

NbL19g24480.1 tubulin_alpha-3_chain [MW = 49.78 kDa]

No. of times detected



log(intensity)



Values from



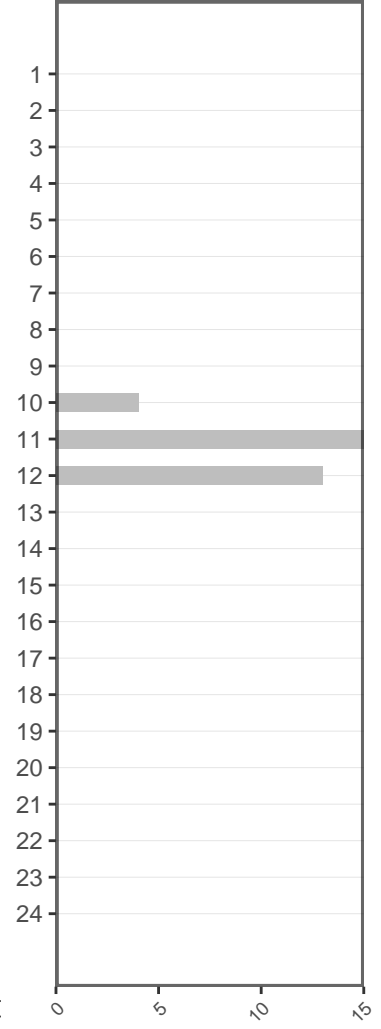
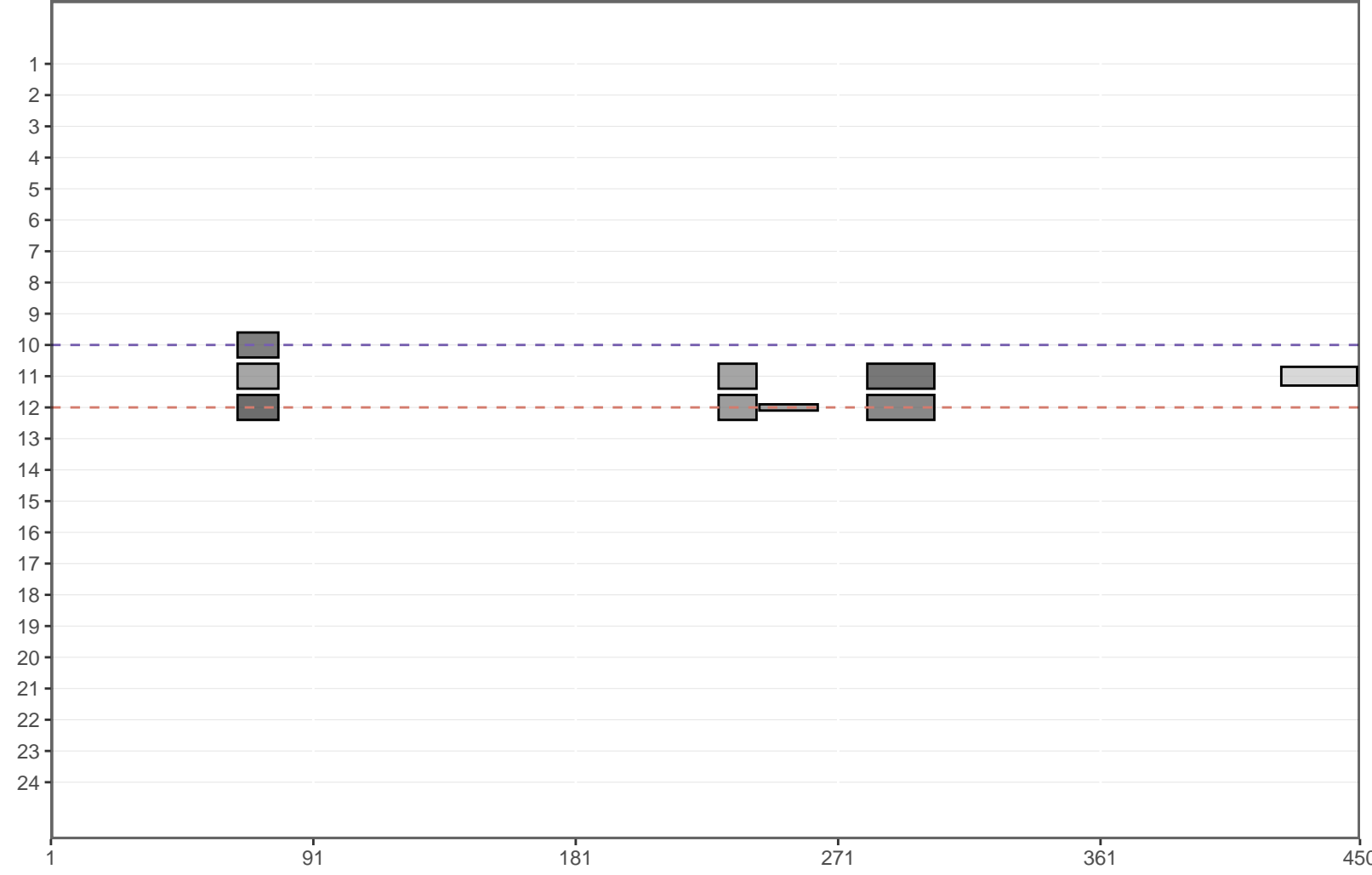
MW indication



Molecular weight

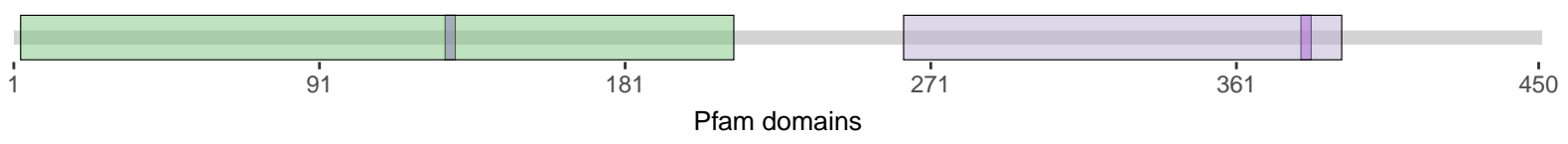


Gel Slice



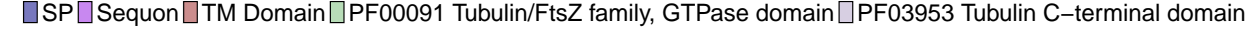
Protein length

Peptide counts over 4 repeats



Pfam domains

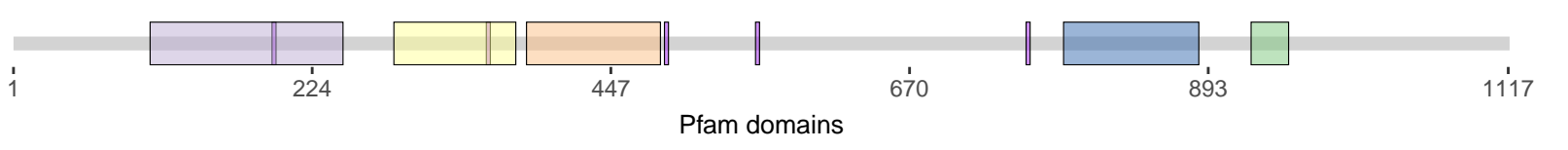
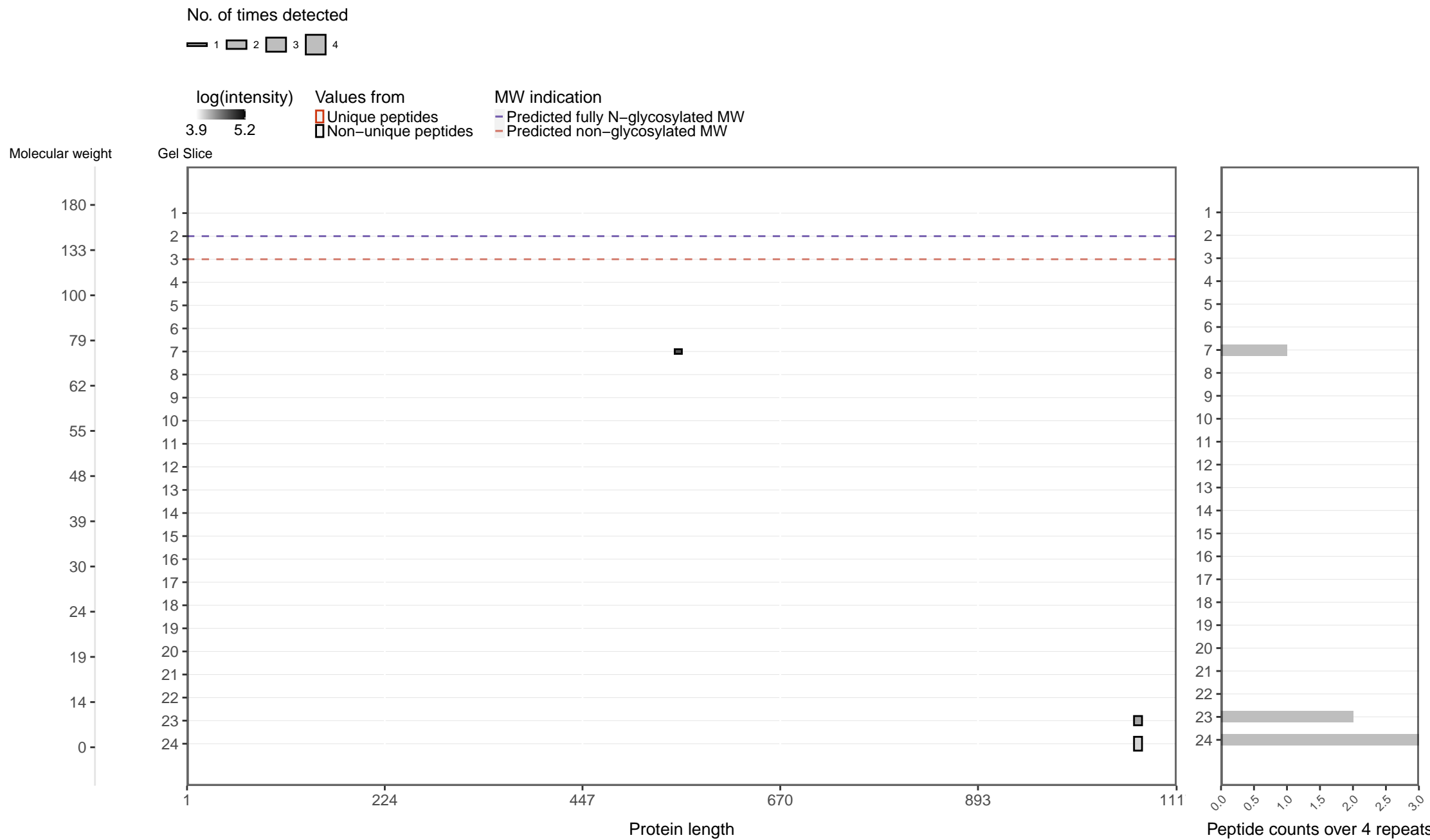
Pfam Description



Protein sequence:

CRRLSDIERPTYTNLNRLLSGHISLTLRFDFGANVDTTEFQTNLVPYRIHFMLSVYAPVISAERKAFHEGLVPEITNAVFERPSSMMMAKDPRHGKYMACGLMYRGDVPKQDVAWAATIKTKRTVGFVDWCFPTGFKGGNYQPPTVPPGGDLAKVQRACMIGNNTAAVEVFSRIQHFQDLMKRAFVHWVYEGEMEEGEFSEAREDLAALEKDYEEVGAEGVDEEDGDDEY*

NbL19g24460.1 importin-5 [MW = 123.81 kDa]



- Pfam Description**
- SP
 - TM Domain
 - PF04510 Family of unknown function (DUF577)
 - PF18808 Importin repeat
 - Sequon
 - PF02985 HEAT repeat
 - PF13646 HEAT repeats
 - PF18829 Importin repeat 6

Protein sequence:
 .KTLV.NATDK.SNR.MLRAK.AMECHL.VGM.AVGKDKFRDDAKG.VMEVLM.BLGG.SGMETDPPF.SYMLG.AWARLKG.LGGDFL.PYMSV.VMPPL.LQSADLKP.DVTISSADSDNELDDSDDDMETFLGDKRIGKTSVLEEKATAC.NMLGCVADELKEGF.YPWIDQVAPTLVPLLKFYRHEEVYRKA.VSAMPELLRSAKL.AVEKGIA.GGRNESVYKQLSDVYVPLVQALHKEPDT.EIGCASMLDALNEGLGSGPLLDDEGGVRSIVDEIKGVIMAS66RKRREARERAKAEFDFAEE

NbL19g24420.1 probable_acyl-activating_enzyme_18_peroxisomal [MW = 80.71 kDa]

No. of times detected



log(intensity)



Values from



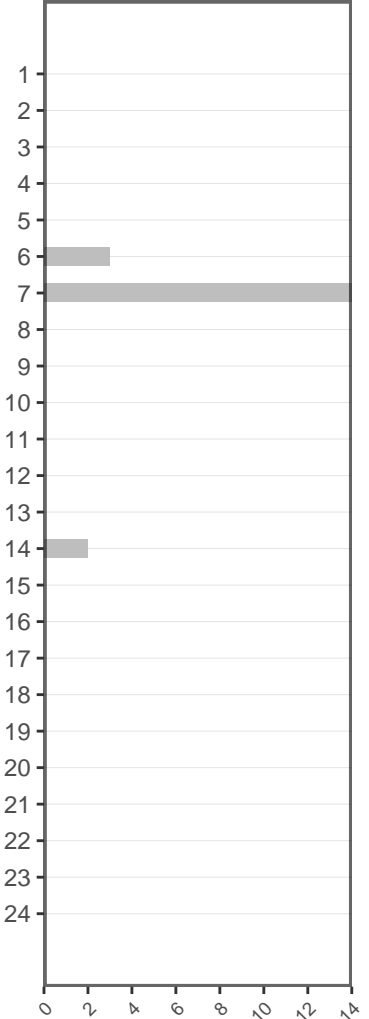
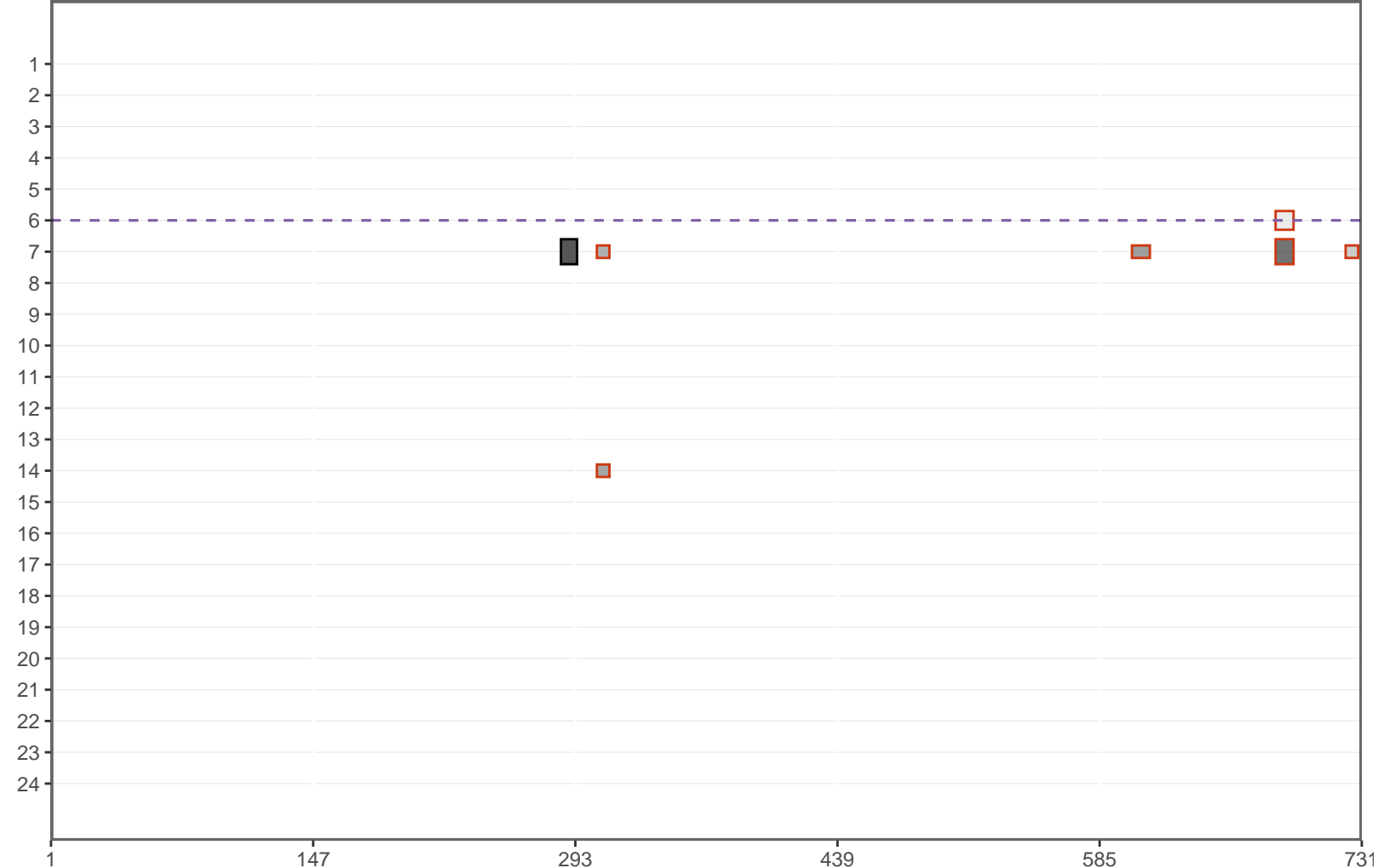
MW indication



Molecular weight



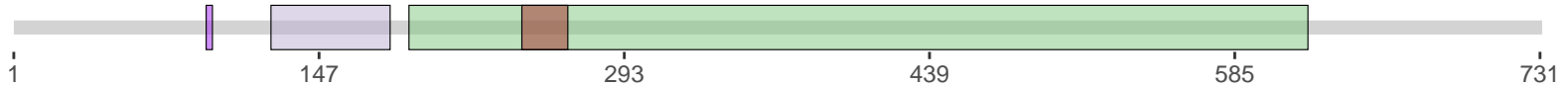
Gel Slice



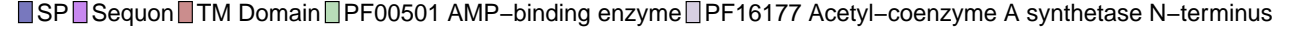
Protein length



Pfam domains



Pfam Description



Protein sequence:

HHQSDISVTNLFSSGTTGDPKAFWTHLSPIRGGAEWNLDRVAGDVGWPTNLGWWMSPLNLYSGFLTGATLALYHSGPLDHGFGKFDQGDVTLGTPVPLKVTWKSTGDMKGLDWRIRRMFASTGEASNVDDDLVLSRVDKPKVIECGGTELSS6YIMGNLLQPAQAGTFSASMTGTFVILDEDGRYPVDDGAGVGEVGLFPTVMGATORLLNADHEKVVYFKGMPMYKDMKLRHRHGDNLKRTVSGVLLVGGRRADDTMNLGGIKTSIEIERVCDRADVCIET

NbL19g24380.1 NADH_dehydrogenase_[ubiquinone]_1_alpha_subcomplex_subunit_6-like [MW = 18.5 kDa]

No. of times detected



log(intensity)



Values from



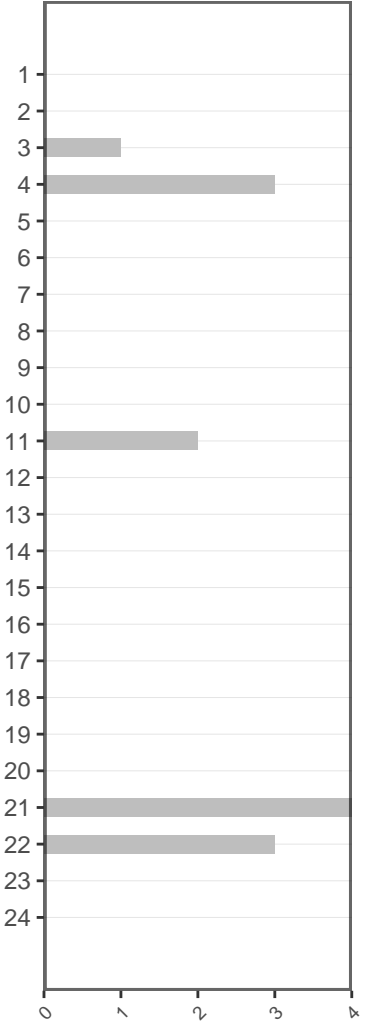
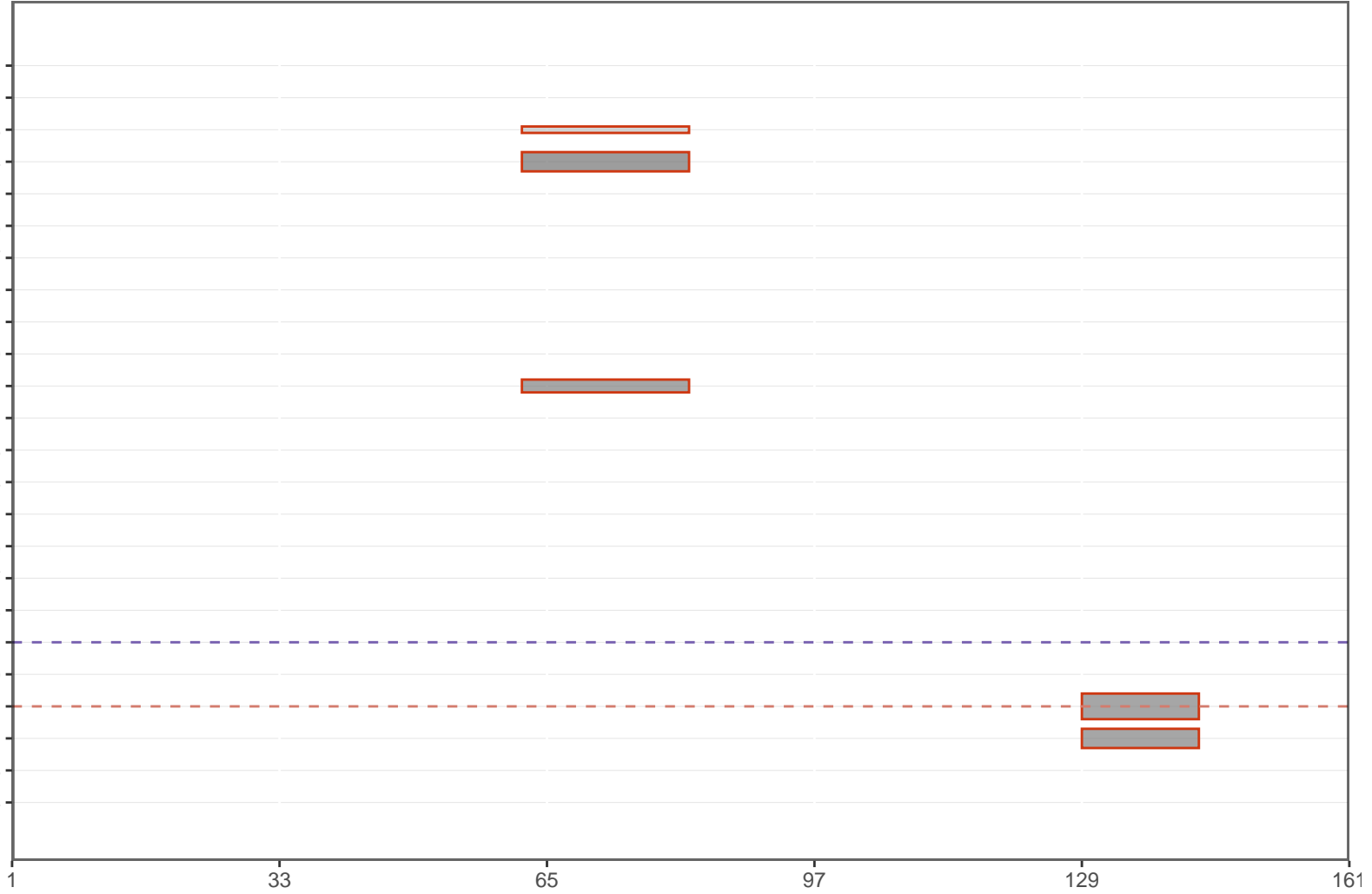
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

JYNYLYDYYVSPSOLREAWAAEVRKNSNVTNPKVIDMLLFGMEELKRFVDSKGRHHVIGKYVYVNGGLVGDLEAKDGGSEFLKIFYSGNYF

NbL19g24250.1 50S_ribosomal_protein_L6_chloroplastic [MW = 25.13 kDa]

No. of times detected



log(intensity)



Values from



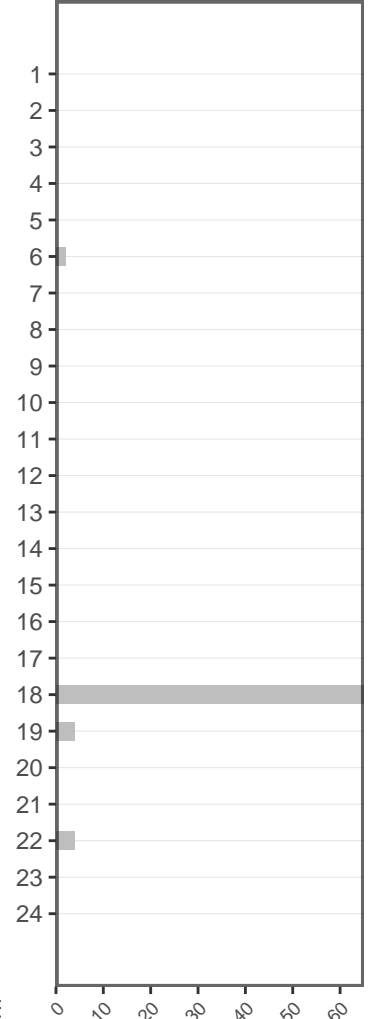
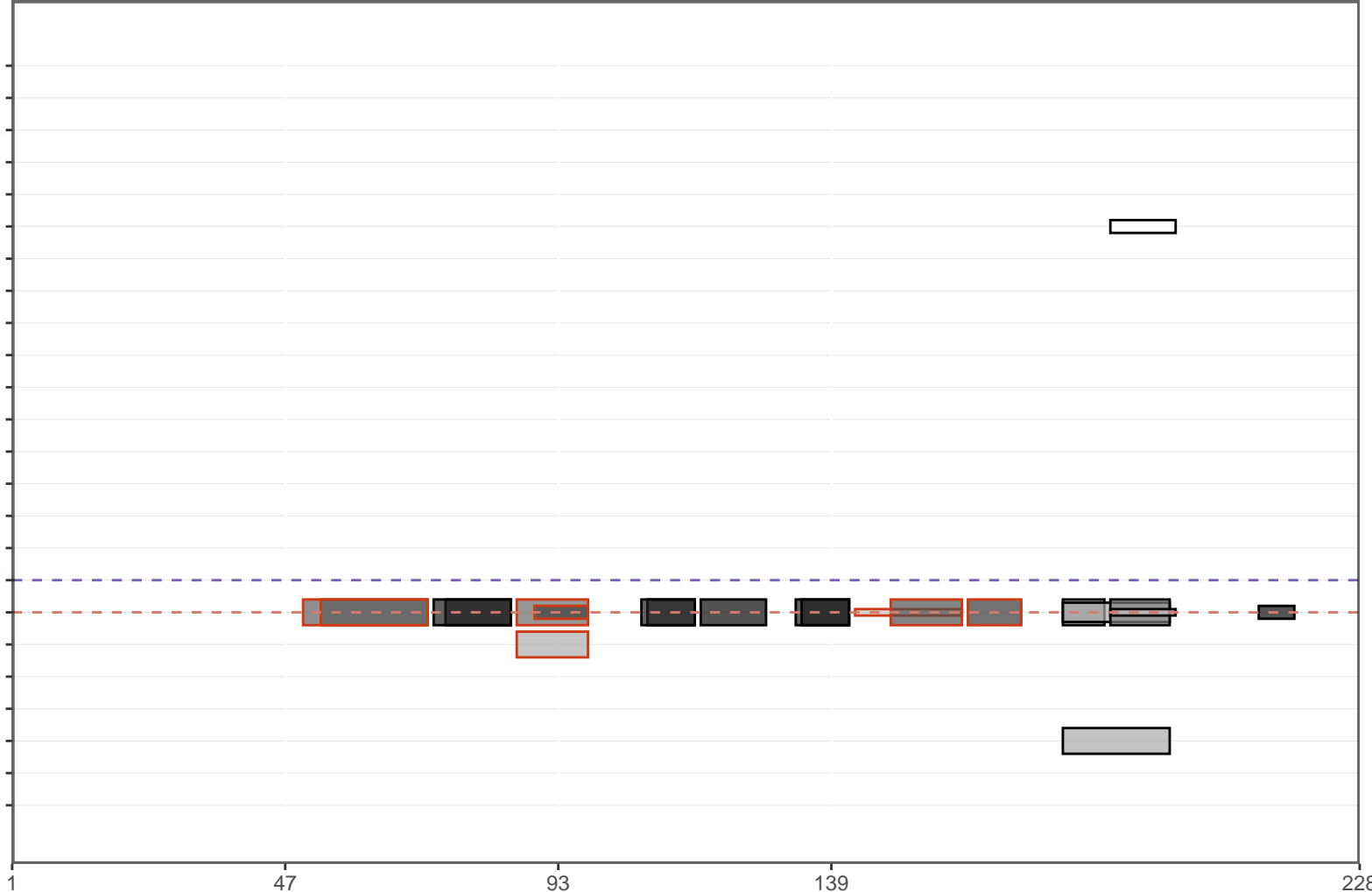
MW indication



Molecular weight

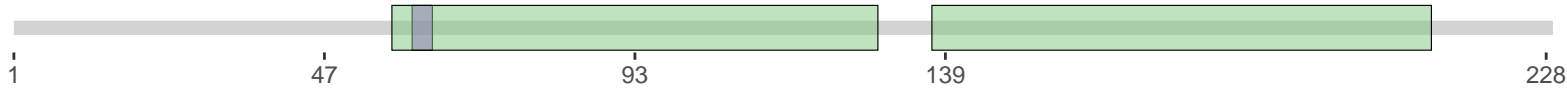


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

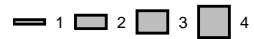


Protein sequence:

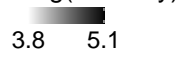
AVETRRANDMIGLFRFLTDMMVGVGKGFKEKLGIVGVYRATVEGKIDVNLGFSHPVMEIPDGLGVKVEENTRTVSGVDNKEHGFAASIRKRWPFPEPKKGVKGVYADEIVRRKEGKAGKKK

NbL19g24150.1 probable_nucleoside_diphosphate_kinase_5 [MW – SP = 17.87 kDa]

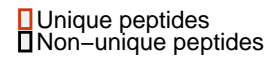
No. of times detected



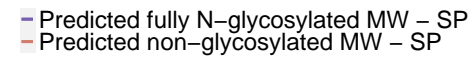
log(intensity)



Values from



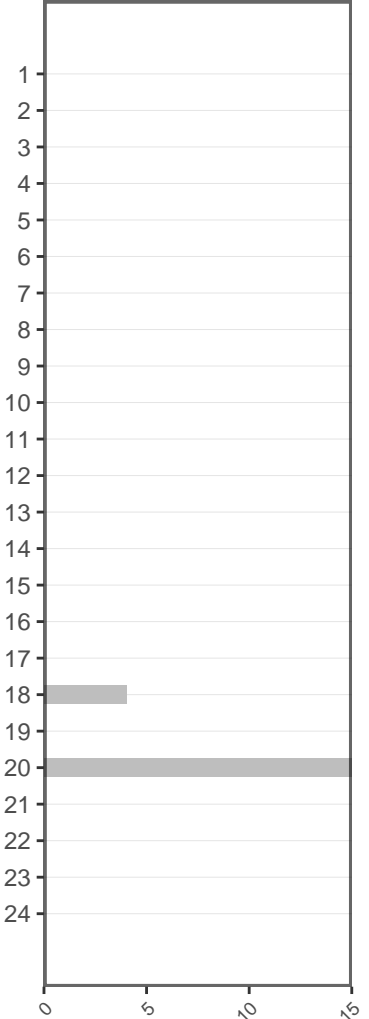
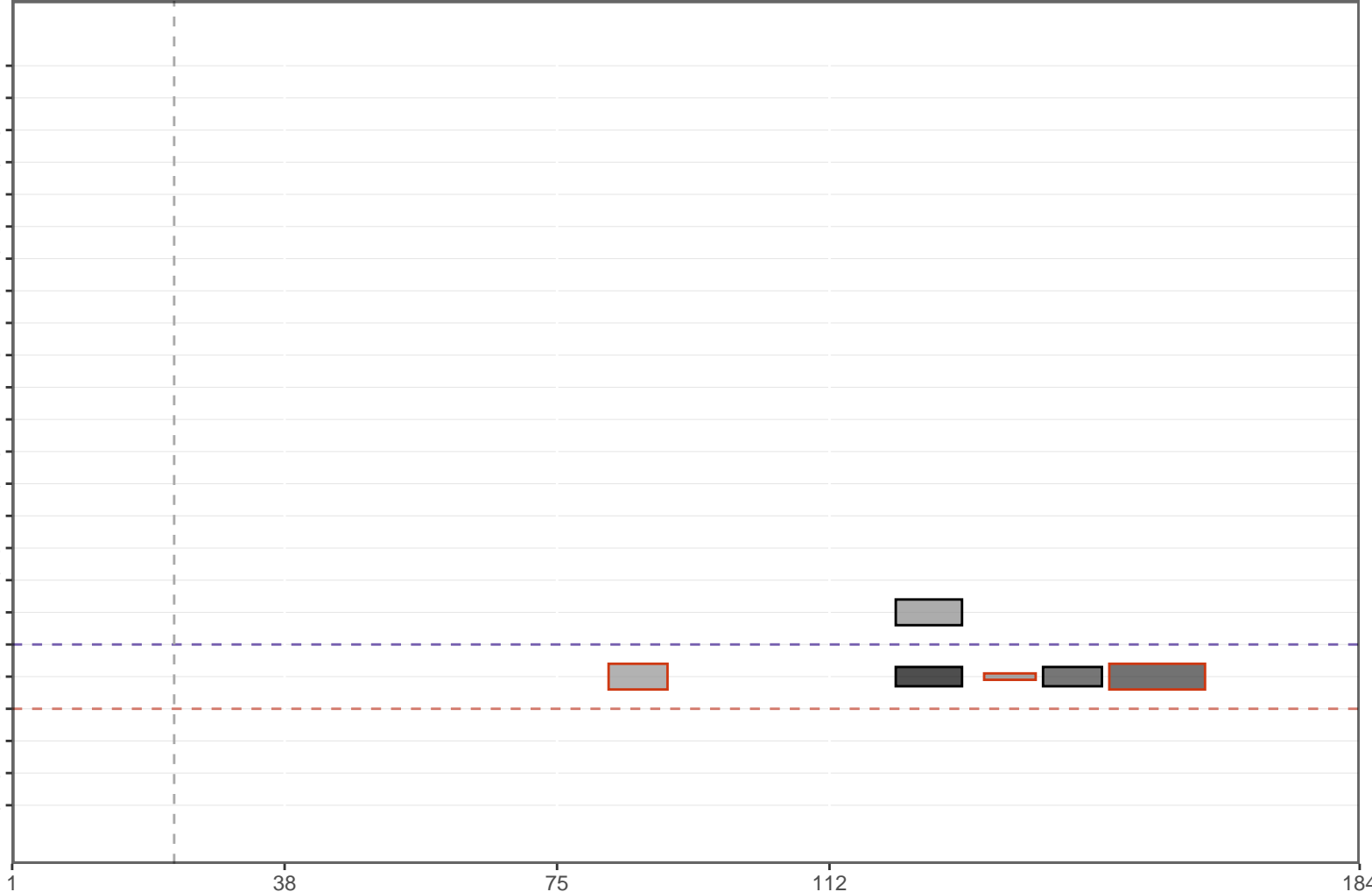
MW indication



Molecular weight



Gel Slice

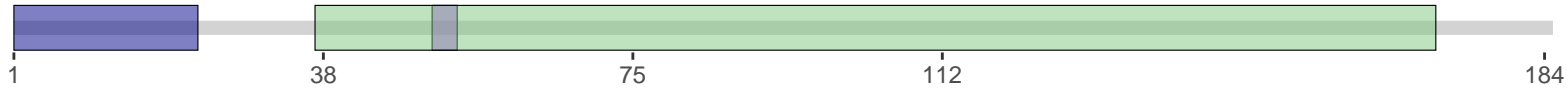


Protein length

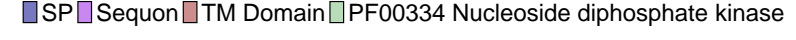


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

INFYAEHSSRSFFPLVEYMAAGPVLIMVLEKGNAAIDWRALHGPTDPLKAKVTHPYSVRAICGLDLQKNQVHGSDSPQGAAREISFFERTSSGHVSKHDEL

NbL19g24090.1 serine--glyoxylate_aminotransferase-like [MW = 46.92 kDa]

No. of times detected



log(intensity)



Values from



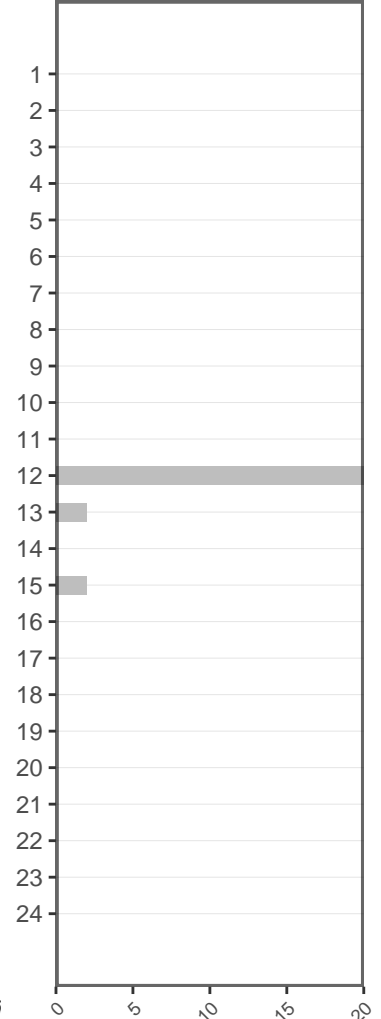
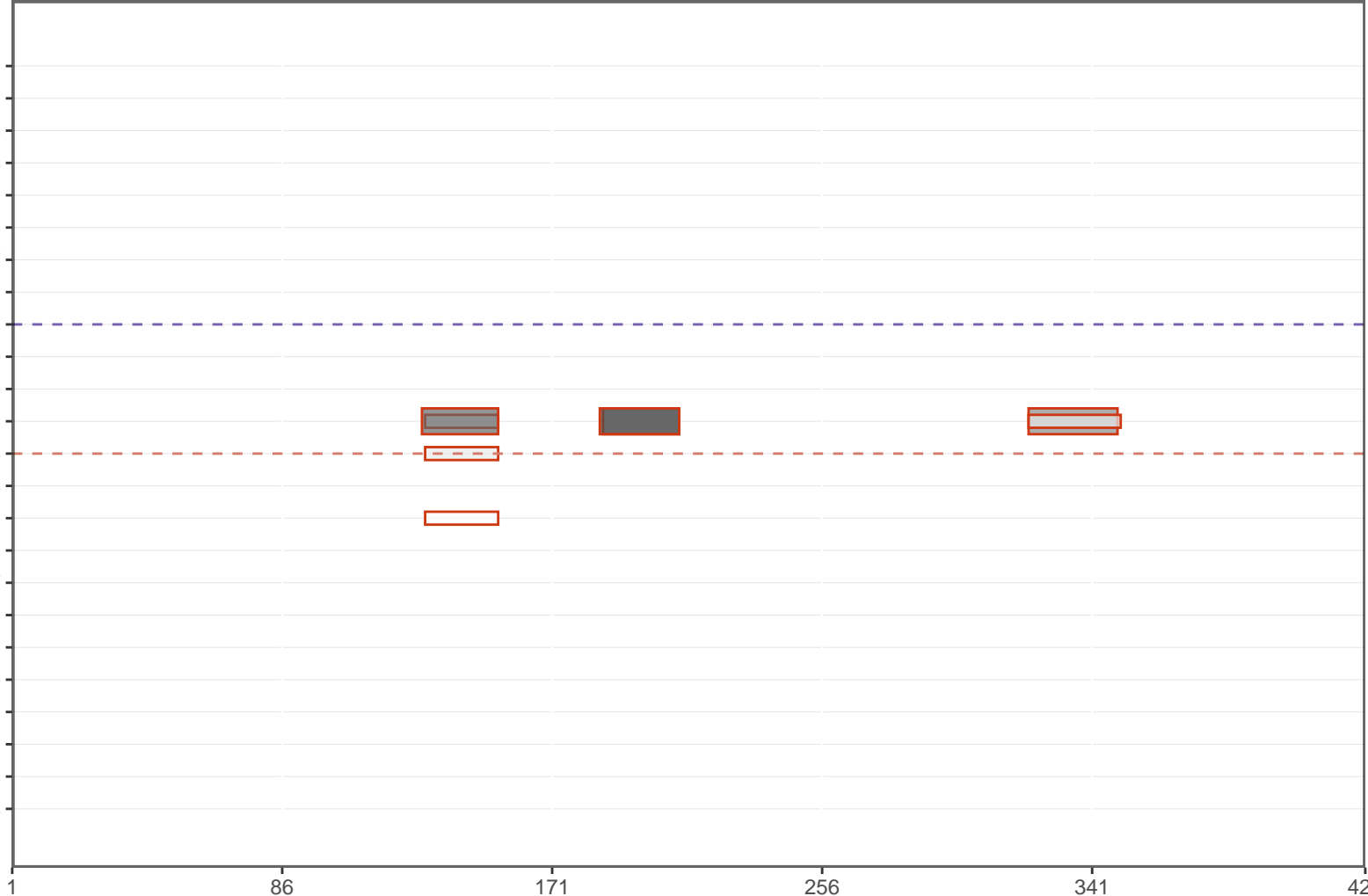
MW indication



Molecular weight

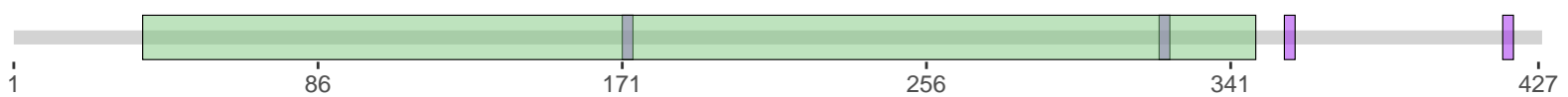


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISSICALDFRMDDEVGVDAVLTGGSKALSLFTGLGIVDASPKALEAAKAKSVRFFDWSQYLFYKMGDTYWFYTFPSIQLLYGLRAALDLLEEGLEENVARHARLGGKATRLAVEAWGLNGTQKEEWFSDTVAWVPPYIDSAEIKRRAWKRYNLSLGLGLNKVAGKVFRIHGLNLELQLLGGLAGVEMVLRKDVGPVWPKFGSGVAAASTFLQNSTPLIPERF

NbL19g23780.1 DEAD-box_ATP-dependent_RNA_helicase_20 [MW = 55.72 kDa]

No. of times detected



log(intensity)



Values from



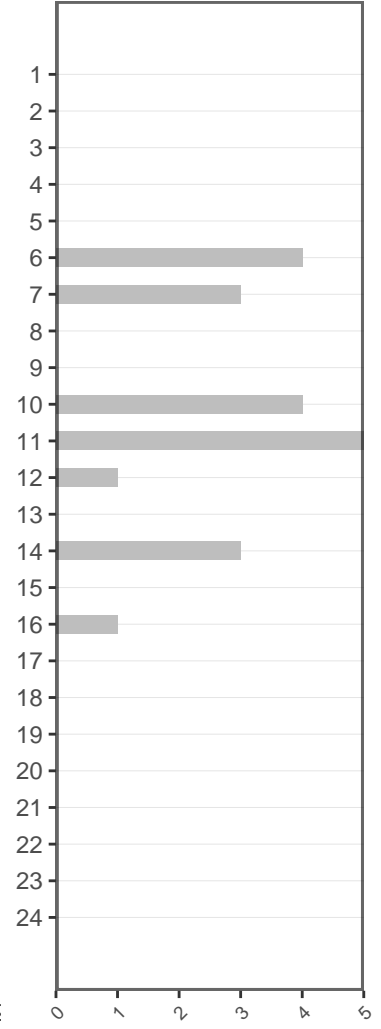
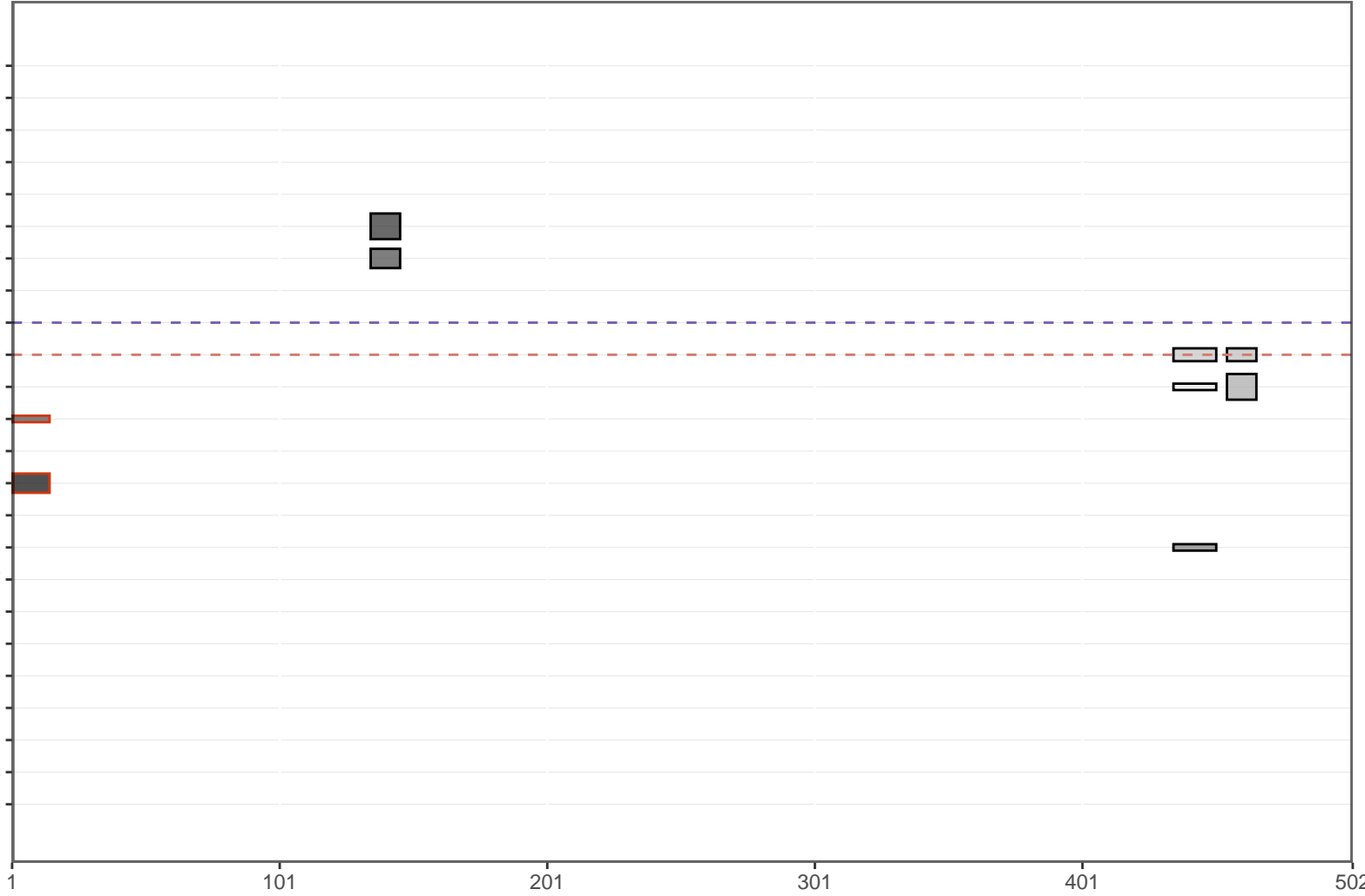
MW indication



Molecular weight

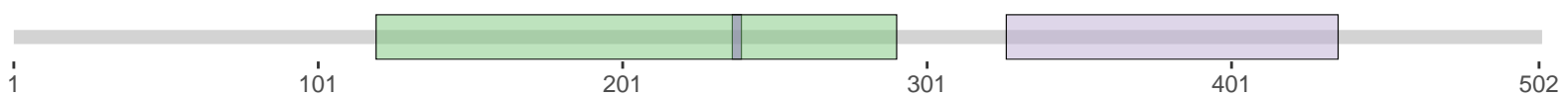


Gel Slice



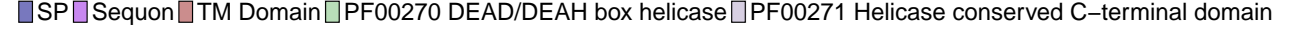
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

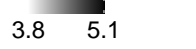
NLRRTYLYLDEADRLMDGFEFQRKIVGDRDRTGLVWSATWPKVEVQLARGFLFNAYKVVIGSADLKANHARGHVEVSEGGKYNLKLLEEDIMDGGRIILFMDTKKGGDQVTRQLRMDDGWPLSHHGDKSGAERDQVVLSEFKAGKSPIMATDVAARGLDKDKVKEVINYDFPGGLEEDVYHRIGRTRGAGAGTAYTYFTANARFAKDLINLEEGQKVSPELAKMGRGAPPPPLGLGGRDRGRGKYGNGRW*

NbL19g23730.1 60S_ribosomal_protein_L28-1-like [MW = 15.8 kDa]

No. of times detected



log(intensity)



Values from



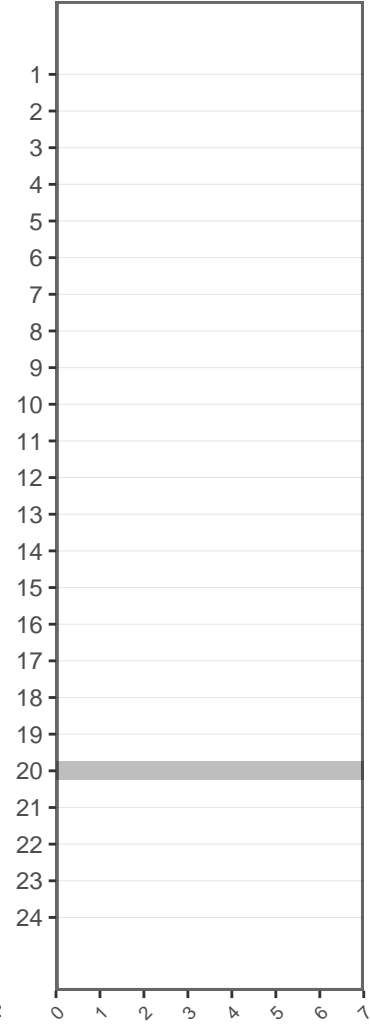
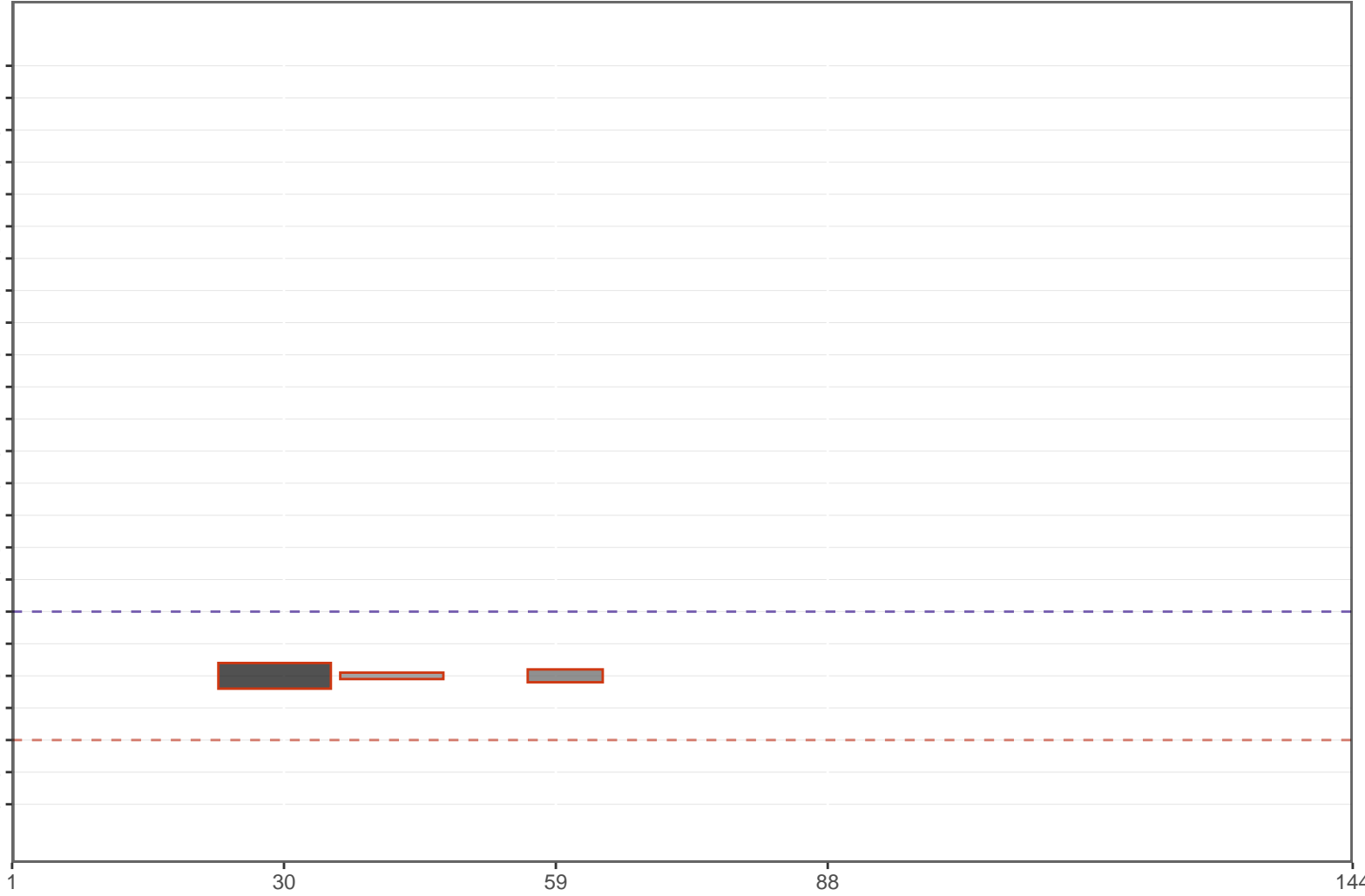
MW indication



Molecular weight



Gel Slice



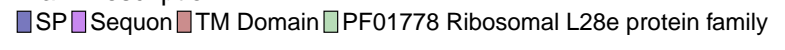
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

JAGGKDDQSVLLATTKTKGKGNKPSLELNKSGAMKKEFRMAKAVTNGVADNYRPLKKAALARLSAVNRSLKVAKEGVKKRNRQA*

NbL19g23700.1 probable_voltage-gated_potassium_channel_subunit_beta [MW = 36.94 kDa]

No. of times detected



log(intensity)



Values from



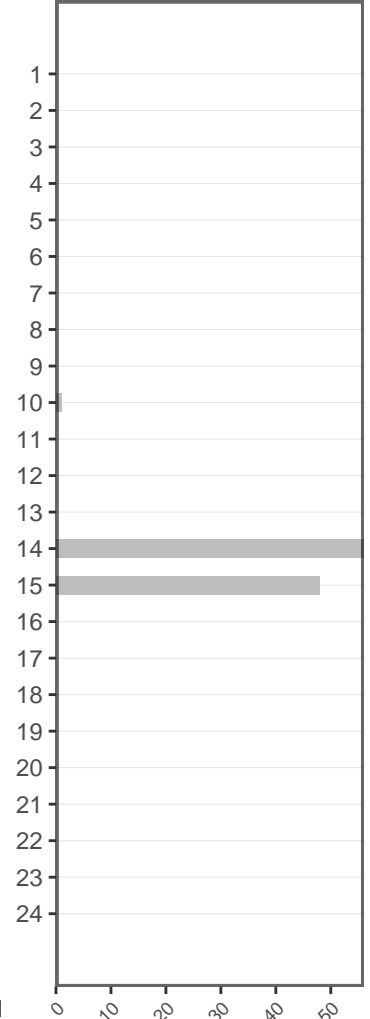
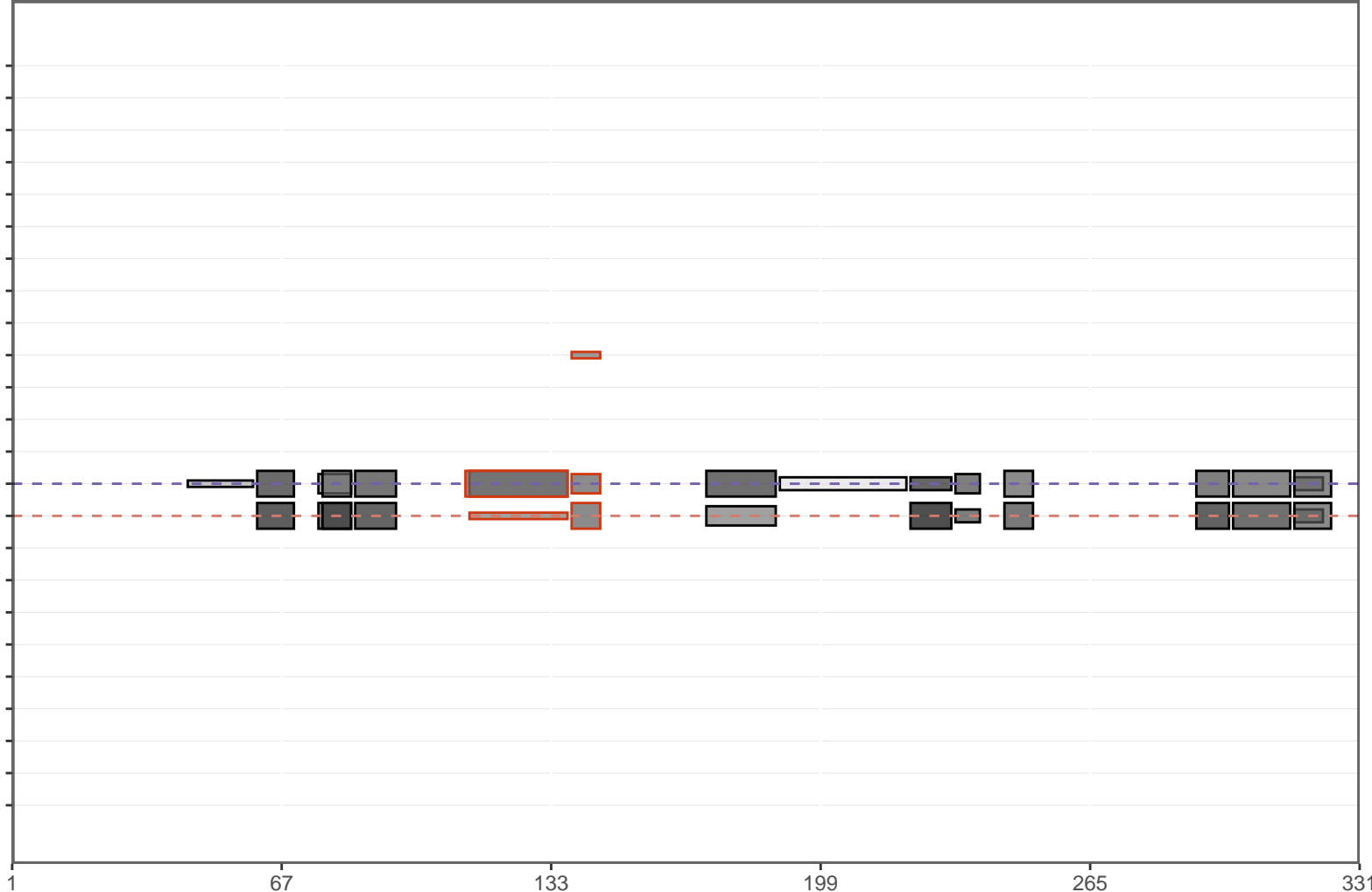
MW indication



Molecular weight

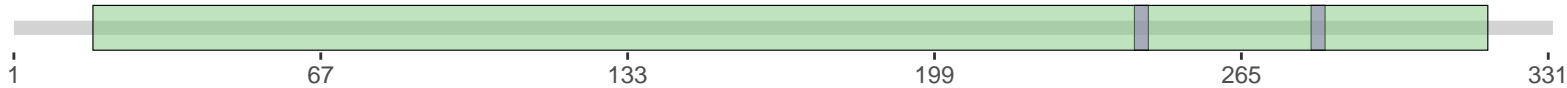


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

WGTSSEVSAQGITTEAWGVAGRLDLVGPVEQPEYNLLSRHKHVESEVFLVYSNVGGIGLTTWSEPLASGVLTKYKAGNIPADRFALENYNLLANRSLVDVLRKVDGLKPIAEGVLPQLAAWGAANPNVSSVITGATKEYVQIEENKAINVIMLTPAWMERIEAVVQSKPKRQDQVYR

NbL19g23450.1 actin-related_protein_2/3_complex_subunit_4 [MW = 19.84 kDa]

No. of times detected



log(intensity)



Values from



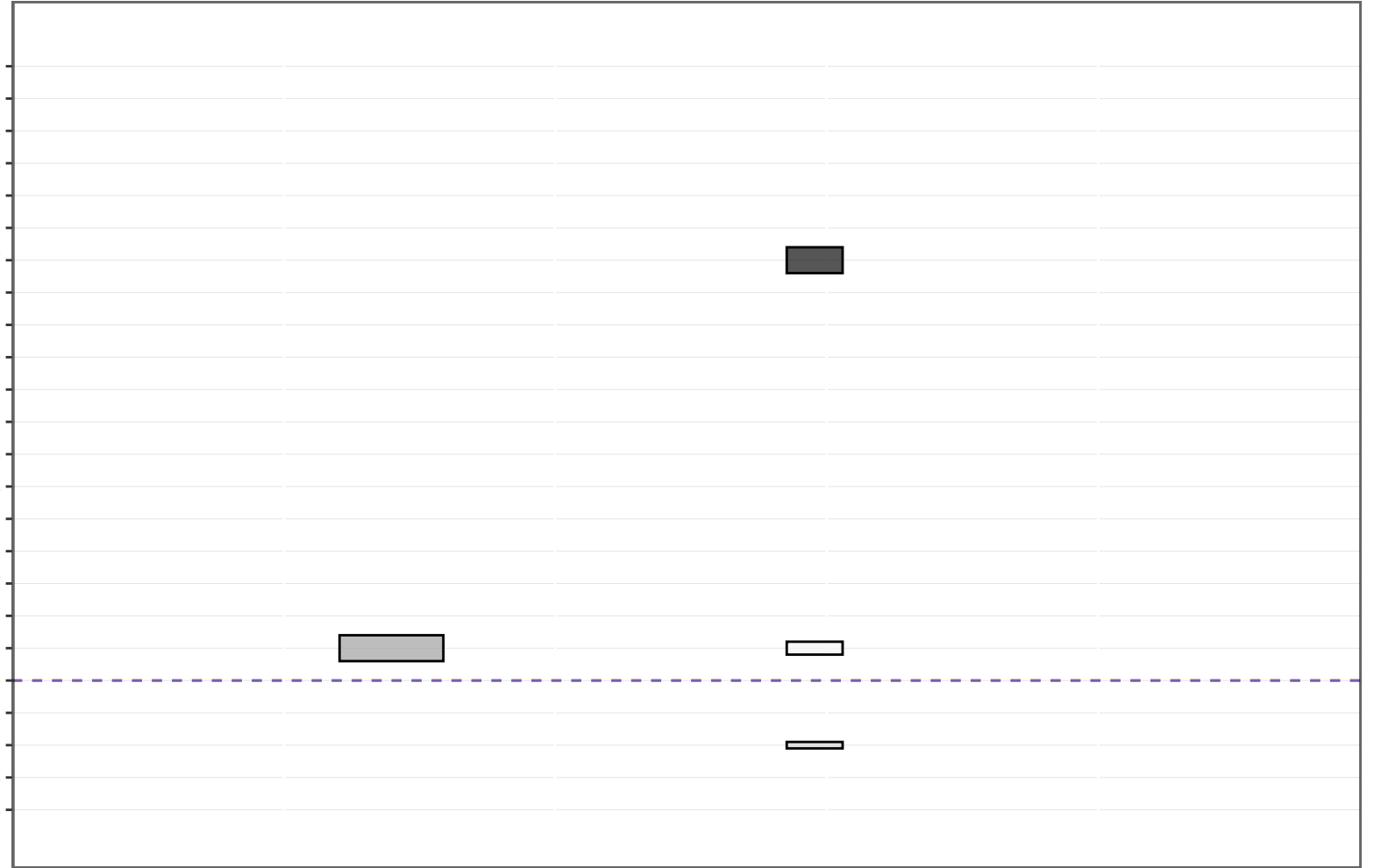
MW indication



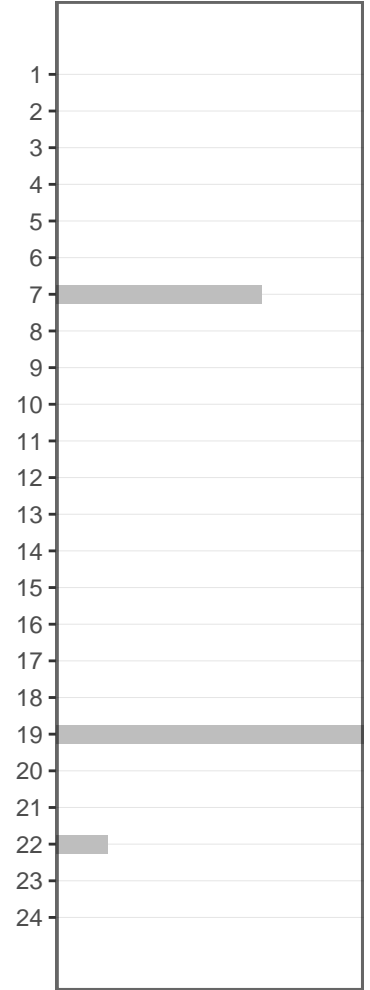
Molecular weight



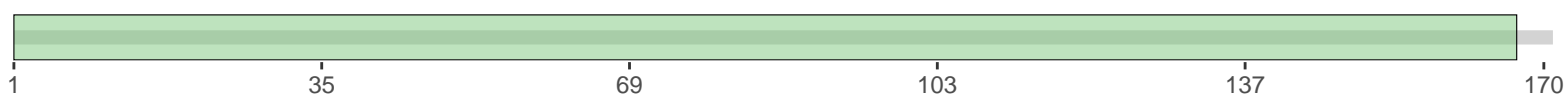
Gel Slice



Protein length

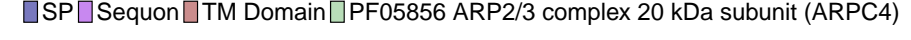


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RISLUKYGSDLELNITKIKFLRFLSMRAEAFQVLRKRPVGGYDISFLITNHYGCEMKGKLIQFVGFMEIDKKEISELKLIVNTRIGLWATEFLKGFV

NbL19g23400.1 serine_hydroxymethyltransferase_4 [MW = 20.68 kDa]

No. of times detected



log(intensity)



Values from



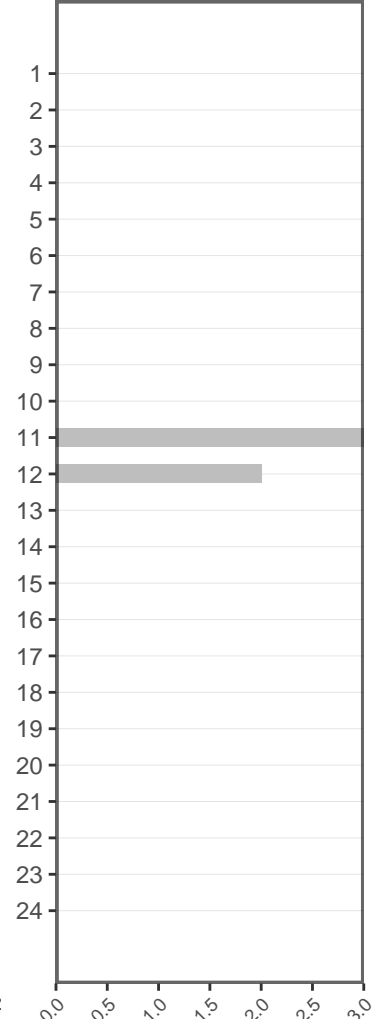
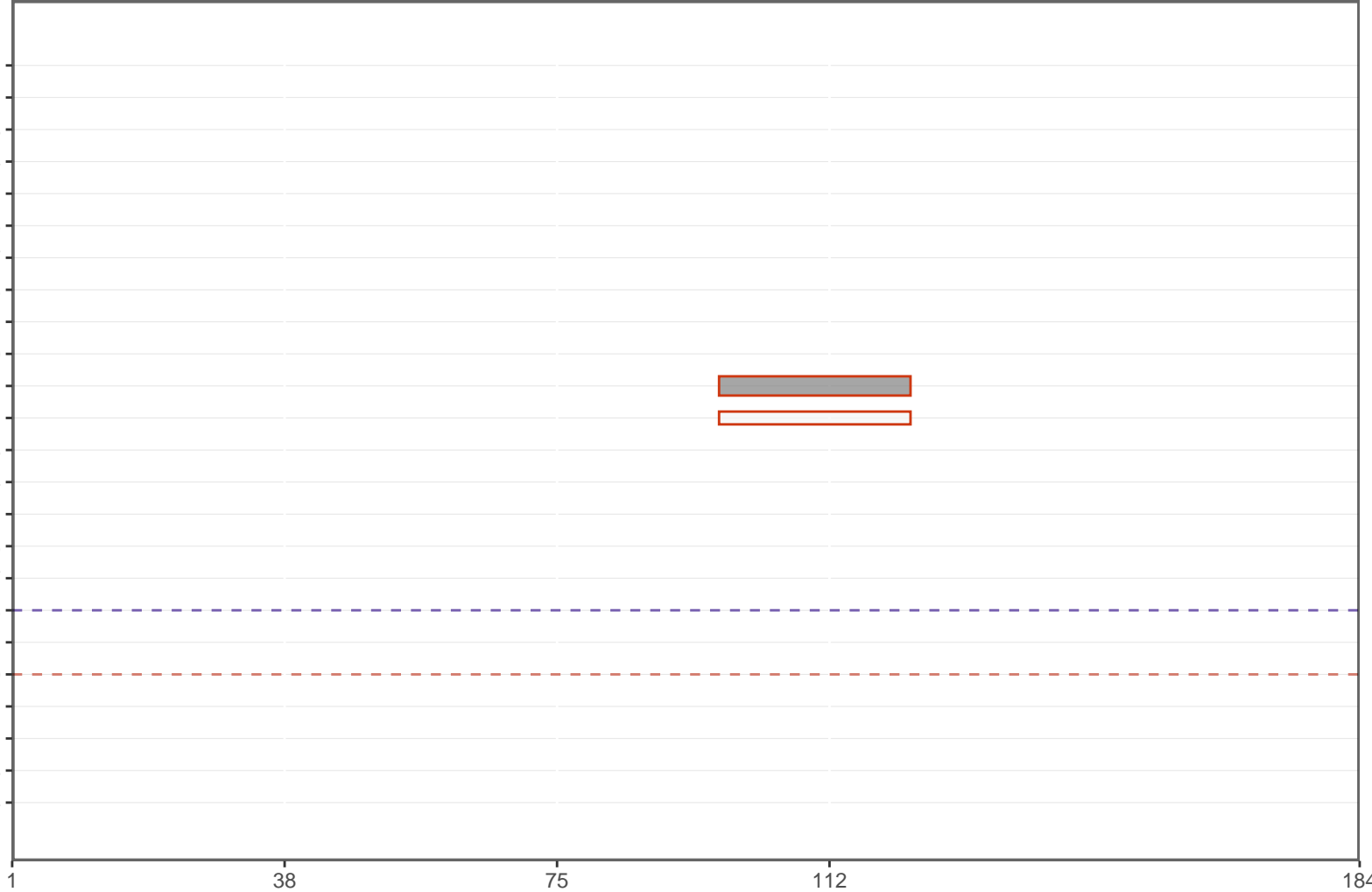
MW indication



Molecular weight



Gel Slice

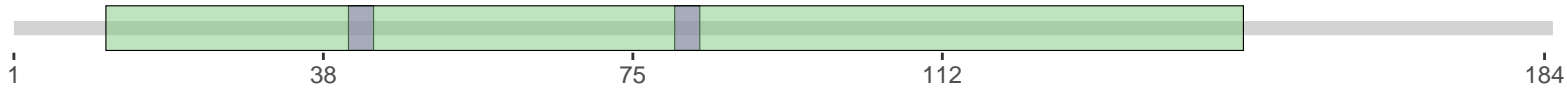


Protein length

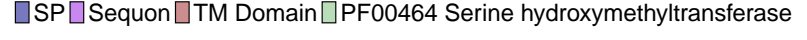


Peptide counts over 4 repeats

Pfam domains



Pfam Description

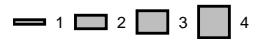


Protein sequence:

INLTSRSLQAQAFYVDPTRWGVNWPVYSGSTANFAAYTAVLNPHDRIMGLDLPSSGHLSHGYYTSGGKKIQLQFLR/VLISWIKLGLIMDWRRHWLGLS*

NbL19g23180.1 signal_peptide_peptidase-like_3 [MW - SP = 55.03 kDa]

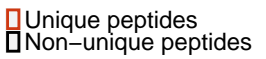
No. of times detected



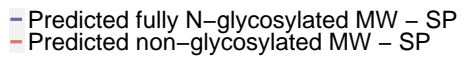
log(intensity)



Values from

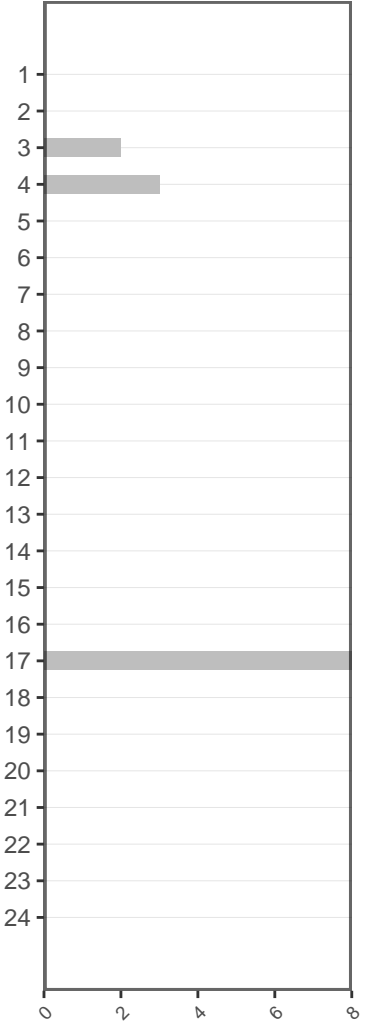
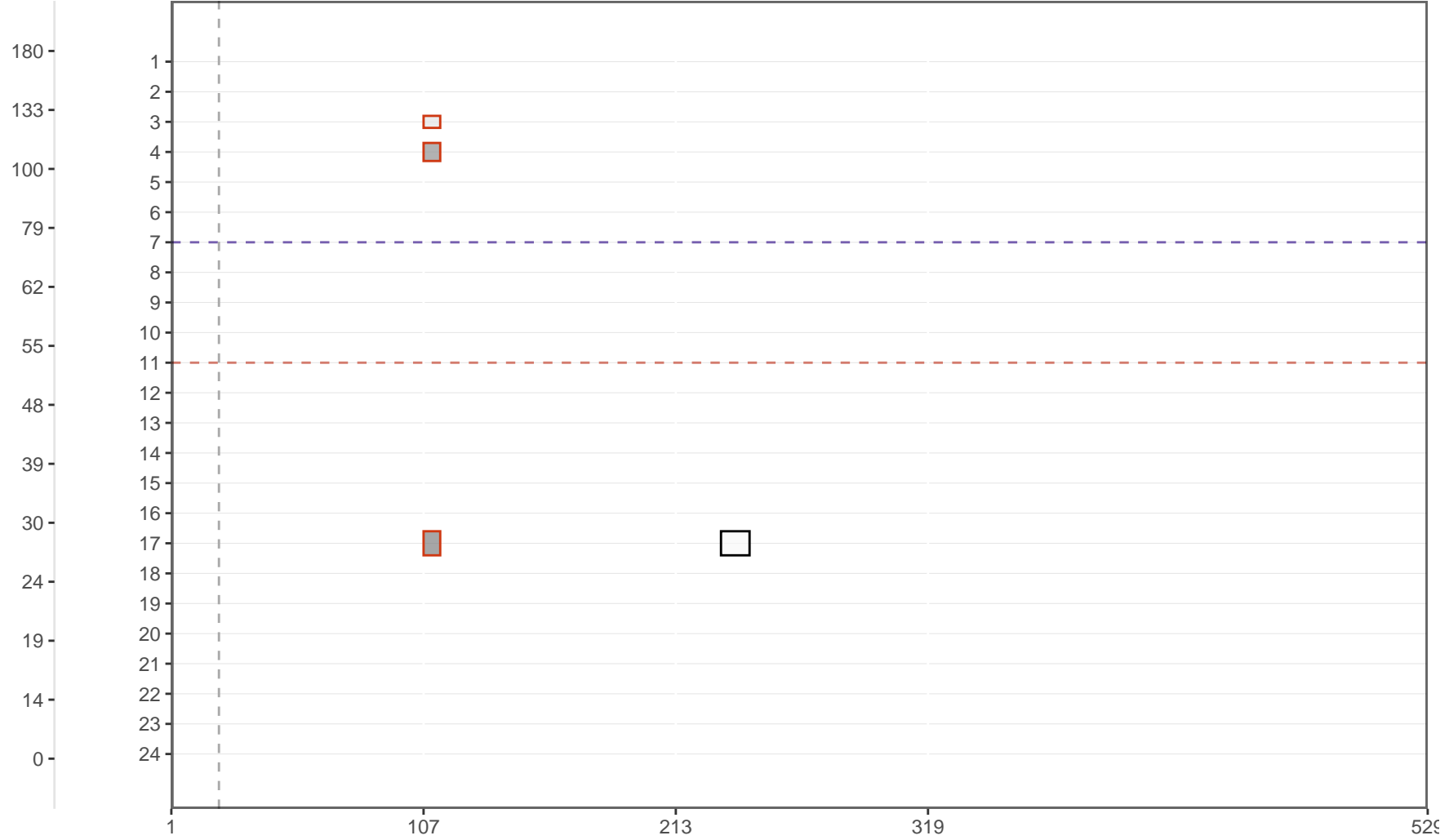


MW indication



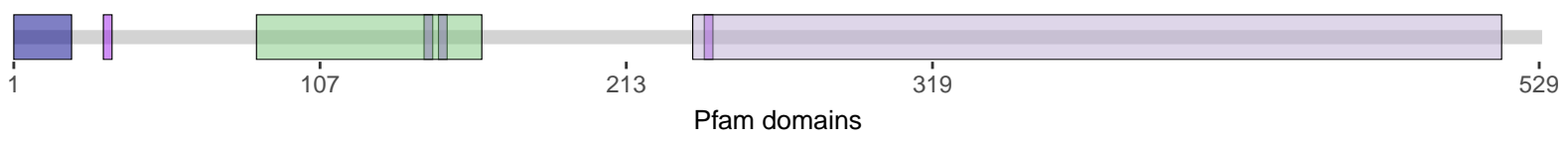
Molecular weight

Gel Slice



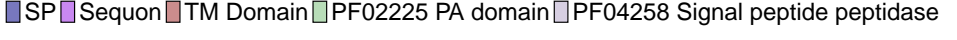
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISASTFLLLLYFTMSAWFLWLLHLFSGIVVEGMHSGHSLVSSKCKGKGRKTLNPLLGEVBSLISLVLCVAFVAFVWATRKAASYVSWGGDLGICMLMFLVQLAGLPIKVKVATVLLCGAFVDFWVFLSPHFHDSVMAVAGGDKAGGESIPMLLRVPRVSDPVYGGYDMIFGDLFPGLLVGFAFRFDKARRKSVLNGYVLLMMVYGVGIGLFTYVGLVLMNHHGDFALLVLPCTLGTYVVLGVLRGELKDLVWVDSSTKVADELLEDA

NbL19g23020.1 5'-nucleotidase_domain-containing_protein_4 [MW = 71.44 kDa]

No. of times detected



log(intensity)



Values from



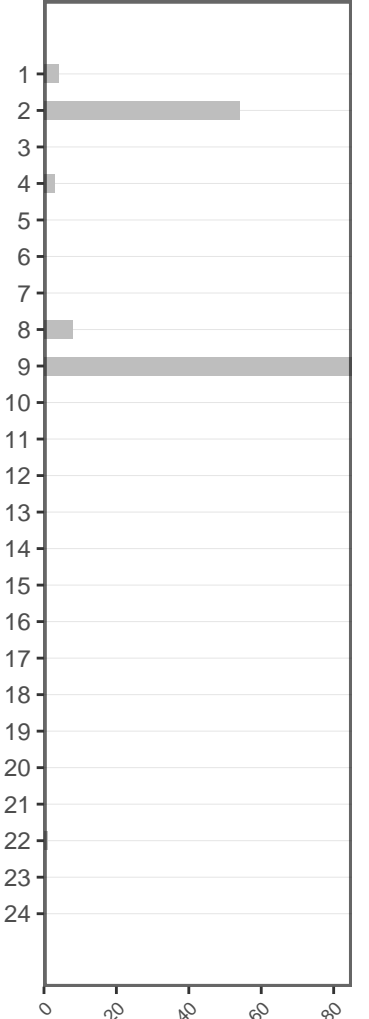
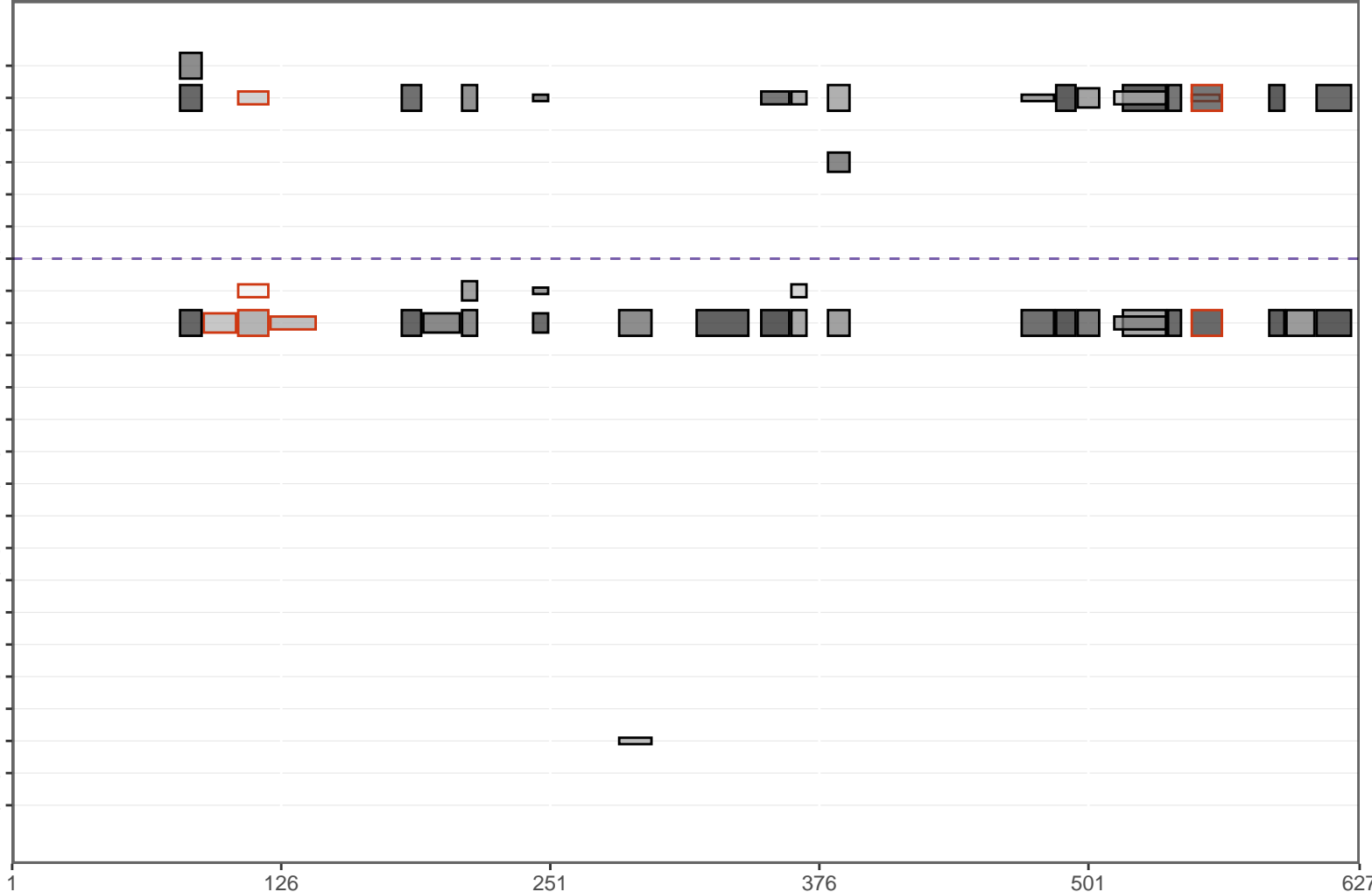
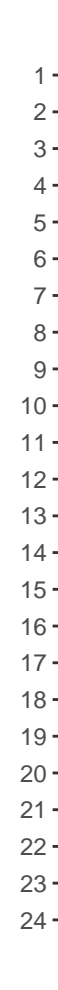
MW indication



Molecular weight

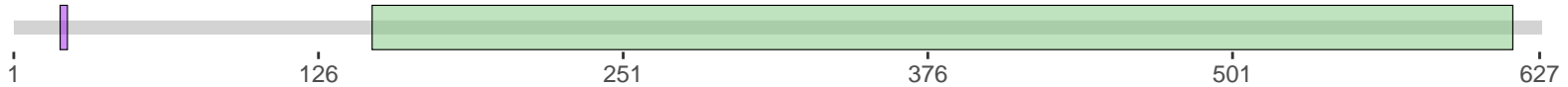


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

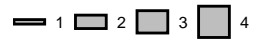


Protein sequence:

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NbL19g22910.1 novel_plant_SNARE_13 [MW = 30.41 kDa]

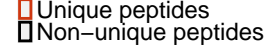
No. of times detected



log(intensity)



Values from



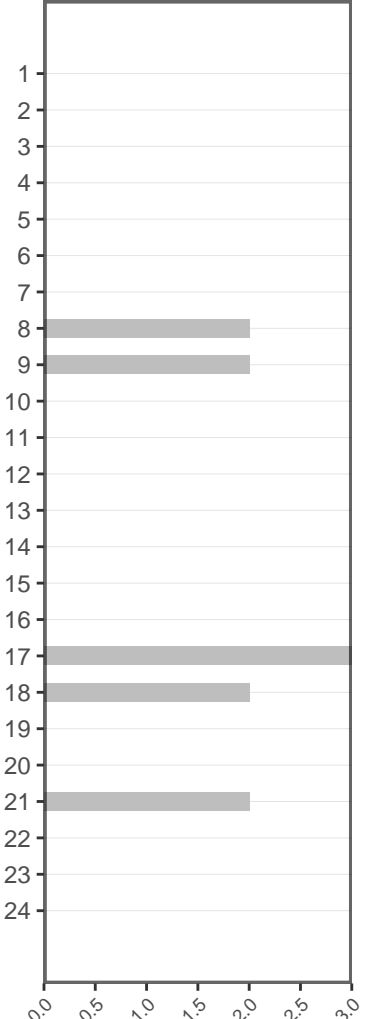
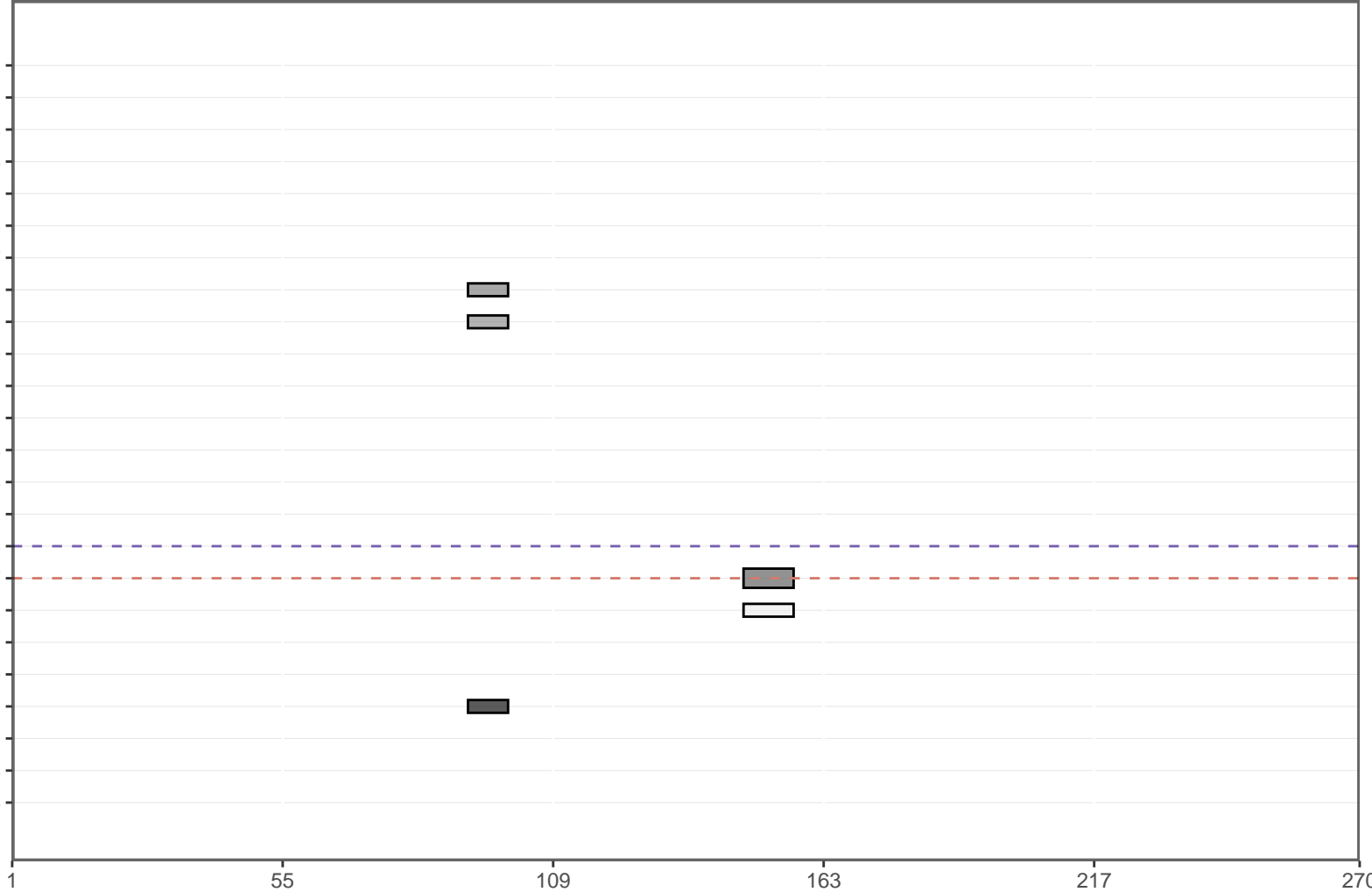
MW indication



Molecular weight



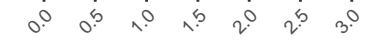
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

ASEPTAEENVQMASAMENGEISAGNKMTDETDAQIERSKGVVHGTIEVSTGTATFLKGGTDDMGRRVNELDTQFSKKAQGLVKEIGRQVATKDCIMLFLVGGVVAIVVKNPNKDRDIPGLAPPAPERLLLYKSGGDFM

NbL19g22860.1 S-adenosylmethionine_synthase_2 [MW = 43.04 kDa]

No. of times detected



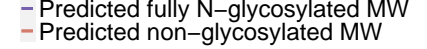
log(intensity)



Values from



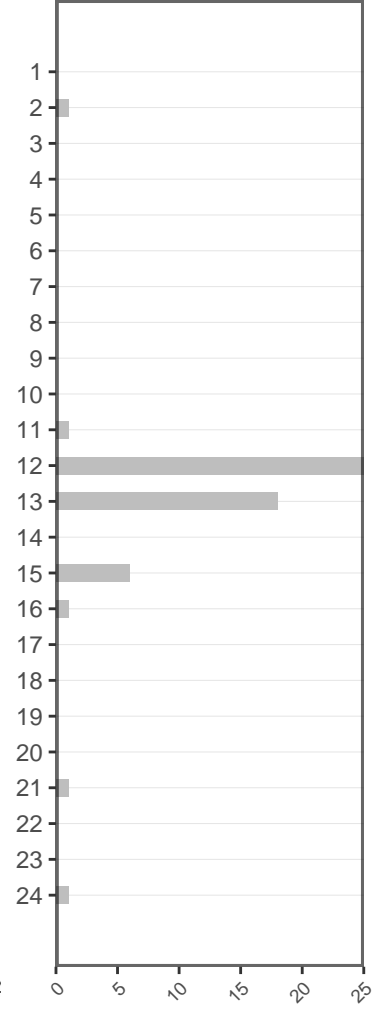
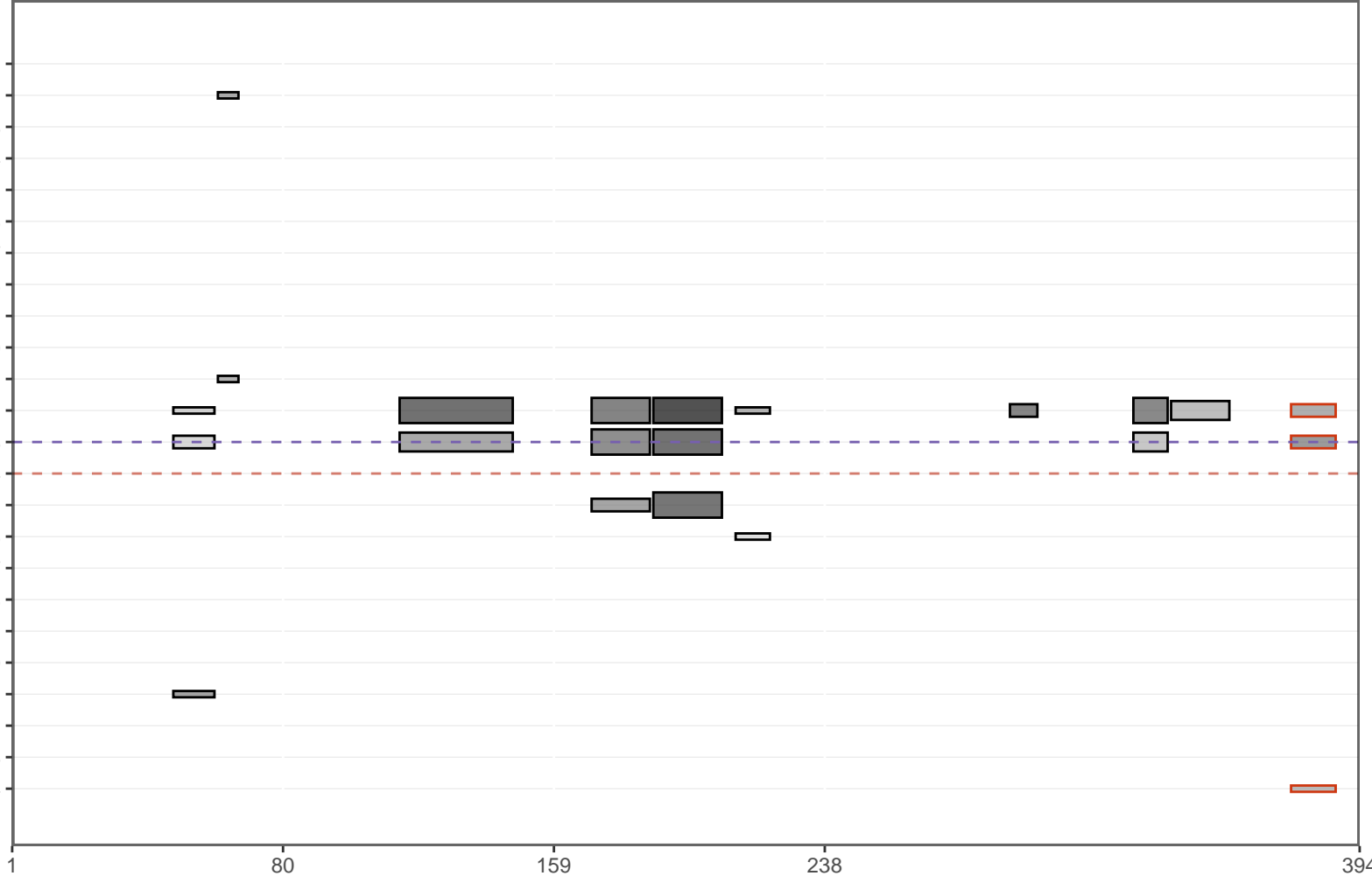
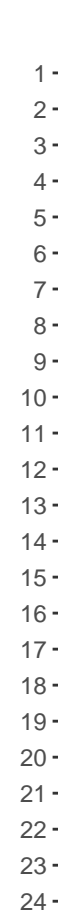
MW indication



Molecular weight

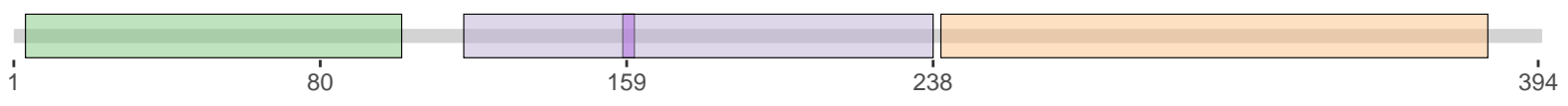


Gel Slice



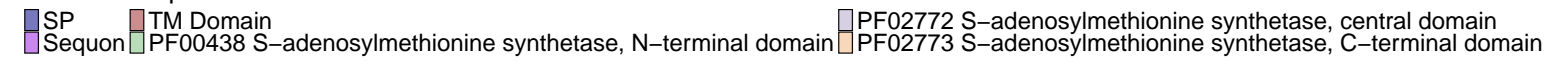
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MVPLRVHTVLISTQHDQVFNDEIARDLKEHVKIPVPEKYLDEKTFHNLNPGREVFGGPHGDAGLTGRKIIDTYGGWGAHGGGAFSGKDPTRKDRSGAVVIRGAAKSIKAVANGLARRGVGVSVAGVPEPLSEVFDYGTGKIPDKELNIVKENFDFRPGMISNLDLLRGGNGRFLKTAAGHFGRDRDPPDFTWEVVKPLKWEKPSA

NbL19g22800.1 ADP-ribosylation_factor_1-like [MW = 20.67 kDa]

No. of times detected



log(intensity)



Values from



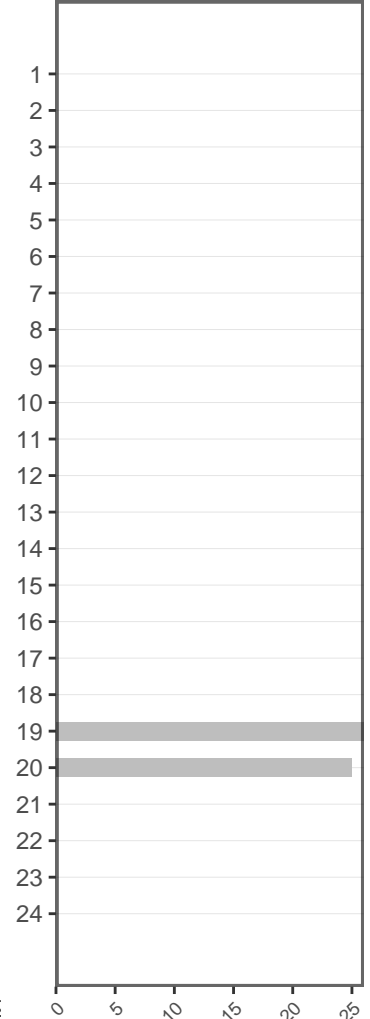
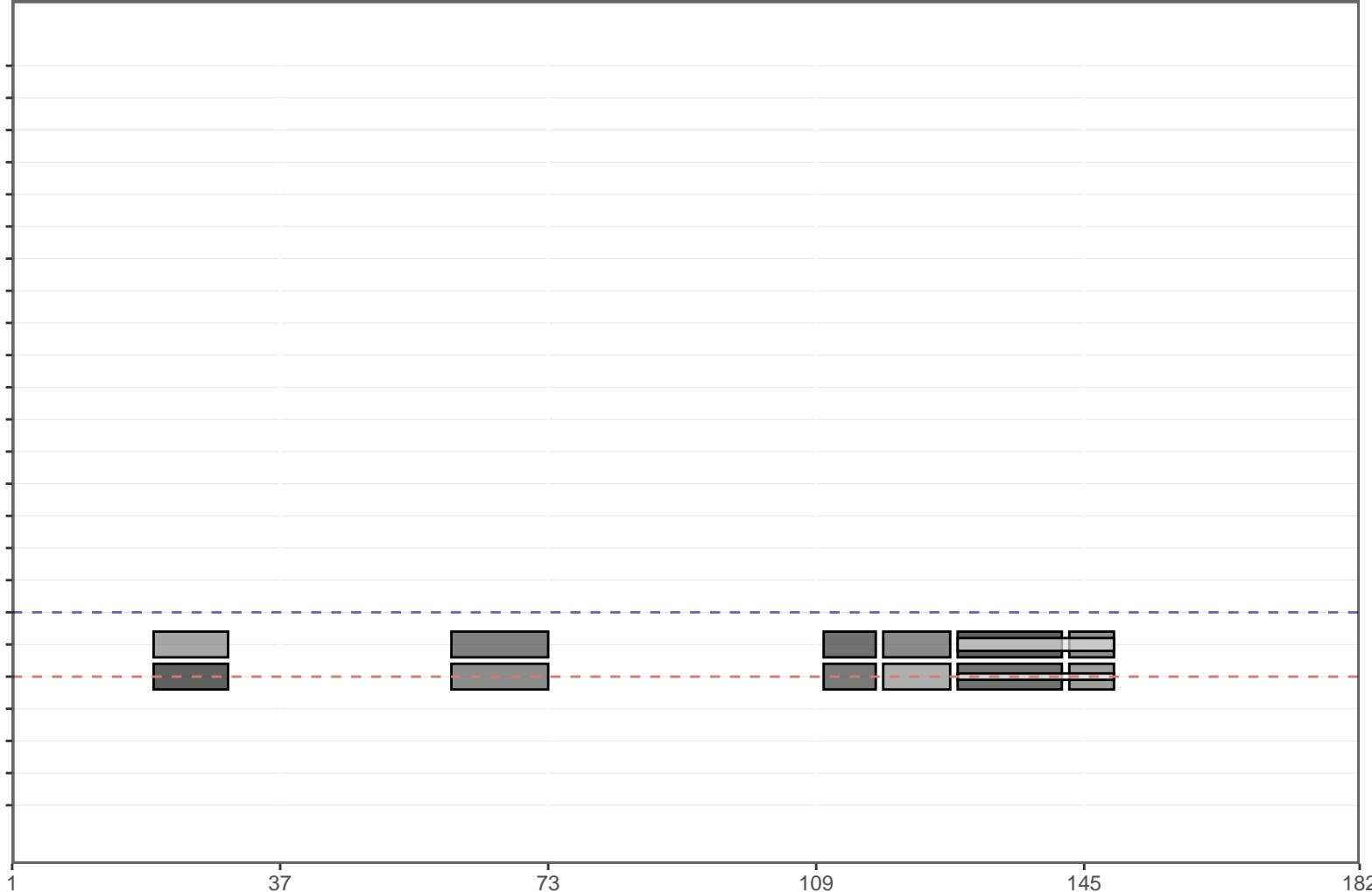
MW indication



Molecular weight

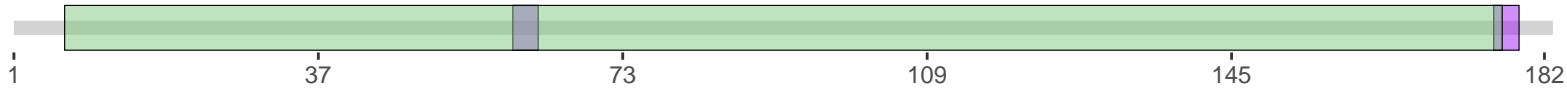


Gel Slice



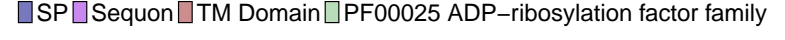
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

HYFQNTGGLFVYVGDNDRDRIVEARDELHRLMNEDELREAVLLVFANKGDLPLNMANAAEITDKLGLHSLRQRHWYIGSTGATSGEGLVEGLDVLNINENKA

NbL19g22780.1 dihydrolipoyl_dehydrogenase_mitochondrial [MW = 16.05 kDa]

No. of times detected



log(intensity)



Values from



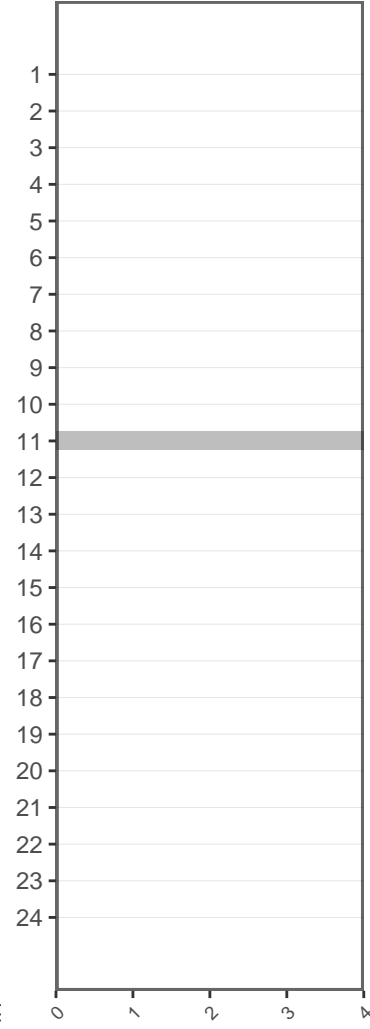
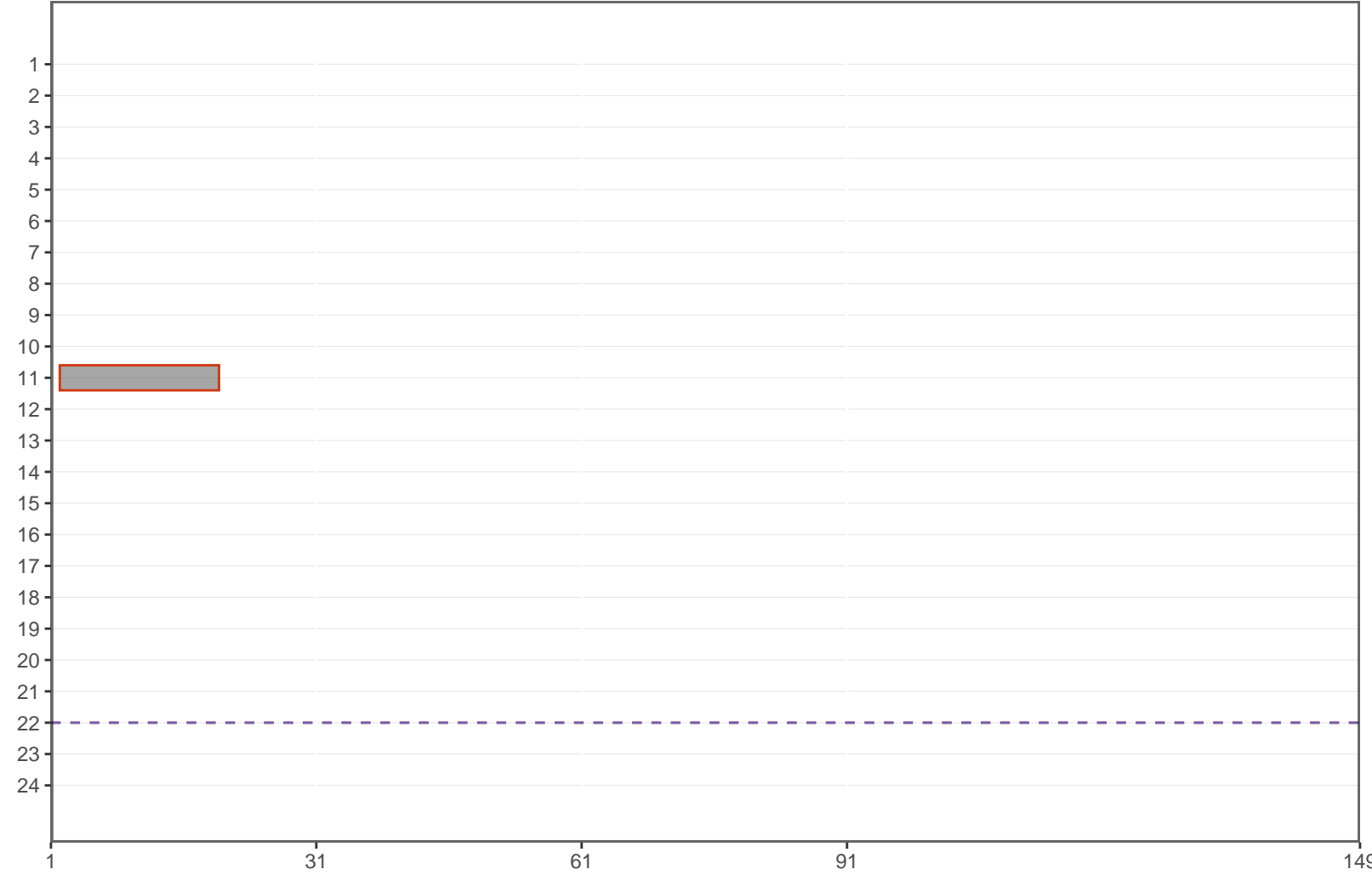
MW indication



Molecular weight

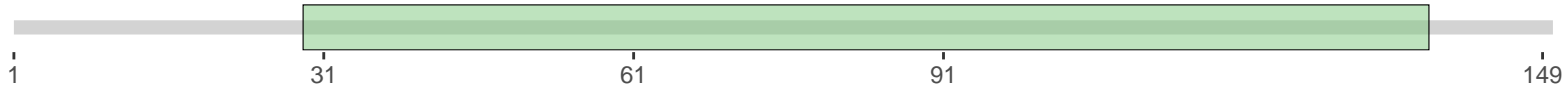


Gel Slice



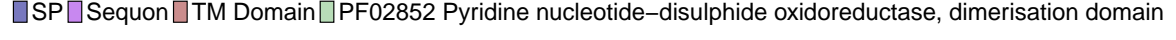
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KFPELANSRKAIDDAEGLVNI/AEKEEDKILGVHIMSPNTGELIHEAVLALGYGASSEDIAETCHAHPTMSEALKEAMATYQKPHIM

NbL19g22710.1 cell_wall/_vacuolar_inhibitor_of_fructosidase_1-like [MW – SP = 15.75 kDa]

No. of times detected



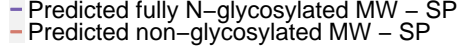
log(intensity)



Values from

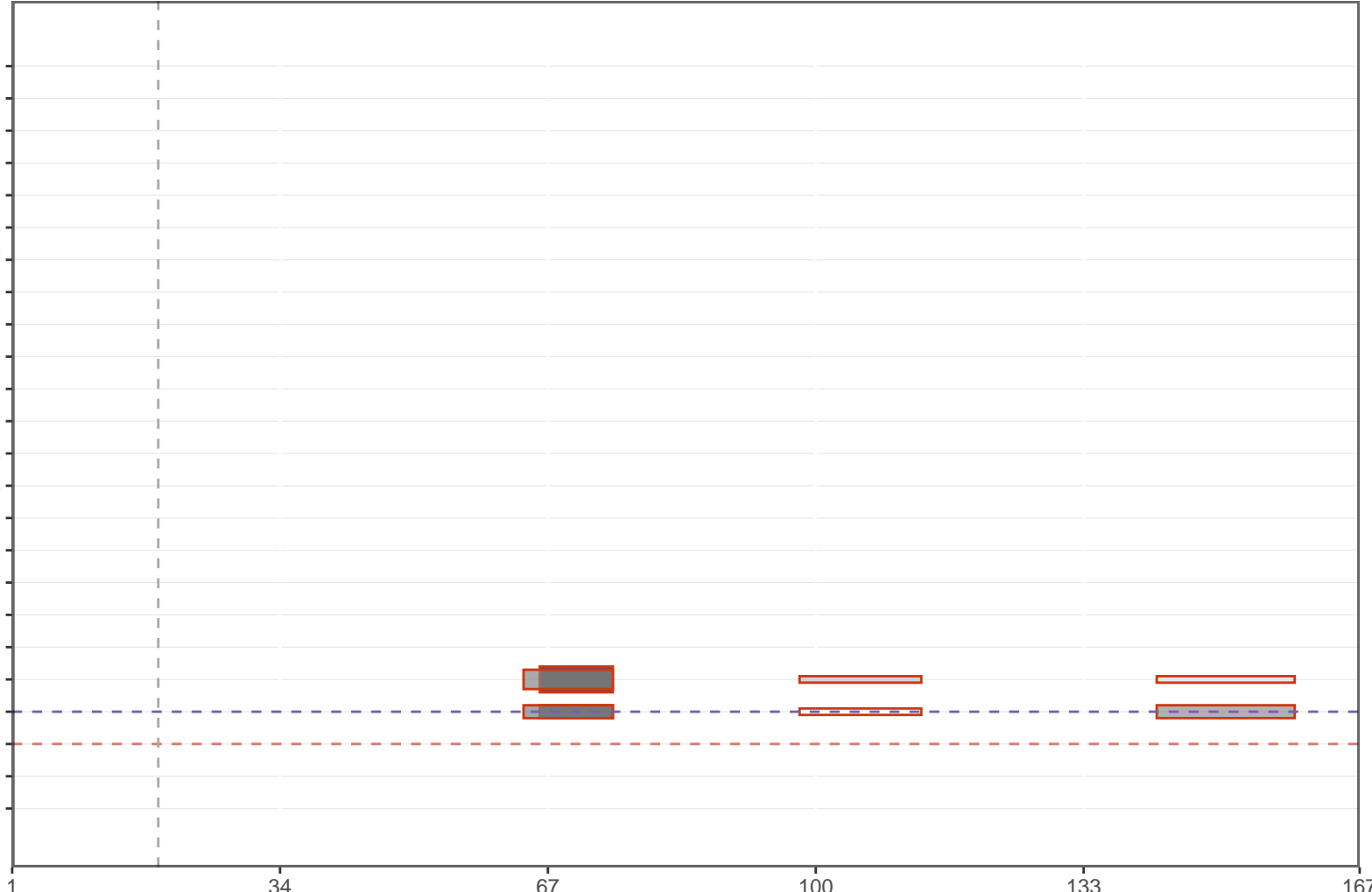
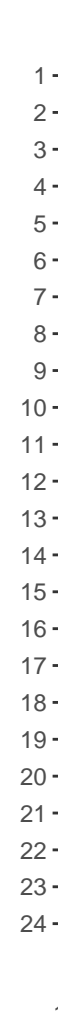


MW indication



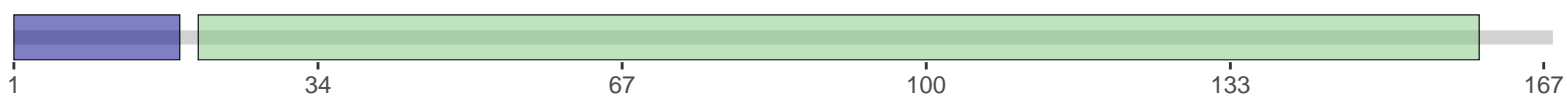
Molecular weight

Gel Slice



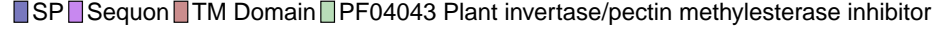
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

/TISKLRHSNPPAAWKGPLKNGAGYKVLTTSLPEAEALTGDKPKFAEDGMVGGSDAQEGEEYFKGSKPLSALNVAWHQLSDVGRAVRRNL*

NbL19g22640.1 ATP-citrate_synthase_beta_chain_protein_2 [MW = 65.63 kDa]

No. of times detected



log(intensity)



Values from



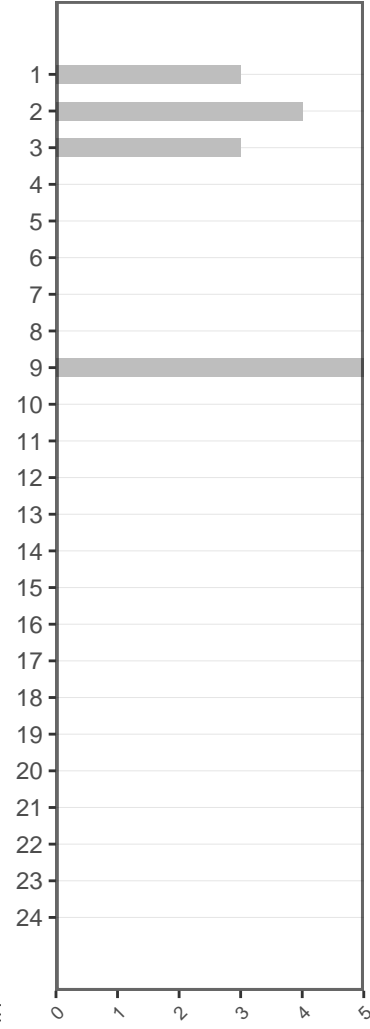
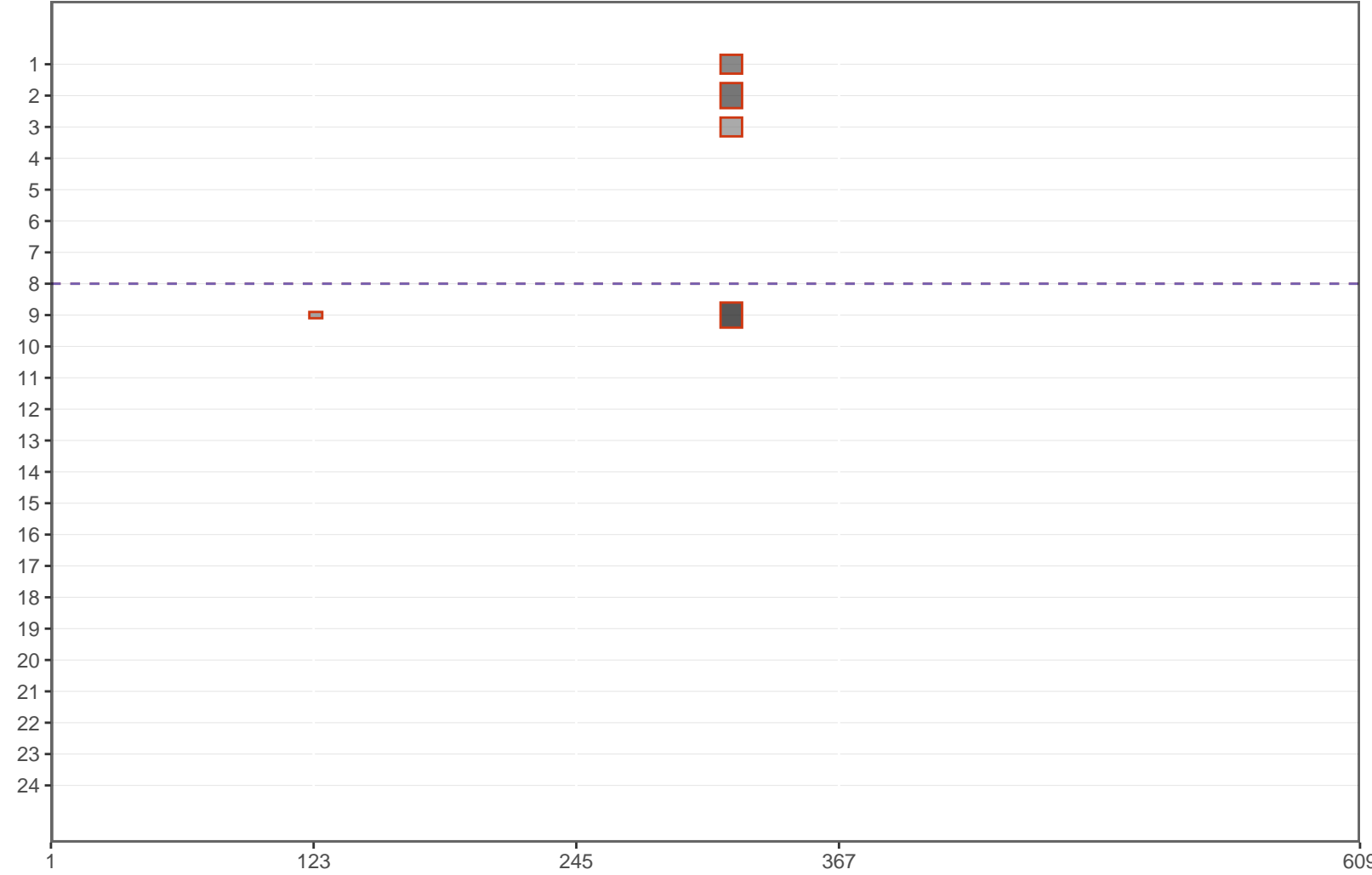
MW indication



Molecular weight



Gel Slice



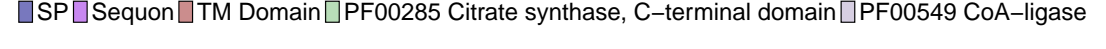
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

JALKDAGAVPTSYEAFEGAIKAEFEGIASDQKTLVKEITPPQIPEDLNTAKSGKVRAPTHIISTISDDRGEPCVAGVPMSSIVEQGLGVSDVBLWFKRSLPRVGRARFIEGILLCADHGPCVSGAHNSIVTARAGKDLVSGLSGLTGRFRFGGAVDDAARYFKDVAIDRGLTPYEFVSEMKKKGRVPGHGRKRDNRKRVFELLQLYARENFPFVKYMEVWGVQVETVTLKANNLVNDGAGSLFLDLLAGSGMFTKPEIDEIVEIGVNLGLFVLAISLIGHTTDDK

NbL19g22510.1 uncharacterized_LOC109241286 [MW = 35.45 kDa]

No. of times detected



log(intensity)



Values from



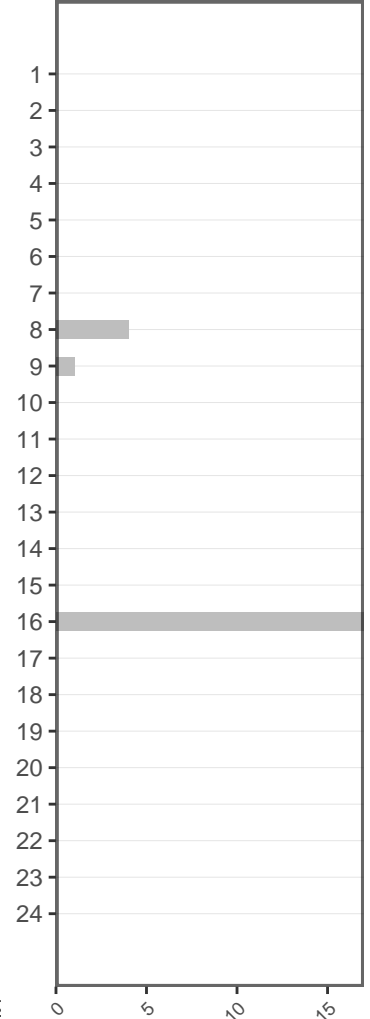
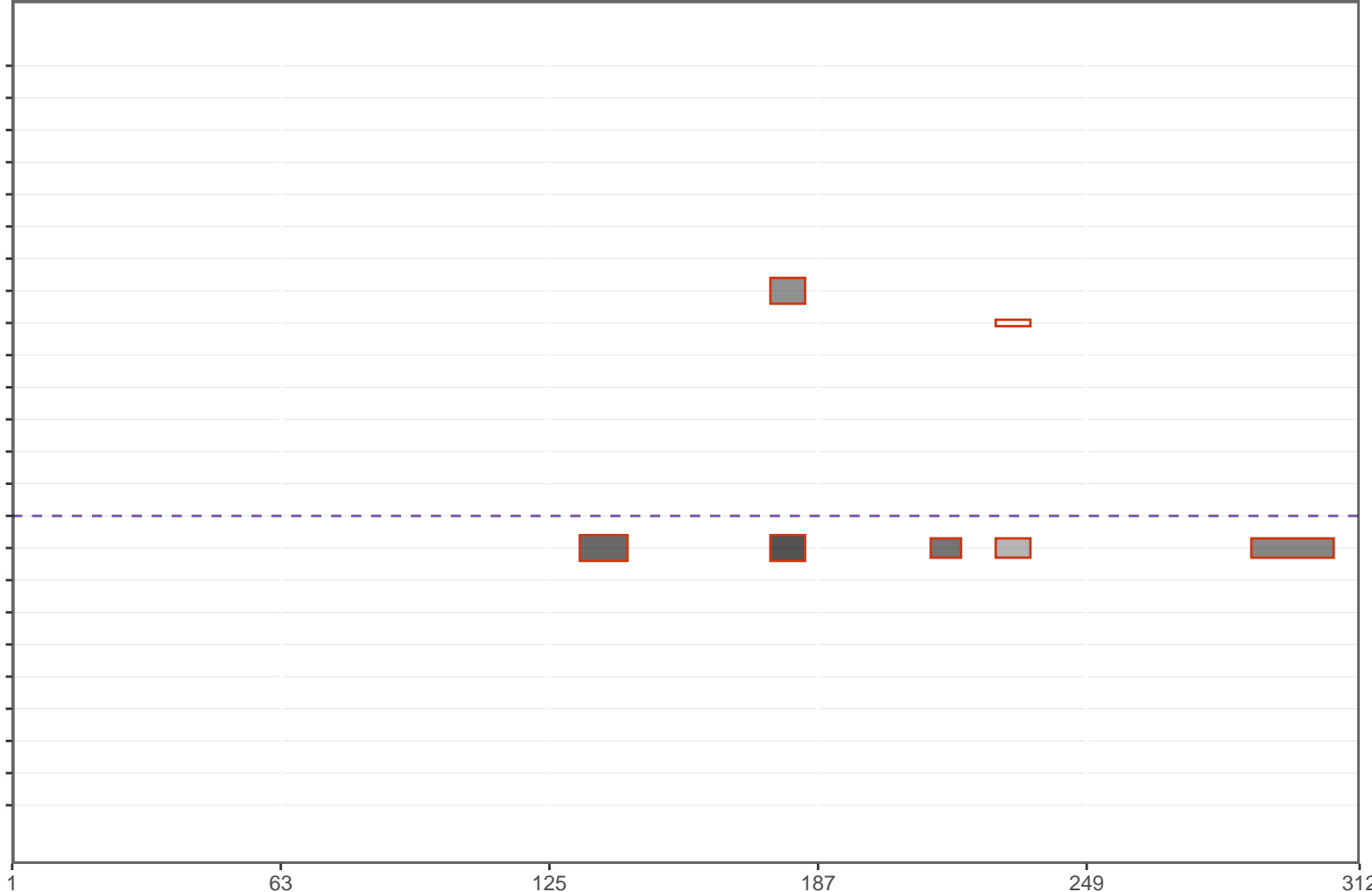
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



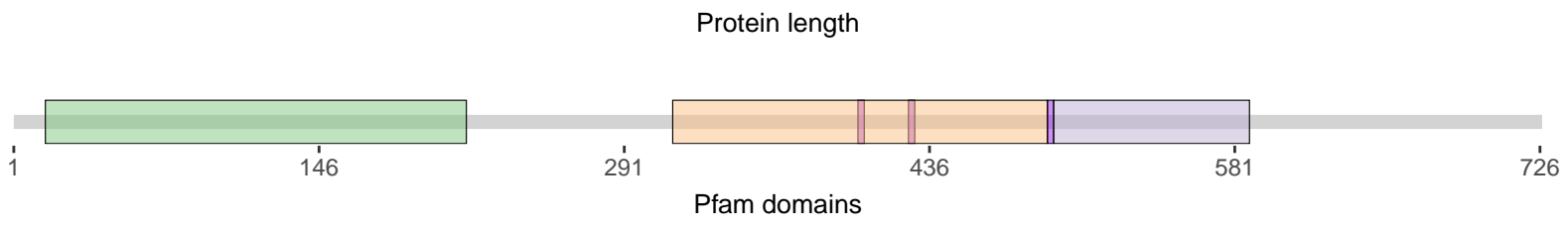
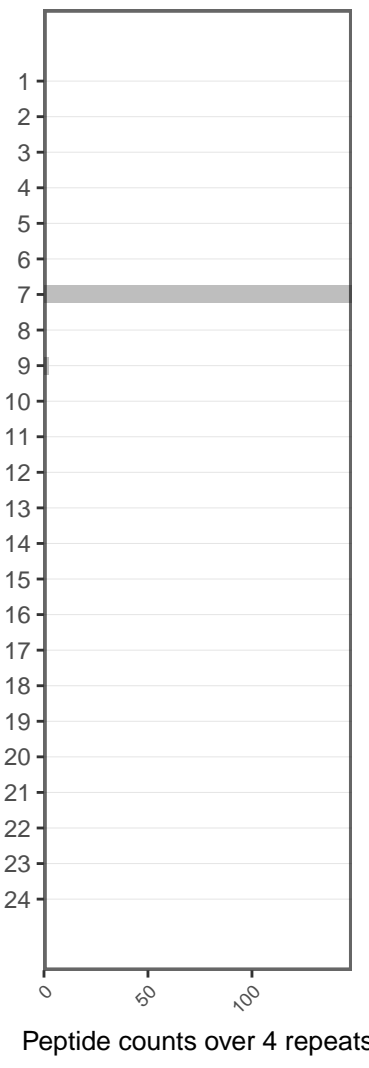
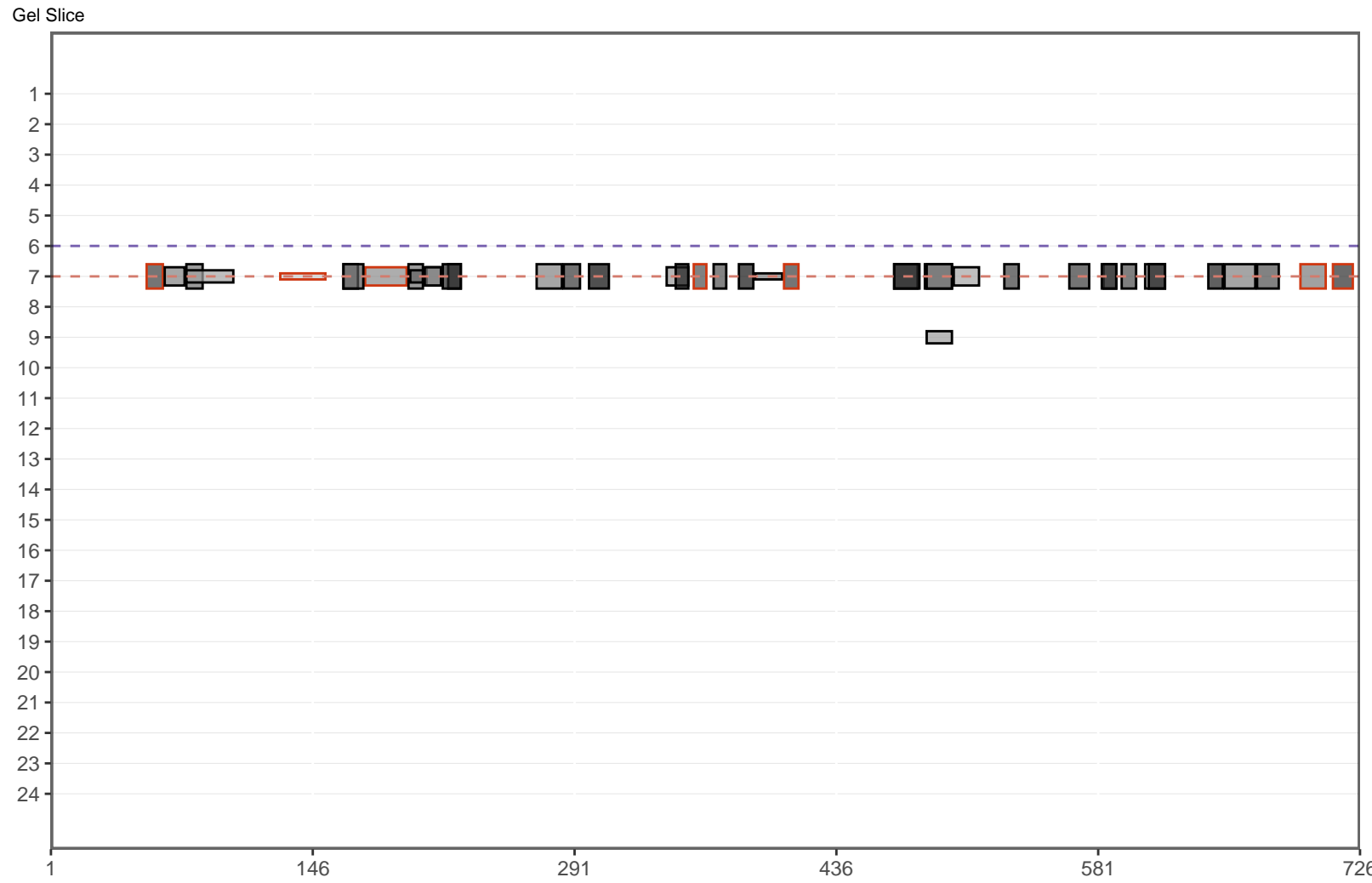
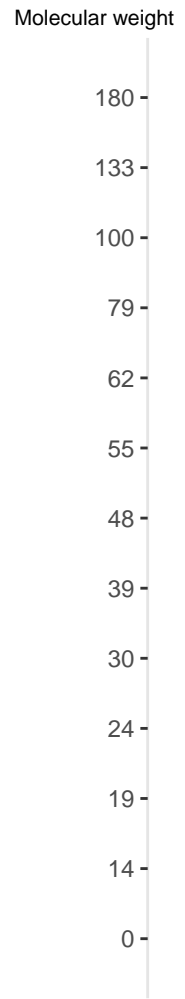
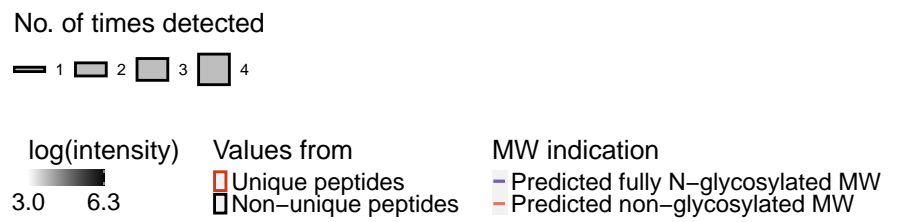
Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

TERGIANPOTKEISSLSVEPCEGETLVTLEFQGRSEPFIERIEHERFLAVIPETLNGFLYINPAICARYSDSEYLYKTRCRGDKGIFPQLVGRYNDIKIWRDILLPCRVLRHDLVAQNLGDVYDFLQHTFLGDRRTIREYLVATTGGSGIMEEPEPELLKRYRGG

NbL19g22470.1 glyoxysomal_fatty_acid_beta-oxidation_multifunctional_protein_MFP-a [MW = 78.86 kDa]

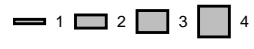


- Pfam Description**
- SP
 - Sequon
 - TM Domain
 - PF00378 Enoyl-CoA hydratase/isomerase
 - PF02737 3-hydroxyacyl-CoA dehydrogenase, NAD binding domain
 - PF00725 3-hydroxyacyl-CoA dehydrogenase, C-terminal domain

Protein sequence:
 IMGRVYKANLQSSVYKKGKMSPEKFEKTLGKGLDYEGRDVMVIEAVIENVSLKGGQFSDLEKYCPSHCLASNTSTDLNLUIGKTKSGDRIGHAFHSPAHVMPLEEVIRTKTSPQIVDLDLVGKGRKRTFVAVVGNCTGFVAVNRIMFFPYTQAALLLVERGTDVYRIDNATKFGMPMGPFRLLGDLVGFVAATGGGFVAVNFERTYKSMPLPLMGEDKRAGETTRKGFVYVDDRKAASPDPEKRYEKAREMGGVTDPLKALNSDKDIEMFFPVA/NEACRVLAEGLAV

NbL19g22450.1 eukaryotic_translation_initiation_factor_2_subunit_gamma-like [MW = 50.74 kDa]

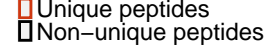
No. of times detected



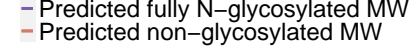
log(intensity)



Values from



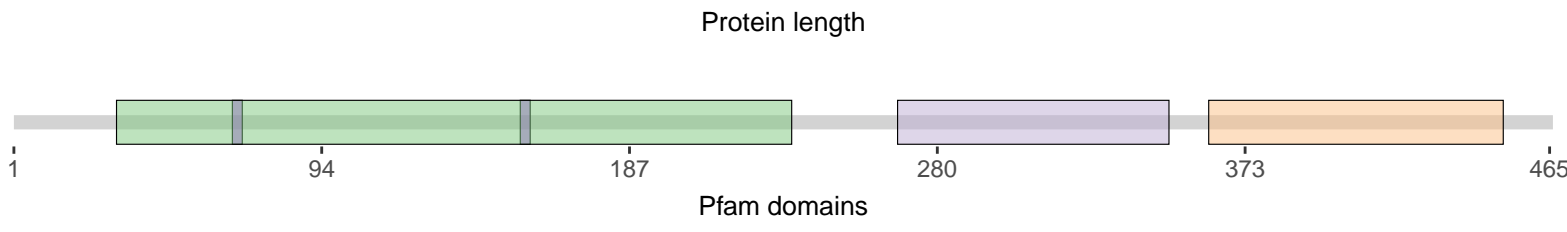
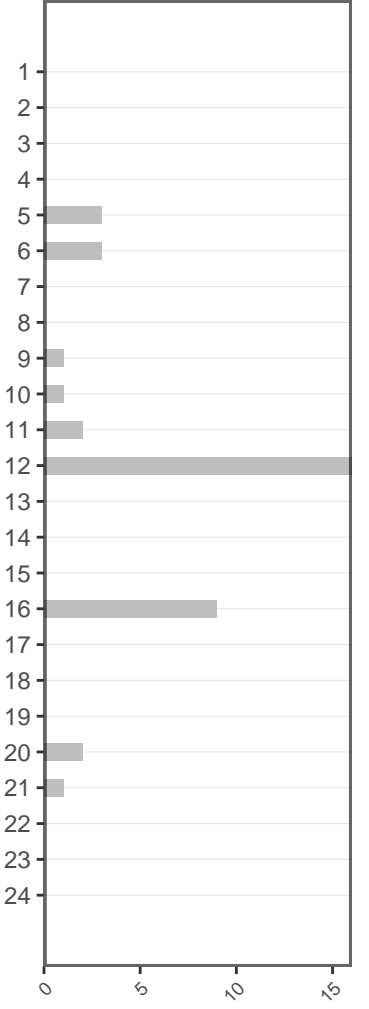
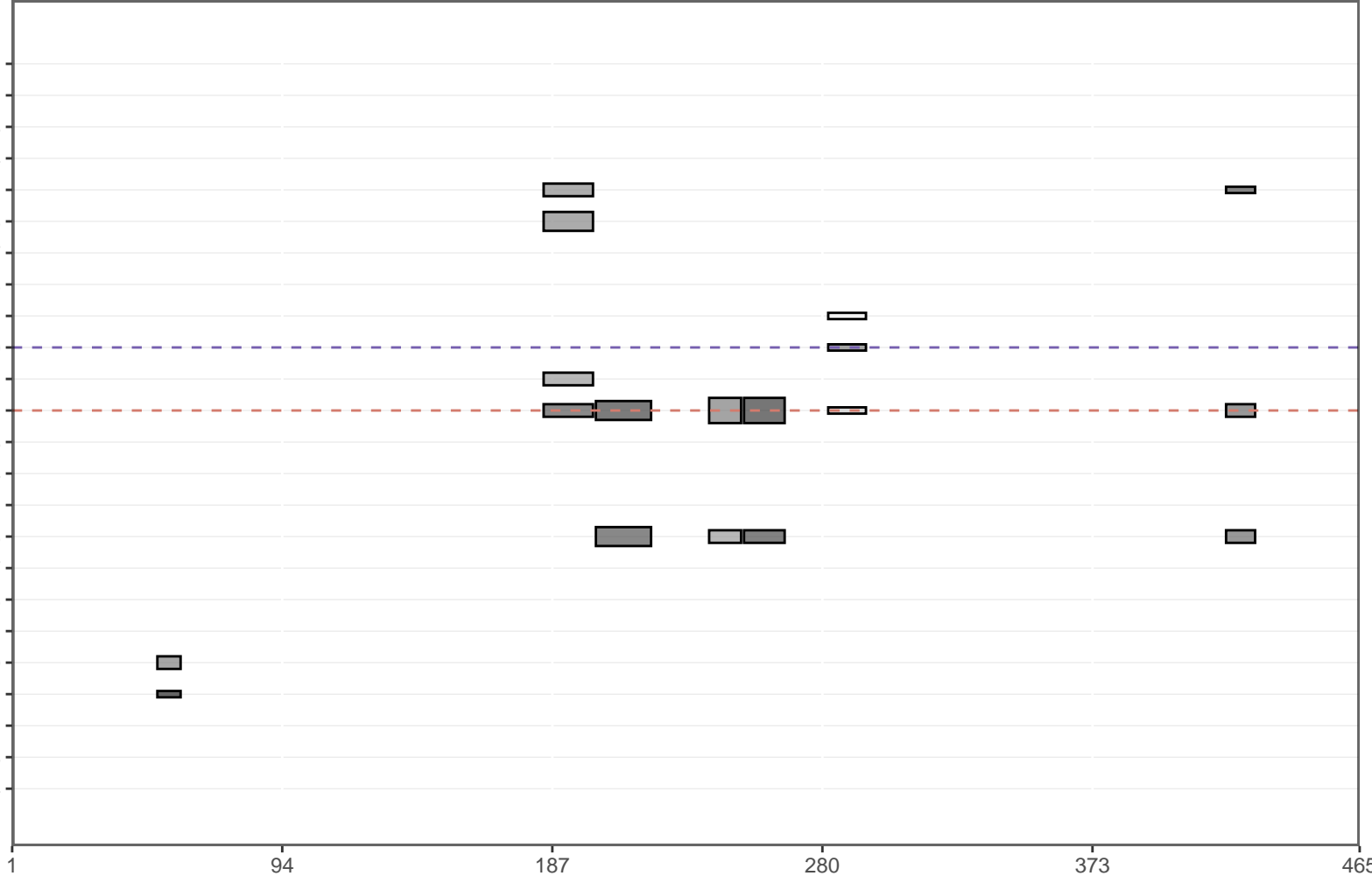
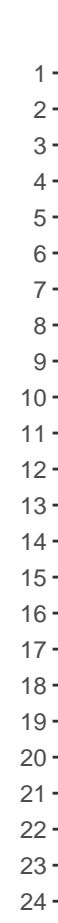
MW indication



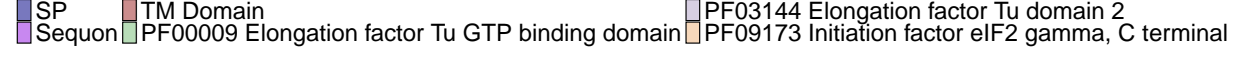
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

IQLKYNDVLAELYWKPKIPERNFISPPNMIWRSFDNKPQFVEDDIRGGVAGGSLKGVLYKNDLIEVRPQIVVYKDESGNKGTPYRSRIVSLFAEQNELQFVPGGLIGVGTFTMDPTLFRADRLVGGVLSGEVSGLPFVFEVLEVNFFLLRLLLGVRTKDSEROGKRVSKLANGEILMLNGMSTGARVWKKVFAKQLTSPVCTSKGEHLSRRREKHWRLLGWGGQAGFLDVPQDPV

NbL19g22340.1 ATP_synthase_subunit_O_mitochondrial-like [MW = 25.84 kDa]

No. of times detected



log(intensity)



Values from



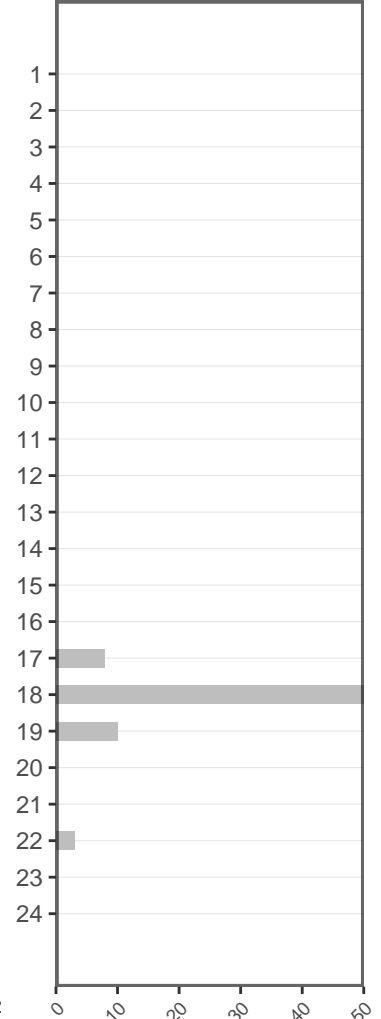
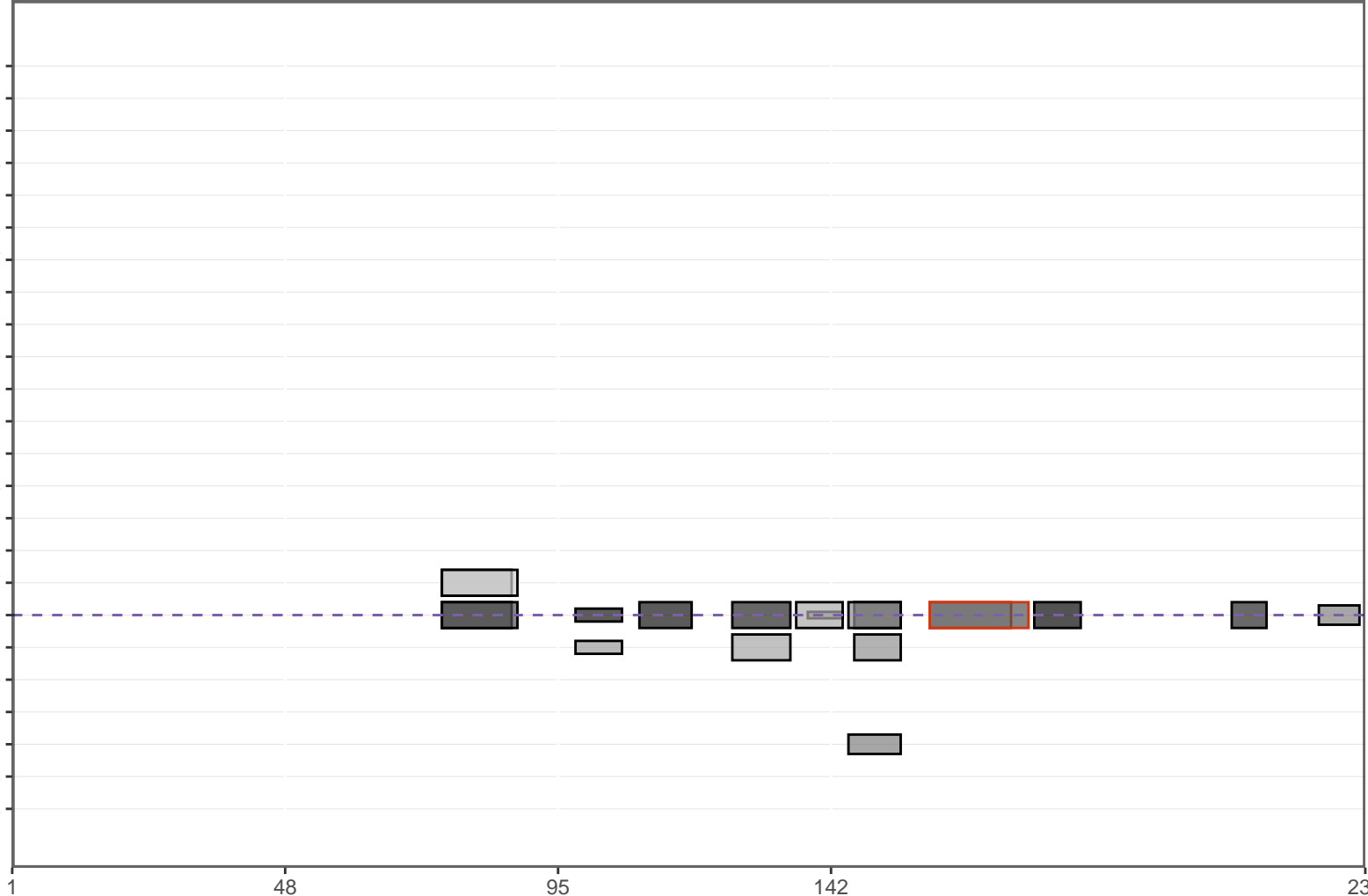
MW indication



Molecular weight

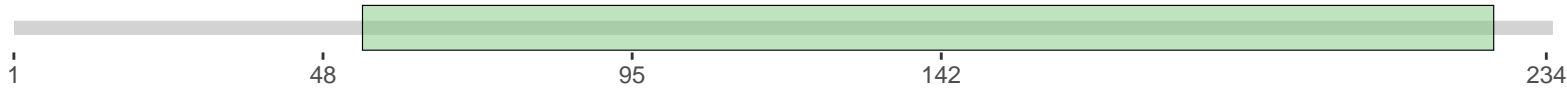


Gel Slice



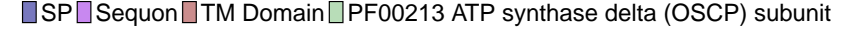
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TDTTRYKASIDICADAKAFGLTRNRLVLAENGRLLKHDIAKRFELTMAHKGELKAVTIVPLPPEEEKELKELTLDQVMGKGGKVNIEGKIDPSLGGLVIEFGQKVFDMRIRTRAROMERLLKEPLNF

NbL19g22330.1 heat_shock_factor-binding_protein_1-like [MW = 12.5 kDa]

No. of times detected



log(intensity)



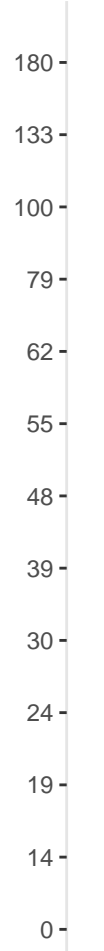
Values from



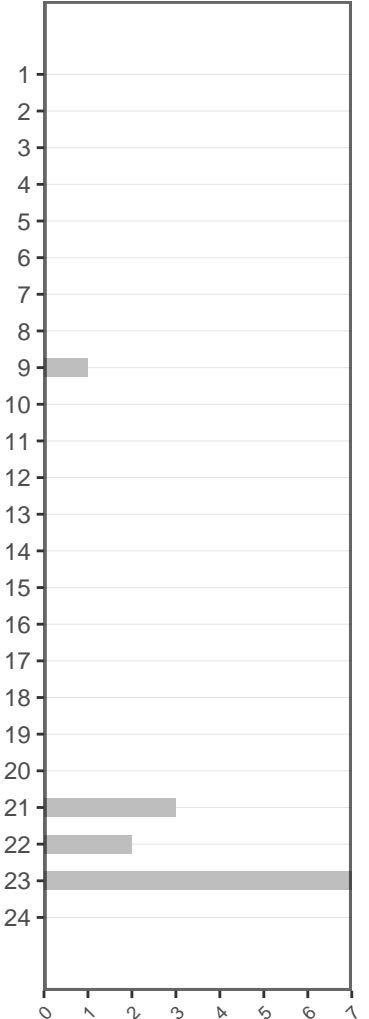
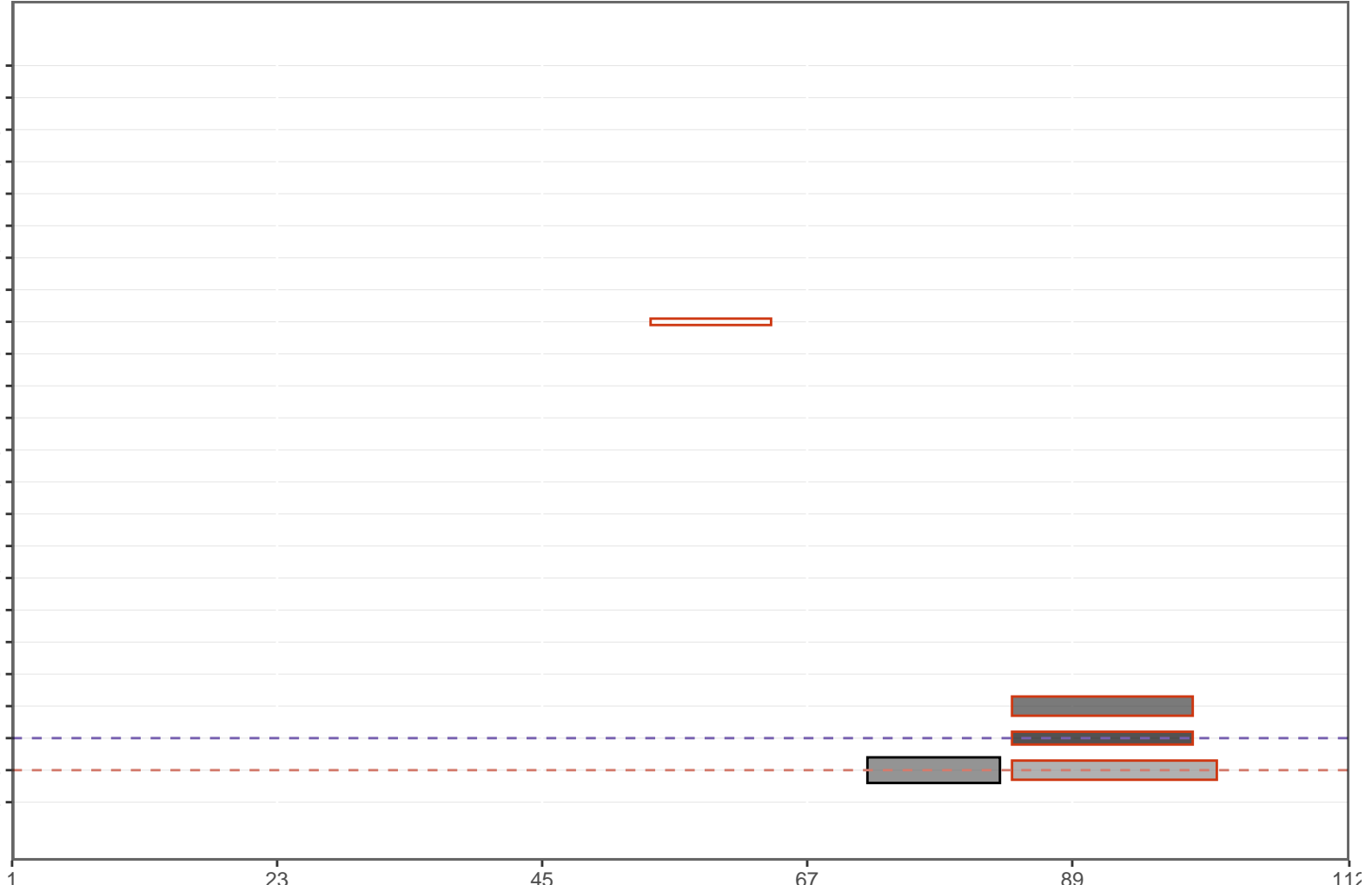
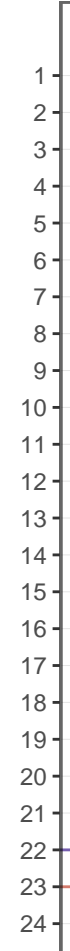
MW indication



Molecular weight

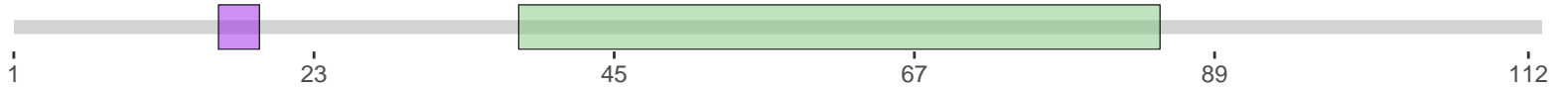


Gel Slice



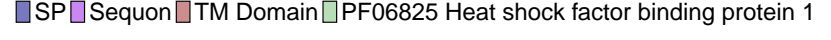
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CVLLGQMQTRFQTMSEGIKIDEMGNRIELEGINDLRAEMGGDGPSPATLKPREEPKTSDDA*

NbL19g22230.1 lipoyl_synthase_chloroplastic [MW = 40.88 kDa]

No. of times detected



log(intensity)



Values from



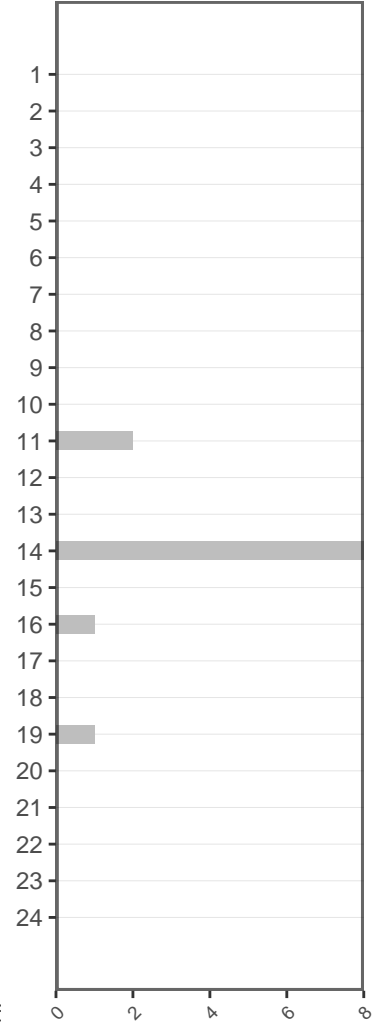
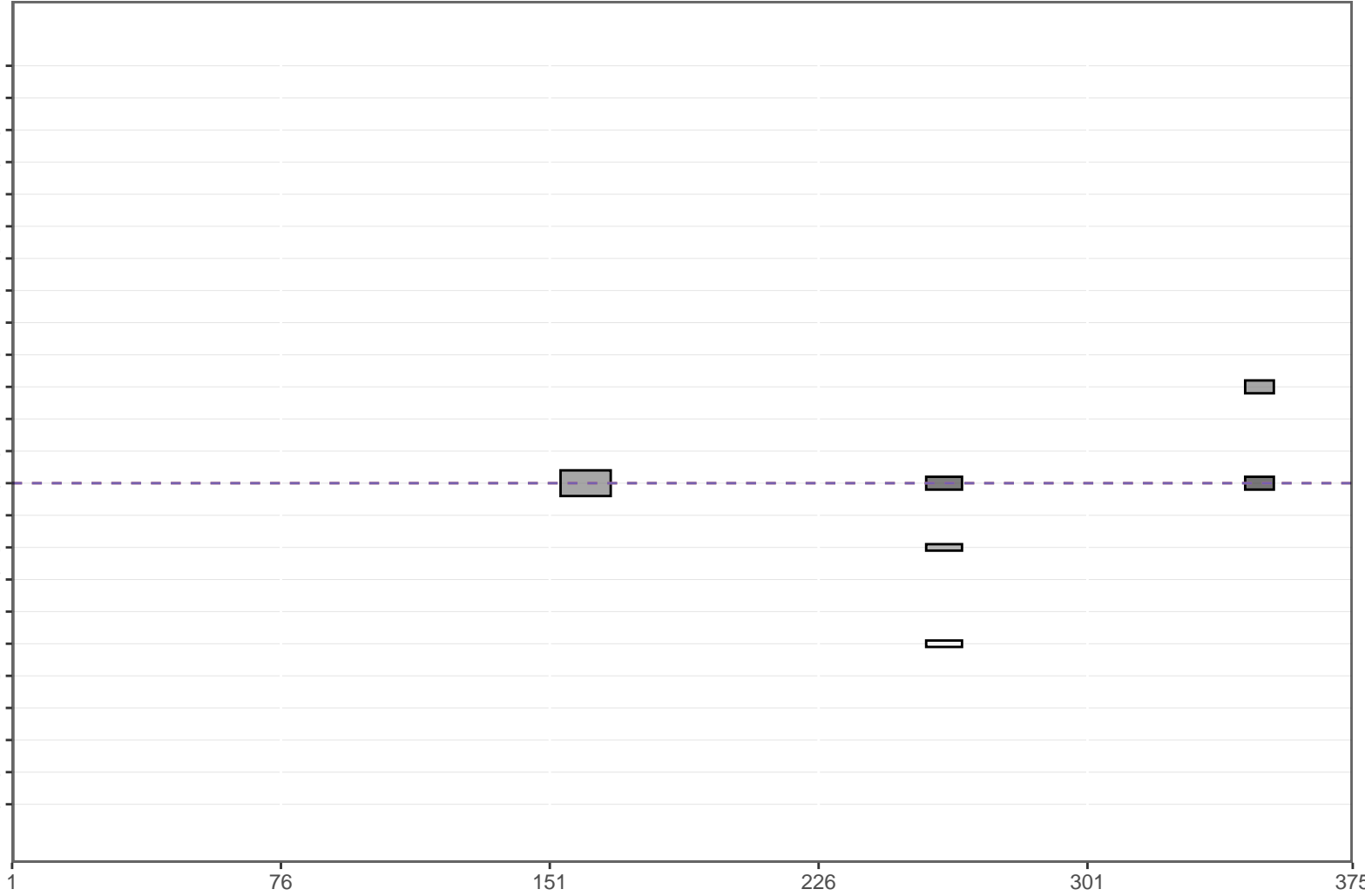
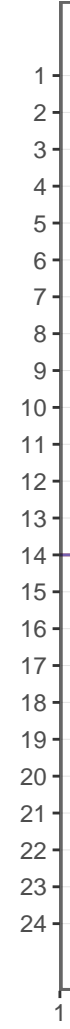
MW indication



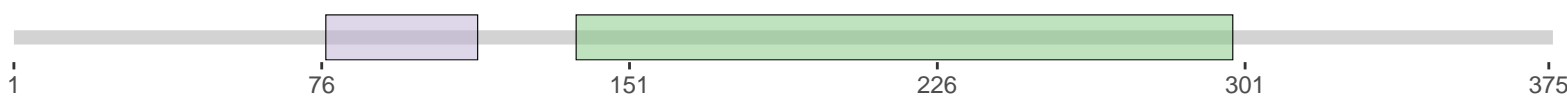
Molecular weight



Gel Slice



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGVDYVLTSLVDRDRLPDGGSGHFVETVKAMKLLKPDIMVEGLTSDFRGDLSEAVSTLVHSGLELVFAHNIETVKRLGRIVRDPFRAGYEGSLVLRKHKLDEKGMKTKTSMGLGETDDELKEAMADLRANDVILTLGGVLPFTPLHLTVKEYVYTPKFAVKEYGESIGFRVYASGPLVRSGYRAGELFVQTMKERTNAY

NbL19g22140.1 signal_recognition_particle_9_kDa_protein [MW = 12.04 kDa]

No. of times detected



log(intensity)



Values from



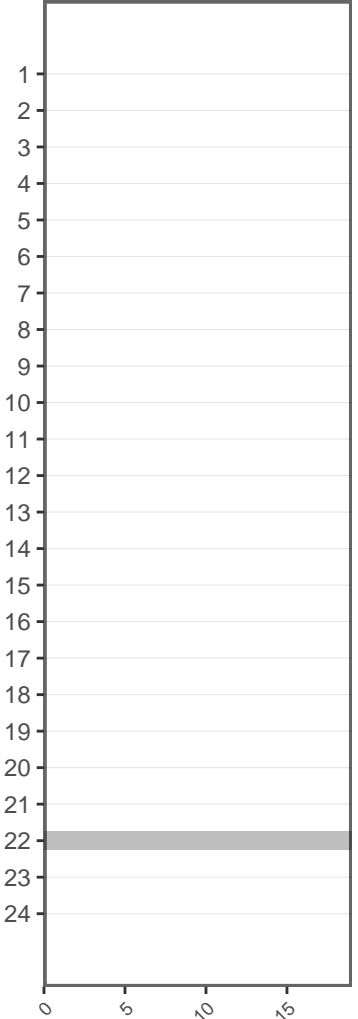
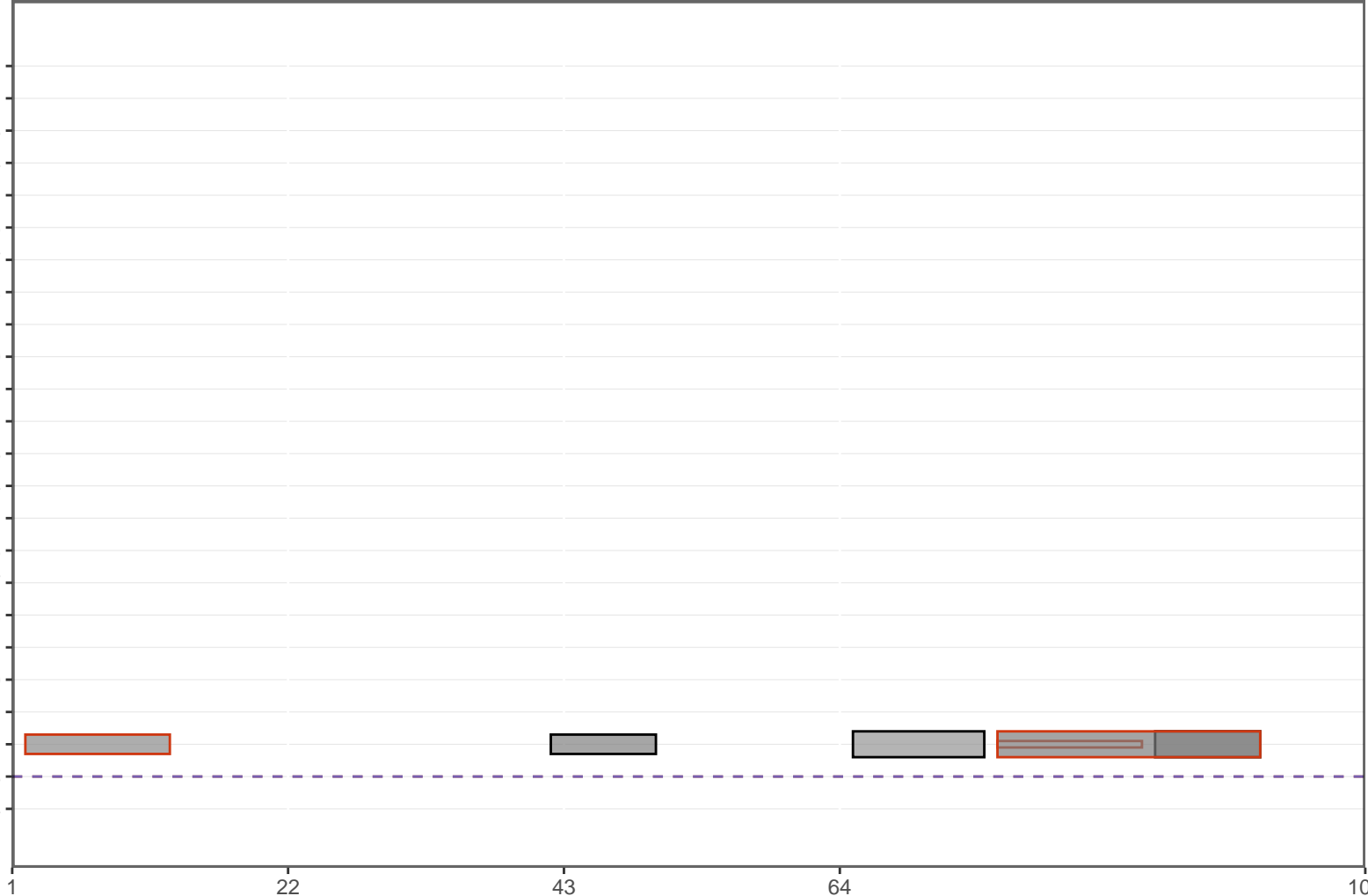
MW indication



Molecular weight

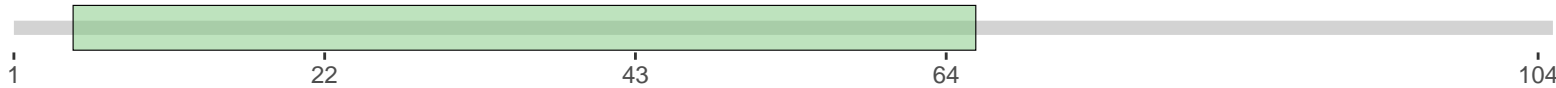


Gel Slice



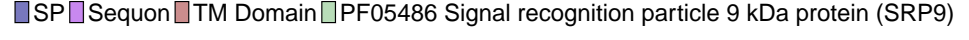
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

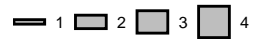


Protein sequence:

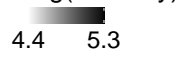
VLKYTDTECKFRFDGAGDAKKMEKLNFFFLMARGPVDISEVGGKGEAEAPKKGRRKQ

NbL19g21970.1 single-stranded_DNA-binding_protein_mitochondrial-like [MW = 26.14 kDa]

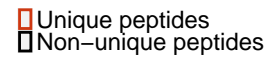
No. of times detected



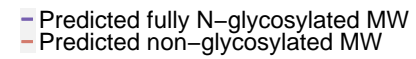
log(intensity)



Values from



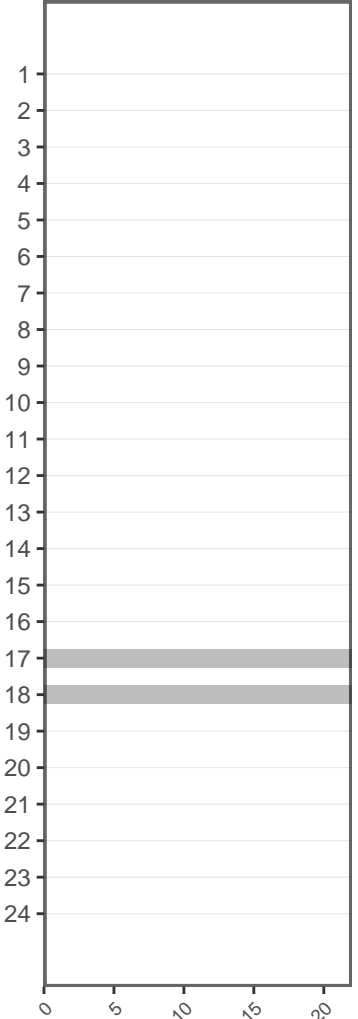
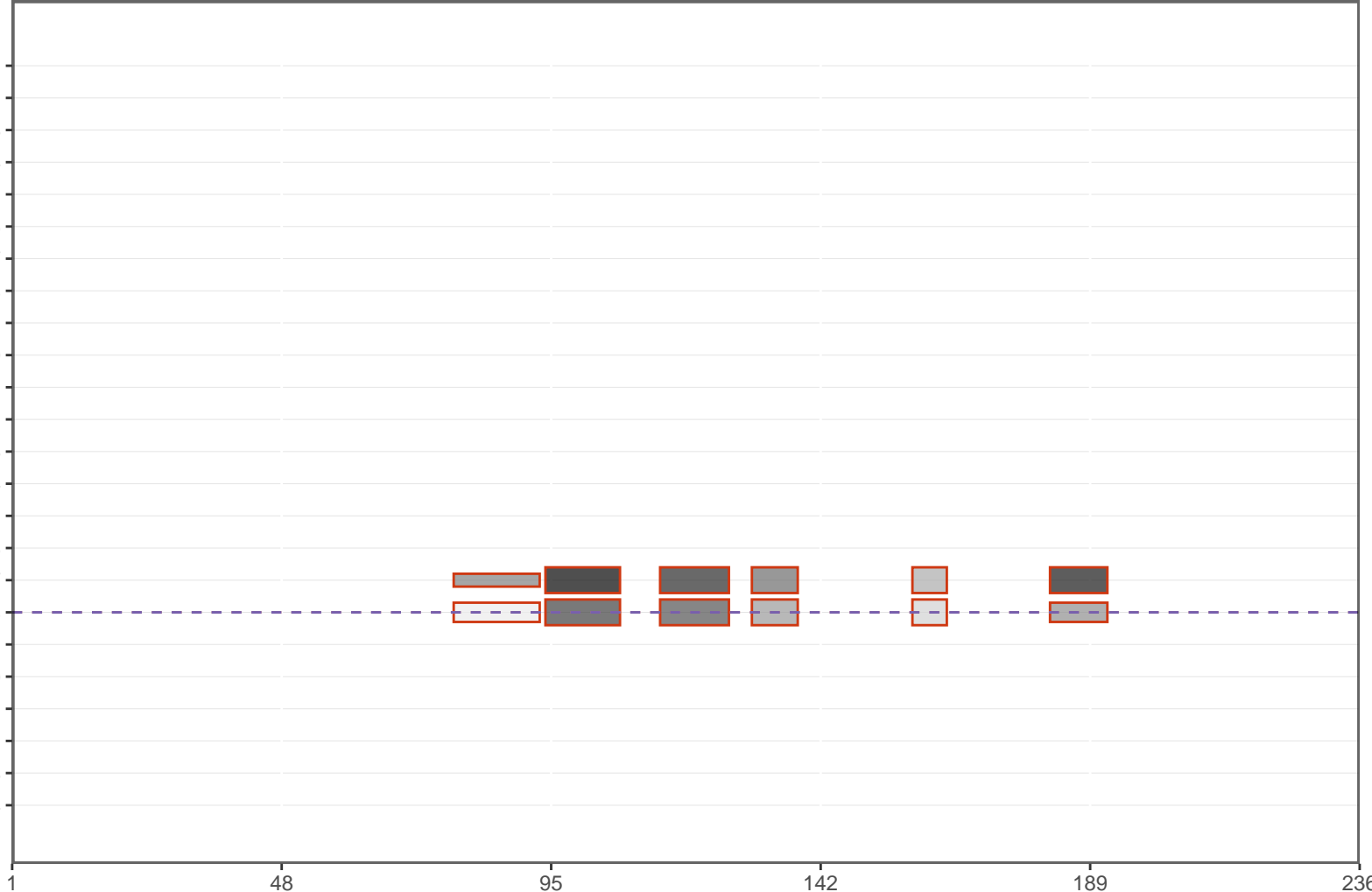
MW indication



Molecular weight



Gel Slice

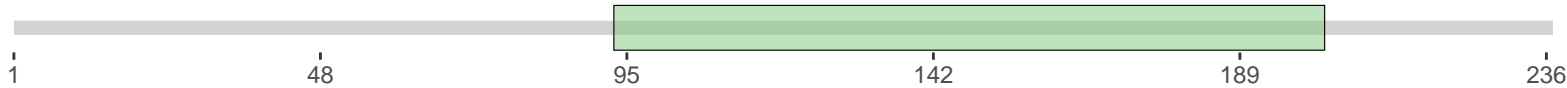


Protein length

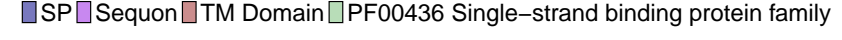


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KKLKSGRSVTLLSLGGTGRNRRRPFDEEPRVWNRCAVQWHRVSVYFPERLGEEMAKSVPGSLYVEGALSKIFDPTGLVRRIRREVLYEEMVWVFLGMLGMKPSHHKQKLGIVTESLRVSLV

NbL19g21950.1 probable_acyl-activating_enzyme_17_peroxisomal [MW = 78.95 kDa]

No. of times detected



log(intensity)



Values from



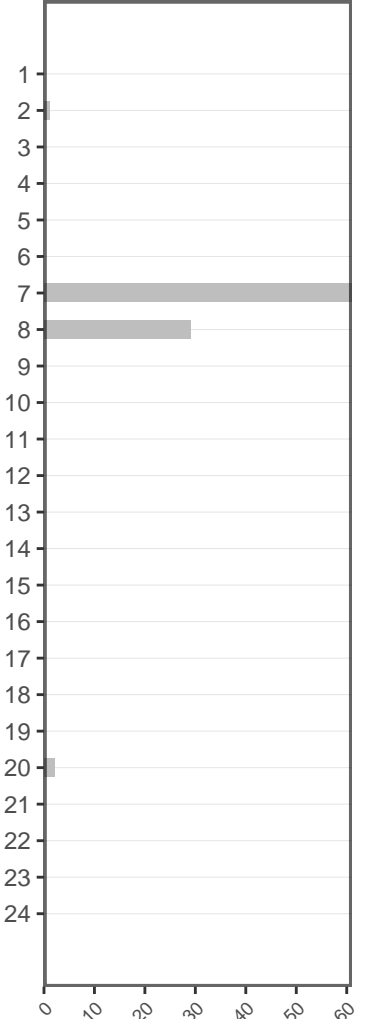
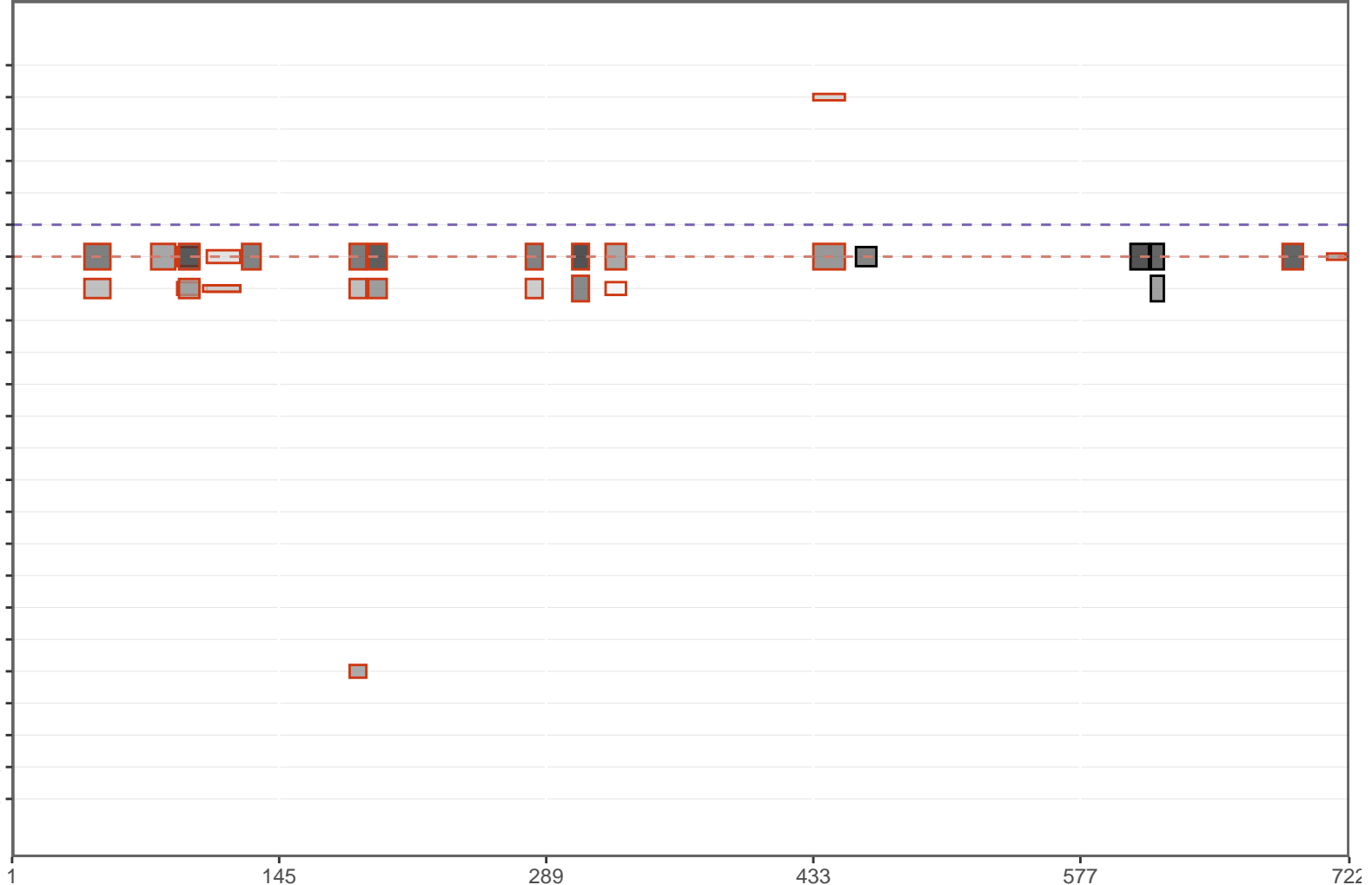
MW indication



Molecular weight

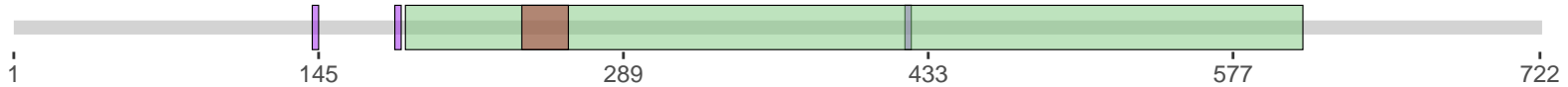


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

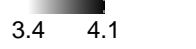
FTNLFSGGTTGEPKAIPIWLLSHFKAAADGWCHMDIKKGGVVAWPTNLGVMMSFVLYASLLNGASIALYNSPLGGFAKFKVQDAEVTMLGVPSPVTRTKANKNSPDGDFWSTRFCGSGTGEASSVDEYLVLMCRAGYKPIEYGGTGGSEVSGSLLQPSLAAFTAVMCGSLHLGDDGLPIPSDVPDGIQELALGPLMFGA6STLNLADHNEIFYKGMPLVNLKVKLRRHGGVDFERTSKGYVHAHGRADDTMLNLGGIKVSSLEIERICNAADENLEAAVGVPPA

NbL19g21920.1 H/ACA_ribonucleoprotein_complex_subunit_2-like_protein [MW = 17.07 kDa]

No. of times detected



log(intensity)



Values from



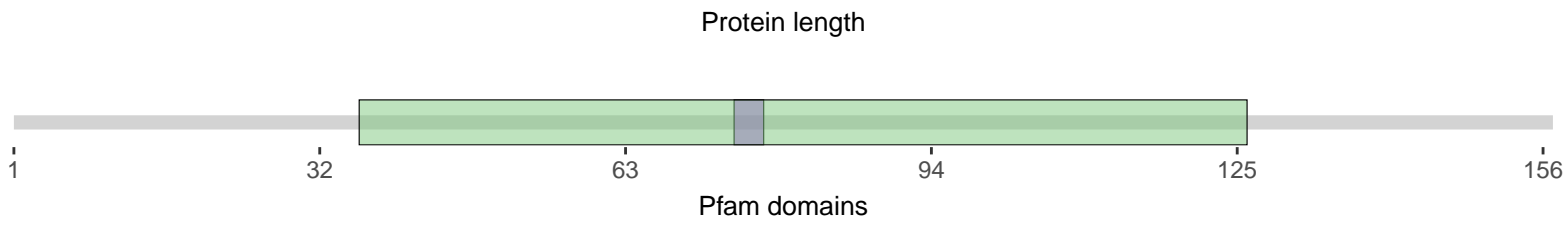
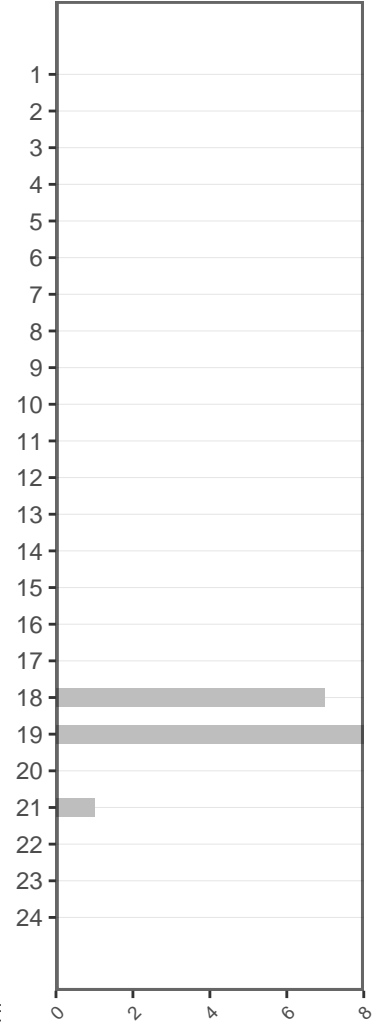
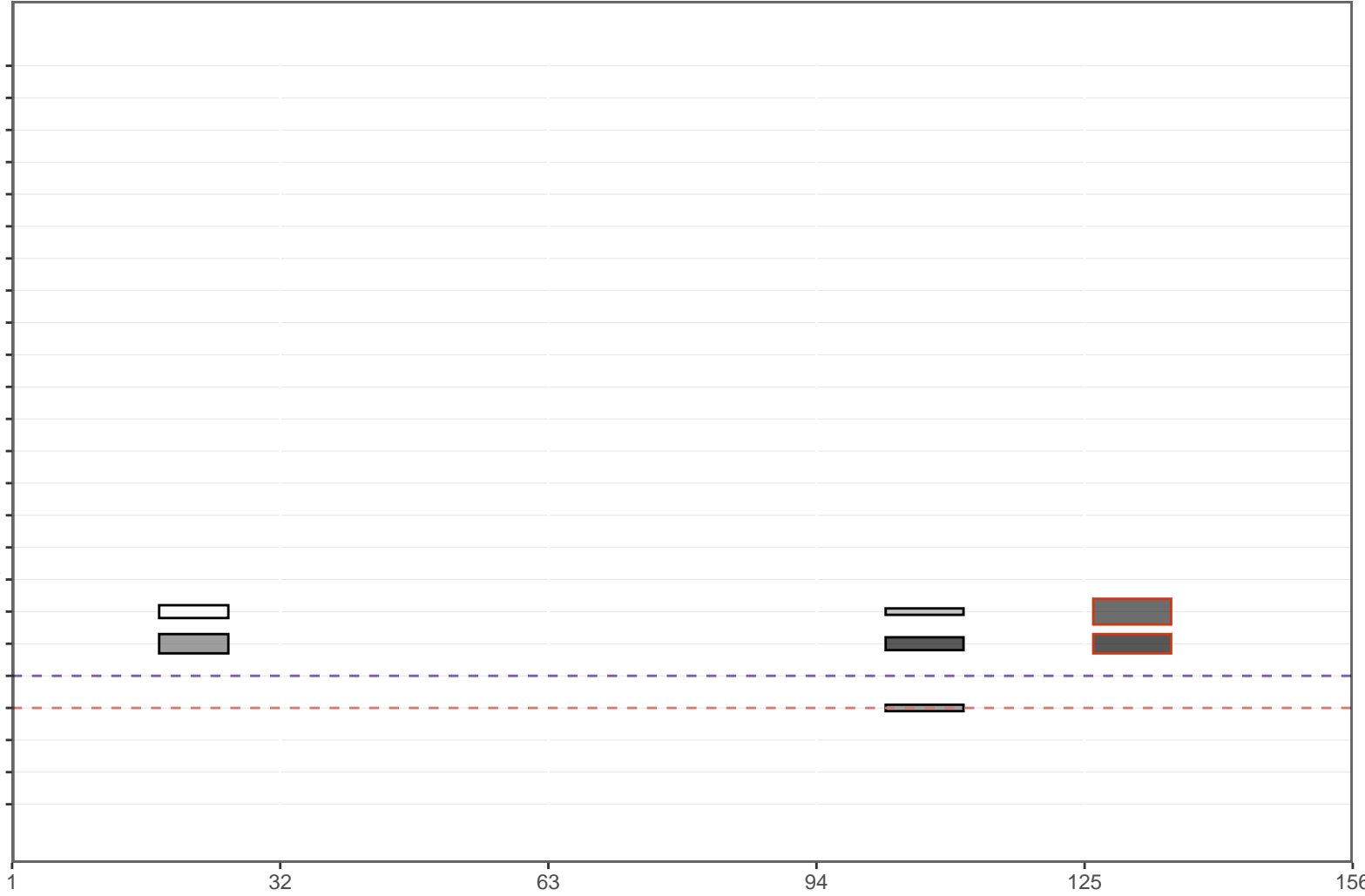
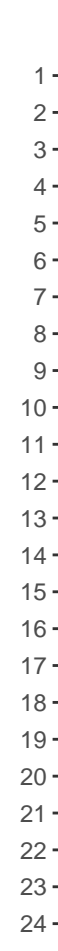
MW indication



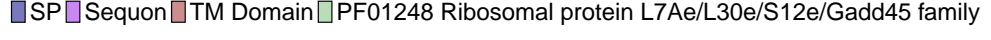
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

QKGVGVAGNSIPDWTHTVPLGEEAEPVYVYVSSKEDLANAGATKRPFGCVLVGTRPAKEELTQEDQEKAKADVDQVVEIGEMASSMF

NbL19g21910.1 agmatine_deiminase-like [MW = 41.57 kDa]

No. of times detected



log(intensity)



Values from



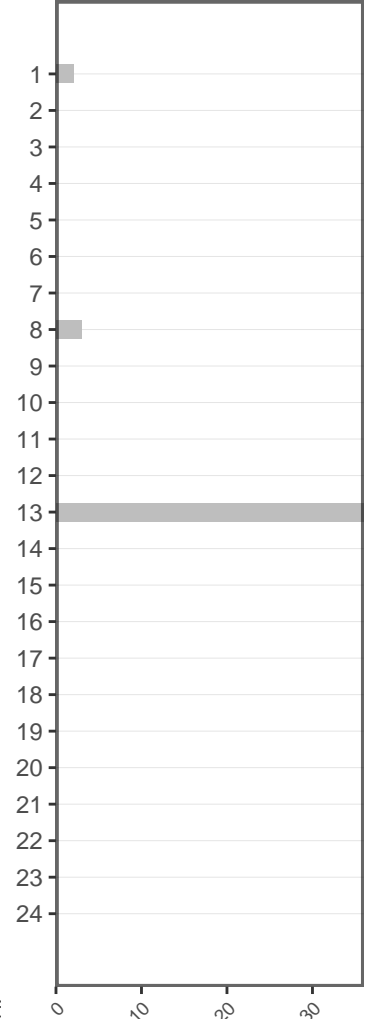
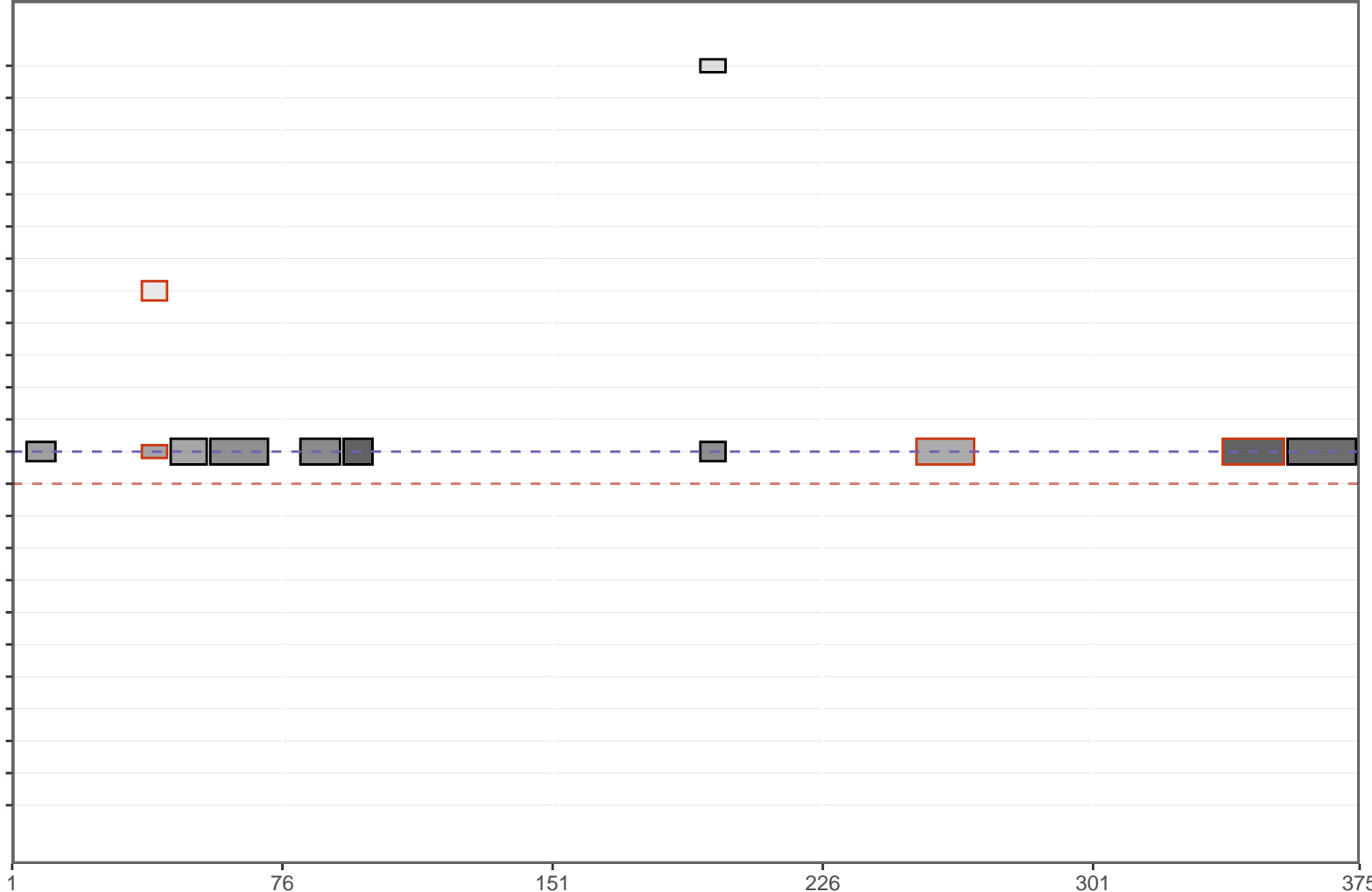
MW indication



Molecular weight

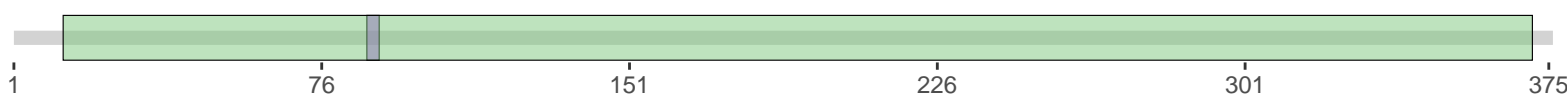


Gel Slice



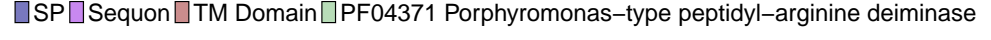
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ITCLTTECLLNKRNPHLSKEGIEENELKAVLGVKRIKIVLPRGLFGDDDTNGHIDNMGCFVPGVLLSWTDDHSDPQYERISIEALSLETTSDANGRLQVQKLVHVPGLCMTDEEADGIFGDDGANPRRTSGTRLAASVYVNFYANGAITPGFGDKKWDDEARVLSLAFDPDHEVYGVGEGAREIVLGGGNHICITGQGFSGP

NbL19g21890.1 uncharacterized_LOC109206323 [MW = 35.25 kDa]

No. of times detected



log(intensity)



Values from



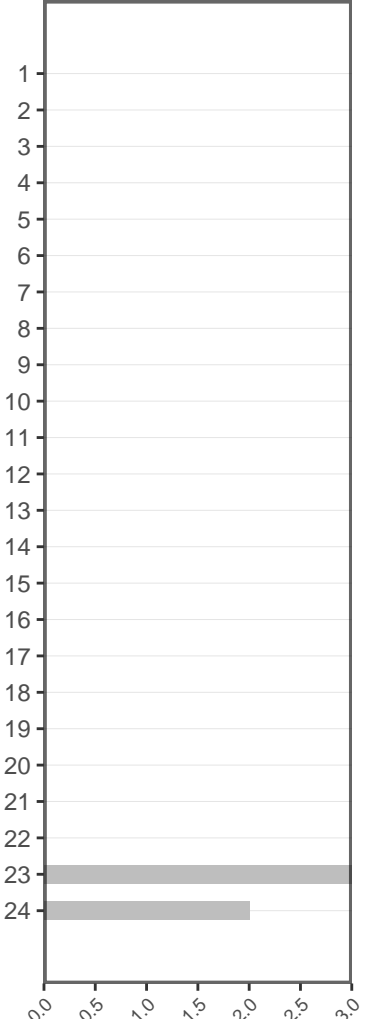
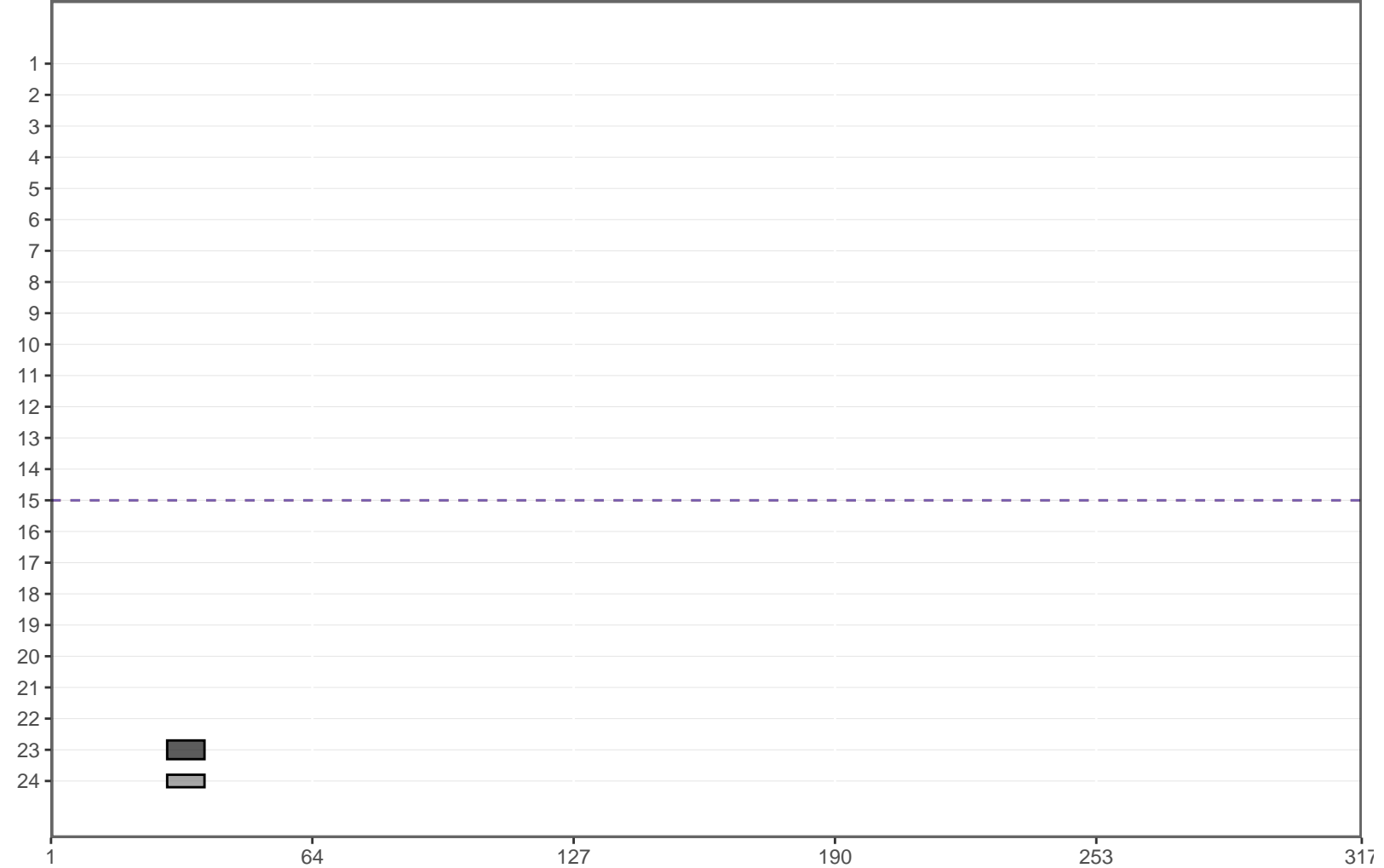
MW indication



Molecular weight



Gel Slice



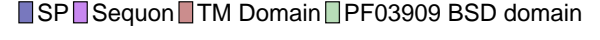
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TDLREFVKGITINTFGDFLEDDSDVSDIPTVSNVRGDLTEFQEKHAKLVLSGVKEISKLRVYELCPRIIMREKFRWIRYFILNSHWAPYEKYMEEAKIKVKEKAGVESEKQLSSAGTTSKPVVEAAPQTNRKXVA6STSDGDLVFLLEGDSDDGPDGDDAFDDDFDKP

NbL19g21790.1 psbP-like_protein_1_chloroplastic [MW = 28.07 kDa]

No. of times detected



log(intensity)



Values from



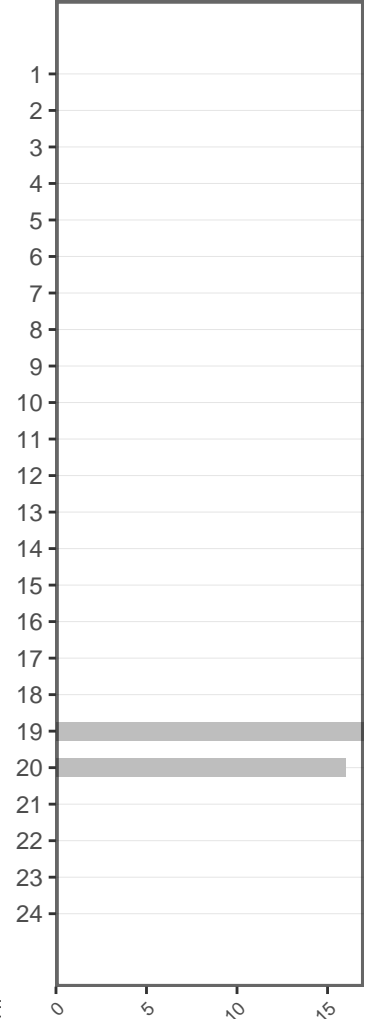
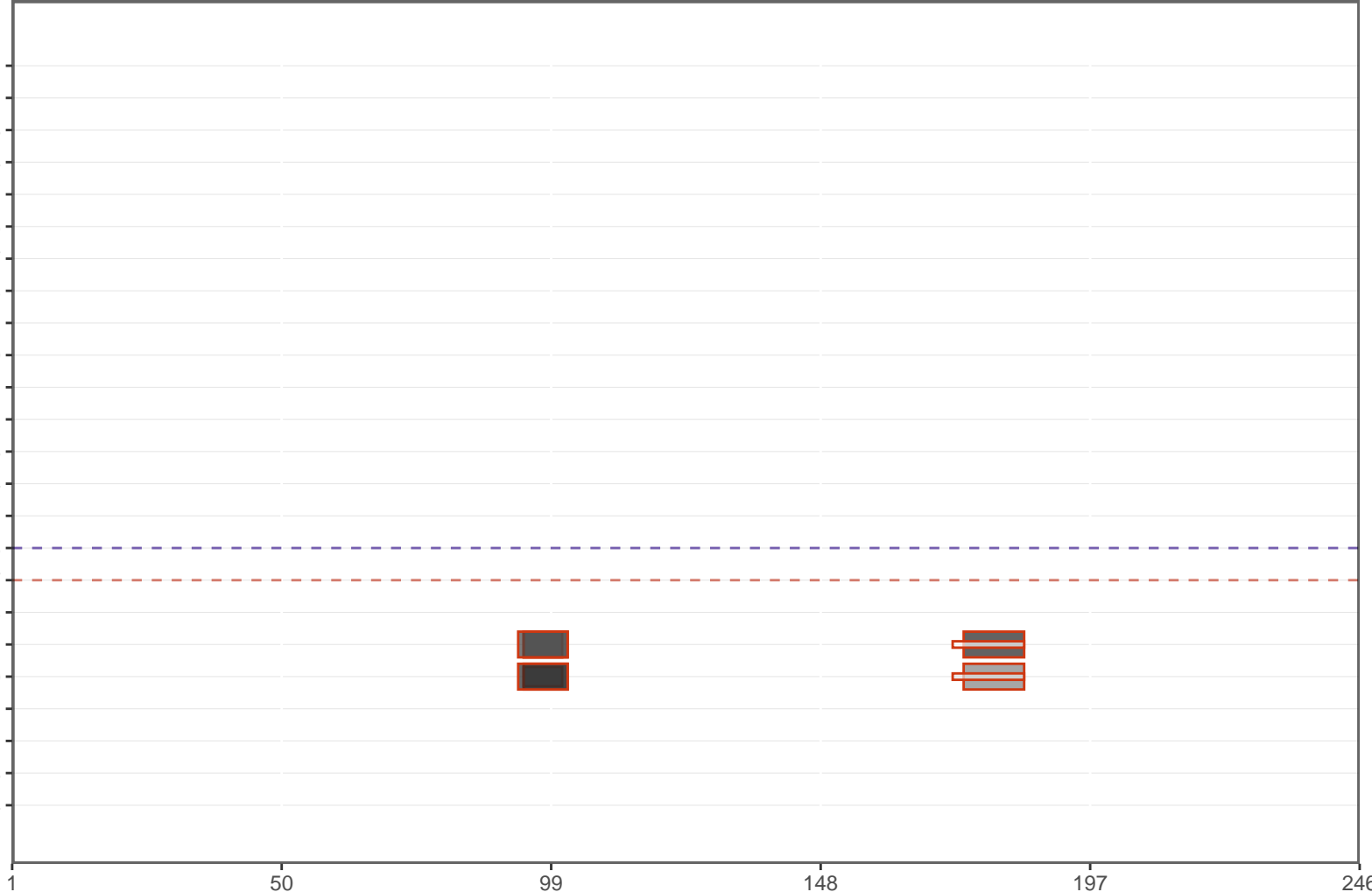
MW indication



Molecular weight



Gel Slice

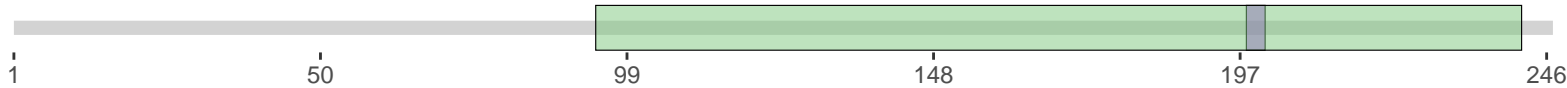


Protein length

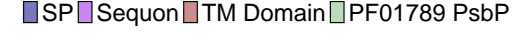


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

FGWGEVVEGGDKVFKDVEPLESVDVNVPTSGDIRDGSPGQVETLUKFLSSPSGKTLIEASEHDIKAYTFEFVQAPNFRHGLTAVGIGNGKFTLTGTGANERRWEKMDRLHTVVDSPQINW

NbL19g21560.1 2-alkenal_reductase_(NADP(+)-dependent)-like [MW = 37.8 kDa]

No. of times detected



log(intensity)



Values from



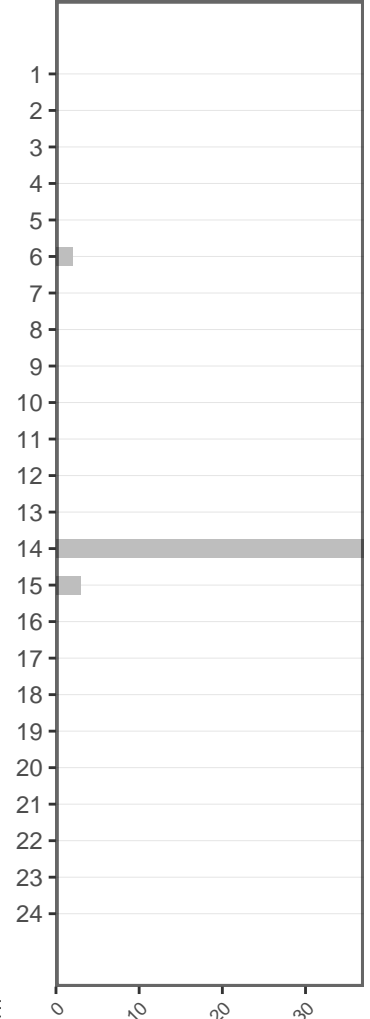
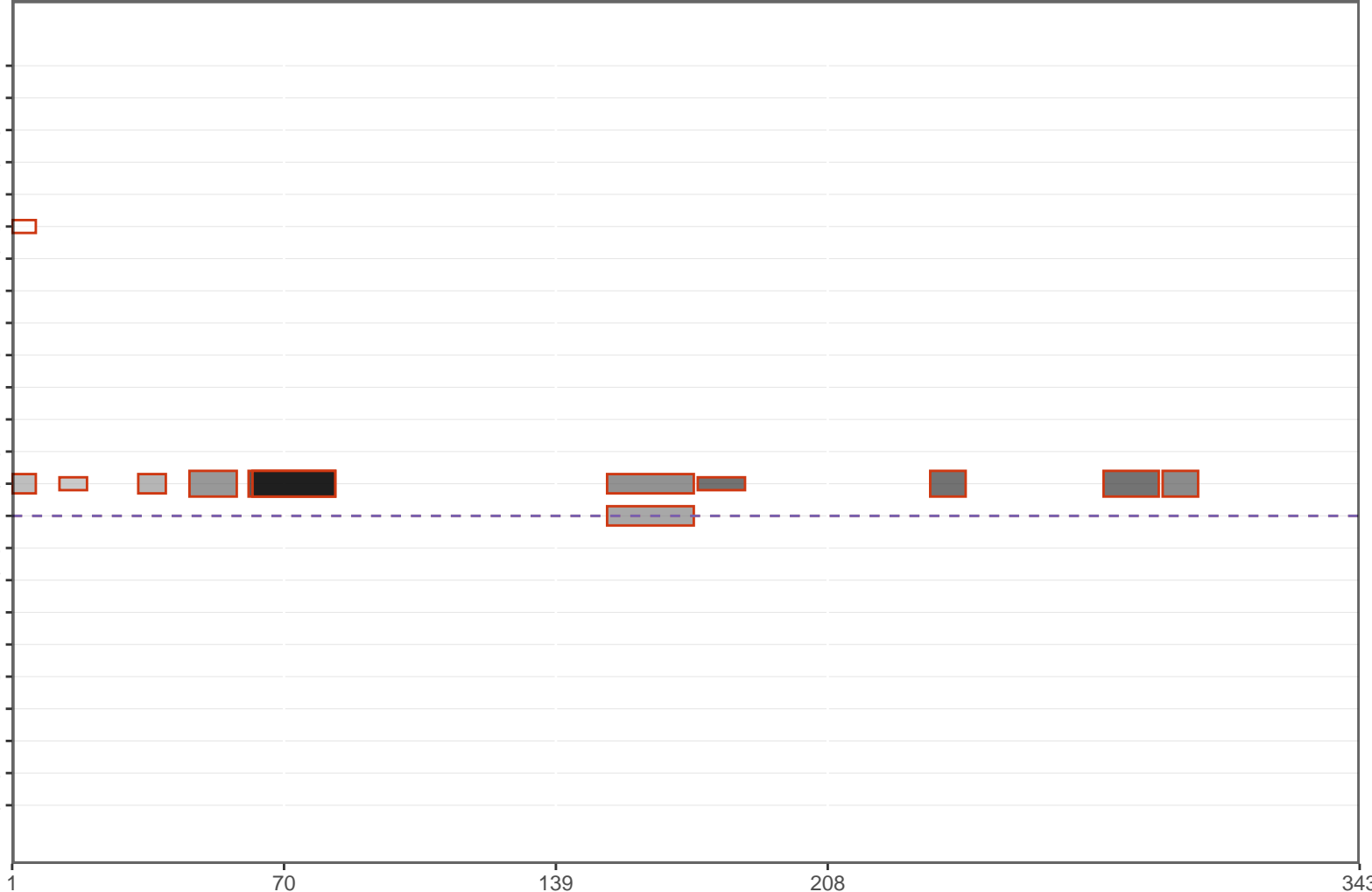
MW indication



Molecular weight

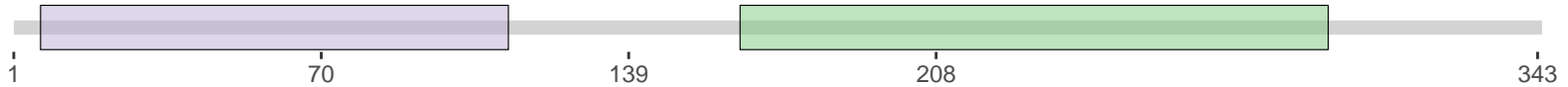


Gel Slice



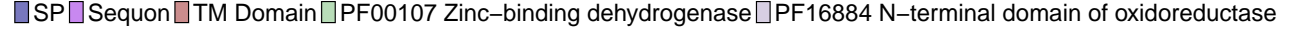
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

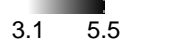
AASGAVGQLVGOFAKLLGGDYVGSAGTKERVDLKNKFGDEAFNKEEGDLSAALKRYFPDGDIDYFENVGGKMLDAVLLNMRVHGRIAVCGFISQYNIQSGPEGVHILFGLISKRVRMGGFLAADYFLLKQKFEVEMTPHKEGKVTVEEDIAEGIESAPGALVGLFSGRNVGKQLRVSR

NbL19g21520.1 UDP-glycosyltransferase_74E2-like [MW = 50.54 kDa]

No. of times detected



log(intensity)



Values from



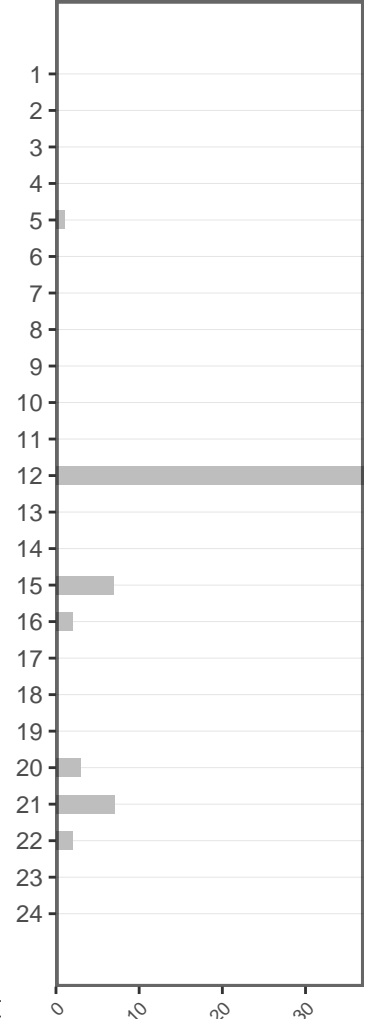
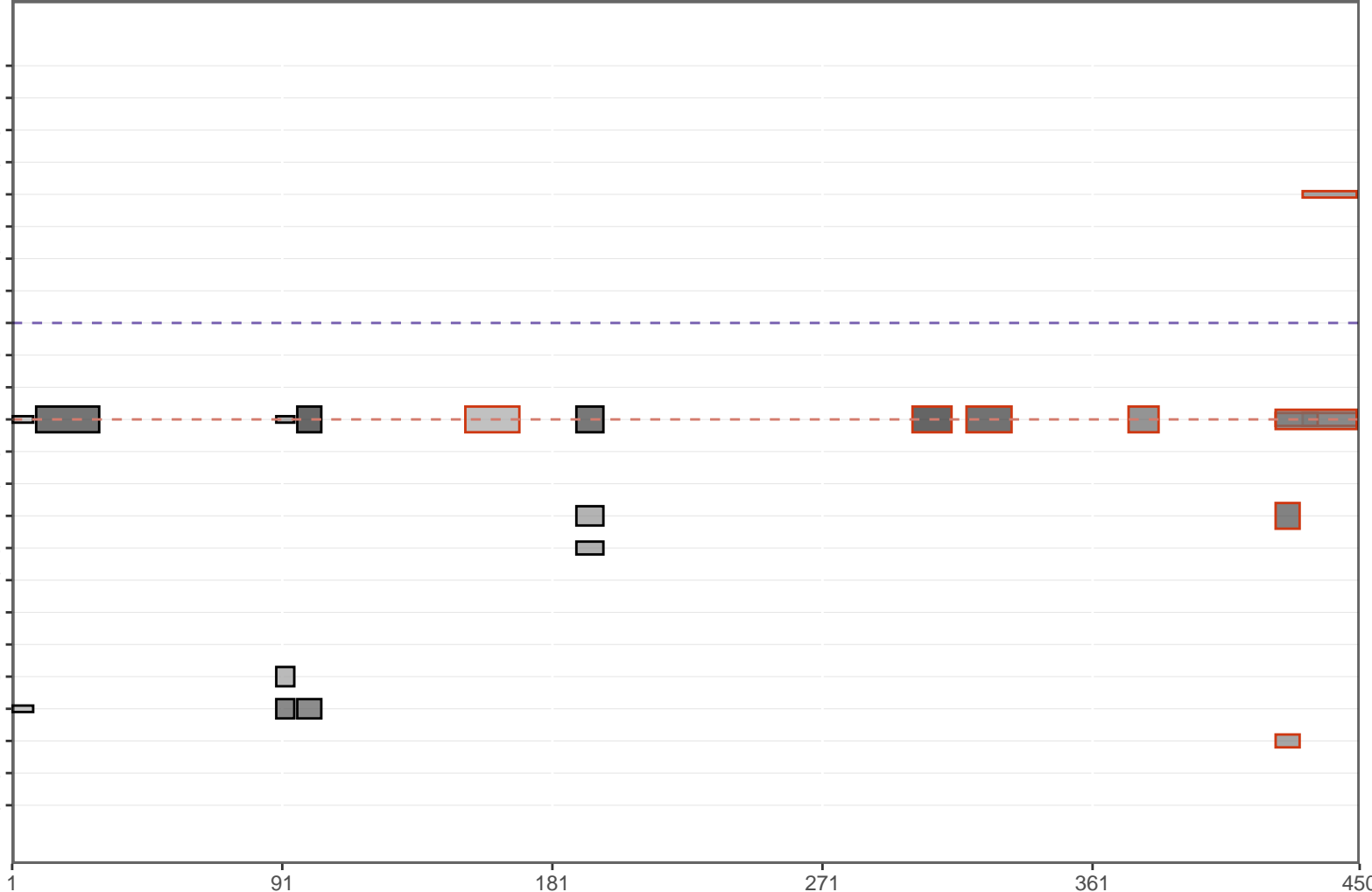
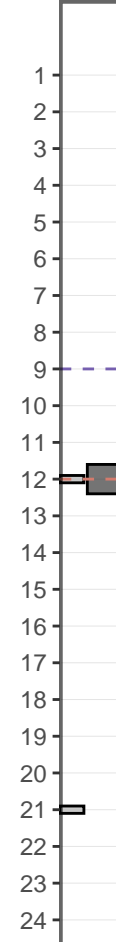
MW indication



Molecular weight

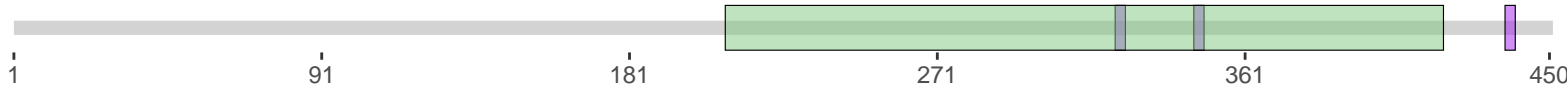


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

WILRTOYSIKTGPVVLGMYLNEVDESLTRPHYETOKKWLDSREIGSVVYVFGSLASLGGKQMEELALGLIMSNEYFLVWVRDTEENKLSNEFMKVKSEKGLTNNWSPQLDLVAHKSIVGFFTHCGDWNSTLEALSLGVPMVQMPQWADGPTNAKFFVDWVGVGRVREYVCKDGVVTRREEIASSEKEVMVDDKKGVMKKNNAKWLAEAAVDKVGGSDKNTEFVQAGNALN

NbL19g21430.1 pathogenesis-related_protein_STH-2-like [MW = 17.8 kDa]

No. of times detected



log(intensity)



Values from



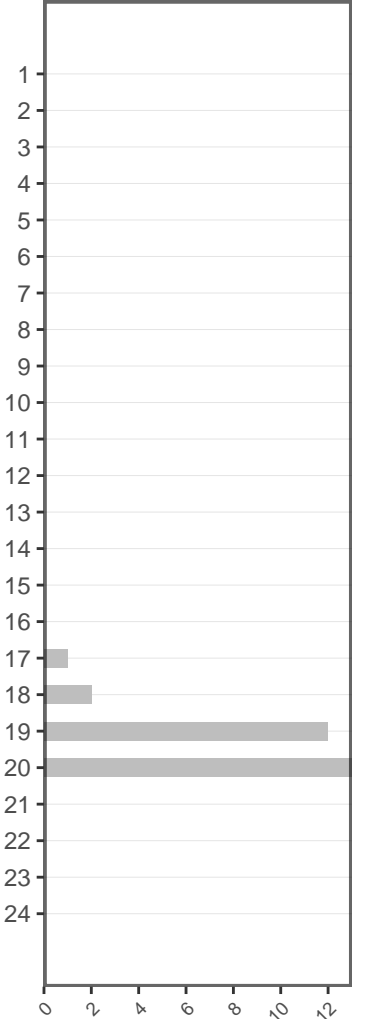
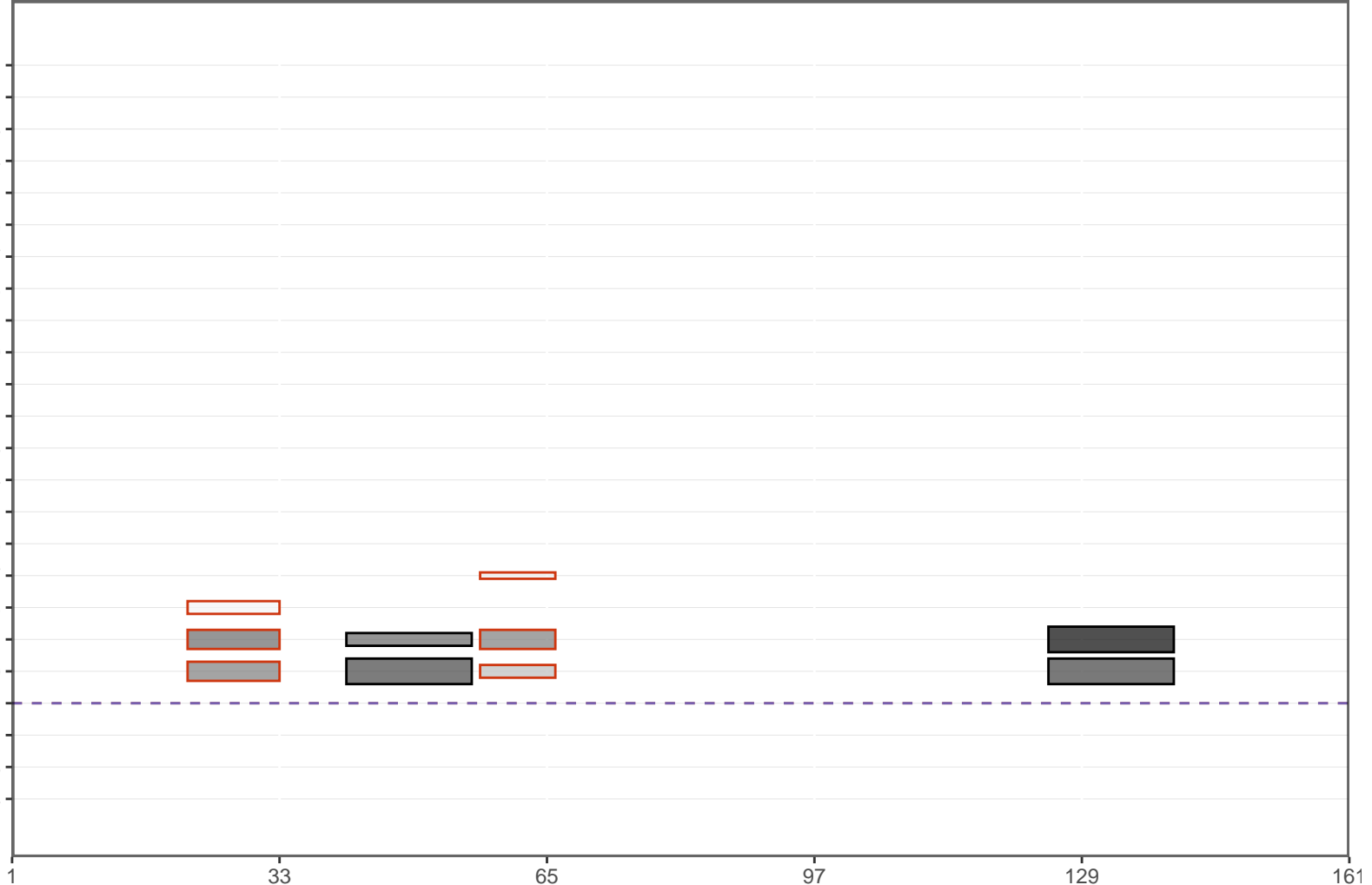
MW indication



Molecular weight



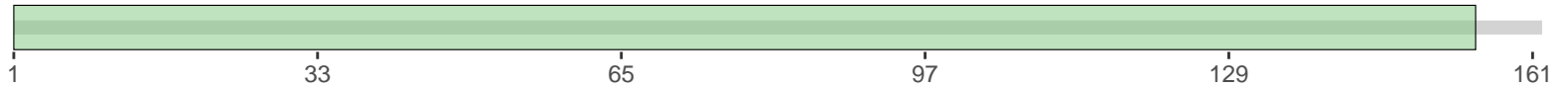
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

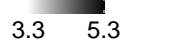
LDLKHVYDDKINAKYSLIEGEVLGENLEIVSWVDFEGSDNGGCKIKTSNHTKDDFVWKEEKEEKEKAVELFKAVEALLANPSSW

NbL19g21380.1 carboxyl-terminal-processing_peptidase_2_chloroplastic-like [MW = 59.91 kDa]

No. of times detected



log(intensity)



Values from



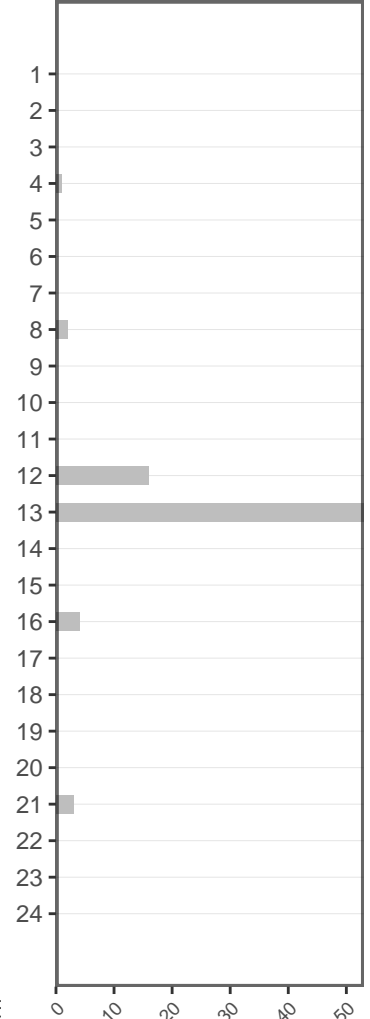
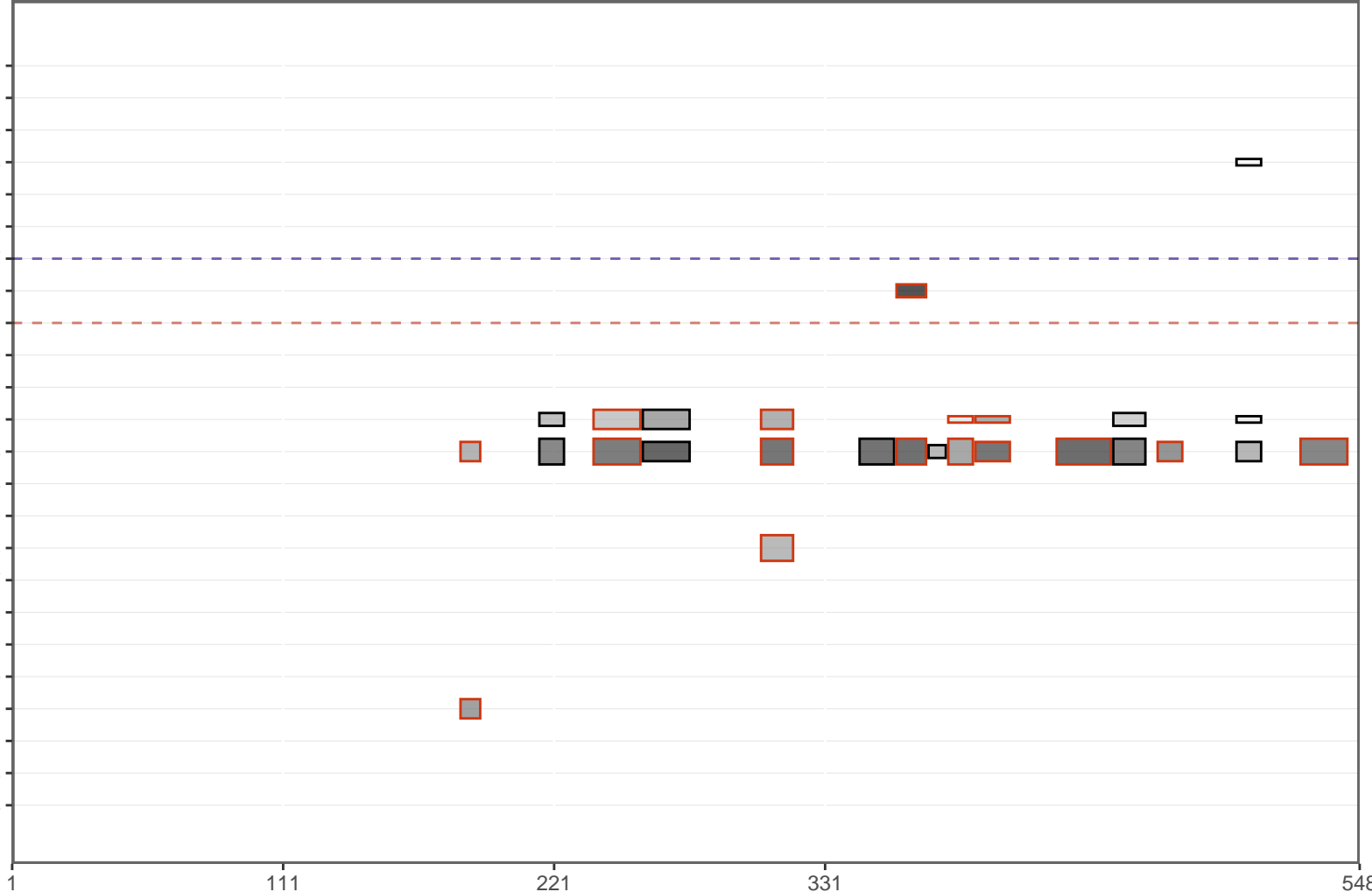
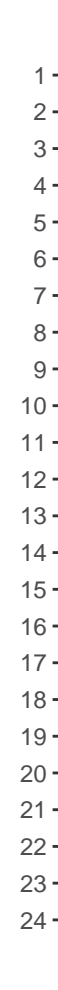
MW indication



Molecular weight

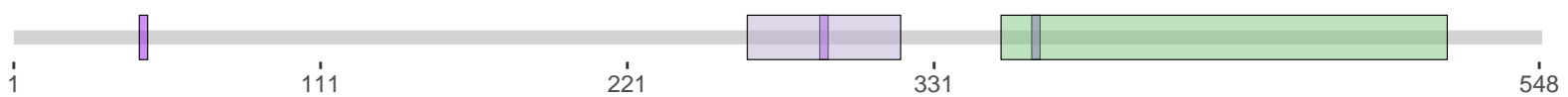


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IPGLVYVSAISPGQADRAIGSSGDHLEINSGTENMGYDAERLGGPEGSGVELTVRRGSETRNLPUREKVSINPVSRIKLPFTGGDDAPGQYKLGSTFNQNASGAKAEIALRKNVNAFVLDLRDNRNSGGLFPEGVEIKWLNKGVHYVIGDGRGRVDYDITDGSNVAASEPLAVLNKGTABASEILAGALKDNKRALIFGETYVGGKKGQGVFQLSDGSGGLAVTVARVETPMNDIKVGVFPHPLPASFPPKDDSEFQNLGNPASAGHNRVLF*

NbL19g21310.1 trans-resveratrol_di-O-methyltransferase-like [MW = 40.72 kDa]

No. of times detected



log(intensity)



Values from



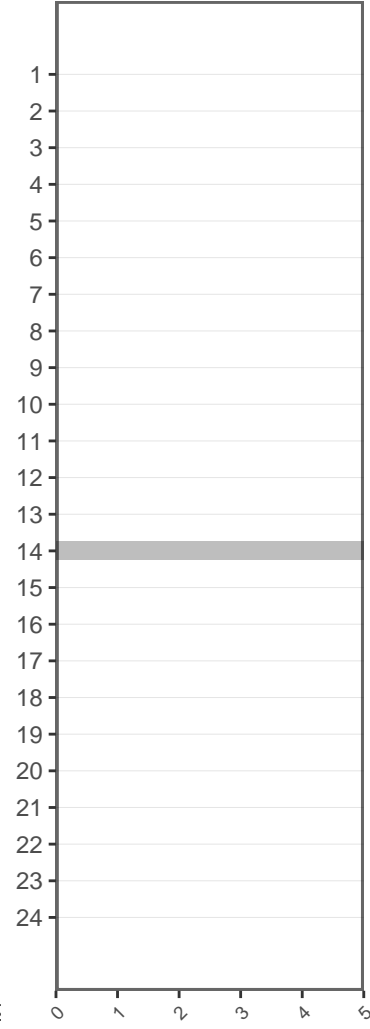
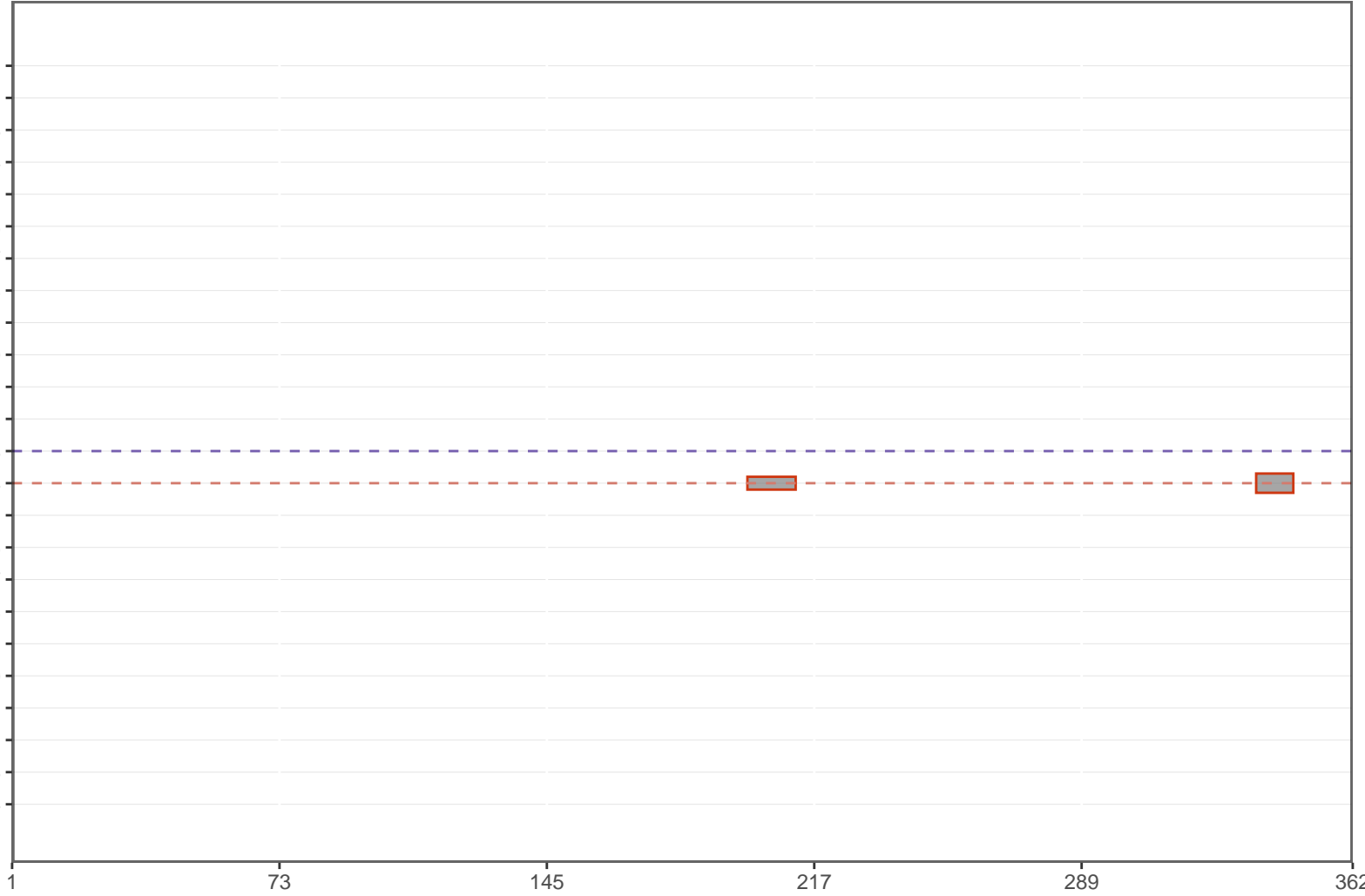
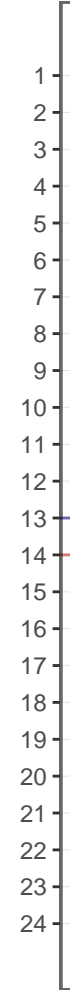
MW indication



Molecular weight

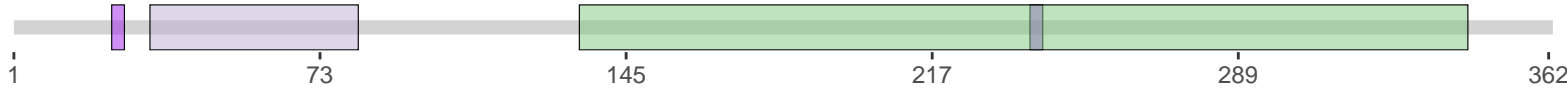


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NCLFNEAMASDARLHISMENKKEVEFGLKSLVDVGGGTGTAKAIAAFPKTNGVFDLPHVIEDCEGRKRLSYVGGDMFKSPADAVLLKWLHDWNEEGIQHLKKEKKAIPSKENGGKVLIDMLDKKEKGDHKFETQLFVDMMLMAMFNSGKERTGGDWANLSTAGFSQKIPVLLGLRRIEIVPI

NbL19g21260.1 transcription_factor_MYB1R1 [MW = 40.48 kDa]

No. of times detected



log(intensity)



Values from



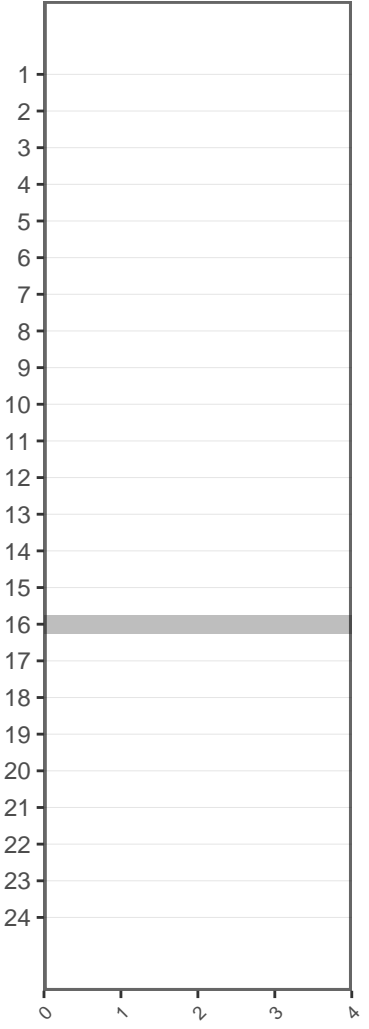
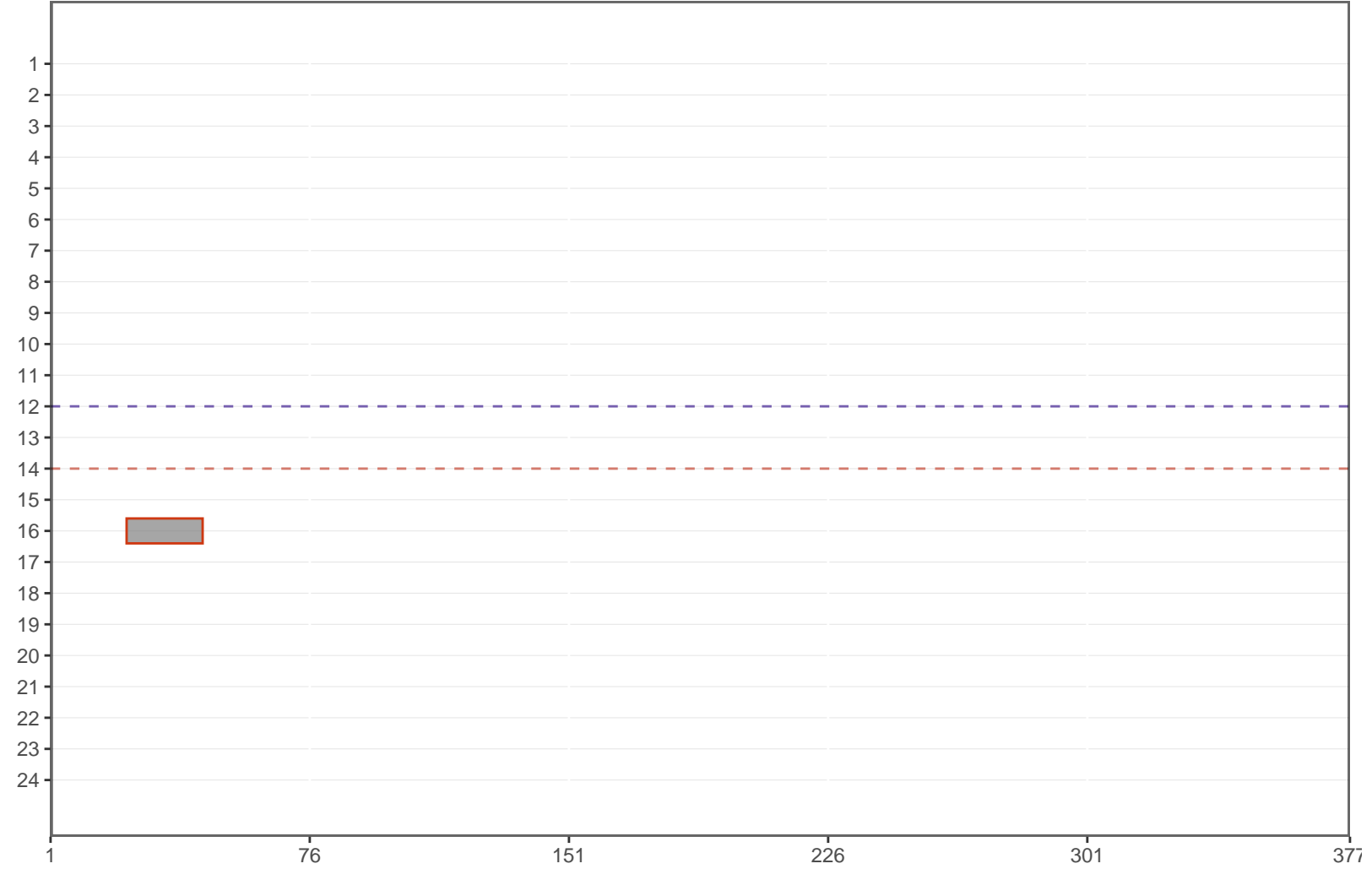
MW indication



Molecular weight



Gel Slice



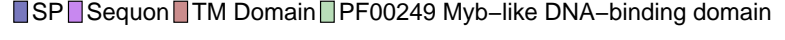
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ITRRKRSSLDIVADTGTDAHPLSEEGFALPPRAIESDKEHLAPATKAESGDFADLPGLDLKLSGDFESMETTASEPVEETKLNITTTDEIPSVYPAFFRWIPVYVSWPNSNAVVPVEDRGGSEPSHHQDKRPIPTVYKPEPVNDELVGMGSLTADAGGGHIEPSLSLKLTAEPVRGSAFHASTPTVKNREITKGETAIPGVV

NbL19g21240.1 NADP-dependent_malic_enzyme_chloroplastic-like [MW = 70.51 kDa]

No. of times detected



log(intensity)



Values from



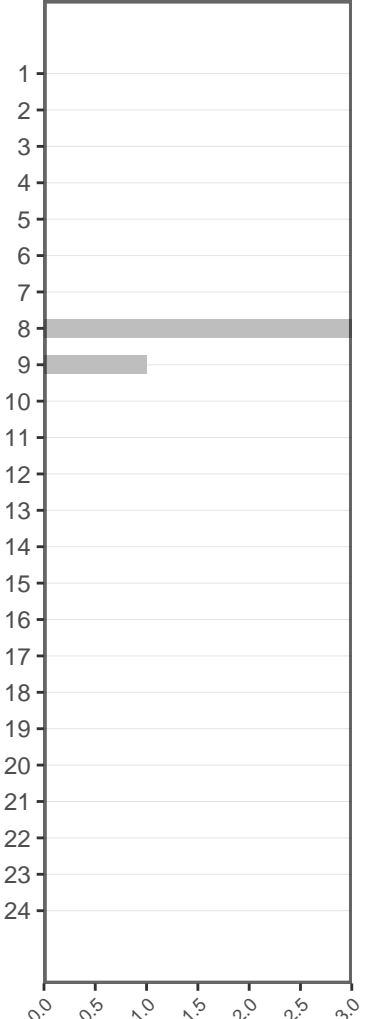
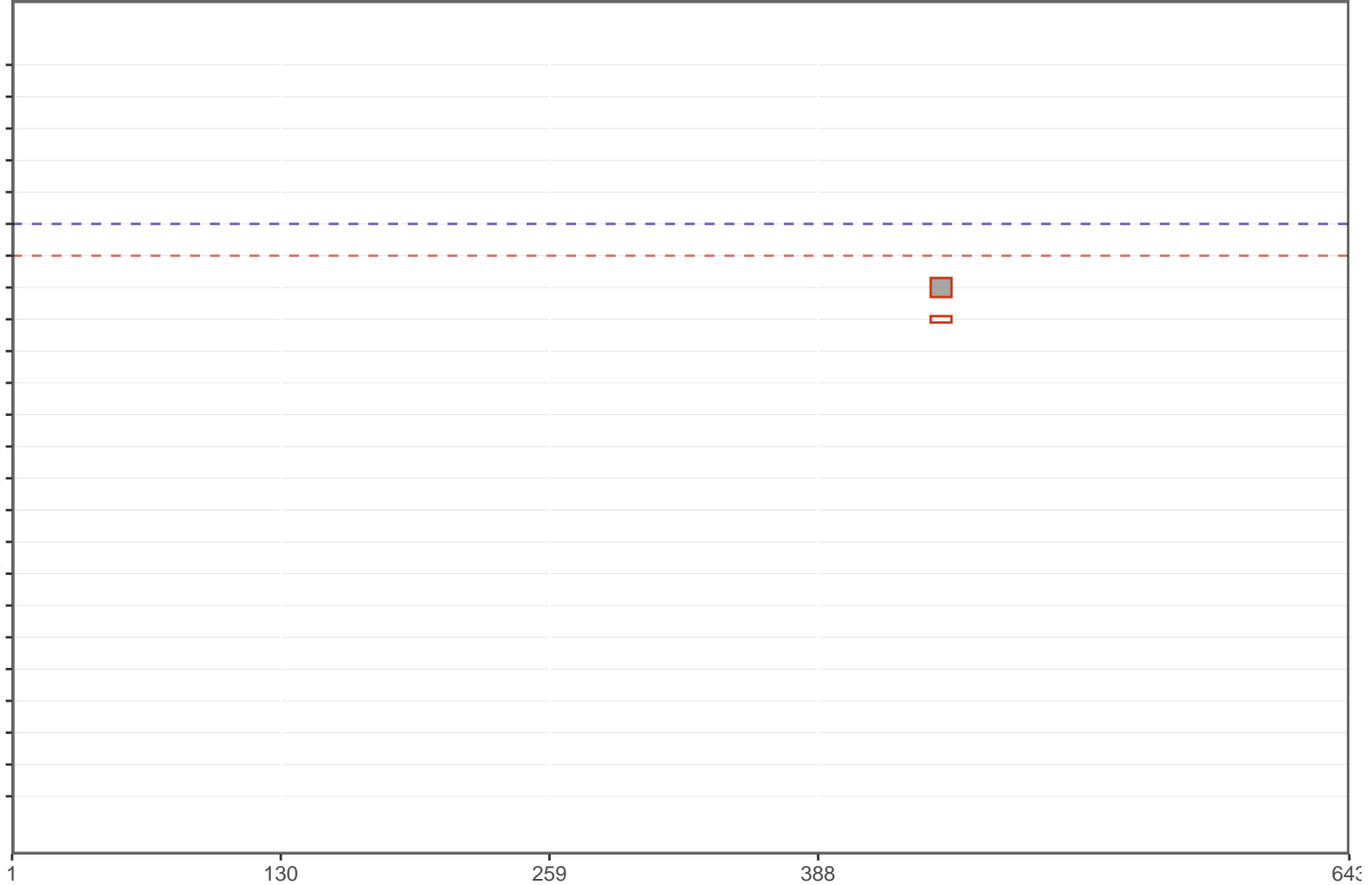
MW indication



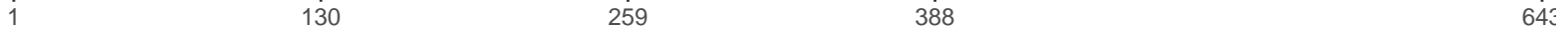
Molecular weight



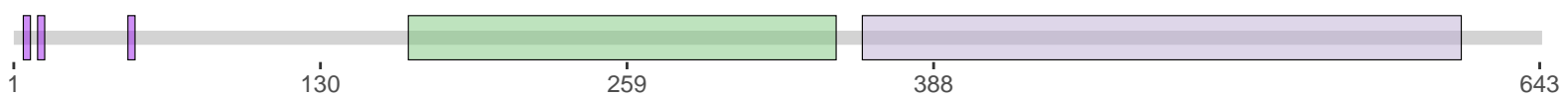
Gel Slice



Protein length

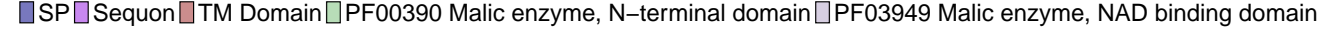


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RGKEYAELFDEFMNAKGNVYGEVLGDFDFANHFADLLAKYGTSHLNFNDIDIGTAVVLAGLMAISLGLVSGTAEHTFLFLGAGEAGTGAELIALEMKGDTGIFLEETRKKIWMLDKGLVFNRMESLQHFKRPAWAEHEPEVKELVNAVKBIKPTVLGSSGAGRFTTKEVGVQVMAFNEKPIIFALSNPTSSQSEGTAEAEANTWSEGRAIFABGSGFPAPVEYNGKQVYASGGANNAYVFPDGLGIIISGARVHDDMLLAASEALAEQVSGENFEKGLYPPFTNIRKISANA

NbL19g21140.1 aquaporin_TIP2-1-like [MW = 24.99 kDa]

No. of times detected



log(intensity)



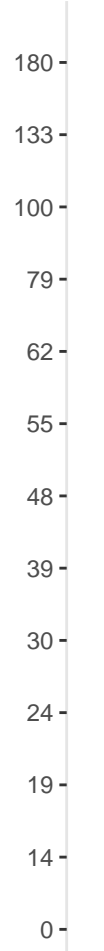
Values from



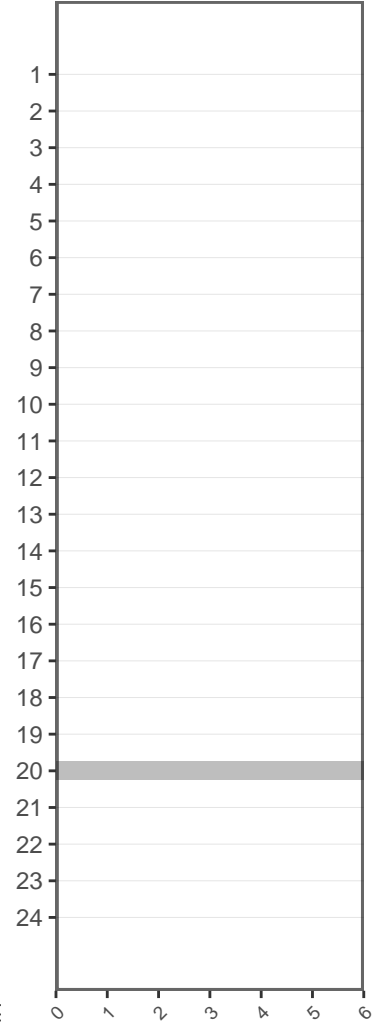
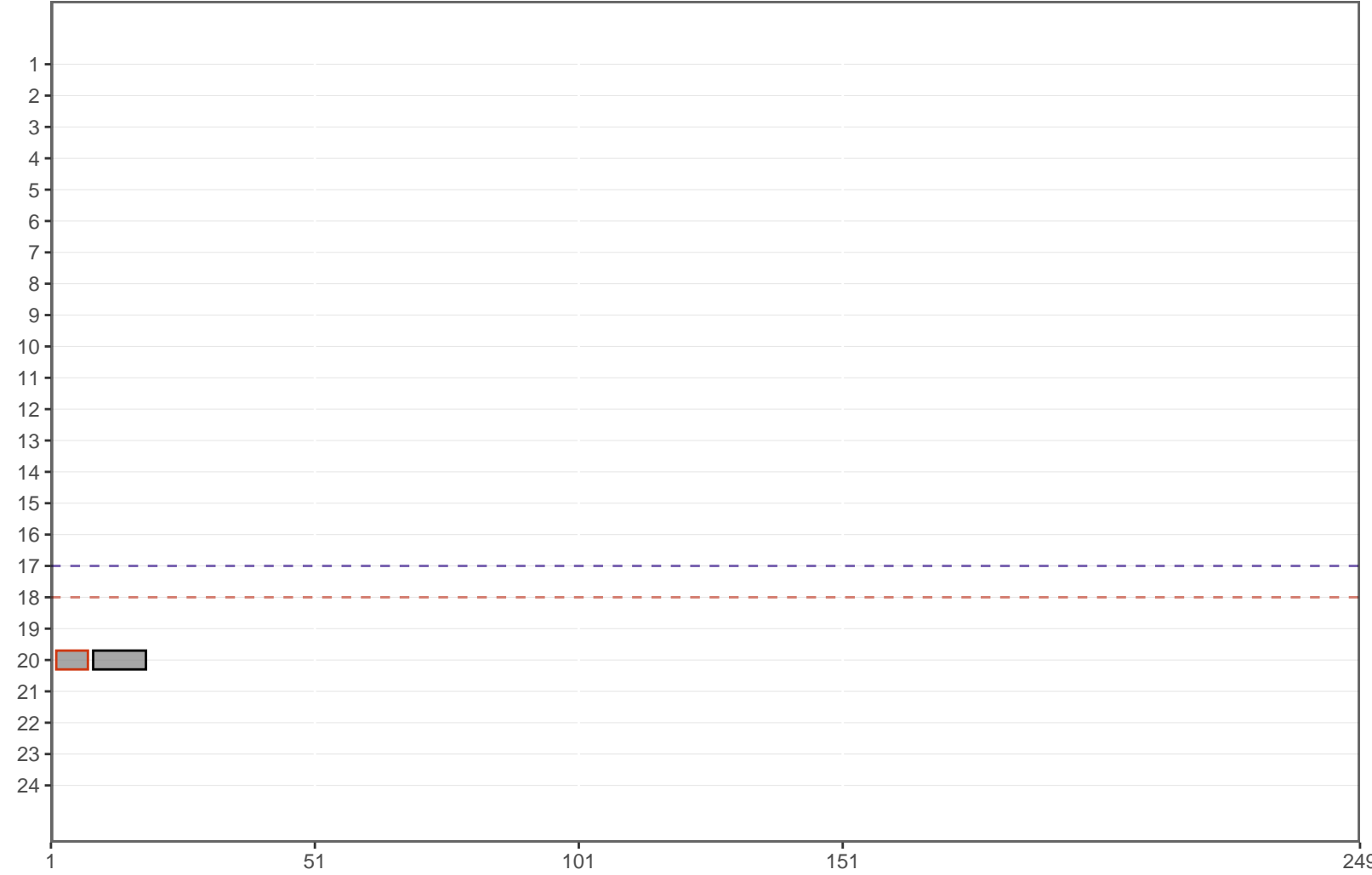
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ITAASTLLKLVVTTGGGLAVPIHSDVAAGVGAEEGVVMEHTFALVYVYVTAADPKKGLGTIPAIAGFVGSANLAAAGPFGGSEMNPARSFGPVAASGNFAGHWYVWVGLVGGGLAGLIVSNVFMNDEHAPLSTEF

NbL19g21130.1 alpha-glucan_phosphorylase_H_isozyme [MW = 80.92 kDa]

No. of times detected



log(intensity)



Values from



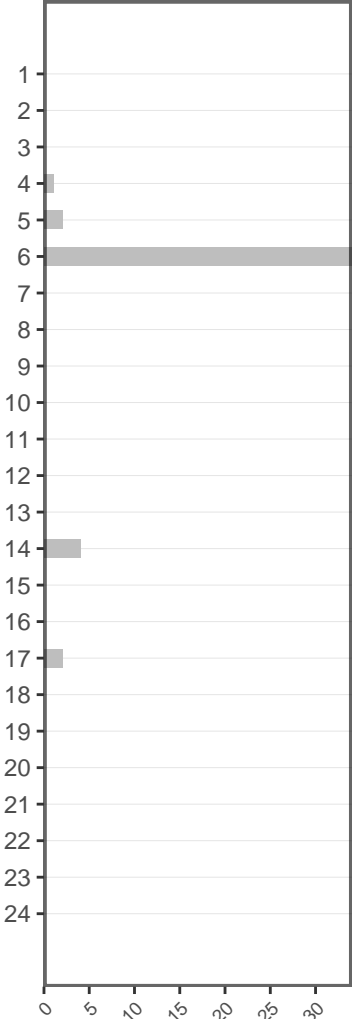
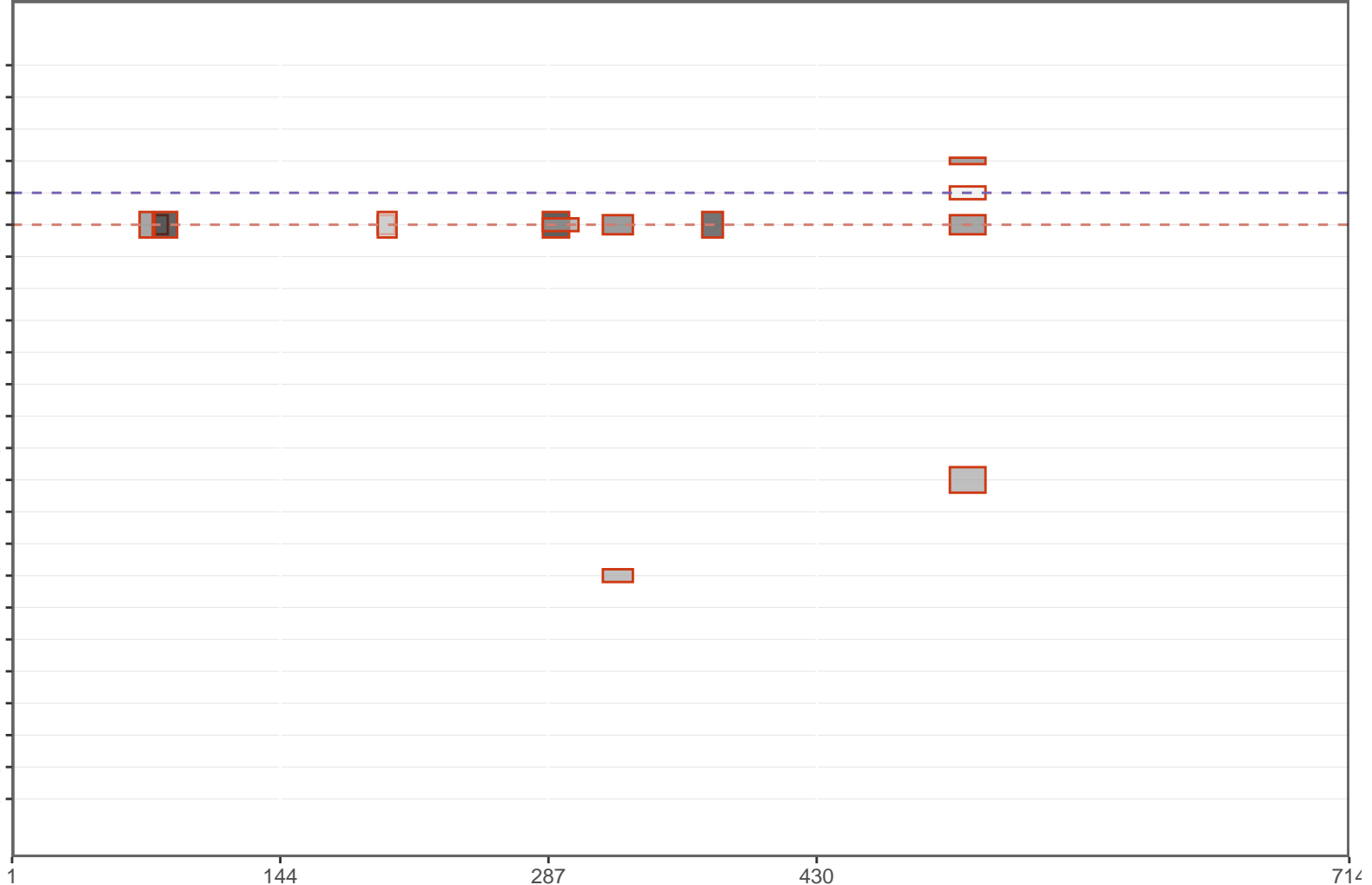
MW indication



Molecular weight

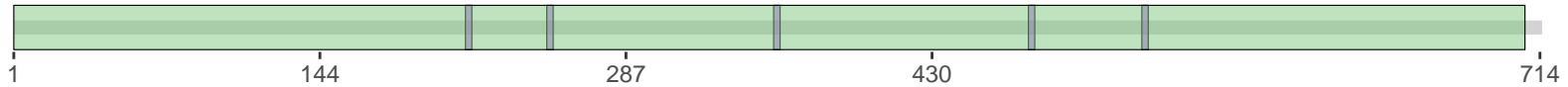


Gel Slice



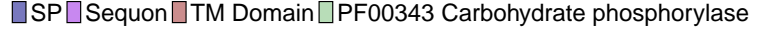
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

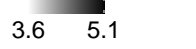
LFADYVSWPTKFGKNTNGTFRRWIRFDSPELBNITKWLKTDQWVTLNLELLANREFADNAELHAEWESAKMANKRLADYVLRVTGVSDPDLFDQVKRIHEYKRLNVLGVYRYKLLKEMSPQERINNTFRVTMIGGKAFATYTNAKRIVLVDVGDHNSDPPNHYLKMVFPVNYVSVAEMLFGQSEISQIHSTAGMEASGTENMKFALNGSLKGLDGANVEIREEIGEENFFLFGATADEVPRLRKEREDGLKPKDPRFEEAKGFRISGAFGTIDYVNPLES

NbL19g21110.1 neutral_ceramidase-like [MW - SP = 81.65 kDa]

No. of times detected



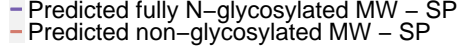
log(intensity)



Values from

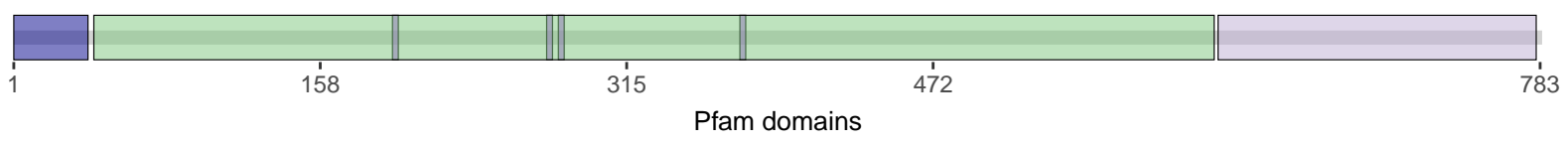
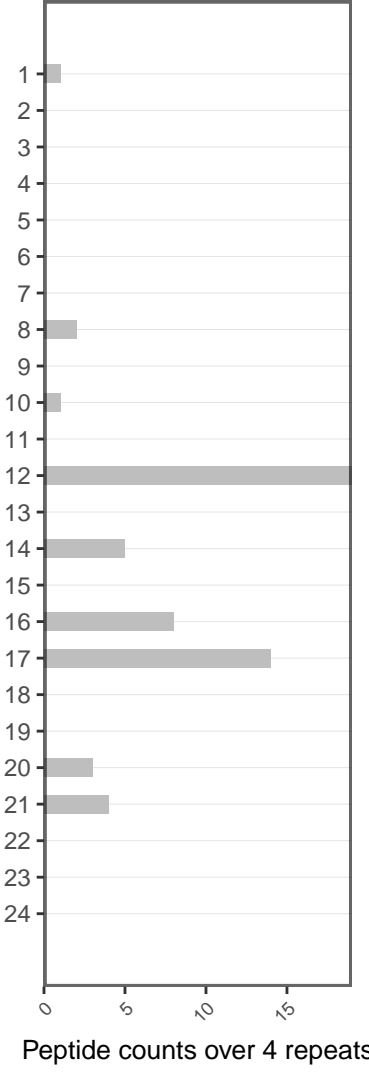
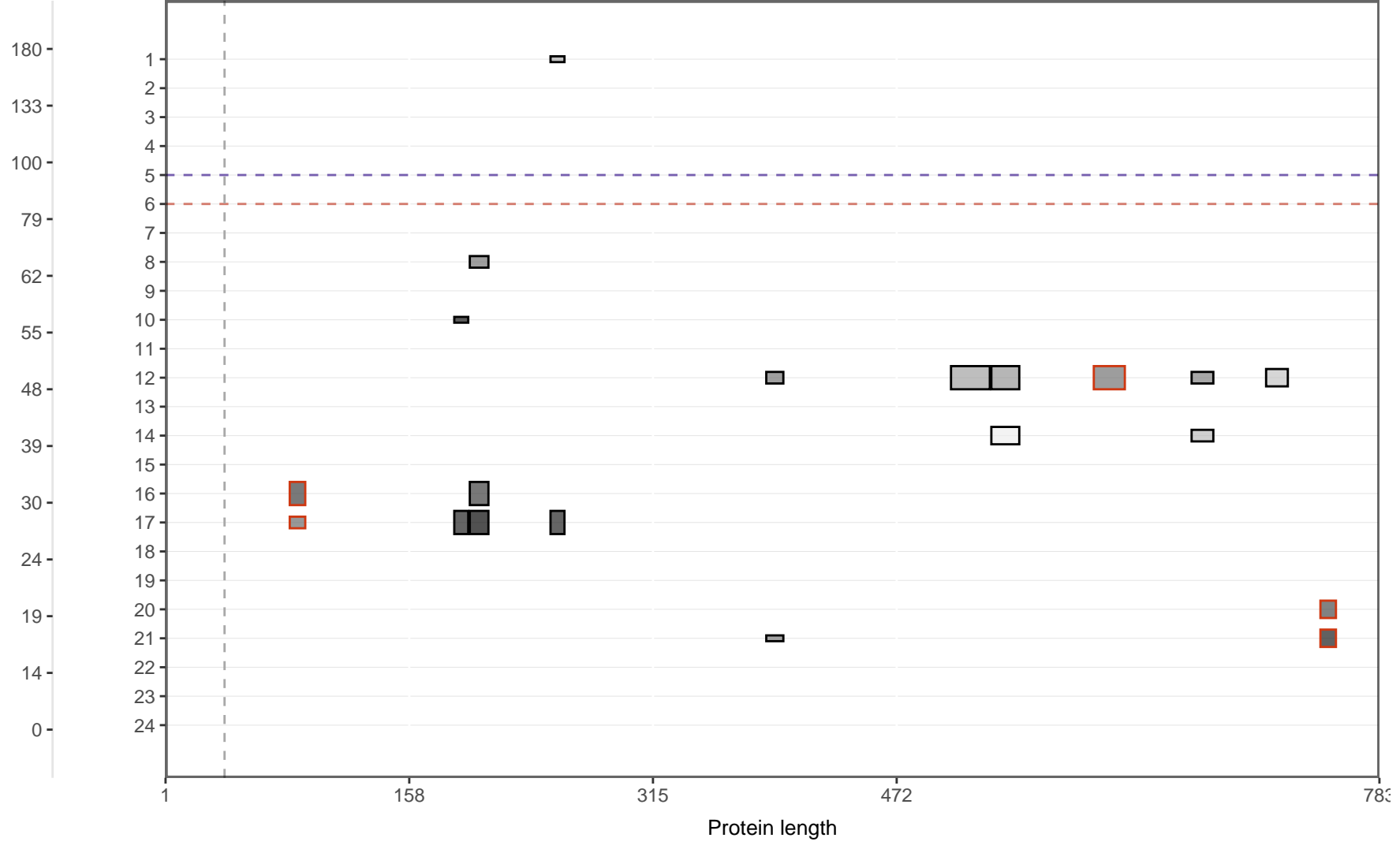


MW indication



Molecular weight

Gel Slice



Pfam Description

- SP Sequon TM Domain PF04734 Neutral/alkaline non-lysosomal ceramidase, N-terminal PF17048 Neutral/alkaline non-lysosomal ceramidase, C-terminal

Protein sequence:

CGGKNELCYGRGPGYDFEFSTRIGERQFKKAVELFNKATEGVKGKVDFRHFTYVDFSNLEVTIPKEGAGETAKTQPAAMGFAPAAAGTTDGGAFDFGQDQKGVFVRLVRLNLRKPKGSEQKQDHPKILLDTGEMKEPYDWPASLPLVQILRIGQLVLEVPGEFSTMGARRLRDAVMMVLTSGGTFKDFDSNHVAAGLNTYVSGVYTFTEEVQIQRYEGASTLYGRHTLGGYQGFRTAAALFTGGTLGAGPQPPNLLGKQGLLPPVMDATPLGSKFGDLTDTVPQI

NbL19g21070.1 50S_ribosomal_protein_L4_chloroplastic [MW = 30.86 kDa]

No. of times detected



log(intensity)



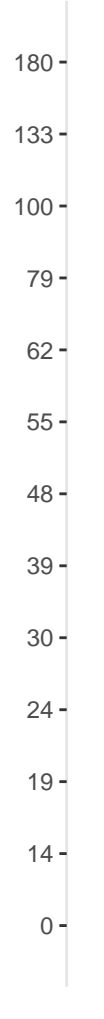
Values from



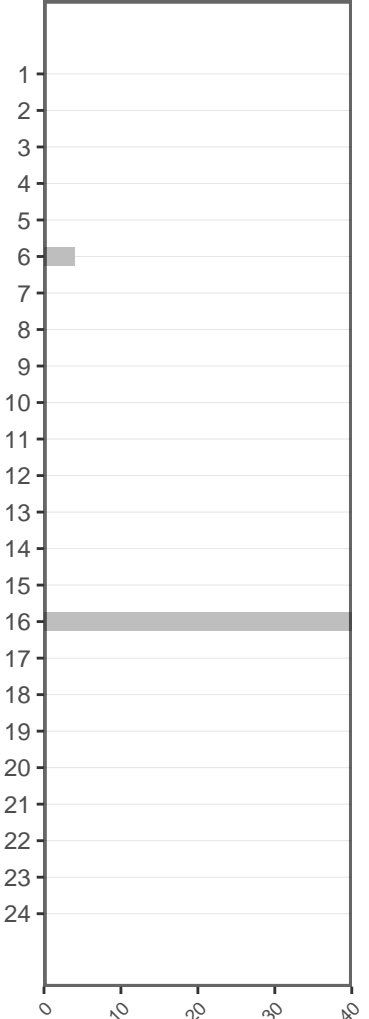
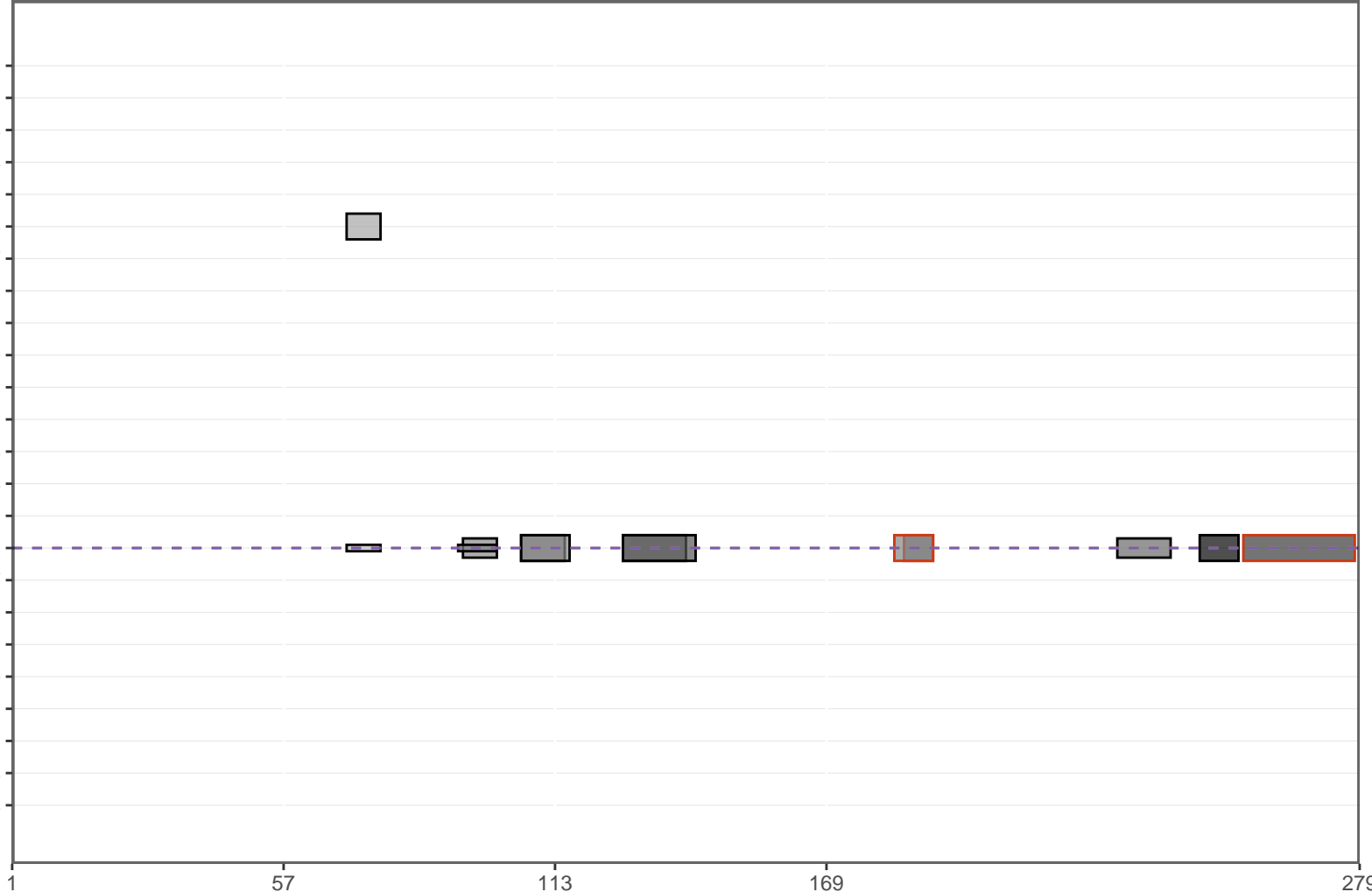
MW indication



Molecular weight



Gel Slice

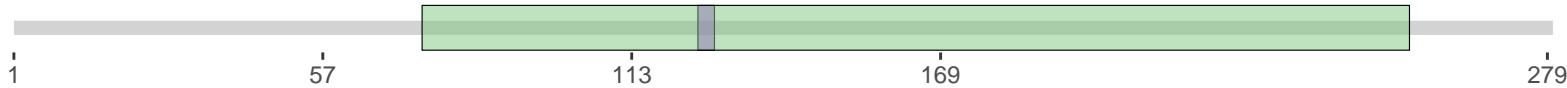


Peptide counts over 4 repeats

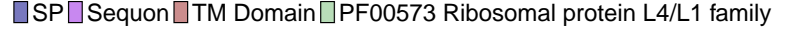
Protein length



Pfam domains



Pfam Description



Protein sequence:

PLRPGGGVVFQPKKDWVWIKNKKEKRLAISTALSSASENTWVEEFNDKFEKPKTKFIDLMRRRWGLDPKESLFLMTEVSDNVLSSRNIGTLKMTPTLNLFDLDEKVLTKSAVDFLNERYGDENEWEEDEKDDGDDGDDGGGR

NbL19g20980.1 probable_aquaporin_PIP-type_pTOM75 [MW = 30.83 kDa]

No. of times detected



log(intensity)



Values from



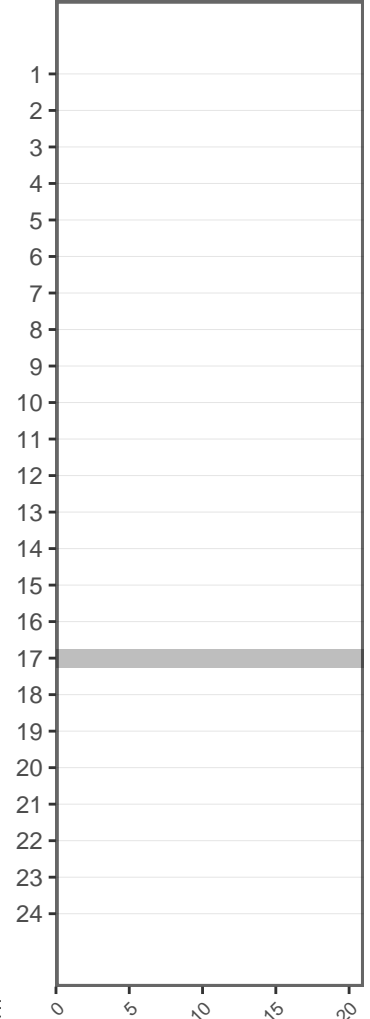
MW indication



Molecular weight



Gel Slice

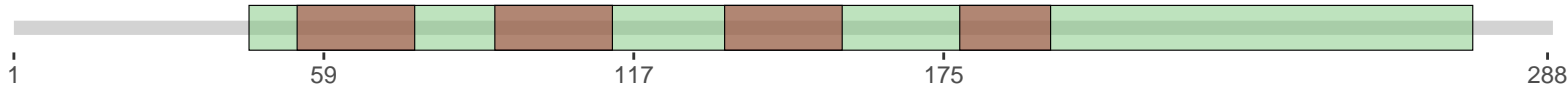


Protein length



Peptide counts over 4 repeats

Pfam domains



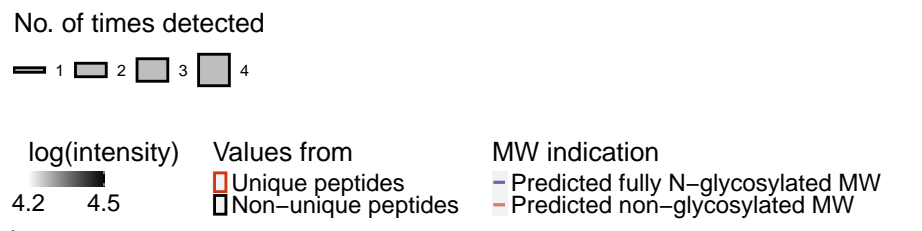
Pfam Description



Protein sequence:

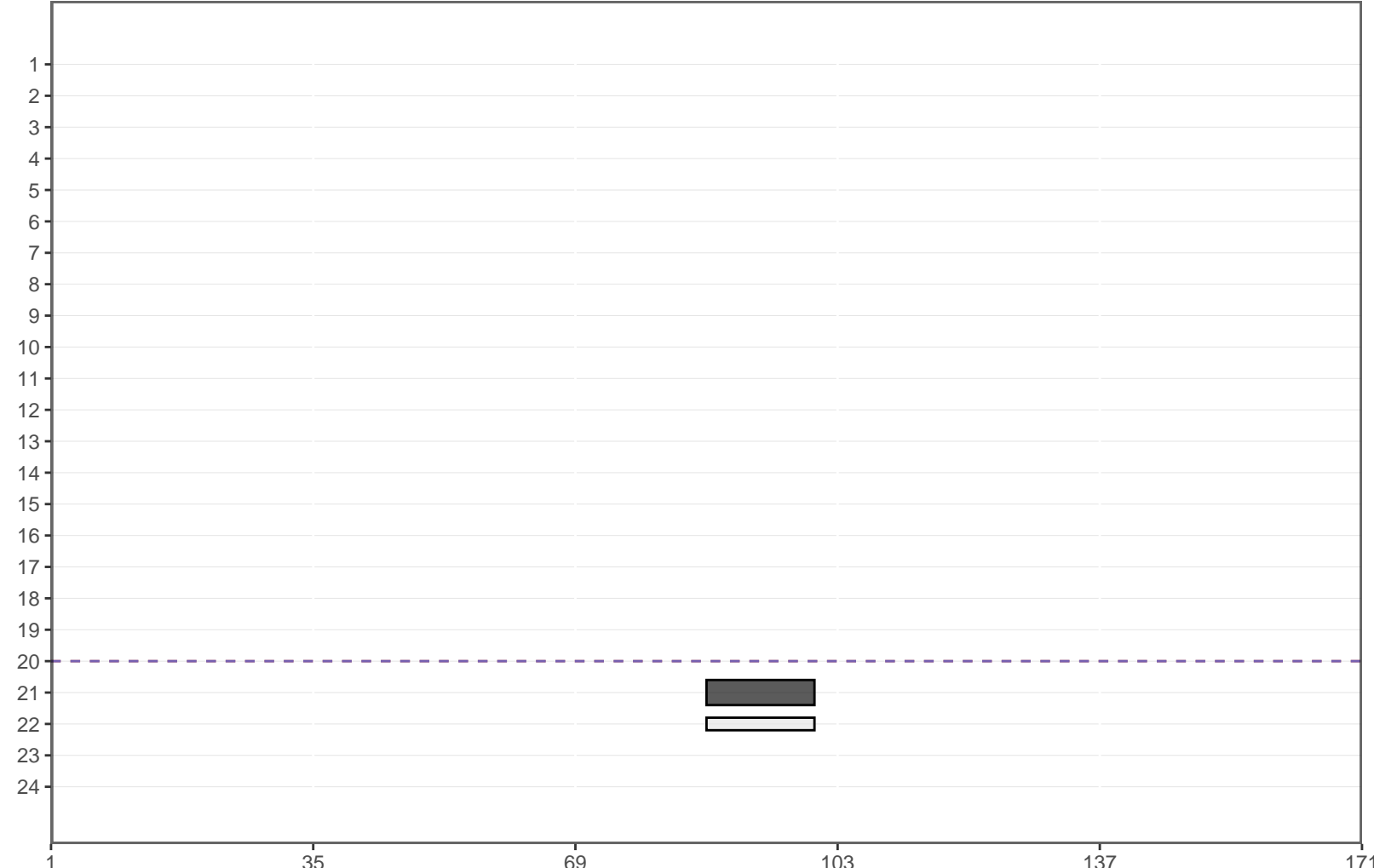
ITRALFYIMVQCLGACGGVYKGFVSPYGRLLGGGANVYVPGYTKGDDLGAIEIGTFVLYVYTFEATDAKRNARDSHVPLAFPLPGFAVFLVHLATIRFTGTGIFNPARSLGAIIFNHDQAWDDHWIFWVSPFPGAALAAVYHQIRAFPFKTS

NbL19g20910.1 putative_cytochrome_c_oxidase_subunit_5b-like [MW = 18.76 kDa]



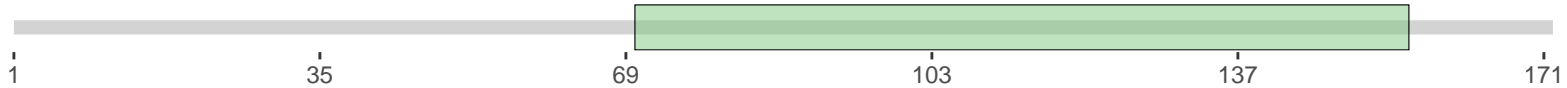
Molecular weight

Gel Slice

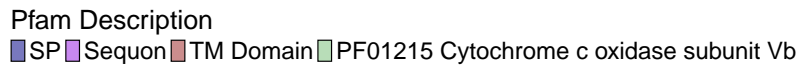


Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:

EELEAELOGRELLDNFPEGPFGTKEAPVVKSYDRIIRVGGCGGEGEDEHDVWVWLEKGGKPKFCVCGGQYFELEVVGPGGPPDGHGSDDEGHV

NbL19g20880.1 uncharacterized_LOC109242909 [MW = 37.21 kDa]

No. of times detected



log(intensity)



Values from



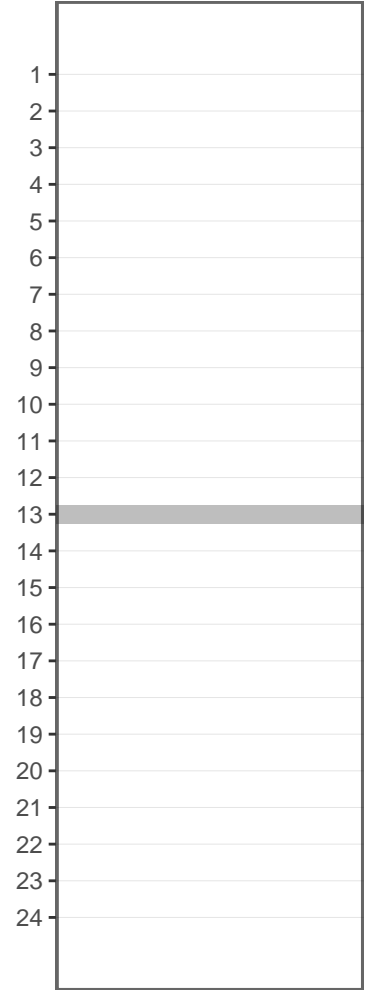
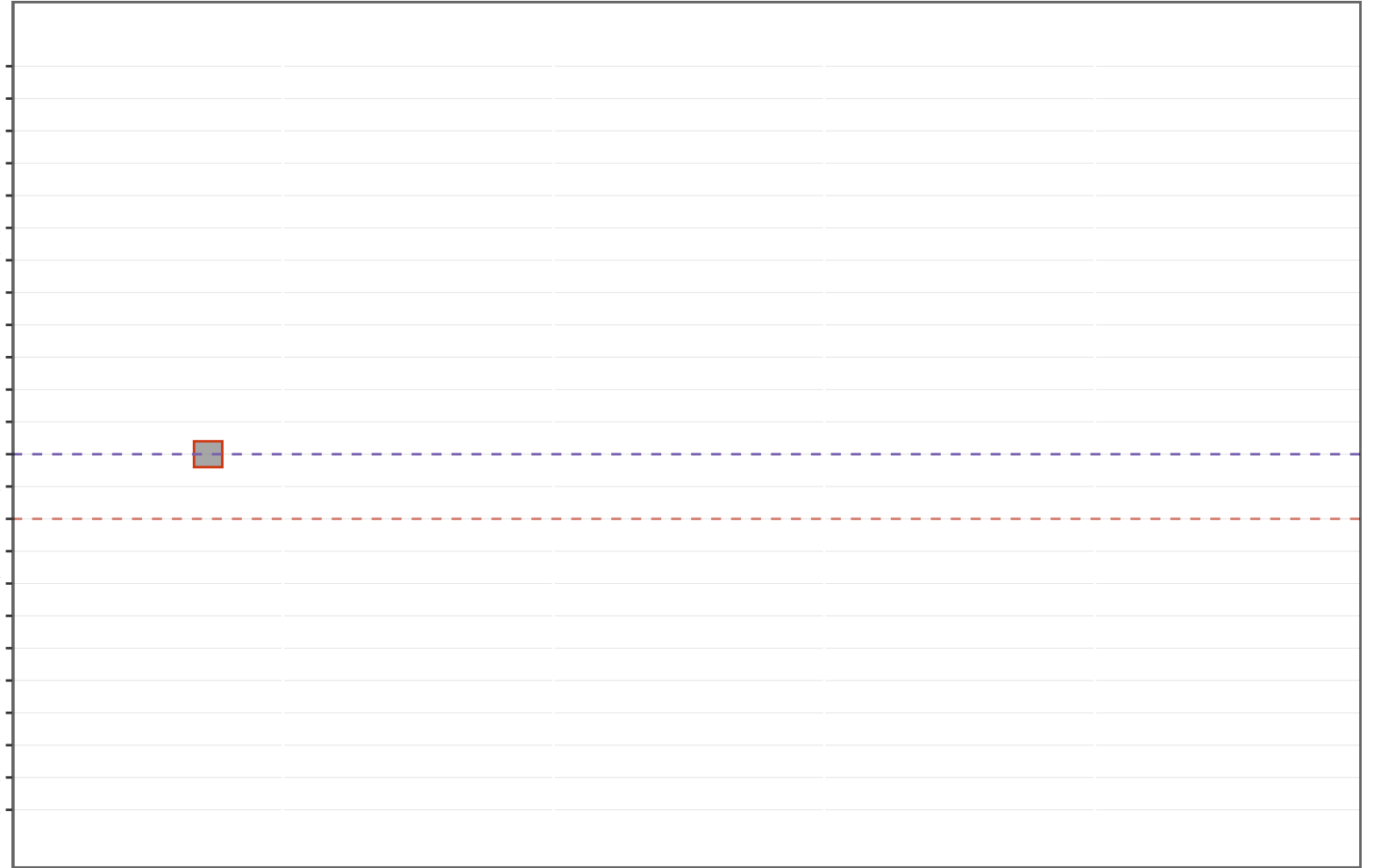
MW indication



Molecular weight



Gel Slice

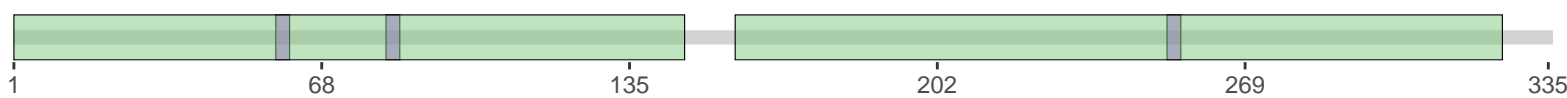


Protein length

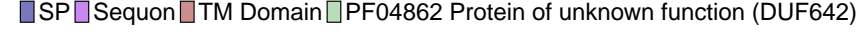


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IRPKGNMLKNGNFEEGPVPFPNTNAGLIPFPNEDDHCFPLPGWIEELKAWKVVDAEHFVPEGKRAVELVAGRESAAGEVTKAGKYDLFSGDANNSCGEGSMLEAFAGKVALGVPMKGGKGGKRAKRLFTAISRRTRVRFLESTNYHMKGNQSSSLGSPVDDVRLVSVRNPRIIP

NbL19g20830.1 coatomer_subunit_beta'-2-like [MW = 103.36 kDa]

No. of times detected



log(intensity)



Values from



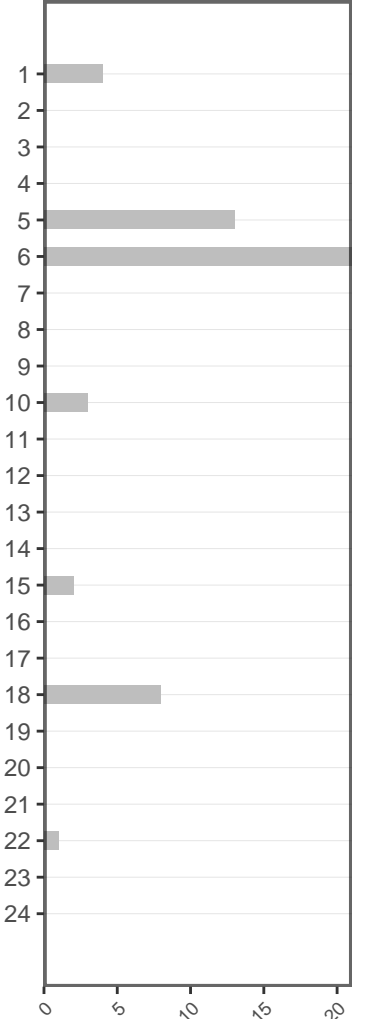
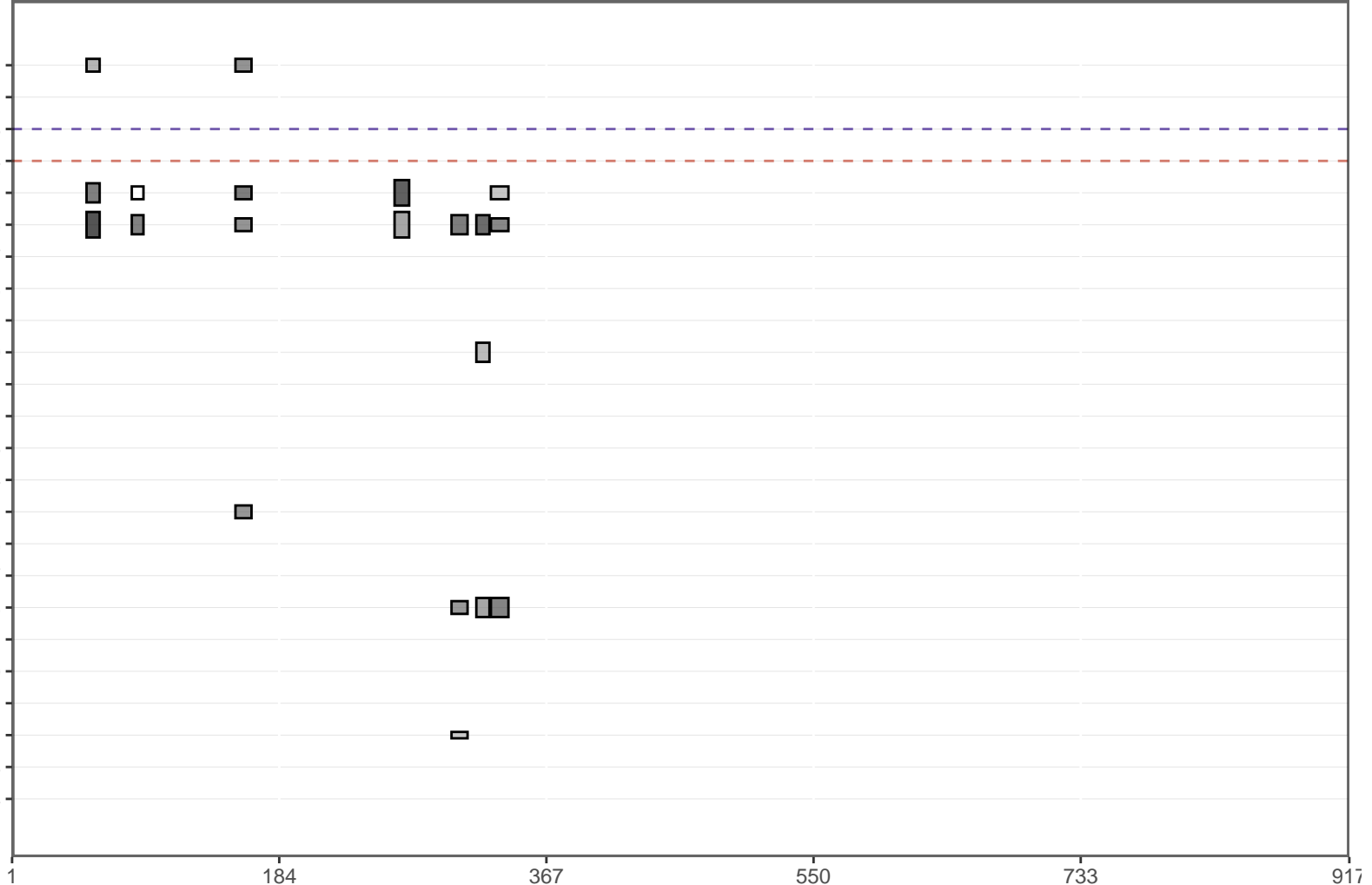
MW indication



Molecular weight

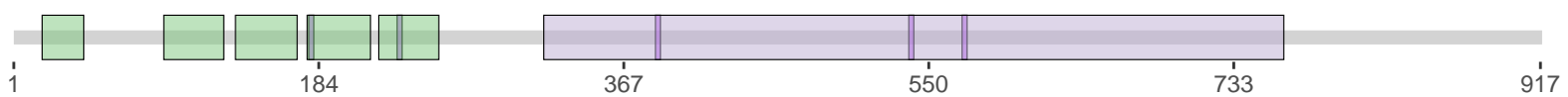


Gel Slice



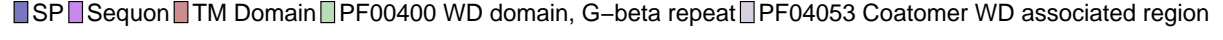
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DFICFYDWAQCRLRRIDVWVKNLYWADSGDLWIAADAGFYLYKYNRQVVAHFDGSRGVDGQGVVEAFELLNEINERVIRTGWVGDGFYVNSWRLNLYVGGVEVTFMFLDRPMLLGLVLANGSRVFLIDKEFNYYGYTLLGLIEYKTLMRGQWDRANEVLPSPRKEHNSVAFLEGRGMIEEALVATLDYRFELAQGLGKLDIAKEIAVWAGSEGWKQLGDLAMSSGRLETAEECLKHANDLSGLLLLYSGLGDAEGITELASFAKEHGKNNVFLCMFLFGKVD

NbL19g20750.1 heat_shock_70_kDa_protein_15-like [MW = 94.36 kDa]

No. of times detected



log(intensity)



Values from



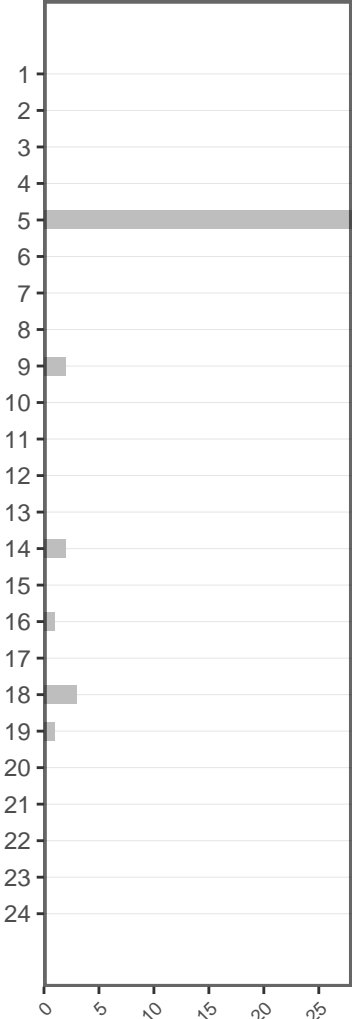
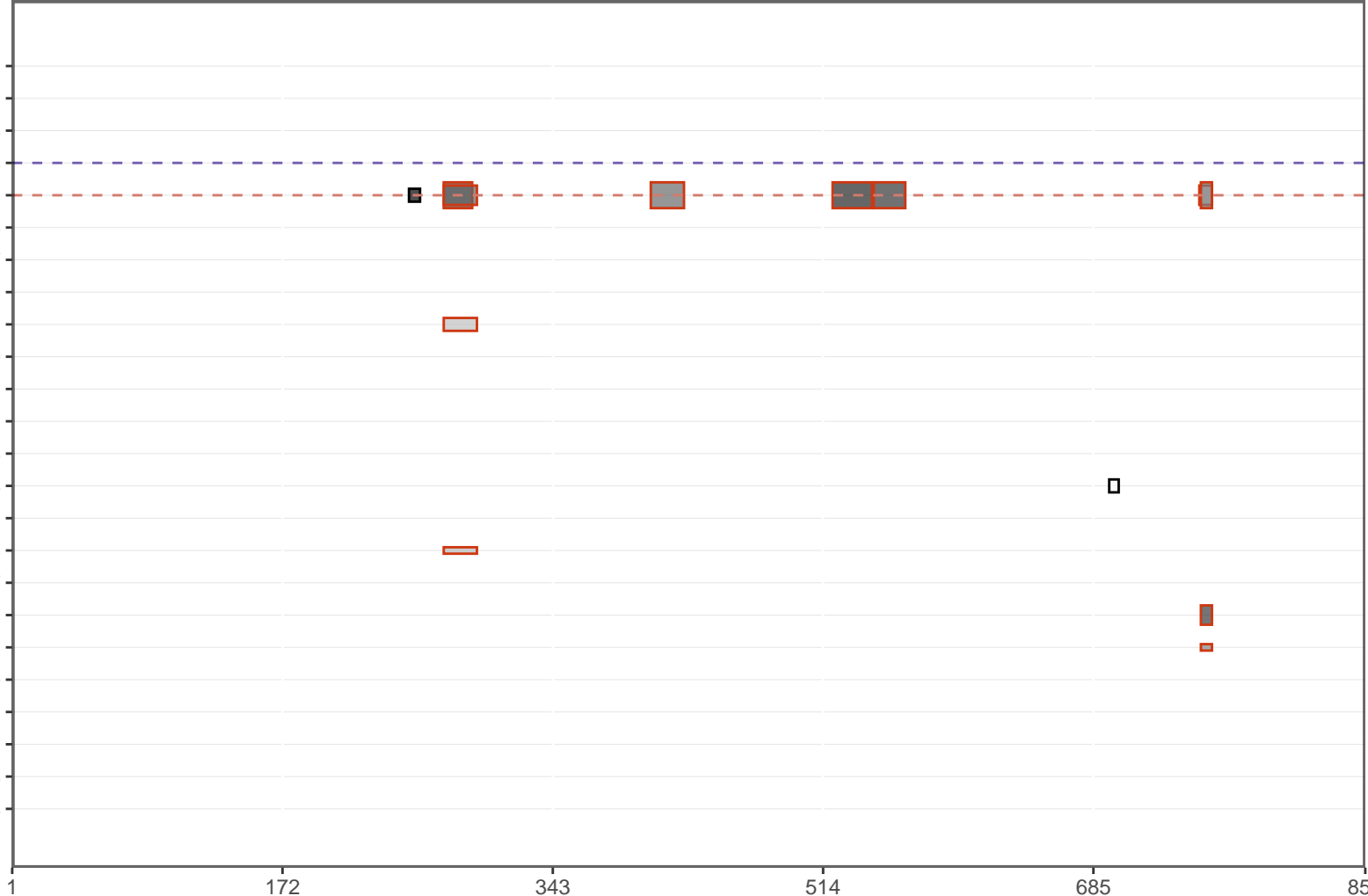
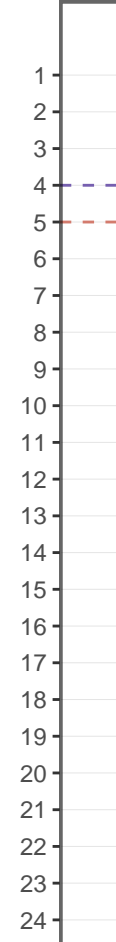
MW indication



Molecular weight

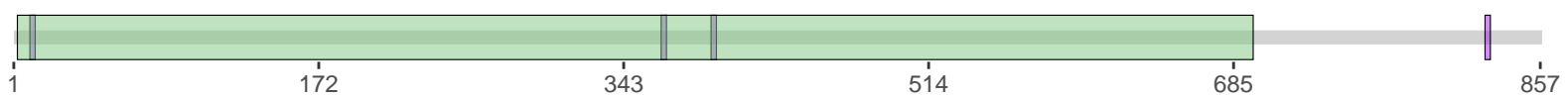


Gel Slice



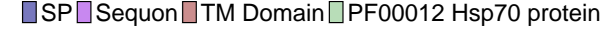
Protein length

Peptide counts over 4 repeats



Pfam domains

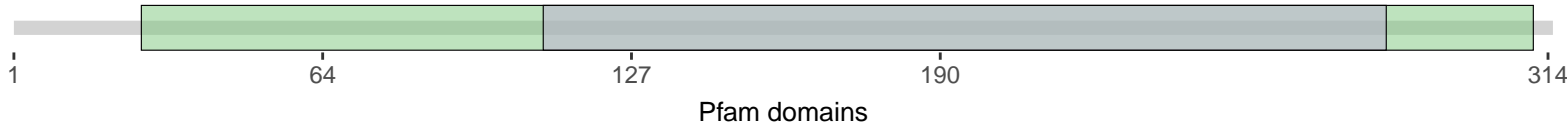
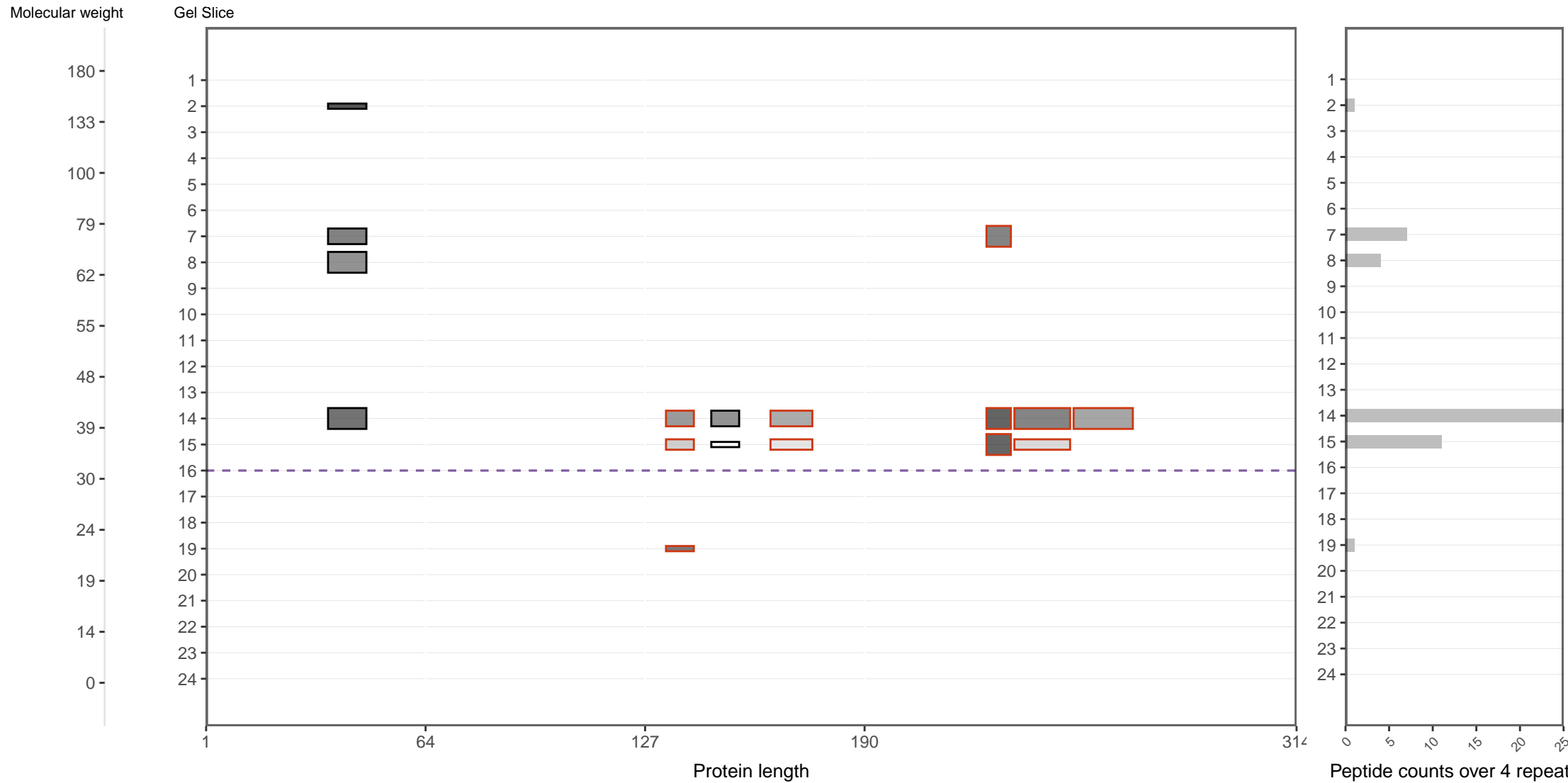
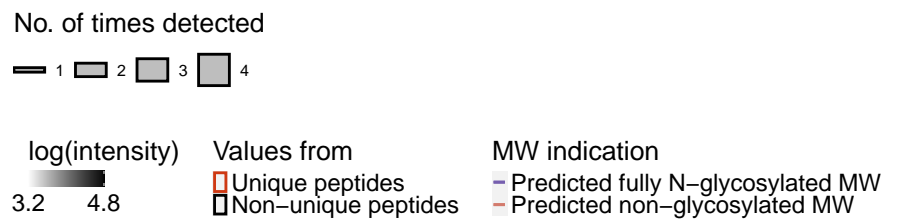
Pfam Description



Protein sequence:

TVFPKGNPPSVKALTYRSGTFTIDVQAVSDELGAPPKIGTYTIGPQSAKGERAKLKVARLNKLVGVVSDATLLEEEVEVPPVREAVKPKMEMDEASGDAHHTTSESDVNDGDAKAGDAAGSANGVPESSGDKPKVMETDAKVGTTKKVVKTSVPLTEVYGAMAADVQKAVKEFEMALGDRVMEETKDKKNVAVVYDMRNKLSDKYGEFVDSEREGFVAALGEVEDWLYEDGEDETKGVYHKLEELKGGDPIEGRYKRYTERGQSVYDQFYCA

NbL19g20710.1 hydroxyphenylpyruvate_reductase-like [MW = 34.11 kDa]



Pfam Description

- SP Sequon
- TM Domain
- PF00389 D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain
- PF02826 D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain

Protein sequence:

FSGKLVGIQLGRIGSAIAKRAEAFGFCFVYHSRBRKPNINIKYGNVVDLAENSELWAGALTEETQGHVNRKVALDALGPKGLINGRGAHVDESELVAHIEGRIGGAGLEVYQTEPEVPERFFGLENVLLLSHAASDVTETGTSMDLVVANLEAHLQKPLTPVLI

NbL19g20690.1 malonate--CoA_ligase-like [MW = 67.75 kDa]

No. of times detected



log(intensity)



Values from



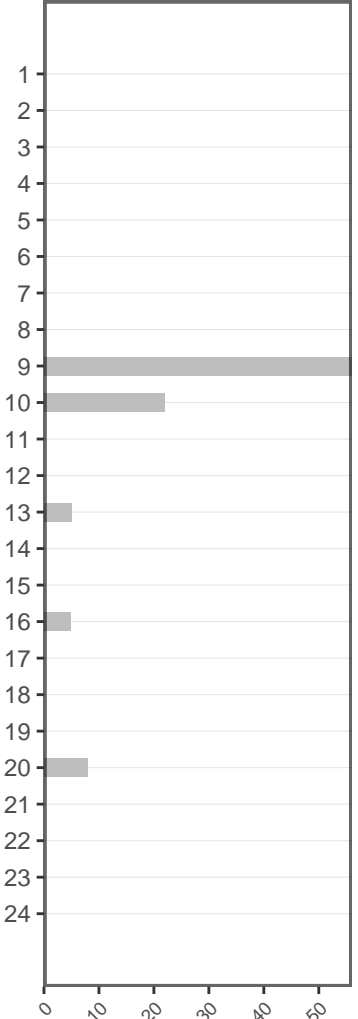
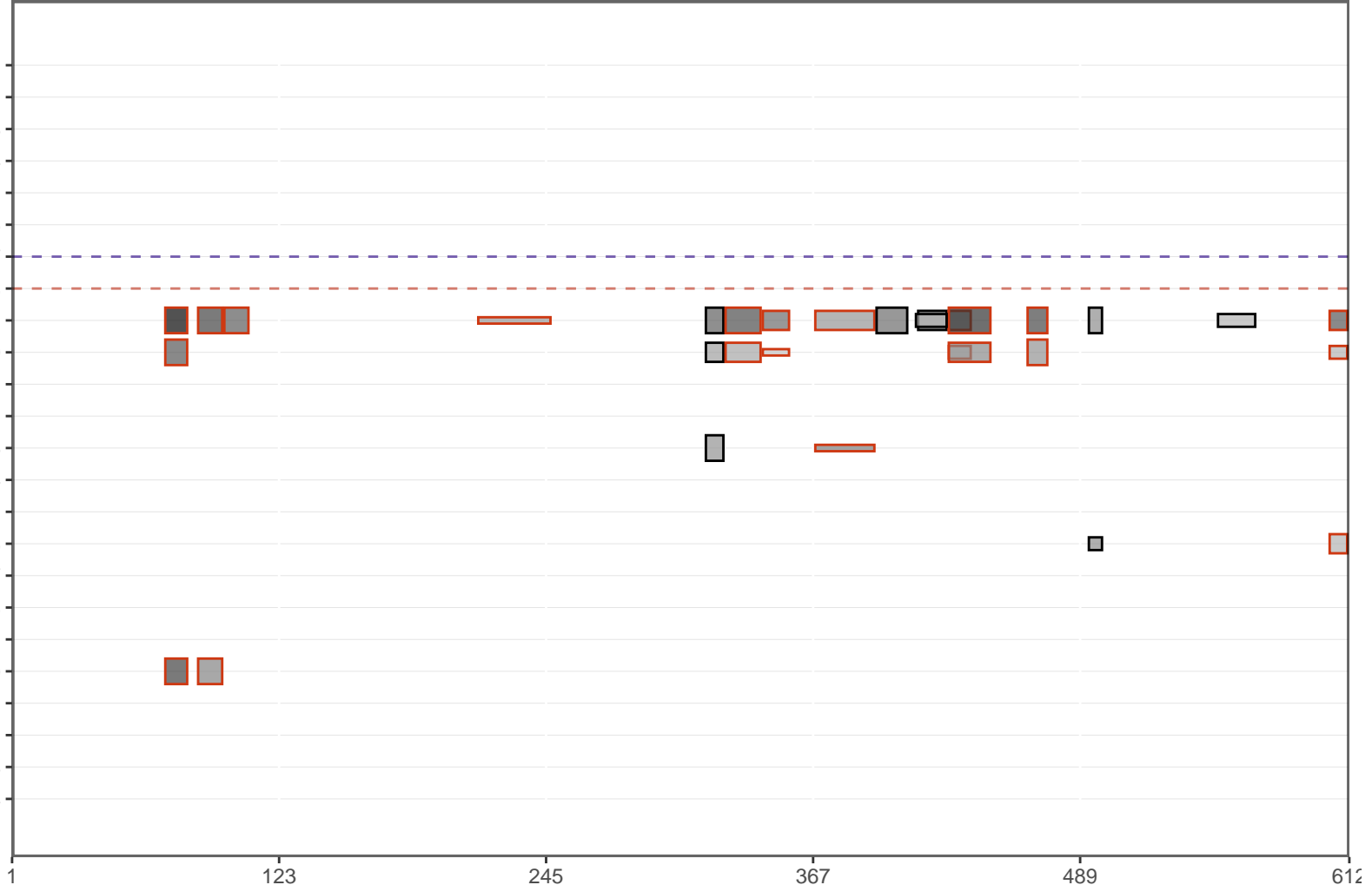
MW indication



Molecular weight

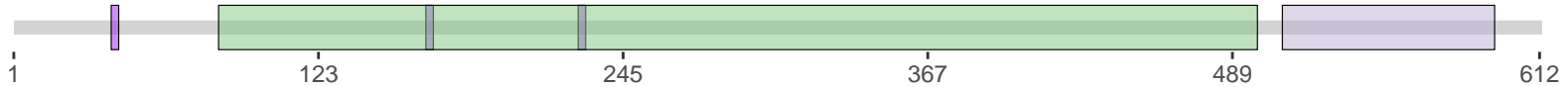


Gel Slice



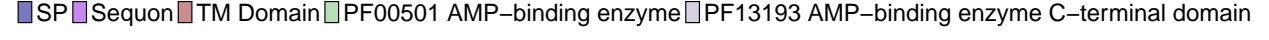
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AGSTVDFVYKFSVRGAWQRWRRESYPTDGTGMNNAITVTFGVPTMYARLLQVYEMDPELKAASASAAHRLRLMMGGSSALPLPVMQGWETVTFGHPILERYGMYTEFVMAISNPIRGRKRGKGTGKPFPGVQAKLLEDESINDKGTGVSLELQKSPSLFREYKWLPEVTKGSGFTDDGDFYKTDGTVTVDEGGYHILGRTNADIMKVGKYLKSALEIEAVLLEHPTISEGCVLGLPKDKYGEVVCIVFPEGKVKRRRDEELKPAFLQELSDWAKEKLAPEYKPTCLFLWDSLP

NbL19g20450.1 cinnamoyl-CoA_reductase_1 [MW = 35.78 kDa]

No. of times detected



log(intensity)



Values from

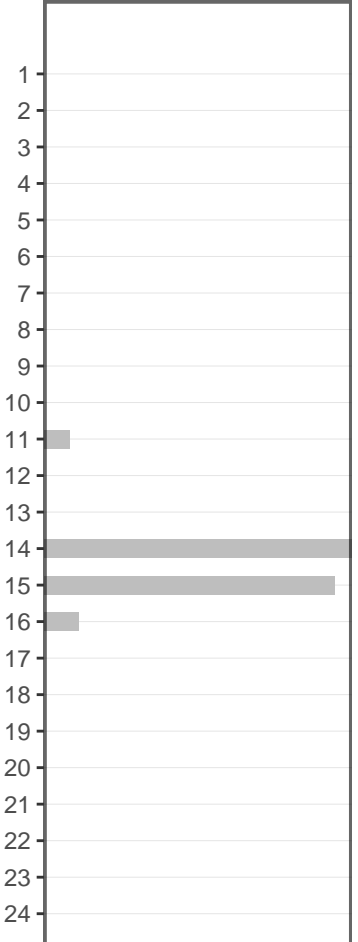
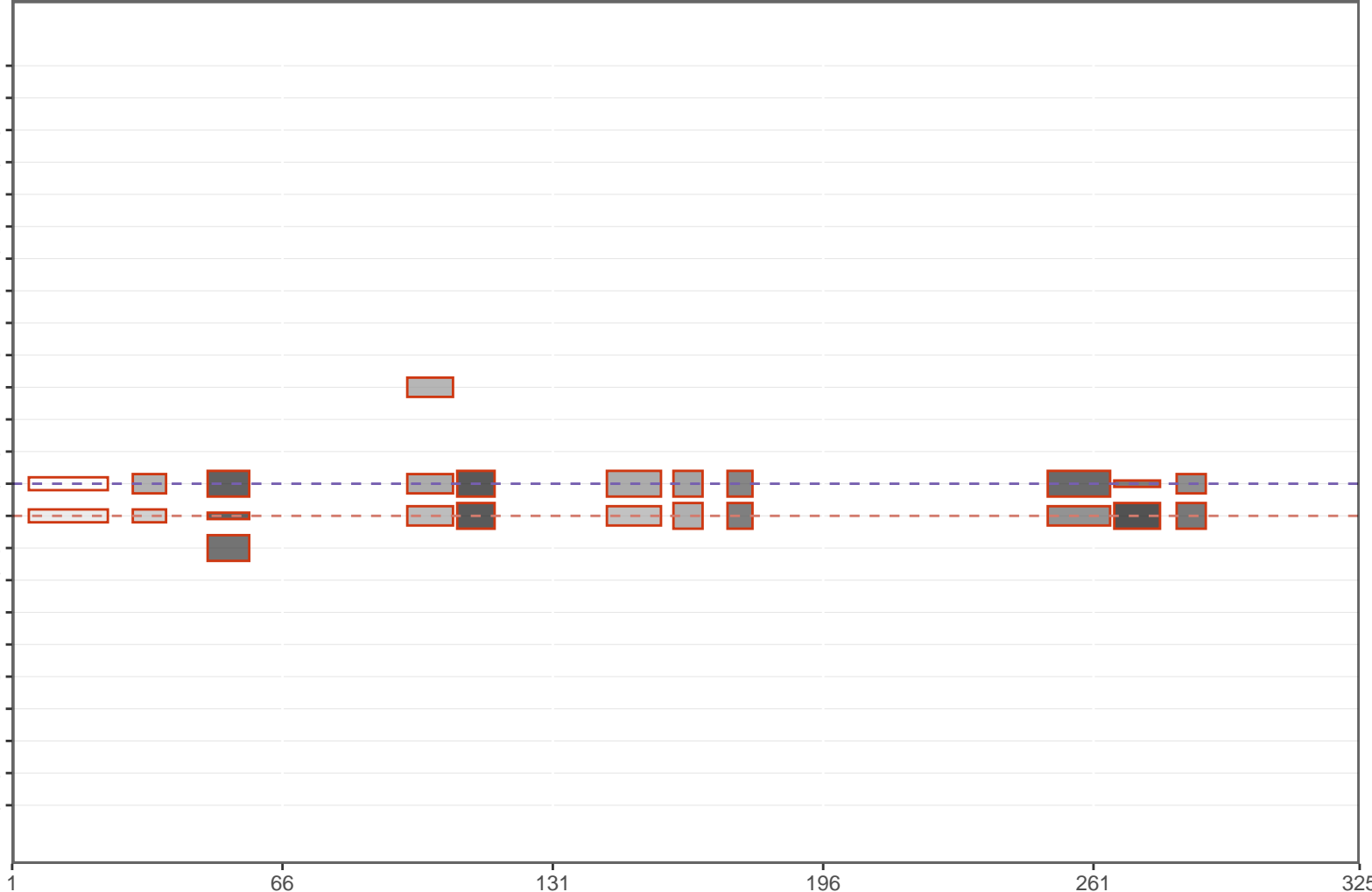
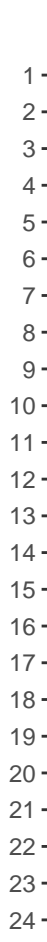
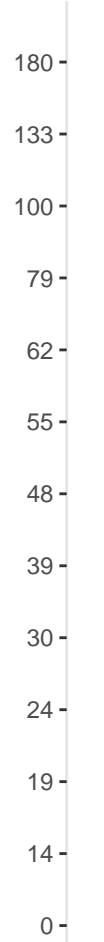


MW indication



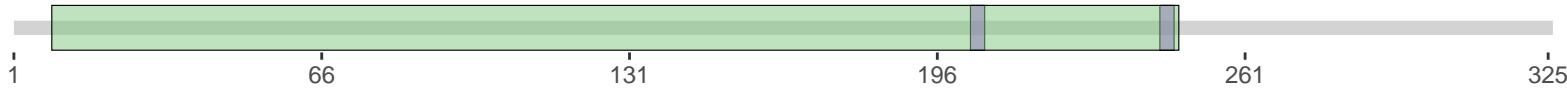
Molecular weight

Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ITDIEYCKGKGVYWYPLSKTLAEKABWEFAKEKLDLHVVNPQTVMGRLPPLTANASMLMLRLGGCTTAVEDFFMGLVHVKDVALAHILVYENSAKGRHLGVEATHYGDFAAKVAELVPEYNPRLPKDTQPGLLRKADGGKRLMDLGLQFDIMEGHIRDSEVSLKMKGFME

NbL19g20340.1 peptidyl-prolyl_cis-trans_isomerase_CYP20-1-like [MW - SP = 19.67 kDa]

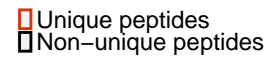
No. of times detected



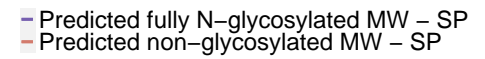
log(intensity)



Values from



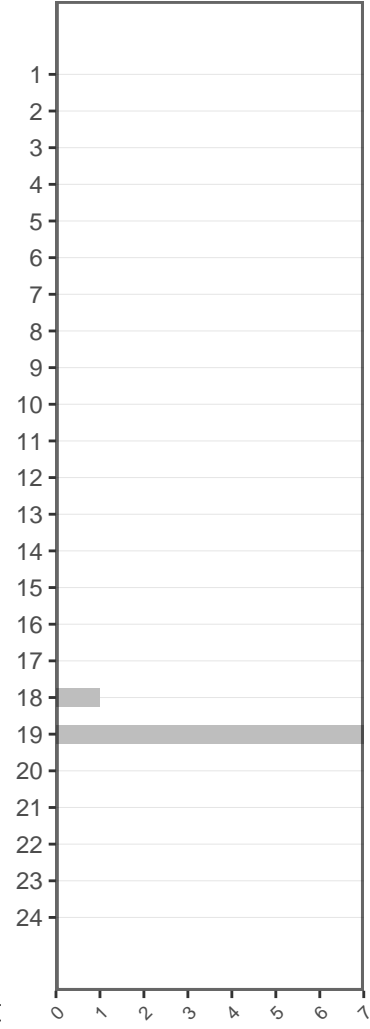
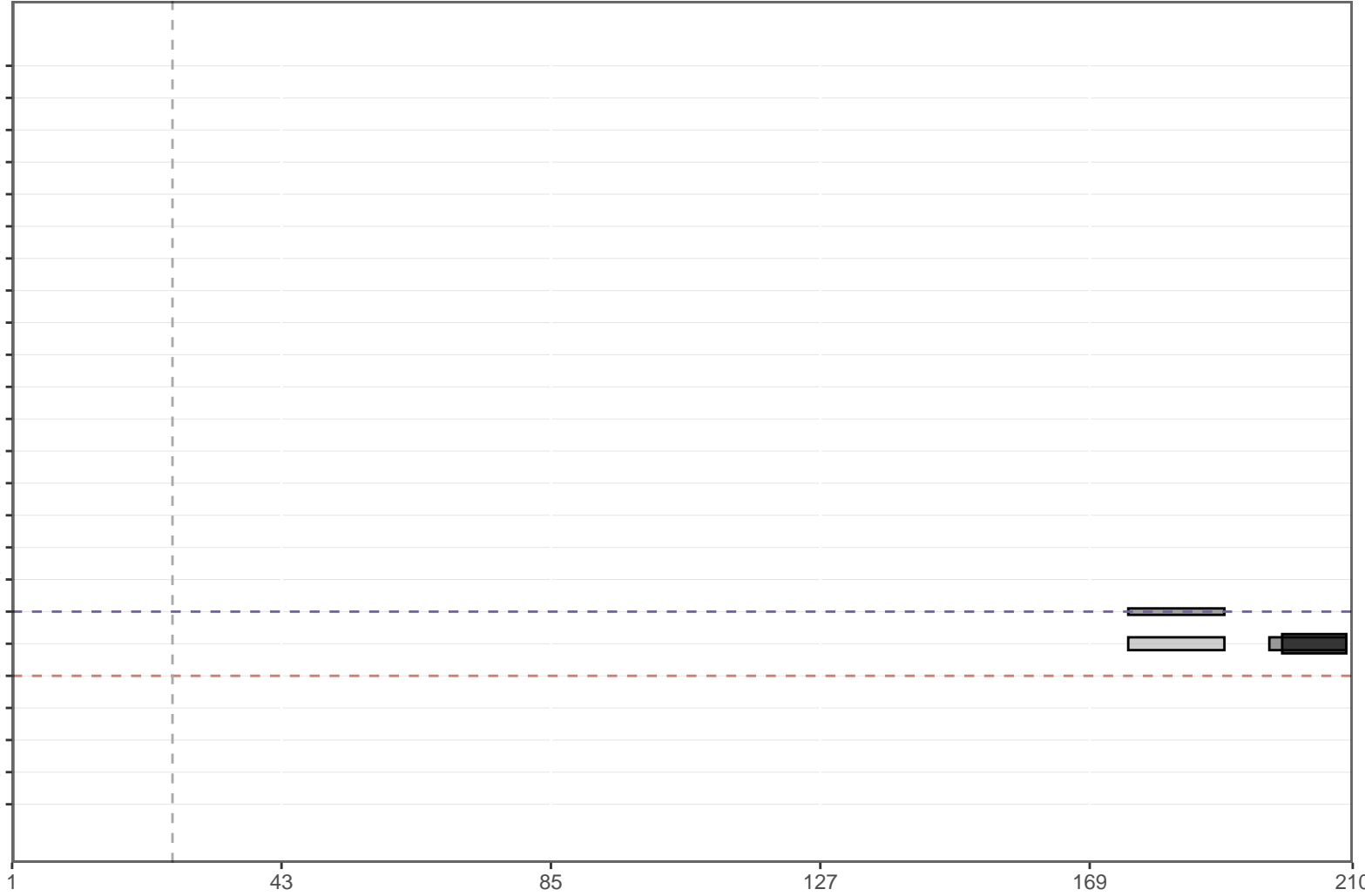
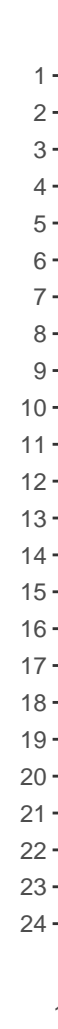
MW indication



Molecular weight

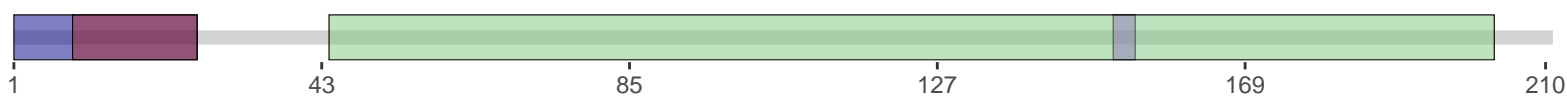


Gel Slice



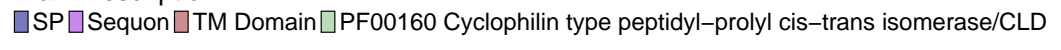
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ISTTRIPSPFLQGGDFLGGDRGGEIVGKFKADENFKIKHTGPLLSEMANAGSDTNSGGFFITVTTSLDGRHVFQKVLGSMVYVYKVEAEGRGGTPEKIVVAESGELPLV

NbL19g20110.1 probable_glutathione_S-transferase_parA [MW = 28.58 kDa]

No. of times detected



log(intensity)



Values from



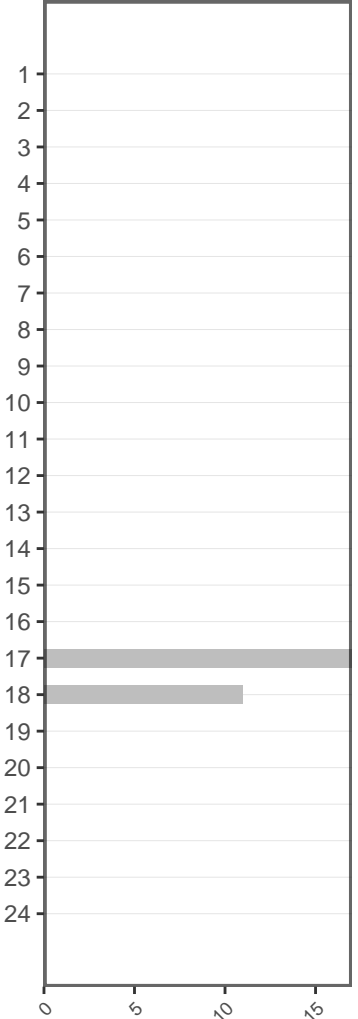
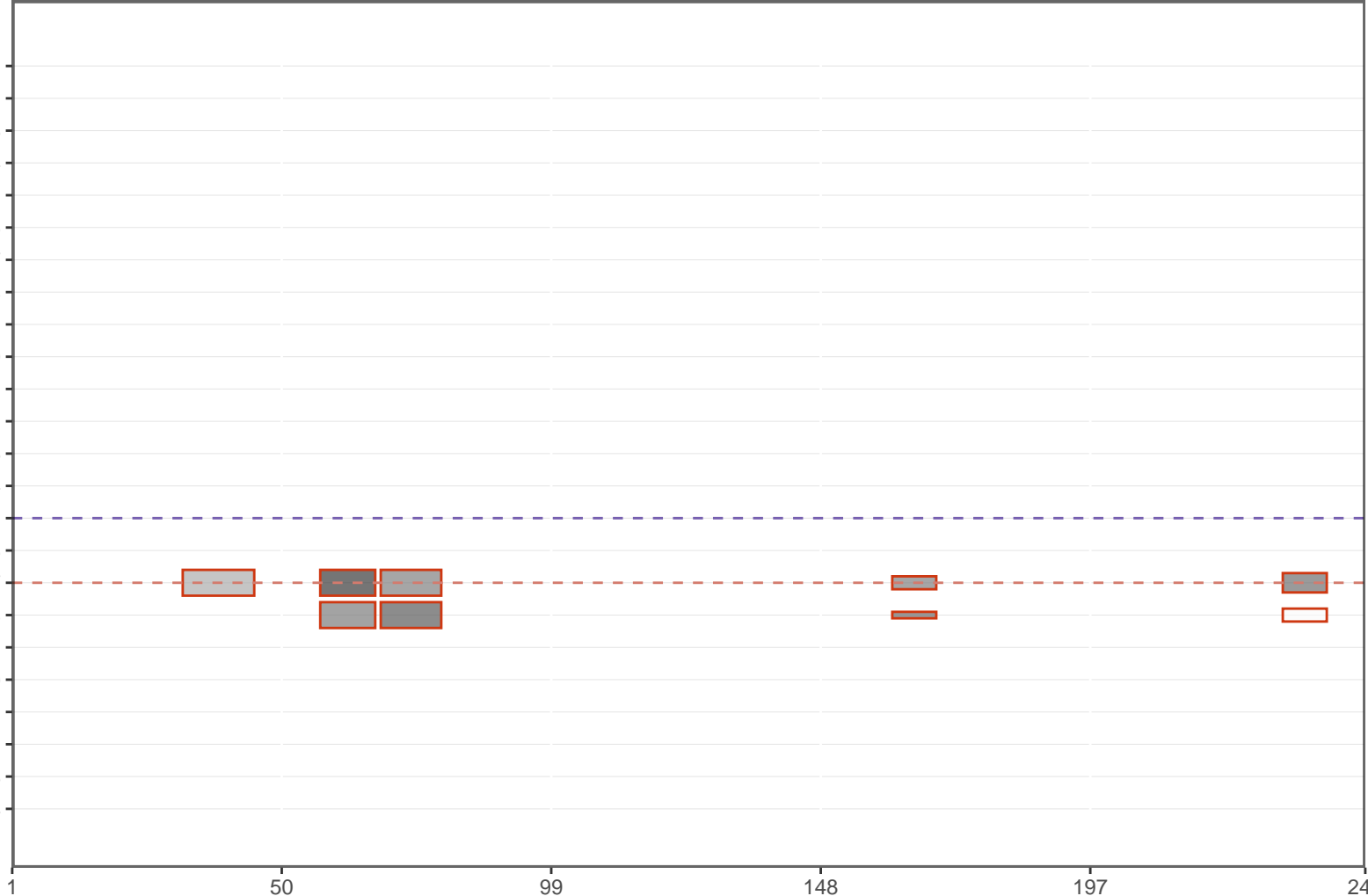
MW indication



Molecular weight



Gel Slice



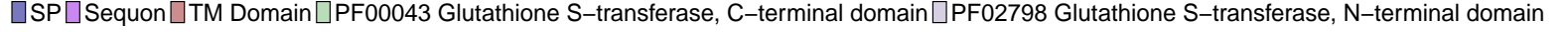
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

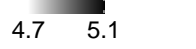
"SDPYEKSRARFVADYDKKYSTGRFRVWSGKGGDGEAKKFLKIFKTLLEGELGKNTYFGDNLGFDVAVLPFTSWFYSVETFRANFSIEAEGPKLWVWAKRGMENEGVSKLPHPKYKDFVLEUKHGLA"

NbL19g20030.1 probable_LRR_receptor-like_serine/threonine-protein_kinase_At1g06840 [MW - SP = 102.38 kDa]

No. of times detected



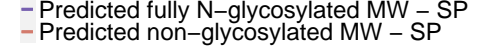
log(intensity)



Values from

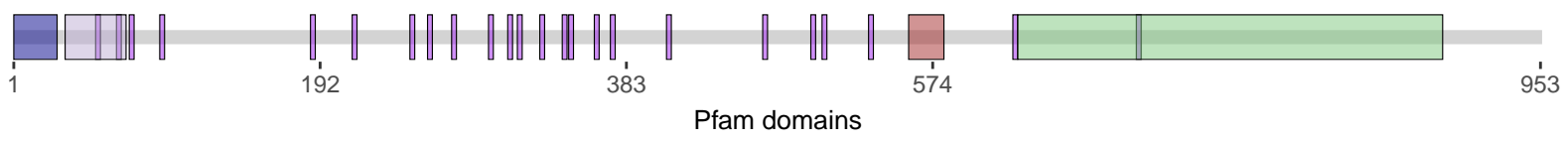
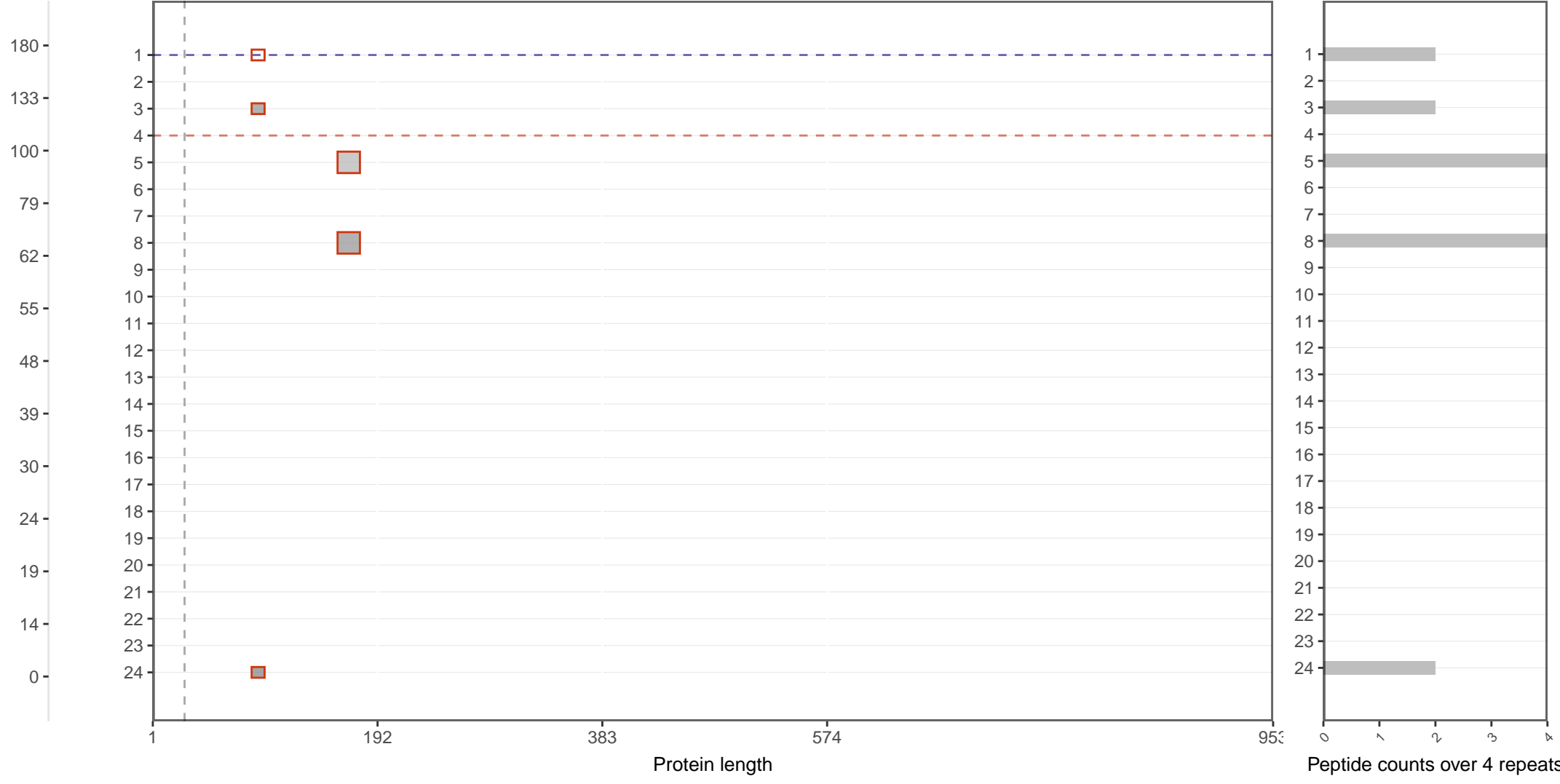


MW indication



Molecular weight

Gel Slice



Pfam Description



Protein sequence:

TSQLKLNQSDLHNTFALEAGPRVIRMYRIFPIVDN666SLFNKBEVLRIRRMFTGVLIPDNDFGPGYELLNFTLADYREFRPP666SISKAGILGVAGAVTISAFVSLVLRHMKKHHHAGSKRNLL666SIVKIDGVKEHFEEFLTATKFNPN666SLVGGGYSKYKGTFLNDGTVVAIKRALEGLGGKKEFLTEIELL666RHLHRRNLVSLGCGEEGEMLVYEFMPNGTFLRDHISGKKEPL666FAMRLRVALGSAKGLVLYHTEADPPFIRDKASILLDSKFLAV

NbL19g19930.1 bis(5'-adenosyl)-triphosphatase-like [MW = 18.11 kDa]

No. of times detected



log(intensity)



Values from



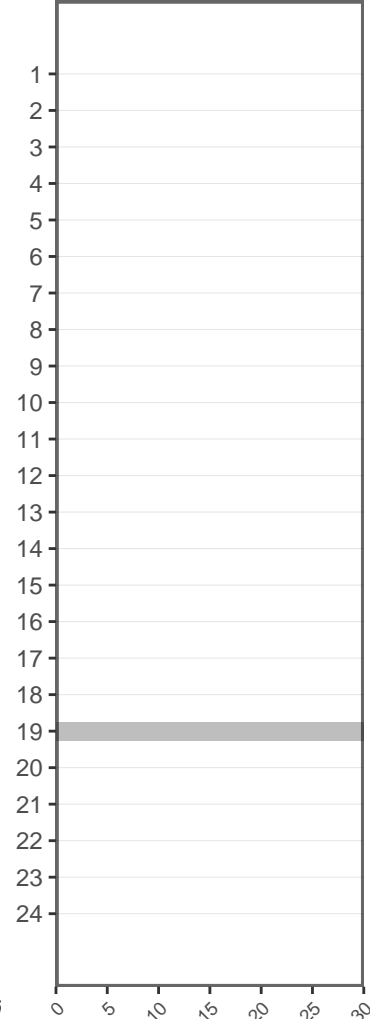
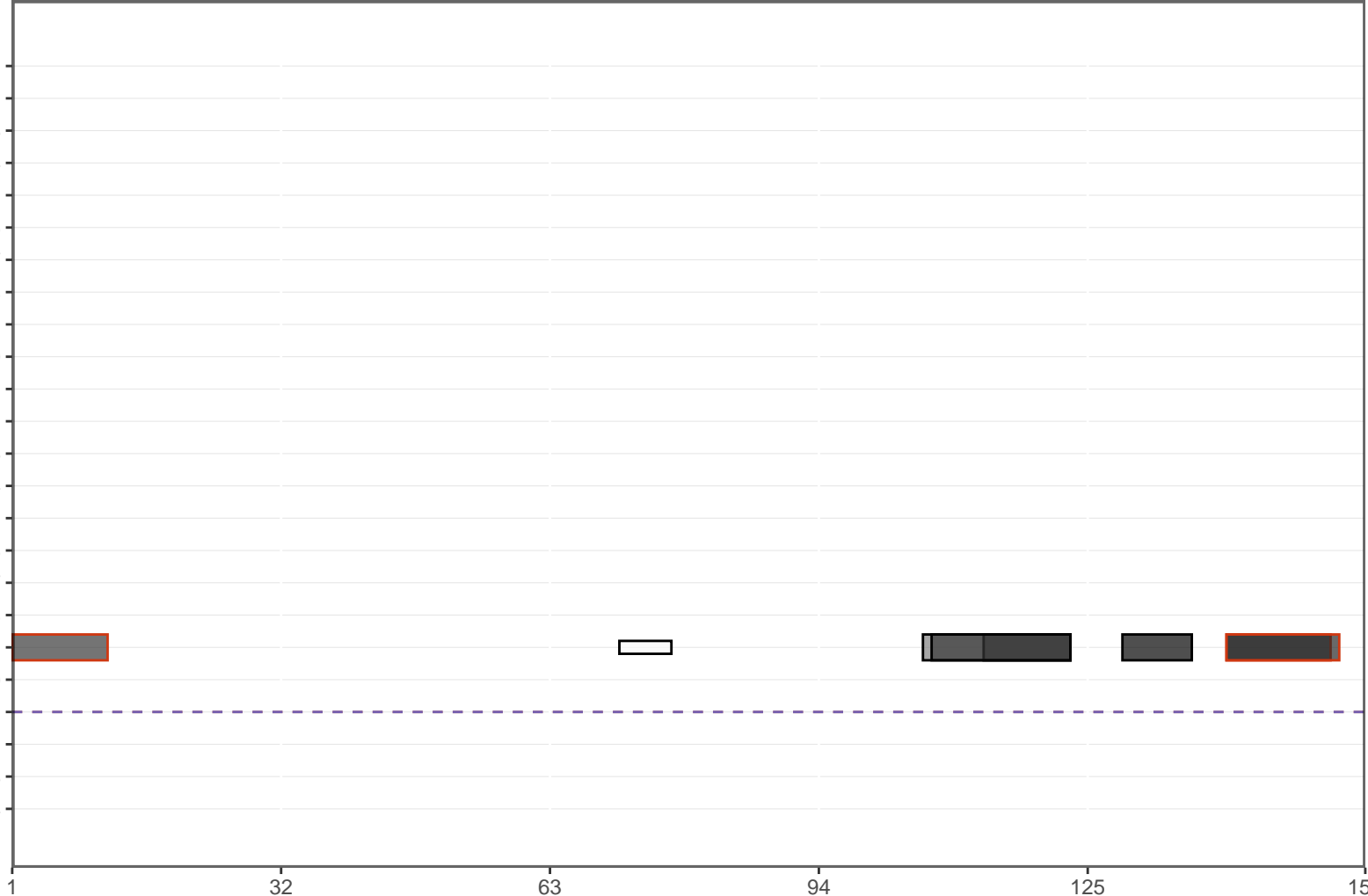
MW indication



Molecular weight



Gel Slice

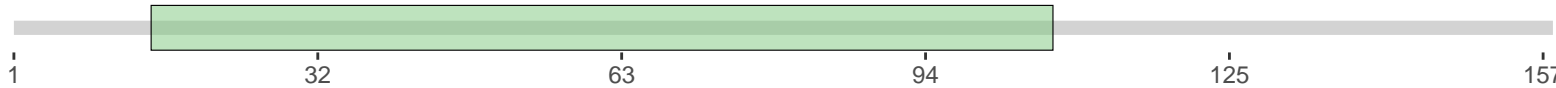


Peptide counts over 4 repeats

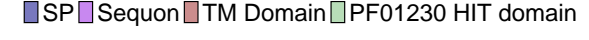
Protein length



Pfam domains



Pfam Description



Protein sequence:

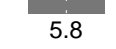
QKVGKQLESYHKASLTFAGDGPAGGTVPHWHIIPKSGDFEKNDENVDALEKEMKQSLDLKDKRDRBIEVMAEEADEYRKL*

NbL19g19920.1 50S_ribosomal_protein_L17_chloroplastic-like [MW = 22.38 kDa]

No. of times detected



log(intensity)



Values from



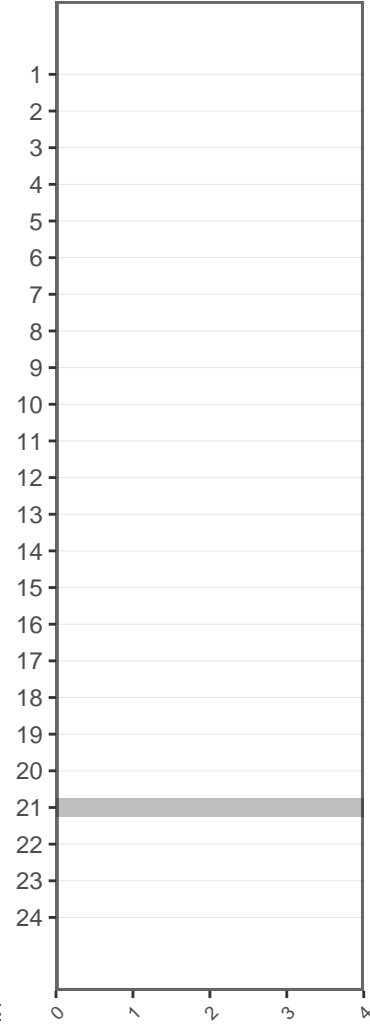
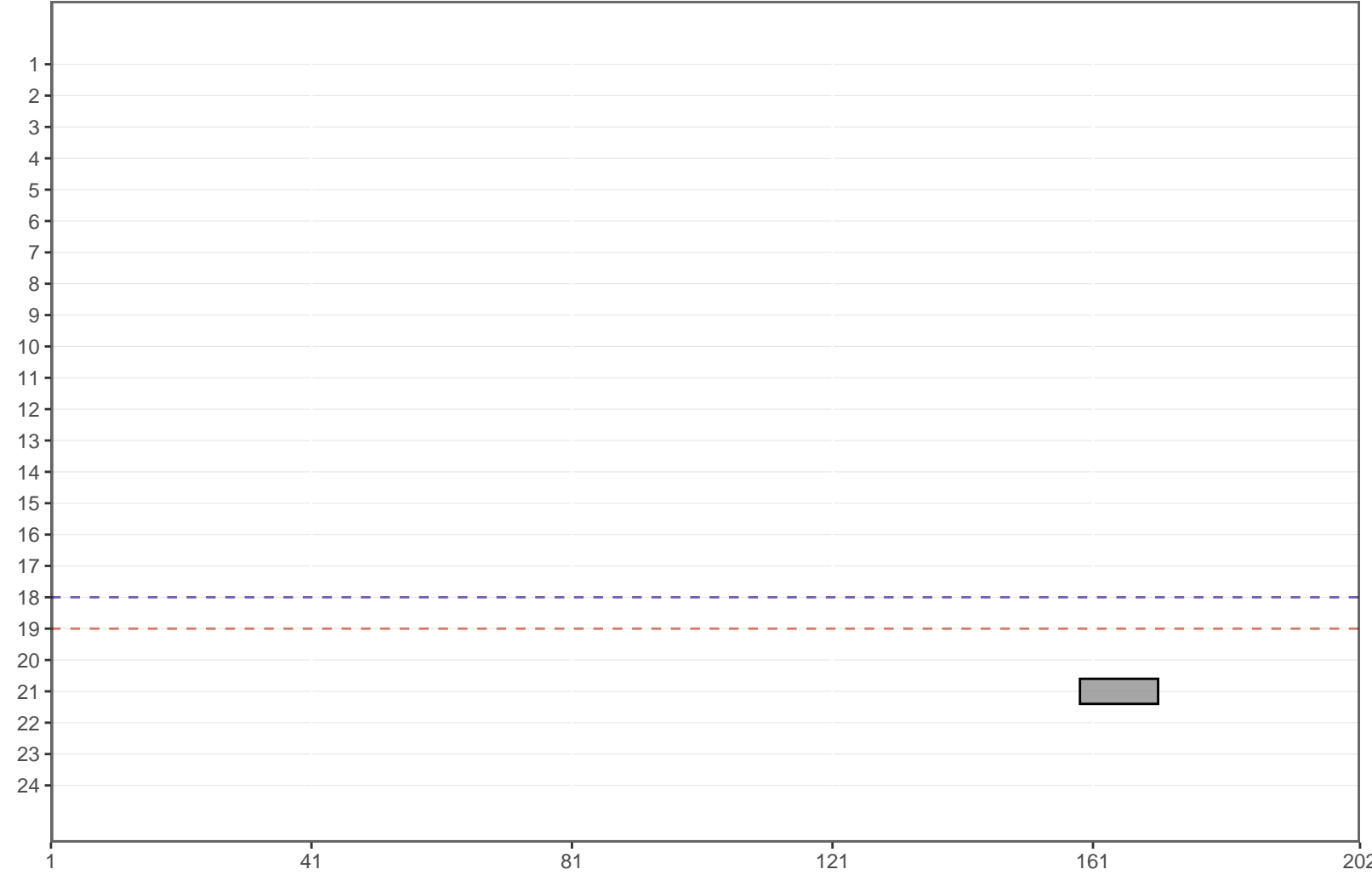
MW indication



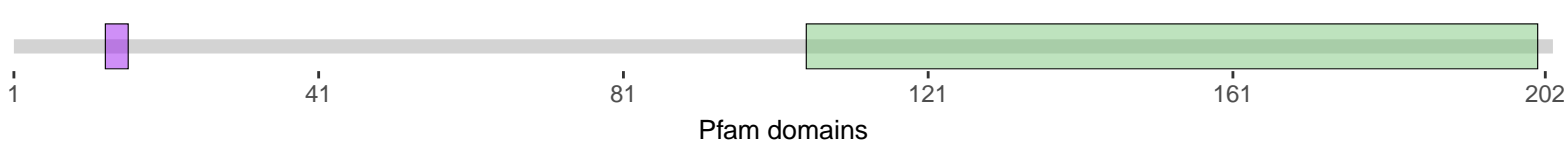
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

SHGRKVPKLNRPDPQRALLRGLTQLLKHGRKTKARARARVKYVDKMITMAKDGTUHKRRQALGFYKQGVHALFAEVPERYGERNGGYTRIRTLPRRGNAPMAYIELV*

NbL19g19880.1 CBS_domain-containing_protein_CBSX3_mitochondrial [MW = 22.57 kDa]

No. of times detected



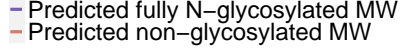
log(intensity)



Values from



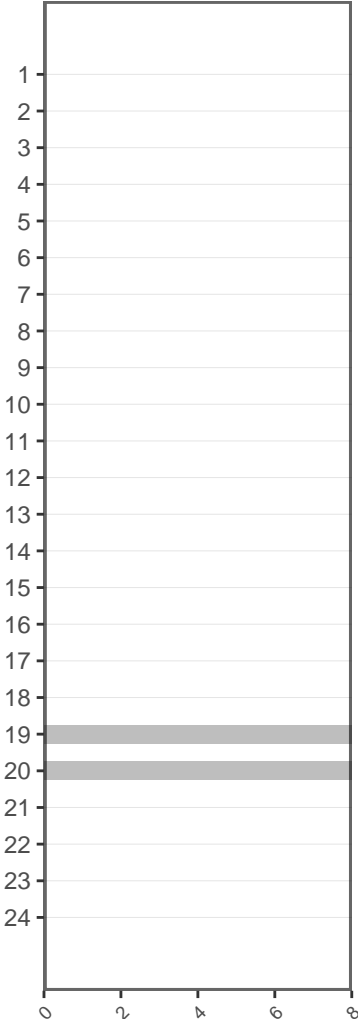
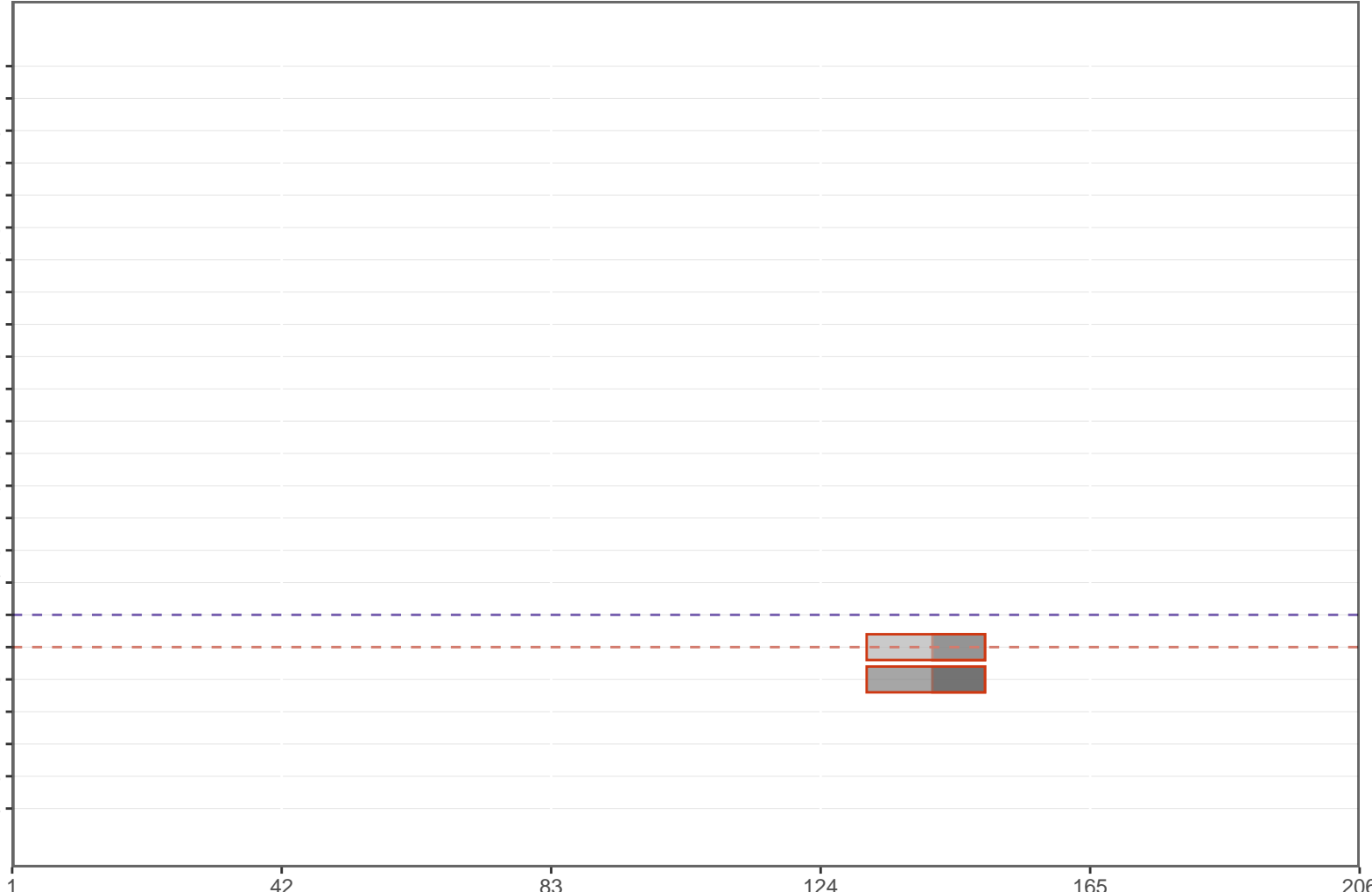
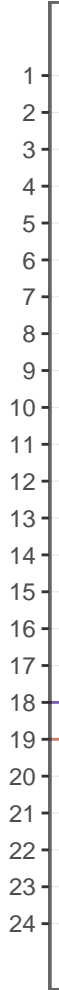
MW indication



Molecular weight



Gel Slice

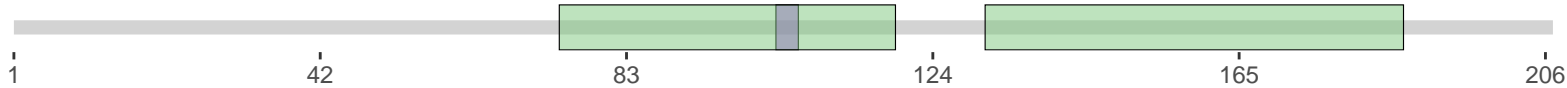


Peptide counts over 4 repeats

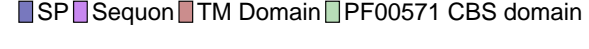
Protein length



Pfam domains



Pfam Description



Protein sequence:

DHNVGLVLYKPKGENKBIAGITERDYLKRVVQGRSBSKTKVGDIMTEENKLIIVTTPETKYLKAMQLMFDNRIRHIFVIDQTGMIGMVSIGDVRVAVVEHREELNRLNAFIGGGY*

NbL19g19850.1 glyoxylate/succinic_semialdehyde_reductase_1 [MW = 30.79 kDa]

No. of times detected



log(intensity)



Values from



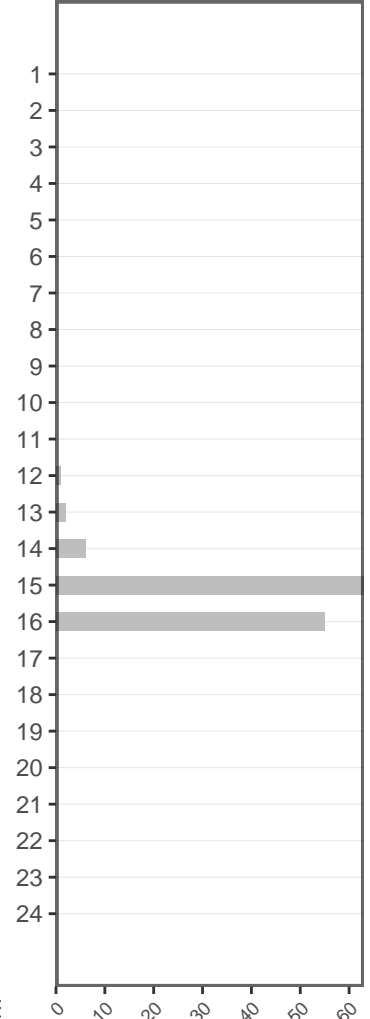
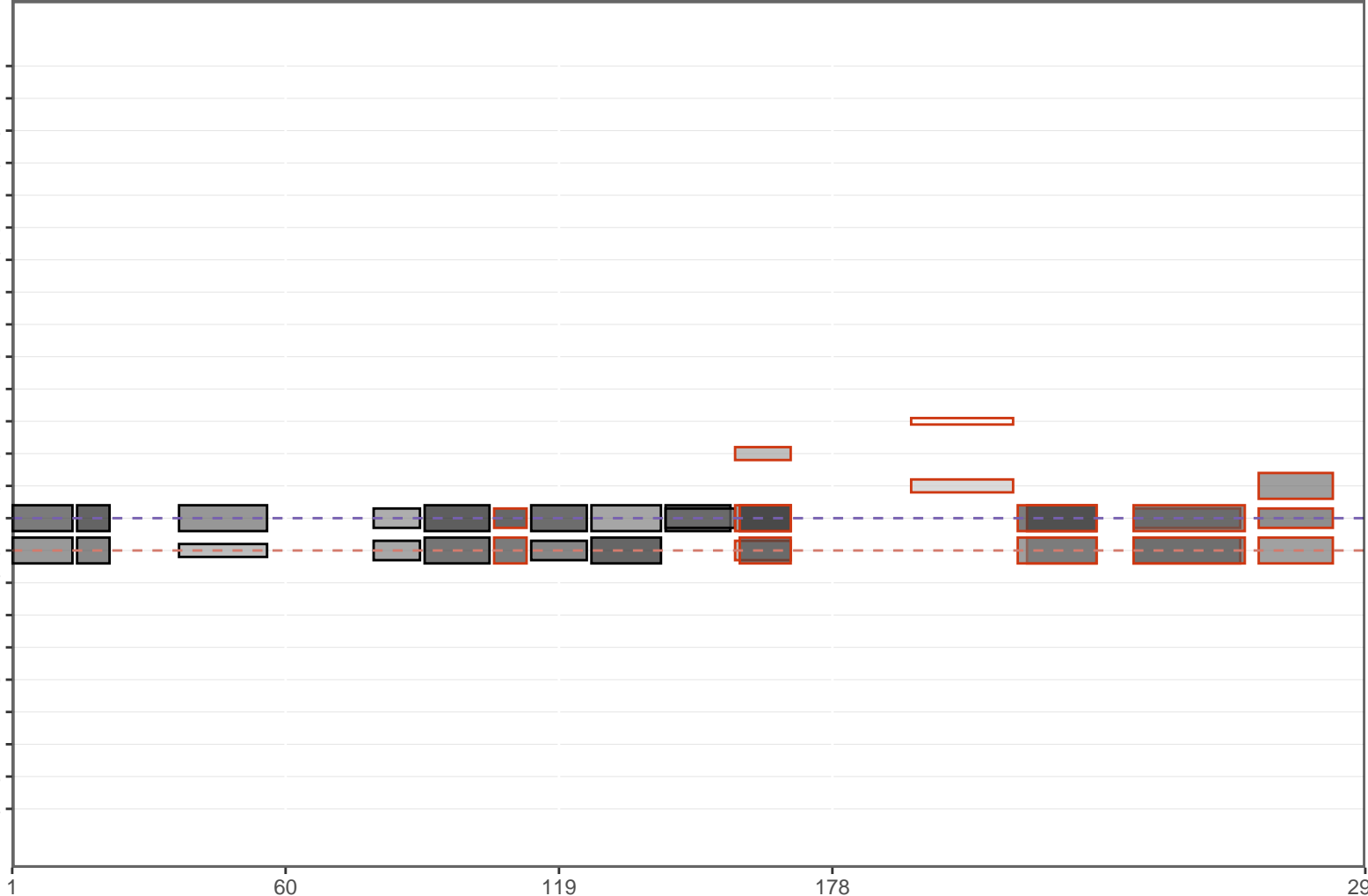
MW indication



Molecular weight

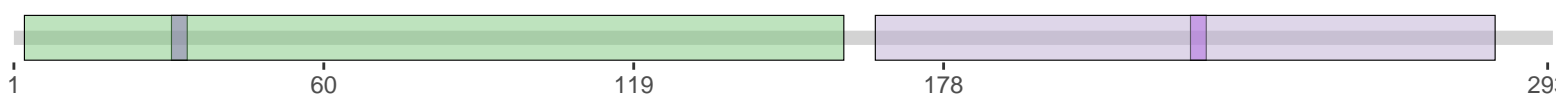


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF03446 NAD binding domain of 6-phosphogluconate dehydrogenase
- PF14833 NAD-binding of NADP-dependent 3-hydroxyisobutyrate dehydrogenase

Protein sequence:

V/LAAGDKALYDQVLPFDVGLGKKSFFLGGVGNAGAKMKLVNMMGSMNMFSEGVLAADKSGLDPKHTLLEVLDLGAIANPFGKGGPMMNNYPPAFPLKHGGKDMRLALALGDENAVPMPVAAAANAEAFKKARSLGLGDHDFSAVFETIRGAQGSST

NbL19g19790.1 auxilin-related_protein_2-like [MW = 105.52 kDa]

No. of times detected



log(intensity)



Values from



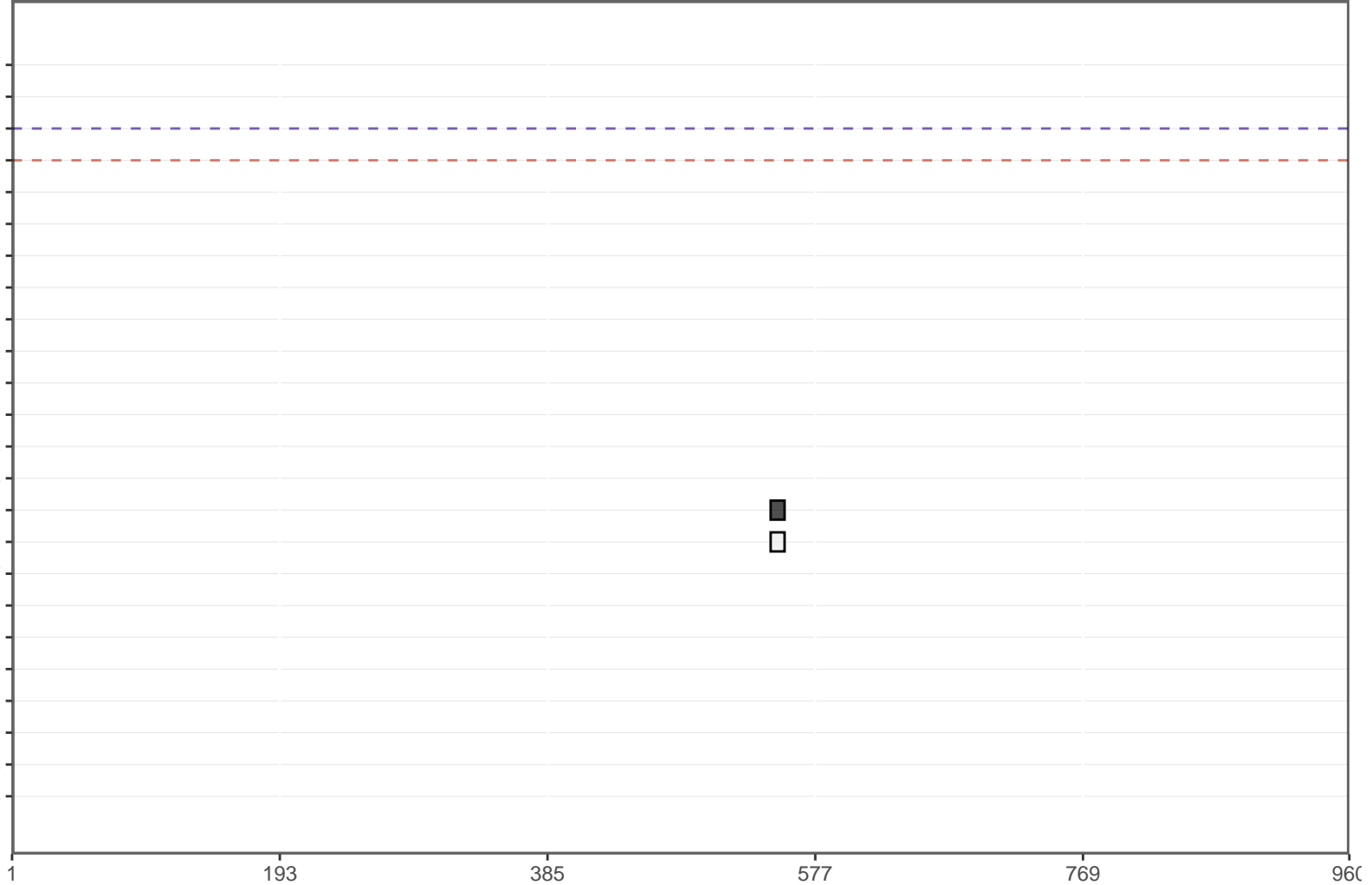
MW indication



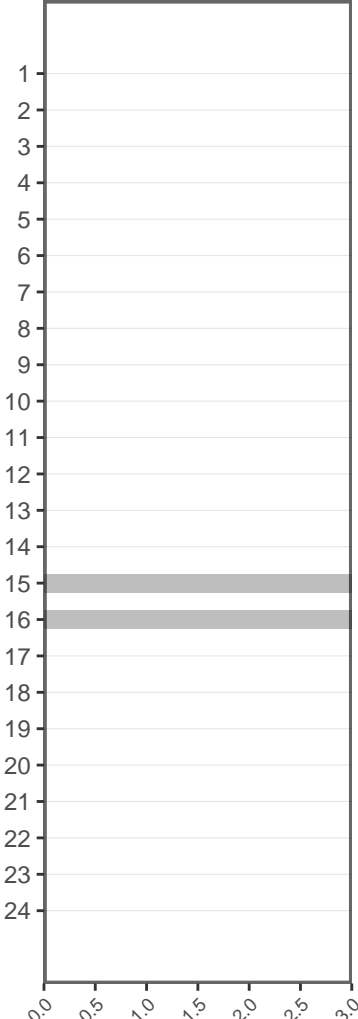
Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

DELEDFARGVPRFSMTDENADALSGEEMNANSVAASAAAMKEAMDRAEAKFRHAAKEVREYEVAKSANKKEAVHLERDEGAINEVOERELGENDERLERENRRREKEEERADRKLREERERTRELEKERARGAVERTREAREARAAVWGARDRAAAEARLKAERAAVEKAAAEARGRAEKAAVQRADAEARERAAVEAKERAEKAAAEAREKEAREKASAVKAAEAERARRAERAAVVERAAAEARERAAAEARERAAAAARMNGQRNDLSEFFSMGRASSAPK

NbL19g19750.1 60S_ribosomal_protein_L5-like [MW = 34.54 kDa]

No. of times detected



log(intensity)



Values from



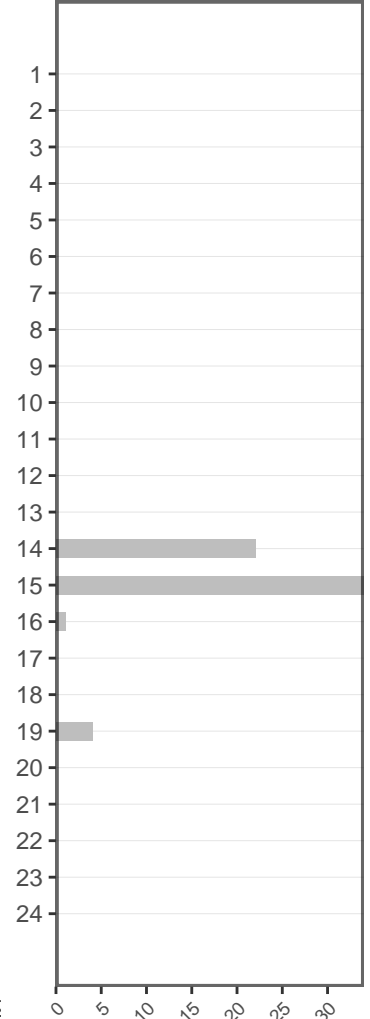
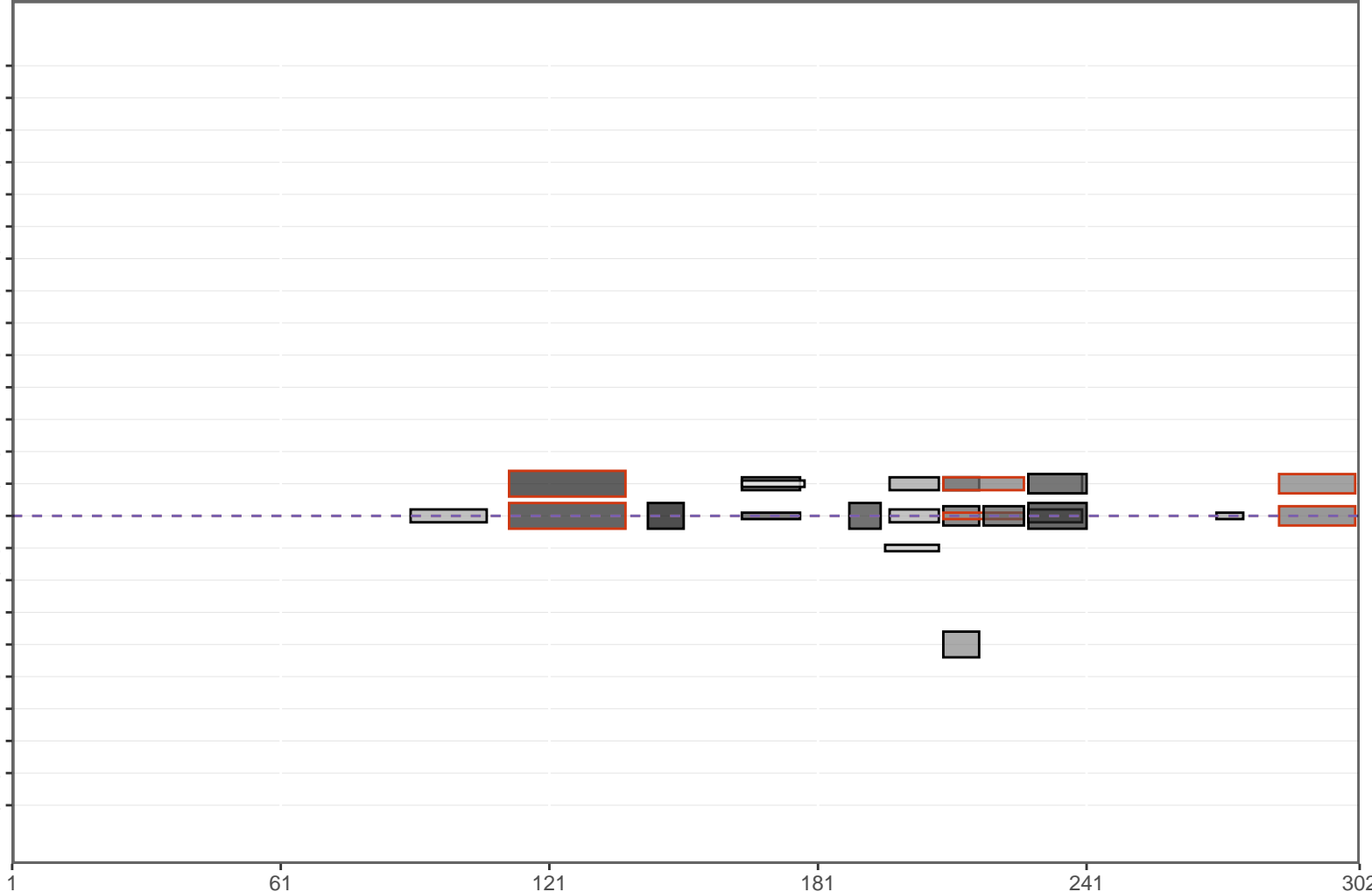
MW indication



Molecular weight

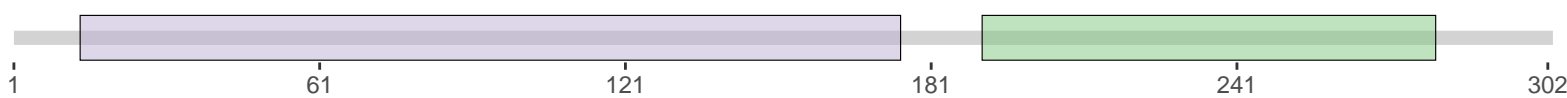


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

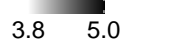
RPFRALLDVLGRLTTTGNRVFGALGALDGLDIPHSKRFAGFSKDSKGLDADVHRKYVYGGHATVMTLTFEPEKYQSHFBEYKGGLEADDLEEMKVKVHAIRADSPKSKSEKQPPKQHKRYNKKLTYEERKAKLIERLNALNSAAGNDDDEEDDD

NbL19g19720.1 ribonuclease_2-like [MW - SP = 26.42 kDa]

No. of times detected



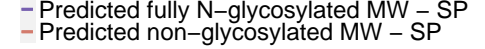
log(intensity)



Values from



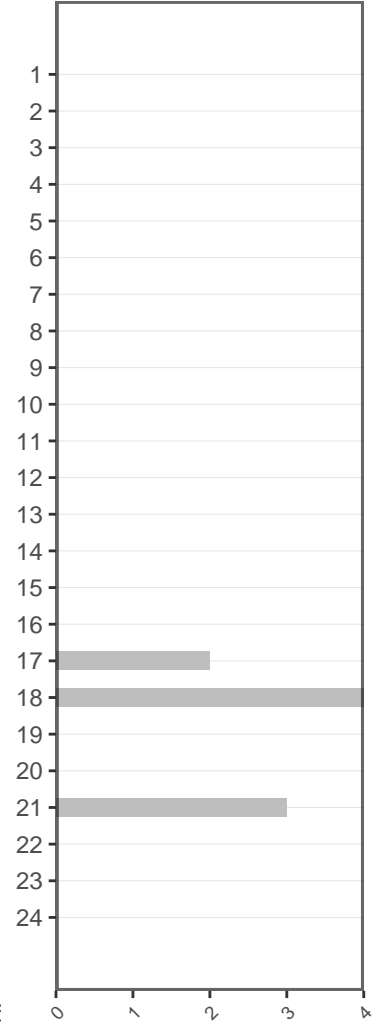
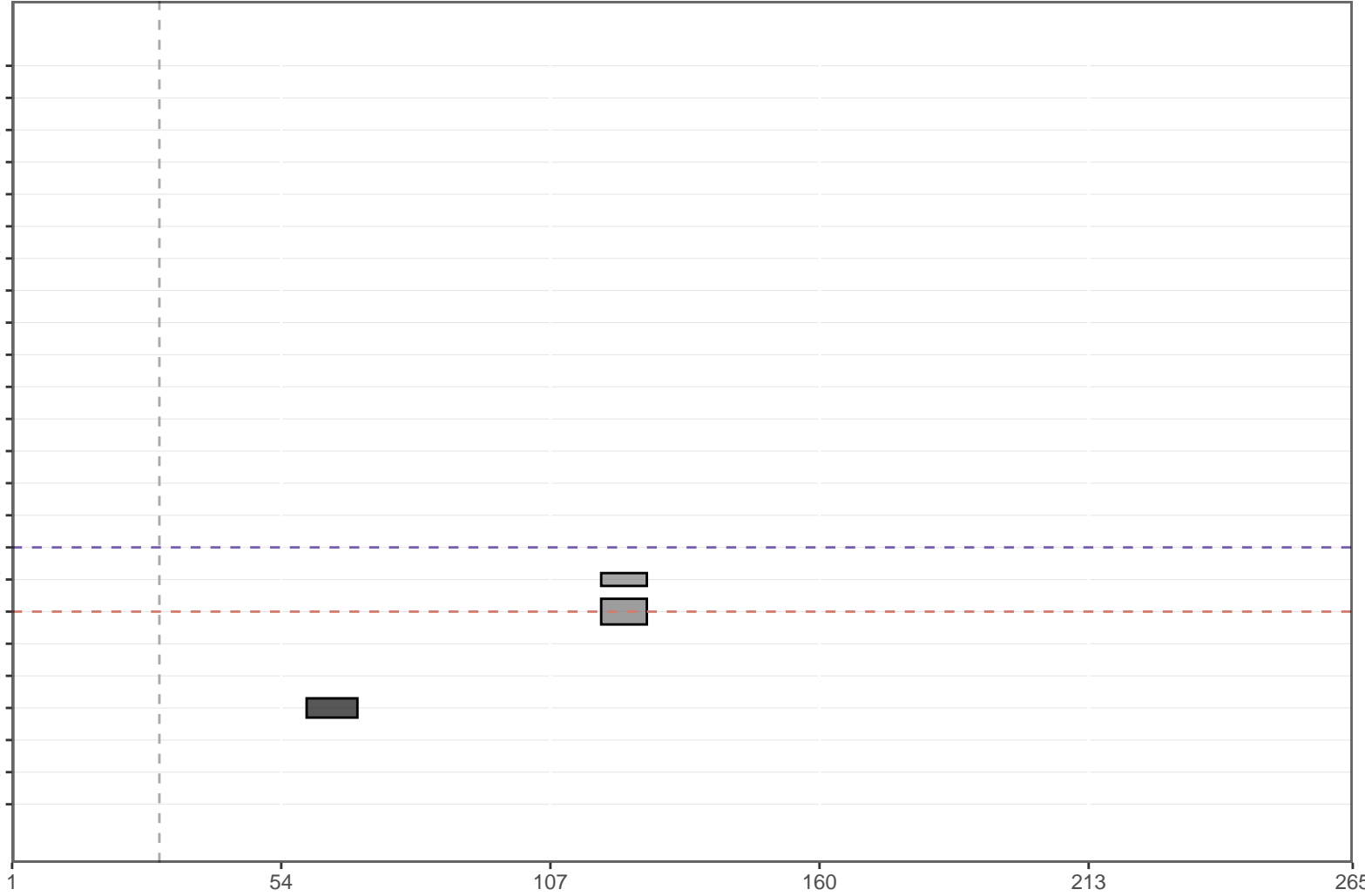
MW indication



Molecular weight



Gel Slice

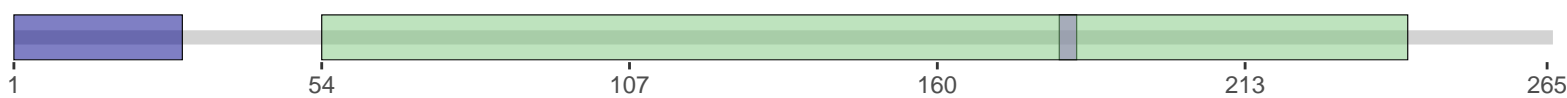


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

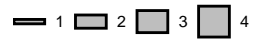


Protein sequence:

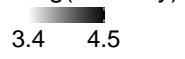
STLLEPLRKYWPSLGGSPRSHHRKGPWAVEKHKGTGAVPVVHDEVEFFLTLNYYFKYVTEVLFQAGYVPSDSEKYPVGGHSSINAFHATPEVTGSGDALEELRQFYKFFPRDCAHDTLSALSRGGCPQVWVLRPHGS

NbL19g19710.1 ATP-dependent_RNA_helicase_DHX36 [MW = 116.31 kDa]

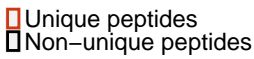
No. of times detected



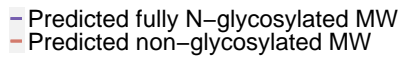
log(intensity)



Values from



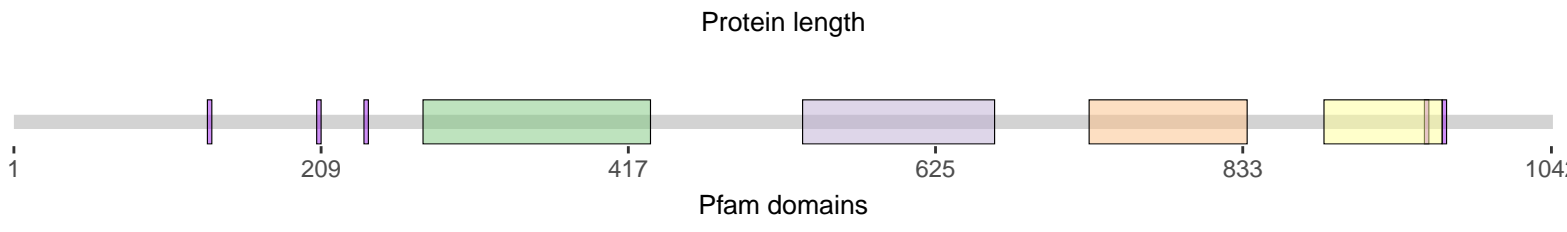
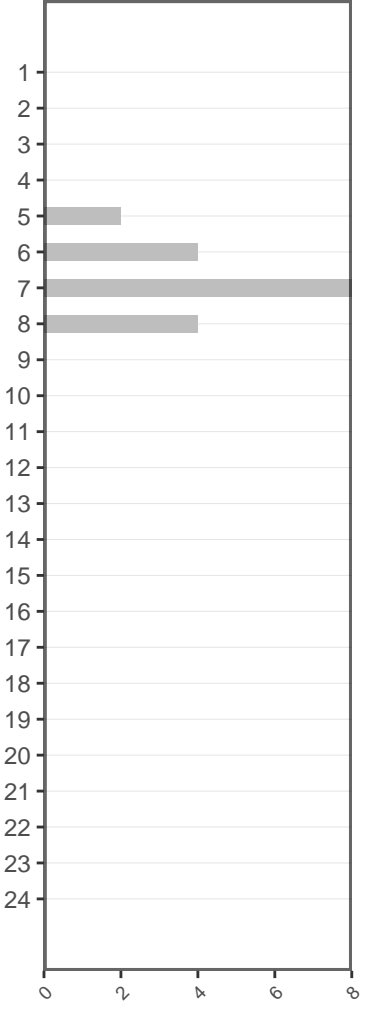
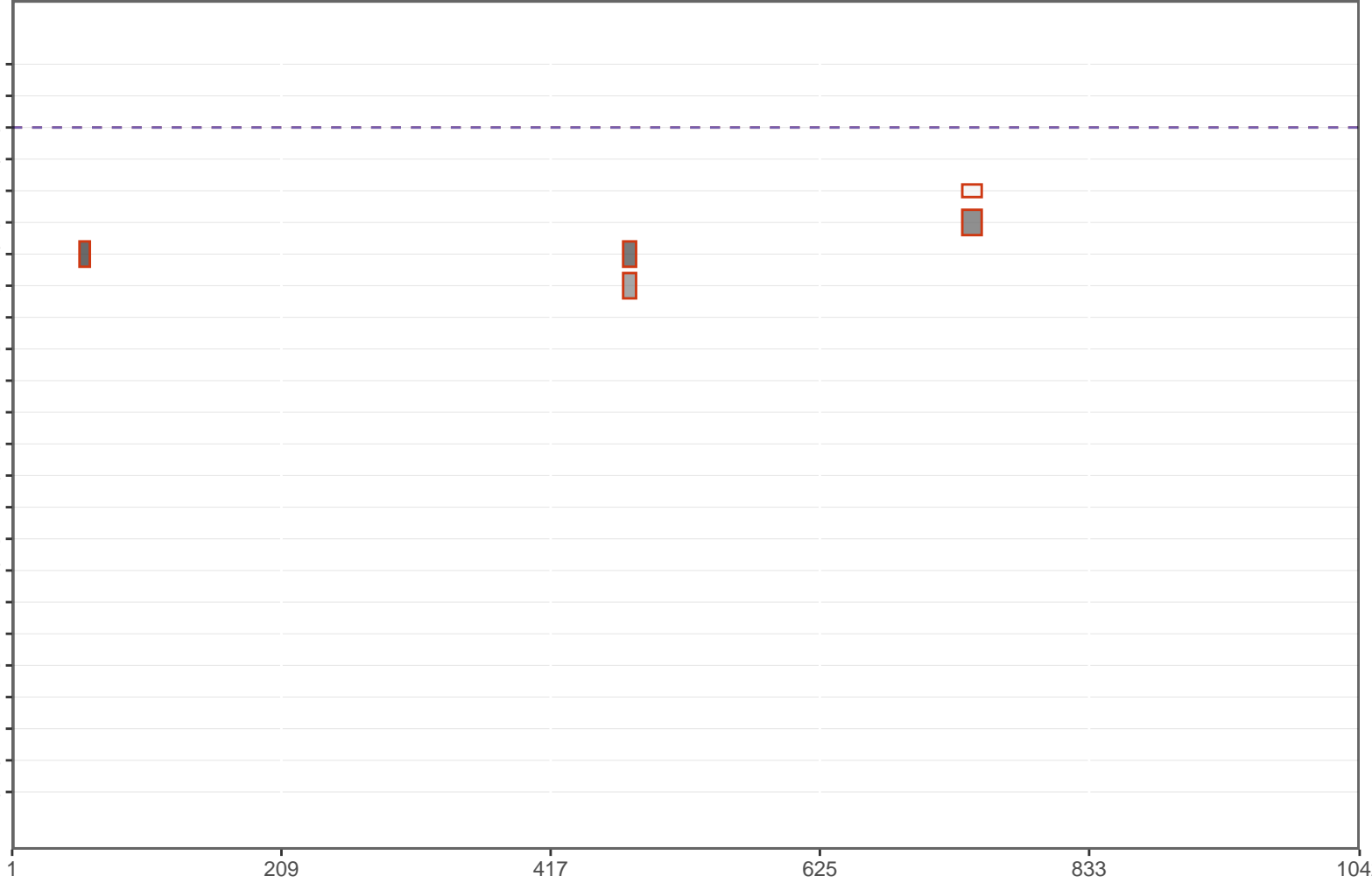
MW indication



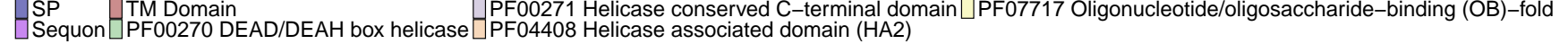
Molecular weight



Gel Slice



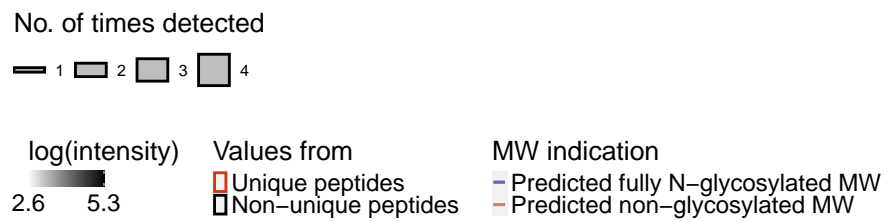
Pfam Description



Protein sequence:

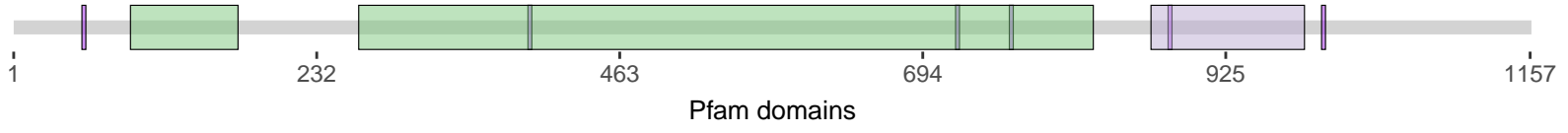
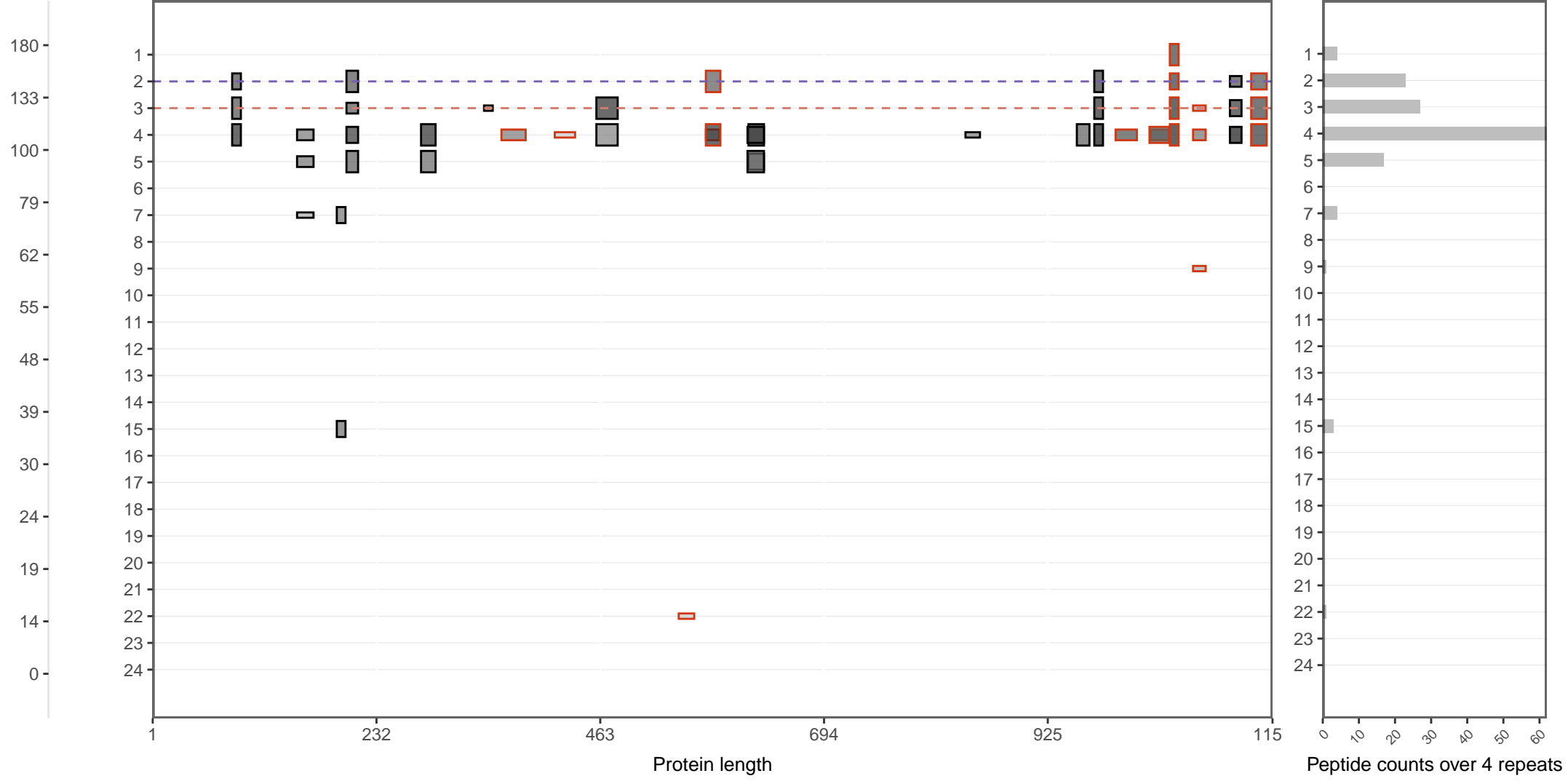
FEDVDIGSHFKCYSMTRRGLAEAWGGSLDLGLVEATIEYICRRREGALVFLTGWDDISKLLDKKANNFLGDTFRKFLPLPHGEMPTINGREIFDRPSANMRKIVLATNIAEESIFIDVVYVDGGKAKETSDALNKLACLPLPWSWKASAHRRGRGRAGRVDPGVYVRLPKLYLDAMPQYQLPEILRPLQELGLGKIKSLQFGAIESFLAKALGPPDPLSVHNAELKTKIGALDDTEELPLGRHLGTLPLVDPNIGIKMLLMGSPQGLNPLRTIAAALAHRRDFVLPINRKEAD

NbL19g19470.1 leucine--tRNA_ligase_cytoplasmic-like [MW = 131.56 kDa]



Molecular weight

Gel Slice



Pfam Description

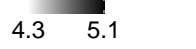
Protein sequence:
 LIRSKLLMNQAVVFSEPEKVMRSRSGDEGVVALTDGWLTYGSEWRKAAEDGLSAMNLYSDETHGFETHLWLNQWAGSRNFGLGTRIPWDEDFLVEISLSDSTVMAYTYVALHLQKGDMYGTDHSGVKPFGQLTDEWVEFLFONGPYPENSLSSSLKEMKQGFQWYFPDLRVSGKDLQNHILFQYHNTAIFPKIHWVPRFRNGHIMLNSEKMSKSTGNFRTLRQAEFFSADATRFALADAGDGMDDANFVFETANAAILRLEIAWMEELVLAESLRS

NbL19g19230.1 ras-related_protein_RABD1-like [MW = 29.38 kDa]

No. of times detected



log(intensity)



Values from



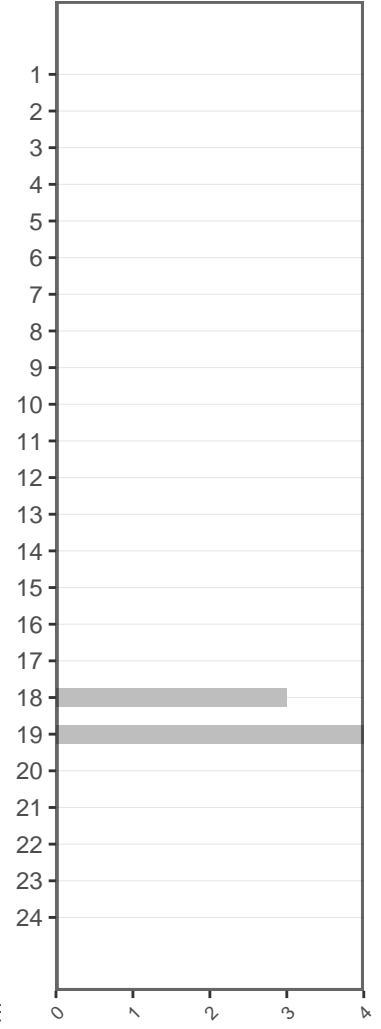
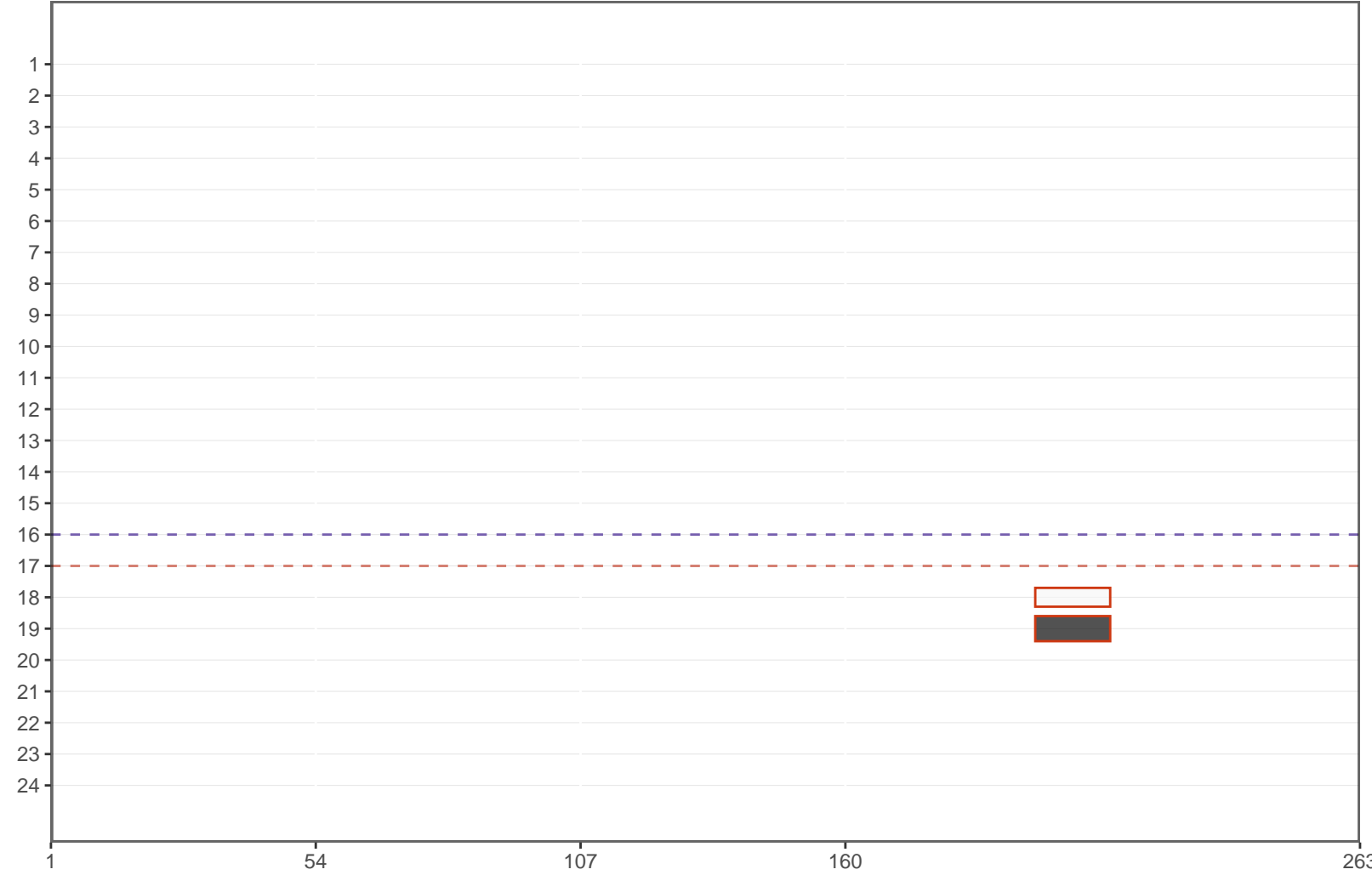
MW indication



Molecular weight



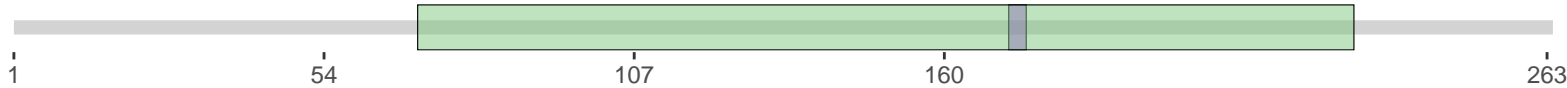
Gel Slice



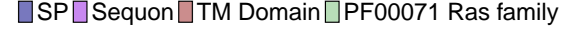
Protein length



Pfam domains



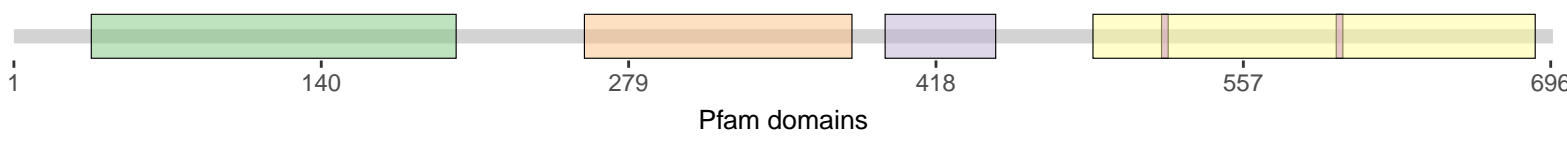
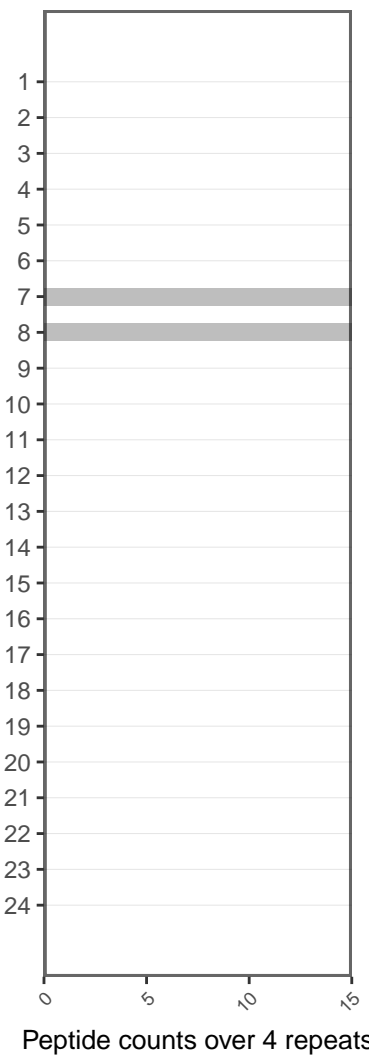
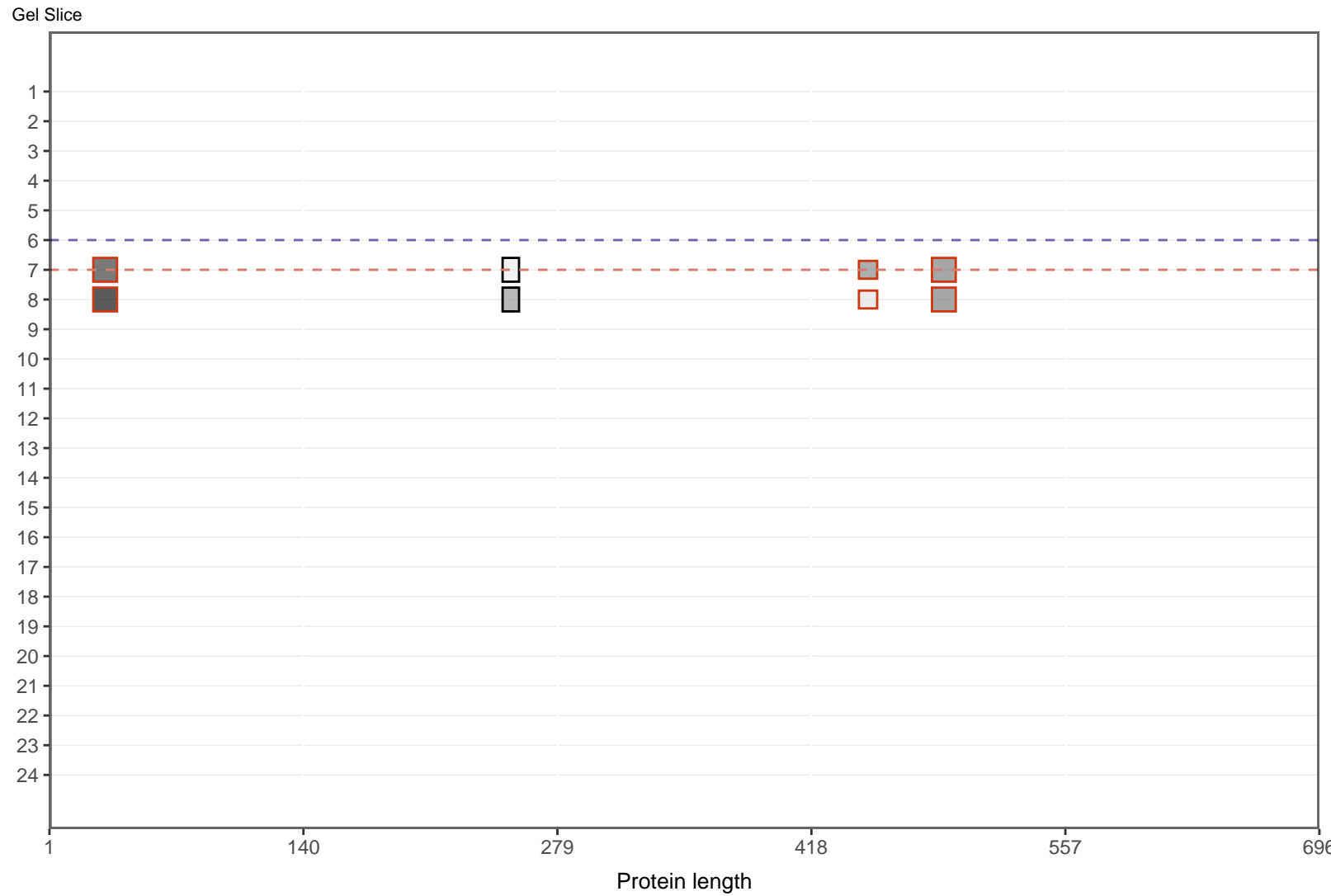
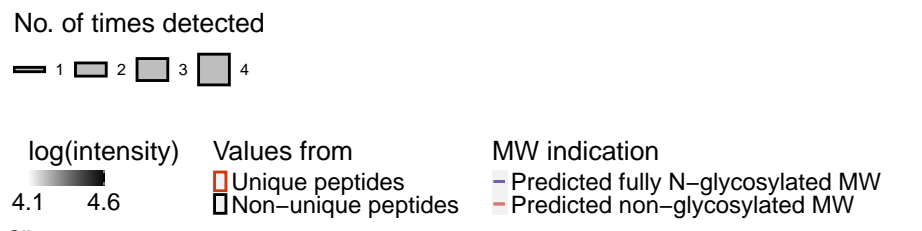
Pfam Description



Protein sequence:

QIWDTAGGERFRITTSSEYRGAHGIRVYDTEKESFDNKKQWLSIEDRYANESVCKLLVGNKGLVFNKVVDTGTAKAFDELGPIETSAKDBNVEGAFLTMAEIKKKMGSGPAGAKNSGGGVQKGGHPTEKNSGCG

NbL19g19130.1 cleavage_and_polyadenylation_specificity_factor_subunit_3-I [MW = 77.37 kDa]



fam Description

SP TM Domain PF07521 Zn-dependent metallo-hydrolase RNA specificity domain PF11718 Pre-mRNA 3'-end-processing endonuclease polyadenylation factor C-term

Sequon PF00753 Metallo-beta-lactamase superfamily PF10996 Beta-Casp domain

Protein sequence:

CVVMMTPGQLGSLRGLFDKWCSDKKNAGVHPGYMVEGLAKTINEPKVEFLQNGLSAPLNMGVHYHFSAHADADGTSFLKELMPPNIIWHGEANEMGRLLKQLKLSLFDAGNTKRTIPKNGDSVEMHFNSEKMAKTVYKLAETPGVGEISGLLWKGFTYQIMAPDDLHFSGLSTANVTQRITPYSGAFVQIHRLLKQIYESVDSGSDTEESGVPRLRHERVTVWGESENHLSLHWITADPISDMVSDGIWALNNSAREMPKRVSDGETLMNEEDAKKAEKIVHAL

NbL19g19040.1 monodehydroascorbate_reductase [MW = 47.05 kDa]

No. of times detected



log(intensity)



Values from



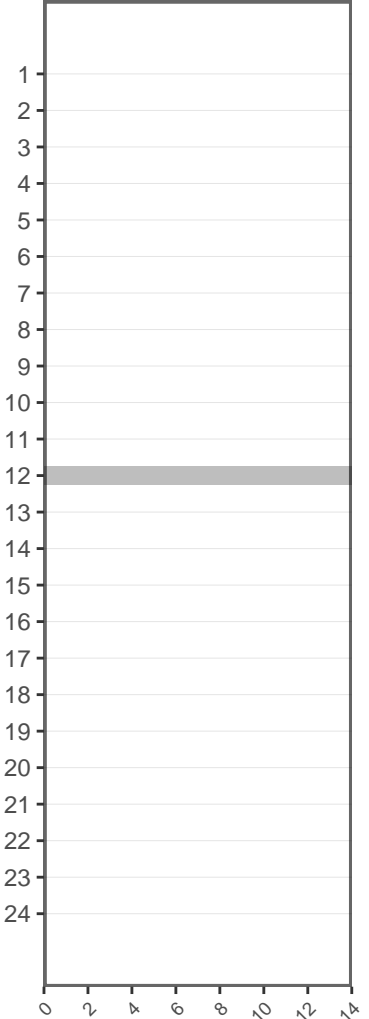
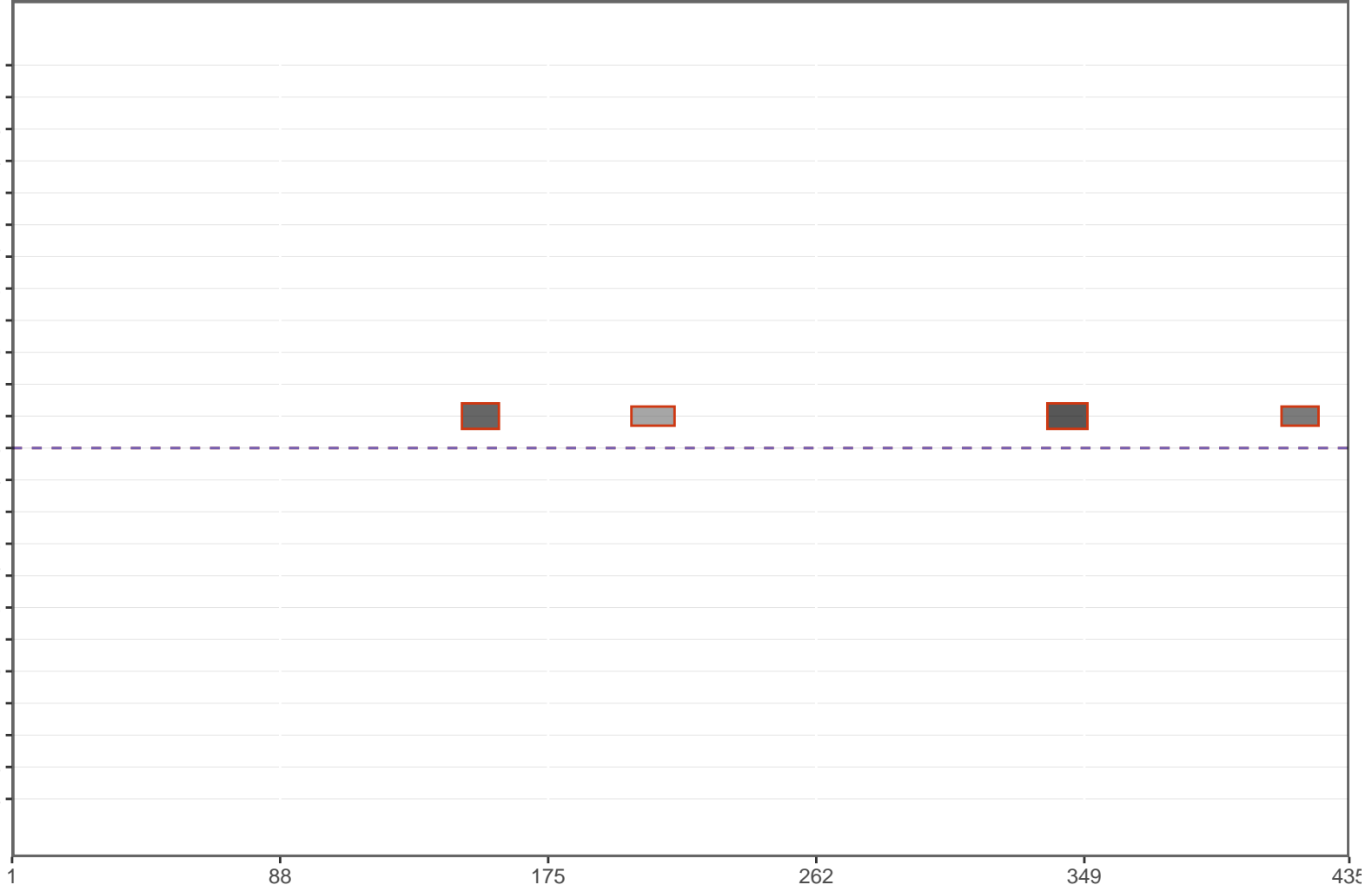
MW indication



Molecular weight



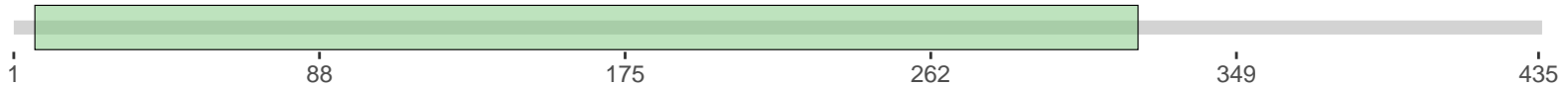
Gel Slice



Peptide counts over 4 repeats

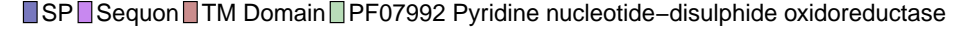
1 88 175 262 349 435

Protein length



Pfam domains

Pfam Description



Protein sequence:

GIAAFYEGYYRNKGVNKKGTVAWGFDTHPNGEVEKVKLKDGRVLEADHVVGVGARPLTLFKGQVAEEKGGKTDFAFFKTSVFDVVAWGDVATFPLKMYSDRRVHEVVDHSRKAEMVAWAFAREGGKSIDVDLPPYVSRADFVWGFYGDVNGETVLFEGDADPNSATHKFGDYYWGDGKVVGVFLEGGTPEENKAAKVAKVGPLVGGLDLQAKEGLSFASKP

NbL19g19020.1 cell_division_protein_FtsZ_homolog_2-2_chloroplastic-like [MW = 49.13 kDa]

No. of times detected



log(intensity)



Values from



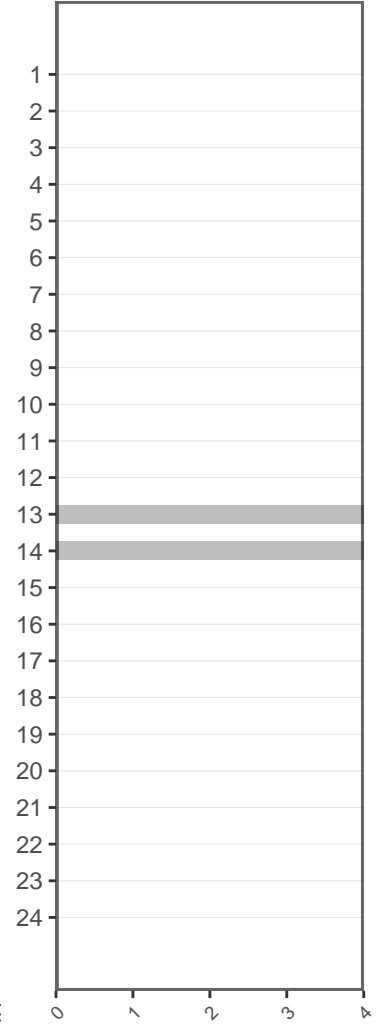
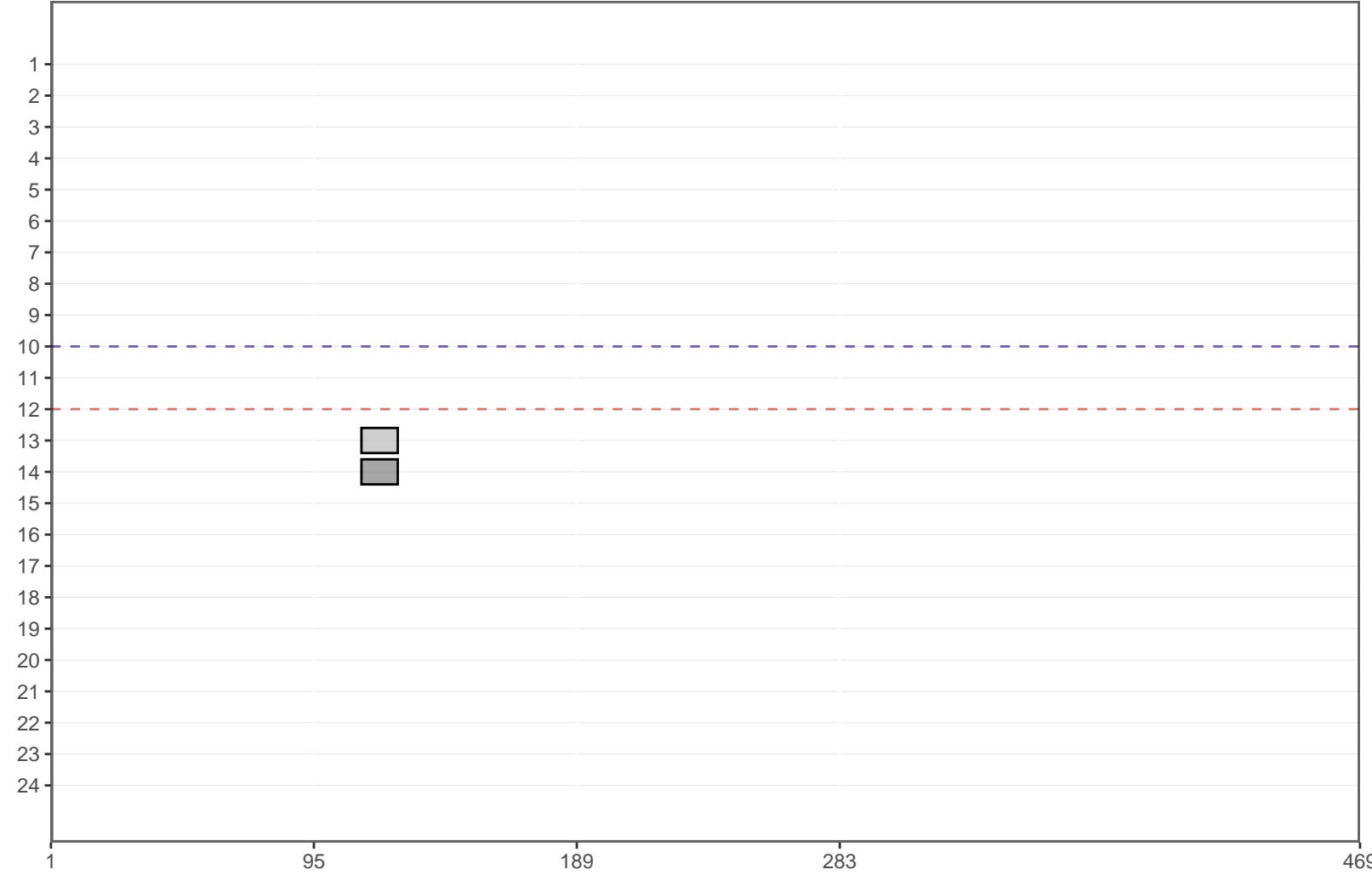
MW indication



Molecular weight

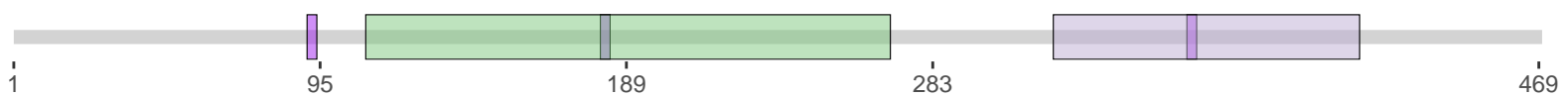


Gel Slice



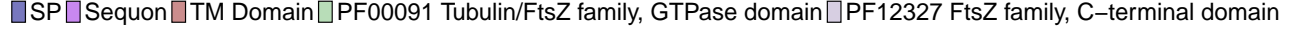
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AGTAKSMGLTYGVITTFPFSEGRRRRAVAGEGHAALRENVDTLVWPNKLLTAVSPSTVTEAFNLADDLRGGVRRGSDIRPGLVWVDFADVRAIMANAGSGLMGIGTATGKTRARDAALNAGSPLLDNGIERATGIVWNTGGSDLTLEVNAAAEVYDLDVPSANLIFGAVVDPISGGVSTLMTGFKRQEESSDGRLLGGNLTGGDASLGSNRRPASFLGEGGSVEPEFLRKKGRSRVPRV

NbL19g18920.1 fatty_acyl-CoA_reductase_2-like [MW = 27.94 kDa]

No. of times detected



log(intensity)



Values from



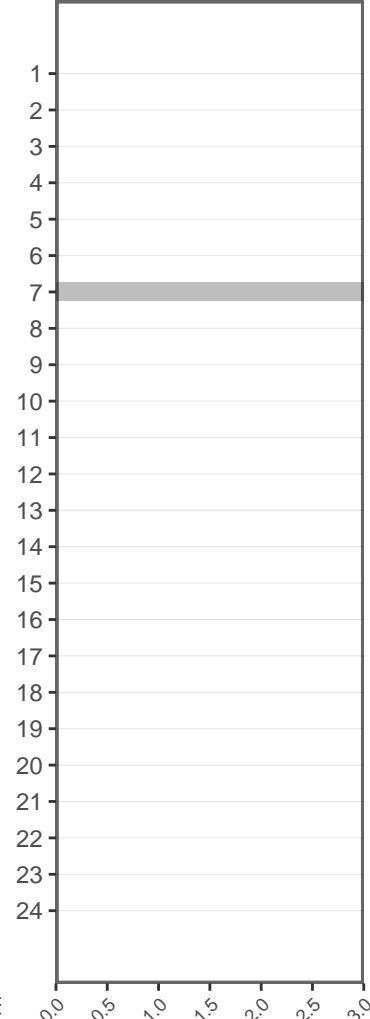
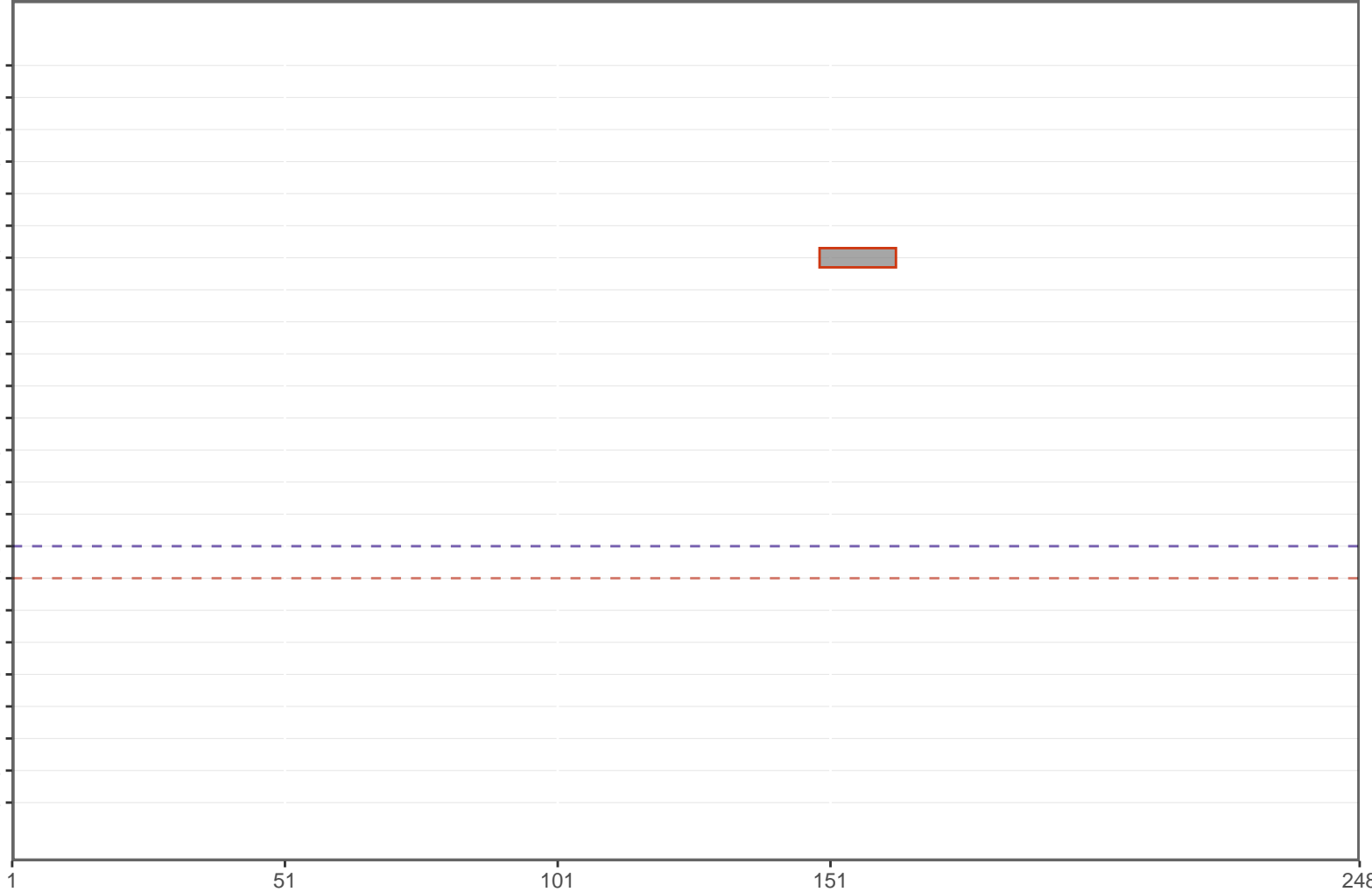
MW indication



Molecular weight



Gel Slice

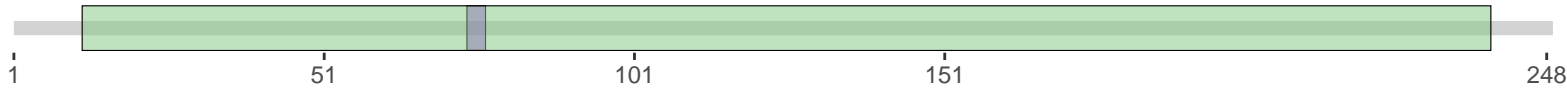


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

STAYANGEREGLLEKFPFMGESITKEKIFSFPTKFPGLNAMSEMDLVKLNKNAITTNLEQIMDTGIERAKLYGWQDTYGFYKAIEMMIDMSRREIPILILRPFVASSFRPEFPFGWQGFRCRPSISGG

NbL19g18850.1 probable_uridine_nucleosidase_1 [MW = 36.72 kDa]

No. of times detected



log(intensity)



Values from



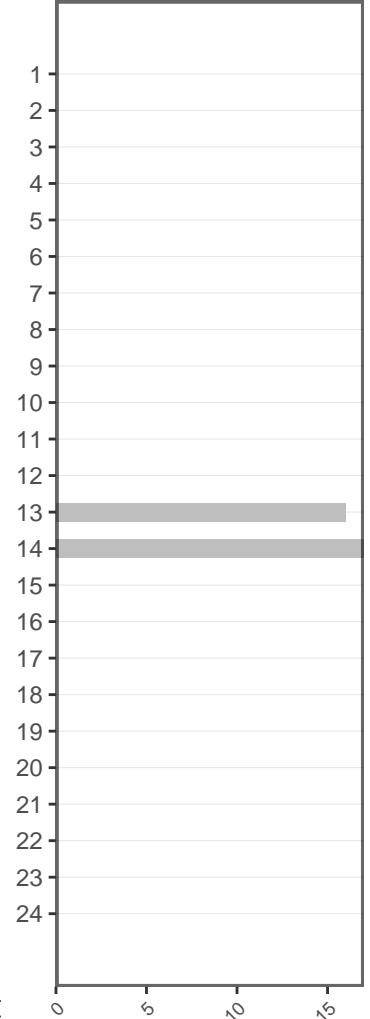
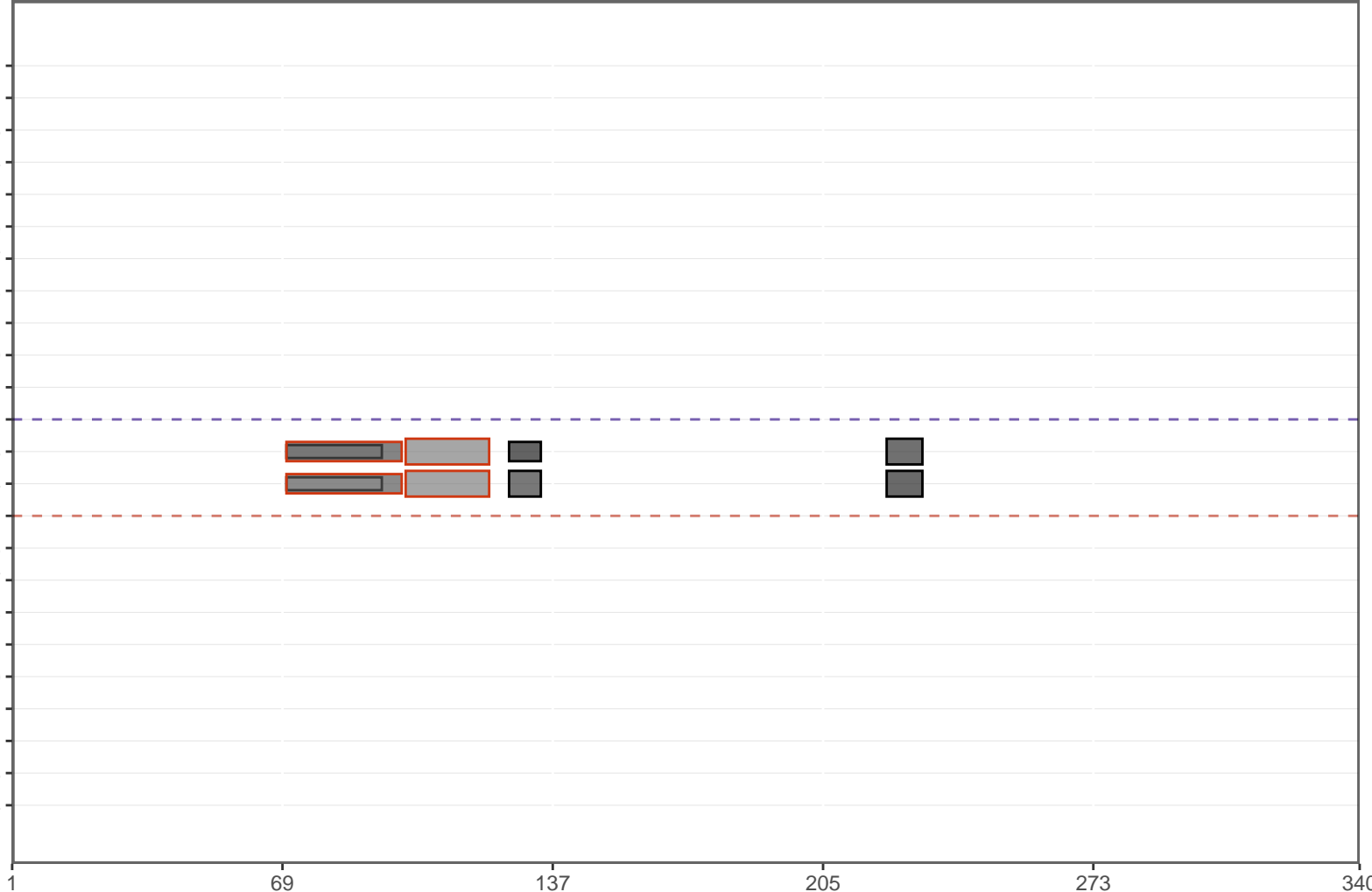
MW indication



Molecular weight

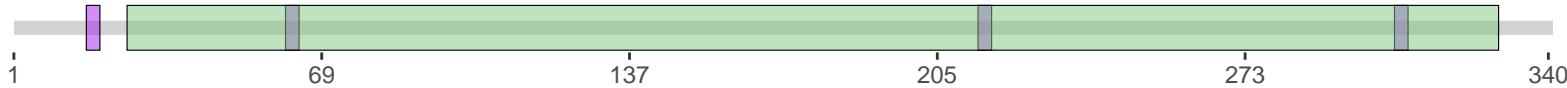


Gel Slice



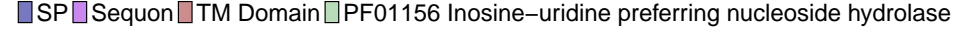
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

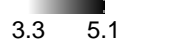
RDSTFASKVKRYVVLGGFFALGNVPAEANIYGDPEADIAFTSGANIDIVGINITQVLTADLEELRQSEGEGHANFLGNMGKFYRDWHVKSDGVYGFILHDPVSPVALVRFELFTFKKGVYRVETQGLGIGHTLMDGGKWKWNTSNPWTQVSPVSWAATVDVDEVLNWKKMLMKP

NbL19g18760.1 glucosamine_6-phosphate_N-acetyltransferase [MW = 17.87 kDa]

No. of times detected



log(intensity)



Values from



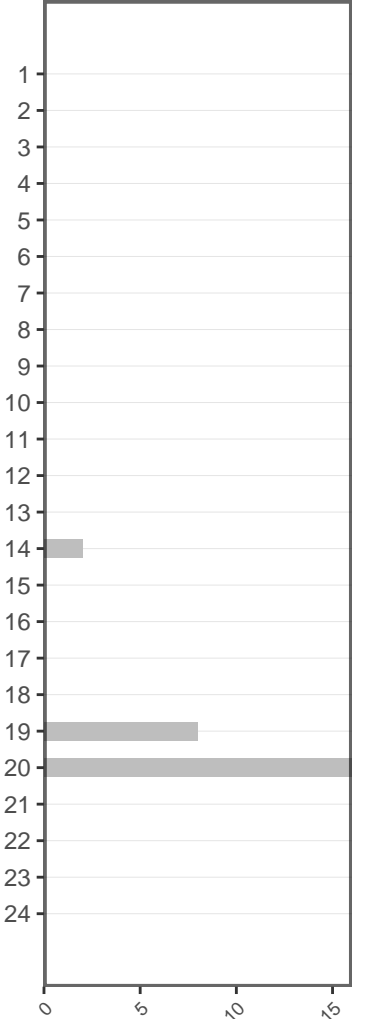
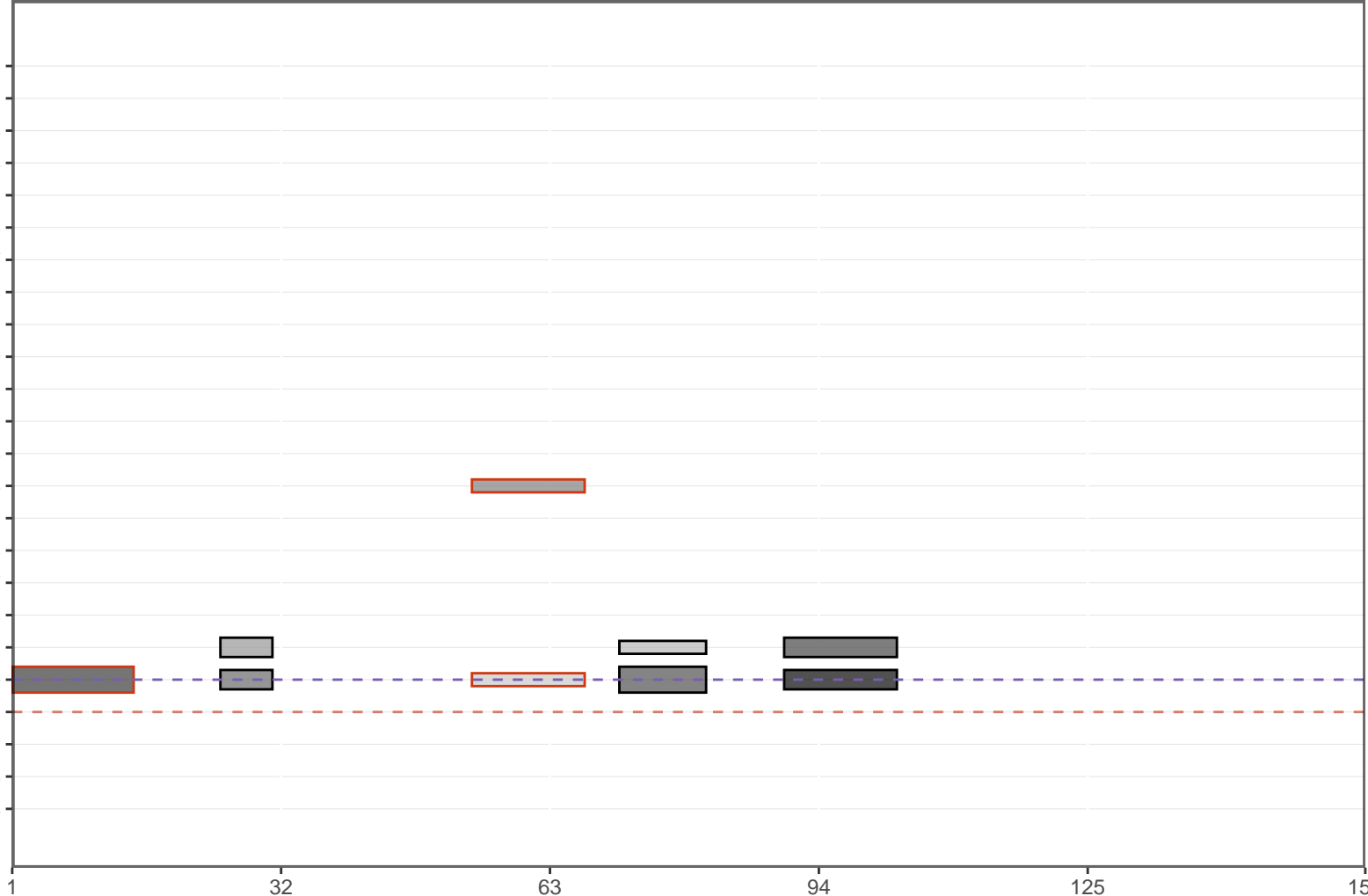
MW indication



Molecular weight

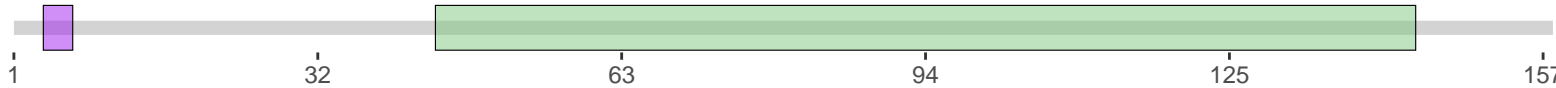


Gel Slice



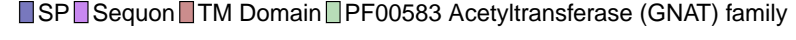
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KSGKIVATGVSVFIEKPKFVRNGGKAGHEDVAVD6STRGMQLKRIEVLANHAVSMGGYKVLDCTEENRPFYEKDGFKKKEIQMVKYFY

NbL19g18720.1 uncharacterized_LOC109242020 [MW = 39.71 kDa]

No. of times detected



log(intensity)



Values from



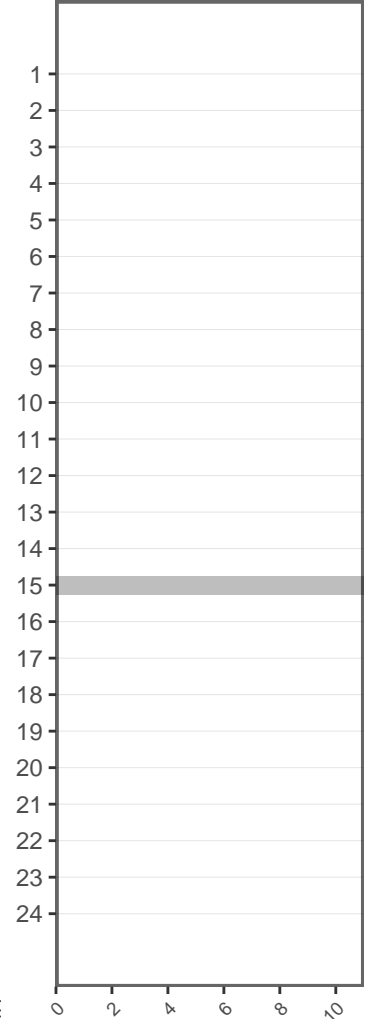
MW indication



Molecular weight

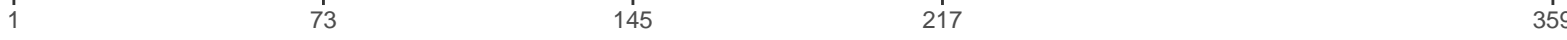


Gel Slice

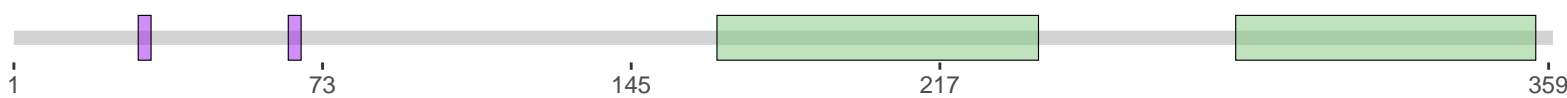


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

ISCPFCRCRVEIVAVLDELDAVYVPCPRNGPNFRPKVGMGGKGGGFPYVDPNTGVEMYESDEIKVLYGKYGDGNVFLMLSLGLLTLTAGFAMIGRMGKGGSSVYRPSKILPKPLEWAVEEPSPFKVRELVLELPHLHGARGSPKRGVLYERVGHFQVYVLEDPNTGVDMFESADIVDLGATVAL

NbL19g18710.1 alpha_carbonic_anhydrase_1_chloroplastic [MW - SP = 27.99 kDa]

No. of times detected



log(intensity)



Values from



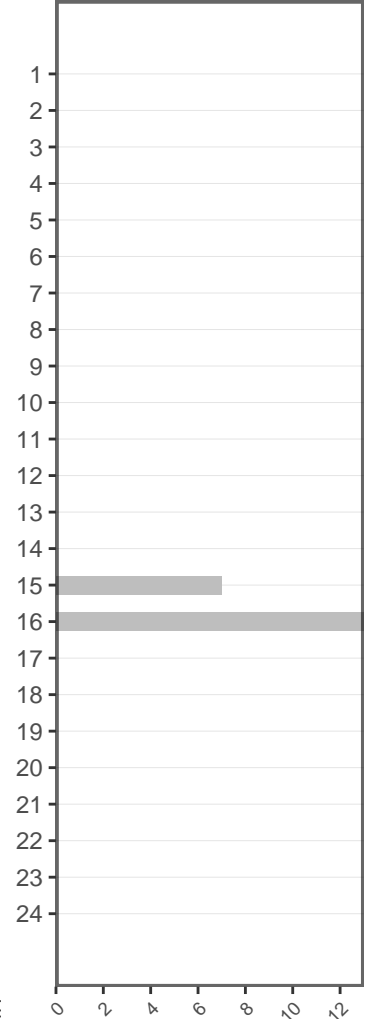
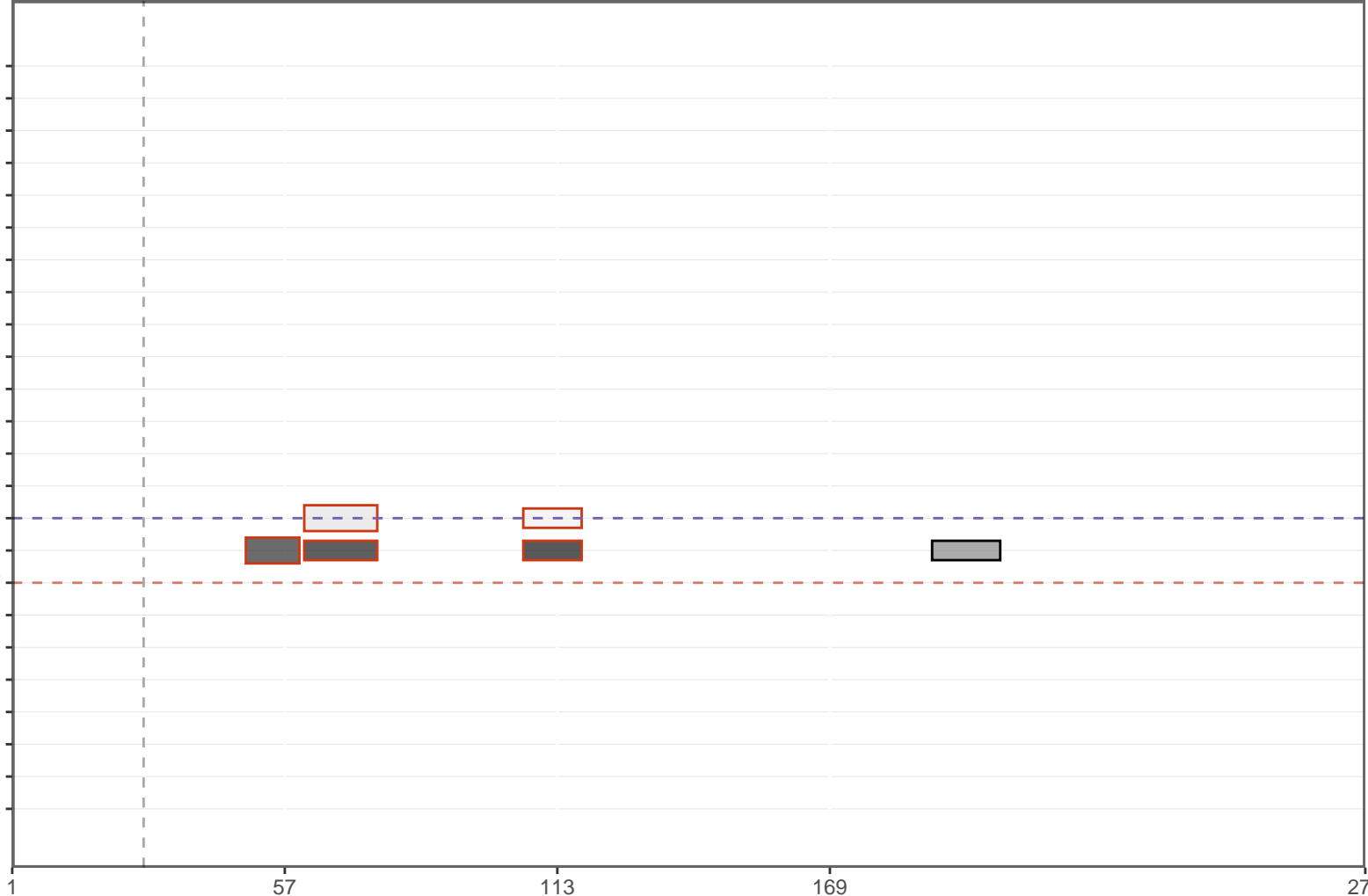
MW indication



Molecular weight



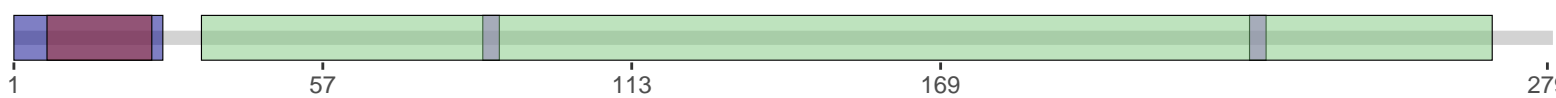
Gel Slice



Protein length

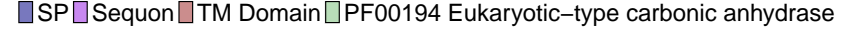


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MHSPSEHRLDGTQYAAELHWHFAEDNSLAVLTFHGHDPDMKLNKLNELARDVASQKETQKLGTDITHEIRKGGHHYYSVTGSLTPPGSENVSWHILGKVRISREGVEALRPLDSRCKRNARPVQPLNGRQIMYEVPNNV

NbL19g18680.1 heterogeneous_nuclear_ribonucleoprotein_R [MW = 53.02 kDa]

No. of times detected



log(intensity)



Values from



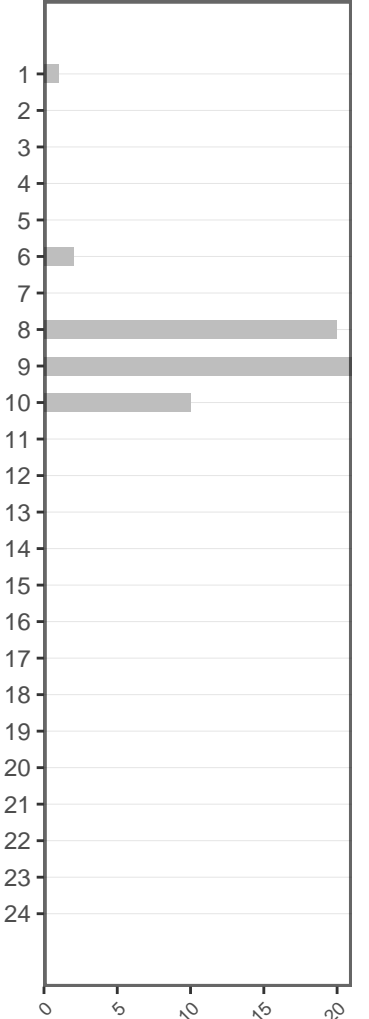
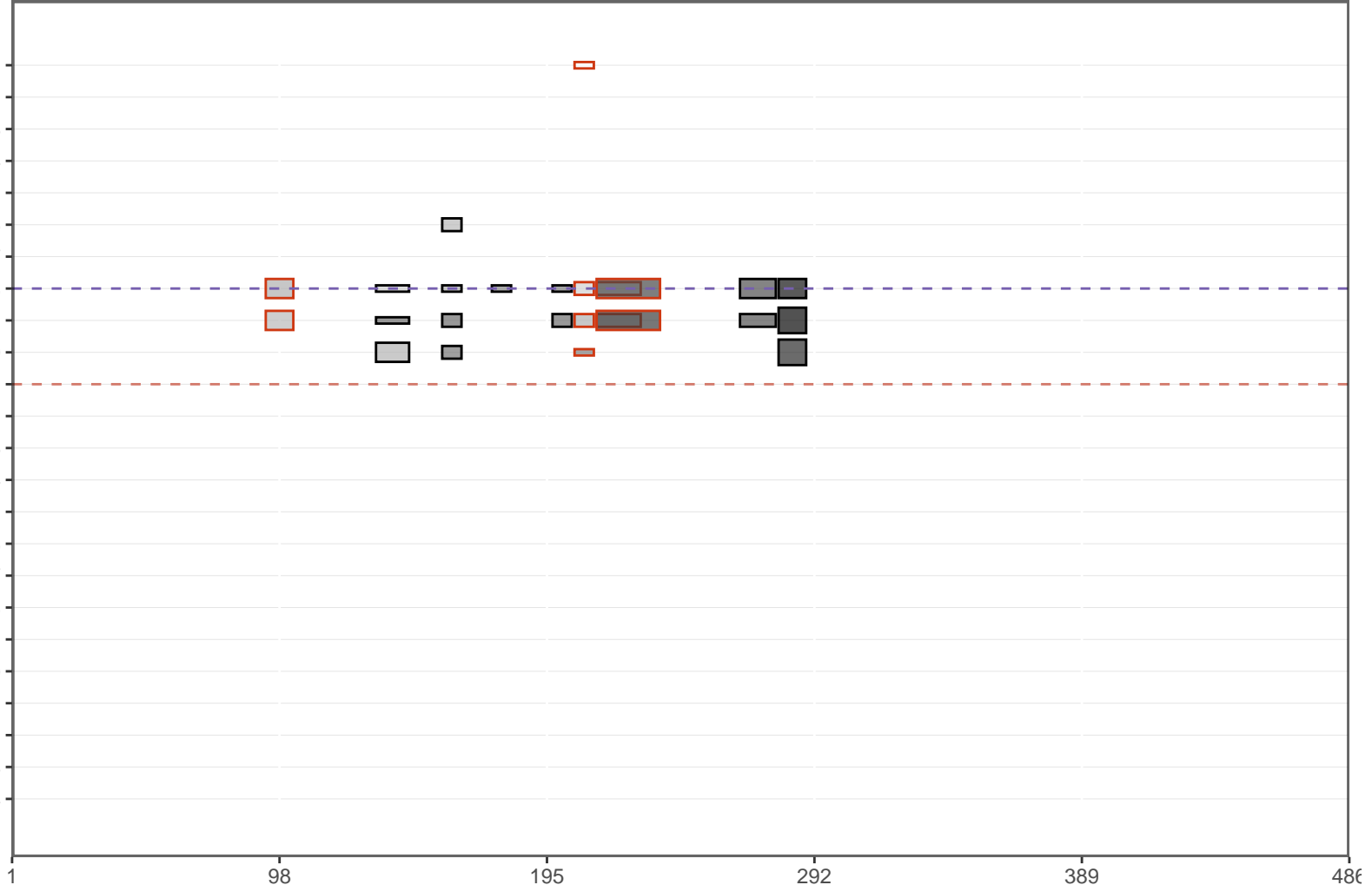
MW indication



Molecular weight



Gel Slice

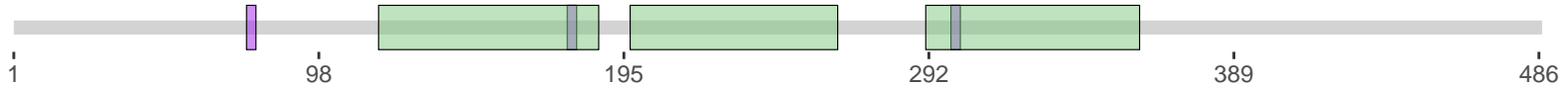


Protein length

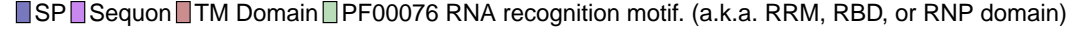


Peptide counts over 4 repeats

Pfam domains



Pfam Description

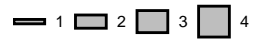


Protein sequence:

INSGRNRGFAFIEYNNACAEYSRQKMSNDKFLDGNAPTYSWADPKNAETAASAGQKAVYYKLNPKNTQDKKELFEHNGKTKVLPKPKGGEGSRVGFVFAERSSAMKALNTEREYEDGKLEGLAKPGADKSSGSSGKGPFLTFYPPRIGYGMVGPYVGSAGYGGAGVGGPLVYGRGASRGLMMPMLLPDGRIVYVGGPCVMHTFLPASRGRSGGGSSGSRGDSGRGRERINPY

NbL19g18640.1 signal_recognition_particle_54_kDa_protein_chloroplastic [MW = 61.91 kDa]

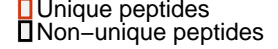
No. of times detected



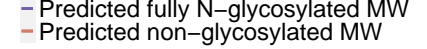
log(intensity)



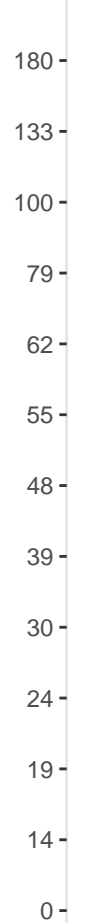
Values from



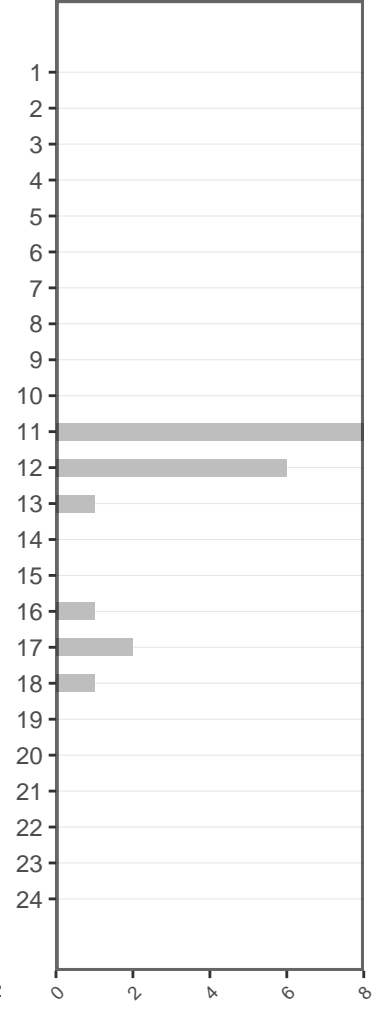
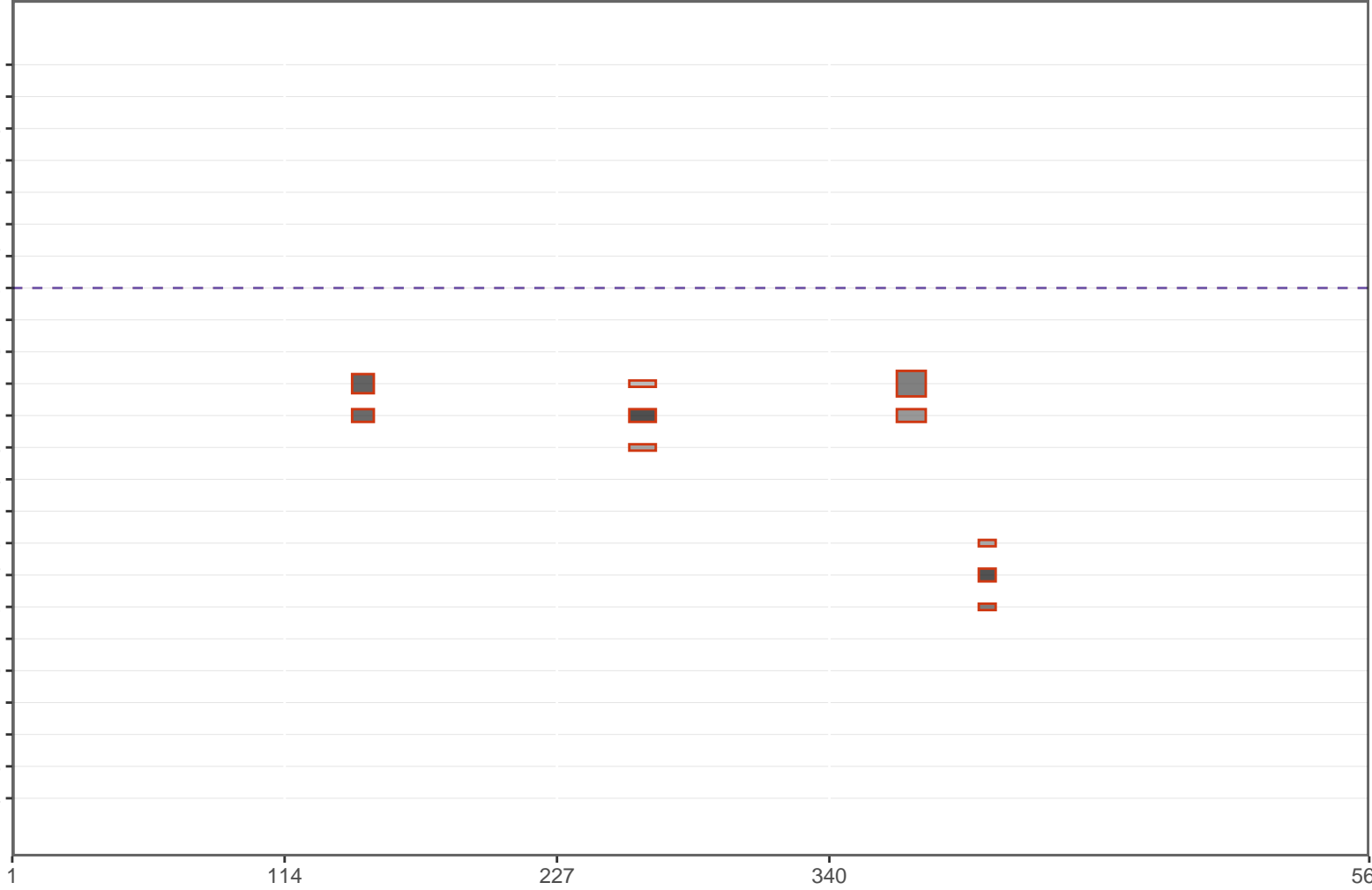
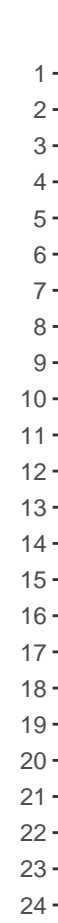
MW indication



Molecular weight

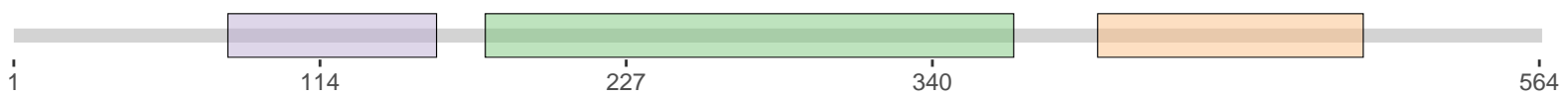


Gel Slice



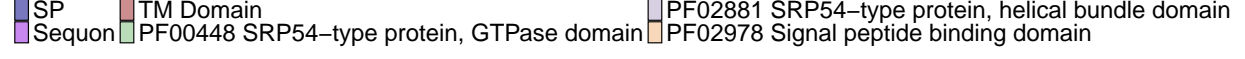
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KKAMMDELKEYKRVLNFTFVLLVDMTGGEEAAALVTFENLEIGTGAMTKLDDGDSRGGAAALSKVEVSGKPKLVGRGERMEDLEFFVPRMAGRLGMGDVLSFVEKAGEVMKGGDAEDLGGKIKMSAKFDNDFLKGTRAVAGMGTSRVLGMPGKGVTPAQIQREAEKSLIMESMIEVMTSEERKPELLAESPRRRKRIAGEGSKTEGGVSQLWOLFQMRVIRKMLMGVMOGGGIPALSNLEELAKTEGKAPPPTGARRKRRESGRKGFADGSTRPGPRGFGA

NbL19g18570.1 1-aminocyclopropane-1-carboxylate_oxidase_homolog_1-like [MW = 40.94 kDa]

No. of times detected



log(intensity)



Values from



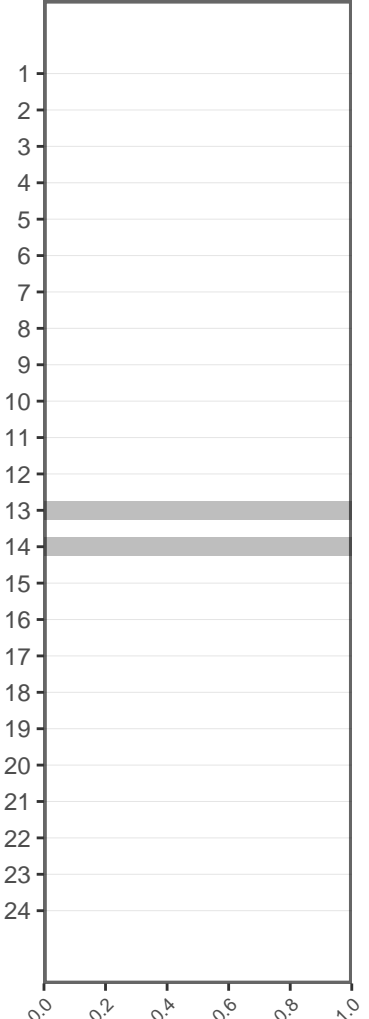
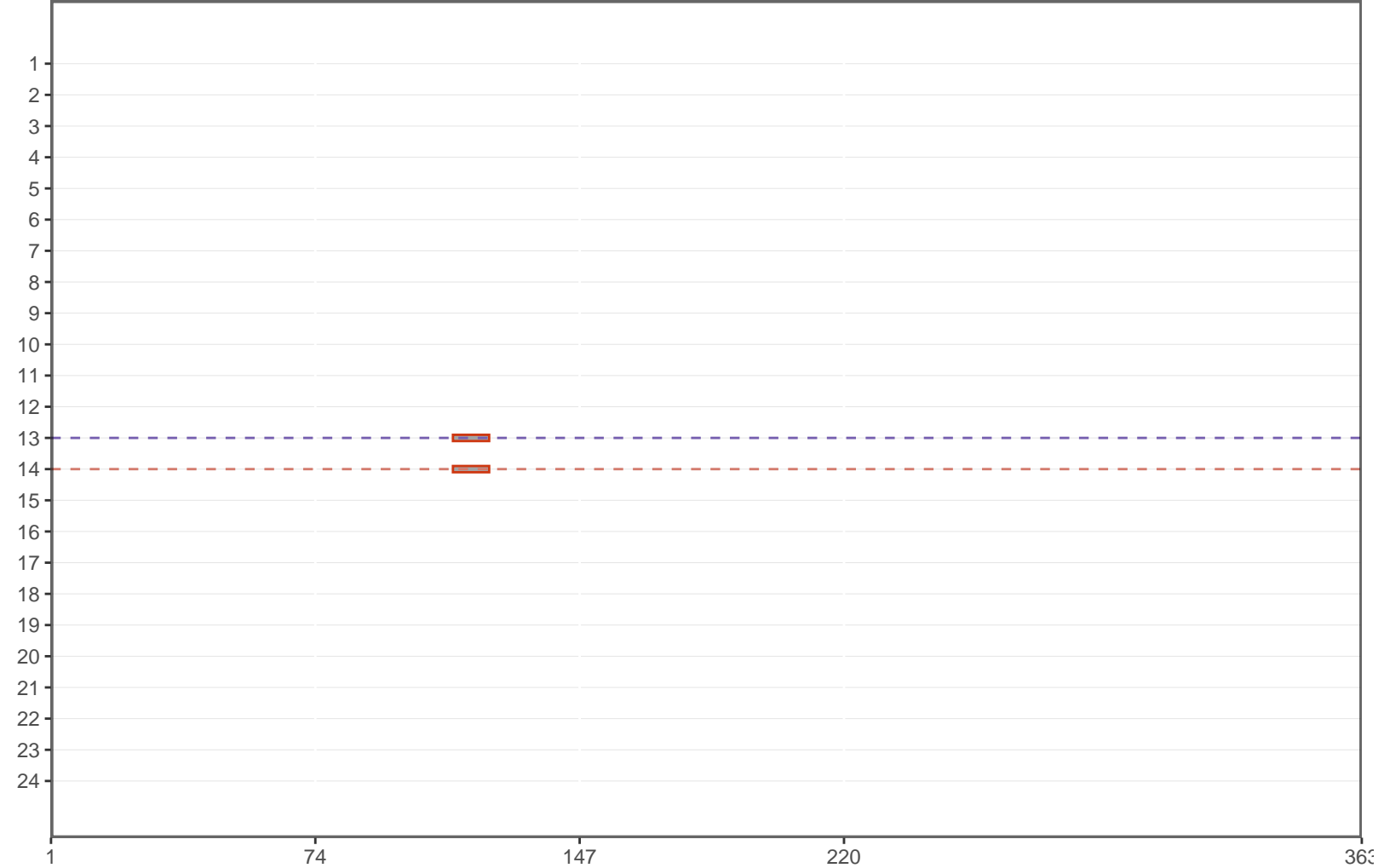
MW indication



Molecular weight



Gel Slice



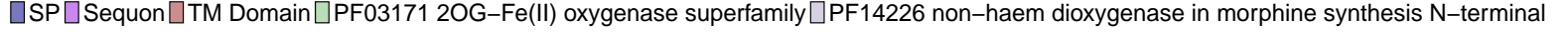
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LPPICRDIKYSSEEWKLGNSLFEELAEGLGLNRNHLTMDGDKGLSVVCHVYVAGPEPELTLGASKHADDGFTLLLDGHHGGLVLRHGNHWVDVPPPTGALVVMADLLQLSNDKFKVEHRVLANHGRPRISAGCFSTFLLAGSRVYEPKELLSDDNPKYKRETTHEVAAYFTAKGLDGTSAHHFRV

NbL19g18490.1 uncharacterized_LOC109237744 [MW = 21.26 kDa]

No. of times detected



log(intensity)



Values from



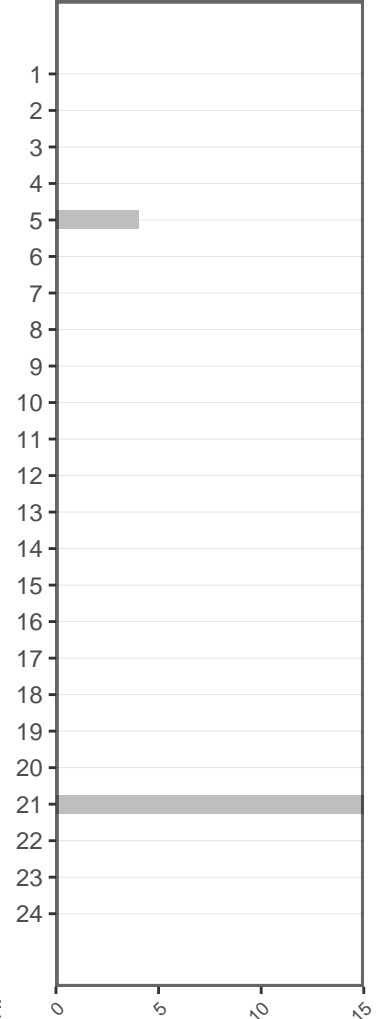
MW indication



Molecular weight



Gel Slice



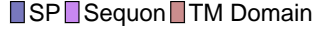
Protein length



Pfam domains



Pfam Description



Protein sequence:

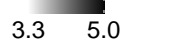
LPFDIDVAFETLLFQWANSLOGGAMLPPLVPLKVDKIPRGARLGGFTVEDAGTEVLVYIDCMVFRITDNGSPFRFRNRNGPSRDKAPDGEPRIMRSLGALGKVEIARV

NbL19g18460.1 beta-fructofuranosidase_insoluble_isoenzyme_1-like [MW = 66.5 kDa]

No. of times detected



log(intensity)



Values from



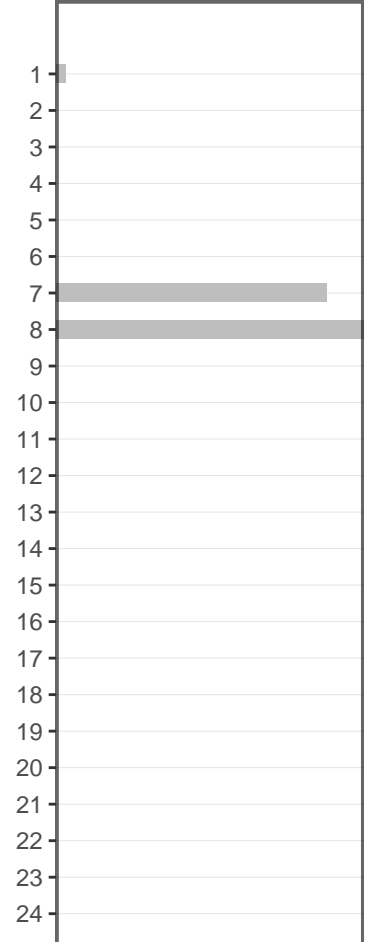
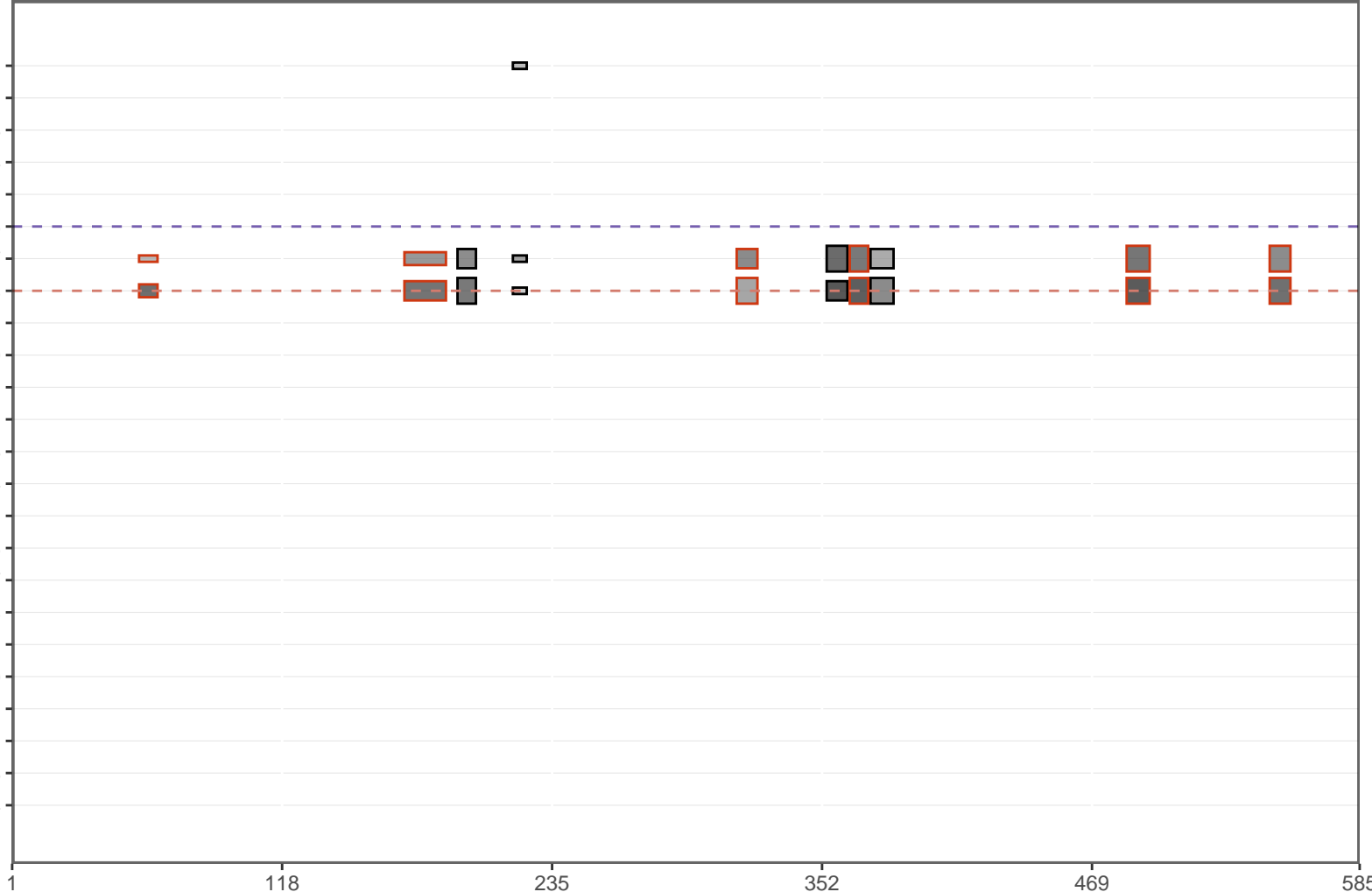
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00251 Glycosyl hydrolases family 32 N-terminal domain
- PF08244 Glycosyl hydrolases family 32 C terminal

Protein sequence:

P L A L F E Y T T G T Y D A K G D R Y P D N T S V D G W N G L R L D Y G M F V A S K S F Y D P S K D R R I V W G W S Y E S D G L F P D N N K G W A G I G T P R R V A L D F S G K G L V Q P V E E L K T L R K G N V L G L S N R L R L K G E K I E V G I T A S G T D V E V T F S F S L K A E P F N G S W A D L Y A G D V C A I K D S T V O G G L G P F G L A T L A S G N L E E Y T P V F R I V F K A Q K K Y V M L M G S D A T R S T E H N A M K P S F A G Y V D M D K D K L S L R S L H S N S V E S F G A G G K I G T S R A Y P T L A H D K A L E F A F N N G T E I T I E T L L

NbL19g18360.1 peptidyl-prolyl_cis-trans_isomerase_CYP18-2 [MW = 18.16 kDa]

No. of times detected



log(intensity)



Values from



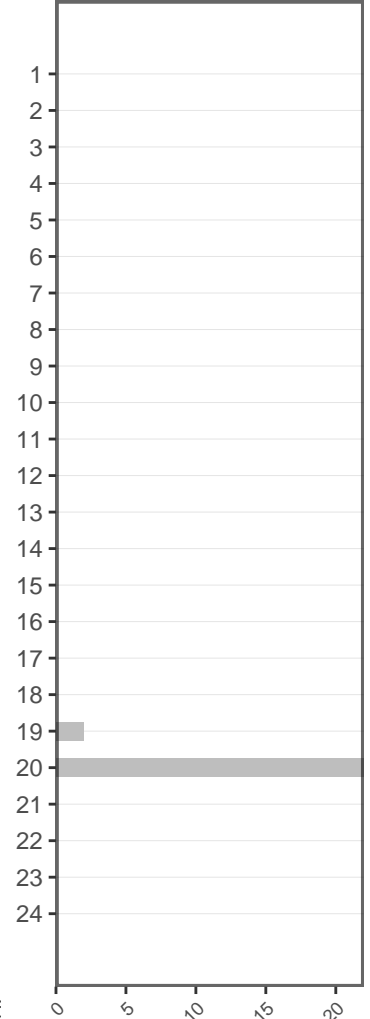
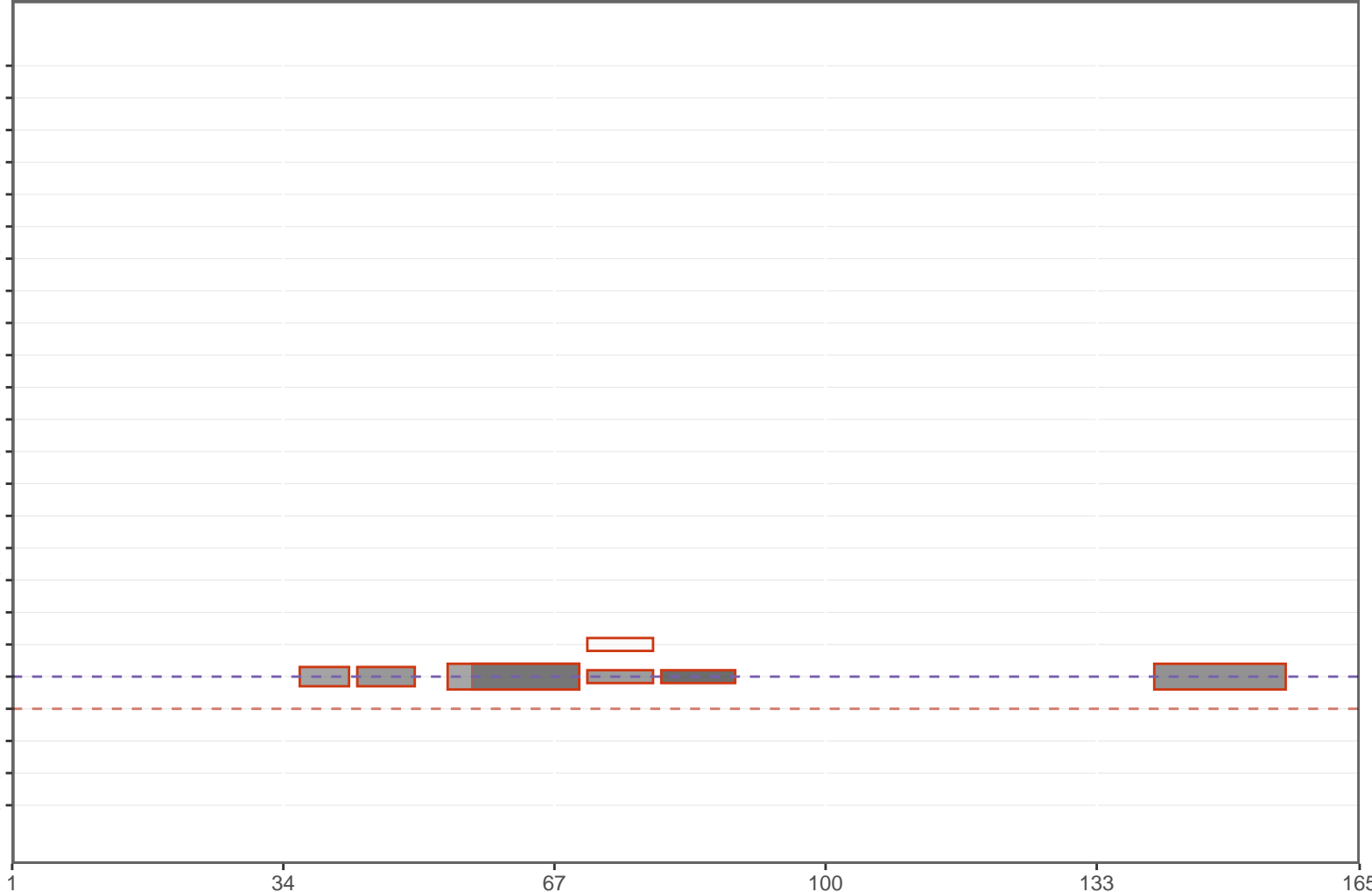
MW indication



Molecular weight

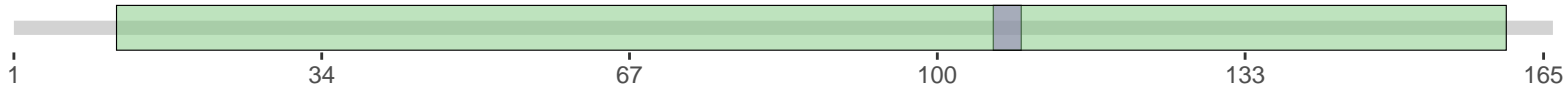


Gel Slice



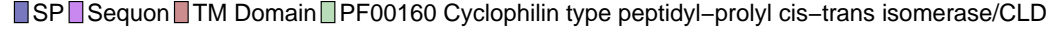
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGRGGESLYGAKFDDENGLKHTGAGHISMANAGPNTNGS6OFFFLAPAGLDDGKHTEFGVRCRGMERKRLGSGVQTDNTRPHIDVHLRTTVKDI

NbL19g18330.1 endoglucanase_8-like [MW = 55.82 kDa]

No. of times detected



log(intensity)



Values from



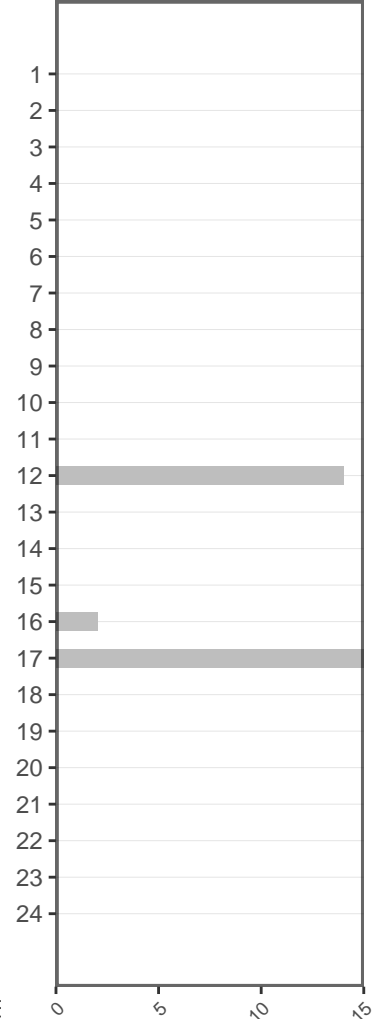
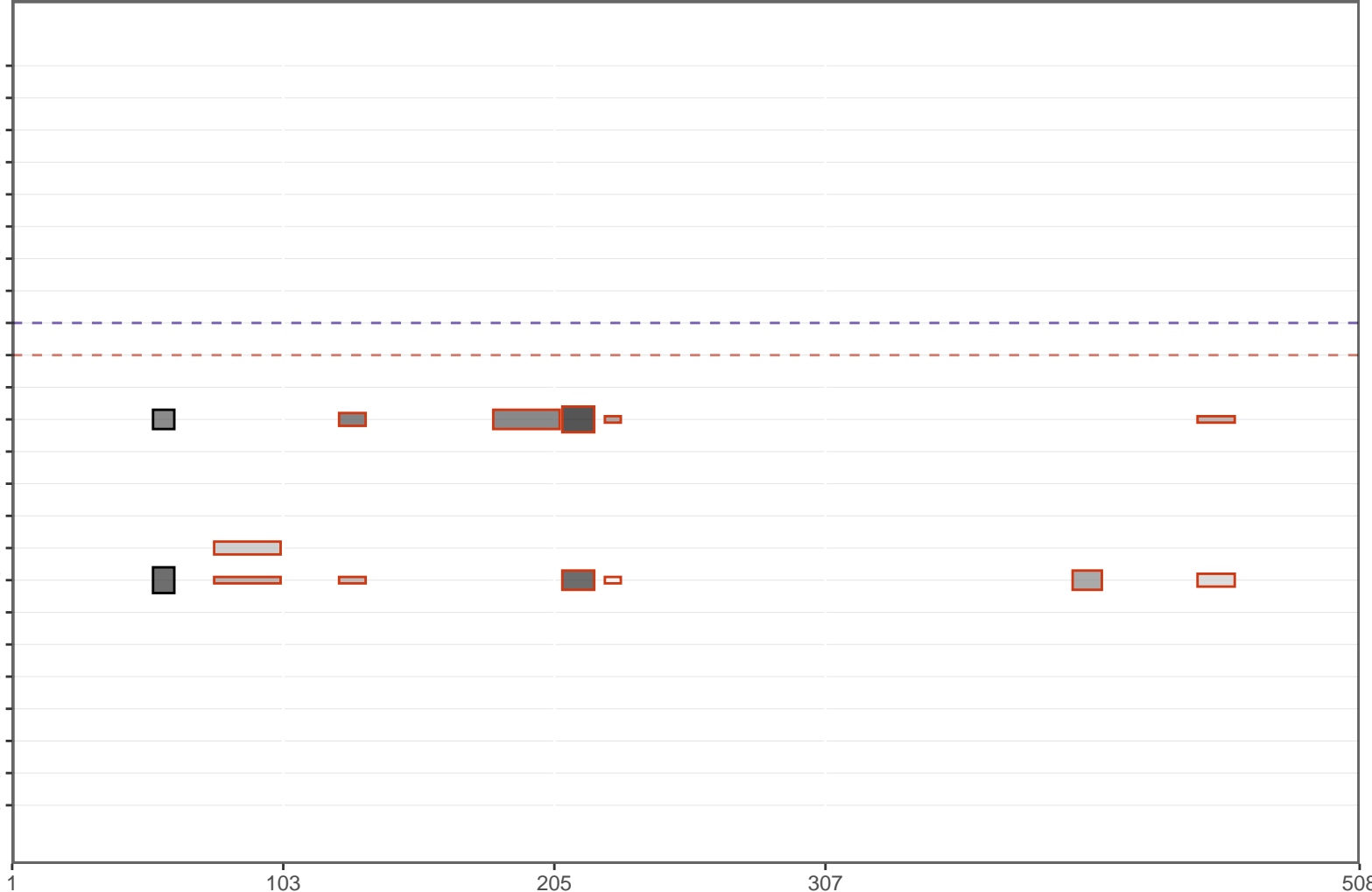
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AVCFPYCDFDGYDELLIGAWLHKATRRRQYREYVKNNEVLRAGDTEINEFGWDNKHAGINVLSEKEVLMGRAADLKSFGVNDADFICBLPGIAHPQVYSPGGILVWPKGVCMQMHVTELSFLLLAYSNLYSHANHAVPGGSMATPALKHKHAKRQVQVYLGDNPKRMSYHMGVGRVPLRIHHRGSLPQVAHPAQIGGGKGGSNYFFSRPNPNPNRLIGAVGGPNITDSFFDARPFDFGSEPTFYVNAPLVGLLAVSAHP

NbL19g18320.1 lysosomal_Pro-X_carboxypeptidase-like [MW - SP = 55.3 kDa]

No. of times detected



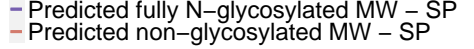
log(intensity)



Values from



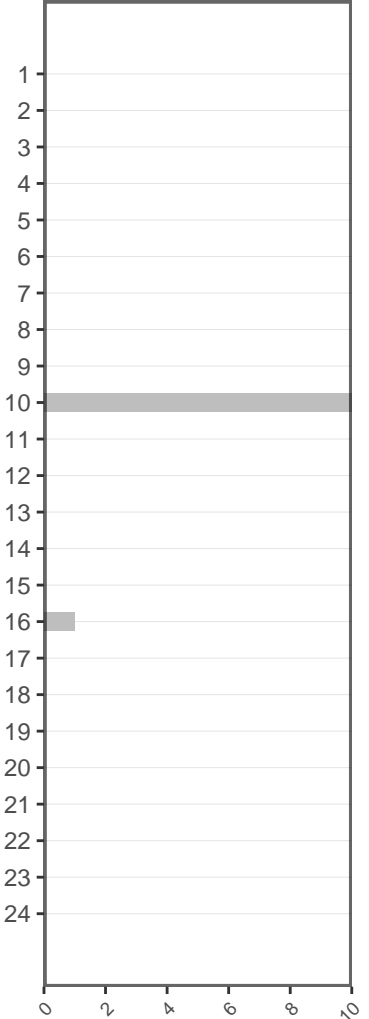
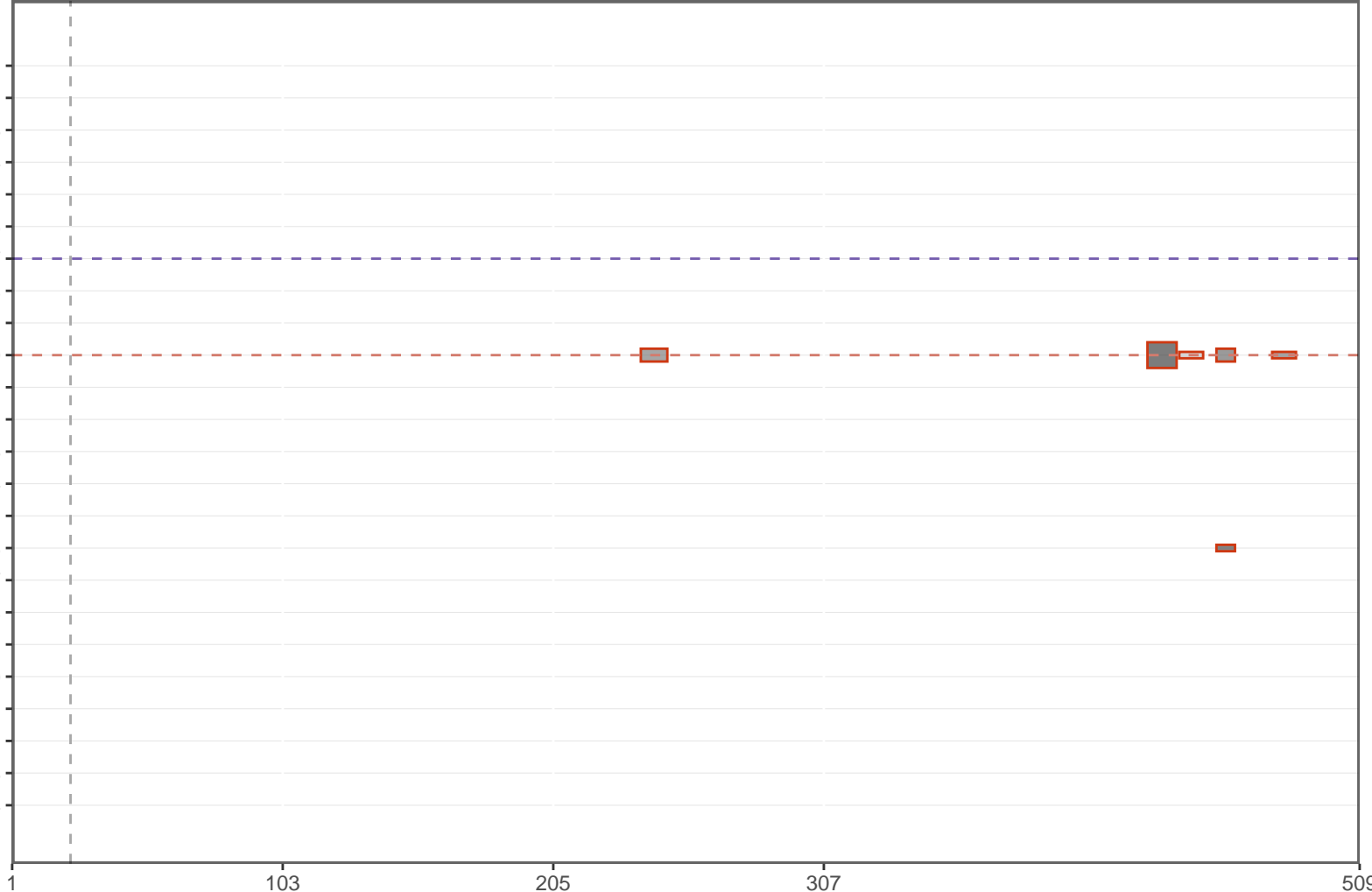
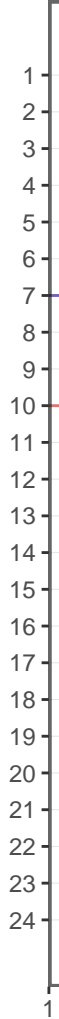
MW indication



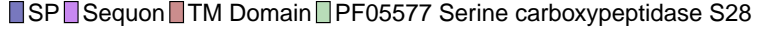
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

EVKGSWVQIEDMAKTTGGGKLRKFRICKNKHSPDGLNVLSTAYTYTAMTDVPTPSNLFNPLFRVYKEMCKAIDDPKSGNDLTKLYGAANIYNYTKATGFNLNDSDFHGLGGWTFWQACTEMVMPDQGNKESIFPPSEWDYNERVRFQKILVDKPRPDWITTEFGGYNIEVWLRKRFGNIFNGLRDPWGGGVLKDKIKGIVAIKEGAAHVDLRWVSKEDPEWLGEVRRAREINIEINWISQVYHITTEFSH

NbL19g18260.1 glutathione_S-transferase_L3-like [MW = 36.16 kDa]

No. of times detected



log(intensity)



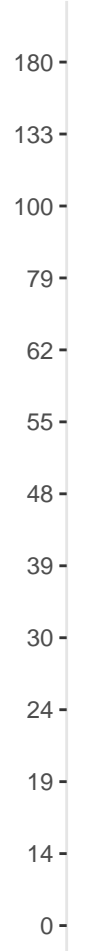
Values from



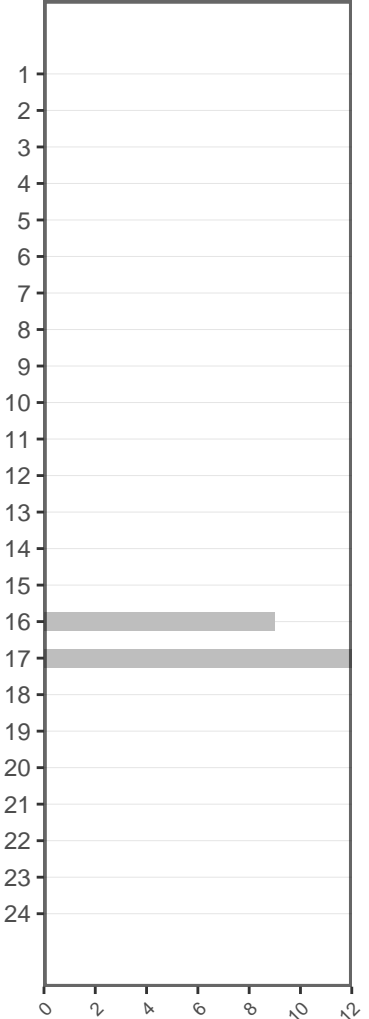
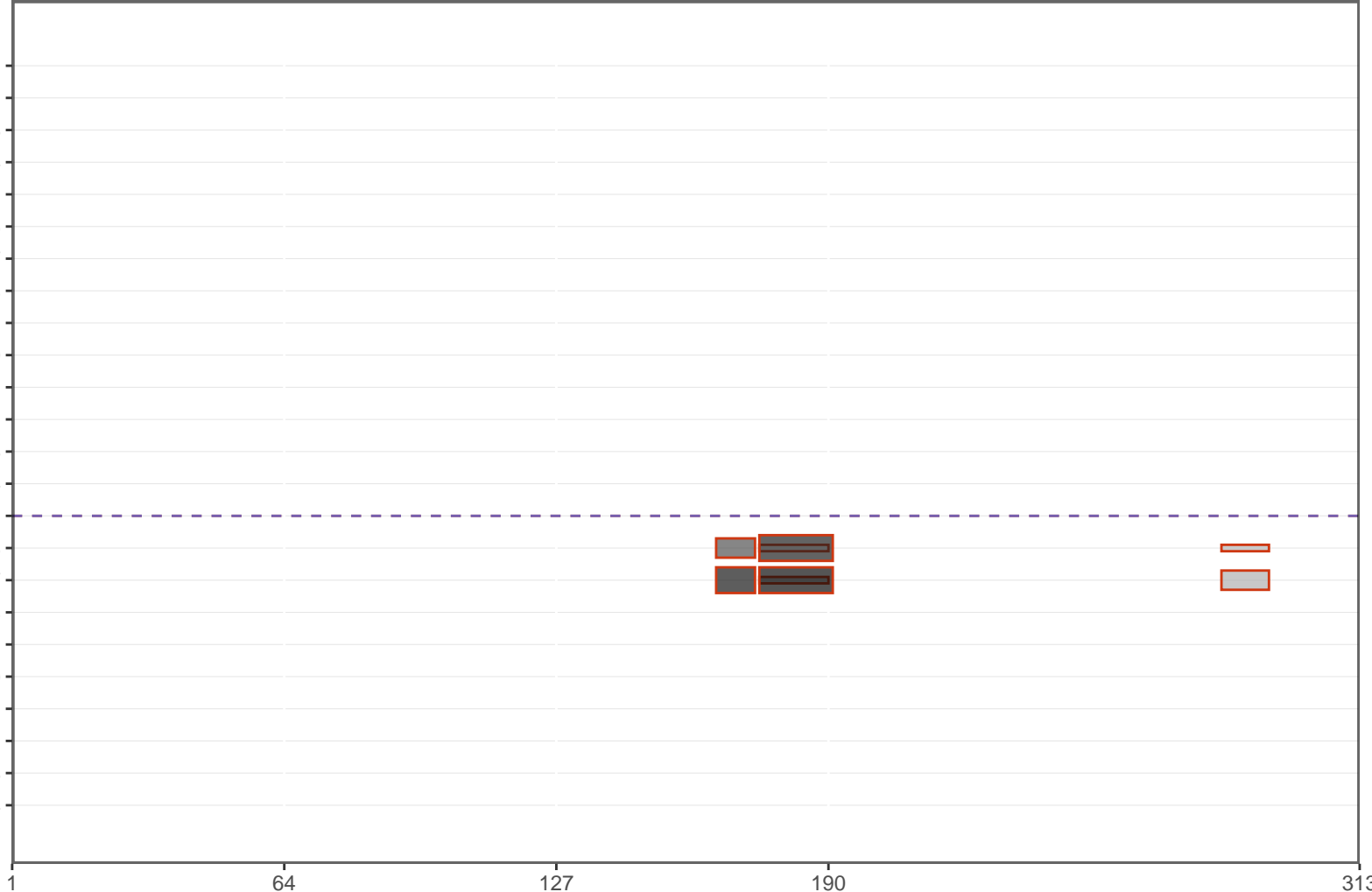
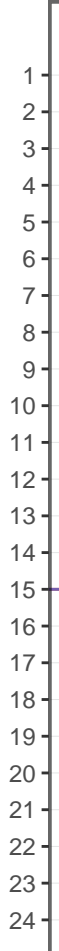
MW indication



Molecular weight



Gel Slice

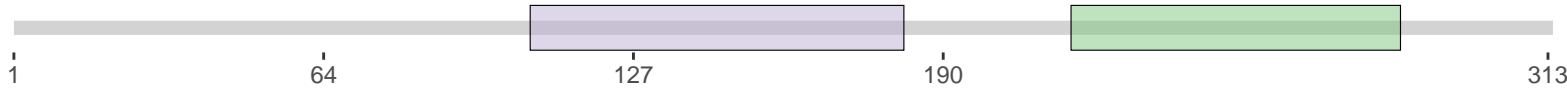


Protein length

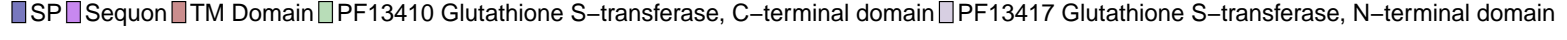


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

YKEKYAENKVPSEHNKIKVIGESLDLTKYVDSNFEFGPSLLPDDPKKQFAEELIAYSDTFVKEVYVGFKKDAGLAGAFDYLEKALEKFDGDFPFLGGFSGVDVAVPIERFQIFLGEVFNVDITSARPKLAWIEEMSNIDGKGTKVLDPKRLVEVYKRRFMA

NbL19g18130.1 uncharacterized_LOC107831931 [MW = 26.85 kDa]

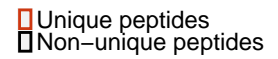
No. of times detected



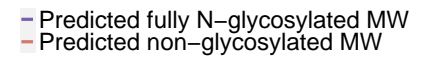
log(intensity)



Values from



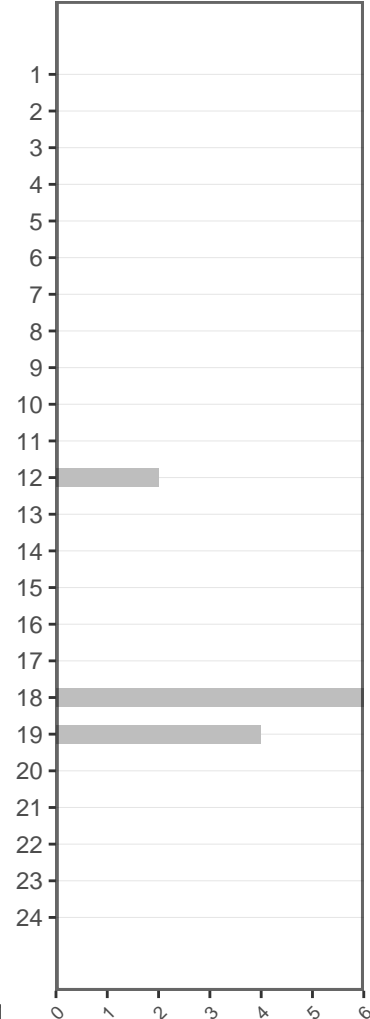
MW indication



Molecular weight



Gel Slice



Protein length



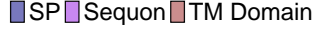
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

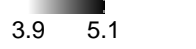
INPNYAPVAAAMQIFPTRNAVDASLRRAVVRTSRILFRMERADROGWDTLPNYDGKTLLOGIPRNALADDERFLGGQYDGGSSIQIFARQGRGDFRPPARVALVGFPSGALAAHAFITNRGFLVNNQIAVRLIQ

NbL19g18070.1 probable_pectate_lyase_4 [MW = 43.89 kDa]

No. of times detected



log(intensity)



Values from



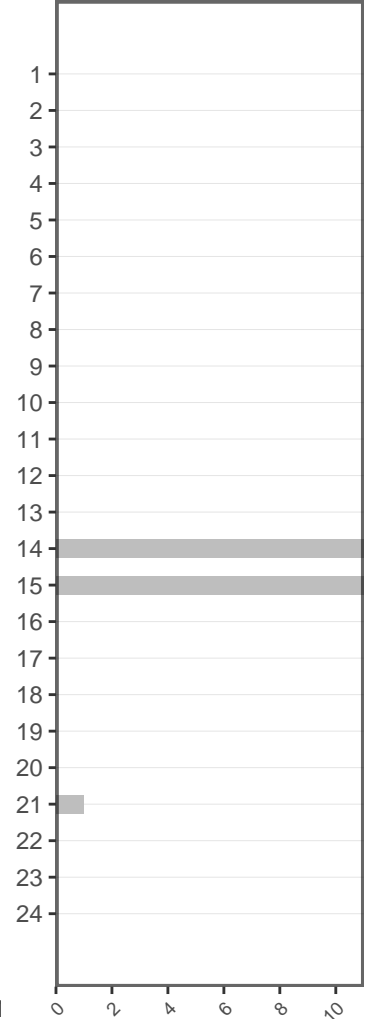
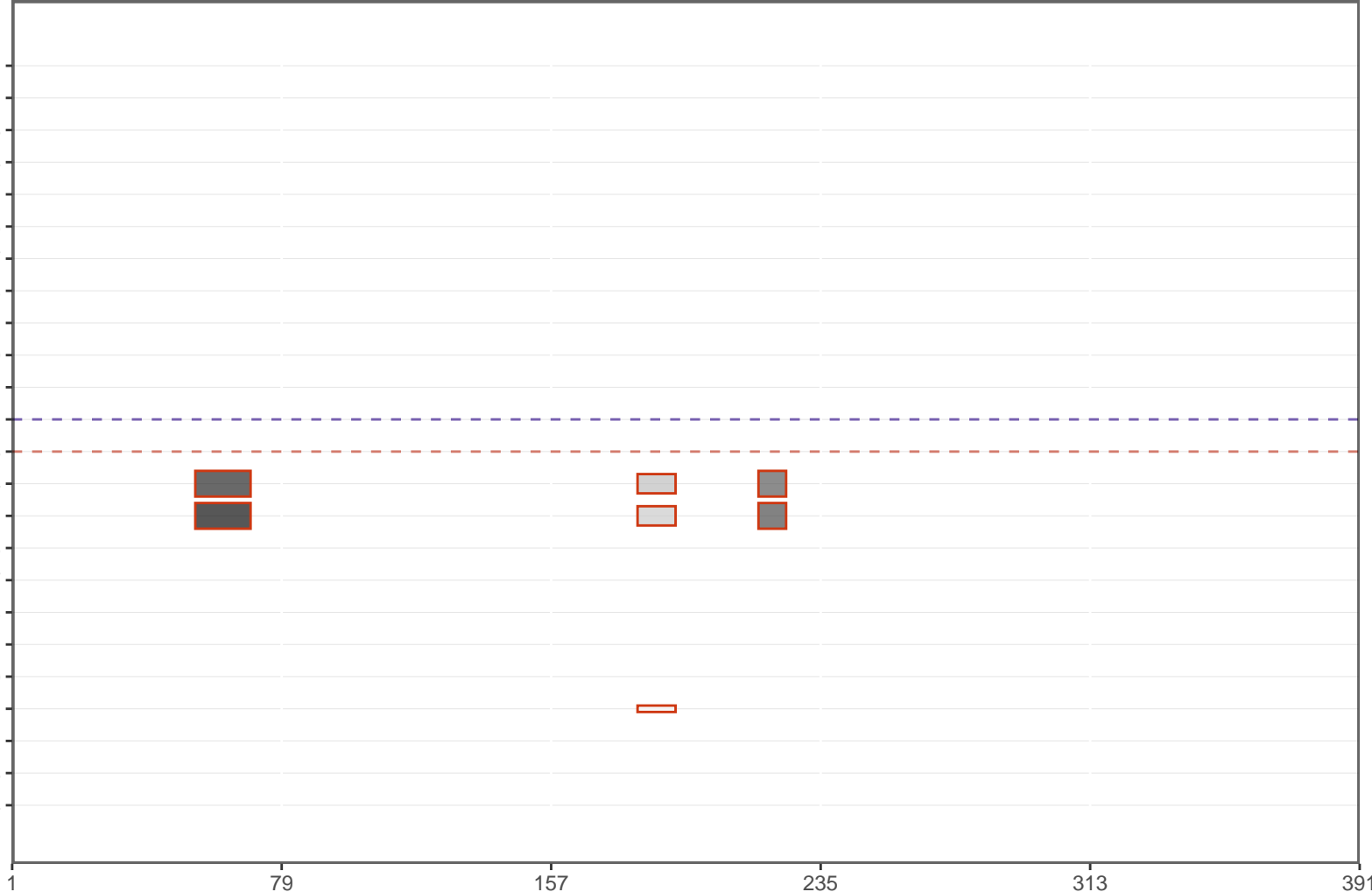
MW indication



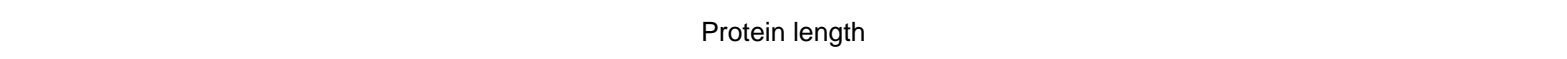
Molecular weight



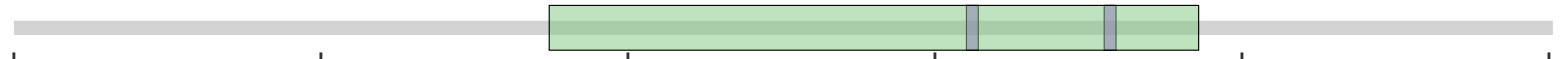
Gel Slice



Peptide counts over 4 repeats

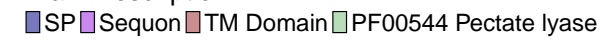


Protein length



Pfam domains

Pfam Description



Protein sequence:

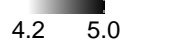
SSDYDAIQKPKSRHWIDRGLSDYDDGLIDTRREFTDYSRCHFSKHKDKTKMLGGDPSNCTDRGMRVTHHCFDCTRGRHPRVRFKGLHLYNTRINWGVYAGVAGVEQYVSDQNYEAGQKVAFKYTEKAAKDEEGCTGSIKSEDDLFDGDTQAGLLPTGSEENFNPCPEFHQTWTVEKPNDAKHLKLGHTGWSRPNV

NbL19g18010.1 protein_SLOW_GREEN_1_chloroplastic-like [MW = 40.2 kDa]

No. of times detected



log(intensity)



Values from



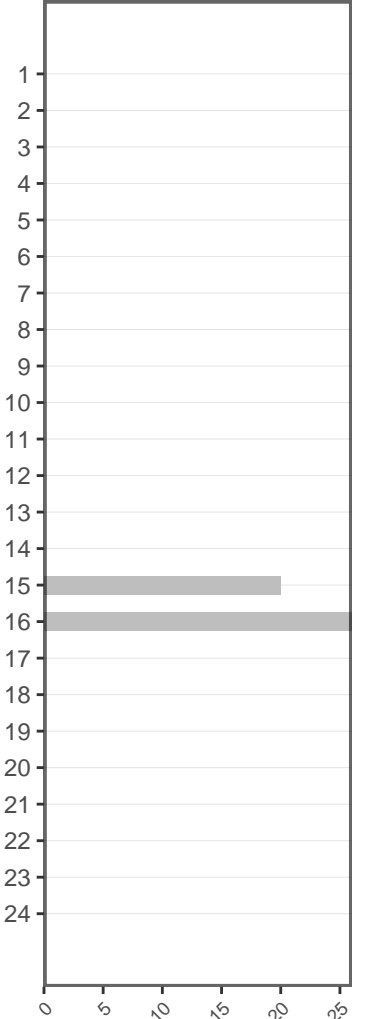
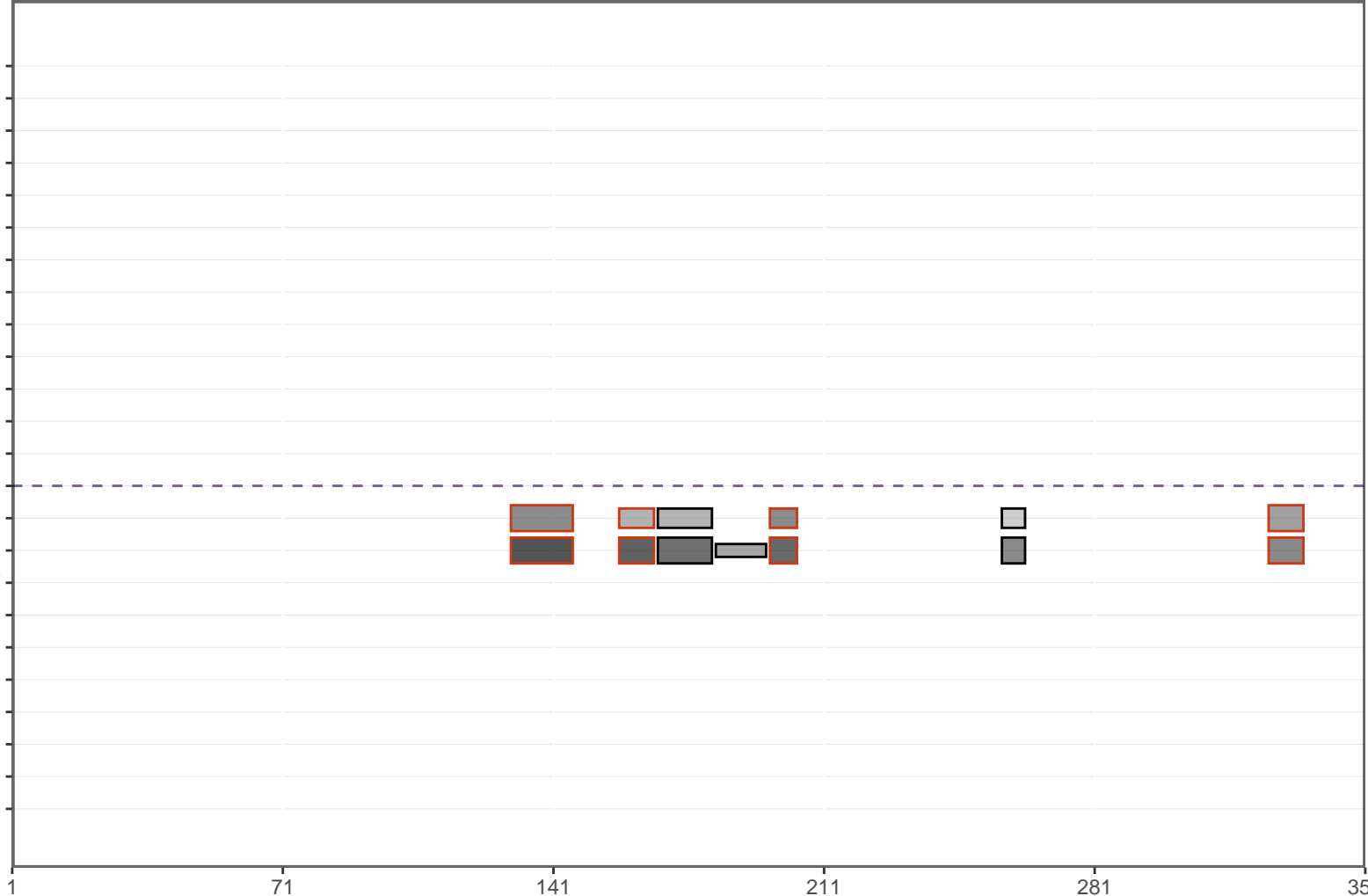
MW indication



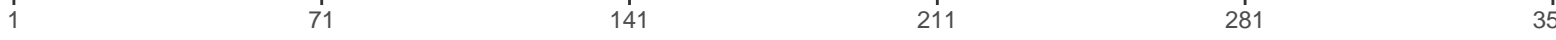
Molecular weight



Gel Slice

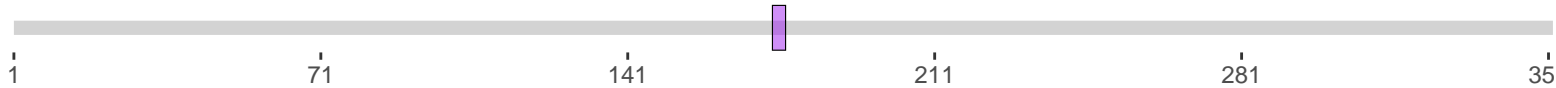


Protein length

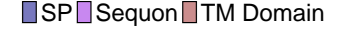


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

10KLEIPEVNESEIVPLMKSHLYNIGVEELAKVGFNELLKDFRVEAYHGLVMAASQDESIDDLKGIEMIEEGMLKCKENKKTDLRDLKLLAGIRVIEGKYEDALKVYVELVKEPRDFRPVYLOGGIYTLRKSSEAEGFEKYRRLVPOGHPVARYFDENMMATKVFAGKVENERAGSKS

NbL19g17980.1 60S_ribosomal_protein_L23a-like [MW = 17.32 kDa]

No. of times detected



log(intensity)



Values from



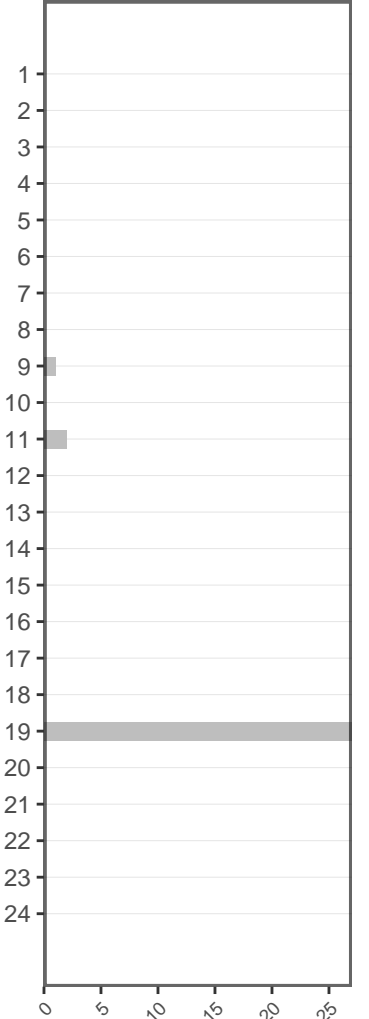
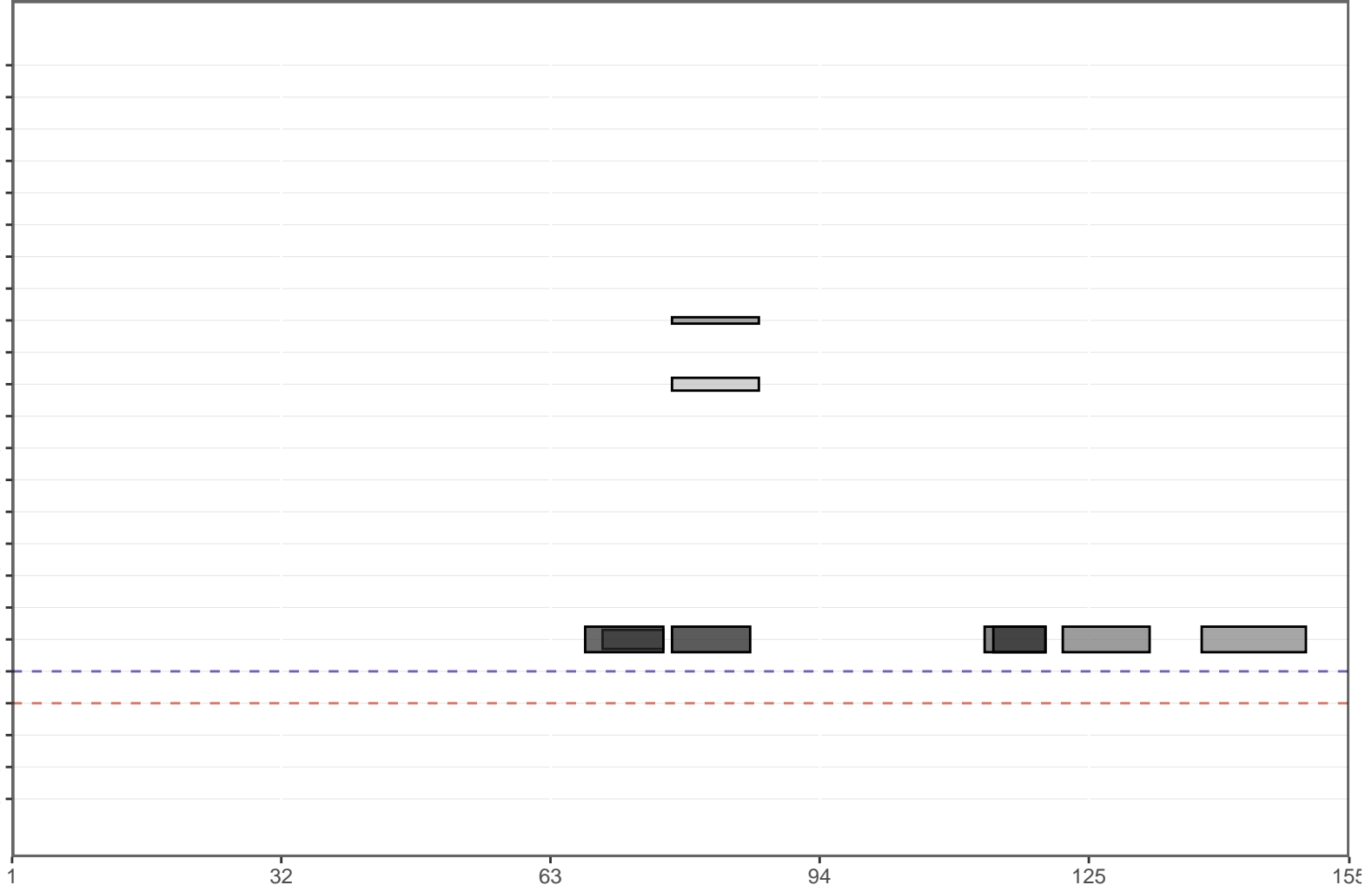
MW indication



Molecular weight

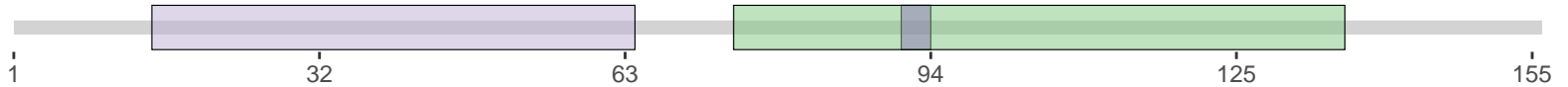


Gel Slice



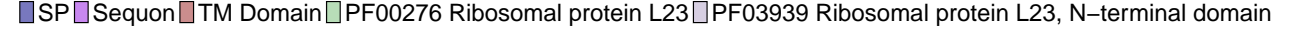
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

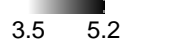
IAPGRNKLDOYGIKAYPLTTEBAMKKIEDNNTLFIYVDIKADKKIKDAWKMMYDQTRKYNFLRIPDGTAKAVVRLTPDVALEIVANKIGIP

NbL19g17970.1 diaminopimelate_epimerase_chloroplastic-like [MW = 39.6 kDa]

No. of times detected



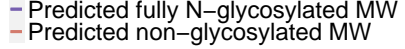
log(intensity)



Values from



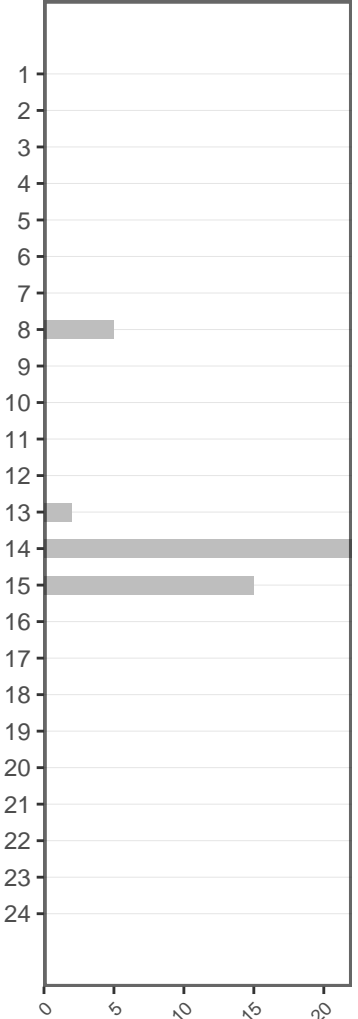
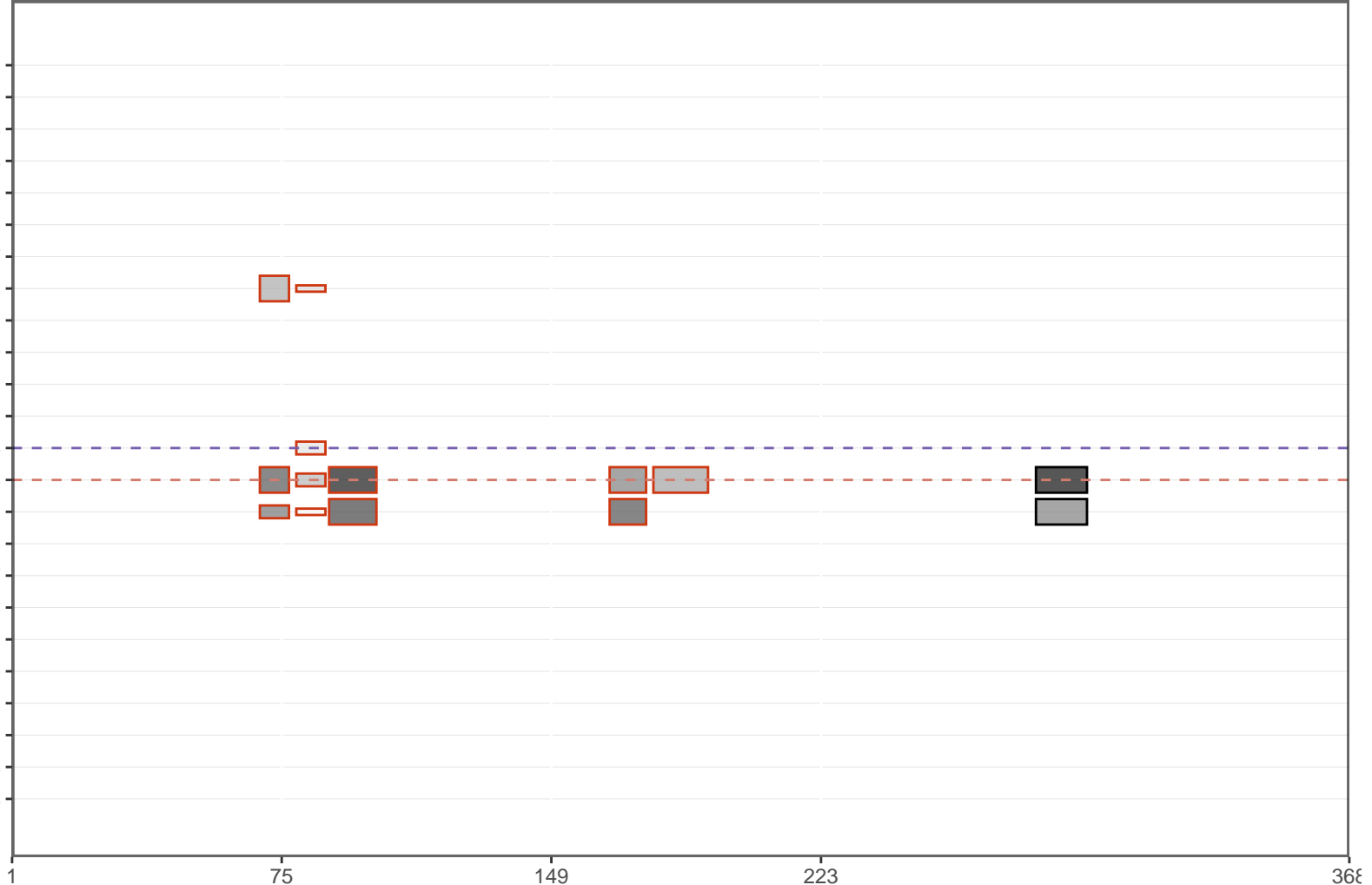
MW indication



Molecular weight

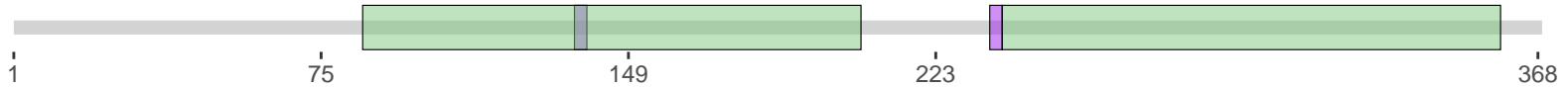


Gel Slice



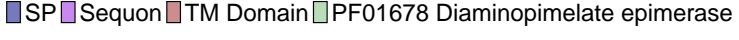
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGKRSFTHTGAGLVPEIREDDGKVRVDMGEPLKASDVPFKLPPNRDGSVVKARLVDGSAWNTCVSMGNPHCVTFGTGQSDLGVDLNLADGPKFHHVMPARTNTEFEVGFSPFHJKMIRWVERGAGATLADGTGAGAVVAWLEDRARRCTVLPDGGFLDEWSEKDNHVMFGPNEVVFYGSVPLV

NbL19g17900.1 probable_23-bisphosphoglycerate-independent_phosphoglycerate_mutase [MW = 52.92 kDa]

No. of times detected



log(intensity)



Values from



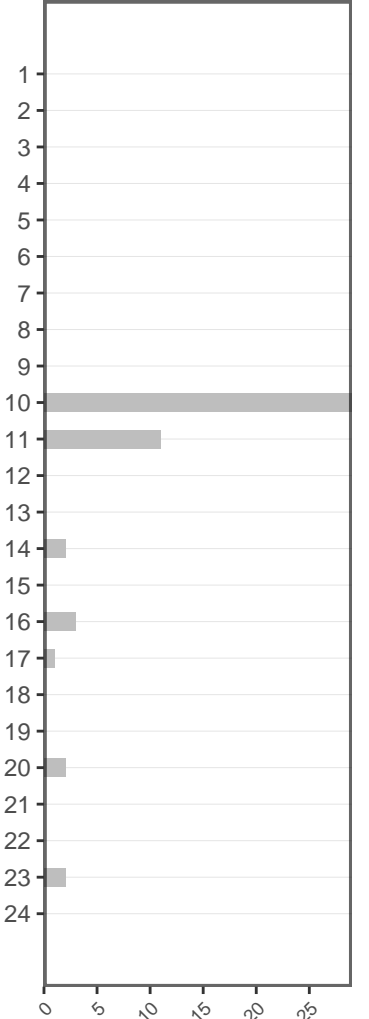
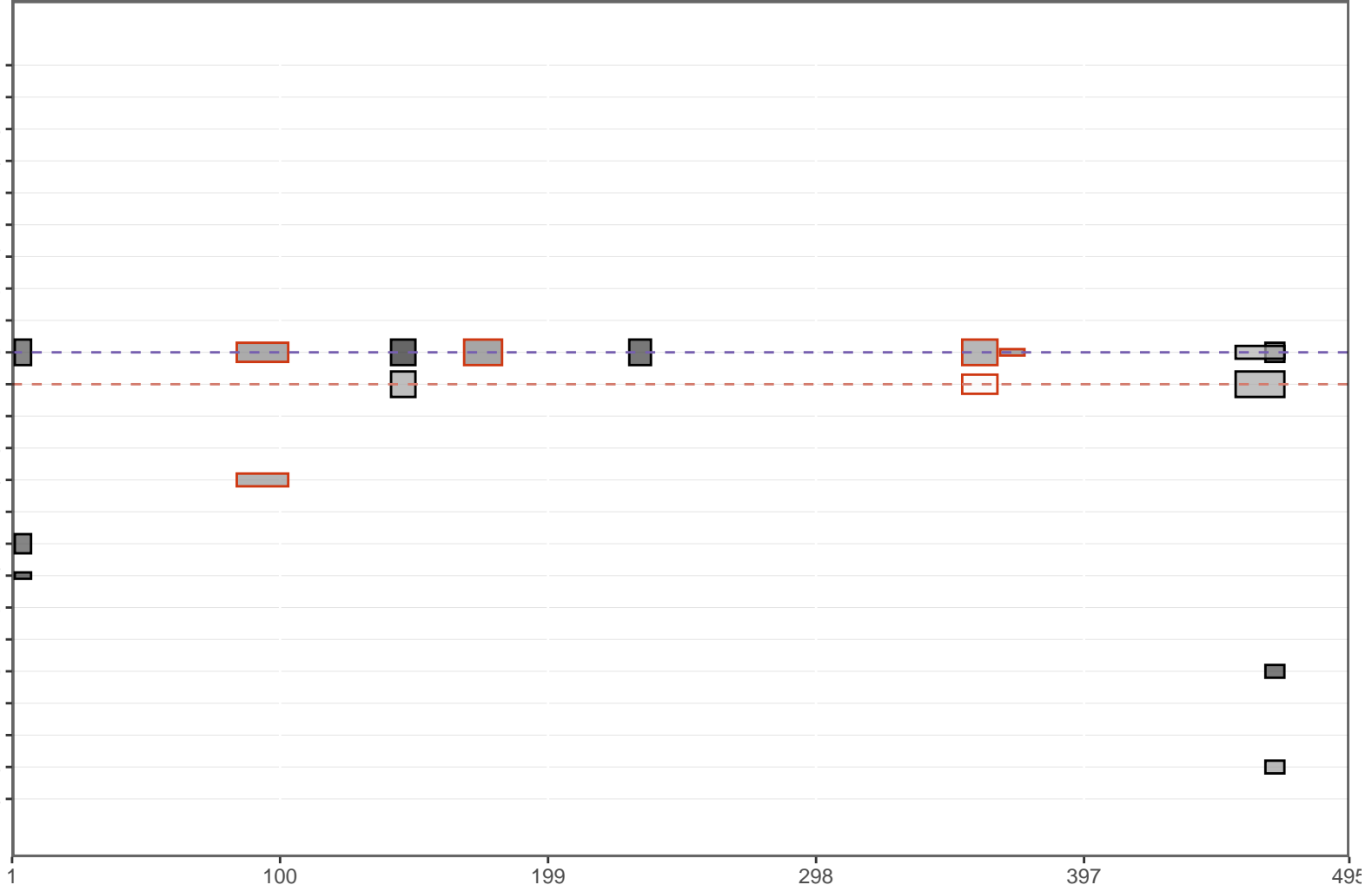
MW indication



Molecular weight

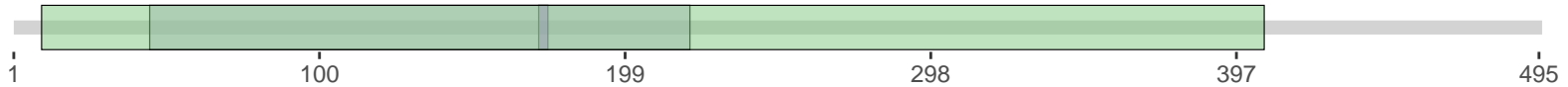


Gel Slice



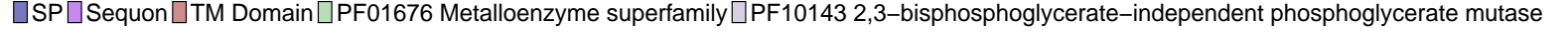
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

L V L R G C G I R E I V A P F E R I H G L W P C M V A P T R I A M G L G L S L G I D L E A P A T G D Y R T L T S K A A A I S K A L S A P L G S C P N F V P Q E D E H K P G R F D G Y D F G F L H K A I D D A G H D K A V F K A K G L E A V D L A G D L A R L L W E A E S T G K F S Y L V G T G D H S T P A V E Y G D H S F E P V F A L G S L K D F V S A L G G A S V L G S I G L D P P F L P S V Q A G E D I D I T R I E E V N K I L G F L A G D S V K F S E A A A R G G L G R F P S E M M G I K A V K L E A V

NbL19g17890.1 soluble_inorganic_pyrophosphatase_4 [MW = 24.46 kDa]

No. of times detected



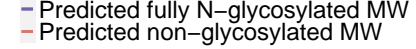
log(intensity)



Values from



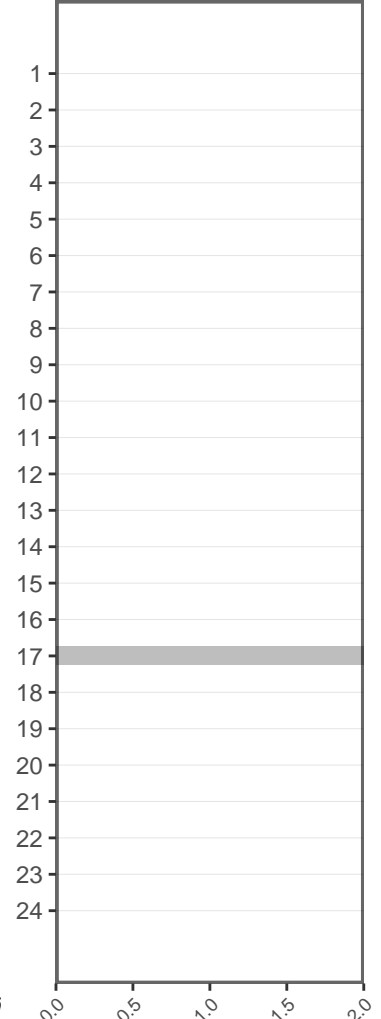
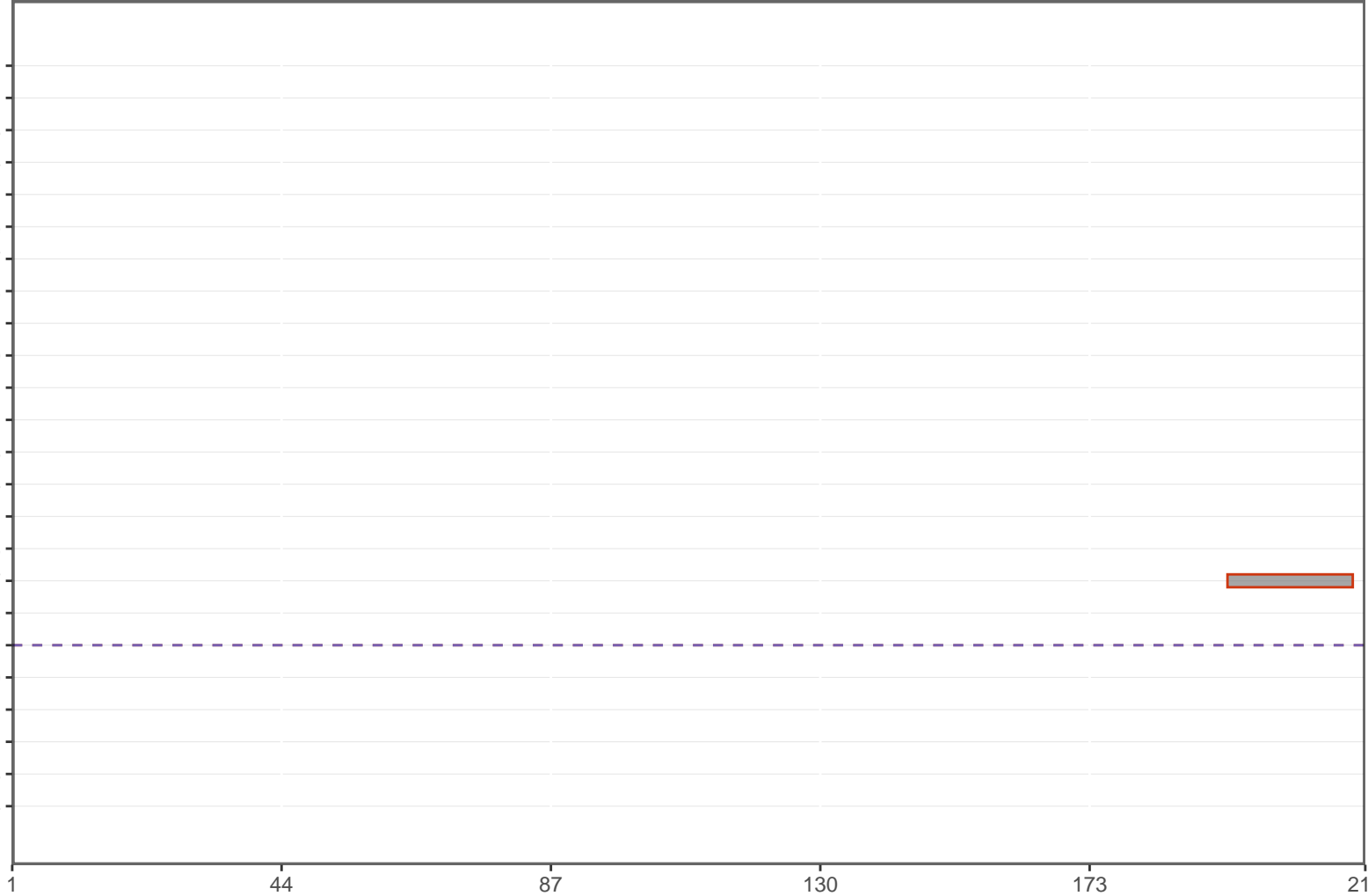
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IPRTLCEDSPLDVAIVMDEPVALPGGFLRAKAIGLMPIMDDGKDKIIVAGADDPKYEYTDIKELPPHRLAERIRFFEDYKKNENKEVAVNDFLPATKAFQAVGHSGDDVADYIVESLRK

NbL19g17870.1 histone_H2A-like [MW = 15.31 kDa]

No. of times detected



log(intensity)



Values from



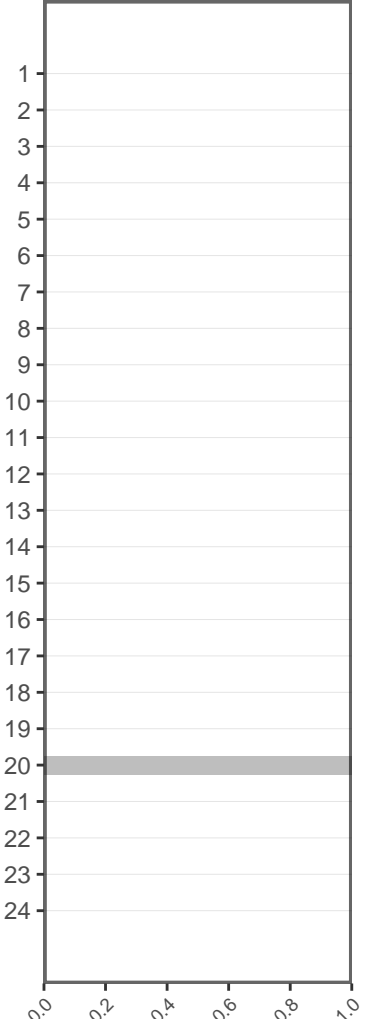
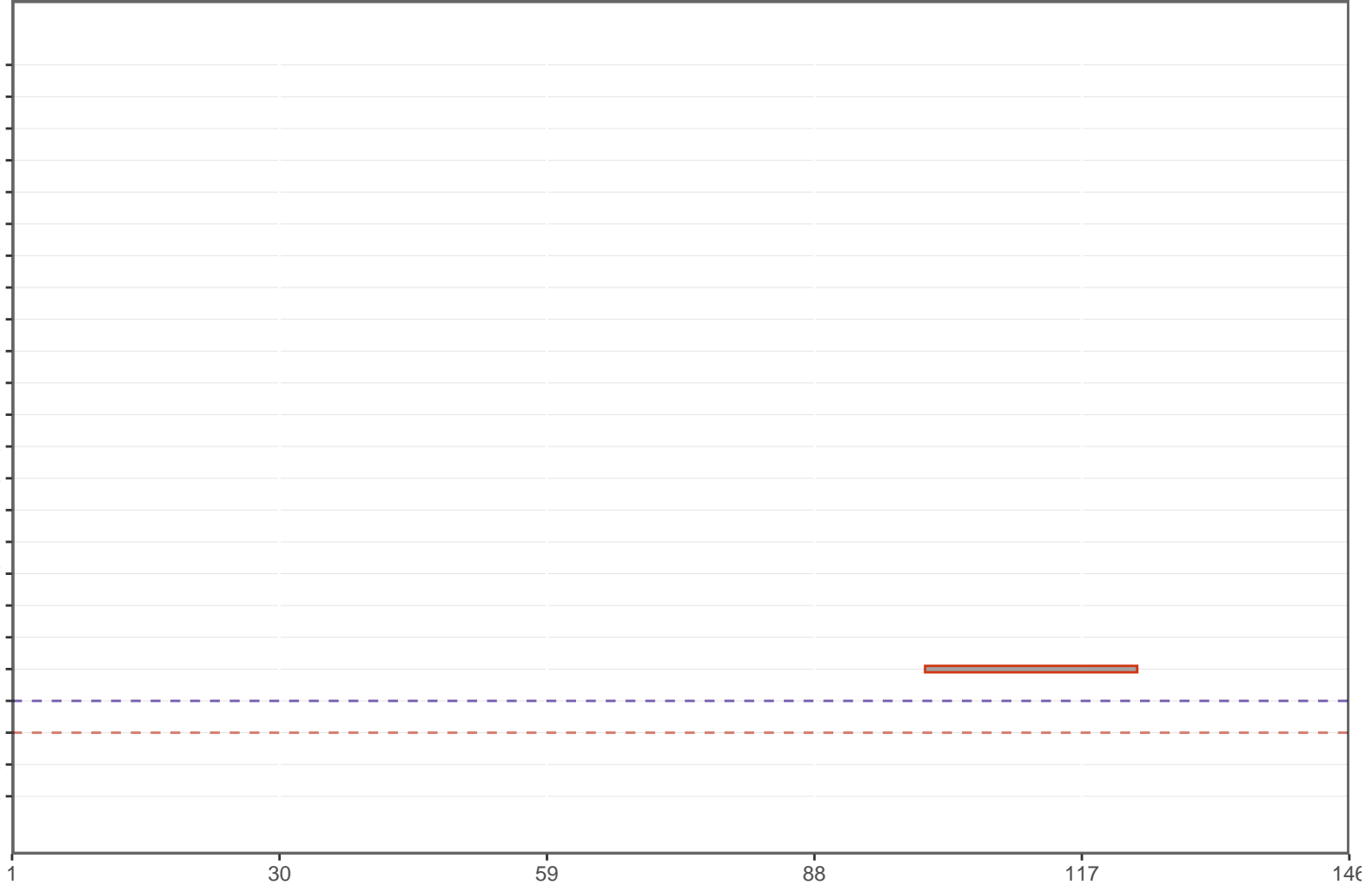
MW indication



Molecular weight



Gel Slice

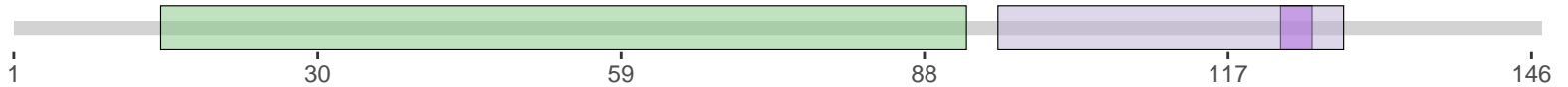


Protein length

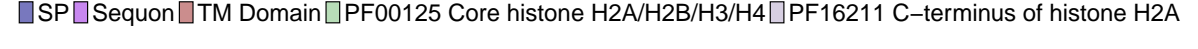


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LEYLAAEVLKLAGNAARDNKKTRIPRHVLLAVRNDDEELGKLLAGVTAHGGVLPNINPVLVLPNKSQKAGKEPTKSPKATKSPKKA*

NbL19g17810.1 actin-depolymerizing_factor_1 [MW = 16 kDa]

No. of times detected



log(intensity)



Values from



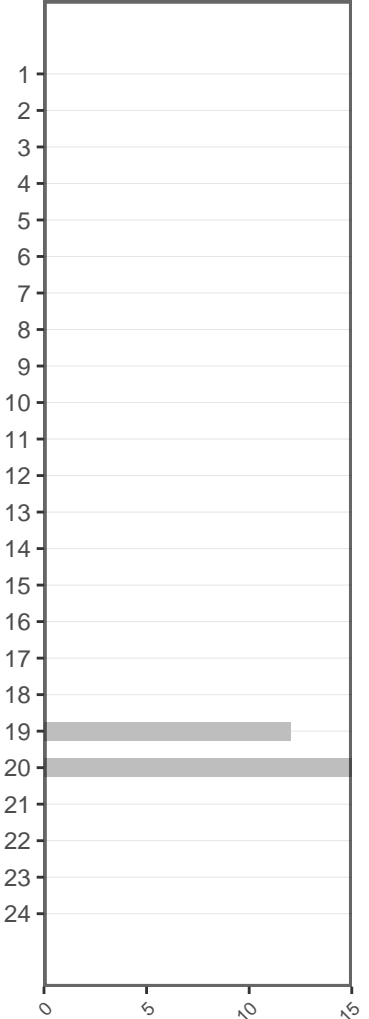
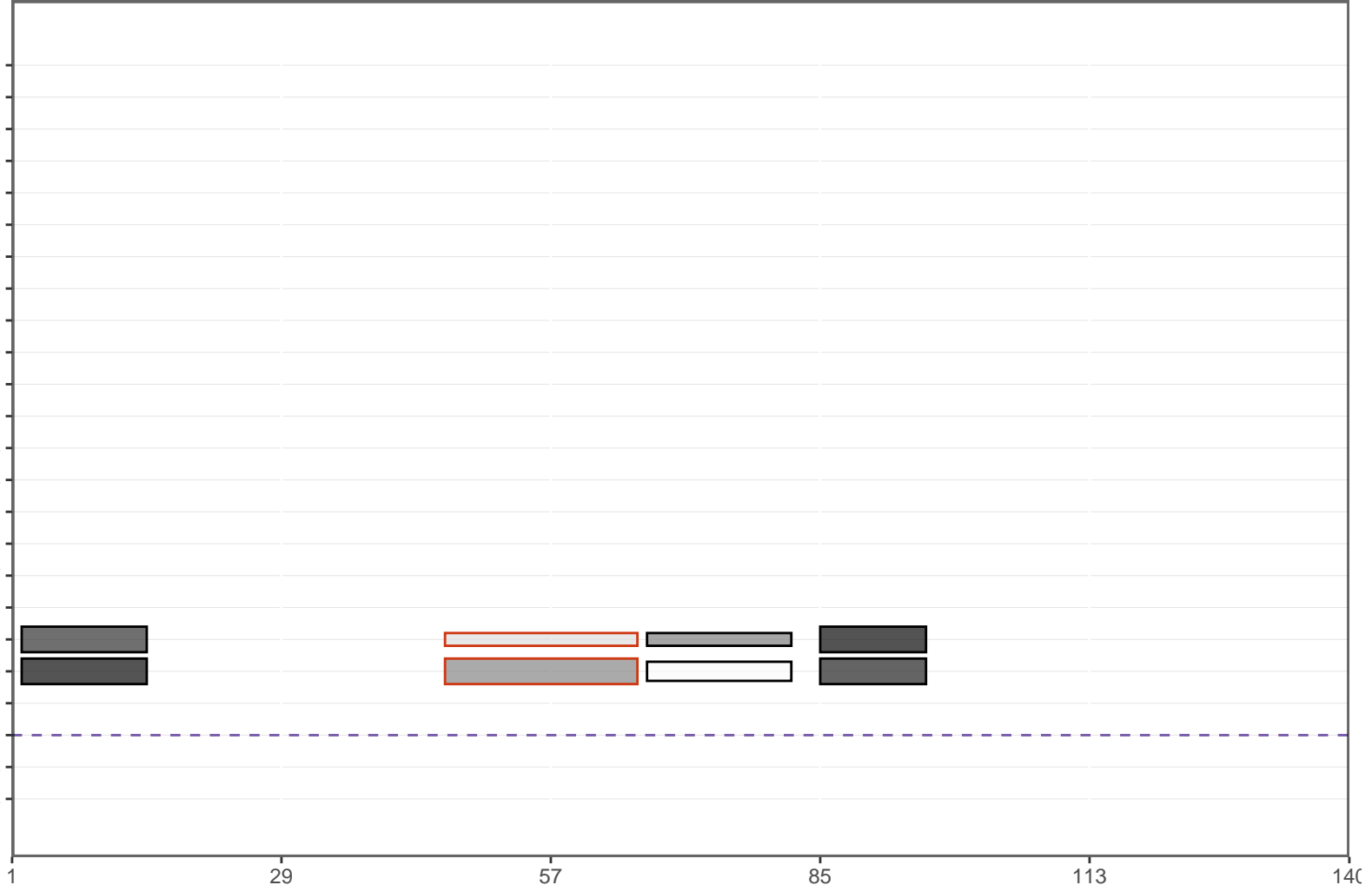
MW indication



Molecular weight



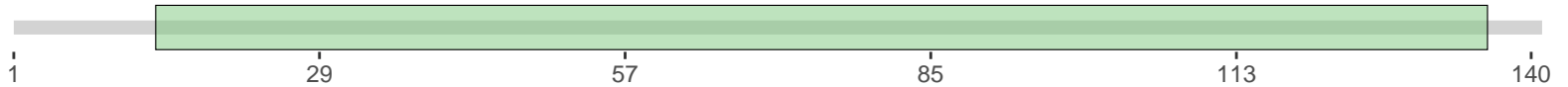
Gel Slice



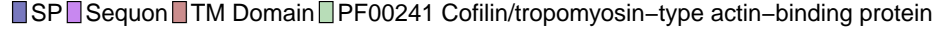
Protein length



Pfam domains



Pfam Description

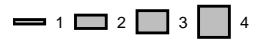


Protein sequence:

AAASLPDNECRYAVVDFDFVTAENQKGRIFIAWSPDTRVRRKIMVASSKDRFKRELGGHVELGATDPTEMGLGVKSRAN

NbL19g17550.1 heat_shock_cognate_70_kDa_protein_2-like [MW = 71.13 kDa]

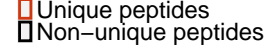
No. of times detected



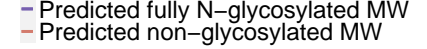
log(intensity)



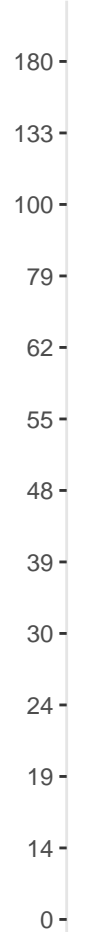
Values from



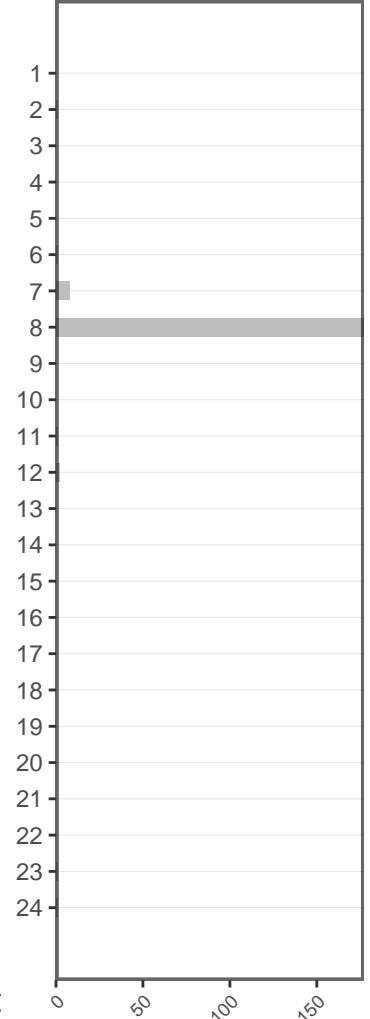
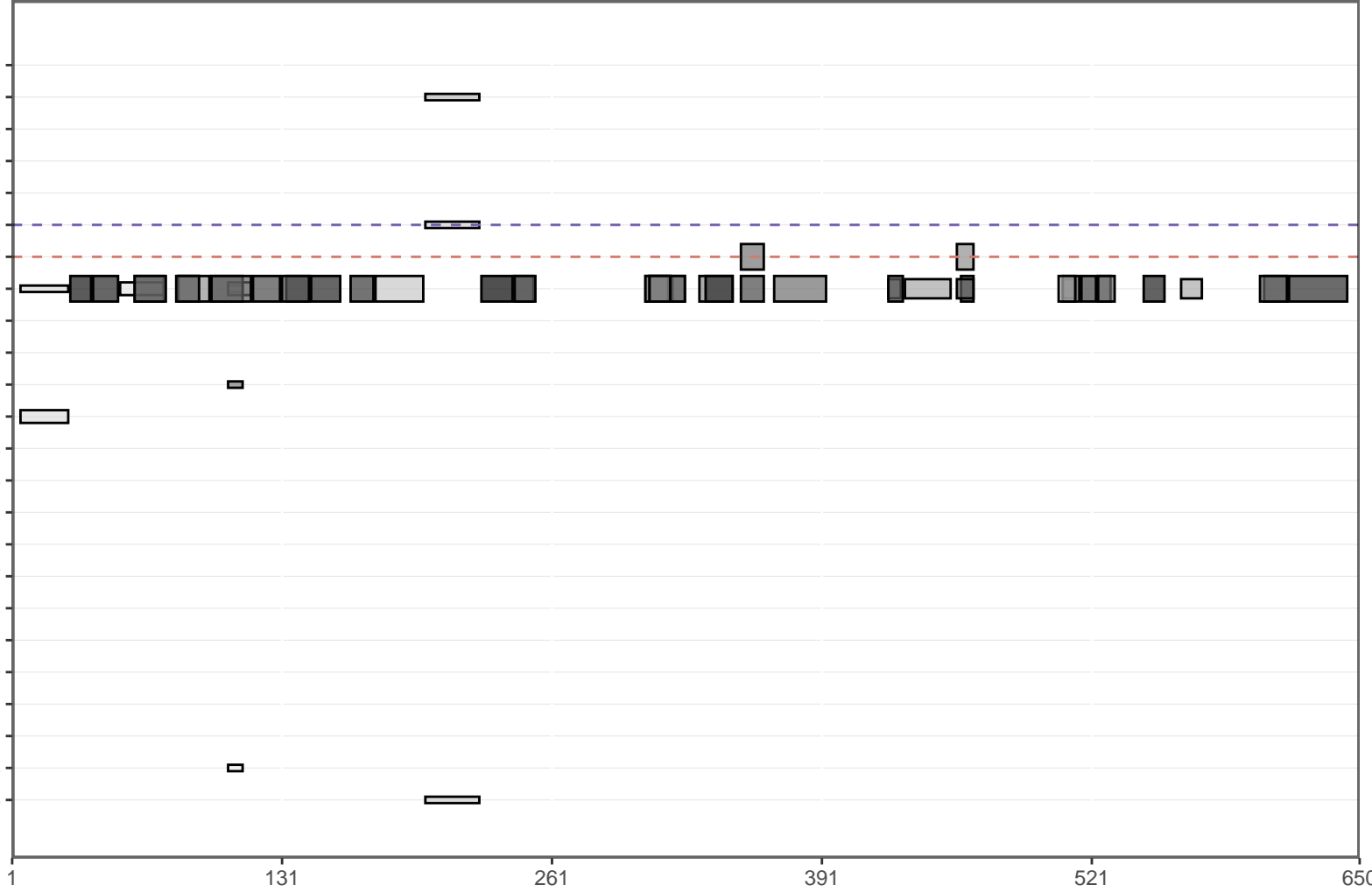
MW indication



Molecular weight

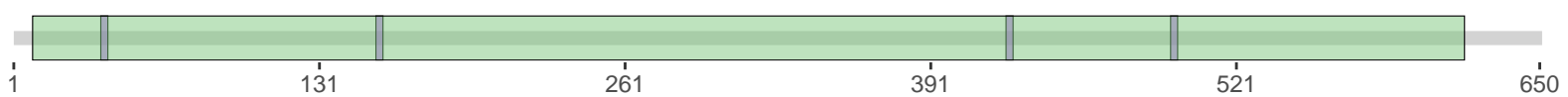


Gel Slice



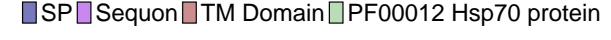
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILFRKCEPVEKLCIRDAKMDKSTHDAVLGGSTRPKVQGLLGGFFNGKELGKSNPDEAVAYGAVAQAALSGEGNEKVDLLLDVTPLSLGLGTAAGVMTVLPINRPTFTPKKEGVFSTVSDNGDPPVLDVYVEGERTTRDNLGKLFELSGIPAPRGVPGITVCFDIDANGLNVAEDKTTGQKNKTTITNDKGRLSKEIEIKMVGEAEKYKSEDEEKKKVVKAQNALENYANNMNTYKDEKIARKLPEADKKKIEDIESAQGLDANQLAESDFEDIKMKELESICN

NbL19g17240.1 ribulose_bisphosphate_carboxylase/oxygenase_activase_1_chloroplastic [MW = 52.72 kDa]

No. of times detected



log(intensity)



Values from



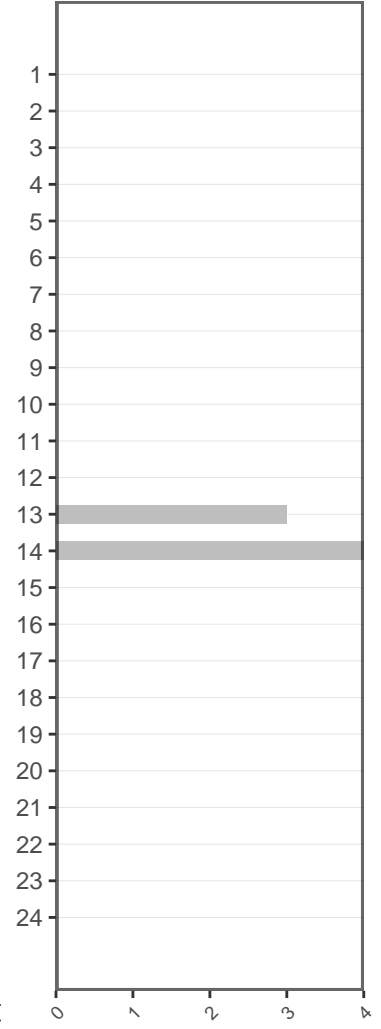
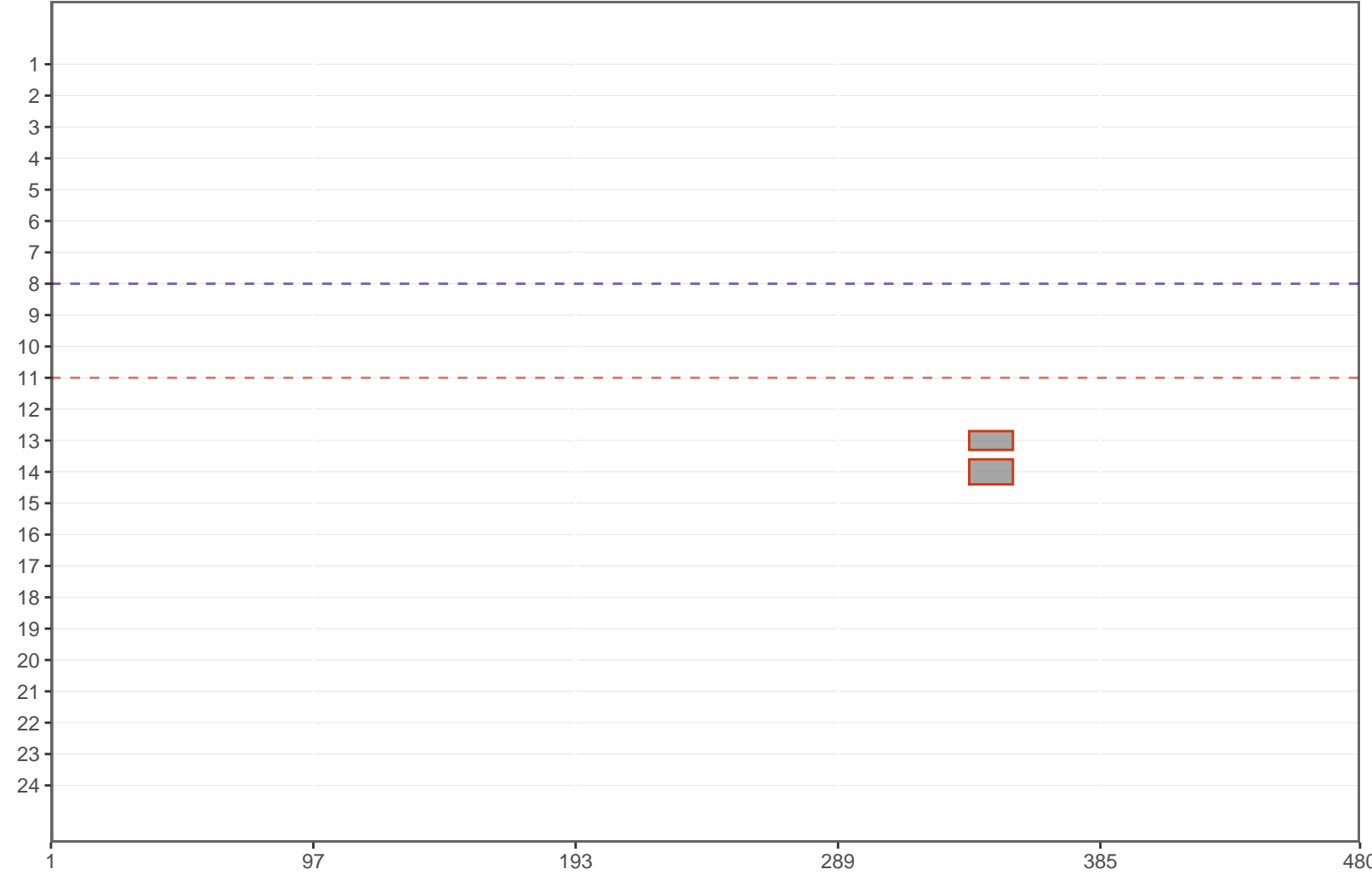
MW indication



Molecular weight



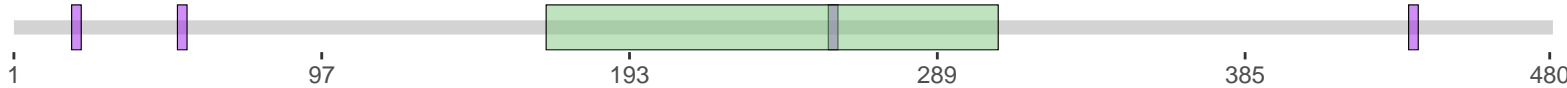
Gel Slice



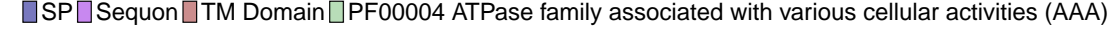
Protein length



Pfam domains



Pfam Description



Protein sequence:

CLFINDLDAGAGRMGGFTTQYTVNNGMVAATLMMIAIDNPNTNVGLPQMYNKGGENARVPIVDTGNDFFSLVAPLRDGRMEKFFYWAPTRDRIGVCTGFRDINPAEDVAVKIVDFPQGSIDFFGALRARVYDDEVKRWVSGTGIENKGDLLNSFDGPPFTFEGPQMTIEKLELVGNMLVQGENWKRVLQADKYLKEAALGDANADAINNGSFFTRKEAQHVDPVYVSGEGTDSIATKLDENSMEDGSGYLFKP

NbL19g17140.1 aldo-keto_reductase_family_4_member_C10-like [MW = 35.23 kDa]

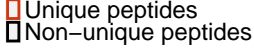
No. of times detected



log(intensity)



Values from



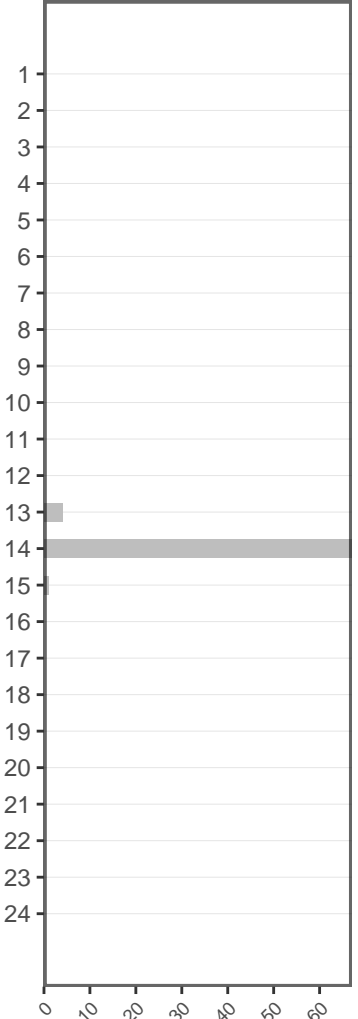
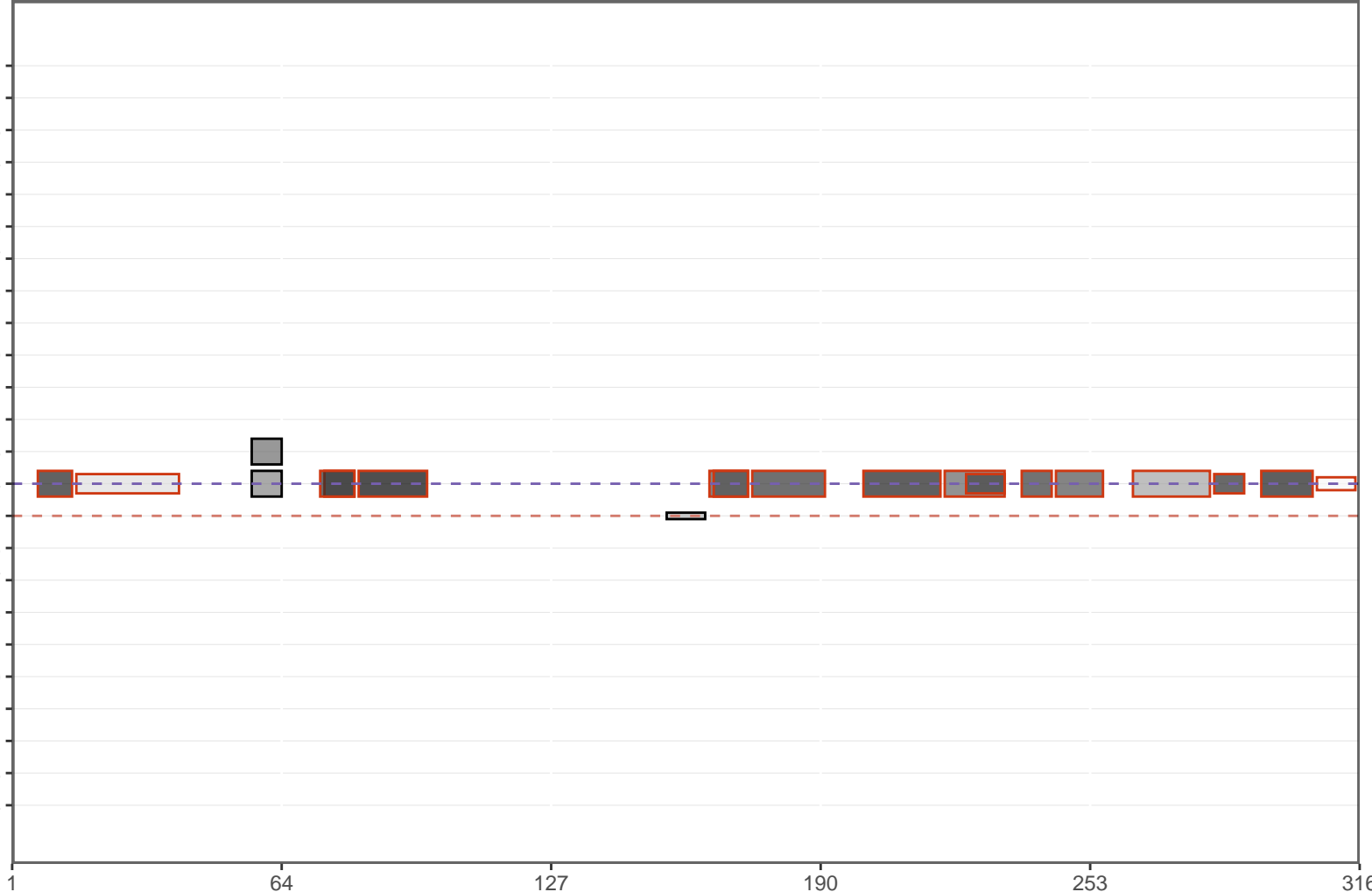
MW indication



Molecular weight

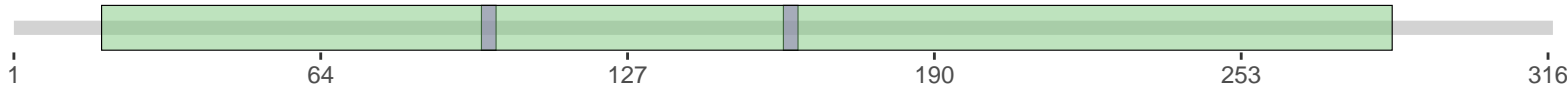


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LYDSQKARAGVSNFSTKRLGDLGVARPPAWNGVEGHPSWQQAKLRFQKSGVHLSAYPLGSPGFTTWLKGDLKGPVWVSWAEKLGKTPALVCLRWGDMGGVLPKSTHARKEKNDLVDWBPDDLFAKFEIPQARLLRGTSPVHEAYGVYRTLEELWDGEL*

NbL19g17100.1 uracil_phosphoribosyltransferase [MW = 36.74 kDa]

No. of times detected



log(intensity)



Values from



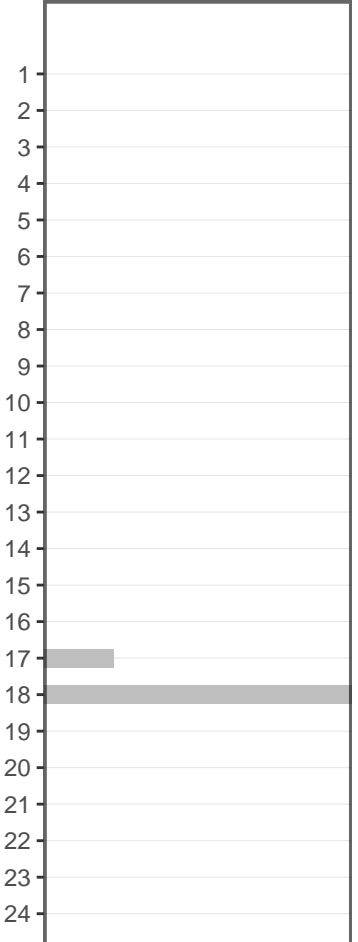
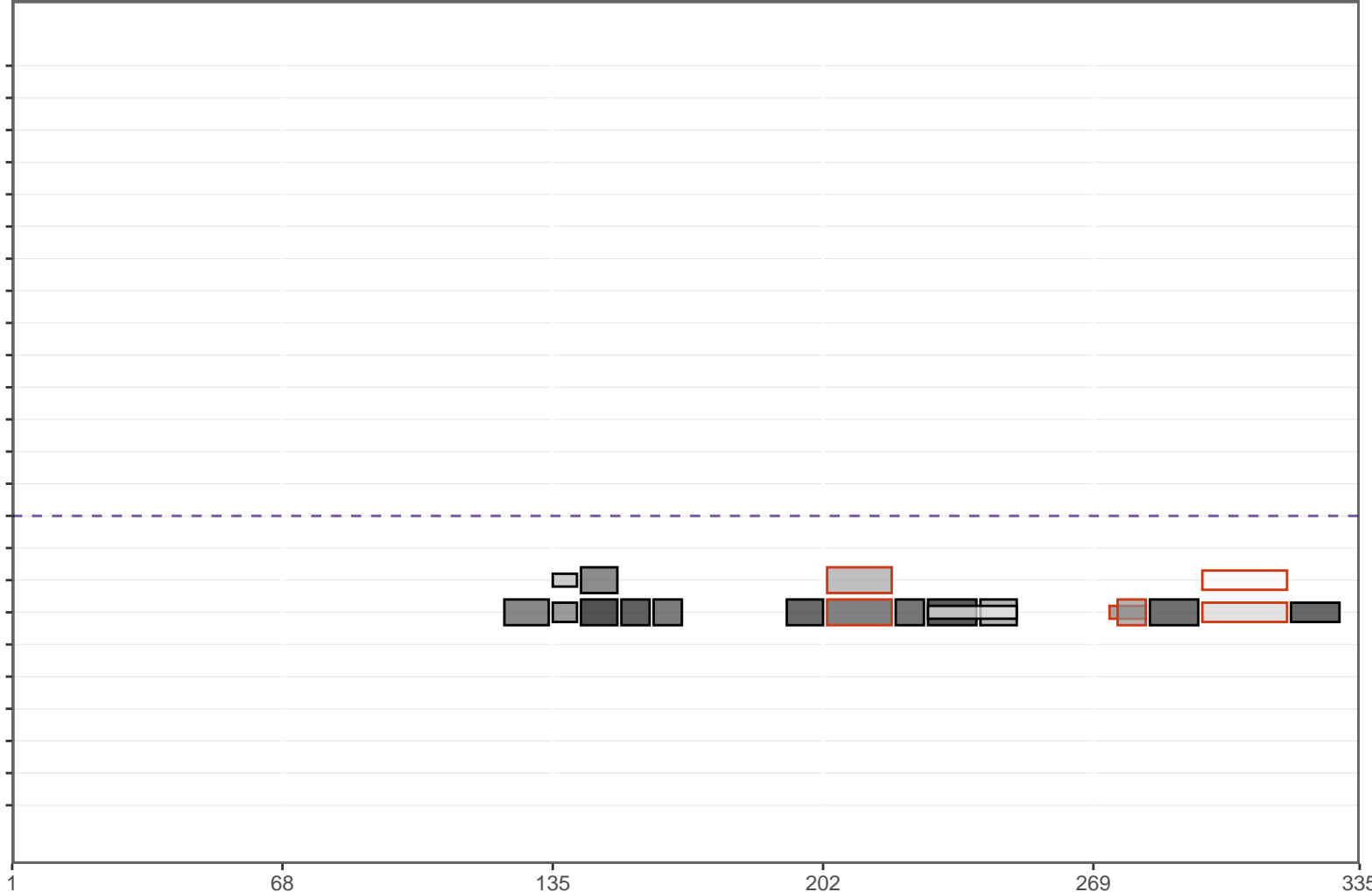
MW indication



Molecular weight



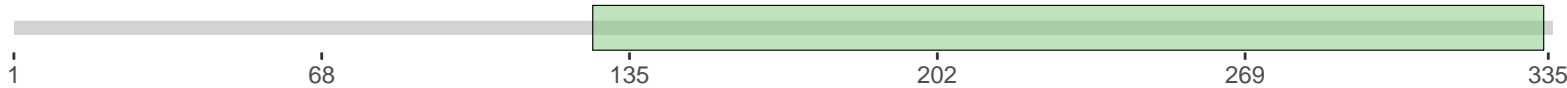
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

MSELGRLLMYEASRDWLPITGEQSPMGVAVSEFVDRPEFVAIVPIRAGLALAEHASSILPATKTYHLGISRNEETLQPSVYLNKLPDKFPEGSRGVFVDDPMLATGGTVAANDLKERGVDSNQKVCAGAPALOKLSENFPGLHVYAGILDPTVNDKGFIPGLGDAGDRSFGT

NbL19g17000.1 NHP2-like_protein_1 [MW = 13.91 kDa]

No. of times detected



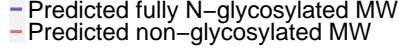
log(intensity)



Values from



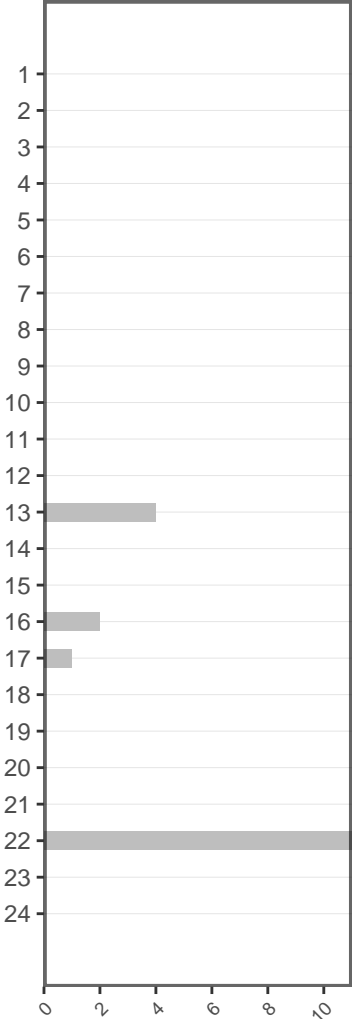
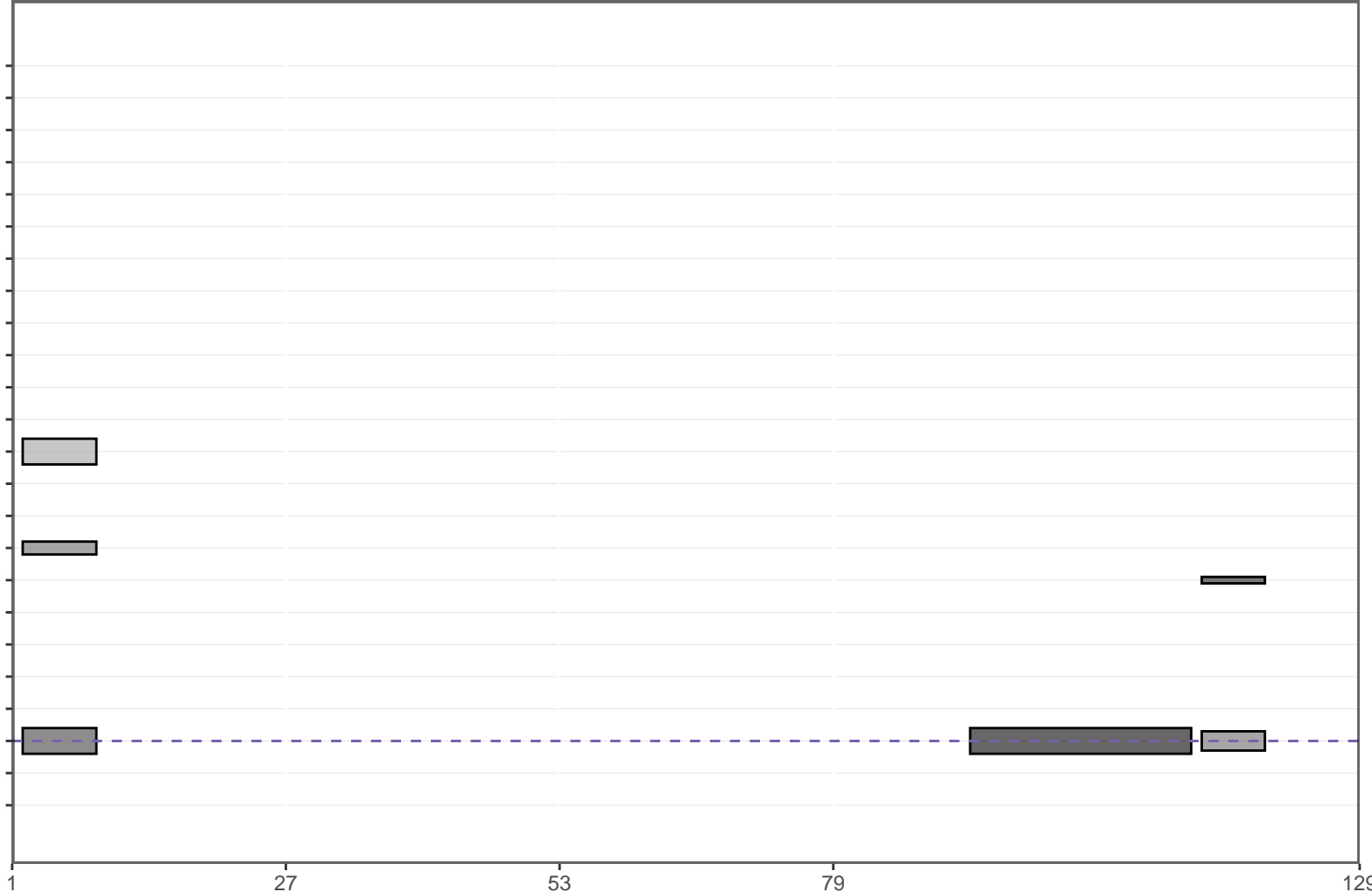
MW indication



Molecular weight

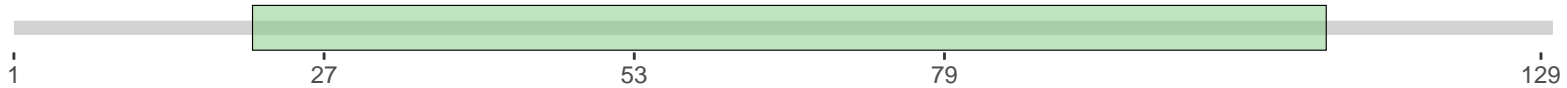


Gel Slice



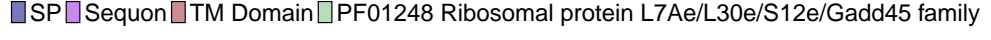
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SEFVYMAADTEPLELHLHLPLLAEDKNVYVFPKQALGRADGTRPVAAGSVTSNEGSOLKSGIQGLKDAEKLKLP

NbL19g16990.1 probable_proteasome_inhibitor [MW = 31.83 kDa]

No. of times detected



log(intensity)



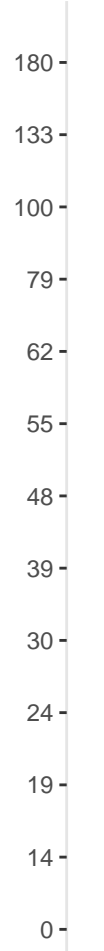
Values from



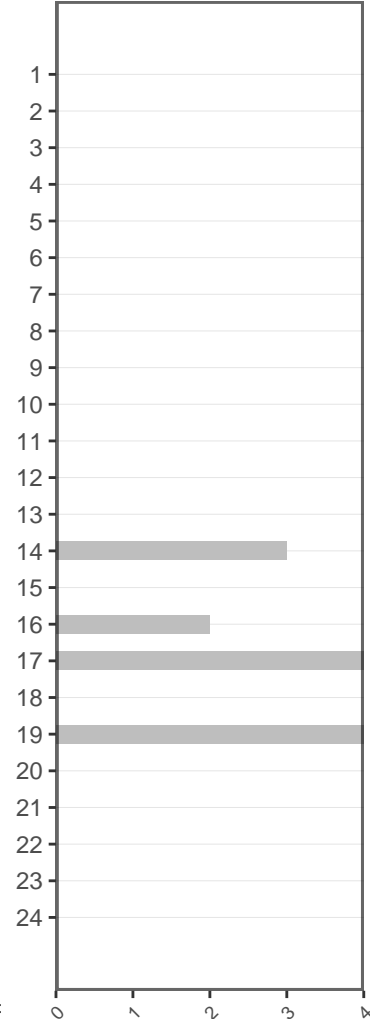
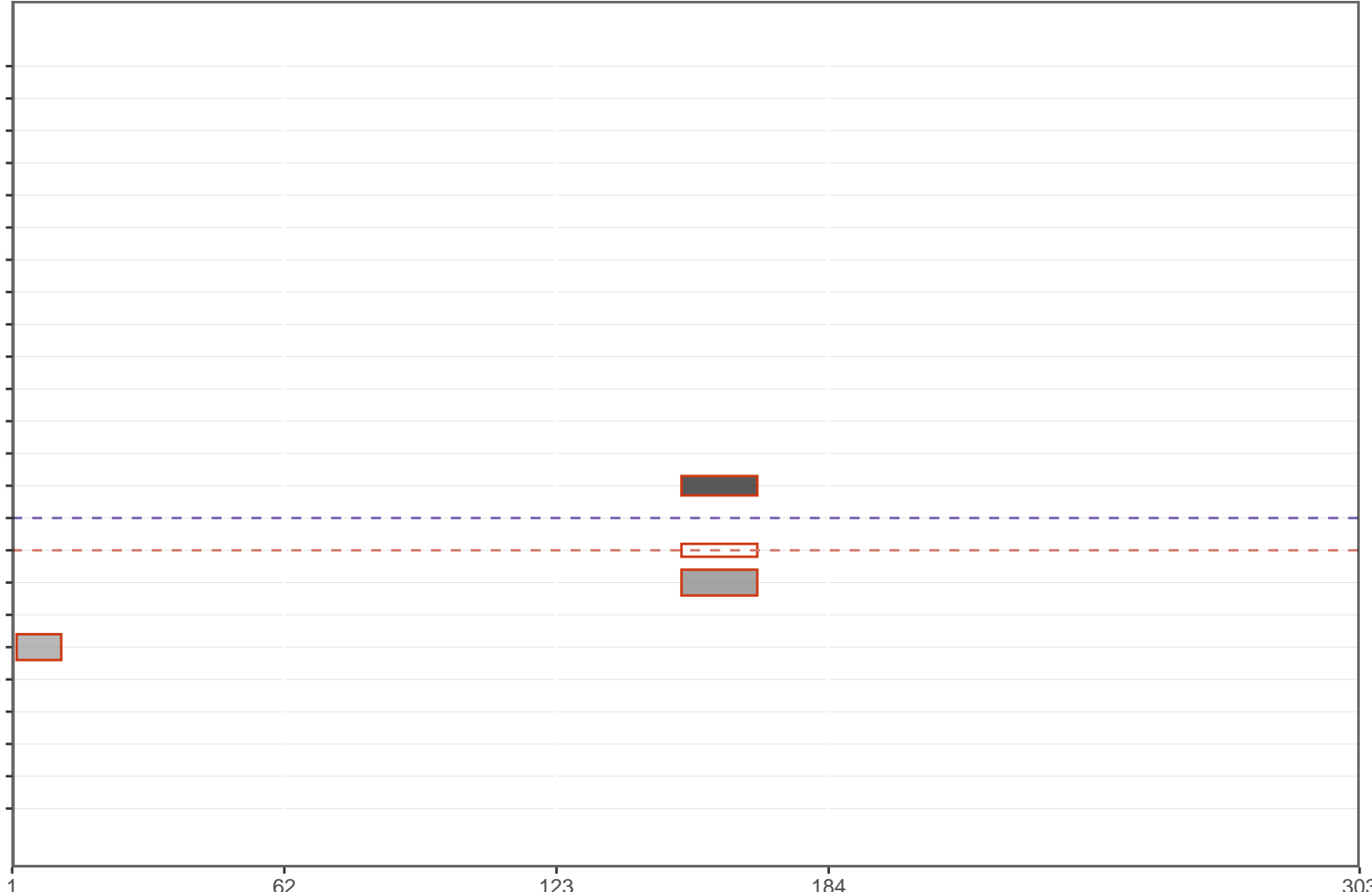
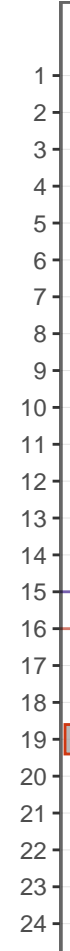
MW indication



Molecular weight



Gel Slice



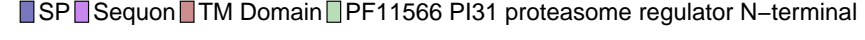
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ELNKEVLSKYSQSSVANSSTQTGSSGGKGLGDEPAERRSQVYQPESSPFGVYVPHPGGGGDLFFGPGAGVYPTKGGGGGSMVGGPDRPFVGGGGDPRLPGLGCPVPPGARFDYVGPDPVPGEPGRFRDRPRRPGGGRPHDLPHPGGSDDFV

NbL19g16950.1 probable_glutathione_S-transferase [MW = 25.47 kDa]

No. of times detected



log(intensity)



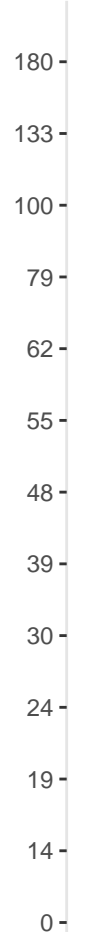
Values from



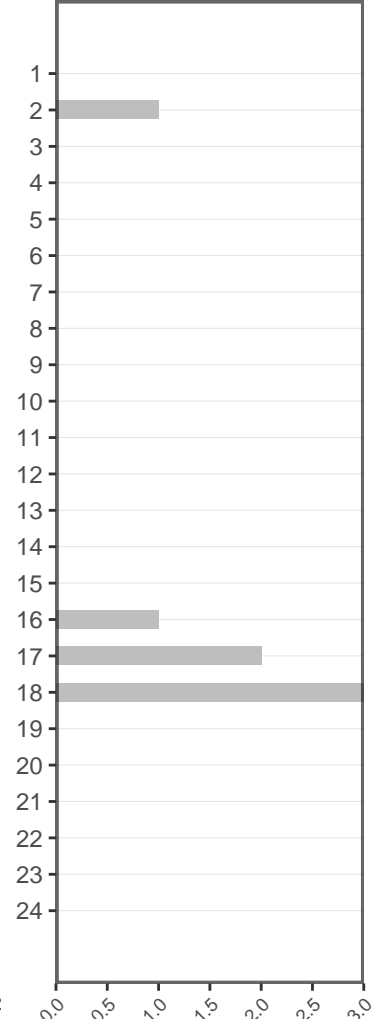
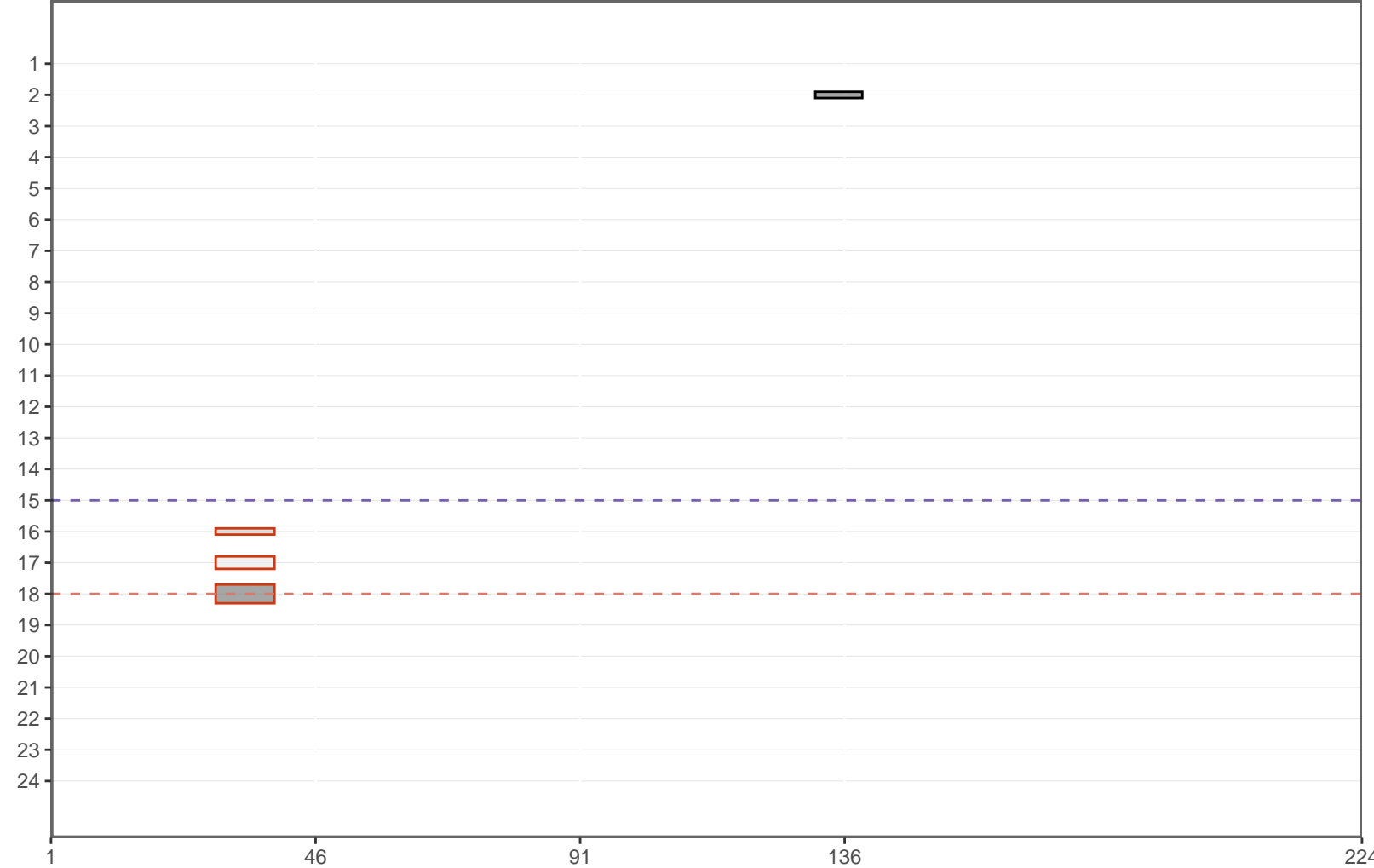
MW indication



Molecular weight



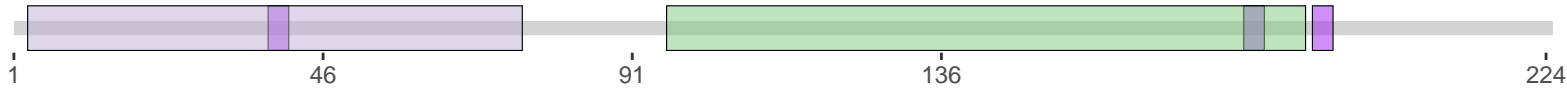
Gel Slice



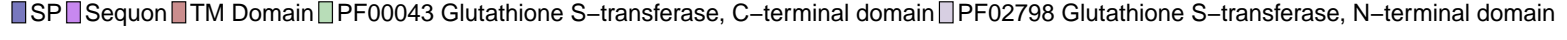
Protein length



Pfam domains



Pfam Description



Protein sequence:

.DDKVTYVNTFLSKGEEGEKAKEGWEMKVLINELKDKKFLVGDKFGFADIAANLVFWLGVFEEASGVLMTESEKFPNFSKRWDEYTNCSGLKESLPPRDELLAFFRARSGAQTTSASAPK

NbL19g16910.1 probable_glutathione_S-transferase [MW = 25.04 kDa]

No. of times detected



log(intensity)



Values from



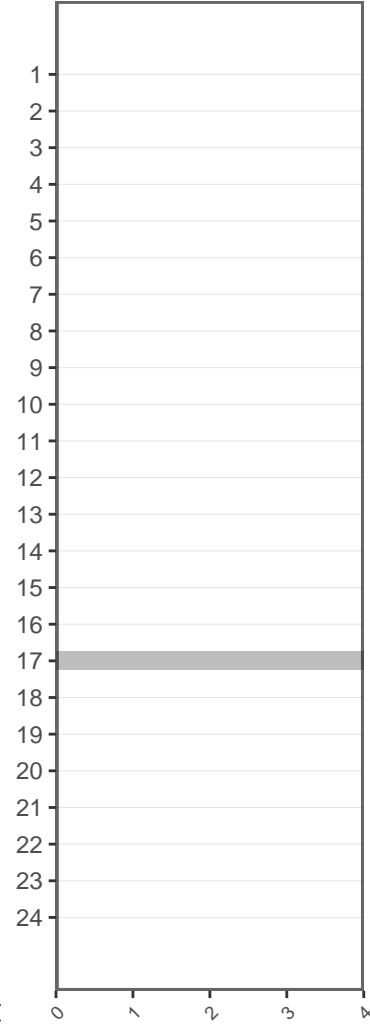
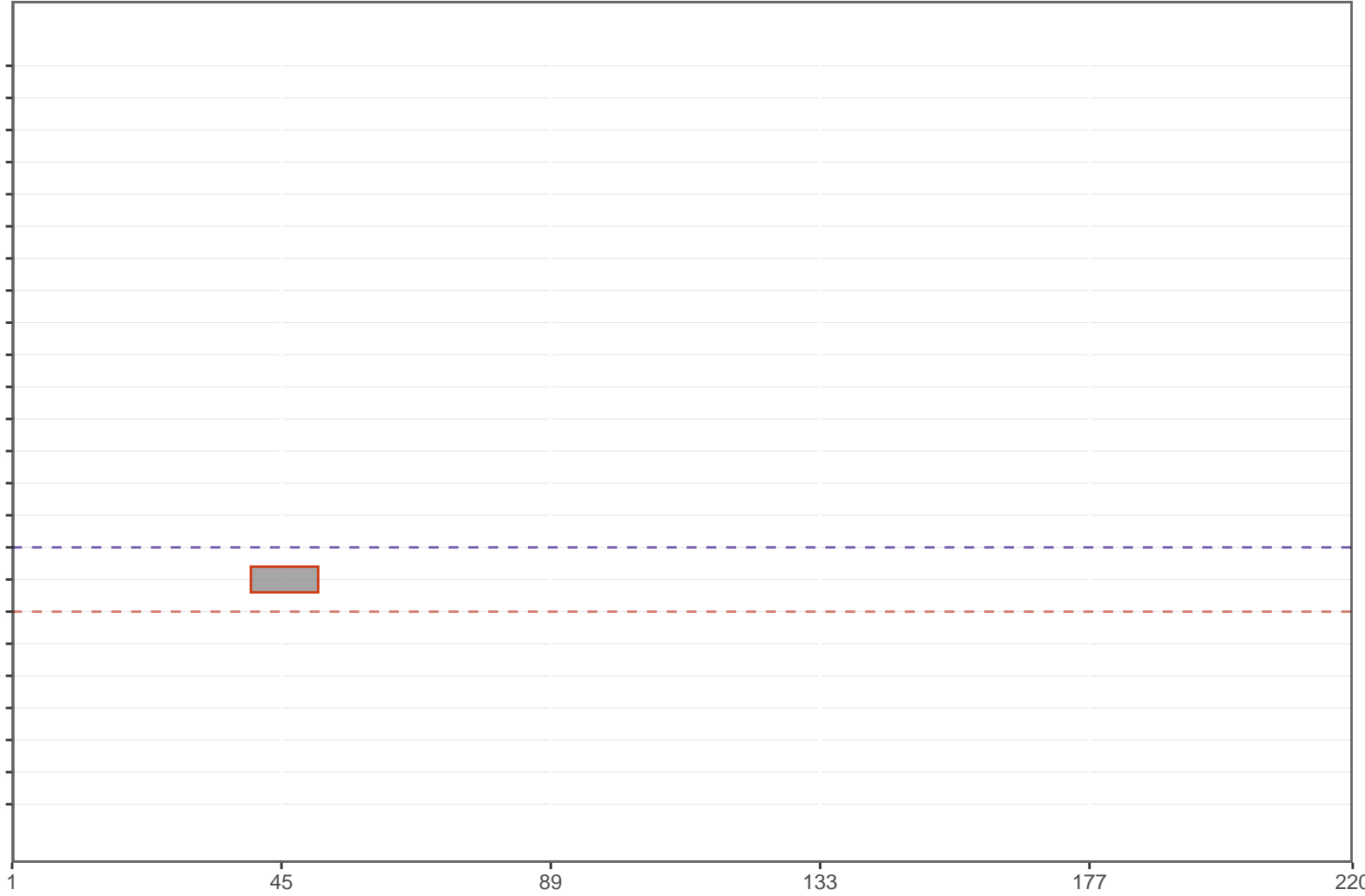
MW indication



Molecular weight

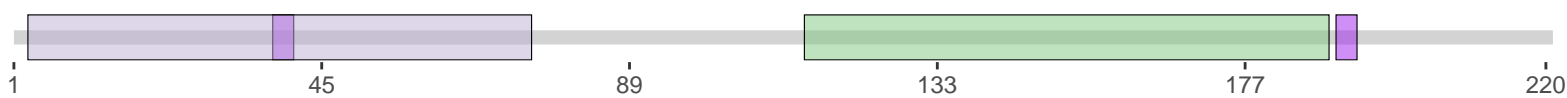


Gel Slice



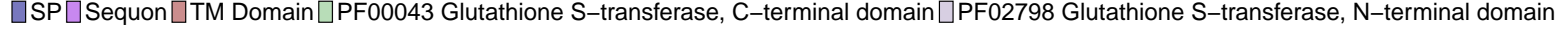
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

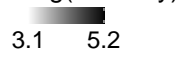
'FEKGGASVGRSFLKGGEGEKAKGQVEMLVLDNEVNDKDKFFVGDKFGFADIAAANAALWLVGLEEASGVLVTRKFFNFGAWRDEYVNGSNKEVLPREDLLALFKARFQAAAA'

NbL19g16900.1 probable_glutathione_S-transferase [MW = 25.38 kDa]

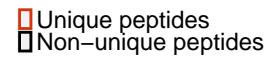
No. of times detected



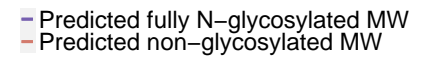
log(intensity)



Values from



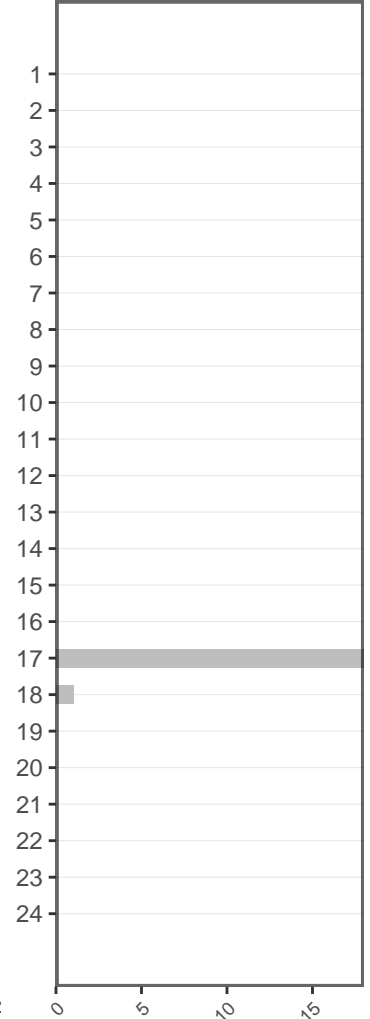
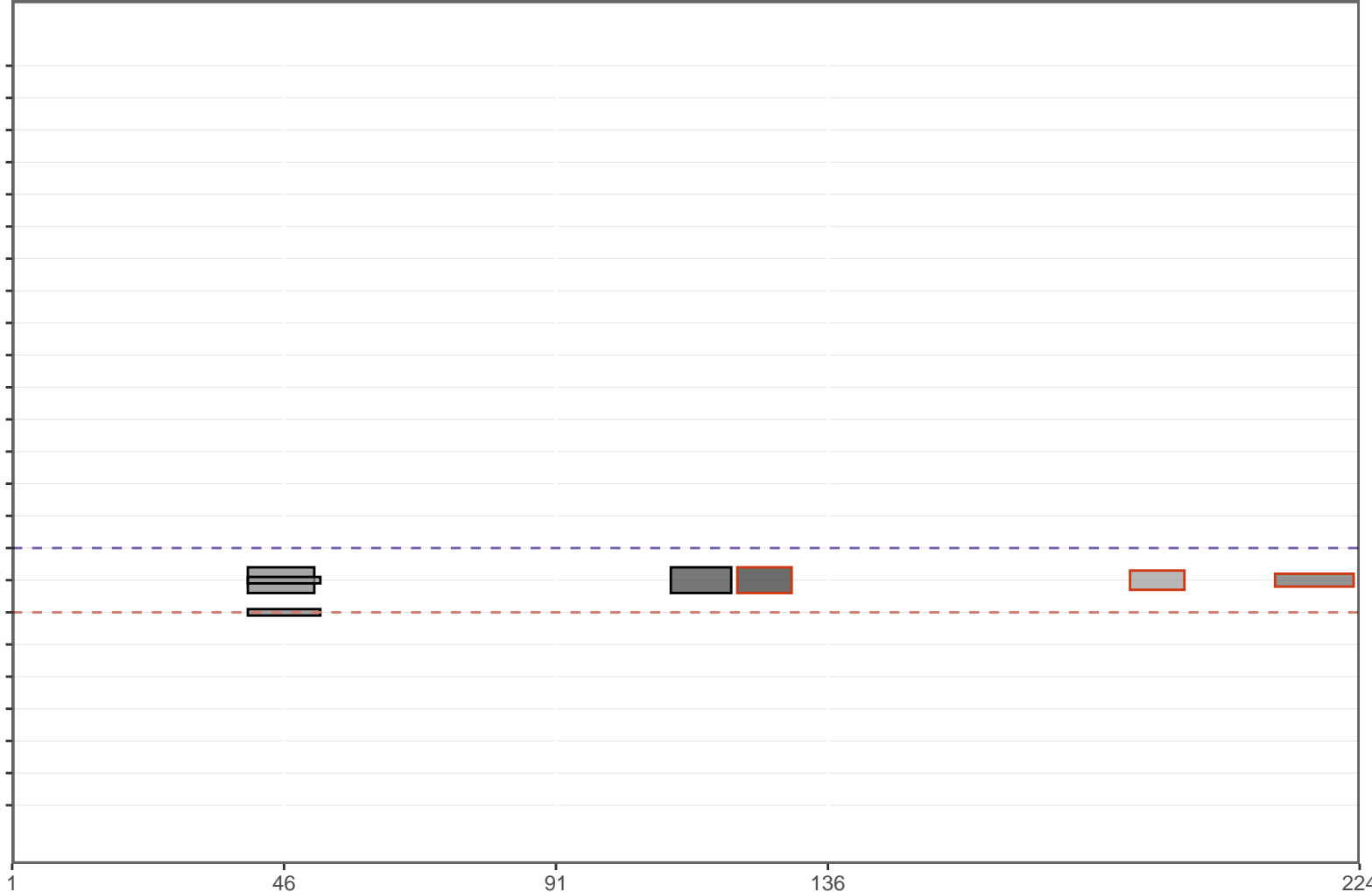
MW indication



Molecular weight



Gel Slice



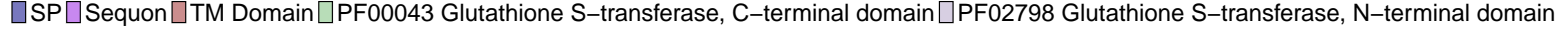
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LEDKYRVAVGKSFYKGGEGEKSKEDAFELIKLIDNELKDKKFFTDGKIGLADIAANFVGLWLVGFEEASGILVTRKFPNFGAWRNEYINGSGNKEYLPRDELVAHFKAHFQAAAAAAAAAPK

NbL19g16890.1 probable_glutathione_S-transferase [MW = 24.92 kDa]

No. of times detected



log(intensity)



Values from



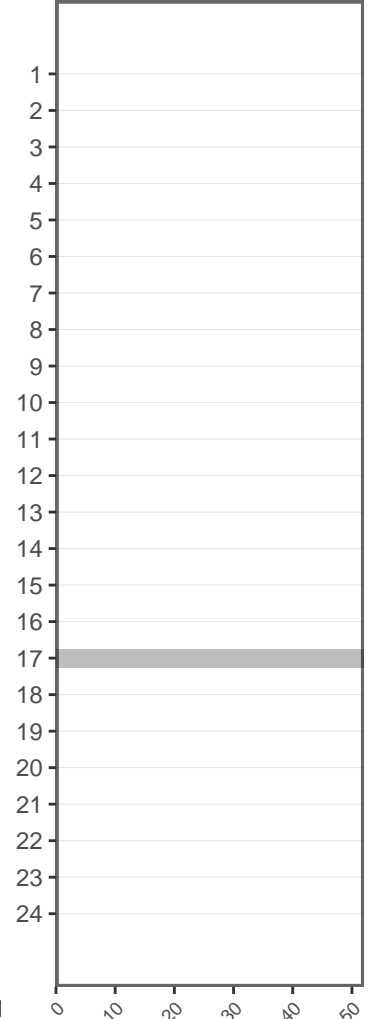
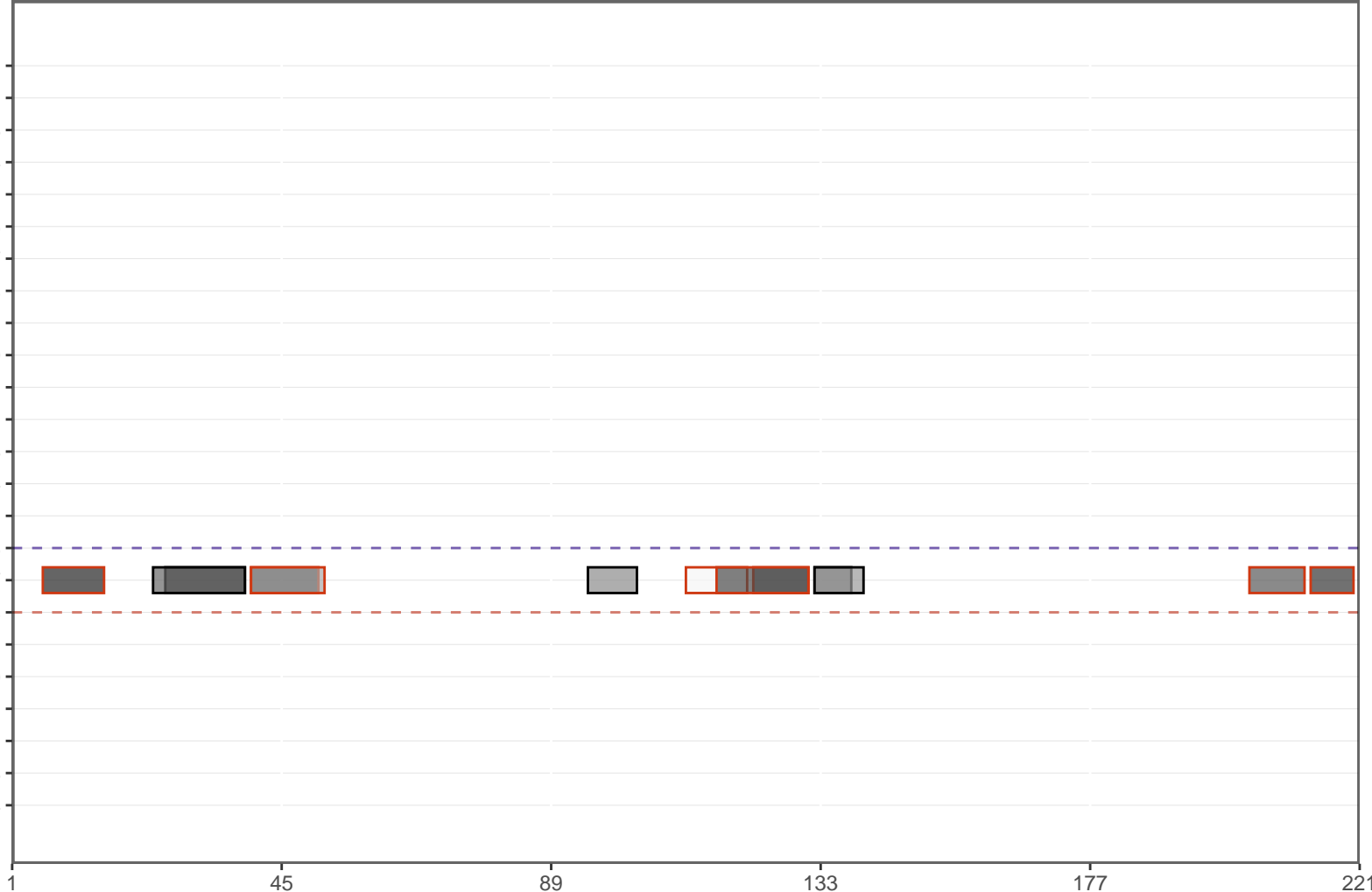
MW indication



Molecular weight

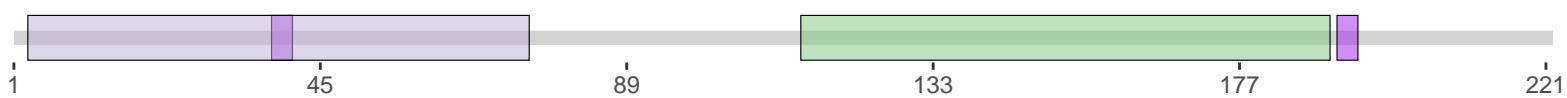


Gel Slice



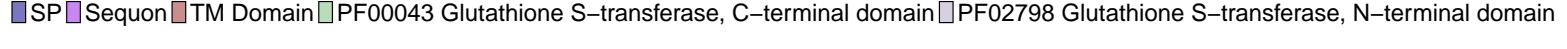
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

NFLDVKCTTIGKALFGKGEESDKAEIEEGELLHLDNELKDKKFFVGDNFQYADIANLMAFWLGIIEEASGVILVTEKFNFCVAKWDEYVNGHVKHEHLPKSRDALLSHFGPRFGTAAAPK

NbL19g16860.1 universal_stress_protein_PHOS32-like [MW = 18.45 kDa]

No. of times detected



log(intensity)



Values from



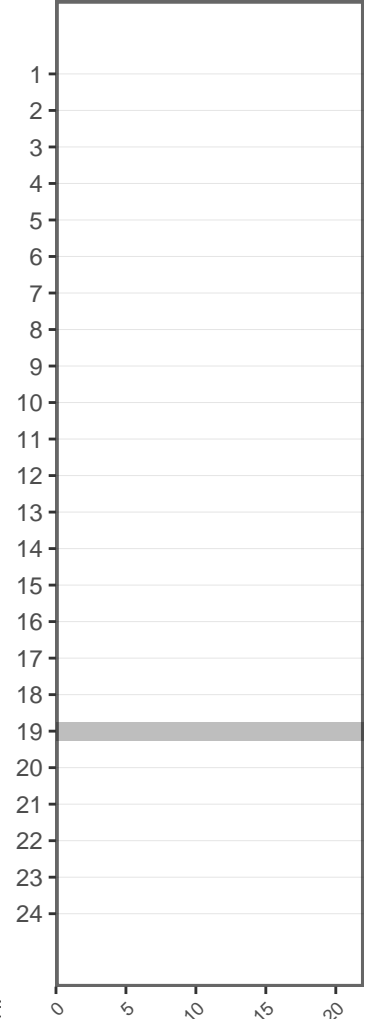
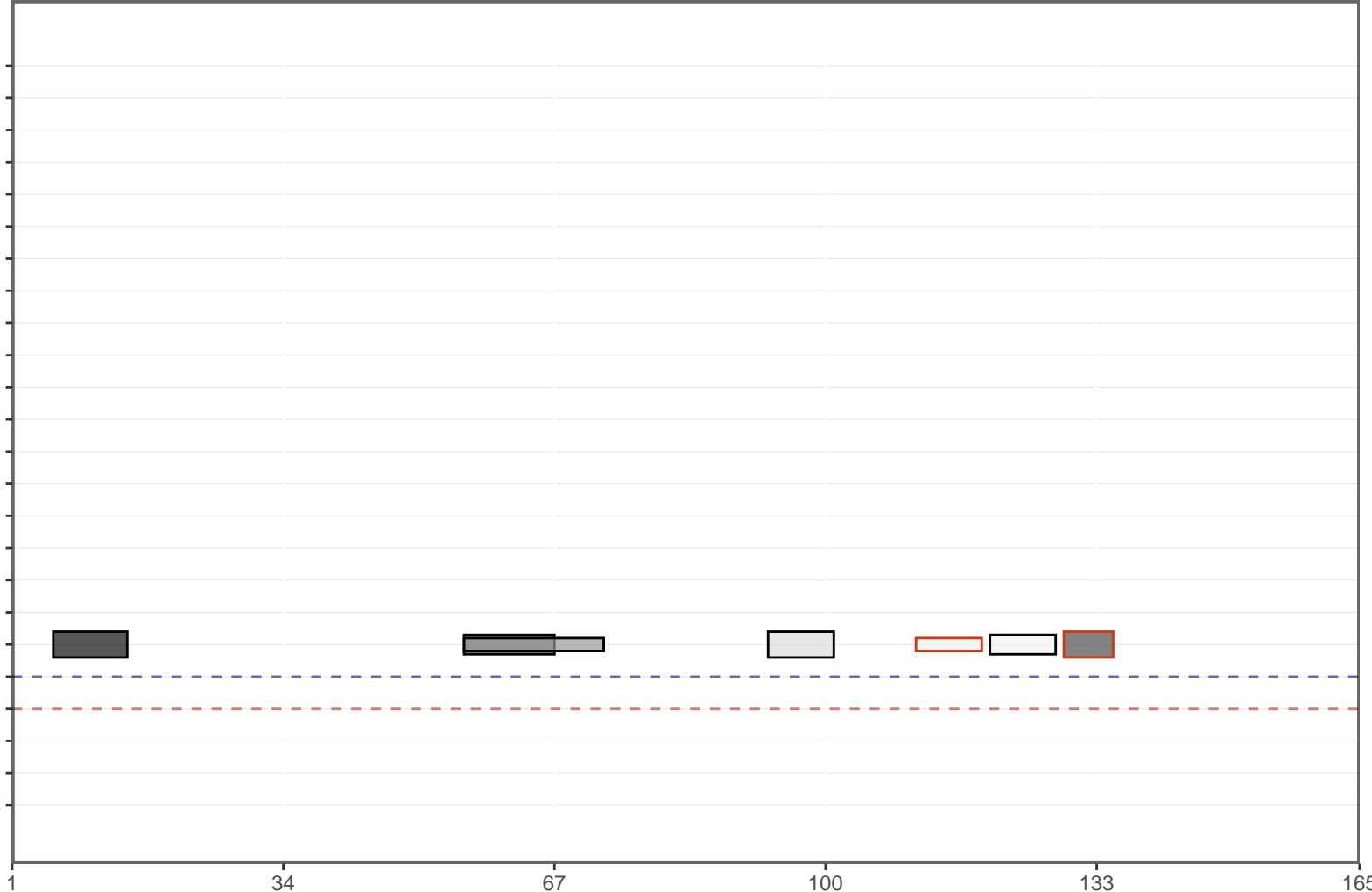
MW indication



Molecular weight



Gel Slice

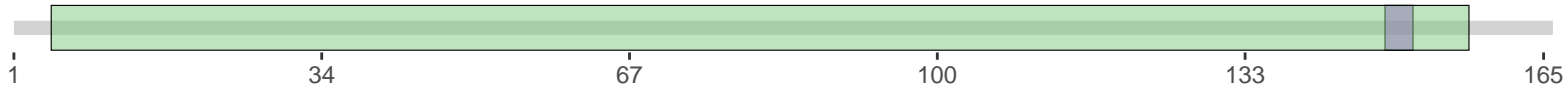


Protein length

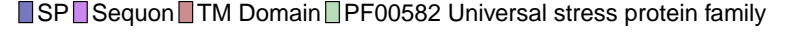


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

EVIMKKYDVEVDIDVLDLDDTATRQKEFTVTKLWYGDAREKLDATEDKLDLSDLVMSRGLGLQRIIMGSGVTNVALTNATGAVTVWKPDPFKH

NbL19g16750.1 fructose-16-bisphosphatase_chloroplastic-like [MW = 44.29 kDa]

No. of times detected



log(intensity)



Values from



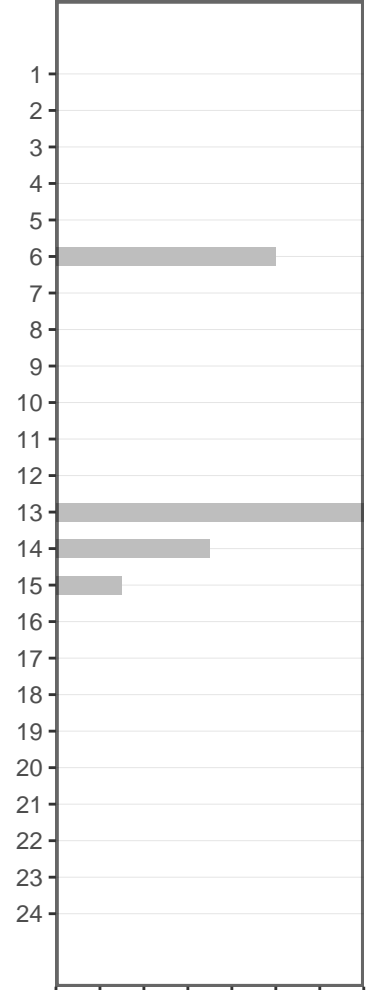
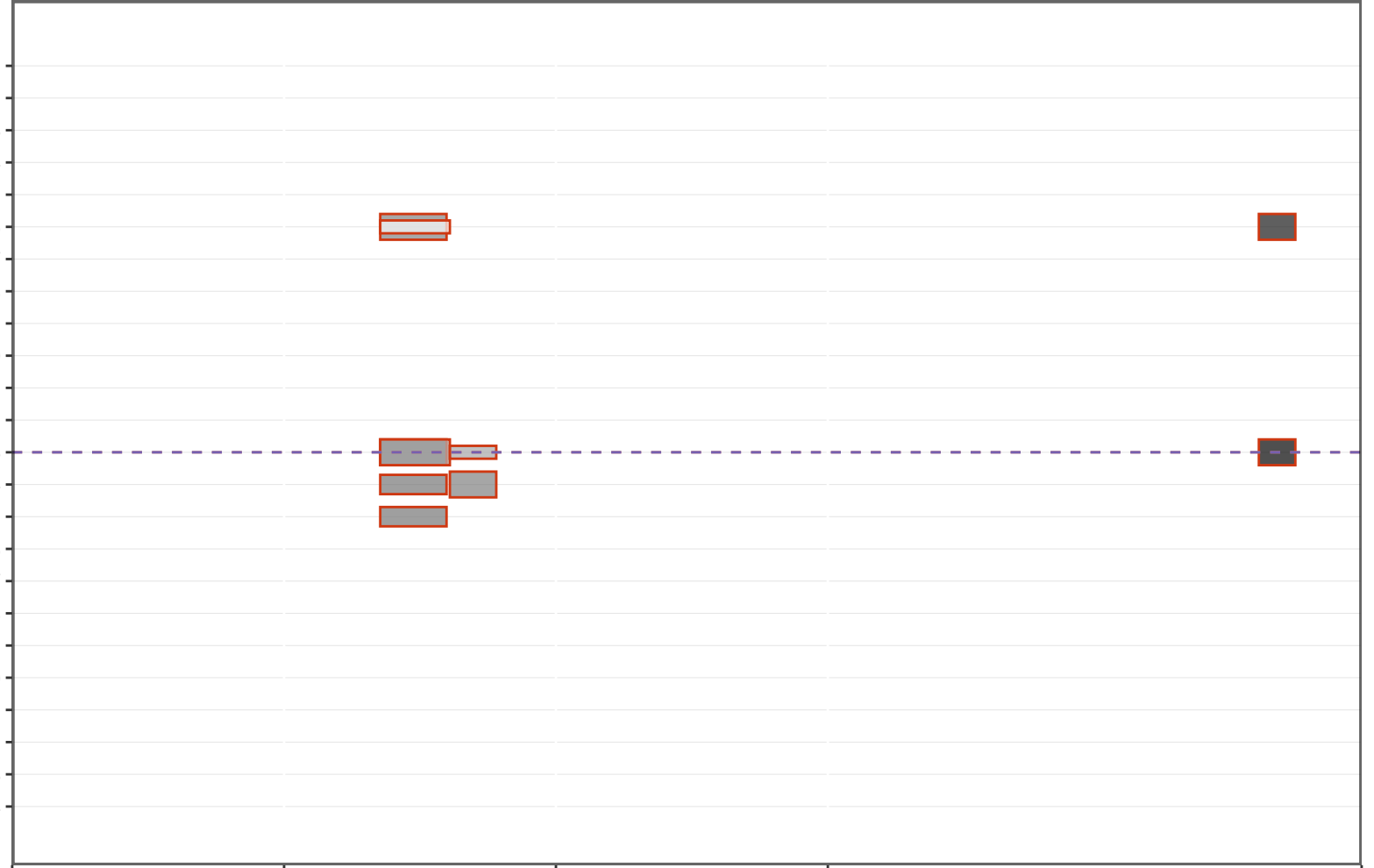
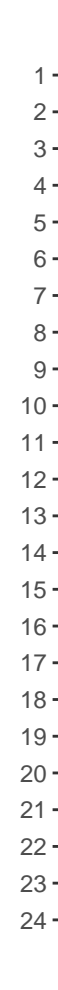
MW indication



Molecular weight

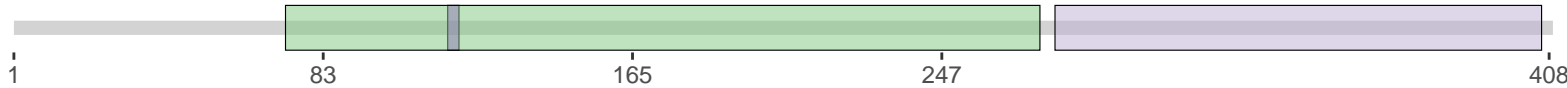


Gel Slice



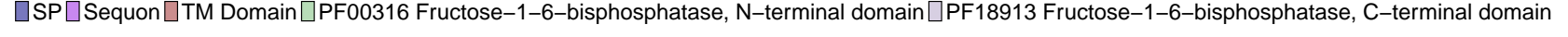
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

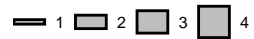


Protein sequence:

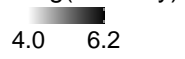
ITGSIFGIYSPNDEGLADHGDDSTLNDVGRGIVAVGQPGSNLLAAGYMS65SIFVFTLGNQVFANLDPMYGEFVMTGENDIPKSGHYSPFNEGHVQLWDDKLYIDDLKDPGPGSGKPYSAHYIGSLVGDHFRTLLYGGYGYPRDKKSKNGKLRLLYEDAPMSFLVEQAGGKGGSDGHQRILDIETENHORVPLMGSTEEVEKLEKYLSP

NbL19g16550.1 proteasome_subunit_alpha_type-4-like [MW = 27.31 kDa]

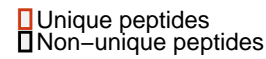
No. of times detected



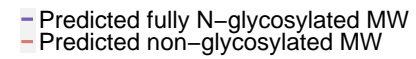
log(intensity)



Values from



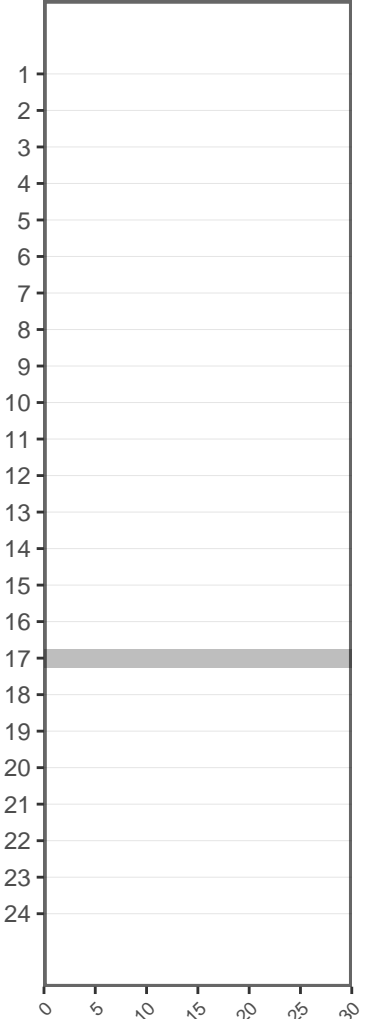
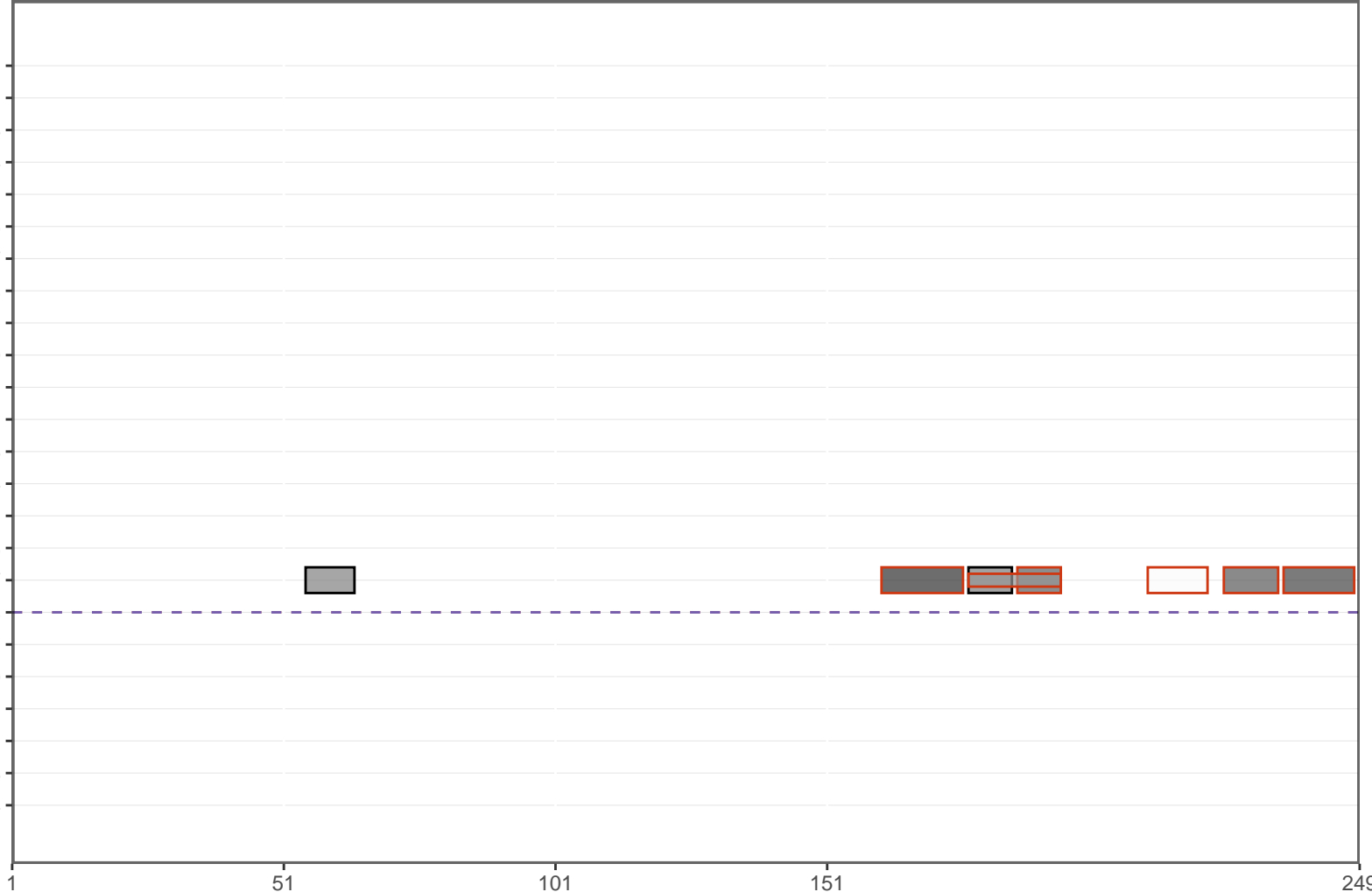
MW indication



Molecular weight



Gel Slice



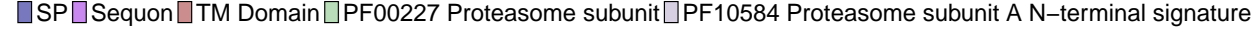
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LCDTKQGYTFQGGLRPFQVSEFLFAGWKNVGFQVMSPDPSGNVGGWKAATGANNGAAQEMLKQDHYDEITREEAWHLVVKLSKTMDSLTSFSEKLELAEVFLVNGKVKYGVHSPPELKLKLVQVGLTQPAADA*

NbL19g16410.1 uncharacterized_acetyltransferase_At3g50280 [MW = 53.21 kDa]

No. of times detected



log(intensity)



Values from



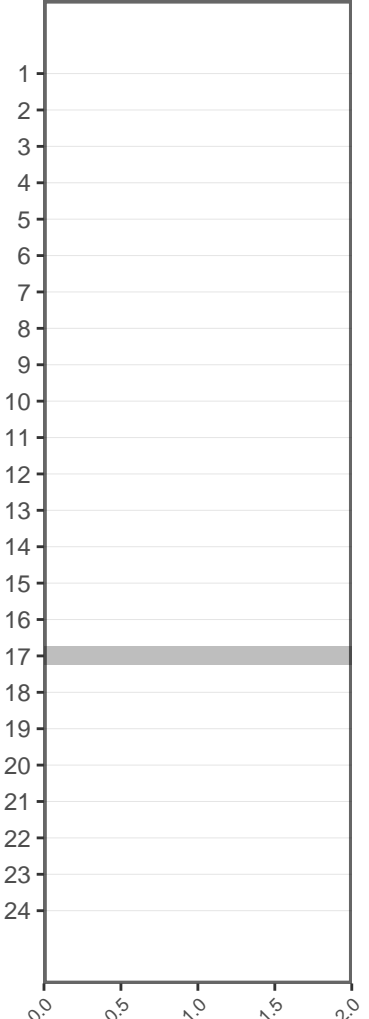
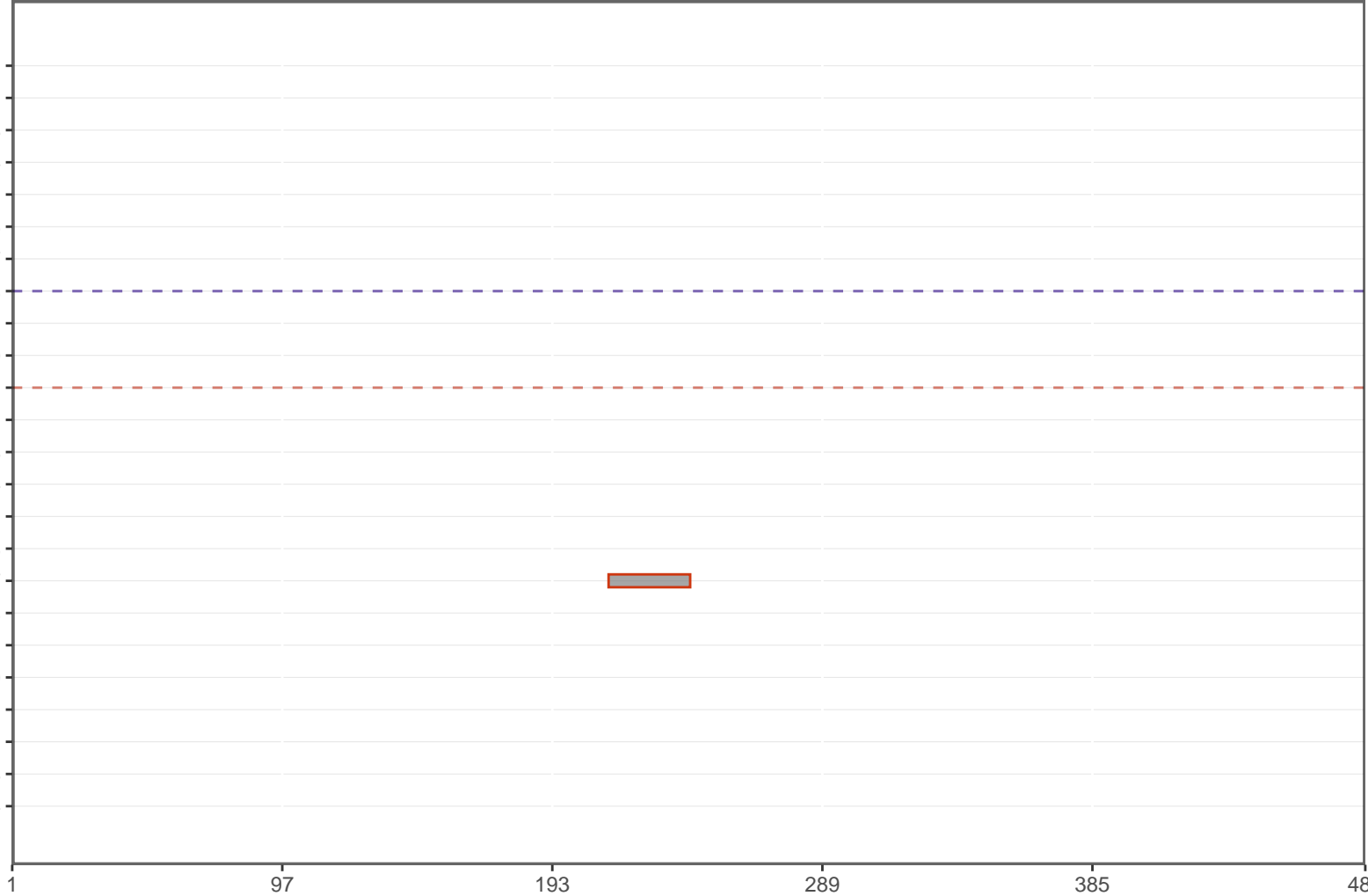
MW indication



Molecular weight



Gel Slice



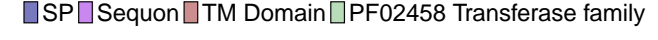
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FSGDEPIREKIFHFEREALKLFRANKMKVANGNGKTKTKITPVNNEPALNGAAVKYTAISEISFQELSAQLWRSVTRAKLGDGSKTTFFRMAVNGRHRLEPKMEPLFYFGNAIGSPTVASVNELLTNDLNSANLLHQNVVAHDDATVRRGVKDWESNPRFLFLGNFDGAMITMGSSRFKFFMNDNDFGWGRPWVWRSGMANKFDGKISAFFRREGNGTVLEVLAPETMAGLEEDMEFVQVGVY

NbL19g16340.1 uncharacterized_LOC104085387 [MW = 46.63 kDa]

No. of times detected



log(intensity)



Values from



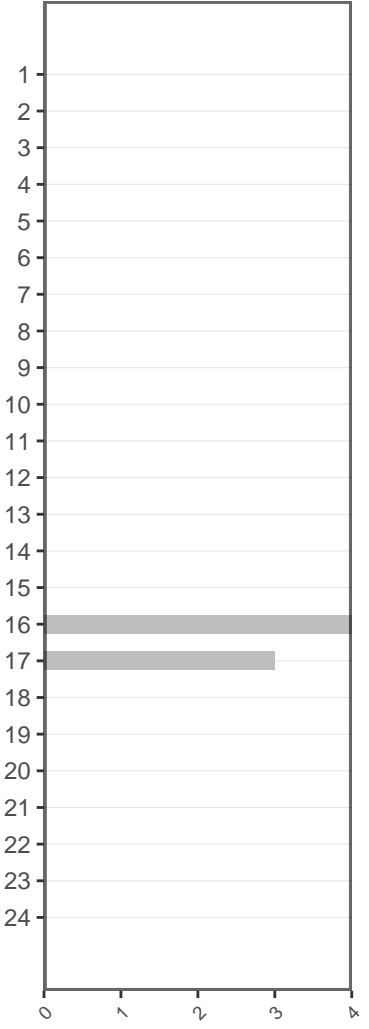
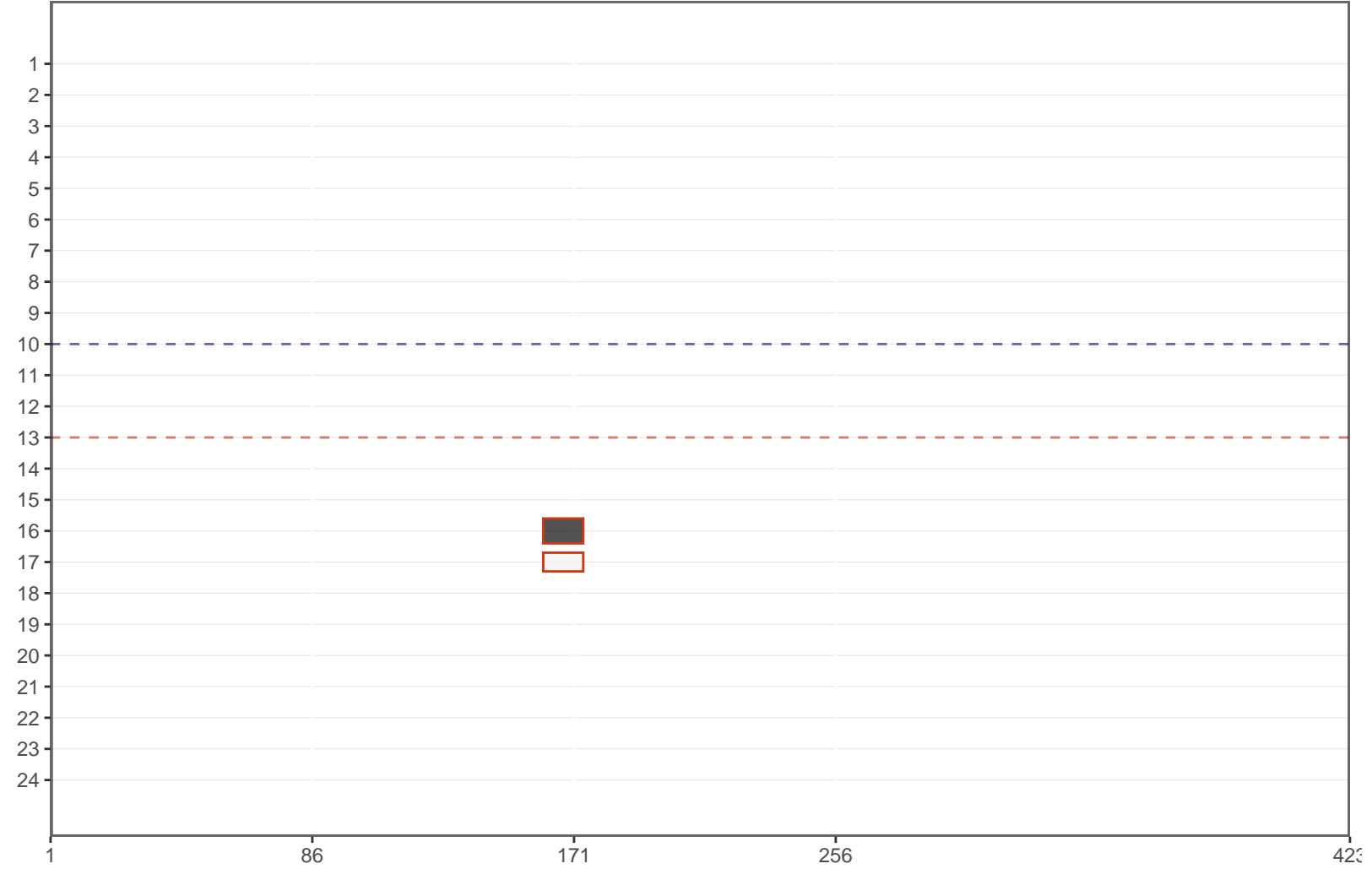
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ITVEEPLAEQSKESAAANPELILAMENLVPTTVVDLEDDVSEKGNKNEVLAMAEINTEVNTIEAKAIGKNGMVFNDEVLSSKEESILVASETVPVLPVPLGTGLVDMDKVIAETLLLDVGMNKVVAEGSLGLKSKFNFPELSLNEEVATDLTHPRETPEMKLNWQEVIRGNEDEKSELVEGGDWPNGKPVKEIFDSDMGWGRITLQKFFANLGFPRKVELEG

NbL19g16270.1 chlorophyll_a-b_binding_protein_CP29.1_chloroplasti-like [MW = 31.08 kDa]

No. of times detected



log(intensity)



Values from



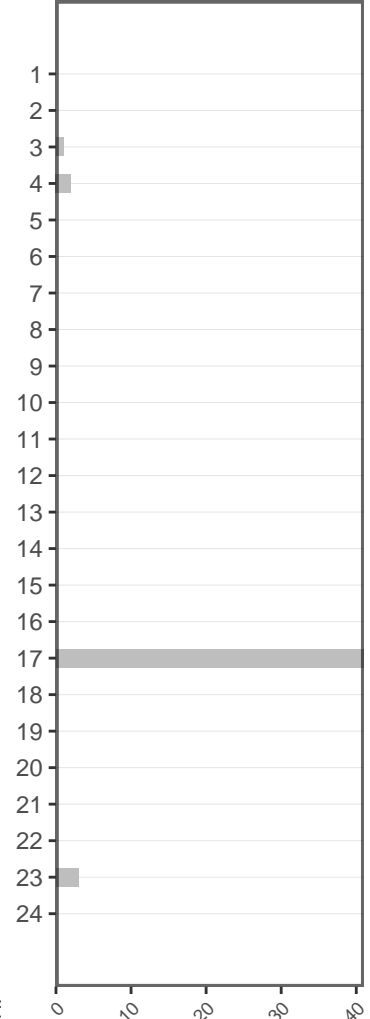
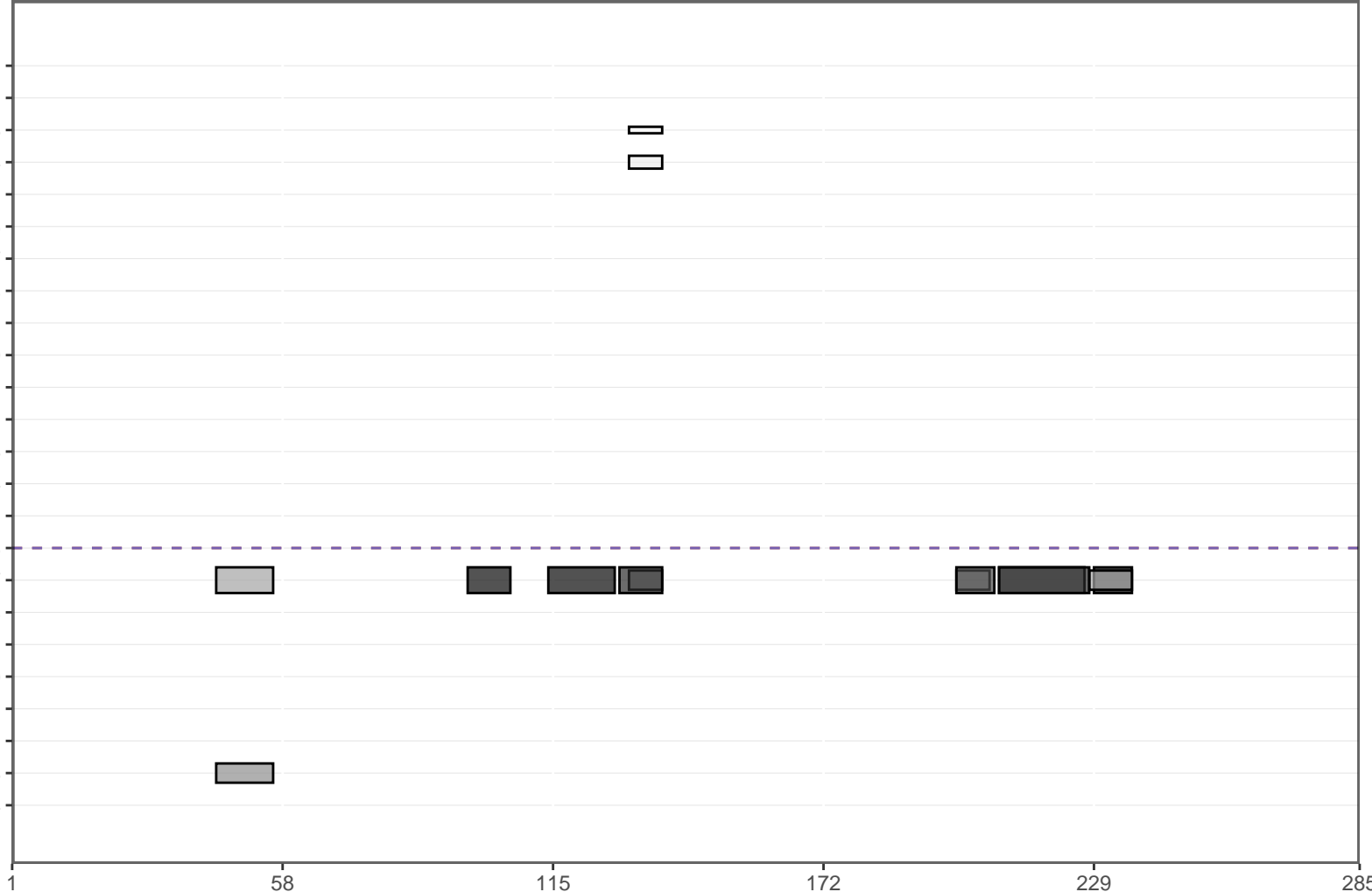
MW indication



Molecular weight



Gel Slice

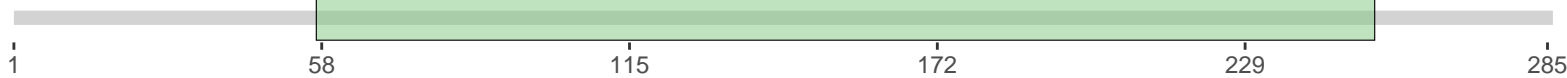


Peptide counts over 4 repeats

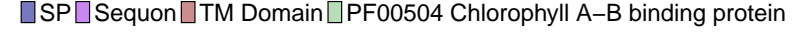
Protein length



Pfam domains



Pfam Description



Protein sequence:

RFRECELHGKRWAMLATLGAALTEVWVSGITWGDAGKVELVEGSSVLLGQPLPFSITLWVIEVLVGHYEFQRNAELDPKRLVPOGSSFDPLGLAADPEKKTALGLAEIKHARLMMWALGFVQAAATGKGPLNINWATHLSDPLHTIFDTTFGFFS

NbL19g16130.1 dnaJ_homolog_subfamily_B_member_4-like [MW = 40.35 kDa]

No. of times detected



log(intensity)



Values from



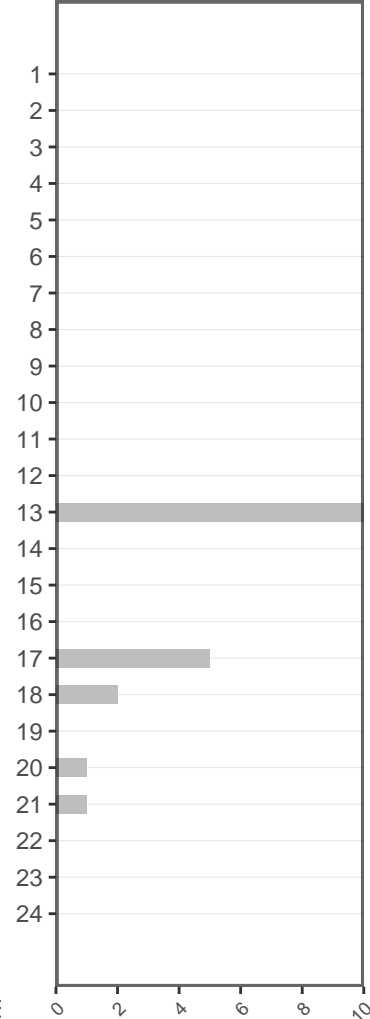
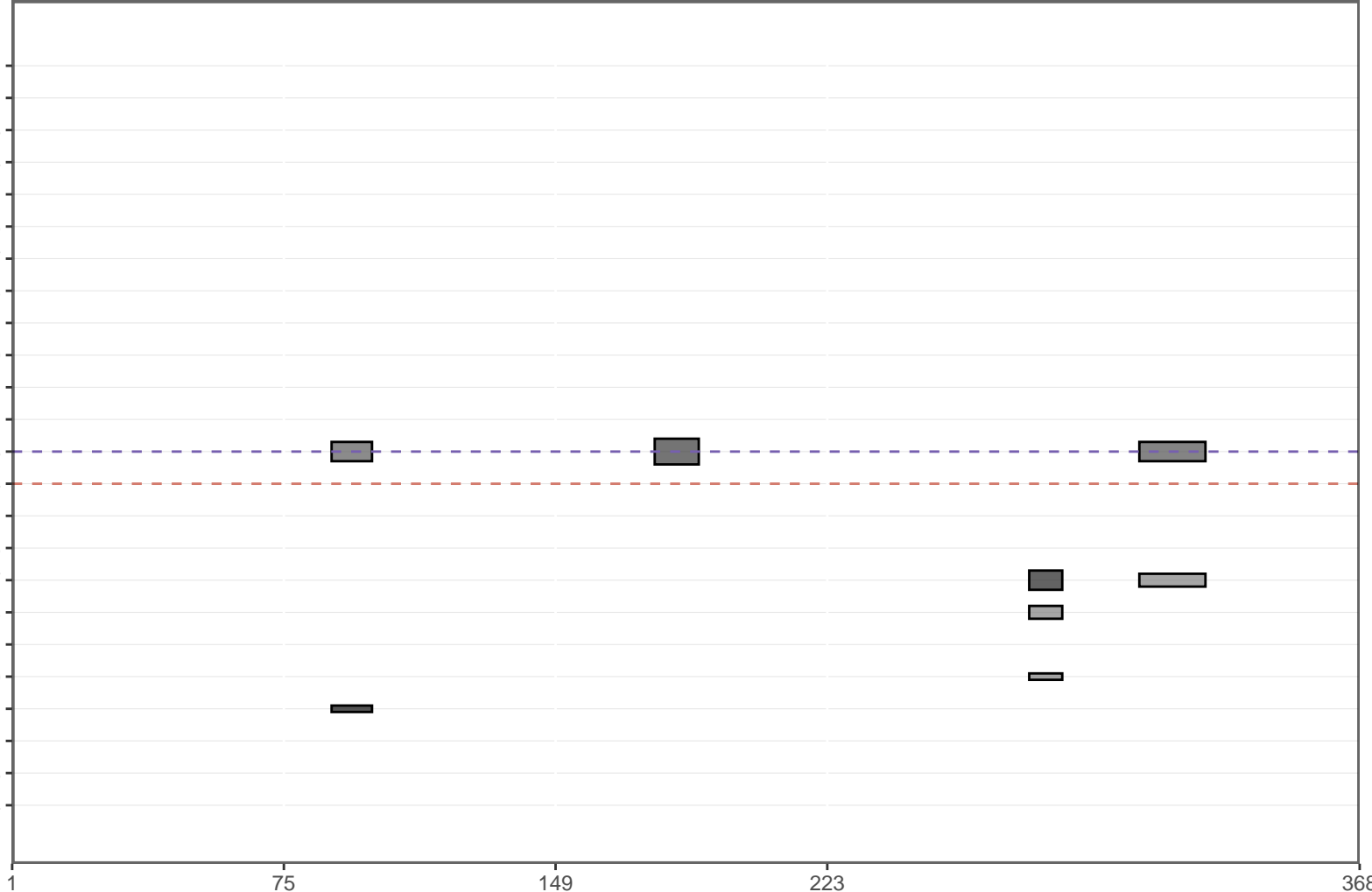
MW indication



Molecular weight

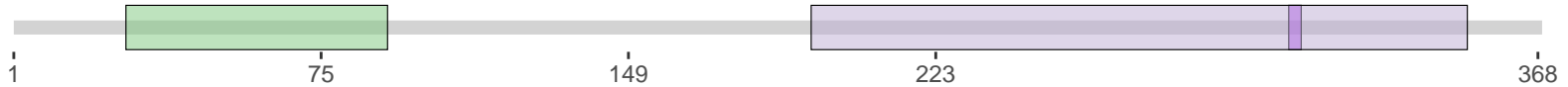


Gel Slice



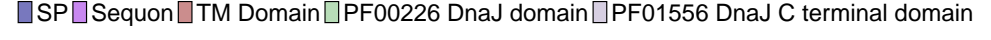
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGMFGEDFTSFRNMAEGEASNNVPRKAAPIERLPGGLELDYKGTTHKMKISREVSQATGRPSTTEELTDKMPGWKKGTITFFPEKNEQRGIPSDLVFIIDEKPHVFKRDGNDLVYTKISLVEALTYAGITLDRNLTPINSHSPNYEEVHKGEKMPKPKKGNLRVFNKFFPSKLTGEQKAGIKRYLT

NbL19g16020.1 bifunctional_monothiol_glutaredoxin-S16_chloroplastic [MW = 35.84 kDa]

No. of times detected



log(intensity)



Values from



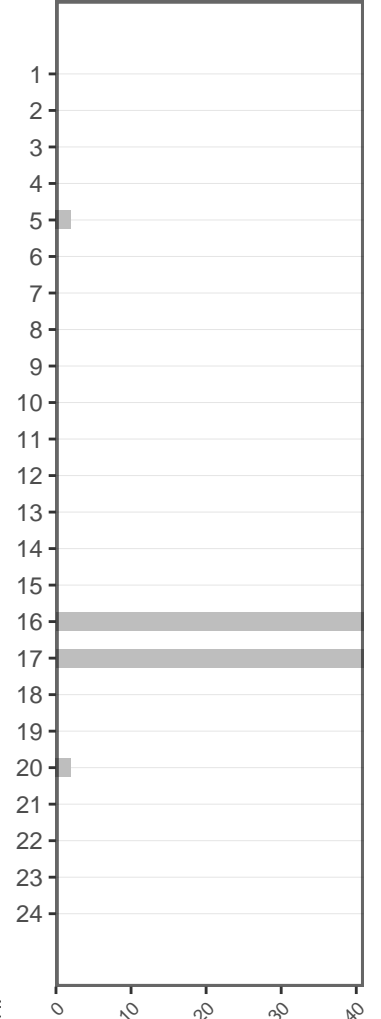
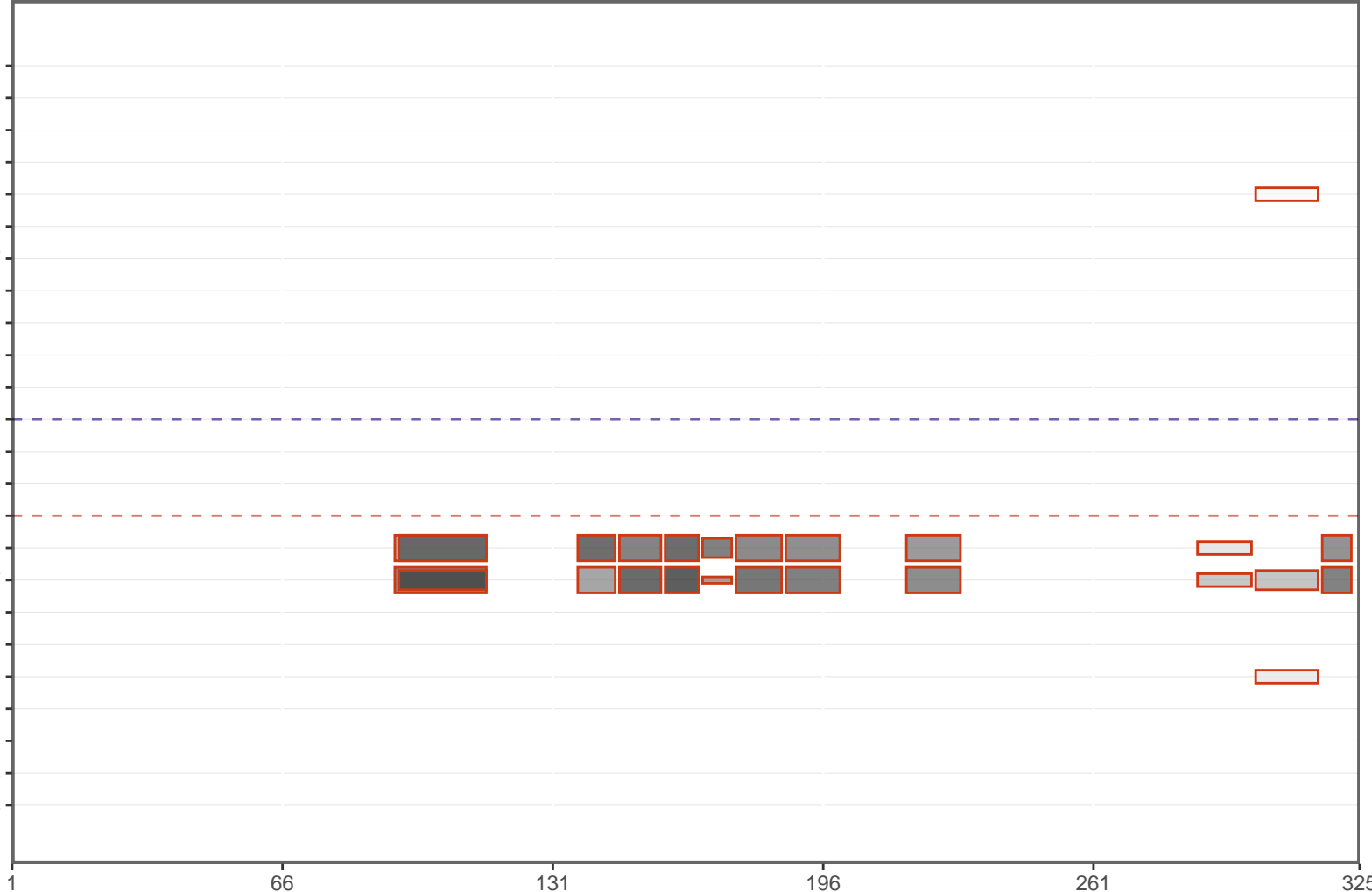
MW indication



Molecular weight



Gel Slice



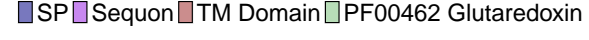
Peptide counts over 4 repeats

Protein length



Pfam domains

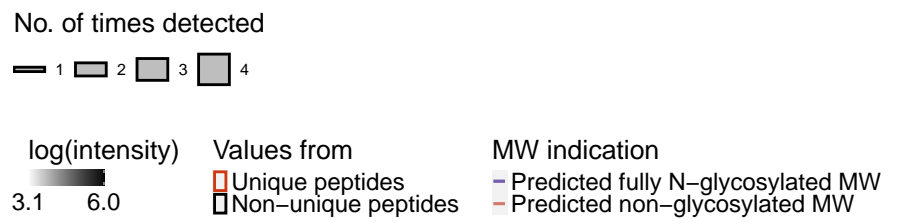
Pfam Description



Protein sequence:

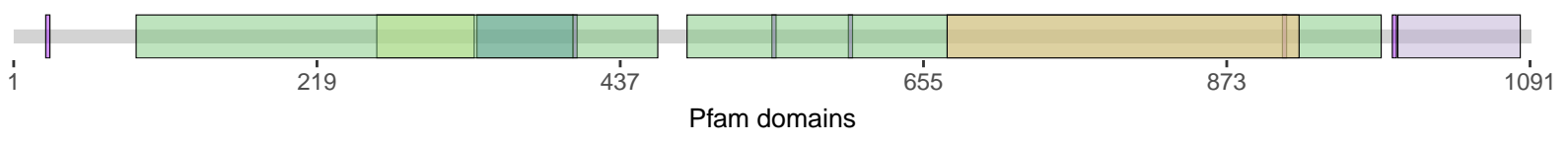
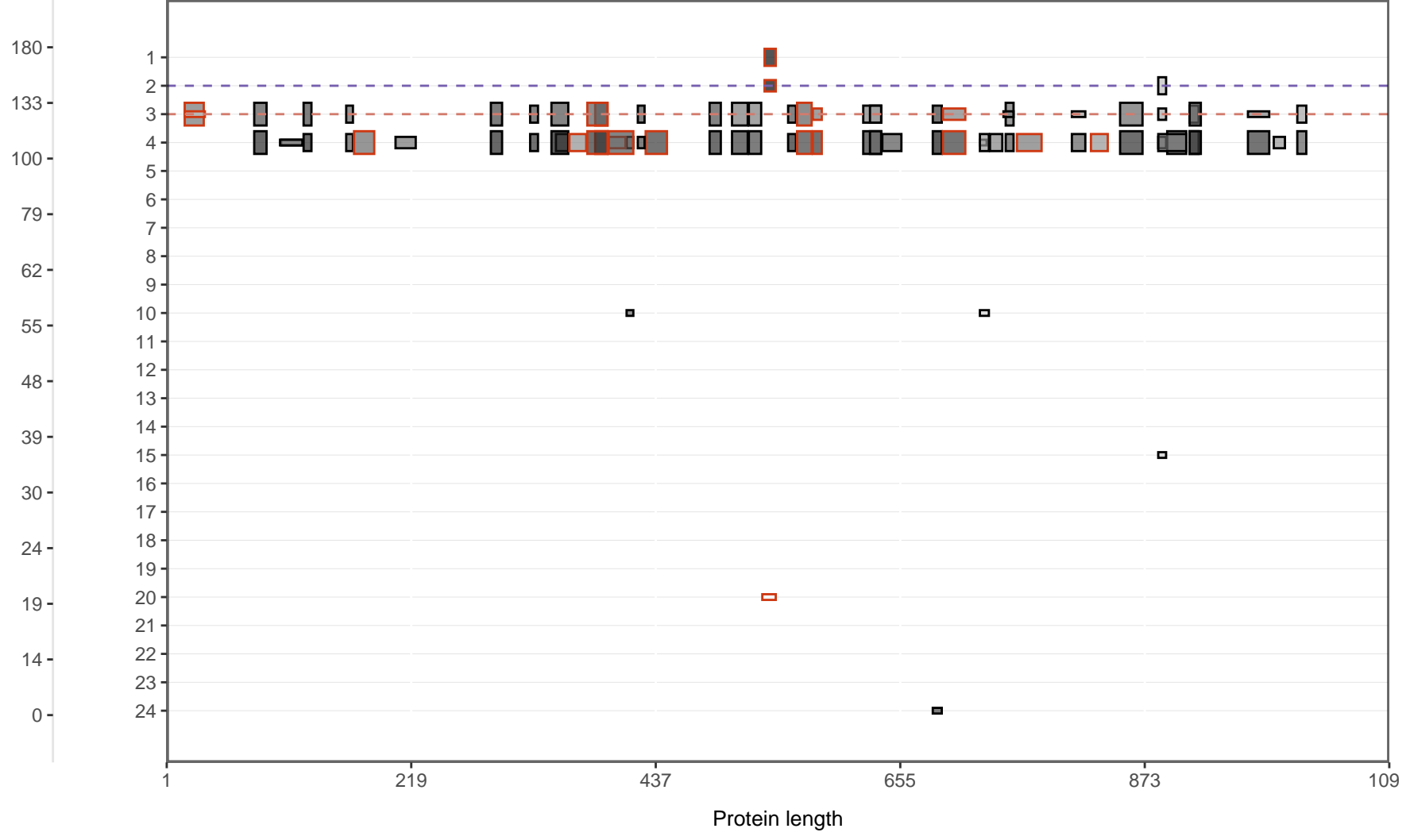
CSNVKGVYDEPNRIALTESEWKSVMEEHAATGKVPNGEPNGSTWWRGPPKPKTDLRLTPGRHVQLTVPLEDLIRLVKENKVAFAIKGSRAPQCGFGSQRVVAMLESEGVDEYEGVDVLDDEEYNYGLRETLKNYSNWTFFPQIFVKGELVGGGDLTSMVEKGEALFLKSE

NbL19g15680.1 ubiquitin-activating_enzyme_E1_1-like [MW = 121.21 kDa]



Molecular weight

Gel Slice



- Pfam Description**
- SP
 - Sequon
 - TM Domain
 - PF00899 ThiF family
 - PF09358 Ubiquitin fold domain
 - PF10585 Ubiquitin-activating enzyme active site
 - PF16190 Ubiquitin-activating enzyme E1 FCCH domain
 - PF16191 Ubiquitin-activating enzyme E1 four-helix bundle

Protein sequence:
CLTTDDVIEKSNLSRGFLFRDWNWGAKSTVAAAAASLNIPRIHEALGNRASPETESVFDDTFWENLGVVINALGNVNAKLVYDGRGLYFQKPLLESGTIGAKNTGMVPHLTFENYGAQRDPPEKQAPMCTVHSFPHNDHGLTWARSEFEGLEKTPTEVNAVNLNPDGHSAMQKAGDAGARDLDRVLEGLDKERNGDTFGDGTWRLRFEDYFADRVKQKLTFTTFEEATTS66APFWSAPKRFPRPLQF6VDBASHLQFLLAASILRAETFGILPQVYKSPQKLAEA

NbL19g15670.1 uncharacterized_LOC107798940 [MW = 37.57 kDa]

No. of times detected



log(intensity)



Values from



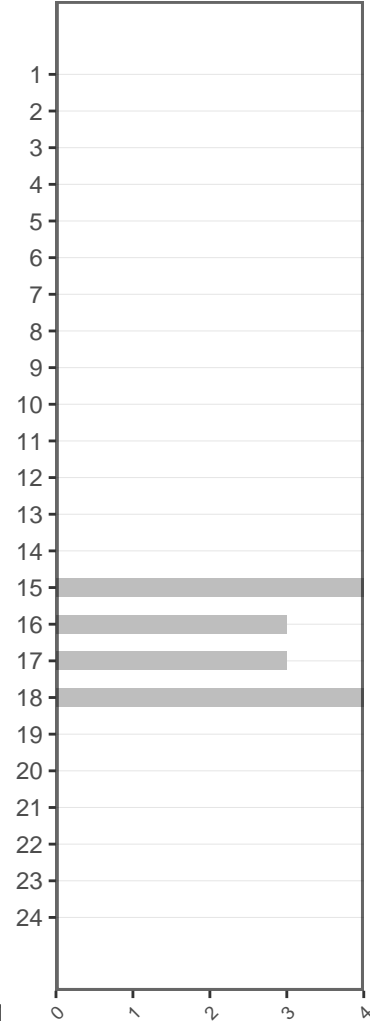
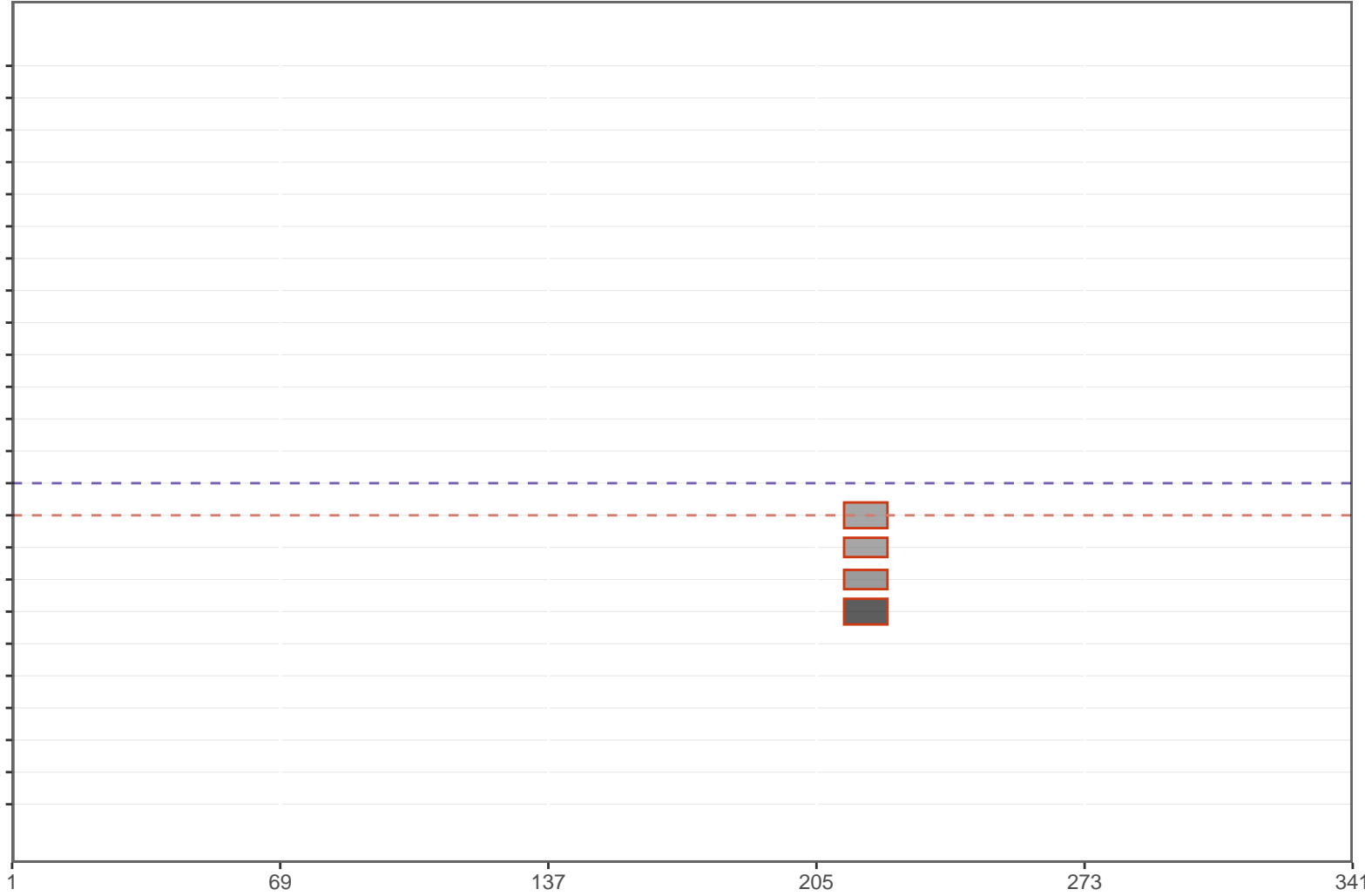
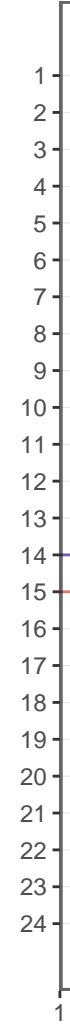
MW indication



Molecular weight



Gel Slice



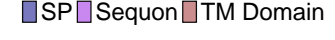
Protein length



Pfam domains



Pfam Description



Protein sequence:

LSHSFTPONAPYLLELPPSLFLLTTPFHEGLHHTHEYAFQYRISTDSFDPKSLDINIGPFRSHYVGFSPSPFLHSCDLRGNPNAEDEKVESLVGKRGKDKGKELDLGAEFGFGRLLNKLMSGDSANYSYTAELHLYDKMLVKLDELARLVETSAAKYLEGENHNMKLRVYKVGLE

NbL19g15230.1 probable_inactive_receptor_kinase_At5g58300 [MW – SP = 67.45 kDa]

No. of times detected



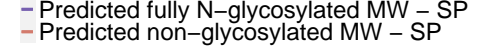
log(intensity)



Values from



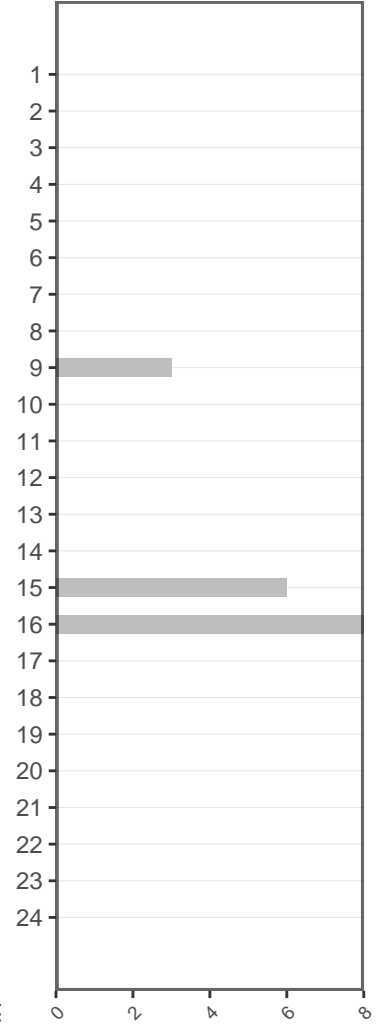
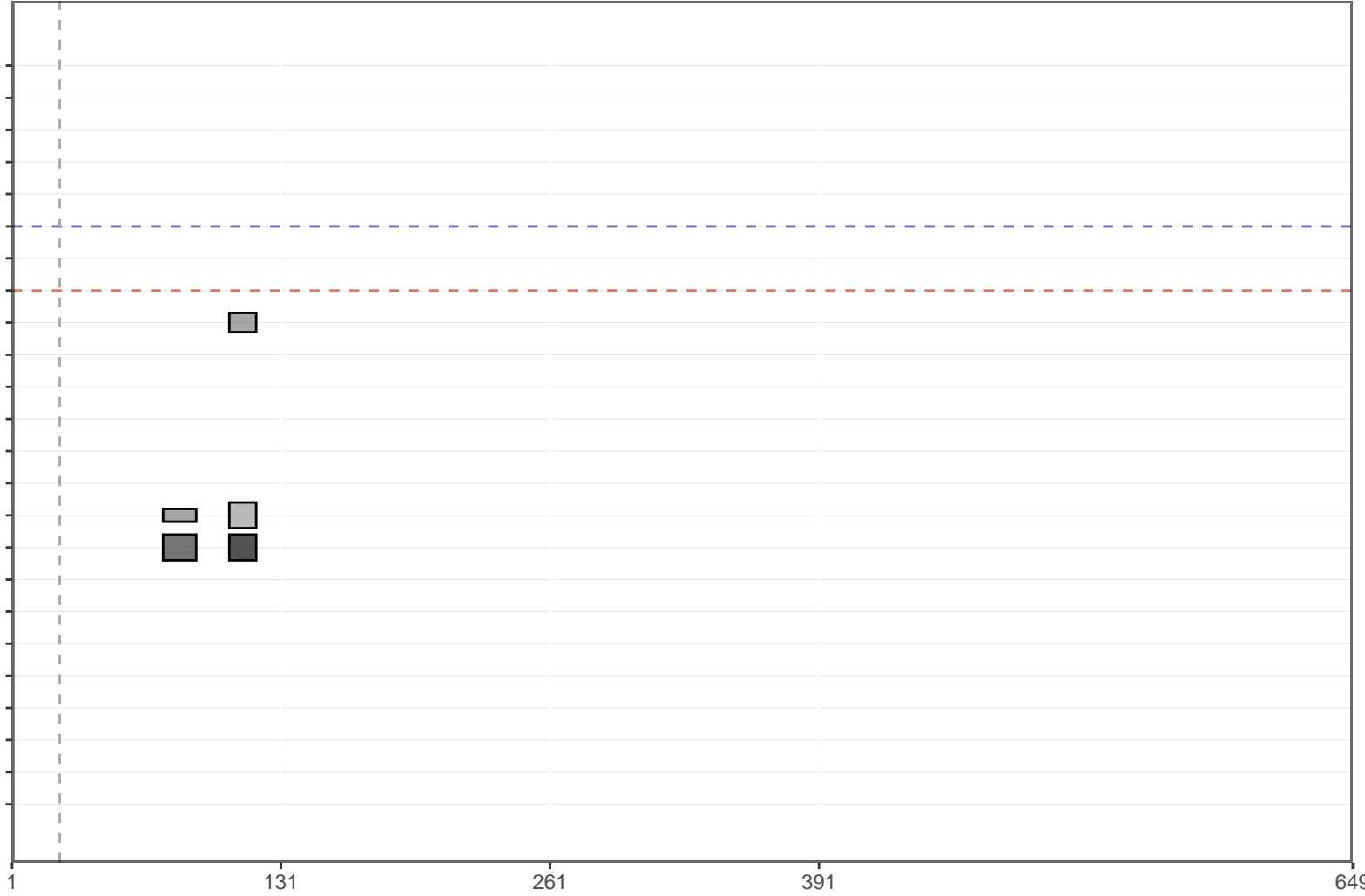
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GSPKQTEDFSSGVGAENKLNLYFFGGGSFNFDLEDLLRASADVLGKSGYGTTYKALEEGTQVWKRLEKVVYVGRREFEGGMEIGTVAQHGQVYALRAYVFSKDEKLLVYDHPAGLSTRMHGNRELGRFLSWESRLRIHGAASGIAHHVAGGKLIHGNIRSNVLTNDNSGGSDVGLTFLMGSPTIPSRVAGYRAREVETRIKTKGSDVYVSGVALLLELLTGAPVQPPHGHDEVDLFRWVQGVVREEWTAIEVFDALIKFQNIIEEMVQMLQIAMACVAKVPEI

NbL19g15210.1 receptor-like_protein_kinase_FERONIA [MW - SP = 93.8 kDa]

No. of times detected



log(intensity)



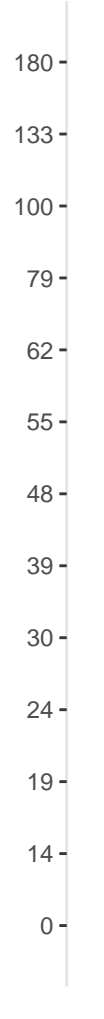
Values from



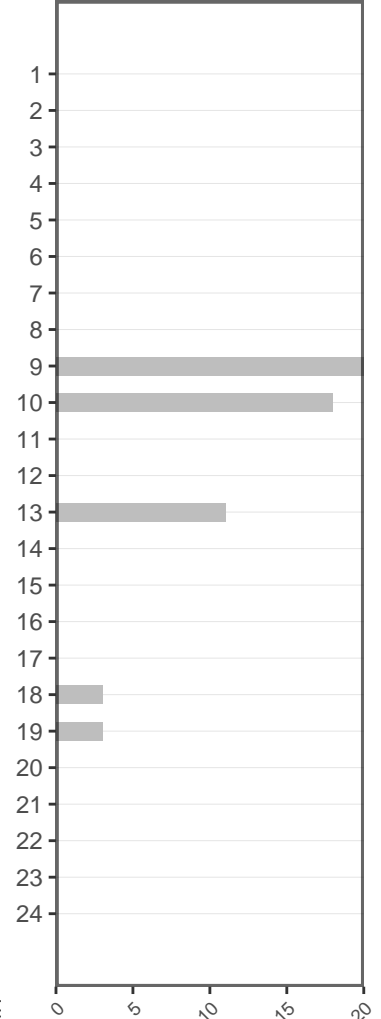
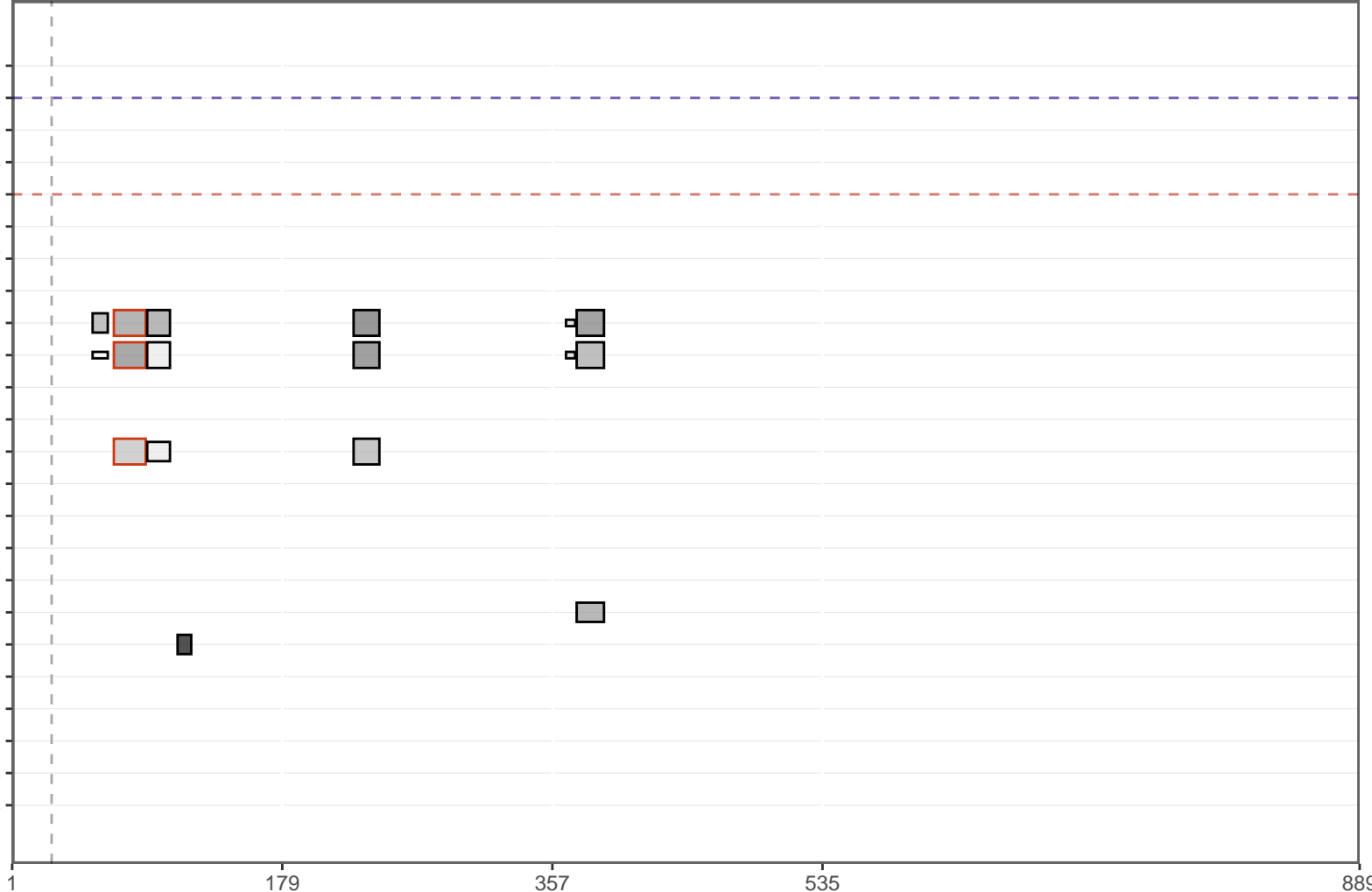
MW indication



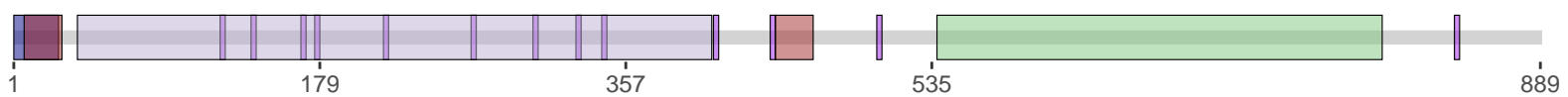
Molecular weight



Gel Slice

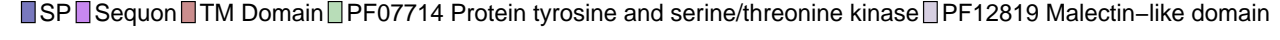


Protein length



Pfam domains

Pfam Description



Protein sequence:

KKGGQSKSNKSAISGGVGGGMAVILGLVGLVTRRRKHGKVGSPDGGPSSGWLPLSLVGNHSHTGSEAKTNTTGGVYASLPSNLRGRHFAEKAATNDFESLILGVGGFGKVKIKRGNPLSEGGVHEFGTEIEMSLKLRHRLVSLIGYCEENCEMILVDDYMAHGTLRHLVYKTKQKPLPWKGRLLDGGGAARGLHYLHGTAAKHTIHRDKTTNLLDEKWWAKVDFGLKTKGPTLDHTHVSTVWKGSGYLDPYFRROGLTKEDVYSGVVLVELLI

NbL19g15060.1 non-specific_lipid-transfer_protein_1-like [MW - SP = 9.78 kDa]

No. of times detected



log(intensity)



Values from



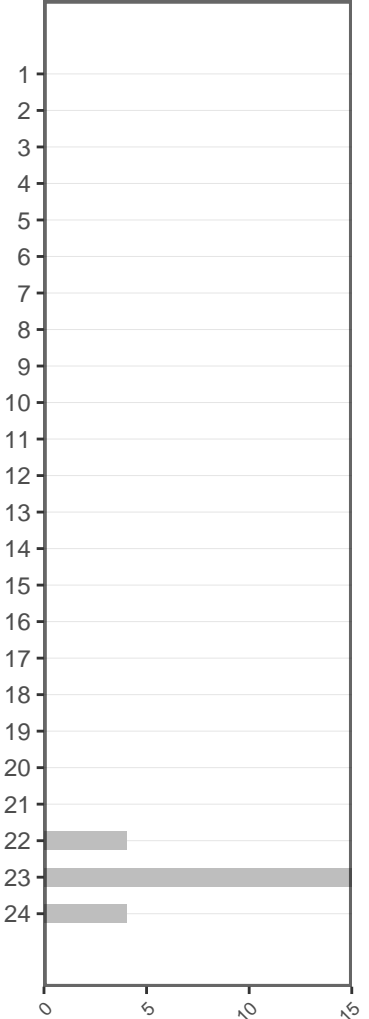
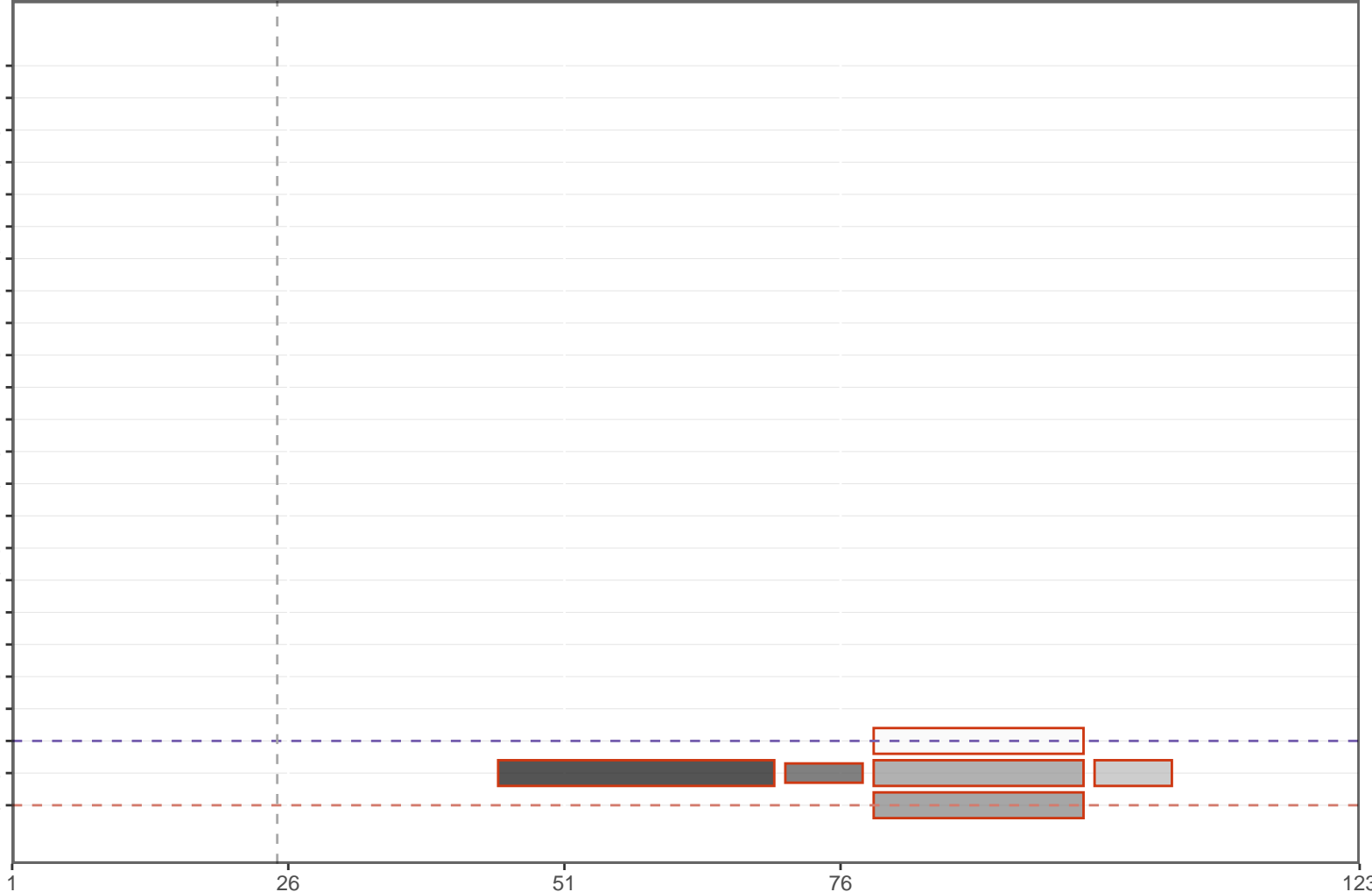
MW indication



Molecular weight



Gel Slice

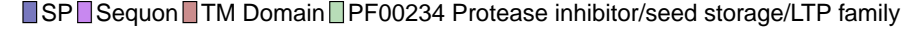


Protein length



Pfam domains

Pfam Description



Protein sequence:

AIKPKCCGINSLNQATSTFDKGTAGCGKSAAGISGNIQLAGLPLKGGVNLPIKISFIDGDTYVSNTHF

NbL19g15050.1 non-specific_lipid-transfer_protein_1-like [MW - SP = 11.38 kDa]

No. of times detected



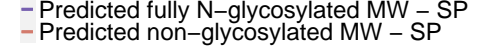
log(intensity)



Values from



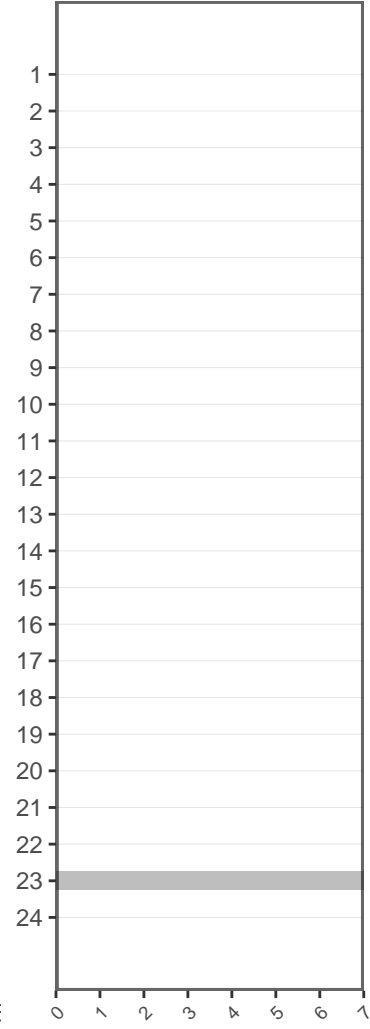
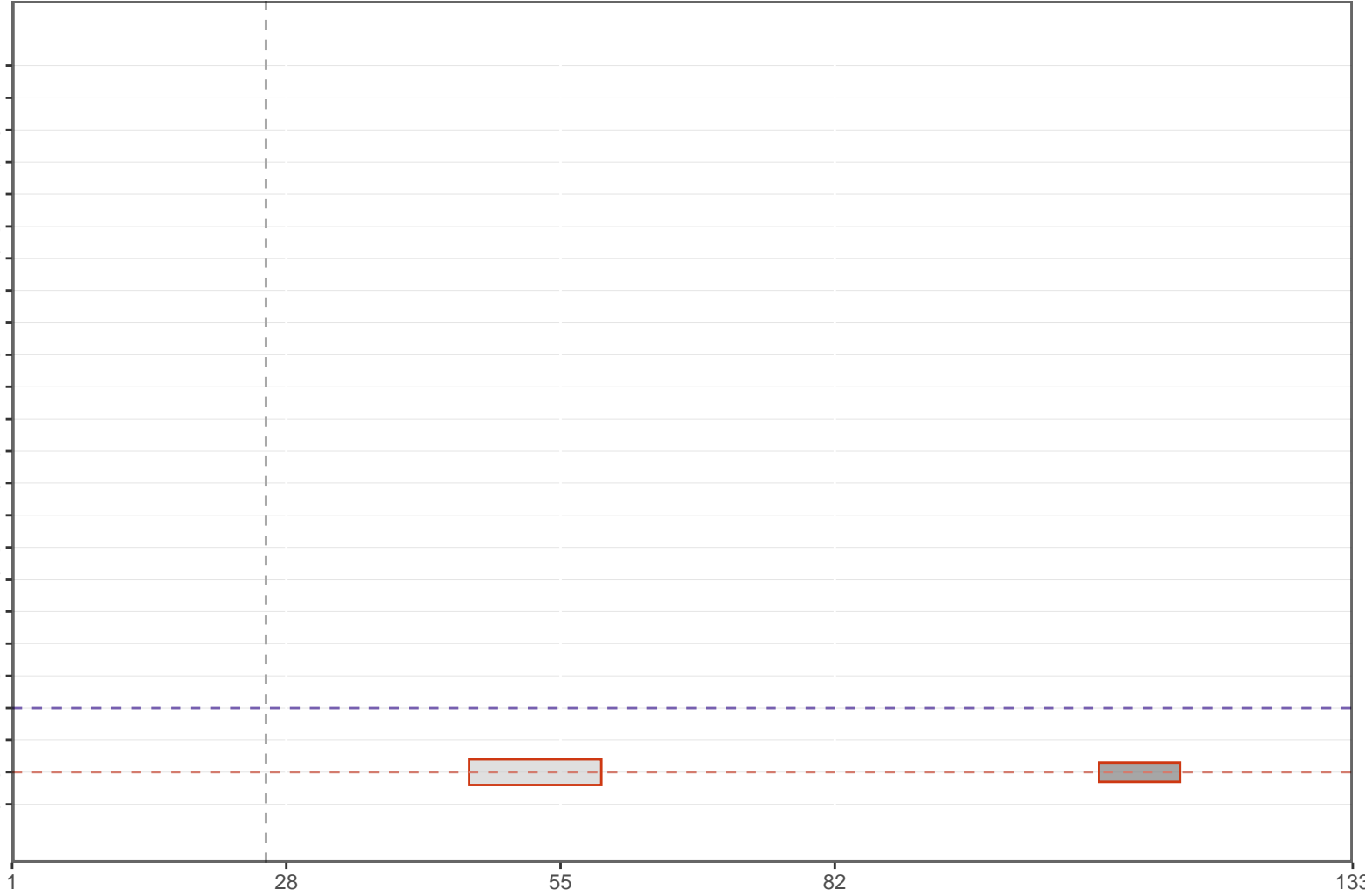
MW indication



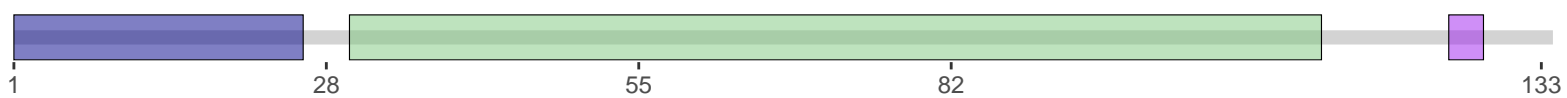
Molecular weight



Gel Slice



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ICCGIRSLFRAAFTDGRGTFVCGMKGAARVHGVLNLAALPREGGVNPFYKISPTDCARVHYVFLNIGHFCAI

NbL19g15040.1 non-specific_lipid-transfer_protein_1-like [MW - SP = 14.85 kDa]

No. of times detected



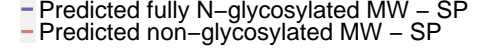
log(intensity)



Values from



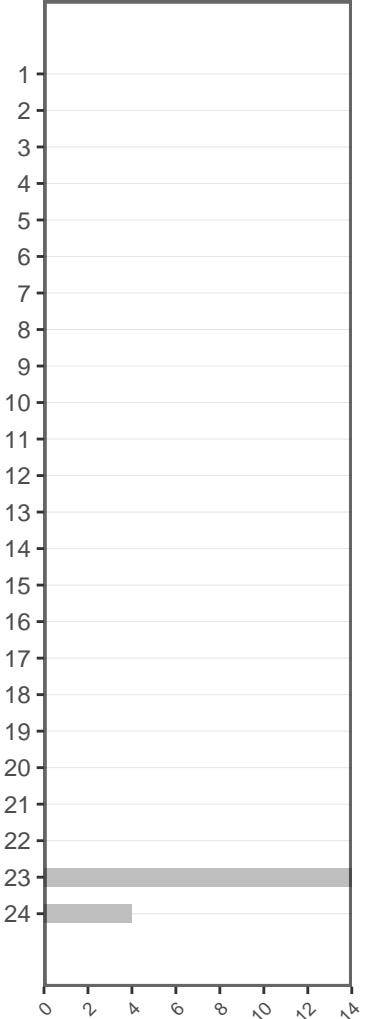
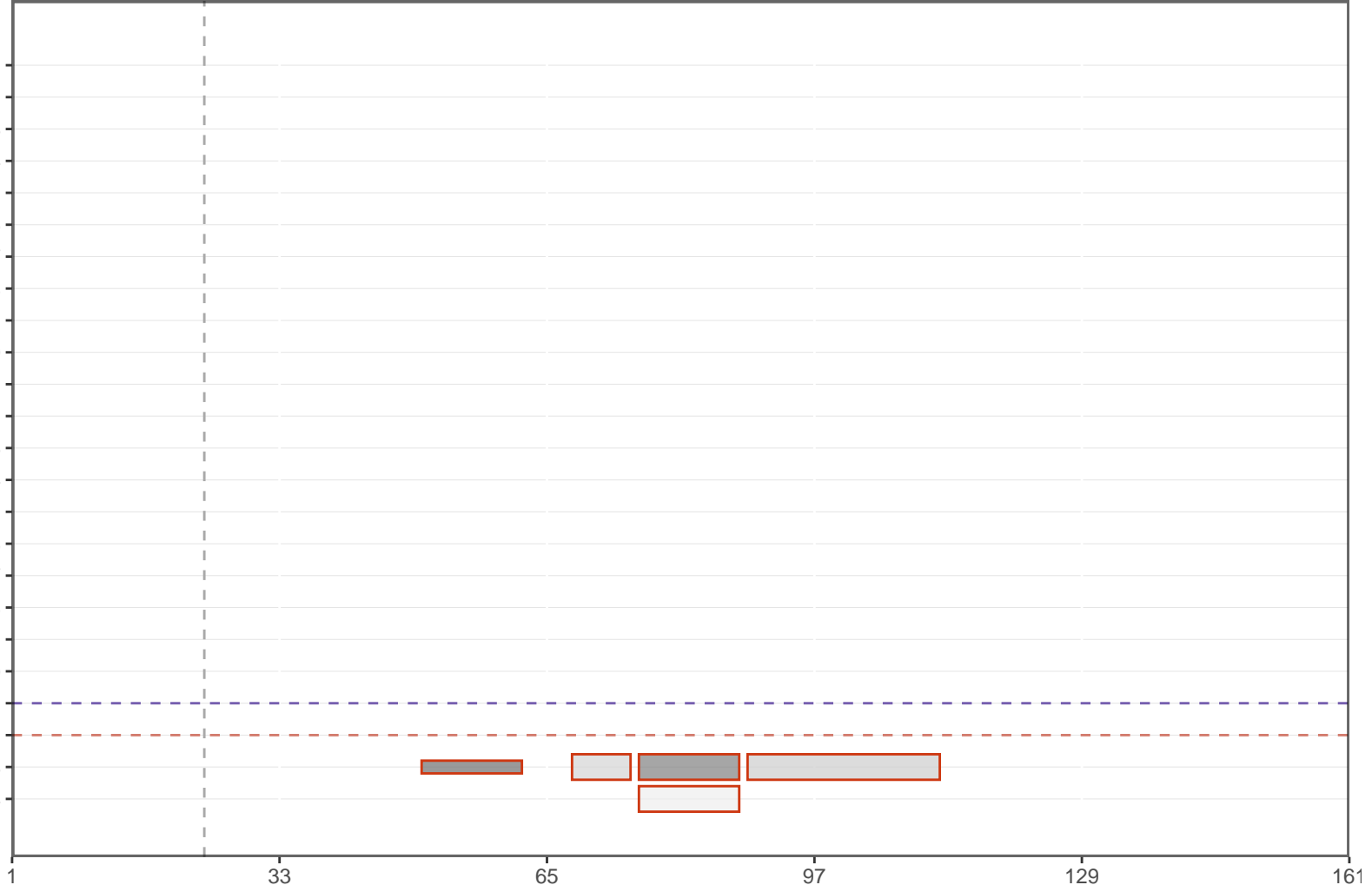
MW indication



Molecular weight



Gel Slice

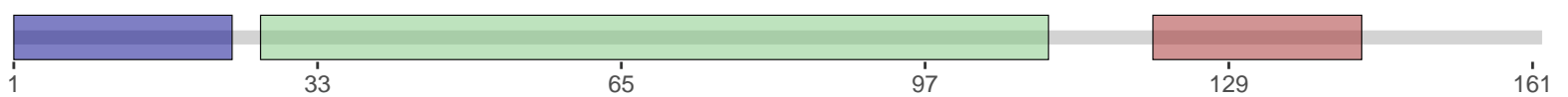


Protein length



Peptide counts over 4 repeats

Pfam domains



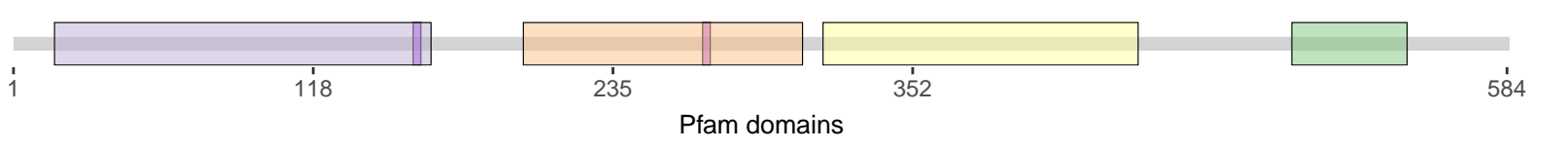
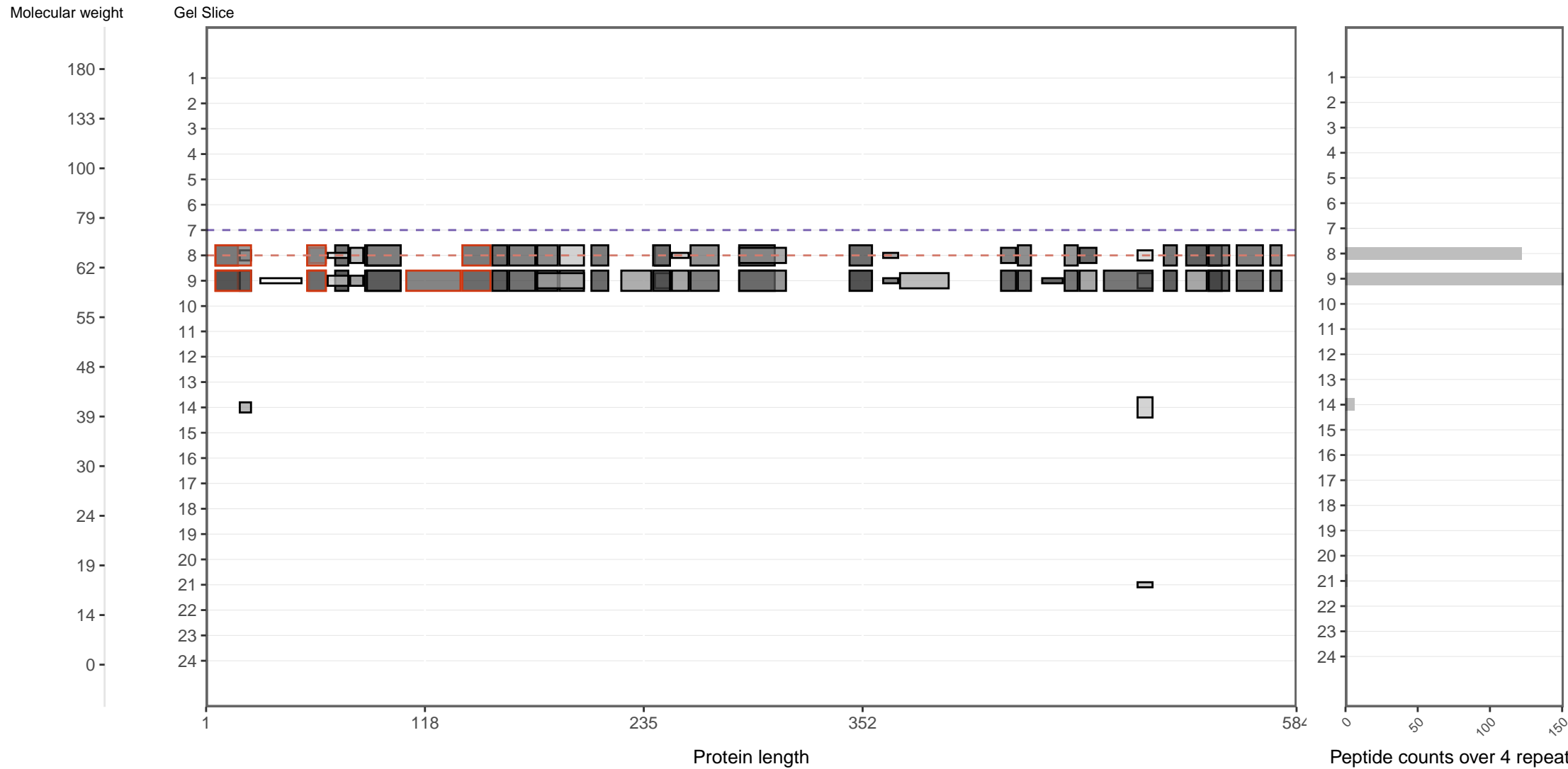
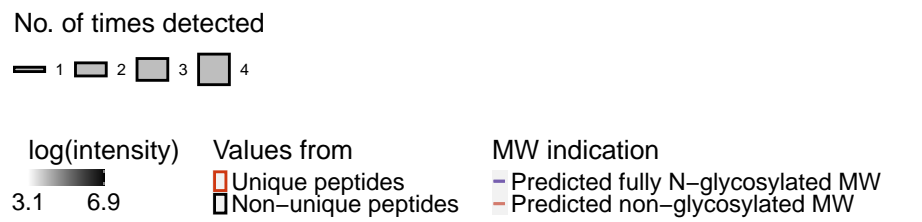
Pfam Description



Protein sequence:

TQDRGTACTCLKLSAAMASGDELGKAAGLPTGGVNIPIWISPTDGGKYLTFLLSHLLLYSGIFSEYPLNLFRLFKGTRRHLYLFFSSRYK

NbL19g14840.1 phosphoglucomutase_cytoplasmic-like [MW = 63.45 kDa]



PF02878 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain I PF02880 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain II
 Phosphoglucomutase/phosphomannomutase, C-terminal domain PF02879 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain II

Protein sequence:
 ARMGLSKSHSEPNPPPEFGAAADGGADRNMILGKRFFVTPSDSVAIAANAVEAIPYFSGGLKGVARSMPFSAALDVAKSLNLFYEVPTGWFQGLMDAGMGGICGEESEFGTQSDHIREKDKGHWLWLAWSLADKNDNLGGEKLVSEEDIVRQGHWTYGRHYHYTRDYENVDAAAGAKELMAHLVKGQSLDEVNKKIKGHSDFGNVYHGDSEFYKDPVDSSEKHKQGRVYLFEDGSRLLVRLSGTSGEGATIRVYIEGQYKPKGKGRDQGEALPLVEVAIKLQKMQE

NbL19g14660.1 heat_shock_70_kDa_protein_16 [MW = 84.35 kDa]

No. of times detected



log(intensity)



Values from



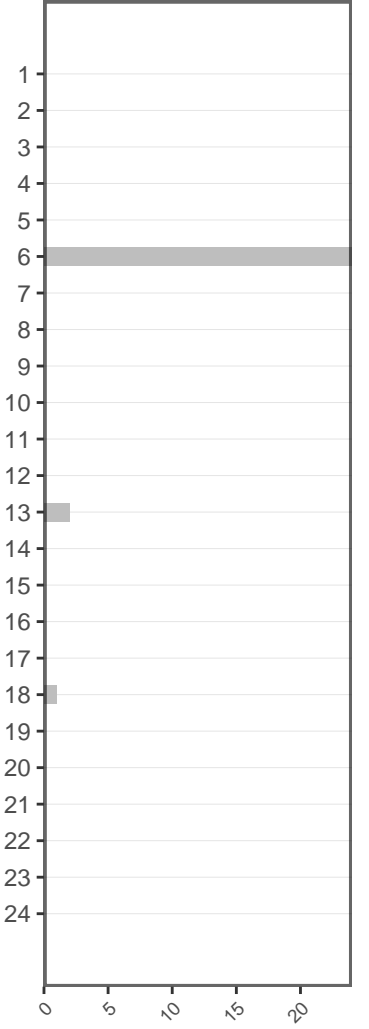
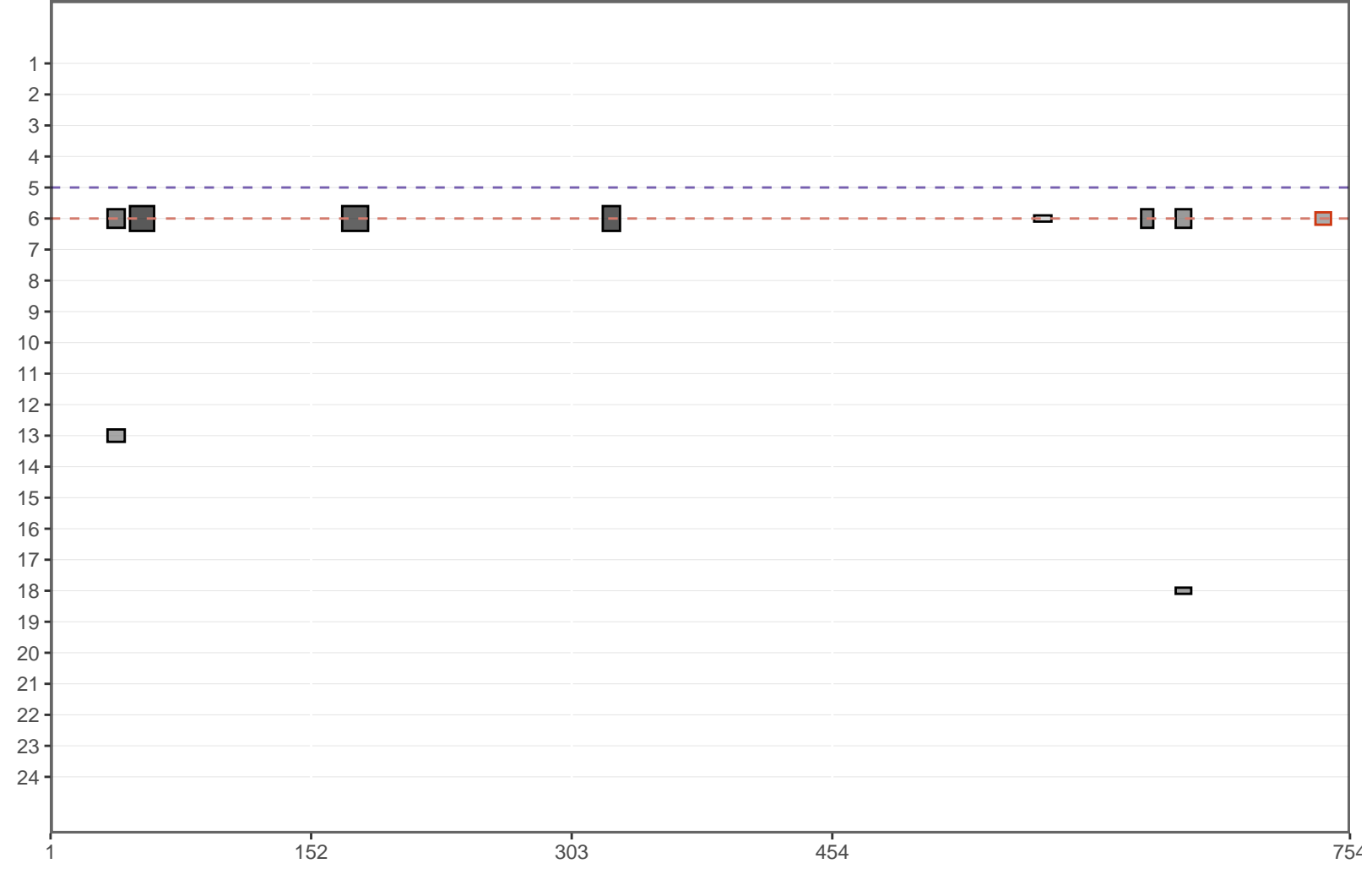
MW indication



Molecular weight

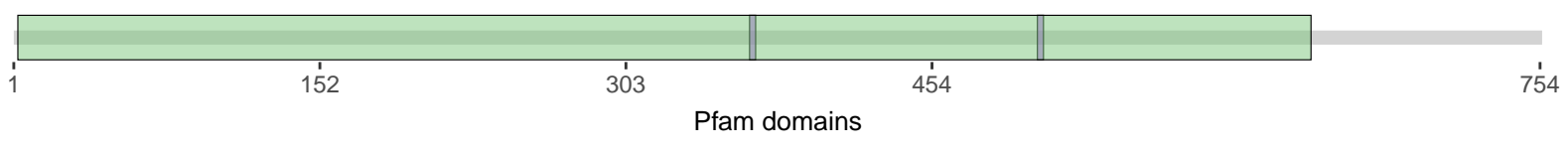


Gel Slice



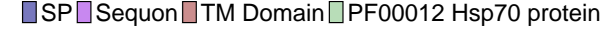
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

/ARGCALQCAMLSPIFRVREVEVQDSFFPFGFASDEGFPVCTLSNGLIFPRGHSPFSKAVLTLGRSTFSYLEAFYTNGLFPPGVSDKISKSTGPFQVPHSEKAKKVKQLNLHGIVTVEGAWLIKDQTSHTSSENNFTDTHAEDMERDDTRKSMVAWRQDIPVSESEVDGGMTLAELSGAQEKECHLAEGDKVPHERTKDKKNTLEAVVYETRNKLLNTYRFGFATDSEREGSCNLQGTTEEWLYEDGGDESEHVVAEKLDLKKMVPENRYKKEETRAQATRNLLNSIVEYI

NbL19g14650.1 UPF0051_protein_ABCI8_chloroplastic-like [MW = 63.93 kDa]

No. of times detected



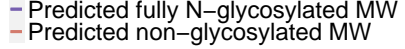
log(intensity)



Values from



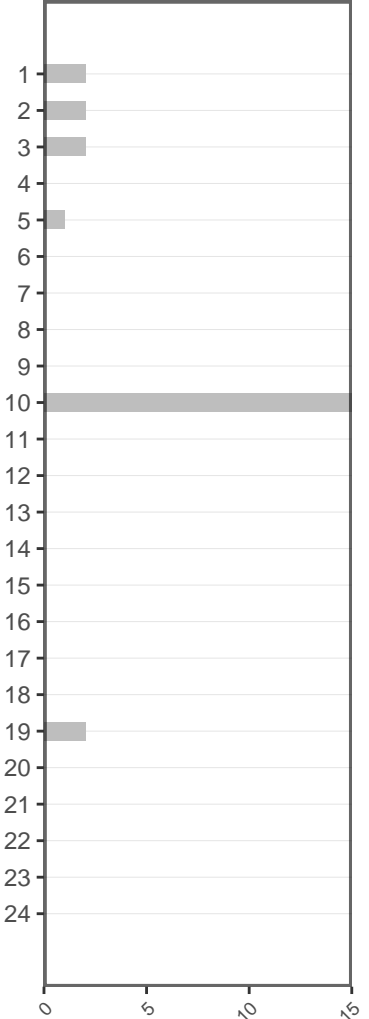
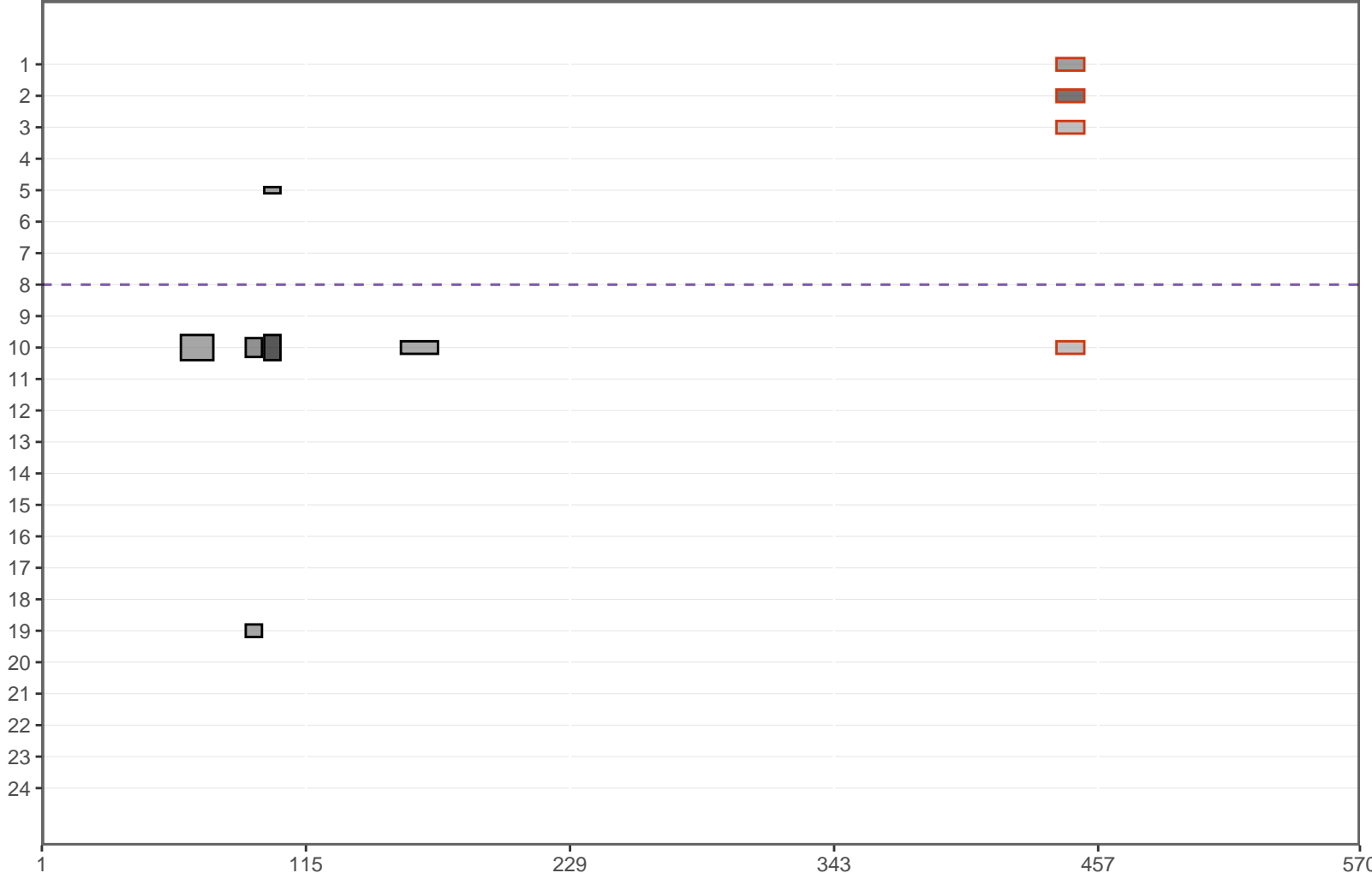
MW indication



Molecular weight



Gel Slice

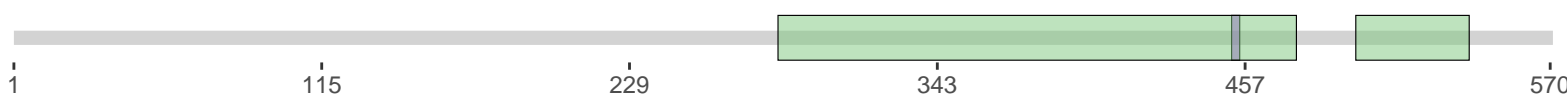


Protein length

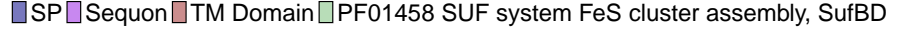


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

YFRNIMETGGFERTLMADEGGFVEVLEGGTAPSPYDNLQHLAAVVELVGHGSAIKYSTVQNWFAAGDEEGRGDYNFVTKRGLGAGARSKISWTQVETGSATWYKPVVLEGGDESVGEFVSGALTNVYGGADTGTMIHKGKNTSRRIKSGIGSAGHSRNGYRGLVGLNAENARNSSGGDSMLIGDAAAANTYPYKQVEGTLFLLLYLWLPDLCMLLAKNPBARIEHEATTSGKGGEDQLFYFGQRGIDKAKMAAMISGFRDWFNLPDFEGAEVYNQLMSLKEG

NbL19g14480.1 zinc_finger_CCCH_domain-containing_protein_14-like [MW = 30.73 kDa]

No. of times detected



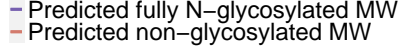
log(intensity)



Values from



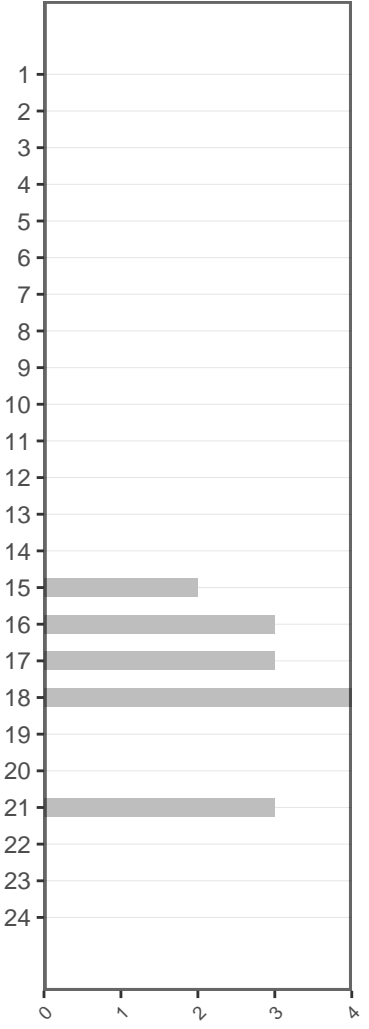
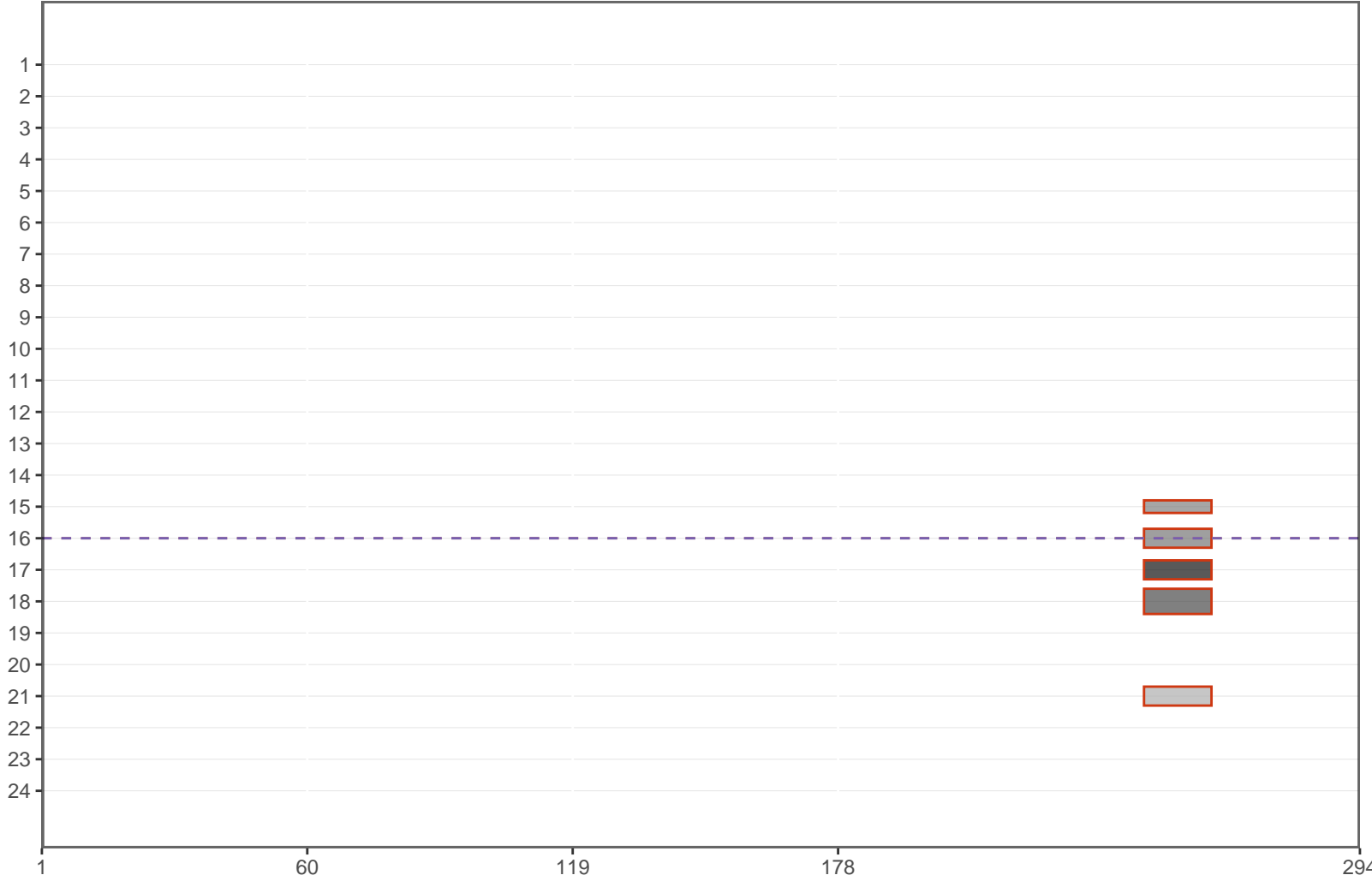
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

QEEPRAMQVGPVPRFGGRNERWVSGPMASFGTSATANISVDSASLAGAIKGGVHSHKQGRGTGAKLARIDHETDKNLNLEEGTFEGQASAMVRELINLSGVGCPDRTPVVPDGAAPRPSNFKTKLGENFAKGSCTFGDRCHFAGAAELRKTGV

NbL19g14410.1 60S_ribosomal_protein_L21-2 [MW = 21.71 kDa]

No. of times detected



log(intensity)



Values from



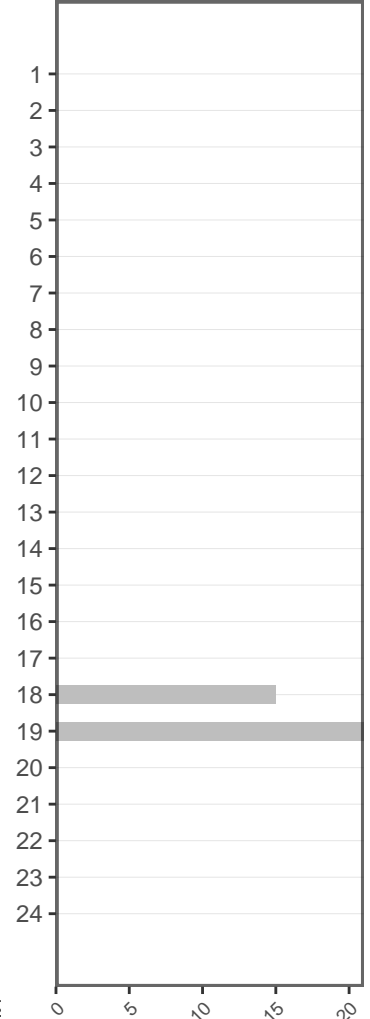
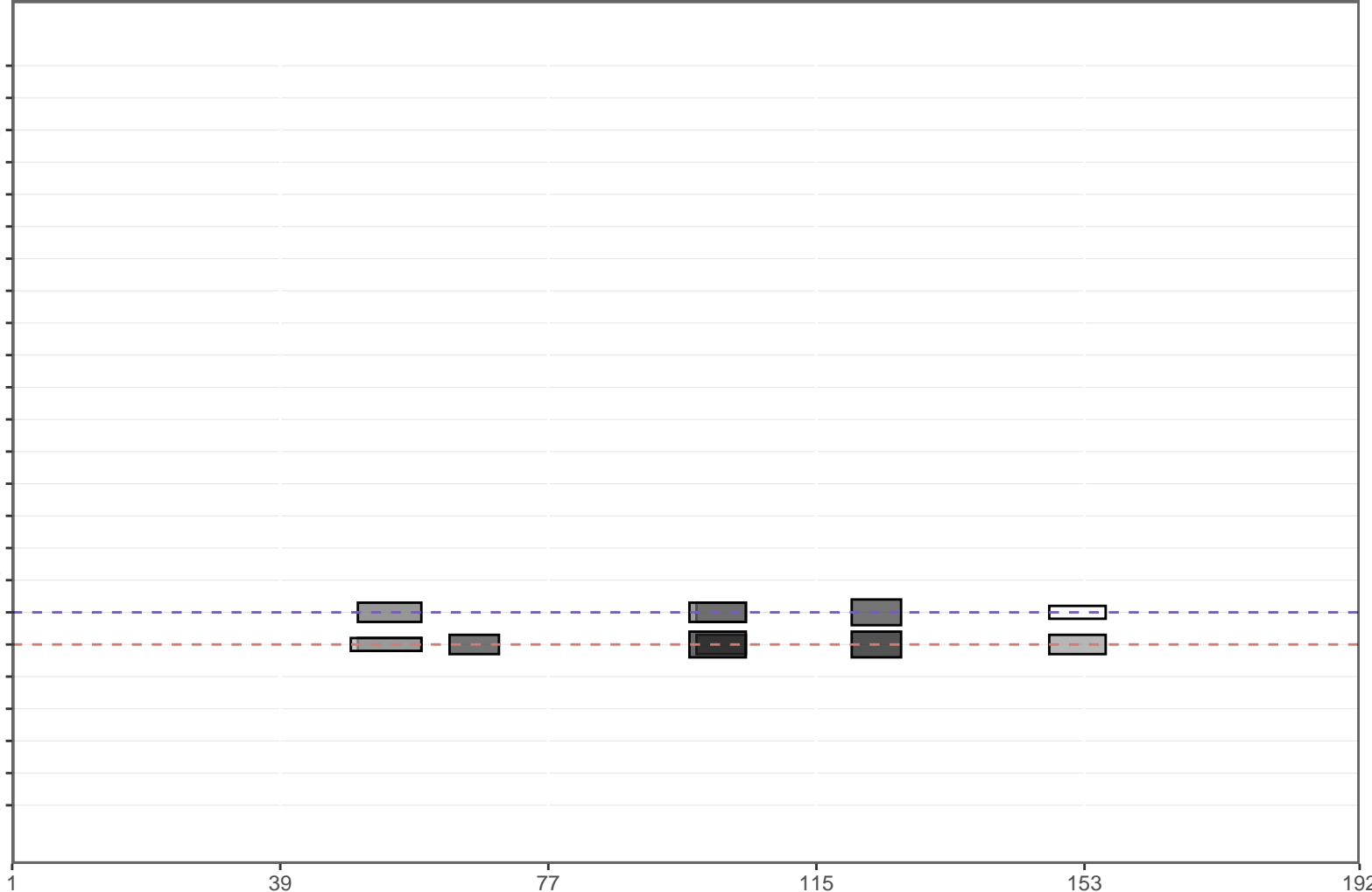
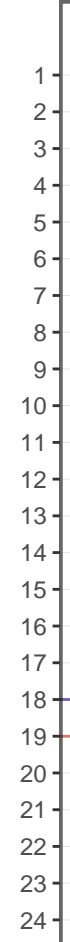
MW indication



Molecular weight

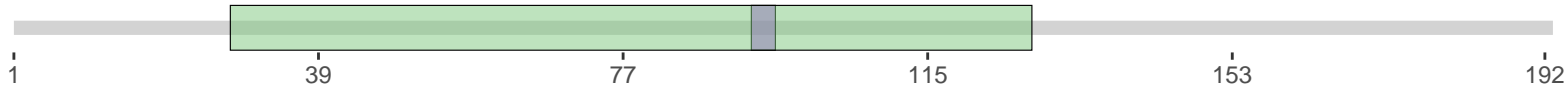


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YHGRTGRWVNTKRAVGVENVKQVFNKILKRIKRIHRIEHWQLSRCTEEVKEIKRINDQLKAEAKARGEVISTKRGPLGPNPFGMVEGATLETVTPYDVAINDLKGCV

NbL19g14270.1 asparagine--tRNA_ligase_cytoplasmic_1-like [MW = 64.92 kDa]

No. of times detected



log(intensity)



Values from



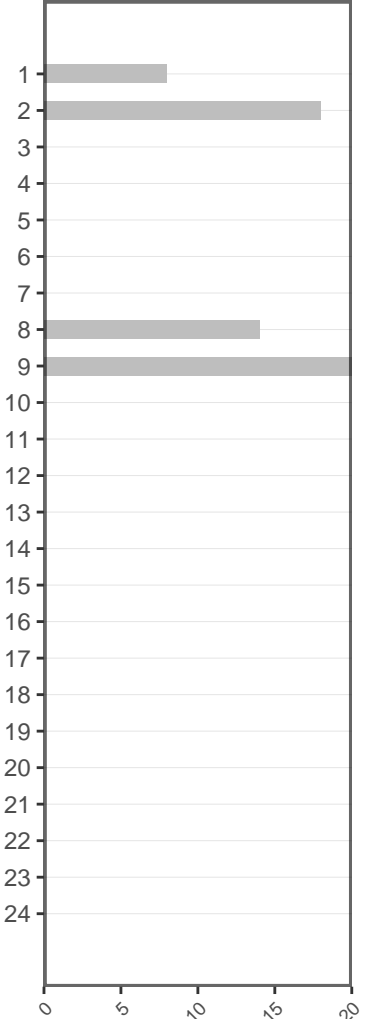
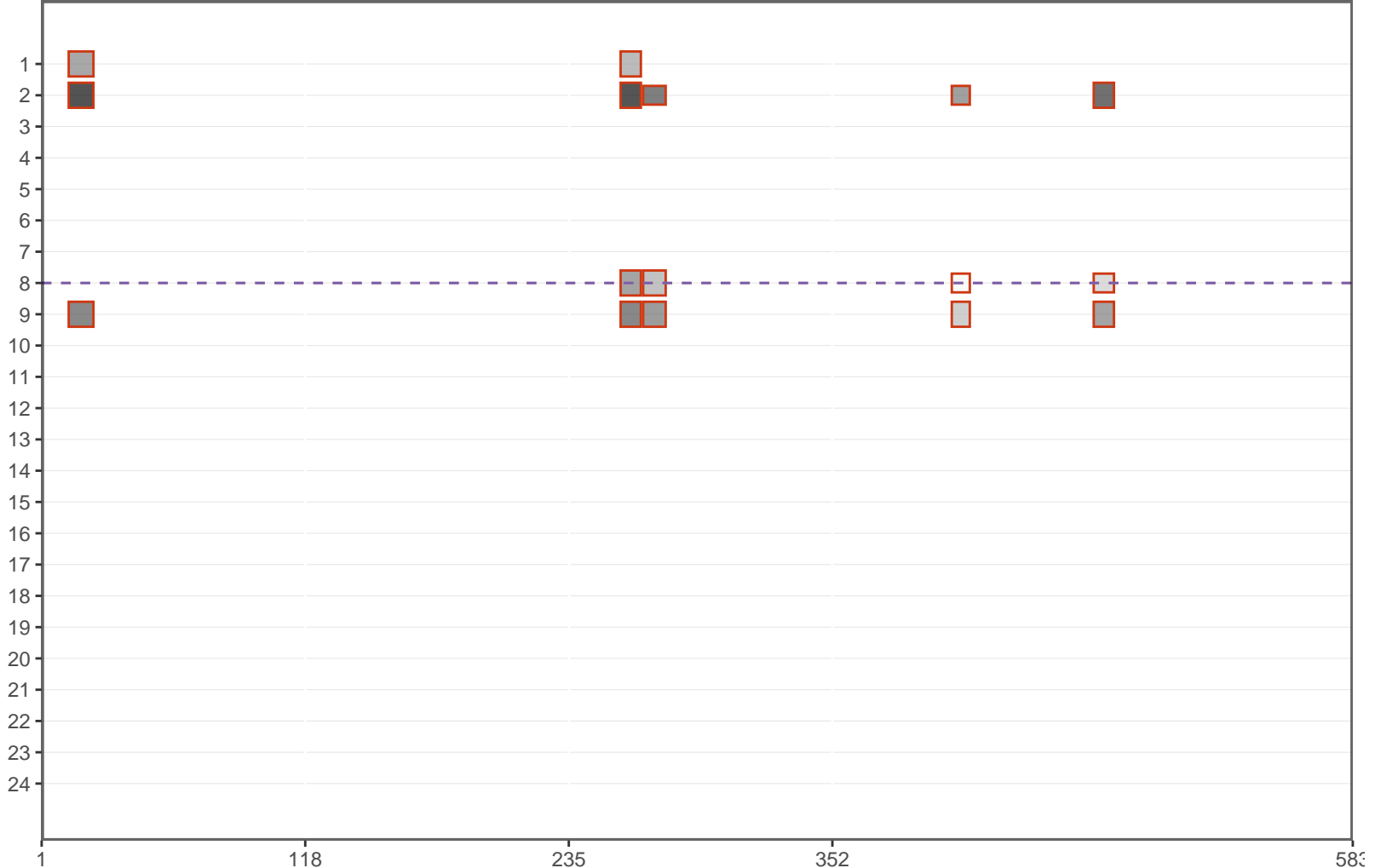
MW indication



Molecular weight



Gel Slice

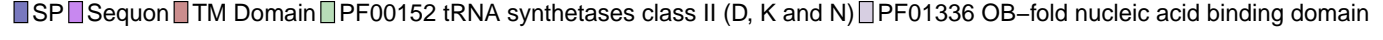


Protein length



Pfam domains

Pfam Description



Protein sequence:

KENLKLQERFKLGERGRLSAGIPKDKGVYSEDFFARGAFLTVSGQLQVETVYAGALSSVYTFGPTFRAEQGHSTRHLAEFCMVVEPEIAFDLQDDMMKCAEAVYKFLQGLLDHGLDQDMERITKFDKIDKLNLRIMVASSNCRYRITYTEAIALEVAVKWKFENKVEVGGIDLASEHERVYTEEHKAPVVFVSYKGIKAFYMKVNEDKKTVAAAMDLLVPRVGEIKGGSGREEDVEVLRTRILEMGLPLEPVEVWLDLRRYGVYKHSGFGLGFERMILFATGIENRDVYPPFR

NbL19g14080.1 bifunctional_protein_Fold_2-like [MW = 32.94 kDa]

No. of times detected



log(intensity)



Values from



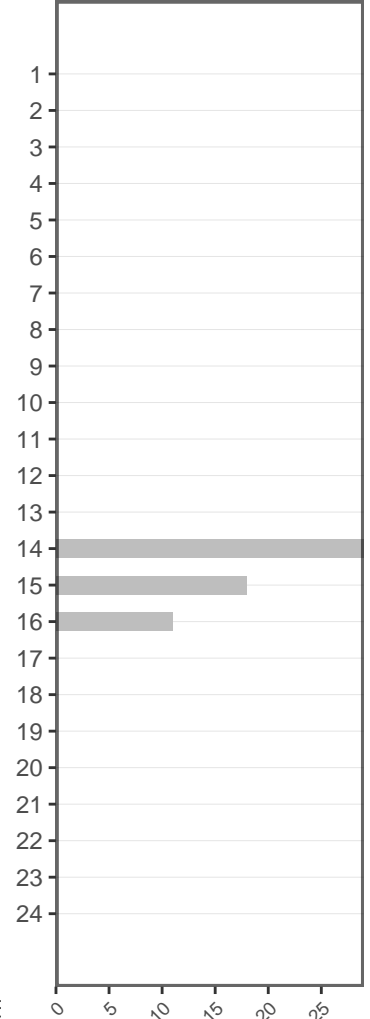
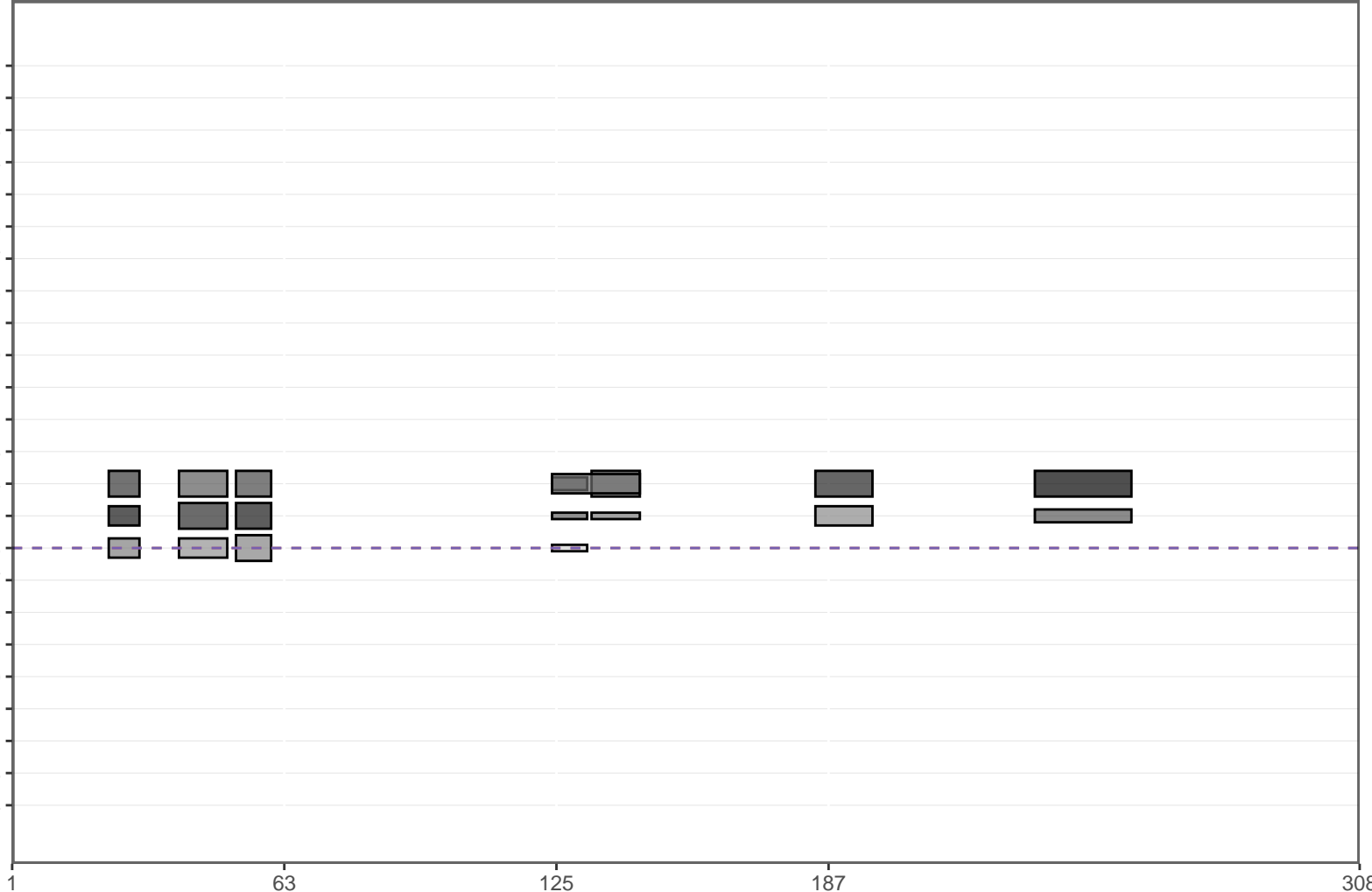
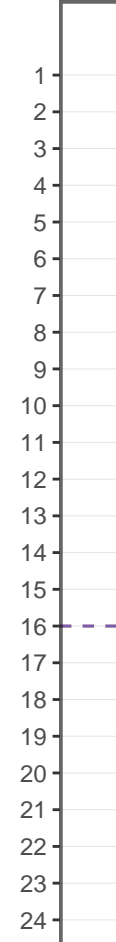
MW indication



Molecular weight

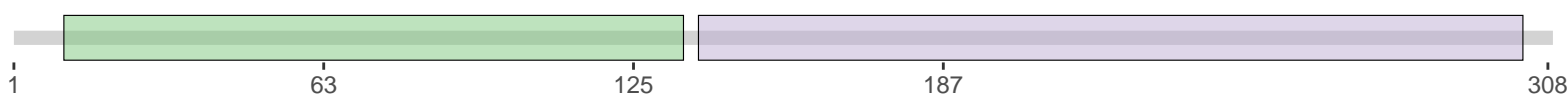


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

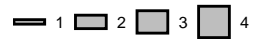
- SP
- Sequon
- TM Domain
- PF00763 Tetrahydrofolate dehydrogenase/cyclohydrolase, catalytic domain
- PF02882 Tetrahydrofolate dehydrogenase/cyclohydrolase, NAD(P)-binding domain

Protein sequence:

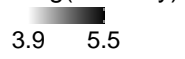
IQGLAMKGRPLFLPCTPKGGIILLHRSGIIGKKNAAVYGRSNVGLFVSLLLKEDATVTVHSHRTKEPEKIVREADIHAAGDAMMKGSWIKPAAVIVGTVNAVDDPTRKSGYRLVGDVDFQGEACEVAGGTFVPGGQVGMFVAMLLKNTLDGAKRVEK

NbL19g14030.1 nascent_polypeptide-associated_complex_subunit_alpha-like_protein [MW = 22.1 kDa]

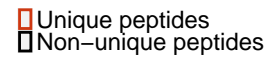
No. of times detected



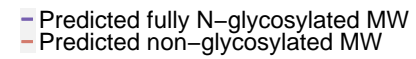
log(intensity)



Values from



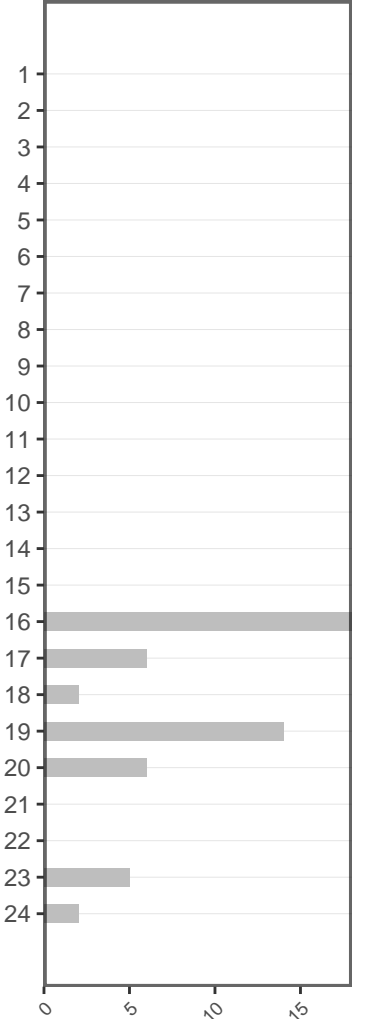
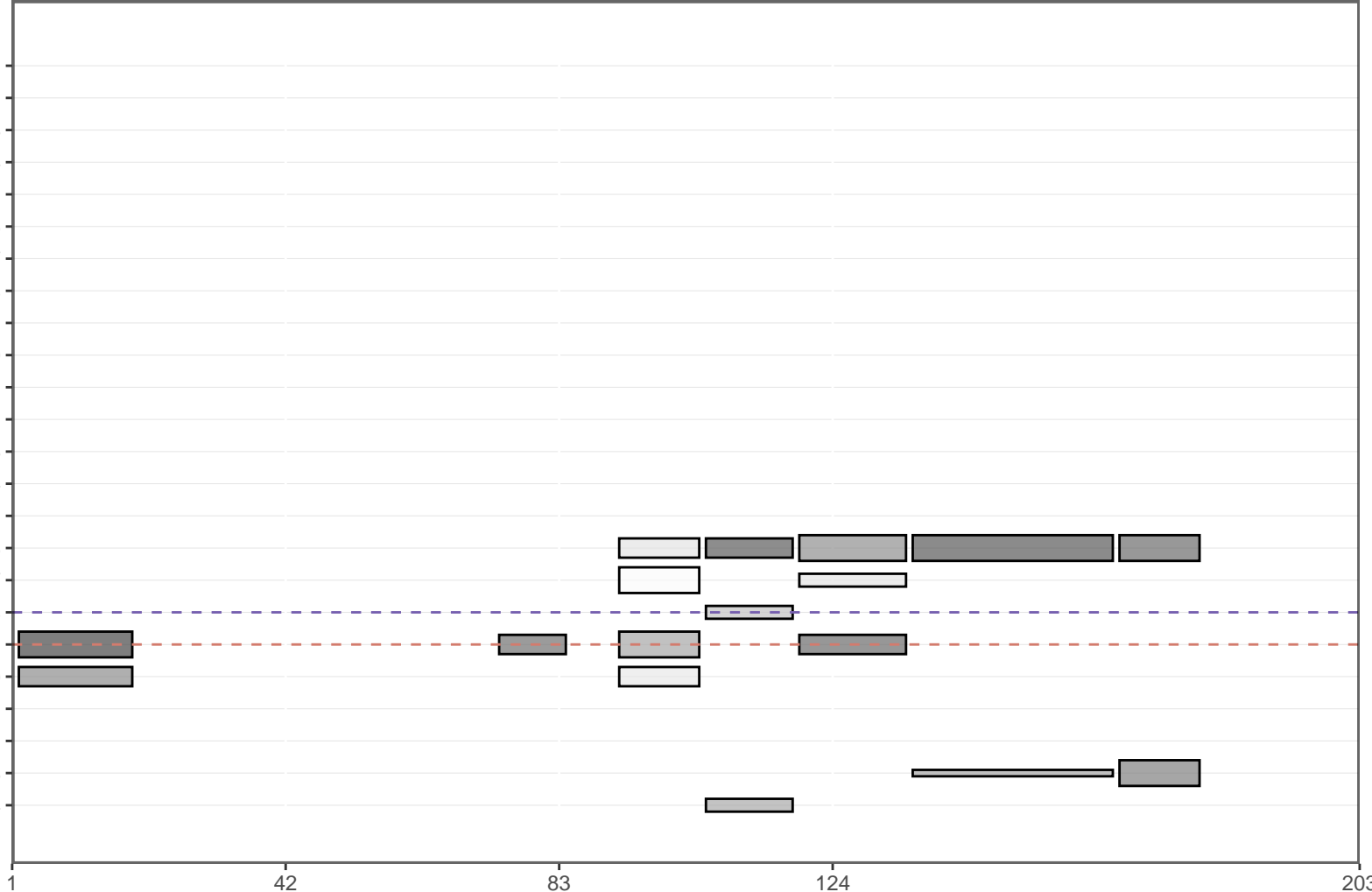
MW indication



Molecular weight



Gel Slice

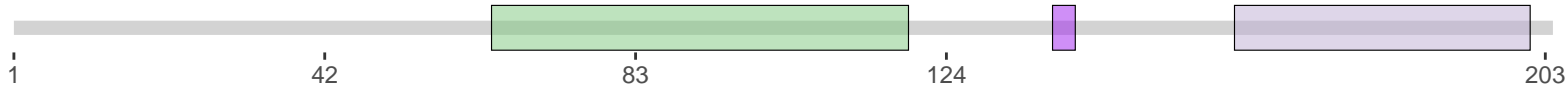


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

VKKSQNLPIYSKPPVFKSPNEDTFVFDGEAKIEDLSSQLGTGAAGFKAPNLSENVISKPEPEPTVAGDDEEDVDETGVEPKDIELMTGAGVSRVAVKALKAAAGDDIVSAMELTN

NbL19g13790.1 thioredoxin_reductase_NTRC-like [MW = 59.44 kDa]

No. of times detected



log(intensity)



Values from



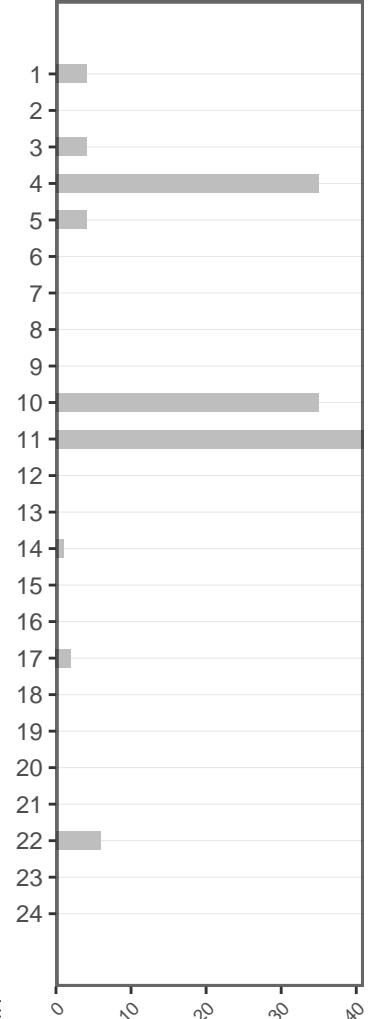
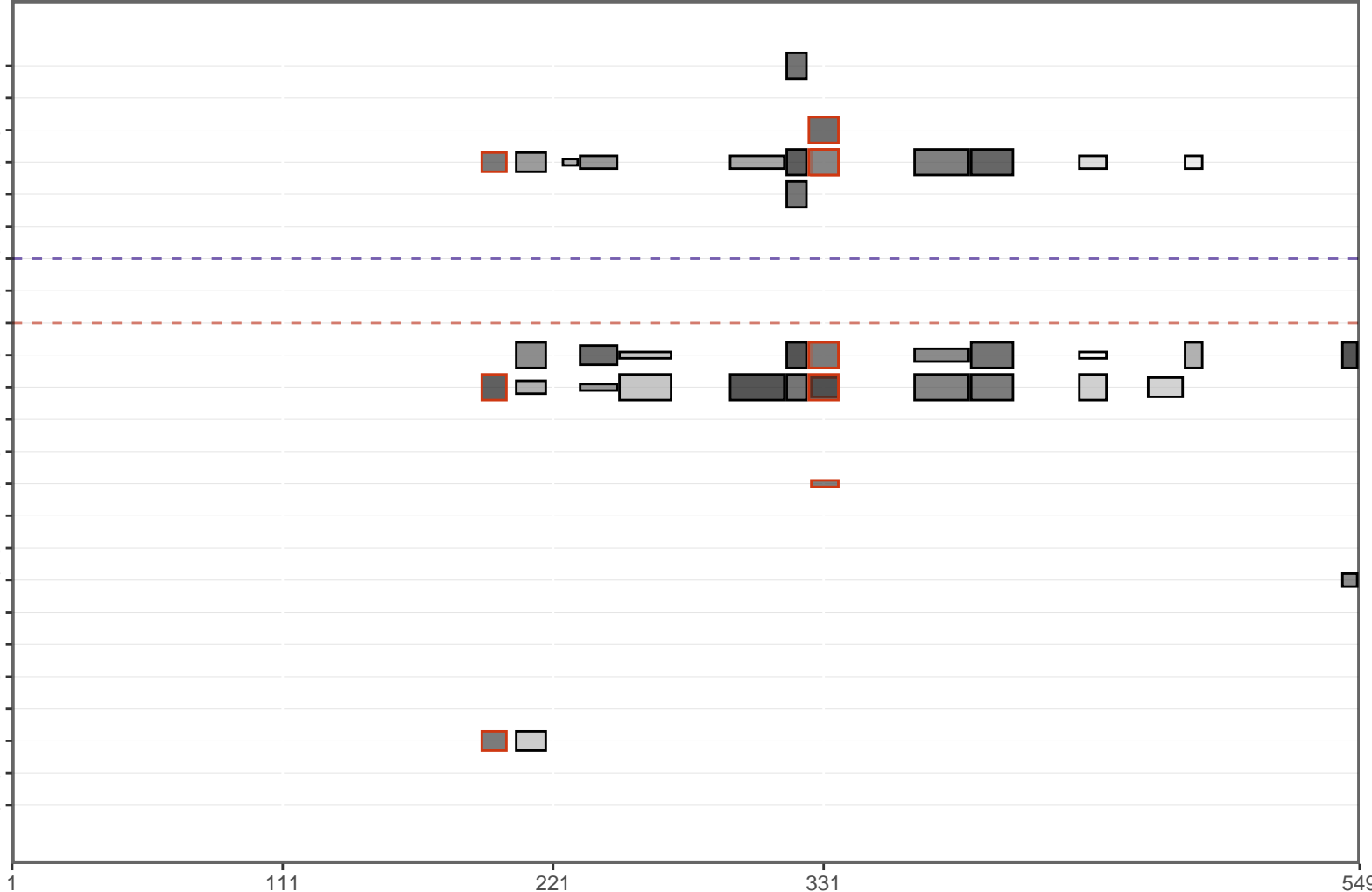
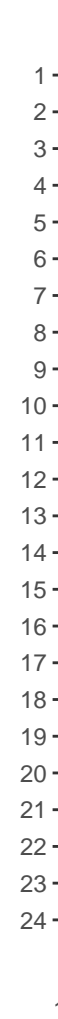
MW indication



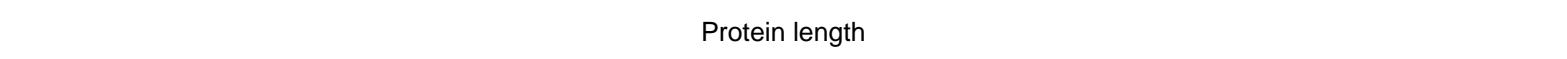
Molecular weight



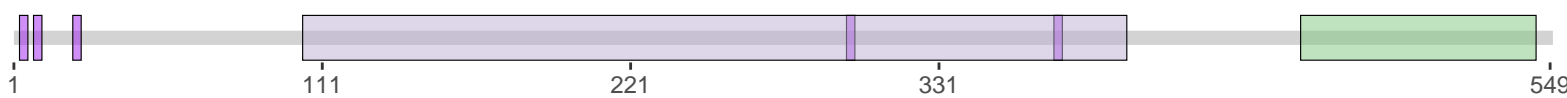
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TEEAITLYARHYHLLVRRKDKLRASAMGDRVFNPNFTVHFNFTETVDVYVSNPKGMSGLRKAADTQEEVLEAKGLFYGIGHSPNQLLEGQVLEDSAGVILVKEGTANTVVEGVFAAGDGHVQDHEWRQAITAAGSGGVVALSVERYLFGKNLIEFHQPHTEEVKELTKQKDVQEGFDITLTKHKGQVALRKLQVHESPRICVLYTSPFGQRTLRKLPILSKVIDEFDQGHVHFVEIDTDEPEIAEAGIMGTPOVQFFRNKEMLRVTSQVWMMKREYRELEAK*

NbL19g13710.1 probable_calcium-binding_protein_CML49 [MW = 35.43 kDa]

No. of times detected



log(intensity)



Values from



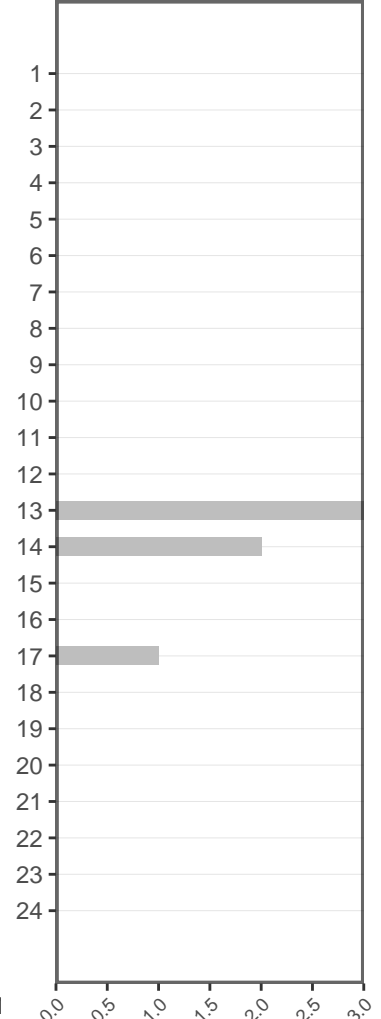
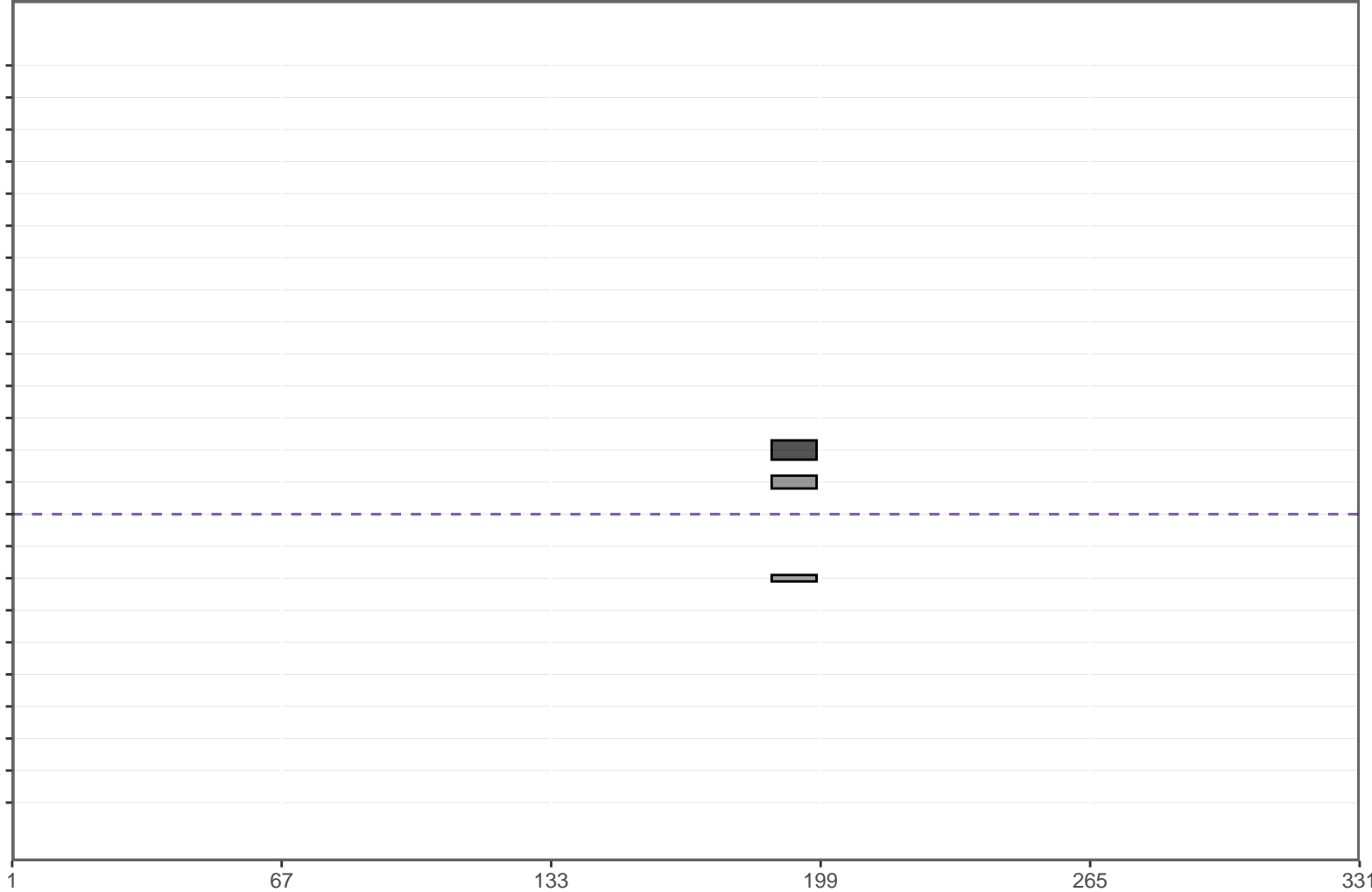
MW indication



Molecular weight



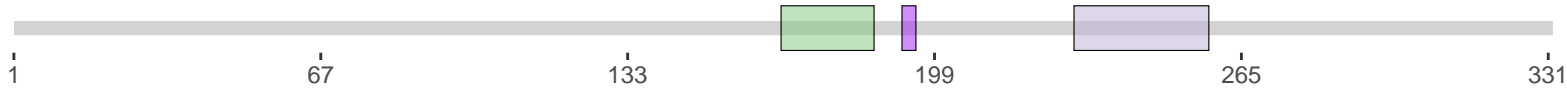
Gel Slice



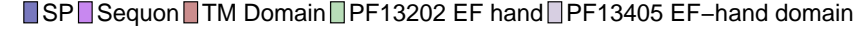
Protein length



Pfam domains



Pfam Description



Protein sequence:

FASLVPSAIFPPGTDPNVAGFQLADGGSGLIIDDKELGKALGSYNGDFSLRTHLLMFLFTNTRKIGKFEFTSVFYSLGEWRGIFERFDRDRSGRIDSGSELRDALLSLGVAWSPILDLLVSKFDKTOGKNAKAEYDFIECDLTVKGLTDKPKKEDASYSGSATFSYEGFMLTVLFLW*

NbL19g13540.1 extensin-like [MW = 29.83 kDa]

No. of times detected



log(intensity)



Values from



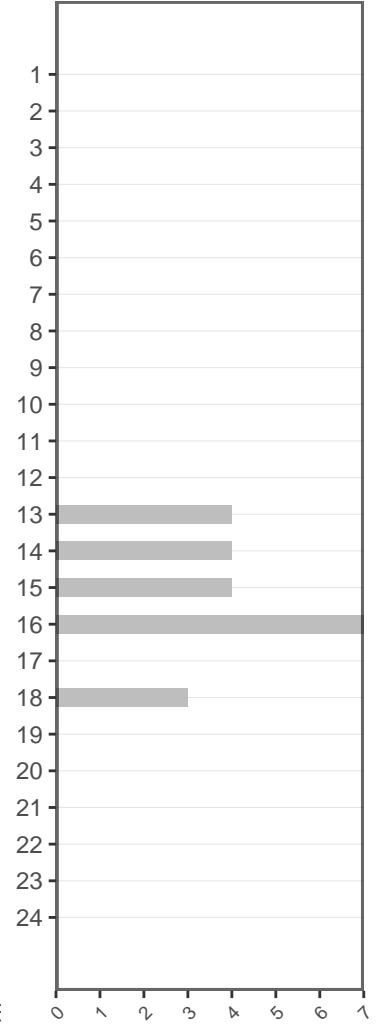
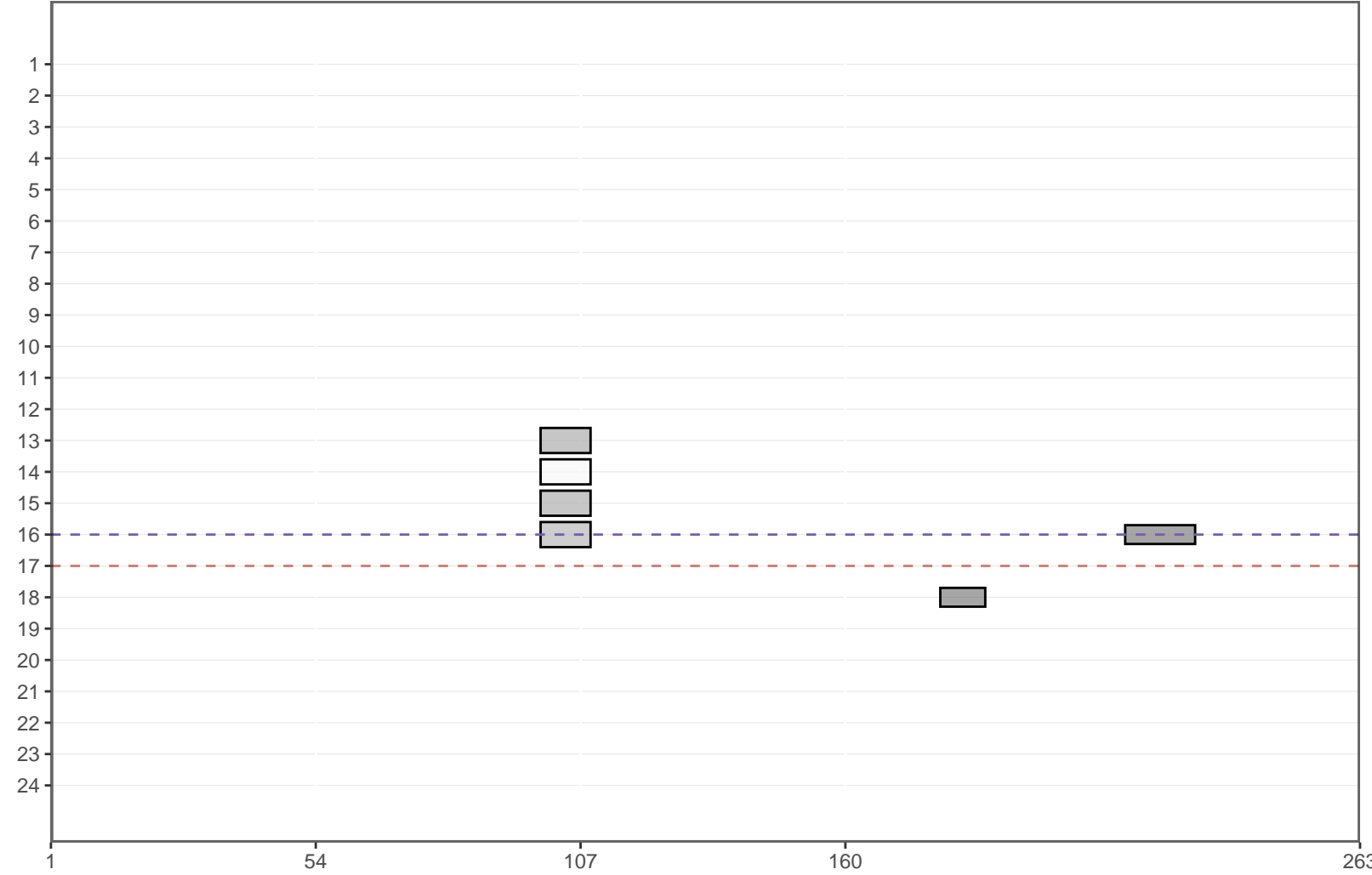
MW indication



Molecular weight

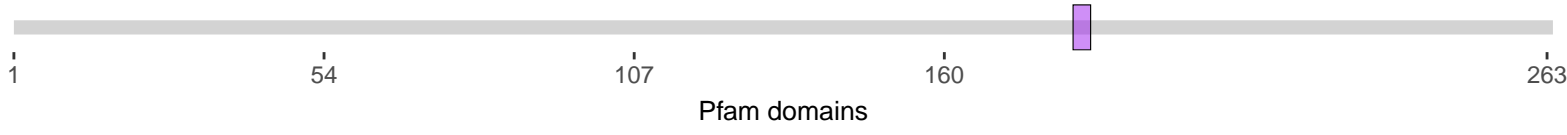


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

PPPPPPSYSSVEHSHHESESEGAHRHDKHHRFGPHVPSFRRHETSHPFELIOLKPFRRVYTKADPNVGLTRDGKVVLLASDDPDRPFQHWYKAERYSTKVADEEGFPFALVNAAGLAMKHVGAASHLCSPLTLMLMRGEGC

NbL19g13520.1 SNW/SKI-interacting_protein-like [MW = 67.2 kDa]

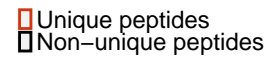
No. of times detected



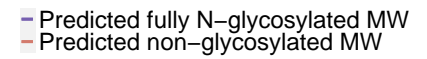
log(intensity)



Values from



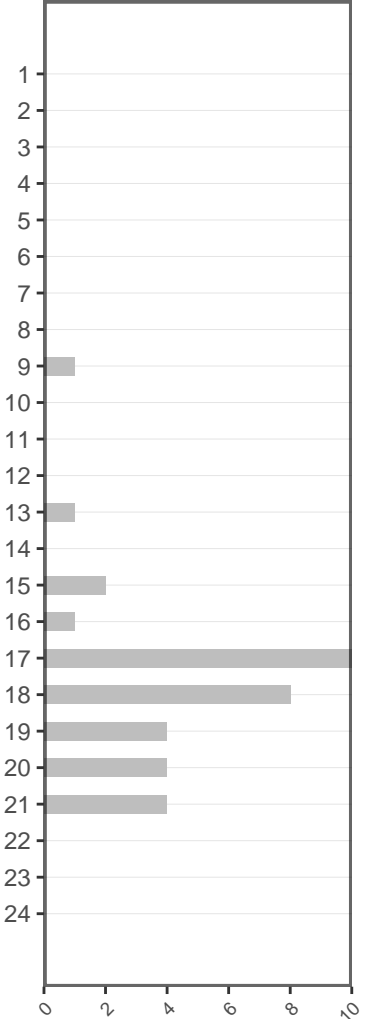
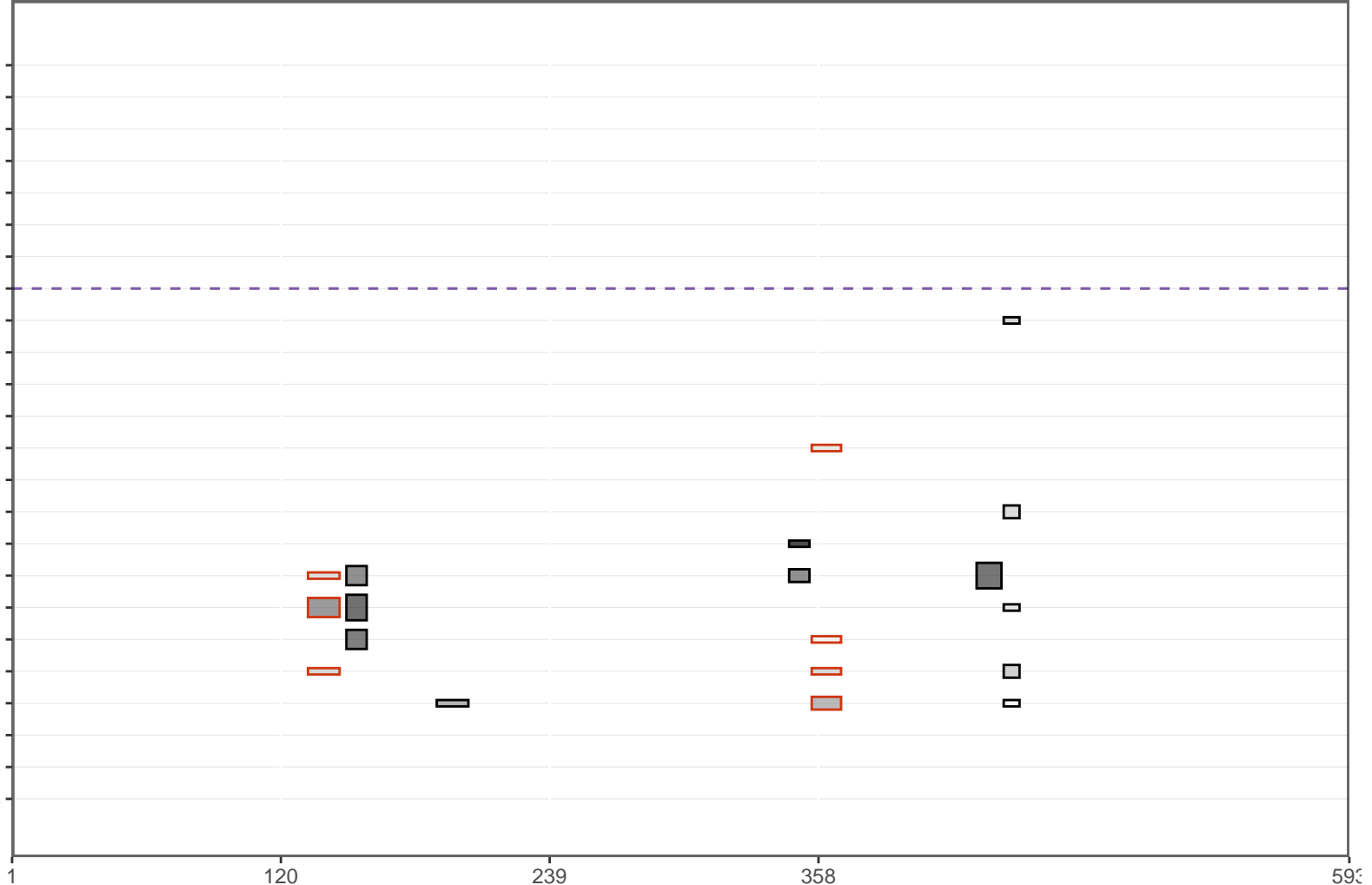
MW indication



Molecular weight

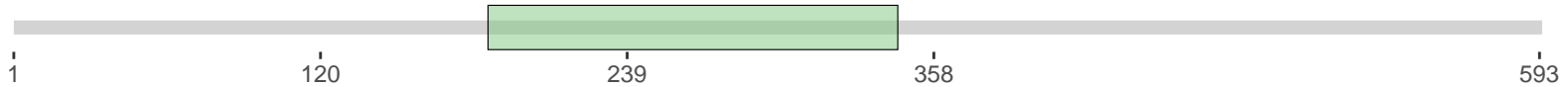


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IVQNDNFALKLEALYAEQKAREAVAMRSKVGKEMMMKEKEKEMELRELARKARSERTGVAPRAERGTVNDQDMSDVDERARDPFKESREDREERLRREKREERERRERERLEAKSDSAMGKSKNTRDRDRDSEKVALGMASTGTSRQEVHYDQRLFNDEKGMDSGDFATDDANNVYDKGLFTAGPTLSTLYRPPKDDADSEMYYGGADEQLEKMKTERFPPDKAFAGTSERAAARDGPPVDFEKEVEEADPPGLDQFLTEVKKGNKAMASYGSGGTMKASA

NbL19g13500.1 cystathionine_beta-lyase_chloroplastic [MW = 51.35 kDa]

No. of times detected



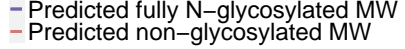
log(intensity)



Values from



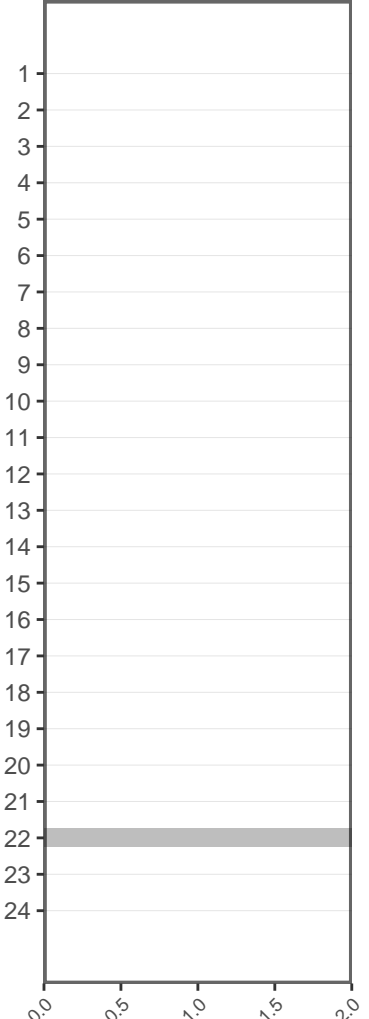
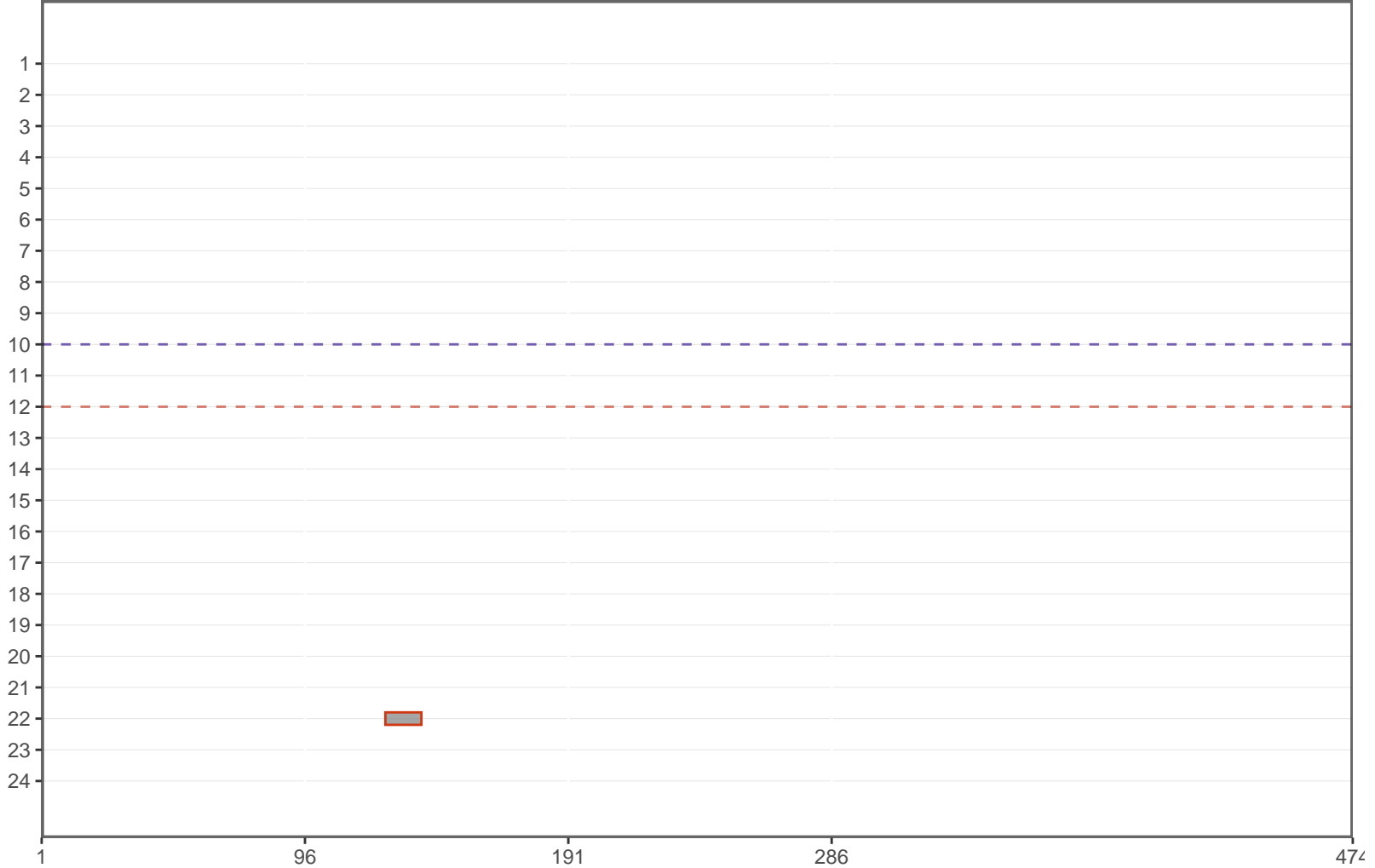
MW indication



Molecular weight

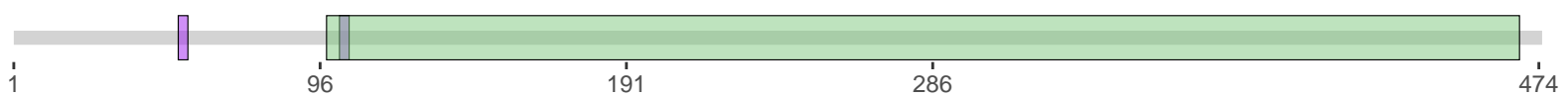


Gel Slice



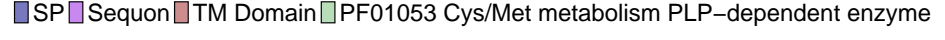
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IAINPOTKLVYLESPFNPRGGKIDIRKAKIAHAGALVLDNBNMSPVFSHPLELGDIVMHSATKFIKSHSDLMAGVLAWRGESLAKEVFLQNSEGAGLAPFDGVLGLRGKTMALRVEKQDGNAGKAEFLSHPRVKKVVAAGLDPHPGRSLHFQGAARGAGVLSFLTGSALSRKVAEATKYFSITVSEFGVKGSLSPCFMSHASIPVEVREARGLTEDLVRIEIVGIEDNDLIDLDVALRTGVA

NbL19g13430.1 protein_STRICTOSIDINE_SYNTHASE-LIKE_10-like [MW = 40.88 kDa]

No. of times detected



log(intensity)



Values from



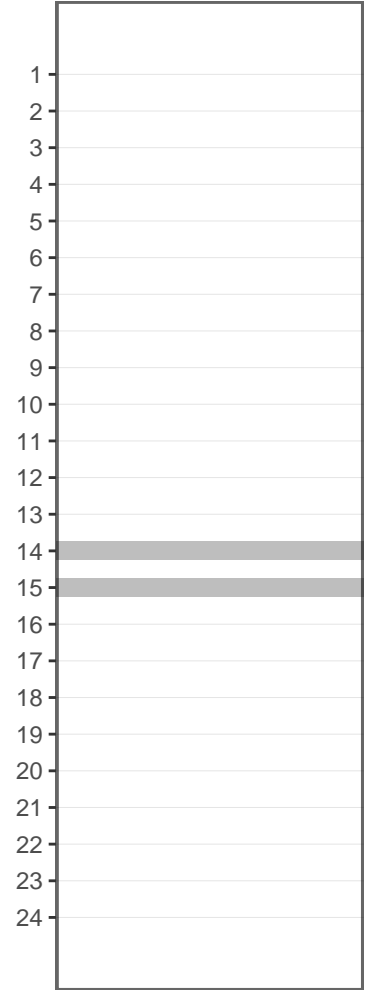
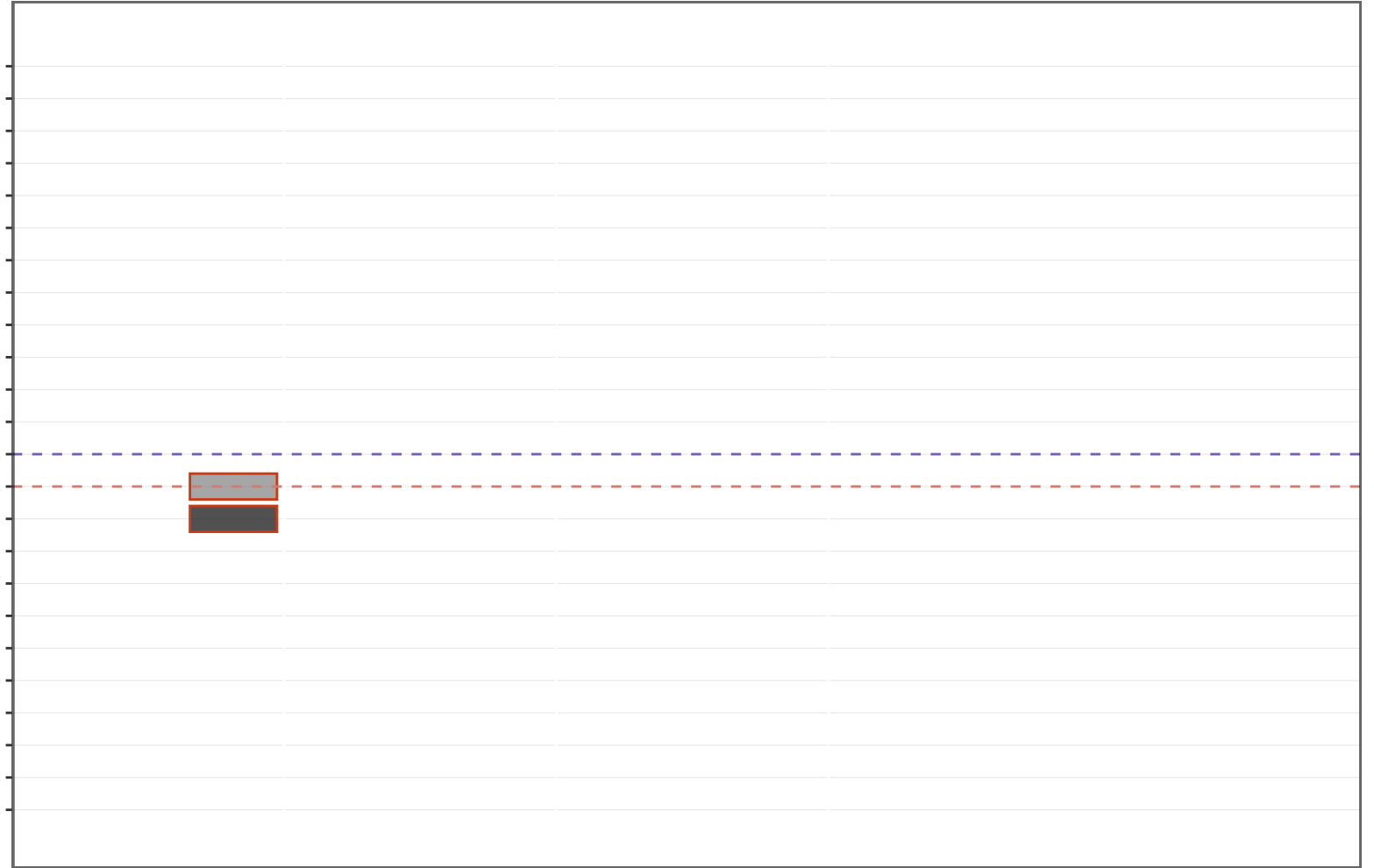
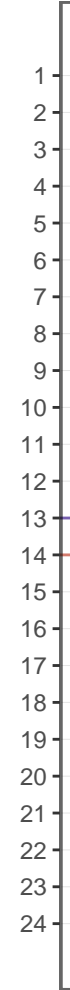
MW indication



Molecular weight



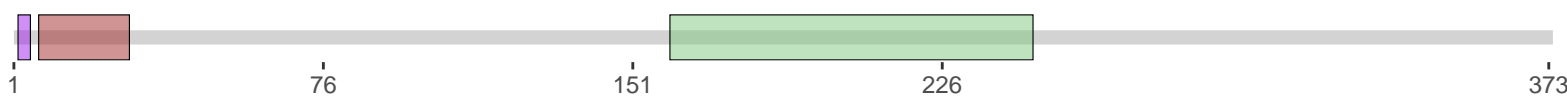
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

DTSTGFRRRQFASVAVIGDRTRGLMKYDKSTKAVTVLLRGLAFANGVLSKDKKFLVIAETSTGRVWYWLKGPDAIGQATFADLPCYDPNIRNRSRGEFVWALHKKRLLARLVTSNGLWGRLLKLPFTFGQHLVLLVGGPPHATAIKLSEGGVLEVEDVSKTKLFLSEVEEKKKGLWGSVLPVFPVGVYELG

NbL19g13410.1 methylthioribose-1-phosphate_isomerase [MW = 39.6 kDa]

No. of times detected



log(intensity)



Values from



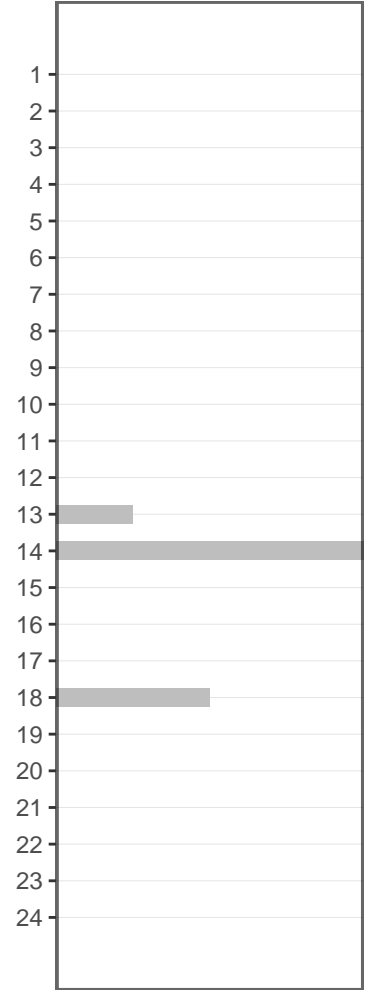
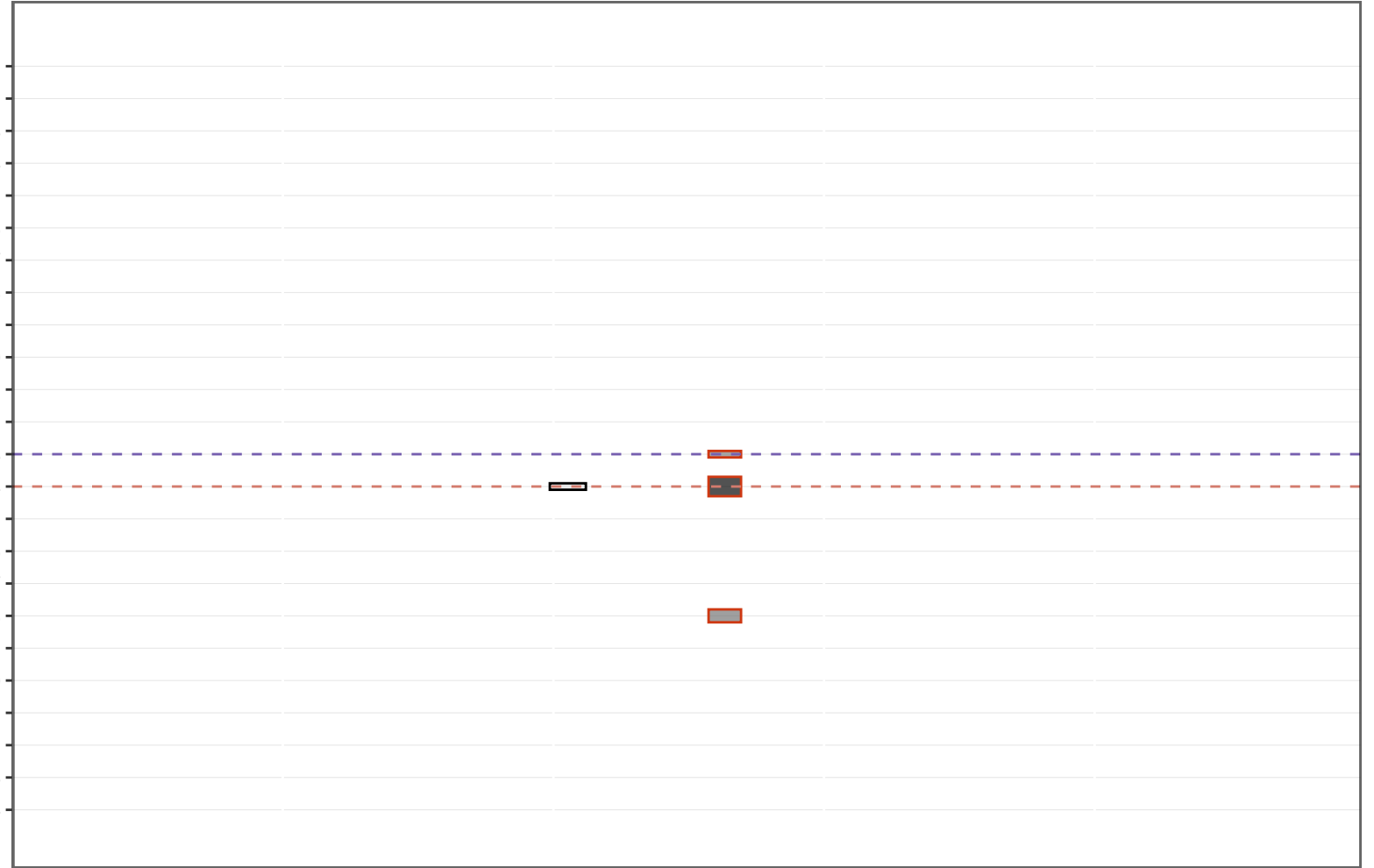
MW indication



Molecular weight

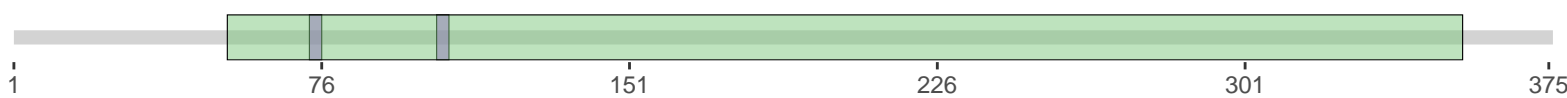


Gel Slice



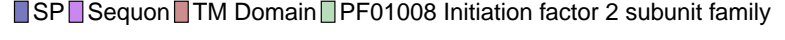
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

HCNTGSLATAGYGTALGVIRALYTDGVLERAYGTETRFNNGGRRLTAFELVHENIPATLADSAALAMNAGRKVAIVGADRVAAGDGTANKIGTNYLAVSAMHGGIPFYVAAPLFTDLSLSSGGEEVIEERSPKELHTRGGLGEGVAASGIVWNPVDFVTPMNLISGITEKGVTRKIGDTDFDIAEFVTKTSGNL

NbL19g13350.1 NAD-dependent_malic_enzyme_62_kDa_isoform_mitochondrial [MW = 70.05 kDa]

No. of times detected



log(intensity)



Values from



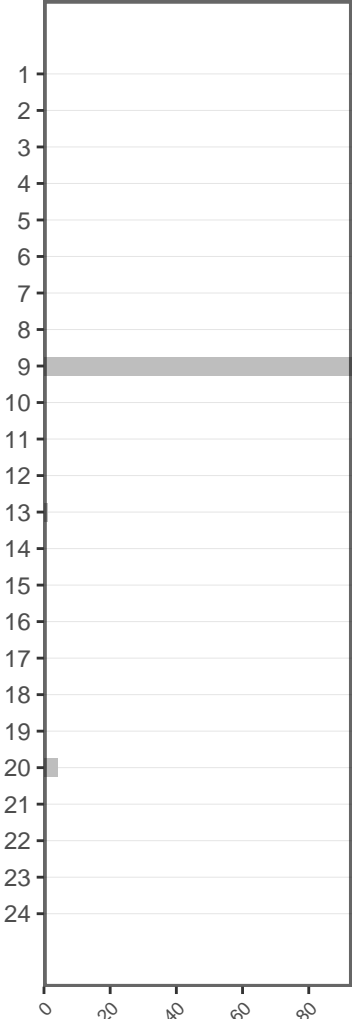
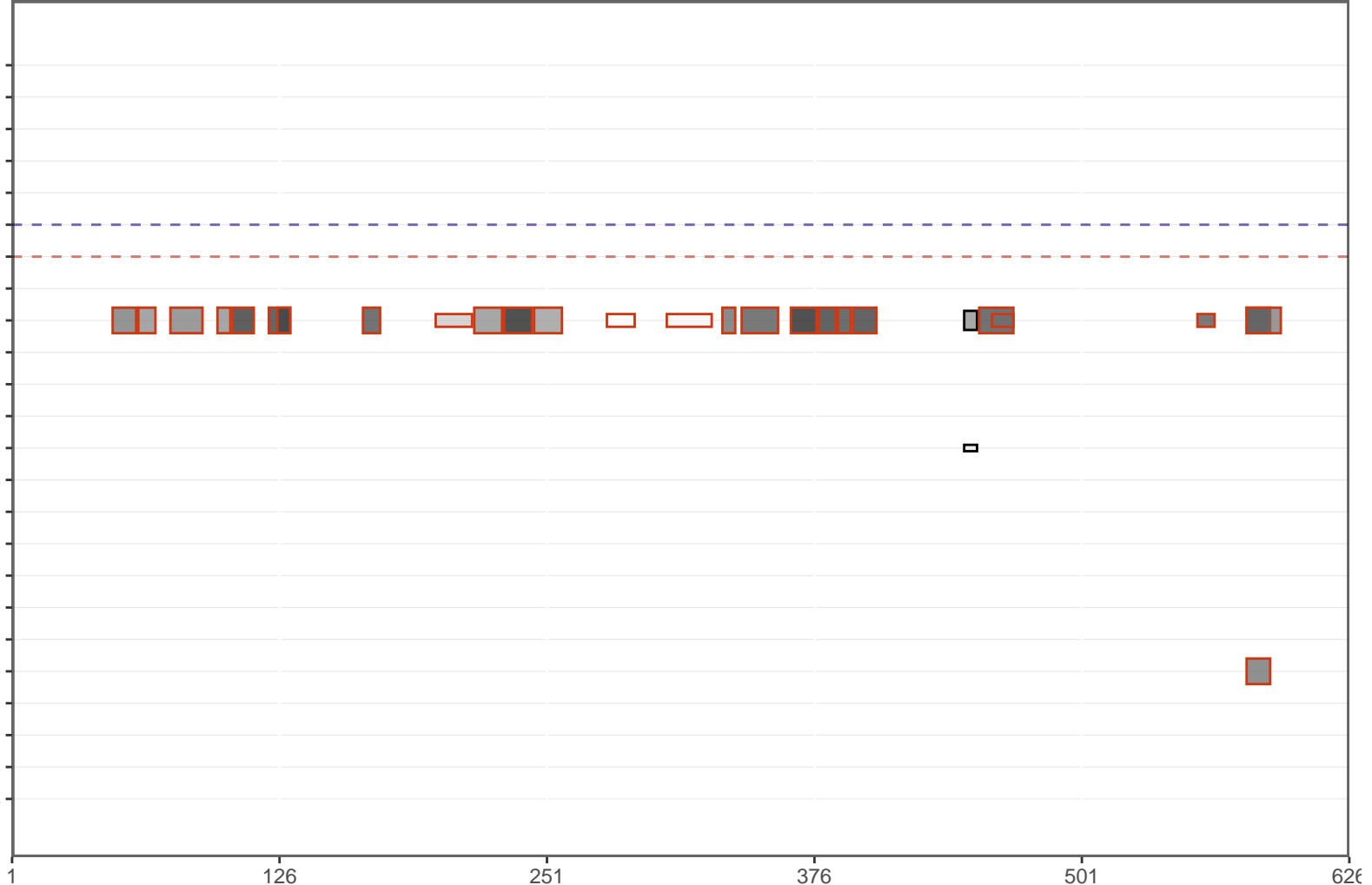
MW indication



Molecular weight

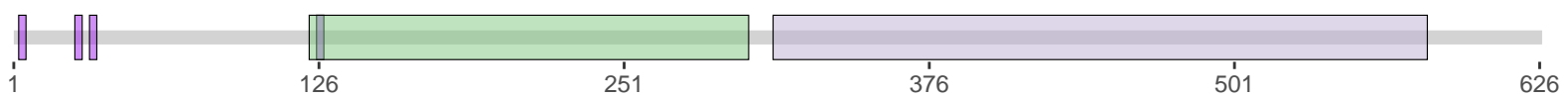


Gel Slice



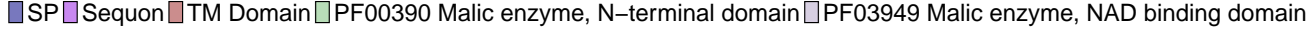
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

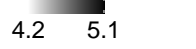
SRYRNNYRMFNDDVGGTAGVALAGLLGAVRAAGRPMDFFPKMKIVVAGAGSAGIGVLNAAKRTMARMLGNTIEAFESARSGFVVVQAKGLFEARENIQDPAKPFARKIKETERQRLREGATLAEVHHQVQKFDVLLGLSVAVGGVGLFSEKVELEAKHSTSTRPAIFPMENPTRNAEGTPEEAFSVGDNIFASGGFPKDVLDLGNHGHVGHGNGANNMFLFPGIGLGTLLGGSRVSDGMALGAAAEGLAAYMSEEDVAKGVVPSISIRIRDTKEVAAVWKEAEEDLAEQYREMDL

NbL19g13340.1 haloacid_dehalogenase-like_hydrolase_domain-containing_protein_Sgpp [MW = 31.65 kDa]

No. of times detected



log(intensity)



Values from



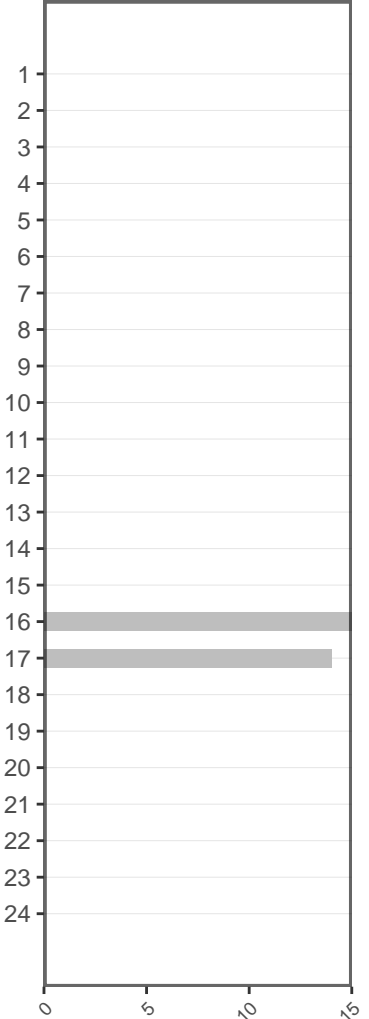
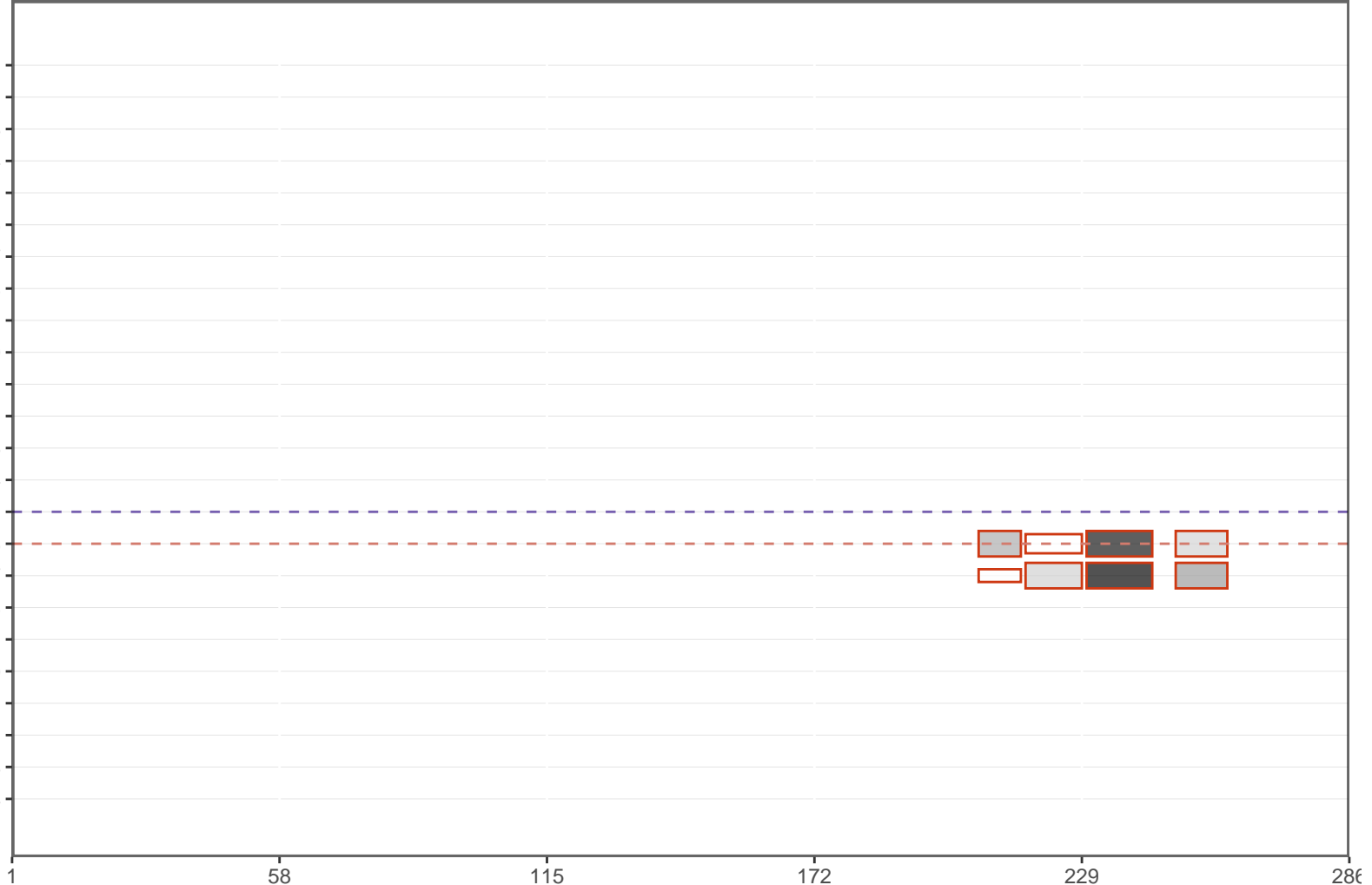
MW indication



Molecular weight

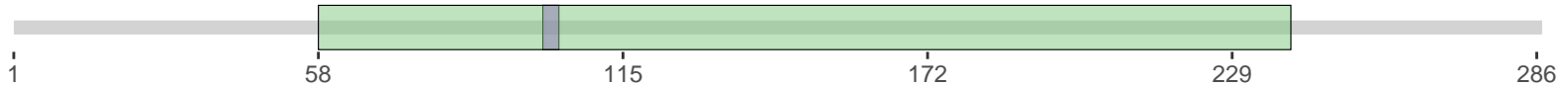


Gel Slice



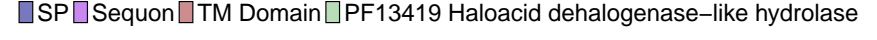
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

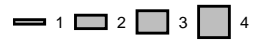


Protein sequence:

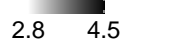
IDMFRKIASEQLKPLNGLEEVKQWIEDHGLKRAAVTNAPRANAEIISMGLADFFELLVIGSEGERAKPFDPVLYKALHELGVSRKHAIVFEDDSIGSIGAGVAAGMPVYVGLGLRINPEKLLSEAGATFYIKDFDKDKLWTALEELEETEVDSEKUKT

NbL19g13270.1 eukaryotic_translation_initiation_factor_2A [MW = 57.89 kDa]

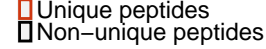
No. of times detected



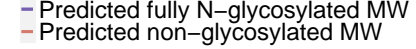
log(intensity)



Values from



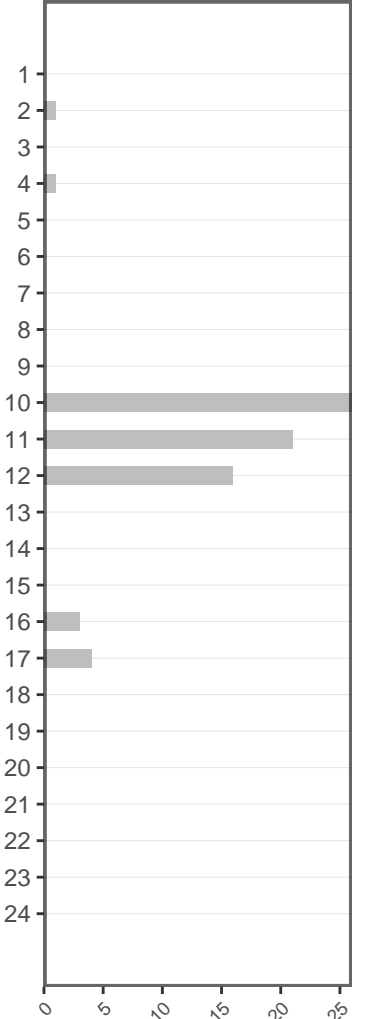
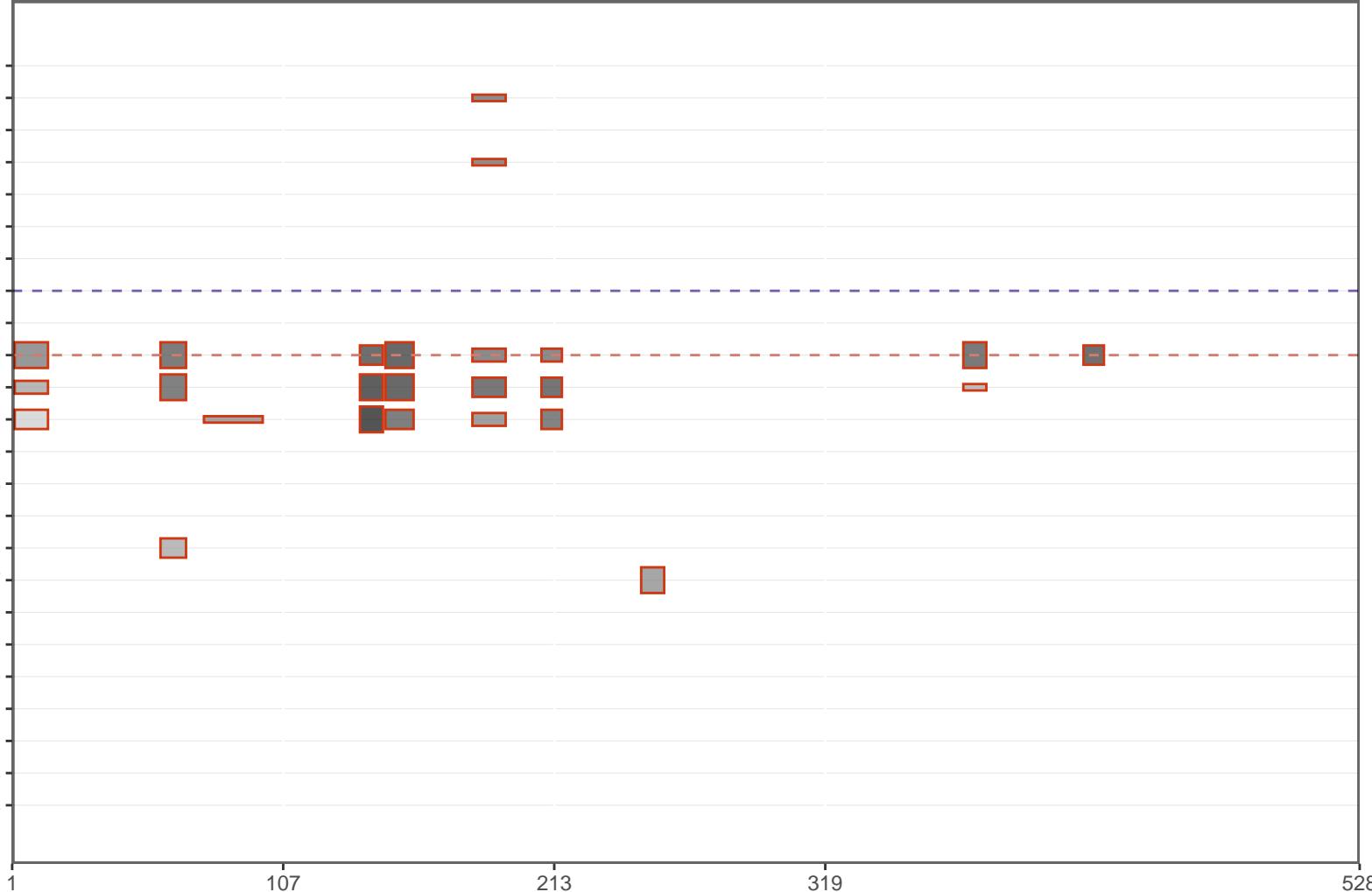
MW indication



Molecular weight

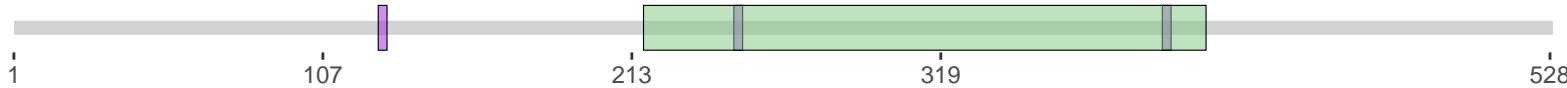


Gel Slice



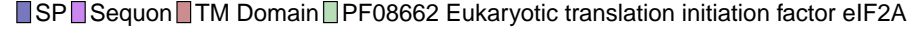
Protein length

Peptide counts over 4 repeats



Pfam domains

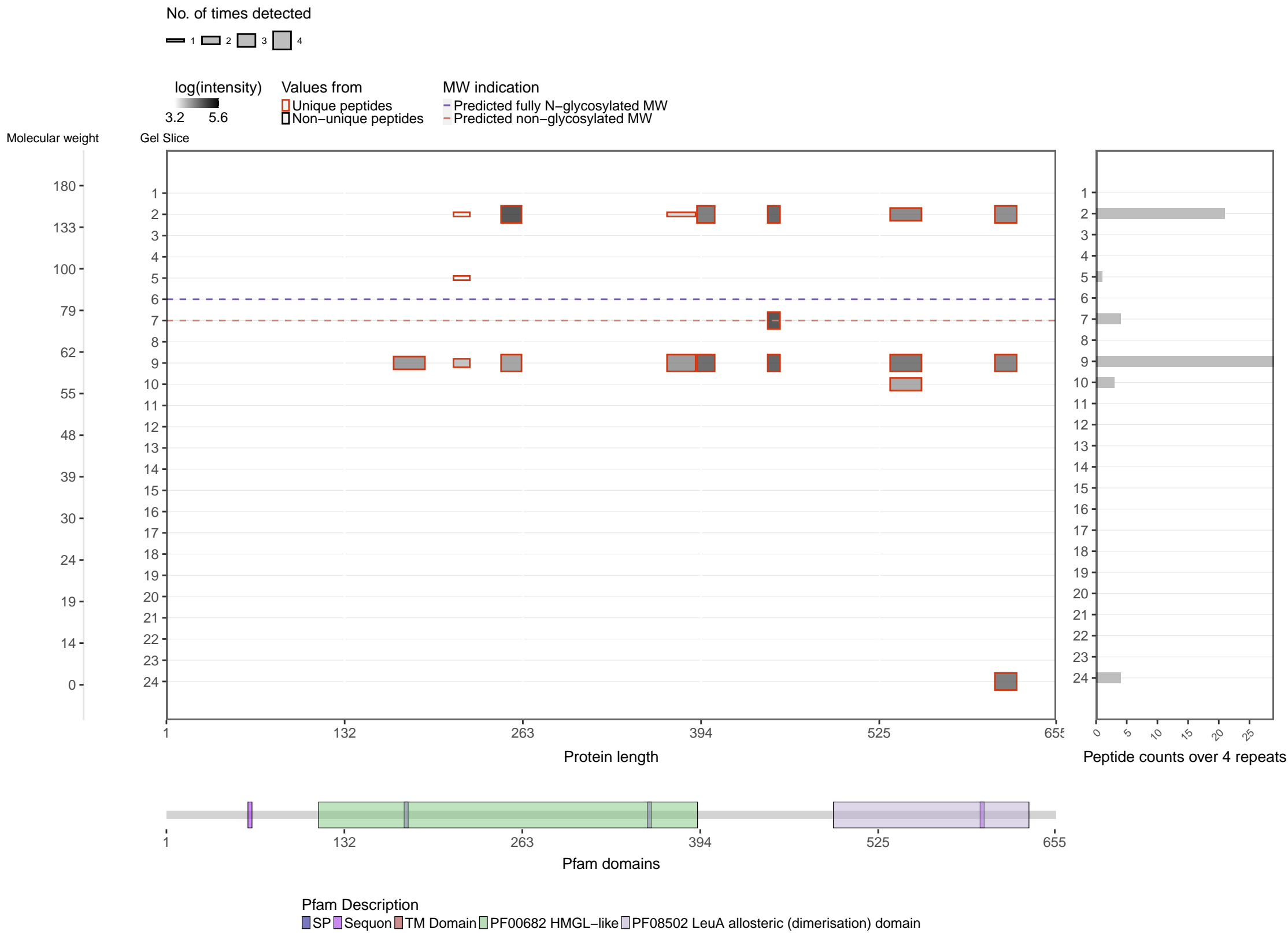
Pfam Description



Protein sequence:

IESKLNLYLTDGTHIEGLVPLRKDGPIDHWGWSYSGKEFAWVYGFPMAMATVFDKIKGNPLLELGTGSPNTRINWPLNGFNLAGFGLNLPDGMAFWDYKIKKGLGTTRAELSVTSEWSPDGRVFMATATAPRLGVNDGKIFHNGSLYFKKMDRLVGVDWKPKPEVKEKFGIEDLVKAVGSKVMDEAKAFQKGGKATGAVPKATQAIKPKATPAPPAKPAVYRPPHAKWAAVDEELFGGSSGELSKNALNKKKREKQREKQTEGASGTGGP-

NbL19g13190.1 2-isopropylmalate_synthase_A-like [MW = 71.24 kDa]



Protein sequence:

CDNDLGLSTANTLADAGAGARGQNEVTINGIGERAGNAGNAGLEEVVMAIKKRGEOVLGGLYTGINTGHHVPTSKMVEKVEEYSGLVQPHKAIVGANAFHESGSHGDGMLKHKDFTYEIISPEIDGLNRANEAGIVLGLSGRHALKSKMLELGYDIEGKELEDFWRFKSVAEKKKYVDDQIALMSDEVFQDPQVWGLADVQIGTGGSLGLSTATVLIKIDSGDGHVAGVGTGFPVDAHAKAVDLVKKVPTLLEVSMNAVTEGIDSIATRVRVIREDDHAFNGSLTLHRTFSGTGA

NbL19g13030.1 beta-galactosidase [MW = 127.97 kDa]

No. of times detected



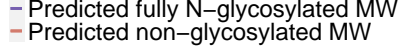
log(intensity)



Values from

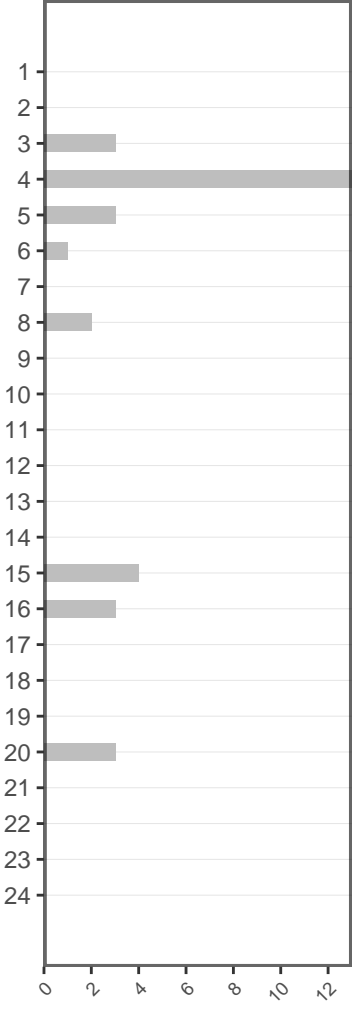
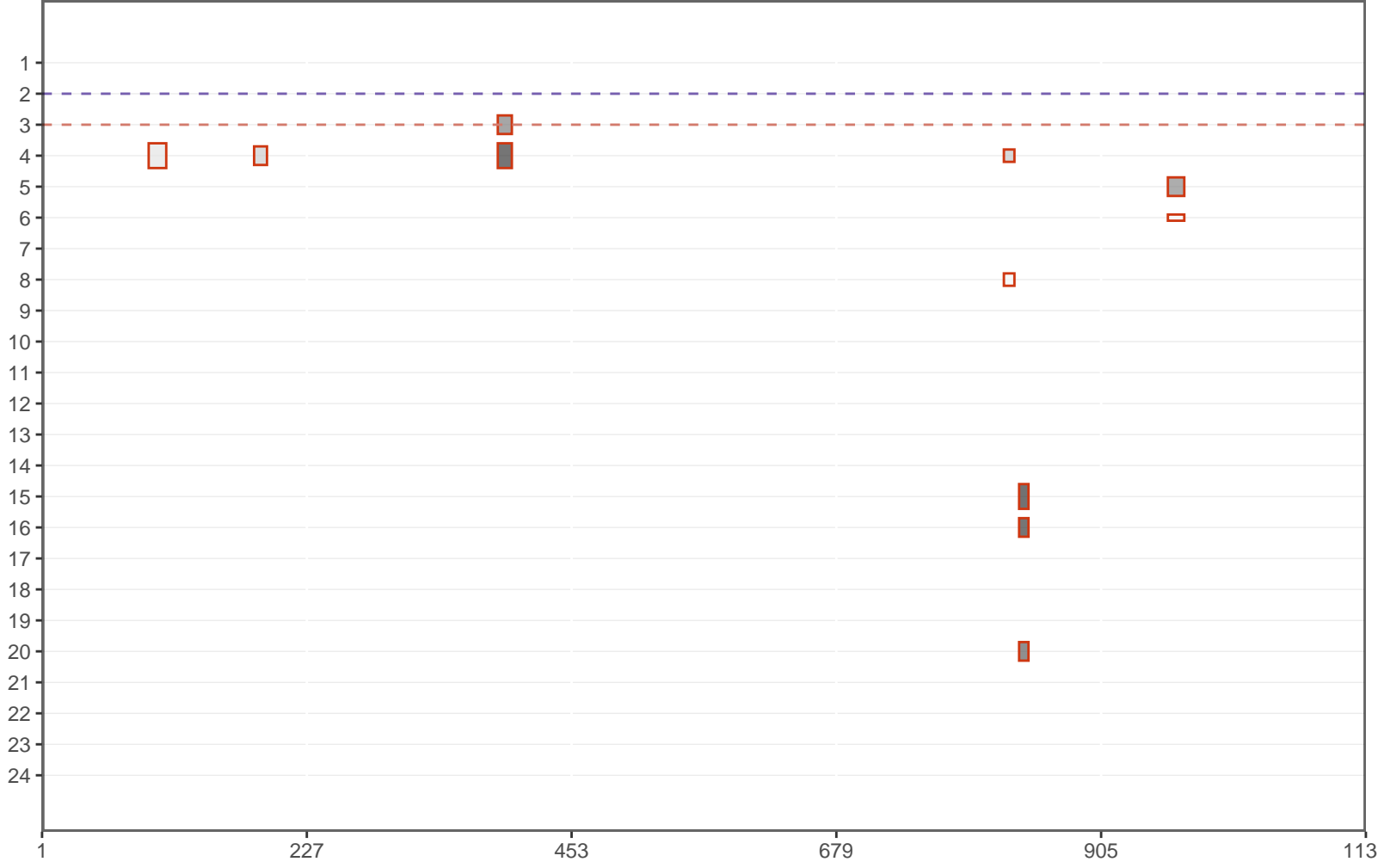
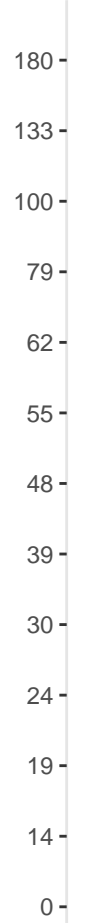


MW indication



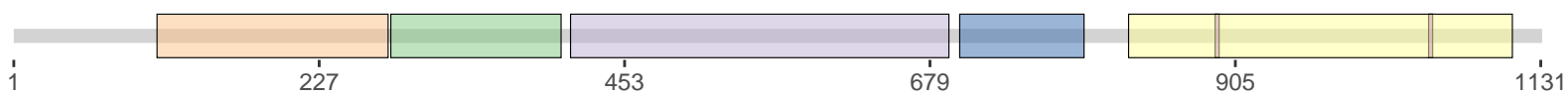
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- Pf00703 Glycosyl hydrolases family 2
- Pf02836 Glycosyl hydrolases family 2, TIM barrel domain
- Pf02837 Glycosyl hydrolases family 2, sugar binding domain
- Pf02929 Beta galactosidase small chain
- Pf16353 Domain of unknown function (DUF4981)

Protein sequence:

/REKDTSLVHYEGGGARTSSTDVCPMVARVSKVIEAKDPTEQRSLHGEYSHAMQNSGNLHKYWEADSTFGLOGGFIWDWADQGLLKEGPRGKMCWVAYGGDFGDPINDLNFQNLGAVWPQRSPFALHEVKEFLVQPKVDFEGVKTMMHFFDTTQALEFNWLLHGDGCELGSGILPLFVIEPGRSHETKWEVGGPWFSAWTSVSAEIGLTKALLHSTRWANNHGLHSTGVLLPNRRRVVPRRIKSTDTLLEGEVLDMMIKVGGNDWELKFNKOTGGIEGWI

NbL19g13020.1 60S_ribosomal_protein_L9-1-like [MW = 22.65 kDa]

No. of times detected



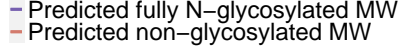
log(intensity)



Values from

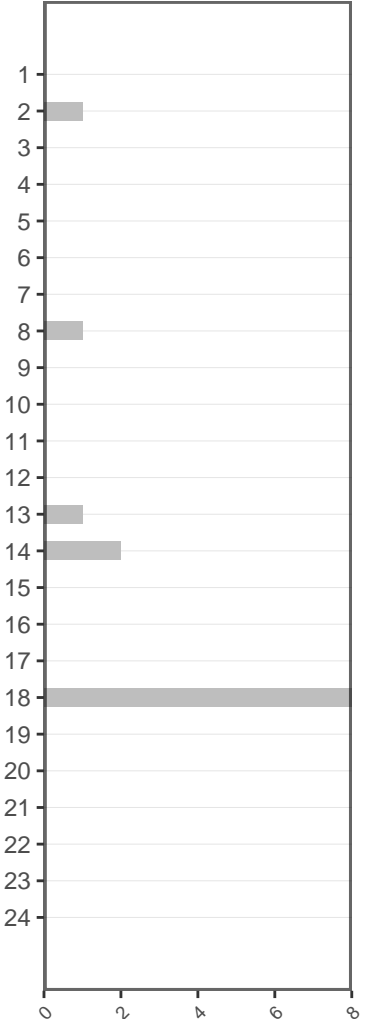
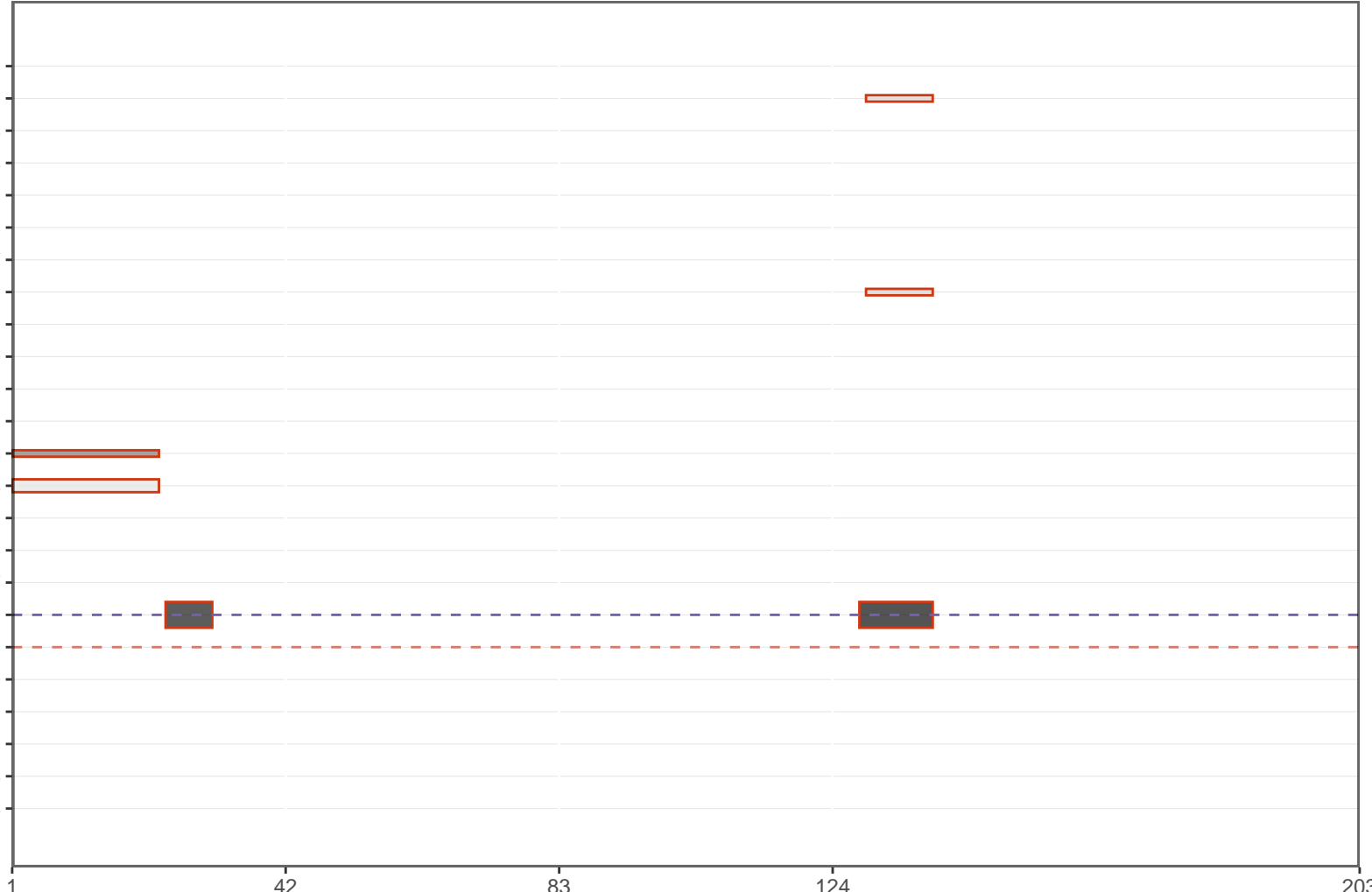
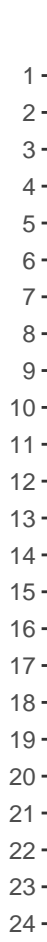
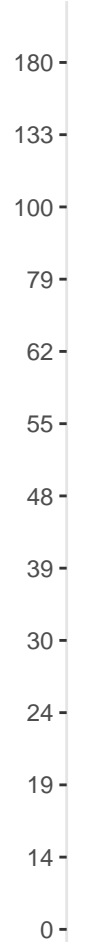


MW indication



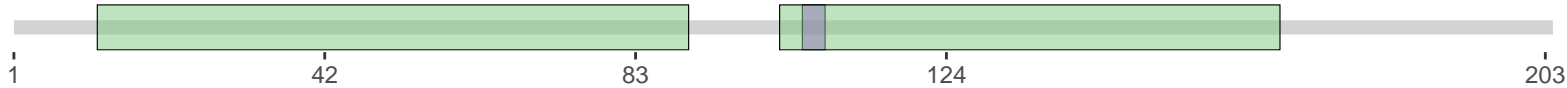
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GGYRYKMFYAHFIPNABITGGNKAIEIRNLFGEKKVKKVDMLEGGVTVRBEKVKDELVDGNDIELVRSALINDVLLFYSSGGGIGALYTFSSBALWISSPFFDRNAM

NbL19g12950.1 hydroxymethylglutaryl-CoA_synthase-like [MW = 51.11 kDa]

No. of times detected



log(intensity)



Values from



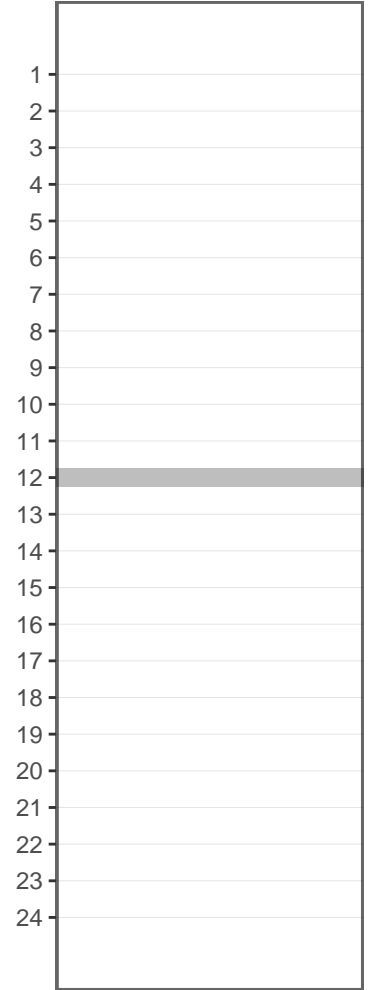
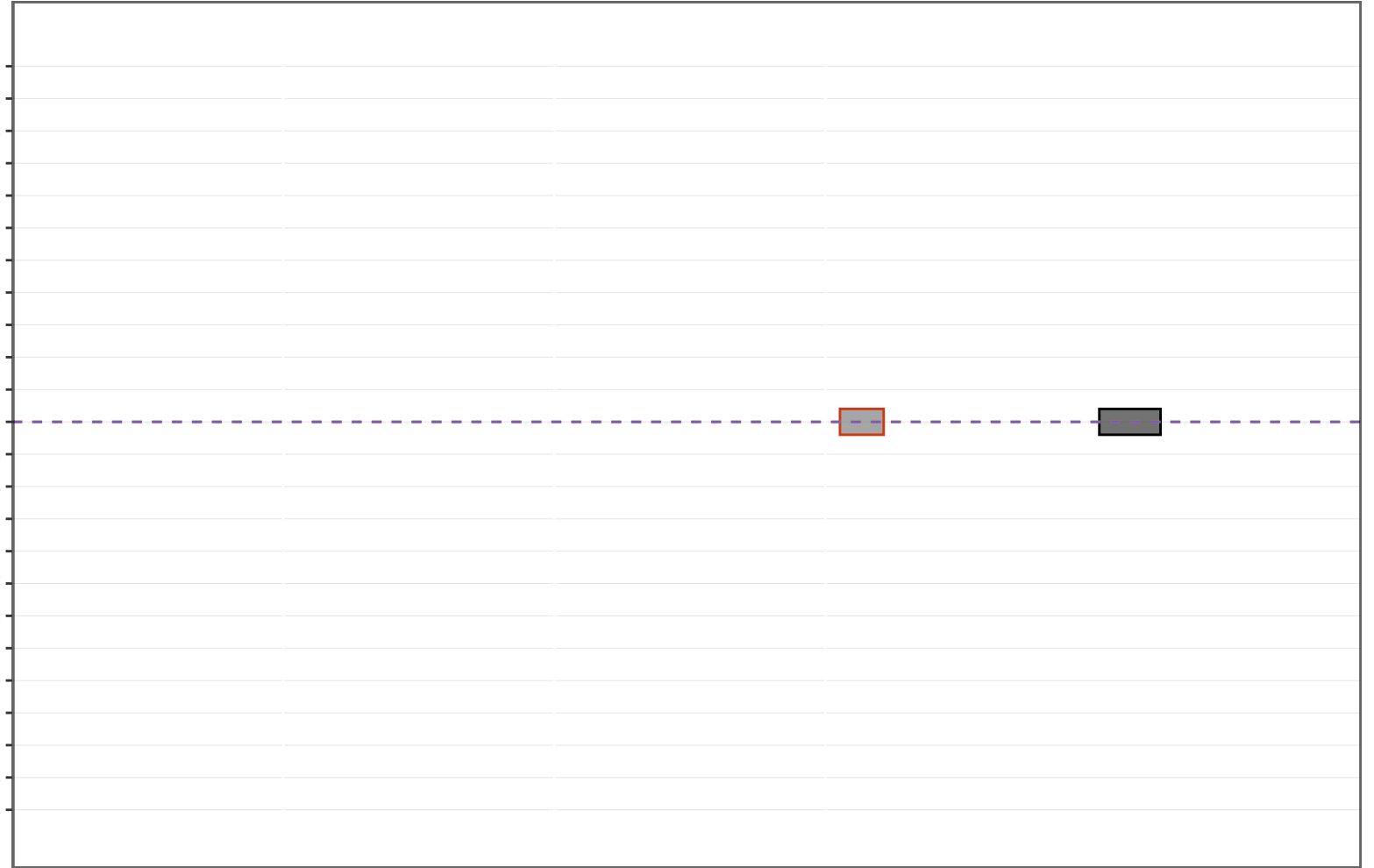
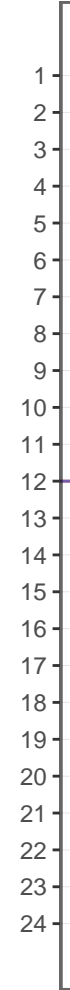
MW indication



Molecular weight

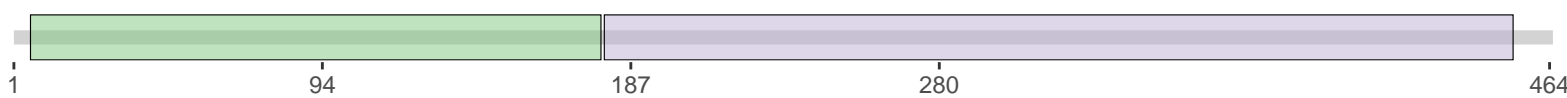


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF01154 Hydroxymethylglutaryl-coenzyme A synthase N terminal
- PF08540 Hydroxymethylglutaryl-coenzyme A synthase C terminal

Protein sequence:

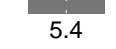
IALDACYSLCNKHEKLEGGKQFSADAAVYFVHSPYKLVGKSFARLFFNDFLRNACGIDESAIEKLPFSSLSGDESYGSRDLKASQGVAKGPFDEKVGPTTLPKGVGNMYTABLYAFAFSLIHNKHTLAGRVMKLFYVGGSGTATMFSGLKLNKNEGHPFSLNENASAMNVAEKLSRHELAPEKFEVEMQLMEHRVGAQDFVTSKDCSLLAPGTYYLFEVDESKYRRFYAKKATENGLNGH

NbL19g12910.1 actin-104 [MW = 41.75 kDa]

No. of times detected



log(intensity)



Values from



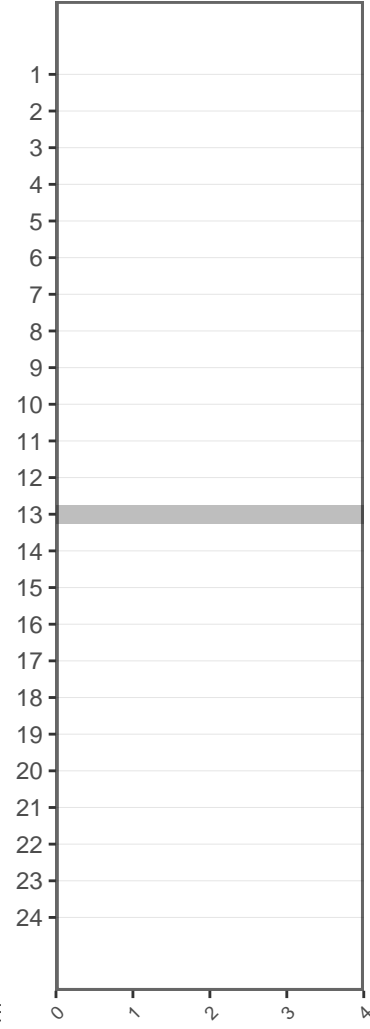
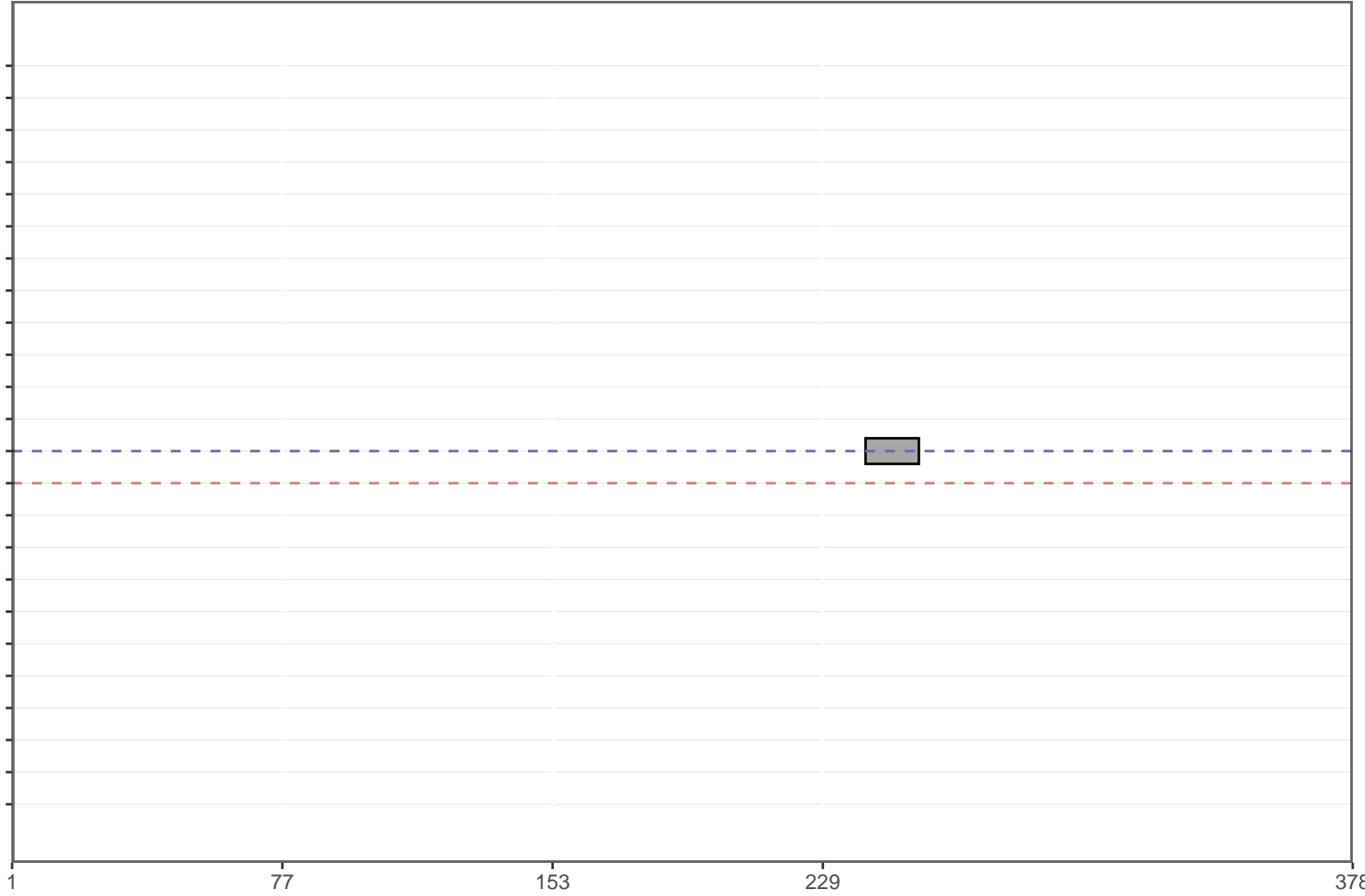
MW indication



Molecular weight

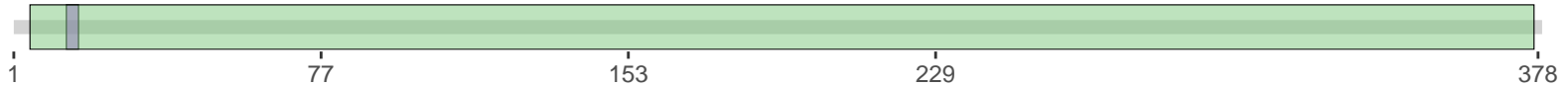


Gel Slice



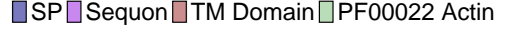
Protein length

Peptide counts over 4 repeats



Pfam domains

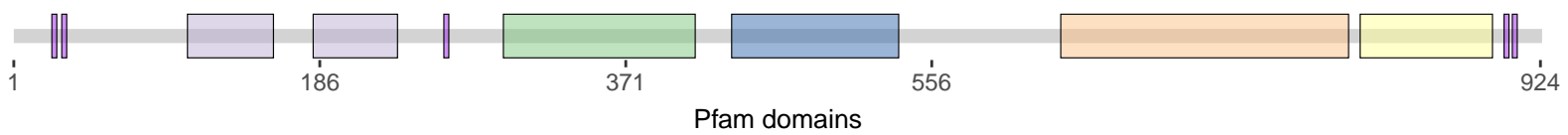
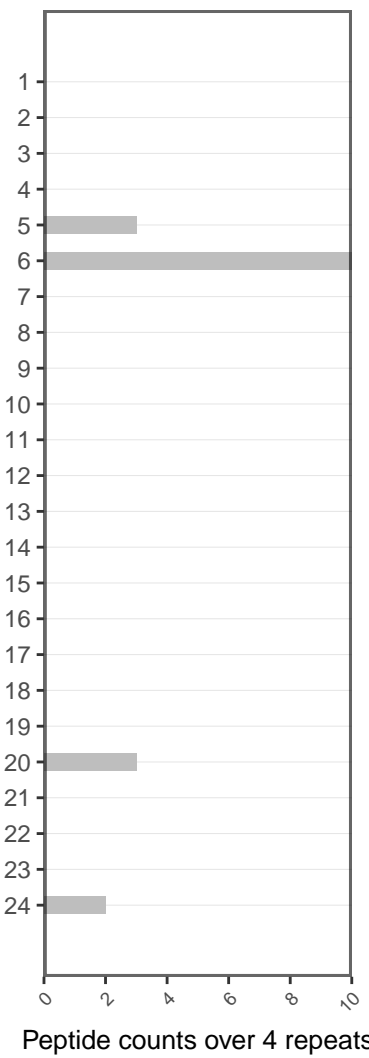
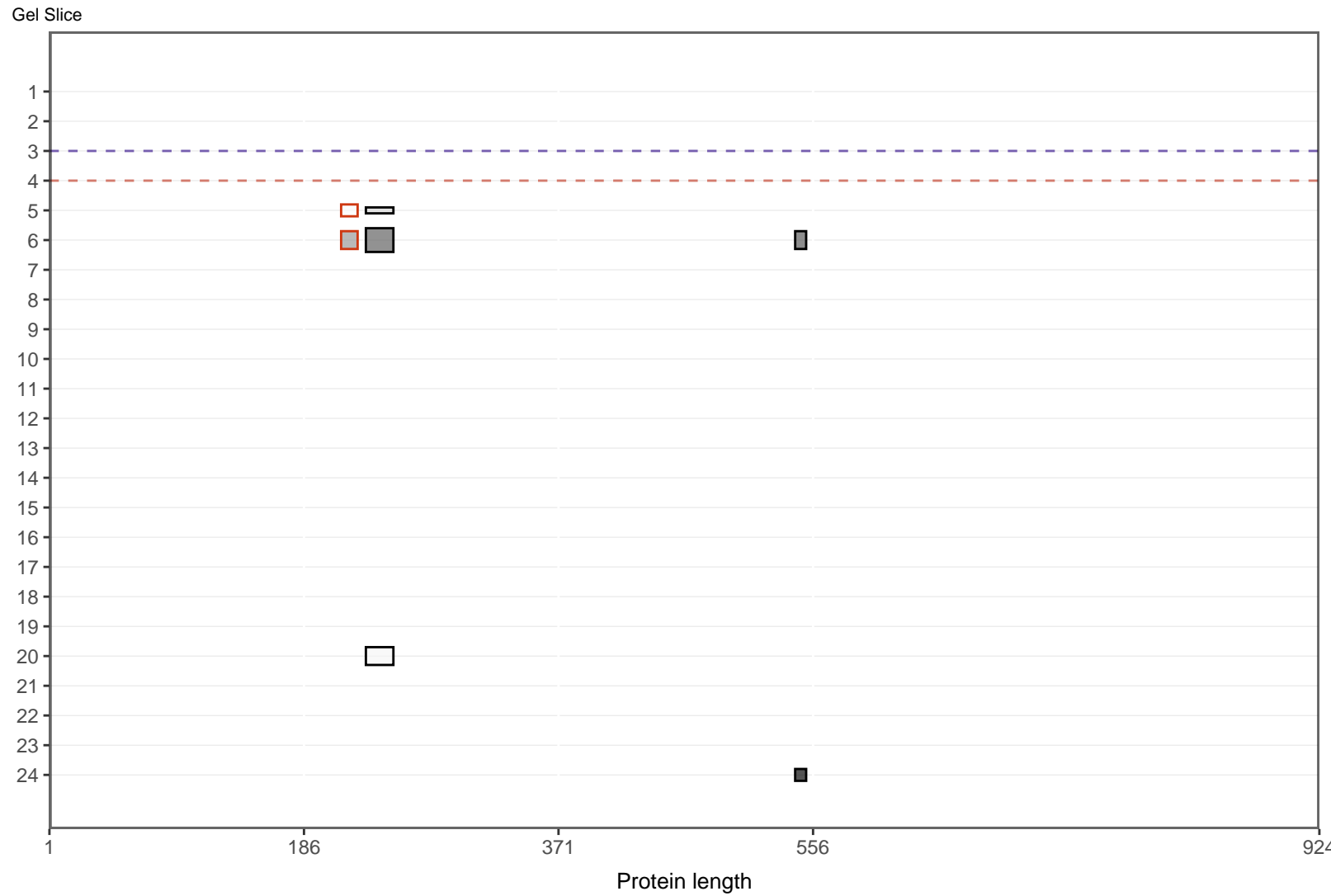
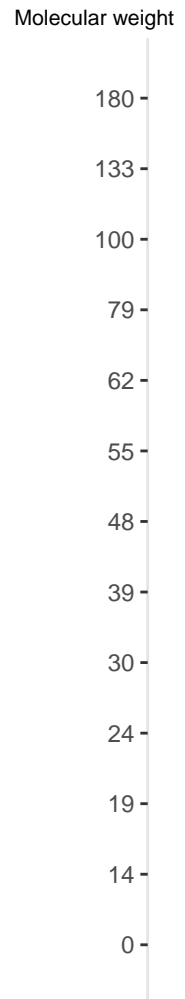
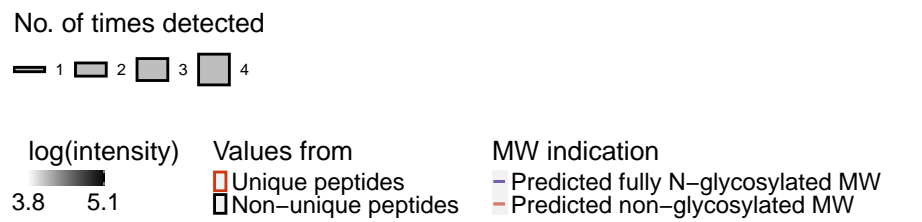
Pfam Description



Protein sequence:

.PHAILRLDLGRDSDTHLMKILTERGYMFTTSAEREIVRDKKELBYVALDFEGELTAKS666VEKVELFDGGHTGAEFRFCPEVLFPQLSLGMEAAAGHETTYNSMKGDVDRKDLGNVLSGGSTMFPGIADRMSKETALAPSEMKIKVWPPERKYVYVWGGSLASLSTFQGMWIKAEYDESGPAVHRKGF

NbL19g12890.1 ATP-dependent_Clp_protease_ATP-binding_subunit_ClpA_homolog_CD4B_chloroplastic [MW = 102.3 kDa]



- Pfam Description
- SP
 - Sequon
 - TM Domain
 - PF00004 ATPase family associated with various cellular activities (AAA)
 - PF02861 Clp amino terminal domain, pathogenicity island component
 - PF07724 AAA domain (Cdc48 subfamily)
 - PF10431 C-terminal, D2-small domain, of ClpB protein
 - PF17871 AAA lid domain

Protein sequence:

YEIHKLYRYTDEALEAANGLSYQYSDRFLPKAIDLIDEAGSRVRLRHAGLPEEAKLEKELRQITKEKNEAVRGGDFEKADELRRDREMDLKAQITLIDKKNKEMKAEEAAGDTGPIVTEADIQHIVSSWTGIPVKEKYSTDESRLKMEETLHTRHGGDEAVKASRRARRAVGLKNPNRPIASFIFSGPTGVGKSELAKLAAYVFGSEEMIRLDMSEFMERHTVSKLGGPPGVGVGTEGGQLTEAVRRRPTVYVLFDEIEKAHPQVFNMLAQLEDGRLTDSKGRVTD

NbL19g12830.1 guanine_nucleotide-binding_protein_subunit_beta-like_protein [MW = 35.91 kDa]

No. of times detected



log(intensity)



Values from



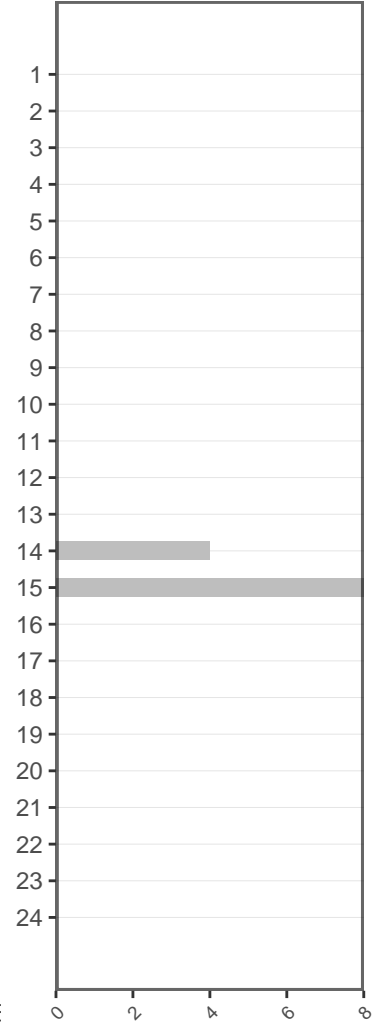
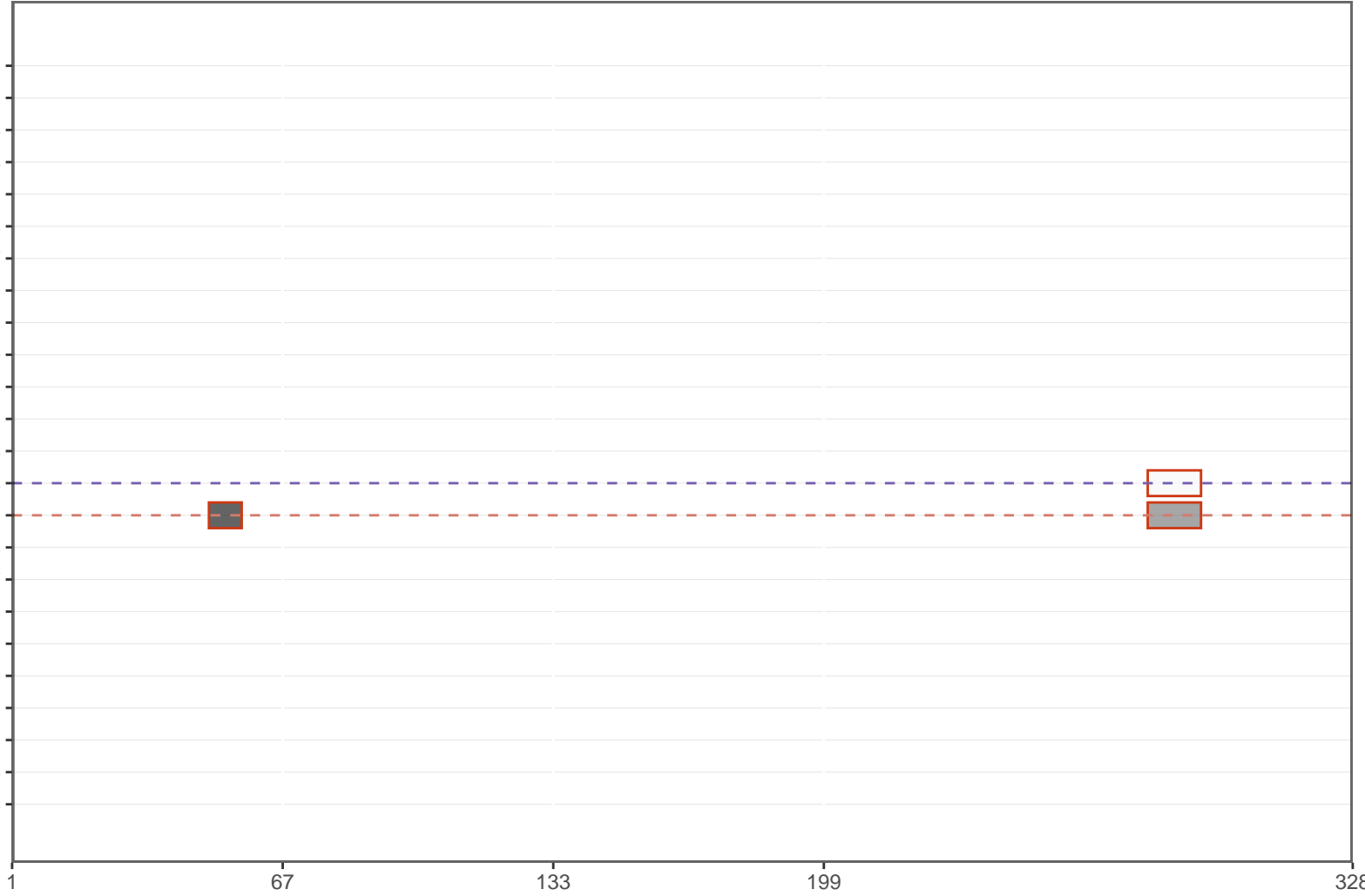
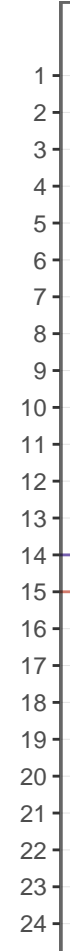
MW indication



Molecular weight



Gel Slice

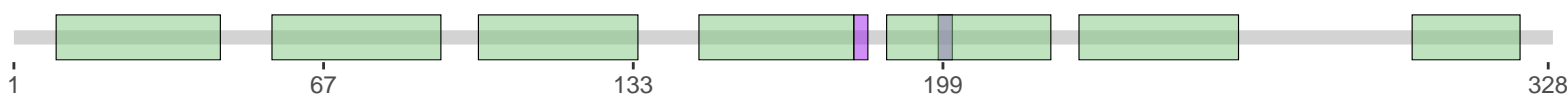


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

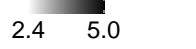
IDWVSCVRFSPNNGPTIVGGWDRTKWNLNGLKRLATLGHTEVYVNTTAVSPDGLGASGGKDDGVILLWDLAEGKLVLEGGSHLSLGFSPNRYWLGATEESIKIWDLESKTIYDDKIKVLDKGETEMSAEQTASGKNKVVYCTSLGWSADGSLFSGVYTDGLRWRWIGIRV*

NbL19g12590.1 actin-related_protein_4 [MW = 48.2 kDa]

No. of times detected



log(intensity)



Values from

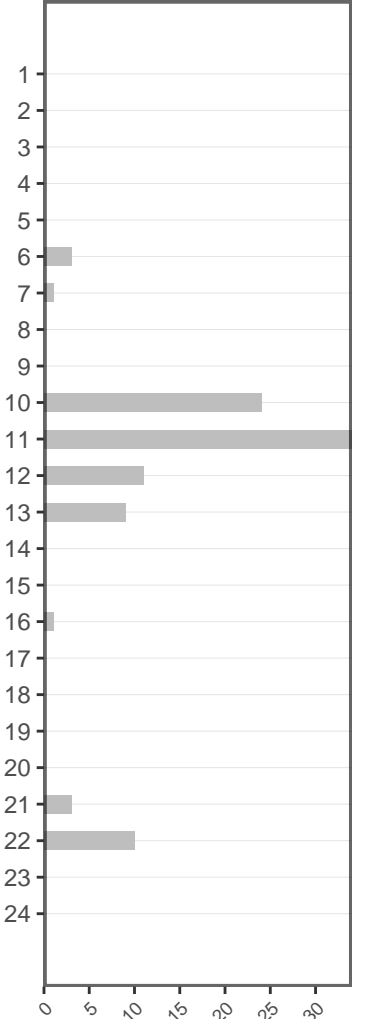
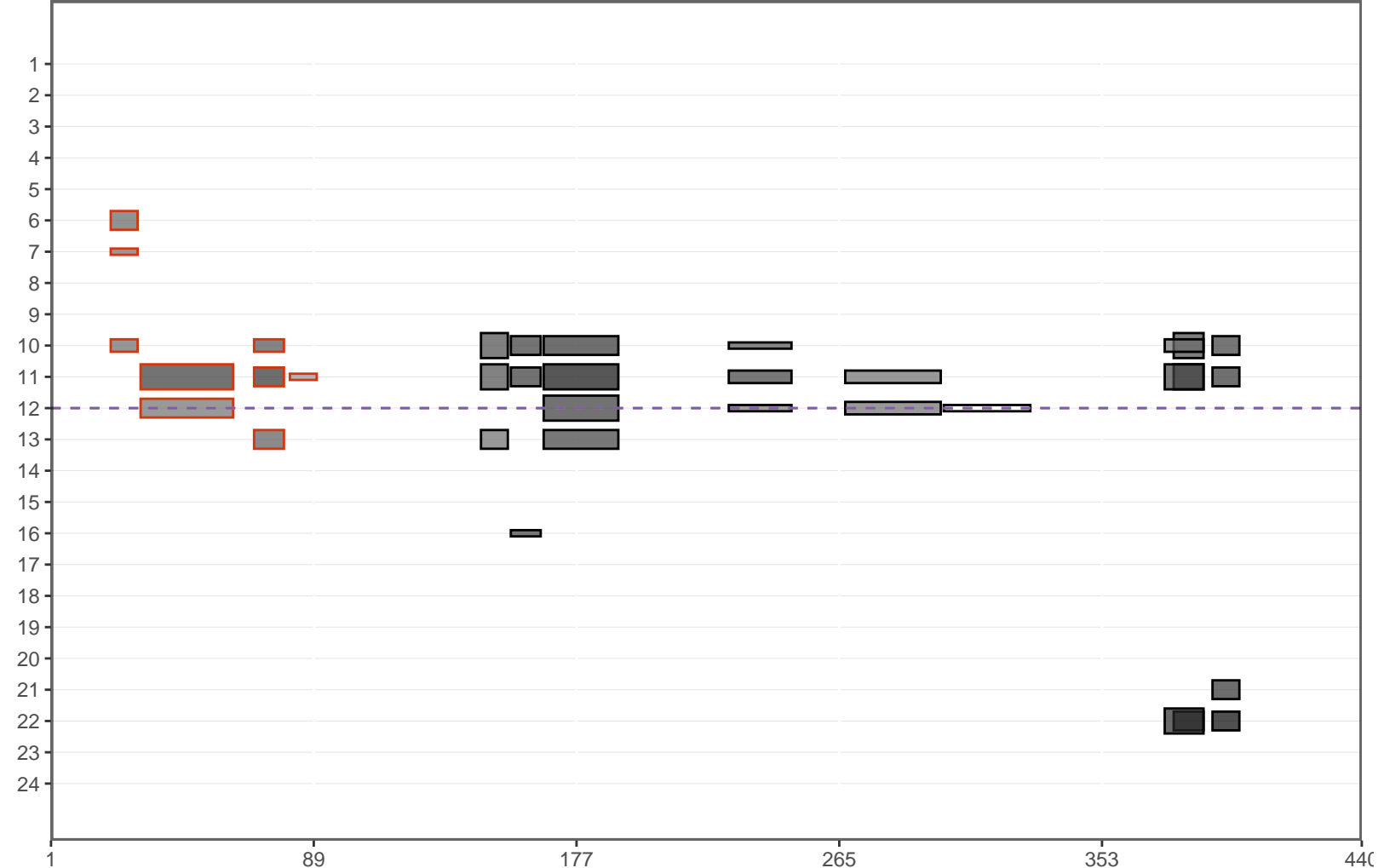
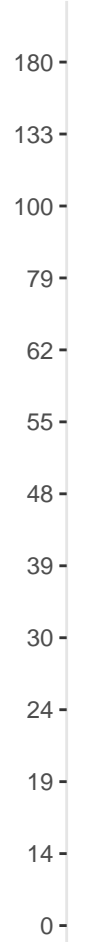


MW indication



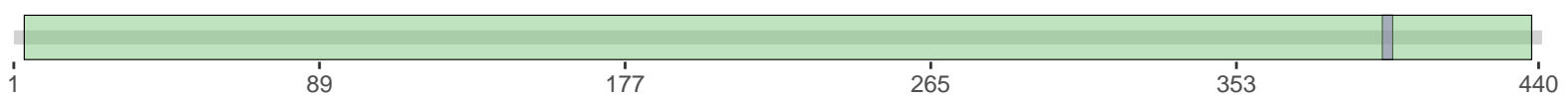
Molecular weight

Gel Slice



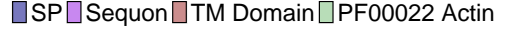
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TDLKLSLEQKGITKPKYVFNKKEIRPGEFGQTVLDLDFPDTTESYKLVQGRRAASDIKCEKVSRAFDPTFYDDSSYENIPFTTSVELPDGQTEVSGADRFPKIPDFNPLVGTIPGMESFAETAASLRGLPQMVEISINKGDVDIRRELFSSILGLHAIAGGTASMOGLKERLEKDLLEESPPAARVYVLAGSNATERRFVWVIGGSLASLGLGFQGMWFSKSEFEHGAAYVQRKCP

NbL19g12520.1 glucan_endo-13-beta-glucosidase_11-like [MW - SP = 42.58 kDa]

No. of times detected



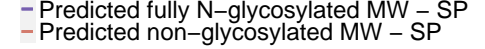
log(intensity)



Values from



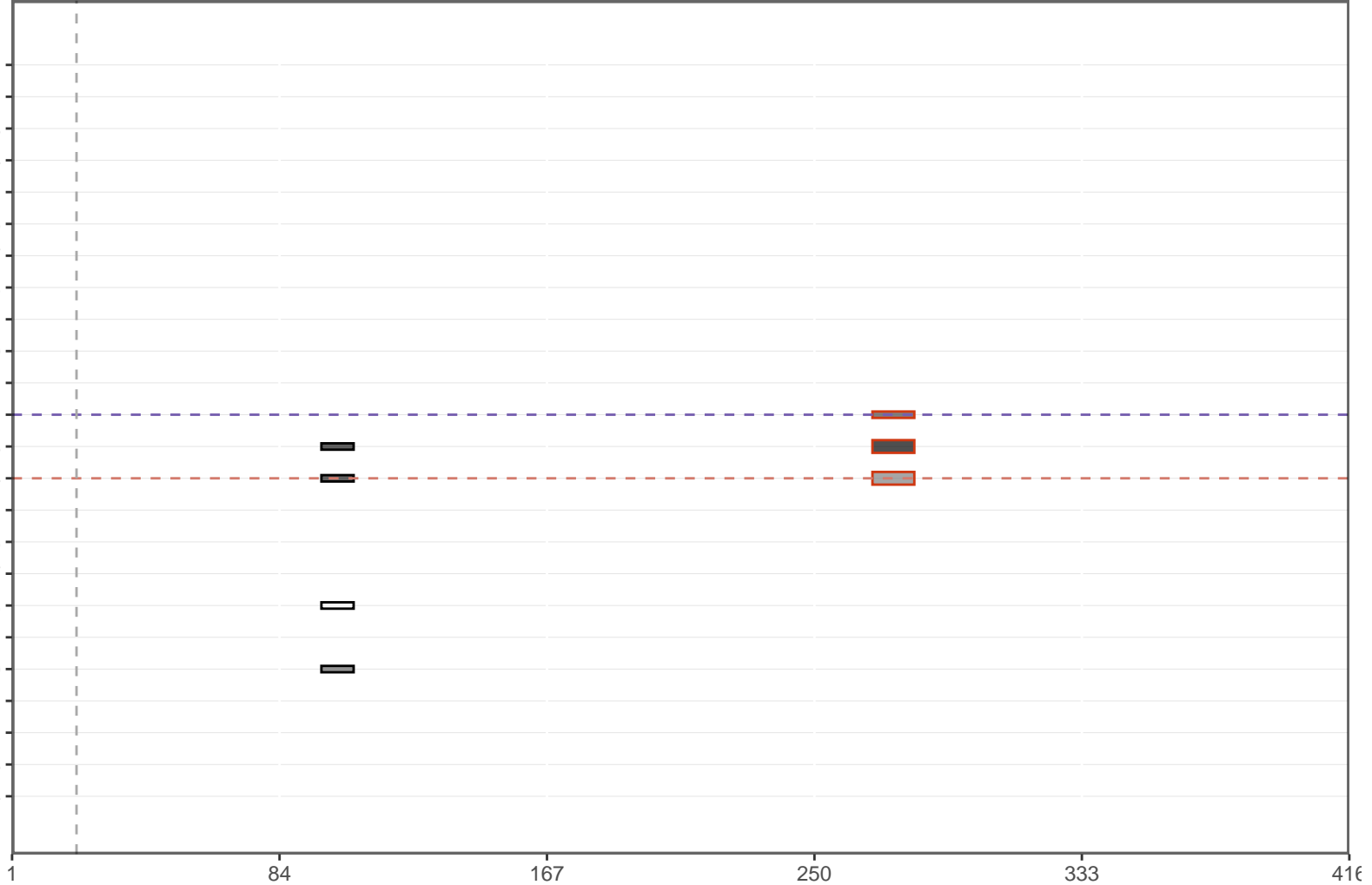
MW indication



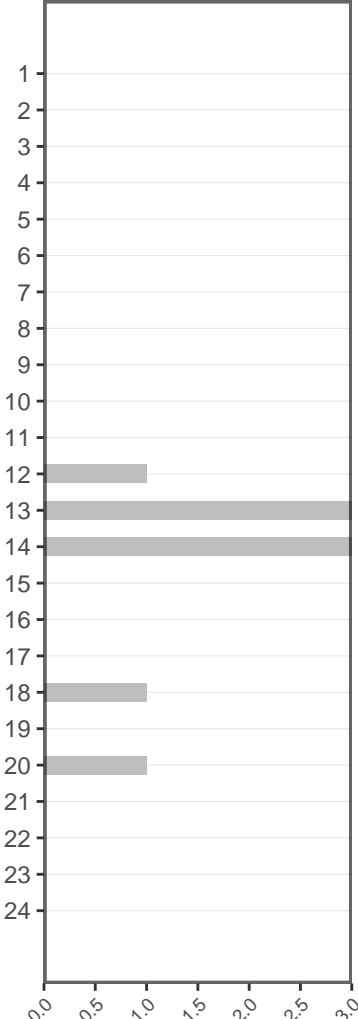
Molecular weight



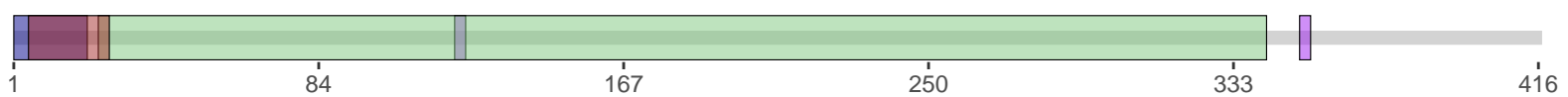
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

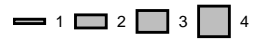


Protein sequence:

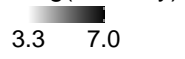
YPYFAYKANPKQVFLDYLVAFLGQNPNGNVDFTNLHYDNNMLYAGIDAVHEALGALGYKKNVQVQISETGWPSKGGDEEVGATPDNARKYKGNLKLIVSGNKGTPLRNFTNLNLYYFALFENLKNKPGPTSERNYGLFKPDGSPRYPLGFGAGINAVGTNBS66RSPAAGTGG66TST66STP6WNSPQVYLFST666RQGFQWKLVLRLHIAGLISLFSQL

NbL19g12500.1 V-type_proton_ATPase_catalytic_subunit_A-like [MW = 68.67 kDa]

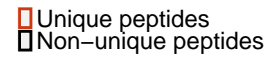
No. of times detected



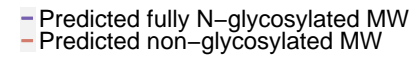
log(intensity)



Values from



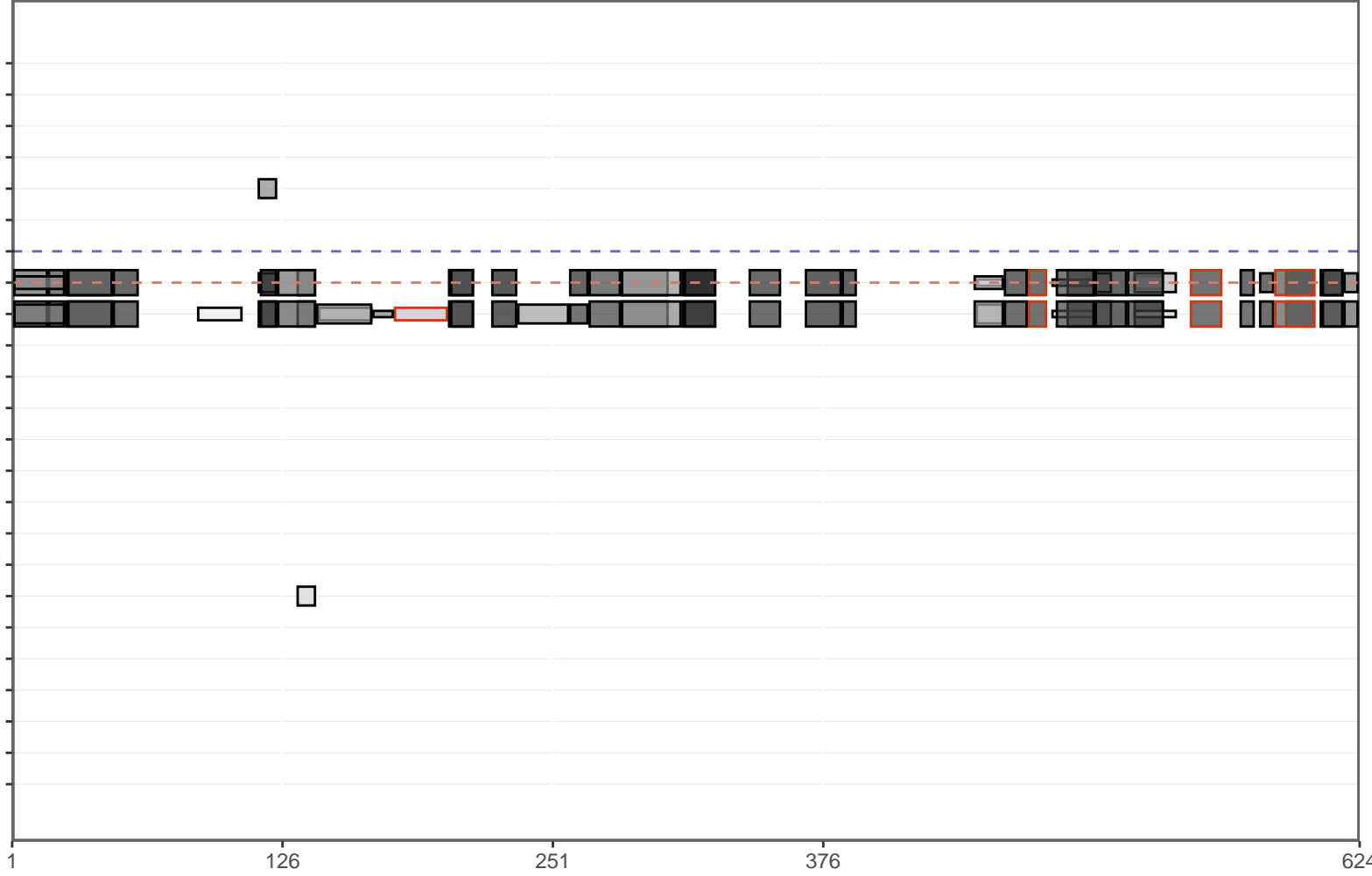
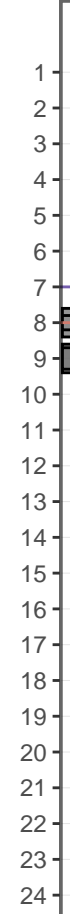
MW indication



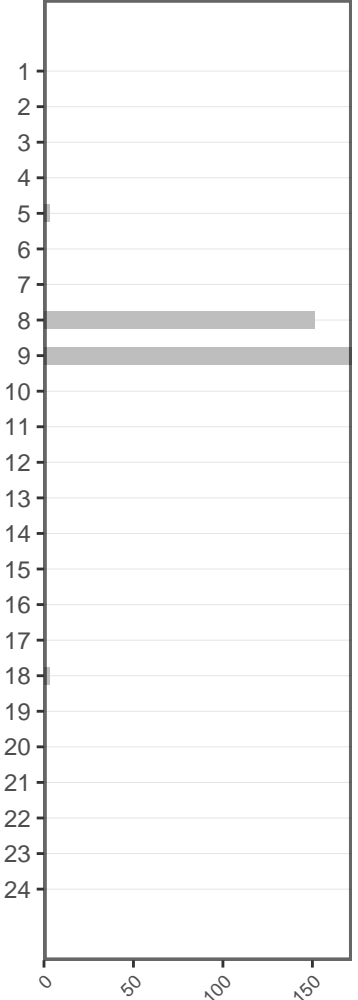
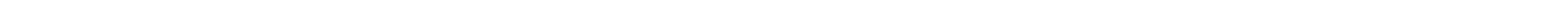
Molecular weight



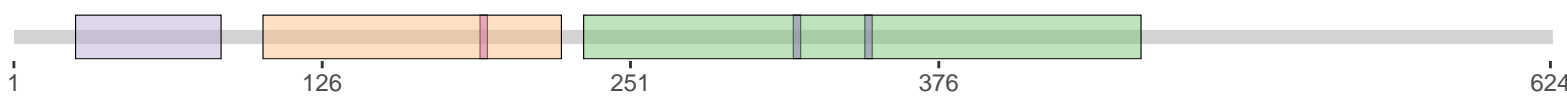
Gel Slice



Protein length

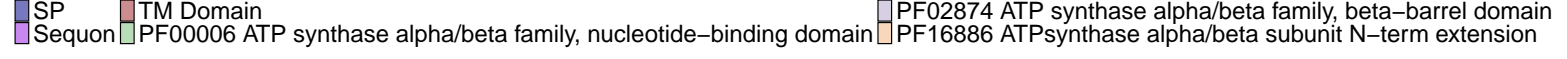


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TLPGREESVMKRTFLWANTENMPVAAREASVYTGITAEVFRMGVNVSMMADETSRWAEALREISGRLAEMPADSGYPWLAARLASFYERAGKVKVGLGPERPTGVSVTWVAVSPPGDFSDPVTSATLGVIVQVWGLDKKLAQRKHFPSPVWALISYKSYGSALESFYKFDADDFIDRTKAREVLRQREDDLNEIVQLVQKDALAETDKITLETAKLLREDPLAGNAFTPVDFKFCDFYKSVWMLRNHHFYNLANGAVERGAAGMDGQKITYLKHRLGLDFYRLVLSQKFEI

NbL19g12370.1 UDP-glucose_4-epimerase_GEPI48-like [MW = 38.37 kDa]

No. of times detected



log(intensity)



Values from



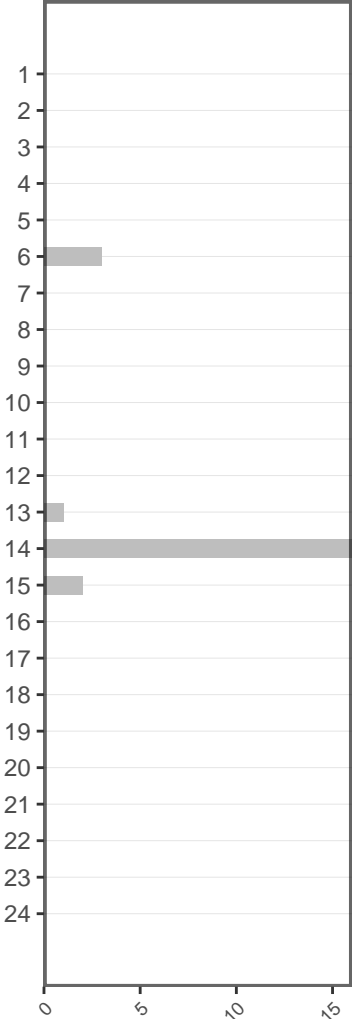
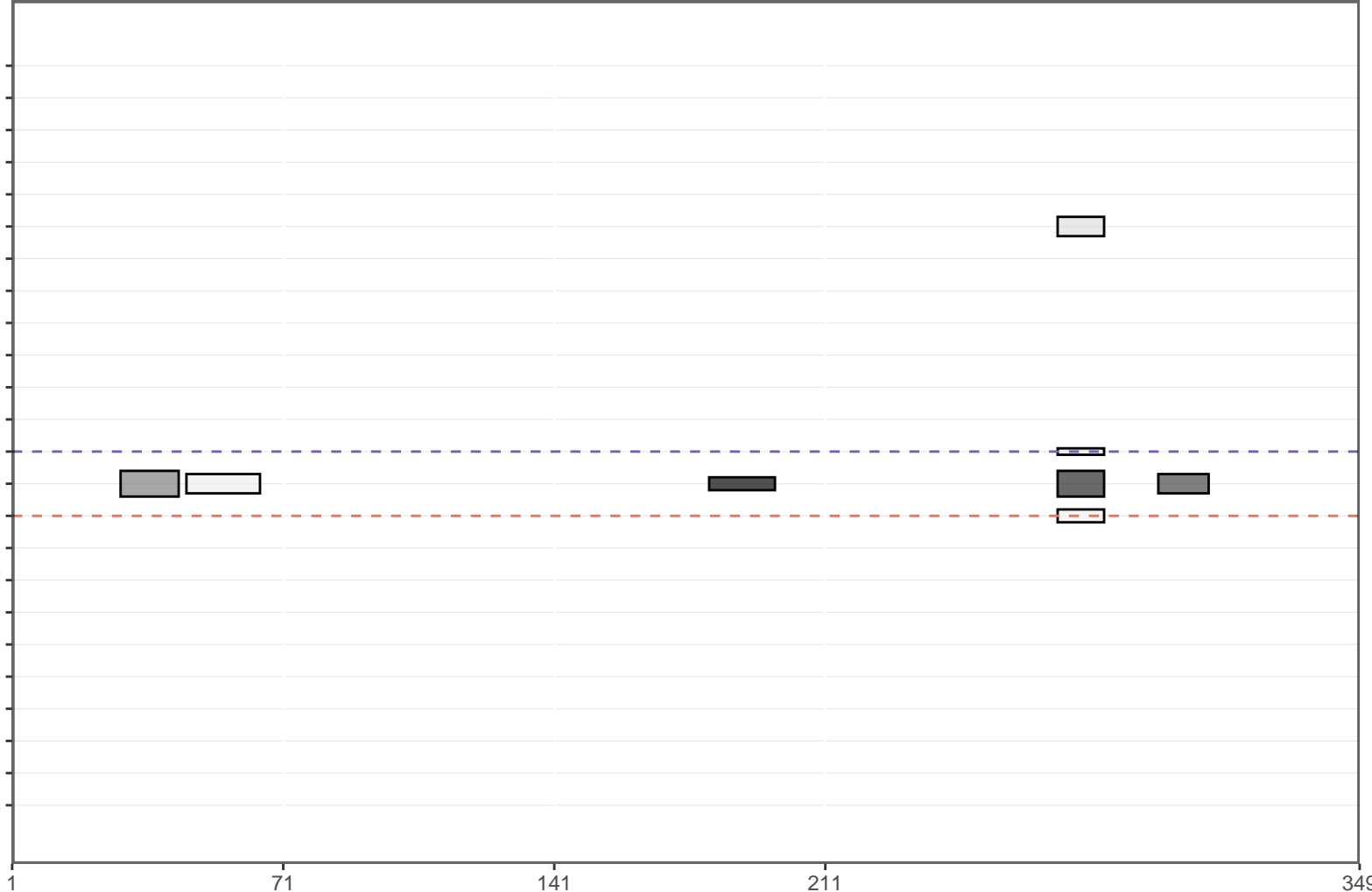
MW indication



Molecular weight

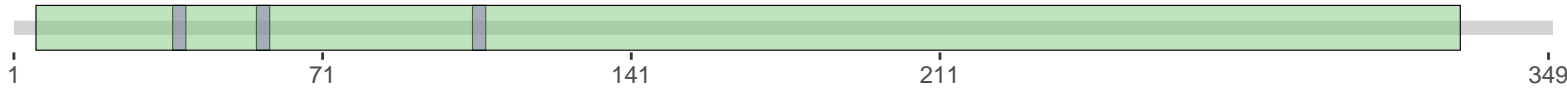


Gel Slice



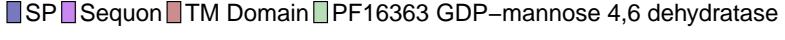
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

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NbL19g12240.1 6-phosphogluconate_dehydrogenase_decarboxylating_2_chloroplastic [MW = 54.27 kDa]

No. of times detected



log(intensity)



Values from



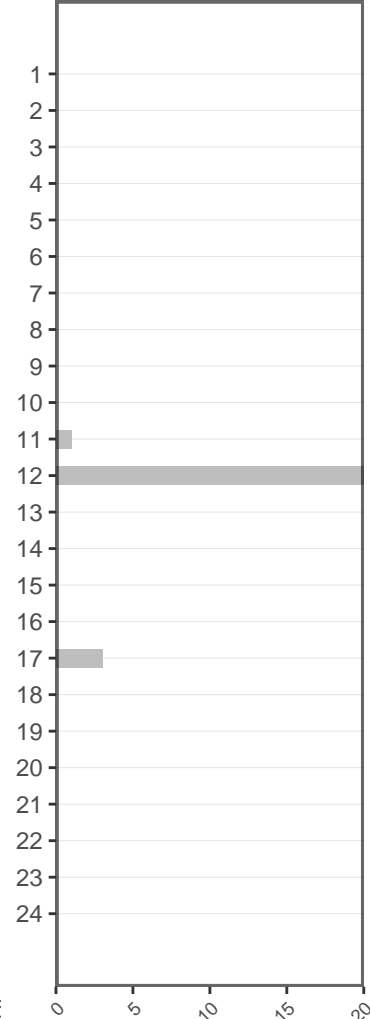
MW indication



Molecular weight

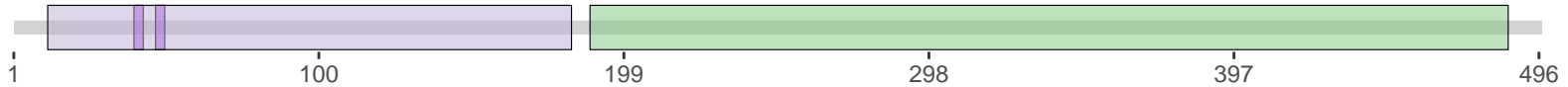


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF00393 6-phosphogluconate dehydrogenase, C-terminal domain
- PF03446 NAD binding domain of 6-phosphogluconate dehydrogenase

Protein sequence:

LESFLVETADIFNVKDEKTSGGELVDLIDKTKMGTGKWTYVGGAAELSLIAAPTIAAELDGRYMSGLKEEREDAAIFKKEGLKEEMNFDYNGASVYKRLLEDYRQALYASKICSAAGGMNLRKAKSAEKGNWNLGEMARIWKGCCIRAVFLDRKKAYGRNPLANLMDPEFAREMVGRGAAWRRVYGLAHRGIVPQMSASLGYFDYTRRRLPANLVGAGRDFVFGAHTYERVDPMPGAYHTEWSKLARKARV

NbL19g12230.1 uncharacterized_LOC109239217 [MW = 39.96 kDa]

No. of times detected



log(intensity)



Values from



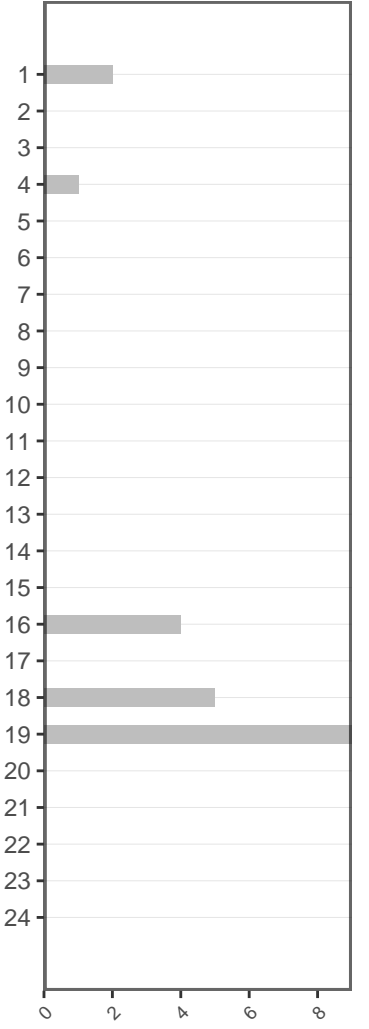
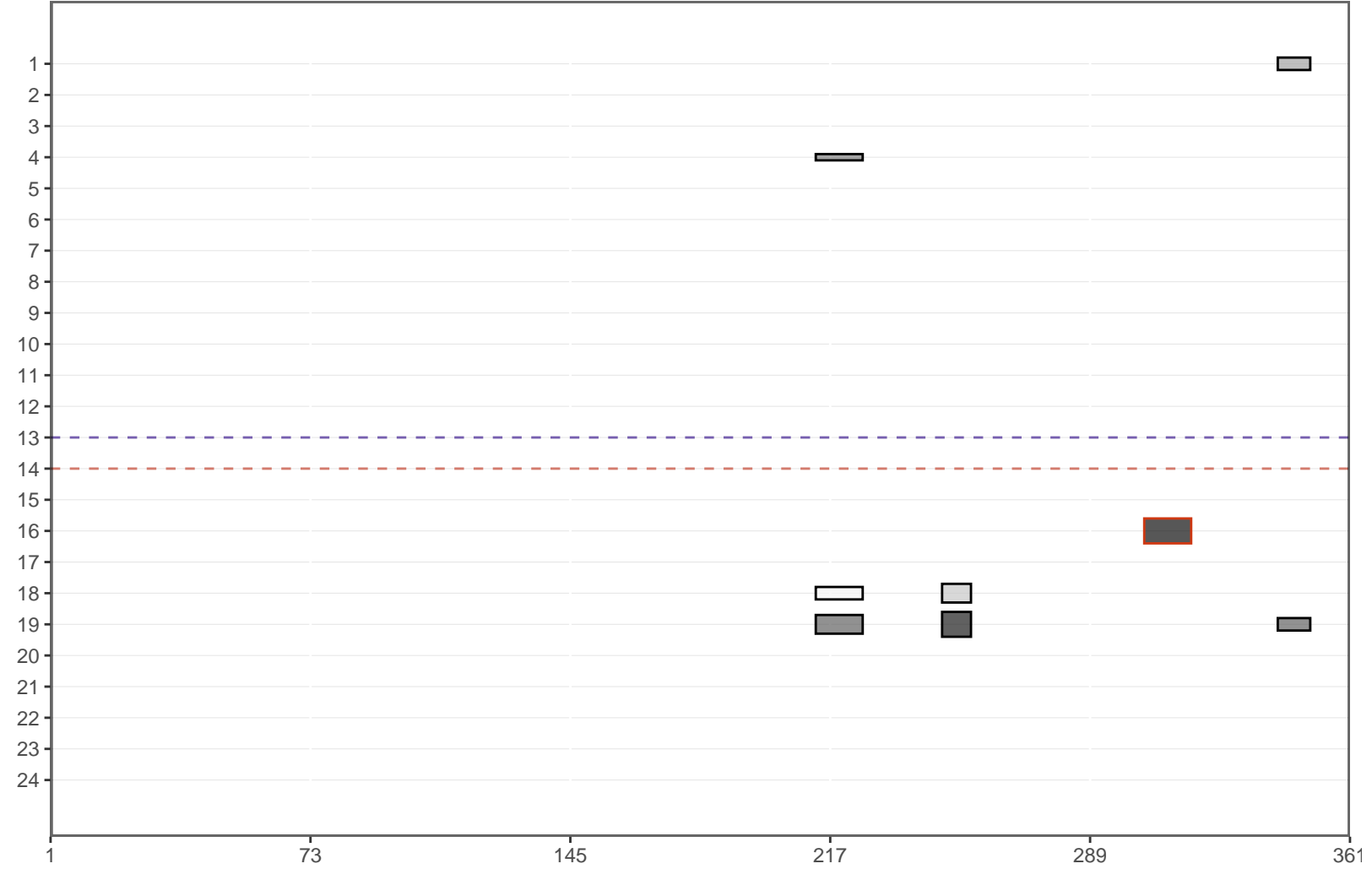
MW indication



Molecular weight

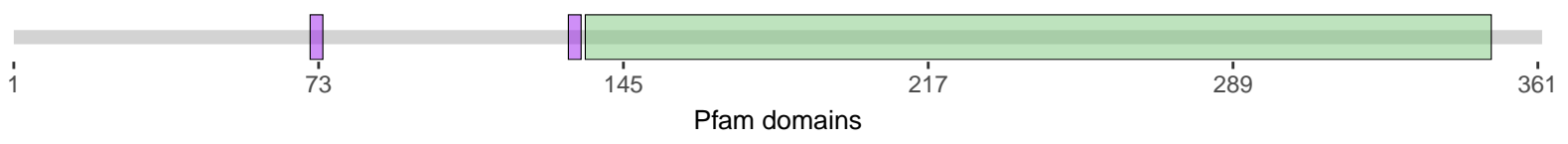


Gel Slice



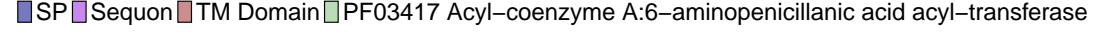
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

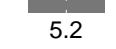
VTYAGELPSCAFGNSHGVAFTLNVPPCEEIEVAGIAGRNFRVSRDLLEANSIEDALARIHSSSEASVGHSEVNIIDTRARRILNVETASRNRIHVHEIGETFPFHANMYLHLQVYKQADDENLSRQKRASSLPKESKDFLALLGDSNAEKYPIVMFGPLLYTLCTAVIDLDEKLTIEGNPKKEQESYVFRLL

NbL19g12210.1 uncharacterized_LOC109238591 [MW = 47.18 kDa]

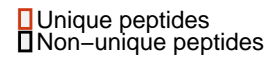
No. of times detected



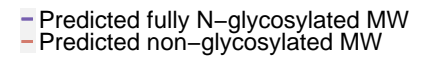
log(intensity)



Values from



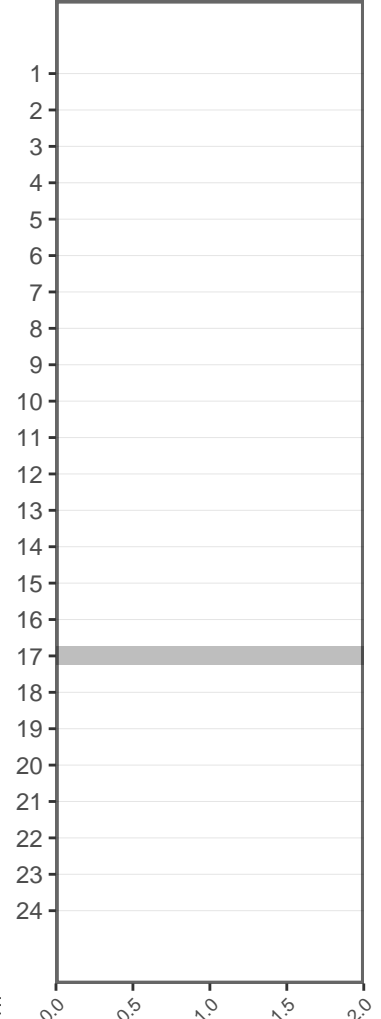
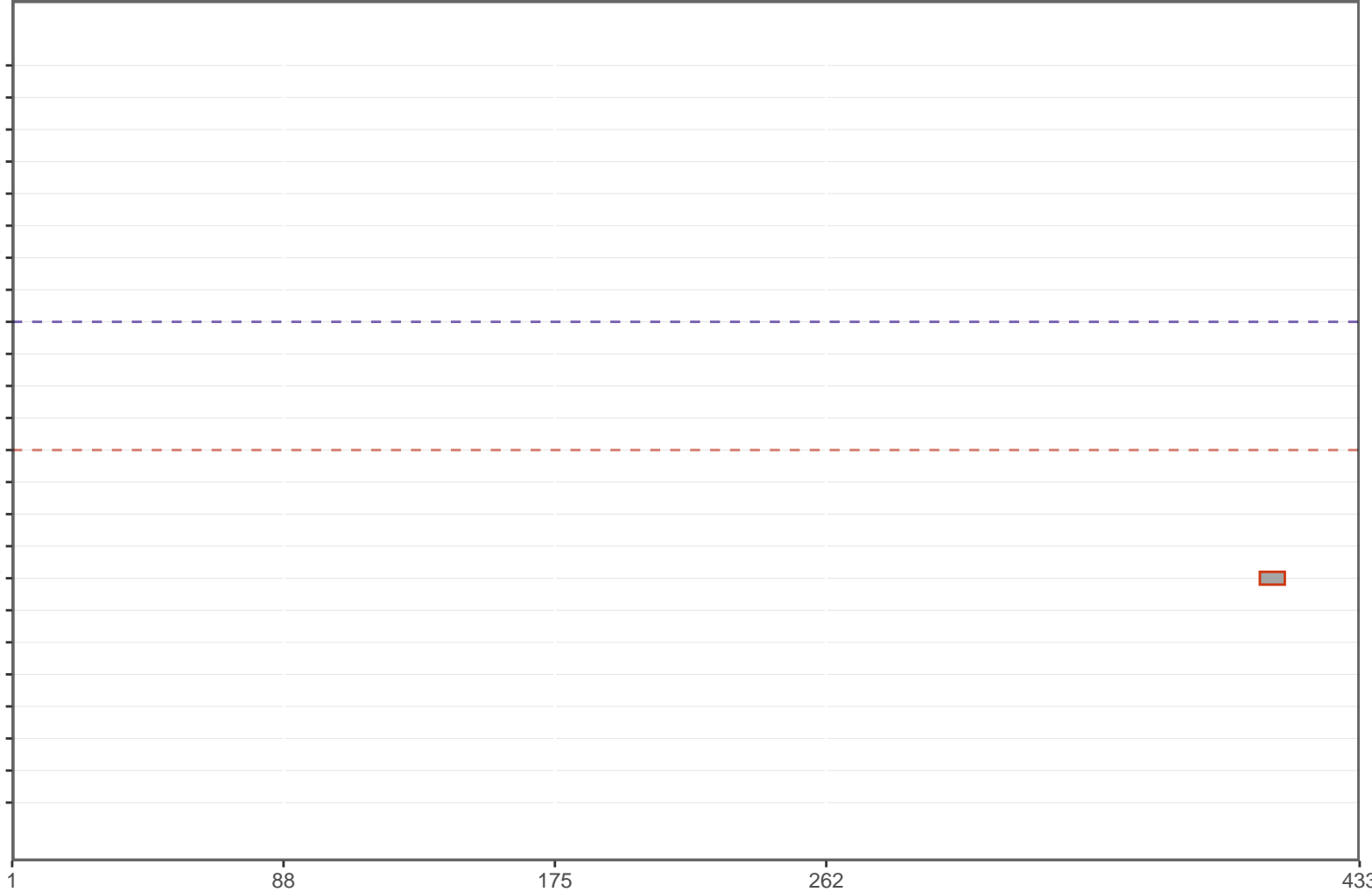
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

ITSKTYCGGRWYKVENLTLFLKGGTGLFVLELGGVTDNIKILPTFGVQVSENVNASTNSDILTMCDERISSEISGASTSEVPPADSPRILVAAATLGEATYSLRQNTTEETFKLLKRPQGVVMKAGKLEKSEKGFAPKPVVGGNNLVEIADGILPGLKRLVGNFRKPKRKGVPVPCGADSRSSPVKFRDSEGFSTSFVNNKPMPPYTRVMKADISEGKLRKIVANGVEPRR

NbL19g12170.1 glucan_endo-13-beta-glucosidase_1 [MW - SP = 53.34 kDa]

No. of times detected



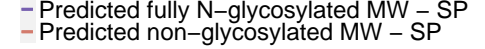
log(intensity)



Values from



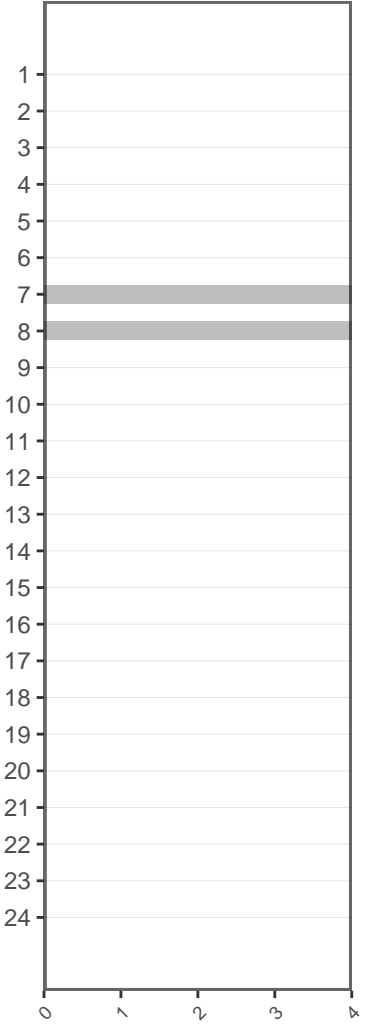
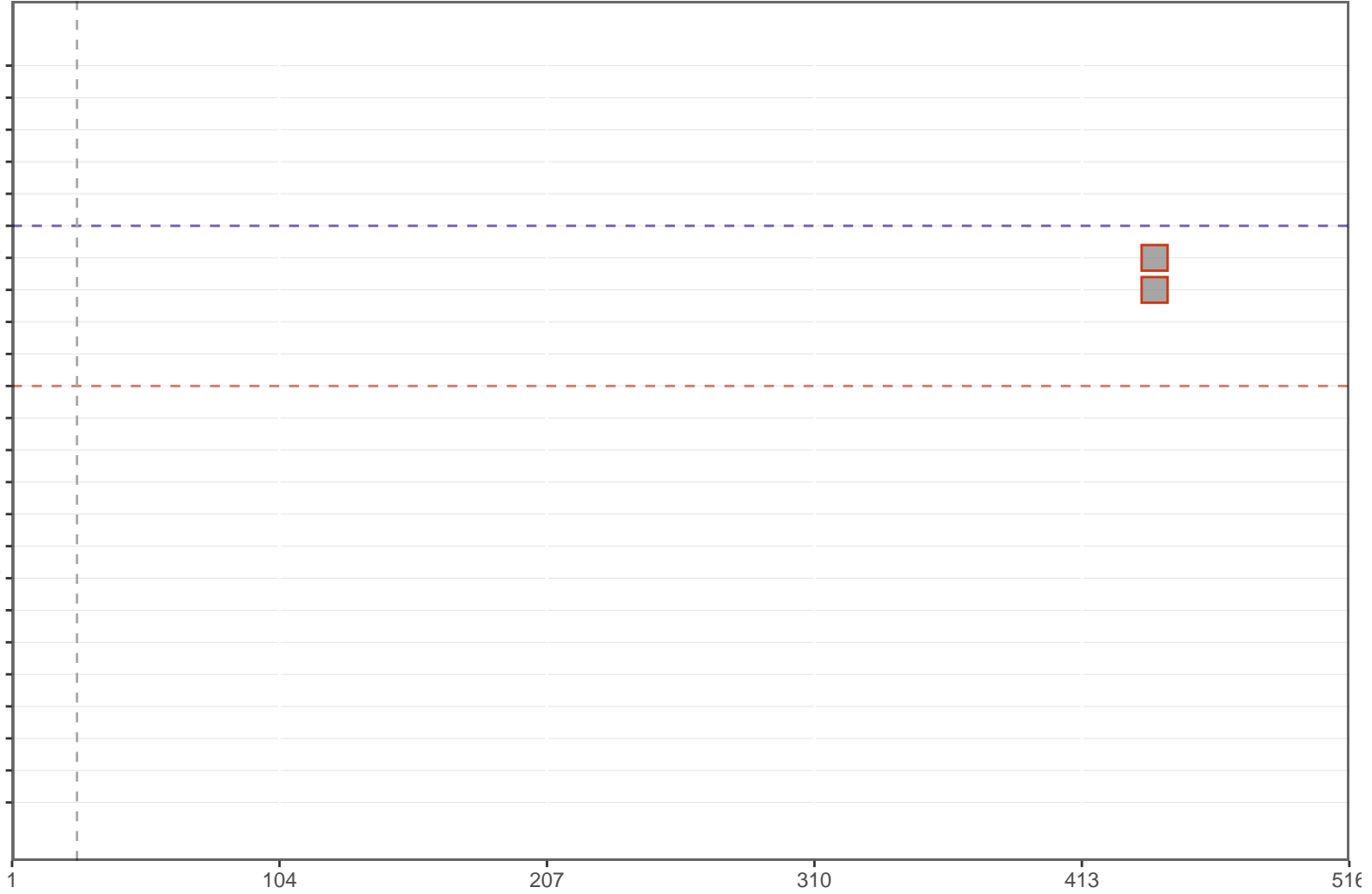
MW indication



Molecular weight

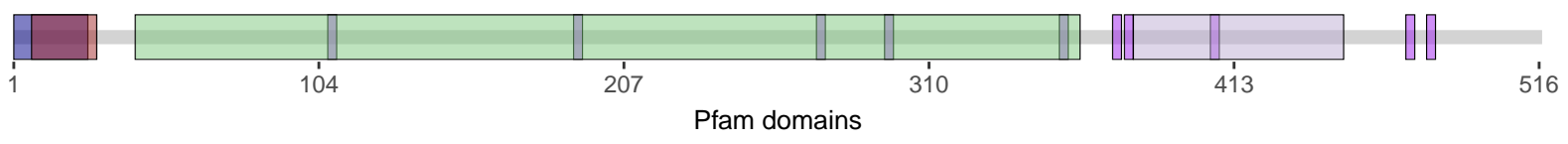


Gel Slice

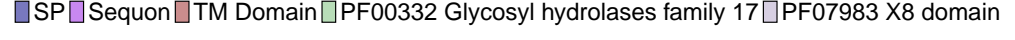


Protein length

Peptide counts over 4 repeats



Pfam Description

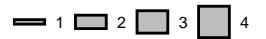


Protein sequence:

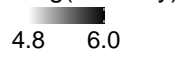
LHLYTNVLDAMDSVYFSMKNLNVDTVLLVETESGWPSPKGDSEKFNATIONADTYNSLNKHIDRSGTFLHPETSSVYVYELFNEDLRSPVSEANWGLFHNSTPVIYLLHVSGGTFLANDTTNGTYGIAMDGVDRKFLGAALDWAGDGPGRANRGEIQPGESCYPFNVDKXNHASVAFDEYVYKSGTSPSGDFKGVAMITTSDFPSHGSCFFPGSKTVSNKTNQVYVNTQASGANTRIVYAGTSLKNNMHLFGVAFGLFYVY

NbL19g12120.1 aminomethyltransferase_mitochondrial [MW = 44.12 kDa]

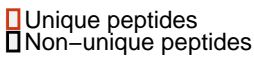
No. of times detected



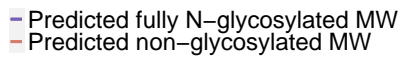
log(intensity)



Values from



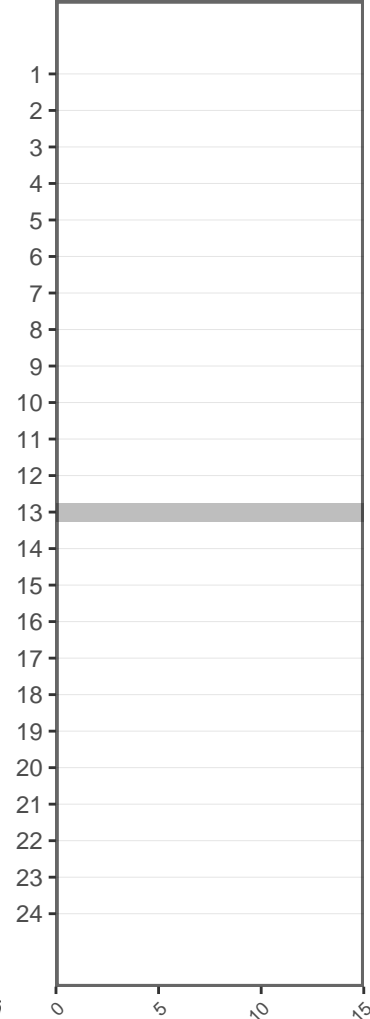
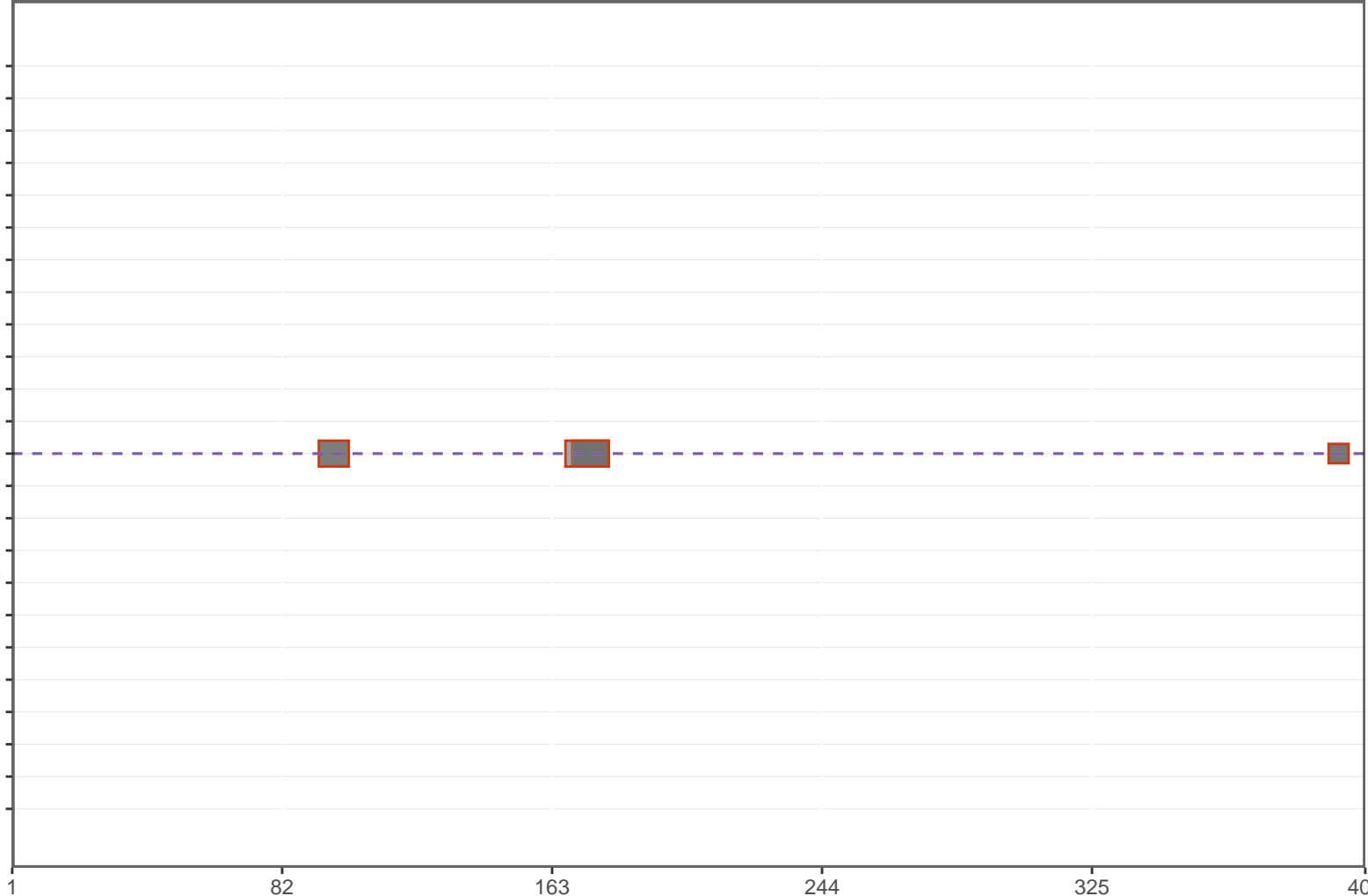
MW indication



Molecular weight

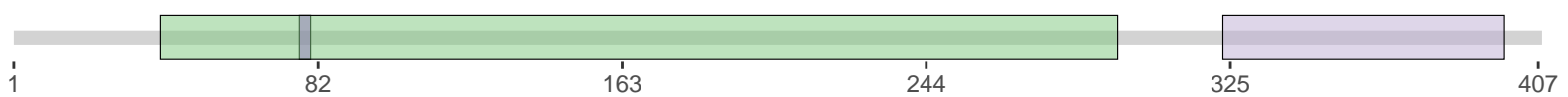


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

SP Sequon TM Domain PF01571 Aminomethyltransferase folate-binding domain PF08669 Glycine cleavage T-protein C-terminal barrel domain

Protein sequence:

AAPVLOHLLTKDQLSNMVFGEFRVLDINGAGFLTRTGVTGDEGFEISVPSENAVDLAKALEKSEGVRLTGLGARDELRLLEAGLGLYGNDMEGHPTPEVGLTWAGKRRRAEGGFLGAELVLDGIEEGPKIRRVGFFSFGPPRHSSEKDDNGNGNGEITSGGSPCLKKNIAMGVYKTNKAGTINAVIVRKGKVDGAVTKMPFAPTKYYKPI

NbL19g12110.1 deoxyhypusine_synthase-like [MW = 27.25 kDa]

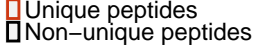
No. of times detected



log(intensity)



Values from

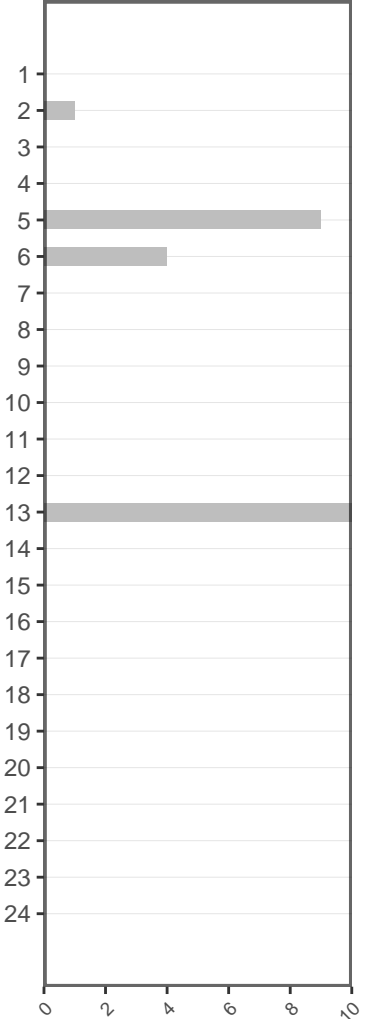
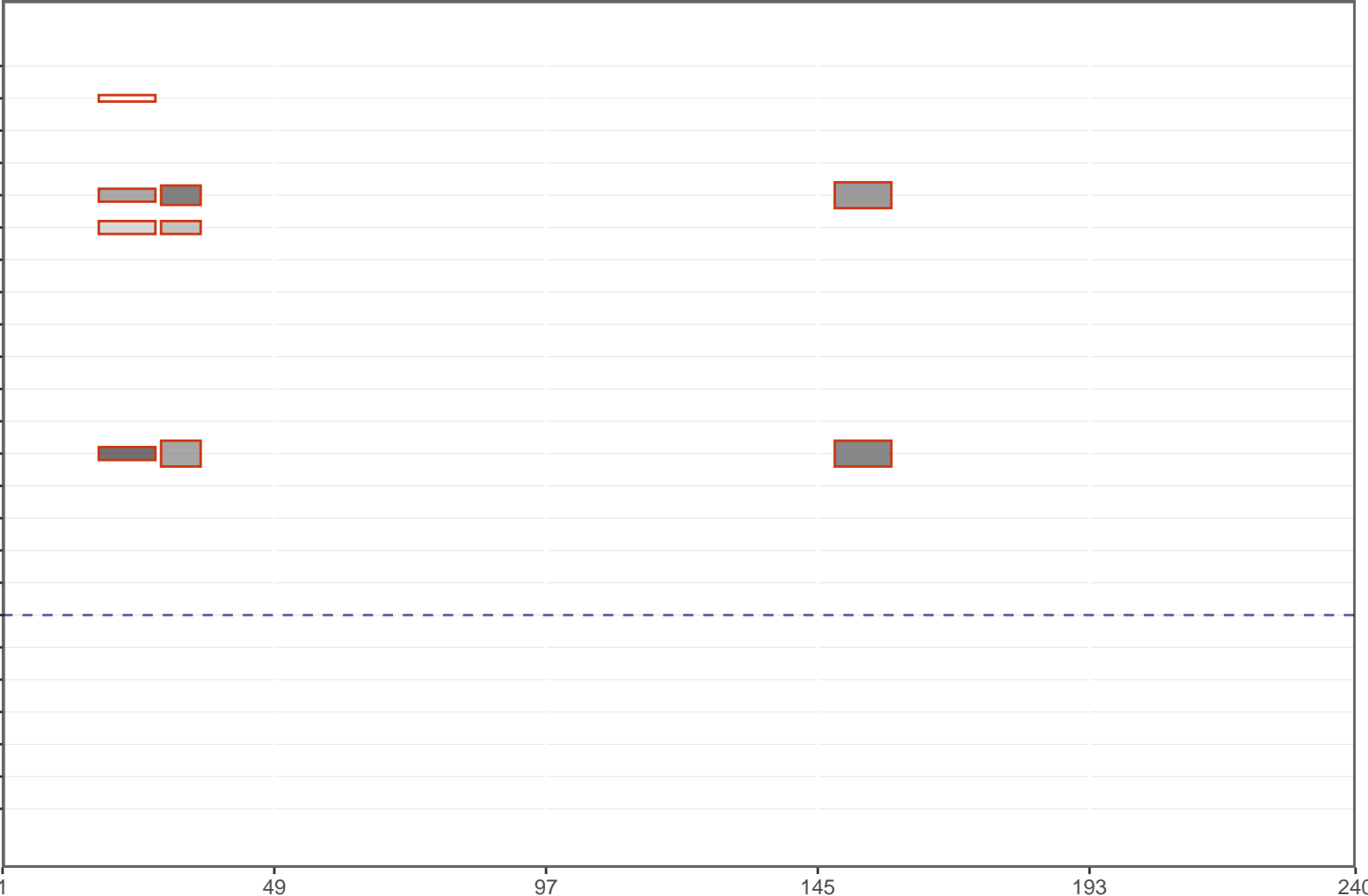
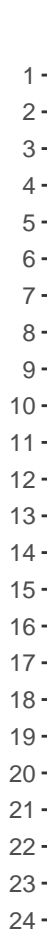
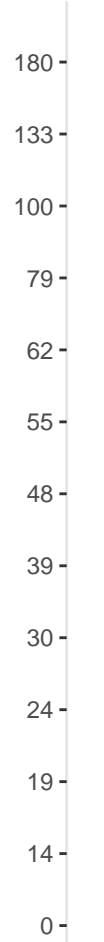


MW indication



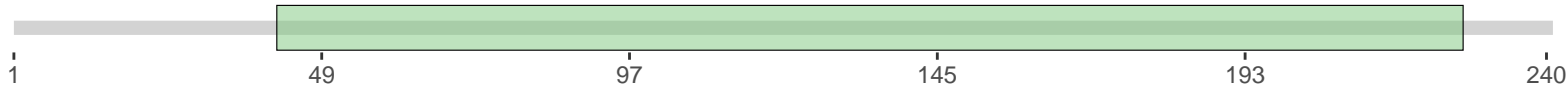
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LLVSSGV RDTIRYL VQHRMVDVAATFAGGIEEDLKG LAFPTKGDPLPGAVLRSGKLNKGNLLVFNPNYKFKFNWIPFDQMYEEQKKEKVLWTPSKVIARLQKEINDETSYLVWYKYNFGSTLGLLFDKI

NbL19g12040.1 proline_synthase_co-transcribed_bacterial_homolog_protein [MW = 30.44 kDa]

No. of times detected



log(intensity)



Values from



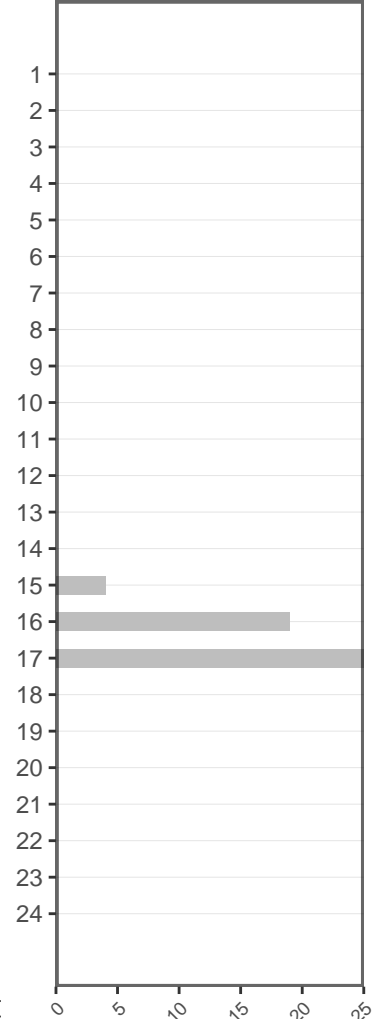
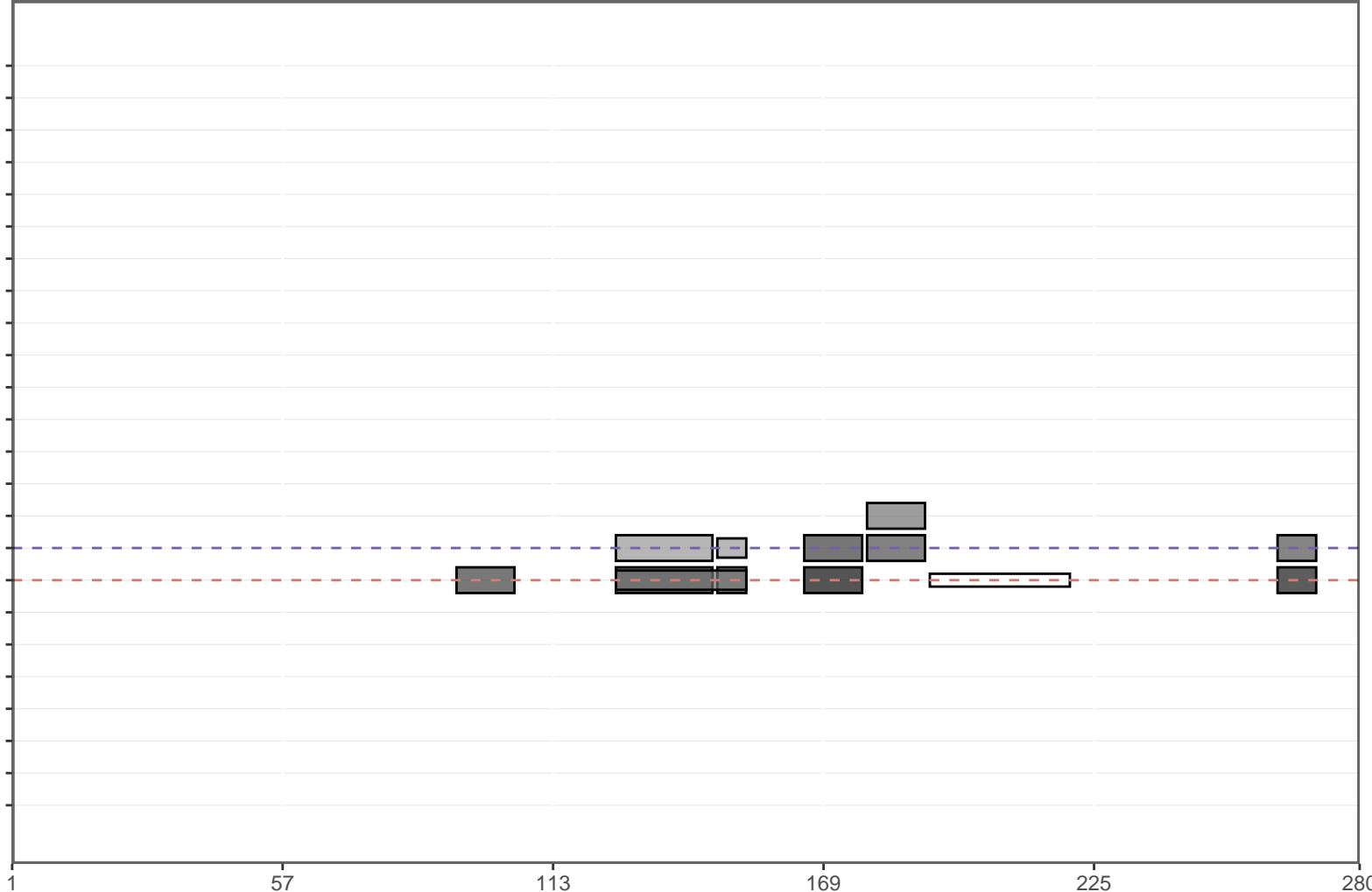
MW indication



Molecular weight

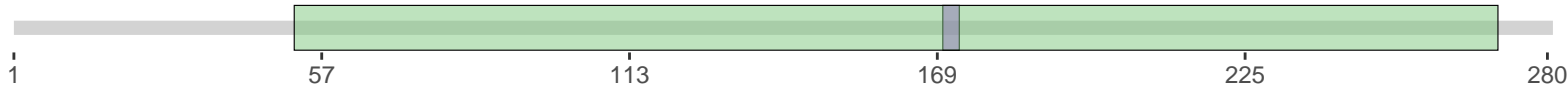


Gel Slice



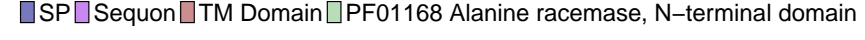
Protein length

Peptide counts over 4 repeats



Pfam domains

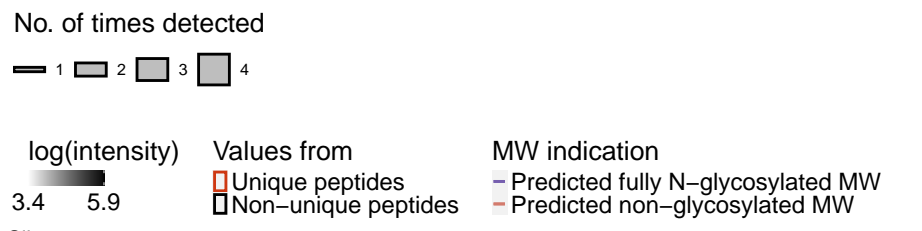
Pfam Description



Protein sequence:

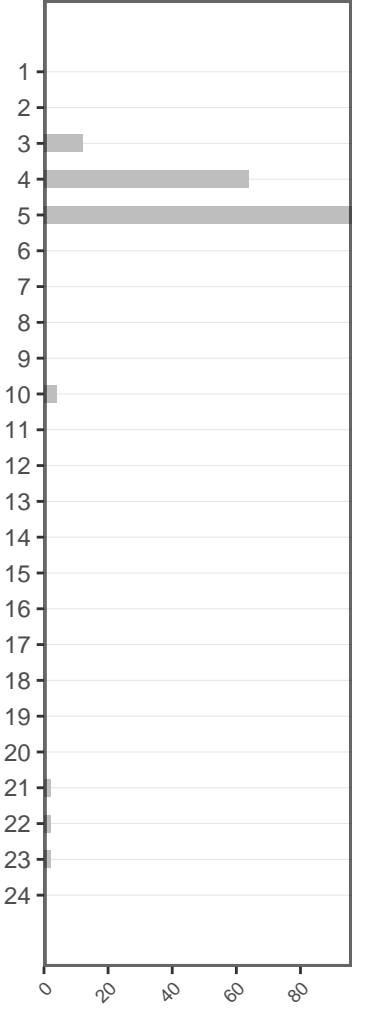
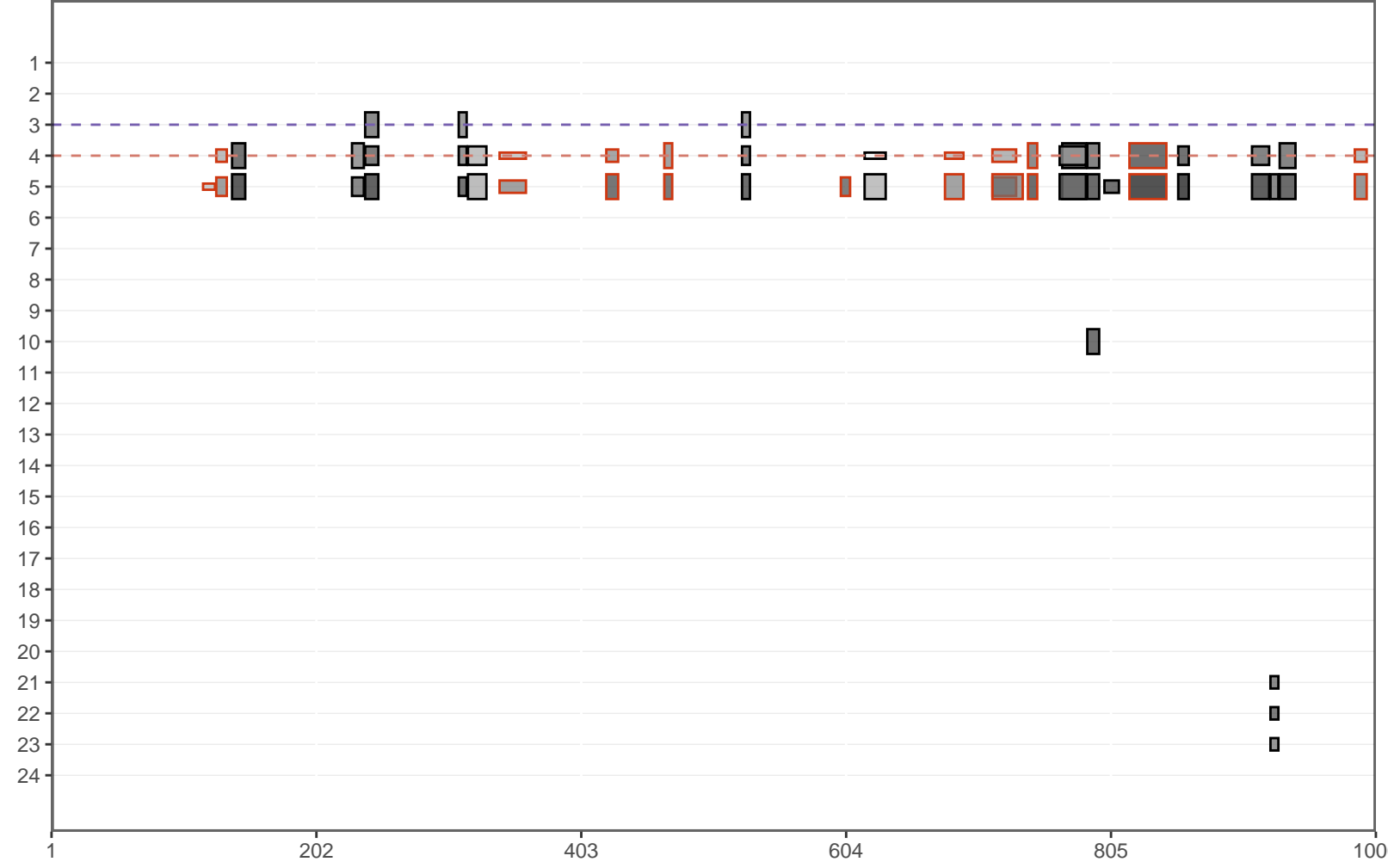
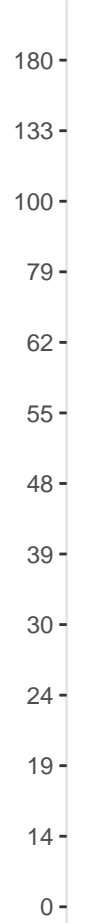
CPLLTGVPNLAMVETVDDKIANGLNRFVAGNIGRPLKLVFQVNTSGEETKSGVEFDGGLLVKHVTSNCPNLEFGGLMTGMPDVTSTPENFKTLVRCRSEVCKALEIPEFGOGEKSMGMSGDFELAVEMSGTINVRVGTSTFGAREYFKKGTN

NbL19g11990.1 leucine--tRNA_ligase_chloroplastic/mitochondrial-like [MW = 113.85 kDa]

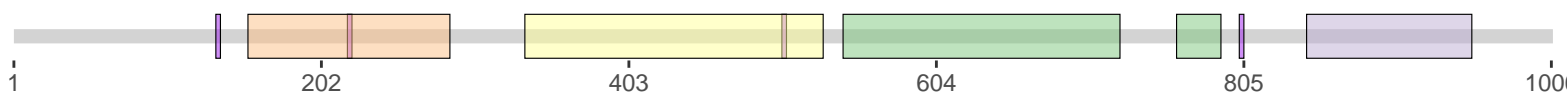


Molecular weight

Gel Slice



Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- Pf00133 tRNA synthetases class I (I, L, M and V)
- Pf09334 tRNA synthetases class I (M)
- Pf08264 Anticodon-binding domain of tRNA ligase
- Pf13603 Leucyl-tRNA synthetase, Domain 2

Protein sequence:

NFERPYSGEETMINASSSESGLDINGLPSKDAASRVQWLEKGGSGKQKYNKLRDLWLFARQRYWGEPIWFLDDTGGEGIPVSETELPLTPELDDFTPTGTGEPPLSKADSWVTKDPLSGKAAARRENTMPQWAGSGWYLRFDMPKNSCALVDKAKEGYWSPFDVYVGGAEHAWLHLLYARFVHKVLYDGVVSTGEPKGVNGHILGEVQYTAGKDDKGNLSADSEVLAELAEYNGEKIPEKVMKGGDFVLRKDPNPNVRLIARAHKMKSRGNVNPDDVLEI

NbL19g11940.1 light-induced_protein_chloroplastic [MW = 34.93 kDa]

No. of times detected



log(intensity)



Values from



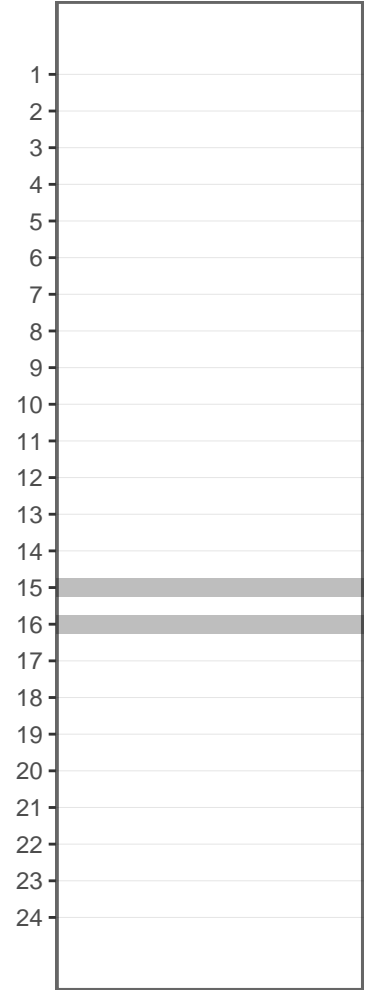
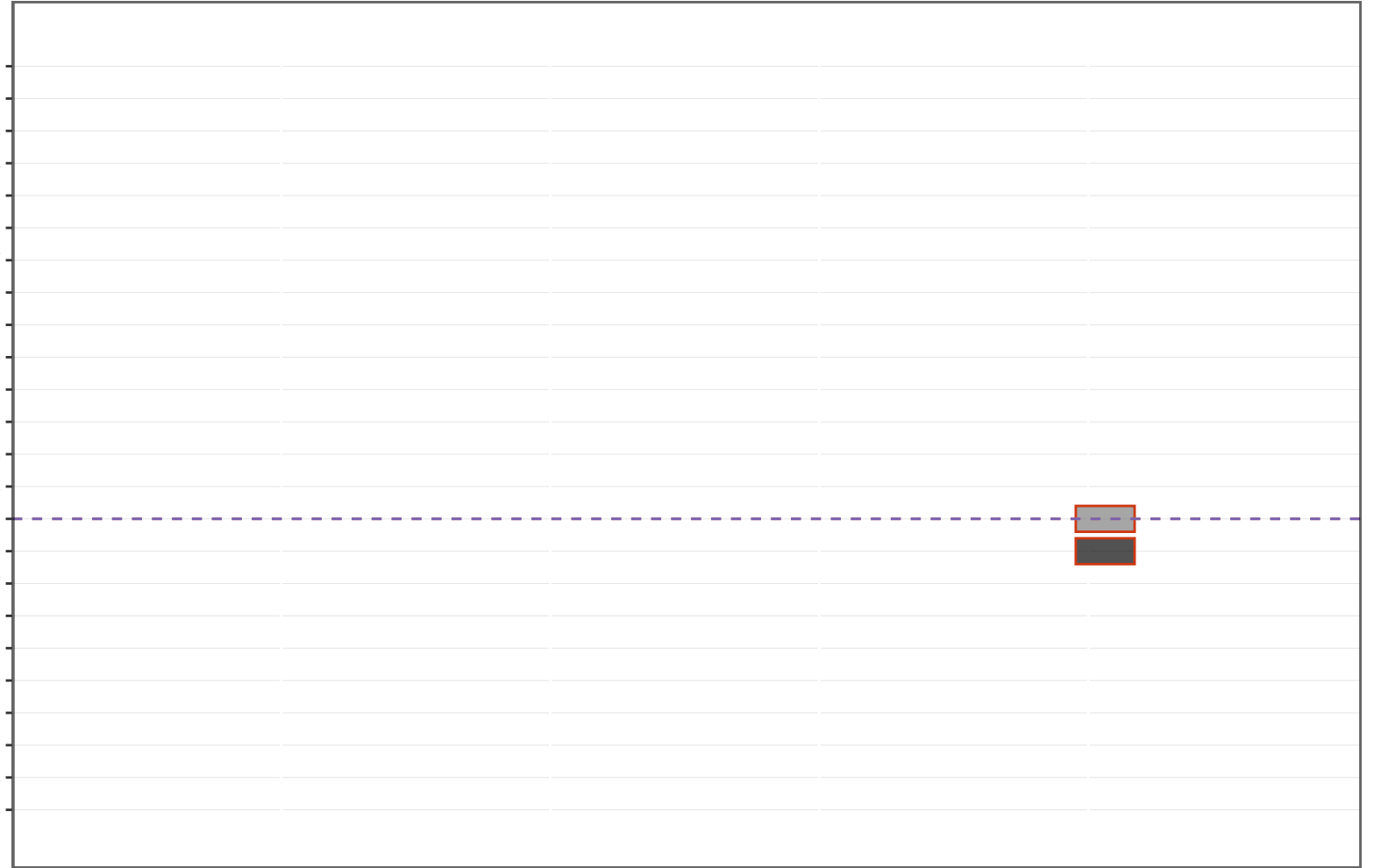
MW indication



Molecular weight



Gel Slice

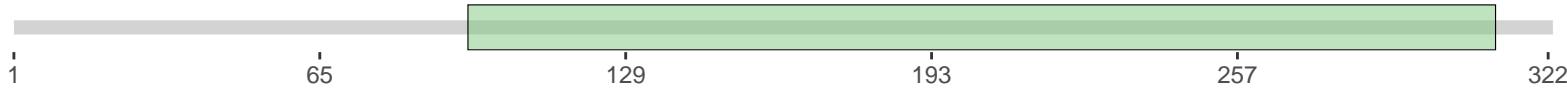


Protein length

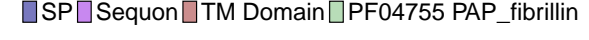


Peptide counts over 4 repeats

Pfam domains



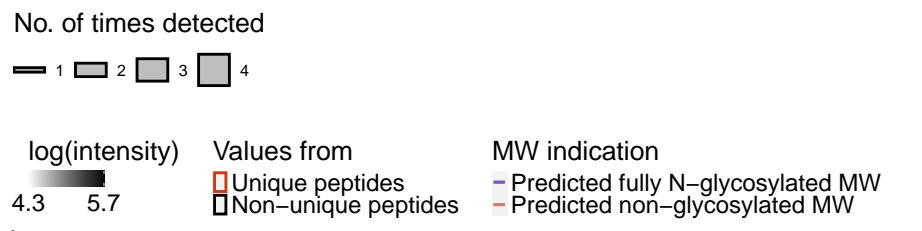
Pfam Description



Protein sequence:

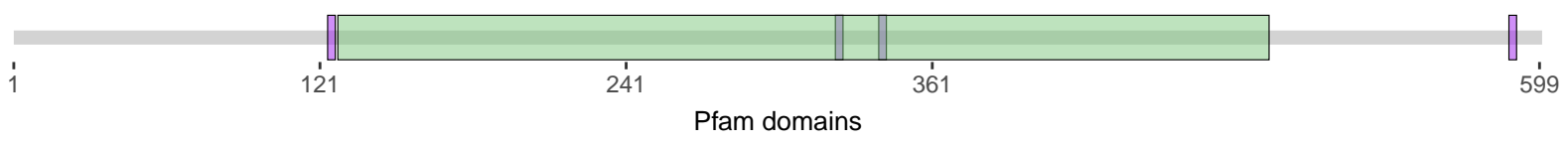
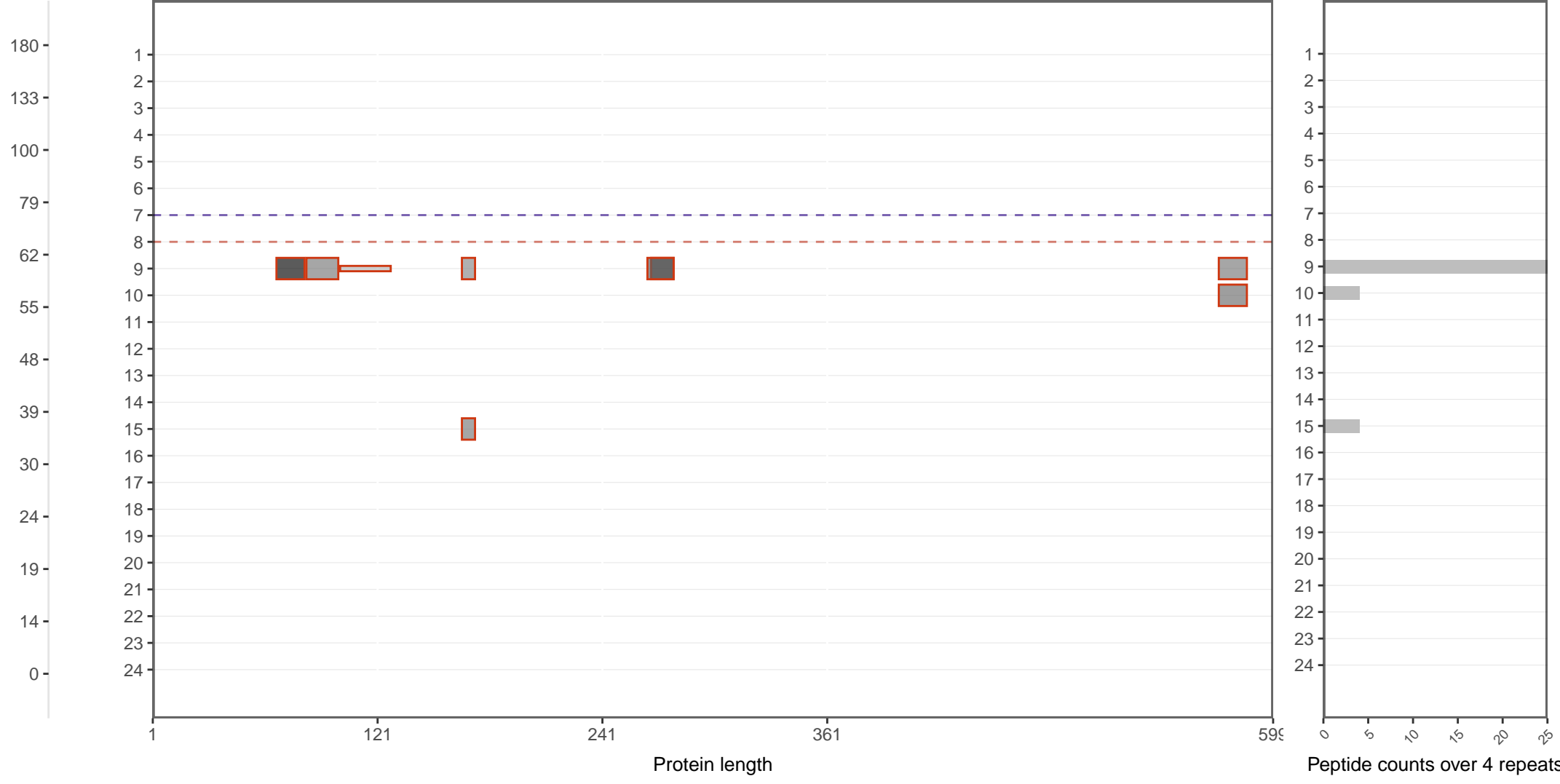
GNWLYATFSQSLFLLSRGFLPLVRIEIGDITDSETFAGVQNVVVFAGPLATTFSTTNAKFEVRSFKRVQKQKDFDEGHGTPQLTDSHELPEVFLGQKDLSPFKGLNIVGQYTABSVAKSISGQPKIPKIPNSNAGSWLLFTYLDDELIRISRGDGGGVFLKKEGSPLLKPT

NbL19g11930.1 pyrophosphate--fructose_6-phosphate_1-phosphotransferase_subunit_beta [MW = 65.17 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00365 Phosphofructokinase

Protein sequence:

GNVMDARSTGKYHFEVRLMGRASHITLICALGTHFNFTLIGEEVFANKLTKLNVTDAIDVIGKRAESGNYGVILPEGLDFIPEIQGLIAELNEILAHVDVDEAGVWKKLTPQCLELFEILLPLAAGEQLLLERDPHGNVQVAKIETKMLQMVETELGGRKGGGYNADFKGGSHFFDYEGRQGLPSNFDSTVGVALGVGAGALLGSKTKLISVGNLAAPVEEVTGGTALMDEVRRHKGKFKPVKIKAMVELEGAPPKFASKREEWALNRYINPQGFVGP

NbL19g11880.1 UBA_and_UBX_domain-containing_protein_At4g15410-like [MW = 32.69 kDa]

No. of times detected



log(intensity)



Values from



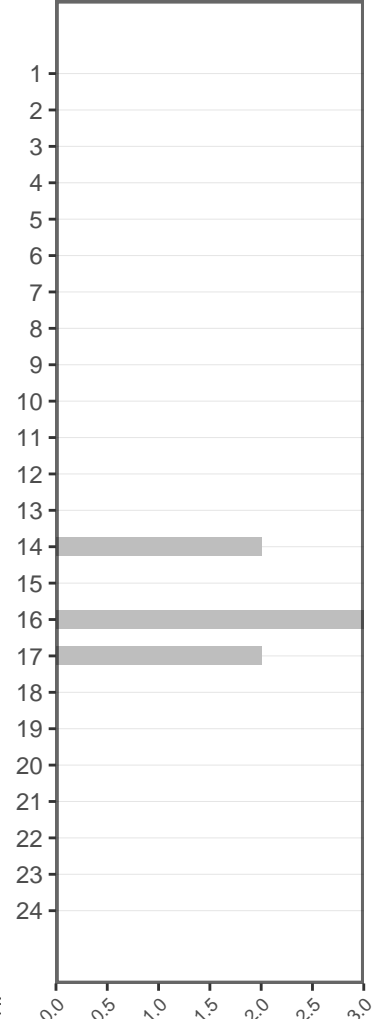
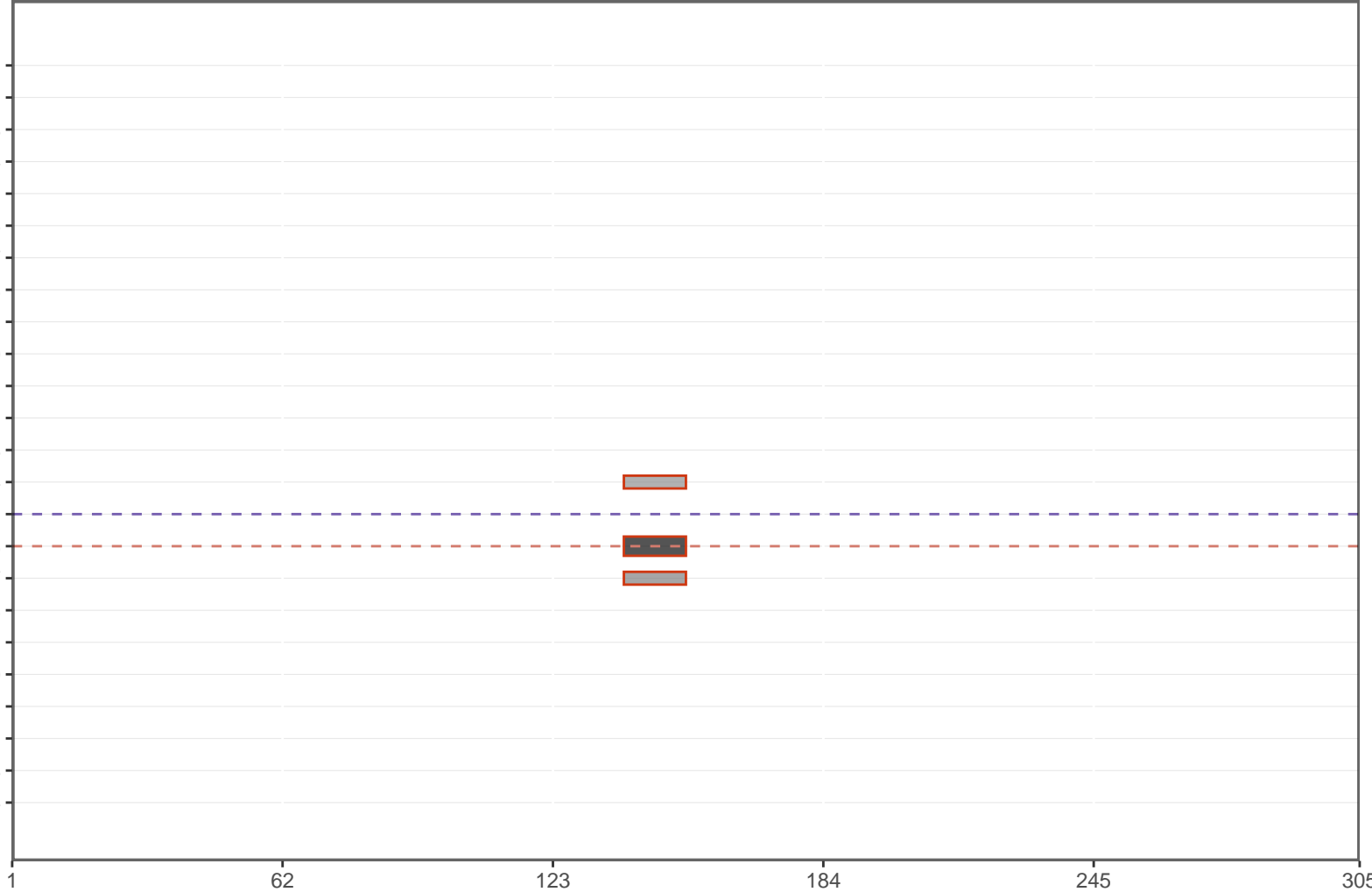
MW indication



Molecular weight

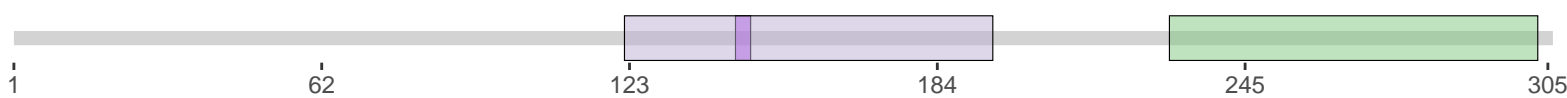


Gel Slice



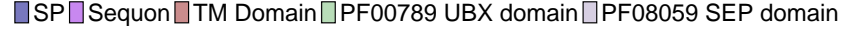
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IRLLDDPENASFLSESTKSECPRELPADTRBQVHGNLIRRDENCPPEKRGVDFQGVGRTLGSSSTPATSEPSASVPTSTAGAPTSILDGSLPSTSLGVRLEDGTRMVAHFNFGQTVGDIRAFIDASRPSNTRAVLLQTVGFPPRLSDPFGTREGAGLANSVVIQKPT

NbL19g11820.1 1-aminocyclopropane-1-carboxylate_oxidase-like [MW = 36.5 kDa]

No. of times detected



log(intensity)



Values from



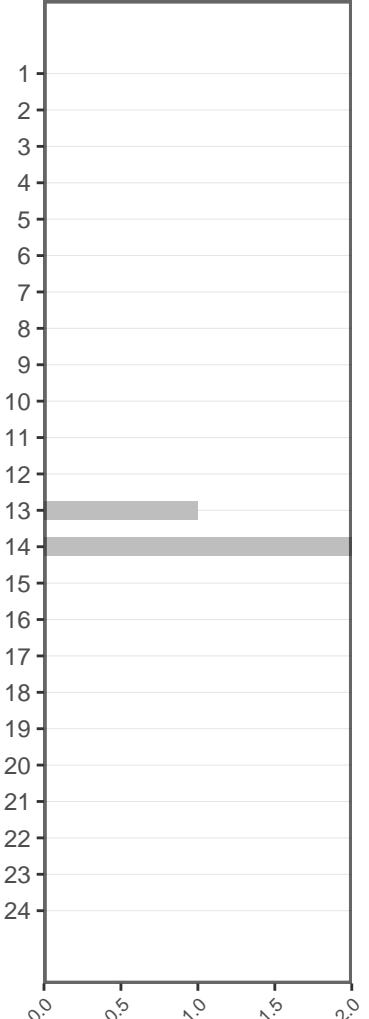
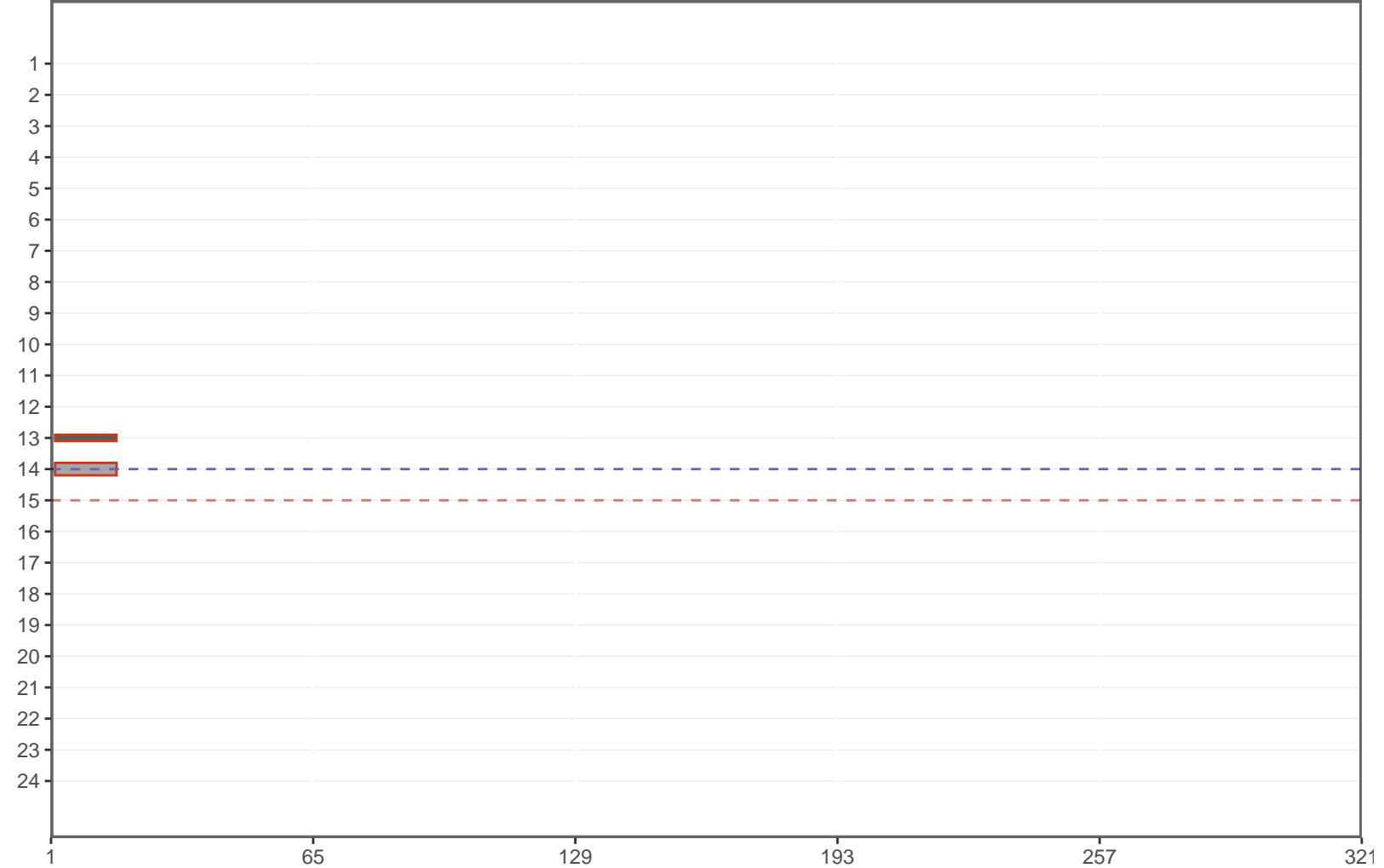
MW indication



Molecular weight

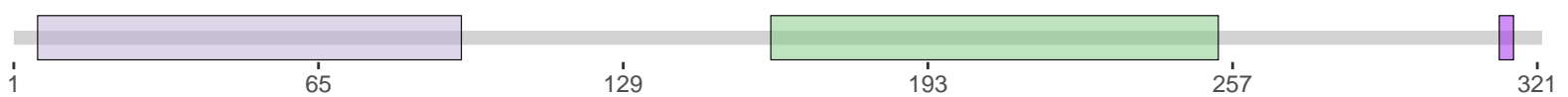


Gel Slice



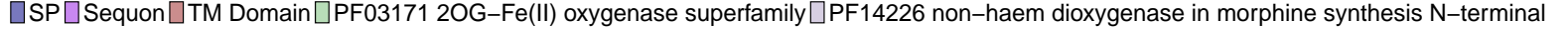
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KVIFYLKGPTGTGKVSNIYPPQPKPELIGLRAHTDAGGLLFGDDKVGSLQLLKDGNWVFPMAKHSIVNLGGDLEVTNGRYKSEHRVIAQDDGTRMSIAISFYNPQSDAIFRPAPELVEKAEENLKYKGFVEDYMKLVAGLGFQAKERFRFEMAKAVETTVNSPIETV

NbL19g11780.1 expansin-A13-like [MW - SP = 26.55 kDa]

No. of times detected



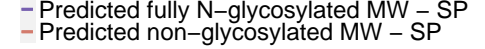
log(intensity)



Values from



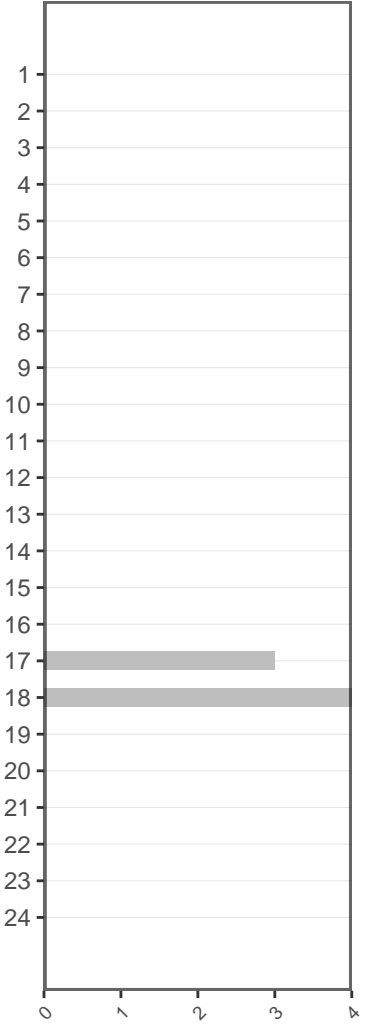
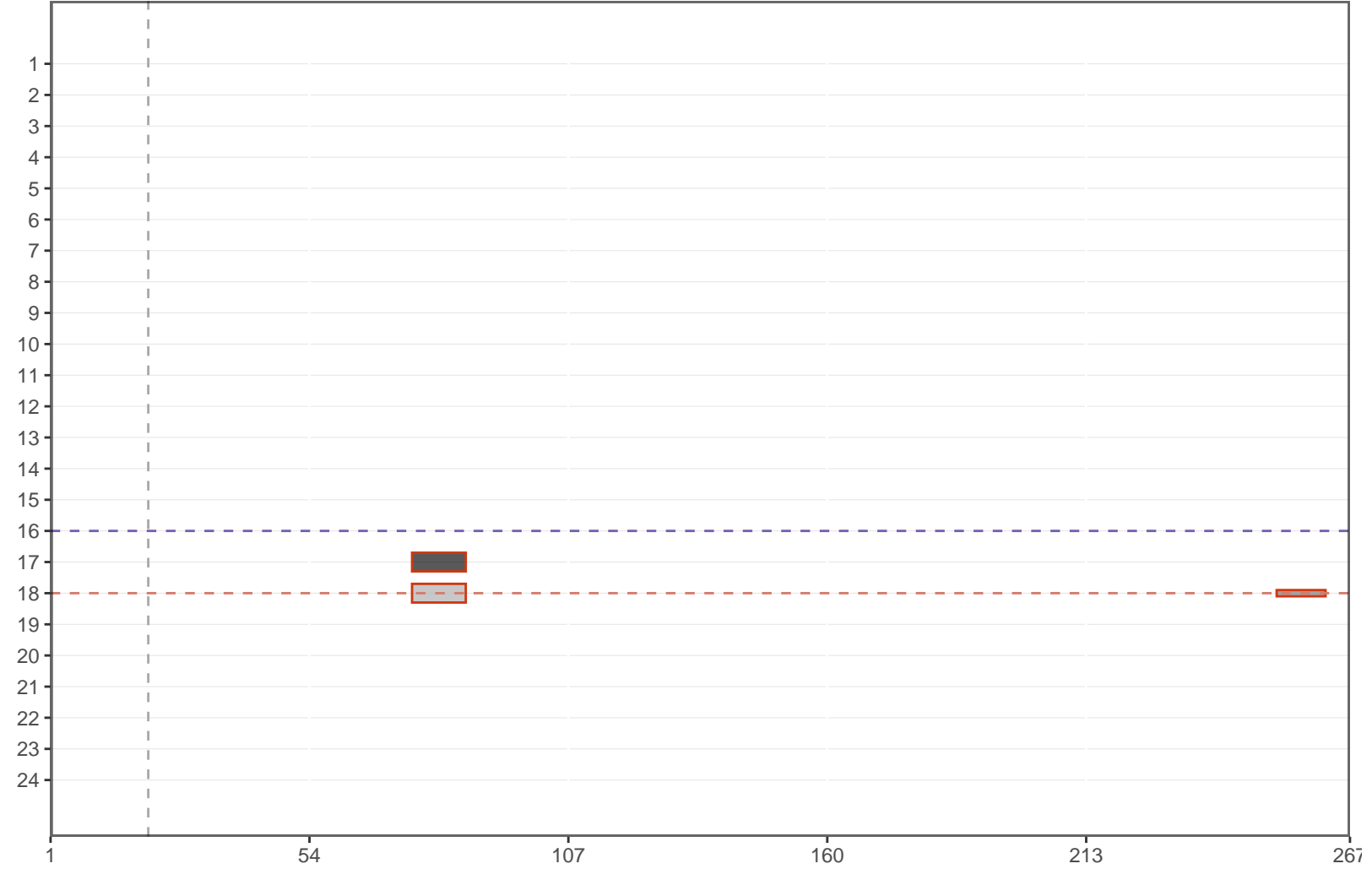
MW indication



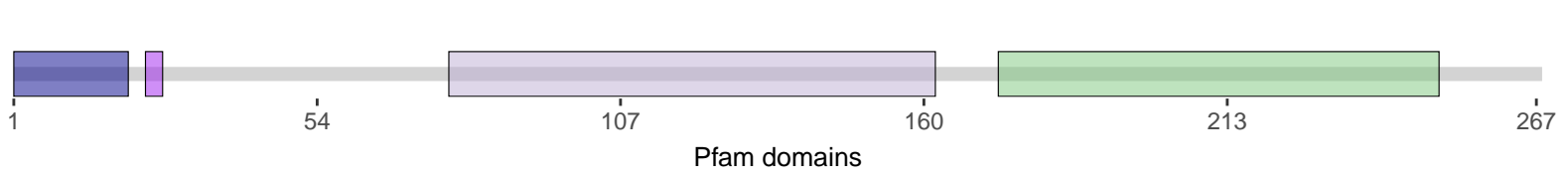
Molecular weight



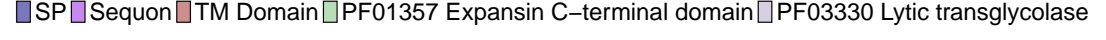
Gel Slice



Protein length



Pfam Description



Protein sequence:

NYGFDVDDGGHCNPNNAHFALPEAFEKIAWKAASNMFGYRRIKRRKEGGVRETMGGAGIFLSEVLSVMAGAGDVAIKIKGSRFGWLPMSRNWGGNWHNADLNKGPLSEFTSSDGVLTSTVNAFKWVNFQGTTEKGGFGSP

NbL19g11740.1 DEAD-box_ATP-dependent_RNA_helicase_21 [MW = 83.1 kDa]

No. of times detected



log(intensity)



Values from



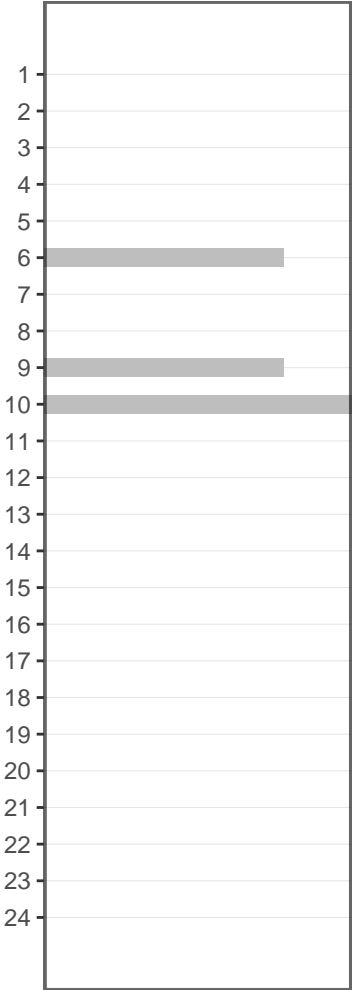
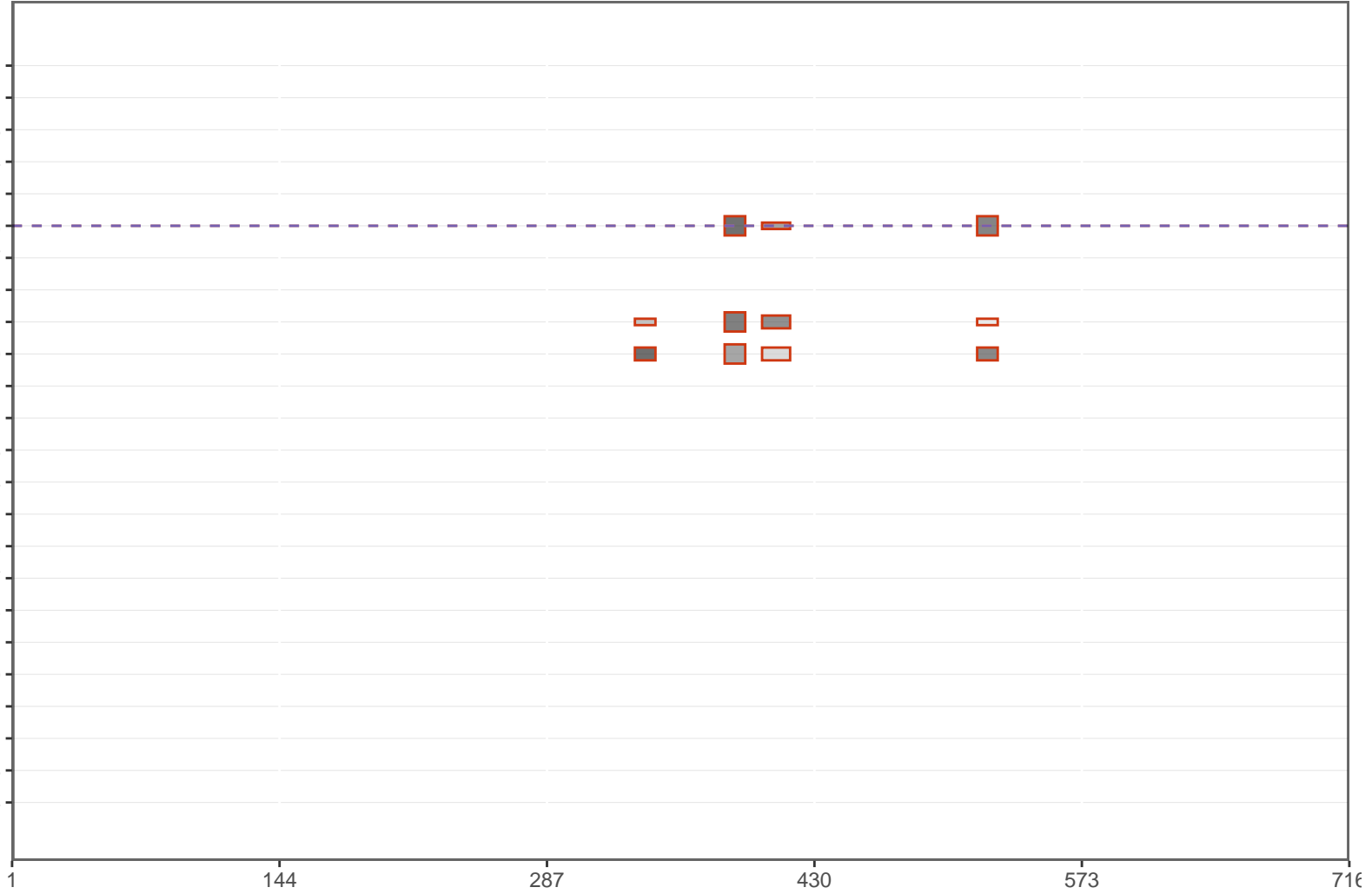
MW indication



Molecular weight



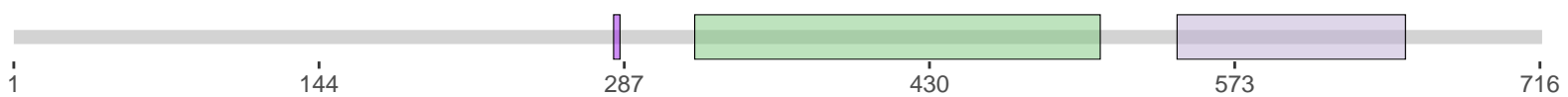
Gel Slice



Peptide counts over 4 repeats

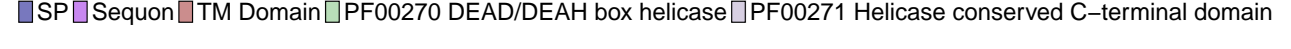


Protein length



Pfam domains

Pfam Description

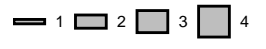


Protein sequence:

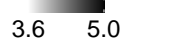
ETGSGKTAFLVLPMLTYTRLPLPSEENEAGFPYAVVAMPTRLEAQGIEDETAKFAHLYGKVVSVVGGQSEEGFRIRGGCEVVIATPGRLLDGLERYGVYKNGGNYVLEADRMIDMGSEFQVYGVLDAMPSSNMPENEDDELDKRYRITTYVFSATMPVWERLARKYLRFNPIVVTGTAGKTTDLTGHVFMVKESEKMYLKLLELDGDKTAVVFNTRKMGADTVAANLKDNGYRVTFLHGGKGGDQREISLEGFRTRKRYNVLVATDVAWRGIDPDAIVVNYDM

NbL19g11550.1 coatomer_subunit_beta-1 [MW = 98 kDa]

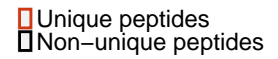
No. of times detected



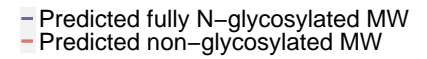
log(intensity)



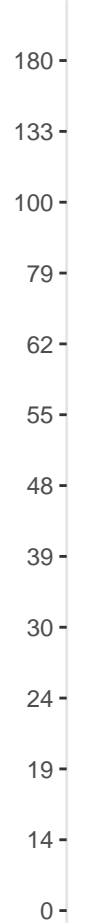
Values from



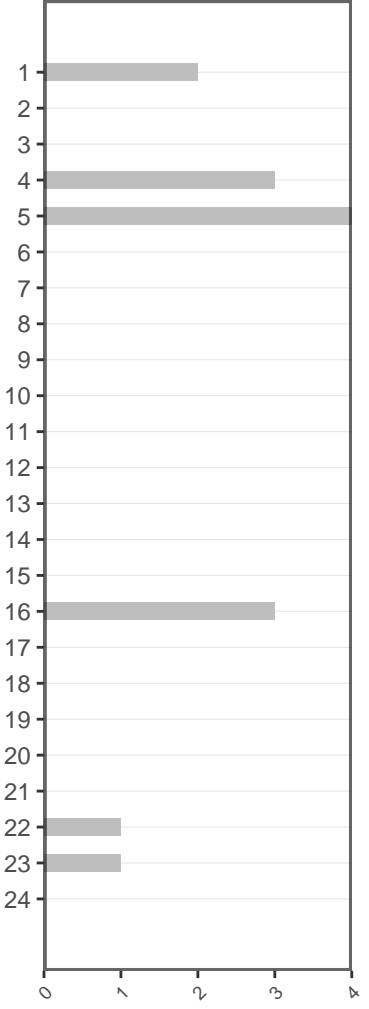
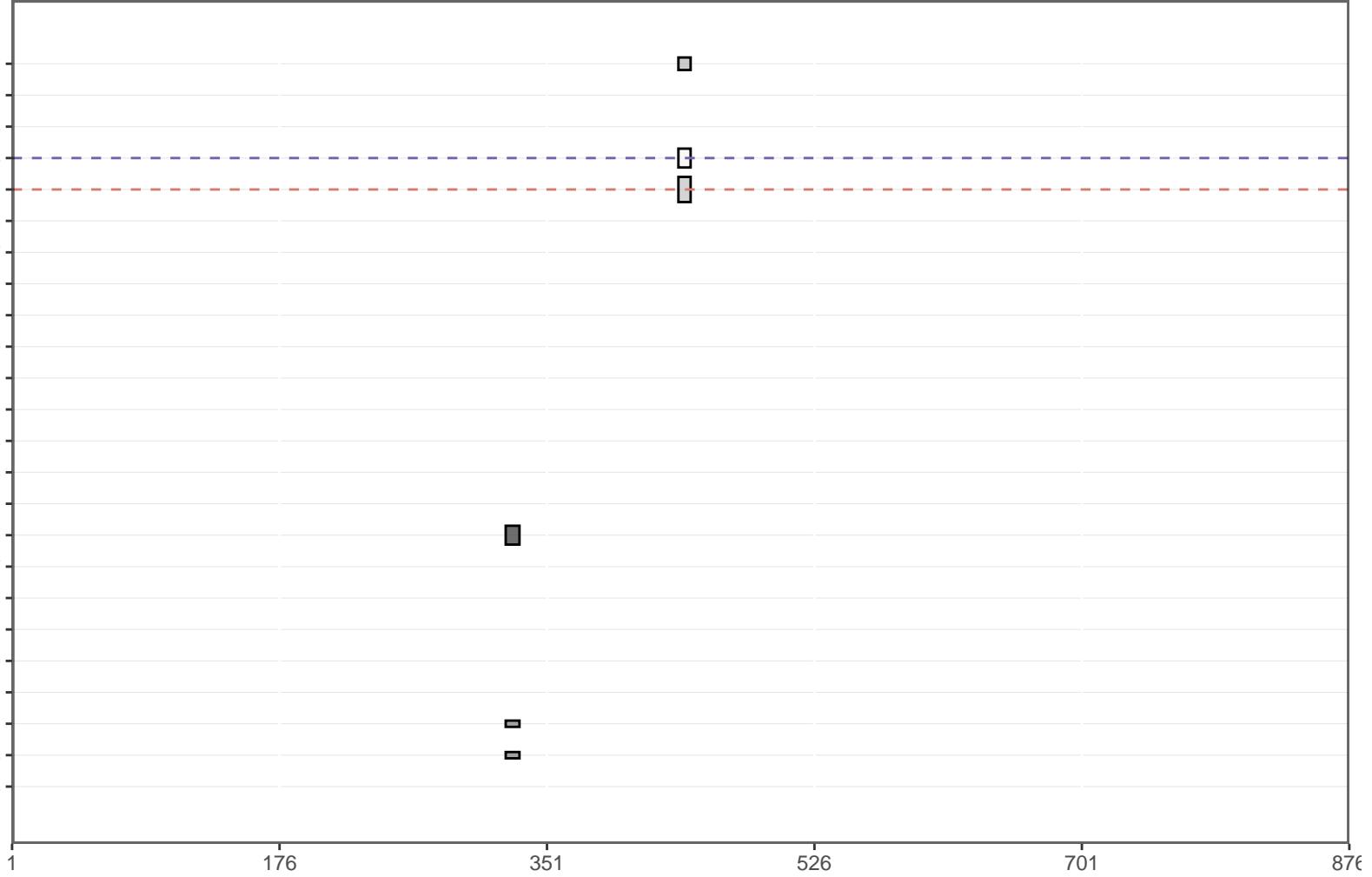
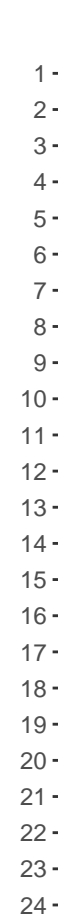
MW indication



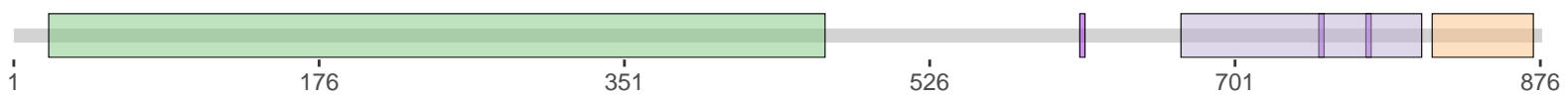
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

*KLRVSVTRLLDTFYQIRARVCGGALWIGEYGLSLSEVEVGGIATKGGDLFFYVSEEESEATDSKKTTPGANSITTVSSRRPMLADGTWATGSAASETVFSPATVGGSLITGNLRLLLTGDFLGAAGVAGTLKILRLLEEVPNSNEVNAKTTNALLIMVSIQLGGGSLVLPHPINDSYDRIVLGRLLCNTGDDEVQIWLSSGRESFVKMLSDKGLRETEEKAKAGTFSFGPDLDYFVHKSRKRMGSLGLEDAVGGDDKHATGEFVNDENDANKLNRVLTGTFSDP

NbL19g11520.1 protein_YeeZ-like [MW = 39.32 kDa]

No. of times detected



log(intensity)



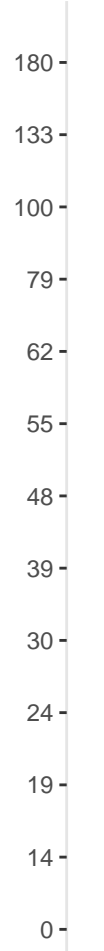
Values from



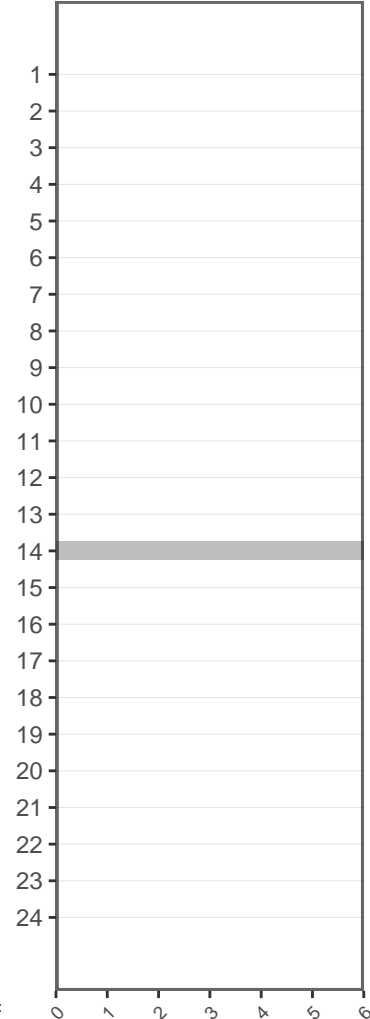
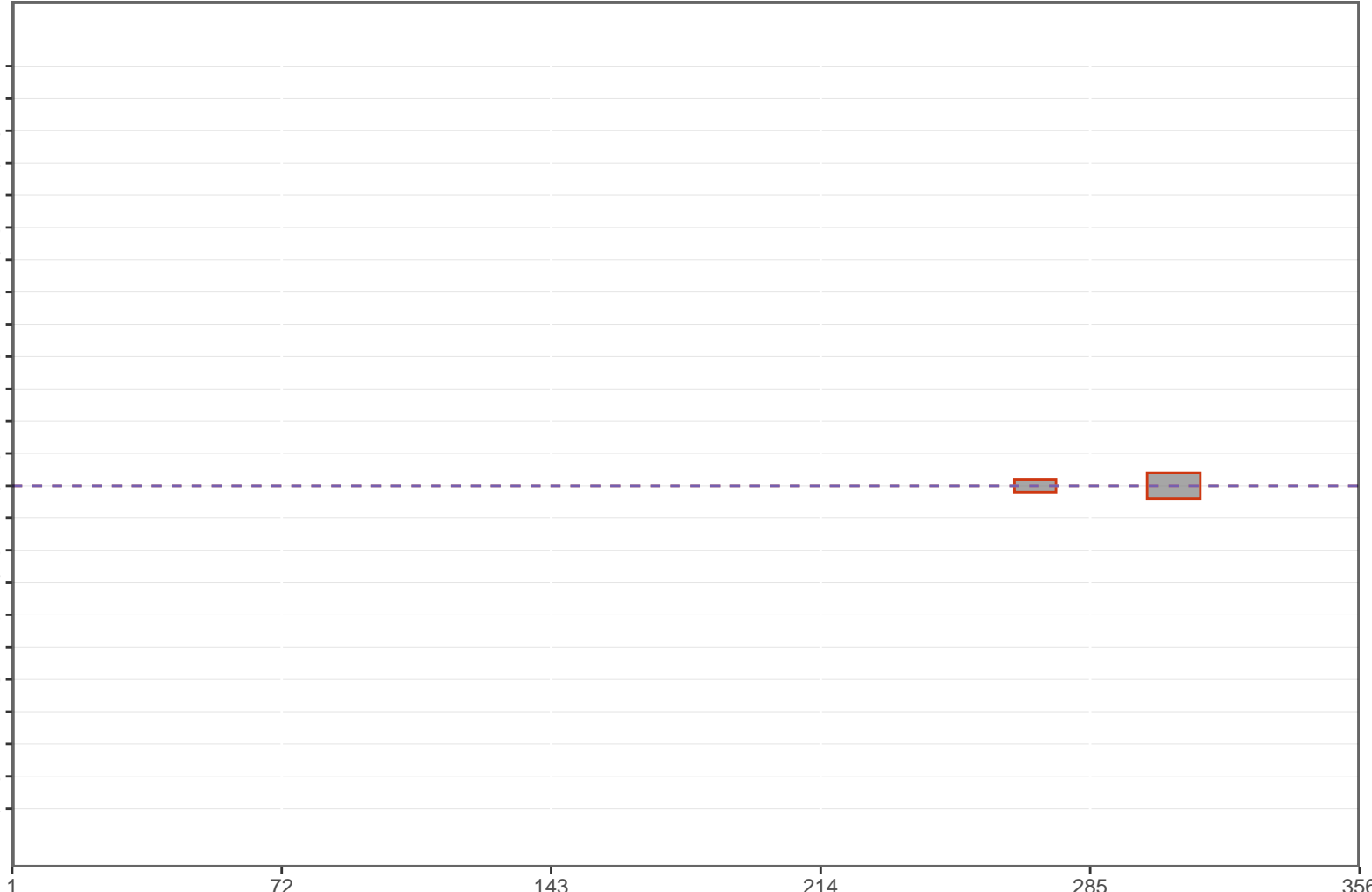
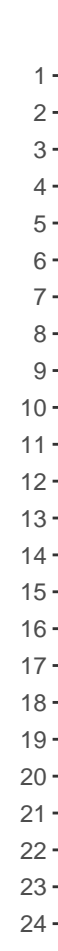
MW indication



Molecular weight



Gel Slice



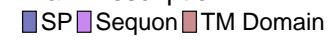
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

GGAWYDEKFFPRPRTESAKARMAAEEGWLHLACDVGVTAGIFRLGGIYDGRSAIDTLKQESLSKGVMRFRSHYTSRIHVAIDICGTLKASIGRPFPGKHYNVVDDDPARELVFTFARNLVEKIKWPHFTSNKSEDAASLNPQGSARGEKRVSNKRKSELAVRLLYPEYEGSLRLEIEMHENPFRGS

NbL19g11360.1 putative_endo-13(4)-beta-glucanase_2 [MW = 80.36 kDa]

No. of times detected



log(intensity)



Values from



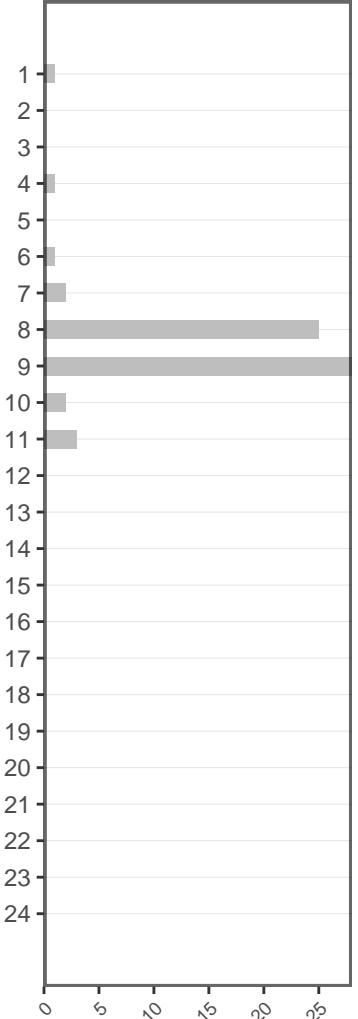
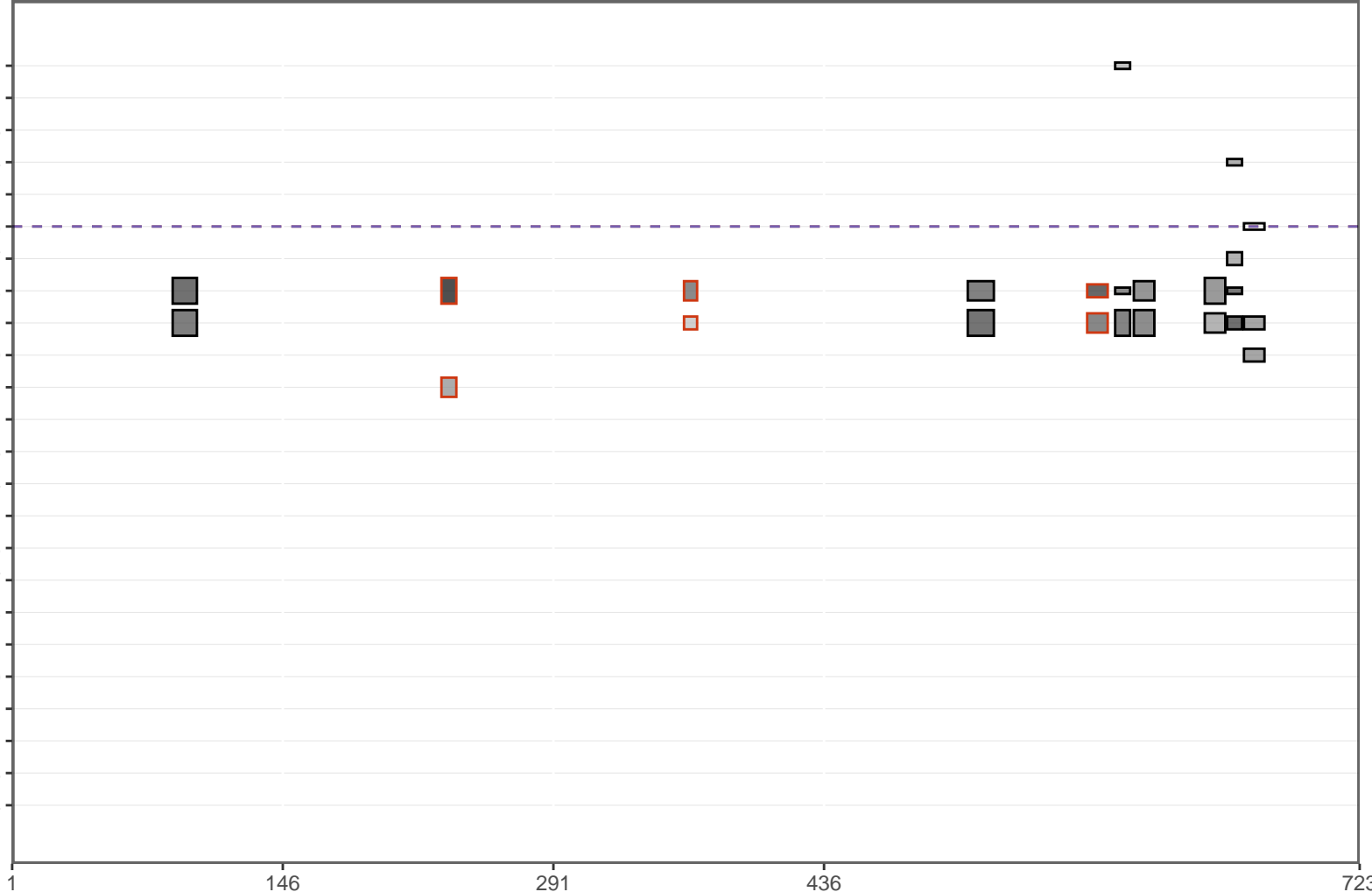
MW indication



Molecular weight

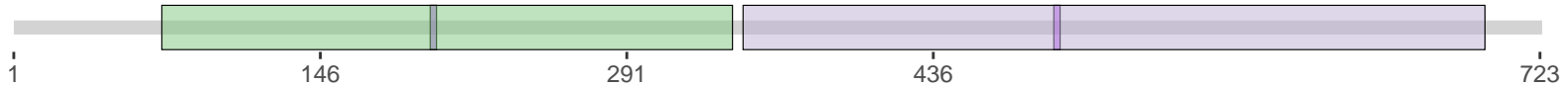


Gel Slice



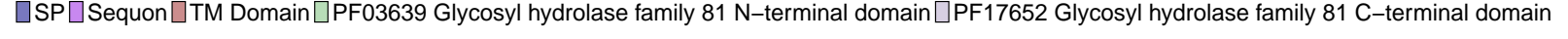
Protein length

Peptide counts over 4 repeats



Pfm domains

Pfam Description



Protein sequence:

SEIDALNKDYVSLLDKSGHFTTSYFYGKLIARAARLALAAIEEYCVLEIVIPTRIRFLKDTVEPWLVEGTFEANGFFYESKRWGGIVTKQGLDGGADFGFGVNDHDFHIFHFLVAIWLAKIDPWRGRKYRPOAVLMAADFVNLRRRANKYKLRKFDLWKLHFWAGGLTEFADGRNGESTSEAVNAYSAALMGLAYGDTNLVANGSTLSAFEIHSAGTWWHNYKEGSLYGDDEFTKDNRYVGVVLVSNKRDSGLWFAPEWREGRLLGKVLPLPTEVLFSDVQFYKLVLEVTLL

NbL19g11280.1 60S_ribosomal_protein_L22-3-like [MW = 13.87 kDa]

No. of times detected



log(intensity)



Values from

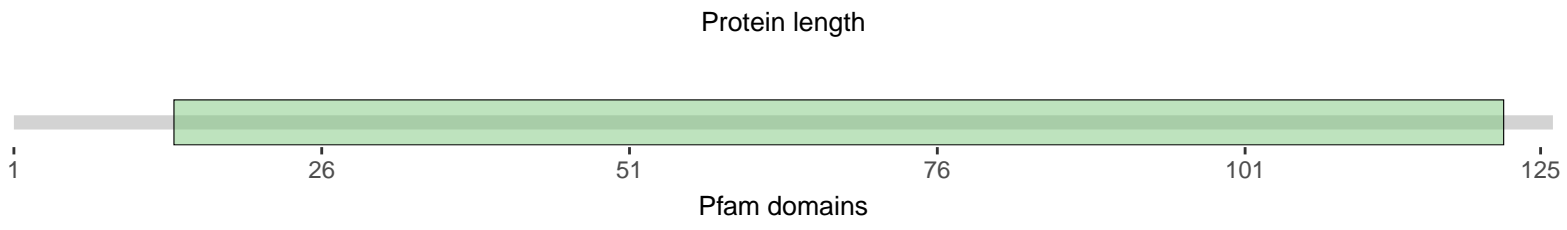
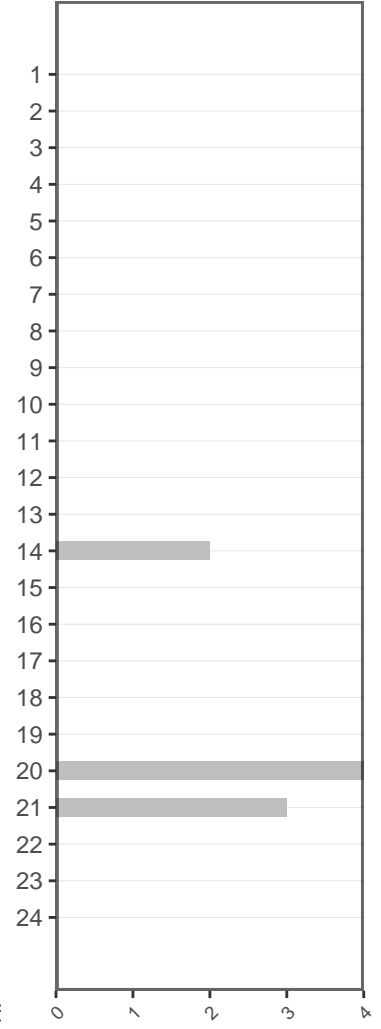
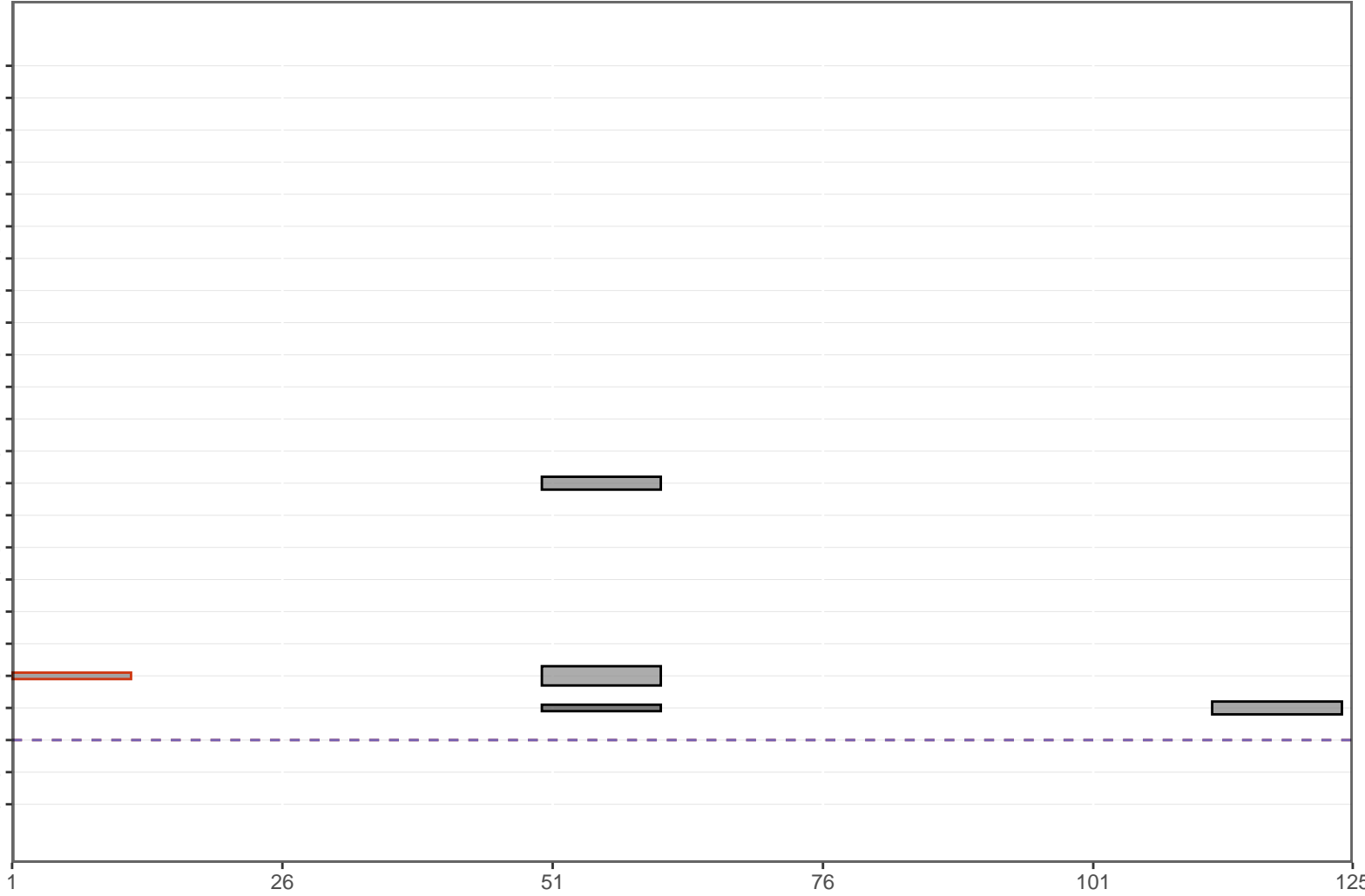


MW indication

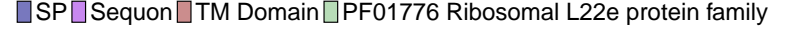


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

AGALGDSVTVTRDKNNTITVTSNFAFSKRVLYKLVKRYLKKNNVVDLRLRVIAANKDKNLYELRYFNAIETEAEED*

NbL19g10960.1 uncharacterized_protein_YwbO [MW = 26.45 kDa]

No. of times detected



log(intensity)



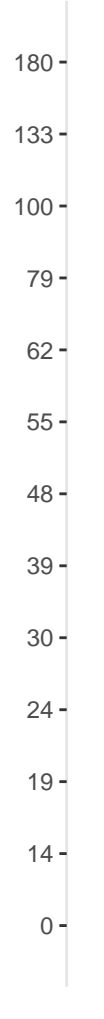
Values from



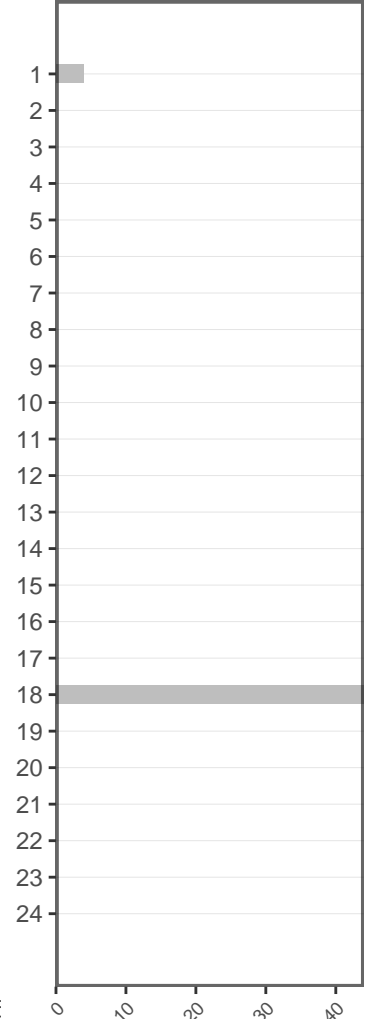
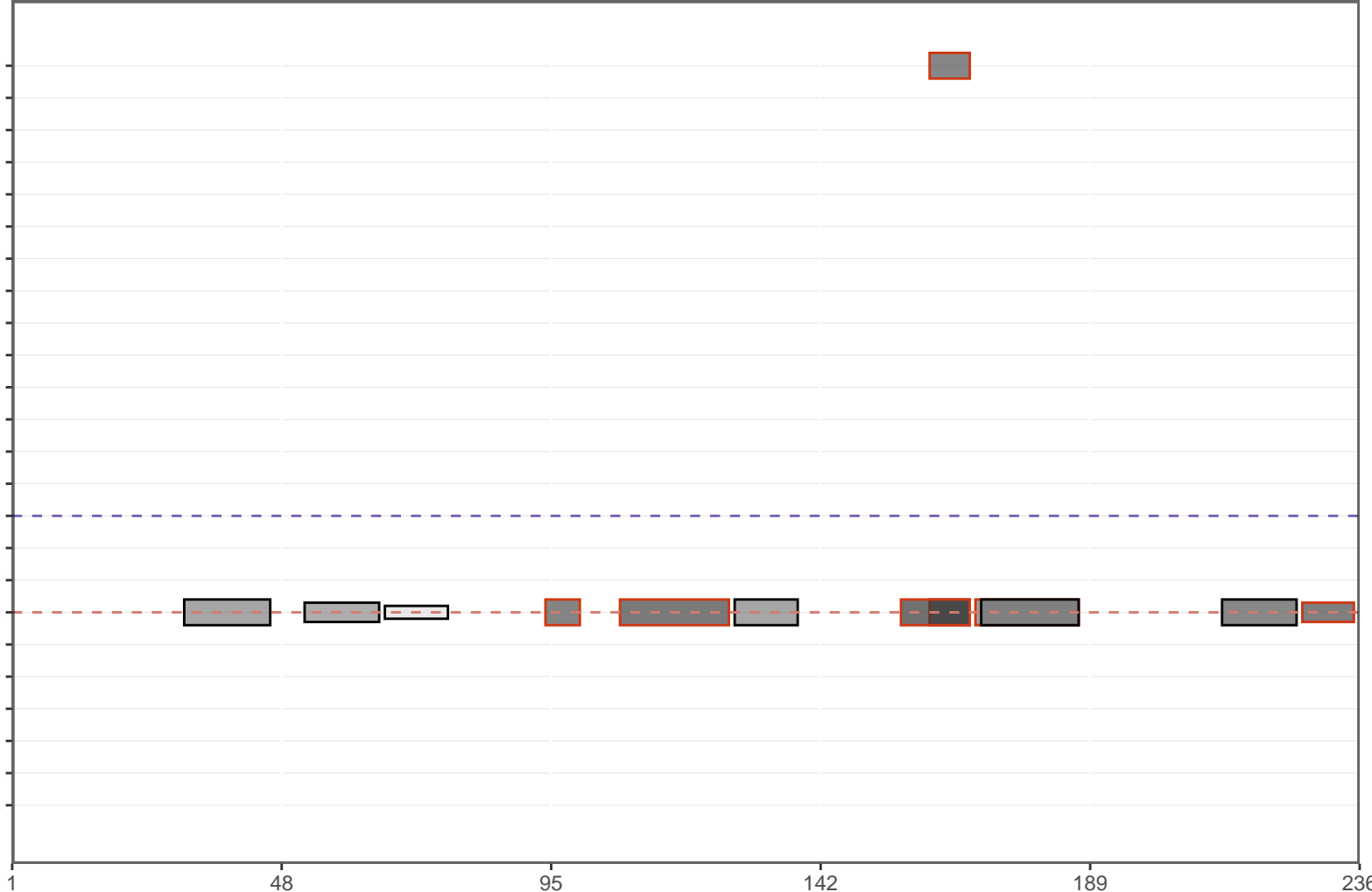
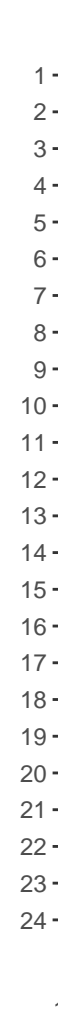
MW indication



Molecular weight



Gel Slice

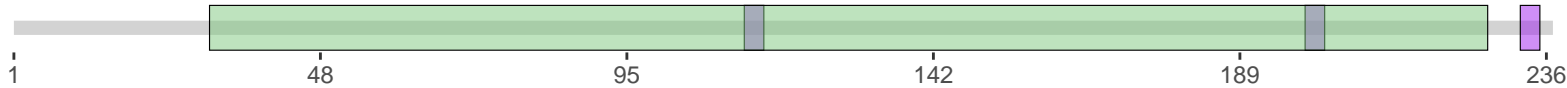


Protein length

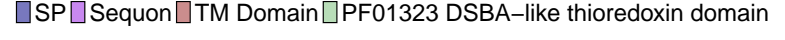


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KGLGLEYNMSGVITGSSLDHSHRLLYFAGGGGLKQNNLAELFLGVFTQGRYIGDRFLVEAARKVGVGGAADFLEDPNNLKEVNEELQYGSNIGVPHFVNLNKKYQLSGGQPPESFRFAQAANTVA

NbL19g10920.1 probable_tRNA_(guanine(26)-N(2))-dimethyltransferase_1 [MW = 65.92 kDa]

No. of times detected



log(intensity)



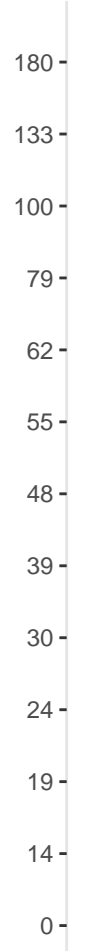
Values from



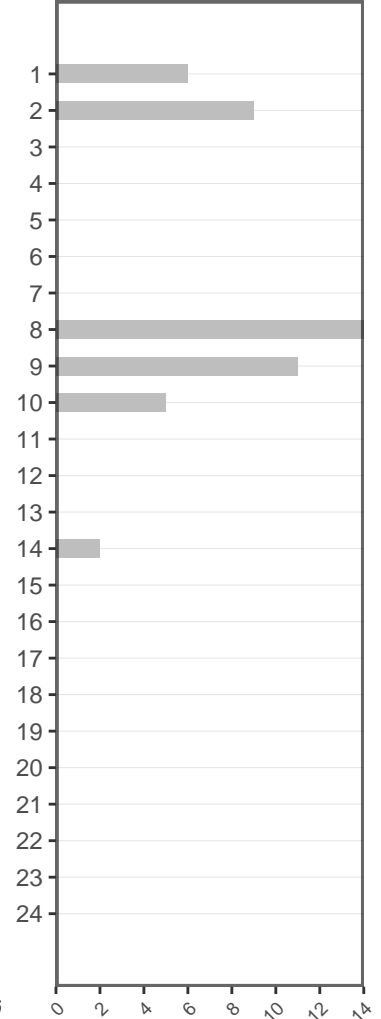
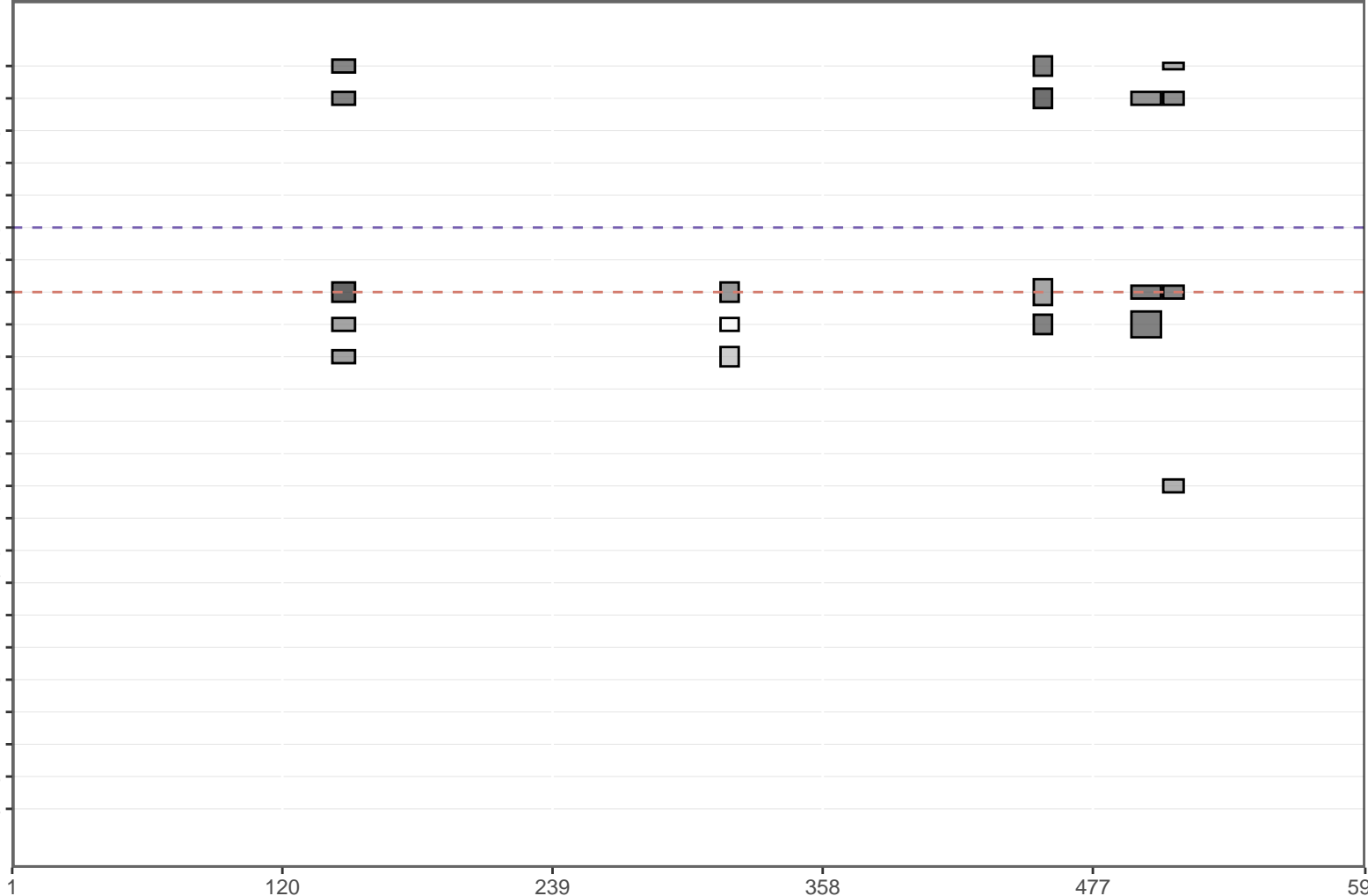
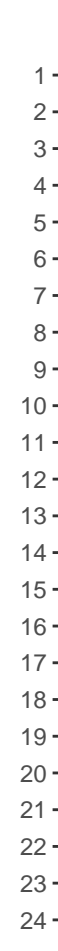
MW indication



Molecular weight



Gel Slice



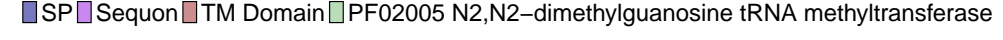
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IESHANRYRYIVPLVLEVMDFYRVEVRYTASDMKSTPLKLSYVYDCTGDSFHLGFQRTVSKNNVRYLPGFGRVWSDGSDGKFKFMGGPIWASPIHGDGEVVAALADVNSMKDRYFVERISAVLTFSEELPDPLFLSLHNLGATLKGTSFSAVFRWAVINGYRIGETHVNFPLGLKTDAPMDVWDMRGWKNHVPKADPDGAGSVLAKEPVLGANFSAIALEKADAKKVARFLNPERHHWGPKLKLRAGRGTSKHVSLGKALGINNHENDGSN

NbL19g10780.1 uncharacterized_LOC109206144 [MW = 14.58 kDa]

No. of times detected



log(intensity)



Values from



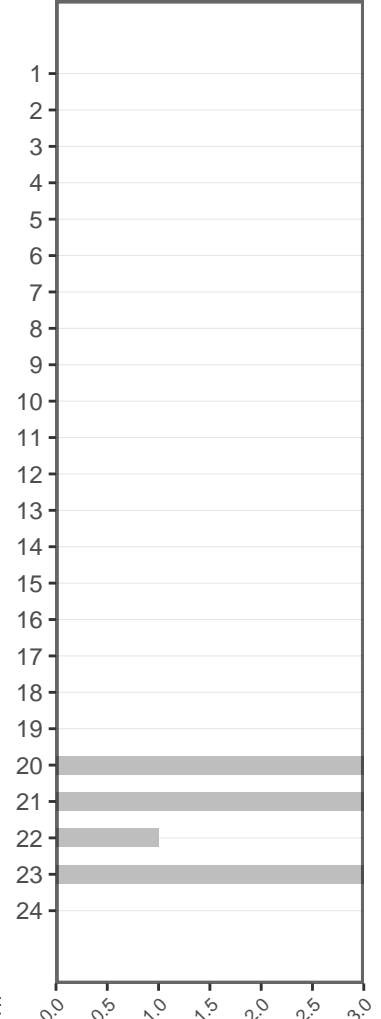
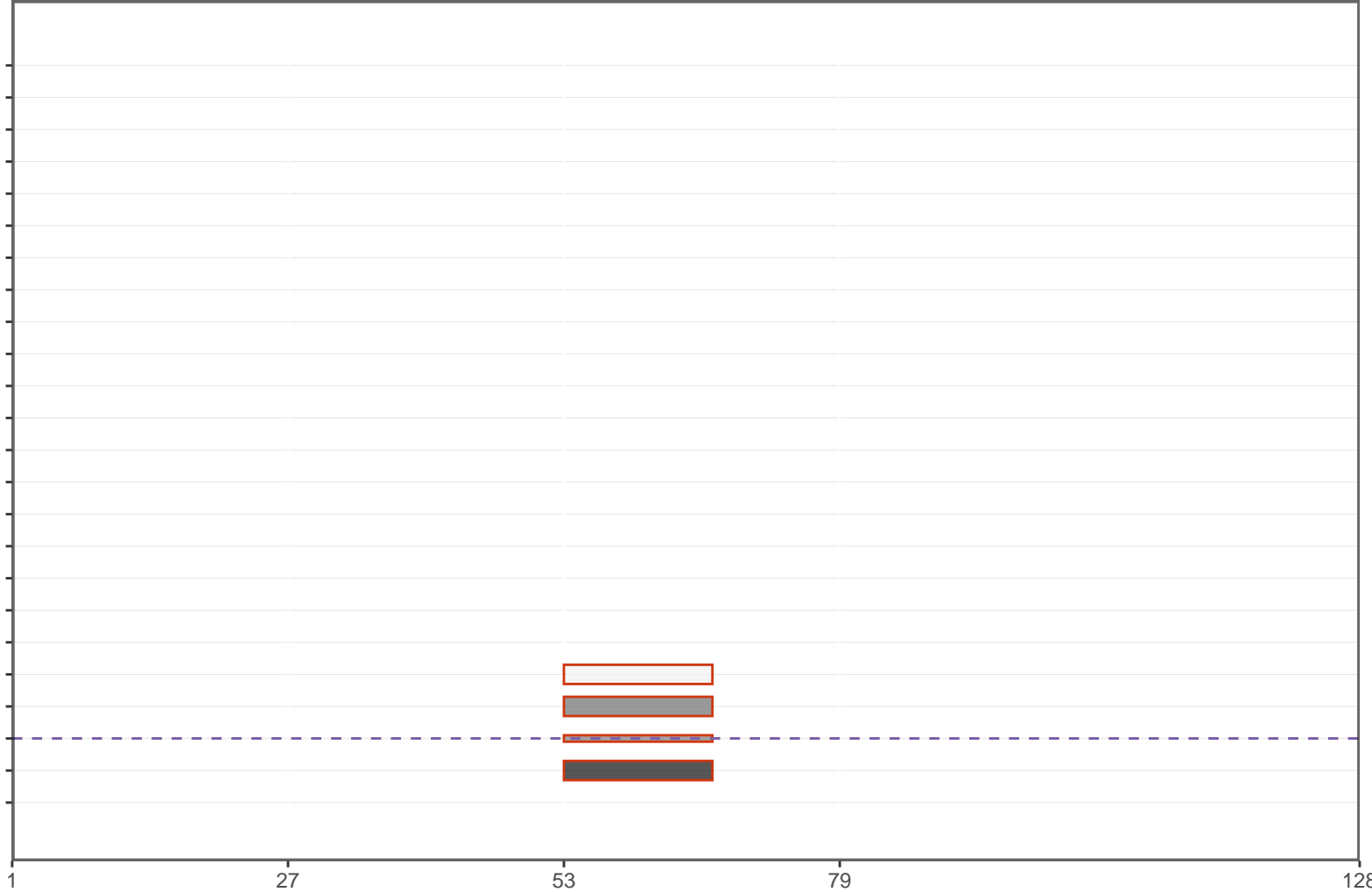
MW indication



Molecular weight



Gel Slice



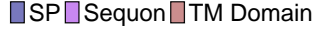
Protein length

Peptide counts over 4 repeats



Pfam domains

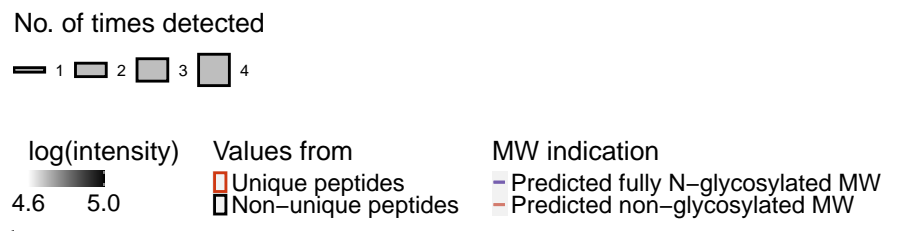
Pfam Description



Protein sequence:

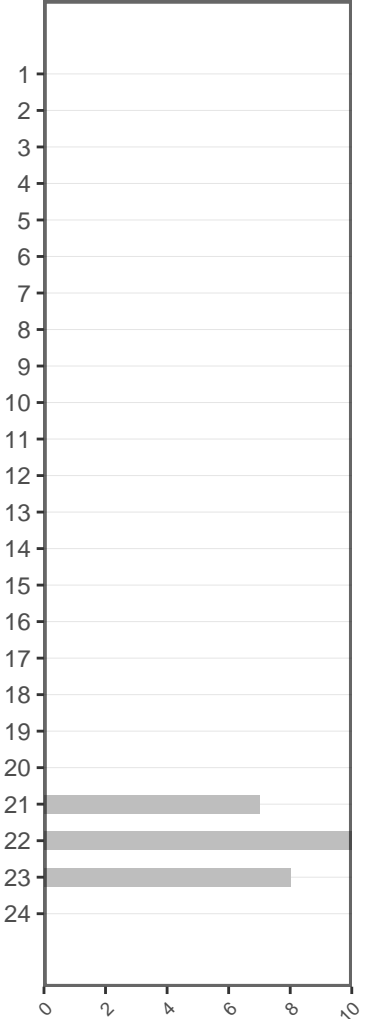
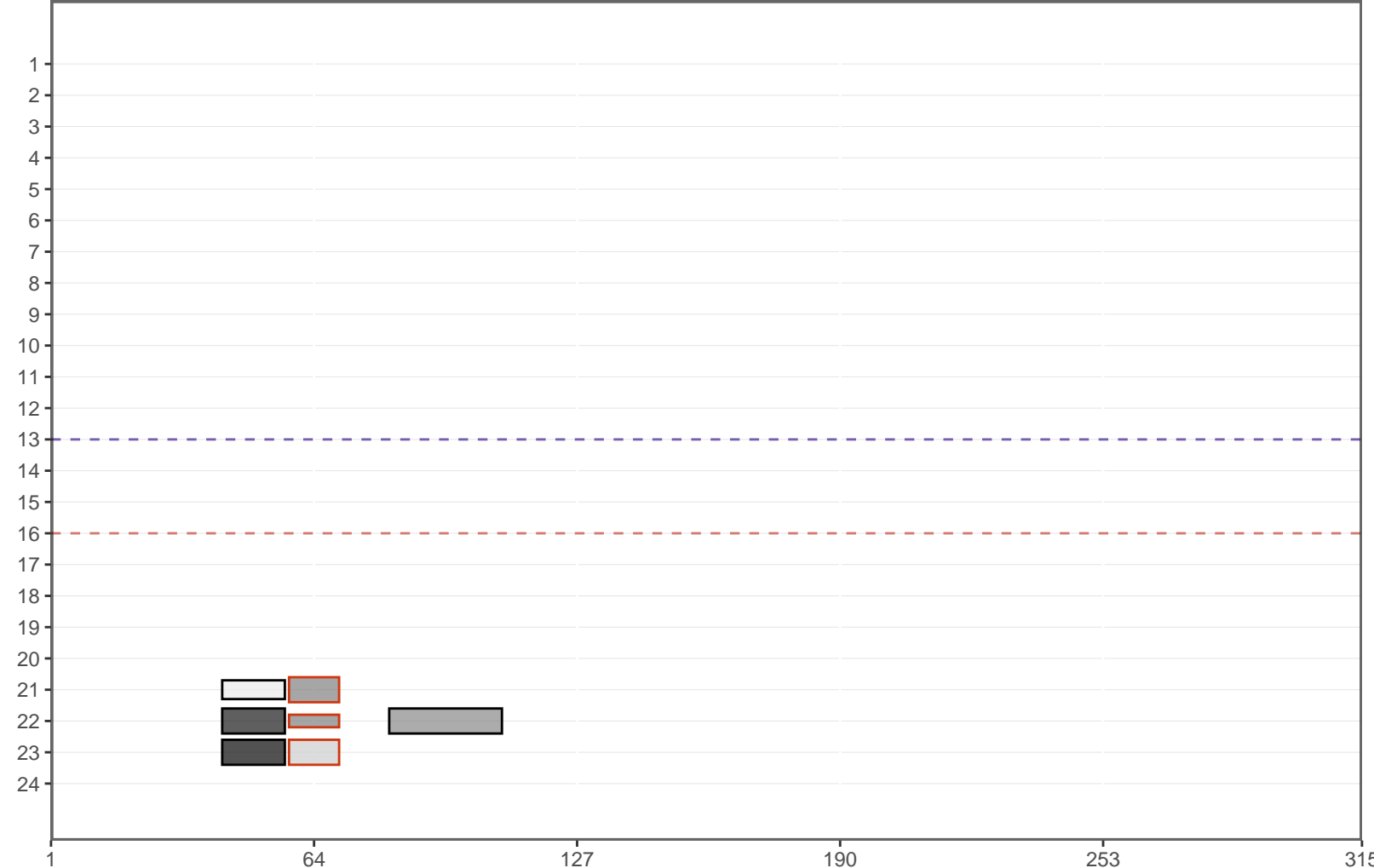
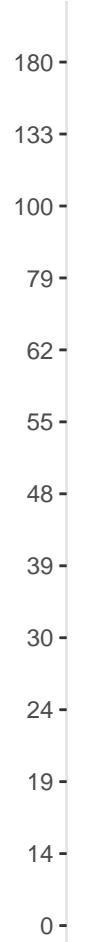
KAIVVPTSDPETVFDIKYFPRDGRNRNRPPIRRTFLNKADVEKMMMEKRTFDVNDFFQPIYIAKVEEDMDAIGGGYK*

NbL19g10690.1 glycine-rich_RNA-binding_protein_3_mitochondrial-like [MW = 31.67 kDa]



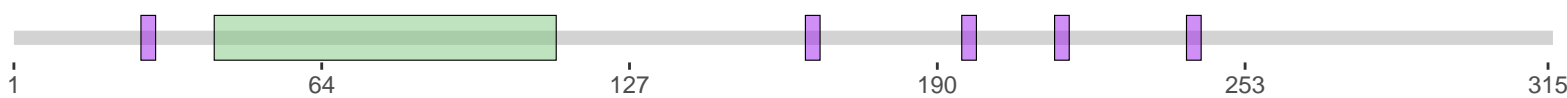
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

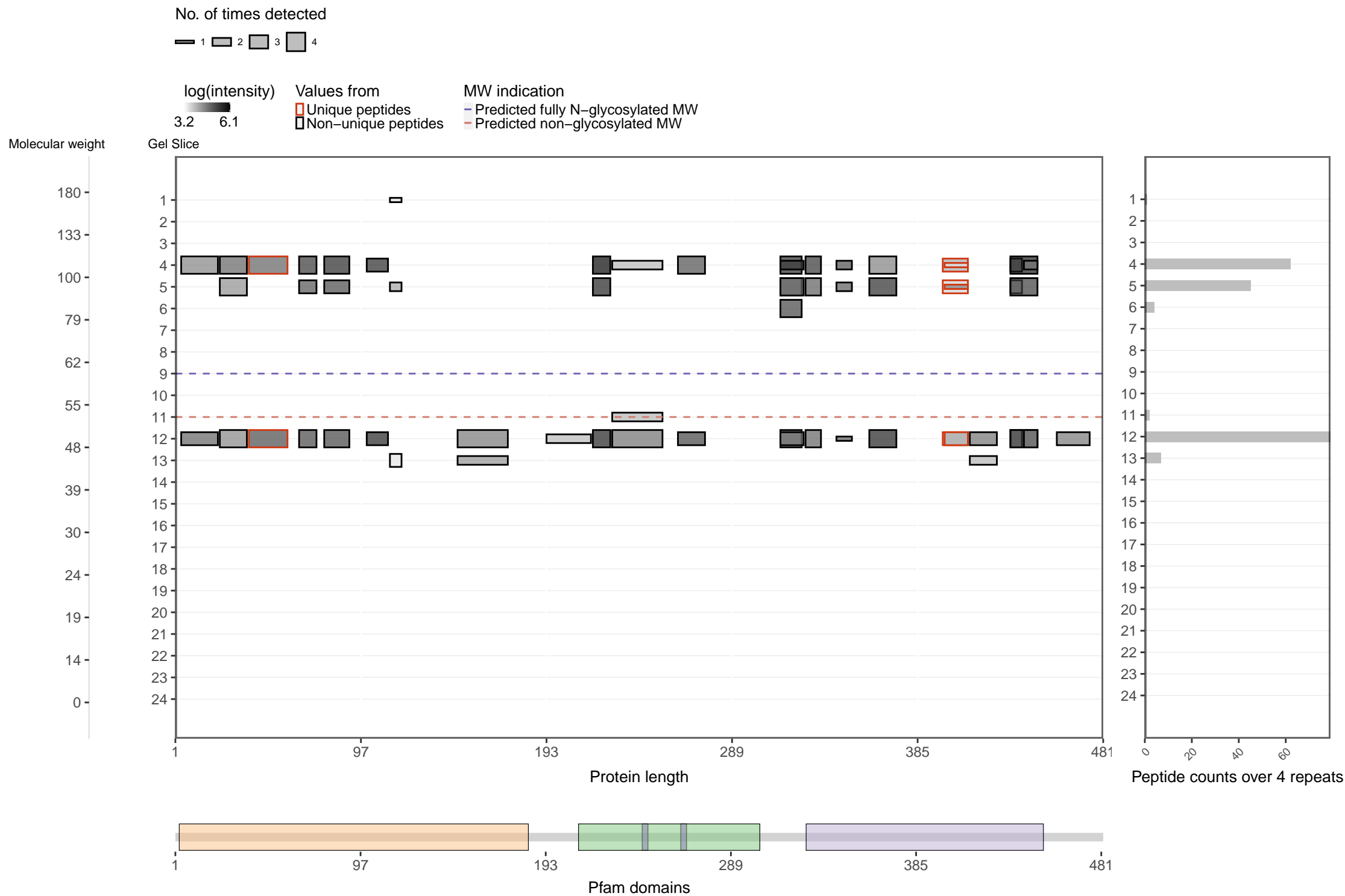
Pfam Description

- SP
- Sequon
- TM Domain
- PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

Protein sequence:

GVAAASNYGGGGYGNBSGFNYGSEGGNSAGAGGYPPTNNYGGGFSAGNTSAGGYSGYGGGSMYGNDSFPAEGGNVGGGVYGSABYGNIPNSNYSGGGNSFSGGGYDGGNSGNGFGEESPAAGFNNGGEGVGVDDGTGSAVNEIEGQETSEGNVYRDDDEDFKDFANTRG

NbL19g10590.1 UDP–glucose_6–dehydrogenase_3 [MW = 53.07 kDa]



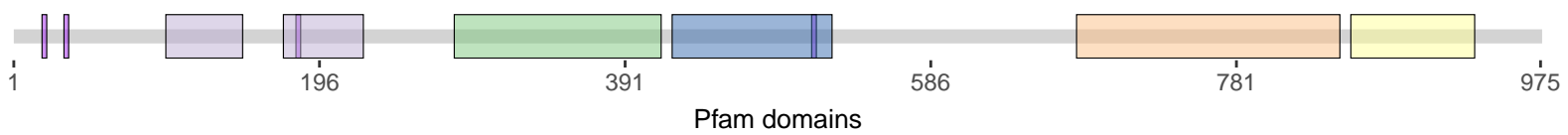
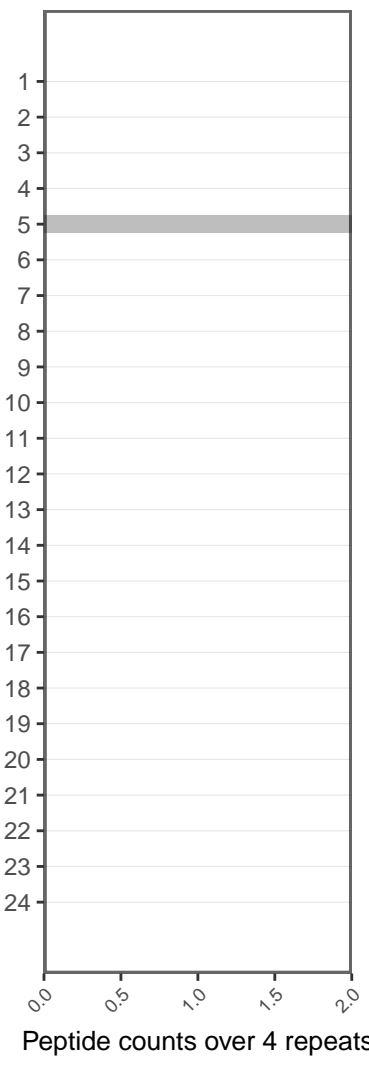
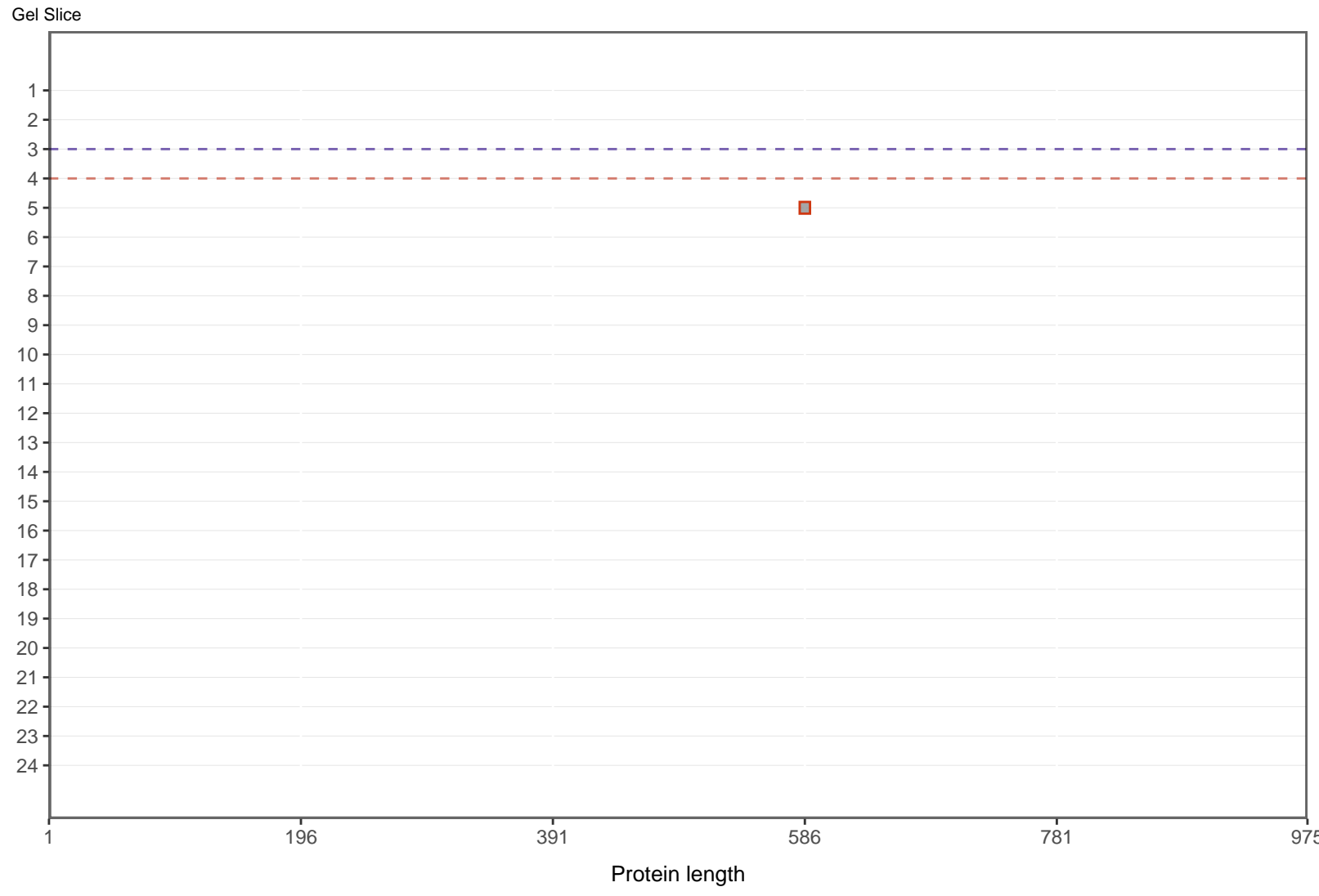
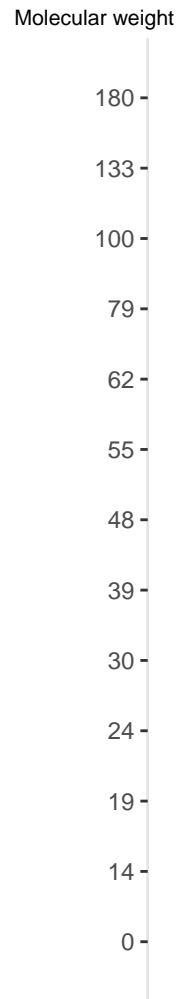
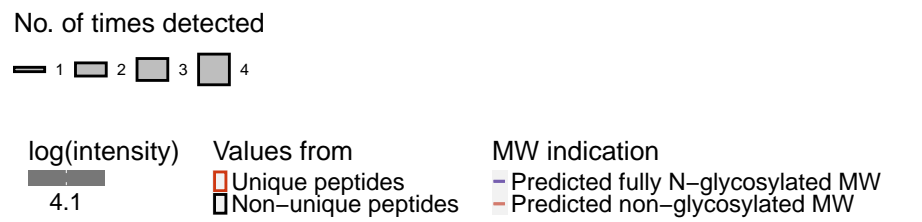
Pfam Description

- SP
- Sequon
- TM Domain
- PF00984 UDP–glucose/GDP–mannose dehydrogenase family, central domain
- PF03720 UDP–glucose/GDP–mannose dehydrogenase family, UDP binding domain
- PF03721 UDP–glucose/GDP–mannose dehydrogenase family, NAD binding domain

Protein sequence:

`INMMSALCEATGANVSGVEVWVGKDRIGKFLNABVDFGSGCFGKDILNLYSGEONGLPEVAEVWVKVQKINDVQKIRFVNRVAAGMNFVTKNKKVALLGAFKKTGTDRETRPVDVCKGLLGDKARLSIYDQVQDGGQKIDLSMNKFDWDHPLHLGPMSPFKKLIVSVTWDAVEAAADHAHVCLTEWDFKTLDYQRIVENMGKPAIFDFGRNVVAVDKLREIFIVYKIGKPLDAWLKDPFAWA`

NbL19g10540.1 chaperone_protein_ClpB3_chloroplastic-like [MW = 109.73 kDa]



Pfam Description

- SP
- Sequon
- TM Domain
- PF00004 ATPase family associated with various cellular activities (AAA)
- PF02861 Clp amino terminal domain, pathogenicity island component
- PF07724 AAA domain (Cdc48 subfamily)
- PF10431 C-terminal, D2-small domain, of ClpB protein
- PF17871 AAA lid domain

Protein sequence:

AAARLKMEITSKPTALDENRAVAKLEMERLSLTNDTKKAKDRRLNRLEAELELSLKEKGAELTEQWEHEKTMTRIGDSVKEEDRVNLEIQGAEREYDLNRAAEKLYGGSDNSLGRQLAAAEKELDEYMKSGKSLRLEEVYTGNDIAEIVSKWTGIPVSKLGGSEREKLLHLEELHKRVVGGDPVRAVAEAQGRSRAGLSDPHRPIASLFFMFGPTGKTEKAKALATVLFNTEEALVRIDMSEVMEKHAVSRLLGAPPQYVGYEEGGGLTEVRRRPVWLFDEIEKHAHDVFI

NbL19g10360.1 chorismate_mutase_1_chloroplastic-like [MW = 40.12 kDa]

No. of times detected



log(intensity)



Values from



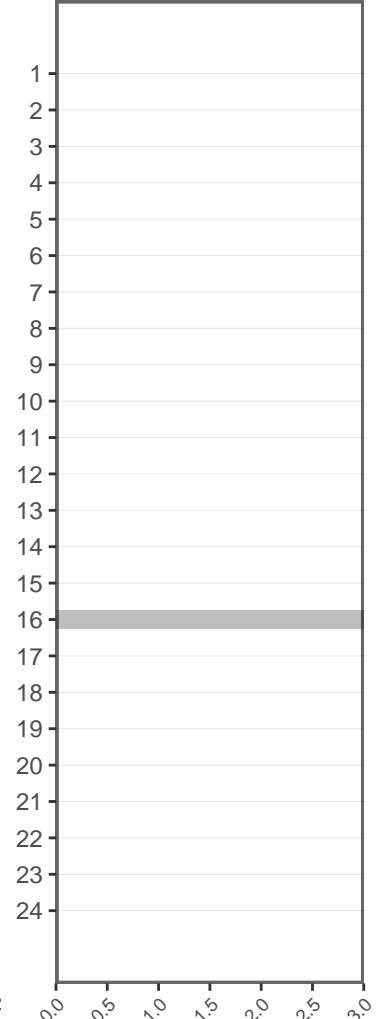
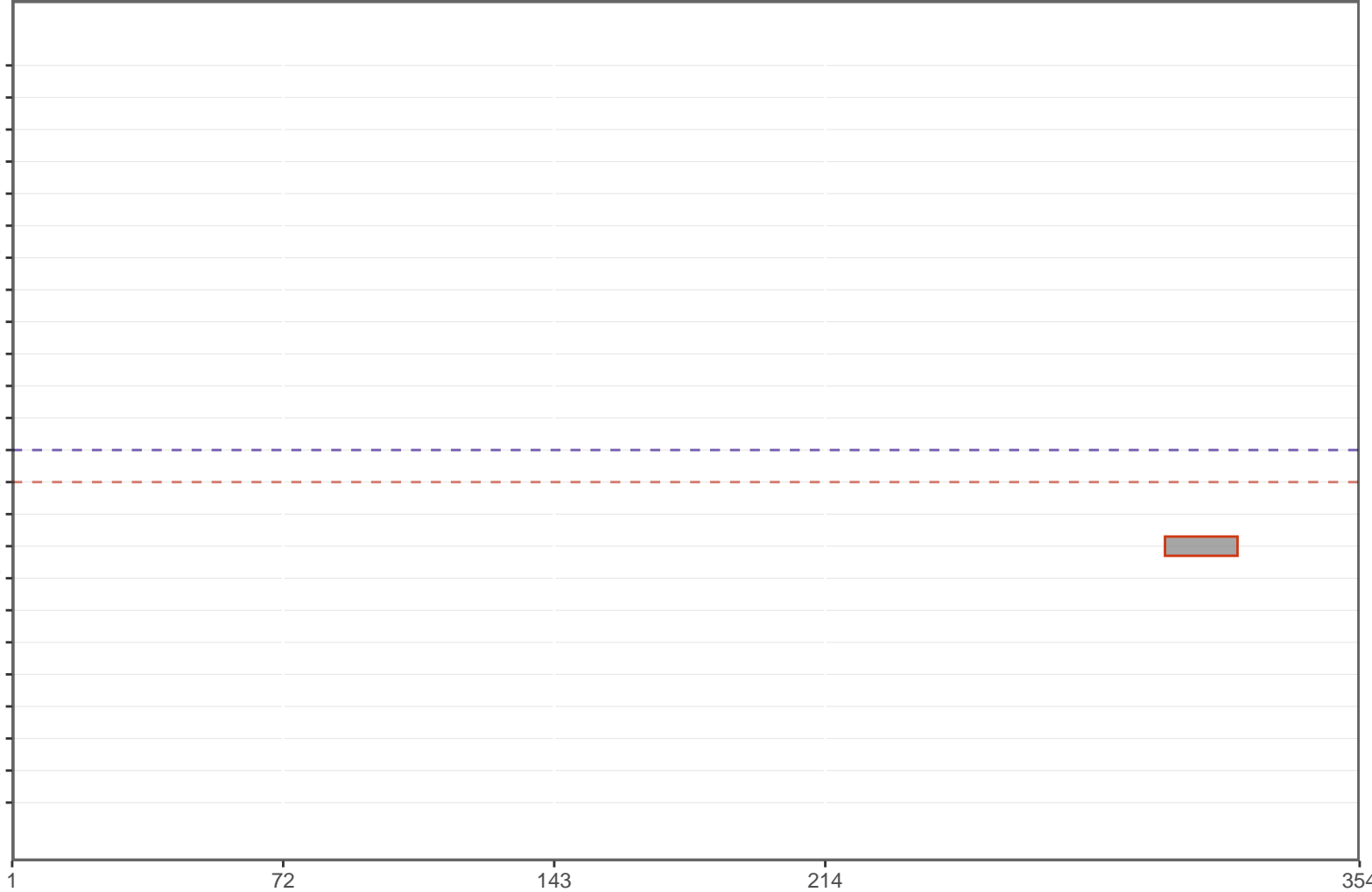
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description
 SP Sequon TM Domain

Protein sequence:

IAKVGRYKSPDEIHPFFPKLPEPMLPFGPKVLHGVADSNINWIKWEMFKNLLPRLVKEGDDGNFGSTAVGDTICLQALSKRIHYGKFAEAKFRASPDVYKAARAGDRNGLMDLLFPTVTEEAIVTRRVEKTRTYGGENINGPENGVDVYKIKPLVAELVGDWIMPLTKEVQVEYLLRRLD

NbL19g10350.1 lamin-like_protein [MW - SP = 16.24 kDa]

No. of times detected



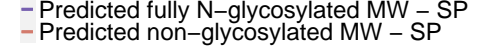
log(intensity)



Values from



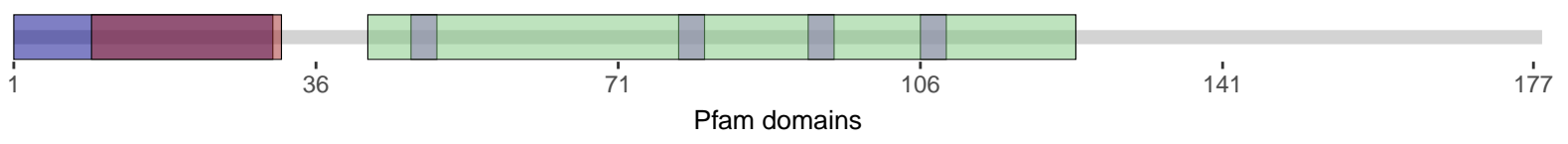
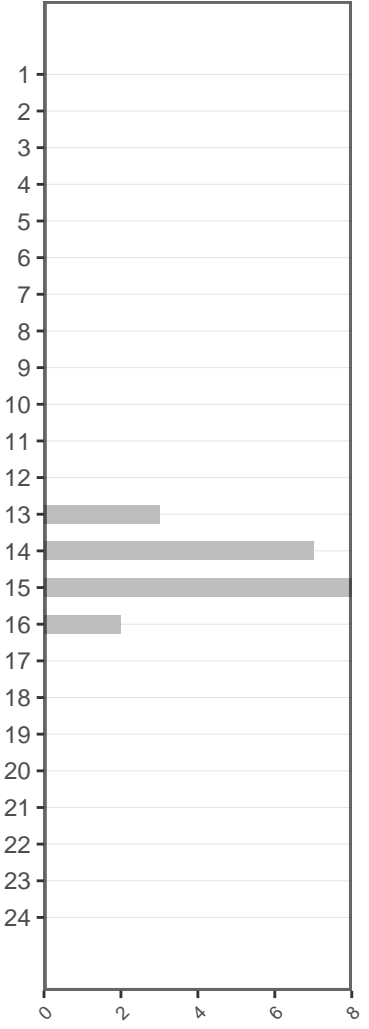
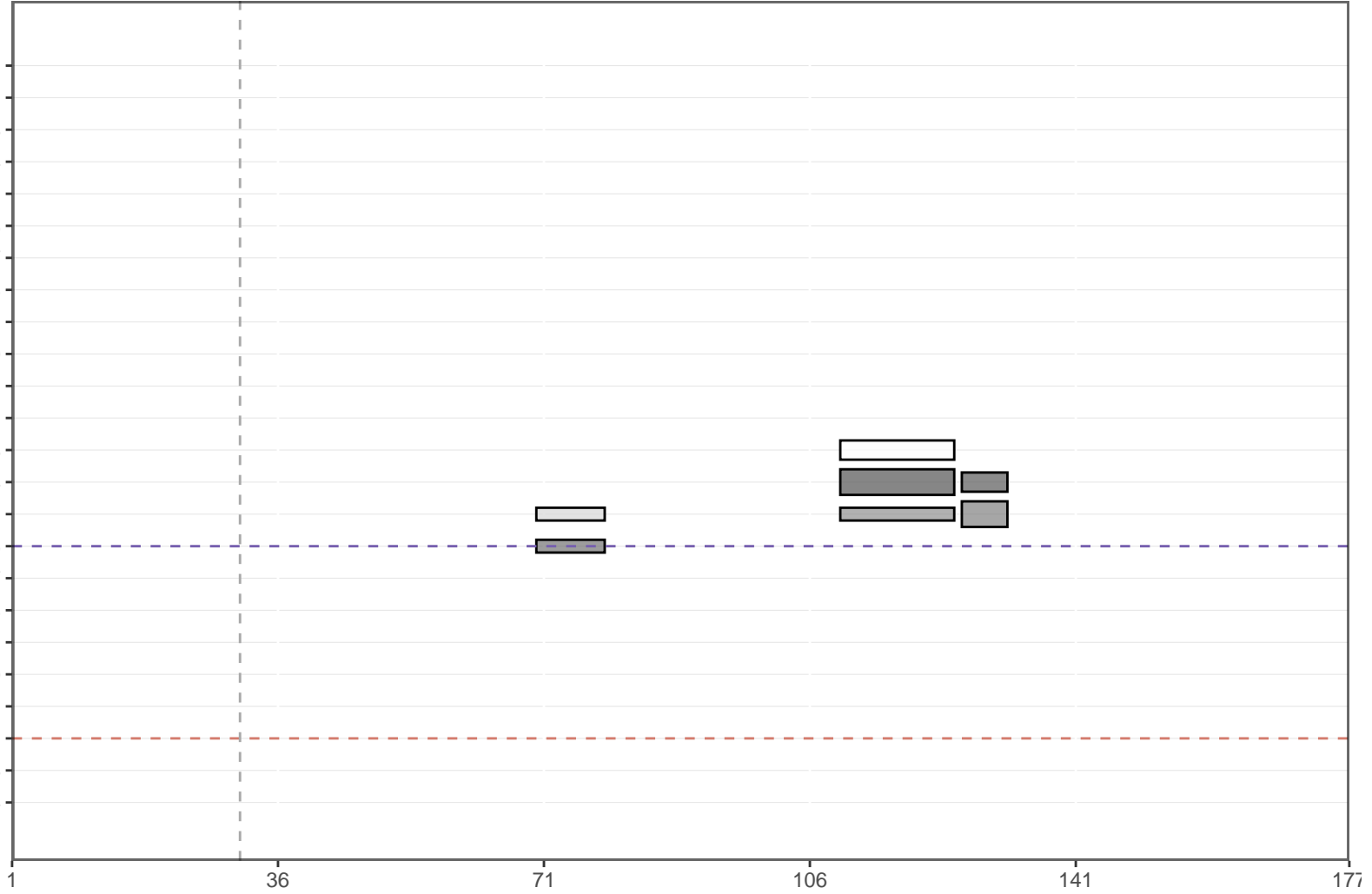
MW indication



Molecular weight



Gel Slice



Pfam Description



Protein sequence:

VLELNKTYNYENCITDHPHNYFTGGRDWPFLNFKTKTYFASGGGLGVGGMKVAHWKAPPPKAPVRSSTNVLTSFTGQILPALFATSANWNAFLRLW

NbL19g10340.1 uncharacterized_LOC107762835 [MW = 46.13 kDa]

No. of times detected



log(intensity)



Values from



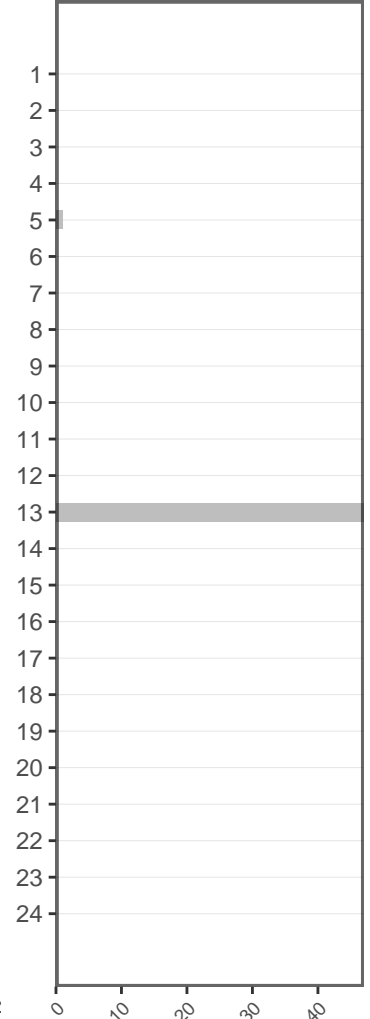
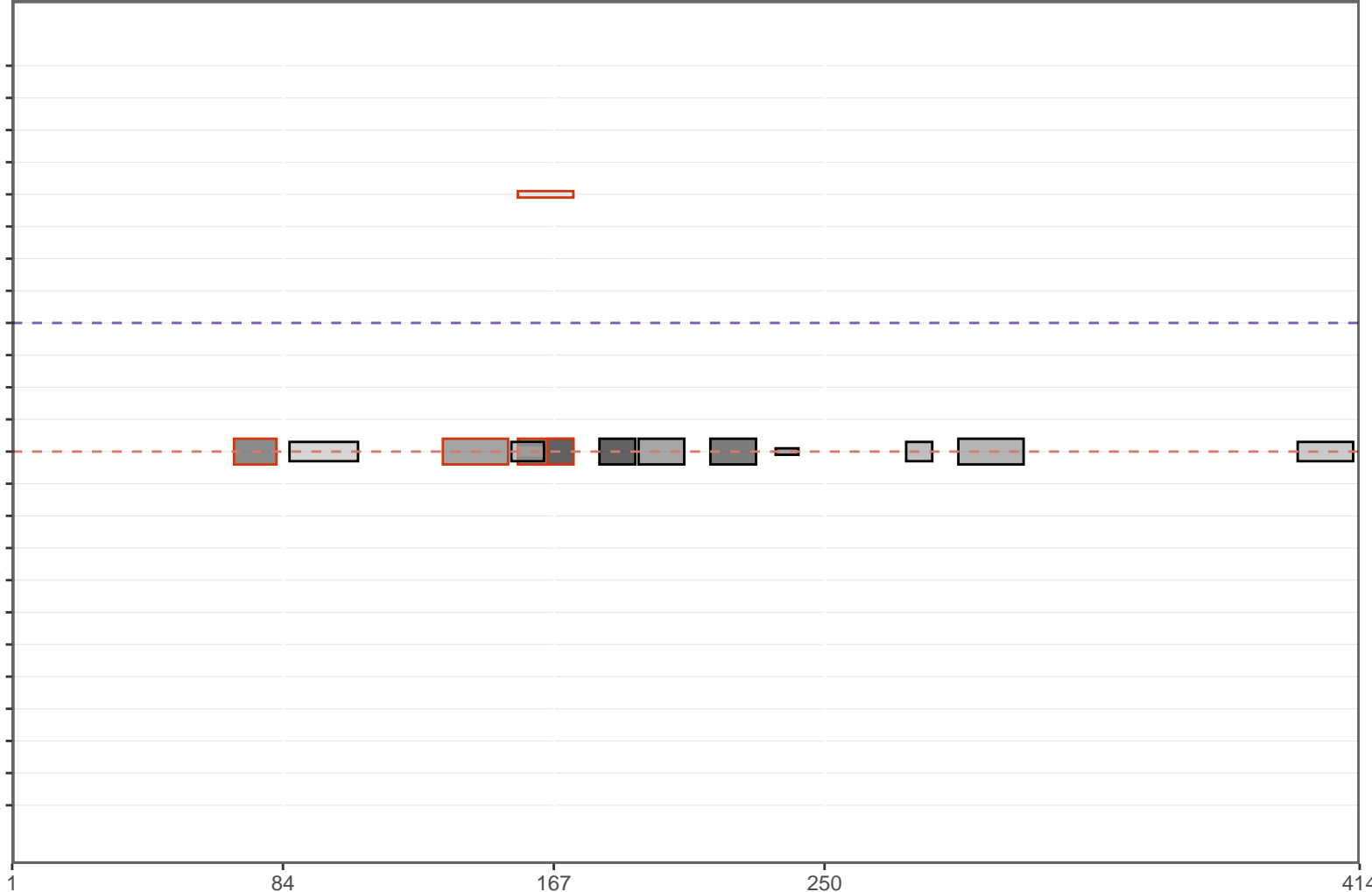
MW indication



Molecular weight

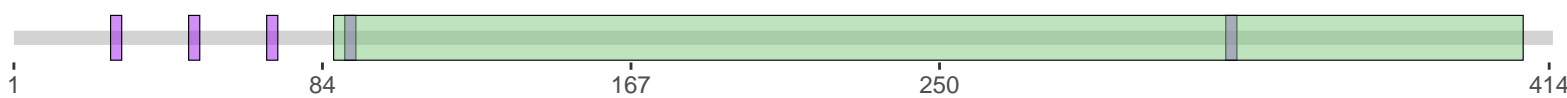


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGYLGEDDGGEESSPRNLLPKKKPVGVEGNLYSLENDKRVRAFHMDPKGILEMLVFLFEERGNKEAIPFDFNFKEDGERIMPHLGTWKGHSLTKRTGVYVGARTEAETLLEMMKDGGLVDDITSTSGASNVTTNHHWTGTISGNLVTFHGGFQTLPLPGGVMGYPSDWNASVQESKSFHLELQWLESPPGKRRRLRTYDVEGLAVSSTVFIESK

NbL19g10230.1 uncharacterized_LOC104214001 [MW = 29.72 kDa]

No. of times detected



log(intensity)



Values from



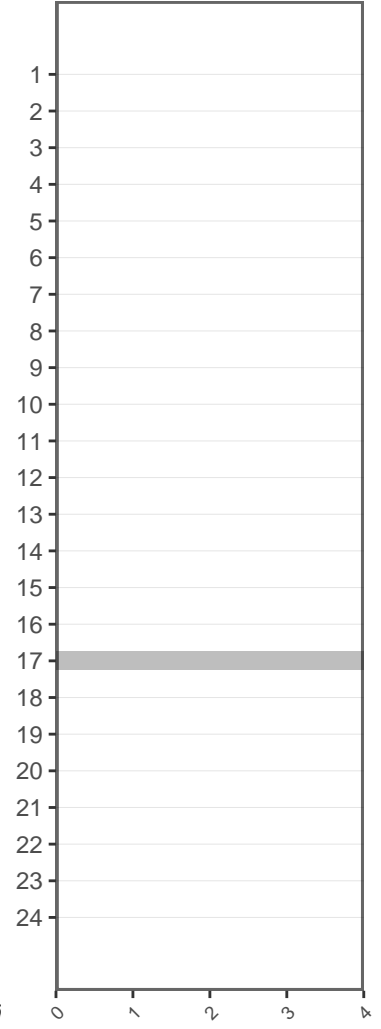
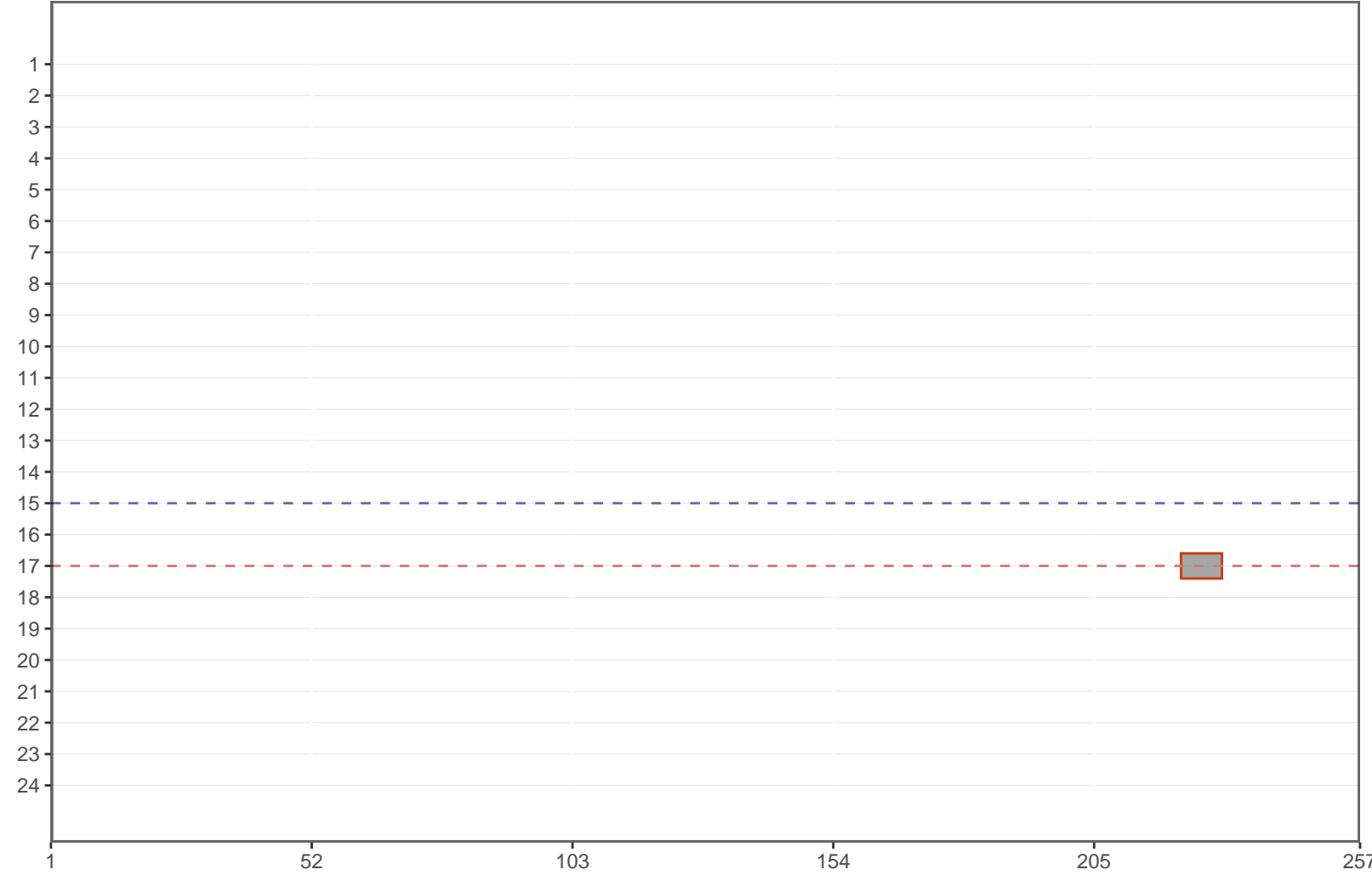
MW indication



Molecular weight



Gel Slice

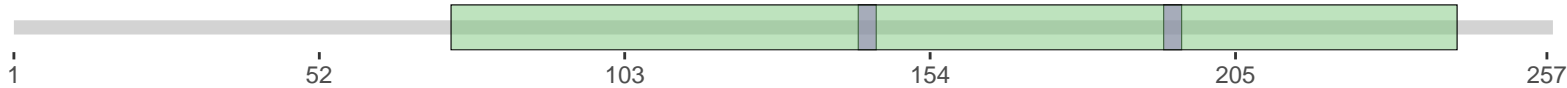


Protein length

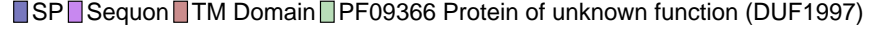


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LTAVPVVNMIRRYKTKGKEVPSGVPTNTSTVLELKHKWOLEGVTEGKPKSEFRINMEGALVPRRGRTRSRKIGHFNMSLGFAPPPMALVPPHVHGHVQTQSVMMKNGESMGMHVRDNLADYTKFKKENYKNEGEDRKY

NbL19g10220.1 uncharacterized_protein_At5g39570 [MW = 27.42 kDa]

No. of times detected



log(intensity)



Values from



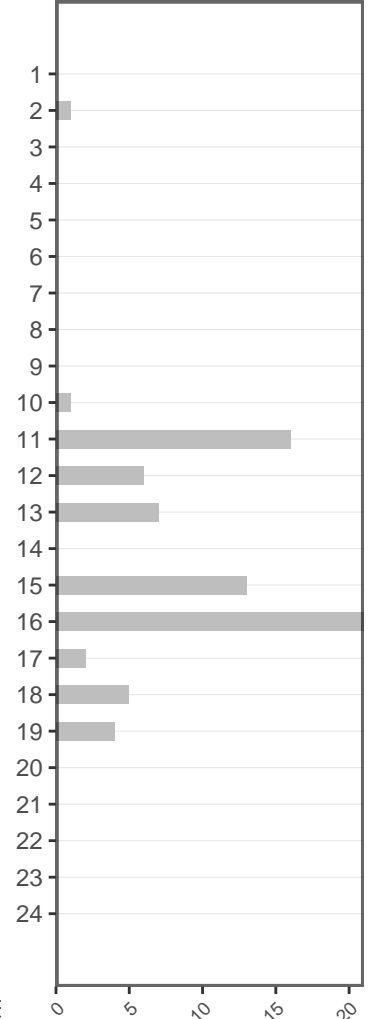
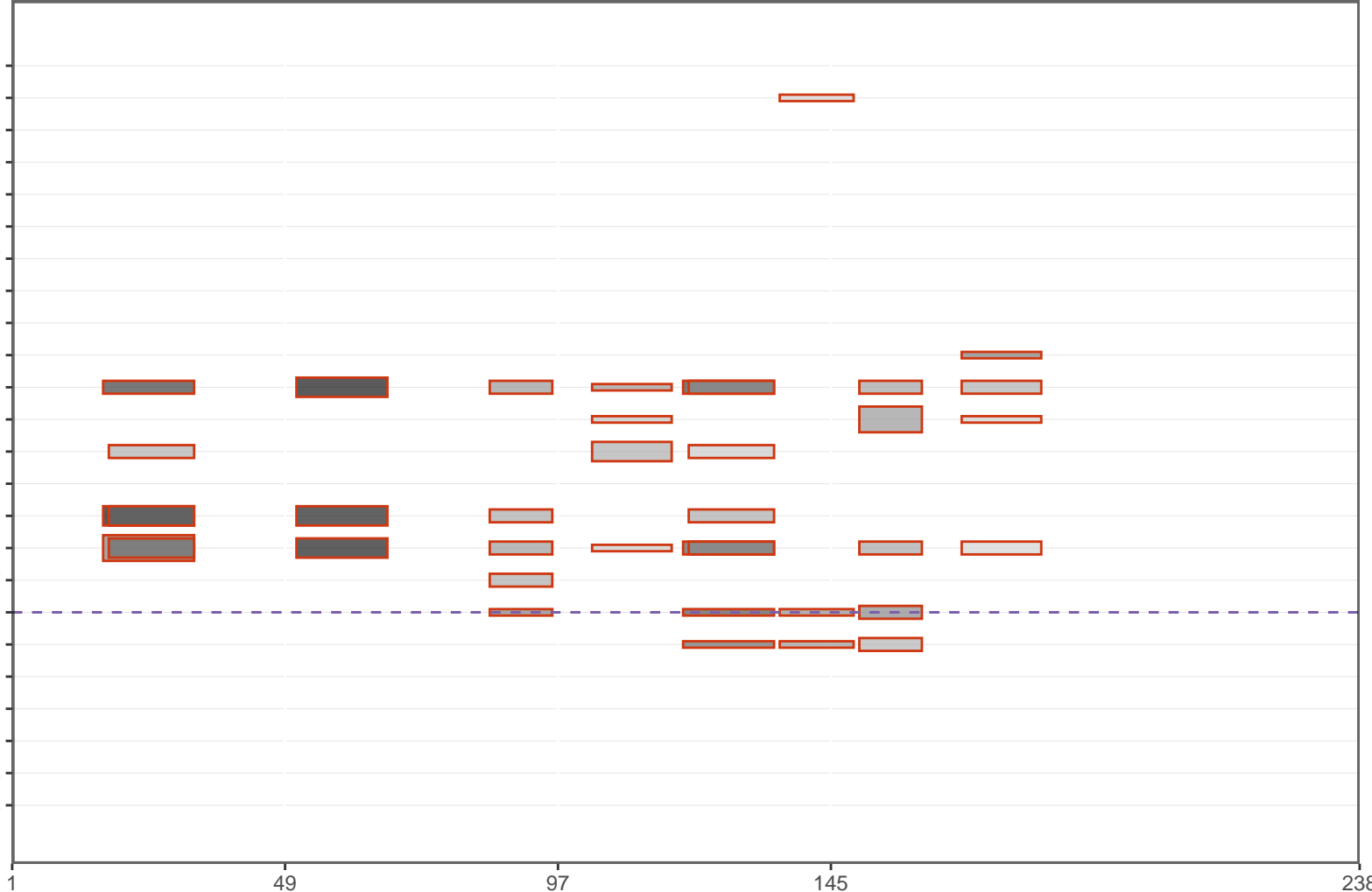
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

IPAPFYGGQYRRKSEVEEPESSVEGGVERKTEPEEDGGGGYGRKPSYGQDEEGERRRPSYGRSSVQTEEGEGYERPRYGRSEEEEDYRRPSYERRAGDDDDGEGYGRKKGDDDDSDDEEKQKHYKHHHRRKHVDD

NbL19g10170.1 cystathionine_gamma-synthase_1_chloroplastic-like [MW = 58.47 kDa]

No. of times detected



log(intensity)



Values from



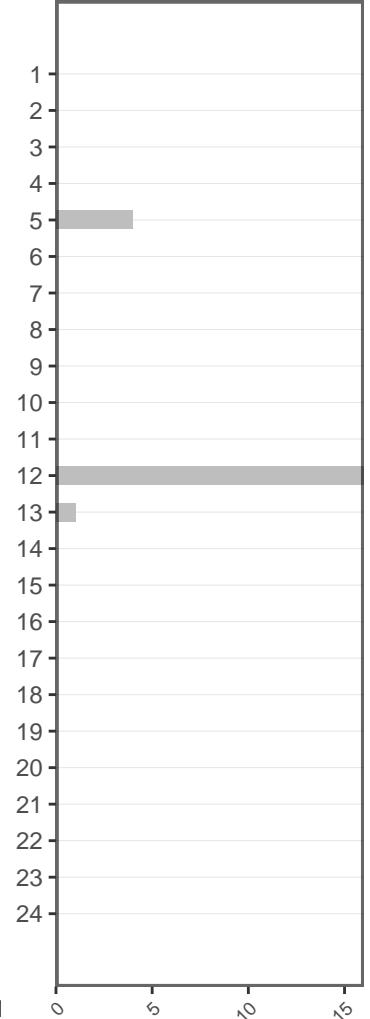
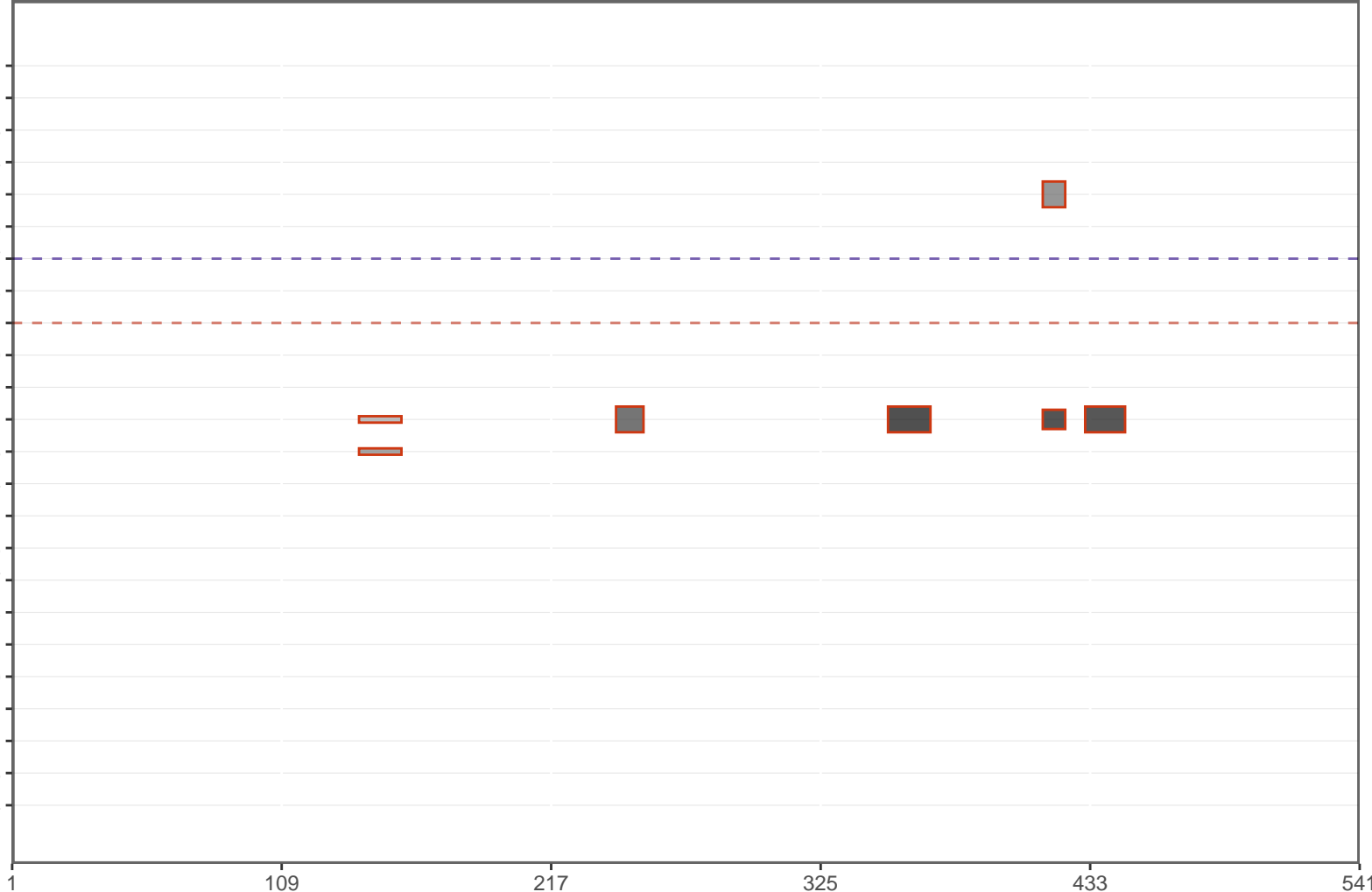
MW indication



Molecular weight

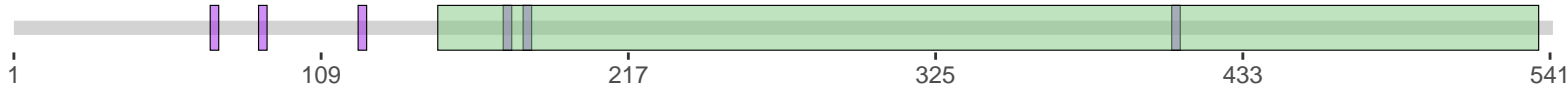


Gel Slice



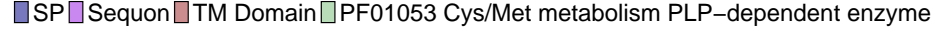
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

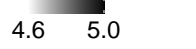
CTRIFETLPKMGITATVDRPADVGALELALNKKVNLFFTESPTNPLRQVDIEMVSKLQHEKQALVQDGTGTFATPLNKKALALGADLVLSATKFLGGHNDVLAGSGGSPVKKVSEIRNLHILGGALNPKAAVLRGAKMQLHLRVGGQNSTALRTAEILEAHPKENELQVRHYYYPGLGSHPEYHAKKQMTFGGGVVSFEVDGDLITAKFVDAIKIPYIAPFGGGGSEVQDQPMMSYVWELGGSDRAKYGMNDNIVRFSFGVEGDFDULKADILGALDGI-

NbL19g10090.1 expansin-A10-like [MW - SP = 23.98 kDa]

No. of times detected



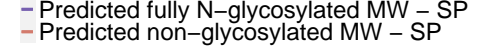
log(intensity)



Values from



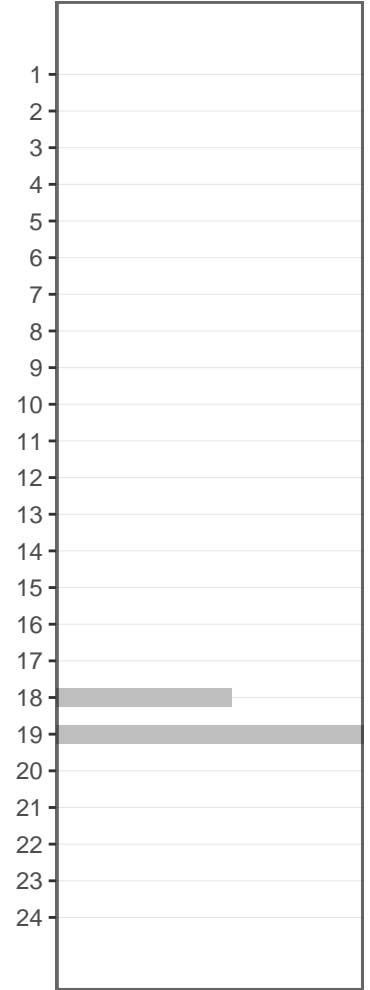
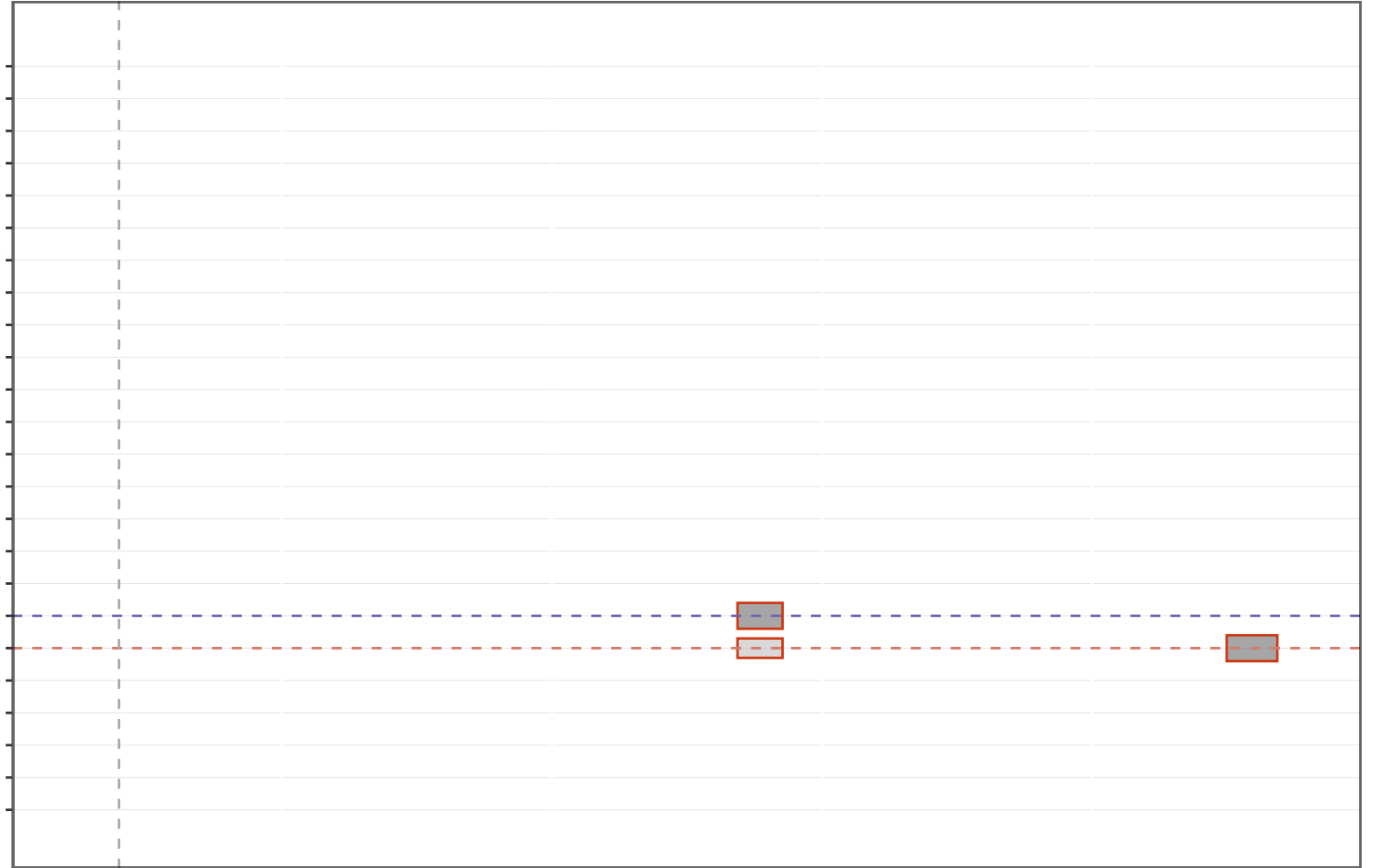
MW indication



Molecular weight

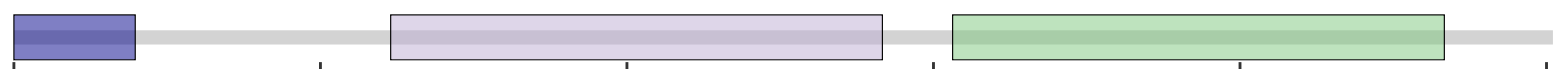


Gel Slice



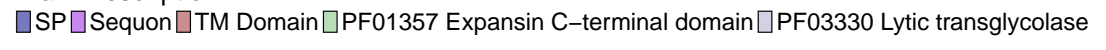
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DPNHF₁FDLSDP₂VLRLA₃QYRGGV₄PNAYR₅RVPCRRRGGIR₆FINGH₇SEYFN₈LVLT₉TVGGAGD₁₀VRSLYK₁₁GGRTQ₁₂WQPM₁₃SRN₁₄WGN₁₅WQNN₁₆ALNG₁₇GL₁₈SK₁₉V₂₀TS₂₁DGRT₂₂V₂₃SYNA₂₄PR₂₅SW₂₆FG₂₇QT₂₈TGG₂₉QFR₃₀

NbL19g10060.1 granule-bound_starch_synthase_2_chloroplastic/amyloplastic [MW = 87.9 kDa]

No. of times detected



log(intensity)



Values from



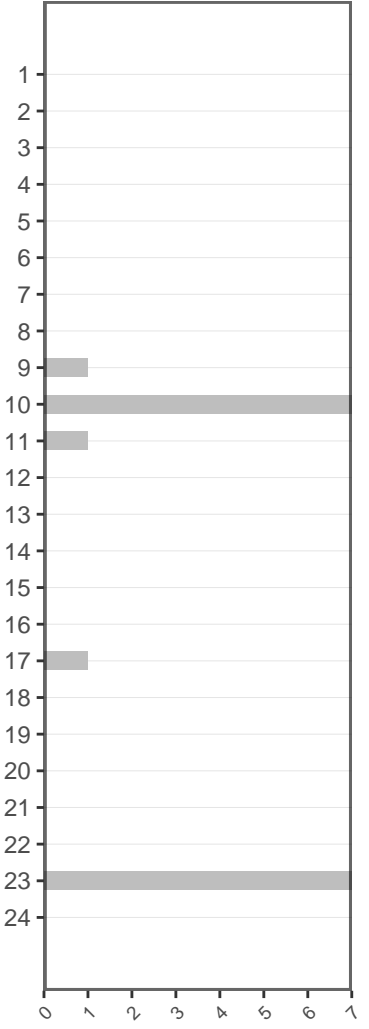
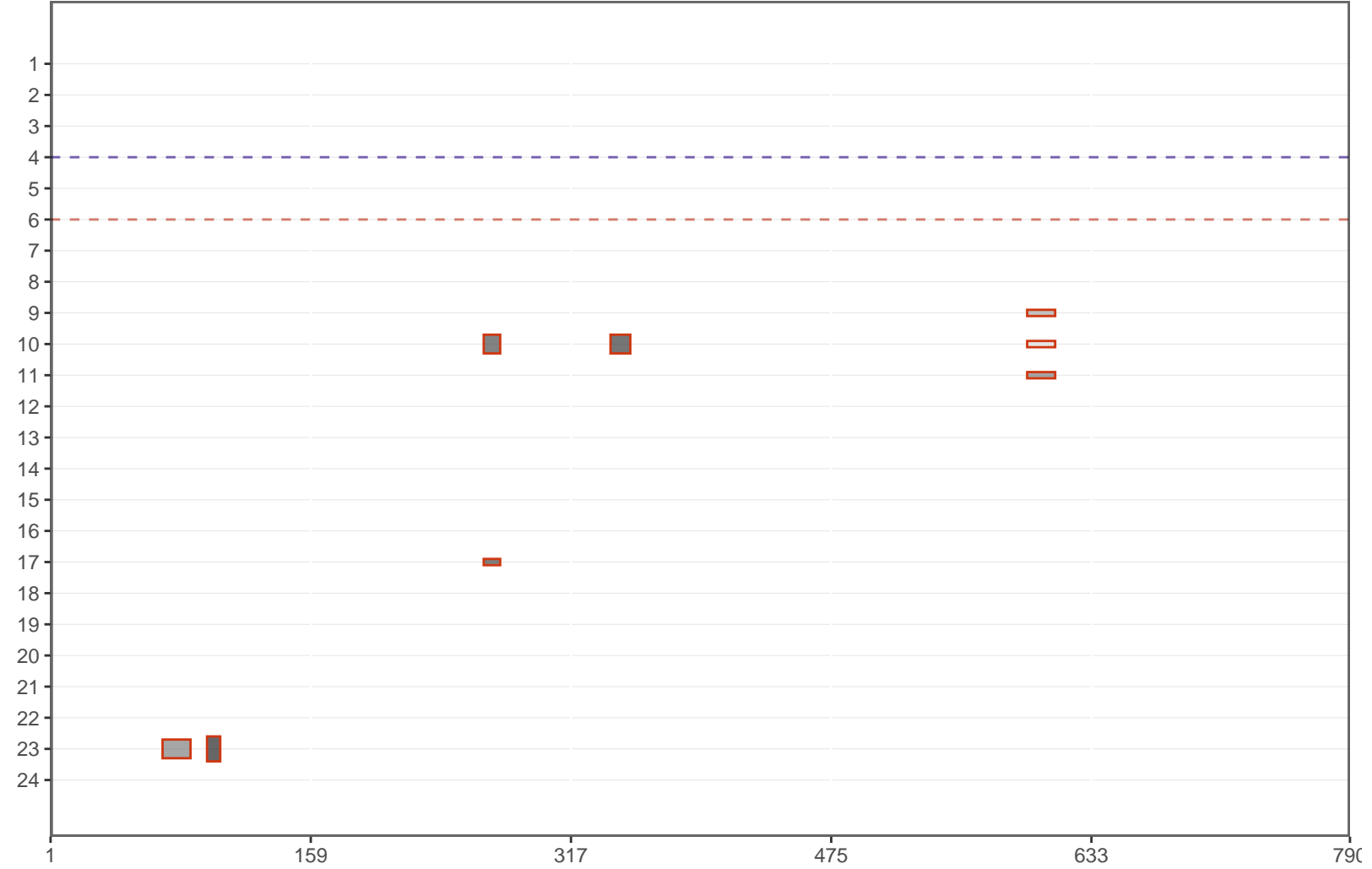
MW indication



Molecular weight

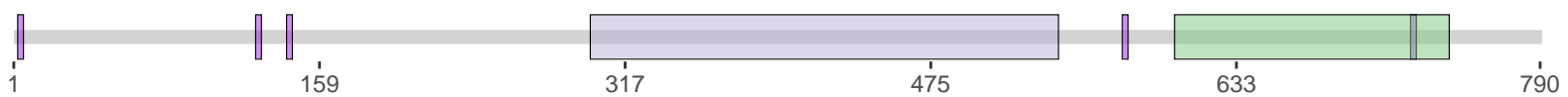


Gel Slice



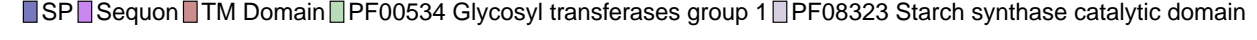
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MSFRIMENNYGGNRVQKRMVLFCKAAIEVPHVPCGGVYGGDNLVFIANDWHHTALLPVYKAYYRDNQGMKYTRSLVHINAHQGRPLDQDFSPVLPPIHMDIFRLVDPVGGEGHFNFAAGLKTADRVVTVSHGYGVELKTSSEGGVGLHEINENDWRLKRGVNGIDTTEWNPELDHLKSGDYYNYSLDLQTKPQCKSALGKELGLPVRDDPLIGFGRLEDPQKGVLDLAEAVPMMGGDGVQLVMLGTGRPLEGLRQFEGGYNDKROVYGFVKTAI

NbL19g09940.1 tubulin_alpha_chain-like [MW = 49.65 kDa]

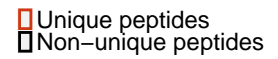
No. of times detected



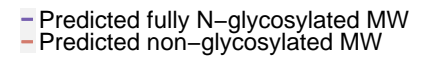
log(intensity)



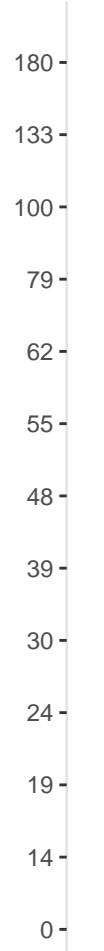
Values from



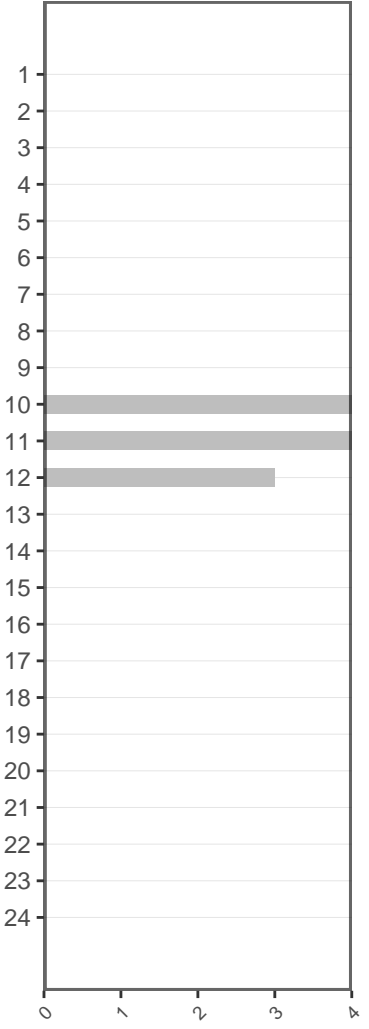
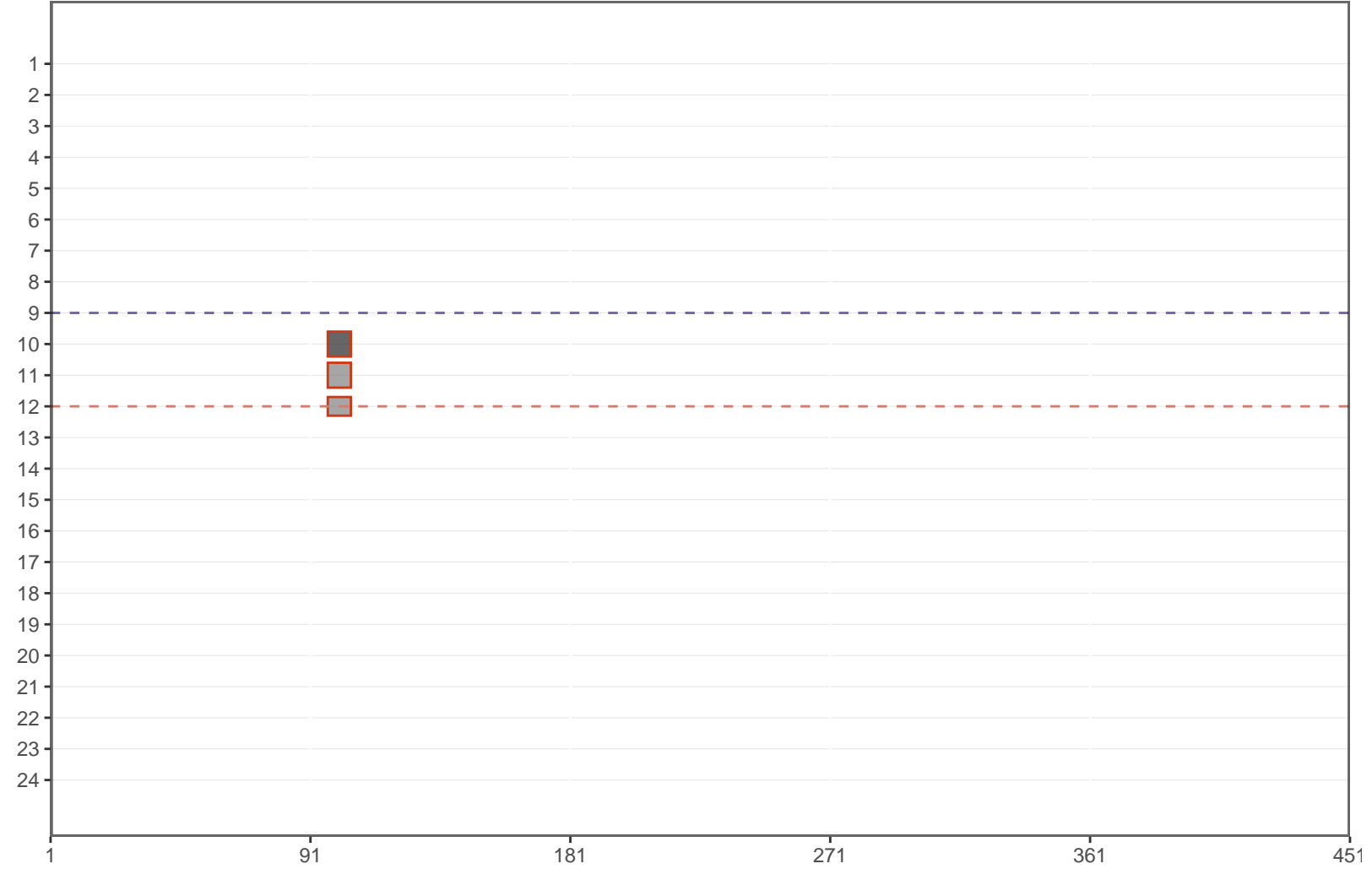
MW indication



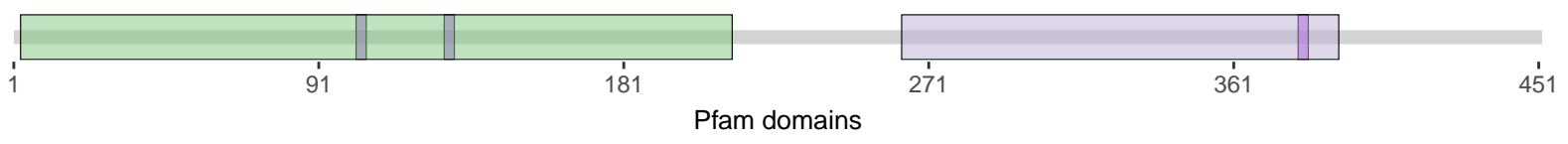
Molecular weight



Gel Slice

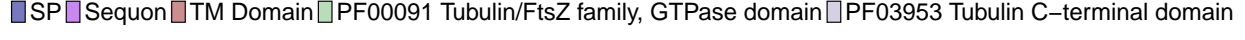


Protein length



Pfam domains

Pfam Description



Protein sequence:

RSKSLDIERPTYTLNLRLSGQVHSSLASLRFDGLALNDVNEFQTNLVPYPRHFHMLSSYAPVSAEKAYHSELVWERTNTAFEPSSMMVKGDRPHGKYMAOGLMVRGDVWPKDVAWAATIKTKRTQGFVDWQPTGFKGGINYQPTTVVPGGDLAKVGRVAVMSENSTVAEYFGRDHKFDLMYAKRAFVHWYVGGEMEEGEFSEAREDLAALEKDYEEVGCESGGDEDDVVEEY

NbL19g09860.1 aldose_1-epimerase-like [MW - SP = 37.14 kDa]

No. of times detected



log(intensity)



Values from



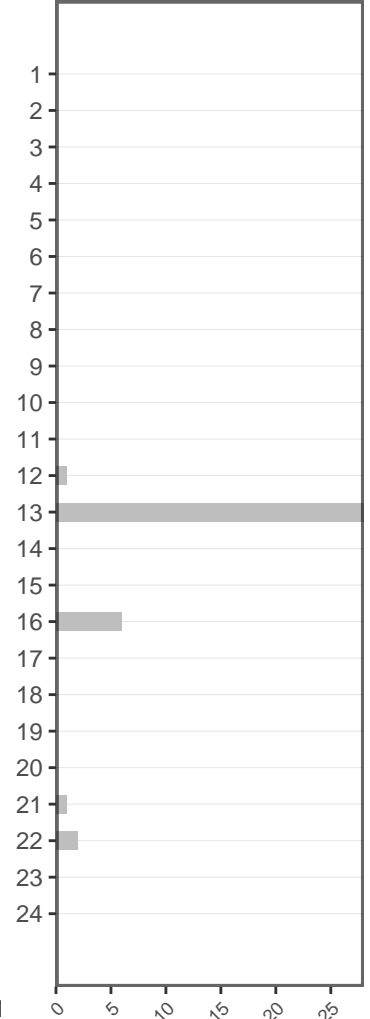
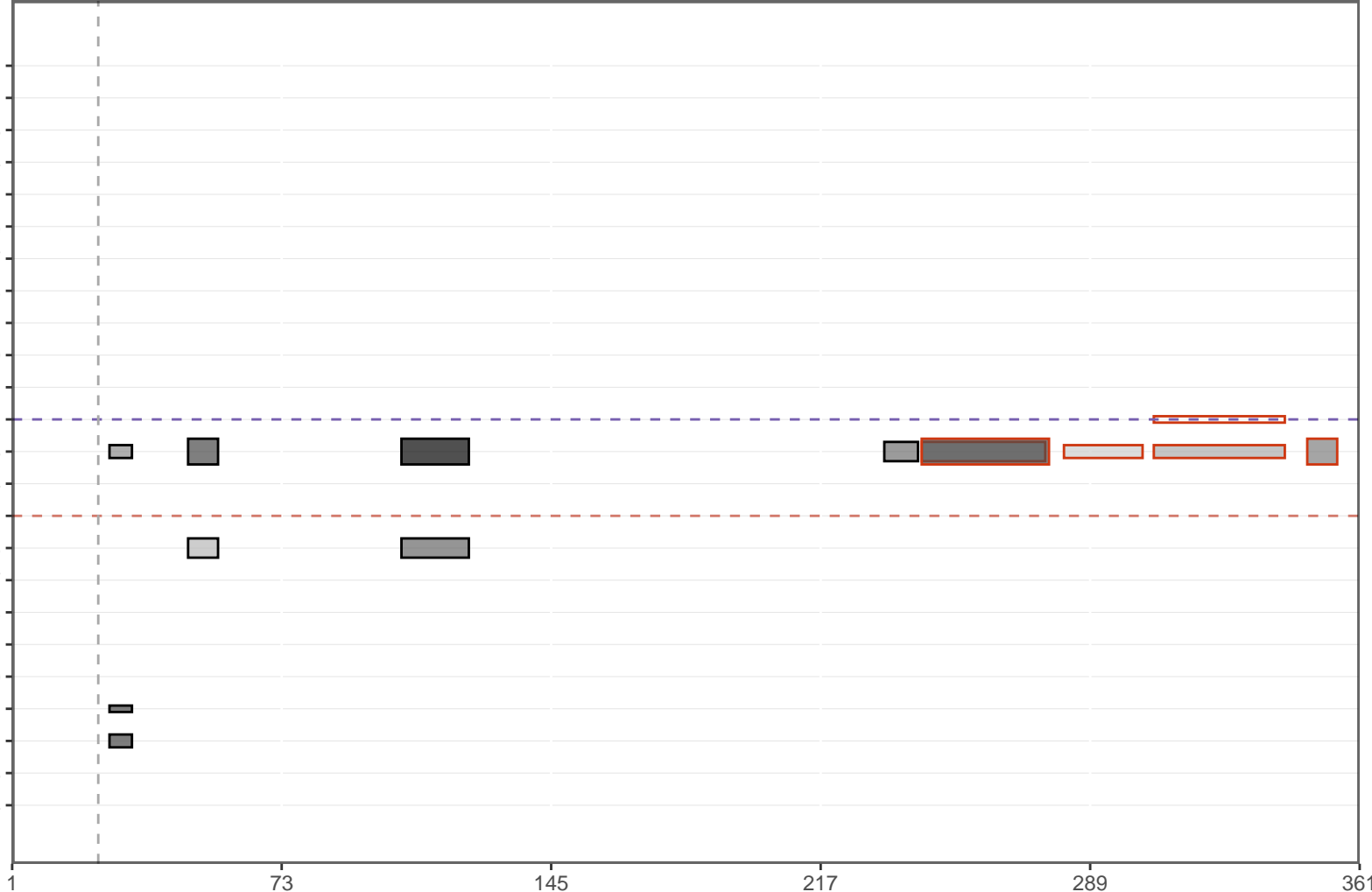
MW indication



Molecular weight

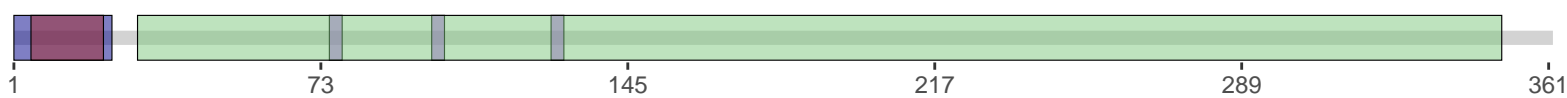
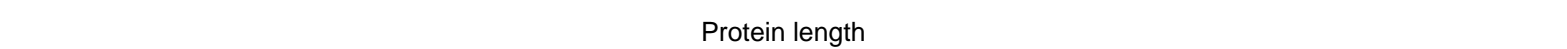


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

YKLSVYAKAKLNKATPVNLQHTYVNLGGHSGSDLSNIVGIFASHITPVDEHFITGTEISPVNNTVDFLKPREVDSGNELGSGYDINVALDSTEEMKPAVAVDKKSGRVMDLQASAPGVGFYTANSLIKGKGGVYVQPHALGFETQGFDDAVNHPNFPSTVIRPKAYTHKMLYTFEMKYWNSY

NbL19g09830.1 protein_IQ-DOMAIN_31-like [MW = 62.22 kDa]

No. of times detected



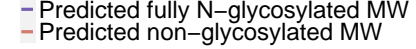
log(intensity)



Values from



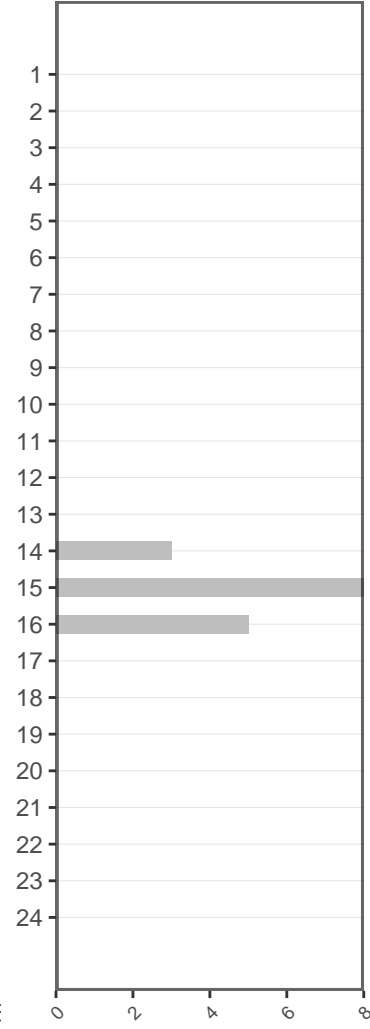
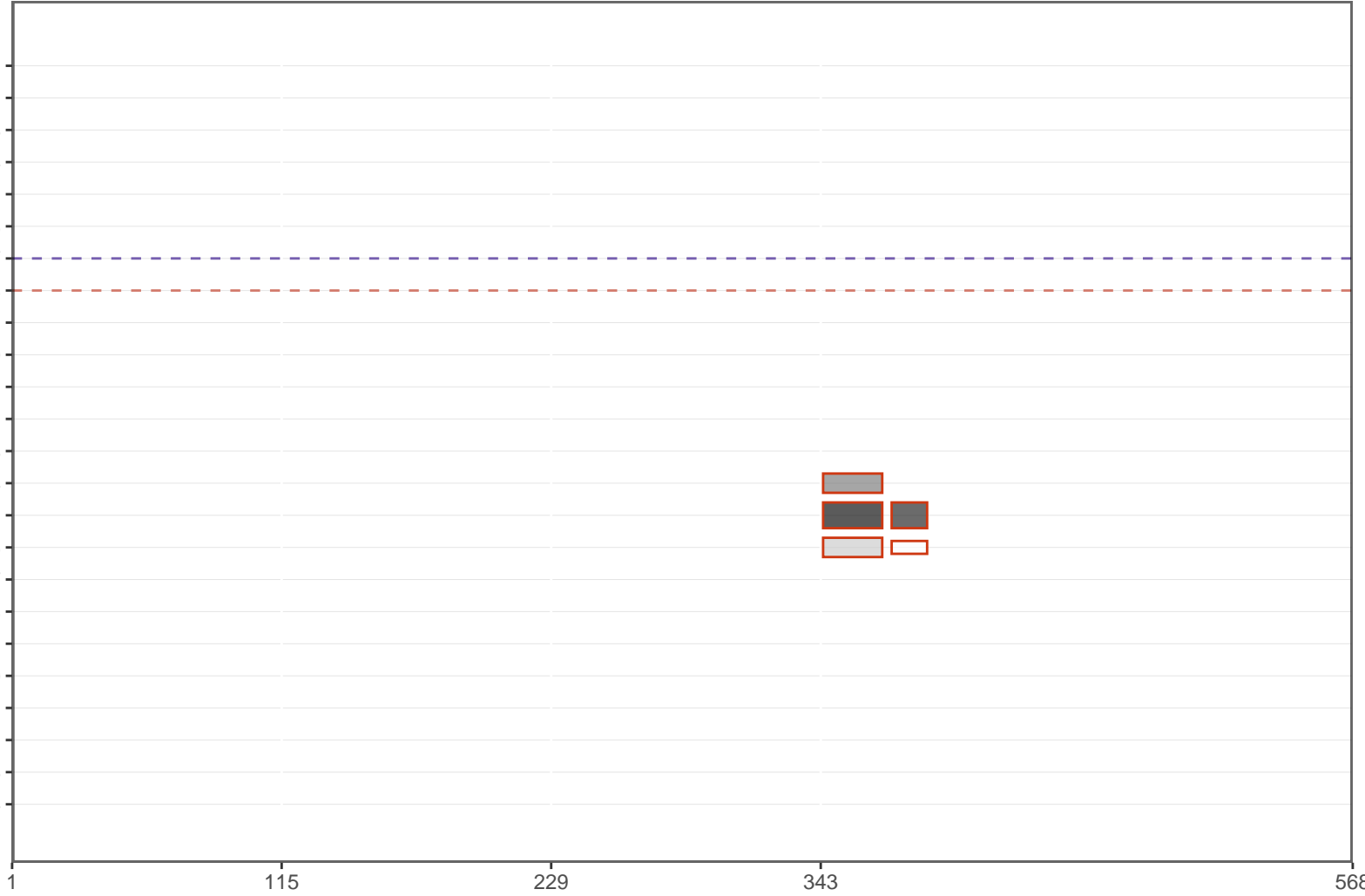
MW indication



Molecular weight



Gel Slice



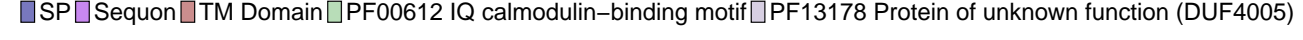
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RSKRSVYKYLTSANGDAWVSSSEPEKTRKRYPRKFSHPHIEPVLDPQNELEKVKRNLRKYSALATPSERTETESSEKVDETPNLAQAQAQAQAQAQAKTSKSSALDVEQIVNNSSEKTRDSEAFSEKLAVTEAPLPVWDEPSNELLHPHTEGQOLEDVGNANTANSPVINEELSMEDHTAKERTRRRKLPPKQENSENISHNTPNVPKMAATQSAKAKLAKGSSAKVSEDDGAENGFRVRRHSLPESSTNGKFNFTSSPRVQRPVQANGKAGNKRAMSSSKDAPSSSEKVL

NbL19g09720.1 thioredoxin_H2-like [MW = 15.57 kDa]

No. of times detected



log(intensity)



Values from



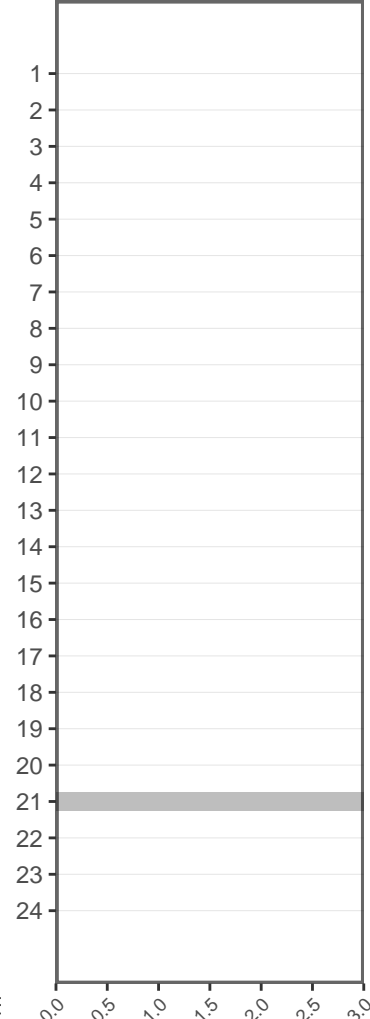
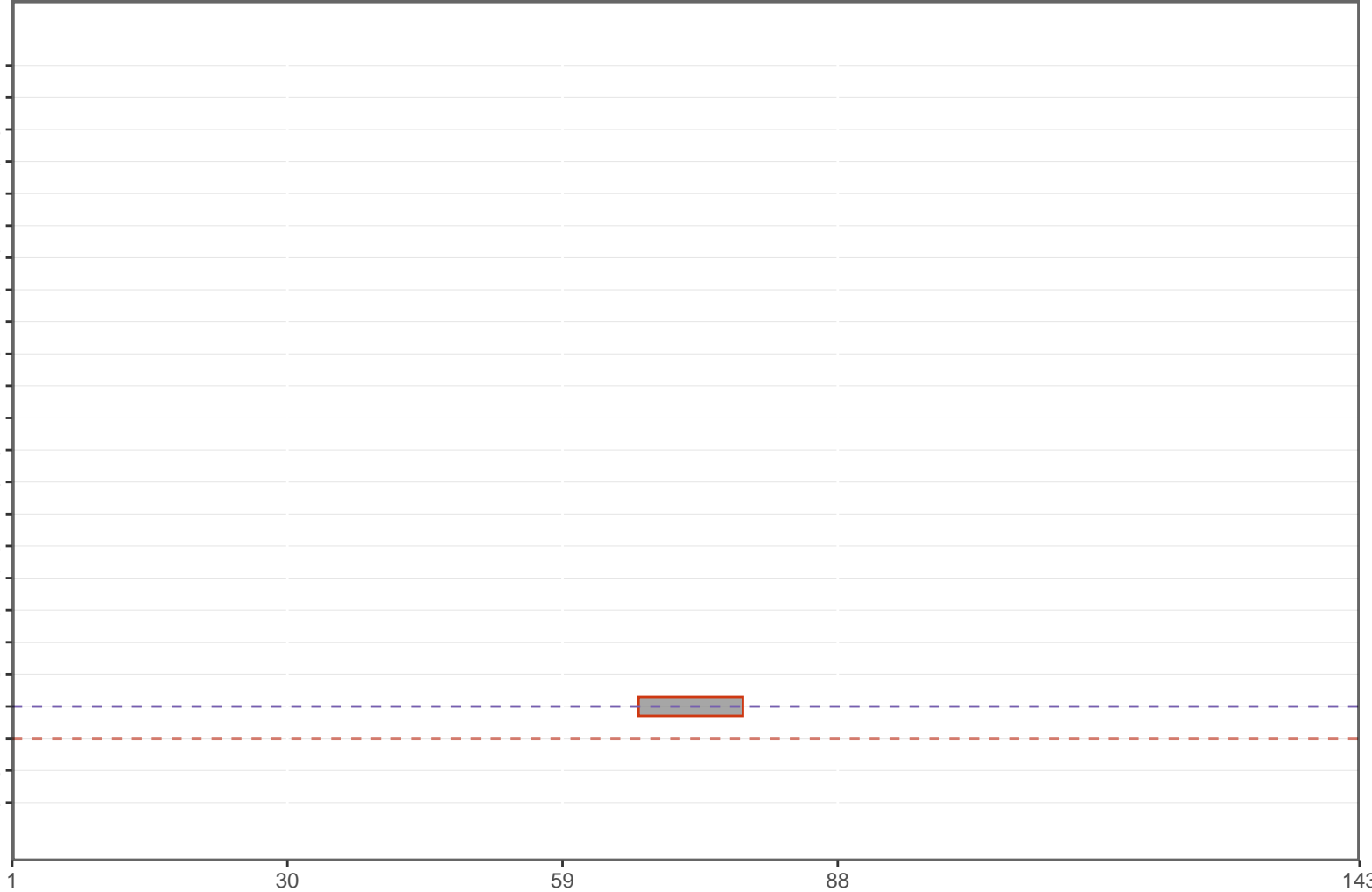
MW indication



Molecular weight

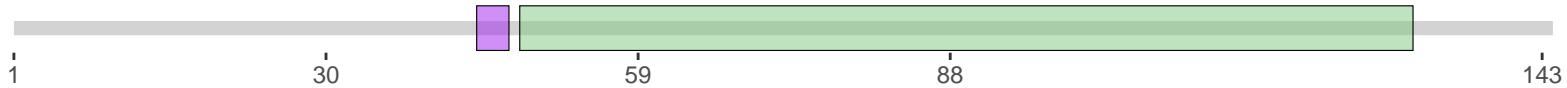


Gel Slice



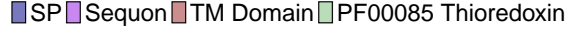
Peptide counts over 4 repeats

Protein length



Pfam domains

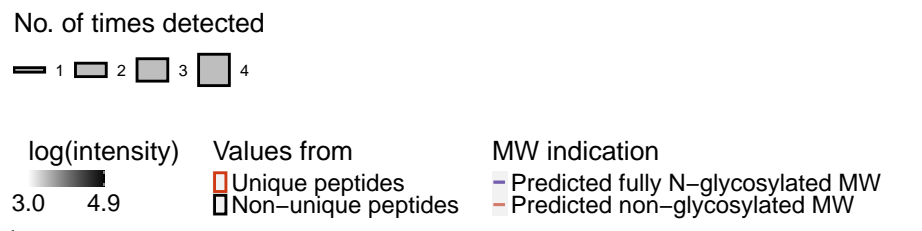
Pfam Description



Protein sequence:

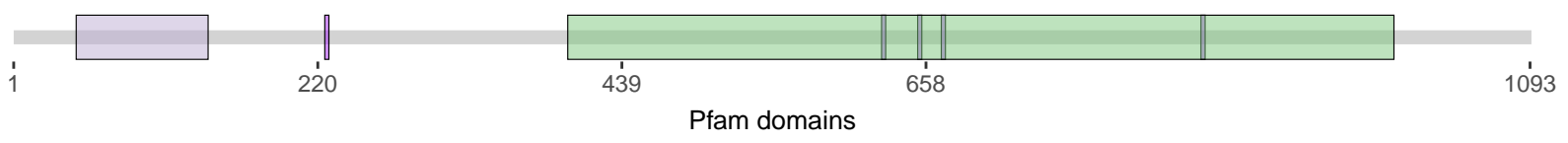
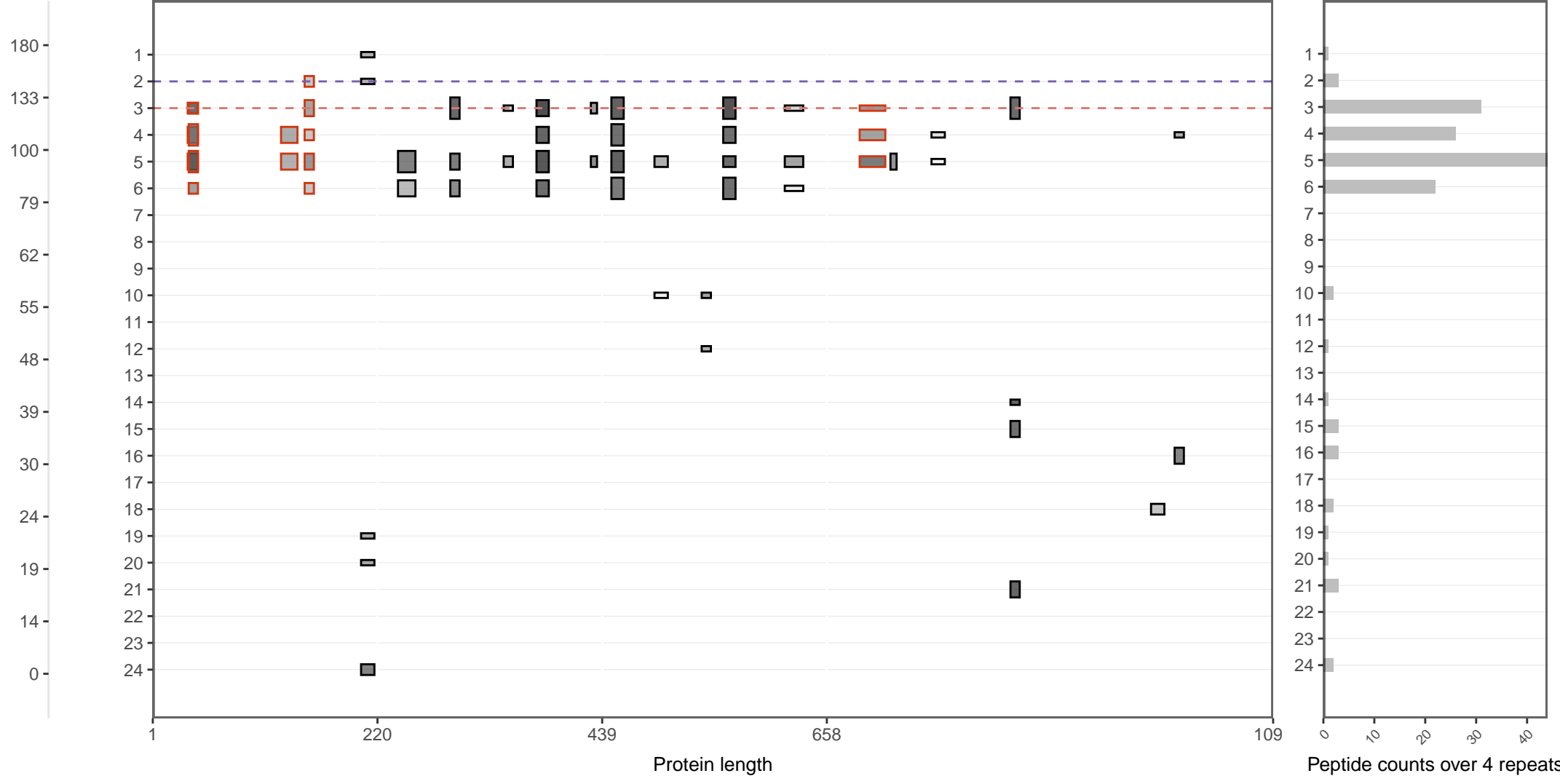
ATWCGPCQKMEPEVINAAMSAKYTDVDFVKIDVDELSDVAQEFVGVGAMPFTLLKKGKQKVEVERVVGAKKDELEKIKIKHREAPKFAA

NbL19g09710.1 inositol_hexakisphosphate_and_diphosphoinositol-pentakisphosphate_kinase_2-like [MW = 124.18 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00328 Histidine phosphatase superfamily (branch 2)
- PF18086 Diphosphoinositol pentakisphosphate kinase 2 N-terminal domain

Protein sequence:
 IALMLVLYKYGSLVLTIMGRKGAELGRVFRNMLVPEGGTGLRLHSTYRHDMLKIVSSDEGRVQMSAAAFANGLLDEGLQTLPLVSLVSKDSSMLDGLDNLNABEMEDAKARLNDIITSGGTRTLHNNQSSSEKPPWVYDGAGLFPNABELLKLKLYTKVTEQVRLLAKEDEEELAEETSPVDMLPPYDGAALGKGTNDVDRIAAGLPGGEGFLMFAFRWRKLERDLNNEARKDRFDITGPDVYDSCKYDLHNSHLNGLDELFTVAQLLADGVPINPEYGNPKOKLIGSKIAARRI

NbL19g09510.1 signal_recognition_particle_43_kDa_protein_chloroplastic [MW = 41.73 kDa]

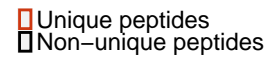
No. of times detected



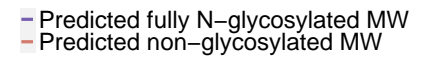
log(intensity)



Values from



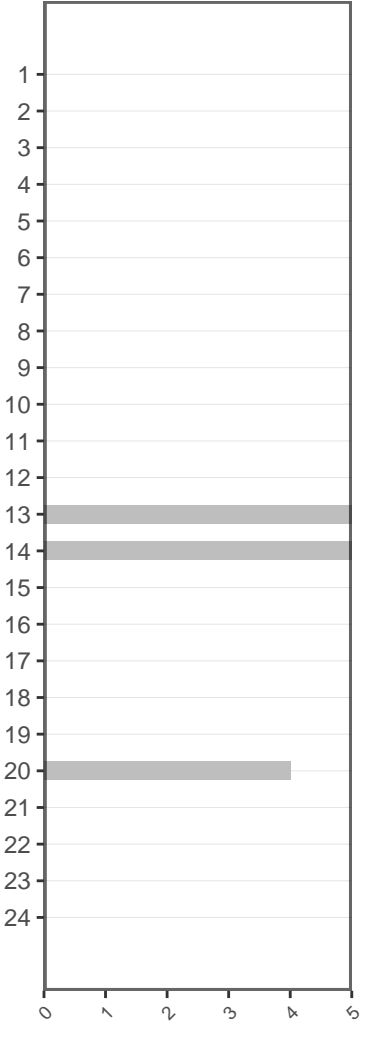
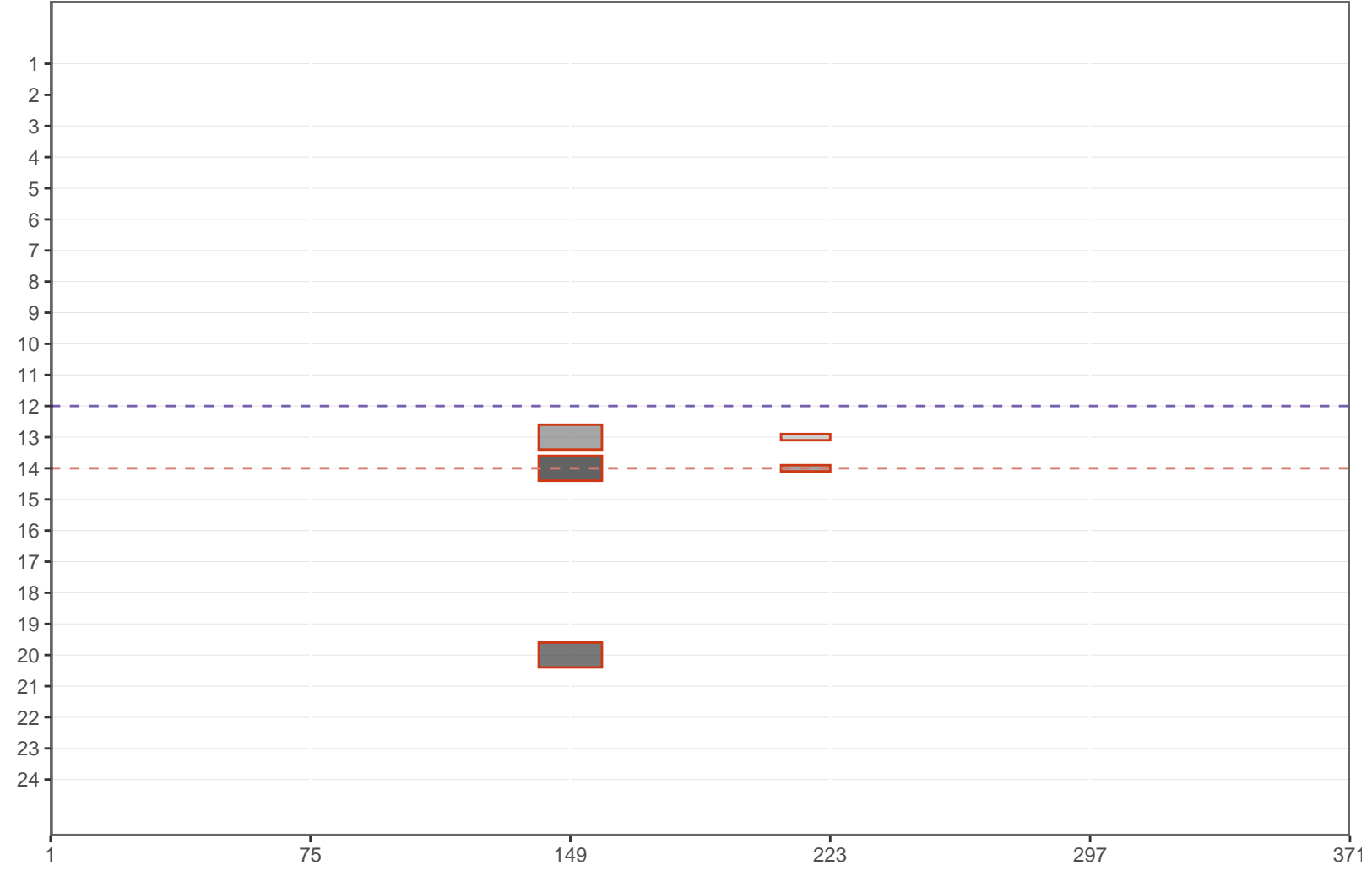
MW indication



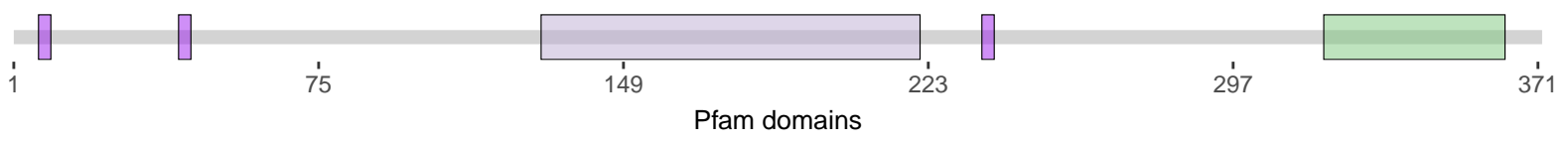
Molecular weight



Gel Slice

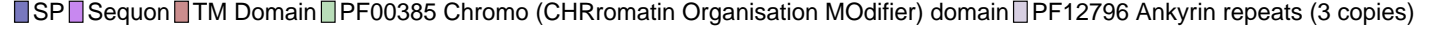


Protein length



Pfam domains

Pfam Description



Protein sequence:

SVKLLAEAGADYDIDRIRNGSLTAJHMAAGYKPDVAKLLIDLGDPEVGDYRGDTPLSARMLNGTPKGNPMDGFARILGLENVVRILEDAFVEYVTVEEILEKRGKGENVEYLVKWKDGEDNEWYKAWVISELDVRFDEAGLEYVAEGILEKREGEDKNGEYLVKWTDEEATVEPEENVDPLLIEDPEKGGQNVVSI

NbL19g09400.1 protein_transport_protein_SEC13_homolog_B [MW = 32.52 kDa]

No. of times detected



log(intensity)



Values from



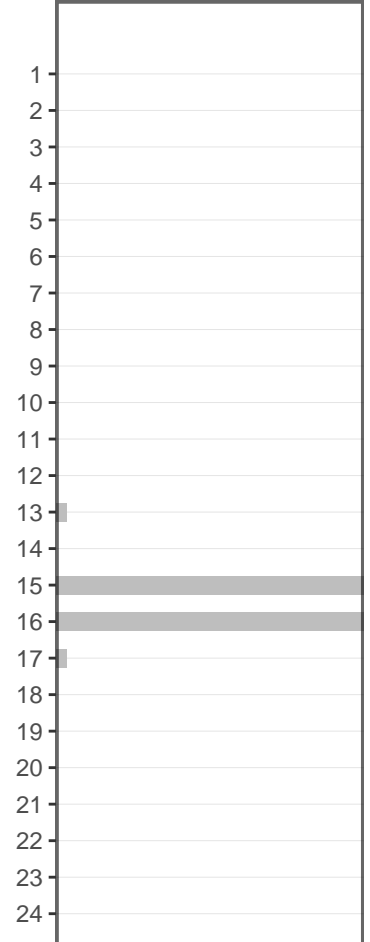
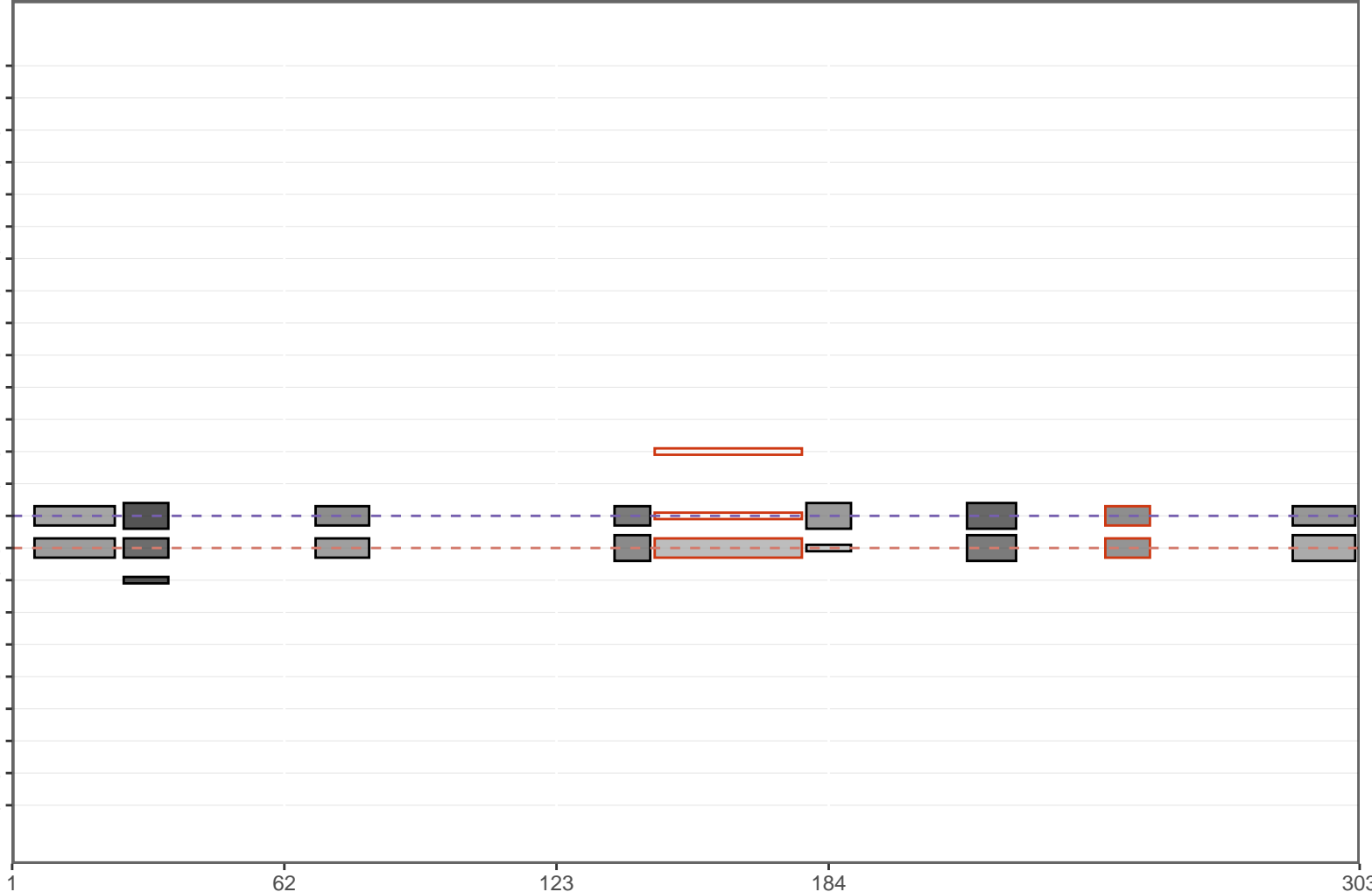
MW indication



Molecular weight

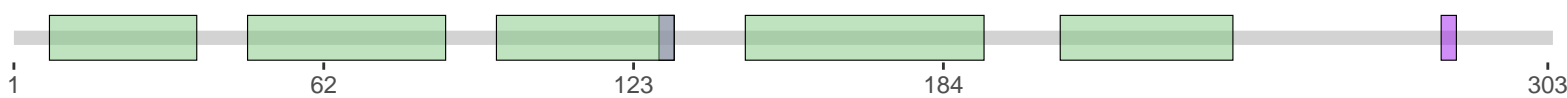


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DTTRIDQAHPIVGVYEVSWAFSPMPGALVGGSALEFVQKLAGGGCDNTVKVWLNNGIHWKMDFFALGMHTNWRDVAWAPNLGLPKSTIASAEDGTVVWTVAKEGGDQWEGNLIKDFKTPVWRVGSWLTGALLAAAGDNNVTLWKEAVDGEWQAGSTVGG

NbL19g09300.1 ferredoxin-thioredoxin_reductase_catalytic_chain_chloroplastic-like [MW = 16.61 kDa]

No. of times detected



log(intensity)



Values from



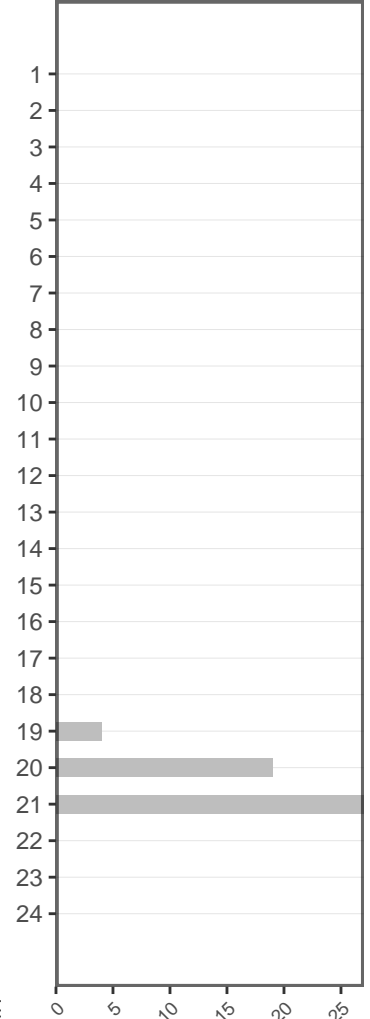
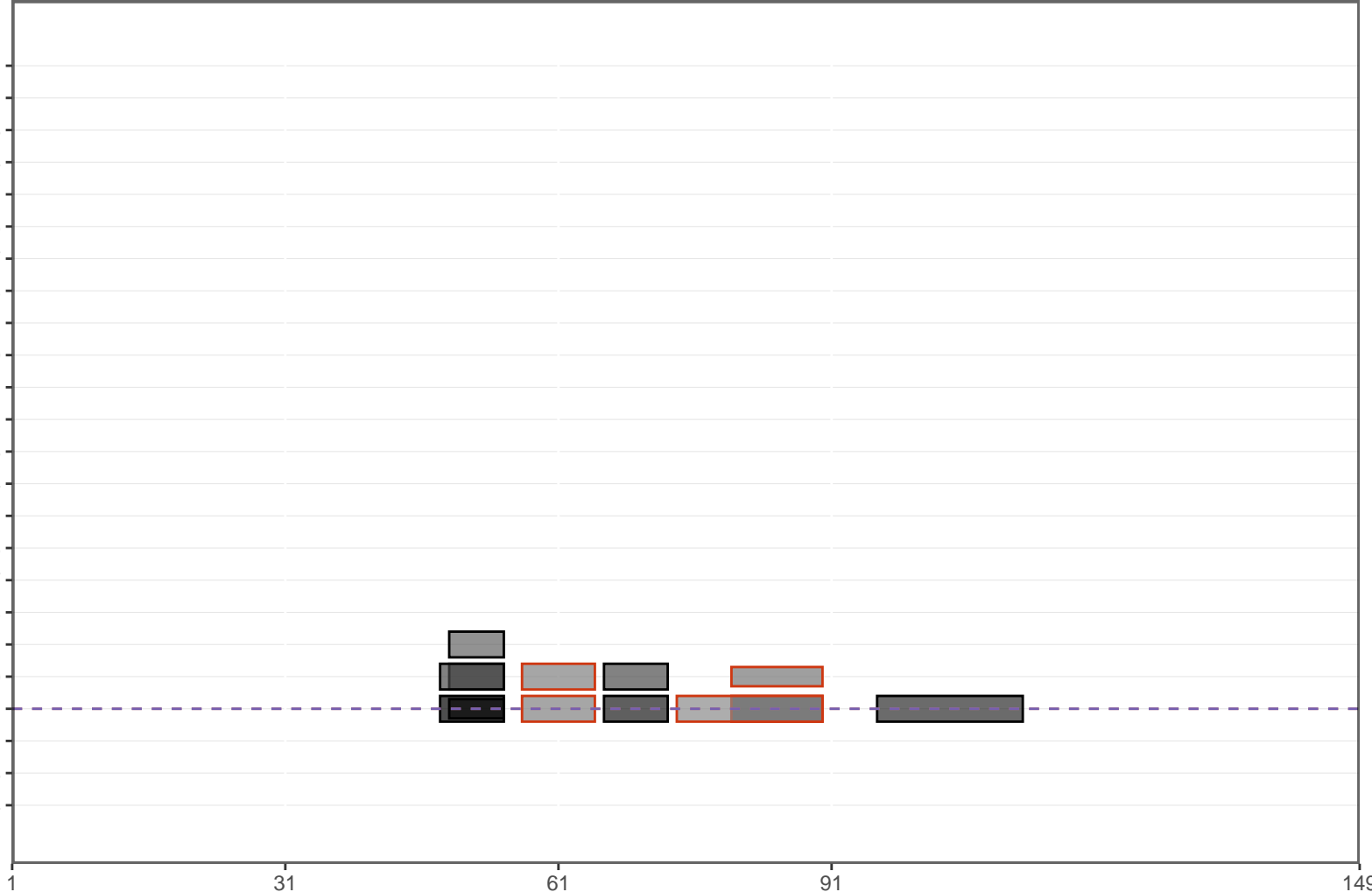
MW indication



Molecular weight

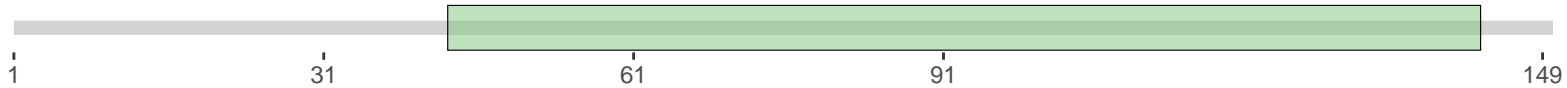


Gel Slice



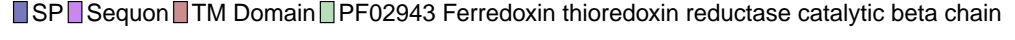
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

MDKGVTSVVIKGLAEHKDITLGAFLGPRHYDDKAAEAGGGFWNGPGVPMRERKECHMLFLTPDNDFAGEEGAIMSEIKETANM

NbL19g09270.1 peroxidase_63-like [MW - SP = 34.17 kDa]

No. of times detected



log(intensity)



Values from



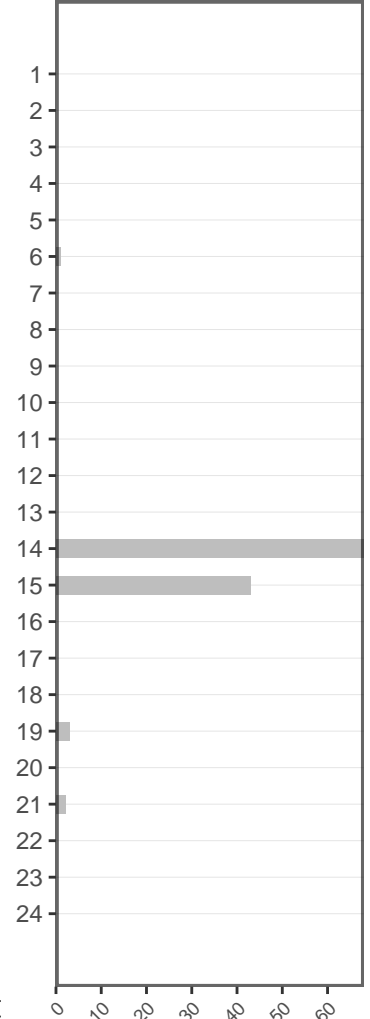
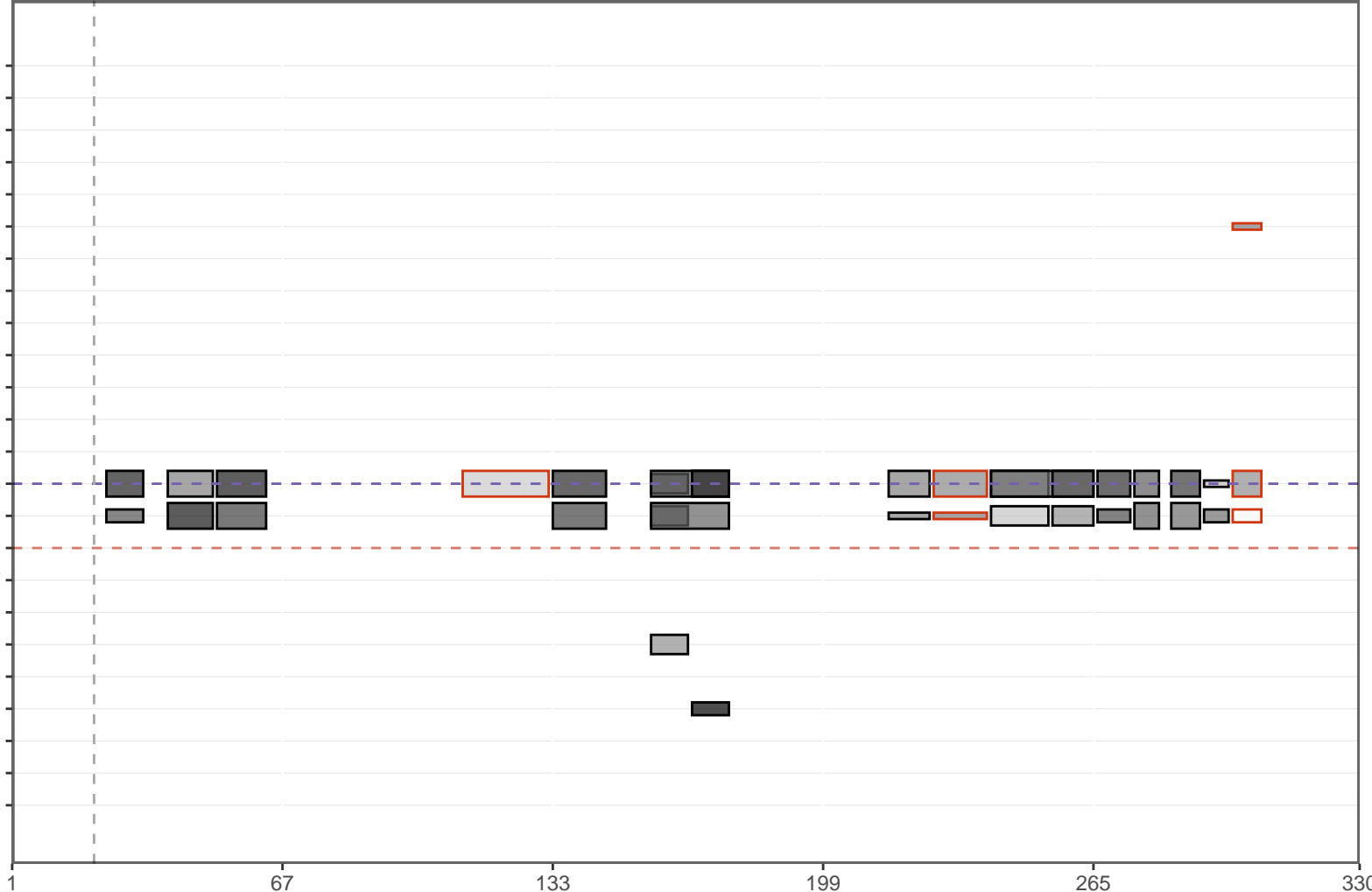
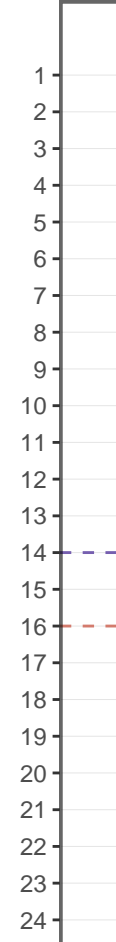
MW indication



Molecular weight

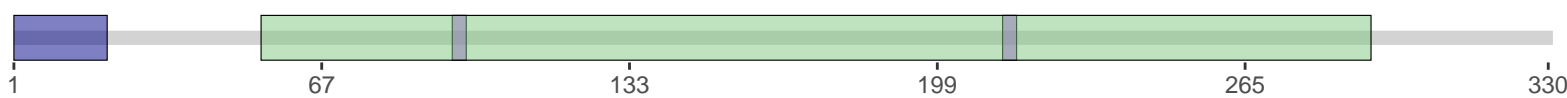


Gel Slice



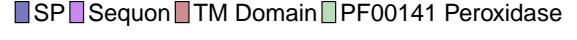
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

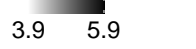
IKASLVEGALPRPTMFMGQIKIFESRGFSTQEMVALSGAHTGFSHCKEFNSDLVYNYKTSQADPSYRFRFAALENAGSNQKDPILSVFNDIMTPNFDMMYYGNLPKGLGLLSSDRGLFSDPRTRHVEEYVRDQNAFKFAAAMQKLESHGVKQKQKGEIRHRQDAFNV

NbL19g08990.1 formate_dehydrogenase_mitochondrial [MW = 42.46 kDa]

No. of times detected



log(intensity)



Values from



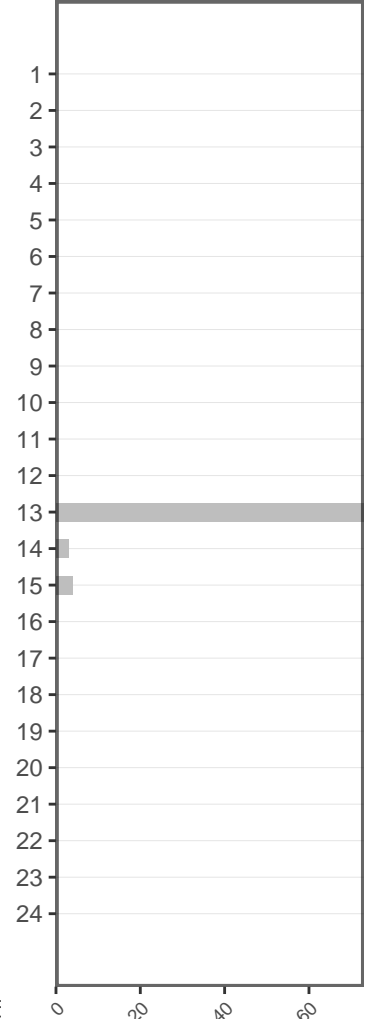
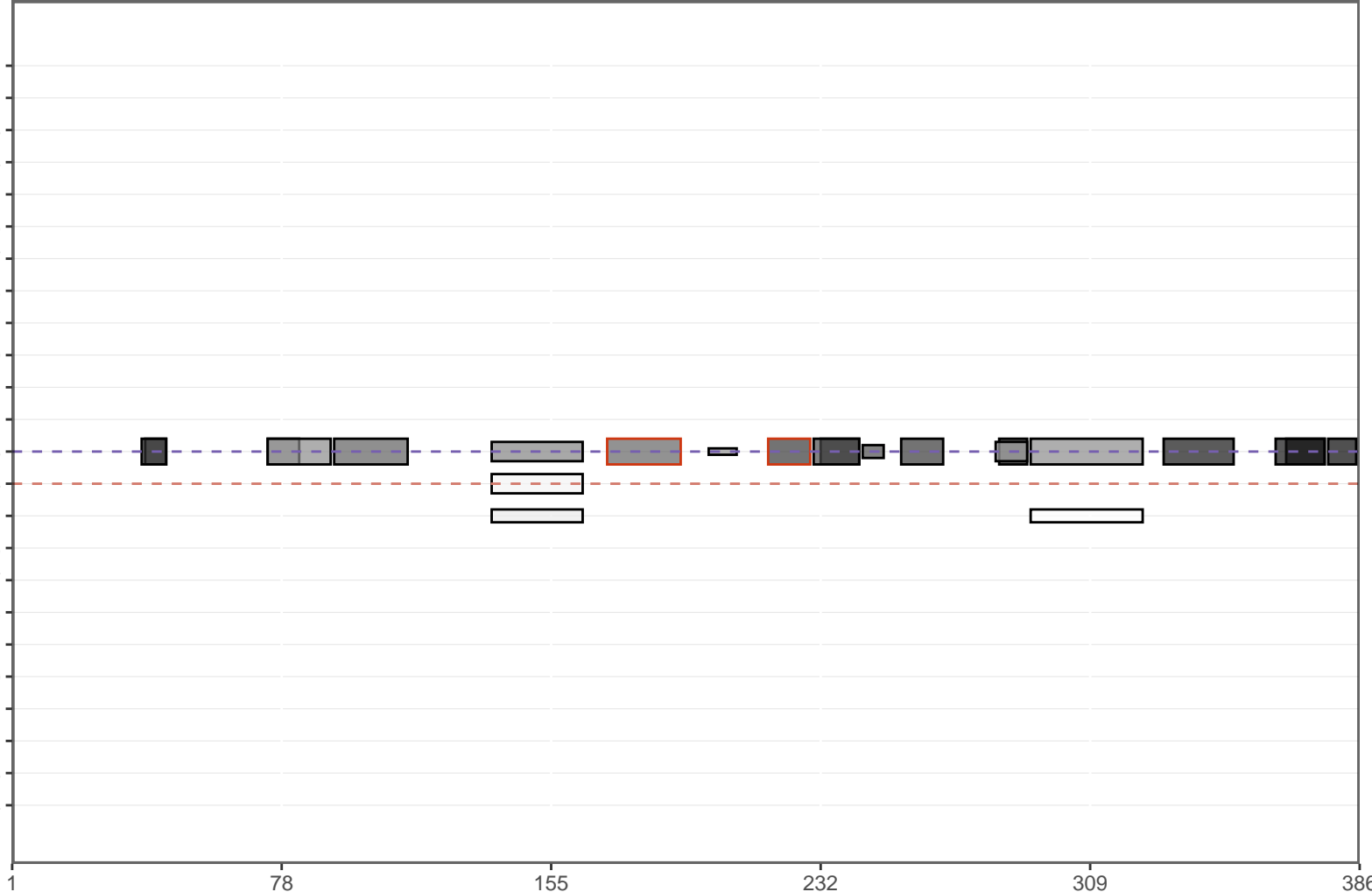
MW indication



Molecular weight

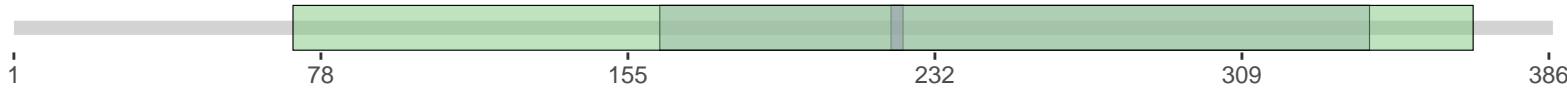


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF00389 D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain
- PF02826 D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain

Protein sequence:

SEWVAGIAYRAYDLEKKTVGTVGAGRIGRLLLRKLPKFCGLLYHDRVKMDSELENGIGAKFEEDLKKMLSKGDIVVANTPLTEKTKGMFKERIAKMKKGVLVVANNARGAMDTGAVVDAENSGHAGYSGDWWYQPAKPKDHPWRWYMPNGAMTHPSGTTIDMLRVAAGTKDMLDRYFKGDFPAQHWYKDGELAPGVR

NbL19g08980.1 protein_farnesyltransferase_subunit_beta-like [MW = 49.86 kDa]

No. of times detected



log(intensity)



Values from



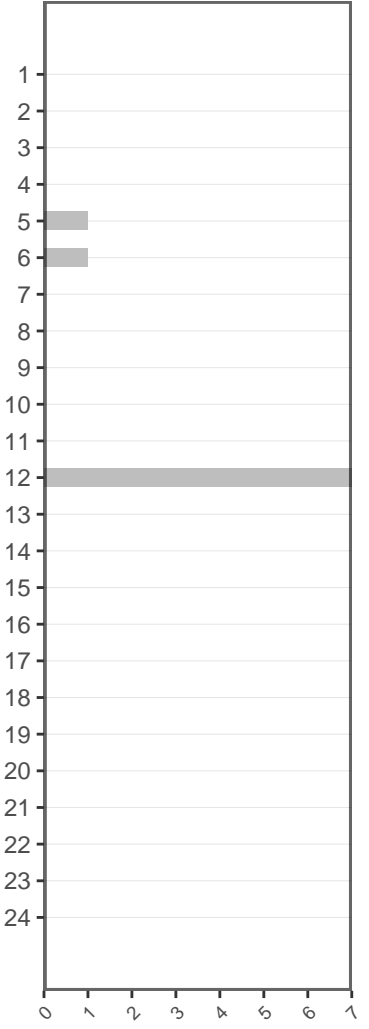
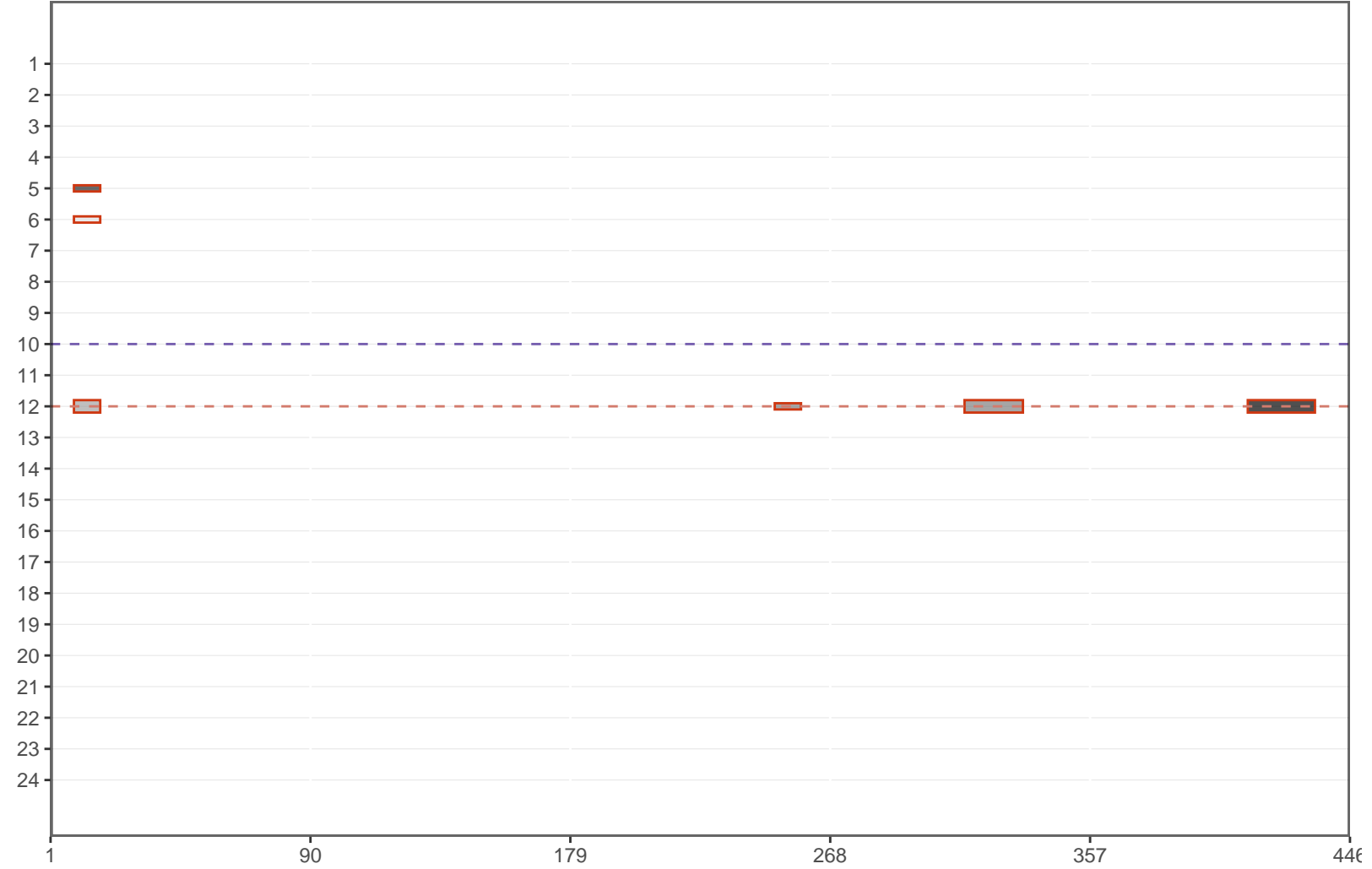
MW indication



Molecular weight

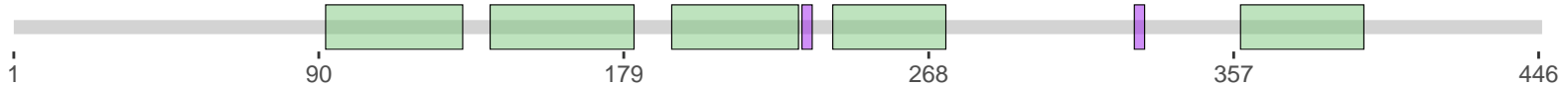


Gel Slice



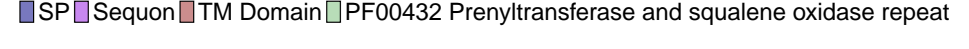
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SEAHGQYTFCCLAAMLIINETNRLDLRLLIDWAVFRQGVGGFGGRTNKLVDGGYSEFWDGAAVFLVDRLKGAYEQLGLSNLSAESADESSSELSDEEKHLEGTSSHGGEGGENASDPTKADTGTDFVNRRIAMQPVDFEYLGQVYLLGSGQDGGFRDKPKGKRDHYHTGYLGLSLGADYQWNTNEADAPLPKDFGQPSQNLLEQIHPVYVLDRYEARFFSCL

NbL19g08930.1 carbonic_anhydrase_chloroplastic [MW = 35.96 kDa]

No. of times detected



log(intensity)



Values from



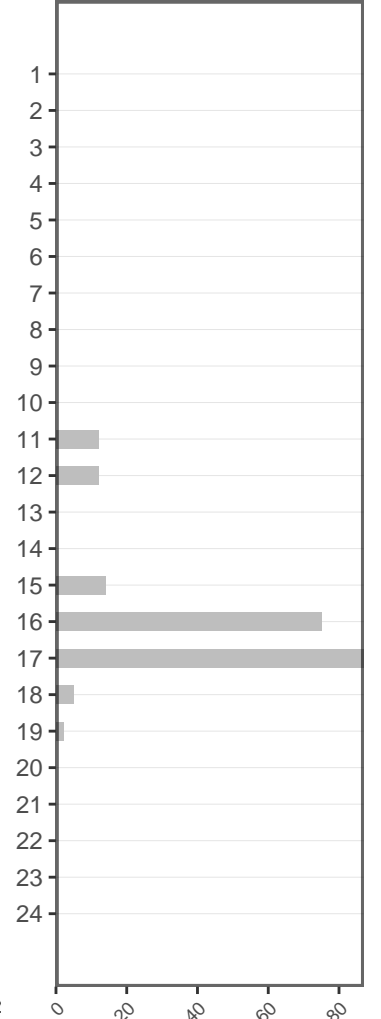
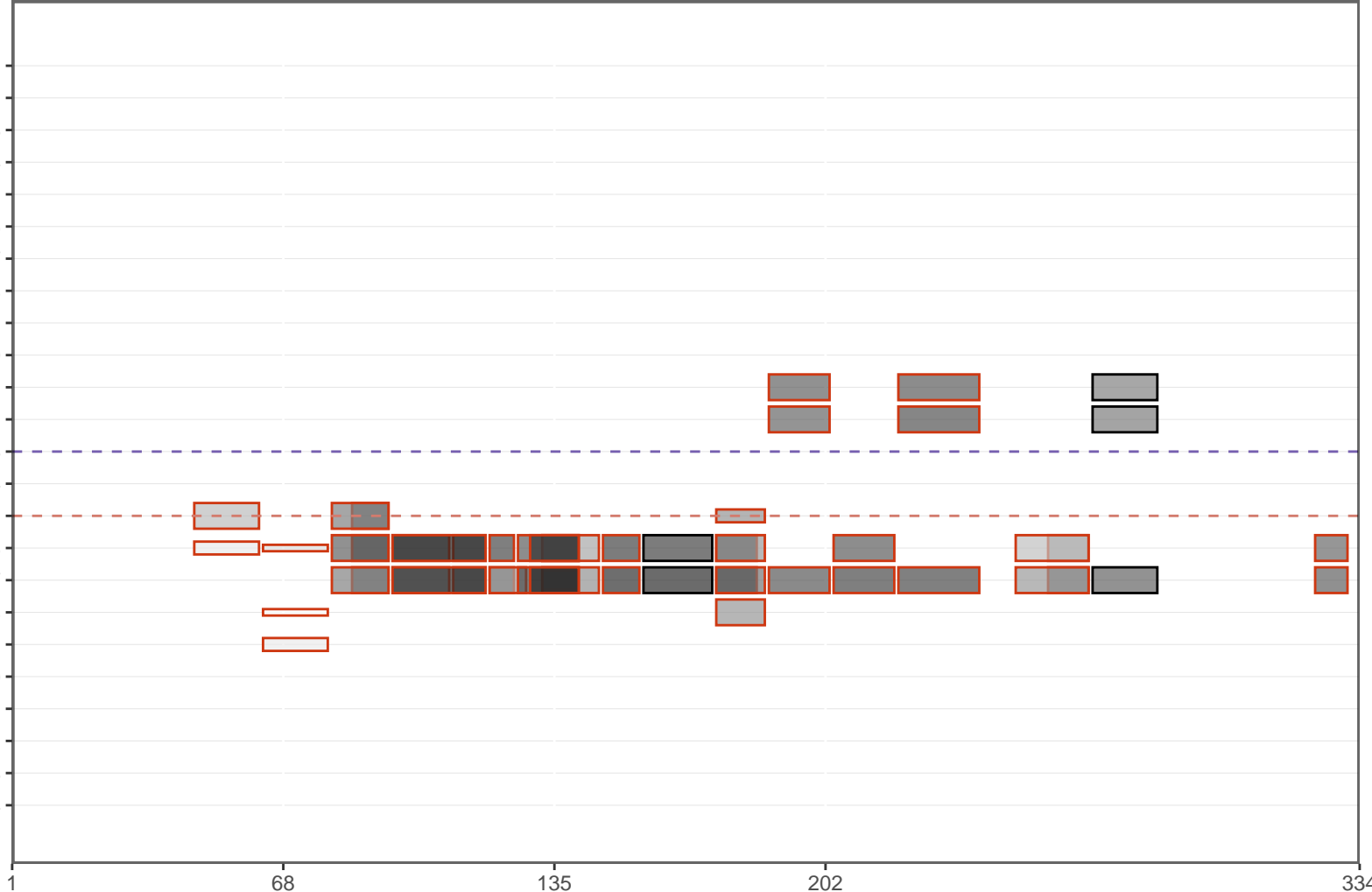
MW indication



Molecular weight

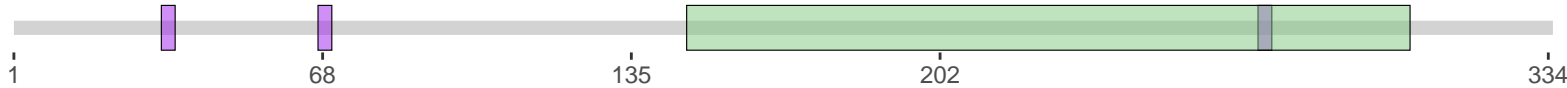


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IRVCPSHLNFOPGEAFVVRNANMVRVDRKTRYSGVGAIEVWVHLKVENIVVGHSGGGKGLMLSPADGGSESTAFIEDWVKKGLPAKAVGGDHWKDFADQQTAGEKEAVVSLGNLLTFVFRVREGLVKVTLAKGGHYDFVNGGFELWGLERFGLSPSLVKNVWASLHWKLL*

NbL19g08840.1 50S_ribosomal_protein_L12_chloroplastic [MW = 22.18 kDa]

No. of times detected



log(intensity)



Values from



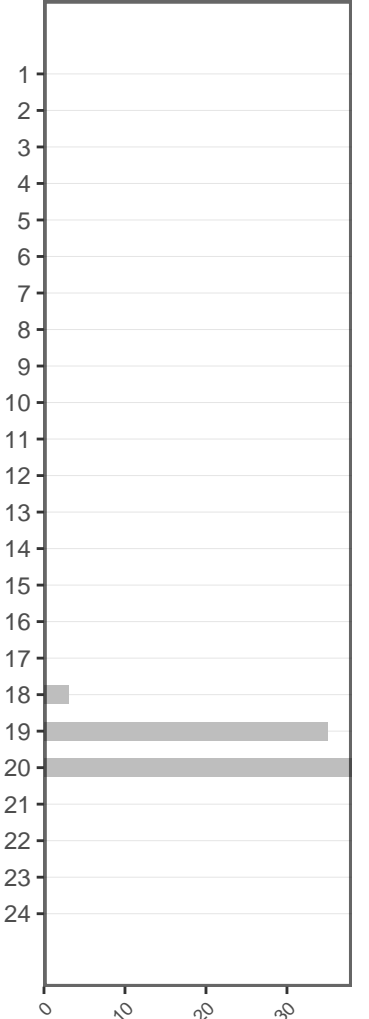
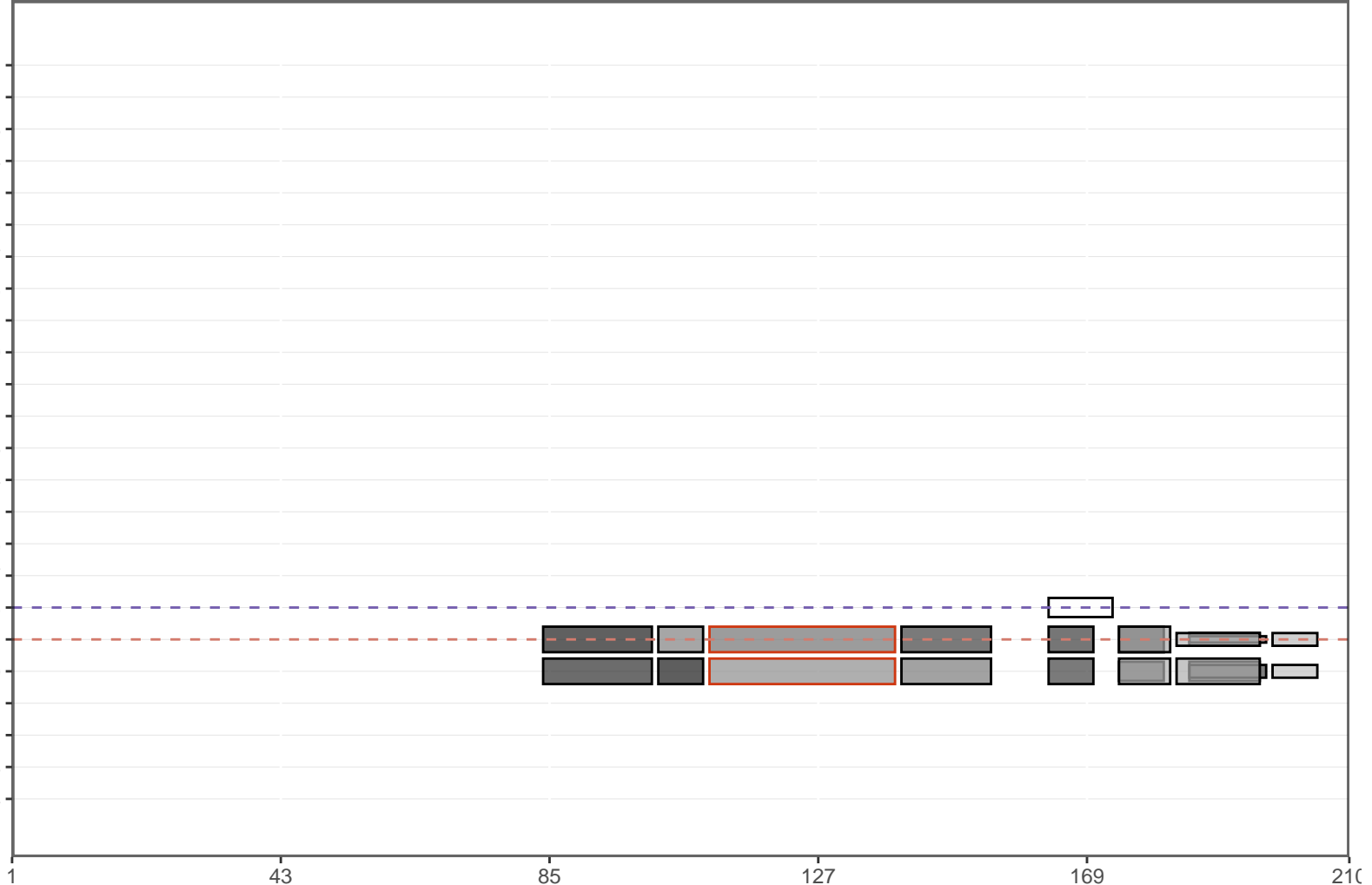
MW indication



Molecular weight

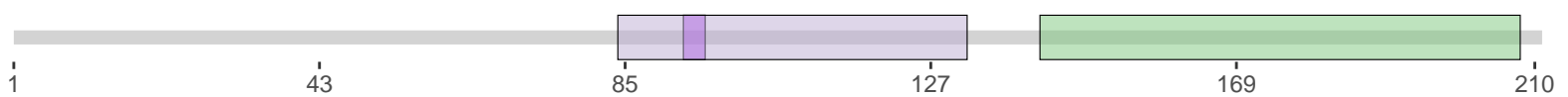


Gel Slice



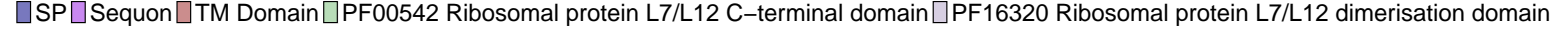
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

INLTLDAQKLVLEYLQDNLGVTAASFAPAAVVAAPGAAAEAPWVEEKTEFDVVIDEVPNARIATIKAVRALTNLALKEAKELIEGLPKKFKEGVSKDEADAKKOLEEAGAKVSIAT

NbL19g08740.1 glutaredoxin [MW = 11.29 kDa]

No. of times detected



log(intensity)



Values from



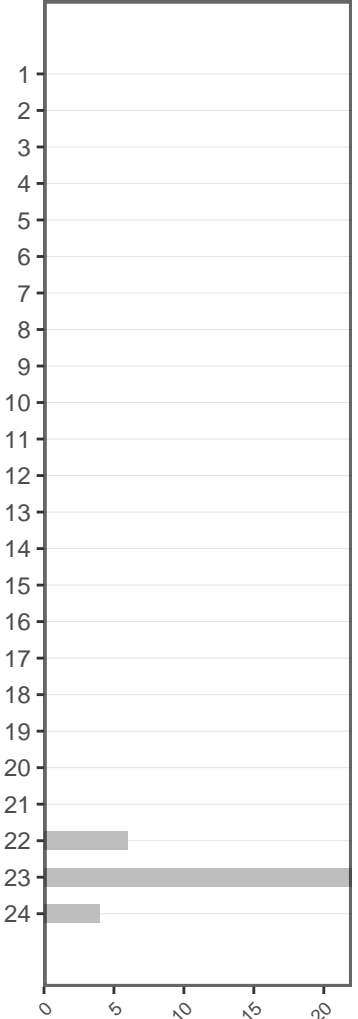
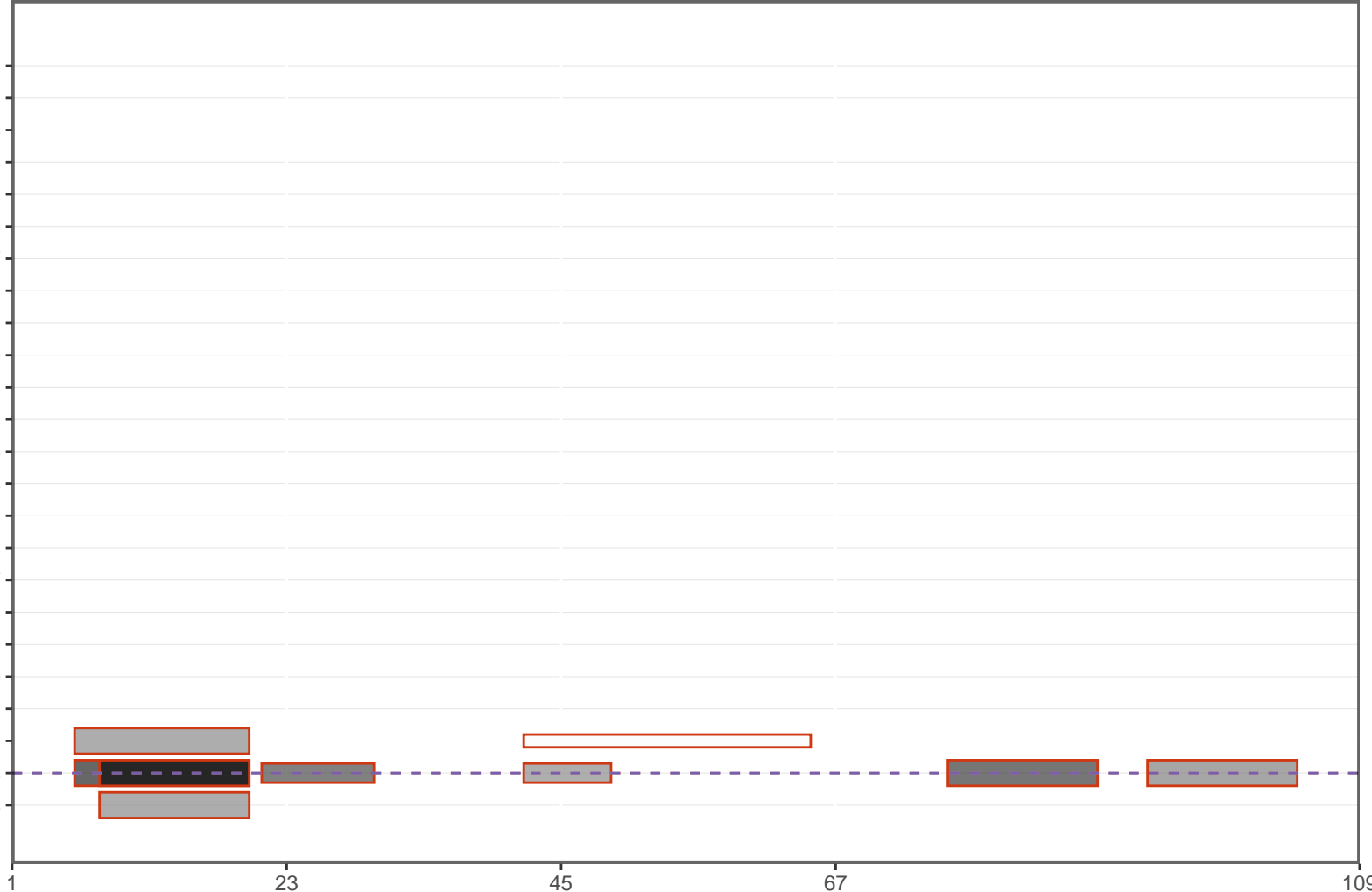
MW indication



Molecular weight

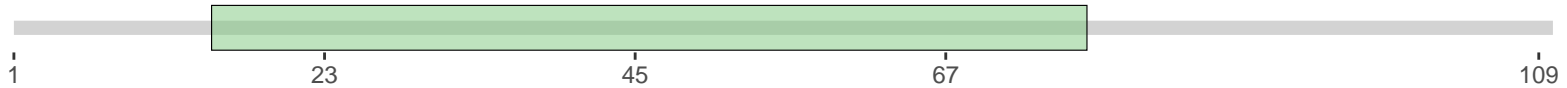


Gel Slice



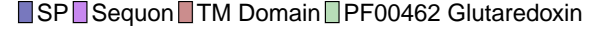
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MAVELDTEKDGSEIGAAIAEWTGQRTVFNFRIGGKHGGDATTALHREGKLVPLITEAGALAKSSSA

NbL19g08650.1 sirohdrochlorin_ferrochelatae_chloroplastic [MW = 22.61 kDa]

No. of times detected



log(intensity)



Values from



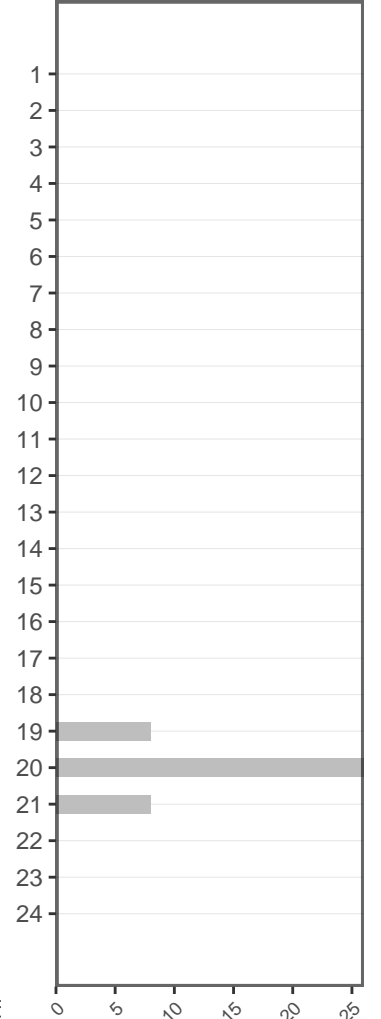
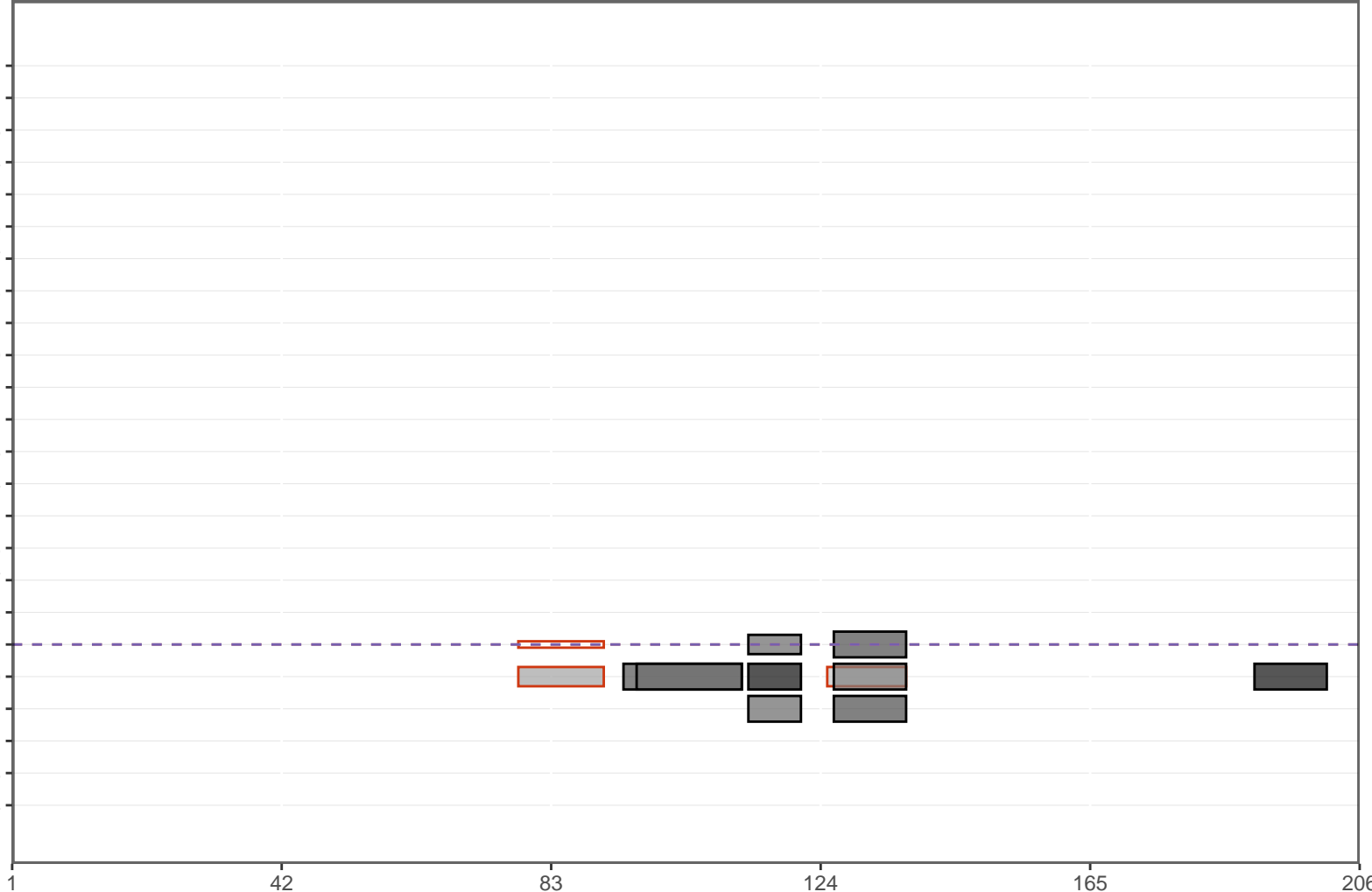
MW indication



Molecular weight

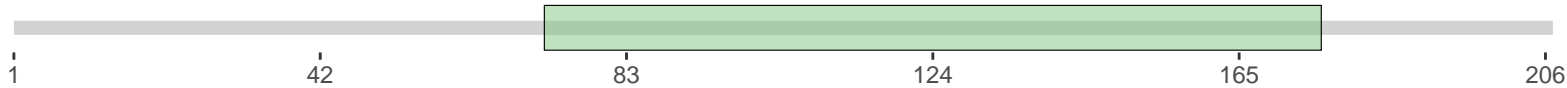


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

#KERTKYPIVEFRIHMELEAERSIRDALFLGVQRGARRIVVSPFLSPGRHWNDIPSLTAAEAKEHFGVSVVITAPLGLHELLVDVNDRIKHQLNHAAGKADEGVCGATGKQGLR

NbL19g08600.1 50S_ribosomal_protein_L5_chloroplastic [MW = 29.53 kDa]

No. of times detected



log(intensity)



Values from



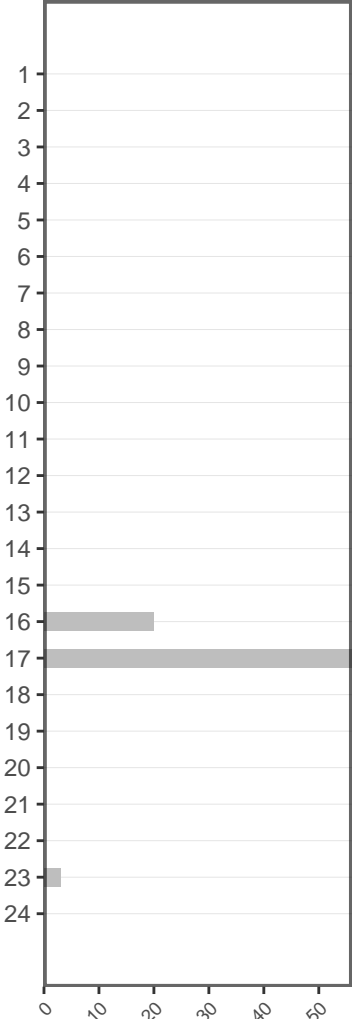
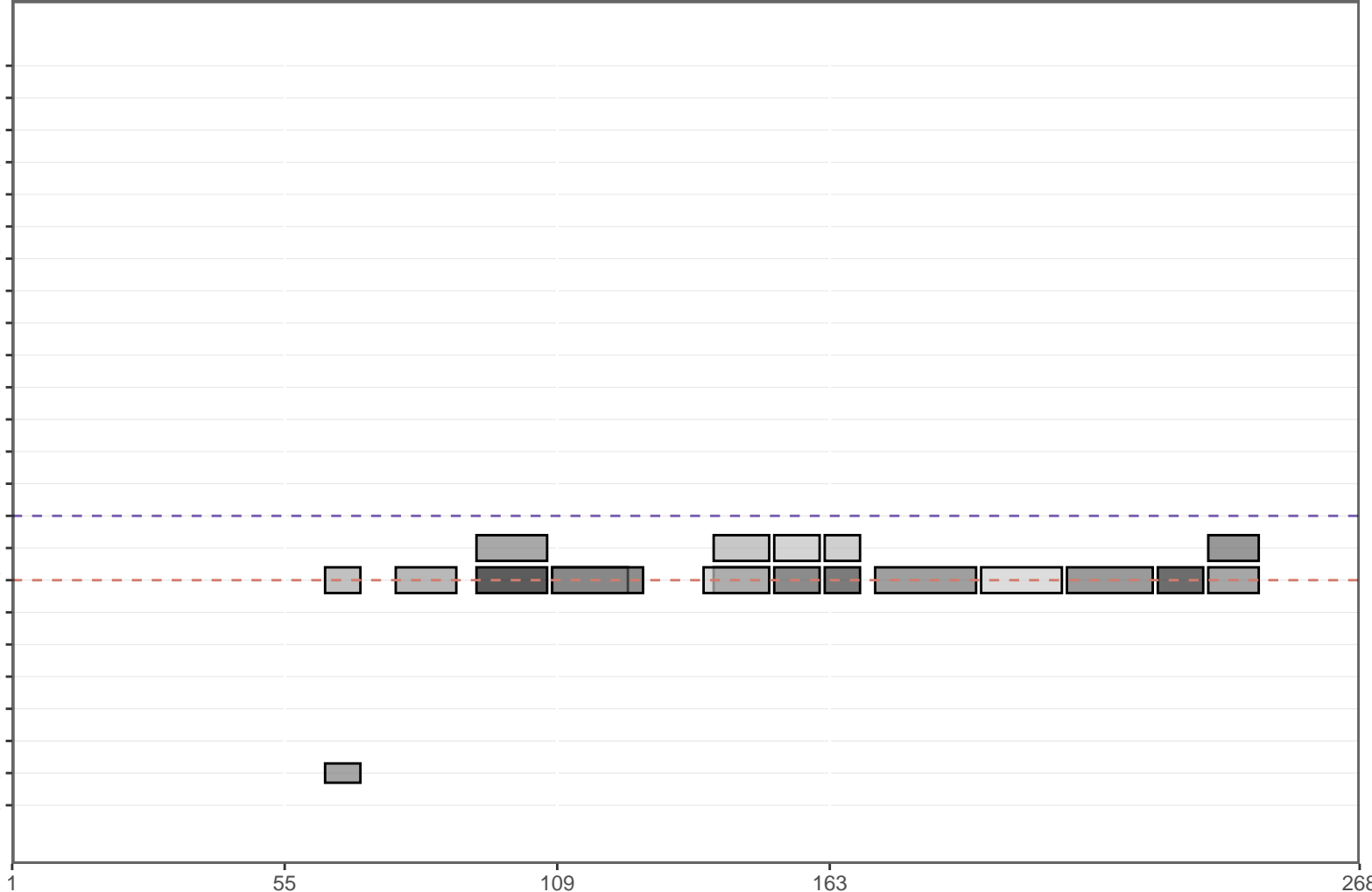
MW indication



Molecular weight



Gel Slice

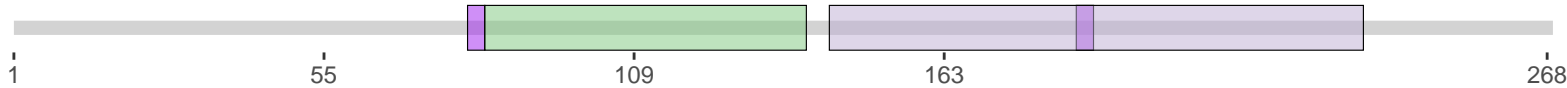


Peptide counts over 4 repeats

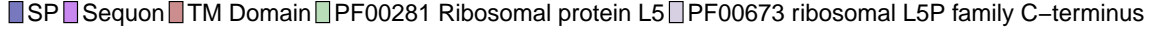
Protein length



Pfam domains



Pfam Description



Protein sequence:

RPVYKTRAKNAUATFNIREGGPLGAVTLRGNMFSFLDRNLNGLPRTRDFGGVNPNSFDGHNYSIGFRQGSVFPFELSVDALGKPRGMVDGTTTAEQKEAHRLLALMGMPFREGAVGGTNNVRRKKLRGHIIFDSKAKGRSR

NbL19g08550.1 titin [MW = 418.08 kDa]

No. of times detected



log(intensity)



Values from



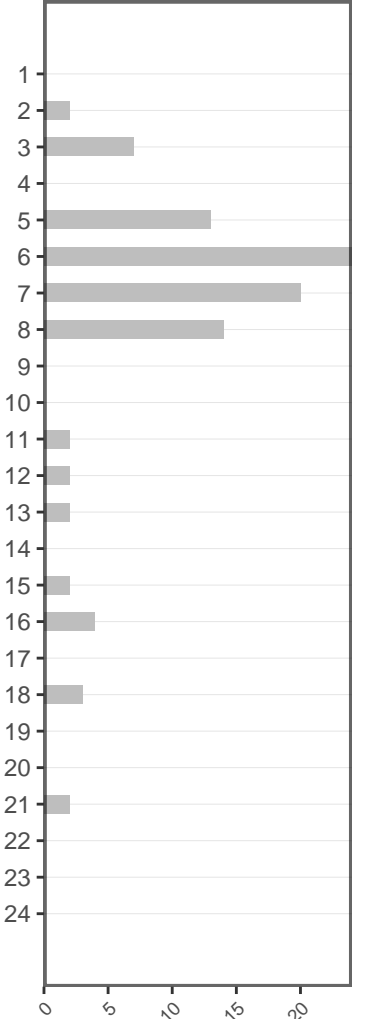
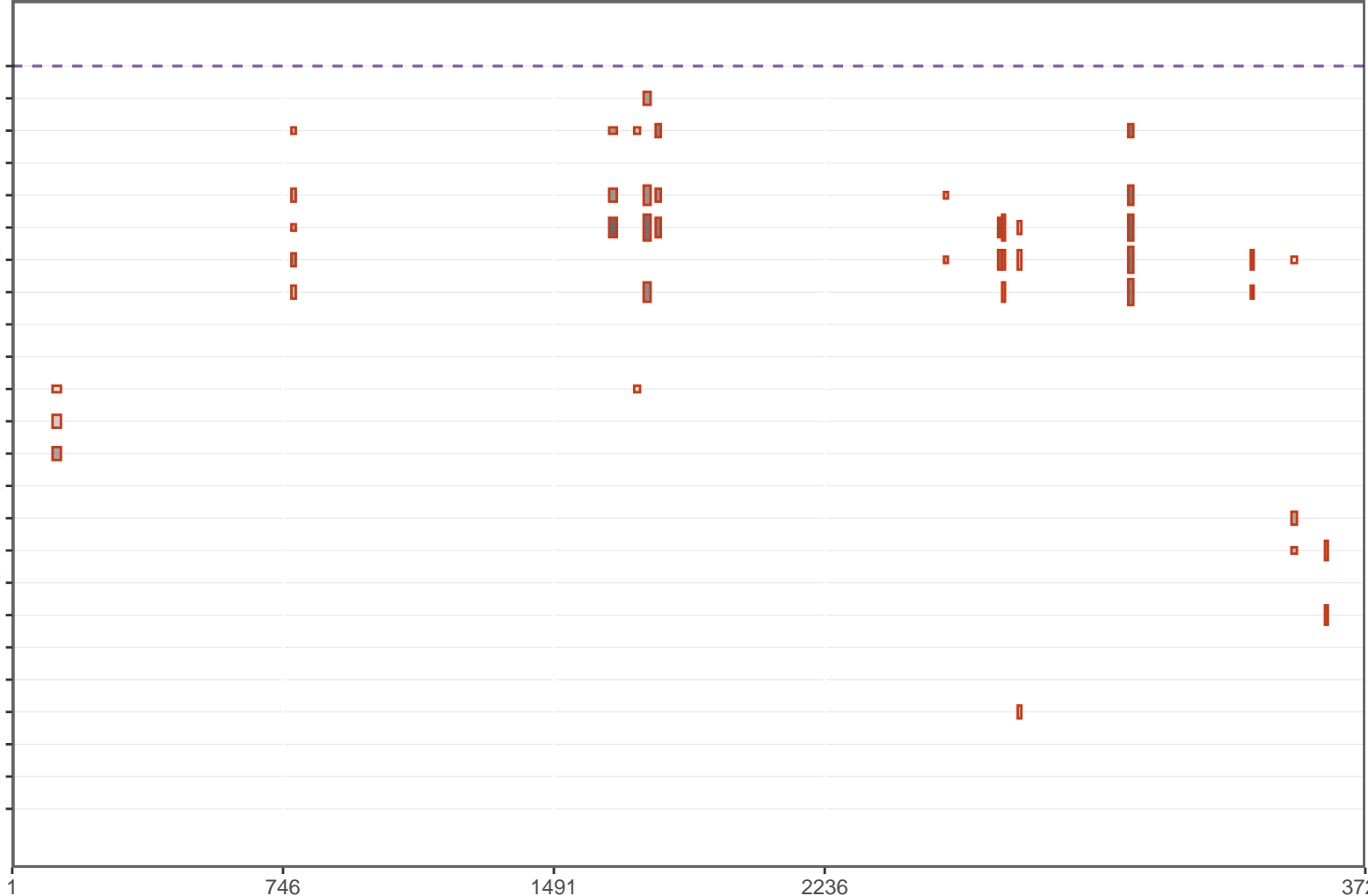
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



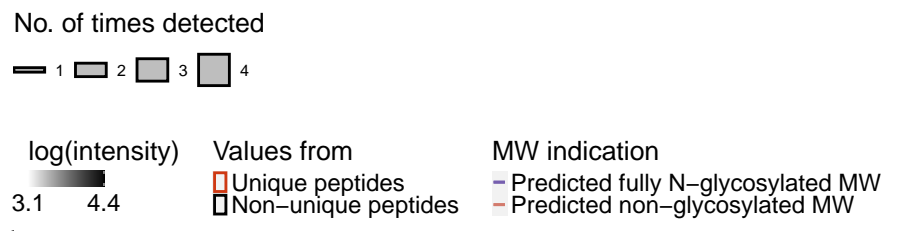
Pfam domains

Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

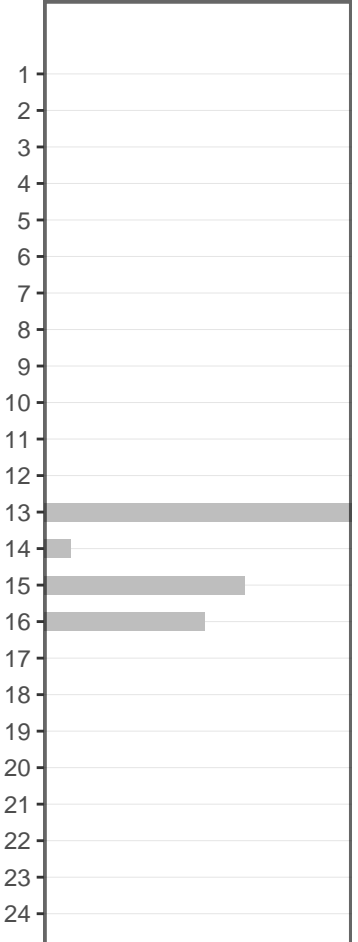
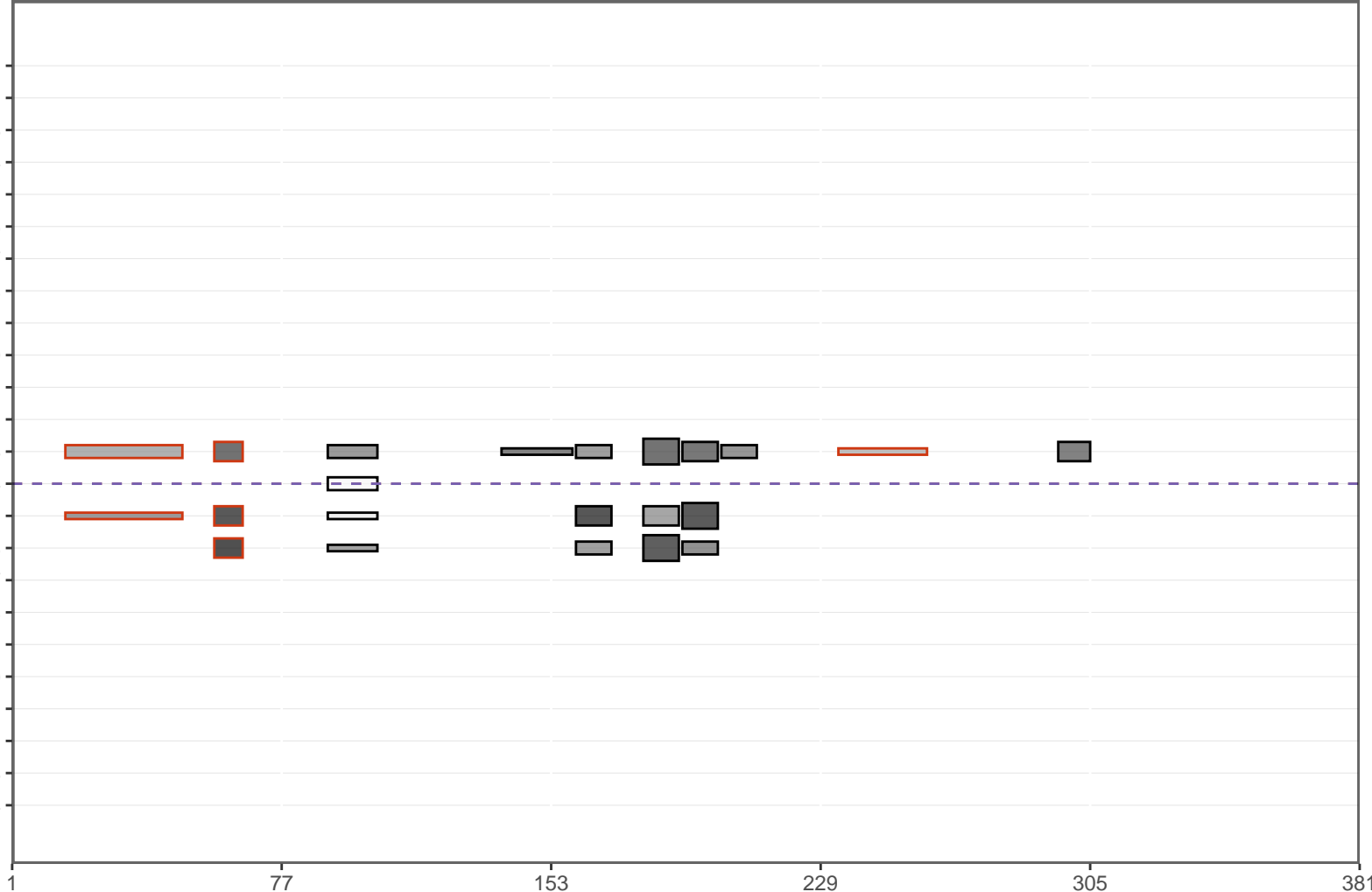
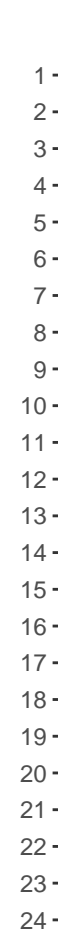
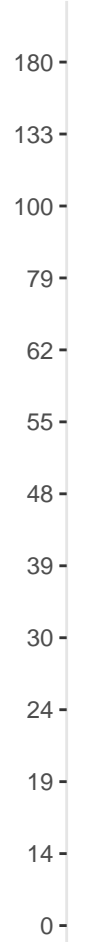
VGGKLEEPVVEQTPKGGWEEETPKELAFEEKPEEPVVEETPEELAVENKPKAVGKHKVTLLEKNPIELNENNDGSPGNTNDAADYLAVEKPEEPKAEKKEEQMAKEKLEEPNVEDKPEKSVIEKSEKLATEETLEEQAGEETPEALAVEEKPDSEAVVEETVEELAEIKPKKETATEKPKPTVTLLEKNMPVVDTKDKNKSEIRPNANNNDVSDYPAVEAMPPEELAVETKVEEPPWILEKPKELAVEETPKTVVEEKPENLAAREETLEPALLEEPEETVEEKPI

NbL19g08480.1 RNA-binding_protein_squid [MW = 39.48 kDa]

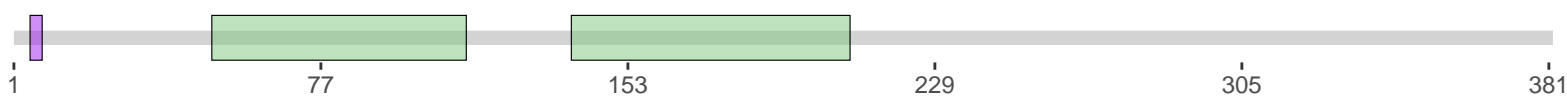


Molecular weight

Gel Slice



Peptide counts over 4 repeats



Pfam Description
 SP Sequon TM Domain PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

Protein sequence:

FDSEKSVEDILANGNRLDFAGTQVEKKAEPKRNAPLPLPATSKRQGHPRASFQGGFDAYGGYGDGDFGAGGPPYRSGGPPYGRSSAYGGYGGAGMGYGGYGGAGYGGFRFEASFQYSSRYGGAFGRGVDVGGYGGPSEGYYGGVAAGSGYGGYGGAGLGGYGGDGTGSSMYGSSRGGYGGAGSGRHPVGR

NbL19g08390.1 glucuronokinase_1-like [MW = 39.74 kDa]

No. of times detected



log(intensity)



Values from



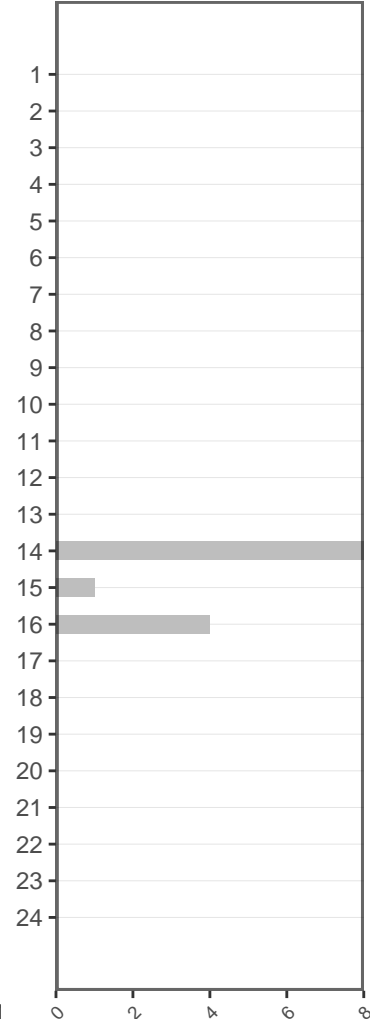
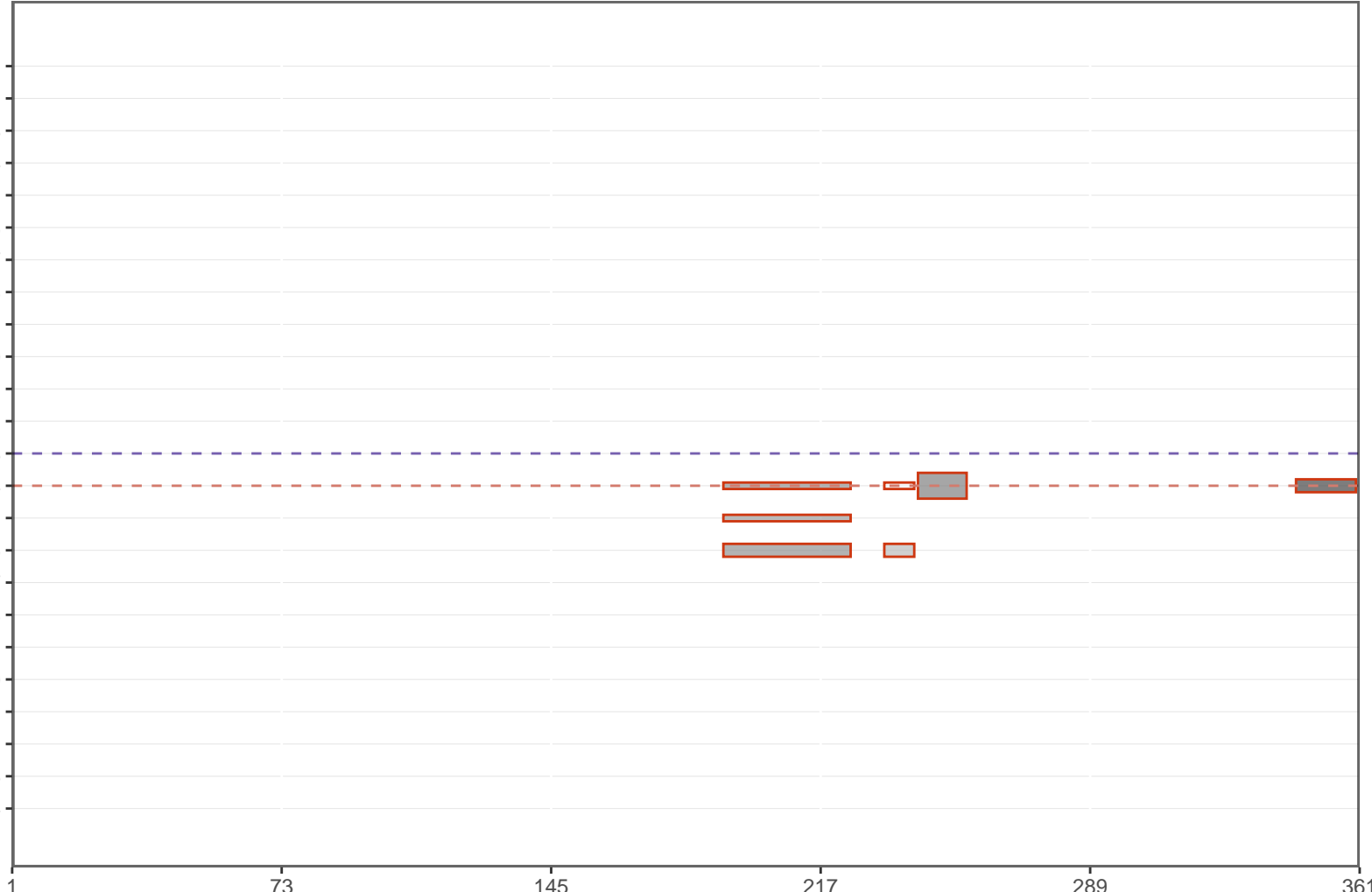
MW indication



Molecular weight

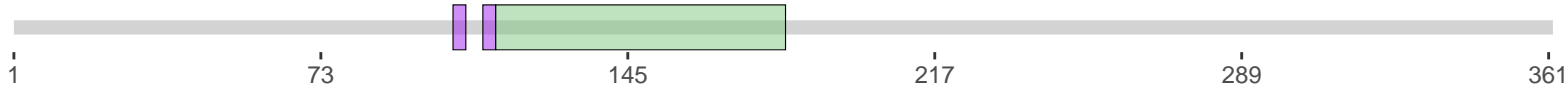


Gel Slice



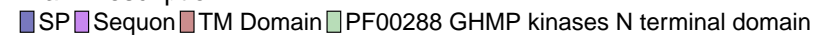
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GLQDRVAQVYGGSLVIMDFGKNHMDLGHGIVTPVDVLLPLLYIAENPDSGKVHSTVQRWLDGDFRSTMEEVANAAEGRKALLEKDKLALALMNHNFDLRLMFGDDALGANIEMVEIARRIGAAASKFTGSGGAVVVFQDPGSGVWQLEDAGHSAGFTFQPKVMPSEFLSEVDLQTPGSH

NbL19g08250.1 ras-related_protein_RABB1b [MW = 23.34 kDa]

No. of times detected



log(intensity)



Values from



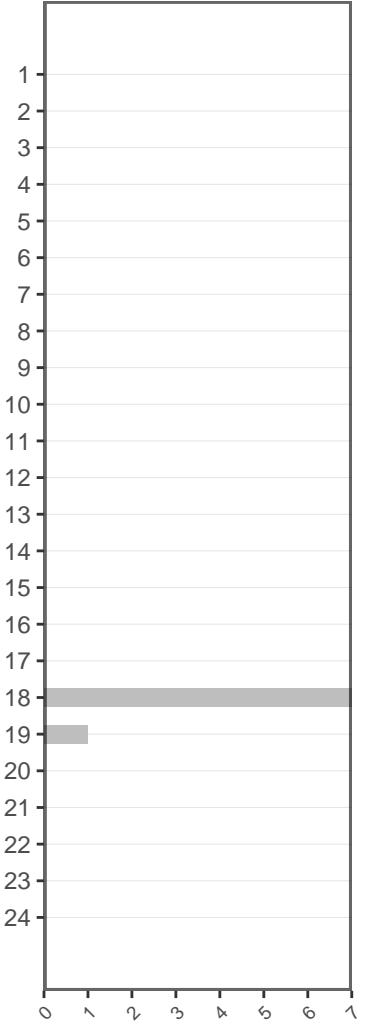
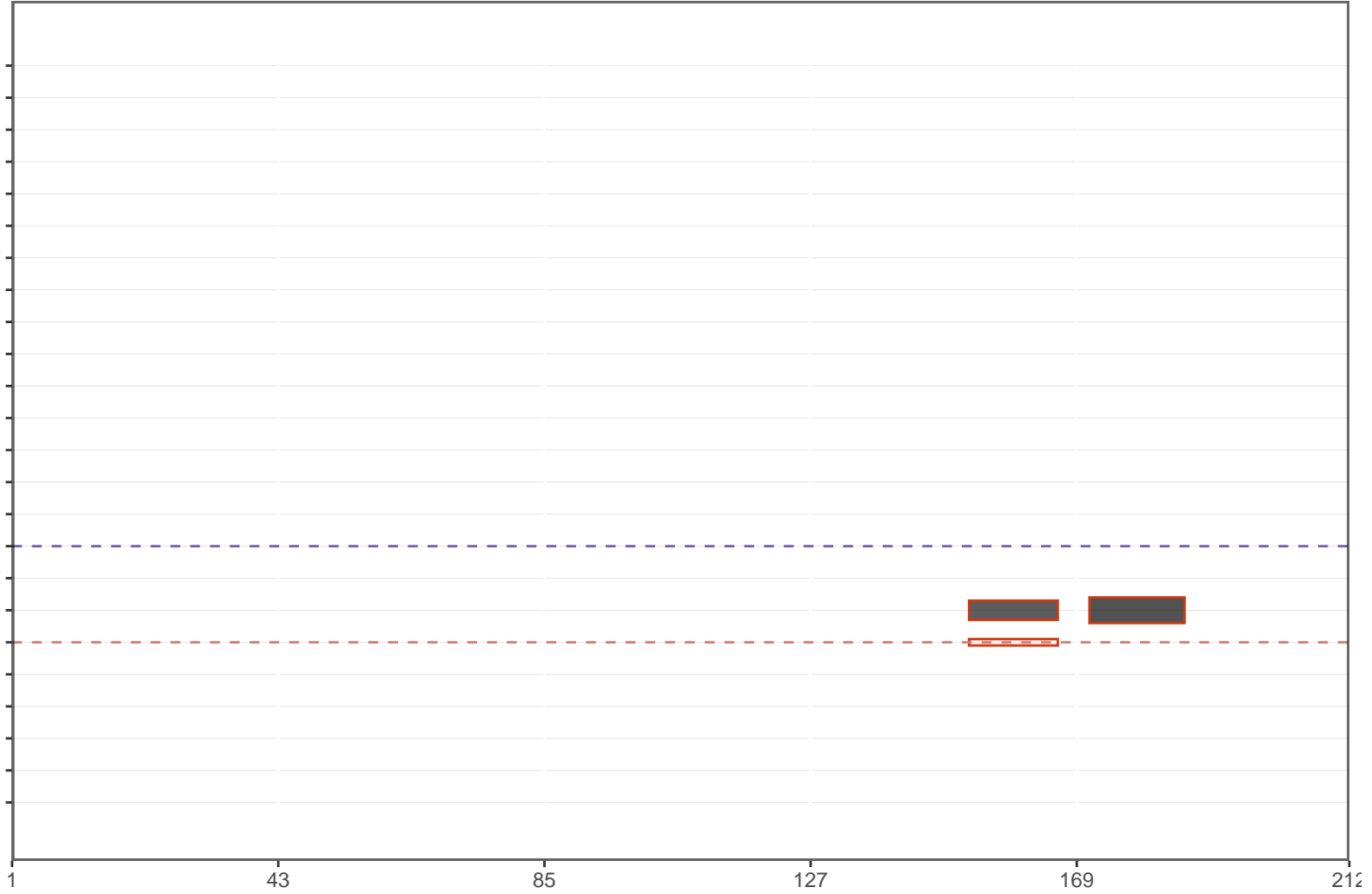
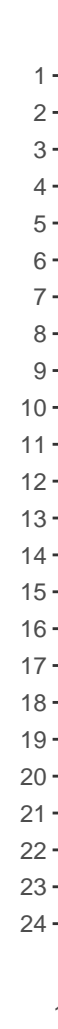
MW indication



Molecular weight



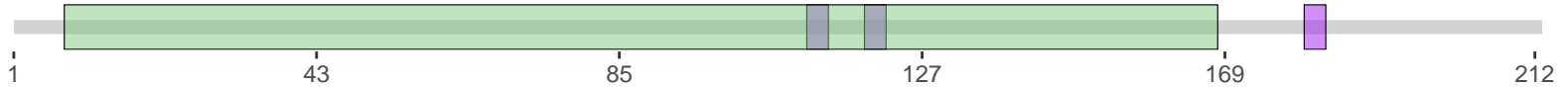
Gel Slice



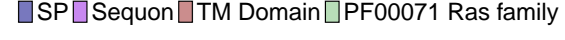
Protein length



Pfam domains



Pfam Description



Protein sequence:

MSLAVLEDAKQIHANPMITMLVGNKEDLHRRAVSKKEEGEAFKENGKLLFLEASARTAGNVEEAFQITAKILQKIDEGVFDVSESSGKIVSYGRTRGGAGPRDGAIAQRGGCCG

NbL19g08220.1 uncharacterized_LOC104120577 [MW = 33.63 kDa]

No. of times detected



log(intensity)



Values from



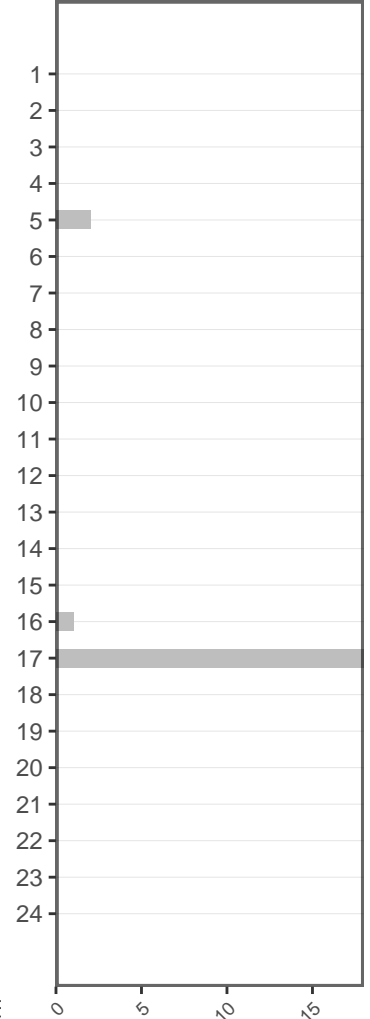
MW indication



Molecular weight

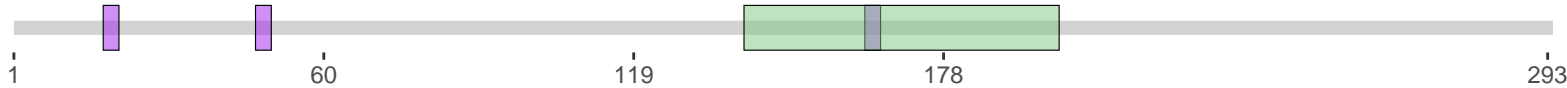


Gel Slice



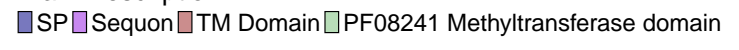
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

NAQELAKNPRLLDYFVFKDLNDDQKLEFENGSFDAVLGTVSGVYLGQPEKVFAEVFRVLRKPGQGVFVFSNRLPFYKRVISAWRRDSTGYGRVQLVGYFGQVEGFTQPEVIRKLPFTGKDDGVAQGNLPSNWMMLQTLGLSASSDPFVAWVAVRNRKPKVHE

NbL19g08070.1 glucose-6-phosphate_1-dehydrogenase_cytoplasmic_isoform [MW = 26.69 kDa]

No. of times detected



log(intensity)



Values from



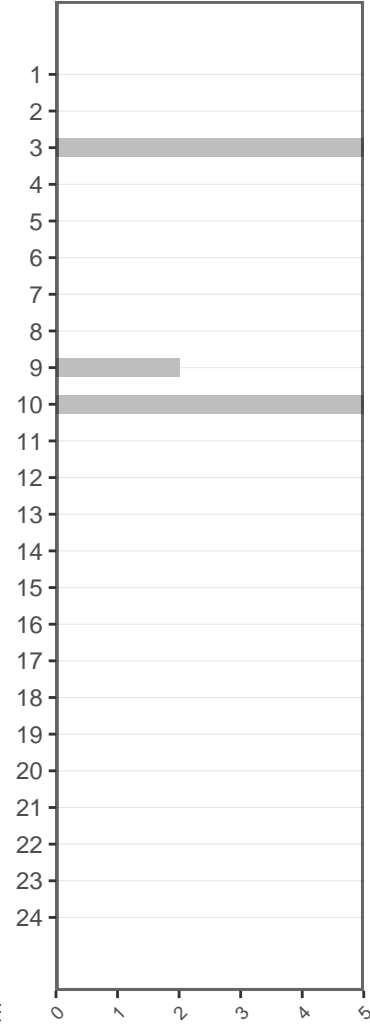
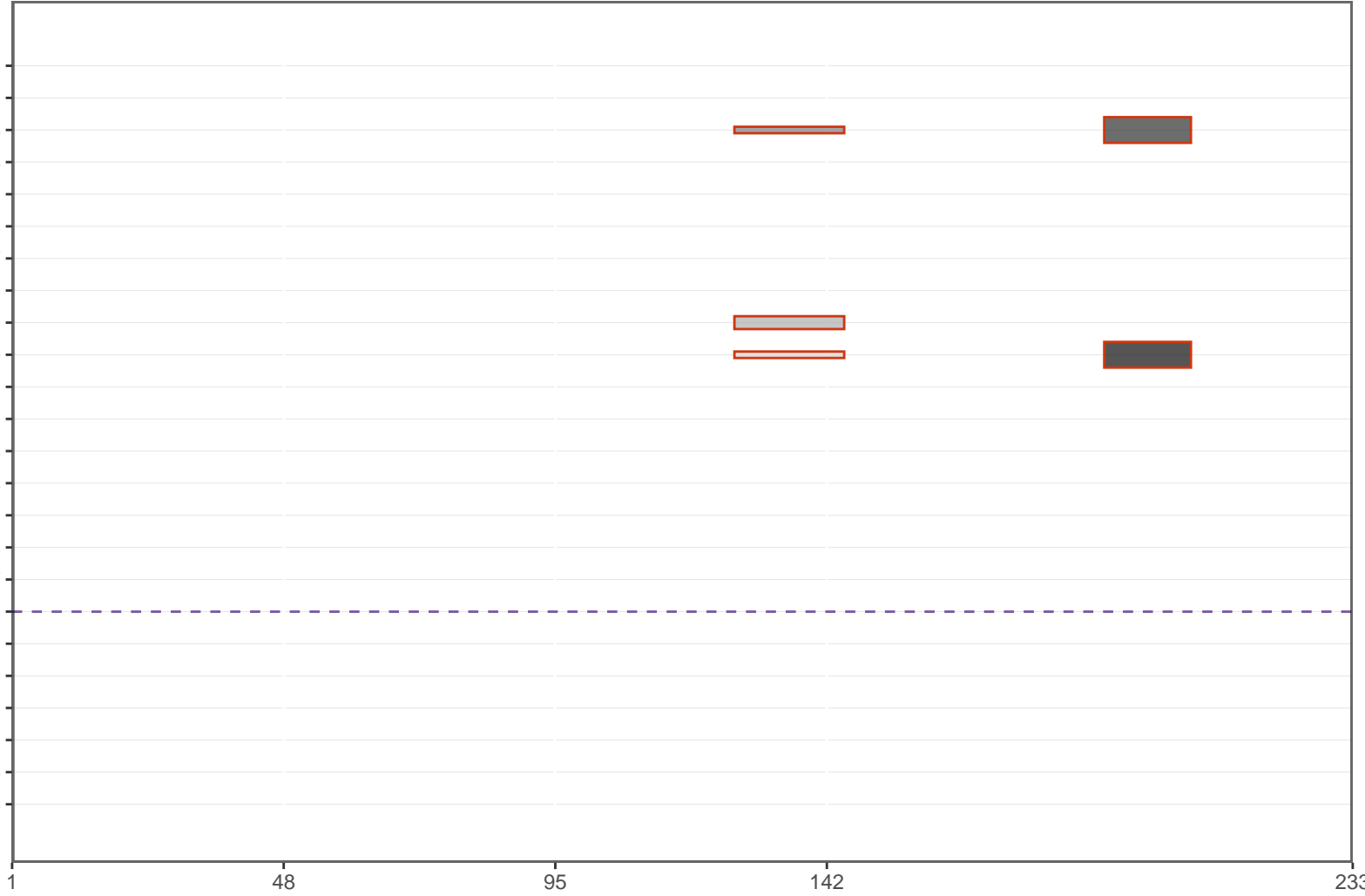
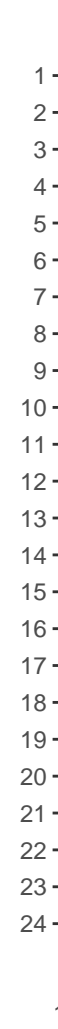
MW indication



Molecular weight



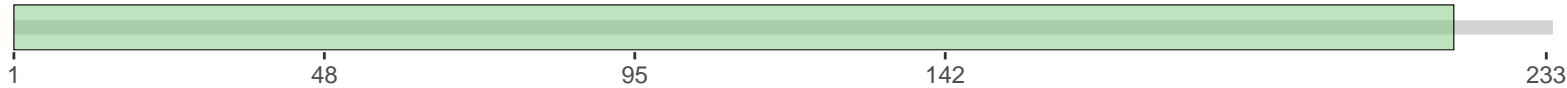
Gel Slice



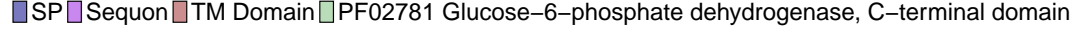
Protein length



Pfam domains



Pfam Description

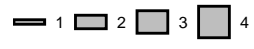


Protein sequence:

IGRNEFVRLQFSEAMFMKLVKPKGLEMSTVQSELDLQYGGRRYGVVPEAVERLLDTRGGDGHFVRRDELKAAWEFTLLHRRIDGGEVKKPKPKGRGPAEDELQNVGVYVQTHGYWIPPTL*

NbL19g07750.1 nuclear_transport_factor_2-like [MW = 24.87 kDa]

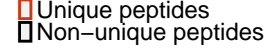
No. of times detected



log(intensity)



Values from



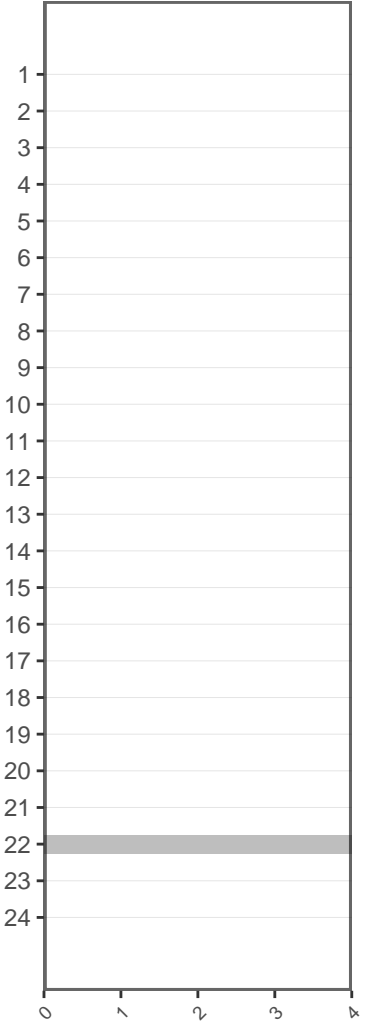
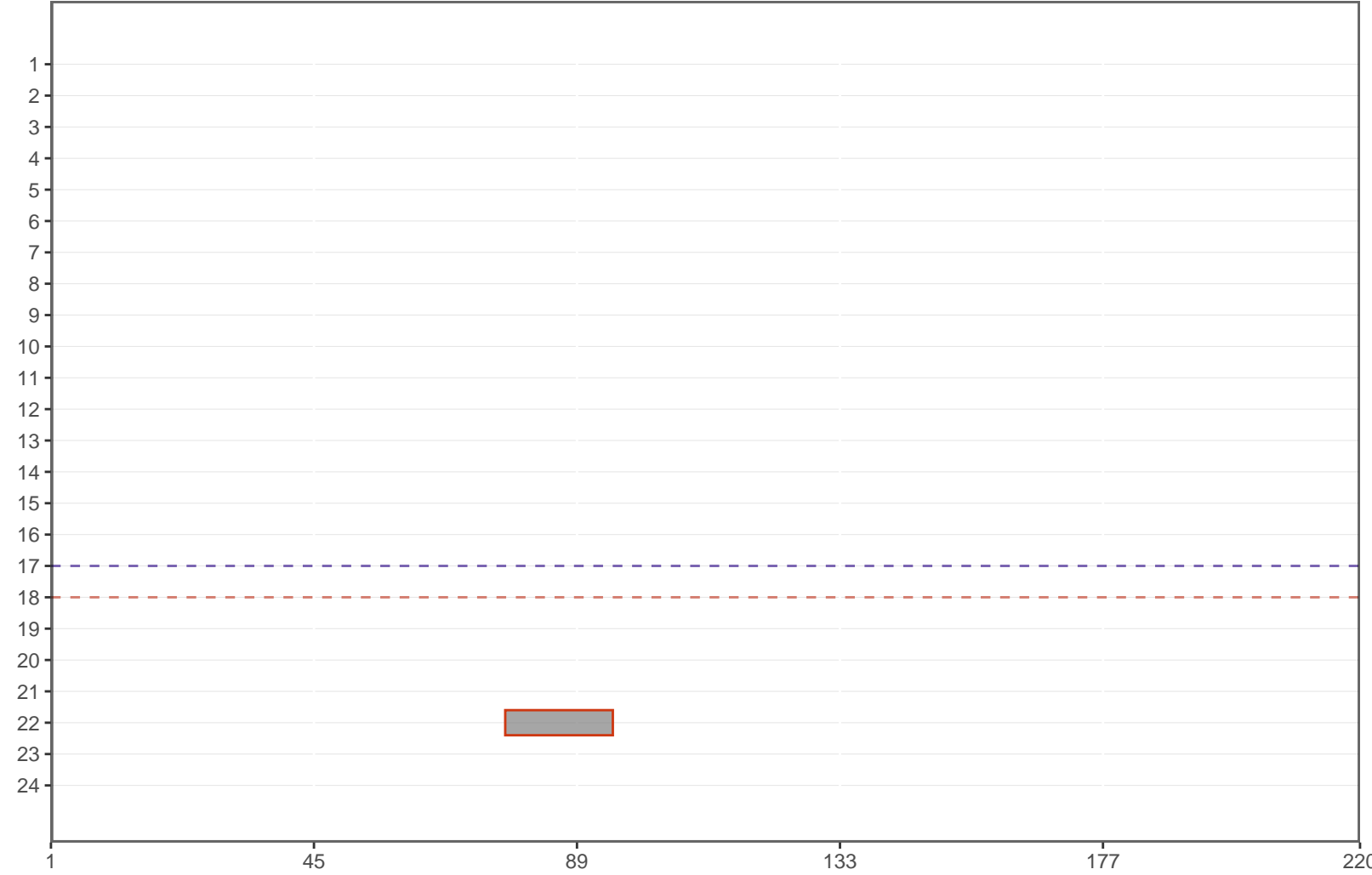
MW indication



Molecular weight

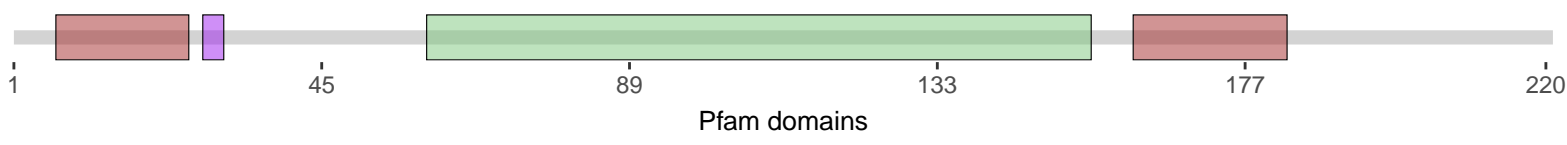


Gel Slice



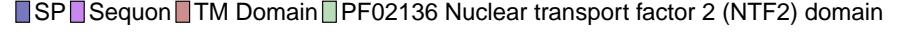
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CGAQHIVAKLTSLPFGQGRKQINIVDQRP66PGMGMLVFSGNLQLPGEHVLKFSQVFSPLRAALLLFFVLFIRIGDMLLYFAISKSHFNRLSKENGWNFDFLFRTPVDFPFRWGRMFKV

NbL19g07710.1 uncharacterized_protein_YciO-like [MW = 33.36 kDa]

No. of times detected



log(intensity)



Values from



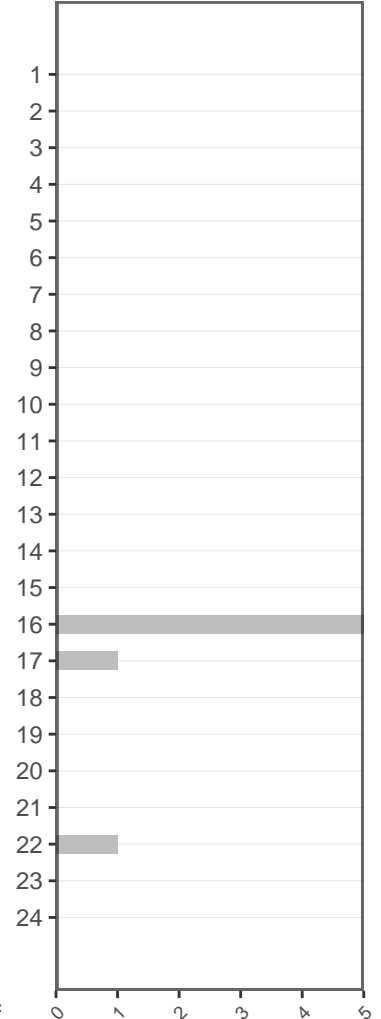
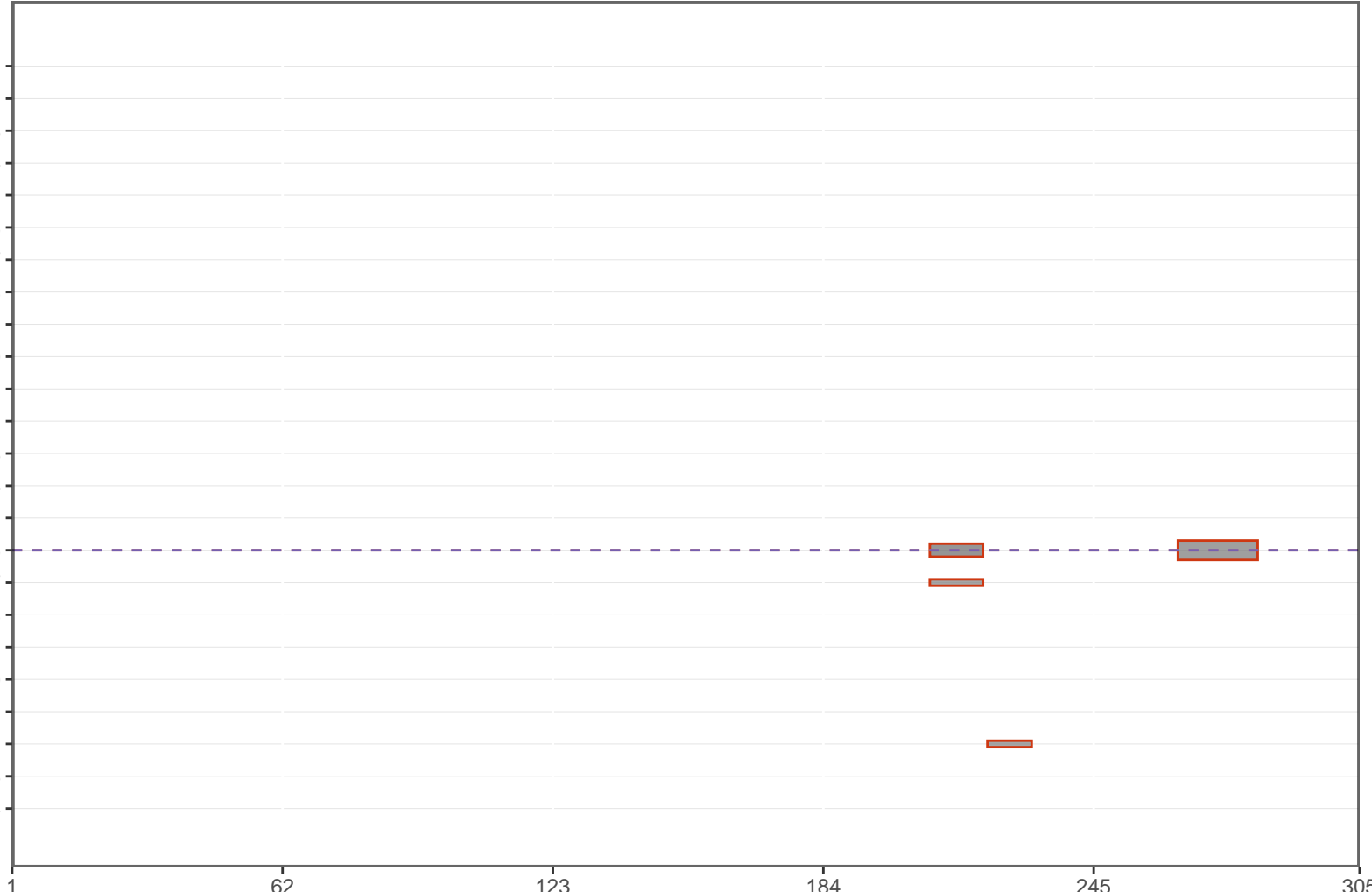
MW indication



Molecular weight

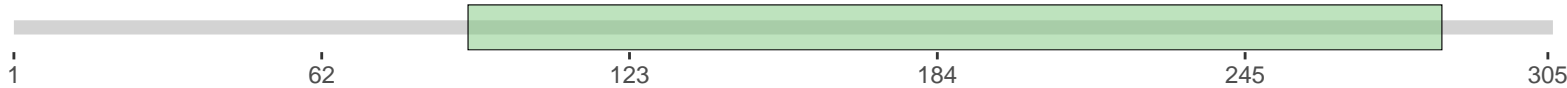


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISFRDIDTYTGFSSGNGGGLTDFRAVHKHLPGPVTFILATASKLQPKGQTRYGTAASRYSRKNKNGVRIPODPVCGALEKMDGPLISTEVKSPFENEWLDPVIADVYGPGEGLDFVVDAGLRVADPSTVVDMTASSPHLRGGKPKGPVMAIEDDDSDARDGN

NbL19g07620.1 basic_blue_protein [MW = 20.95 kDa]

No. of times detected



log(intensity)



Values from



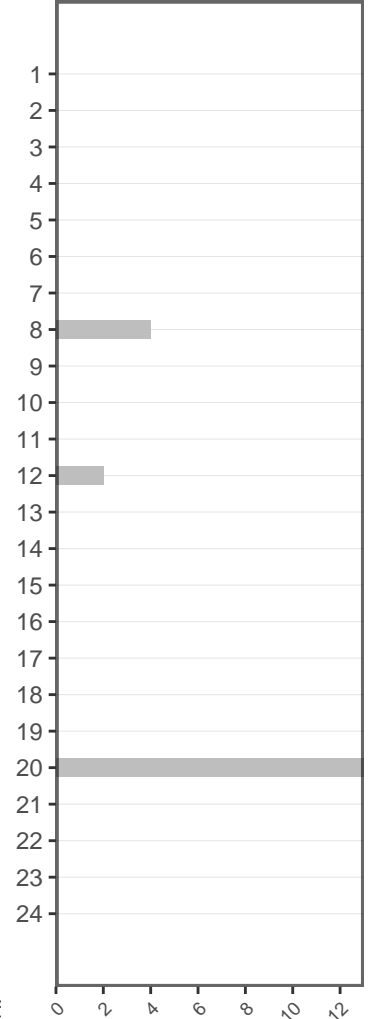
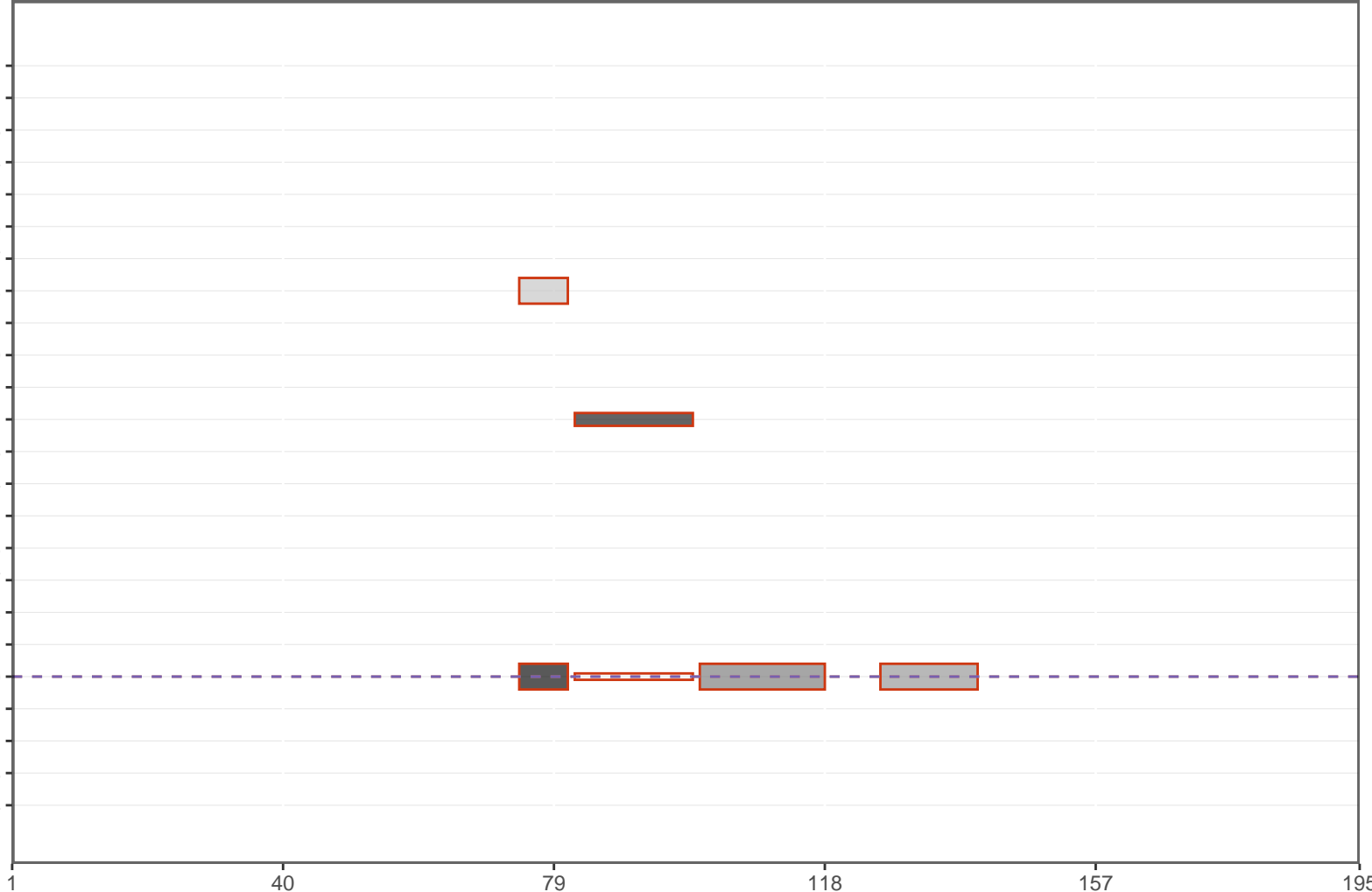
MW indication



Molecular weight



Gel Slice

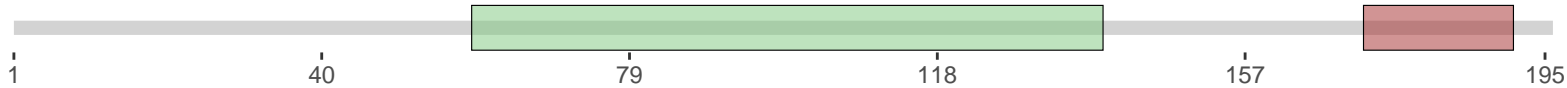


Protein length

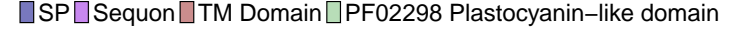


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IGLHSVVEGESAYKSGDTSSSVNSMSAGNDVAVLNKPKTRVYFACGTAGHCDGGMKLKITVTGNAPSNQAAATSSNPSSESVADSRRFSTAFFTFVAVIFIGMALVFLQ*

NbL19g07360.1 mitochondrial_phosphate_carrier_protein_3_mitochondrial-like [MW = 39.22 kDa]

No. of times detected



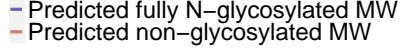
log(intensity)



Values from

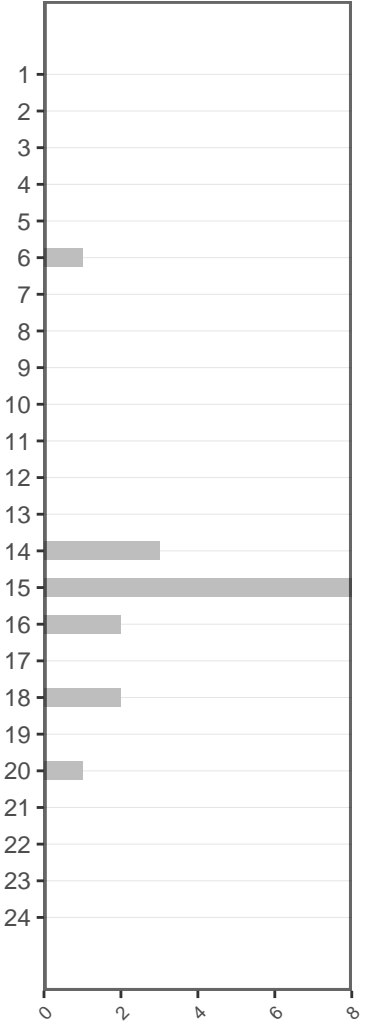
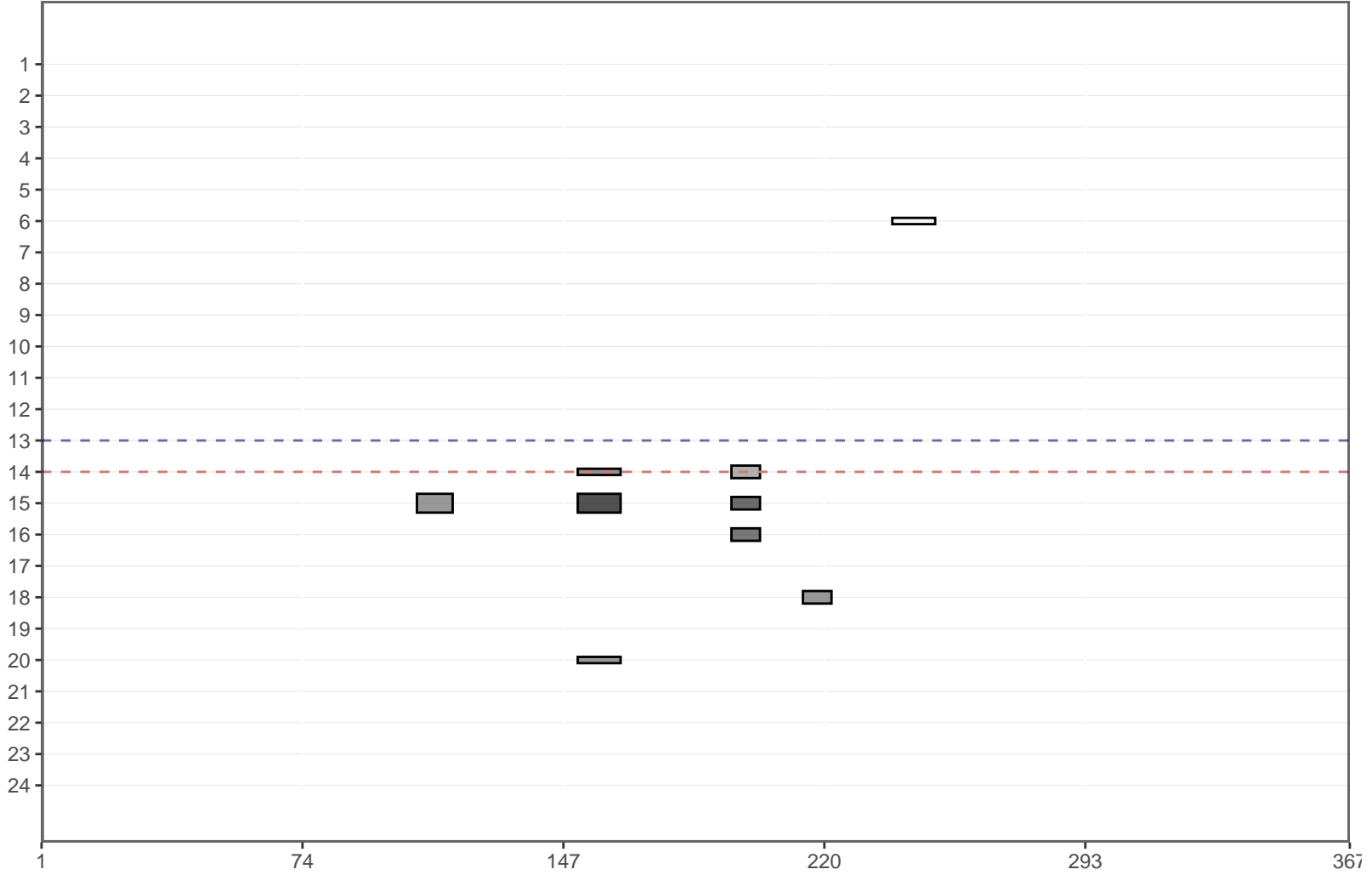


MW indication



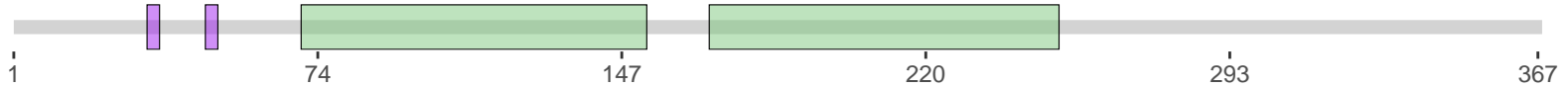
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AGSASAEVADIALGPFEEAVKRVGDTGPGFARGLSGDLKPKFRSEGTMLGKGLPLVWGRGIPKTMKMFASFETIVEMIKYHAFKPKNEGSKTMQLGSGFAGGYAGVFGAIVSHPADNLVSLFNNAKGATVSDAWKMKMVGSLFTRGLPLRIVMIGTLTGAGQWGYDAFRVYVGLPTTGGVTPAPMASEVAKV

NbL19g07210.1 acetyl-coenzyme_A_synthetase_chloroplastic/glyoxysomal [MW = 86.21 kDa]

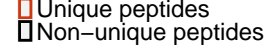
No. of times detected



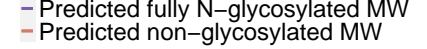
log(intensity)



Values from



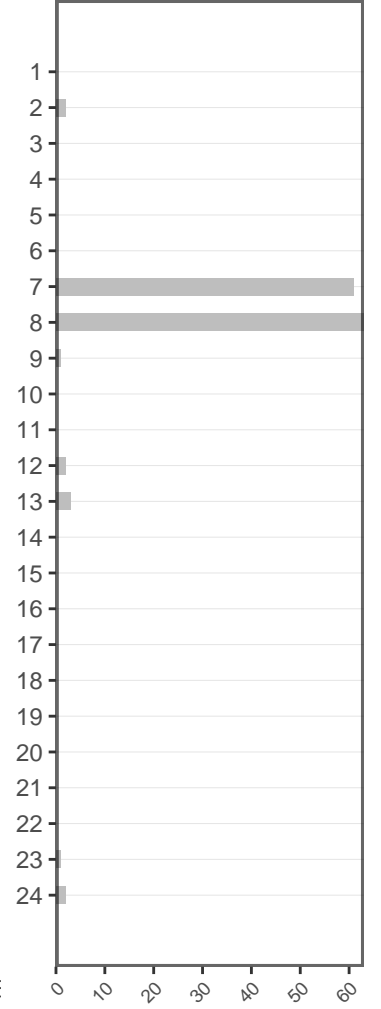
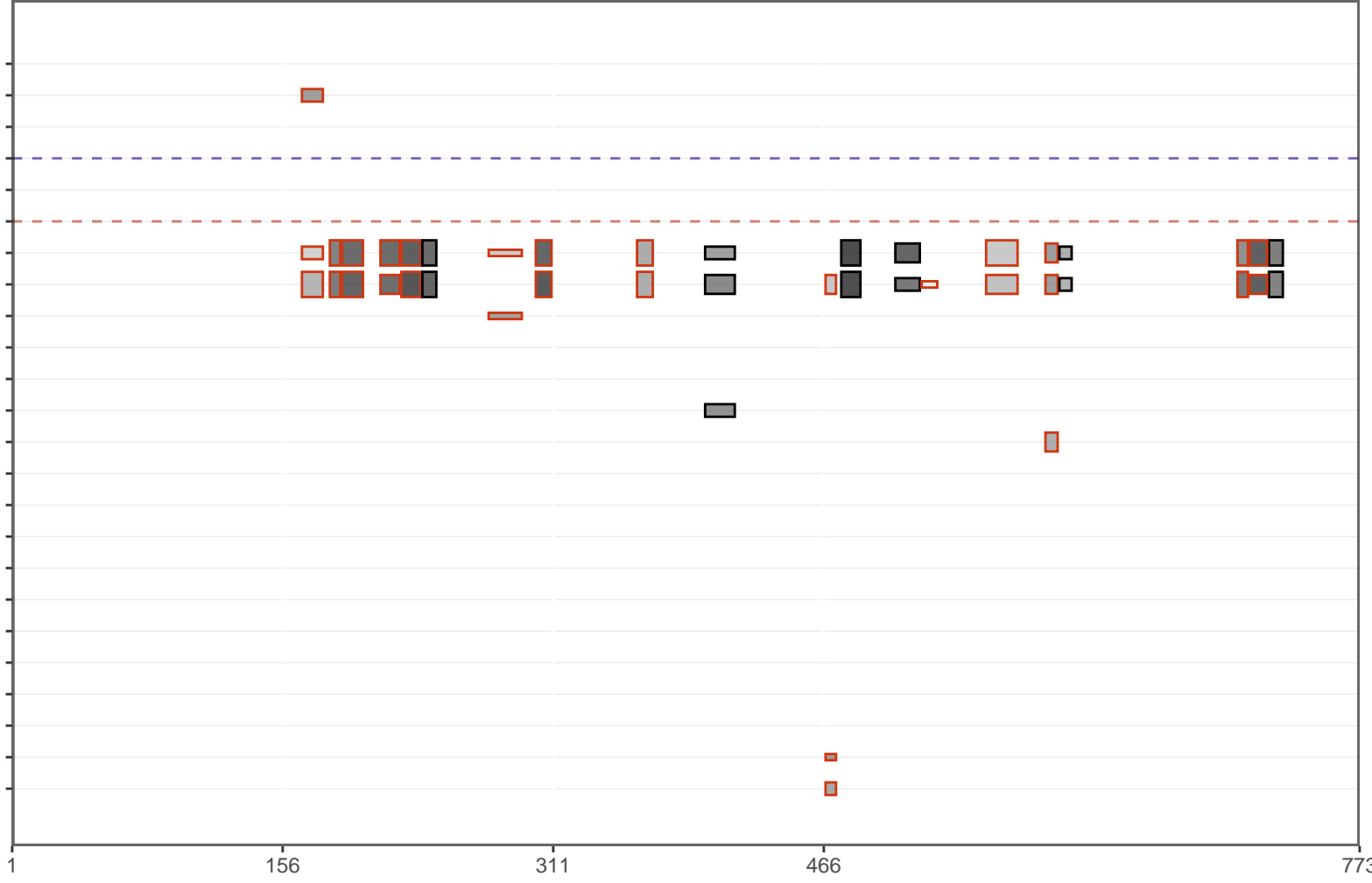
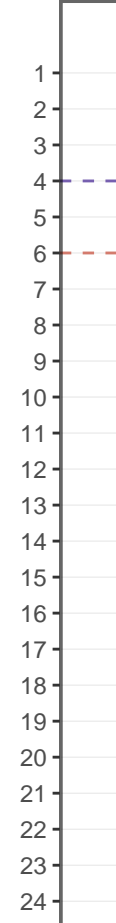
MW indication



Molecular weight

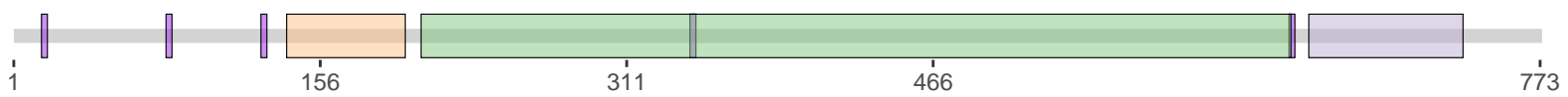


Gel Slice



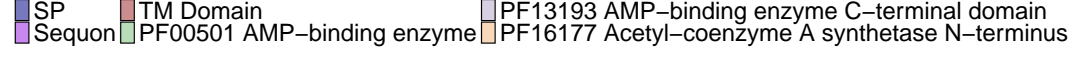
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

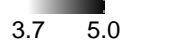
MVEVDAEDPLFLVTSGGTKPKGVLIHTGGYMYTATFKYAFDKYKPTDHWGTADGGWITGHSHVYVYRLLNGATVIFEGAPSPYDAGRGWDIDKDKVIFSYTAPTLVRLMLREGDDEHVSRYSRKSLRVLGSGVSEPNPAWRWFFNVDGARQPSIDFTVWQETGGFMITLPLGAWPKQKPGSATFFPFKVGPIVDEKGVIEIGEGSGYLGVKNWPGAFRTLVDGHERVYATYFSAFPQYVYFSGDGGSRDKDGYGWLTRGVDDVNWVSGHRIGTAEVESALVSH

NbL19g07200.1 beta-glucosidase_18-like [MW - SP = 57.03 kDa]

No. of times detected



log(intensity)



Values from



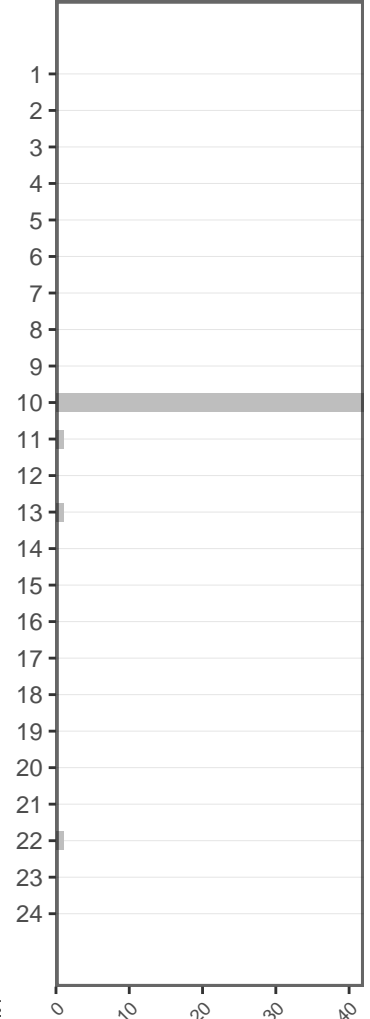
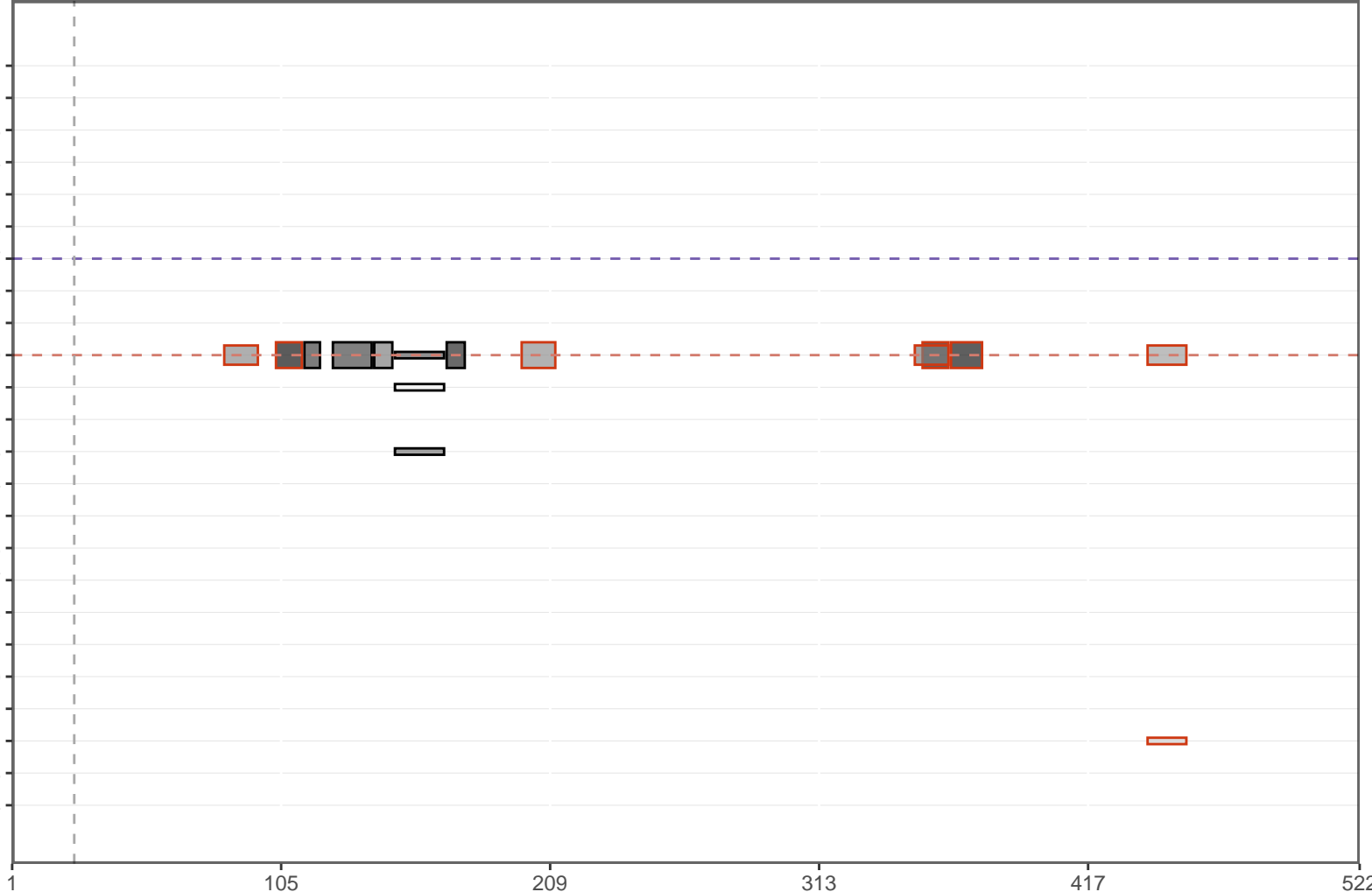
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SHAAAVSYRTRYQKRGGGMIGLNDGWVPEVYNSSEDAATQRARSPVNWFLDPIILGRYFMEMVQELGHLPDFVNDLSKLSYGLDFIGNYYTAKYKDLGYSAGEHGKHTWSEGGYFVTKEDGVYIGDPTFVDLFLYDGMKKKVMYMKDRFNMTFMVITENGAENENLNPISDTDLNDHRVWYMHSHVNLNLANAIREGADVRGYSYVWBLLDNFEWLDGYSRFRFGLHYVFTNLERTPKFSATRYKELMVFNFHGLEHTAQQ*

NbL19g07190.1 phosphoribosylamine--glycine_ligase-like [MW = 55.25 kDa]

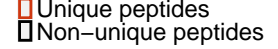
No. of times detected



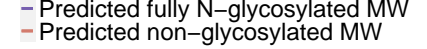
log(intensity)



Values from



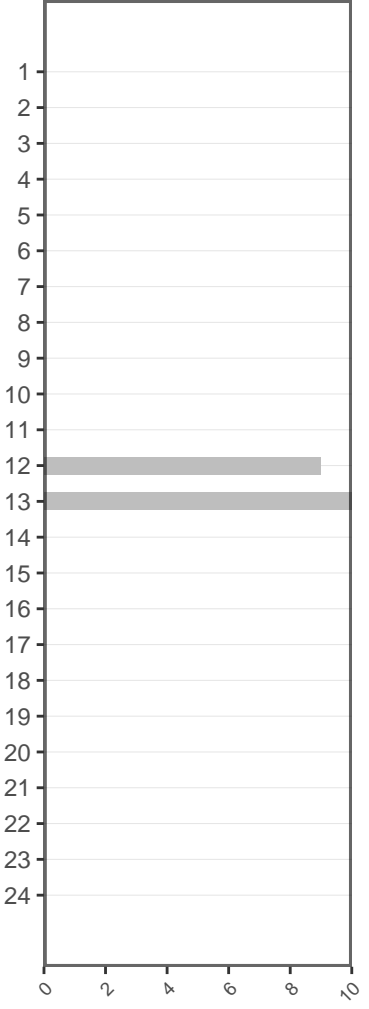
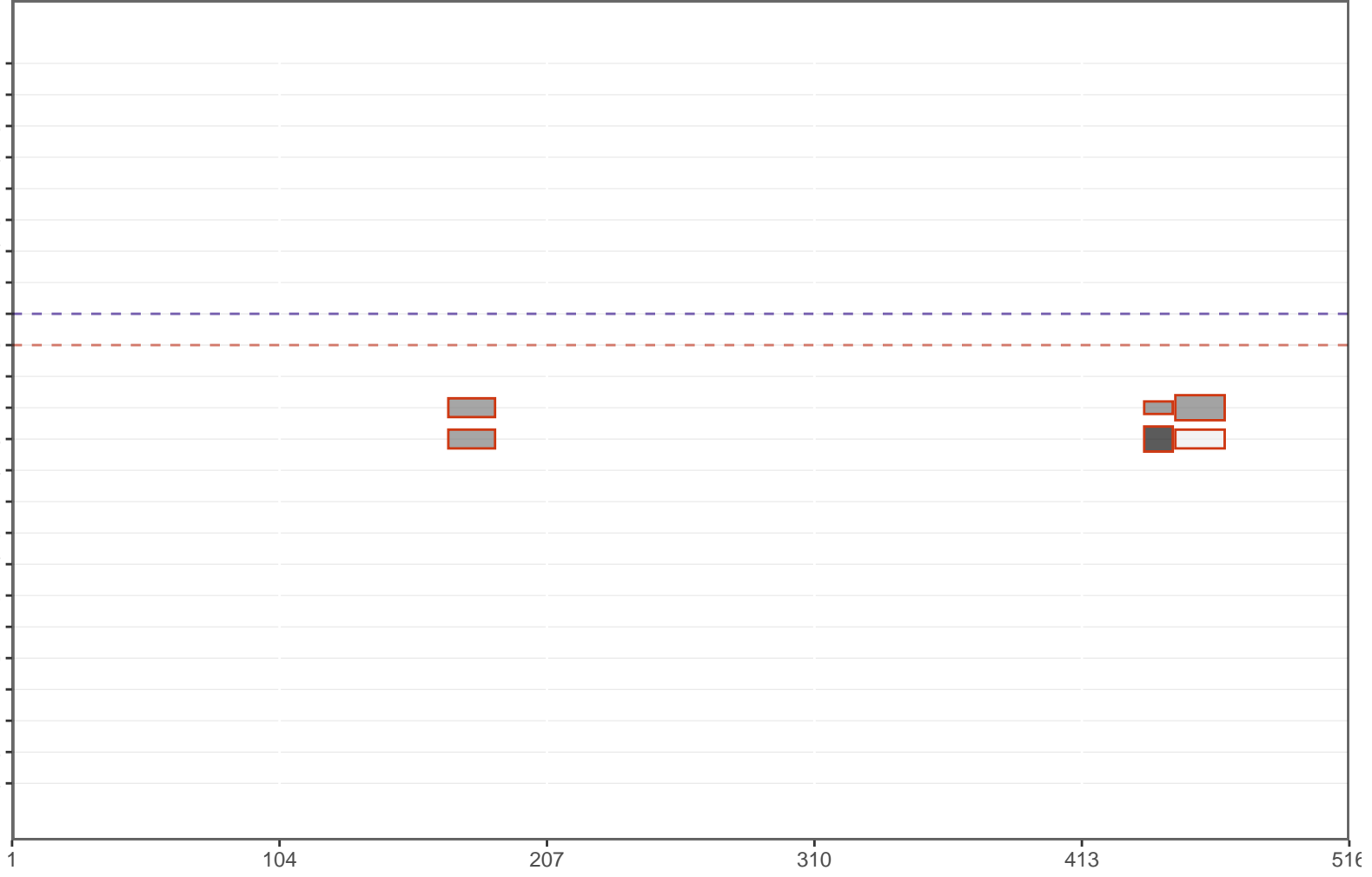
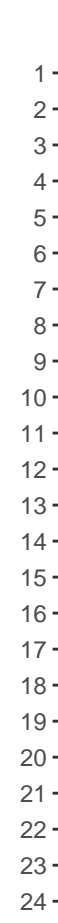
MW indication



Molecular weight

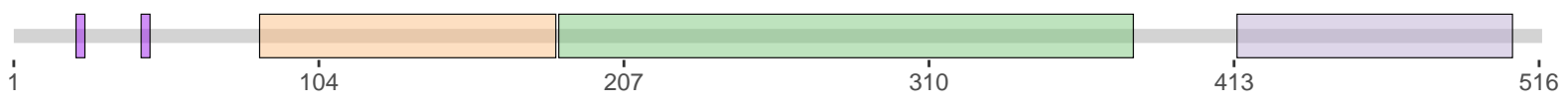


Gel Slice



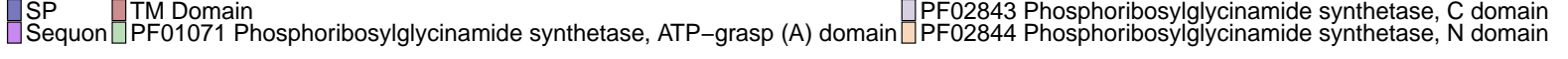
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EAVDSMLVENVYFGSAGSRVVEEYLEGEEAFAFFALVDGHEAIPLESGADHKRRVGGDGTGPNFTGGMGAYSPAPVATKELQGVVMEIHLPTVGMMAEEGKPFVGLVAGLMIKKSGLPALIEVYVRFQDPEQGVLMVRLESQLVKLLAACRGELRGLVSLQWSPGAMVAVMANKGYPGSYQKGTVIHKLEEAEGVPSVVKVTHAGTAFDQGNFIAAGRVLGVTARGEDLEKARDRAYGAVEGISWPGGFYRRDQWRALHQKQYS

NbL19g07040.1 oxygen-evolving_enhancer_protein_3-2_chloroplastic-like [MW = 24.19 kDa]

No. of times detected



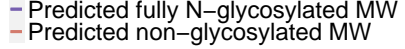
log(intensity)



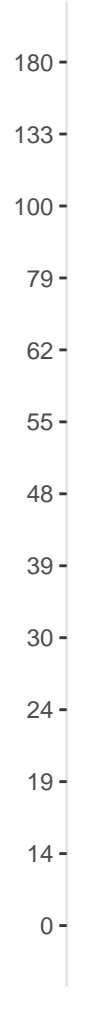
Values from



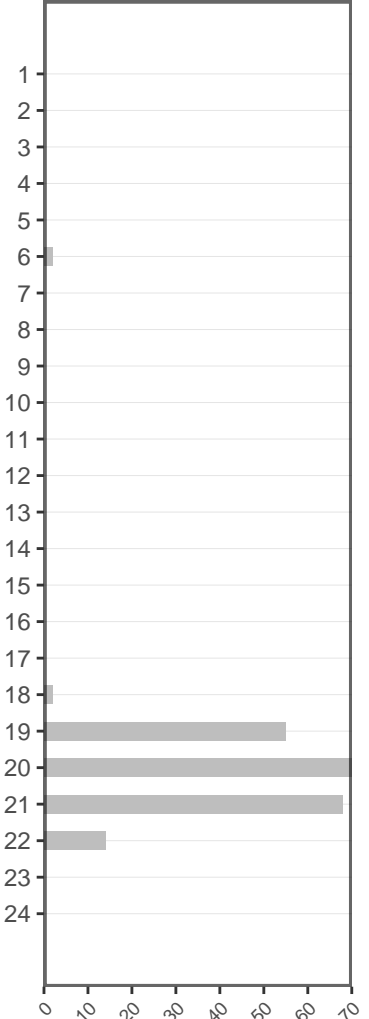
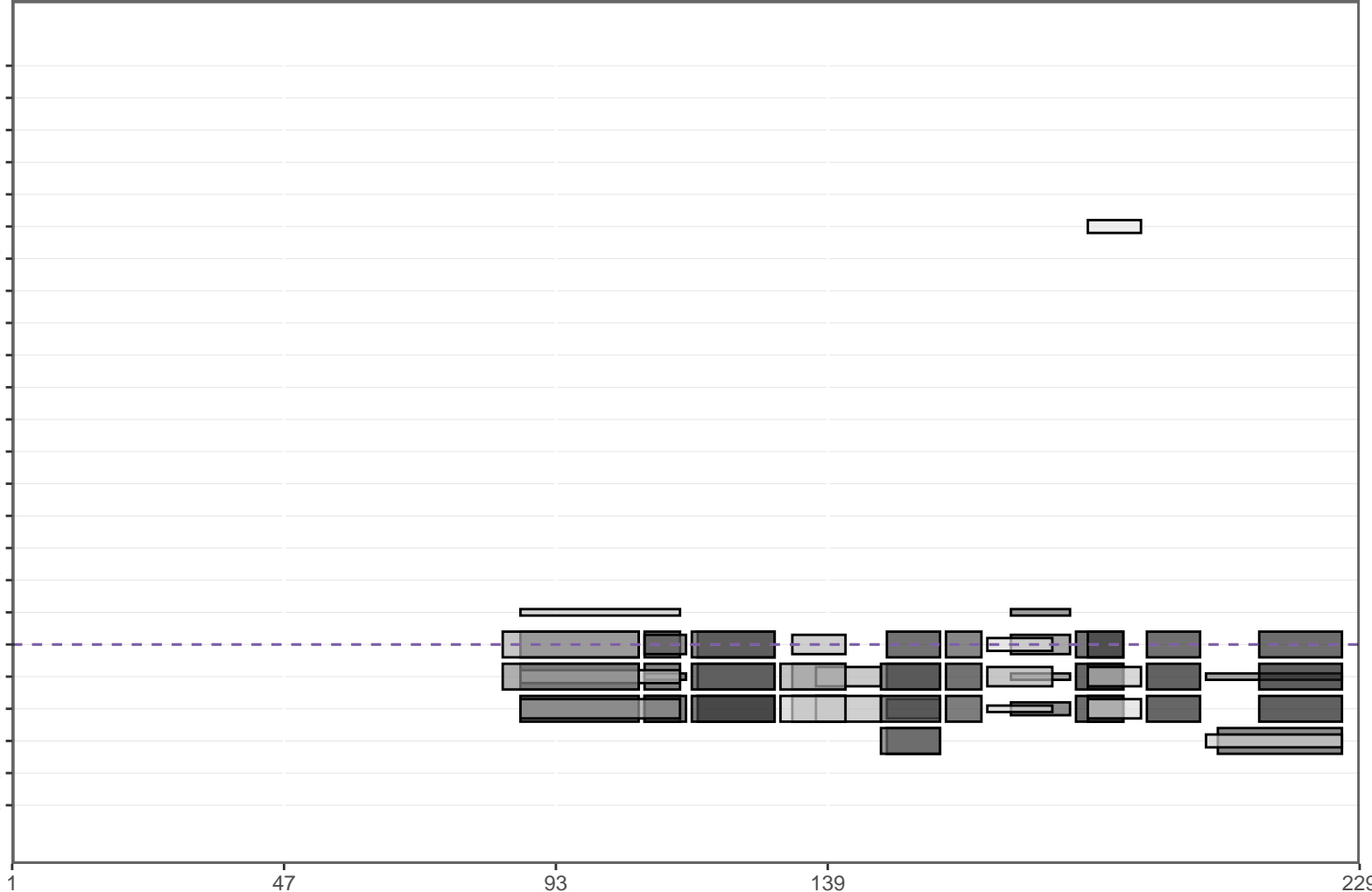
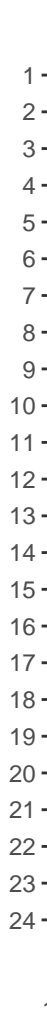
MW indication



Molecular weight

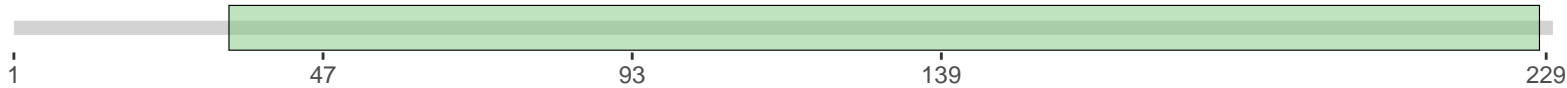


Gel Slice



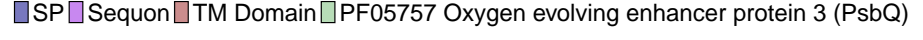
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LNISDEARDFGLPLKRFYLGPLTFRAEAGRKKDSAKEIVSVKVFIDKKAWPYVQNDLRLRAEYLRVLDKTVISAKPKEEKGLDGLTGLFKRTISDLHAAKTKNSPEAEKYVAETVSTLNDVLAALG

NbL19g06980.1 (-)-alpha-terpineol_synthase-like [MW = 62.89 kDa]

No. of times detected



log(intensity)



Values from



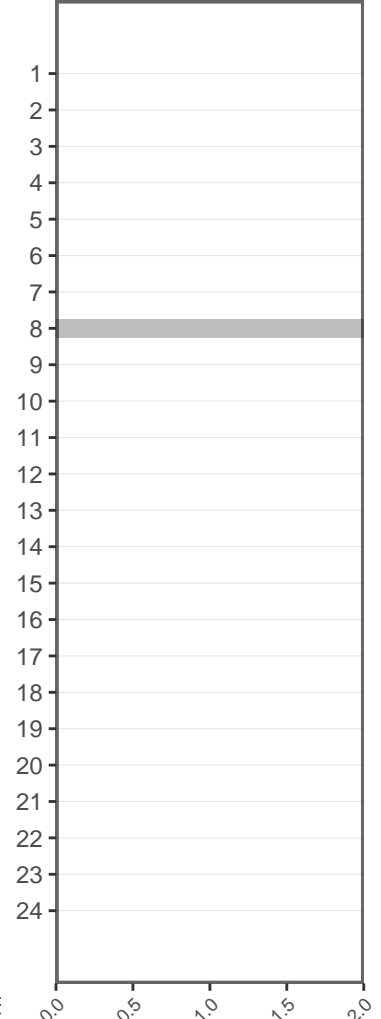
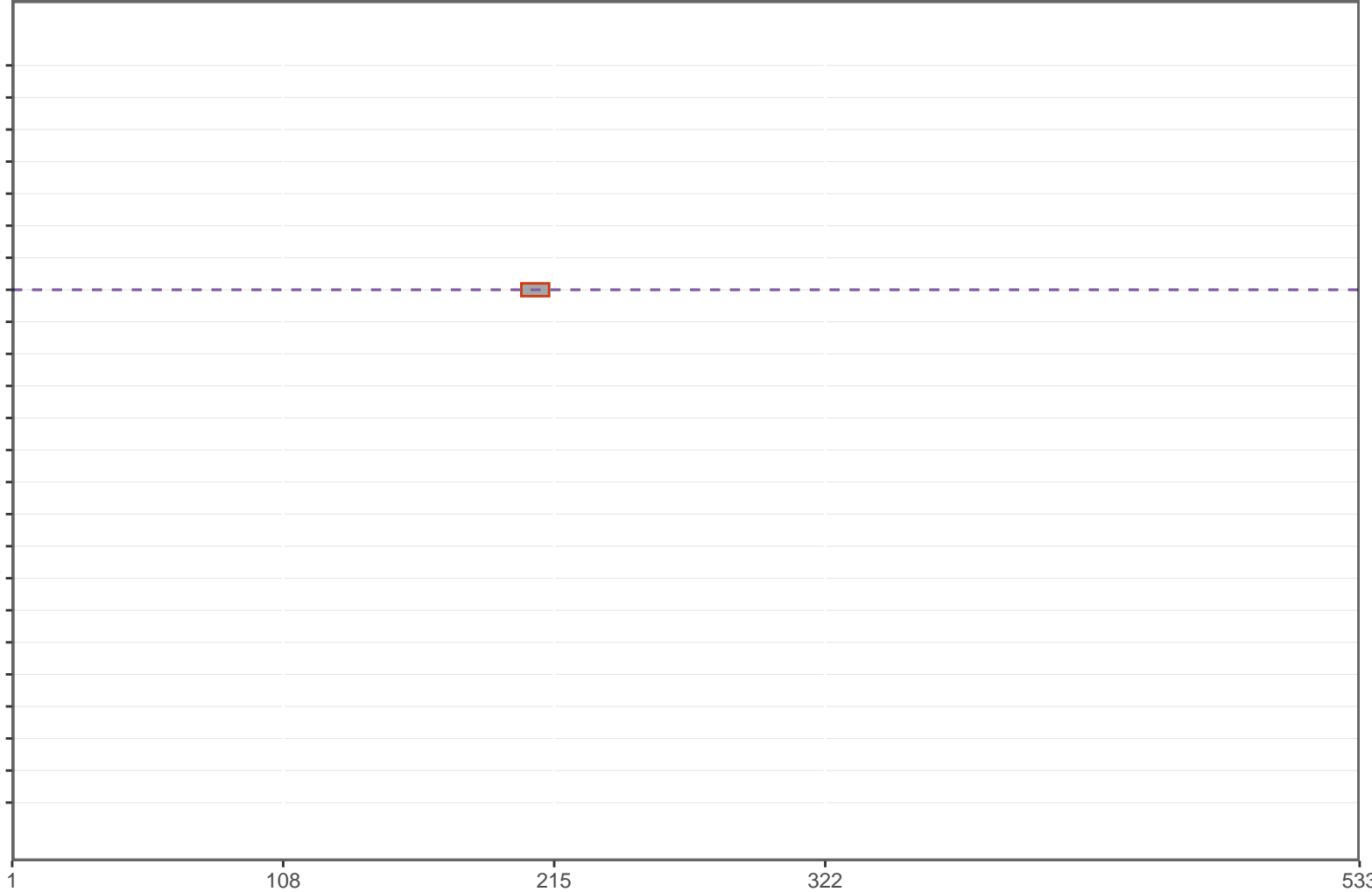
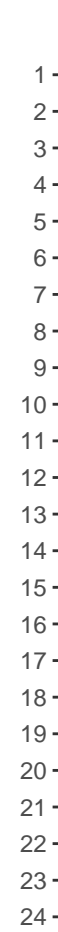
MW indication



Molecular weight



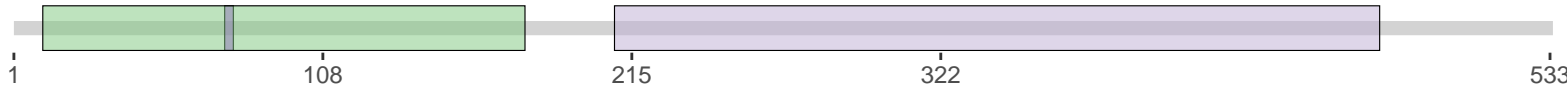
Gel Slice



Protein length

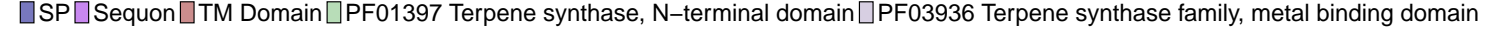


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

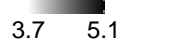
RLVEGFLWA/GFTPNPQFGDYCRKFTSLGVALTTDDYDVGVTMDLELFTDVRWDNIAERLPQMKDFLALFNAMNELAYDLKEGGFSKSHGQWANLCKAYLLEVVWYQSGRYTSLNEFLRNAWITNTGPKLIMHAYFGITNPKKEELEGLKNYPNIEPRLRLFLANDLATSFDKIKKGGDKLKSIGVYMHESGRSEENARNYINKLIDGTWKMMNKDLRGGSSFKDFRTTAMNARIADQMYGHGDDGFGIPDRETKDRIRSLFFEPNLS

NbL19g06930.1 DAG_protein_chloroplastic-like [MW = 25.42 kDa]

No. of times detected



log(intensity)



Values from



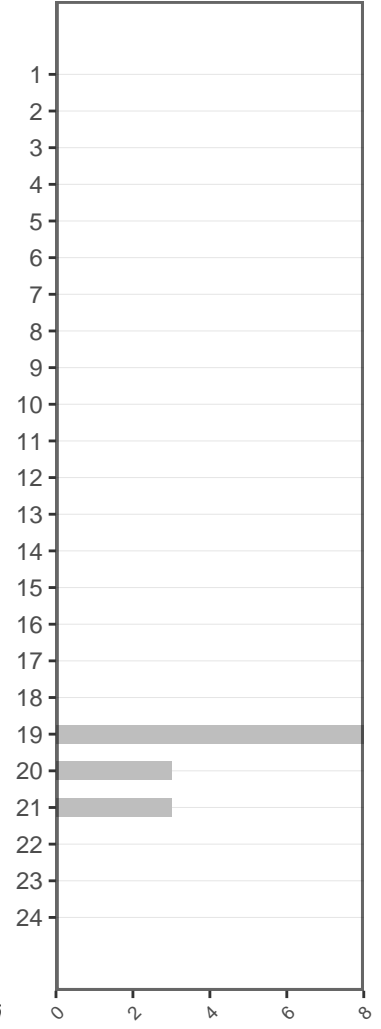
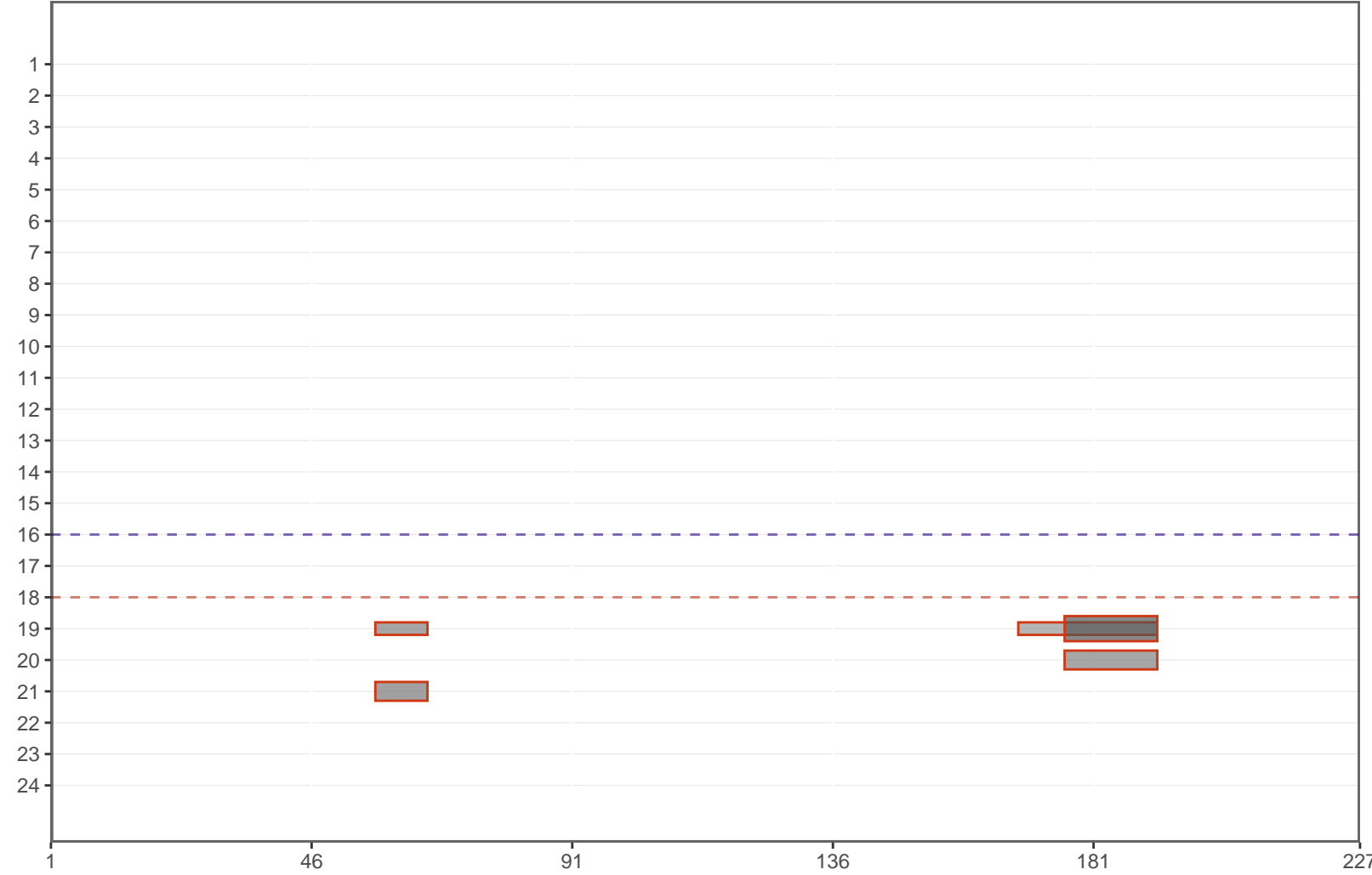
MW indication



Molecular weight



Gel Slice



Protein length

Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

EQMIDTYLNLATVAGSMEEAKKMMVAFSTTTTGFQGTVSEETSEKFKGLPGVLLWLPDSYHVDVANKKIVGGDKYNGEIPDQVPTVQPKQNNRTRKSKKAVVRRRDGPPPERTKGEAAPESSE

NbL19g06910.1 probable_NAD(P)H_dehydrogenase_(quinone)_FQR1-like_1 [MW = 24.95 kDa]

No. of times detected



log(intensity)



Values from



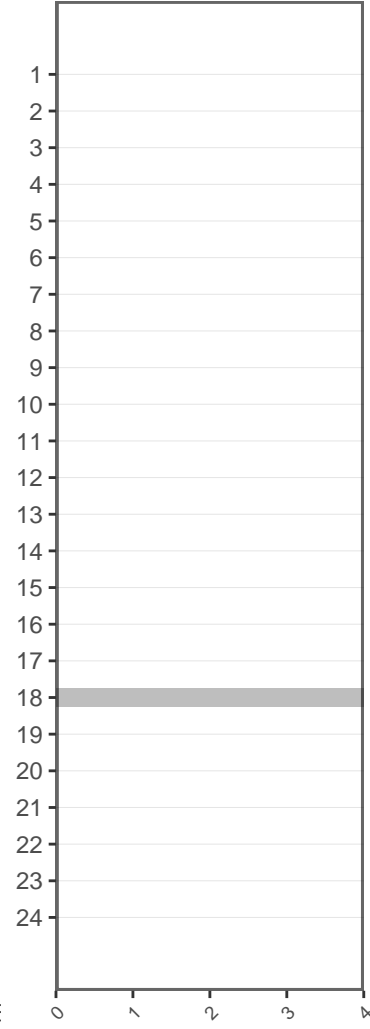
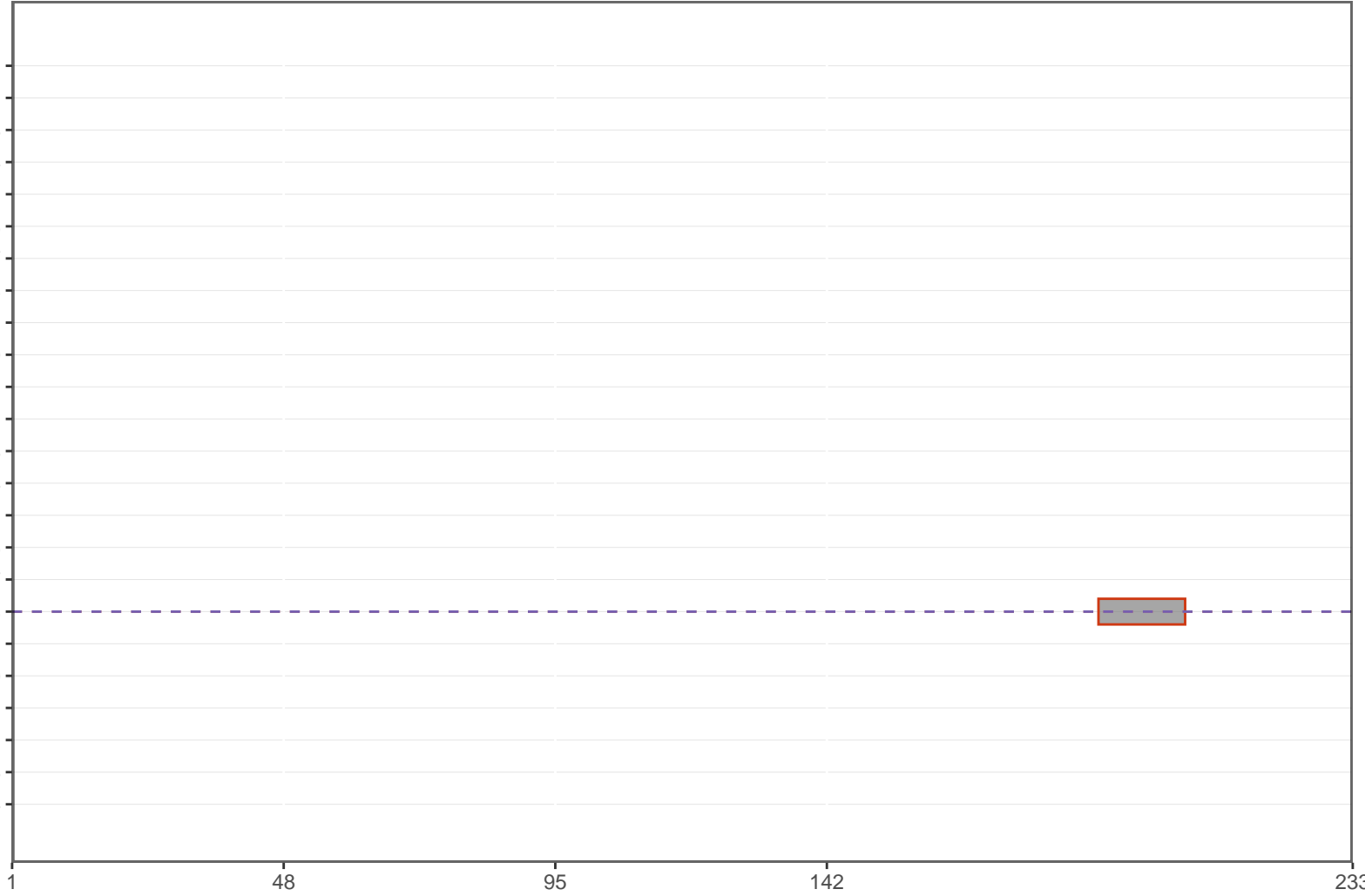
MW indication



Molecular weight

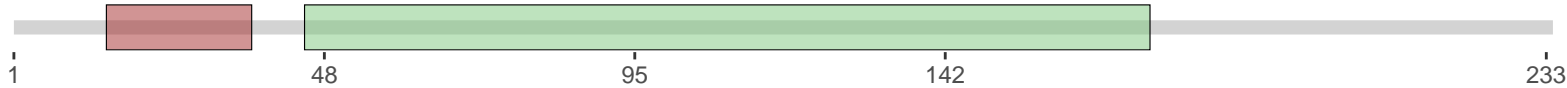


Gel Slice



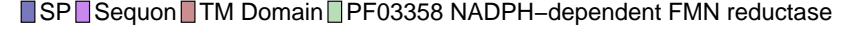
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

GPPTRFQMMAACFKAFLDATGGWRTGQLAGKPKGLFYSTGSGGGGGTFLTAFTQLVHHQGMFVPIGYTFGGGMFEMENIKGGSPYGGSTYAGDGSRGPTLEMEQAFHGGKYHATTKLKGSA*

NbL19g06780.1 suberization-associated_anionic_peroxidase-like [MW - SP = 35.98 kDa]

No. of times detected



log(intensity)



Values from



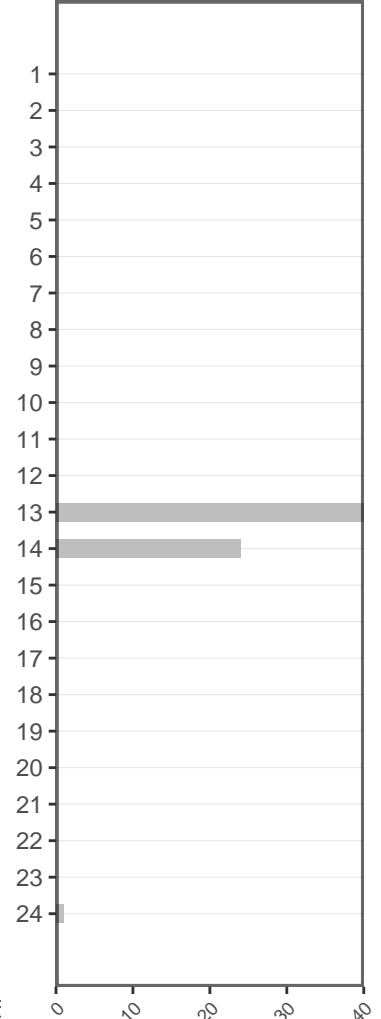
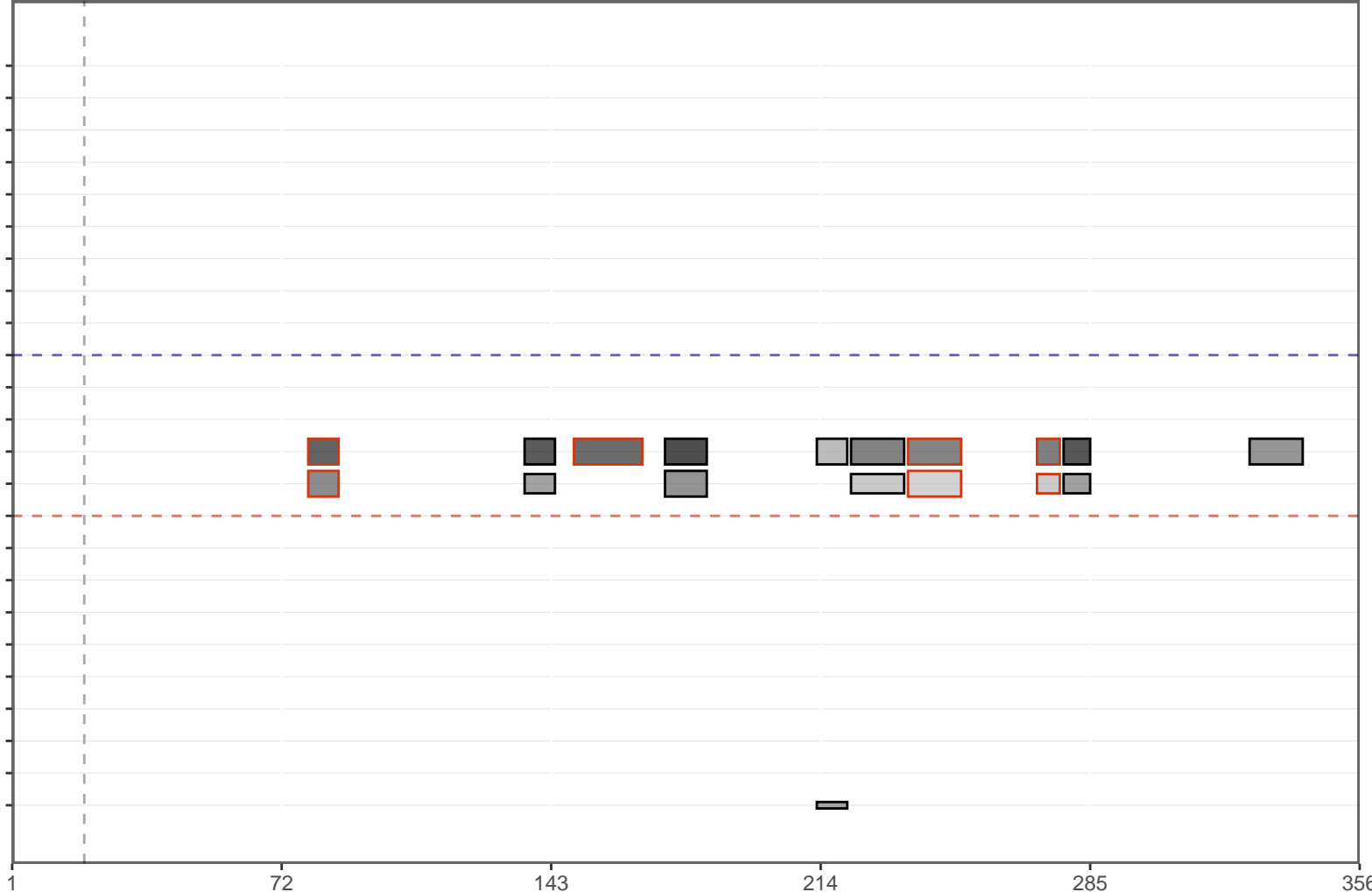
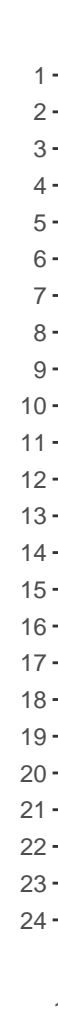
MW indication



Molecular weight

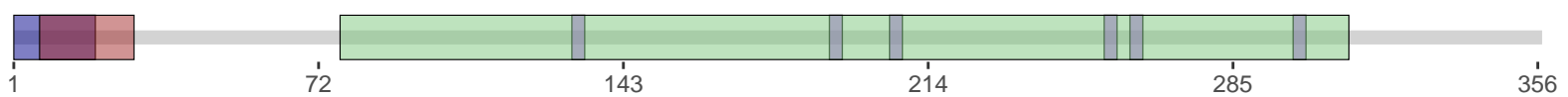


Gel Slice



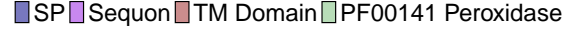
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DSVVKLGGQYTNALGRDRARENFTGALGQLPAPFDNLTVQLQKFNKFNAREMVALAGAHYVGFTRGAVAGNSFNVPAARLQGNCGVPGNDTNLGRLDRTFWDFRVYFQDLNRNGDGLFSDGVLGTNTTAAVVTYSNNGAVFLGDFAAAMKMGNLPPSPGAGLEERVCSRNPSSVSM

NbL19g06760.1 suberization-associated_anionic_peroxidase-like [MW - SP = 36.4 kDa]

No. of times detected



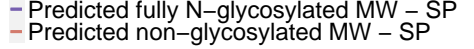
log(intensity)



Values from



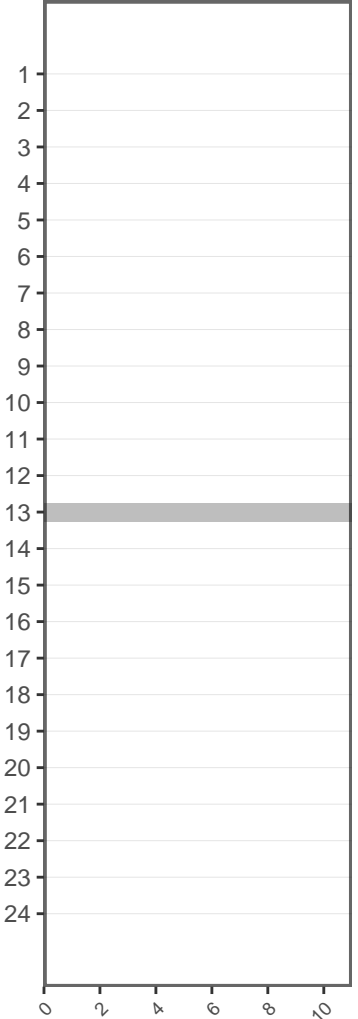
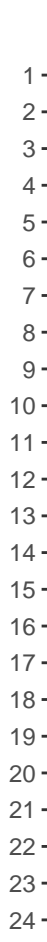
MW indication



Molecular weight



Gel Slice

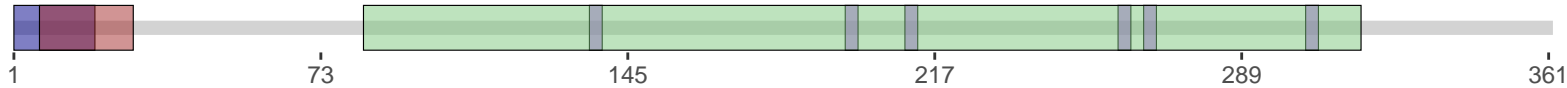


Protein length

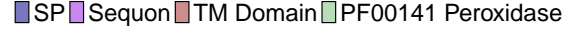


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

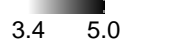
VARDVYKLGQGGQYHVALGRBDARAANFTGALQLPAPFDNLTVALRKFNDKNFNAREMVALAGAHVTGFRCTVAGNSNNVNPAAALGQNGSVTQNDTNLQGLDFTTWFVDFRVYFDGLNRNGGLFSDQVLTGNTTAAVITYSNKGAVFLGDFAAAMIKMGNLPPSPGAGLEIRDVGSRVNPSVAVEM

NbL19g06700.1 uncharacterized_LOC104219407 [MW = 26.2 kDa]

No. of times detected



log(intensity)



Values from



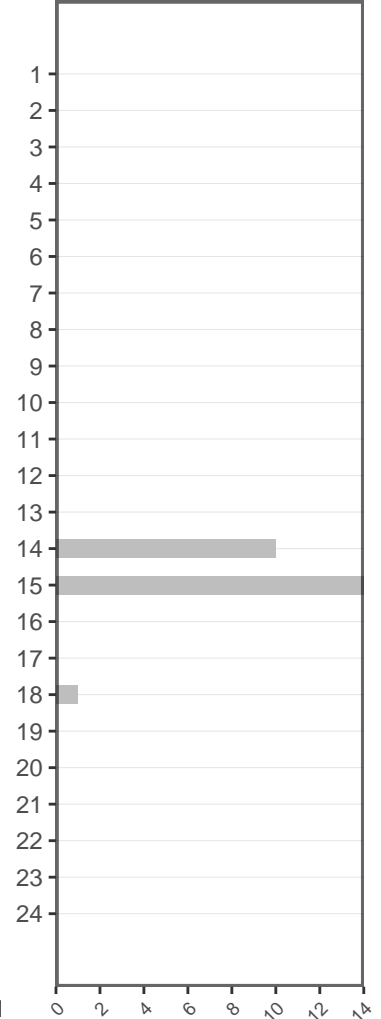
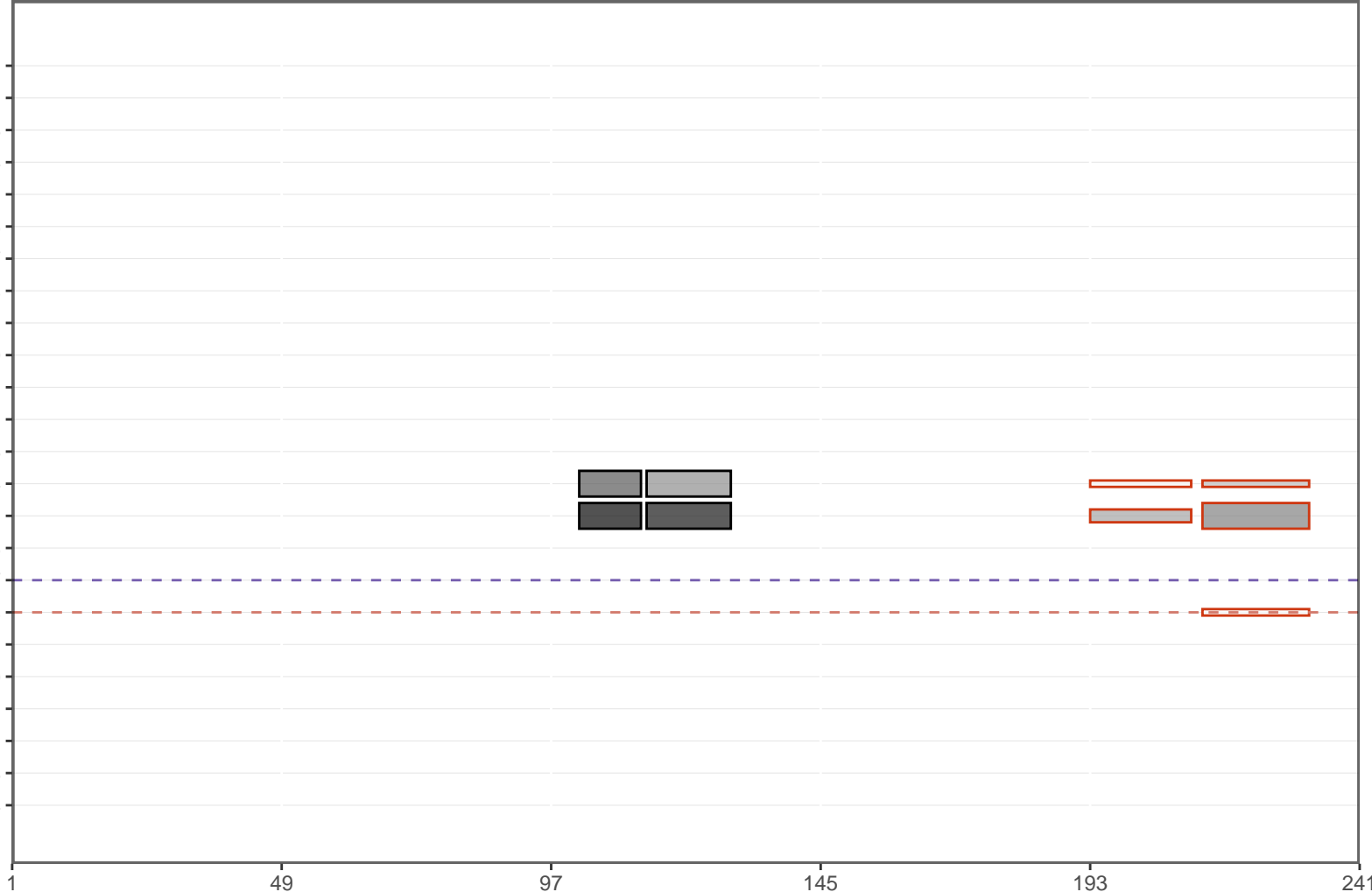
MW indication



Molecular weight



Gel Slice

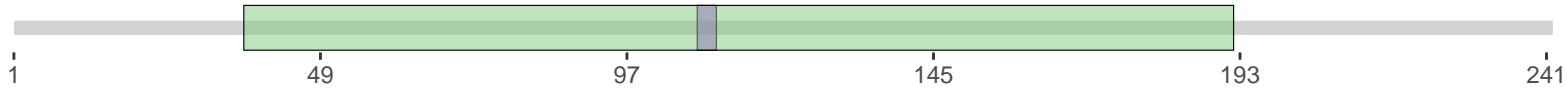


Peptide counts over 4 repeats

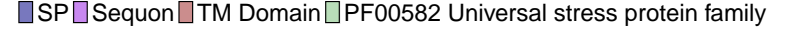
Protein length



Pfam domains



Pfam Description



Protein sequence:

IFTTTKANDLAQPLVEGNPFKIHVKDMMKERLGLLEVERLGLSAVIMSGRFGASRRSISKGRLLGVSSEYCVHSHVCPVVVRRYFDKDGVAADDANEGSVKKTDLHPVPEDEPIYHDAEDKAADEKAS

NbL19g06660.1 uncharacterized_LOC107758959 [MW = 44.9 kDa]

No. of times detected



log(intensity)



Values from



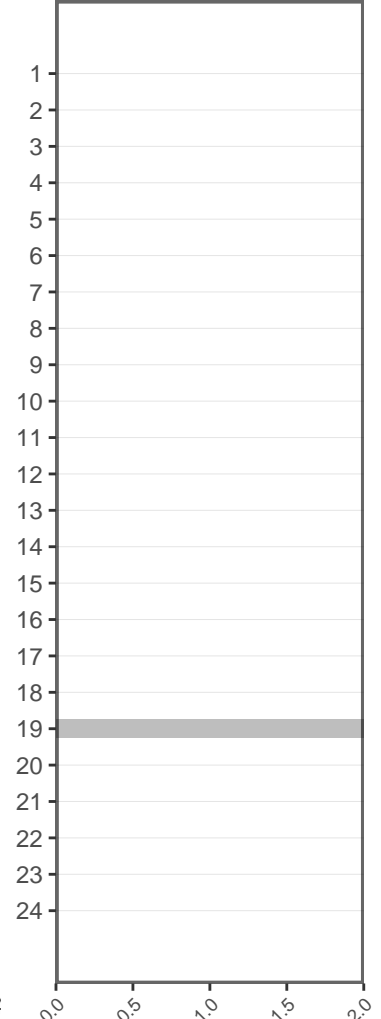
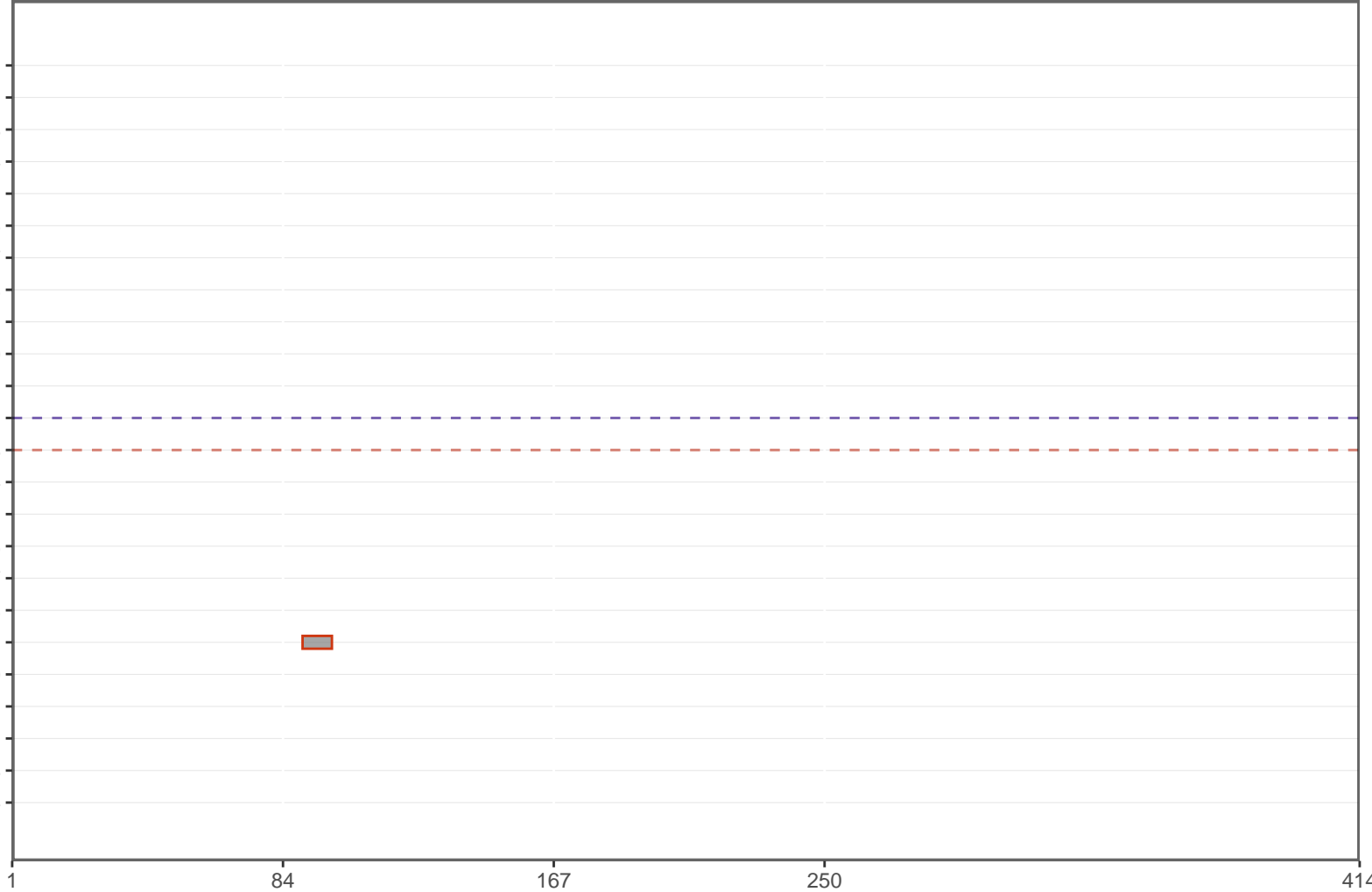
MW indication



Molecular weight



Gel Slice



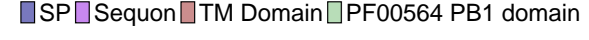
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

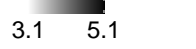
/PDIYLFGLDAADDPRESRFGRKINISDPGSPAPPIVSGPVGVSSTMTSSAMTMDLPVTKPKPKNPVTESEKTFVGRDQGPVYVPGSPLWHYRPTVGTPIVYVYVDPVHQDQSGIPVQSIPIRMRAPVYVHFPPVPPNQLPVGYPVPSIGDYGMRPVMGVDPNFEFAAARVYVTEGTNGQMMVYGFVNSGVVPGVGLLAGEEMDQPGNDKAGRVSDI

NbL19g06540.1 putative_PAP-specific_phosphatase_mitochondrial [MW = 44.21 kDa]

No. of times detected



log(intensity)



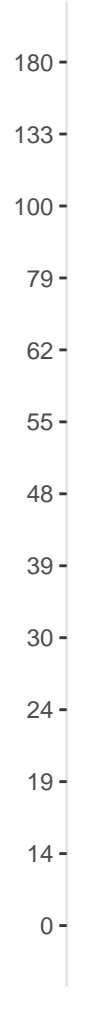
Values from



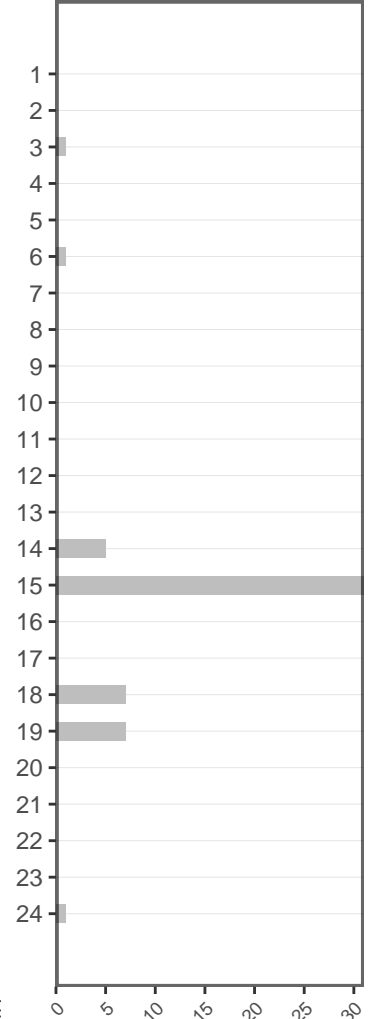
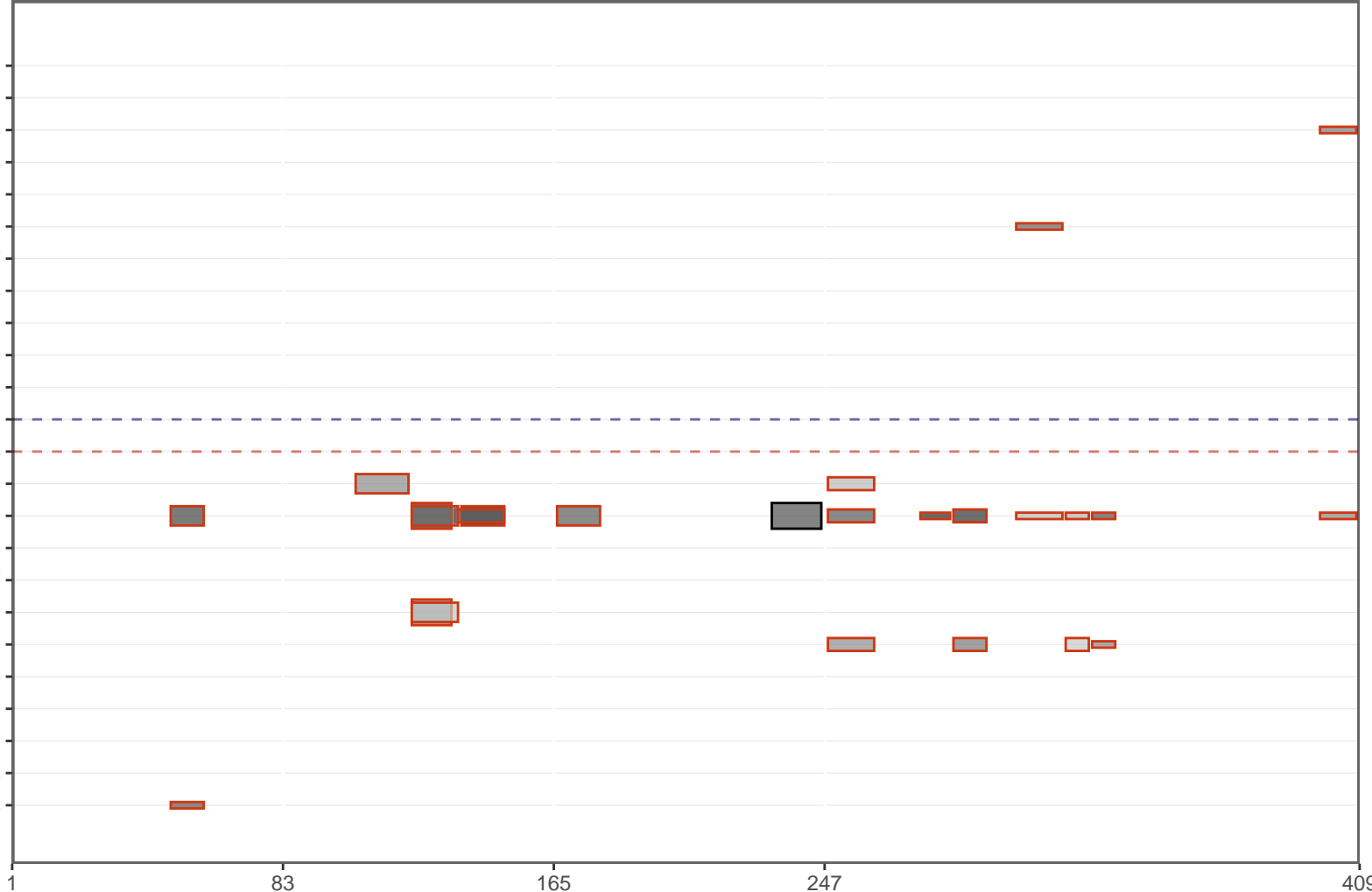
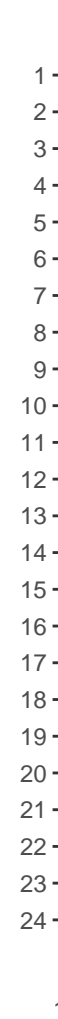
MW indication



Molecular weight

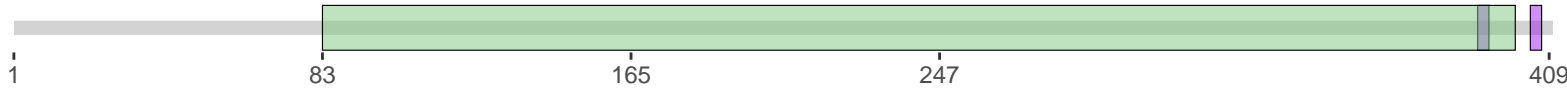


Gel Slice



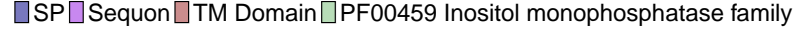
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILALVVEGQVLYVMGCFNWDDDCSENSVGVQES66SRGIMVSHVCGGTWTKRLSDILTFESSHTWTRGVD6DGMVEGARFTPE60GSKPLPLVDFDAKRDSENGKGNLILLASDC6SLCKYLMVAGSRASVYIGRKNATBIKIVDHWVGHGIVHEAGGKVTDWAGG6FDMAADDTERRLIIFP6GGVAVTNGSLHKKIGMIS6NS6LV

NbL19g06530.1 vesicle-associated_protein_4-2 [MW = 30.44 kDa]

No. of times detected



log(intensity)



Values from



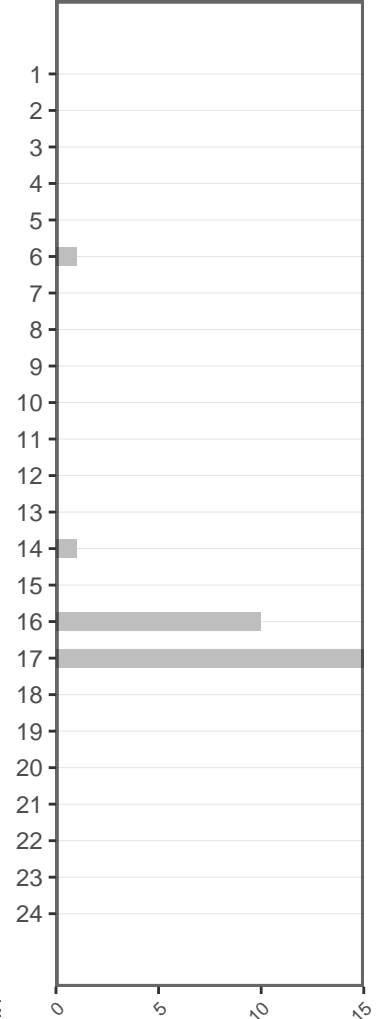
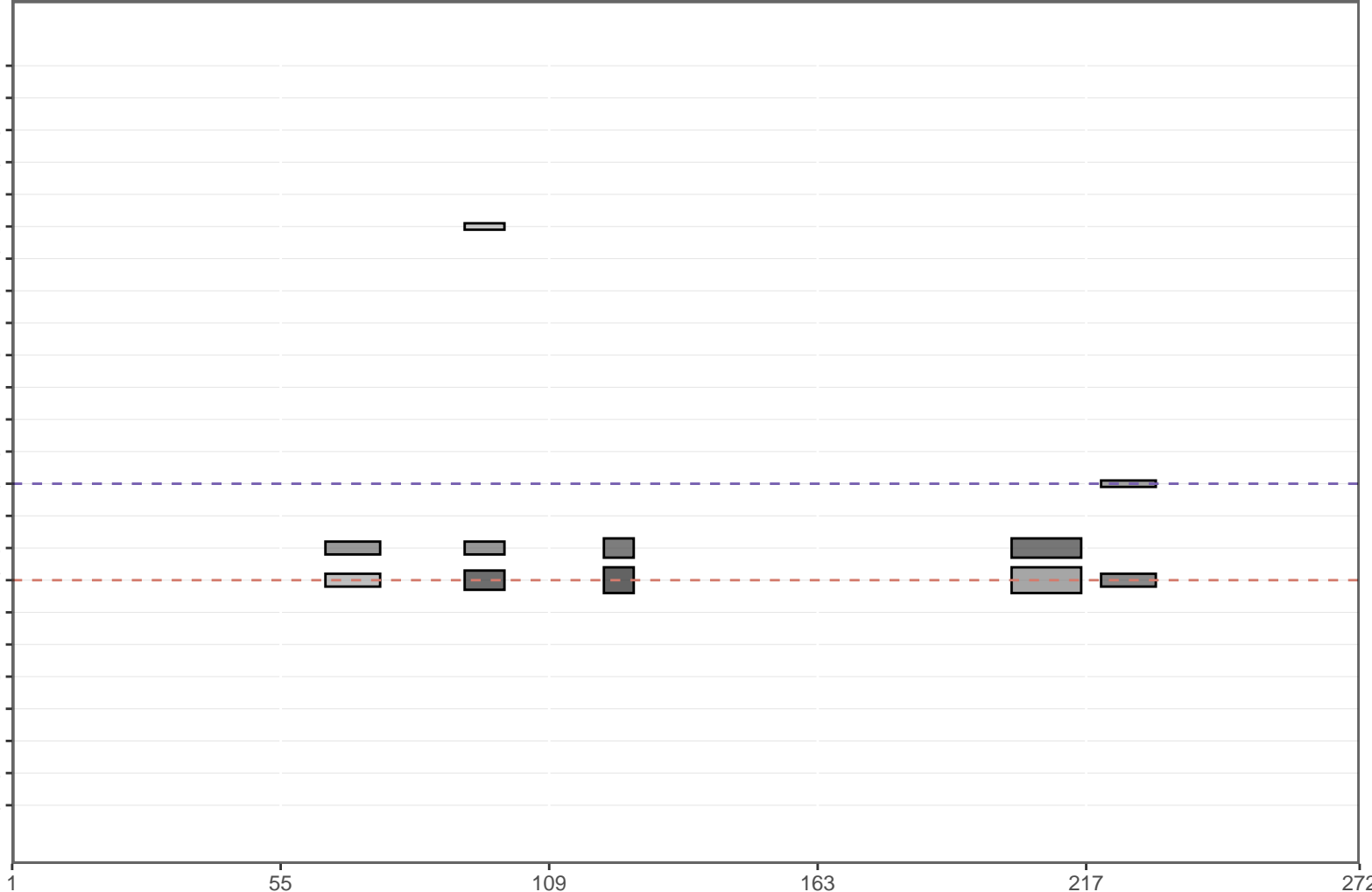
MW indication



Molecular weight



Gel Slice



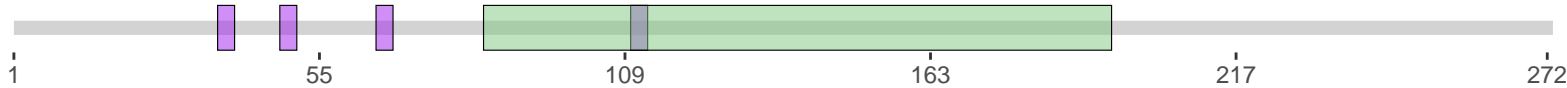
Protein length



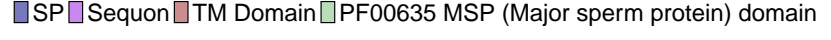
Peptide counts over 4 repeats



Pfam domains



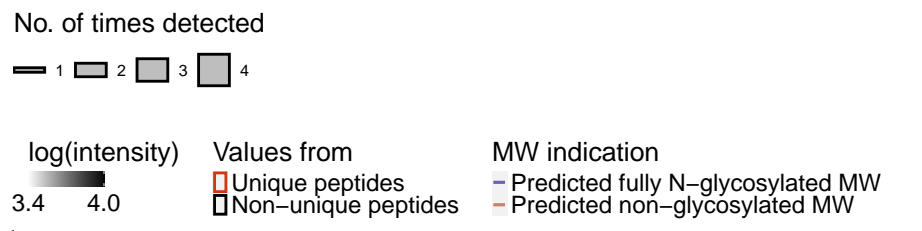
Pfam Description



Protein sequence:

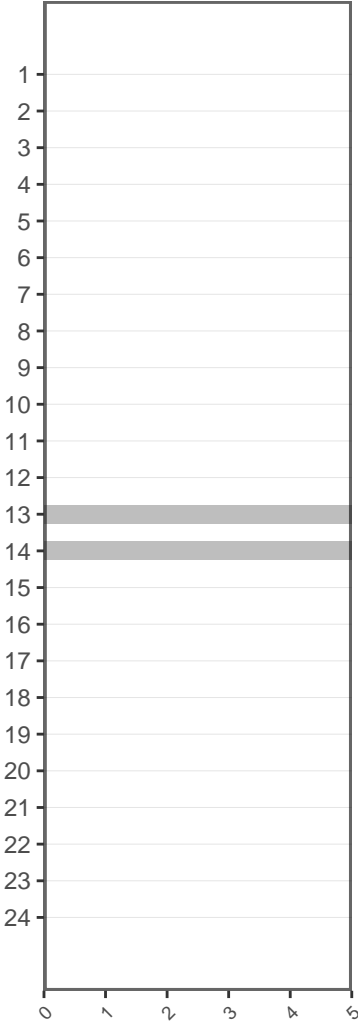
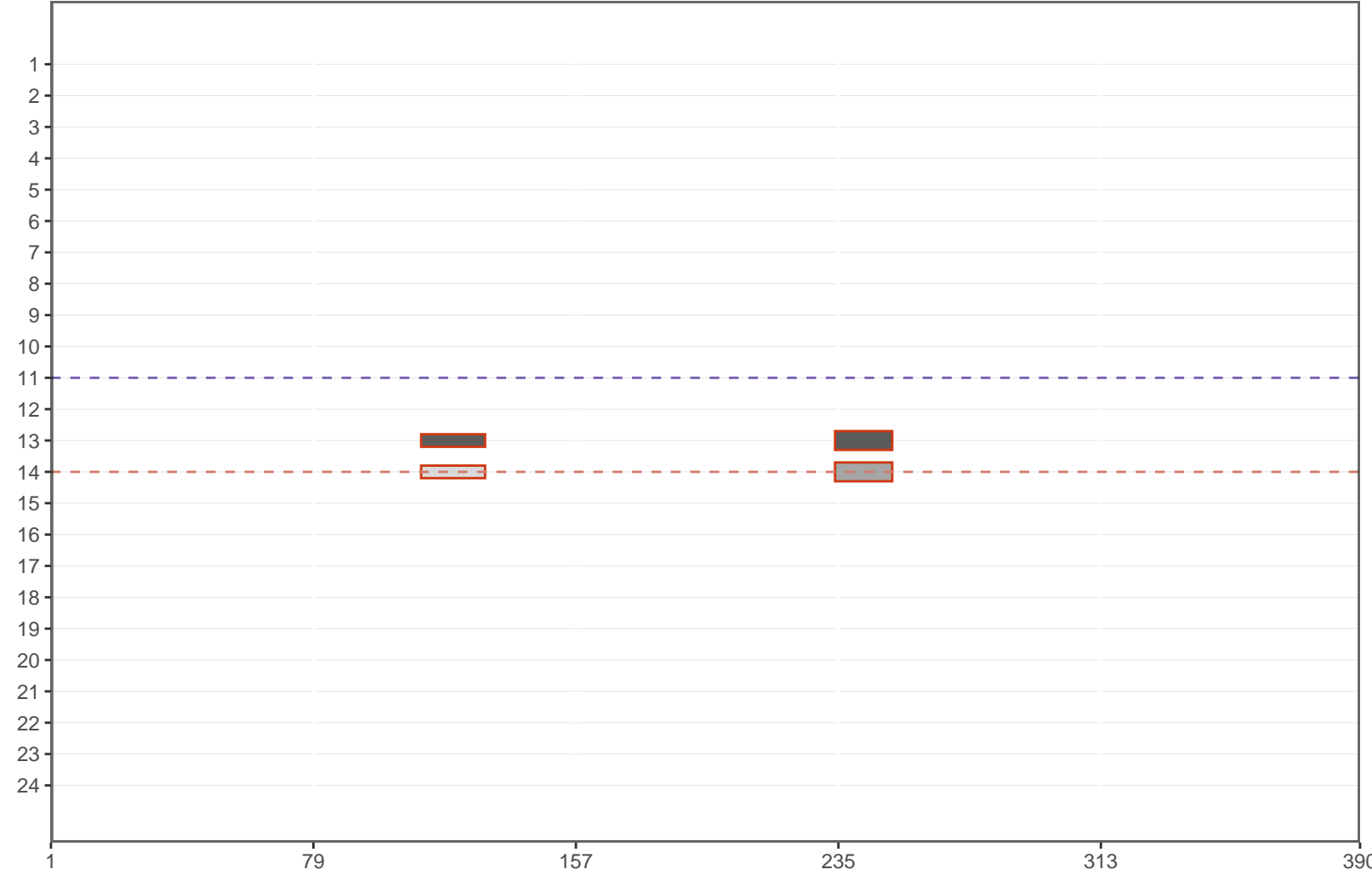
ITAPKSCFMRPFGAILAPGEGSIATVFKFVEHPENNEKPKMDQKSKVKFKHMSLKVKGPMDEVVPELFDQKQDQVAVQILRVFLQVLRPSPAFKELKROLAEADALEARKPKPEDTGRWIKGELVDEWKERRERYLARGQVQEGVDSV

NbL19g06420.1 bifunctional_riboflavin_kinase/FMN_phosphatase-like [MW = 42.83 kDa]



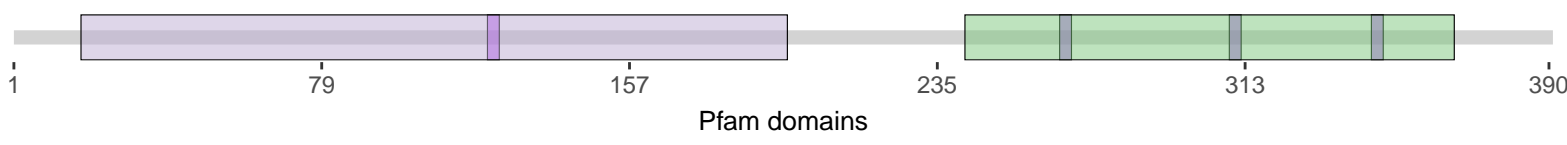
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain PF01687 Riboflavin kinase PF13419 Haloacid dehalogenase-like hydrolase

Protein sequence:

IPGVTAGKAAGMAVAVPRLAKGSHLYTSADEVINSLLDNLQLEKWLPLAFQDRREGTLPLEPWYHGGPIKGFGRGKVLGPTANLSPEGYSAILSEHPAGVYFGWAGLSARGVYKMMVMSGWNPFVFNTEKAEPLWLDHFDNEDFYGEELHLVVGVYRPEANFSSLEALAKIHEDRKAERALELPGVLYKDDPYLKIQLHGDV

NbL19g06320.1 calmodulin-binding_protein_60_B-like [MW = 69.31 kDa]

No. of times detected



log(intensity)



Values from



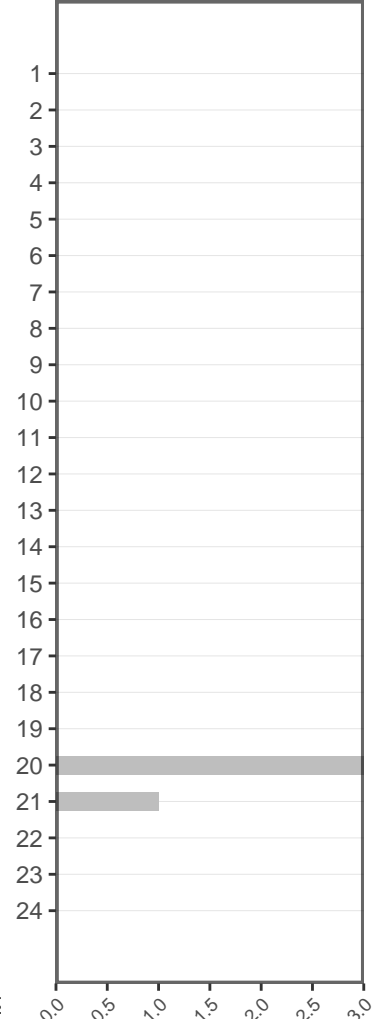
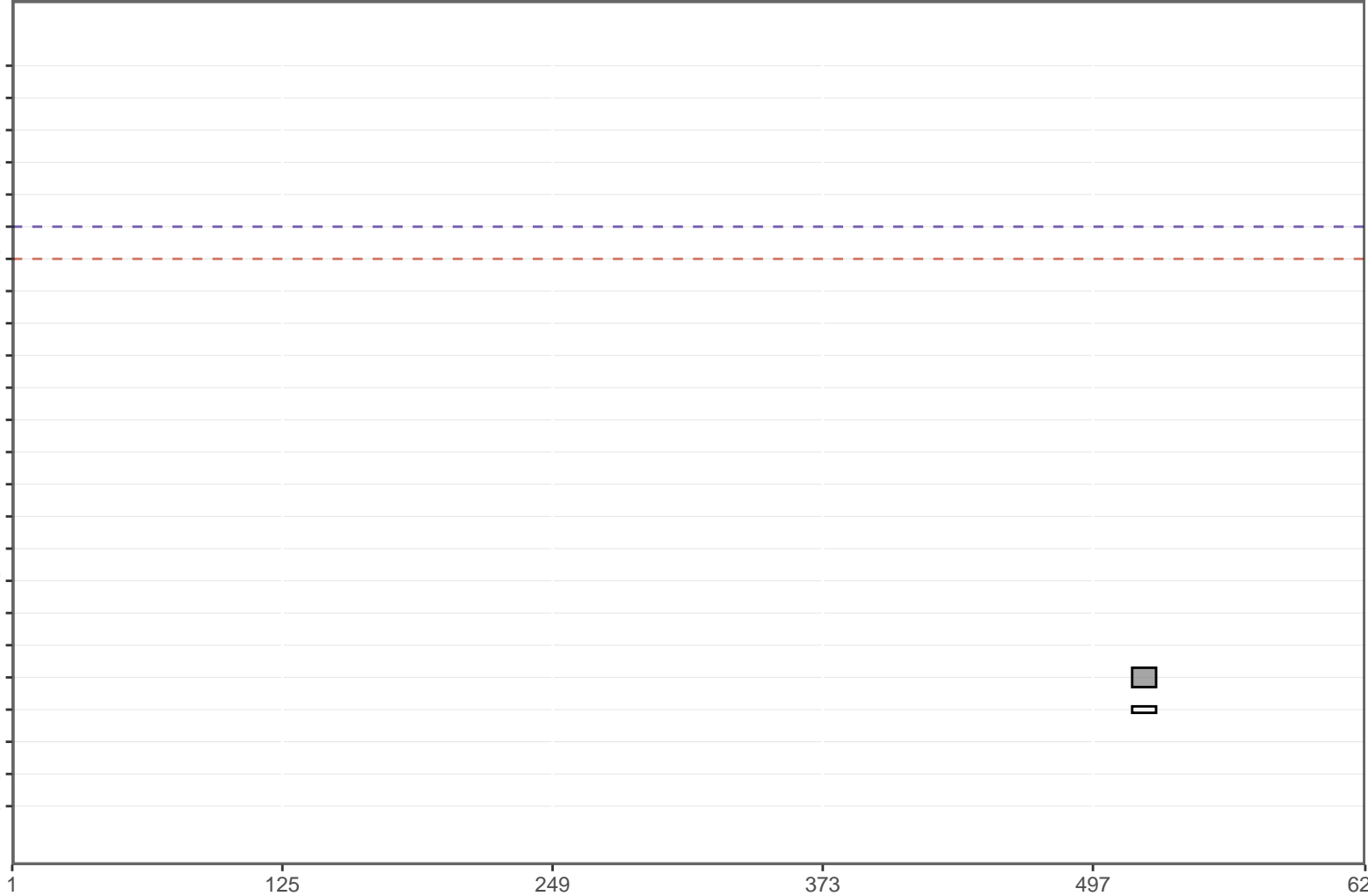
MW indication



Molecular weight

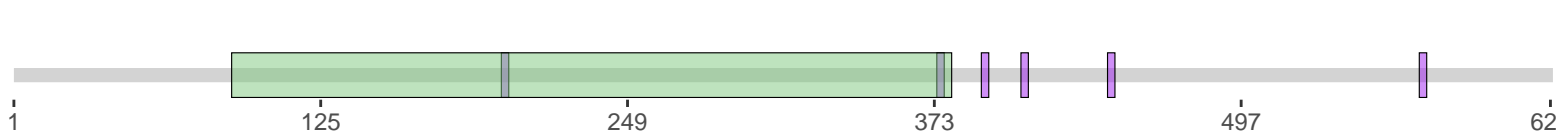


Gel Slice



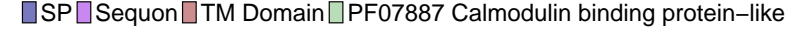
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

GMVDALVEHAKTCVIGGKLYVYPPDMRNVGVVFNINVELGGLGGGQYHVDLSENGKVVYDTLVKQAYGNWTHVEYDGLKLLSGGNKTSVASGNVLTIGSNNHSTFDDGQNLPLPAPISSEGPANNINLNGDGYNEISLSSRYTMDPQRMNINLNGMQLNGASFPQNLHGTGGGAGPHGSEMLALRPPQPMSSYFAASEPNPKYGAEDFLTEEERMRSHMLENEDEMQLHLLRIFSMGGGHASGGSEENYQVGGSPMPNMSSTFGFDEDRTRSSGK

NbL19g06300.1 eukaryotic_translation_initiation_factor_3_subunit_J-A-like [MW = 25.18 kDa]

No. of times detected



log(intensity)



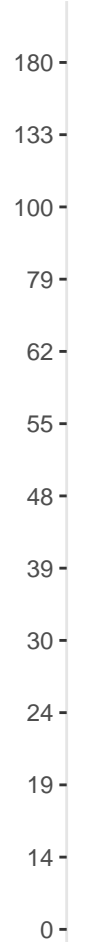
Values from



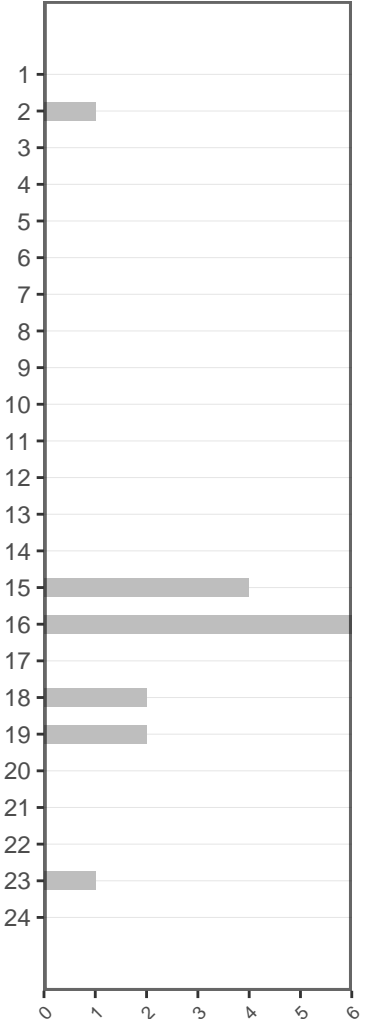
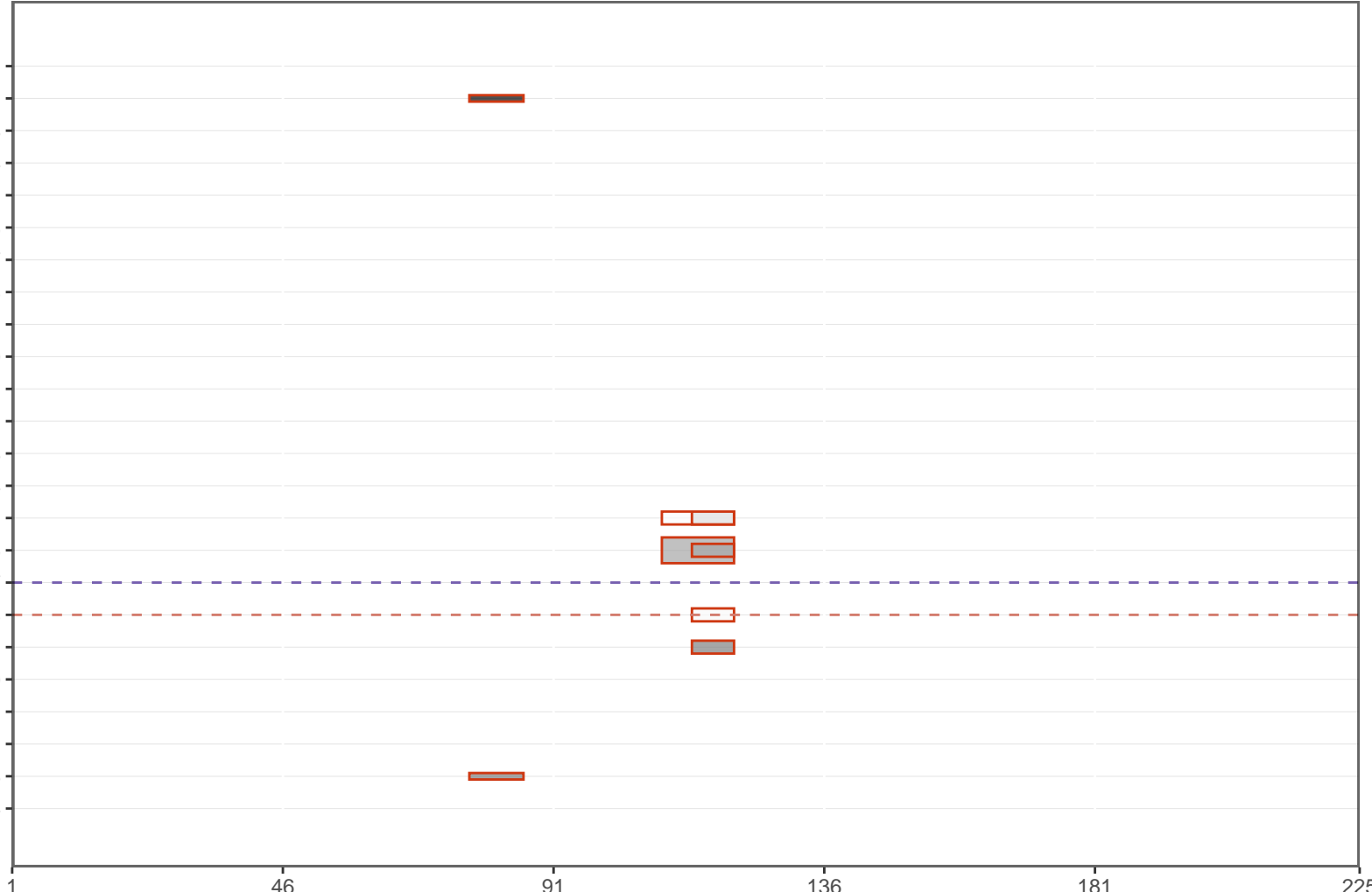
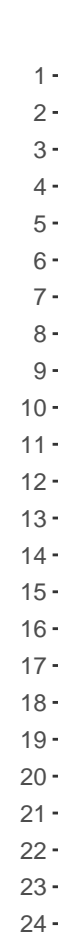
MW indication



Molecular weight

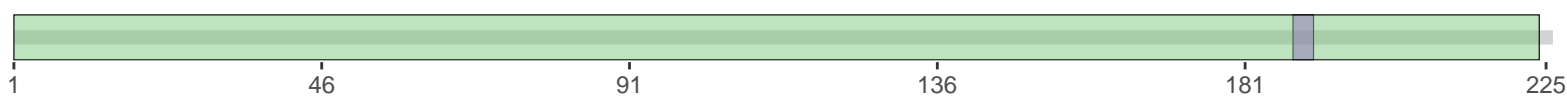


Gel Slice



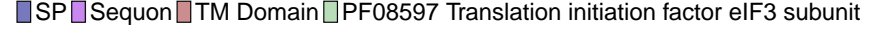
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

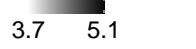
YKSTAELEFATKGGDQKTDNFIPIKSENFLELYAEIISHKLRIPYEKSVHYHGLKAVMRLSMTALKGADAKEIASVTAANEKKAKEANASKKKAGAKKQIHVDKADAEAVVNAVYDGYDDYDFM

NbL19g06240.1 glucan_endo-13-beta-glucosidase-like [MW - SP = 48.89 kDa]

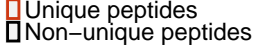
No. of times detected



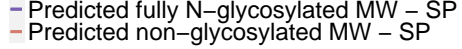
log(intensity)



Values from



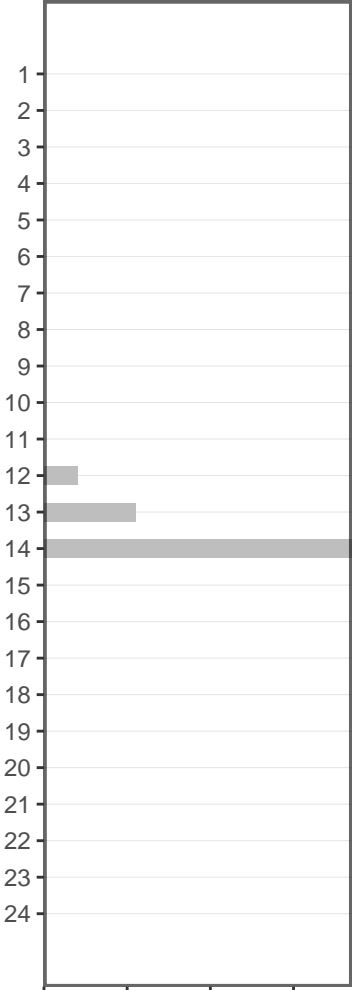
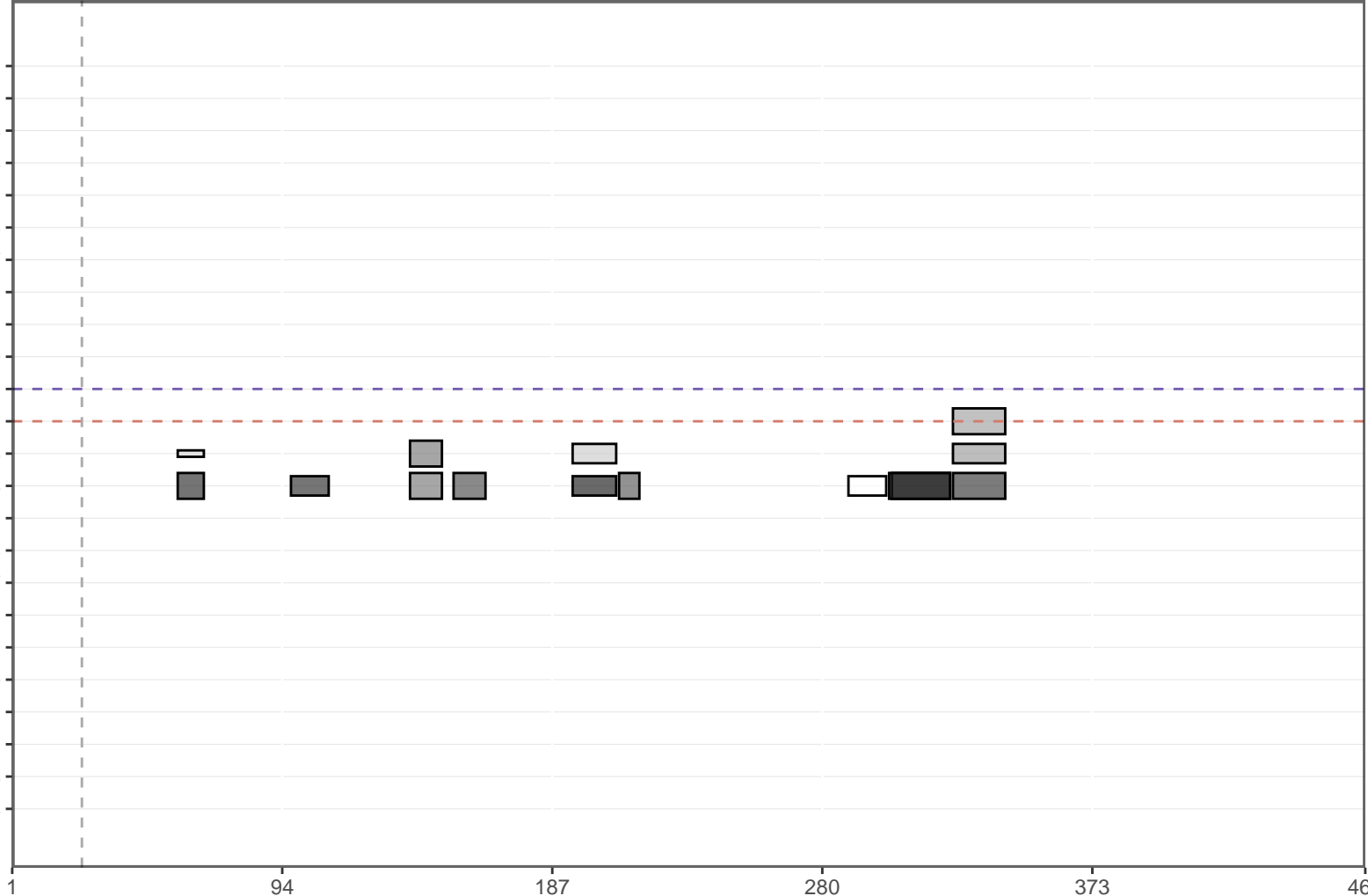
MW indication



Molecular weight



Gel Slice

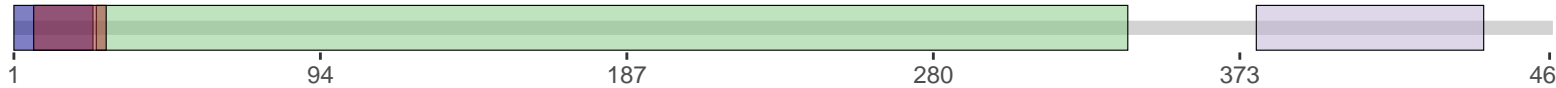


Peptide counts over 4 repeats

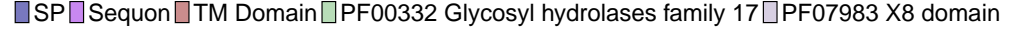
Protein length



Pfam domains



Pfam Description

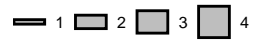


Protein sequence:

FSKRWYTNSTFDMLLDAVMMVRLKYSVDEIVAAETGWPSSGSGSEFPGCTVENAASVYNGLLRKYNSGTGTPLMFNRKIETVYFGLFNENTKRPQSTAEIRNGLFRPQTFVYVNGVLYKGEQAGPTALPAPRNGNGNKGQPTSPVRRPESKVFQMKPAEATDAQLGENVYVSGDGDCTPQAGGPGFNPNTIRSHAAAFVMSVYVQREGRNAFNQDFAGTGVVASADPKKHSKLLFLG

NbL19g06220.1 endonuclease_4-like [MW - SP = 31.06 kDa]

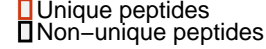
No. of times detected



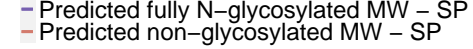
log(intensity)



Values from



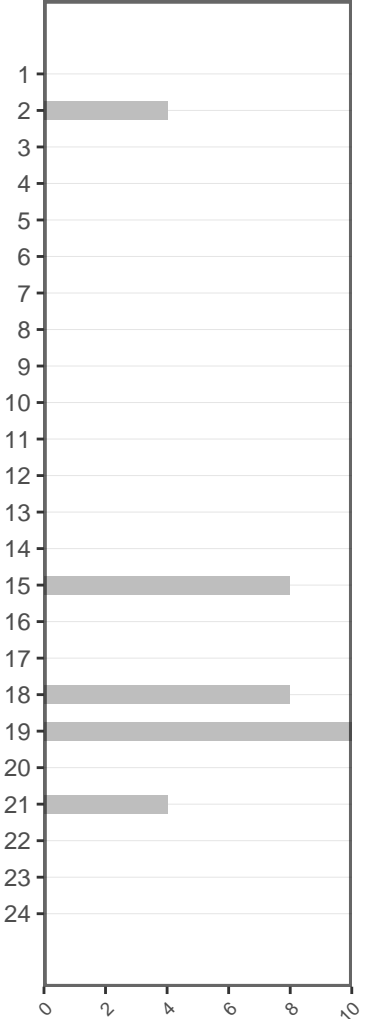
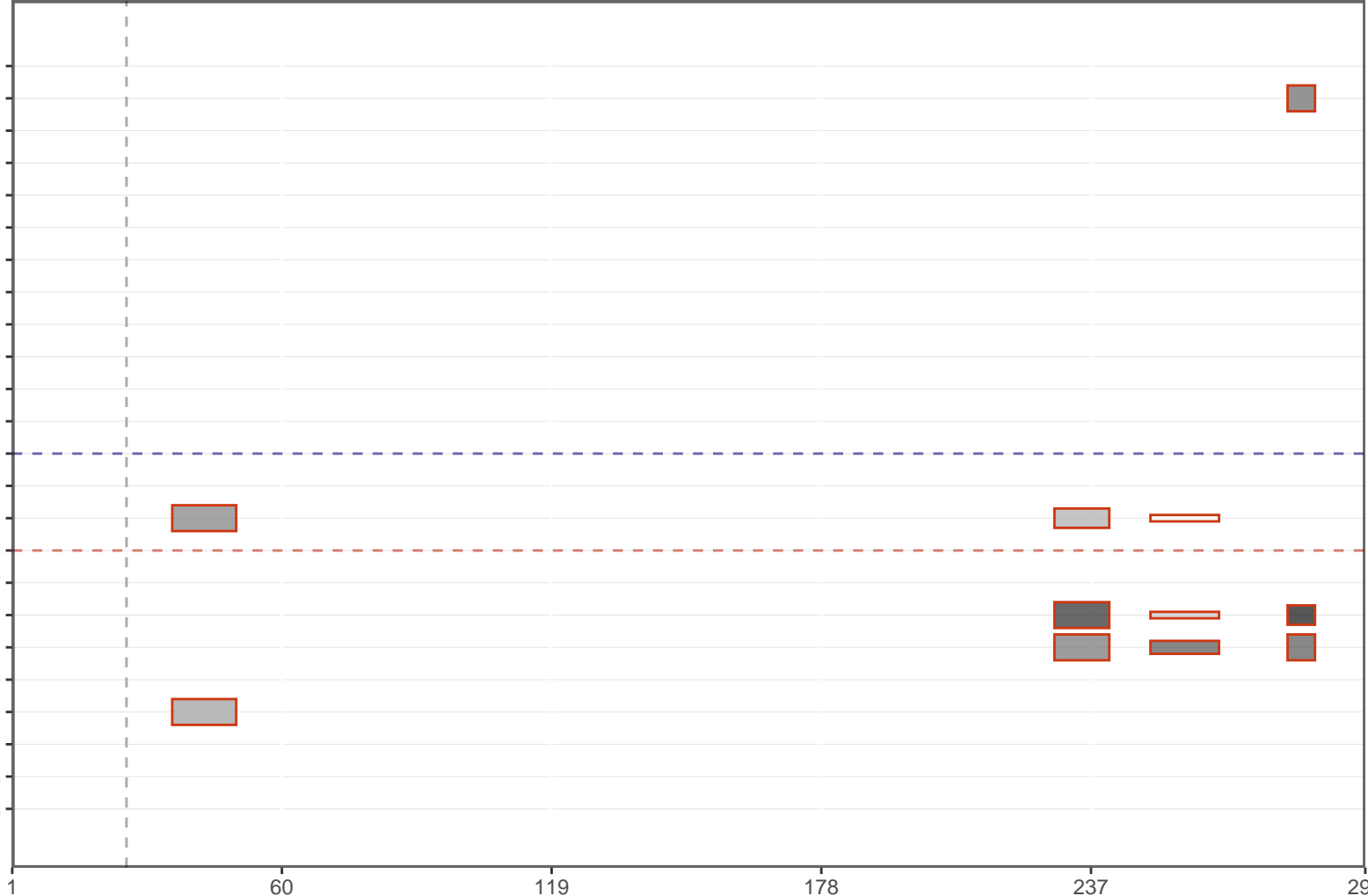
MW indication



Molecular weight



Gel Slice



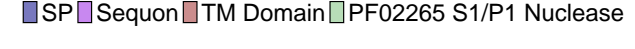
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EKYNLTEAMFLSHFVGDVHGPHVGFVGDVGNIVVWRKRKLNHJHWDTMIESALKTYKSDLTLMGALLRNITDEWSDVPSWENCKMVGCPDPYASEVSRVLRACKFAVRNATPGSTLGGDYFLSRPLVVEKRLAQSGIRLAEVLRFRFSKQFTAQ

NbL19g05870.1 clathrin_light_chain_1-like [MW = 34.84 kDa]

No. of times detected



log(intensity)



Values from



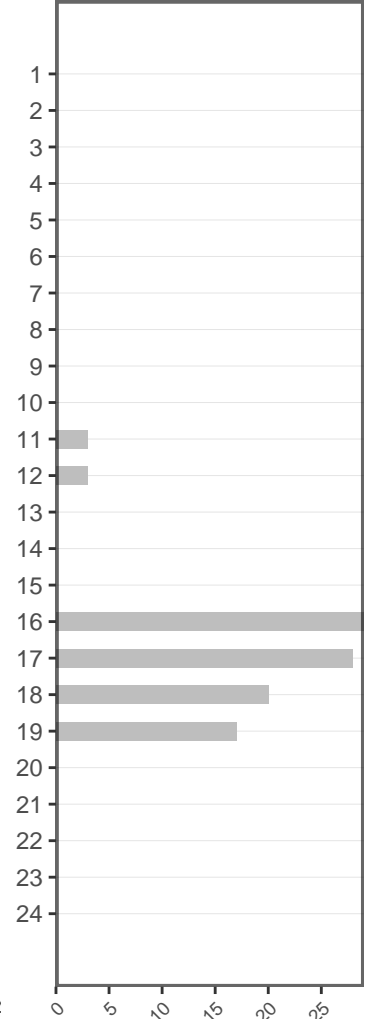
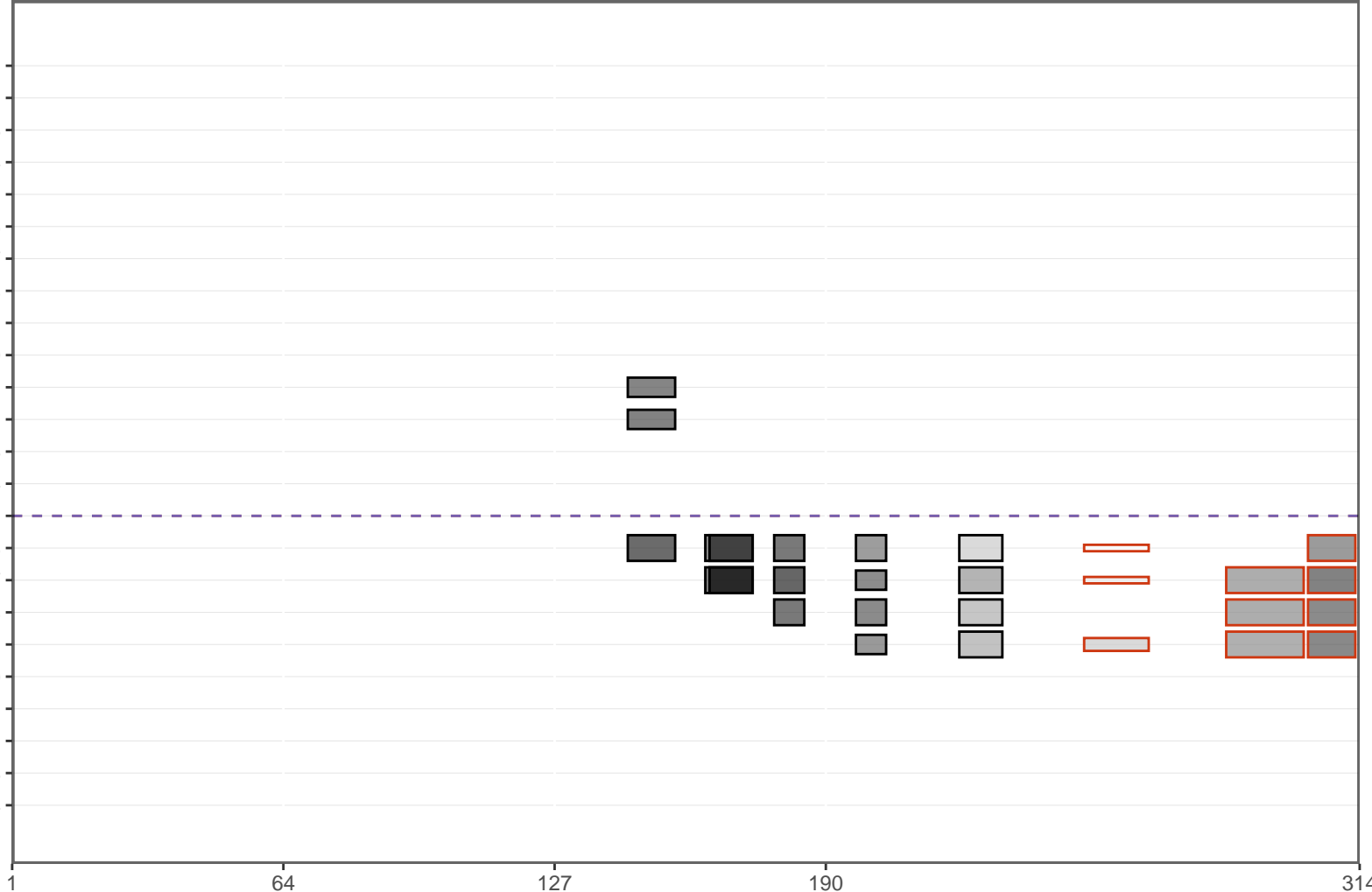
MW indication



Molecular weight



Gel Slice

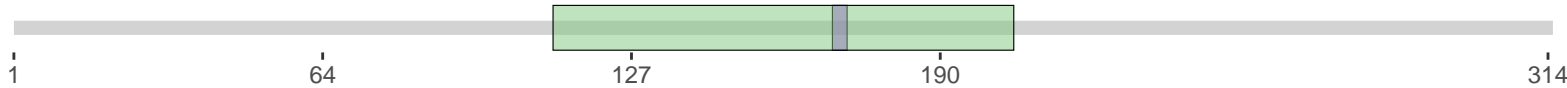


Peptide counts over 4 repeats

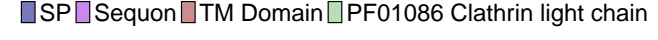
Protein length



Pfam domains



Pfam Description



Protein sequence:

IRNIDIEEGEEYKAFYEKRLKLVETNGSTNREKEKLVLENGDKFHKAEADKQYWKAAELPKVEATEKKGRNKDGEKPEVTVVQGPKPKPTELSRMRHLLKIKHSPPFHMPPIPPPPPKDAKAGKDGKDAKVKDKSNKAKDEAPNGHSDAPPDPAKVTQTSEEPVAAE

NbL19g05830.1 30S_ribosomal_protein_S5_chloroplastic [MW = 36.85 kDa]

No. of times detected



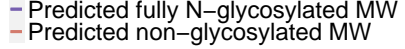
log(intensity)



Values from



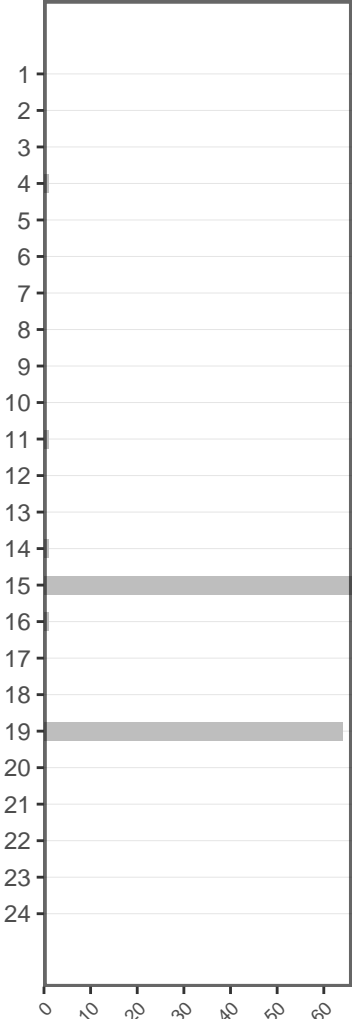
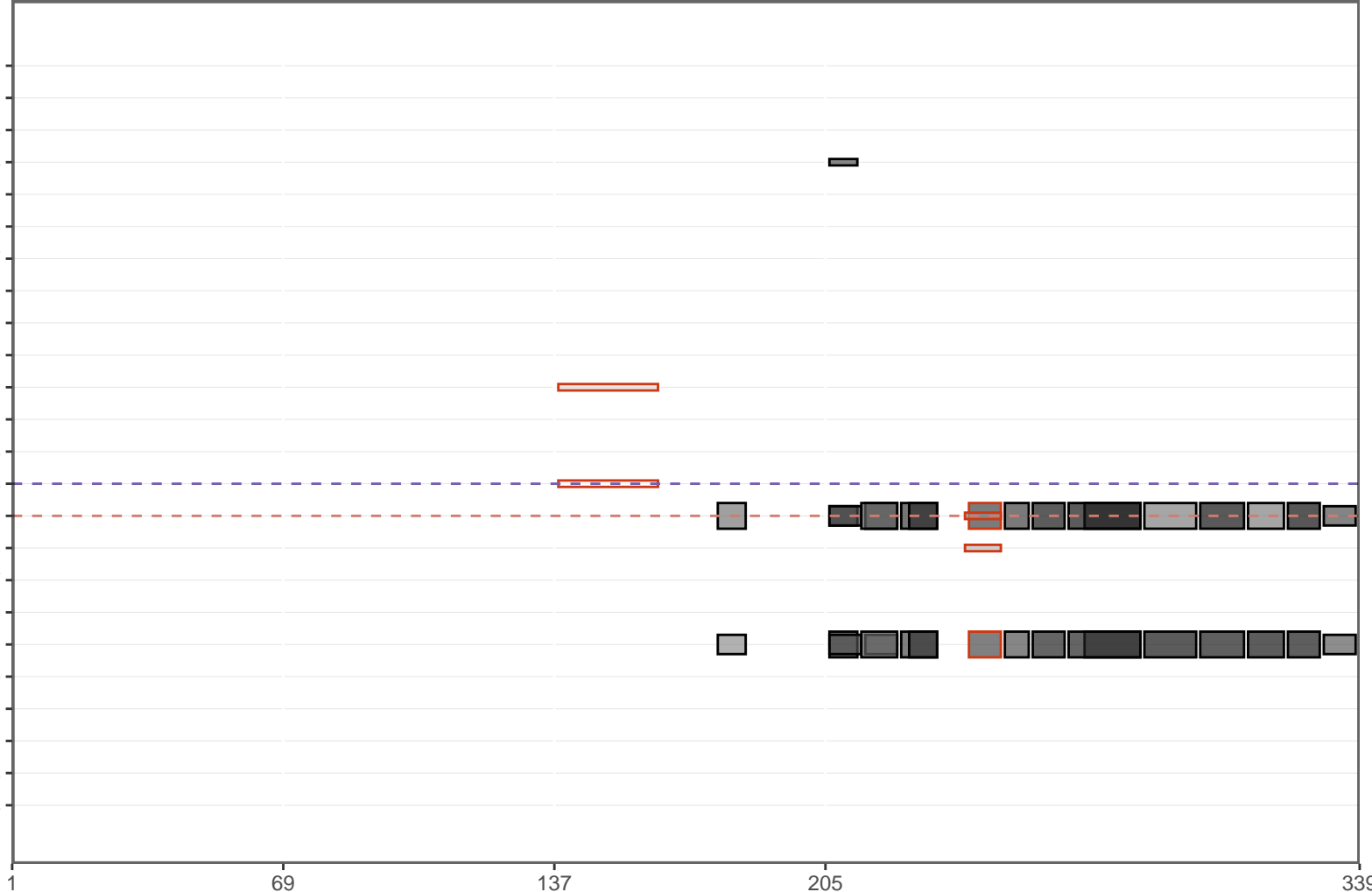
MW indication



Molecular weight



Gel Slice



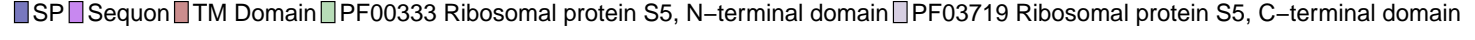
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DSKLYKTTAFGKTKNEKAKDGFDERVVGQRVRRVTKVKGKGLHFRRAIVVGDHKGGVGVGKAKEVIAVQKSAVNAARRNITVPMTRKYLTFPHRSEGDGFAARVMLRPAAPGTGVAGGAVRIVLEMAGVENALGKLGNNLNARATVVAQDGMRFSEVAGERGIPMEELWK*

NbL19g05770.1 pistil-specific_extensin-like_protein [MW - SP = 25.44 kDa]

No. of times detected



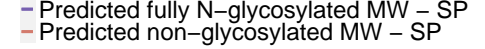
log(intensity)



Values from



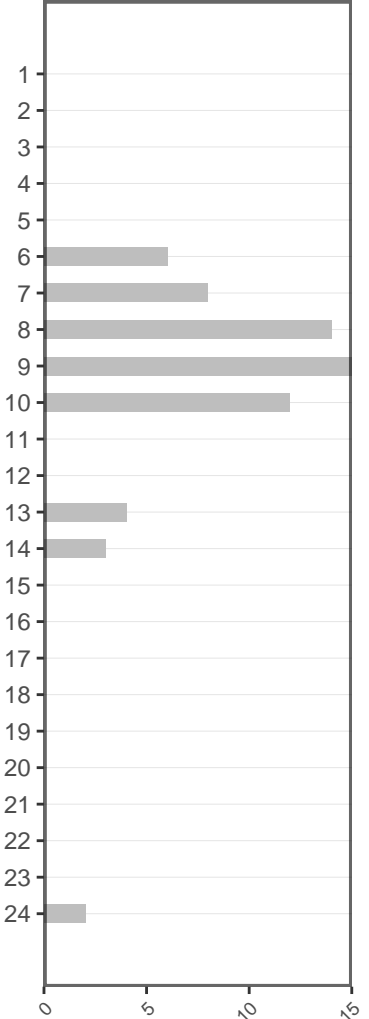
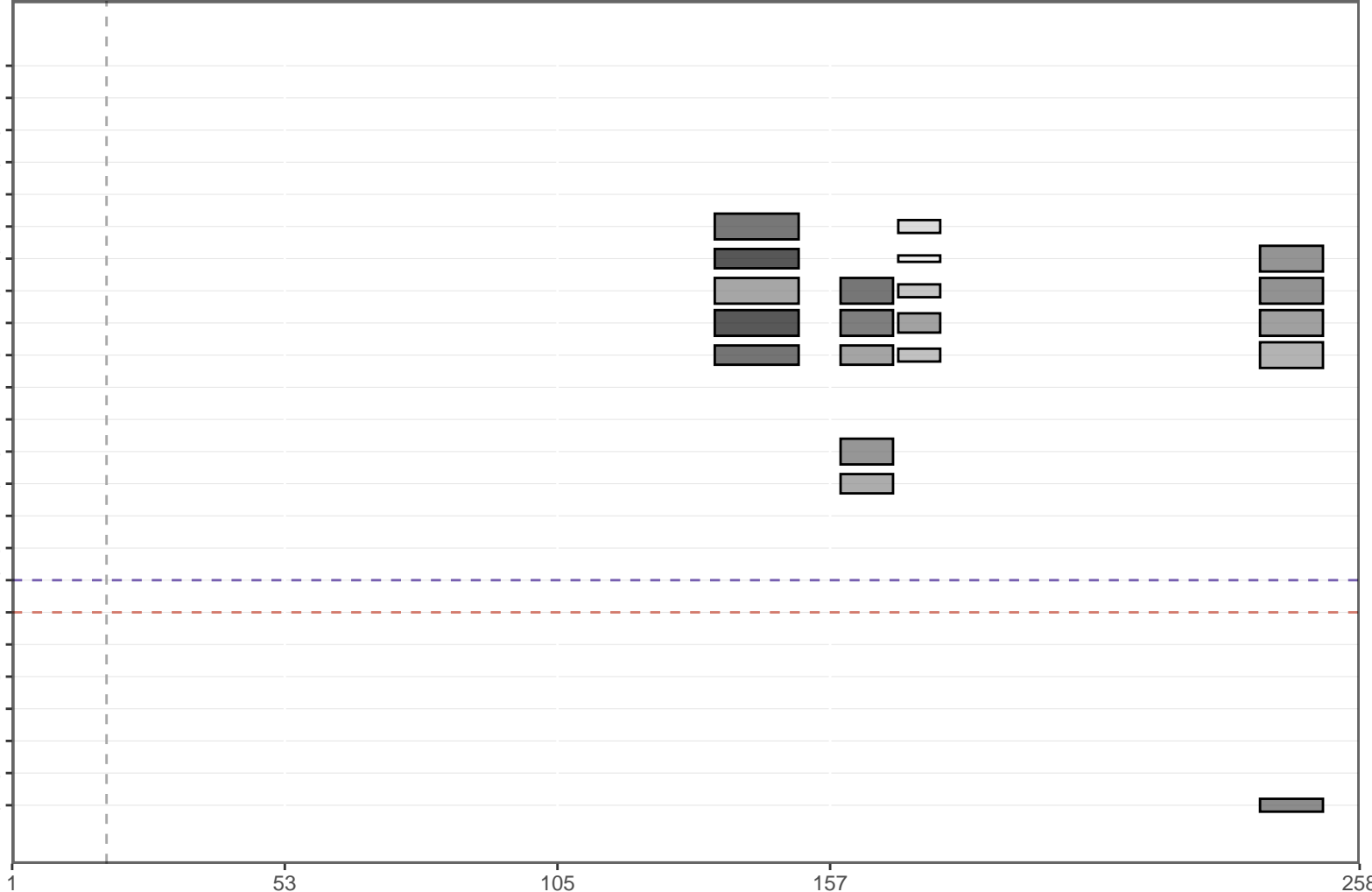
MW indication



Molecular weight



Gel Slice

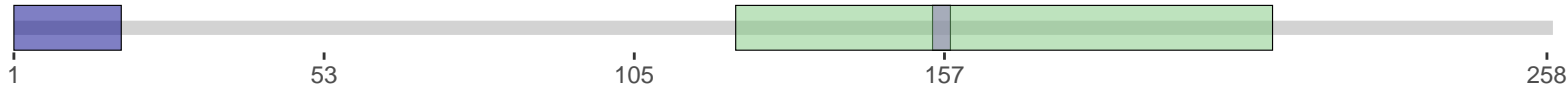


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

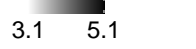
TRNFVGVVGVGVVYCKSEKQYRGIIDLLGASPIQGVAVLHAGNTRHYHILTAIGTTRDKNGYFFIQPKWLTAGYHKQKFLANKPKAEGVPTNFHNGGAGAMLVPLFPPPEPMISKPVDSGETGVKLENVGPFAPERSKILPCKG

NbL19g05700.1 eukaryotic_translation_initiation_factor_3_subunit_D-like [MW = 65.58 kDa]

No. of times detected



log(intensity)



Values from



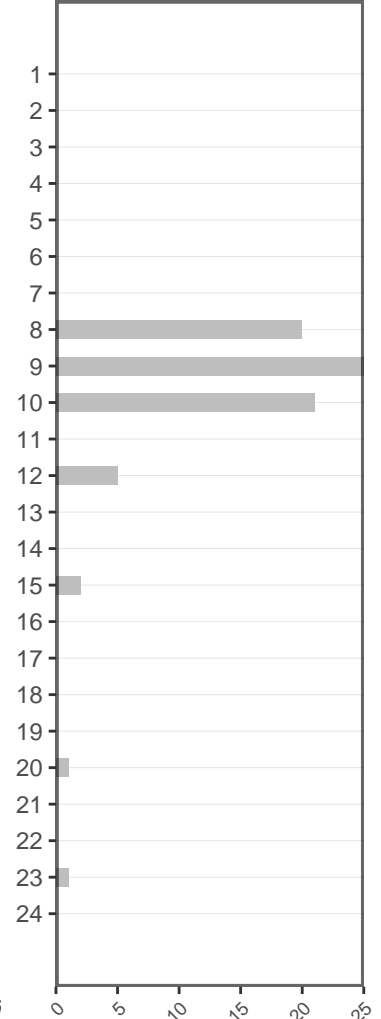
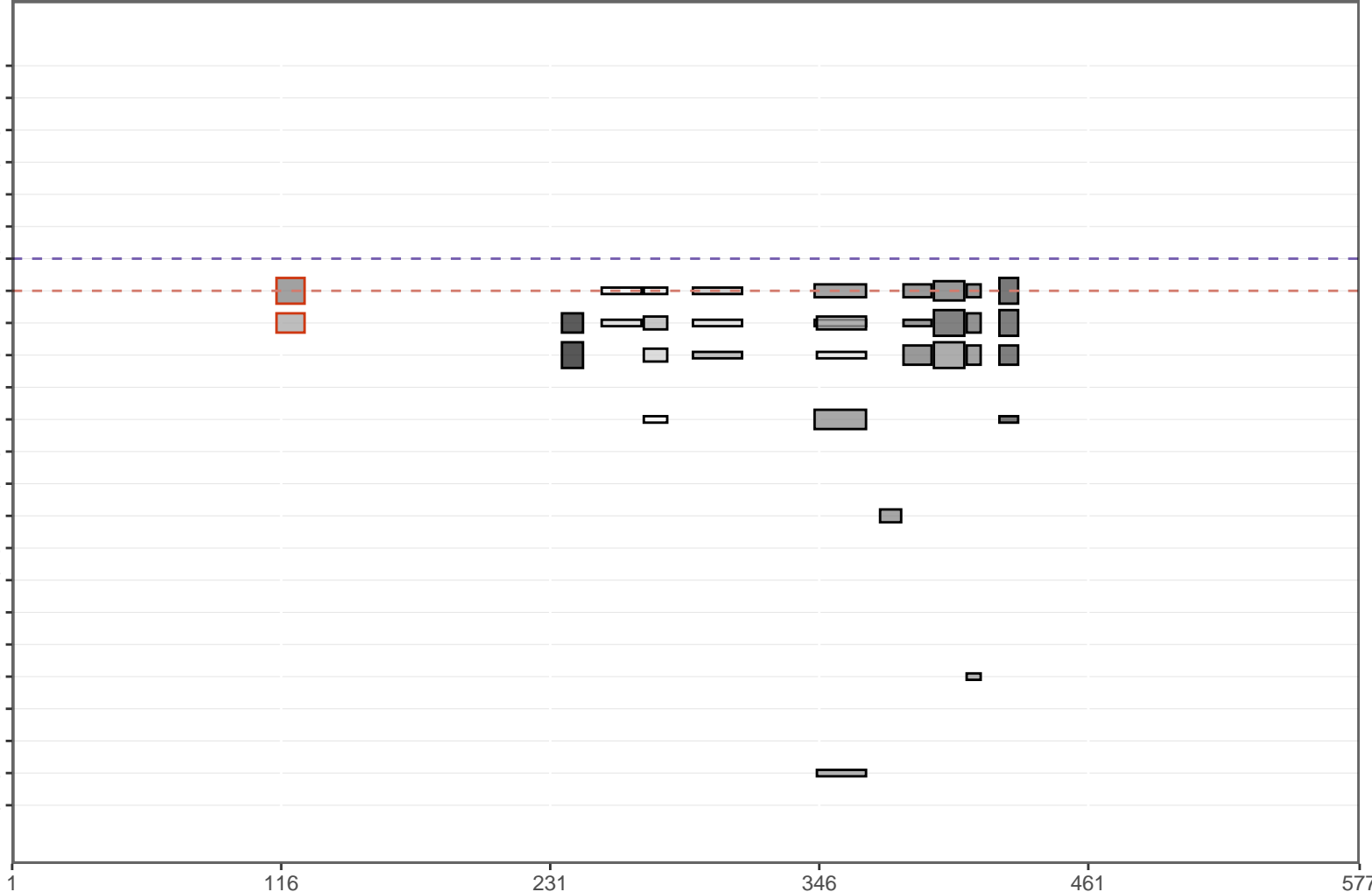
MW indication



Molecular weight



Gel Slice



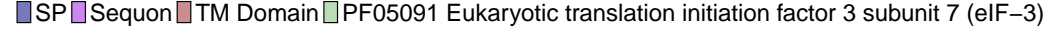
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IDIVVQRVGNKLIFFBKRDGSGQLDLEVHETSGELFDPVKKDDNSAHSLSVEAAAYINGNFSGGVLRDGGKLNNDYDFNPFATEGEEVASGVYRFRWKLDDDTFLVARGEVQSVYEVNNGRSFLTNALNEFDPKYGGVDWRKLETGRGAVLATELKNNAKILAKWTAGALLANADMMLKGVYGRVYRPHDFHVLVAAGYKPKDFAAGINLNTSNMVGIVNSVDLGMKLNKGYKLVKDPKQVRIYVPPRAFENDVVEEPLPEDEGVGPPPTEDMGOAEANGVN

NbL19g05590.1 metal-independent_phosphoserine_phosphatase-like [MW = 34.03 kDa]

No. of times detected



log(intensity)



Values from



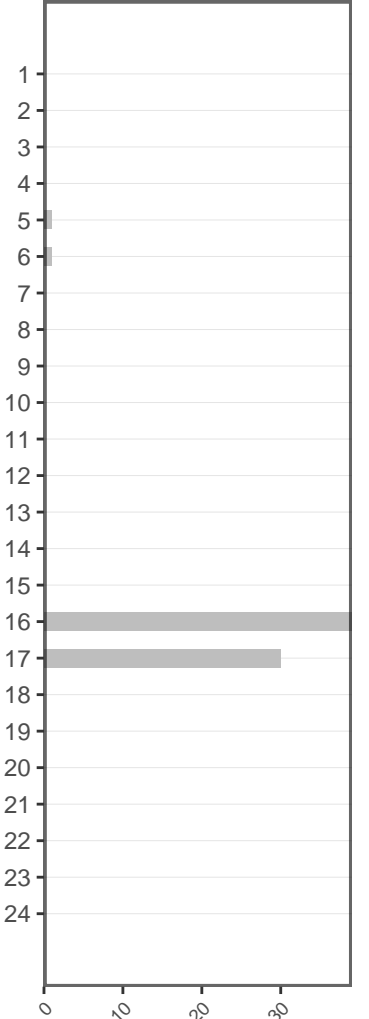
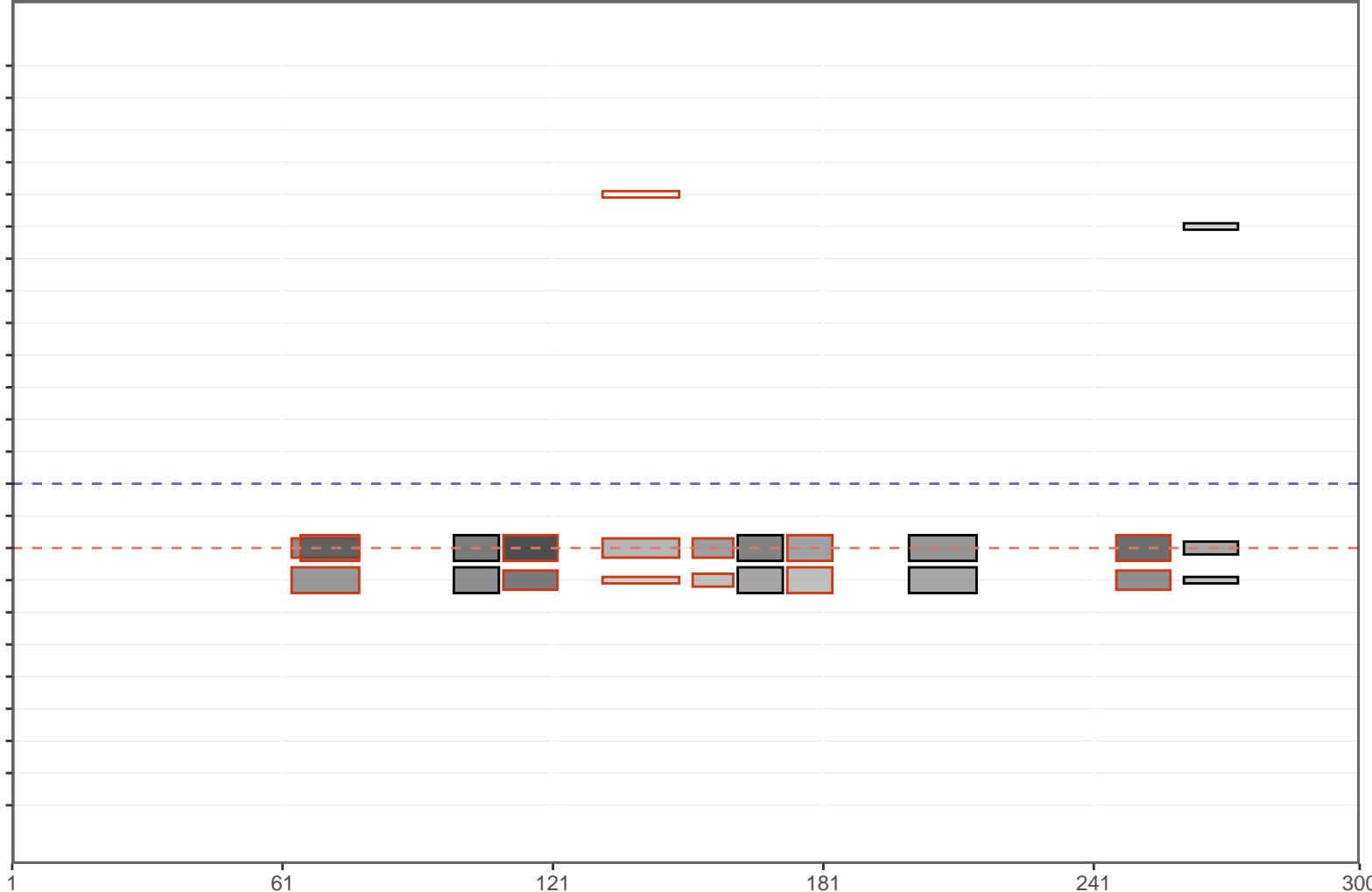
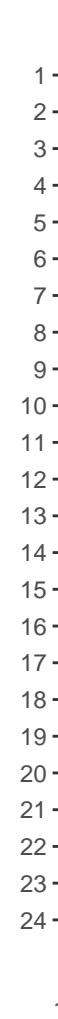
MW indication



Molecular weight

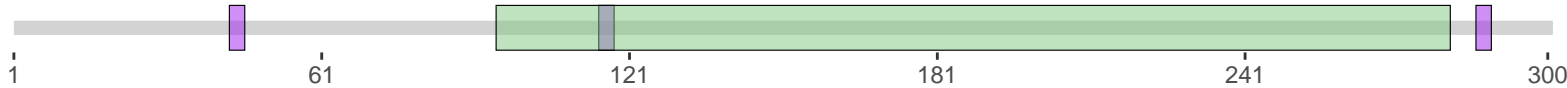


Gel Slice



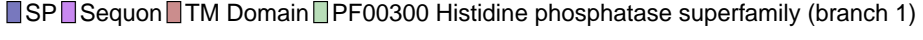
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VHFDGCFSSPSRAKTAEMVGGKEPLVFLDLSKEAHYVLEGMKEDAKRIYKPYKTTWREDFSNFVDGYYPLQKLWGRAVEAWEEILLTPGENFLVYTHKSLRALIGTALGLGPERFRFRVDNNGGLGVFKFKNGEAMLHSLNMTAHMYTDHWHY*

NbL19g05540.1 molybdopterin_synthase_sulfur_carrier_subunit [MW = 13.33 kDa]

No. of times detected



log(intensity)



Values from



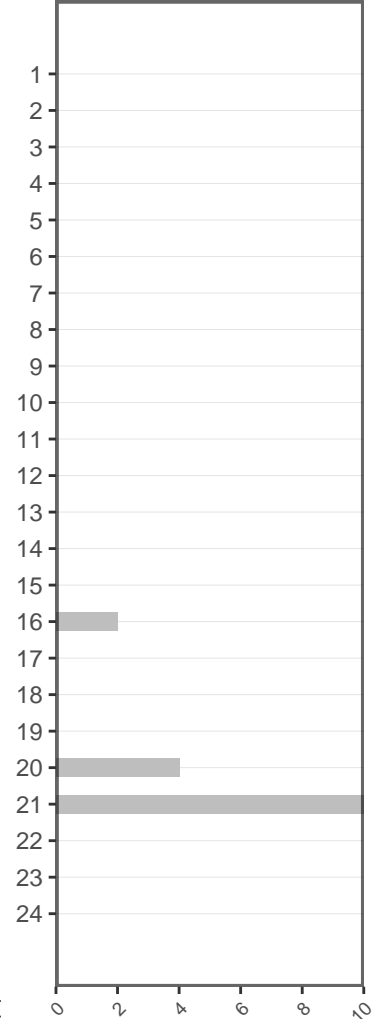
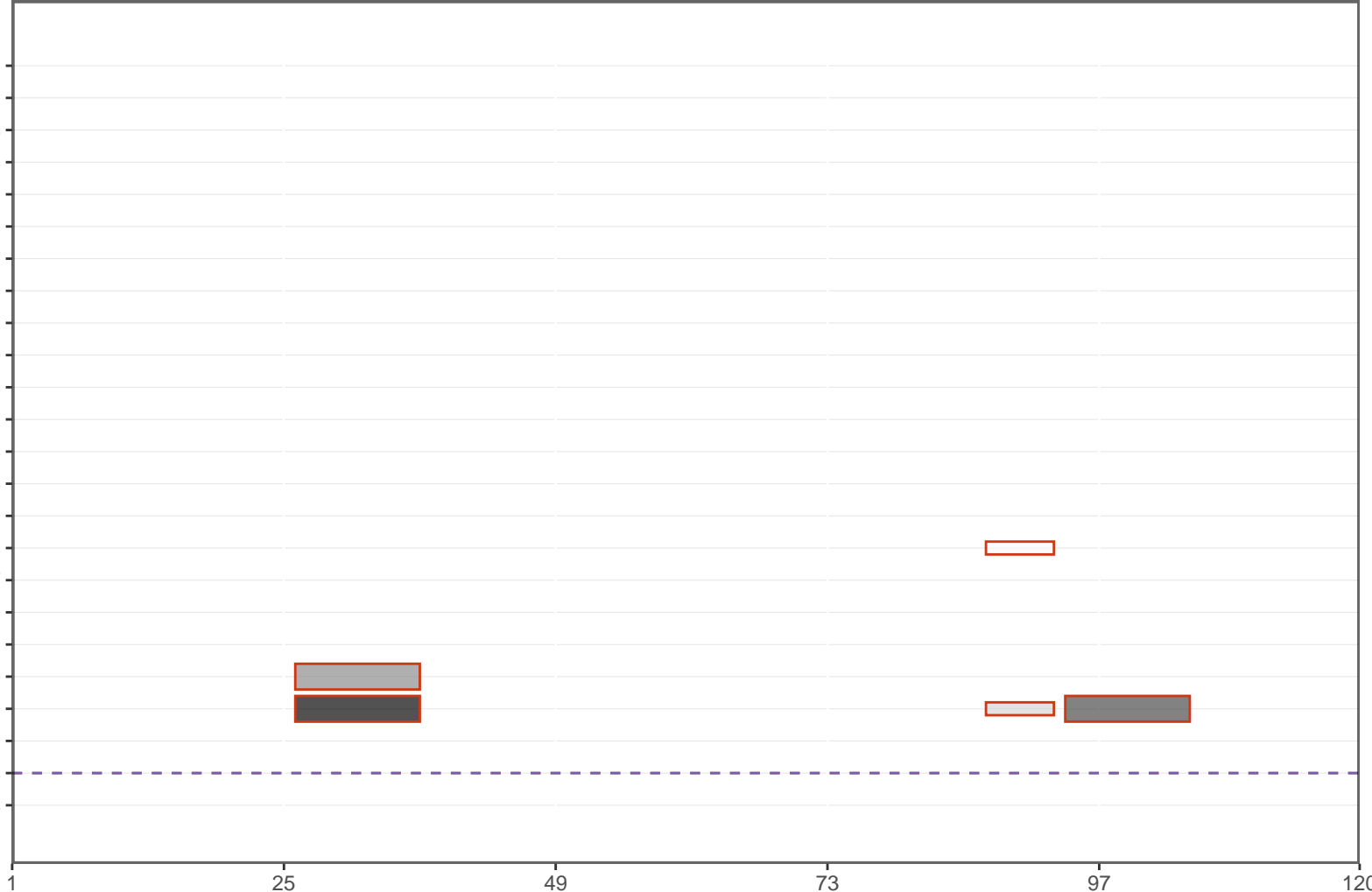
MW indication



Molecular weight

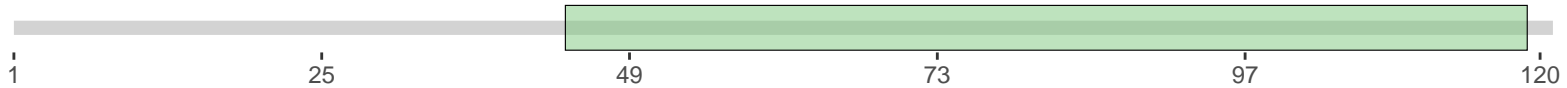


Gel Slice



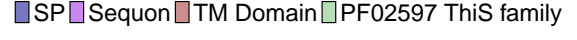
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VRARDLTGMTMPLEVSYSGTAGDGLNKVGRFRPRLEERIRGMLLARNEEYTPSEFTYKDGDELAIIPRGGG

NbL19g05470.1 14-dihydroxy-2-naphthoyl-CoA_thioesterase_1-like [MW = 17.1 kDa]

No. of times detected



log(intensity)



Values from



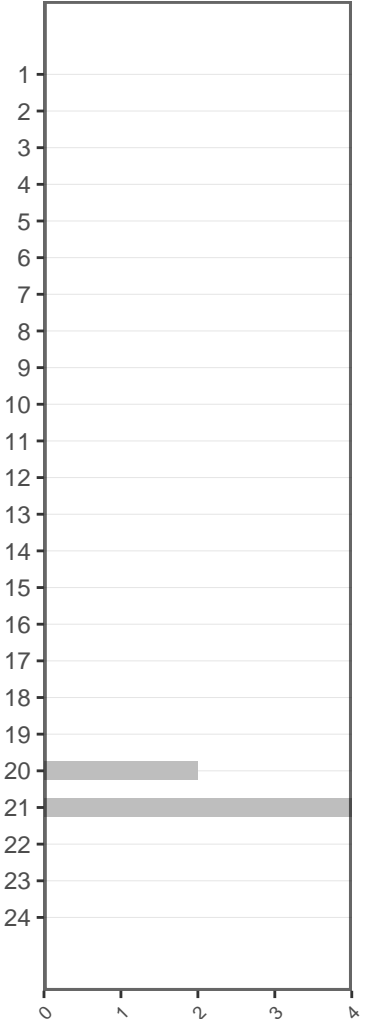
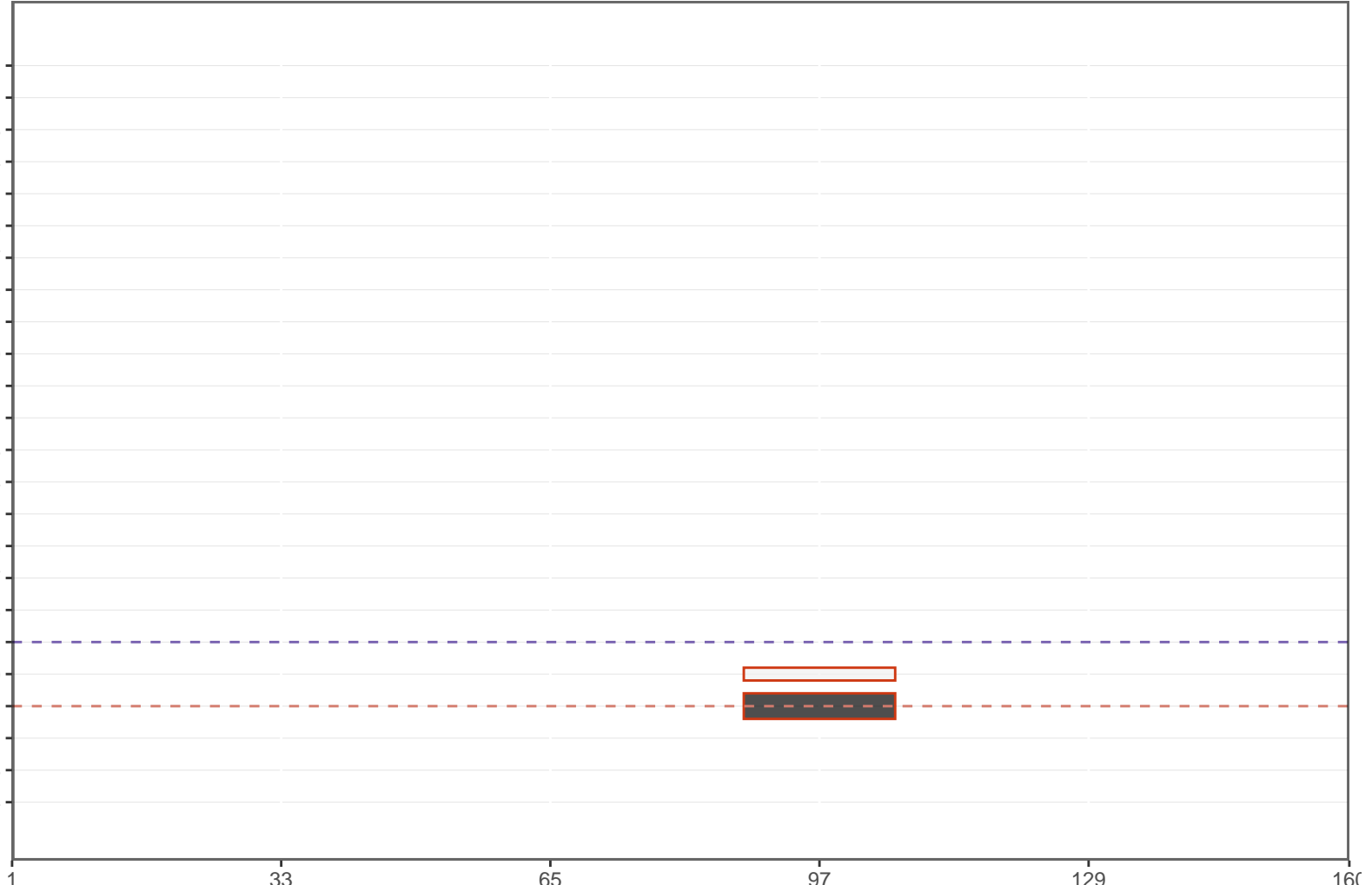
MW indication



Molecular weight

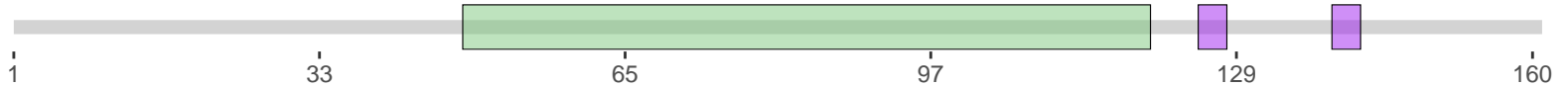


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AHMASGFGRRVAGVQLGSHHLEKSAHIGDLVFAEAVPNIKGRTHWVEVGIWKIDPNNEENKTLAASRVLTKANMSPENAKDAVNLKRYAKL

NbL19g05160.1 uncharacterized_protein_At4g28440-like [MW = 17.54 kDa]

No. of times detected



log(intensity)



Values from



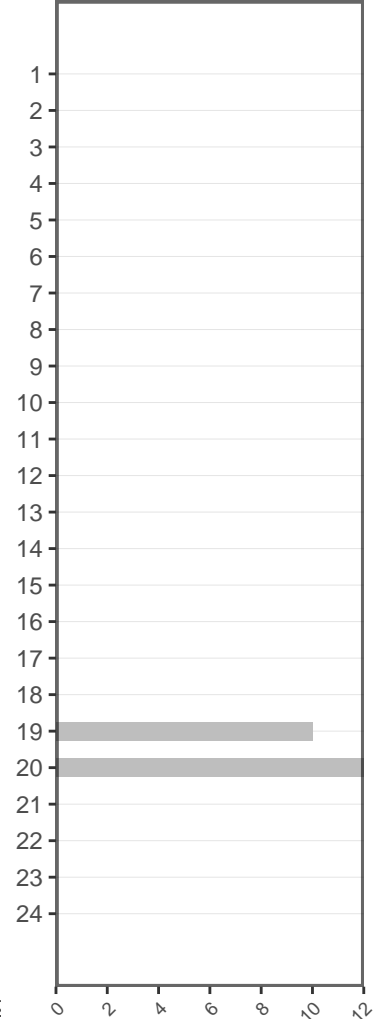
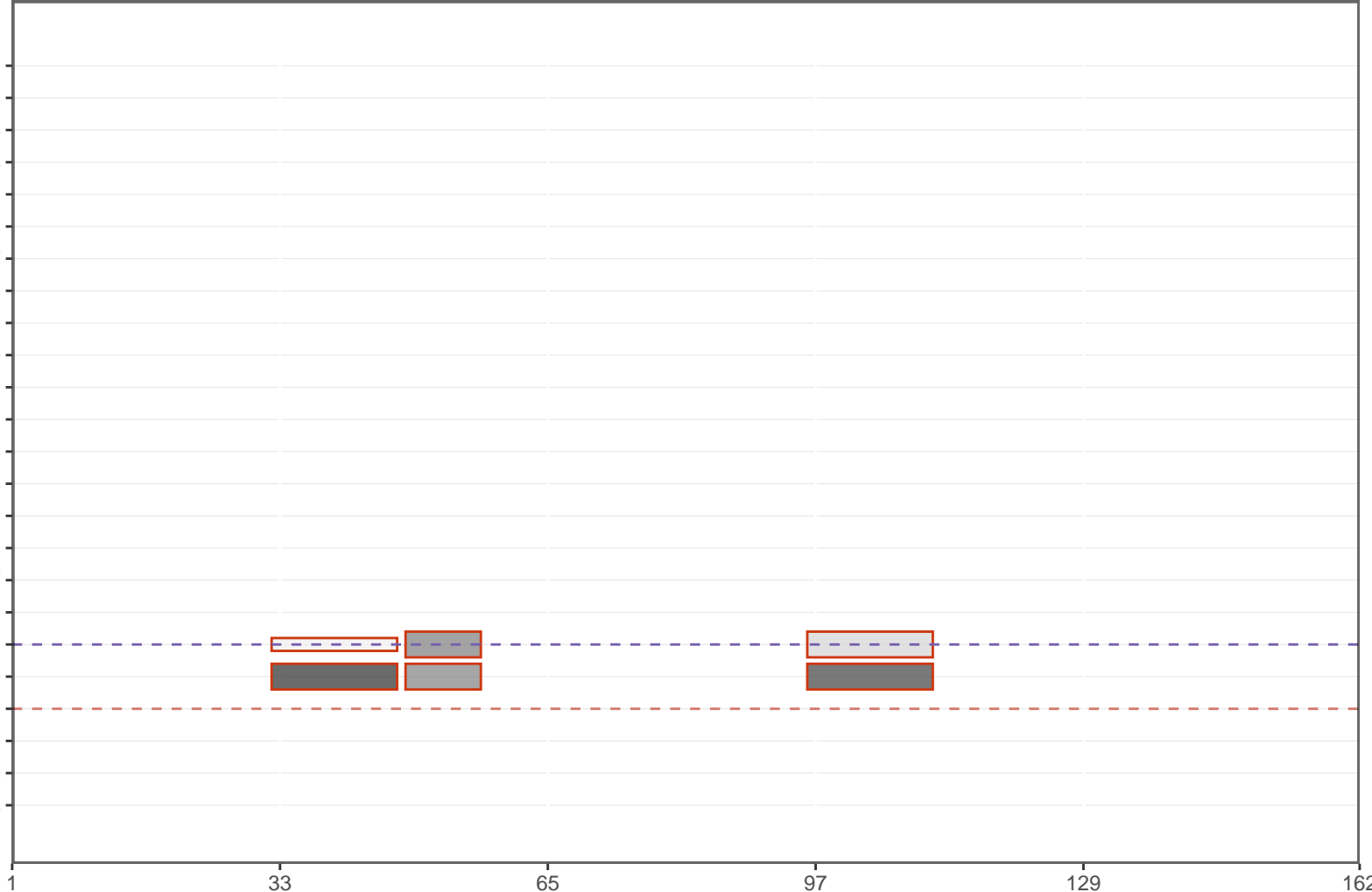
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RVPKRPQONTRISEGLVGDDEGGILFTARDGVDMMKPDATHLRNAKIDMFKGSMRLAVDKWGRVEVAERTFVYNEENLGLVEVELVAEE

NbL19g05100.1 glycogen_phosphorylase_1-like [MW = 92.51 kDa]

No. of times detected



log(intensity)



Values from



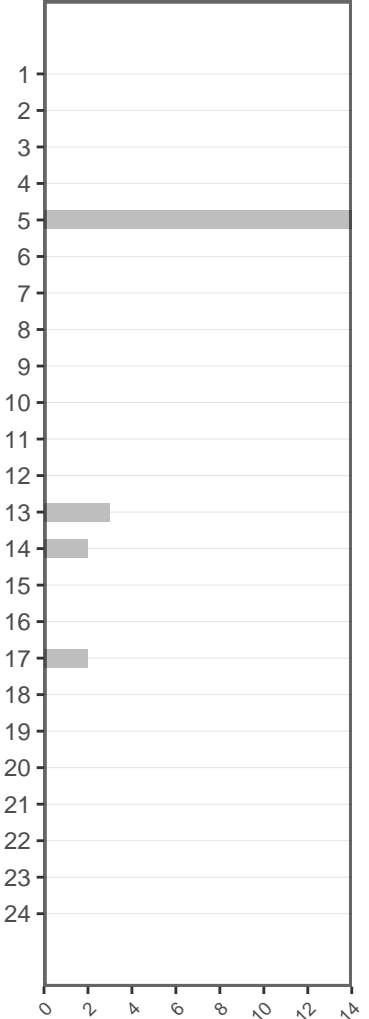
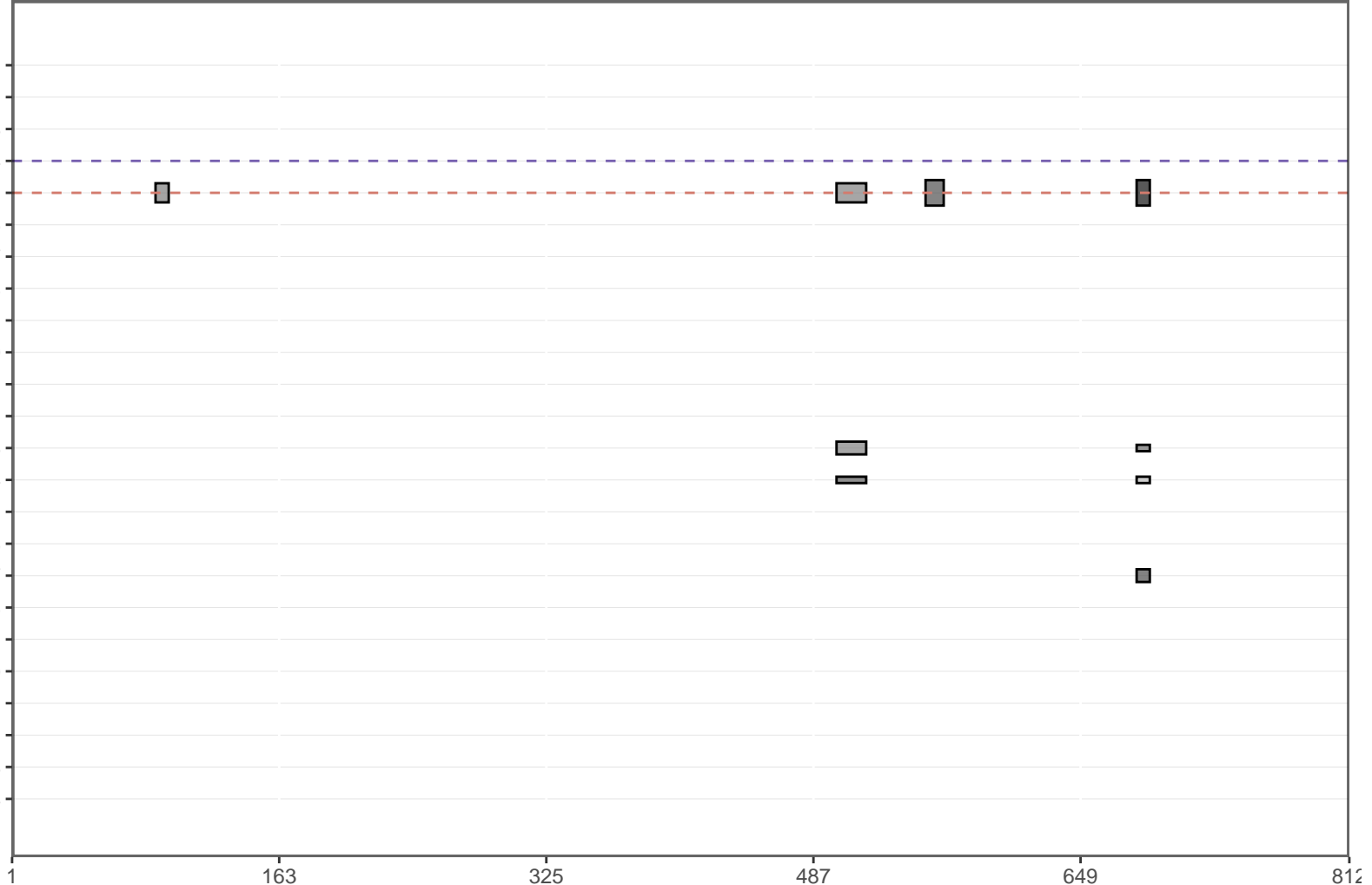
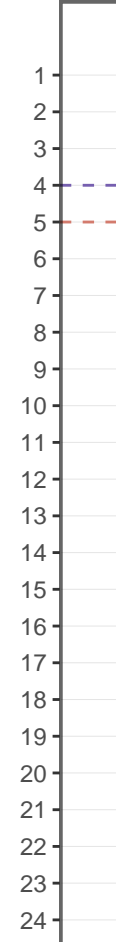
MW indication



Molecular weight



Gel Slice

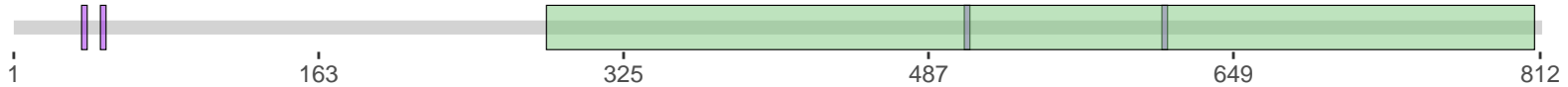


Protein length

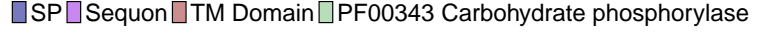


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

...VWPAESVEAWDNPFGYGRNANLRWAAKPSDGYDMESVYTTGDVYNAVNRGKAETISNLYPDGRSVOGKELRLKGGYFFVGSALQDHRFRKDLHNFDEFPEKVALGINDTHPSIAIAEVMRVLVDEEHLDSKAWGIAGKIFSVTHAVQPEALEKVPIDLLGSLPRHLEIYEINVLMEELKRLGGDYDLSRMSIEEGAWKGRMANLSLACGHTYNGVSRHLLETLEKTRVFKDFYELWPKQFKTKNGVTQRRLVWVSNPLOSIEKWLGTAEWIRNVDIAK

NbL19g04820.1 GDSL_esterase/lipase_At5g45950 [MW – SP = 37.79 kDa]

No. of times detected



log(intensity)



Values from



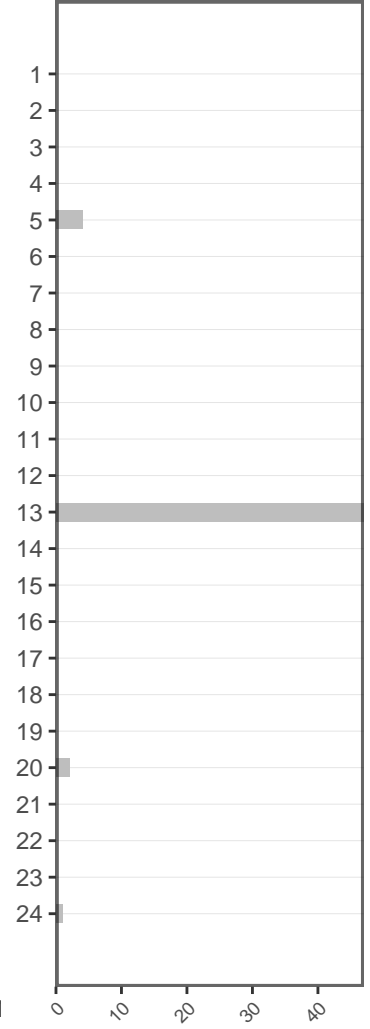
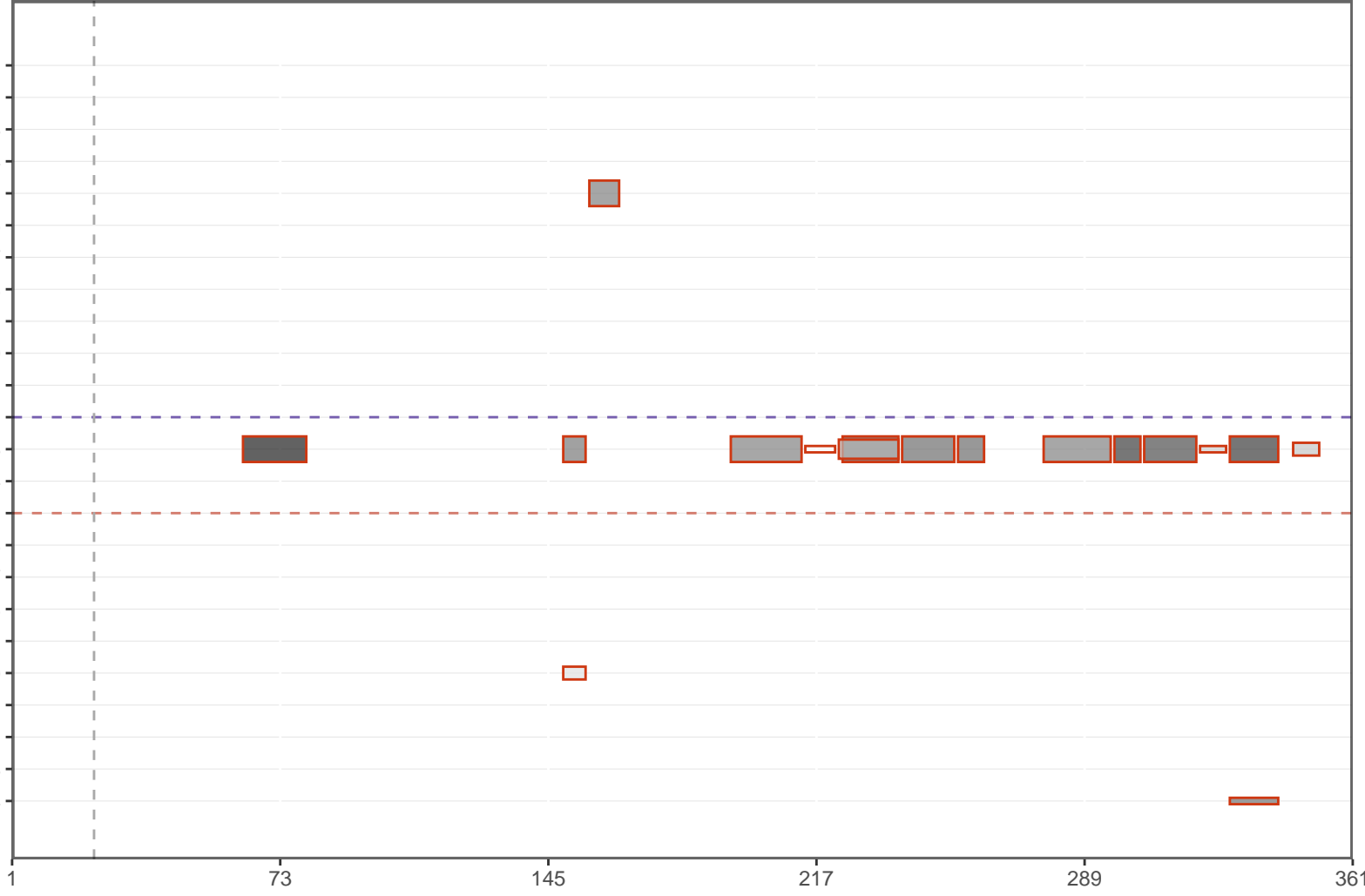
MW indication



Molecular weight



Gel Slice



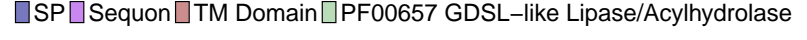
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MKNALYLSMGTNDFLGNFYFEVERSGKYVVEGYNQFLHISMFTHKVDIHHGVGARLLAVGVYPLFGCEPLRTRRDETKGDDDLNKKVAFSFLNKLKRELGTLLKRLFGKASFIDYISQIEAVGNPKHFGFEETSKGKCCGCTGTTTEYGETKGLLTGADRTPQFVFDVAWHPSEKMKMKIMADEALKSINADLFS

NbL19g04710.1 GDSL_esterase/lipase_At5g45920 [MW = 26.32 kDa]

No. of times detected



log(intensity)



Values from



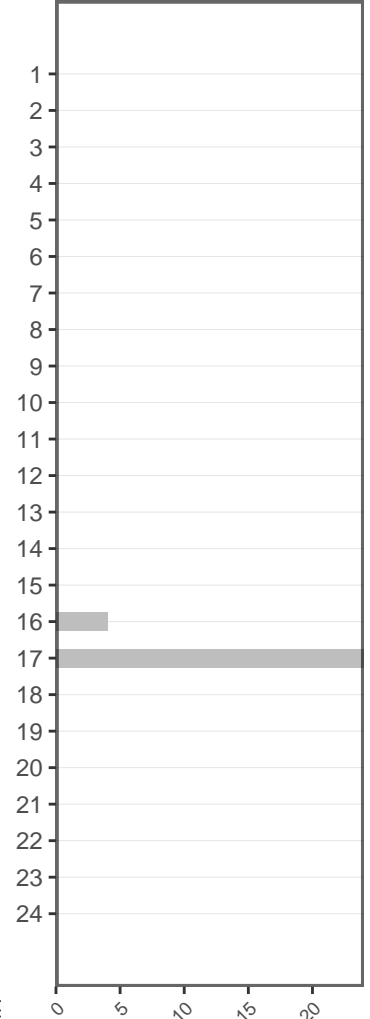
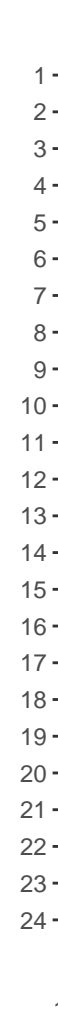
MW indication



Molecular weight

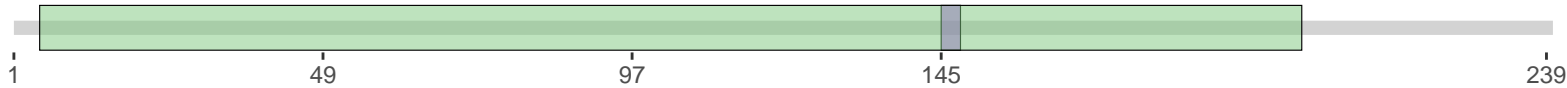


Gel Slice



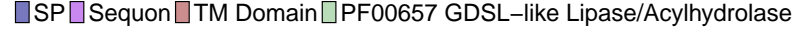
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FLKGRWPTTQVILISPPRIDEPARLLYPIFIENKLGIPERTNETAGNYAKASLTVAAEGGVLAVDLWTRMGQIPGWGTAGLSDGLHLKTKGNEIFEEVVEALKKKGLSEVETLAWDLVINEIDPNDPLKSFEGII

NbL19g04660.1 GDSL_esterase/lipase_At1g28600-like [MW = 43.02 kDa]

No. of times detected



log(intensity)



Values from



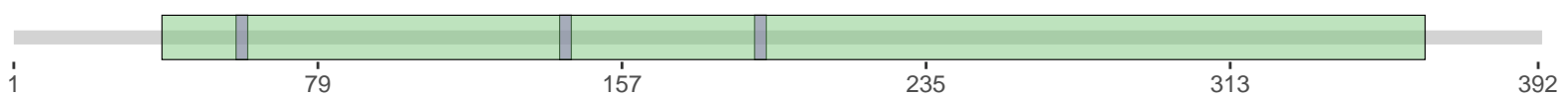
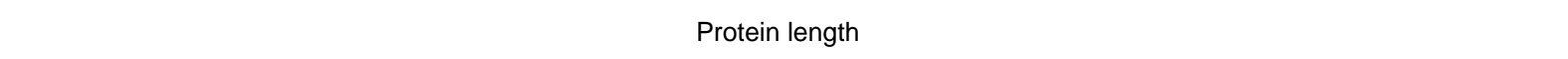
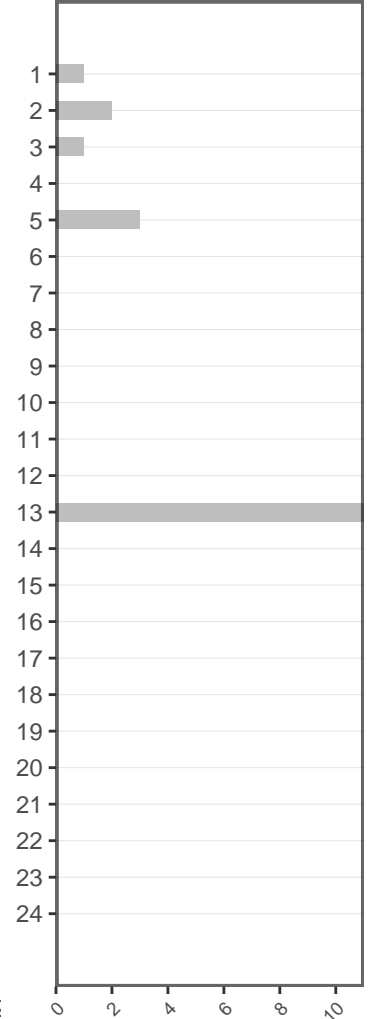
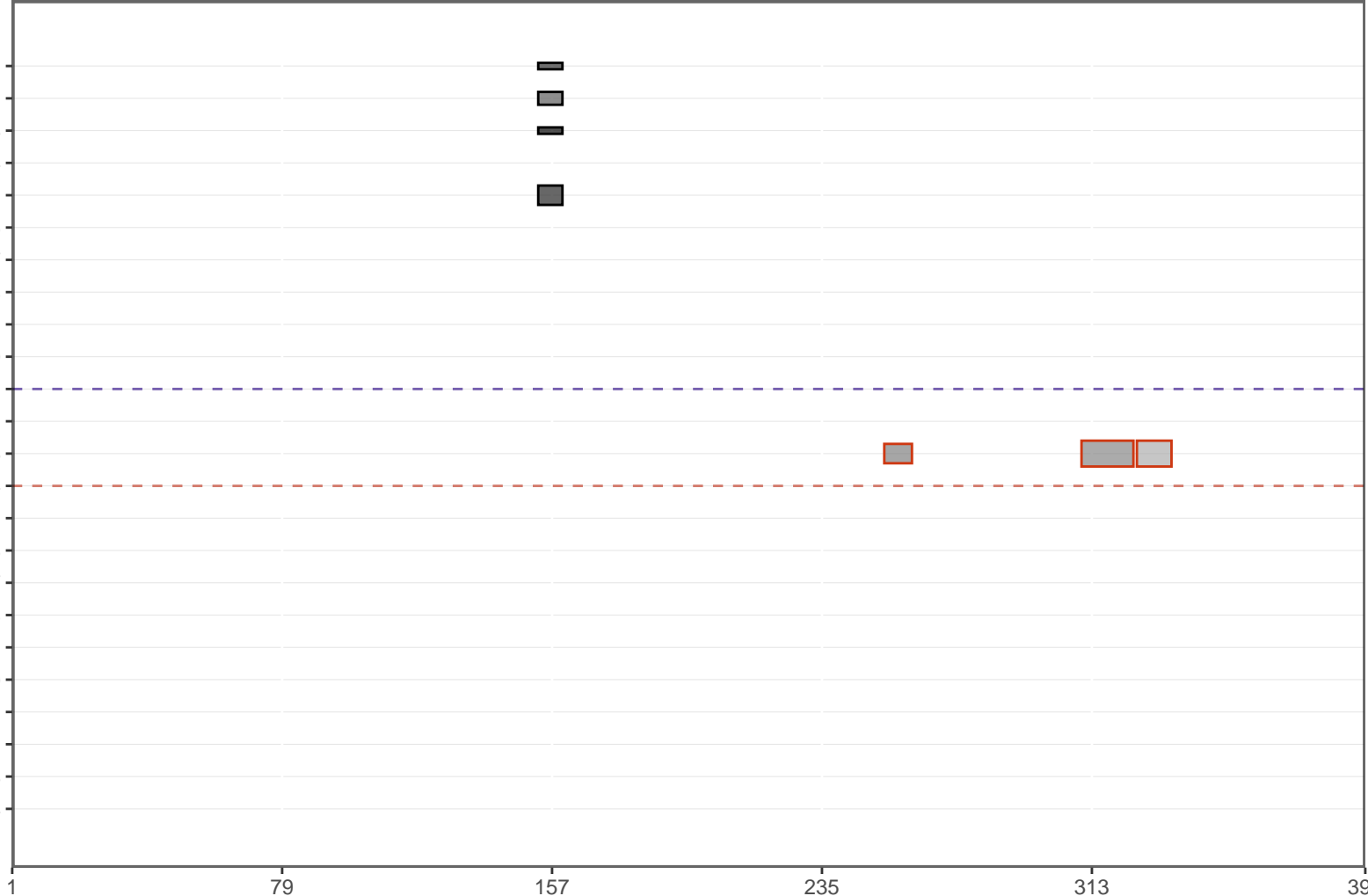
MW indication



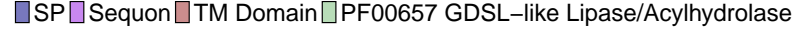
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

DFNYGFLGNSTKKEEVESEYVFWWNTTSSAIGELGASTLVVFGDLPIGGSTAVLTKFMHSDKENYDPKTCGNLWLNRFSGHYNELLGKELHLRELYPSATIYADYVNAAMGEFYVHPMSHGFTKALDAGCGAGGPPNFKFAVCGDPPARNIGSDTSVVAEWDDGVHFEAAVKLARGLLEGTFTFPPLPKFTFPNPIAHFDS

NbL19g04650.1 phospholipase_A1-II_1-like [MW - SP = 44.01 kDa]

No. of times detected



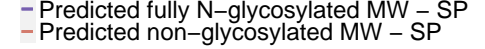
log(intensity)



Values from



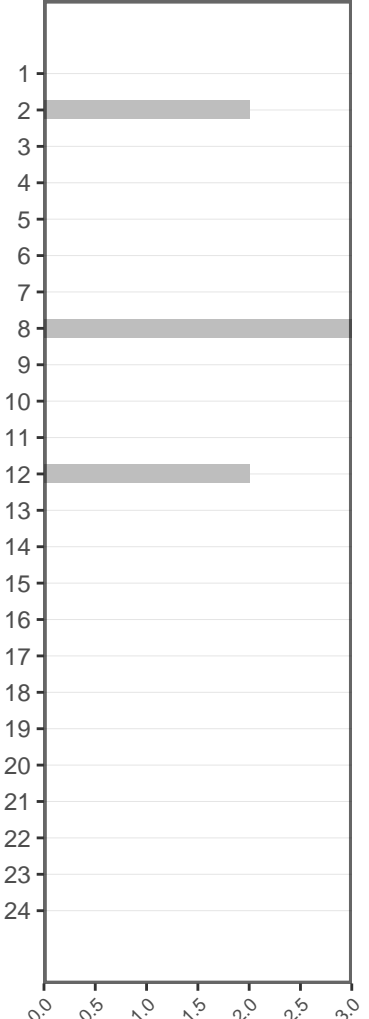
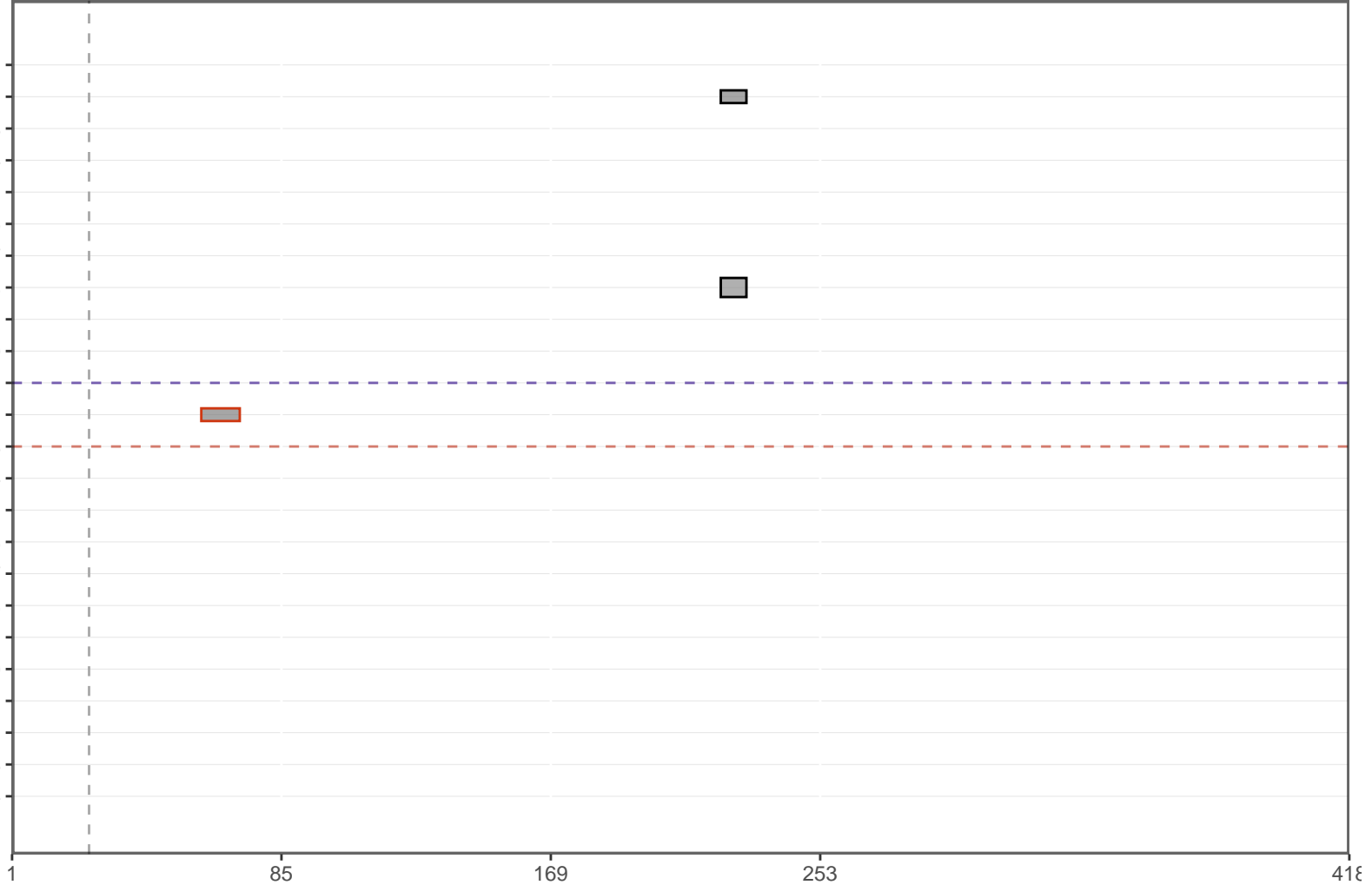
MW indication



Molecular weight

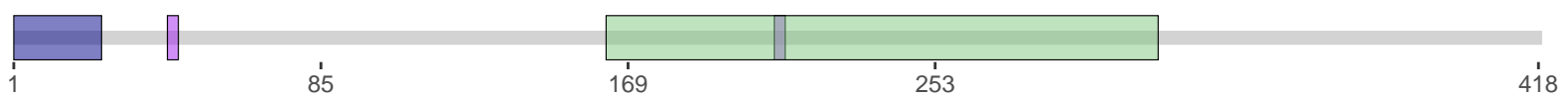


Gel Slice



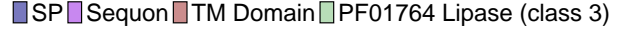
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

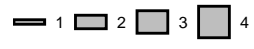


Protein sequence:

IHGWSYVTSNDSRFFPKASARDGVLEGEVRLVEGYKNEETFTVTGHSMGAATLNADVDSNGFNKGFPTAFLFASPRVGGDNFKTKFEKLNLRALRVRNAPDVPNYPLLGYSDVGVQLDDITTKSTYKPGPDESQWMMDCVYMHGVAGNGGSGKGFLEVGHDSVYNNKYLDAKDEYGVPSGVAWVEKNKGMVGGQDGSWLMHDEDDL

NbL19g04630.1 protein_trichome_birefringence-like_37 [MW - SP = 39.09 kDa]

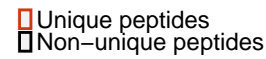
No. of times detected



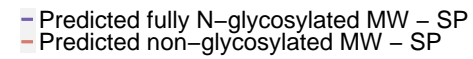
log(intensity)



Values from



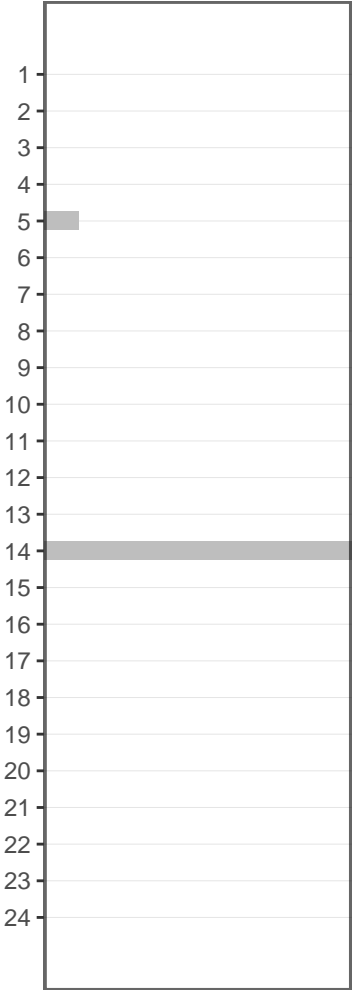
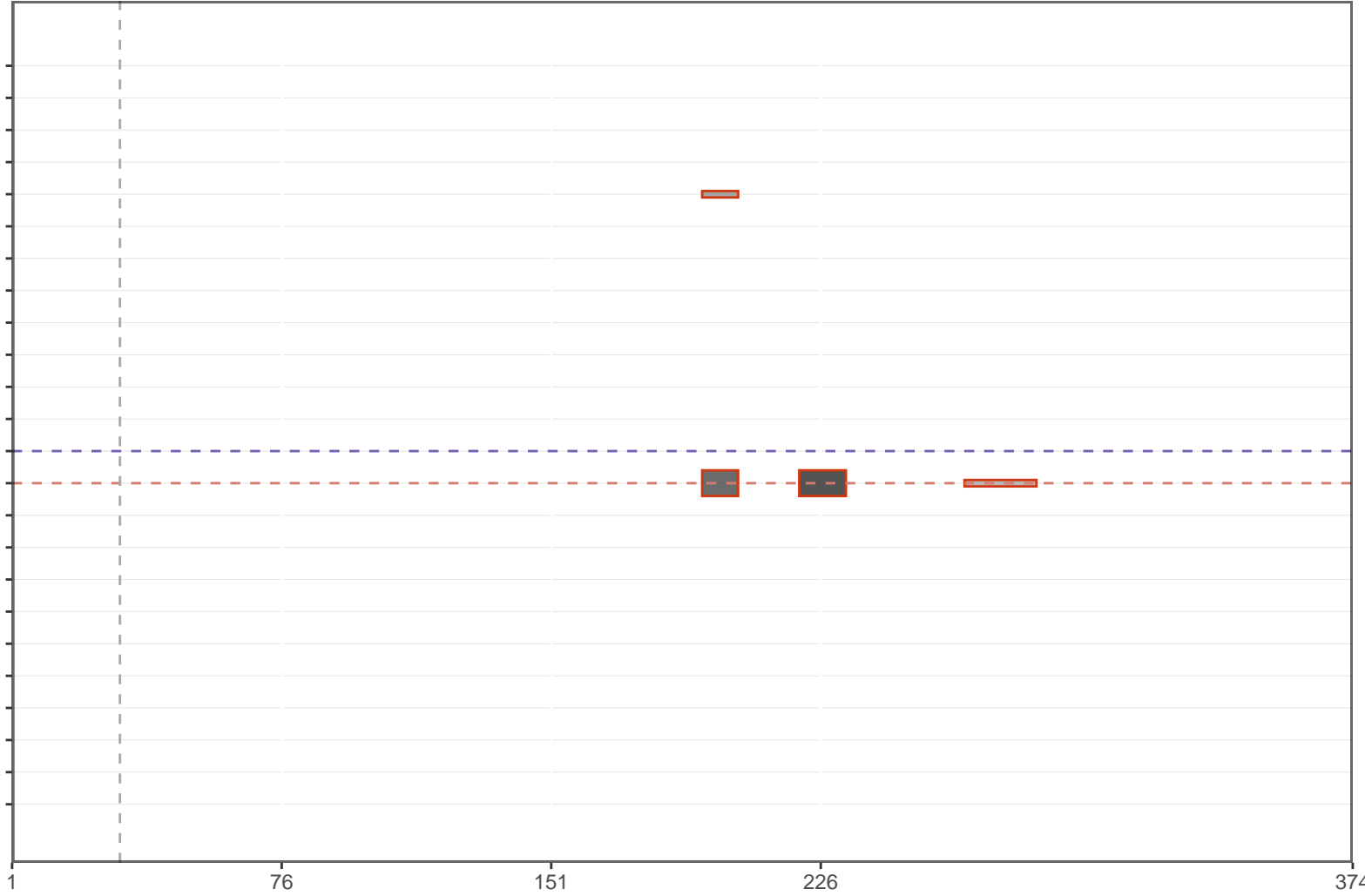
MW indication



Molecular weight

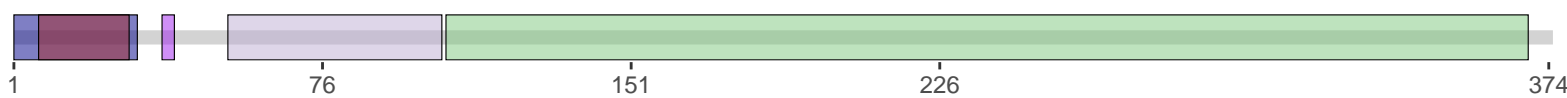


Gel Slice



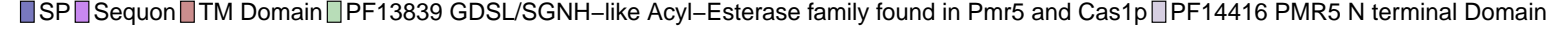
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

TYLIDVIREKIGRYLALDGGGGDAKMGMDLIFNSHWHTKGNSSGPWQVYDGGSKVTKMDRLMAFYKGLTTWGRWVDRINVDSSKTRVFFQGISPTHYMGTEWGGSTKNGNSEQMLAGSTYKAGTASAVVNNKLNRMKTPVYLLDITFLSGLRKAHPQVYSGDHPGVDCSHWCLPGLPDTWNGLLVAMIM

NbL19g04120.1 ras-related_protein_RABA1d-like [MW = 24.14 kDa]

No. of times detected



log(intensity)



Values from



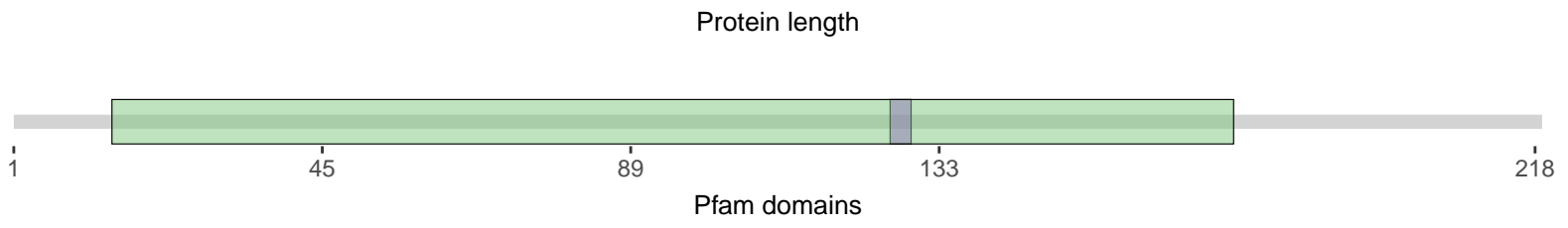
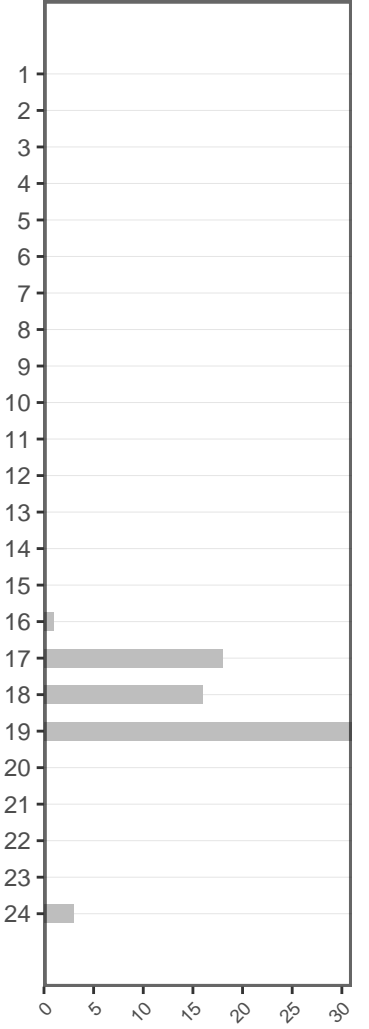
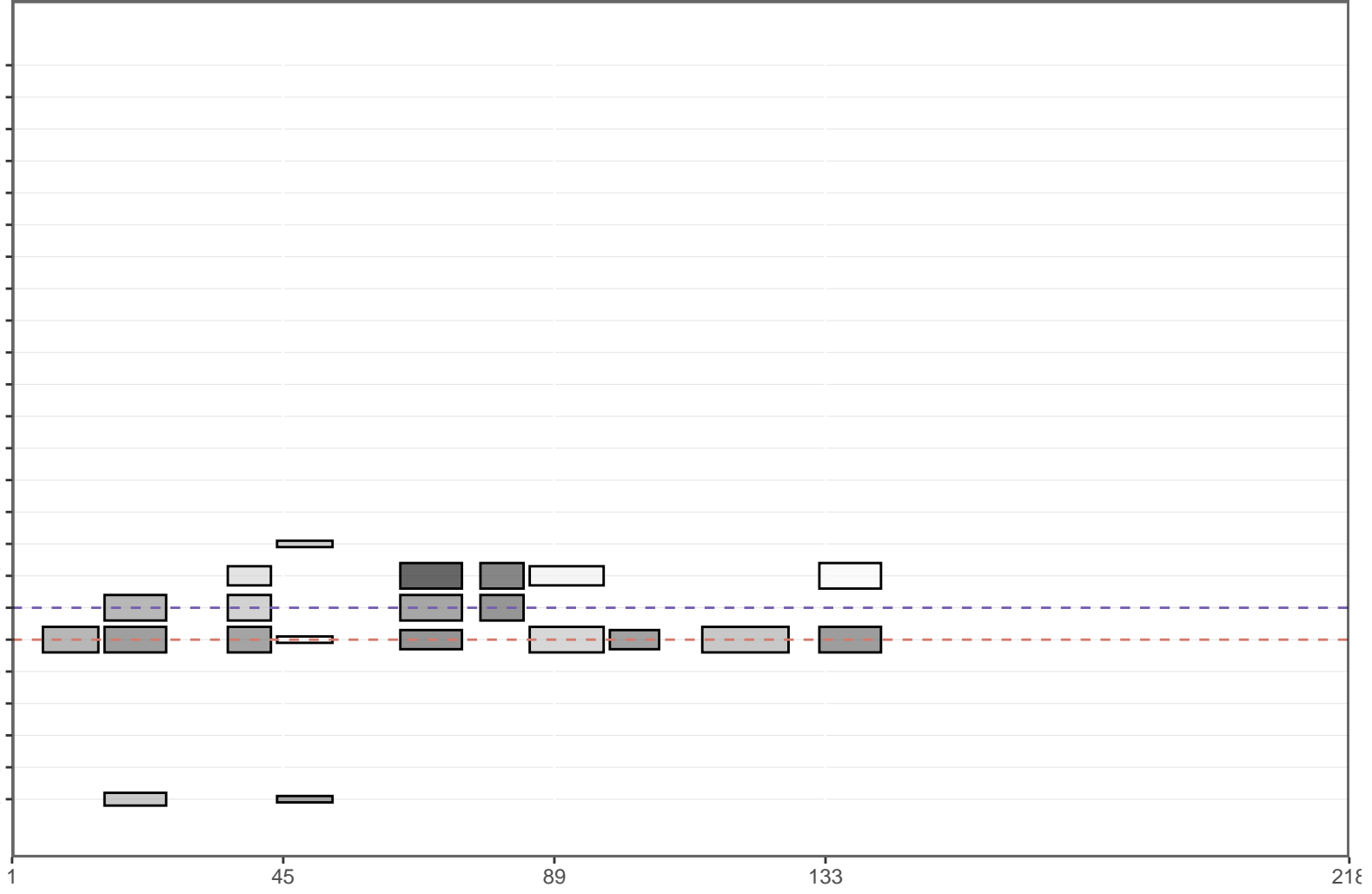
MW indication



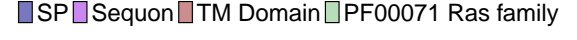
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

1HSTFENVERVYKELRHDTPNIVMLVGNKSDLRHLVAVSTEDGKSFAPKKEISLYFMETSALEATNVDNFAFELTEIHHVSRKAMENGENGNANVPPQGEKIDGKEVSDVKKTGCGST

NbL19g03830.1 histidinol_dehydrogenase_chloroplastic-like [MW = 55.4 kDa]

No. of times detected



log(intensity)



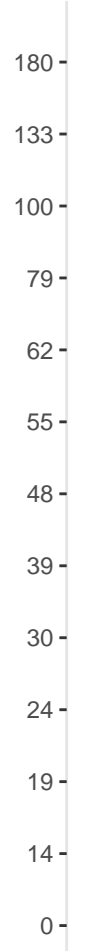
Values from



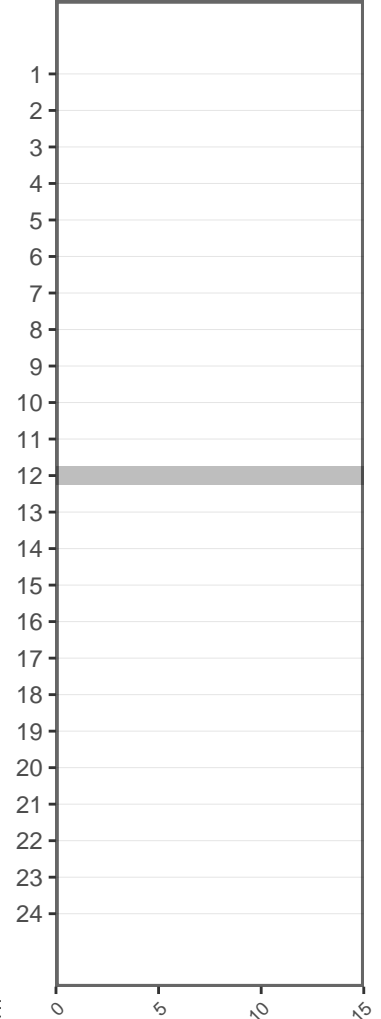
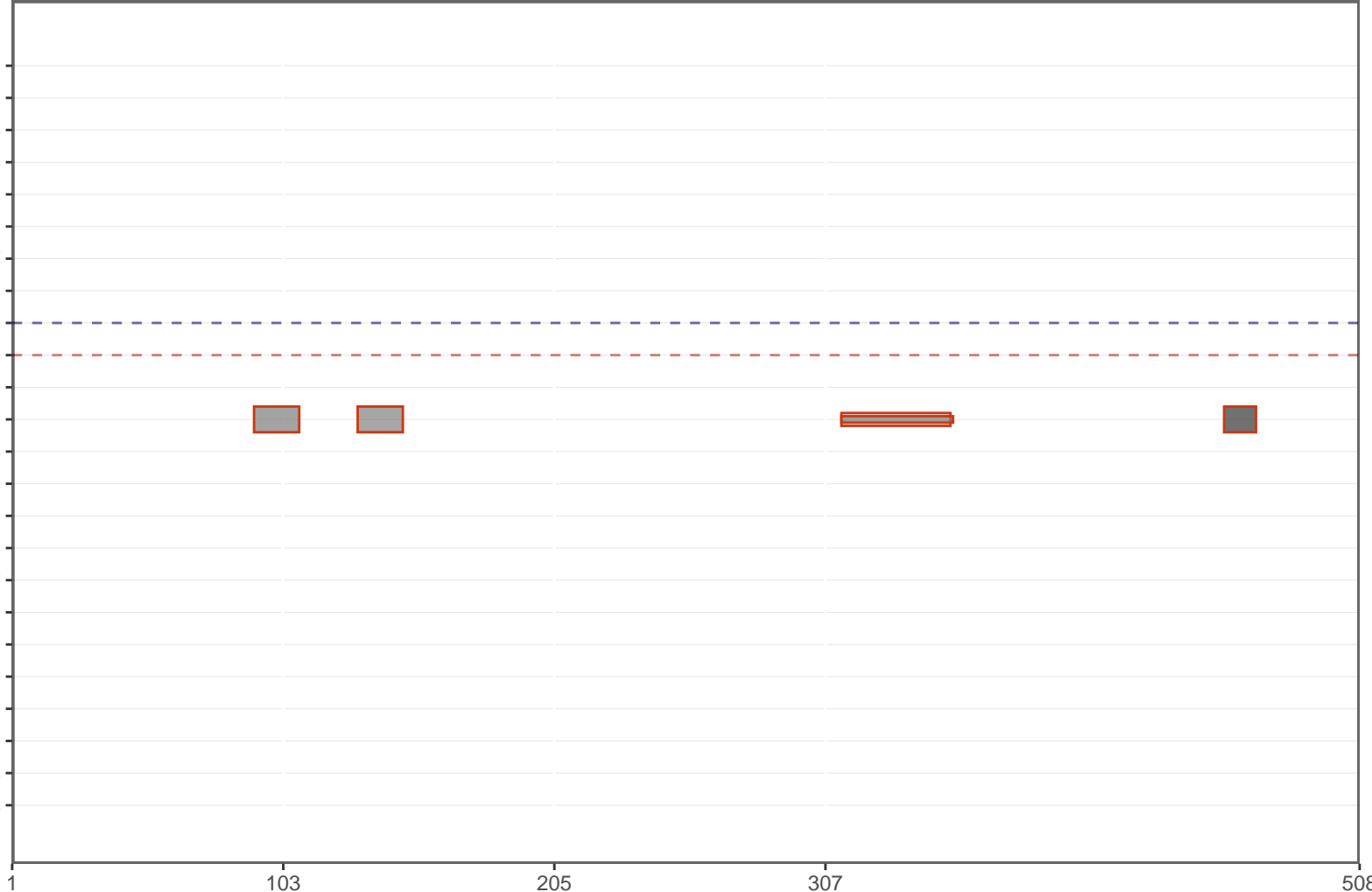
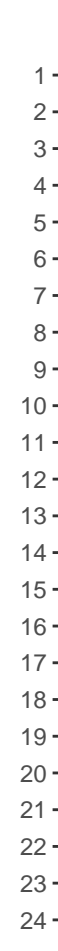
MW indication



Molecular weight

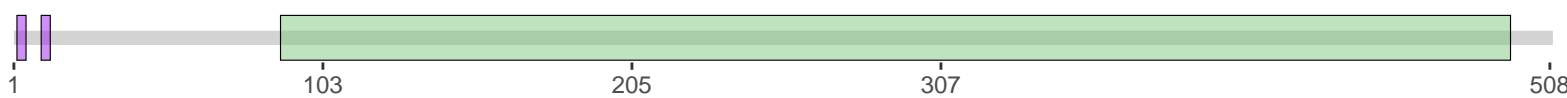


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

GVTHLKAGGADQASAMAWGTESCPKVEIKYGPNGVYTAANKMILQNSEAMVSDIMPAGPSEVLVADKHSSPWHVAADLLSDAEHGPDGQVLLVIAGDGDVLDLNAQEEIRKGGALPRGEFALGALSHSFTVLARDMLEAIFSNMVAPEHLINVNEAEKRWESLHENSAGVFTMGQWTPESVGDVAGSTNHVLPYTYGVARMYGGVSLDFLKYTFVQSLTEGLKNI GPVYENMAEVEGLDAHKRAVTLRLQDEARQVQHSR

NbL19g03780.1 MACPF_domain-containing_protein_CAD1 [MW = 63.38 kDa]

No. of times detected



log(intensity)



Values from



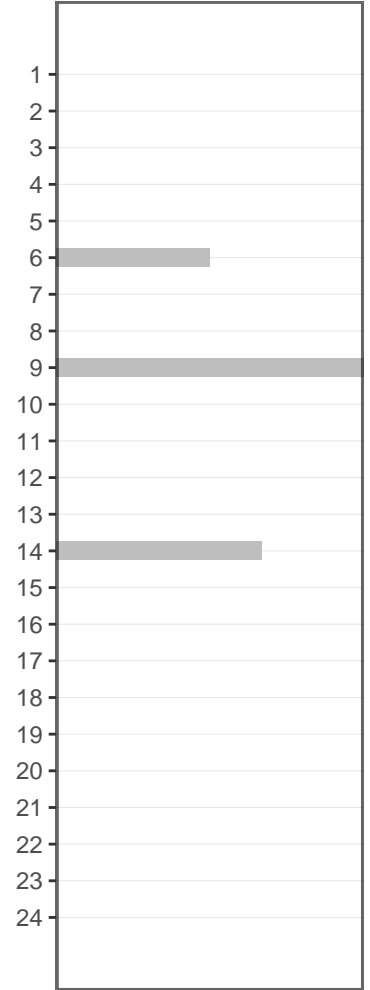
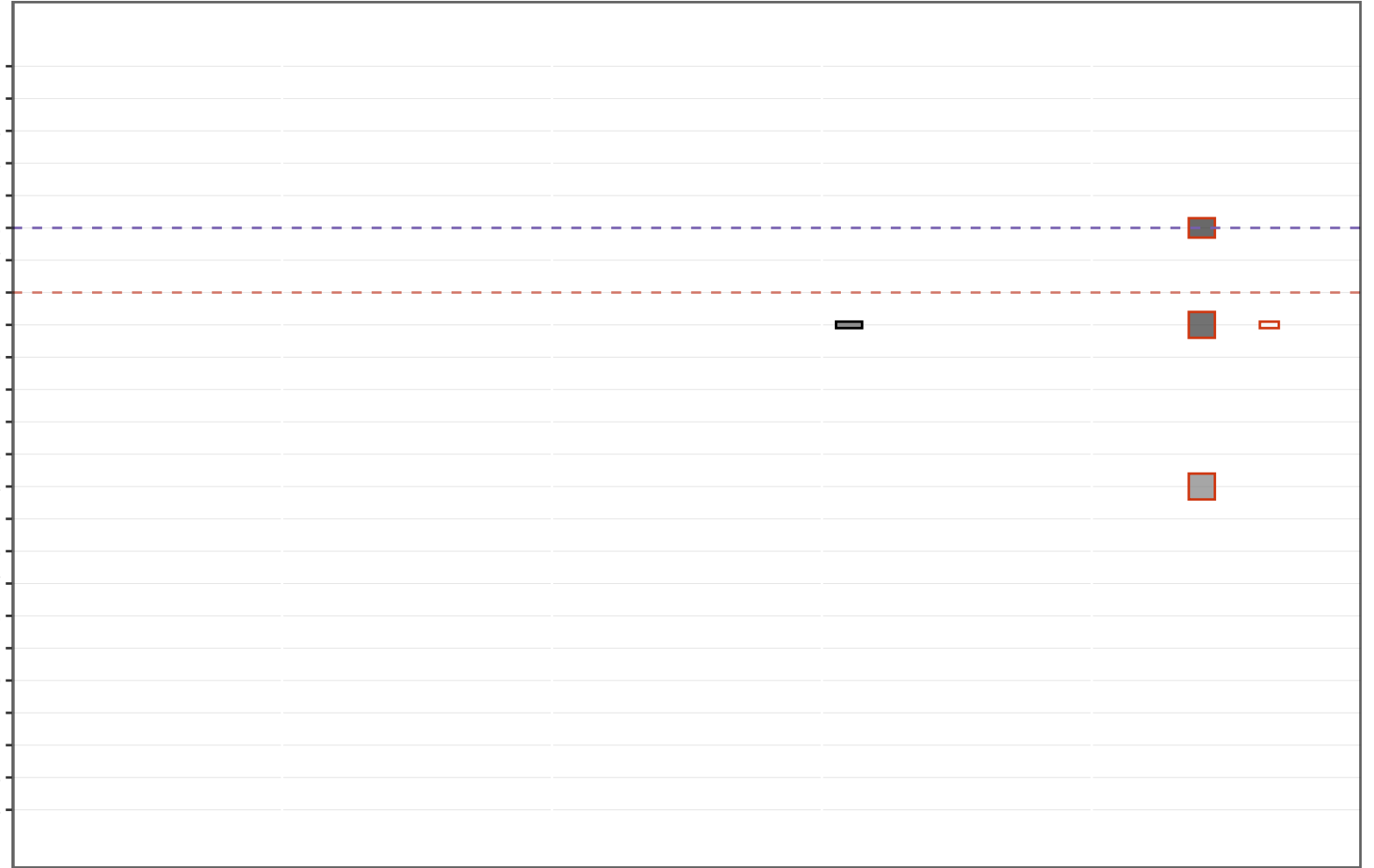
MW indication



Molecular weight



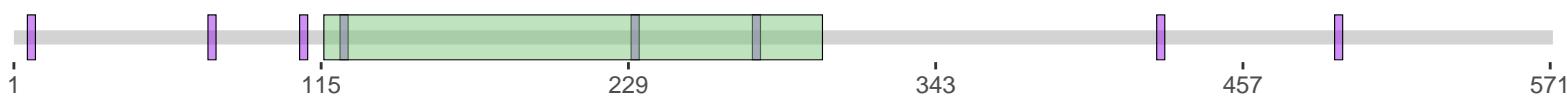
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

IMTFTPIVLSLEEYPGKYLRSRAIELLVEYKPPIEDLQYFLDFQIARWAFPEQNNLQRKEPVCASLQFSLMGPKLYSPDQVTVGRKPFVTLRLSLSEGGKKNRLEVLQHLVSLPKLQPHWDTHMAIGAPKWKQPEEGDSRWFPEPKIWNFSEHVTAPIEHTFETSLGDLGGVYVITGAGLGFVDFGAKSVLHLKLLFSKVPQCTIRRSVVDHSPNLSAVGRIDGSSLSLMNEKTAENKRGDSSSQMGKLANIVDTEMKSGPQDAPGHVLTGAKLGV/DKGGVLRVYKSL

NbL19g03760.1 serine/threonine-protein_kinase_HT1-like [MW = 53.32 kDa]

No. of times detected



log(intensity)



Values from



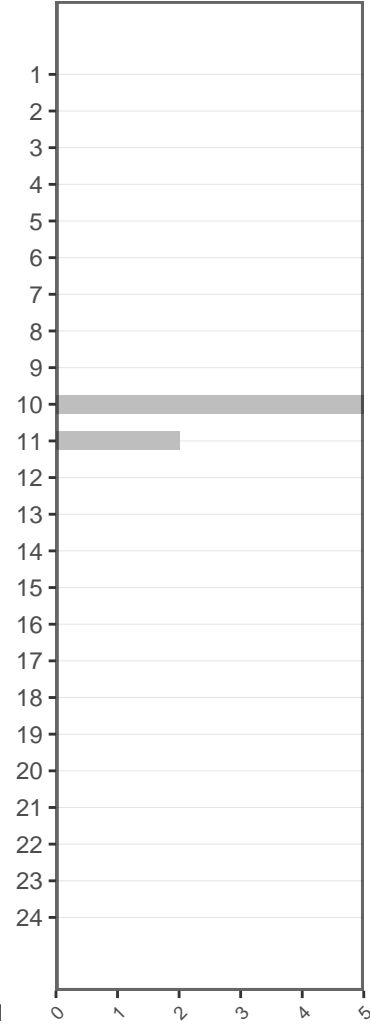
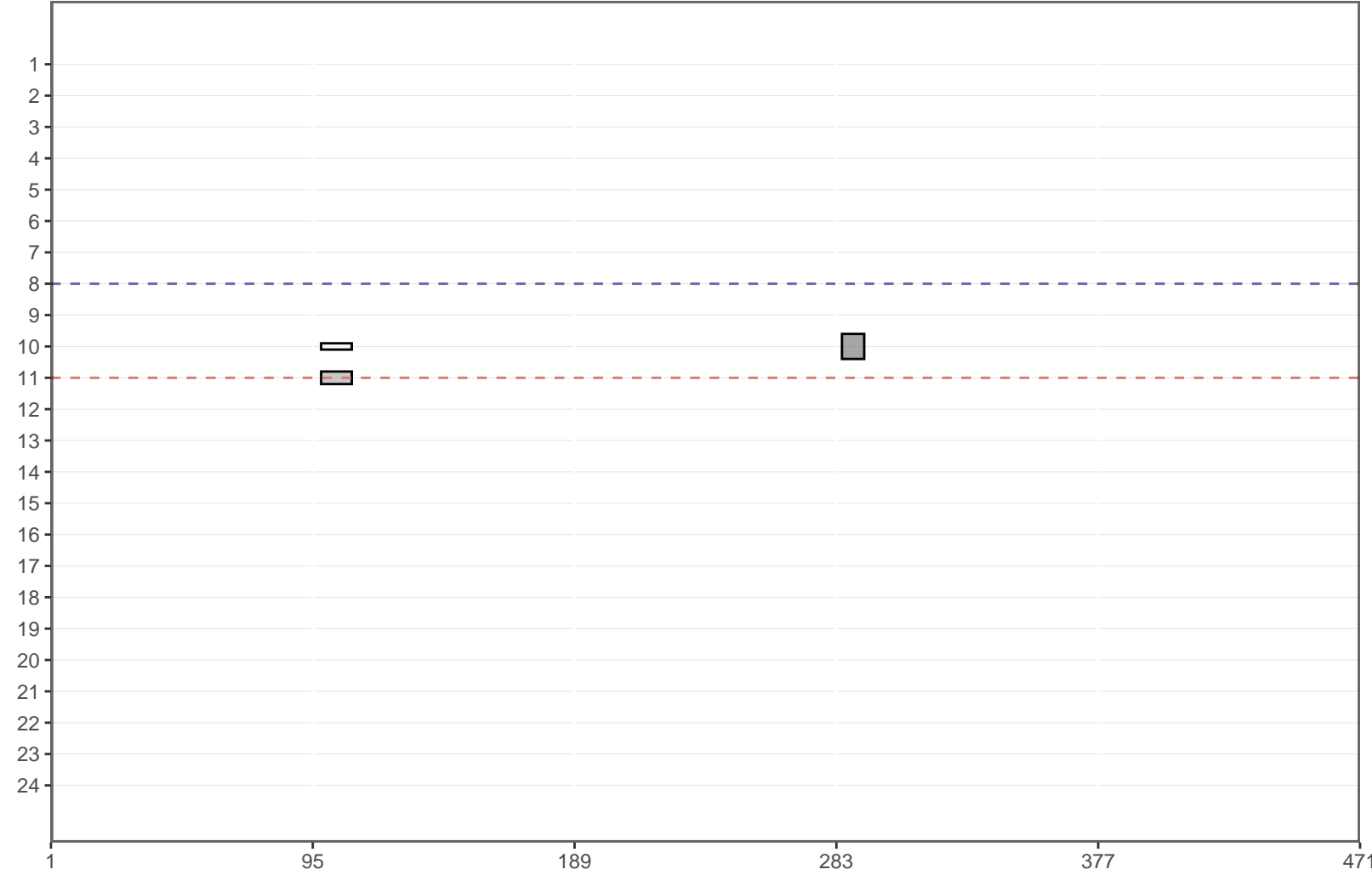
MW indication



Molecular weight

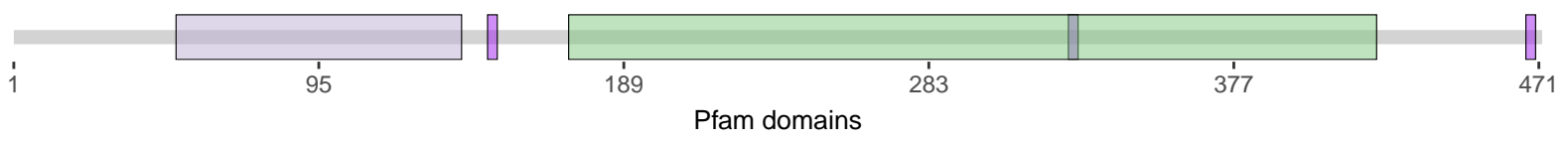


Gel Slice



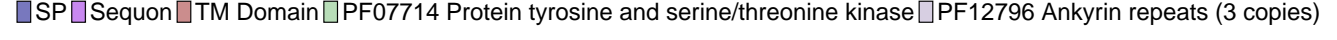
Protein length

Peptide counts over 4 repeats



Pfam domains

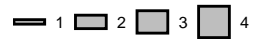
Pfam Description



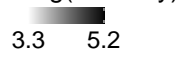
Protein sequence:

LGAVTQSSPMMVTEYLPKGDHAYLMKEGRLRPTKAIKRFAMDIARGLNLYHEIRPEAIHRDLPEPSNLRDDTGHKLVADFGVSKLKVTRNWKEDKPLTGDNTSGRVYAPKVFKNEEYDVKVDFVFSFALLQEMEGDPPHAKIESEVAKGYAAKERPPKAPKGFYAHGLRLEECQWNEKPLRPFKQIPRLSDYTKFGHKRRRWKVRPMKGFQNFEMAKKDKHSELSSRNGGSGSRNRP

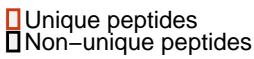
No. of times detected



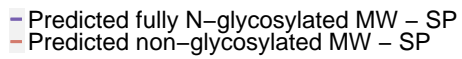
log(intensity)



Values from

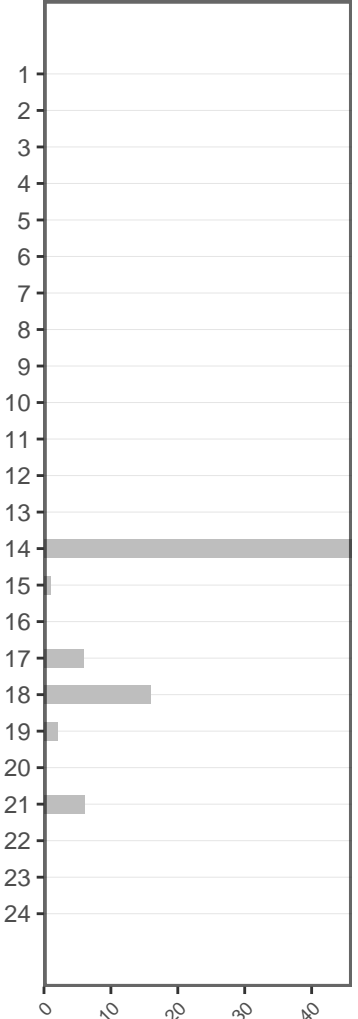
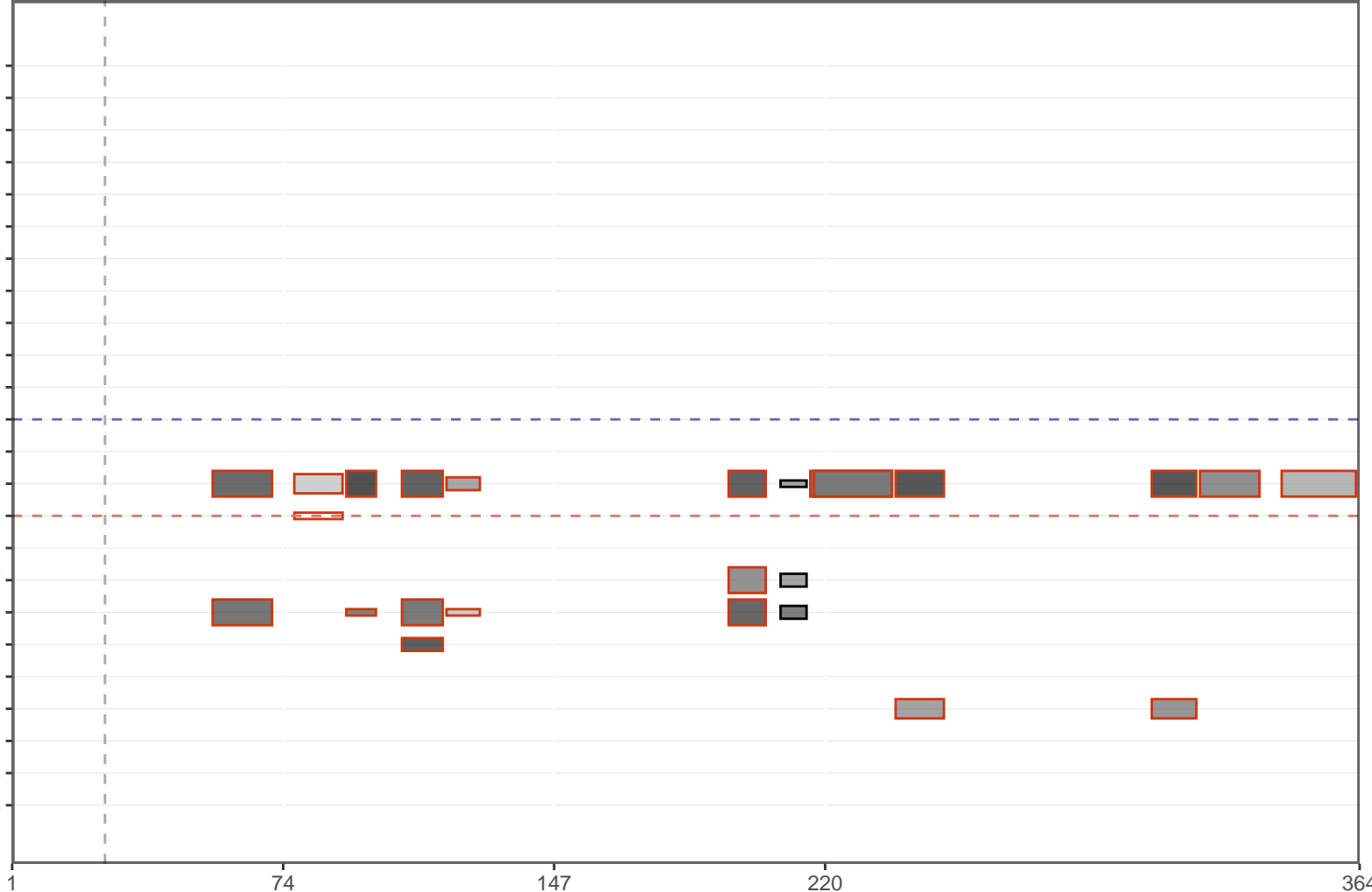
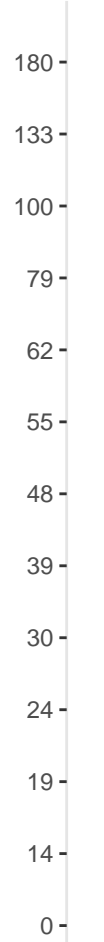


MW indication



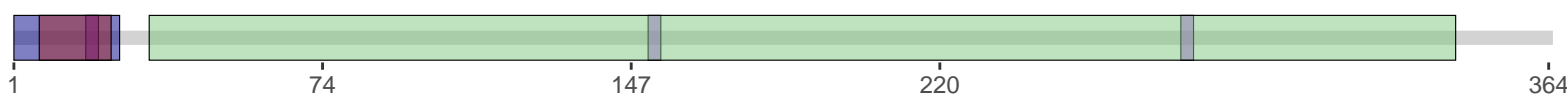
Molecular weight

Gel Slice



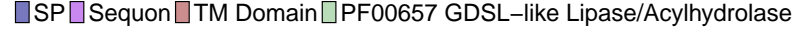
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IMGNNDYINNYLMPGFYPSGLLYKPKYATILAGDYVYKQLKTYSYGARKVAVFGLGSGVGGIPAEIDNYGTDKSPCVDSINSALVKEVDKLPKMDNFNINLPNANFNINITSIAIGDPAIGITNLADPCCEISSFRAKGGQSYEGSAGNDRASHYFWDGFRHTEVPNKVTAERAYTALLPTDVAVFPDISHLALL

NbL19g03700.1 GDSL_esterase/lipase_At1g29670 [MW - SP = 37.18 kDa]

No. of times detected



log(intensity)



Values from



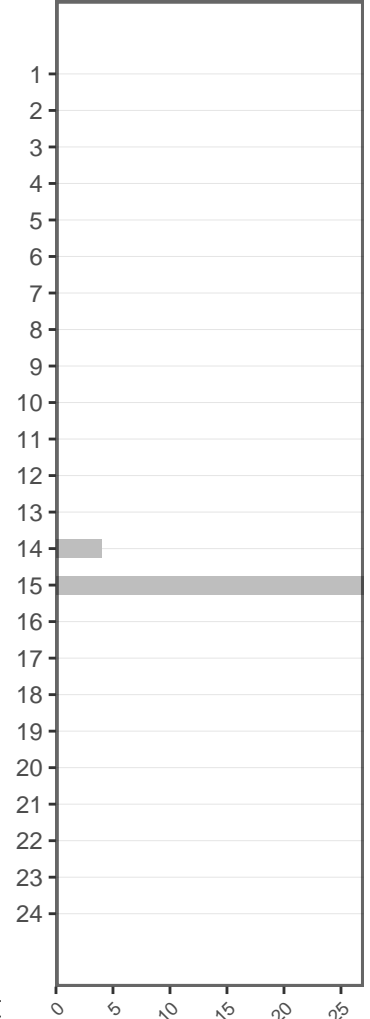
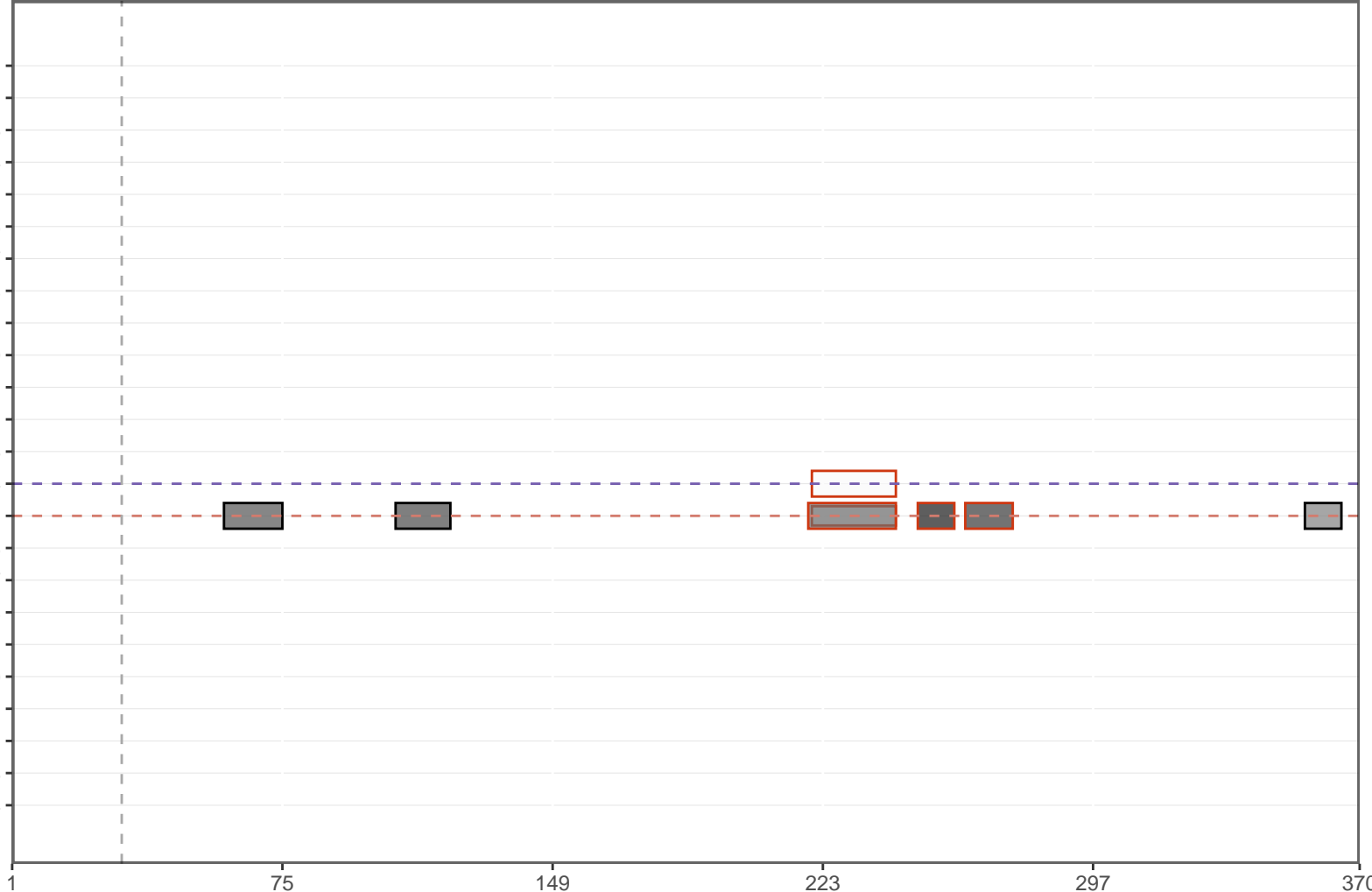
MW indication



Molecular weight

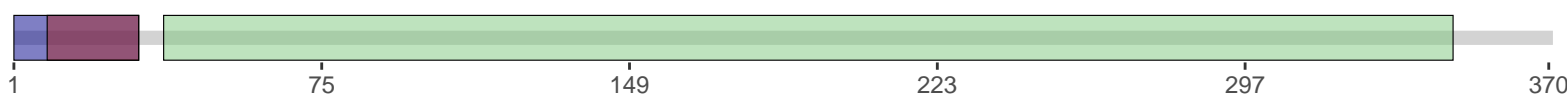


Gel Slice



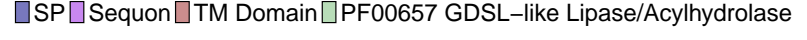
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GSNDYLNNYFMPLVYPTSGRTTFEGVAVLQGYTQGLRLRYNNGARKFALIGVGGGGSPNALQGNPDGRTGVGRINAVGLFNASKLKAVALDNLNNTPDKFIYINAVGIFGDLNPSAFGLVSTNAGCCGGRNNGGITLPLFQRPGRNRNGYLFWDAPHTPEVANNVGRREYRAGKSEDAVYFDISRLAQL

NbL19g03690.1 GDSL_esterase/lipase_At5g45670-like [MW = 43.6 kDa]

No. of times detected



log(intensity)



Values from



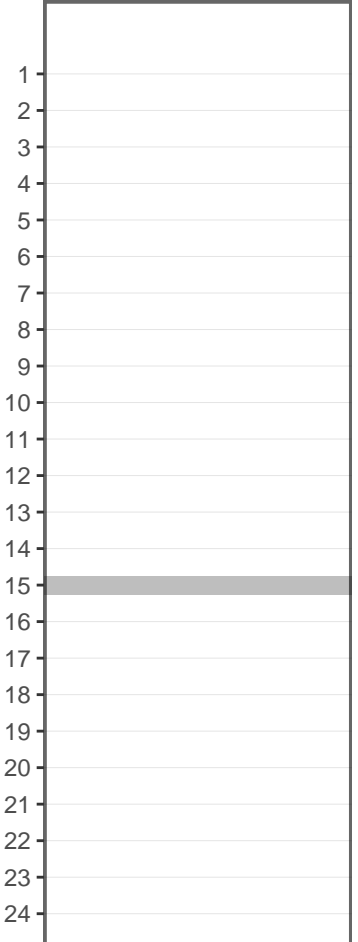
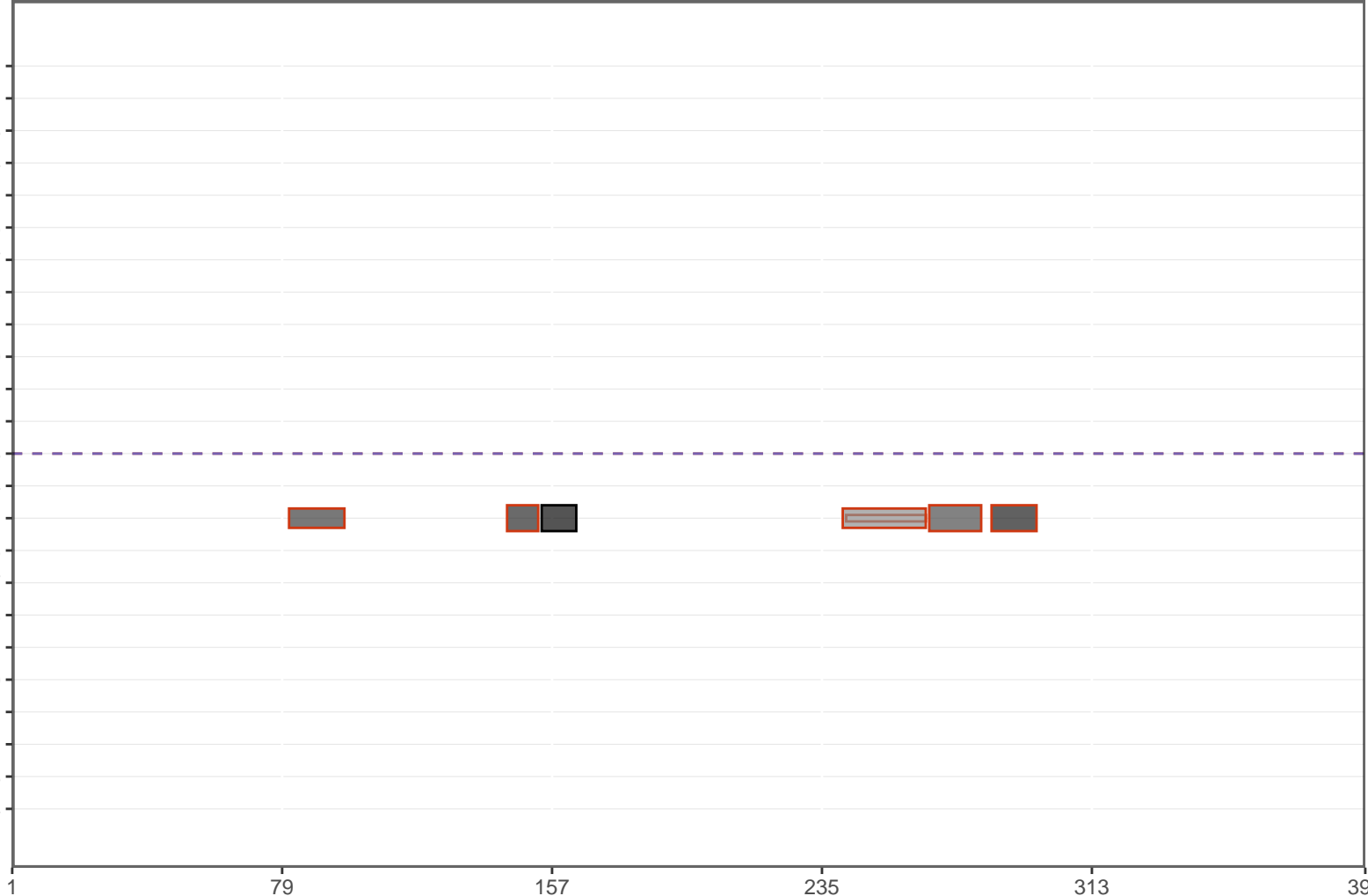
MW indication



Molecular weight

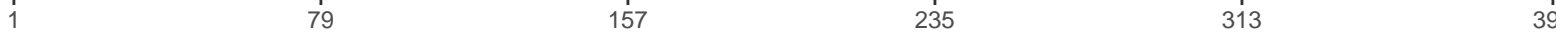


Gel Slice

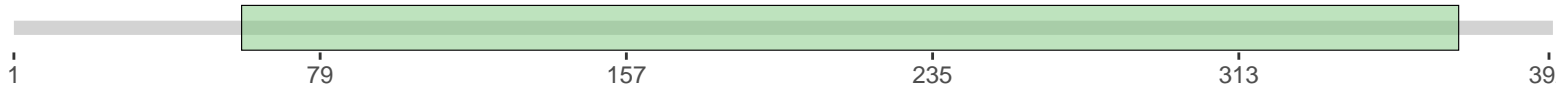


Peptide counts over 4 repeats

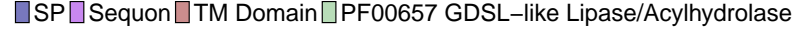
Protein length



Pfam domains



Pfam Description



Protein sequence:

YLSKCYISGLGSDNIDLNINFMPLVYFSTRGFNPEGVADVLGGYFQQLKLYDYGARFKVLLGVGGGCGSPNLSLAGNSPDGRTGVGNINWANGIFNRLRGLVGVDFNSNTPKAKFYINAVDFGLDIDNPEAFGRFRVITNAGGGGVGRNNGGIGTGLPLGNPGRNDEYLFVDAFHPGEAANVWGRREYRAERPDSYDFDQRLAQL

NbL19g03660.1 subtilisin-like_protease_SBT5.6 [MW - SP = 80.79 kDa]

No. of times detected



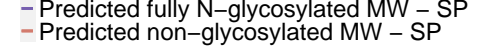
log(intensity)



Values from



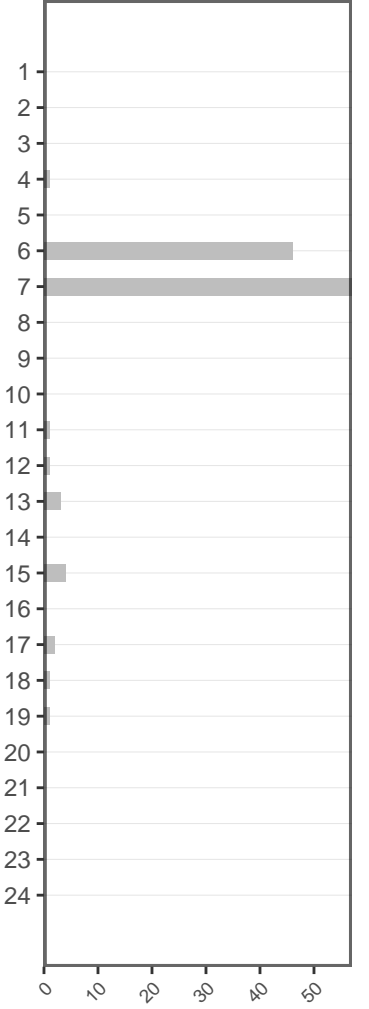
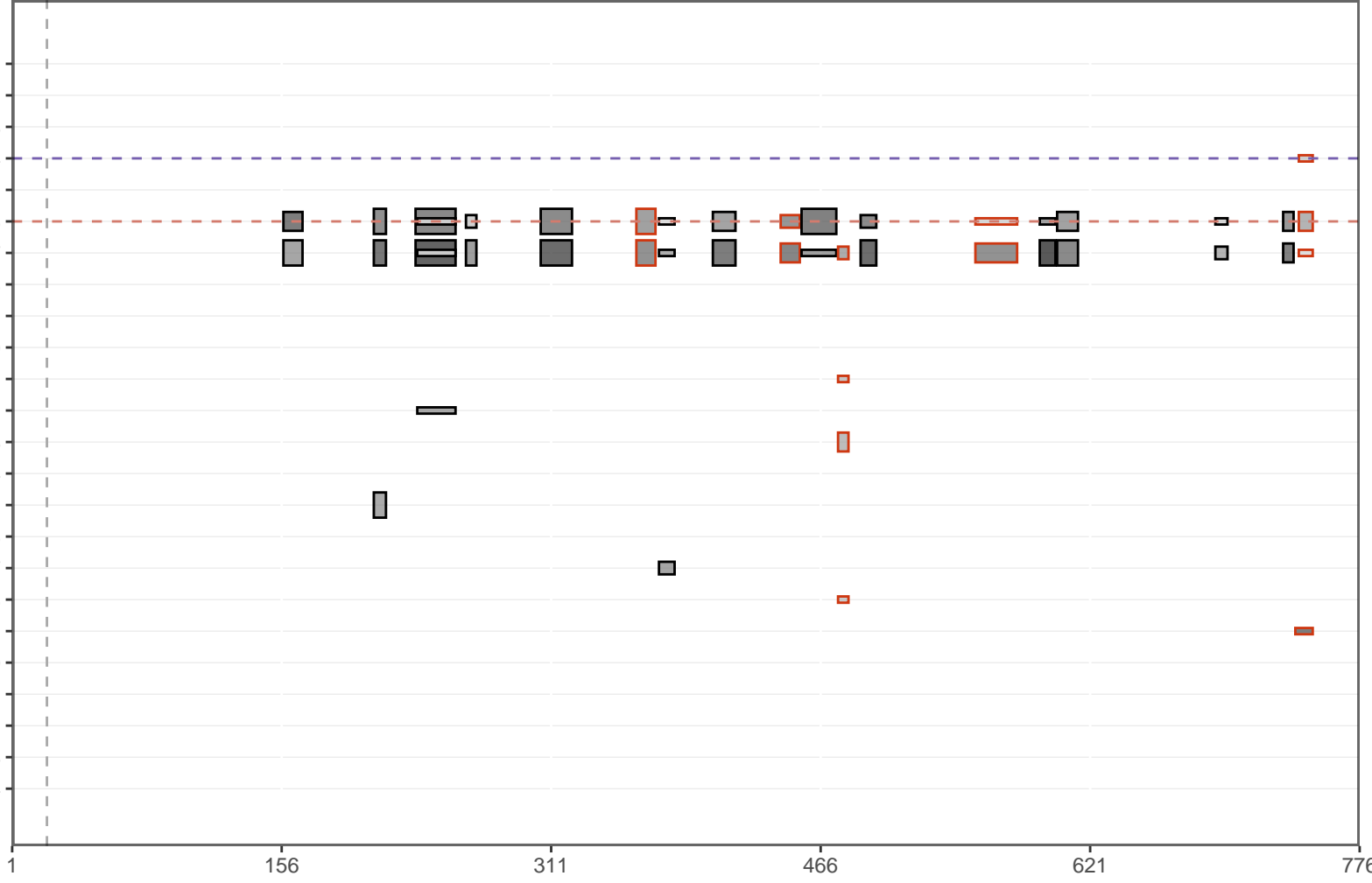
MW indication



Molecular weight



Gel Slice



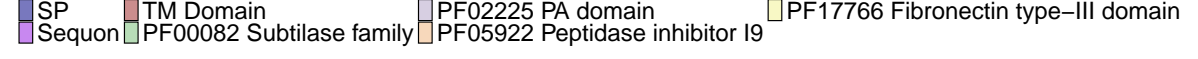
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MGQTVTPYKLEKXKMPLYVAGQVNSNVTKDVAGGQLPQSLSPKKAAGKIVLGRNGTRVYKGGVEVNRAGGIGVLDGNSKANGAELVADPHFLPQVAKVAVQIKVYNTKSPVAWVFKVTLVHSGKAPVYMSFTSRGSAVAPHLKRPDITAPGLNLAWVGGSSPTKLDIDRRVDVYNISSGTSMSGPHVGGAAALLKAIHPTVWSSAAIRRSALITSEAGLRNNVGEQITDASGKPADPFFQGGGHRFRPKAAADPGLVYDASVGDVLLFLGASGKDLKSKFCPKXSHLP

NbL19g03370.1 carboxyl-terminal-processing_peptidase_1_chloroplastic [MW = 50.46 kDa]

No. of times detected



log(intensity)



Values from



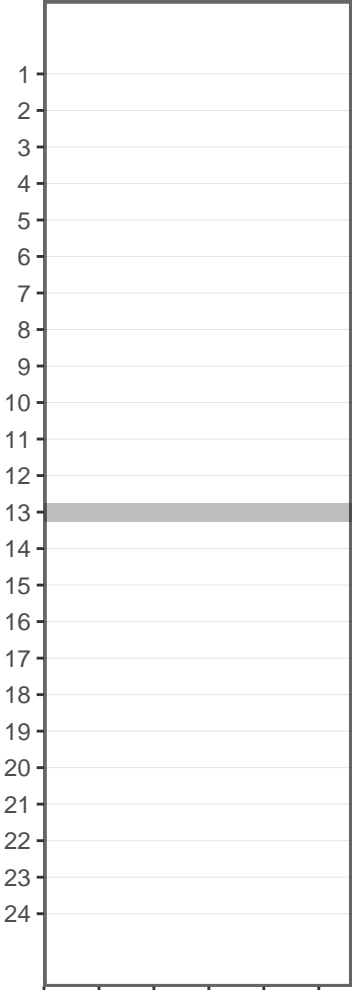
MW indication



Molecular weight



Gel Slice

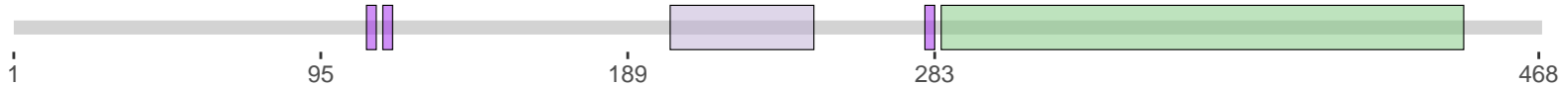


Peptide counts over 4 repeats

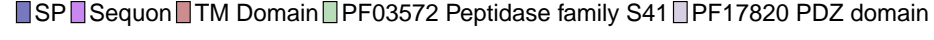
Protein length



Pfam domains



Pfam Description



Protein sequence:

SVNVRDKSAFEASILLGPGSTFVNMVKKHNGDGVQSDIVQRGSIKPTVYFRLGKENGSEVGVYRLLKDFNARLKDVTAKRLEGMSASDFVLDKRDNLGGVQAGIEIAFLFNEGDTVETVGRDPPQYRRNIWAEAPLTPAPVIVLNKKTASASEVATLHONGRAVVGDKTYGKGLQGVFELPQGGVWVTGKRVYTFNNLNDINGNDVDFRNFPAWNEVTHLSKGRKPGGG

NbL19g03350.1 uncharacterized_LOC109236735 [MW = 89.52 kDa]

No. of times detected



log(intensity)



Values from



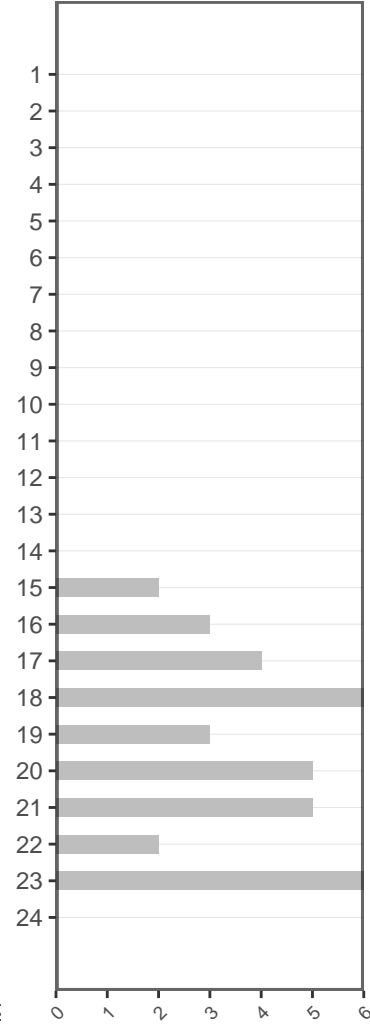
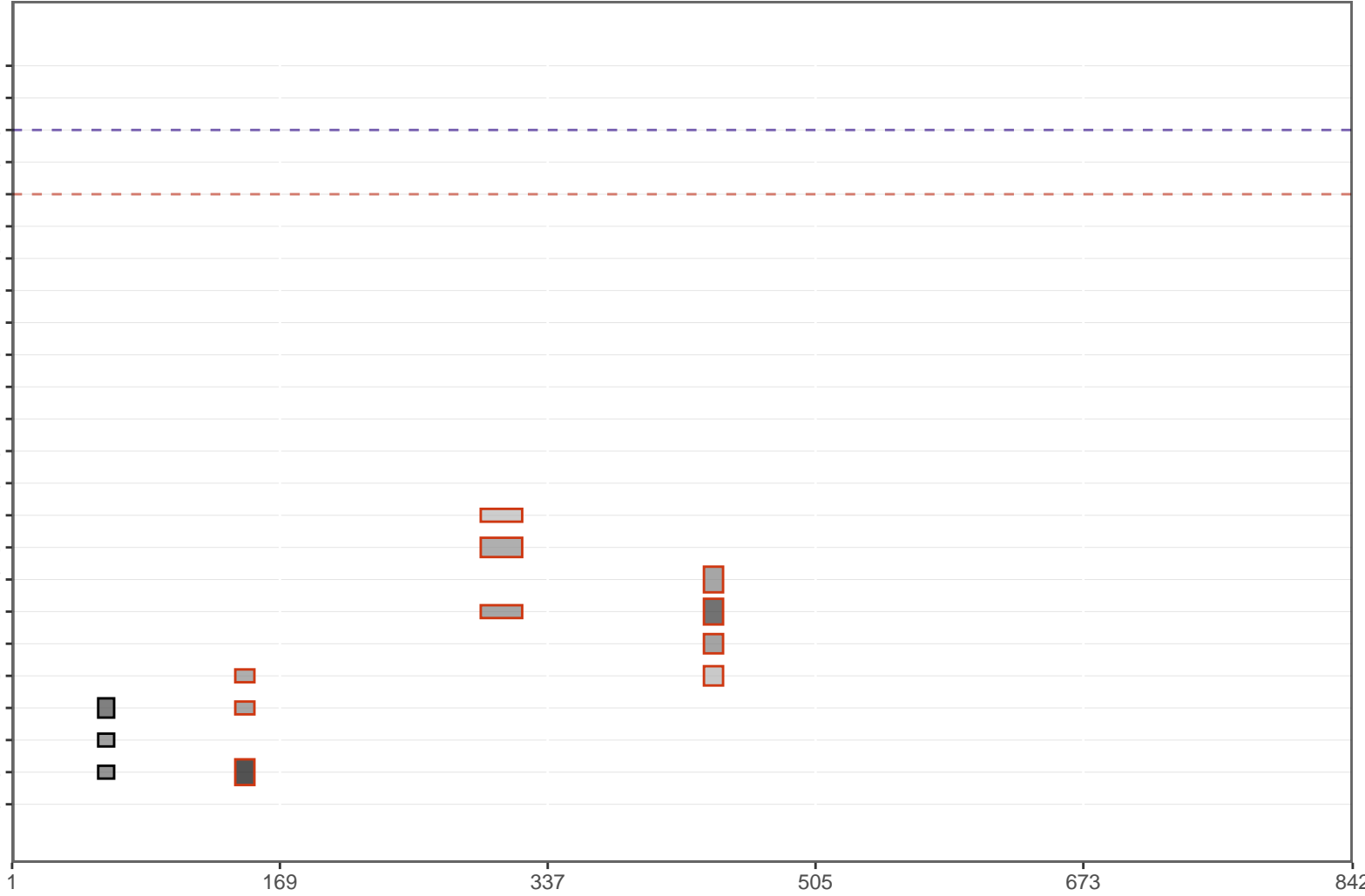
MW indication



Molecular weight



Gel Slice



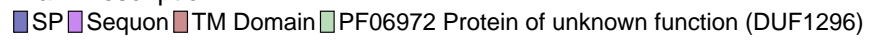
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GIGSFSGLPLASAAKSGLEEDAPKIVGSSAGHLGSRAPRYVYDDESLGHASEENLYHRTNASSGNVDEPSASQPEGLKTELSEHGNGYVYPSAGQYTYETAQQLTAAFSGQPTGSHMNLASFNNMAFTNLSLPTLLAANVHAGRESDPYVYFSSATGAMPKTYGNGVSESGGSTMPELRTVYFGSAGPSPQTLGCTGVTTGPAVPHGLAVHPYSGPTLPLGPFANMRYFPMPQSYTYMPSAFQPPFAGNETHYQGLAVALPQYKNEVYVSSLPQASGVASC

NbL19g03130.1 nuclear_pore_complex_protein_GP210 [MW – SP = 210.28 kDa]

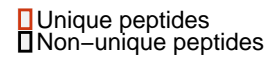
No. of times detected



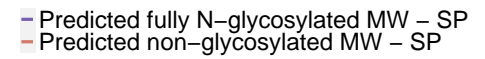
log(intensity)



Values from



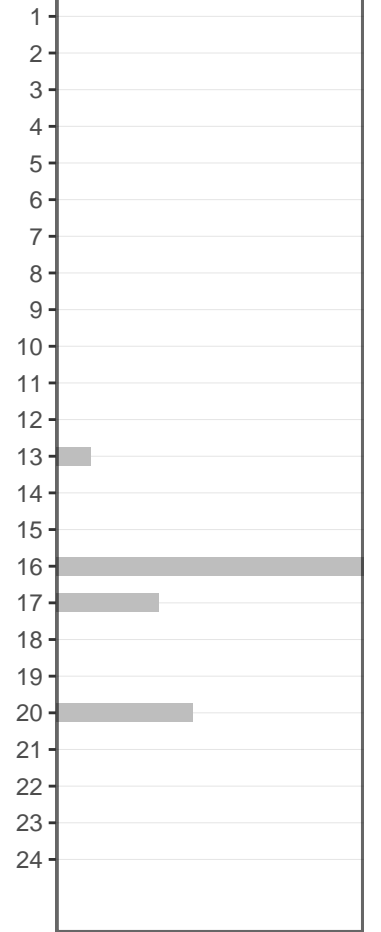
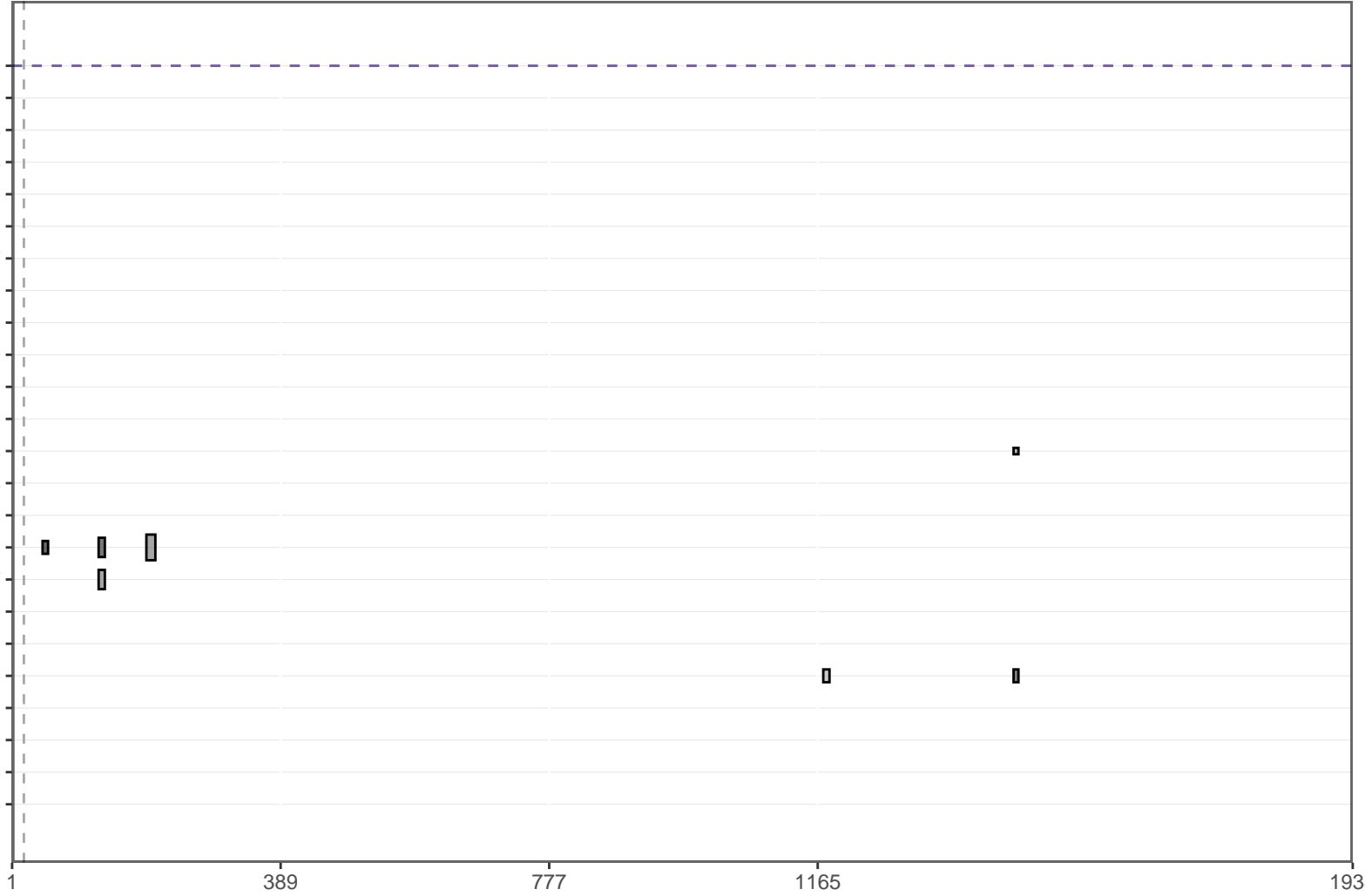
MW indication



Molecular weight



Gel Slice



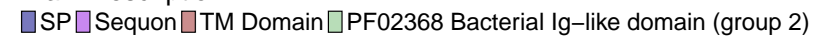
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

YLNIDAKLNLSITGGSGFDAAVNDTHMETGPAAGLGGTQLLLAKKLGTAIVTRDVGGLAPLSTFSVQVADVDWIKITSGEELGMEGGSLINFLAGVNDGNFTDSSGGVYMNHYHEDHVELVNEDDLGGCGDDGYYMFPNFRIRAMRLGVTTLYSARQHTDHELGPQKVEVYAPRRIHPEDIFLPGASVYLVTRGGPKTGAVAFVMDNEWVYHTATGRVTSATSPGNSTIAAKYRNGDIFGDAFGAEVKVGVPS66AMLNVGSEGLAVGRMPFPPSLSEGL

NbL19g03120.1 uncharacterized_protein_ycf23-like [MW = 31.66 kDa]

No. of times detected



log(intensity)



Values from



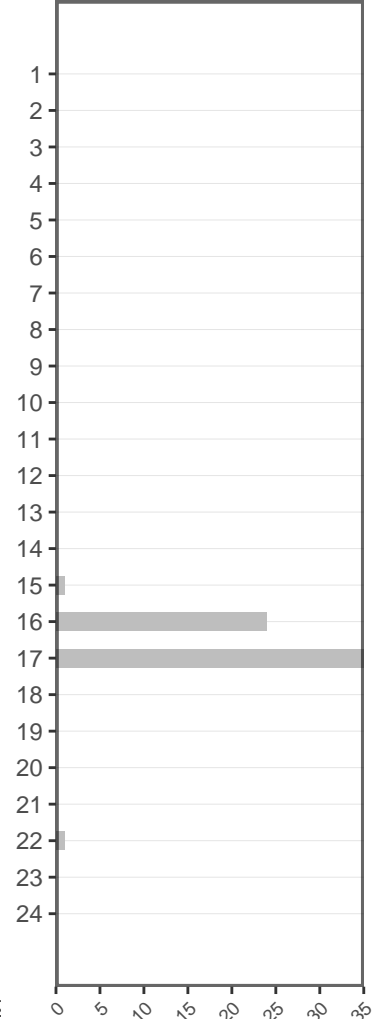
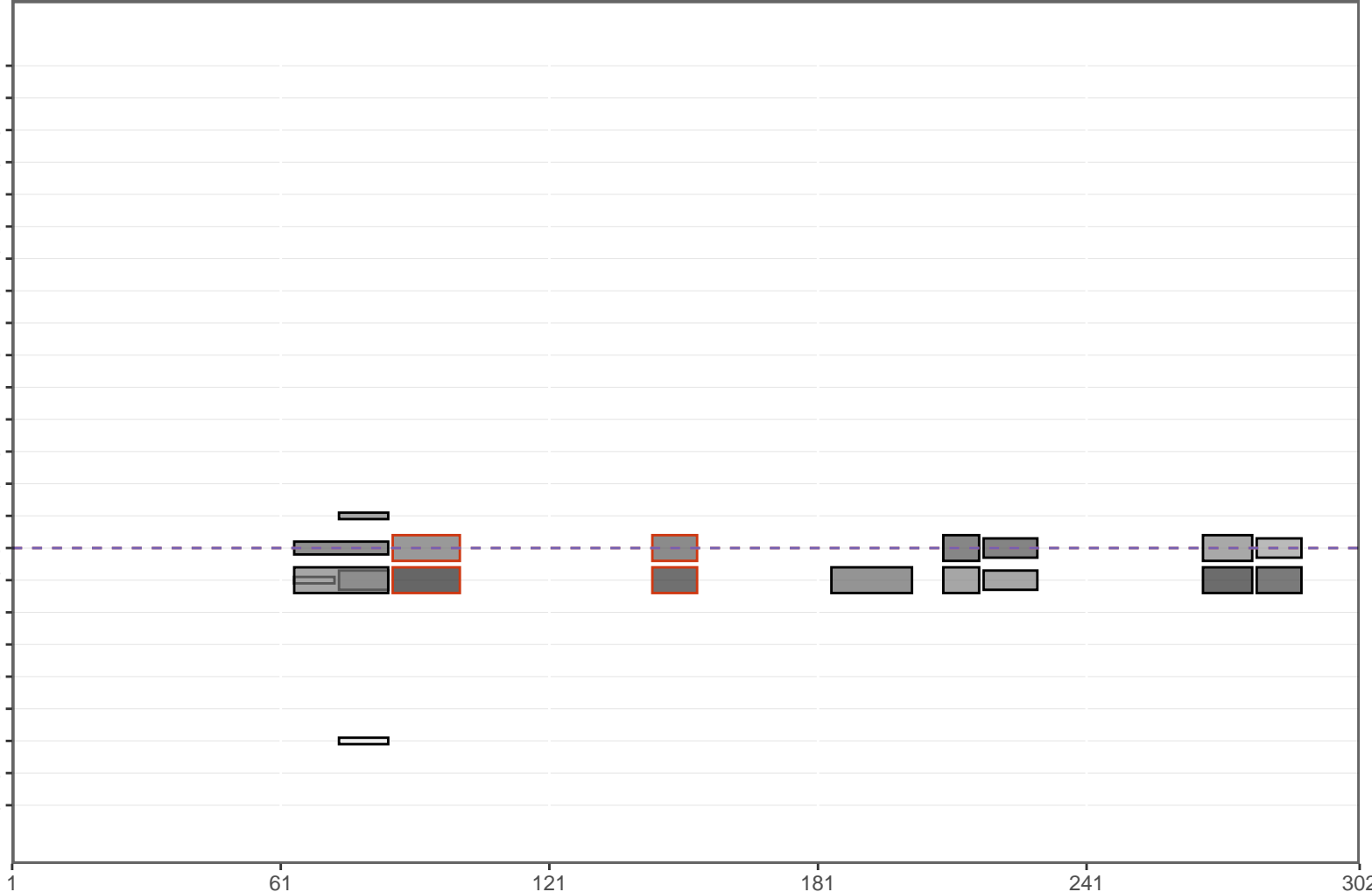
MW indication



Molecular weight



Gel Slice

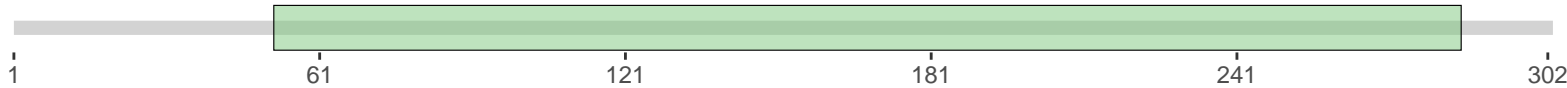


Protein length

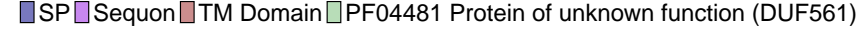


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

DSFYKGLVFTPEGLKIKTKETKRILPSPVLEVTVPHTLSLDPDKLAELEQEGVDIKQTEGGKSTPSKAGVLEKIKATPTLAAAYSIRAVNIPVMSGSLGAVTAPMATAGAAAGVGVGSAANKLNQDQVMAIEVKSIHSLGLSTKQNLFECSGLRL*

NbL19g03110.1 3-oxoacyl-[acyl-carrier-protein]_synthase_I_chloroplastic [MW = 49.99 kDa]

No. of times detected



log(intensity)



Values from



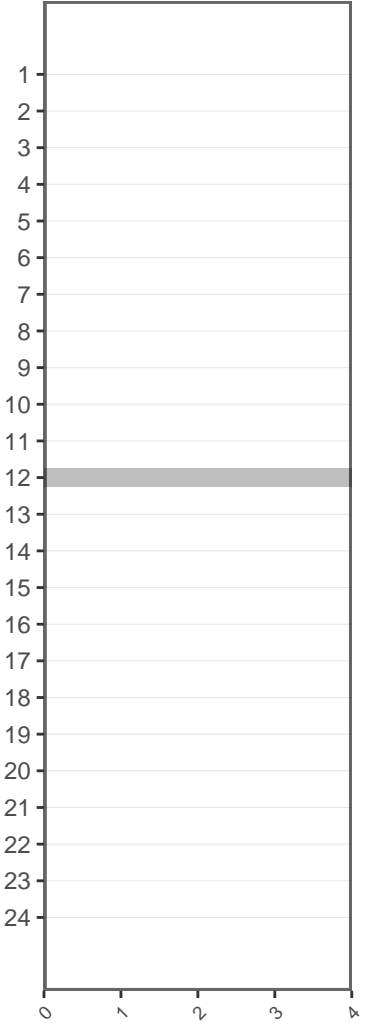
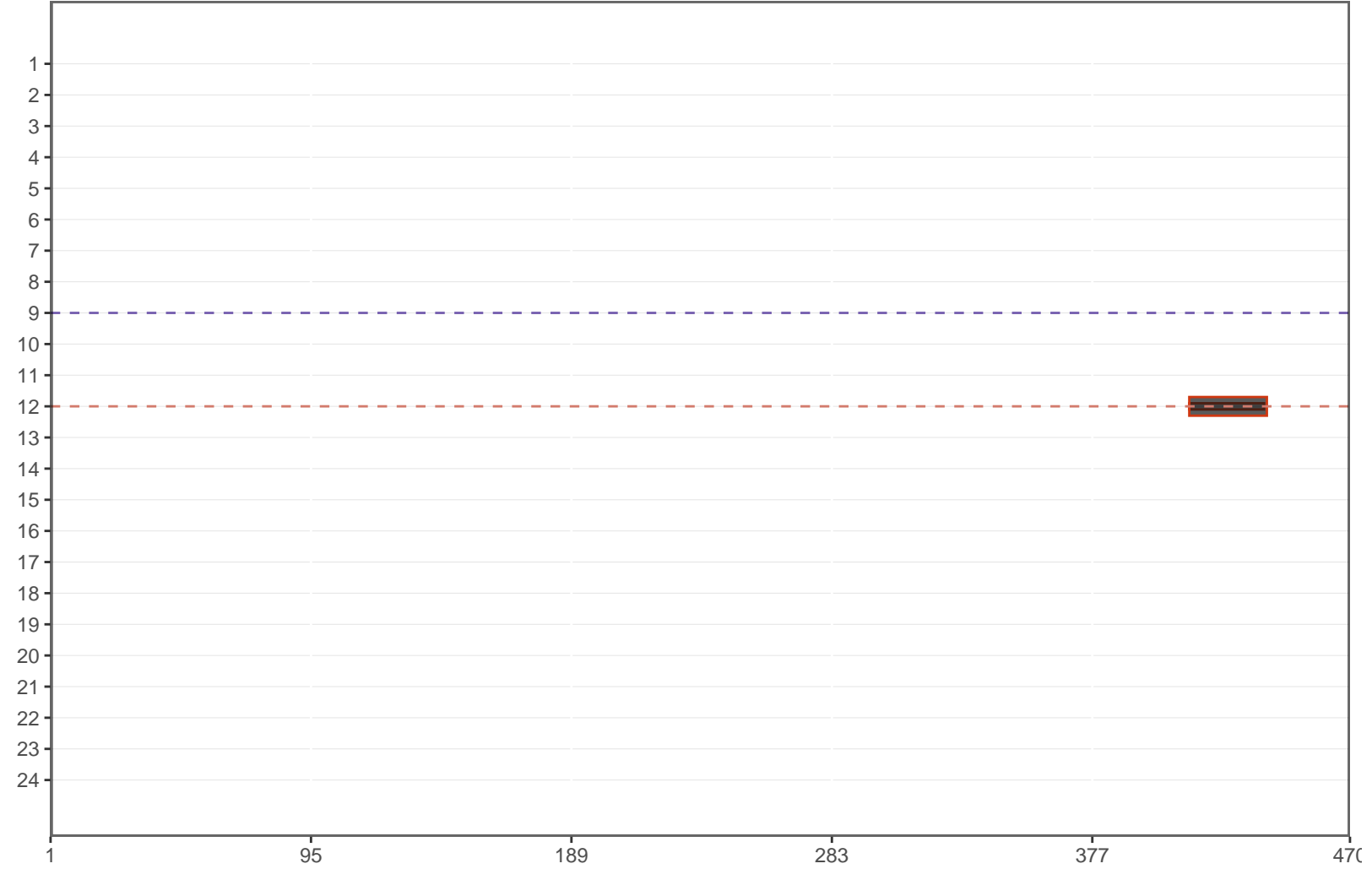
MW indication



Molecular weight



Gel Slice

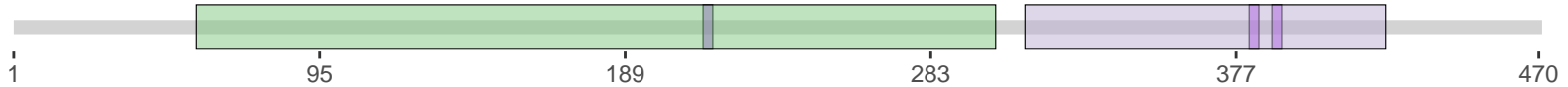


Protein length

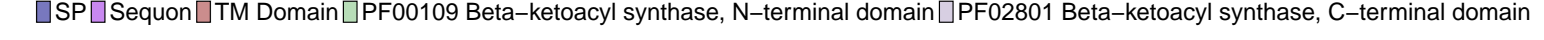


Peptide counts over 4 repeats

Pfam domains



Pfam Description

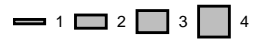


Protein sequence:

NYCFYAAANHRRGEADLLMAGGTEAARINGLGGFVACRALSGRRNDPQGTASRPVWDEKERDGFVMEGAGVLMESLEHAMKRGAPAAIEVLGGAVNGBAHHMTDPRADGLGVSSGIGSLEDAVGVPEEVNYYNAHMTSTVGDIAEVLNAKKVFKNTSGIKMNTKSMIGHGLGAAGGMEAMTVAITGQWVHPISINGFNPESGVFEFDTVPNKKGGHEVNVGIGSNVGFSGGHNSVAVFSAFKP

NbL19g03100.1 DNA_replication_licensing_factor_MCM3_homolog_2 [MW = 94.57 kDa]

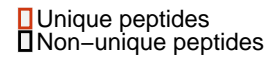
No. of times detected



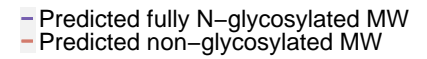
log(intensity)



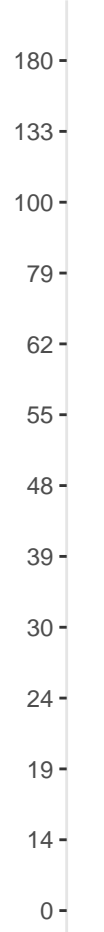
Values from



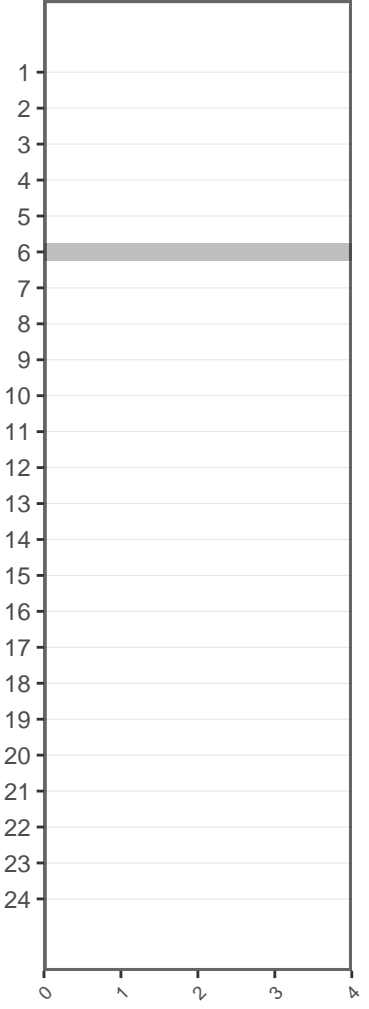
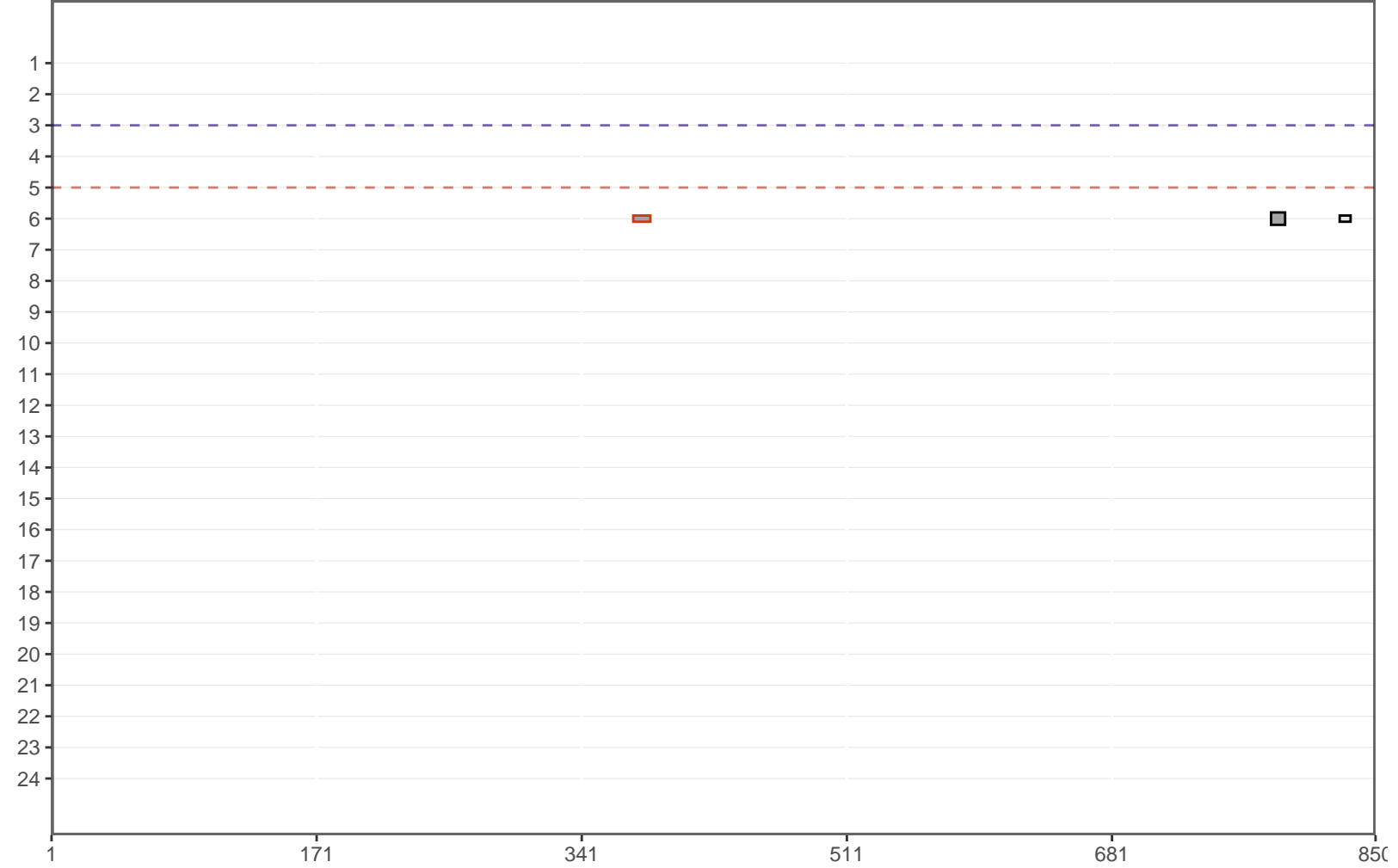
MW indication



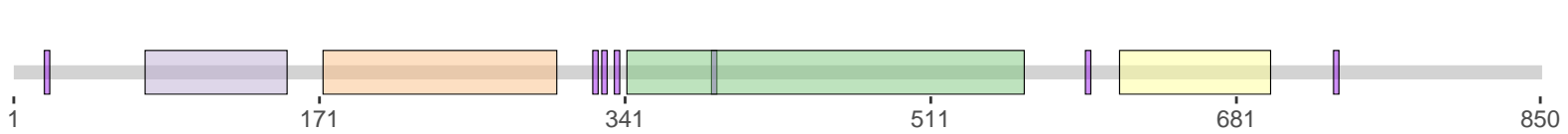
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

LLRAIMNIAPLAISTFGRGSSGVLTAAVTSDGETGERLEAGAMVLAADRGVYVGDDEFKMDGDRVAHEVMEQGTVTIAKAGHAGLNARCGVAAMNPNYGVYDRSLFTTKNGLPDSLLSRFDLLFVLDQMDPGVDRLLSEHVLRMHGVRTDGGSSFLDONSRYEEGTEKDEMPVYVYKHNRTLHGNENRRKDKTLTGFLKTYHYAKNRHPPELDEASDHATAVAELRSASTNAKTGGGLPITARTLETIRLSTAHAKLKLRRQVFKSDVDAALQVLIHFAIYHQLTEI

NbL19g03090.1 uncharacterized_LOC104243949 [MW = 50.11 kDa]

No. of times detected



log(intensity)



Values from



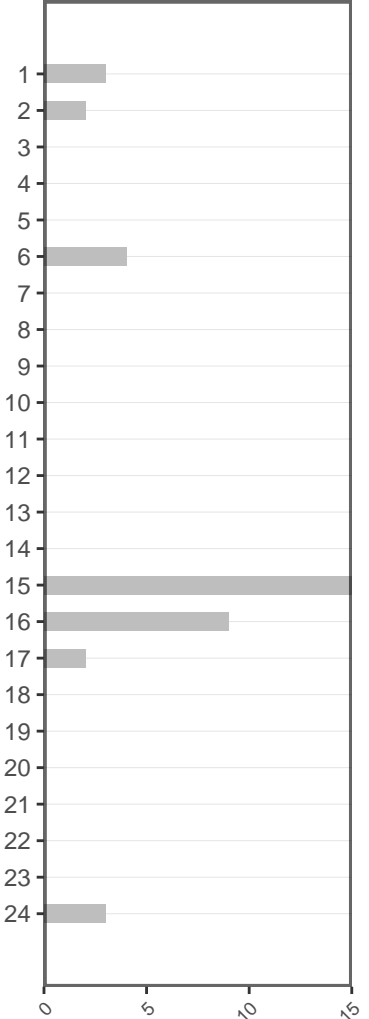
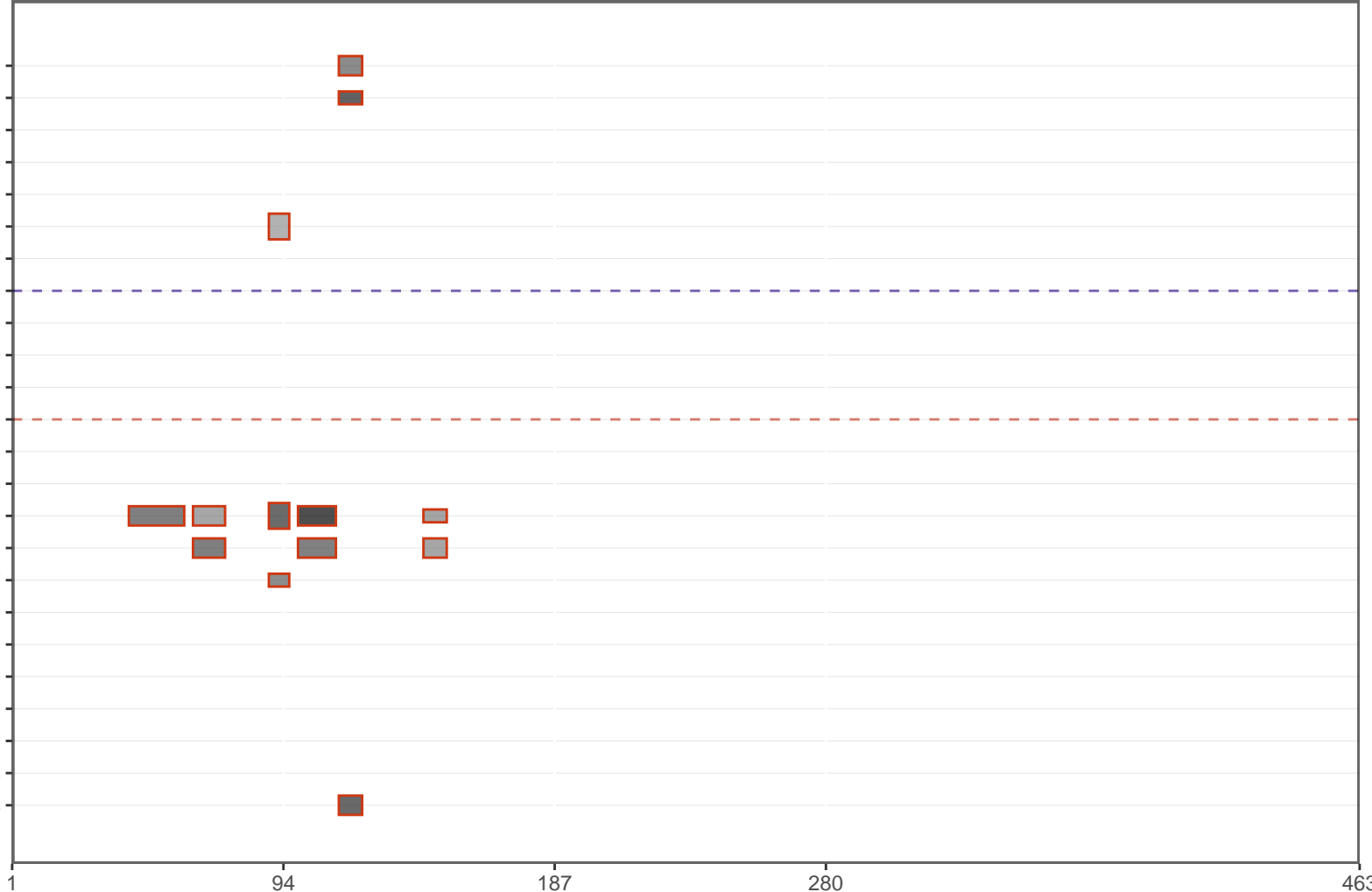
MW indication



Molecular weight



Gel Slice



Protein length

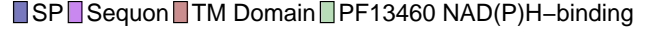


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

HPVSSSOTLDSLSLVSGSMNDRASHMEYRRGGGRFRSRPSELVWNLVLTGCAIYVDDGQKNAFYAGSEPTGNGGFGVSEREYNELFKYRAEKQTSQVATVAGPDTFVAGNFAFVGGSSPLEQWVYDAAAGDHSGNKKLLGNAYSGFLPNVTLANGSGQTKAKGVGGENPLFPEVTLDEVLVYVPGGPNFASVRLTRALAEVILLMTLLLCRTAVRDRRLLEQDLNGTDFTLTH

NbL19g03000.1 urease_accessory_protein_G-like [MW = 30.67 kDa]

No. of times detected



log(intensity)



Values from



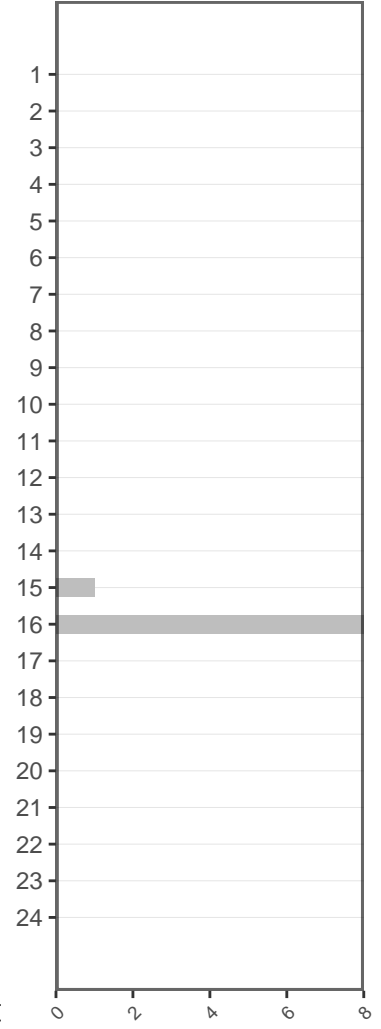
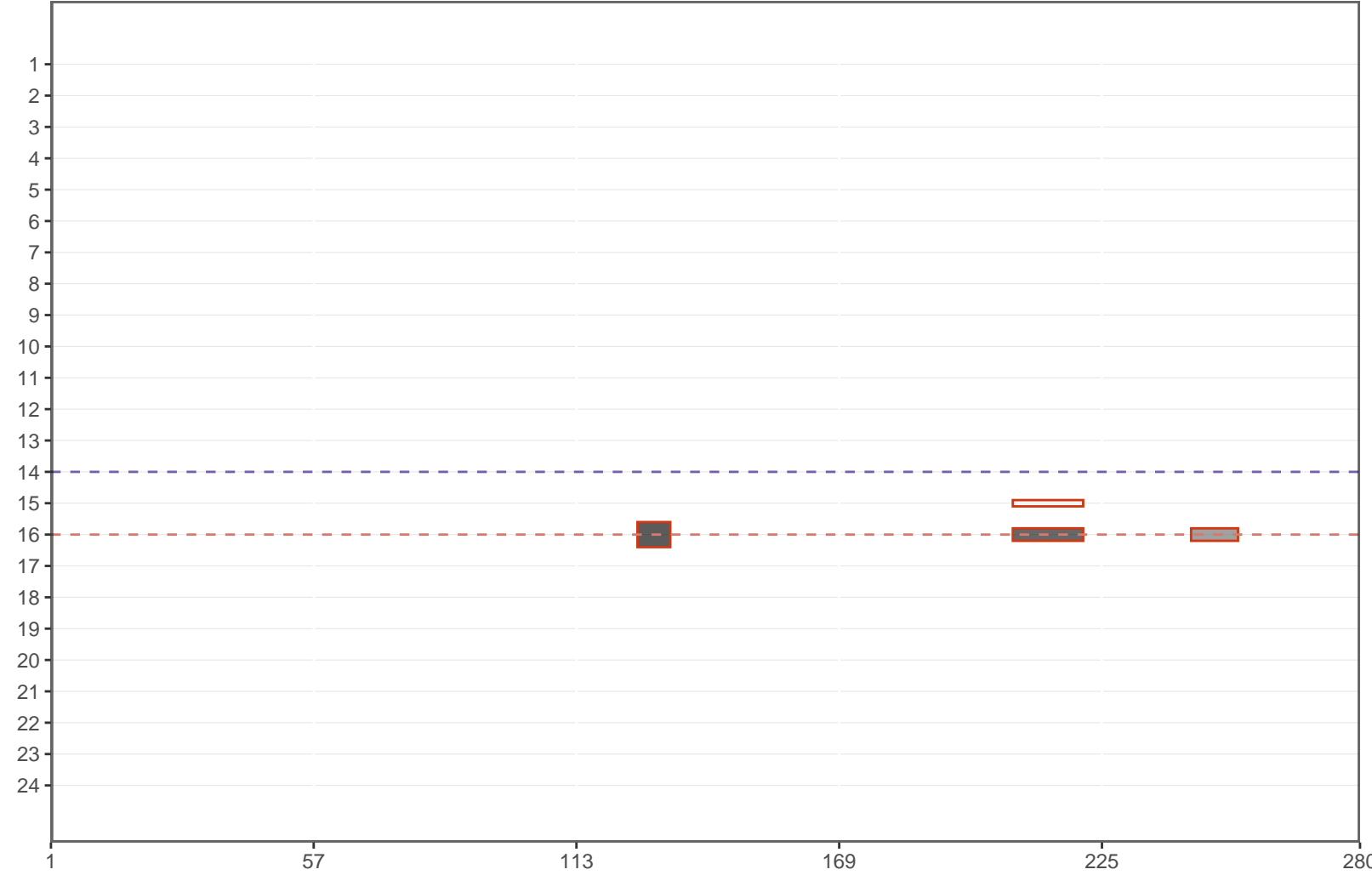
MW indication



Molecular weight



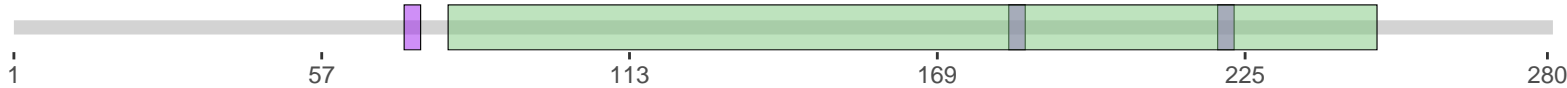
Gel Slice



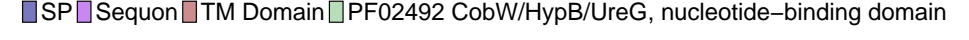
Protein length



Pfam domains



Pfam Description



Protein sequence:

KHIGALPEERIRAVETGGCPHAAREIDISINLPLLEELSNLYKADILLCEGGDNLAAANFSRELADHRYIDVSGGDKPRKGGPGTGDALLVWKTDLAAAVGADLSVMERDALMRDGGPFVFAQVKEVGVGVEDIVNHLQAWAVATGNKKH

NbL19g02860.1 leucine-rich_repeat_receptor-like_serine/threonine-protein_kinase_BAM1 [MW - SP = 108.91 kDa]

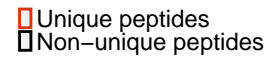
No. of times detected



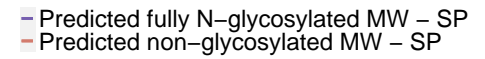
log(intensity)



Values from



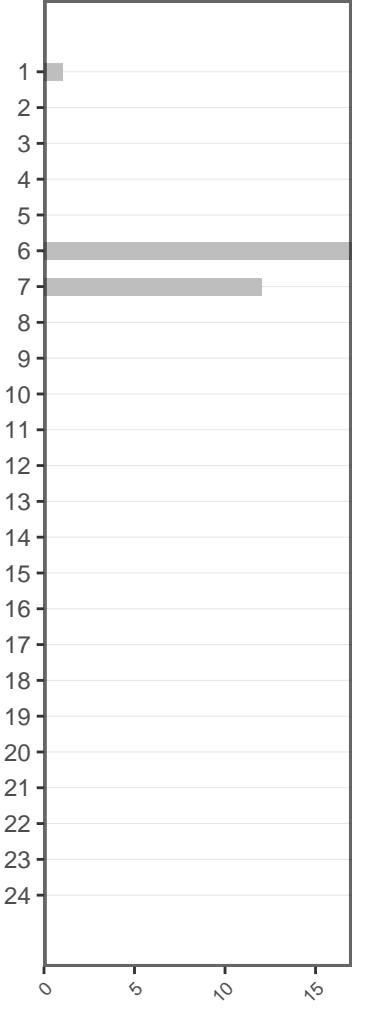
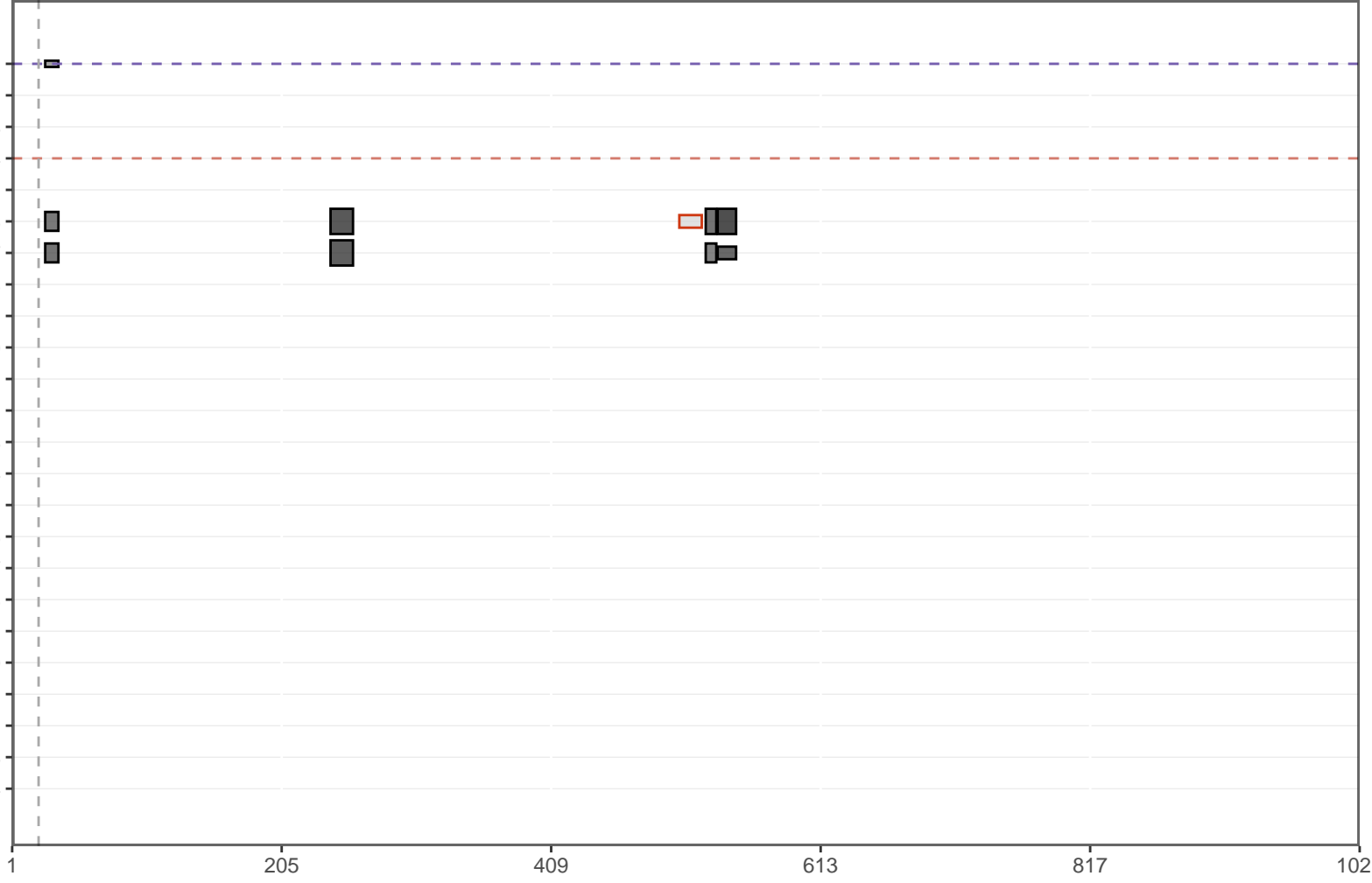
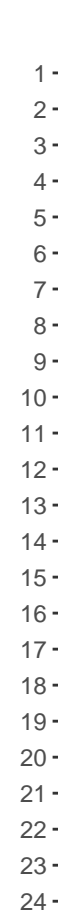
MW indication



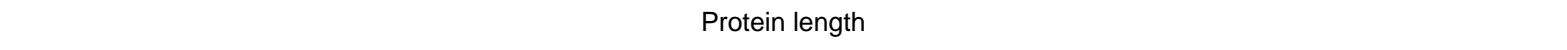
Molecular weight



Gel Slice



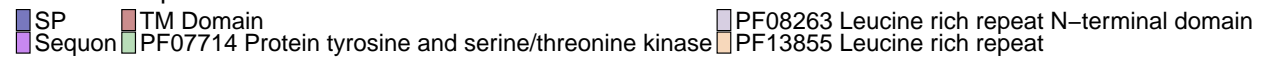
Protein length



Pfam domains



Pfam Description

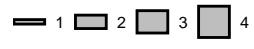


Protein sequence:

QLSKDFSHNDLSGPAPEISKKLLTYVDLGRNLDSEIPEITGMRLINLYNLNRNHLVGSPPISMDLSTVDFSYNFFDGLVPCGTGQGFYFNYSFGNPDLOGPGLGPKCKEYVDGVGSPHQRGALSPSKMLLLVGLLVGSIVFAWAIKARKLKAASEARAWKLTAFORLDFDGDLDLSEKNEIKGGAGIVYKGVMPGGEHWAKRLPAMSRGSEHDHGFNAEIQTLGRIRHRHVALLGFGSNHETNLLVVEYMPNGLGEMLHGKGGHLLIWDTRYKAVI

NbL19g02790.1 COMPASS-like_H3K4_histone_methylase_component_WDR5A [MW = 35.45 kDa]

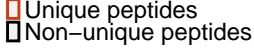
No. of times detected



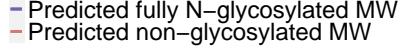
log(intensity)



Values from



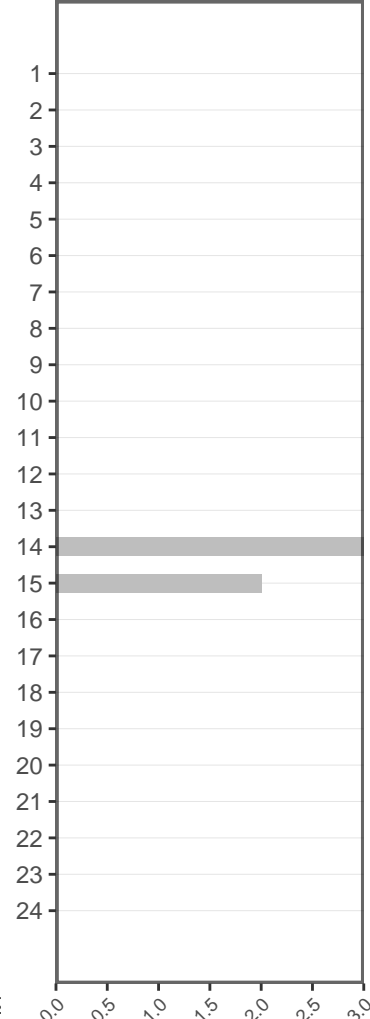
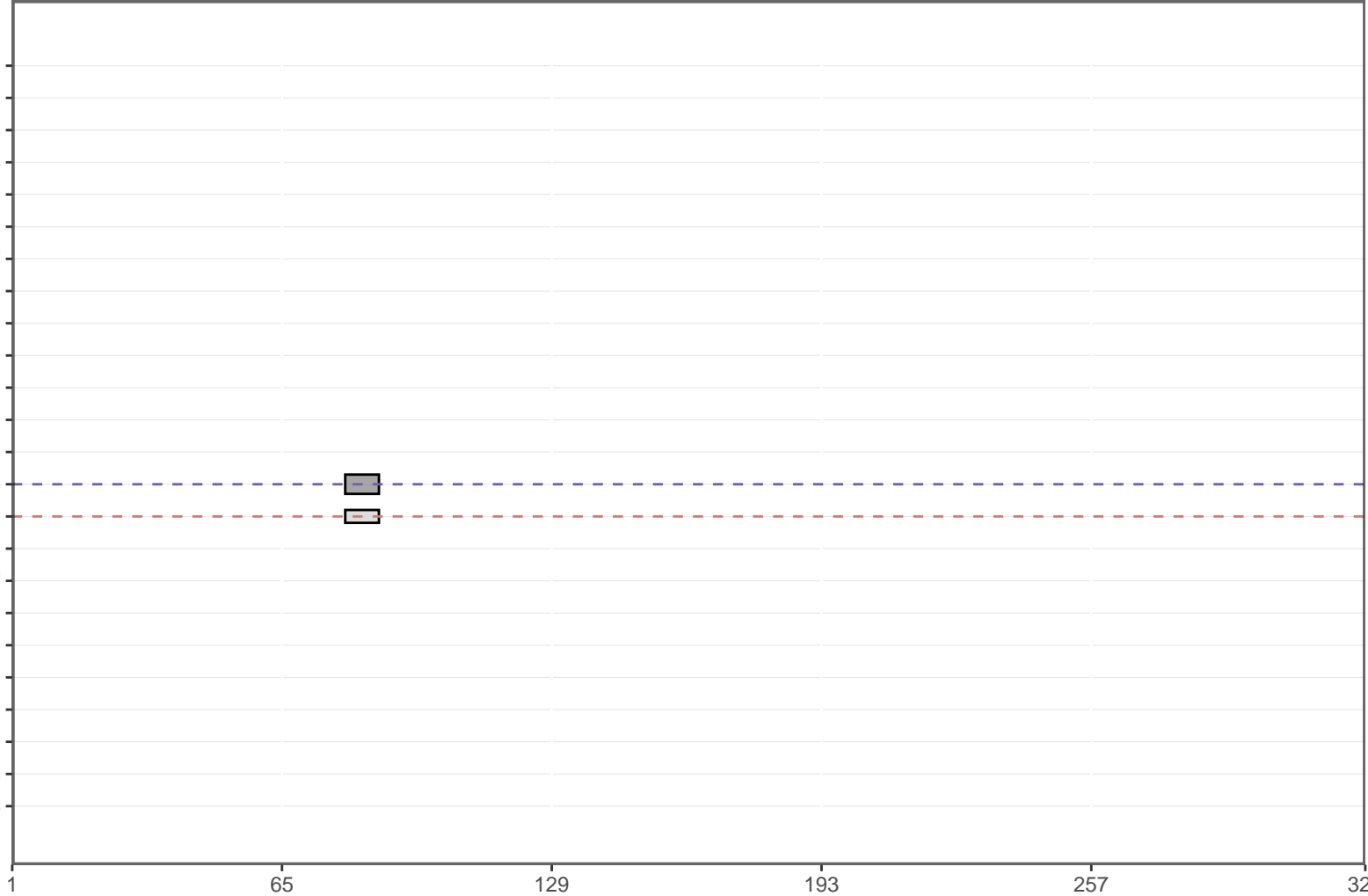
MW indication



Molecular weight



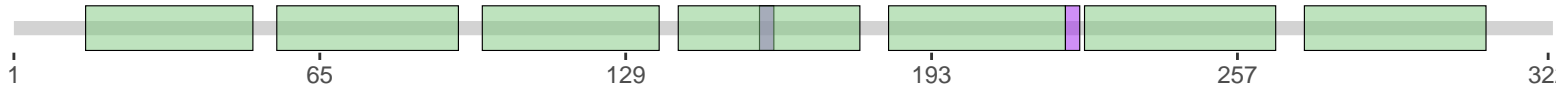
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

PAHSDPVTA/NFNRDGLLVSSSYDGLGRWDASTGHCMKTHIDENPVPVSEVVFSPKSPNGKFLVGLDNTLRLWVFTGKVLKTYTGHANSKYGVSSFTSDGKIVYVSSGSEDNQVYLVWELGSRKIVQKLEGHDTDTVIVACHPTQNMIA6SGLGNKKT/KKWTGAGRDESEDMT

NbL19g02730.1 probable_beta-D-xylosidase_6 [MW - SP = 83.95 kDa]

No. of times detected



log(intensity)



Values from

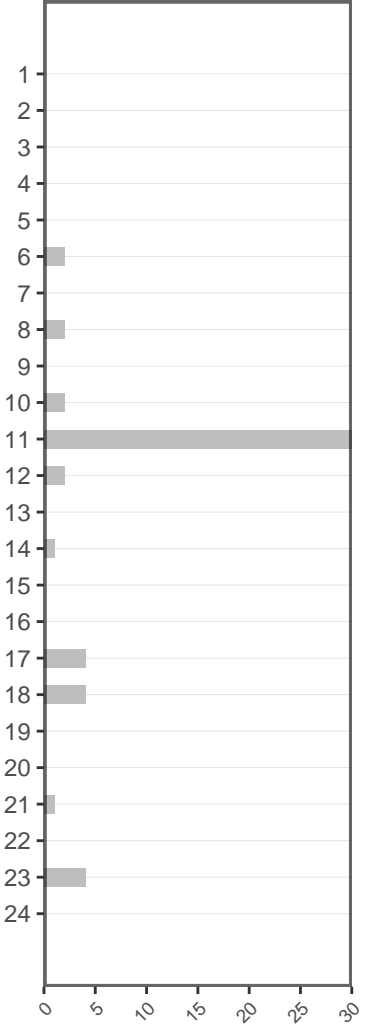
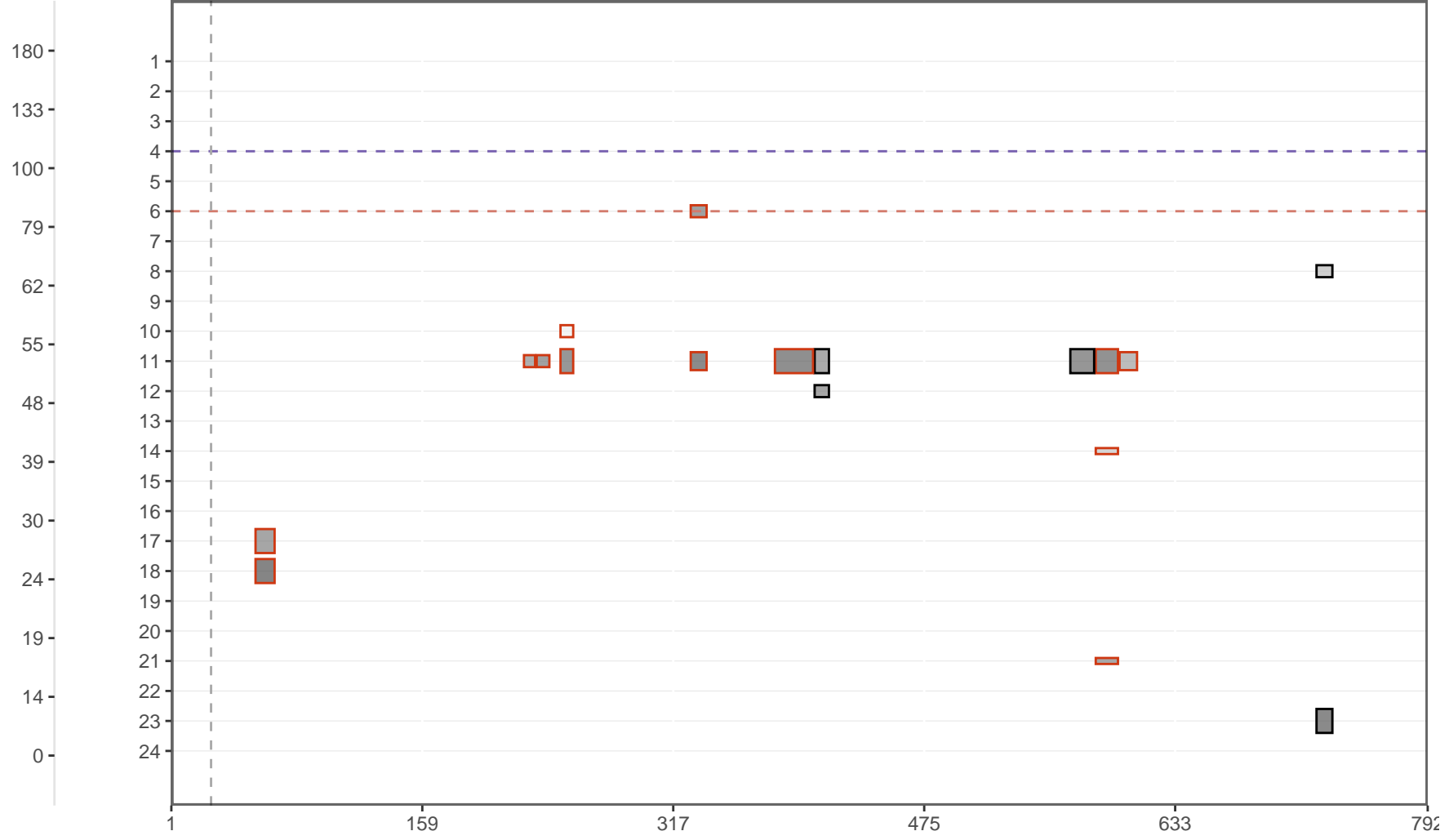


MW indication



Molecular weight

Gel Slice



Protein length



Pfam domains

Pfam Description

SP Sequon TM Domain PF00933 Glycosyl hydrolase family 3 N terminal domain PF01915 Glycosyl hydrolase family 3 C-terminal domain

Protein sequence:

GLFDGNPADGGFANFGAEDVSGSKHNLNLDADAROGVLLKNDKIFLPLDKTSVSTLAVGPMANVSSPGGTYGGVPOKLSKREGFHRHNRITLVAAGLDVGGNSTGGFQDASIAKEADYVVAAGLDLSEETEDHDRIYKLLPLPGQGANVITLAAASKPHILVLTGGGPDVDFSAEKDPRIASLWVWPGETGGKALBEVFGYGNPNPGKLPVTVWLESFTKVPMTNMMNRADPSNGVYGRBVRVFTGDWLYGFGHGLGVTFSBQLLSAPRRLSLAKSNRKRSLI

NbL19g02580.1 probable_fructokinase-6_chloroplastic [MW = 42.05 kDa]

No. of times detected



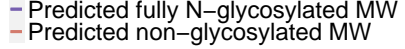
log(intensity)



Values from

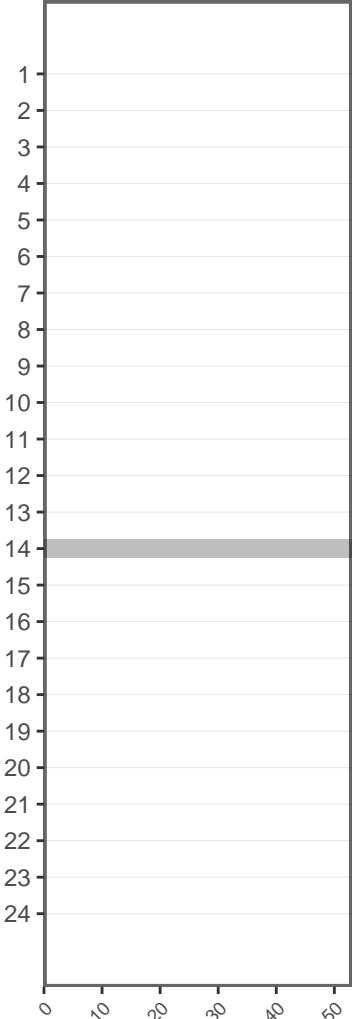
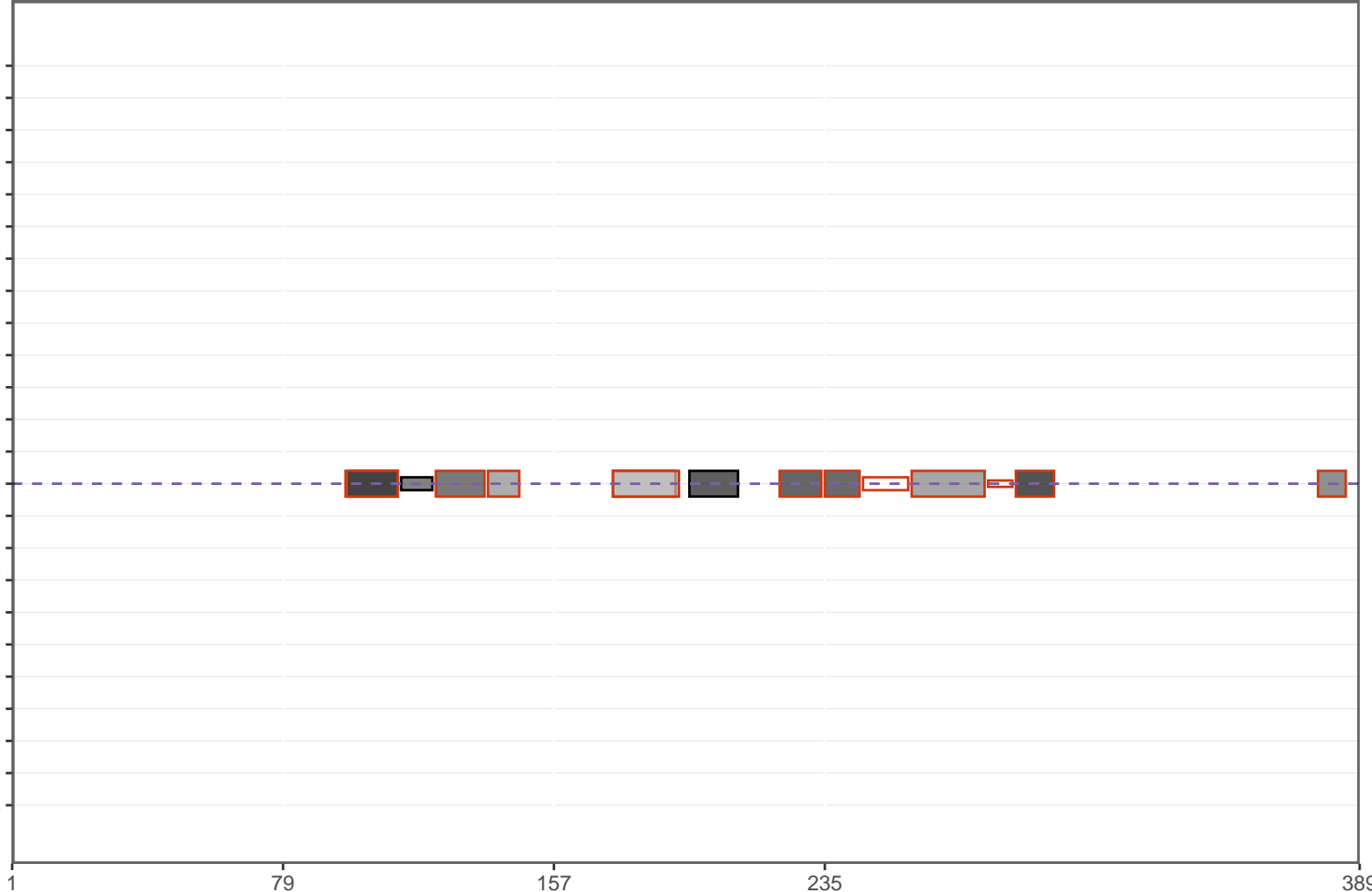
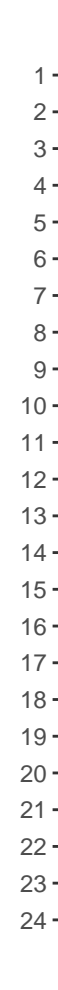


MW indication



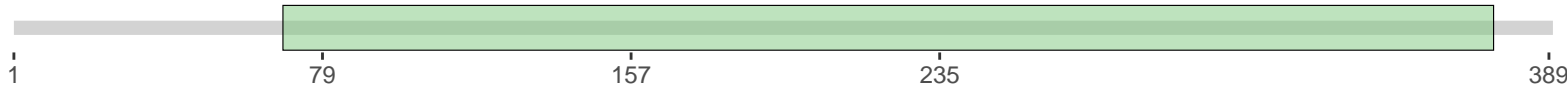
Molecular weight

Gel Slice



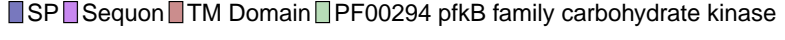
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DMLLQEDLDELIRKAKIFHYGSLTEPGRSAHMAATRAANDAGVLEVDPNLRLPLWPAEIAREGLSWETAQIKISEEISFLTQGEDPYDDNVRKLVHPNKLILVTEGPEGCRYYTKDFSGRIVKGLKVDVDDTTGAGDAFVAGLSQLASDVSLLQDEDKLRDALCFANAGSALTVMERGAIPALPTREVVLNLLKSVS

NbL19g02480.1 protease_Do-like_7 [MW = 122.68 kDa]

No. of times detected



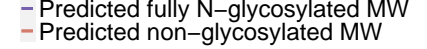
log(intensity)



Values from

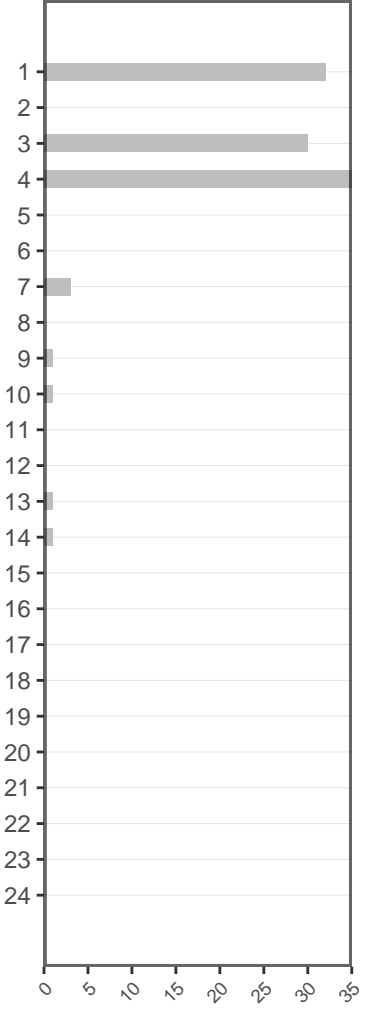
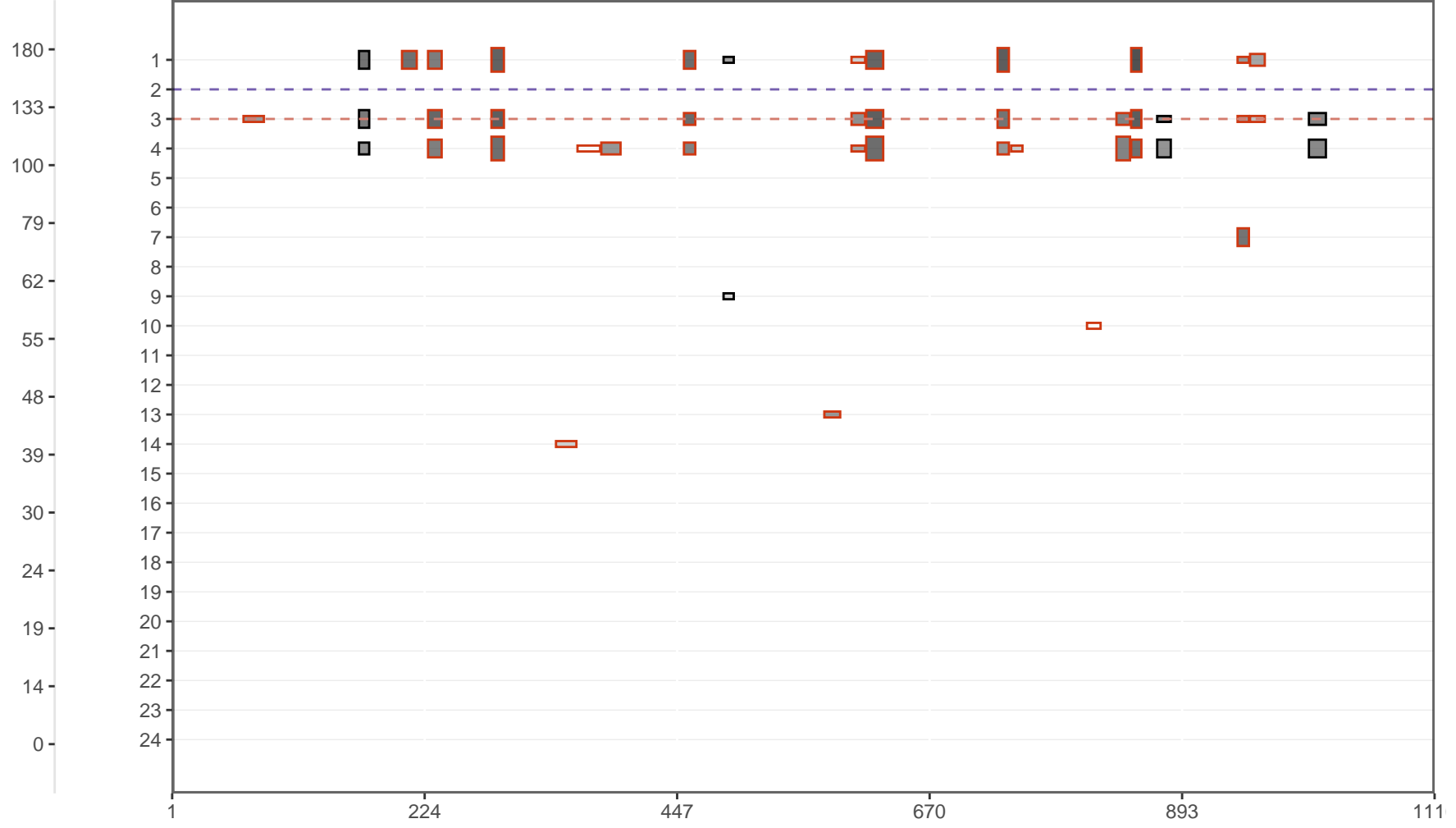


MW indication

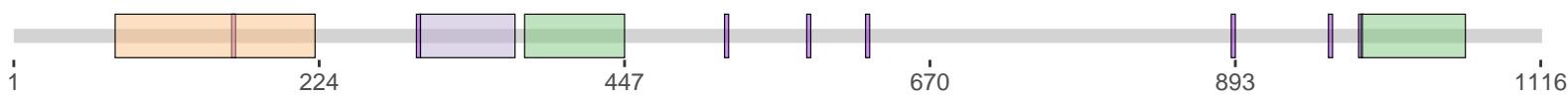


Molecular weight

Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

DGVNMTSCDDVTEGNSDSDSAGTKRRVVENFSADGSDVITDRSLNDRHREERFDSDGFLDQALRDGGAAPAAANASVAERAEPTLVMFEVHVPBLCLDGVHGHFFGTGTGVVHSGNMLLWVDRKNTVAWGVSDMLSFAPAEIPGEVVFVLFHPVNFALVAWDPALGAAAAASAVRAEELLFDPALRRGDDSVYLVGLGRSLQATSRKSVITNPEAAVNWGSDCPFRVATNMEVELDTPDFGTFSGVLTDERGRVQALWGFSTOLKYGGSSSEIDHOFVIRGPI

NbL19g02450.1 pyridoxal_kinase [MW = 37.43 kDa]

No. of times detected



log(intensity)



Values from



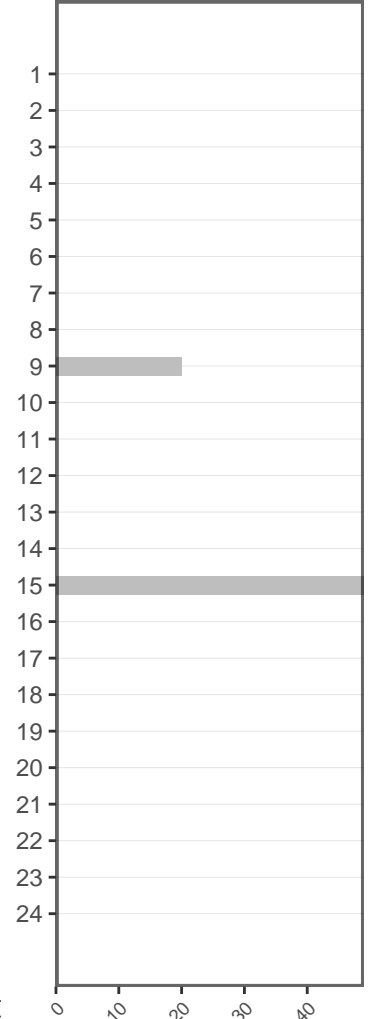
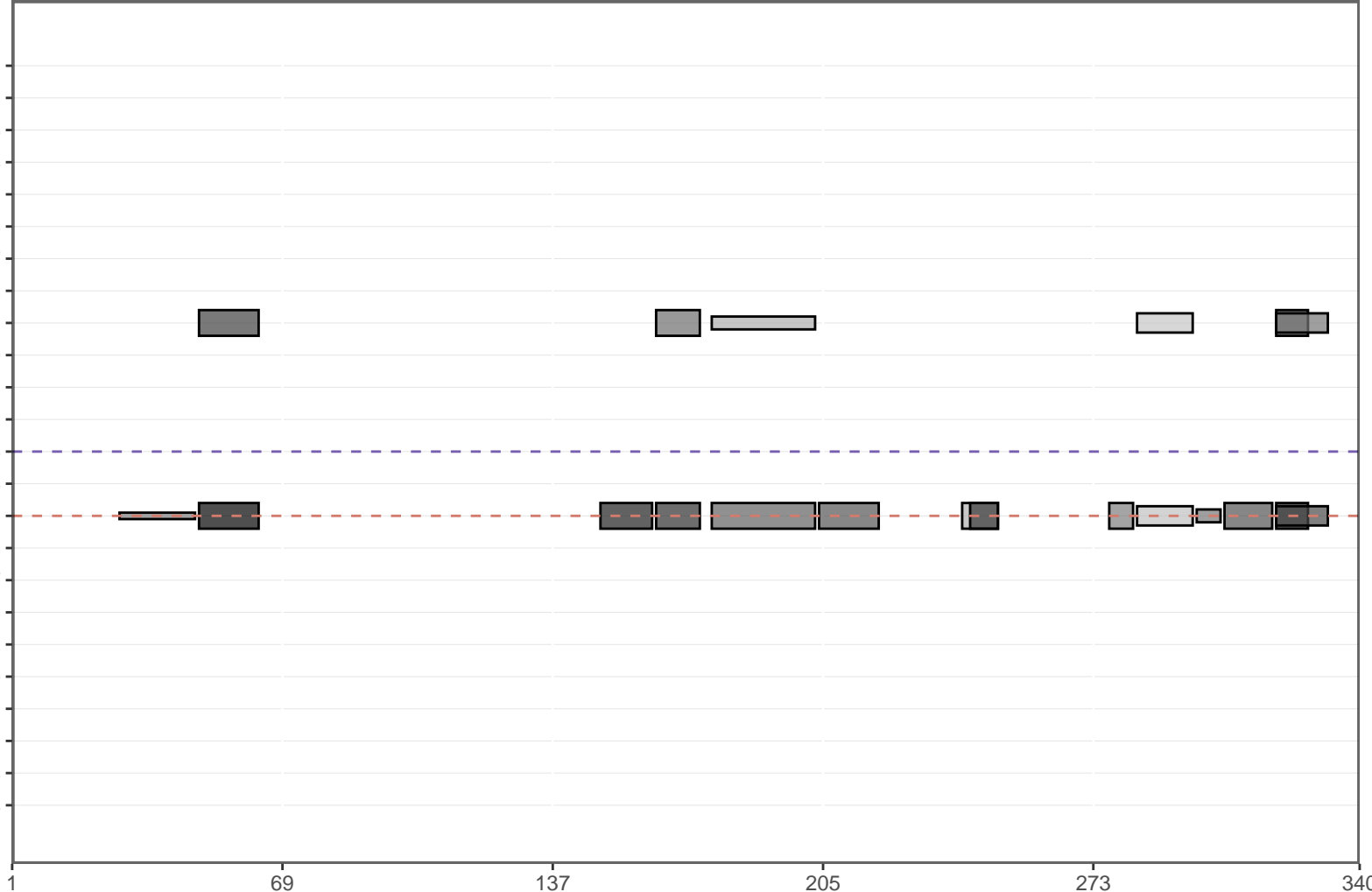
MW indication



Molecular weight



Gel Slice



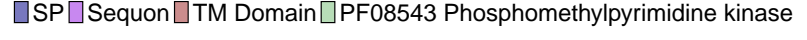
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

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NbL19g02400.1 methionyl-tRNA_{formyltransferase}-like [MW = 38.92 kDa]

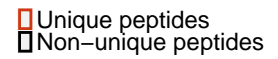
No. of times detected



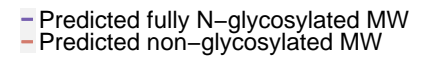
log(intensity)



Values from



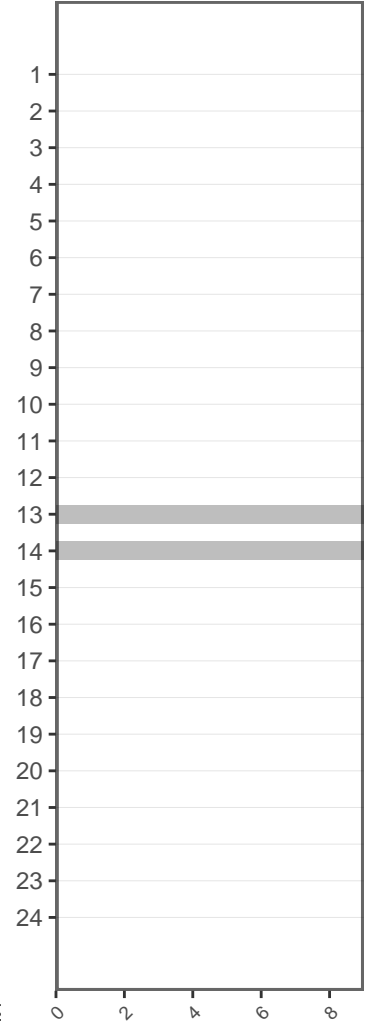
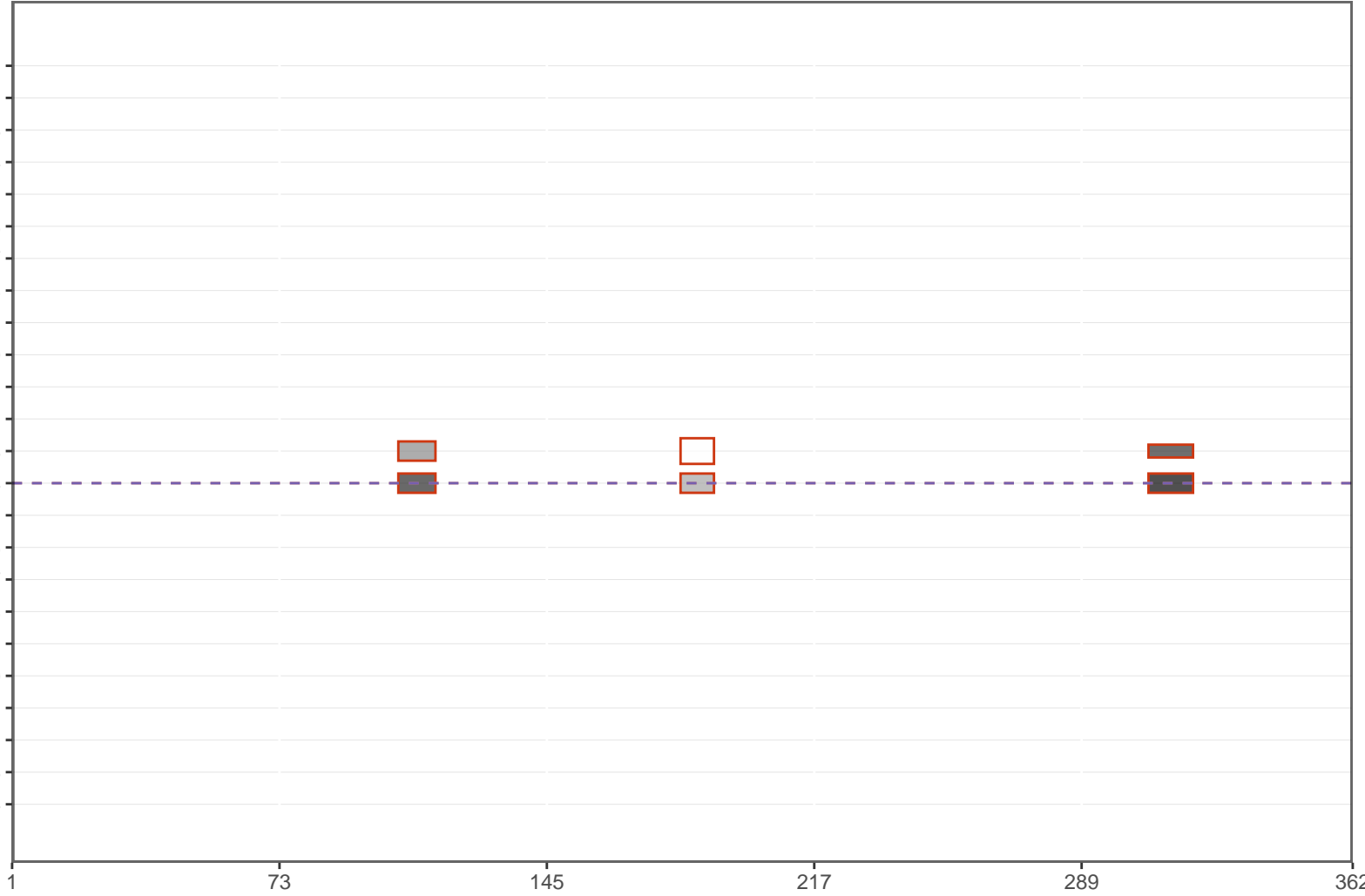
MW indication



Molecular weight

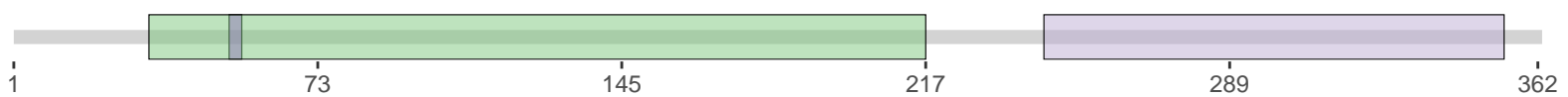


Gel Slice



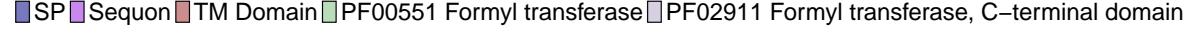
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

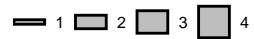


Protein sequence:

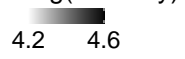
SVKETGVSLAYTVRKLEMDAGPVARERVTDDGKAPDLLELDFALGSKLLIRELPBIFDGSASGRAEEGDDSKATLAPKTFPEESWLFDEDDAQLHDKVRAFAGWPGTRSRRLMVDPSGGESSSELEKNITRYYGGIRSGDDETNDVLFTRKGSIVPQGGGTALEVLELQLPKRAWNAASFVNLGRGQLKR

NbL19g02380.1 ATP-dependent_Clp_protease_proteolytic_subunit_3_chloroplastic [MW = 20.67 kDa]

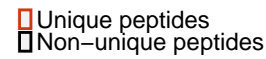
No. of times detected



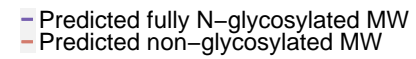
log(intensity)



Values from



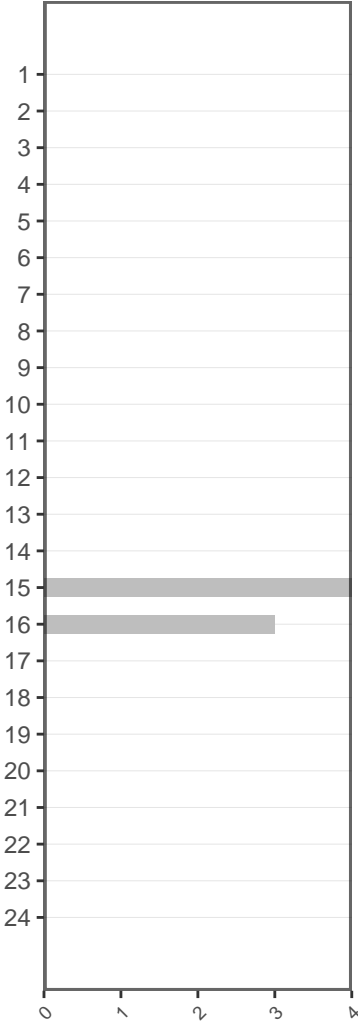
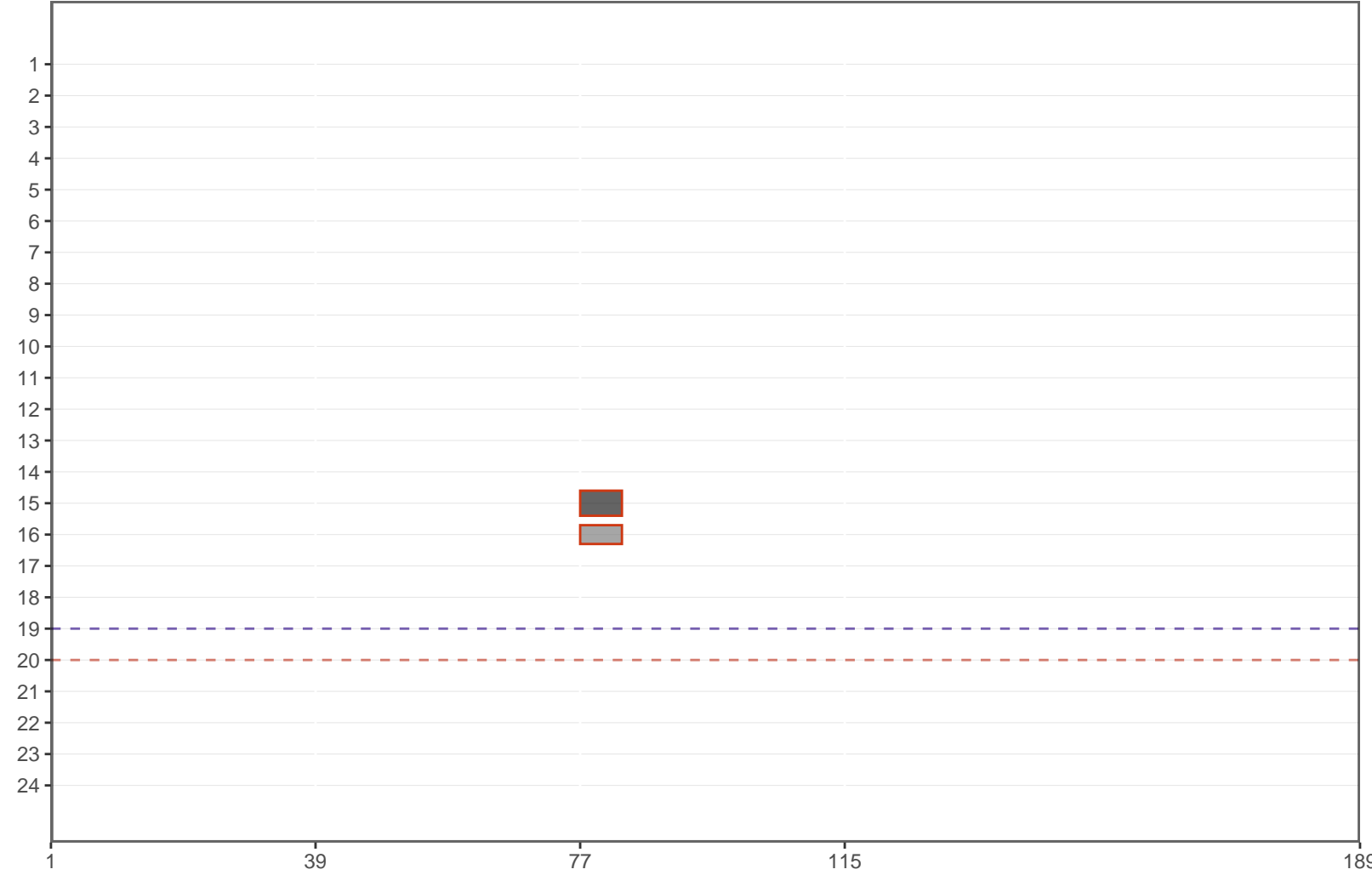
MW indication



Molecular weight



Gel Slice

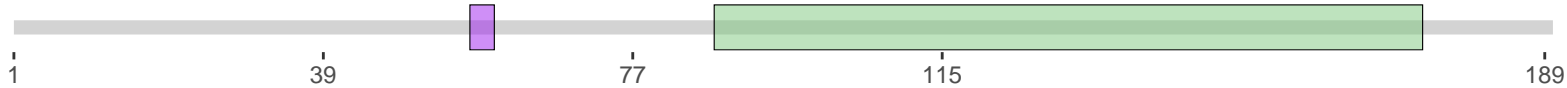


Protein length

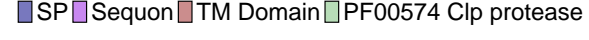


Peptide counts over 4 repeats

Pfam domains



Pfam Description

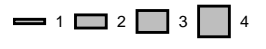


Protein sequence:

PPFEELDTTMLLRQRIFLGGVDDMTADFVIGQLFLDLEDQKDKIRLINSFGSVTAGMGVYDAMKMKKADVSTIGMGLAASMGAFSSHLAARERGTCRTQD

NbL19g02300.1 ATP_synthase_subunit_beta_mitochondrial-like [MW = 59.82 kDa]

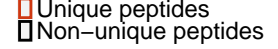
No. of times detected



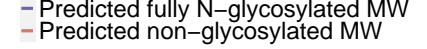
log(intensity)



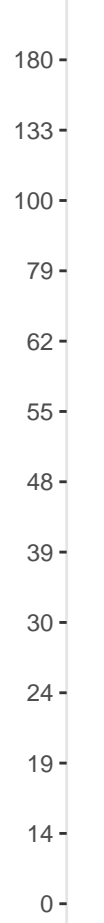
Values from



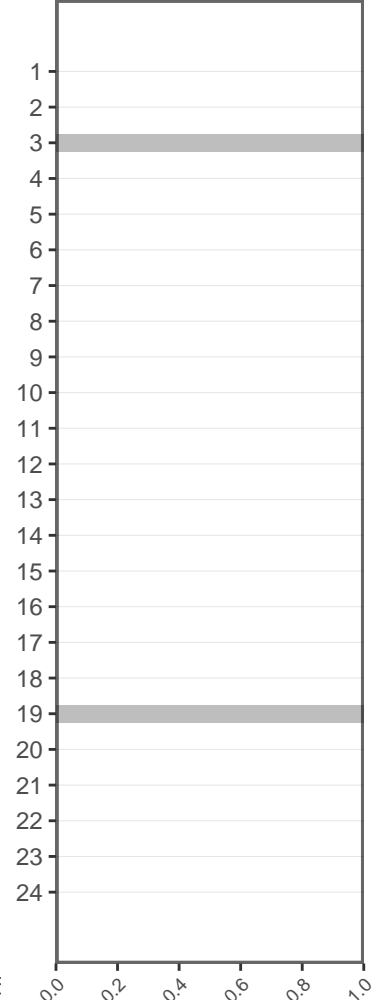
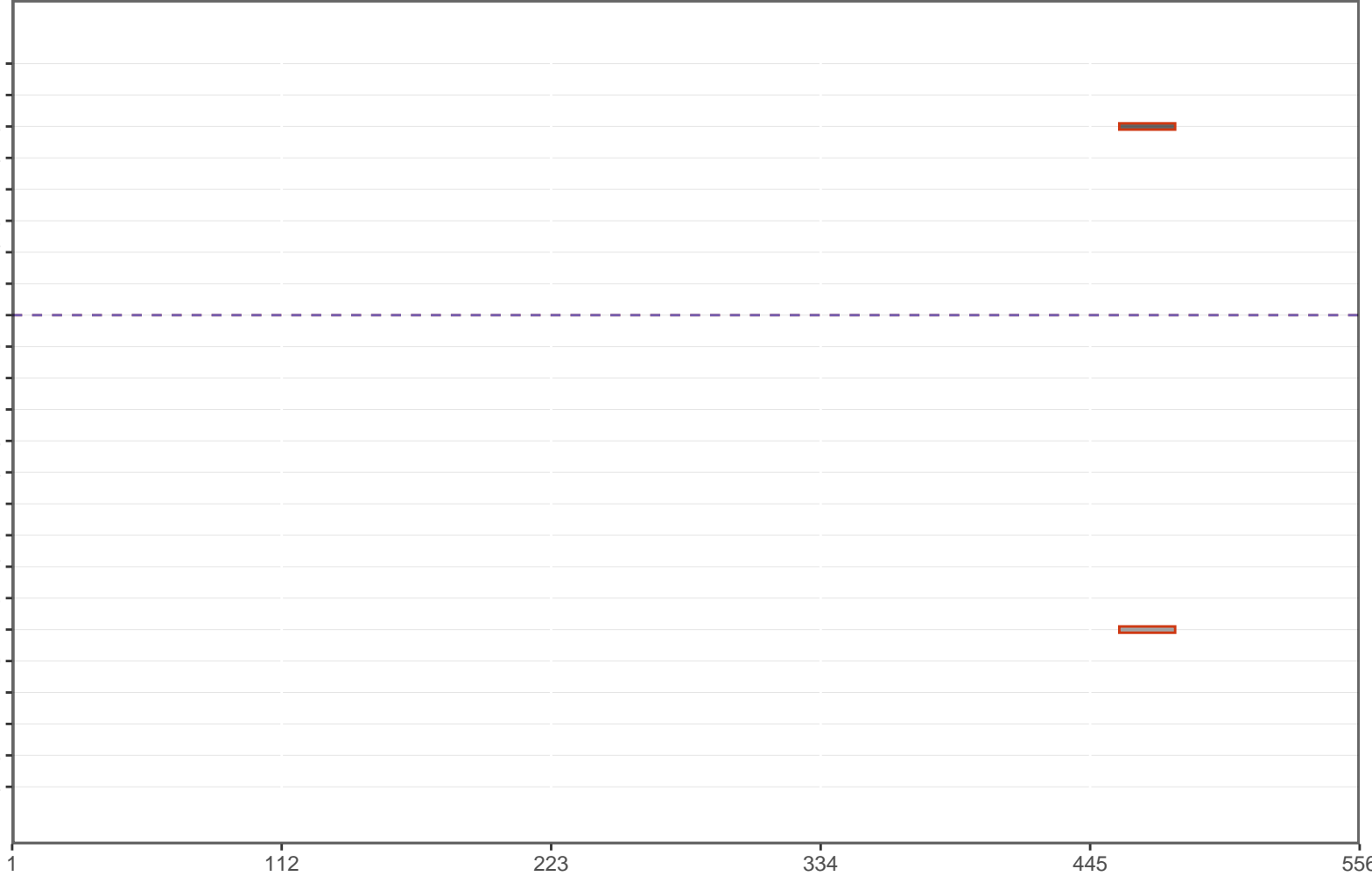
MW indication



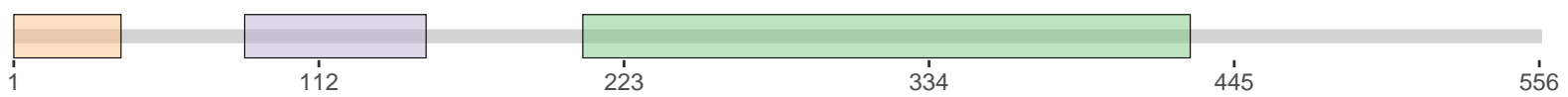
Molecular weight



Gel Slice

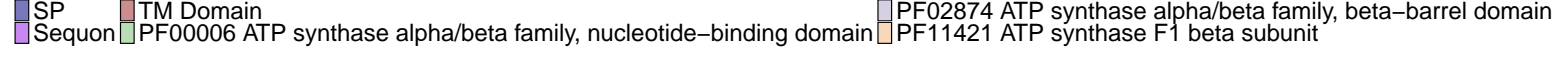


Protein length



Pfam domains

Pfam Description



Protein sequence:

INDLYRMEISGVINKLGDKGEKALVYGDMMNEPPGARARVGLTVAEHRFRAEAGDQKLLFDNFRFTQANSEVSGALLGRIPSAVGYQPTLATDLGGLGERITTTKKGSTFVQAIVYFADDLTDRPMTTFAHLDATVLSRQISELGYFAVDPLDSTSRMLSPHLGEDHYNTARGVQKVLGNVKNLGDIIALGMDLSEDDKLTVARARKIGRFLSGPPHVAEYFTGAPGKYVLDKESIGSFGQGVLDGKYDDLSEGSFYMVGGEIVAKAEIKASATS*

NbL19g02270.1 2-hydroxyacyl-CoA_lyase-like [MW = 61.41 kDa]

No. of times detected



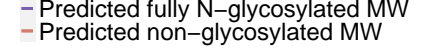
log(intensity)



Values from

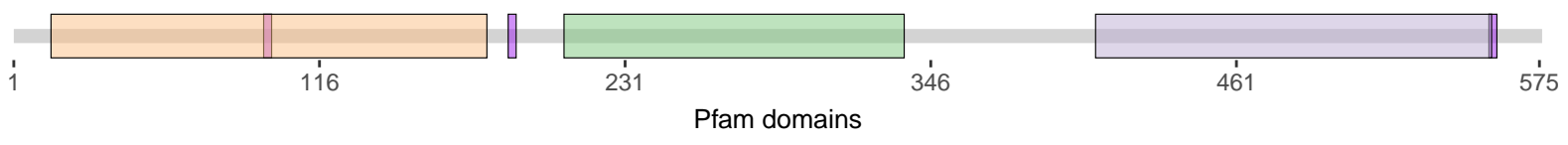
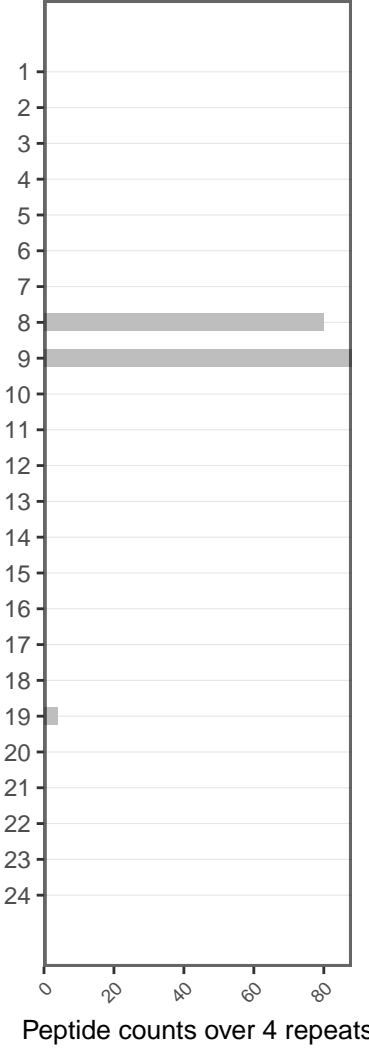
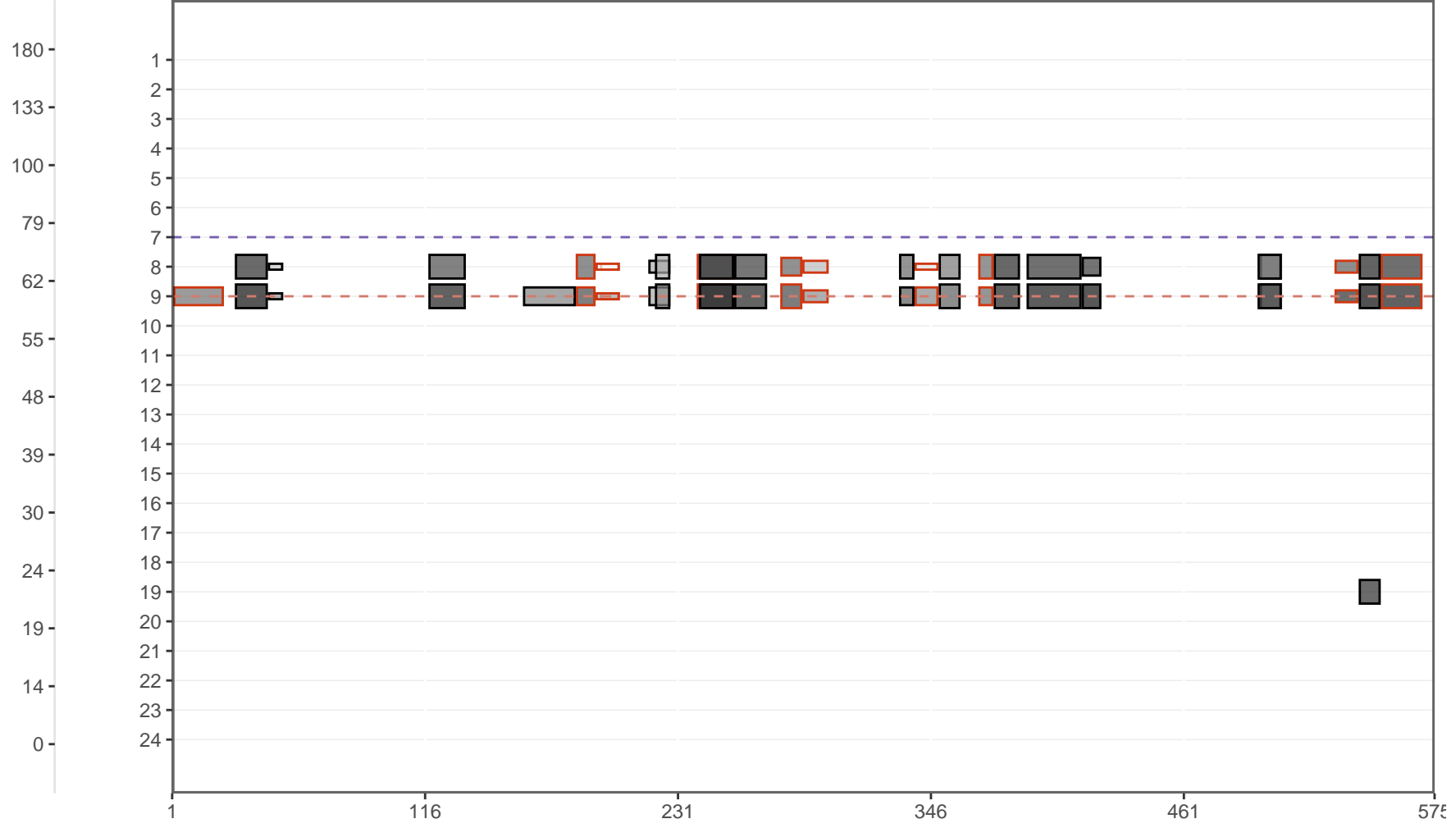


MW indication



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00205 Thiamine pyrophosphate enzyme, central domain
- PF02775 Thiamine pyrophosphate enzyme, C-terminal TPP binding domain
- PF02776 Thiamine pyrophosphate enzyme, N-terminal TPP binding domain

Protein sequence:

GKCDVALVGLARLNWLLHFGESPKWKKVFLVDVAEEIEELRKLGLIGDATKVVEMLHKVKDDPFLGKSHPWVEALAKKSKENAKMEAGLTKGVVFFNFMTMRIRIDALGVSSPAPVVVSEGANMTMDVGRBLVQTEPRTRLDAGTWTGTMGVGLGYGAAAVSCEPLVAVVEGDSGFGFSAMEVETLVRVQLPVAIVFVNGGVYGGDRRNPEEITGPKYKEDPMTSFPVPGASVHLLIEAFGGKGVLVGTPDELRSALSESFARKPWVNTIDPYAGAESGF

NbL19g01990.1 chloroplastic_group_IIB_intron_splicing_facilitator_CRS2_chloroplastic-like [MW = 26.86 kDa]

No. of times detected



log(intensity)



Values from



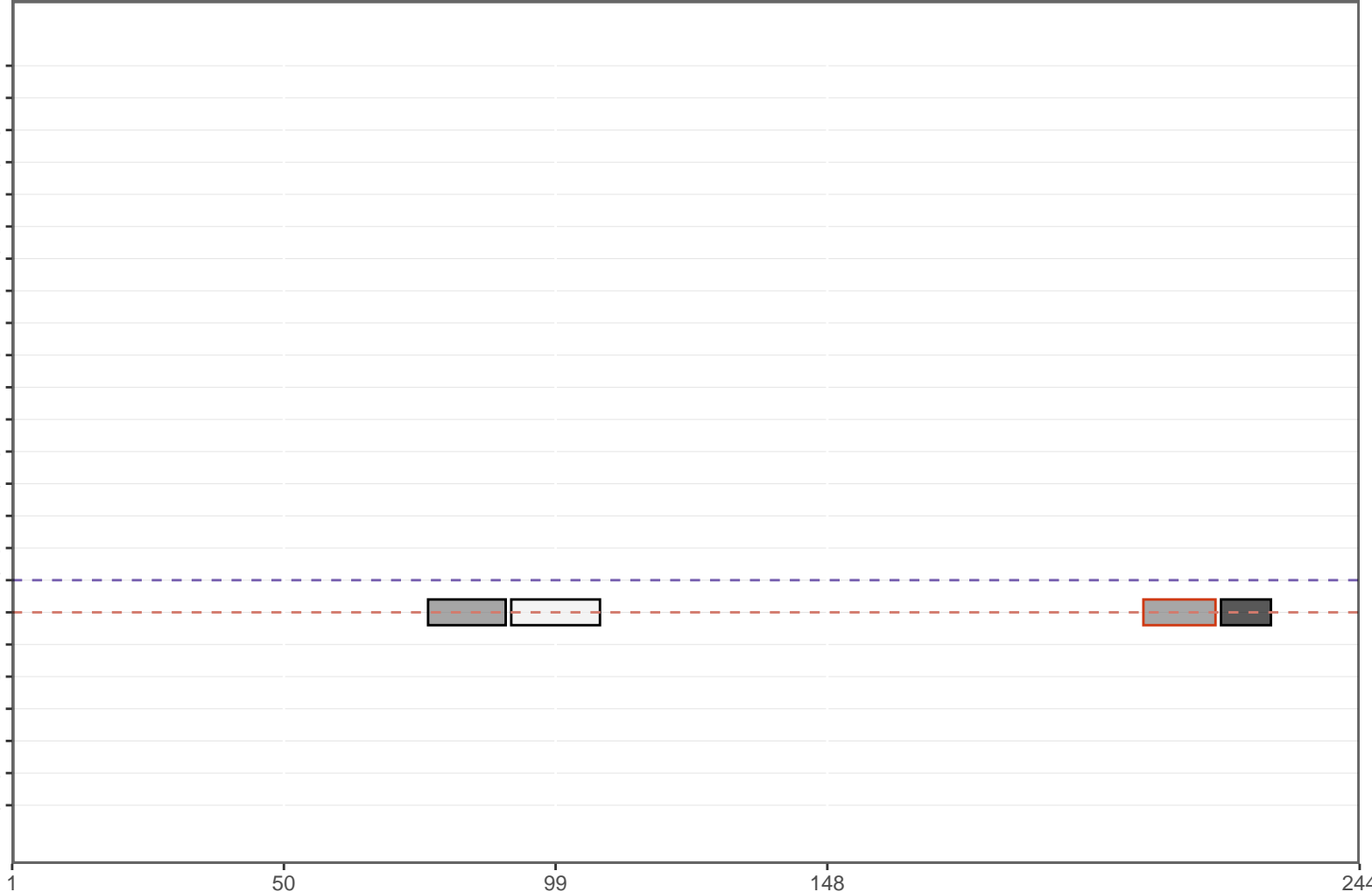
MW indication



Molecular weight



Gel Slice

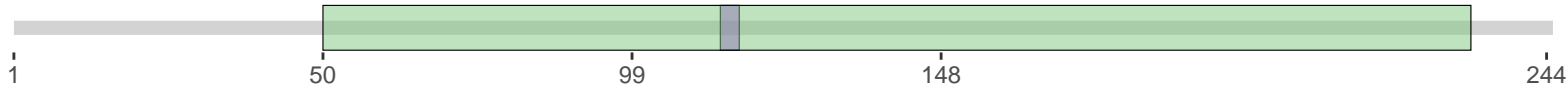


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

YMNFSGESVGFPLAAYGVPLRHLVYDEMFLFNGVLRLOPKGSHGHSHNGKVKMEHLDRREFPFQIGKGNPPTMDMKAVLLQKFSDIERKGVDAFDQGVAVRRTVLEFGFSRIIRFNGQKYWHV

NbL19g01960.1 ribulose_bisphosphate_carboxylase_small_chain_S41_chloroplastic-like [MW = 20.37 kDa]

No. of times detected



log(intensity)



Values from



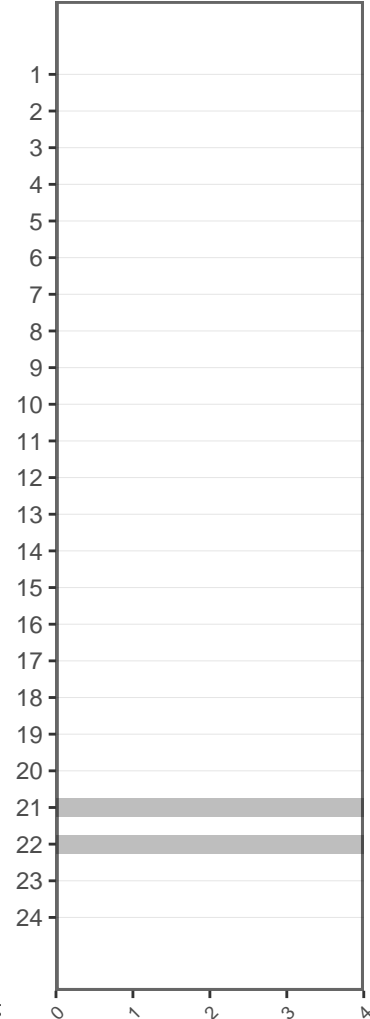
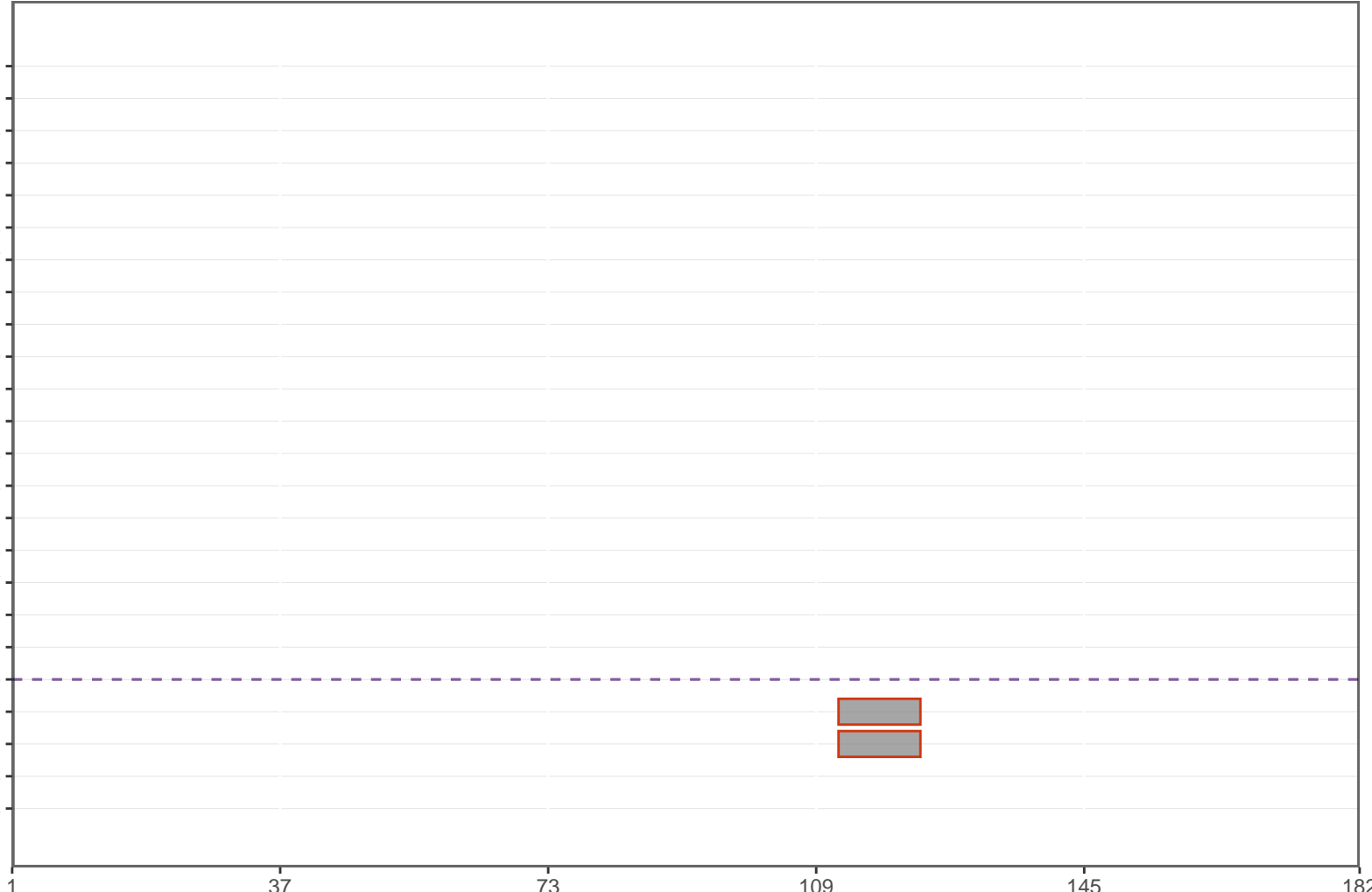
MW indication



Molecular weight

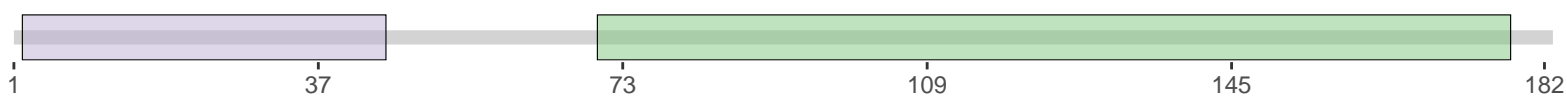


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00101 Ribulose bisphosphate carboxylase, small chain
- PF12338 Ribulose-1,5-bisphosphate carboxylase small subunit

Protein sequence:

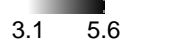
LSLVEQLLSIEIYLKNGWVPLEFETEHGPFVREHHHSPDYDGRYWTMKLPMFGGTDATQVLAEEVAAKAVPQAWWRHGFDNVRQVGGISFIAYKPEGY

NbL19g01770.1 T-complex_protein_1_subunit_zeta_1-like [MW = 58.97 kDa]

No. of times detected



log(intensity)



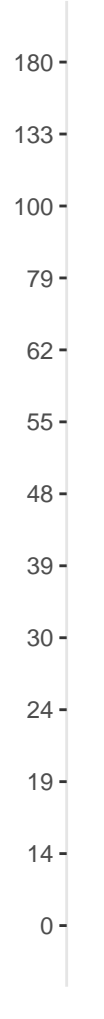
Values from



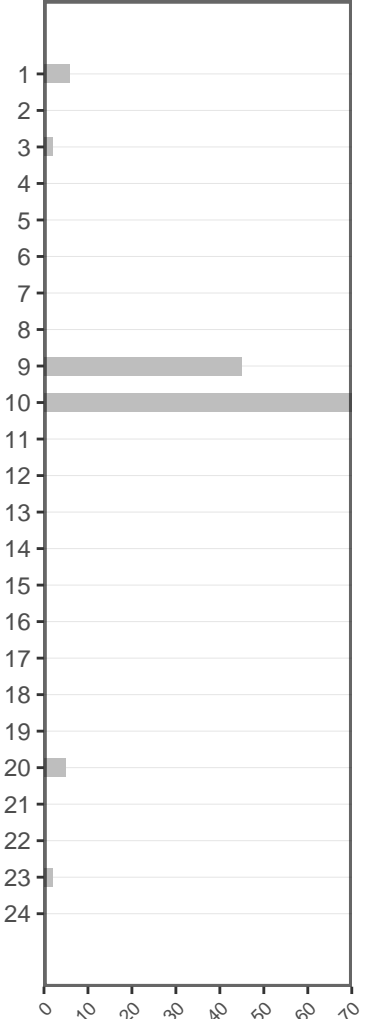
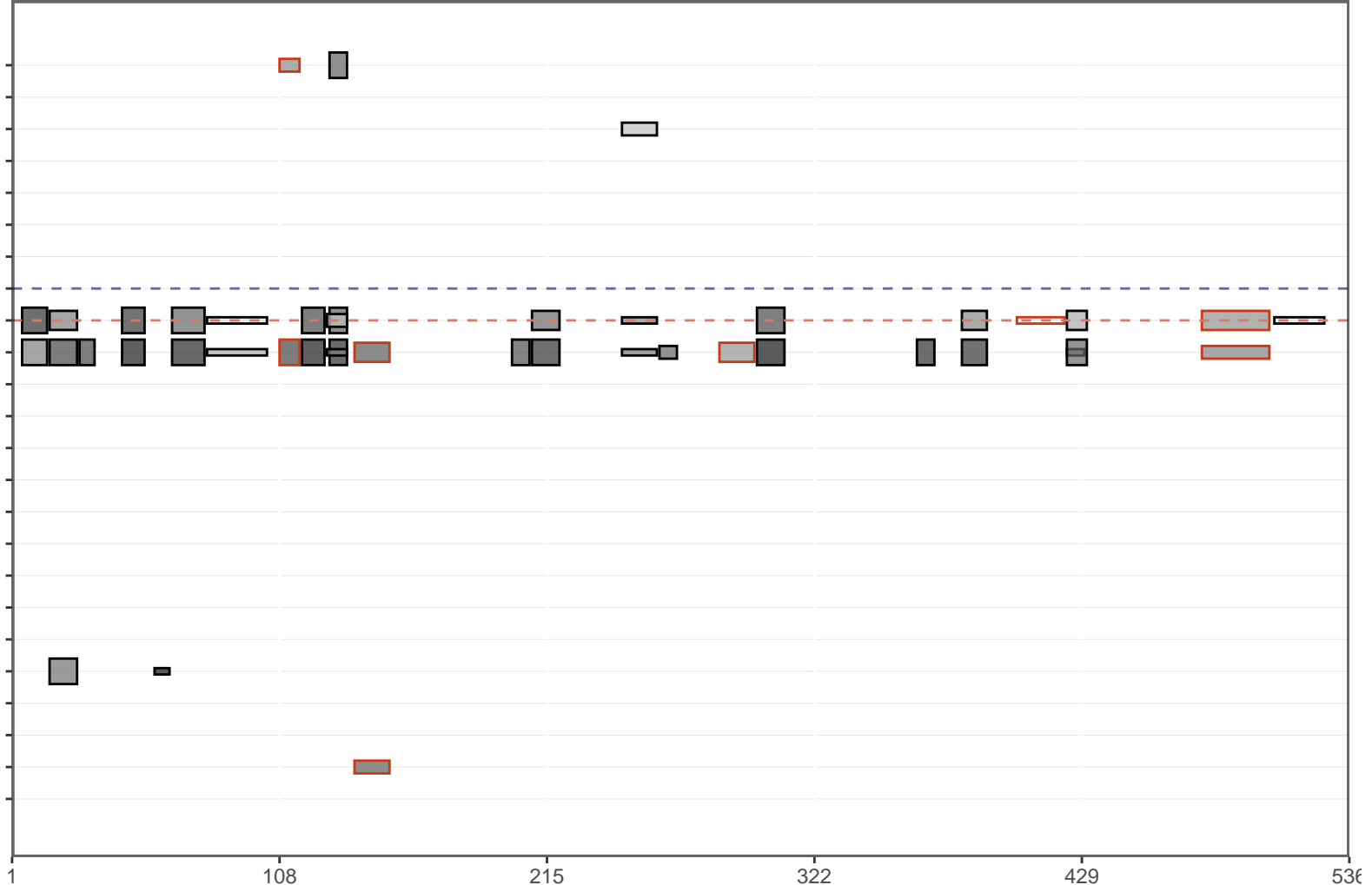
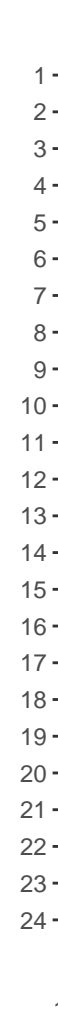
MW indication



Molecular weight

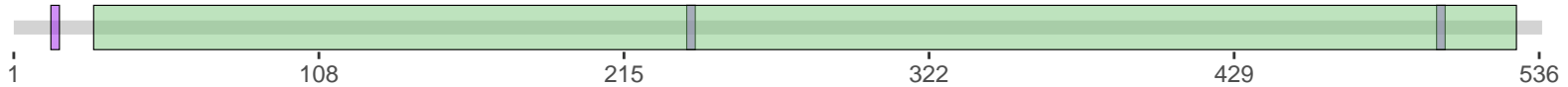


Gel Slice



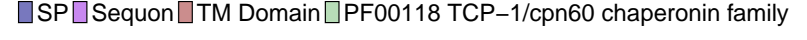
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NAEQREAAVAERRSVDERVQKIDKNKVCSSGNNENFVWQKGGIDPSPDLARAGIHLRAKRINMERVLACGGDAVNSVDDLTPEGLGWAGLVYEHVLEGEKYTFVENKKNPHSCTLIKGFNDHTIAGKDAVRDGLRAVKNTEDEAVLGGAGAFVAAQGLYNEVKKTVKGRADLGVFAFANALLVIRKTLAENSGLDTGQVIAITGEHDKGNVGLNHTGEPIDPQMEGIFDNYSVKRGIHNSGPIASOLLVDEVIRAGRNMRKPT---

NbL19g01710.1 allene_oxide_cyclase_4_chloroplastic-like [MW = 30.28 kDa]

No. of times detected



log(intensity)



Values from



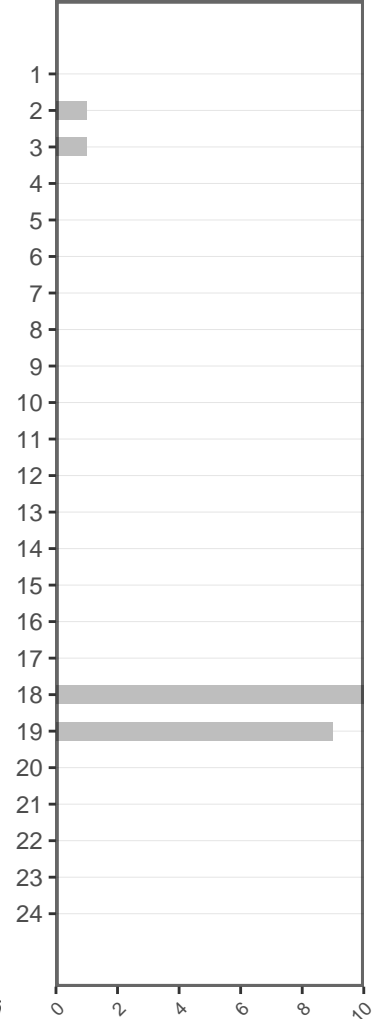
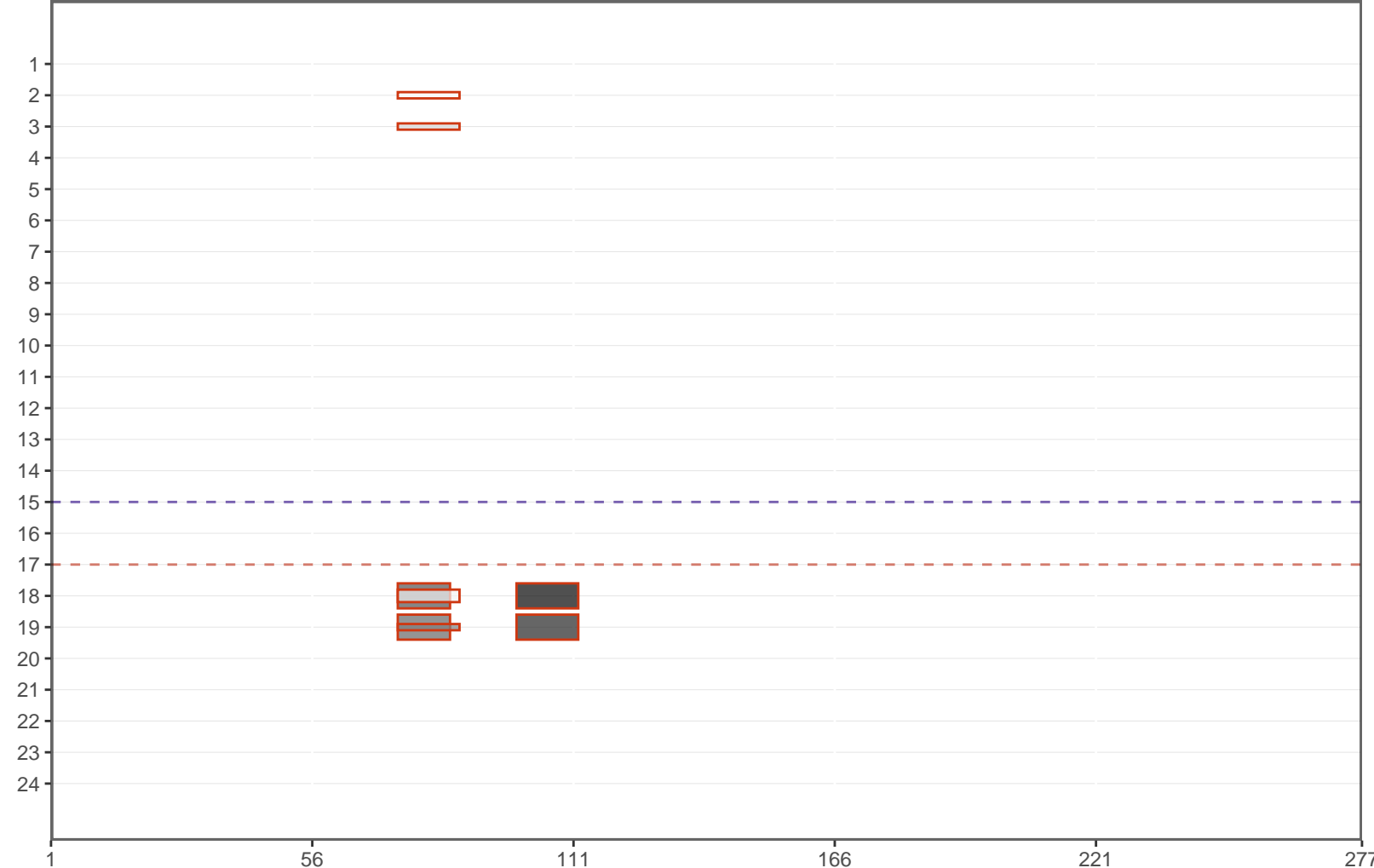
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

YVKKRIFSLYFLMLKLYIFQLYTGDLKKRIGFTAGLILNHEEEKKDRYEAYSFYFGDYGQIAVQSSYLTYEDTYLAVTGGSGIFAGVSGGVKGGIIFPKFLFYTYLKGIDPLSELLVAVPPSPFTVEPEAKACEAGATVKNFTN

NbL19g01520.1 60S_acidic_ribosomal_protein_P2-2-like [MW = 14.1 kDa]

No. of times detected



log(intensity)



Values from



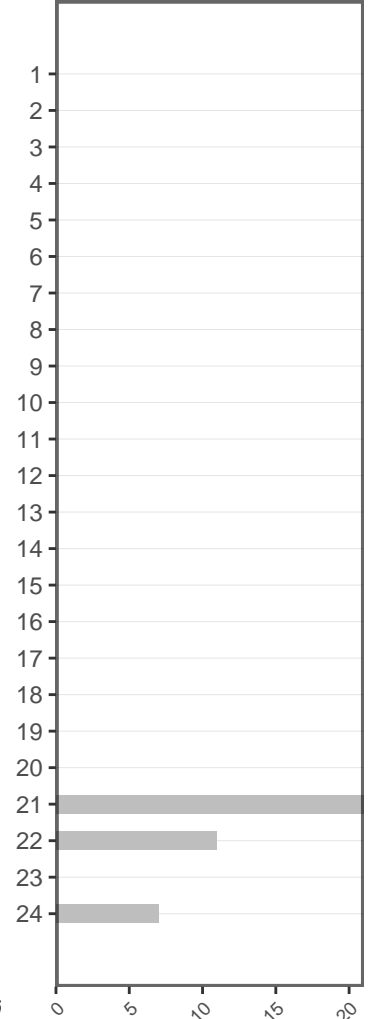
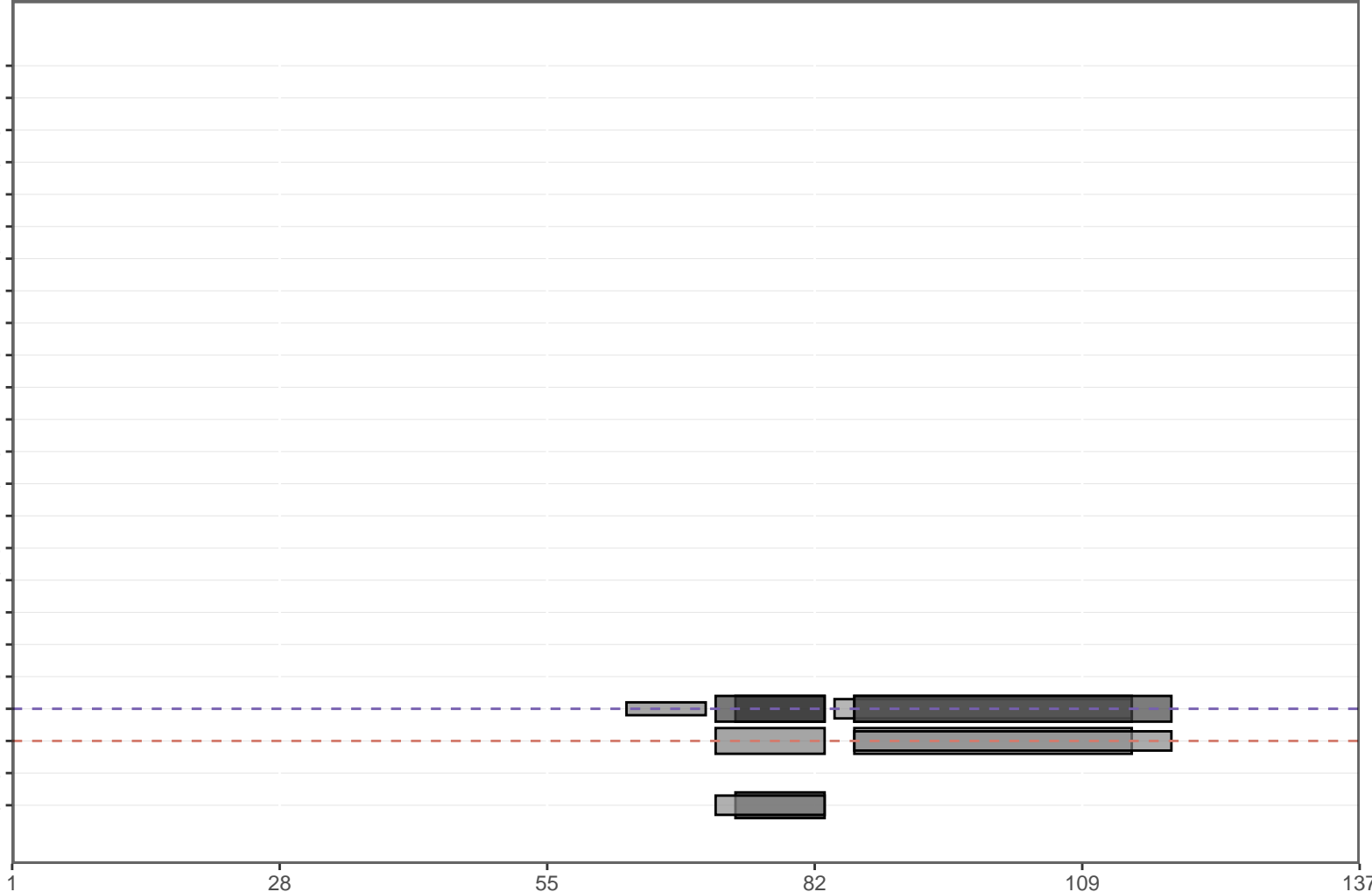
MW indication



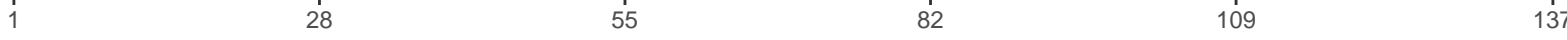
Molecular weight



Gel Slice

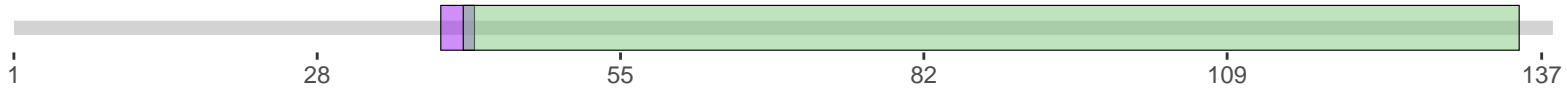


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

AEADDRIELLLSQVYKDKITELIANGREKLAVPAGGGGVAAAPTGGAAAAAPKEEKKVVEEKEEDDDMGFLFDI

NbL19g01430.1 succinate_dehydrogenase_[ubiquinone]_flavoprotein_subunit_1_mitochondrial [MW = 69.39 kDa]

No. of times detected



log(intensity)



Values from



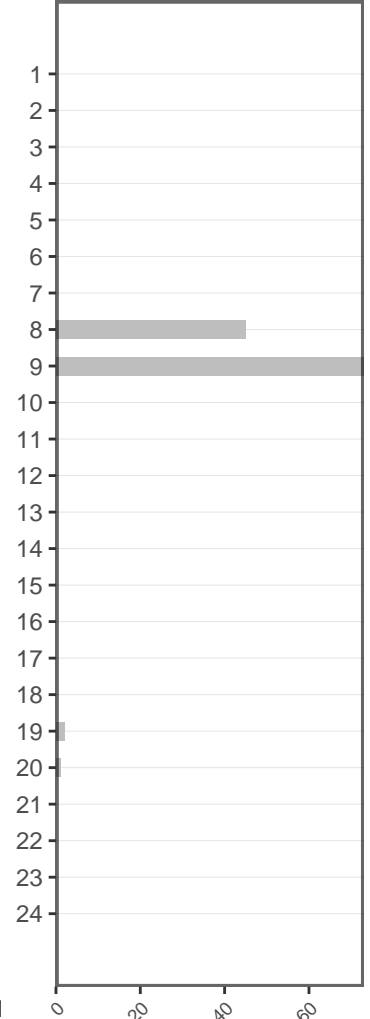
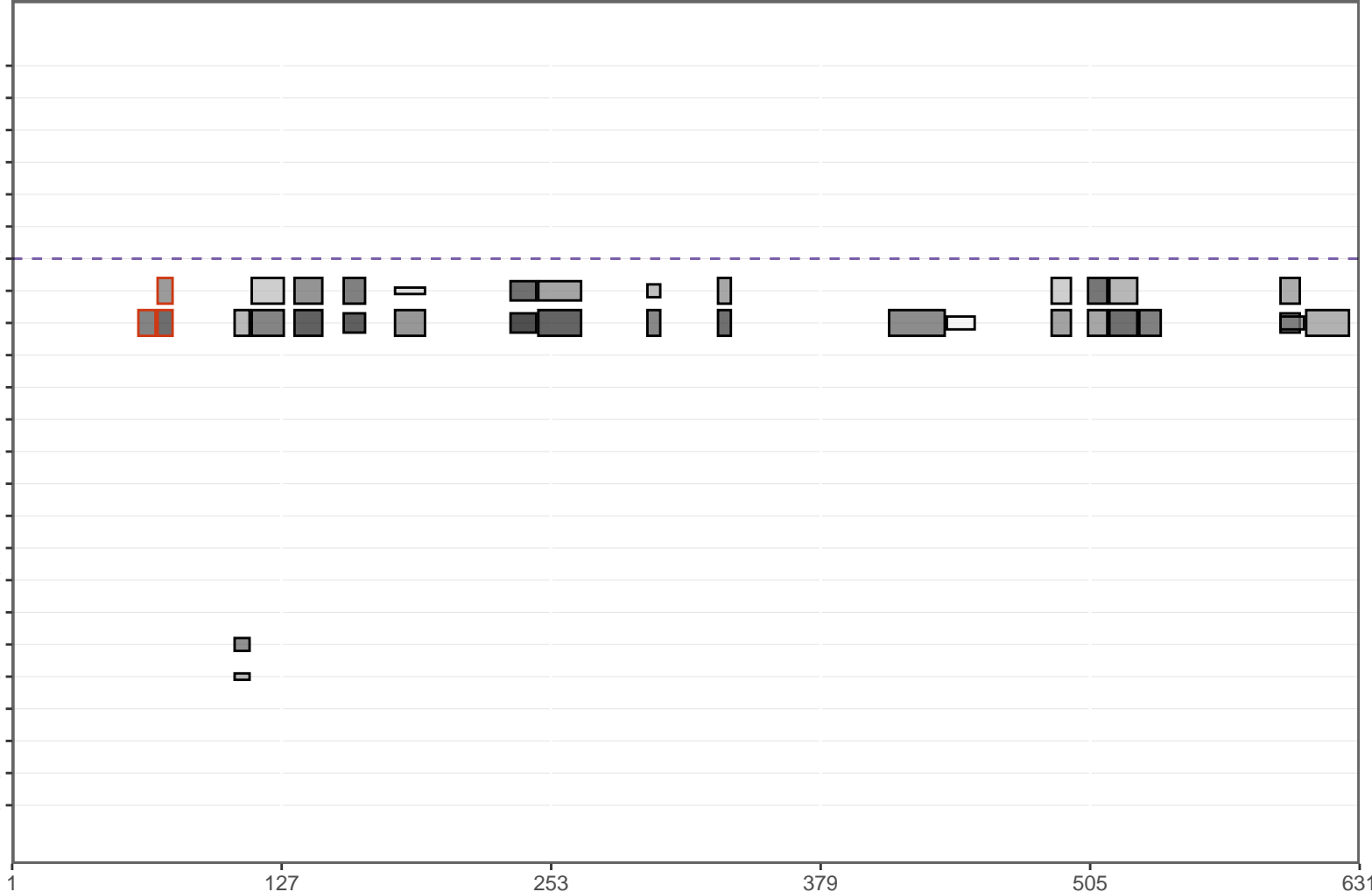
MW indication



Molecular weight

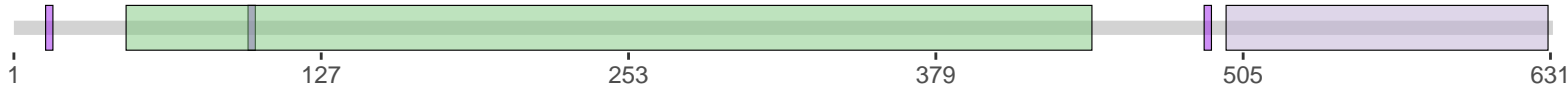


Gel Slice



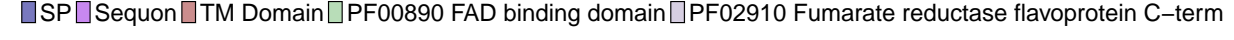
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SGILRNSEGERFMERVAPTANDLARDVVRSMTEIREGRGVGLKDHVYHLNHLNLPPEVLKERLPGISBETAIFAGVDVTKRNPVLPVYHYNMGGIPTNYHGEVVTKGDNDPAVVPGLMAAGEAGASVHGANRLGANSLLDVIIVFRGACANRVAEKRPGENKPKLEKDGERTIWLDKRIRNSNGSLPTSKIRLNMGRVMMQNNAAVFRTOETLEEGGGLDKTVEGFHDVQLKDRSLVWNSDUETIELENLHINAGITMHSAEARKRGAHAREDFTKRDEKVM

NbL19g01370.1 maf-like_protein_DDB_G0281937 [MW = 29.27 kDa]

No. of times detected



log(intensity)



Values from



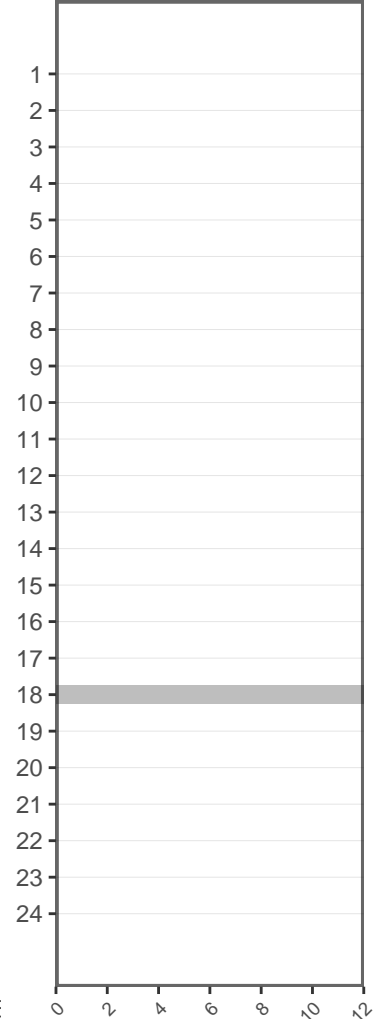
MW indication



Molecular weight



Gel Slice



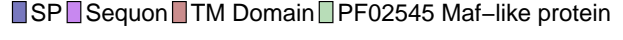
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

KADAMSRLETTDHLLEENTHPFLITADTVAWYGGHREKPKPSKKEARGPKSYSGGGQATVVGSEVVVTLNLTGIRKGAWERSEVVFHEIPDEVIDLIEEGHINWAGLMLKHPFLFPFDVTVGTADHVMGLRSLRTEKLQEAAL

NbL19g01220.1 laccase-11-like [MW - SP = 59.37 kDa]

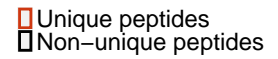
No. of times detected



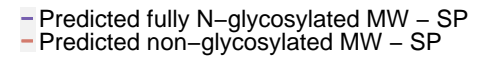
log(intensity)



Values from



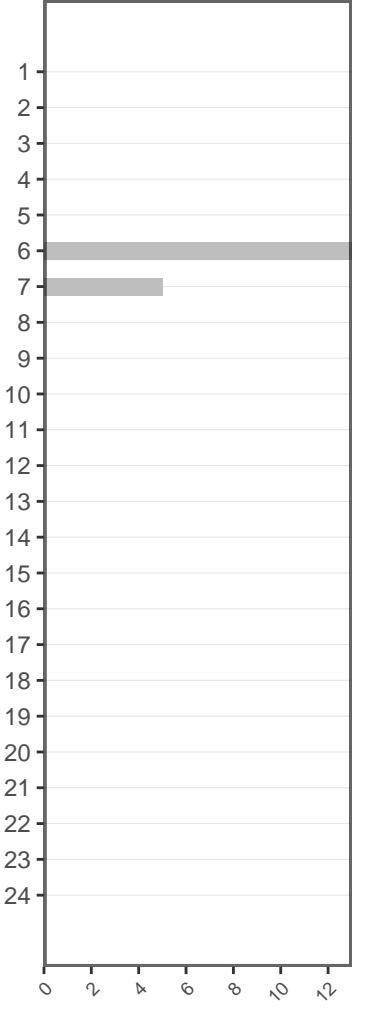
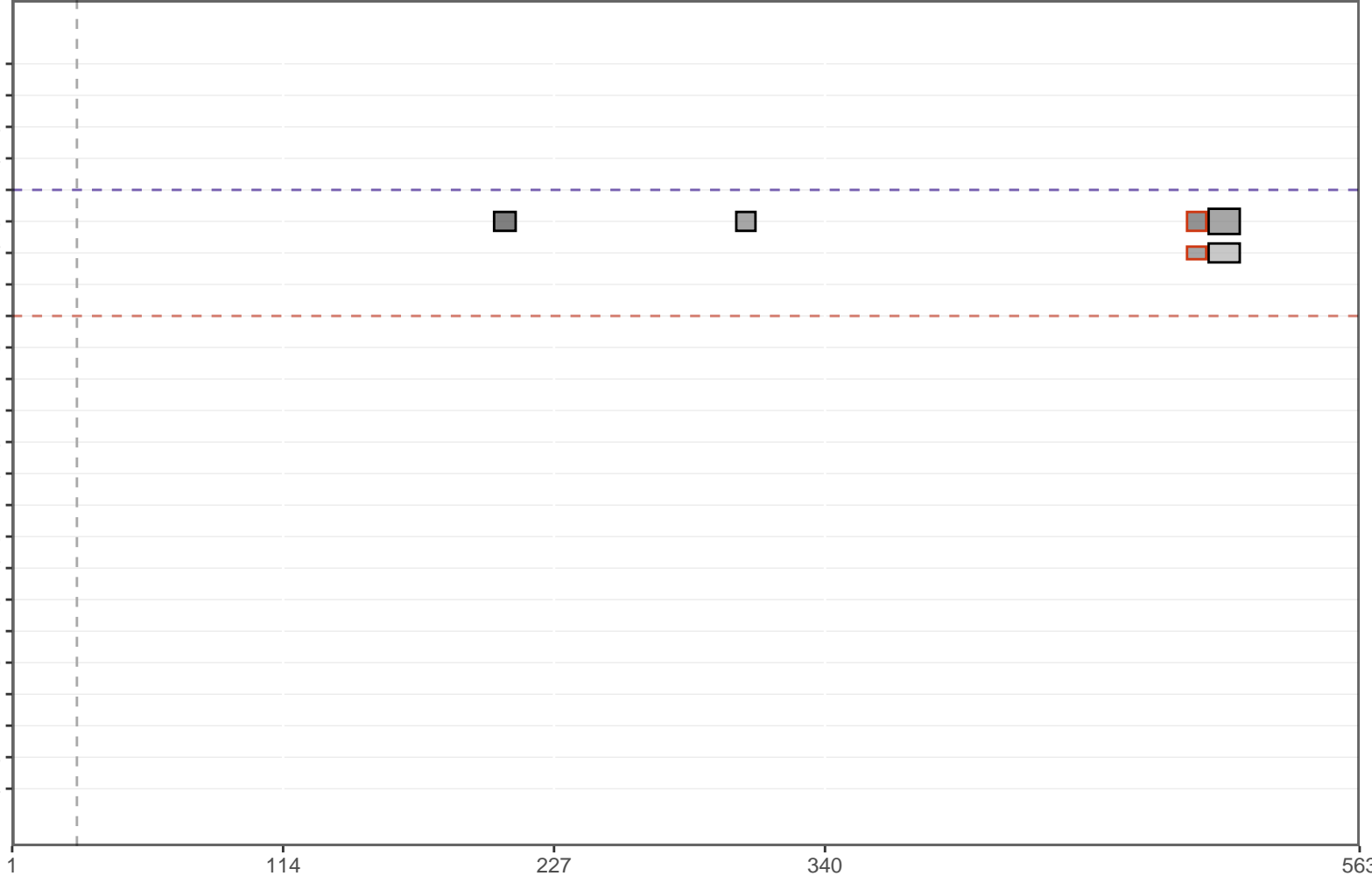
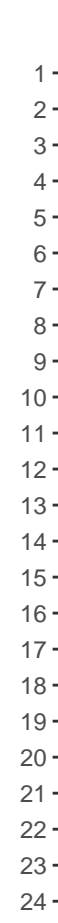
MW indication



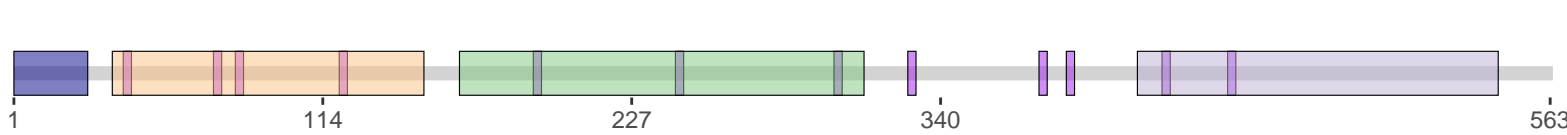
Molecular weight



Gel Slice



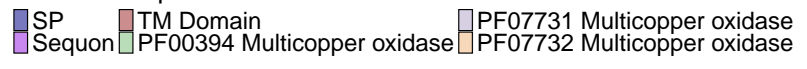
Protein length



Pfam domains



Pfam Description



Protein sequence:

IPQGTNLLVRSASVPGRFVMAARAFMDAPISVINKTATAIFGYPGIPESVLPKLPSPAGNDTDFALTYNEKLIKSLNTPKYPANVPLNVDRIHLFTVGLGHPCTCLNGTRLTASLNTFFSMPTALLGAIHYFNKGVYTPDFDKPPTFPNFTGAPLSTANLRTNLGTRLNKIAFNSTVELVIGDTNLLSEVSHPFHLHGYNFVAGTGTGSGNFDPKDPKYNLLIDPIERNTVGVPTGGWTAIRFRADNPNGVWFFHGHLELHFTGWLKTAFLVEDGPGSDHSLPPPKDLPRC*

NbL19g01150.1 soluble_inorganic_pyrophosphatase-like [MW = 24.07 kDa]

No. of times detected



log(intensity)



Values from



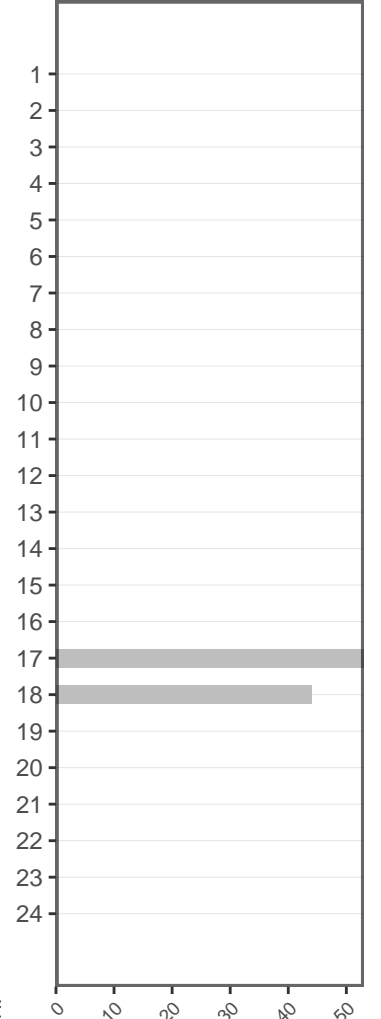
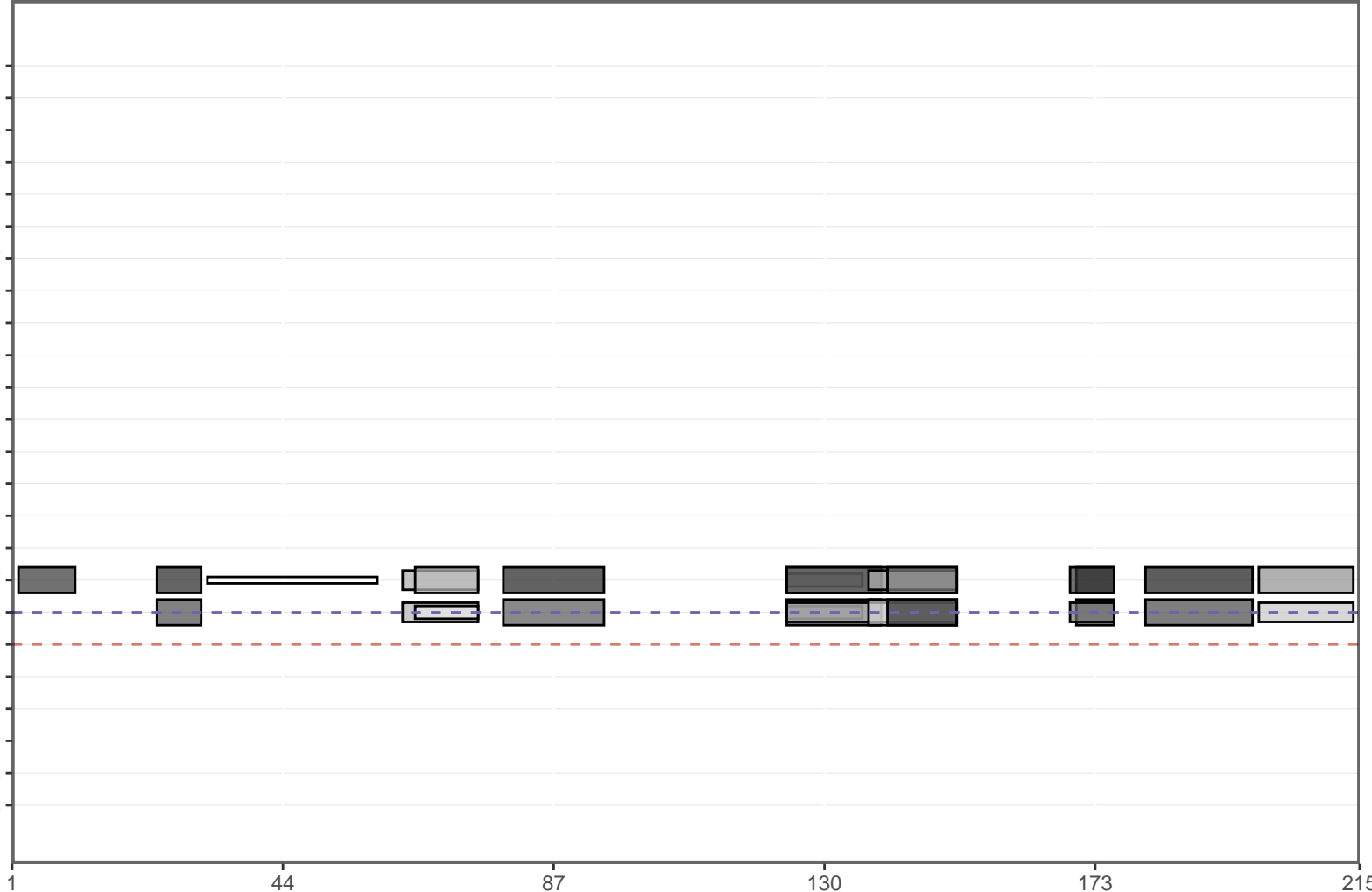
MW indication



Molecular weight

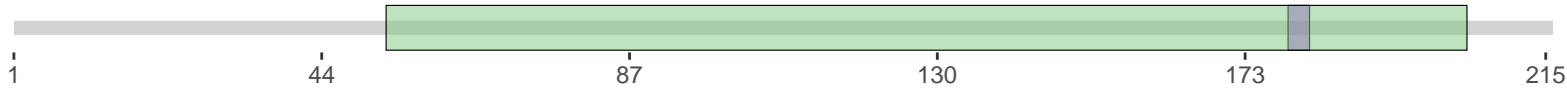


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

PRTICEDSDPMVLSLMGEPVLPSTFLRARAIQLMFMIDGEGKDKKIIVACADDFRFRIHYSIDKELPPHRLAEIRFFEDVKKNNENKSVAVEDFLPAKAAVDAIKYSMDLVAISYVEELRK

NbL19g01070.1 uncharacterized_LOC109238053 [MW = 53.01 kDa]

No. of times detected



log(intensity)



Values from



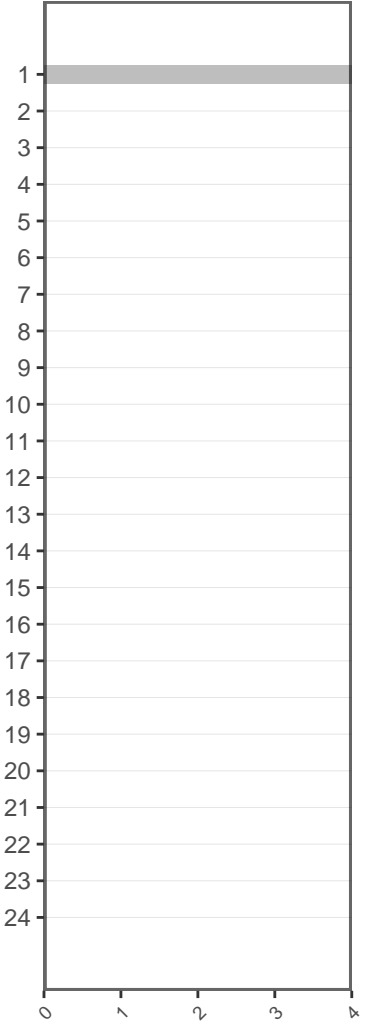
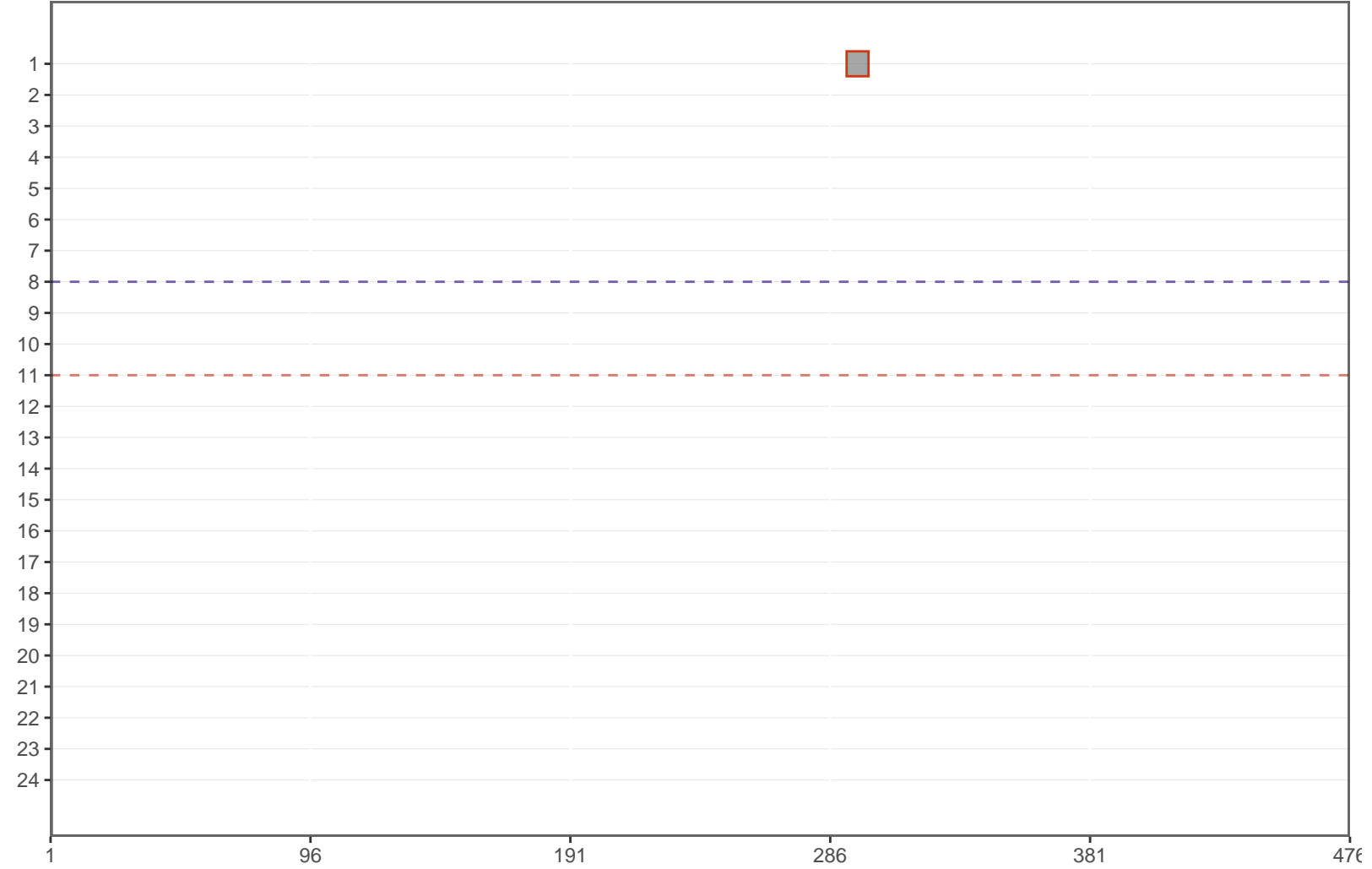
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

DDFFDPOEELSLVYKNGESENNGGLGRGVSAMTPLGEFYDAWEELSSGNGPQIPHTDFENELREIRLSLLMEIEKRKHVEEALGNMGTQWRIRQREQLSLVGNFFPCFPAAGDGLNEGLDQDVEDLFGQYHVRVFSDSIGRGIKAEVEIEMEAGIEKNIEMARLWDLKLNHYEAVNREMDSQRNGEAIETARRLRHRRKRRKQKWIWGSIAATITLGSVAWLWVYFSAERASSSSNGSHLEGDGTSEL

NbL19g00880.1 peroxidase_72-like [MW - SP = 33.81 kDa]

No. of times detected



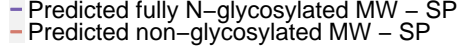
log(intensity)



Values from



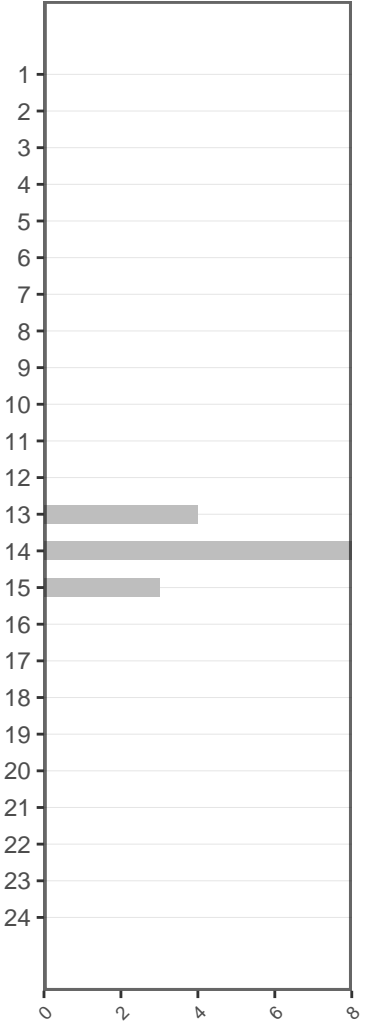
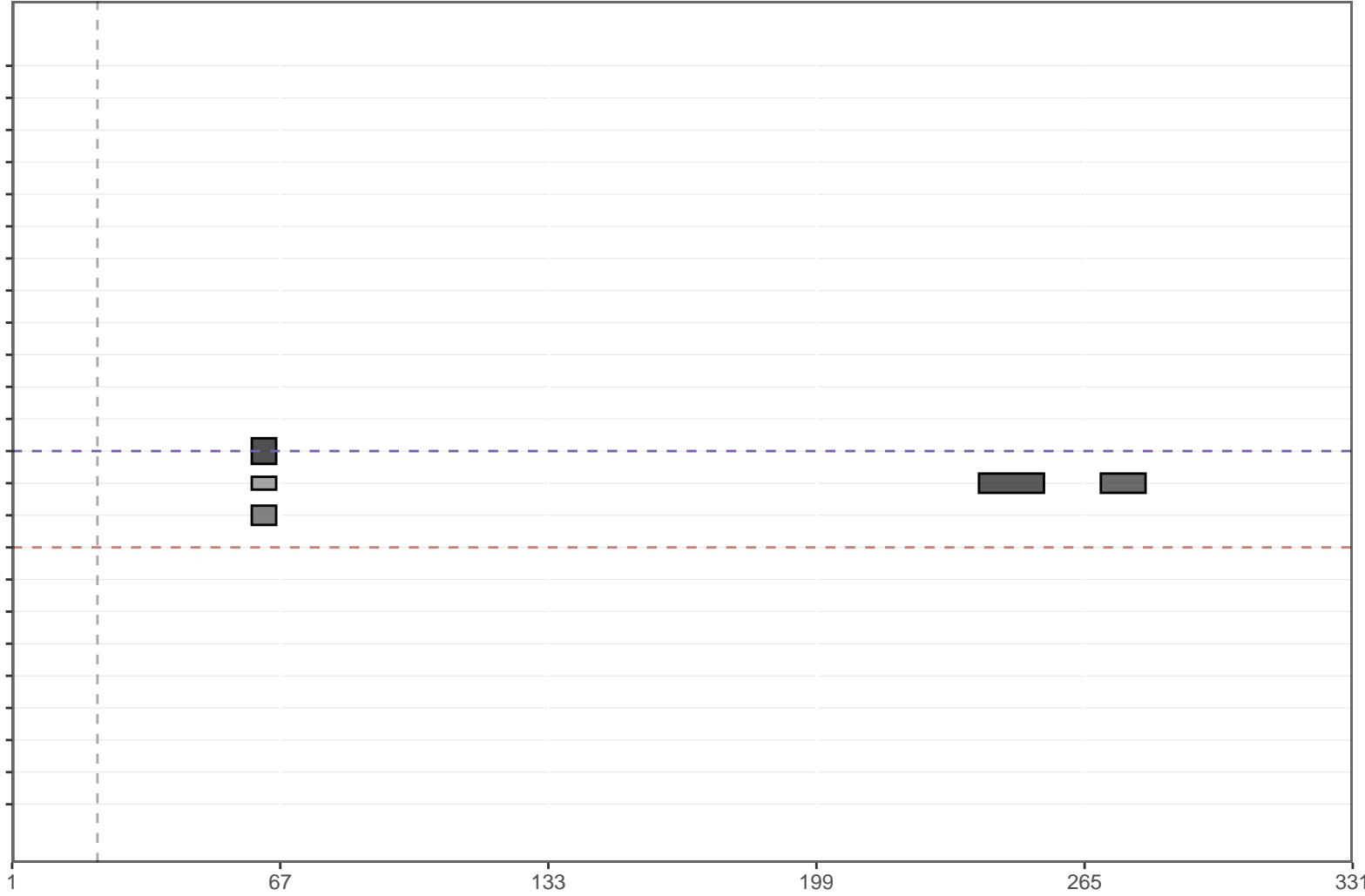
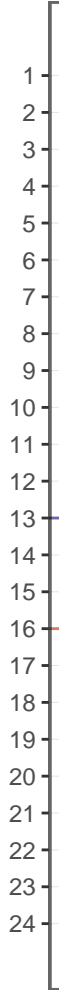
MW indication



Molecular weight

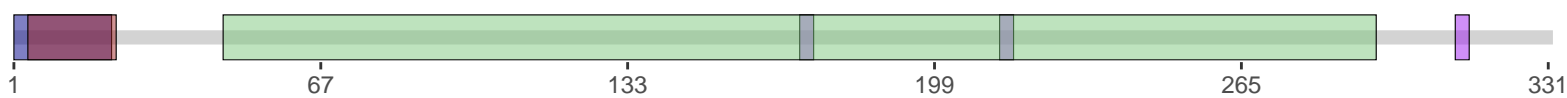


Gel Slice



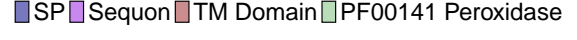
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

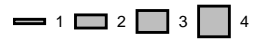


Protein sequence:

ISRSASLGGSNINIPFNNITFDTLKFKRQGLDLVLDVALSGSHIQRGRTSFRQRLVNDGSGNNQPDSTLDQSYAAGLRNRCPKSGGDDNIFLFDVSPFKFDNSVYFNKLLASGKLLNEDQVLAATKSGASLALVKGVAENNAFFEFHFAKSMVMKMGNSPLTGGSSGEIRKRCRMVY

NbL19g00840.1 CDK5RAP1-like_protein [MW = 70.67 kDa]

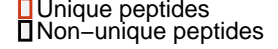
No. of times detected



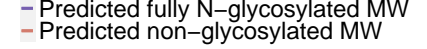
log(intensity)



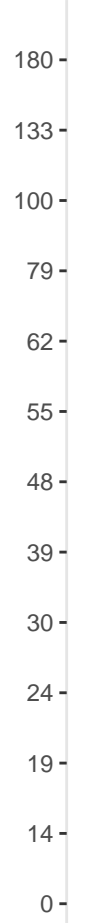
Values from



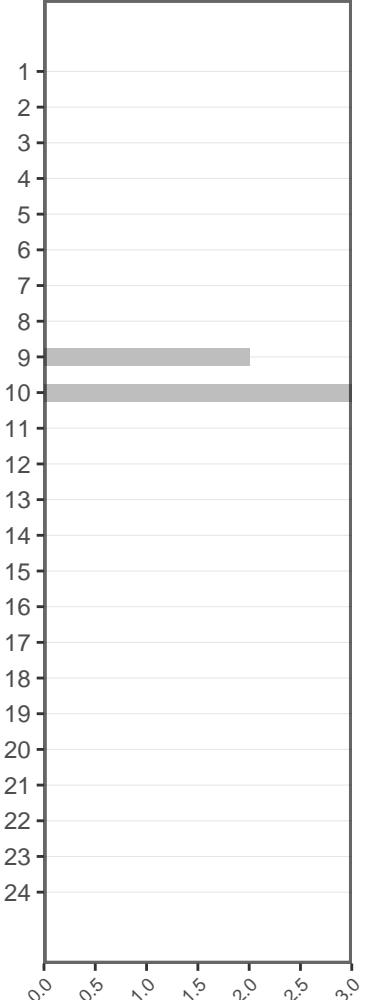
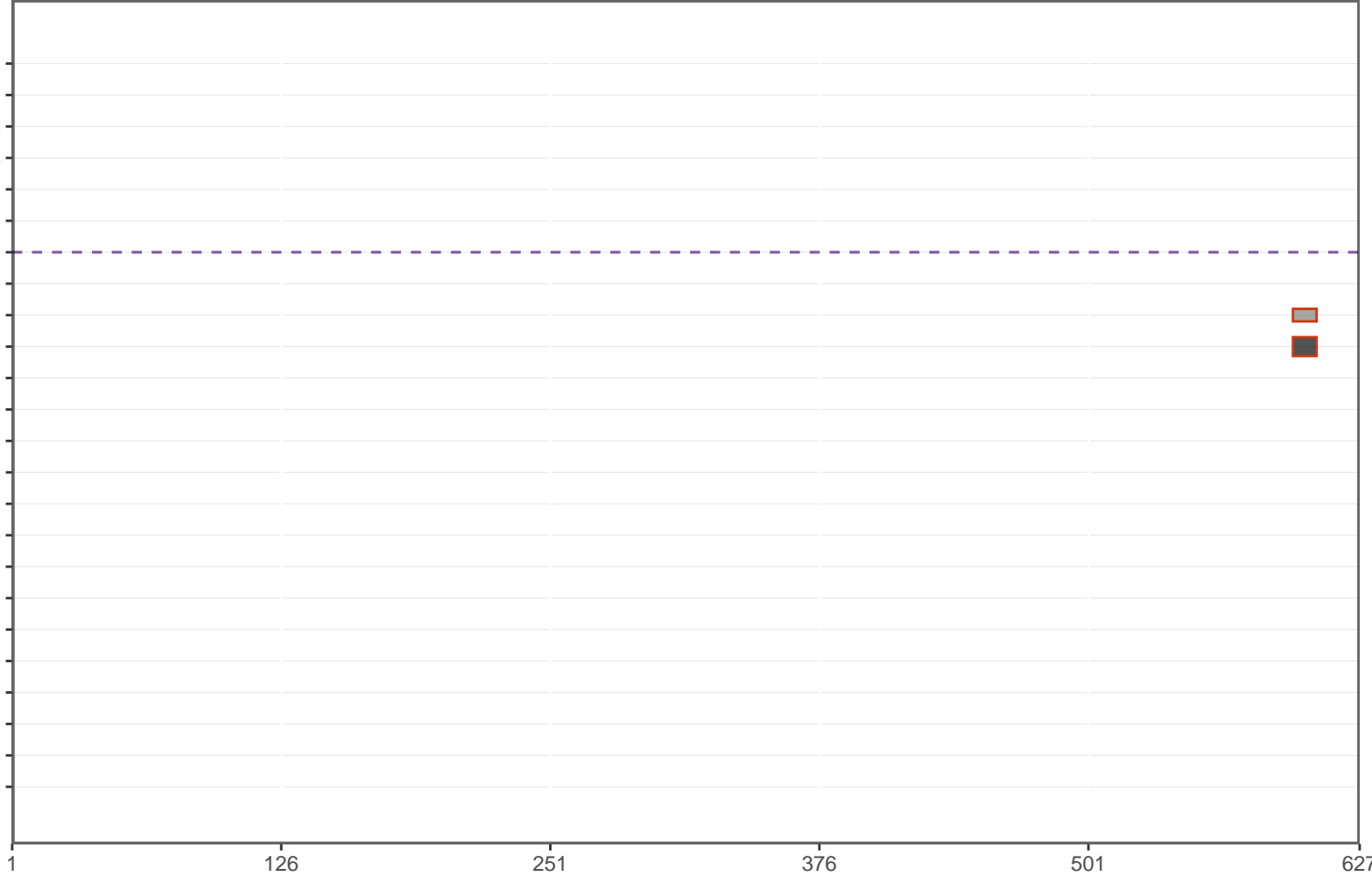
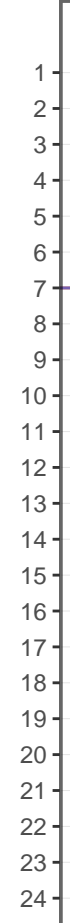
MW indication



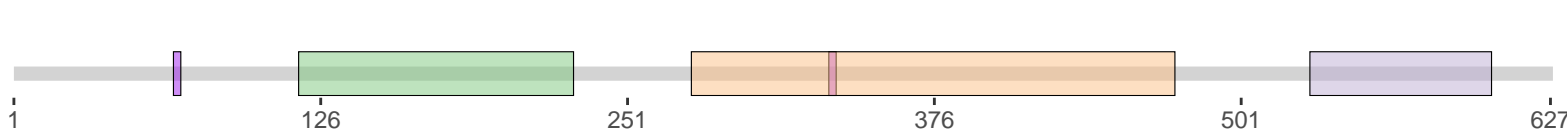
Molecular weight



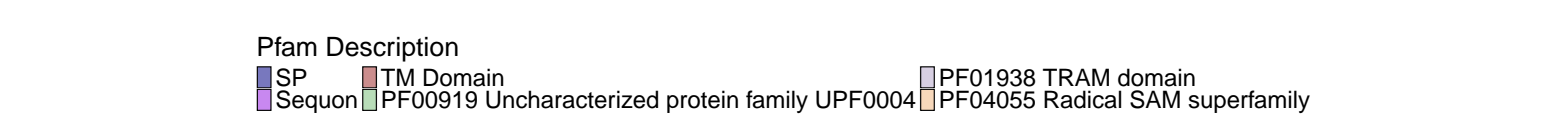
Gel Slice



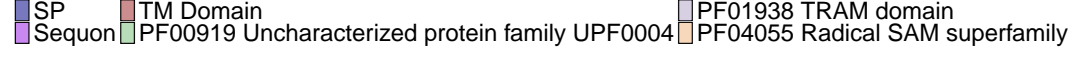
Protein length



Pfam domains



Pfam Description



Protein sequence:

ISRPVESIVKEVLELWKEGVKEVTLGGQVNSVNDTSQVENPKERFVSWELSDGFSMCKVYKHVGLRFADLLRLATEFFEMFRYTSHPKDFPDLLVYMRDRYVCKSHLFRGSGSSAVLERMRDGYTREAVLDLVKIRIDPDMGSSDFFGFCGETEEDHEDLGLVAVGYDMMVAFVSMREKTHAHRKYVDQDAPDQKQRRLTELEAFRGSTGGNYDSKIGTLGLVVEGPNKRAPDTELGKSGDRGRVGFANLFPDPKXVDNNGKRNPKGGDYVEVHTKST1

NbL19g00810.1 thioredoxin_H-type_2 [MW = 12.99 kDa]

No. of times detected



log(intensity)



Values from



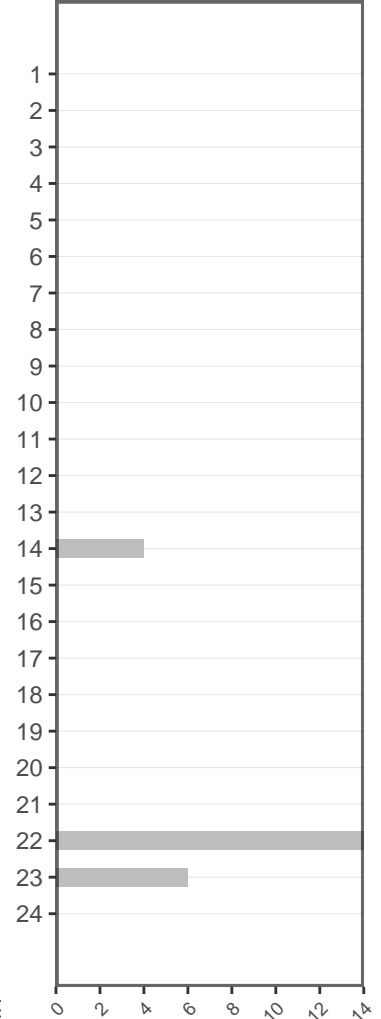
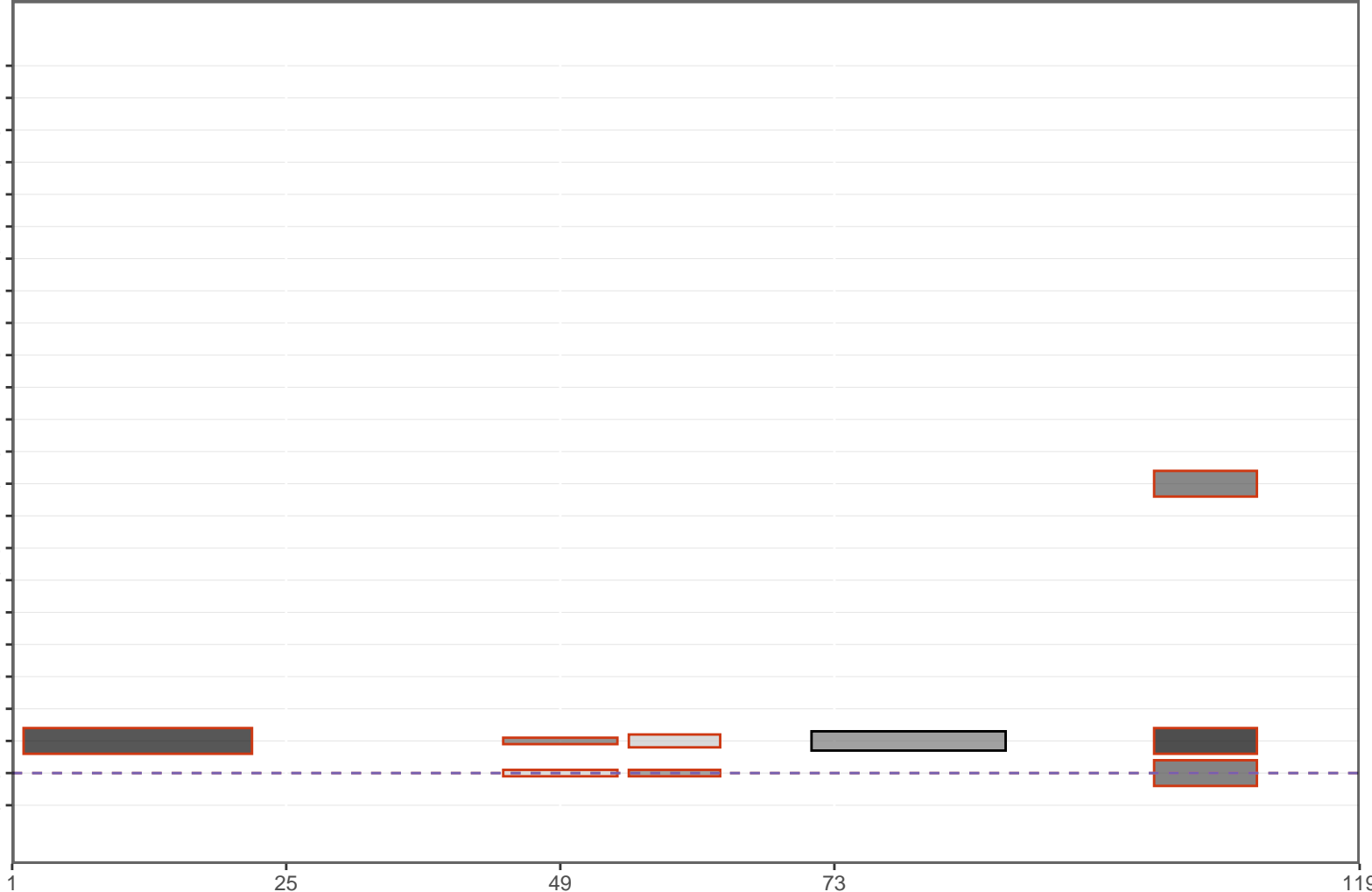
MW indication



Molecular weight



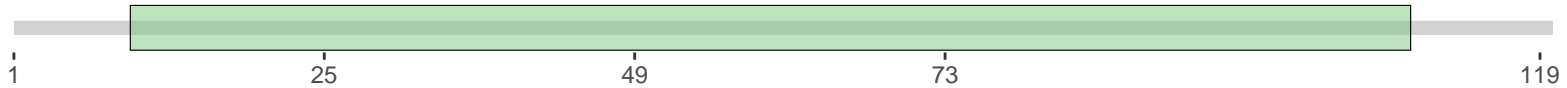
Gel Slice



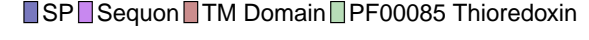
Protein length



Pfam domains



Pfam Description



Protein sequence:

APFFFAELAKKPTVYFLKIVDDELKSWTDWAVEAMPFFMLKEGKIVDKVAGAKKDELGGTAAKHSIGTSA*

NbL19g00680.1 fructose-bisphosphate_aldolase_1_chloroplastic-like [MW = 42.75 kDa]

No. of times detected



log(intensity)



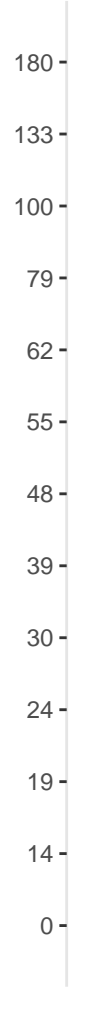
Values from



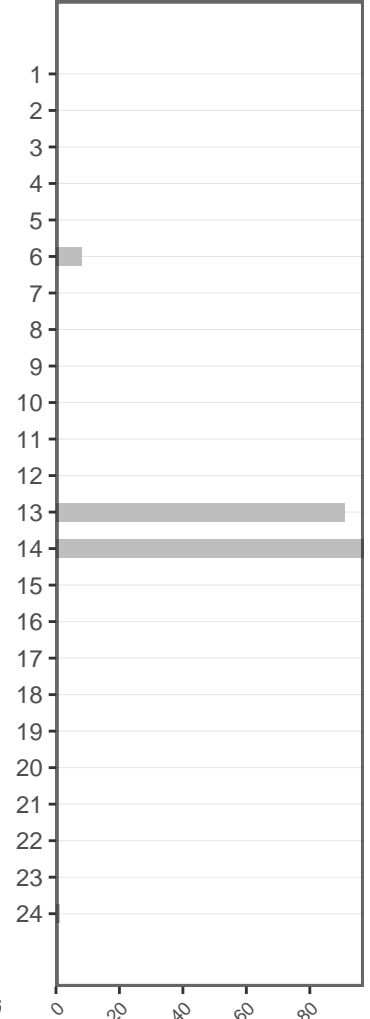
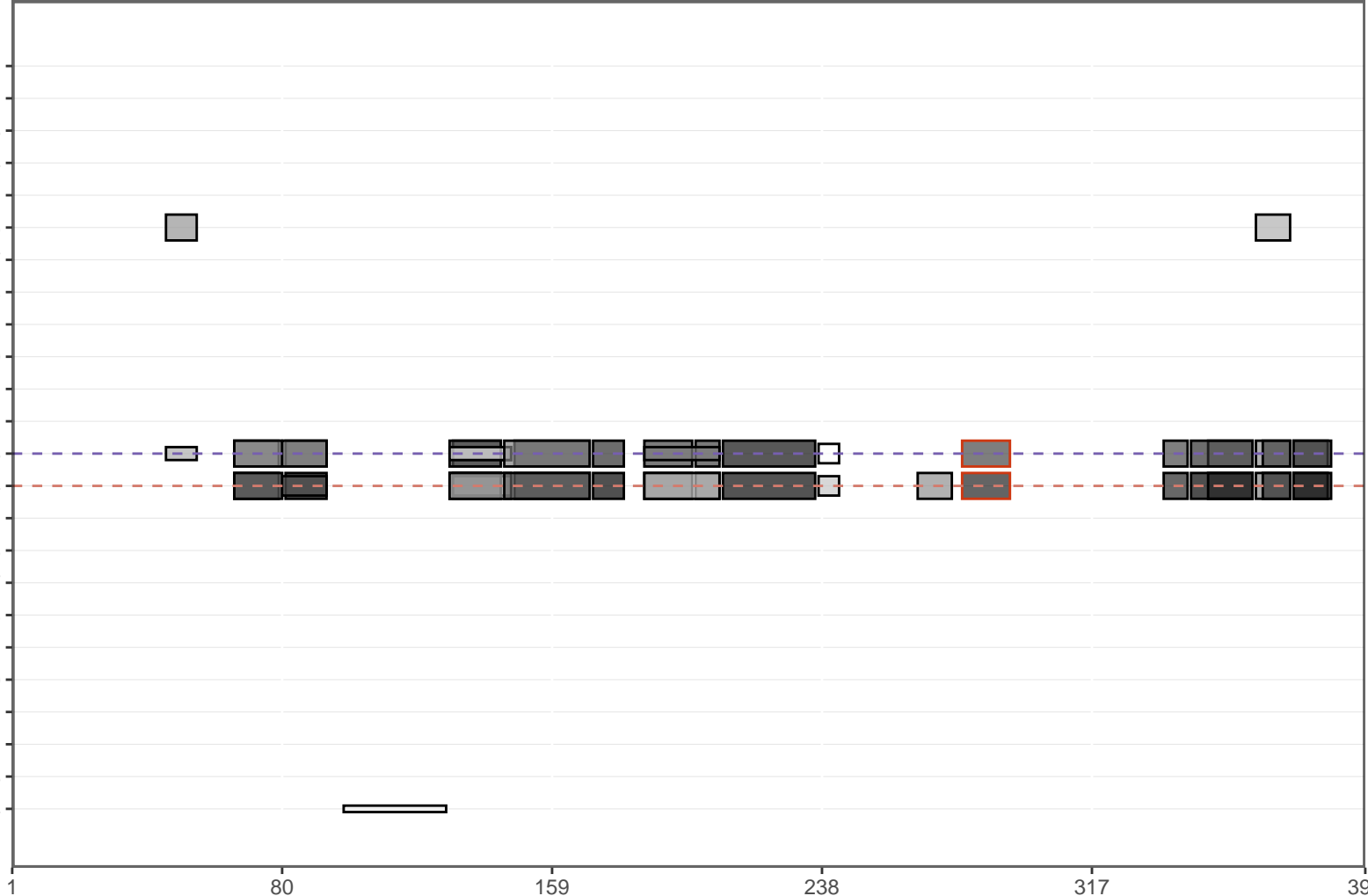
MW indication



Molecular weight

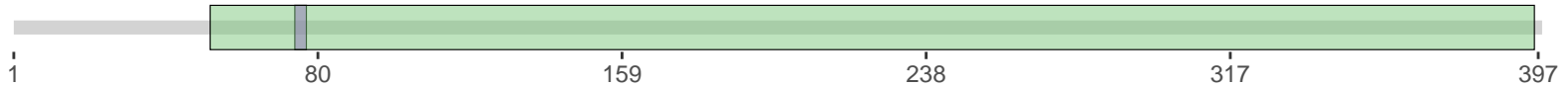


Gel Slice



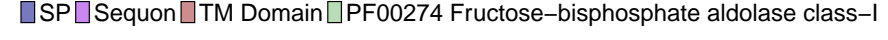
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

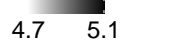
VVSIPIGPSALIVKEAAWGLARVAISGDNGLWPIVEPEILLDGEHNDIRTFEVAKKVVAEVFFVLAENNVMEFGLLKPDMVTPGAEGERATPHQVDYDTLNLRLRQRPVPGIMFLSGGGSEVEATLNLNAMNGGNPWHVFSFYARALQNTGLKTKTWGRPENVAQAEALLVRAKANSLAQLGKYTGEGESEEAANKGMFVKGIVVY

NbL19g00300.1 50S_ribosomal_protein_L3_chloroplastic [MW = 30.03 kDa]

No. of times detected



log(intensity)



Values from



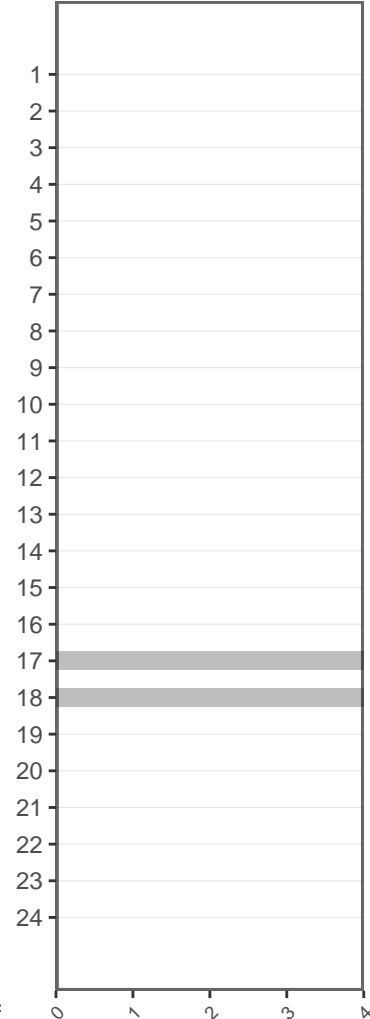
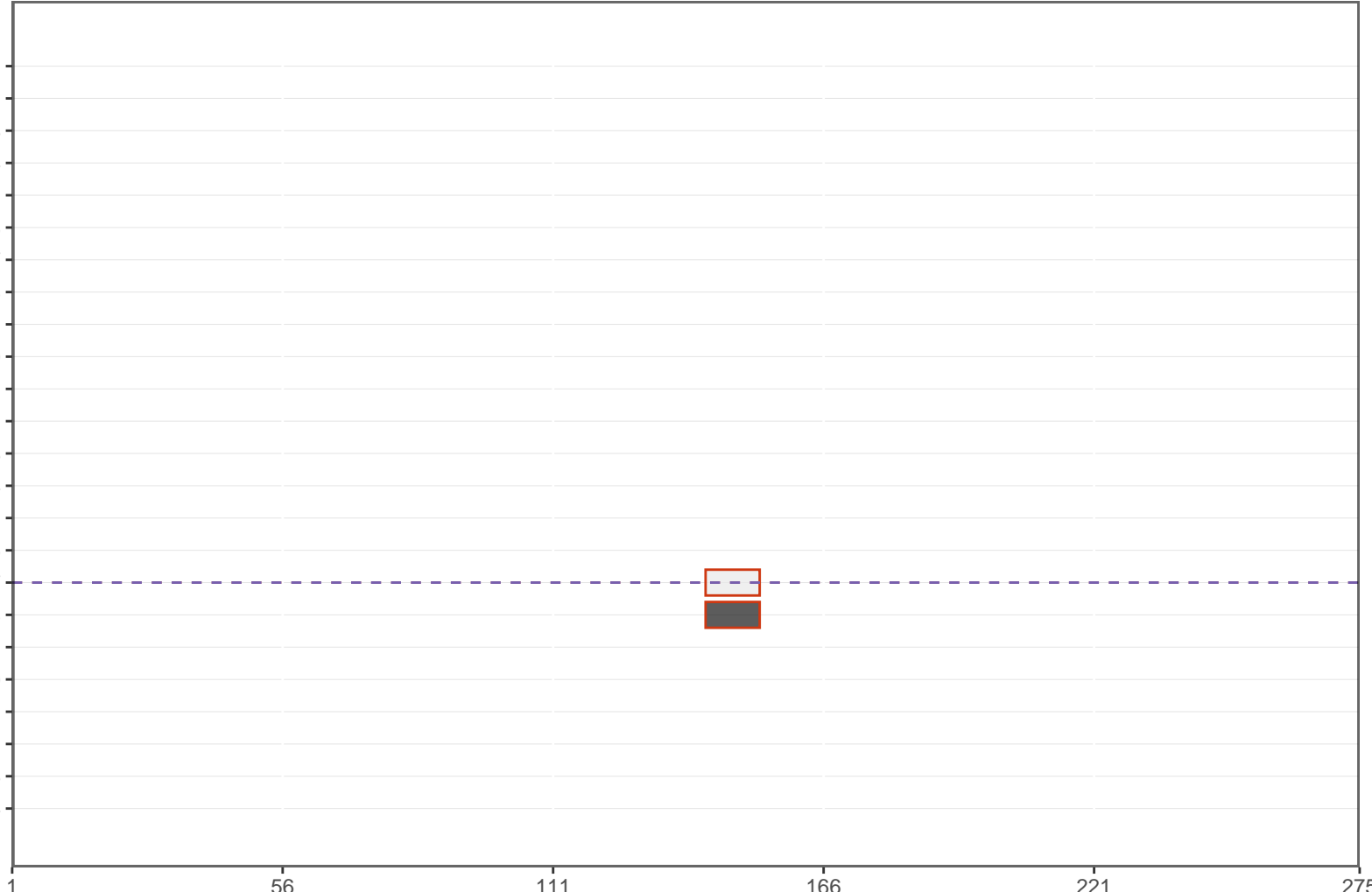
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

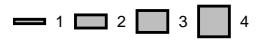


Protein sequence:

SHLEKSGIPLRLQEFRLGGIDGFEVTKQLDFGELFKEGDLVDSGTTGKGFQGGKRRHFKRGGMTHGSKSHRQLGSGAGTTPGRVYKGGKMPGRMGSTKRRKIRKLIKVKDDDLNIMIKGALPGKPGNLLRIAPKIVGKNPKV

NbL19g00260.1 zinc_finger_CCCH_domain-containing_protein_44-like [MW = 30.62 kDa]

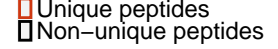
No. of times detected



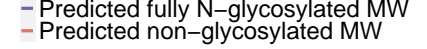
log(intensity)



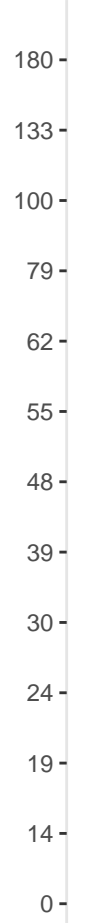
Values from



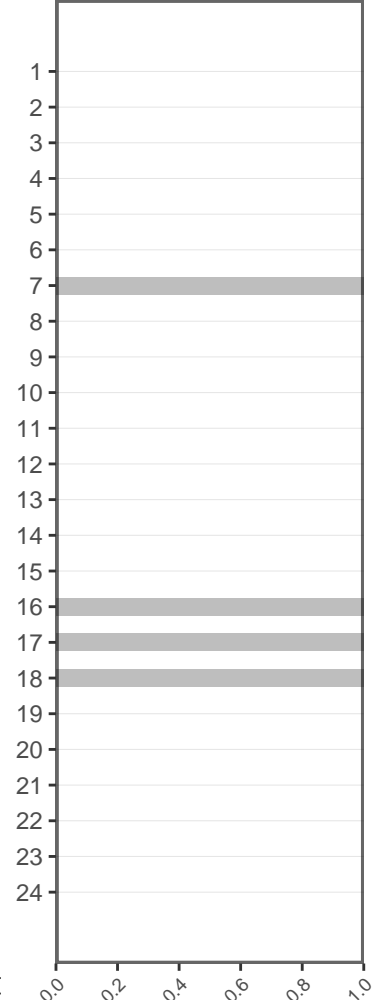
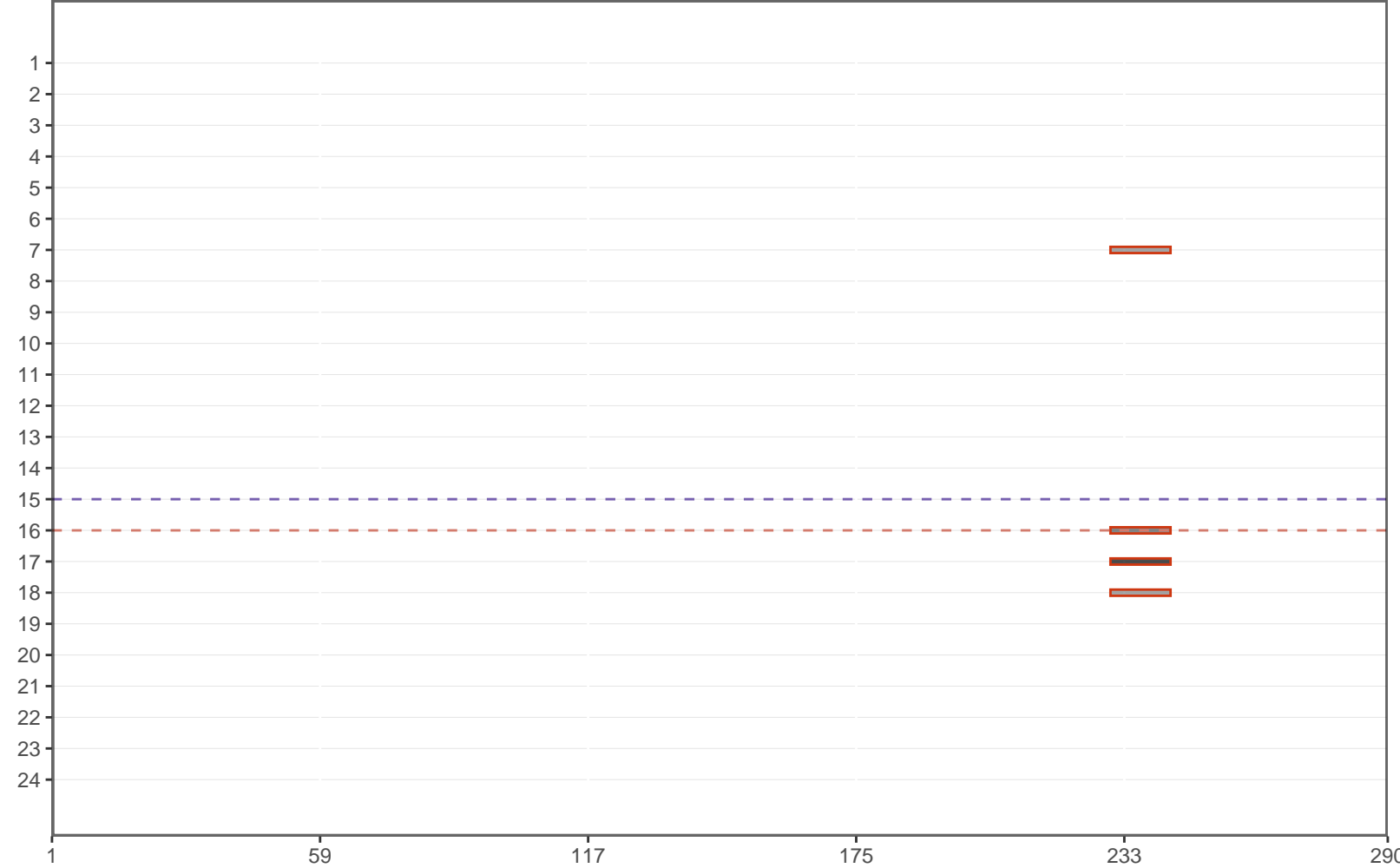
MW indication



Molecular weight



Gel Slice



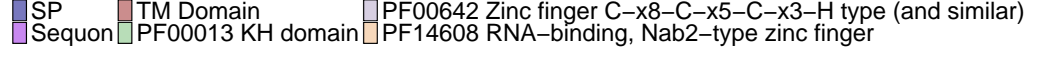
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

[APVYDDFGAAGPPEPRFFDGHKPKGQPRMATNFGASATTTISIDAAAGTIGRNGVNSKIGKRLTGVLSEKDHETDSNRRNELOGTFDQINGASAMVREIHSNVTPTGGPKNTGPFARGPAGPFKTKMCSNFSKSGSOTFGKCKHFAHGASELQKPLA]

NbL19g00190.1 protein_GrpE-like [MW = 42.46 kDa]

No. of times detected



log(intensity)



Values from



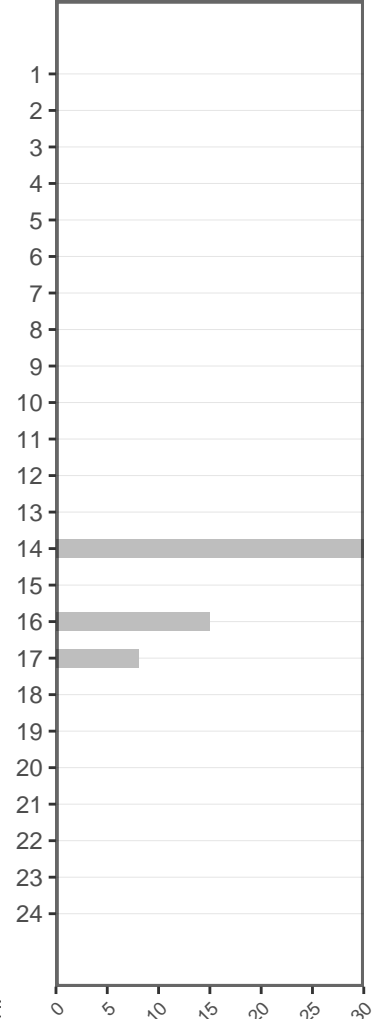
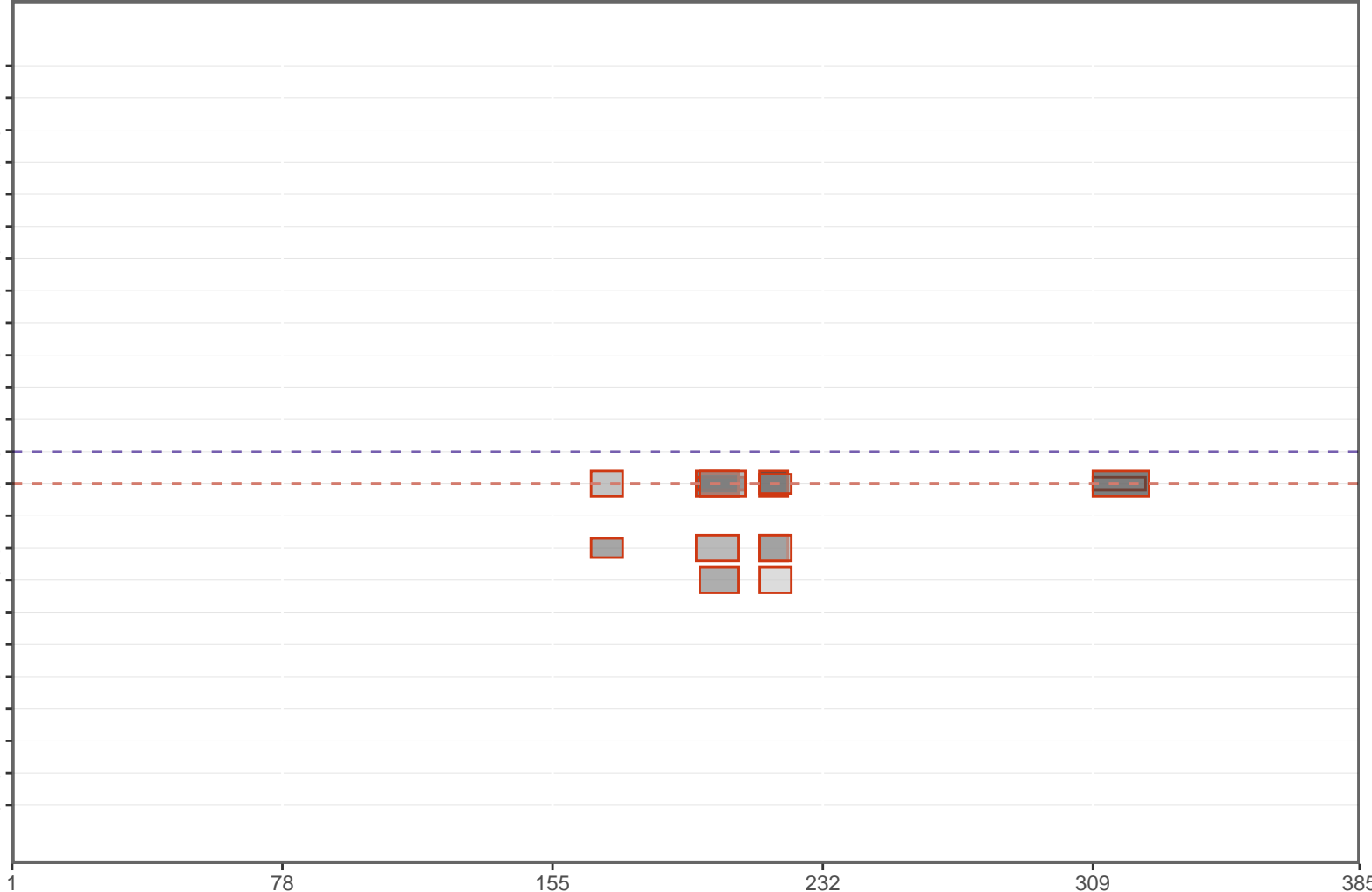
MW indication



Molecular weight



Gel Slice

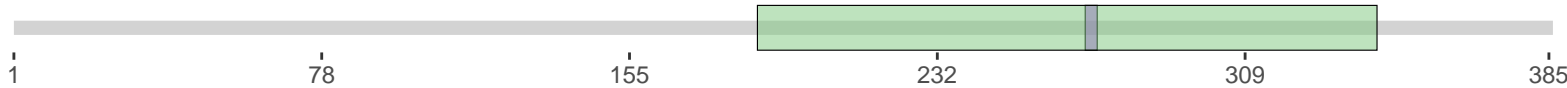


Peptide counts over 4 repeats

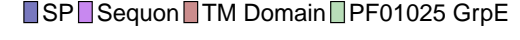
Protein length



Pfam domains



Pfam Description



Protein sequence:

ISLKSIEIKELORVKVABLTLEELSSERDRVLRISADFNFRKRTERERLSLVTNAGGEVVEKLLVLDINFERAKMQKATEEGEEKINNYGSIKGFGEKLSGLGVETVDTVYKPFDPRLLEHAIMRDESEEFEEGVLEEVKIKFKLGDRLLRPSMKVYSAGPGKPKETAEPKKEEQHKVVEEKSEEGTATAGDEGTGEGGN

NbL19g00170.1 replication_protein_A_14_kDa_subunit_B-like [MW = 14.75 kDa]

No. of times detected



log(intensity)



Values from



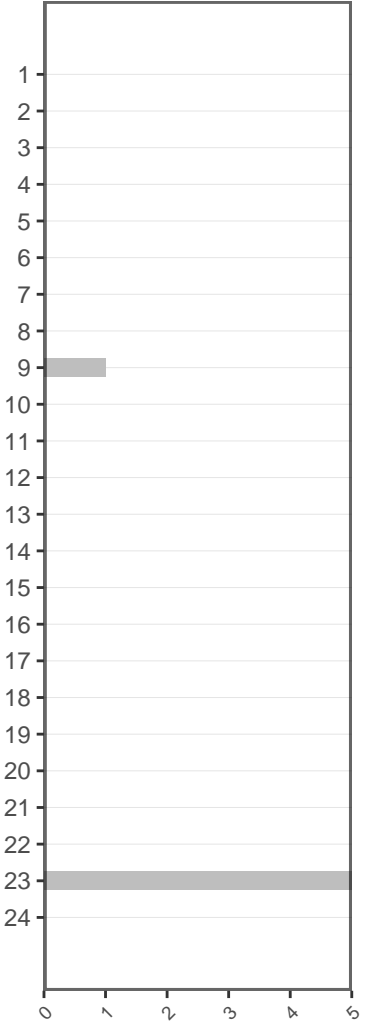
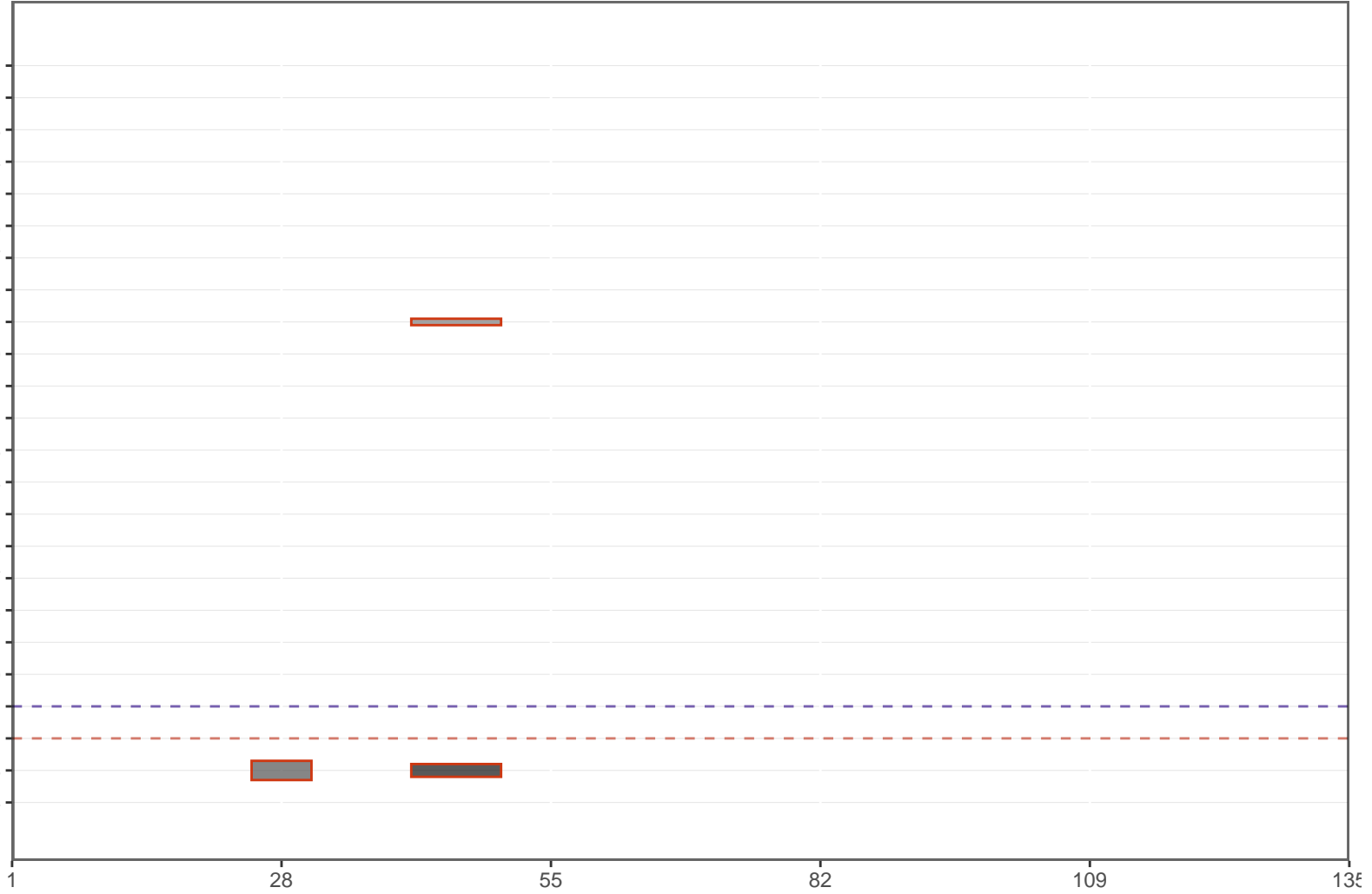
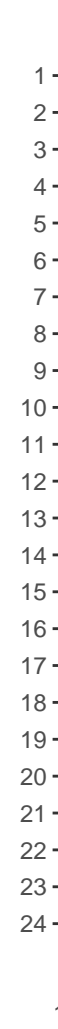
MW indication



Molecular weight



Gel Slice

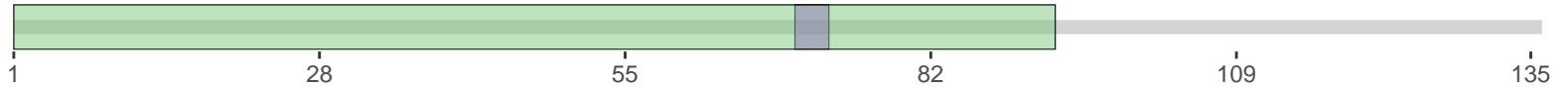


Peptide counts over 4 repeats

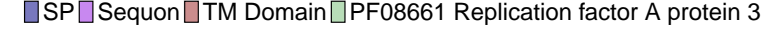
Protein length



Pfam domains



Pfam Description



Protein sequence:

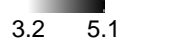
PGPLTTFVEVIGADENSGRAEWSNFGDTLGLTLDHSMNFDNVLSHVGRWVWVNYDQFLGLLGVGSALAKKFTNDL*

NbL19g00150.1 BRASSINOSTEROID_INSENSITIVE_1-associated_receptor_kinase_1-like [MW - SP = 21.02 kDa]

No. of times detected



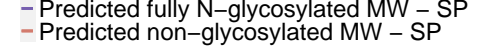
log(intensity)



Values from



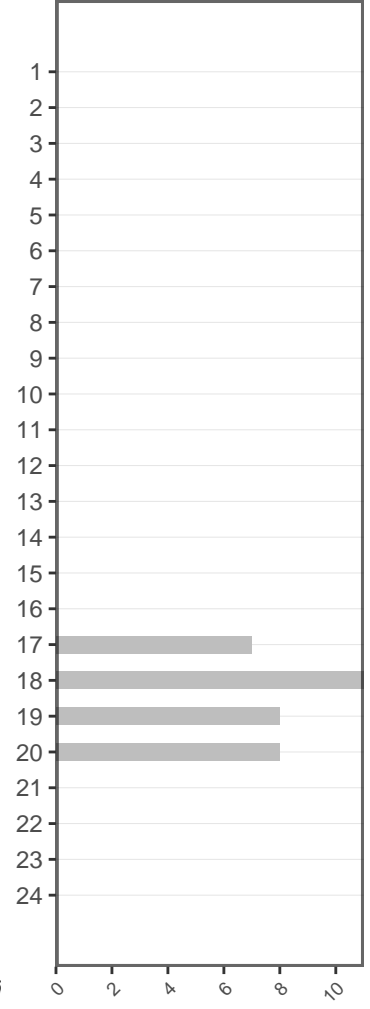
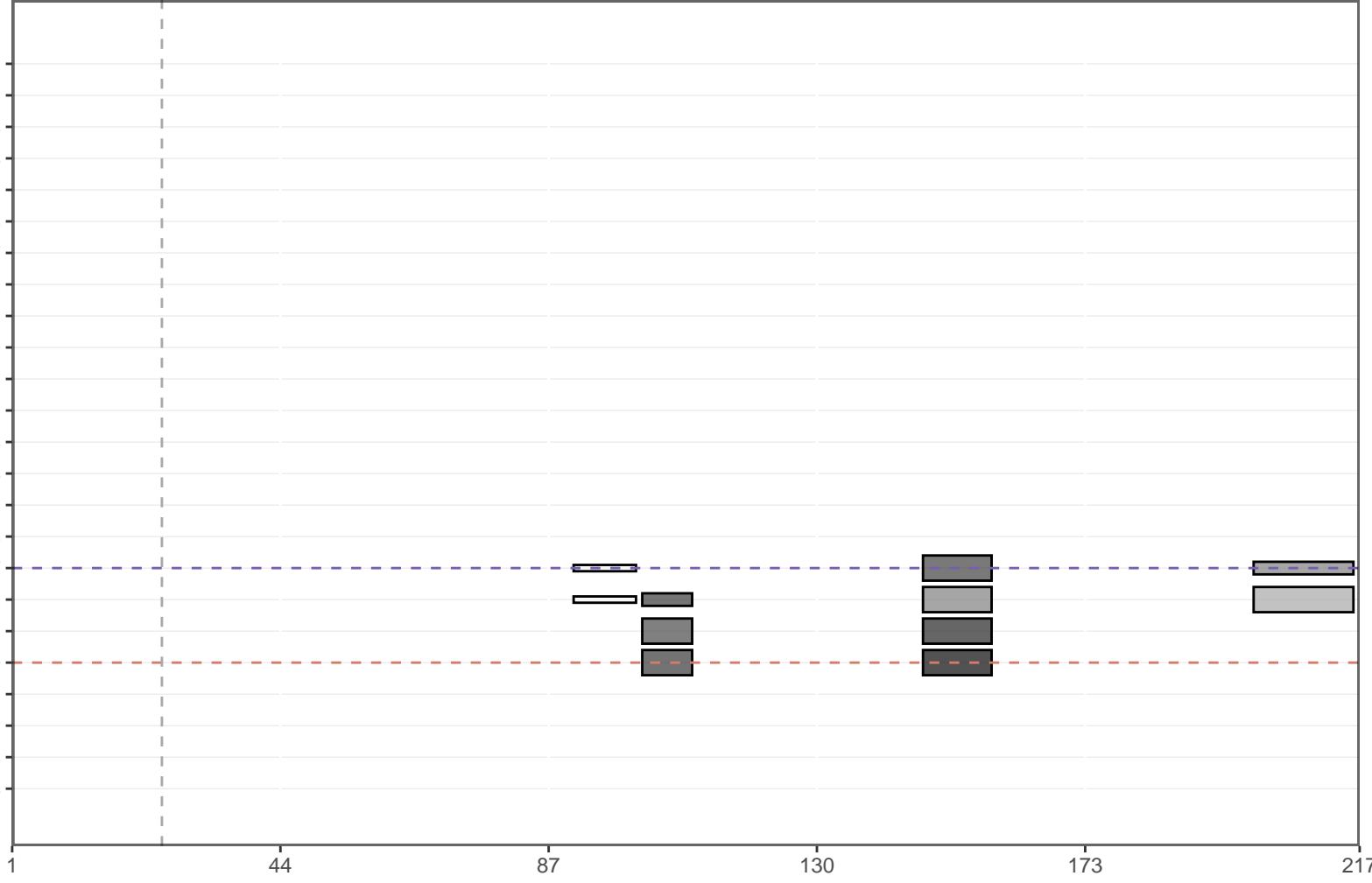
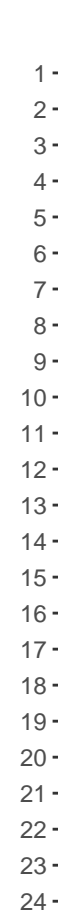
MW indication



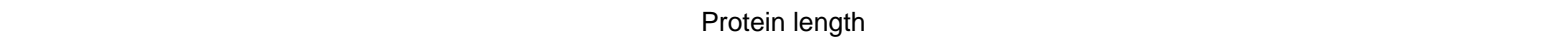
Molecular weight



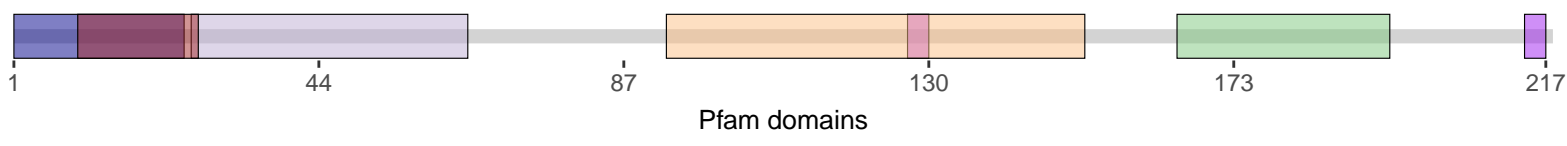
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

IQYLYLYKYNIGDTPKELGNLKBUSLSDLYNNINSGTIPPSLGLKLNLFRLNDNDLGTGPIPRELSSVSLKVVQVDSNNLGGTPTTSGPFEHPLNFEHNPRLEGPELLGLASVDYDNGS

NbL19g00140.1 glycine-rich_RNA-binding_protein_2_mitochondrial-like [MW = 29.7 kDa]

No. of times detected



log(intensity)



Values from



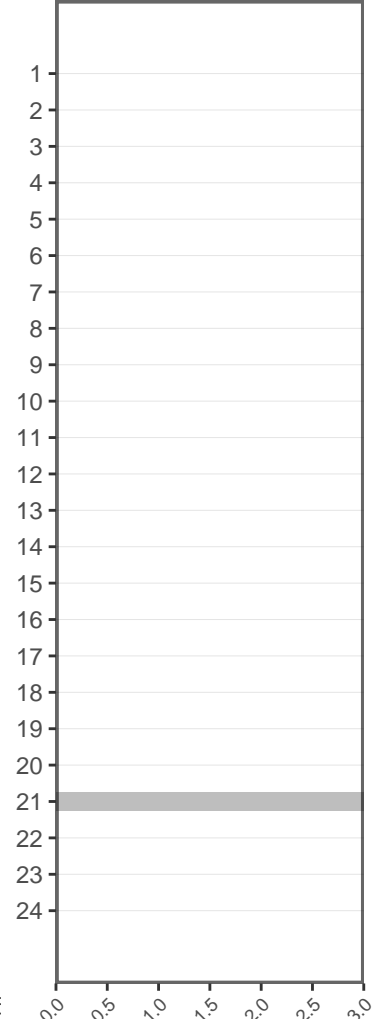
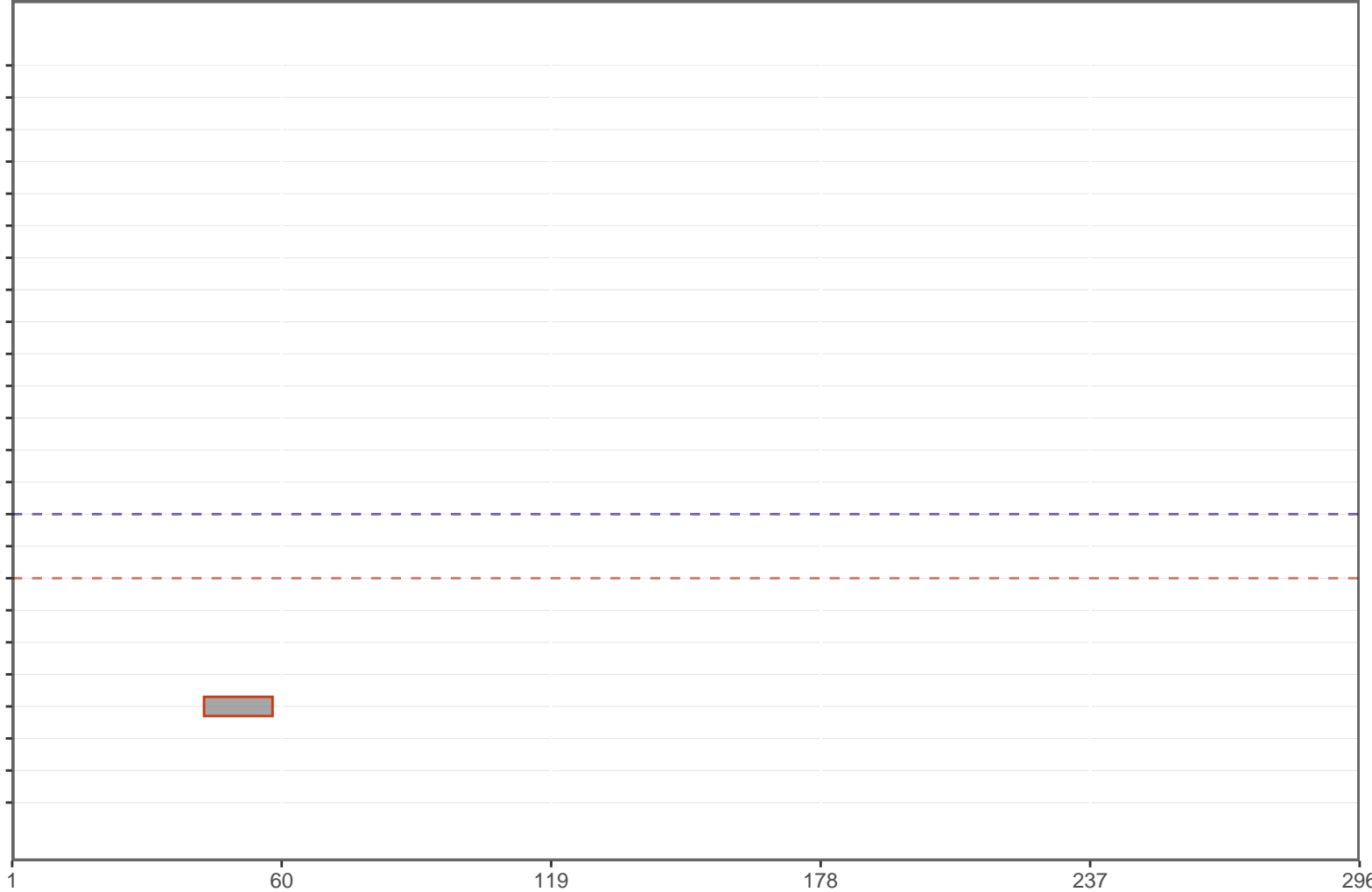
MW indication



Molecular weight



Gel Slice



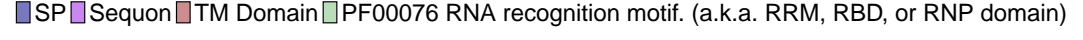
Protein length



Pfam domains



Pfam Description



Protein sequence:

GGFGAGGYGGGNYAGGYGGGNYAGGYGGGNYAGGYGGGNDVVTGSGYANNYTGSESSFGFGTSGGNFFSGDGYAENQNLDMAAAGSDTYGTGEAANSFTSSFGNDQFGNVDTSNQAETGDVNSPVDAGEDYRDDNVEGGDANRRV

NbL19g00110.1 50S_ribosomal_protein_5_chloroplastic-like [MW = 15.98 kDa]

No. of times detected



log(intensity)



Values from



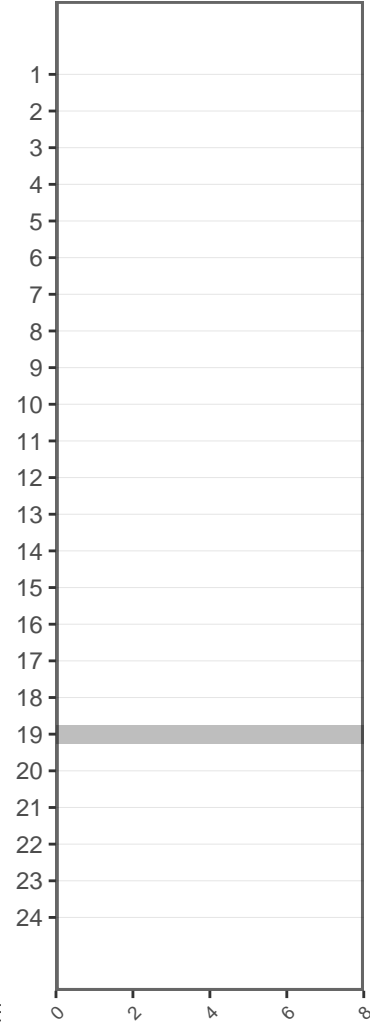
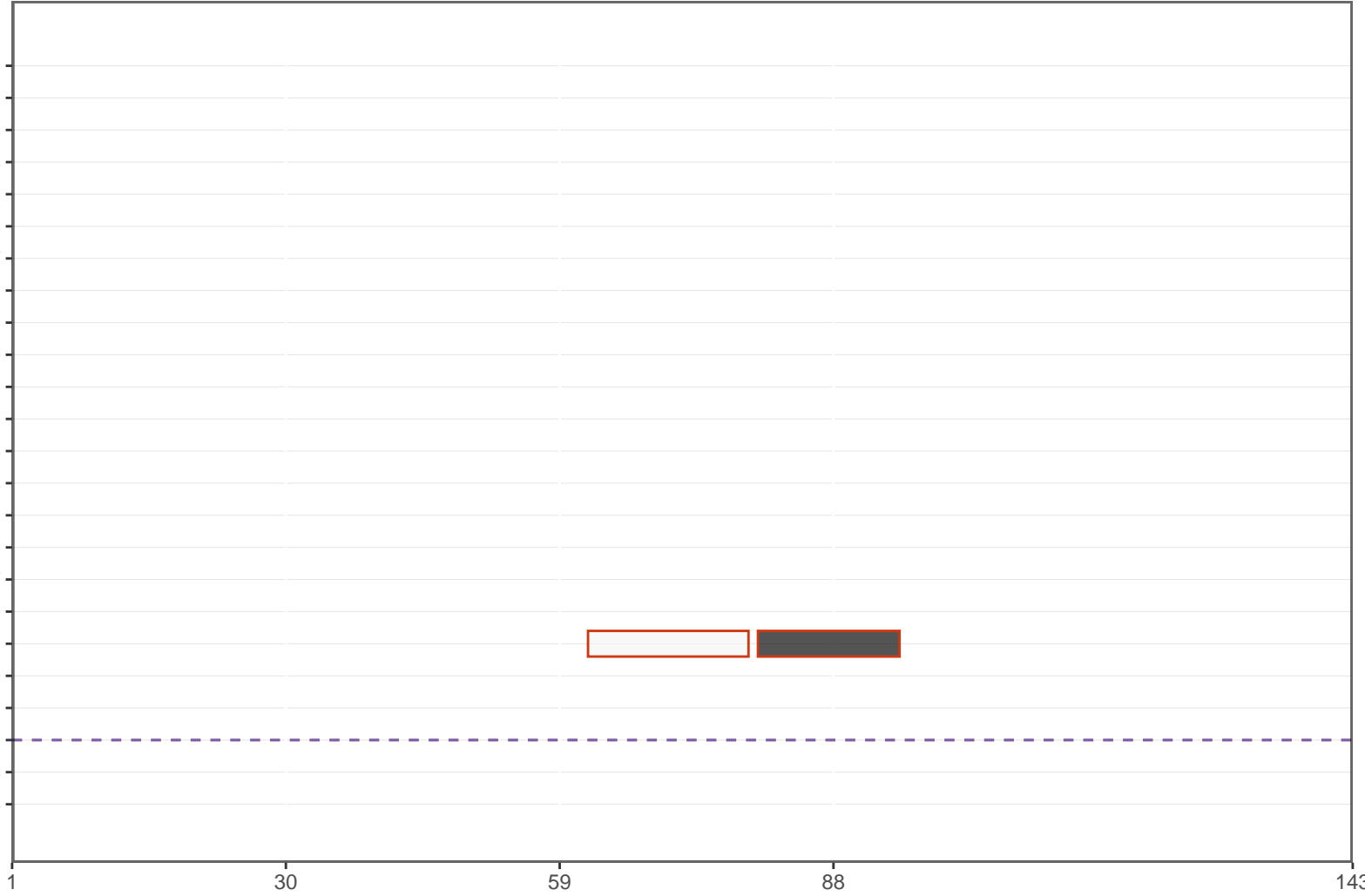
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

GAADIDVGSNDNPEPAPKNEEESVPVENLPLEEKLOGKLDQKMMKLAQKRLRLRKRHLRKKGRWPPSKMKNKNV

NbL19g00100.1 splicing_factor_3B_subunit_1 [MW = 141.25 kDa]

No. of times detected



log(intensity)



Values from



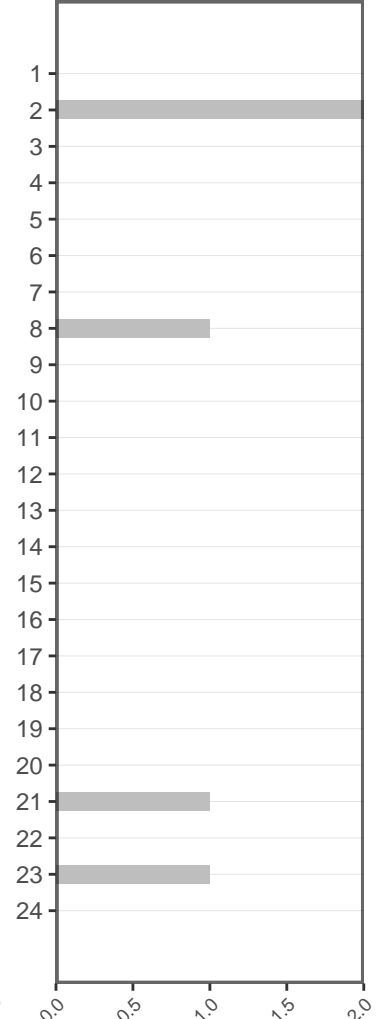
MW indication



Molecular weight



Gel Slice



Protein length

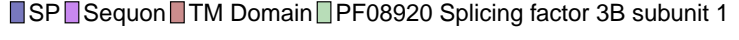


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KSIWQARHITGKIVGGIALLGCAVPLHRSLRVEIHEHGLDENGKVRITITALLSALAEAAAPYGESFDSVLKPLWKGIRSHRGGVLAFLKAGRIPLMDAVYASVYKVEVMVILREFGSPDEEMKKVKKVKGCCVSTEGVEPDIKRDILPEFFRNFWRRMALDRRNKQGLVETTVKIANKVGVDIVGRIVEDLKDSESEPYRRMVMETIEKVVANLGAASDIDRLLELLDGLVAFGEQTSDDANMLNFGAVWVNALGGRVKKPKLPGKGTIKWRLNKKSAKYRQQAAADI

NbL19g00040.1 phytanoyl-CoA_dioxygenase [MW = 32.09 kDa]

No. of times detected



log(intensity)



Values from



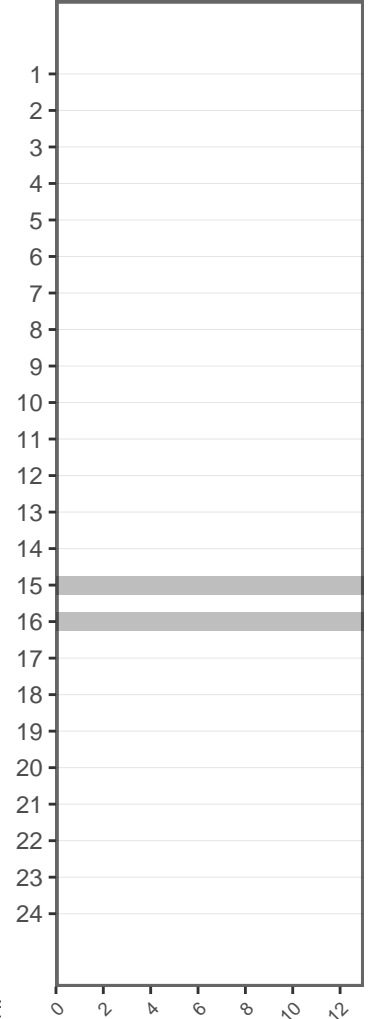
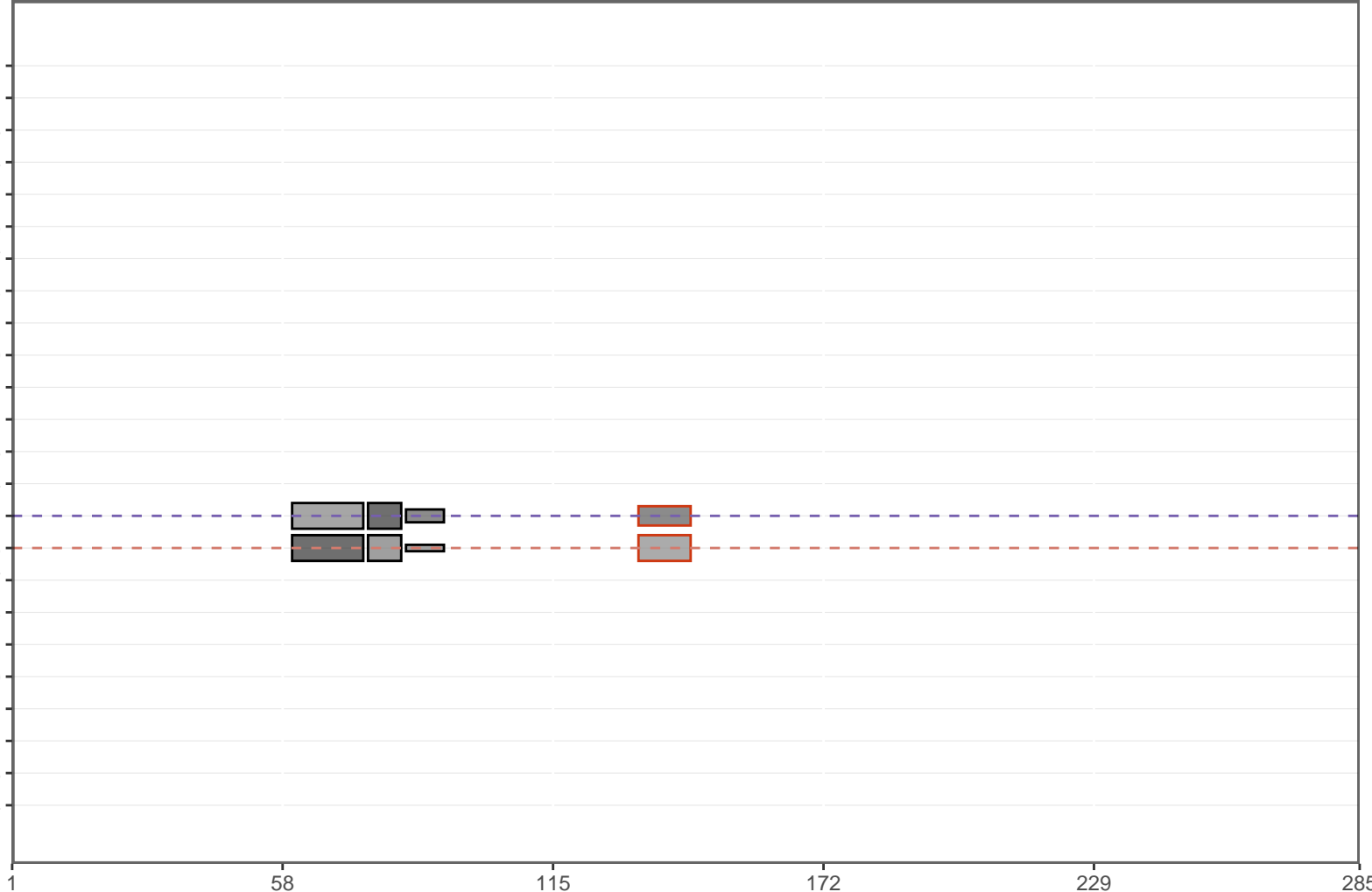
MW indication



Molecular weight



Gel Slice

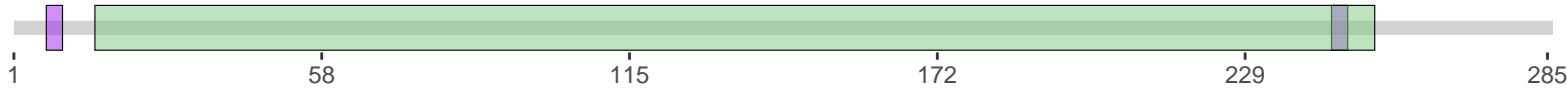


Protein length

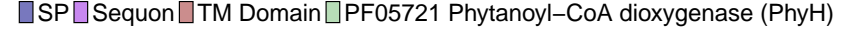


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

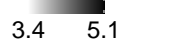
LGYSPLVQSMYFKGPGIGGVEVPHQDNFLVTEPTTCTGLWLALEDATINGGLWAIIPGSHKDGILVRRFLRDENGVHFDKPSPCYYQKDFPLEVKAGSLVIVHGDUIHGDFENKSEKSRHAYSLHVVDTNGDKWAEDNWIRRNVDPLVLSG

NbL18g20630.1 xaa-Pro_dipeptidase [MW = 55.79 kDa]

No. of times detected



log(intensity)



Values from



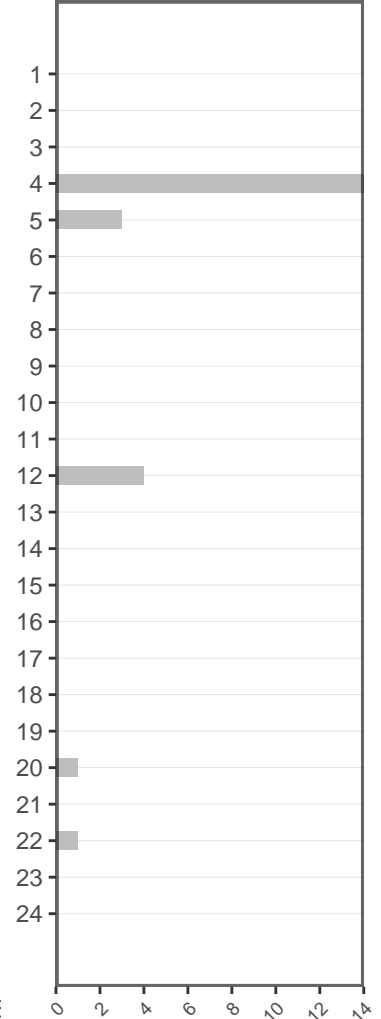
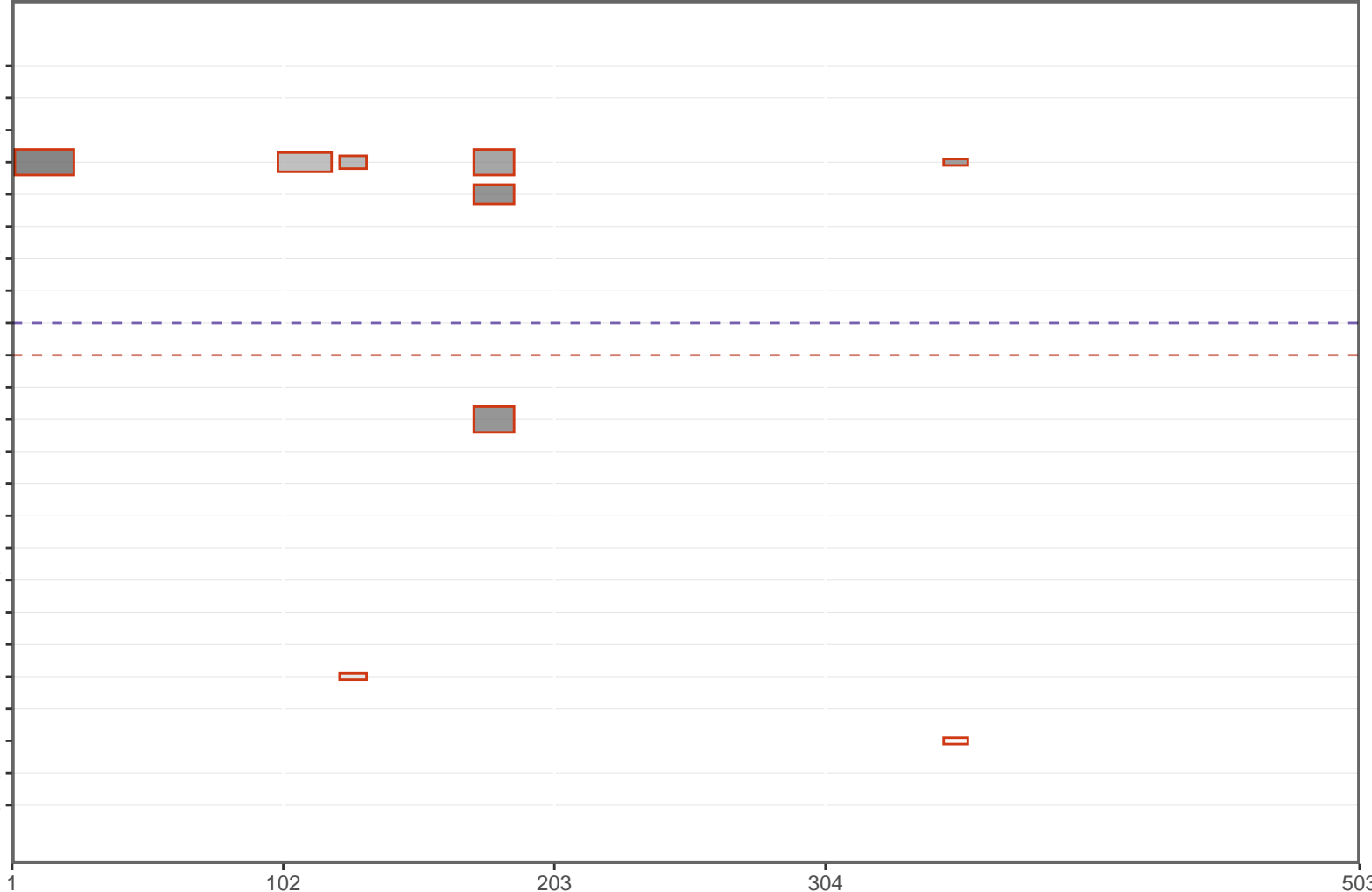
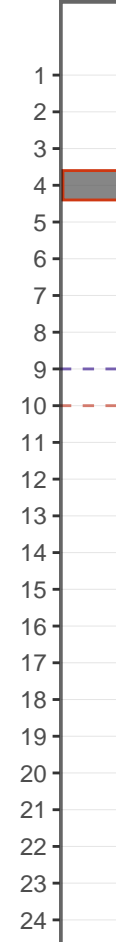
MW indication



Molecular weight



Gel Slice



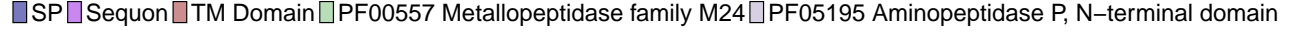
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SCRHCSYTCICATGNSAVLHGHAAAPNDKTLREGDMALLDMGAEYHFYGSDDTGSFFPANGKFRDQSLVYTAFLDMDHDAVISAMEPGVSWDMHKAERKILVSLKGHLLVGDVDMKMTTERLGAVFMPHGLHLLGDTHDPGGYLKGAERPKPEGLSRLRSKLLLEGDMVTFEPGCFIDALLLPALLESPEVSEFFNHCENRFRAGFGVRIEEDVGTANGCINMTKGRKIEIEAVMAGVWPWPKTKTFPBGNGKV

NbL18g20450.1 uncharacterized_LOC107790078 [MW = 34.94 kDa]

No. of times detected



log(intensity)



Values from



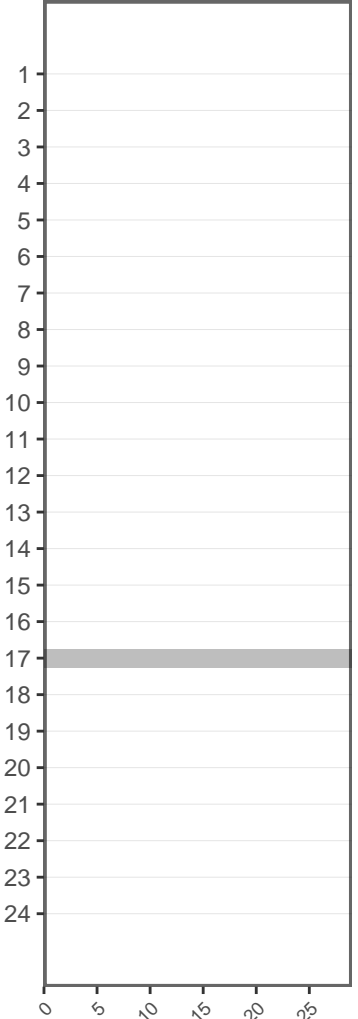
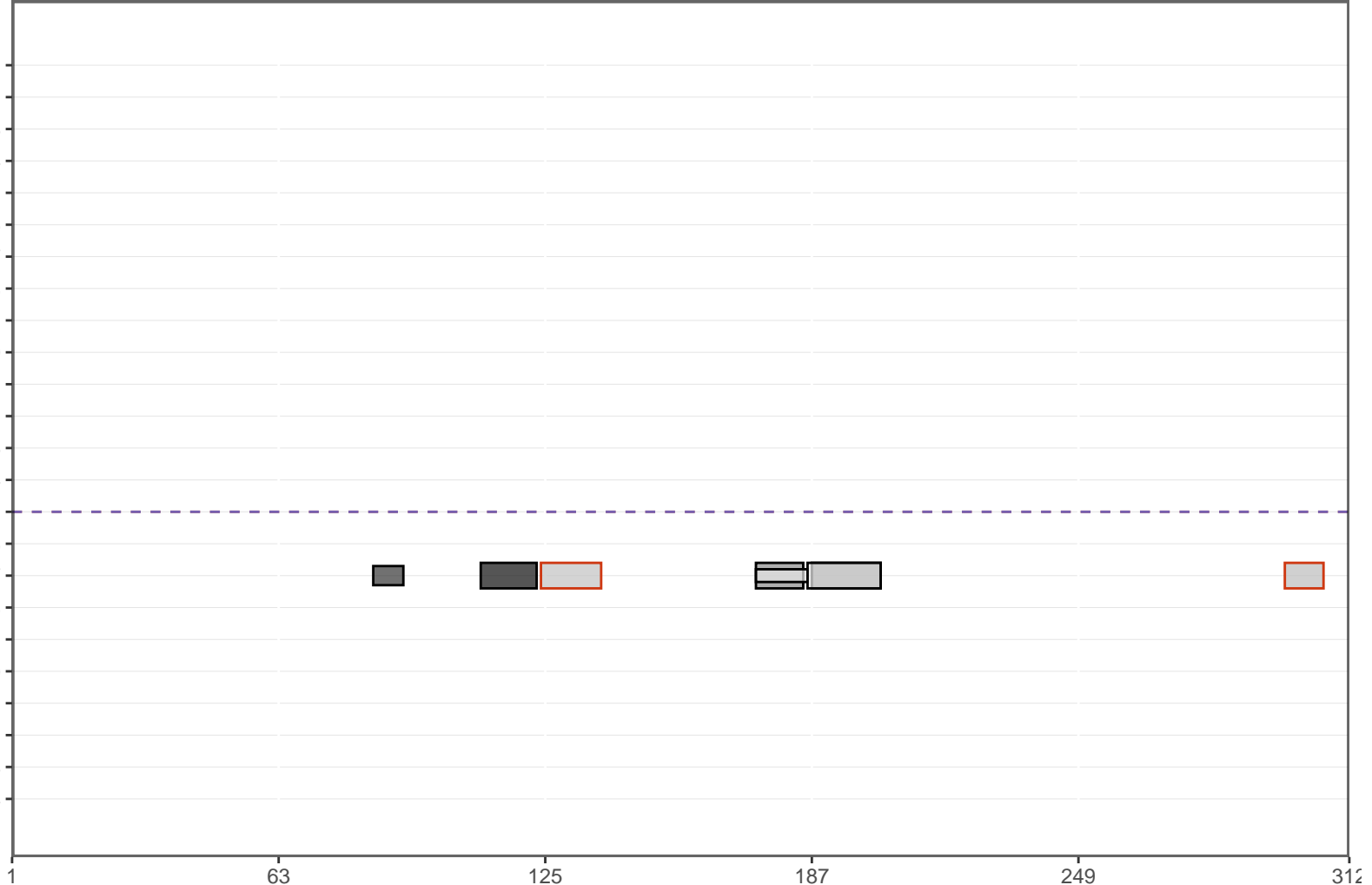
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

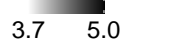
VLPSSNAPGVILDMSSWVSHYFAGYKQERIVGMGLNEELKRNPLVTEYVVDLNSNPKLPLFGDNTFDITNIVSVDLTKPLDVKEMSRILKHGGLAMSFENRQFFTKAISEWTSFGDADHVMVIGSYFHYAGGFEPGQAVDISPNQRSDPMVYVSRKIATV

NbL18g20430.1 cytidine_deaminase_1-like [MW = 35.49 kDa]

No. of times detected



log(intensity)



Values from

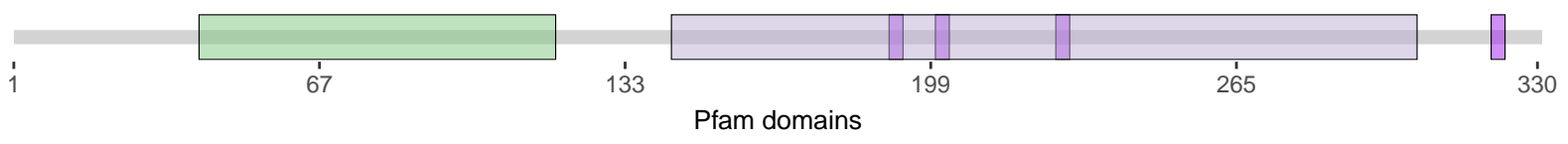
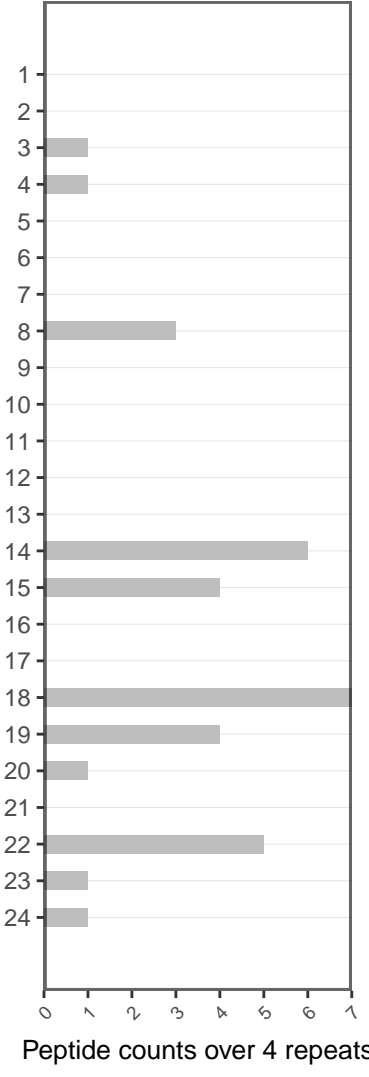
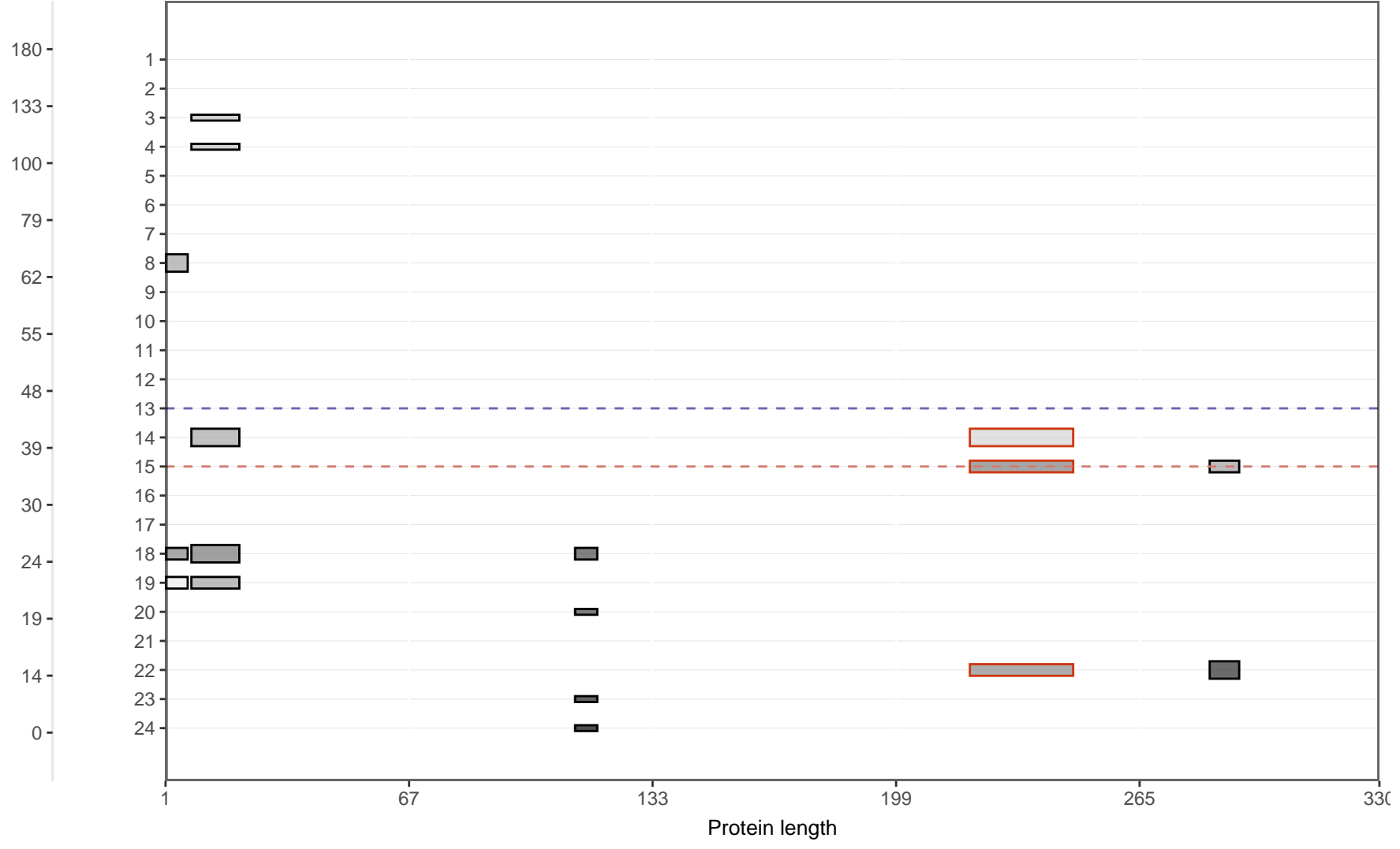


MW indication



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00383 Cytidine and deoxycytidylate deaminase zinc-binding region
- PF08211 Cytidine and deoxycytidylate deaminase zinc-binding region

Protein sequence:

FDLLDGETPLLLERHNGFELNDNHADLGNFSDNSKRVNGVNLGNFGFKKTETENTLNLKIAALEANDSHAPYSGCPGVALMDSKGVKRGVYVESAVNPLSLGVAALVAVVAGGGGGYERIVAAALVEKEGAKVRGEDTTKLFKVMSPKGLRIVNCSFAKNGCI

NbL18g20390.1 ectonucleotide_pyrophosphatase/phosphodiesterase_family_member_3-like [MW = 54.85 kDa]

No. of times detected



log(intensity)



Values from



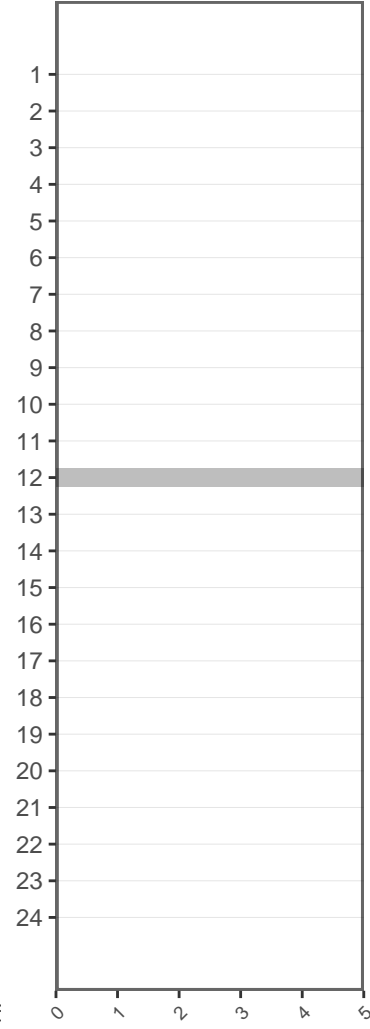
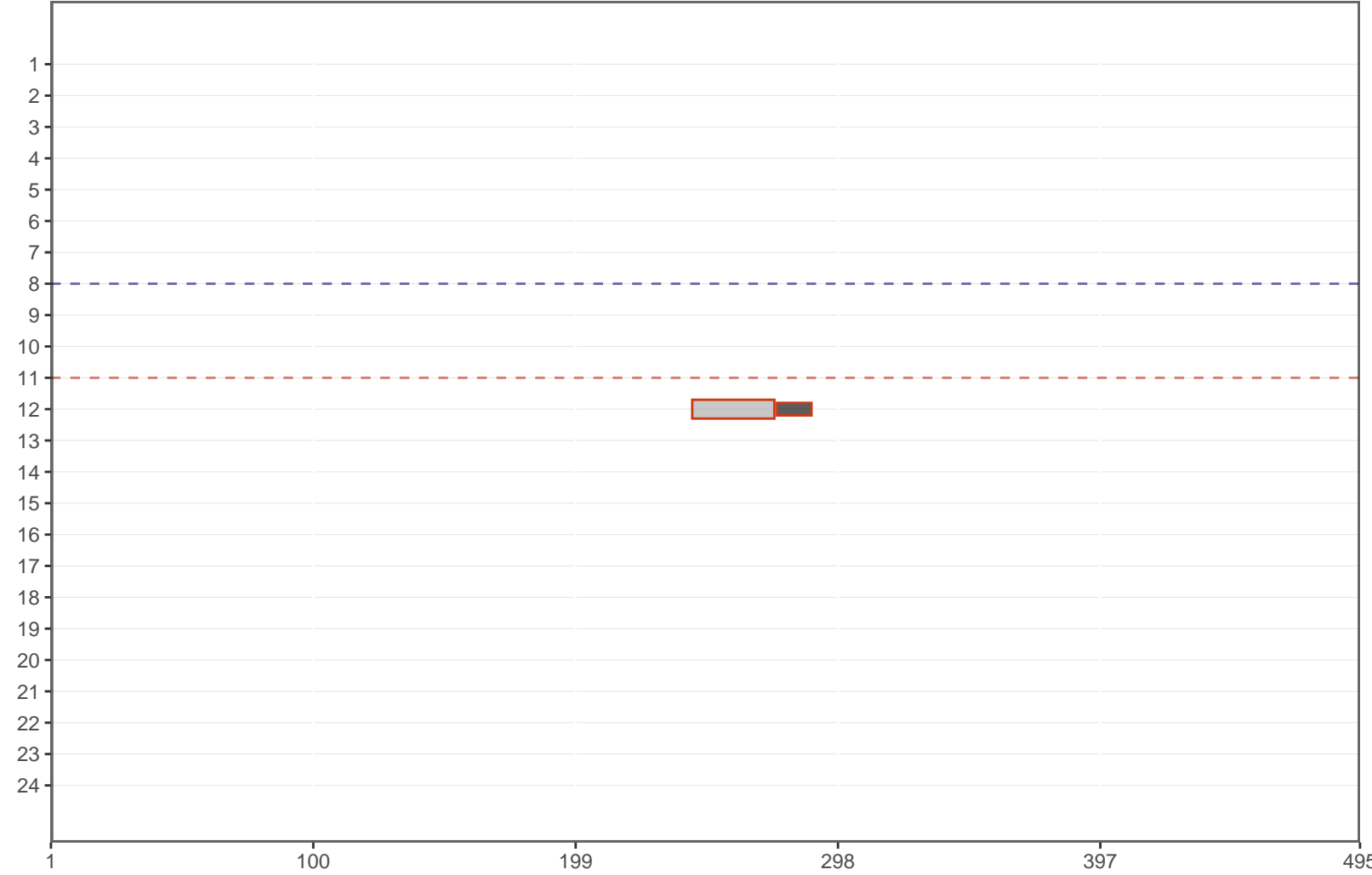
MW indication



Molecular weight

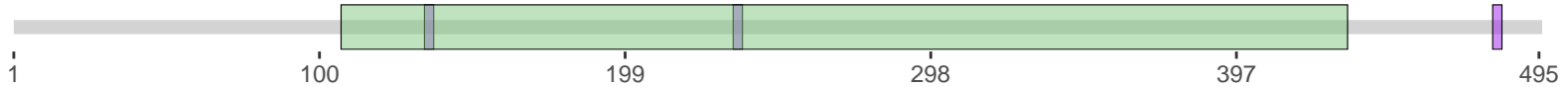


Gel Slice



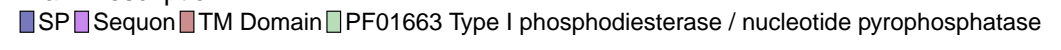
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GSVYFEEKRVDTVLSNFQDLIDIEIPFMTLYFEDPDHGHKVGPDPPQTEAVARVDMIGRLRGLLEERGIVFEDNIMVGDHGMVGTGDKLFLFLEDLAFVWIEIKGWISYSPLLSIRPPASYSAKDVVTKMNEGLKSGKVGNGGVLKVKYKEELPARLHYFASDRNPIIQLDESPKVEQKSKRKECGGSHGVDNAFFSMRTIFAHGPRFARGSKVTSFENVGIVNLTLLNQGASNGDTTSFPKTLIPSH

NbL18g20290.1 WD-40_repeat-containing_protein_MSI4-like [MW = 57.46 kDa]

No. of times detected



log(intensity)



Values from



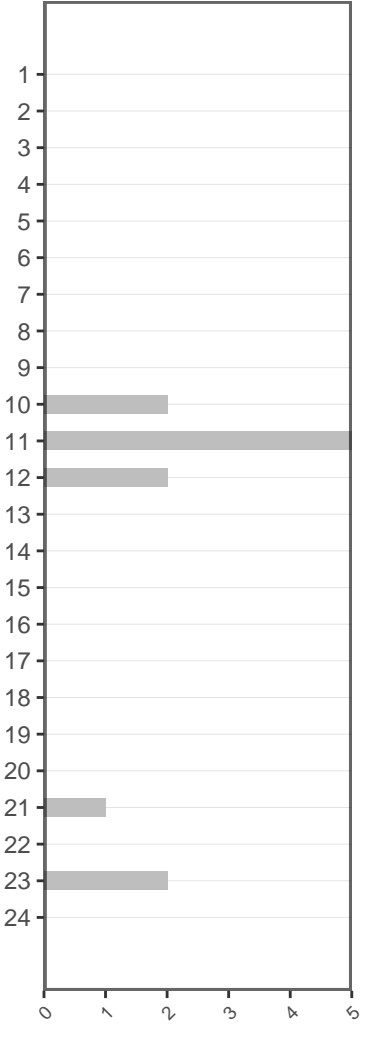
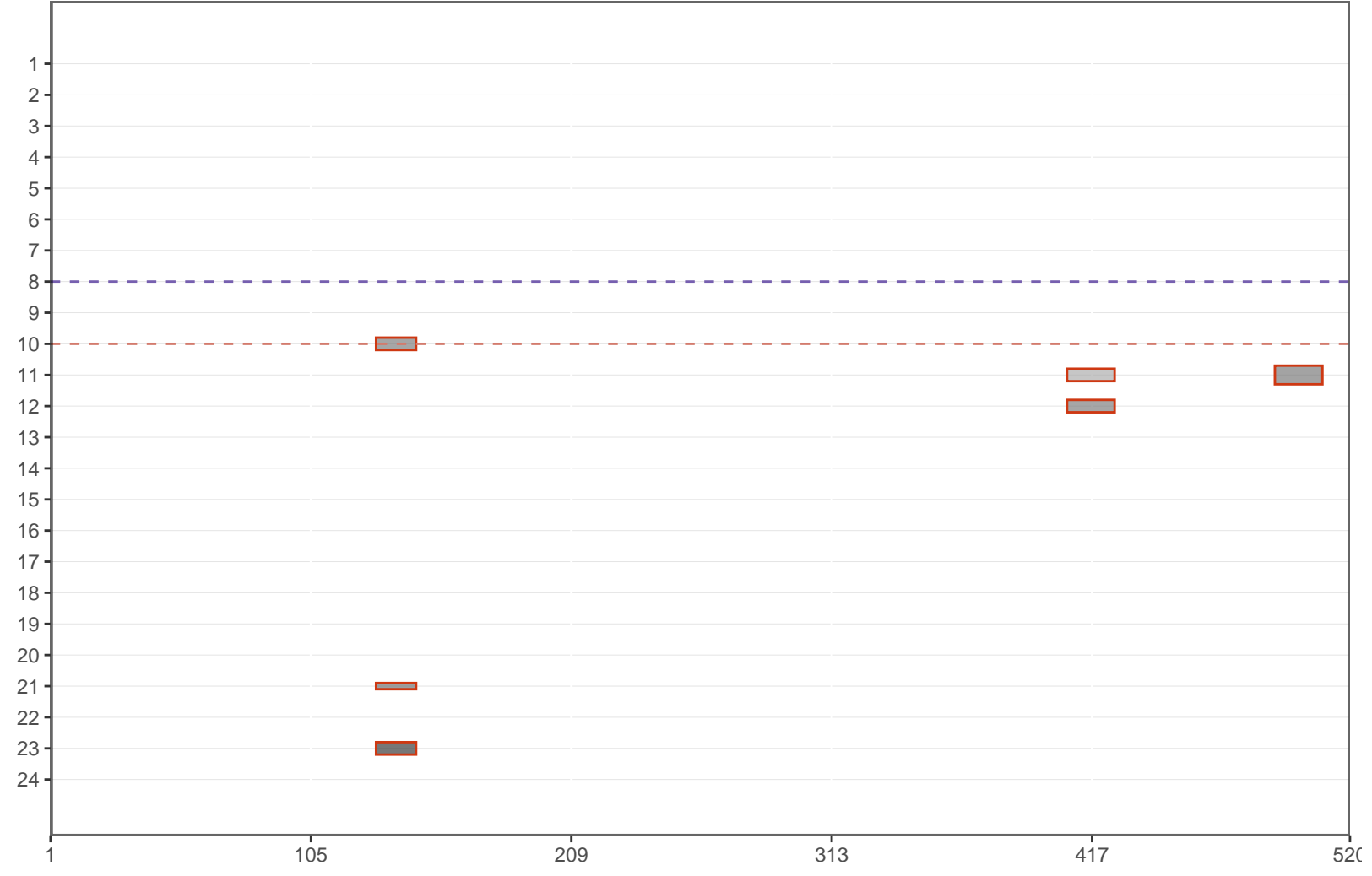
MW indication



Molecular weight

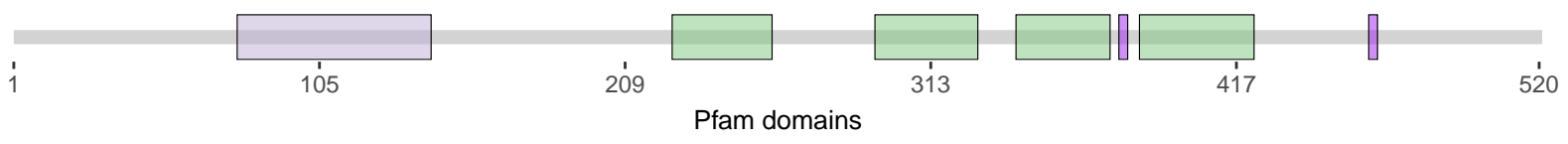


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

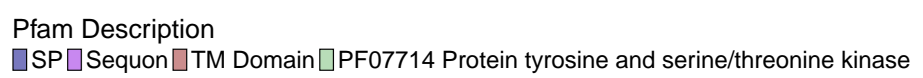
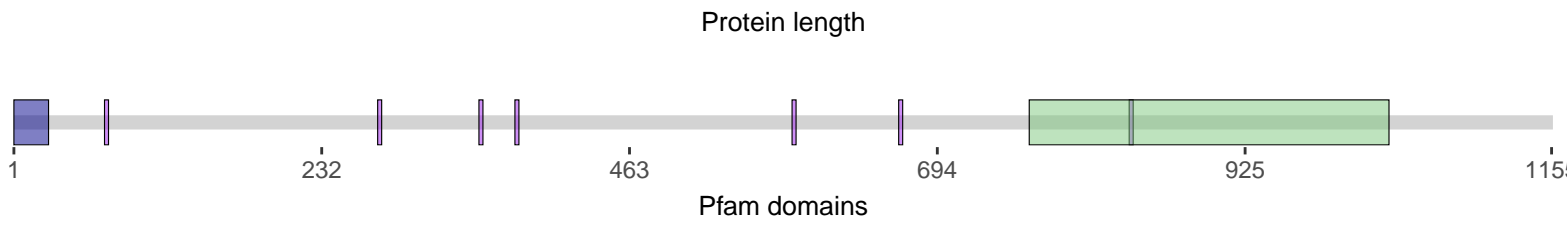
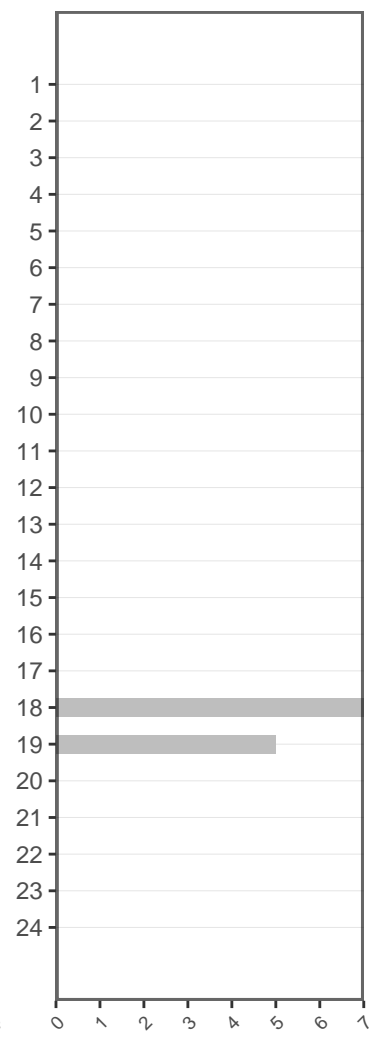
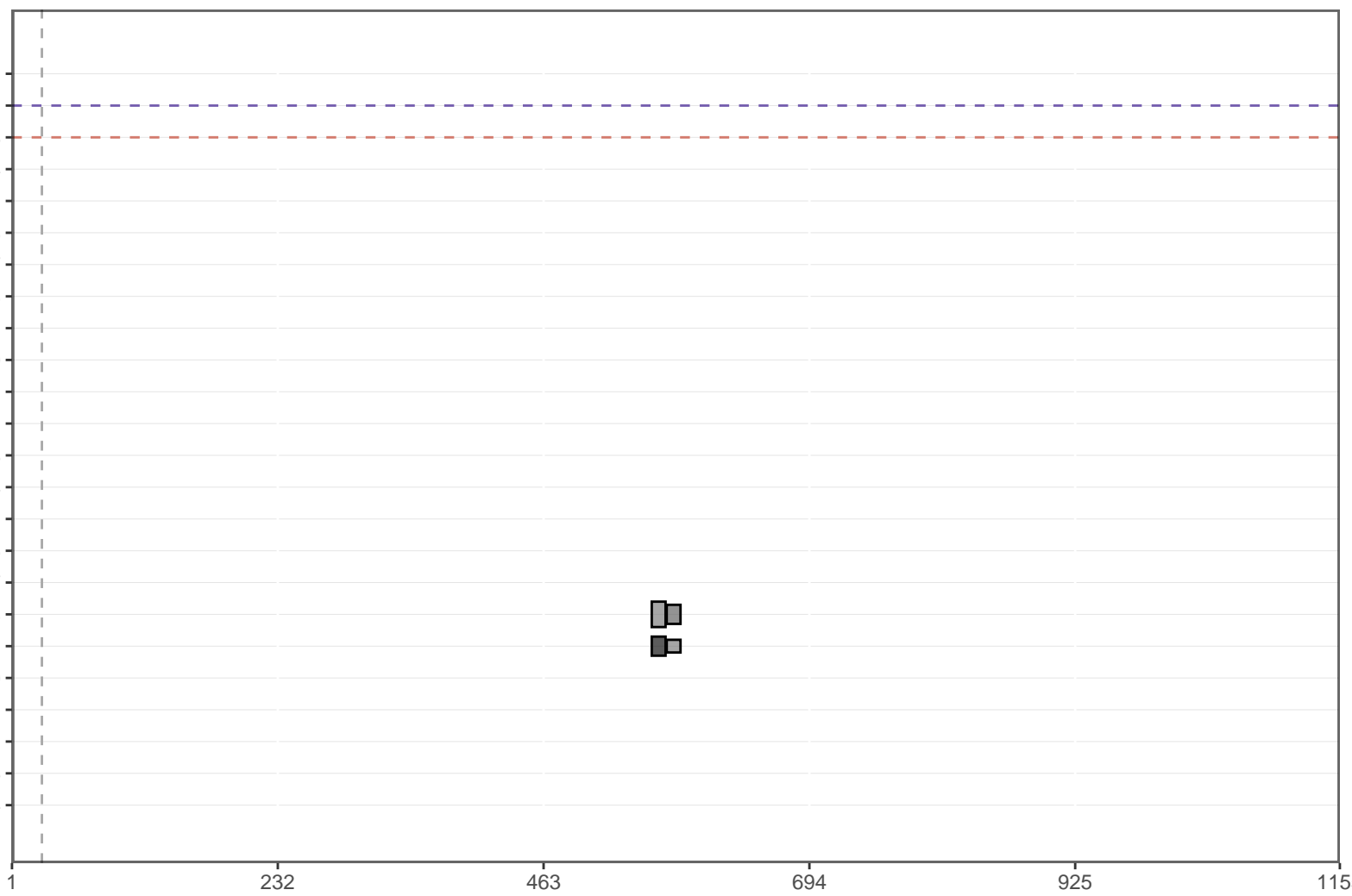
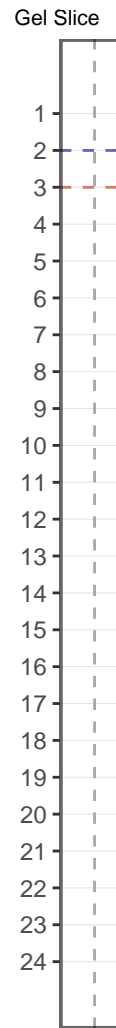
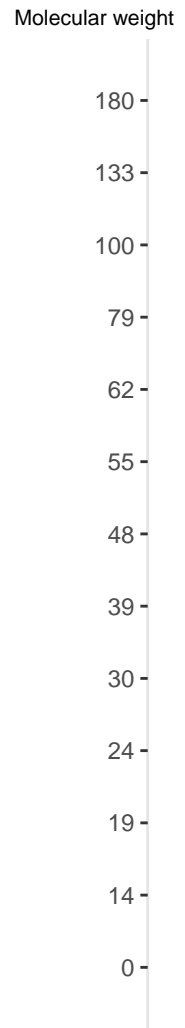
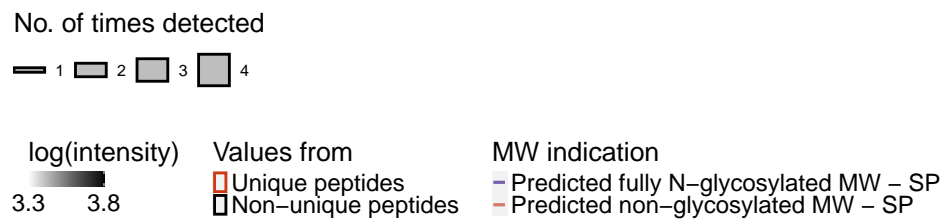
Pfam Description



Protein sequence:

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NbL18g20260.1 receptor-like_serine/threonine-protein_kinase_ALE2 [MW – SP = 120.55 kDa]



Protein sequence:
 EKTIVLIDVLP LGEKFNFTALTSQRFWKGVLIKASLFGDGVV LNVGYPLPPPPAAASEIDTIGSRPYDGNRRITQPLGVGVSGQRHKSGPNRSVIAVVLGASAVLGGAAVWVLLFRHRDHGGGSDPTSPFTLPLSLAKSGSIAASMGIRPNPGLFSSSFAANTGSARTFSSSEIERATDNFNENARVLCGGGFRVYVSGVLDGGMKVVKILKRDDGGGGRFLAEVEMLSRLHHRNLVKLIGDIEERSRLVVELMPPNGSVEHSLHGVDKESPLDWHARMK/

NbL18g20240.1 translation_machinery-associated_protein_22-like [MW = 20.68 kDa]

No. of times detected



log(intensity)



Values from



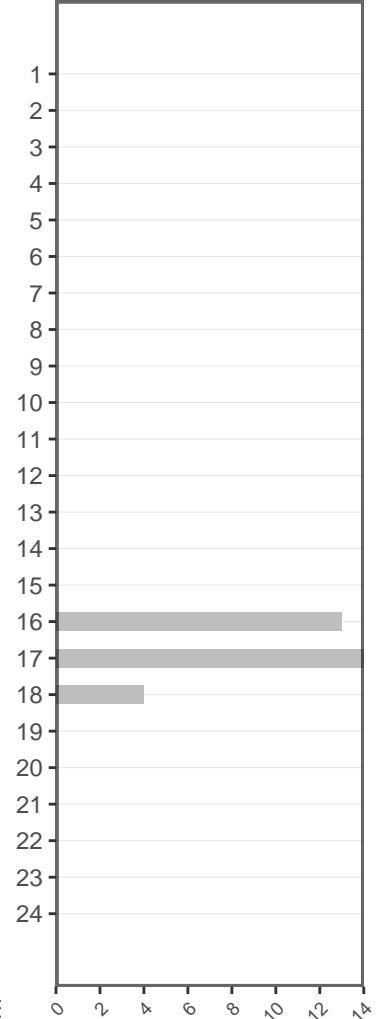
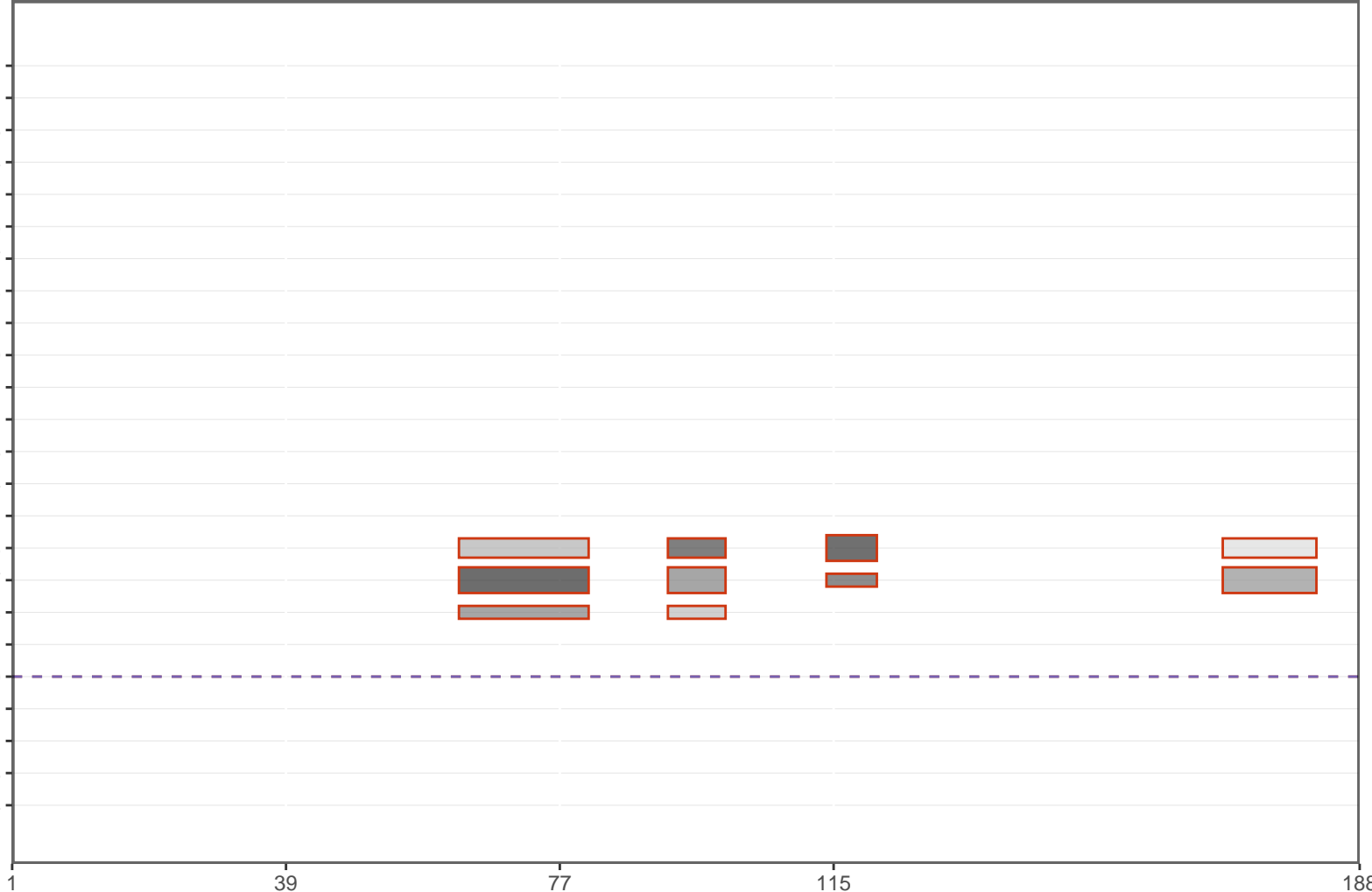
MW indication



Molecular weight

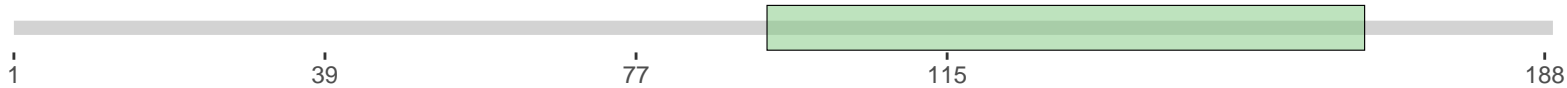


Gel Slice



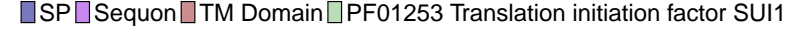
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

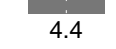
IEVLRLLPGGKIKKQKQKGEIEKIVTRNKRKISITIKGLELFGVKLSDAKKLGKFKATGASVVKGPTKEKQIDVGGDFYDVIDFITETWRDVPESAFFIEDGKVKVPA

NbL18g19830.1 WD_repeat-containing_protein_VIP3-like [MW = 34.79 kDa]

No. of times detected



log(intensity)



Values from



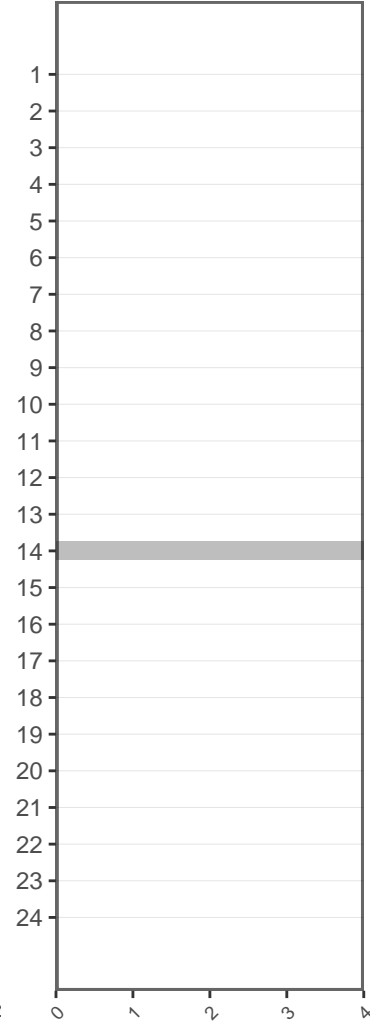
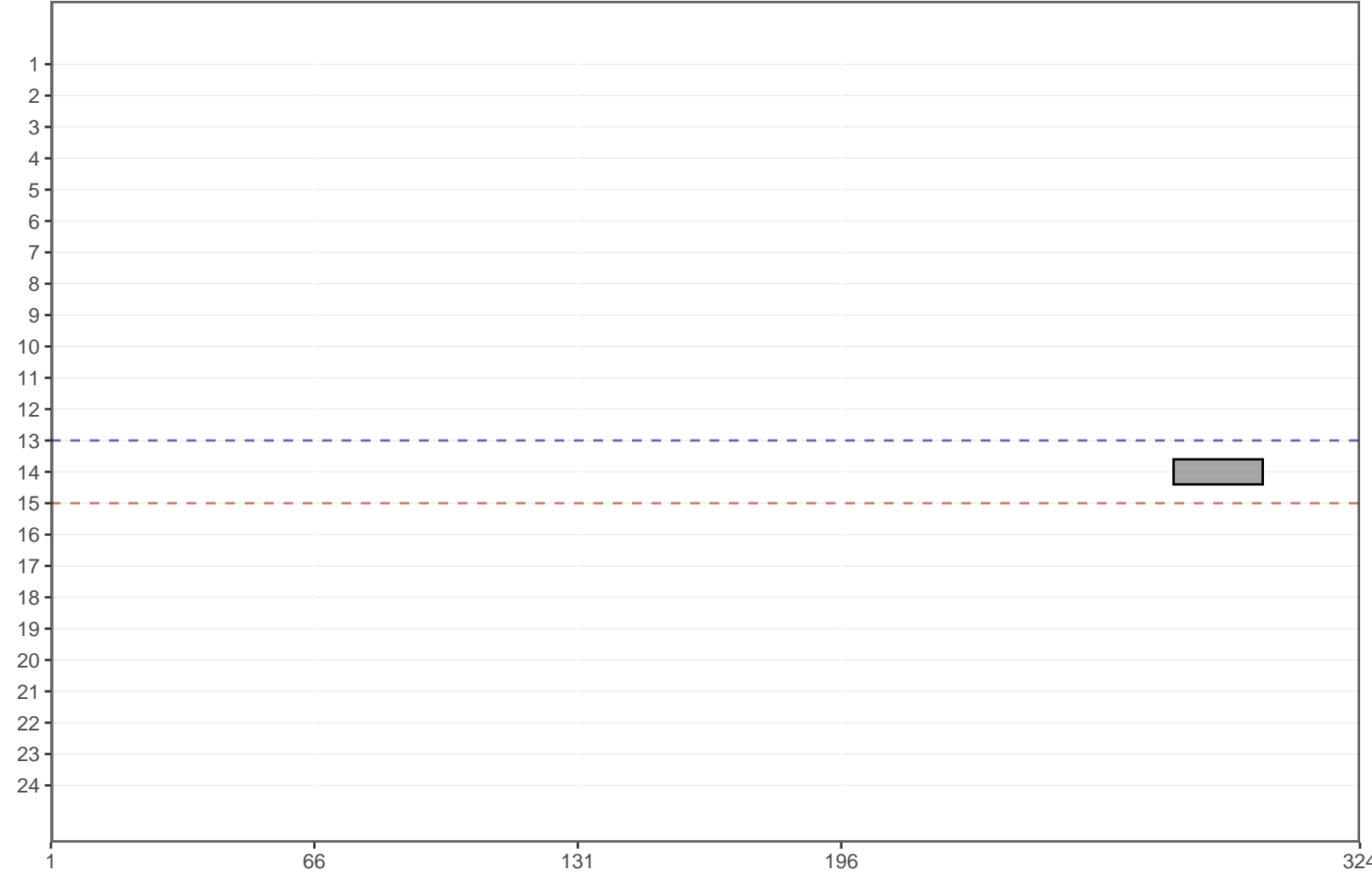
MW indication



Molecular weight



Gel Slice

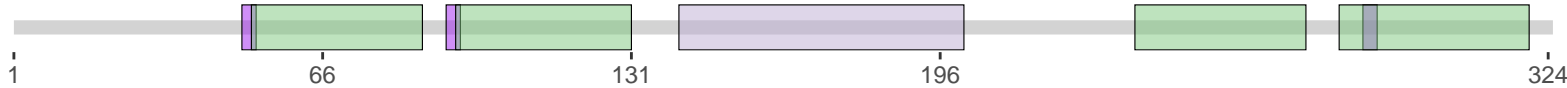


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IPSEKSGNKYLYLSWAWNPQGRLLAGGSEVDGTSIVFDVARAKFLHFLLEGHEMPVRSGLVFSPSHIDSRILFSAEDDGHVHYDAEGKTLFSLGSHAWLSEVDVSPDGAAMATGSSDKTVRLWDLKMRATGTLTNHTDGVWVWVAFGPTERTVRSGLASVSDOKSIFVGYE

NbL18g19750.1 PHD_finger_protein_ALFIN-LIKE_4-like [MW = 27.73 kDa]

No. of times detected



log(intensity)



Values from



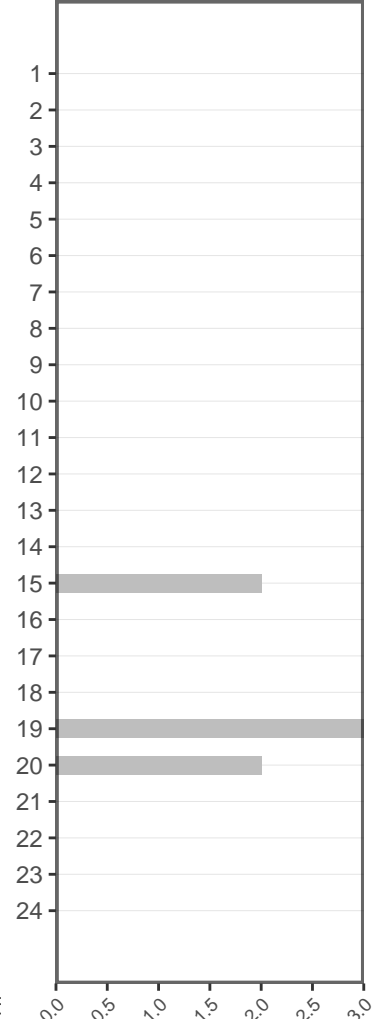
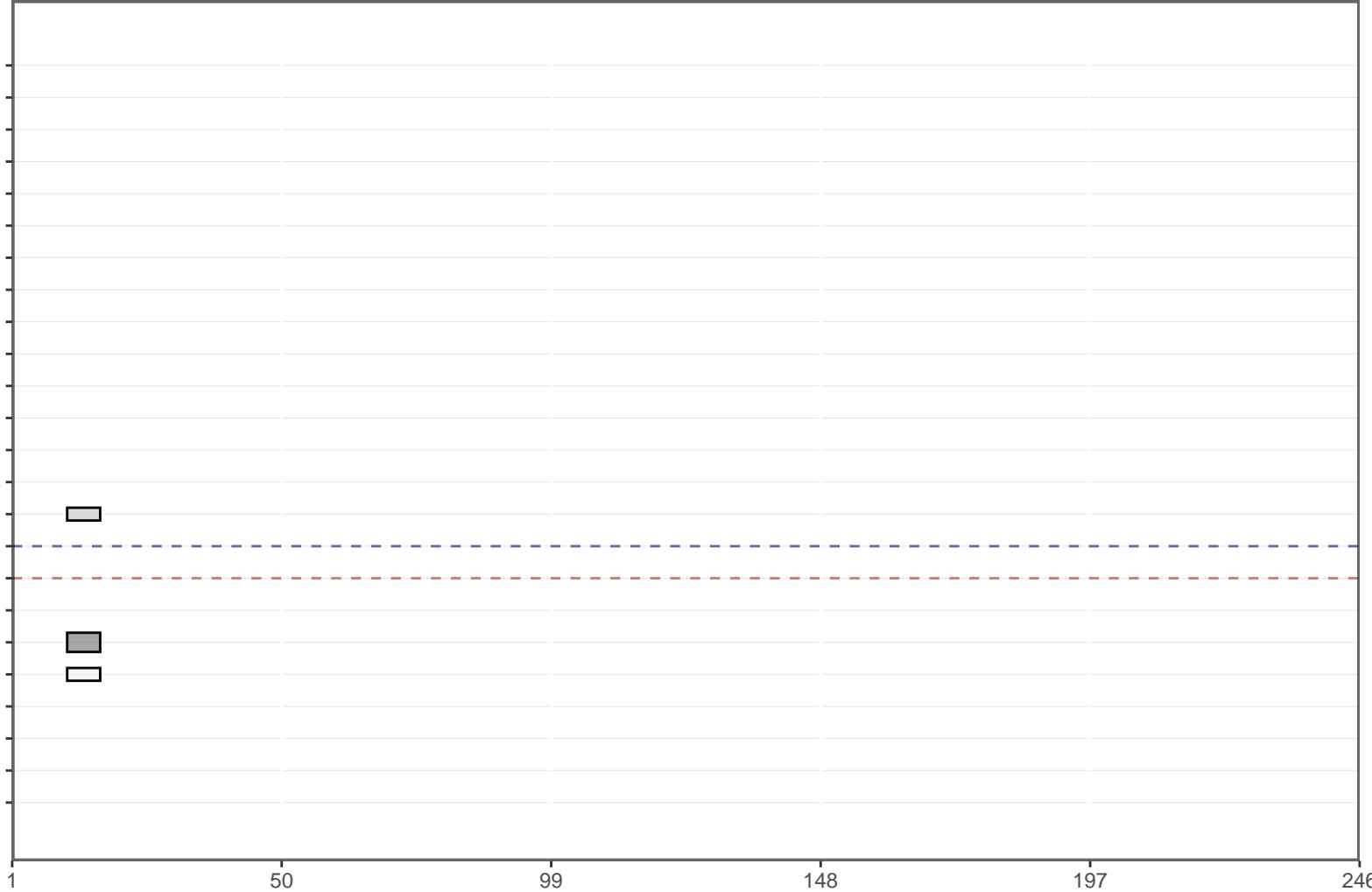
MW indication



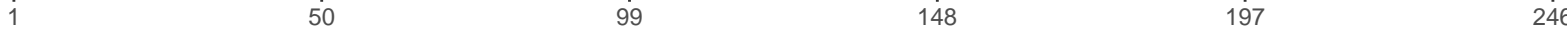
Molecular weight



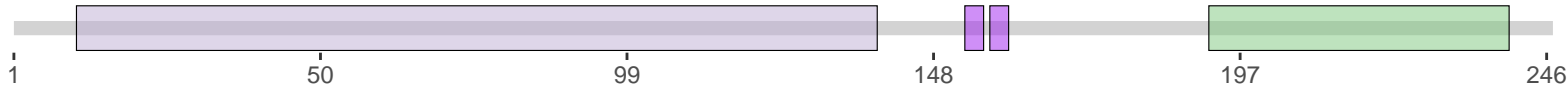
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

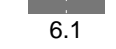
SARFGFDKTRKCLFNMINDLPTFVEVTGVAKKGVKDRBTEHHSNKNKSNKSNKAGVSKAHVDEDDGLDEEEDHGDTLGGAGGENYASDEFWIGGDCIQRWFHKGKVKITPARAEHKGKYPGCGNKRSGP

NbL18g19710.1 40S_ribosomal_protein_S3-1-like [MW = 26.43 kDa]

No. of times detected



log(intensity)



Values from



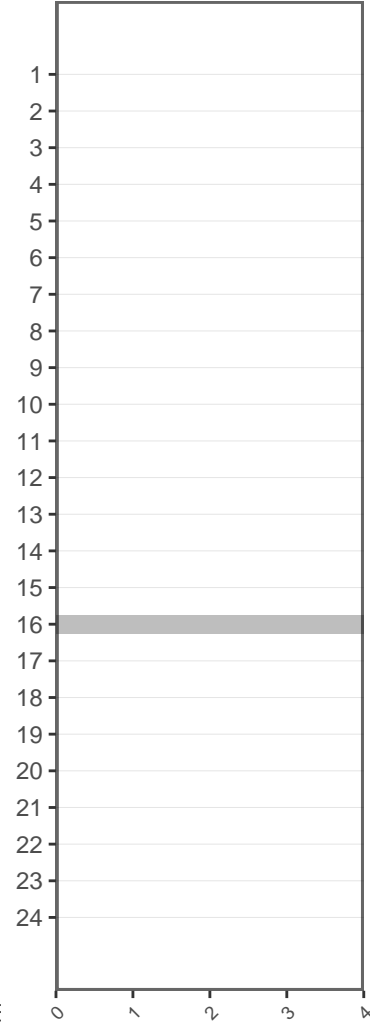
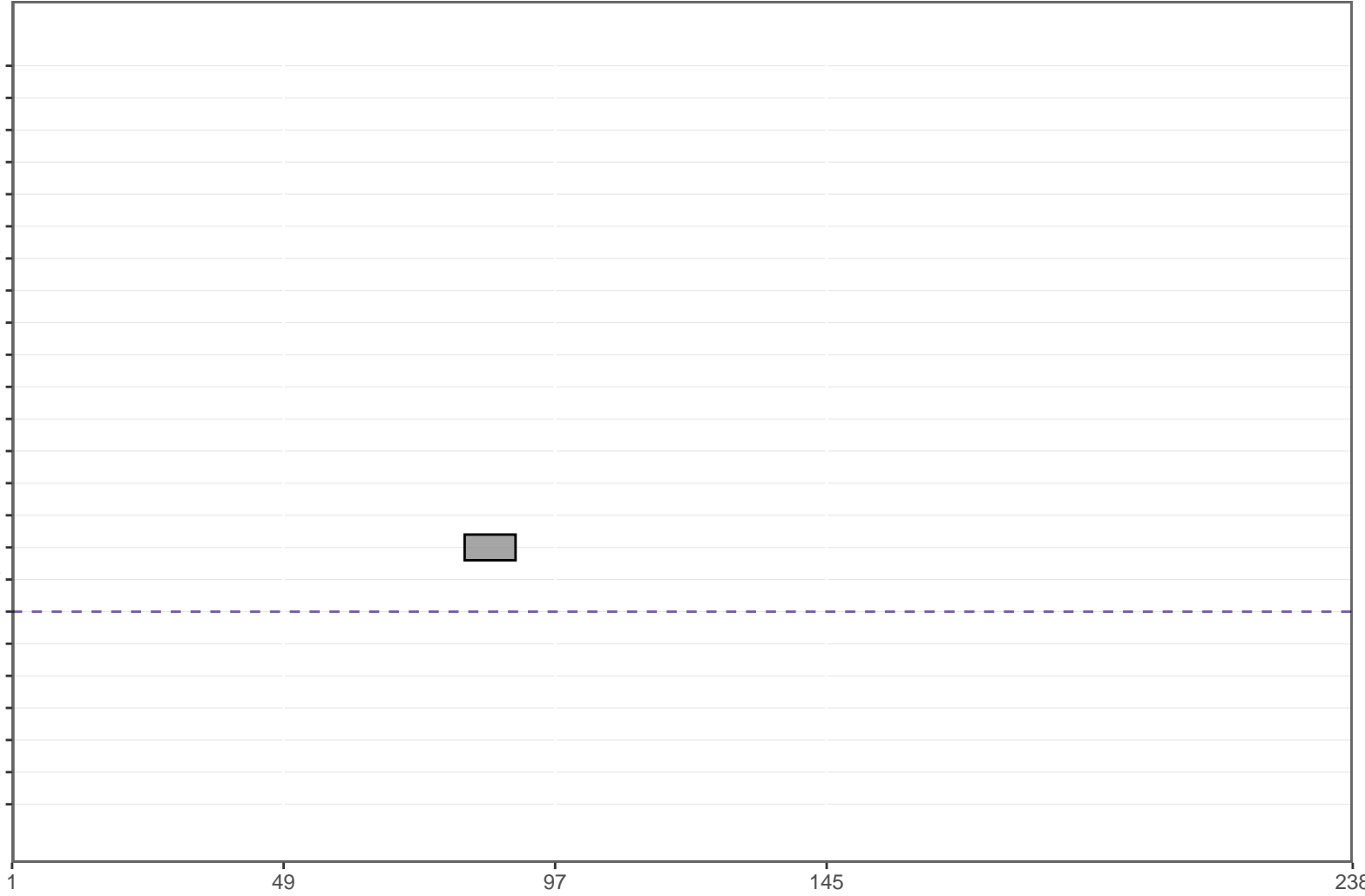
MW indication



Molecular weight

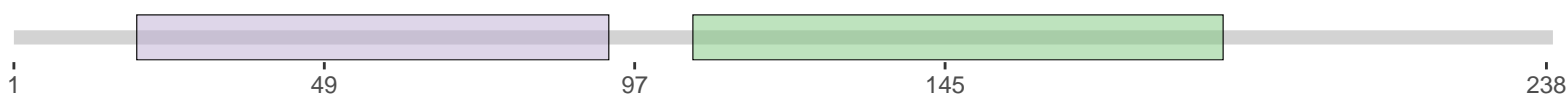


Gel Slice



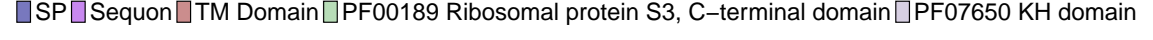
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YKLLGGLAVRACGYGLRFIMESGAKGGEVIVSGHLRAGRAKSMKFKDGYMISGGQPWKEYDIAVRHLMRGGVLGKWKWMLDWDPKGKGGPTTLPDLVTHPPKKEEEVYNPDPAPVDEIVSPIS

NbL18g19670.1 stress-response_A/B_barrel_domain-containing_protein_UP3 [MW = 31.82 kDa]

No. of times detected



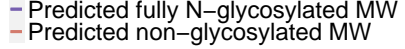
log(intensity)



Values from



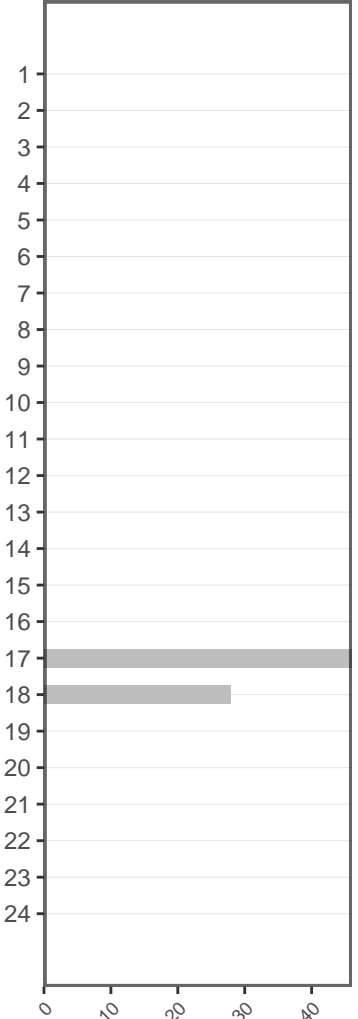
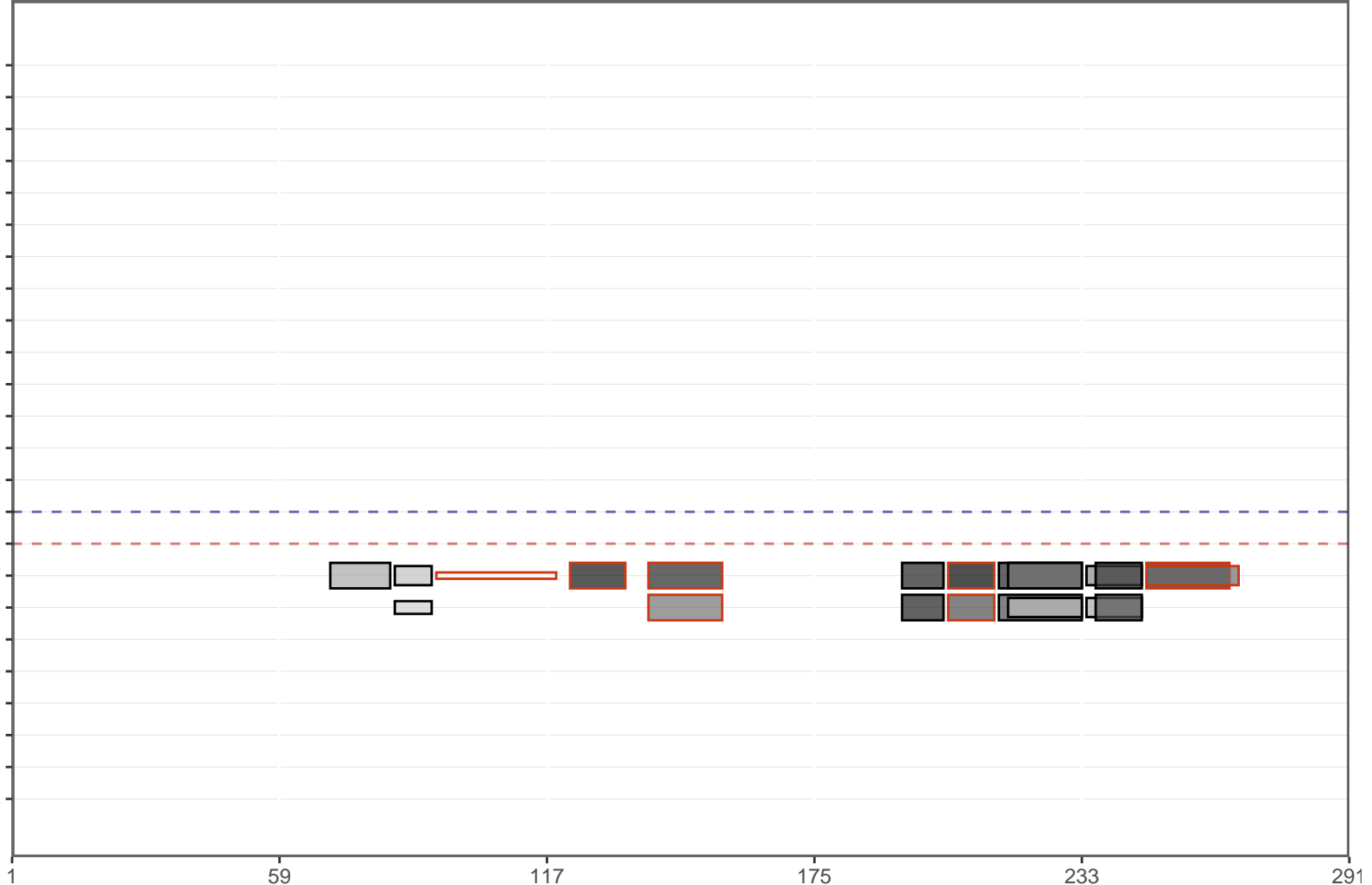
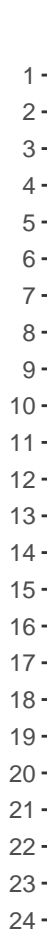
MW indication



Molecular weight

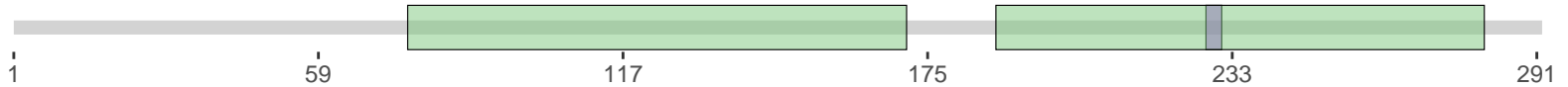


Gel Slice



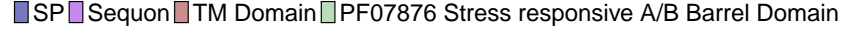
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

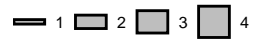


Protein sequence:

IRYKSKDLADYSAMPDHSVHKEVYLPVDDIMAVDWPTDFSGPIEVPPGSAIRVTFLLKLNKLGENEKSGQLNAVGGKEKFPQIEQLTVGENFSFGRAGKGFSAIAVFKGVNLELEAEAGTELANEQKEKVRDFLDGIVVVVDVAVPPTQSAEL

NbL18g19380.1 protein_trichome_birefringence-like_14 [MW = 55.35 kDa]

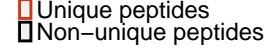
No. of times detected



log(intensity)



Values from



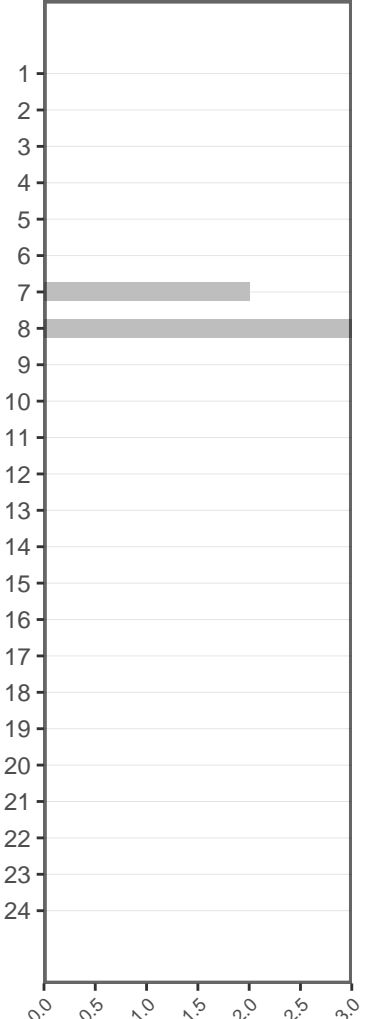
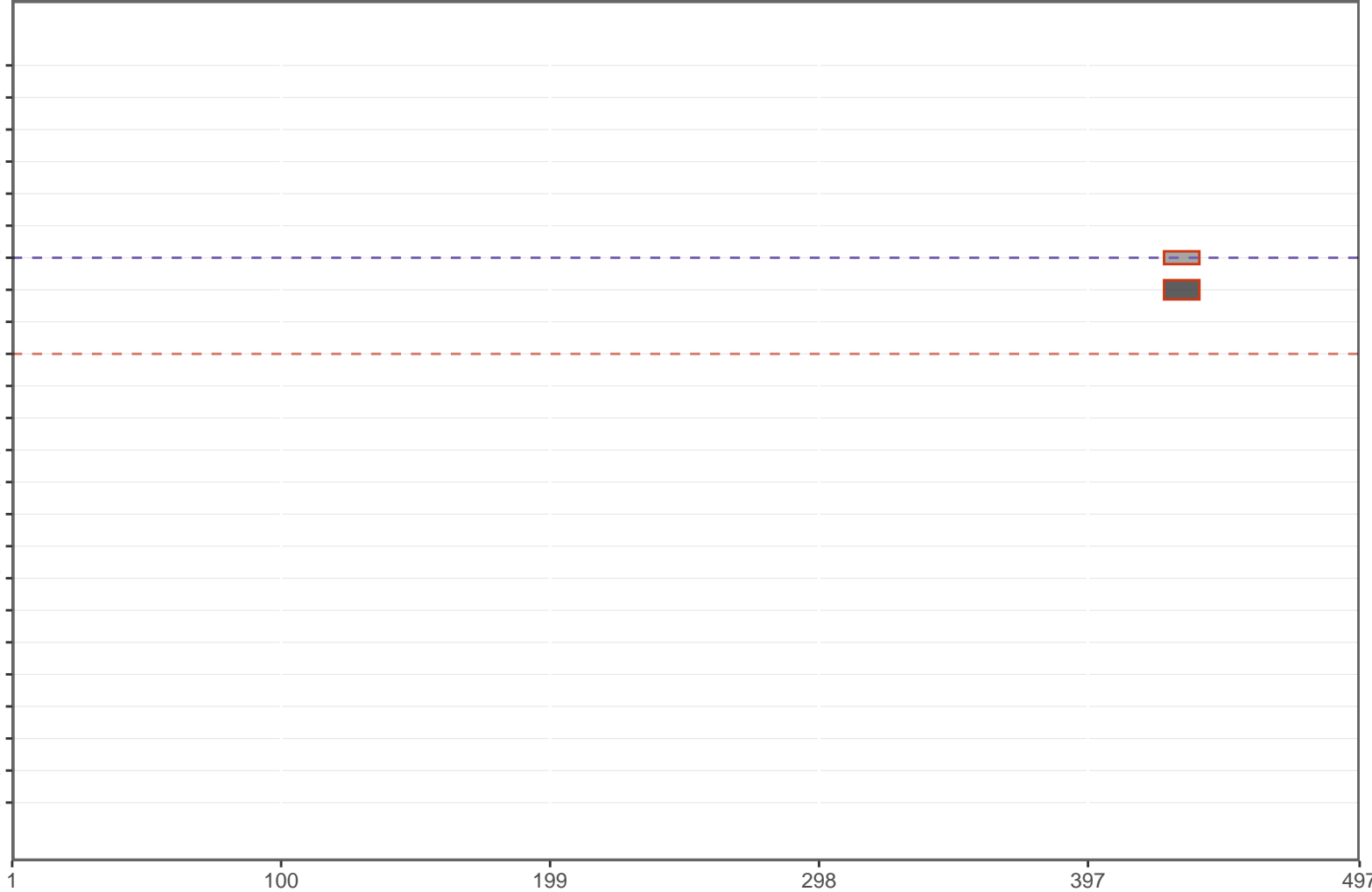
MW indication



Molecular weight

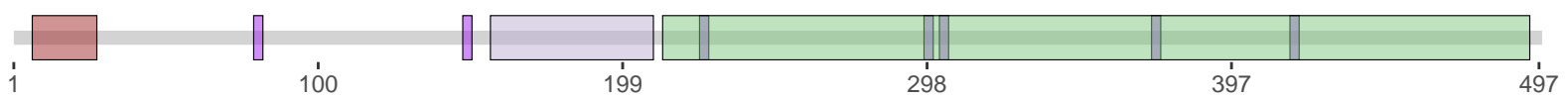


Gel Slice



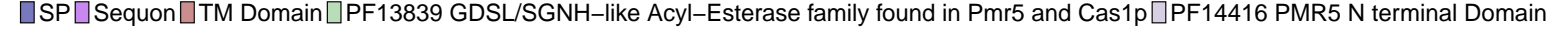
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

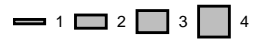


Protein sequence:

ROFQSLMCMITGGEDRPDLVDRGVEYGLVKARGAKRPDGVWYRFPQTQTFLYYWSLGLNLTPIINAFNPATDVAHMLDRPFLSLRFLRFDFLVLNTGHHWNRKLNANRWVHVHGVDPNTRKADAGANNFTHSIINWVNSQLPKHPLGLKVFYRSIPIRHFVNGDWTGGTCGINTTFLAGKVEVLQDSESSD6TAARAVKGTAVKLLDITAVSELREGHISRYSIKATPGMGDCLHWLPGVPTVNEIFAGL

NbL18g19260.1 beta-galactosidase_15-like [MW - SP = 89.71 kDa]

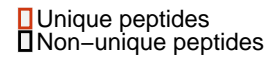
No. of times detected



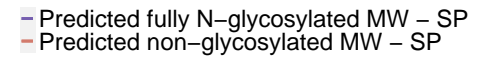
log(intensity)



Values from



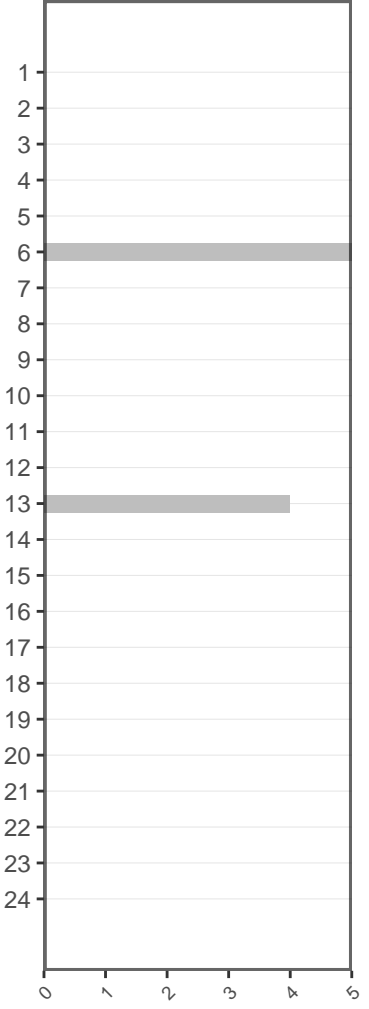
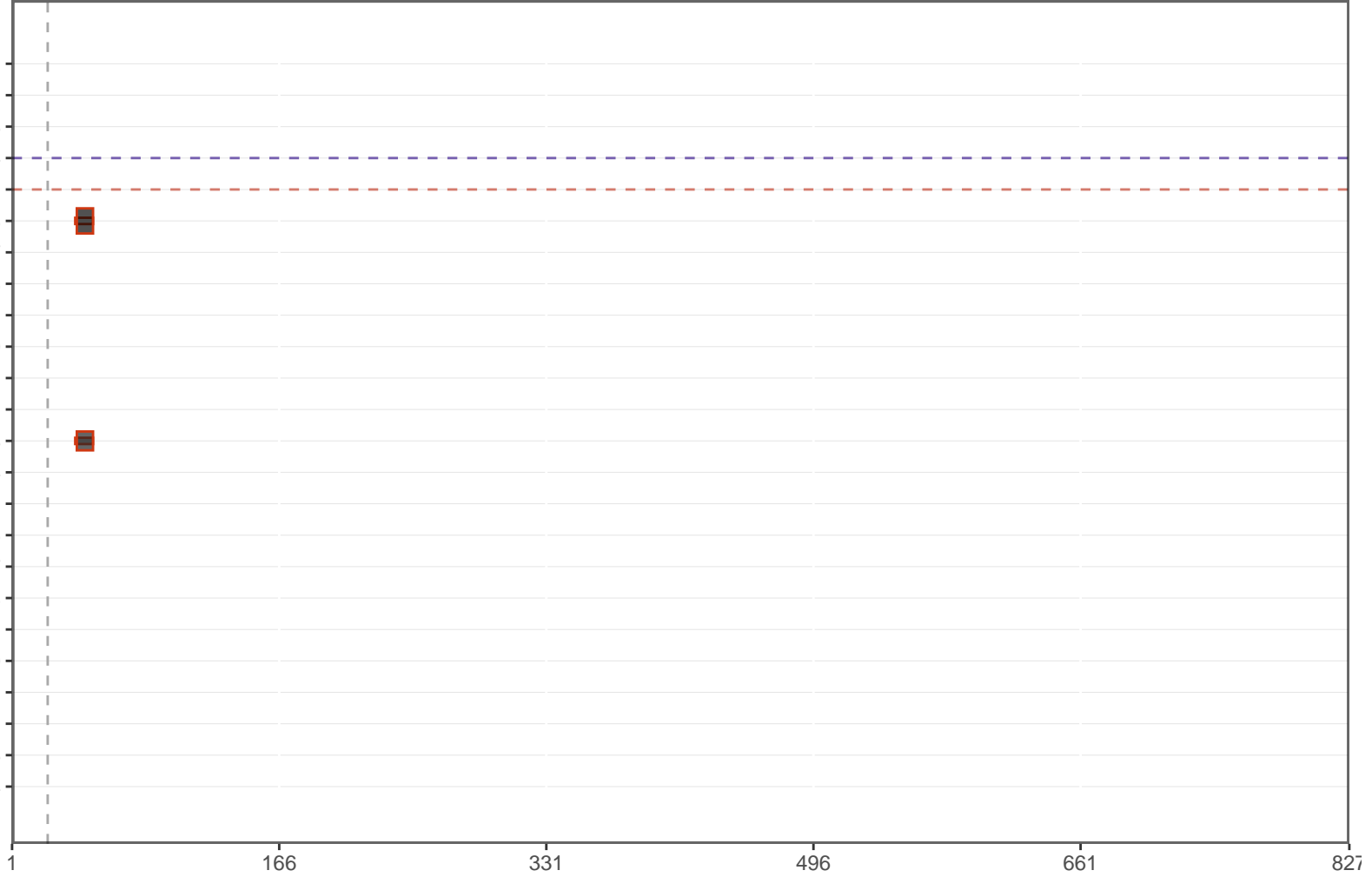
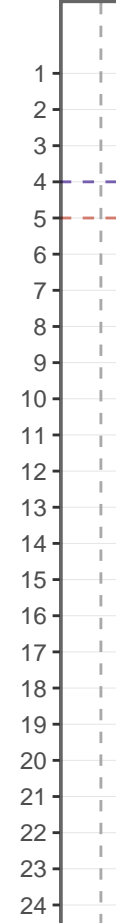
MW indication



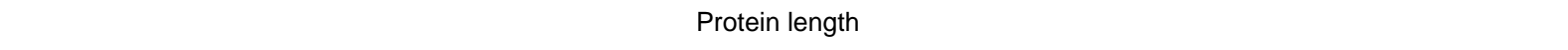
Molecular weight



Gel Slice

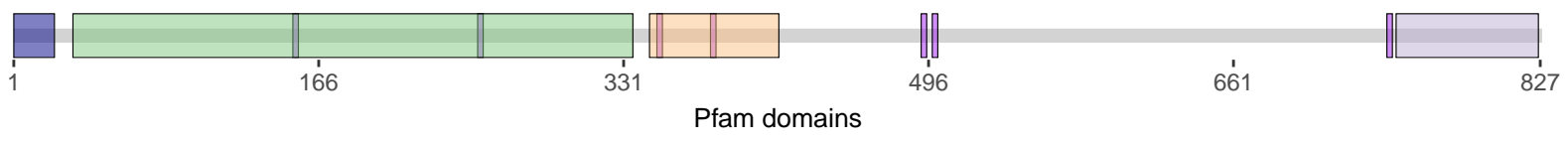


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LPDCKTEVYNTAKVNTQTSVMKKNSDAENEPASLQWSWRPEKDEAVVLGRGQSSAHELVDQKVNANDVSDQMWMTNHYIGKNDPIWTDNMTLRLRVNGSGHLLHAYVNGGYLGGWATYGFNYYFEKQVWLNPCRNHLLSATLGLQNYGAHFDTVQGGPGPVEIKGNQDSEVYKDLSSHKWSEYKVDLNGNKKLFSGNPKFENGWQFSGQVPIRNMRTWYKTTFKAPLGNLDPVVVDLQGLGKHAWINGESIGRYWPEKLAEEGGSTDLCDYRKYGPDKC/

NbL18g19210.1 3-oxoacyl-[acyl-carrier-protein]_synthase_II_chloroplastic-like [MW = 53.04 kDa]

No. of times detected



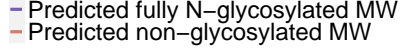
log(intensity)



Values from



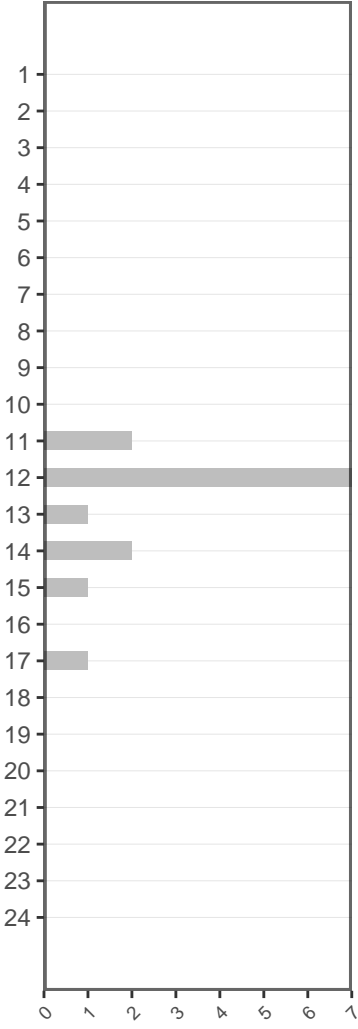
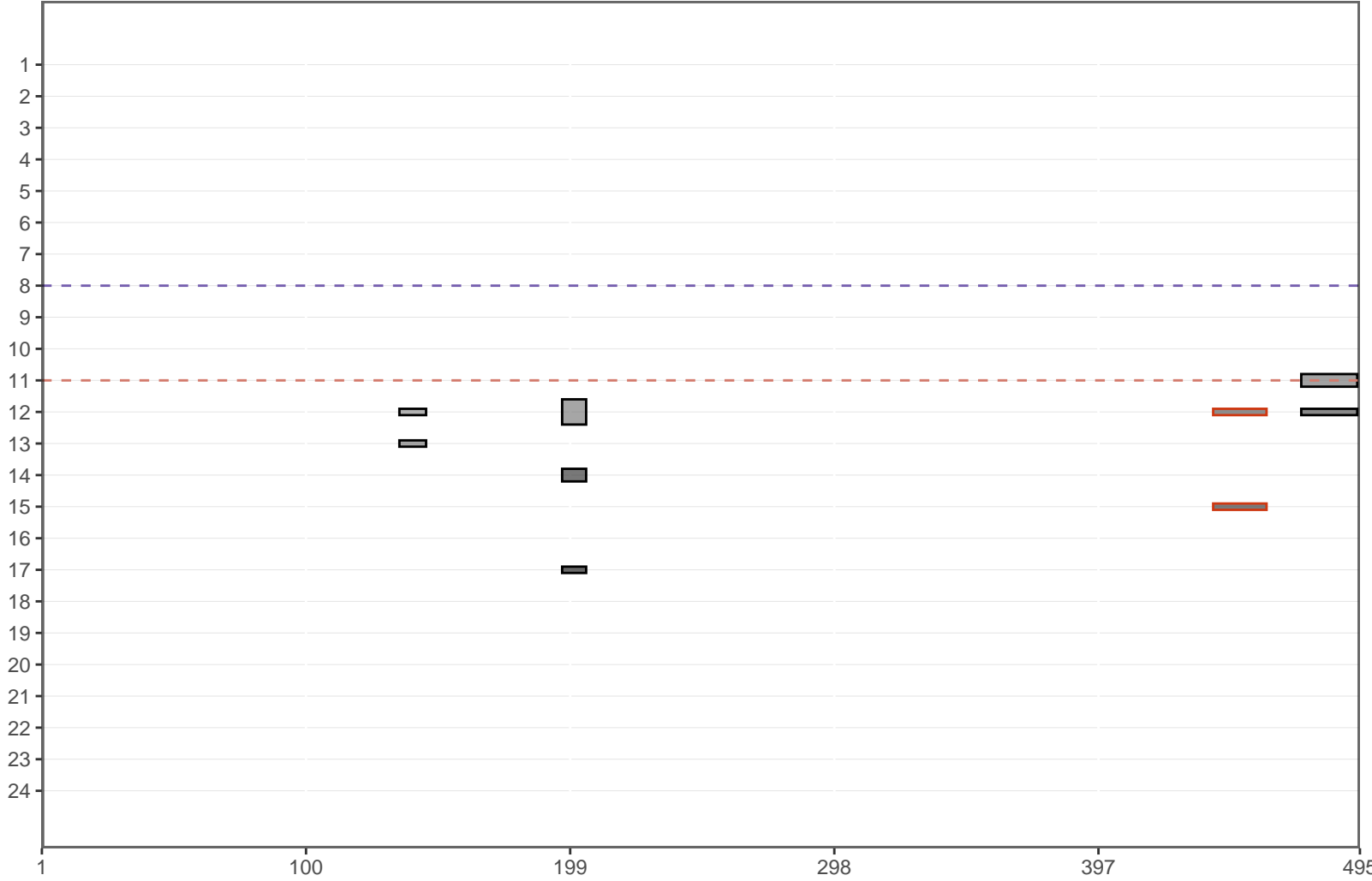
MW indication



Molecular weight

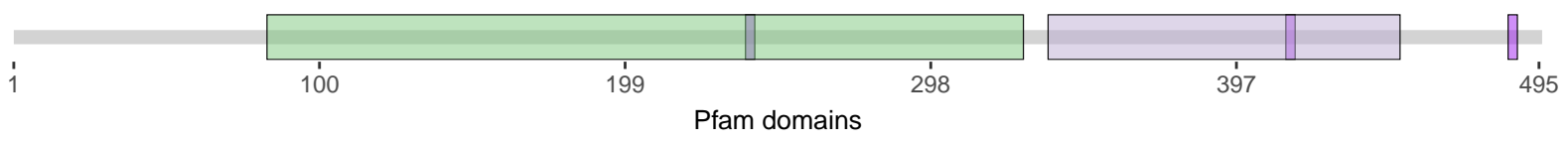


Gel Slice



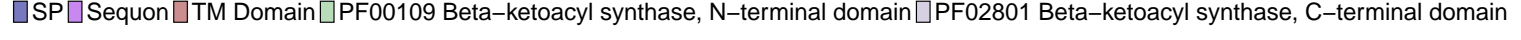
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

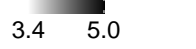
MLQVIMGPNYISITADATENFGILNANAHIRGEADLMLGGSDAAIPIGLGGFVGRALSGRNGDRRAERPWDGSRDGFVMGEGAGVLVLEELHAKQRGATVAEFLGGSTFDAAHMTPEHPPEGTGVLGIEKALAGSGVSKEDNNYNHAHATSTLAGDKIEVQALLYCFGQNPPELRVNSTKSMIGHLLGAAGAVEATQAIRTGWVHPNINLENPDEGVDFTRLVGPKERLDKRVKLSNFSFGGGHNSILFAPYK

NbL18g19190.1 21_kDa_protein-like [MW = 16.77 kDa]

No. of times detected



log(intensity)



Values from



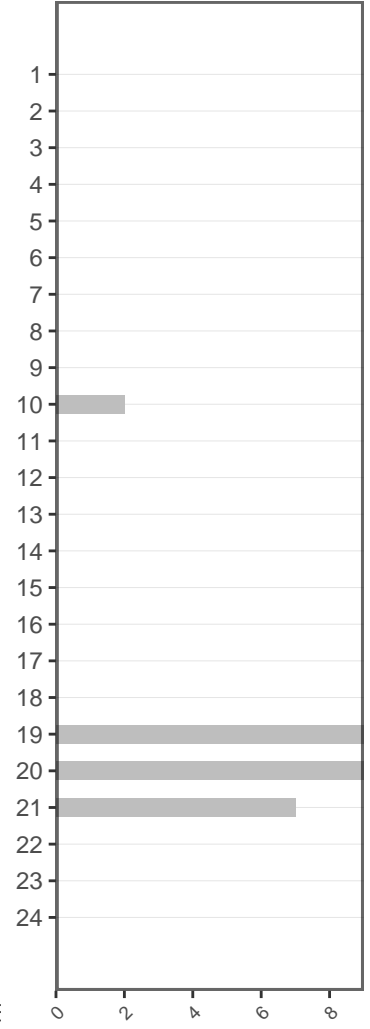
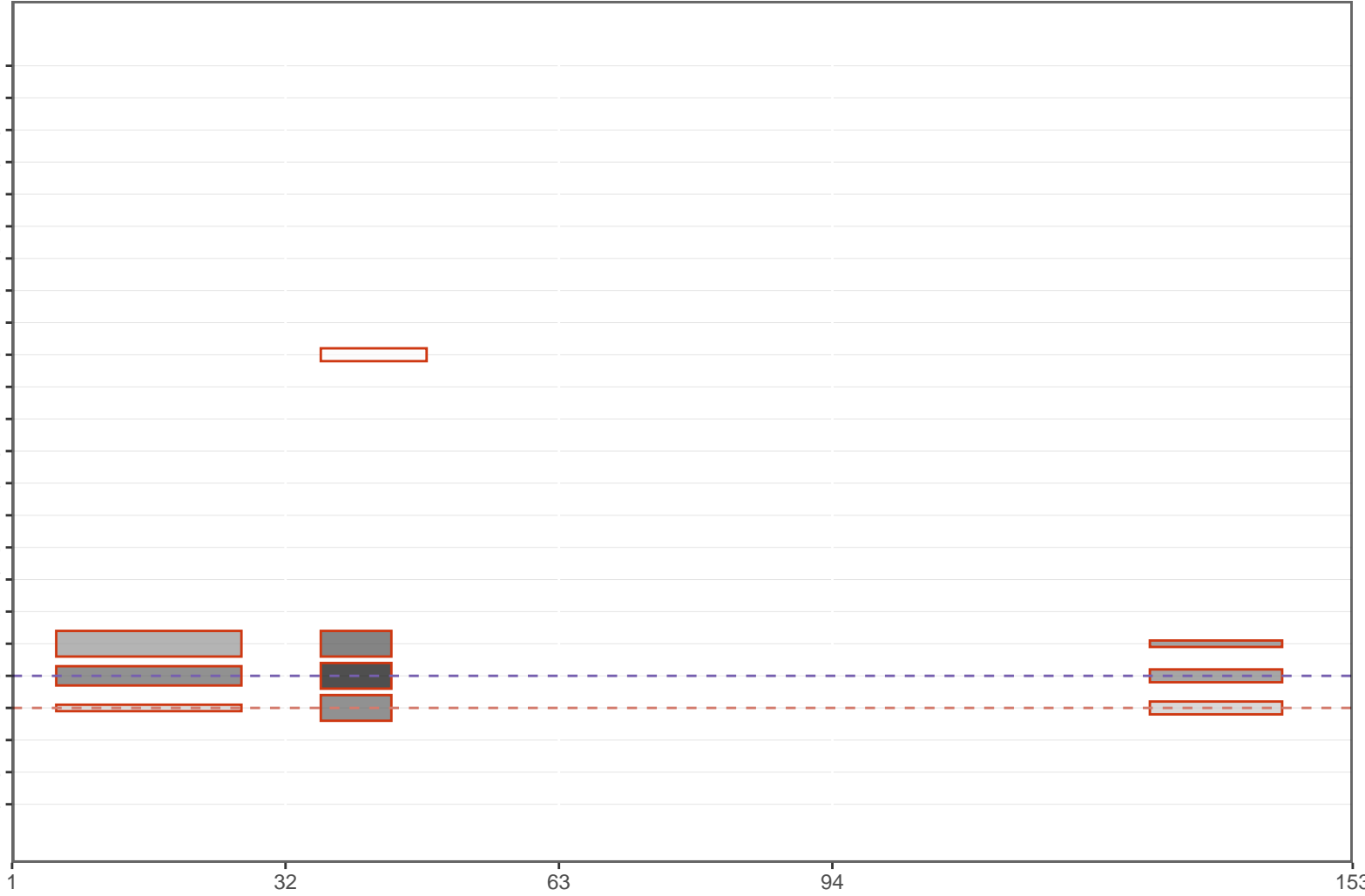
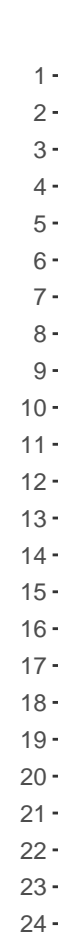
MW indication



Molecular weight



Gel Slice

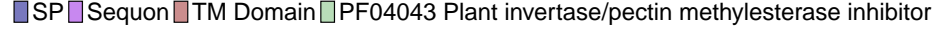


Protein length



Pfam domains

Pfam Description



Protein sequence:

DSMDLSKTLSELKHLKSNKAFKQGMENLETWVSAALNEDTQDGFKEIDGKLRGDKRKRITFNARVTSNANLYLNGLDDGRNKTAHP

NbL18g19130.1 peroxiredoxin_Q_chloroplastic-like [MW = 23.59 kDa]

No. of times detected



log(intensity)



Values from



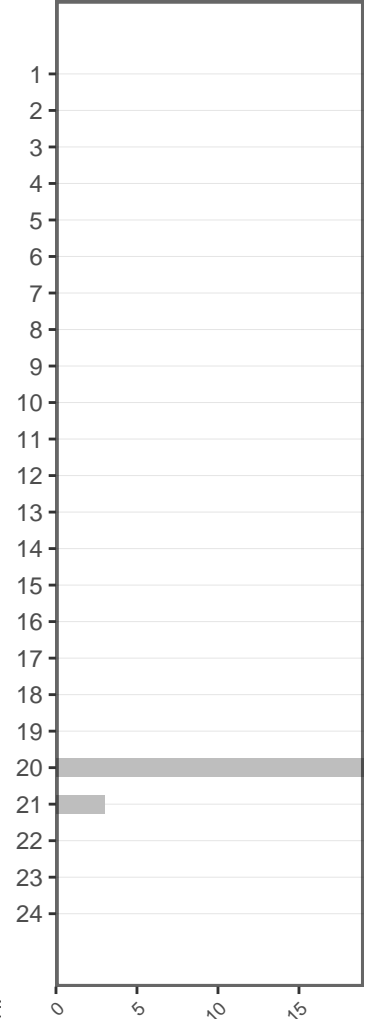
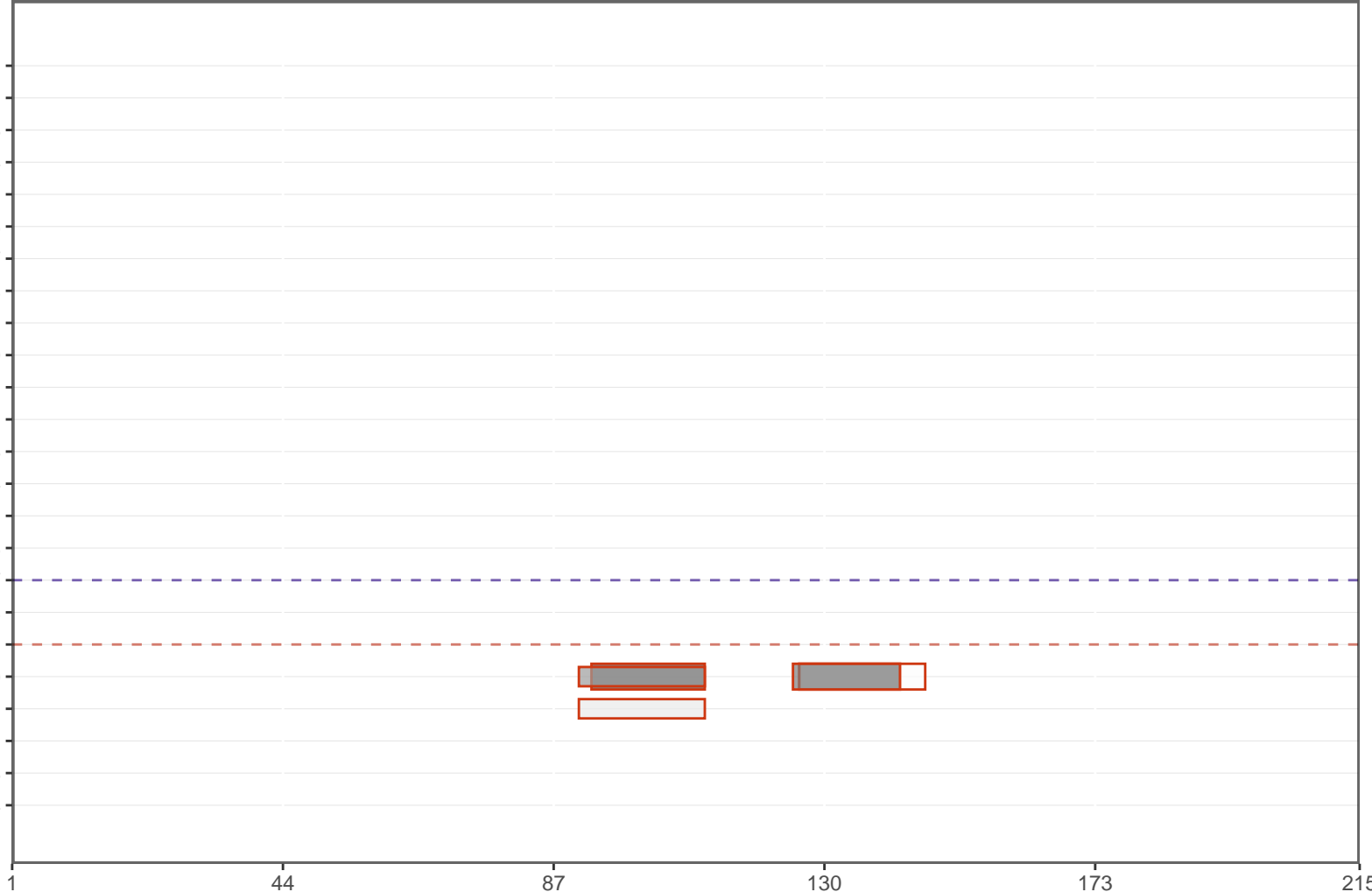
MW indication



Molecular weight



Gel Slice

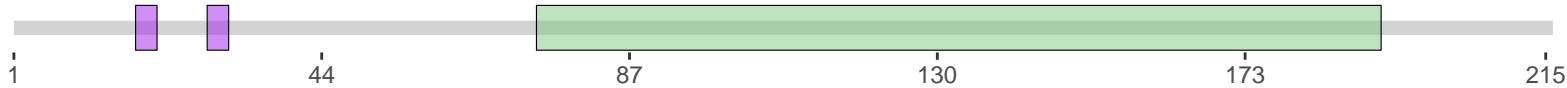


Protein length

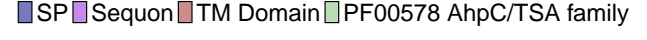


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VVVVYYPADETPGGTGAGAFRDSYKFRKAGAGVVGISGDDPMSHKAFKKYKLPFTLLGDEGNVYRKEWIGPGDLFTLPGRGTVLDKNGVWQLYVNGFGPERKHIDETLKLGLSL*

NbL18g19090.1 sucrose_synthase-like [MW = 91.19 kDa]

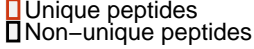
No. of times detected



log(intensity)



Values from



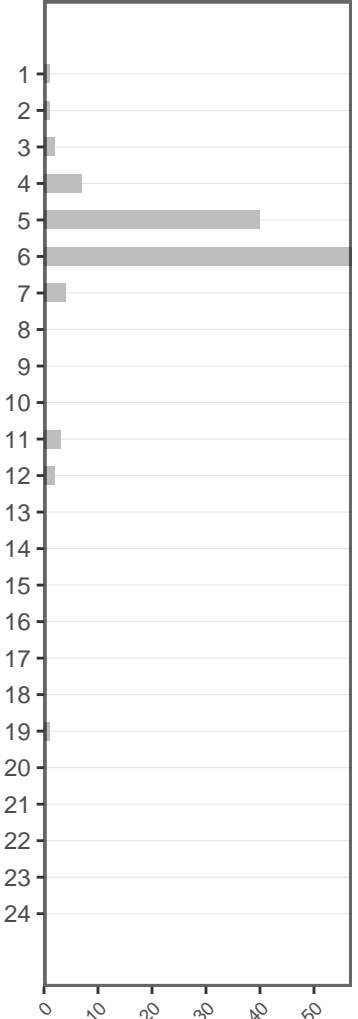
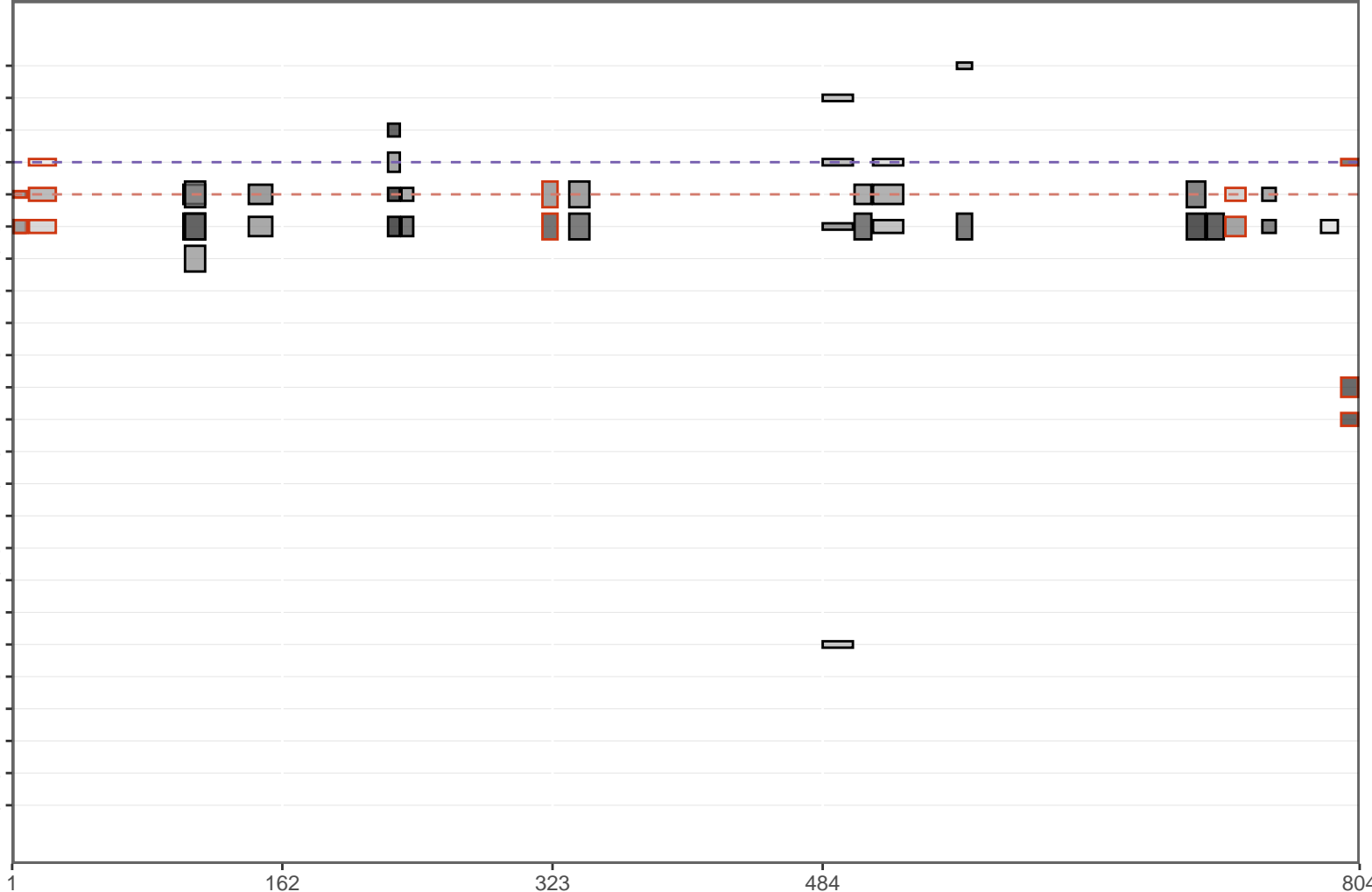
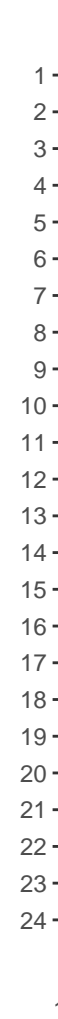
MW indication



Molecular weight

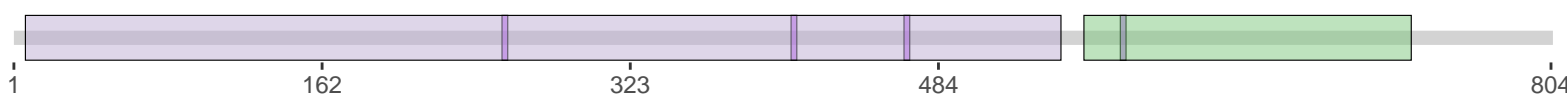


Gel Slice



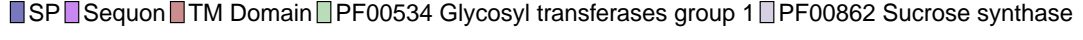
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

..EELVKELOAKPDLIENYSEGNLAABLAKKFGATQGTIAHALEKTKYPNISDLNWKKFFDDKYHFSGQFADLFAMNHSDPITSTFDQEIAGSNKNTVGGYEGHATFMPGLYRVYHGGIDFDPKFNIVSPGADMISYFFYTEKEKRLTFNFAEIEELLYSPVENKDHGLVKDRNKPIFTMARLDRVKNLTCGLEWYAKNARRELNLVVVGGDRRKEKDLLEGAEKMKMYDUETYNLNGDFRWISSGMNFRVRNGELVRYIADTRGAFVGRPAEYAFGLTYVESMTCGLPTF/

NbL18g19080.1 sucrose_synthase-like [MW = 92.49 kDa]

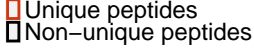
No. of times detected



log(intensity)



Values from



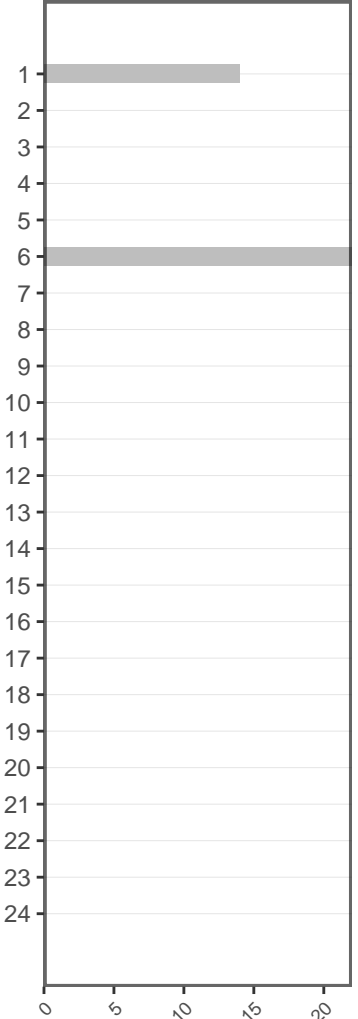
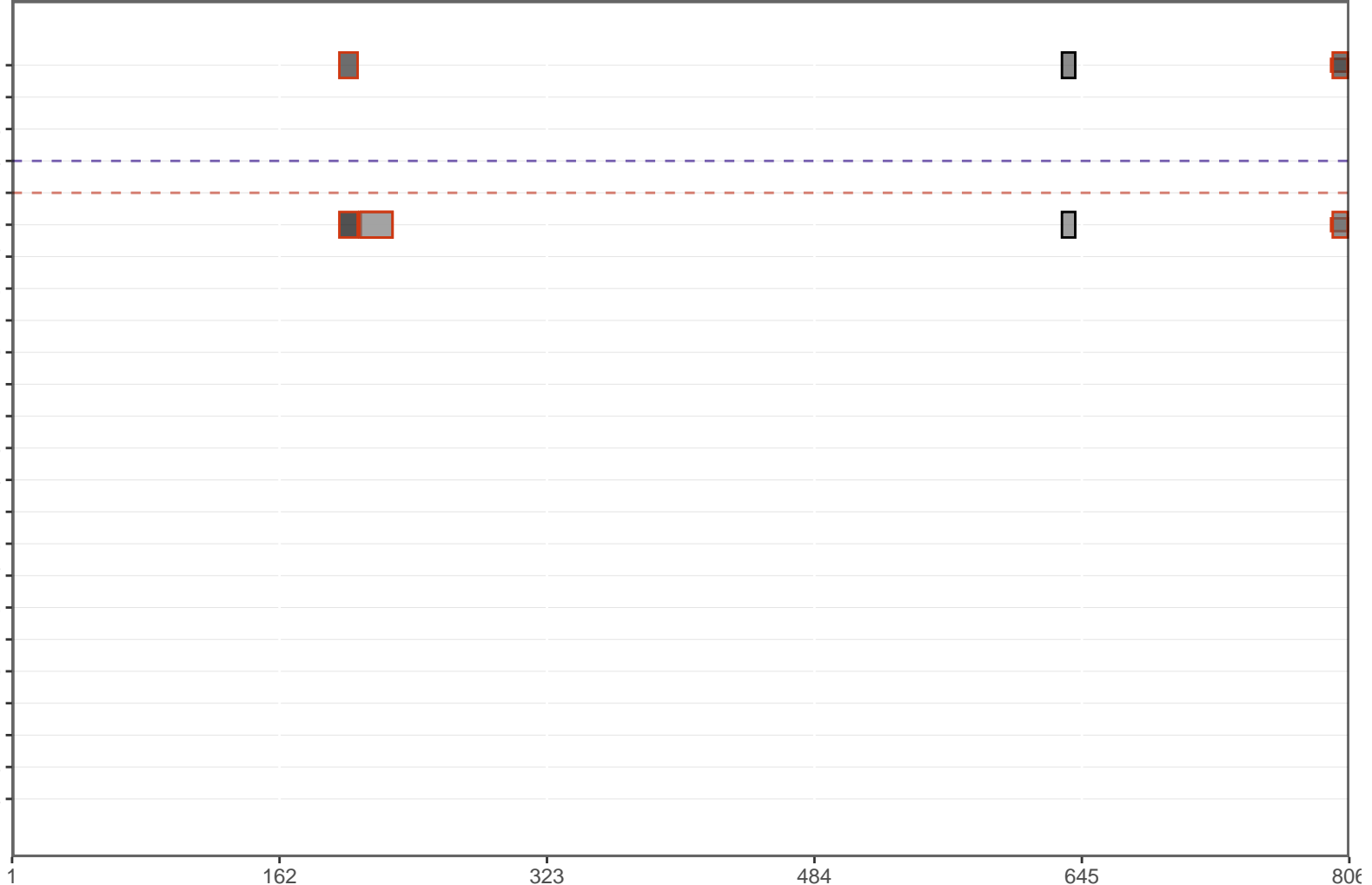
MW indication



Molecular weight

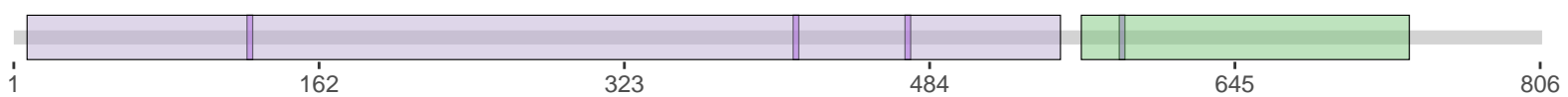


Gel Slice



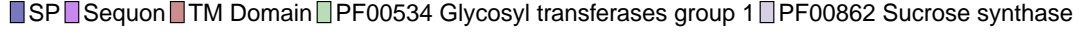
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

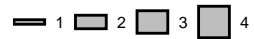


Protein sequence:

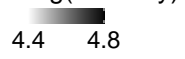
FTTEDVAKEIAAELGAKPDLHGNYSSEGNLAASLLAKLGVFGCTAAHALEKTKYFDSDIYKPKFDEKYHFEAGDTADLIAMNHTDFRITSTFQEIAGGKDTVGGVYHMAFTMPLGIVYVHGGIDVFDPKFNVISPGADMNLYFPYFEKEKRLTAWHPHIEELLFSDVFNDEHDTGLKDRNKPIFTMARLDRVKNLTVGLVELYAKNPRLRRELNLVWVGGDRRKEKSDLEEQAEMKMYELUKTHNLNGQFRWISSGMNVRNGELRYIADTRGAFVQRFAYEAFGLTVVEAMTGGI

NbL18g19060.1 eukaryotic_translation_initiation_factor_3_subunit_K [MW = 26.2 kDa]

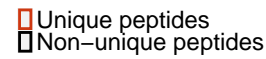
No. of times detected



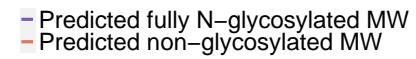
log(intensity)



Values from



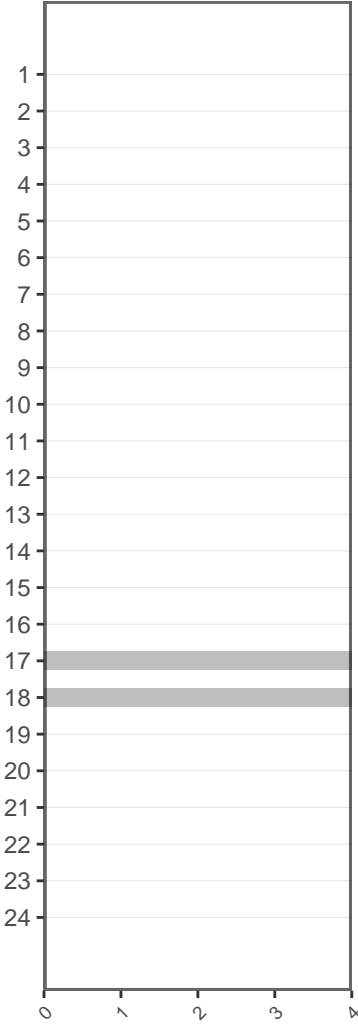
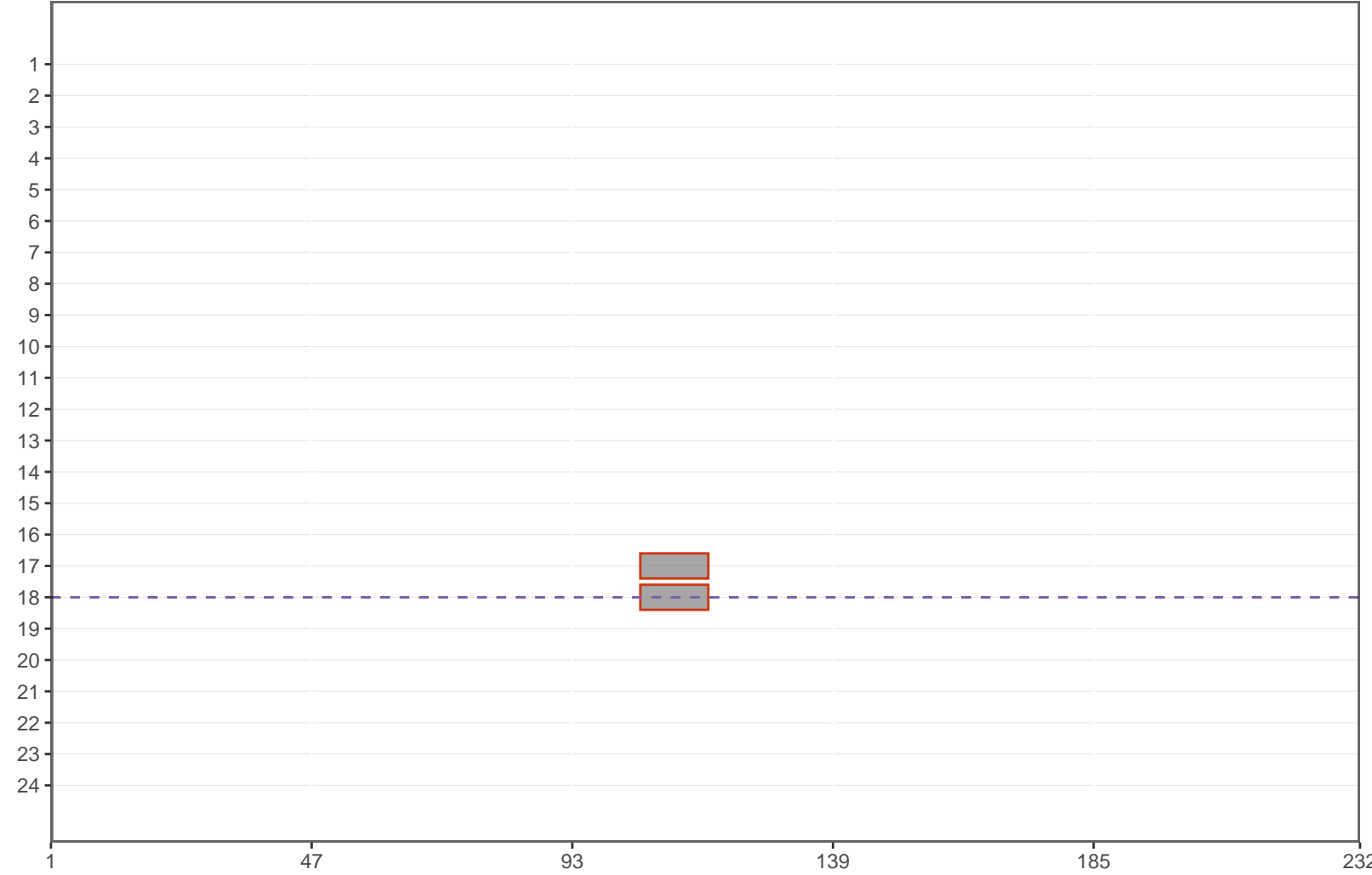
MW indication



Molecular weight



Gel Slice

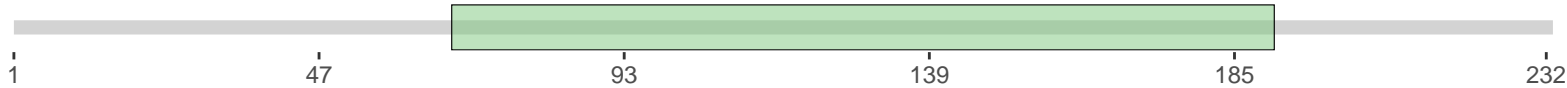


Protein length

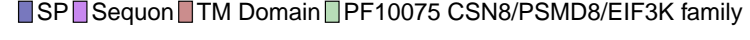


Peptide counts over 4 repeats

Pfam domains



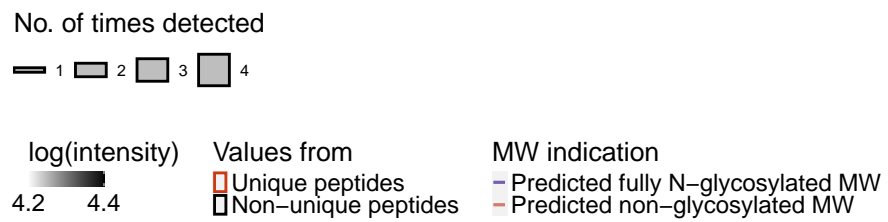
Pfam Description



Protein sequence:

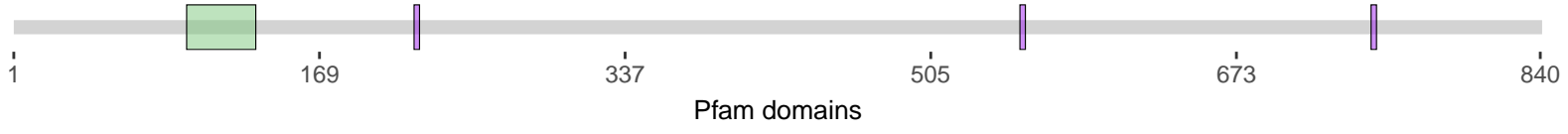
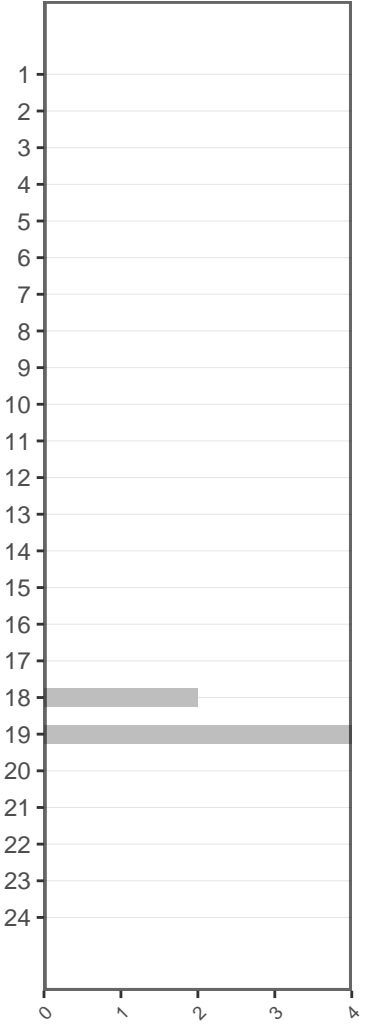
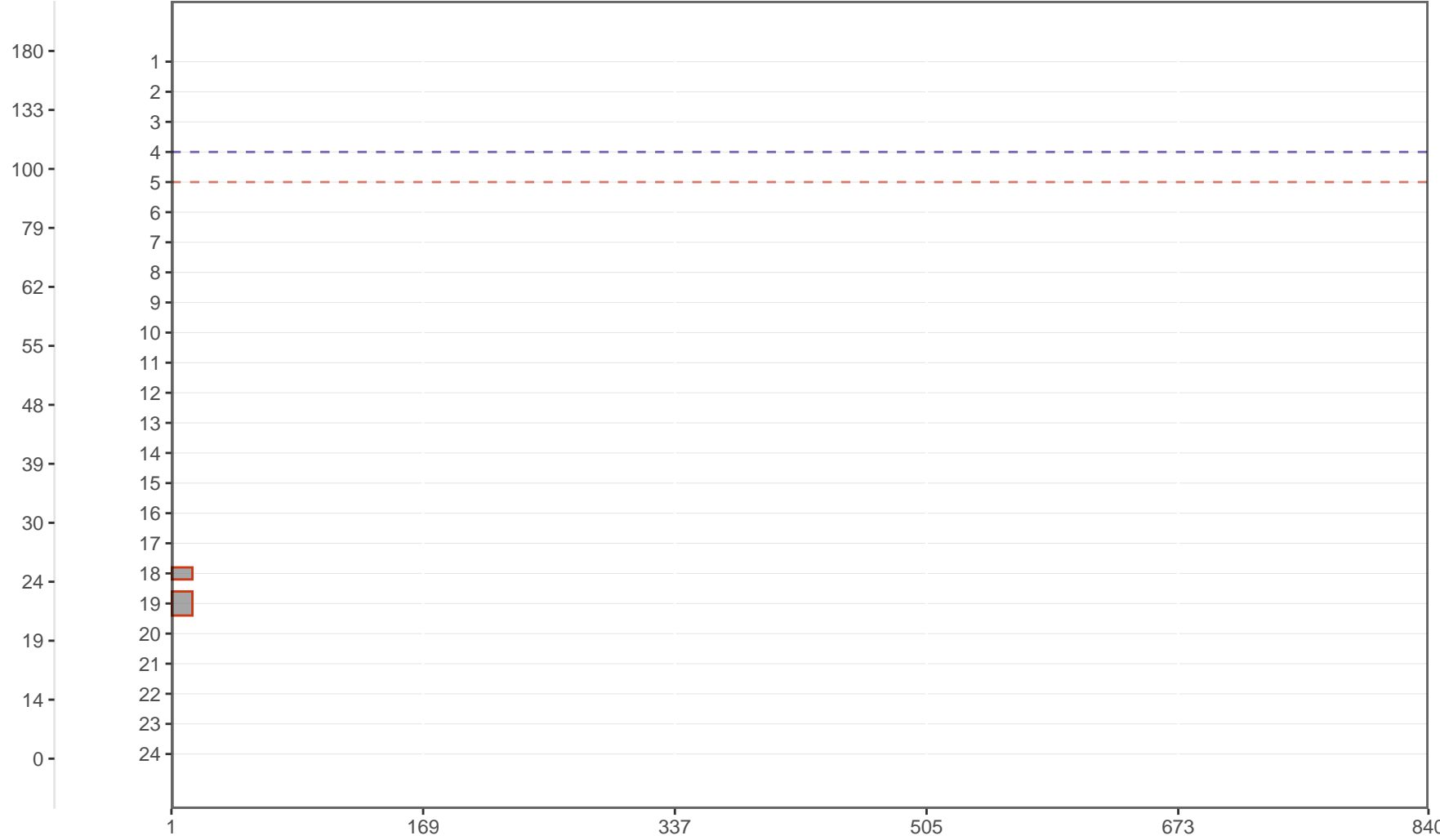
DFKTLVLSHYLETARFRGFVDEAAKRHVEVWPGFEGAILAWVHLSYFYQKVPRAVAEANEGLSLOKFLHGVSNNGWVIEKGGKGGQLTLPPTFENHPELKKNTADSVFLEHVTREPLG

NbL18g19050.1 microtubule-associated_protein_TORTIFOLIA1-like [MW = 92.53 kDa]



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain PF12765 HEAT repeat associated with sister chromatid cohesion

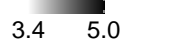
Protein sequence:
ISVMKAVKESAEITRSHHDEYEVYHDDKGCESGSGENLFPDNFORKEVMGSHGIDEASLGTPLGTSQHVVEEIEEGRYFGGTQDRRLDSTTLESGKLVHGGCHVAKEMLSVRKQLLDIENKGNLDDLLKEFTTNVDLMSMMQMKVAGLEGMDRIMASELSYGGGRGDFLFTKFMKRSPVSWASRLSTYTPRPQVDHPHRKFSLLPTKGMMDVQEERTLVKSRSSSFRITQNLDMWTDIAAKGGGYPVKGKGVHKNSSGGGTHGGGLRRNNDVFSRISTTNAKQF

NbL18g19030.1 prefoldin_subunit_1 [MW = 14.83 kDa]

No. of times detected



log(intensity)



Values from



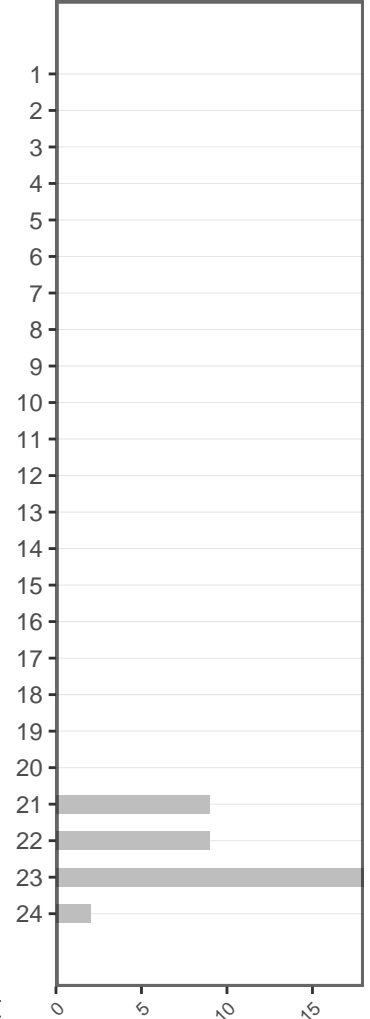
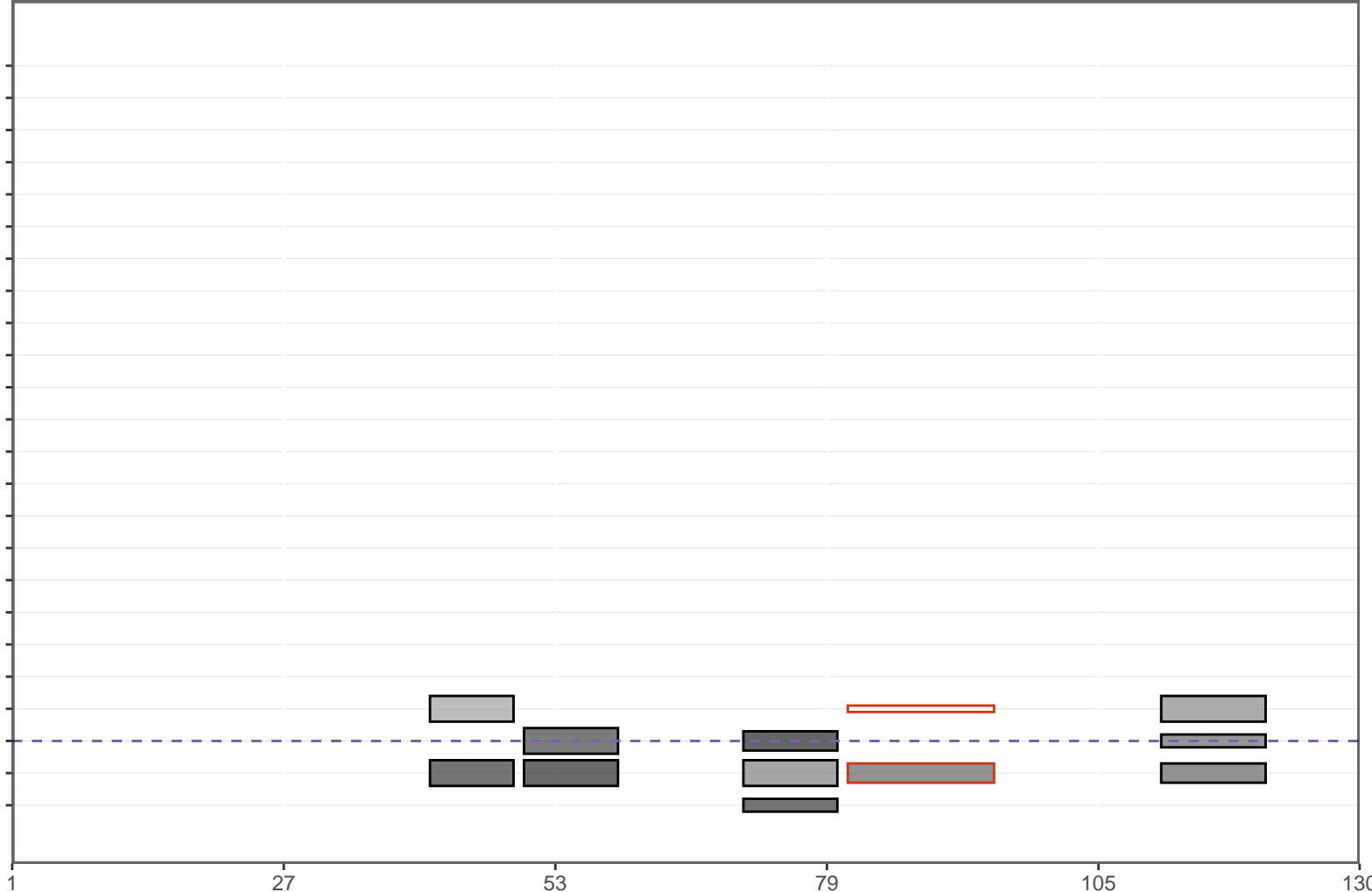
MW indication



Molecular weight

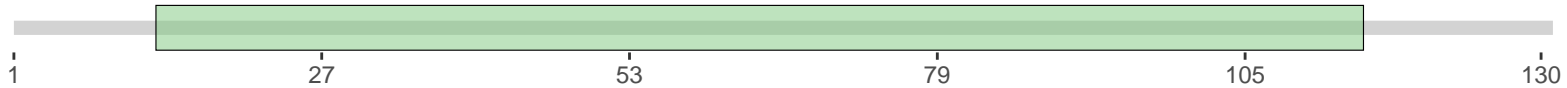


Gel Slice



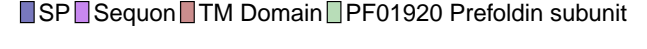
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SDDTNTYKAGMRFLEPKFTVLMDEGEQKLDKETAIASLQTSKEYLEKHLAEVENNLRLLGGDFGLARQIMTMSVA*

NbL18g18900.1 pyruvate_dehydrogenase_E1_component_subunit_alpha-3_chloroplastic-like [MW = 47.9 kDa]

No. of times detected



log(intensity)



Values from



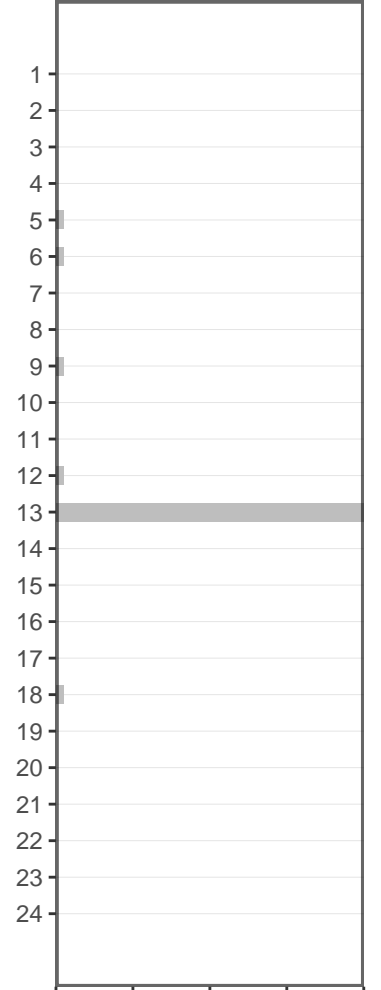
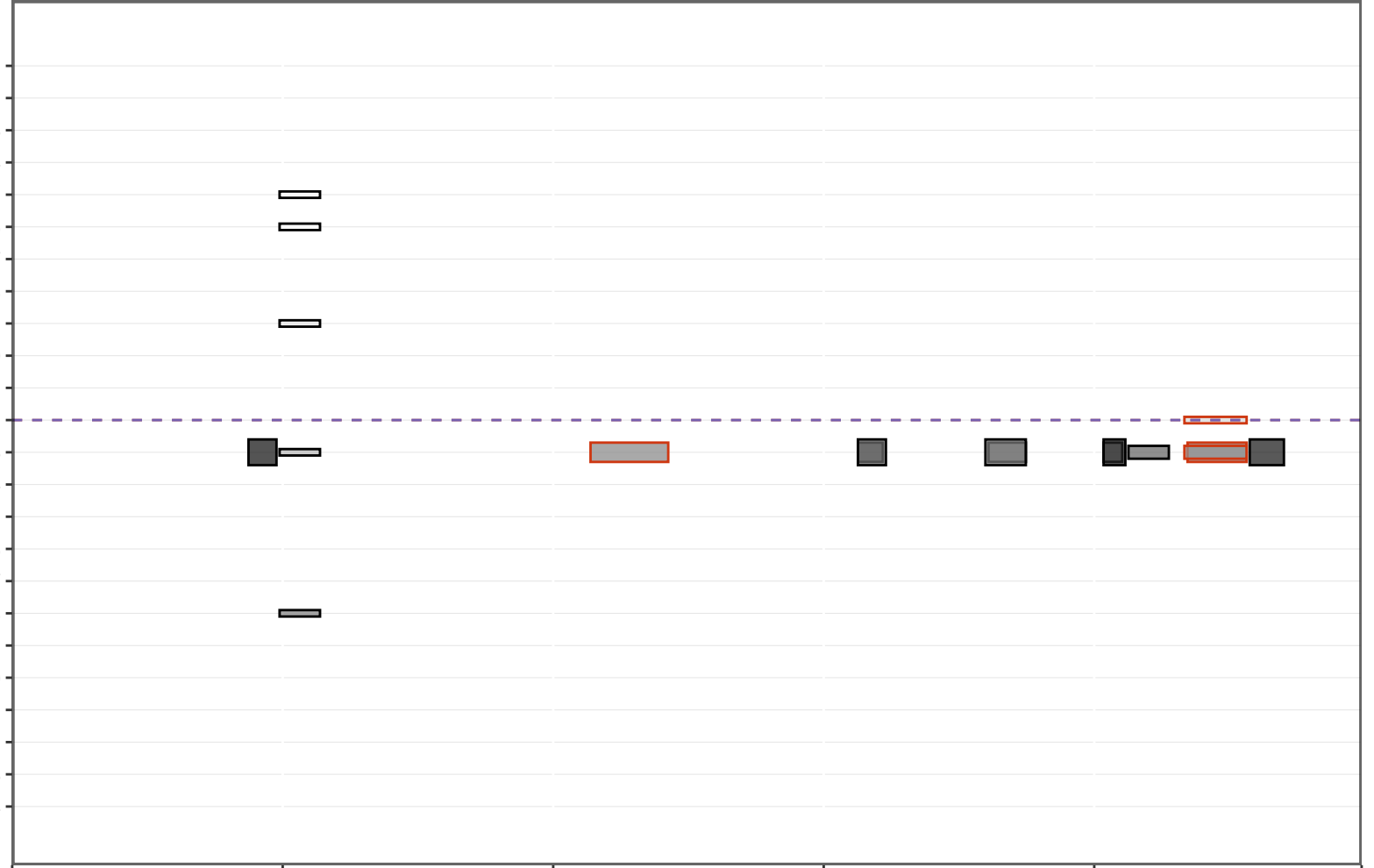
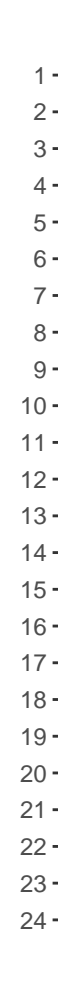
MW indication



Molecular weight



Gel Slice

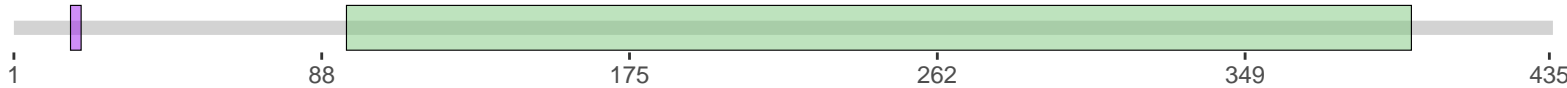


Peptide counts over 4 repeats

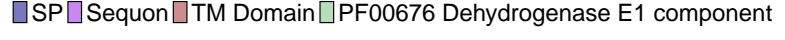
Protein length



Pfam domains



Pfam Description



Protein sequence:

JAGAAFTSKYRREVAKEADCDHVLAFFGDGTGNGDFYEGELMAALWKLPIIFVENNLWAGMSHLRSTSDPEIWKKGPAFGMPGVHVDGMVLYKREVAKEAGRRARRGGEPGLTVEGETYRFRGHSLADPDELDPAEKNHYATRDPTALKKVMFENNLVSEAEKAKDKKDEVEEVEFADASPVPKRSOLLENVADPKRGGFGIGDPGRVRCEDPKFTEGTANV

NbL18g18770.1 gamma_aminobutyrate_transaminase_1_mitochondrial [MW = 41.62 kDa]

No. of times detected



log(intensity)



Values from



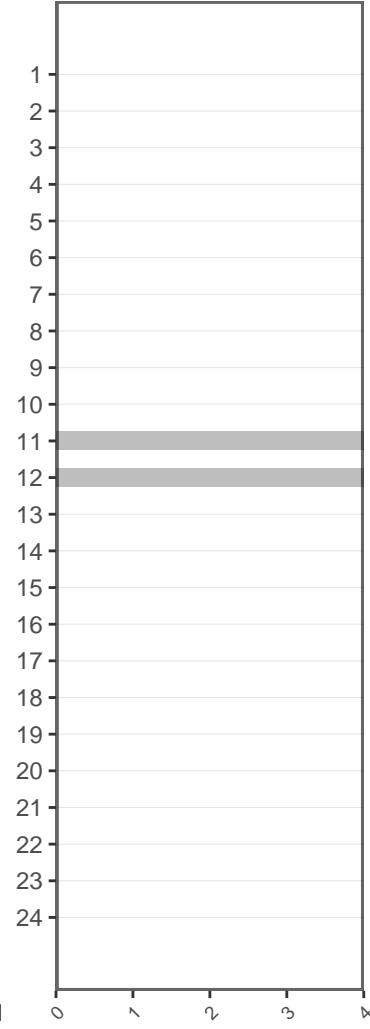
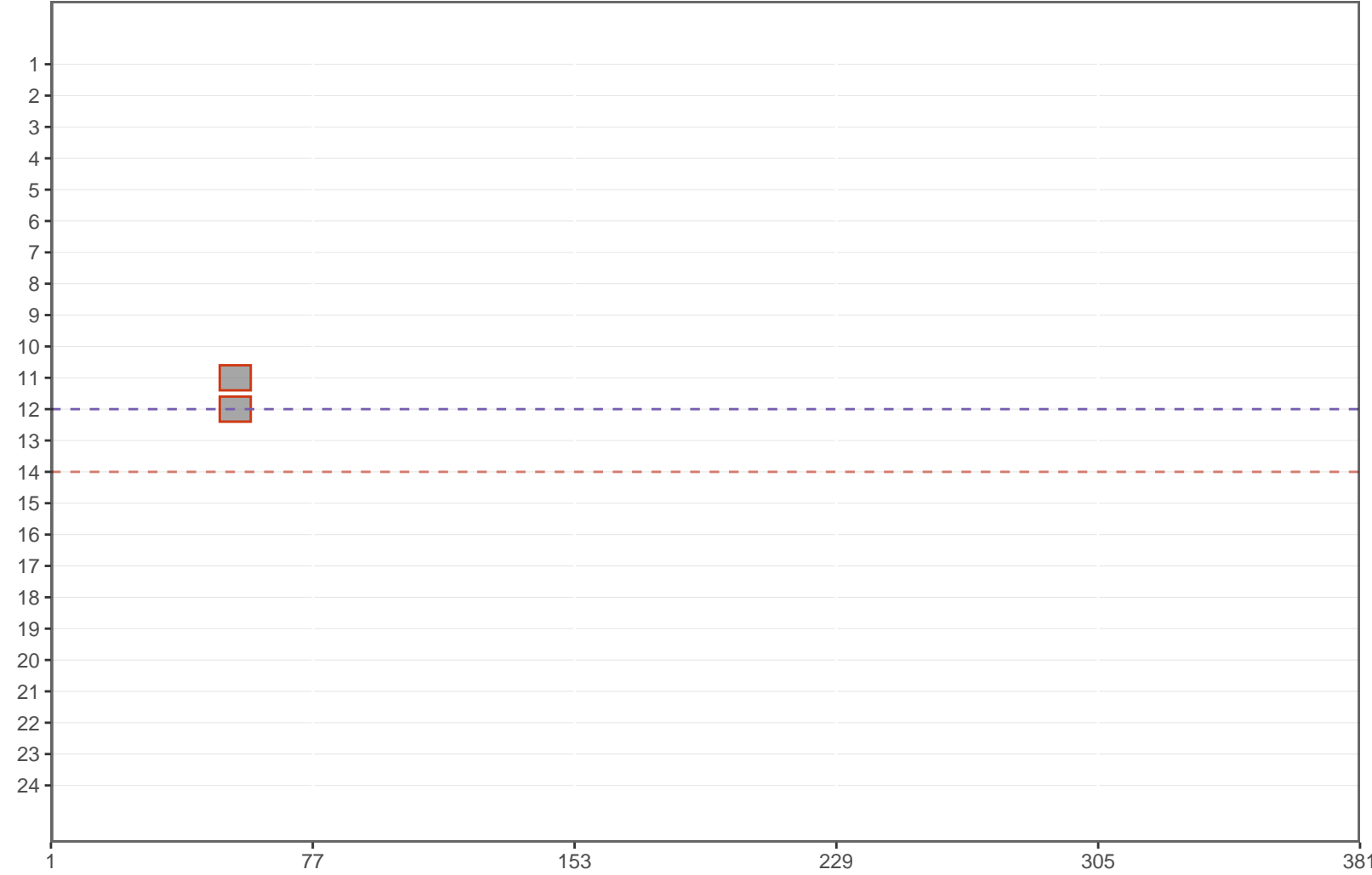
MW indication



Molecular weight

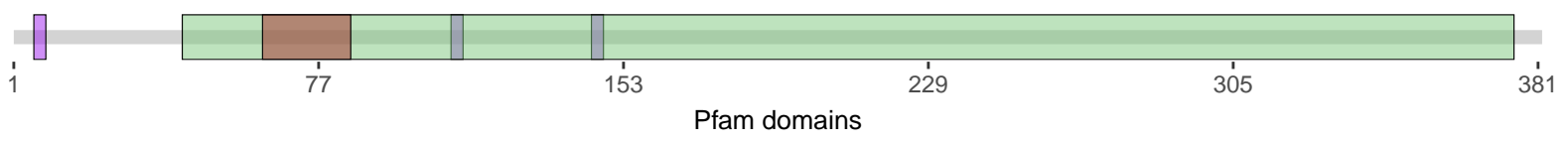


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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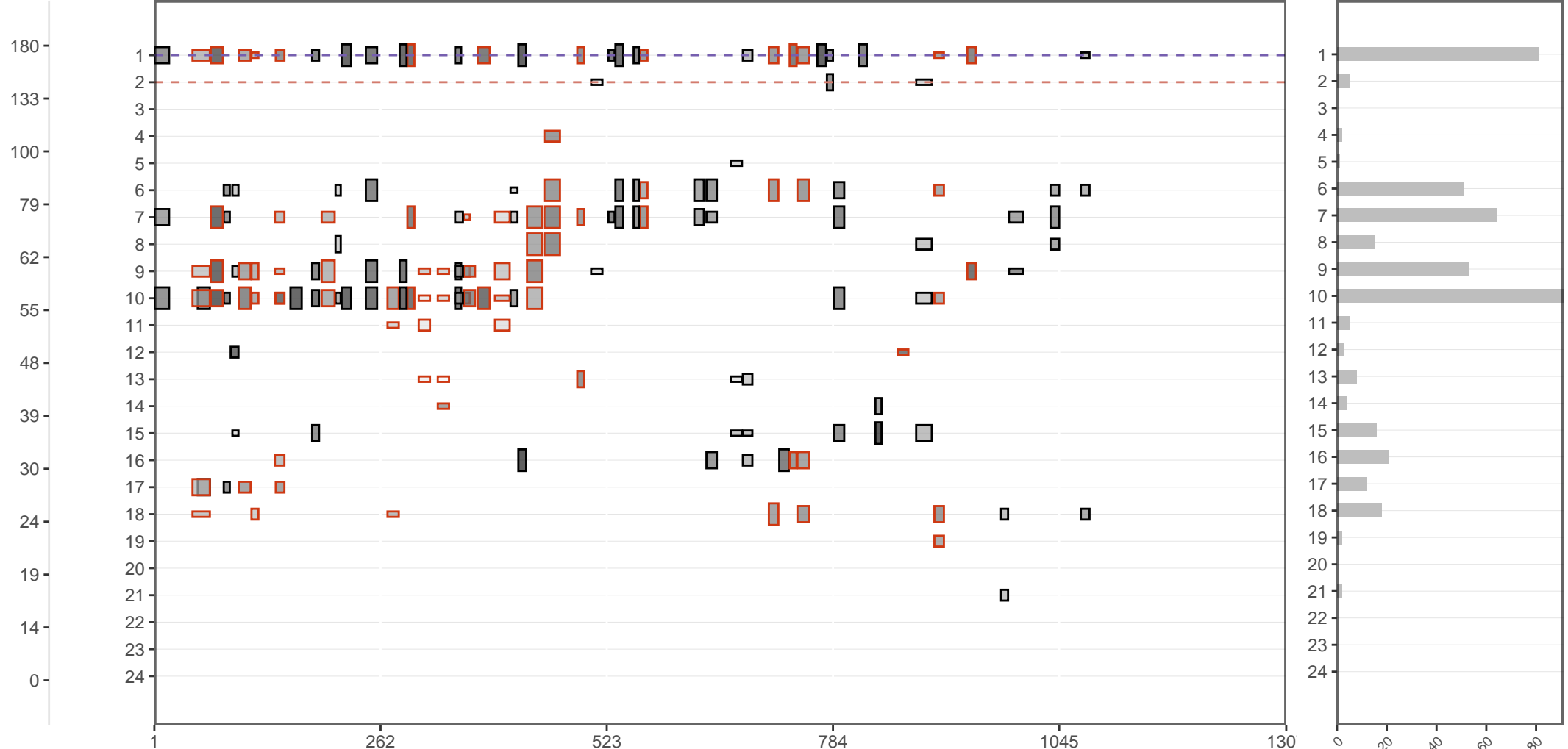
NbL18g18760.1 myosin_heavy_chain_cardiac_muscle_isoform-like [MW = 146.68 kDa]

No. of times detected
 1 2 3 4

log(intensity) 2.9 5.6
 Values from Unique peptides Non-unique peptides
 MW indication Predicted fully N-glycosylated MW Predicted non-glycosylated MW

Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfm domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

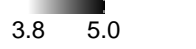
IQELEEQISTLEIKGVVAEVEKSHADRASELEAEVEAFQMKSS66LEVALTEETKEKEKELSGGLNVTYEEKKQVYANSVKEKLAETENLLEVLINELNVTQQRLEGIEDNLNAAALKEGSLMEKLSAEQLEQQGRVLEQATARSIELESLSLHDTLKRDSKELKIGATGKFKVTRDSEAGTLNEKLSKAFEDQLKSYEEQAKSTEFSSFAWKEELDGLVWKLASSETQNEQDKKILAEKKAADLSENGQLAETNMLKKNRVDLEQGLNSARAEKAEAVQCLVSHMNTITLSI

NbL18g18740.1 60S_ribosomal_protein_L27-3-like [MW = 15.68 kDa]

No. of times detected



log(intensity)



Values from



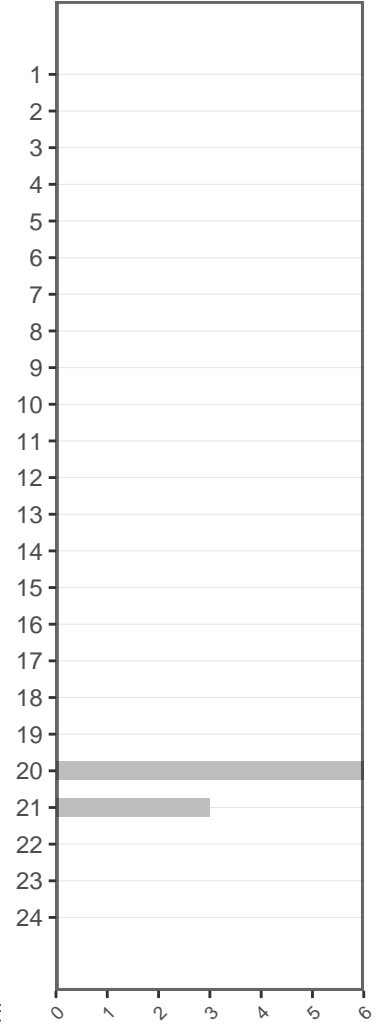
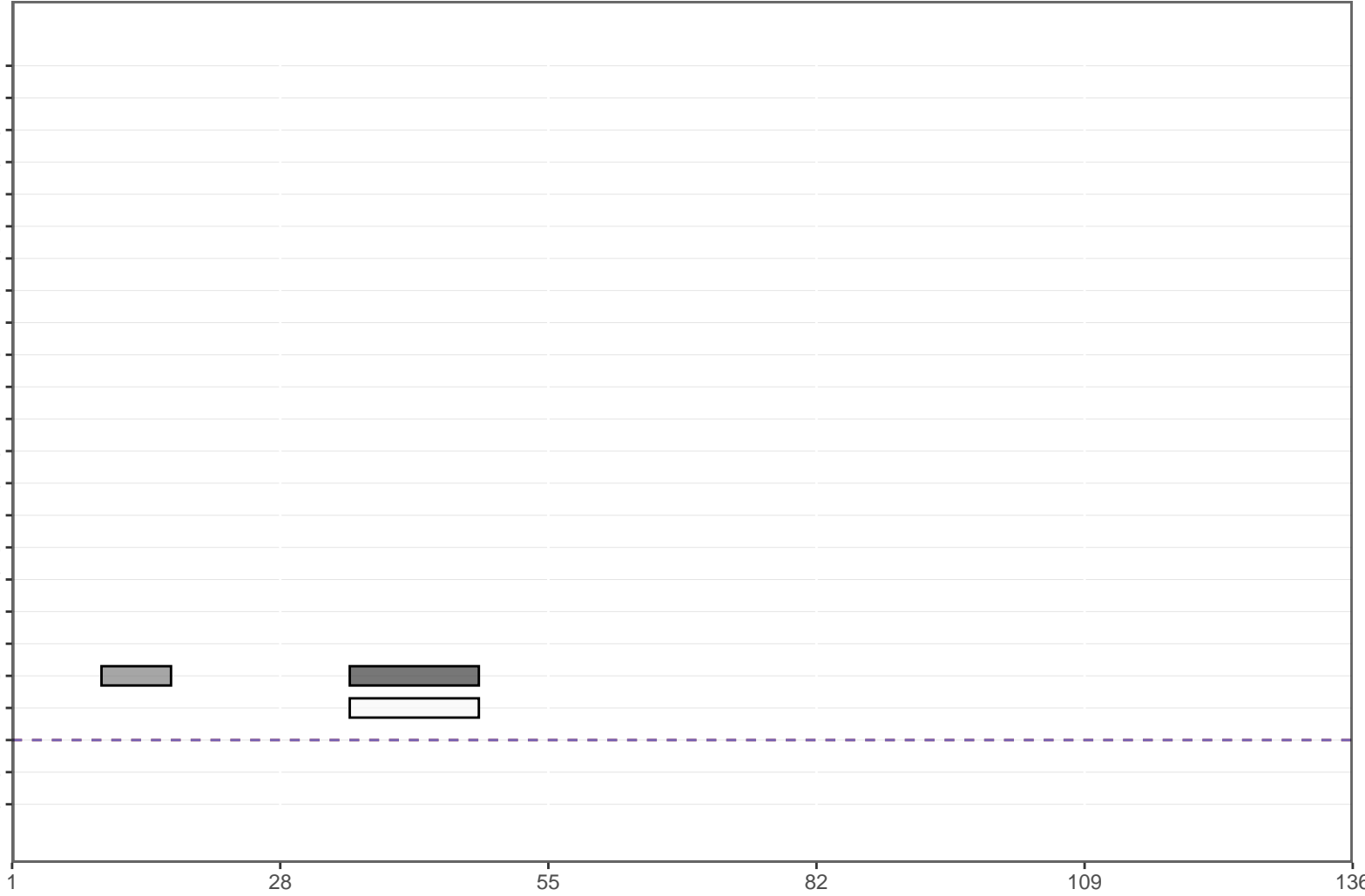
MW indication



Molecular weight

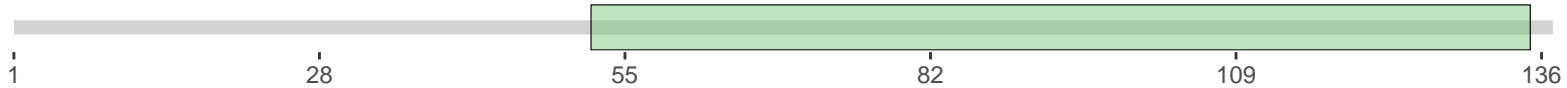


Gel Slice



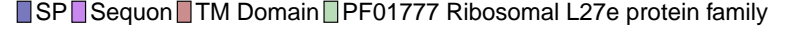
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

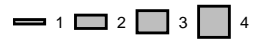


Protein sequence:

RKDSDKGQAKKSRVKTFRILNINHMPTRYFLDVLKEAVTVDLGSGSRDKKVTAAKEAKAFEEFRFTGNINRWFSSKLRP

NbL18g18640.1 heat_shock_70_kDa_protein_17 [MW – SP = 96.92 kDa]

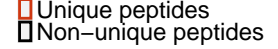
No. of times detected



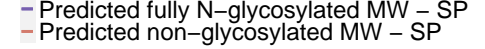
log(intensity)



Values from

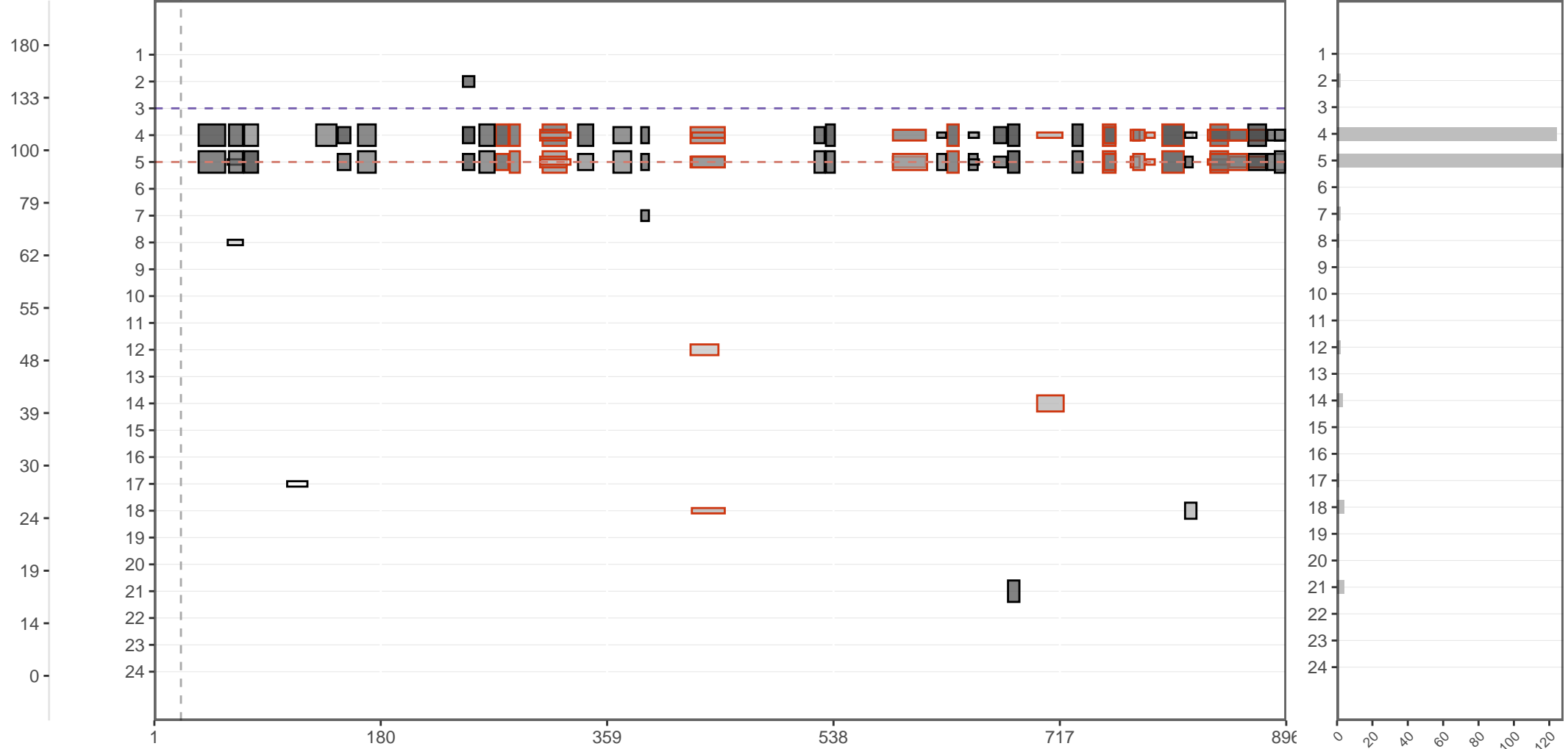


MW indication

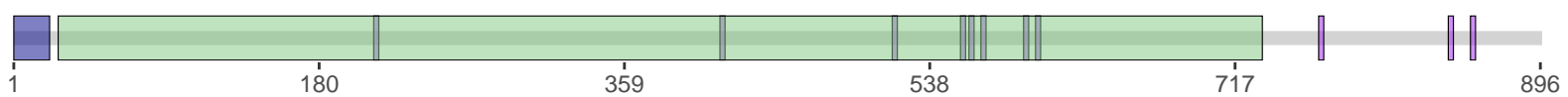


Molecular weight

Gel Slice

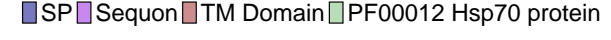


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IYDGAQLPKDESTKQLLPRMKLPSKMFBSVHVKDFEVLAVESDDFLPPQTFPLTFAQYVAGLADTSEKYASLNLGAPKAKLHFLSLRSGISLDRADAVIEVTEVVEAPRRMLTVDNSTASNTSTEGSPNTEESSEKLNADDNSNNSNDGPNAGD6STTSLSEIKLKKRTFRVPLKIDKTAGTGCDALLKESLNEAKSKLEALDKKDEERRRRTAELKNSLEGVHYDTRKLESEDFANIGTSGERGSPFIEKLDEVGELWLYDGEDASATQFKKRLDELKAGDPFFRIP

NbL18g18610.1 uncharacterized_oxidoreductase_At1g06690_chloroplastic [MW = 40.32 kDa]

No. of times detected



log(intensity)



Values from



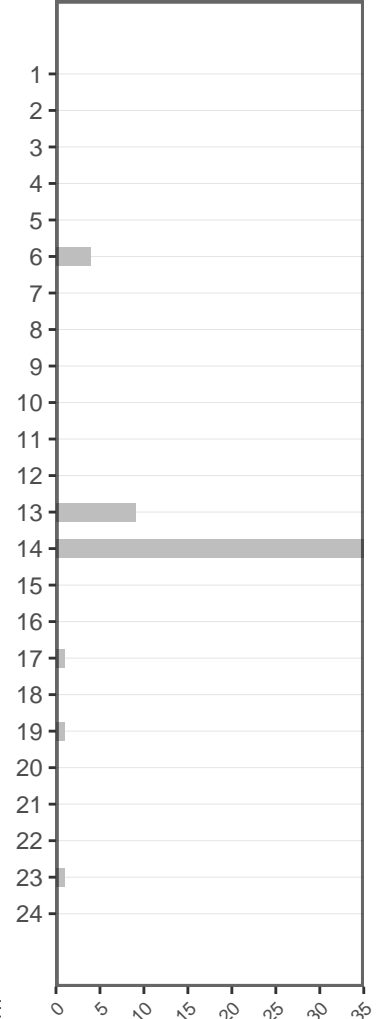
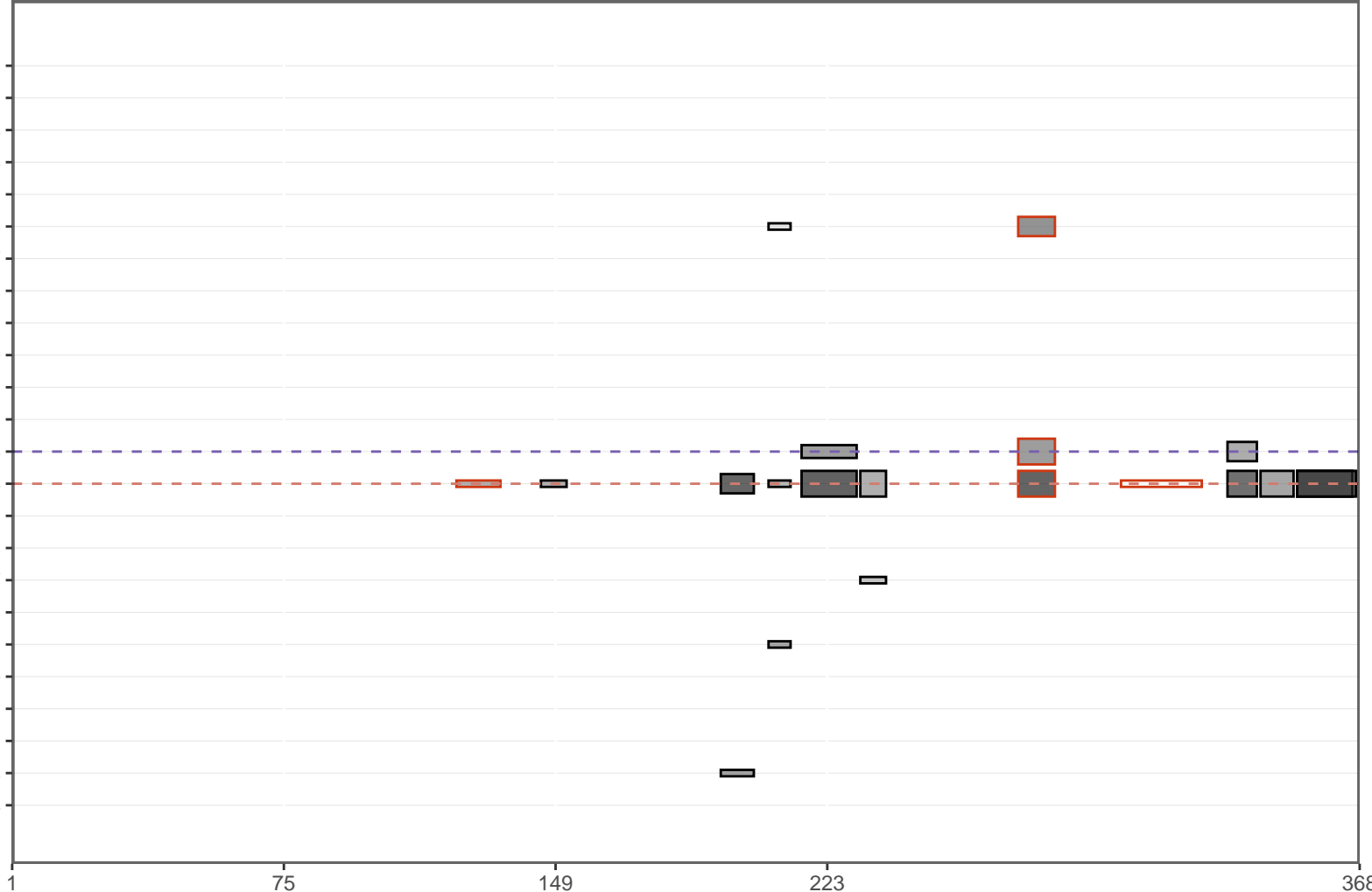
MW indication



Molecular weight

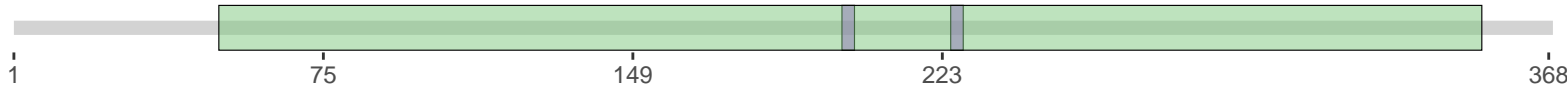


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL18g18480.1 23-bisphosphoglycerate-independent_phosphoglycerate_mutase-like [MW = 61.06 kDa]

No. of times detected



log(intensity)



Values from



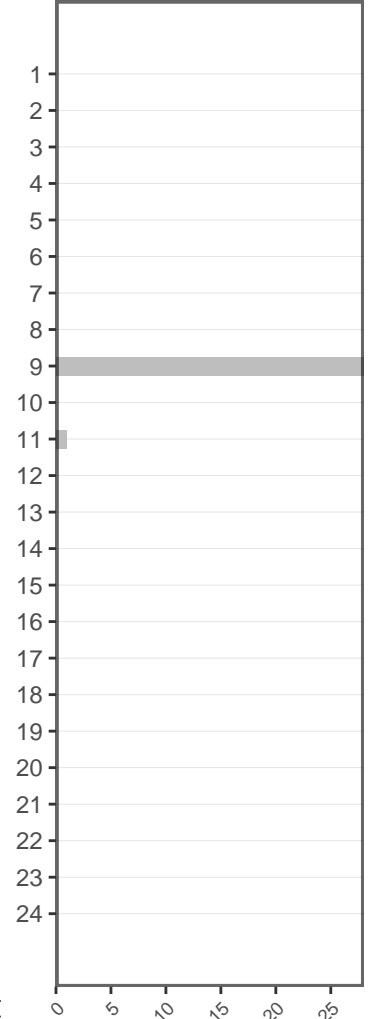
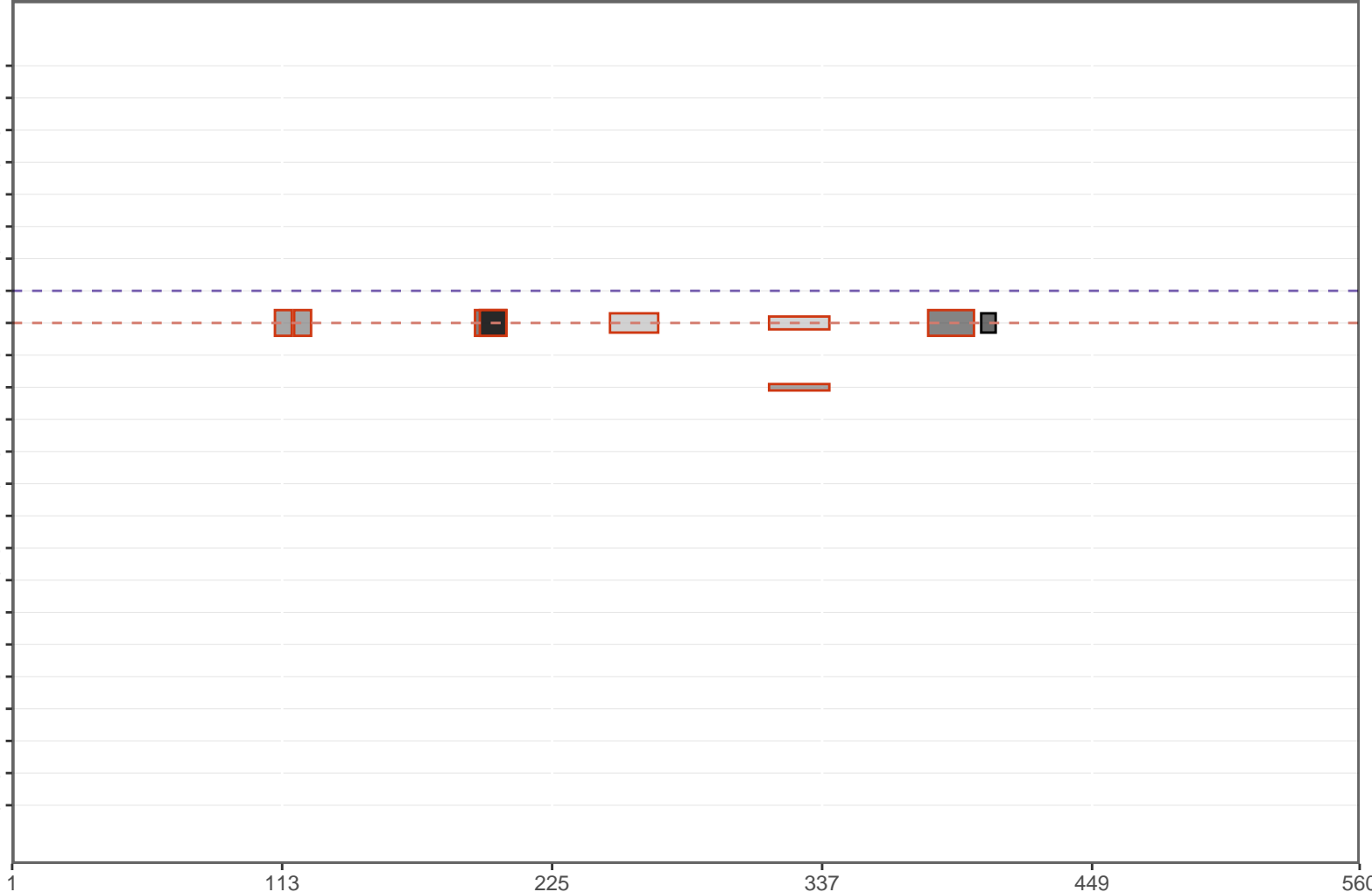
MW indication



Molecular weight



Gel Slice



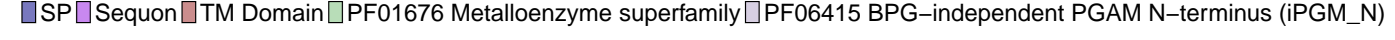
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VDDYQKPYGPIIDGDAVVTFRADRMVMLAKALEYENFDKFRVVRPKIRVAGMLQYDGELOLPSHYLVSPDDIRTSGEYLVIRNGVRTFAGSETYKFGHVTFFVWNGNRGDFYFNKLEEVYVEIPSDSGITFNVKPKMKALEIAEKTRDAILNGYDFDQVRLNPNMGDMVGHYTGDKATIEACKAADEAVKMLDAIEGVGGYLVTDHGNAEADMVKRNKKGESALDKNGANGLTSHTCPEVPAWGGPGLAPGVVRFRRDLPPTGGLANVAATFMNLHGVEAFPSDYEPSLIEVVC

NbL18g18460.1 enhancer_protein_2-1_chloroplastic-like [MW = 28.55 kDa]

No. of times detected



log(intensity)



Values from



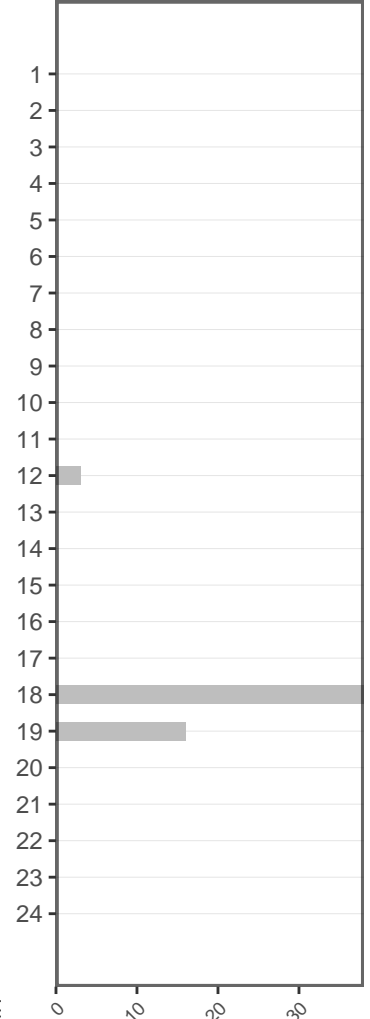
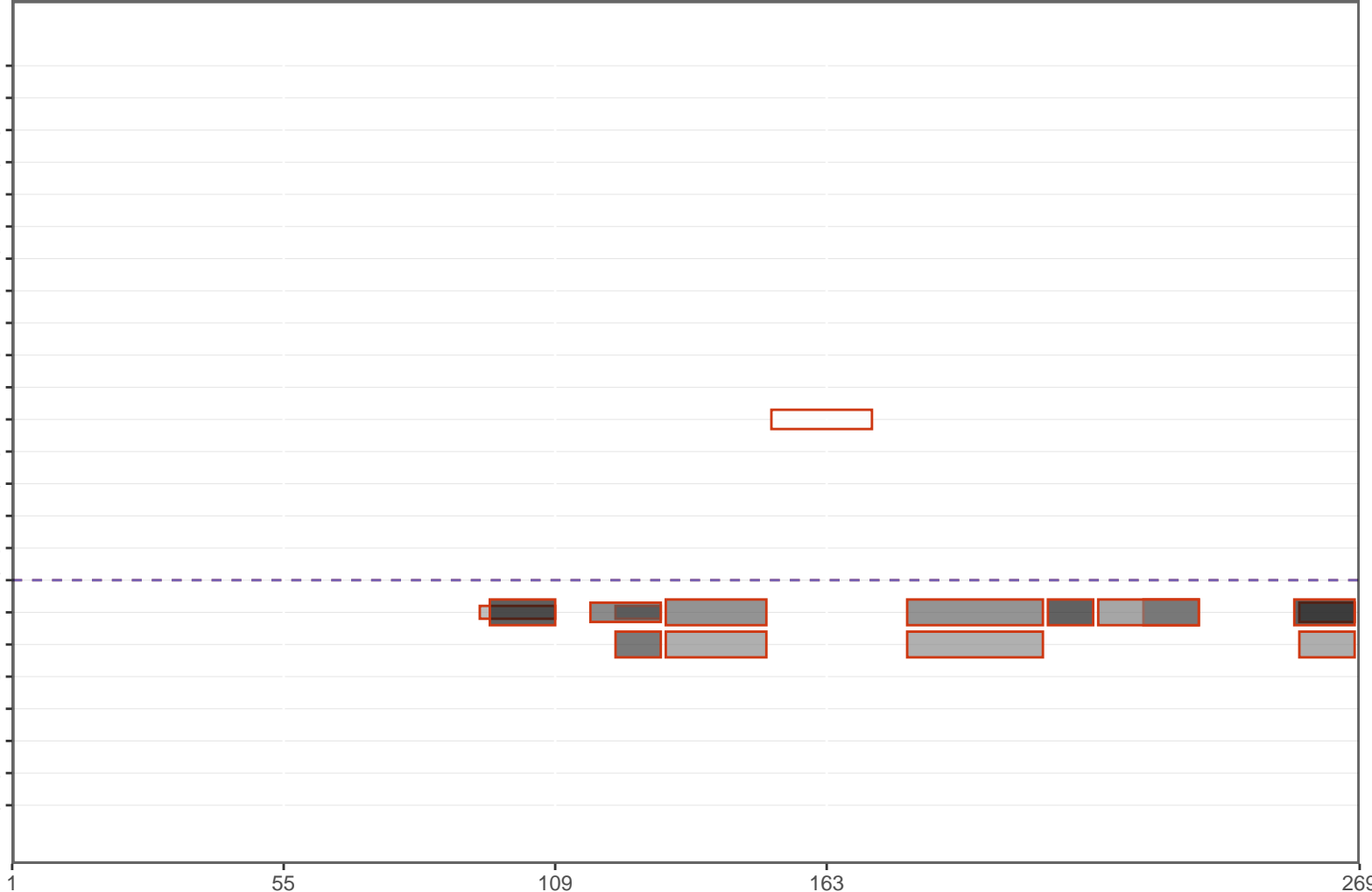
MW indication



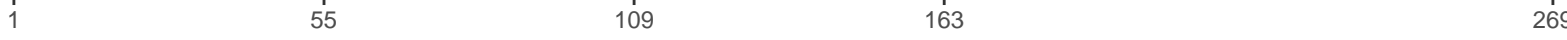
Molecular weight



Gel Slice

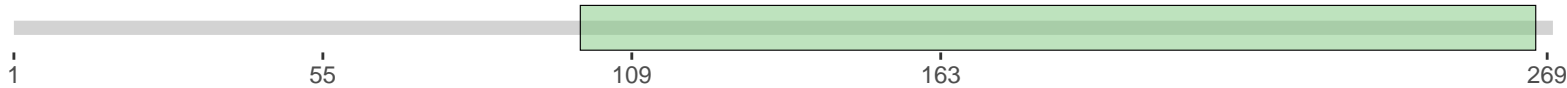


Protein length

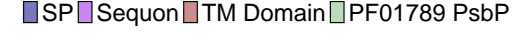


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

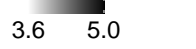
<EVEFPGVLRVYEDNFDSLSNLVTVPTDKKISITGYGSPPEFLSQVDLLGKQAVFGKTDSEGGFEGGAWATNLEASSTTVGGKEYHLSVLRTRADGDEGGKHQLSATVNDGKLYICKAQADGKRWFKGARKFVENAATSFVA>

NbL18g18270.1 uncharacterized_LOC107810187 [MW = 26.64 kDa]

No. of times detected



log(intensity)



Values from



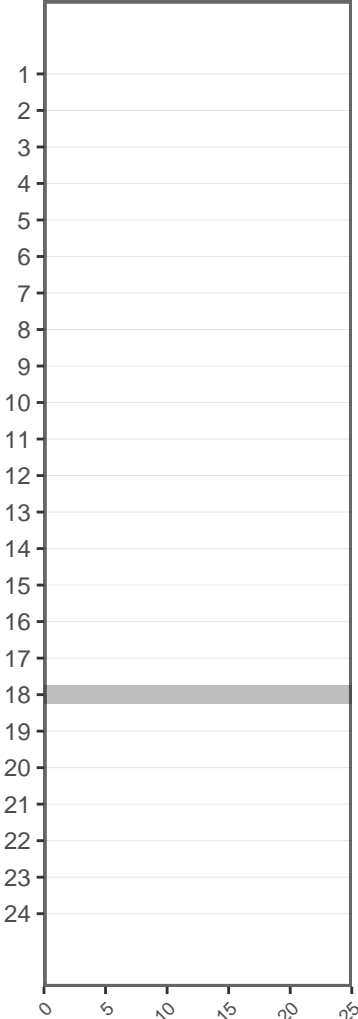
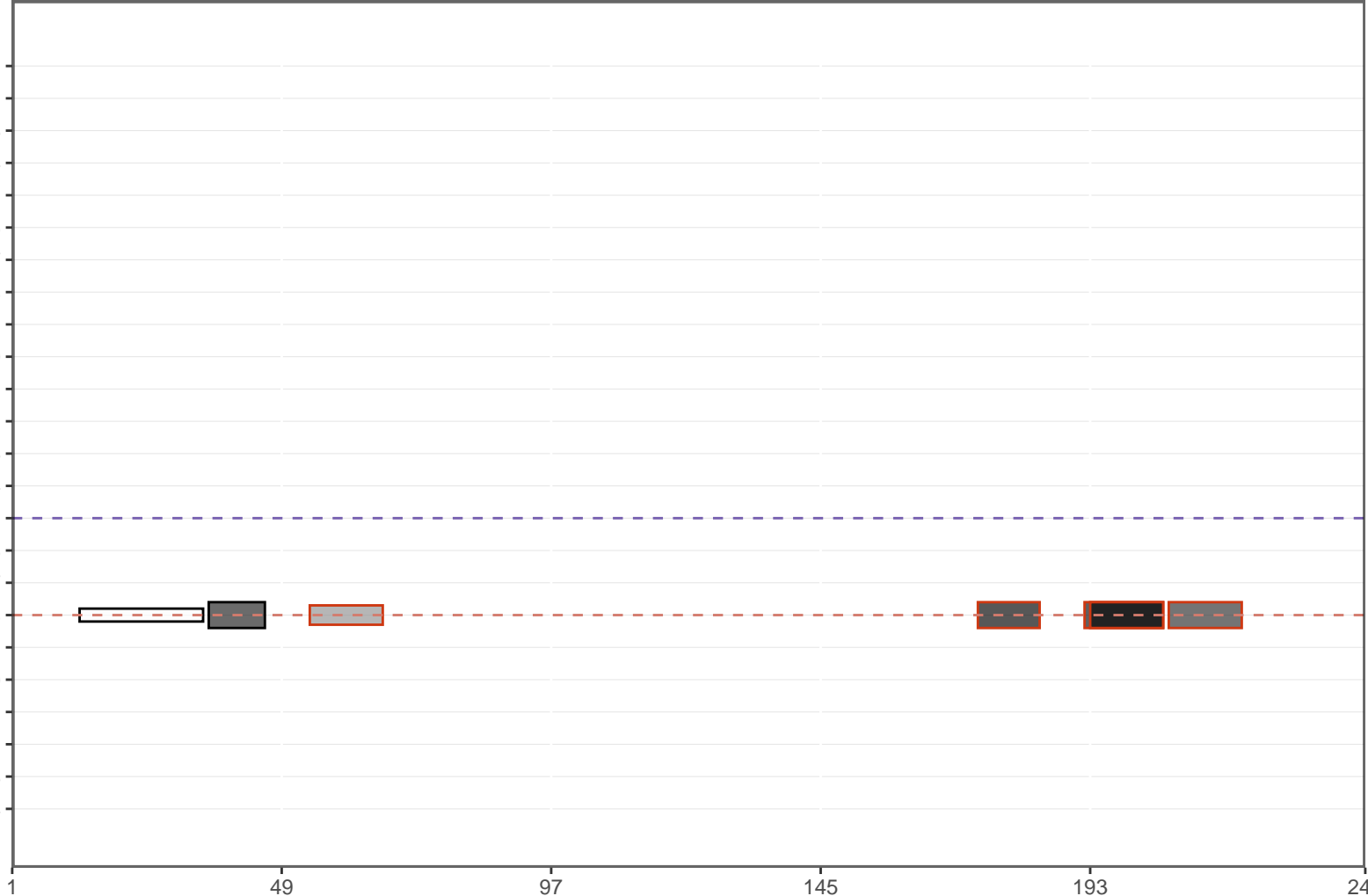
MW indication



Molecular weight

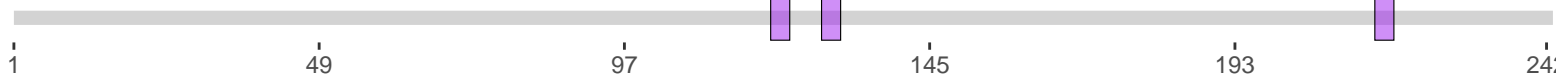


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

PFLVTDTKLMENRRTSVGVDNIEVYGLGVGASGSLTKALVFNLQSSPPSLGIFHEQLACLQLQVRLVNLPTVYVWGGKGGKLRKRTSEDELEVHEIGRHLASFSSLNFSAEKIAWDATKSSRETQEPWRALVQ

NbL18g18210.1 uncharacterized_LOC104231634 [MW = 66.42 kDa]

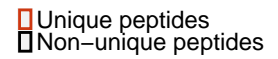
No. of times detected



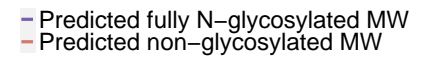
log(intensity)



Values from



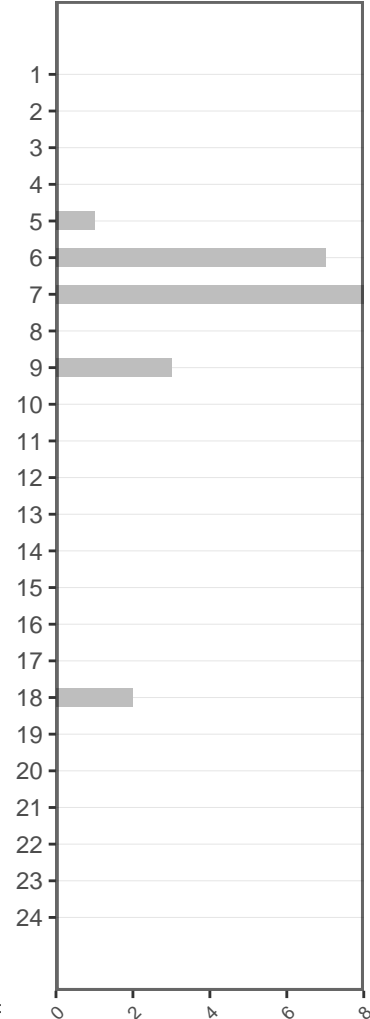
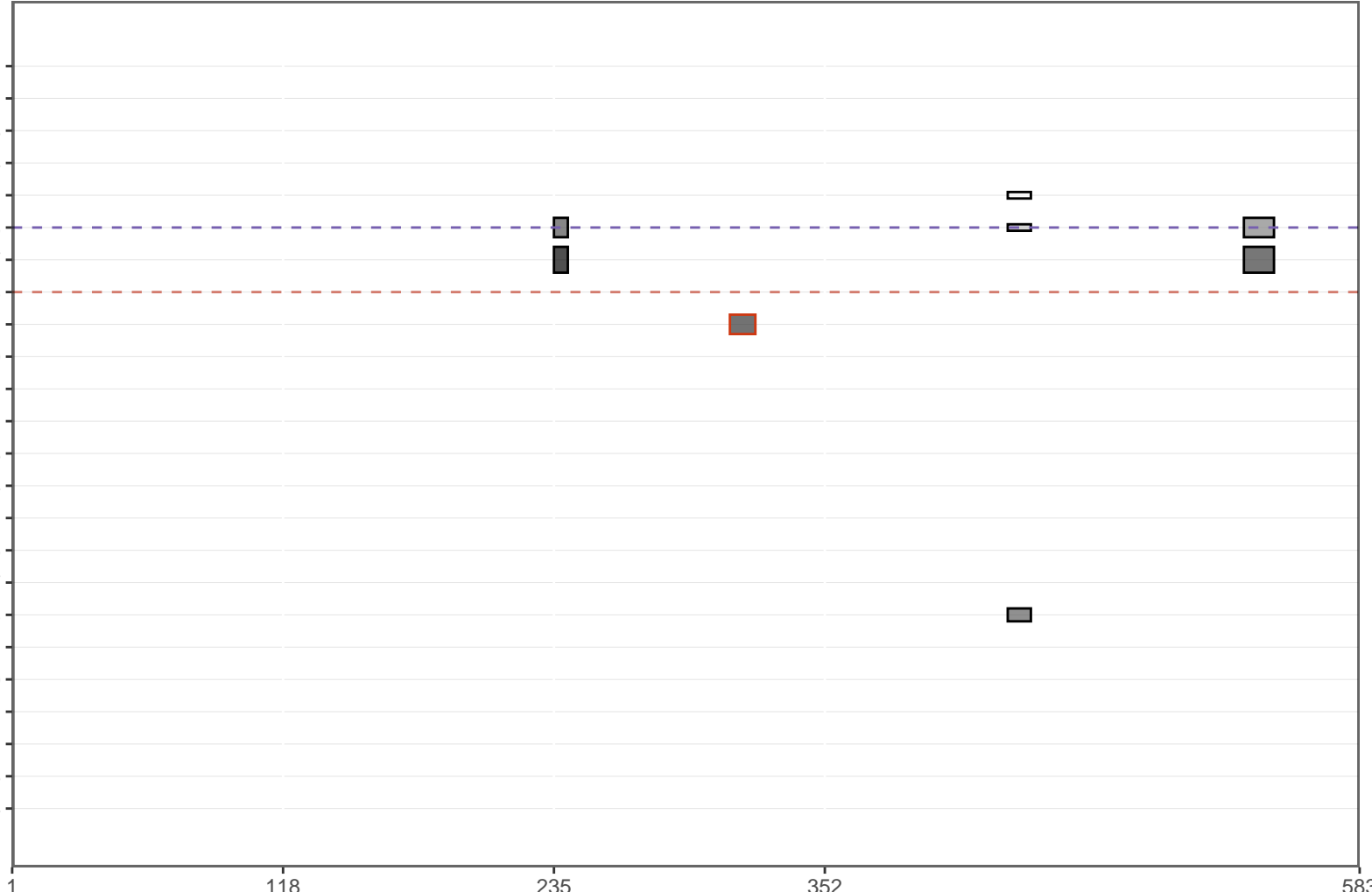
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

SGGGORCKSMNINLWSEFMDALGEAGYLNRLIMDLTGLNKIKYTSGGVDEEGKDFRFYDFEHLKDSAVLDDVQFVWSDWKNWKKDRLLGLHLVEDFRITPKLSEVQDTLMKFKGSEVQPNWYRVRCEGETESVGRPHLWVKSRRLLMDVSAVASRLNWDVDDVHYVRRGEKARNREMMWPHLAEDTSPESLLETLOGKIDDRNLVATDEPDTSSFFDPLKDKYSTHFLDEYKDLWDENSDDWYAEAKLNGNPIVEFDGVMRVSVDTVEFRGKKQIETFDLT*

NbL18g18180.1 heterogeneous_nuclear_ribonucleoprotein_1-like [MW = 35.55 kDa]

No. of times detected



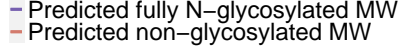
log(intensity)



Values from



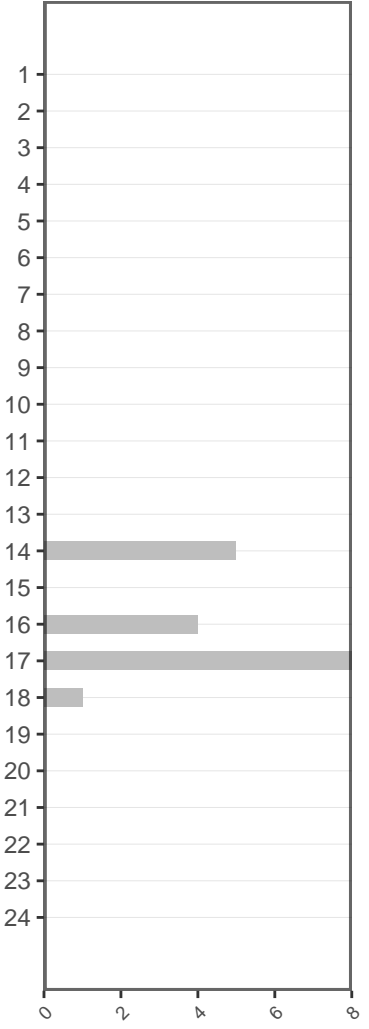
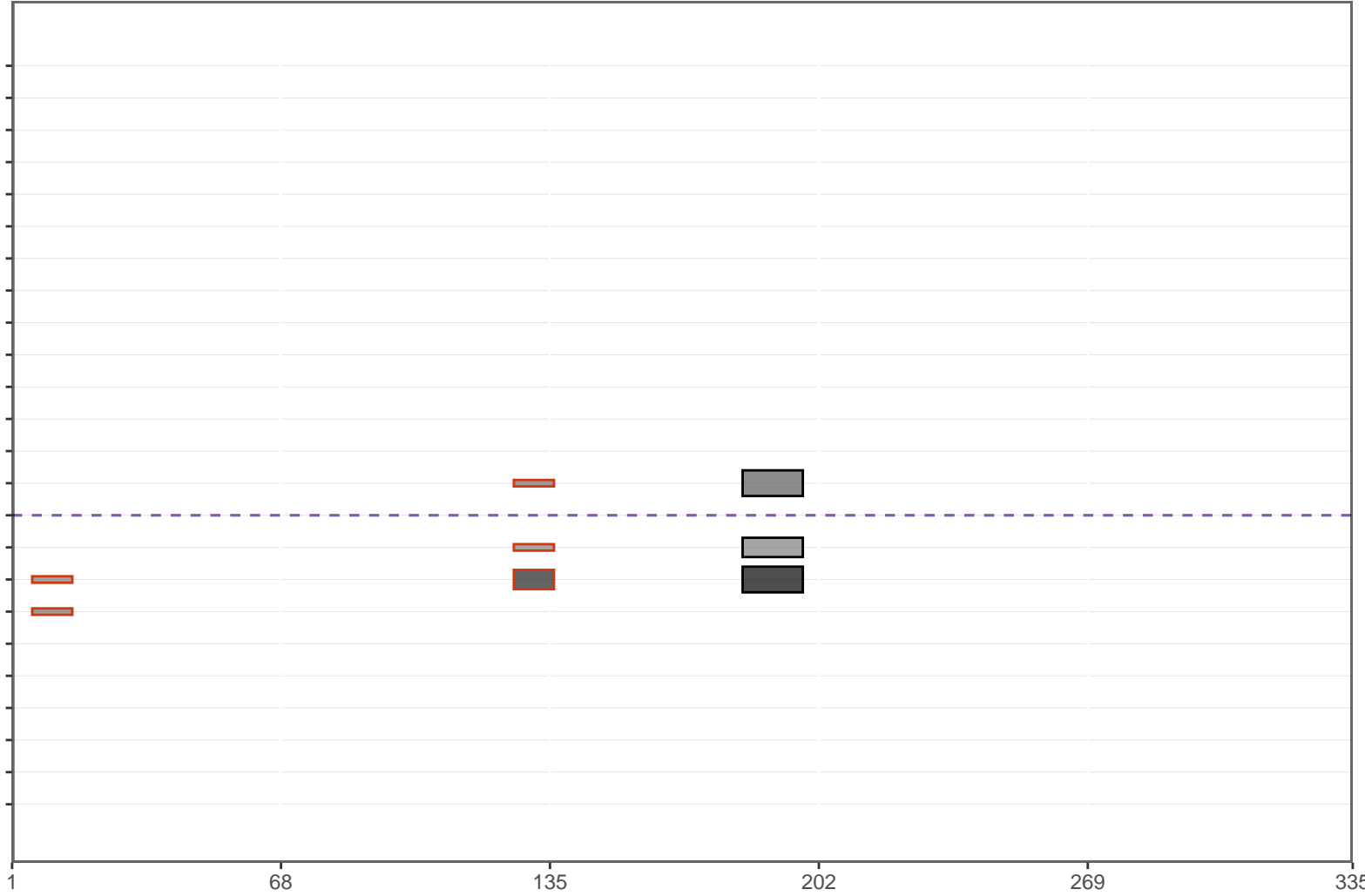
MW indication



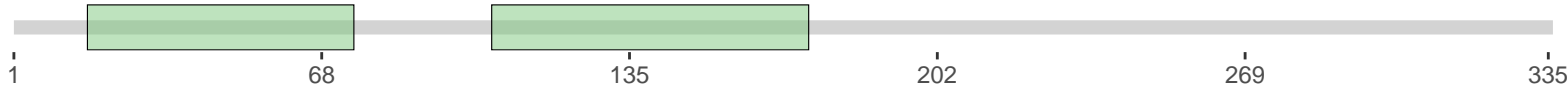
Molecular weight



Gel Slice

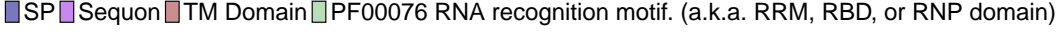


Protein length



Pfam domains

Pfam Description



Protein sequence:

AEGNRIDIMMGTCVVEKKAEPKPFNFAAPAYGSDRGRGVGDEYGGFGNSYSGFSGGFGPMEYRSGFARGEYGGGDFGRRYDFGVRGDPRLGYSSRFSGVAAFGGGYGGGSLGYSYRGGGGYGGYGGVGFDPABVEGSPGAGYGGPGGLYGTTRAGYEGSSGRVHPYER

NbL18g18080.1 acetyl-CoA_acetyltransferase_cytosolic_1 [MW = 41.28 kDa]

No. of times detected



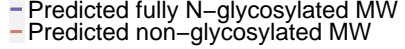
log(intensity)



Values from



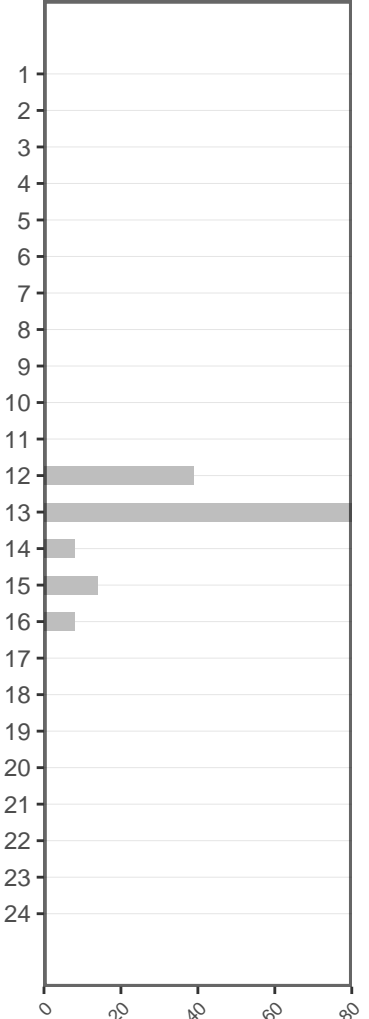
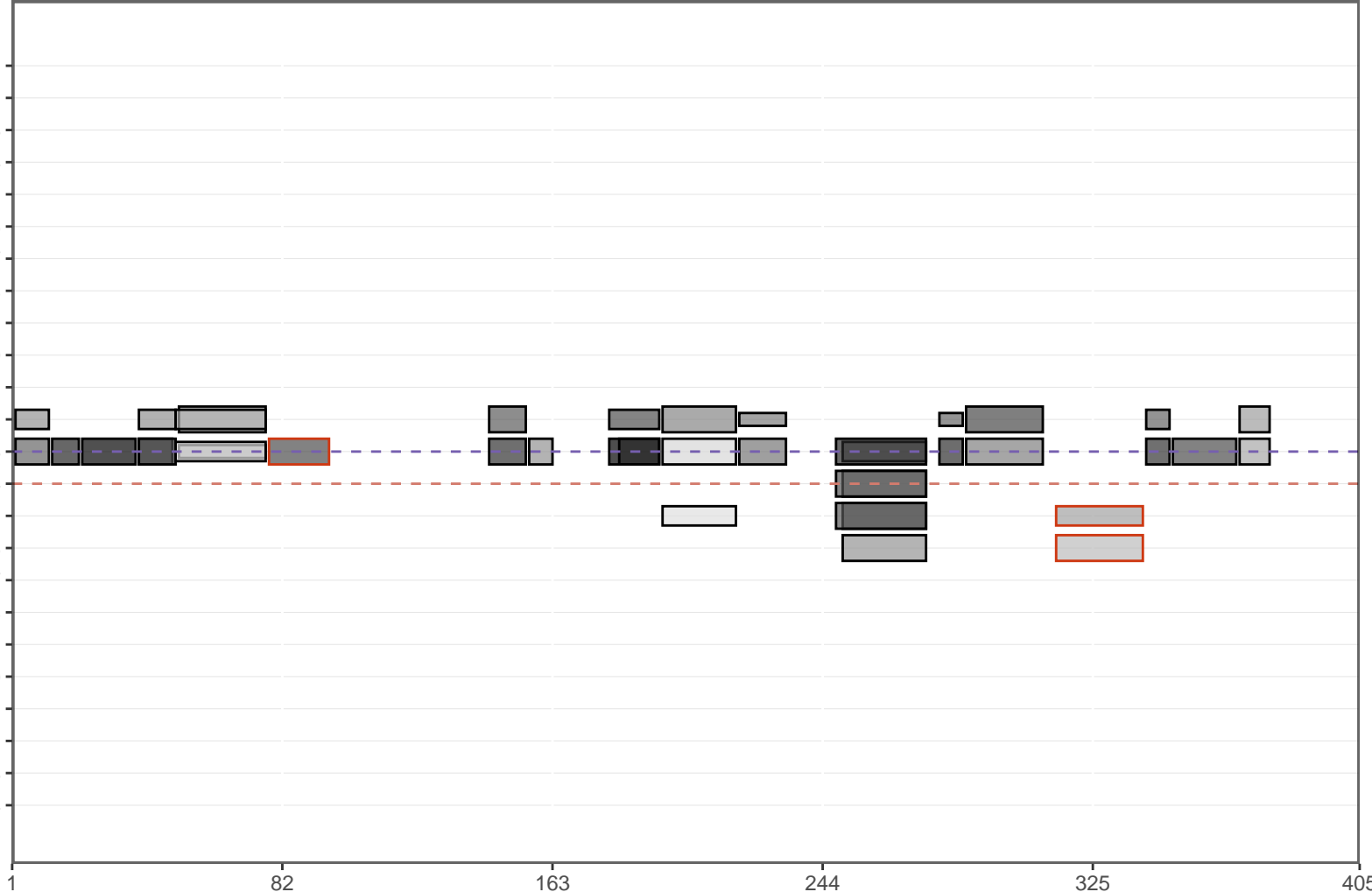
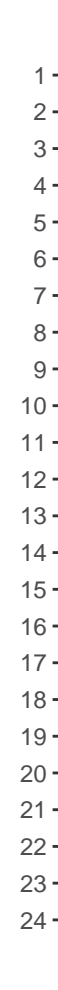
MW indication



Molecular weight

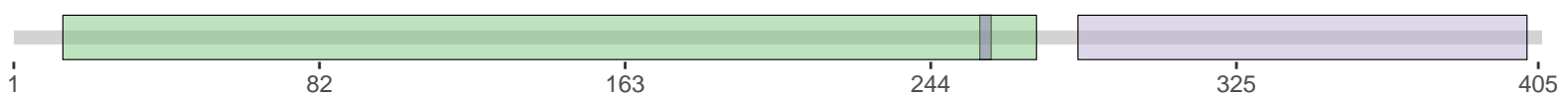


Gel Slice



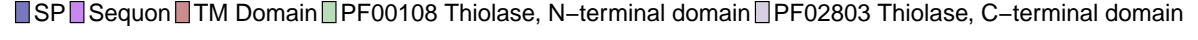
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MAVQSFERGIAGQAGAFWEIVVEVPGGRGKPSIVDKDDGLGKFDGAKLRKLRPFRKDKDGTVTAGNASGISDGAALVVSQEKAKILGLNVIQKISGVADAAQAPLFTTARLAPKAKSSLEASQIDFYEINEAFVSLANQKLLGLNPFKRVNHHGAVSLGHPGGSGARILVTLGLVLRGKNKYGAAQVGNQGGGASAIIVLELL

NbL18g18030.1 fasciclin-like_arabinogalactan_protein_2 [MW - SP = 48.02 kDa]

No. of times detected



log(intensity)



Values from



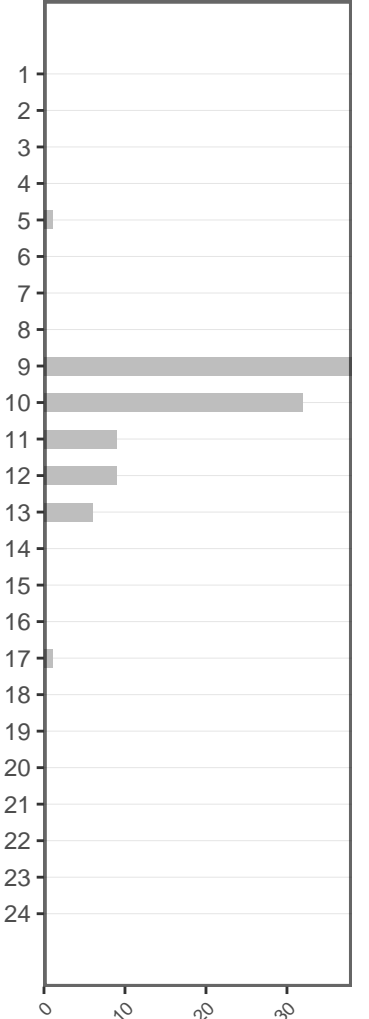
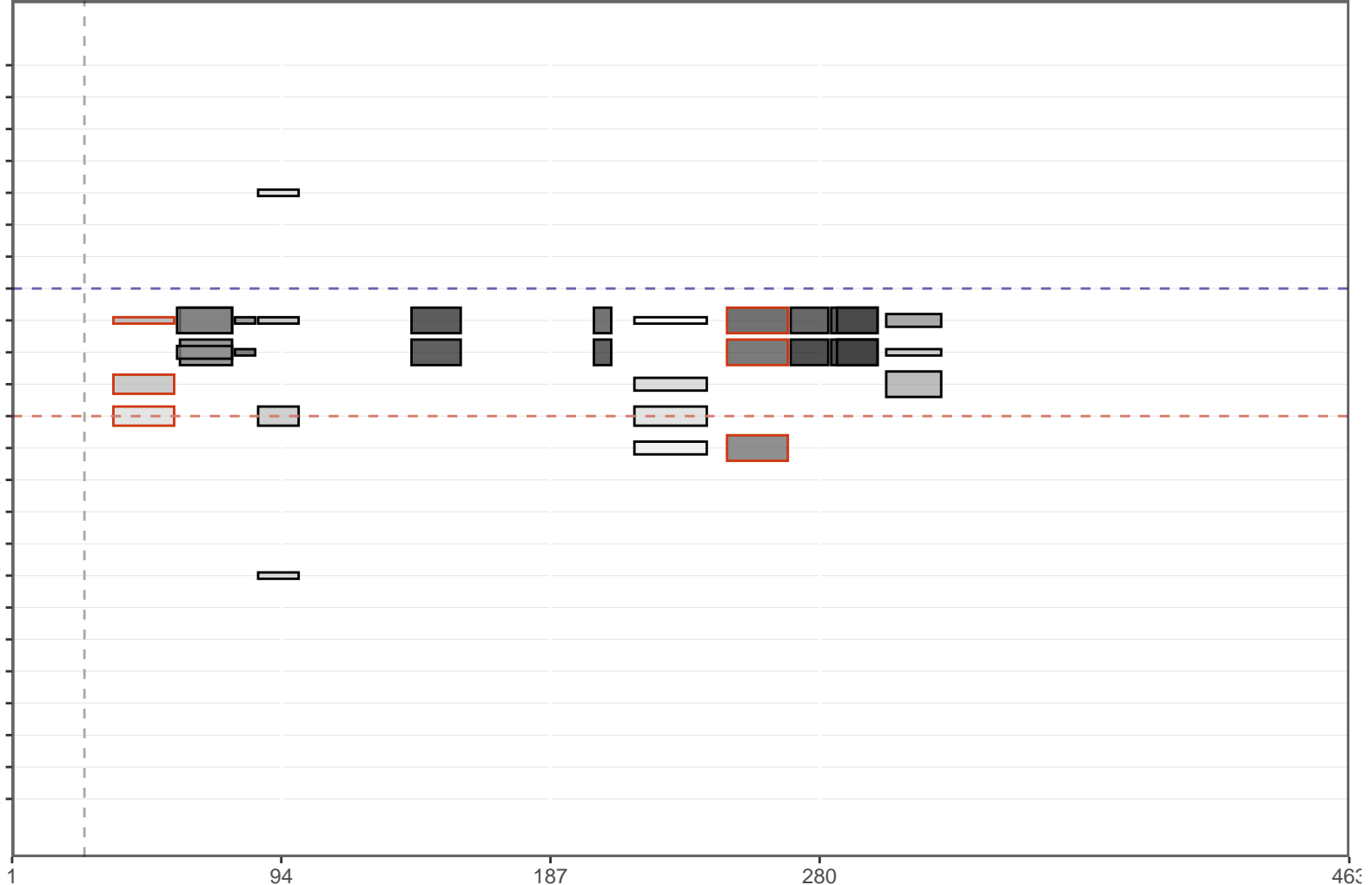
MW indication



Molecular weight

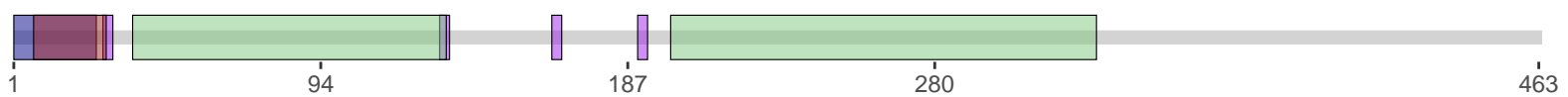


Gel Slice



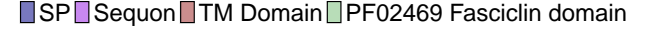
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGLTVFCPTDGLVINGFMPKFKLTKDGAPELLYHGVPVYVNLGLMKKNNGLMNTLATEGKNKYDFTVQNDGDDVMLKTKVVTARISGTLVDEEPLVYKVDKLLPRELKFVFAEFPAPKPKGSKKKKGGDDDDVDDSDAPEPSPDDEDAPADESENINGAIVSEVGFCTKERMKKERKXKXEGNRRNGRQKRKTKTKKKEGRRNGRQKRKTKTKTEGNRRIGREKRRKTLTFLGIP

NbL18g17790.1 levodione_reductase-like [MW = 29.73 kDa]

No. of times detected



log(intensity)



Values from



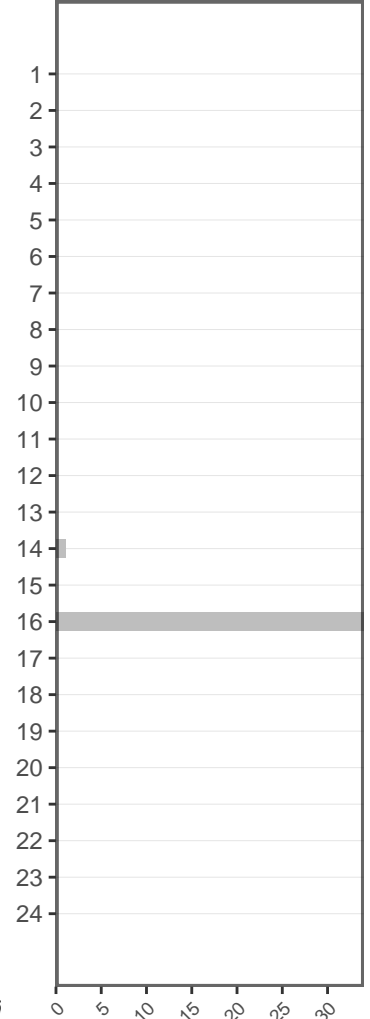
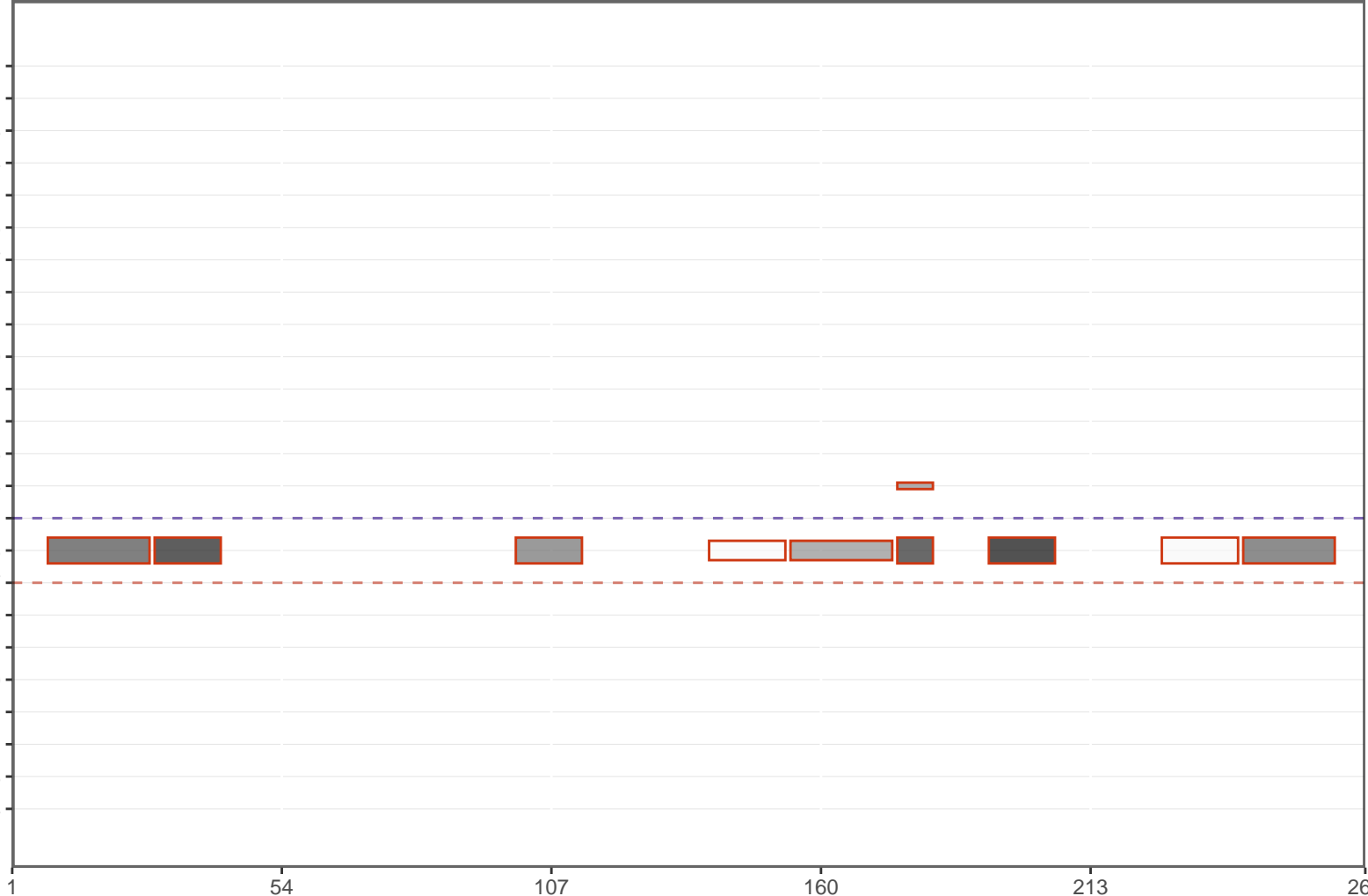
MW indication



Molecular weight



Gel Slice

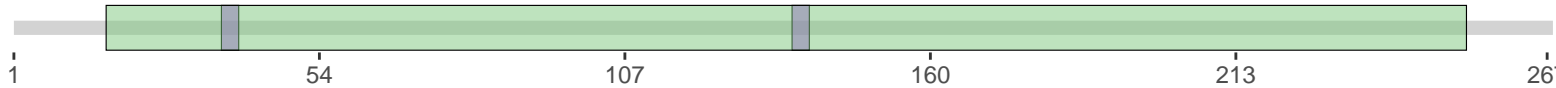


Peptide counts over 4 repeats

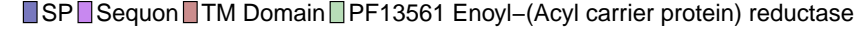
Protein length



Pfam domains



Pfam Description



Protein sequence:

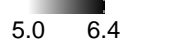
AGWYLLKCIKRMARDNKSGGSNFLTSGAERGIYGGAAAYGSGAAGMDQLVRLSALEMKHKHQRVNGISRGLHLEDEYPMBSVQKERAEKLTKEAAPLNRLVDVRRKDLASTVYVLSDDSRVMTGTSIFVDGAGSLVRRPMSRYM

NbL18g17720.1 chlorophyll_a-b_binding_protein_37_chloroplastic-like [MW = 28.6 kDa]

No. of times detected



log(intensity)



Values from



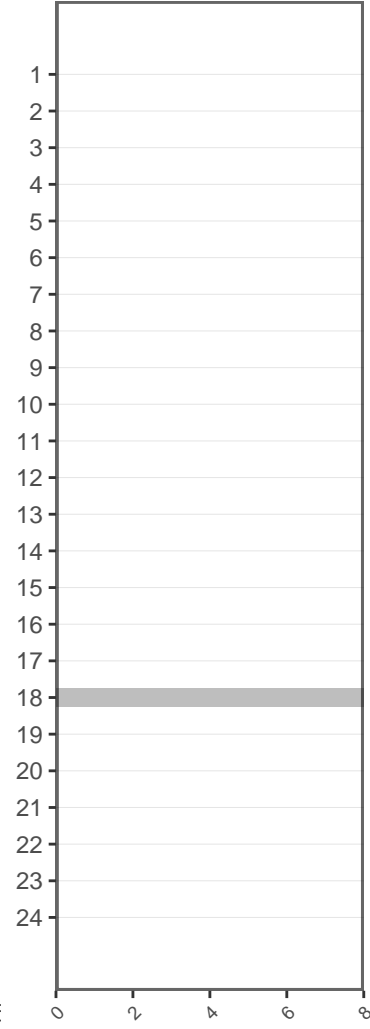
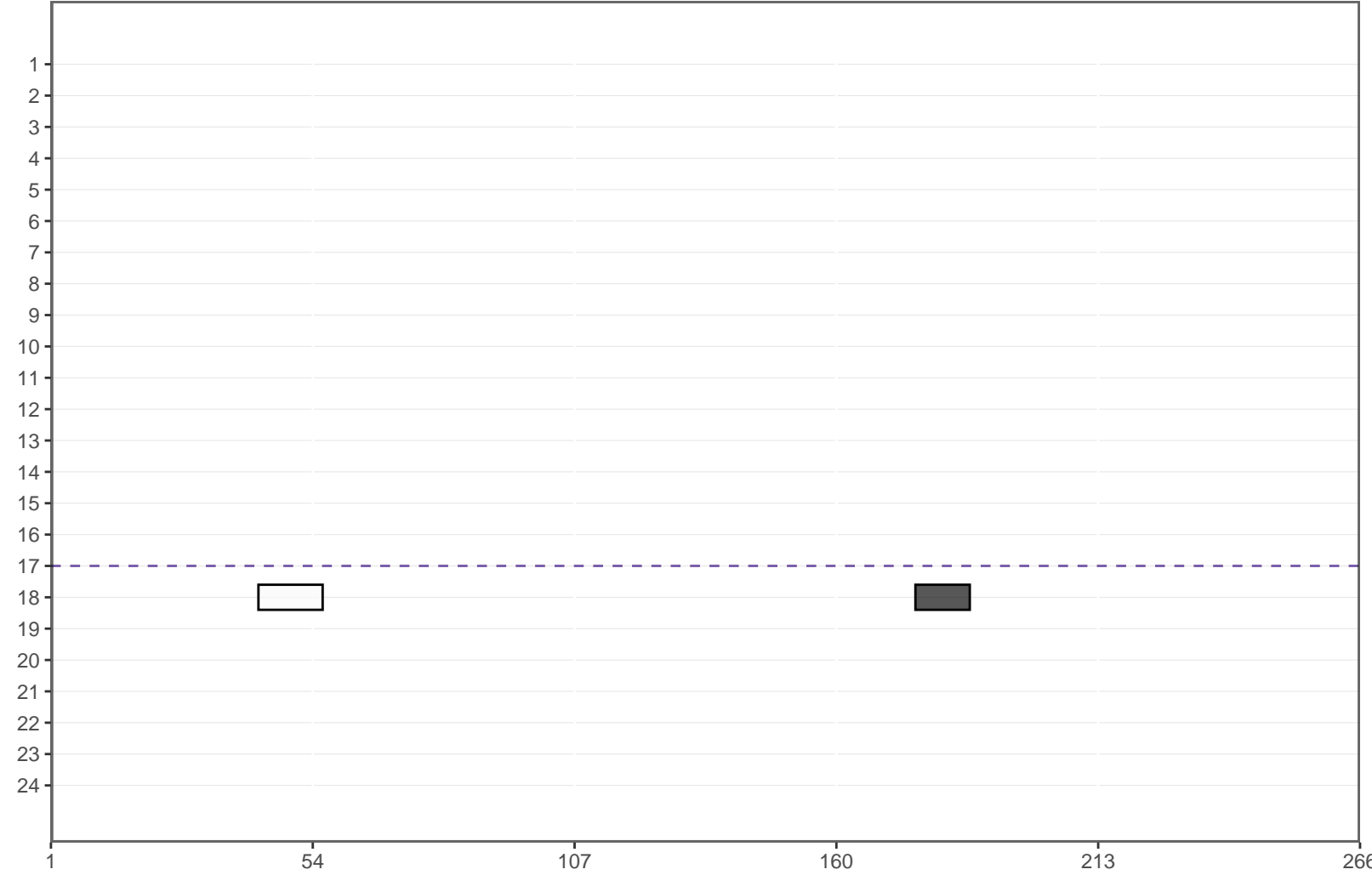
MW indication



Molecular weight

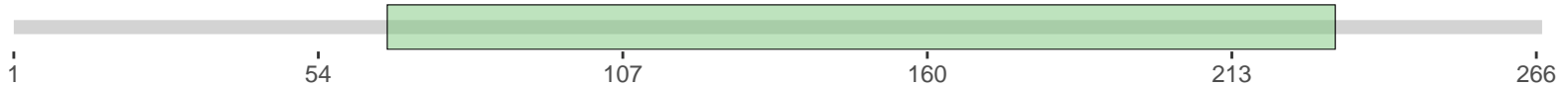


Gel Slice



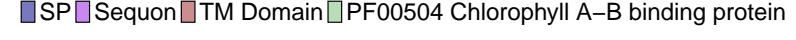
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKKGVKFGEAIVFKAGAQIFSEGGLELGNPNLVHAGSILAWAGQVVLVGLIEGYRVGGPLGEGLDKVPQGAFDPLGLADDPFAFELKVKIKNGRLMFSMFGFFVQAIVTGKGRLENLFDHNDPVAWNAWAFATNVPVGGK

NbL18g17540.1 cytochrome_b561_and_DOMON_domain-containing_protein_At5g47530-like [MW - SP = 41.28 kDa]

No. of times detected



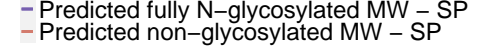
log(intensity)



Values from



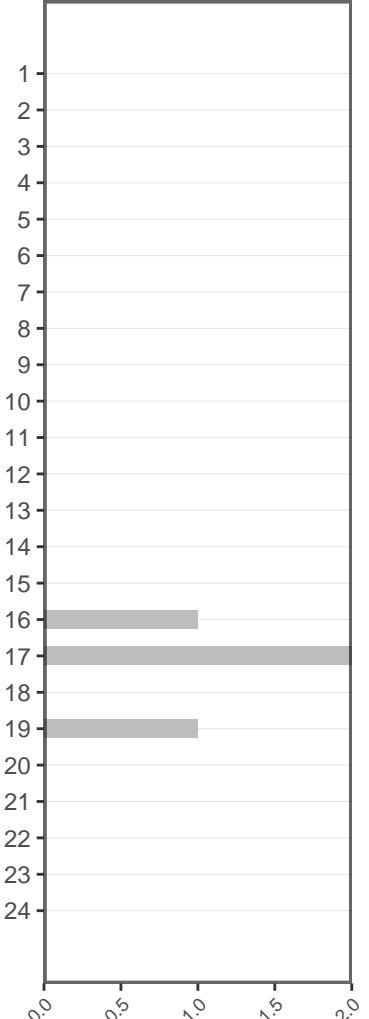
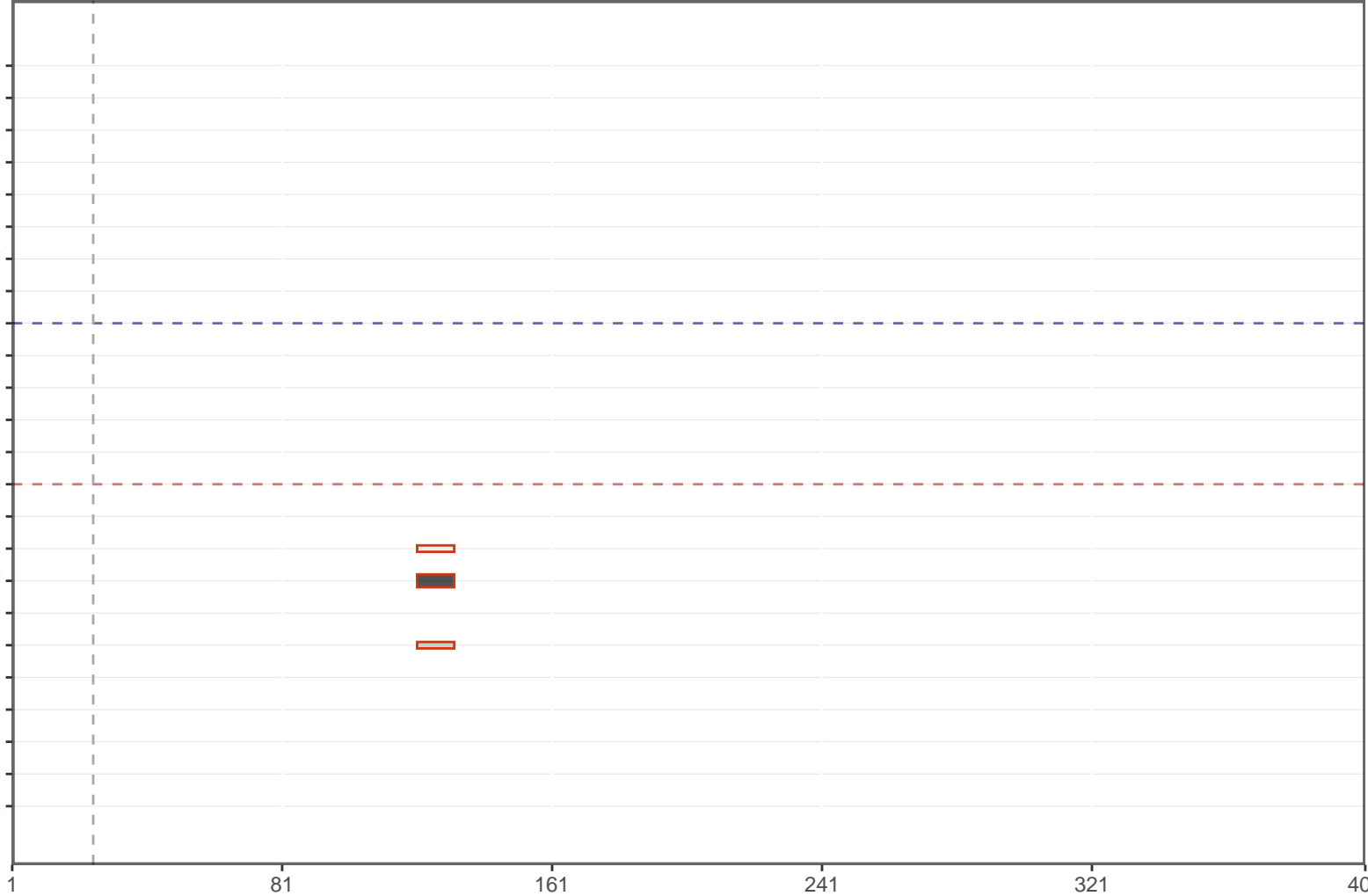
MW indication



Molecular weight



Gel Slice



Protein length

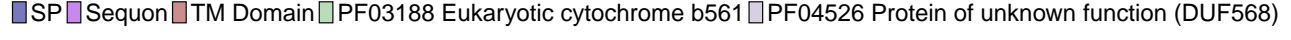


Peptide counts over 4 repeats

Pfam domains



Pfam Description

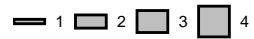


Protein sequence:

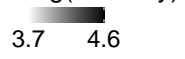
SVDFATGQLNDGGGISTGRKRNVHGVNLNAVSWGVHMPMGSAVFARLYKVFESANPWFLHWAGTSAVAVGVAGWGTGLKLGSDSVGKFTTRHRIGHTFLGLGVFALLLRPKDPKHYRLVYNNVHHSIGYVLSLGIANVFEGFDALNGGKHWKRAYTGVIALGMAVLEAFTWFKRKRKTDENKILGNGTNGVNGYNGTHTQGP

NbL18g17530.1 threonine--tRNA_ligase_chloroplastic/mitochondrial_2 [MW = 77.82 kDa]

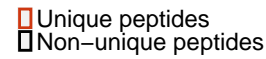
No. of times detected



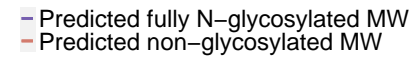
log(intensity)



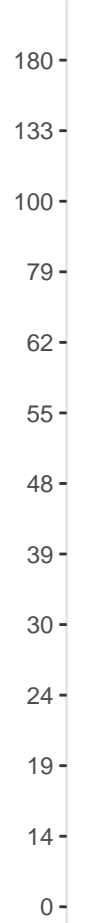
Values from



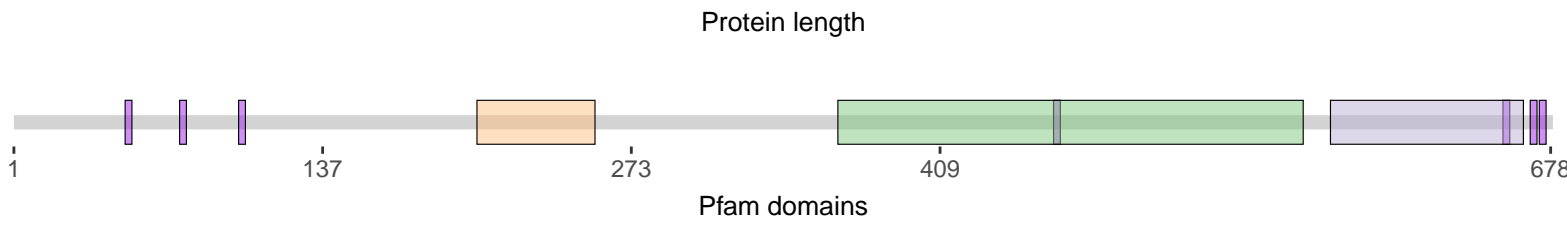
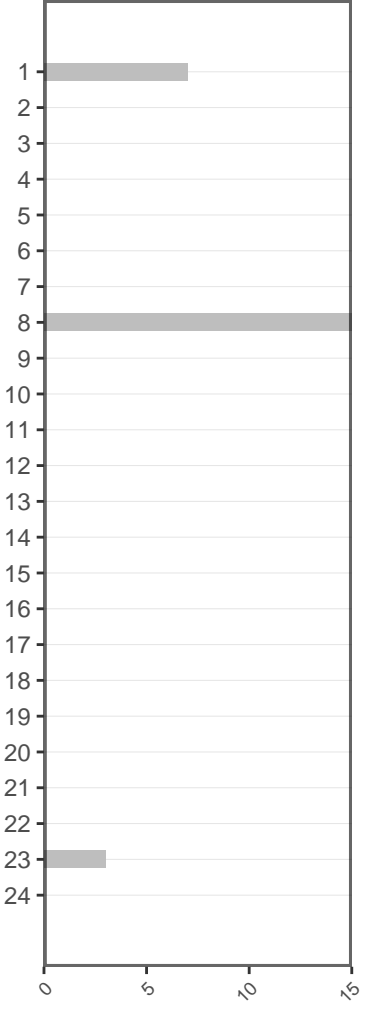
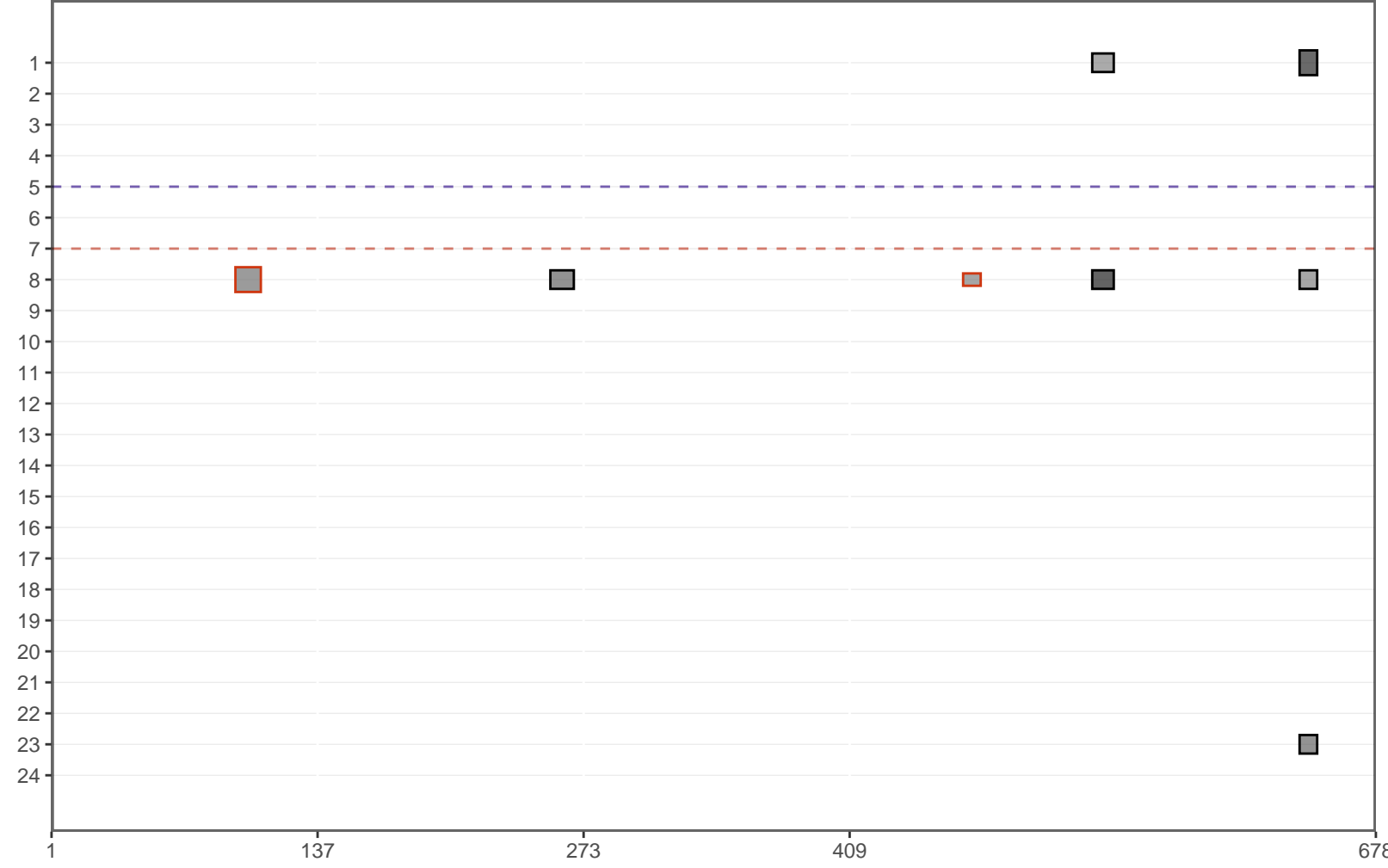
MW indication



Molecular weight



Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00587 tRNA synthetase class II core domain (G, H, P, S and T)
- PF07973 Threonyl and Alanyl tRNA synthetase second additional domain
- PF03129 Anticodon binding domain

Protein sequence:

RGYDLLTPIHAKADLWIKGHLDFYKENMFDQMEIEEELGQRFMPNGPYHVALYKRLHSHYRDFPVRVAELGTVYRYELSGSLHGLFRVGRFTQDDAHFQLEDDQKDEIRGVLDTLEELQGFQDKYEVNLSRPEKAVGDDIEWQKATSKDALEDKQWVSVGTDDGGAFYGNIDLKIEDLGRKWDG6STGVDNLPQRFDITVYDSNGERKRPMIHRVAVLGSLEFFGVLENYAGDFPLWLSFGQARVLPVFTDQGLQYGVNEVGNKLIKASGRIVEVCSGERLPLKI

NbL18g17520.1 fasciclin-like_arabinogalactan_protein_7 [MW – SP = 25.75 kDa]

No. of times detected



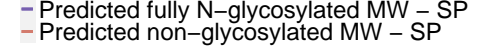
log(intensity)



Values from



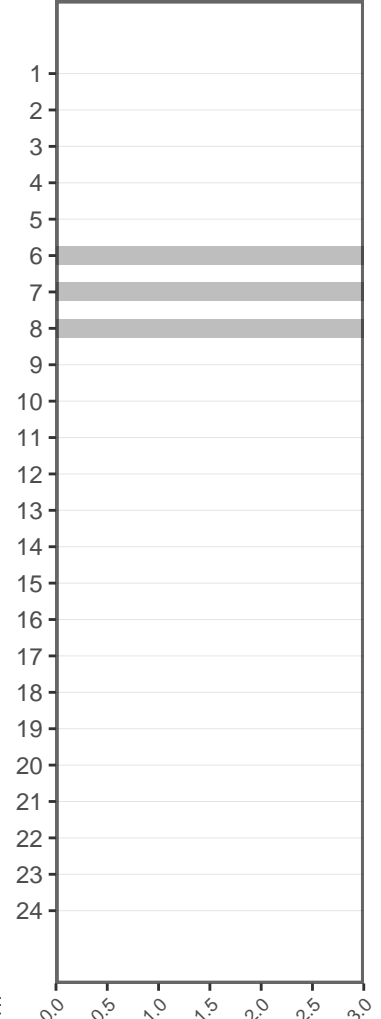
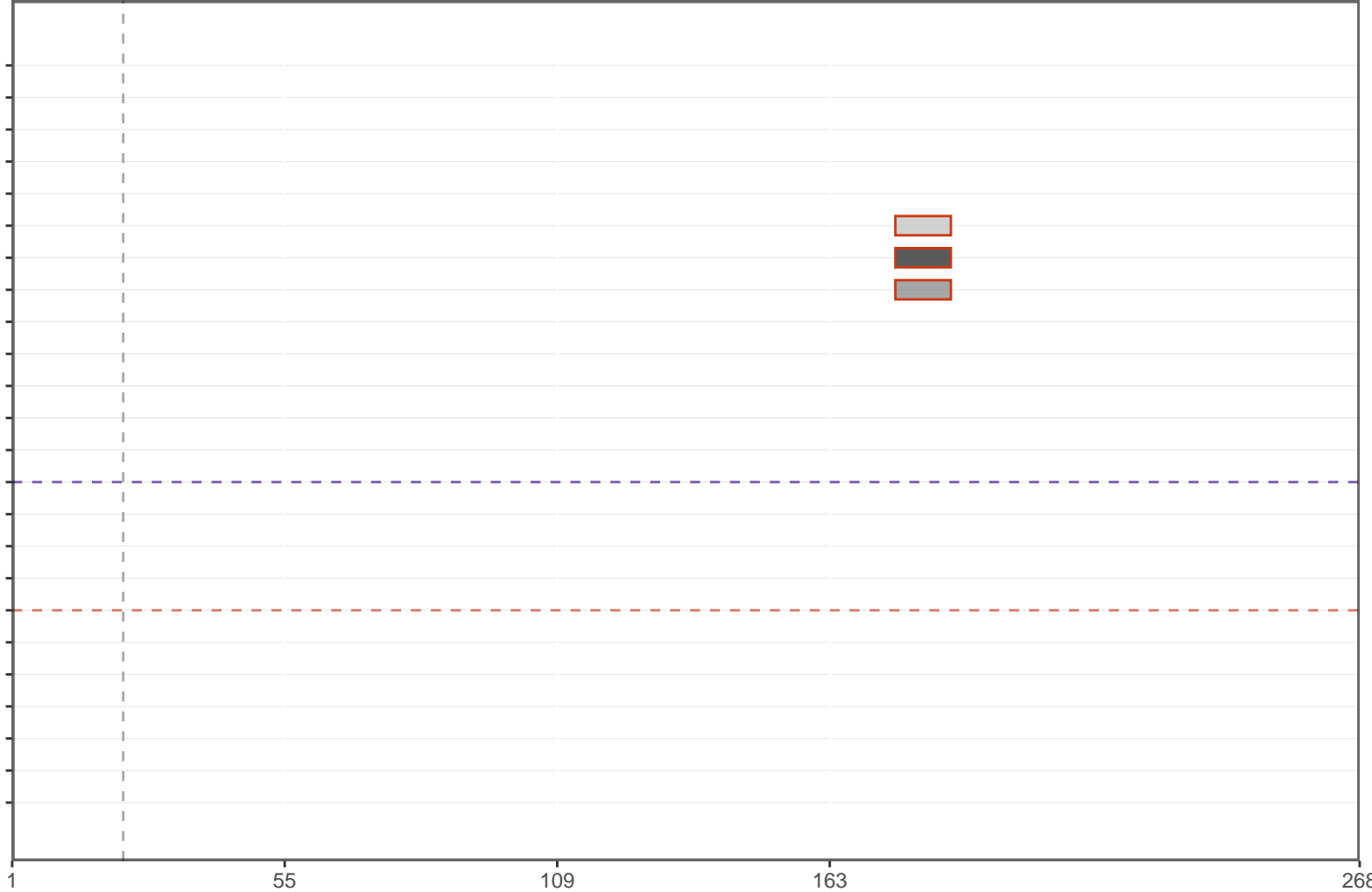
MW indication



Molecular weight



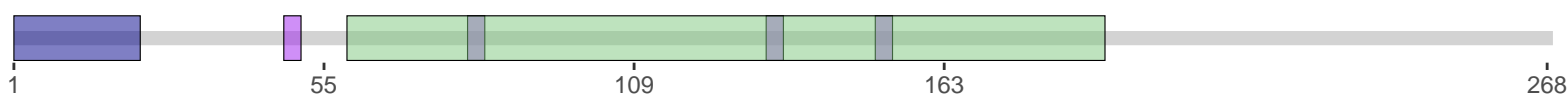
Gel Slice



Protein length

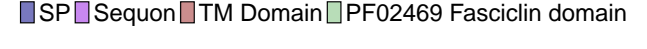


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YYSLADKNIKLSDMSPNITFAGNLYSLNFTDSDGTVHLNSGWSRTRKVSARVTAFFWVYQVQKVLKPEAFQGTDLPPMPKPAFAPETDTRPTADSPAADGTGKARAAAQSDSSSPSASHGRMSEWGLNHLVLIAGGFLMFLI

NbL18g17470.1 chitin_elicitor_receptor_kinase_1-like [MW - SP = 65.34 kDa]

No. of times detected



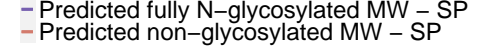
log(intensity)



Values from



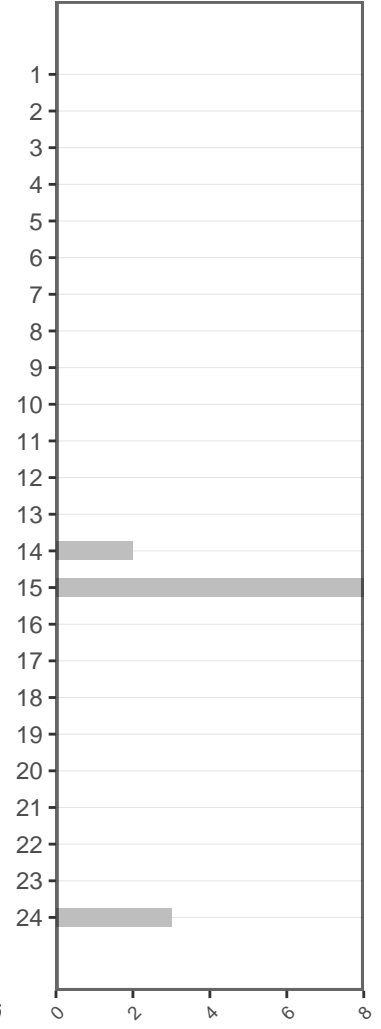
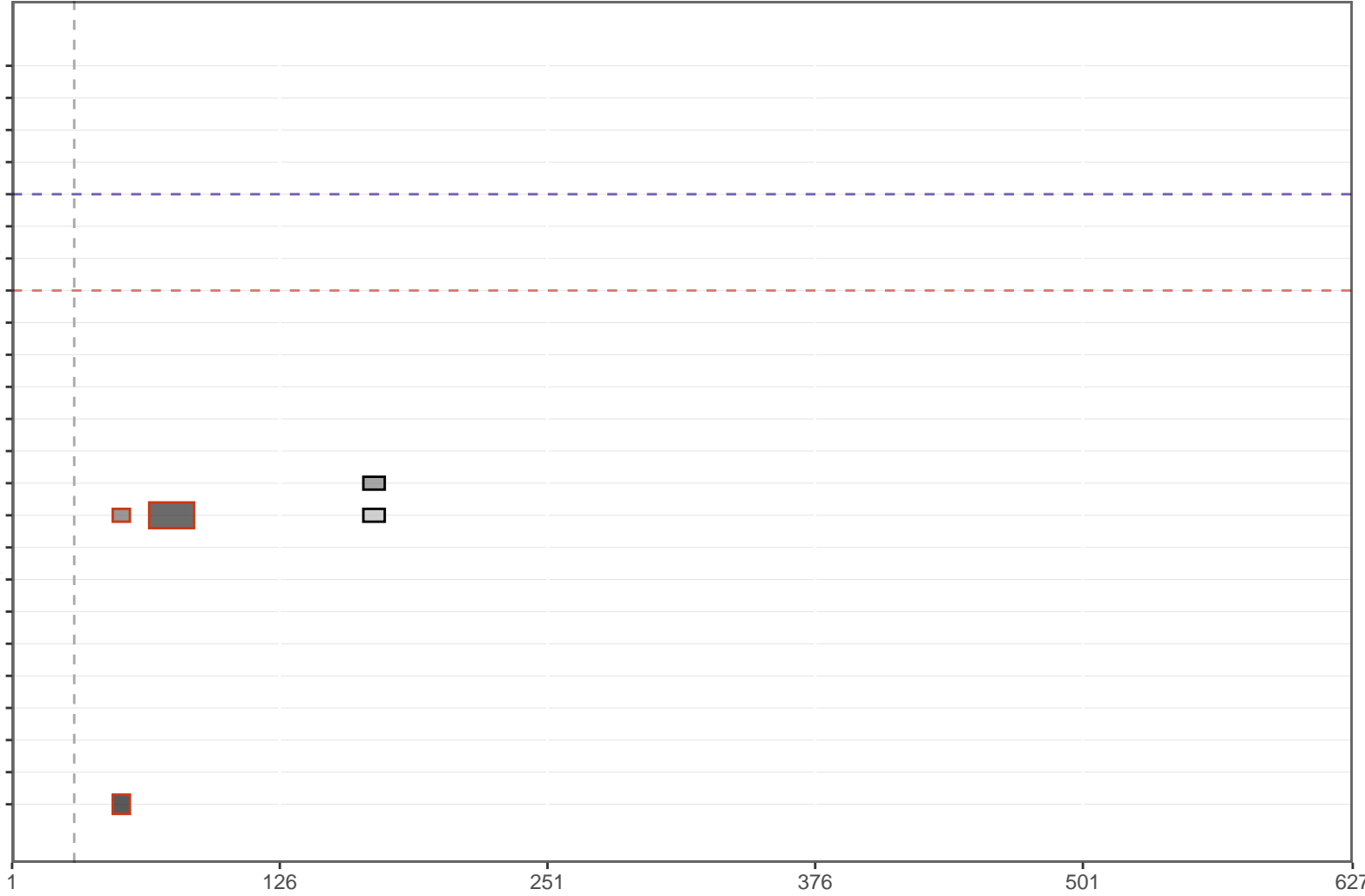
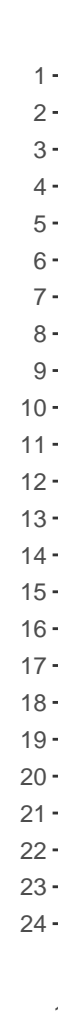
MW indication



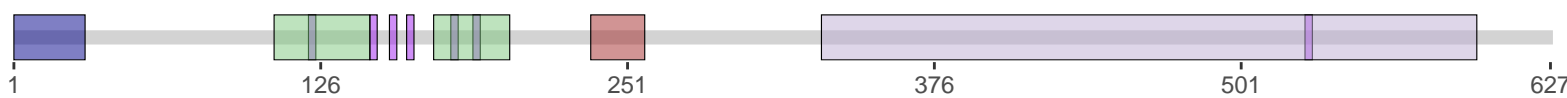
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

SPFLSGITVYDKSVEFTYEELATATDFBANKKIGGGFGAVYVAELRGEKAAKKMDMEATREFLAELKVLTHVHHLNLRLLIGYVEGSLFLVYEVVENGHGGHRLGTGRDPLPWSTRVQIALDSARGLGVHEHTVYVYHRRDKTANLIDKPHAKVADFGLTKLTVVSSSSLQTRLVGTFGMPPEYAGYGDVSPKVDVYAFGVLLYELISAKAAVAPNESVTEKGLVLFEEVLRNGPEPDEDLRLKLVDPRLGNDVPLDQVIRKMAQLAKACTHENPLRPSMRSIVVAMT

NbL18g17430.1 uncharacterized_LOC107779001 [MW = 16.98 kDa]

No. of times detected



log(intensity)



Values from



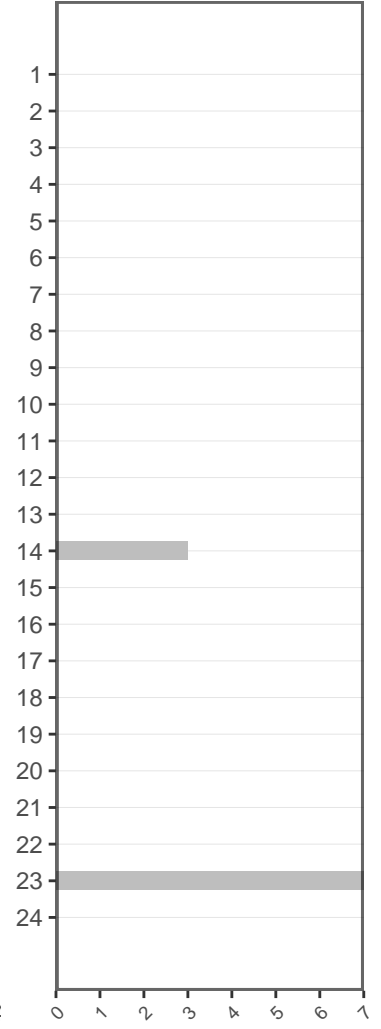
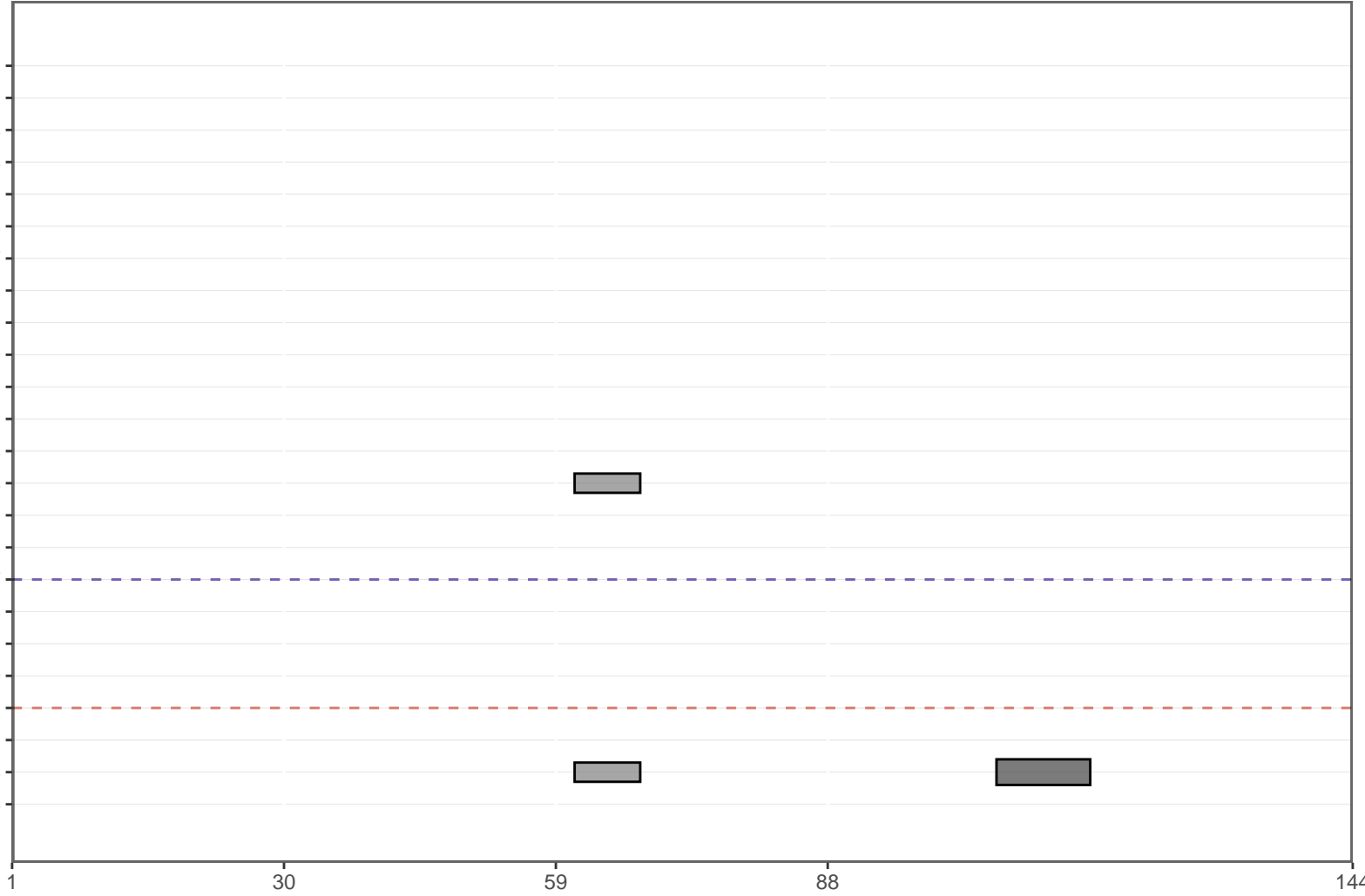
MW indication



Molecular weight



Gel Slice

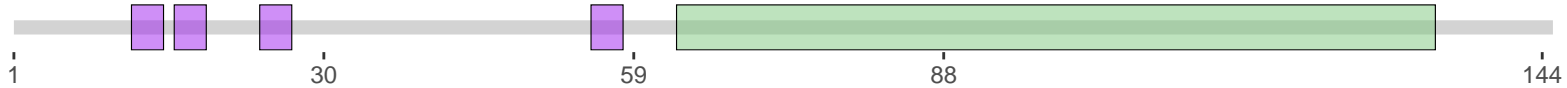


Peptide counts over 4 repeats

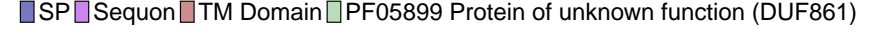
Protein length



Pfam domains



Pfam Description



Protein sequence:

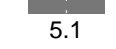
LMELGVPRVSMVKTGKGLPQDWHVDLVHIEEGEVRRVPEGGGRFMQFVAGDLVRYPKWFEADLYFNDYGERVYFRAYGDS

NbL18g17300.1 small_ubiquitin-related_modifier_2 [MW = 12.06 kDa]

No. of times detected



log(intensity)



Values from



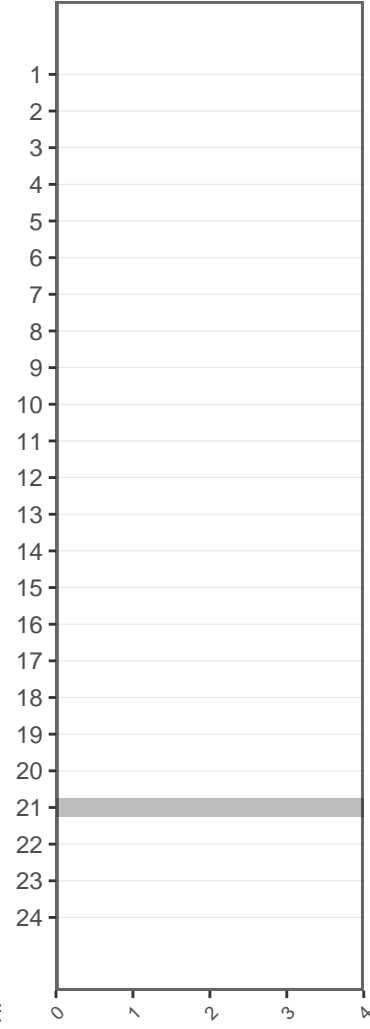
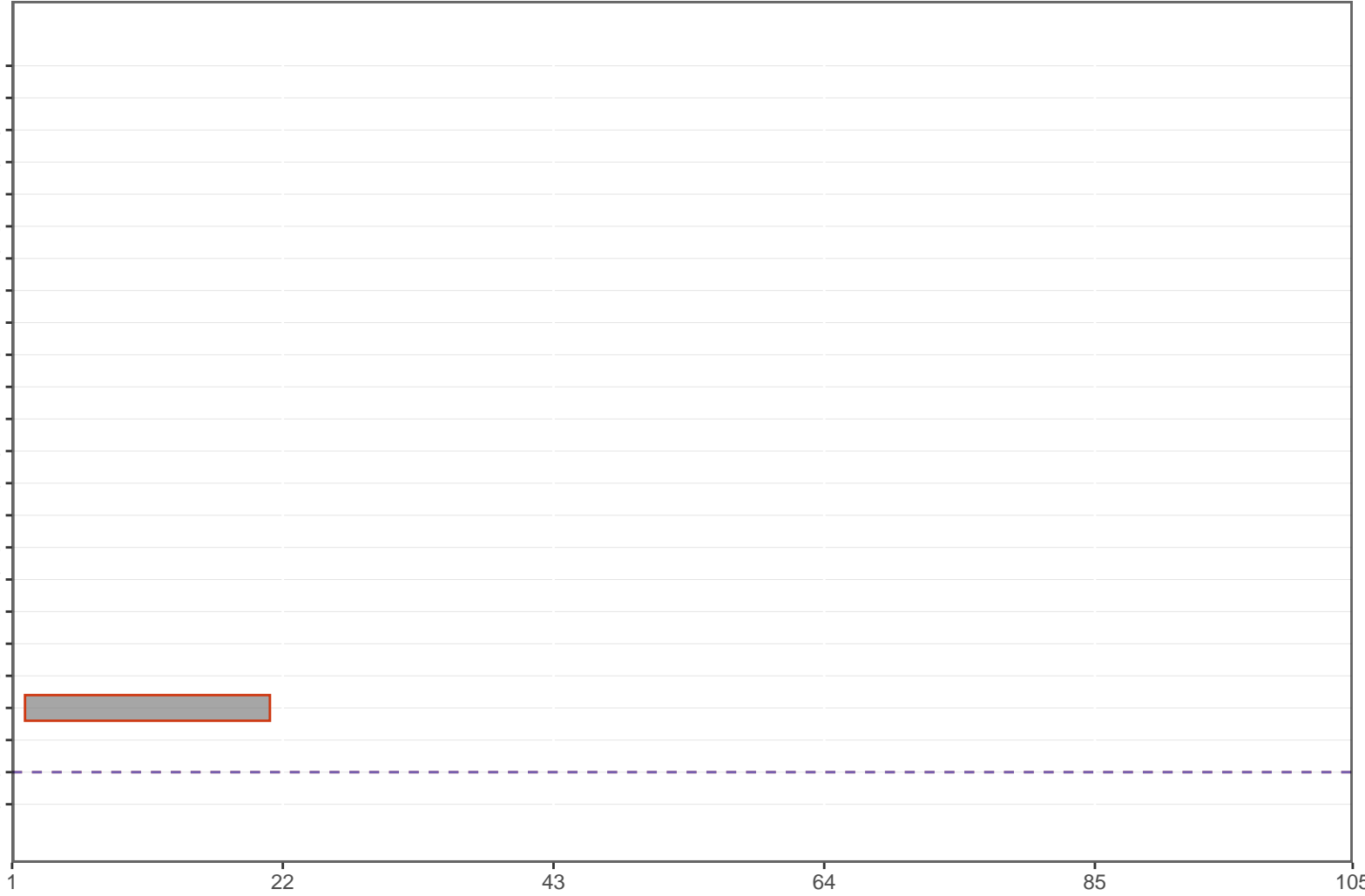
MW indication



Molecular weight

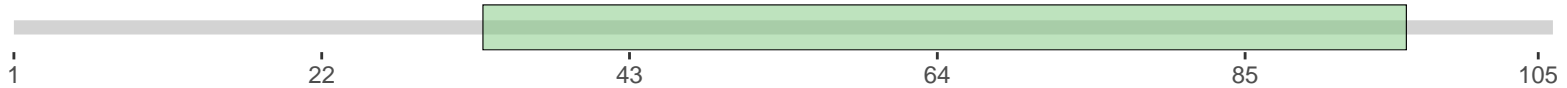


Gel Slice



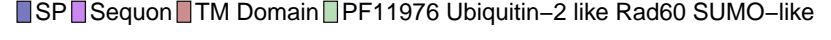
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FRKRSTQLKLLMNAVGDQGVDFNFAFLFDGRRRLRAEGTPDELEMEDGDEIDMMHGTGGSTV

NbL18g17280.1 nifU-like_protein_4_mitochondrial [MW = 30.8 kDa]

No. of times detected



log(intensity)



Values from



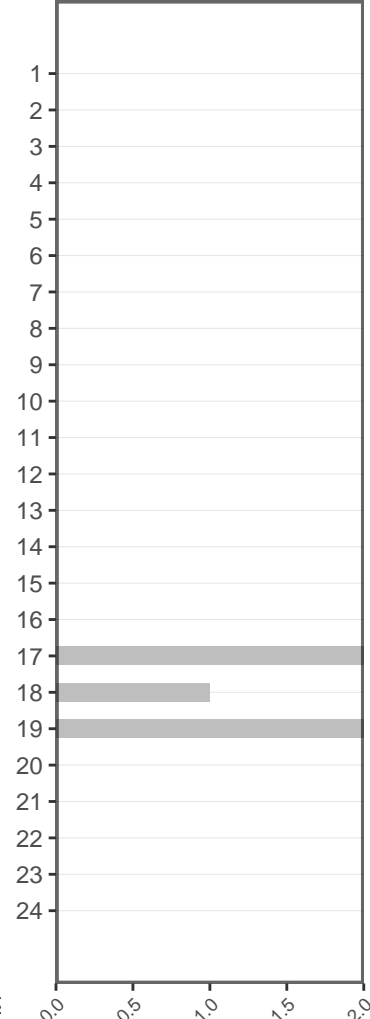
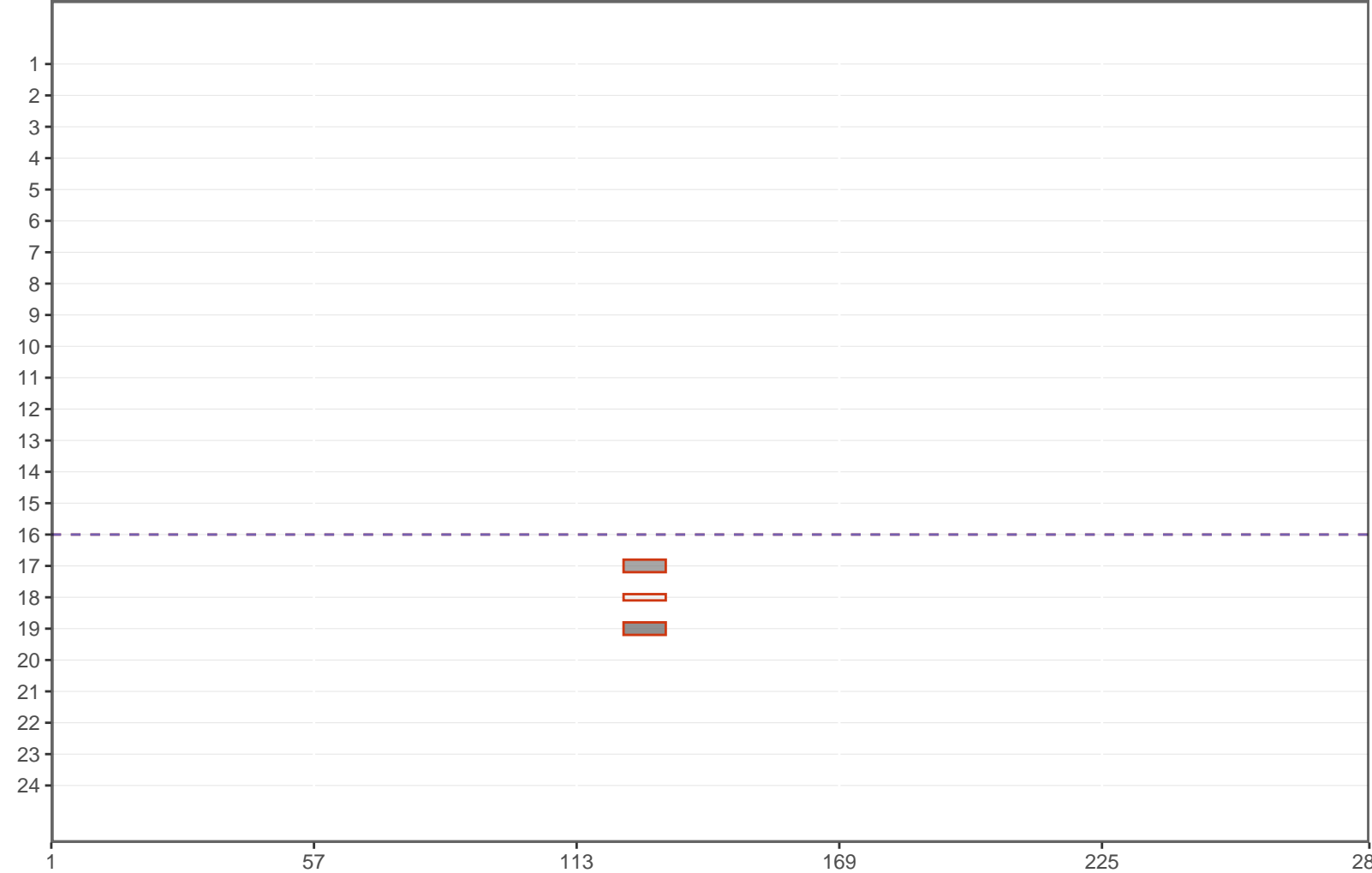
MW indication



Molecular weight



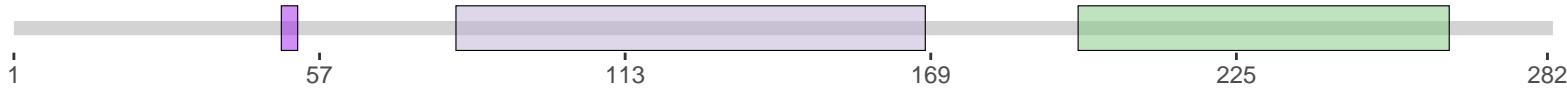
Gel Slice



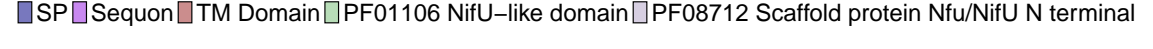
Protein length



Pfam domains



Pfam Description



Protein sequence:

GISRVFGSDFTVYTKSEDAIGWDFLKPFAAAMDYSSGKPLFLDGSSTAGMDTAHEDDSETVAMKELLETRIRPVAQDDGGDIYRFGDLDRGVLKMMQAGGCGPSSSVTLKSGIENLMARHYPEVKGVEGEMDDDEEHLGTGVPVE-

NbL18g17220.1 protein_disulfide_isomerase-like_2-3 [MW - SP = 44.7 kDa]

No. of times detected



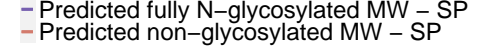
log(intensity)



Values from

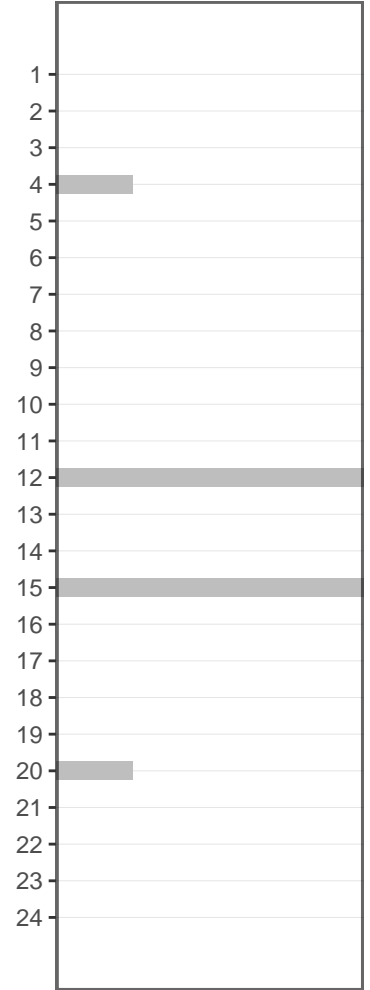
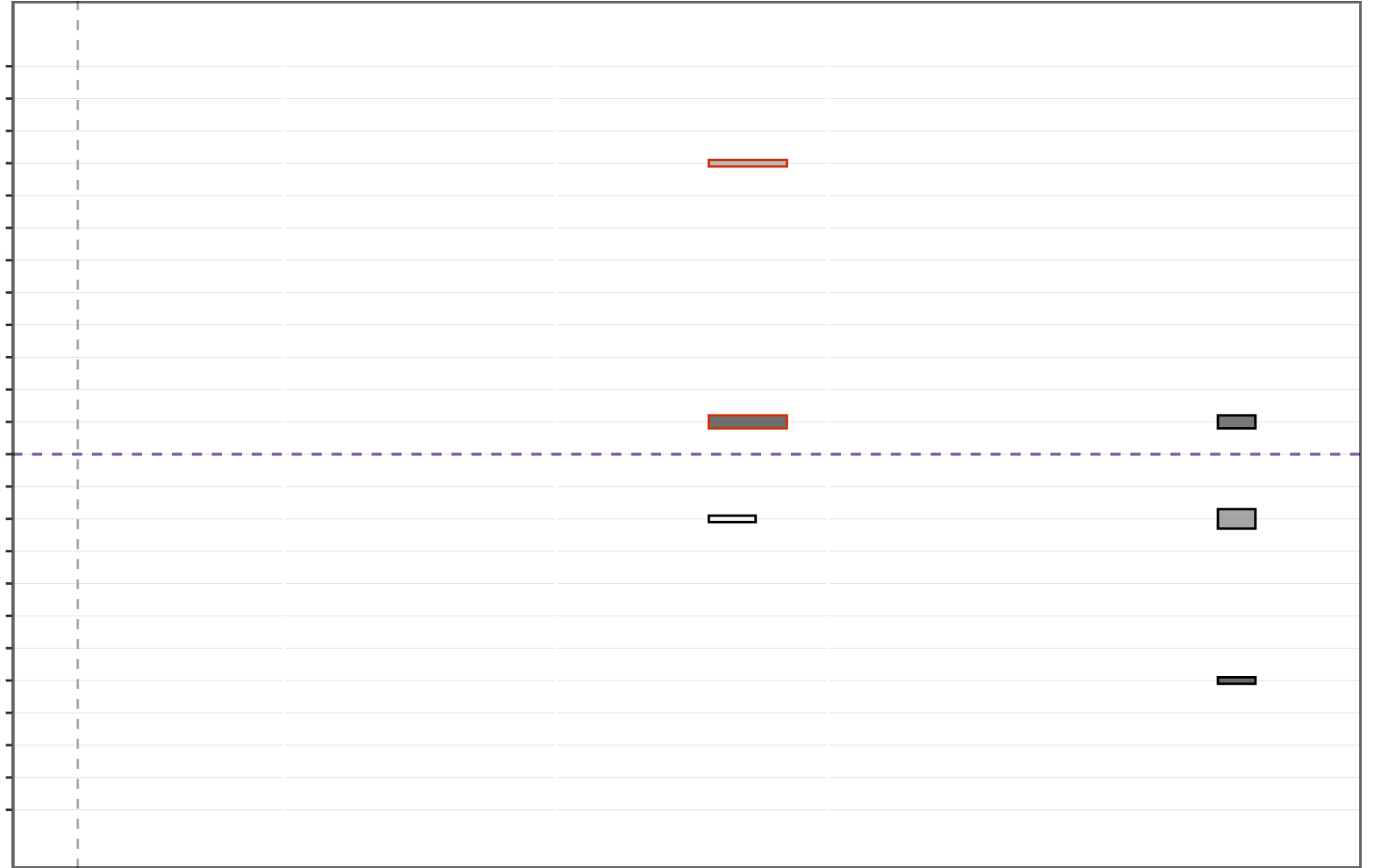


MW indication



Molecular weight

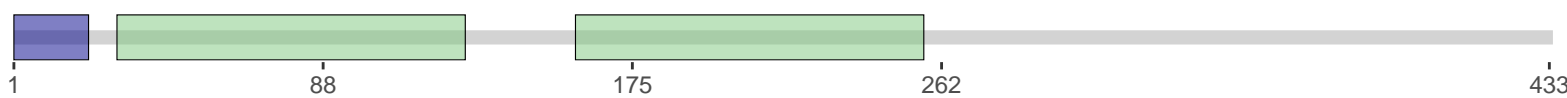
Gel Slice



Peptide counts over 4 repeats

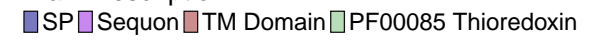


Protein length



Pfam domains

Pfam Description



Protein sequence:

GVKVLGHVDCDAEKSLMRNRYVGGFTLVFGADKESFVYEGARTAAAEISFGIEGLETRVAPPEVIELTSPDMEEKGNBAAGFVFLPDLDSKAEGRNKYLEMLLSVAEKFRNPNVYVWVAAGNDPDLKHHVGVGGYGYPMWALNKKGVYAPLKSAGFRGPIIDFVKEAGLGGKGNLPLAATPSVITEAWDGGKDGHEEDEFSEELMGDDTRNKDEL

NbL18g17210.1 GDSL_esterase/lipase_At4g26790-like [MW - SP = 36.16 kDa]

No. of times detected



log(intensity)



Values from



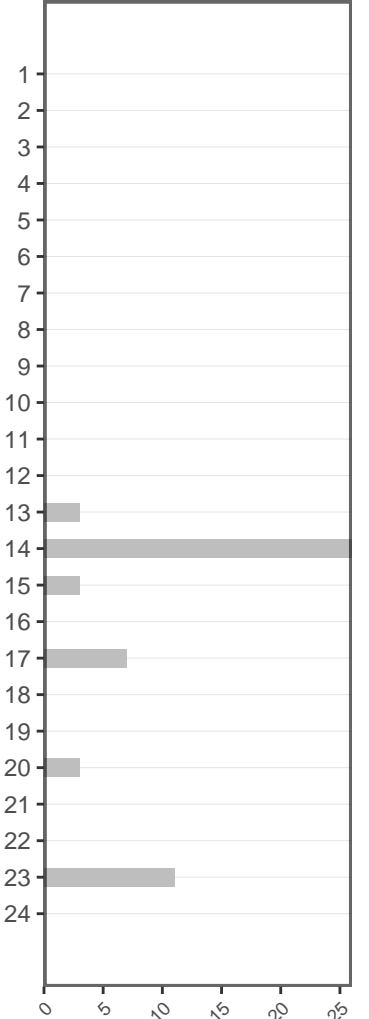
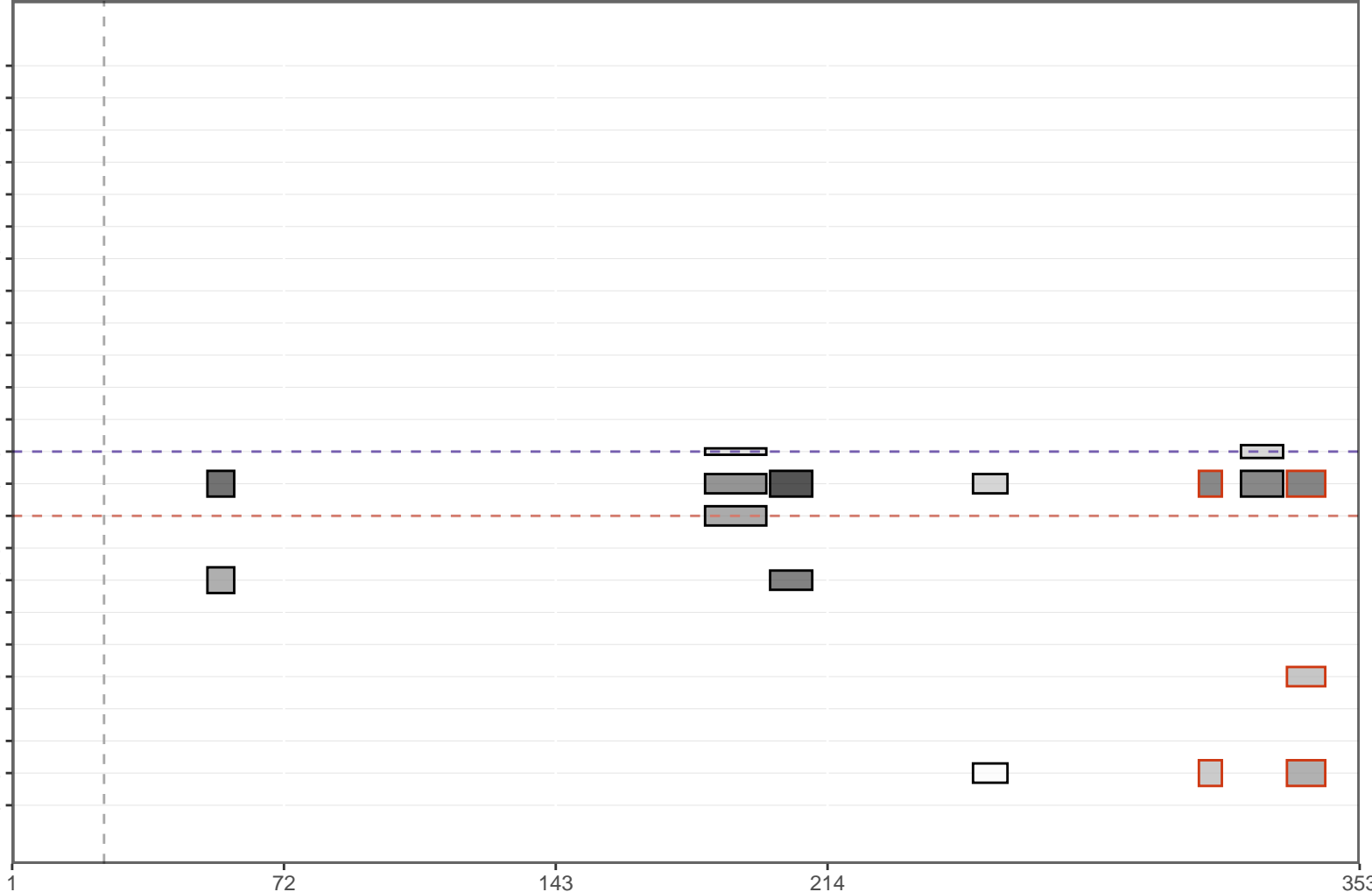
MW indication



Molecular weight

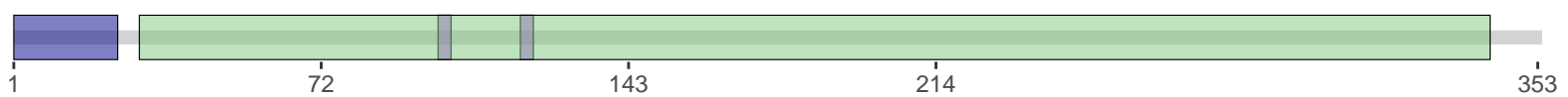


Gel Slice



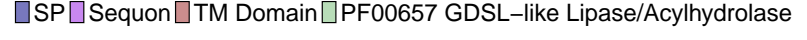
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GTNDIENLYTTPQRREQYTVDQYGTFLGIANNFVTLNLYGARKISLGGLPFGMCPLEKRTSNVANGNEGLESNVAMNFNDKLSGLVIELNKLKELSGIQVLELNPYINMLGMKNPSSYGFEEVASLACCATGLFEMGVACDRYVLFQKGDANKYFWDFAFHPTKTEKDGADHVVKTALSKFLA*

NbL18g17030.1 1-aminocyclopropane-1-carboxylate_oxidase [MW = 35.58 kDa]

No. of times detected



log(intensity)



Values from

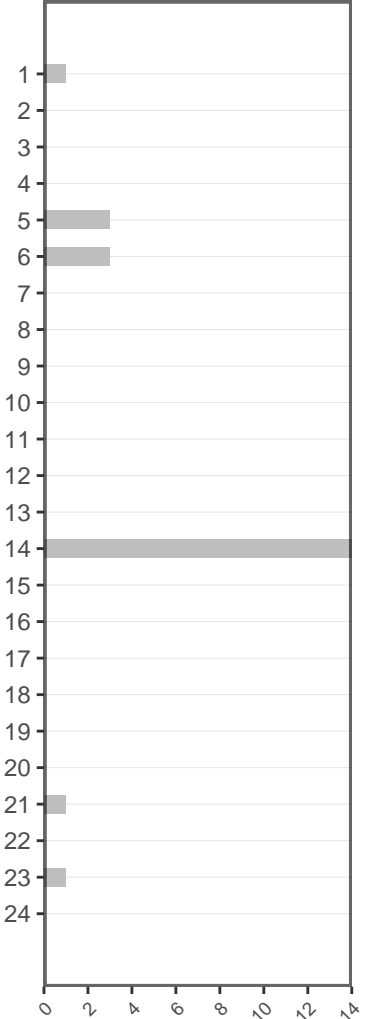
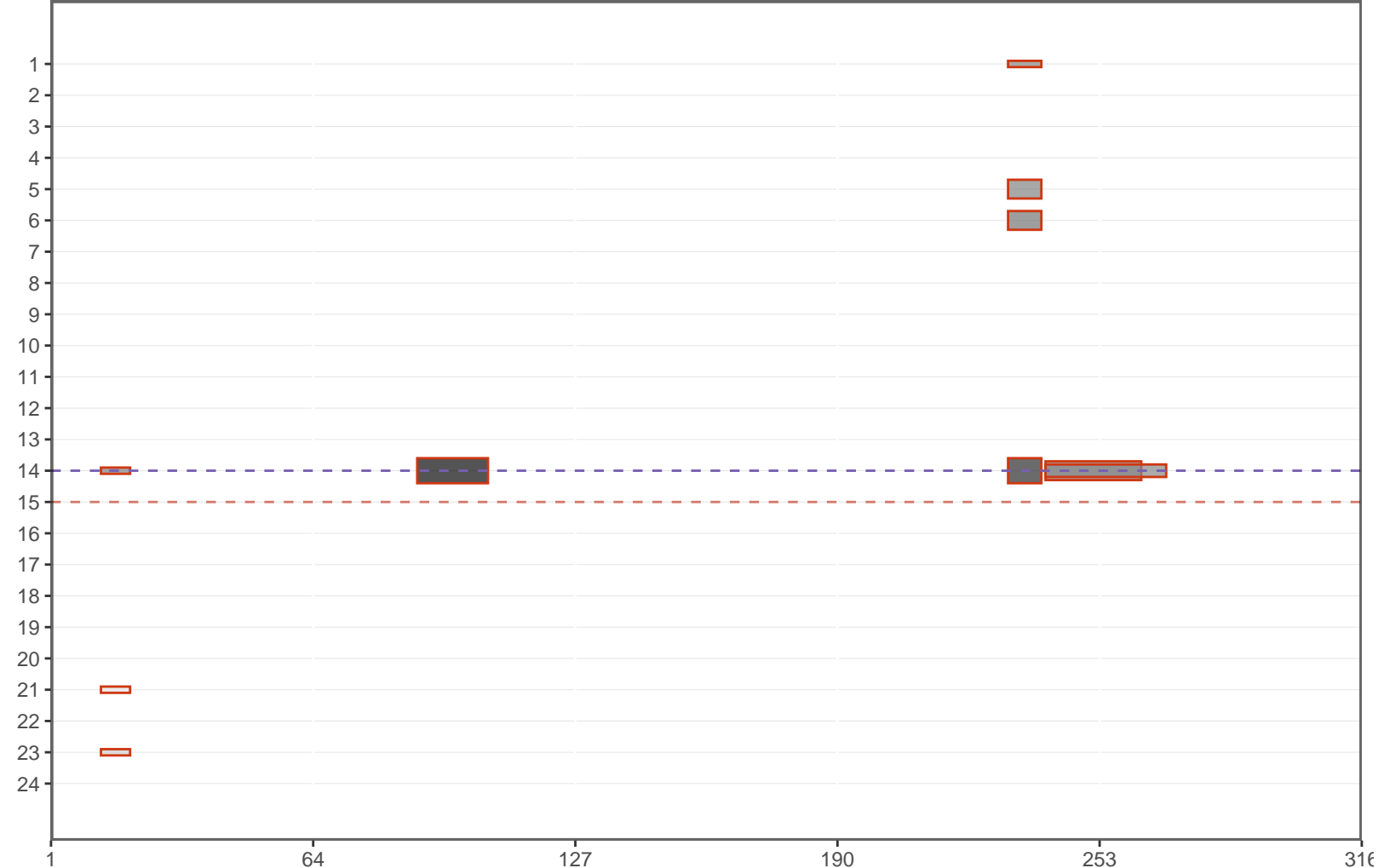
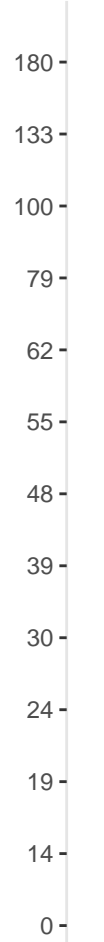


MW indication



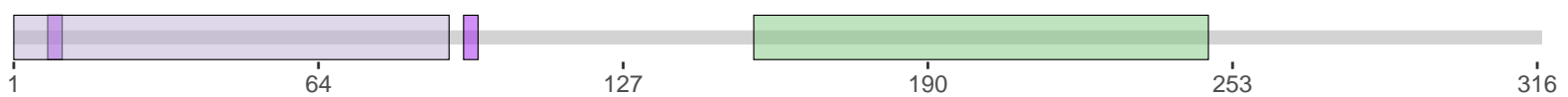
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

SP Sequon TM Domain PF03171 2OG-Fe(II) oxygenase superfamily PF14226 non-haem dioxygenase in morphine synthesis N-terminal

Protein sequence:

3TKGPNFGTKVSNYPGPKPDLIKGLRAHTDAGGHLLFDQDKVSGLQLKDDGQWIDVPPMRHSIVNLDGQLEVTNGKYKSVNHRVITGDTGRMLSLASFYNPGGDAWIFPAFALVEKDAEESKAVYKPFVDDYMKVYGLKFDQAKEPRFEAMIKAMETGVKCDPIATAV

NbL18g17000.1 uncharacterized_LOC107024435 [MW - SP = 10.94 kDa]

No. of times detected



log(intensity)



Values from



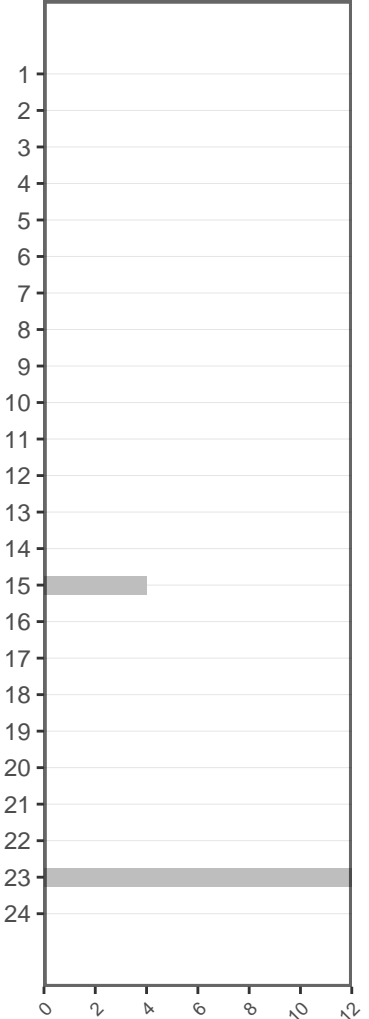
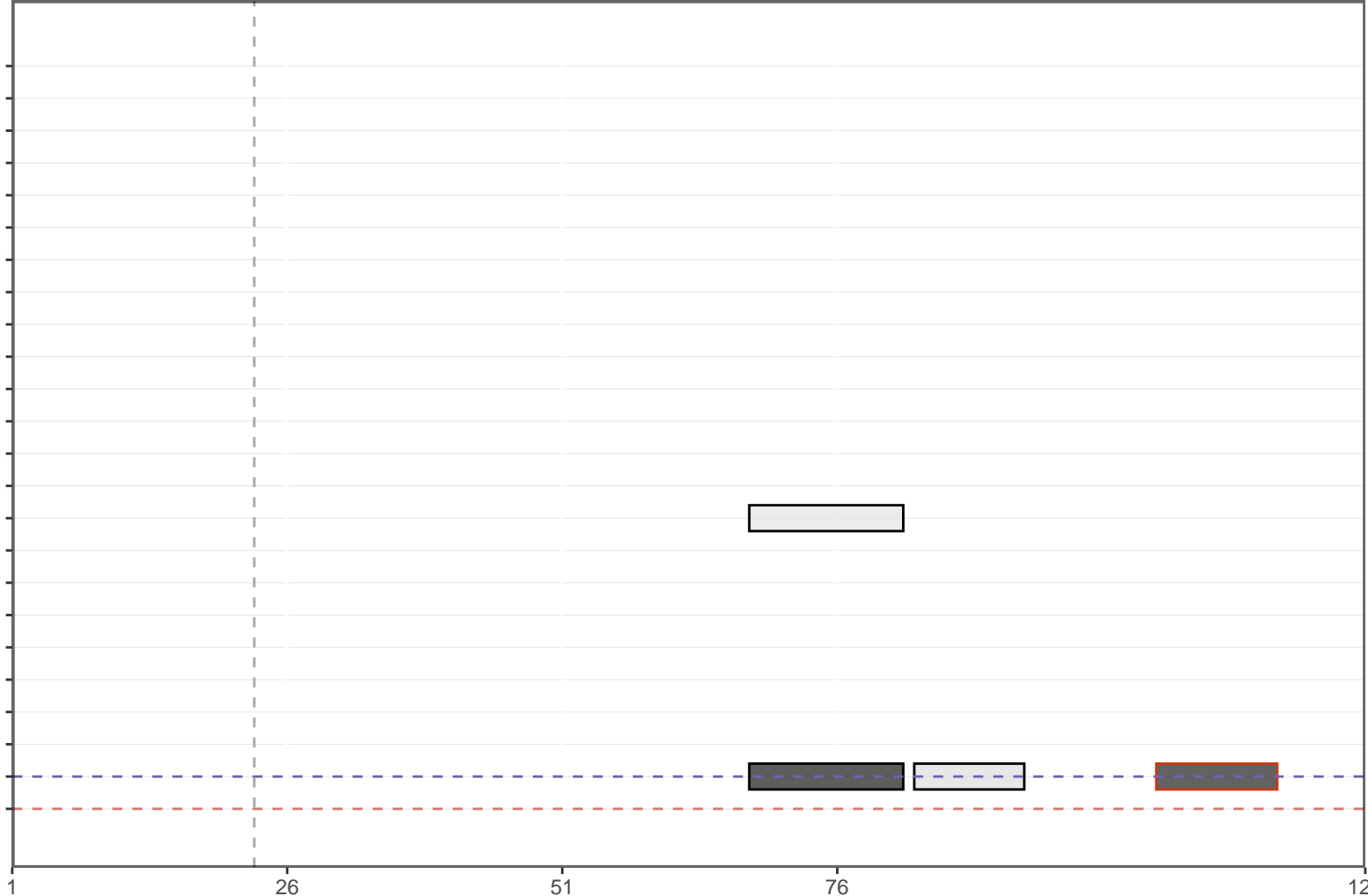
MW indication



Molecular weight



Gel Slice



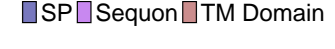
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

FPTEESPLVSVLDCGELWVTVSESEGHVLDLKEGLGTAATINRIVGRRRVSKVIGSGTGETTRVRCFSDP

NbL18g16990.1 benzyl_alcohol_O-benzoyltransferase-like [MW = 50.78 kDa]

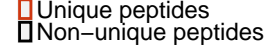
No. of times detected



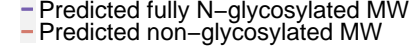
log(intensity)



Values from



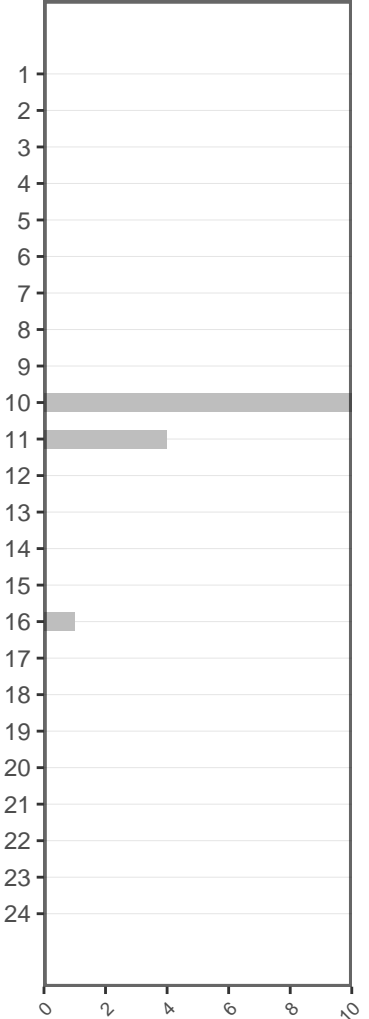
MW indication



Molecular weight

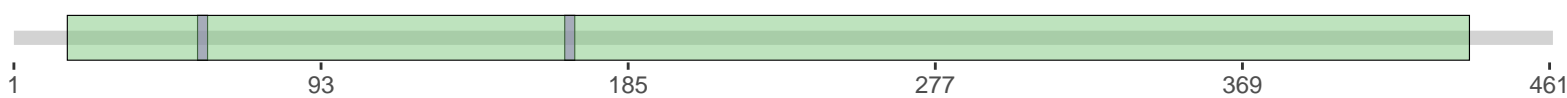


Gel Slice



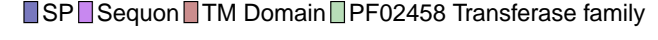
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IEYDEVPTKGTIFLDDMWHKSEFFGDPSEVSAALRREVPQHLHGKSTFELLTAVLWRGRMTSLKPDPEEEVRYLGNVARSRFNPLPTGYYGNAFAPVWTTAAKLSKNPLGFALVELKTKADVTEEVYKESVADLMVAKGRPHETVVRTYLVSDVTRGGFGEVDFGWAKPVYGGPKGGVGAIPGVASFYIPFKNKKGENGVPIQLPGFAMETFKELDGMKGVDFVNTKYAIRPAL

NbL18g16950.1 probable_lipid-A-disaccharide_synthase_mitochondrial [MW = 51.85 kDa]

No. of times detected



log(intensity)



Values from



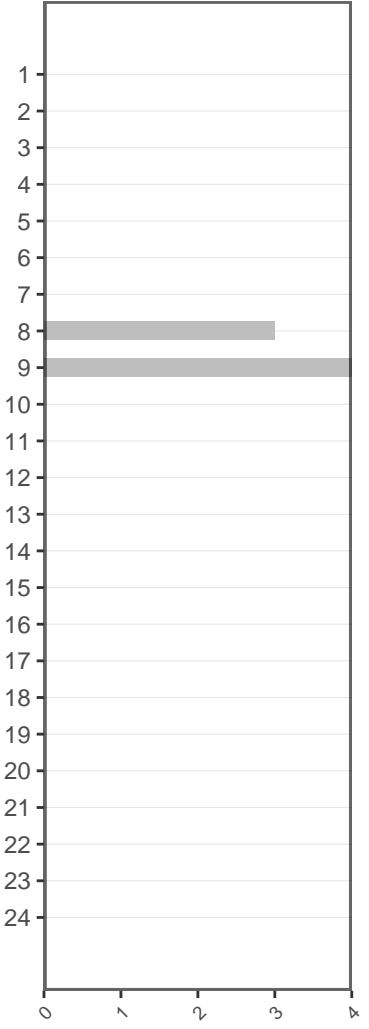
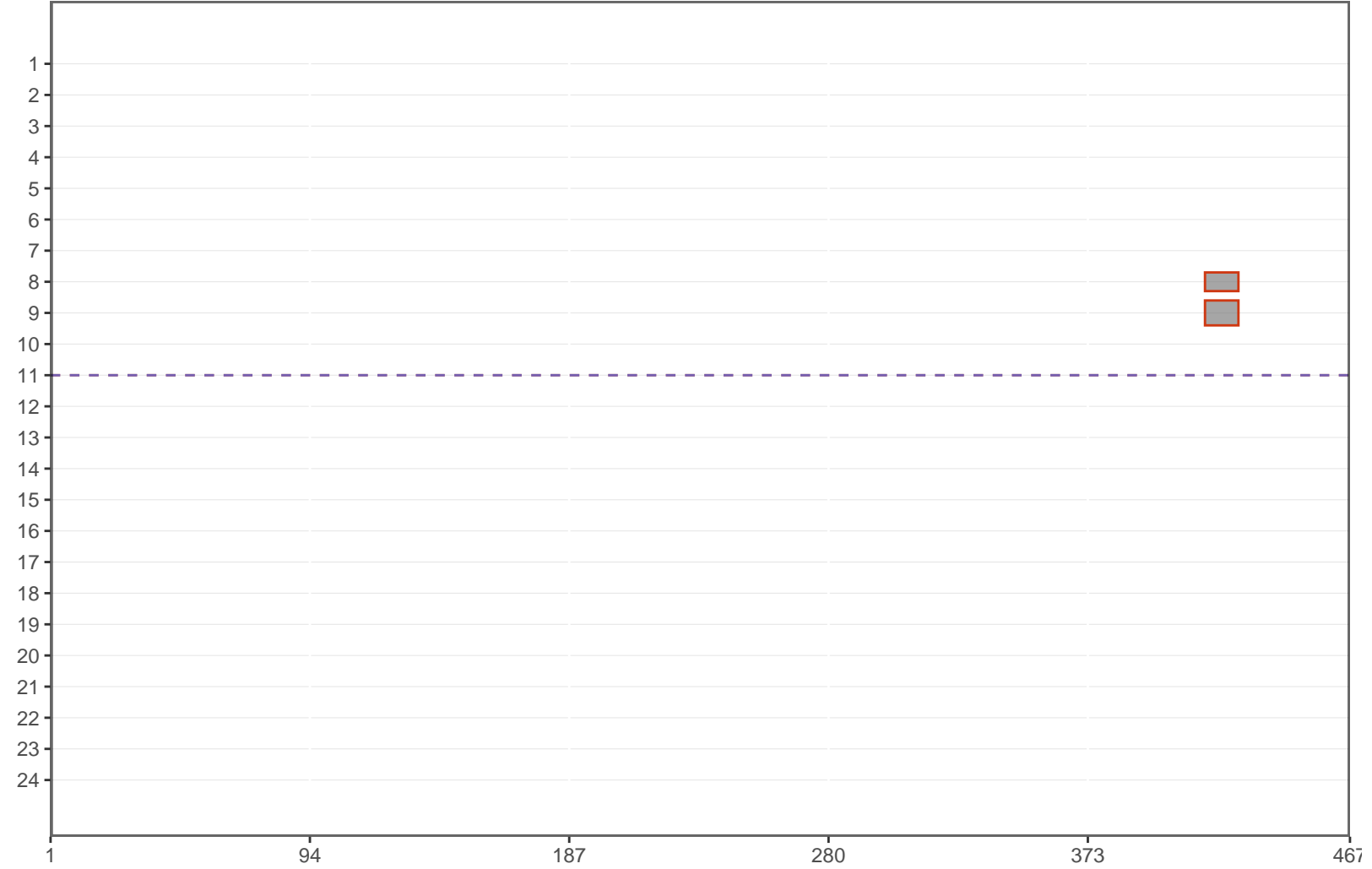
MW indication



Molecular weight



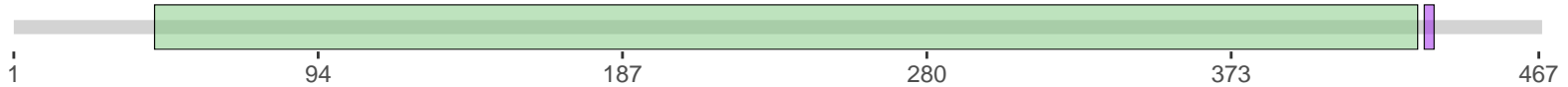
Gel Slice



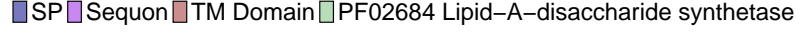
Protein length



Pfam domains



Pfam Description



Protein sequence:

DFQVQDATERRYHQGNAAFLTDHGSSGSPVILLPGRRGQVEYTRMFSFSSLEHLKGSFPDLVAVHVPNGHVEDHDKAVKWPSSVVLVPGSGHQMKYNSFSSASVALGSGTVMVEVQLARLFCVAVRAHLTELVRHKATIPVLSLNLDDSAHPEALFRDCTPKLASLLKDLMLDDDLREKGFNAEEVLDLIRPKMKNSGSGTGGEMVPLSDGAPSMVAWAWLYSRNKLE

NbL18g16710.1 universal_stress_protein_PHOS32-like [MW = 23.77 kDa]

No. of times detected



log(intensity)



Values from



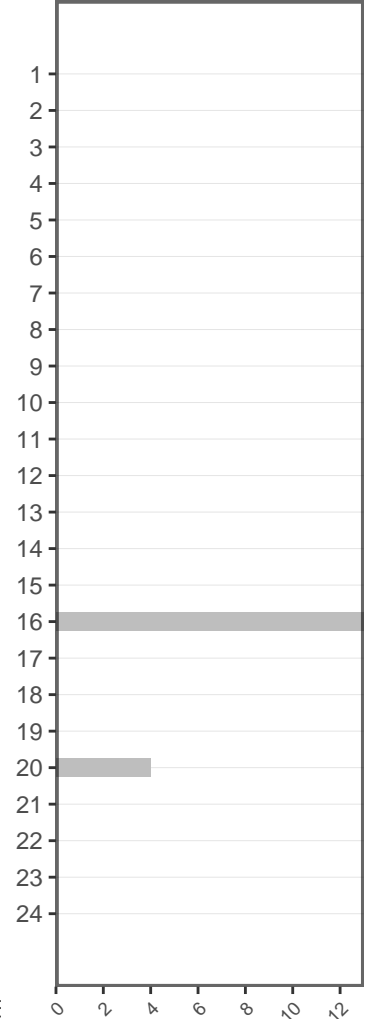
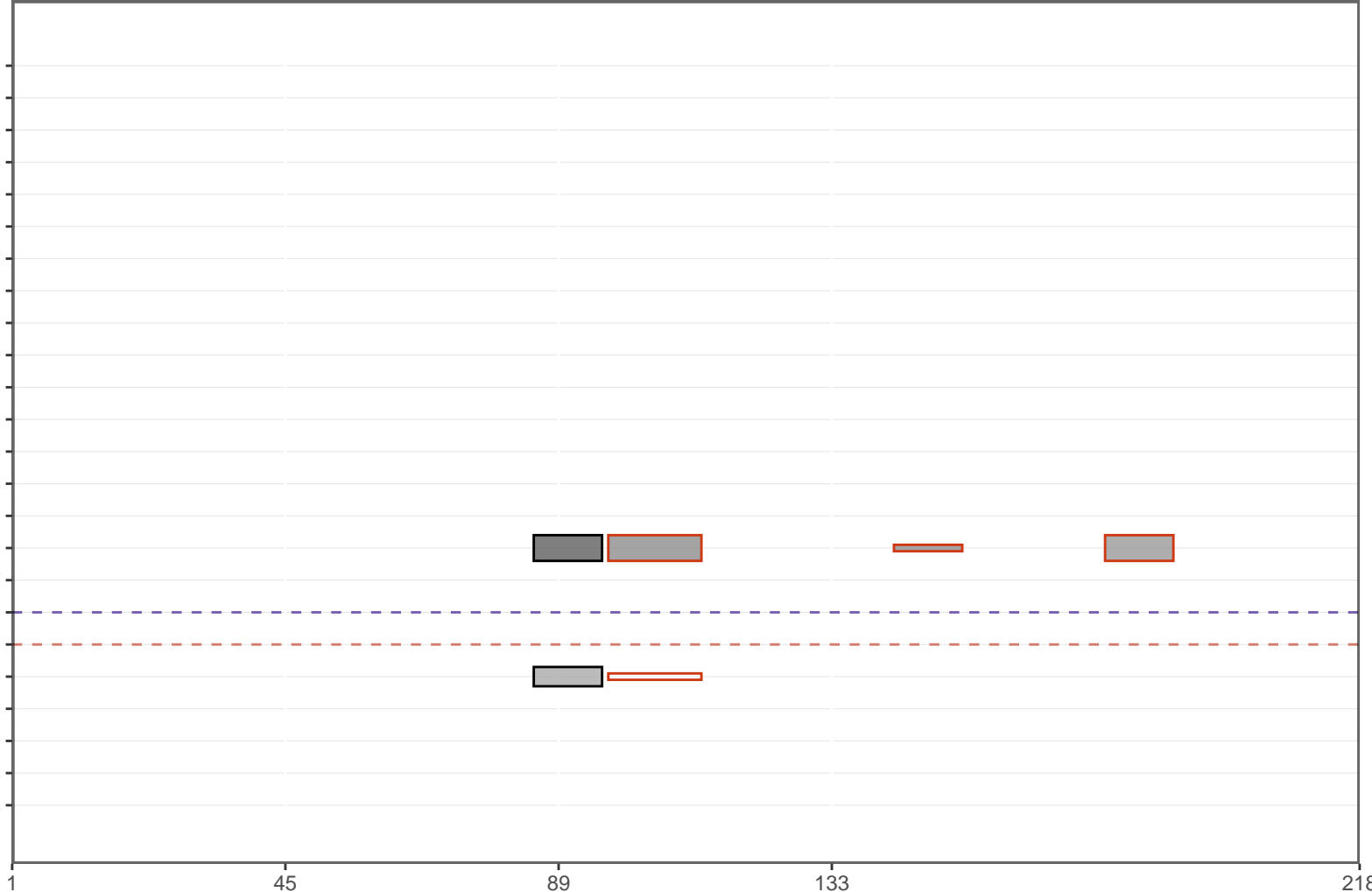
MW indication



Molecular weight

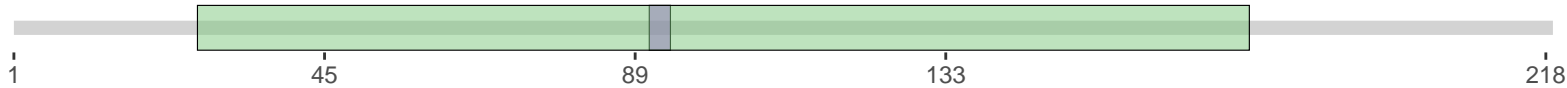


Gel Slice



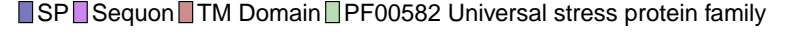
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ATQLALPLVEANVPIKIHVKDRDMKERLGLVEGLGLSAMIIMSGRFGATSSGFIKIKLGVSDVHHCICPVVVVRYPODDGGGVKKAIVAEALPPVPEEVEVHHDDDELTKGG

NbL18g16280.1 aconitate_hydratase_cytoplasmic [MW = 108.85 kDa]

No. of times detected



log(intensity)



Values from



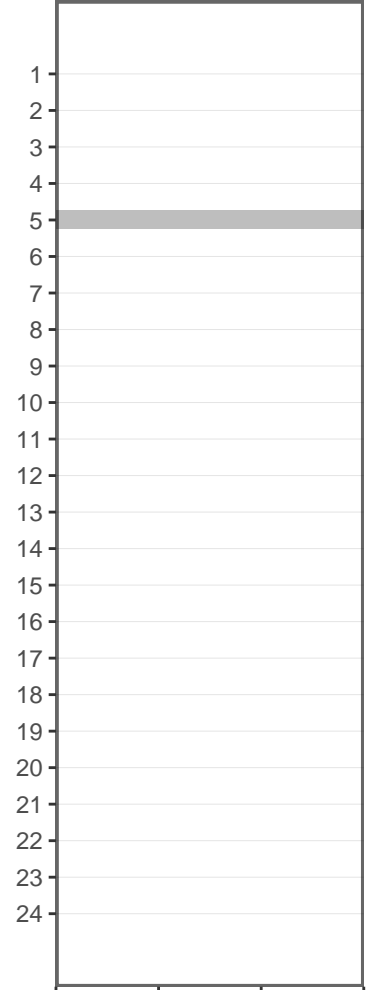
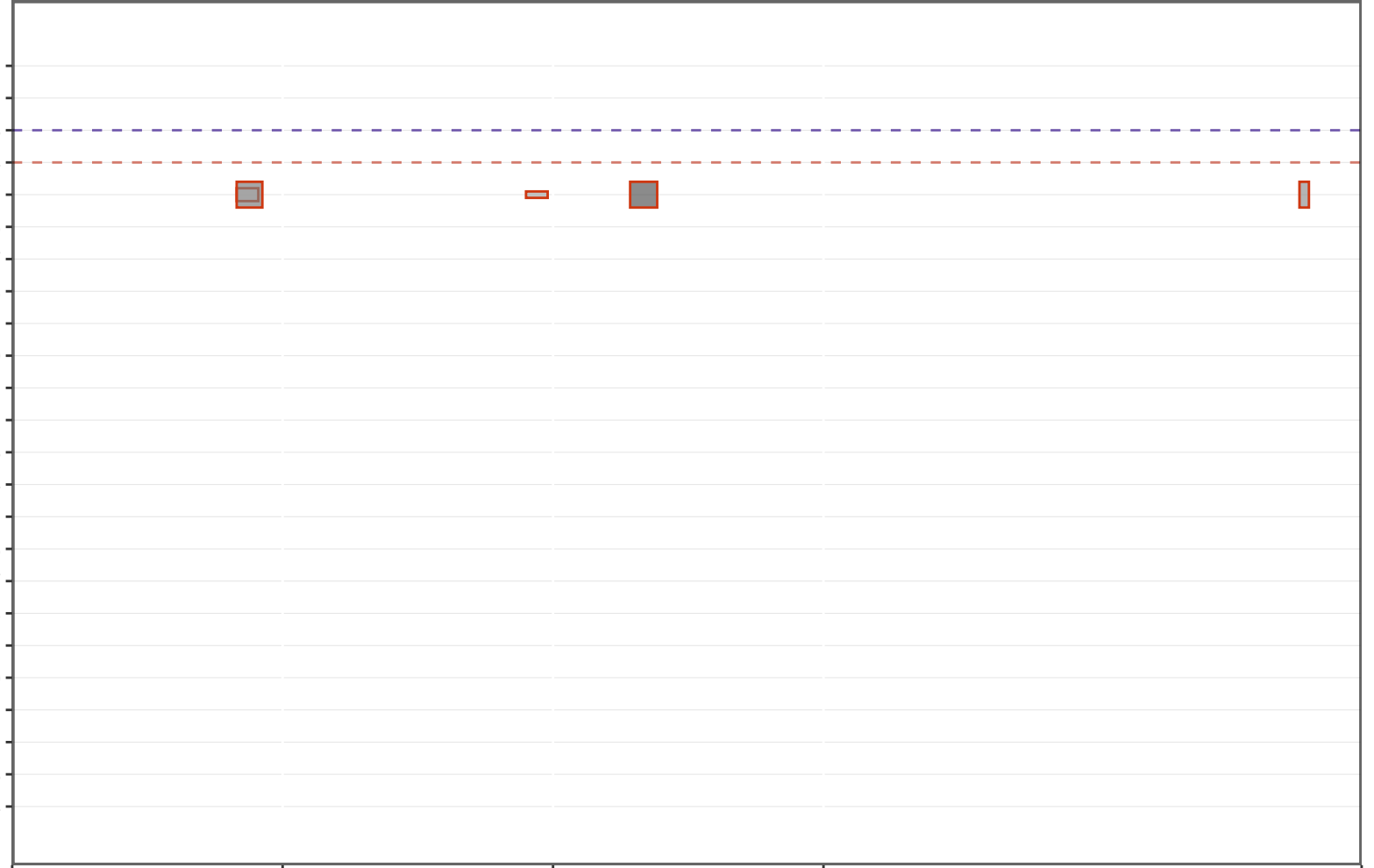
MW indication



Molecular weight



Gel Slice

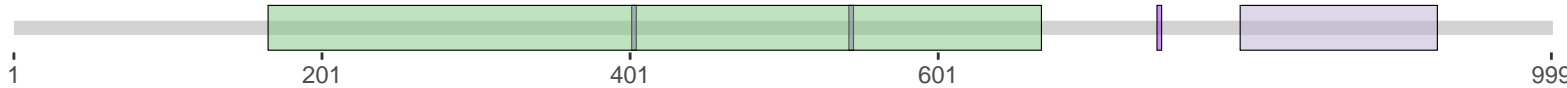


Peptide counts over 4 repeats

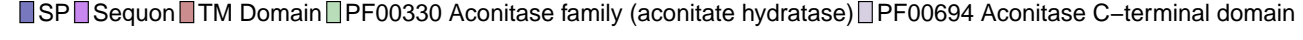
Protein length



Pfam domains



Pfam Description



Protein sequence:

*LKEKMSDWHACLBNKVGDFKGFVAPKEVGDKVAKFDHFGDPELKHGSAVAATSGTNTSNPVSVMGALVAKKAKASELGLHWKPVKTSLAPGSGVYTKYLLKGLKYLKGGGFNVYGGTTCIGNSGDLDESVASISENDVAAAALSGNRNPFEGRYHALTRANKLASPLVVAALAGTVDIDFENKDRGVGKDKDVFYFRDWPSTEEIAEVVGGSVLPDMFKSTYEATKGNMVALELVPTAKLVSWDPNSTYIHEPPVFKGMMDPPGPHGYKDAYCLLNFGL

NbL18g16090.1 cyprosin-like [MW - SP = 53.42 kDa]

No. of times detected



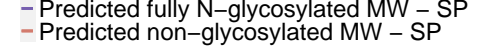
log(intensity)



Values from



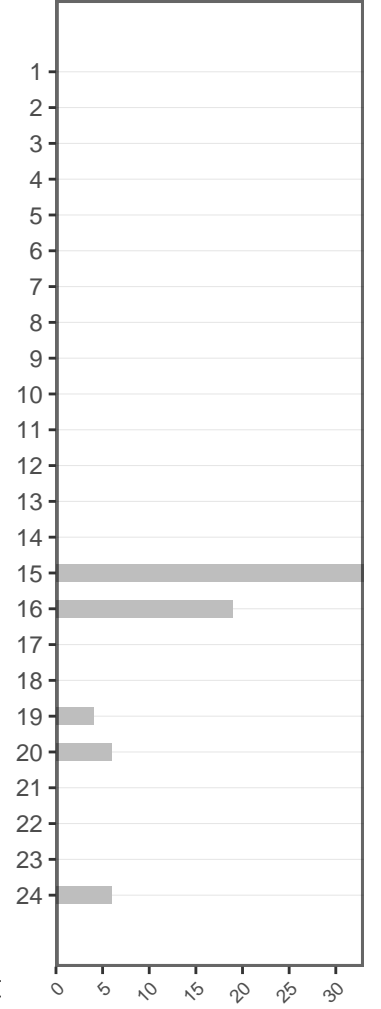
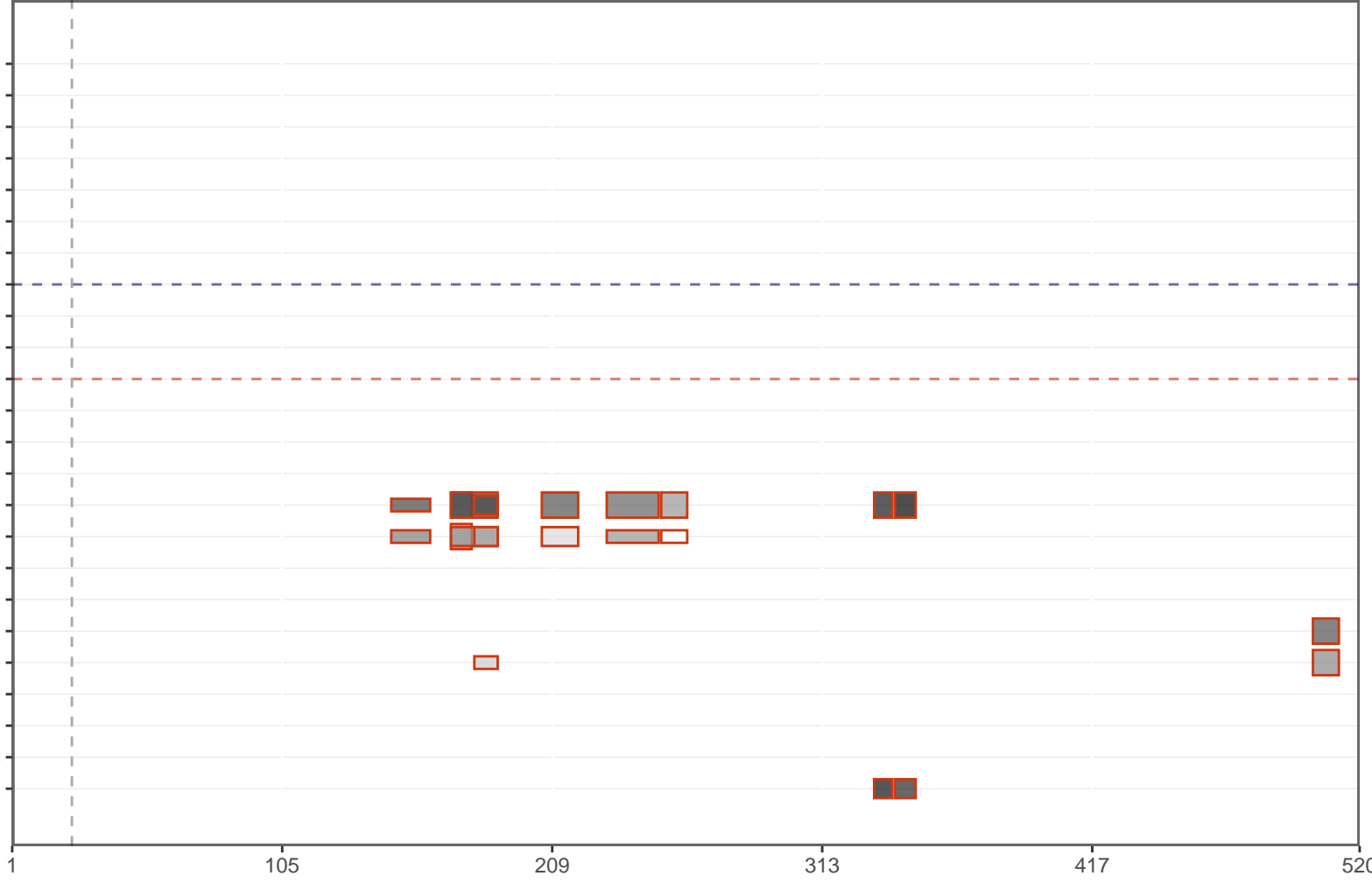
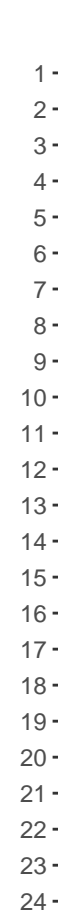
MW indication



Molecular weight



Gel Slice



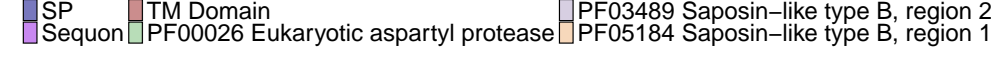
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FKGEHTYYPVTHKGVWGFDMGDLVWGGETTGISSEVGHVYVWFDGGGGCAIDSGTSLLAGPTTTRIQNHAGASGVVSGECKSLVTEYKTLIDLLKSAAPKQKSGKLGSSDGGSDVSMIEVVDKHNAGSNGLGDMDCRVCEMAVVMQNGMRRNETADSHYVYVGLGDRLLPSPMAGEAVDQGSLSAMPVNSFTIGNKTFDLPQQVYLVGVEAPVAGQSGFTALGVPPRGRPLWLGDFVFMGRVHTVFDVGNBRVGFEEAAV

NbL18g15780.1 lipoyl_synthase_mitochondrial [MW = 47.75 kDa]

No. of times detected



log(intensity)



Values from



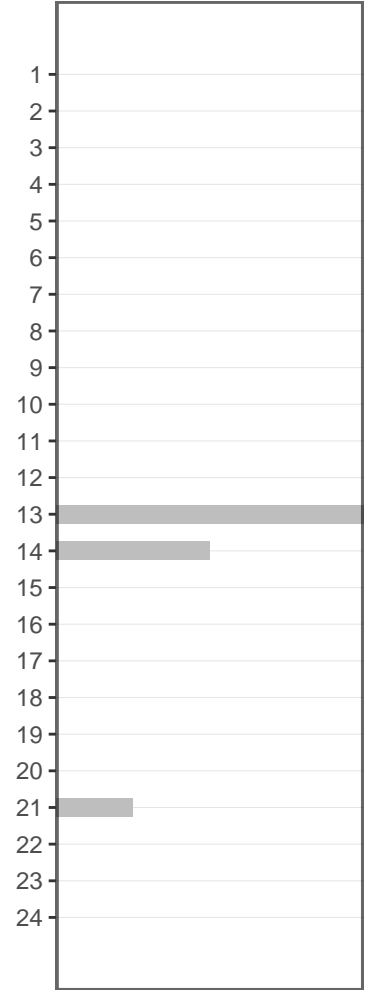
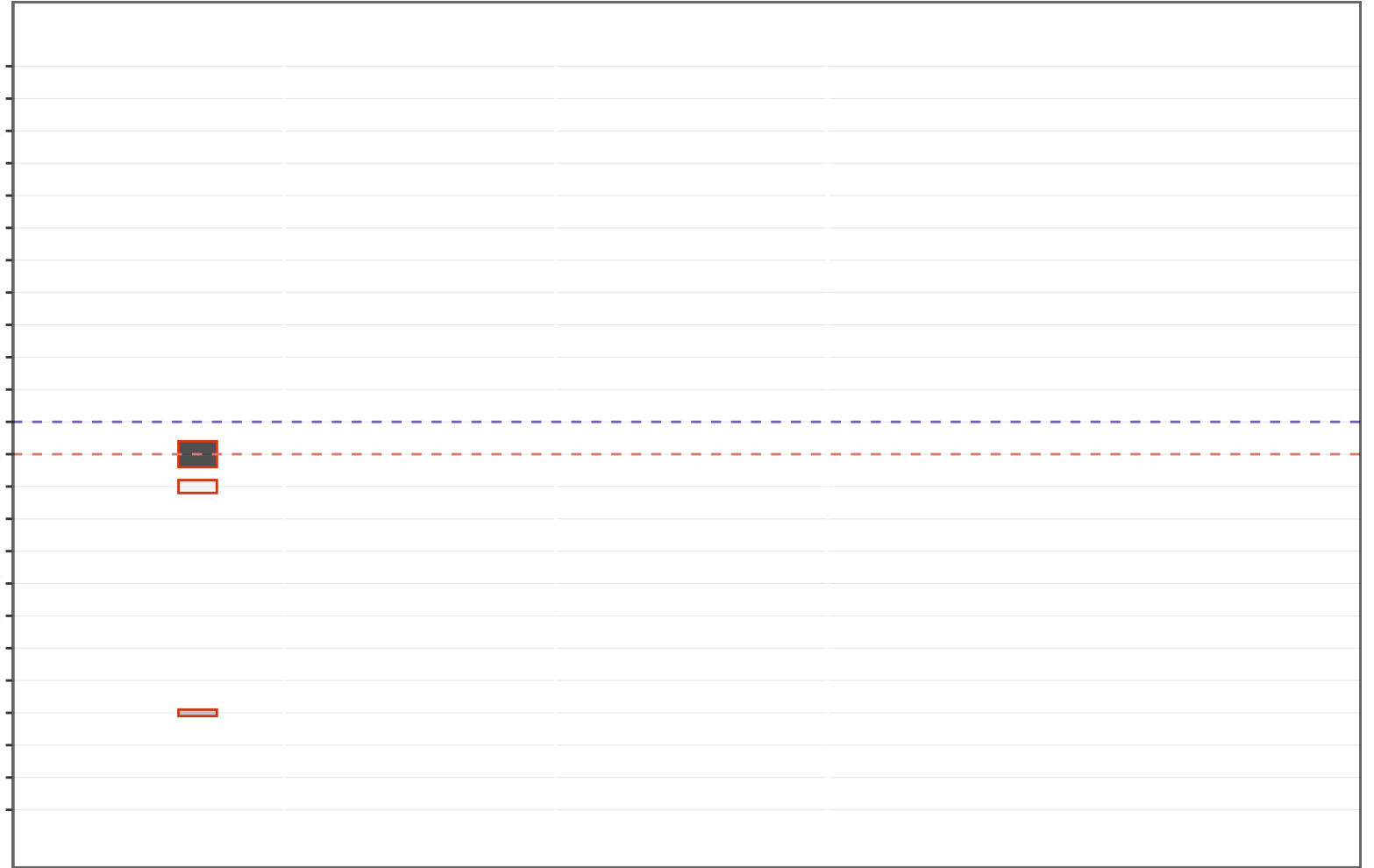
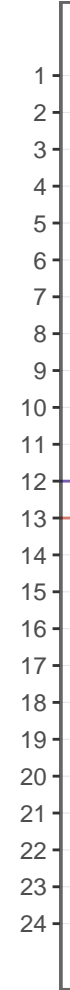
MW indication



Molecular weight



Gel Slice



Protein length

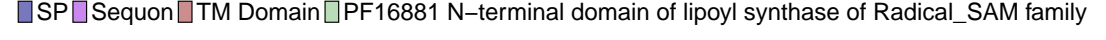


Peptide counts over 4 repeats



Pfam domains

Pfam Description

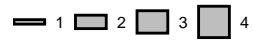


Protein sequence:

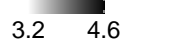
CGSHFTETVQKLLKALKPNMIEALKLVFFLLSSIVIKGERFKREARRGTTVALFCPKARINGLKSAAWFRPREKOGKERELSEVDGGLGFYFKLIGISTLLFFQNICFEWDCKPCNISESSLDCCGDFGDKFLLFFSFLSGLFLLFSAFLPSFLFSSFLFFGSSGTCSSYFVSVLLFPLGSAFFFLKRRDTSRVWVTEILLNNMMLPLGFGFAFA*

NbL18g15600.1 polyadenylate-binding_protein_2-like [MW = 71.84 kDa]

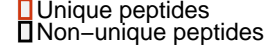
No. of times detected



log(intensity)



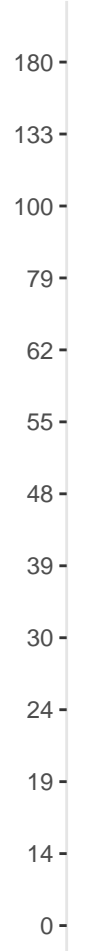
Values from



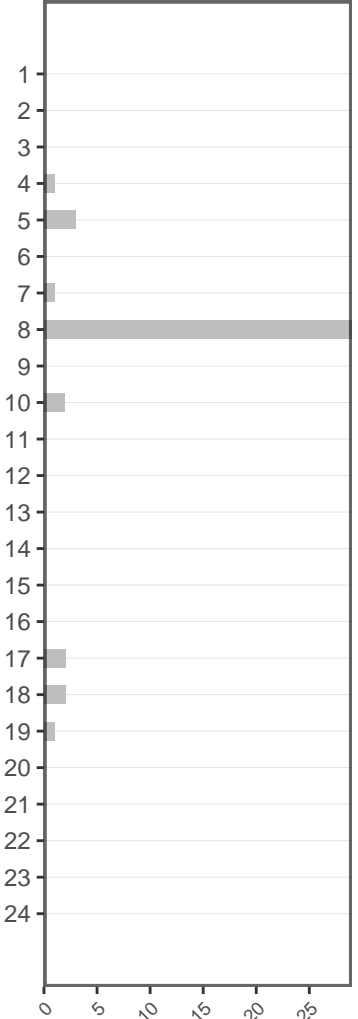
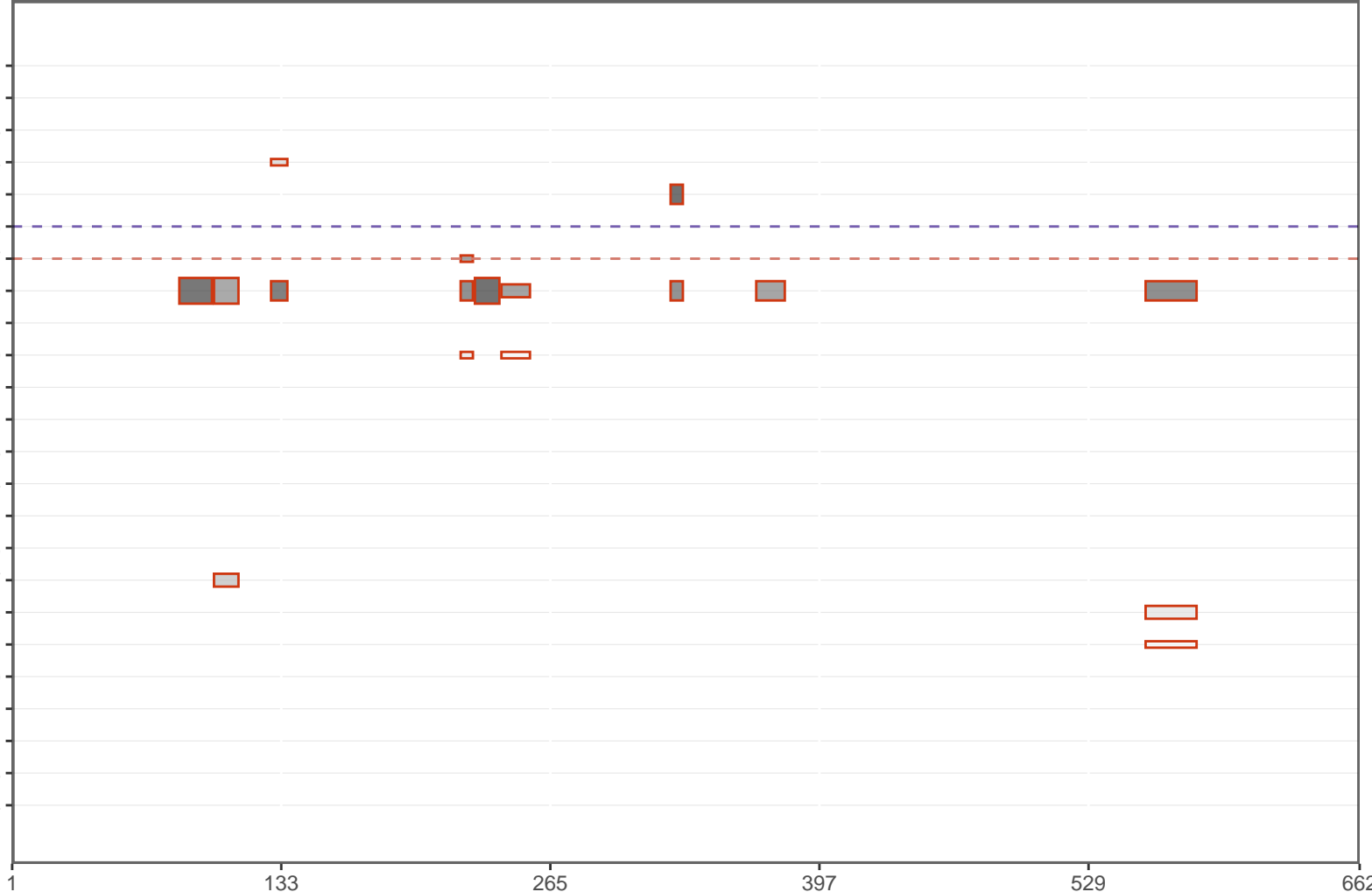
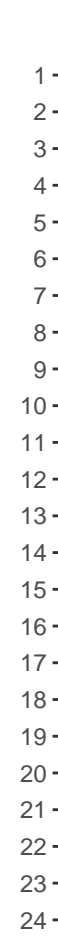
MW indication



Molecular weight

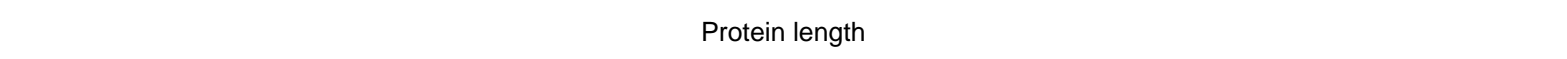


Gel Slice

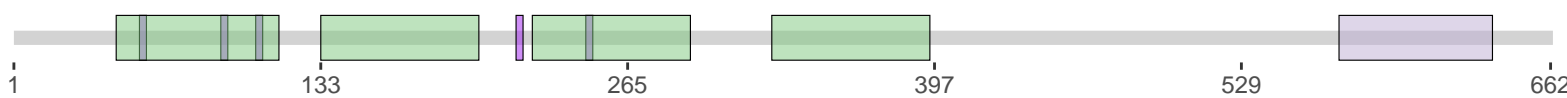


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

IGVLYIKNLDITIDDKLKEIFSEFGTIVTSGKVMRDPGSRGSGGFVAFSTPEEASKALSEMNGMKMIVSKPLVVALAGRKEERRAMLGAGFSGLRPVAAAMASMPMPMPYPGAPGMSGGLFYGGAFPPGMIPPGAGFVYGGQLAPGMRPGGAPLRFDFMPLVYGGGGGGGRPGRRGAGFVGGTGGPMPMMGGMLPRGMRYRPPGRNGGEAPTPLAGMLSVPYDMGGMLPREAAMSGPMPSTLASALANAPPEQQRITLGESEVPLVQLEIHEAAK

NbL18g15550.1 subtilisin-like_protease [MW = 87.81 kDa]

No. of times detected



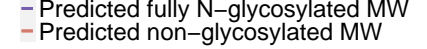
log(intensity)



Values from



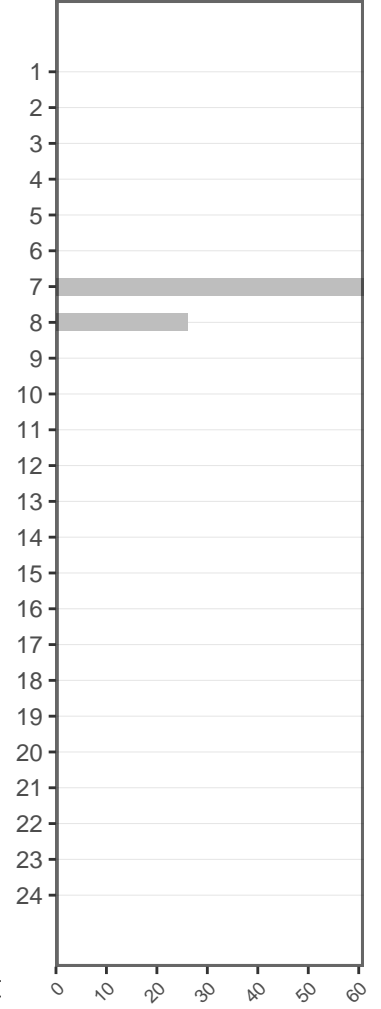
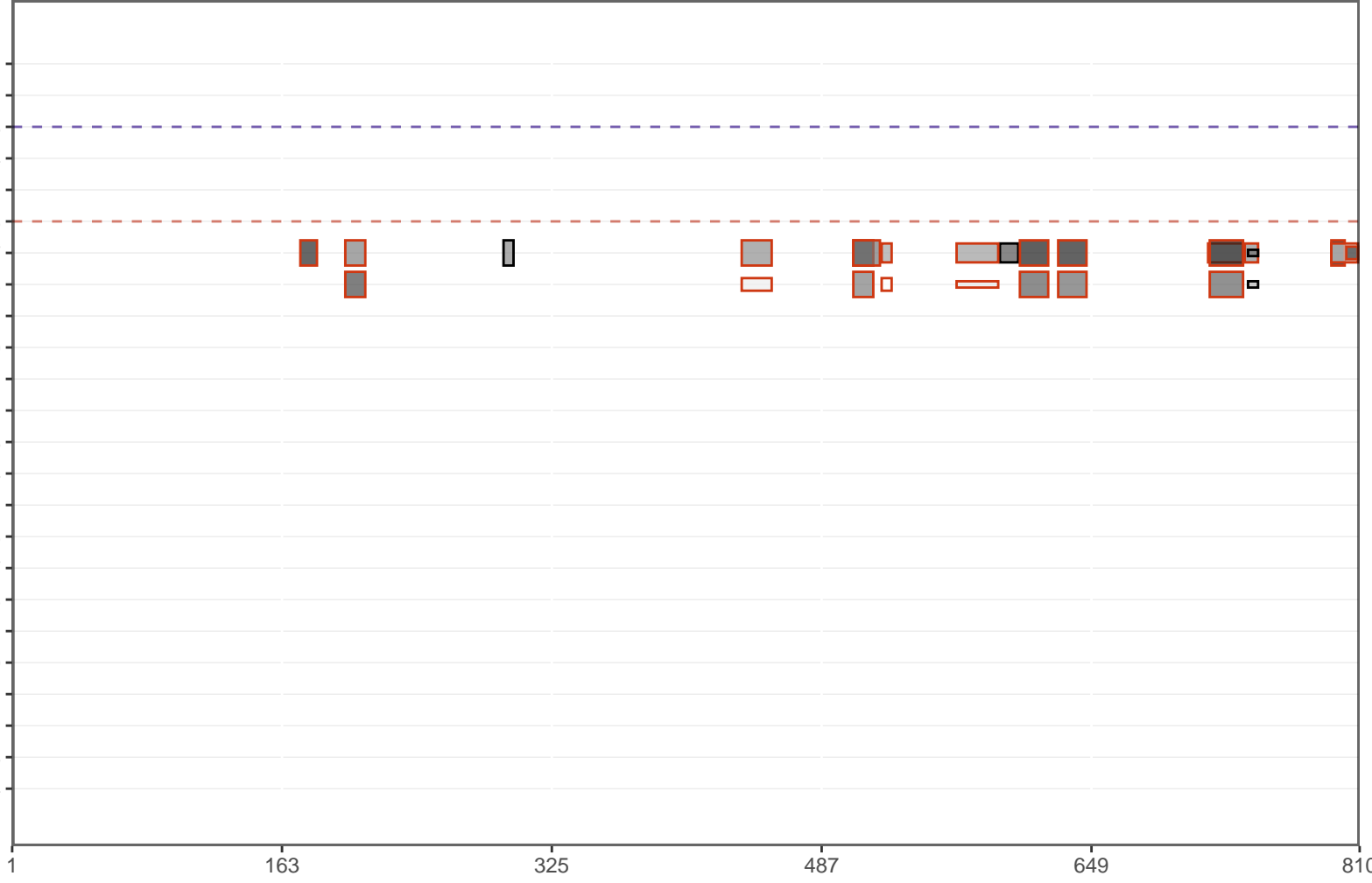
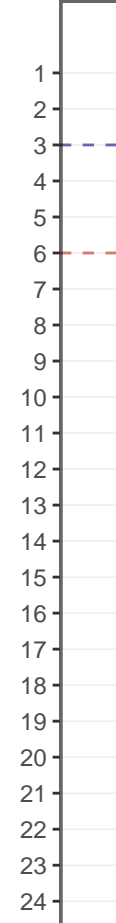
MW indication



Molecular weight

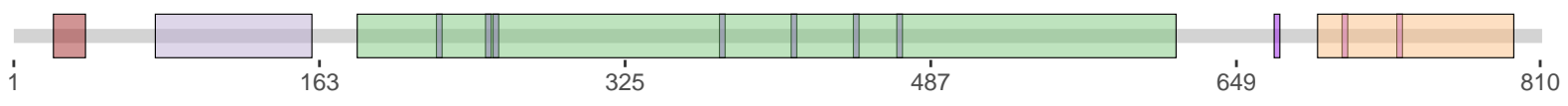


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

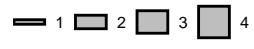


Protein sequence:

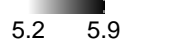
LTLLGNGVSPGLSLVPGNSSE66SLVVEGDDKELQKNAKKEVVLGDKNDVGEHYVYWRNSKAVAGAVFITNTDLEFYLQSEFPVWFLNQGEGDKVLEYIKGNSAPKGLKLEFQVTHGAKPKVATVYSGRGRSPGPKLKDLMAPGAILAGWPDGSPVTDVTEGKLFNFNIISGTSMSGCPHAGSGVAALKAAHPEWSPKAIKRSAMMTTSTALENTQSPRIGKRNKAAATPLAMGAGHIDPKALDPGLYDTPGDVYVLLGALNFTSKGIRKTRSSSYTCNSPS

NbL18g15390.1 snakin-1 [MW - SP = 7.07 kDa]

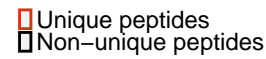
No. of times detected



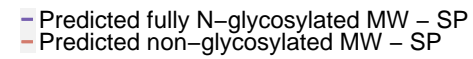
log(intensity)



Values from



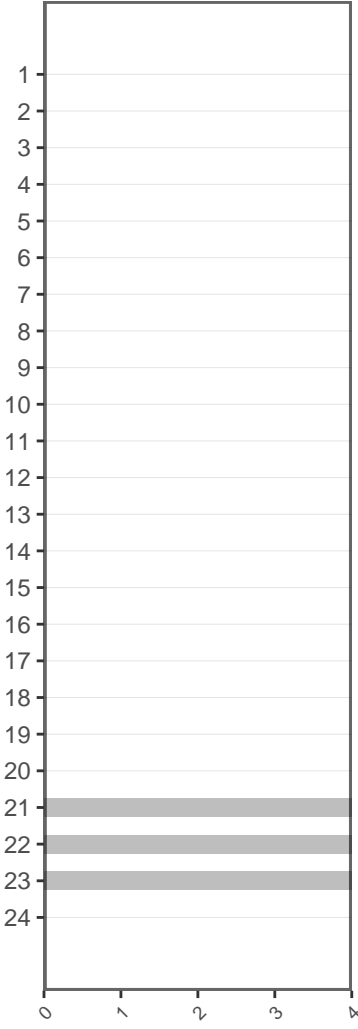
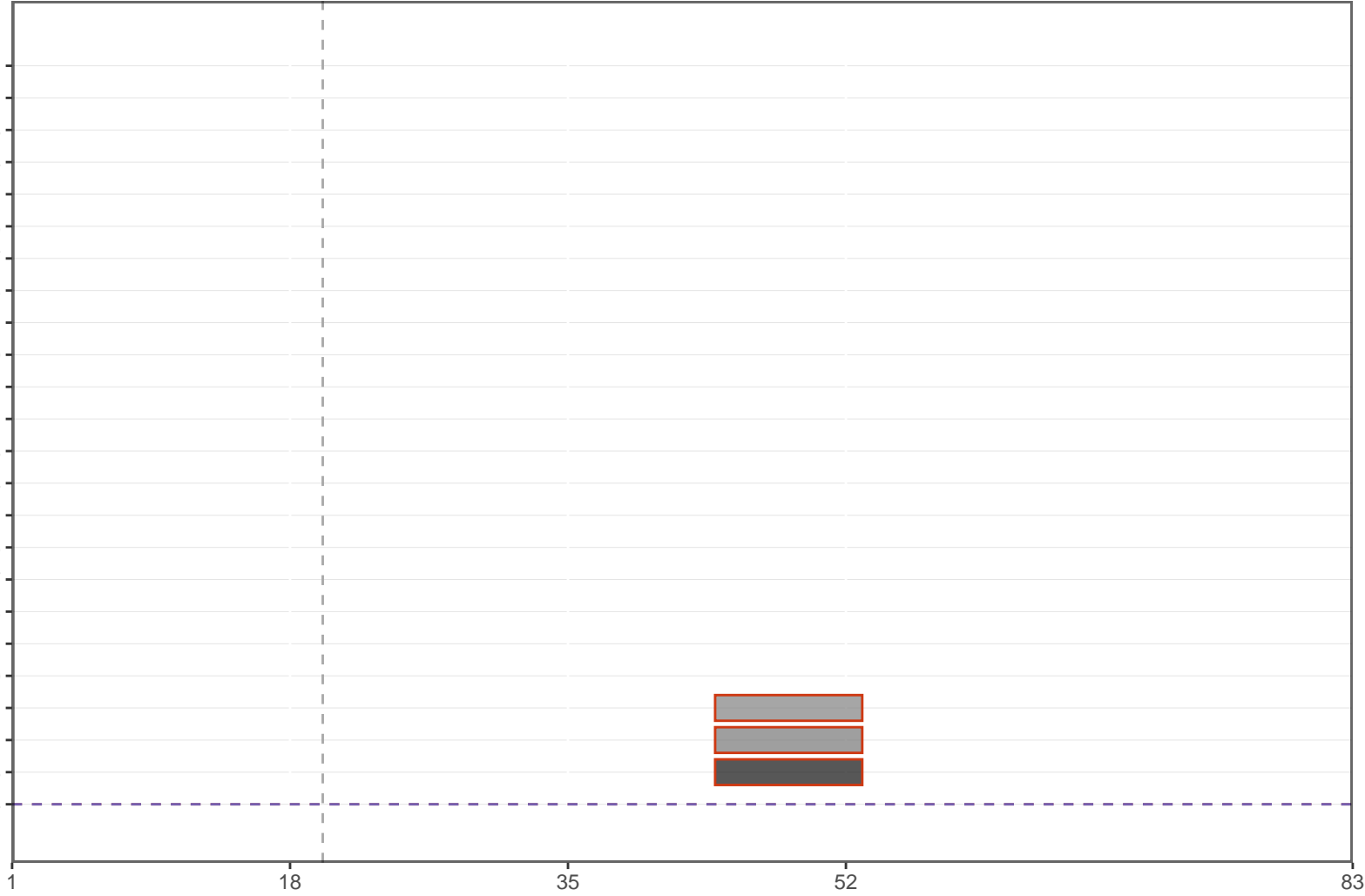
MW indication



Molecular weight



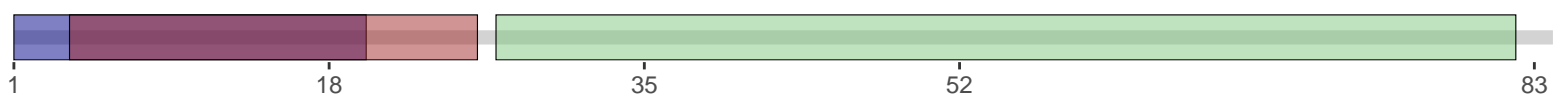
Gel Slice



Protein length

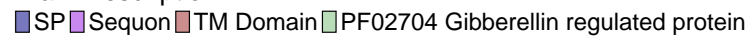


Peptide counts over 4 repeats



Pfam domains

Pfam Description

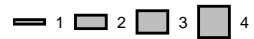


Protein sequence:

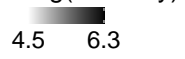
RCAKAGVMERCLKWGGDGECKGVPGGTVGNNHGCPRYRDKKNNKGNPKGP

NbL18g15140.1 adenine_phosphoribosyltransferase_1-like [MW = 30.08 kDa]

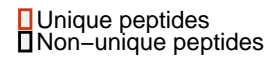
No. of times detected



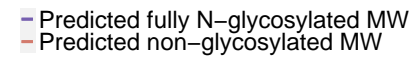
log(intensity)



Values from



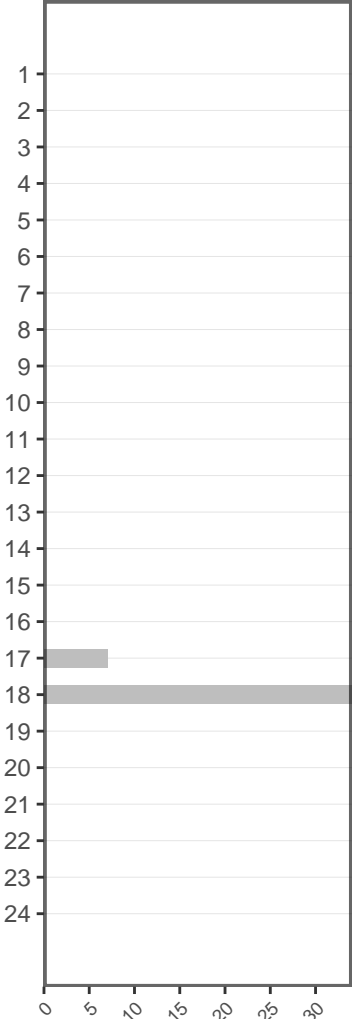
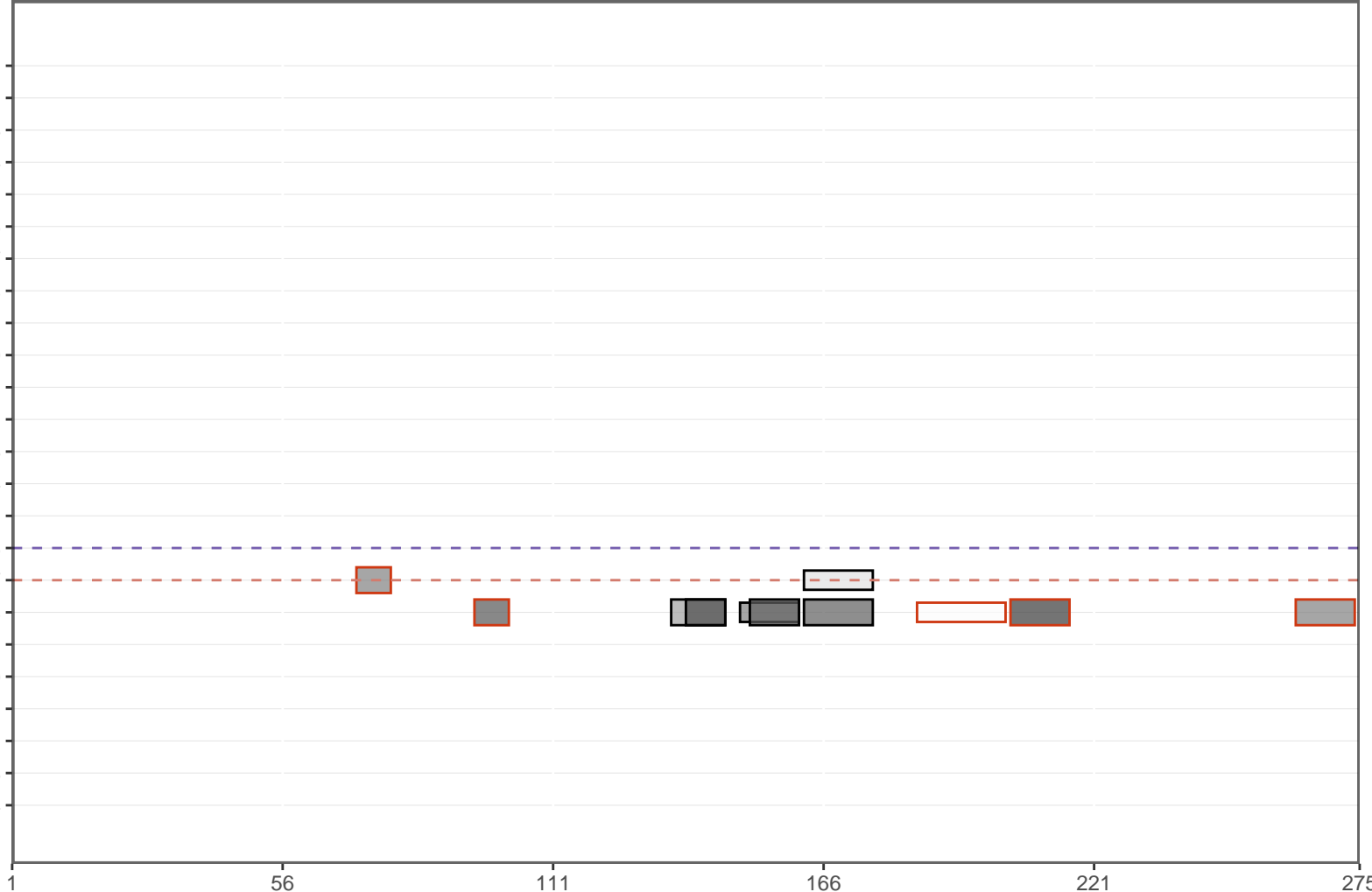
MW indication



Molecular weight

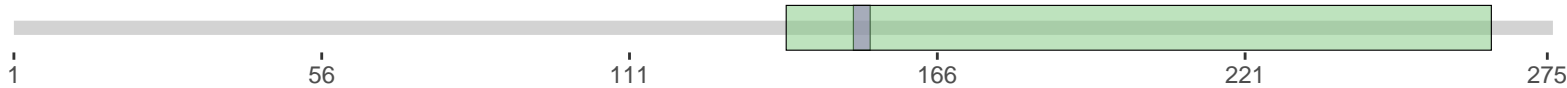


Gel Slice



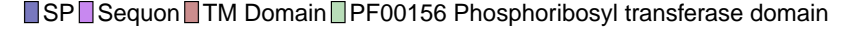
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IDITLLLLDTKAFKDTIDLFVVERKDKNINVVAGIEARGFIFGPPALAAAGAKFVPMRKPKNLPGEVISEEYSLEYGTDKIEMHVGAVQAGERALVDDHATGGTLSAARLLERVGVVEVACGLIELPELKGDRRLGDKPLFLVLSGT

NbL18g14970.1 LIM_domain-containing_protein_WLIM1-like [MW = 21.62 kDa]

No. of times detected



log(intensity)



Values from



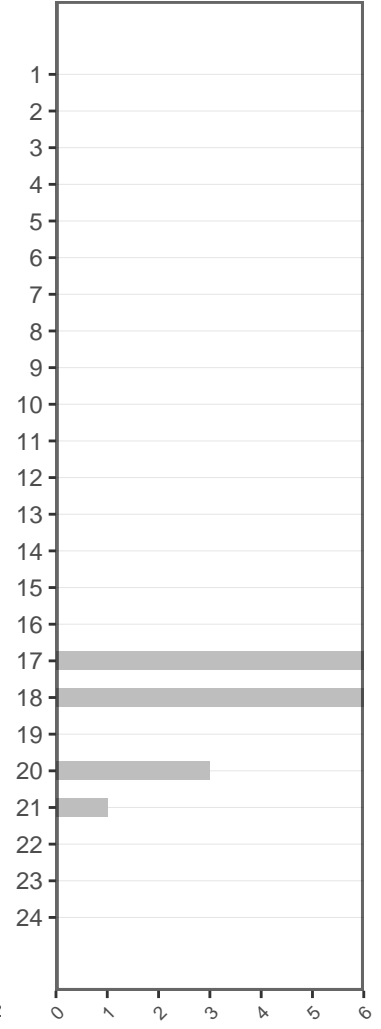
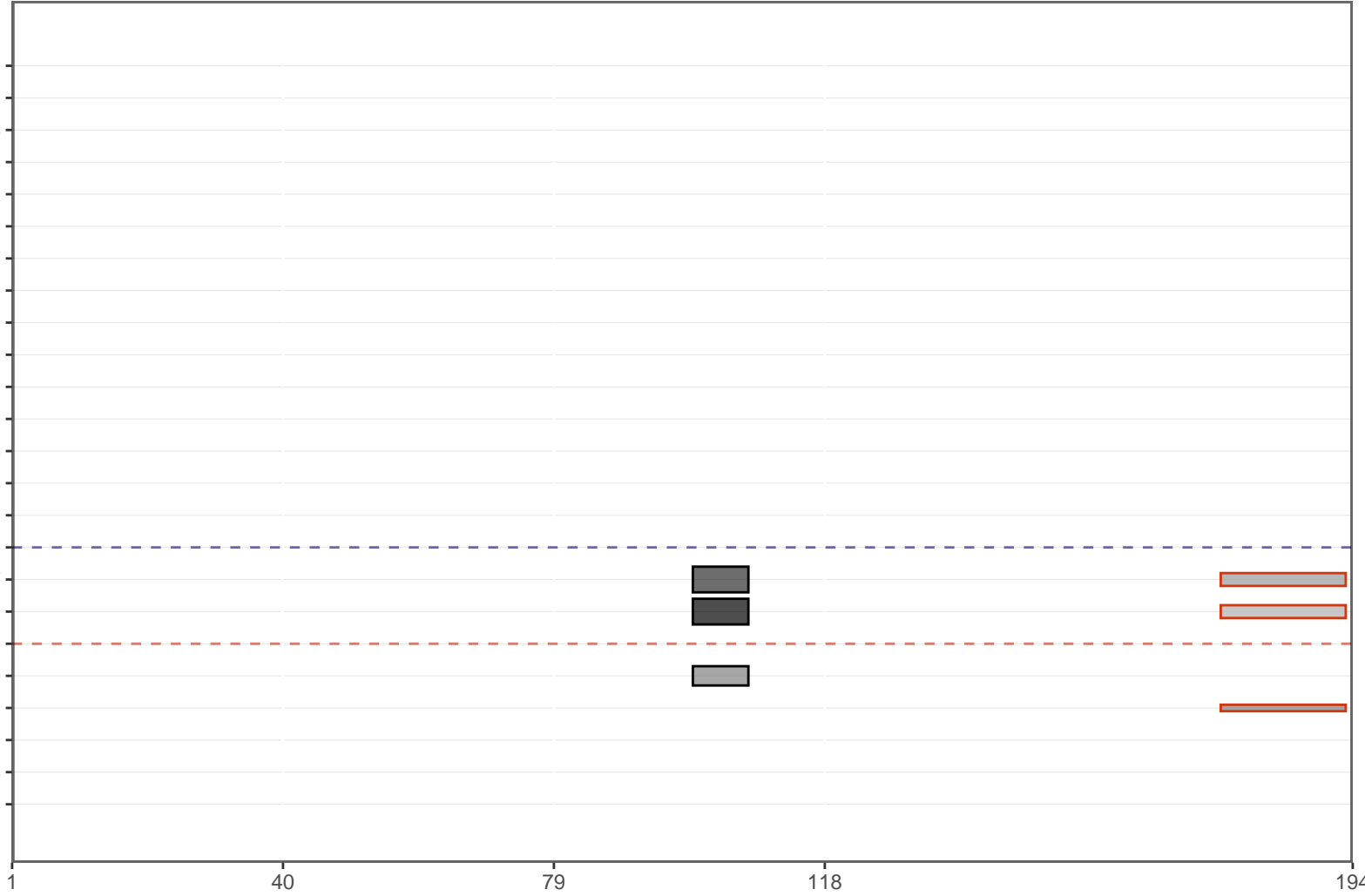
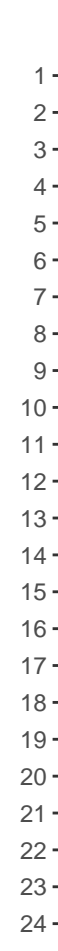
MW indication



Molecular weight



Gel Slice



Protein length

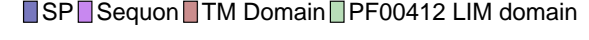


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

PGQKPIDSEKPOVAVVTEFMFGGTRKFGGKKTVPTEKVSVNGTPYHKGFKDSHGSGGVSPSNVIAHEGRLYGKH*HQLIKEKGNLSKLEGGHQNSTTTTTEVTAES*

NbL18g14840.1 serine_carboxypeptidase-like_7 [MW - SP = 49.86 kDa]

No. of times detected



log(intensity)



Values from



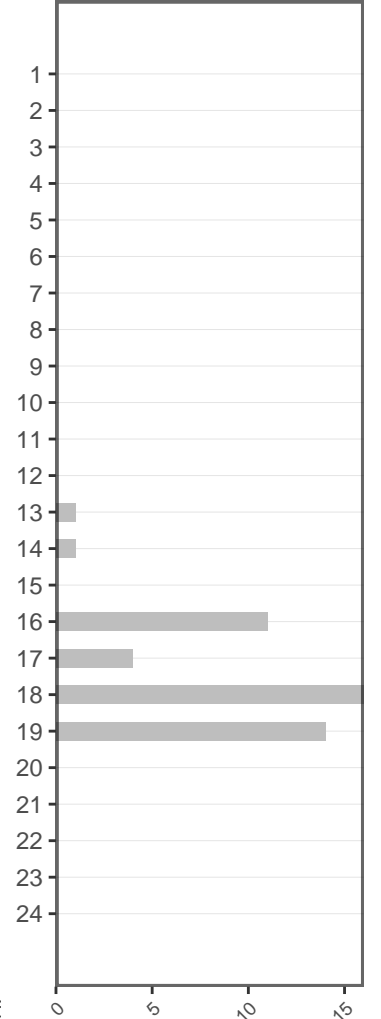
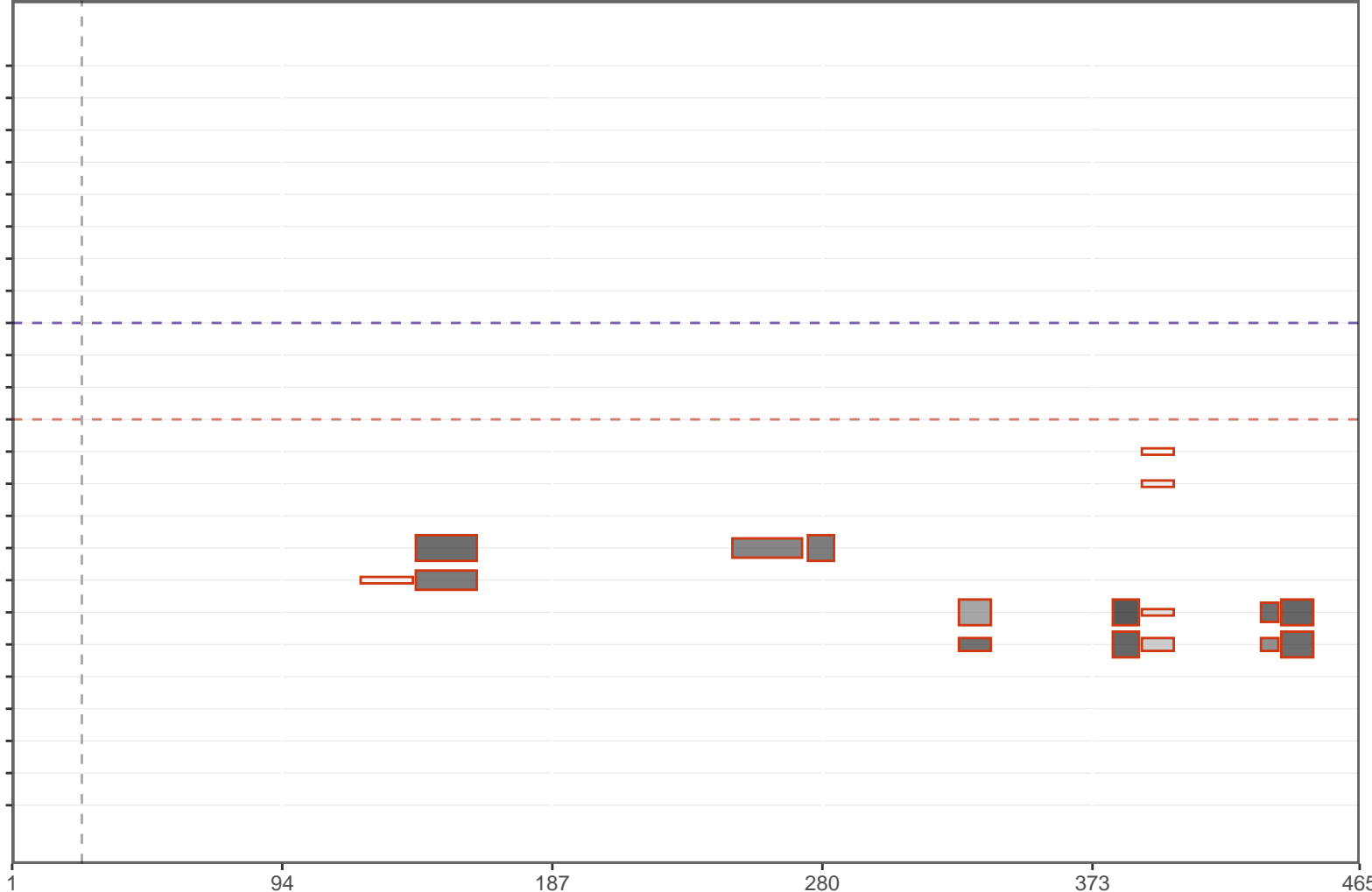
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YEIPFAYGAGLISDELVEELKRNKNGEYQNTDFPNTQGLDGHFTFHELLKRINNPHELEPKQGFASPKPHLLFGQRRLNWKFHQLNPNPQGLPALKRNDWYKHSTHWADDGGVREALHRIKGTGKWKVRCASLQVGTTFMSSIPYHANNLSAKGYRSLYSGDHDKVVTFLESTQAWIKSLNVEYDQDWRPWWVDNQVAGYTRSYENRMTFATVKGAGHTAPEYKPREGLAMLRWMSCKPL*

NbL18g14580.1 branched-chain-amino-acid_aminotransferase_2_chloroplastic-like [MW = 42.81 kDa]

No. of times detected



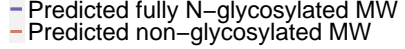
log(intensity)



Values from



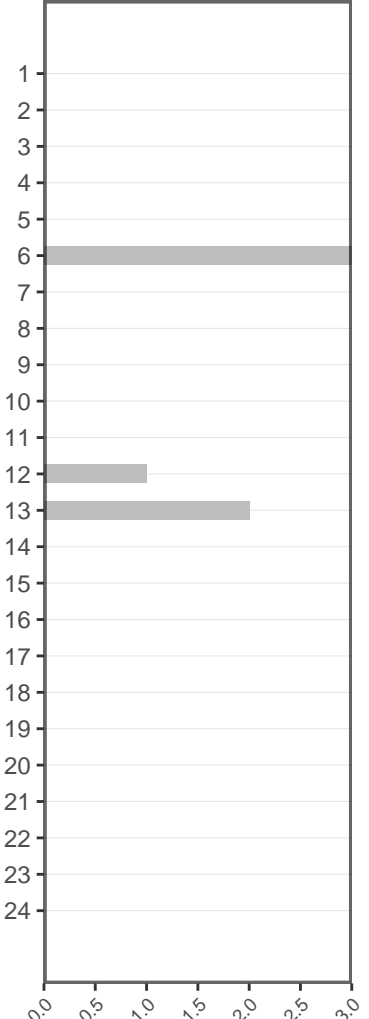
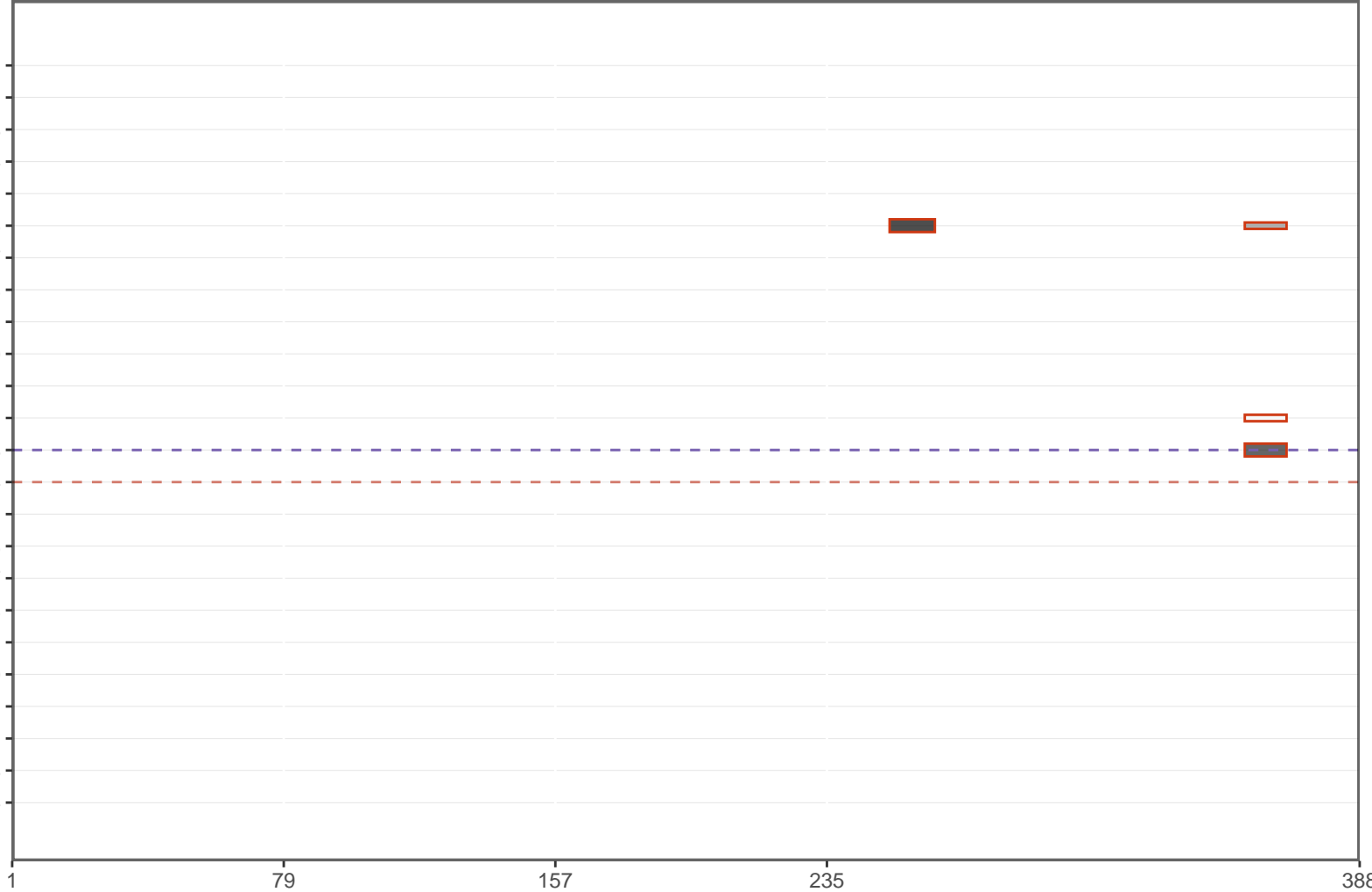
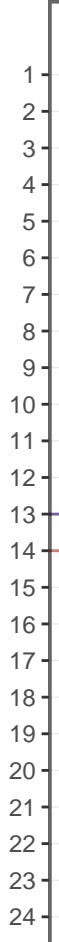
MW indication



Molecular weight

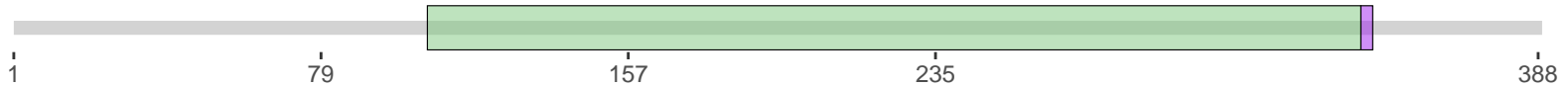


Gel Slice



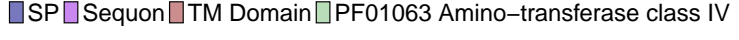
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

.MGSGA/LGVAPAEYFLVYSGFVGNVFKDGTALSLVYVEEFHRSALGGAGRIKSIYVAPVAKMARNNAKGGKFTDVLVLDVNNKYIEEASBSNLFVKGKIVSTPKAKGTILEGVTKKSAIDAHDLGYQVEERAEAEELNTADEVFCGTALGVAVVGNITVYKGGKIEYKISSEMISGQLNRLVIGRGTIEGRKRWVVEVW

NbL18g14390.1 xylulose_kinase-like [MW = 61.44 kDa]

No. of times detected



log(intensity)



Values from



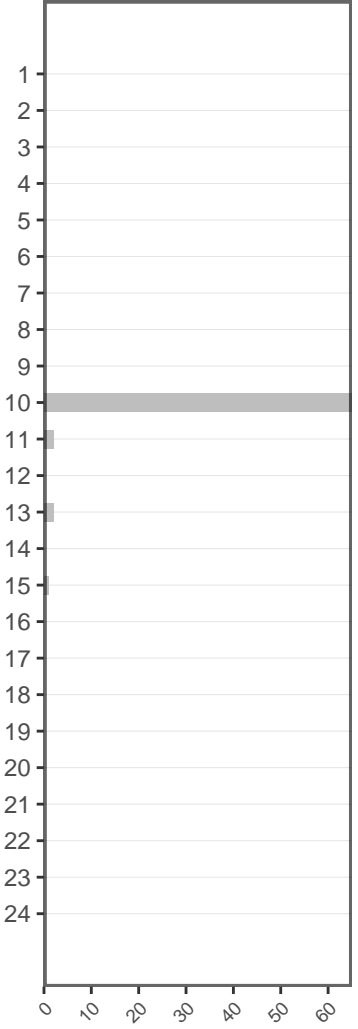
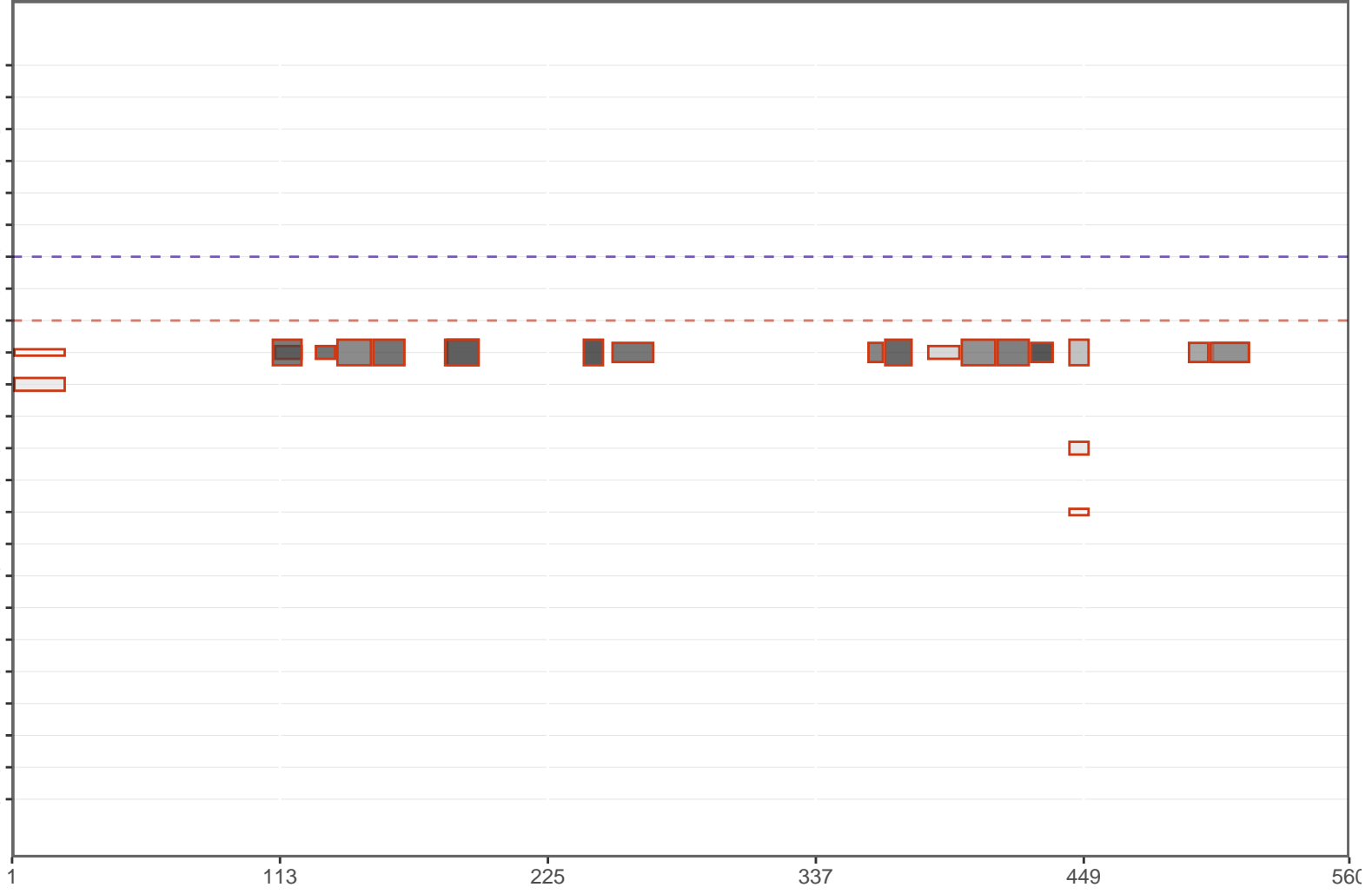
MW indication



Molecular weight

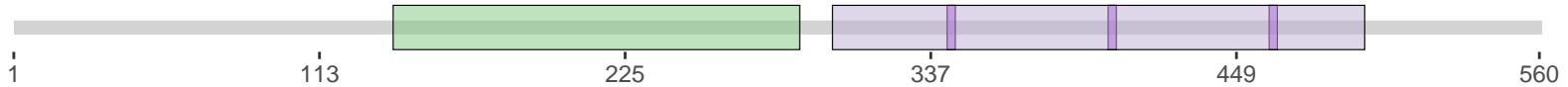


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00370 FGGY family of carbohydrate kinases, N-terminal domain
- PF02782 FGGY family of carbohydrate kinases, C-terminal domain

Protein sequence:

ERYHFSKDCCLIQVSGDNPNSLAGFLNTPGDLAVSLGTSDFVFGITKHNPSEGHVFPNPDTESEVMMLGKYNGLAREDRNINVAEKSWDFNKYLGQTPPLNSGRDLGYKDFEFLPLPVGFHRYLENTFGDGLGKHEVGEFDPPEVRAVEGGFLSKRAHERFGMPSPPKRIATGGASANSLSLALBIFGCDVYFVGGPDSASLGAALRAAHGWLGSKGNFVPSISMVMDNMDKTSLNCKLAATAGDQGLKVAKYAMLMKKRIENRNLVEKGLR*

NbL18g14320.1 60S_ribosomal_protein_L14-1 [MW = 17.07 kDa]

No. of times detected



log(intensity)



Values from



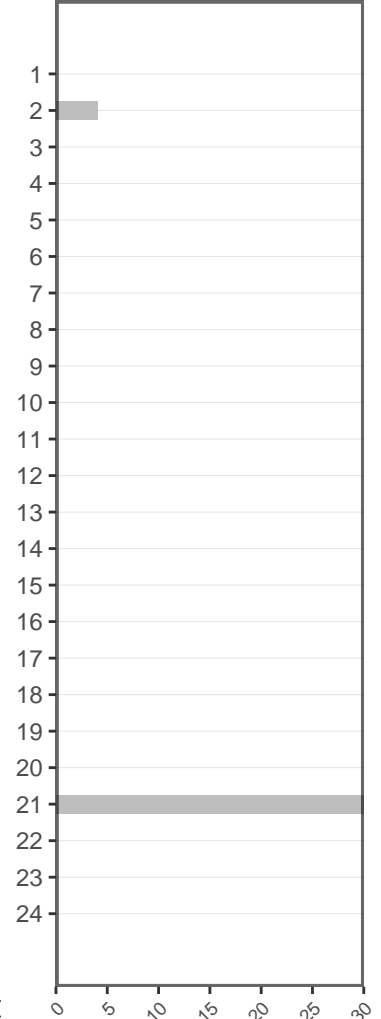
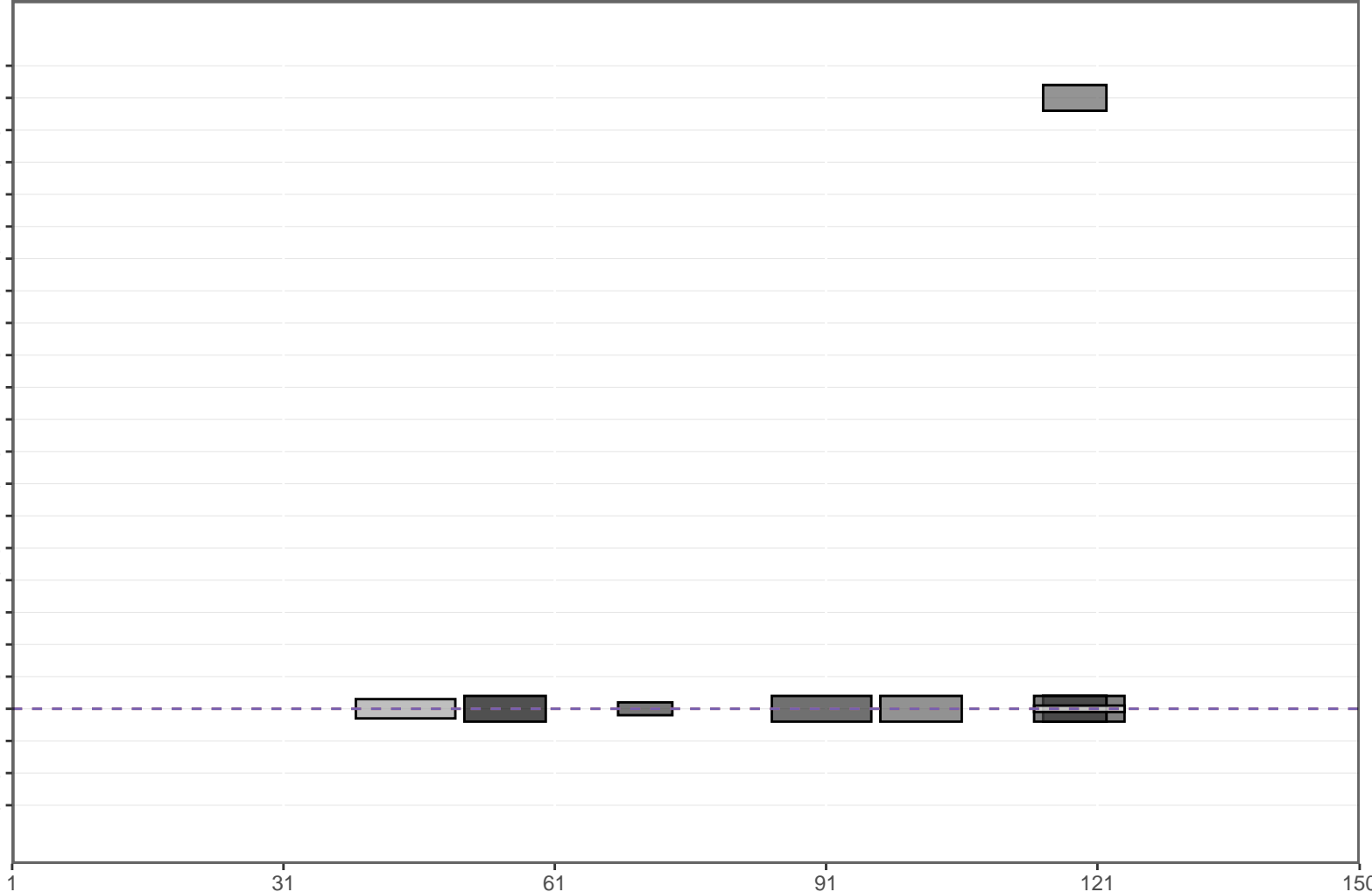
MW indication



Molecular weight

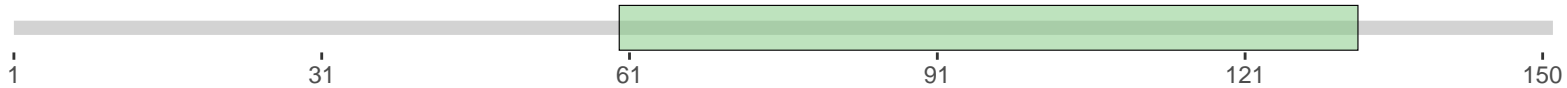


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

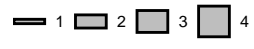


Protein sequence:

IQINFKRLSLTDKIDKIPKPKKTLVAMDAADVNNKWESSWGRKLVQKRRASLNDFRFKLMLAKIKRAGVVRGELAKLKKETVAI

NbL18g14290.1 E3_ubiquitin-protein_ligase_UPL2-like [MW = 403.04 kDa]

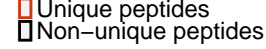
No. of times detected



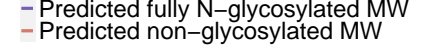
log(intensity)



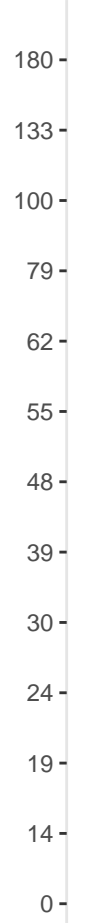
Values from



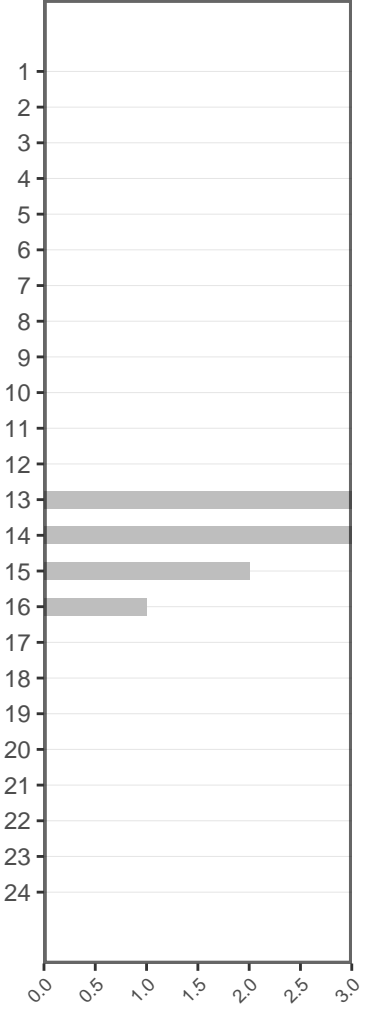
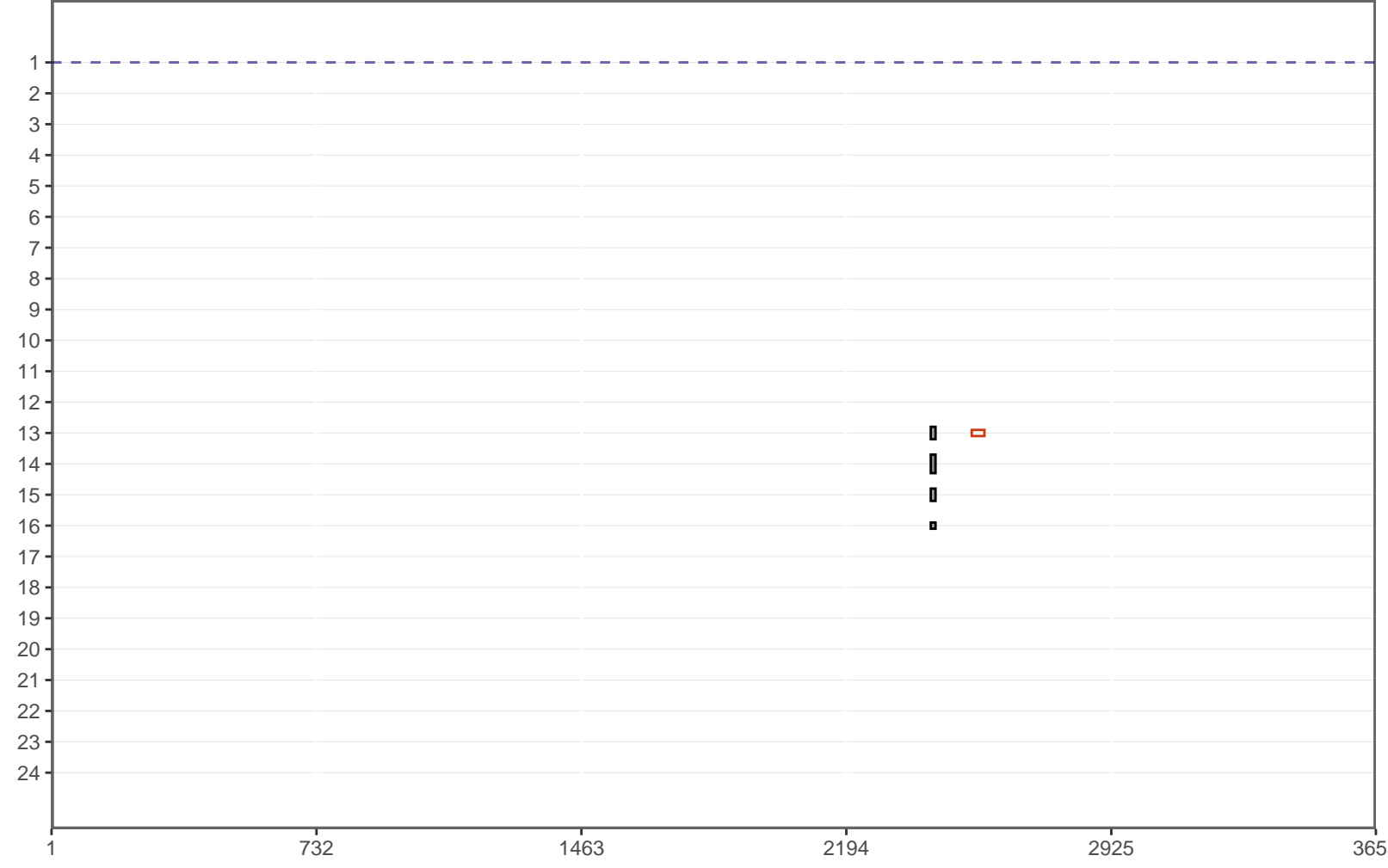
MW indication



Molecular weight



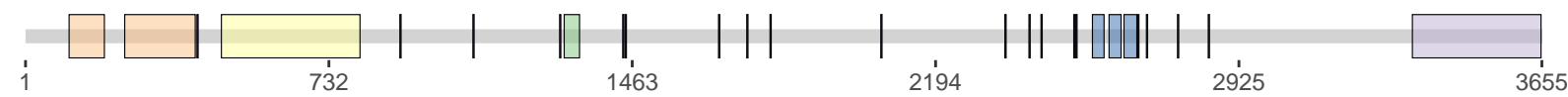
Gel Slice



Protein length

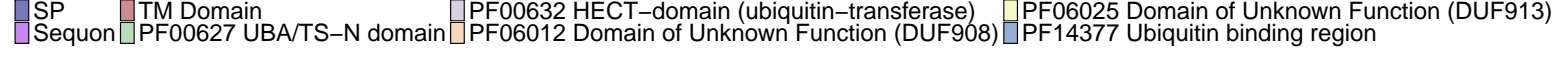


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

3SHLSASMAKIVFLKLLTEFLMVTASVHLLRRDSEVSSGIAAPQRSPFGHVTGGIFPHLHKFLPHSKSRKERKTDVDRQKLSRASGQFLVAGVRSREARKRIFTEINSVFDQVELEKGFRAPTDQAFIDLLNQLTARAPPTGSSISAEASATFDVGLVHSLRALHVLDELDTGSSKVVTVGVKYLELVTKEHVHAAESNAGKGGEGSTKTDGLSGPPTNDAFALQTNETAGQPNGNPVPTDHEGFGASGNFGGSEAVTDDMEHDDQDGGFGPSNEDDYMEH

NbL18g14060.1 phosphoglycerate_mutase-like_protein_1 [MW = 31.4 kDa]

No. of times detected



log(intensity)



Values from



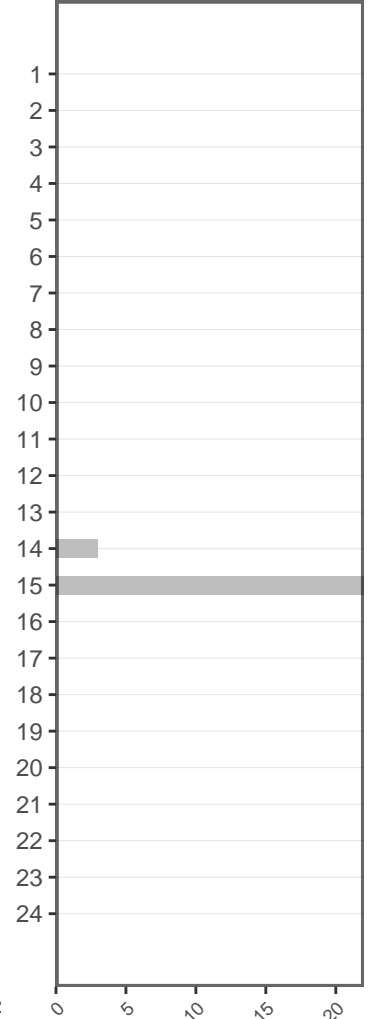
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

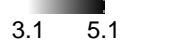
AVEGCRHLYVWGDNRRISEYKPLFADFSLIEGDDDLWEFDRRENEHLAARGMEFLRWLWTRKEKEAVVTHSGFLHLSAFGNDCHPDVKNKICRPFNNGELRGMVHIREMIGSD66STNYPKPKPGVDVPSDNTYKHHPDGLSN

NbL18g13960.1 phosphoenolpyruvate_carboxykinase_[ATP]-like [MW = 82.61 kDa]

No. of times detected



log(intensity)



Values from



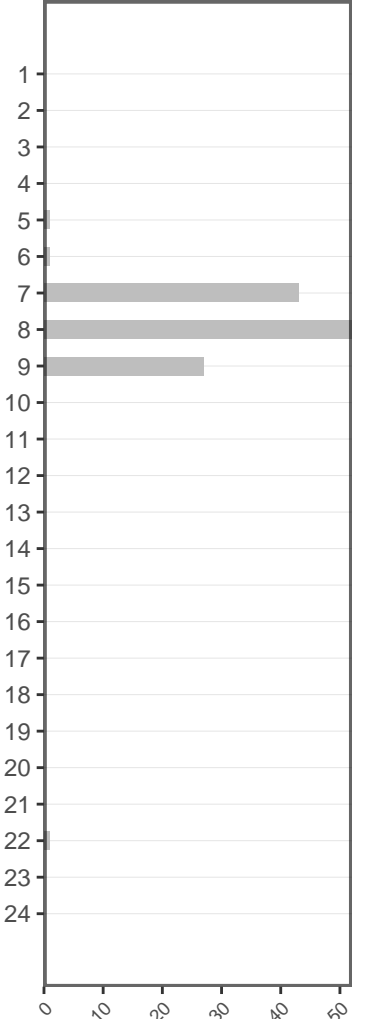
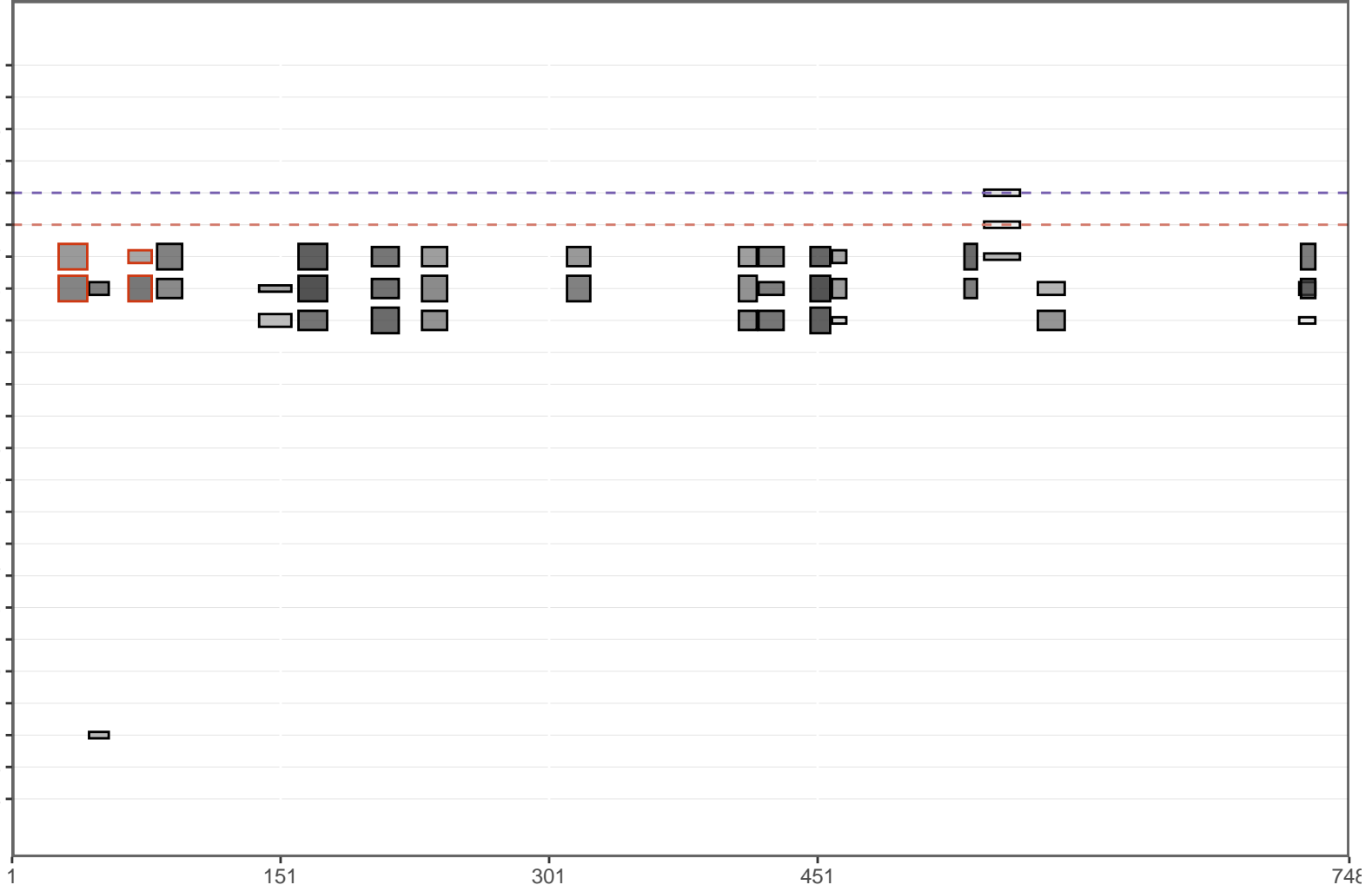
MW indication



Molecular weight

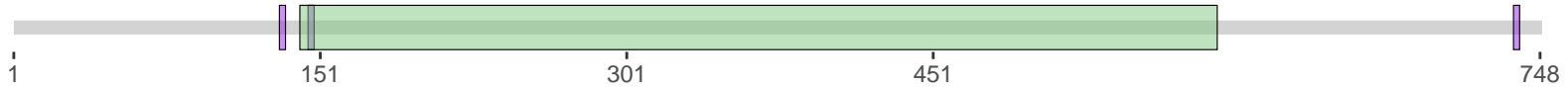


Gel Slice



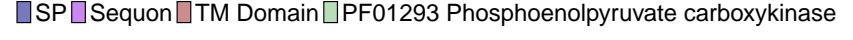
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

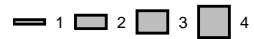


Protein sequence:

FFQLSGTGKTTLSTENRRLYHGDDHGWSDHGVSNIEGGCVKGDLSREKEPDWNAIKFGLVLENVVFEEHTRFVDAWADKSVTENTRAVYPIEIPNAKIPGVGFHPKRVNILLAGDAFGVLPVPSKLNLAQTMVHFISGYTALVAGTDEGKEPTATFSACFGAIFIMLHPTKYAAMLAEMKMKHGATGWLNTGWSSGGVGSRRIRKLYATRKIDAIHSGALNANVYKTEDGKEPTATFSACFGAIFIMLHPTKYAAMLAEMKMKHGATGWLNTGWSSGGVGSRRIRK

NbL18g13950.1 ubiquitin-fold_modifier-conjugating_enzyme_1 [MW = 13.64 kDa]

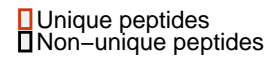
No. of times detected



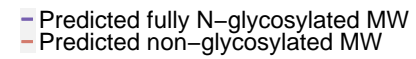
log(intensity)



Values from



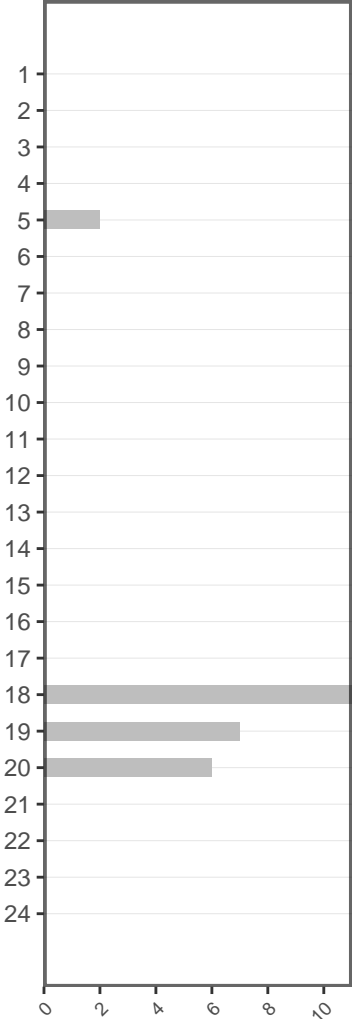
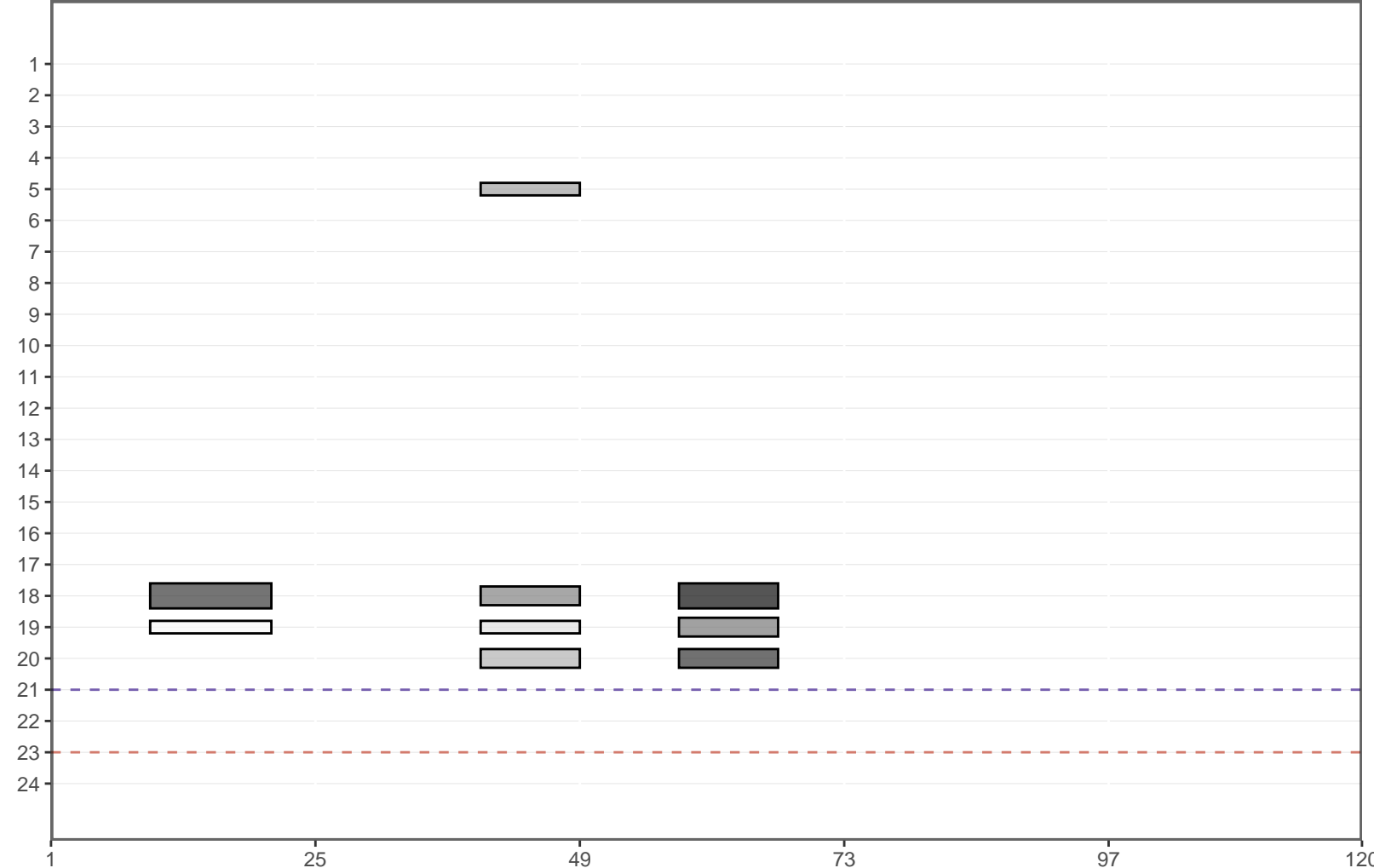
MW indication



Molecular weight

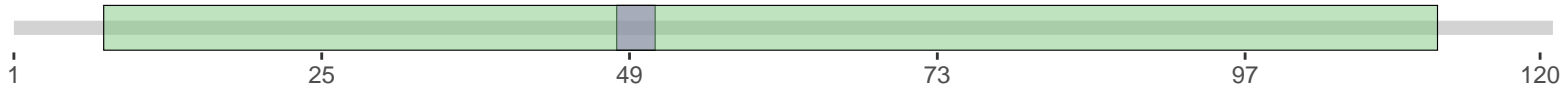


Gel Slice



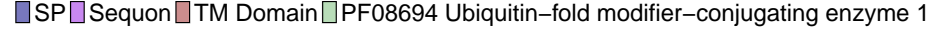
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

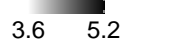
INLSKNDWFRISANPEGRWKGKQWYHNLKYEFDLQDFVYPTAPLELPELDGKTEKVTSLQVF

NbL18g13800.1 geranylgeranyl_transferase_type-2_subunit_alpha_1 [MW = 81.33 kDa]

No. of times detected



log(intensity)



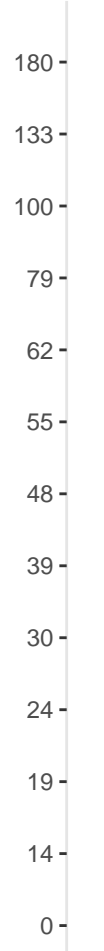
Values from



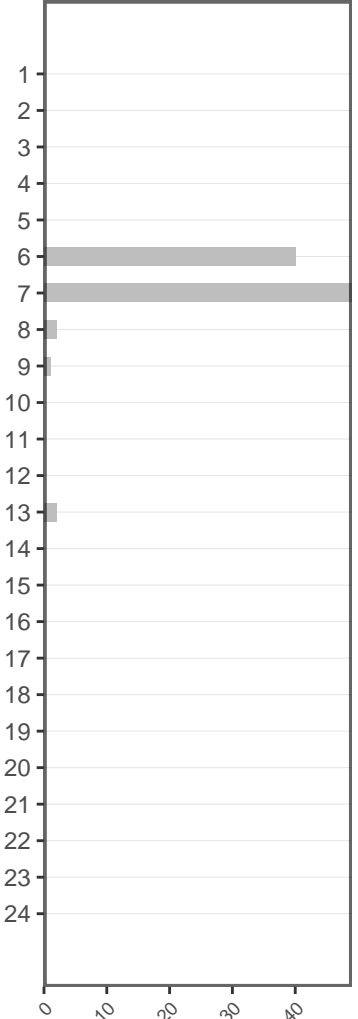
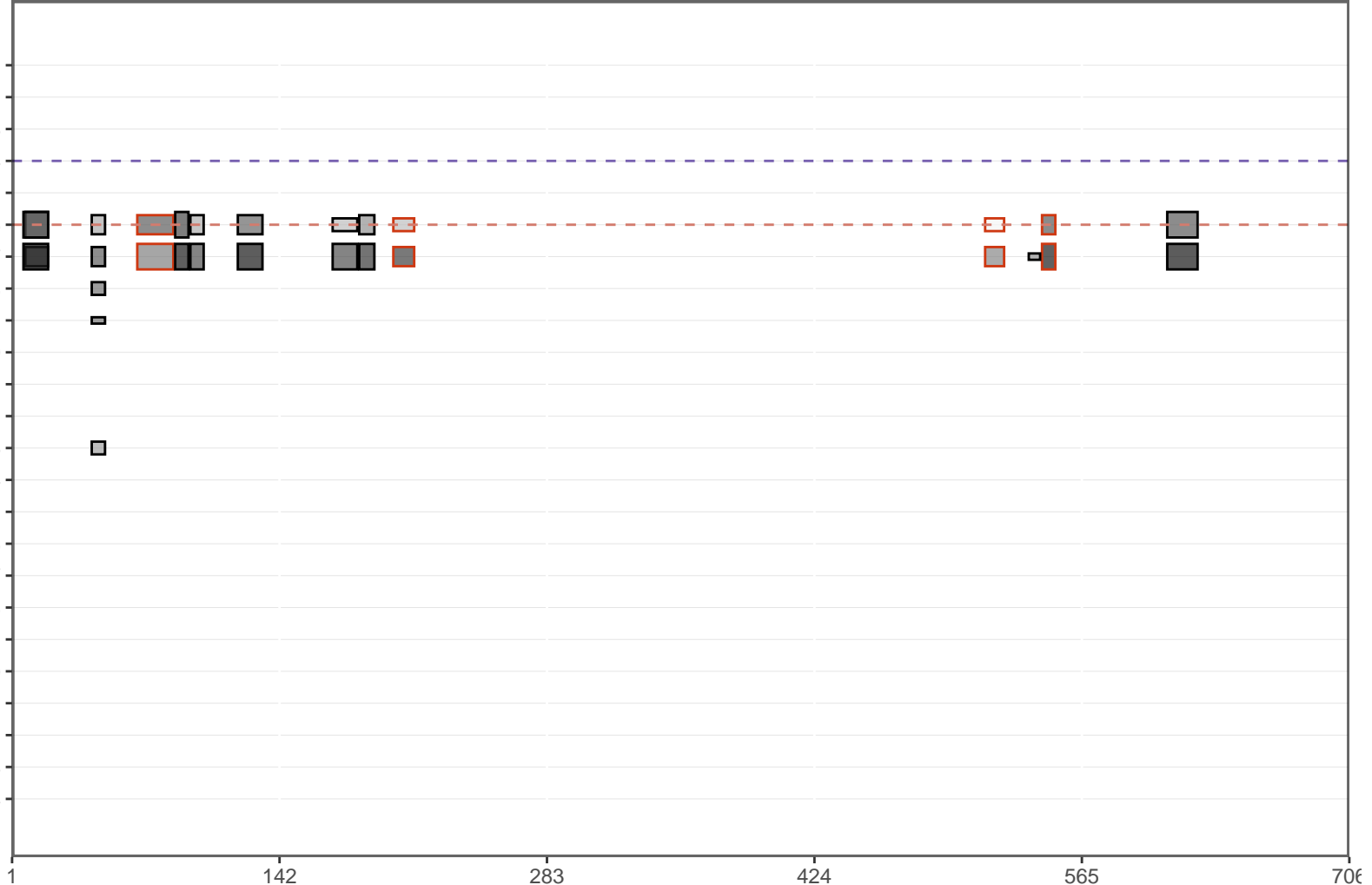
MW indication



Molecular weight



Gel Slice



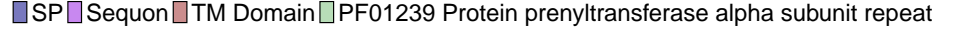
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

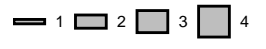


Protein sequence:

IANSUKAYQVYKSLARSGQIFSGTGVHGMNSHIAFTVSPYRSEHVDLKNKEKISWVNDSEFGTHERPQFESVLANLFIHERTKVDEKVDYQVWVYTTVQNEILYRELLATMNGKIGKLTARLLMAHDTLMAHSDTMSYTGTSHGNSFHSHTERLQVLEDKMKMPAHPHFHYQDEVLSVLLKQHSNGELLLKHGCKYRDPSPKINFLRFDLNLGRGSMERKLLWVQVLDLNNQLGSLGELVEMQLTGLNVSNNKLGFTALEPLRLLRSLKVLDSIYNEIGAHSDTRRYLCSPP

NbL18g13760.1 NADPH--cytochrome_P450_reductase [MW = 76.81 kDa]

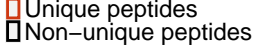
No. of times detected



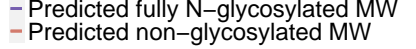
log(intensity)



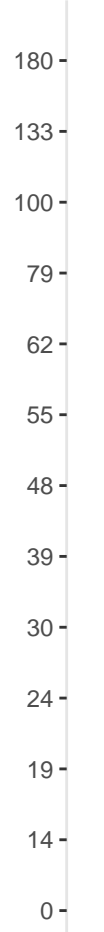
Values from



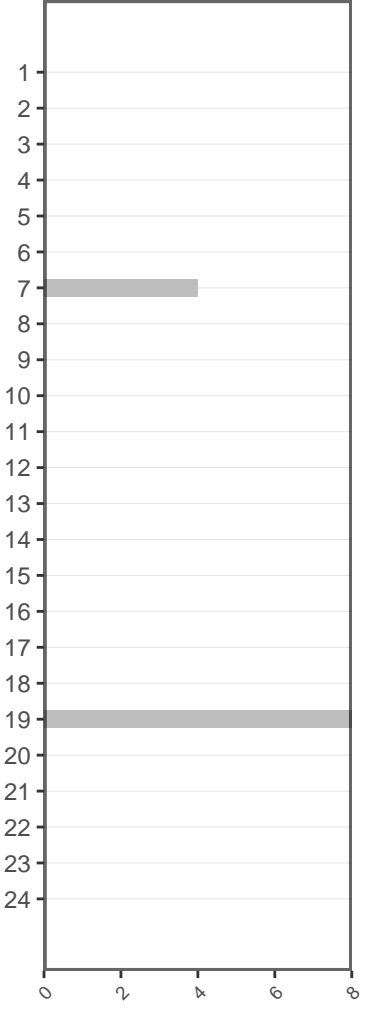
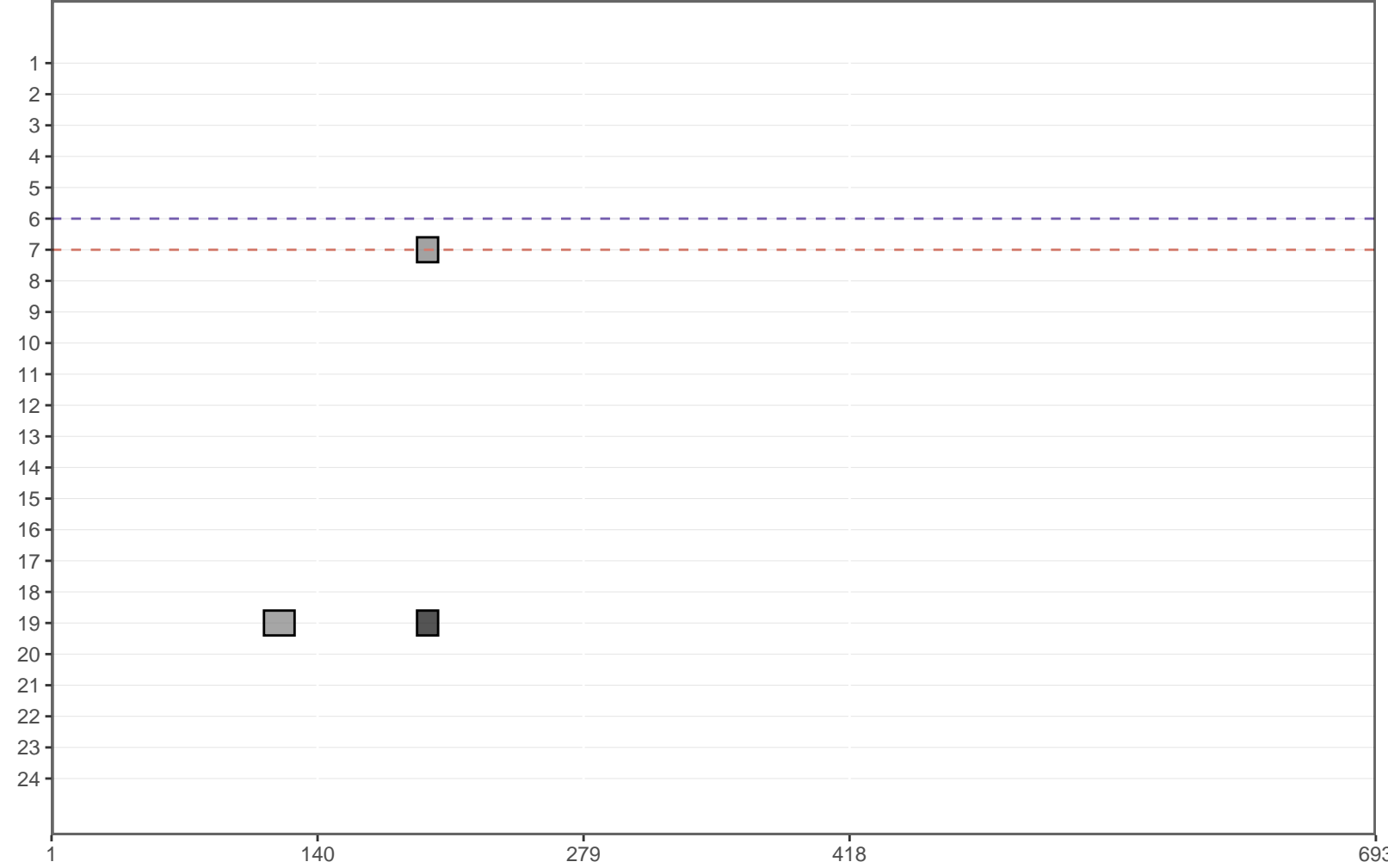
MW indication



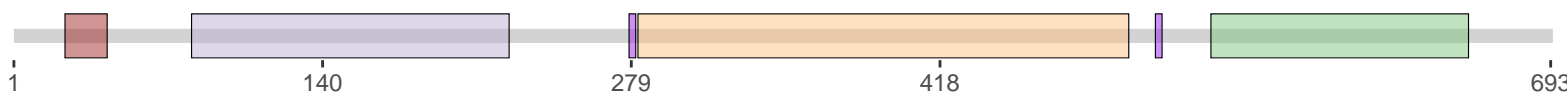
Molecular weight



Gel Slice

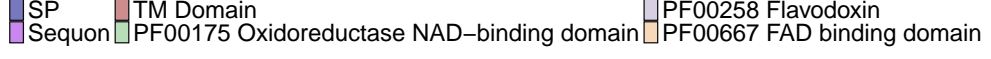


Protein length



Pfam domains

Pfam Description



Protein sequence:

EVVEAARLLGQSLNDFSHDKEDGTALGGSLPPFPDPCTLRARLARFADLLNPPRKATLVAIAHAAEPEAEKLFASPGQKDEYSAAWVAAGRLLLEVMAEFFSAKPLGVFFAAWAPRLGPRVYSISSSPRFAPARIHVTGALVYGTPTTGRHKHKGVGSTWAKNVAPEKSGNCGESAFIRFIRPNFKLPVDPSPVPIVMVGGPTGLAPFRFGLQERAALKEDGAGLGFALFFGCRNRRMDPIYEELQSFVKGQVISELIASFREGPKQEVYQIKMLEKLMTYEQI

NbL18g13540.1 glutamate_dehydrogenase_B [MW = 44.47 kDa]

No. of times detected



log(intensity)



Values from

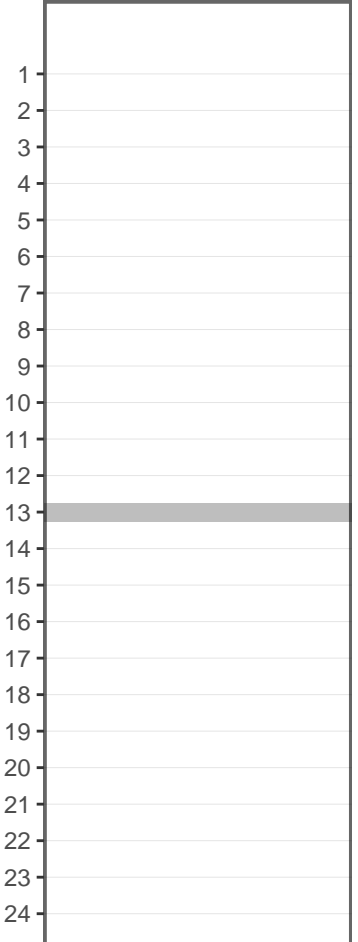
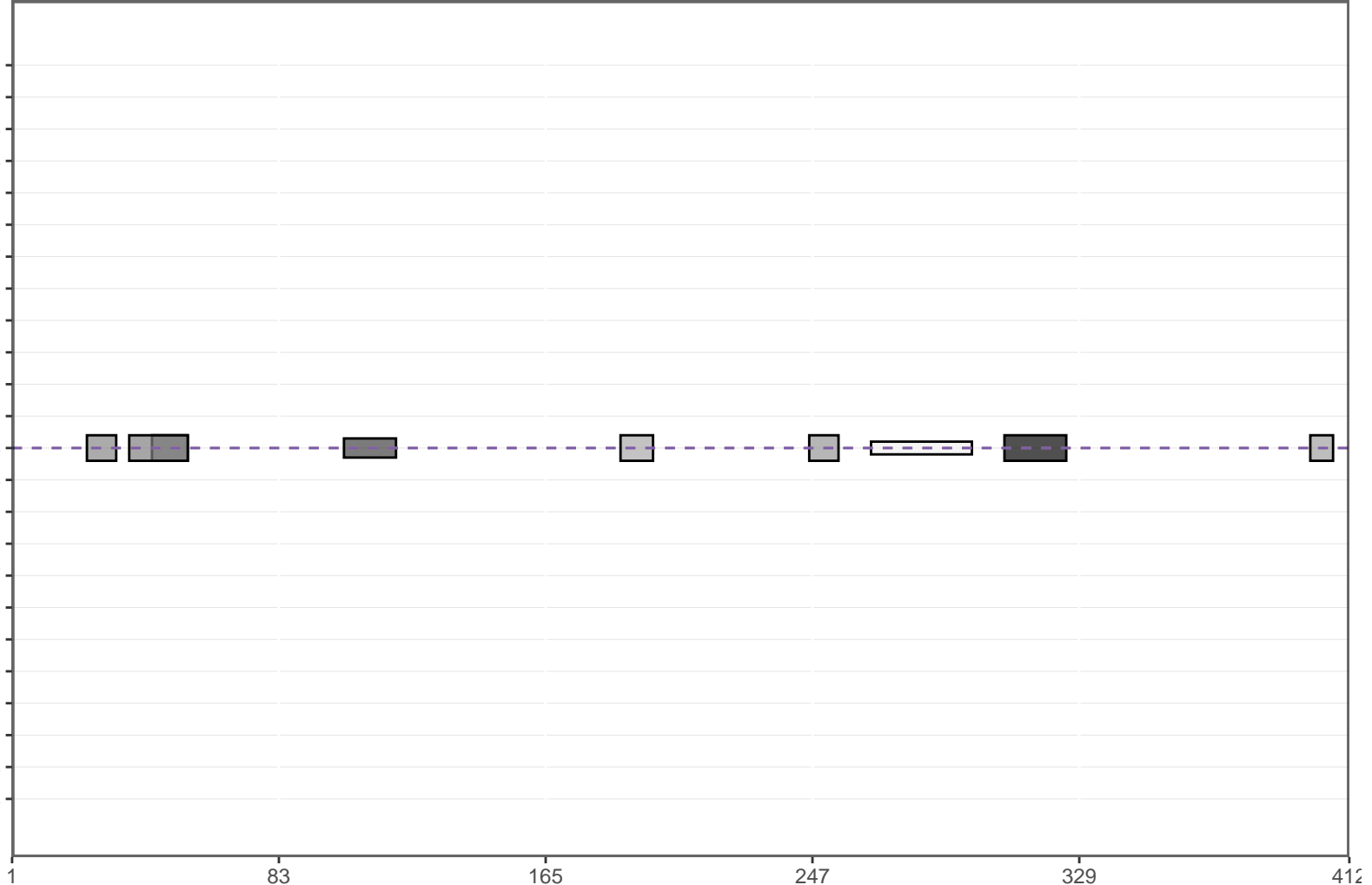
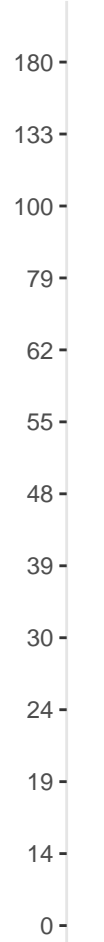


MW indication



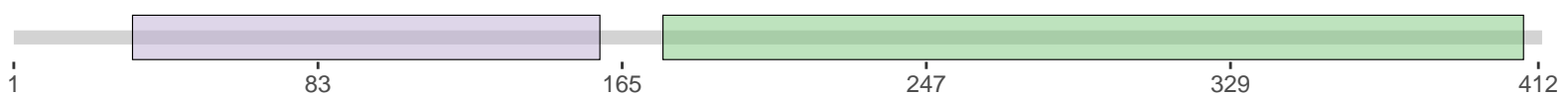
Molecular weight

Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00208 Glutamate/Leucine/Phenylalanine/Valine dehydrogenase
- PF02812 Glu/Leu/Phe/Val dehydrogenase, dimerisation domain

Protein sequence:

EAALLRDHGKSIAGGRFVVDGFGNIGSEWAAGLTFEGGGKIVVSDITGAKNKNGIDIALLKHVKENRGVYGFHGDSDIPNSILVEDGGVLPALGQVNRDNDKAKKAFVEAANHPDPEADELAKKGVILFDIVANSGGVTVSYFEWVQNIQGGFMWDEERVNTELKAMNRRGFKVDKMDCKTHNGDLRMGAFTLGVNRVATATFLRGWEA

NbL18g13530.1 protein_ASPARTIC_PROTEASE_IN_GUARD_CELL_2 [MW – SP = 43.94 kDa]

No. of times detected



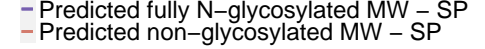
log(intensity)



Values from



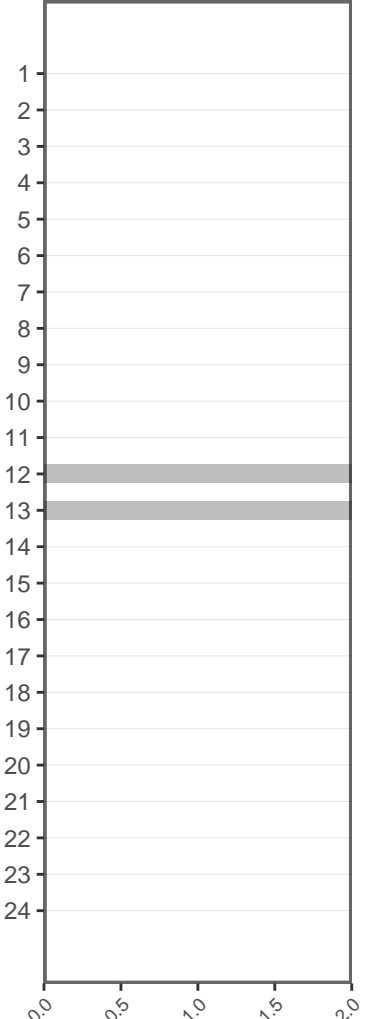
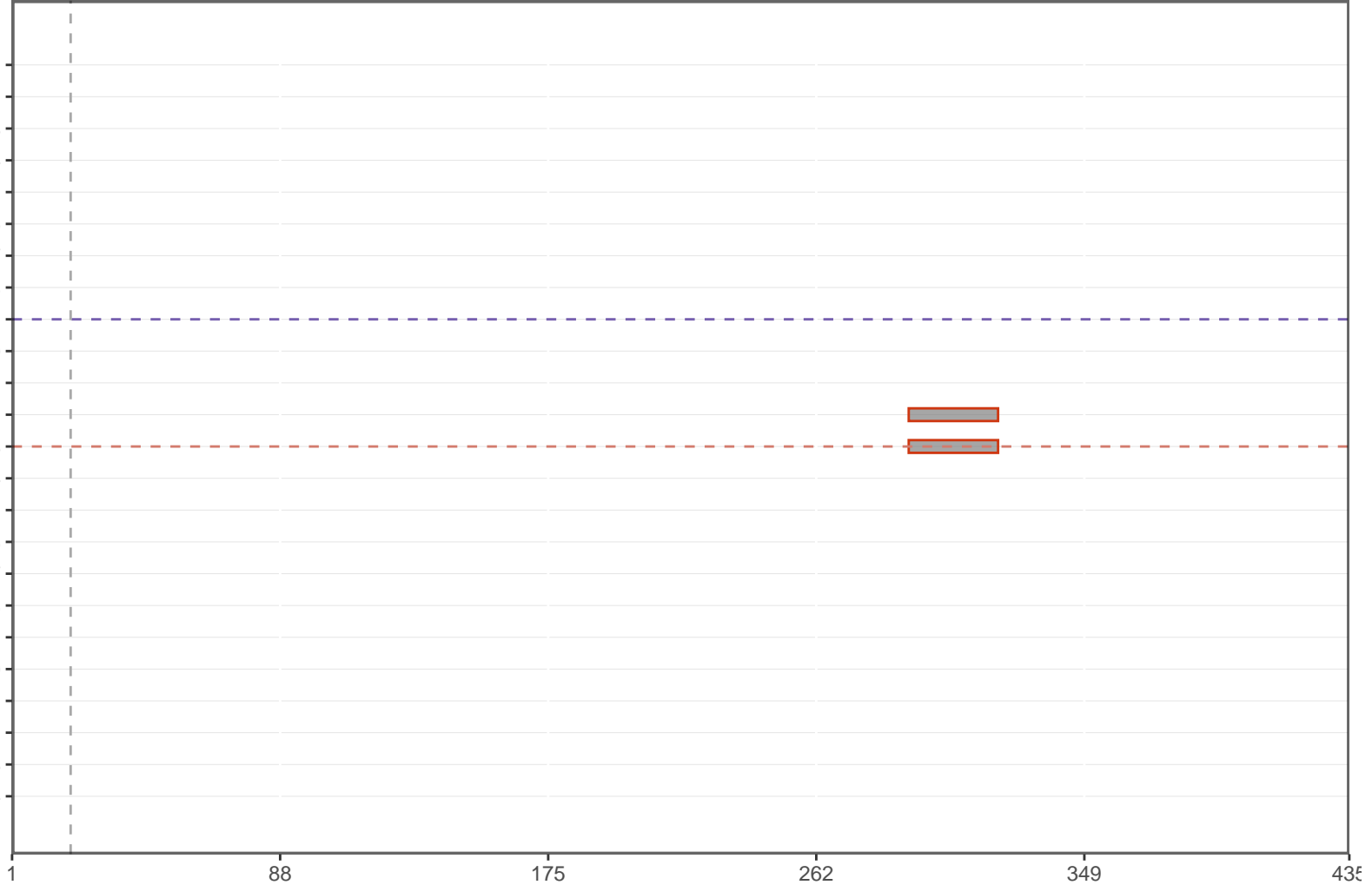
MW indication



Molecular weight



Gel Slice

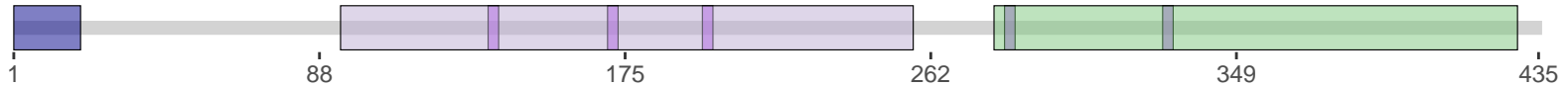


Protein length

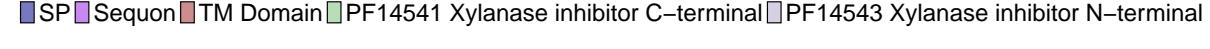


Peptide counts over 4 repeats

Pfam domains



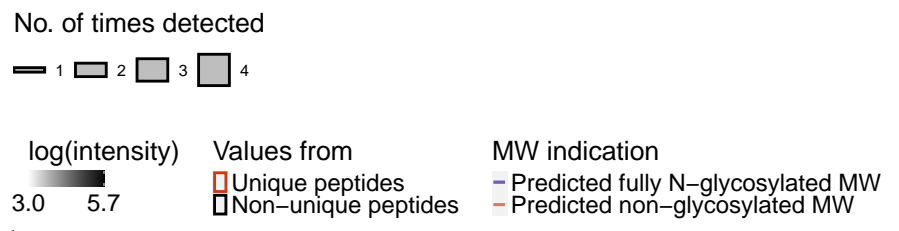
Pfam Description



Protein sequence:

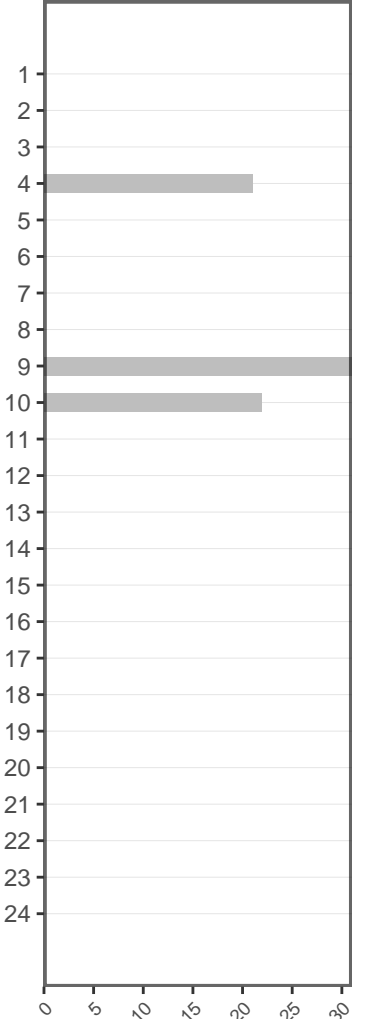
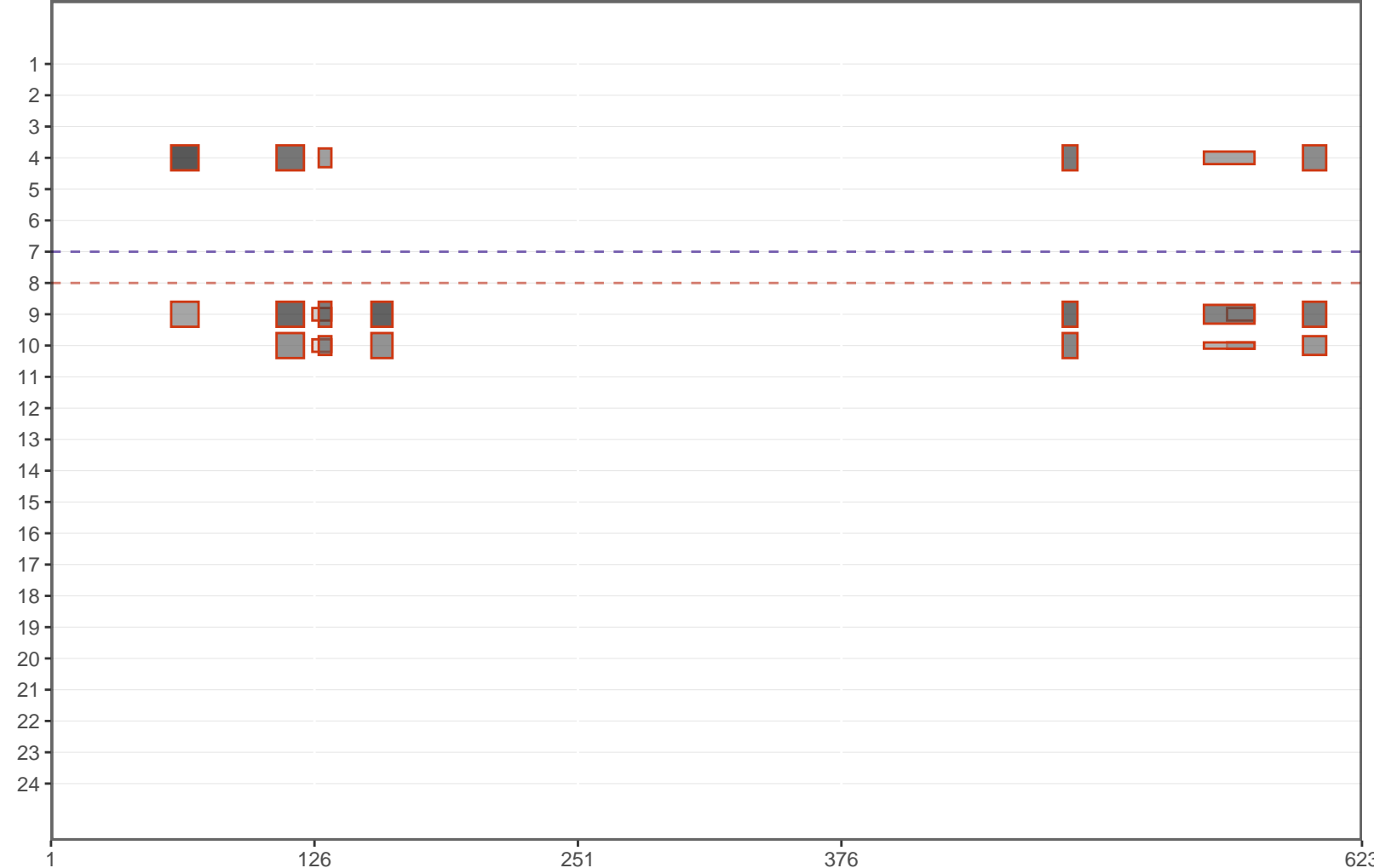
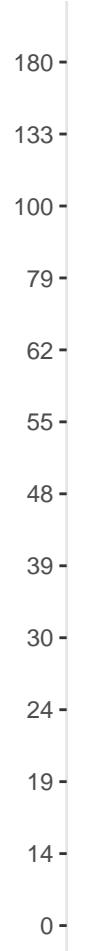
ICISAISSGSIIPQGLLGLGRSMELLGQGSABLYSSEVSYQLPFRKRYVYFSGSLKLGPLGGPKNKFTLLKKNFHRPBLVYVNLTGISVGRVLPVPIAPELLAFDMNTGAGTHDSGTVTRFRVQVFNATRDEFKQVGGPFSSLGAFDTGFASTNEAVAPATLHFTGMDLVLPMENTLHSSASPAQLMAAAPPTNLNSVLNVIANLGGQNLRIPLFDANRSLGIARELGN

NbL18g13490.1 glucose-6-phosphate_isomerase_1_chloroplastic [MW = 68.04 kDa]



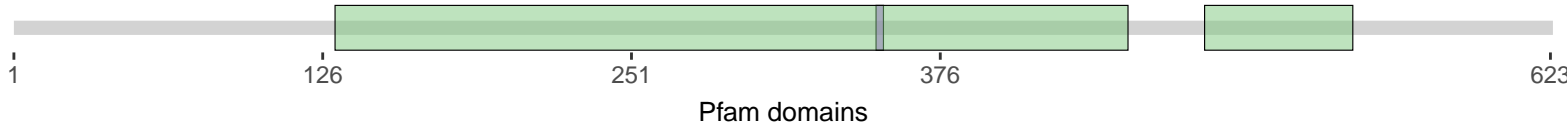
Molecular weight

Gel Slice

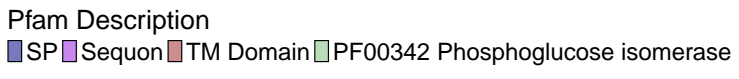


Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:

IEGWLARFPMFDFVAGRTSELSAVGLLPAALGGINREMLTGAALMDEANRTTVYRDRPALLALGLGWYATDGVGSKDMVLPYKDSLLLFSRYLQQLVMEISLGEKFDLGNRYNGGISVYGNKSTDQGHAYIQQLREGVHNFATFIEVLRDRPPGHGWELEPGVTOGDGFLGMLGTRLSALYANNRESISVTVGVEYTPR6VGLVLYERAVGHVSLVNNAYHGPQVEAGKKAAGEVLALGKRVLAVLNEASGKDPVEFLTLEIADRHCDEEEMTYKIAHMAANDR

NbL18g13430.1 14-3-3_protein_10 [MW = 32.9 kDa]

No. of times detected



log(intensity)



Values from



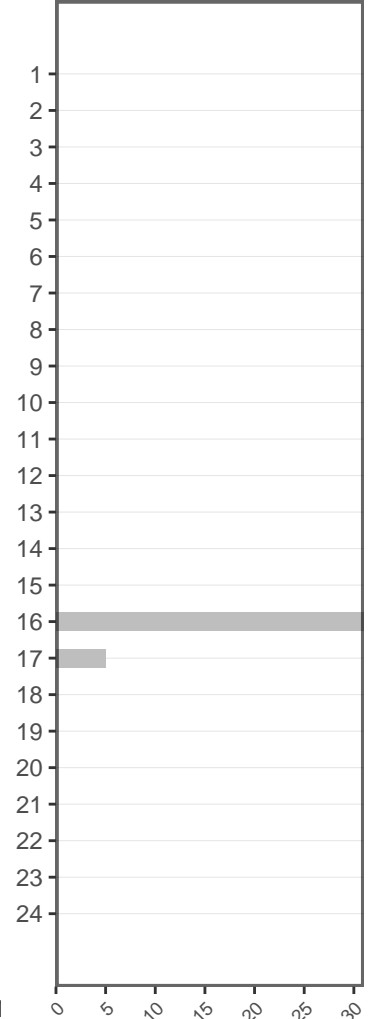
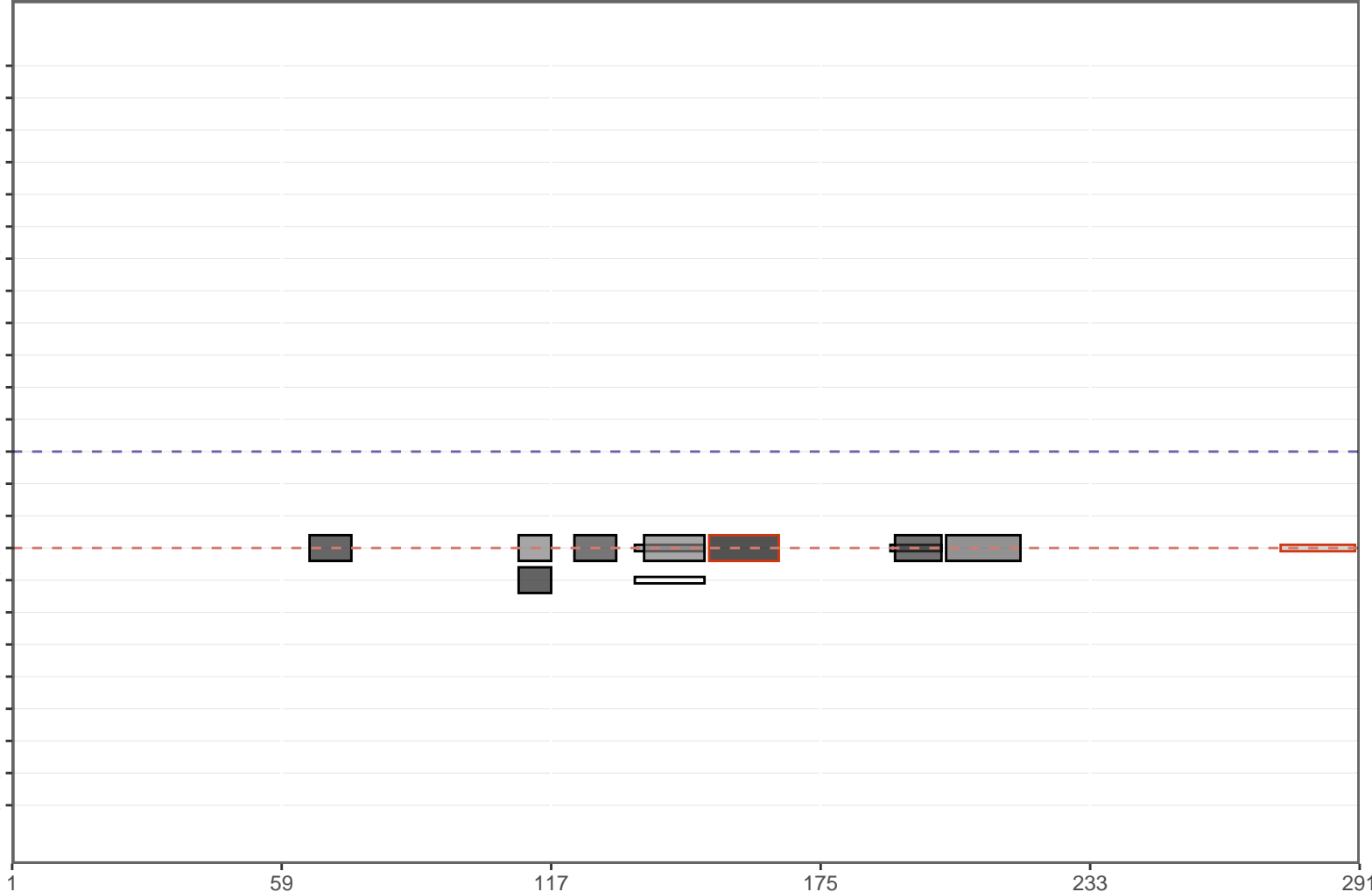
MW indication



Molecular weight



Gel Slice

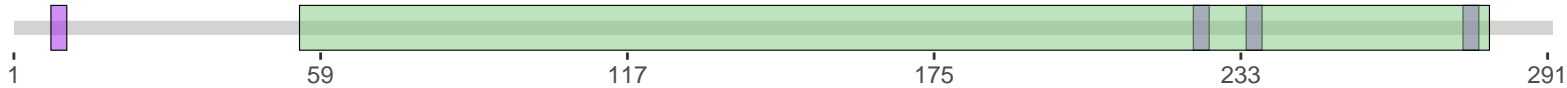


Protein length

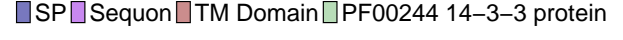


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

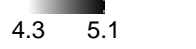
IRGKVENLLETVCAGLKLLEENLEPSASTGSESRVFLKMKGDYYRYLAEFRKVDGRKGAEDTMSYKAADEIALDLPTPIRLGLALNFSVYFVEILNSGDKACSMKQAFEEAAEELDTLGEESYKDSFLIMQLLRDNLTLWTSADGDLDES

NbL18g13420.1 protein_CutA_chloroplastic [MW = 19.92 kDa]

No. of times detected



log(intensity)



Values from



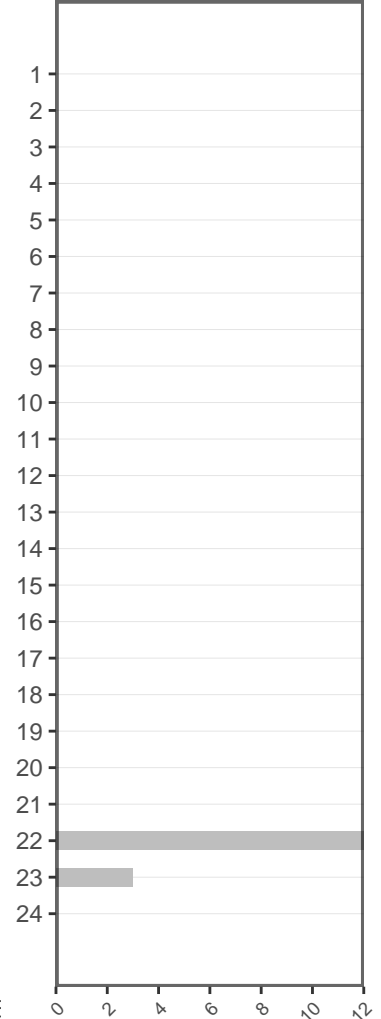
MW indication



Molecular weight



Gel Slice

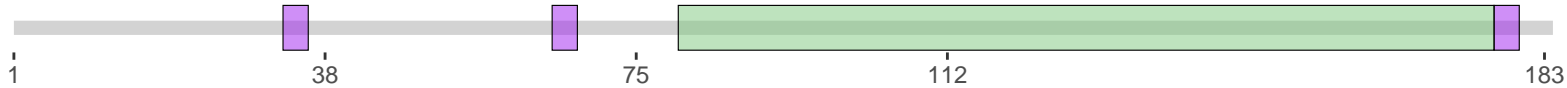


Peptide counts over 4 repeats

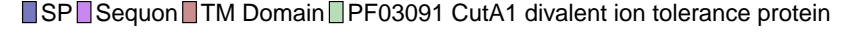
Protein length



Pfam domains



Pfam Description



Protein sequence:

IIIVVYTPNKLGGKLAGSVKELASGVNRPQVESVYVEWEGKVGTDSEELIHKTRSELLEALTEHVKANHEVDVPEVIAMPVGGSPQYLEWLNKNTREK

NbL18g13260.1 28_kDa_ribonucleoprotein_chloroplastic-like [MW = 32.77 kDa]

No. of times detected



log(intensity)



Values from



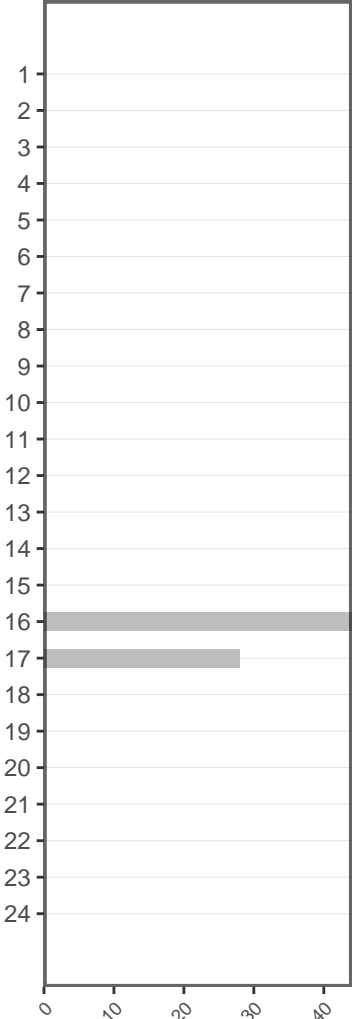
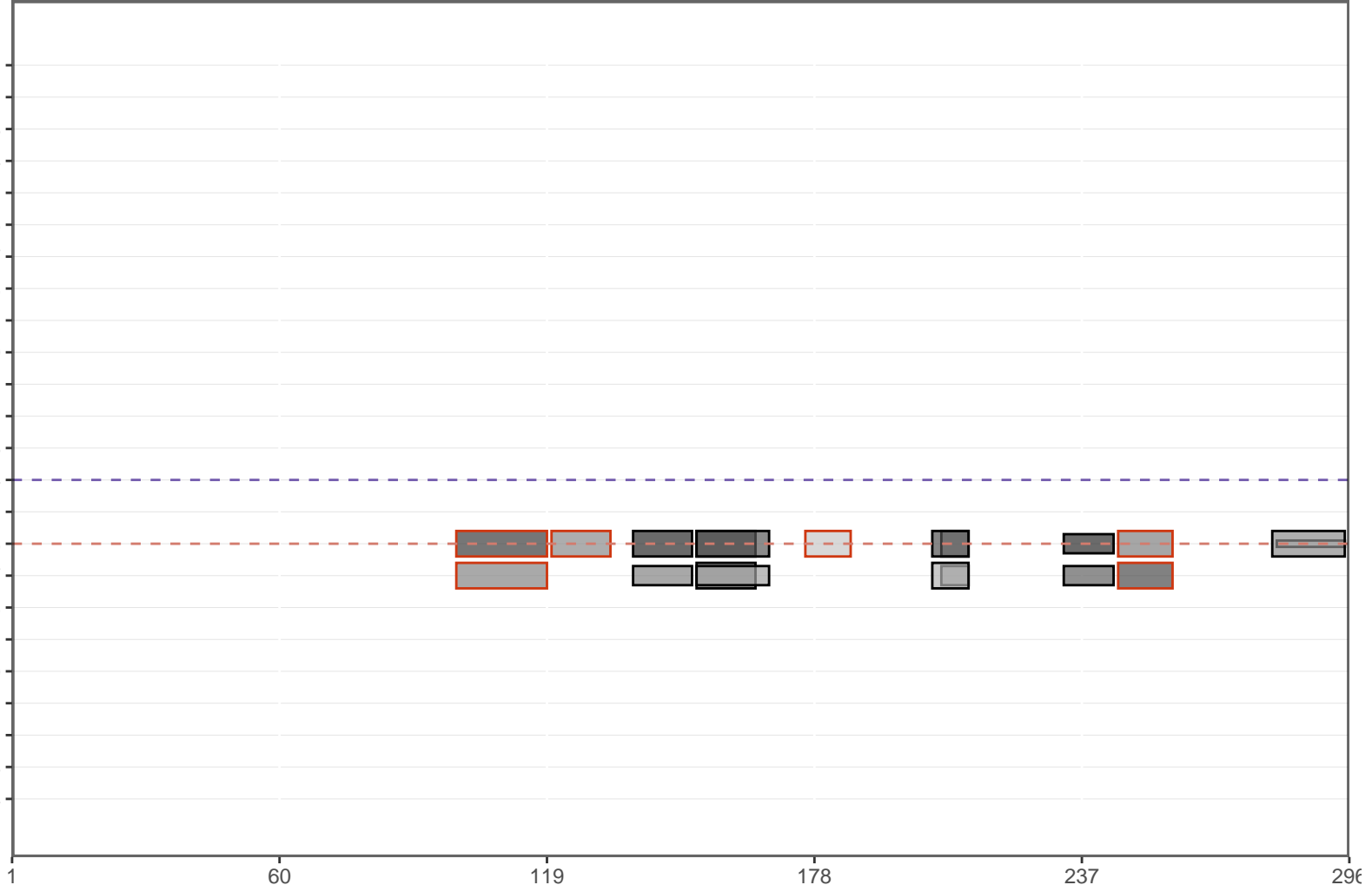
MW indication



Molecular weight

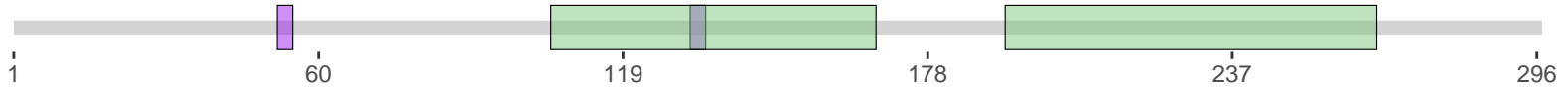


Gel Slice



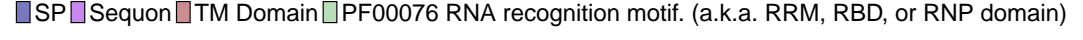
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SRGLVFTMGSHEEAKAVLENLEAVELEGRPLRLAWAKPKTKPKP6PLPKPLFVHNVFNVLHFEARSKDLMEFFKANGADVSAEIVFNSDNRPRRAGYGFVFNKVEADLSSFEKEMGRPRIRVAHAKRFLRGETKMLQSGEVSSEIISVAE

NbL18g13160.1 thylakoid_luminal_29_kDa_protein_chloroplastic [MW = 37.52 kDa]

No. of times detected



log(intensity)



Values from



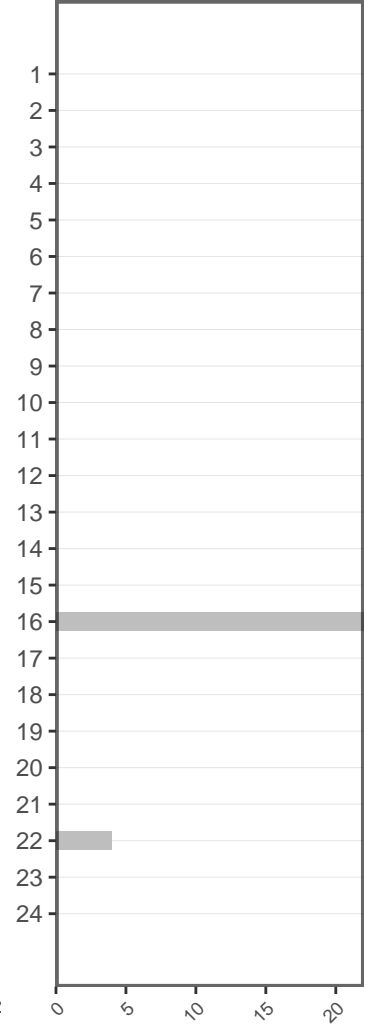
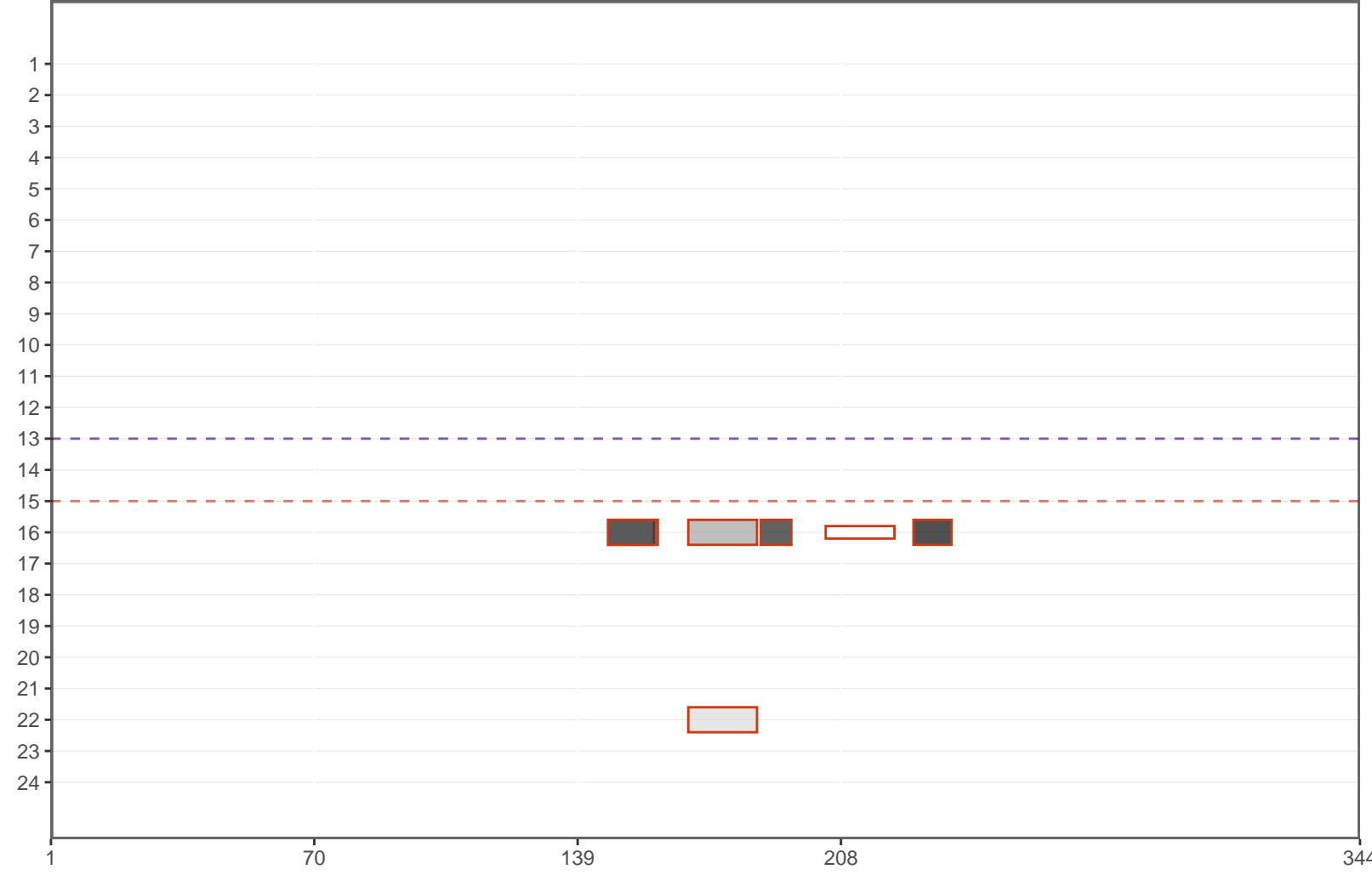
MW indication



Molecular weight

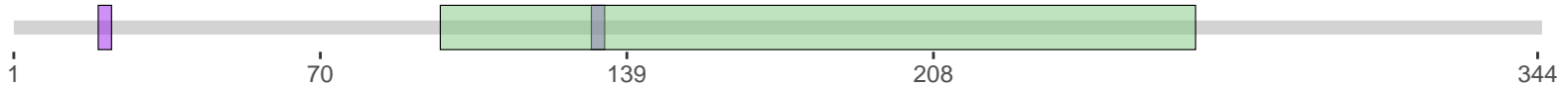


Gel Slice



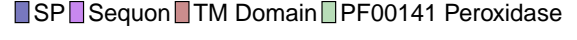
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IDADSKGSPISYADLHQLAAGBALNKTFLASAIRKGGGNVEKBSLLYSAYGNSGNGWGLFDRQFGRSDAGEPDEGRVQWKKAVGEMKDKFKAVGFGPRQLAVMSAFIGPDGDATEALLANDPEVIVPWGKYGSRLETYSRRTDYEVDLFTLTKLSGLGGQINYEAYSYPVQKQVTKLKL*

NbL18g13150.1 serine--tRNA_ligase_chloroplastic/mitochondrial [MW = 59.96 kDa]

No. of times detected



log(intensity)



Values from



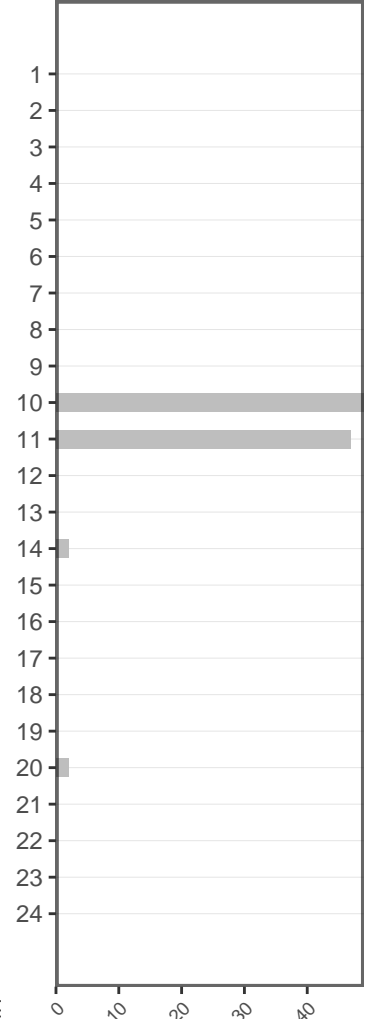
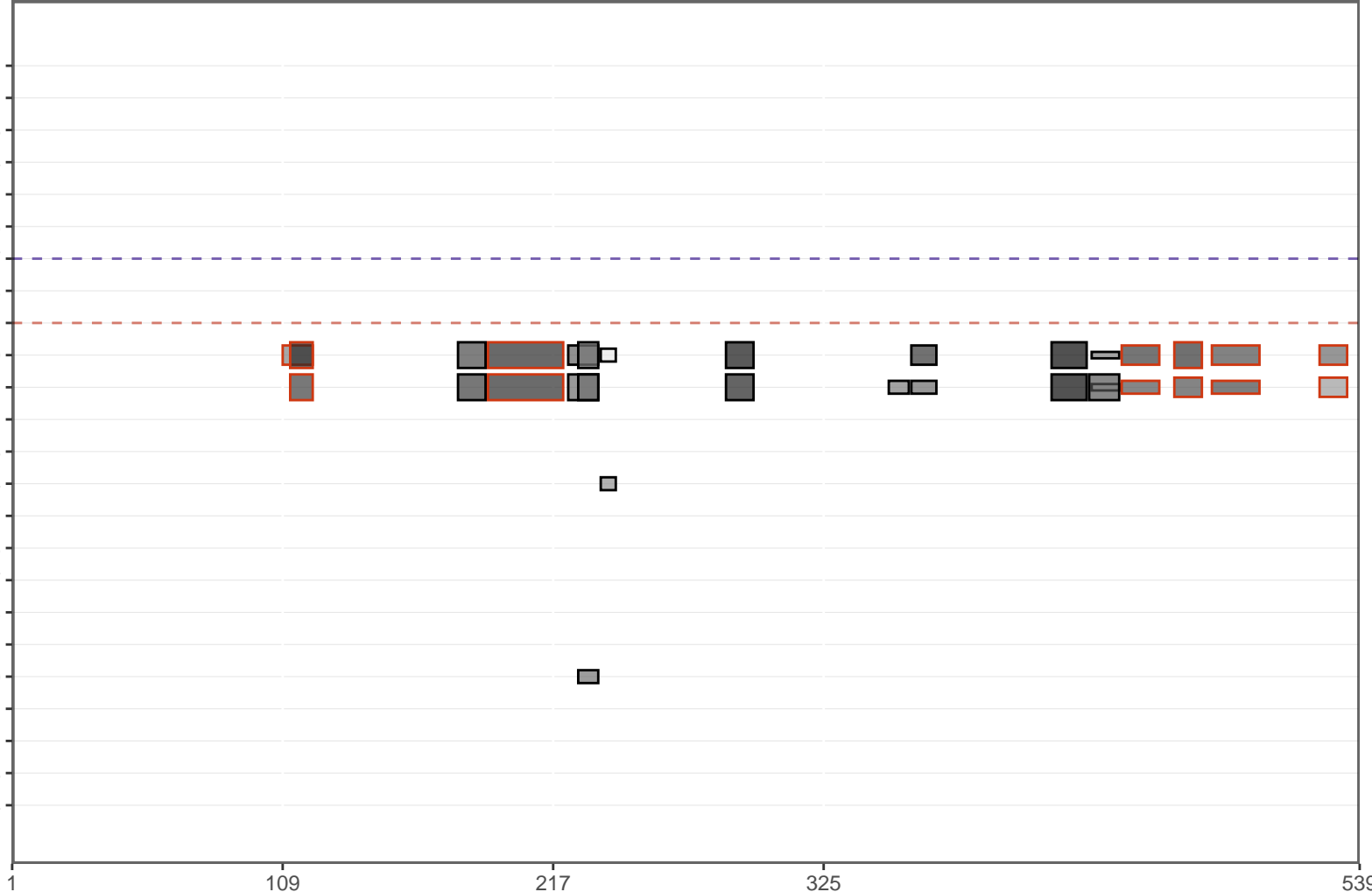
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00587 tRNA synthetase class II core domain (G, H, P, S and T)
- PF02403 Seryl-tRNA synthetase N-terminal domain

Protein sequence:

"SGSKFYLLKNEAVLEEMALVNWVSEAMKRGFPLTTPPEVRS6VWEKCGFDFPRGNTQVYSEIENSDDGLGTAETIPVGGHMDLSE6SLPLKYWFASHCFRTAEAAAGAAATRLGLYRVHGF5KVMFILCRPDESD6VYHEELIEIEDLFS6LGFHFKTLDMASGDDLGAIPVRFKFDVEAWMPGLGRVGEISSAENGTQYSRRLLGRVYRPEPSA6SSPKKNTAPQFVHTLNATAGAVPRMVLLENFQGEDG6SVVPEPLR6FMGGLGHIKPKHIGN"

NbL18g13120.1 cytochrome_c_oxidase_subunit_6b-1-like [MW = 19.83 kDa]

No. of times detected



log(intensity)



Values from



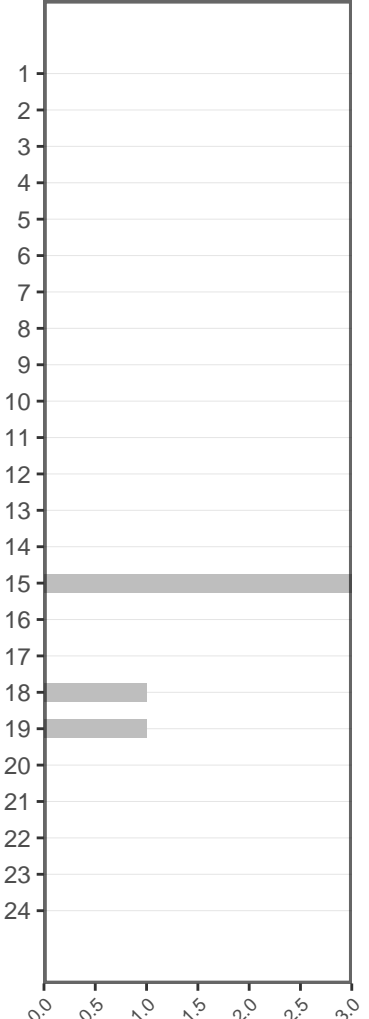
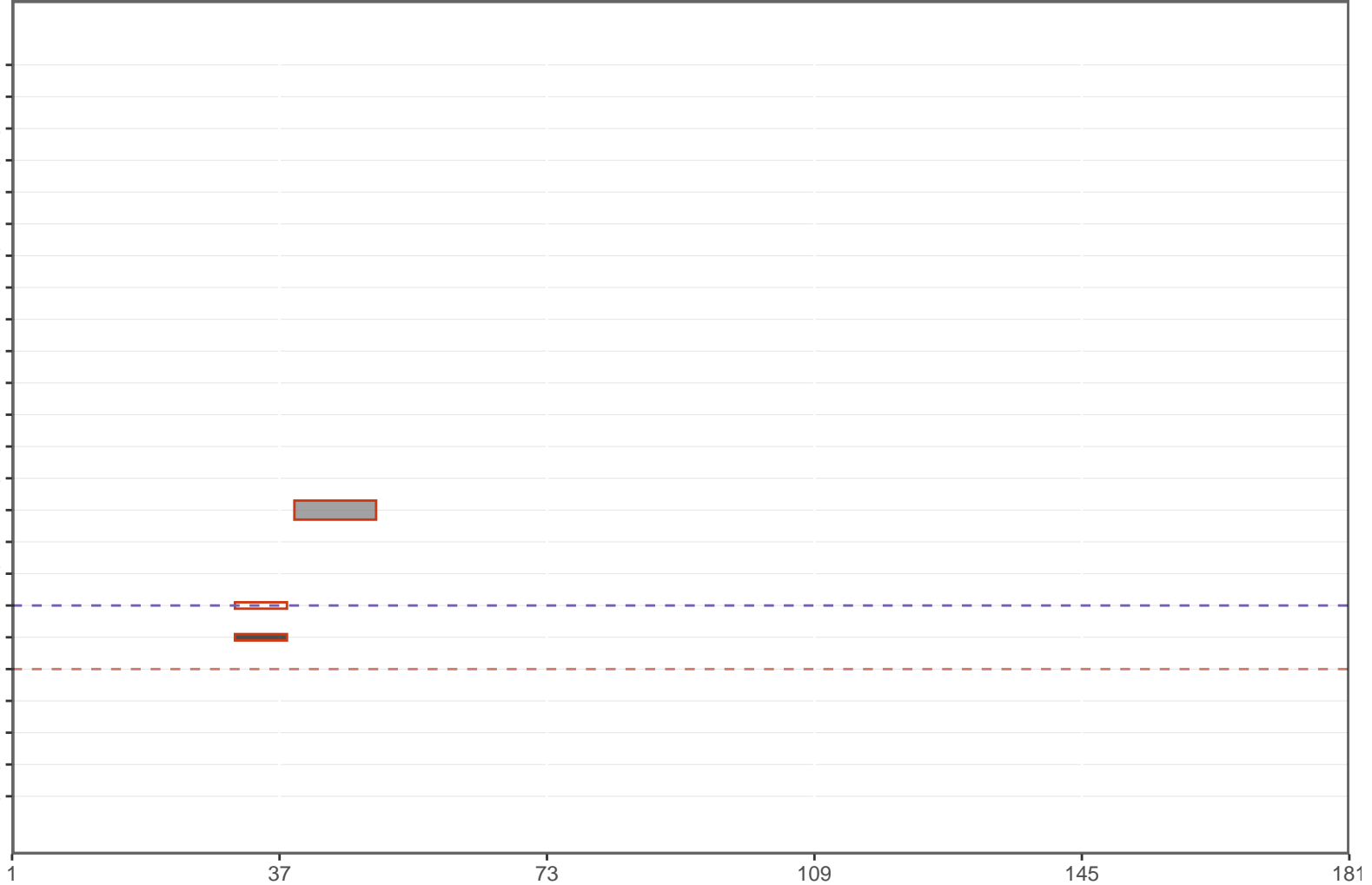
MW indication



Molecular weight



Gel Slice



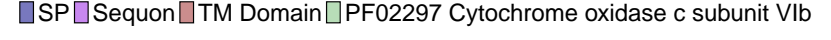
Protein length

Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

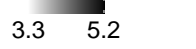
VEASSDESSESTEDTETSGNEESAVETPEIKLETAADFRFRPFTNGTRHGFTRVVEYHRCAVANKGEGAPEGDKFANYRRLGCPGEWDRWNEGRENQTFPGPL*

NbL18g13010.1 probable_carboxylesterase_2 [MW = 36.95 kDa]

No. of times detected



log(intensity)



Values from



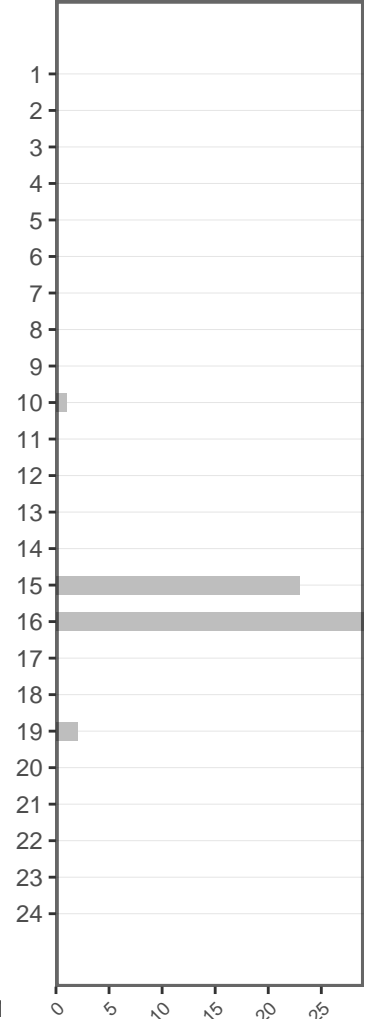
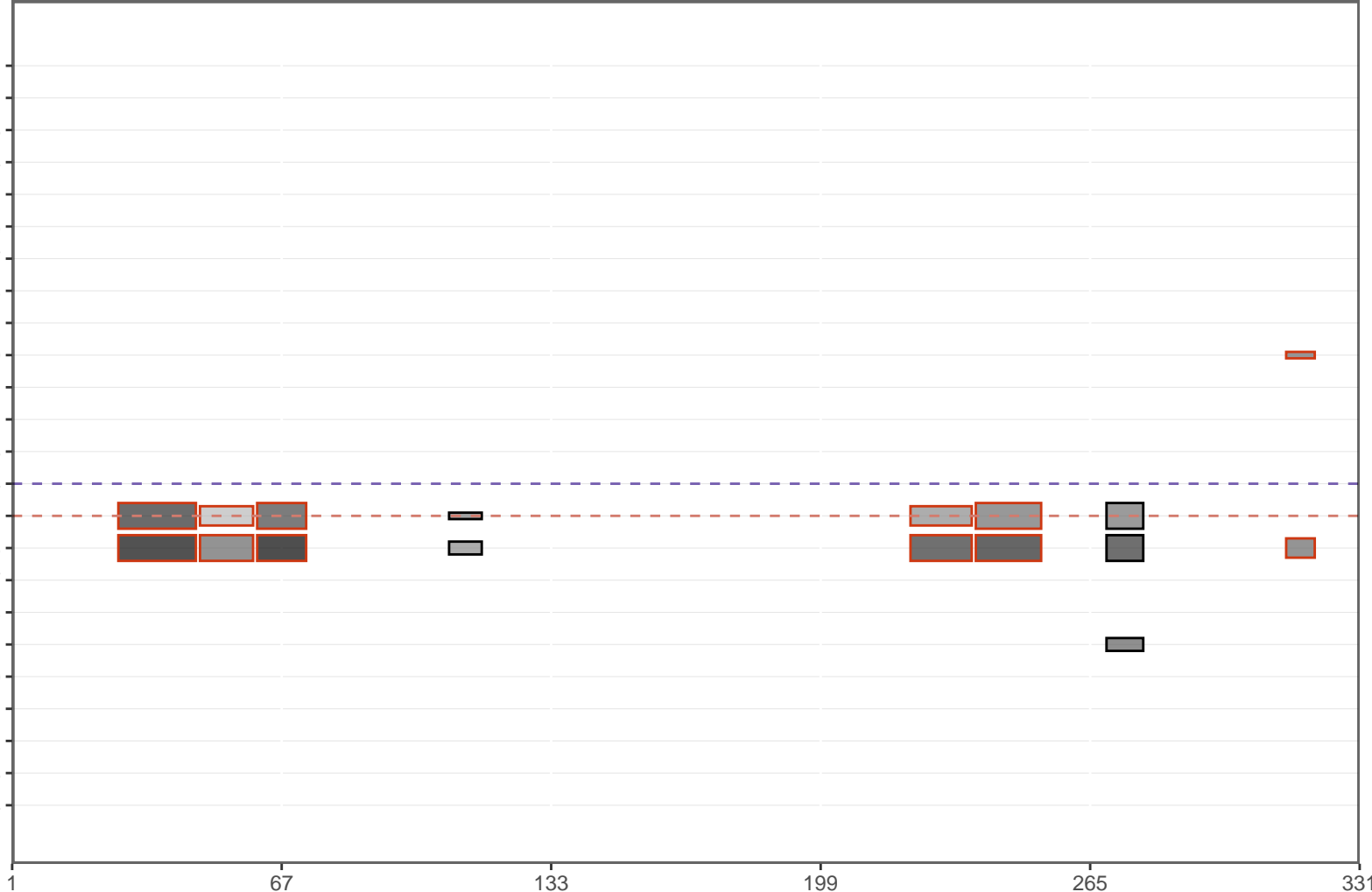
MW indication



Molecular weight

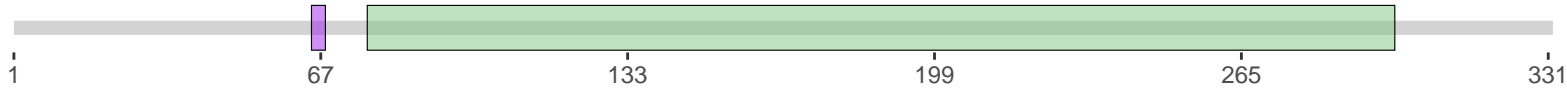


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

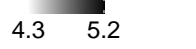
NFGRVFLSGDSAGANAHNLMAAGVPELMDIGVALHPYFWSGGSGEALYPKKAAHVDRLWAFVCPENPNDPRINPMFEGAPLTSLGGRRVLIIVAEKDKLDRGWAYGALGRGGWMDVVVQETEGEDHVFHLNLLGGQKSKDLIKNLAHFFNREMPFLKKH*

NbL18g12750.1 ornithine_carbamoyltransferase_chloroplastic-like [MW = 43.22 kDa]

No. of times detected



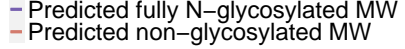
log(intensity)



Values from

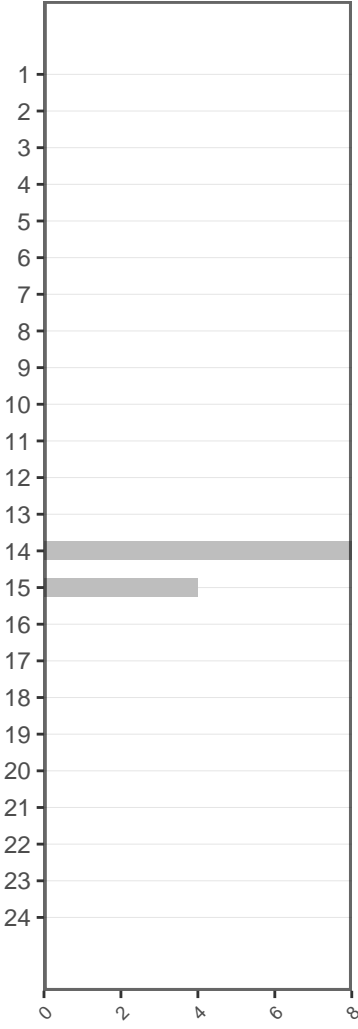
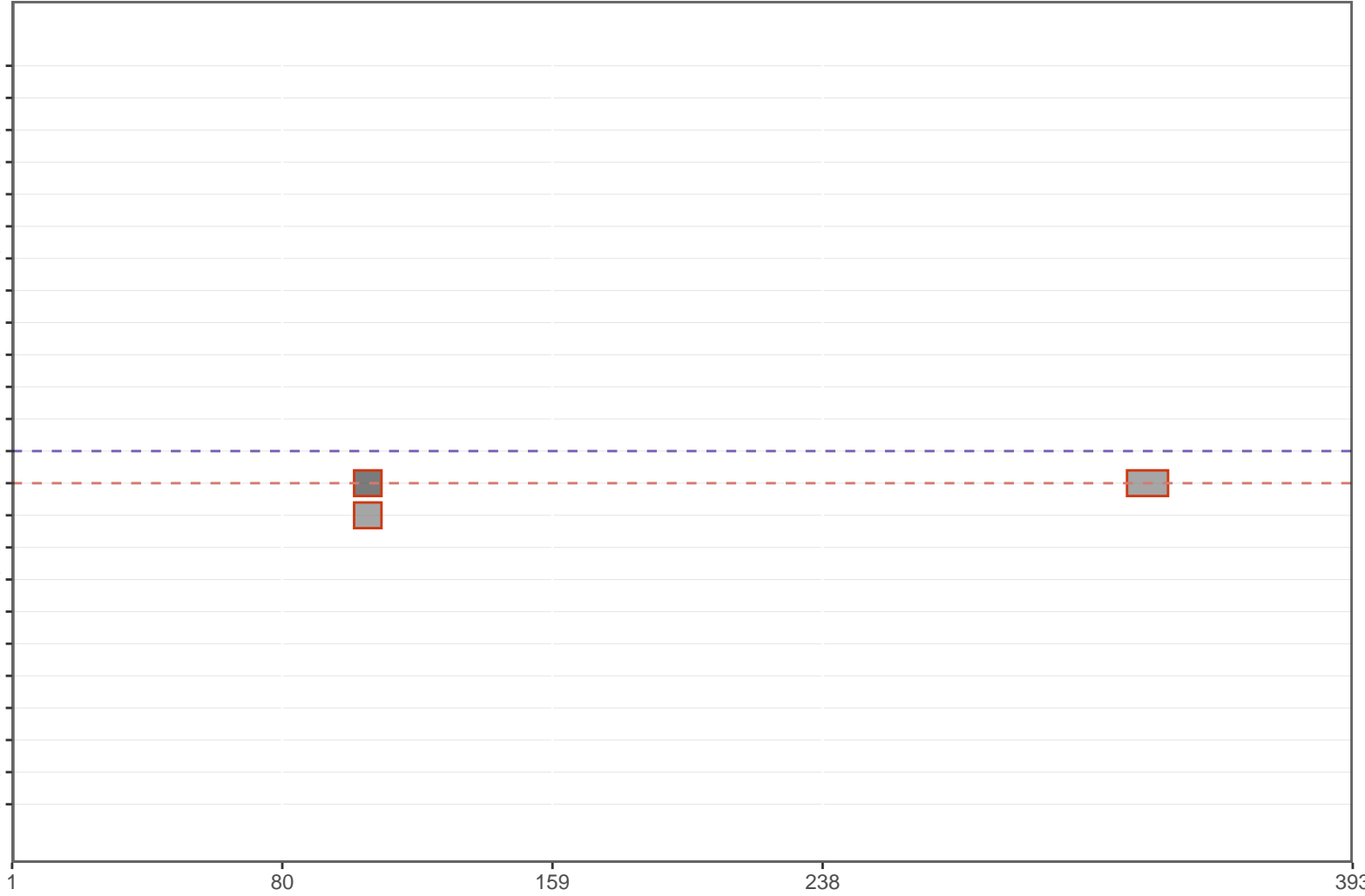
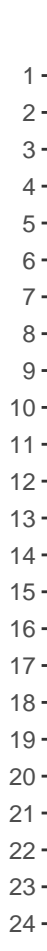


MW indication



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00185 Aspartate/ornithine carbamoyltransferase, Asp/Orn binding domain
- PF02729 Aspartate/ornithine carbamoyltransferase, carbamoyl-P binding domain

Protein sequence:

IIIMARVFAHQDILDIAKATVFPVINGLTDVNHPPGQIMADALTMIEHVGGLETKVAVVYGGDGNVHSEWLLLSAVPFHFVCGACPKGFEPDGETVEKARGAGVSKIEITNDPKAVRGADVVVYDVAWSMGGKKEAAHRRRVFGGFGVDEELMLKLAGGKAYFMHLLFAERGVETDGVKVEAPNSVFPQAEIRMHAGNAIMLHVLGL*

NbL18g12390.1 alcohol_dehydrogenase-like_7 [MW = 41.88 kDa]

No. of times detected



log(intensity)



Values from

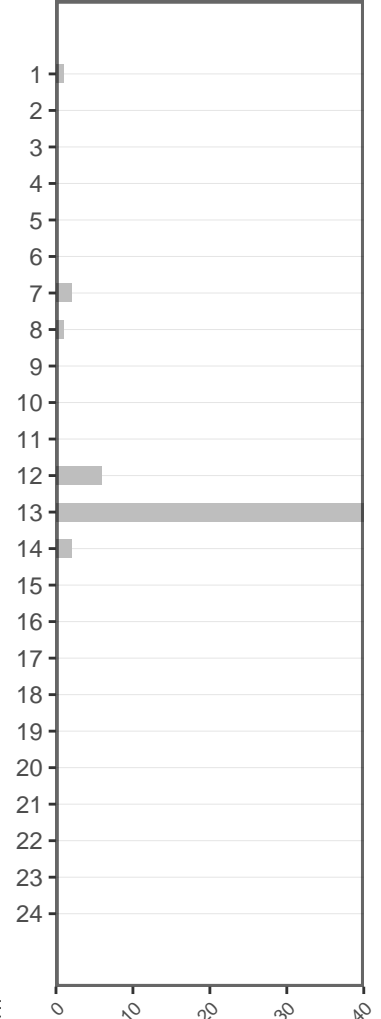
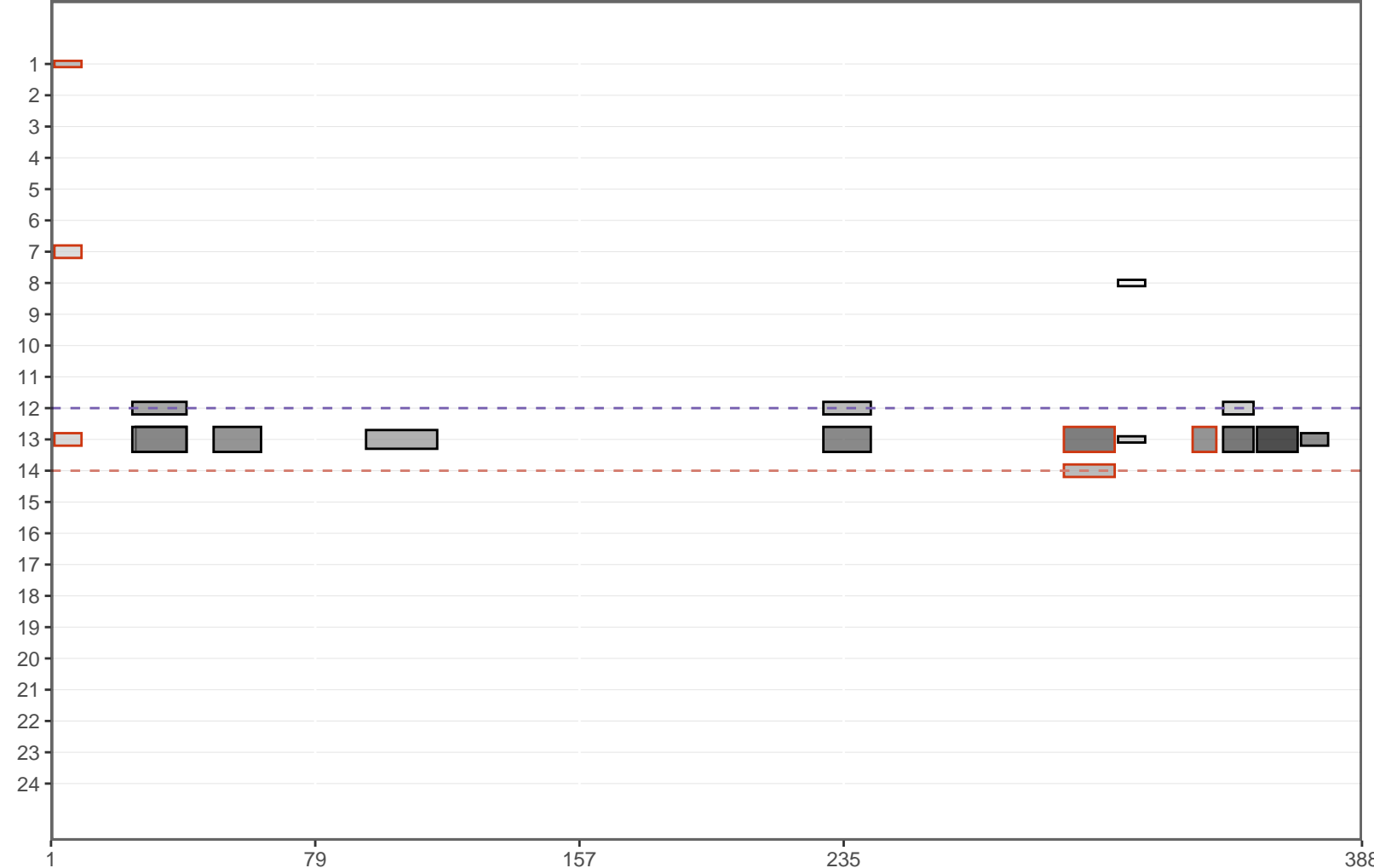
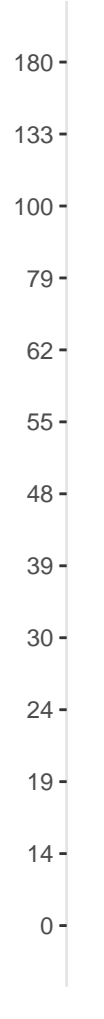


MW indication



Molecular weight

Gel Slice



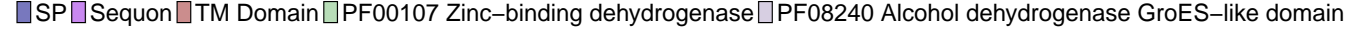
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

"SCVSTGLGAAFKTANVEFGSTVIFGLGAGLWAEGARICGATRIIGVDINSDFEIKGDFVDFVNSFSFGDKPIBQVNMETNGGADYCFEYVGLGTVAQEAAYAGRRKQWGTIVLGVDPKPGADITKSEFDVLSHGKTLMSLSLFGGLKPKSDIPFLVKRYLDELQLDKPFVTHEVVFQDNKAFDILLAGGKSLRCVIMD"

NbL18g12280.1 aspartic_proteinase_Asp1 [MW - SP = 42.69 kDa]

No. of times detected



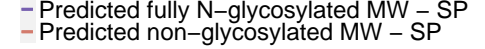
log(intensity)



Values from



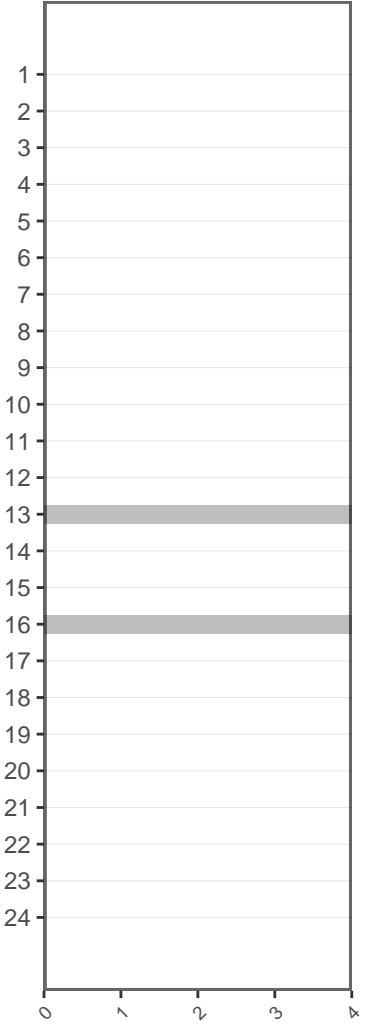
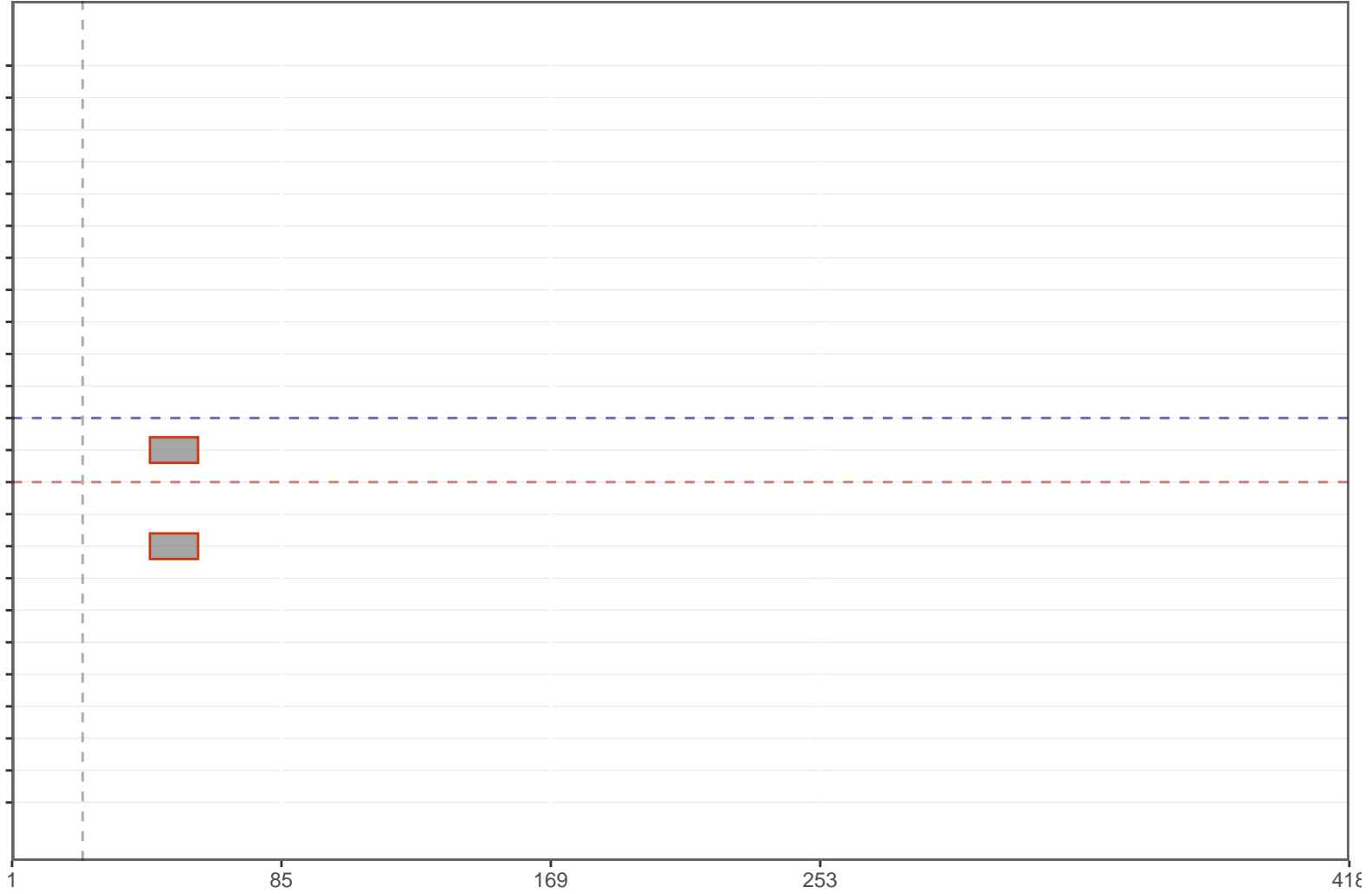
MW indication



Molecular weight

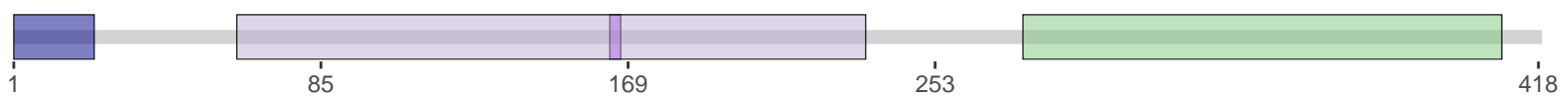


Gel Slice



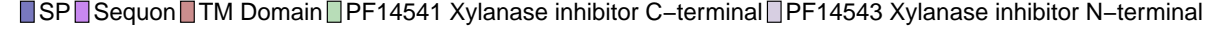
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

GILGLNGKSSVLSQLESGLIRNVVGHCLGGGGGFLFFGGDVLPSGGVWTFPIVRSSEKHYVSLGPADLLFSGDAGKGIPIFDGGSTYVYNSKAVKILVSSKIKDNTKQLTDAVDDKSLPVDVWKGKSKFSIHDAKFFKPLTLEFRKAKNVQLPLPEAVLVRTEHGNLGLDGTVEVGLGNVNLGGDSMVDKMKVYDNEKQGGGWVPAKCNLPI

NbL18g12270.1 catalase_isozyme_1 [MW = 56.85 kDa]

No. of times detected



log(intensity)



Values from



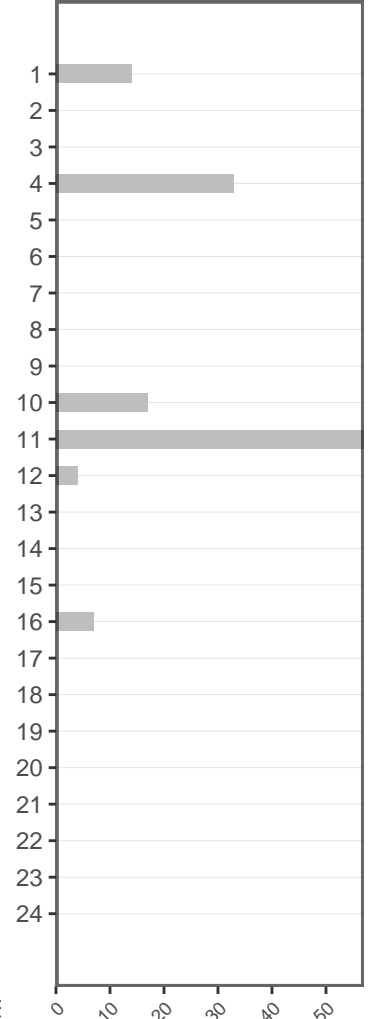
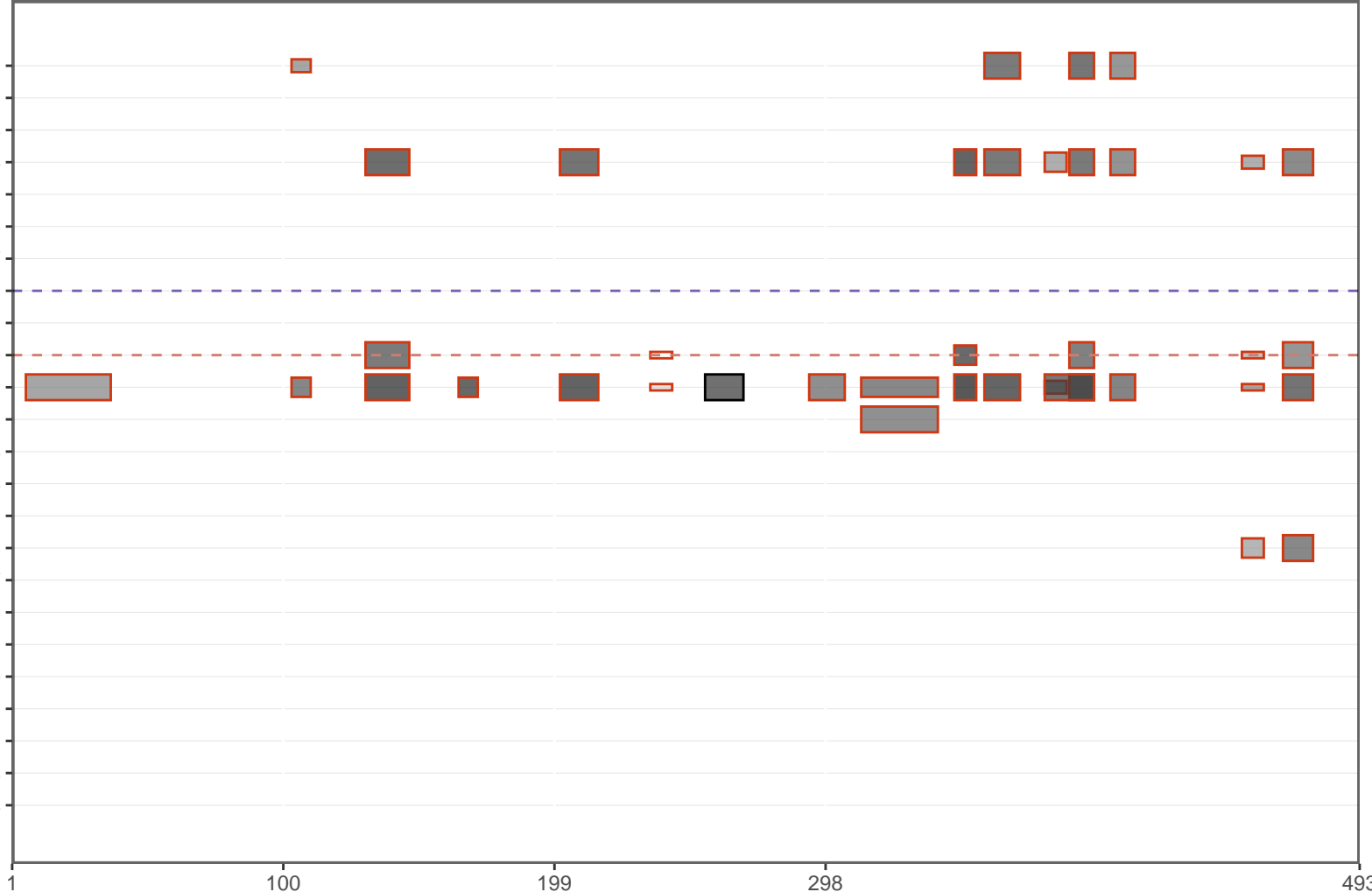
MW indication



Molecular weight

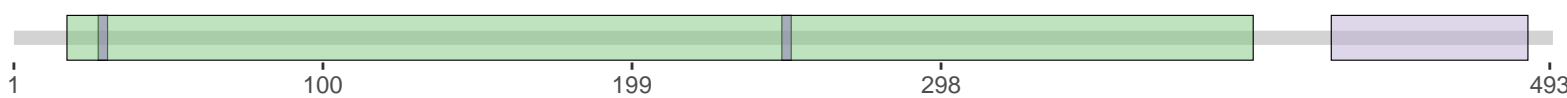


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

MSEEEAIRVGGTINSHATKDLVDSIAAGNYPEWKLFGIMDTEEDVDFKDFDPLDVTKTWPEDELFLMPVGRVLVNRNIDNFFAENEGLAFNPHGVPLGYSEDKLQTRIFAVADTORHRIGPNYMDLPIVAPKCAHINNHKDGAMNFMHRDEVDVLPSPFDPRGRLHAEGYIPSRVLTGRREMVEIKENNYKAGERYRSWEPDRDGRVYKWKVVEHLSDPRVTEYRISHWISYLSGADKSGGQKVASRLTKPTM

NbL18g12180.1 psbP_domain-containing_protein_3_chloroplastic-like [MW = 28.34 kDa]

No. of times detected



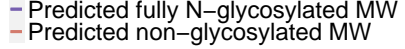
log(intensity)



Values from



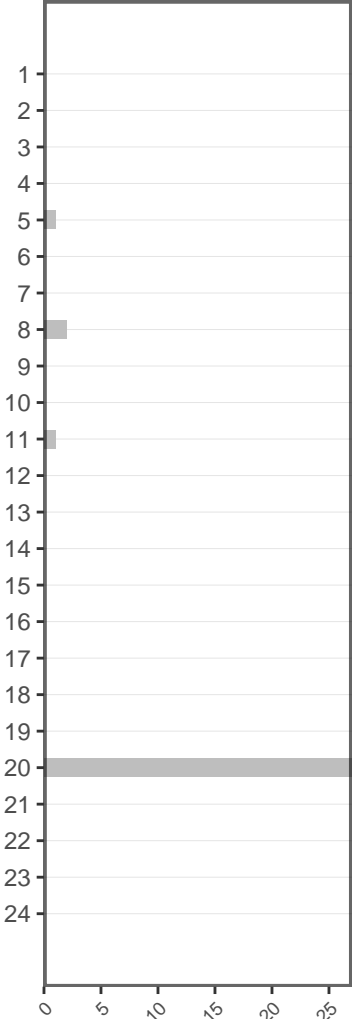
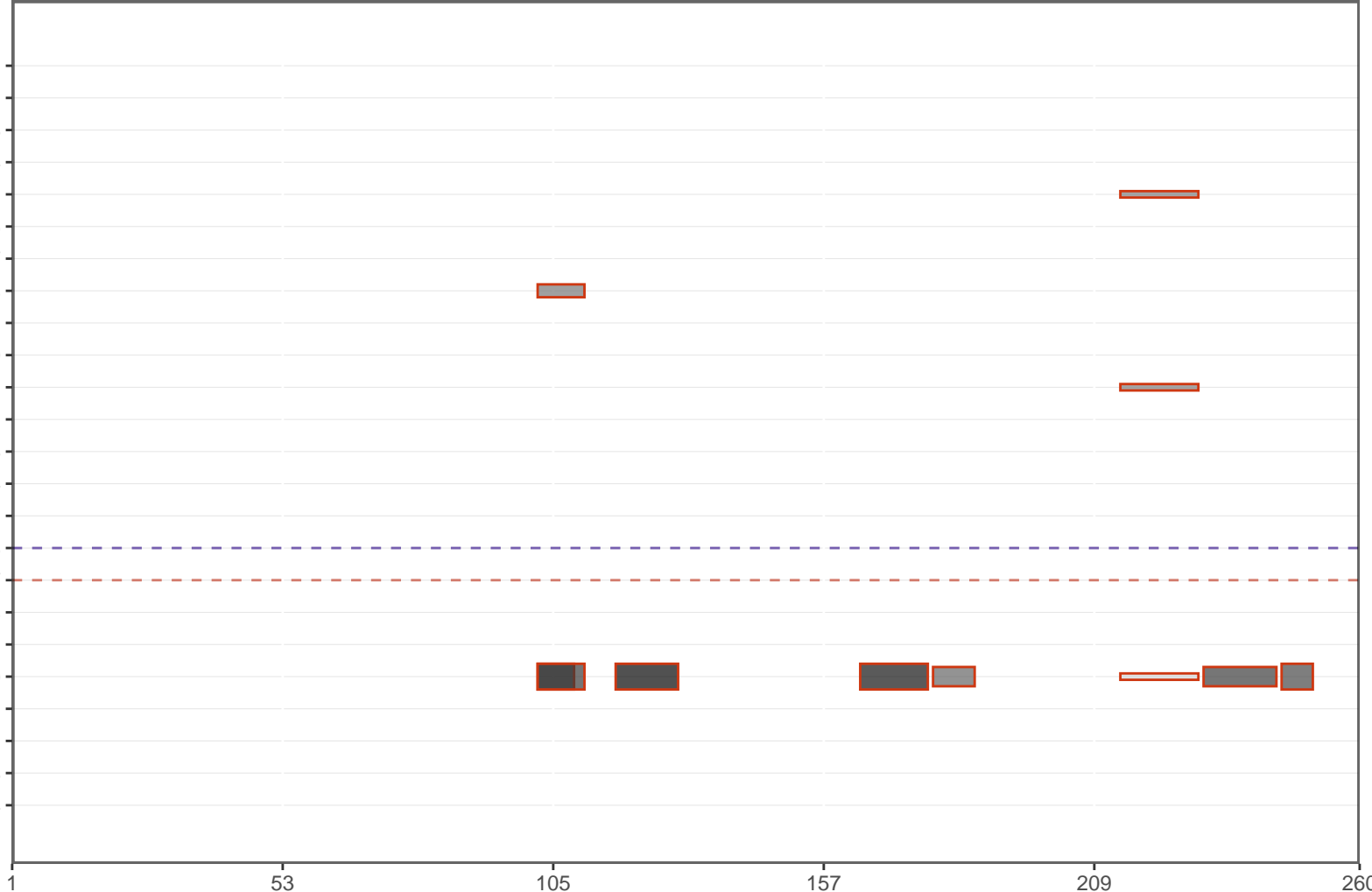
MW indication



Molecular weight

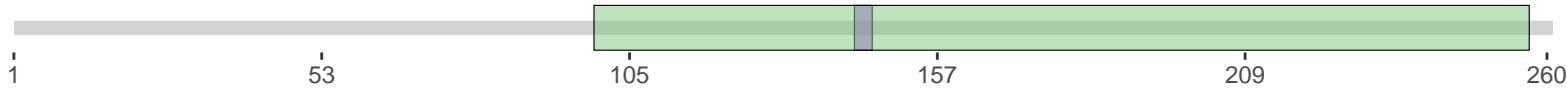


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YVQIGAGEGDCVRLSLAFYFDGEASNTNVSIVTSLGADFTKLESGFKVDAFAENIVSGLDRSWORPRGDKWAKLIDSKASKGLYIEVETLONPGGSLRLHLFSLVGLIADNGVYRNYLTGTGDFDEEAKEYGAGVEKAVSFRLLI

NbL18g12170.1 pyrophosphate--fructose_6-phosphate_1-phosphotransferase_subunit_alpha-like [MW = 67.18 kDa]

No. of times detected



log(intensity)



Values from



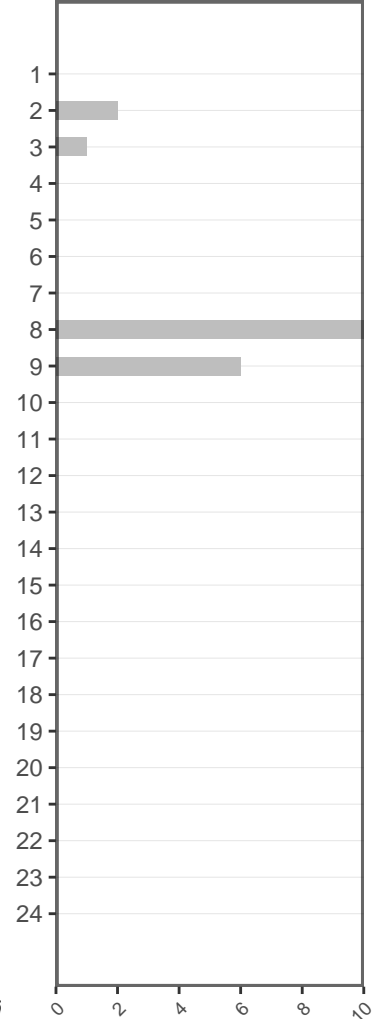
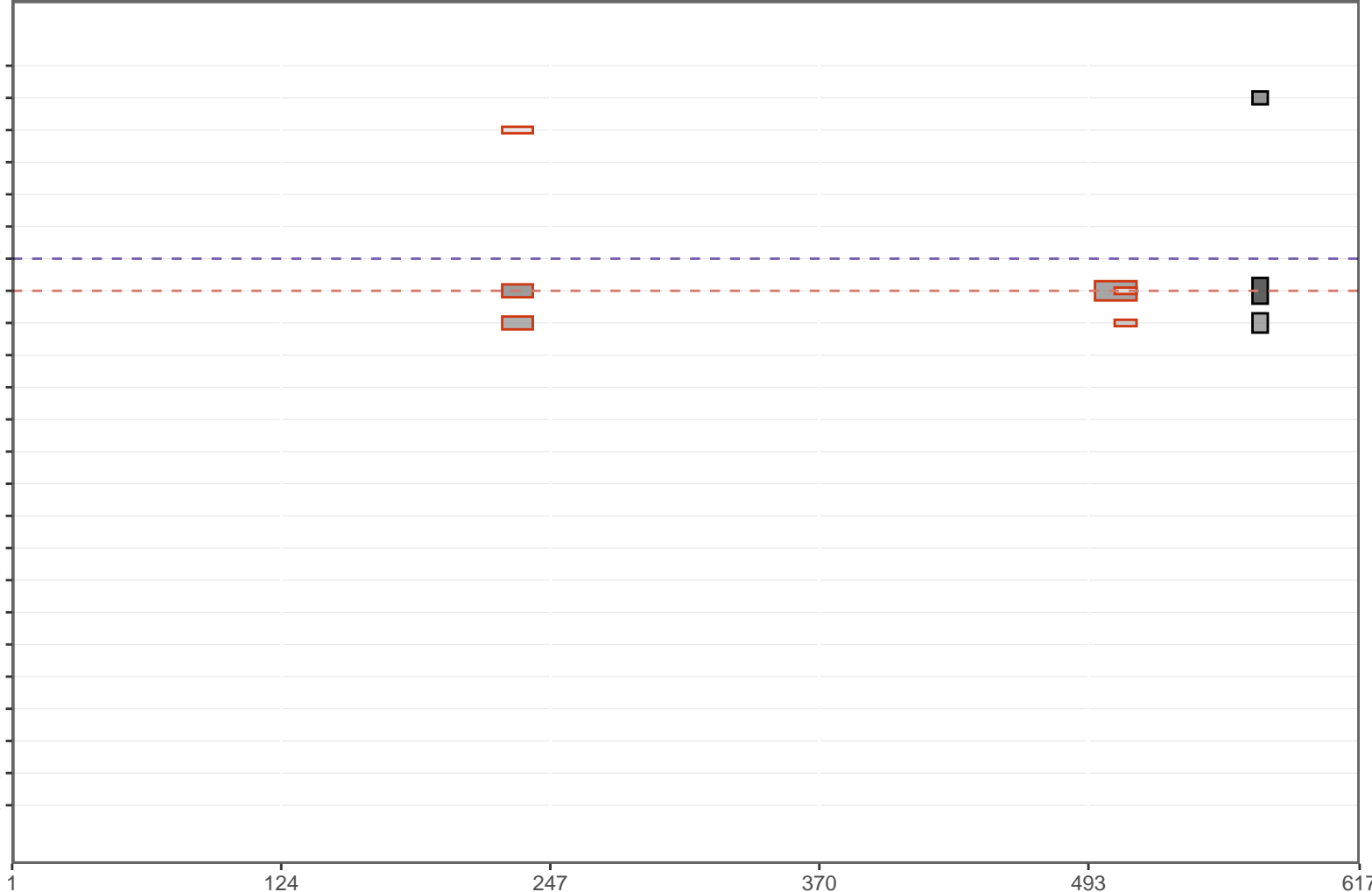
MW indication



Molecular weight

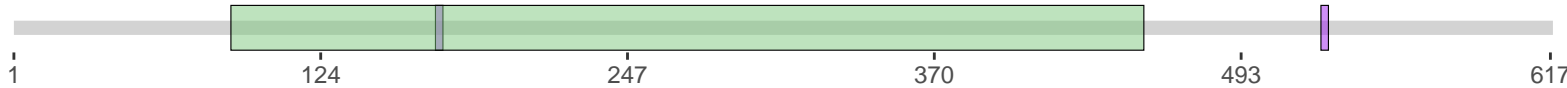


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

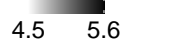
KLTLDITNKICDAVQARAEGDKNHGVLPEGLHESPEVYVALLGEIHGLLRGGVADKISGLSPWASALFEFLPFKIKOLLVPESSDASQLSQIETEKIAHLVETEMNKRLEKGTYKGGKFNACHFFGVDARGSLPSKFDGWAYVLGHICVHILAAGLNGYMATVFNLNKHVHWKRCAAAFITAMMTVKRYRGRGPNAAIKRPAVHPTTVDLKGKAYELLSQNTKFLLDVYRNPGLGFDGPGADAKAVTLGVEDGDYMGRIKILGEVLDKVRRTYKPGCCSDV/LKA

NbL18g12160.1 UPF0047_protein_YjbQ [MW = 22.5 kDa]

No. of times detected



log(intensity)



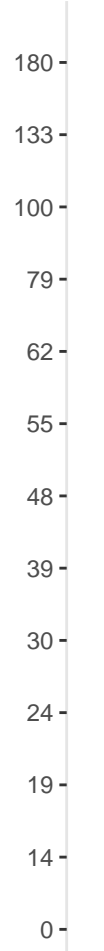
Values from



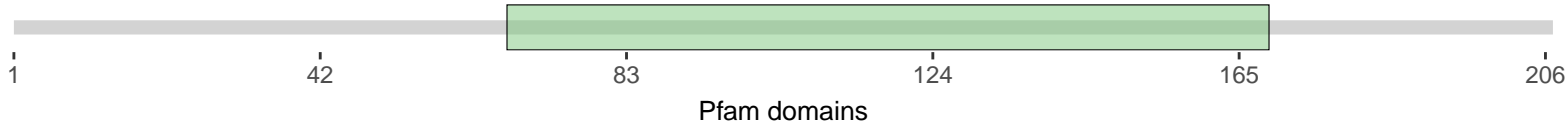
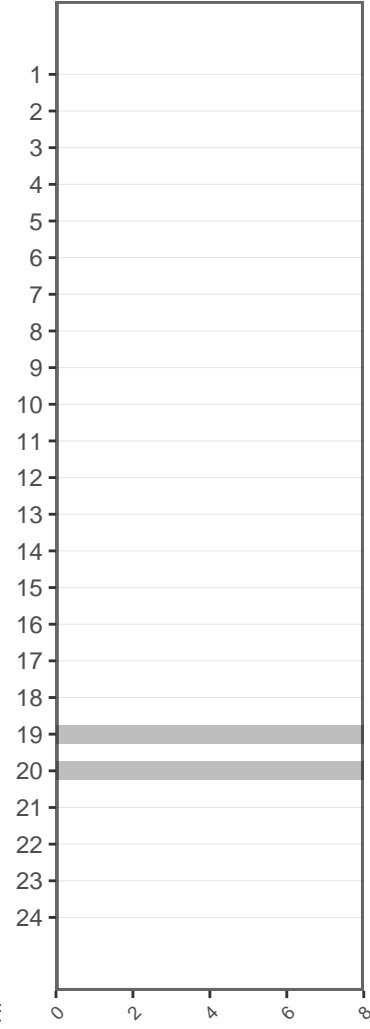
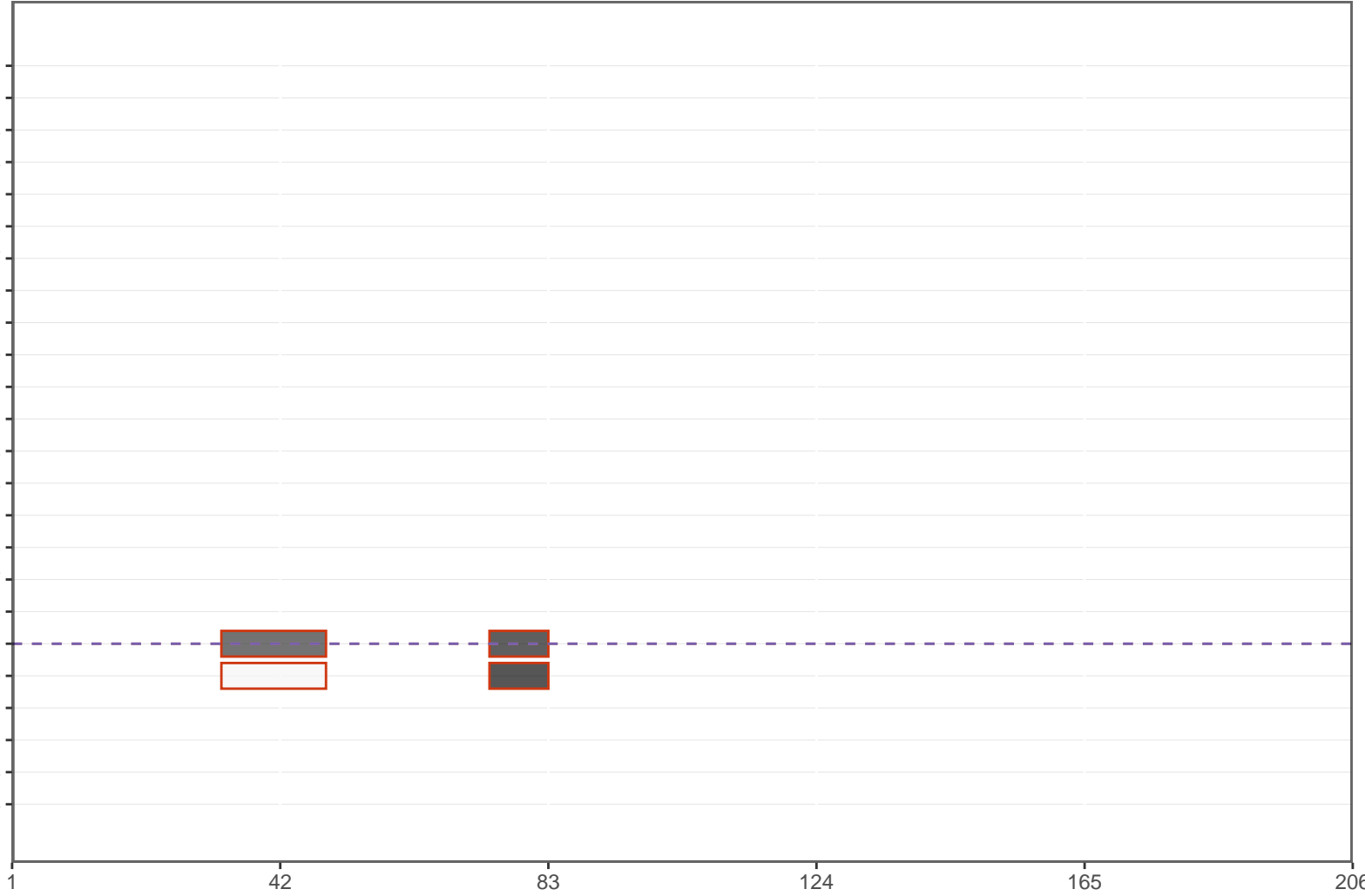
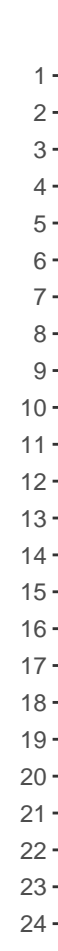
MW indication



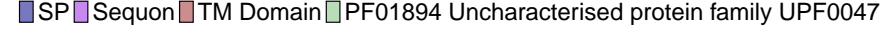
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

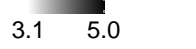
LDHTSASLTINENYDSVRRDQTFELNRVWPEGISAPWNKFLGPDQDMPNKHGSMFGDTLSEIPITDGLNMGTWGLPSSAEEEPWQLGIWLGEHRDATPRRIFLNGM

NbL18g12080.1 tryptophan--tRNA_ligase_chloroplastic/mitochondrial [MW = 49.77 kDa]

No. of times detected



log(intensity)



Values from



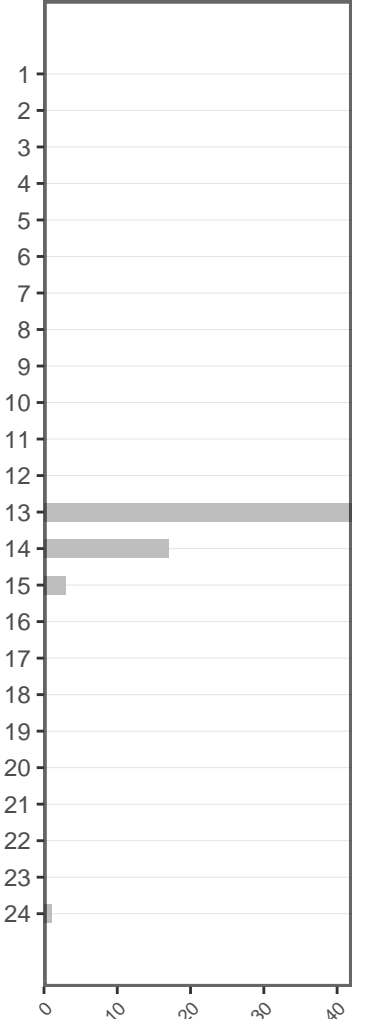
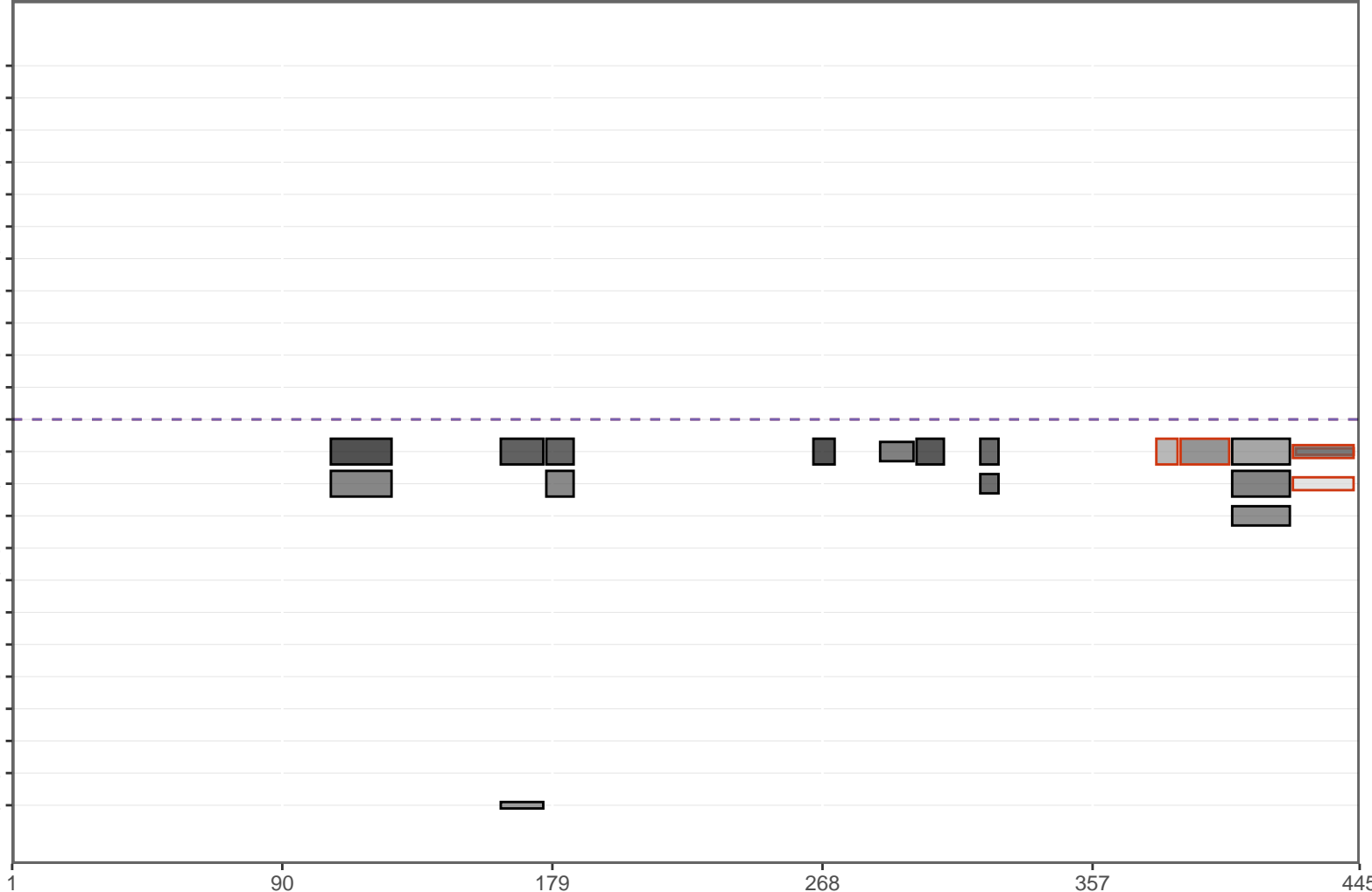
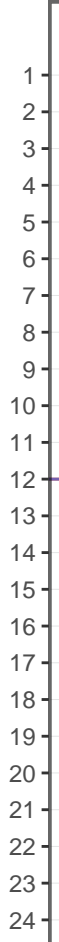
MW indication



Molecular weight



Gel Slice

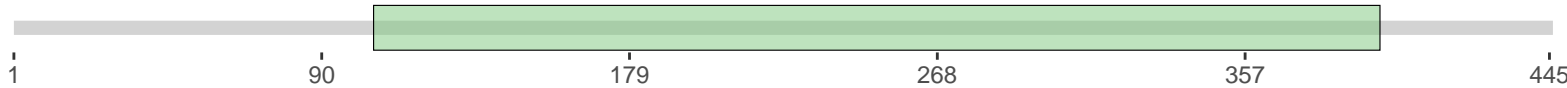


Peptide counts over 4 repeats

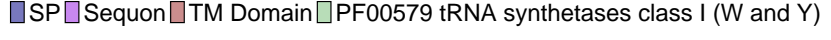
Protein length



Pfam domains



Pfam Description



Protein sequence:

KEKSRKAGDENVSWLLTYFVLMADLLYQSDFFVVGEDDQKHLELRELAEKRVNLYGGRKWKLLGGRRGSSFKVPEPLIPFAGARIMSLTDGLSKMKKAPSDGSRINLLDQKDVIANKKIKKTKTDSFFQMEFDNLERPEGNNLLSIVGLVTKTKGVAEECRDMNWGTFKLVLTDAIVDHLRPIQVRYEEIVSDASVLDGVLAEAGARKAADVADVTNNVYQAMGFLRR

NbL18g12010.1 serine_hydroxymethyltransferase_3_chloroplastic-like [MW = 31.26 kDa]

No. of times detected



log(intensity)



Values from



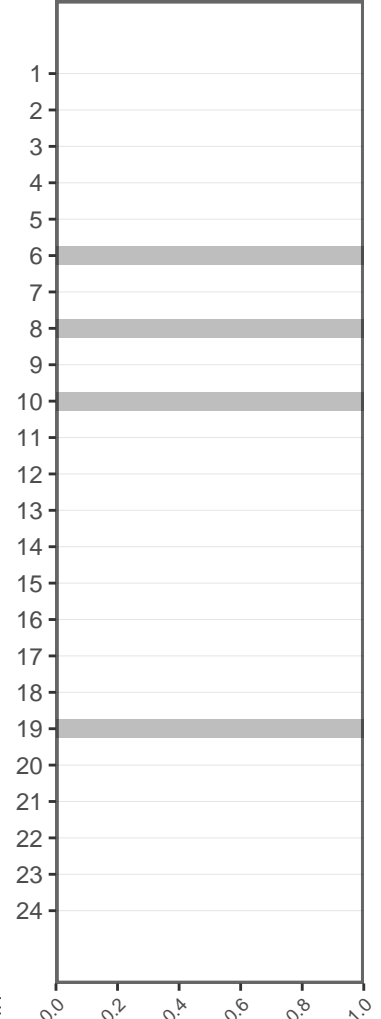
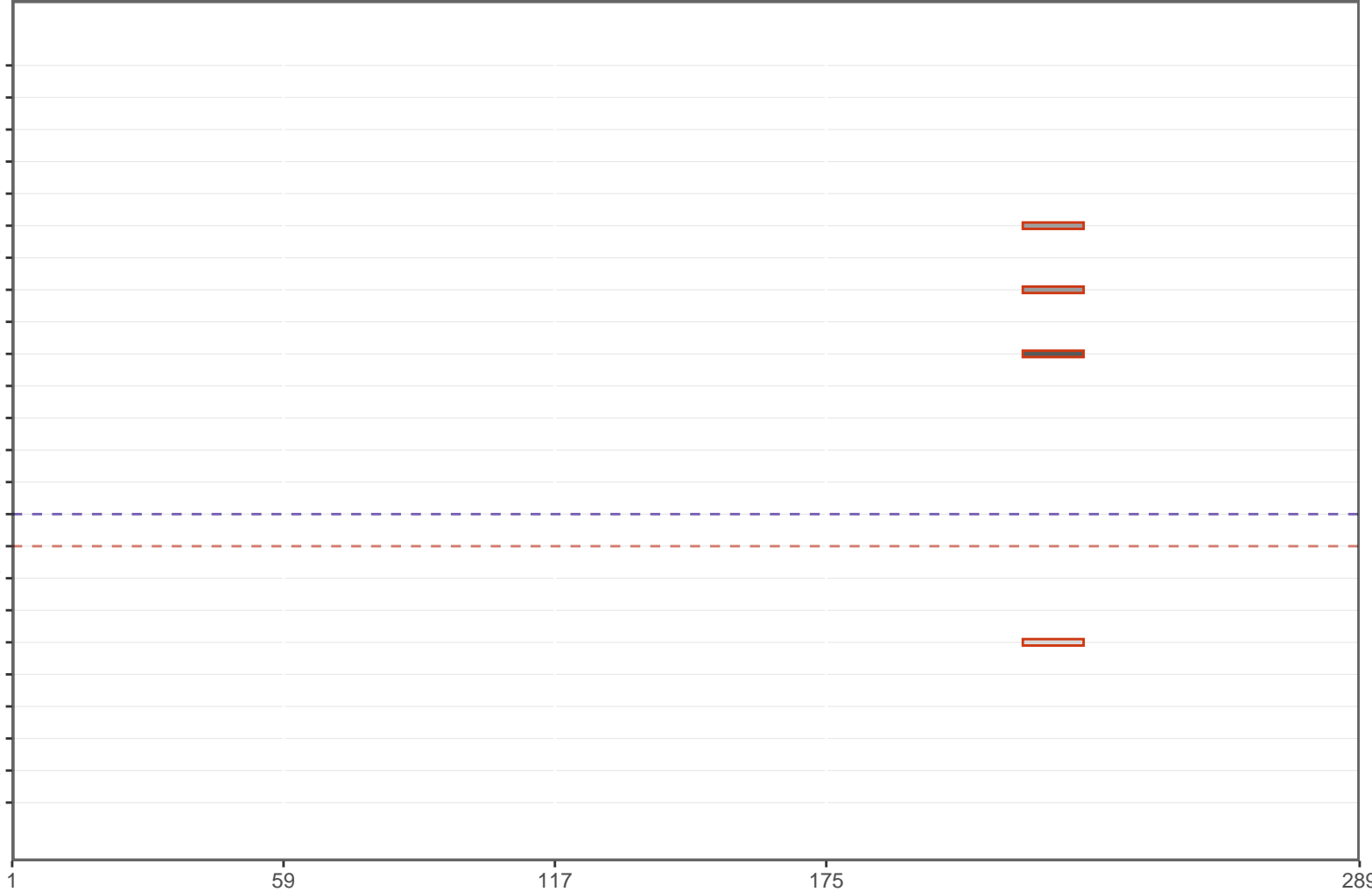
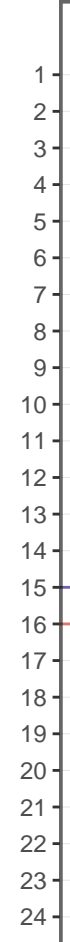
MW indication



Molecular weight



Gel Slice



Protein length

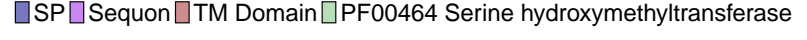


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IEQLPKRYGCGNEYDELEKIQGERALAAFNLDGKGWGVNVPRLSGSPANFEVYTAALNPHDRIMGLDLPHGGHLSHGFMTPKRRVSGTSHVFESMPYRLDESSGLVDYDMEKTAELFRPKLIAGASAYPRDFDVPKQAGLNCFIRSSAGRGCC

NbL18g11940.1 far_upstream_element-binding_protein_2 [MW = 67.71 kDa]

No. of times detected



log(intensity)



Values from



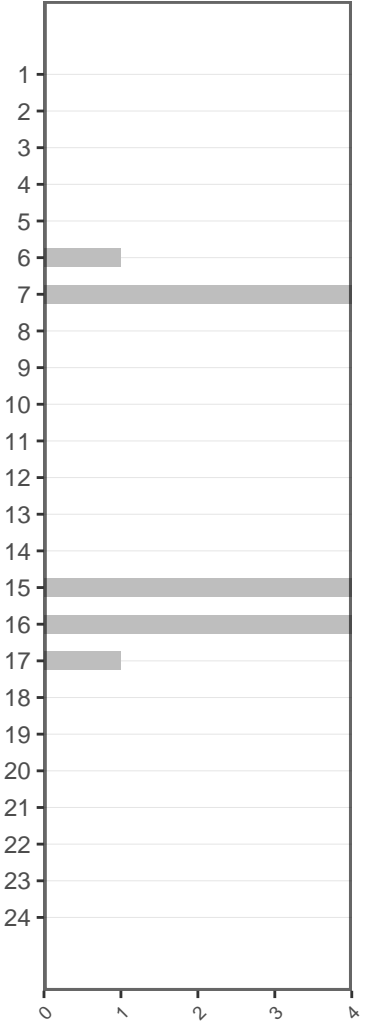
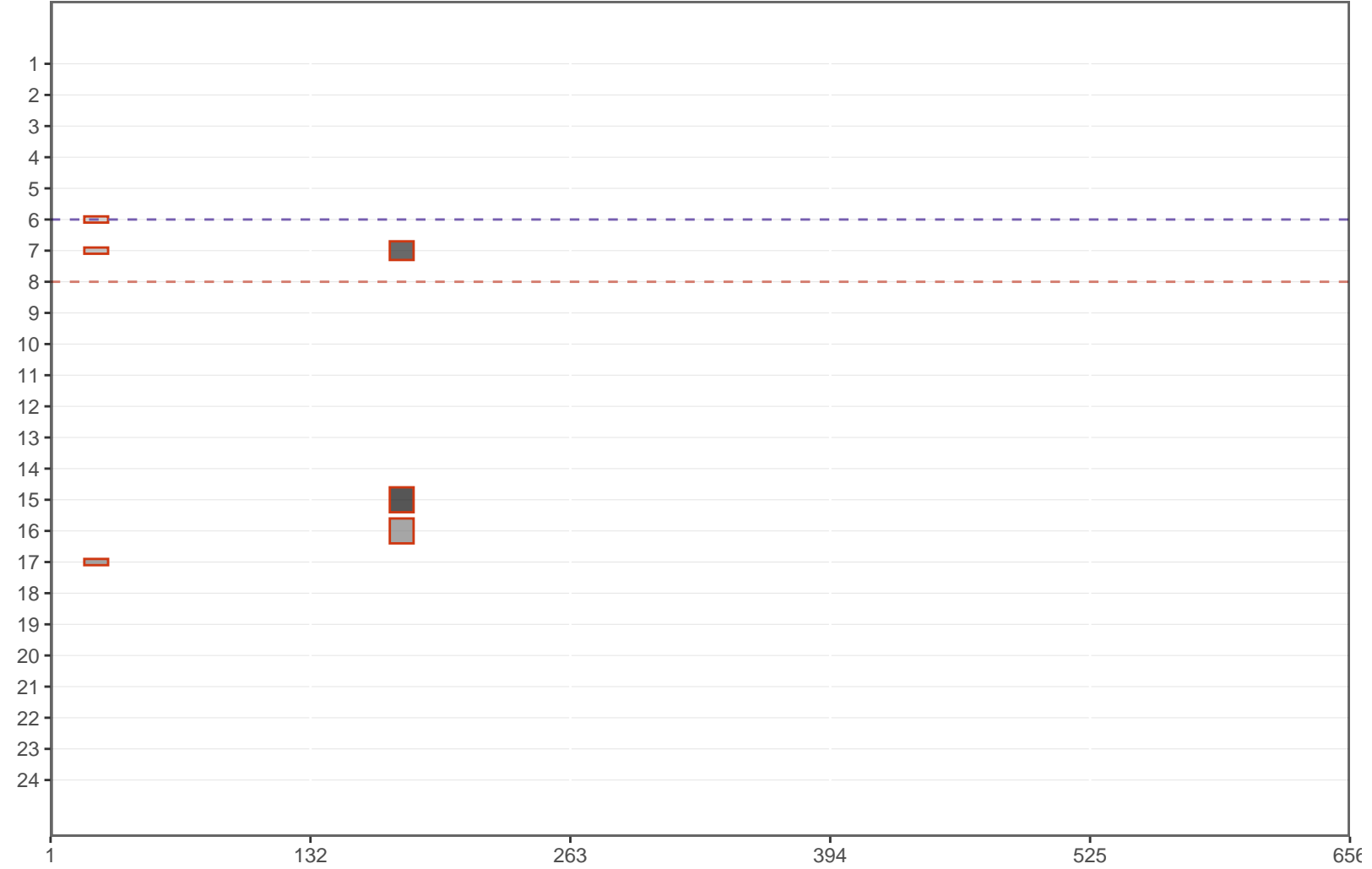
MW indication



Molecular weight

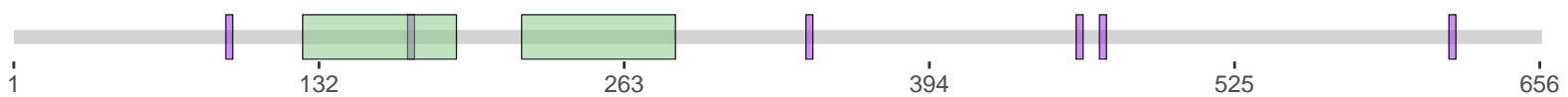


Gel Slice



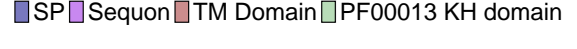
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

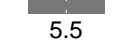
DPLGYGVYQPCAYPGRSPQYNTSGDFVGVFPQPSAGYASGWDGTASGNQGGSGGGYDYVINGQAPPDQGGTFCGTAASTNSAYGYNQLSASGYSQGGAYSGDGYGGYHAPFQSGYGGTGYEQGGGYSAAAGYGNASNPTEGGNSYGTGGDGGAPPPVGGSEATGGGGYFSGGGTAAGYGMPTSGGGYGTTPPAGVAEYSGAPQTKPKPSPGPAWGGPQGGSEADGGYAGPPPMRPGYVPGGAADGGALPDDGTLRPPASGYGAPTAPGYI

NbL18g11750.1 60S_ribosomal_protein_L7-2 [MW = 30.82 kDa]

No. of times detected



log(intensity)



Values from



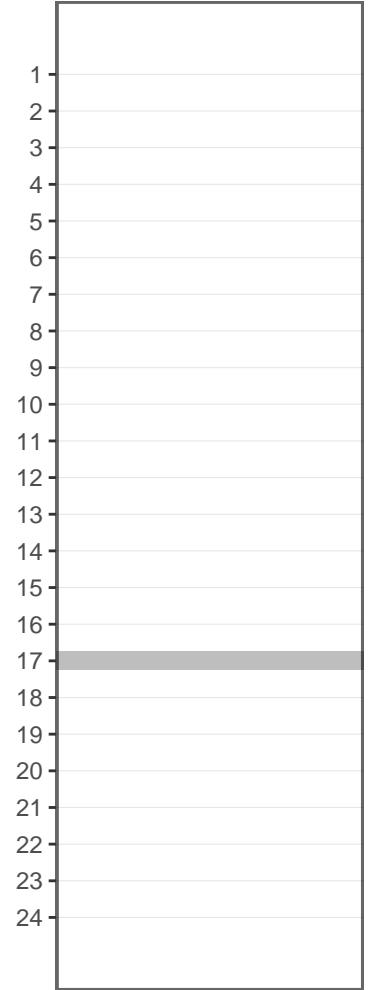
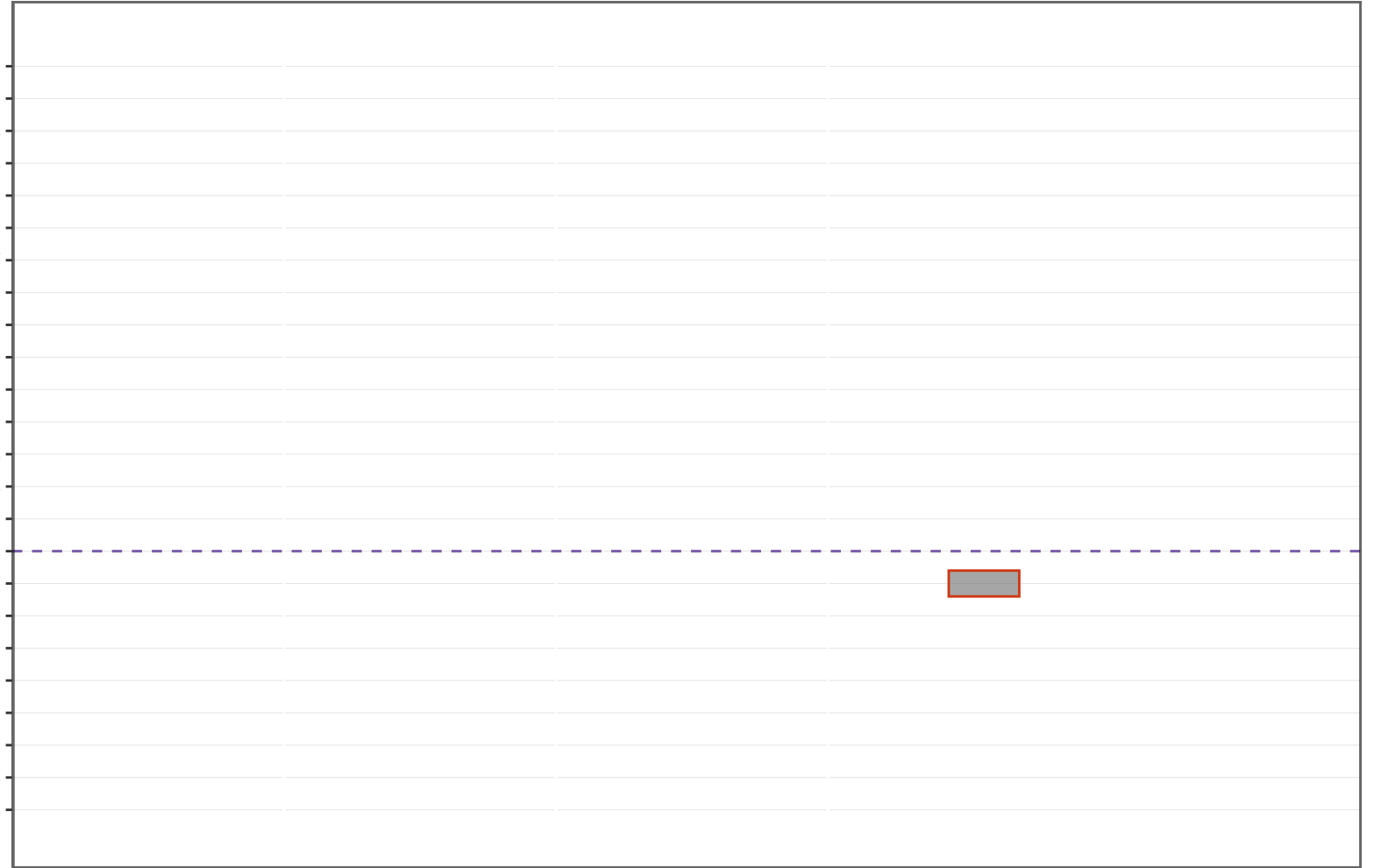
MW indication



Molecular weight



Gel Slice

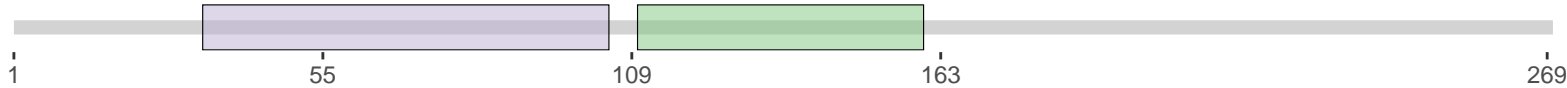


Protein length

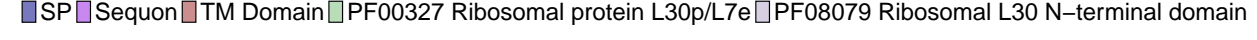
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

IAPDQTKKLLQLLRDQIFNGVFLKVKATVWMLHRVPEPVYTYGYPNLKSRELYMKRGYGLDKRRIALTDSIEGALGKHGICAEULVHEIMTVGPHKEANNFLWPFQKAPLGLGKXXXXRHHYVEGGDAGRENYYNELRRIMV

NbL18g11660.1 40S_ribosomal_protein_S6-like [MW = 28.32 kDa]

No. of times detected



log(intensity)



Values from



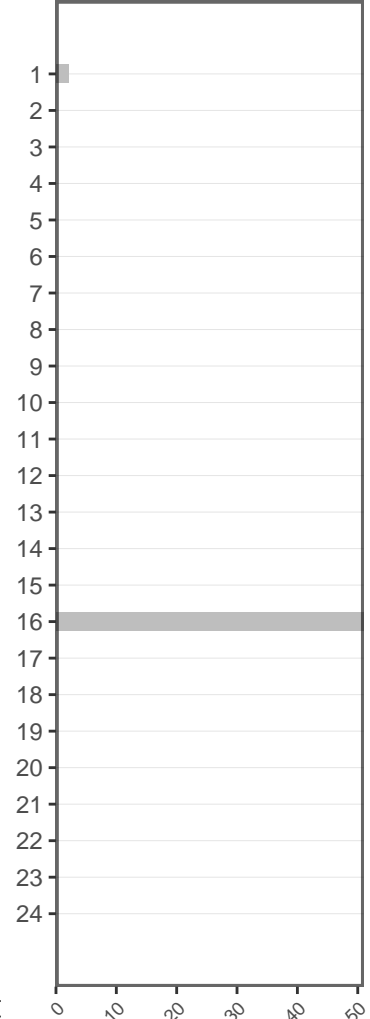
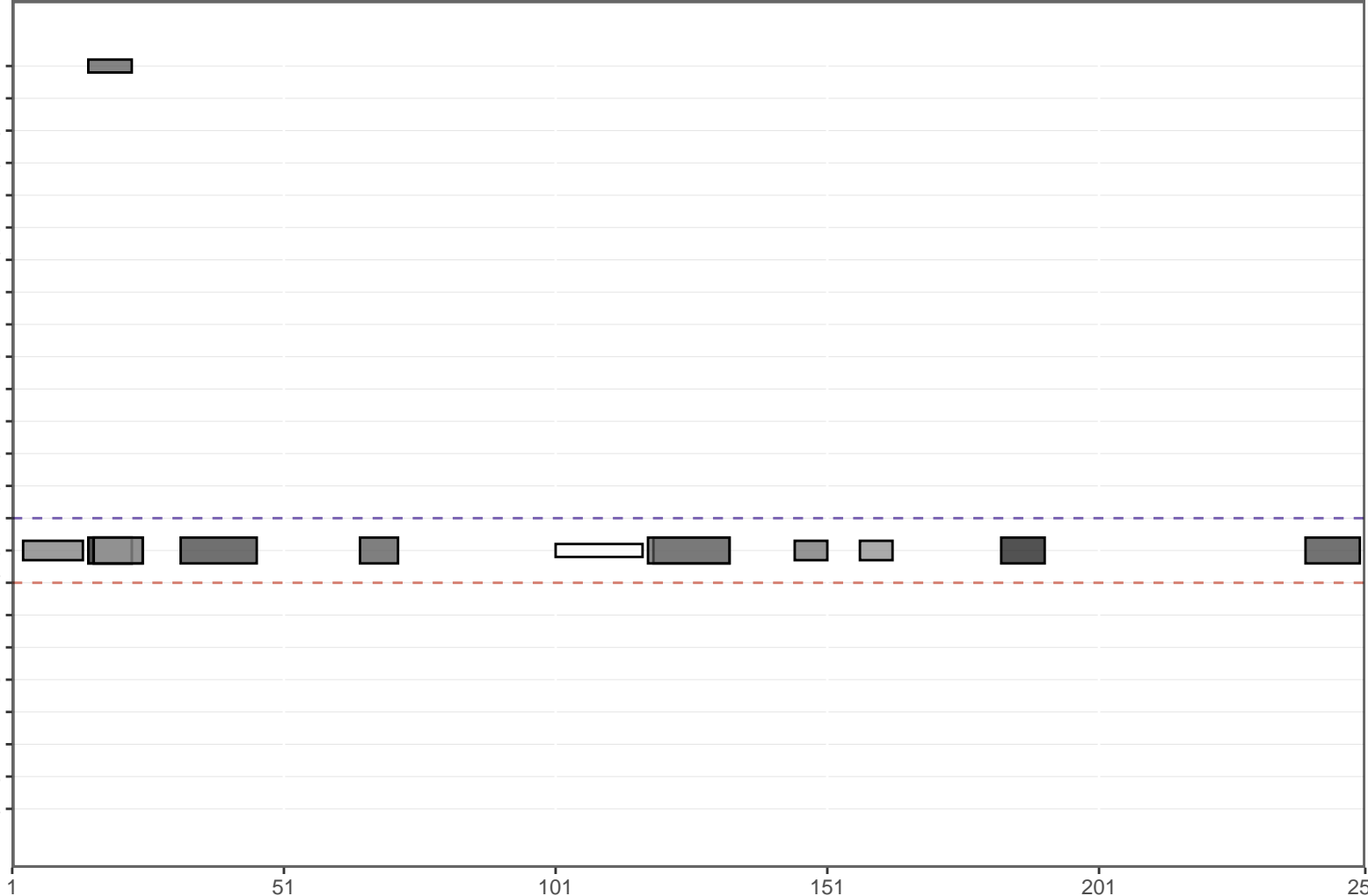
MW indication



Molecular weight

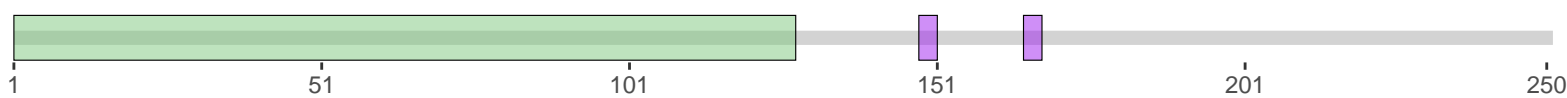


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

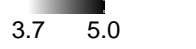
/LNLYVKKGENLPGTDFTEKPRMRGPKRASKIRKLFNLSKEDDMRKVYNTYRINFTTKTKKASKAPKIGRLVPLTFLQKRRAIADKKRIAKAKSEAEVYKLLATRLKEQRERREESLAKKRISLSAASKPSIA*

NbL18g11560.1 probable_protein_phosphatase_2C_59 [MW = 31.49 kDa]

No. of times detected



log(intensity)



Values from



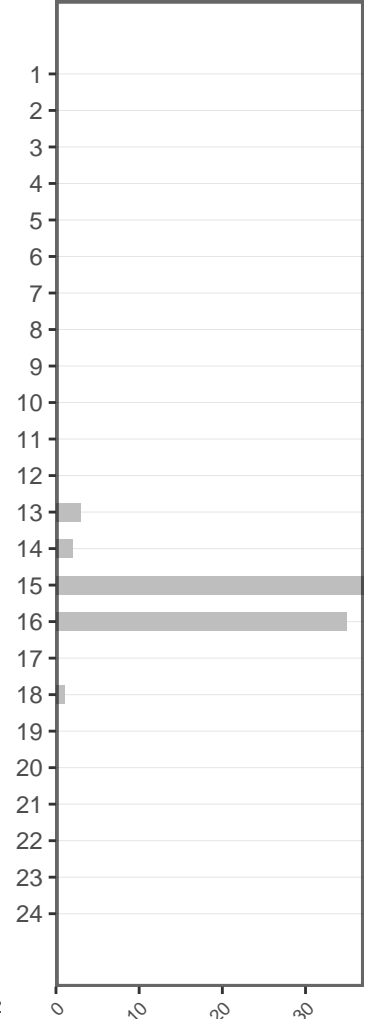
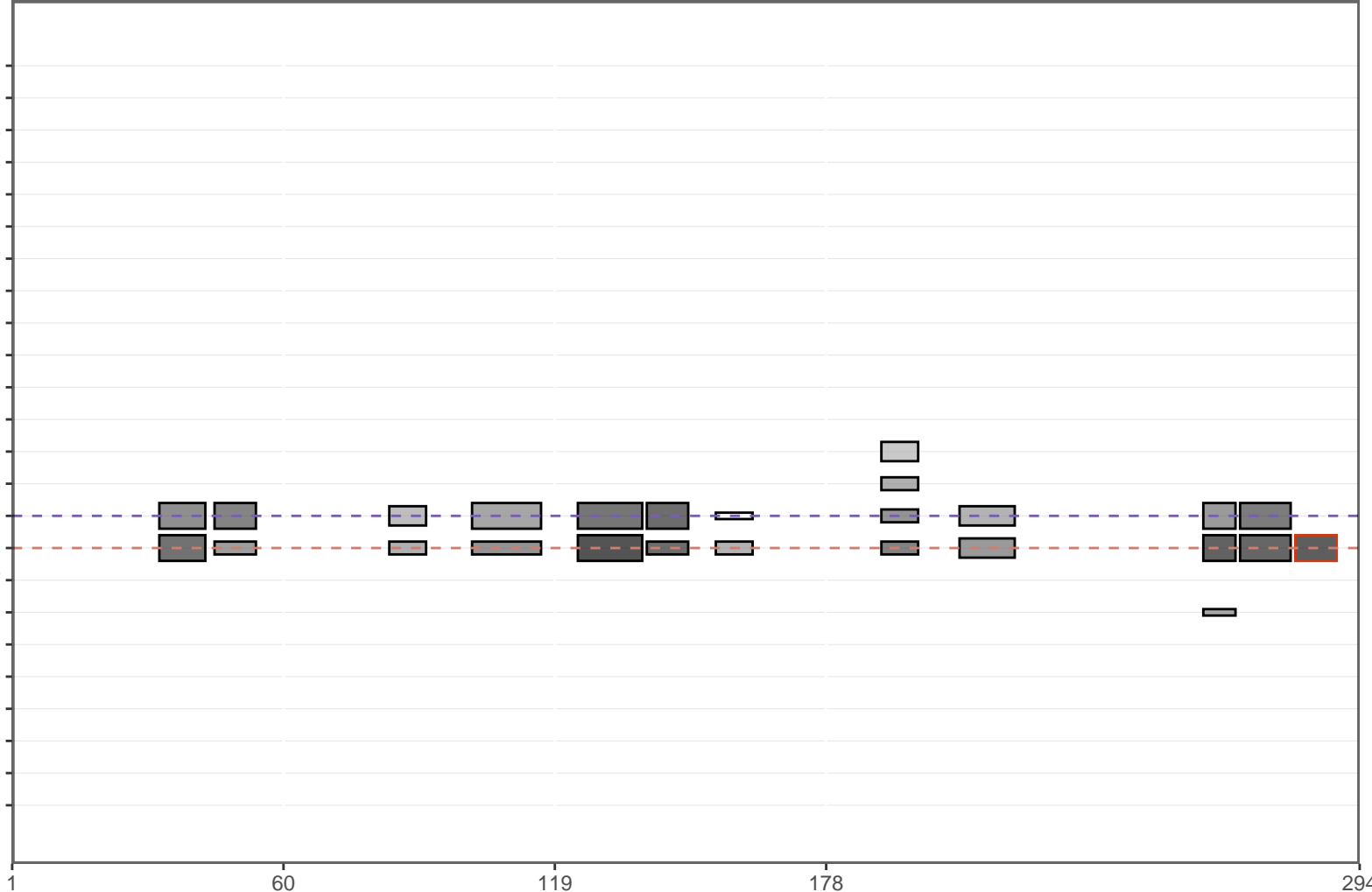
MW indication



Molecular weight

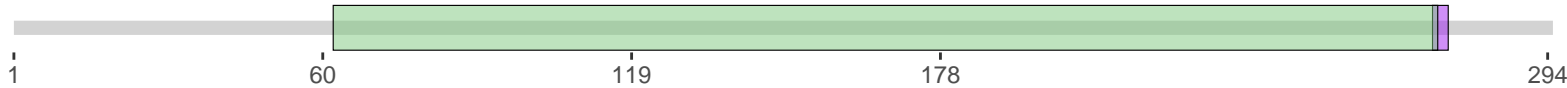


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

YGDRLLVAVNGDSRAVIGRGGTAVSRDHKPDGTDERRGRLEDAGGPFVWAGTWRVGGVAVSRAFGDRLLKGVVADPEIQEIKVDGSLFELILASDGLWVVTNEEAVSMVKPIQDPEEAAKRLMGEAYGRGSADNITVAVRFLNGEIGSRGVSVA

NbL18g11540.1 apyrase_2-like [MW = 51.2 kDa]

No. of times detected



log(intensity)



Values from



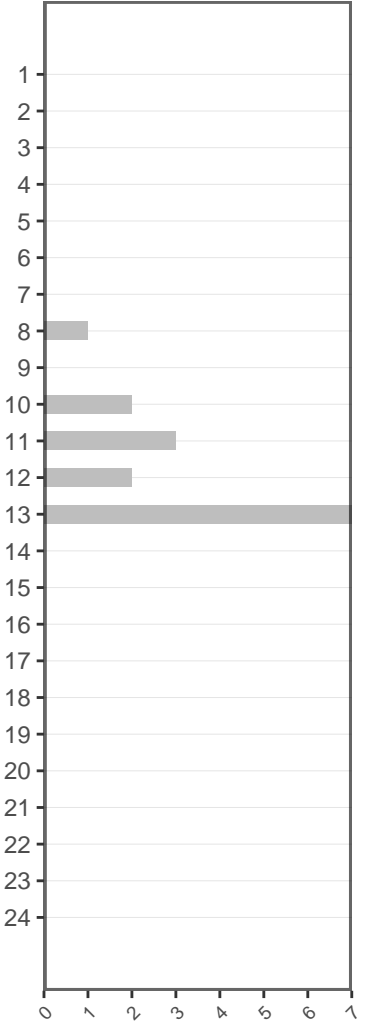
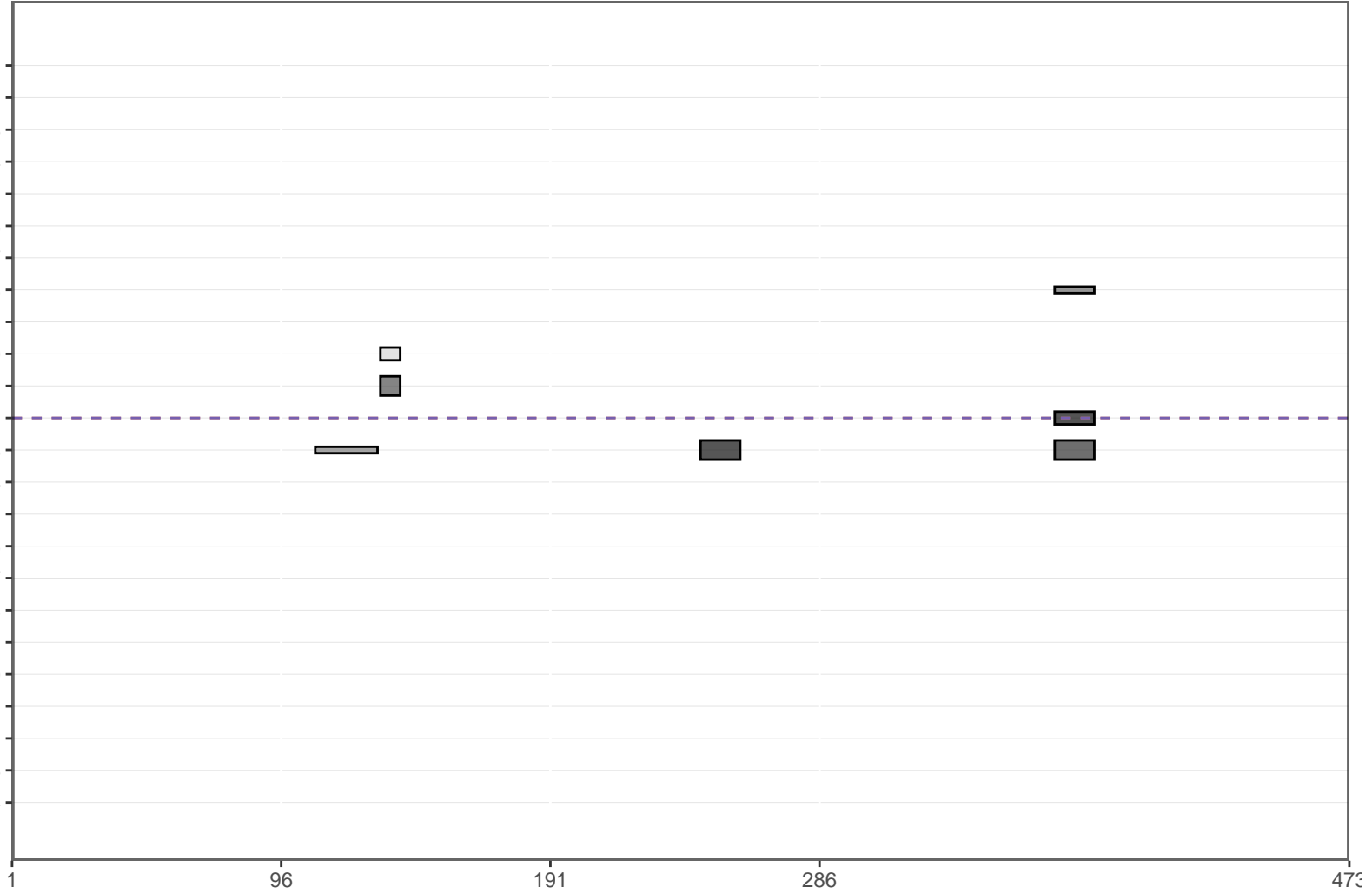
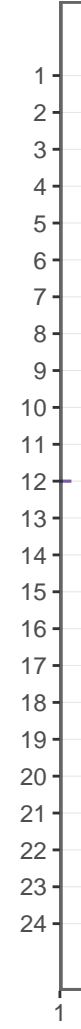
MW indication



Molecular weight



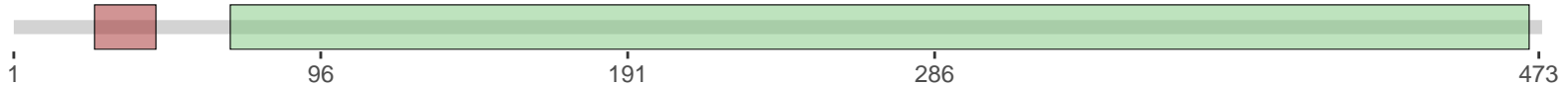
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

SVYQMAVALESDDGKAPKVSDDGDTYVDEMVLKGTQYLYVHSHVHLYGLLAARAELKATDEGGSPCLGGYHGGYKYGAVYFASAMSOGSGSLSSGCRVSLKALKVNEPTCTHMKCTFGDYYNNGGGGGGKGMFVAFSFFDRAAEAEMINPSLAWKVRPVDYVESAAGRAGETGLEGAKSAFPRVDPDLPLGMDLVVQYTLVDFGLDPQGGHTLVKVKVQYKNSLVEAAWFLGSAIEVAISLT

NbL18g11510.1 67-dimethyl-8-ribityllumazine_synthase_chloroplastic-like [MW = 25.46 kDa]

No. of times detected



log(intensity)



Values from



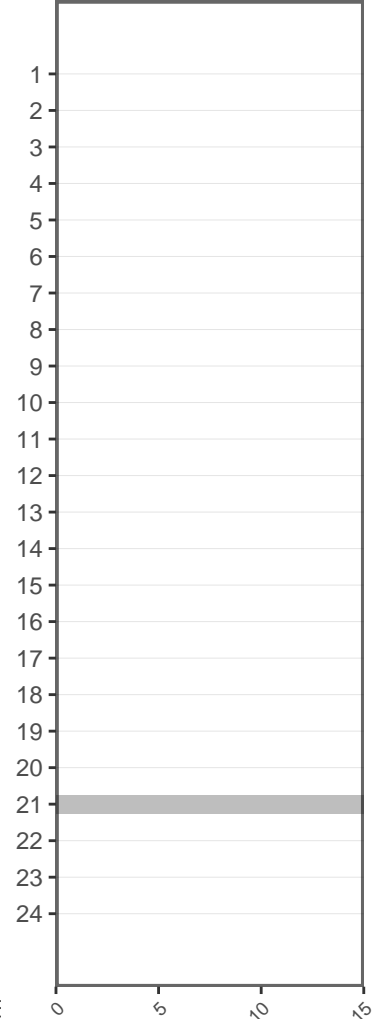
MW indication



Molecular weight

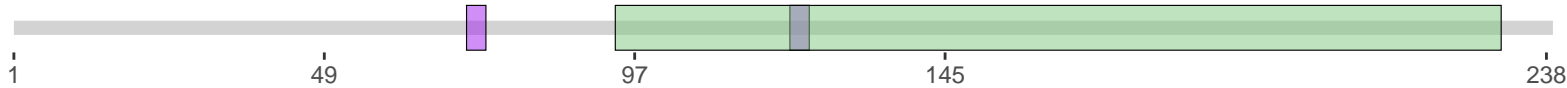


Gel Slice



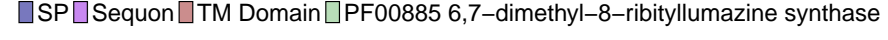
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LITKLLLEGALETFKXNSVREEDDVAWPGCFEIGVVAQQLGKSKYQALGIGAVIRGDTSHYDAVNAATSGVLSAGLNSGTPCFQVLTGDTLEQAFNRRVGGKAGNKAETALTAEMALFEHHLKV

NbL18g11320.1 uncharacterized_LOC109236326 [MW = 30.24 kDa]

No. of times detected



log(intensity)



Values from



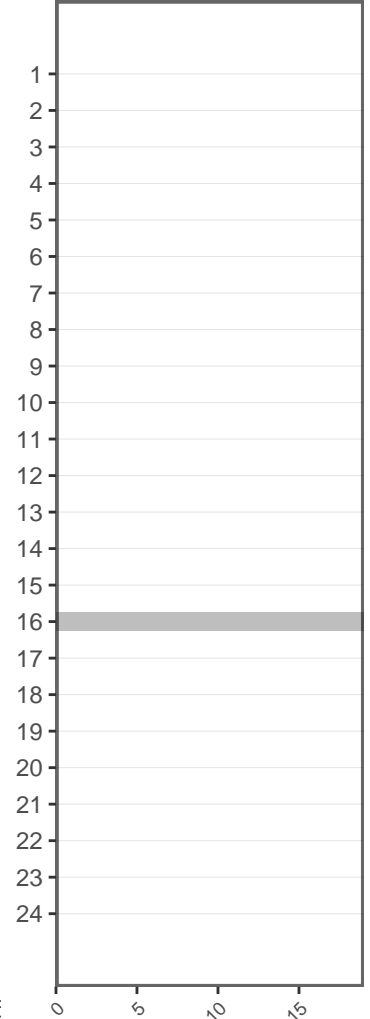
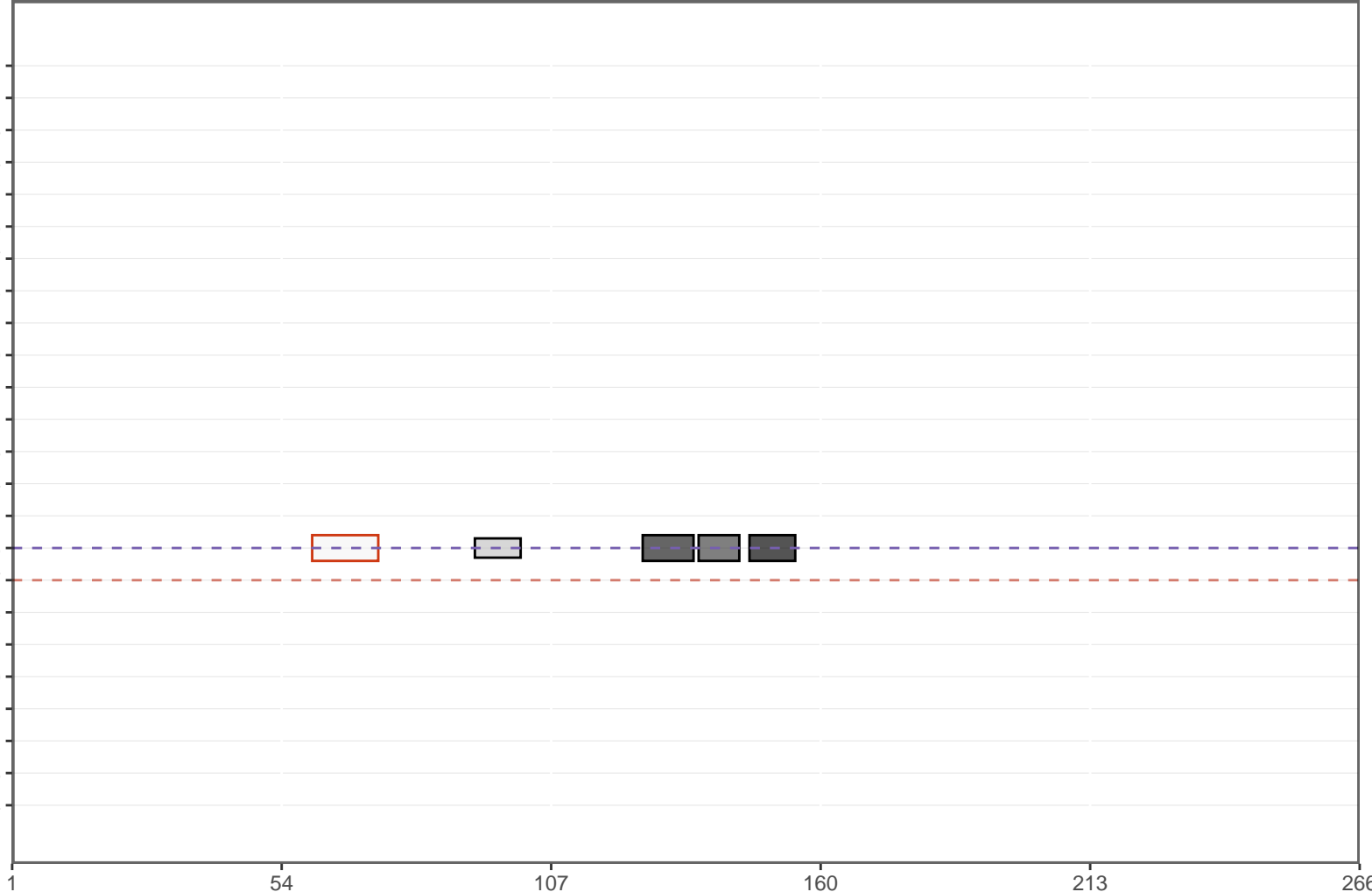
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

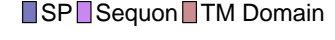
Protein length



Pfam domains



Pfam Description



Protein sequence:

LYSKVFGQVGDFTSLRENDYVFGNRKFGGNAGBTRGRWHHTFSLWDEWEMINMAYLKLPRKRAPEYRQARDHSDFCRMKDYLRGGEFINRTISTLDSHFVSTLSELELKFDCPDDEKFMPSRLLGKQEELESFESSEGNVILGSM

NbL18g11300.1 polycopene_isomerase_1_chloroplastic [MW = 61.73 kDa]

No. of times detected



log(intensity)



Values from



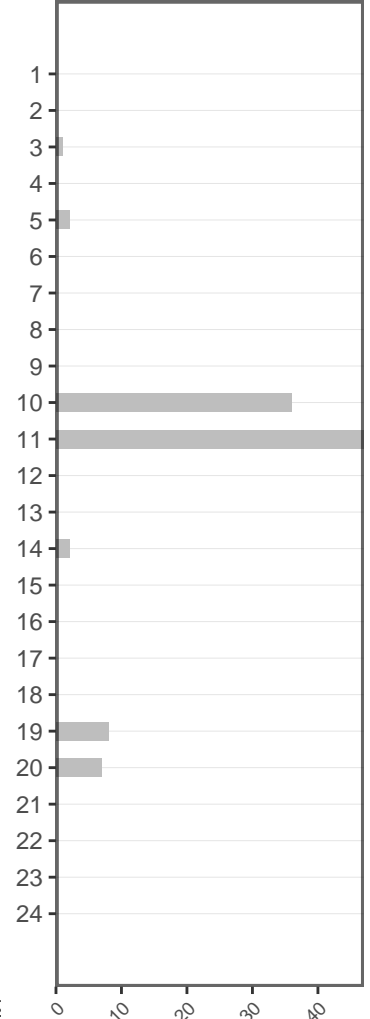
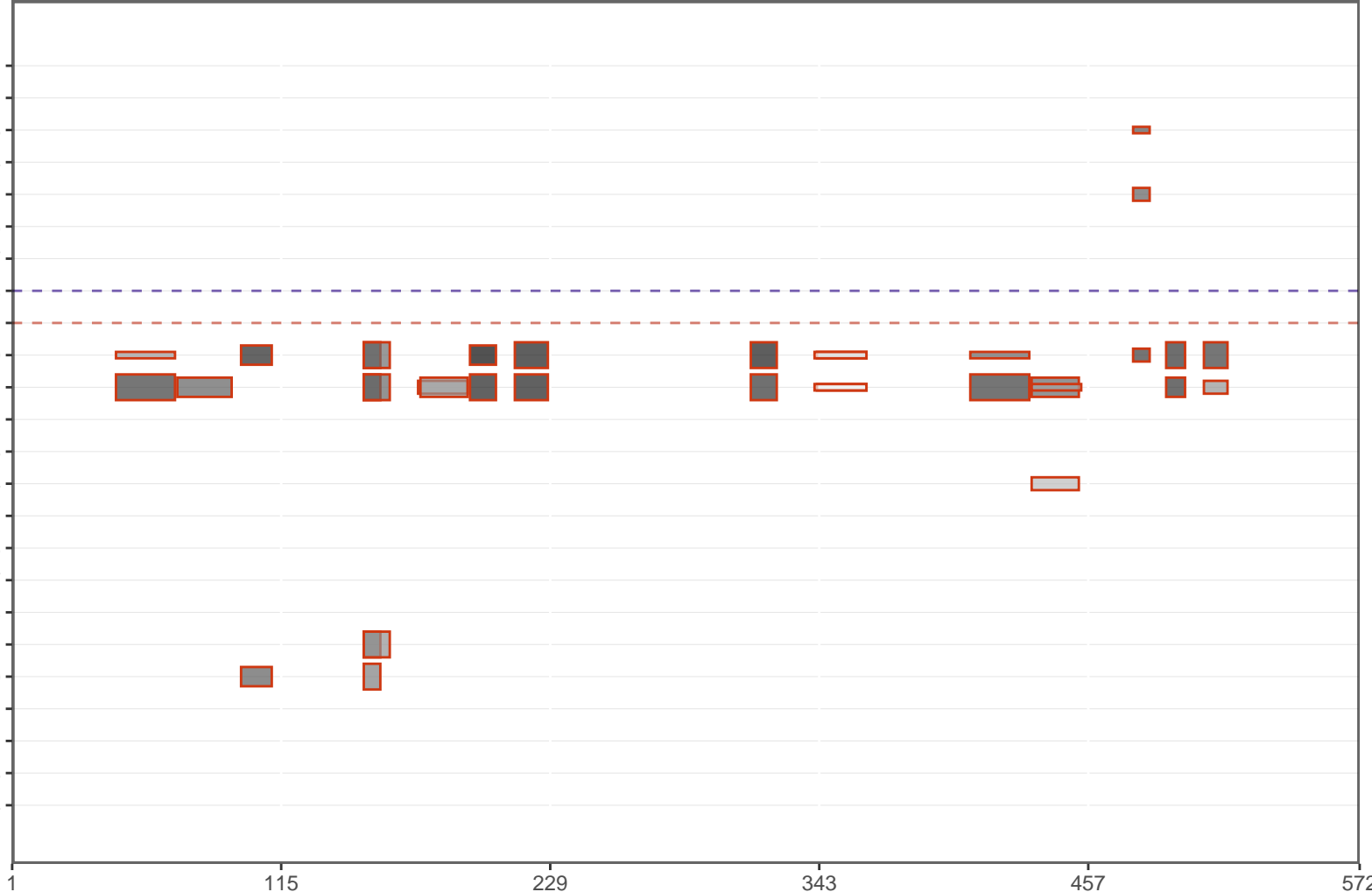
MW indication



Molecular weight

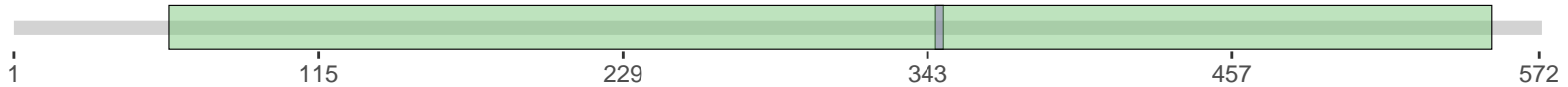


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FSEVYKPCQTLLEYPLGGGAVDALVRLGKFGGRISLKSHEVNIIVENGRVAVGKLRGGGFVRAKKAIVSNASMWDTLSLFLFVLPKSYRDNKSTPQGESFMHLHGFDAEGRDDLGHIIHVDWRDGRVDADQNVAVLSPVLSPLNAPPQKHLHAYTPGTPEFEEWEGLDLRRSNEVKNKAERSEVMMRAVEKALGPGFRNREKVEKLVGTPLTHKRFLLRNRTGYGPMLAGKGTFFGHSTPIPQLWCCGGDSTFPFGVWVAWAGGSMANSLVVAEHSLLI

NbL18g11220.1 glutathione_S-transferase_U9-like [MW = 25.5 kDa]

No. of times detected



log(intensity)



Values from



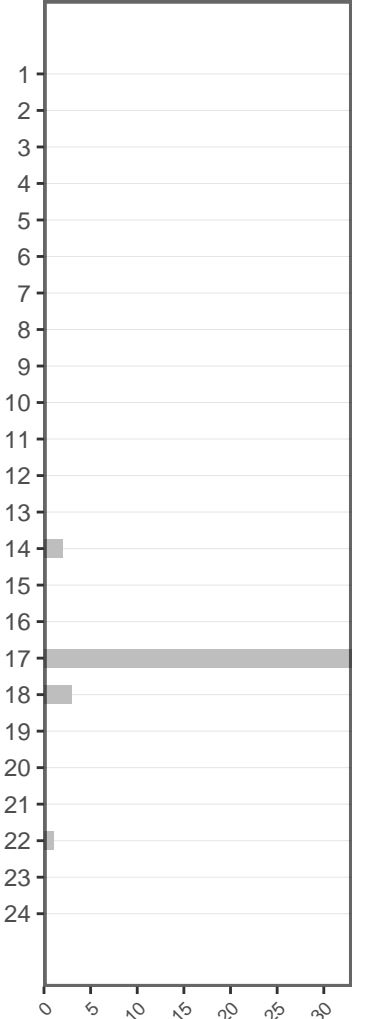
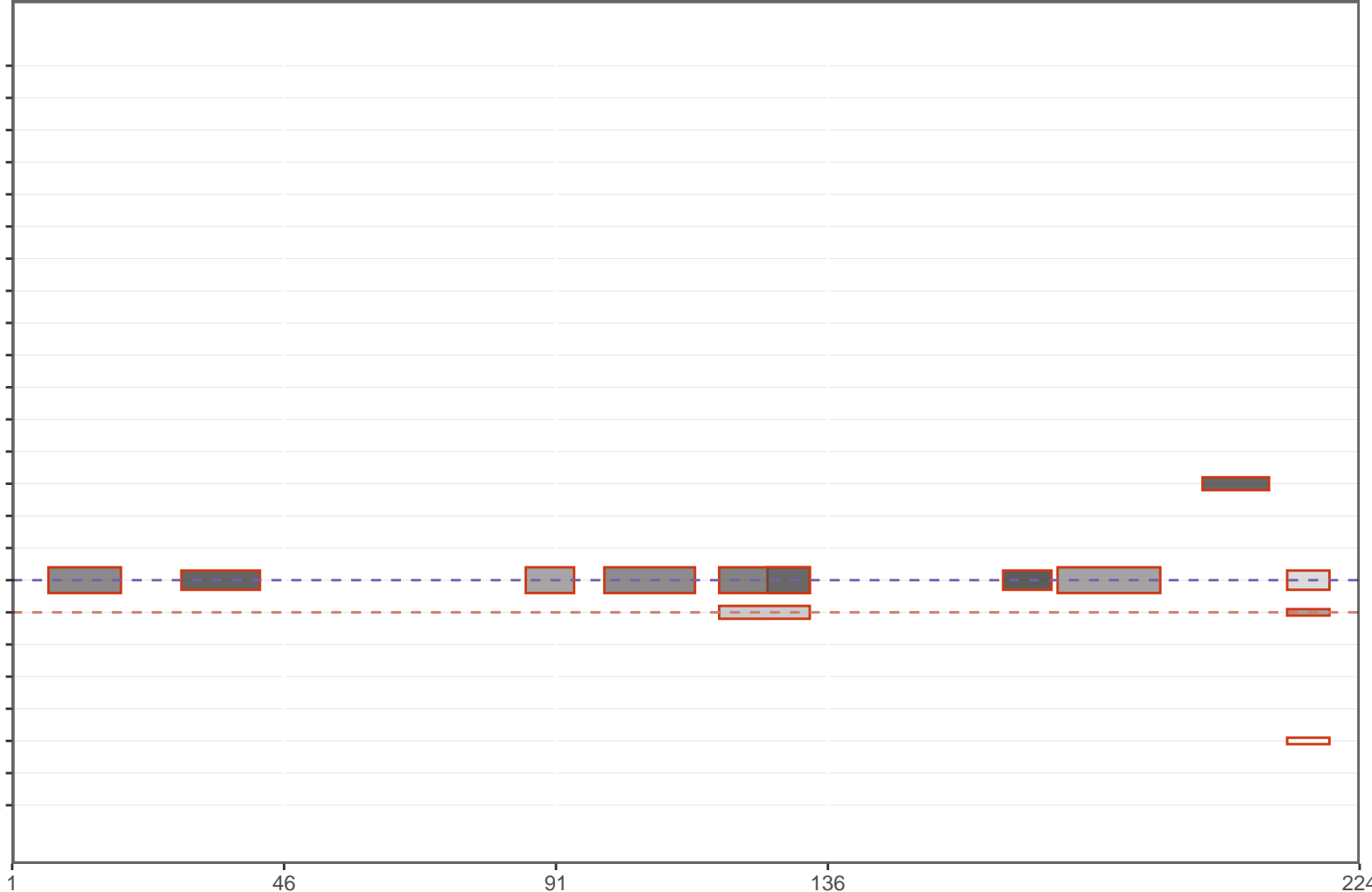
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

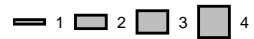


Protein sequence:

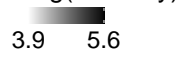
RFVANYIQHLPSTAKLWKSTGEEGEKALEEVLKIRLEKGIPEHIGNEFGLGILLVITFGSHKAYEDLVGWKILVPENNPLLSGQVTSKELPLVKEICPPYDMLLKLKIRYENALKSTHY

NbL18g11190.1 flavonol_synthase/flavanone_3-hydroxylase-like [MW = 36.18 kDa]

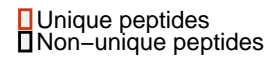
No. of times detected



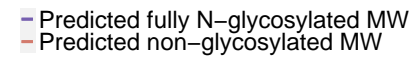
log(intensity)



Values from



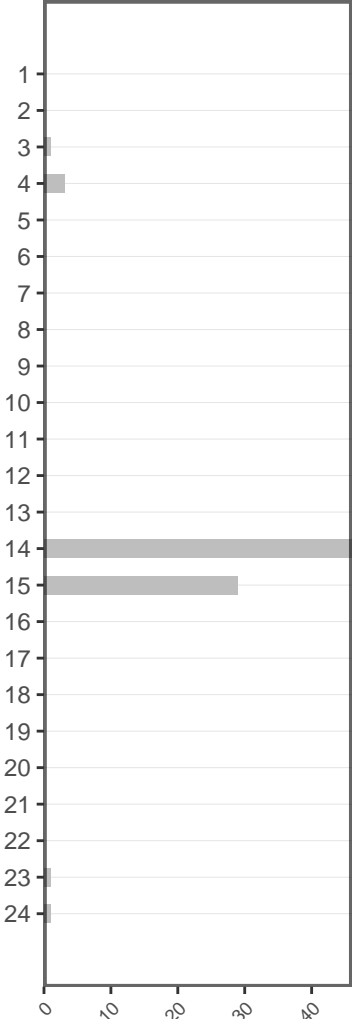
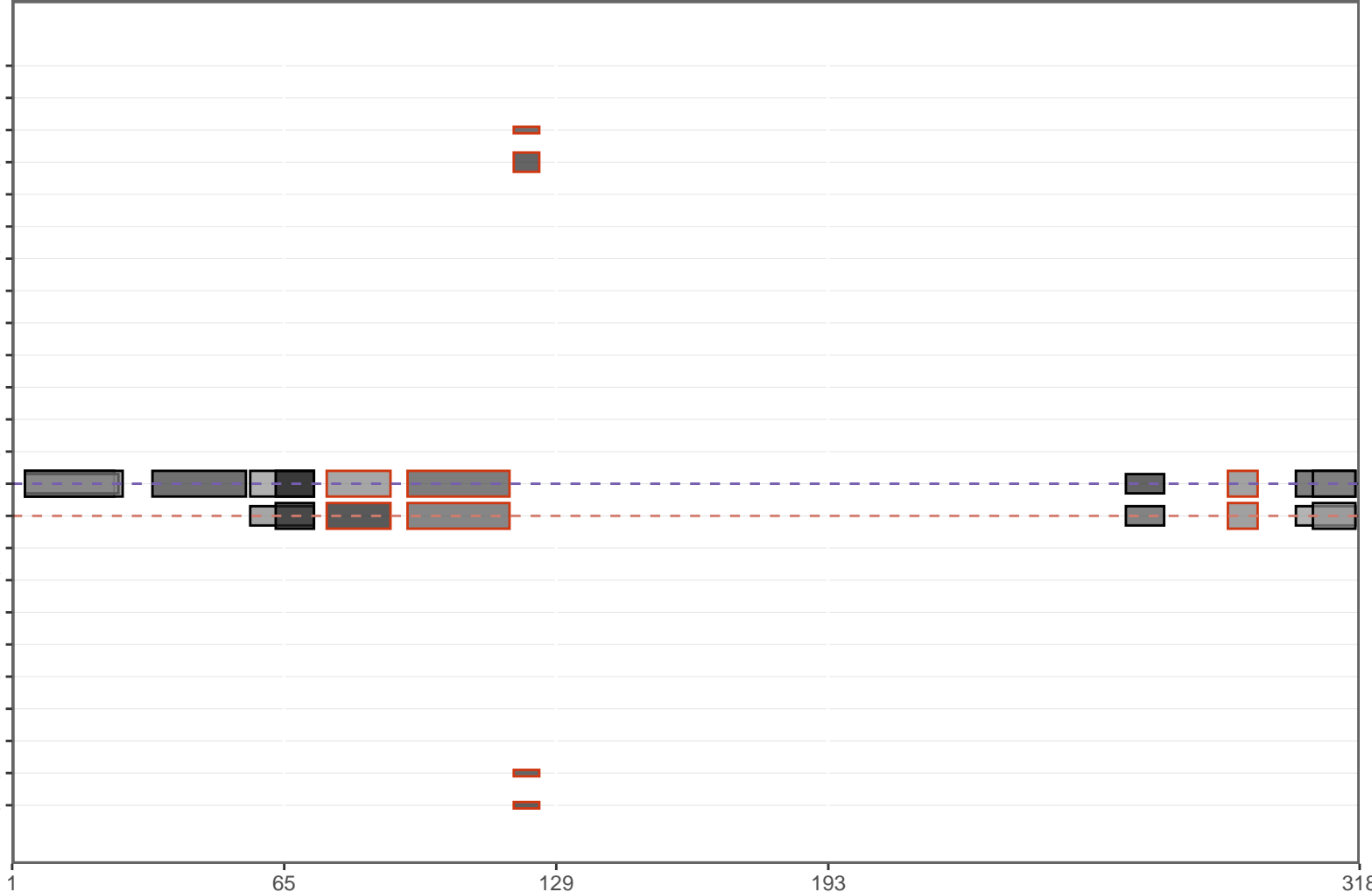
MW indication



Molecular weight

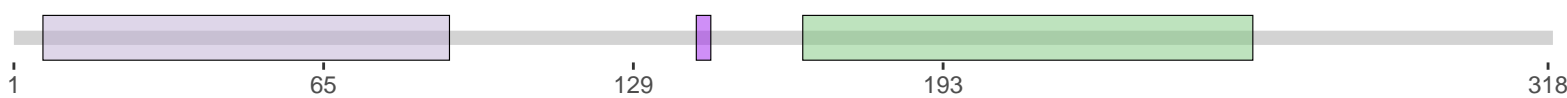


Gel Slice



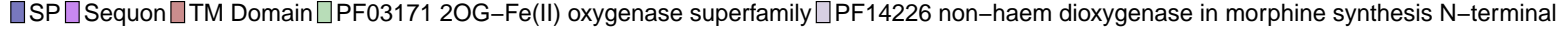
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

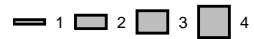


Protein sequence:

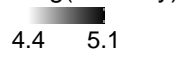
ILPPNCLKDYNDNRGADLLLSGRVFRATEMEDNGASGHDRPVVLGLFQDDAGLEVLVDGEWIPVTRIEGALVFHSDVGLVLTNDKVFSPHQVLRPKGKSRVVFVFFYNLNGEKWVEPLQDFQKEIGEPKRYRFQYKDFGAWWKEKLNRPVVRHEDKXLSLITFASATN

NbL18g11080.1 flavonol_synthase/flavanone_3-hydroxylase-like [MW = 36.12 kDa]

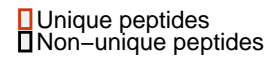
No. of times detected



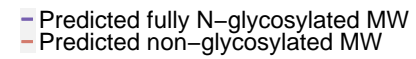
log(intensity)



Values from



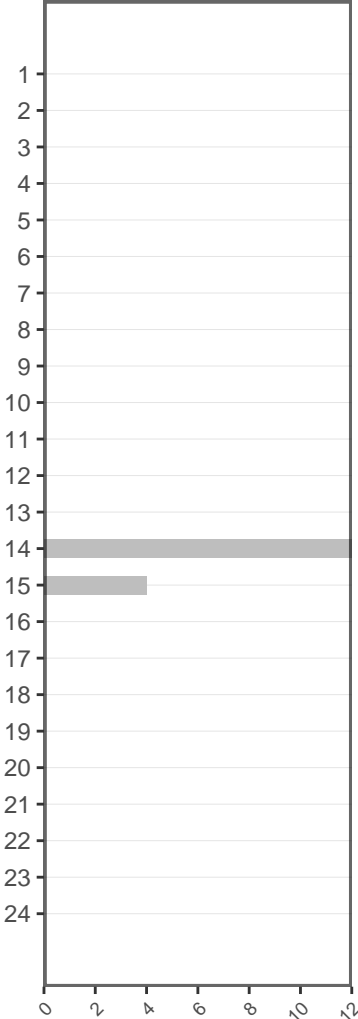
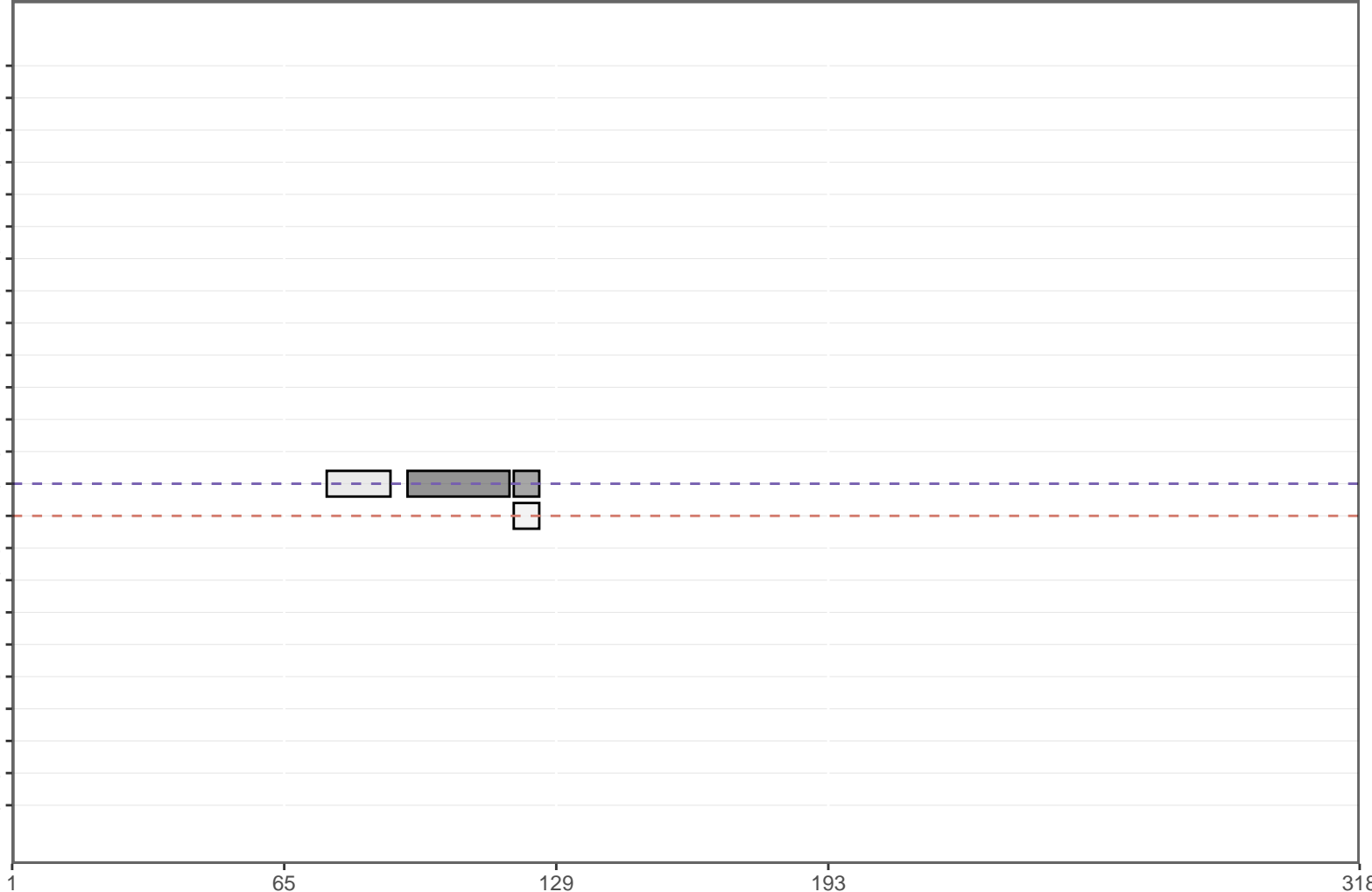
MW indication



Molecular weight

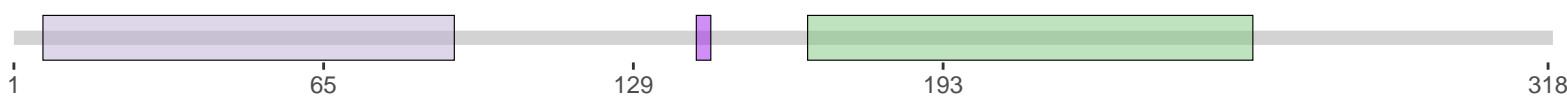


Gel Slice



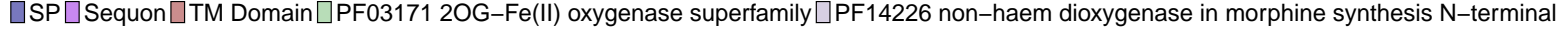
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GLPPNCLQDYNDRDADLLSGRYFPTMEMEDNGANSHGDPVAVLGLFQDDAGGLEVLIDGEWIPVTPTEGALVPHQDMLQVLTNDFVSPFHQVLRPKGKSRVVFVFFYNLNGEKWVEPLPDFQSKKEGPPKRYKFKQYKDFGVIRVKEKLNPPARHEDKTSLITFASATN

NbL18g10900.1 uncharacterized_LOC107799956 [MW = 31.48 kDa]

No. of times detected



log(intensity)



Values from



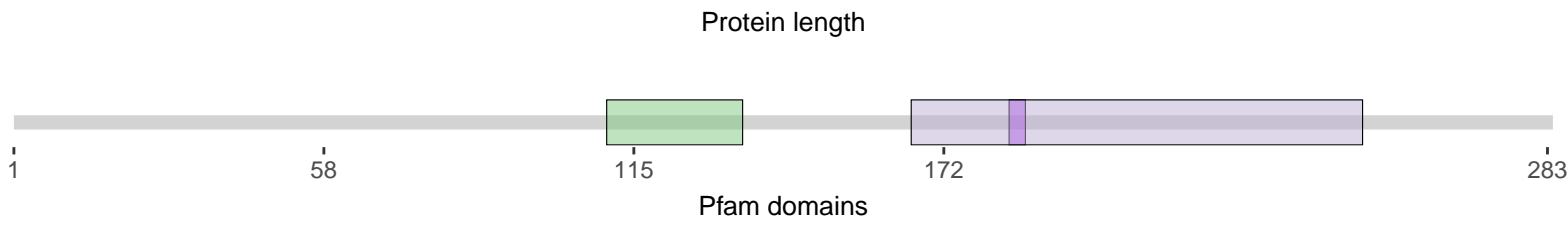
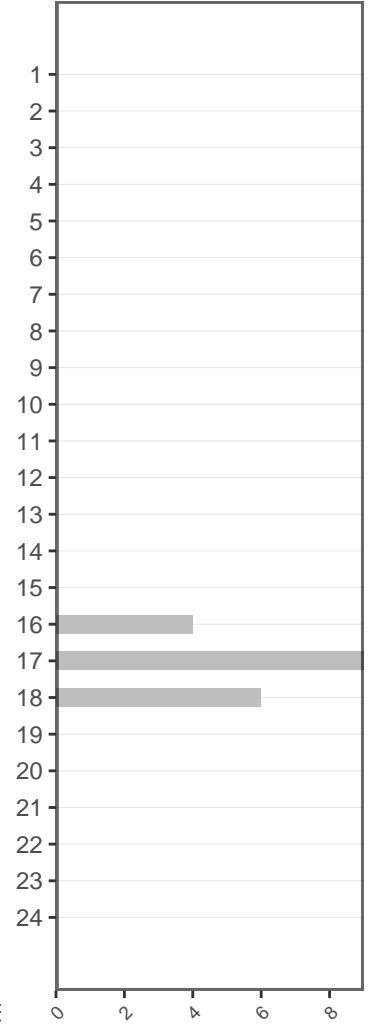
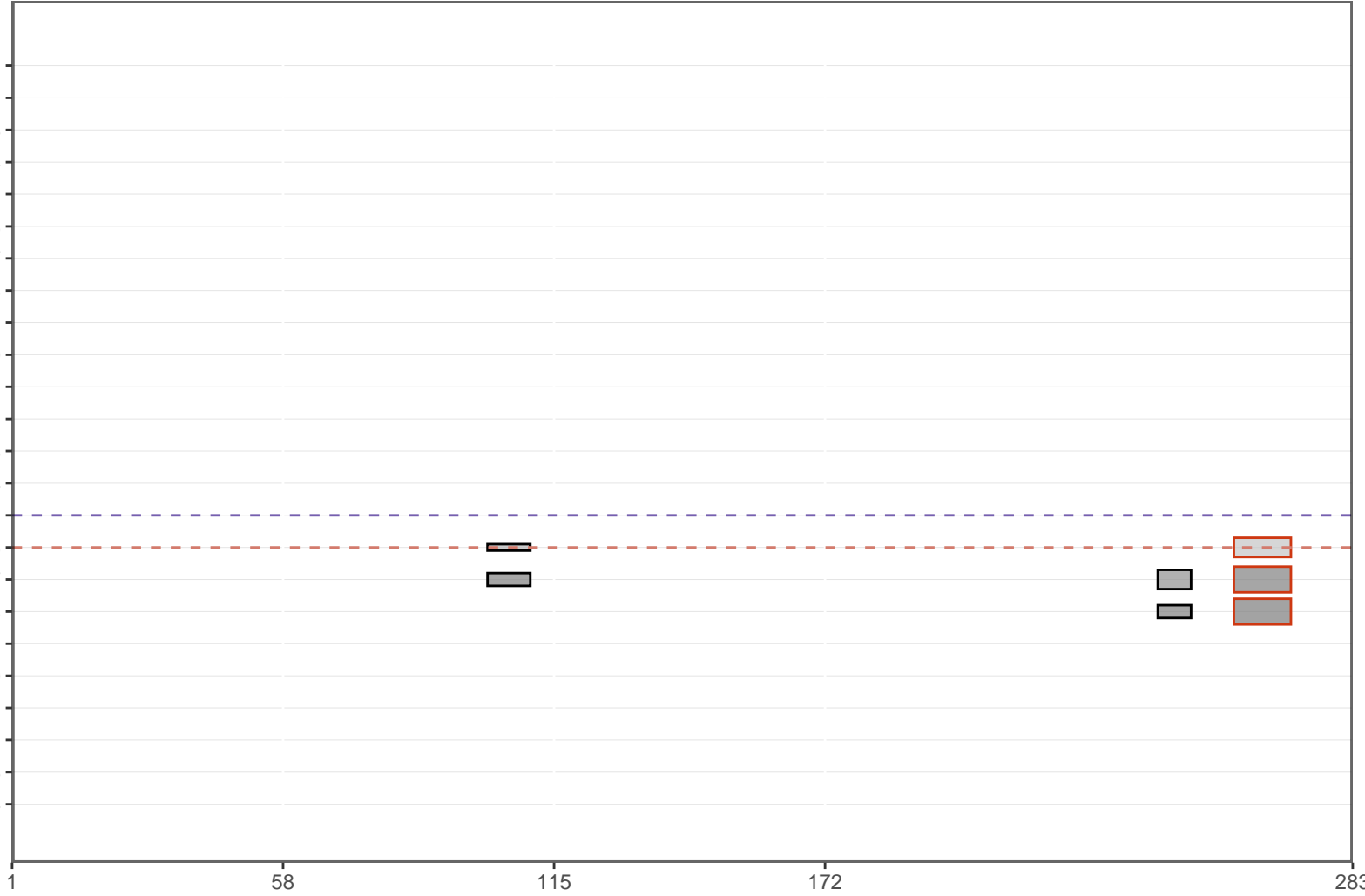
MW indication



Molecular weight



Gel Slice



Pfam Description
 ■ SP ■ Sequon ■ TM Domain ■ PF02151 UvrB/uvrC motif ■ PF04379 ApaG domain

Protein sequence:

AAARYRDELKDVAPHLLKSGSDATLGIKRVQVRVYIEGRSHPKGLYFFAYRIRITNEDRPPVQLLRARHWITDANGKTNVWGGVIGEQPILPNTGFEYSAGPLGTPNGRMEGGDFEMKHDKVSRRTFNVAIAPFSLKLVGGSDGDTFSDGQ

NbL18g10890.1 60S_ribosomal_protein_L44 [MW = 12 kDa]

No. of times detected



log(intensity)



Values from



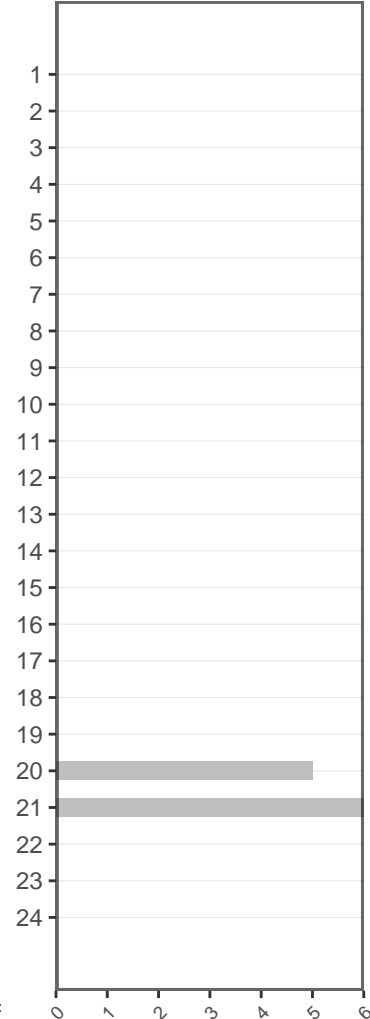
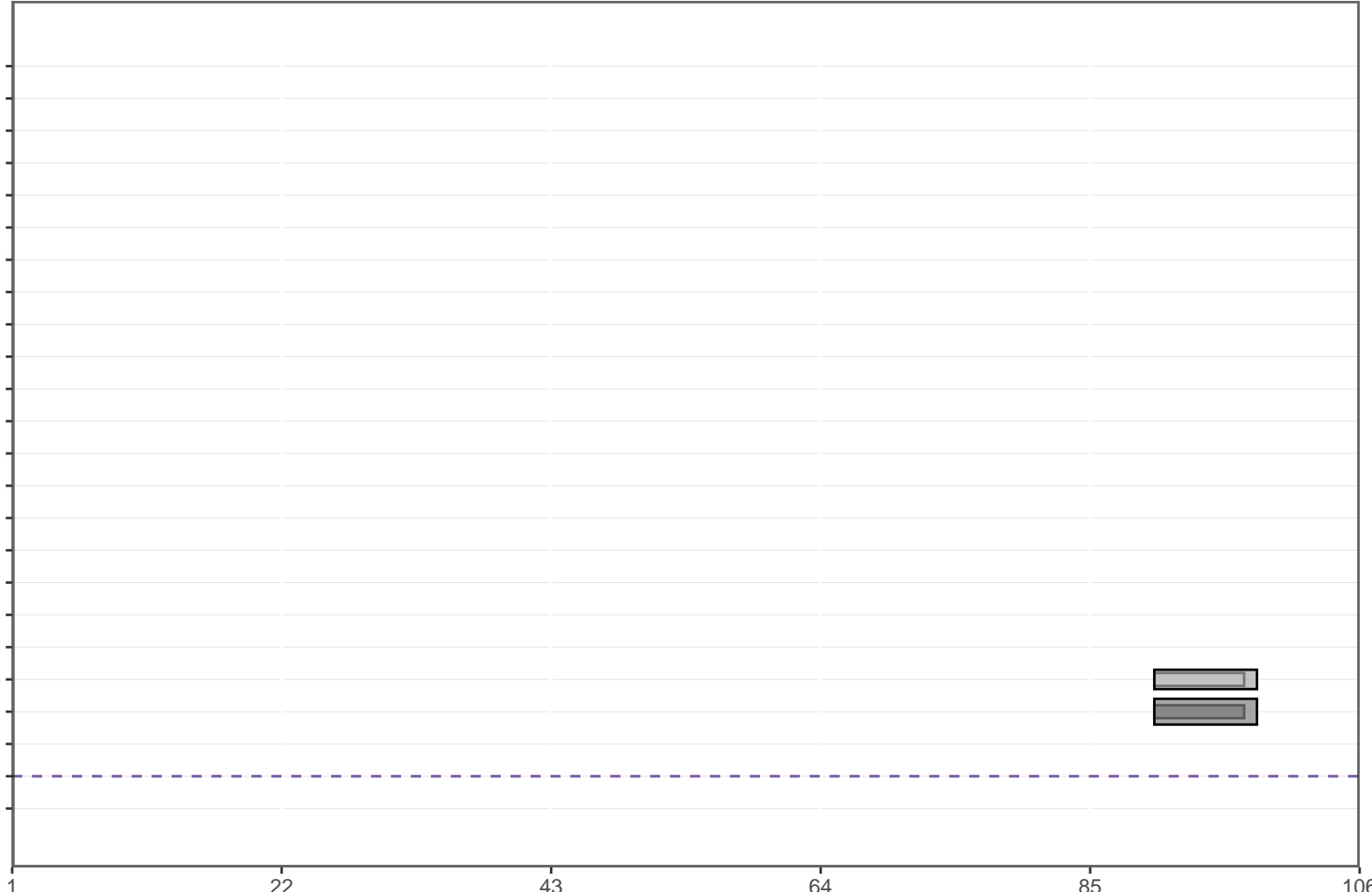
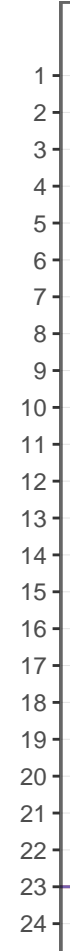
MW indication



Molecular weight



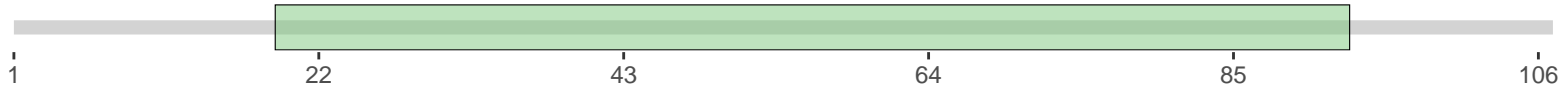
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

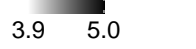
RRYDRKQSGSYGGGTRKPVFHKAKTKKIVLRGGGGGKHVSGHPKPKGHFEIGGDKKGGKGTSLF

NbL18g10730.1 indole-3-glycerol_phosphate_synthase_chloroplastic-like [MW = 45.02 kDa]

No. of times detected



log(intensity)



Values from



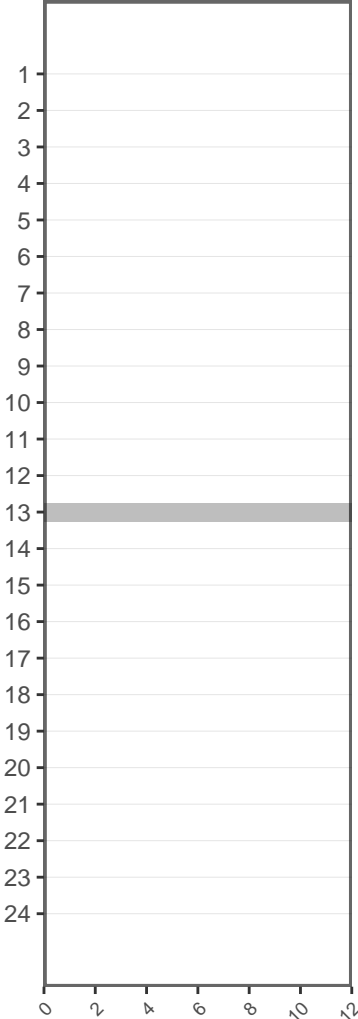
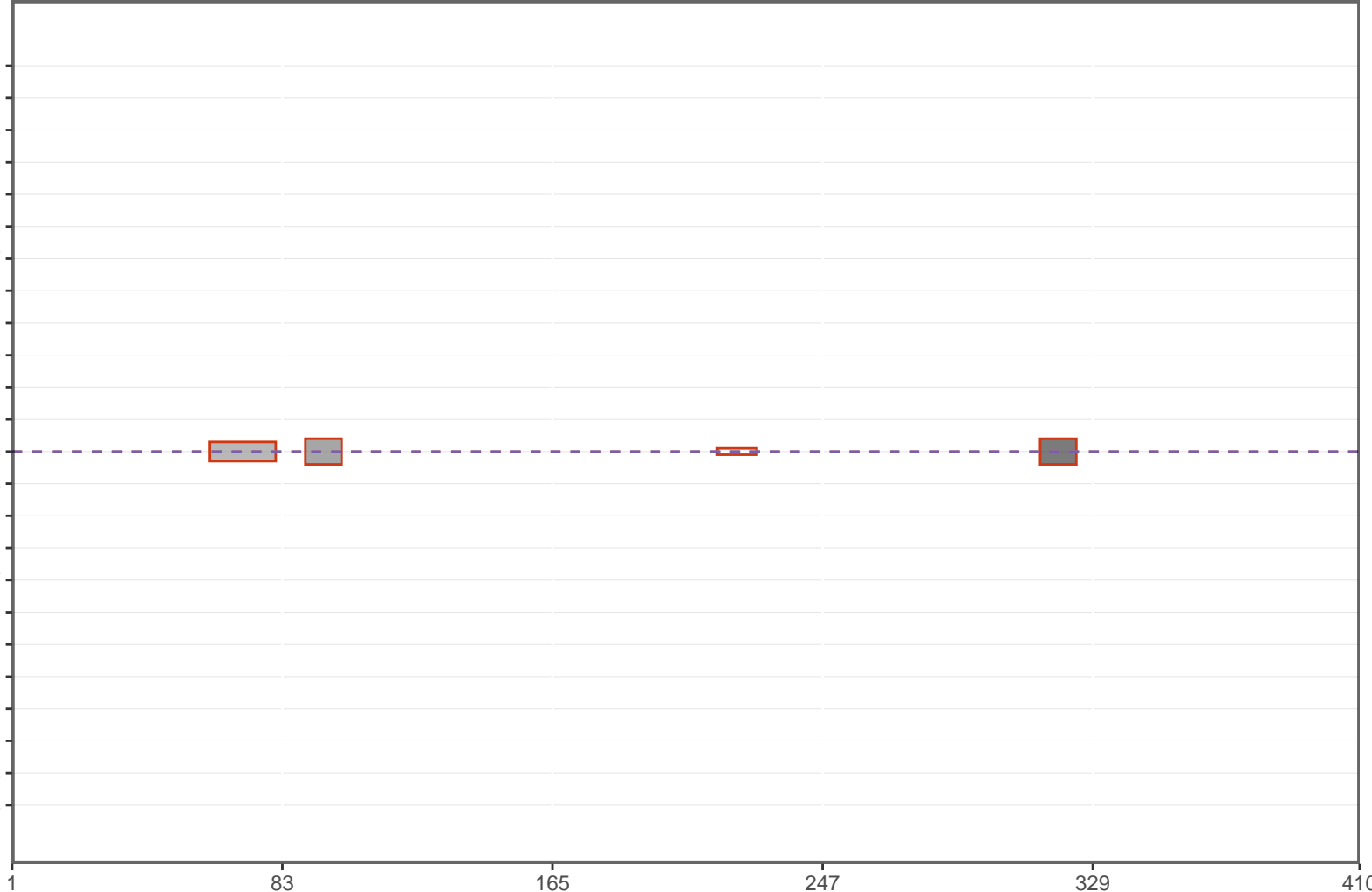
MW indication



Molecular weight

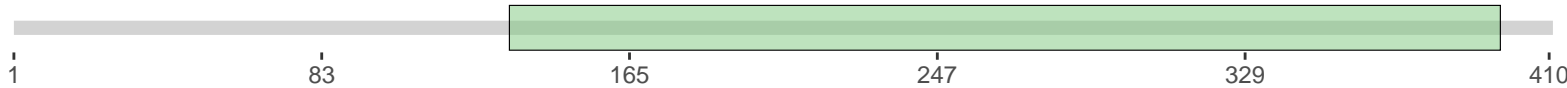


Gel Slice



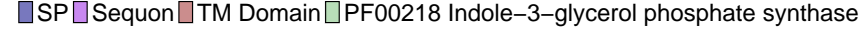
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KASPGRGVLREDFNPVMAKAVEKGGAGLGLVLTDEKYFGQSFENLEARNAGVECPLLGKEFVDAWGGYFARIRKADAVLLAAVLPFLDIMVYTRKIKLGLTALVEVHDEREMDRVLRIDGIELGNNRDLGTFKVDENTKLNLEGERGKRHKEGIVVGSGLFTPDWVYQEAAGVAAVLGSESLKQKDKPKGIRLFGKDKDSCGSPS

NbL18g10720.1 31_kDa_ribonucleoprotein_chloroplastic [MW = 34.51 kDa]

No. of times detected



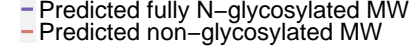
log(intensity)



Values from



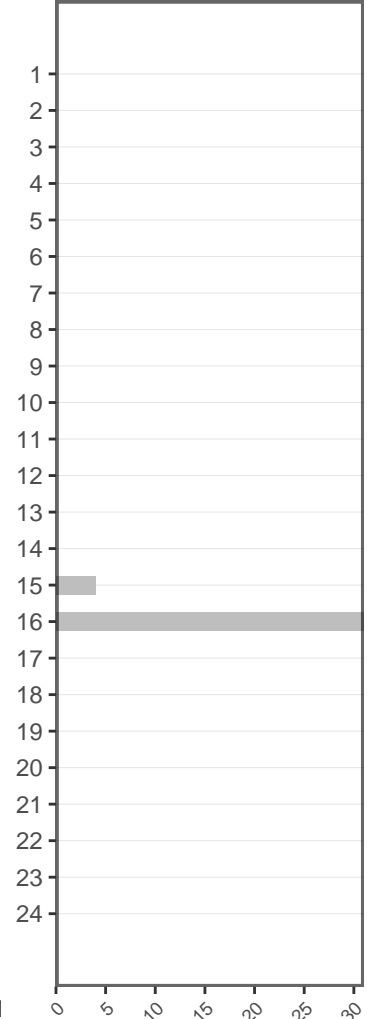
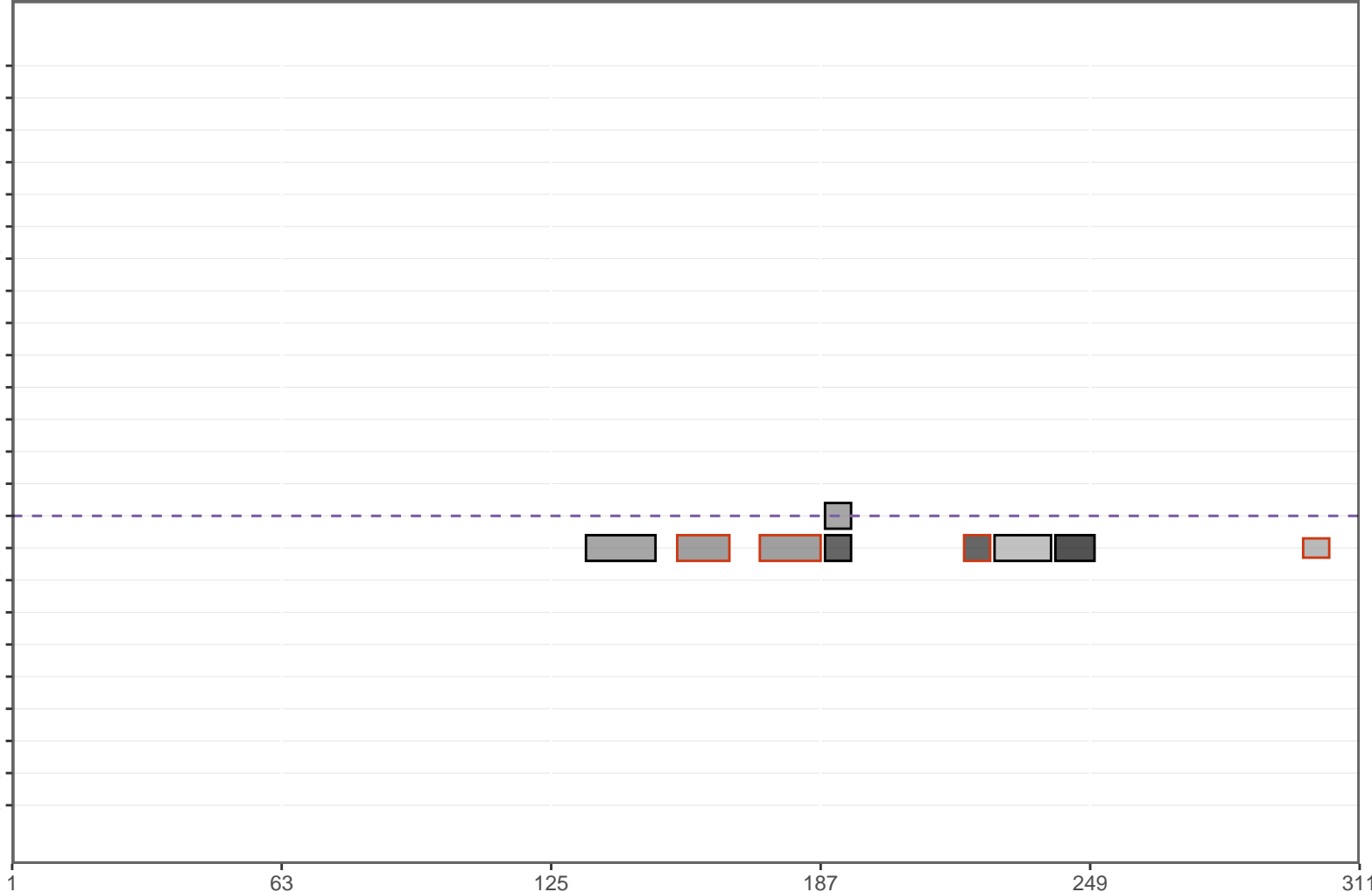
MW indication



Molecular weight

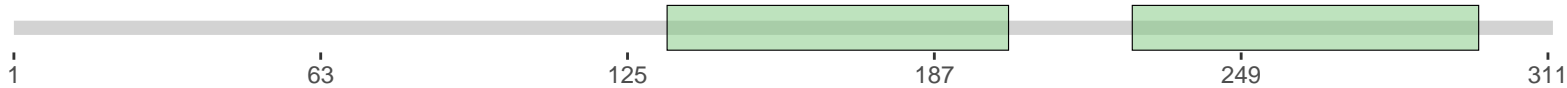


Gel Slice



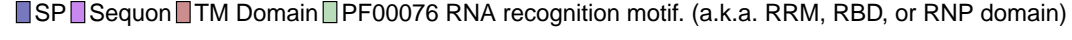
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

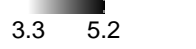
GLARLFKAGVVEAEVWNRDIDGSRGFGVVTMTVEAEKAVEMVNRVQVNGRLLTWNKARRGERPERPPRTFEGSYRIVYVGNIPWGIIDARLEQLFSEHGKVVBARVYYDRETGRSRGFGVVTMASEAEMSDAIAIADGSLDGRTRVWVAEDRGRARNTF

NbL18g10610.1 adenylate_kinase_4-like [MW = 26.74 kDa]

No. of times detected



log(intensity)



Values from



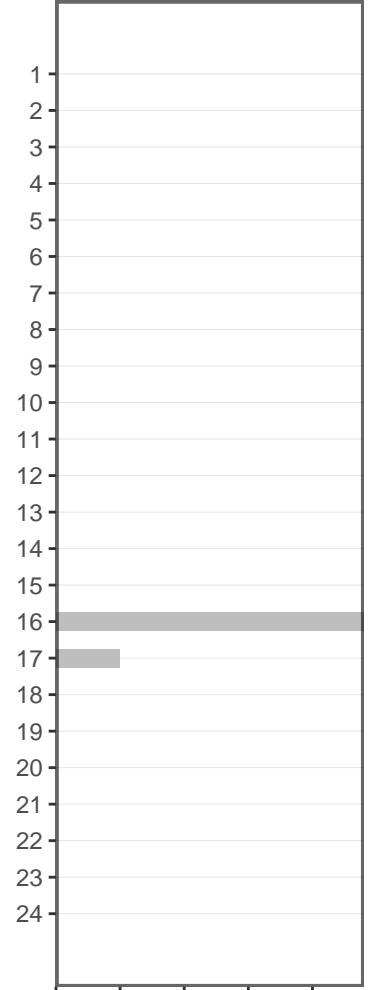
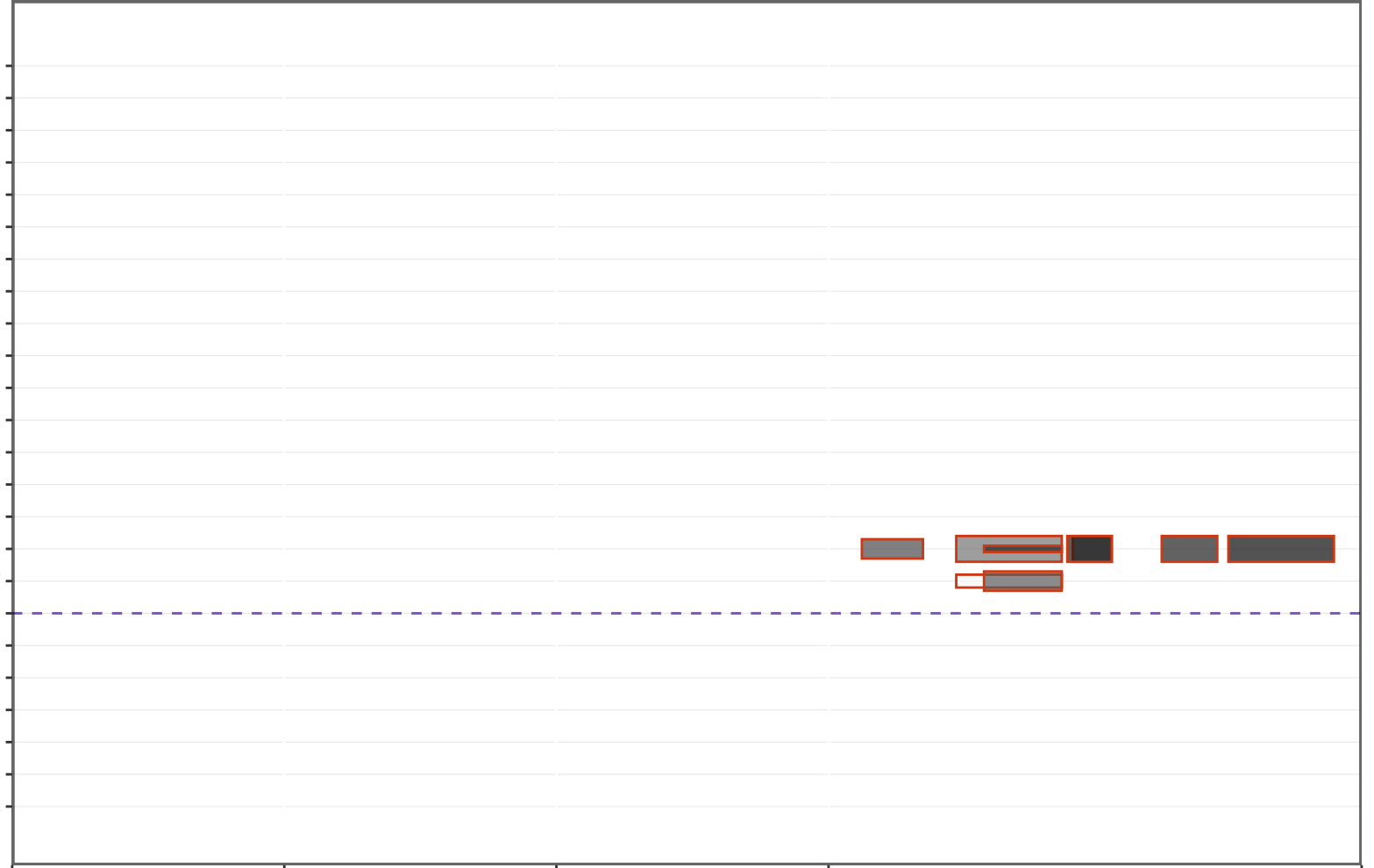
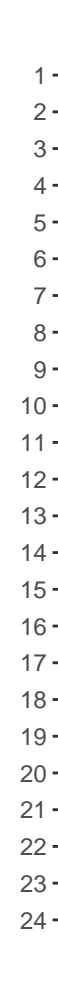
MW indication



Molecular weight



Gel Slice

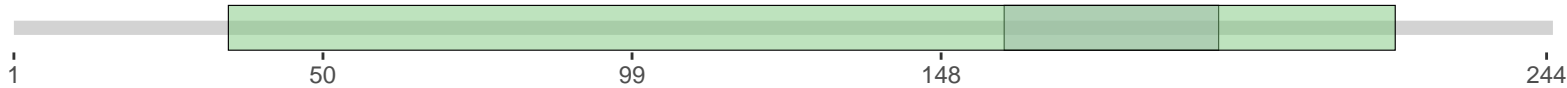


Peptide counts over 4 repeats

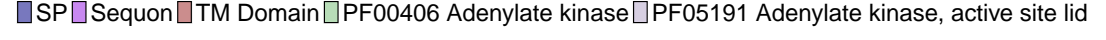
Protein length



Pfam domains



Pfam Description



Protein sequence:

KGFLDGFPRTYVQAEKLEDEMLGNRGTWKVKNLNFADDALEERITGLWIHPASGRSYHTKFAPKVYVPGEDDITGEPLIGRKDDTAVFKSALESFHRDTEPVDYVYKKNMVMVNLPAEKPRGTVTSEVKKALS*

NbL18g10590.1 uncharacterized_LOC107817829 [MW = 10.95 kDa]

No. of times detected



log(intensity)



Values from



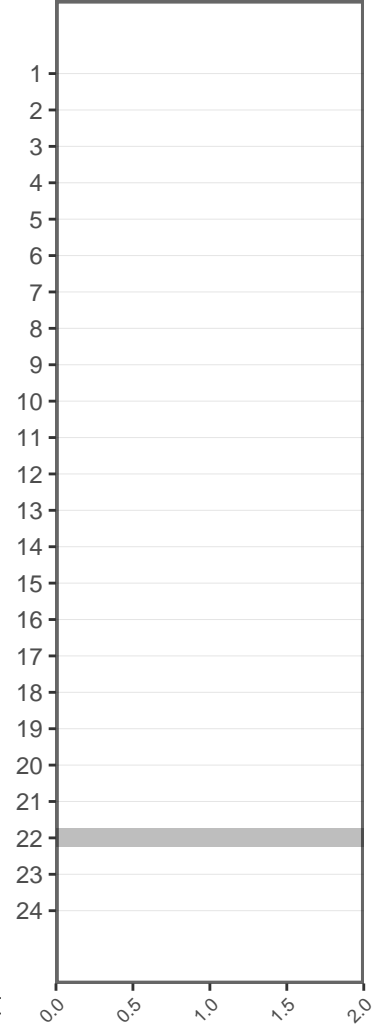
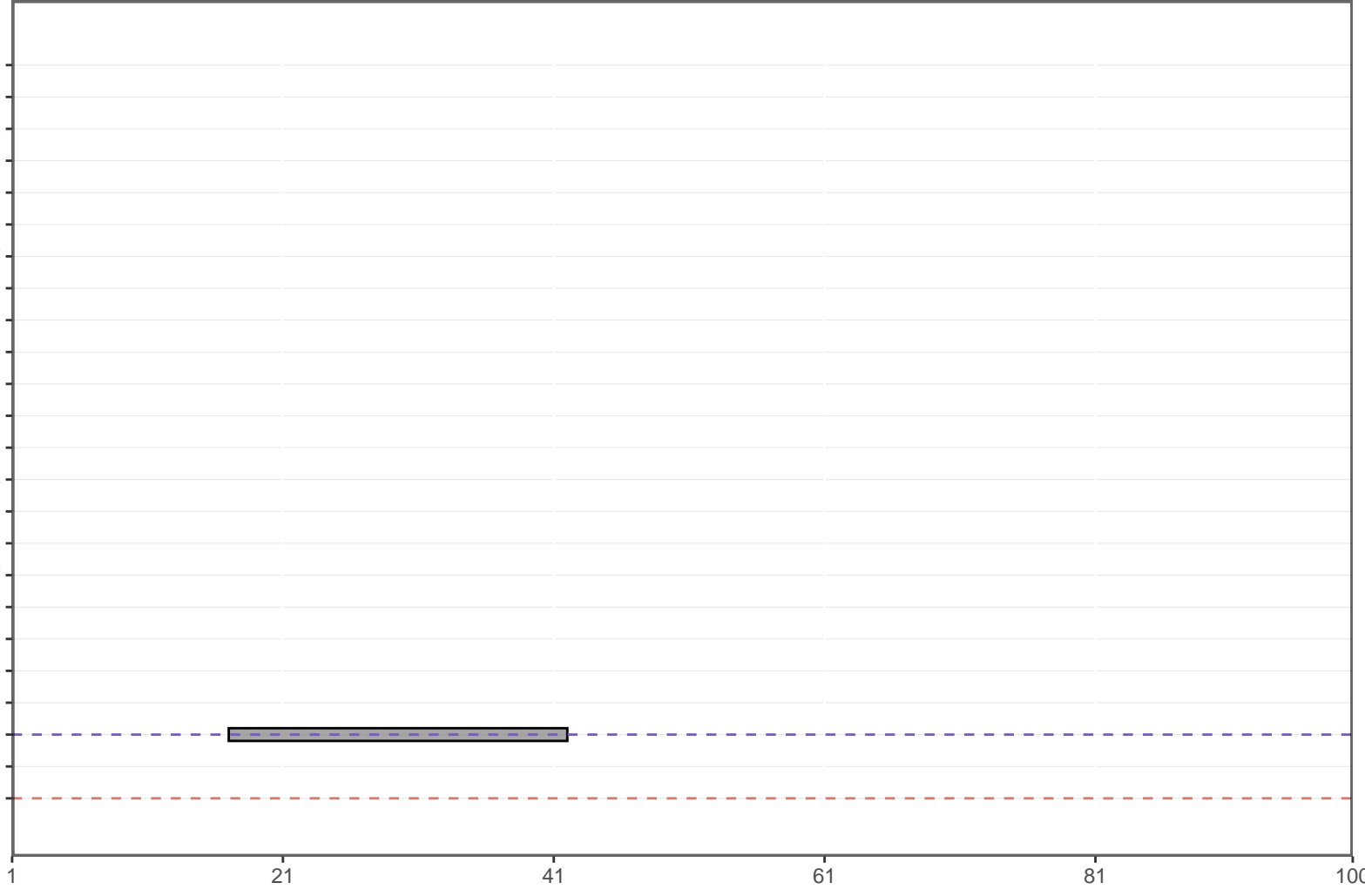
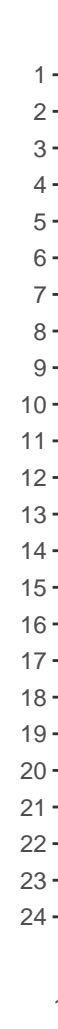
MW indication



Molecular weight

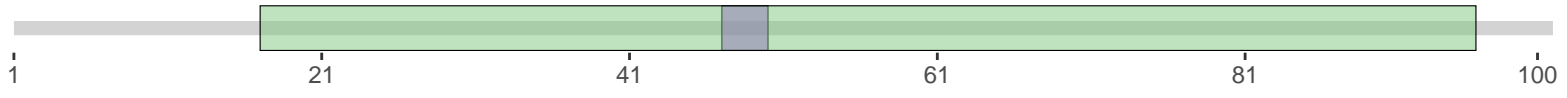


Gel Slice



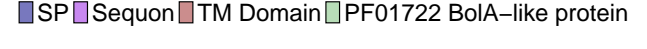
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SHAAVKEGGTNETHFNNKIVSKFDGGLVKKRHRMVEELSDLELGGHLSIAKTPKEAGM*

NbL18g10550.1 pyruvate_dehydrogenase_E1_component_subunit_beta-1_mitochondrial-like [MW = 40.55 kDa]

No. of times detected



log(intensity)



Values from



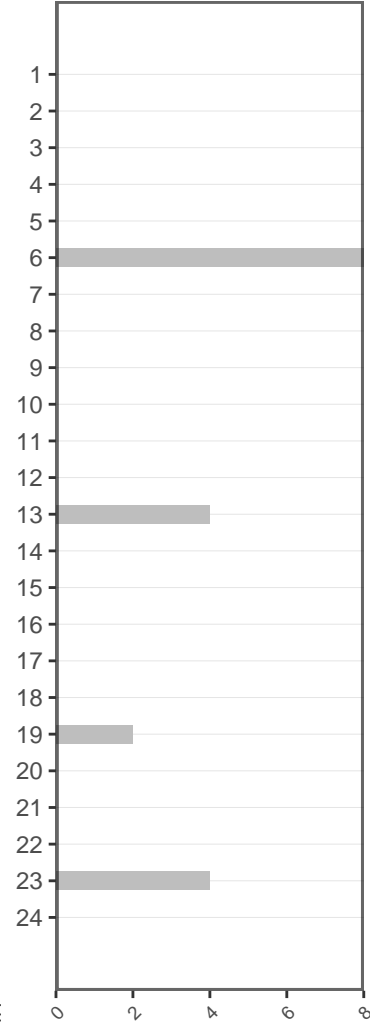
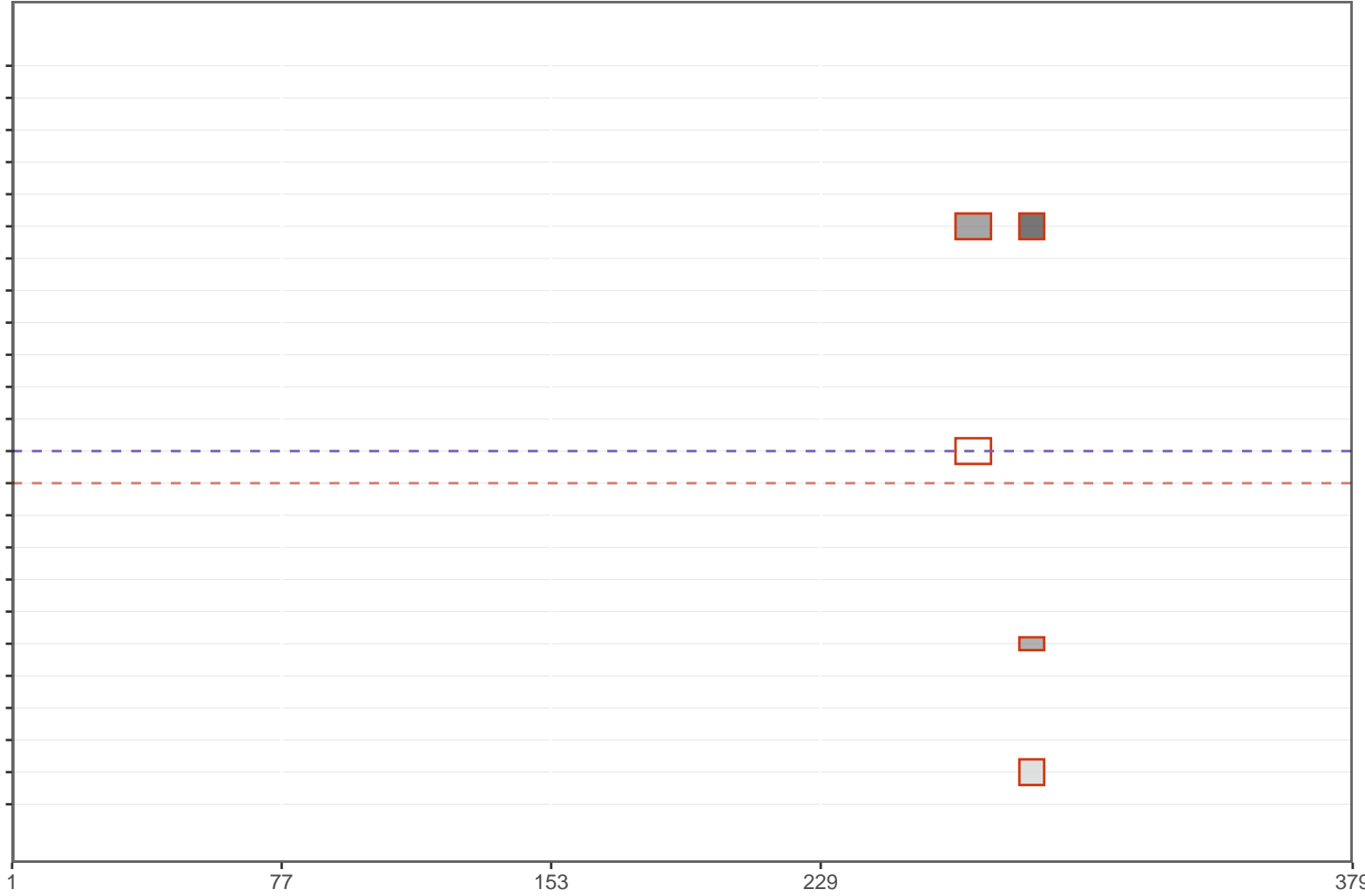
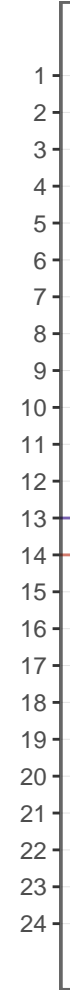
MW indication



Molecular weight

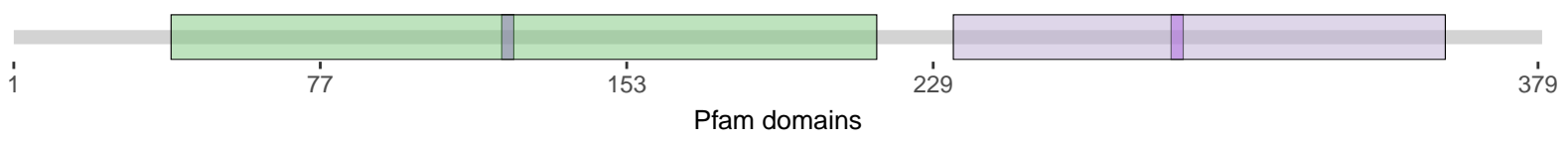


Gel Slice



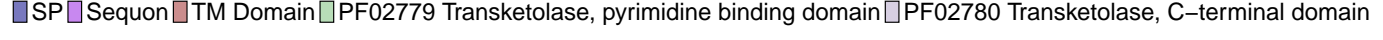
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ICPLGLKYLAPYSSESDARGLLKAARDPDPVVFLENELLYGESFPVSAEALDSSFLPFGKAKIELEGKDVTTITAFSKMVGSAKAAEILAKEGISAEEVNLRRIRPLDRSTNAEVRNTRNLRTVTEEGFPQHGVAEIGASVVEESFEVLDAPVERISGADVMPMPYANLERMAVPGVEDVRAAKRADYRSAGKSKVPMATV

NbL18g10400.1 protein_IQ-DOMAIN_14-like [MW = 54.31 kDa]

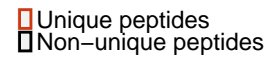
No. of times detected



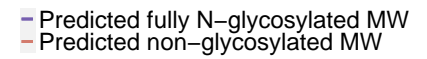
log(intensity)



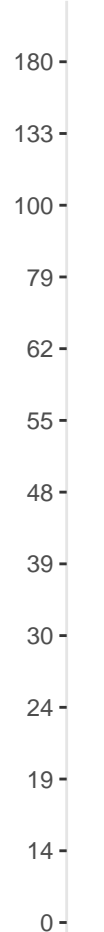
Values from



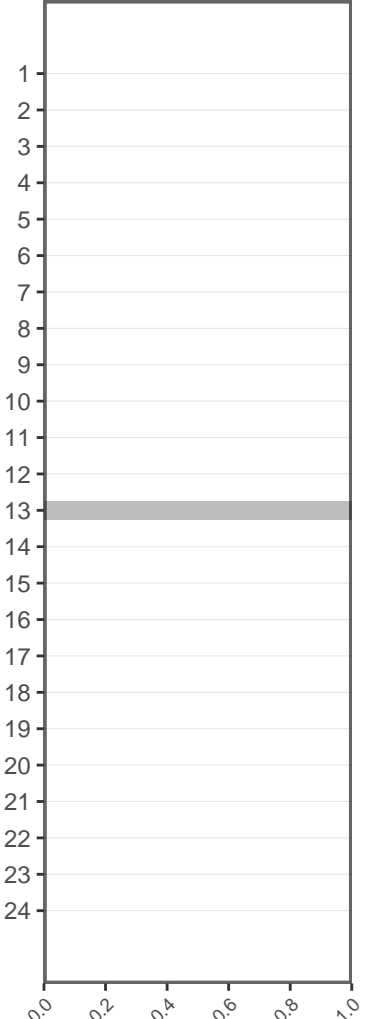
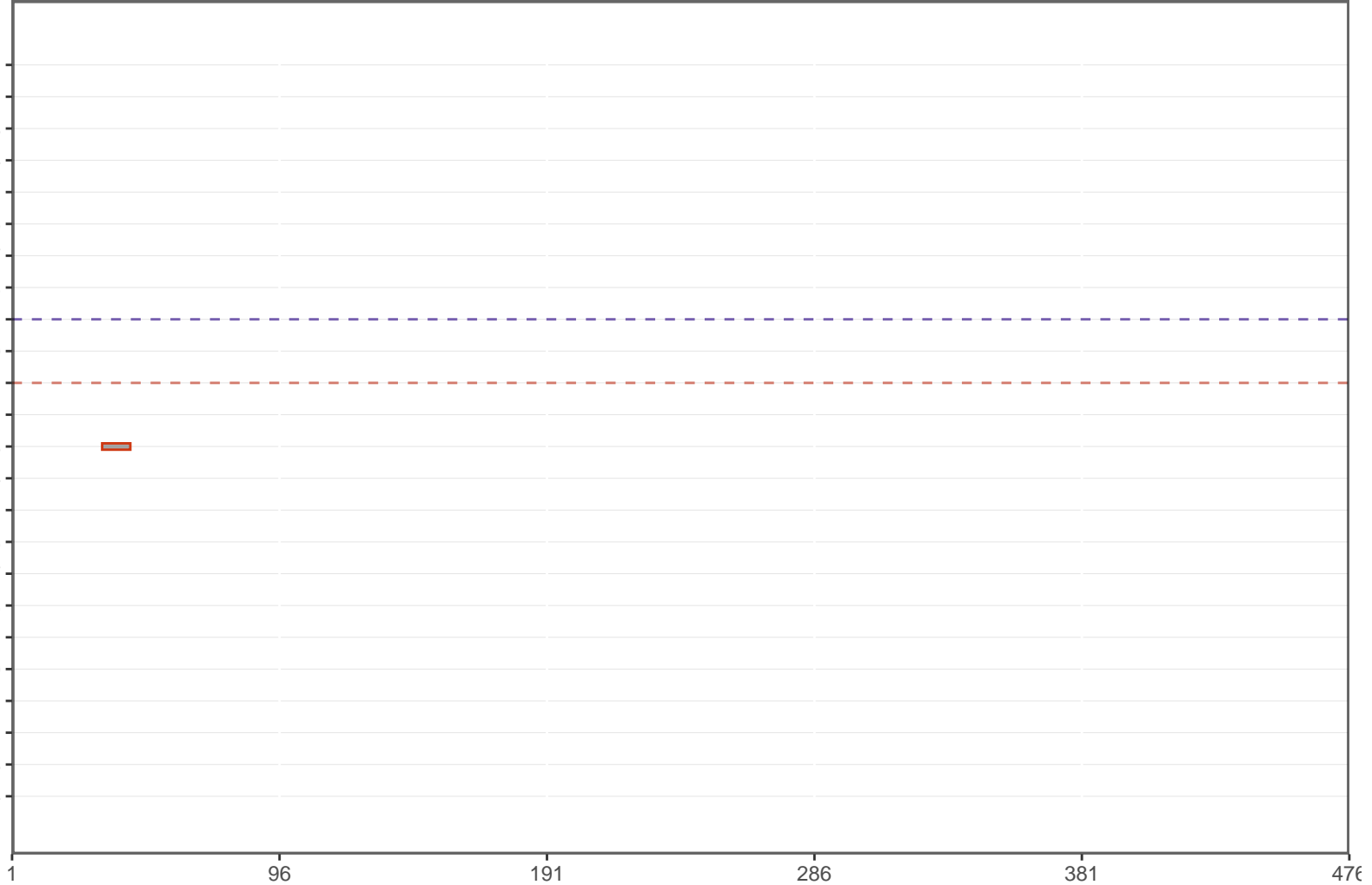
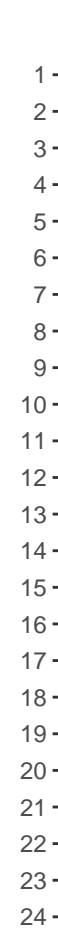
MW indication



Molecular weight



Gel Slice



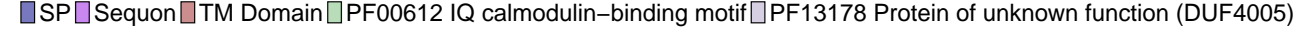
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MSHALEKVEALLQKAKEAAGRENTLFAFHSKMMWTKNEDTSSVKELDENMRVYFHRDGRNGRTLSRASDQPRDCKNEVDTAGVSDSDYDFWRLRNGFYQDKQKILGSAVPSPLRNGVQGNLTHSAFTPTSKMKNLVHSASPRDRREERSHRMTLLSRKANEPNMTTASAKARERSHSAPRRMLTPPEREKTSAAANKRLSFPQGTGNETVTSDDGPLDHLRLVSPGWKVEVTEPRDHY

NbL18g10370.1 uncharacterized_LOC104217540 [MW – SP = 68.67 kDa]

No. of times detected



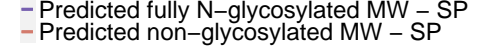
log(intensity)



Values from

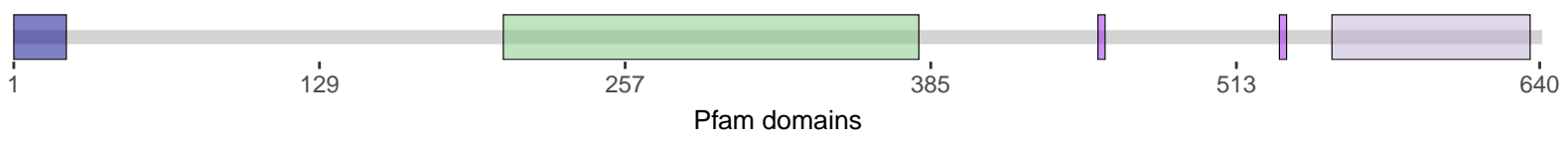
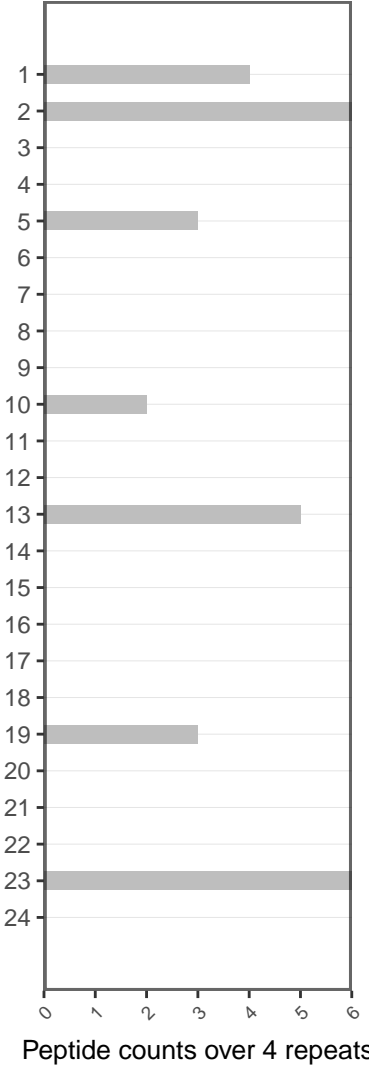
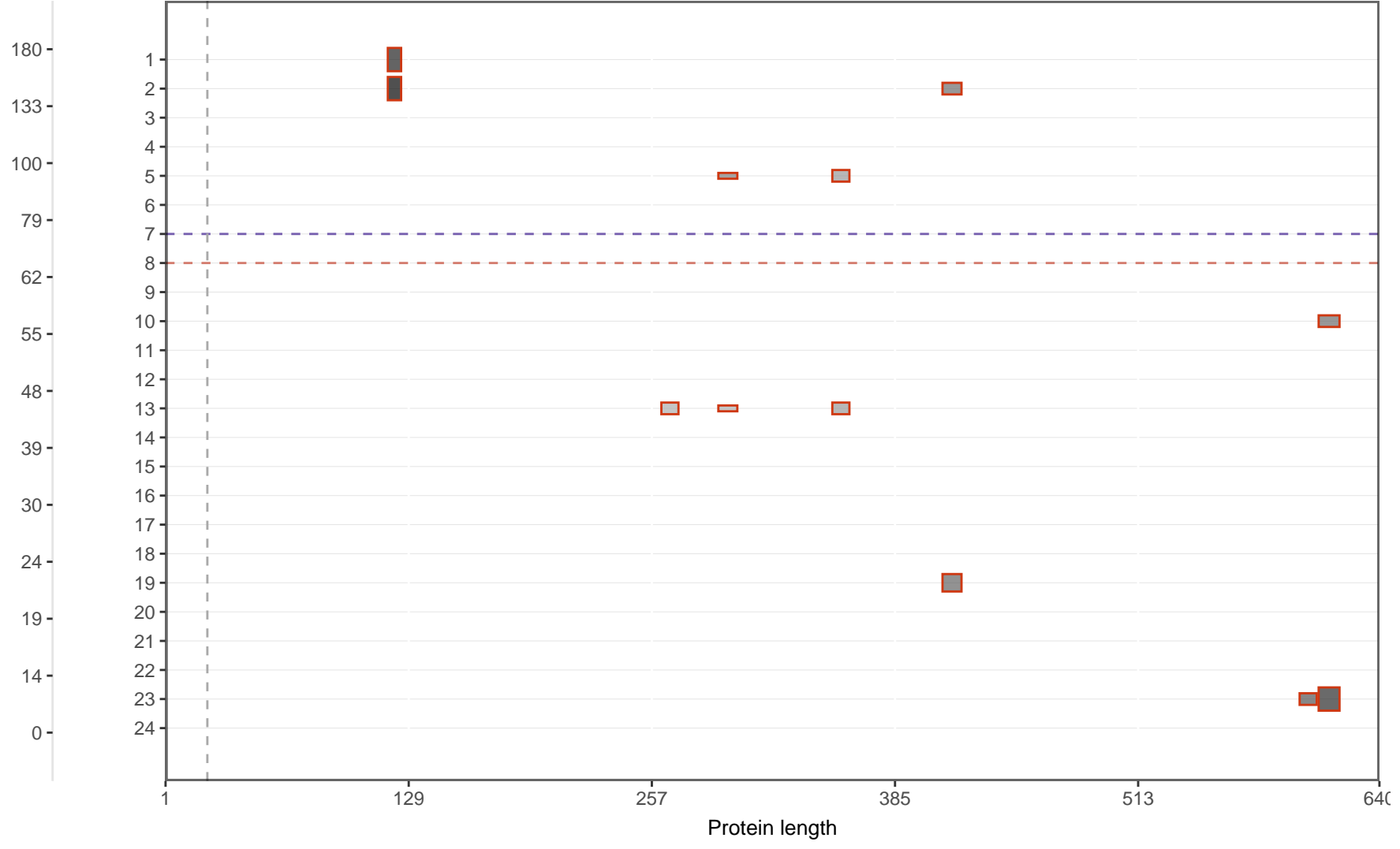


MW indication



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF16499 Alpha galactosidase A
- PF17801 Alpha galactosidase C-terminal beta sandwich domain

Protein sequence:

KSIWPLDMLPLGWLTDAGSNLGPFRNCRLNLDGRTQVTLWSMVRSLPFGGDMRKLDDTFNLLNPTLLENWFSNNMEFRVYTGSLSPGHGLTHNSKNEKGTSSVSETRVLALRSCDKVKNANGWSTKVLNDVAVGVWEENSNNHTSFFGLYKRKAPLSEGEEMVYHQSHGKLLHLVTERTELGFASGNRKLTSKESRGSFRCRSHANGIWEIINNNGTLKNSYVGLGASLDIVKASPGDVRSLWATGRRRGEIYLAFFNLNNGVTEMSAKISDIAKAPKI

NbL18g10340.1 uncharacterized_LOC109235488 [MW = 13.05 kDa]

No. of times detected



log(intensity)



Values from



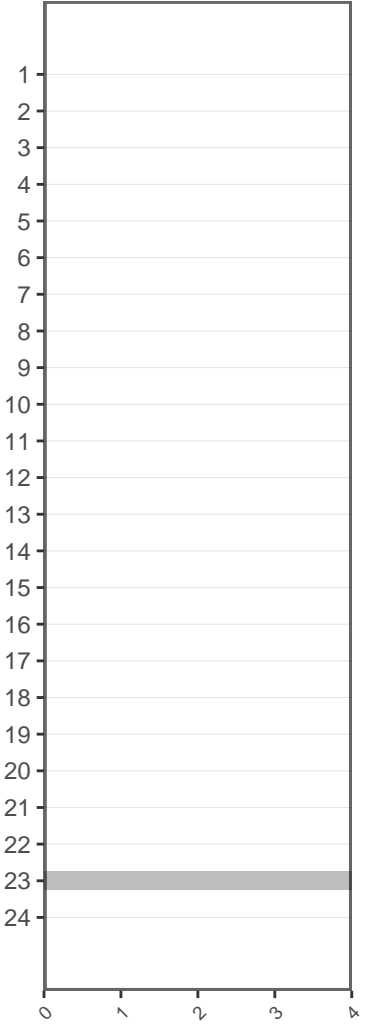
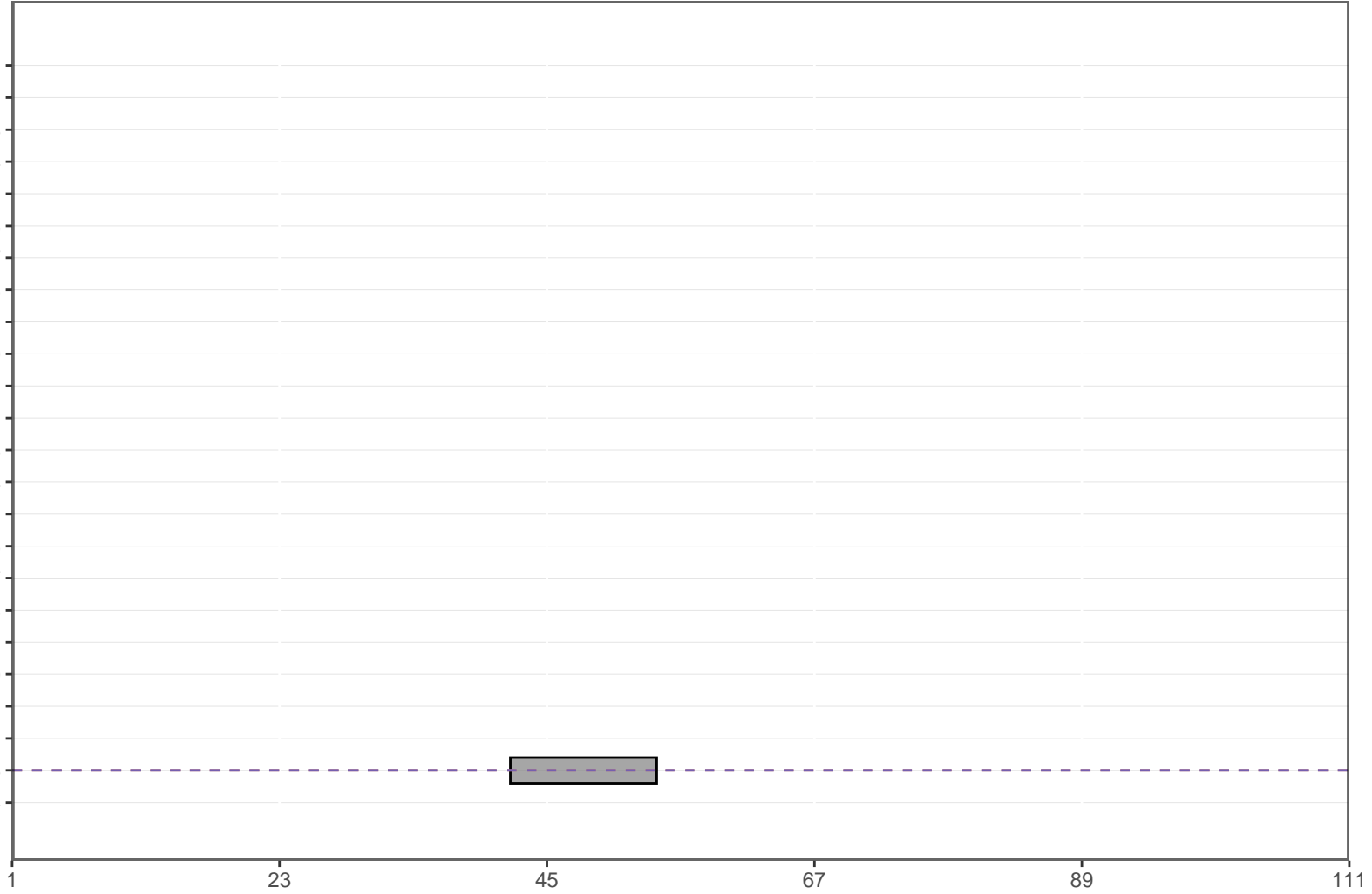
MW indication



Molecular weight



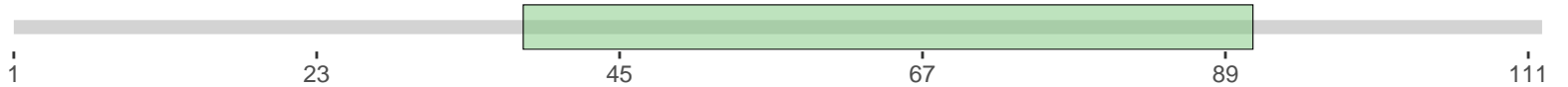
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

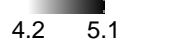
NNLDOALFLMORAMQSSGMEELIKREGLHHKNEKRVLARKLLERKLRGGDLARKLKSILKIKVRLG

NbL18g10270.1 uncharacterized_LOC107778361 [MW - SP = 59.56 kDa]

No. of times detected



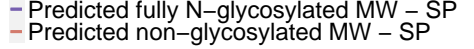
log(intensity)



Values from



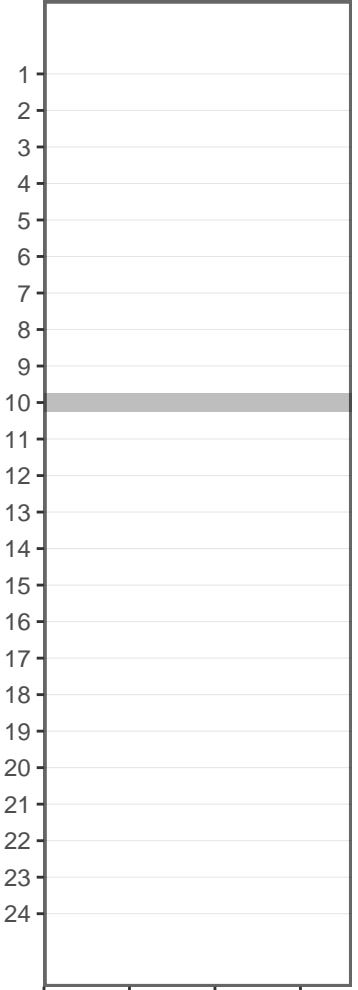
MW indication



Molecular weight



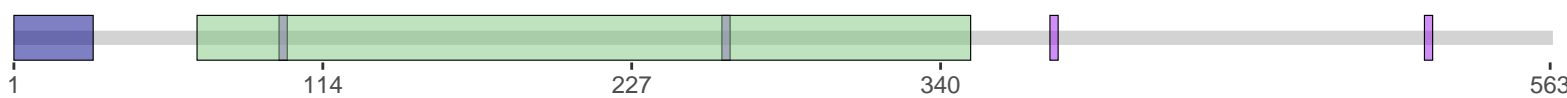
Gel Slice



Peptide counts over 4 repeats

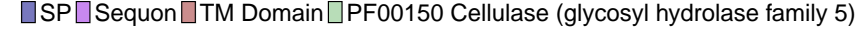
1 114 227 340 563

Protein length



Pfam domains

Pfam Description



Protein sequence:

MEHRYGFTDGDYWGDDSANQAGVNLNDMVKGTFLVGGVPLFVSEFGVDGRGTNYNDNRYFNGLFLGLAAELDFDQWALWTLVGGVYLRDGVVGLNEVYGVLDWVNRDIRNSGFLERVSAIREPFGSPGVYETRLHKVIFHPKTLQVRRRTSFLQPLFELGSGSEAAAARVYAPQKTLVIGTYFLGQADKIGERPKLGIKGGDDSGKWTETSGSKMHLGSKLHDATSVGLVDENNVVITQTKGLSTNDTDDPQSGQWFKHIDSTRVYTKTKKEFLQKPIRFLARSFFGS

NbL18g10240.1 tumor_protein [MW = 18.76 kDa]

No. of times detected



log(intensity)



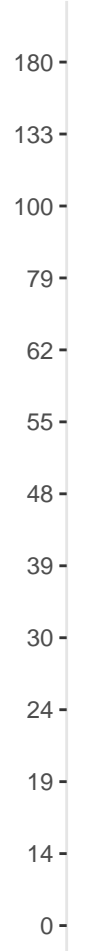
Values from



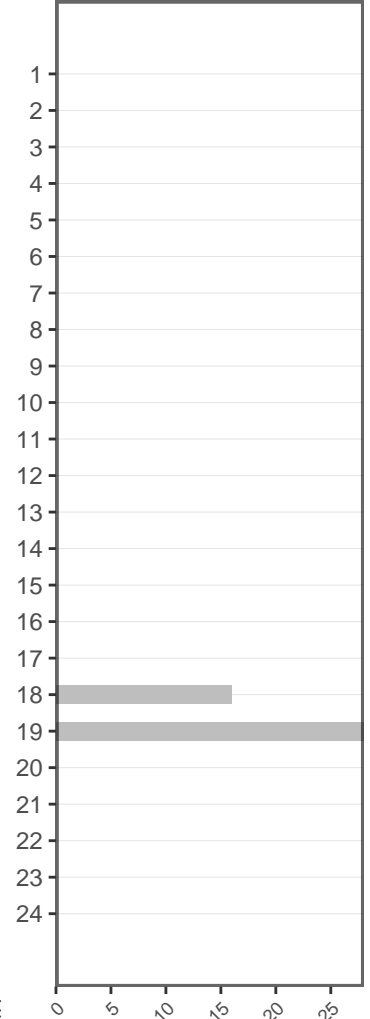
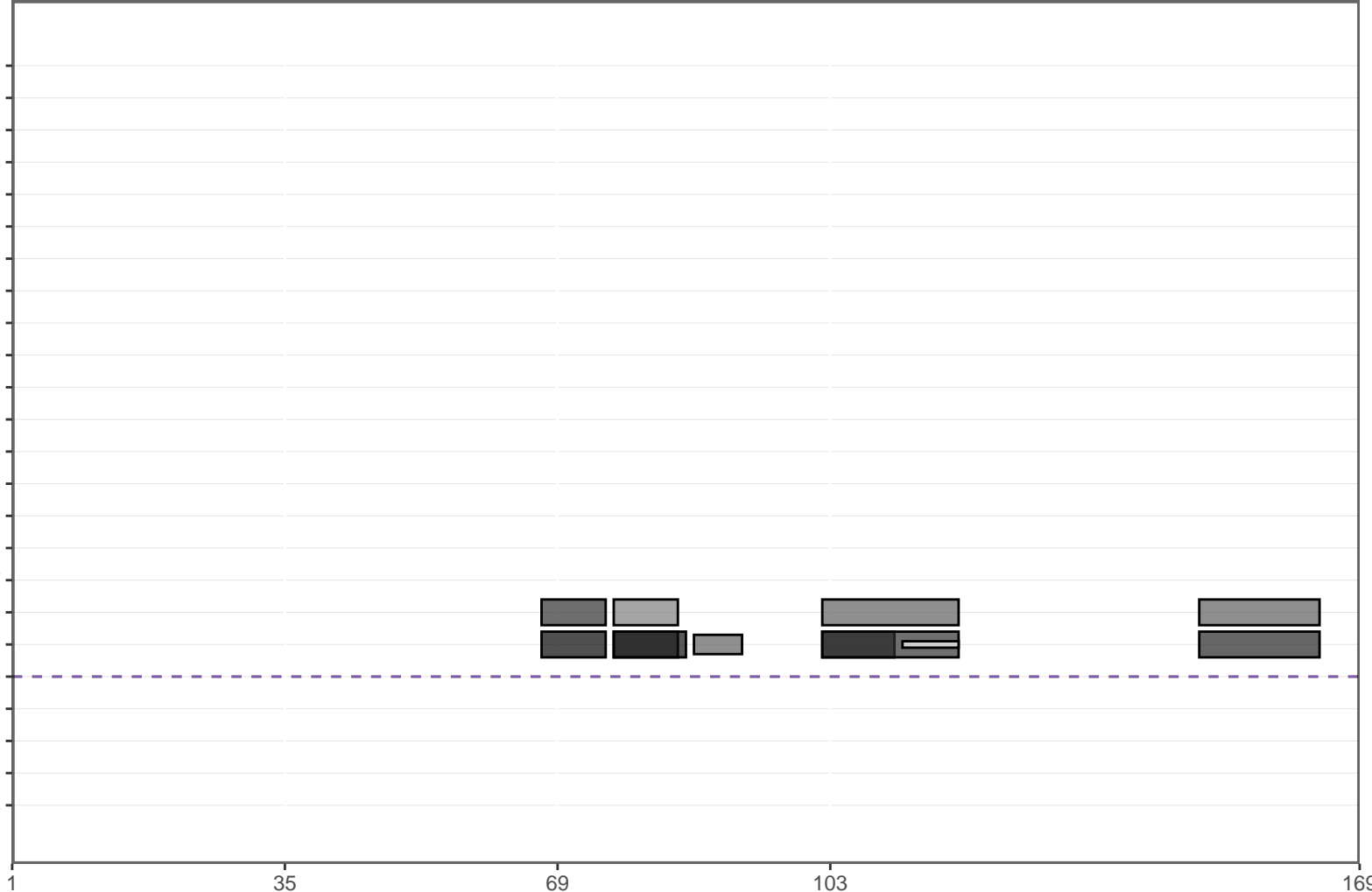
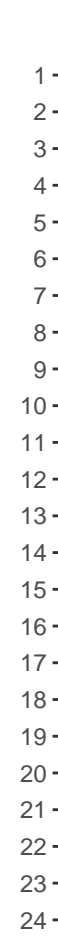
MW indication



Molecular weight

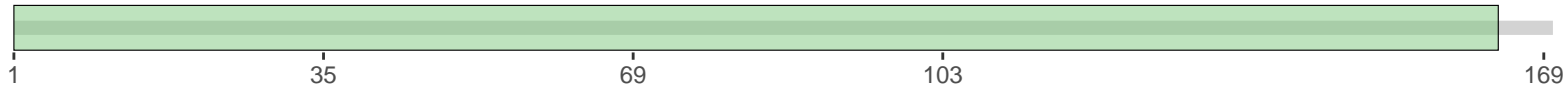


Gel Slice



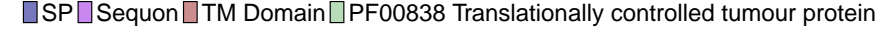
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VDTFRLEQPSFDKIKGFVVMKKYKIKLTKLGAEGEEVFRKNNIGGATRYLLSKLSDLQFFVGEEMADDTGMVFAYKDGATDPTFLVLAHGLKEVQD

NbL18g10190.1 putative_protease_Do-like_14 [MW = 46.37 kDa]

No. of times detected



log(intensity)



Values from



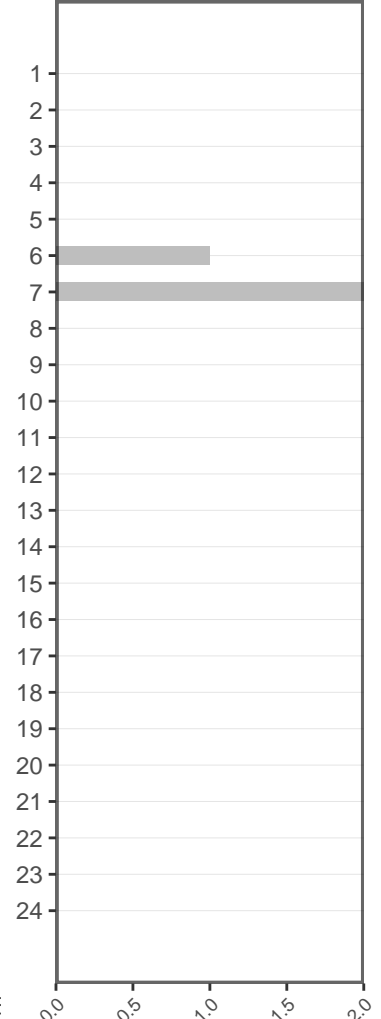
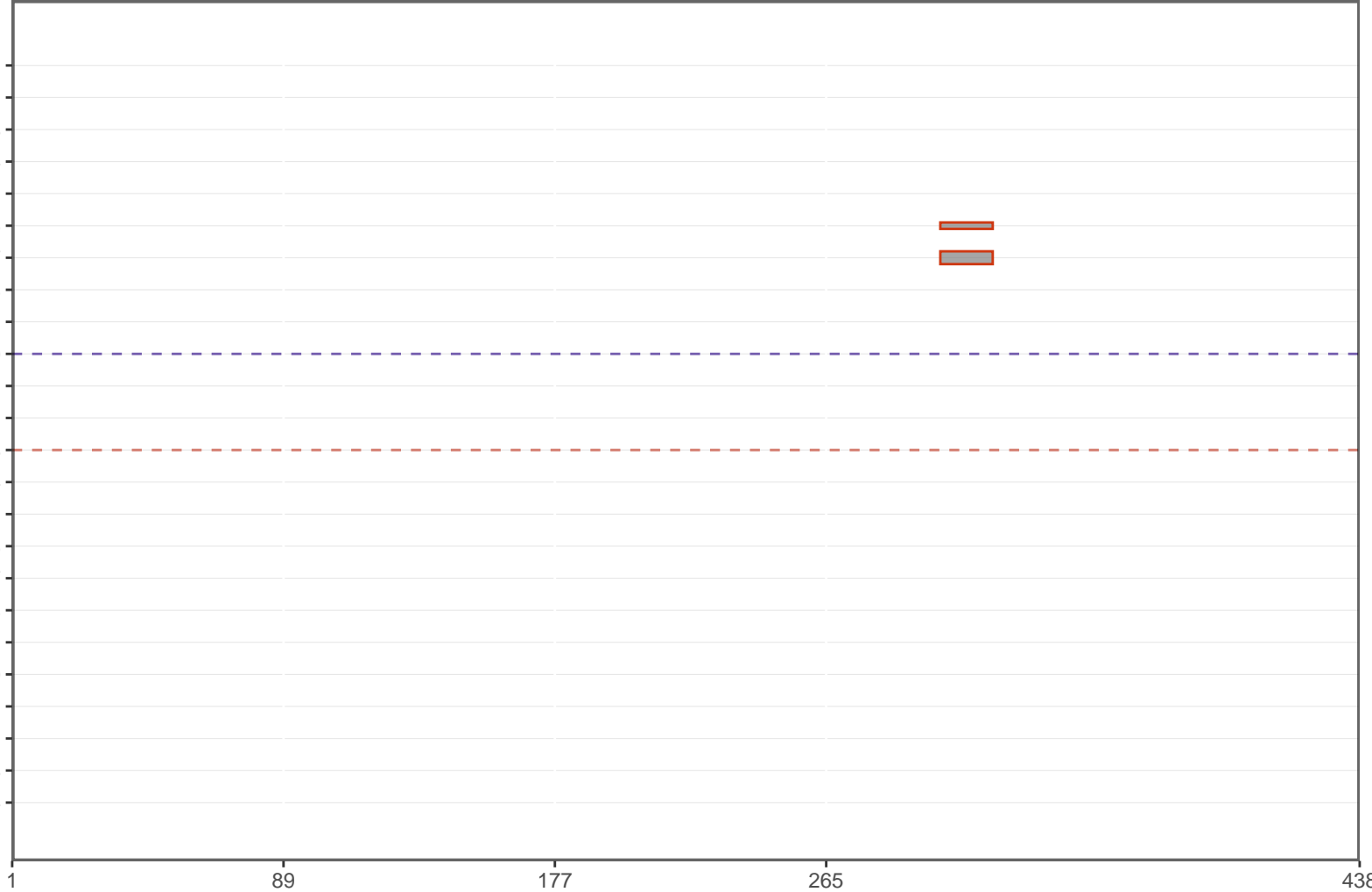
MW indication



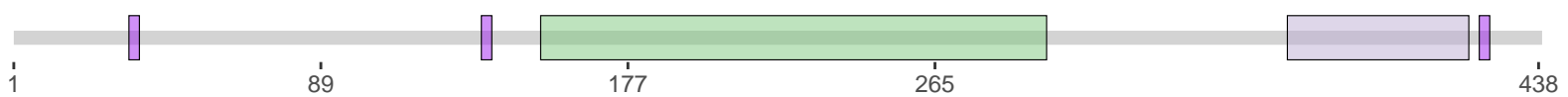
Molecular weight



Gel Slice

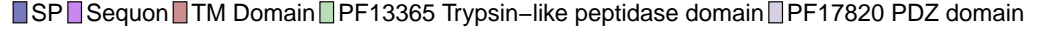


Protein length



Pfam domains

Pfam Description



Protein sequence:

DAIVYKIKSKTFLPTAKLGTSMLRPGWVAVMGGPLSLQNTTITAGVSGVDRKSSDLGLGMRREYLGTDGANAGNSGGPLVNVDDGEVIGVNMKVLAAADGLGFSVDEVTYKIDHFKKRGVIRPWLGLKMLDLNDMVAALGGERDPSFKVKNKGVLSMVTFGSPADGAGFHPSEVVVEFDGKPVGSIKEIDMGENLQKLTAVKRNANATATLTVPEEANPDM

NbL18g10090.1 amidase_1 [MW = 45.14 kDa]

No. of times detected



log(intensity)



Values from



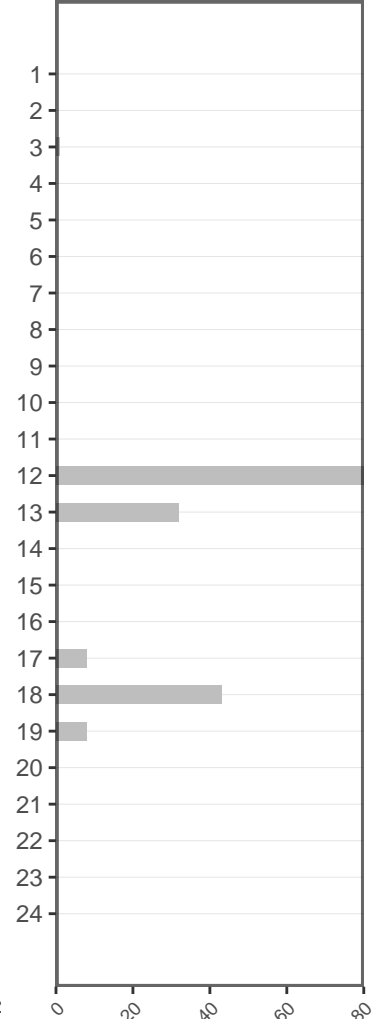
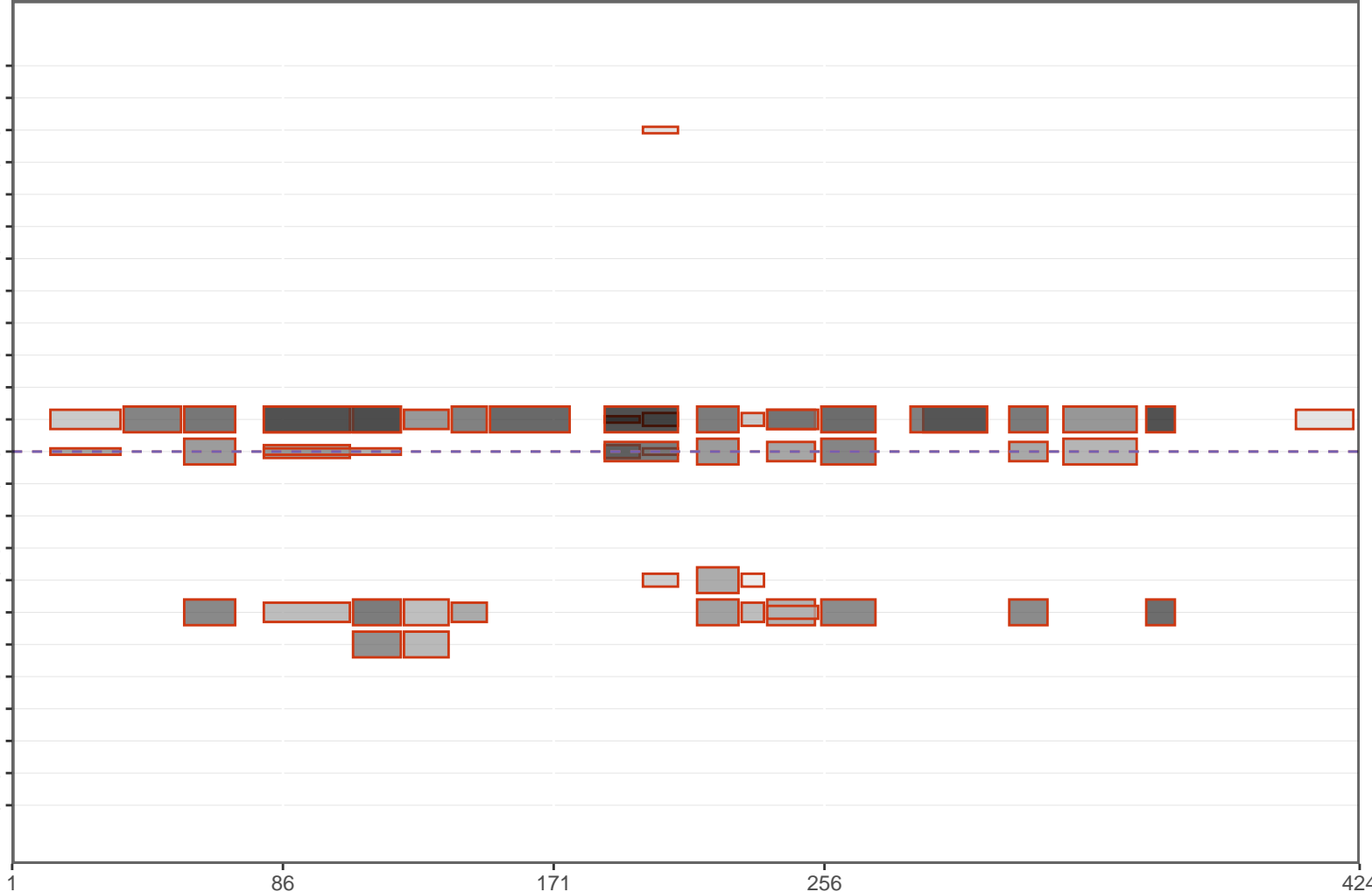
MW indication



Molecular weight



Gel Slice



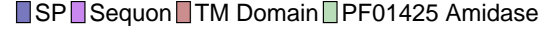
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

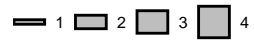


Protein sequence:

/RPTNIIAEDCFKLLDSKSNGLIEVLVNVEKLVGSHMKIKYVSGDVEIGNVPLNKFMTPTGTGNDSEYFPLLRLLSAAAMRLLQRYEFKENHGEWVSTVKKPLGPGIAERVWEALKATDENIDVGHVSAELRAALTALLGDGGIAPITVPGPPPKLRGETSALLEGFRVAFSLLSIAGVSGFGQVSIPLGMGDNIPLISVLSLVRKHSGLLLEDAEAIHNLKI

NbL18g09960.1 eukaryotic_translation_initiation_factor_4B1-like [MW = 70 kDa]

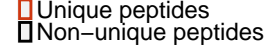
No. of times detected



log(intensity)



Values from



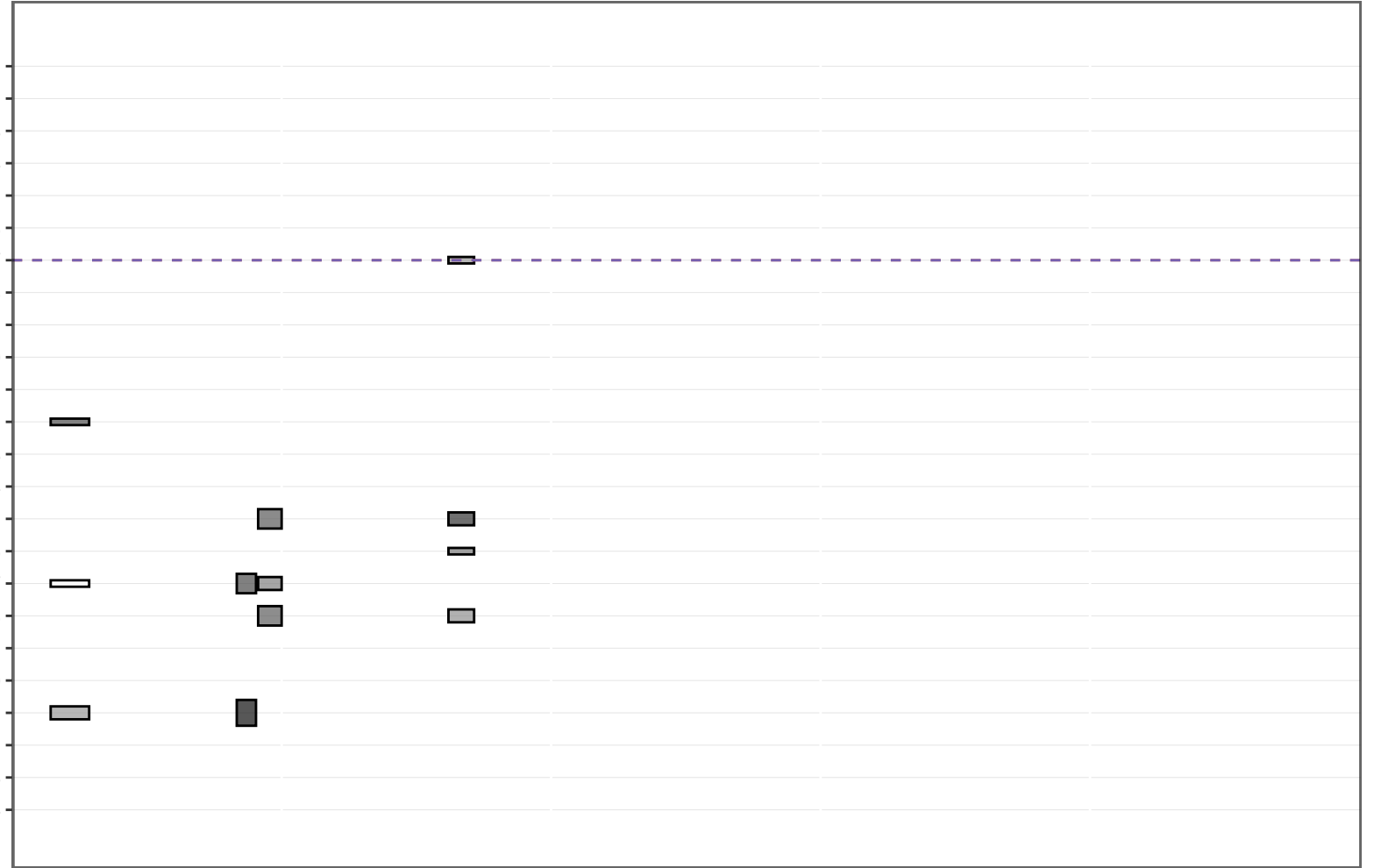
MW indication



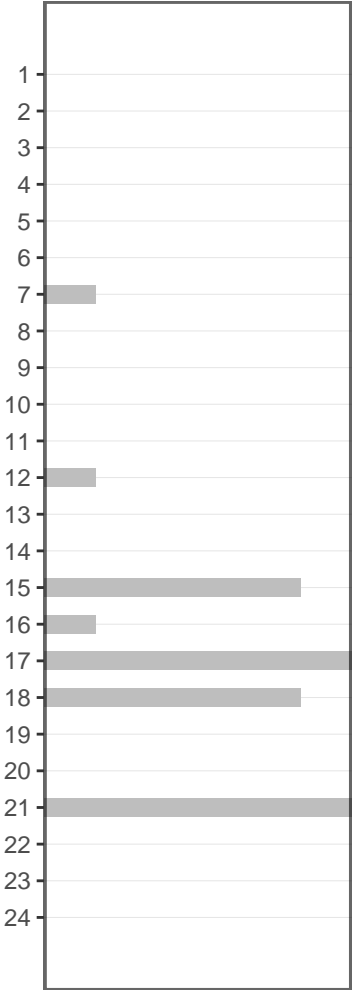
Molecular weight



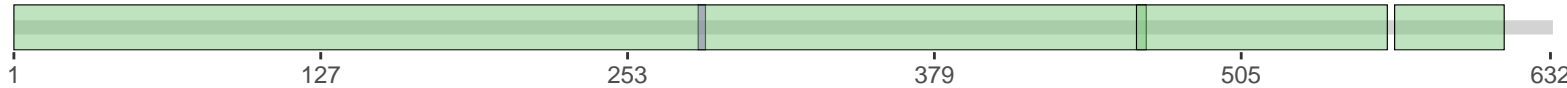
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EEVLAEGLDVWVGLDMEIEVWVGGSRPTSGS6SRP65SH6AFSE6GPAWLGGGVMEVWPKKVPNFRDAPKPREVLEEKGLDWWKIDLELEHRRVDRPTEETEEKLNKKEEIEHLRKEAMQ65GHGDTNLGVVNPKDRDLELLIRDLDLDDKVRFGKRPQ66AGRERNLKEEIEQLRKEAMQ66GGDGTNLGNLNGKERELELLIRDFDKVVRF67KHQRPG68GG69VTLGPERL69GSASVE69RRAGEQIDRPRRGG69AWARPTDPMERPRR69GVDSWARPNEQV

NbL18g09950.1 GDSL_esterase/lipase_At3g26430-like [MW - SP = 39.69 kDa]

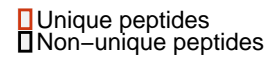
No. of times detected



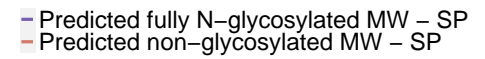
log(intensity)



Values from



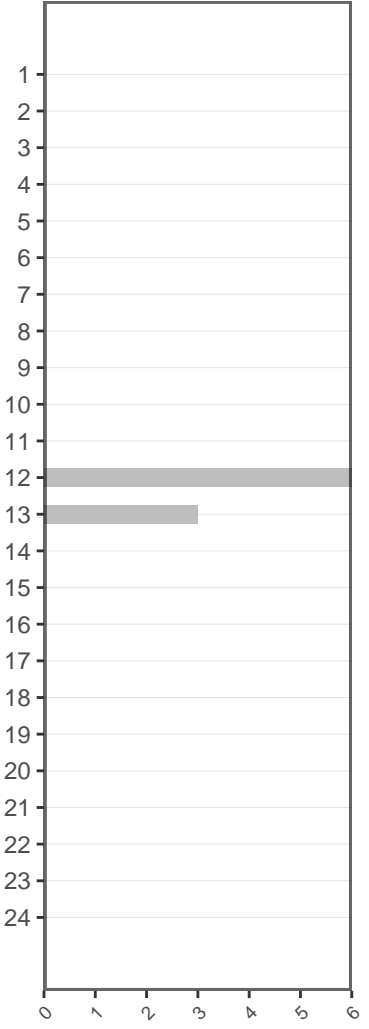
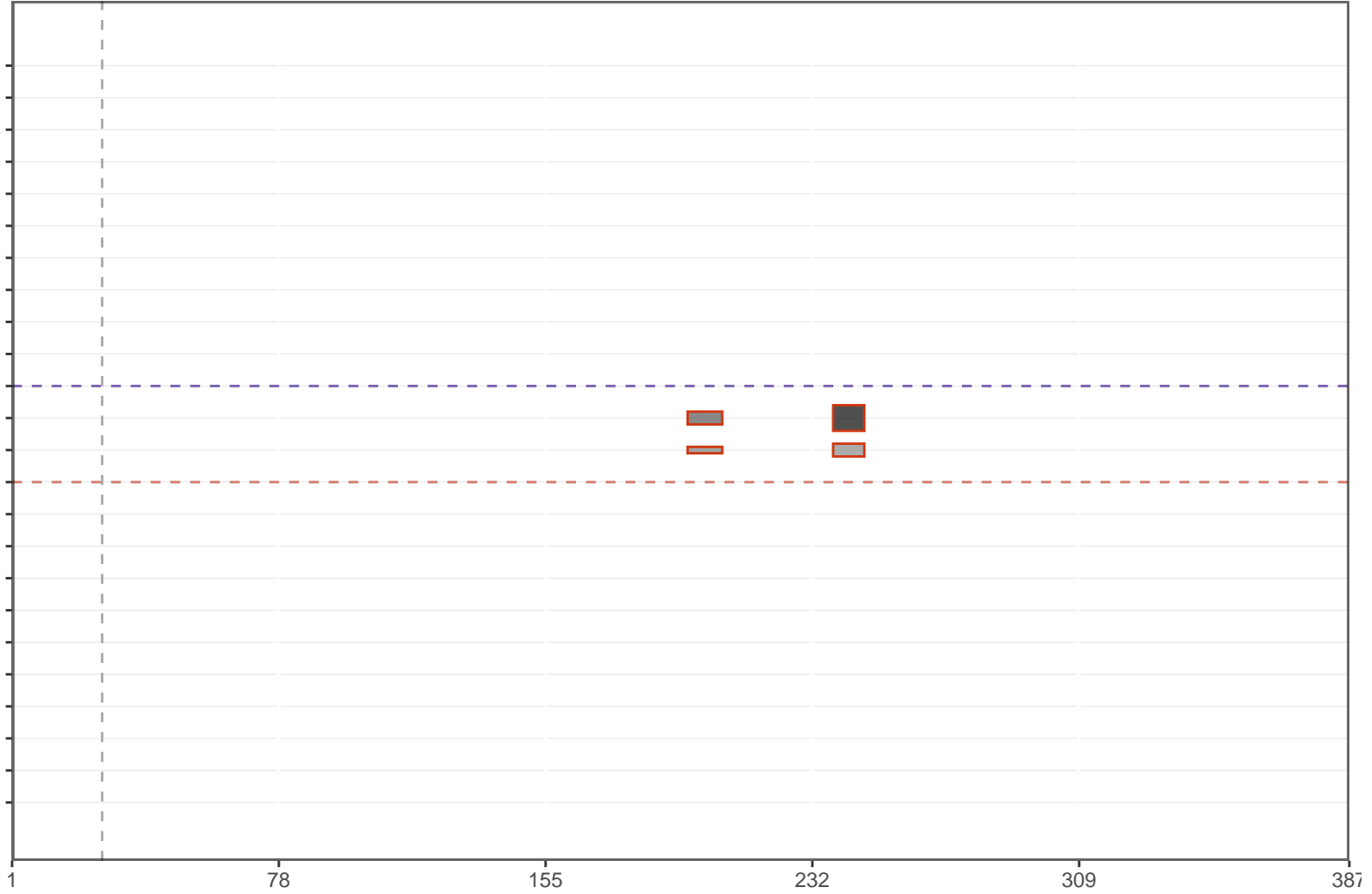
MW indication



Molecular weight



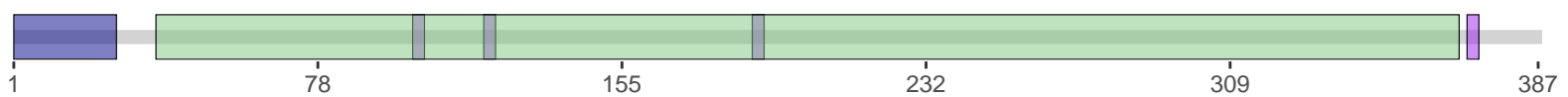
Gel Slice



Protein length

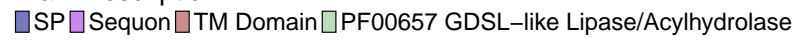


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GYFLMISTDQVRANVPQMLMGFRVTKIDYDEGGGRYFVHNTGFGVLPYLDRLFLTAQIDKAGGASFPFNKAGYFNKLIKETVQLRKLPLAALTYVDVYSAKYELSHANKHGFHFPLRACCGHGGKYWNMNHGGGSKKVKGKEIMLGGKDKDPSVRINWDGVHYTEAANRWVFEKVIKNGSYSDPFLPLNMAGHKQI

NbL18g09690.1 peroxisomal_primary_amine_oxidase-like [MW = 86.25 kDa]

No. of times detected



log(intensity)



Values from



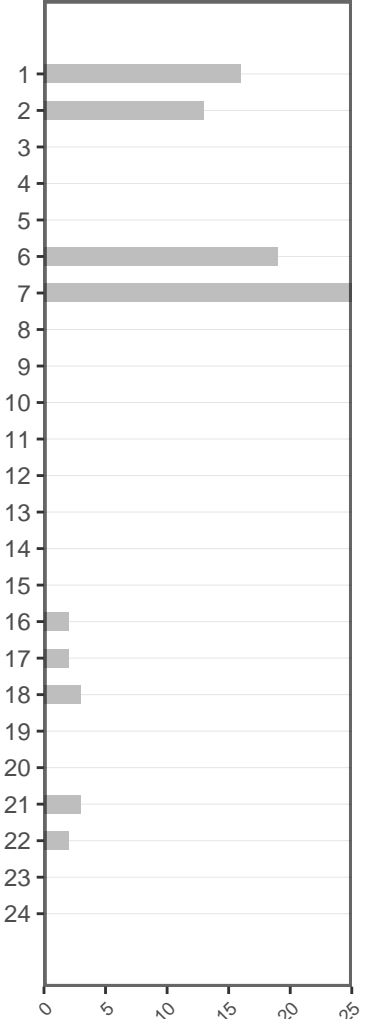
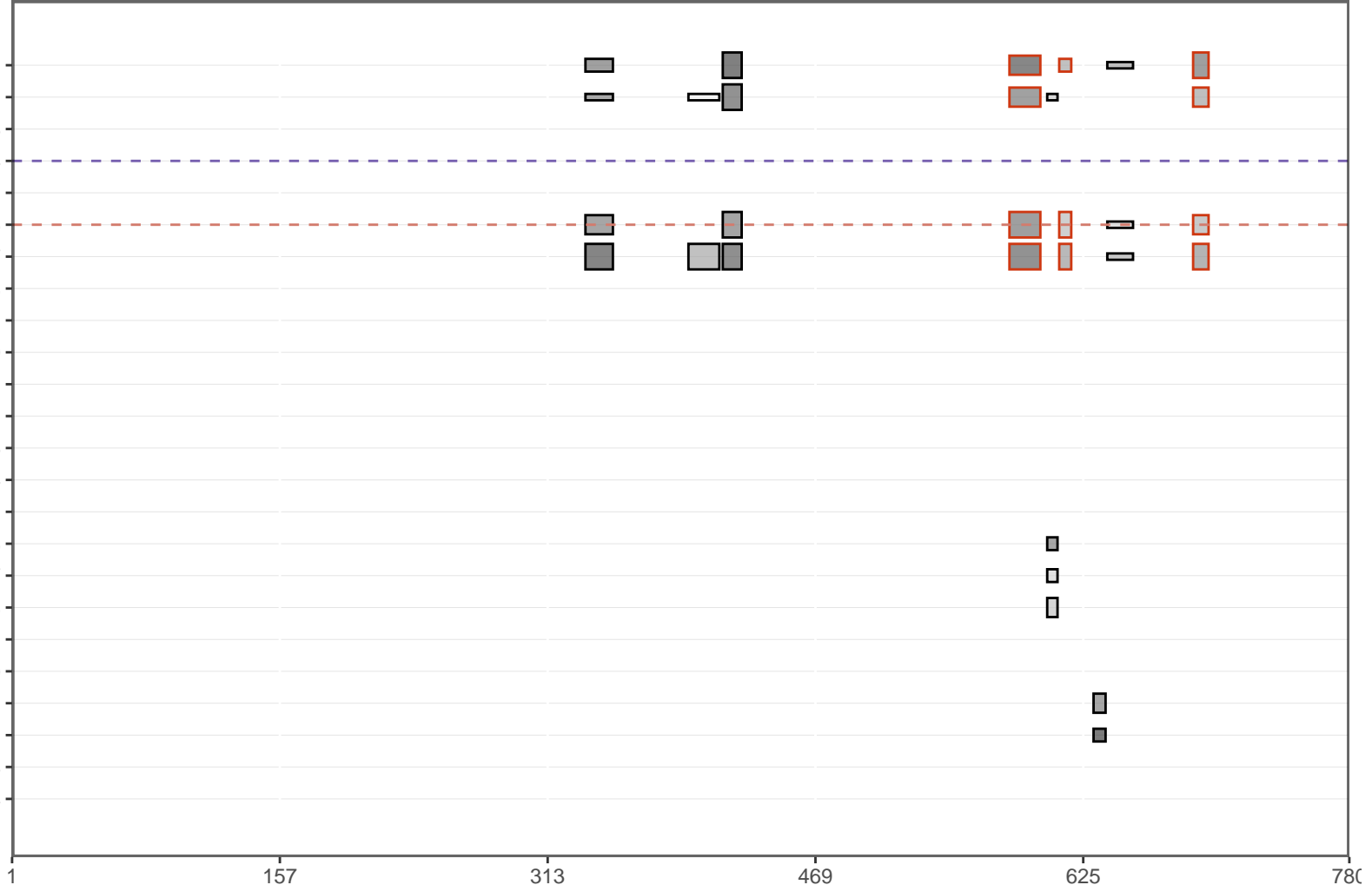
MW indication



Molecular weight

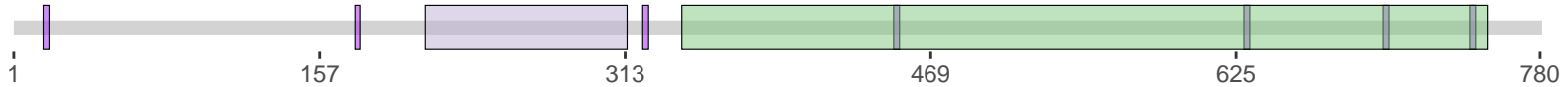


Gel Slice



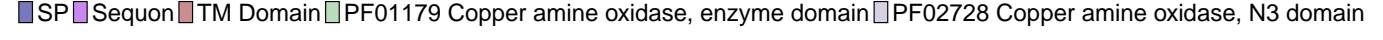
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

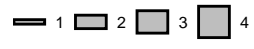


Protein sequence:

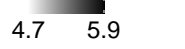
/VDSRGRFPVAHRLRFEMVYPYSDPNEPHYKNAFDAGDEGLKNAHSLKKGDDGLGKRYKFDHFTNFTGGVETIENGVGLHEEDHGMKWKHQDWRITGLAEVRRSRRLTVFICTVANNVEYGFYWHFYDGDKEAEVKITGLLGLALLPGEVRYKGTIAPGLVAPVHQHFFVARMDDMVDCKPGEAHNGVVEVNAIRVEPPGENNVHNNAFYAEERLLRTELEAMRDGKPLTARHWIRNTRTVNRTGGDTGKLVPGTNGLPLAGSEAKFLRRAFLXKLNWTT

NbL18g09650.1 glutamate--glyoxylate_aminotransferase_2 [MW = 53.48 kDa]

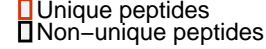
No. of times detected



log(intensity)



Values from



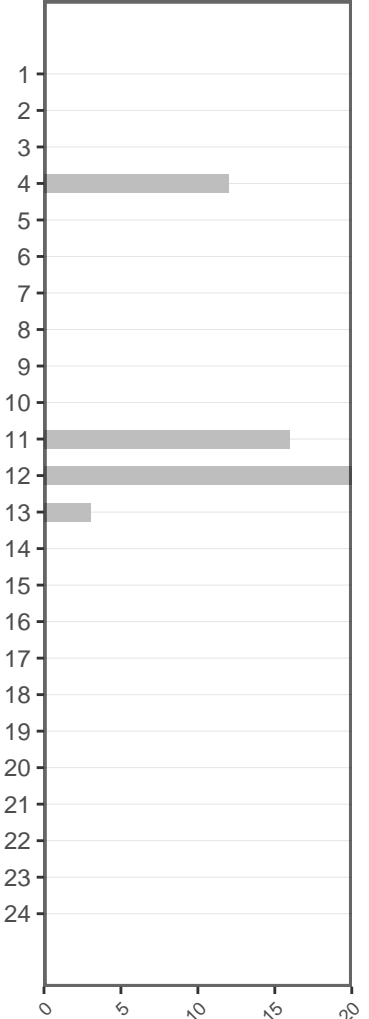
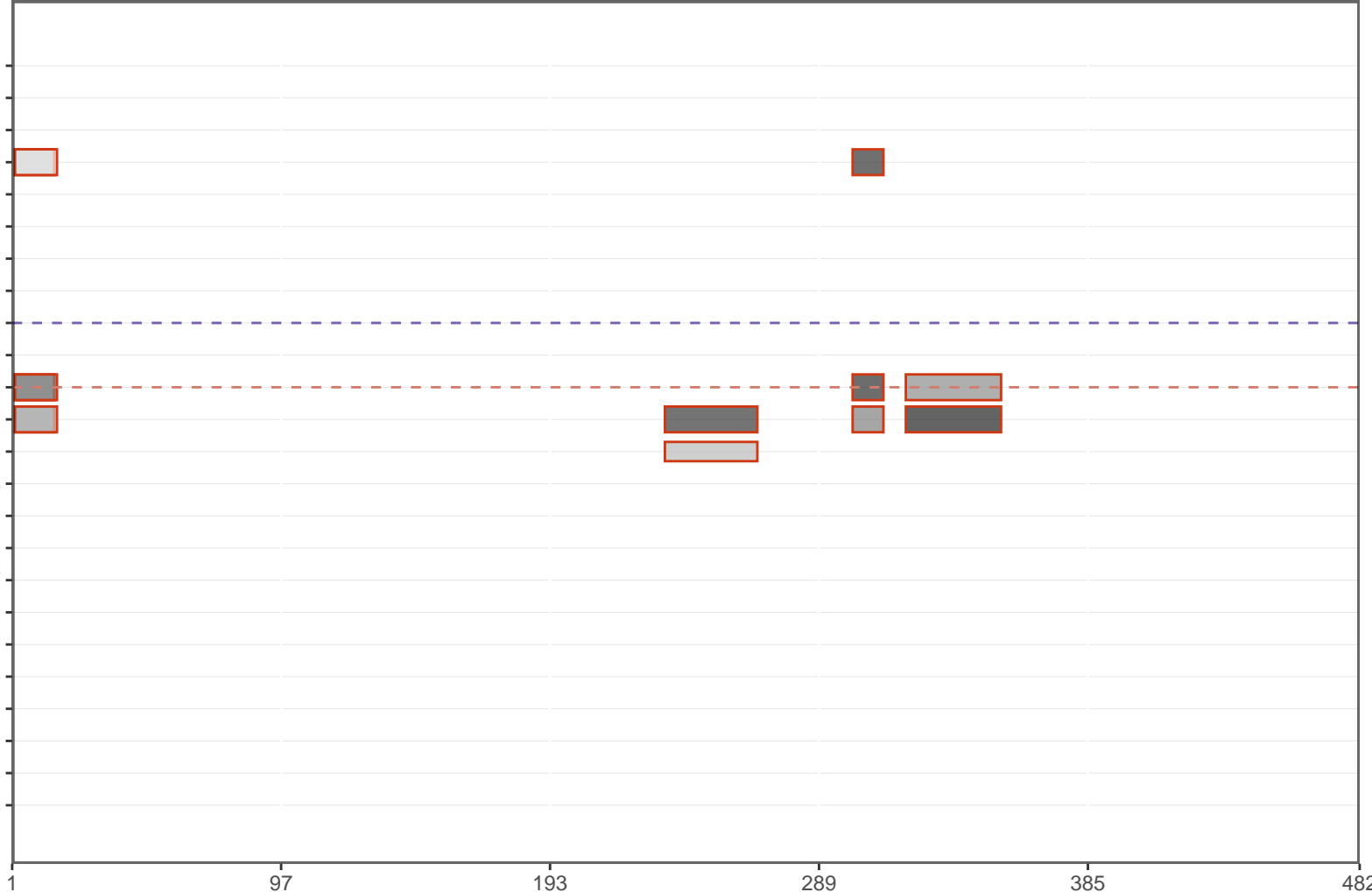
MW indication



Molecular weight

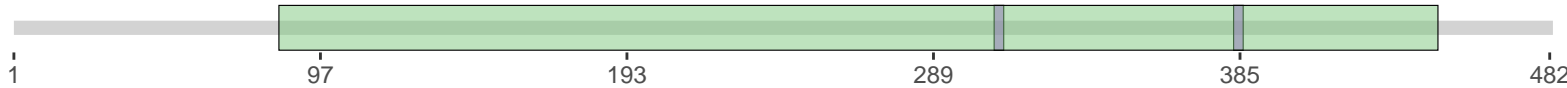


Gel Slice



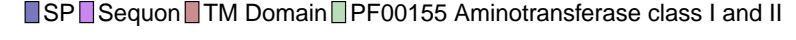
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

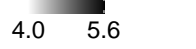
ANLKGIDFCHQESILLGDEVVQGNVYDERRFFISARKVLLDMGPPRISKEQLQVSHFTVSKGYWGEQGRGGYFEMTNSPKVVEIKVVASILSPNVGGIFMGLMVPKPKGDEVDQVYREKGLLESLRKRHMMTDGFGNSGRNVVGNFTEGAMYSFPQRLPDKAEAAKKLGVKVPVYGLRLLLEATGISTVPSGSGFQKKEGVFHLRRTLLPAEEDMPAAMSSPKKFNDEFMEQYEDHRGVSRM

NbL18g09500.1 cysteine-rich_receptor-like_protein_kinase_2 [MW - SP = 69.77 kDa]

No. of times detected



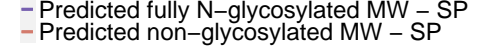
log(intensity)



Values from



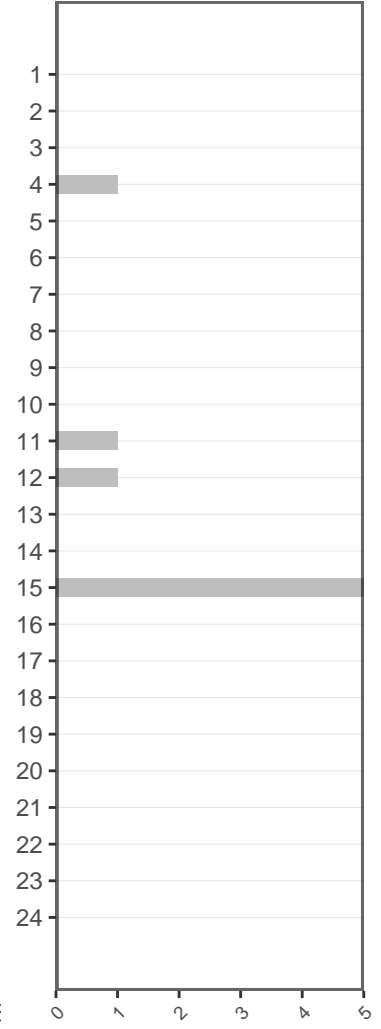
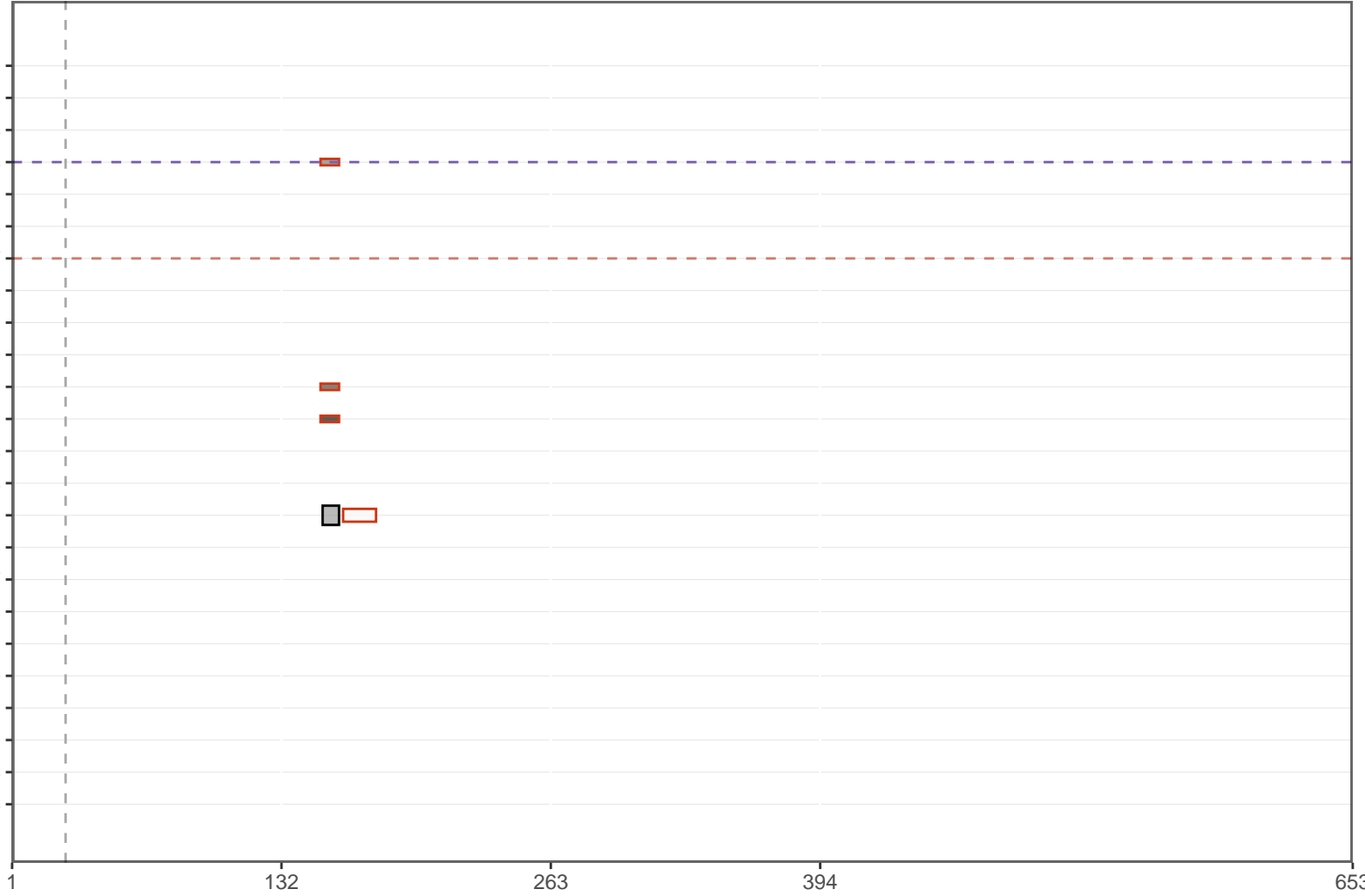
MW indication



Molecular weight



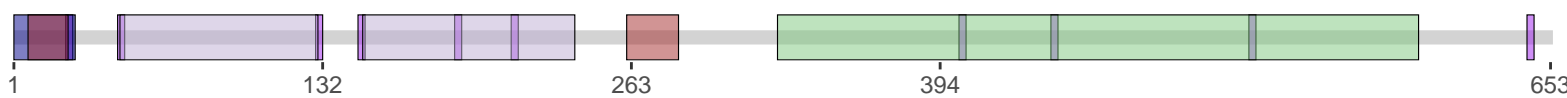
Gel Slice



Protein length

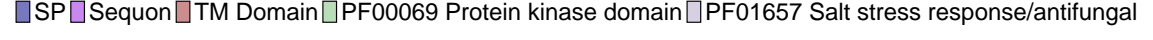


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IFKYSTLEKATGSFDEVNKLGGGGFVYKGVLDGGRVIAWRLEFNKHRVADYNEVNISSVEHKNLVRLLGGSCGGPESLLVYELFNGSLDRIFDFPSKGGKTLNWEKRFEEIGTAEGLVYLHENNRTRIHRDKAKENLLDSRLRAKIADFGLARFQEDKSHSTAGTLGYMAPEVLAHQGTEKADVYFQVLLLENTGRQNNRSGKTEVSDLSIAWQHFGHGRVKEELFDPNLMLNHYHTINWKEVLRVHVHGLLCTQEVPGLRPMSKALQMLYKKEEELPA

NbL18g09260.1 ATP-citrate_synthase_alpha_chain_protein_2 [MW = 46.5 kDa]

No. of times detected



log(intensity)



Values from



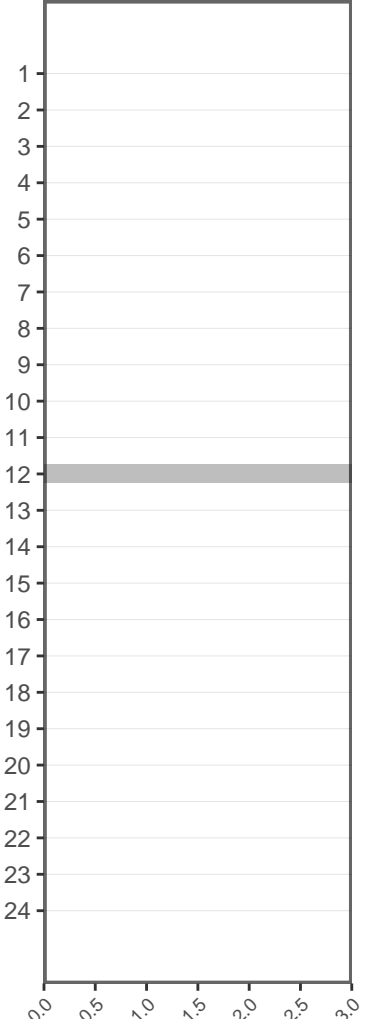
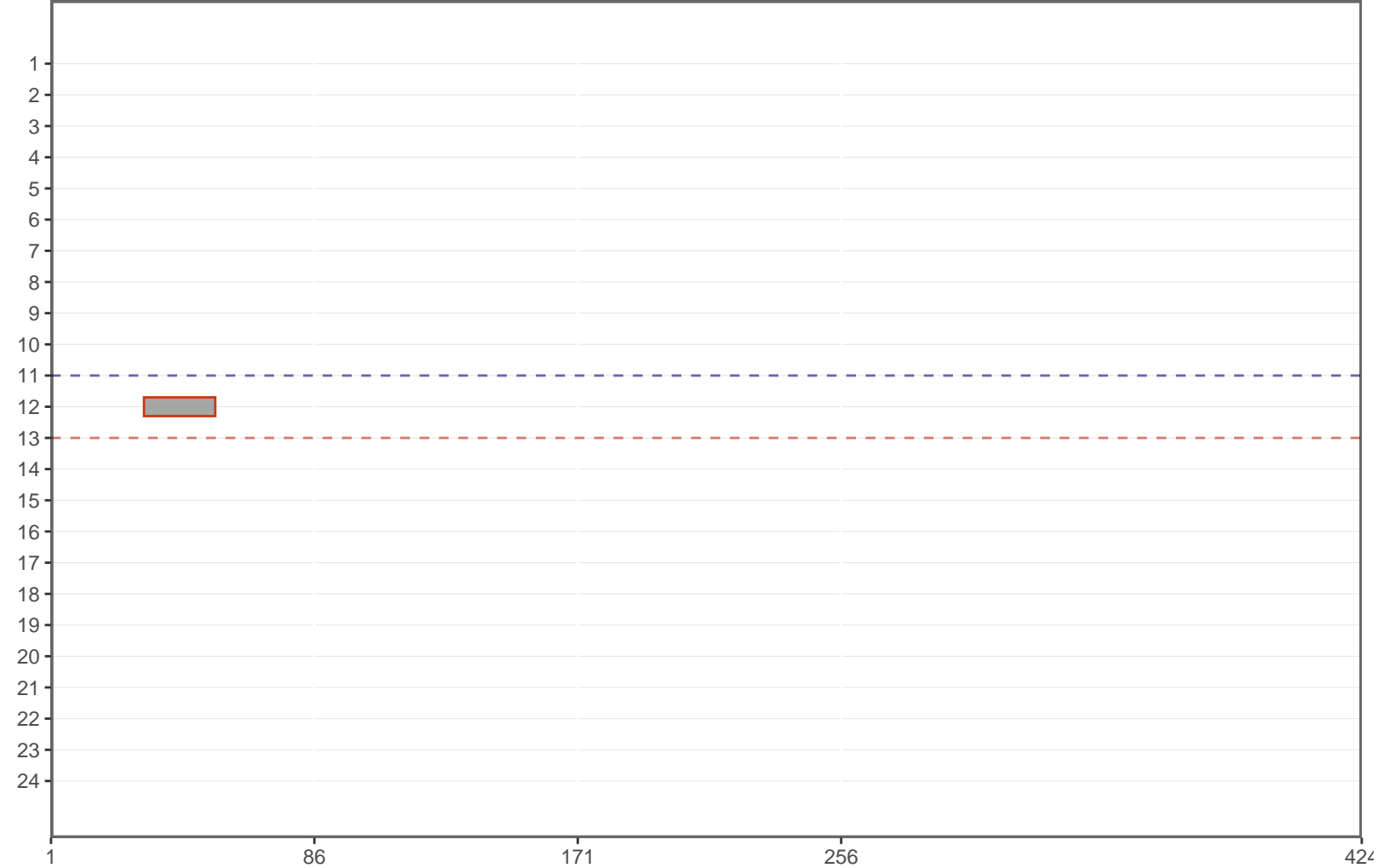
MW indication



Molecular weight



Gel Slice



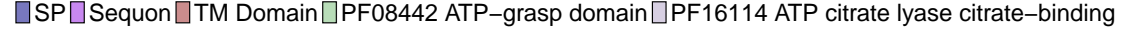
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

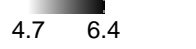
INPFAIVEGKPYPLDMRGELEDDTAFKFNKKNWGNIEFPLPFGIRVMSATEFRIHGLDEKTSASLKFTVLFNPKGRIMTMVAGGGASVHYADTVGDLGVAELGNVAEYSGAPNEEVLQVARVVDICATANPDGRKRRAIVGGGIANFTDVAWTFSGIRALKEKEKSLKAARMQIFVRRGGFNVQKGLAKMRSLSGEEIGPIEVYVGPATMTGICKQAEIGTAA*

NbL18g09140.1 2-methylene-furan-3-one_reductase-like [MW = 41.11 kDa]

No. of times detected



log(intensity)



Values from



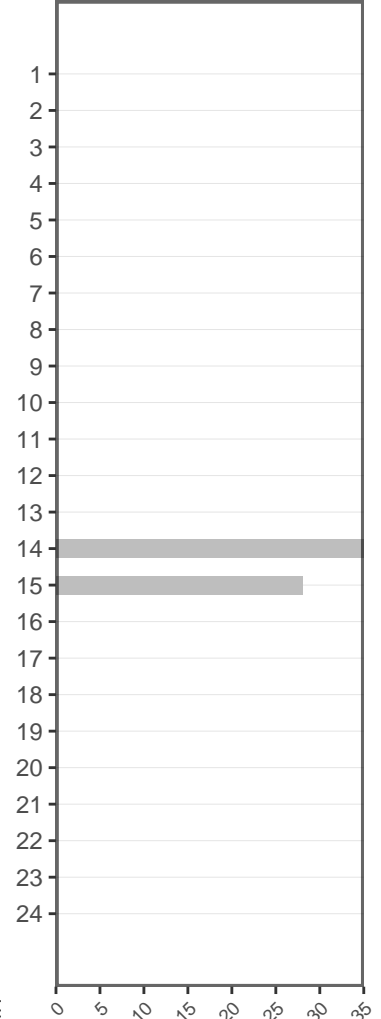
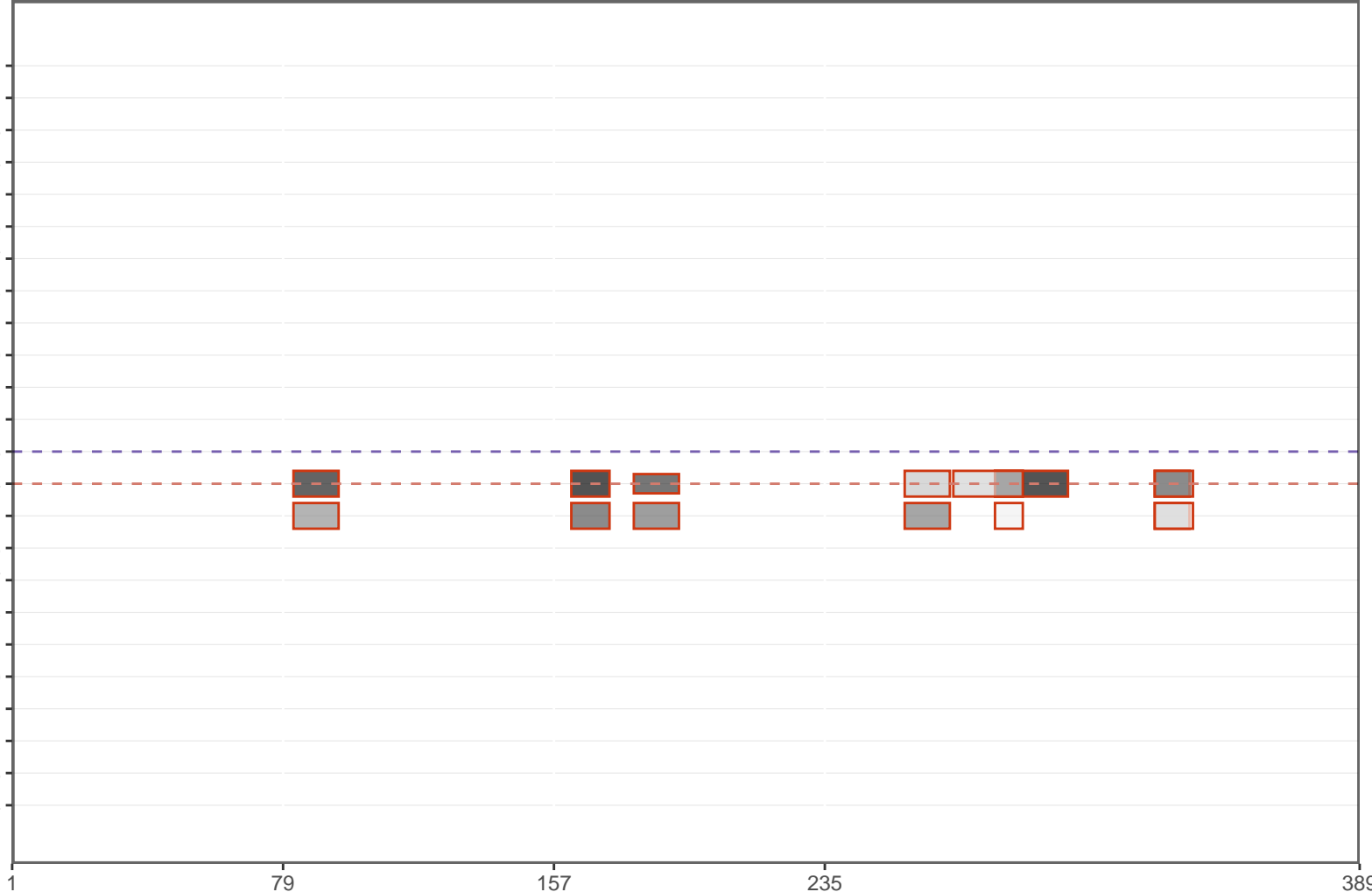
MW indication



Molecular weight



Gel Slice

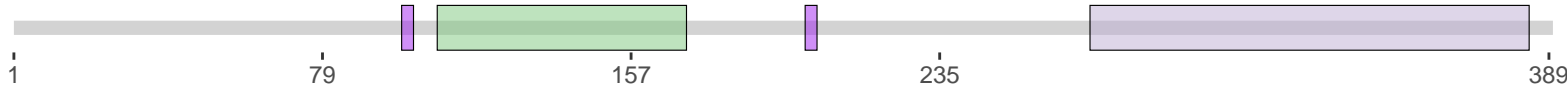


Protein length

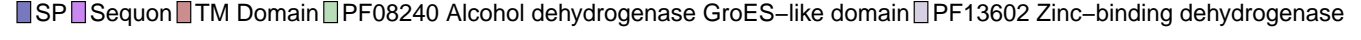


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

QFGSLAEFTAV(EENLVAIKPKNLGFAEAASLPLAETAVEGLEKAGFSAKGSILVGGAGDVGSLVQVAKKHVFGASKVAATSETGRLELLKSGADLAIDYTKNFENLPEKFDVYDTVGGGEKAKVAKKEGGSVVLTGAVTRPGFRFVFTSGEMLKKPKYLESGKPKPVDPKGFPPFDKVAEAFSYLETGRATGKVVHHPV

NbL18g09130.1 carbonic_anhydrase_2-like [MW = 33.23 kDa]

No. of times detected



log(intensity)



Values from



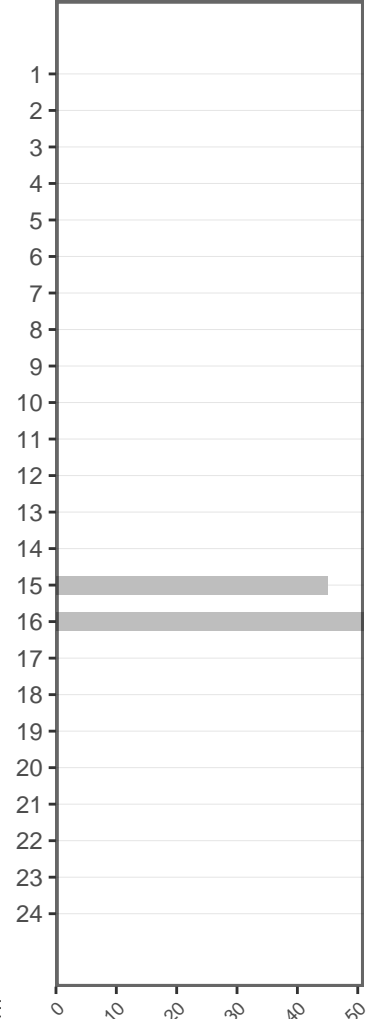
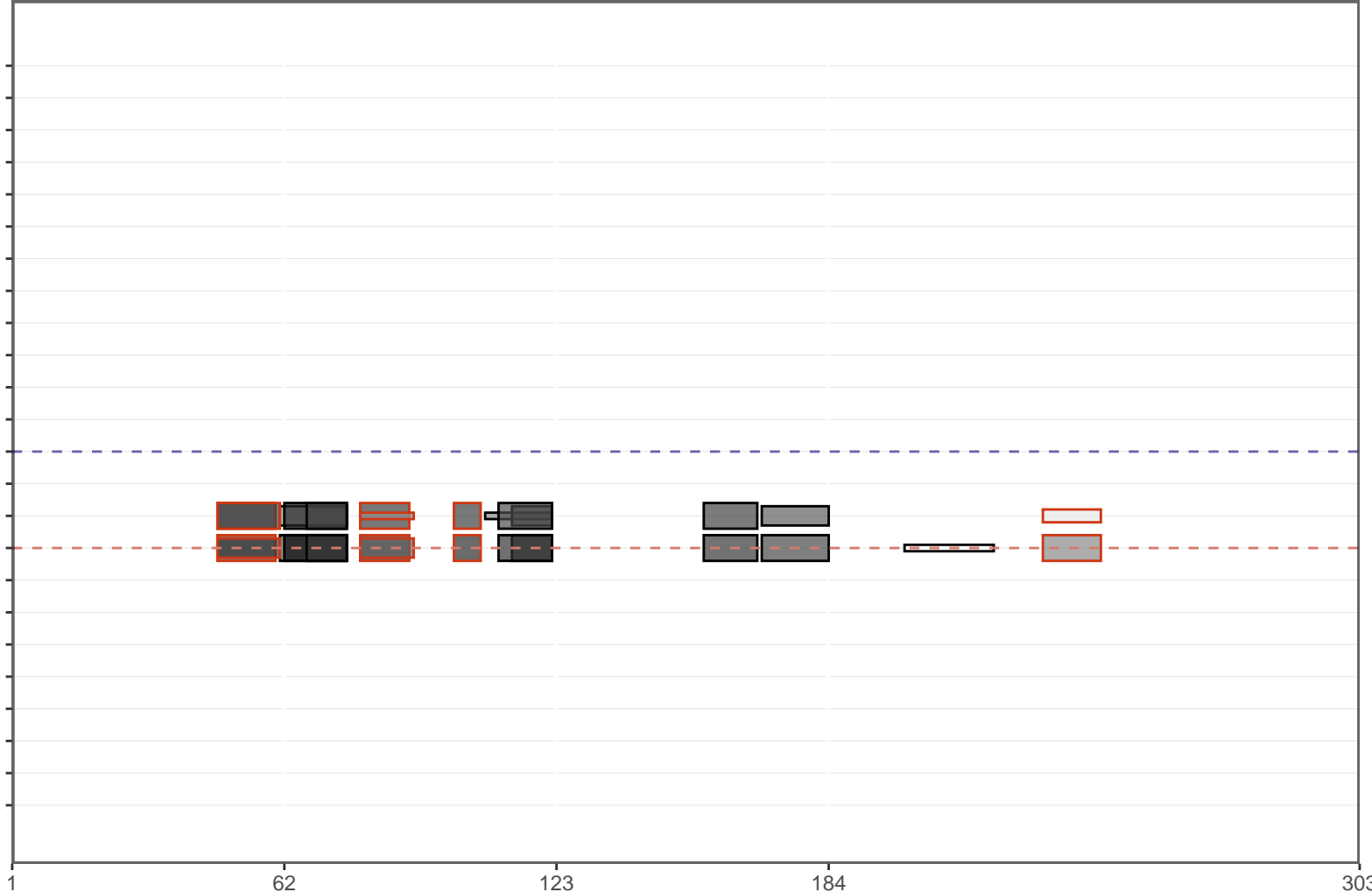
MW indication



Molecular weight



Gel Slice

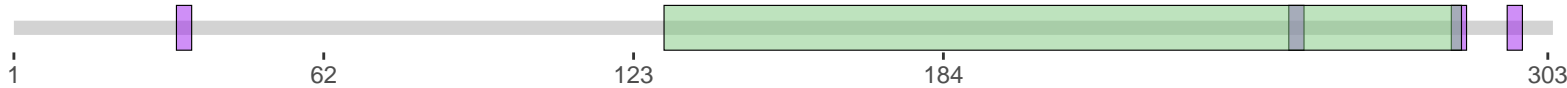


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

CPSHILNFQPEAFVVRNINMVPFDGTRKYSGVGAAYEVAWHKVENLVIHSGCOGGIKGLMSIPDDGGSTNSDFIEEWKICLPAKAKVKAECCHLNPFTEGQTRLEKEAVNVLGNLLTFYFVREAVVQKSLALKGGHYDFVNGSFEIWNIDFNLRPEVSL*

NbL18g09040.1 RNA-binding_protein_25 [MW = 106.19 kDa]

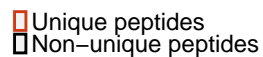
No. of times detected



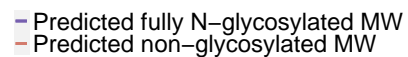
log(intensity)



Values from

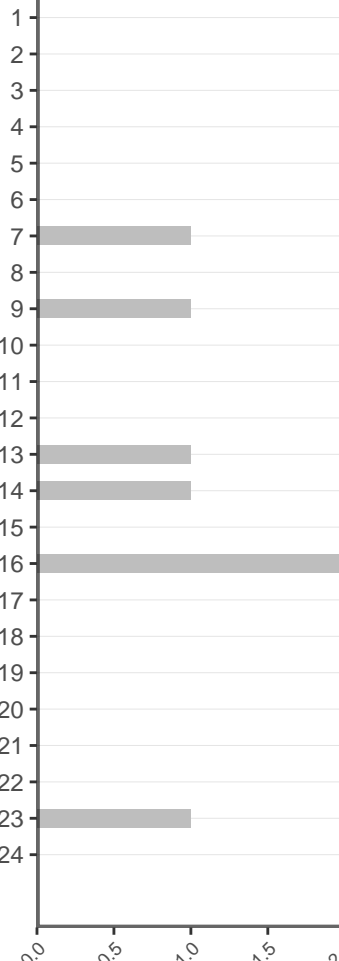
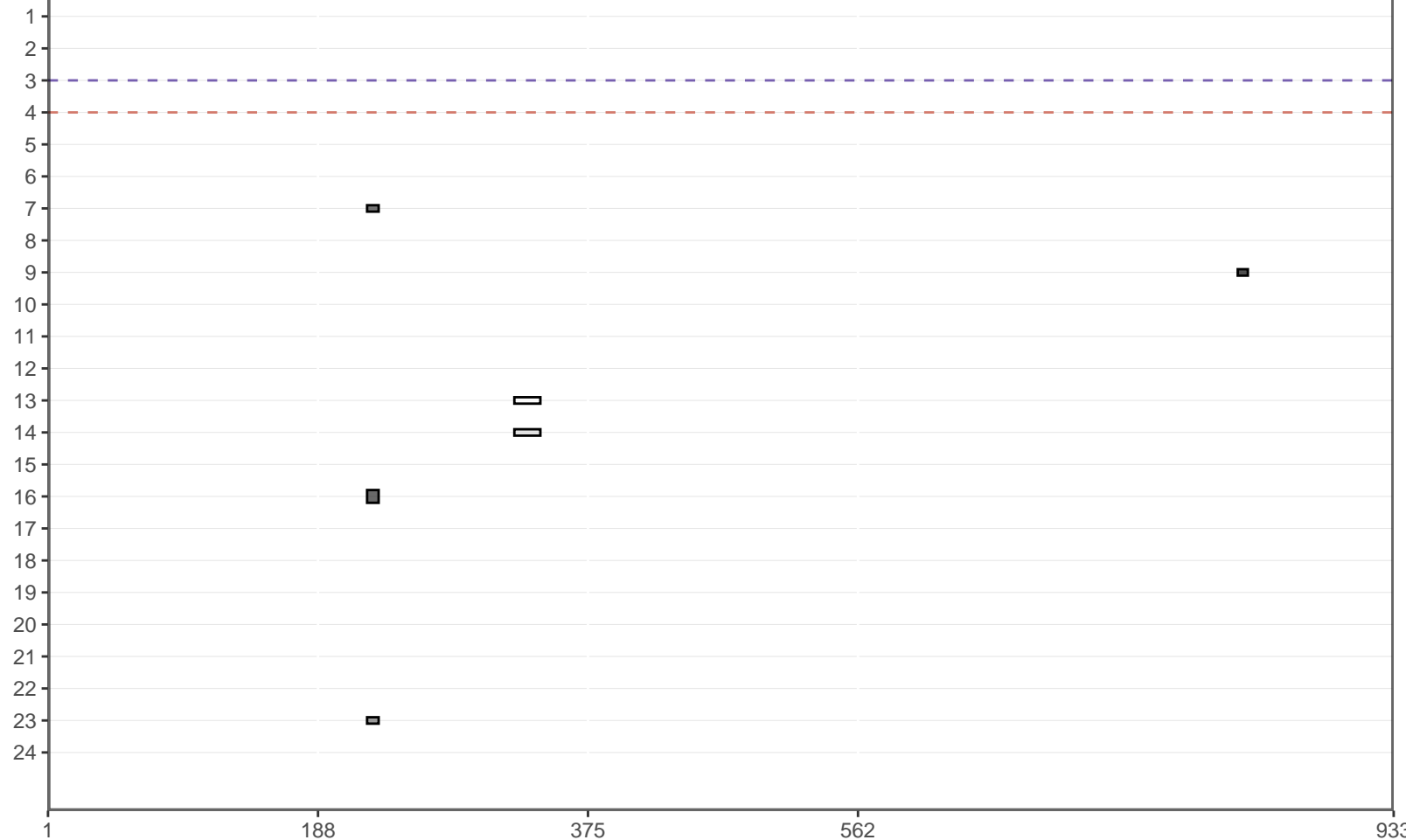
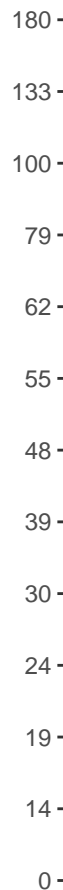


MW indication



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

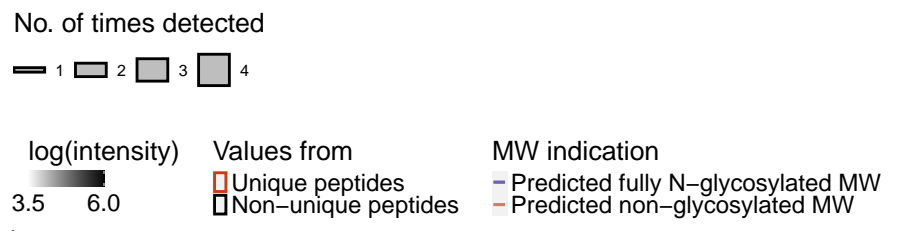
Pfam Description

SP Sequon TM Domain PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) PF01480 PWI domain

Protein sequence:

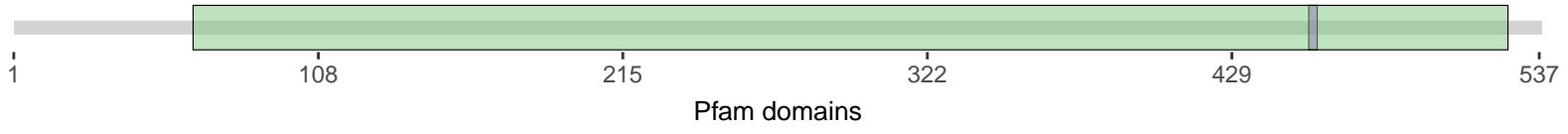
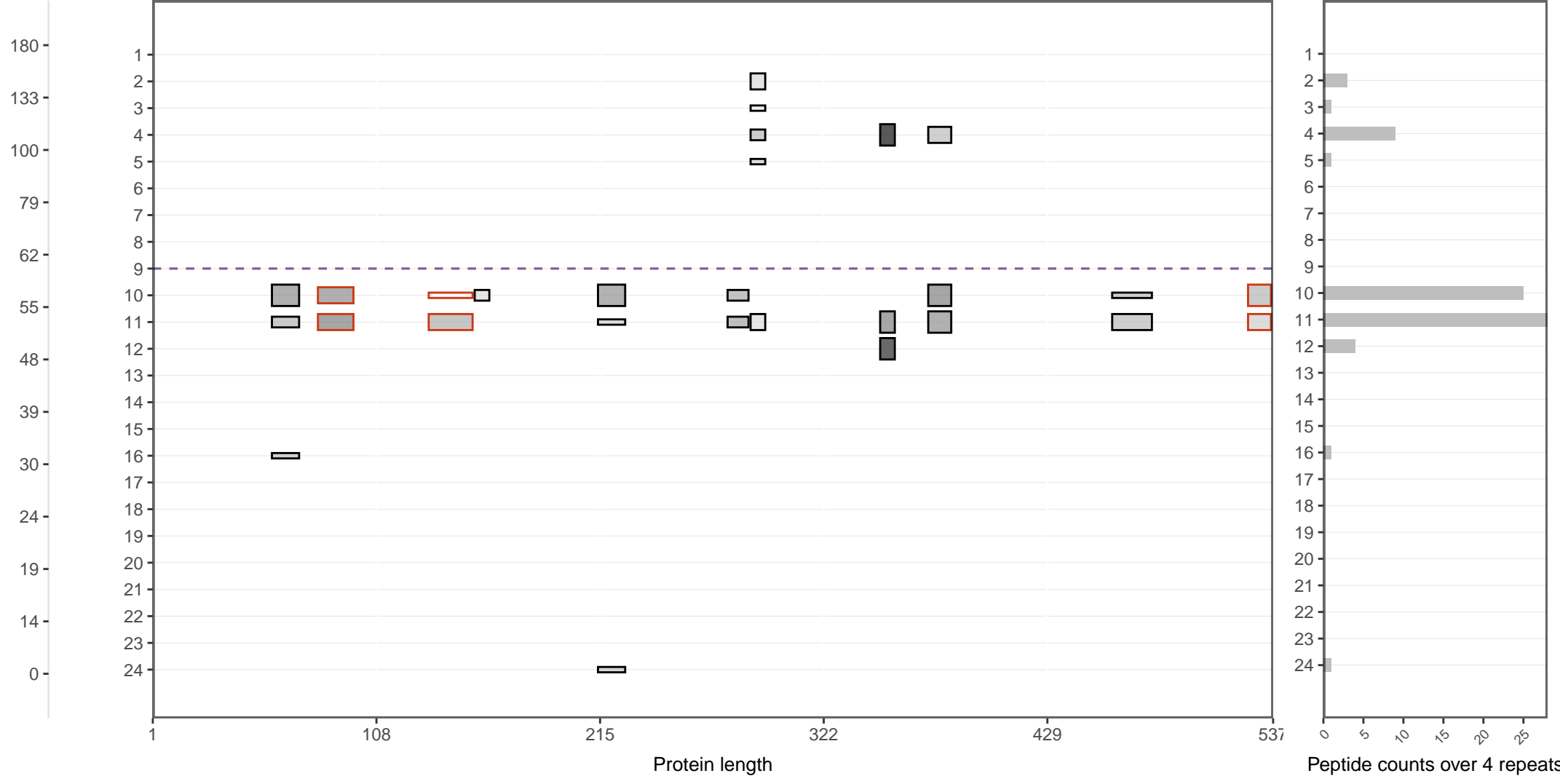
IKKADISSPDIHRRIIDRRERDRERDLKREKERELERYERERERGERAKREKERDYKIREDERRYVREKEVEEKEREREYWRKKEREREREKERADGERKWDINEGEREDEGDYVRKHRTSDEERKRKRROREKEDDLADRLEKEEEIEAEKRRADEEHQKKEGEFEALKILSGHLANGREKAVSHEENLESQDKNETAHQNLGGDGGIVQNGTDEESVLAATASSDMKHSNAPAKRFGGLGSGKRAAVPQVFNADDEDTQKEKMRPLVDYIEDERIVMVPQPSISE

NbL18g08970.1 aldehyde_dehydrogenase_family_2_member_B7_mitochondrial-like [MW = 58.53 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF00171 Aldehyde dehydrogenase family

Protein sequence:

SFGPTAGAPLCSIMDVSKLAFTGSDTQKAILSLAASKNLKFPVLELGGKSPFVIGEDADIDTAVEGAHFALFFDGGGCGGAGSRTYVHEKYVDFLEKAKARALKRTYDGFKSGTEGGPGDQKGFDMIMNYRQGDGSGATLETGGERLGERGYIKPTVFSNFKDMLAQDEFGLVDSIKFKDLDDVIRRANNSRYGLAAGVFTQNDTANTLRLRVGTWVWVNCDFDFTDFGQYKMSGHGREKGEYSLKNVLGKAVVPLNPAWL-

NbL18g08950.1 synthase [MW = 38.14 kDa]

No. of times detected



log(intensity)



Values from



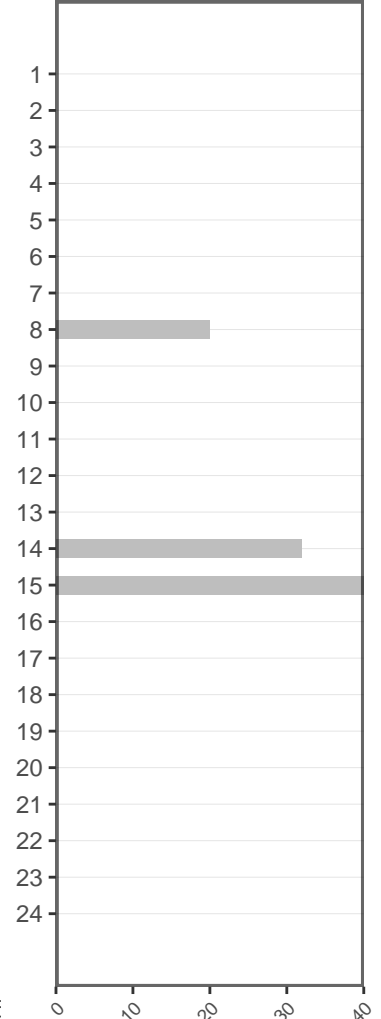
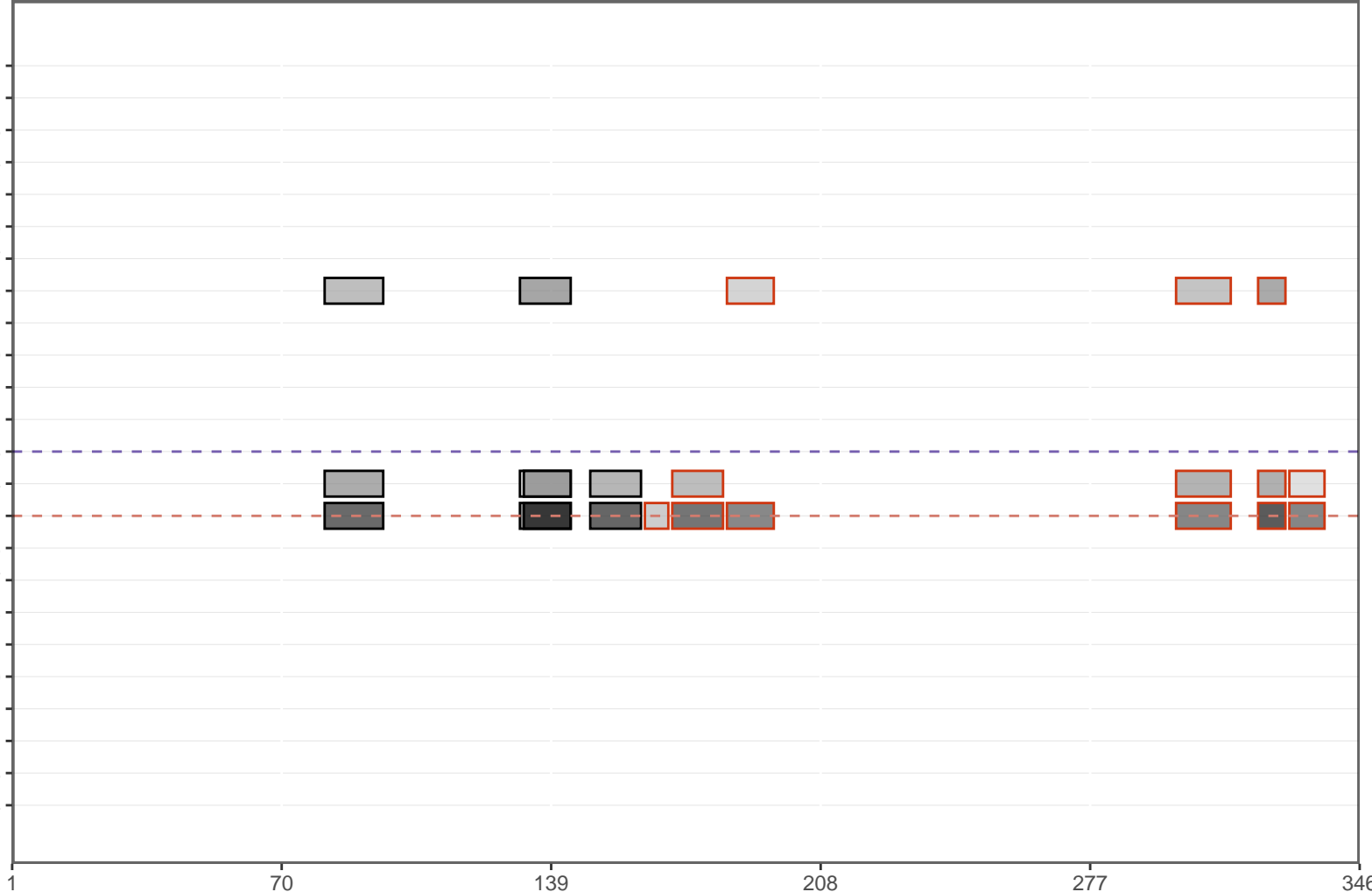
MW indication



Molecular weight

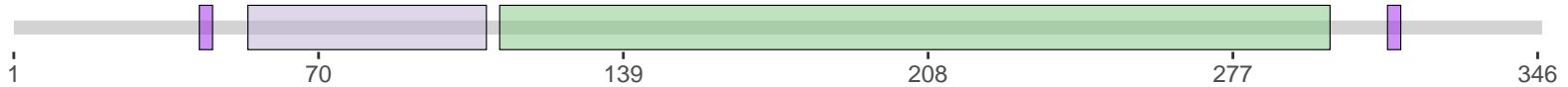


Gel Slice



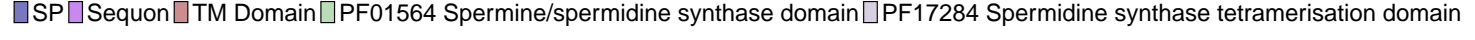
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ICEDIKMVEVSKQFFFDVWGWGVEDPRVNLHIGDGVAFLNKVAAGTVDVIVDSDPDPAGELFKPFPEIARALRPGGVSTGAEGIWLHMHEEIVANGRUFIKGSVWYAWTTVTPYPSGMIFMLGSTEGRVDFKINPNIPDEDDVSHNKTLGPKLKFYNSLHKASFCLPFAKRVIESGKI

NbL18g08850.1 AP-1_complex_subunit_gamma-2-like [MW = 96.03 kDa]

No. of times detected



log(intensity)



Values from



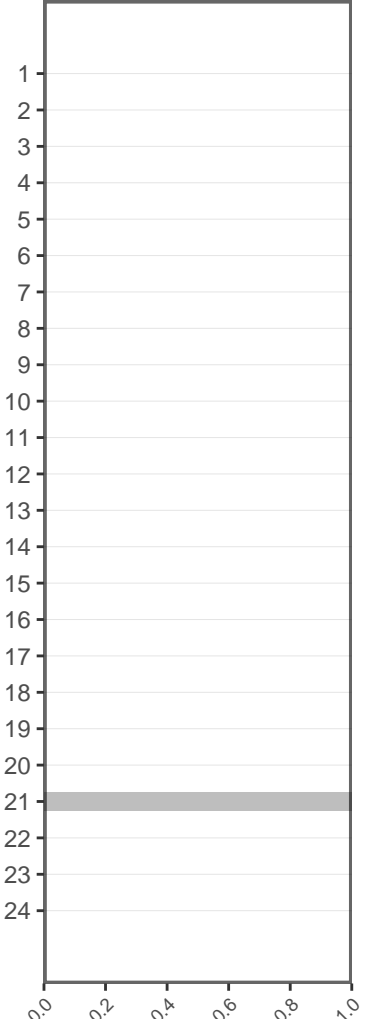
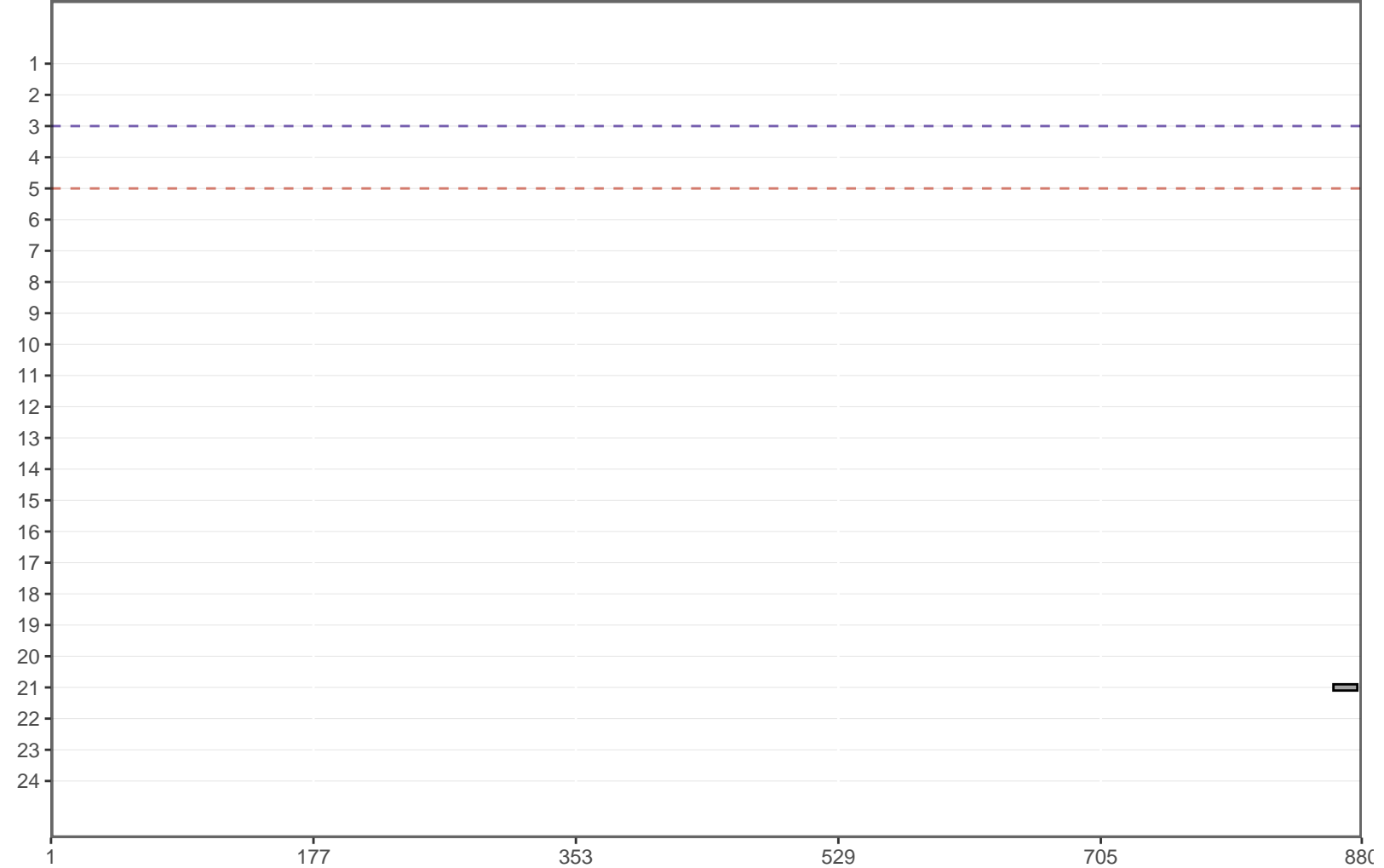
MW indication



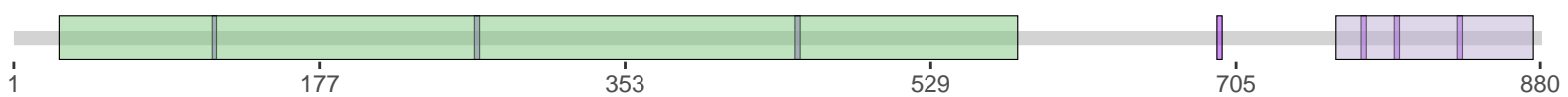
Molecular weight



Gel Slice

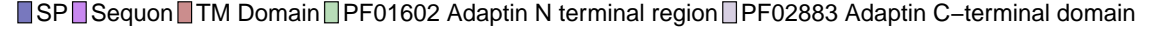


Protein length



Pfam domains

Pfam Description

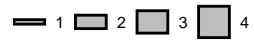


Protein sequence:

PEAGNYKDEYVHSLFVITNANLHGVAWRSLRAVGAAGEGETLRVAVWVWCGEYEDMLVNNAGRLDIEEPFVTESDAVDVVETSIKSHFDLFTGAMCLIALLLKLSERFFPCGGRINDIVQYKGFVLELQRAIEFNSVIERHONRIPGLVERMPVLDATYSGKKKAGSLPAGSTSGGVVNLNPGVWKPATPLVLLDL6SDVAAPSS6GDFLQDLGVDLAFV6SGSGTNGAGKGTDLVLLDL6LIGTPAN6SPFTTGV6SP6NVDIR6PVCLLDLR6LSSP6SFS1

NbL18g08830.1 threonine--tRNA_ligase_mitochondrial [MW = 53.09 kDa]

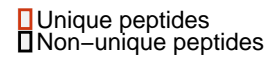
No. of times detected



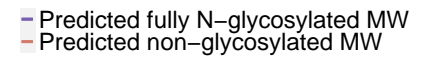
log(intensity)



Values from



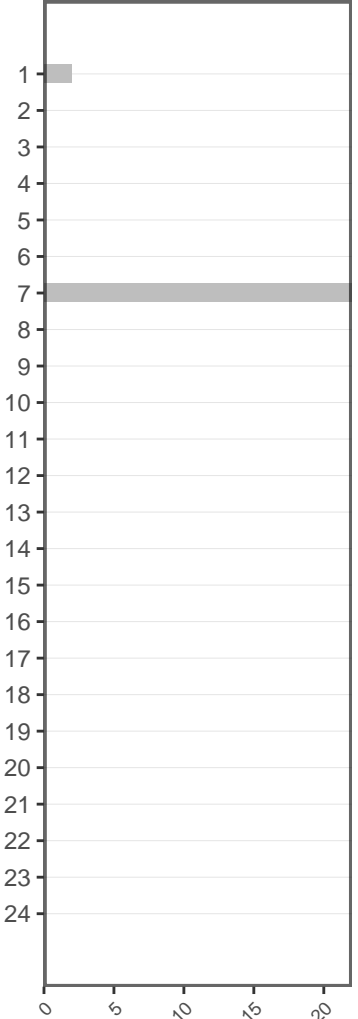
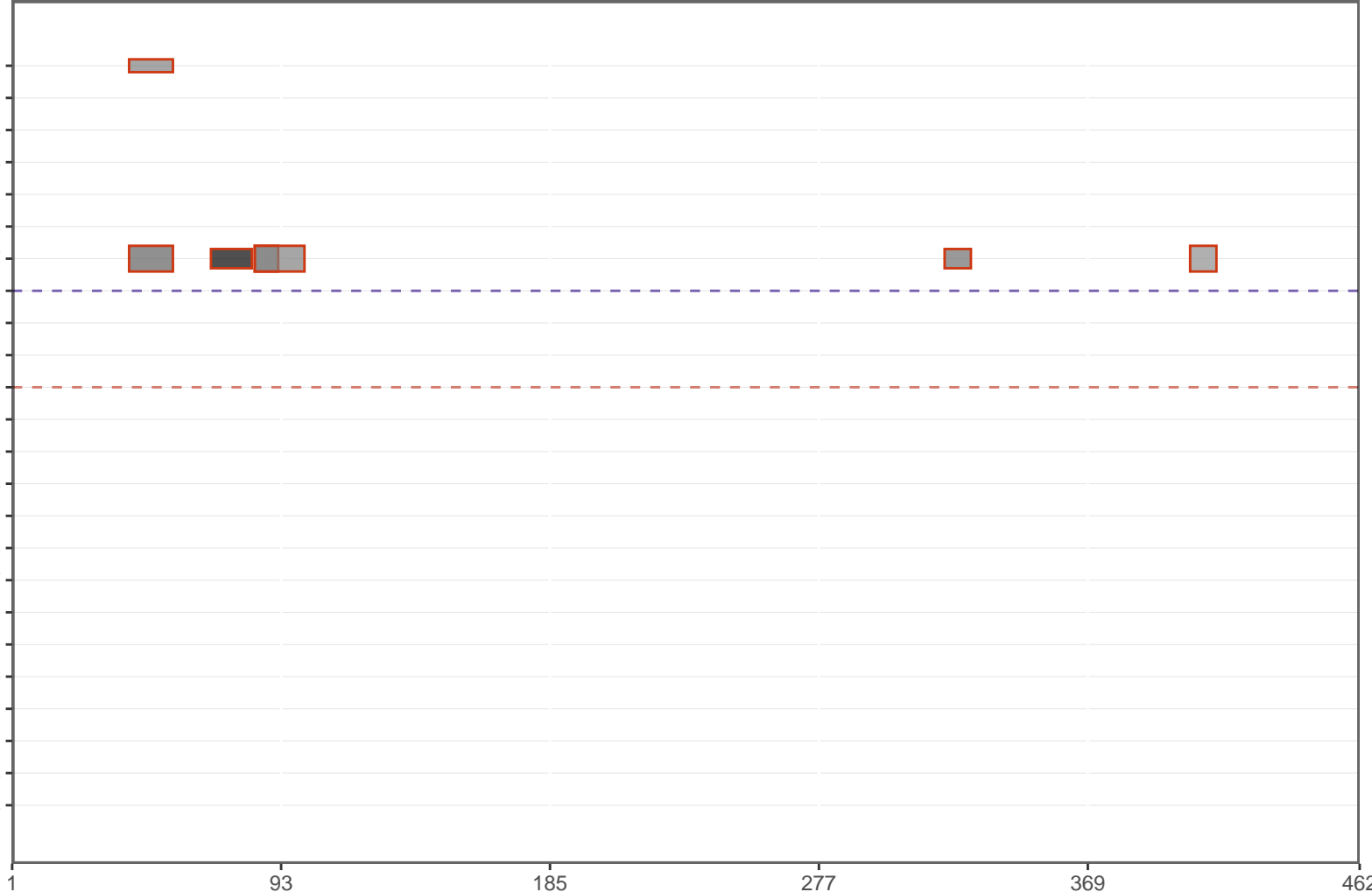
MW indication



Molecular weight



Gel Slice



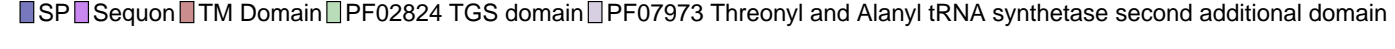
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

VSEKQPFERIEVSRGGALDMFSDNRKVEIKDLPEDKTFTVYRGGPLVDLGRGPHIPNTSEVKALACTKASSAVWRGDKRESLORVYGI6VYFDKIKLQKYLAMEEAAKQYKRELTAKGELFFHSL6LPGSCFFLPHGARVGNKLEFIKHQVYKRGYEEVWSPNAYNMQLWETSQHAANYKENMFVFEIEKGEFLKPMNGPGHGLLITEFVPTGSHSVAWLTLEFYTGMRPVVHLLA*

NbL18g08760.1 MLP-like_protein_423 [MW = 16.82 kDa]

No. of times detected



log(intensity)



Values from



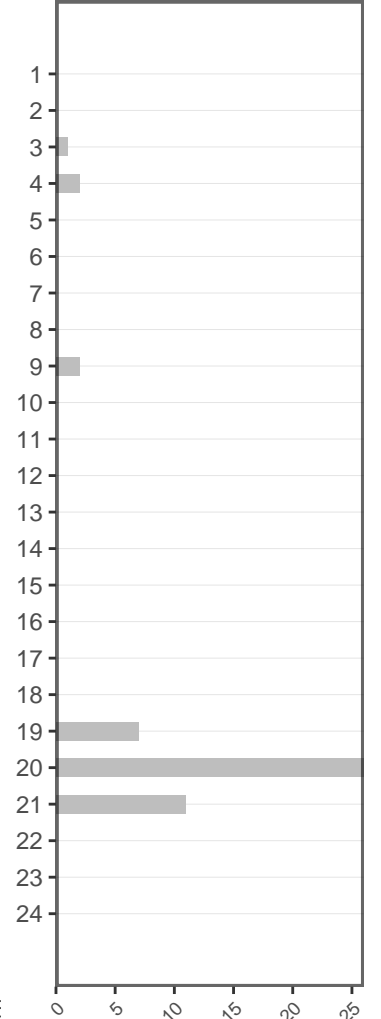
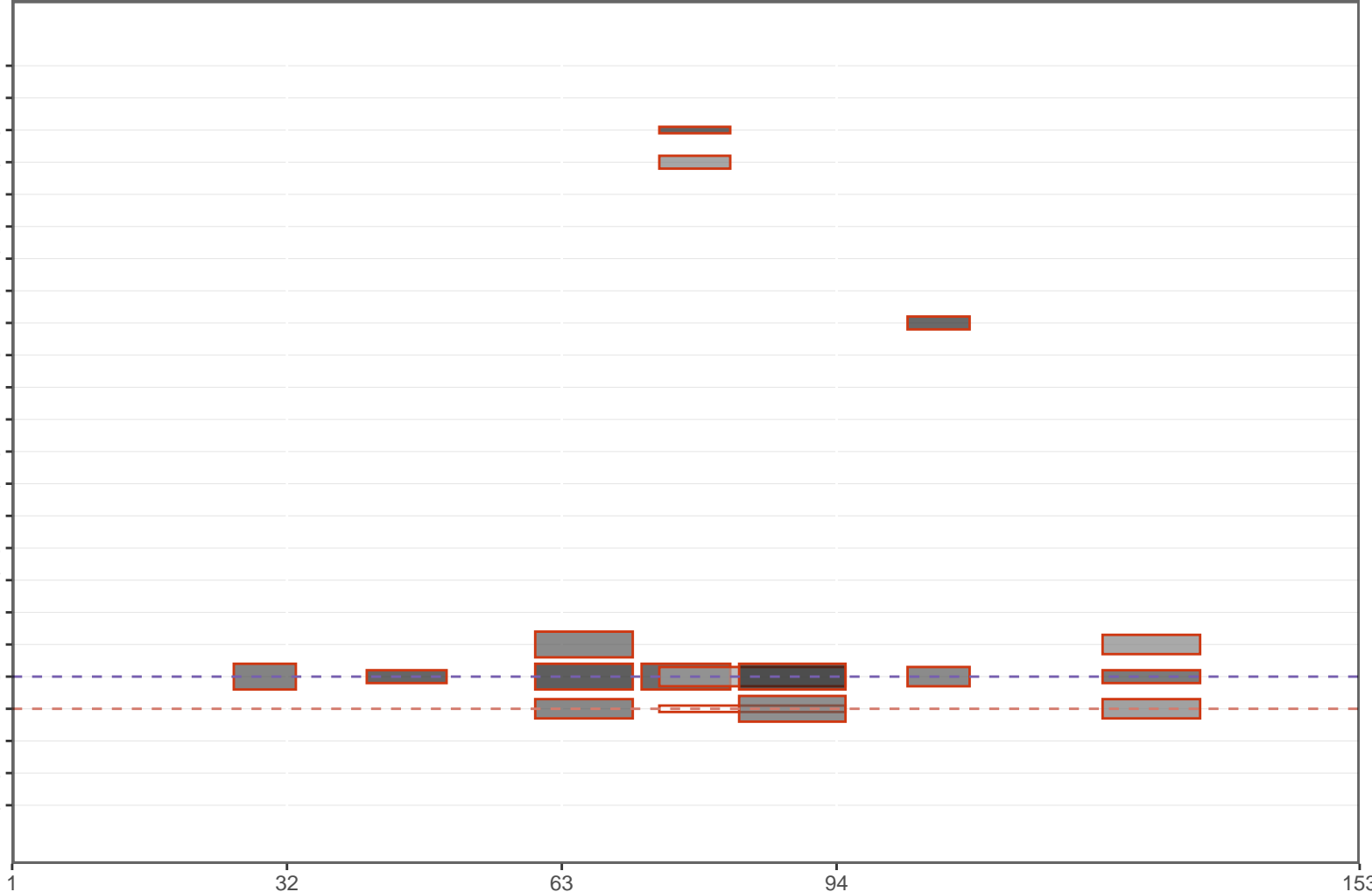
MW indication



Molecular weight

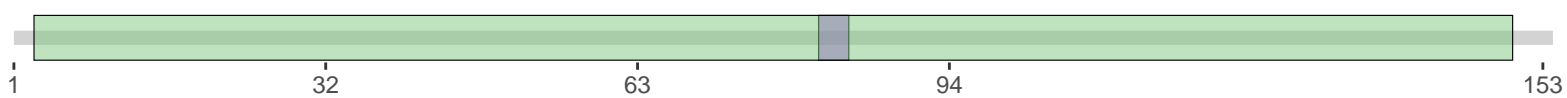


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SSPLVTFAXEKIESVDEGNKTVVYVVDGETMKYKYSFKGSLTVSPKGDGSSLVYKWCGEFEKASDEVPEPOLKDFAVKFKDLDAVLGA*

NbL18g08740.1 30S_ribosomal_protein_S13_chloroplastic [MW = 21.93 kDa]

No. of times detected



log(intensity)



Values from



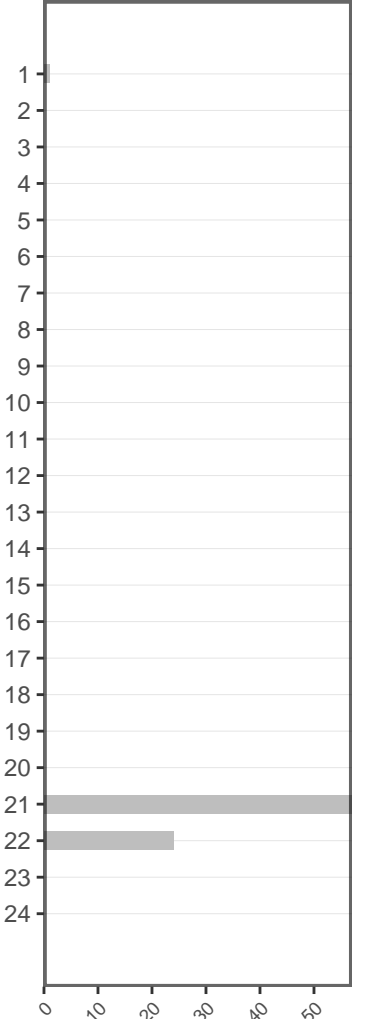
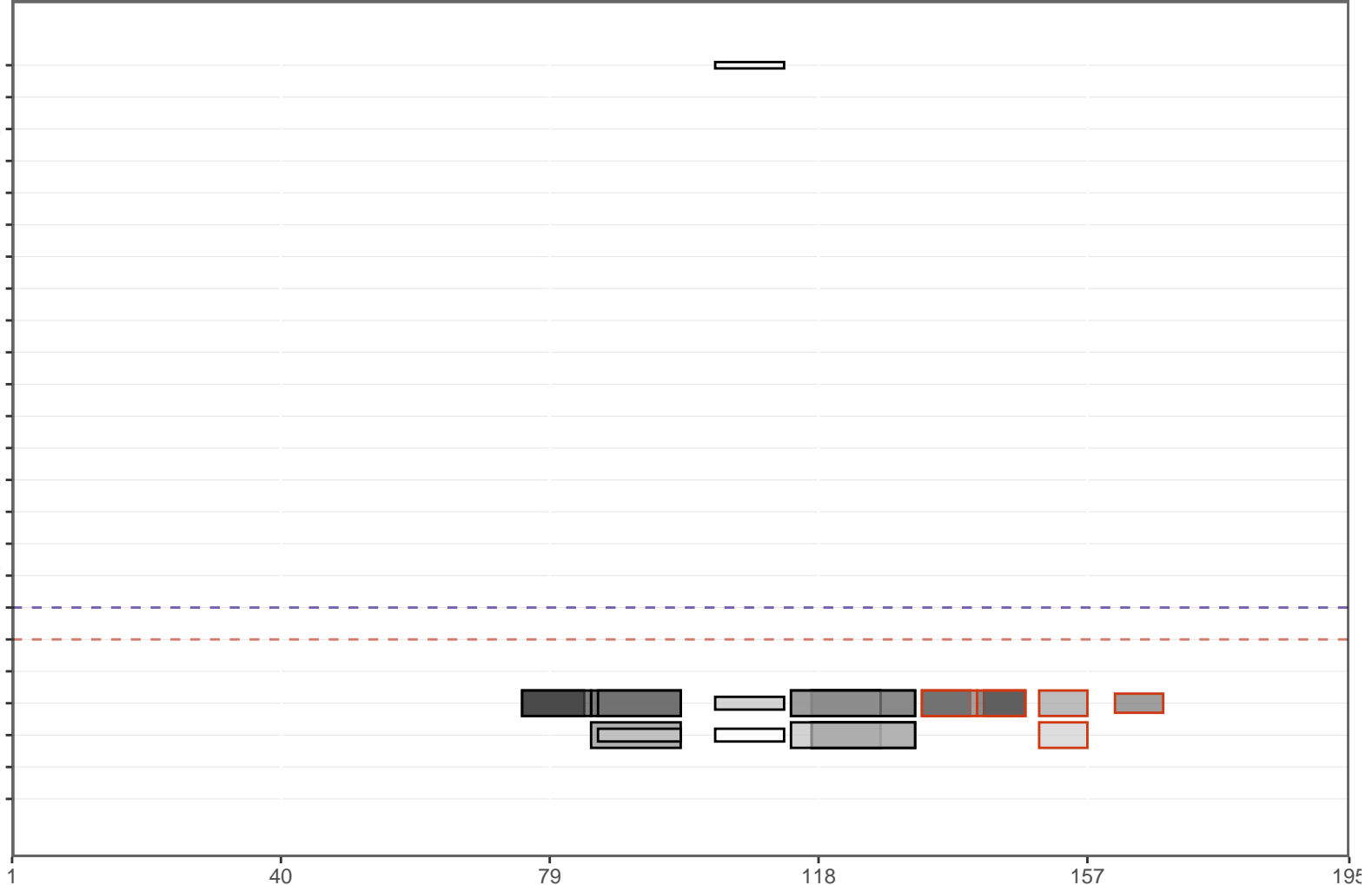
MW indication



Molecular weight

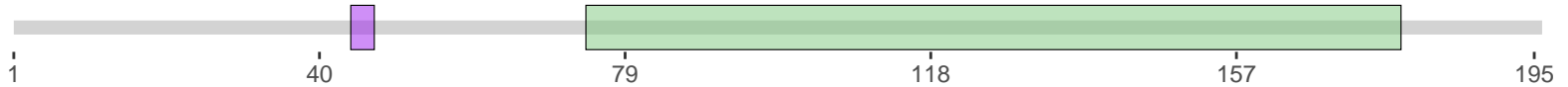


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RVFEALQYIHGIGRTBARGILVDLGIENKIMKDFBEEELFLRDEVSQYMEGDLRRFNALAIRLKEIGQYRQVRRHQGLPDRGRRTNNGRLLKGGKVAIAKQKAPR

NbL18g08630.1 uncharacterized_LOC107812748 [MW = 40.41 kDa]

No. of times detected



log(intensity)



Values from



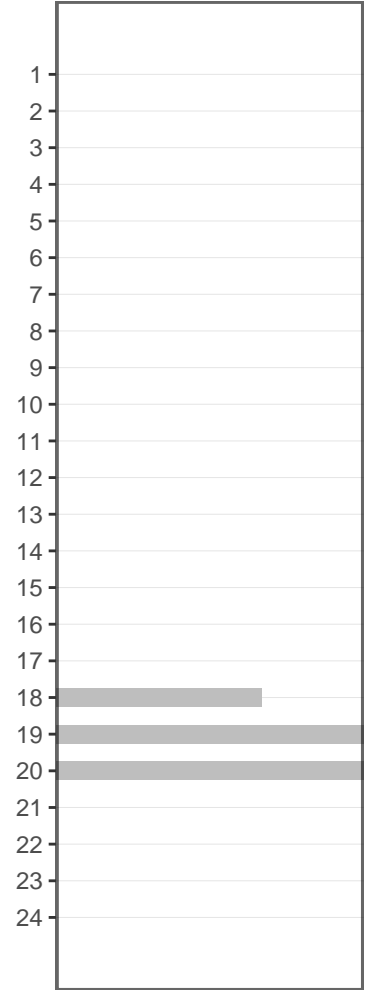
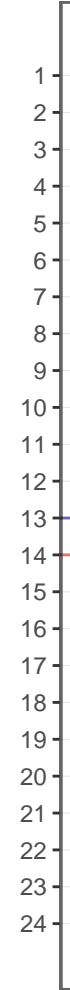
MW indication



Molecular weight



Gel Slice



Protein length

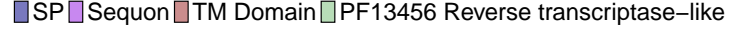


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

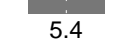
KSGTSDHLPIKRSQEMMSEYADVGSVAVPNDIRKHVKIEHKKGDQVLAIPSGGRGCTLEFDGASKGNPQAGAGAVIRADDGSLTGRLEGLGWATSNHAEVRAFILGLKVALSKGFTNIRVGGDSKLVCMQGGGLWVKNNQINATVFEQAKGLKERFLTRRHVLRRESGSDADQGANLAVELAEQGGQEEIEK

NbL18g08550.1 uncharacterized_protein_At4g28440-like [MW = 13.82 kDa]

No. of times detected



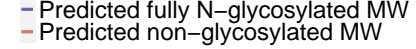
log(intensity)



Values from



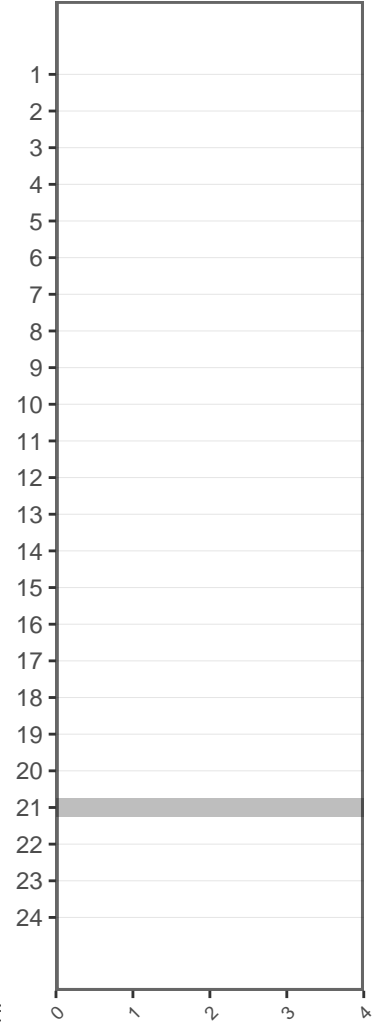
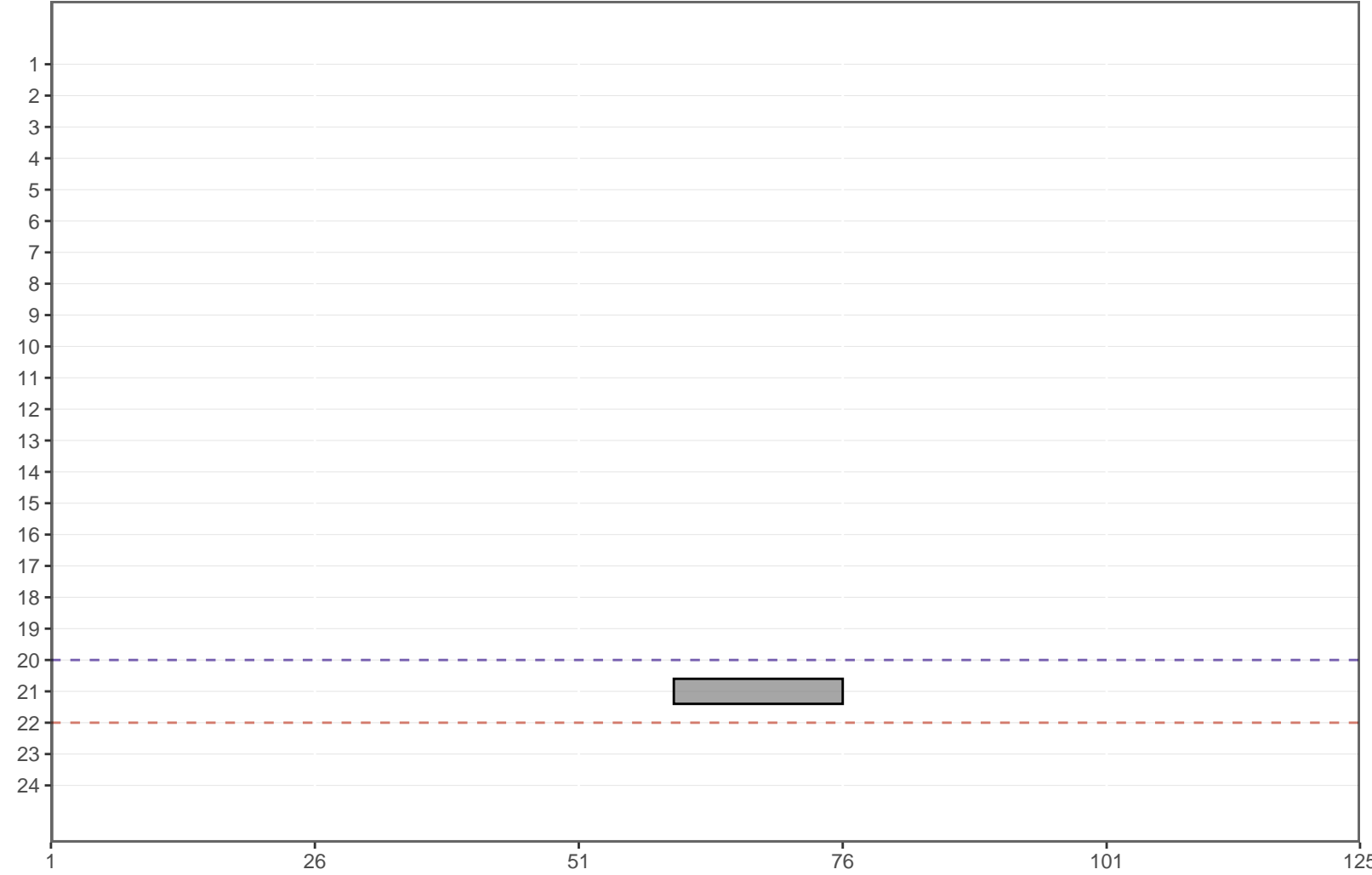
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



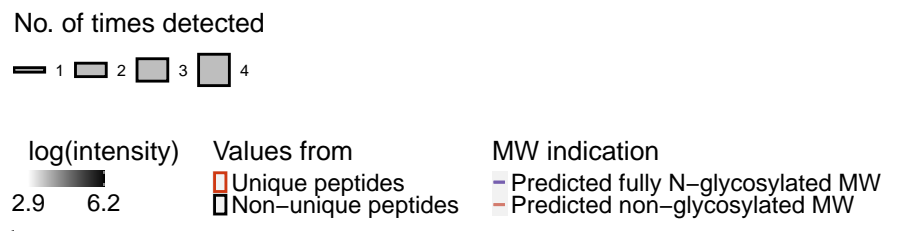
Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

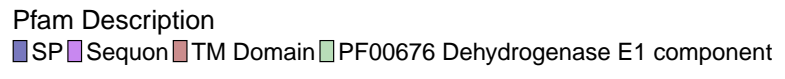
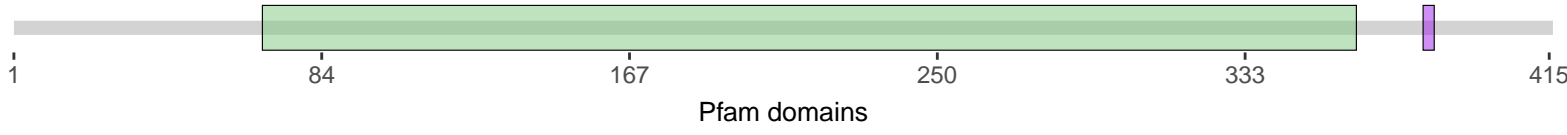
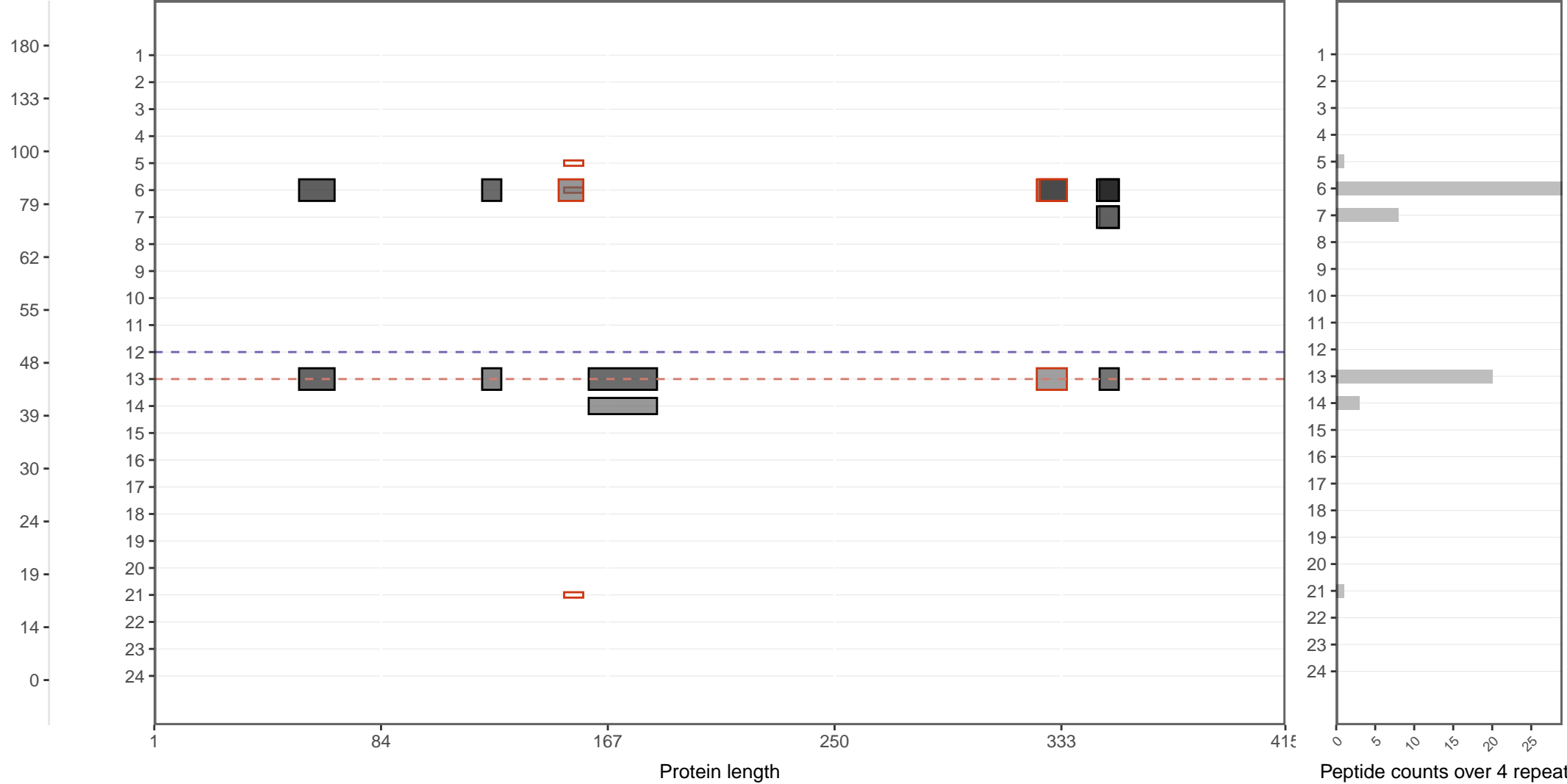
DETGIIETARNDQVDLIGEGSTLVTKAKVDMFKGSMRLAVDRFGRIEVGPGASFSVDGDNMSLIEFERVDVYV

NbL18g08290.1 pyruvate_dehydrogenase_E1_component_subunit_alpha_mitochondrial-like [MW = 45.9 kDa]



Molecular weight

Gel Slice



Protein sequence:

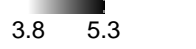
MTYDGAANDCQLFEALNMAALWDLKPLVGENNHVGMGTAEWRAAKSPVYKRGDVYVPLKVDGMDALAVKGAGKFAKEHALKNPHEMDTYRHHGHMSDPGSTRTRDSEIGSVRGERDPIERIKLILAHDSIEKELKDIEKEKRNIVDEAIKAKESPMPPDPSELFTNYYKGFGEVQNGSNHGFELNVLKATVSRNGVMIAQFLEHII

NbL18g08060.1 HIPL1_protein-like [MW = 78.01 kDa]

No. of times detected



log(intensity)



Values from



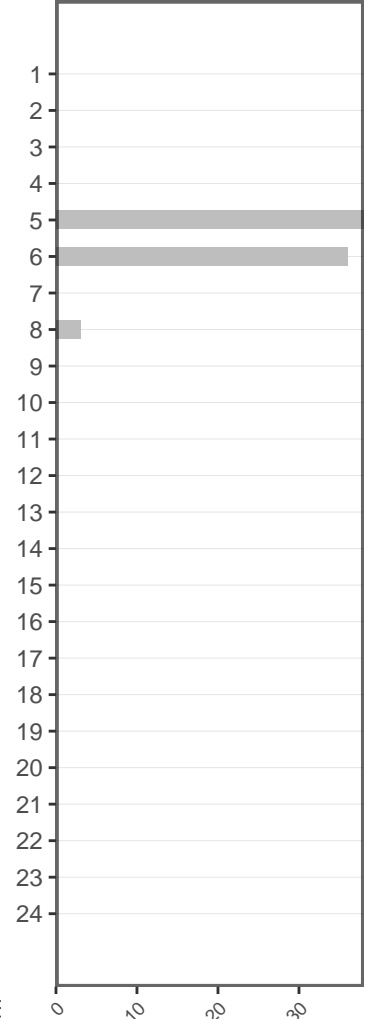
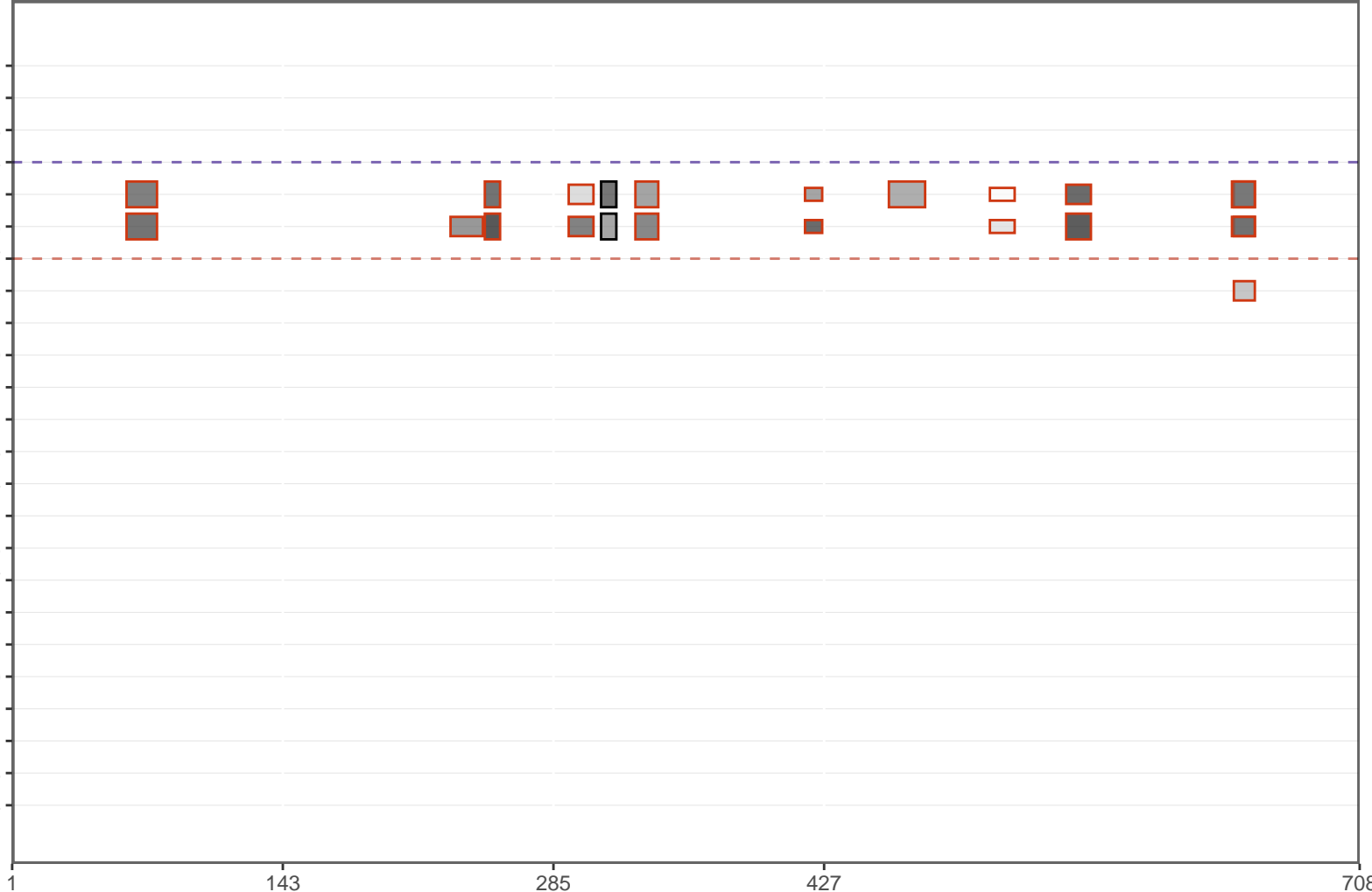
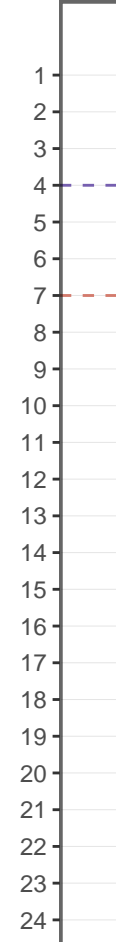
MW indication



Molecular weight

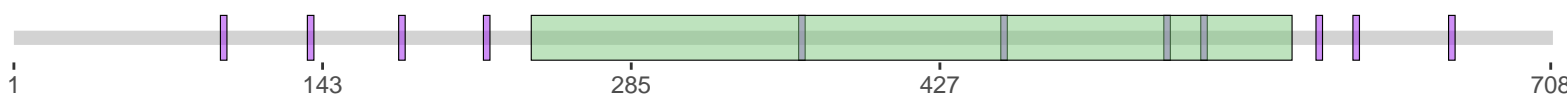


Gel Slice



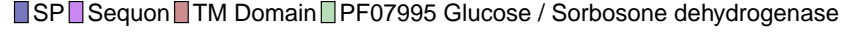
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

QNSDDNKQPCQYHTVAEFSVNGTAPNPKAEKAPSEVRRIFMTGLPFTANHGGLFQPEDGVLVMTGGDGGKGDGFNFAGNKKSLGKIMRVDINDP6GEEISDLGHWGNVSVPRDNPYS6DKDLGPEWALGLRDPVWRCGFDGERPBYFCADYGDDQYEEVDITRGGNYGWSMVEGPFPRFNKASADD6MDRFPVLGVNHSDNKEVGSAAISGGYVVRKTDPGYGEVYGDLYANFNFWAAGENPNYNSGNFTFRDIPFSGAHD6PLNCSVYNSPLPALC

NbL18g08050.1 glutathione_S-transferase_U17-like [MW = 25.33 kDa]

No. of times detected



log(intensity)



Values from



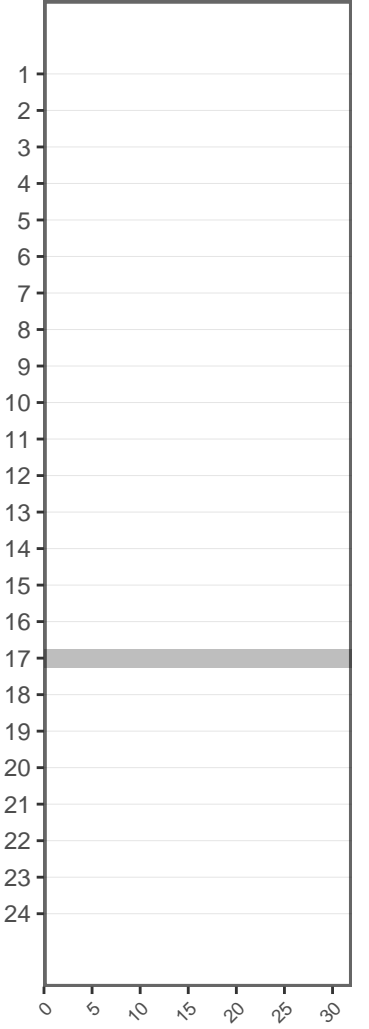
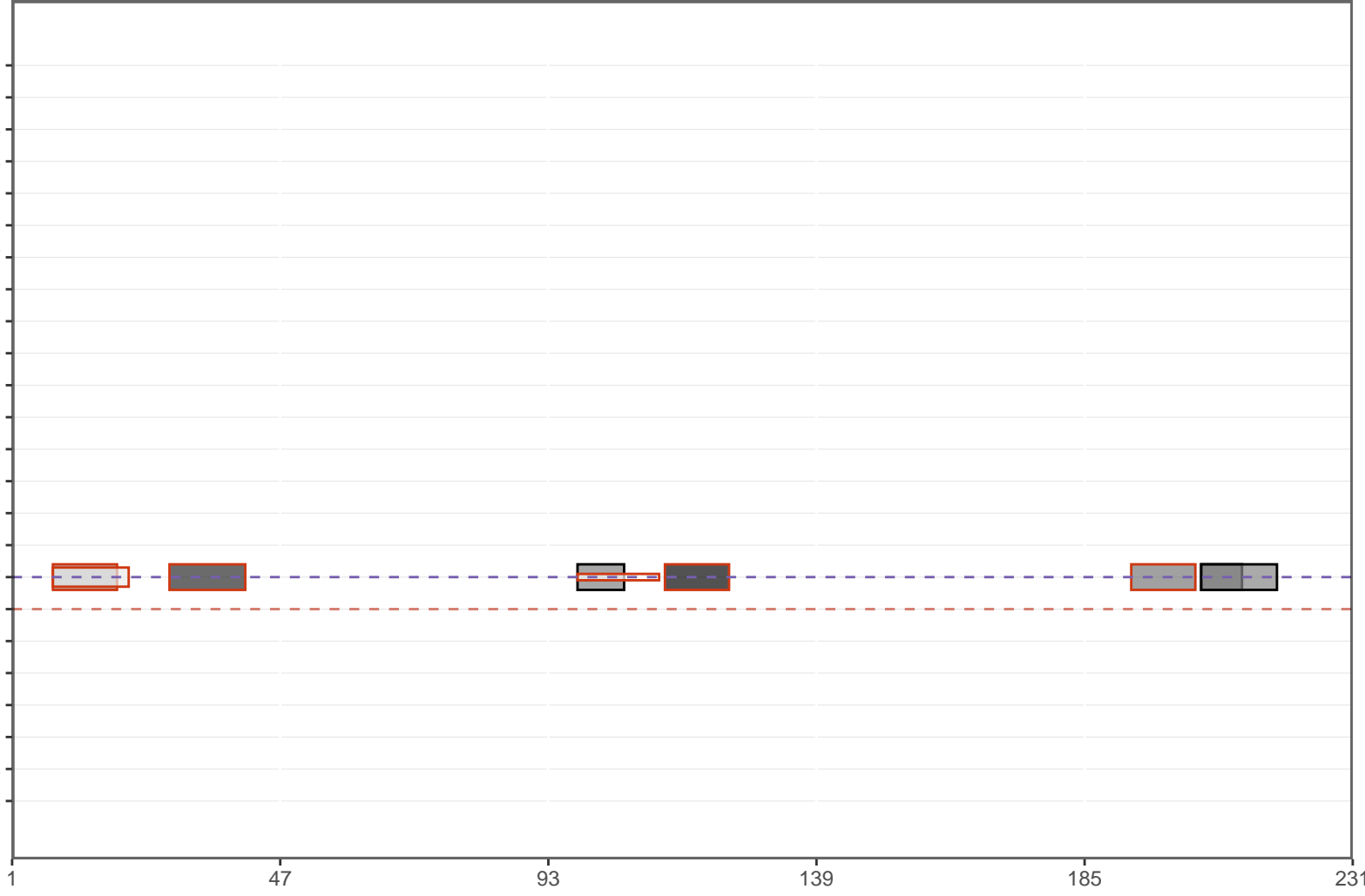
MW indication



Molecular weight

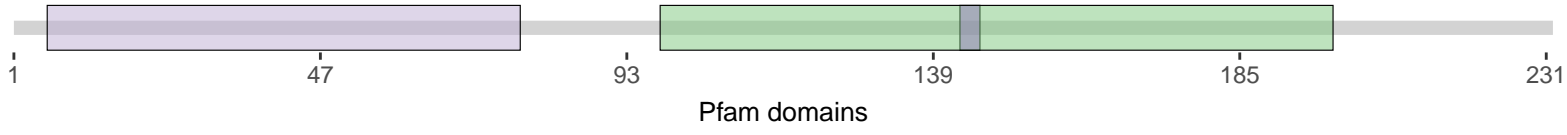


Gel Slice



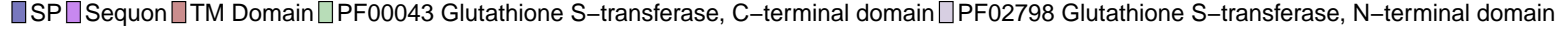
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SKWFFAMRGIAAAGGEDAGKATEPVEGLVLEDAFKNGSEGNKFFGGDKIGYLDALGGFLGWMRVTEKLNKLLDEVKTPGLQKWAEDFGADSAVKDMFPTDKLAEAAKVMKIRAGASS

NbL18g08000.1 tetratricopeptide_repeat_protein_38 [MW = 57.38 kDa]

No. of times detected



log(intensity)



Values from



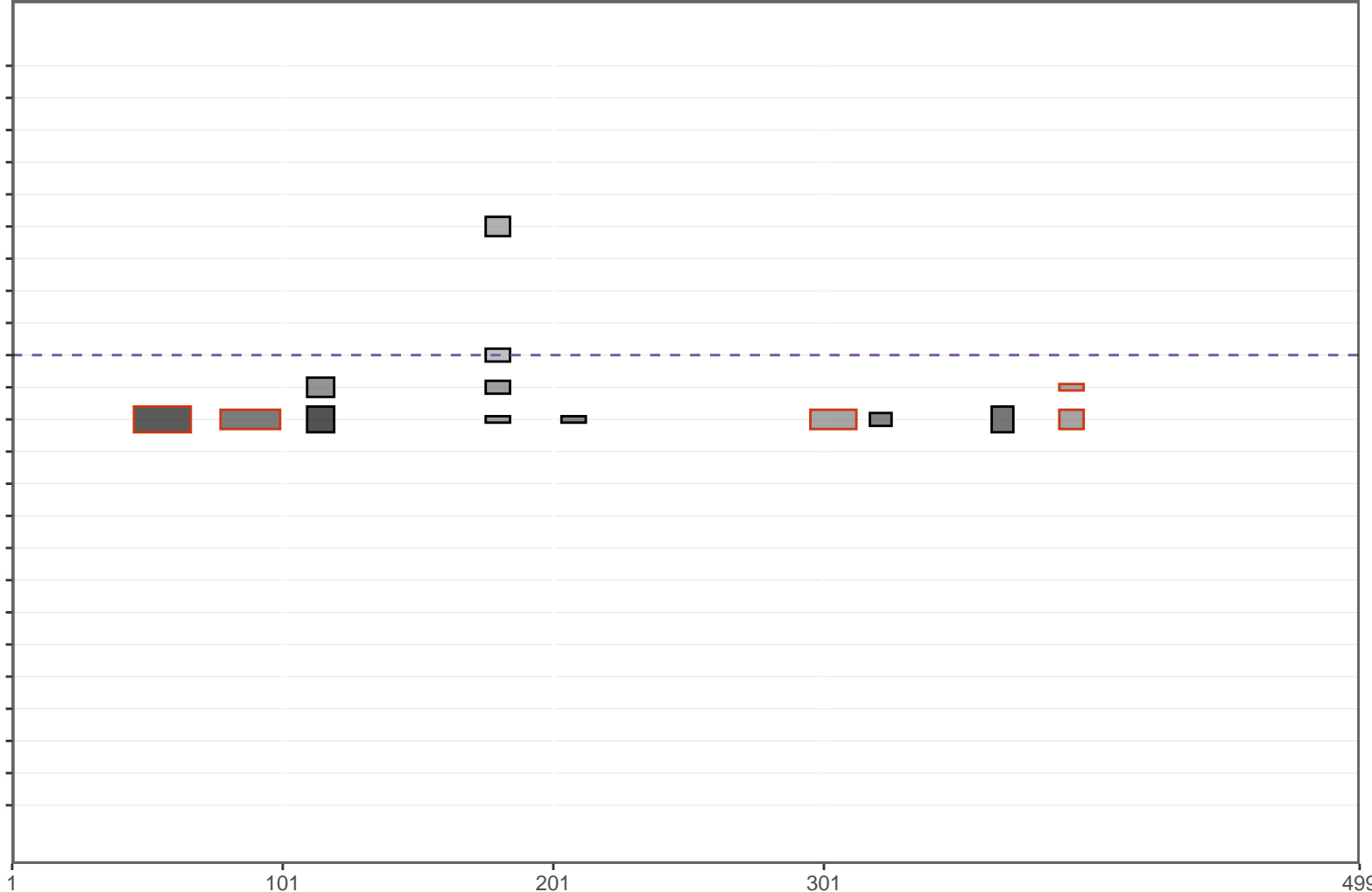
MW indication



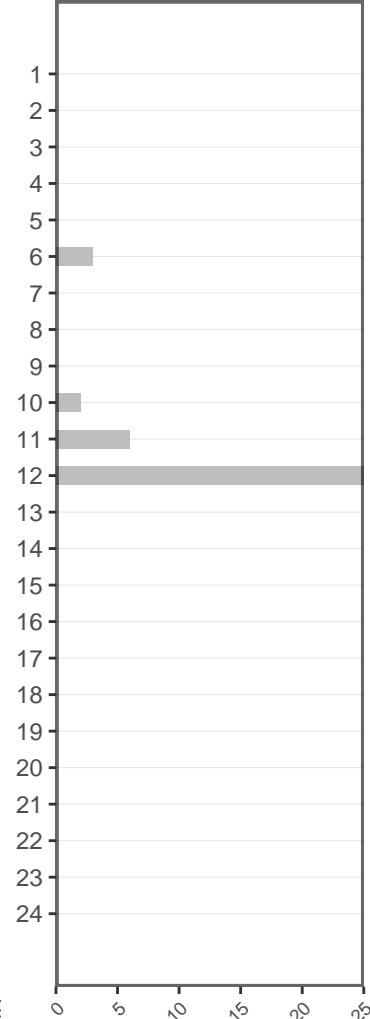
Molecular weight



Gel Slice



Protein length

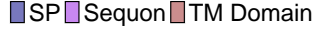


Peptide counts over 4 repeats



Pfm domains

Pfam Description



Protein sequence:

CEAVQFMKCSRTWSLSLSSFMVTHNHWVHVALDYLEGHSQMEKVRDVFQDNHWKELERSDASPEVYLVNVLGLLLRVYVROGINVFGDRLKLADLCTNFKAFVLEWHLDVAVVWALSFTGEVKAELLEGLKSRMSKMTKKQRHMQRAMLLAELFRYKGENERALELLGEPFDANVYKIGASDEGLDFVNEVWITMLNSGQVTKAIGAIERGLKREGTPTFLWRLEKYSMSRKQEAIDAGKAGALEAAVFD

NbL18g07960.1 uncharacterized_protein_At1g27050 [MW = 24.87 kDa]

No. of times detected



log(intensity)



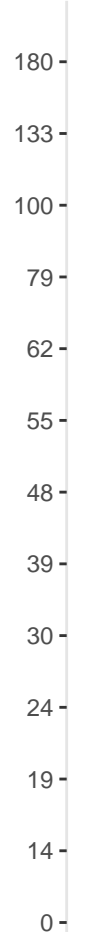
Values from



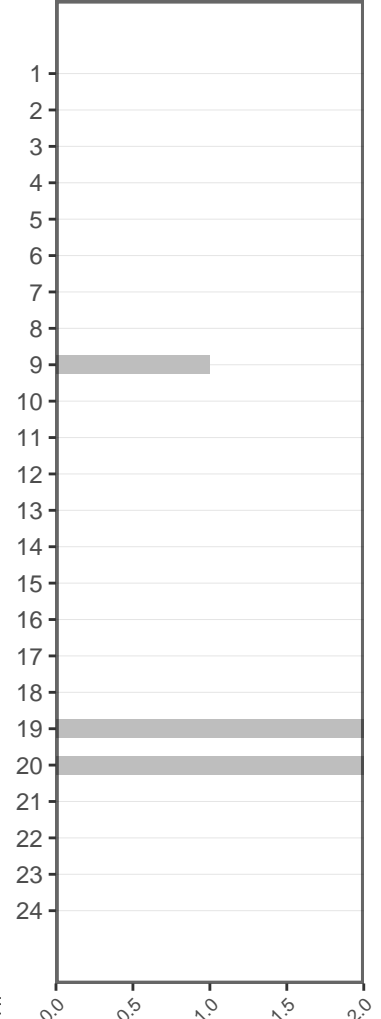
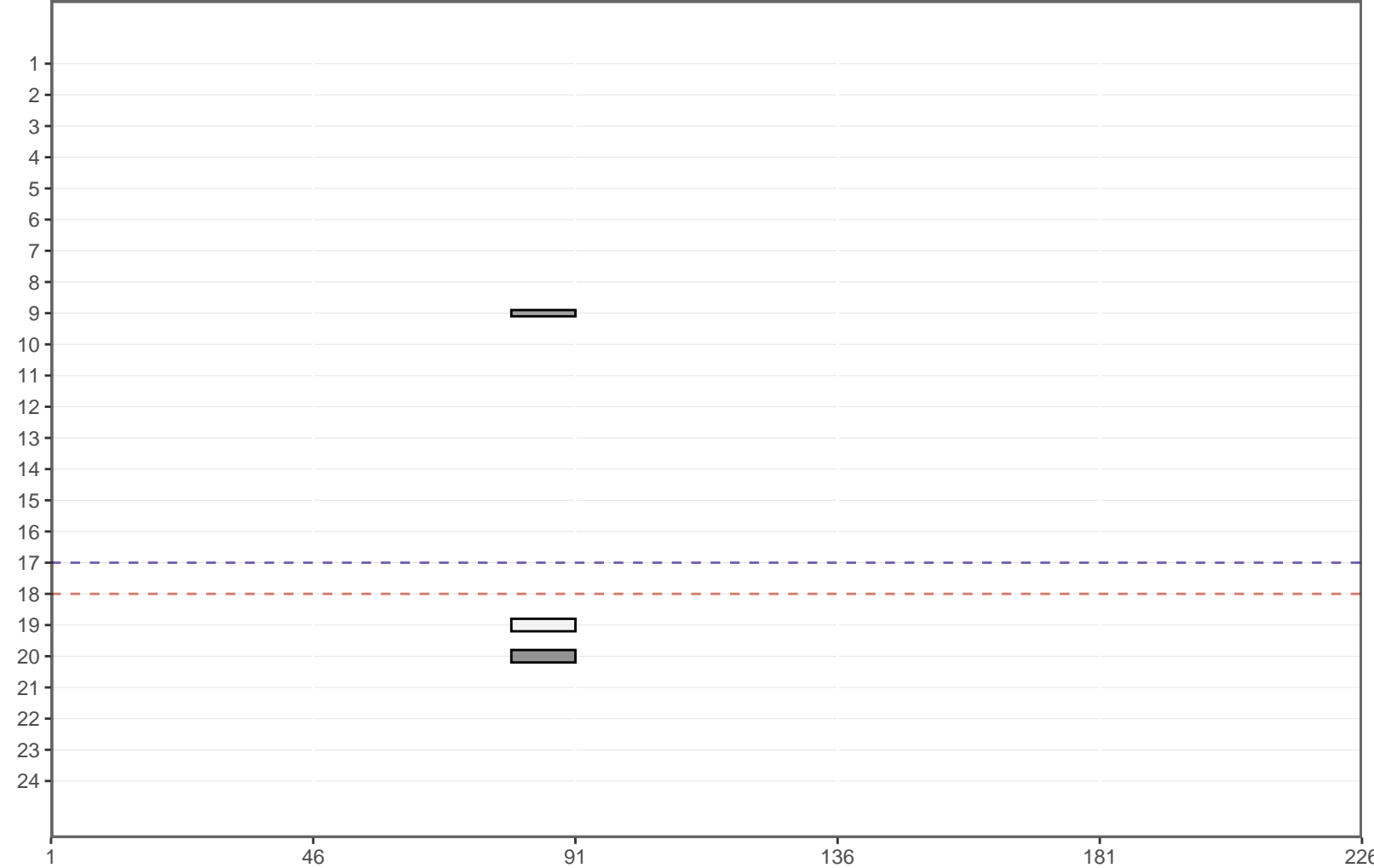
MW indication



Molecular weight



Gel Slice



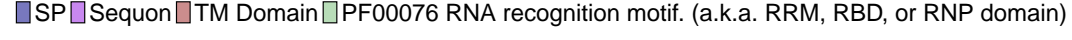
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NAVAGSSFPITLHISKPIGVWATDHPQWKEGVMRKDGLSTVAKLVRAEIPLRHRGNRLGSAVNPKDEDNDNAGNHRGHVSTRLGEFDNAGNDRGHVSTRLVEFVYKGRERWVDDLI

NbL18g07870.1 uncharacterized_LOC104243986 [MW = 42.67 kDa]

No. of times detected



log(intensity)



Values from



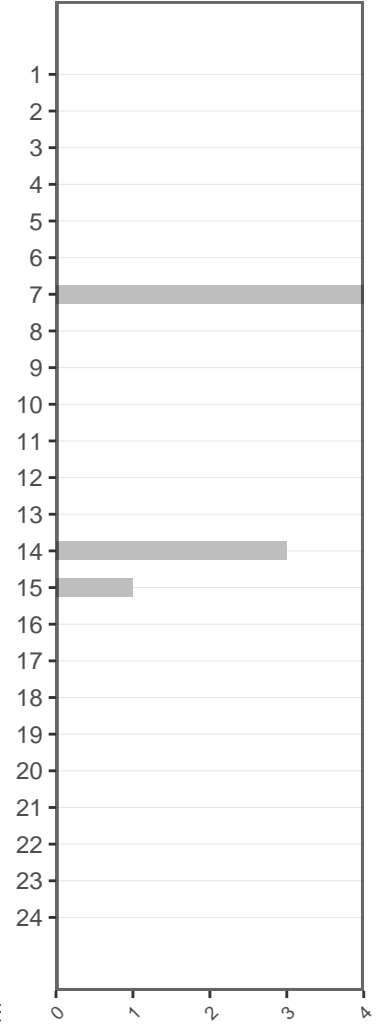
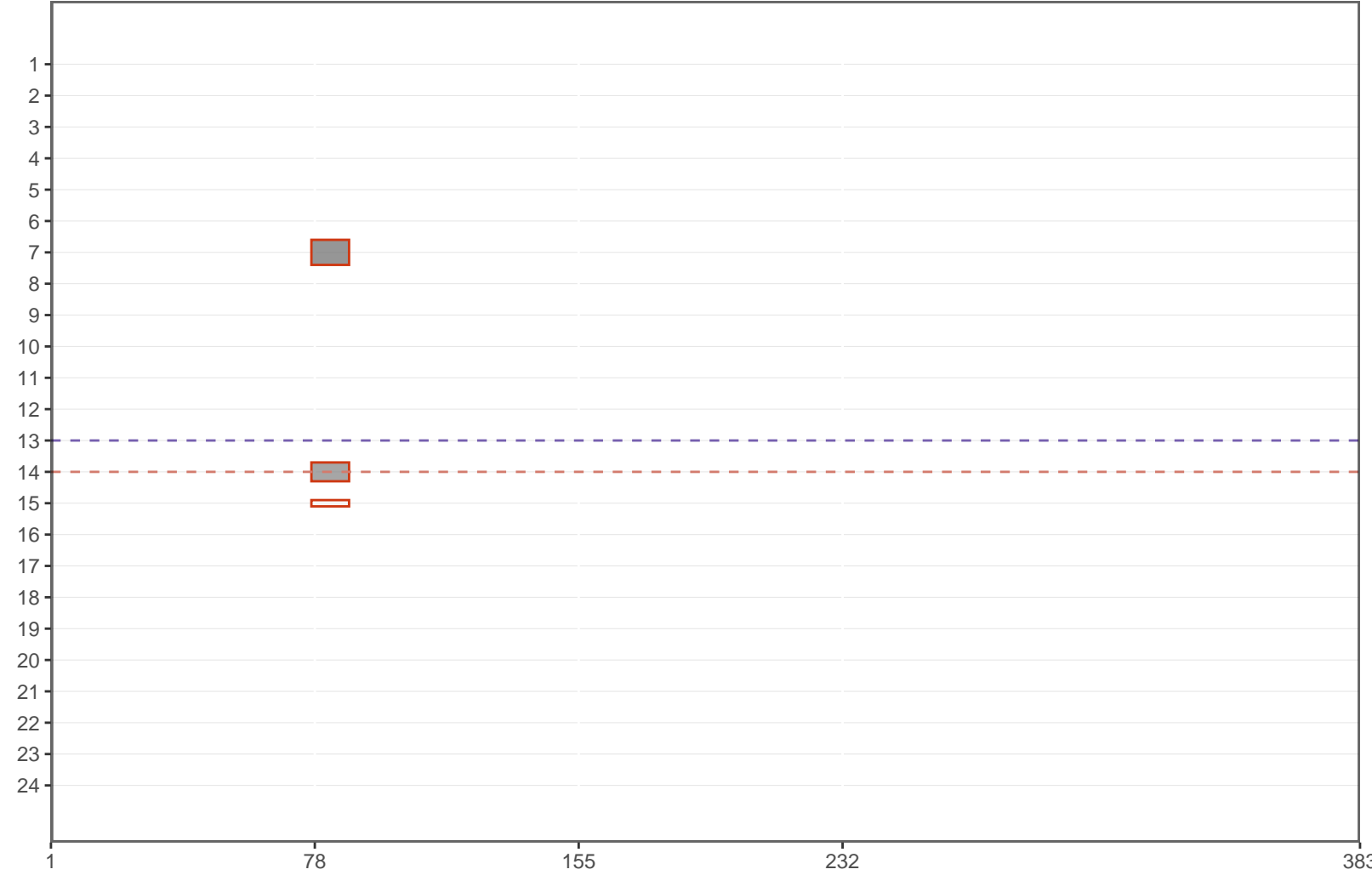
MW indication



Molecular weight

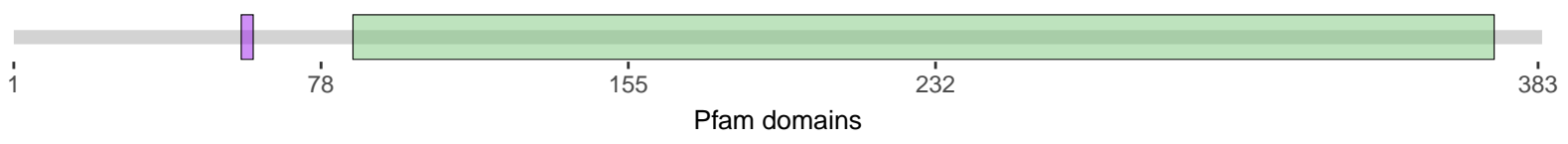


Gel Slice



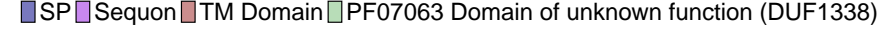
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RGSGVNGPLPRIFBELLVGLSPEAGDVKYKTDISGCGKEVYALASAFGTLTWKPFYSEFGQLARESEYAAWTLVNGYALNHVITSTHRLTSLNLSIGNLNGFEKNGNLNISEGGVLYVSPDGLLGGSTVADSTFFEFSDGITEAWPFSEYFAERLVALPQYKDLPEKVEEFHRRDGFVGNADKIFESTKDKDLTRAAV

NbL18g07850.1 single-stranded_DNA-binding_protein_WHY1_chloroplastic-like [MW = 29.43 kDa]

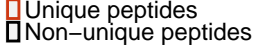
No. of times detected



log(intensity)



Values from



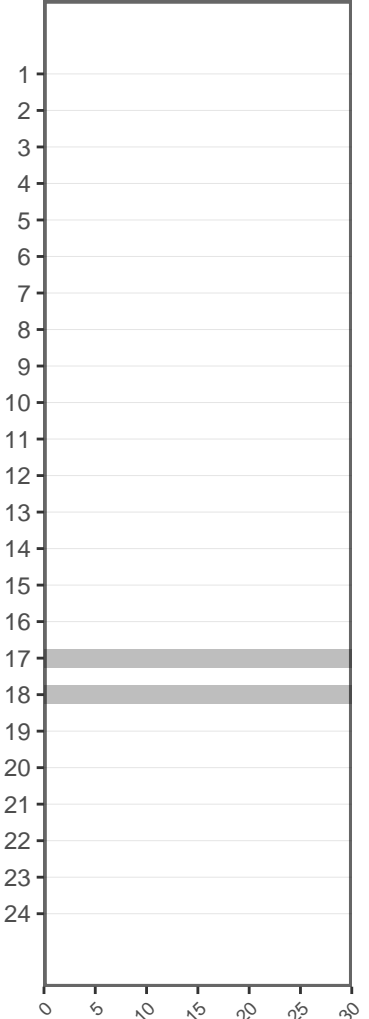
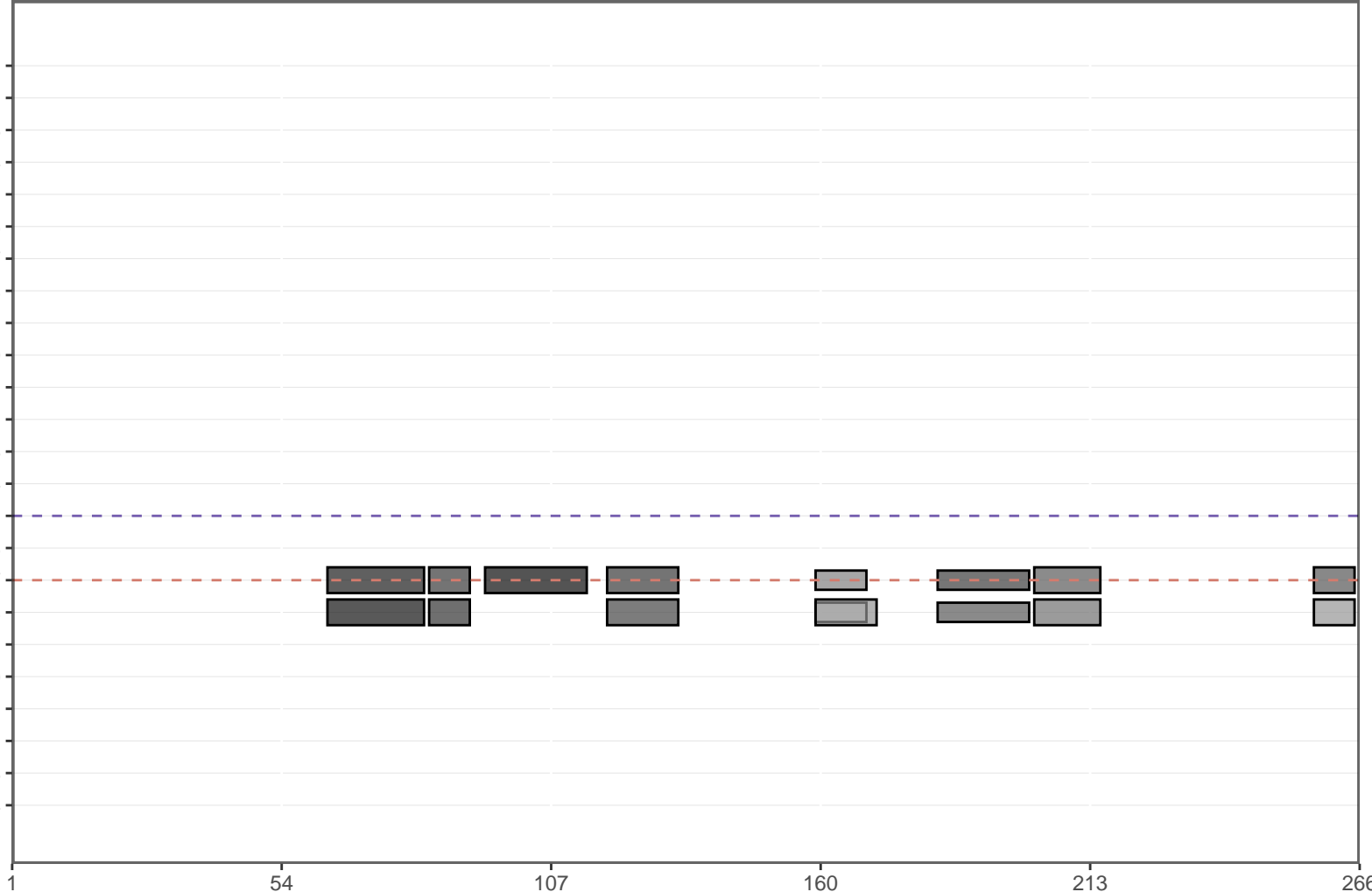
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

FVLLQFAPAGVYRQYDWDGRKGVFSLVETEMGSLISFGAKDSCEFFHPDKNGRDEGKVRKVKVKEFLPDGSGHFFNLSVQNKLNLDENIYPTKAEFALISAFNFVYPLLGWHTAVNSFKPEQASRNNANFRSGADLEWR

NbL18g07810.1 fumarate_hydratase_1_mitochondrial [MW = 50.36 kDa]

No. of times detected



log(intensity)



Values from



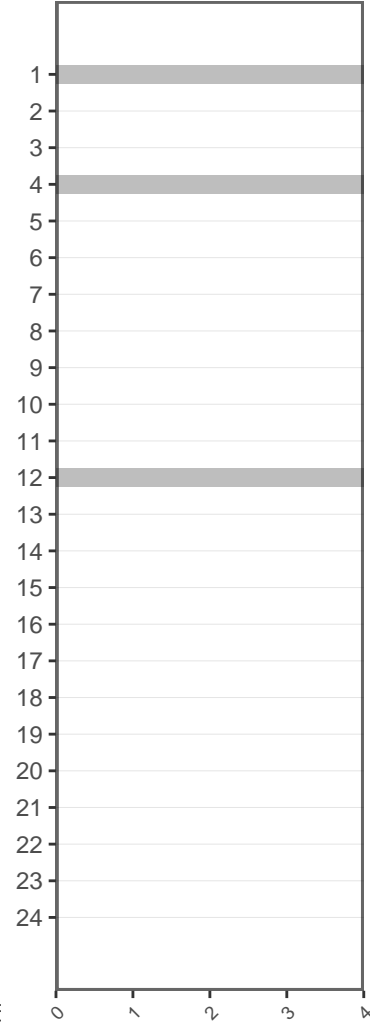
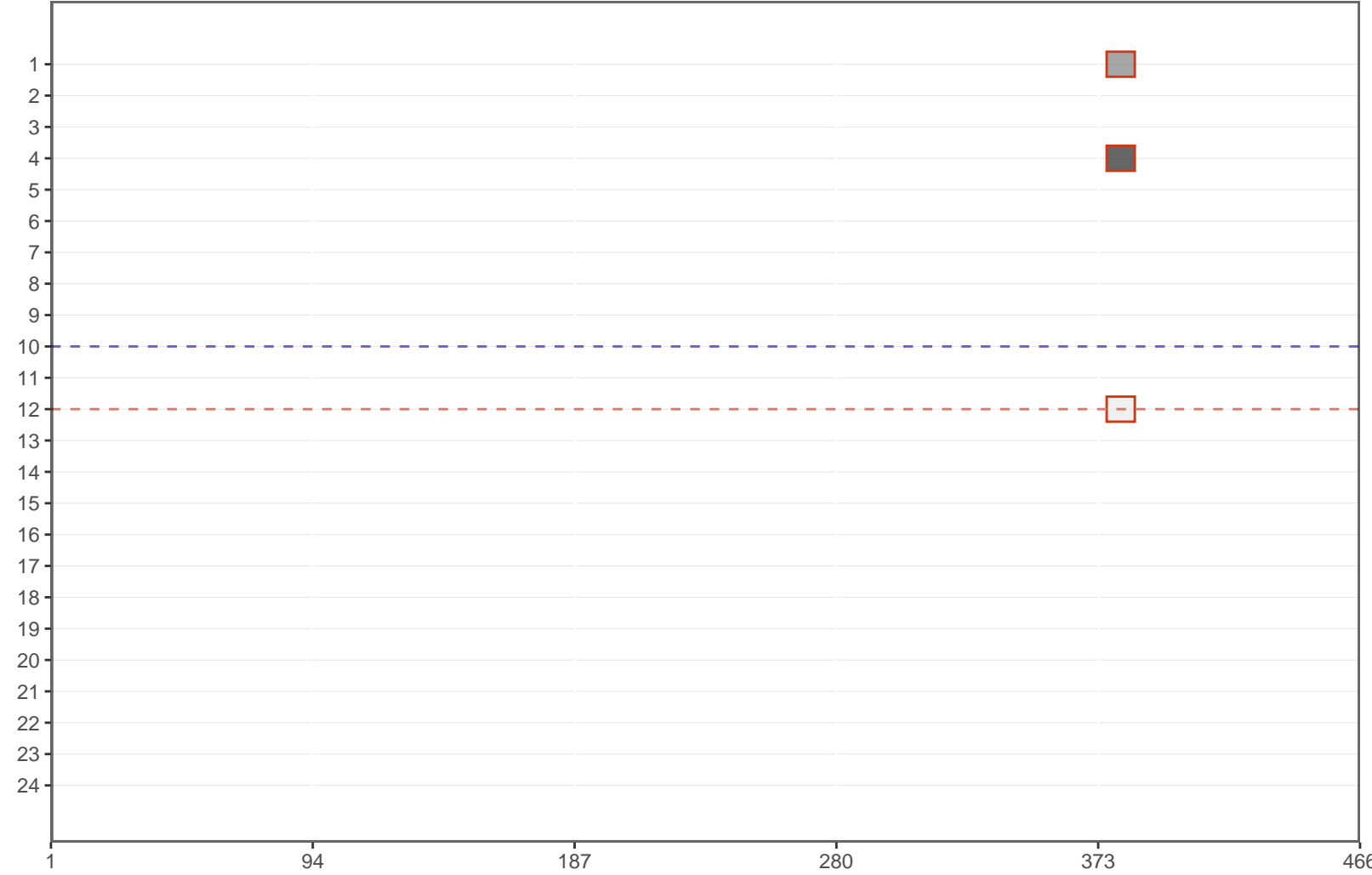
MW indication



Molecular weight

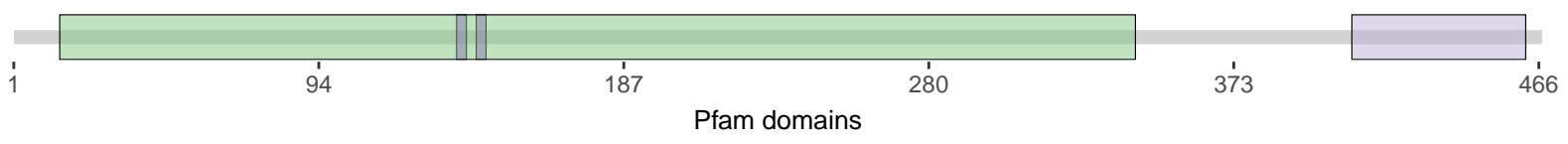


Gel Slice



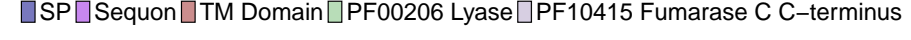
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LPIMYQIQGGGTAWGTGLNTRKGFDRKAAVAEETNLRFVTAENKFEALAAHDAFVETSGAVNTLAASLMKVGNDIRFLGSGPROGLGELIPENEPSSIMPQKVNPTQGEALTMVCGAGVMGNHVAVTGGSSGHFELNFKPFIAMNALLHSVRLIGDASAFERKNGVRGQANRERIDKLLHESLMVLTGLNPKIGYDIAAAWAKKHEGTSLSKDAALNLGVLKEEFDGFVPEKMGFTD

NbL18g07620.1 40S_ribosomal_protein_S9-2-like [MW = 23.01 kDa]

No. of times detected



log(intensity)



Values from



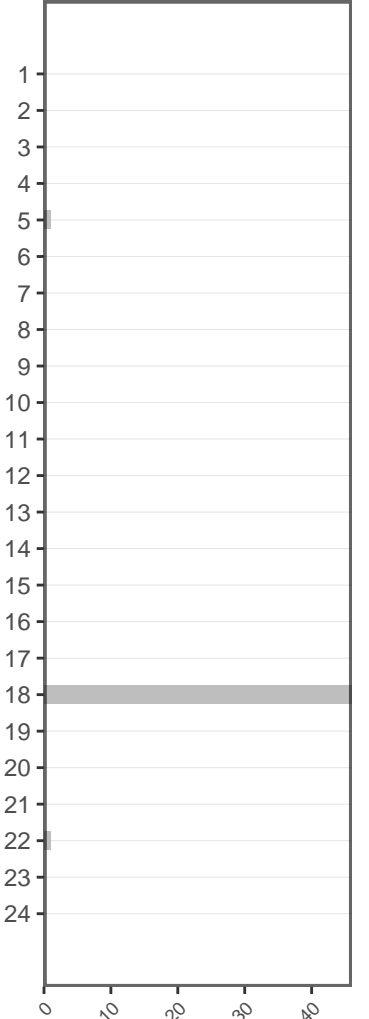
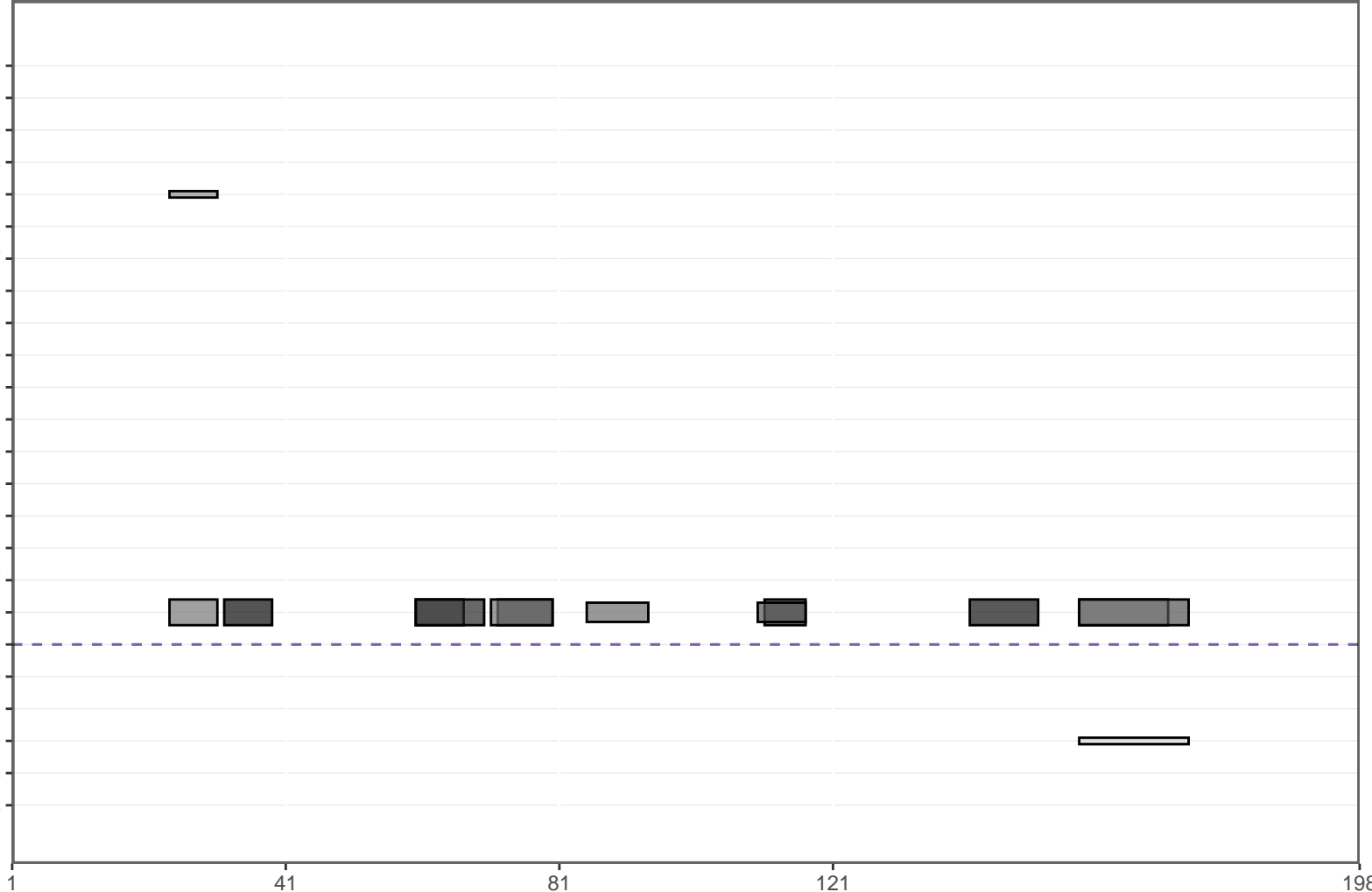
MW indication



Molecular weight



Gel Slice



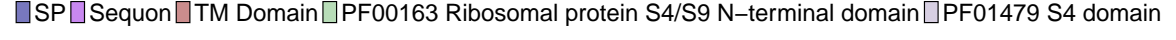
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILLDESQKLDVYVLSLTVENFLERRLGTLVFKTGMAKSHHARVLRGRHVRGRQVAVVPSFMVRVDSGRKHDFSLTSFPFGGGRPRGRVRRKNGKAAAKAKAAGGGDEEED

NbL18g07420.1 60S_ribosomal_protein_L34 [MW = 13.77 kDa]

No. of times detected



log(intensity)



Values from



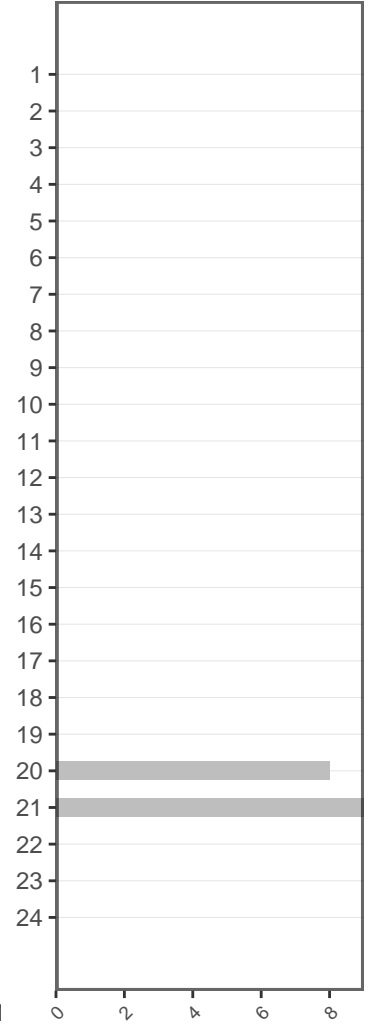
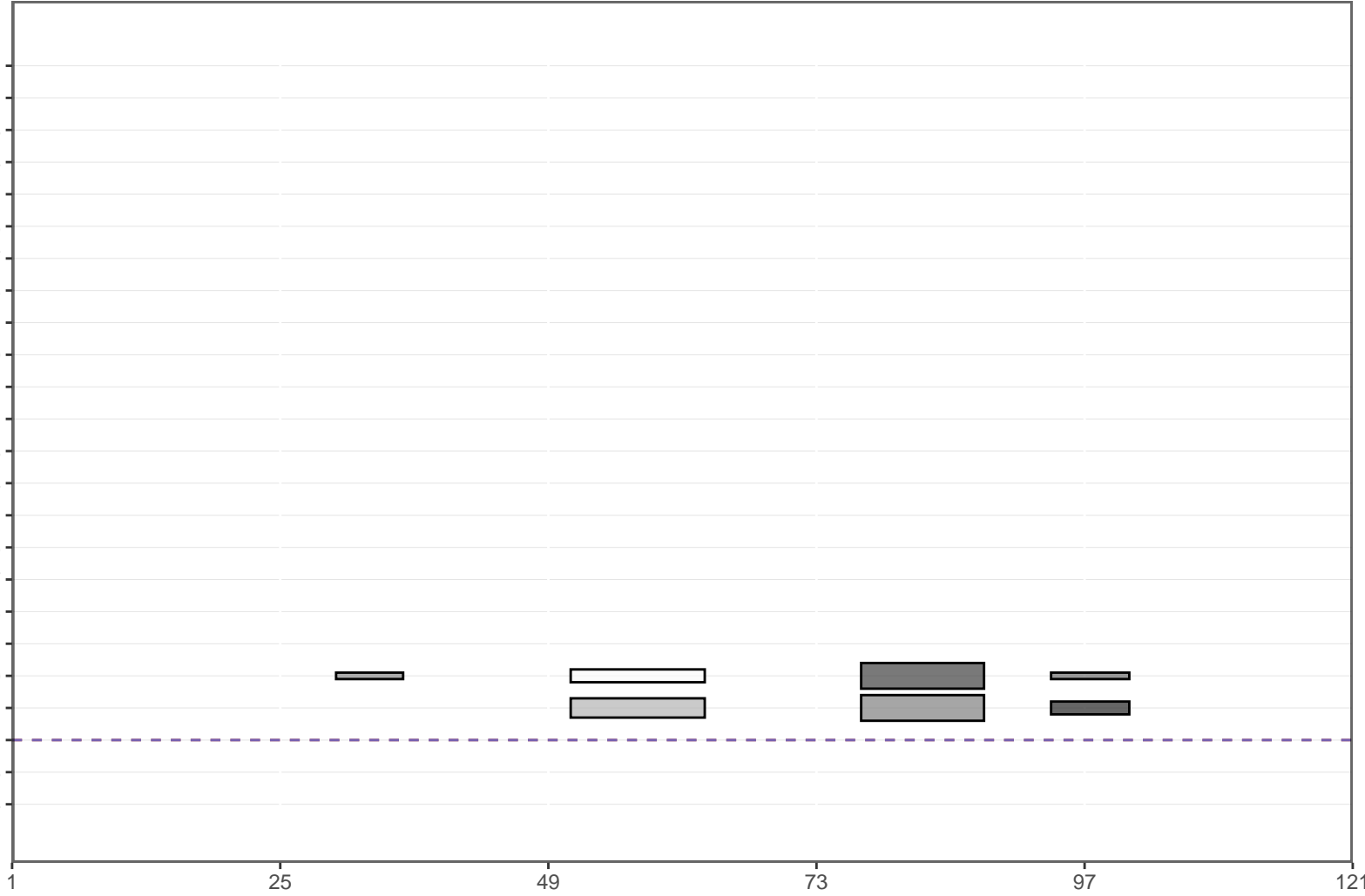
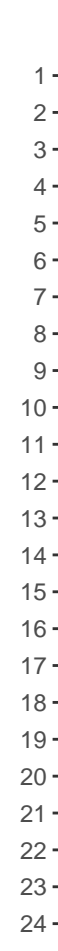
MW indication



Molecular weight

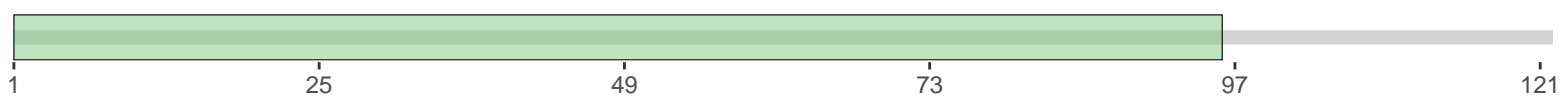


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

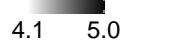
ITGKRIQGPHLRPTETVKRSLRSNRRTVNRAYGGVLSGSAVRERIRAFVLEEGKIKKVLKIKQKAKEKLAKSE

NbL18g07140.1 intracellular_ribonuclease_LX-like [MW = 32.47 kDa]

No. of times detected



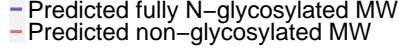
log(intensity)



Values from



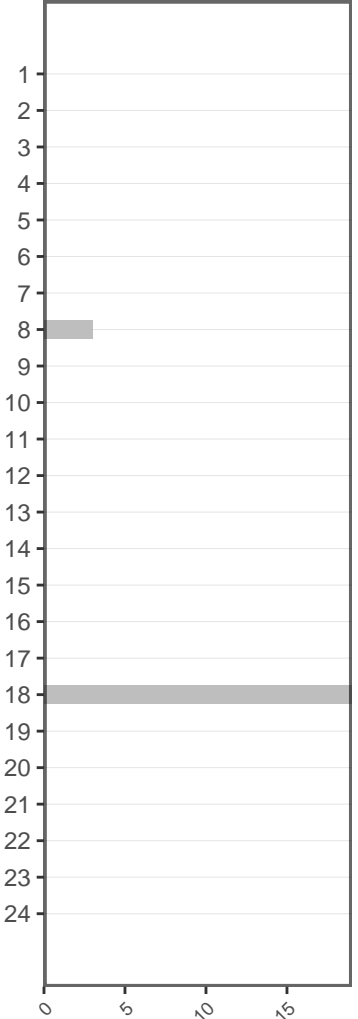
MW indication



Molecular weight



Gel Slice

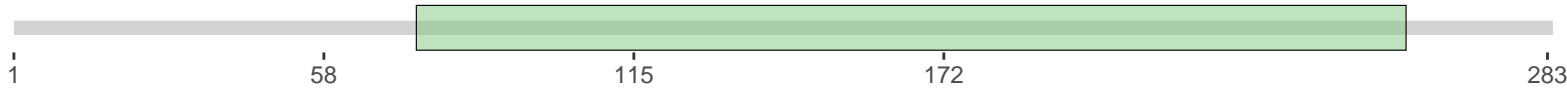


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



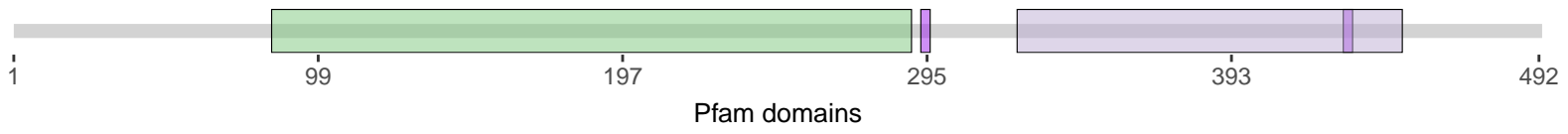
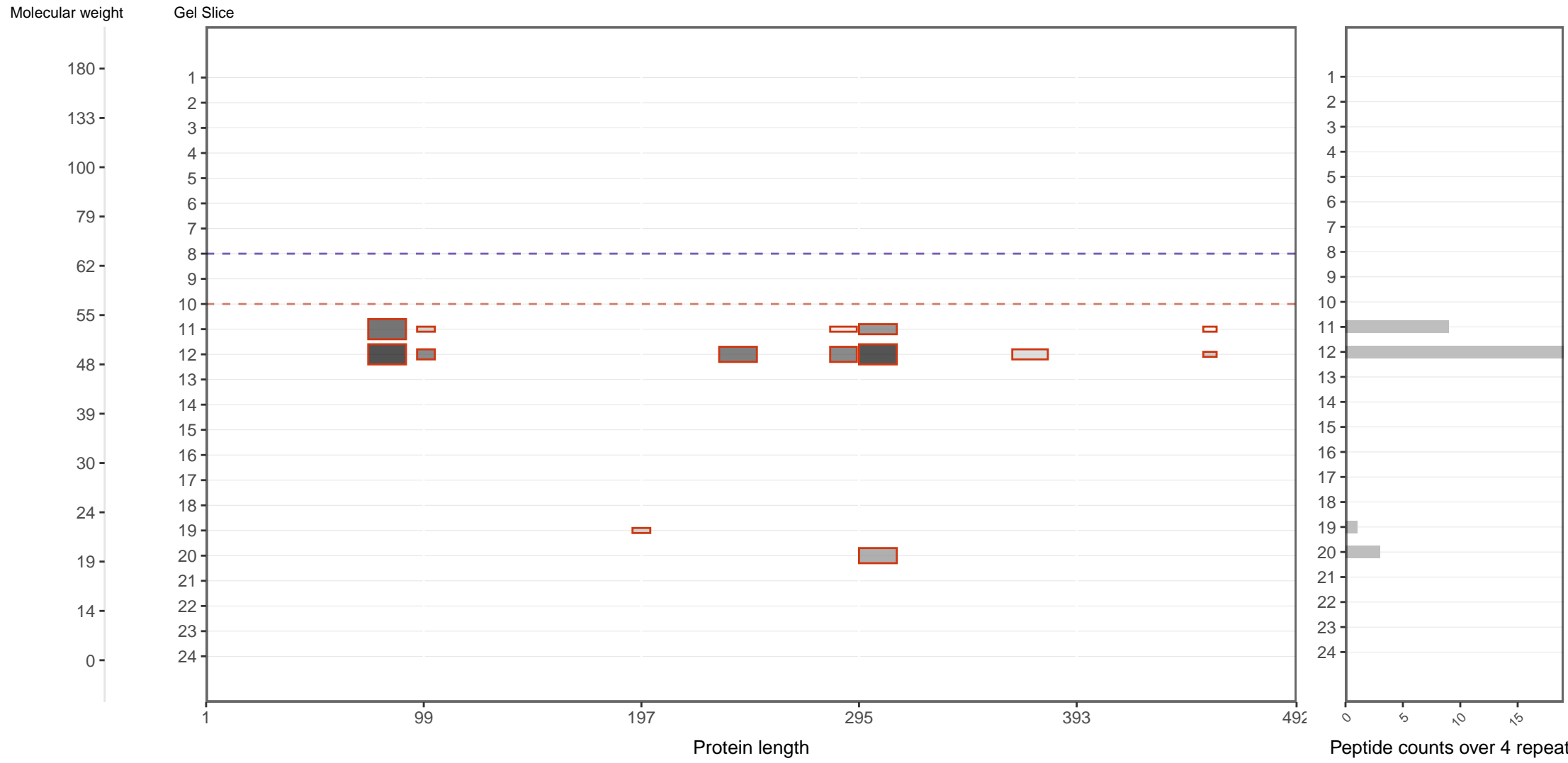
Protein sequence:

SLDESKISDLSTMEKNWPLACPSGSDGVRFWSEHWLKHGDTGALGERAVFQAALDFRKKSLLENLKNAGITFRNGEHVSLKIKKAEQGVGHSPIYEGNVDTGNGHQYGVYMCVDTKATDFIDCPVFPHGRGGGSKIEFFPFSDDHAEF

NbL18g06980.1 ribulose-15_bisphosphate_carboxylase/oxygenase_large_subunit_N-methyltransferase_chloroplastic-like [MW = 55.99 kDa]

No. of times detected
 1 2 3 4

log(intensity) Values from MW indication
 3.1 4.5 Unique peptides Non-unique peptides
 Predicted fully N-glycosylated MW Predicted non-glycosylated MW



Protein sequence:
 RNQNLLVPPADLTNHNARVTTEDHAAHEVRRPQWLFVWDLFSLRSLPKAKAGDQFQYDQNKKNADMLDYGFIKPEASARDAFTLLEISESEDFYQDKLDAETNGIGETAYFDIKIGGSLPPTMPIRLRLVALGGTDFALLESIFRNSVWGHGLPLVSRANEELCKVVRDACKSALSGVHTTIEDEKLMEOGNLSTRQLGAVGIRLGEKKVLRKQIDNIFRERRELELDELEVYGERRLKDLGLVGEQGDIFWEK

NbL18g06970.1 uncharacterized_LOC109214564 [MW = 19.96 kDa]

No. of times detected



log(intensity)



Values from



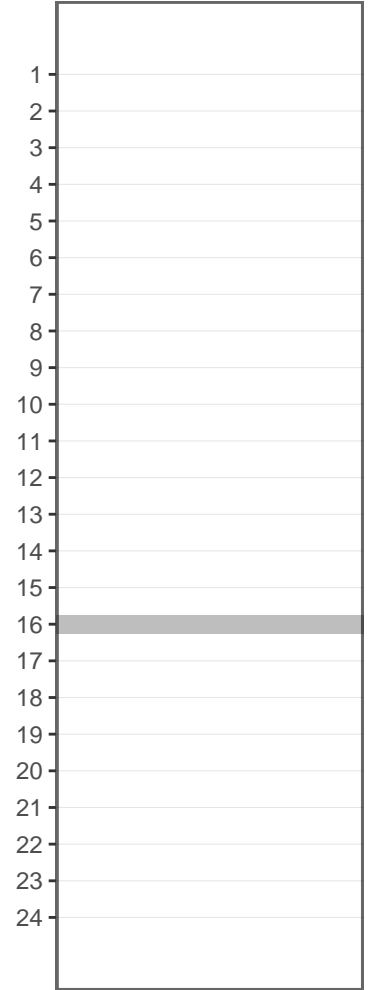
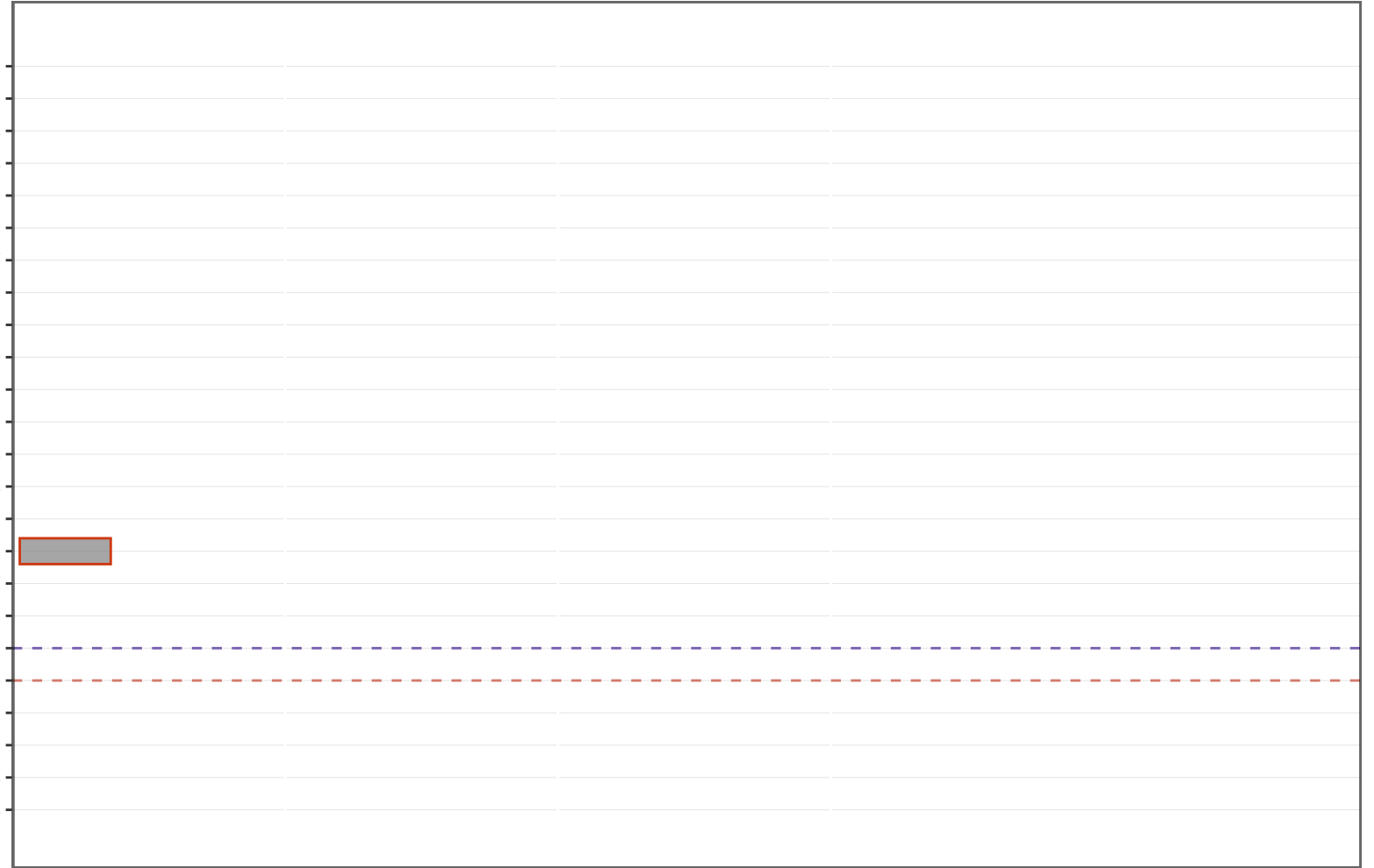
MW indication



Molecular weight



Gel Slice

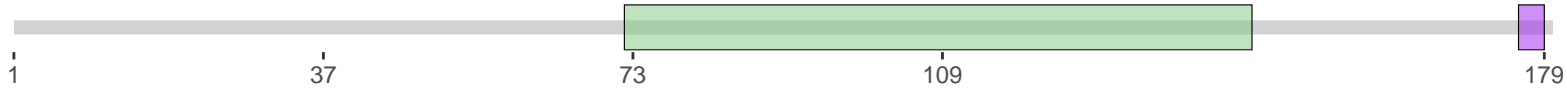


Protein length

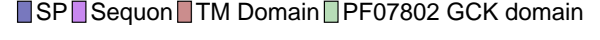


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

CLFMKGGGCKDEFHWEKIEEGEKNEKEDIVKGFVTSALKKMEAHSDYAPIFGAEKAAEALEKELKKEKEKEEQRNDADALGSVSDPTLDGNNSG

NbL18g06930.1 extracellular_ribonuclease_LE-like [MW - SP = 22.51 kDa]

No. of times detected



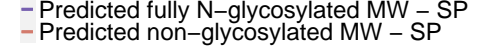
log(intensity)



Values from



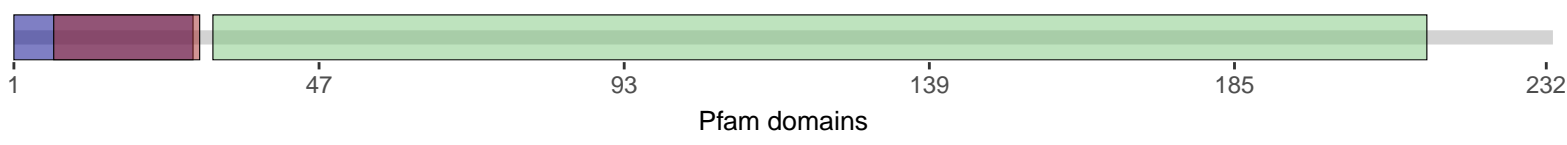
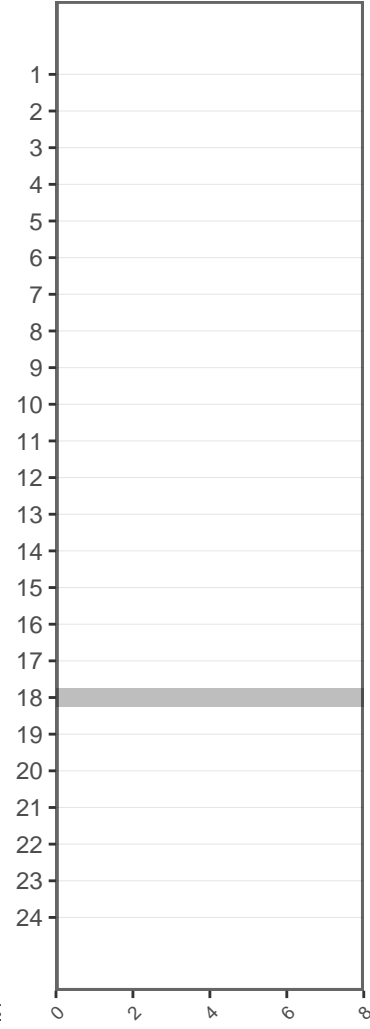
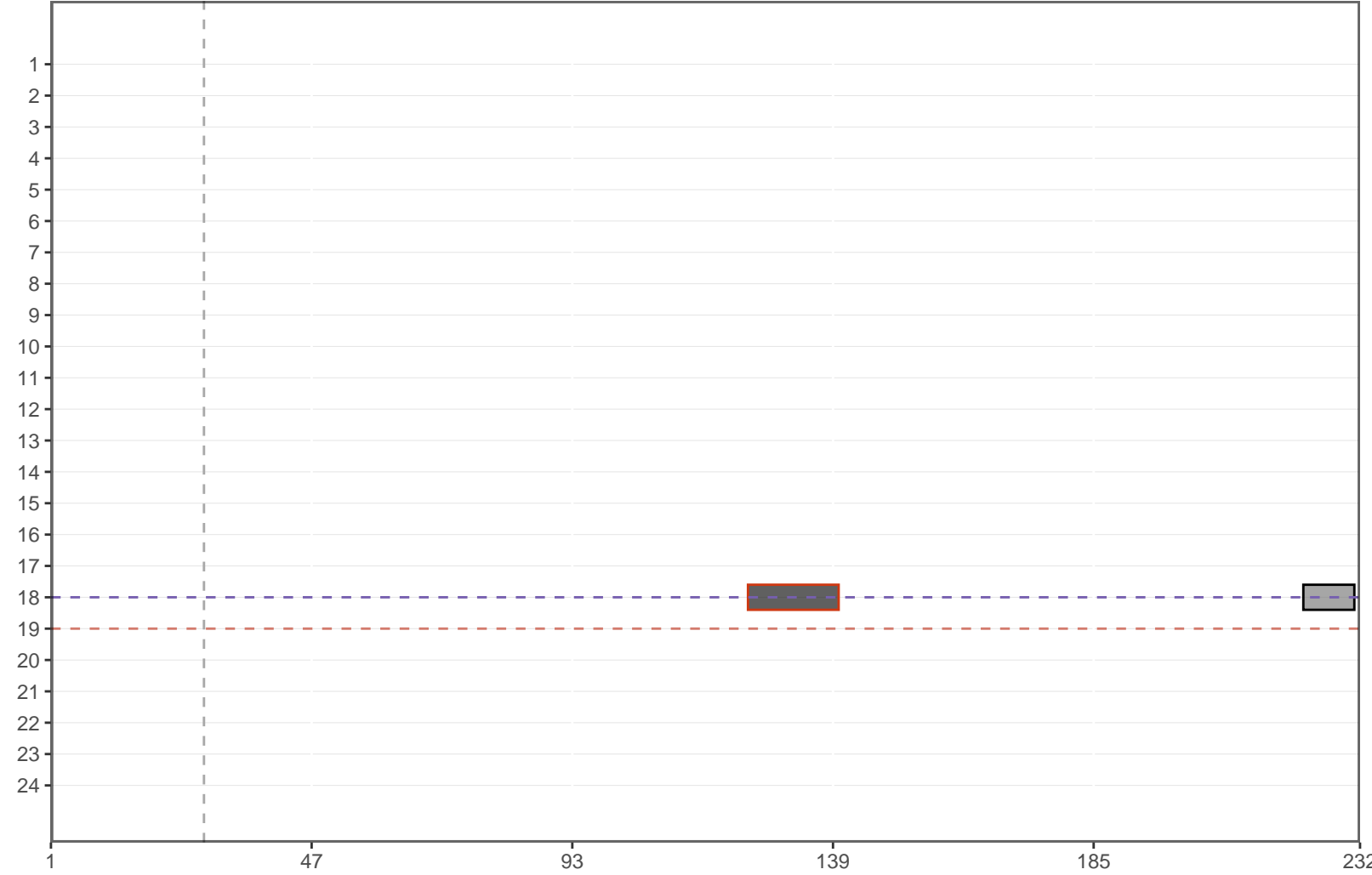
MW indication



Molecular weight



Gel Slice



Pfam Description

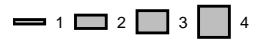


Protein sequence:

MPVTLACPSGTGSAFWSHEWKGKGTGAENVFDGHHGVFMKALDKNINLELQAGINPDGDFYSLNSVKNARSAIGYTPGECNVDESNGSLGVYKGVGDGSGENLIEGPFVFRKGGSGSIEFFTP

NbL18g06660.1 alpha-14_glucan_phosphorylase_L-2_isozyme_chloroplastic/amyloplastic [MW = 111.4 kDa]

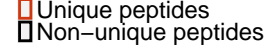
No. of times detected



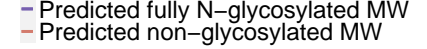
log(intensity)



Values from

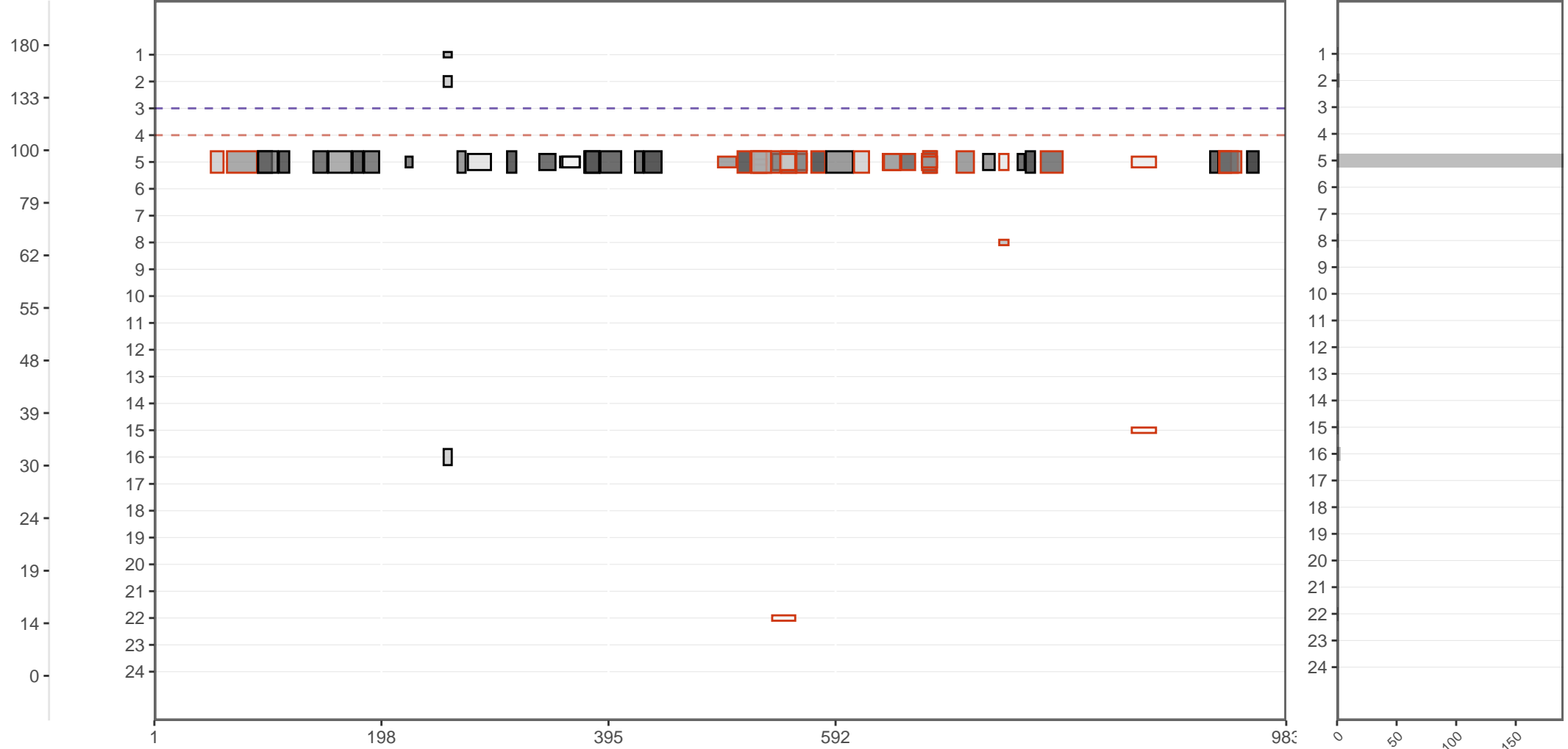


MW indication



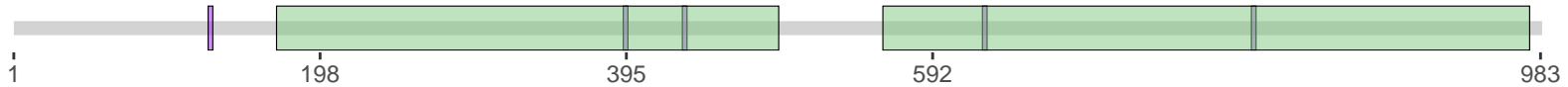
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

.LQELNQMRLLENVEIP6SVLELLIKFEEGKEHAEEPVKWETQVEVGGEGGKDDTKDDEETAANKAETAAEEETKVEKVAEADPDQANARIFGSDPNQGVVRRMANLVVGGHAVNGVAEHSEIVNGEVNFEFYELWPEKFGNKTNGVTPRRVLSFCNPELSDHTKWTGSDDWLVNTEKLAELRKFADNEELGSEWRKAKRSNKKIVSLKEKTGYVVSFDAMFDVQIKRIHEVKRQLNFGIVYRYYKMKMESPERRKEKFPVRVCFPGKAFATYYQAKRIVKFTD.

NbL18g06610.1 probable_pectinesterase/pectinesterase_inhibitor_41 [MW = 12.6 kDa]

No. of times detected



log(intensity)



Values from



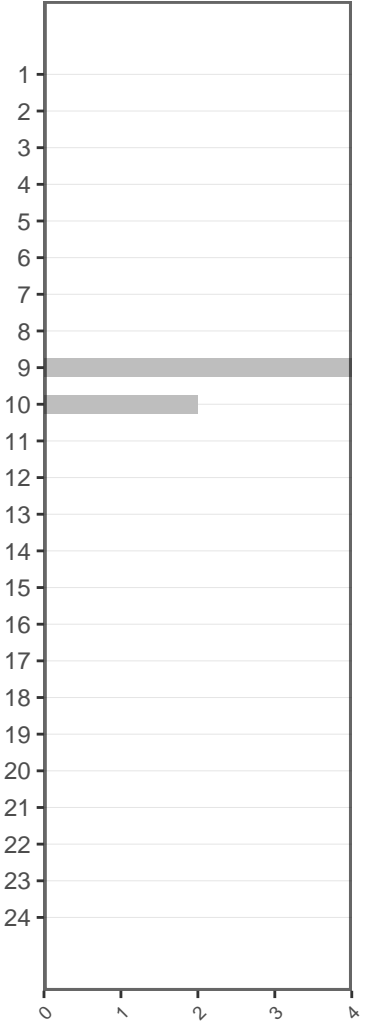
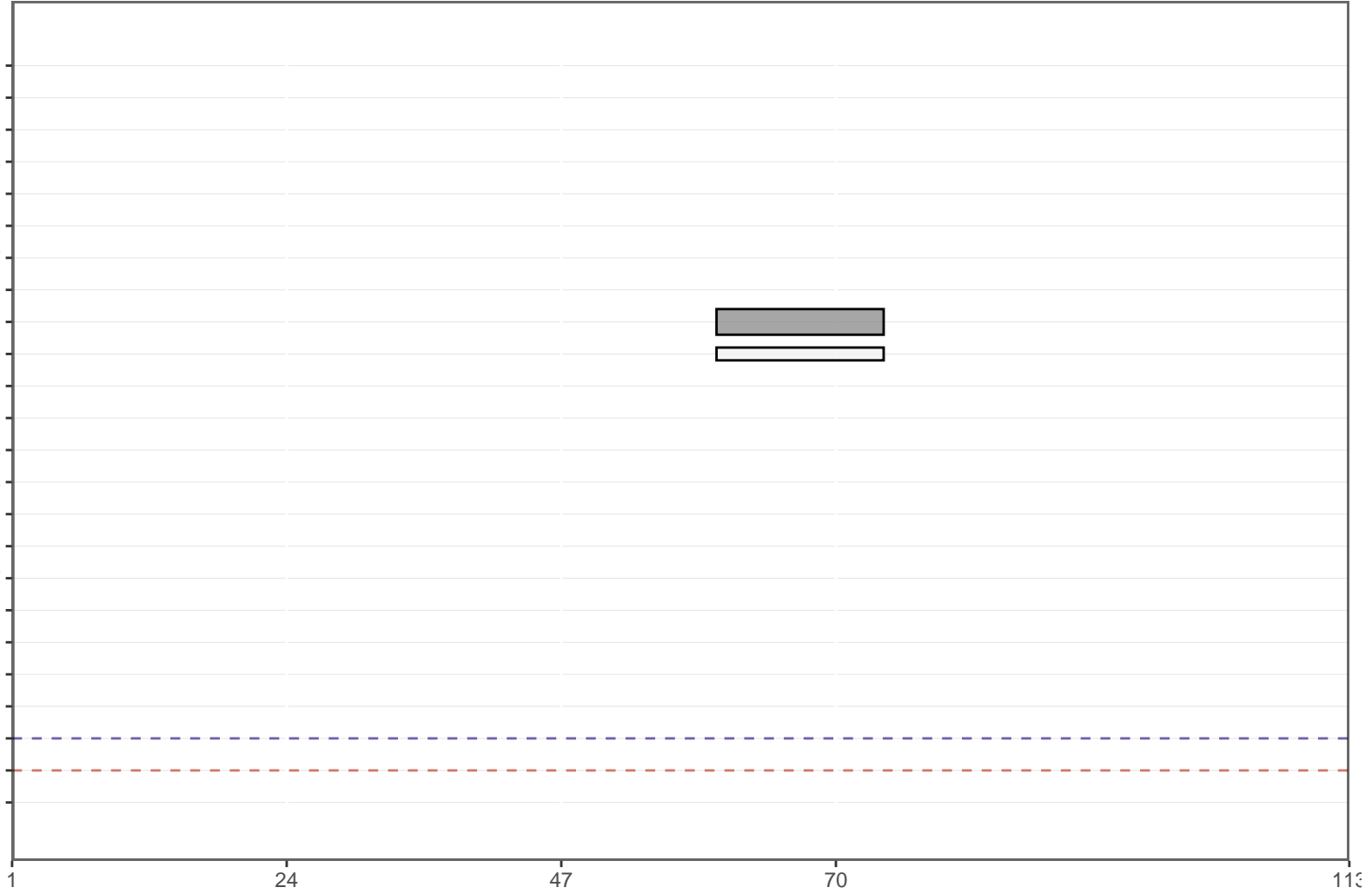
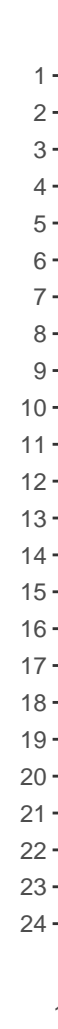
MW indication



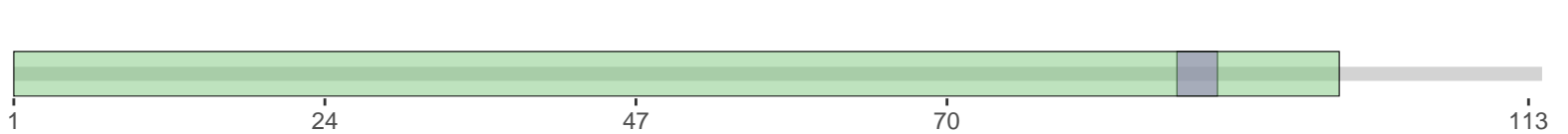
Molecular weight



Gel Slice



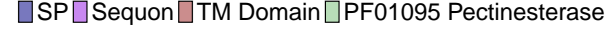
Protein length



Pfam domains



Pfam Description



Protein sequence:

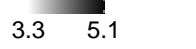
1FGNAAAVFQNCNLYRPLPLPQGFNATAGGRDINQNTGISHHNGITTPSGGGRTVASTNLLSRVEGI1

NbL18g06590.1 probable_mitochondrial-processing_peptidase_subunit_beta_mitochondrial [MW = 57.17 kDa]

No. of times detected



log(intensity)



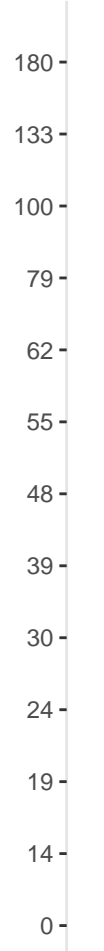
Values from



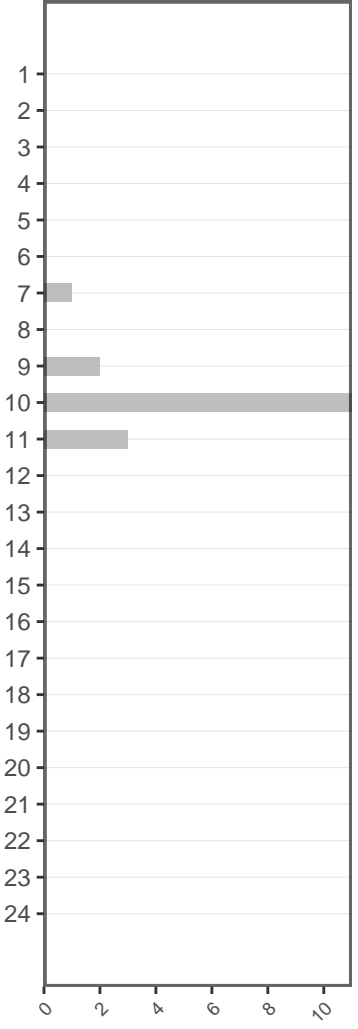
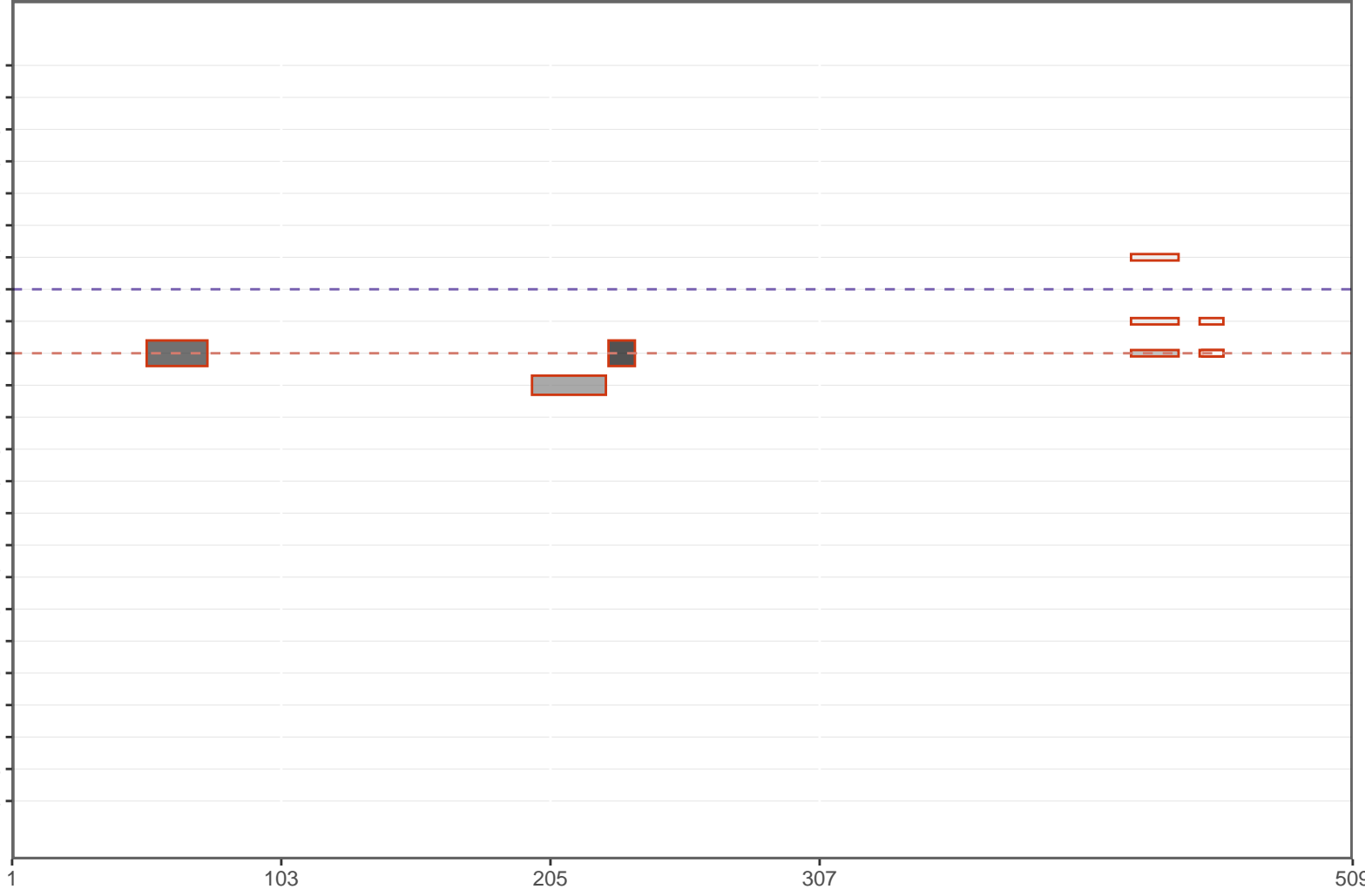
MW indication



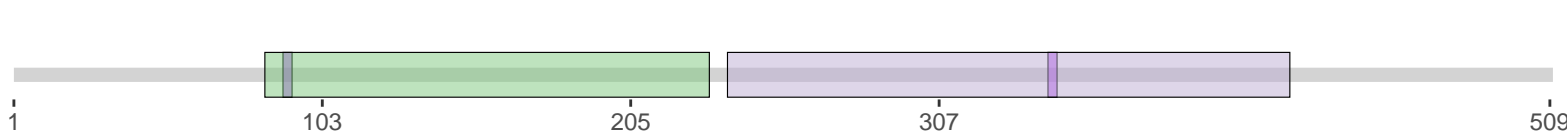
Molecular weight



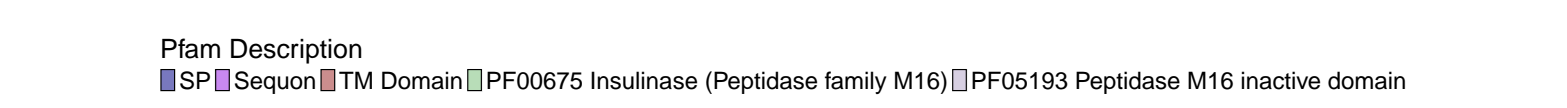
Gel Slice



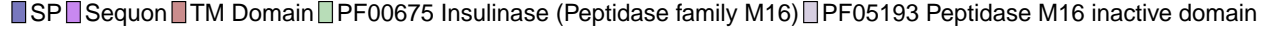
Protein length



Pfam domains



Pfam Description



Protein sequence:

IQDYISTHYGAIKRMVISAAGAVKHEDEVVELKHKHFTKLSNPFITSGQLVADEPAFTGSEIRHDDDLPLAGFAVAFSGASVWTDPPDGIALMVMQGMKLGWVNTKGGGKHMSSSELVQRVANEIEAEVMAFNNTYKDTGLFGVYAEAKPDGLSDLAIVIMQGGKLGKLYRVSEADVIRARNDLKSMLMHDGGGPTAEDIGRGLTYGRRIHAELFFRRIDRVADTVKRVNRRVFDLDRDAISARGPDLPDYNVWFRRTYWLRY

NbL18g06520.1 pentatricopeptide_repeat-containing_protein_At1g26460_mitochondrial [MW = 69.29 kDa]

No. of times detected



log(intensity)



Values from



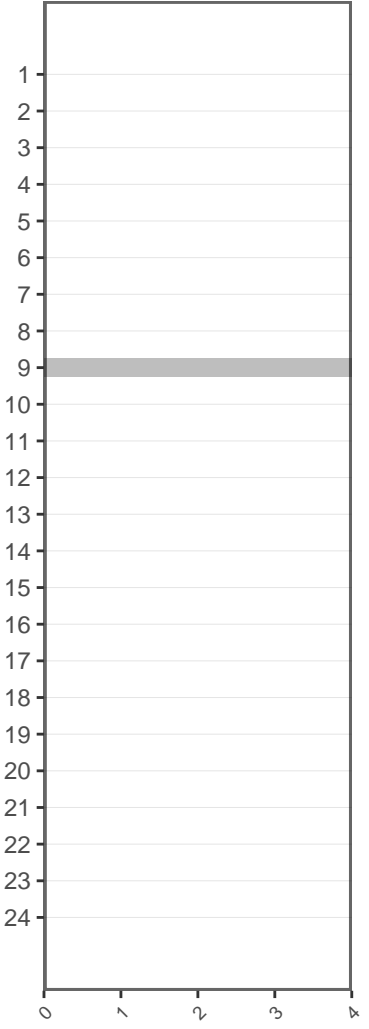
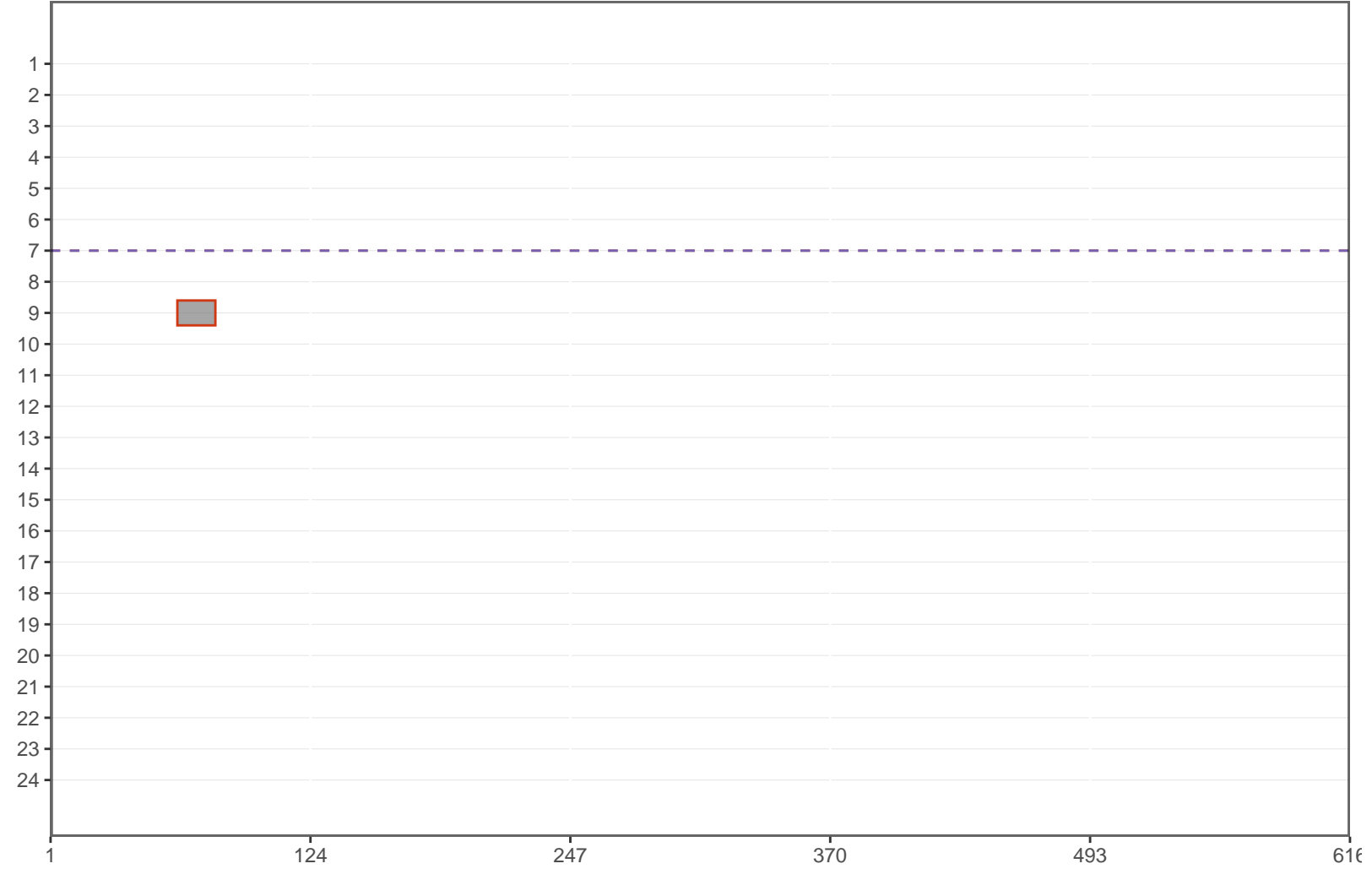
MW indication



Molecular weight



Gel Slice



Protein length

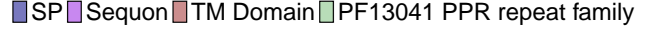


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

HLADVALQADNSLAFSSLEFFVWVVRGESVRRPPVLSVDEGLLVAALGTAGRTYNKLLNGAWEVLRSLRQMRAPNPEFLAKYAHASLGLQNFATLHEFEKAVGSSKEESAELFSPFTTLNPLVACGRNGFVTLDEVVYQLENLSRADPPYKSEVAALNDVILGCANWDRAYGTFAAIESSFGLVDPDHYNALYFAKLGKRDEATKYVEHFMDLGVWPNEMTYSLLDVAHLKREPKAASVVDENVHAGYKPKEMLKKRRRTREMDYESDORVEELAK

NbL18g06440.1 probable_inactive_purple_acid_phosphatase_1 [MW – SP = 66.47 kDa]

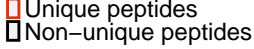
No. of times detected



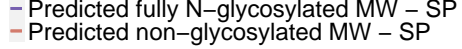
log(intensity)



Values from

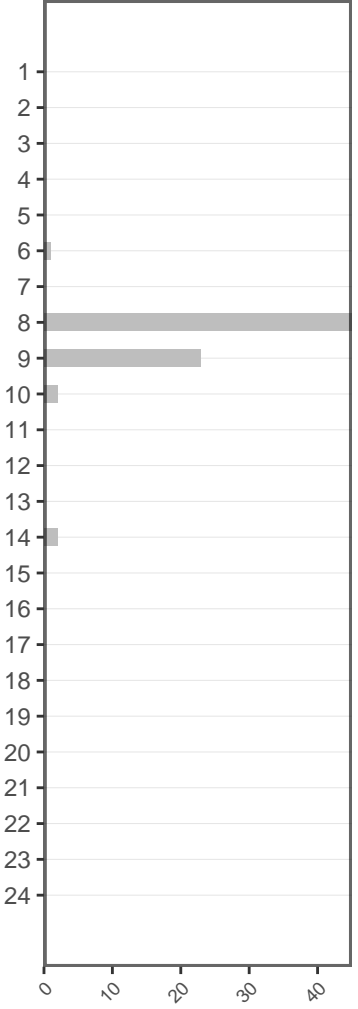
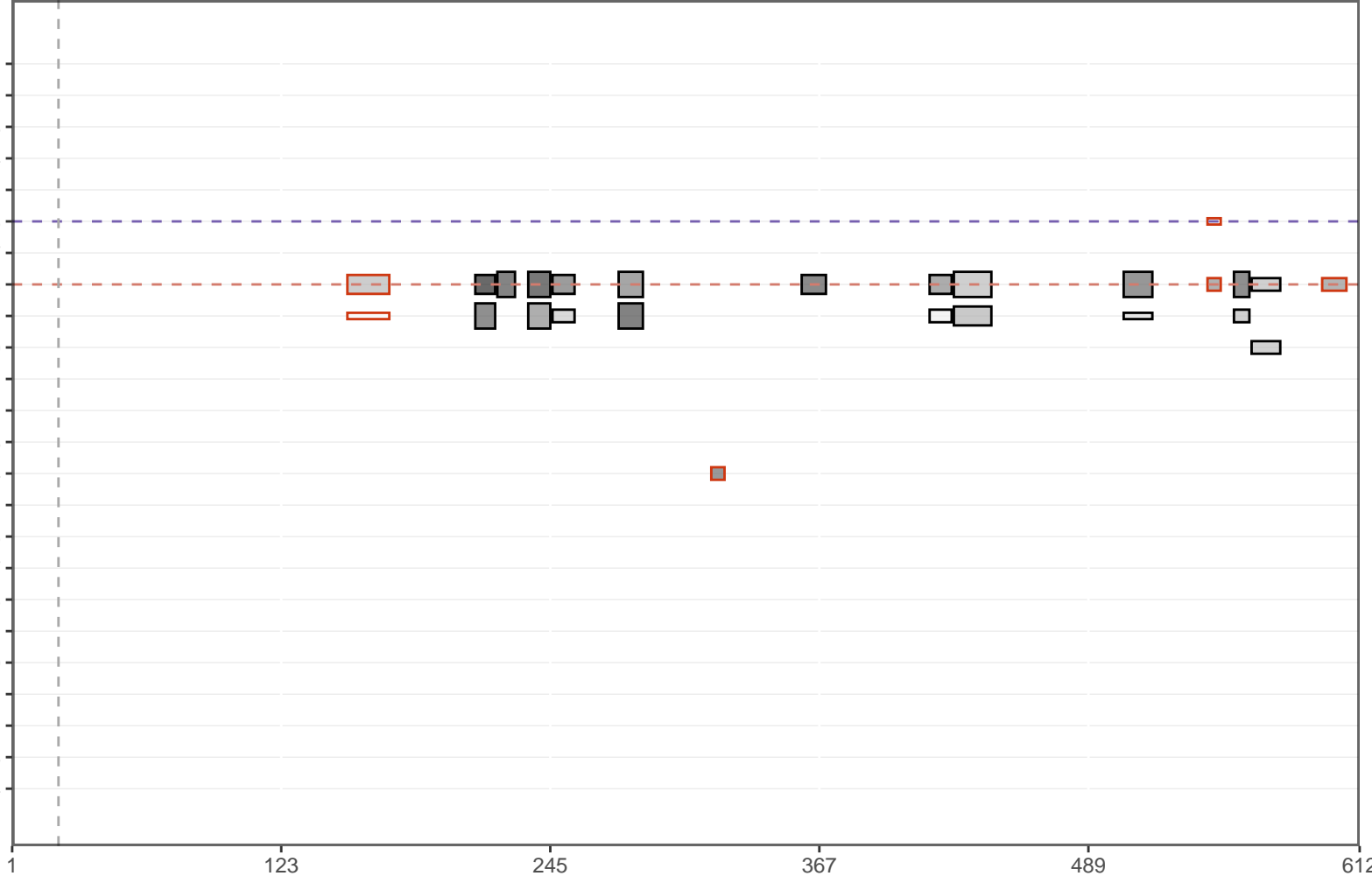
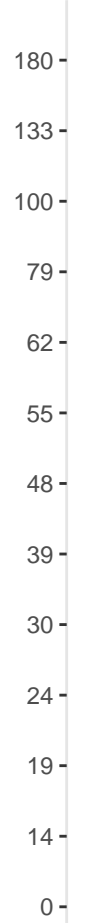


MW indication



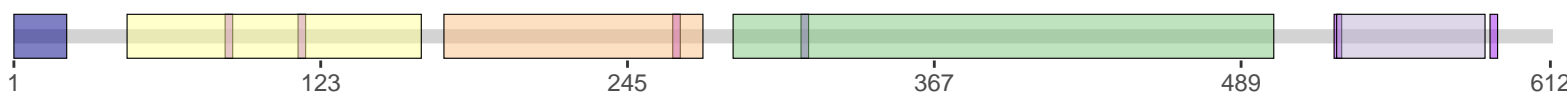
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00149 Calcineurin-like phosphoesterase
- PF16656 Purple acid Phosphatase, N-terminal domain
- PF14008 Iron/zinc purple acid phosphatase-like protein C
- PF17808 Fn3-like domain from Purple Acid Phosphatase

Protein sequence:

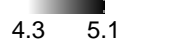
SKEEADGSNYYNQYQPGSLNTRFKGVGDKNDLVFHIGDPIYANGVLSQWDGFTSGVEGITSRVPYMAASGNHERDWPDSGSEYGNKDSGGEGGLVAGTMEYFPAENRDKFVYSTDYGMFRFGIADTEHDWRGTEGYEFIEHGFASVDRQKGPWLFIAHRVLGYSSGGDFYADEGSGFGPMGRSGLQKLVQKYYVDIAVGHVHHNYERTGPIWQNTCTMNEKNSYKGTNGTHVWAGGGGAGLVKFTSLTRKWSIFKQDYGFVYKMTAFDHSALLFEYKSRDQKV

NbL18g06260.1 probable_6-phosphogluconolactonase_1 [MW = 29.2 kDa]

No. of times detected



log(intensity)



Values from



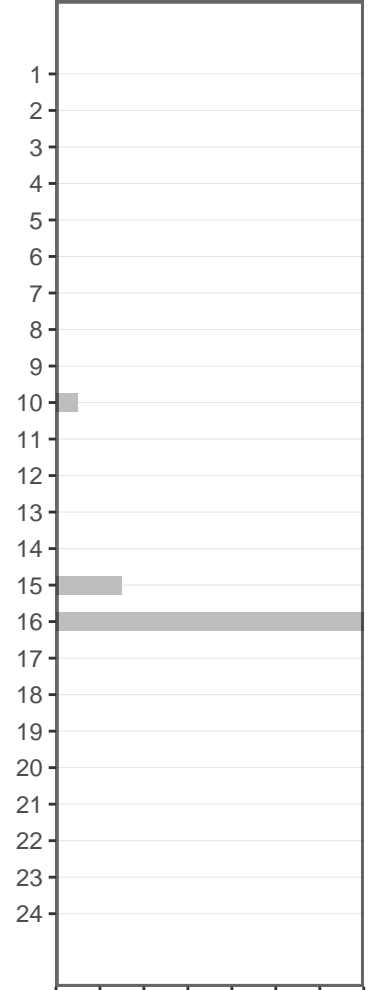
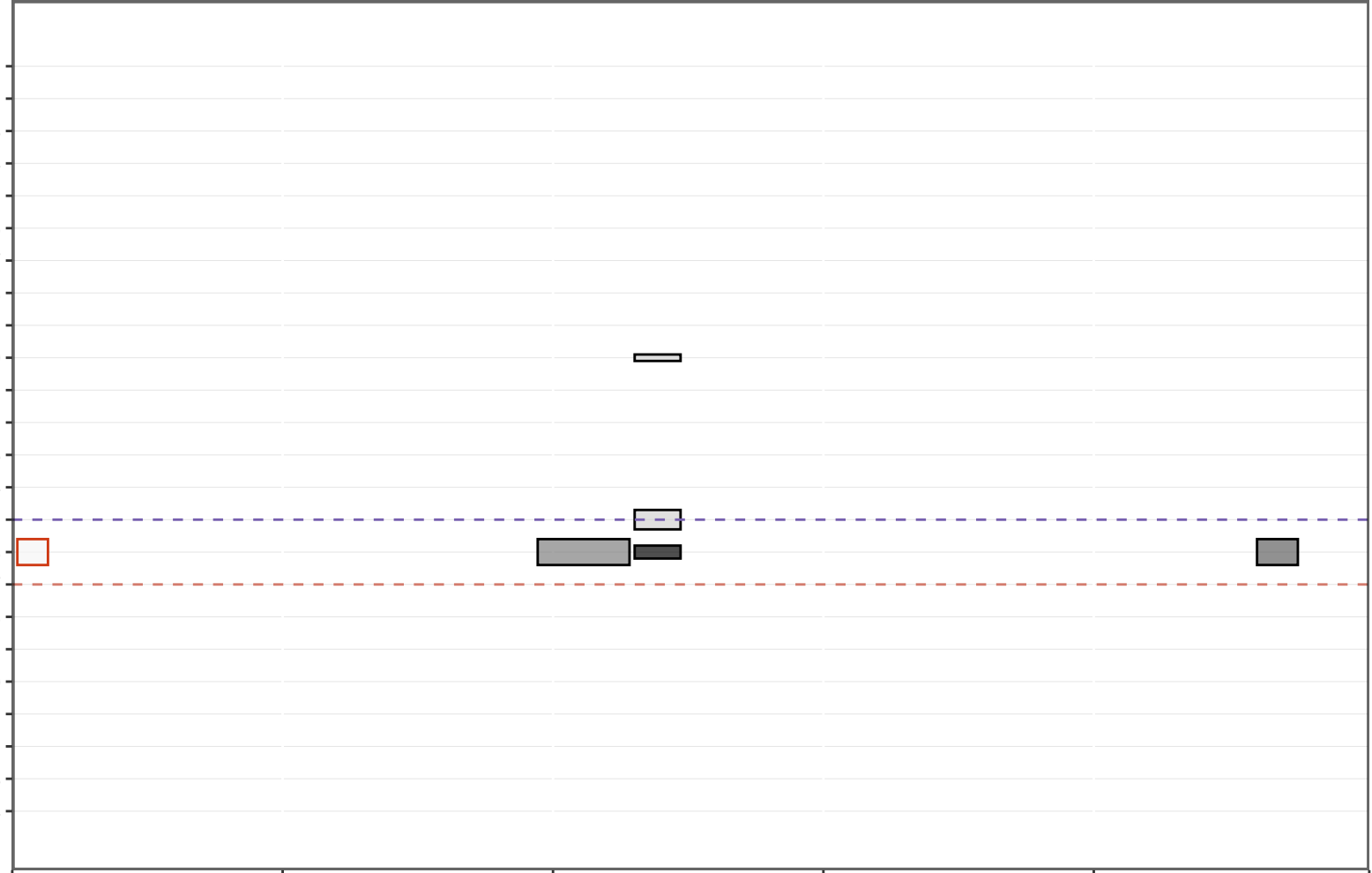
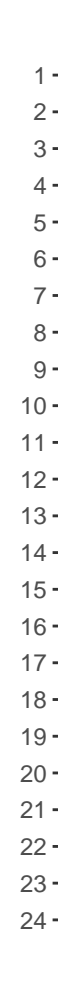
MW indication



Molecular weight



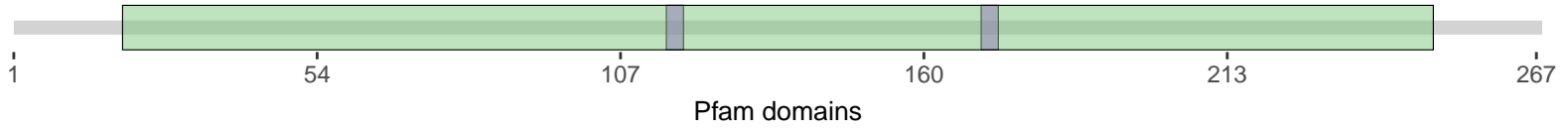
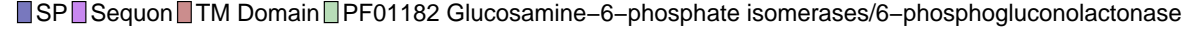
Gel Slice



Protein length

Peptide counts over 4 repeats

Pfam Description



Protein sequence:

IAEKAAEDYEFYIRGLVRRTRVHVSDDISDQPKFDLLKGMGGDDHWSLFFNHHILDEKEEWWVFLTDSQPKPPPERISFTLPVINSAGNVAIVATGSSKAEAVHLAIDDDGPECPKSPKMMVQPSKGNLVWFLDKAAASKLDGAKFSE

NbL18g06250.1 uncharacterized_LOC104234369 [MW = 72.8 kDa]

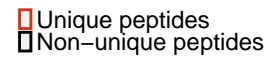
No. of times detected



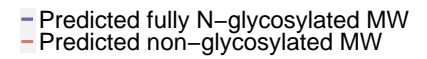
log(intensity)



Values from



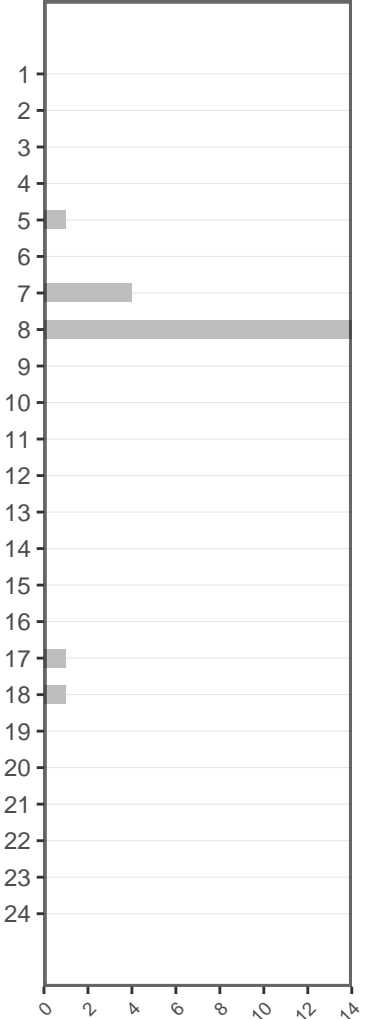
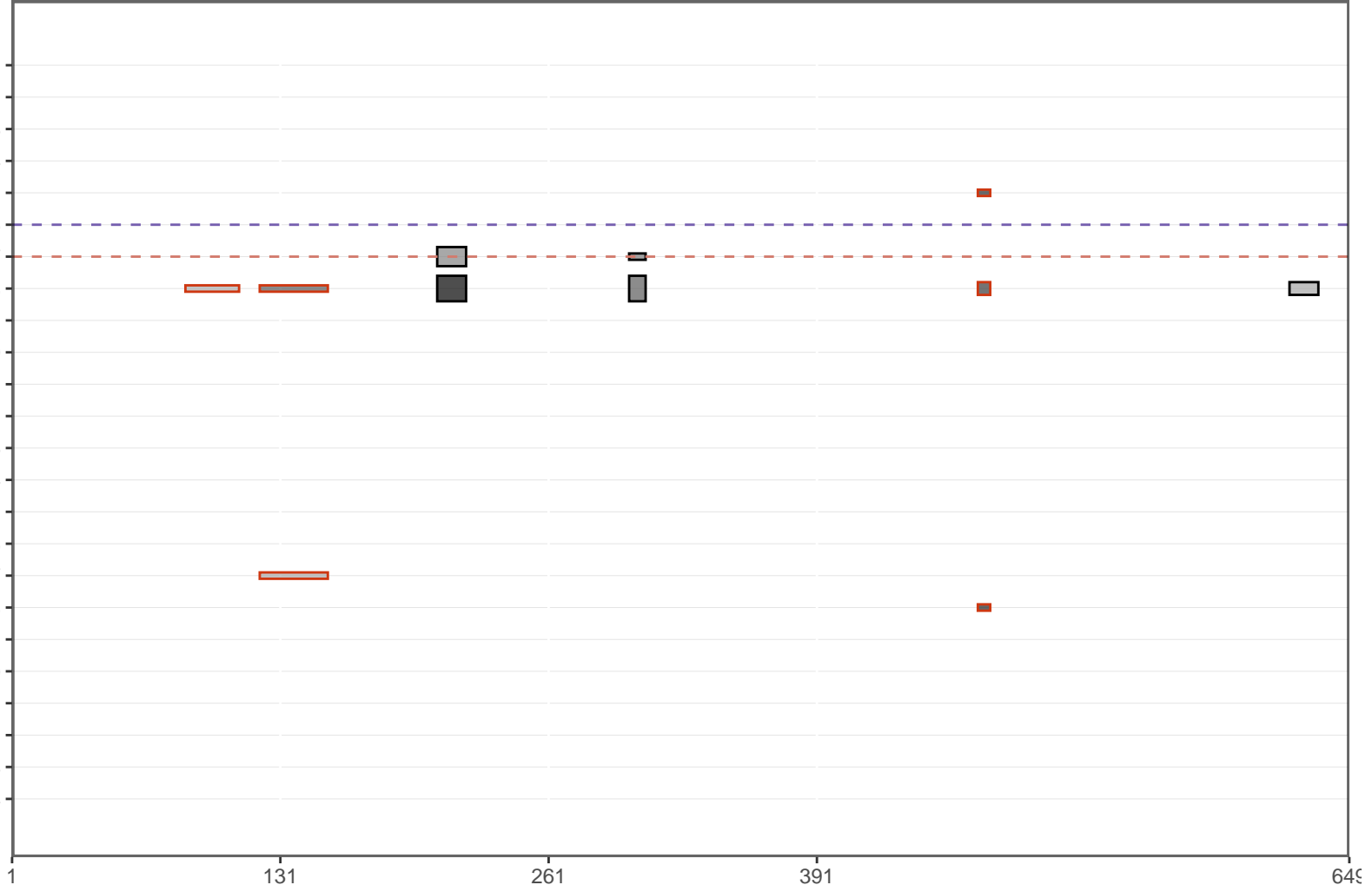
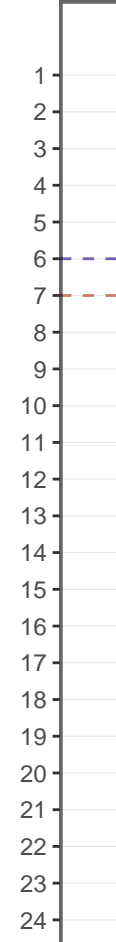
MW indication



Molecular weight

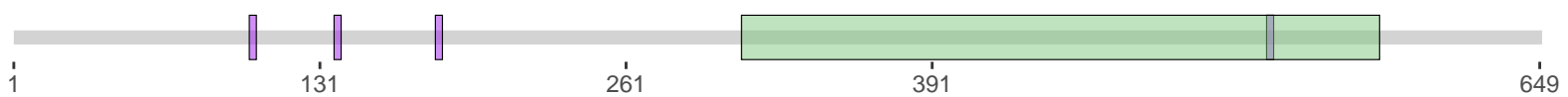


Gel Slice



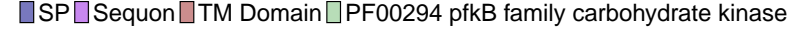
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

RMKDAIVDPEKFRSPGGSSNVAALASLGGKWFAMKLGDDDFGDSLVFMNINKVQTRVRLDSSKATATFMMKGRGGLRMTTTPKSAEDSLKSEINDLKEAKMVFYFTSLLDFNMLTLRATKIKSLGGVVFYDNLFFLWESGGKAKTFDQAKDLADIEVTGDELEFLGKPKPERFDTKDNRSKFTHYDPEVIAPLWHENLILFVYNTGTSKIHYYTKEHNGAVLGLIEDVPLTPYVTSMSASGGDIAGIRMLTVQPHLMTKGYLERTLYAISGVV

NbL18g06200.1 alpha-14-glucan-protein_synthase_[UDP-forming]_1 [MW = 41.18 kDa]

No. of times detected



log(intensity)



Values from



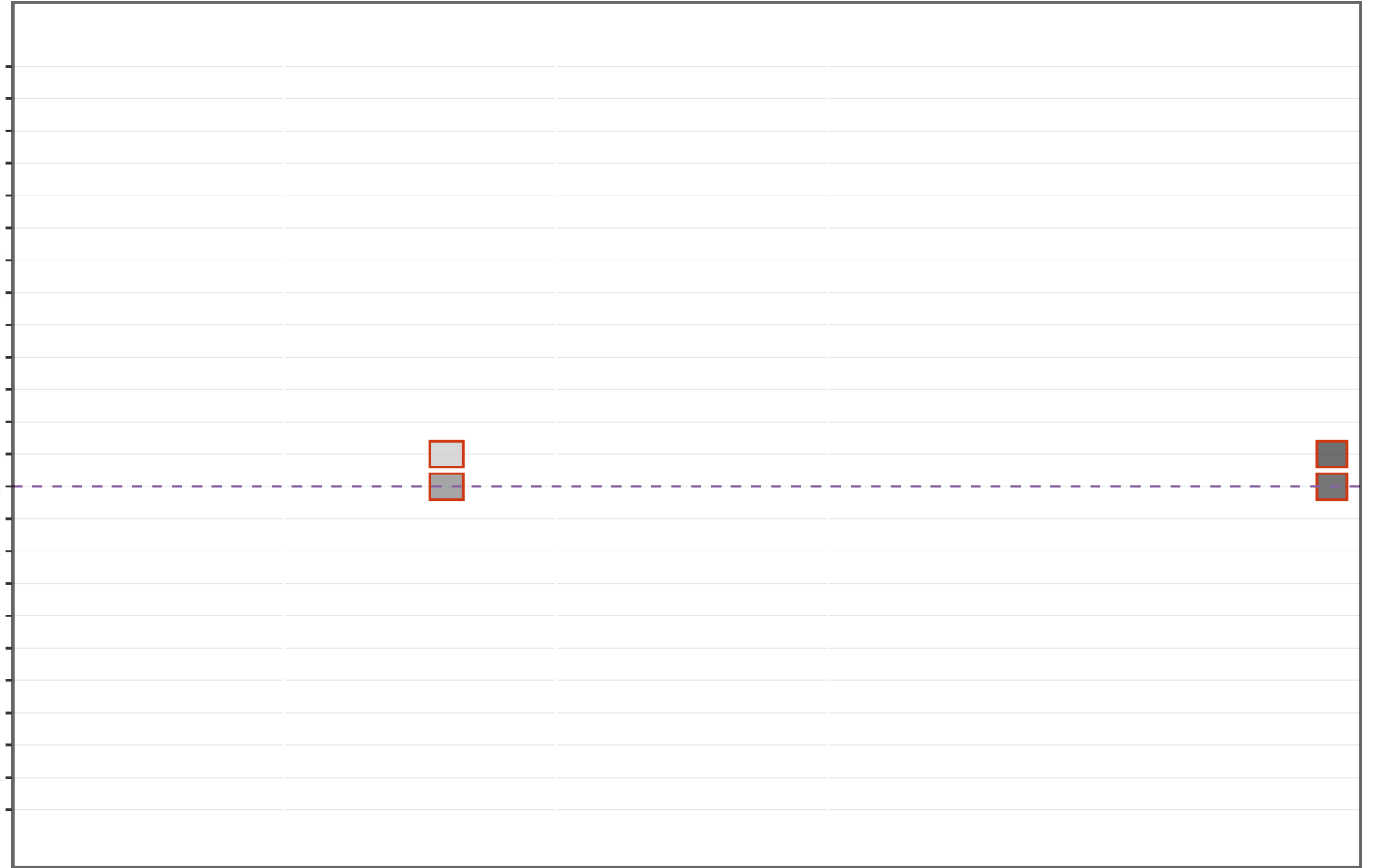
MW indication



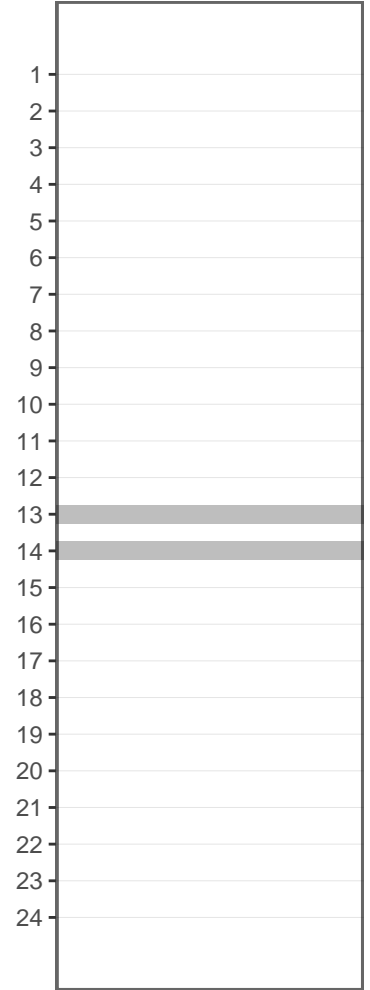
Molecular weight



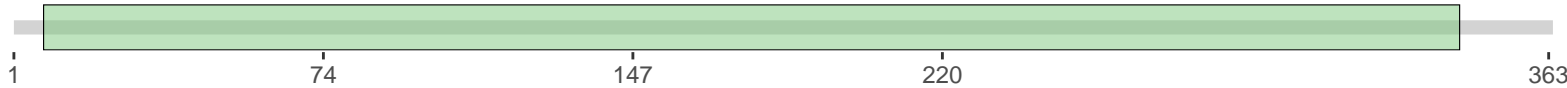
Gel Slice



Protein length

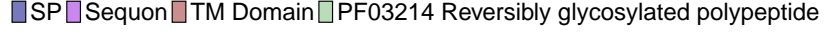


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PDYDPTQLVXPHERNTRVYDAVMTSPKGTLPFMGGMNLAFDRRELIGPMYFGLMGGGPIGRYDDMMAGWCTKVICDHLGLGKIGTGLFVWHHSKASNPFFVNLKKEVNGIFWQEEIHPFFGAATFFKKEKTVGGCYLELSKGVKDKLSDIPYFTKLGDMVTVIEWAWDELNPITGENLAKLSIADGPAKAAK

NbL18g05980.1 chalcone--flavonone_isomerase [MW = 26.41 kDa]

No. of times detected



log(intensity)



Values from



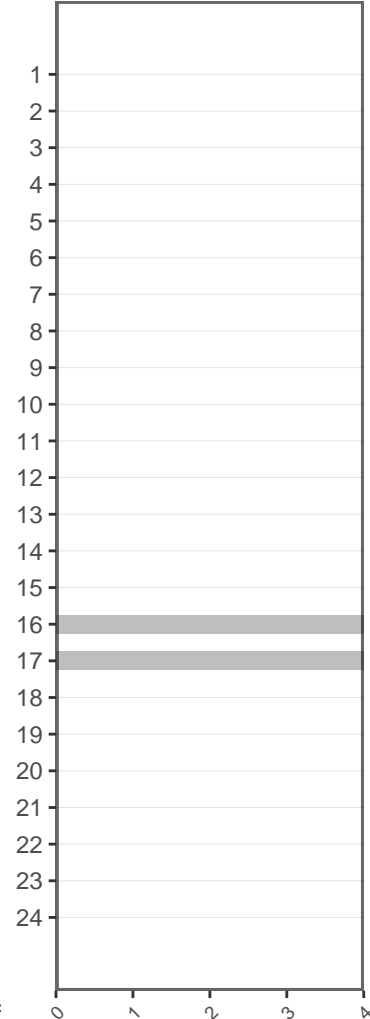
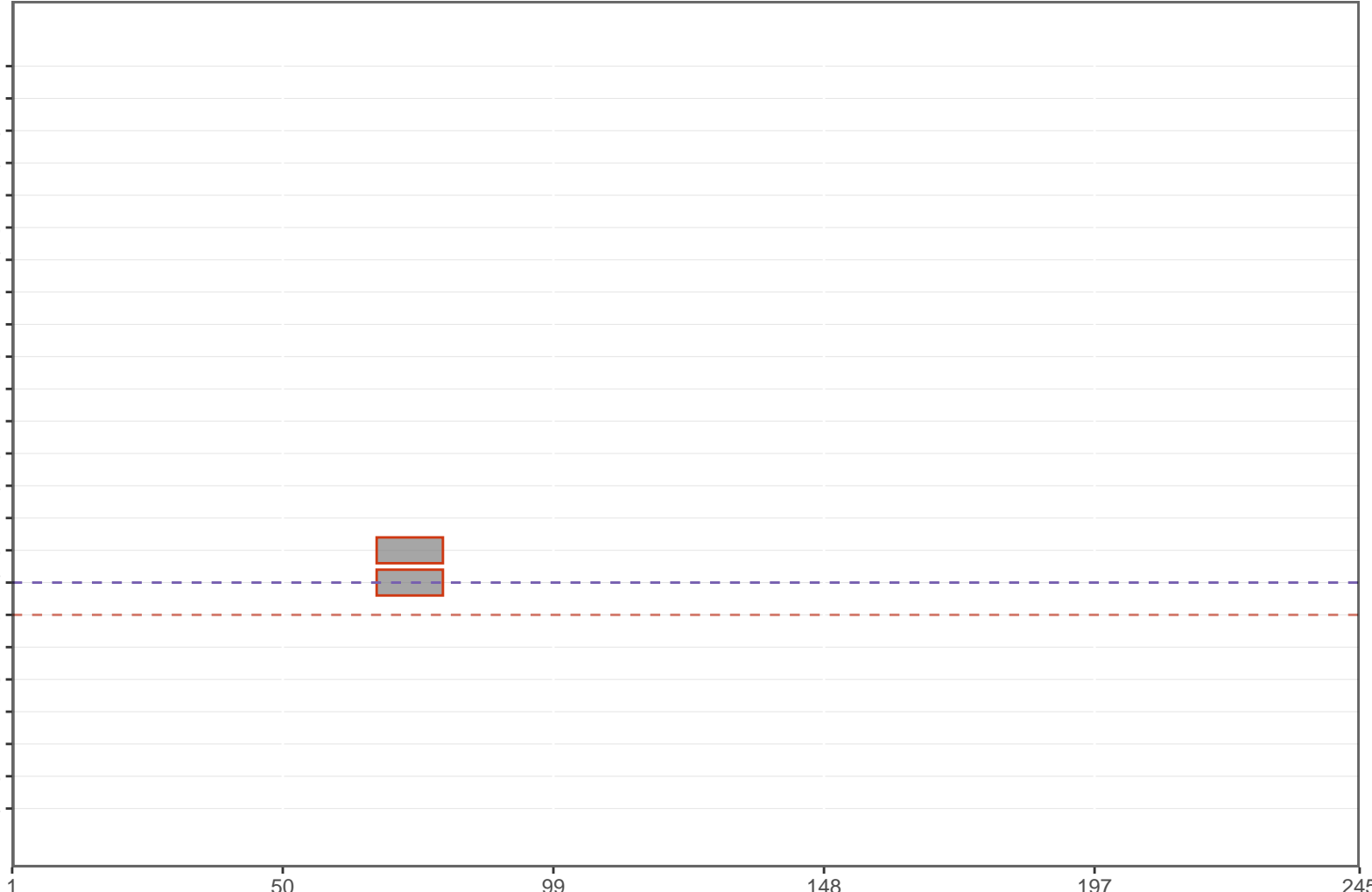
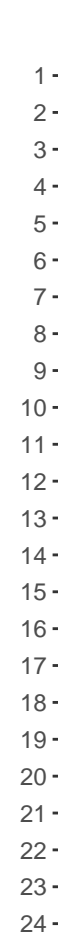
MW indication



Molecular weight



Gel Slice

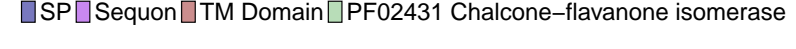


Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

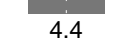
ENCVAHWKAGITYTDAESGAEELNFGNETFPGLGASLFTGSPVGAITIFIKDDITTTGNAWENKQLEAVLESIGIKHGVPAAKGSIAERVSLLLKKYGEVFPVGEKPKNGKSSDPVNEDKPTIAEIGV

NbL18g05950.1 uncharacterized_LOC104233992 [MW = 29.66 kDa]

No. of times detected



log(intensity)



Values from



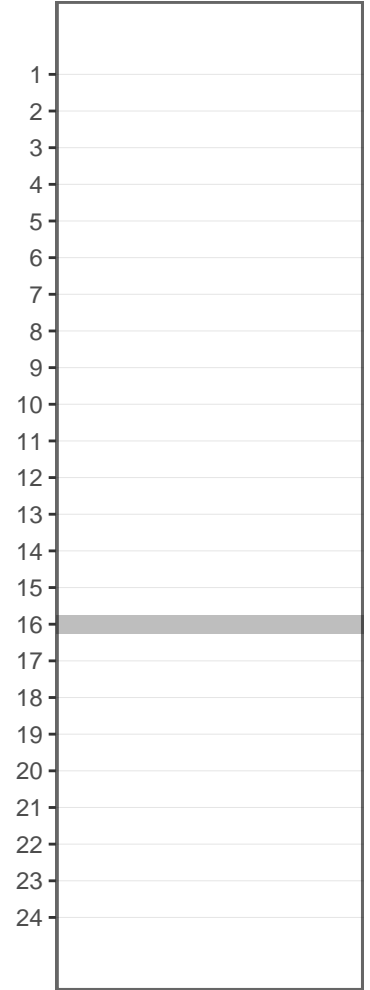
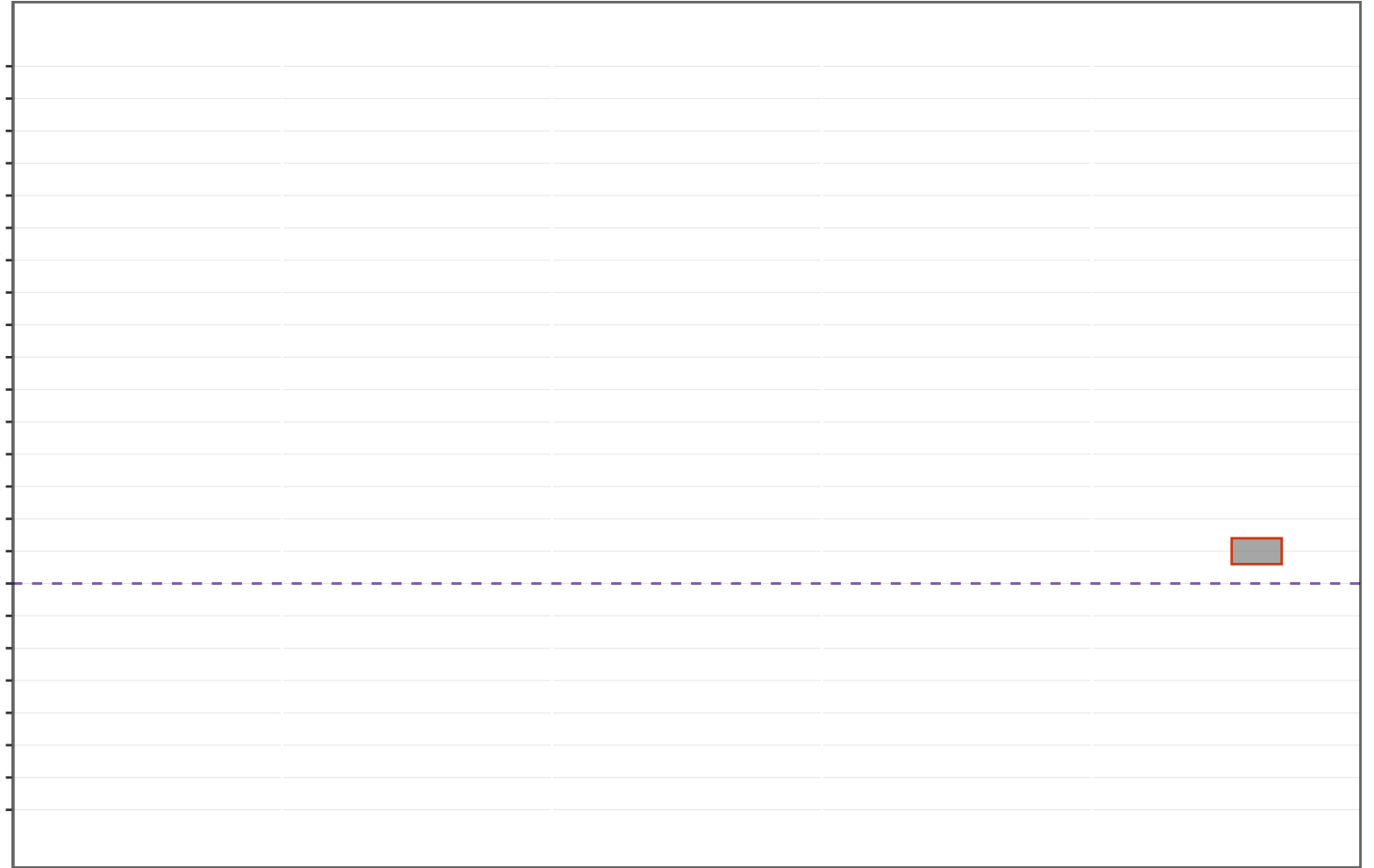
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains

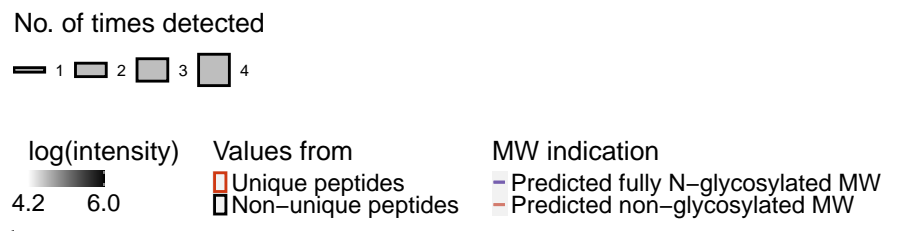


Pfam Description
 SP Sequon TM Domain

Protein sequence:

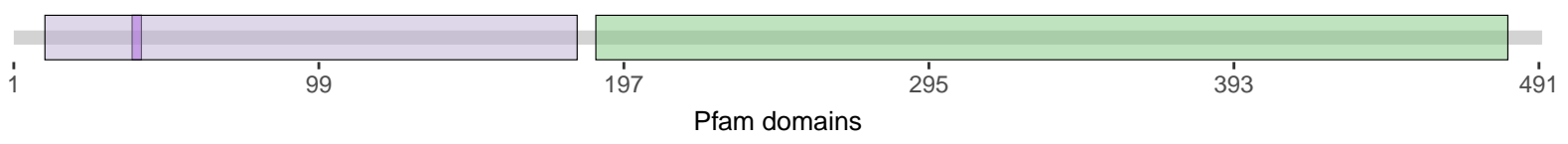
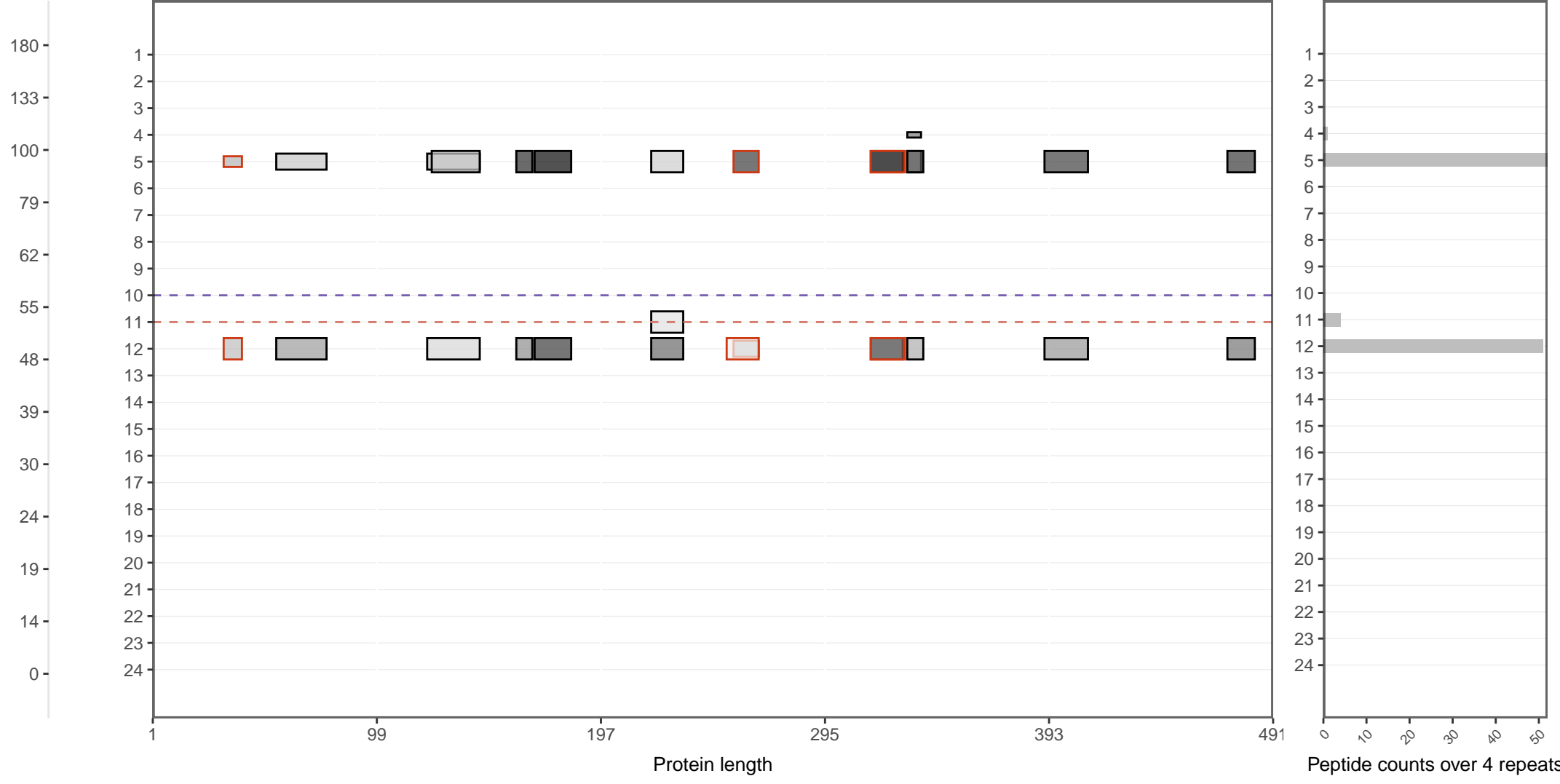
LVANLLIGEQIPEKVALDSDIRSNFRGKLSFDEAFARFKLESSERKGGKADGHQDSPLVKGADHLPGGVVDGLAALLSRDGLKKIRGTLGVSWPEAGISVLSIKLLKLDVLSGVNHNKVDGLEEFELKLRNKKDFLDSELYT

NbL18g05920.1 6-phosphogluconate_dehydrogenase_decarboxylating_3 [MW = 54.05 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00393 6-phosphogluconate dehydrogenase, C-terminal domain
- PF03446 NAD binding domain of 6-phosphogluconate dehydrogenase

Protein sequence:

VNKGELLSFLLEITADIFGKDKADGHVLDNVLKTKGMKGTGKWTGQAAELSVAPTIASSLDRFLSGLKDERVGAANKVFKSSGVSDLVVEGPDKGLIDDRKALYASKIGSYADGMNLRKAEKVEKGDWDLKGLGARLWKGCCIRAFIDRDKGAYDRNPDLANLLVDEEFANKEVVERGSAWRRVVGLANGSIGTPOGMSLSLAFDQYRRELRANLVQAGRDVFGAHTYERTDMPCARHTEWFKIARQSKI

NbL18g05770.1 heat_shock_protein_90-5_chloroplastic-like [MW = 51.78 kDa]

No. of times detected



log(intensity)



Values from



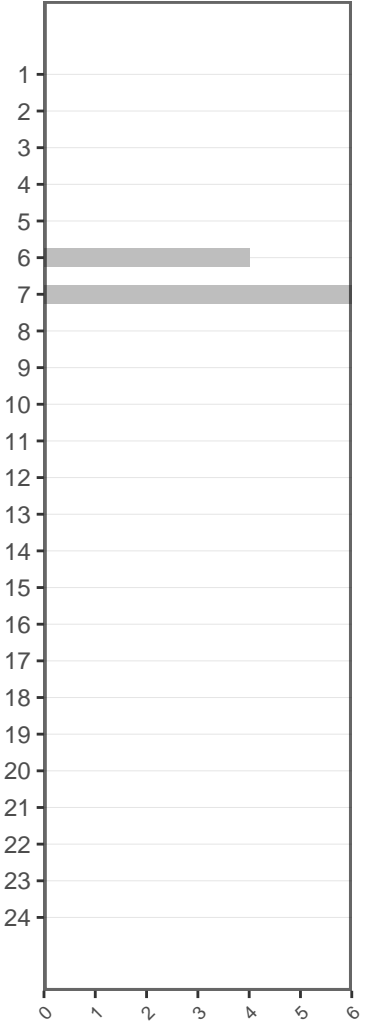
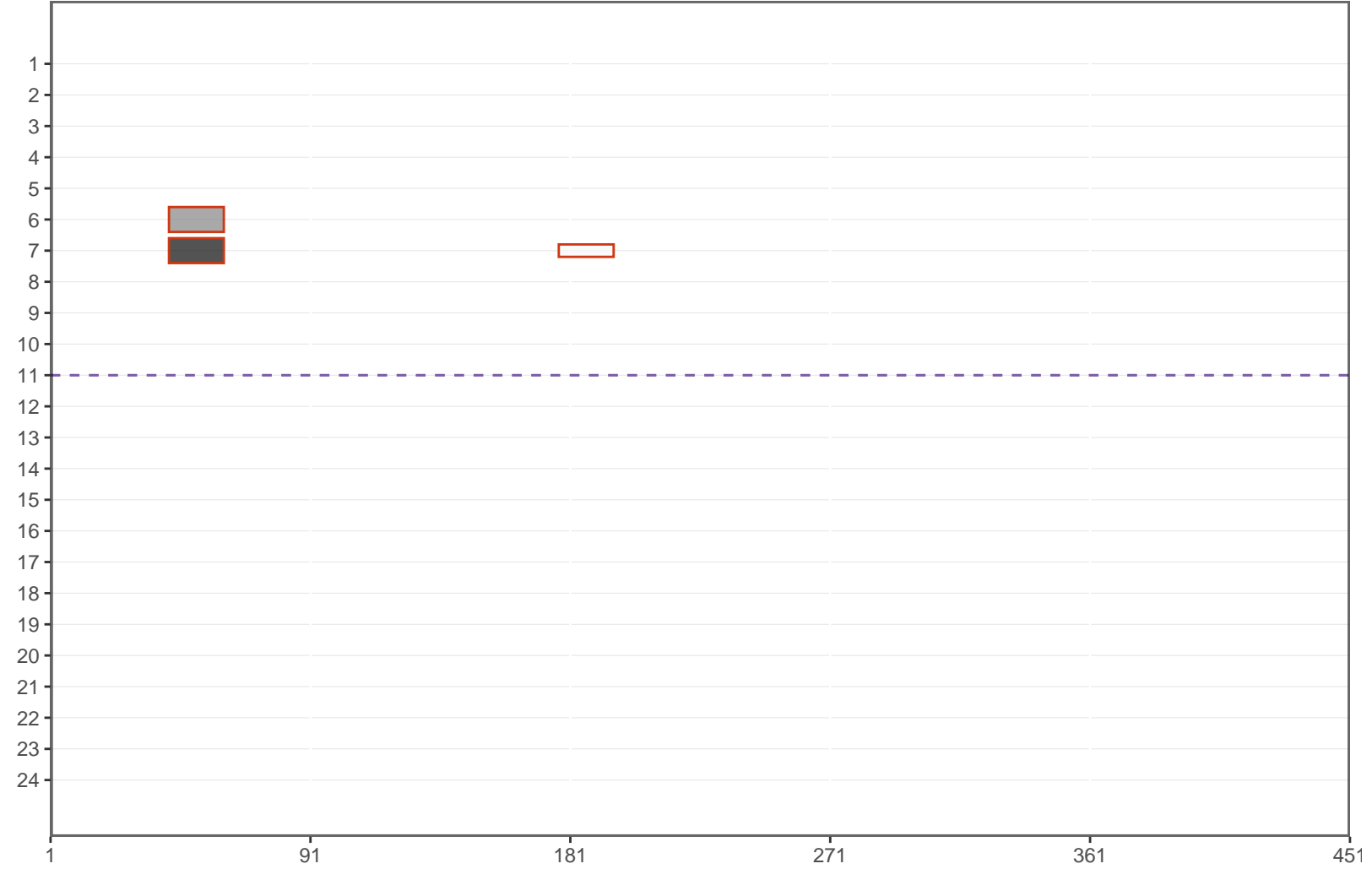
MW indication



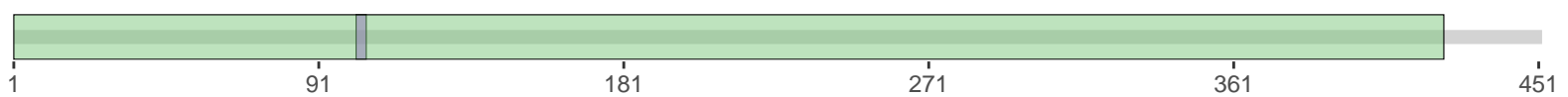
Molecular weight



Gel Slice

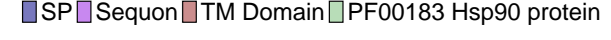


Protein length



Pfam domains

Pfam Description



Protein sequence:

EKLIVQKGEVLYLVPEIDEVADNLFYKEKFFVDISKEDLELDDDDVEKEREAKGEYVLLGDWIKDGLGDKWVAVGVSKRLSSSPCVLVSGKFGVSWANMERLMRAQTLGDTSTLEFMRRRLVFNPDHPVWDLNAAAGKNAPOSSGDKRAVELLYDTALISSGFTPDSPAEELGNKYDMMAMALGGRWGRSSEDESETSVETSTESDAGSAEVSEVQVVEPSEVIRTESNDIWE

NbL18g05620.1 phosphopantothenate--cysteine_ligase_2-like [MW = 36.24 kDa]

No. of times detected



log(intensity)



Values from



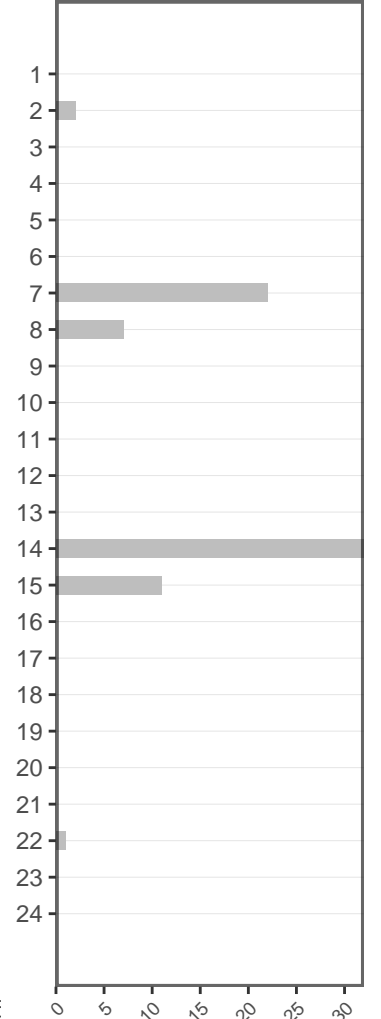
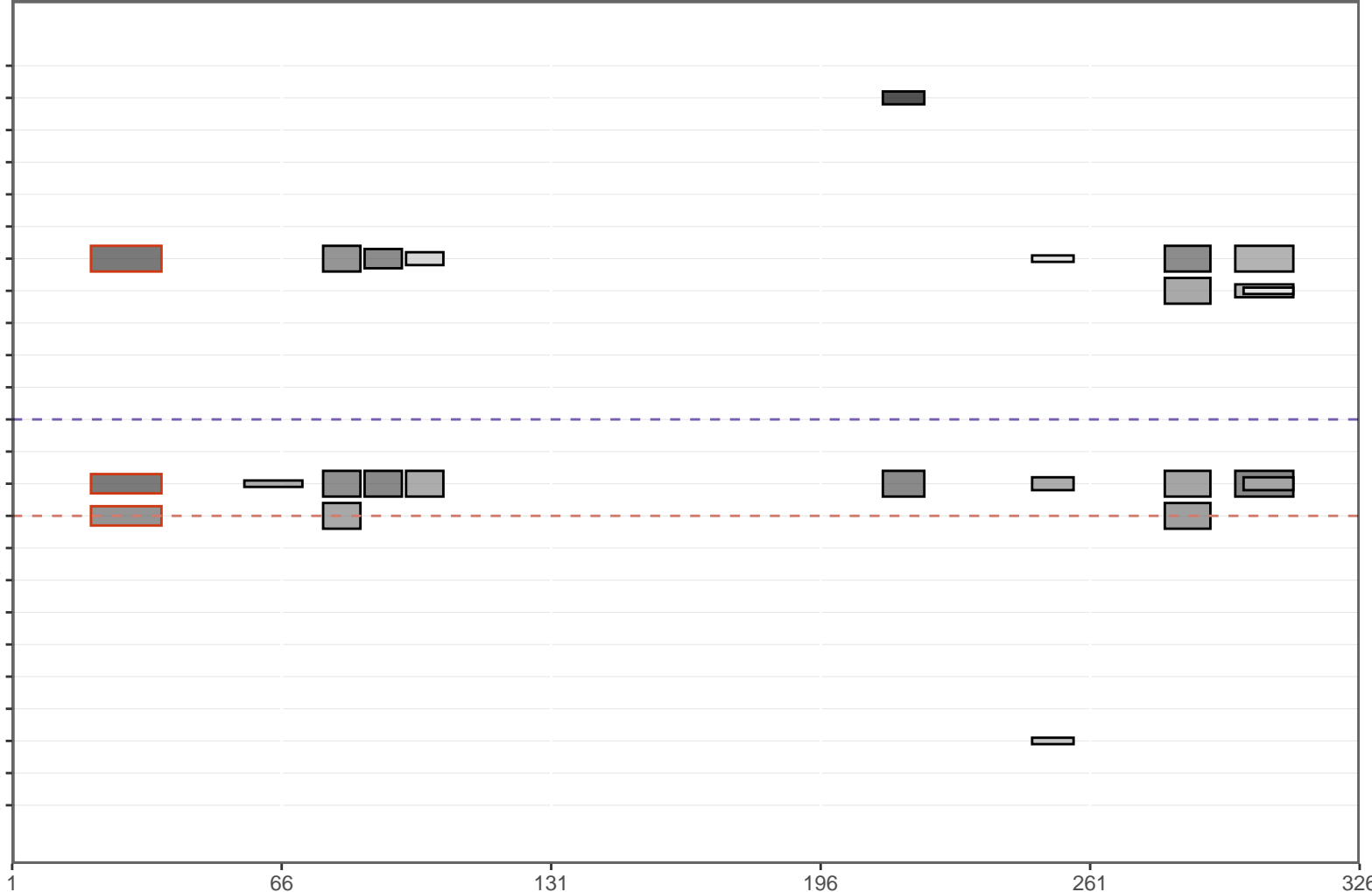
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

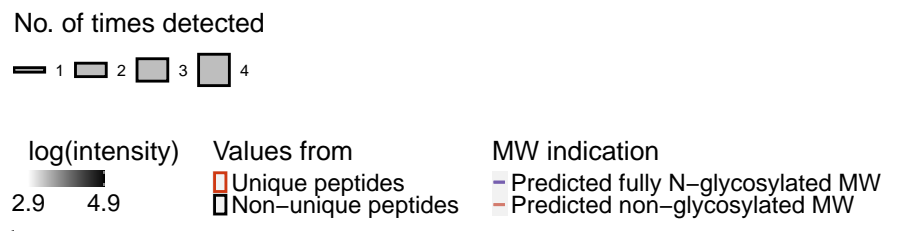
Pfam Description



Protein sequence:

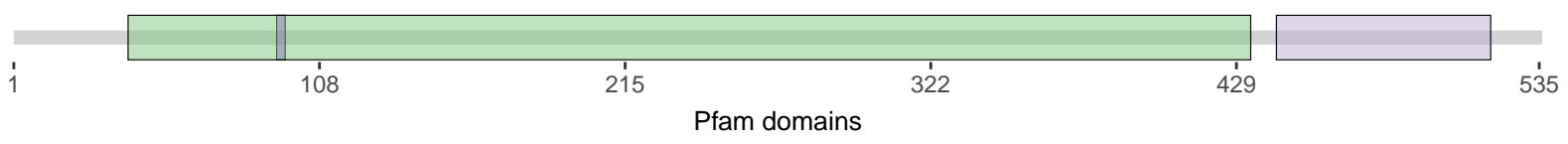
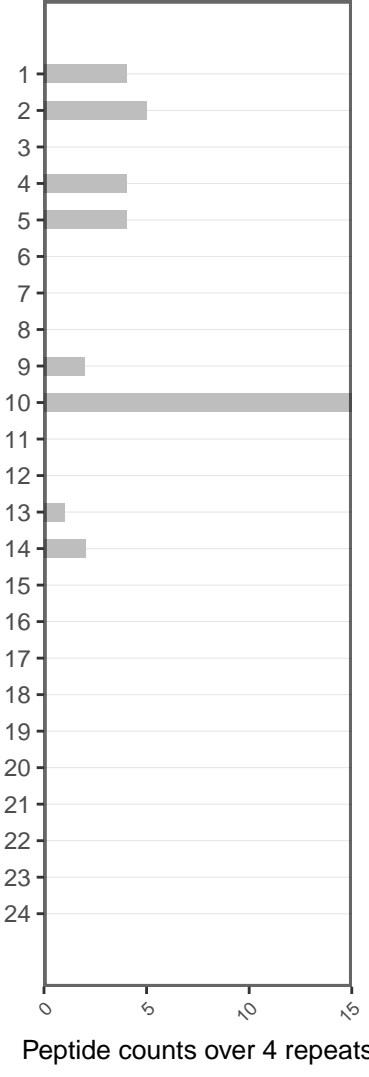
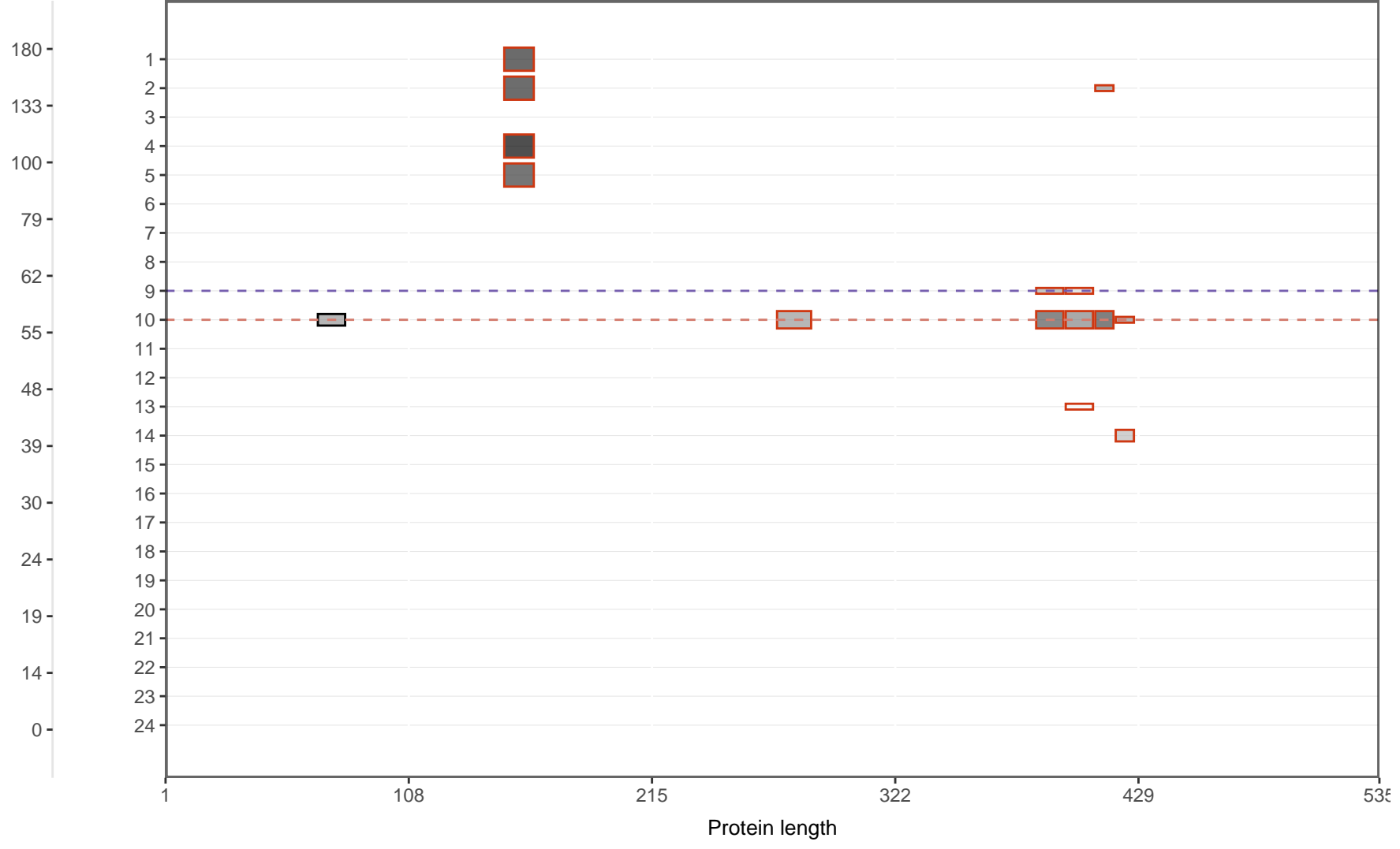
NRSAVNGSFLKLPFTTFEYLGRLRSLRSLRSGP6GMFYLAASDFYVPWESMTVHKDGG6GLMRLAQVPKMLYLRNEWAPVAFGIFKLETDITDILLGKADMLKHYKMMVAVNELSTRKEEYVWTEGEKTVRRDKTQAGADVEDPLIKLVMDVHSAVYKHSDA

NbL18g05470.1 4-coumarate--CoA_ligase-like_9 [MW = 58.35 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00501 AMP-binding enzyme
- PF13193 AMP-binding enzyme C-terminal domain

Protein sequence:

MRRKMLKAVEKFKYTGILVAPPPIVAVAMAKGKSVTSGYDLSLVAWGSGGAPLGHKQVQAFSDKFPNTVFGVGLTETSGAAFRATTEMLRGDSVGRLLIATEAKVDPDTGIALPPGEGELWKGPTMGGVYGDPKATSETLVPFGWLRDGLQYDHRHGVLFVDRLLKELIKYKQVQVAPRELEQLLQSHPDVDAVFPFDEEAGGVPMFVLRPQSGALDKEGVDFISKGVAPYKRRVAFVSGIKPKNSGKILRKLRRIRPQSKL

NbL18g05350.1 uncharacterized_LOC107789946 [MW = 14.02 kDa]

No. of times detected



log(intensity)



Values from



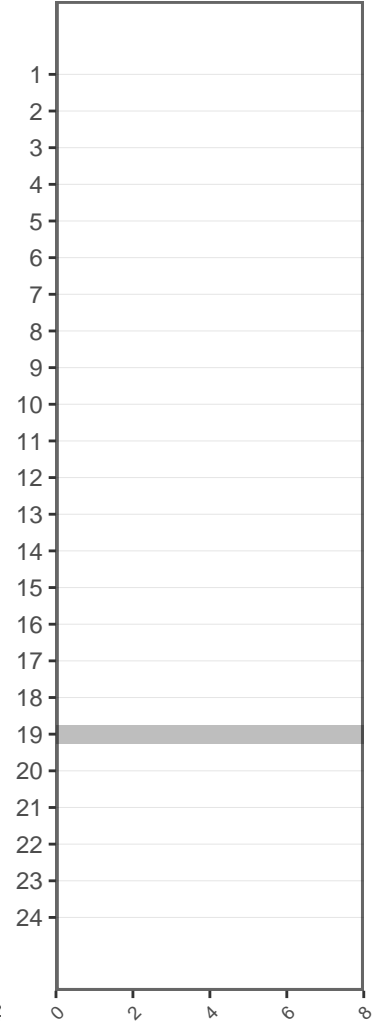
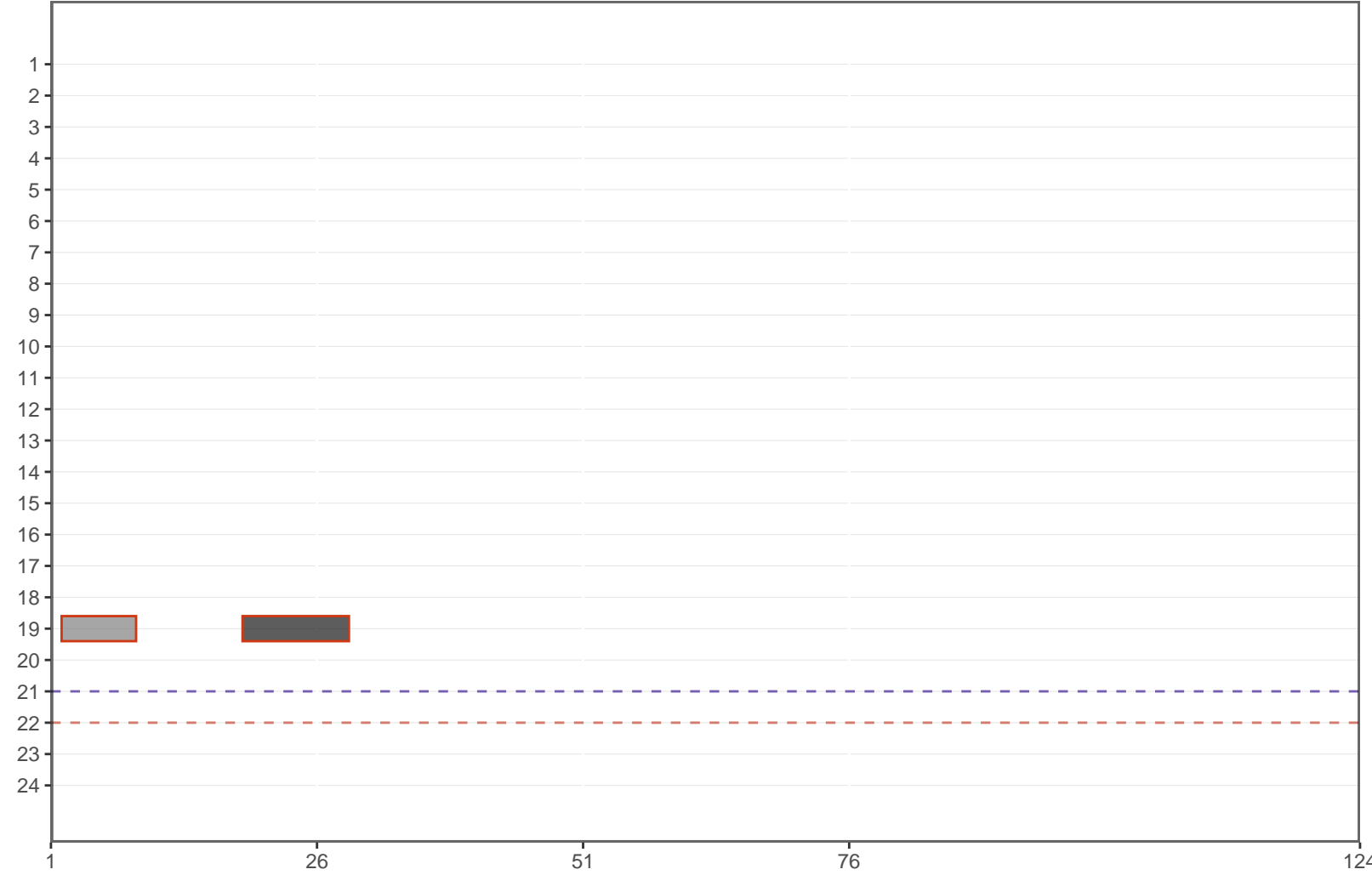
MW indication



Molecular weight



Gel Slice



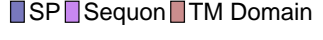
Protein length



Pfam domains



Pfam Description



Protein sequence:

EEIFSEMGIQPRFGLAGLGGKINMFEEDRDLMHFYFVAKEMAGEEAEELGPDGFAERLKMQGNLGSNWRG

NbL18g05300.1 ATP_synthase_subunit_alpha_chloroplastic [MW = 60.15 kDa]

No. of times detected



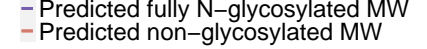
log(intensity)



Values from



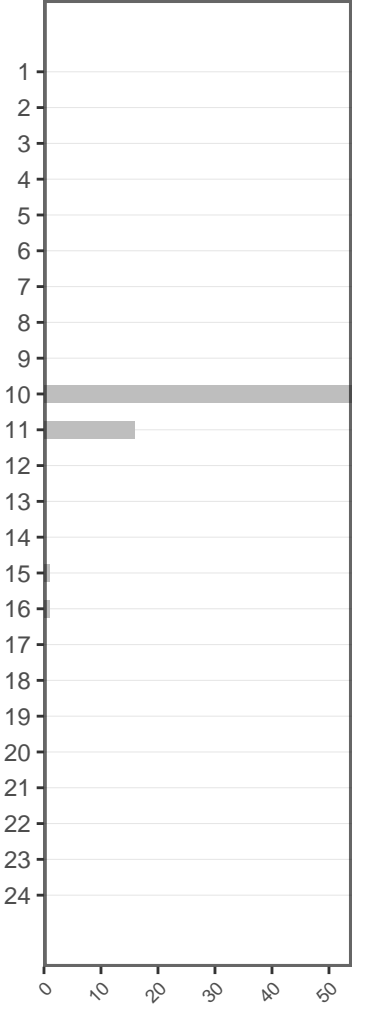
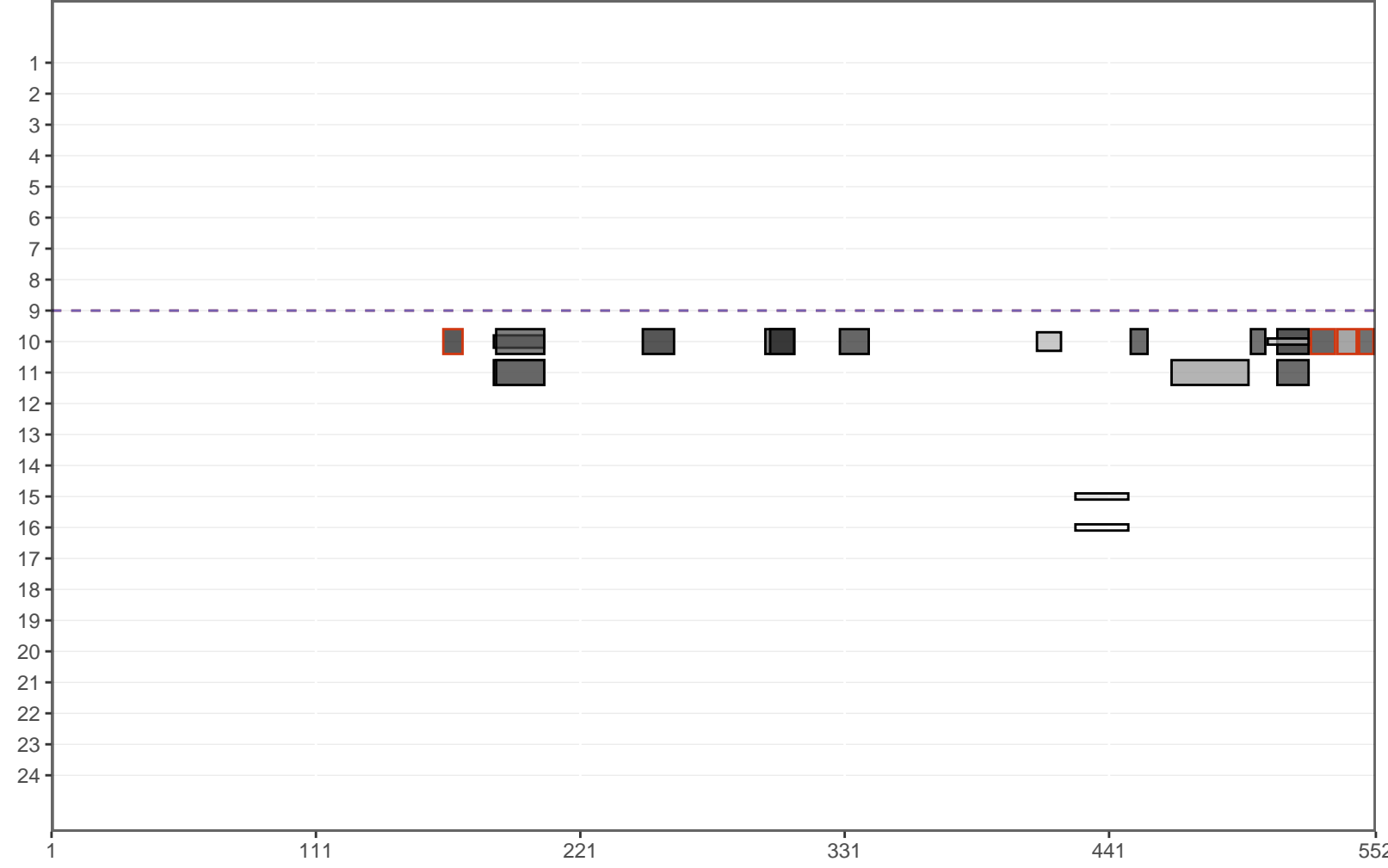
MW indication



Molecular weight



Gel Slice

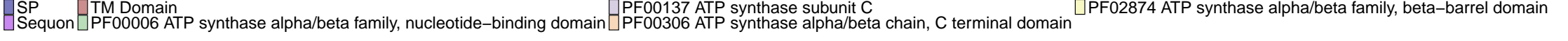


Protein length



Pfam domains

Pfam Description



Protein sequence:

EYTVVAETADSPKTLGHLAPYTGAAALAEVFMVRRHRTLHFDOLSKGADAVRQMSLLLRPPGREAYPGDFVYLSRLLERAAGLSSSLGEGSMTALPIVETGGGDSVAIPITNVISITDGGFLGADLNFSGIRPAINVGSIVSRVGSAAQIKAMKVAQKLELELAGFAELEAFAGFASDLKATQNLARGRRLRELLKGGSGAPLTVEEQIMTHYGTGTNGYLDLSLEVGVKFLVELRTYLYKTNKPFQGEISSTKTFTEAEALLKEAAGEGMDRFLGEOA*

NbL18g05240.1 50S_ribosomal_protein_L27_chloroplastic [MW = 20.57 kDa]

No. of times detected



log(intensity)



Values from



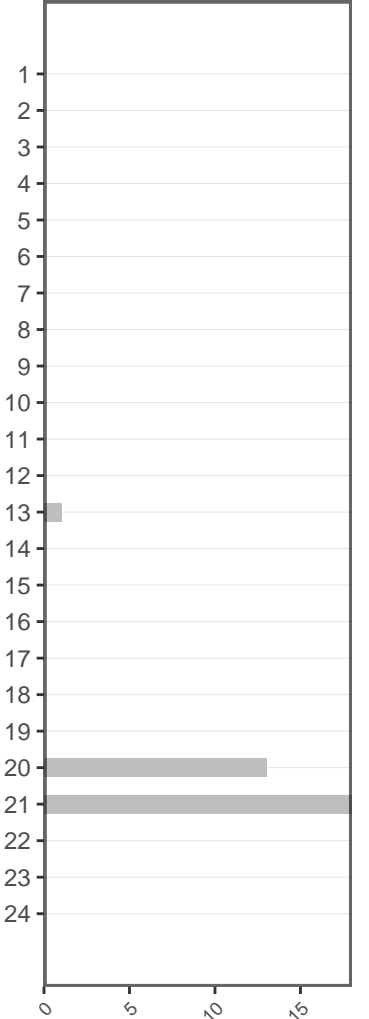
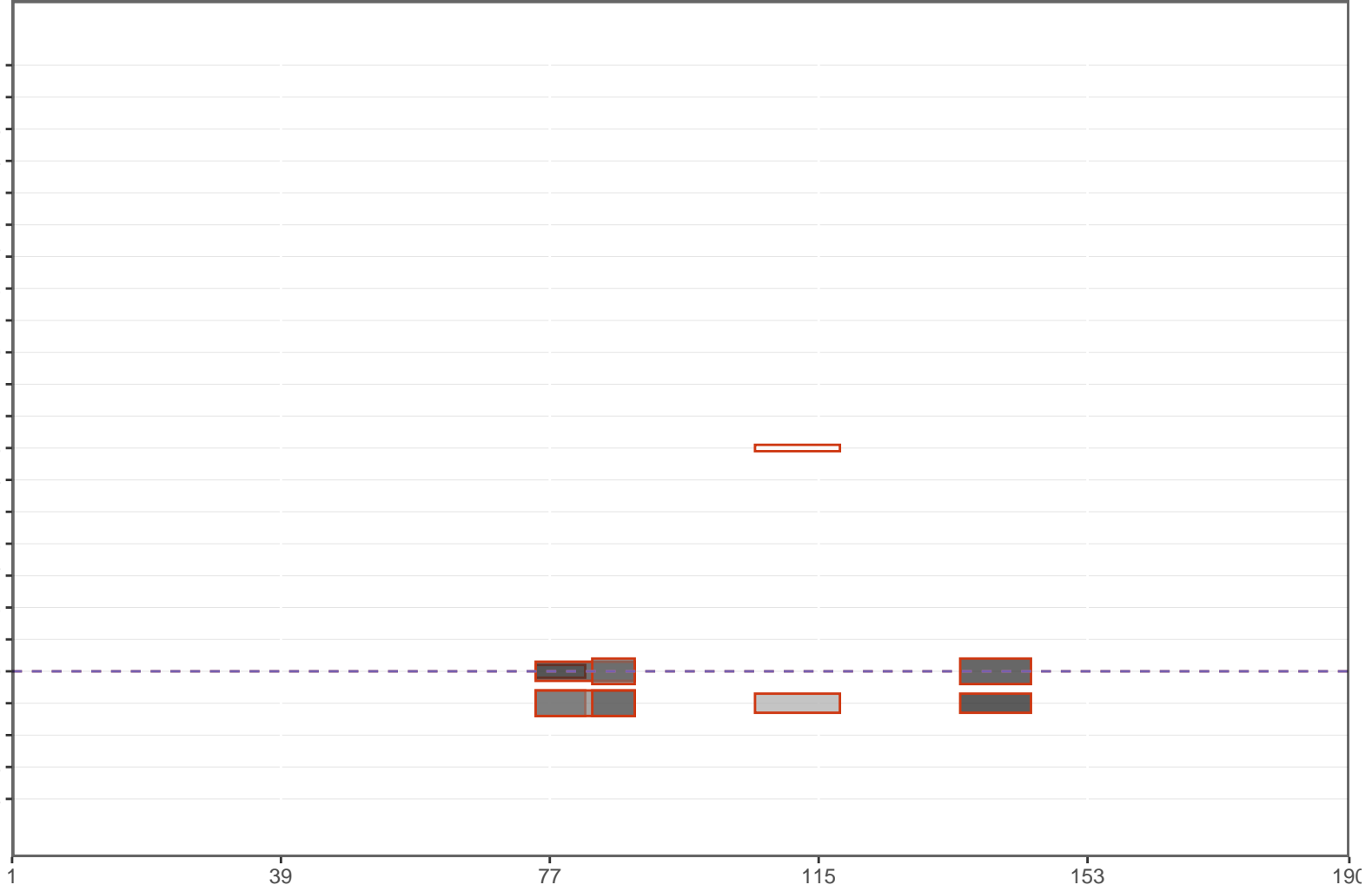
MW indication



Molecular weight

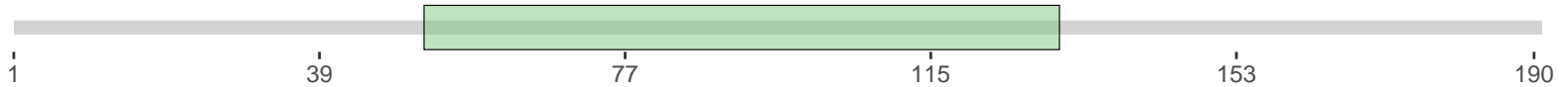


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KPGSIVRGRGTYKHPGRNVLGKNDHTFSLIDGLVWFKFGDPRRKKISVYPREVQFENPNBYRNRKRRESFRVGRERRKARREGVILQPSILAFAPESSEDTPSPGQ

NbL18g04880.1 ATP_sulfurylase_1_chloroplastic-like [MW = 52.15 kDa]

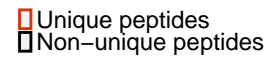
No. of times detected



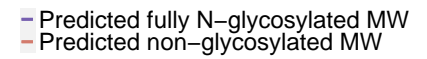
log(intensity)



Values from



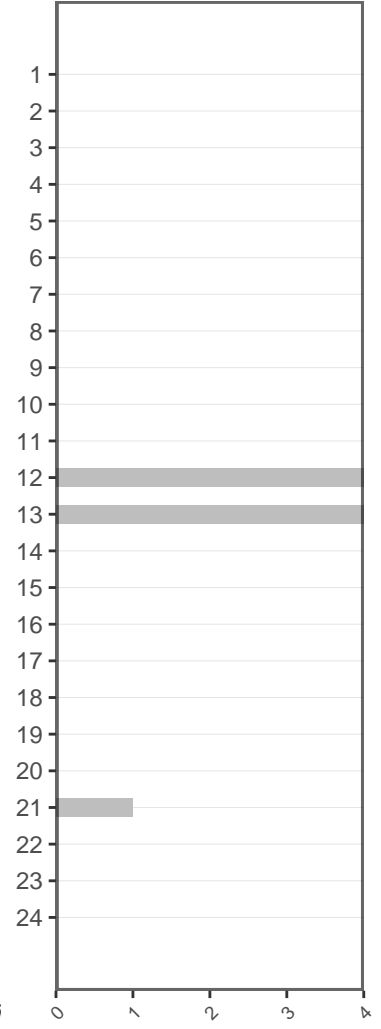
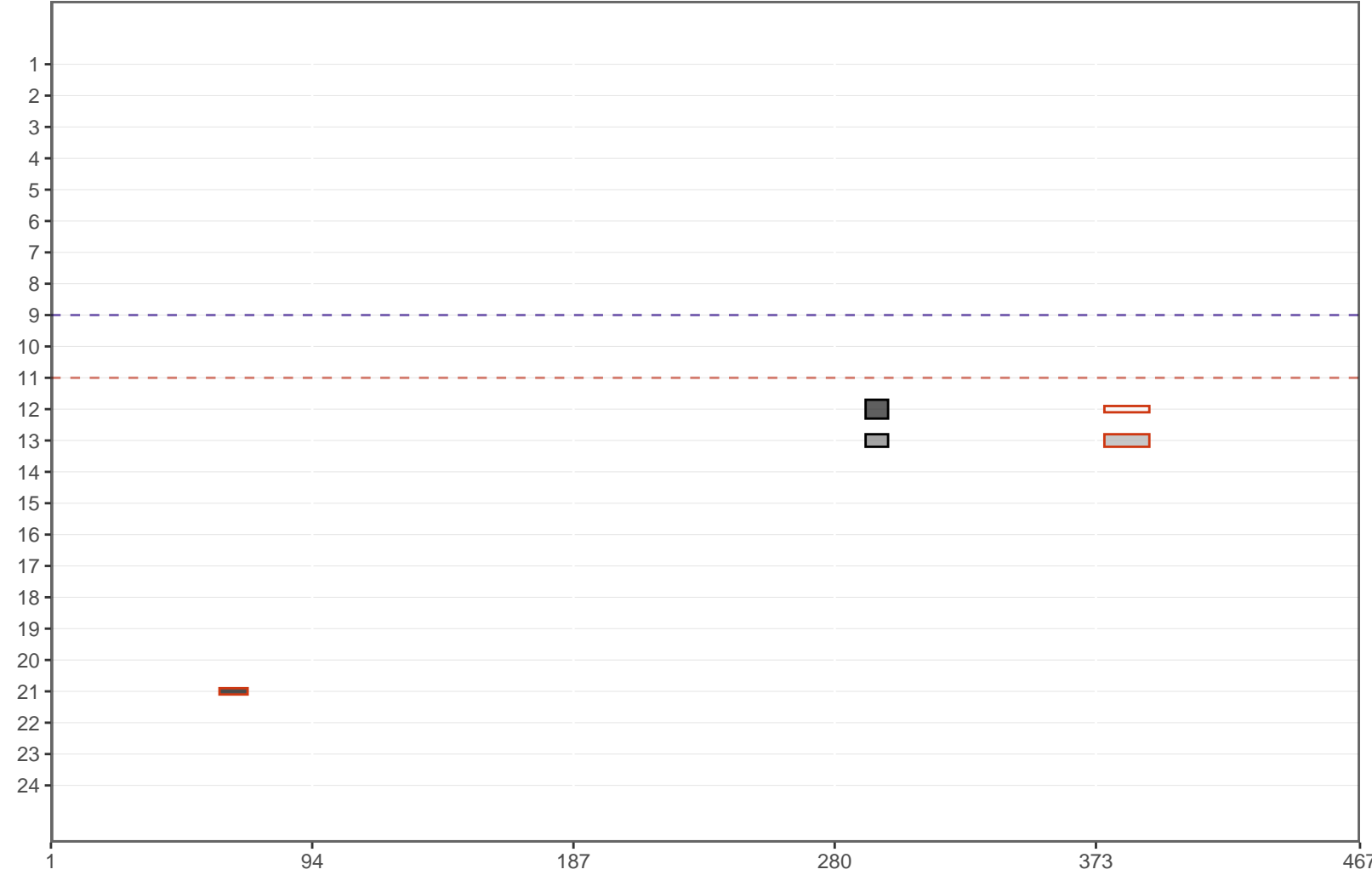
MW indication



Molecular weight

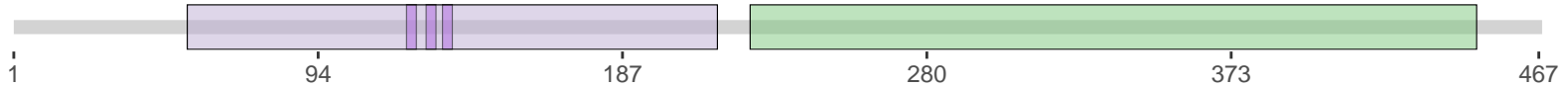


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IRFRLSPAELRDEFFRRNADAVFAFQLRNPNVHNGHALMTDTRRRLLLEMGYKNPVLHLPGLGQTKADDVPLQWRMKGHEKVLDDGLDPEFTTVSIFSPSMHYAGPTEVQVHAKARINAGANFYHGRDRAGMGHFLKRDYDADHGKVKLSMAPGLEQLTLFFRVAAYDKTGNKMAFFDPSRPQDFIFSGTKMRALAKNKESPPDGFMCDFGQVWVLEVYDLSLSTENGRIPQVPIV

NbL18g04860.1 2-methyl-6-phytyl-14-hydroquinone_methyltransferase_chloroplastic-like [MW = 38.07 kDa]

No. of times detected



log(intensity)



Values from



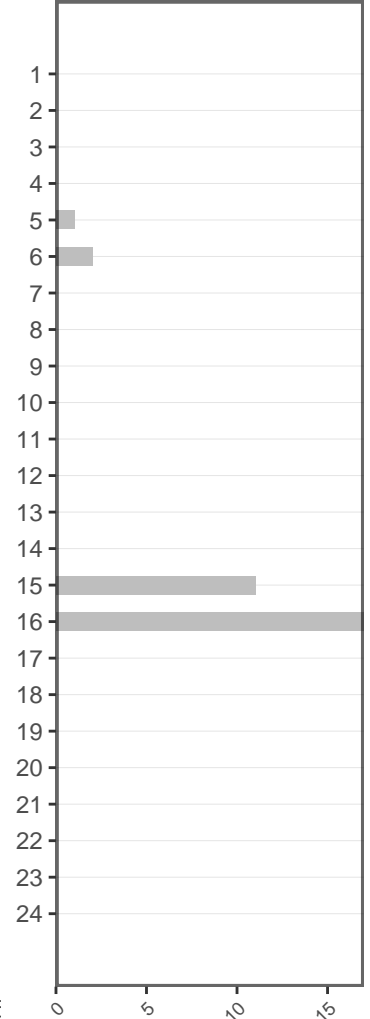
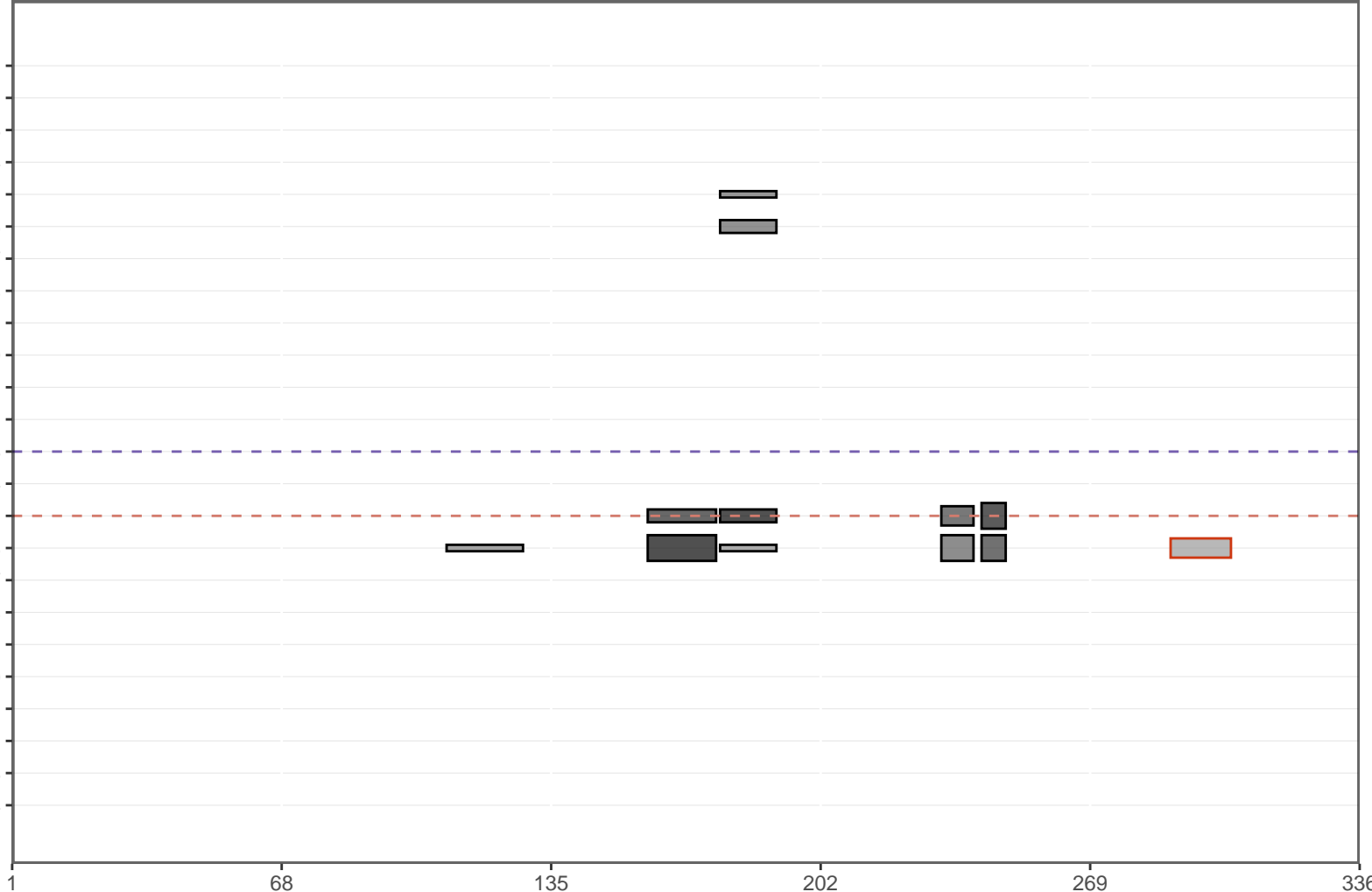
MW indication



Molecular weight

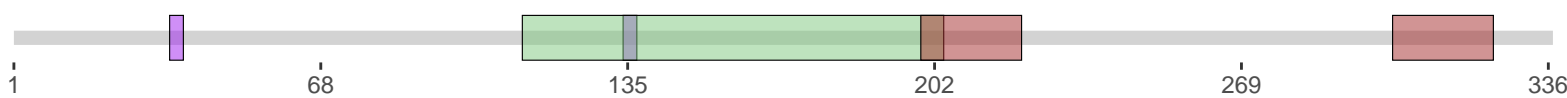


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CECKLECGDAEDLFPPTDFDRVYVSGSIEYWPDPGRGKEAVRVLTIQGGVAQLGIPVYPSFVLSRFADMMMLFFKKEEYIEVFKKAGFAQVVKLRIGRQKRWYRGRVRRHGLMGSQVTVGKPYFGESFLQLGPKVEVSKPKVNFVFLVRFLLGTAATPYVVLPIVYVMLKDDITPKGGPI

NbL18g04830.1 pyruvate_kinase_isozyme_A_chloroplastic-like [MW = 63.11 kDa]

No. of times detected



log(intensity)



Values from



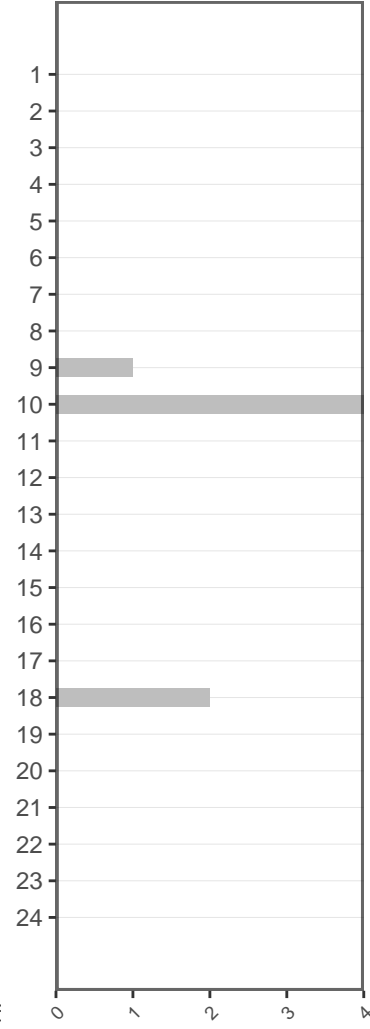
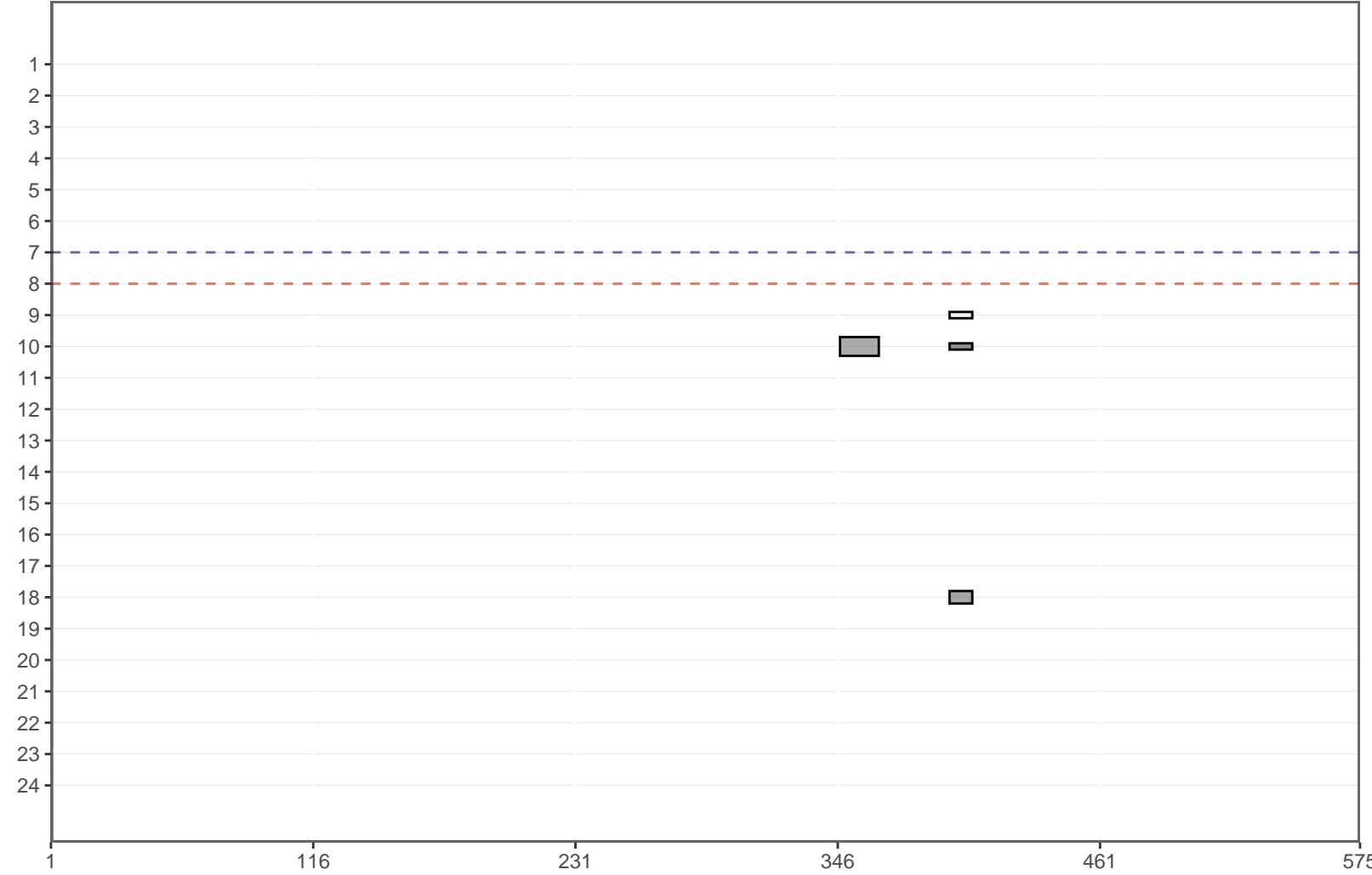
MW indication



Molecular weight

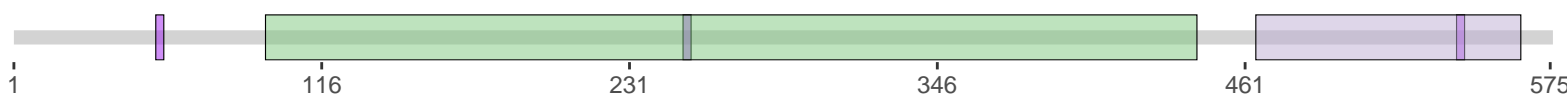


Gel Slice



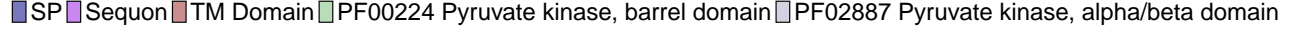
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SKDVLIDDFGAEIGVDFIAVSEFKSAEVIKHKYKIKHSPNSDAVIAKIESIDSKNLEEIHQASDGMVARGDLGAQPLEQVPSQQGRIVQLCRQLNKPVIASQLLESMEVPIPTRAEVAADISEAVRQRGDALMLSGESAMGGYPEKALGVLKSASLRISERSVREGQKHVEVELPSIASFTGSSIEEIGNSAAGMANNLEVDALFVYTRNGHMAALLSRGRPCGRPFATTTTTSVRRRLNLQWGLTPERLGFSDNIMESNLNFTFSLKARGMVRGGDLIAVSDMLSQIOM

NbL18g04770.1 acylamino-acid-releasing_enzyme-like [MW = 66.34 kDa]

No. of times detected



log(intensity)



Values from

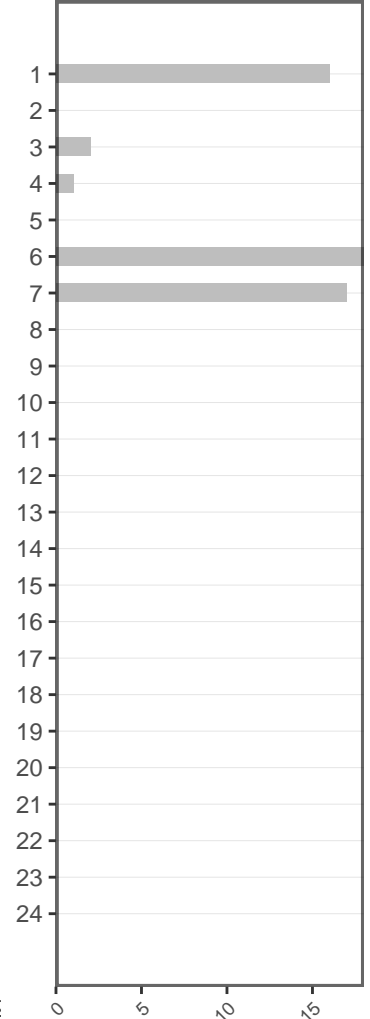
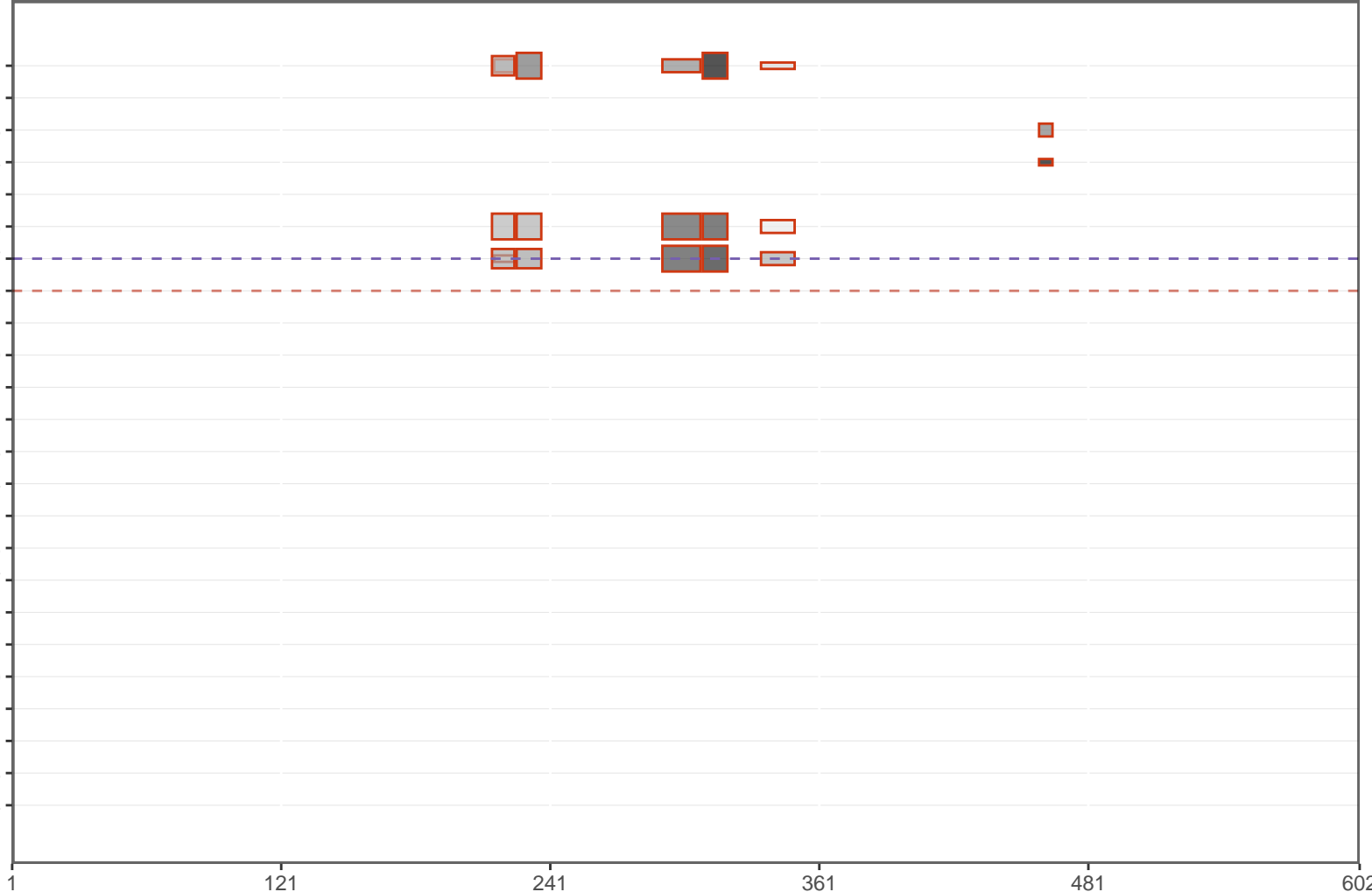
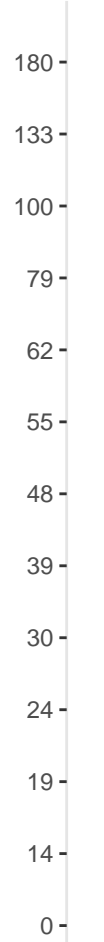


MW indication



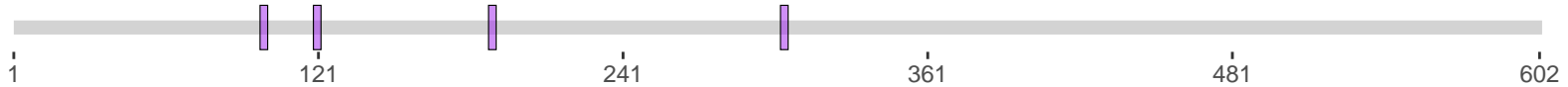
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



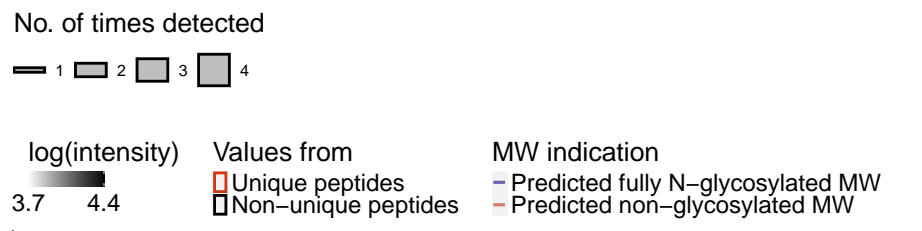
Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

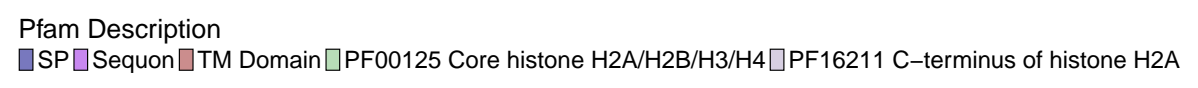
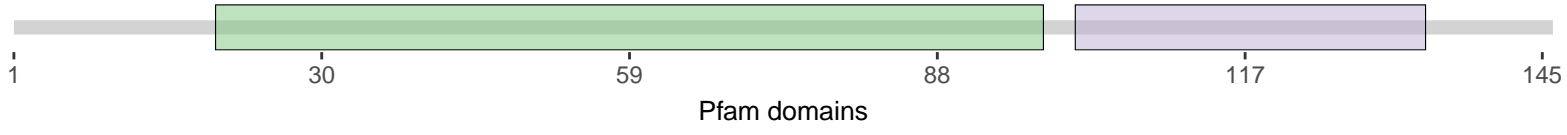
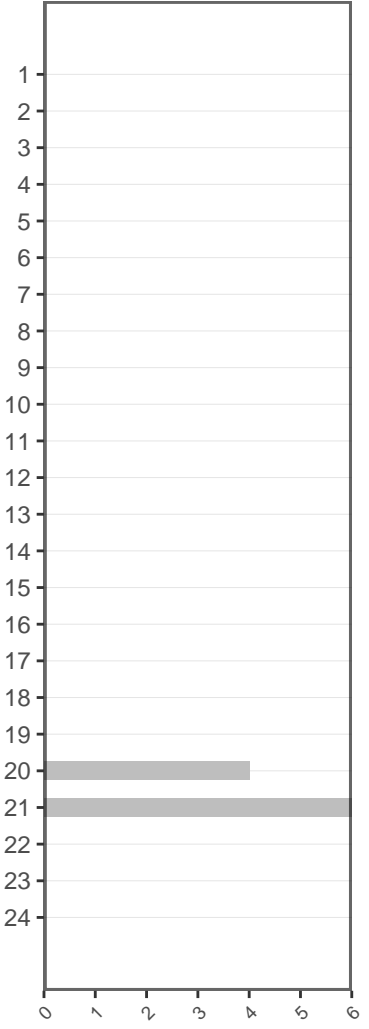
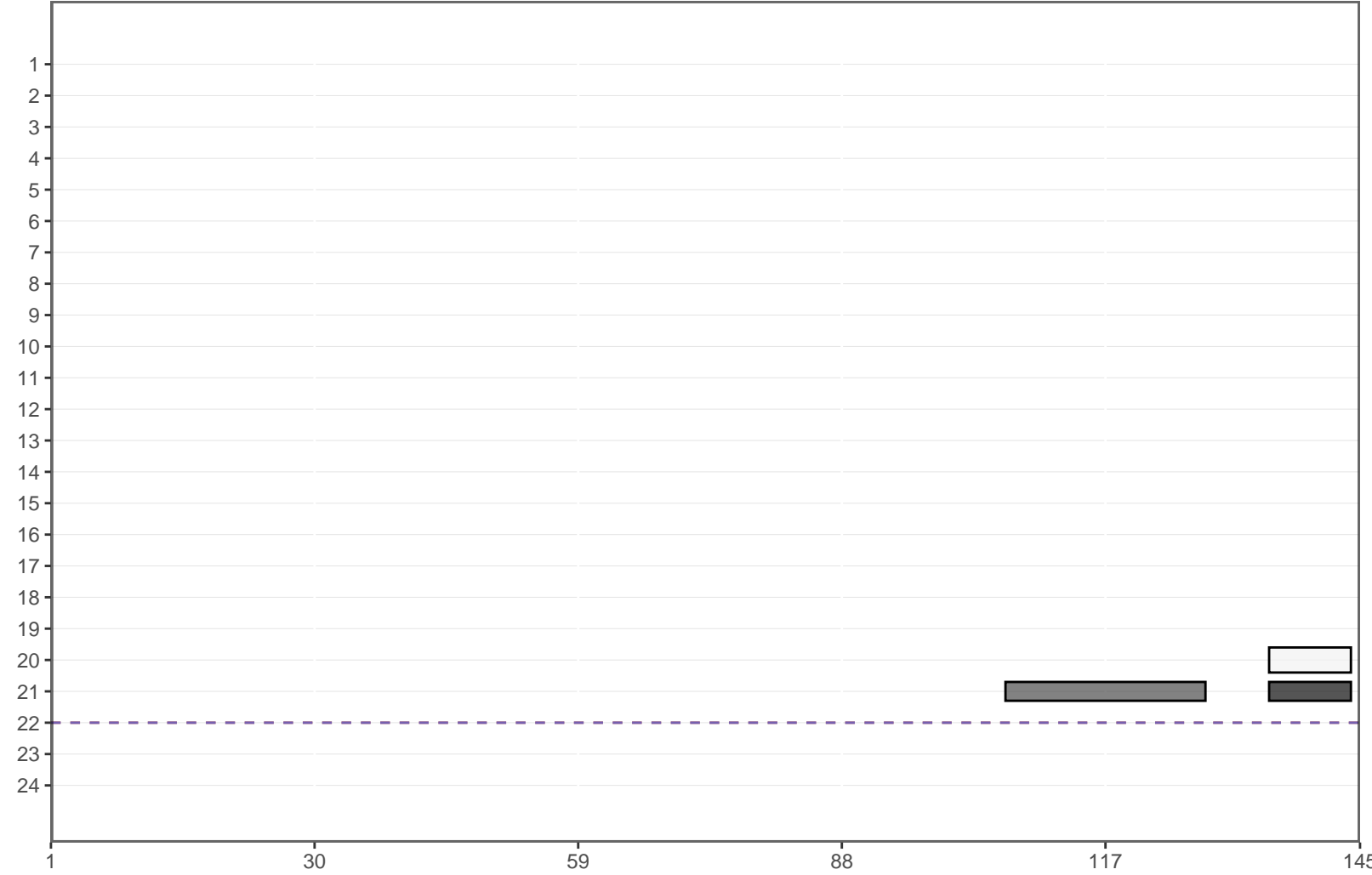
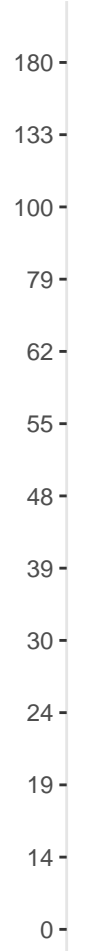
IAPFSKSDIHGSGTHAADNVSPKILTQSI65AYFRFSPDGKLLFL6ARNSVD5WHAHSATGSLHRI65W5FNGKPTDPAKIDVVPVVMCPEDGCFPLGYCYVPSRPSWSDGVTML65W65G5TQAI65NVV56GVYRISPGTFS65WVLLQDGDGNIAV65SPVDVPAKYGSLVHKAEAEASW5WLDV65PIR65SERVTSLL65RQFSIMRIPVRDSEKLTGASKPYEARFV65SK65GRNYYDPLVYVHGGPH65VLL65SF65K65LAF65L65GLY65LLIYYR65SL65LVRKQ

NbL18g04730.1 histone_H2AX-like [MW = 14.92 kDa]



Molecular weight

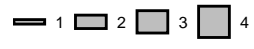
Gel Slice



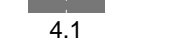
Protein sequence:
 YLSAVLEYLAEEVLELAGNAARDNKKNRIPRHIGLAVRNDDELEKLLGGVTANGGVMPNHNQLPKKAGSGKGDIGSASGEF

NbL18g04640.1 ADP-ribosylation_factor-like_protein_5 [MW = 20.94 kDa]

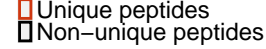
No. of times detected



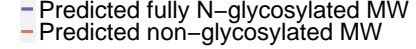
log(intensity)



Values from



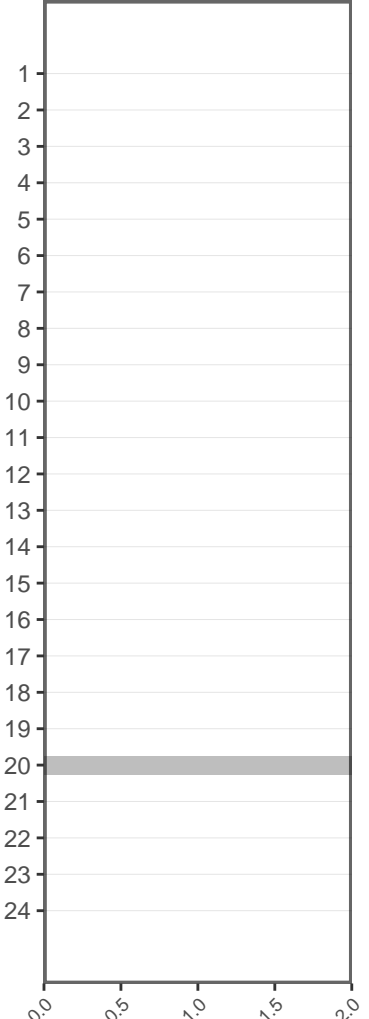
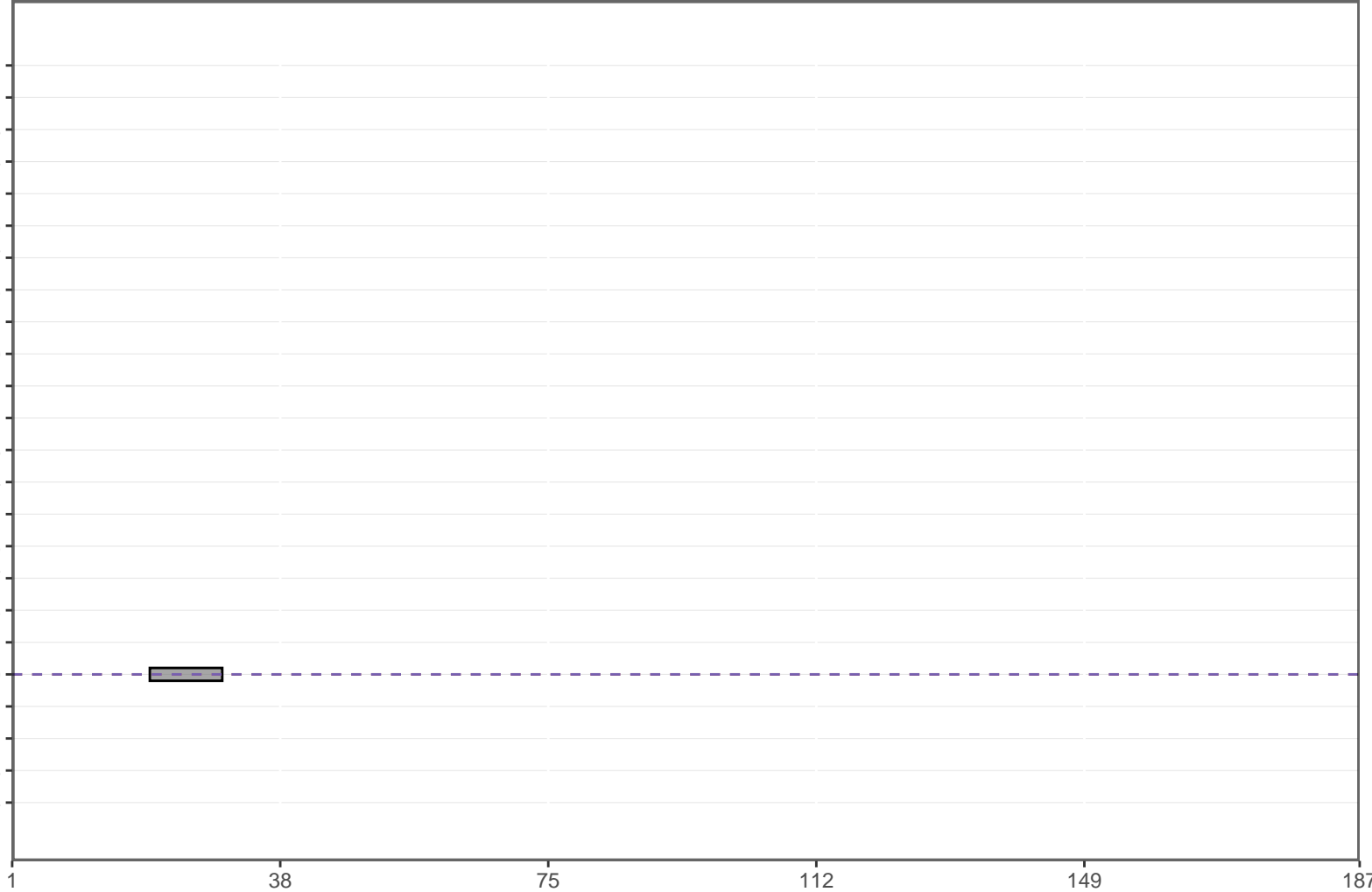
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

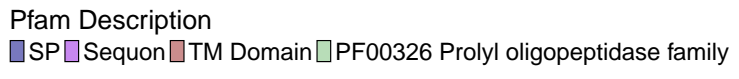
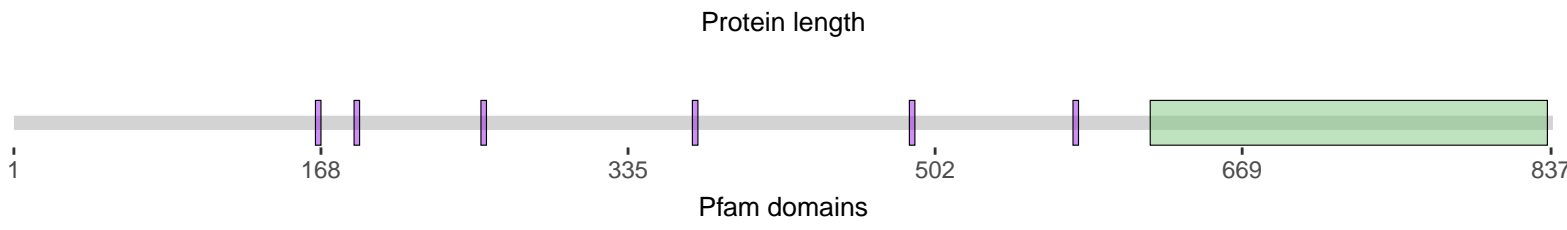
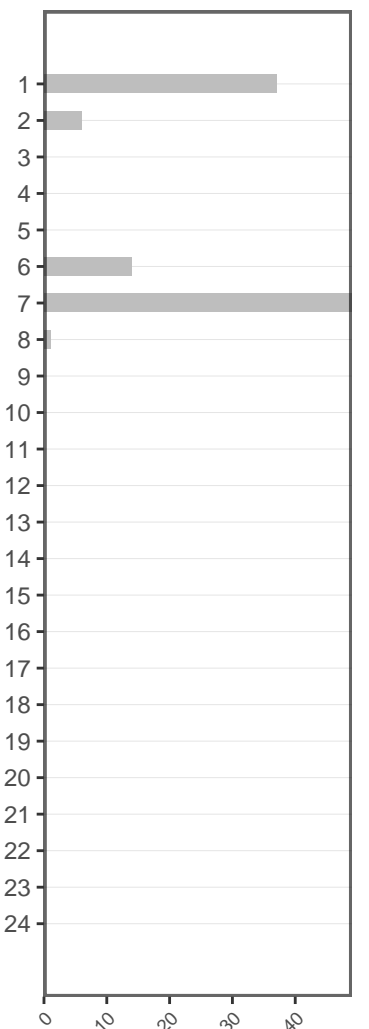
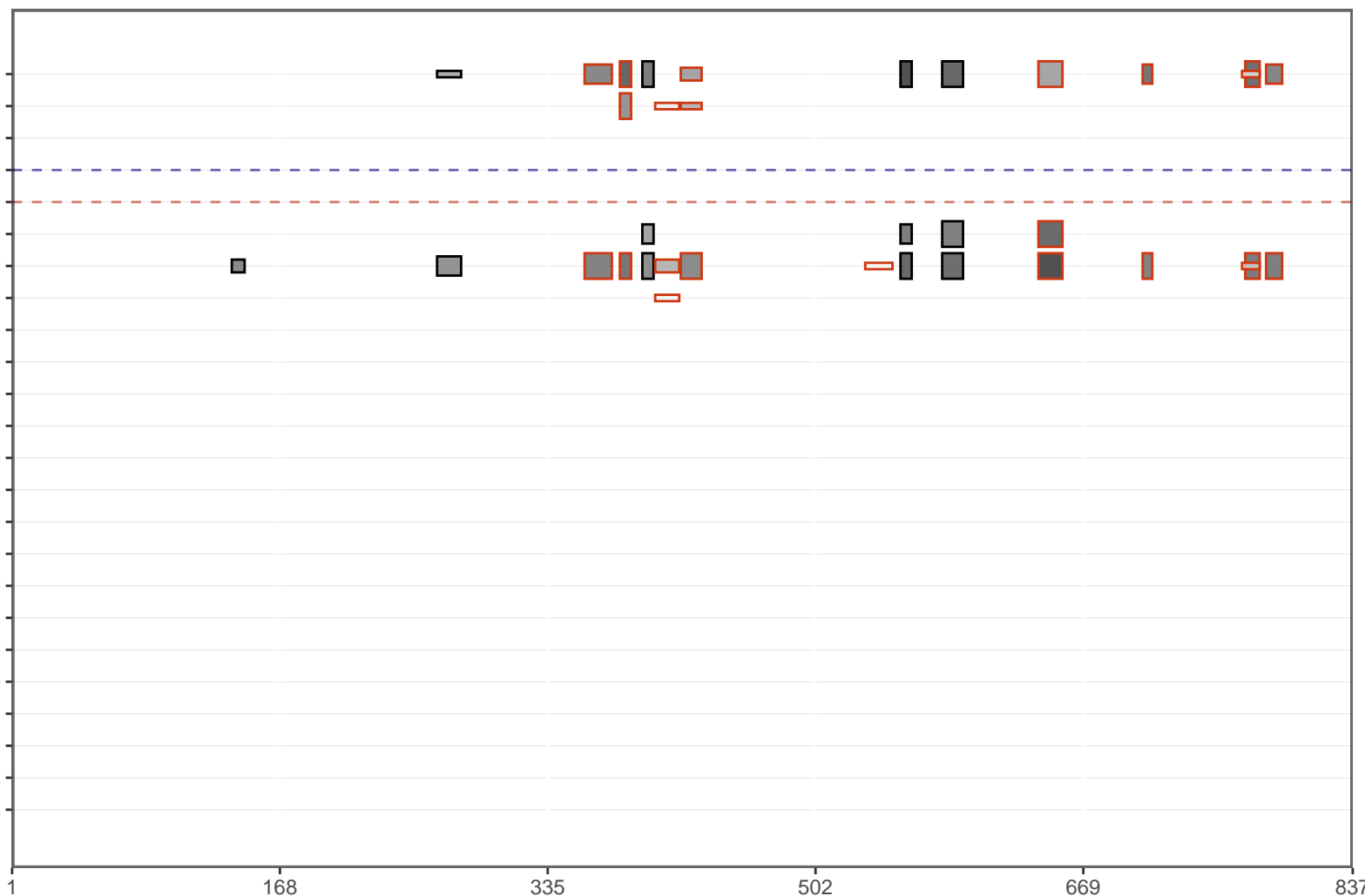
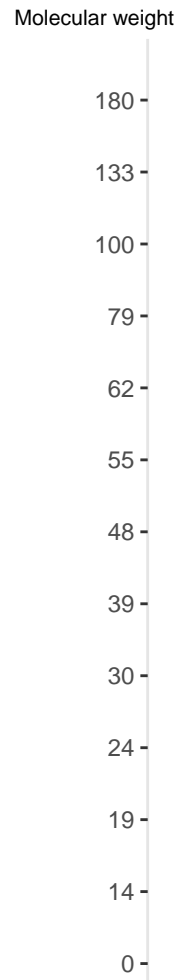
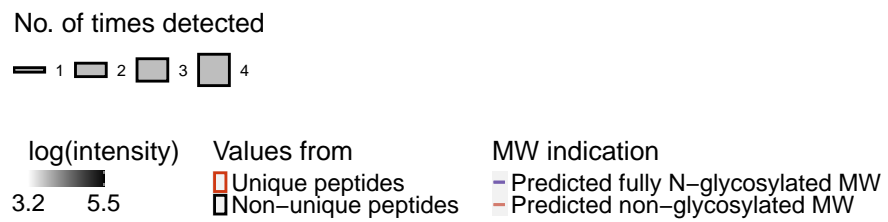
Pfam Description



Protein sequence:

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NbL18g04600.1 acylamino-acid-releasing_enzyme-like [MW = 91.52 kDa]



Protein sequence:
 SSVDSWAHSATGSLHRIDWSENEKPTDAKIDVFPVAVMCPEDGGFPGLYGVYVLEKPKWISDGYTMLSSEWVGSTQVIEVNVISGNSIRISLGDSEFSWVNLALDGDNIHVGSPFDVDFPAIKYGLVRKASTAEAGWISWLVGSEPIGKGEKVTSLLSRQGFIMRIPVRDIEQNTLKGASKPYEAFVSSKFRFRNVDPLVVLHGGPHSVLLSFSFKLAFLSLGLYSLLLVWYRGLGFGEEAVDGLPKIGSDQNDVLAIDHVIKGLADPKMVLGGSHGGFLTHLGG

NbL18g03900.1 chlorophyll_a-b_binding_protein_50_chloroplastic-like [MW = 28.41 kDa]

No. of times detected



log(intensity)



Values from



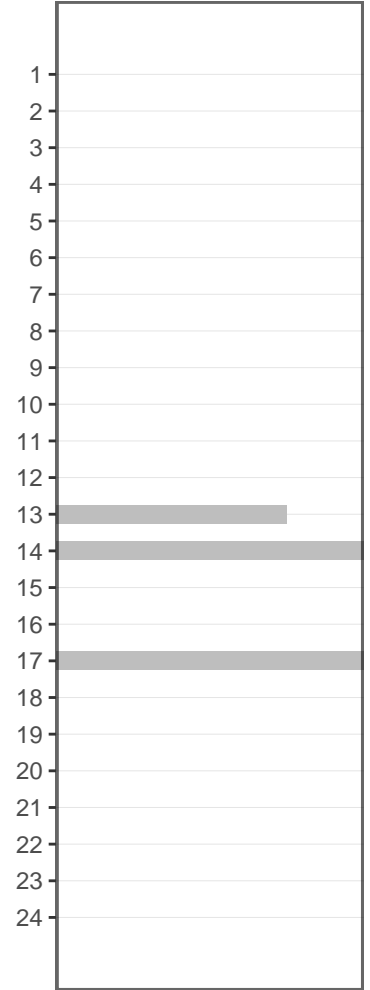
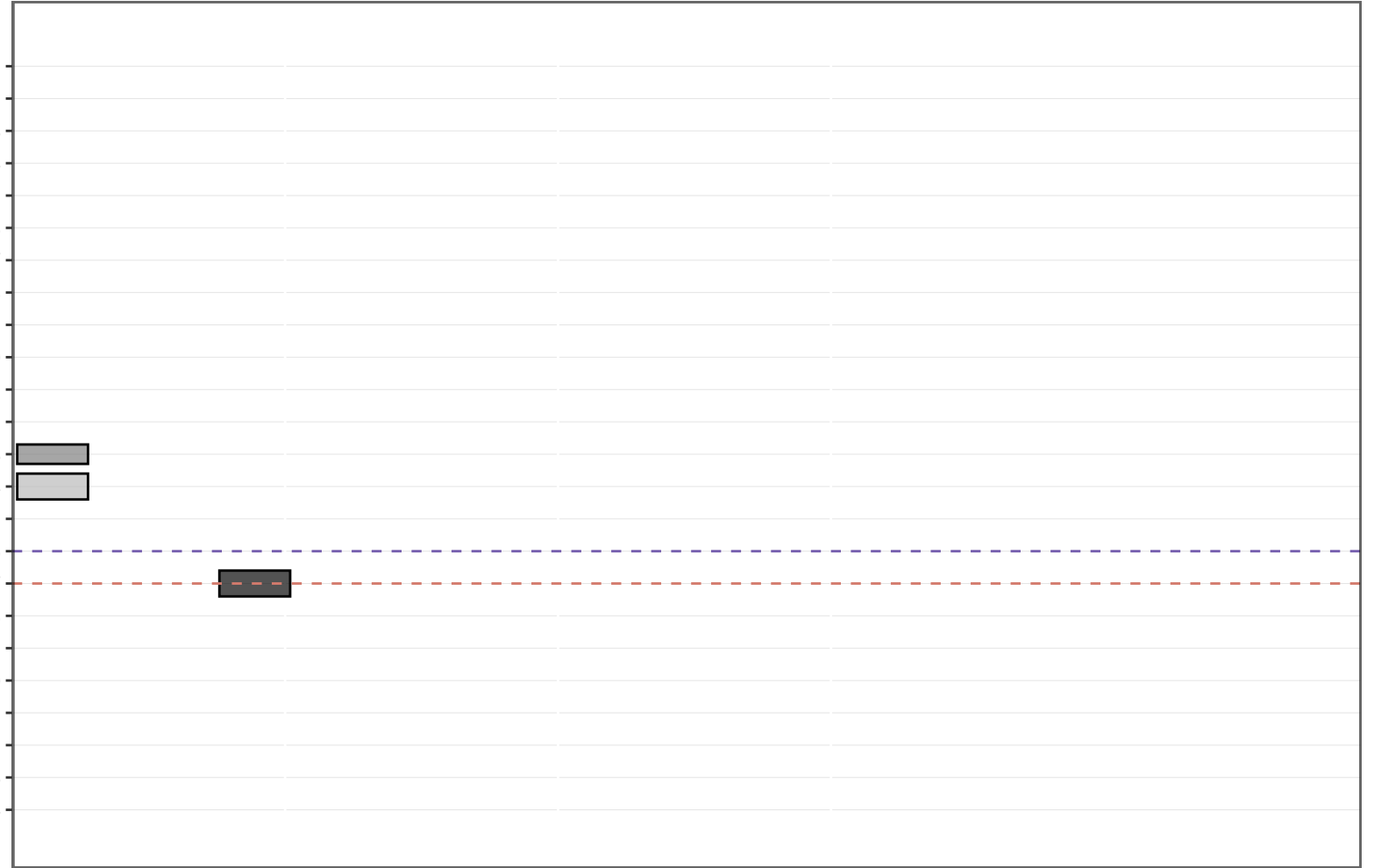
MW indication



Molecular weight



Gel Slice

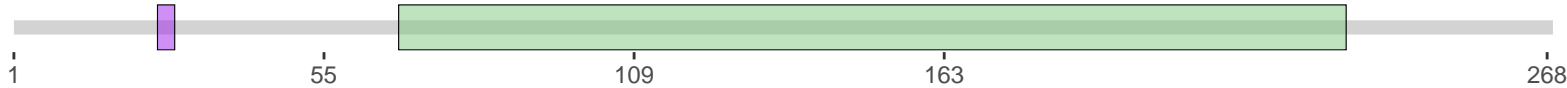


Protein length

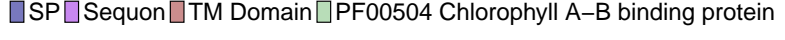


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ARNGYKFGAEVYFKAGSGDFSEGGLELGNPBLVHAGSLAWAGQVLMGAVEGYRVAGGFLGEVVDPLYPGGDFPLGLADDPFAELKVKIKNGRLAMFEMFGFFVQAVITGKPLELADHLTDPVYVNAWAWATNFVPGK

NbL18g03850.1 chlorophyll_a-b_binding_protein_40_chloroplastic [MW = 28.7 kDa]

No. of times detected



log(intensity)



Values from



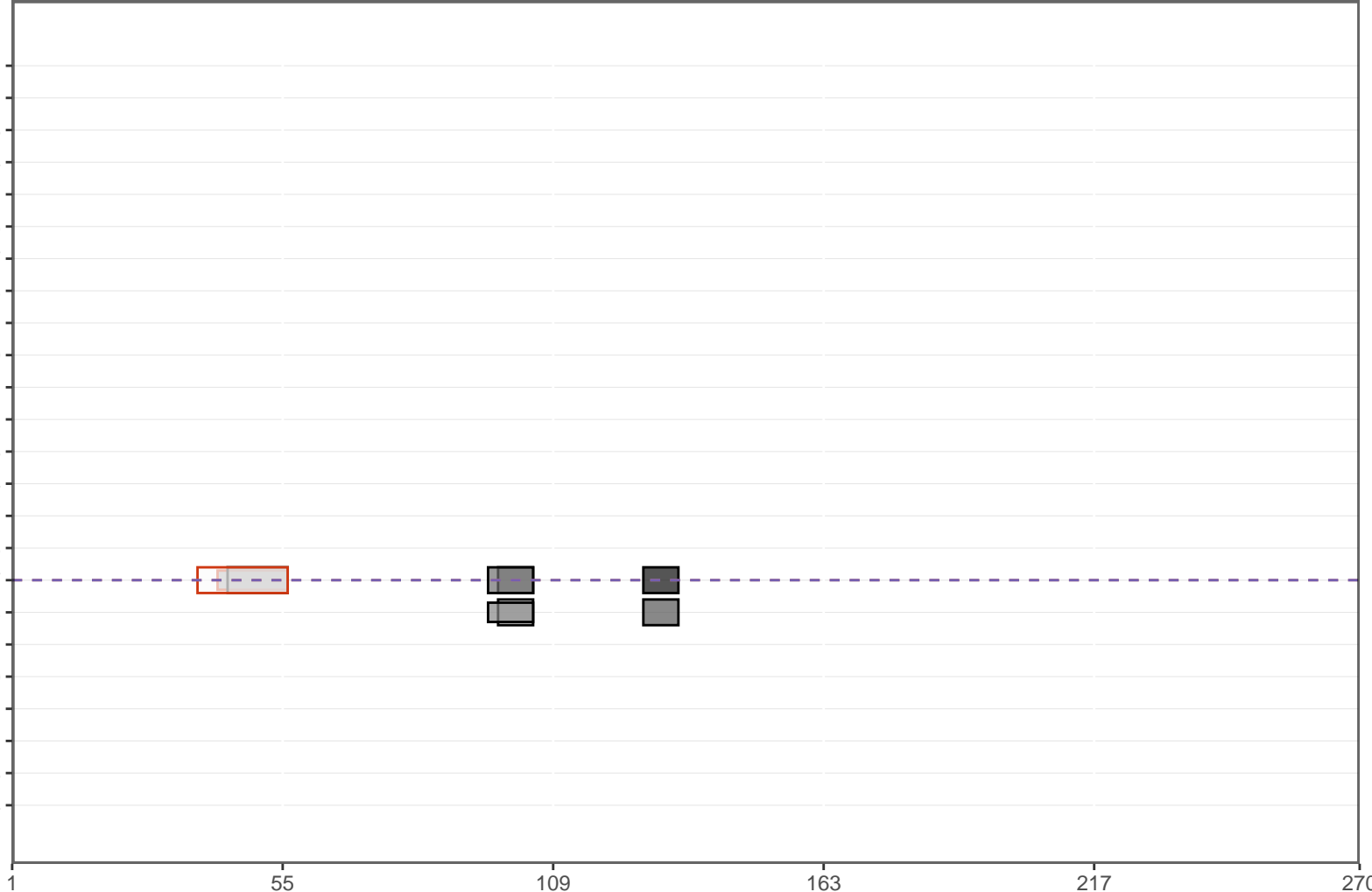
MW indication



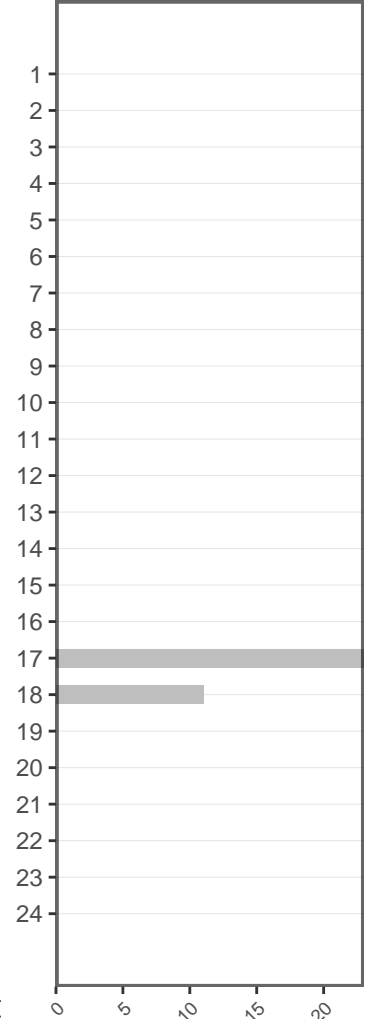
Molecular weight



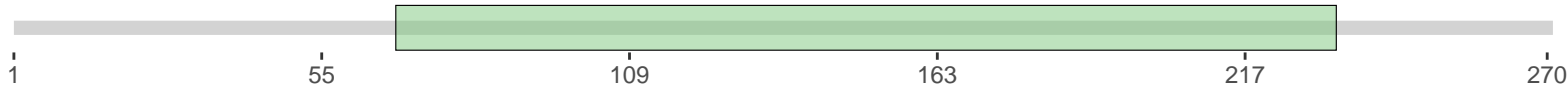
Gel Slice



Protein length

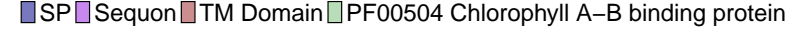


Peptide counts over 4 repeats



Pfam domains

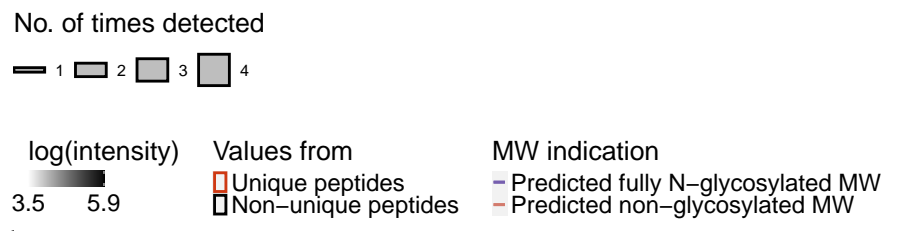
Pfam Description



Protein sequence:

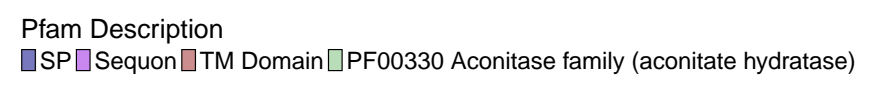
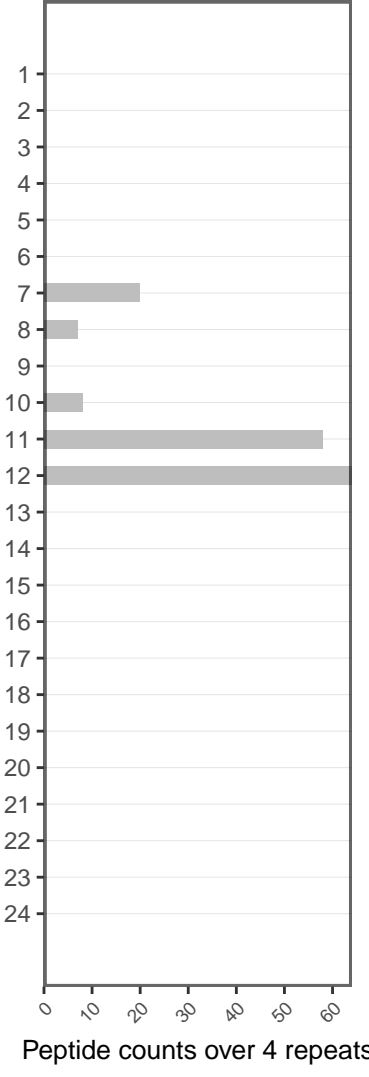
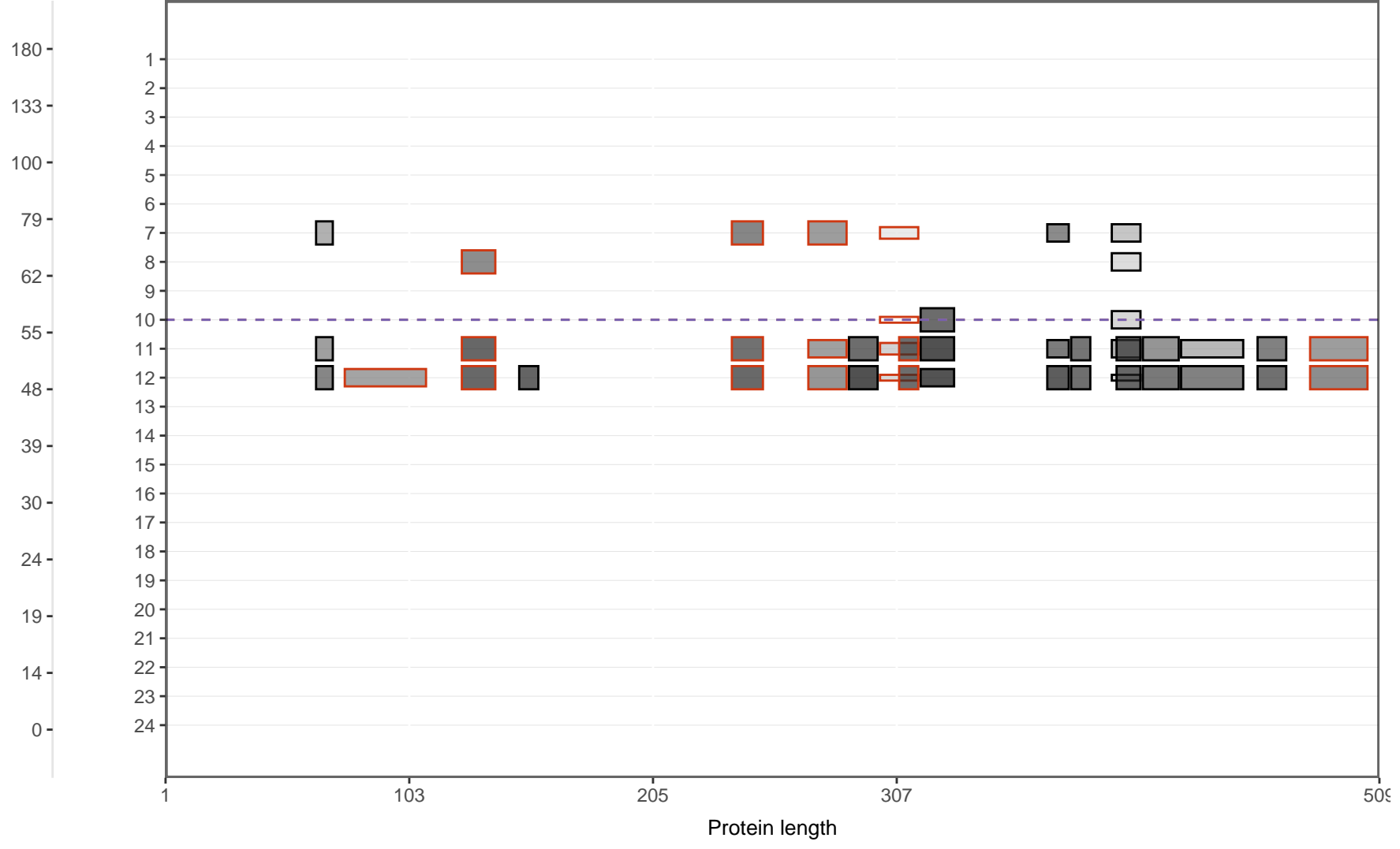
RNGVYKGEAVWFKAGSQIFBEGGLDPLGNPSLVHQAQSLAWAGQVYLMGAVEGYRAGGPLSEVVDPLVPGGFDPLGLAEDPEAFELKVKKEIKRGLAMFSMFGFFVQAVTGTGKPLENLADHLADPANNWAWATYVYLPLEN

NbL18g03810.1 3-isopropylmalate_dehydratase_large_subunit_chloroplastic-like [MW = 55.21 kDa]



Molecular weight

Gel Slice

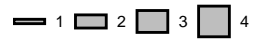


Protein sequence:

IEMPDYLLAKDLIQGSEISVAGATYKAMEFVSGTVESELGMEERMTLGNMVEAGGKNGVHPADKTTYDYLEGRITSPYEPVYVSDGARYLKEVRFDISKLEPLVAKPHSPDNRALAREKDKKIDRVYSGCTGGKTEDFMAAAKVFASGGKWKVPTFLVPTQKVMMDVYSLFVPSGGKTKGQIFEEAGGDTFASPSGGAGLGGPKDTPYARMNEAQVGVSTTRNRFPGRMGHEGGHVLASPYTAAASALTVTDRPREFLQ

NbL18g03510.1 pleiotropic_drug_resistance_protein_1 [MW = 140.5 kDa]

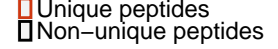
No. of times detected



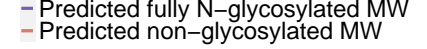
log(intensity)



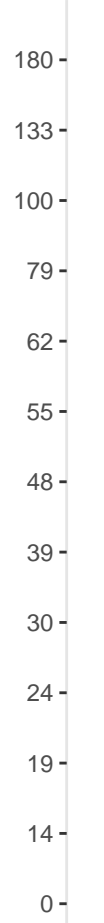
Values from



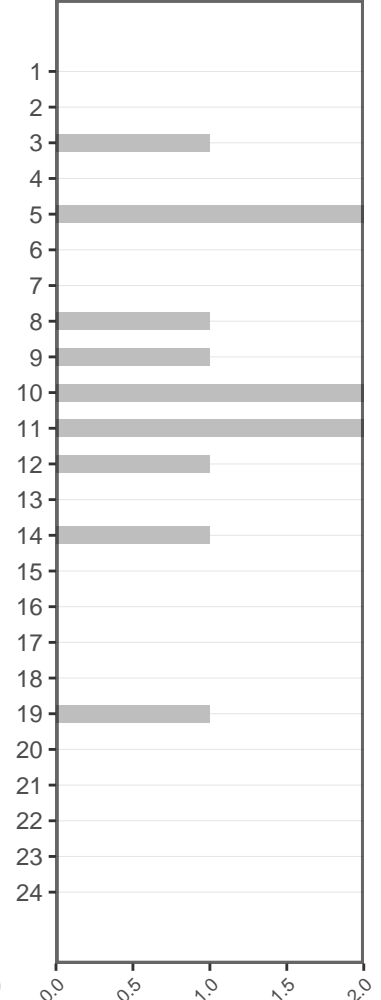
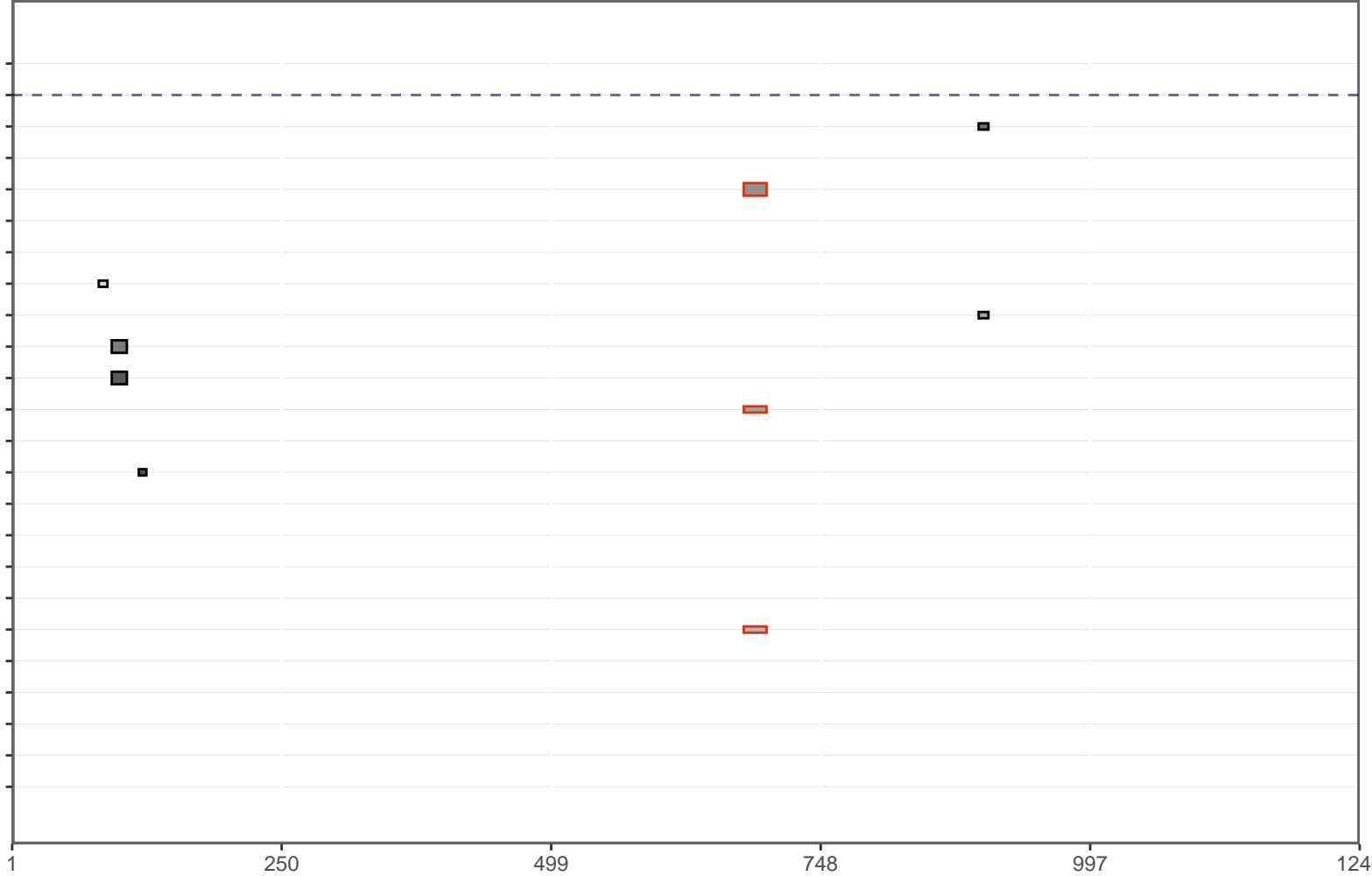
MW indication



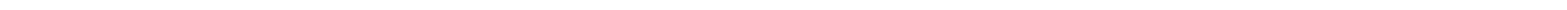
Molecular weight



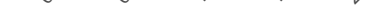
Gel Slice



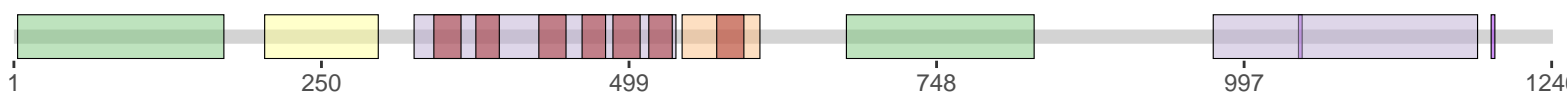
Protein length



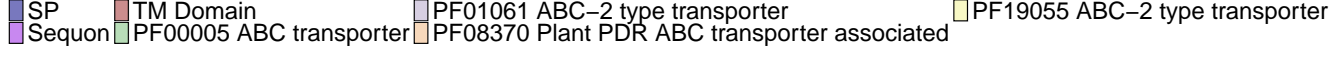
Peptide counts over 4 repeats



Pfam domains



Pfam Description

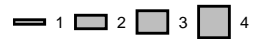


Protein sequence:

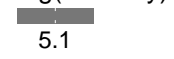
NENTSSPQITSTKEGDSVNEENKKGKMLVDFDPIHIFDFEIVYGVDMPEMREGGTSENRLVLLKVEVSGAFRPGVLTALMGVSGAGKTTLMVLAGRKTGGYDGGKIKSGYPKKDETFARISGYSQGNIDHSPVTVFESLIVSAWLRPQDVEQKRMFMVEEVMQVLTSLRSALVGLPGVNGLSTEQKRLTAVELVANPSIIFMDEPTSGLDRAAAAAMRAVRNTVDTGRTVYVCTHQPISDIFEADEFELFLMKRGGQEHYVGLPGRGSHLKIYFESIPGVSKYK

NbL18g03310.1 histone_H2B.3 [MW = 15.96 kDa]

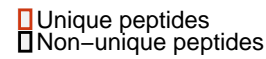
No. of times detected



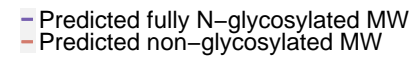
log(intensity)



Values from



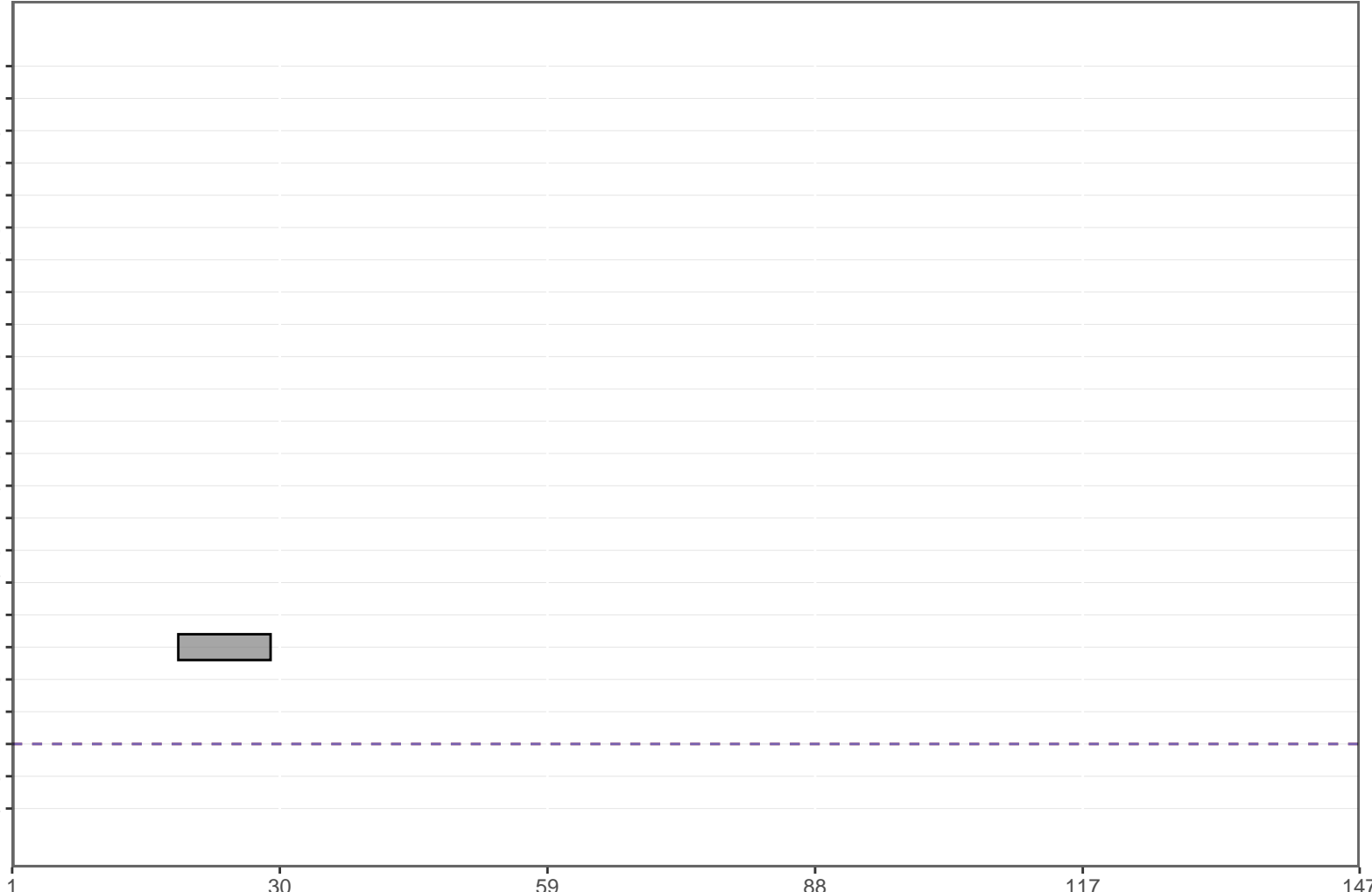
MW indication



Molecular weight

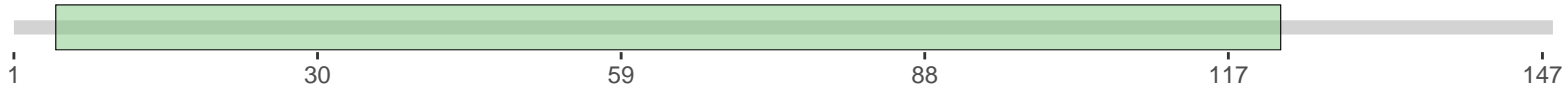


Gel Slice



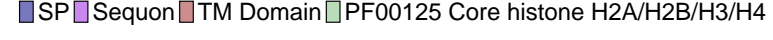
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

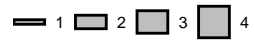


Protein sequence:

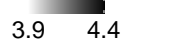
YKIQYFKVLRKQVHPDQIGSSKAMGIMNSFINDIFEKLAQESSRLRYRNKKPTTTSREIGTAVRLVLPQELAKHAVSEGTAKVTKFTSS

NbL18g03130.1 bark_storage_protein_A-like [MW - SP = 34.47 kDa]

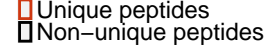
No. of times detected



log(intensity)



Values from



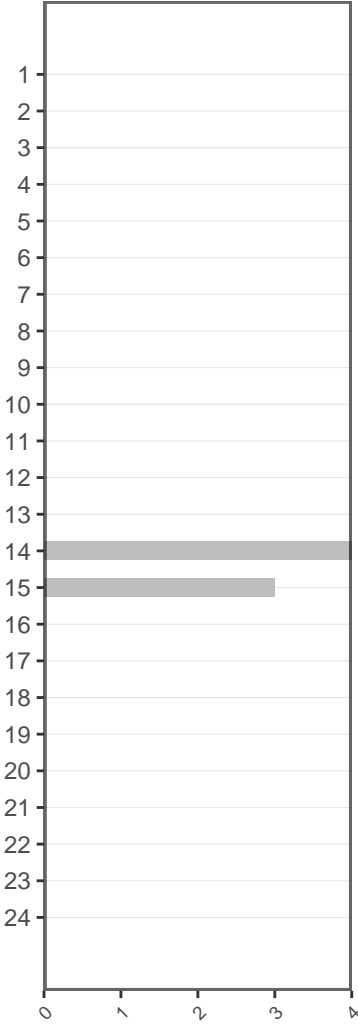
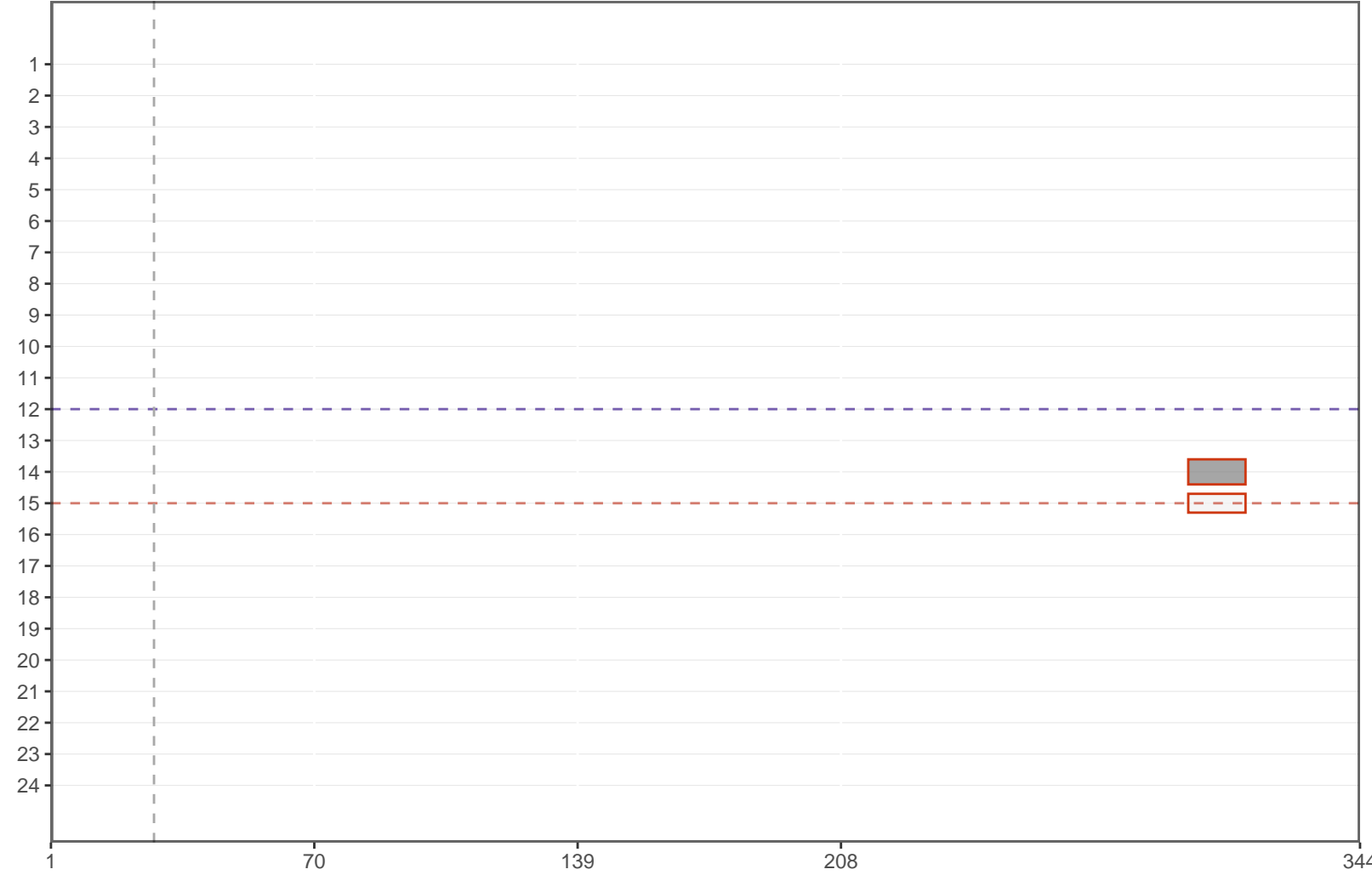
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MLEPNDFAQDFDKHNAKPGGDKNLGRVGVSTEGFVSTSGEINVPQRPVWFNTRKNLWASHLGGMKLEGGANSTMCLPQPKLVVGLKIGATSNFFIDNAAVYDFLRFKTFGVTSLOMESSAVMTGLENGYPIAIRGVSDLAGTGEQGNTRILFGPLAALNTAKVVISFVSLPQNVISKF

NbL18g03090.1 pyruvate_kinase_1_cytosolic-like [MW = 57.62 kDa]

No. of times detected



log(intensity)



Values from



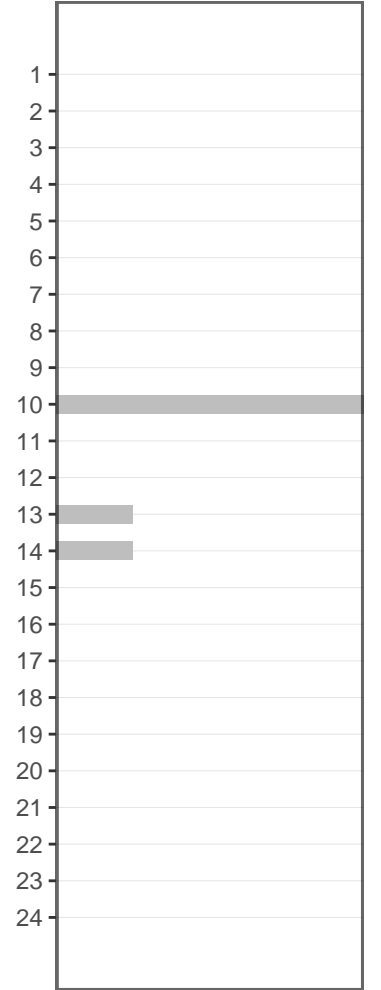
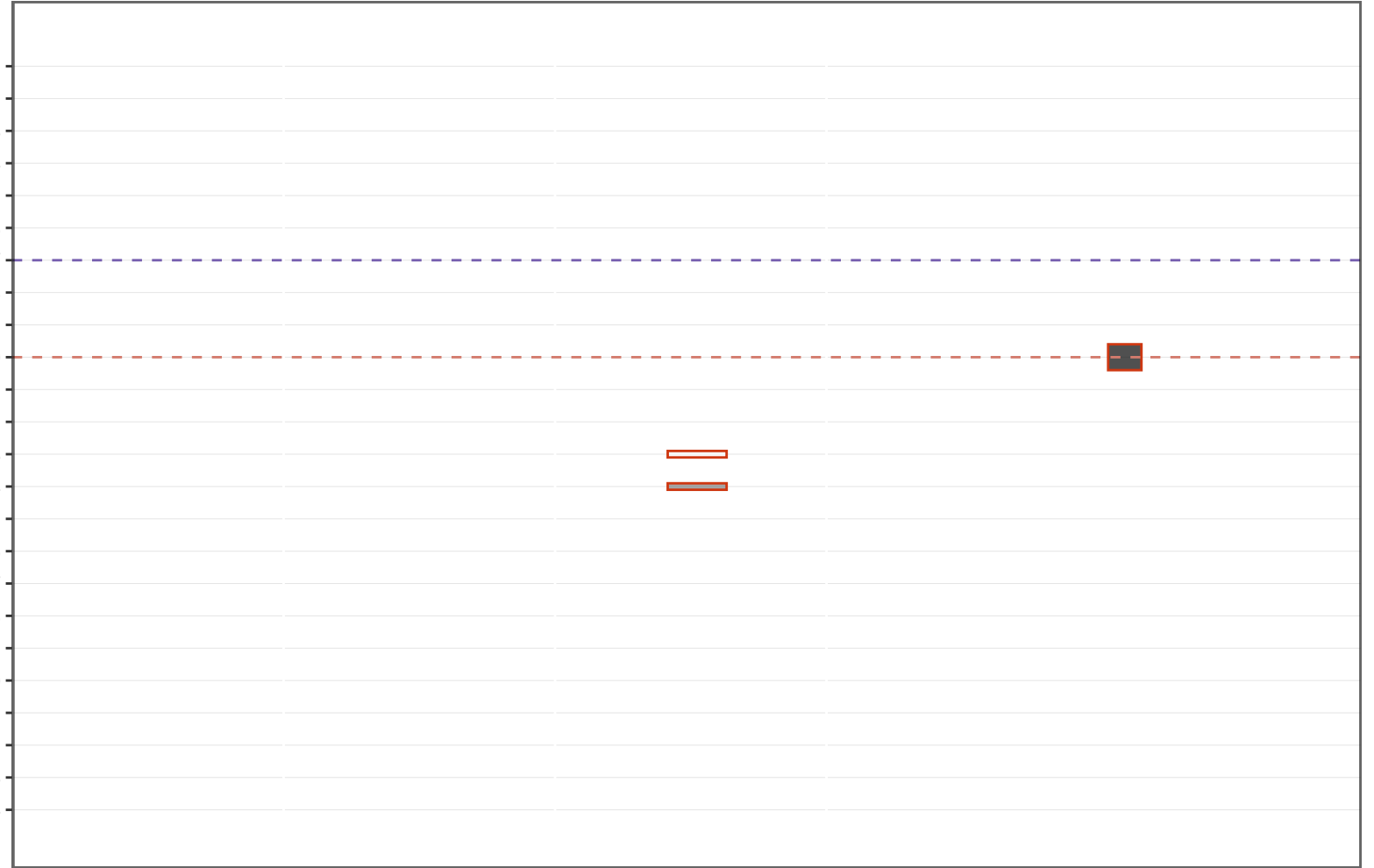
MW indication



Molecular weight



Gel Slice

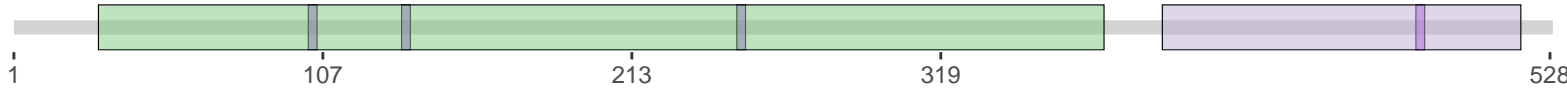


Protein length

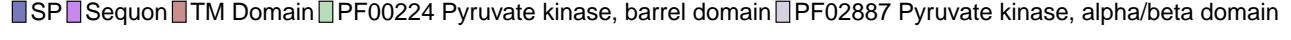


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ITQIFAKIENVEGGMANFDEILEEADGILSRGNLGDLPPEKVFLLFQKAHHKGNMAGKPVVTRVVDGEMTDNLRPRRAEATDVAWAVLDGSDAILLGAETLRLGLVPTETISVIGKCAEAQVYNGDVFYKRAKYYVGEPMTHLESIASSAVRAAKVWASVIGFTSSGSAARLIAYRPPMPVLSVIVPRLKTNDLRLWTFSGAFQARQSLVIRGLFPLIADPRHFKESTNATDESVLKVALDHGKTAGVYKPHDRVVYFQKVGDSVYKHELEN

NbL18g02860.1 neutral/alkaline_invertase_3_chloroplastic-like [MW = 73.53 kDa]

No. of times detected



log(intensity)



Values from



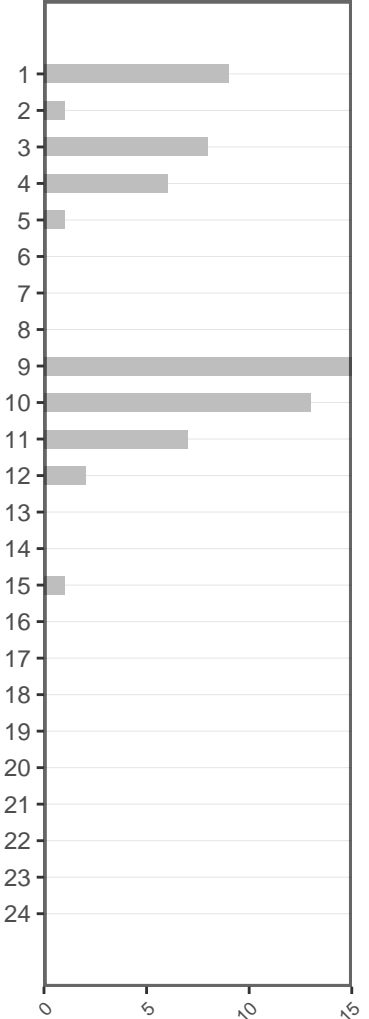
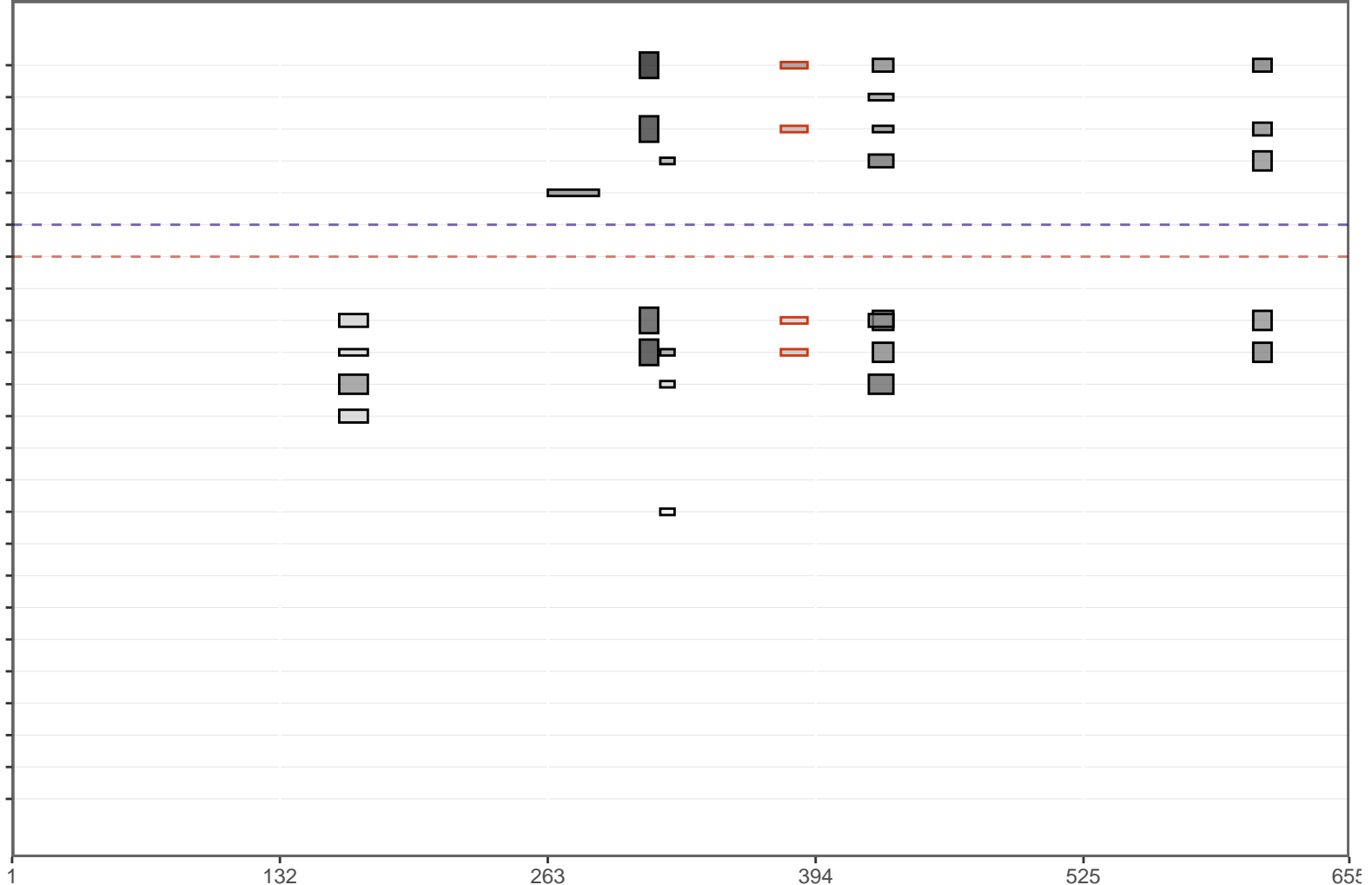
MW indication



Molecular weight

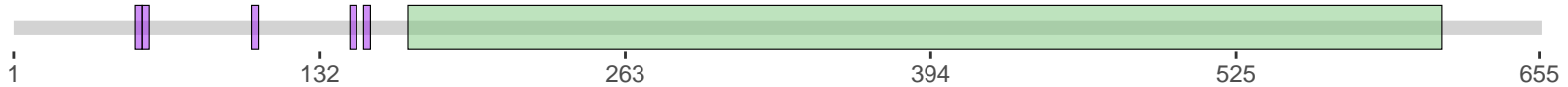


Gel Slice



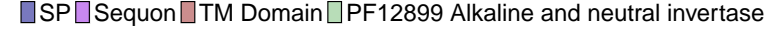
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

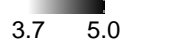
LSVQERIDVOTGIKMLRLGLADGDMFPTLLVTDGSGMIDRRMGHGHLEIQALFHSALLGAREMLTPEDDGSAIDLIRALNLRLLVLSFHREYVYWDMMKLEIYRYKTEEYSDVANKFNFYDGGFWLVEWMPNKGKGLYIGNLQPAHMDFRFFSLGNLWGVVGSLLTDEQSHALDLIEAKWGDLDVMPFKICYPALEGGGEWQITGGDPKNTFPWYHNGGAWPTLLWQLAWASMMNRPPIAAKAAVEAEKRIERDKWPEYDTRKARFVGGKARLFOTWYSIAGYLVA

NbL18g02750.1 nifU-like_protein_4_mitochondrial [MW = 30.86 kDa]

No. of times detected



log(intensity)



Values from



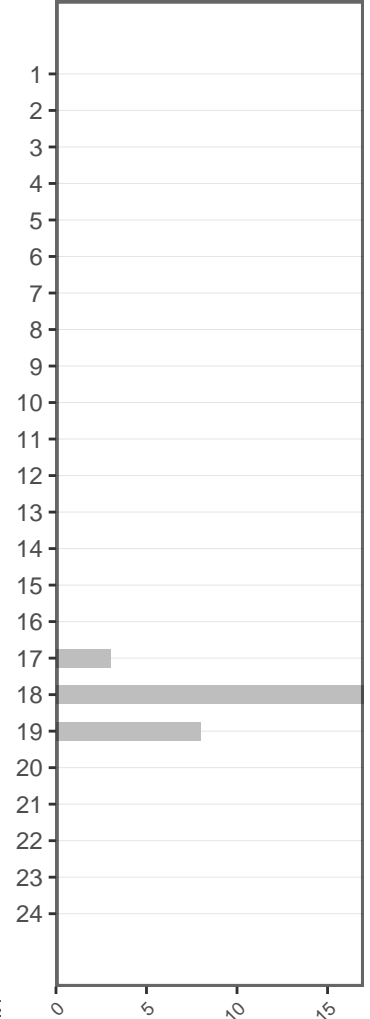
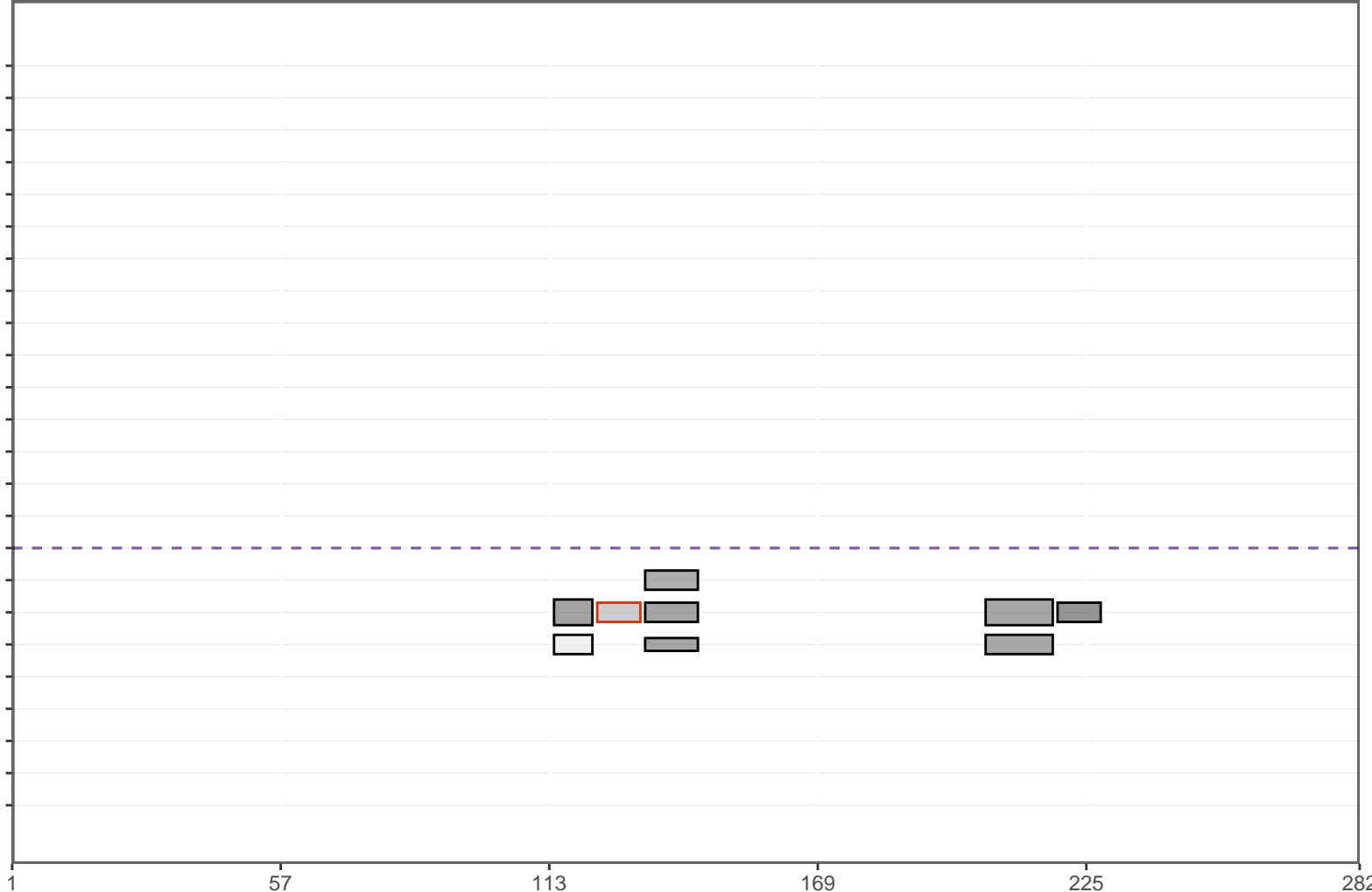
MW indication



Molecular weight



Gel Slice

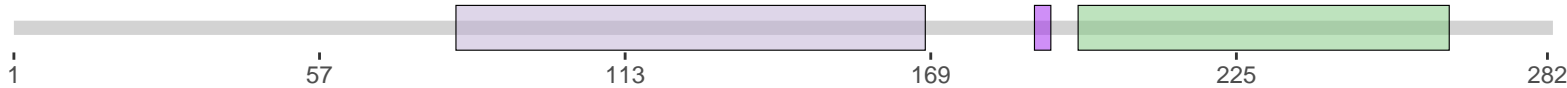


Protein length

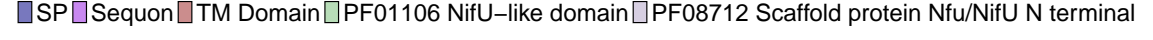


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SITRVFFGSDFYVTKSSDASWDFLKPEFAAIMDFYSSGKPLFLDNTAASMDTAIHENDESETVAMIKELLETRIRPWGDDGGDIVYRQFDLDTGIVLKMGGACGGPSSVFLKSGIENMLMHHYVPEVKGVEGEMDEDEEPGLTGAPVE*

NbL18g02710.1 probable_aspartyl_aminopeptidase [MW = 59.77 kDa]

No. of times detected



log(intensity)



Values from

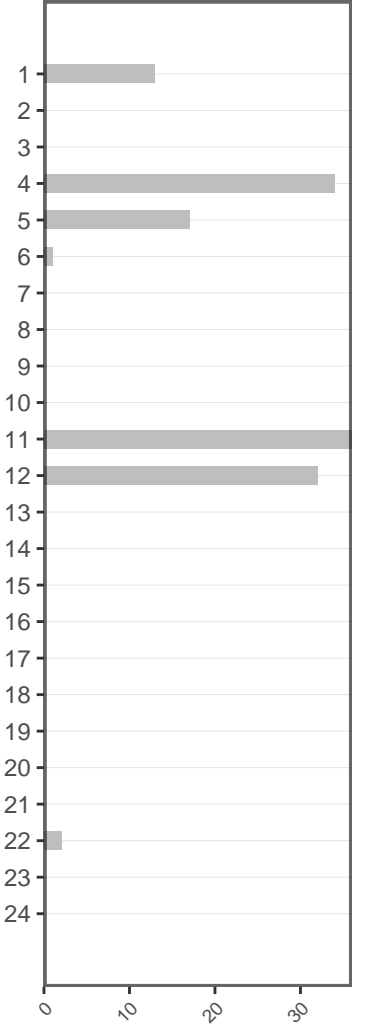
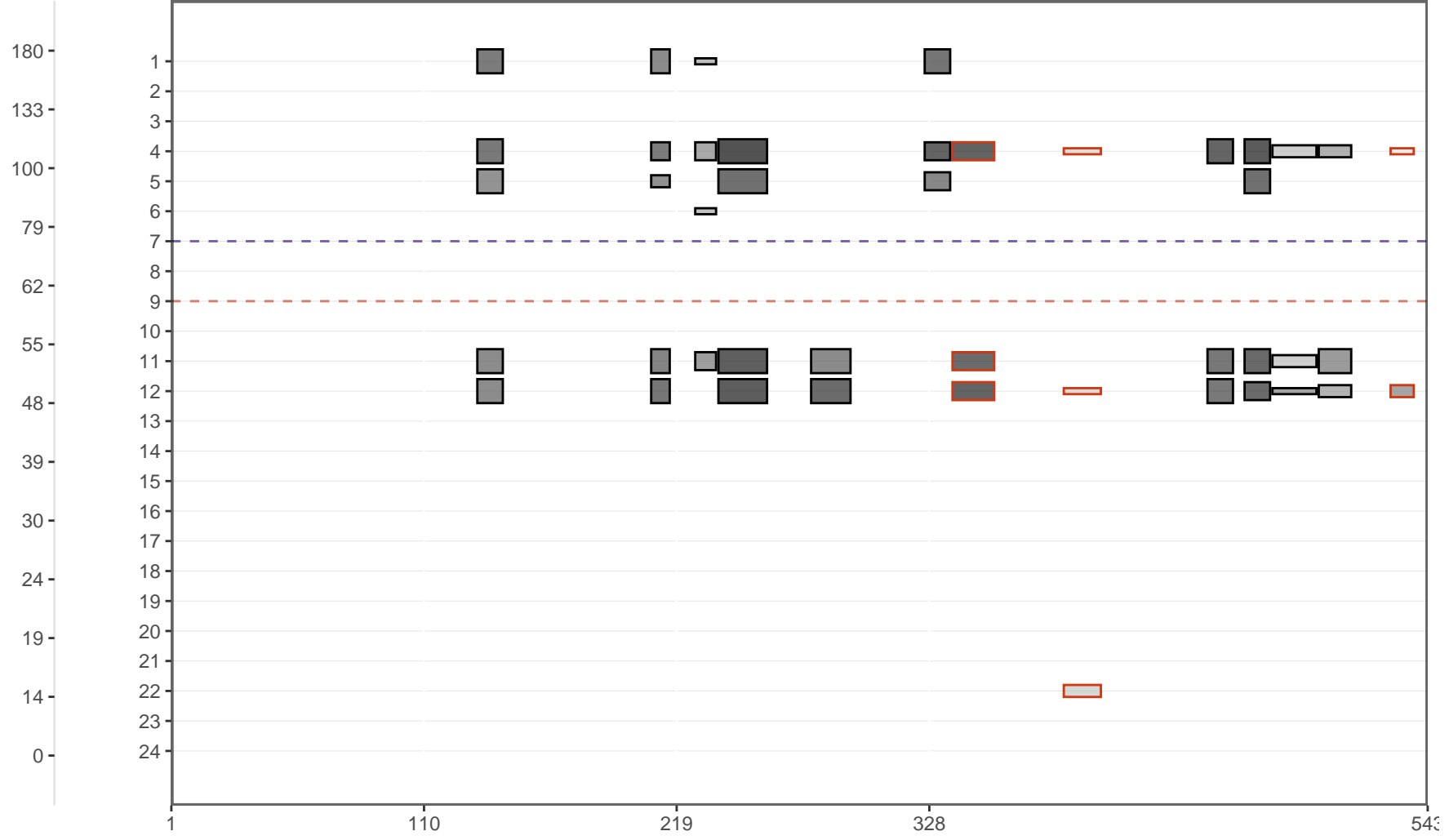


MW indication



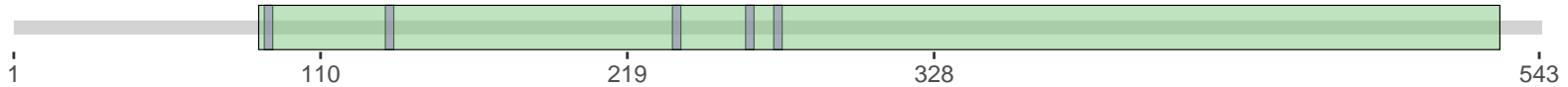
Molecular weight

Gel Slice



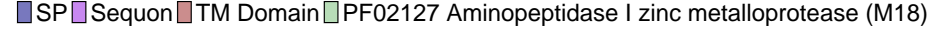
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TENATDSTKSNVSSSKDYYHQLLGLSDLSKIDDDVVELNIGDTQRPGLGGANNEFIFGRLNLAASFQGLRALVDGCTLPEDLSNEHARMALFDNEEVGSDGYSQAGAPTFMEAMRRITDGMISHQSGAGSDDFARAIRHSLFVADMAHGVHNFVQKHEEHRPELQKGLVKKHANNQRYATSGVTSFLFKEVARLHSLPTQDFVWRNDMGGGSGTIGPLASGVGIRTVDOGIAQLSMHVRVREICGKEDIDWAYKHFKAFVLTSSIDRKLVD

NbL18g02680.1 diphosphomevalonate_decarboxylase_MVD2-like [MW = 46.55 kDa]

No. of times detected



log(intensity)



Values from



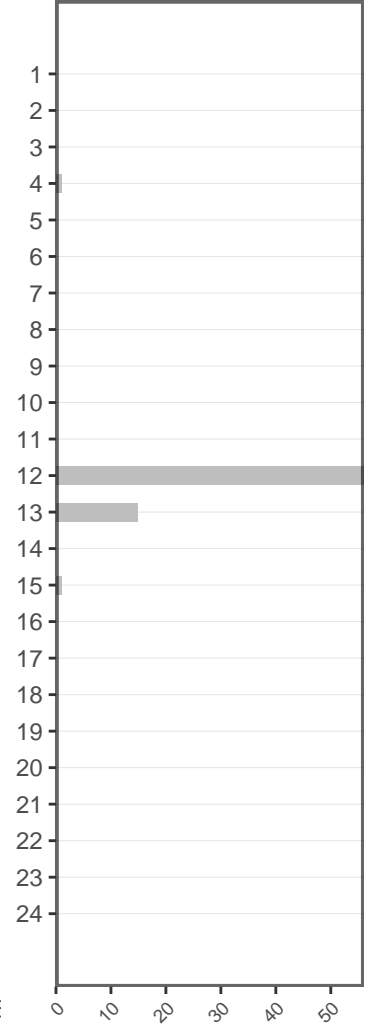
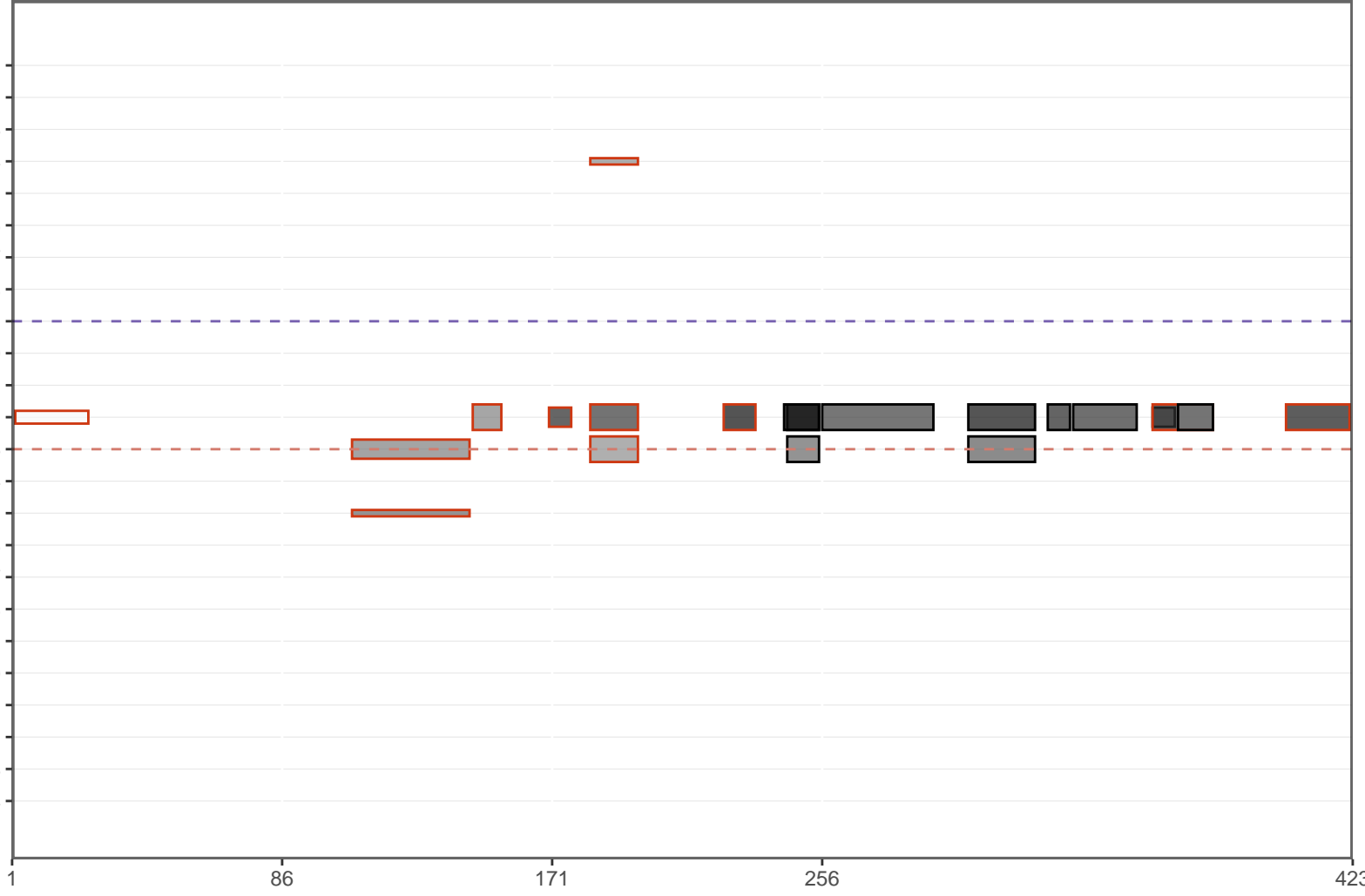
MW indication



Molecular weight

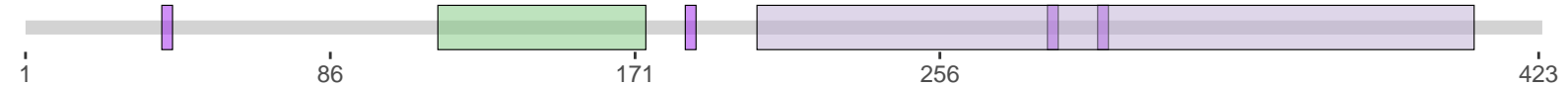


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00288 GHMP kinases N terminal domain
- PF18376 Mevalonate 5-diphosphate decarboxylase C-terminal domain

Protein sequence:

EKHVDELVIAAVYSSRQKETSSTGMRDVTVETSAIHERRAKEVVPKRKQMEEAQNRDFFPTFAQLTCAAGSNGFHVAVGMDTSPPEFVYMDTSHRVIGGVQEKVWRSEGTQVWYTFDAGNVLVLRNKAATLMLGRLLFFPFPNSDGLNSVYVIGDKSLKADAGIDKDVLEALSPPEKDKVYPAQYKGEIVYFICTRPGRGPIVLTDDSLALNPETGLPKV

NbL18g02620.1 ACT_domain-containing_protein_ACR12-like [MW = 35.4 kDa]

No. of times detected



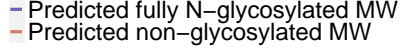
log(intensity)



Values from



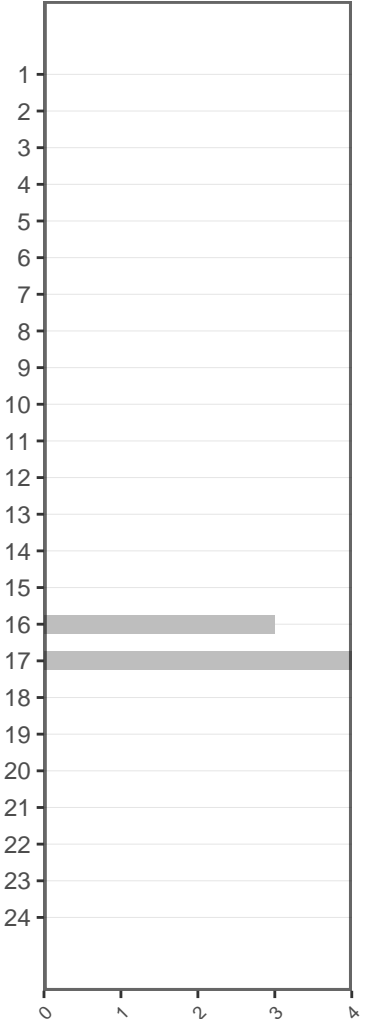
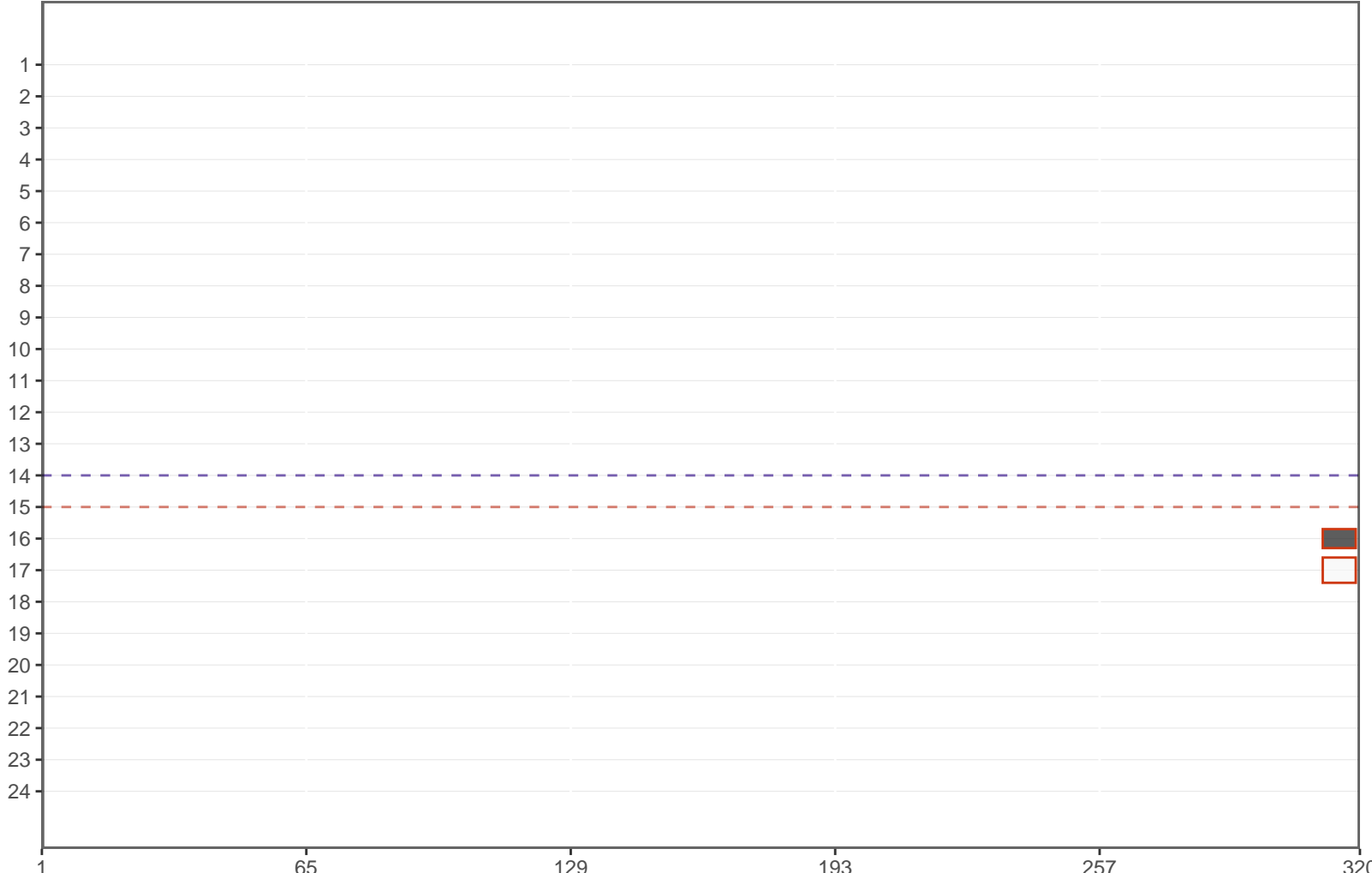
MW indication



Molecular weight



Gel Slice

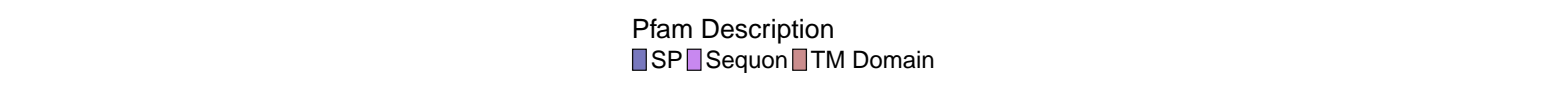
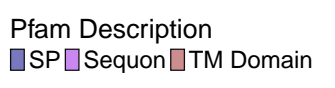


Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:

LKDLGLDLYKGIIVTEGSKVKKTKFLTRLDGTGRKVEDPDLLEIRLRITISLKIYHPESSEGLAMGEAFQIKAPEKPKDQDIATHHVKDDGSKRSLHVEIADRSGLLVEVVKMADINDVESAIEDTEGLVAKDKFYVSYRGAALNSLSGLVNLGLRFLRRPETDEESY

NbL18g02590.1 ferredoxin_root_R-B2-like [MW = 16 kDa]

No. of times detected



log(intensity)



Values from



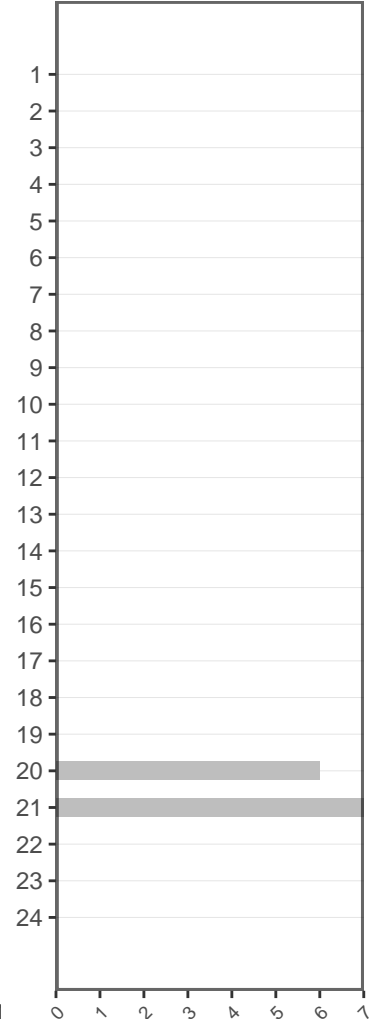
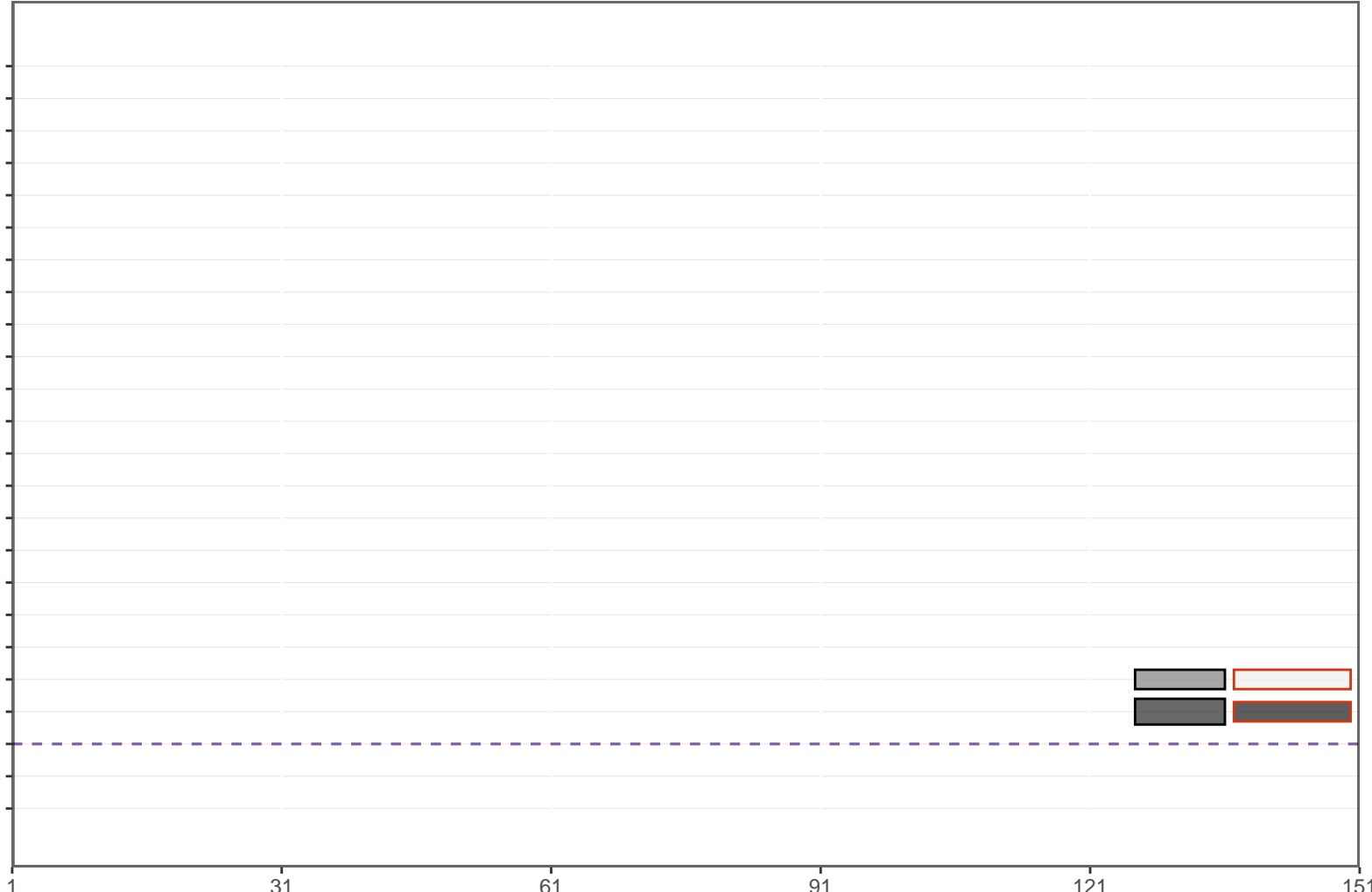
MW indication



Molecular weight



Gel Slice

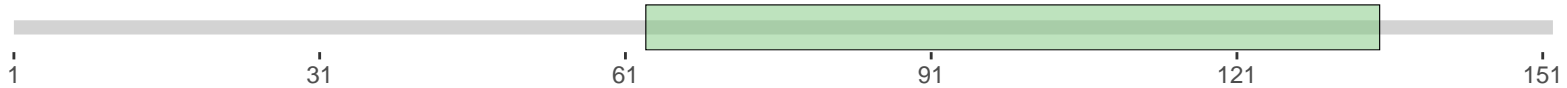


Peptide counts over 4 repeats

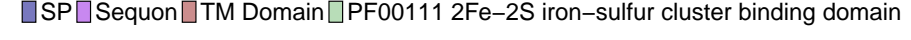
Protein length



Pfam domains



Pfam Description



Protein sequence:

MGTEIEIVSDCOYHLDAEADAGLELPYSGRAGSGCTCAGQLVSGVDSQSEGAFLDDQDMENGYLLTGSIVPRSDCVHTNKEEYH

NbL18g02520.1 5-epi-aristolochene_synthase-like [MW = 63.22 kDa]

No. of times detected



log(intensity)



Values from



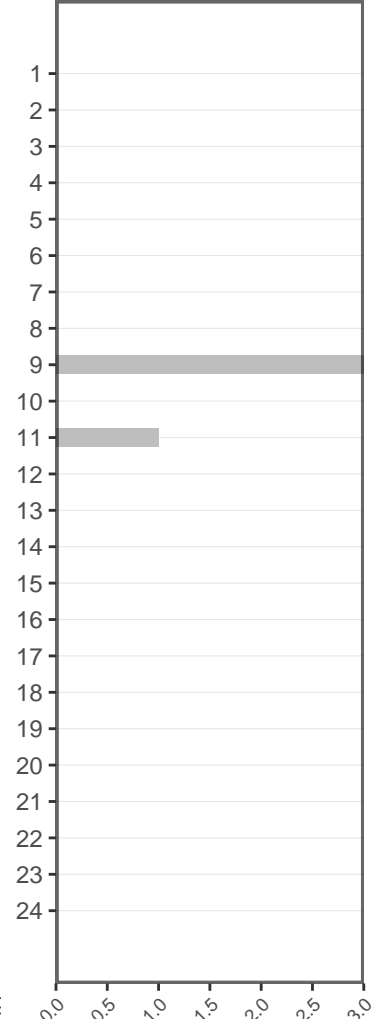
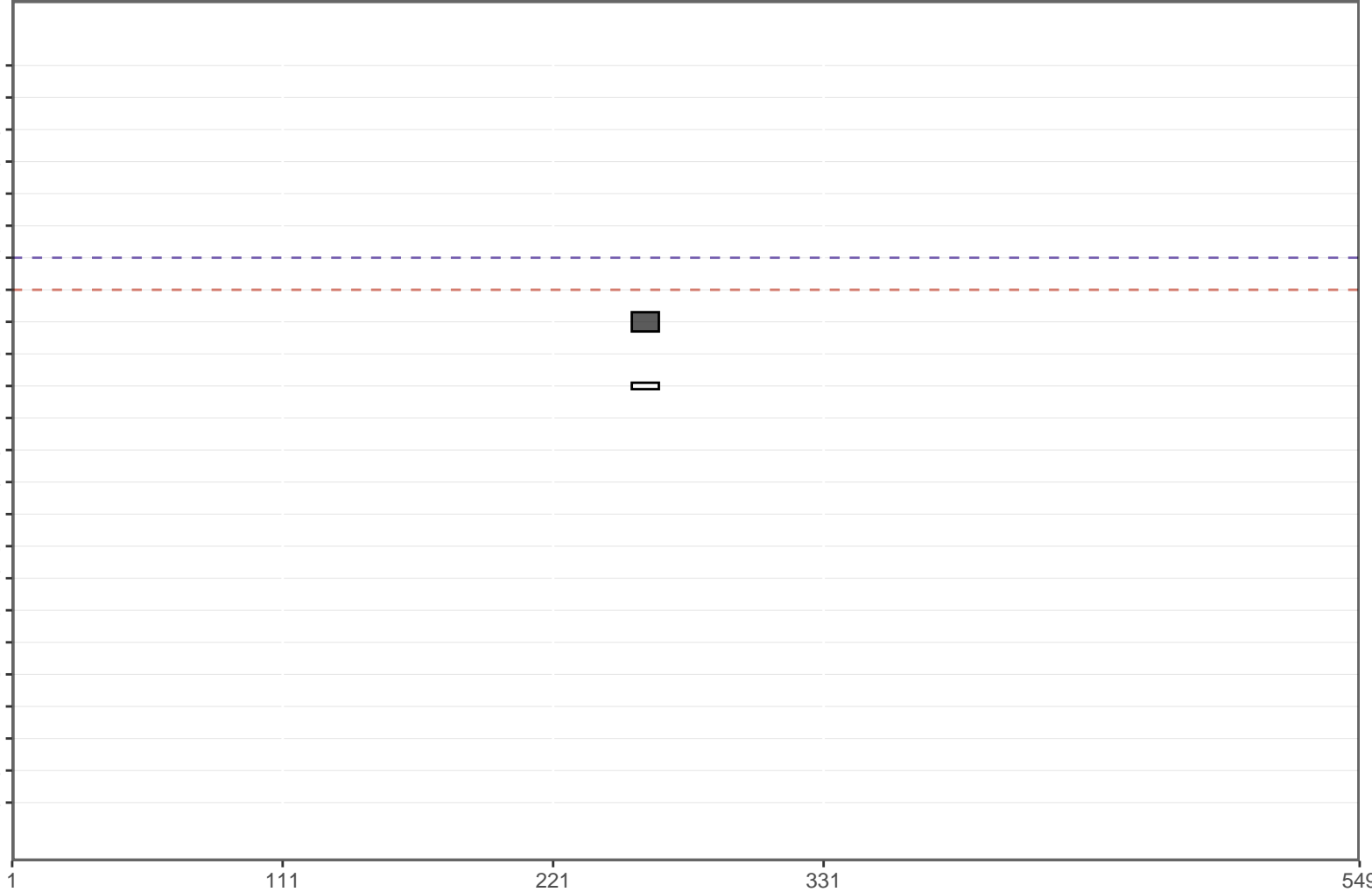
MW indication



Molecular weight

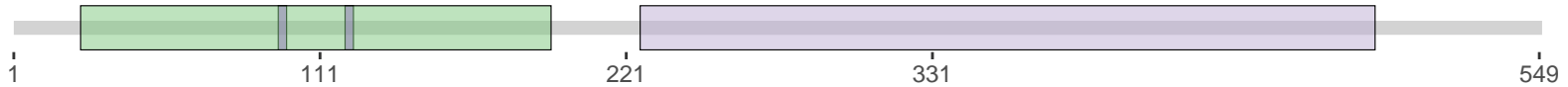


Gel Slice



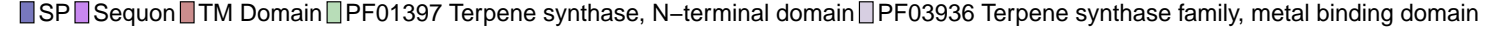
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

"YARDRVVECYFVALGVYFEPQYKARVLMKVTSMISVDDTDFDAGTGVKELEVYTNAGRWDINEIDRLPDYMKLEAYKALDLDNDVKEKELSSAGRHLVGHAIERMKVIRVNYNEVSTWFIEGKPPVTEYLENALATTTYYLATTSYMGKMKVTERDFEWLKSNPKILEASVIGRVDVDTATYVEKSRGGHATGIECGMRDVGIGISTEAMTKFQEMEAAWNDLNEGLLRPTTFFVTEFLSRILNLRARIVETVYHNLDDGYTHPEKVLKPHIALLVDSIEV"

NbL18g02510.1 5-epi-aristolochene_synthase-like [MW = 63.24 kDa]

No. of times detected



log(intensity)



Values from



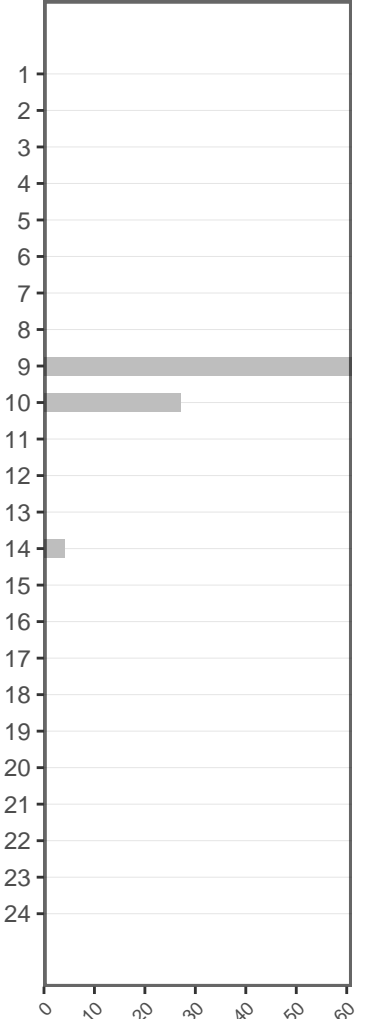
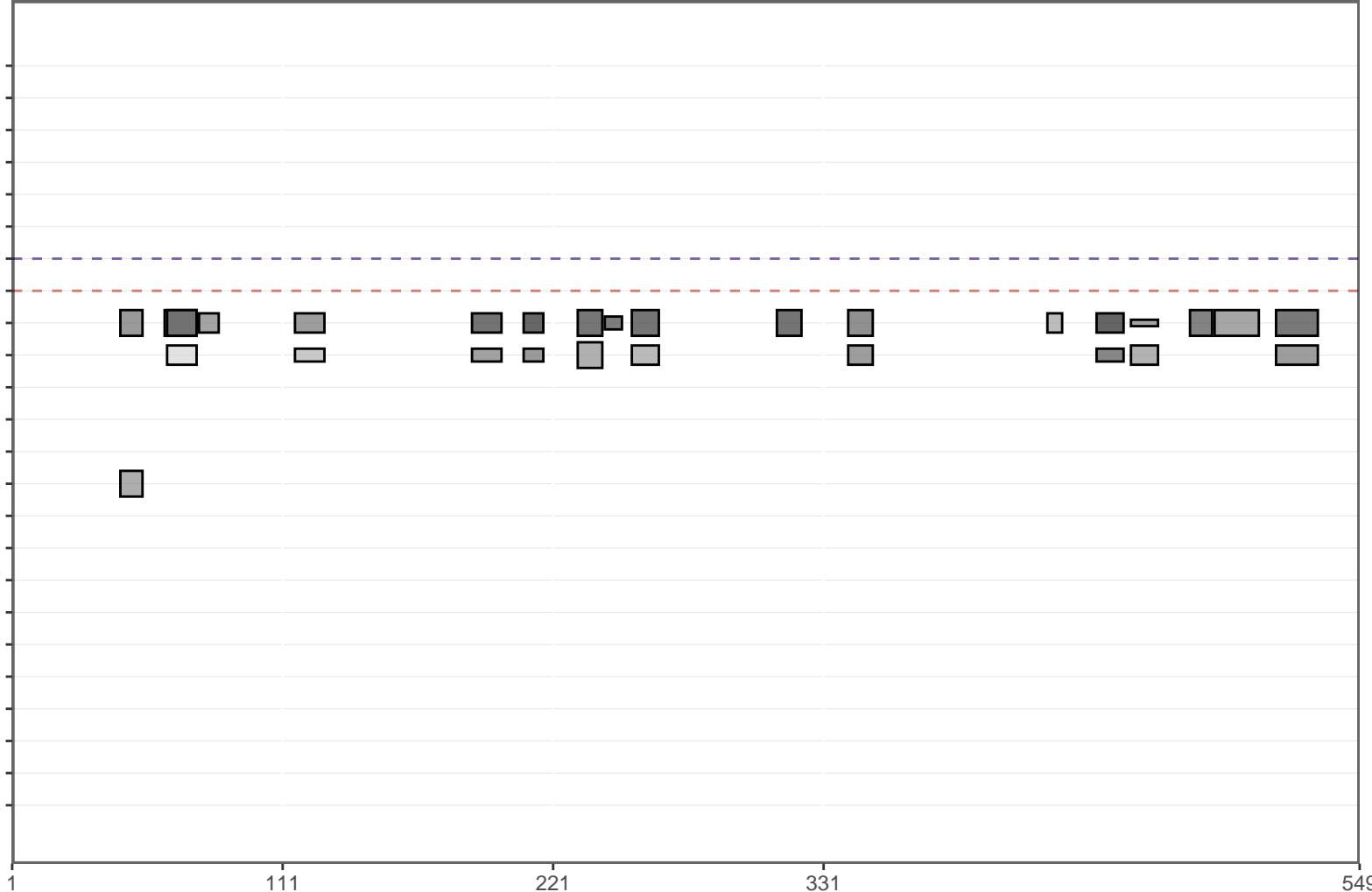
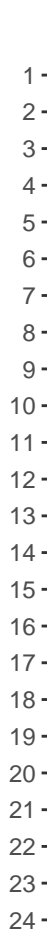
MW indication



Molecular weight

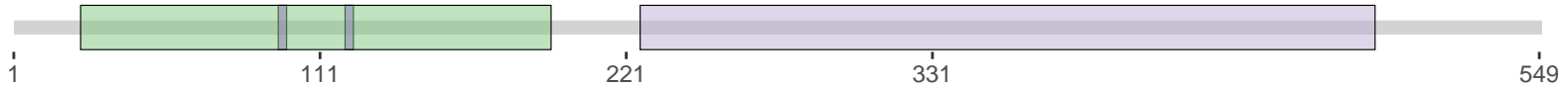


Gel Slice



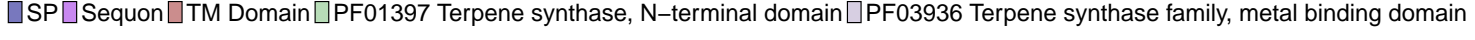
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

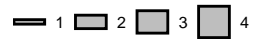


Protein sequence:

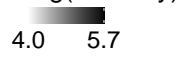
"YARDRVVECYFVALGVYFEPQYKARVMKVTMSISVDDTDFDAYGTVTKELEVYTNIAQRWDNEIDRLPDKMLKLYKALDLYNDVKEKLSASGRHLVCHAIERMKEVVRNVVESTWFIEGKPPNVEYLSNALATTTYYLATTFSYMGMDQVTERDFEVLKSNKLEASVIGRVDDTATVEKSRGQATGIECCMRDYGIGTTEAMTKFQEMAEAAWKDLNEGLLRPTFPVSTEFLSRLNARIVEVTVYHNLDSGYTHPEKLVKPHIALLDVDSIEY"

NbL18g02400.1 nudix_hydrolase_26_chloroplastic-like [MW = 26.02 kDa]

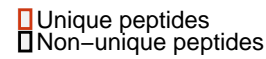
No. of times detected



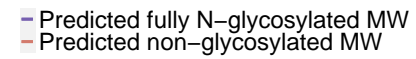
log(intensity)



Values from



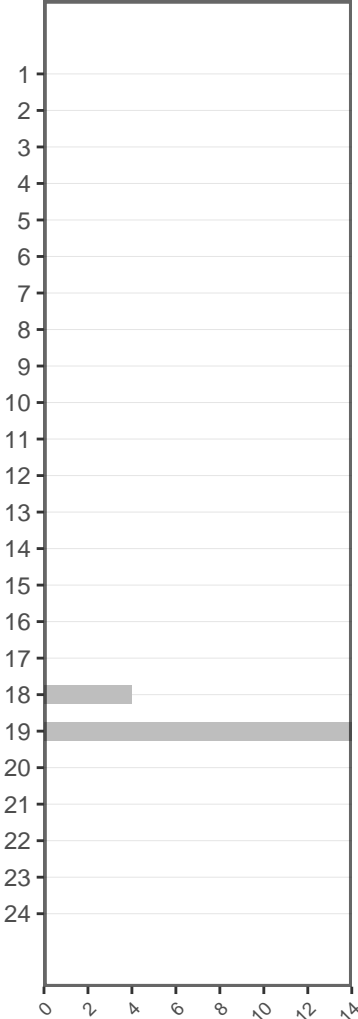
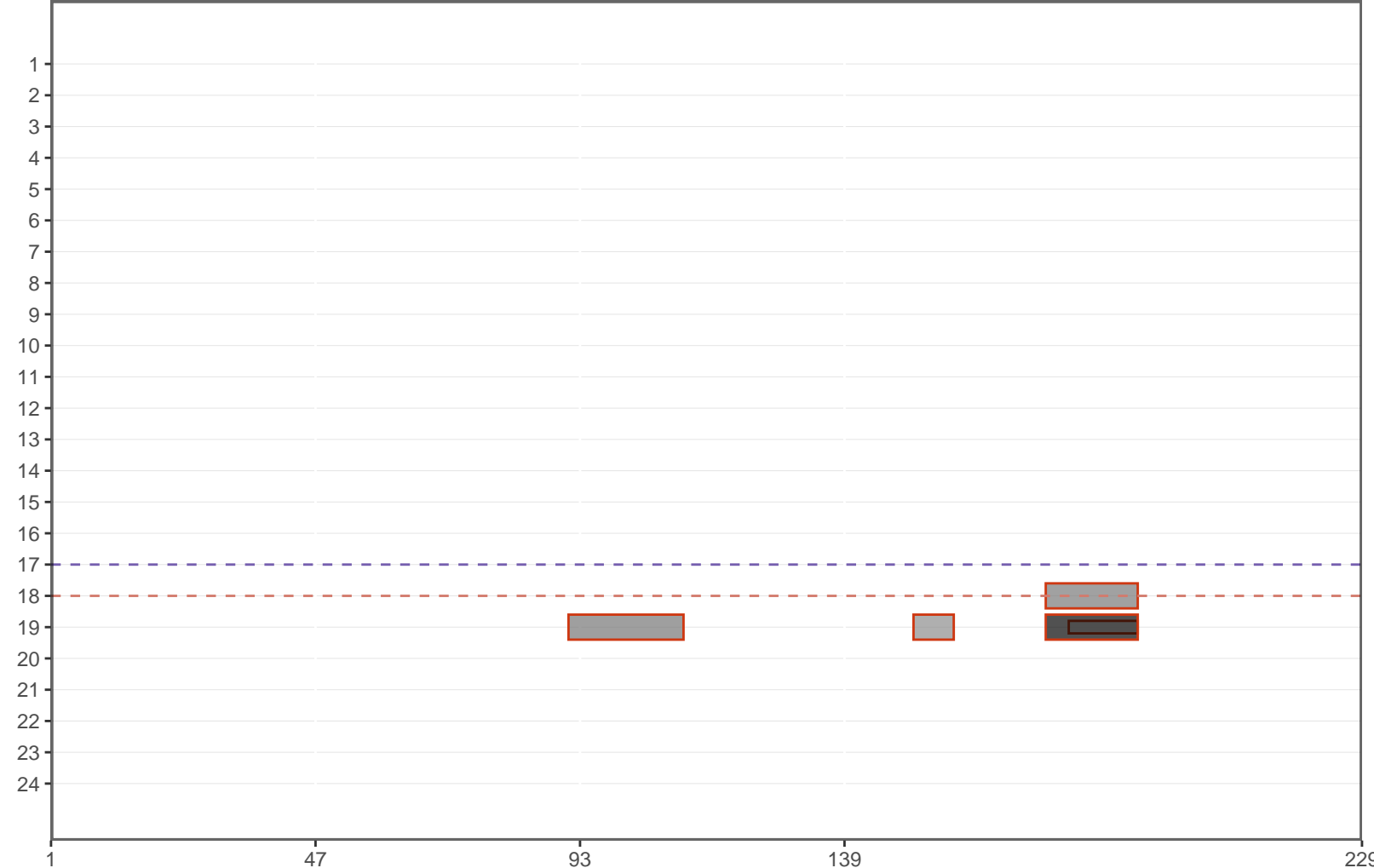
MW indication



Molecular weight

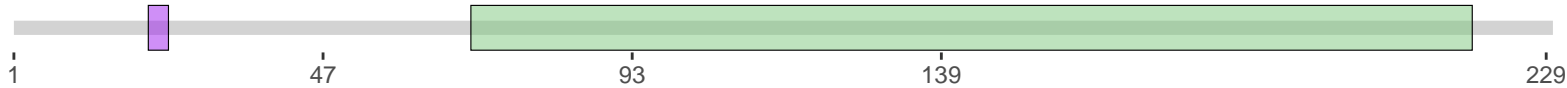


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IYDESEDRNAAIRELREETGVTSAEVAEAPHHLTYDFPPDVRKLRHQWGSQWKGQAQKCMENSRFLFKFTGKDEEINLLGDGTEKAEFGGEVSWMSPEQVVEFAADKPKPVYKEVLSVFSQVFL

NbL18g02360.1 vacuolar_protein_sorting-associated_protein_60.1 [MW = 25.95 kDa]

No. of times detected



log(intensity)



Values from



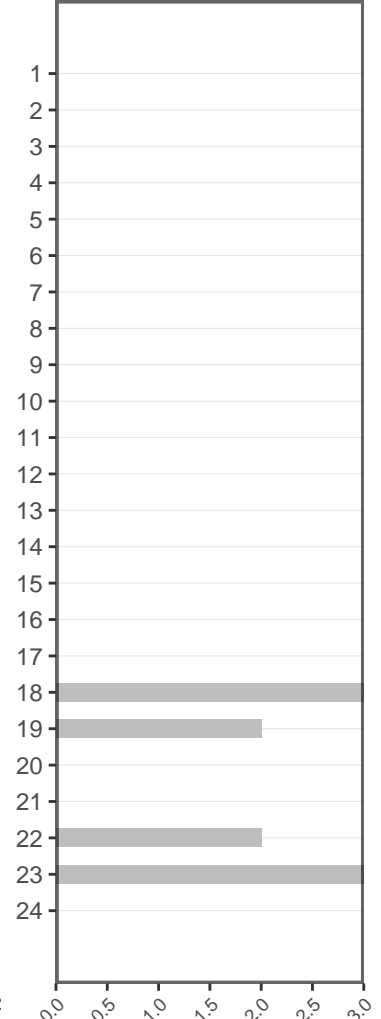
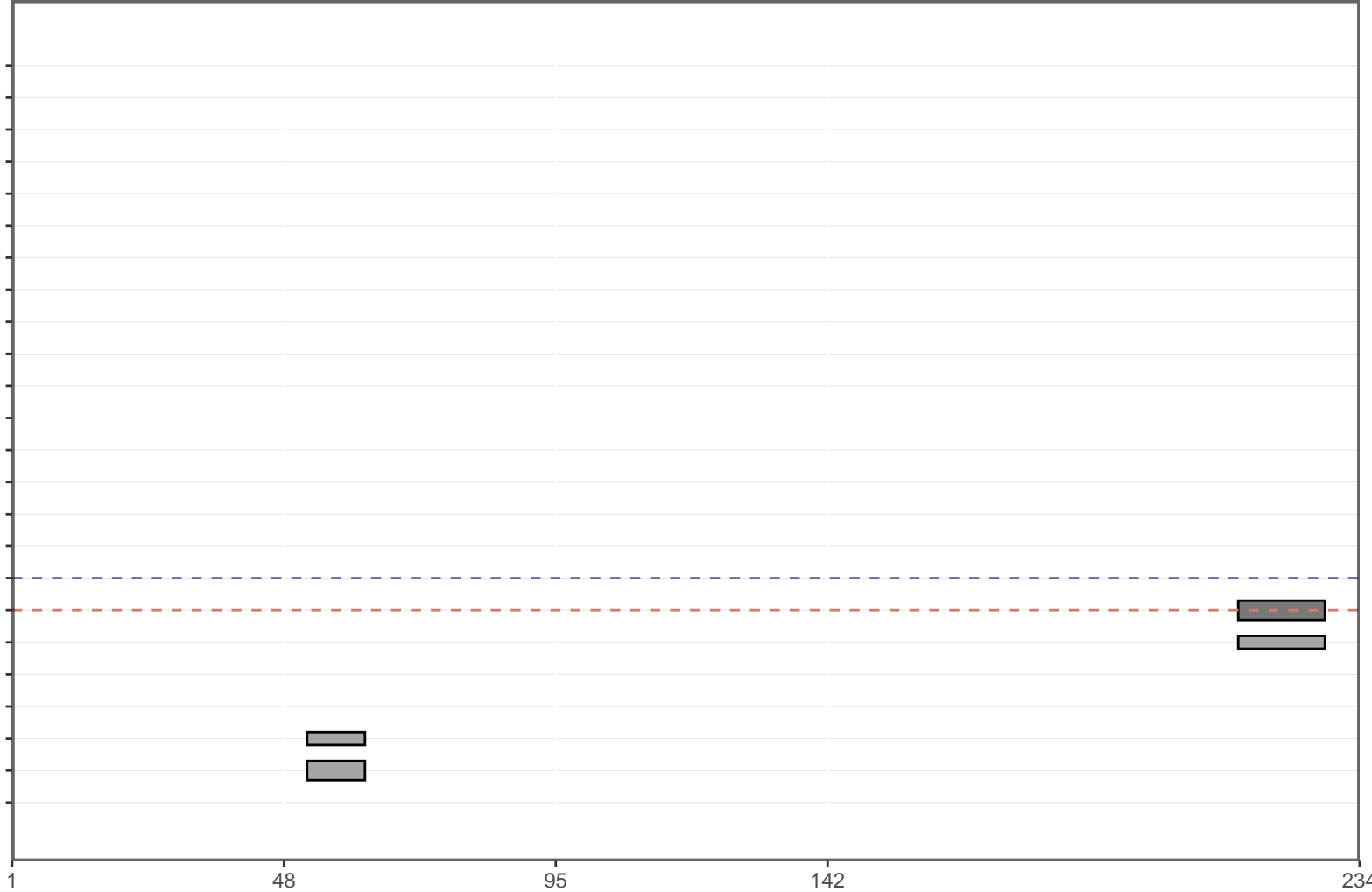
MW indication



Molecular weight

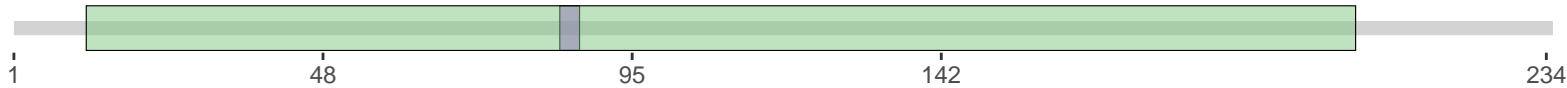


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

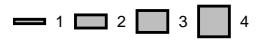


Protein sequence:

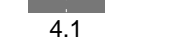
ITMSALKSANKELKGMKFTKINDINLGGEMDLMDVSNIEQESLGRYSVPPDDDEEELMGELDLAEDMDTEGGGVPEYLOPEPDLDAELSLRPAPTGHAPMPMPGRANPQADDELGLFVPRASRG

NbL18g02330.1 dnaJ_protein_homolog [MW = 46.56 kDa]

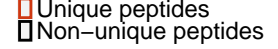
No. of times detected



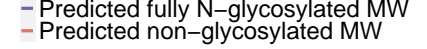
log(intensity)



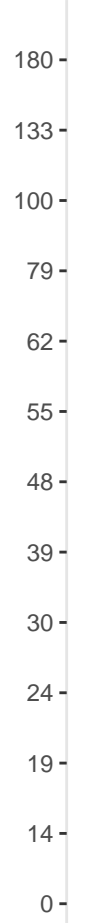
Values from



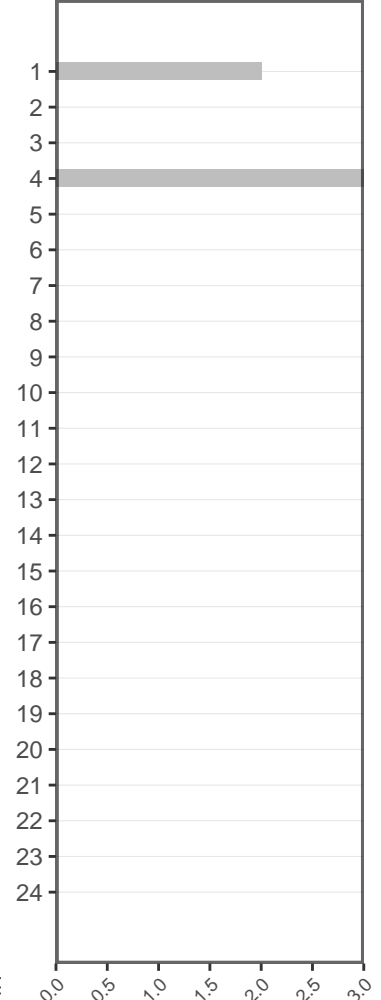
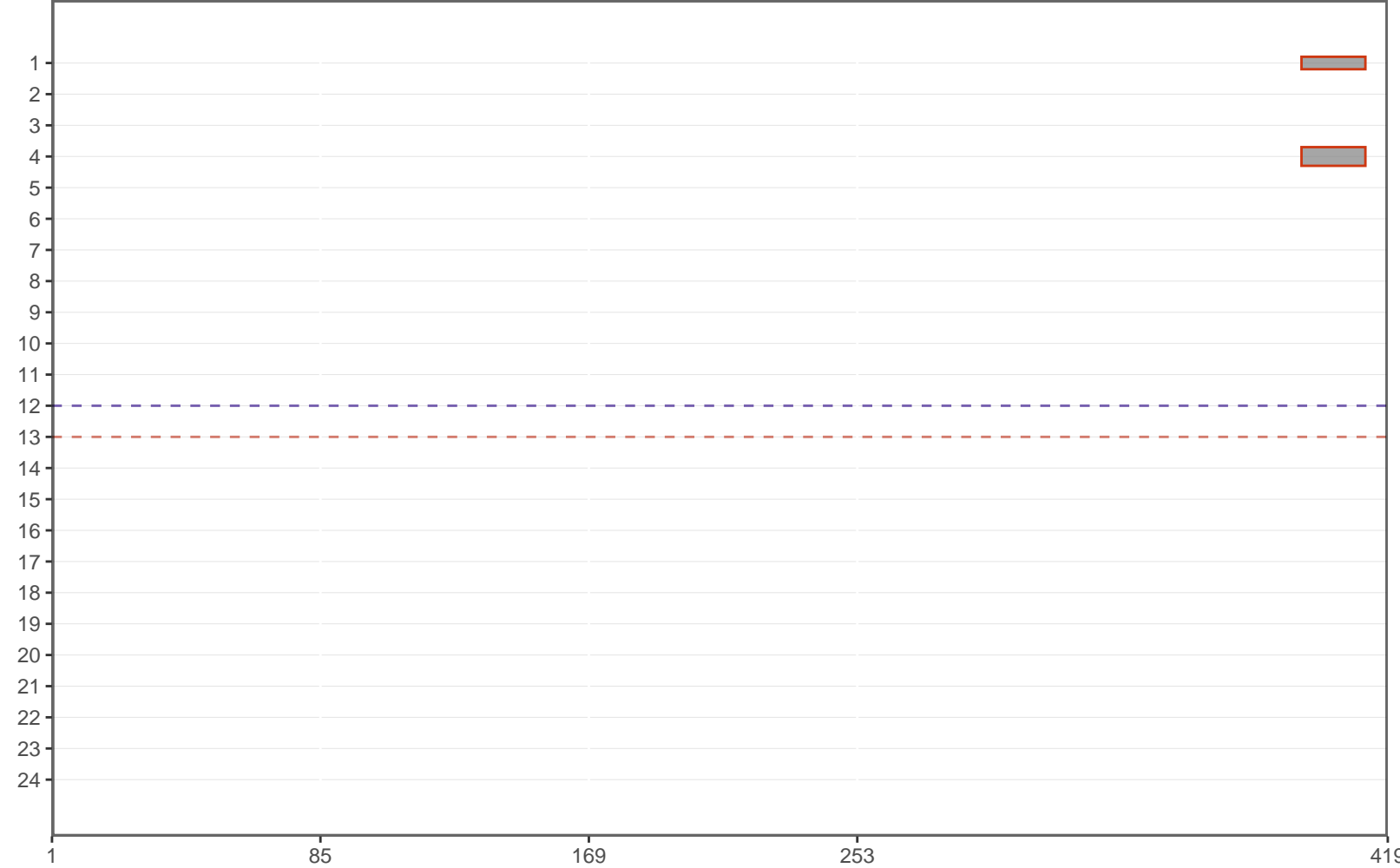
MW indication



Molecular weight



Gel Slice

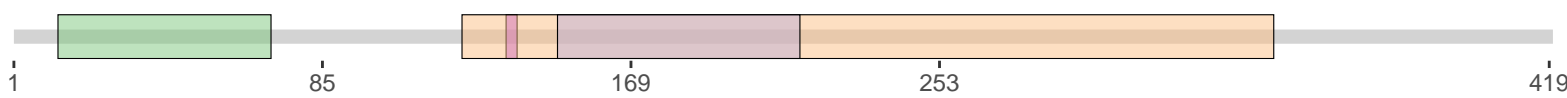


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

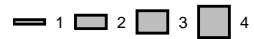


Protein sequence:

ICKGTGETINDKDRPQDGKGVKVEKLVHVEKGMQNGKIFRGEADEAPETTTGDIIVFLGQKEHPKFRKGGDQDFVEHTLTLTEALGGFQFILHLDMRQLIKSGDQGEVVKPQDFKANDCEGMFMYGRPFMRGKLYHFTVDFPESLTPEGGKLEAVLPPKPKMEVSEMELEDCEETTLHDEVNIEEEMRRKGGAAQGEAYDEDDMPGGAGRVQGAQQ

NbL18g02290.1 mitochondrial_acidic_protein_MAM33 [MW = 25.26 kDa]

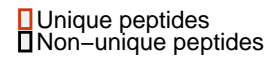
No. of times detected



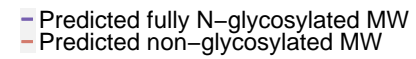
log(intensity)



Values from



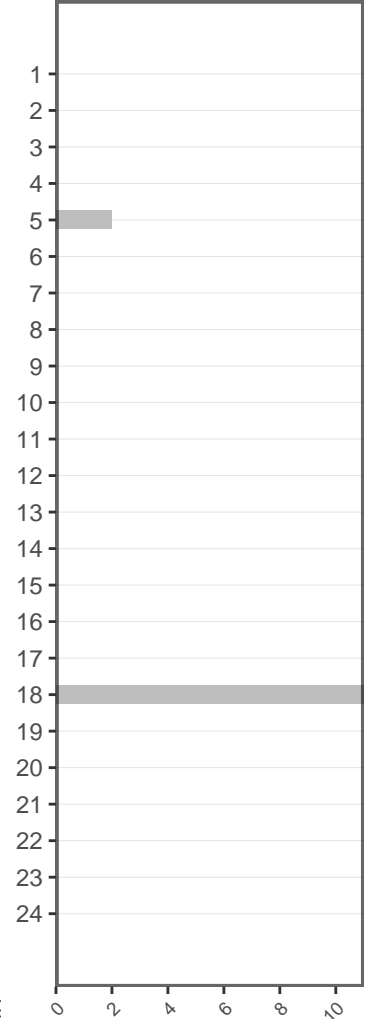
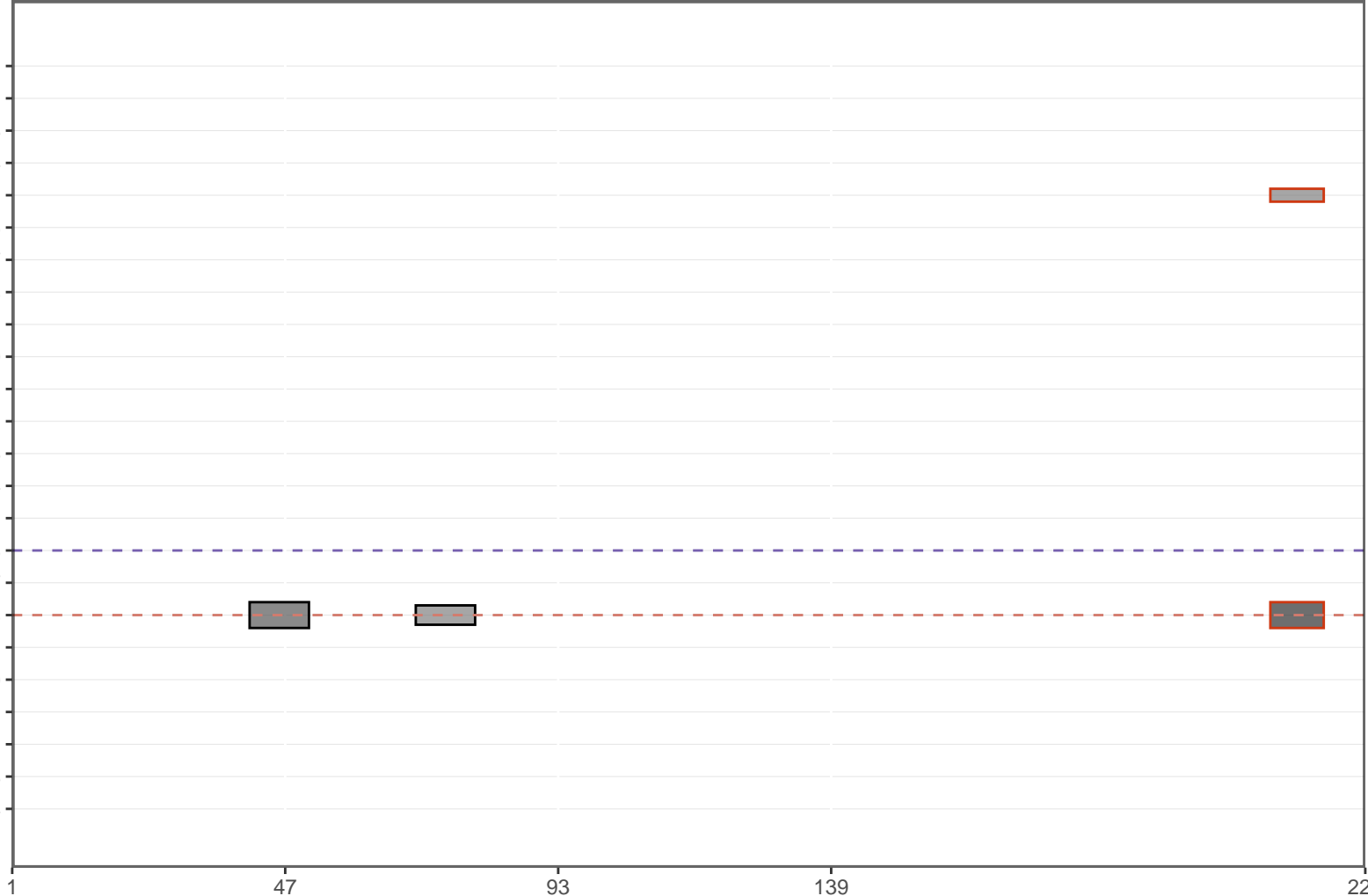
MW indication



Molecular weight

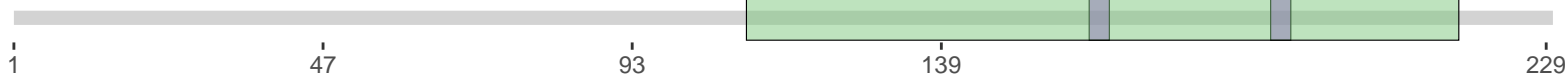


Gel Slice



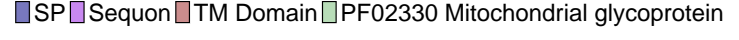
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

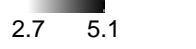
GGDEEDGQNLFLHVDISKPGGKSLHFLGGLYDPLGHSVLSRPKAESTGFLAVPTNYSQPVFDDDEAMRDALHRFIEERGINESLFPFLQAWLVYKDRNLMLRWFRTVGSVLNDRKGGSSHA

NbL18g02240.1 ubiquitin_carboxyl-terminal_hydrolase_12-like [MW = 130.72 kDa]

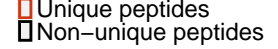
No. of times detected



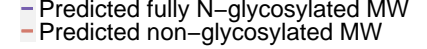
log(intensity)



Values from



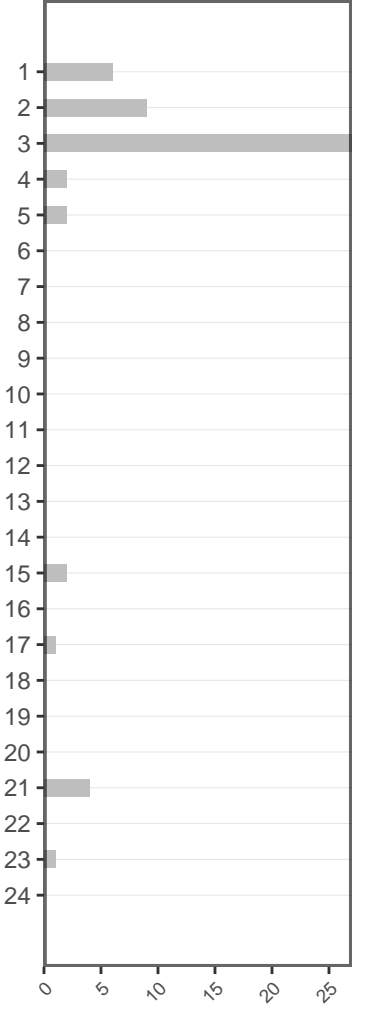
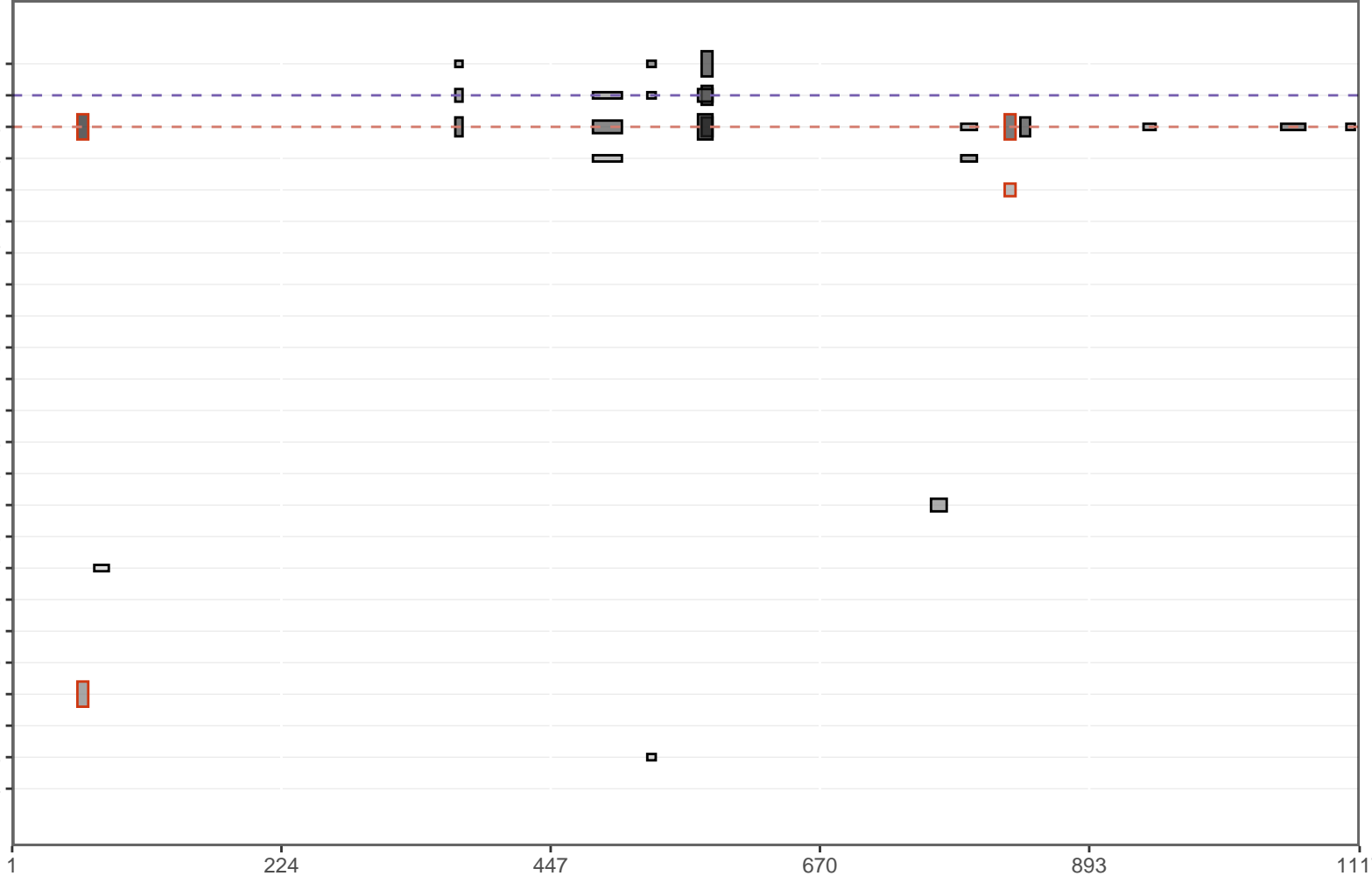
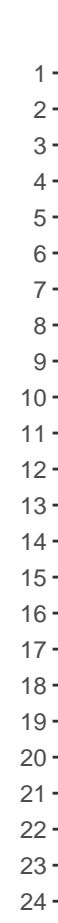
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00443 Ubiquitin carboxyl-terminal hydrolase
- PF00917 MATH domain
- PF12436 ICP0-binding domain of Ubiquitin-specific protease 7
- PF14533 Ubiquitin-specific protease C-terminal

Protein sequence:

YRLLKDEDEKQKRKEAEAHLYTKVARDEDLGEGIGKEIFDLVDHDKVRSFRIGKGMFTQFKEEVAKELGIPVQGRYALWAKRQNHLYRPNRPLTPQEEAGSGVGLREVSNNKANAELKLFLEVEFGDLRPPPEKTKEDILLFFKLYDPLKKEMRVAGRLFVKGSGKPLELPLKLNELSGFSFQDEELFEEIKFDPNVMGEPIDWKLTRFGSGLEDDGDFGKPLRSQTSQEGYRFDVPSFLEYVHNRQVVRFRSLEKSKEDDFSELSKQNNYDEVERLAR

NbL18g02180.1 GDSL_esterase/lipase_At5g33370-like [MW = 41.52 kDa]

No. of times detected



log(intensity)



Values from



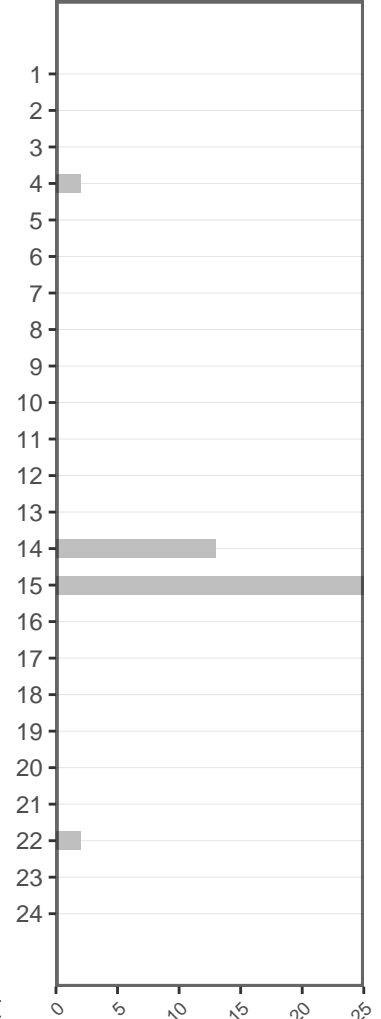
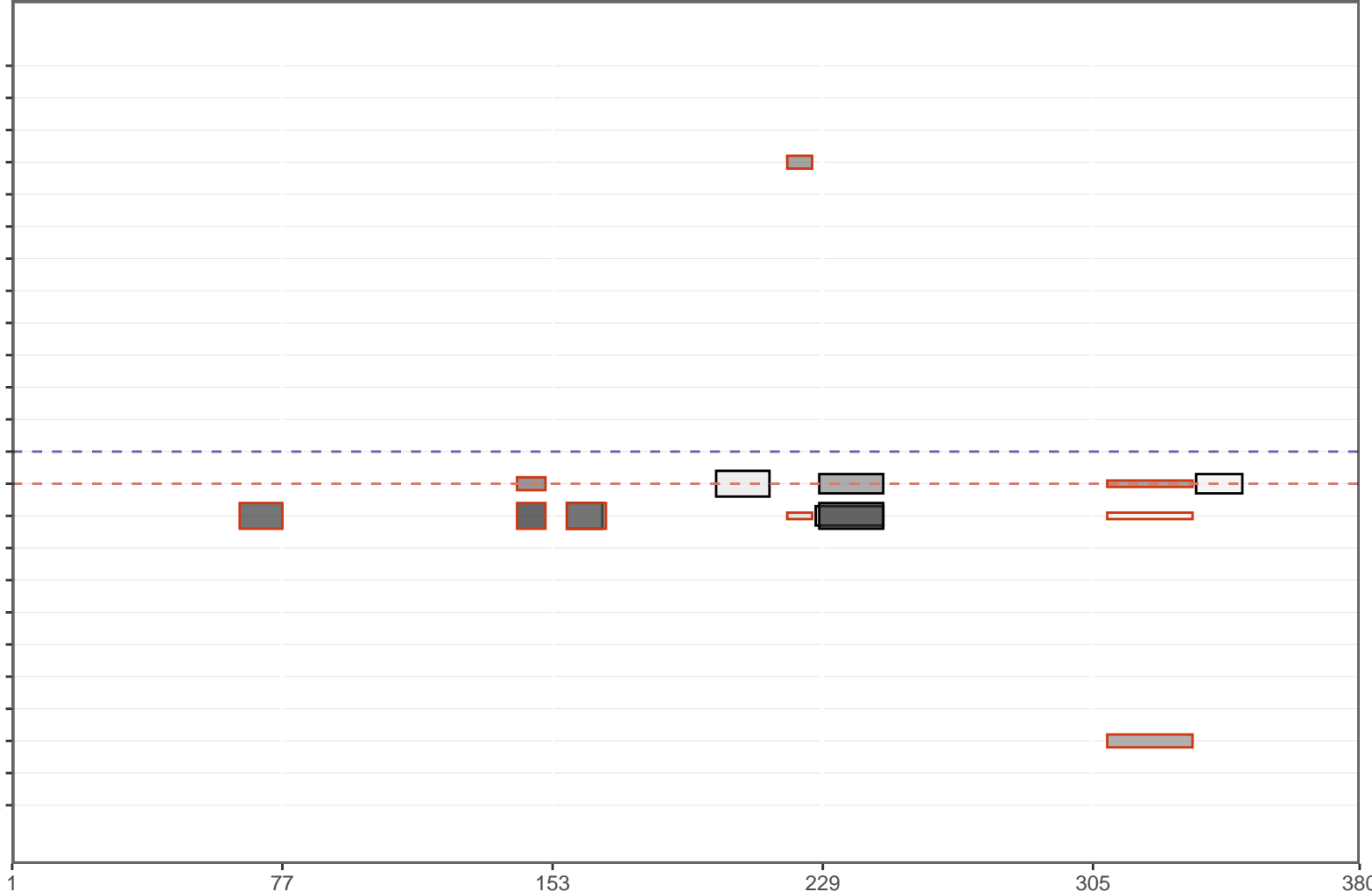
MW indication



Molecular weight

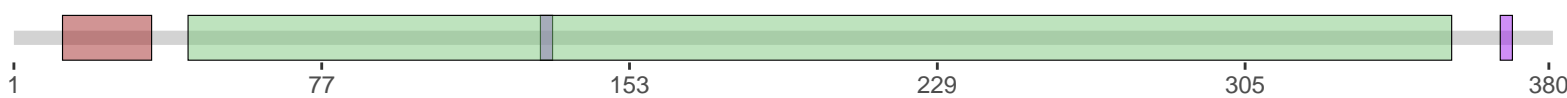


Gel Slice



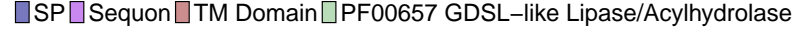
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GNDFNNYYLVPNSARERQYALFDVPLFISEYRKLRRVYDLGRRVLTGTGPLGGVPAELADRNRNGECAGVELGQAALFNPLQTMGLDNLTELGNGFAANTGQMHDITNPAQYGFITSEKAVCGGPGYNGLGLCTPLNGLGNRDVFAFVWDPHPHSEKANKIVGGIMTGSDDYANPMLSTIMAMDMA*

NbL18g02050.1 HMG-Y-related_protein_A-like [MW = 18.23 kDa]

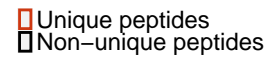
No. of times detected



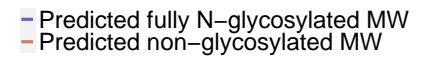
log(intensity)



Values from



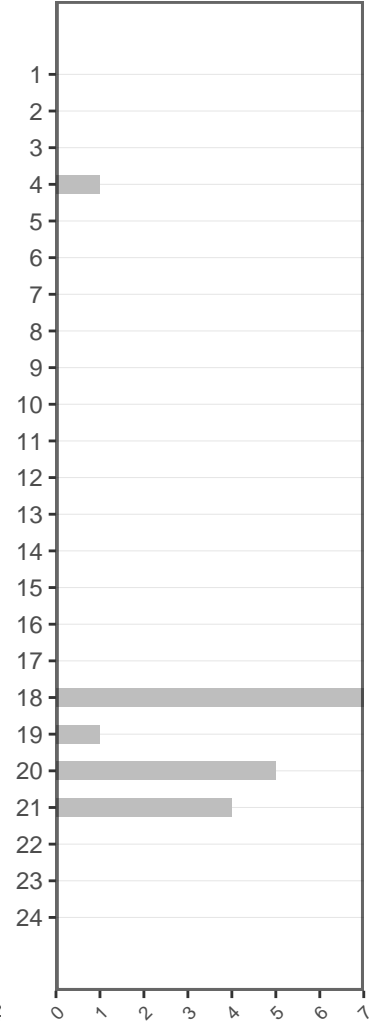
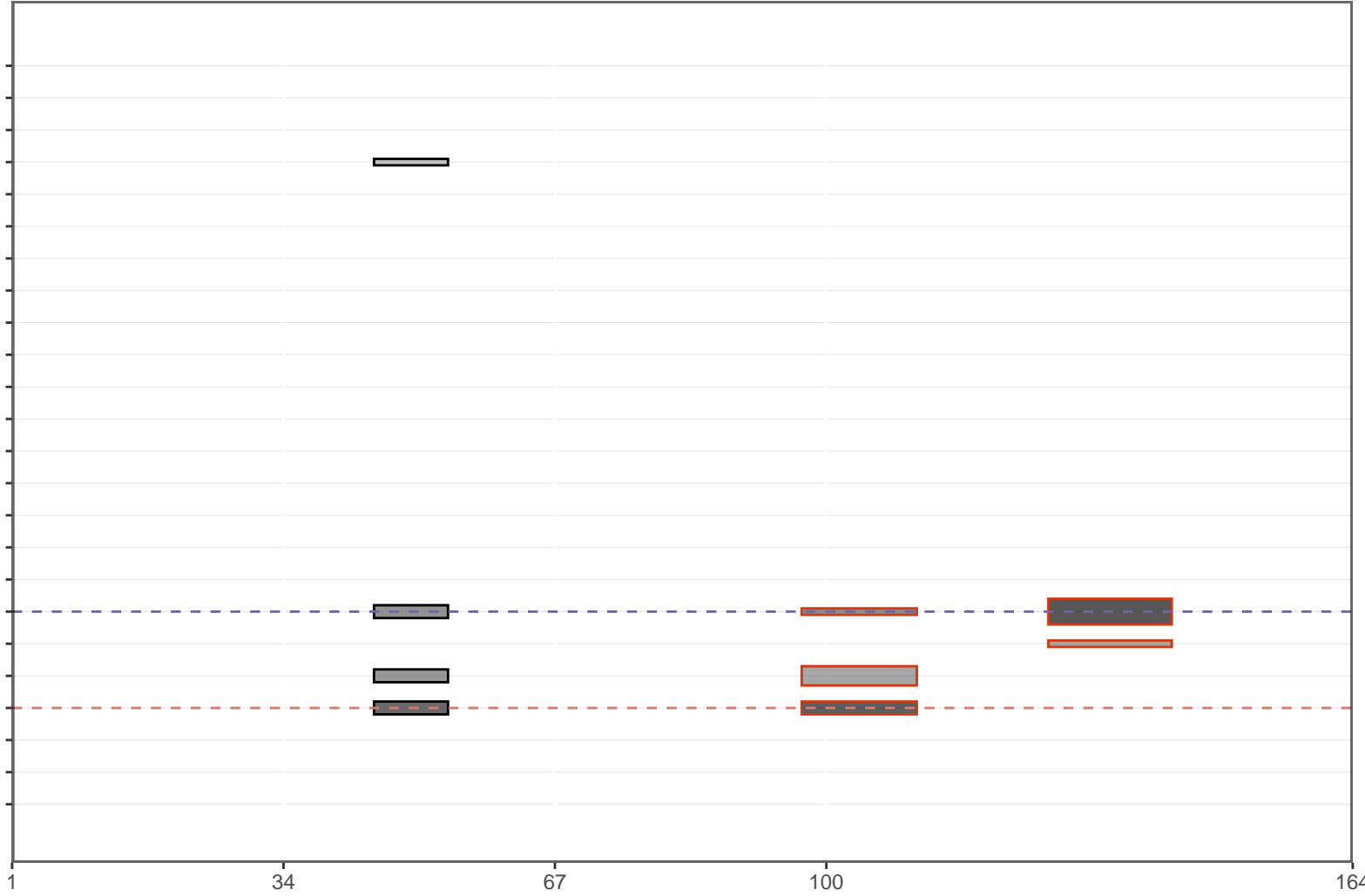
MW indication



Molecular weight

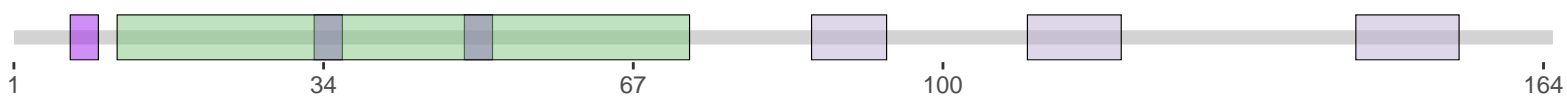


Gel Slice



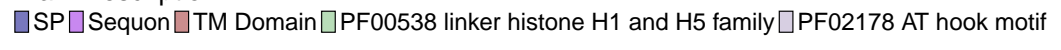
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FLKINNYKPGPNVPPKRGRRGRFPKPKTTLPGDTEHASKRPRGRPKKDPNAPPTPKLKPITVFINSANPVSKTGRPRGRPRKVKPKQDAGNVE

NbL18g01810.1 probable_isoleucine--tRNA_ligase_cytoplasmic [MW = 135.05 kDa]

No. of times detected



log(intensity)



Values from



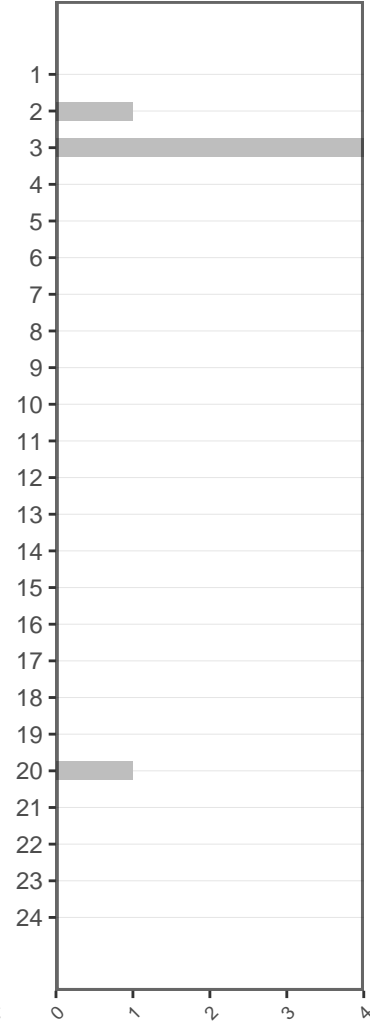
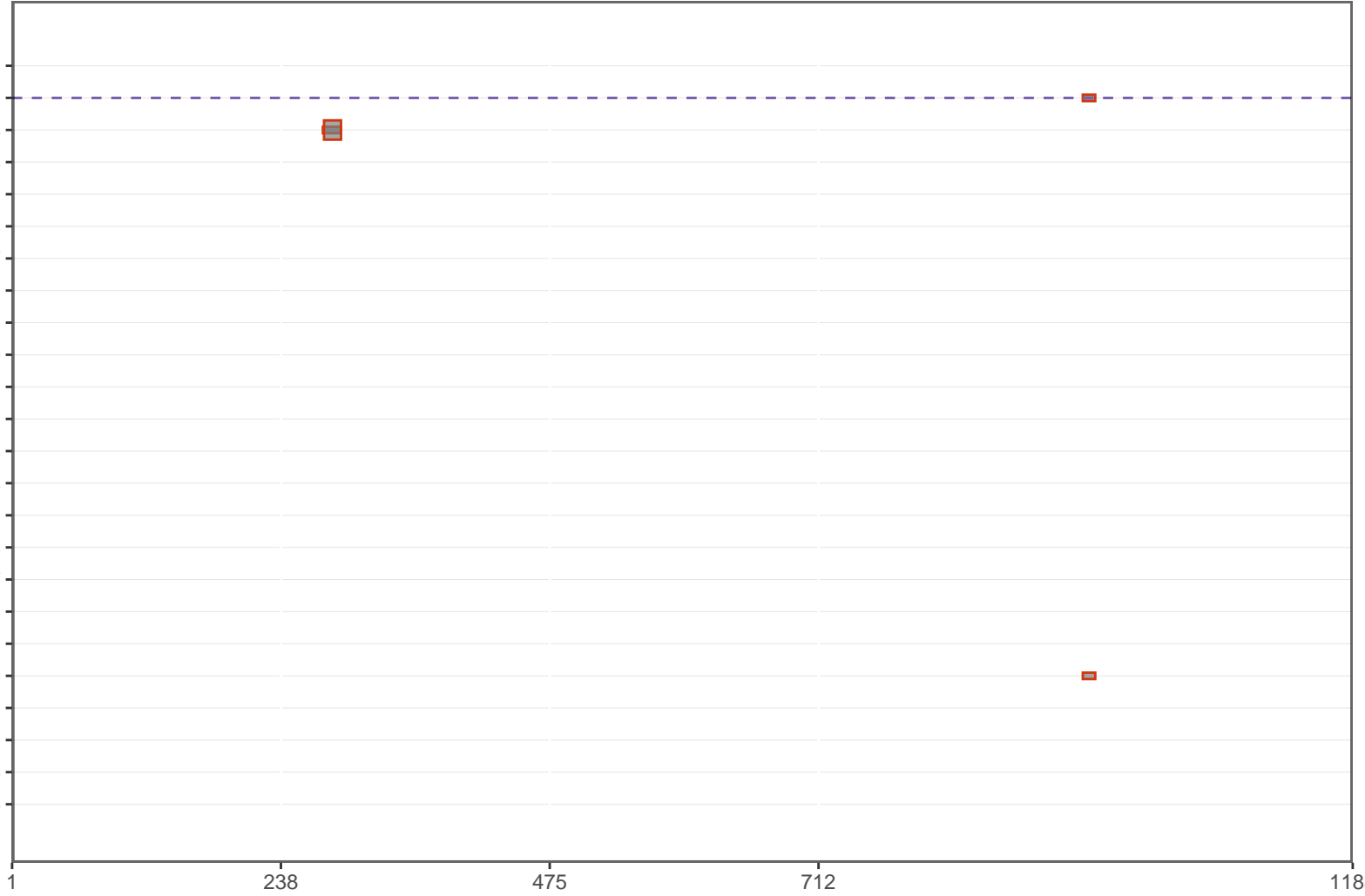
MW indication



Molecular weight



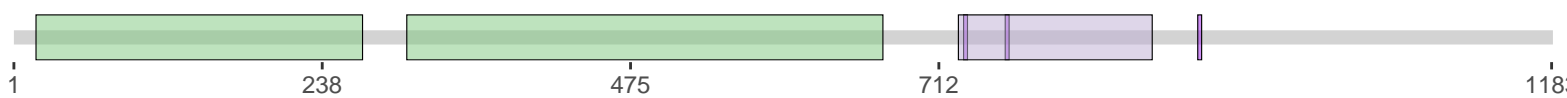
Gel Slice



Protein length

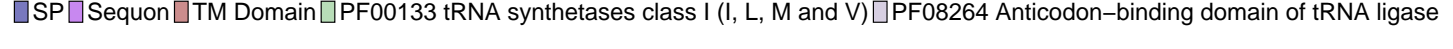


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YPFENVLEFENFPGHFVAEGLDQTRGWEYFLMVLSTALFGKPKFRNLKNGLVLAEDGKMKRKLKYNYPQPEVINDYGDALRLVYLNINSPVRAEPLRFKDKGVFAVYKDFLPPWYNAVRFVGNKRLKLEIDGFGFPPTDQKLGSSNVLQDQWNSGTGLVHFVROEMDAVRLYTVVPLKFLNLTNYYRFRKRRLKGRTEGGDGRITALSTLFLVLLTSCKAMALPTPFTEVLYGNLRKYKGSSESHYGSYFPEVEGKRWERIEGSVNRMMTIDLARNIRERHN

NbL18g01780.1 60S_ribosomal_protein_L6-like [MW = 25.45 kDa]

No. of times detected



log(intensity)



Values from



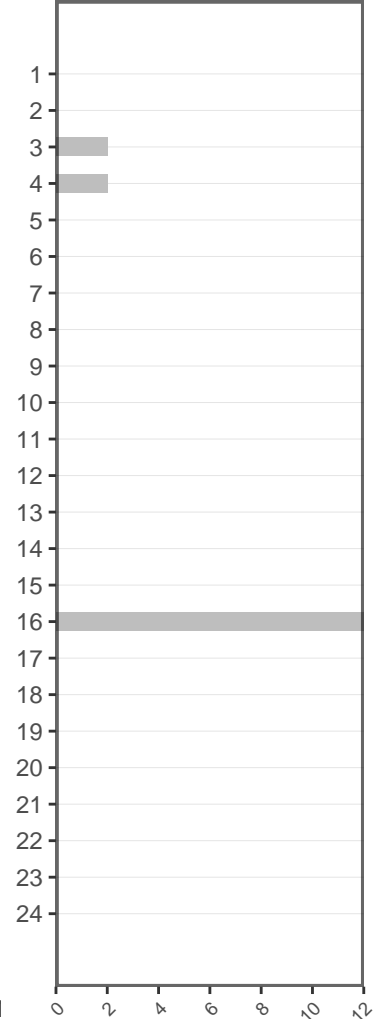
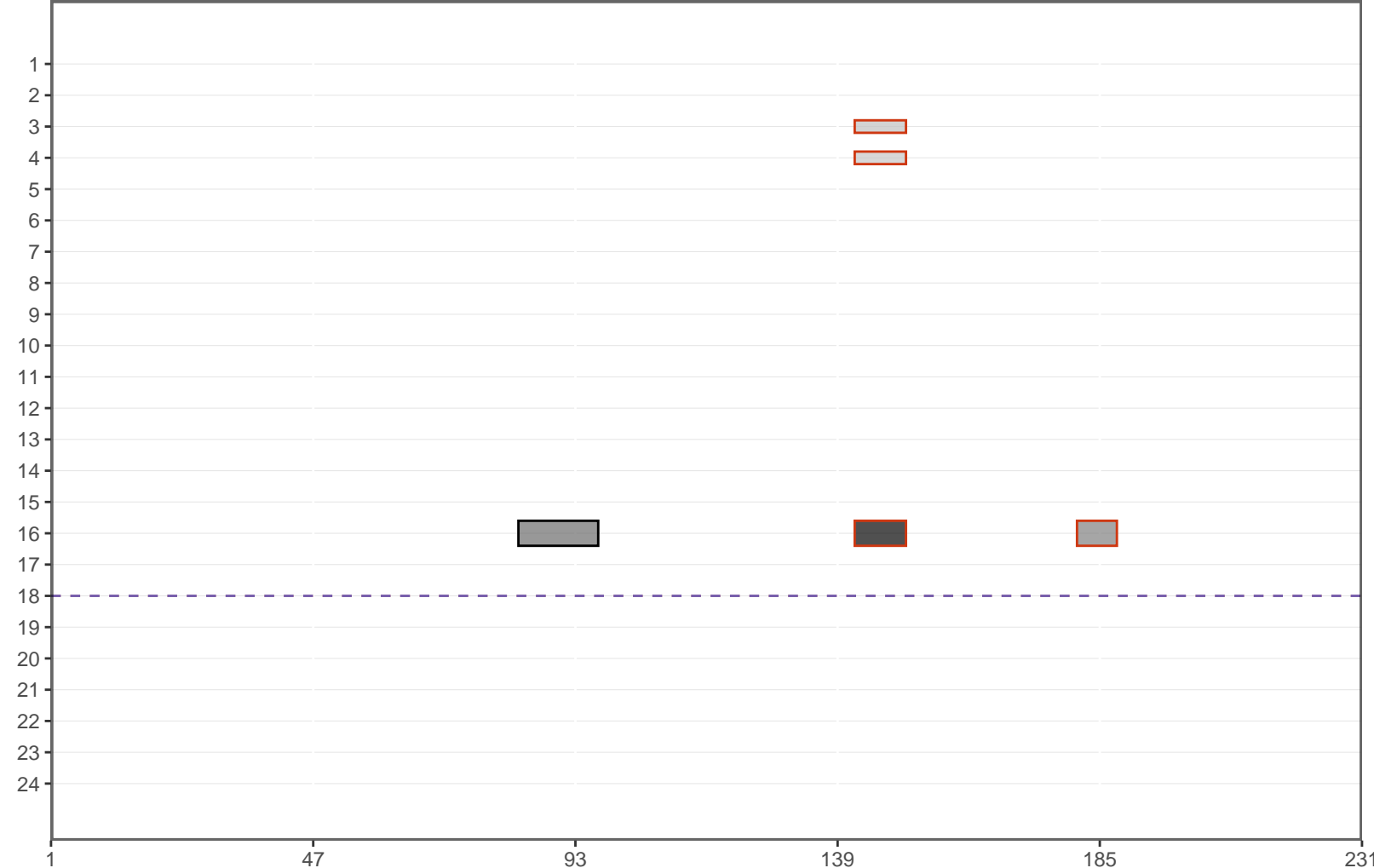
MW indication



Molecular weight

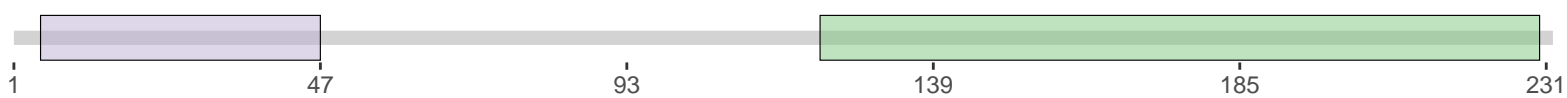


Gel Slice



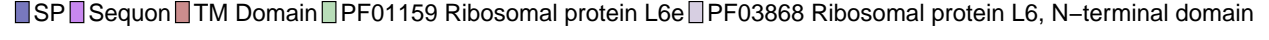
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VFLKGLKSGLLLVSGPFLKNGVPLRRVNGAVVGTSTKVDISGVSVEKFDKDYFAKGAENKGGKGGEGEFFFEDKKEKNVLPDEKDDQKAVDEALIKAVEGVPELKAVALSARFLKSGMMPHELVF

NbL18g01770.1 phosphoribosylglycinamide_formyltransferase_chloroplastic [MW = 33.07 kDa]

No. of times detected



log(intensity)



Values from



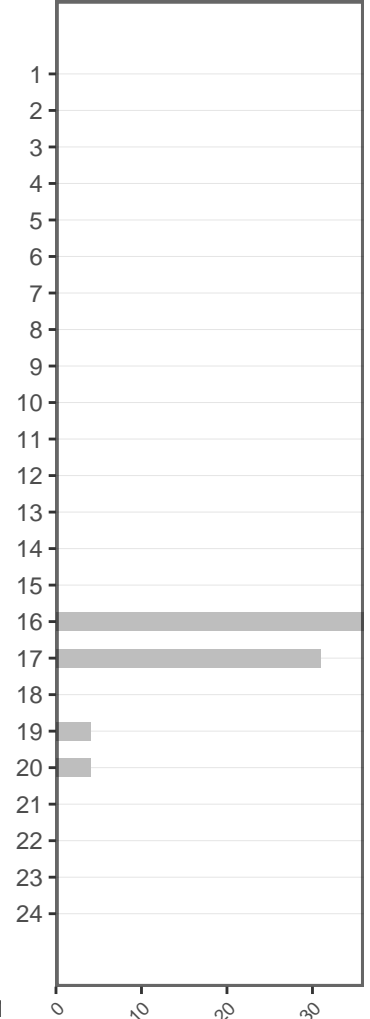
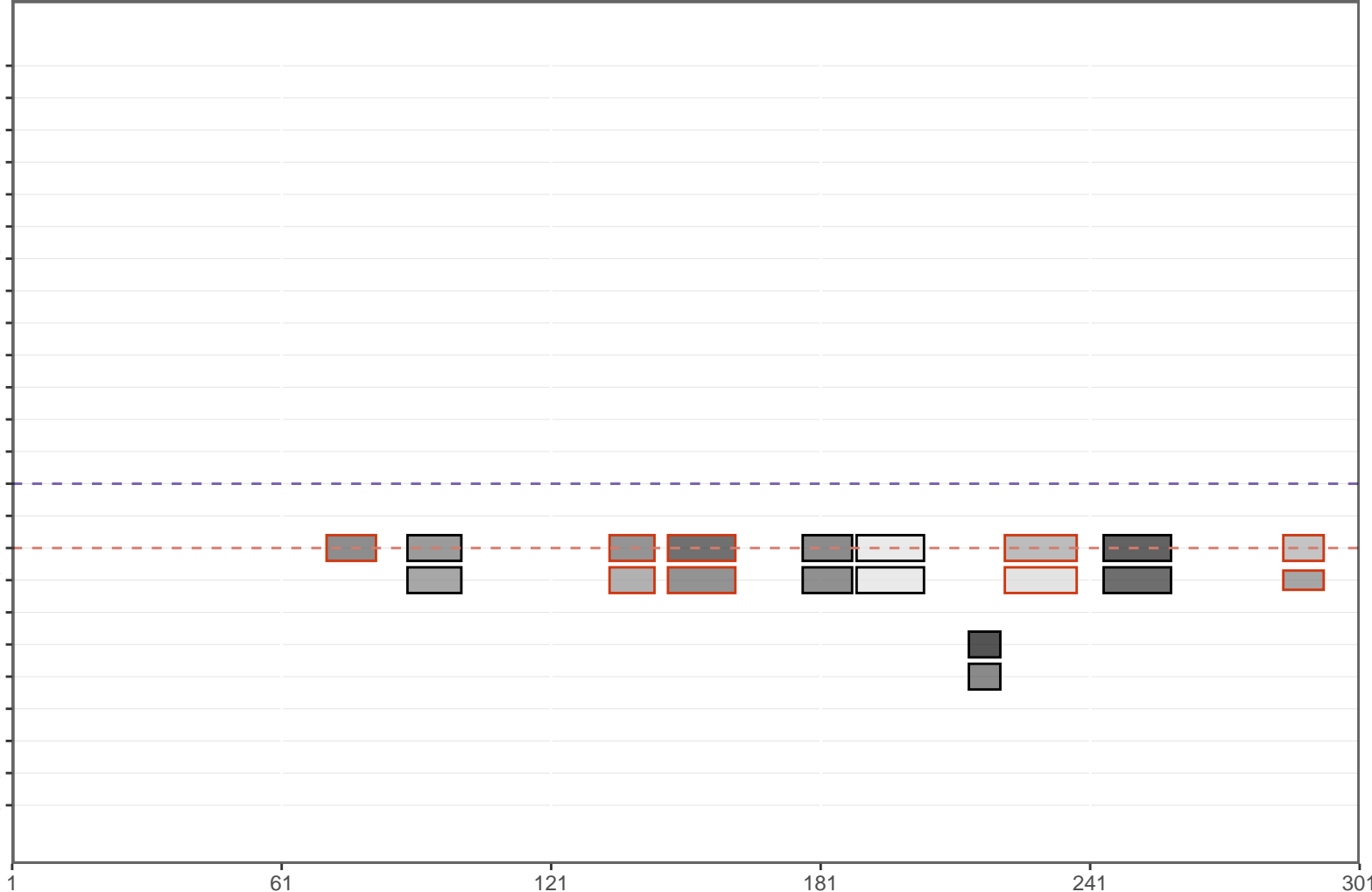
MW indication



Molecular weight

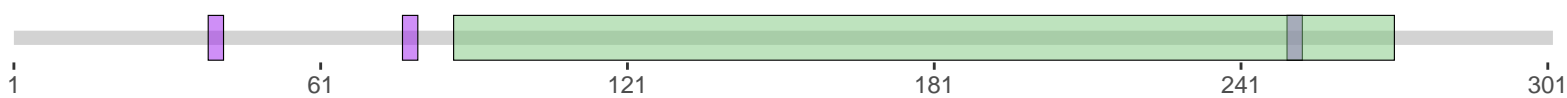


Gel Slice



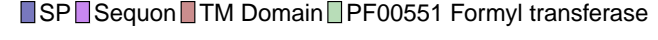
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IPVILFPAKGTSEGLSEEDLVGALRTYNDIFLLAGYLUKIPTELVAQAFRRISFNHPSLLPFGGKGYGAKVHKAVASGARVSGPTTHYVDEHYDTGRILAQRVVPVPLANDTADTLAARVLQEEHKLVVEVAALCEERIVWRGDDVPLIGSEKDPNQYK

NbL18g01740.1 acyl-protein_thioesterase_1-like [MW = 28.01 kDa]

No. of times detected



log(intensity)



Values from



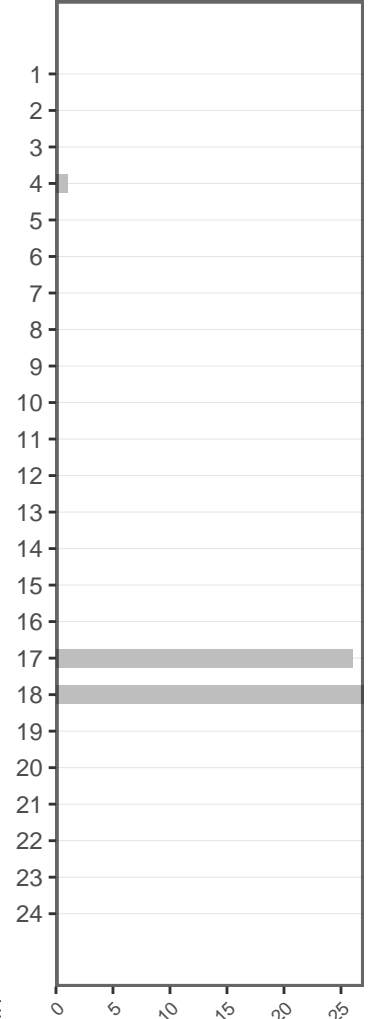
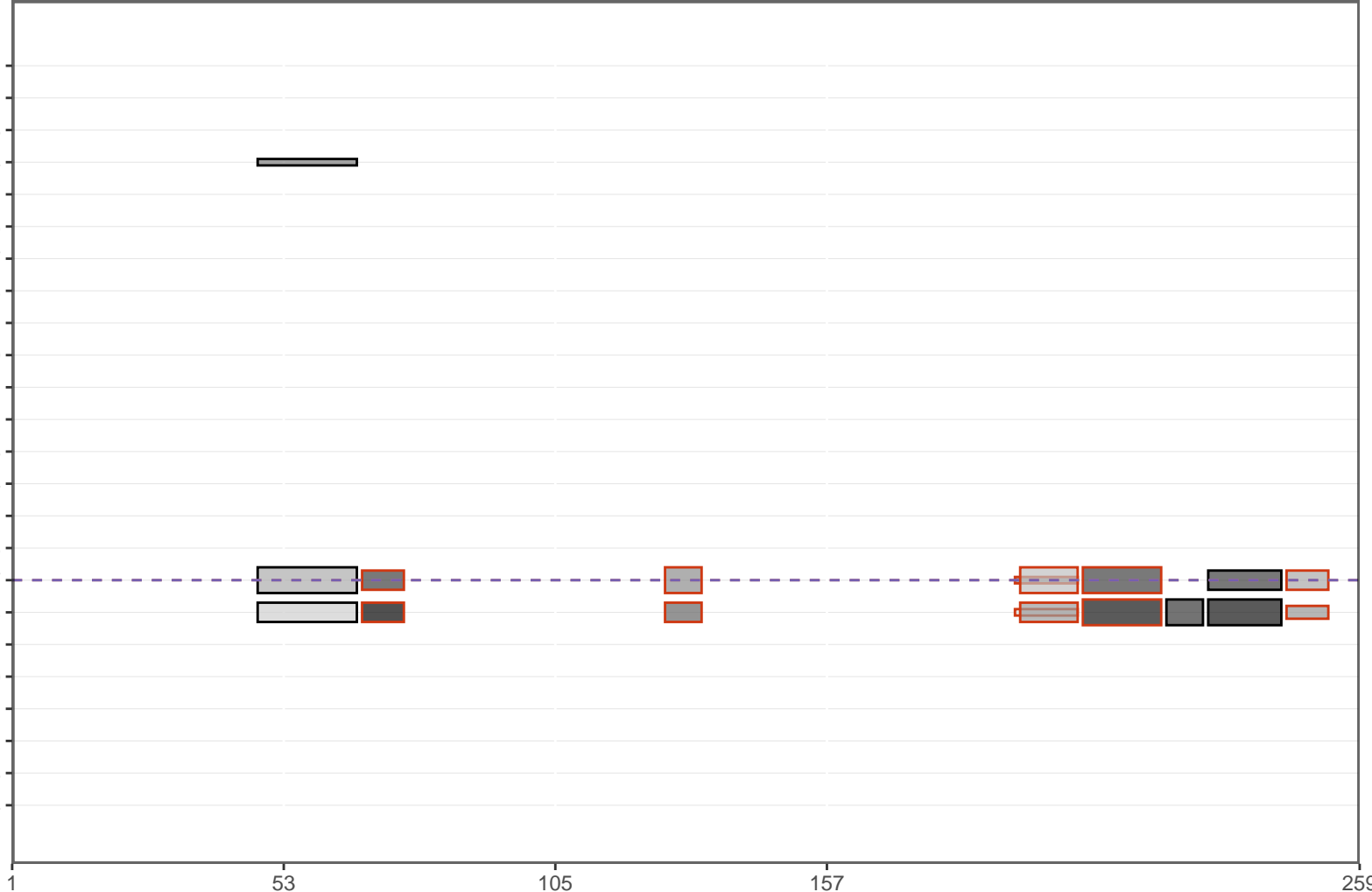
MW indication



Molecular weight



Gel Slice



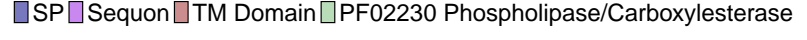
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

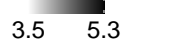
ISQLKAVNINHAMDKEDAGTNPINFCGFSGGALTLASVLLPKTLGGGAVFSGVWVFNNSALEKGTPEAKKTPILWSHGADRTLVFEAGGAGPPFLERAGMTCEFKAVPLAHNSINNEELKNELEWKPRLQNS

NbL18g01690.1 tropinone_reductase-like_3 [MW = 27.18 kDa]

No. of times detected



log(intensity)



Values from



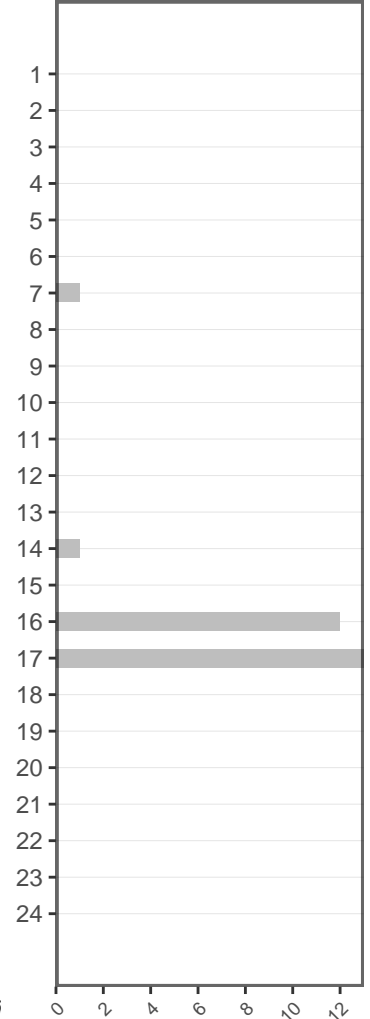
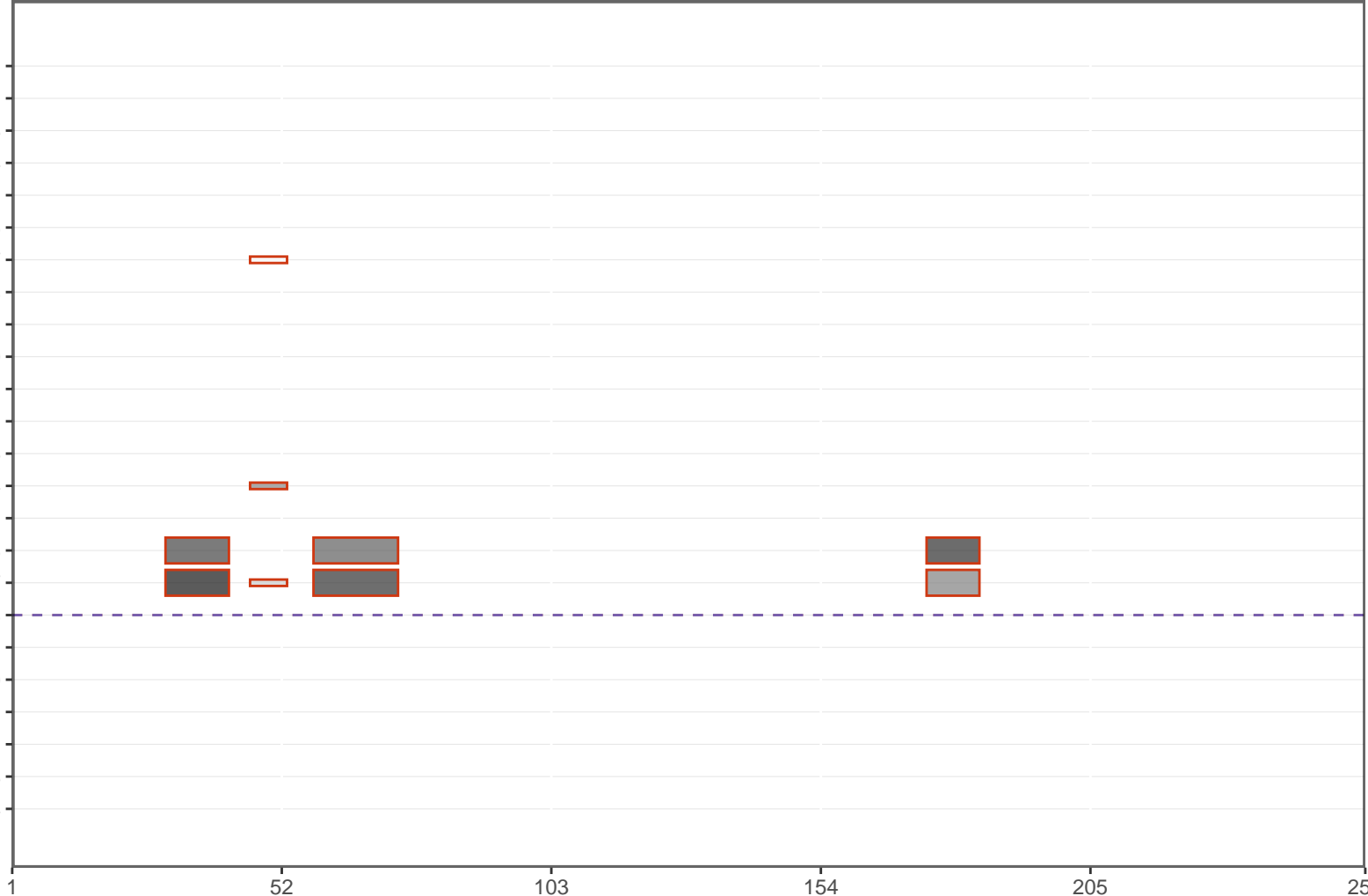
MW indication



Molecular weight



Gel Slice

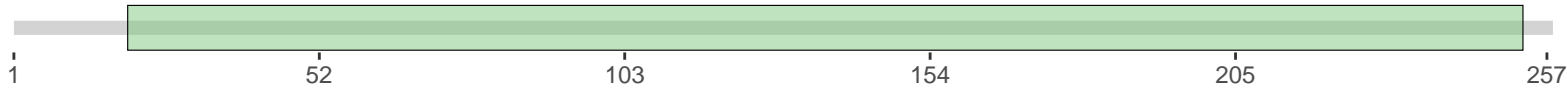
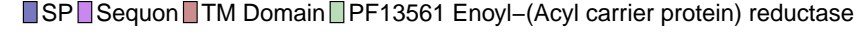


Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

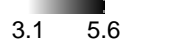
WQNYKAILLQIHGDAPLQKGSVYHISIAGYTPRAMGMGVTKTALLGLTKALAEAMPNTRVNSIAPGFVPTTHFAEFTGNANVRRELEAKTLNRLGTTQDMAAATAVLASDDAAVYVGETLVWGGMHRLL

NbL18g01640.1 UTP--glucose-1-phosphate_urydyltransferase [MW = 54.7 kDa]

No. of times detected



log(intensity)



Values from



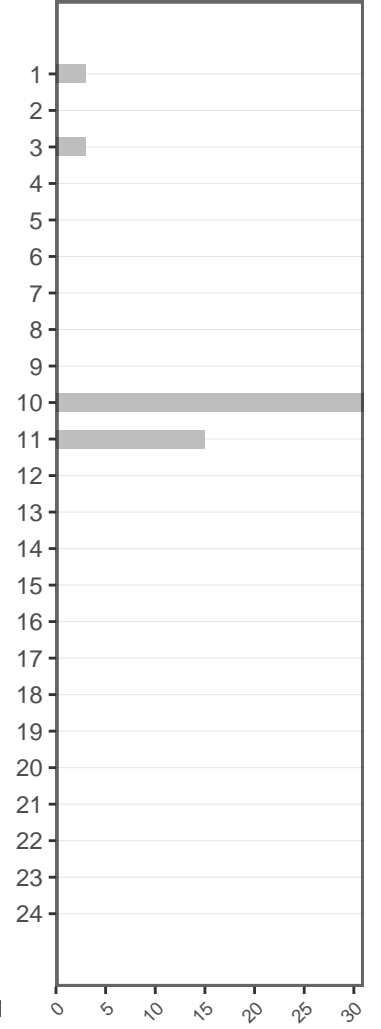
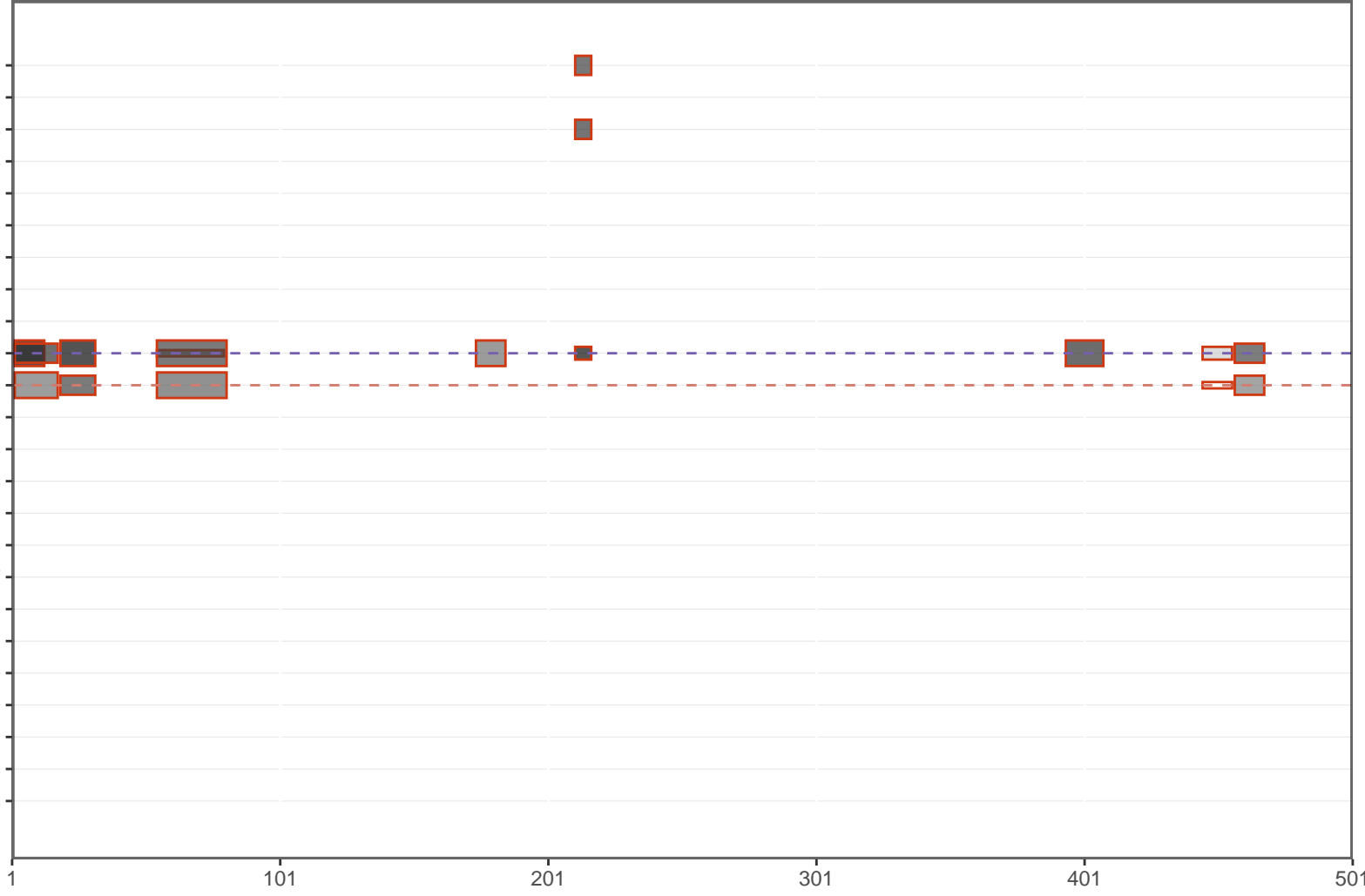
MW indication



Molecular weight

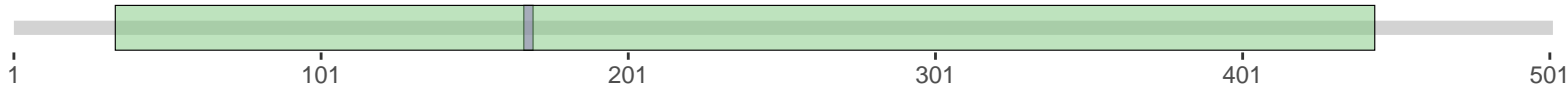


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VDLKLNLIQNKNEYMEVTPKTLADVGGTLLSYEGKVKVLEIAGVPRDEHVNFEKSIKPKFNTNLLWNLNANRILVEADALKMEIHPNKEVGDGKVKVLETAAGAANKFFDRAIGVNVPRSRFLPKKATSDLLLVQSDLYLTDEGYVIRNPARSDPNPNSIELGPEFKKVNFLGRFKSIPSEIHLDELKVTGDVWFGSGITLKGIVVAISGVKLEIPDGSVANKVQFTLAPNGAARYRFTSFDFPVTGFRISMDF

NbL18g01600.1 isocitrate_dehydrogenase_[NADP]-like [MW = 57.88 kDa]

No. of times detected



log(intensity)



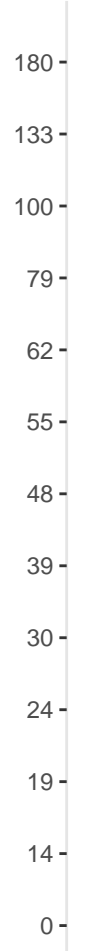
Values from



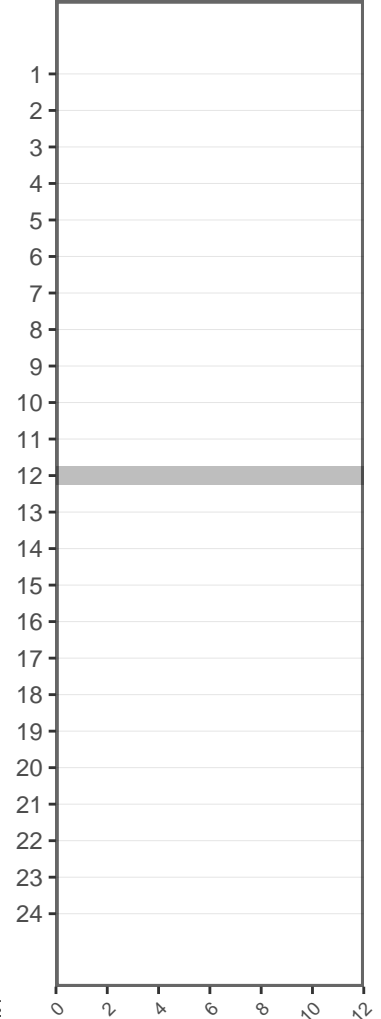
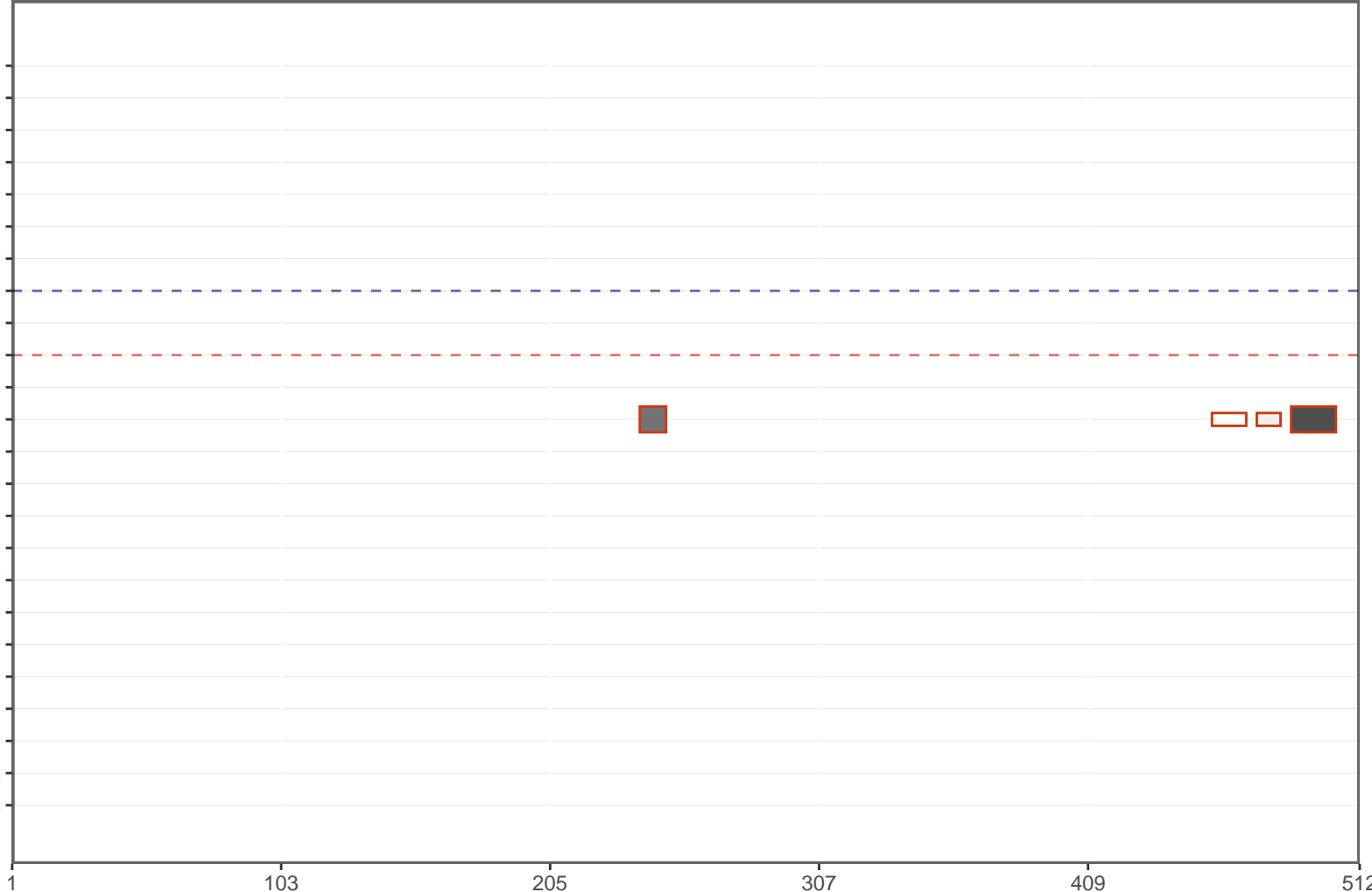
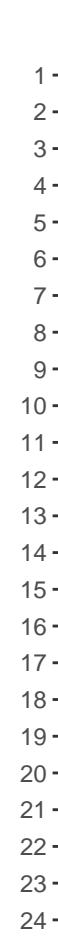
MW indication



Molecular weight

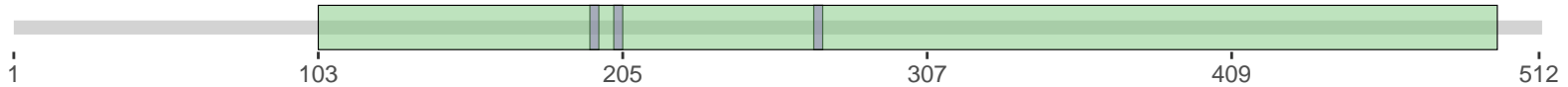


Gel Slice



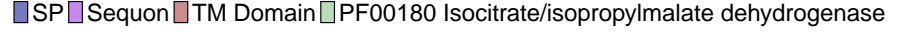
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RPQKIKLVFYPEGDKDETEFEVYNTFGAGGVLSMYNTDESIRSFSAEASMMAYQKWPVYLSKNTKTKKRYDGRFKDFGVEVYENWELKFEFAGIYWEHRLIDDMWYALKSDGGYVWAGKNYDGDVQSDFLAQGFSLGLMTSLICPDGKTIKTESEAAHGTVTRHYRHHQKGGTSTNSIASIFAWTRGLAHRRAKLDNNAALLDFTKLEAAGVAVENGMKTKDLALVHSGKVAHQVANTEEFIDVADELKARLLKAVP

NbL18g01590.1 glutamate_decarboxylase [MW = 55.86 kDa]

No. of times detected



log(intensity)



Values from

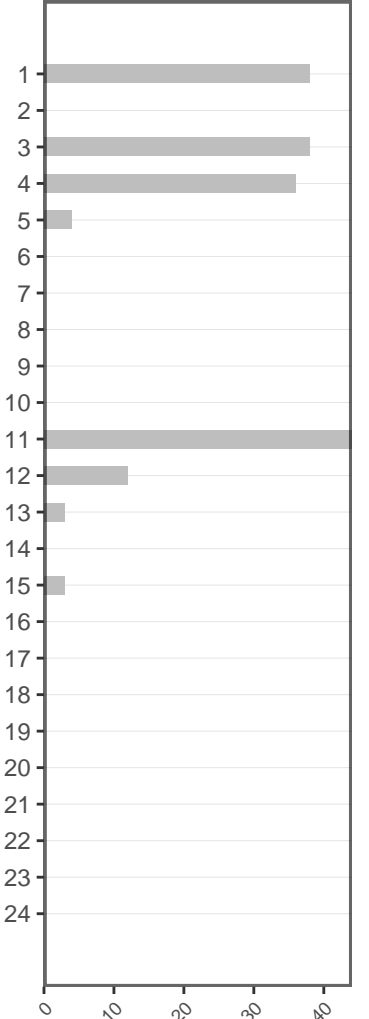
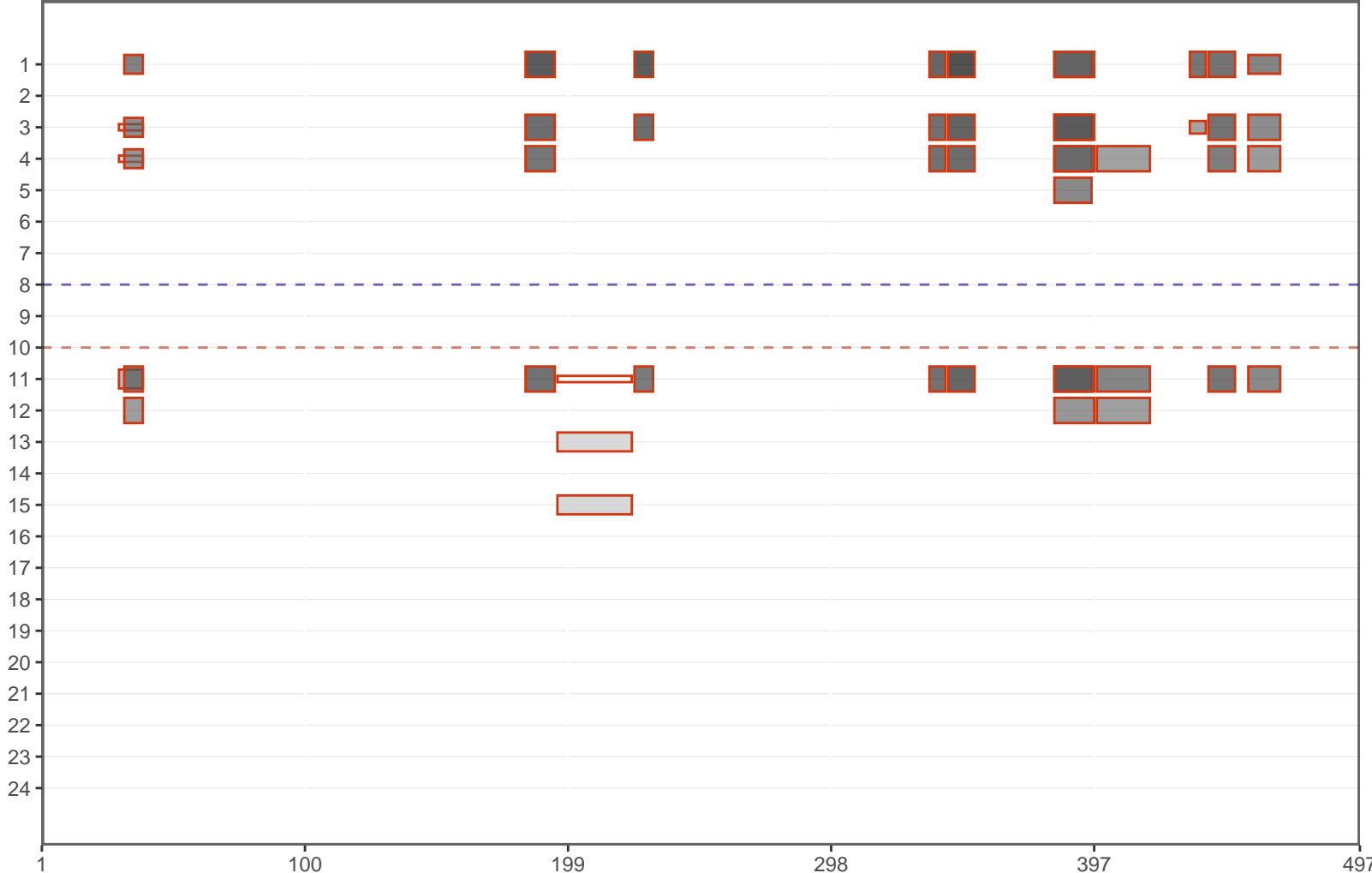
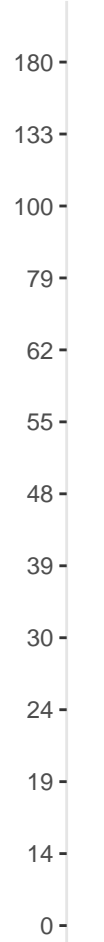


MW indication



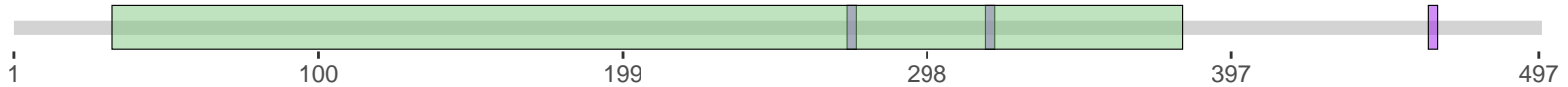
Molecular weight

Gel Slice



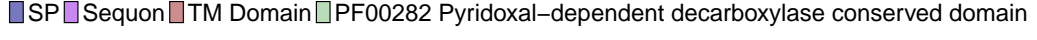
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LETGVDTPHHVDAAGGGAFAPFLYPELEWDFRFLPLKSNVSGHKVGLYAGIGWAWRNKEDLPDELFINHNLGADGPTFTLFRSGKSSGVAQYQLRILGFEGYKVMENGENARVLRLEGLKSGRFNISKIIEGKPLVAFSLKDNQSHNEFEISETLRRFGWIPWVTPMPNAGHVTYLVLRVYREDFSRTLAERLVMQVMDVYKVLHELDLTPGRVNAKLAFAANGSGVHKKTDREVGLVETAAWKLVADKKKKTNGVD

NbL18g01390.1 30S_ribosomal_protein_3-1_chloroplastic-like [MW = 22.47 kDa]

No. of times detected



log(intensity)



Values from



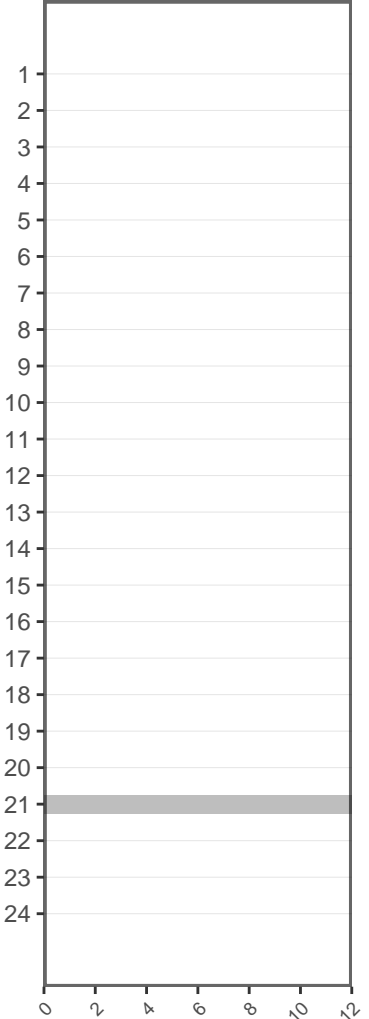
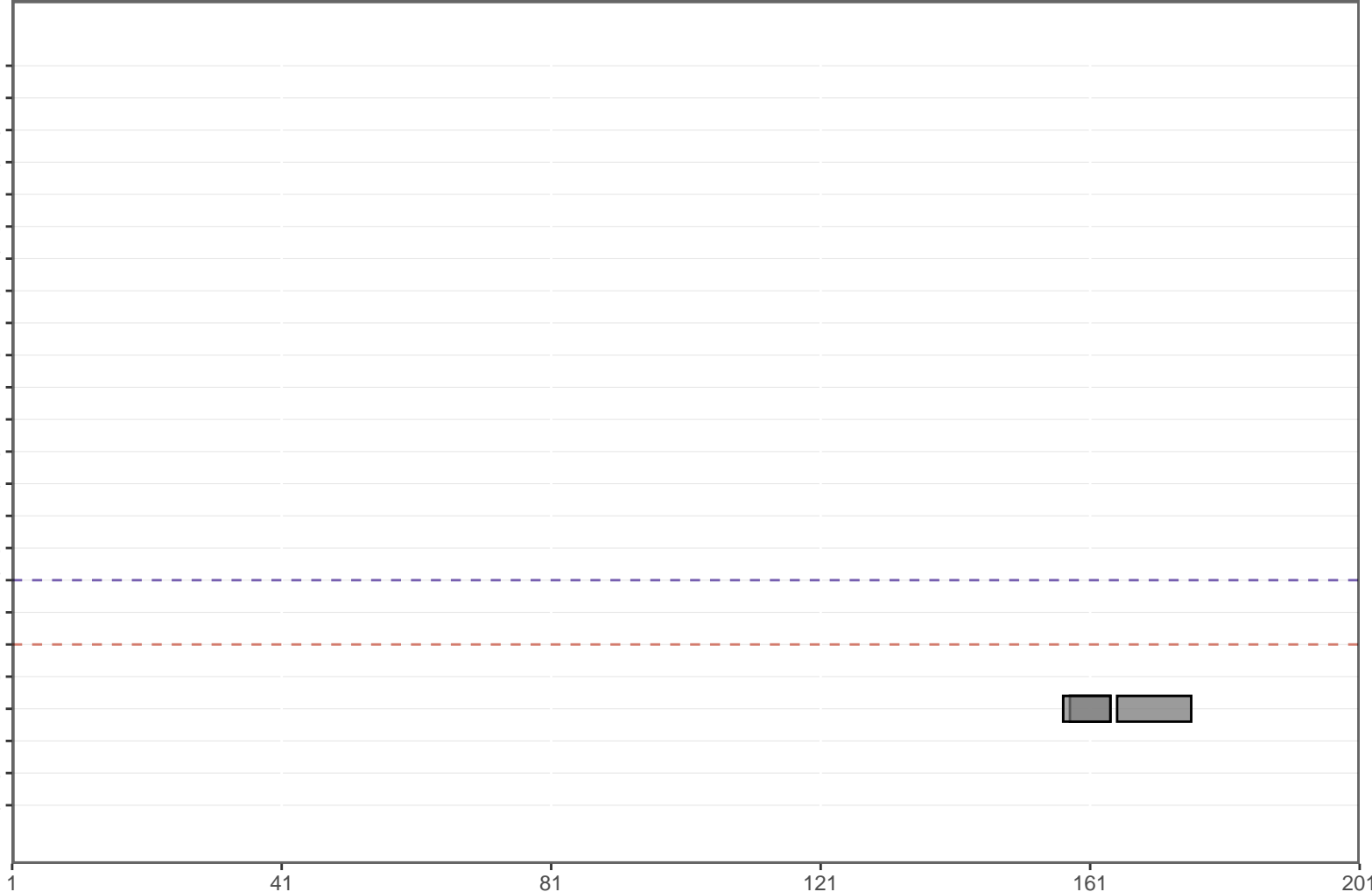
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

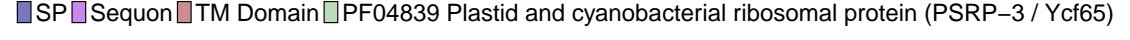
Protein length



Pfam domains



Pfam Description



Protein sequence:

TETELVTTDTSVVOEIENTDGGKKVIEKPRLLVLFKFIWMEKNGLGLDQVLPVGHGVPLSPYFFVPRKDAWEEELKTTLEKPKWISGKGMILLNGATDINLWGGSGNLSP

NbL18g01300.1 alpha-xylosidase_1-like [MW - SP = 102.24 kDa]

No. of times detected



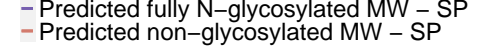
log(intensity)



Values from



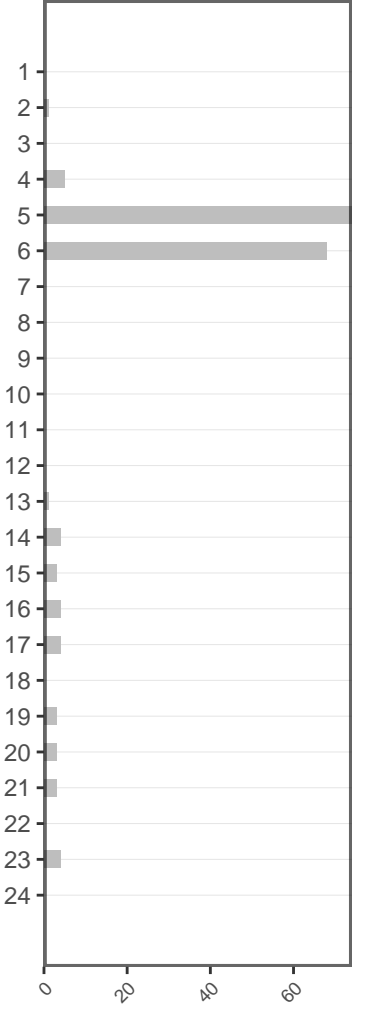
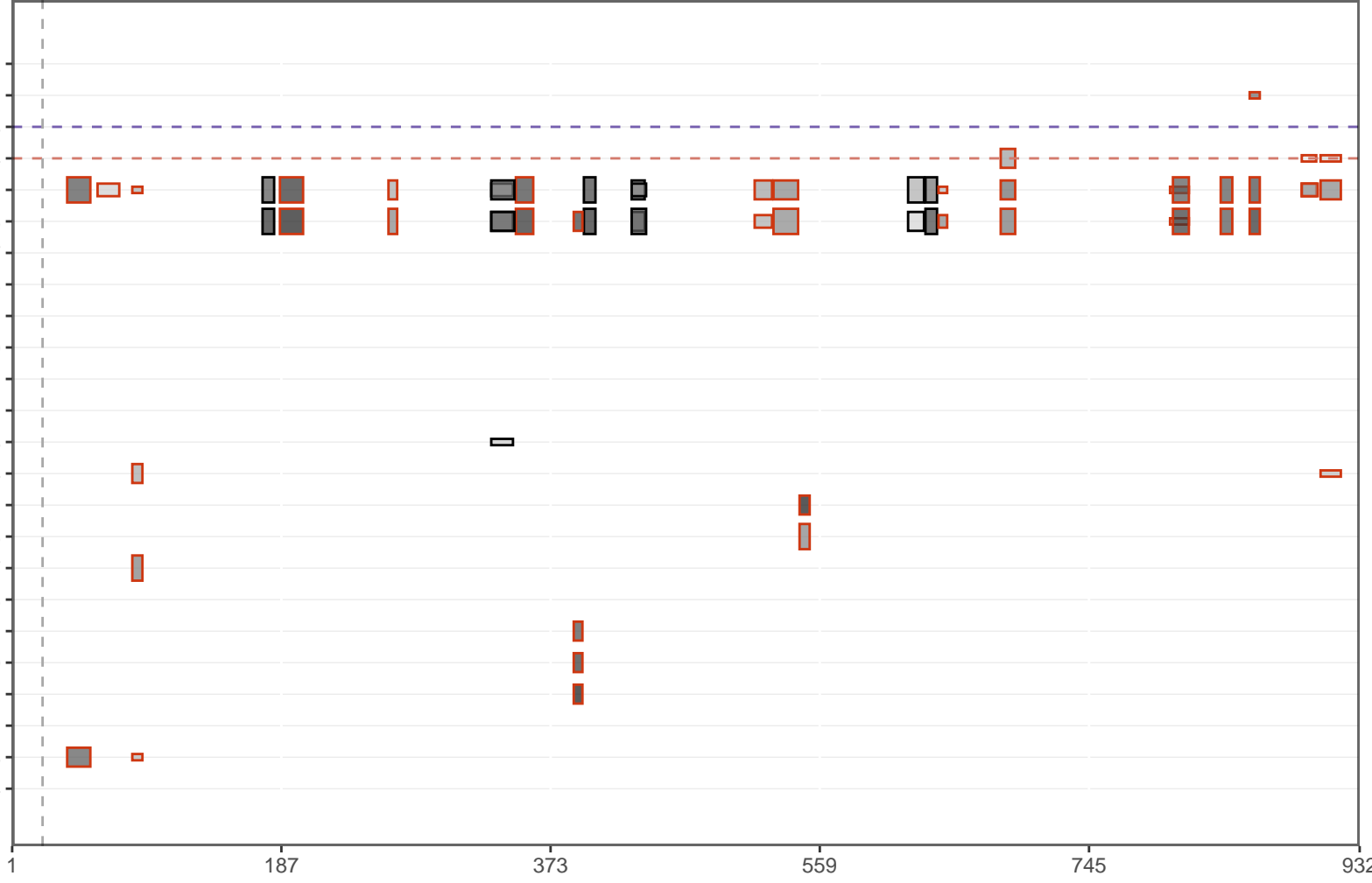
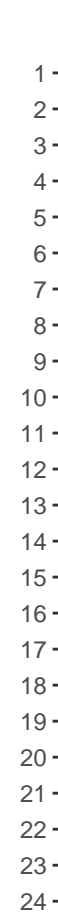
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

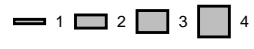
- SP
- Sequon
- TM Domain
- PF01055 Glycosyl hydrolases family 31
- PF13802 Galactose mutarotase-like
- PF16863 N-terminal barrel of NtMGAM and CtMGAM, maltase-glucoamylase

Protein sequence:

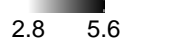
IYSNFCTGLCTPEGRIGPNGTGFQWWDGLDKNVSTKWDQPPYKINA6GIGAPIGYKTIATSAHYNQVREYDAHSLYGFSEAIATHKGLQALEGRPFILSRATFVGGHYAAHHTGDNKGTWEDLRVSGISTVLNFGIFGVPMAGSDKCGFYKAPTEELNQRWIEVGAIFYPSRSDHANNYSFROELVQWKSVAAGARNALGMRVYKLLPYEYTLTYEAHTTGAPIARLFFSFPNPKLVGVTQFLIGSSVMVSPVLERGKTEVKALFPDPTWYKLFDMTQAVYTKPEYLYL

NbL18g01100.1 glutamine--tRNA_ligase [MW = 90.51 kDa]

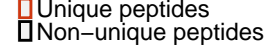
No. of times detected



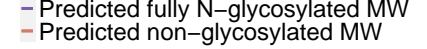
log(intensity)



Values from



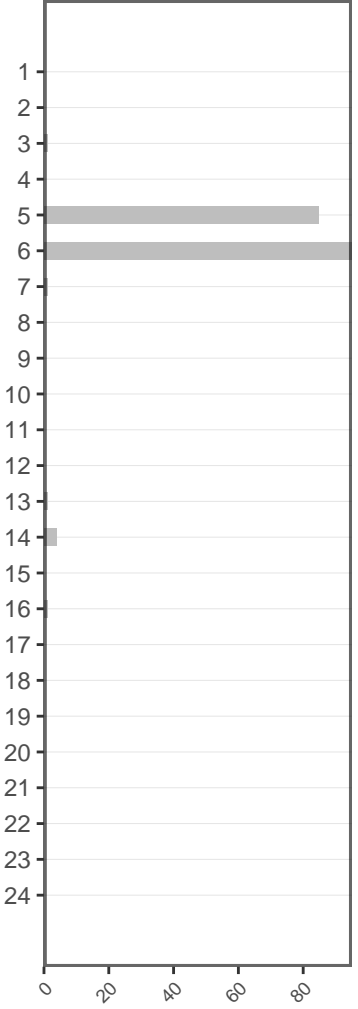
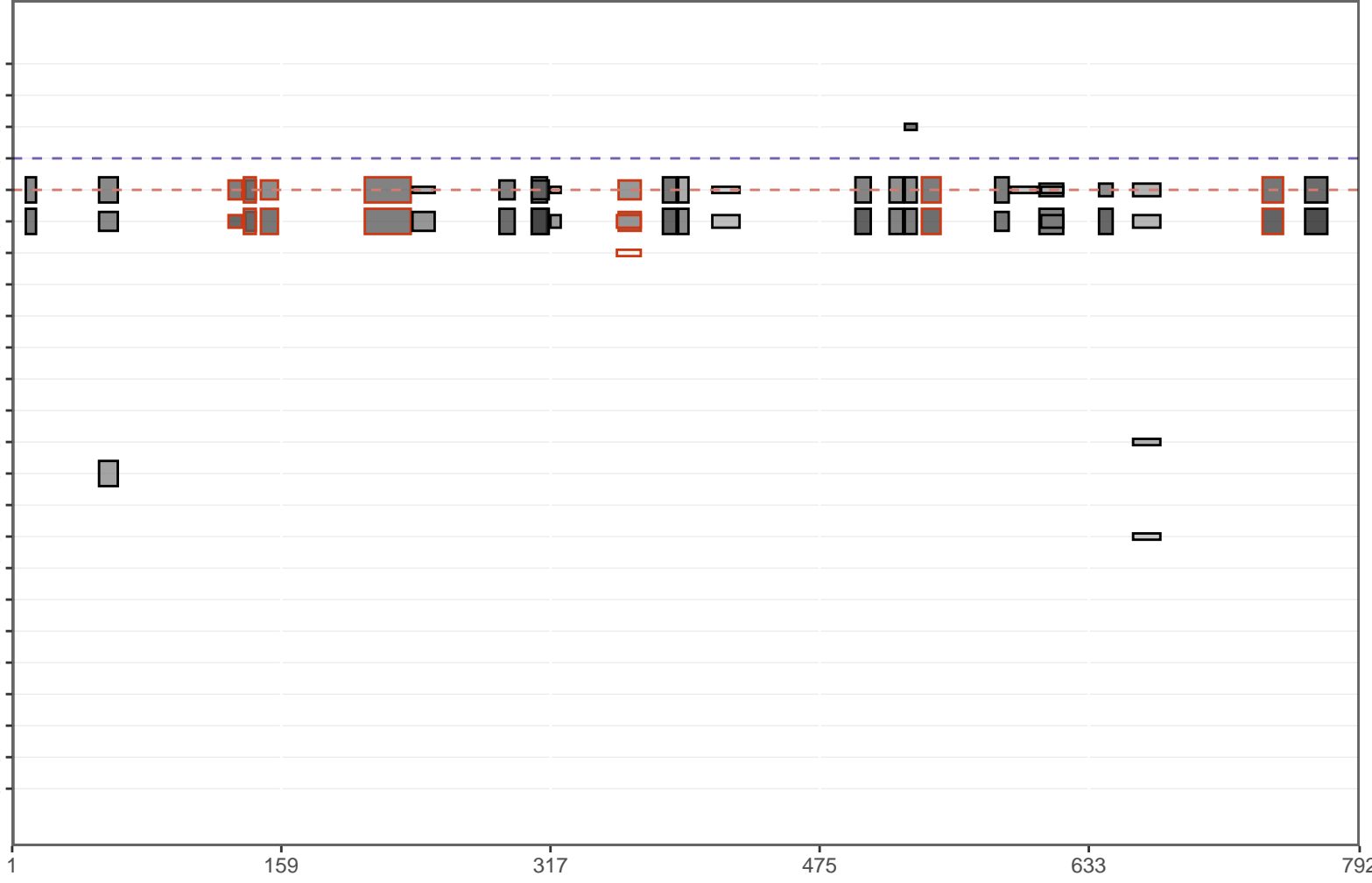
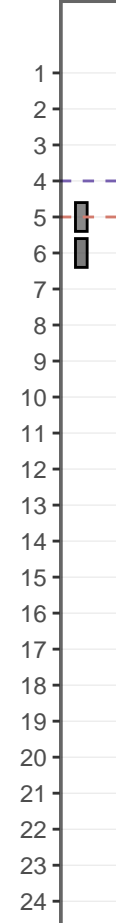
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Description

- PF00749 tRNA synthetases class I (E and Q), catalytic domain
- PF03950 tRNA synthetases class I (E and Q), anti-codon binding domain
- PF04557 Glutaminyl-tRNA synthetase, non-specific RNA binding region part 2
- PF04558 Glutaminyl-tRNA synthetase, non-specific RNA binding region part 1

Protein sequence:

RRPEESLRLLFDEMKKGMIDEGKATLRMKGMQSDNFMVYDLIARRIKFTPHAGDQWGVYPEYDVAHGVDSLENTHSLGTLFEFETRRASVYVLLDALGLVYGFVWEVSRNLVNTVMSKRKLNRLVTEKWVDGWDDPRMLTLAGLRRRGVASTANAFVIRGIGTRSDGSMHLGRLEVYHREELNKTPARTMVLNPLKVVITNLEAGLVTDLDAKKWPEAPINDASSFYVFFSRYVYIERTDFRLKDKGKVFGLAPKQKVLRLRYPIKGTDLVLAADKETVLEIRAEYD

NbL18g01080.1 cysteine--tRNA_ligase_2_cytoplasmic-like [MW = 63.8 kDa]

No. of times detected



log(intensity)



Values from



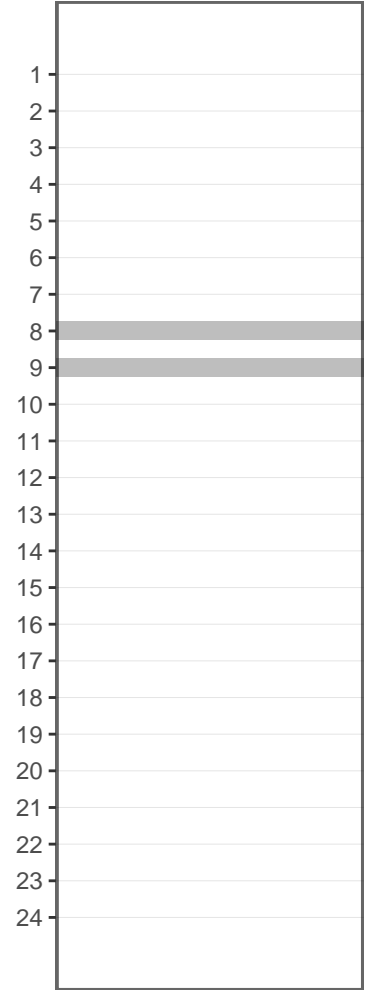
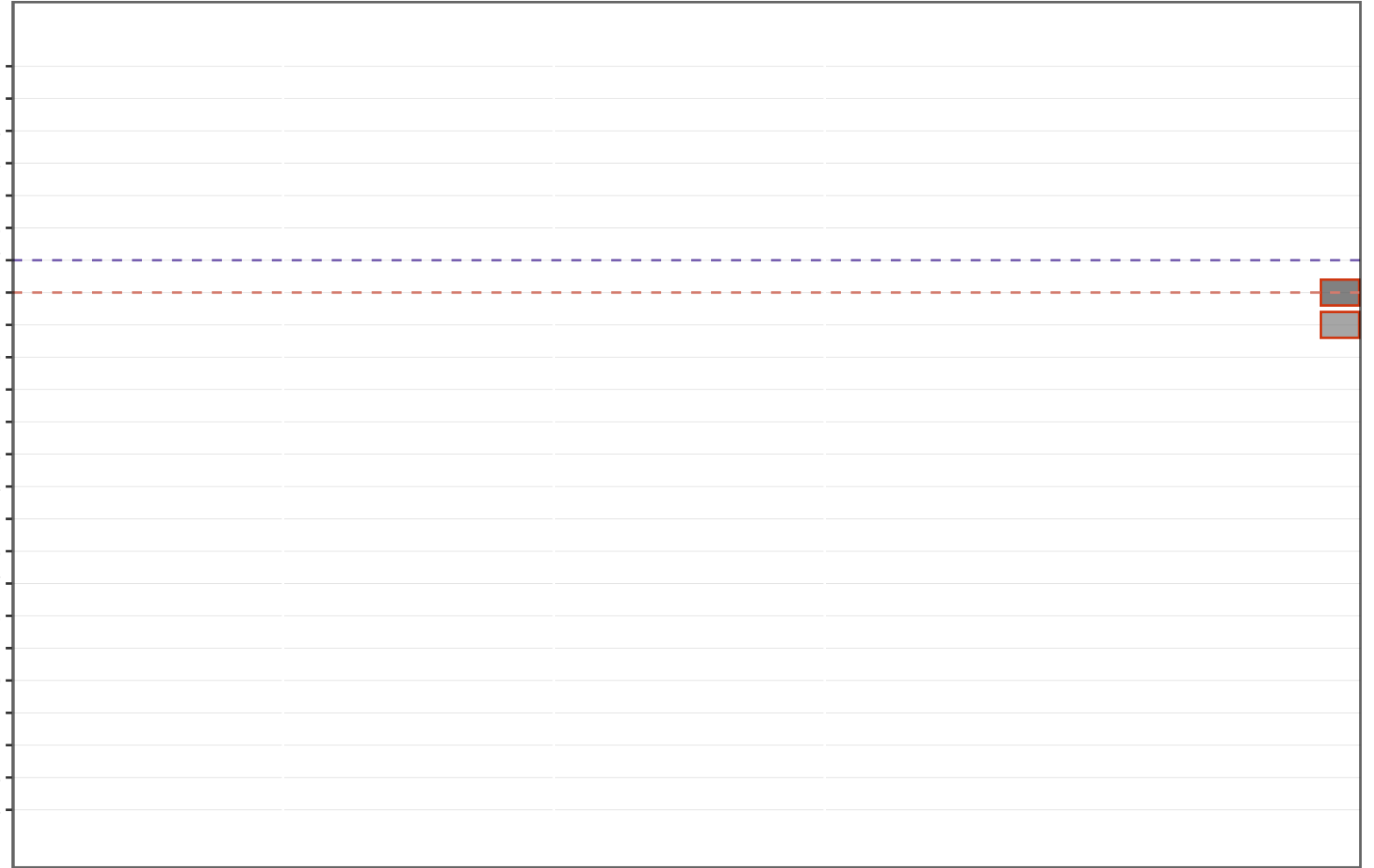
MW indication



Molecular weight



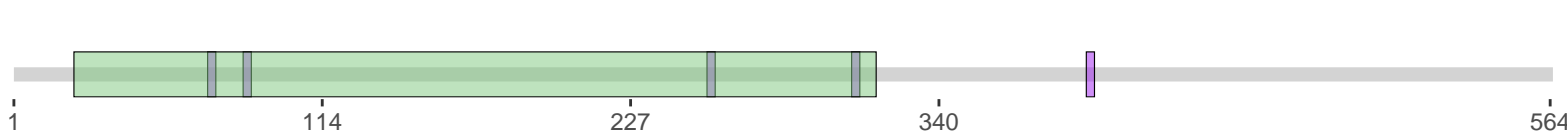
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

IDDEKMSKSLGNFTIREVTRLYHPALRYFLGLGMHYRSPVNYISIQIEAISESVFYLYKQLHDCDEALSVFQGGTETETEVIRGVRSVPAAGECKKLRNELETHLSDLLHTPTLNAALGEALRLMNSLNLKPKKQKQGLSAVLSLAELLKVKAVLDVLDLGLLSSTCAEVLGGFKERALKRAELFEEDLHAEERTLARKNKEFARSDQIRSDLVAKGIALMDIGTETVWRPQVRSPEPEQGFAPFVQGEQSAAVQKKEKPAAPSGQKGSAAAPQKEGPIAPLQOEOPIVRI

NbL18g00530.1 fruit_protein_pKIWI502-like [MW = 33.43 kDa]

No. of times detected



log(intensity)



Values from



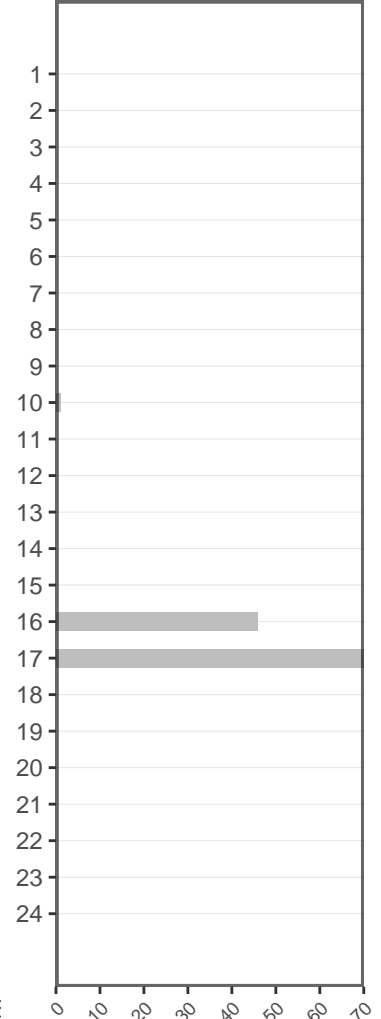
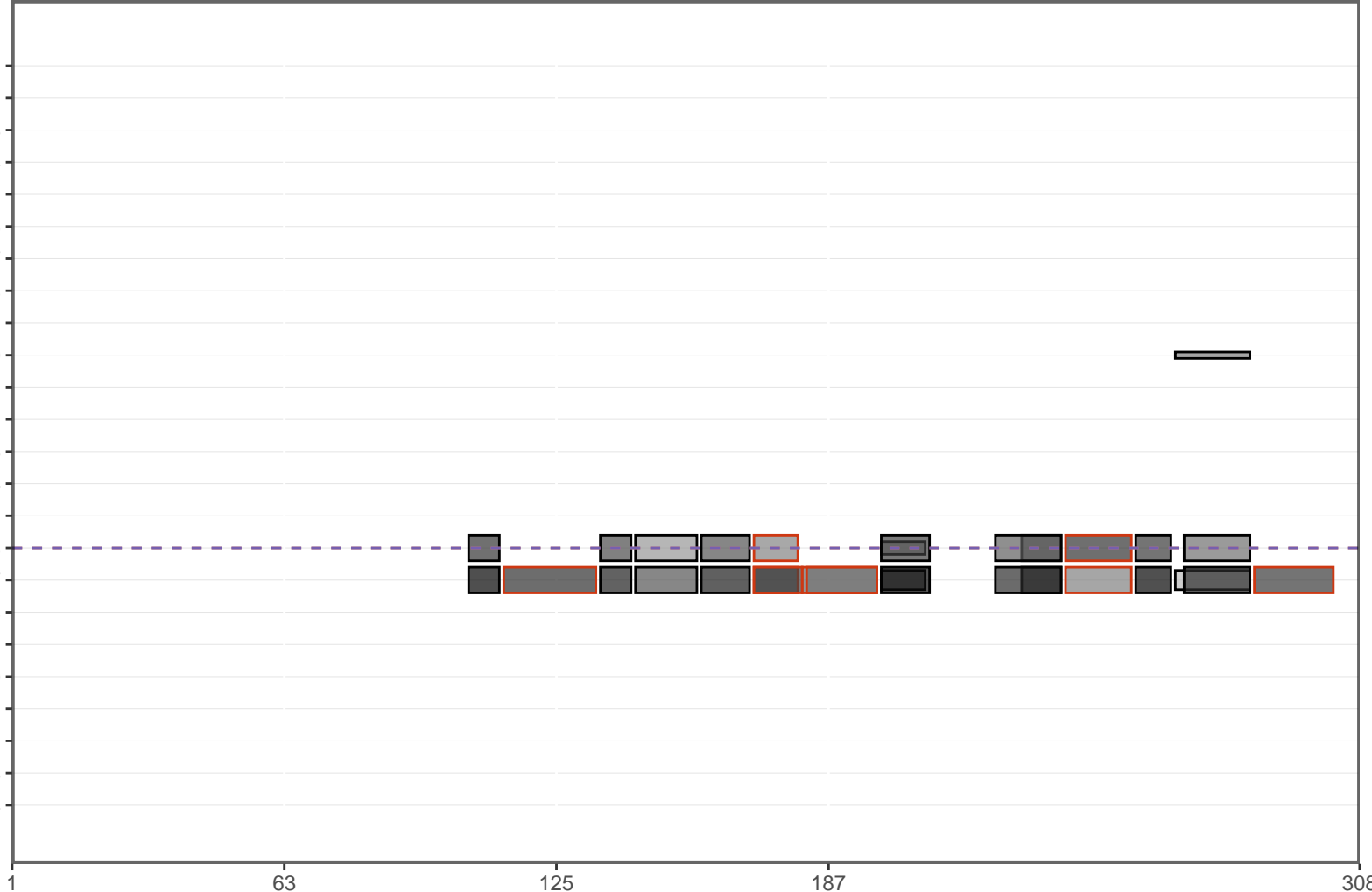
MW indication



Molecular weight



Gel Slice



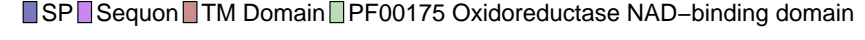
Protein length



Pfam domains



Pfam Description

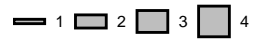


Protein sequence:

SISGSTAELLCCOLKGDVVELSGVMGKGFDLQISPKKYQTLIFATGGGSPIRSLIEAGFSADKRSDVRLYVGARNLKRMAYGDRFENWASG6VWVVPVLSGPDADWTGERGVQAAAFARAKNFPOSTGAVLGGGKGMAEVITALLADGVSTEKLNKPF

NbL18g00520.1 ATP_synthase_subunit_beta_mitochondrial-like [MW = 66.27 kDa]

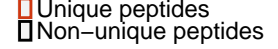
No. of times detected



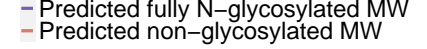
log(intensity)



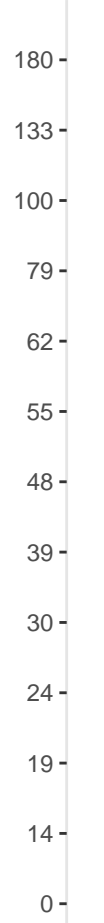
Values from



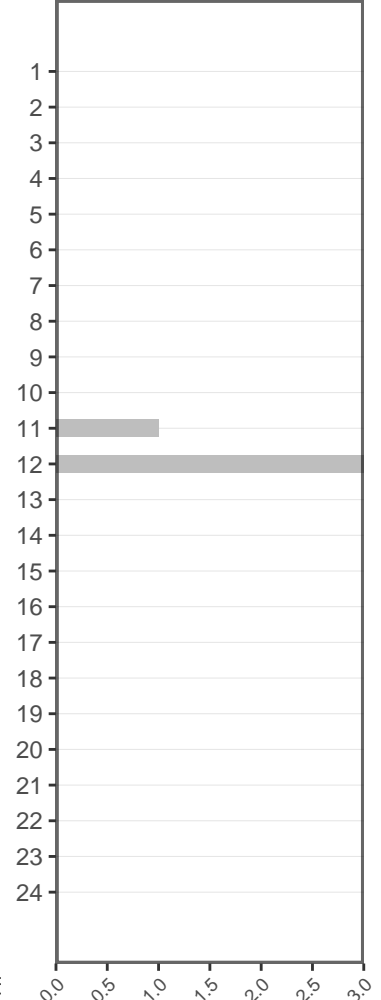
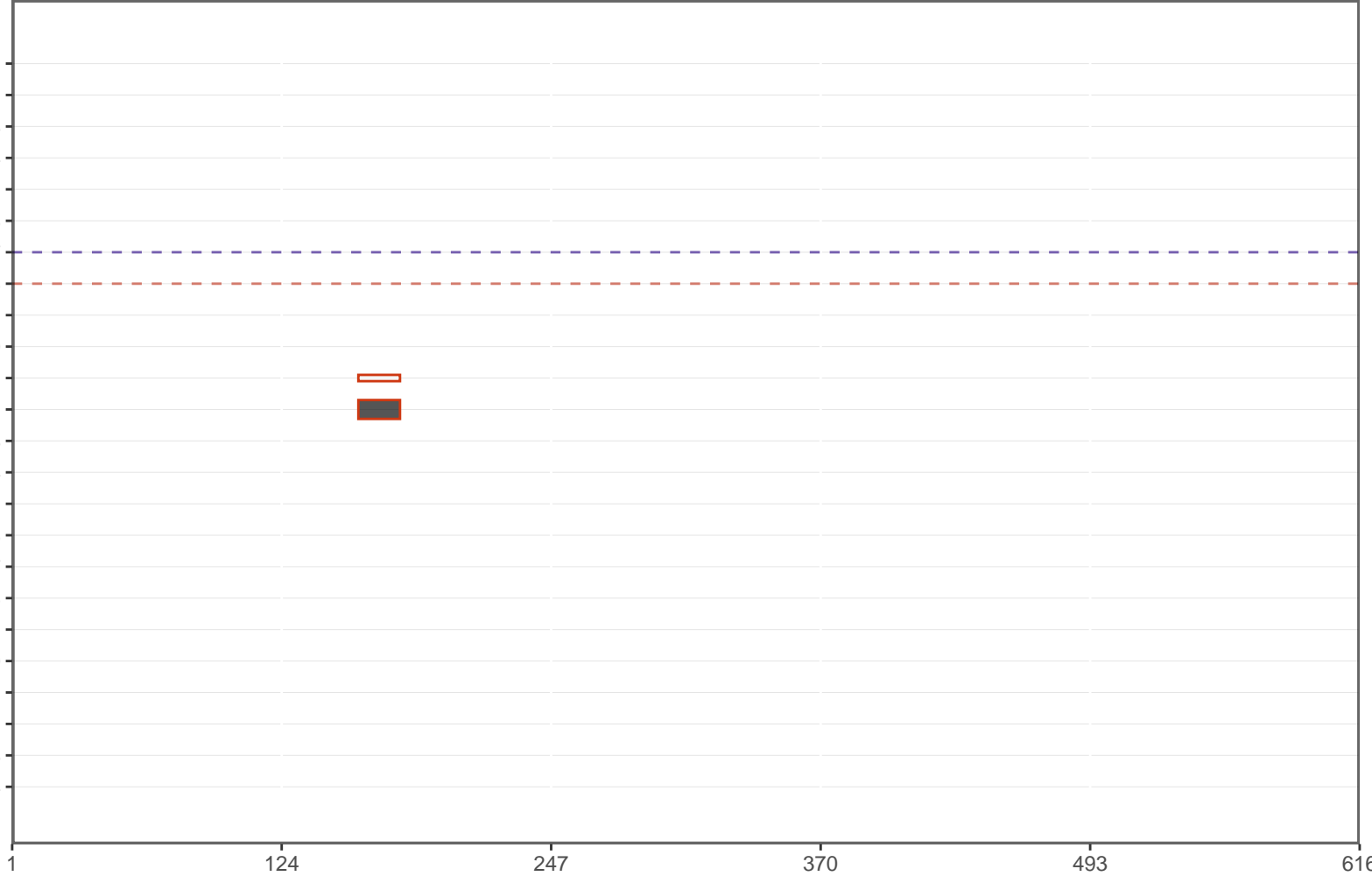
MW indication



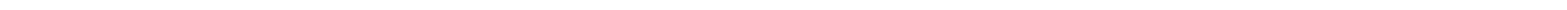
Molecular weight



Gel Slice



Protein length

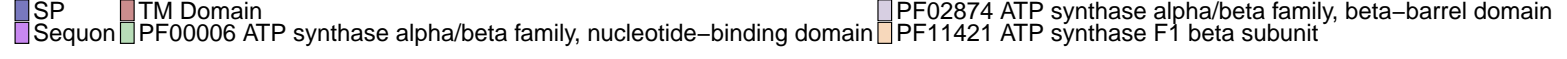


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

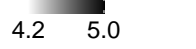
ITVLMELNNVAKAHGDFSVFAGVGERTRREGNDLYREMEISGVKIKGDKSSEKCALVGGMMPEPPGARARVGLTVAEHRDAEGGDVLLFDINFRFTGANSEVSAALLGRIPAVGVYQPTLATLGGIGERITTTKKGKSTSVQAIYVPADDLDPAPATTTFAHLDDATVLRGISELGNFVADPLDSTSRMLSPHLGEDHYNTARGVQKVLGNKYKLGDIIALGMDELSEDDKMTVARARKIGRFLSGPPHVAEFTGAPGKYVDLKEISNFDGKLDGKYDDLSEGSPT

NbL18g00010.1 60S_ribosomal_protein_L31-like [MW = 13.91 kDa]

No. of times detected



log(intensity)



Values from



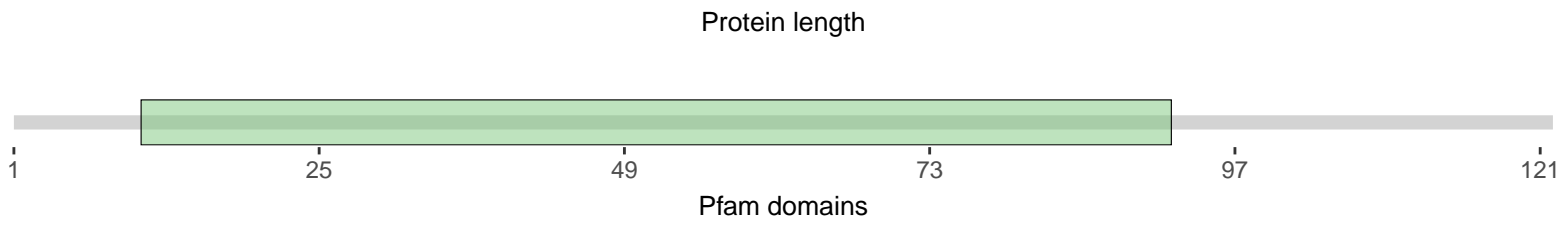
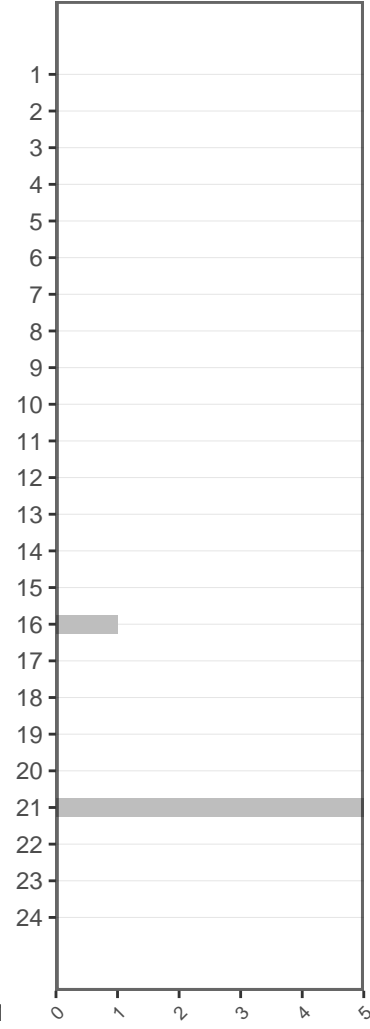
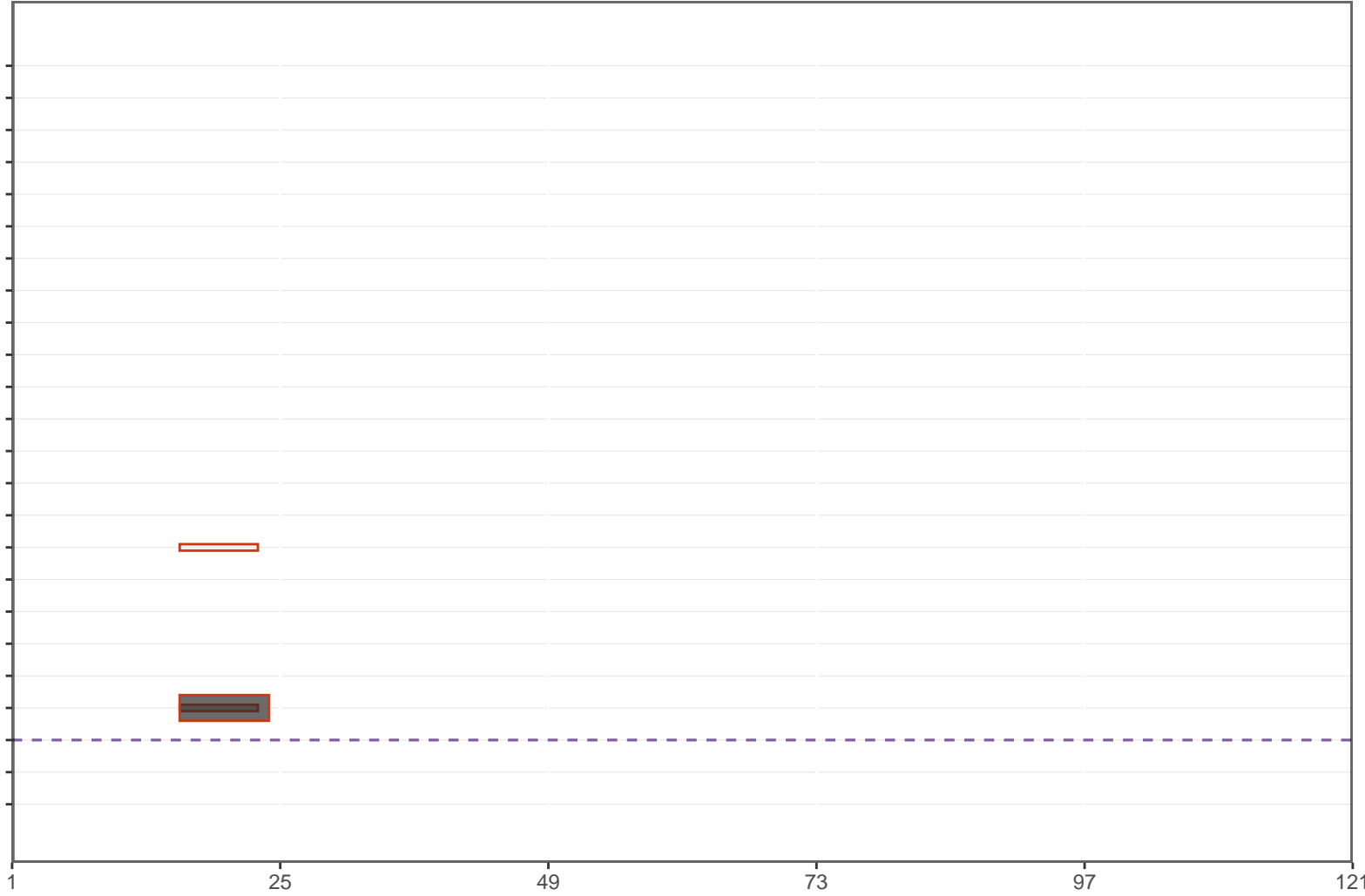
MW indication



Molecular weight



Gel Slice



Pfam Description



Protein sequence:

AMSTKDIRVDVGLNKHWSRGRVPRRVRVRIARKRNDDEDAKEELVSLVTVTEPPELGLGLTKIEEDD

NbL17g28270.1 nuclear_pore_complex_protein_NUP98A [MW = 105.87 kDa]

No. of times detected



log(intensity)



Values from



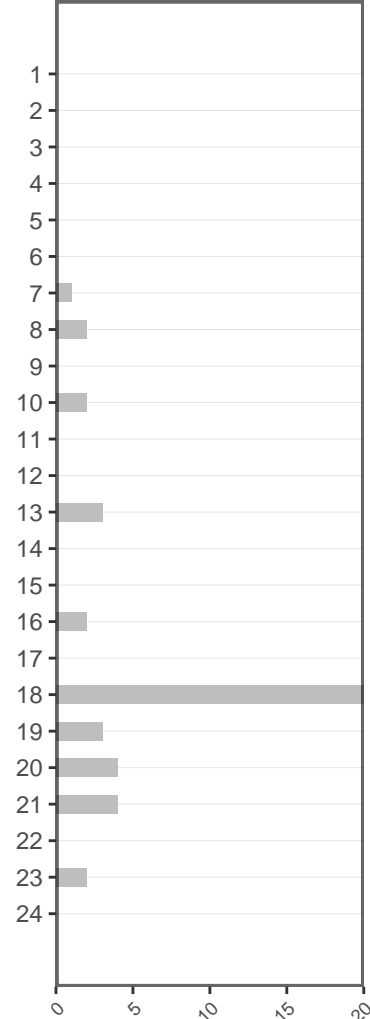
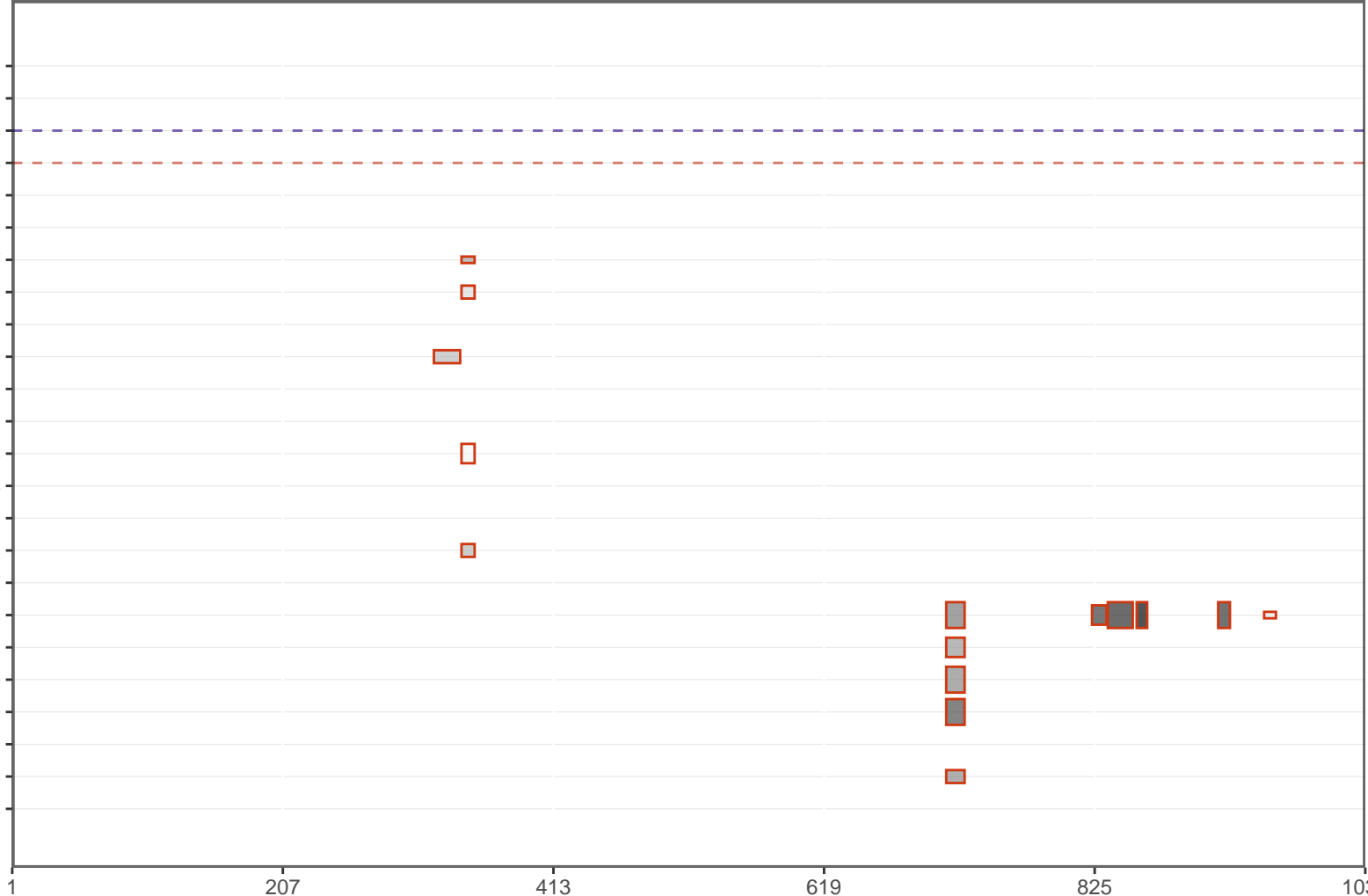
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

*GPSLSFGNTQSSPLFGQETTPFSGGTS6AFGGTAS6FGG66TPAFGG6NLFSTP6TGF6G6NLF6SAPLLNTSNT6GFGGTTPL6LSTPF6LQTP6G6T6P6F6S6N6Y6G6T6G6G6A6S6FG6G6T6P6L6F6Q6P6A6N6G6S6V6A6D6P6W6T6N6F6G6T6L6P6M6P6M6S6I6R6T6G6T6S6S6I6Q6Y6G6S6L6P6V6D6K6P6V6R6I6S6L6L6T6R6H6L6Q6R6R6V6L6P6A6R6K6Y6H6P6T6E6G6A6K6Y6P6F6S6D6E6T6P6T6K6A6L6F6V6R6N6R6N6P6R6L6V6R6L6D6W6P6S6R6G6L6K6V6S6S6K6Y6T6P6A6H6N6G6K6I6P6V6F6A6P6T6T6S6A6D6K6D6L6

NbL17g28220.1 soluble_inorganic_pyrophosphatase_PPA1-like [MW = 24.12 kDa]

No. of times detected



log(intensity)



Values from



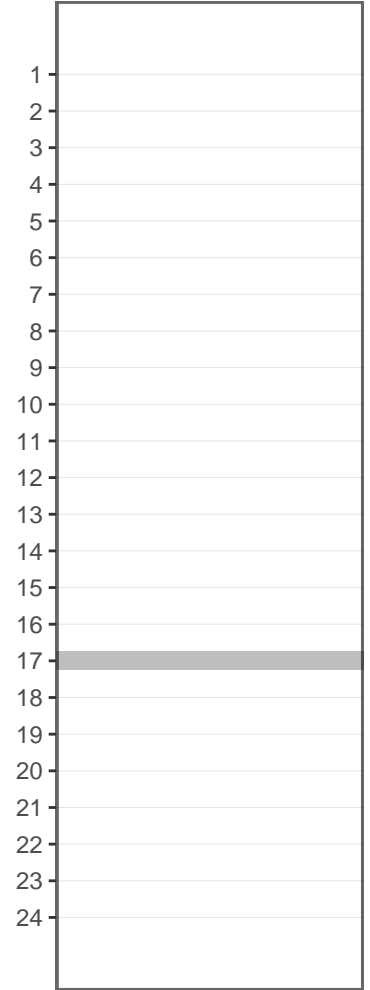
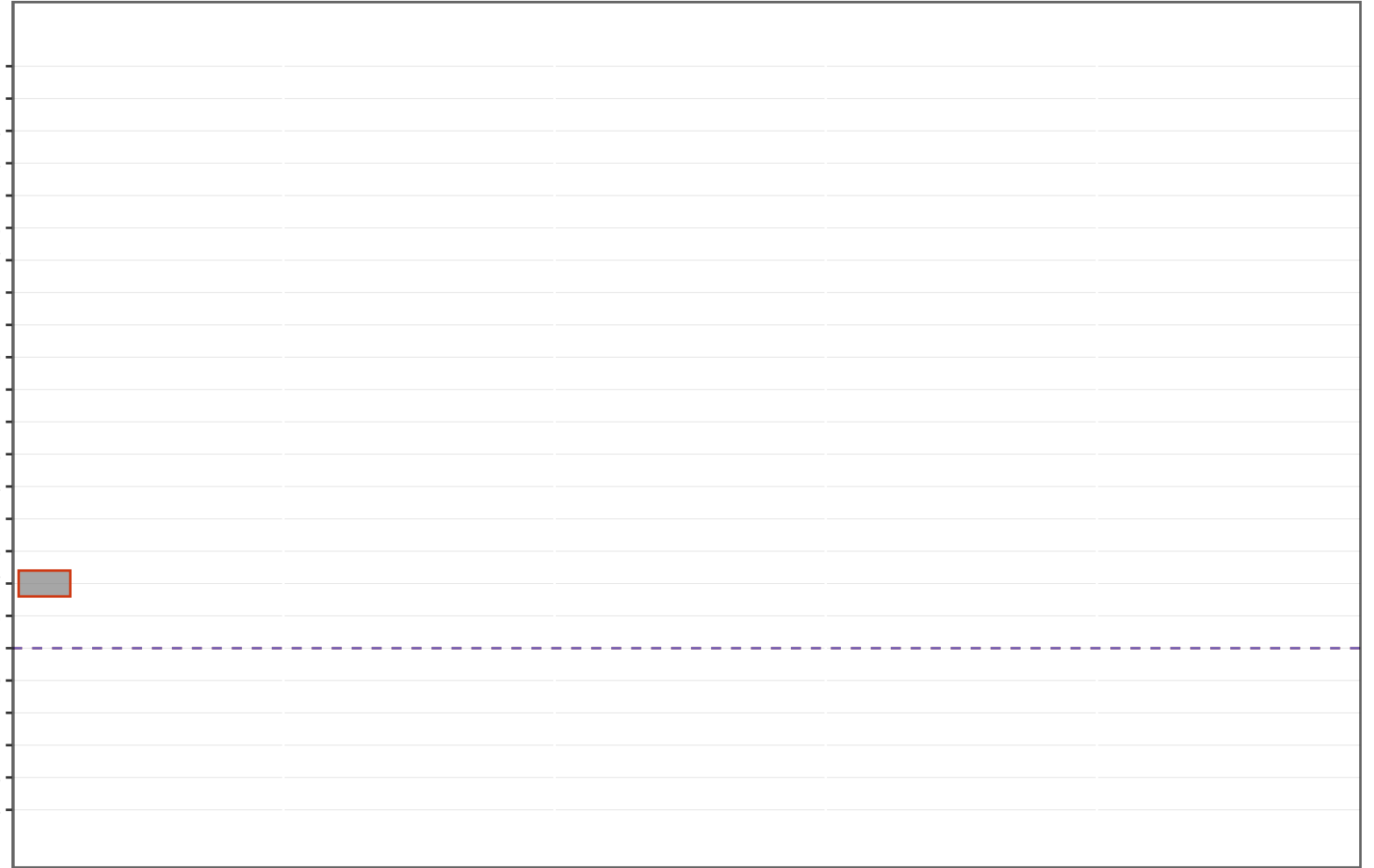
MW indication



Molecular weight



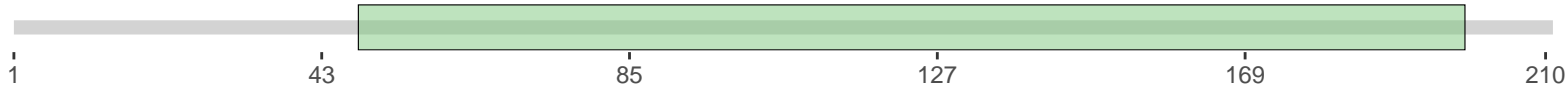
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

MLCEDNDPMDVLLVLDGEPVLPGGFLRARAGLMPMDGGGKDDKIAGVADDPEYRHYTDINQLAPHLAEIRRRFFEDYKLENKEVWNEFLPNTAVDAIGYQMDLVAEYLGTLRK

NbL17g28120.1 putative_glucose-6-phosphate_1-epimerase [MW = 34.21 kDa]

No. of times detected



log(intensity)



Values from



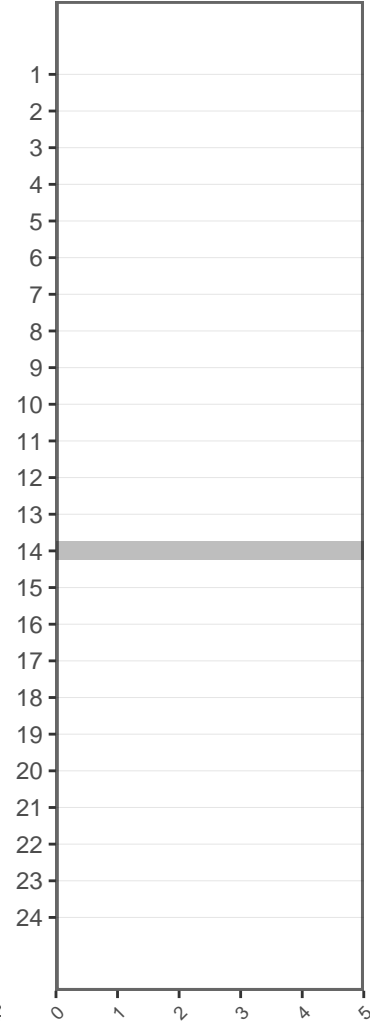
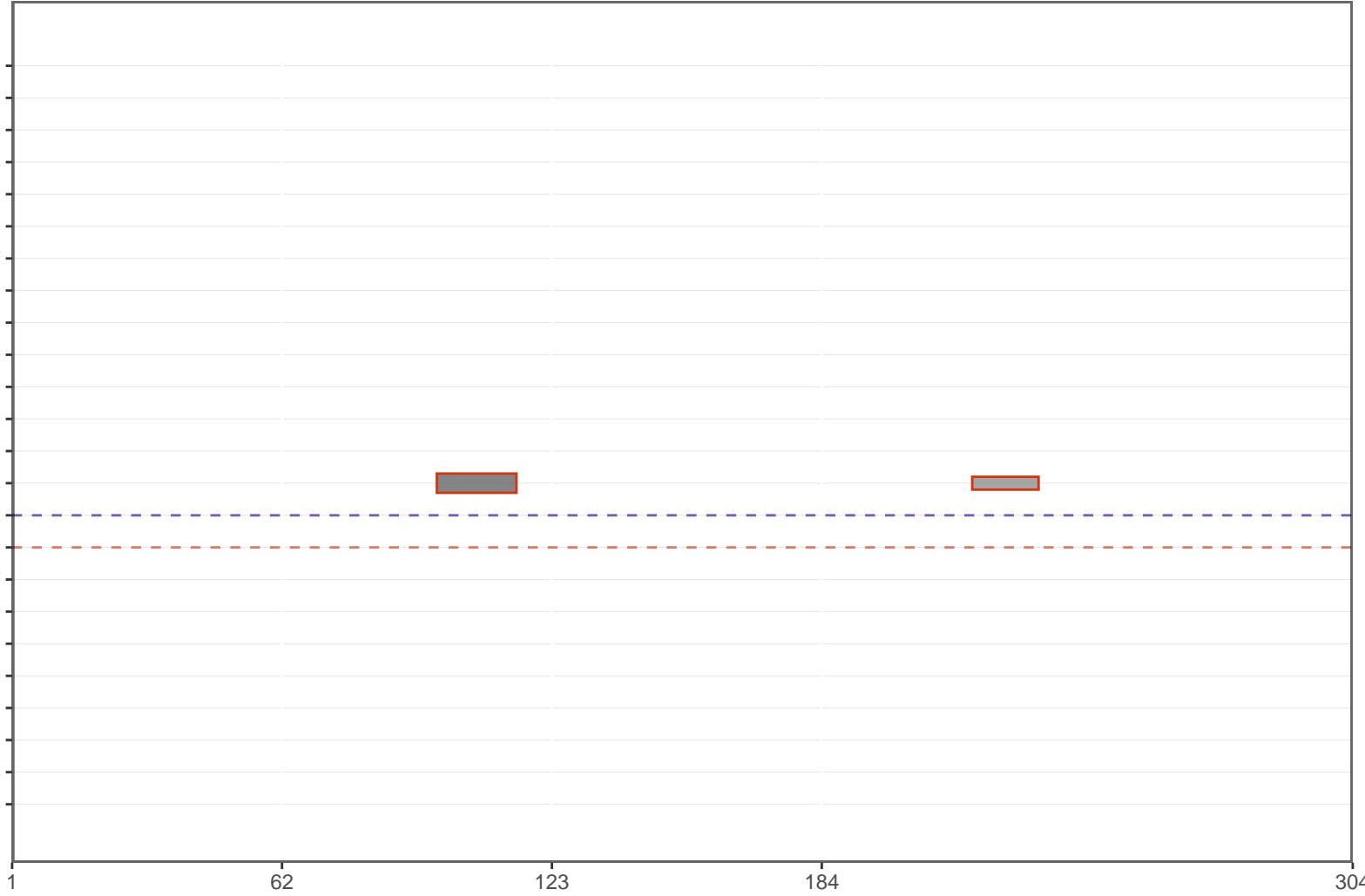
MW indication



Molecular weight

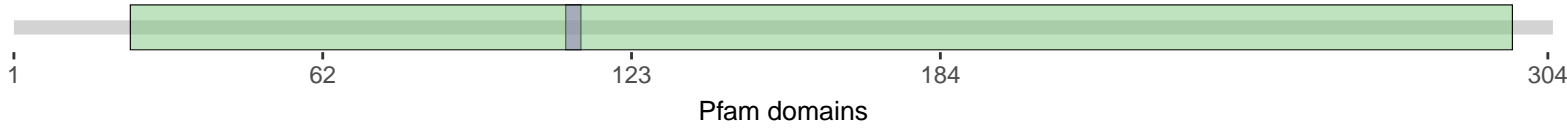


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TEFRLRVTLAVDGSITUSRIRRNKPKPFSSBIAVHTYFALSDISEVRLGLELETLDYLDNLCNRRERFTGGDALTETEVDRIYLTSSDVIAFDHEKRTFKVIREGLPDVAWVNPWEKKKKTADFGDDEYRHMLCVDSAAIEKPTFLKPGEEWTRGLELSVMPSS

NbL17g28080.1 myosin-11-like [MW = 159.57 kDa]

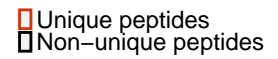
No. of times detected



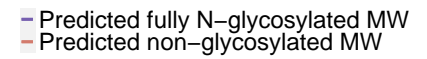
log(intensity)



Values from



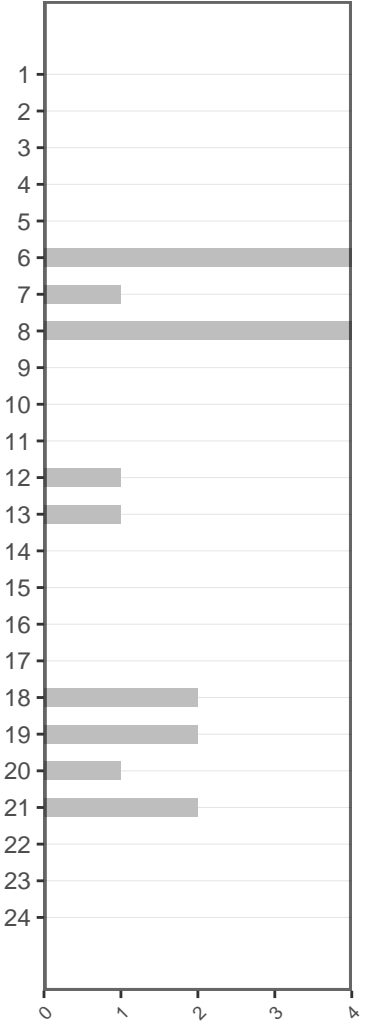
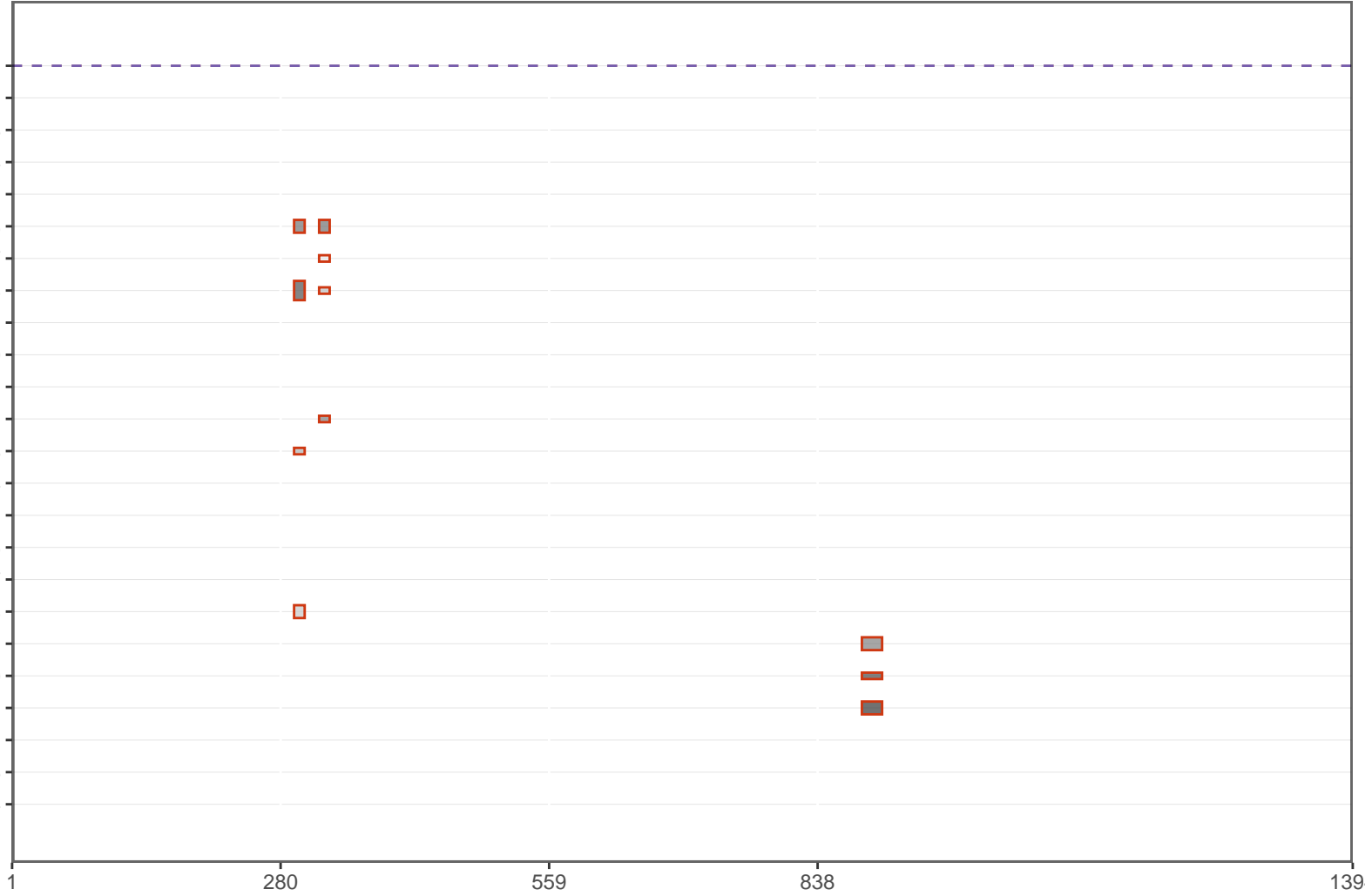
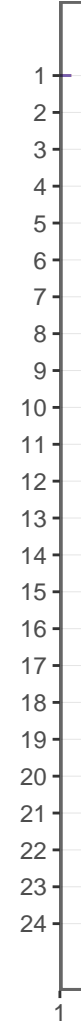
MW indication



Molecular weight



Gel Slice



Protein length

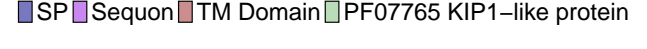


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

...OKKLEDVQNEASTGNALTEEVNELSGQDELGKERGGLELAERGGKQESTESLAGAENQNTFELSQQVDSQDEKLGKEQEEAFVKKLVEEKDGLVVQVNDLQAEVYKLGEGQNTLEENISSANNENNLLTEEGYFLKGLSELENTLVKVVDEHEALQKKLELVQNESSTQGLALTEEVNELRQGGELLGTEKSGLELVLTERGKLGESTESLAGAENQNTFELSQQVDSQVLETKLKEKEEADGKLVVEEKDGLVVQVNDLQAEVYKLGEGKSTFEENISNTENNLLKKEEKESLLKTSLEI

NbL17g27940.1 probable_polygalacturonase [MW = 53.73 kDa]

No. of times detected



log(intensity)



Values from



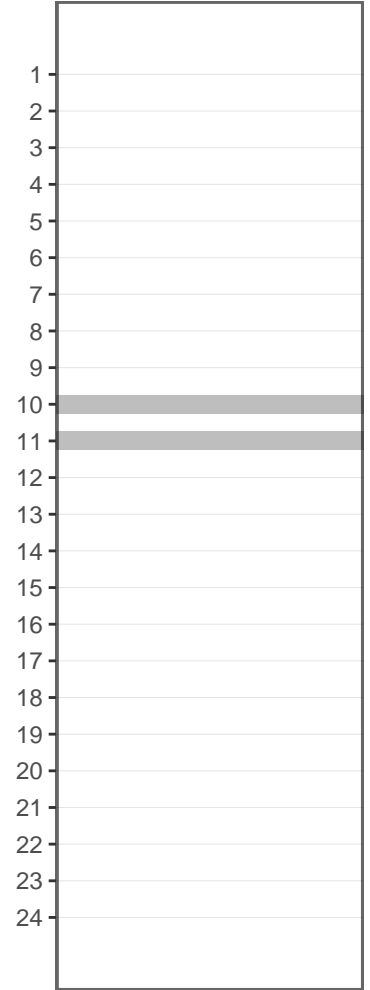
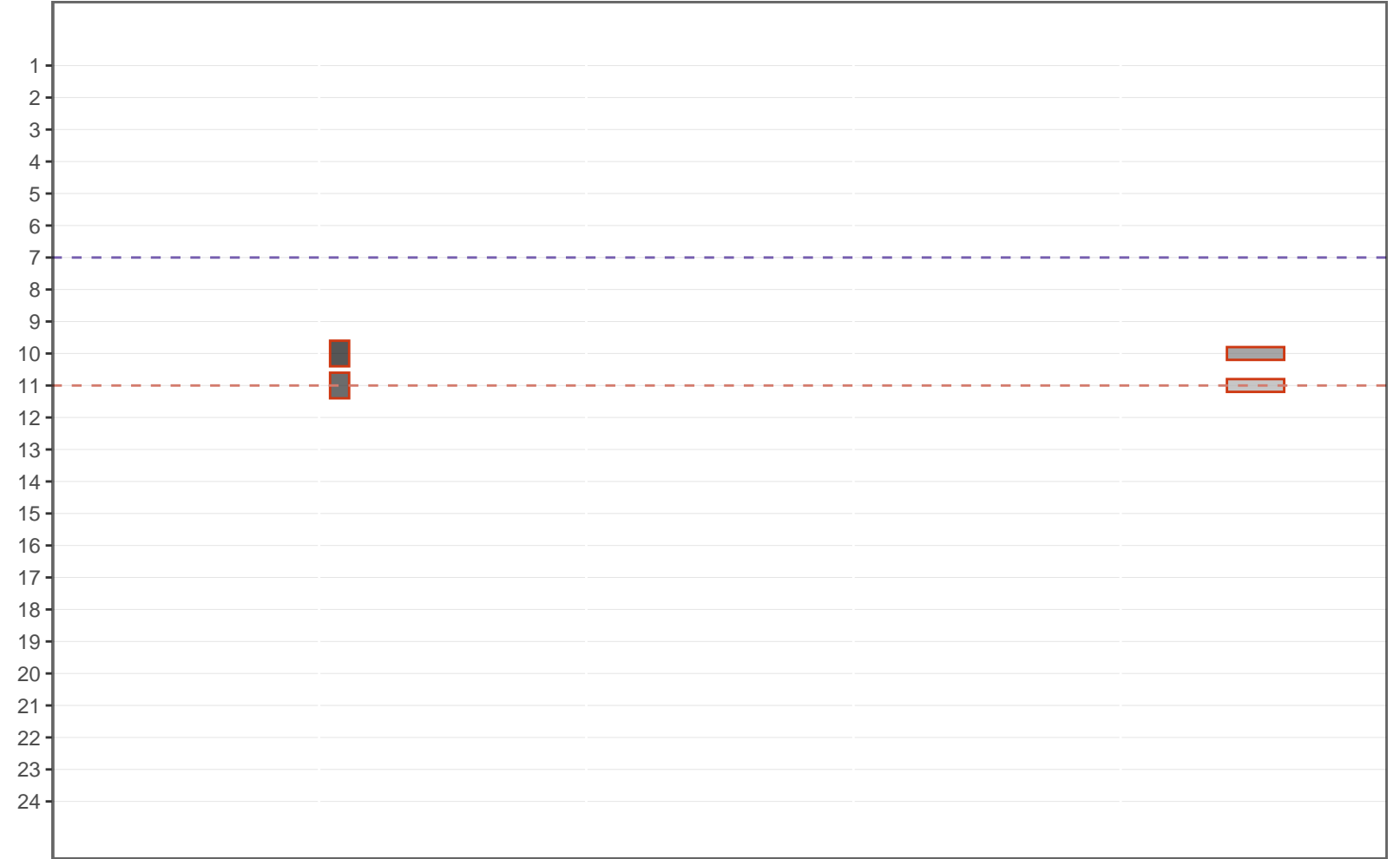
MW indication



Molecular weight

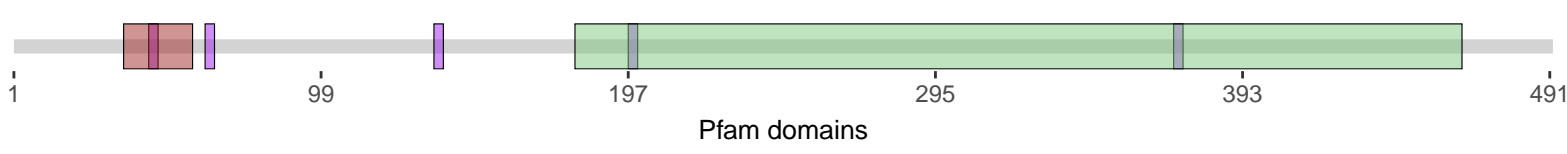


Gel Slice



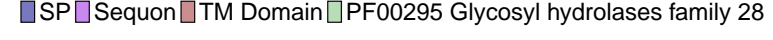
Peptide counts over 4 repeats

Protein length (1, 99, 197, 295, 393, 491)



Pfam domains

Pfam Description



Protein sequence:

IRGIISNIFKNSPFWNHPVCGSNVIRVYTLAPADSPNTDGDIPDSSSHVQIEDSVYSGDDLWVKSGVDQYSGVYGRPSHGHTIRRTIGSGSPFAGVAGSETGGGVDVLAEHNLFMGDIYGHKKTNGRGRGMRINTVSNVYMENTRTGKAGVDGHPDKEFNALPVGKIKKDWGEKVLQAGLRGLKNSFFSGICLNLHGNKPGPRNSPWKGSVDVGAAGVSPWPCSELTSSGQGTGAGSTSF

NbL17g27850.1 long_chain_acyl-CoA_synthetase_4-like [MW = 25.45 kDa]

No. of times detected



log(intensity)



Values from



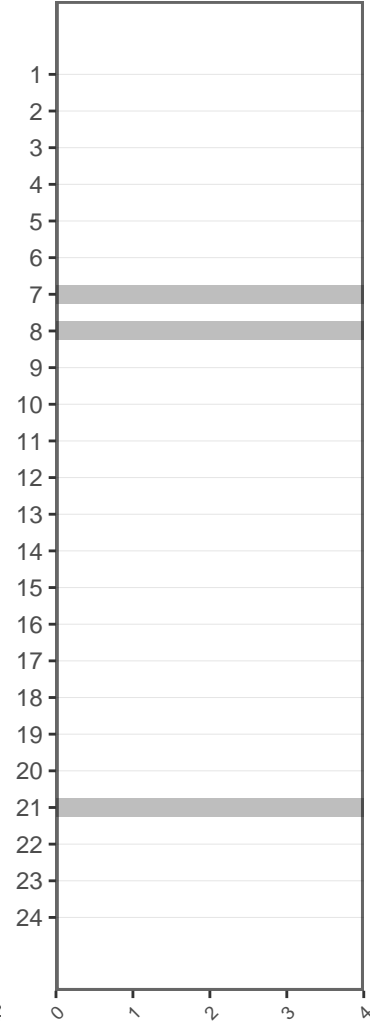
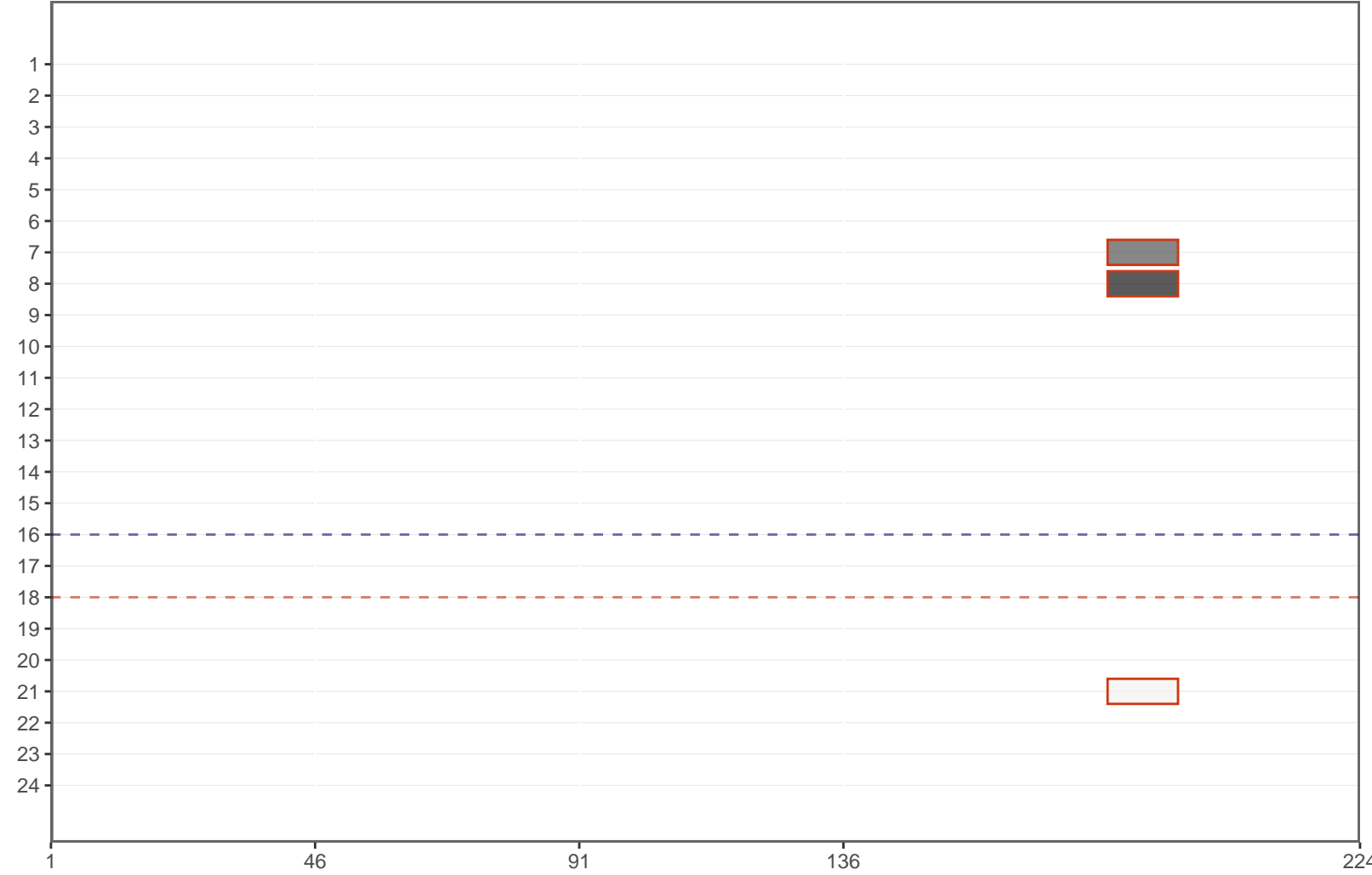
MW indication



Molecular weight

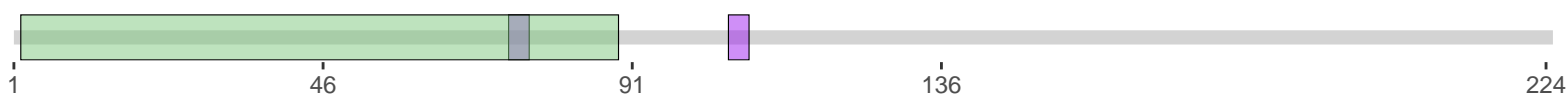


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NLENYGNSSLDISWYGNFSFESFLWLNPNGRAGEVWAGQNGISGDFDGLGENPKVKEYLGLTKAGKEKRLKGFEFKAVHLDAQPFDMERDLITPTFKKRPQLLYKYYKISLLIGWML*

NbL17g27770.1 nucleoside_diphosphate_kinase_3-like [MW = 25.75 kDa]

No. of times detected



log(intensity)



Values from



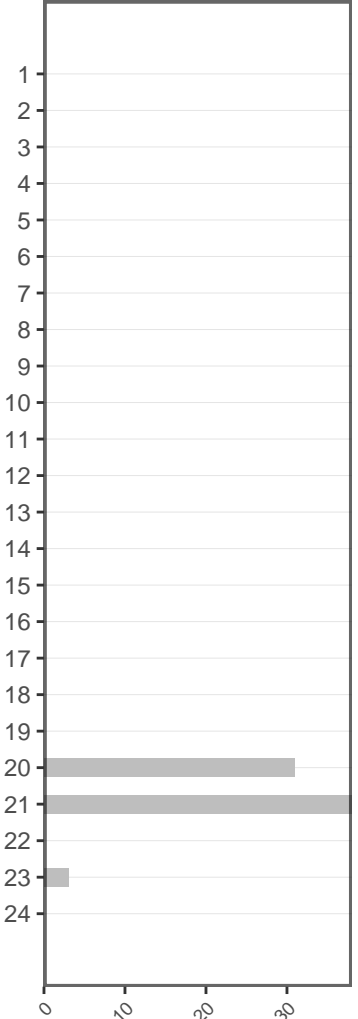
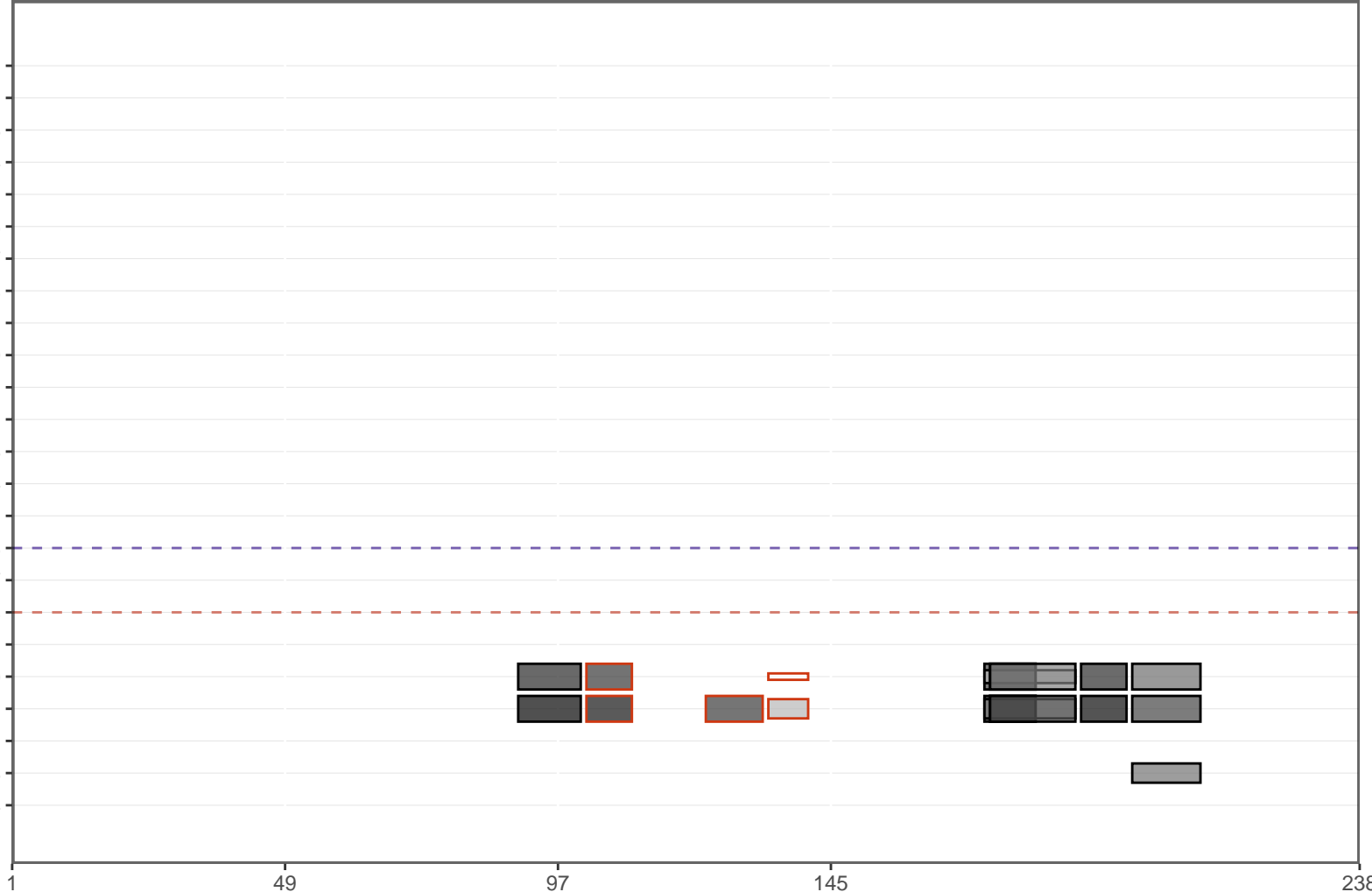
MW indication



Molecular weight

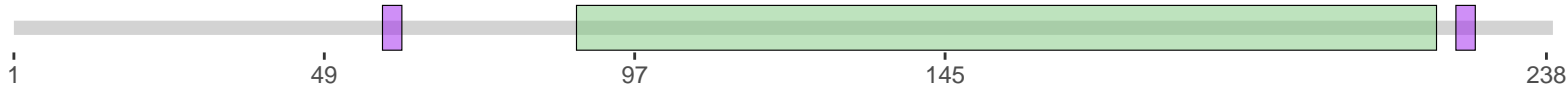


Gel Slice



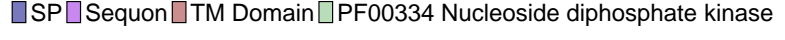
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SEIIARFERKGFKLLWKKVIVPEKFAQKHYYDLGERFFNGLGDFL6SGPVLAMVWEEGQVIRYGRKLGATDPKSEPTIRGDLAVVGRNIHSGDGPETAKDENLWFKPEELNNTSNSEKRWVYGDN

NbL17g27710.1 uncharacterized_LOC109210112 [MW = 22.28 kDa]

No. of times detected



log(intensity)



Values from



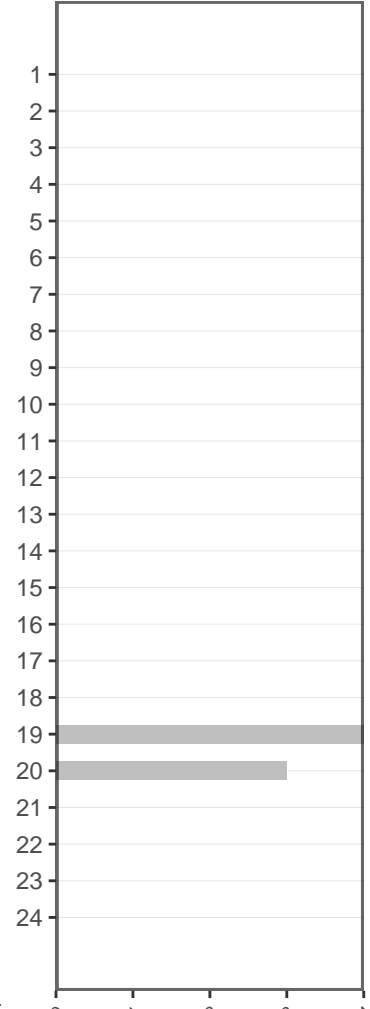
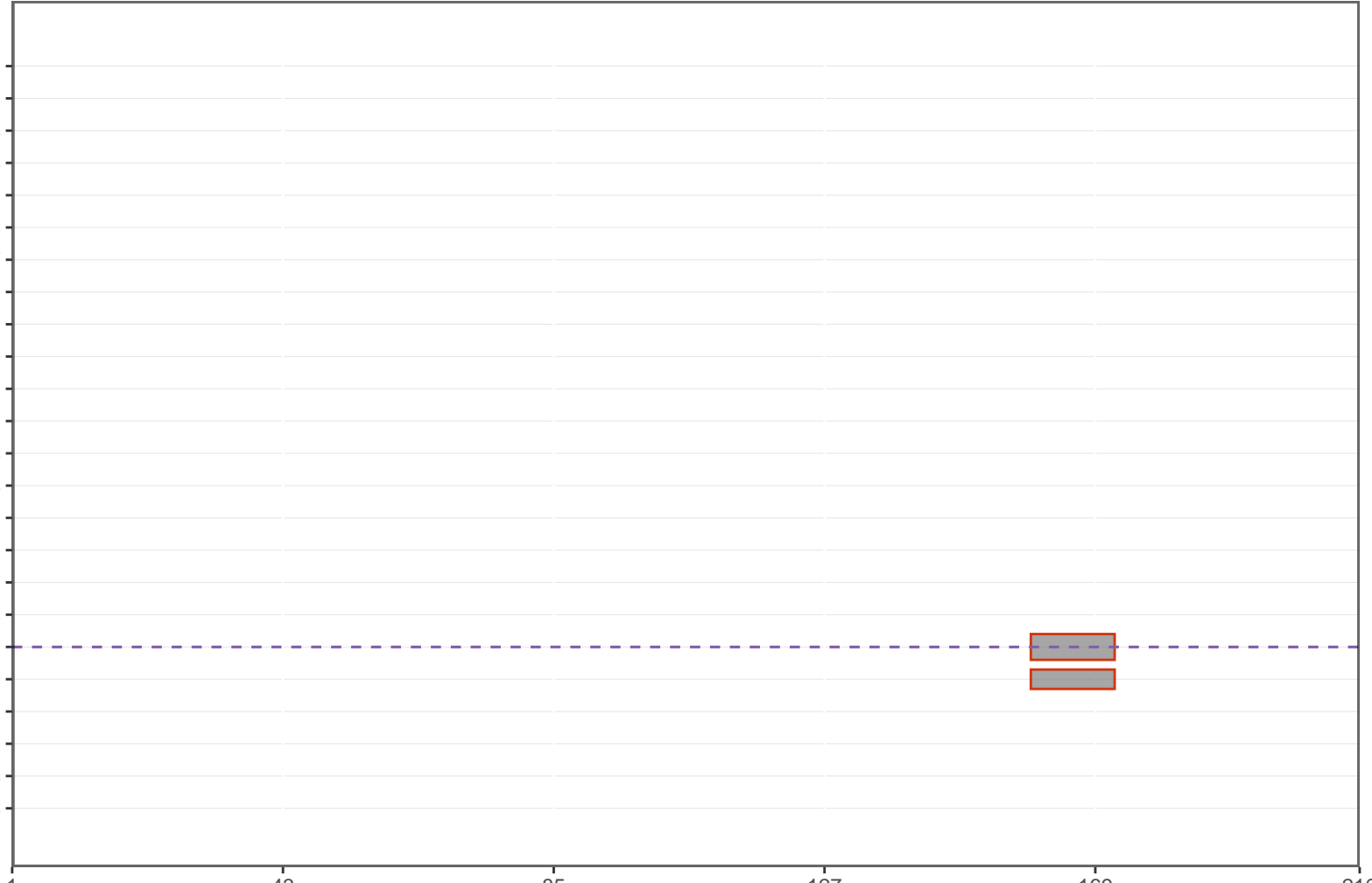
MW indication



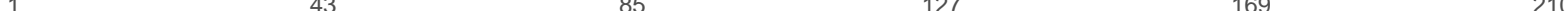
Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description
 SP Sequon TM Domain

Protein sequence:

INDESTVLPFGAGGAGGREGREEIRGNGEGRIKGGIATVPGFGWHPKAYRPGPFVASGGRYRRFGGMDDEVVSGSGRGRASSAGTDAEVQSSLFGRKPSRFGNLNLIAPVRH

NbL17g27580.1 signal_recognition_particle_19_kDa_protein-like [MW = 15.29 kDa]

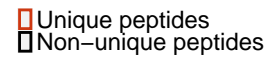
No. of times detected



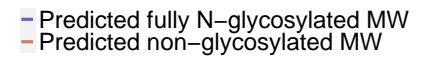
log(intensity)



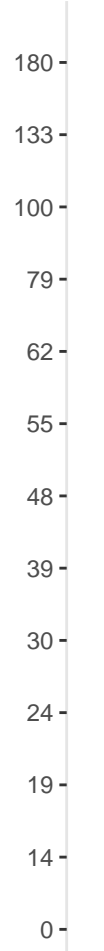
Values from



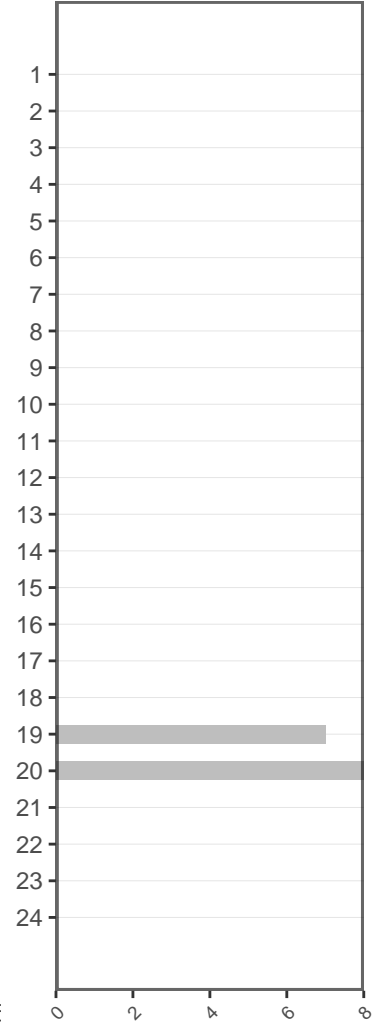
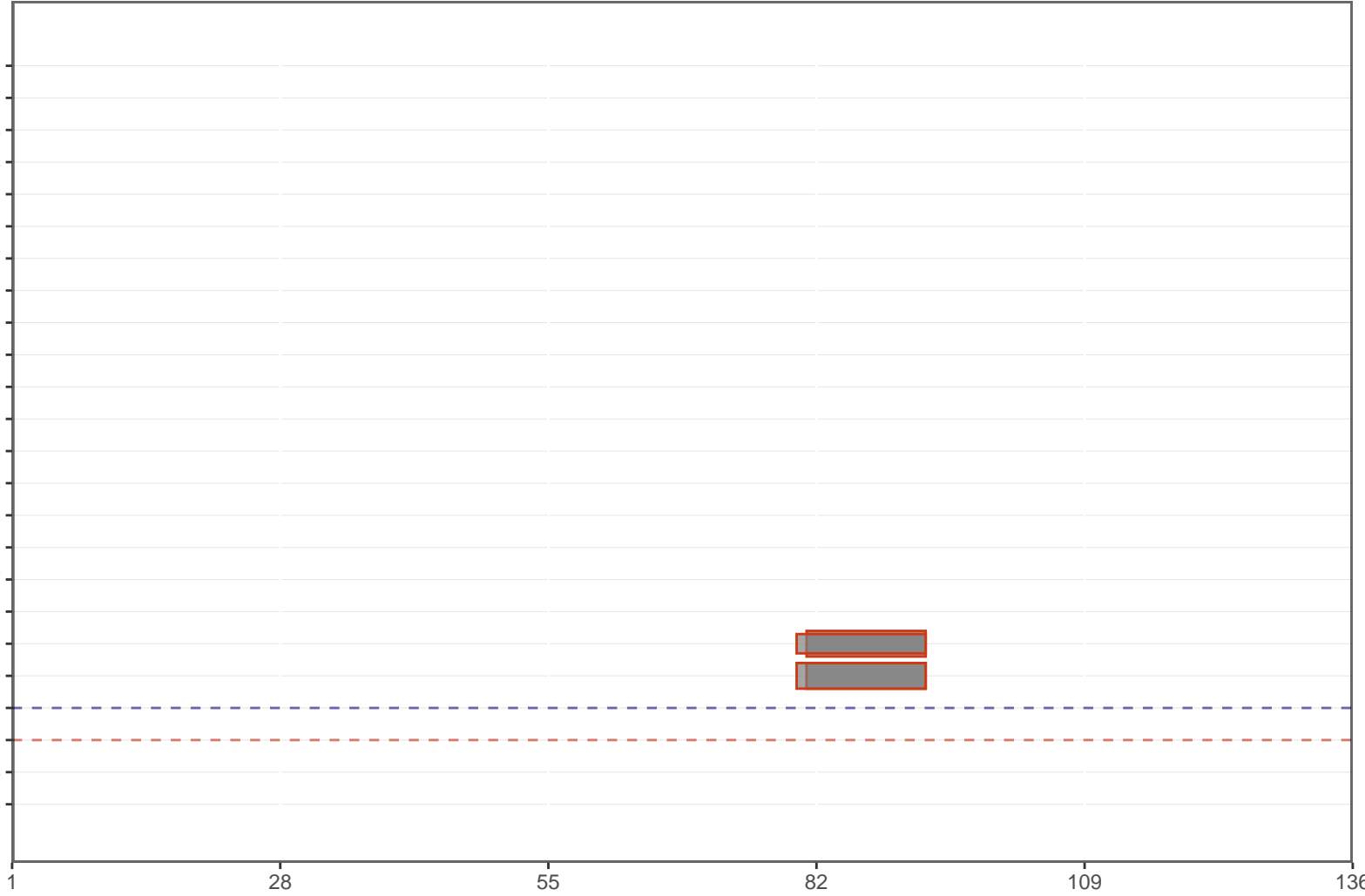
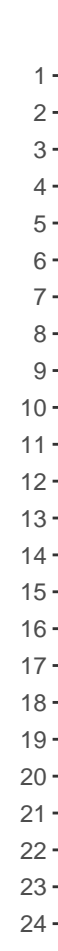
MW indication



Molecular weight

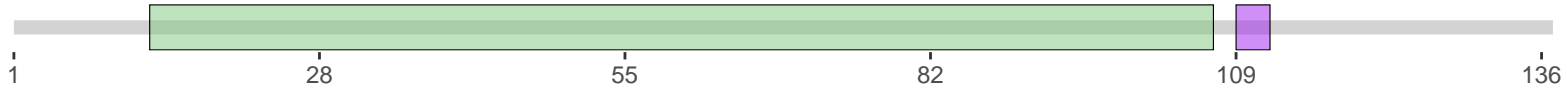


Gel Slice



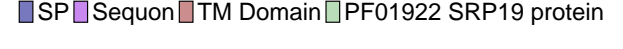
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AIELDKAYPRDFMGRGVRVRLIKKEDGTTYNPAISRSRGLMHVAELVRKHFNRTKKQEPASSAAGSSKSGKGGKKR1

NbL17g27510.1 luminal-binding_protein [MW – SP = 70.53 kDa]

No. of times detected



log(intensity)



Values from



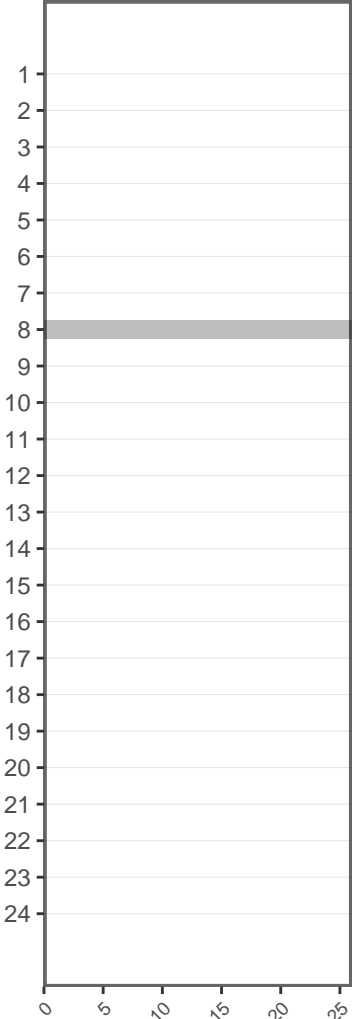
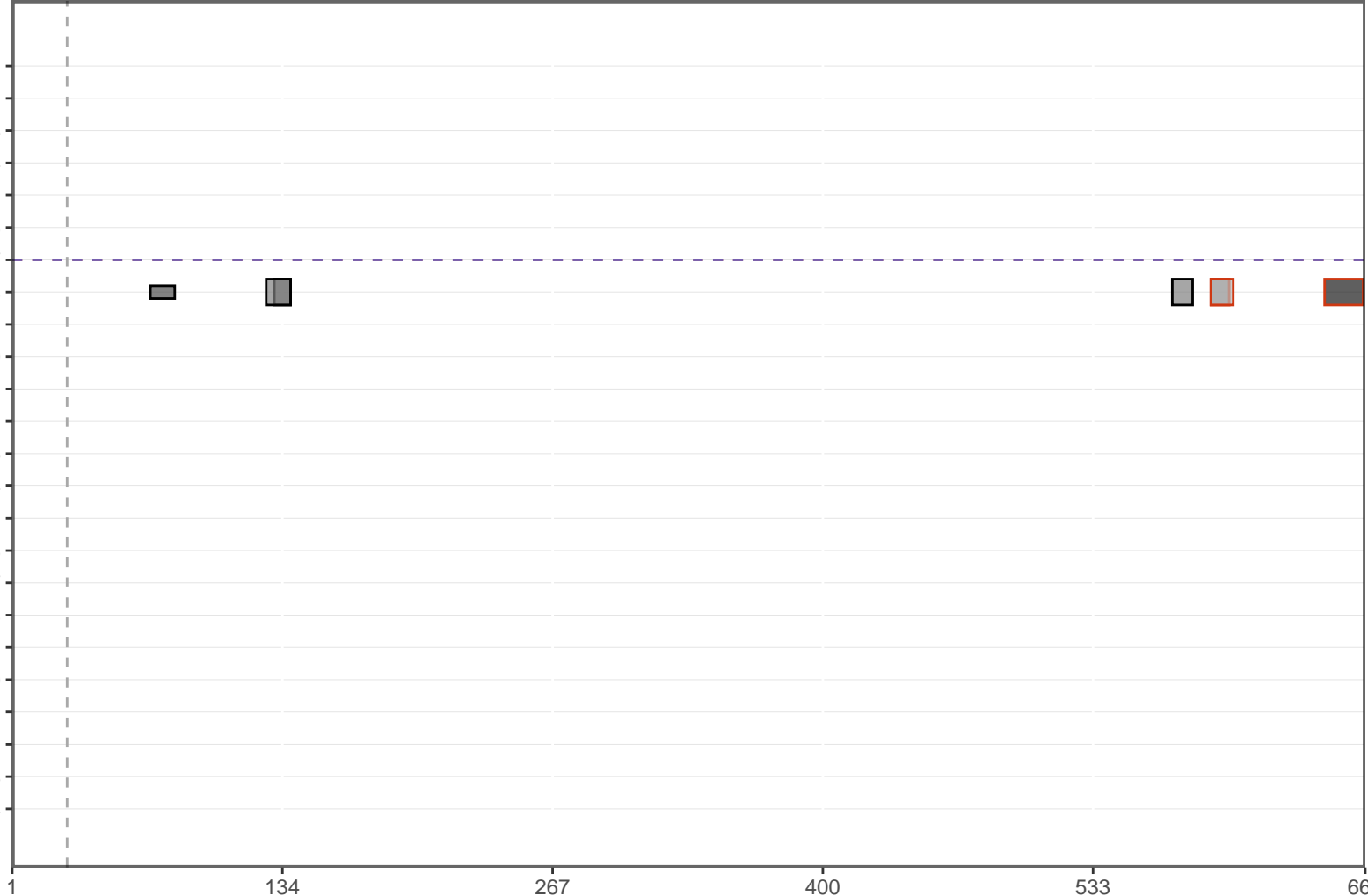
MW indication



Molecular weight



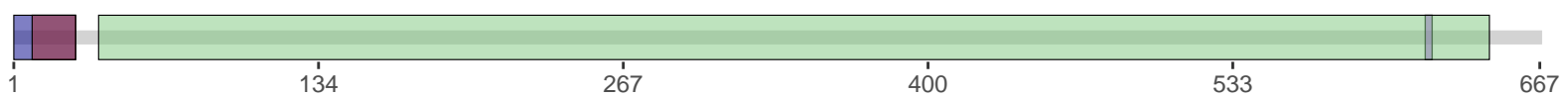
Gel Slice



Peptide counts over 4 repeats

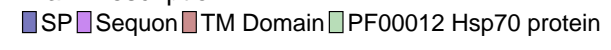
1 134 267 400 533 667

Protein length



Pfam domains

Pfam Description



Protein sequence:

IDFSEPLTRARFEEELNDLFRKTMGPKKAMMEDAGLEKNQIDEIVLGGSTRIPKVGQLLKNDYFDGKPKNGVNPDEAWGAAVGGILSGEGGDDEKDLLLDVAPLTLGIETVGGVMTKLPKIPNTVPTKKSQVFTTYGDDGFTVSGVFEGERSLTKDRLGLKFDLGIAPAPRGTTPQIEVTFEVDANGILNVKAEKDKGTGKSEKITTNDKGRLSGEEIERMVRRAEEFAEEDKKVKERIDARNLSLETYYNKNKNGINDKDLADKLEBVEKEKIEATKALELWLDGNS

NbL17g27460.1 probable_trehalase [MW – SP = 63.48 kDa]

No. of times detected



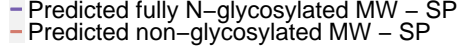
log(intensity)



Values from



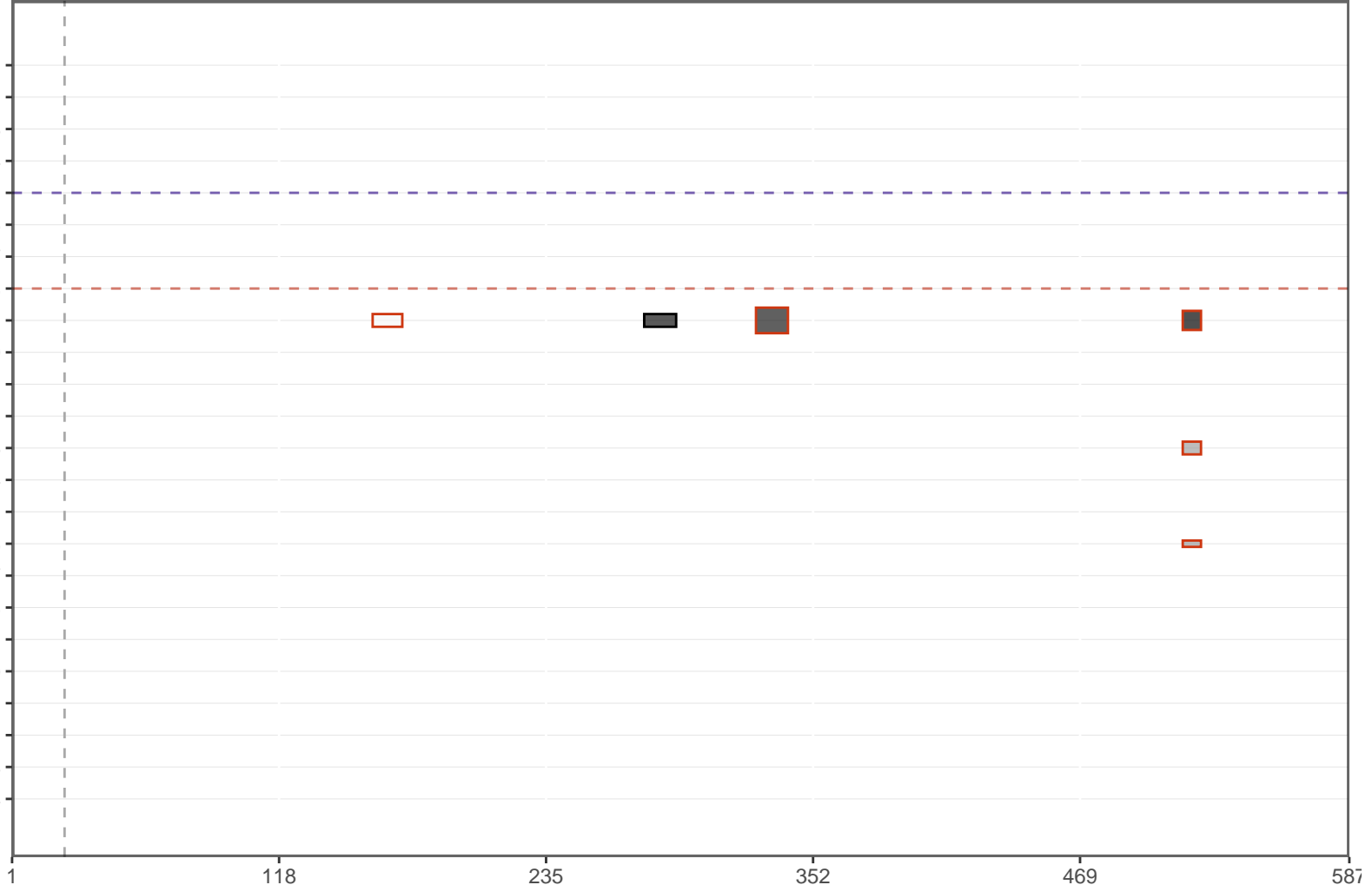
MW indication



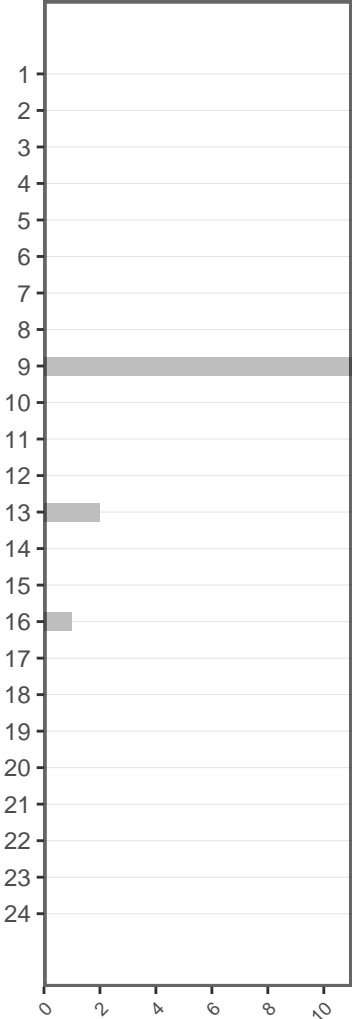
Molecular weight



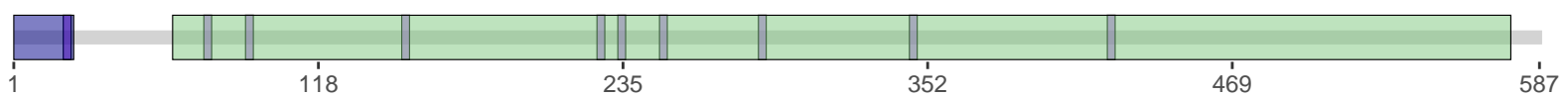
Gel Slice



Protein length

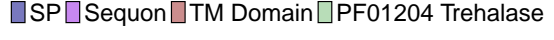


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IQGNSHLSLRYYAMWNNRPPSSSTIDGETAKLPLNGEKRLQYRDVASAAESGGWDFSSRWMRNGSDLTSTTTSIPVDLNAFLKMKELDAFLANLVGESSIHAFTEASGNRQKAMNSILWNTMGGWGLDYLWLNQNSNTSEDPHYWEDLHGNKGSFASNFVPLWAEILLNSDDITTKQYVQGLKSSGLLQPGIATLNTGGQWDFPFGWAPPLQIHIEGLRERLEEAKLAEDAVRWIRRTNYWAYKKTGAMHEKYDVTKGGAYGGGGGEVYPTQTFGWANGVLLALEE

NbL17g27220.1 uncharacterized_LOC107784855 [MW = 64.25 kDa]

No. of times detected



log(intensity)



Values from



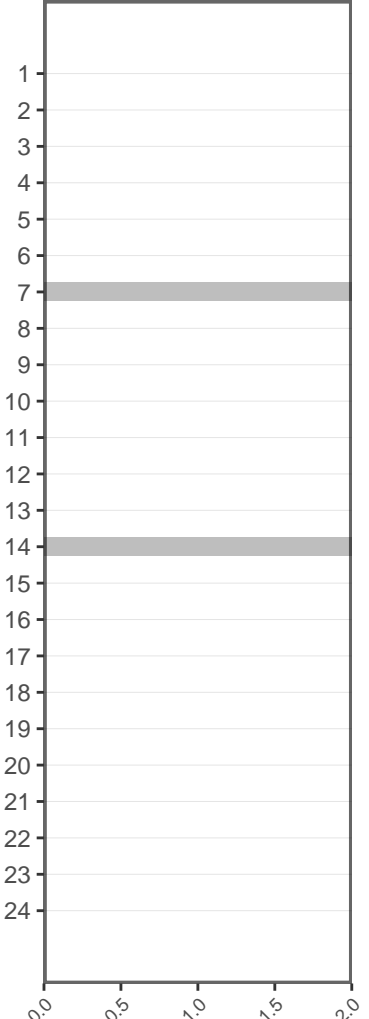
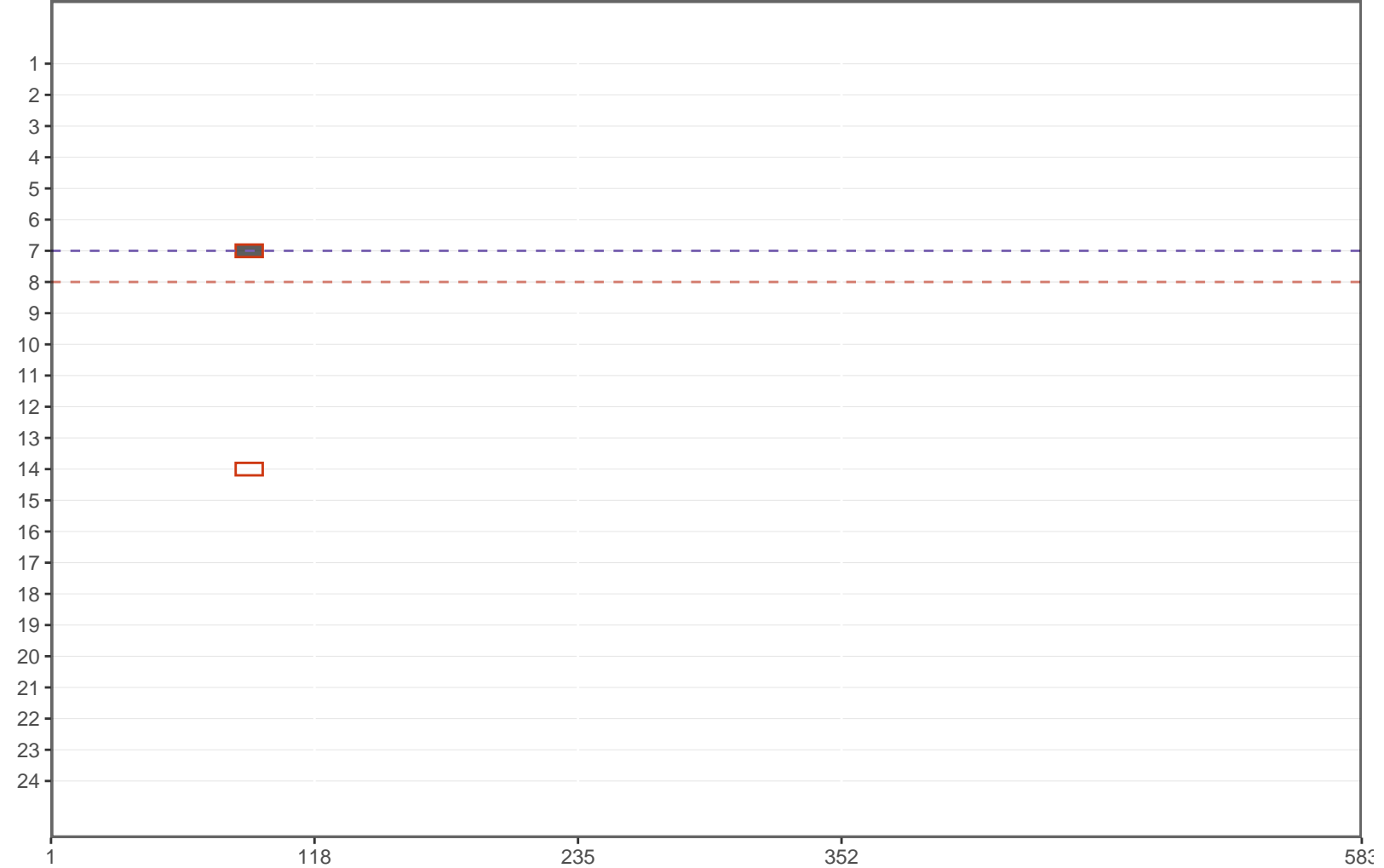
MW indication



Molecular weight



Gel Slice



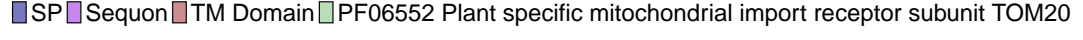
Protein length



Pfam domains



Pfam Description



Protein sequence:

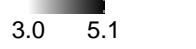
ISDRAKIRGRTEAEELWKGATNVEKAVGLNWNWSPQALNNWGLAGELGSAIVFRREKLTIVKTAISKFRRAIQLGDFDHRAYNFGTVLYGLAEDMSRTGGAVNTKDISFNELYSGSAHYAAAHAKLPNYSVYTSALKLVIRSMVQNLLEGSWYVQLGSCNEVLSKALIVFQLPLPLKVVSLTAPPDAGNPLAFHSDWKRGGFVLNHEGLGQISKVDQRHMSRSLGSEADTSPNGGAIKVDVDFDVSVSAGSDLTLPFGAGLIGDTHGPPVYMIADSEWESLWVLDARLRYTIGARC

NbL17g27030.1 granule-bound_starch_synthase_1_chloroplastic/amyloplastic-like [MW = 34.66 kDa]

No. of times detected



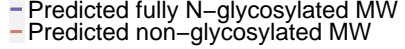
log(intensity)



Values from



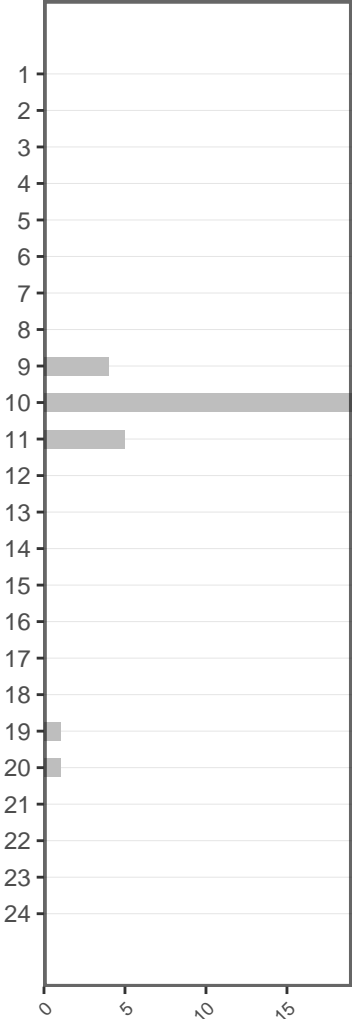
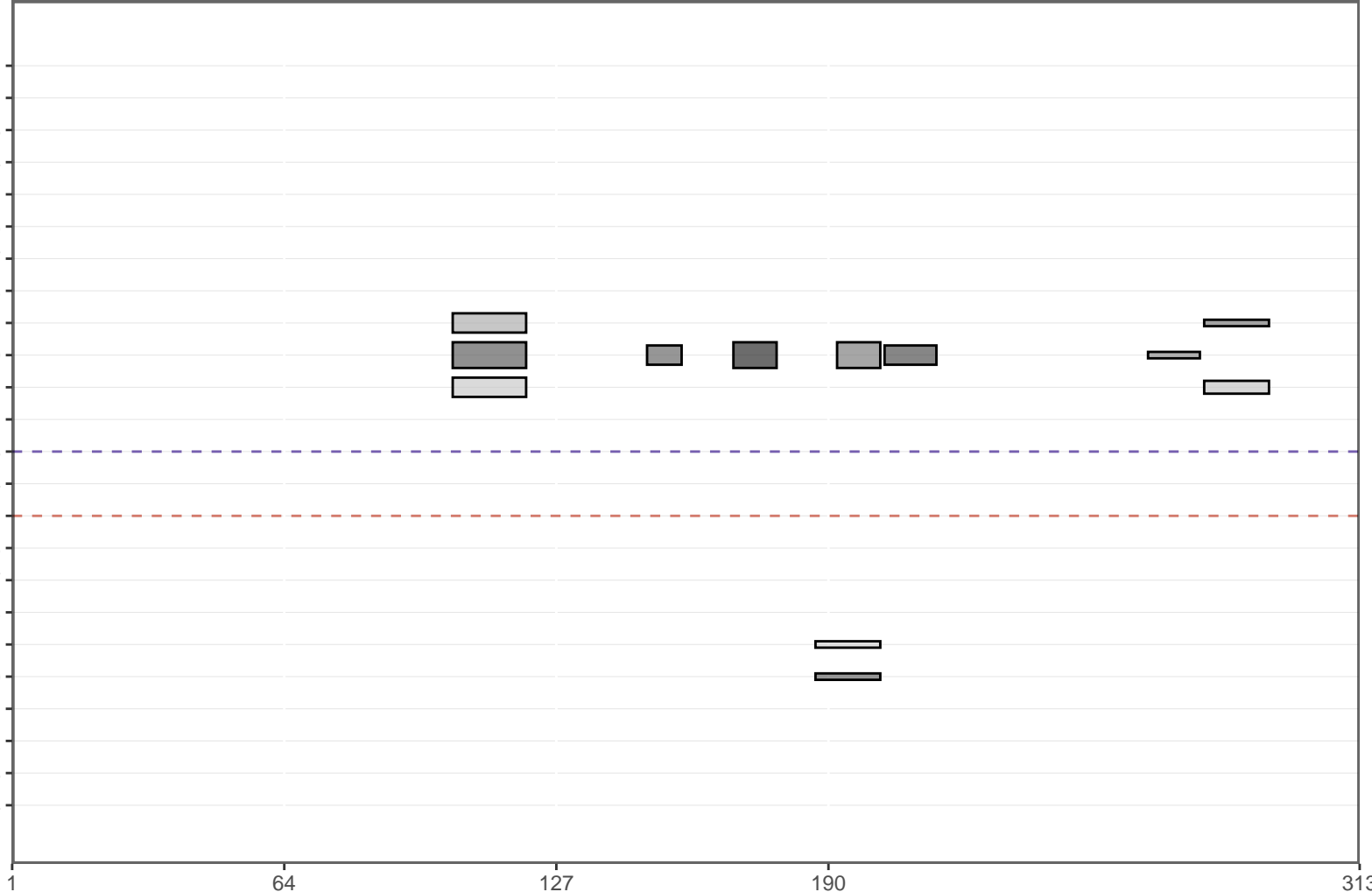
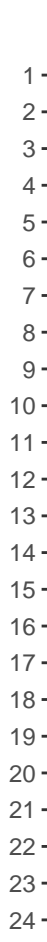
MW indication



Molecular weight



Gel Slice

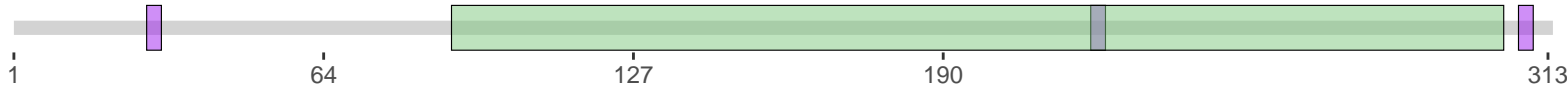


Protein length

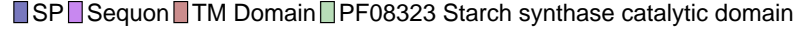


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VVEIKYGDQKIEIVRFHGVKRGVDRVFDHPMFLKVVWGTAKVYGPYKAGDYLDELRFSLDQAALEAPRVNLNGSEVFGSPYGEDVFIANDWHTALLPGLKSMYQSRGVMNAKVAFCNINAVGGRAFSDFSLLNLPDEYKSGSDFDFIDGVEFNISWNGTDFP

NbL17g26920.1 reticulon-like_protein_B4 [MW = 30.05 kDa]

No. of times detected



log(intensity)



Values from



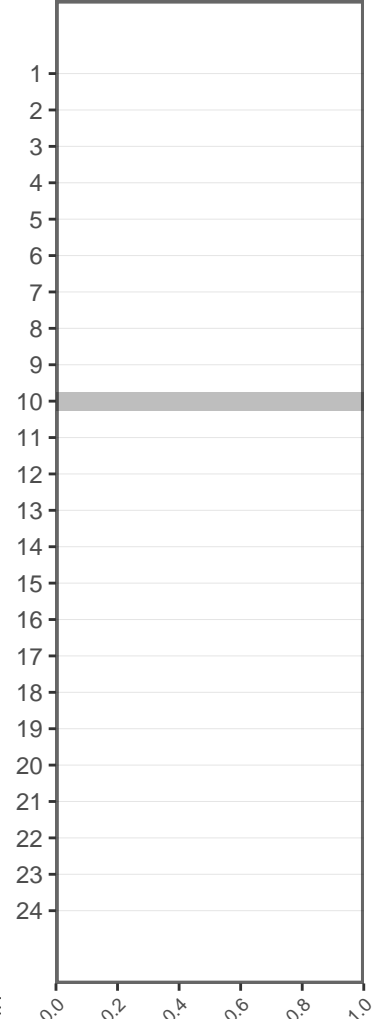
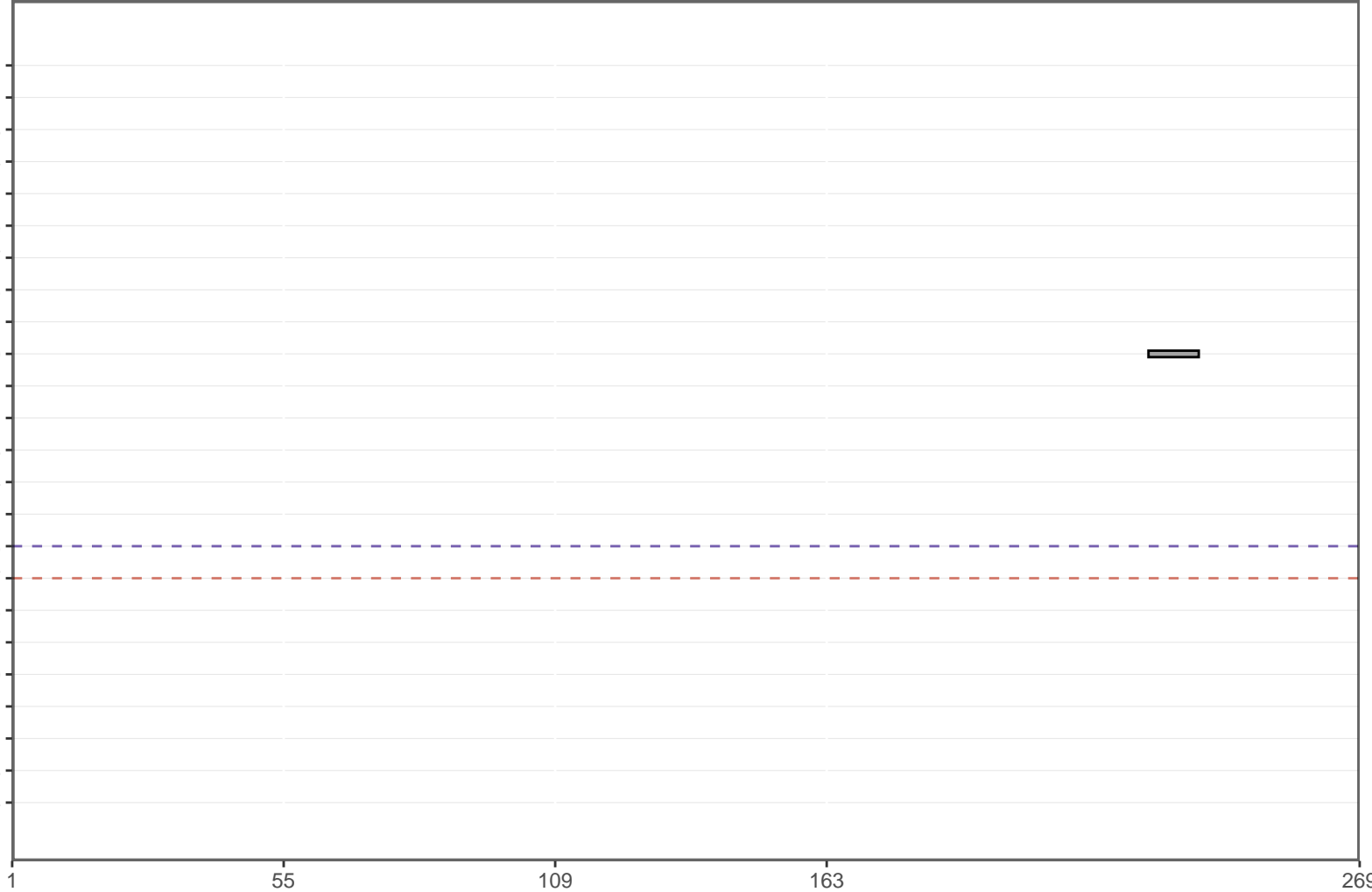
MW indication



Molecular weight

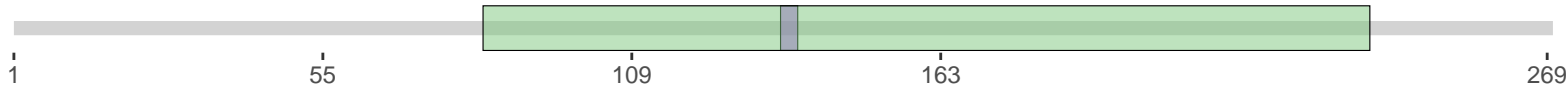


Gel Slice



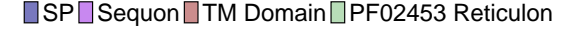
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

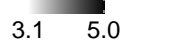
LCHGLIYALAGLFLWNSAFHKISAPHEVHPKPKVLEFATGLRNEINRAFAVLEIAAGRDLMFLMVGQWILSVLGGCCDFLGLLYHWVLLHTVPLVPEYKEDDIDGFAEKAPHELKKGQYGVDFMAYLSEKIPRGLRDKKKA

NbL17g26860.1 endoglucanase_18-like [MW = 57.18 kDa]

No. of times detected



log(intensity)



Values from



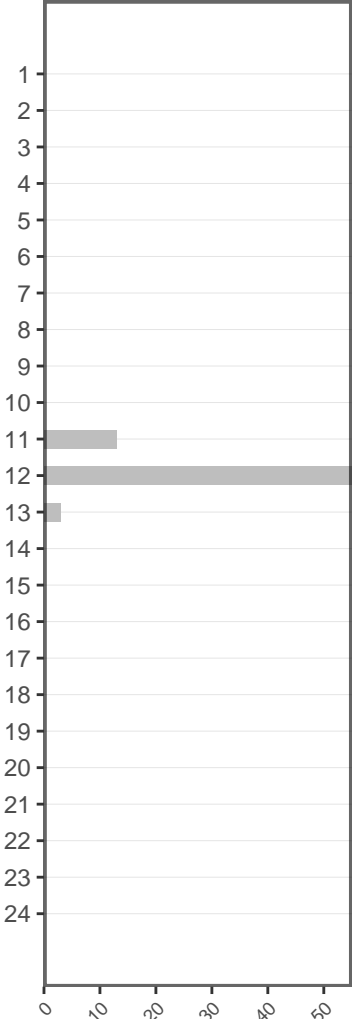
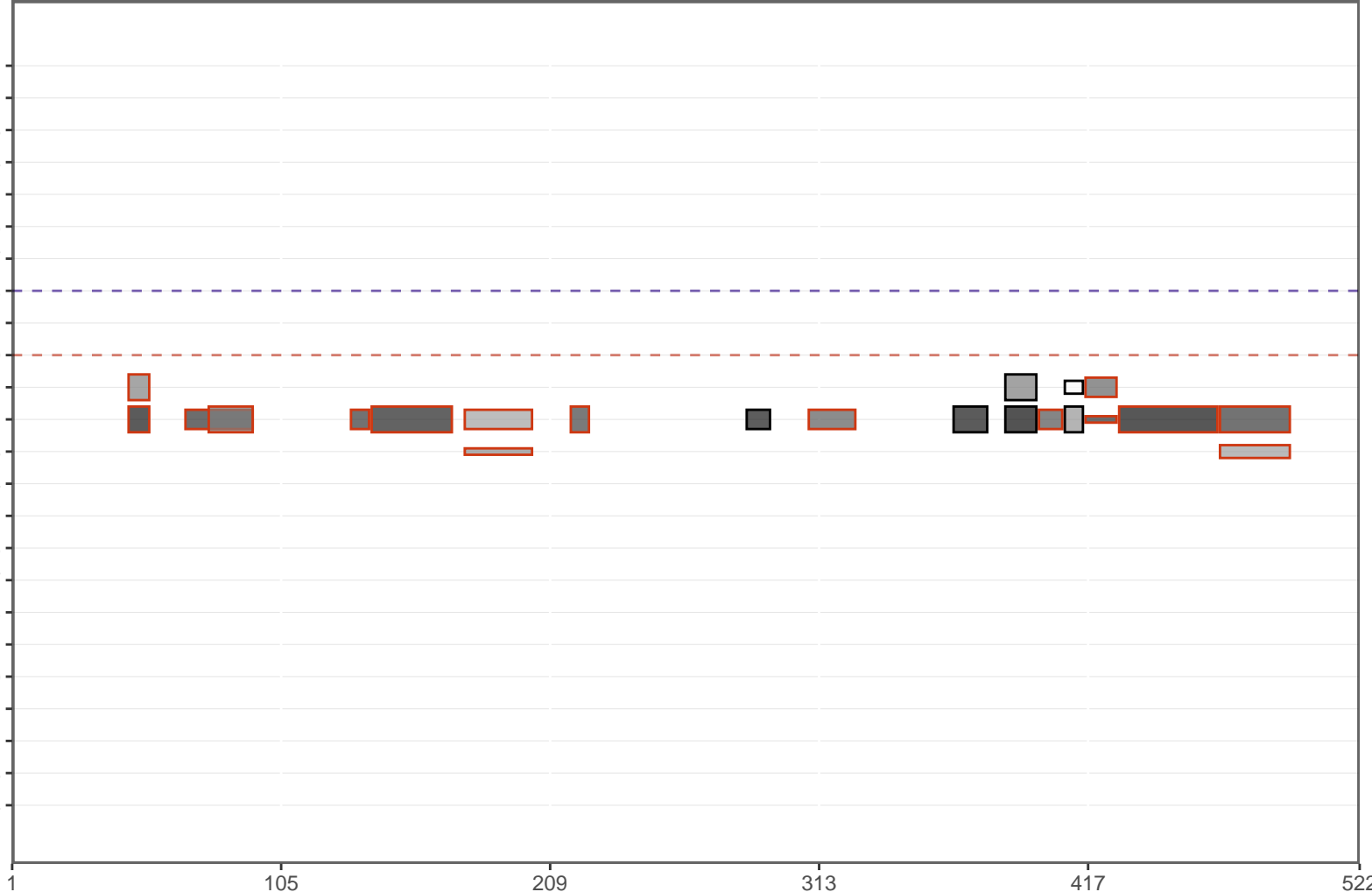
MW indication



Molecular weight

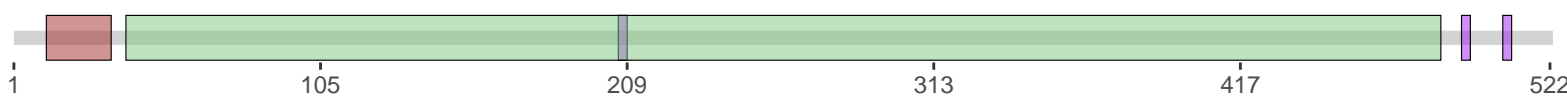


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

VLYKAGGGNNYLYNASSNGGWSQWTEFSDWKNKFAAGQTLKLEFLNKGKSELEKFKKDKADSFICALMPGSSSIQKTFPGLLYTRDSNLYGVYTGATMVFMSYKVLKLETAGKGGVTCGGVTFSTSKKSFANQVDVHLGNPLKMSYMYGFGSKYPTQLHRRASSIPKHHPTKRVGNDGYSWYNSKNPNFNIHVGAVGGPNSGGDGFADRSREYSHSEPTTMMNAAFVGSVAALNDSKVEGSLQMPQLNKTTFYDRGSKNLY

NbL17g26730.1 mitogen-activated_protein_kinase_homolog_MMK2-like [MW = 43.77 kDa]

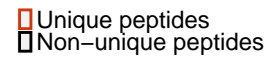
No. of times detected



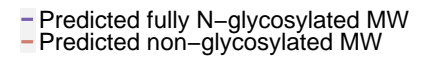
log(intensity)



Values from



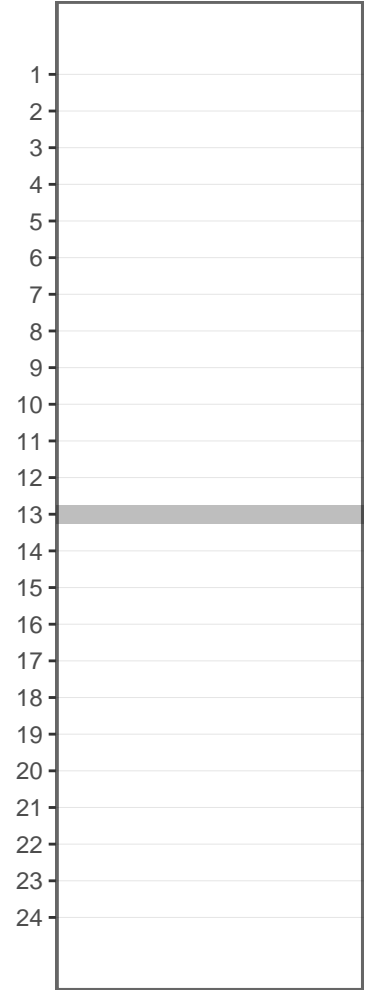
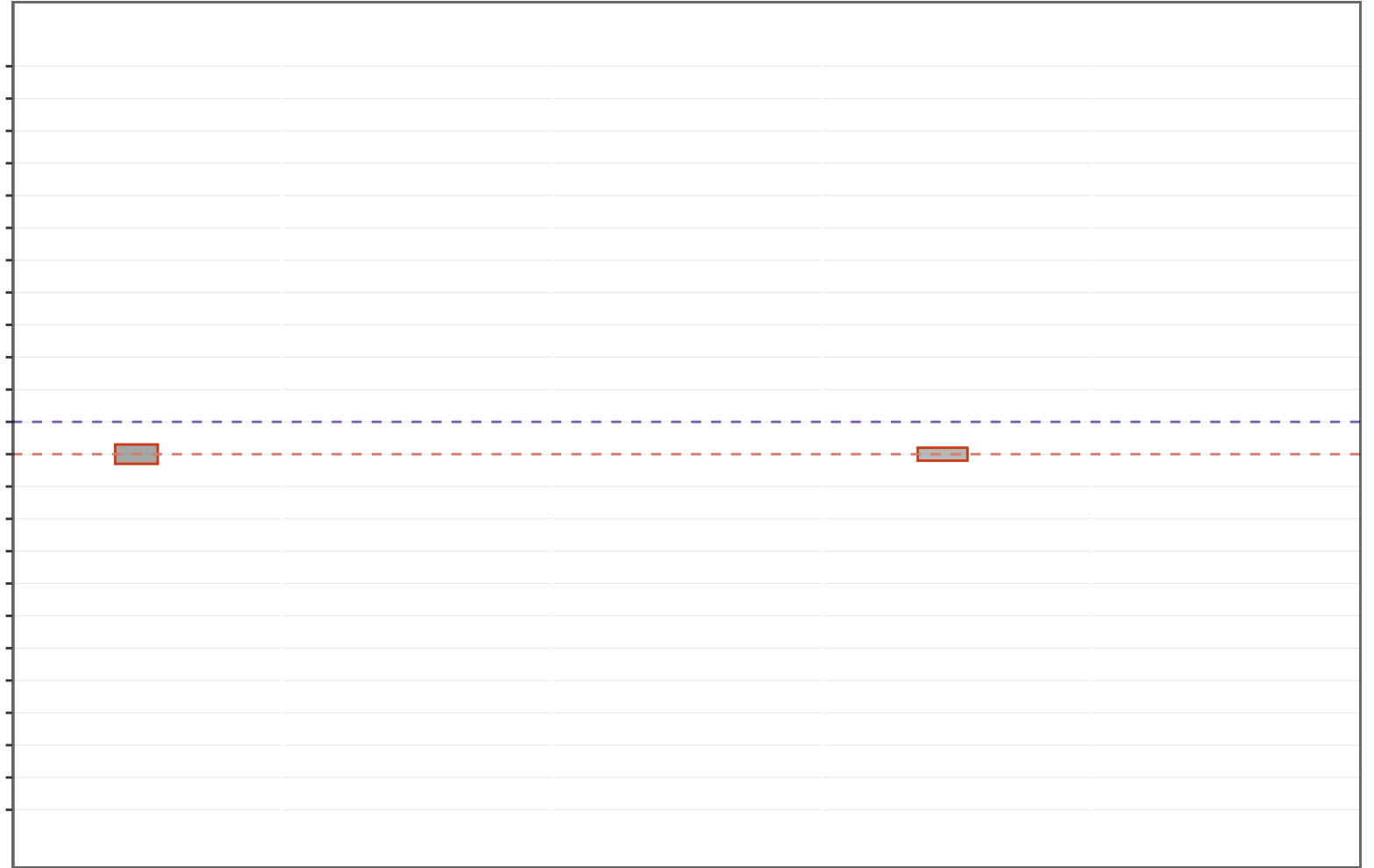
MW indication



Molecular weight



Gel Slice

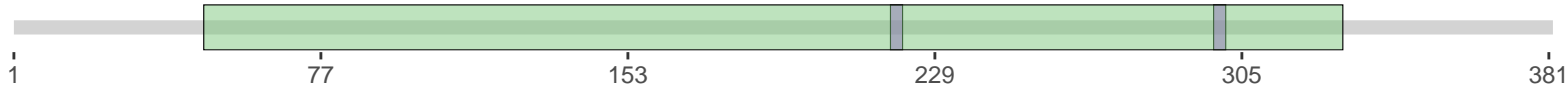


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

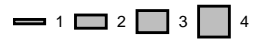


Protein sequence:

.IANCOLKIGDFGLARITSETDFMTEVYVTRWYRAPELLNNGSEYTAANDVWVGGHGEIMTRPELFGKDYVHQLRLITELLGEPDDASLRFLRSNARRYYRQLGCKPKGQFSARFFNMSTLAIDLEKMAVFDPTRRITVDIALCHPFLSLLHNDDEPICRPRPFDFEQPSITEENKELWKEGVKFPYDFVELKI

NbL17g26610.1 beta-adaptin-like_protein_B [MW = 99.81 kDa]

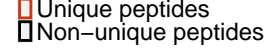
No. of times detected



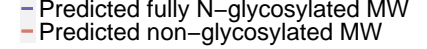
log(intensity)



Values from



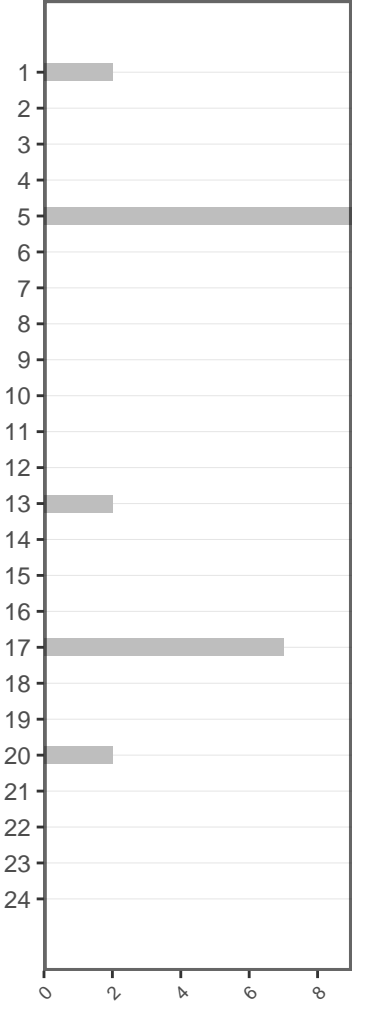
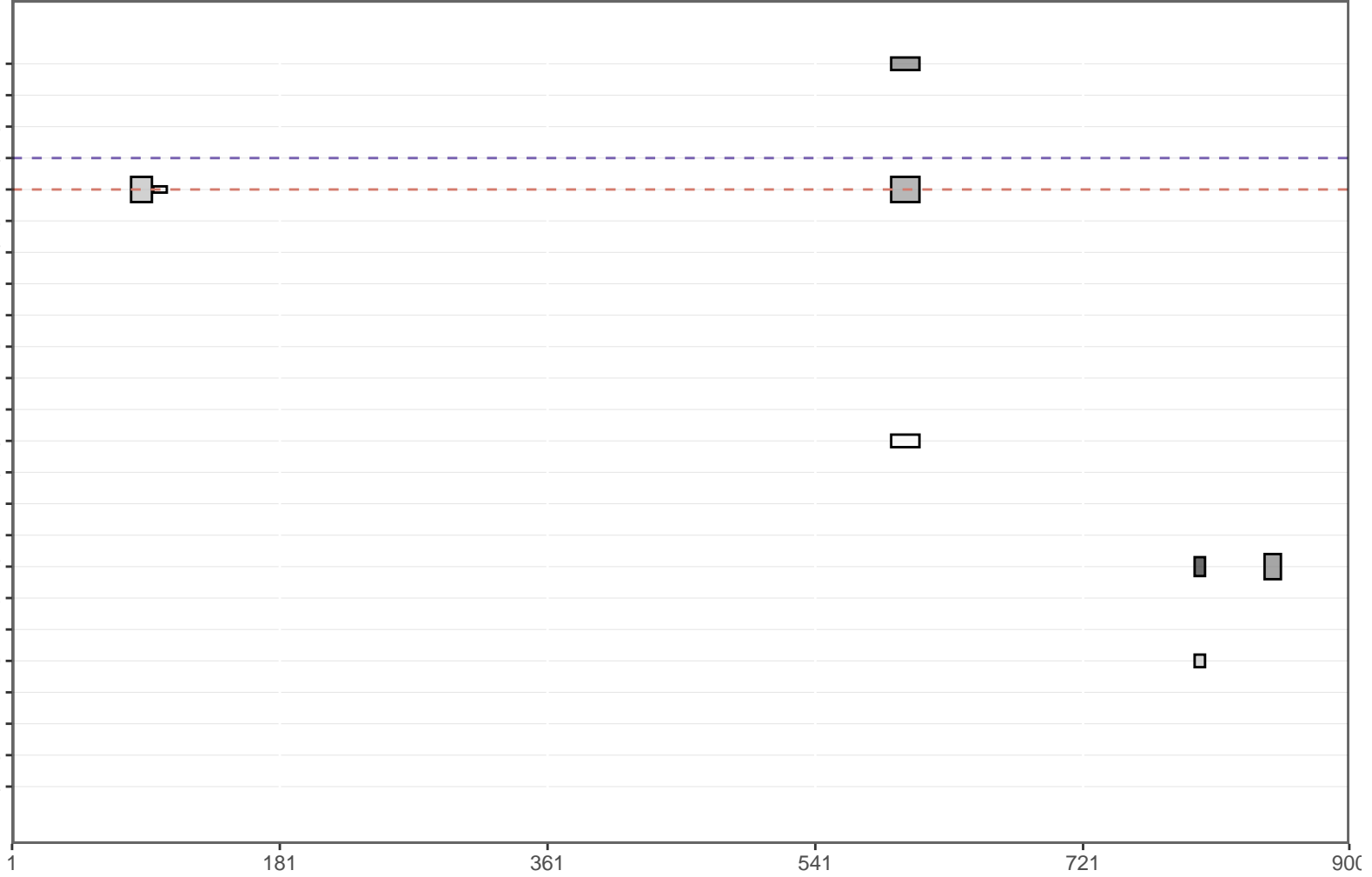
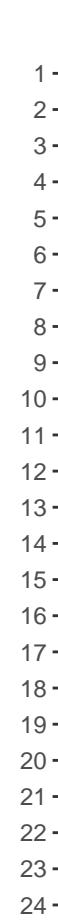
MW indication



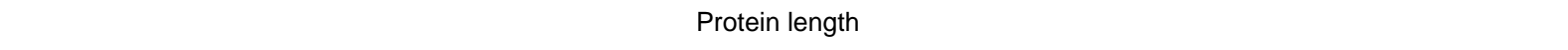
Molecular weight



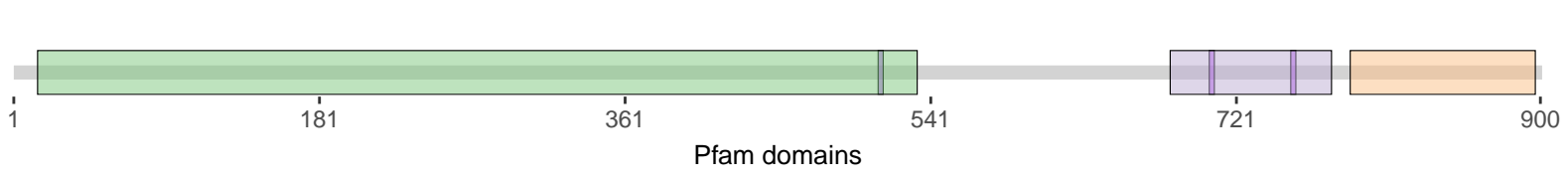
Gel Slice



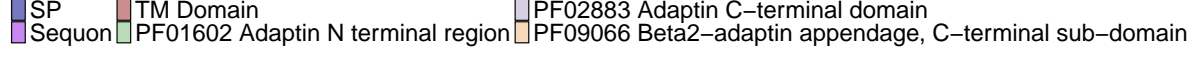
Protein length



Pfam domains



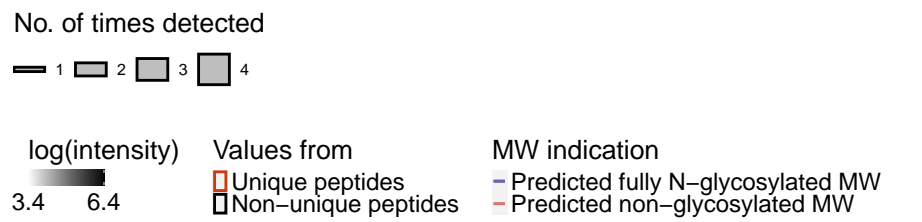
Pfam Description



Protein sequence:

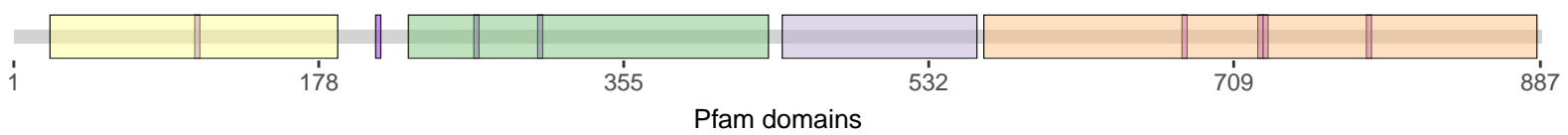
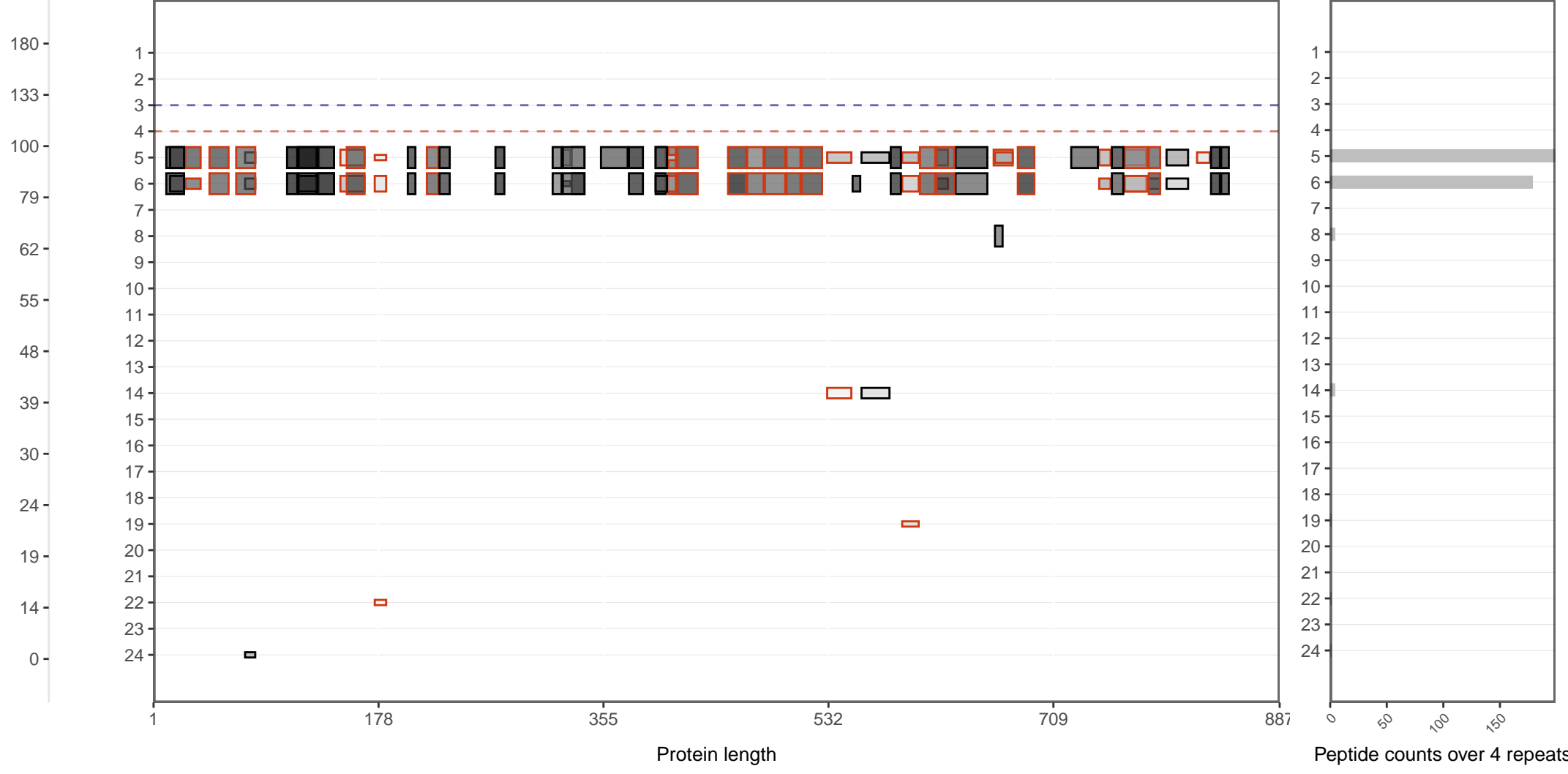
EAKASMIWIGEYAEIRIDNADELLESLFESFPEEPPGVQLQLLTATVKFLKPKTEGPGQMGVVLNNAVIVETDNPDLRDRAYHWLLSTDPAAKDKVLAEKPIVGDGNGQLPDLLELLENLATSIVYHKPEAFVTRVKTQRTTEEEVADAGEQGLSDSPRVAEESGAEPPASAAARAGHRAARGPAPAPAPALPDLLDLGMNDNSNAIVSDGPRTRGPPLPVLPVASTGGGLQISQILRRDGGVYFYSMMFENNTQVPLDGFMIQFNKNTFGLAAGPLOVPLLF

NbL17g26530.1 puromycin-sensitive_aminopeptidase [MW = 100.13 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF01433 Peptidase family M1 domain
- PF11940 Domain of unknown function (DUF3458) Ig-like fold
- PF17432 Domain of unknown function (DUF3458_C) ARM repeats
- PF17900 Peptidase M1 N-terminal domain

Protein sequence:

IRDANNADFNFLWYSGAGTRWVKTNNYNAESHFTLSKFSQEVPRPTPGGSAKEPVPFVAVGLDSSGRDMPLESDVYHDKLEFSAGSGGWHHTVLRITKKEEFVDFDKFKPIPLRFGFAPIRLESGLTDSLLFLLAHDSDFNRIWEAGGVLAARKMLGLVADFGGNKALVLPQDFVGGIKSILTSSLDKKEFAKATLPCVGEIMDMMTVAQDPDAVHARTRFRKQLASELKEELLFTAKNNRSGGAYEFDHNNMARRALKNALVYKLSLEDPETILLLENYRATN

NbL17g26470.1 short-chain_dehydrogenase_TIC_32_chloroplastic-like [MW = 34.51 kDa]

No. of times detected



log(intensity)



Values from



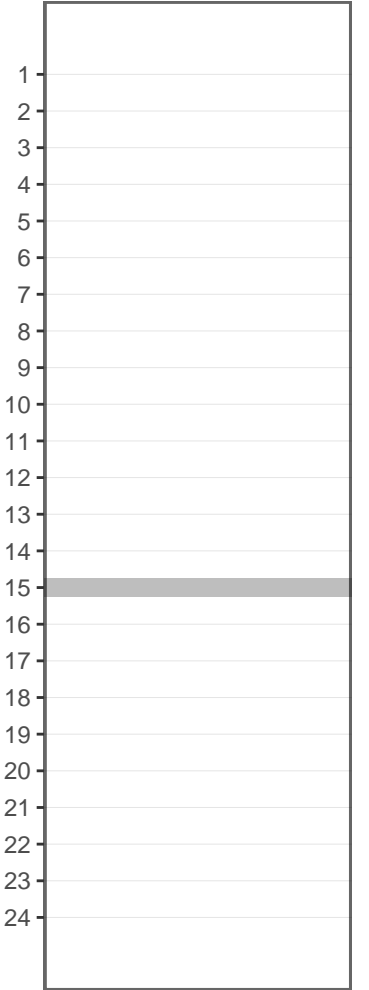
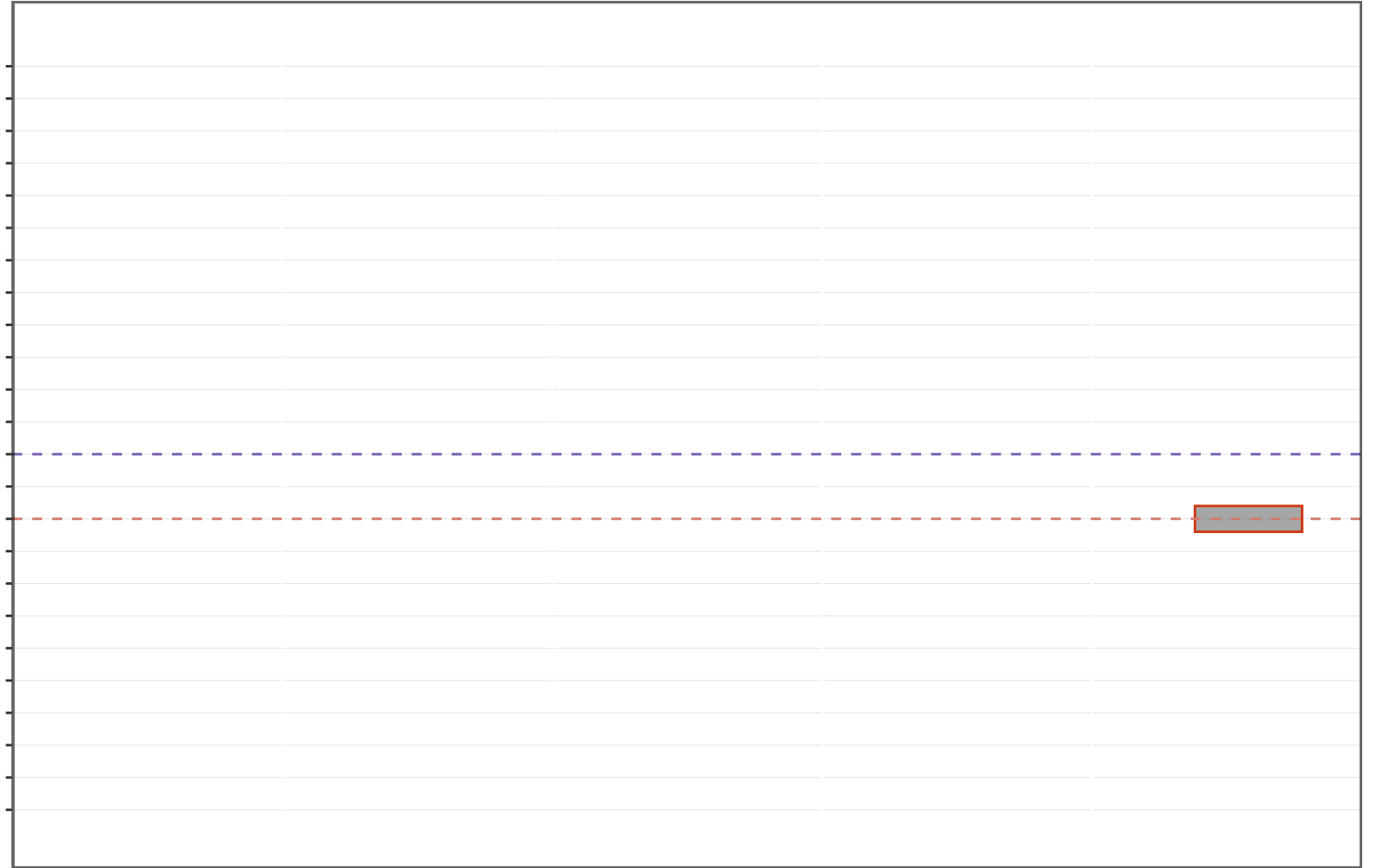
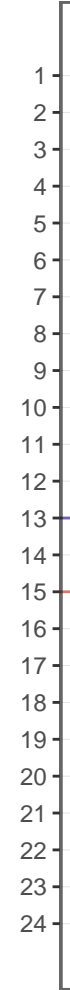
MW indication



Molecular weight



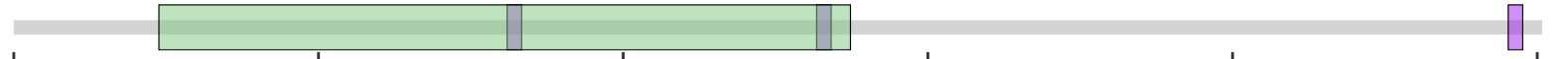
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

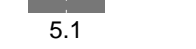
TNLLLENLNTAQGSHKEGRIVNVSMSGHKFTYRIGRFDKINDKDEYTSWVAVGGQELANLHANELARRFKDEGLEITANSLHPCGAINTLMRHQNLIEGIVNNGKYFKIDIPGCAITTCYVALHPQVYKIGISGEYFSDSNWPTTSHATDTLAKKLIWDFSLNLTQPGQ

NbL17g26460.1 aquaporin_PIP-type_pTOM75 [MW = 30.76 kDa]

No. of times detected



log(intensity)



Values from



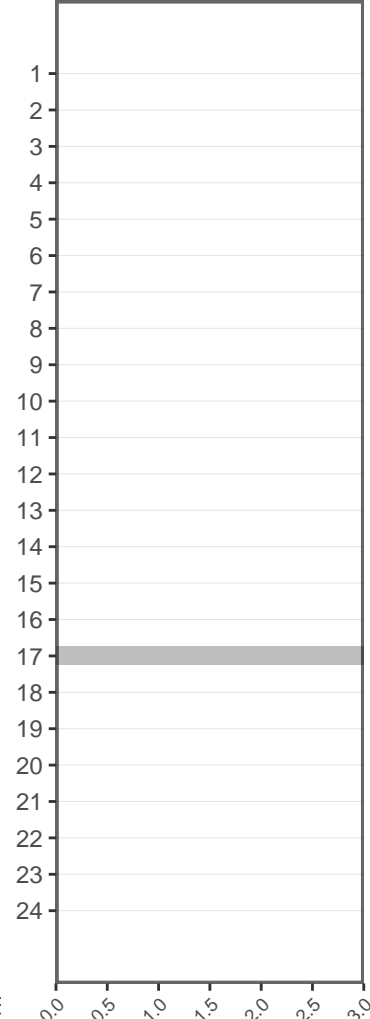
MW indication



Molecular weight



Gel Slice

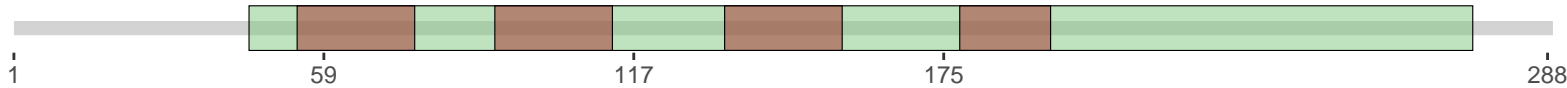


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

LTRAFVYVMOCCLGAGGAGVYKGFMPYQRLGGGANVNPQYTKDGLGAEIGTFVLYVTFVSDAKRNARDSHVPLAPLPQGFVFLVHLATPITGTGINPARSLGAAMVNDHAWDDHWFVWGFPGAALAAVYHQIRAPFHKSS

NbL17g26400.1 GMP_synthase_[glutamine-hydrolyzing] [MW = 64.12 kDa]

No. of times detected



log(intensity)



Values from



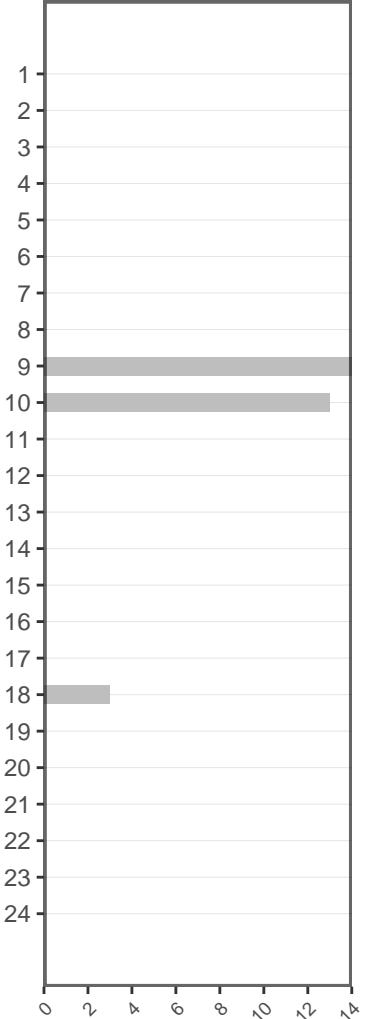
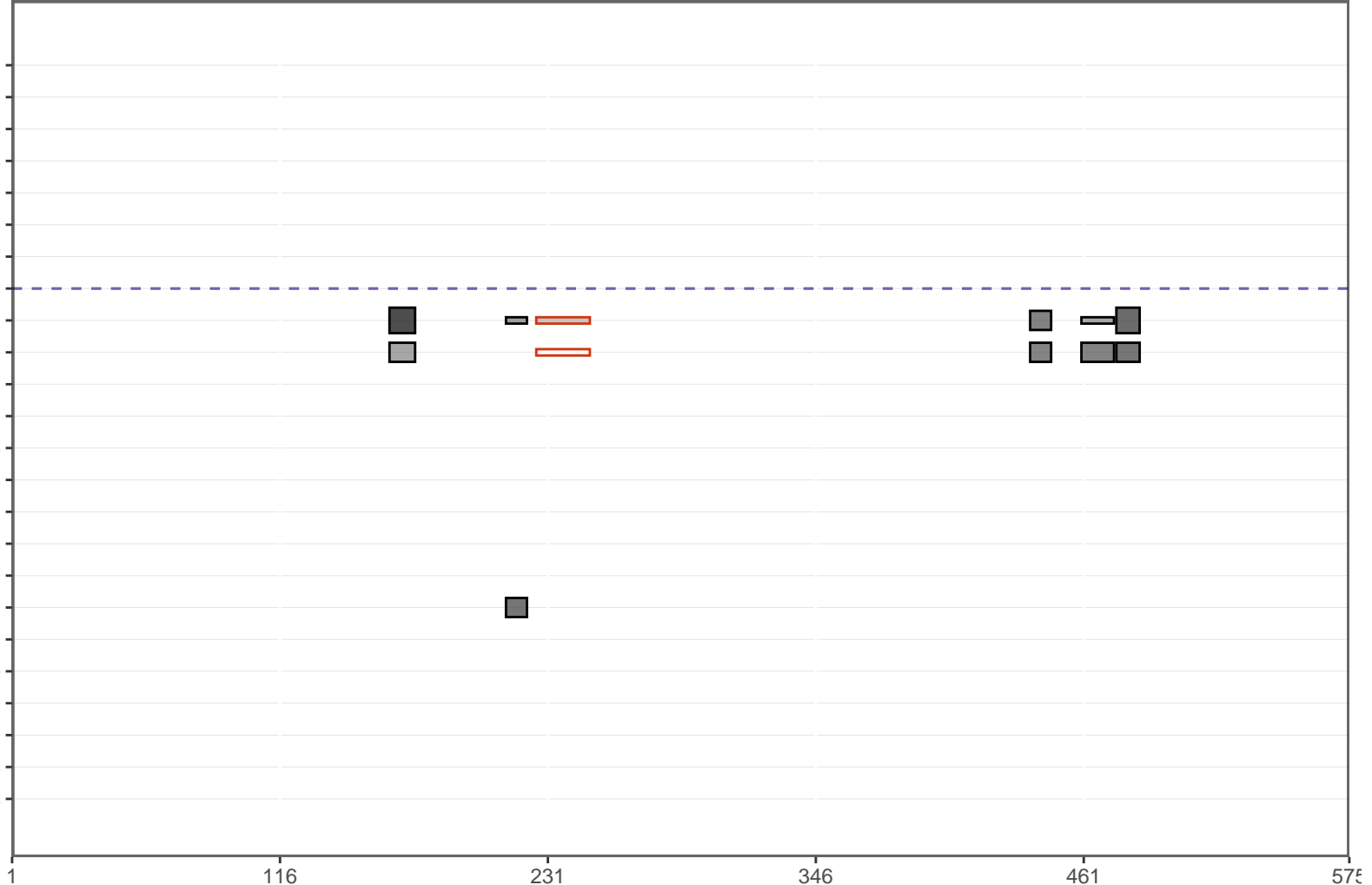
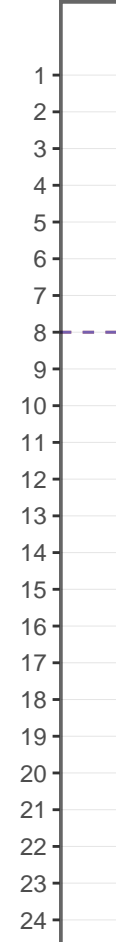
MW indication



Molecular weight



Gel Slice

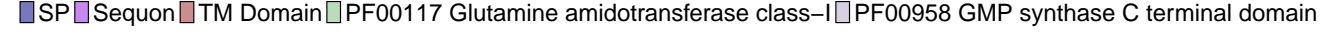


Protein length



Pfam domains

Pfam Description



Protein sequence:

CEERVMDLFEKRLHLPVTVQVDATEEFLKLGKGVTEPEMKRRIKGFNFDLFGHDVEKKVGGKPTLVLDGTLVPOVIESCPFPQSGSRTHGHTKSHNNVGGVLMKMLKLEPLKLFKDFEVSFOLLKLLHSLHYFFLTLGKGLVLDLSCFTPLISGIVRELGKILDSDFLKRHPFPCGLAVRIPGDTAGNGLDLRGVDFEIGSIREAKYDEWQAFVFLPKVTYGVGGDGRTHSHAWALRAVTSQDGMADWYVDFKFLDQVSRKGNVIRGVNRI/LDITSKPSTEV

NbL17g26310.1 glutamate--cysteine_ligase_chloroplasic [MW = 58.98 kDa]

No. of times detected



log(intensity)



Values from



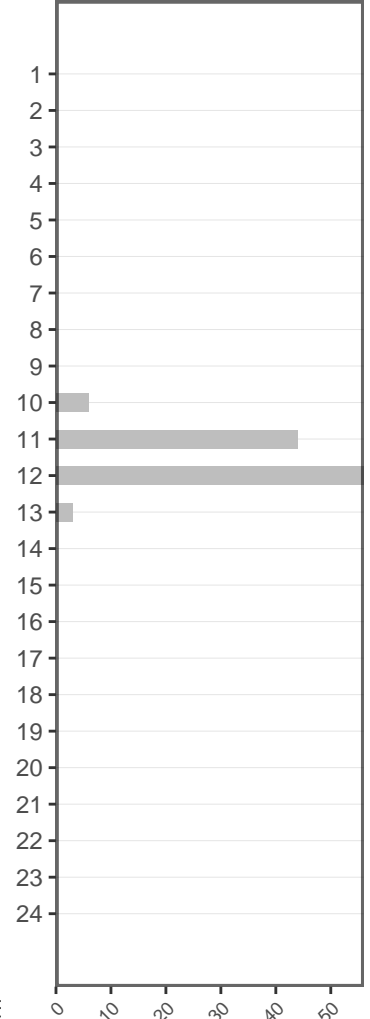
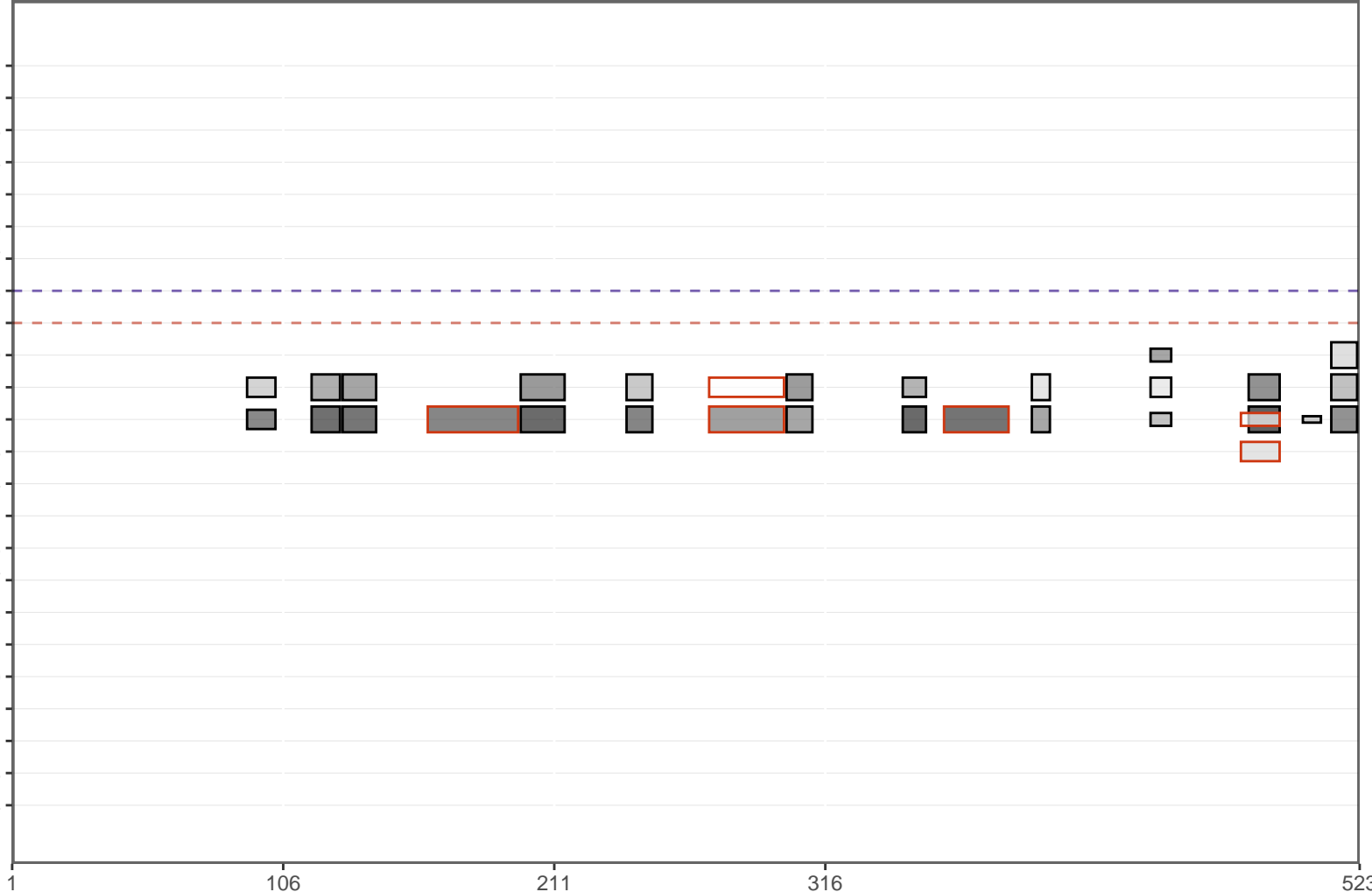
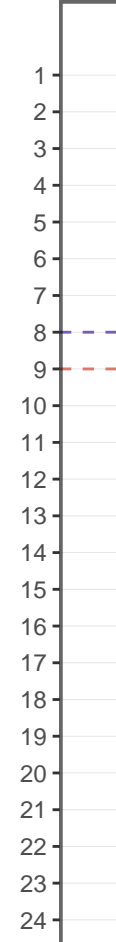
MW indication



Molecular weight

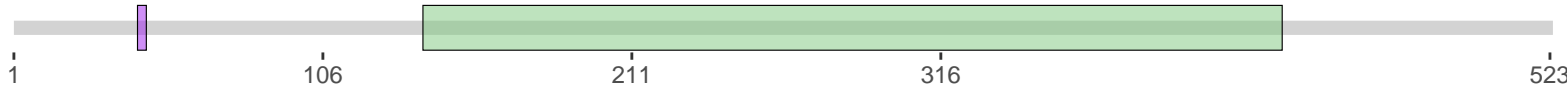


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RTCTVQVNLDFSSSEAMIRKFRAGLALQRIATLAFANRPETEGKPNGLSMRSHWTDIDNIRAGALPFVFDHSGFGEQYVDVALEVPMAFYVYRKKKYDCAGMSFRDFMNGKLPPIPGDVPFLNDWENHLLTTFPEVRLKRYLEMIRGADGGFVRRRLGALPFAVWGLYDEVLSQTVLDMTSDWTAERREMLRNKVPPTSGLKTFPRDGLLKHVAGDVAVLAKEGLERRGYKETGFLNEVTEVVRTGVTRAKLLELYHGKWKGRBVDVFEELY---

NbL17g26250.1 probable_phospholipid_hydroperoxide_glutathione_peroxidase [MW = 25.99 kDa]

No. of times detected



log(intensity)



Values from



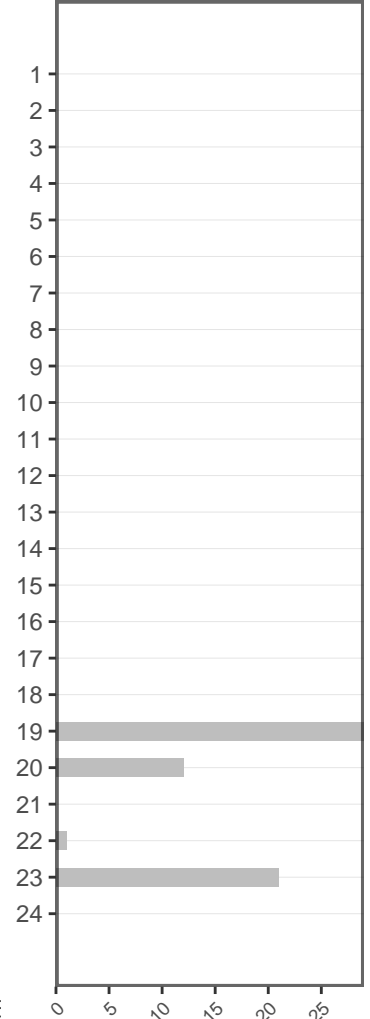
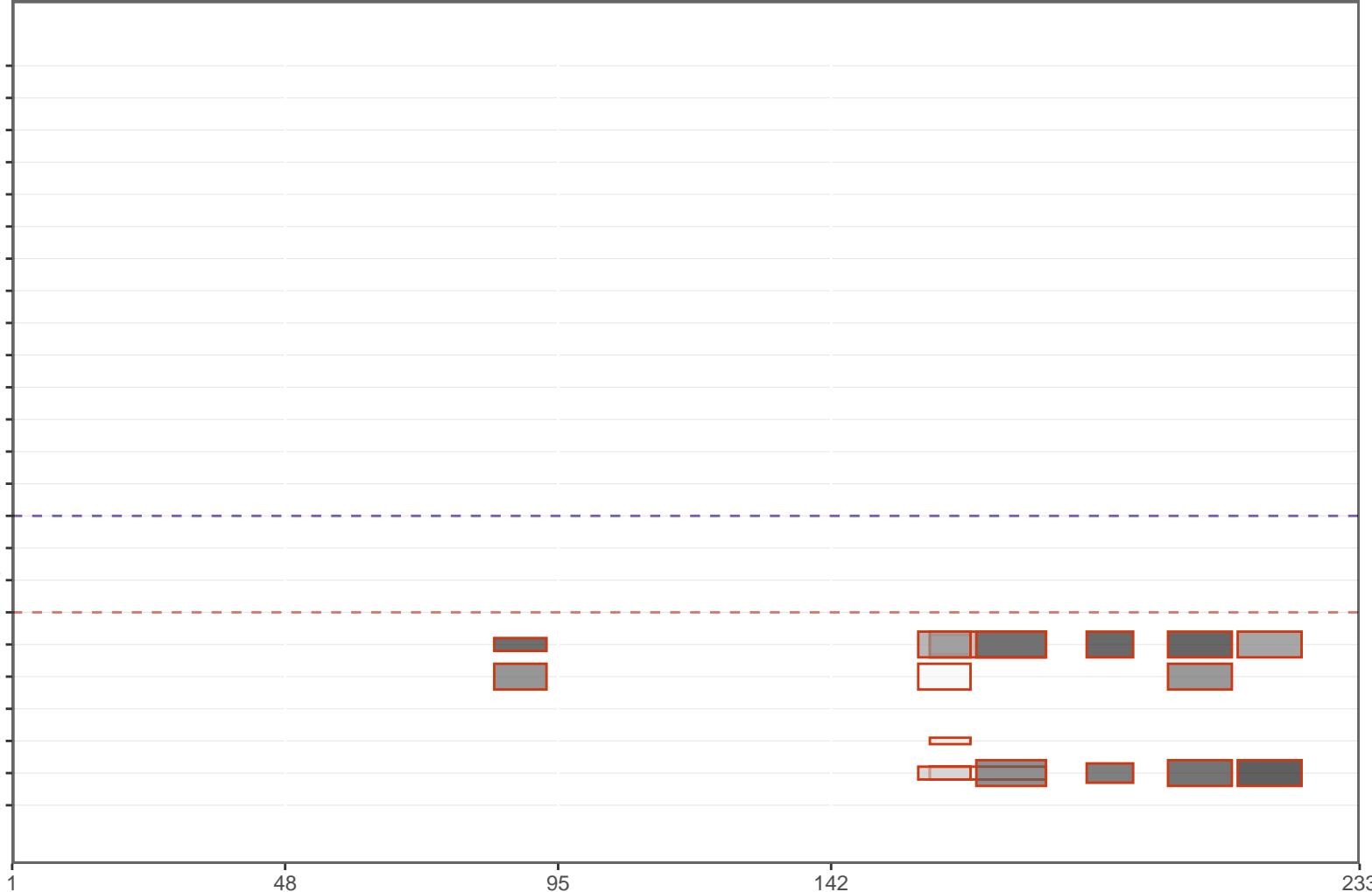
MW indication



Molecular weight

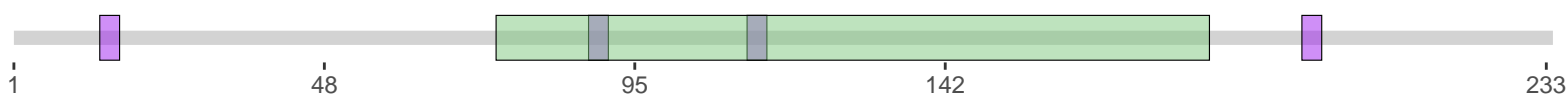


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

COLTNSNYTDMTERKKKKYKDGLEILAFPCNGFGGDEPGSEIEIGNMVTFRFAEYPIFDKVDVNGDNAAPLYKFLKSEKGGFFGDSIKWNSKFLVKEGNNVDRYSPTTAPAEEMKDKKLLGVA

NbL17g26230.1 probable_phosphopantothenoylcysteine_decarboxylase [MW = 23.09 kDa]

No. of times detected



log(intensity)



Values from



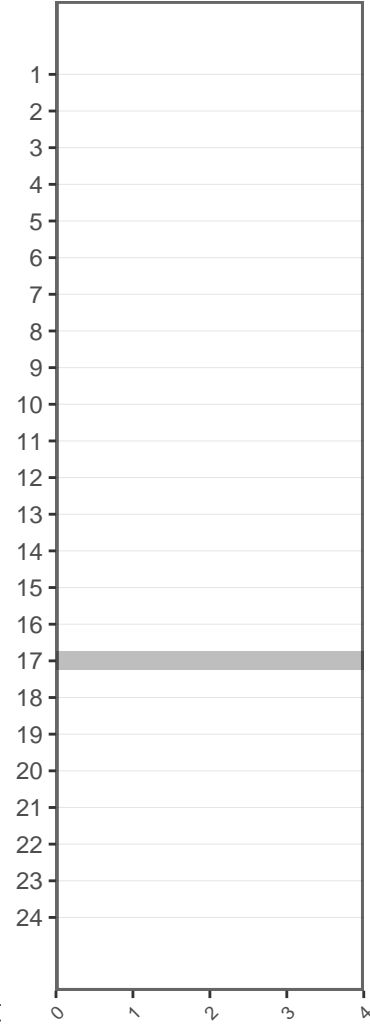
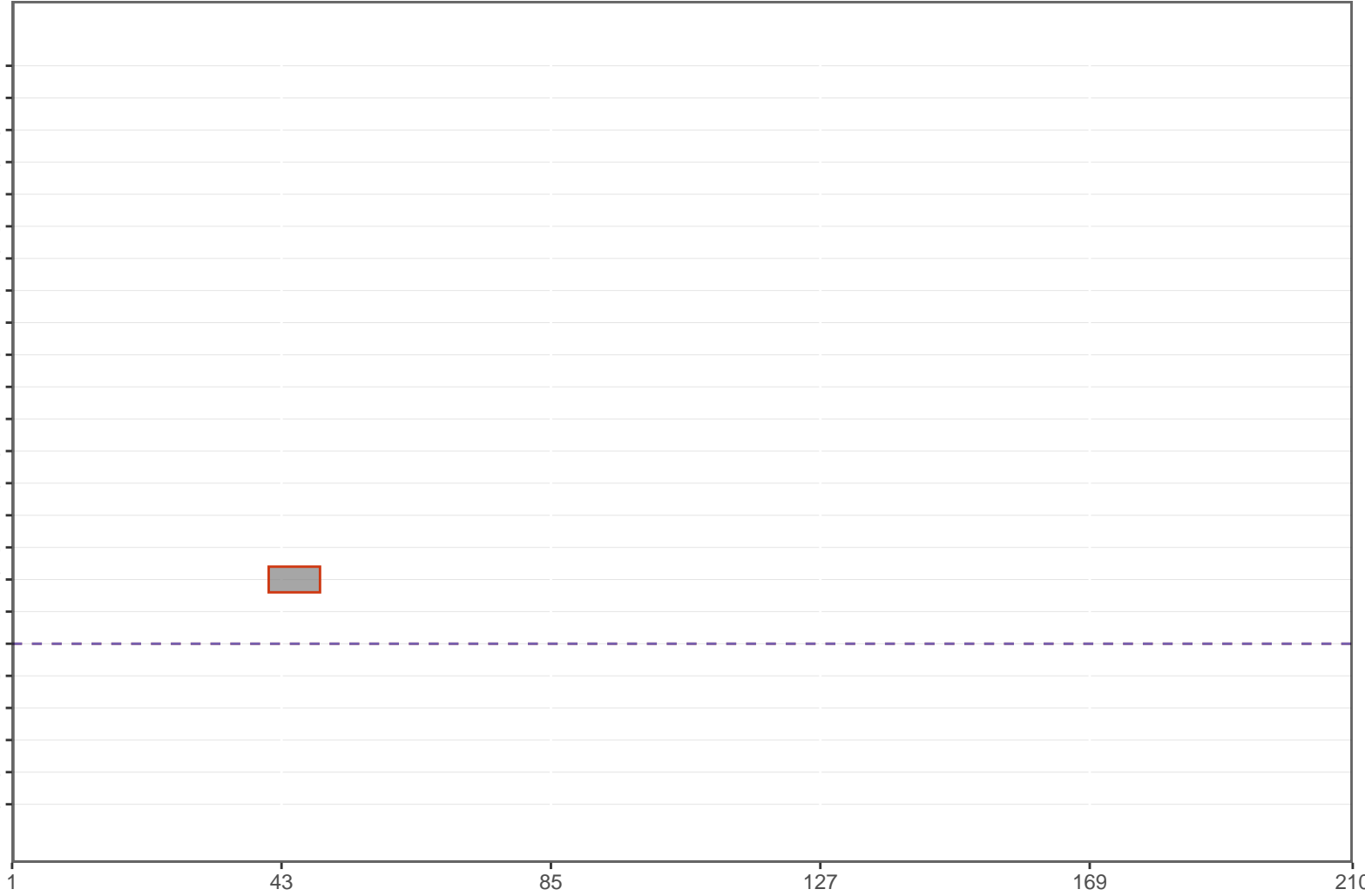
MW indication



Molecular weight

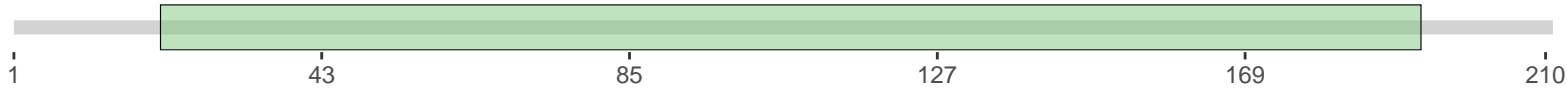


Gel Slice



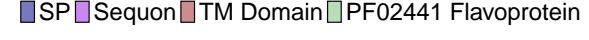
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILRRWADIMIAFLSANTLGIKAGGLGDNLLTGVRAWYDKPLFVAPAMNTLMWVNPTEKHLVIDELGSLPPVSKRLAGGDYGNQMAEPLIQAVRYYDAQLRGGSNVA

NbL17g26060.1 elicitor-responsive_protein_3 [MW = 16.07 kDa]

No. of times detected



log(intensity)



Values from



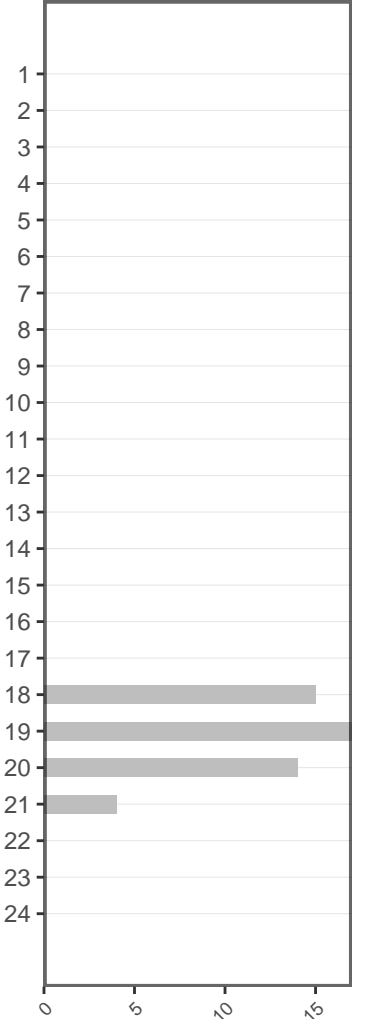
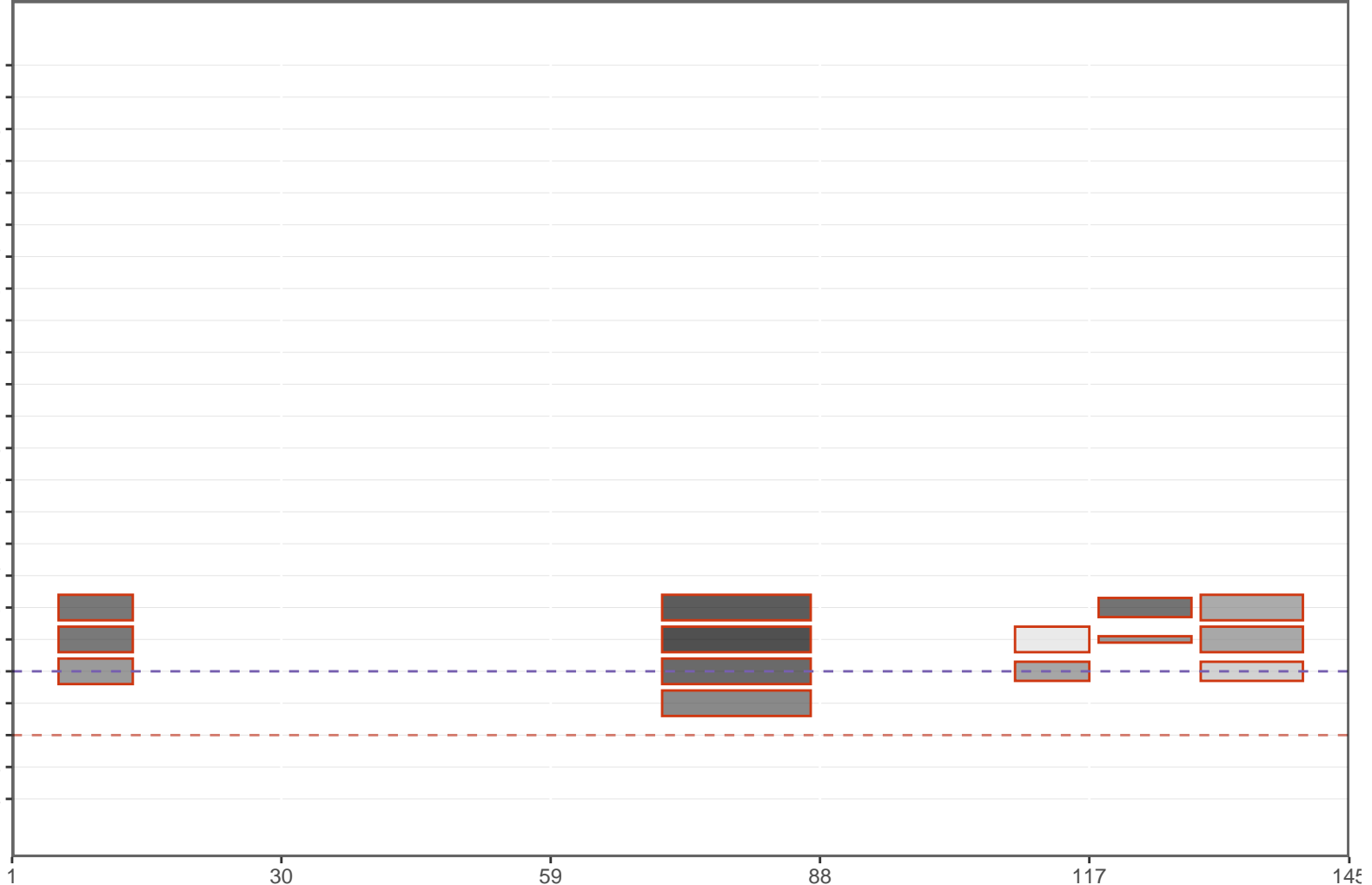
MW indication



Molecular weight

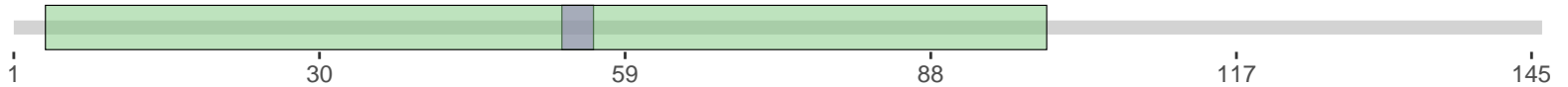


Gel Slice



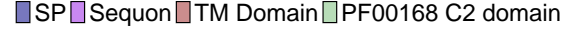
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

'SISGQVEELFLKIMSDSDVGEDDFVGEAKPIEPVSGEGSPTTAVNWNNEEYGGERSVSLFTFPQEDRDVEQEEGYPGGWKESTV'

NbL17g26040.1 bifunctional_UDP-glucose_4-epimerase_and_UDP-xylose_4-epimerase_1 [MW = 39.3 kDa]

No. of times detected



log(intensity)



Values from



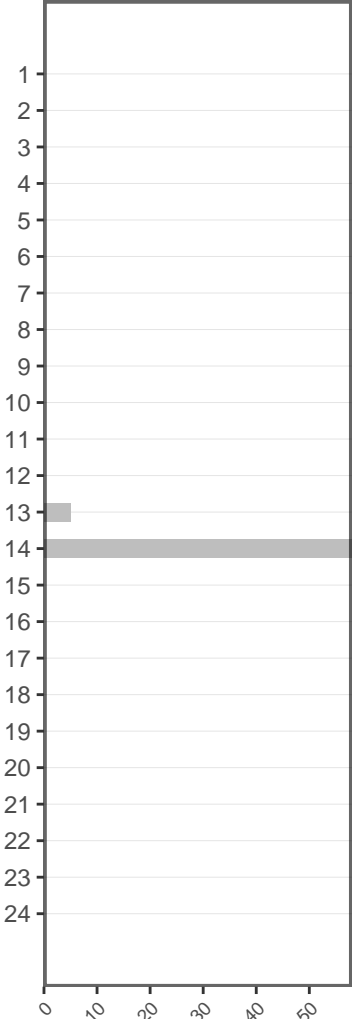
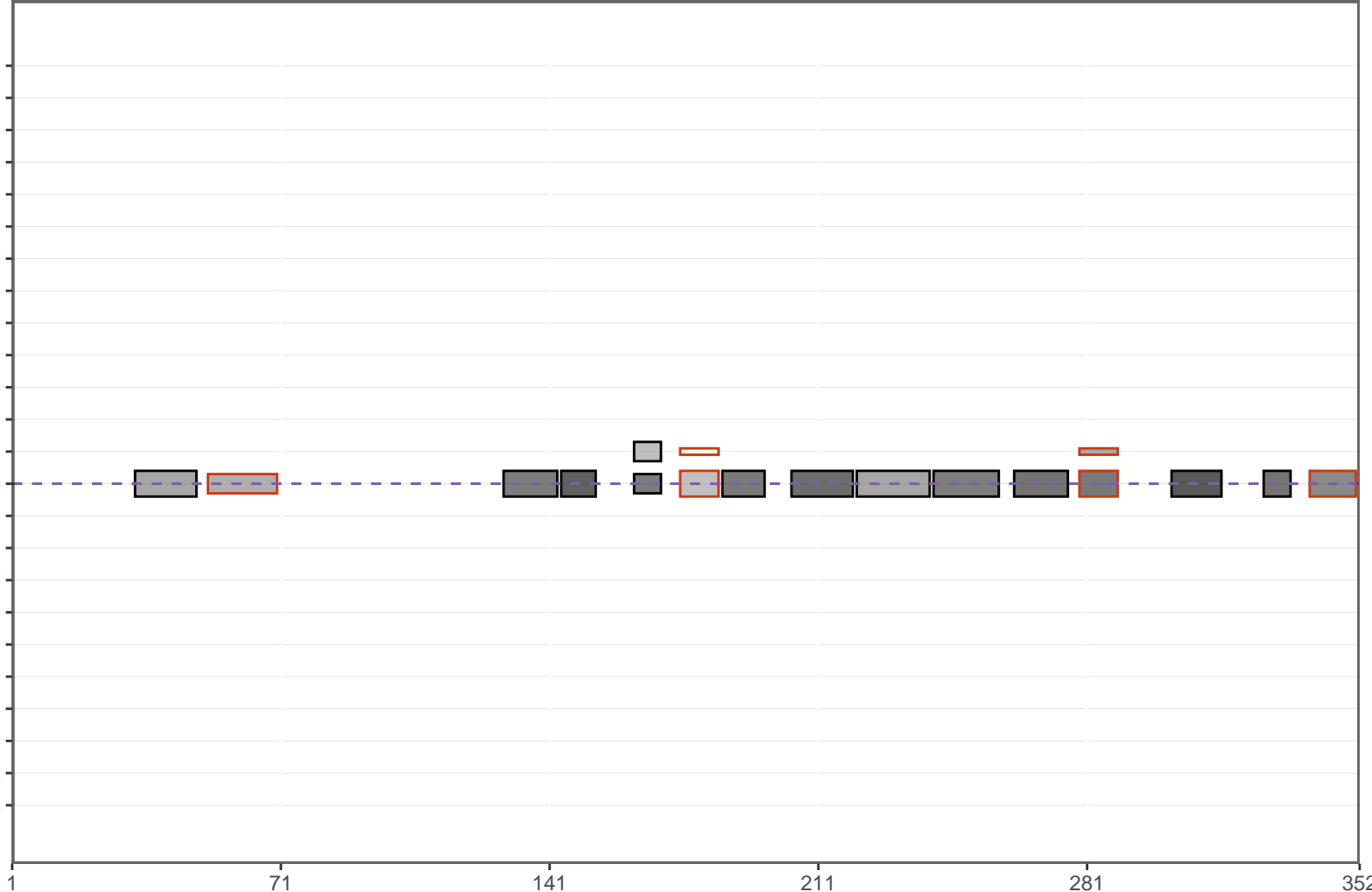
MW indication



Molecular weight

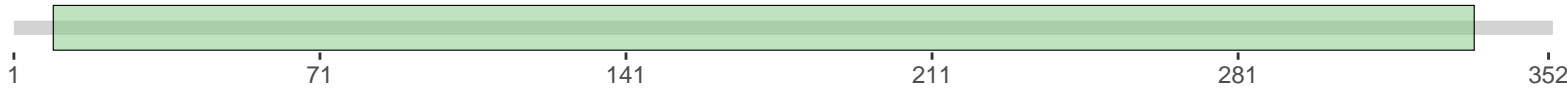


Gel Slice



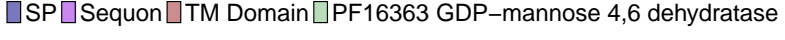
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

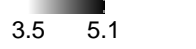
..EEIARDIQKADAEVWISILLRYFNFPVGAHESGKLGEDPRGIPNLMMPYIQQVWGRLELPELVYGTDFPTDGTNRDVIHVMIDLADGHVWALGRLLKGNLDLGVWVNLGTGKGVLEMMVAERASGKFLKMPRRRPGDATVAVSTKAEKELGWKAKYGDMDCRDQVWVWASGNPVGWYQSKP

NbL17g25940.1 plant_UBX_domain-containing_protein_8-like [MW = 66.83 kDa]

No. of times detected



log(intensity)



Values from



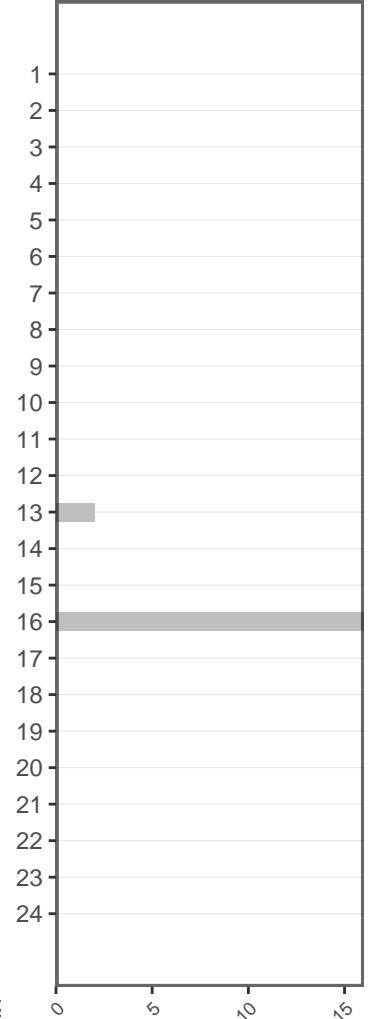
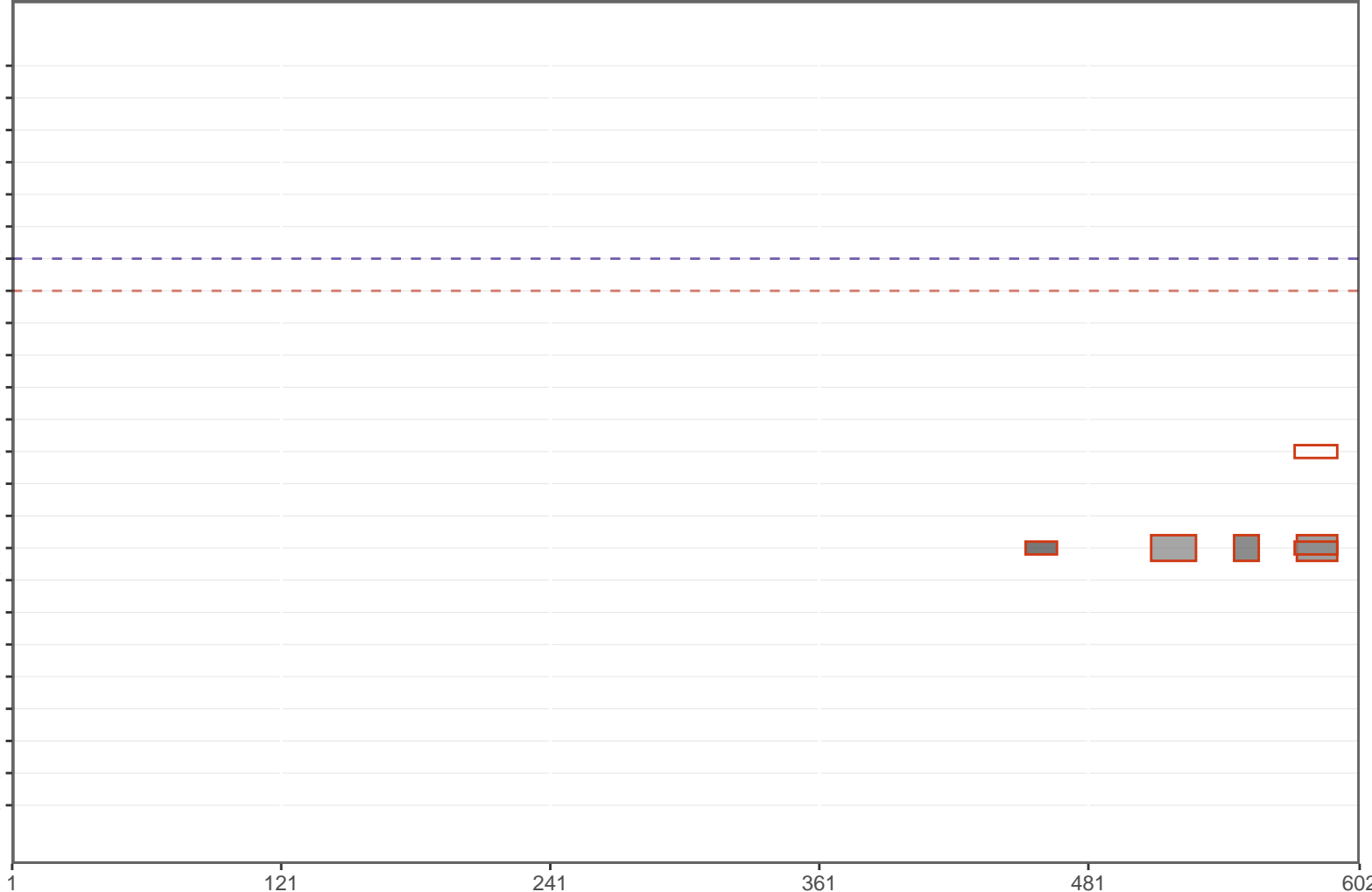
MW indication



Molecular weight



Gel Slice



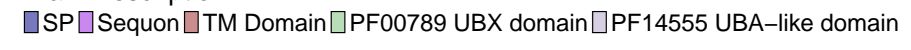
Peptide counts over 4 repeats

Protein length



Pfam domains

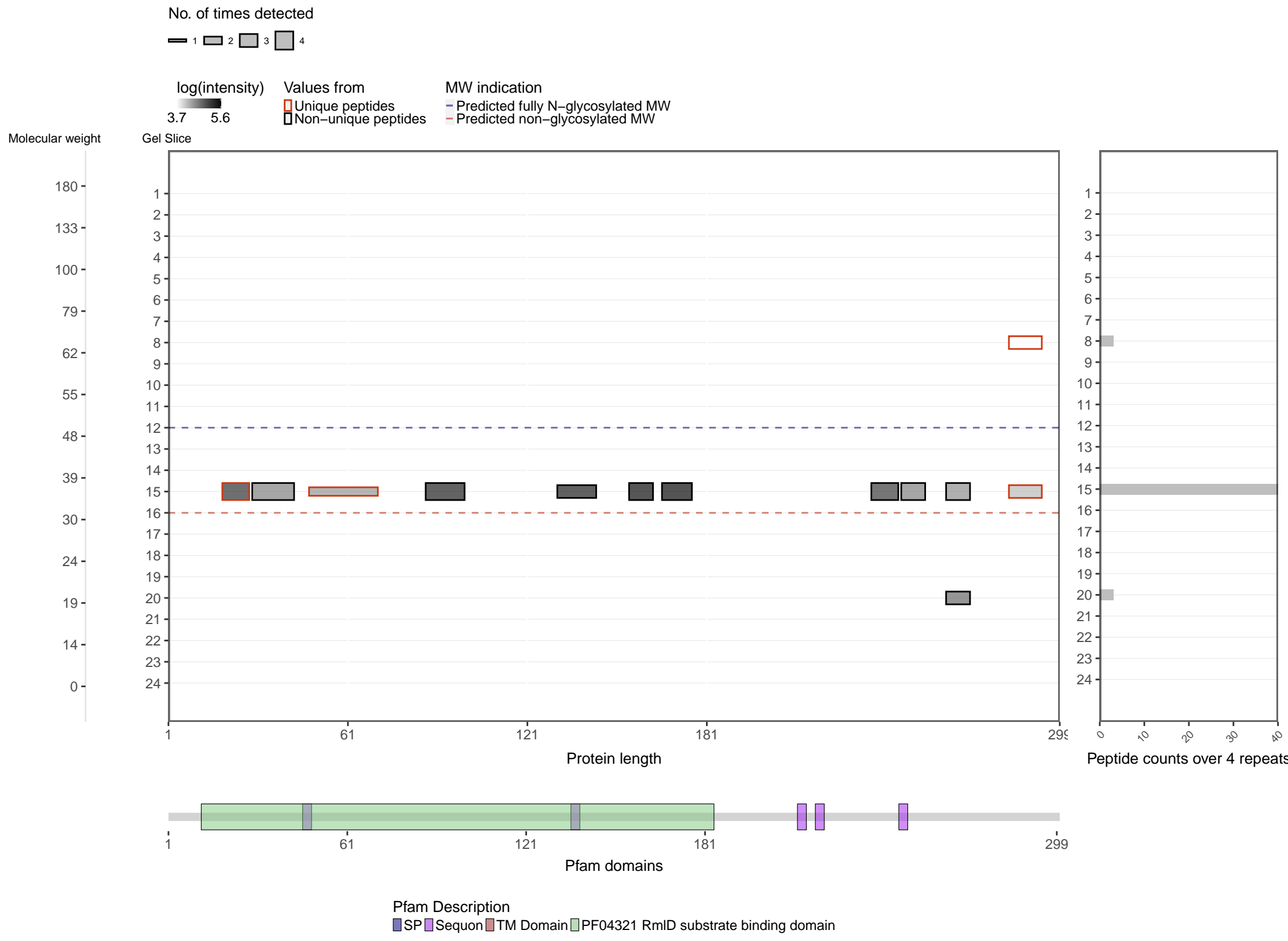
Pfam Description



Protein sequence:

EGYKPAEEDERKGTSTNGRQFRSEVGSSEVDFDEADLEEEPLWRRRKPISSGSETAQDIEEHVGSPLSSPQHDNLRSPRNGADFFPSDEWGGISLEHDEAVMEEAALFGGIFEGGGYRLFNAPHQLMNGVEGPMGPYQWHMPRRPSPBLVQRLLRREGQDDYHTALQADREKELKAAKEAAALEEKROEEESRRKAAEEKEMEROLAAKEASLPDEPTADNENAVNLVWMPDGGRRRRLFKSDRLGVLFNVDVGRVWPKGTVRLVRYPRRAFSC

NbL17g25820.1 bifunctional_dTDP-4-dehydrorhamnose_35-epimerase/dTDP-4-dehydrorhamnose_reductase [MW = 33.47 kDa]

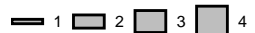


Protein sequence:

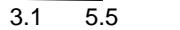
NFTGSPYKTKAMVEELLKKNYDNLVTRVMPISADLTNPRNFITKTRVYDKVVDIPNEMTLDLLEPISLEMAKRNLTGAVNFTNPGVSHNIELEMYRDVDFSGVKNFTLEEGAKVWVAPRSNIELDASKLEKPEEMKSIKESLIEVYFKPNRKTPTVAI

NbL17g25810.1 phospholipase_D_beta_1-like [MW = 95.71 kDa]

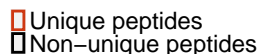
No. of times detected



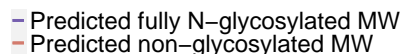
log(intensity)



Values from



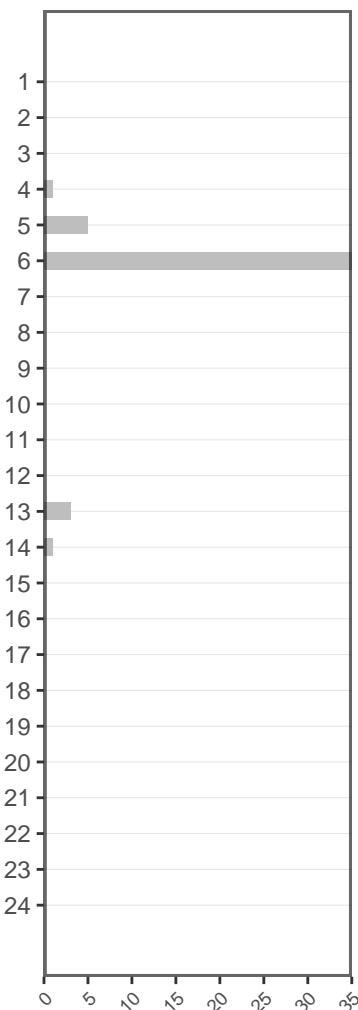
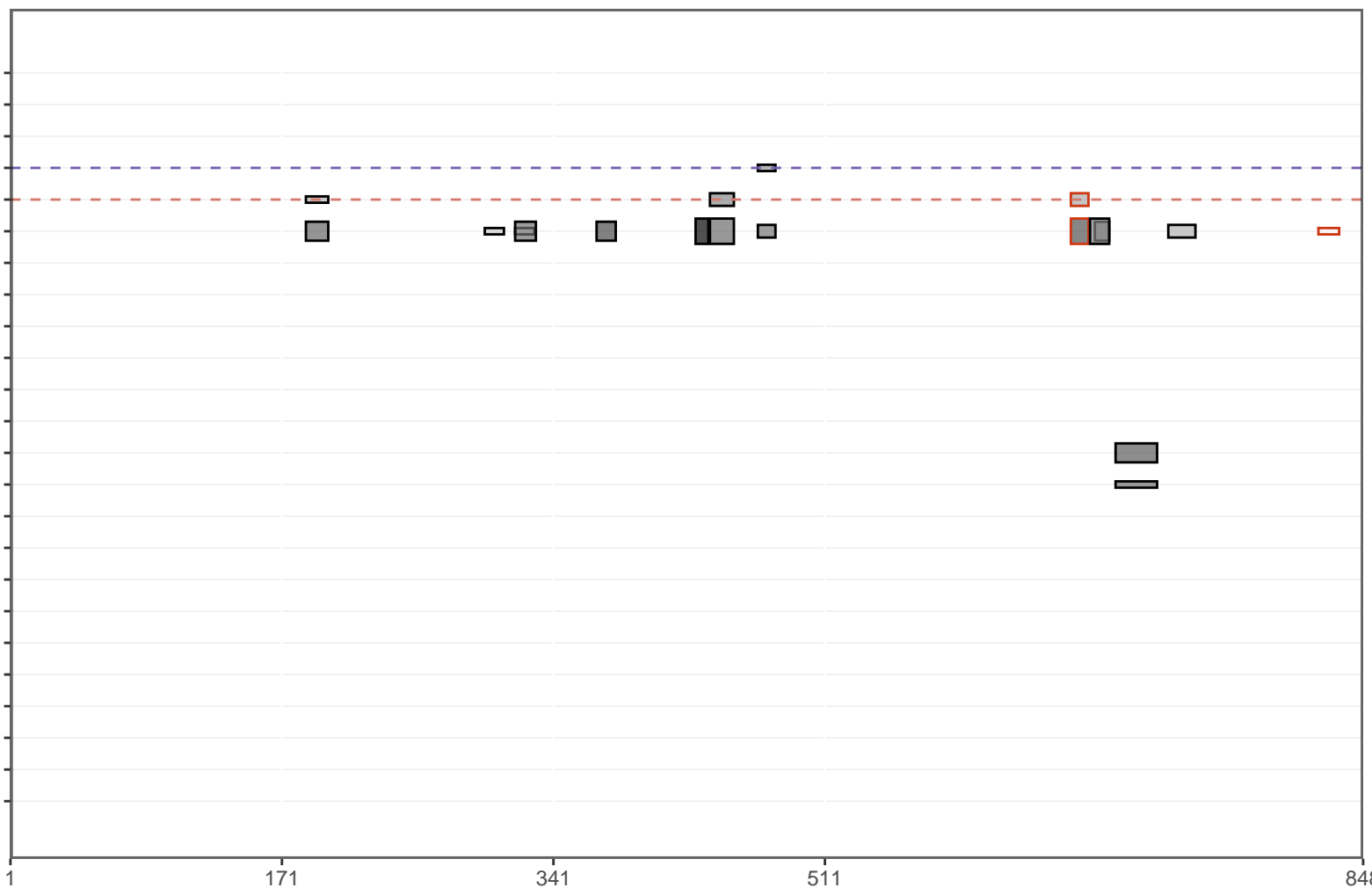
MW indication



Molecular weight

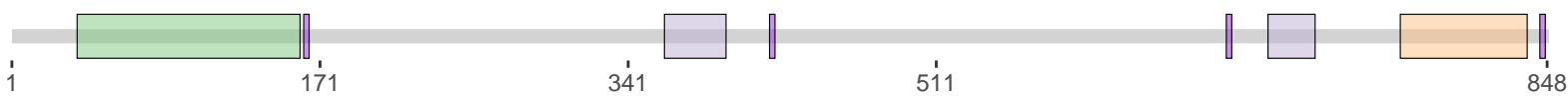


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- PF00168 C2 domain
- TM Domain
- PF00614 Phospholipase D Active site motif
- PF12357 Phospholipase D C terminal

Protein sequence:

/HKKDYHCPNYTGFTTGCPREPWHDLHSRIEGPAAYDVLNFEERWLKASKRHGLGKMKASODDALLQLDRIPDLKIAADVPLCLREDDADTVHWQIFRSIDSNVWGFPKDKPEATNKNLVCGKNYLDMSHTAYKAIKAAAGHFVIENGVYFLGSSVWVWNYQNLGANNLIFMEALKAANKIRANERFSVWVPMWPEGVPTSTATQRIKLFWGHNTMGMMVETWYKALVEVGLENTYEPDQHLNFFLGLGAREVQEGGNNTVWKSFKATPQELGKSRRFMTYVHSGMP

NbL17g25740.1 uncharacterized_LOC109240160 [MW = 138.05 kDa]

No. of times detected



log(intensity)



Values from



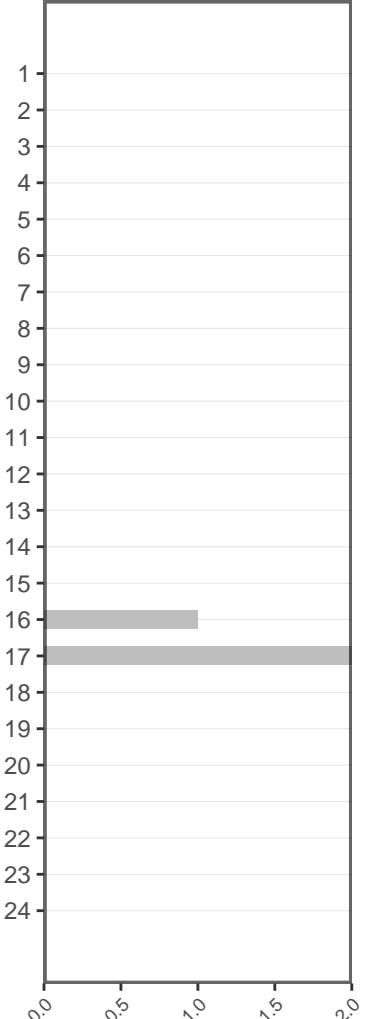
MW indication



Molecular weight



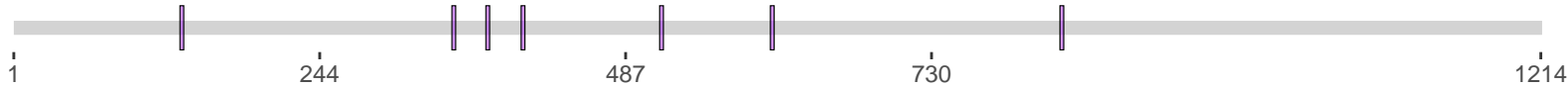
Gel Slice



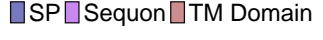
Protein length



Pfam domains



Pfam Description



Protein sequence:

ITLSWFLNQSANTAHYHPAFYEKREDLNINGLREARTDPGPNRSR6RSFQTSKSKHVFSTSDLPFGDALSDGDPKLIHDGPNLKGKYPGEVAS5CFMSEFMFELDSP6CAYGNLFGDPKKGSPALLAFETGARQMYH6SR6PR6GRLLFFVFDRAAFPH6TRPALFTNLYNRCHKDSGLYQRNKERGDNLAPDIRR6G6SGEKRKNH6KTTIVRGGFYRKTPTFWFGTDHNY6MESAKHVELPGEELGTGTRR6ENHLNGGDCIS6FVPH6SNV6GSK6T

NbL17g25630.1 subtilisin-like_protease_SBT1.2 [MW - SP = 77.37 kDa]

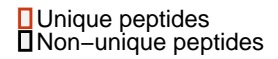
No. of times detected



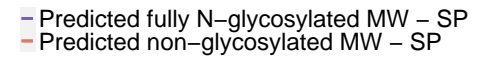
log(intensity)



Values from



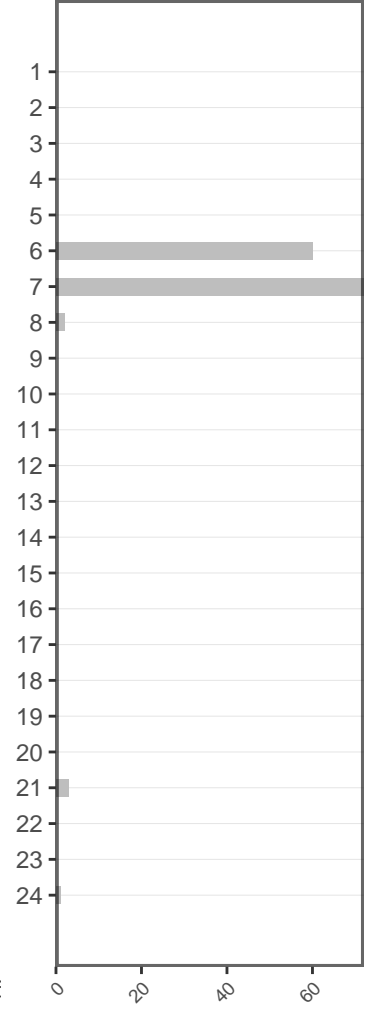
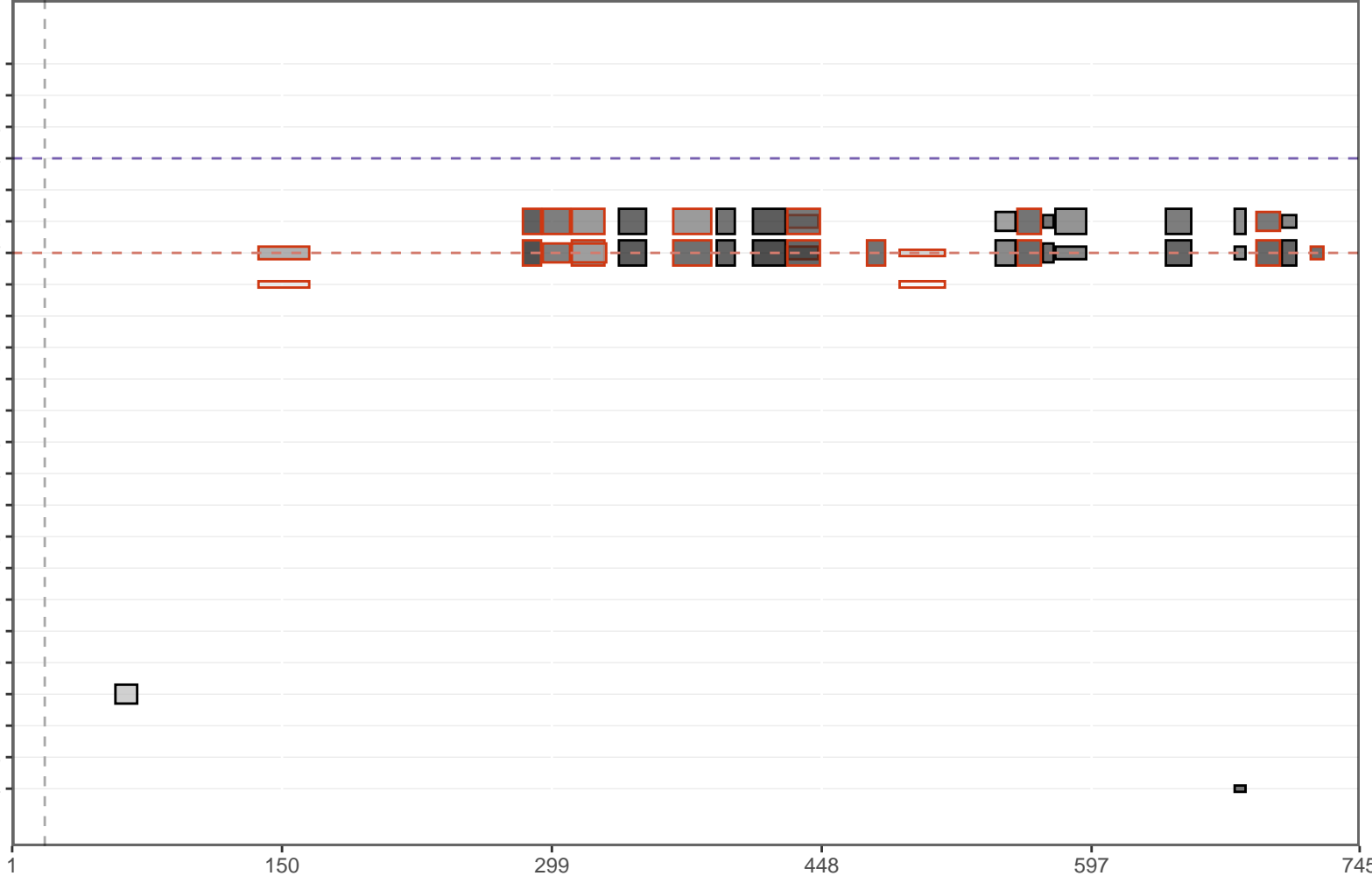
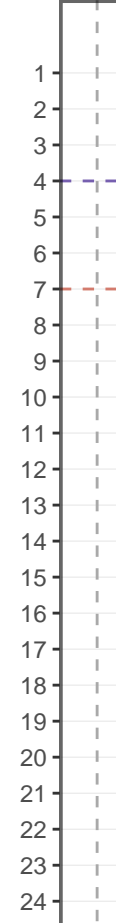
MW indication



Molecular weight



Gel Slice



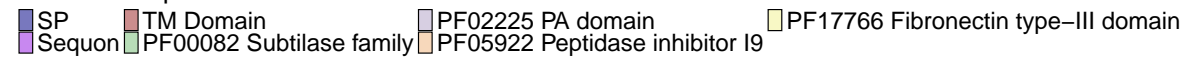
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FTLFDVKEKIVHEQIPVAFPGISGLTDFPSIRGKIVVGLVGGGVRTVQKGVVNDAGGVGMILNPEDEGVTKSAEAVLFLALGVSDADGKIKLAVNSTENPVAATFTHTGTVLGGKNAPVAFSFRGPRSEASRGLKPKDIKPGVNVLLAAWPTGVQNNKNTKSTFNISGTSMSCFHLGGIAALLKSVKPDVWSPAAKSAAMTTDTLNLAKNPILDERLSPADIFAIQAGVAVNPSRANDPGLVYDTPFEDVYVPLCGLNKYNTRREVGLKGGKVNQSEVKKIPEAGLNYPFSFSLRSTP

NbL17g25620.1 copper_chaperone_for_superoxide_dismutase_chloroplastic/cytosolic [MW = 34.1 kDa]

No. of times detected



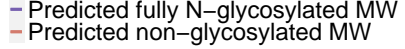
log(intensity)



Values from



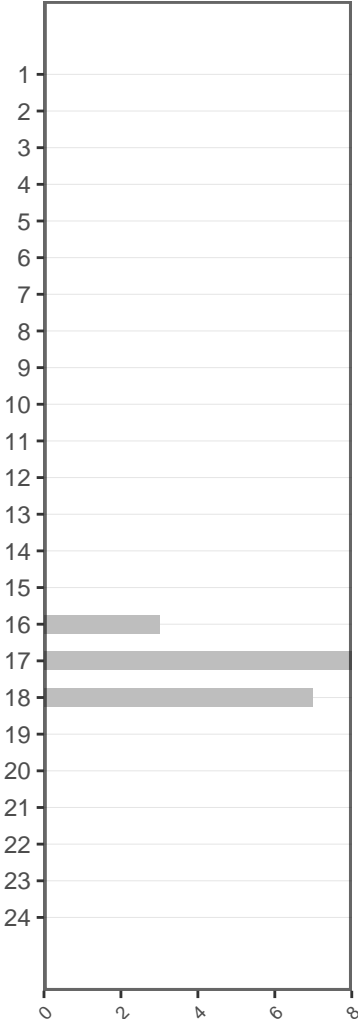
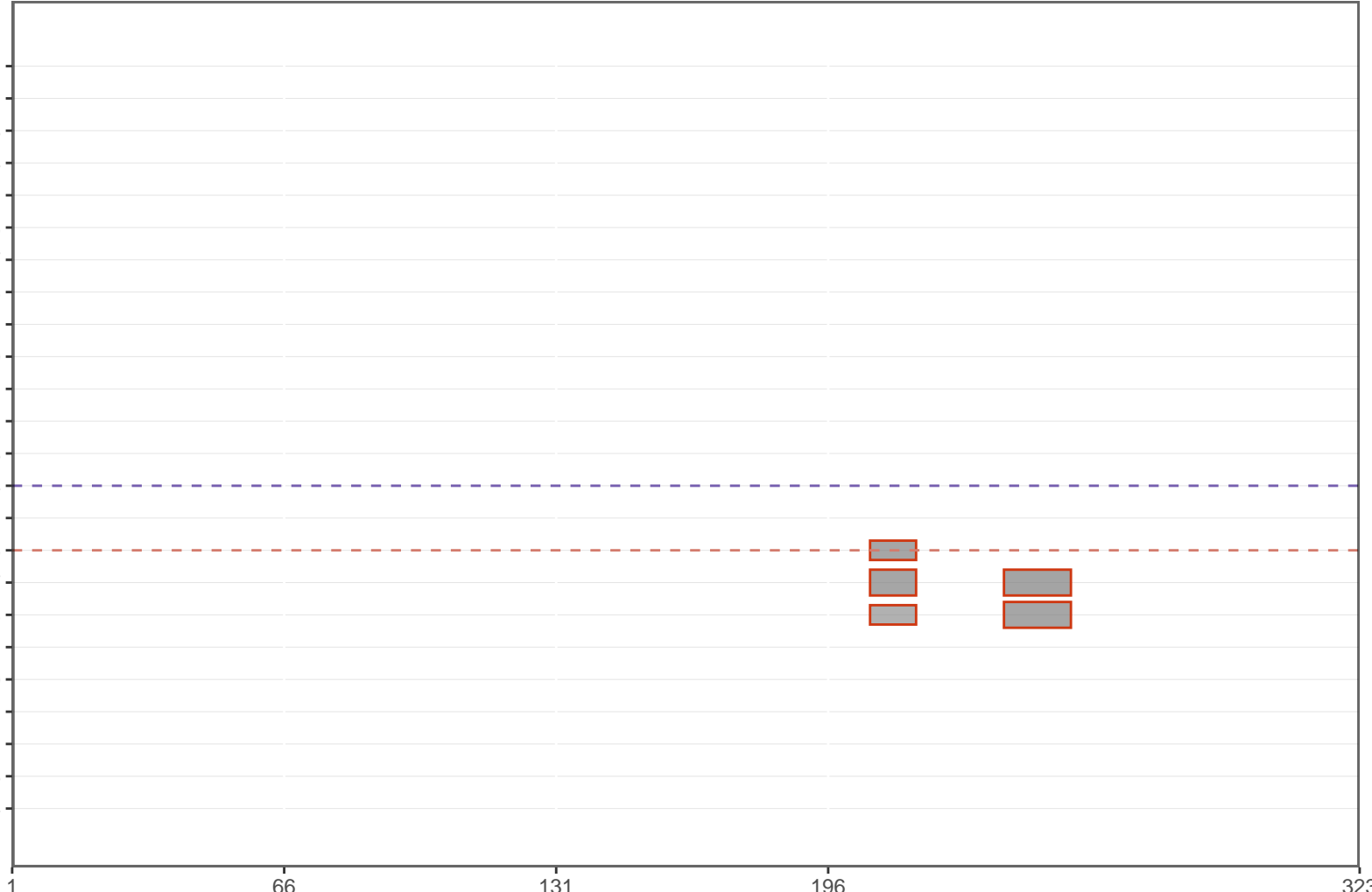
MW indication



Molecular weight



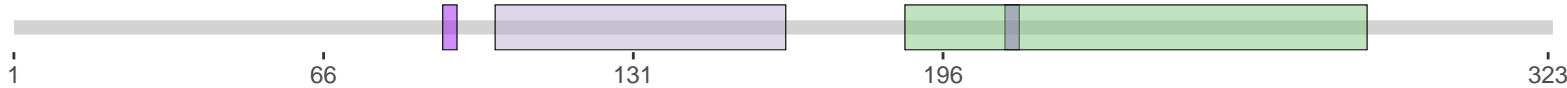
Gel Slice



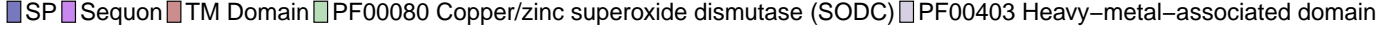
Protein length



Pfam domains



Pfam Description



Protein sequence:

SSPVKILTELEQTGRKARLGGGVDFDLISAWAEFKGSDFGVRLAGVNIELTRIEANFSGLSFGKHAWISNEFGDLTRGAABTGKLYGPPVGDGLGTLVDGKGEAFYSGAKEKLRVADLIGRAWVYSTDKSDPLKAAVIARSAGVGENYKLGDTGDGTTIWEATNKLY

NbL17g25610.1 enoyl-CoA_delta_isomerase_1_peroxisomal [MW = 26.85 kDa]

No. of times detected



log(intensity)



Values from



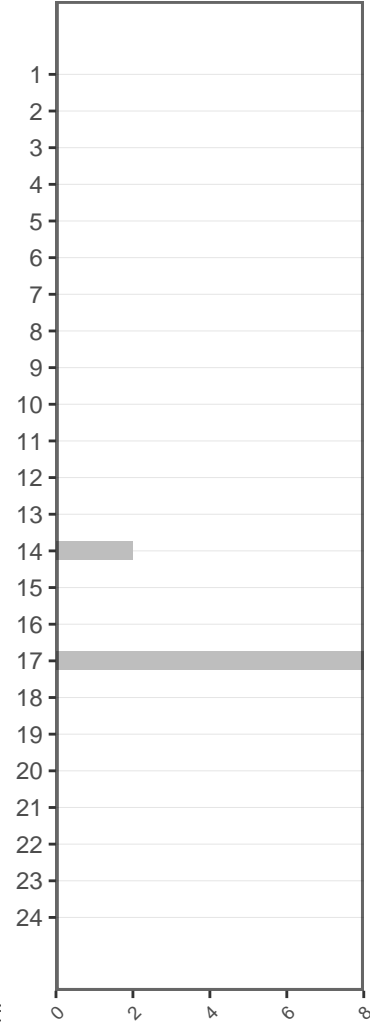
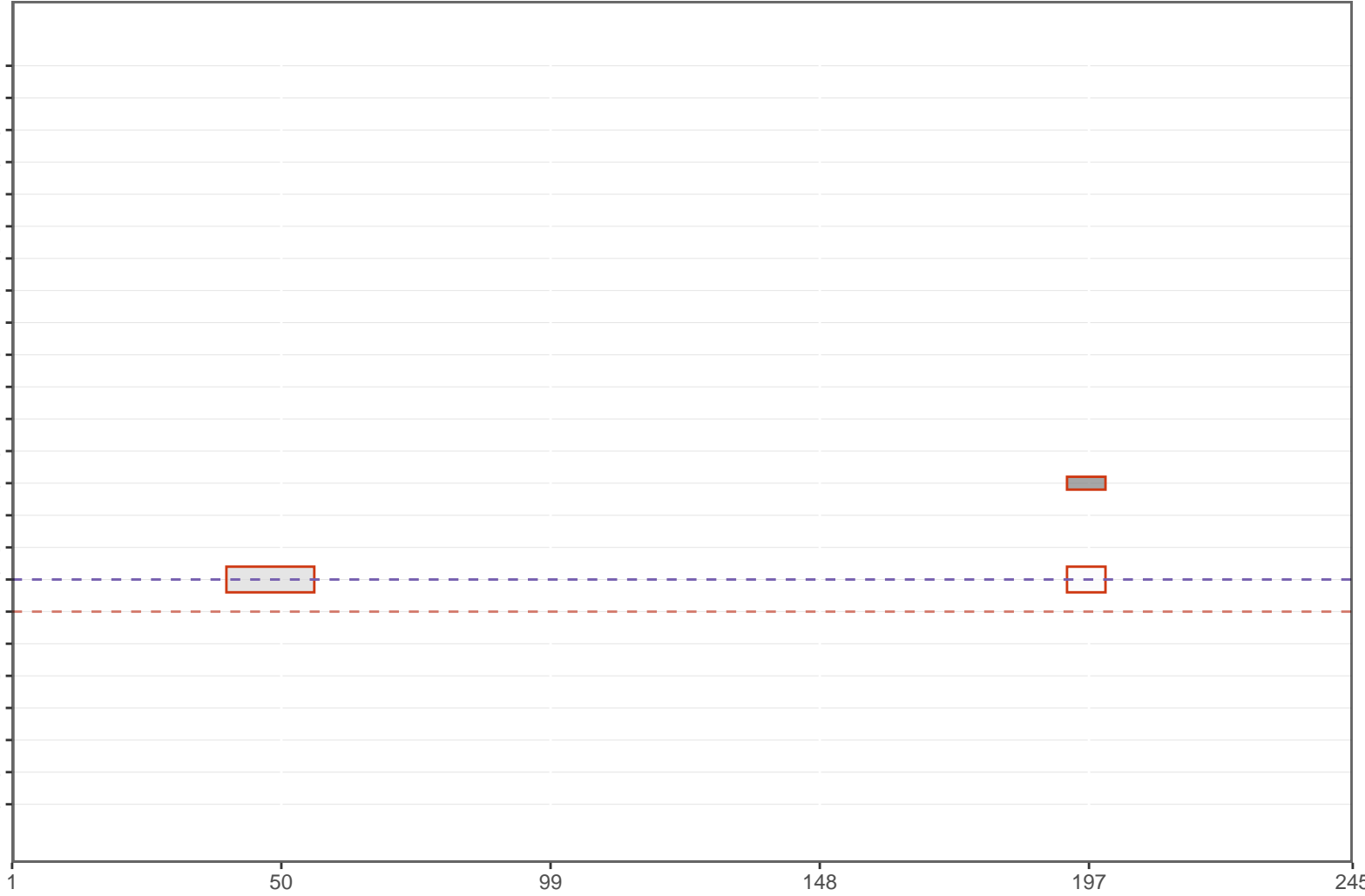
MW indication



Molecular weight

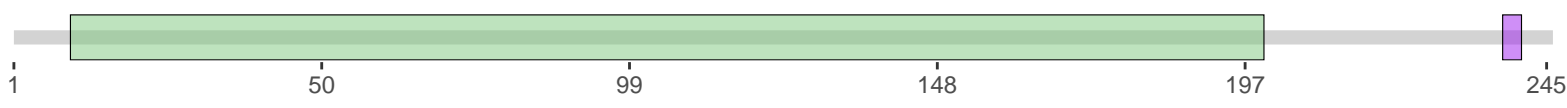


Gel Slice



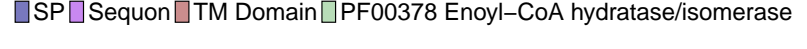
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

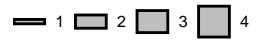


Protein sequence:

.SHDYLNRKDDGFLGMSLELDGKFKPWFVFLVLLKGVGSPWVWREVLVKSAMTAEMGVEMAVDSAHSGAETVEAANRLGEEVSRNWDGNVYDGRKTLVOLLNLSLGSDETGVHYGEEKPKTLGRLL

NbL17g25510.1 probable_LRR_receptor-like_serine/threonine-protein_kinase_At1g12460 [MW - SP = 92.52 kDa]

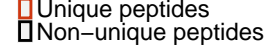
No. of times detected



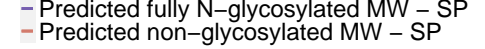
log(intensity)



Values from



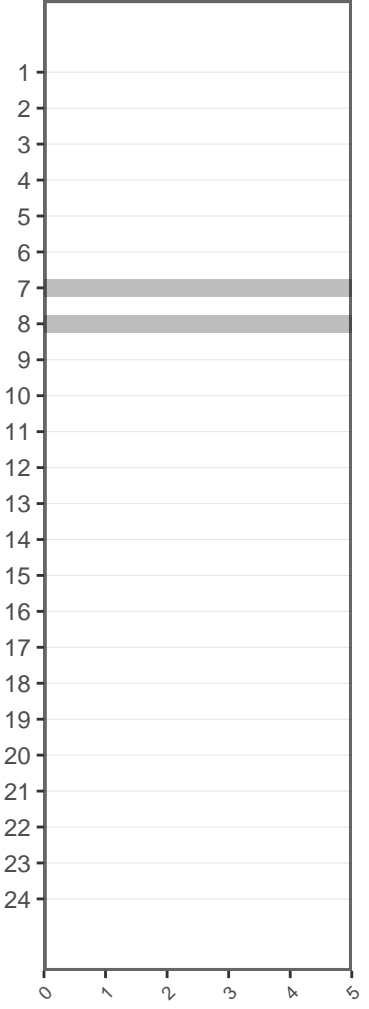
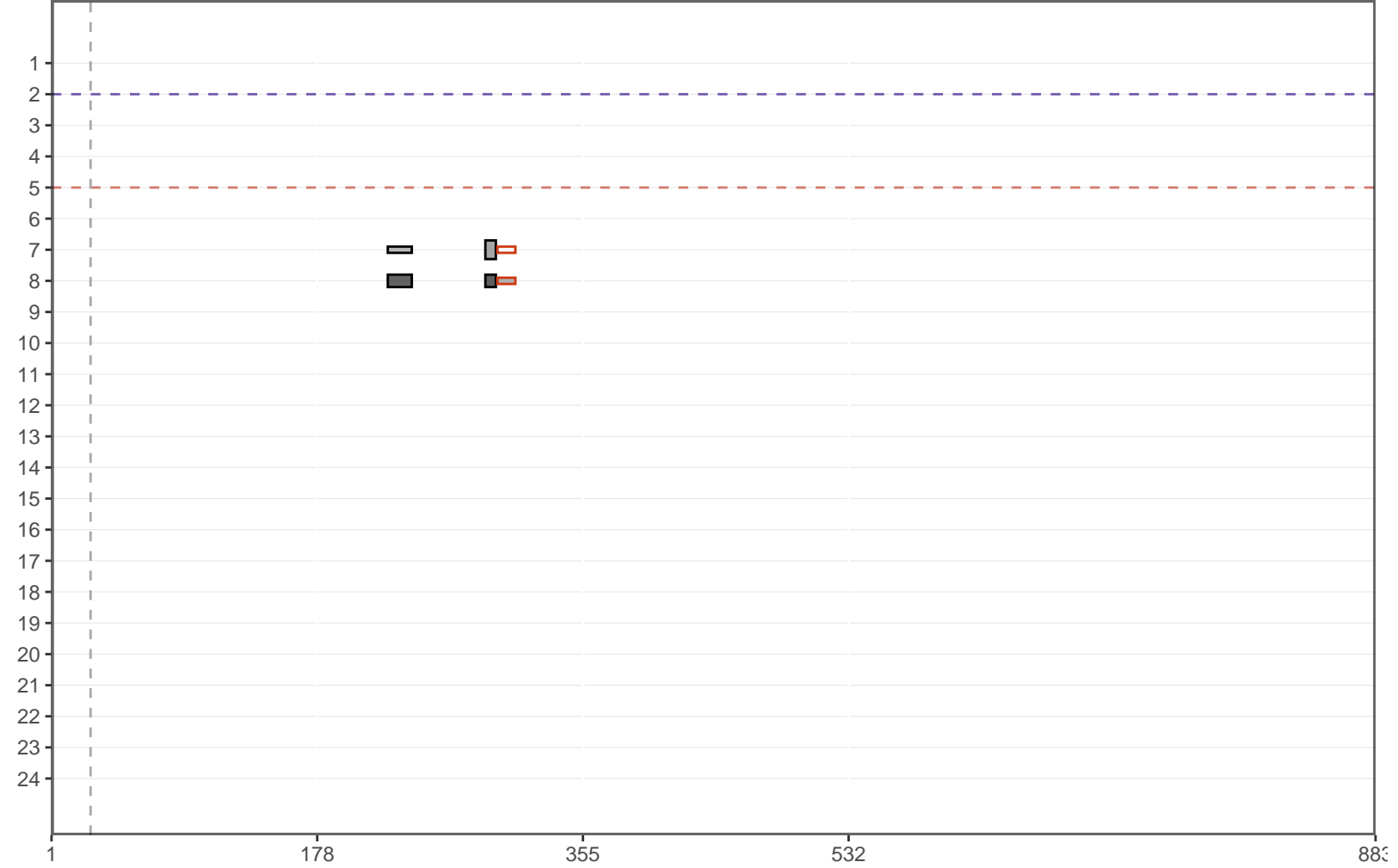
MW indication



Molecular weight



Gel Slice

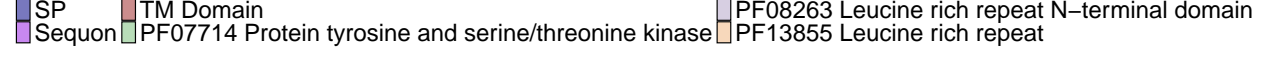


Protein length



Pfam domains

Pfam Description

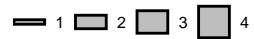


Protein sequence:

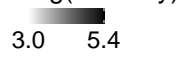
NLSNLHFLDLSQNLKGGSPVAGLGNLHNLTHFNISVYVNLGGAPISBEGQGFQPSAFFHNSGLGGAPLQVSCYPSGAPAVKPKRLLSASAVAVAAVLTGVLTITNKKARRRRRADETHIVESTPLASTESNIVGKLVLFKTLPSKYEDWEAGTKALLKESLGGGTGCVYRTSFEFGGVSIAWKKLETLGRINQDFEFGEGRLGTLHHPNLVALGGVYVSSSMQLLSEFVFNQGNVYNNLHGLVYPTGTGQVPELWPRRFQAVGTARALAVLHEDCKPPVLIHNV

NbL17g25390.1 ATP-dependent_Clp_protease_ATP-binding_subunit_CLPT2_chloroplastic-like [MW = 29.13 kDa]

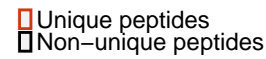
No. of times detected



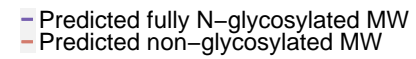
log(intensity)



Values from



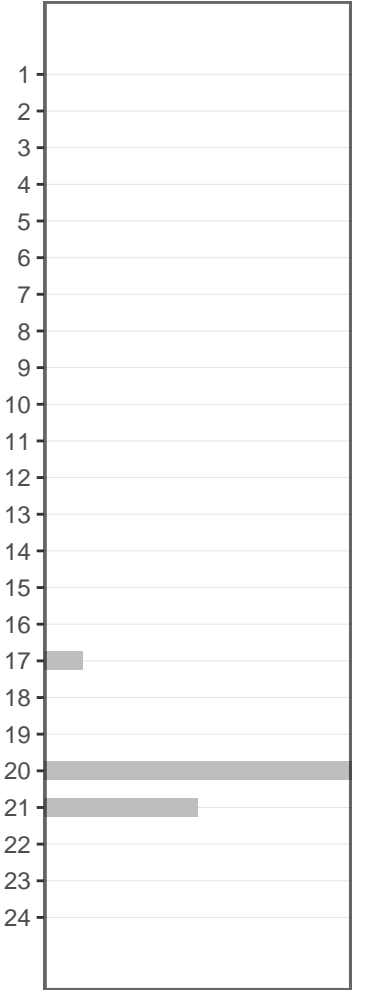
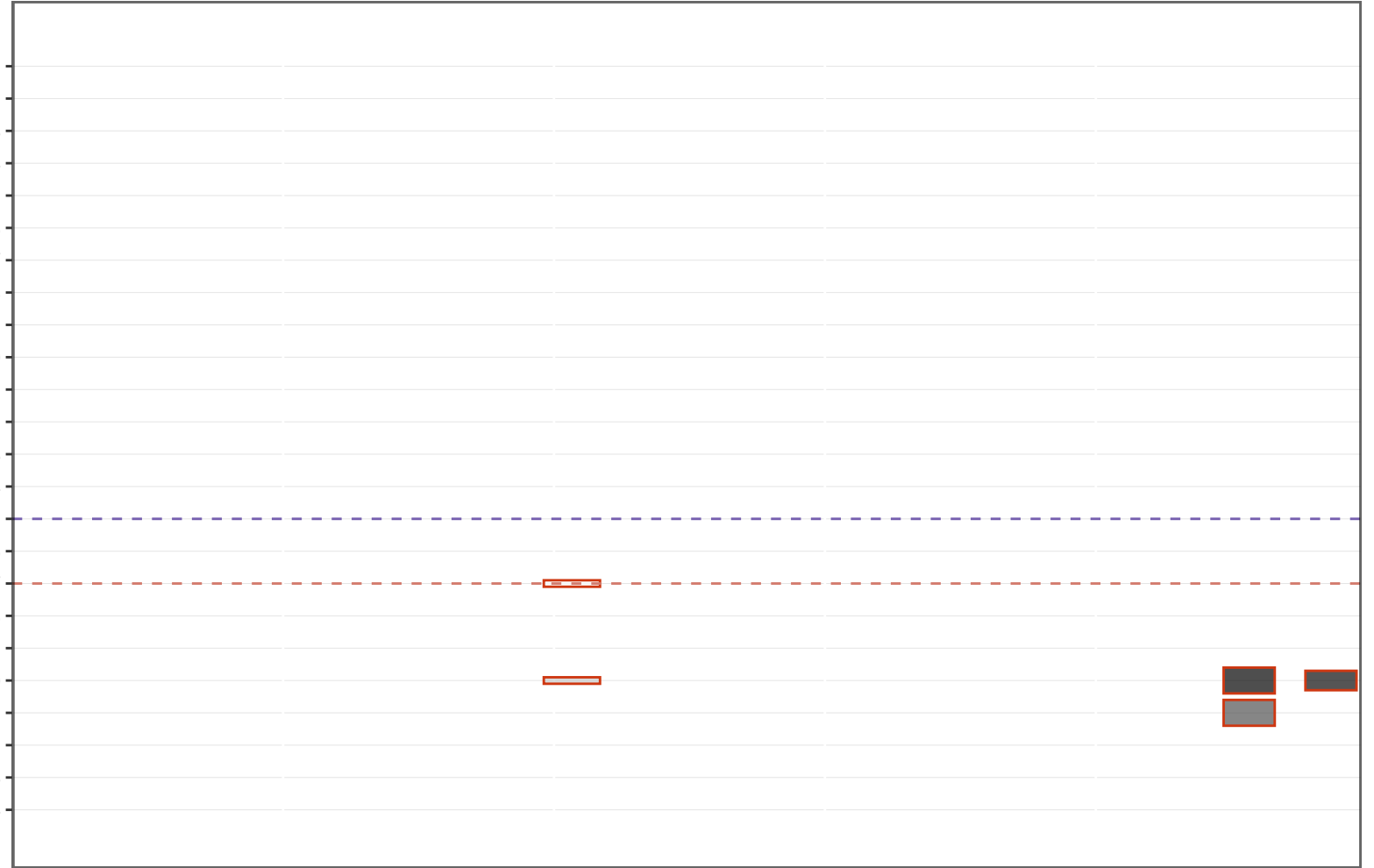
MW indication



Molecular weight



Gel Slice

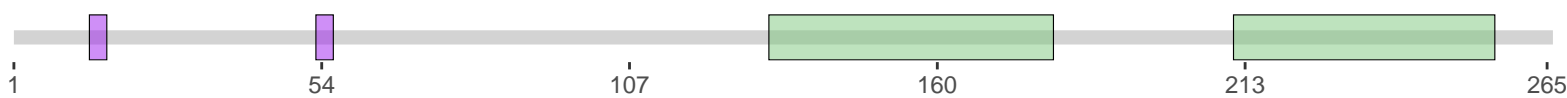


Protein length

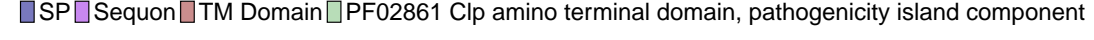
Peptide counts over 4 repeats



Pfam domains



Pfam Description

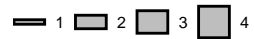


Protein sequence:

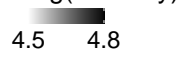
KAIKSFAMGELIARALKYPTTGTTEALLMGLEIGETNFASKYLRRANSIFLFRVREETIKYLGKADMMWFFSPEHPPLTDDGKALDVALDEKLKSSDNGEITFTTHLLGVWSQVSGSPGYKILSALGFNDEKADLKNVISEPQFVDD

NbL17g25360.1 ATP-dependent_Clp_protease_proteolytic_subunit-related_protein_2_chloroplastic-like [MW = 36 kDa]

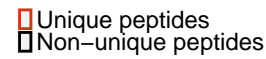
No. of times detected



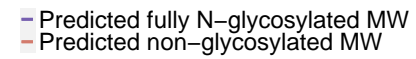
log(intensity)



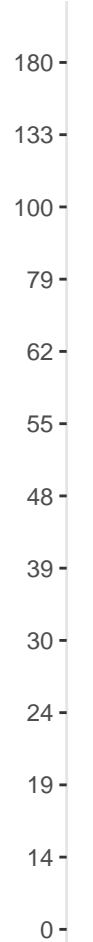
Values from



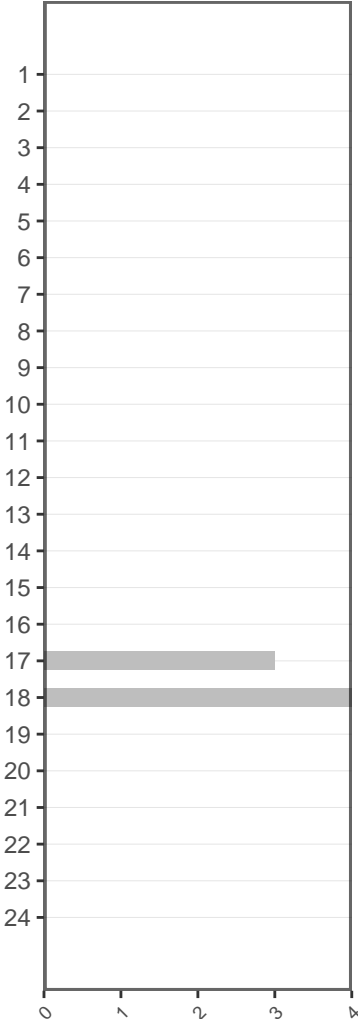
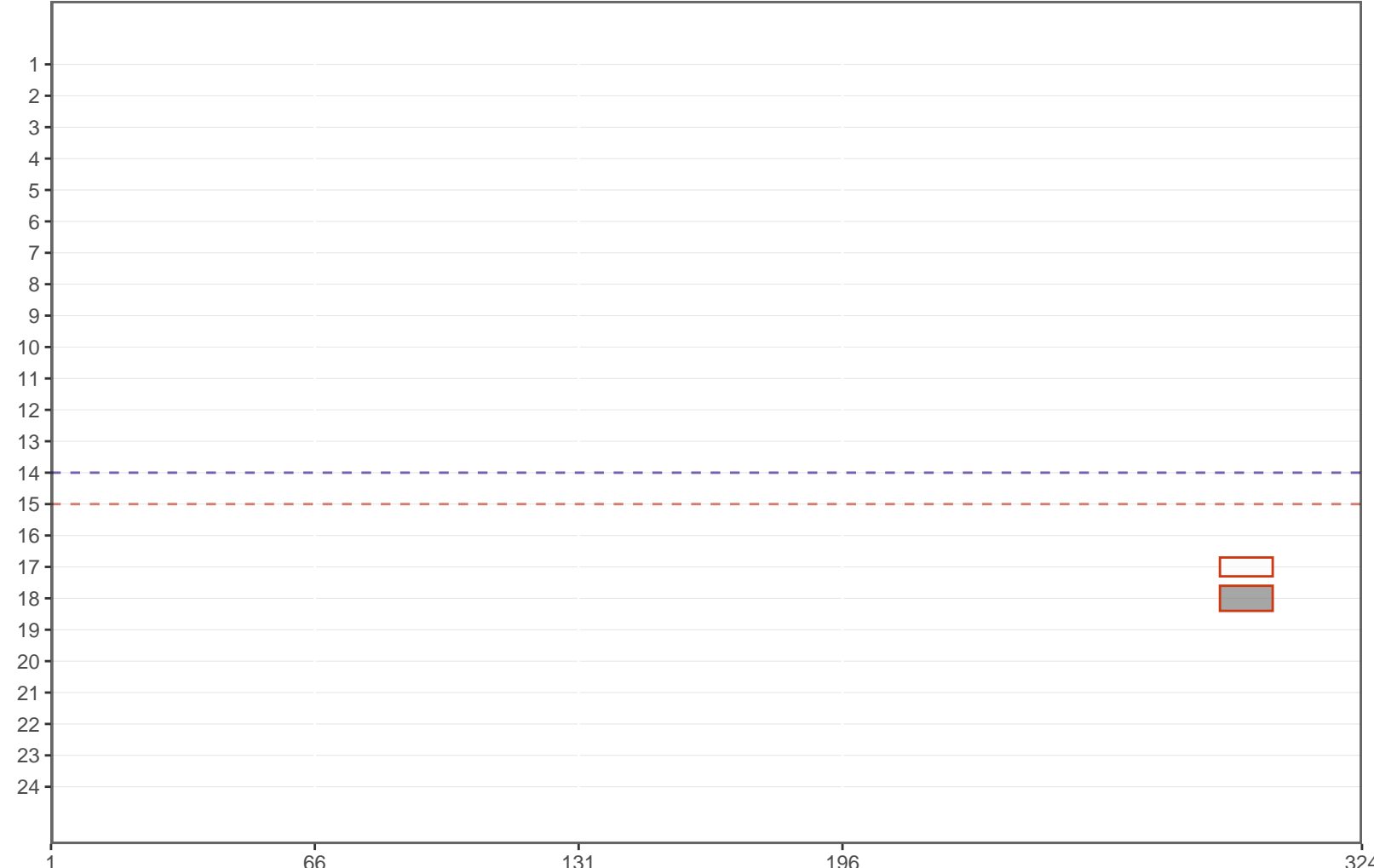
MW indication



Molecular weight

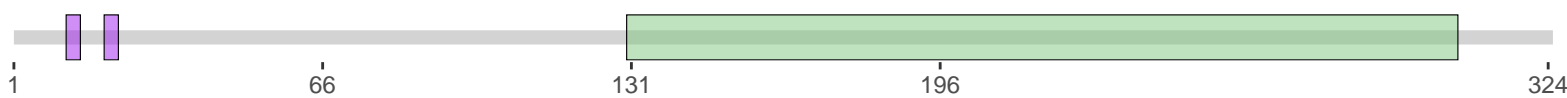


Gel Slice



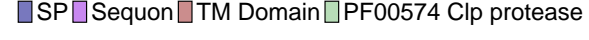
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

QHIDEEFSNQLATMLVLDSDSDSKKLYLNGPQGGDLTFPMAYDTMDSLKBVAGTHGVGWAYNLAGFLLAAGEKGNRFAMPLSRHLAGPAAARGDADIRNEADELLRIRDFLKELAEKTDGQVPEKWHKDLSRMKRFNAGEALEVGLDRVRRPRIKADAPRIKDTTAGLG

NbL17g25240.1 peptidyl-tRNA_hydrolase_ICT1_mitochondrial [MW = 26.3 kDa]

No. of times detected



log(intensity)



Values from



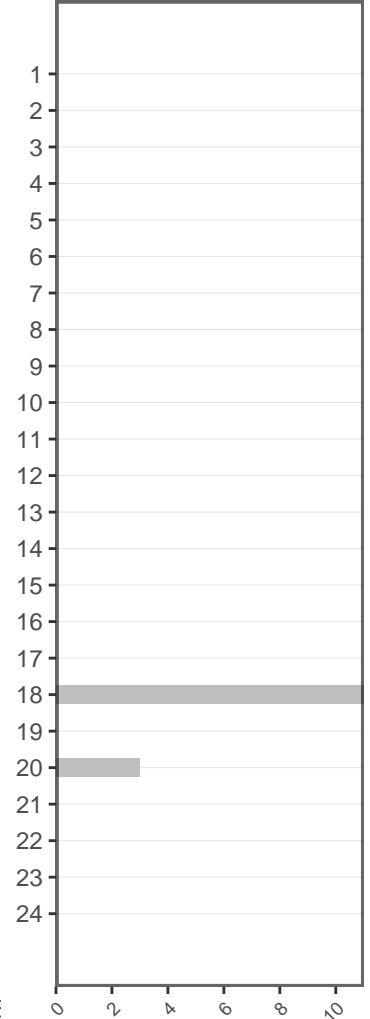
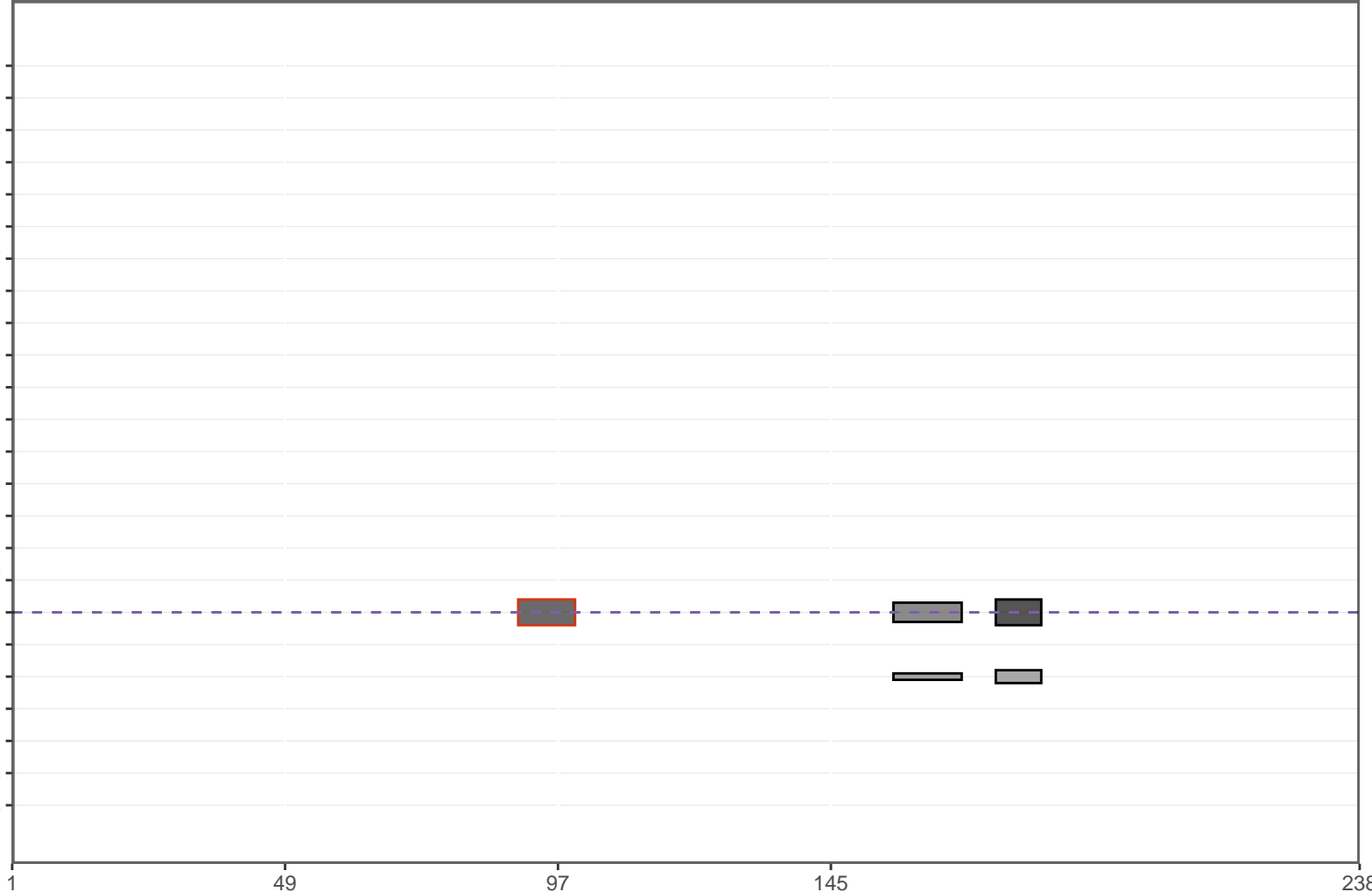
MW indication



Molecular weight



Gel Slice

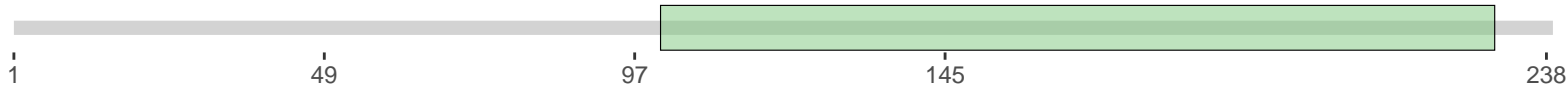


Peptide counts over 4 repeats

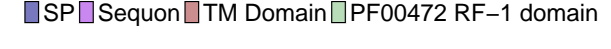
Protein length



Pfam domains



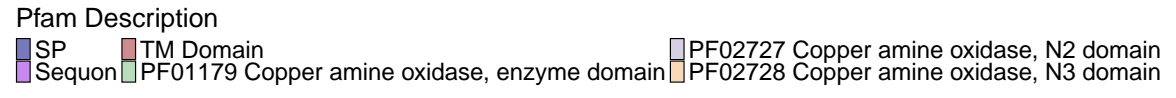
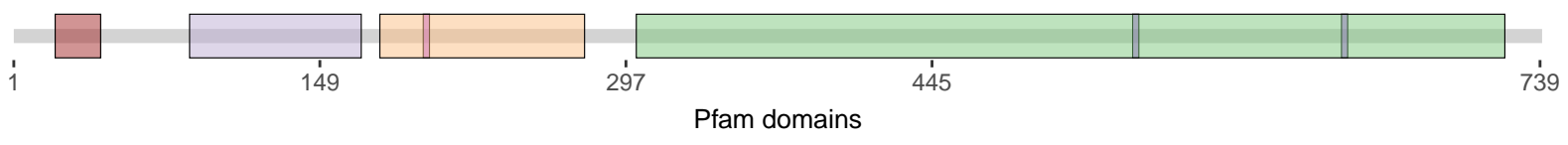
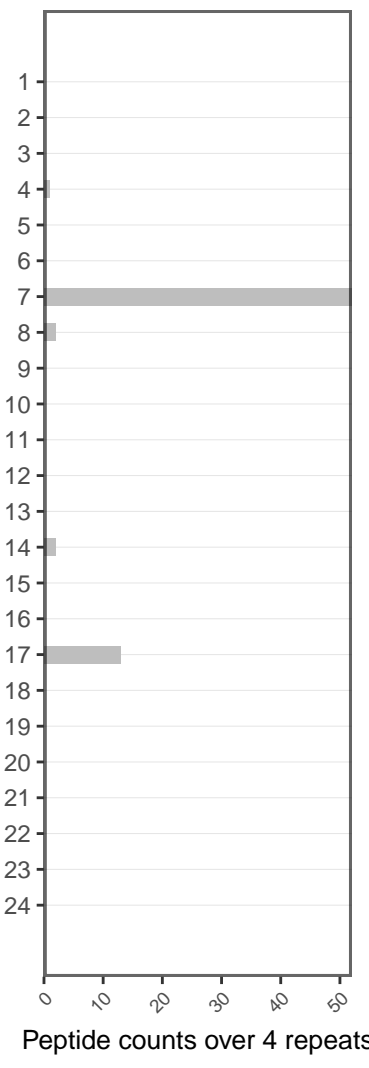
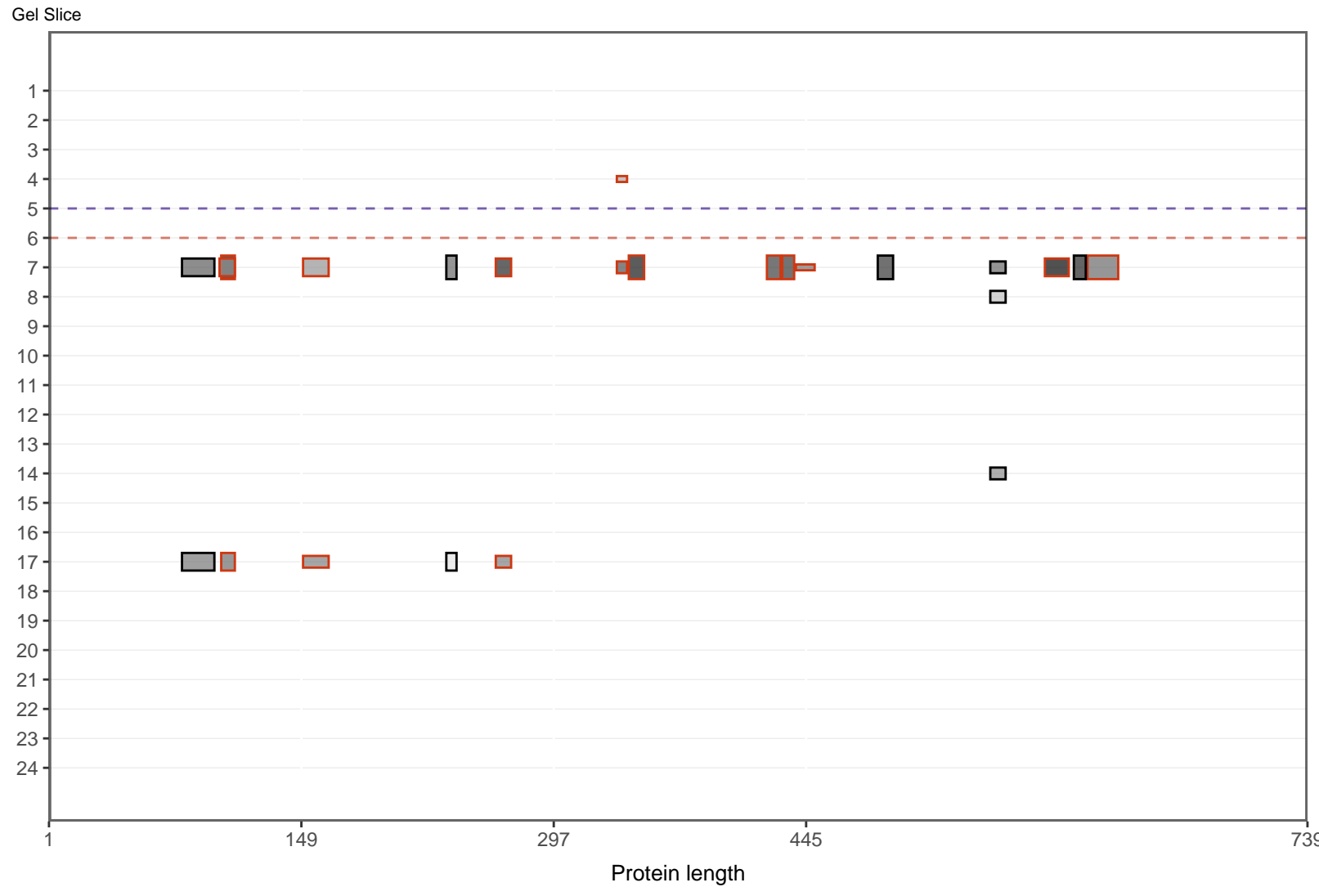
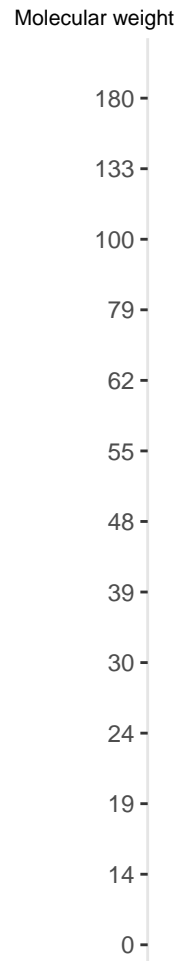
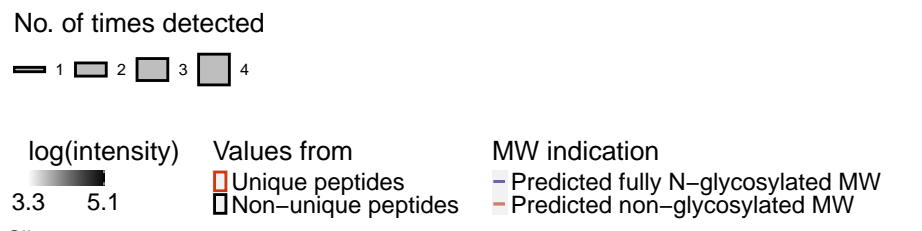
Pfam Description



Protein sequence:

/NFARSGGPGGQNNKKNKTRVDMRFNKNVAVLSDRVREKILGMENKRNKNDGELVISEKTRTGKGNMEDALSKLQAIDAASVYPPPPSEEQVKRIAKLAAGERKRLNKKKAGSGKKAIRREKDGWD

NbL17g25180.1 primary_amine_oxidase-like [MW = 83.54 kDa]



Protein sequence:

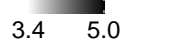
TSELFVPIYMDPSDAWYFKTYMDAGEVFGGLGAMFLDPLNDGPRNAYYMDGVFAADGTPYRISNMIGVFERRVAGDGGWRHAEISPTGLFRRVRRKVTLLVRRMAASVANYDQVVDWEFQTDGLIRAKVGLGILMKGSPYYMMNGVNGNEVLYGTLLENIGVHHDHYHTRHLDMDIDGSGNNEFVKNLQKATTSPPGESPRKSEYLRVRRVAKTEKDGAKLKYDPSSEPHVNPNEKSRVGNPAGYKIVPGSTAALLLENDPPQKRGAFSTNNGWVTPYNESEQWAGL

NbL17g25120.1 uncharacterized_LOC104104568 [MW = 28.48 kDa]

No. of times detected



log(intensity)



Values from



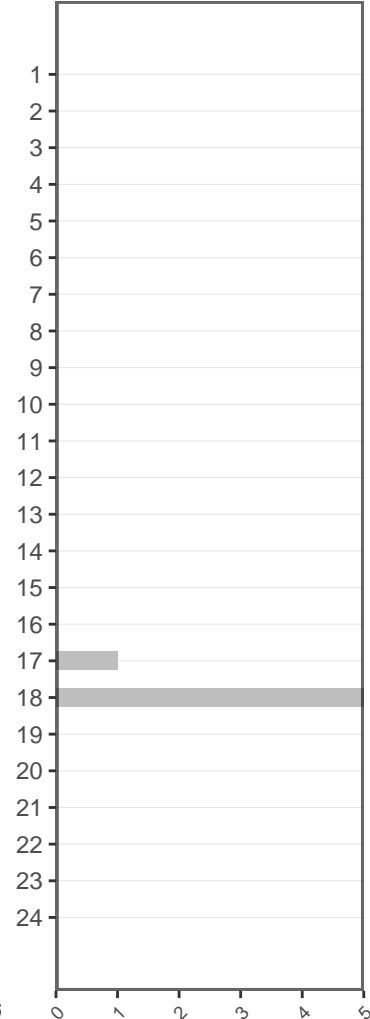
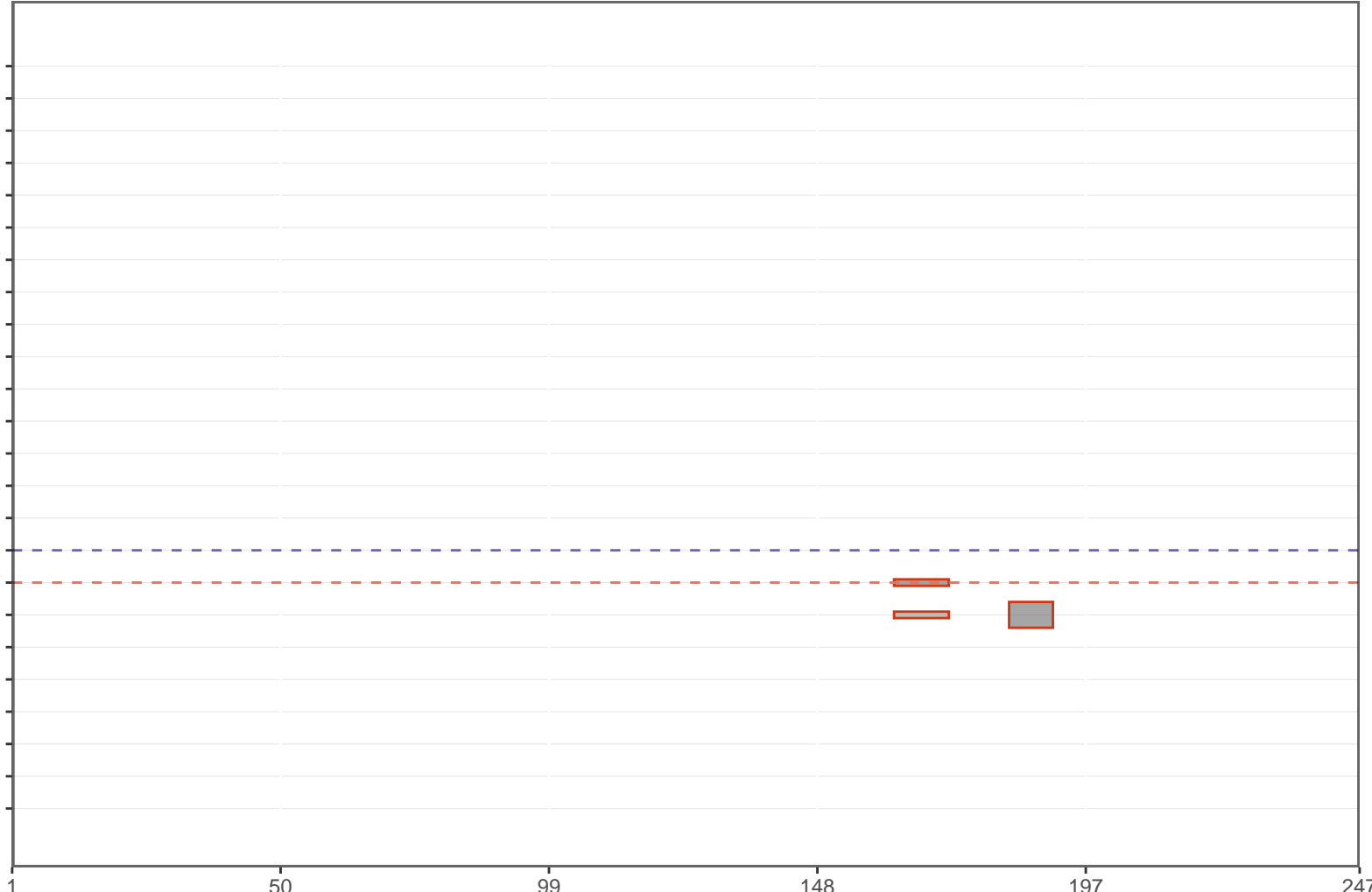
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats

Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

EAQIEIEFARLRPRNLKEFFDHLQVEVGLRFSMTKTKGVEDRLIELEAGKALQEAFAFDKMEADIVATKKNLTELTSKDKVKATLLOLVERNELNRPPLTLLDENATAHVNGKGAAYMEKLRGLVLYLTV

NbL17g24960.1 protein_IQ-DOMAIN_32 [MW = 97.86 kDa]

No. of times detected



log(intensity)



Values from



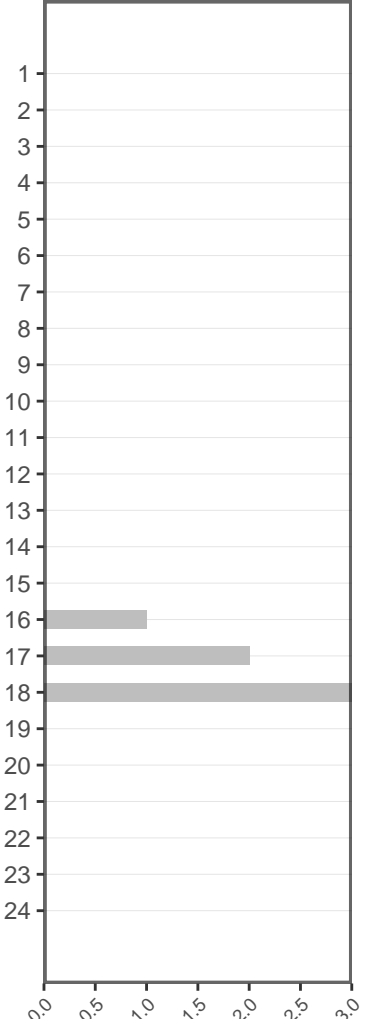
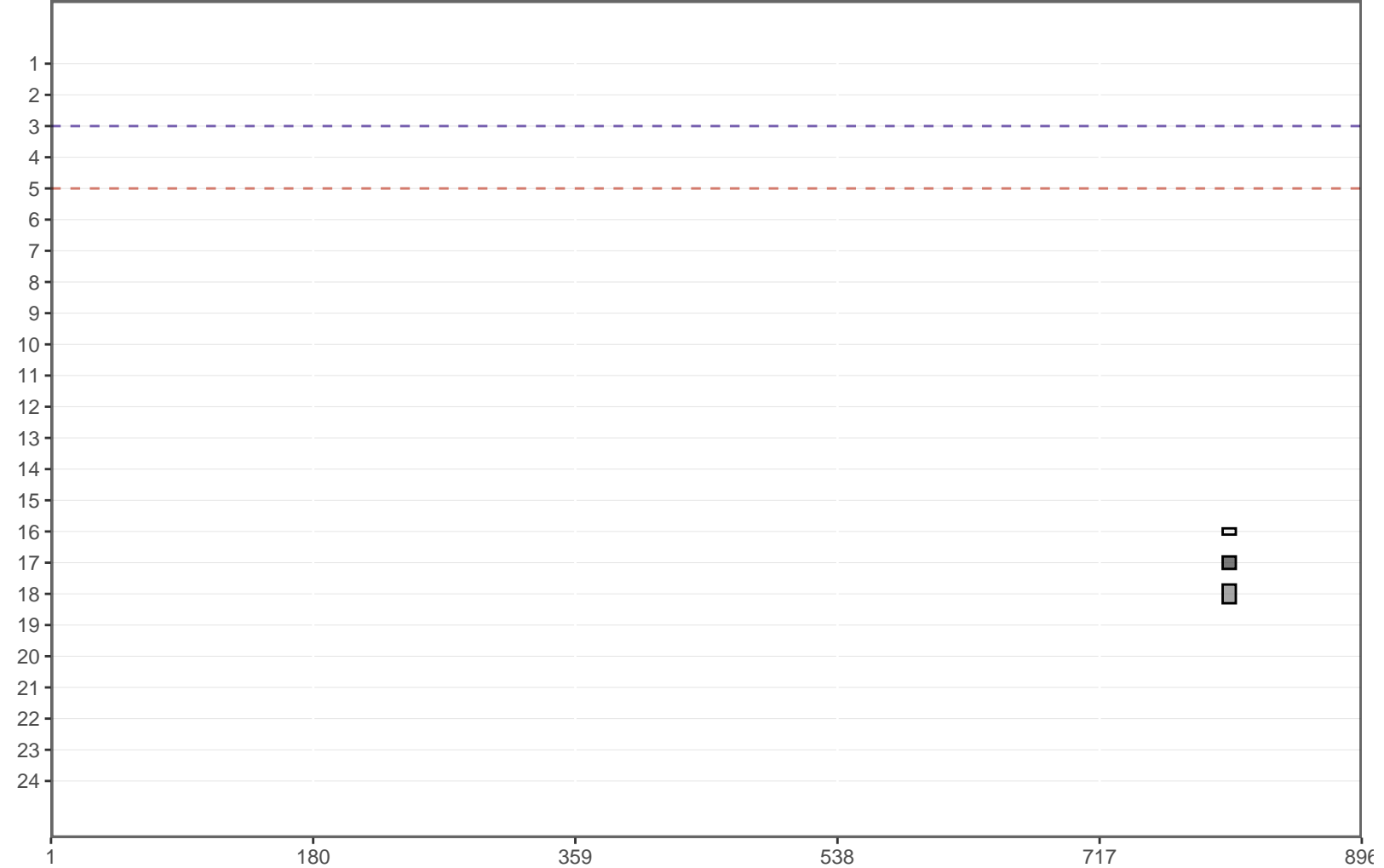
MW indication



Molecular weight



Gel Slice



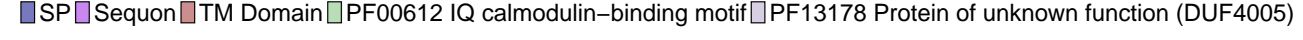
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

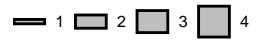


Protein sequence:

APLLESDHELITYDADSLVGVADIPVPPGPGNVDETNSRDDNFQSPITQYKESELLPESETNSFPKATEADSDDTLHSLTVEPPETESKQVYHGSRKSNPFAAAGTKFEELTSAANKSTKISLNSNKTDESSSEDTFSGIDQSGFGARETAMSEASVPHSTRAQVGSSECGTSLGSGSTLDEPDRFEVSGAREFEQELKPGVYQTGHNKSGNGYPHGGDNDNLHSDNVQTGTEDPTDANSELKQVMVSSDLSHHEEKPENNVSEVQIEGEAKTRLHKVYSPDASPRSHVT

NbL17g24900.1 5'-3'_exoribonuclease_3-like [MW = 122.11 kDa]

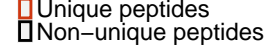
No. of times detected



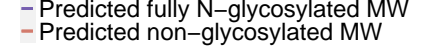
log(intensity)



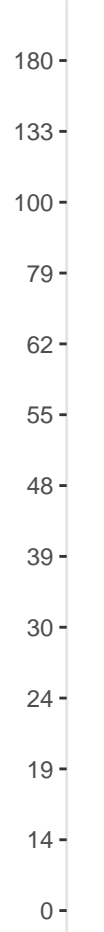
Values from



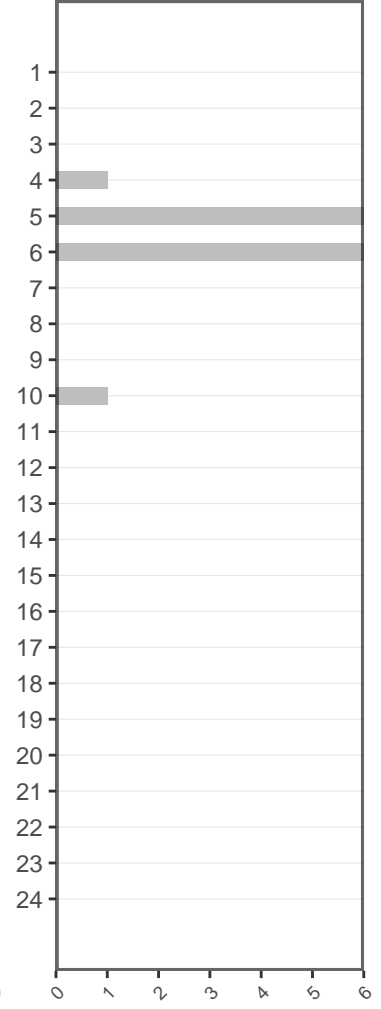
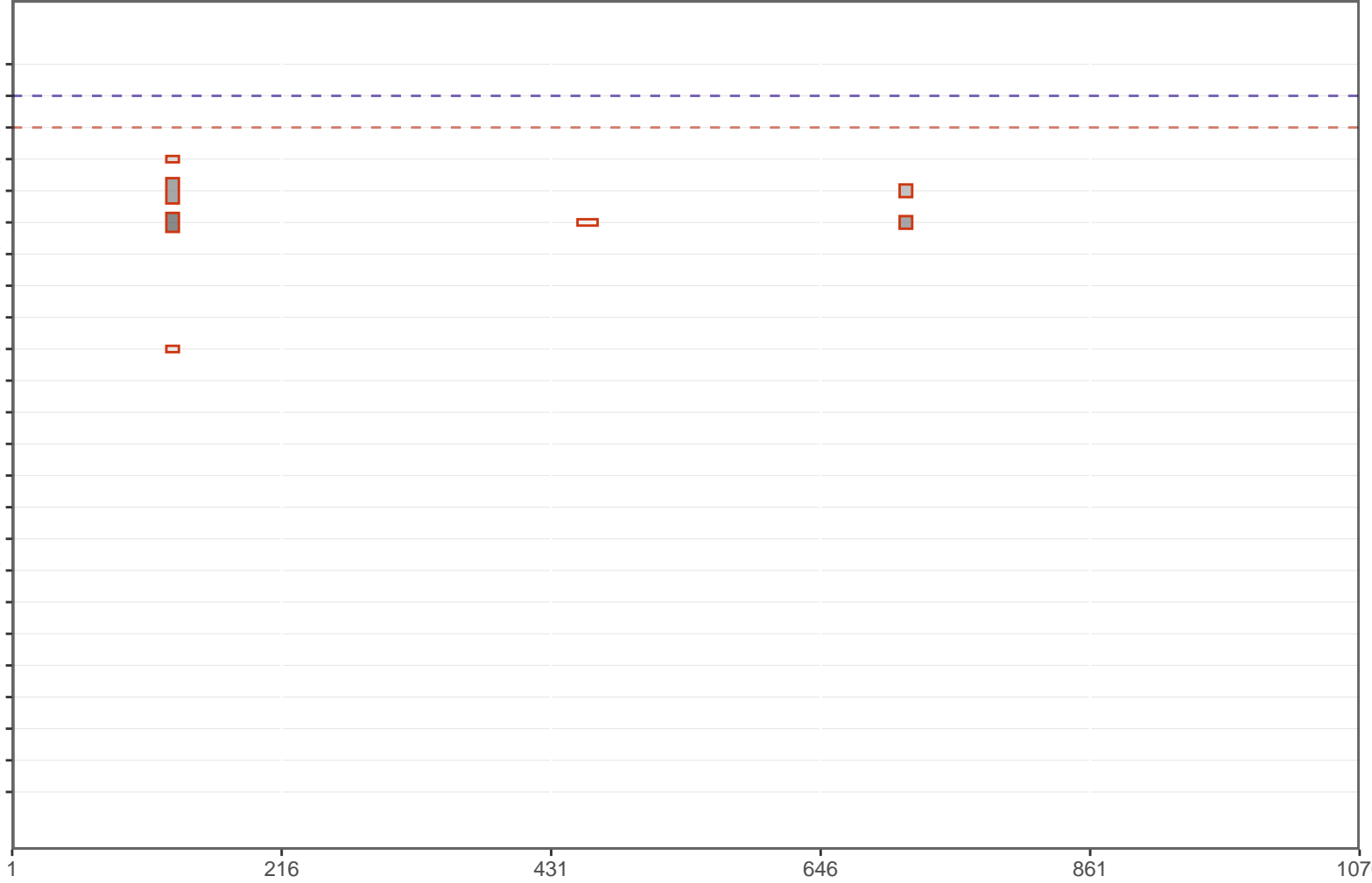
MW indication



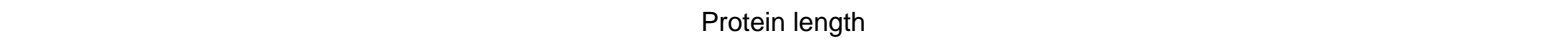
Molecular weight



Gel Slice



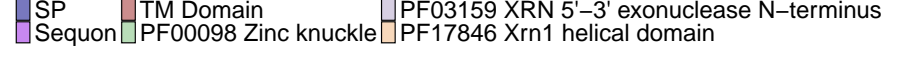
Protein length



Pfam domains



Pfam Description



Protein sequence:

IKLREKNDVFNSEHPEDKIKLGVPGWKERYEERKFSAKTPEEMEEVRRKQVLLKYTEGLQWMMHYHYEGVGSWQWFYVYHYAPFASDLKDISELNITFELGSPFKPFNGLLGVFRAASAAHALPLQVRQLMTDPSNIDFYPTDFEVDMMNGKRFSGWGIAKLPFIDEARLLAEVAKVEHTLTSEEARRNBNVMDMLFVLSLHPLSPYIFSLDRGKQLTQERVEVVKERLDPKSGGGMNGVHSLMGDPPPIFRSPIDGLEIDMDNGVIGAYRLEPFIHQITRPPYGVIF

NbL17g24880.1 endoglucanase_2 [MW = 57.17 kDa]

No. of times detected



log(intensity)



Values from



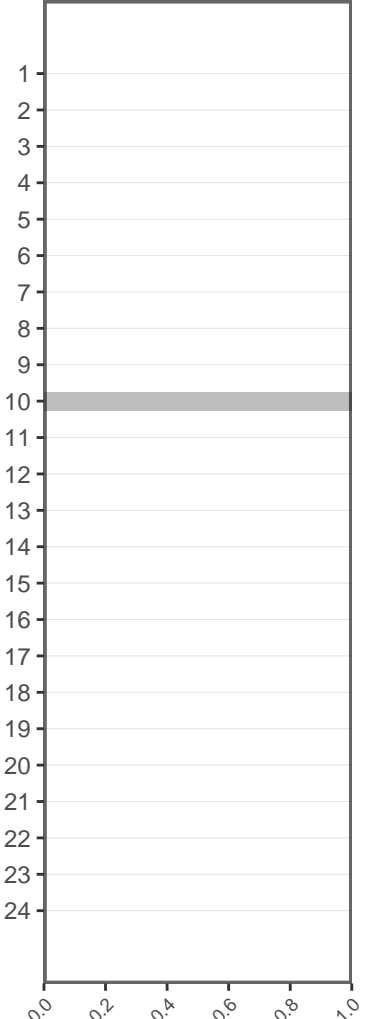
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EVATYVNSITGYDELLWAAGWLYHATGDGQSYVDATGKNAQDFGNGFNPAWFWGSDWNLGAGTGVLLSRVFFDQKGTNSSETLQEVKRTAEAVMGGLLPKPTATSRDTGSLIWEVWNLQHPVAASFLAVLYSDVMLFRTAKTNGSDAVTPSLDRKFAISGADYVLDGNPKMEHLGVGDNPQYVYHHRGASPKDADTQKDGKWKWLDSTERNPNVATGALVGGPFLNETYIDSRNNSMQAERTTYNSAVIVGLLGLVTTSSVVGSEFT---

NbL17g24850.1 probable_diphthine_methyl_ester_synthase [MW = 30.19 kDa]

No. of times detected



log(intensity)



Values from



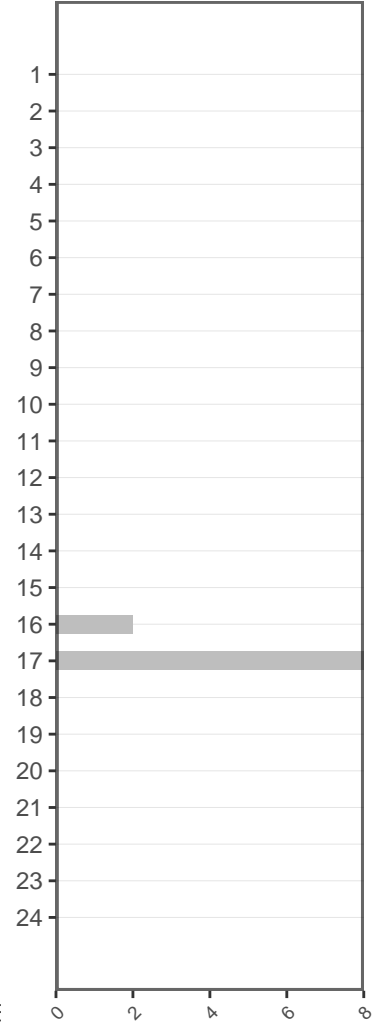
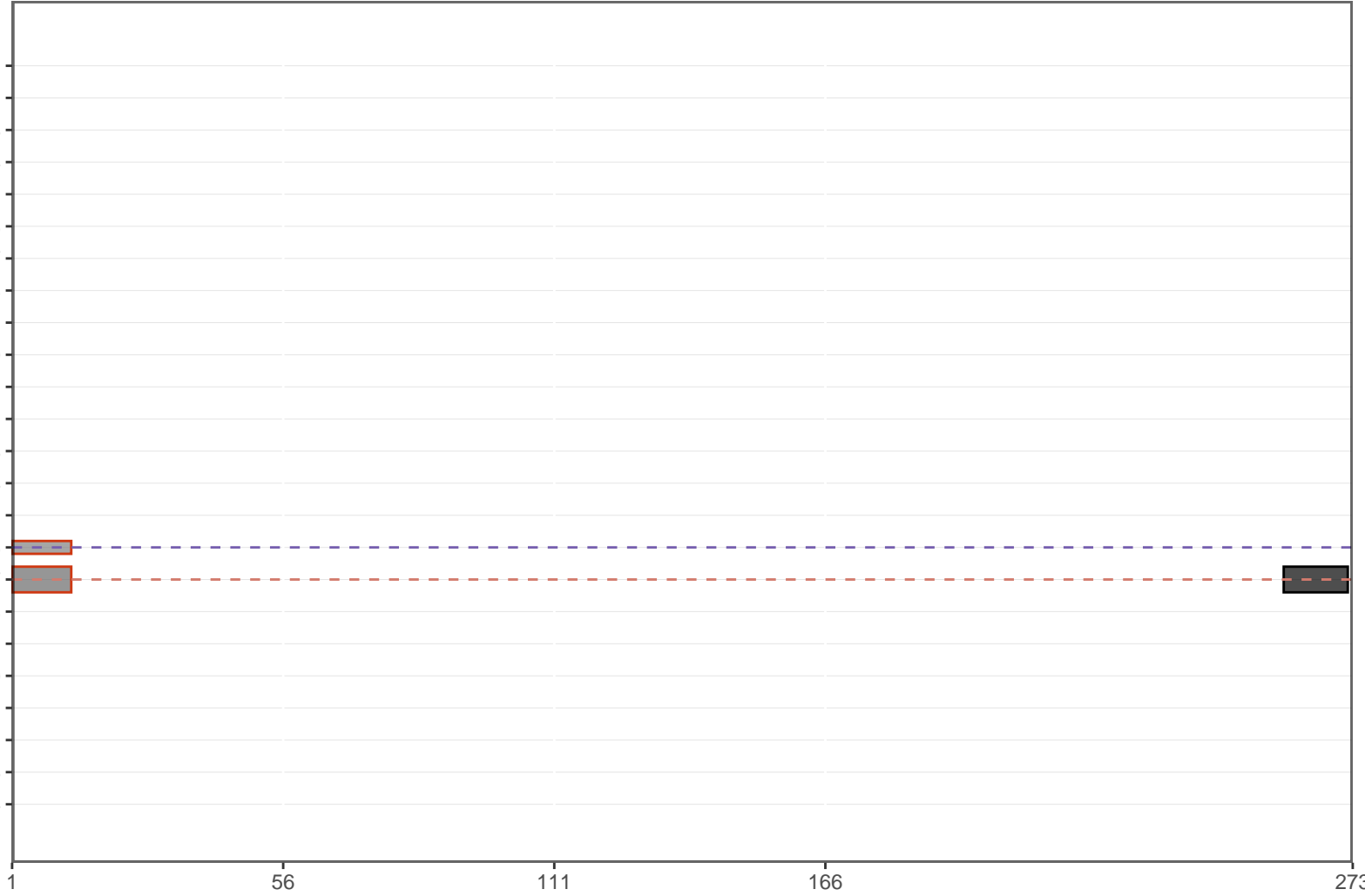
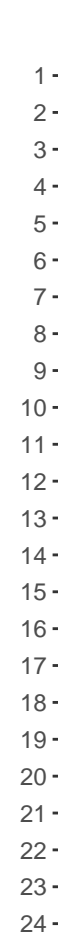
MW indication



Molecular weight

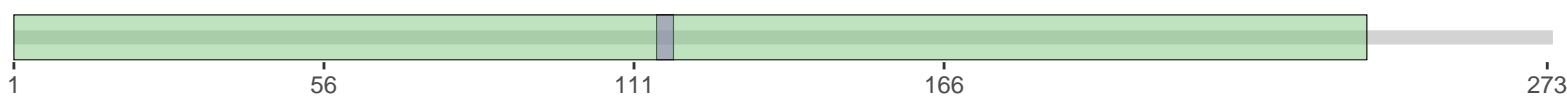


Gel Slice



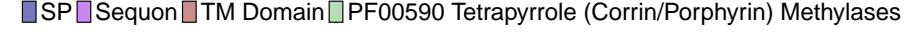
Protein length

Peptide counts over 4 repeats



Pfam domains

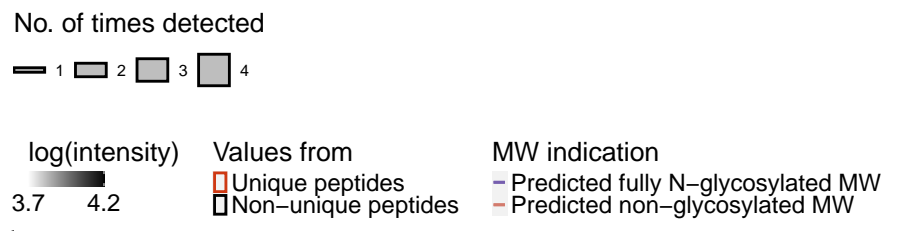
Pfam Description



Protein sequence:

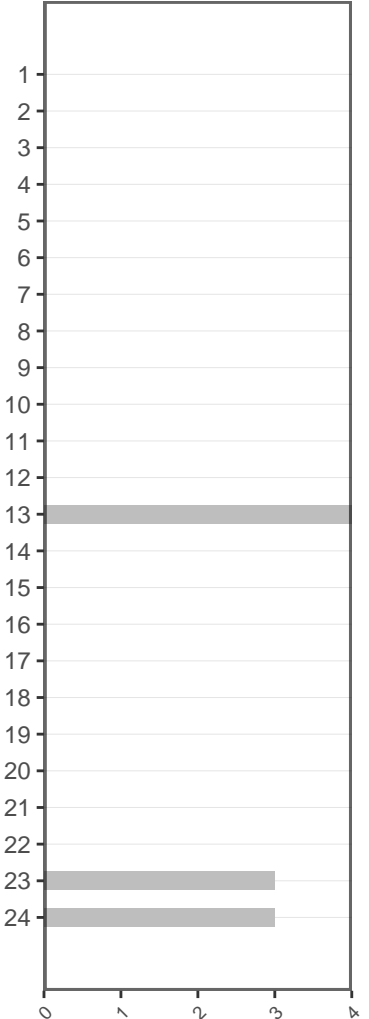
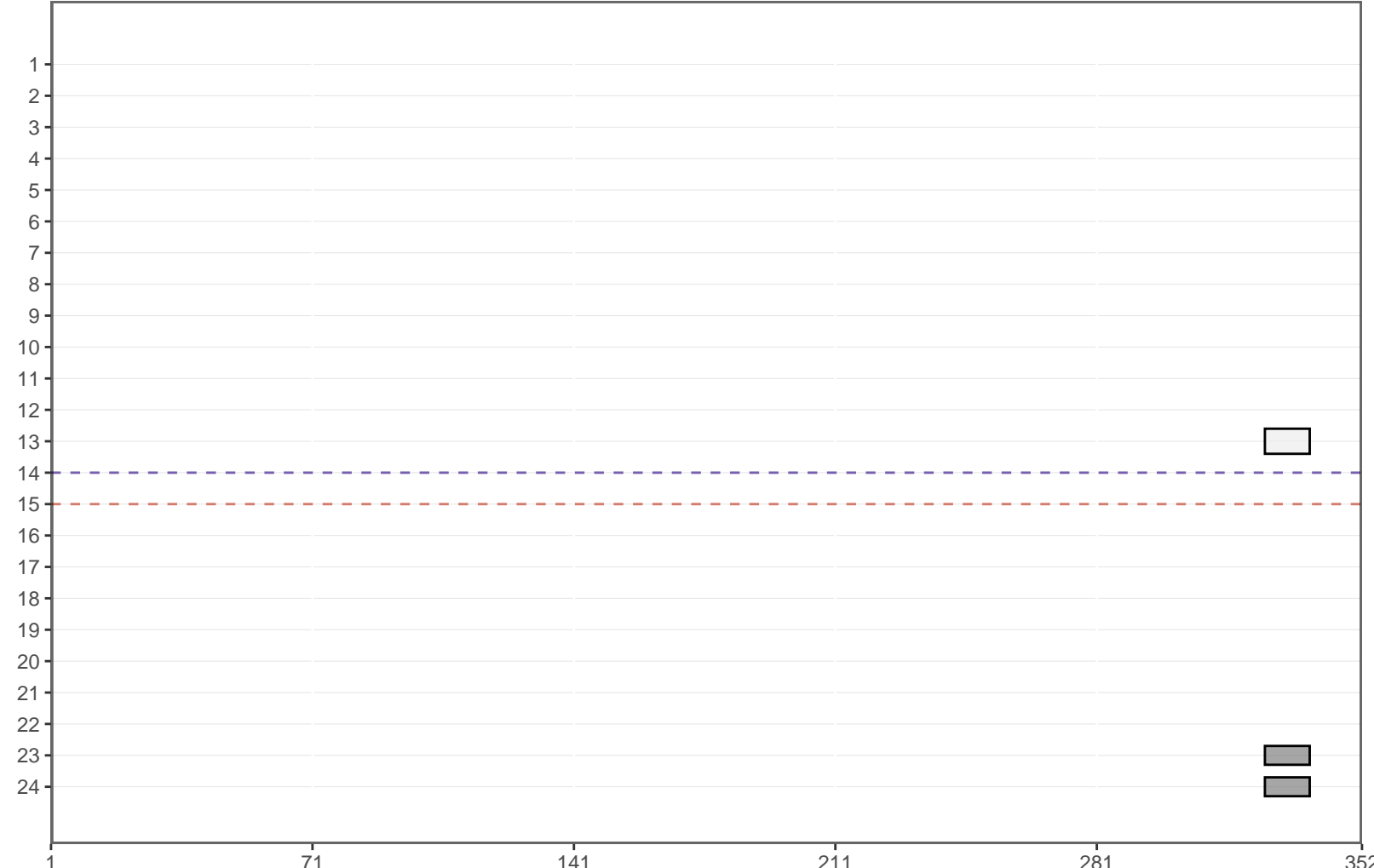
ICGLQLYHYGETVSIPIFFETETWRPDSFYENIKRENKLGHLHTLGLDIRVKEPTIEGLCRGKKQYERARFMTVNTAIEQLGEVEEARGESVSGENTICVGFARLGSDEQKVVAGSMKOLLTDFGAPLHGLVIVGKTHFVEEEMLEFYGLI

NbL17g24780.1 alkylated_DNA_repair_protein_alkB_homolog_8-like [MW = 38.52 kDa]



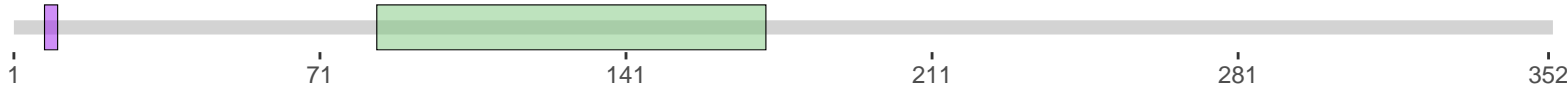
Molecular weight

Gel Slice

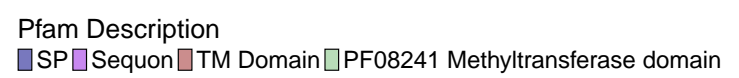


Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:

VVKKGGCLTYVAREGEEDLSLVEKWTPLNGRYAEWIGPGPRVTRPSPTLESPEAEENGAGEQLKDLHAKSKVKSEVMDISIGDKGRSLGGSGKGYAEQGEFFVPHLPHYHRAEVSGASAWLAGLAKKDDKGGVYVYRYYHVFSEGELERLVSGLDNALVDFRYDKSNWGLFE

NbL17g24570.1 GDSL_esterase/lipase_EXL3 [MW - SP = 36.69 kDa]

No. of times detected



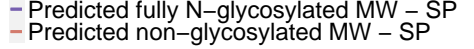
log(intensity)



Values from



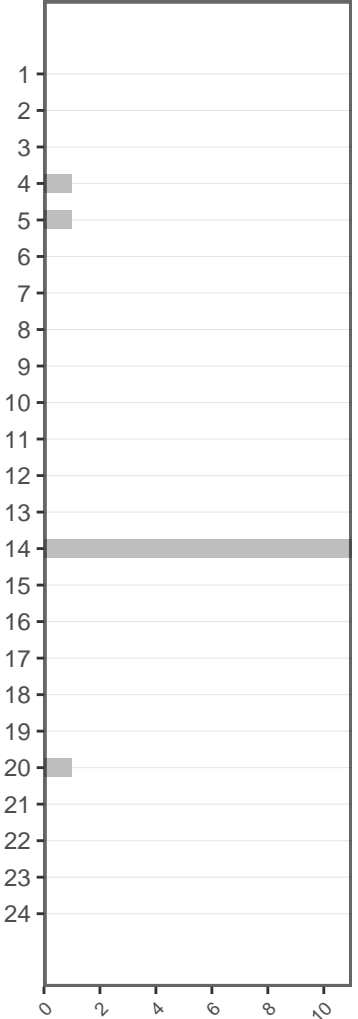
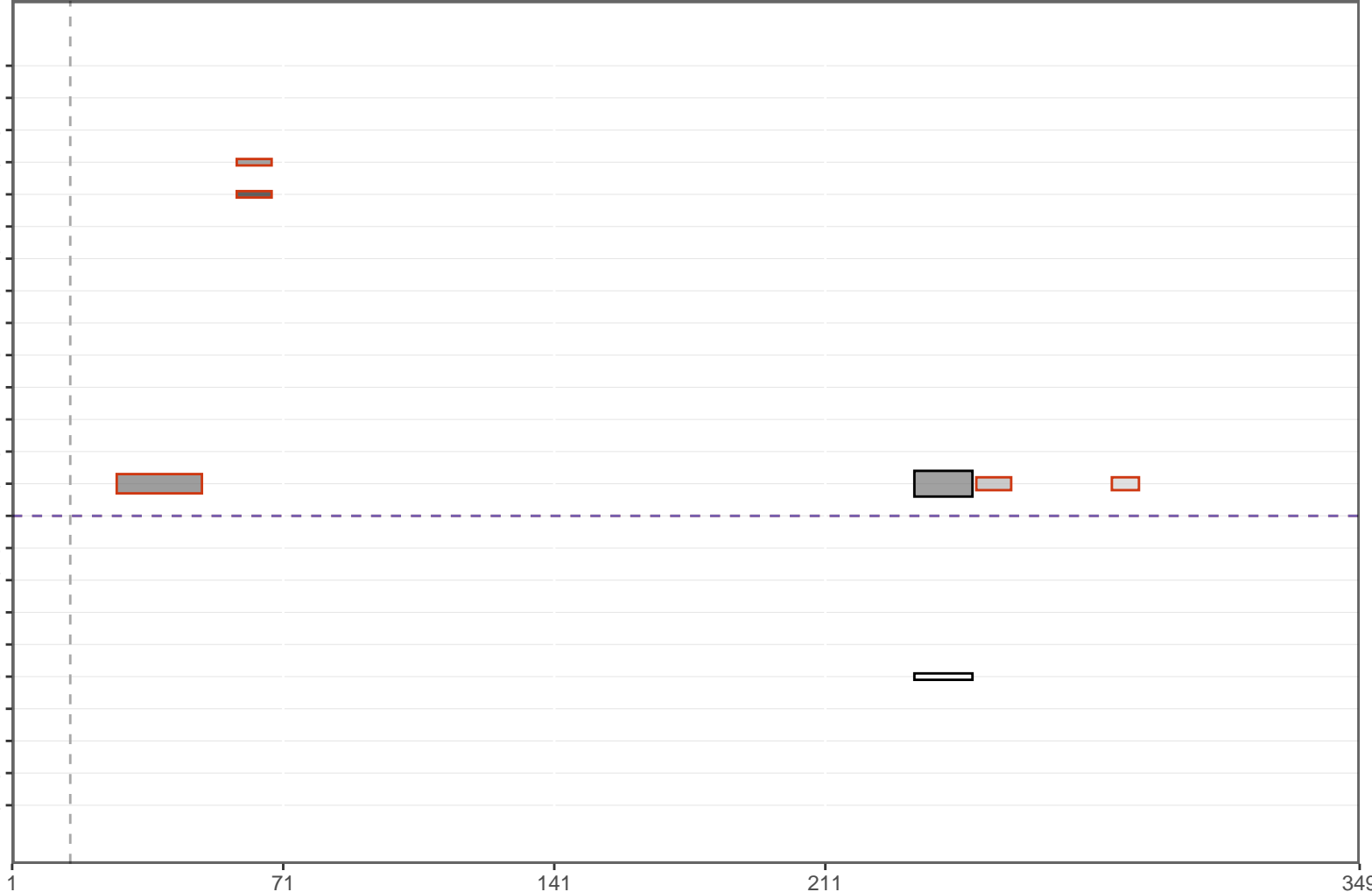
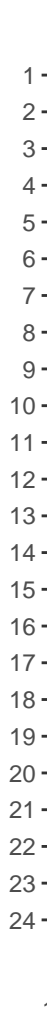
MW indication



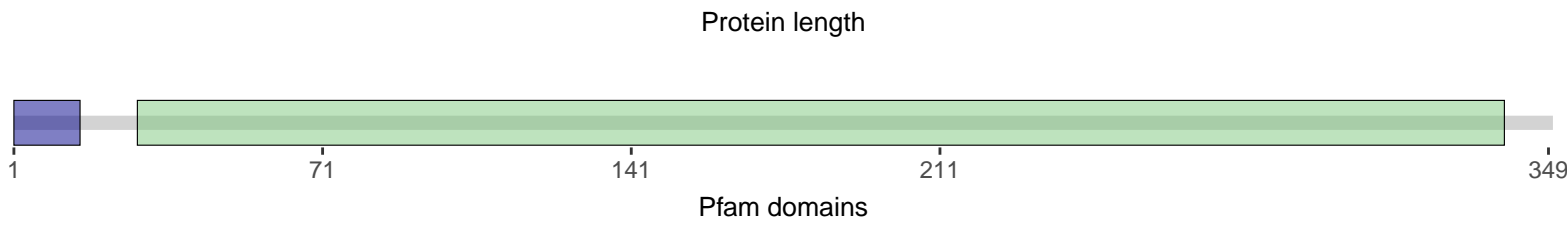
Molecular weight



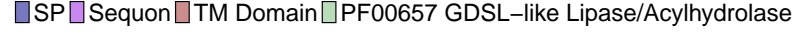
Gel Slice



Peptide counts over 4 repeats



Pfam Description



Protein sequence:

LVAGSDDIANTYITAGIRLKGQDSNYTNFMDYKVSERLQELVKLGARKVGFDFGIPPLGGLPSQRRLAGGFNRVQVEEYNGAAELANTRKLSAELNSLSKYLPQSKLVFDIYINPLDINVPQKYGLEEVEKGGDGTGKIEVTLGNKFSGTGEDDTKYFFWDSYHPTKNGYRILVDQLKKYINFL*

NbL17g24520.1 uncharacterized_LOC109224900 [MW - SP = 13.94 kDa]

No. of times detected



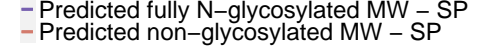
log(intensity)



Values from



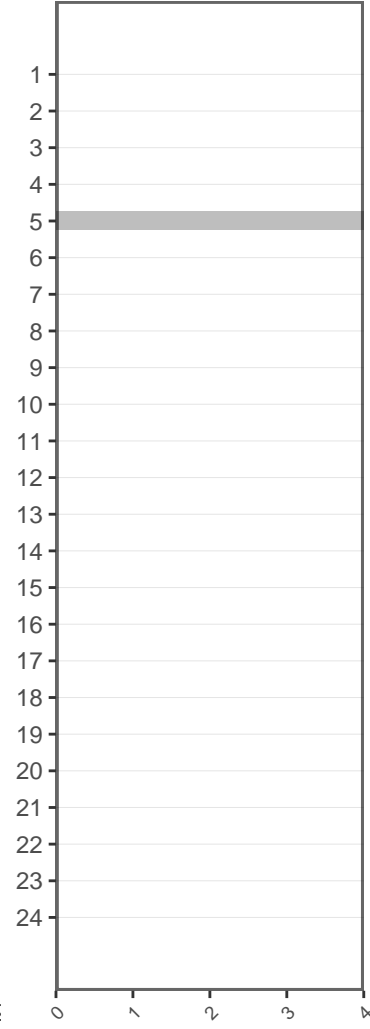
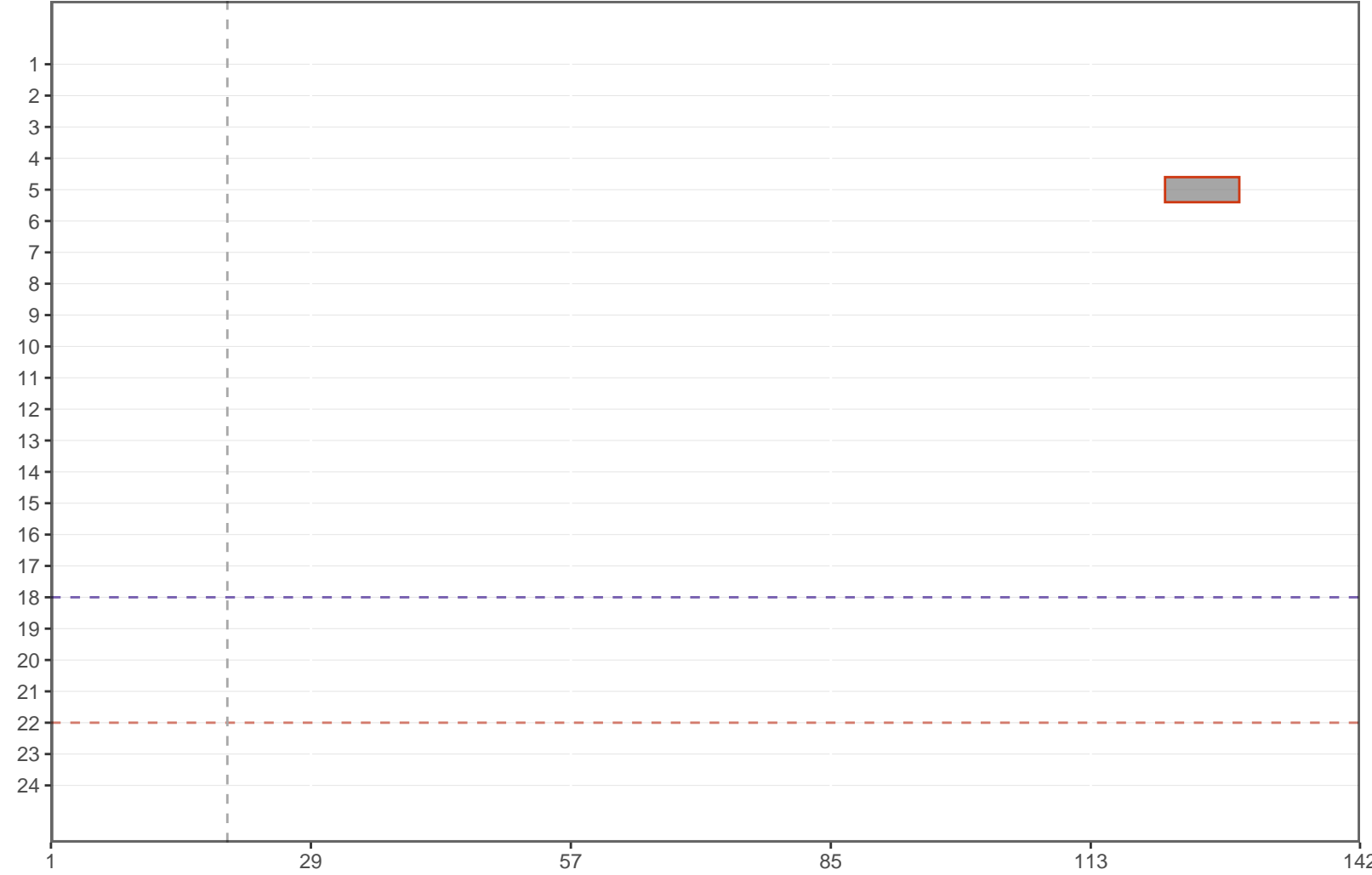
MW indication



Molecular weight



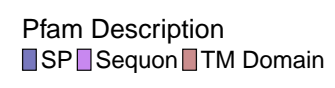
Gel Slice



Protein length



Pfam domains



Protein sequence:

I/DNRRYNELDV/SMEILNLTKEHSETENNTSGTMEKEGDNLMSGSETVIGNEIN/VSSSVRRKFDLHCELDKFLIGENFMSRN

NbL17g24350.1 expansin-A11-like [MW - SP = 25.21 kDa]

No. of times detected



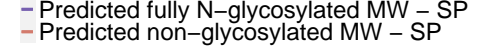
log(intensity)



Values from



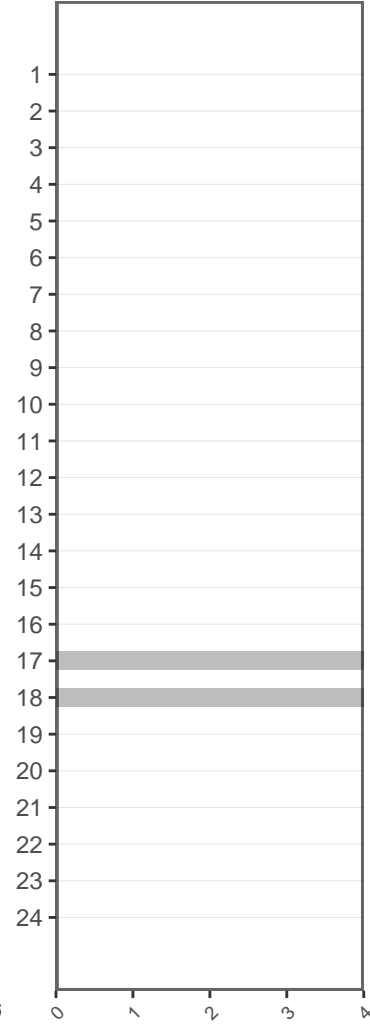
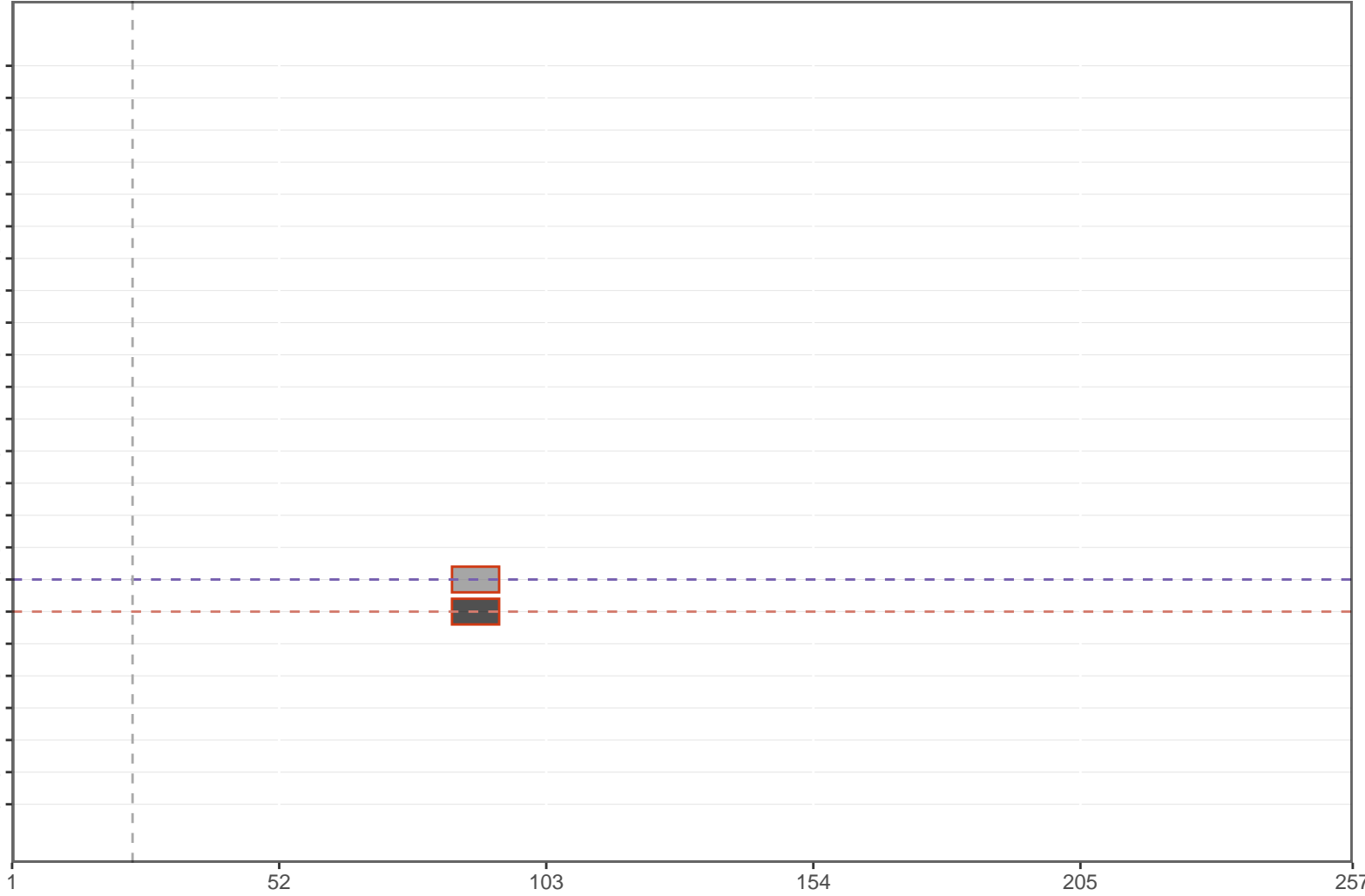
MW indication



Molecular weight



Gel Slice



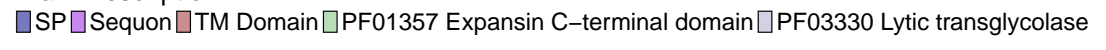
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

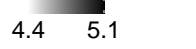
PSYNGGVICNPPRPFRHFDMAQPAWENHGGYRGGVPAVLYQRIPGVKKGQVRFETINGRNYFELLMISNIVGAGSAGSVQIKGSKTNWMTMSRNRWGANWGSNLYLNGDFLFRVYTTDGVTKTFLNAPSNWHFGQTYSTEINP

NbL17g24340.1 ribonuclease_P_protein_subunit_p25-like_protein [MW = 28.13 kDa]

No. of times detected



log(intensity)



Values from



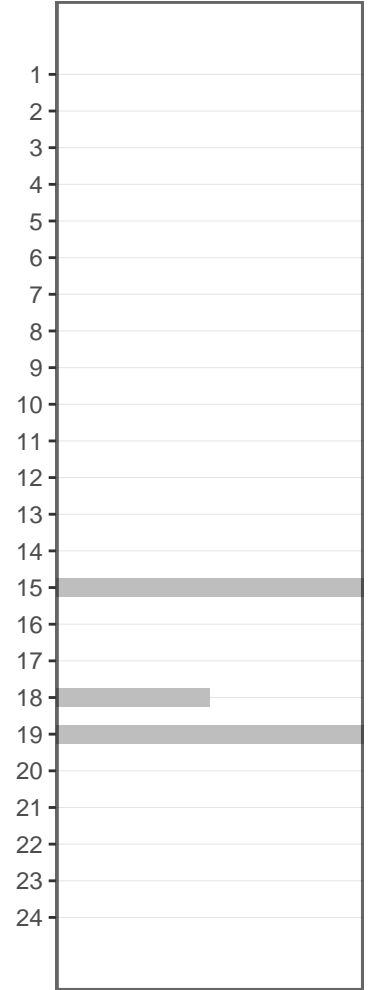
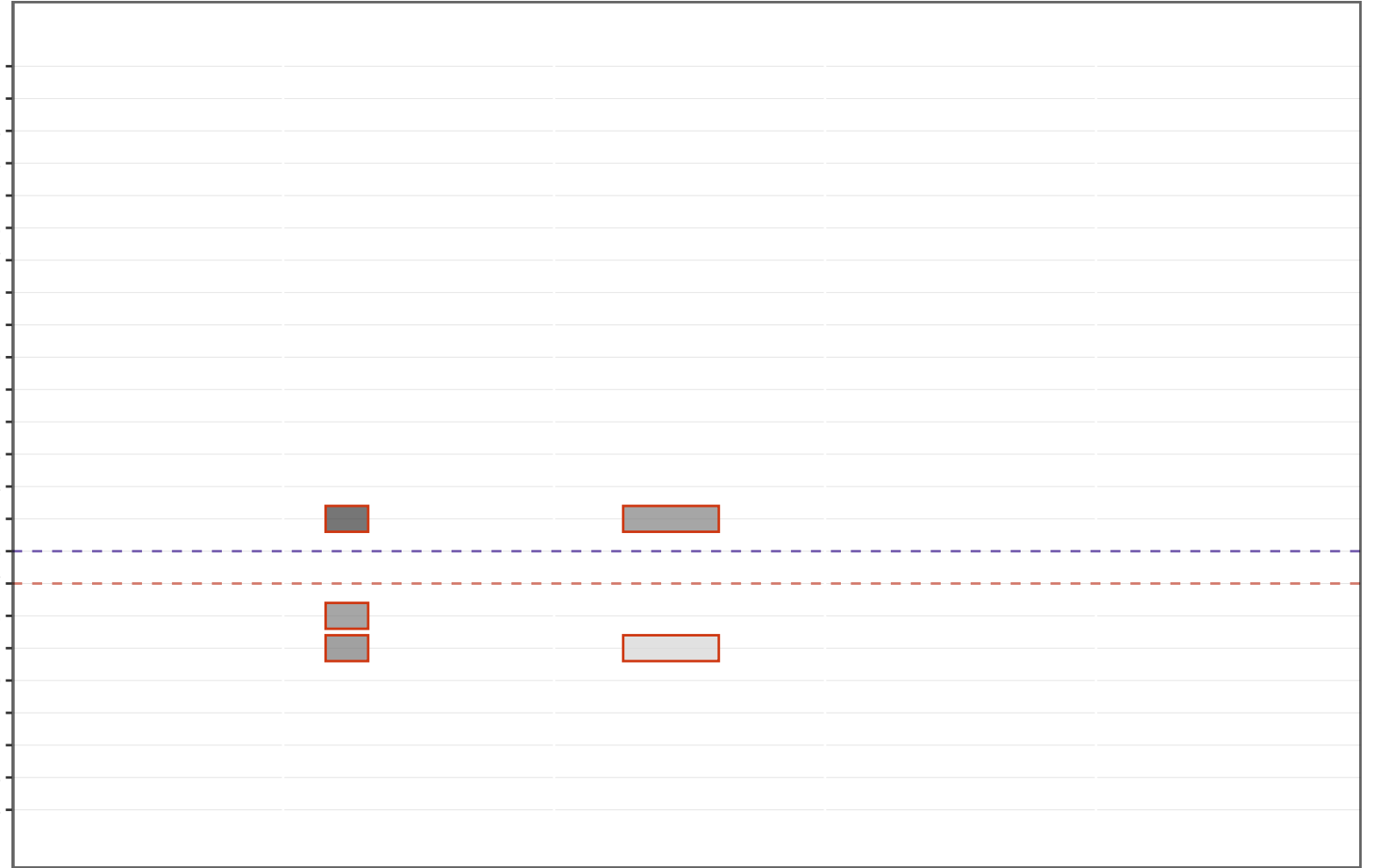
MW indication



Molecular weight



Gel Slice



Protein length

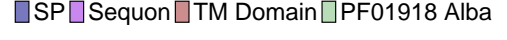
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

/GYQPLPADQ/KVLTDFD/DGEGSPGGRRGRGRGRFRFAGNGFMSAEYDDGGYDNRNRYGRGRGRGRFRGRGRGYNPQDTQDAGFYNGEAPMGGRGRGRGRGRFRFRITTPHGGGA

NbL17g24230.1 thioredoxin-like_protein_CDSP32_chloroplastic [MW = 33.5 kDa]

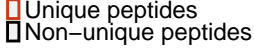
No. of times detected



log(intensity)



Values from



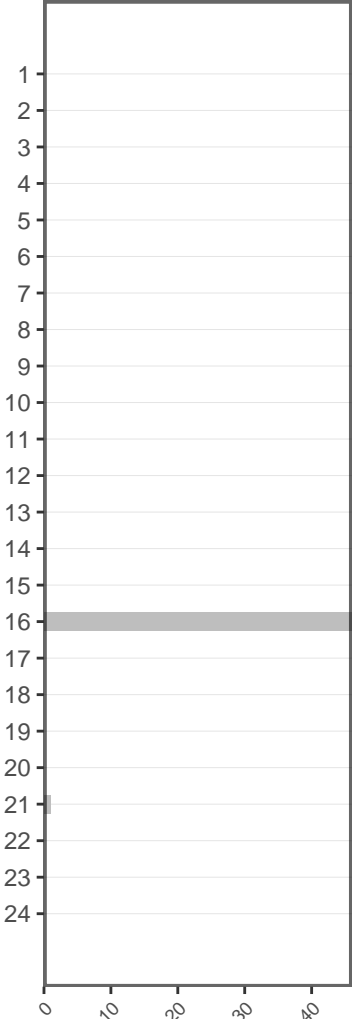
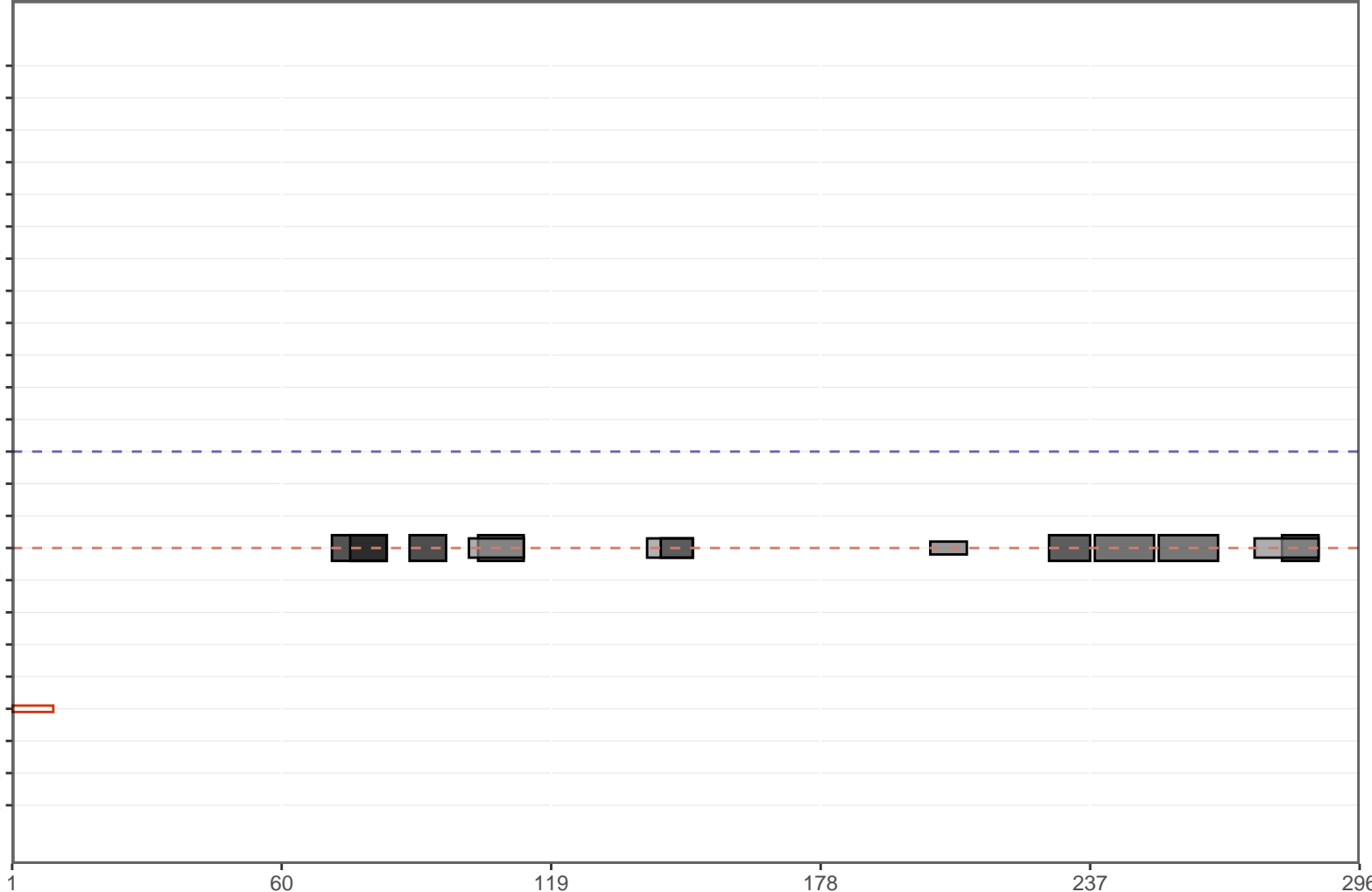
MW indication



Molecular weight

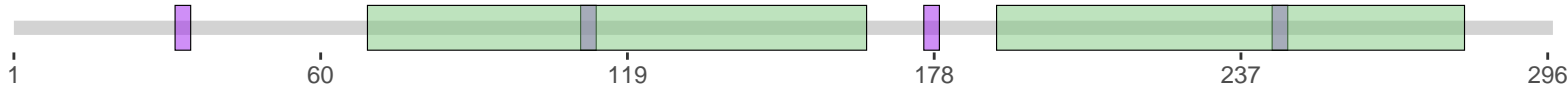


Gel Slice



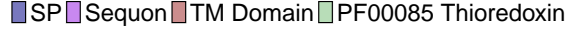
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

REKINKYPHFNFYKSMERHEEEEGKPDQLAGDLYYGDNHSEVQLHSRDEVEKLDGKIKLVLGVGLKHGPGVWVPTVWIKLSRGMADTVVFARMGDEGDSMQLKMDVAEVPVTLFIREGEKGRVYGGKGLIGEILRYGGVRYTY

NbL17g24160.1 tRNA_pseudouridine_synthase_A_mitochondrial [MW = 64.29 kDa]

No. of times detected



log(intensity)



Values from



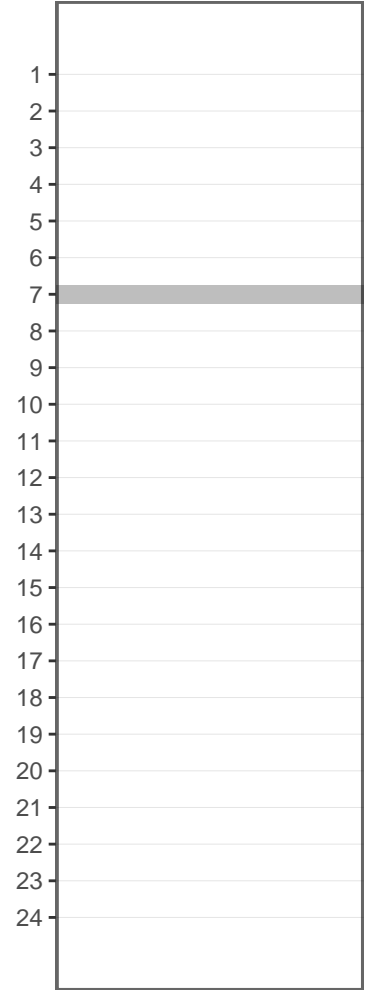
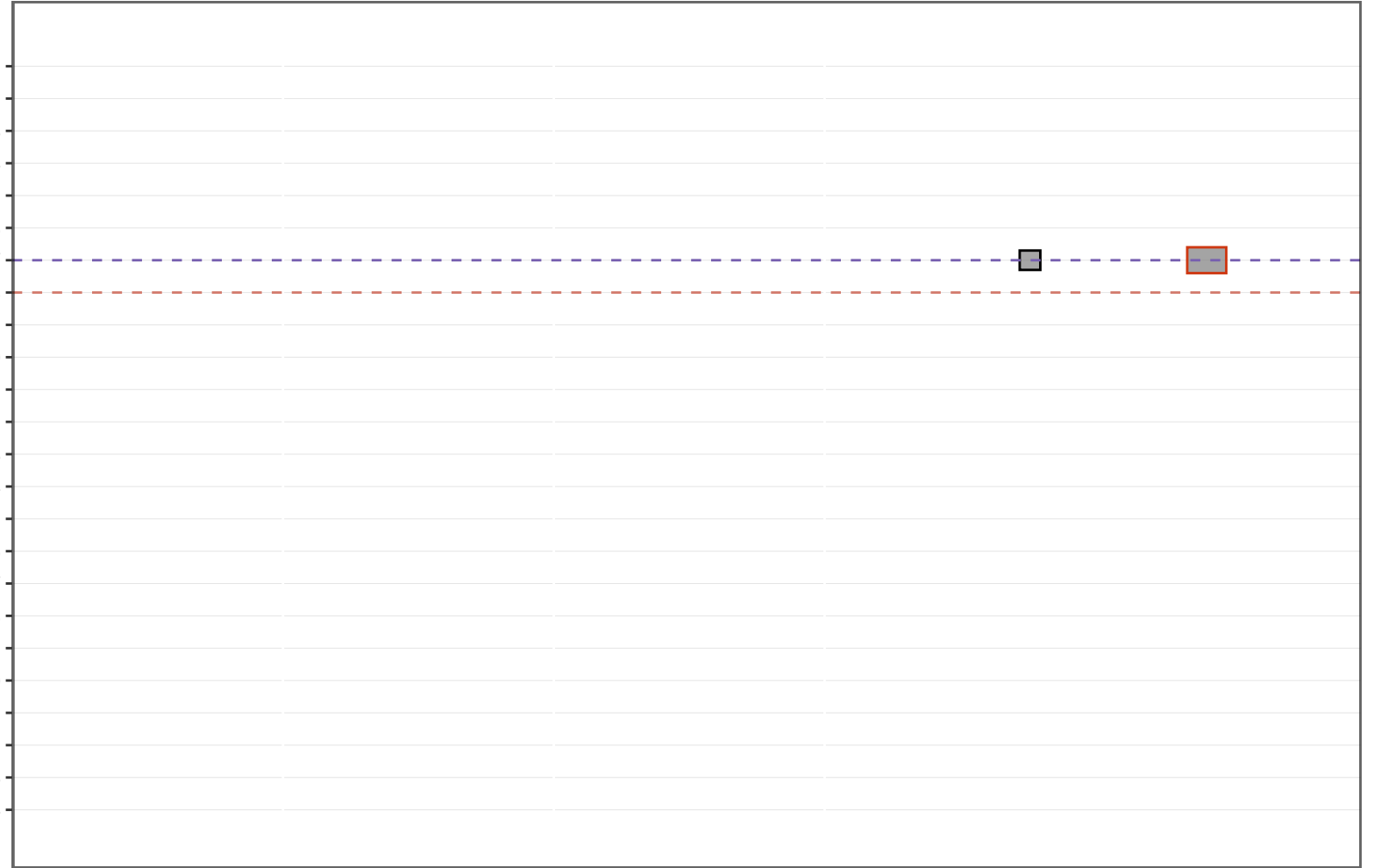
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

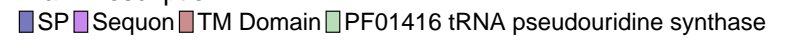
1 119 237 355 589

Protein length



Pfam domains

Pfam Description



Protein sequence:

EEVEKGDENAKAIDEGVEESVFSYGEKEKERNRLKYYEGTHNPHNFFTRTKADDPAAKRYHISTANTINNVVEGIEFVKDEVVGGSFMLHGIRKMLGLWAIMRNDAPESLQGTAFRRDNNVPMAPVEVGLYDEGFTSYNKRKWDTHEEVSLKAYTEAAEEFKMKYVYSHASTEHDGDMALWHLNLRNYPDLRQVDNGNSAGASDGKAVEAVEAGVGVANNGESTDNNNSAGAVDQSKAGEAIEAGLGSVNDGESTDNNVAGAGDGSSEYETVVEVQLSGV

NbL17g24120.1 enoyl-CoA_hydratase_2_peroxisomal-like [MW = 34.08 kDa]

No. of times detected



log(intensity)



Values from



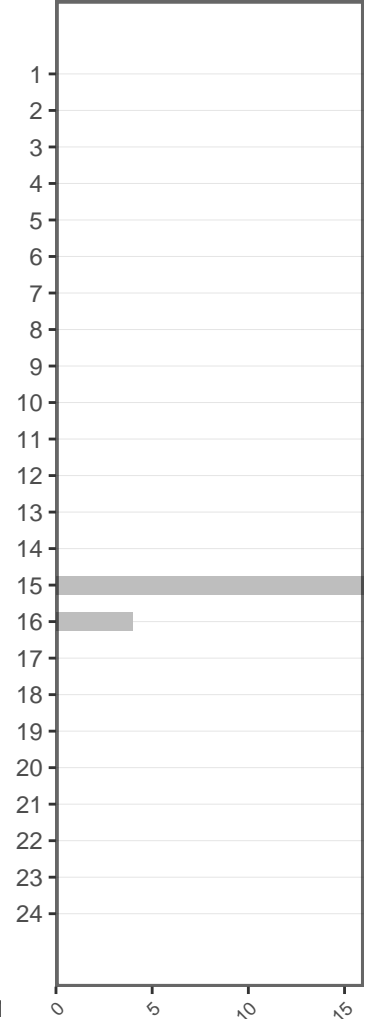
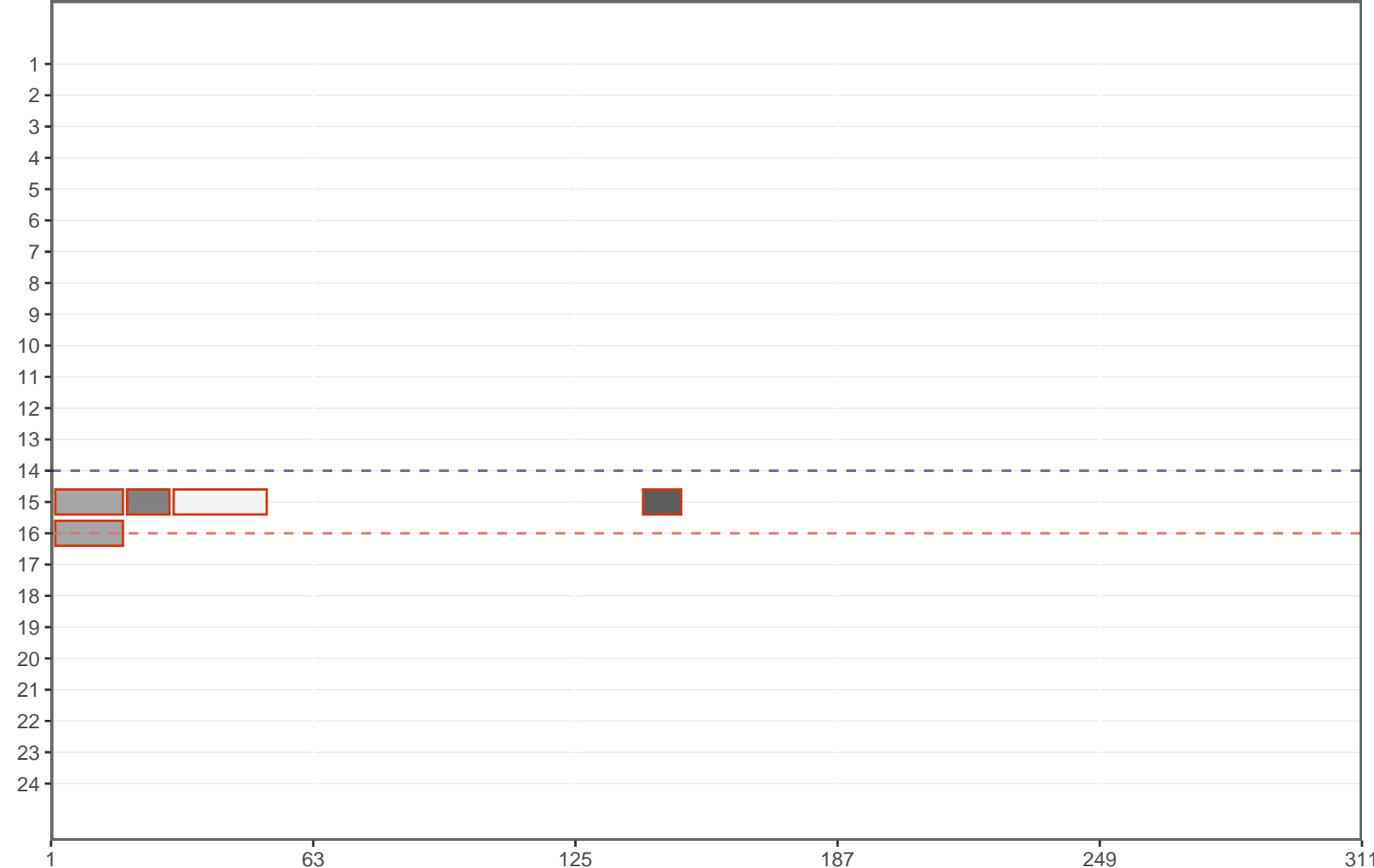
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

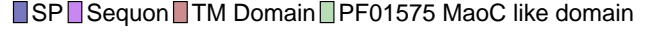
Protein length



Pfam domains



Pfam Description



Protein sequence:

I V E P L C M N R M S I Y L R G S G G F K S R P Y S Y E R N P E N G T A F P K I P K G Q P F A V F E G G T Q A S G A L L Y R L S G D Y N P L H S D P L W A S I A G F E R P I L H G L C T L G F A I R A I R G I R G D H T L K S I S G R F L L H Y V P G E T L I T E M W P E A S R V I Y Q W V K E R N R A W L L G F V D L D R I N S E L

NbL17g24100.1 L-ascorbate_oxidase_homolog [MW - SP = 57.77 kDa]

No. of times detected



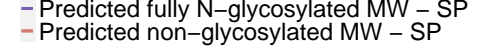
log(intensity)



Values from



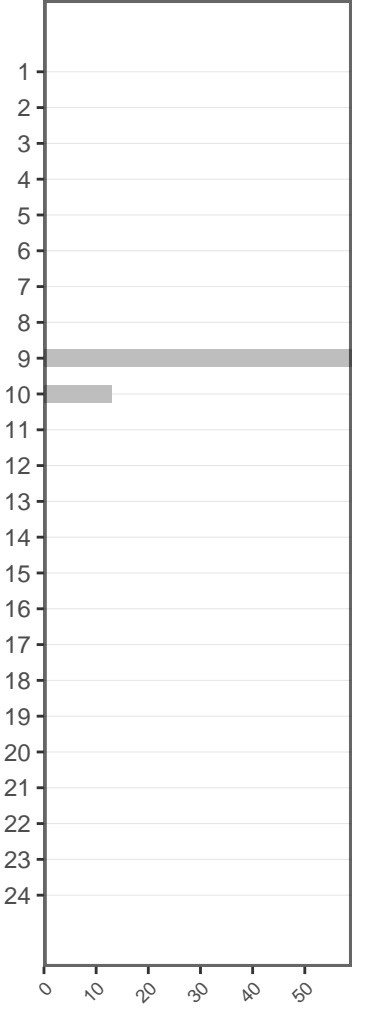
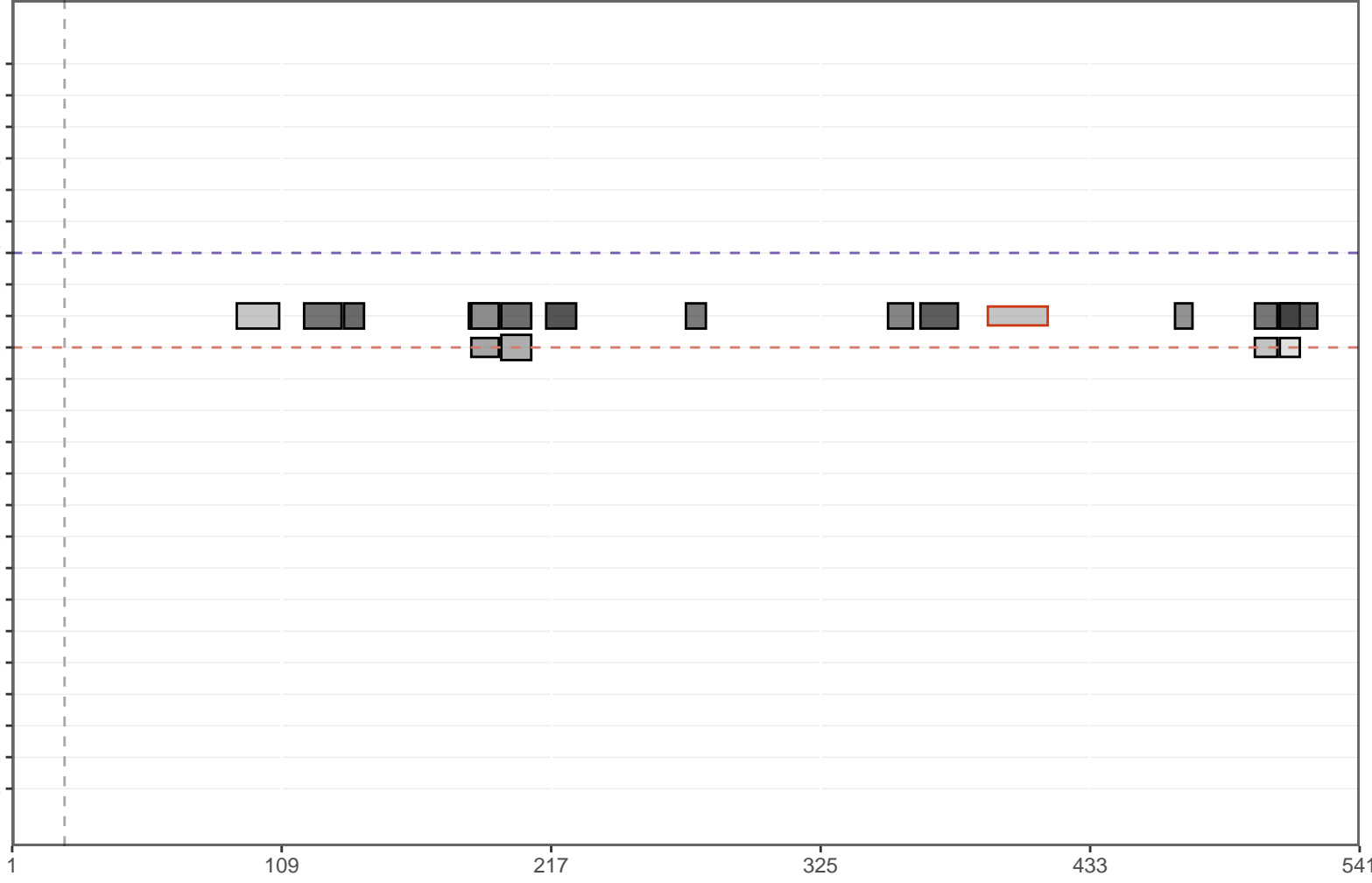
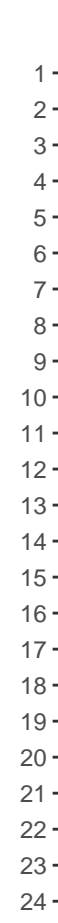
MW indication



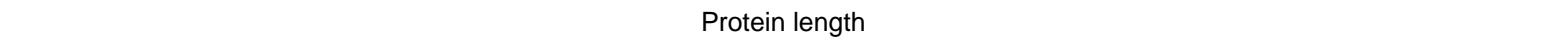
Molecular weight



Gel Slice

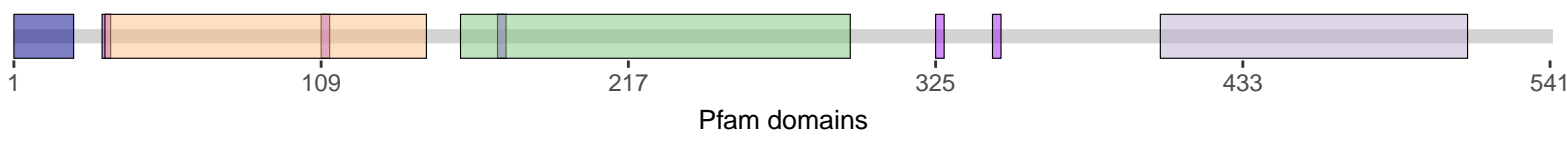


Protein length

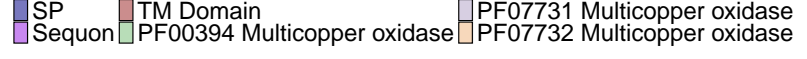


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VLTADDEAKDHYVYVSSRFTSQVLTFTGVVHYENSNTPVSGPPRPGFTIQDWLNGARSRITNLGASGPRFNPQGSYHYGMNTRTRIRLASAGQVNGKQRVYVNSVFLPDTPLKLLDFKVGGRVGSISDAPSGGGIFLDSVLGADYRGRFIEVFENNEDIVQSWHLNGYDFWVYVMDGGQWQTAQRSGVYLRDVARCTTQVYPKSWTAYHALDNVGMVNLRTFQWQYLGQQLMRYVYTTSTSLRDEVPVPRNARLGGKAGRHTRPL*

NbL17g24020.1 ATP-dependent_zinc_metalloprotease_FTSH_chloroplastic [MW = 76.02 kDa]

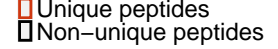
No. of times detected



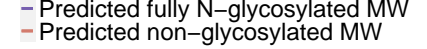
log(intensity)



Values from



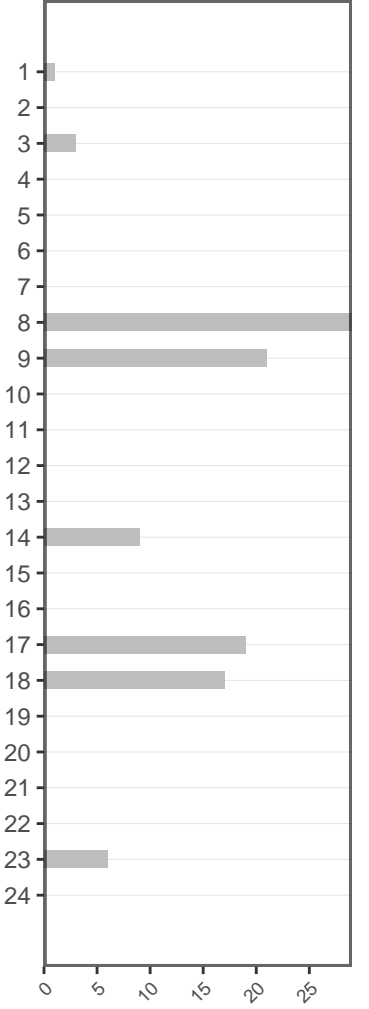
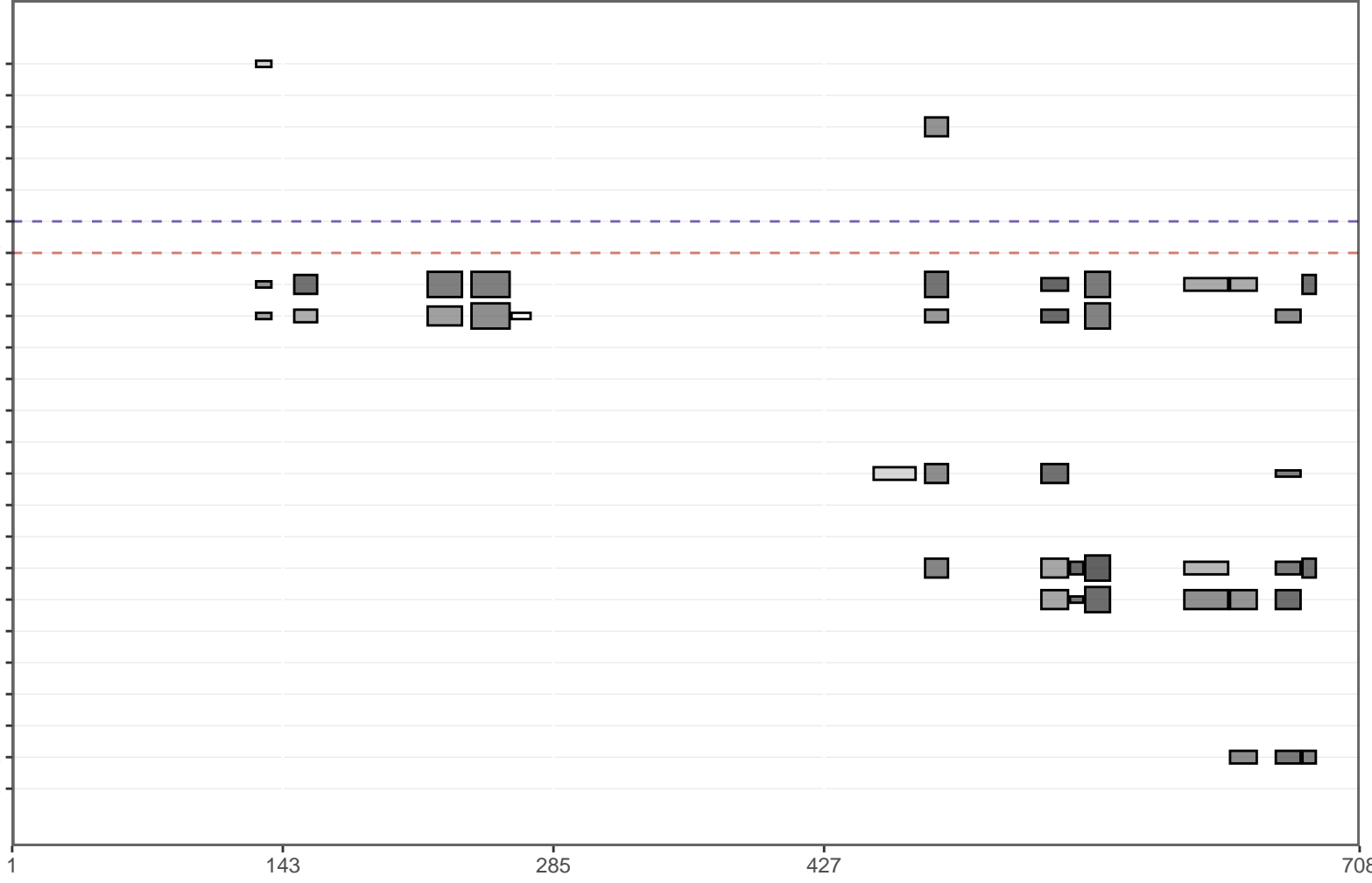
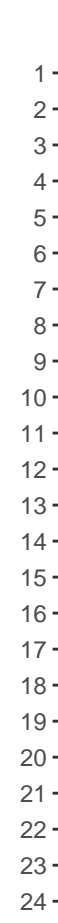
MW indication



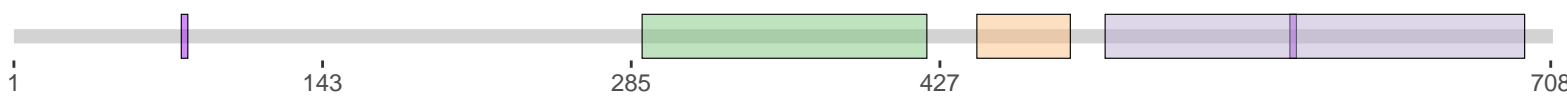
Molecular weight



Gel Slice

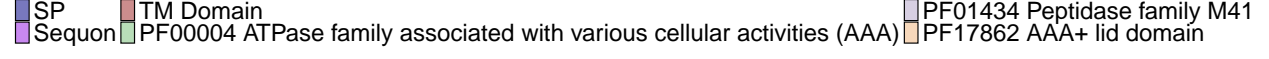


Protein length



Pfam domains

Pfam Description



Protein sequence:

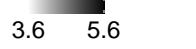
IKAKSKAPCVTIDEIDAVGRGRGAGMGGGNDEREQTNLLITEMDFSGNSGVVLAATNRPOVLDLALLRPGRFDRQVTVDRPDVAGRIKIQVHRGRKALAKVDFEKIARRTPTGFTGADLQNLNNEAAALAAARRELKEIKSDEISDALERIIATGPEKKNVAVSEEEKKLVAVHEAGHALVQALMPEYDPAKISIPRGGAGGLTFFAPSEERLEGGVSRVLENGMAVAGGRVAEEVFGDDNVTGAEKDFMAGVSRVARGMVERLGF8KKIGDAVIGGGGCGNPFLOQI

NbL17g23970.1 uncharacterized_LOC107816208 [MW = 37.39 kDa]

No. of times detected



log(intensity)



Values from



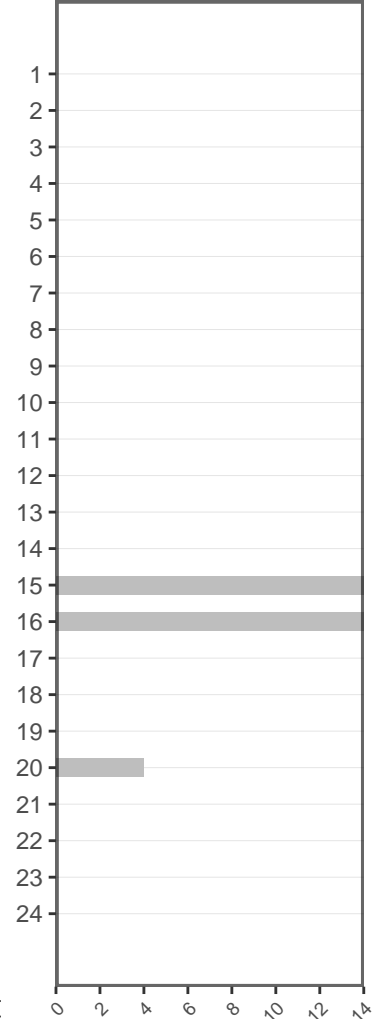
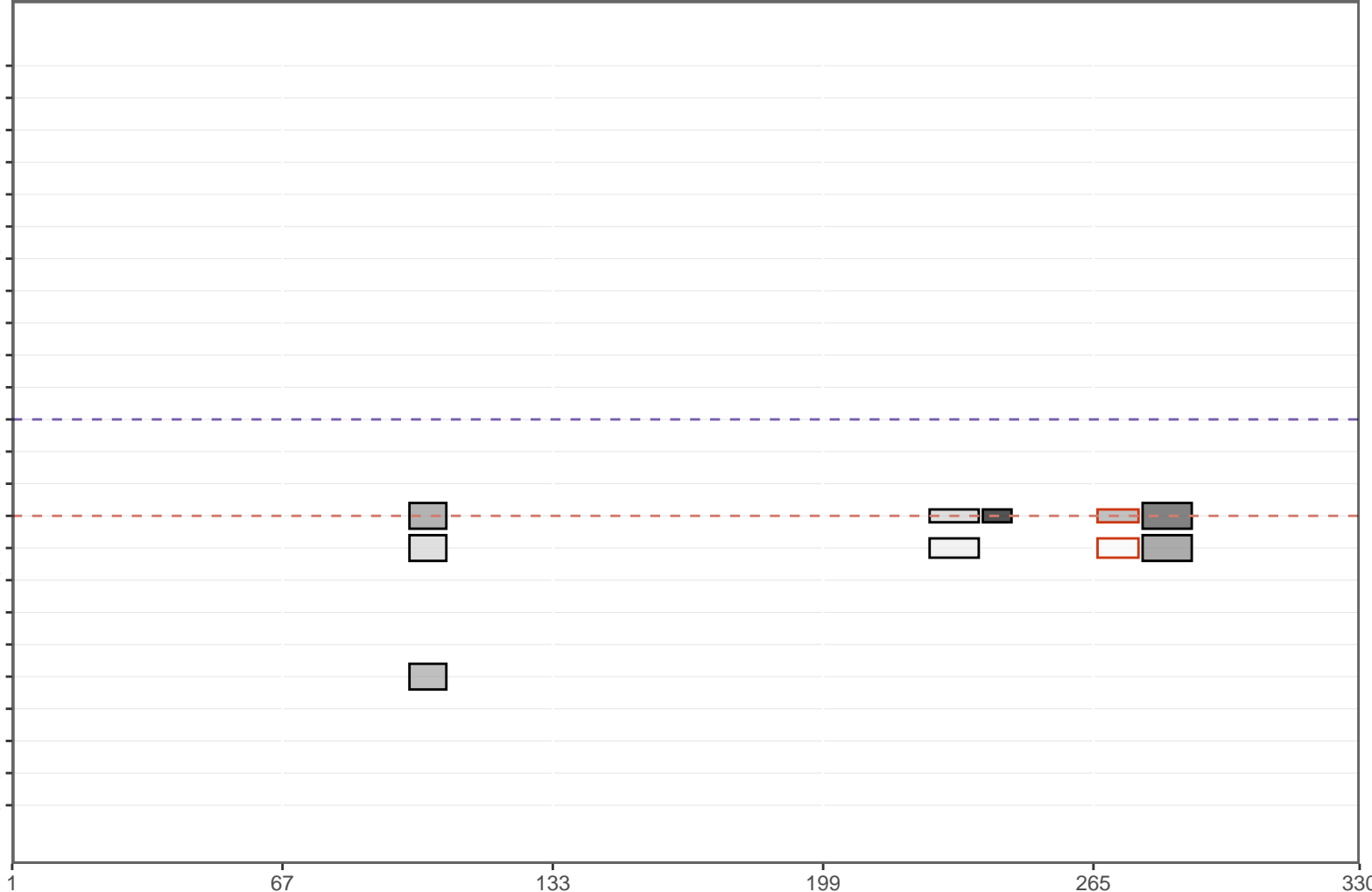
MW indication



Molecular weight

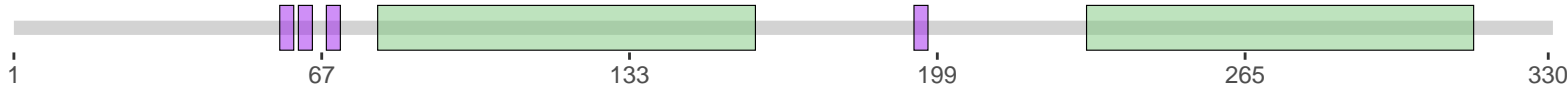


Gel Slice



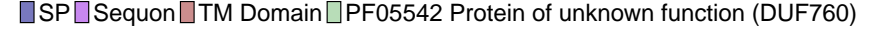
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IQFRRLLEQOSLEQALPEAGEEKSDPQASGTQKKVYGEVIRWISNVTGPEKDALKYHELLEAEVEELNRQMERIKSGGGYNELLEVLKTLFQNKELSTAGEDVILAMNSFKIRLWASDPSQMKTVTETSAPELAKLLVLMVGYGSRINIEVRFDMERVLGTPPKLAEPPGENI

NbL17g23910.1 14-alpha-glucan-branching_enzyme-like [MW = 98.34 kDa]

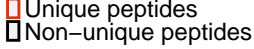
No. of times detected



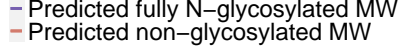
log(intensity)



Values from



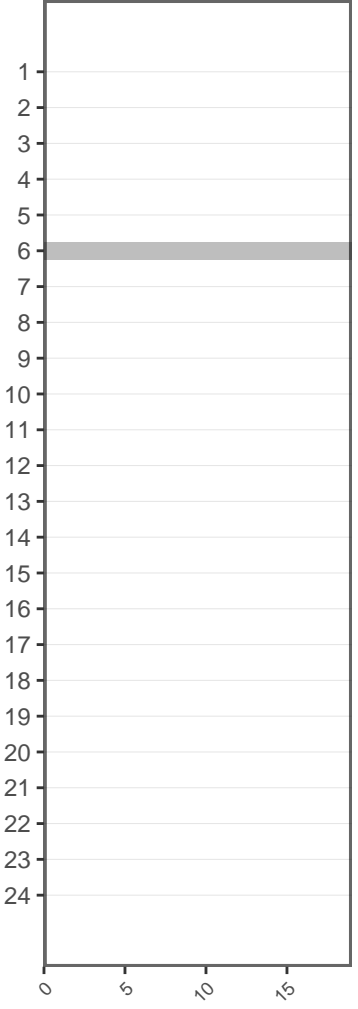
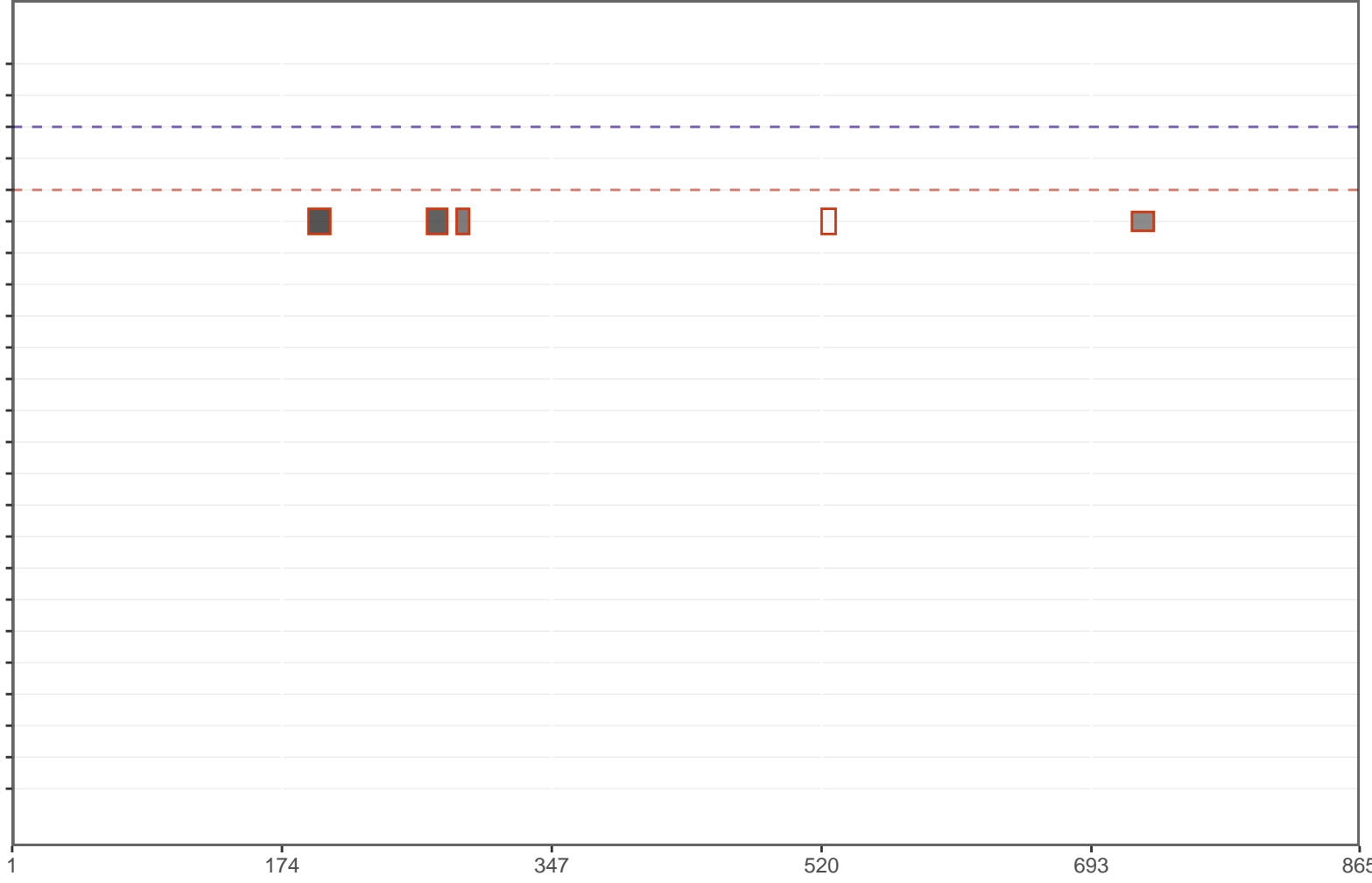
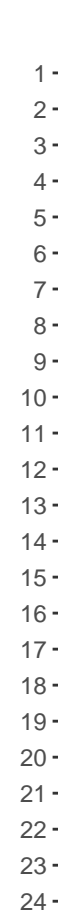
MW indication



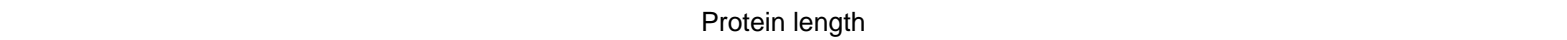
Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

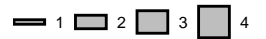


Protein sequence:

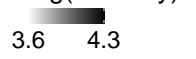
IEYNFDGFRDGGITSMILVYHGHNGFTGNVHEVFSDATVDVAIVMLANLNIKIFFDATVAEDVSGMPLGRPVSEGGGFDYRLAMAIPDKWIDYLNKNDDEDSVSKKEVTRSLNRRVYTKENIAVAESHDDGSDGDKTIAFLLMQKEMVSGMSGLTDASPVVDRGIALHKMHFFETMALGGEGYLNFMGNFEGHPEDWDFPREGNHNSYDKRRQWNLADSEHLRYKFMNAFDRAMNLSDEKFSFLASGKGVSTDEDNKVVWFERGDVLFVFNFPENTYGYK

NbL17g23850.1 WD_repeat-containing_protein_LWD1 [MW = 38.97 kDa]

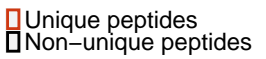
No. of times detected



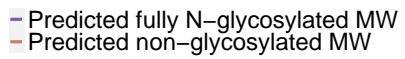
log(intensity)



Values from



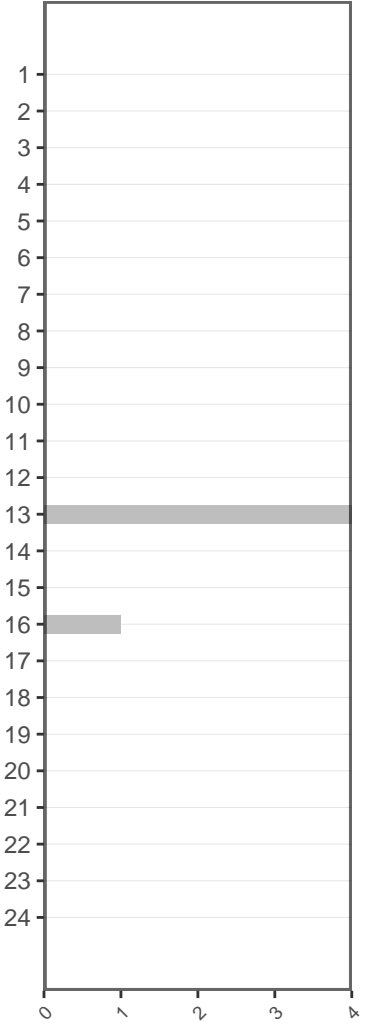
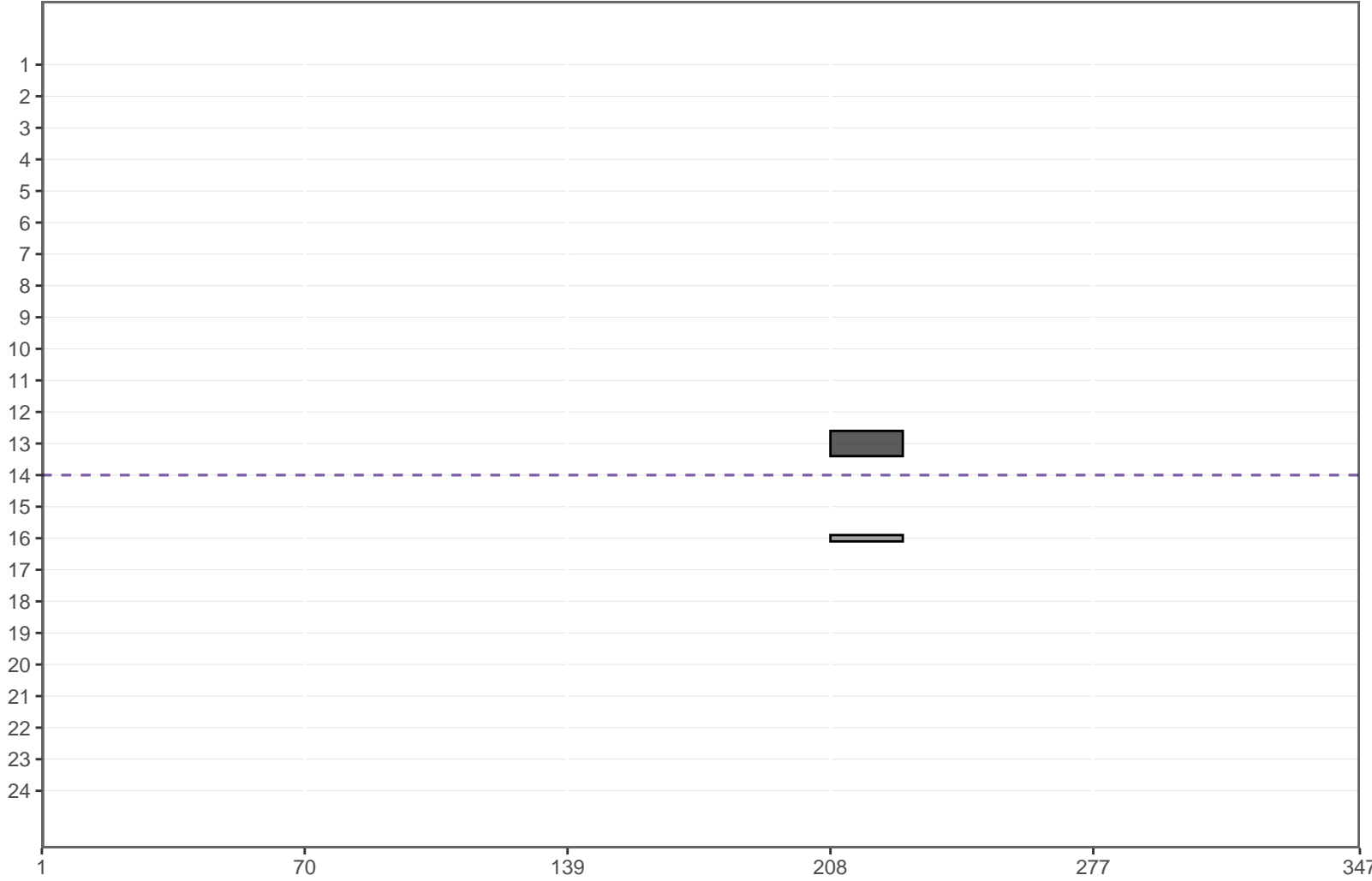
MW indication



Molecular weight

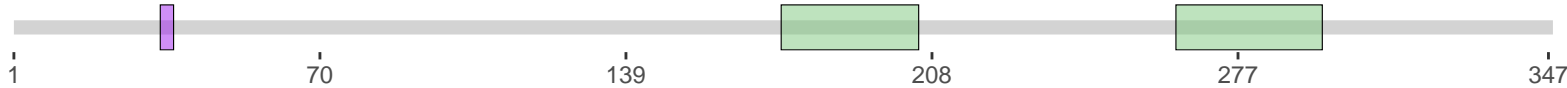


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

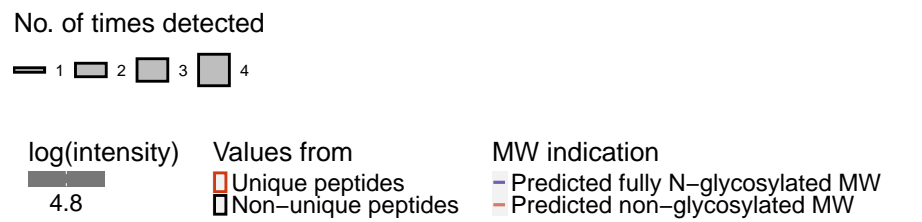
Pfam Description



Protein sequence:

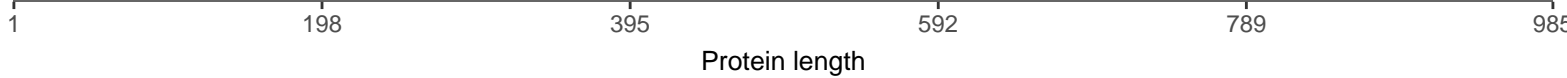
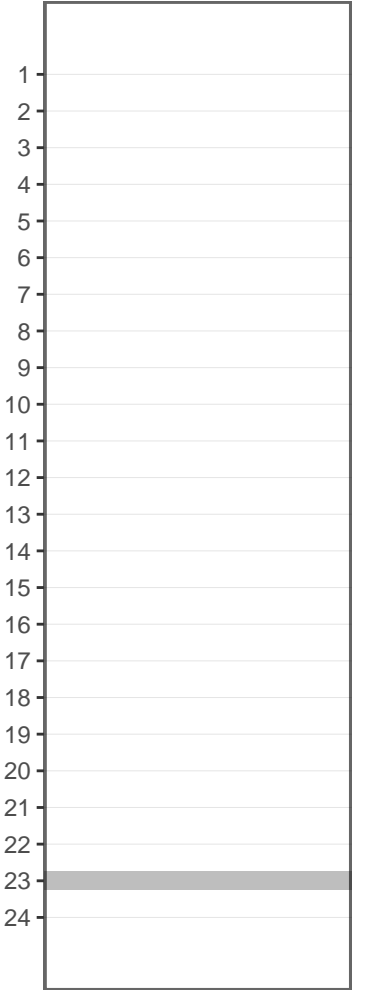
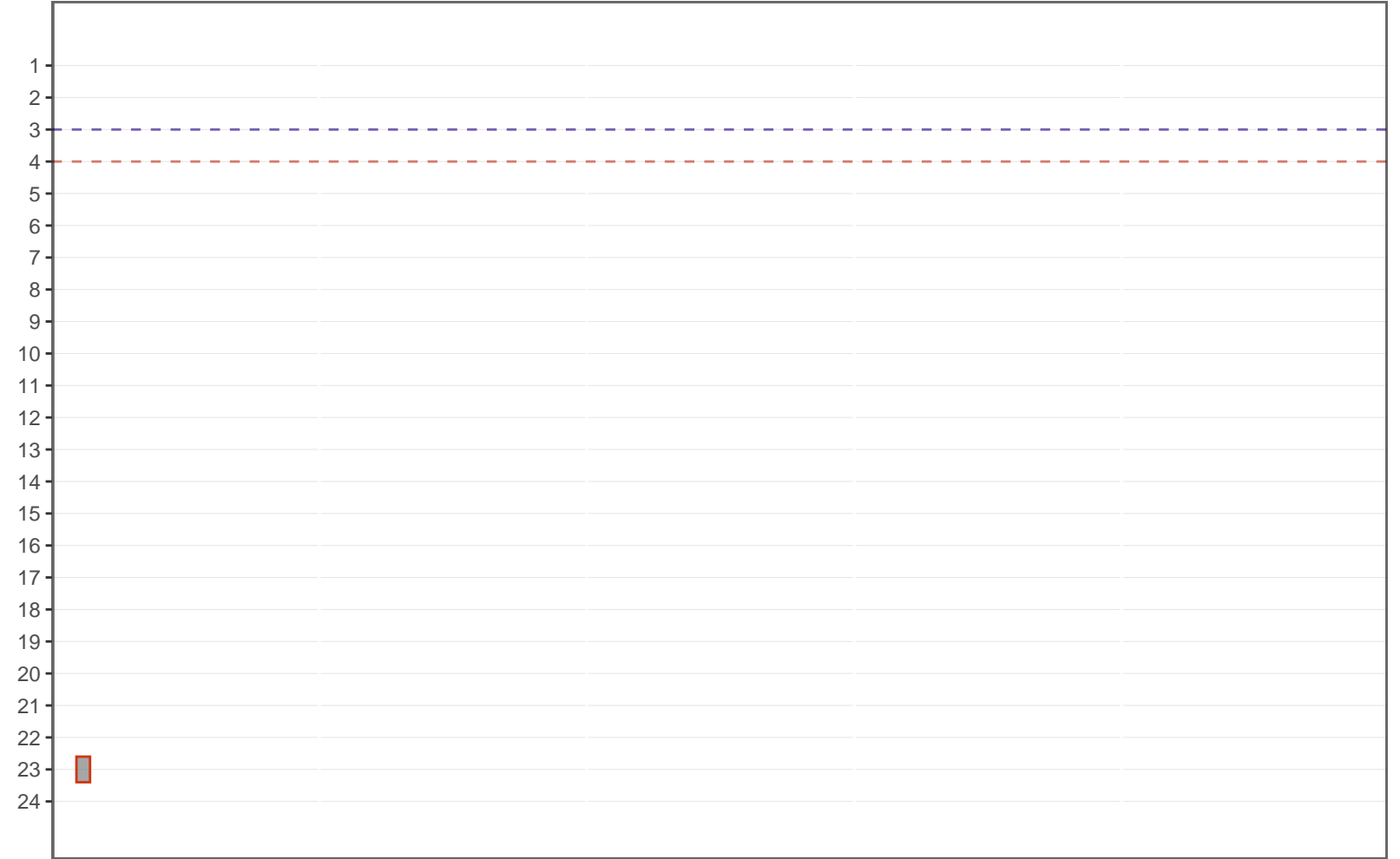
ICTIWDIERETVDTGLIANDKEVYDIAWGGVGVFASVSDGSRVFDLRDKHSTHYSSEPDPTLVRLGWNKGDPRYMATIMDSAAKVVLDHDFPTLPVVELGRHQASVNAIAWPHSSCHCTAGDDSGALWDLSSMGDPIEGGLDPLAYTAGAEIQKQWSSGGPQWVAIFSNKLGILRV

NbL17g23740.1 epidermal_growth_factor_receptor_substrate_15-like_1 [MW = 107.52 kDa]



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain PF12763 Cytoskeletal-regulatory complex EF hand PF13202 EF hand

Protein sequence:
 SLPLGVPQGAIFPOLRPPIDGAFPGPDRSMGFNDGNARATSHNSHMDQLSNGEONMLEPKREDAWAGEKDESKDNLVLDREKLEFYRRTKMDGLVLYKSGDNRNLREITERALADKREAMELAQKYEKYYGVAEASKLTIEEAFRFDTQERKLELQGAIRKMEGGGADGLQVRAADRVQHDLEELLKALADRSKQKHELNKSTALIELPFGVQGPPEISAAWDEEDWDFEDEGFSDFAAPANKSTNGKESPIHGDDSPDSMSNADTKSENYSAKGNNNFETDI

NbL17g23690.1 uncharacterized_LOC109224789 [MW = 17.59 kDa]

No. of times detected



log(intensity)



Values from



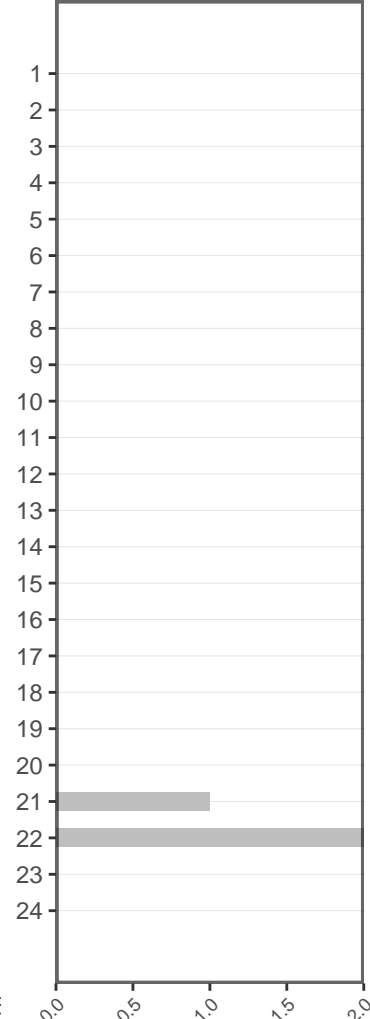
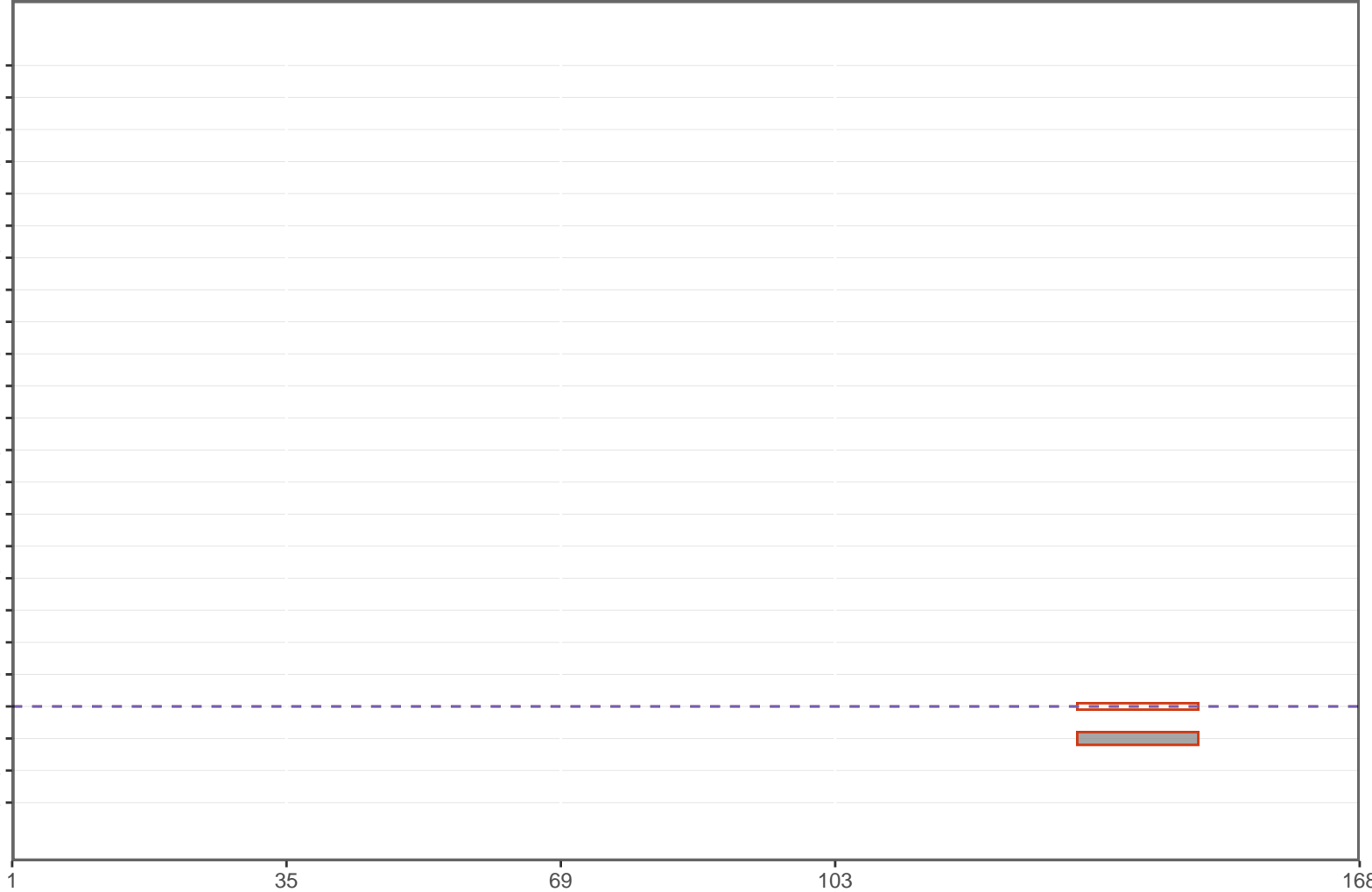
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGIFVGGFYLGGILVGTLLGGVFLGHSKALAGADKKDLMRKLPKFIYDEDKALEKQRKLAEKIDQLNSADDISTQLRSDDTFNGAAVNSDDVEAVV

NbL17g23640.1 protein_canopy_homolog_1-like [MW - SP = 18.78 kDa]

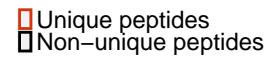
No. of times detected



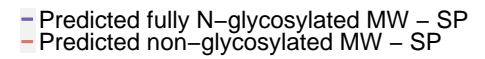
log(intensity)



Values from

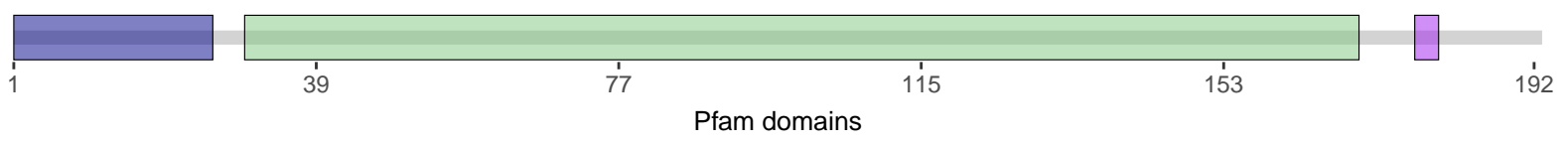
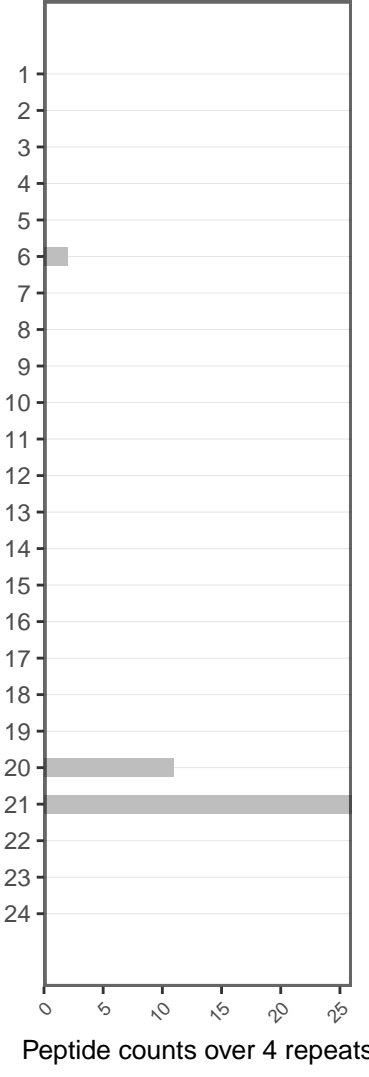
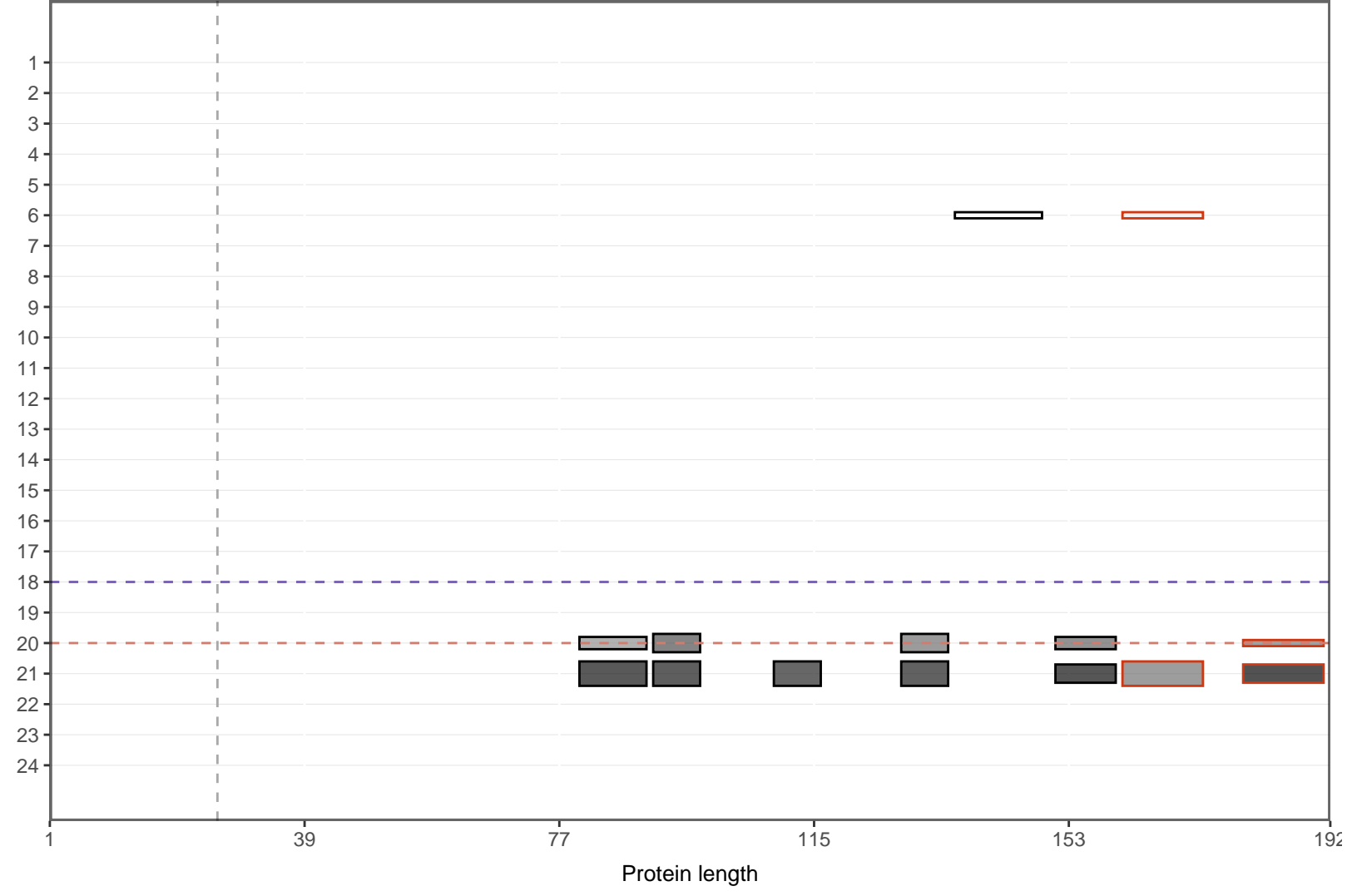
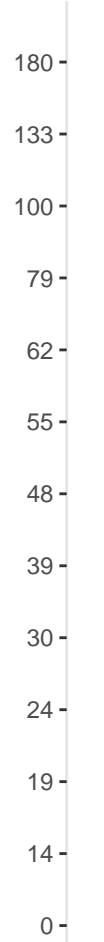


MW indication



Molecular weight

Gel Slice



Pfam Description
 ■ SP ■ Sequon ■ TM Domain ■ PF11938 TLR4 regulator and MIR-interacting MSAP

Protein sequence:

DLCCEKMDQYTLKIKVDSSTKTKWIKVWVWDLKLNKGEARAHKAKISFSGRLLLEQTEDDFTFLMKKGGVGVGVDVSKVLDGELSNVGNKGSNNKTVGDNEDADRELI

NbL17g23590.1 peptidyl-prolyl_cis-trans_isomerase_FKBP18_chloroplastic [MW = 24.73 kDa]

No. of times detected



log(intensity)



Values from



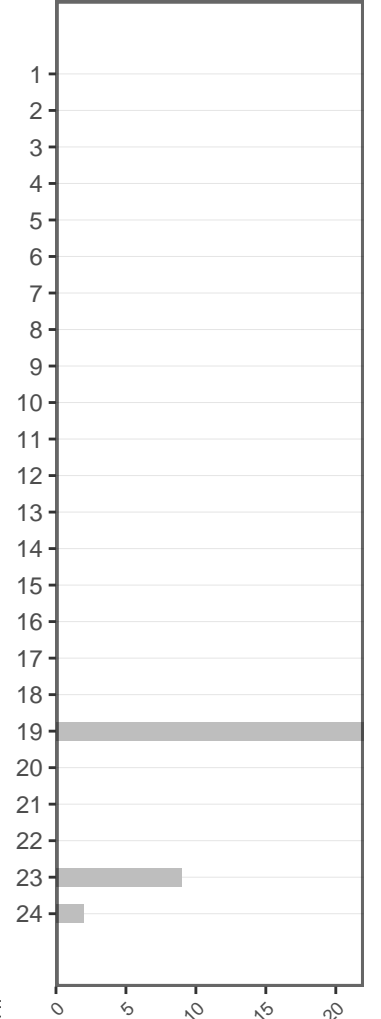
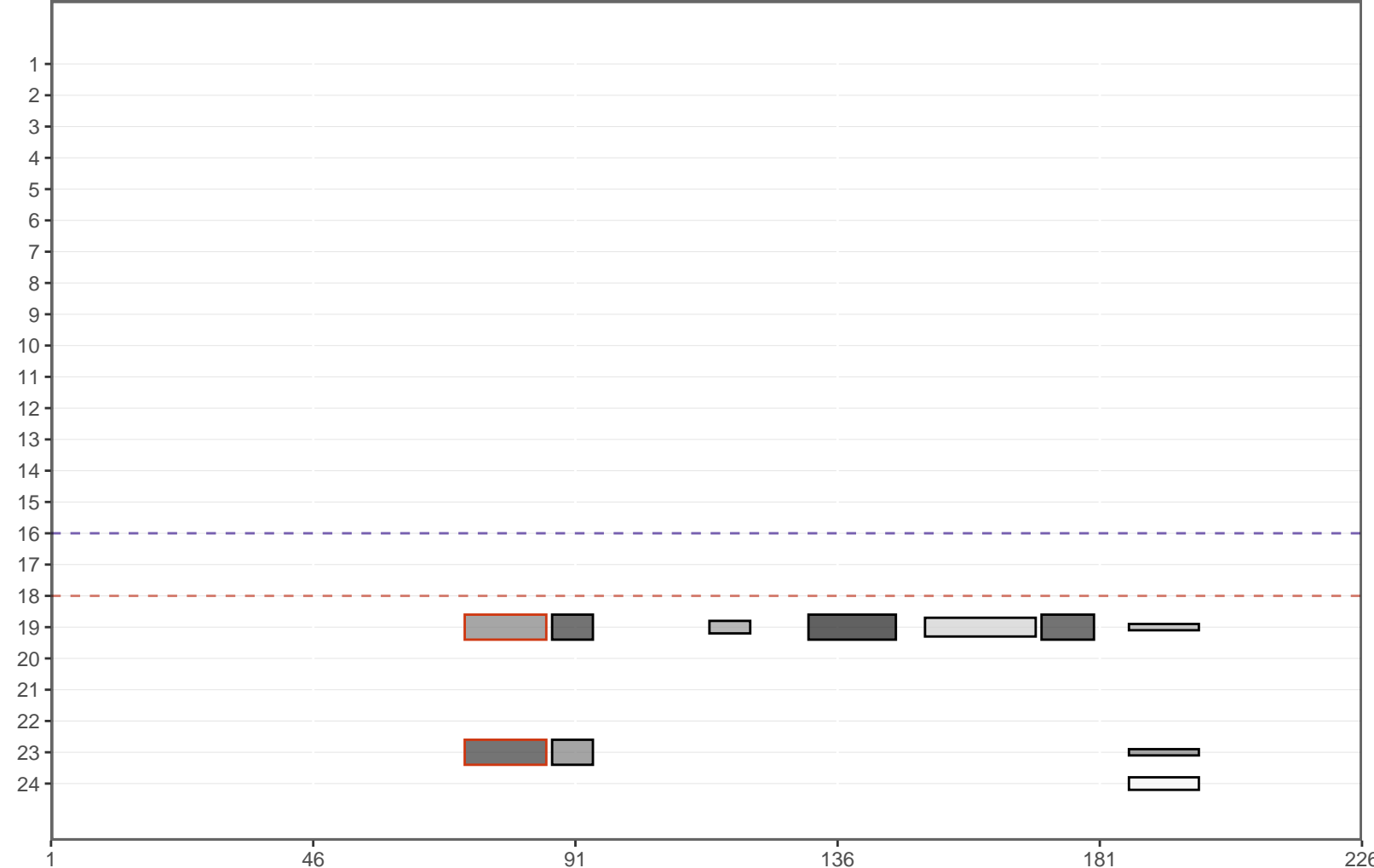
MW indication



Molecular weight

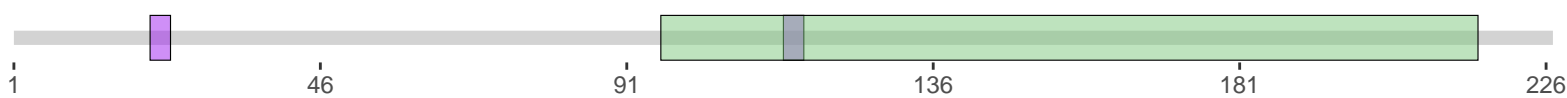


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

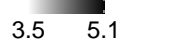
ISTVGVHFECLYRNTAVSRRESKLLAGNRHSGPYEFQVGGAPPKGRKRDFVDNPNGLFSAQAAPKPKKAMYITTEGMKVGKRTVWVPEAGYGRGMNEIPPGATFDLNIELLEVKKPEKQ*

NbL17g23490.1 xylem_cysteine_proteinase_1-like [MW - SP = 37.04 kDa]

No. of times detected



log(intensity)



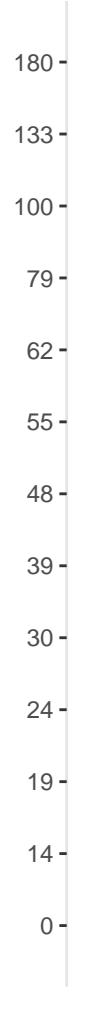
Values from



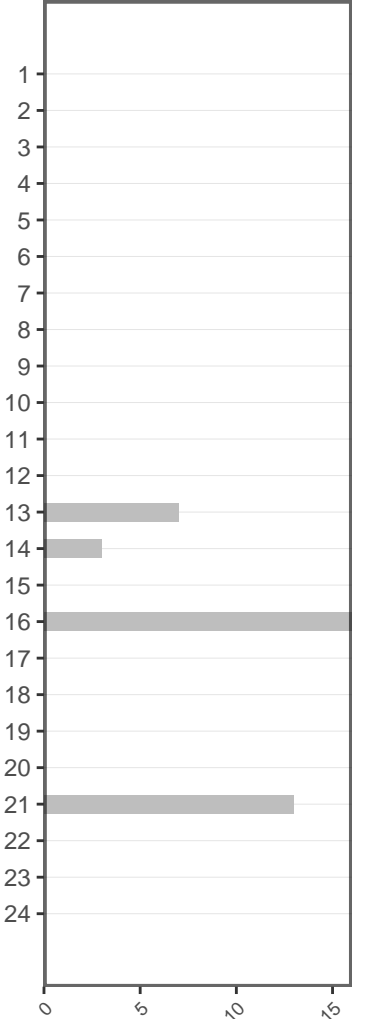
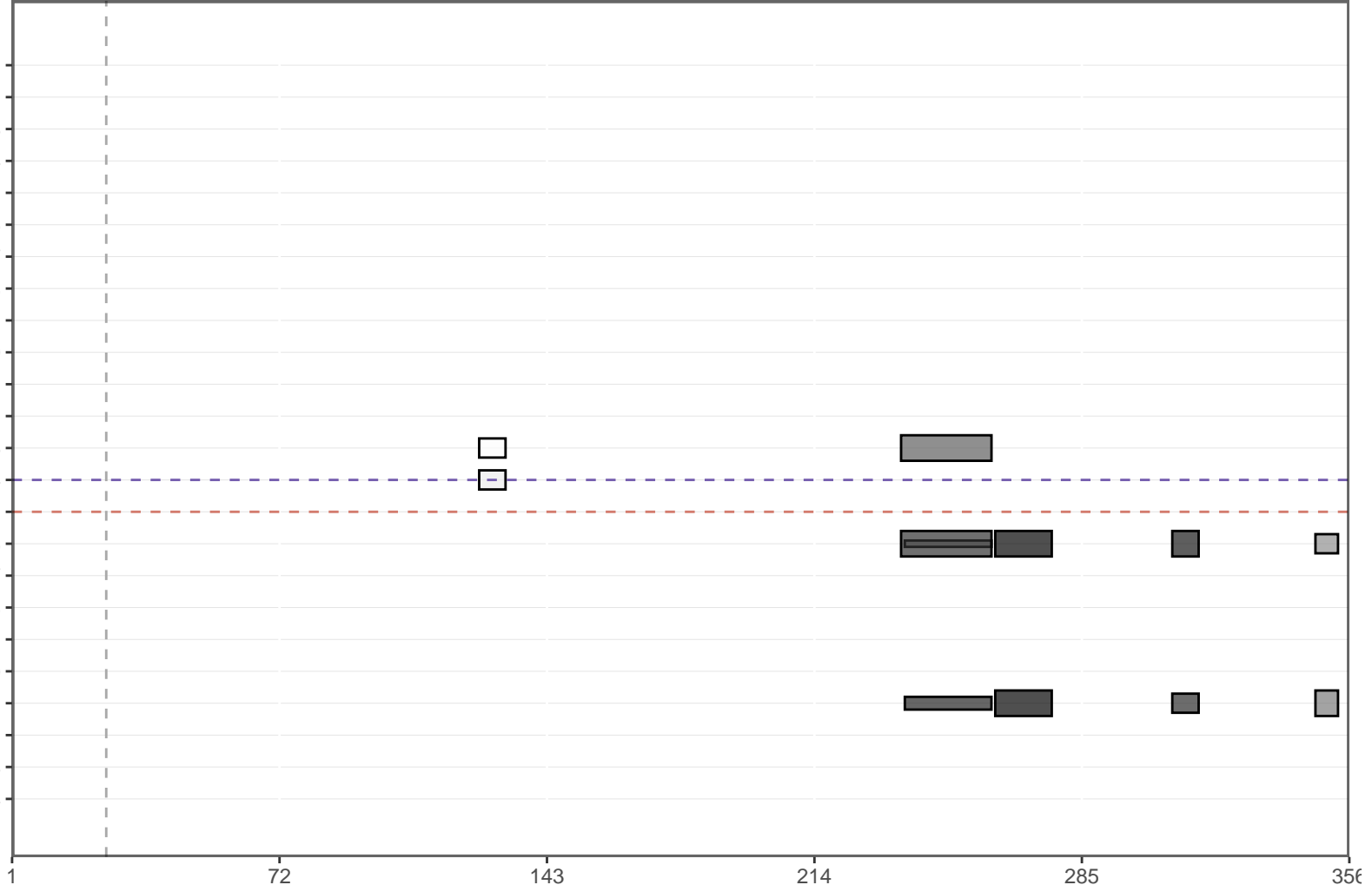
MW indication



Molecular weight

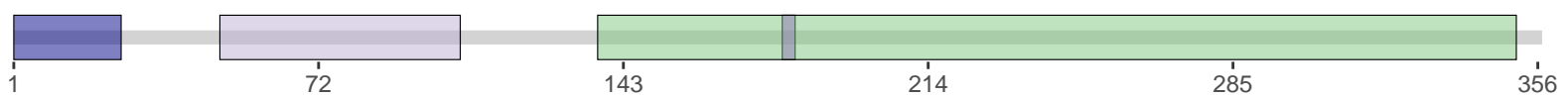


Gel Slice



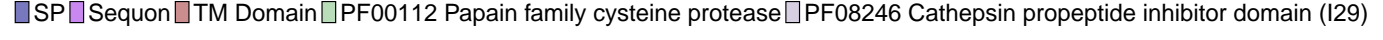
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AAVEGINQKTKGNLTELSEGELEIDGDTFTYNNQNGCNGGLMDYAFQFHSNGGLHKEDDYPYLMEEGTCNEKRDESEVATIDGYHDVPAFDEQBLKALANGLPSVAIEASGRDFQFYGGGGYFDGHGDTLHDGQVAVGVTTKGADHIVVNSVSPKHWGEGKGFIRMKRINTGKAEKGGKGNMVSFVKKK

NbL17g23450.1 increased_DNA_methylation_3 [MW = 19.91 kDa]

No. of times detected



log(intensity)



Values from



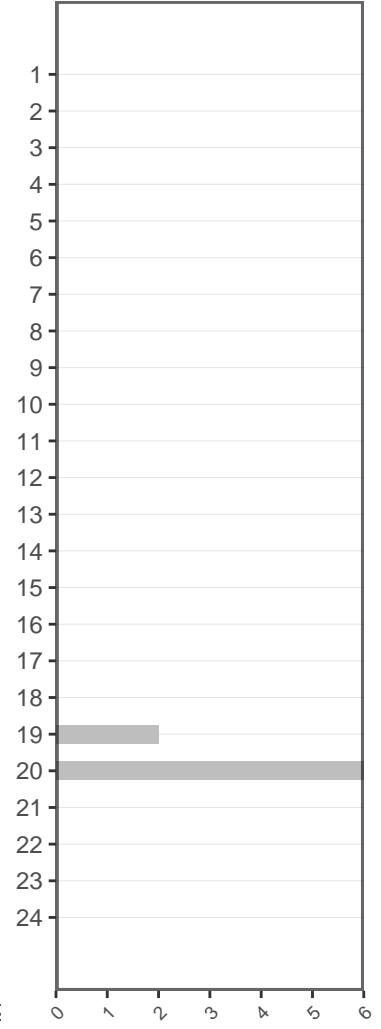
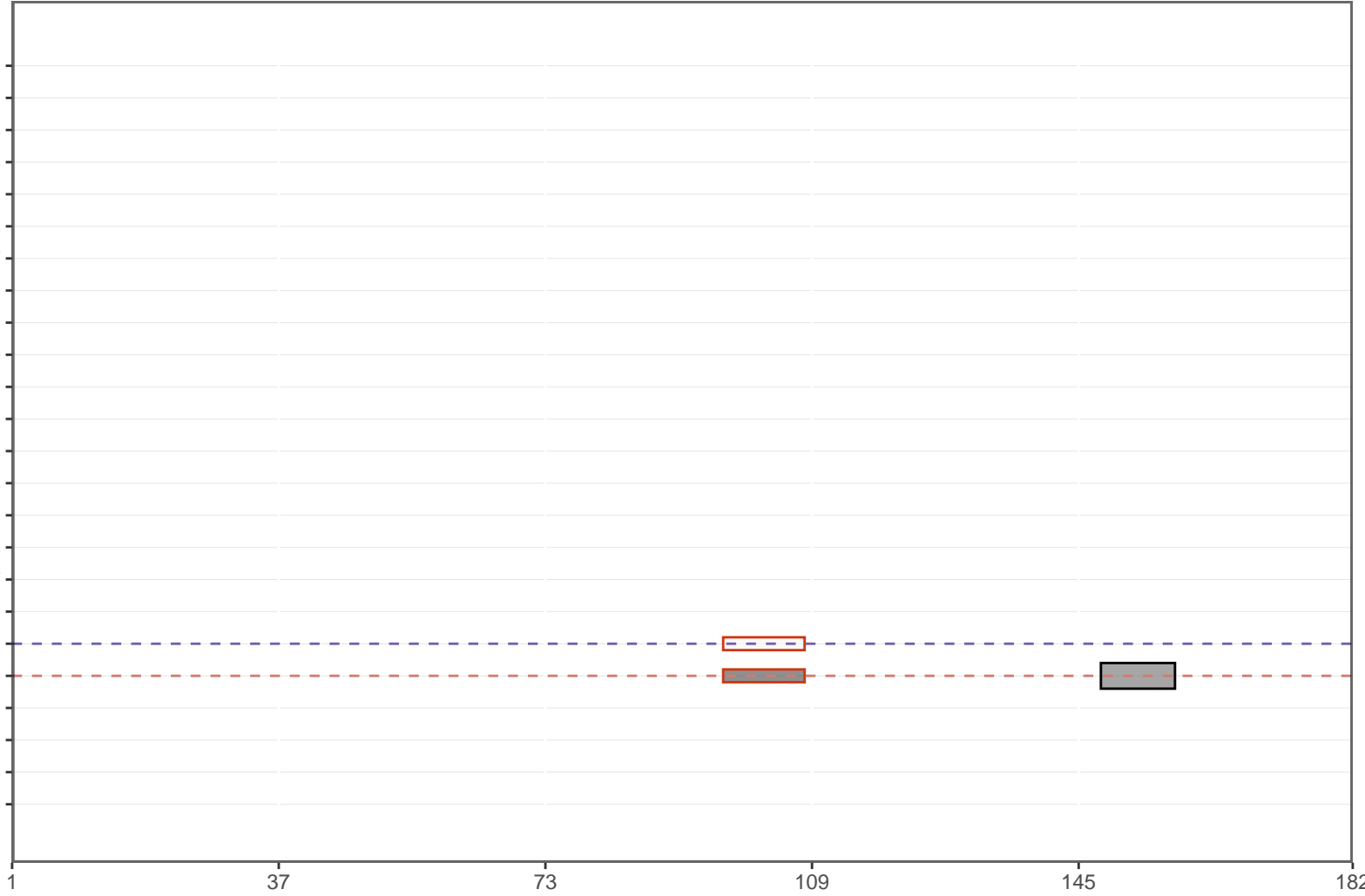
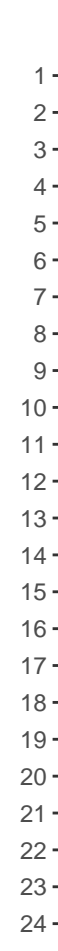
MW indication



Molecular weight



Gel Slice



Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

SVRRKCNKCDIQREGVRVREGVITSGDLKNSPKDYEMKVGQLSPGPFVTFNLPGPVDPRLGERRFRSDGLEIVLKYRIPVSAEGLPENWYNGSFPK

NbL17g23380.1 cinnamoyl-CoA_reductase_2-like [MW = 37.37 kDa]

No. of times detected



log(intensity)



Values from



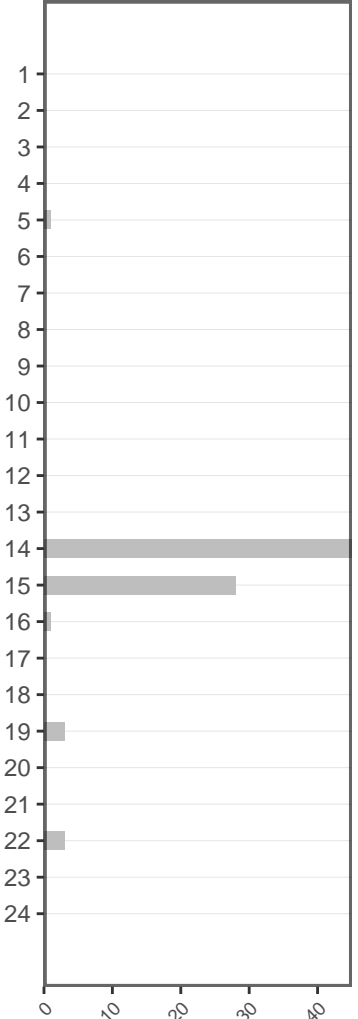
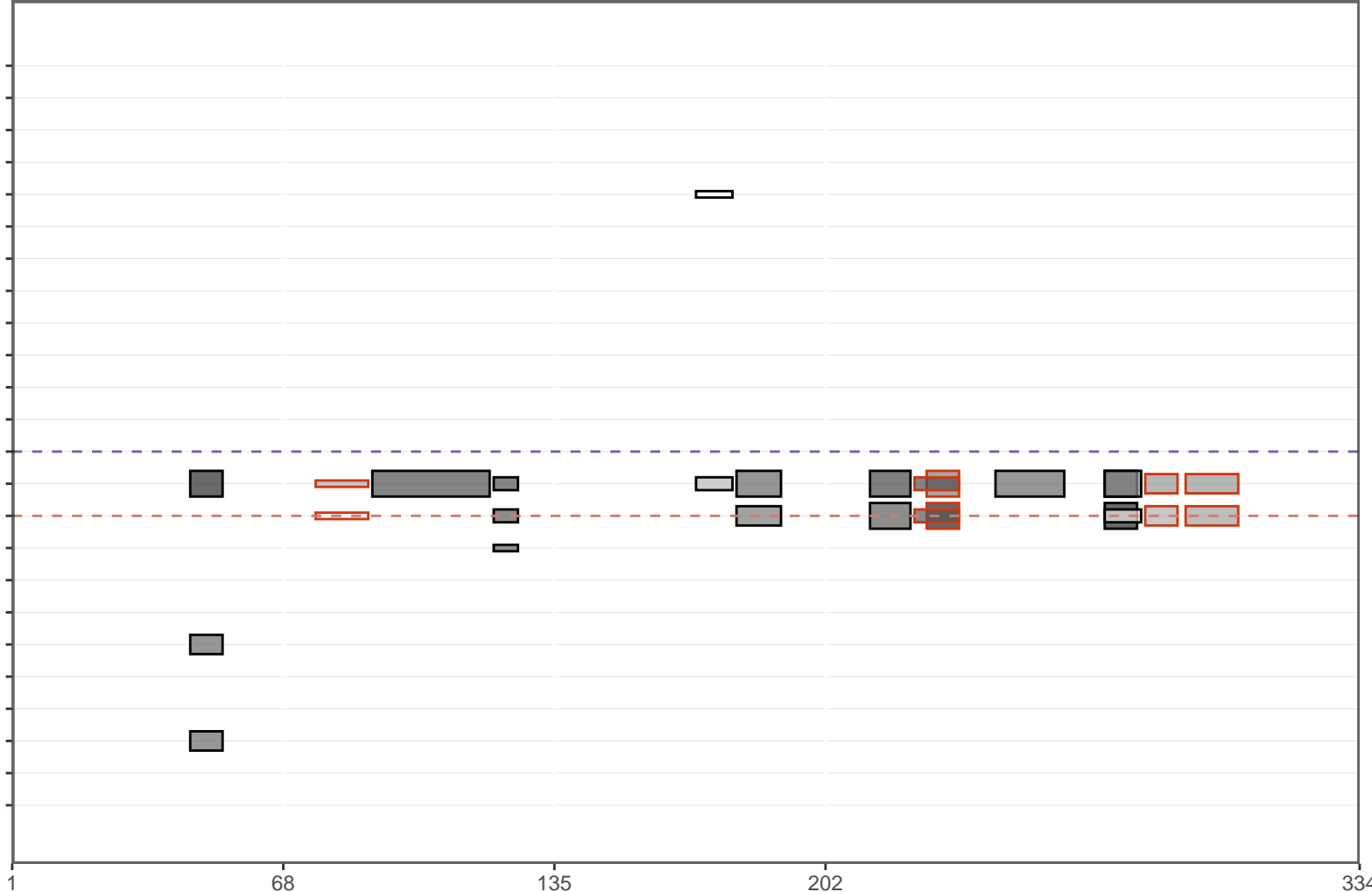
MW indication



Molecular weight

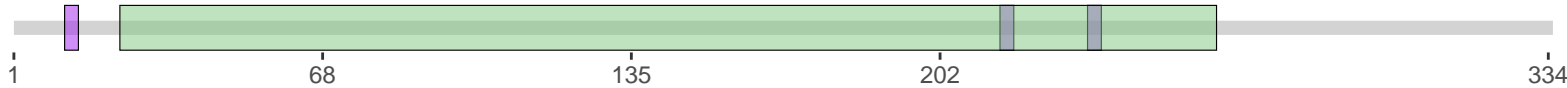


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

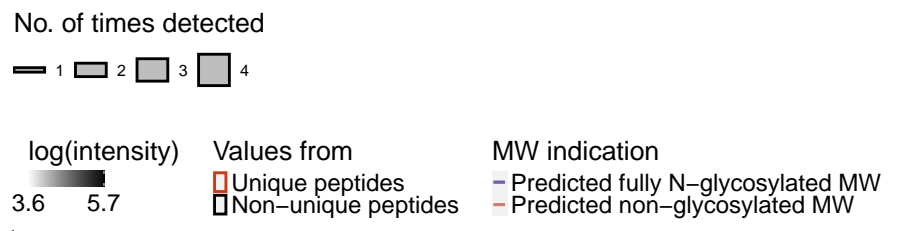
Pfam Description



Protein sequence:

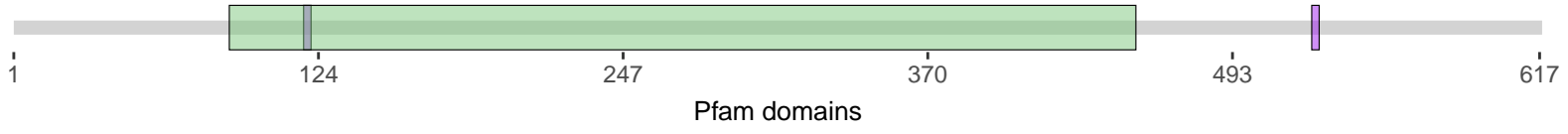
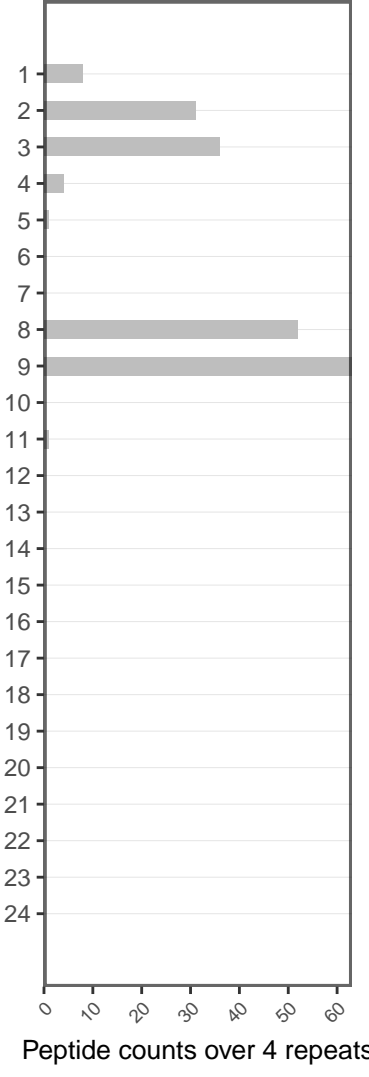
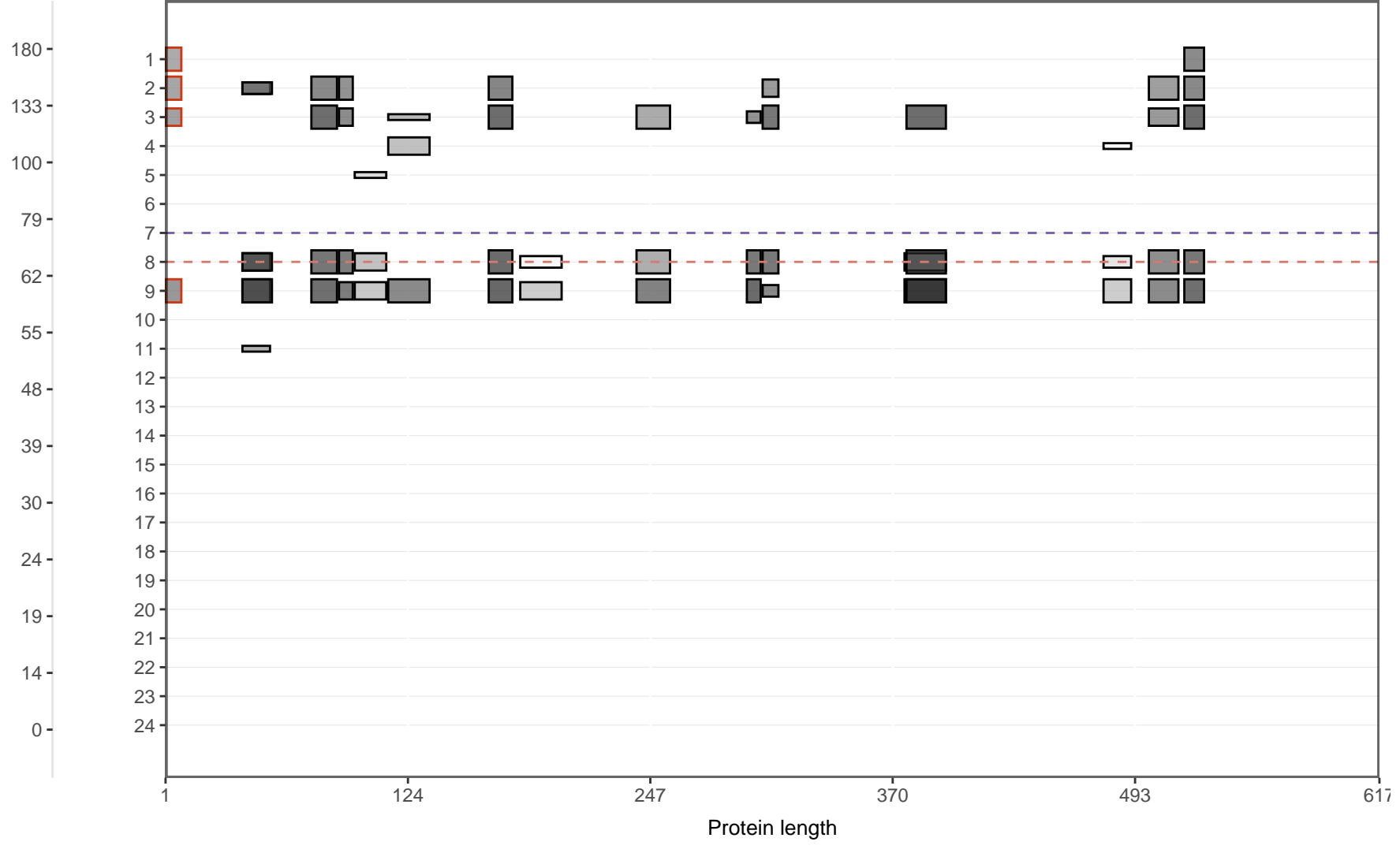
YKIDTCVSDSEYKATNWWYSGSKTMAETEAWSYAKGGGLDVLVLPTRVWGPMLGKTTNASSLLKLLKEGYEELKNTFRFDVRLAEALVLYEKPEAEGRHGMHAKANGDGLVMDLNRYYPNVYFKRFETDVRREEGSYSTEKLLKLGWKRPLEETLDAVESYKAGILD

NbL17g23280.1 pyrophosphate--fructose_6-phosphate_1-phosphotransferase_subunit_alpha [MW = 67.36 kDa]



Molecular weight

Gel Slice



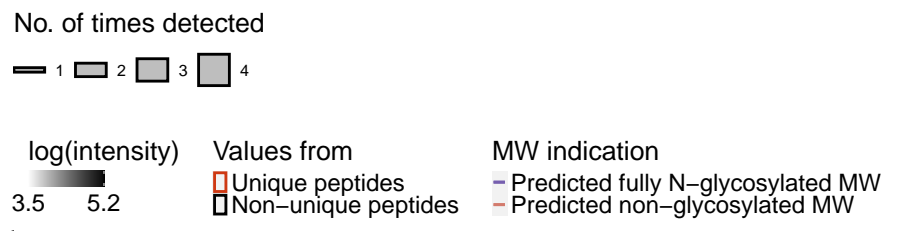
Pfam Description

SP Sequon TM Domain PF00365 Phosphofructokinase

Protein sequence:

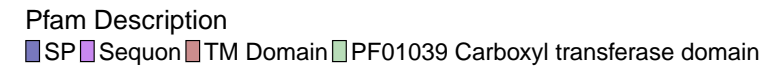
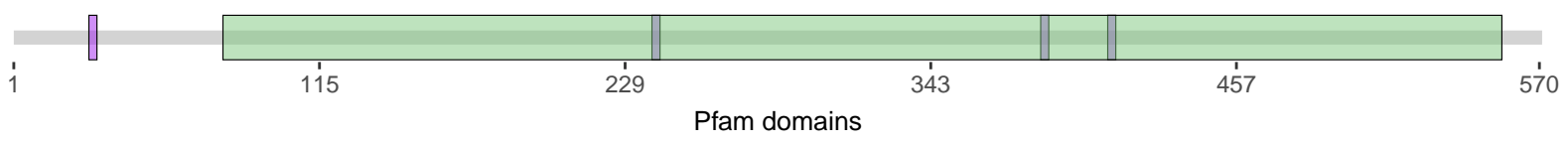
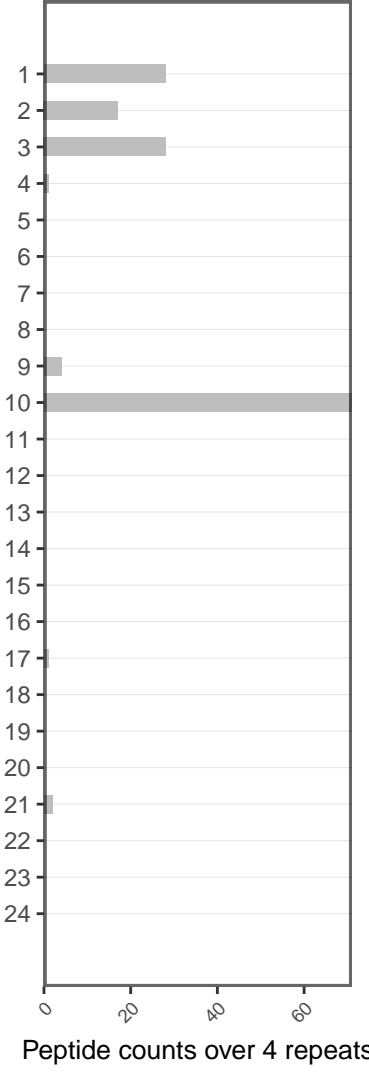
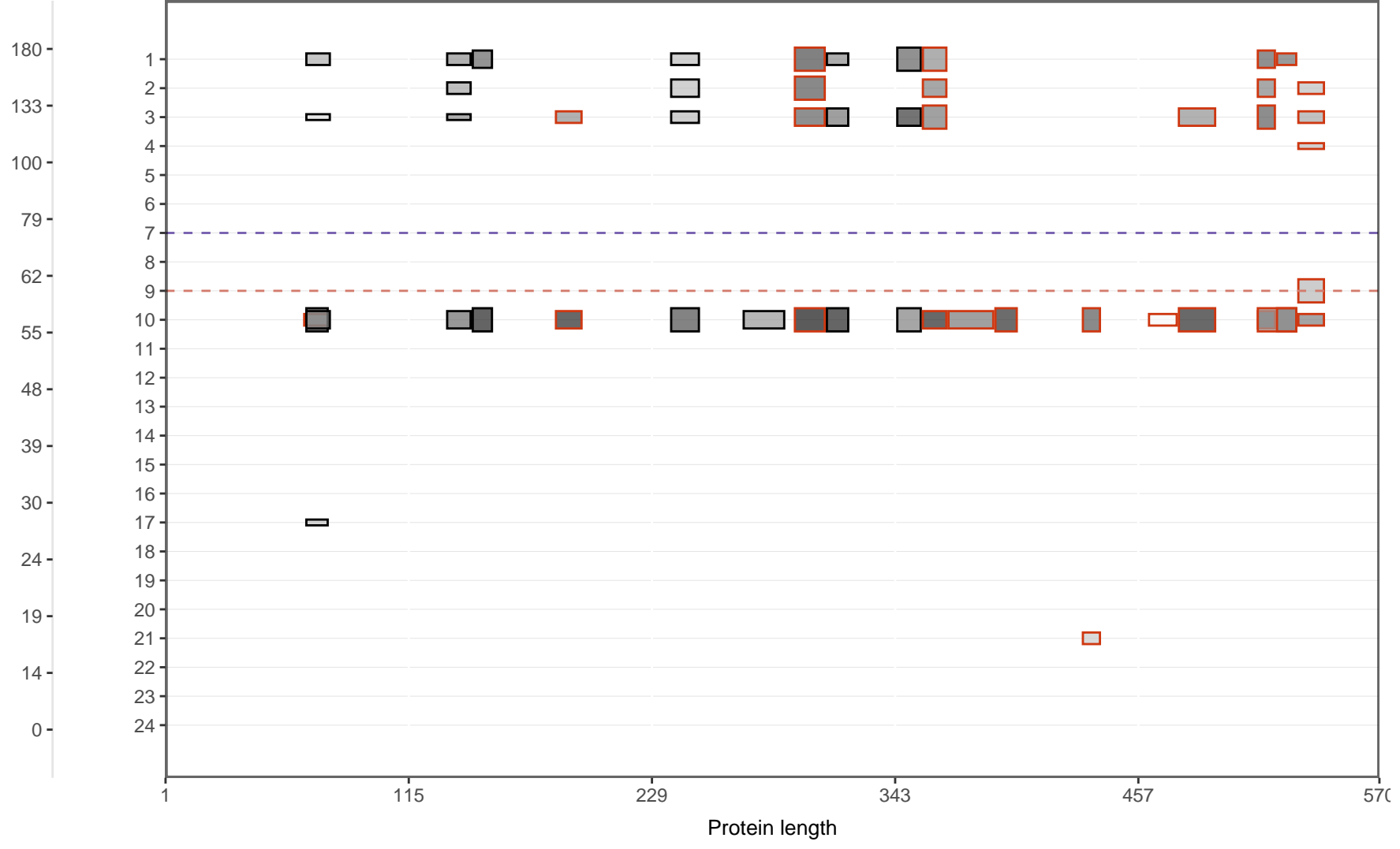
SKLTFDITKICDVAQARAENHDKNHGVILLPEGLIEIPVYALLGEHGLLRQGVASADKISSQLSPWASALFEFLPVFIRKQLLHPESDSSAQLSGDIETEKLIHILVETEMNKRKKEGTYKGNFNAICFFGYQARGLSPKFKDCDVAWVLLGHVGHVHLAAGLNGVMATVTLNKNPNKWHOGAAPSAMMTVKRYGRGPKASIGVPAIHPRTVQLKKGKVEYLLSQNATKFLLEDVYRNPGPLGFDGPGADAKAVTLGVEDGDYMRINKLGEVLEKVRTIVKPGCSQDVLI

NbL17g23180.1 methylcrotonoyl-CoA_carboxylase_beta_chain_mitochondrial [MW = 61.59 kDa]



Molecular weight

Gel Slice

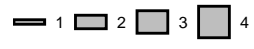


Protein sequence:

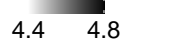
SGVSDYFAHDELHLAGRNIVKNIHMAGGPEASGGTRADYKELFVYKELRTIAPTDLKQPFDRVIRVARIIVGSGEDEFKLYGTTLVTGFORIGGQPFVGLGNGLIFENESAGKGAHFIELCAQRNPLIFLGNITGFMYGSKSEASGIAKAKAMVAVSCAKVFKITVYVGGFAGAGNVMCGRAYSPNFMFFVFNARISVIMGGPQAAGVLAQVEKATKKKGGWAKEEENFKAEVVEAYDREGSPVYATRLWDDGDHPDTRKILSLGHSASLRGPETTKFGVFR

NbL17g23170.1 thioredoxin_M3_chloroplastic-like [MW = 19.95 kDa]

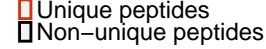
No. of times detected



log(intensity)



Values from



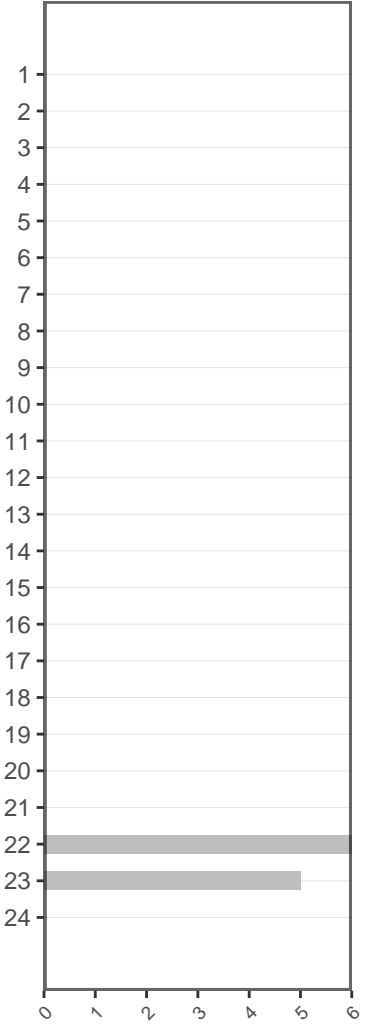
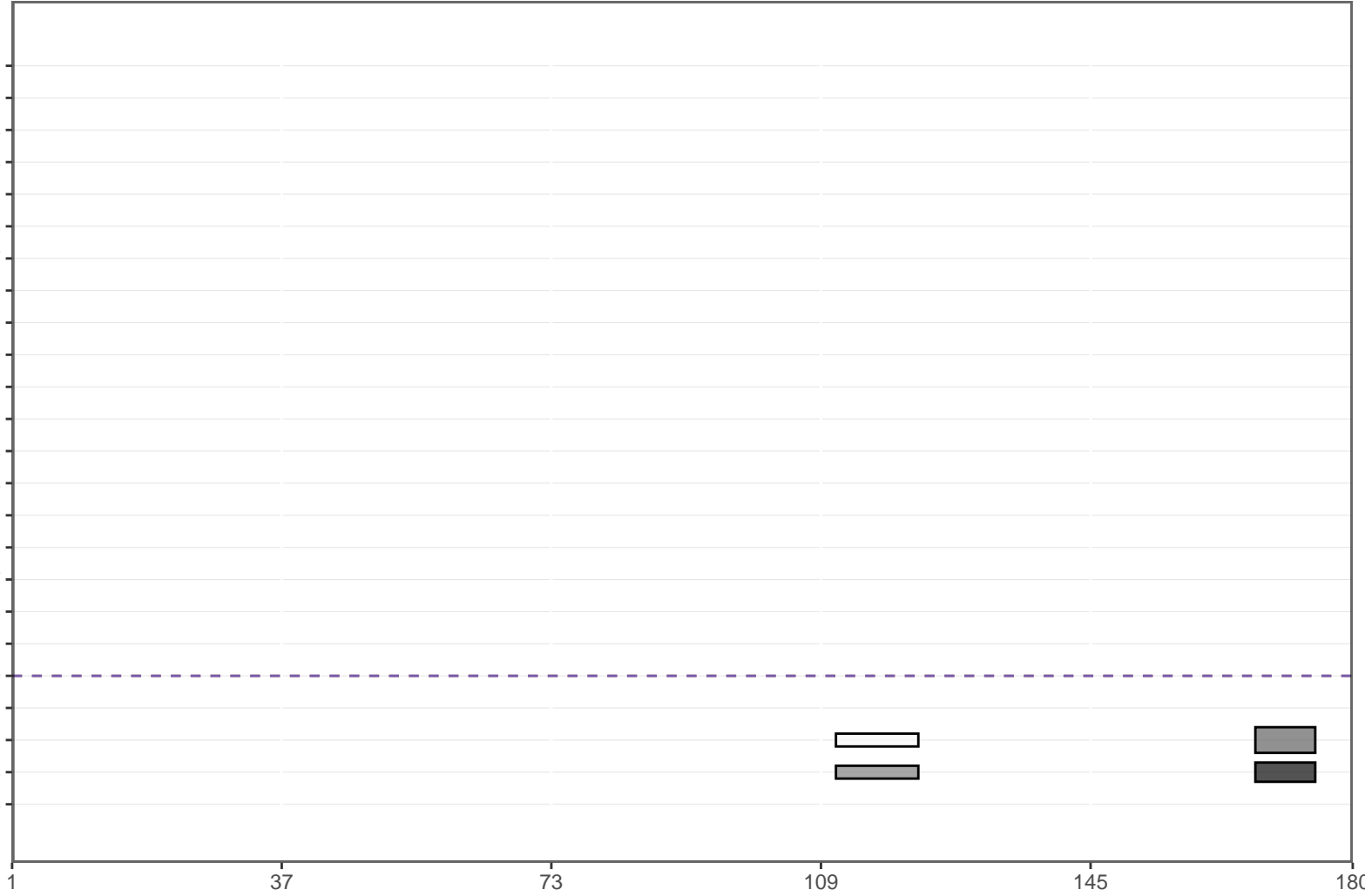
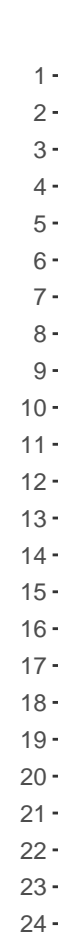
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

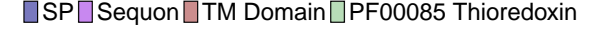
Protein length



Pfam domains



Pfam Description



Protein sequence:

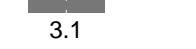
EVVTAKSVKELLSDDTLVLFVHFATWCGPGGMVHRVDEIAEYSGRLKGVLDADSESGIAEDYDKAVFVLLFRNGEKGDSEVIGTMPKEFYVAGIERLLAS*

NbL17g23140.1 PI-PLC_X_domain-containing_protein_At5g67130-like [MW = 52.03 kDa]

No. of times detected



log(intensity)



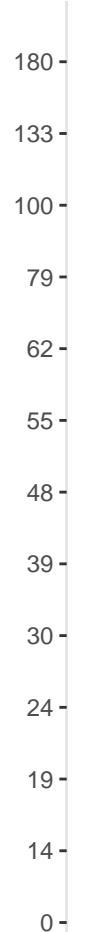
Values from



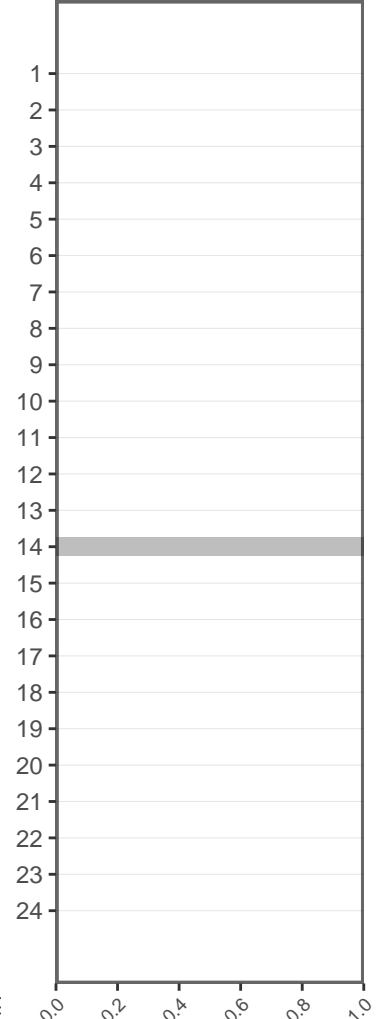
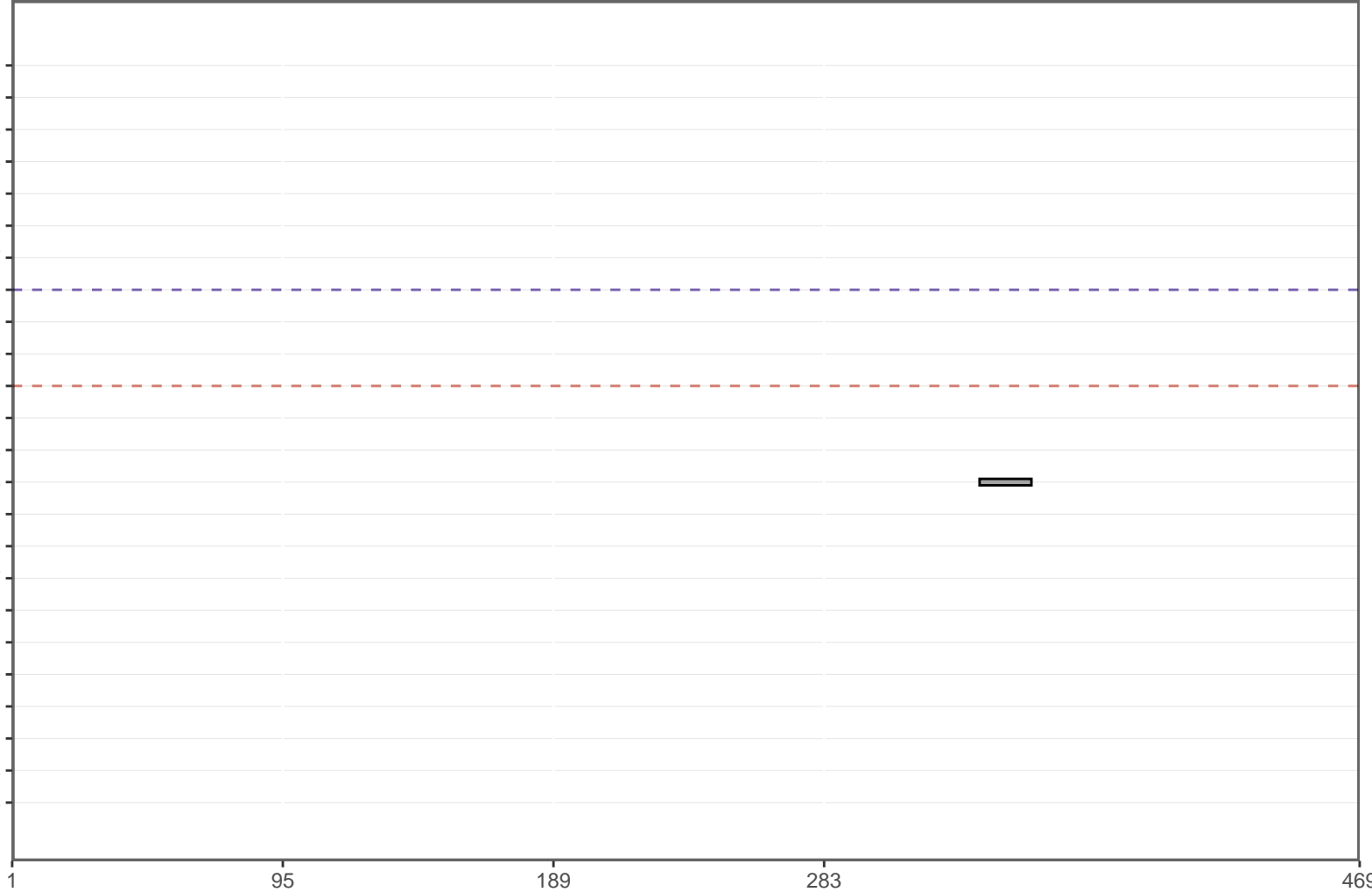
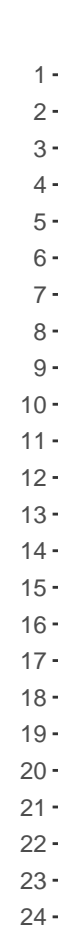
MW indication



Molecular weight



Gel Slice



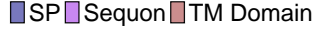
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EANPSDITYIEDYVRSPNGLTKLFDAGLRKRFVFRVSRMPNNGGEWPTVDDMVGRRNQLRVVFTSKSAKEPSEGIAYEWRVYVWENGYGNGMKGPGCPNRAEISSAMDNKTSLVLMVYFPDAPDFQAQKHNSAPLNMMTTQHEAAGKRWFNFVAWDFYKRSDDGGGAPEAVDVAHGHVCGGTNIASGCKEHMTYIGIGELPEPRISPVTPAAAKNETSFSNFGQPKLQWLLGTTLMSEFLI

NbL17g23090.1 caffeoyl-CoA_O-methyltransferase_6 [MW = 27.78 kDa]

No. of times detected



log(intensity)



Values from



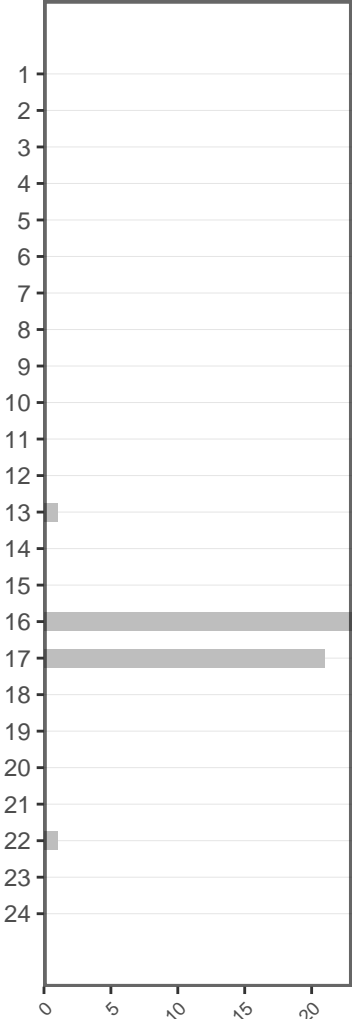
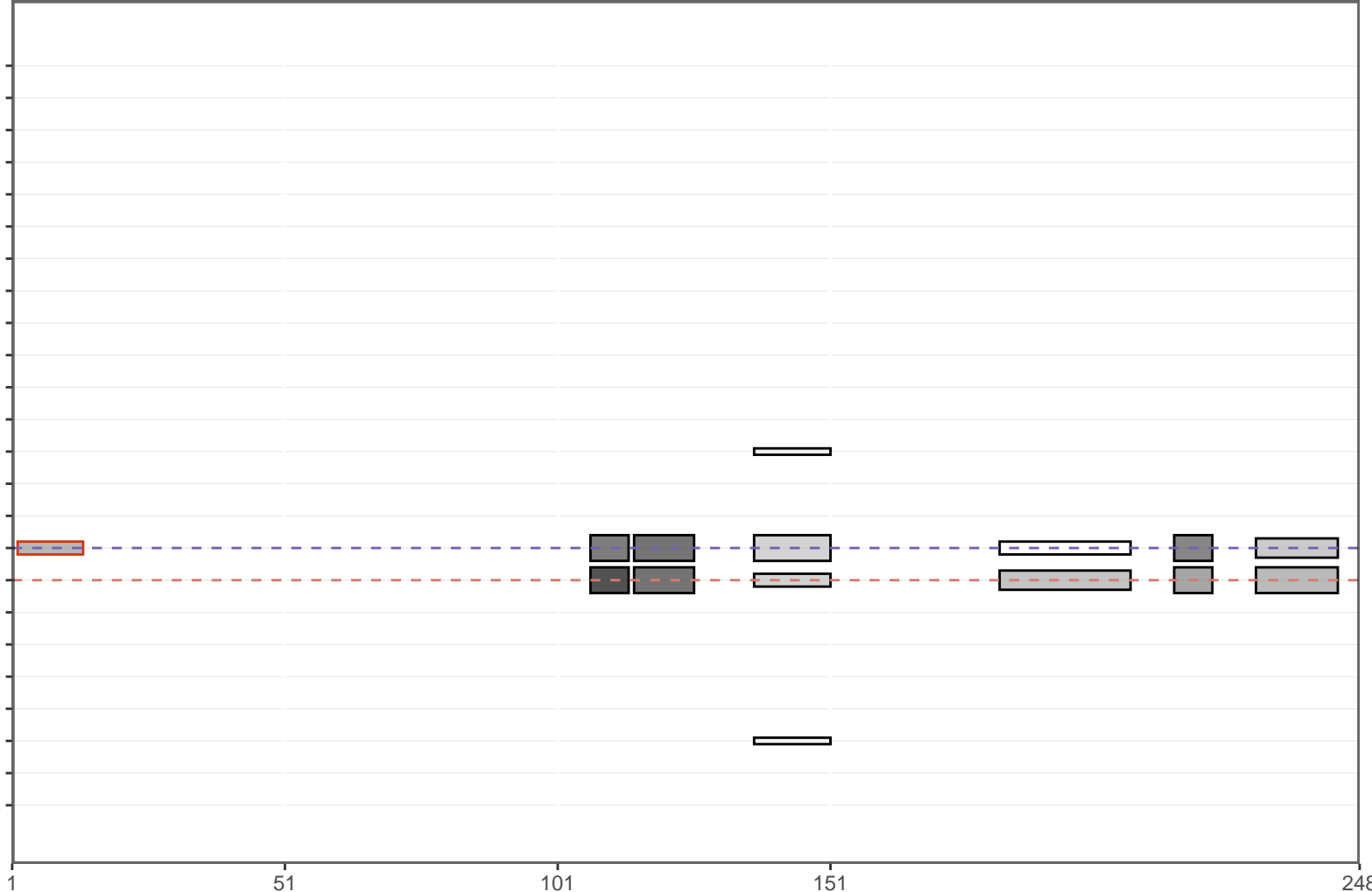
MW indication



Molecular weight

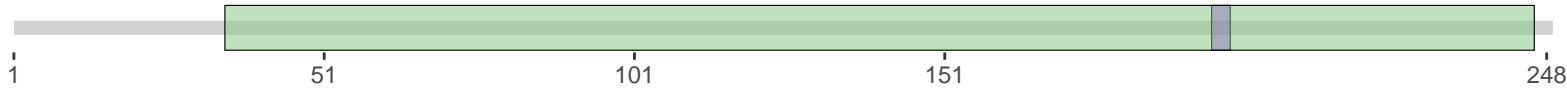


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ADINRENYEIGLPVQKAGVAHKIDFREGPALPVLIDLMVEDKNNHGTDFRFDADKDNVYHKRIELVKVGGVGYDNTLWNGSVAAPPDPMRKYVRYRDFVLELNKALAADPRIEICMLPVGGDTLGRIN

NbL17g23020.1 CBS_domain-containing_protein_CBSX1_chloroplastic-like [MW = 26.4 kDa]

No. of times detected



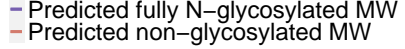
log(intensity)



Values from



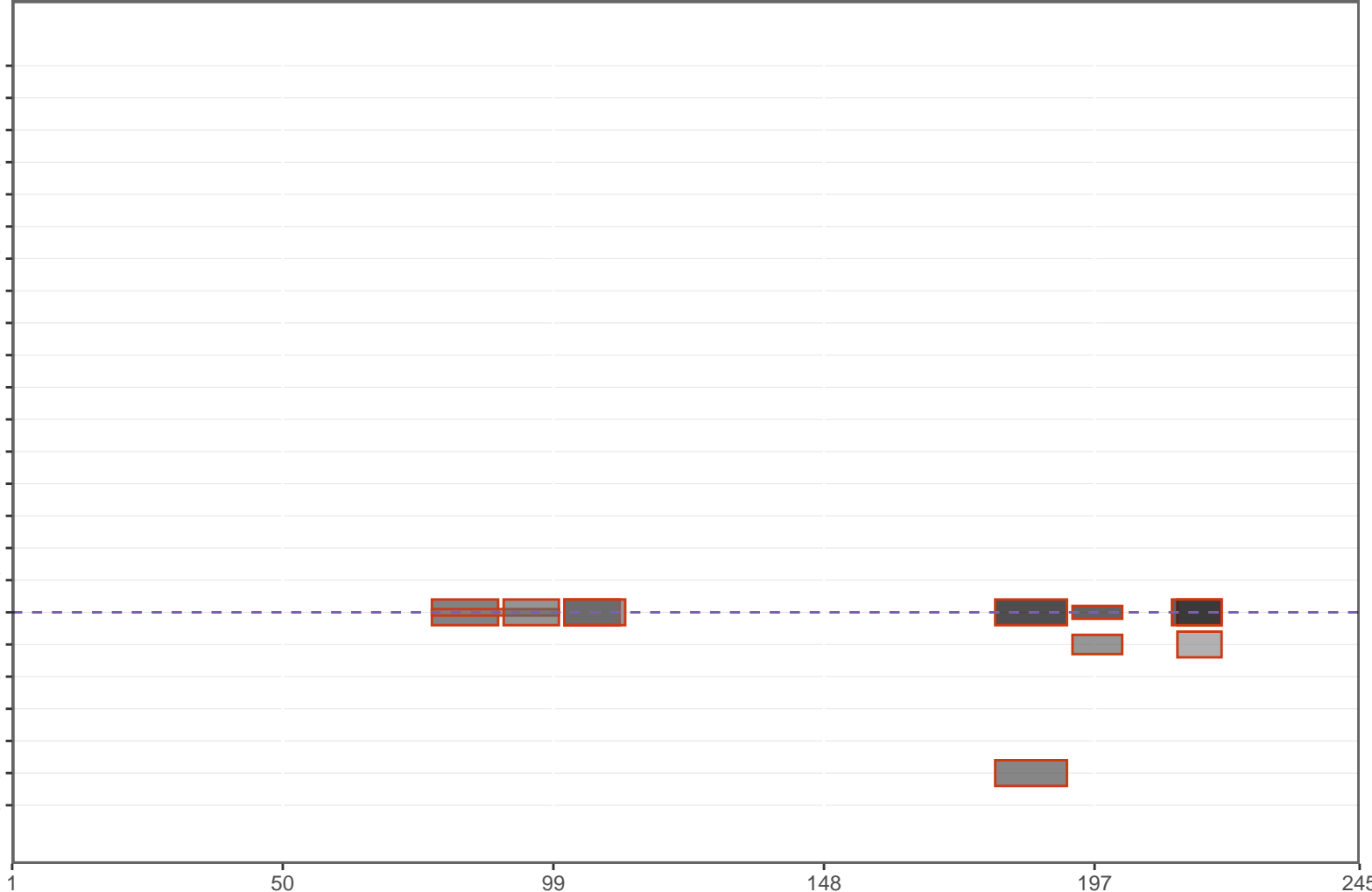
MW indication



Molecular weight



Gel Slice

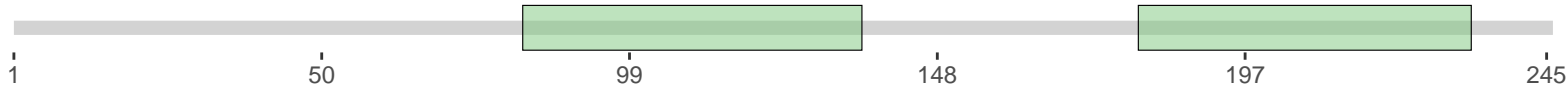


Protein length

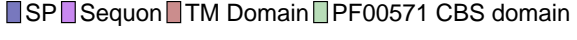


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VEKRYTGLPVIIDDDNVLGVVSDNLLALDPSISGIEGTGADTNLFPVDSTWTFNEVQKLLKTKNGKVVGDVMTPTPLSRENTNLEDAARLLGQTKYRLLPVVDVGGKLVGITRGNVYRAALGIKRTIDQ

NbL17g22990.1 scopoletin_glycosyltransferase [MW = 53.77 kDa]

No. of times detected



log(intensity)



Values from



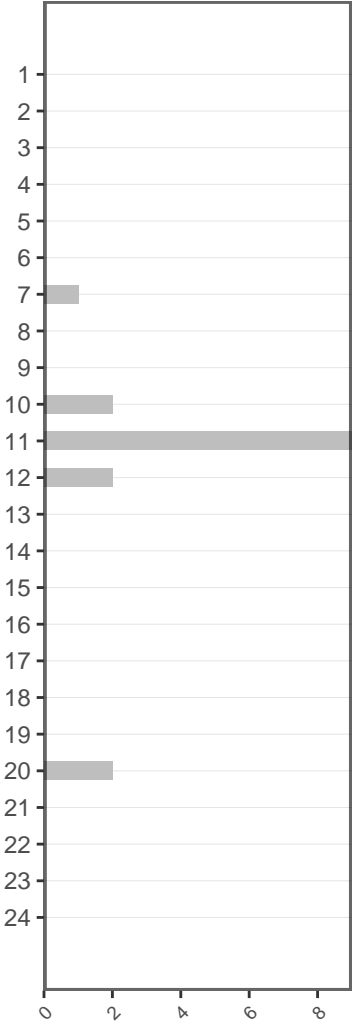
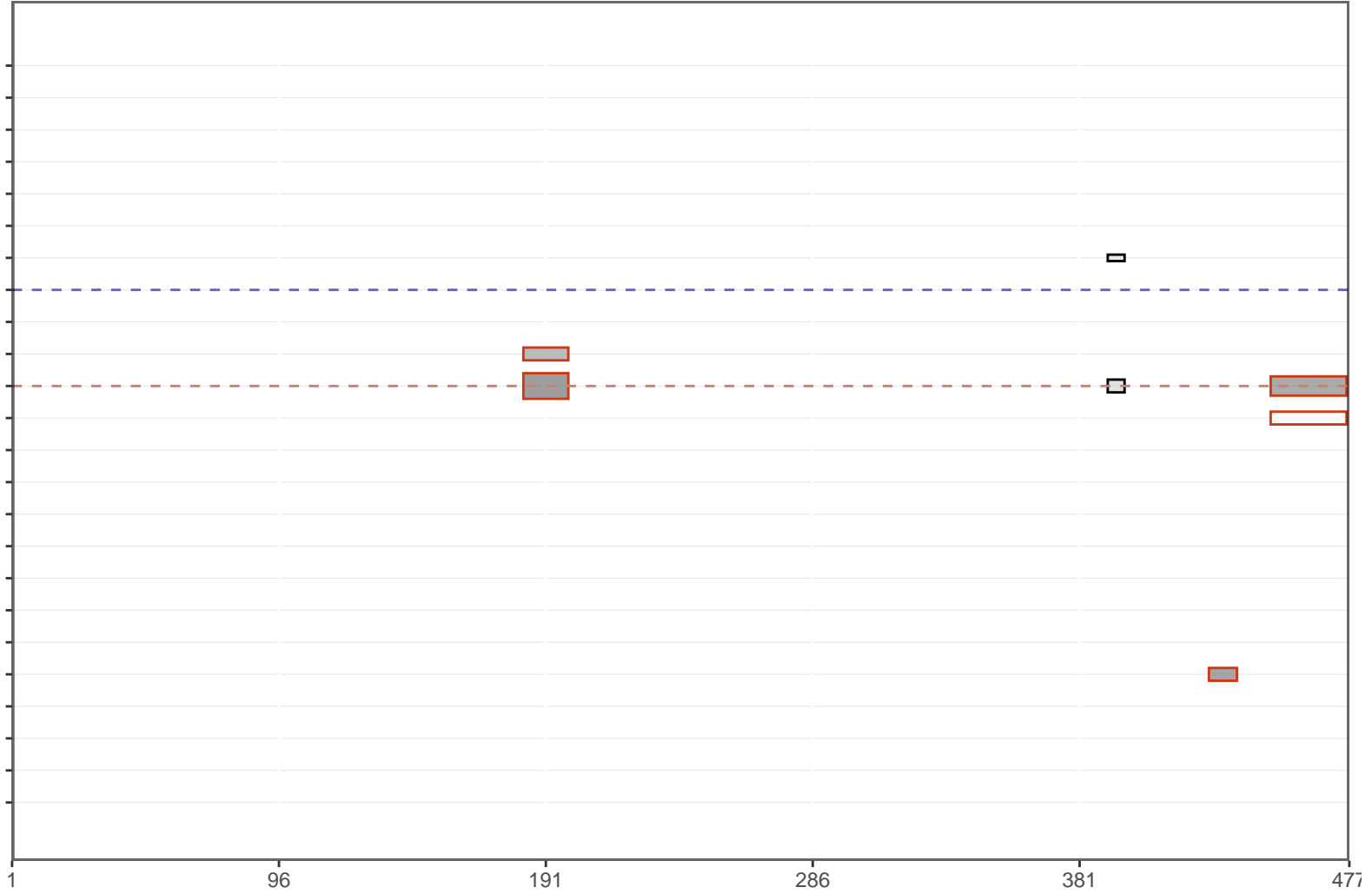
MW indication



Molecular weight



Gel Slice



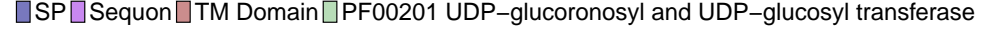
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

HYTKVLGRRAWIIGPLGMCNRDIEDKAEKGRKSSDKHEGLKWLKLDKPKSIVVYIGFGSVANFTASQLHELAMGIEASGGDEFWVVRTELNDKDLPEGFEEETREKGLIRGWAPQVILDHESVGFVTHGQWNSLLEGVGGVPMVTFVFAEGFFNEKLVTEVLRITGADVSGHWRRSASEGVKREIAKAKQRVMVSEEAEGFRNRAKAYKEMARKAVEEGGSSYGLTLLLEDISTYESTGH

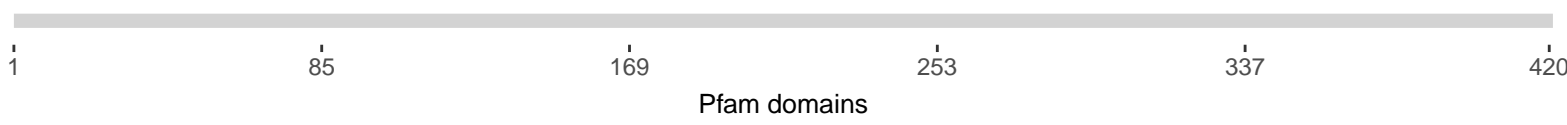
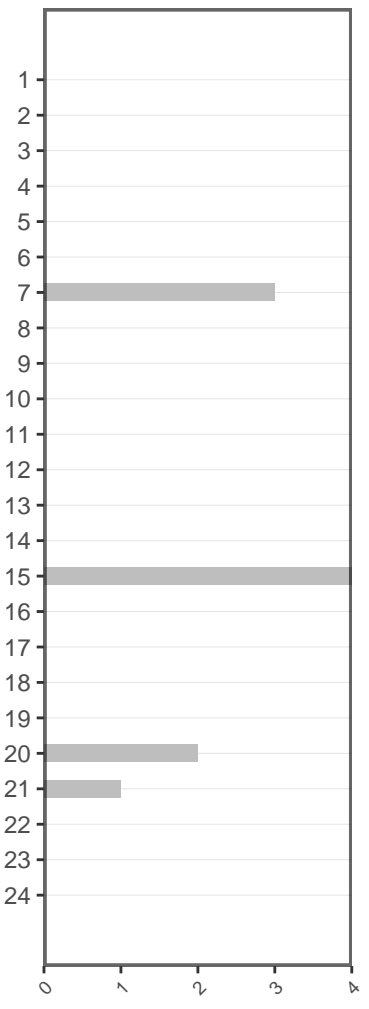
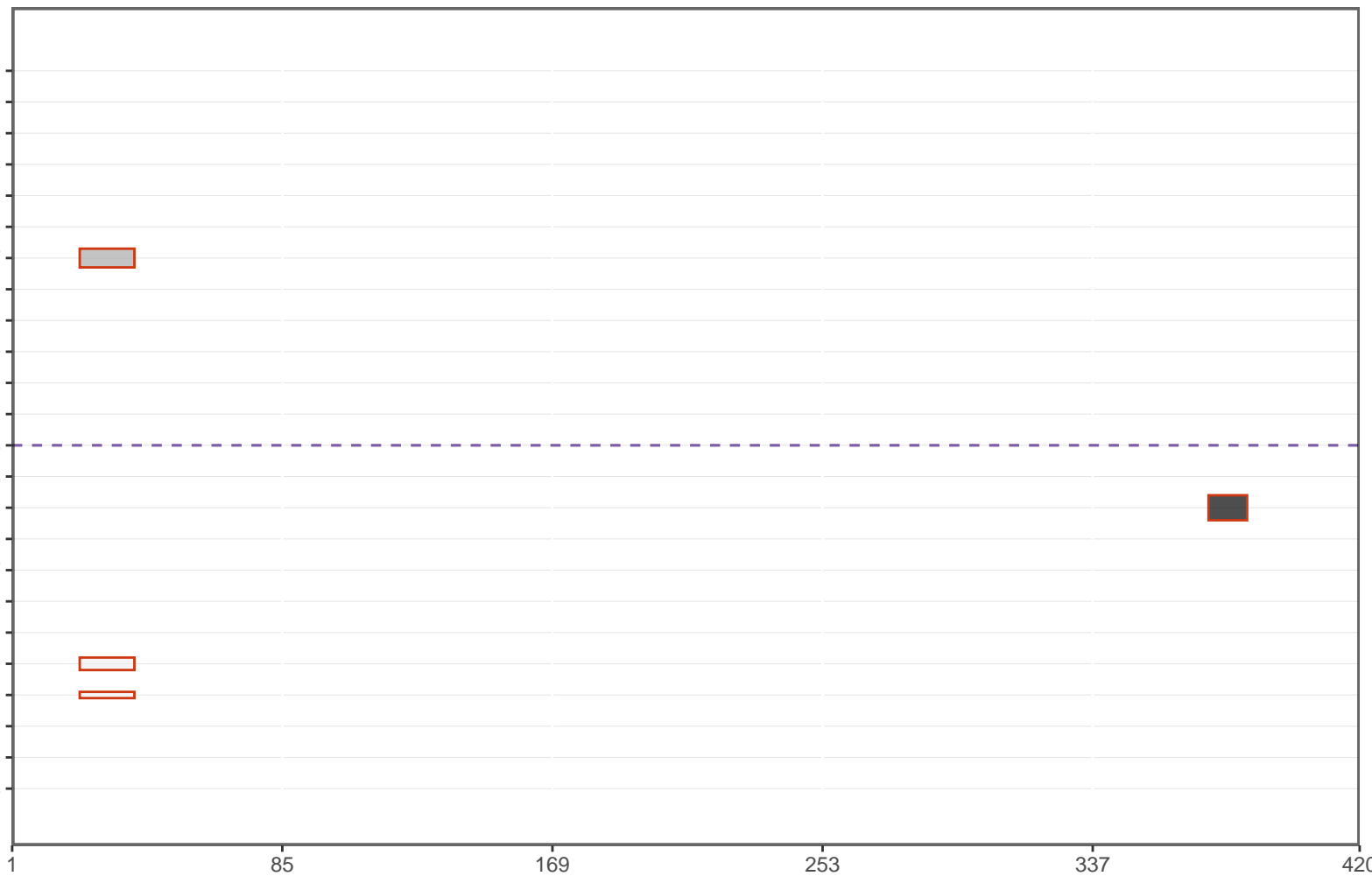
NbL17g22970.1 phosphatidylinositol_345-trisphosphate_3-phosphatase_and_protein-tyrosine-phosphatase_PTEN2A [MW = 46.86 kDa]

No. of times detected
 1 2 3 4

log(intensity) Values from MW indication
 3.5 4.7 Unique peptides Non-unique peptides
 Predicted fully N-glycosylated MW Predicted non-glycosylated MW

Molecular weight
 180
 133
 100
 79
 62
 55
 48
 39
 30
 24
 19
 14
 0

Gel Slice
 1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24



Pfam Description
 SP Sequon TM Domain

Protein sequence:
 YKYNLCSEELYDASLFEKGVGFDFDHNCPKGLISFGGSGAYGWLKEDIENVVVHKAGMARTGLMISLLVLLKLGVMVLFQFFPTAEEGMDYVNGKRCVDGKGLVFGQIRVYKFERILMVFNGENGPGRGMLRGFRLLHRCPPVWIRKPSIVSDHNGVLFSTKKHPRTKELSPEDDFVTSAPKGVVVFALPGEPLAELAGDFKHVHFGGGDFWV

NbL17g22960.1 elicitor-responsive_protein_1-like [MW = 26.28 kDa]

No. of times detected



log(intensity)



Values from



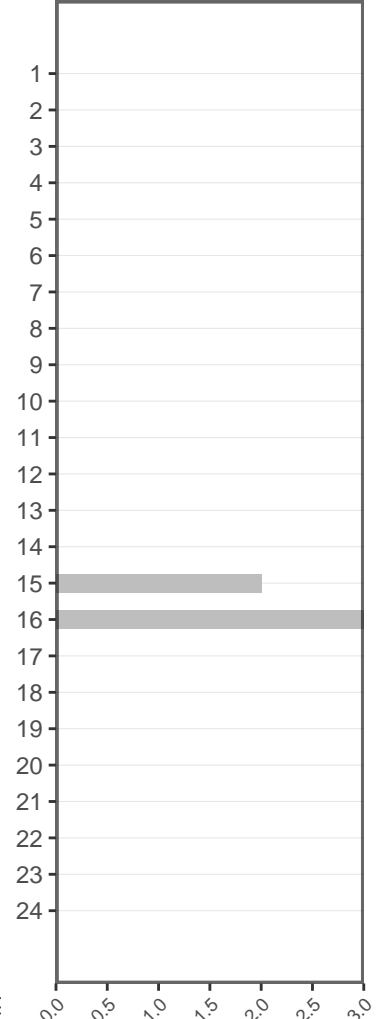
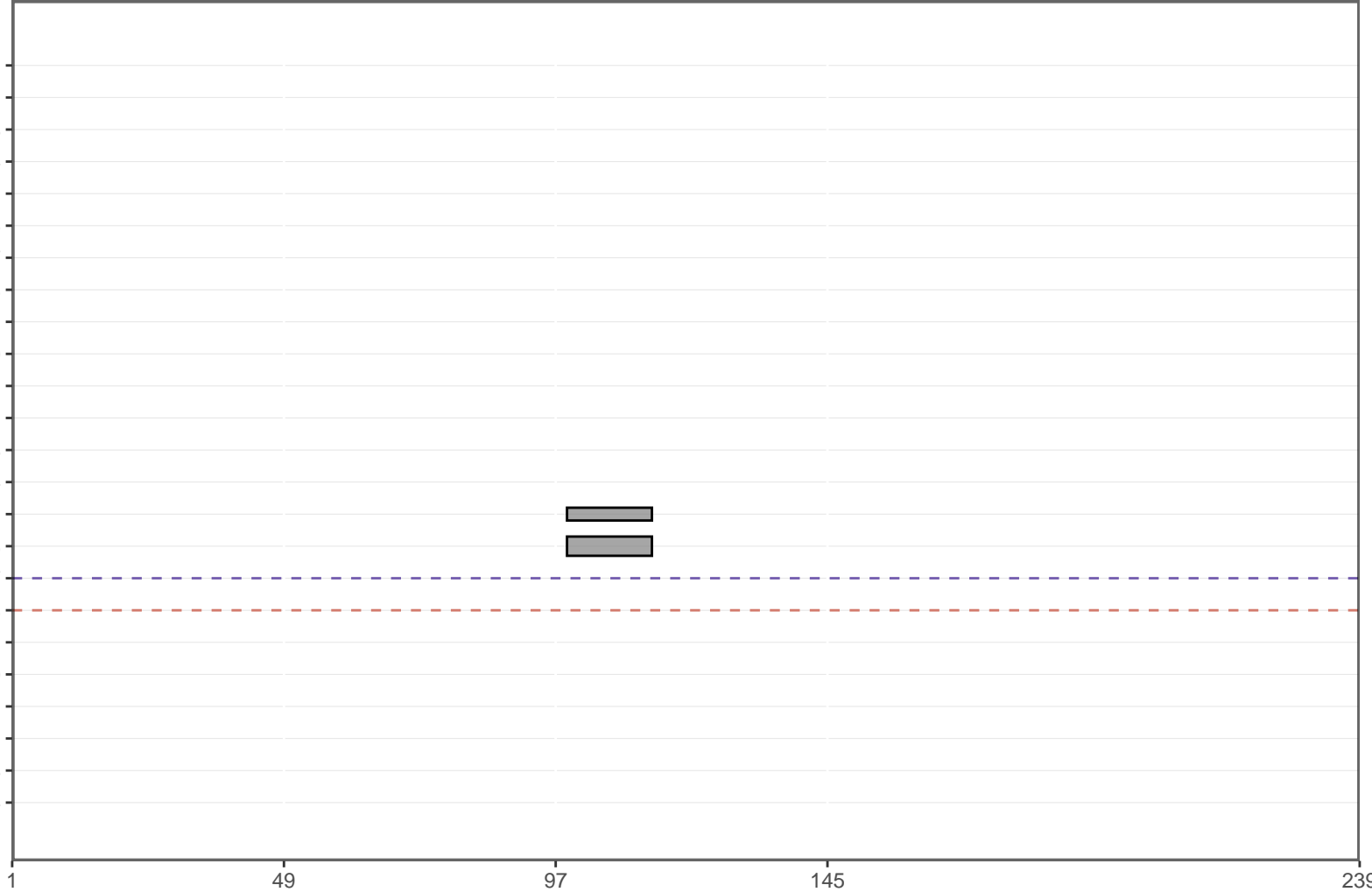
MW indication



Molecular weight



Gel Slice



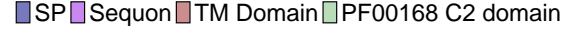
Protein length



Pfam domains



Pfam Description



Protein sequence:

IAWPIQTKGRHAGEVRLIMHYANASNPTEVAPSAAPVADPQAPMYSVPPHLAGYPTTAAGQTPSPVAVPPHSAVPPSPVPPQTAVPVAWPPPSAVPPVSVPPPSSGDSVPPGPGYGGTYPPRPV*

NbL17g22930.1 cyclase-like_protein_2 [MW - SP = 27.88 kDa]

No. of times detected



log(intensity)



Values from



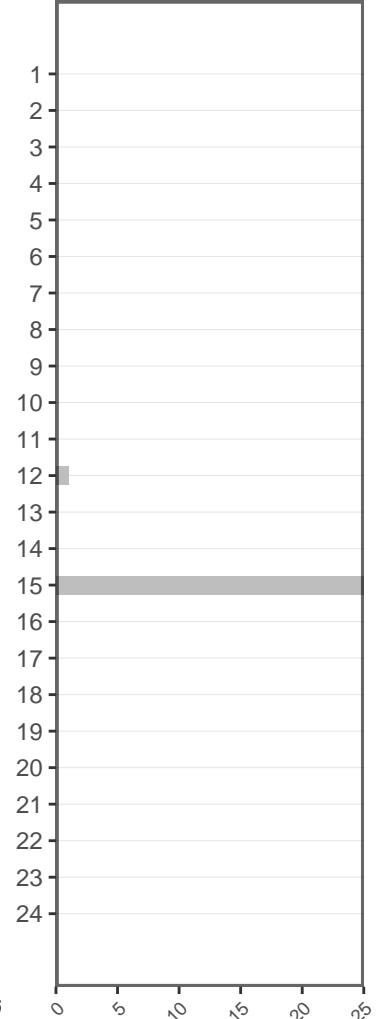
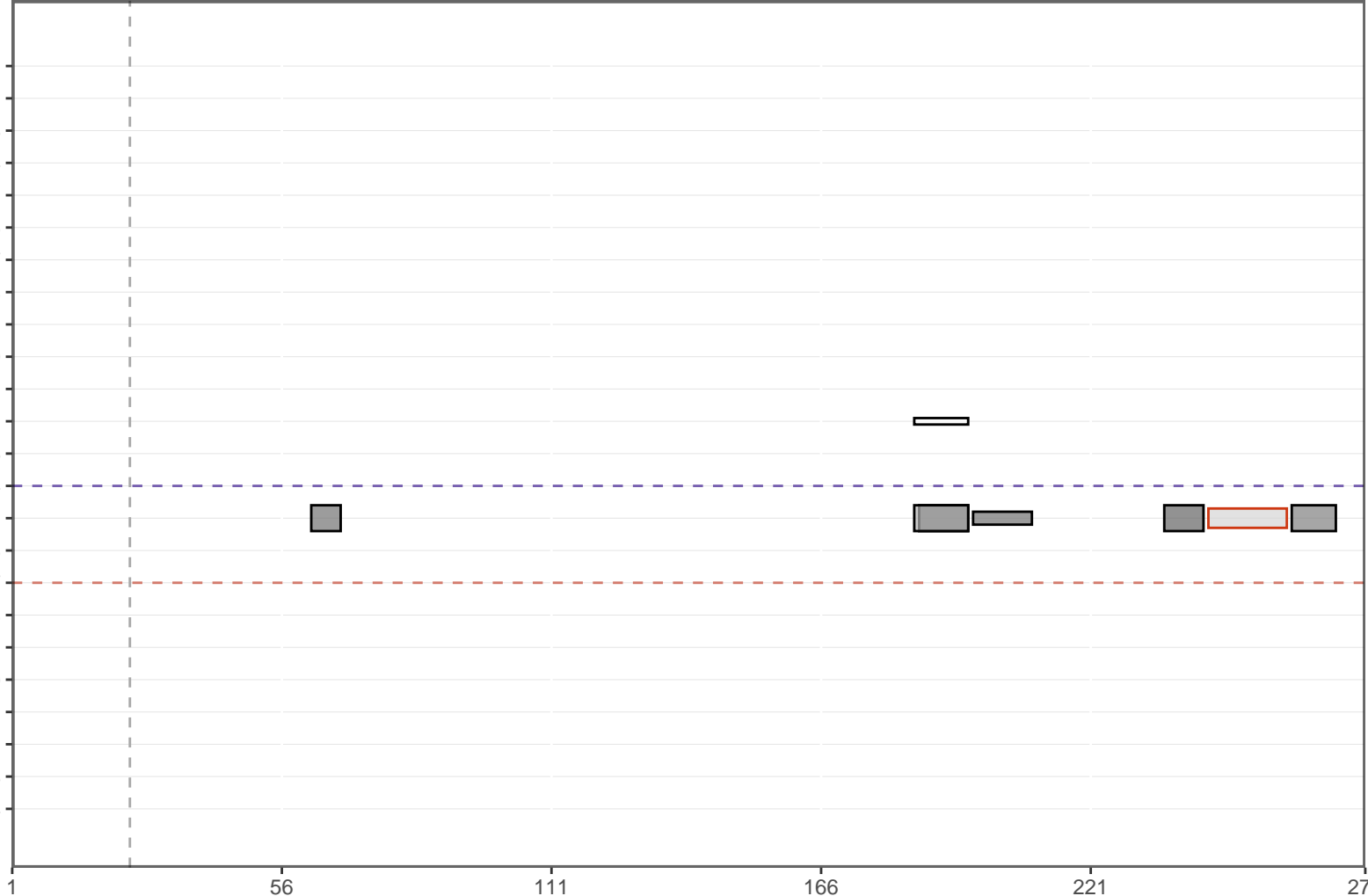
MW indication



Molecular weight



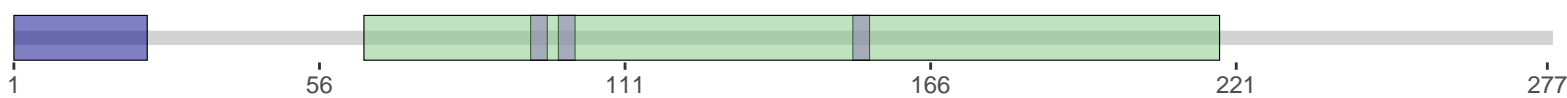
Gel Slice



Protein length

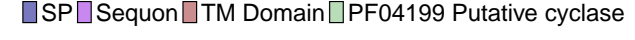


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YFDAGFDITLDELVNGPALVVDPRKNTADVMSLSHPKGVKRVLFRFLNDRRLMVKKAFDTSYVGFMDGAGVAVNTDKLVGSEVLSVAFFDILPSHLVFLKREIRLVEGLKLDDETGVYVHQLFLRLLAGEGSPRGLIK

NbL17g22910.1 stress_enhanced_protein_1_chloroplastic [MW = 14.74 kDa]

No. of times detected



log(intensity)



Values from



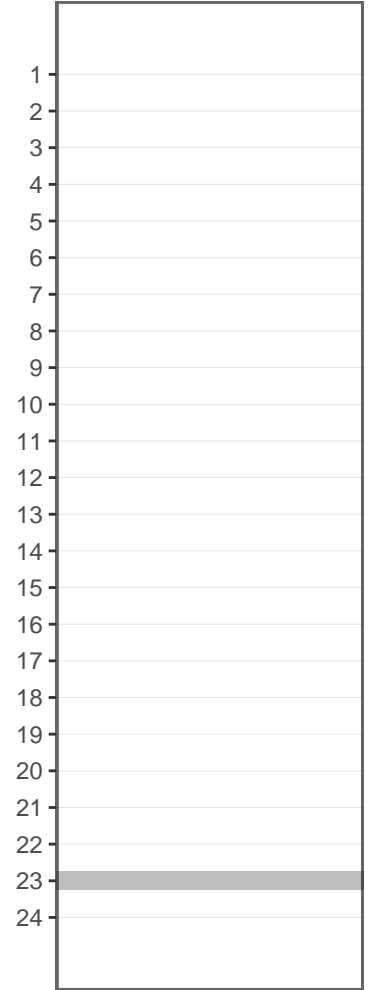
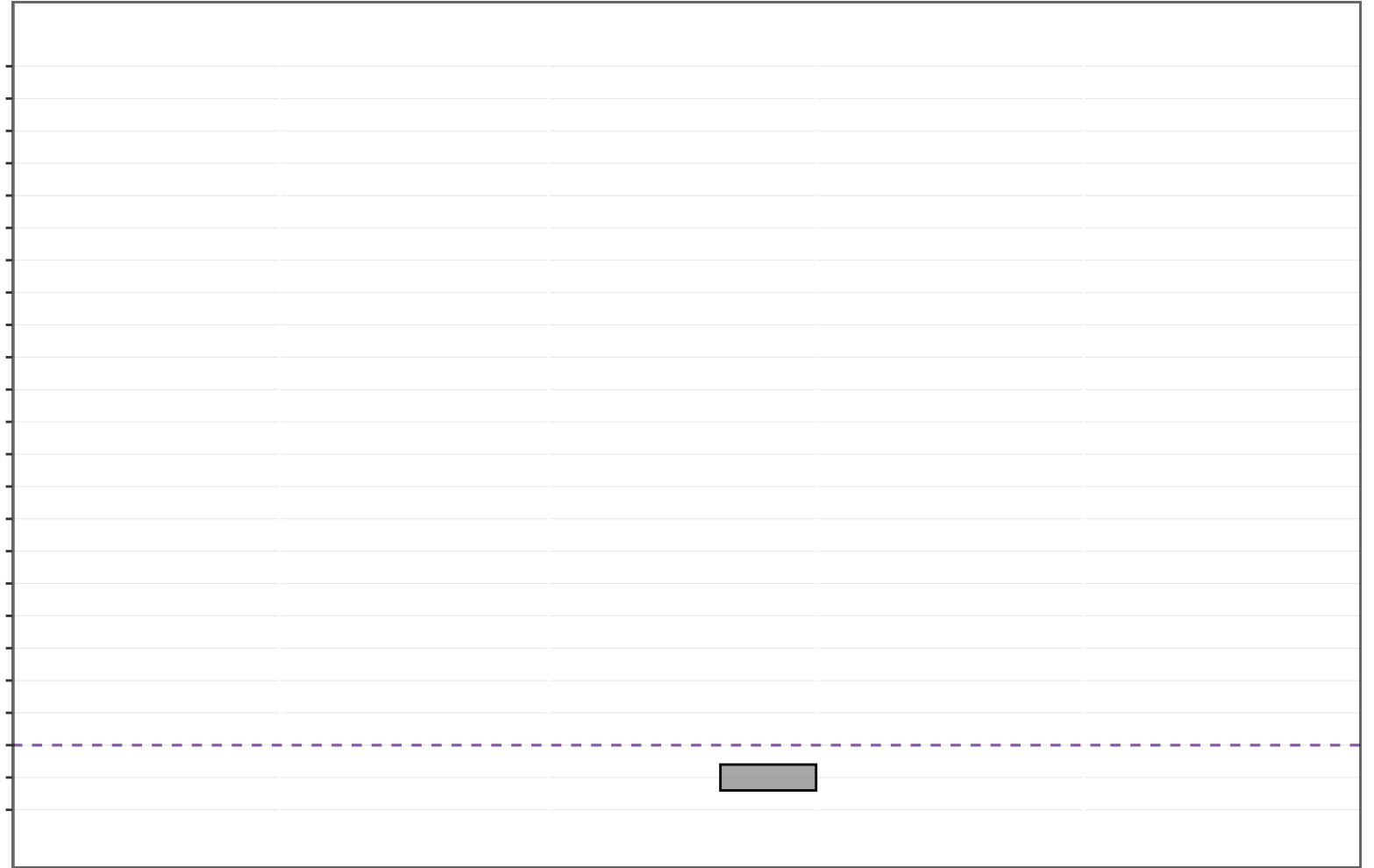
MW indication



Molecular weight



Gel Slice



Protein length

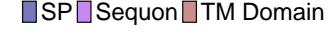


Peptide counts over 4 repeats

Pfam domains



Pfam Description

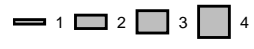


Protein sequence:

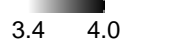
AIPSRATSYVIRCGG6TRKEESNLDVWGR6AMVGFVAIV6VEIATGKLENF6V7GPIPTALVALVGLTAVFIFQ6ASKV

NbL17g22820.1 methylthioribose_kinase [MW = 48.02 kDa]

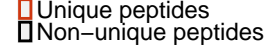
No. of times detected



log(intensity)



Values from



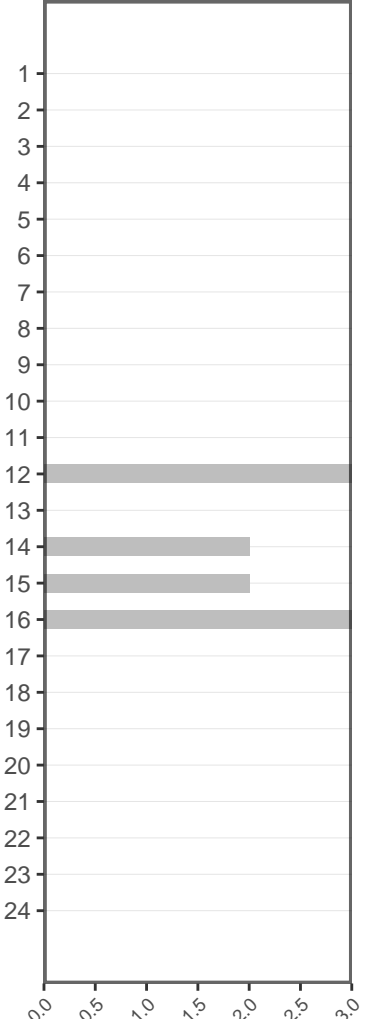
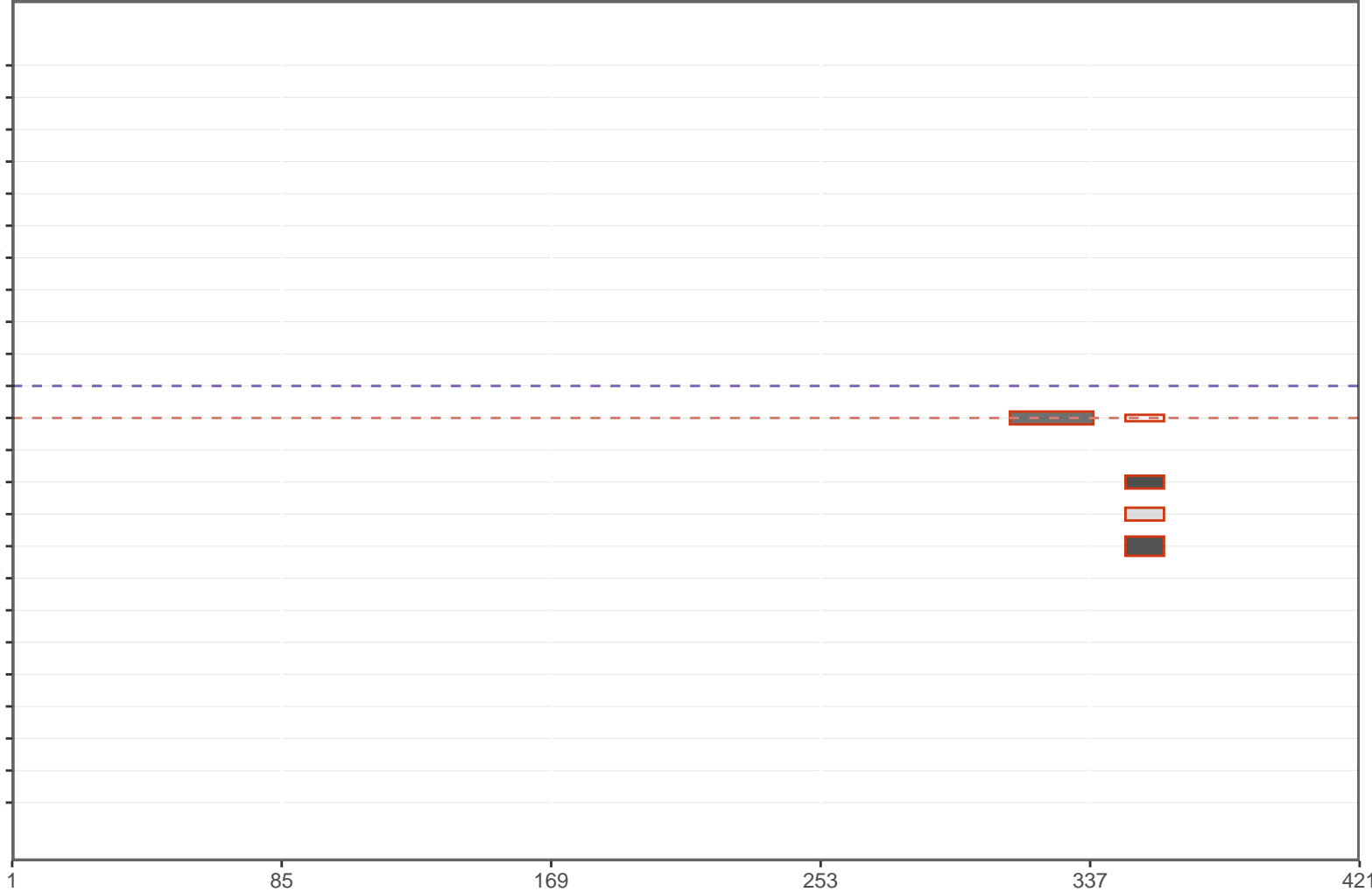
MW indication



Molecular weight

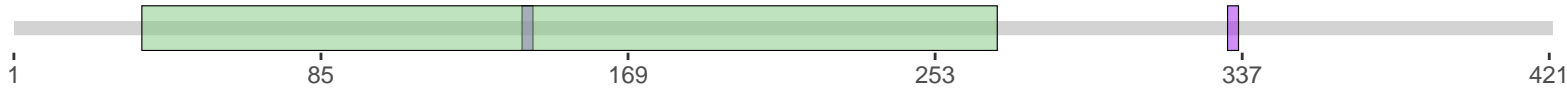


Gel Slice



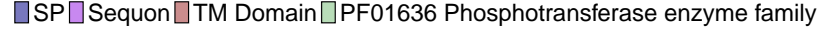
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PYLDAEAVRNDSLKEVAELKSKFGRAGALHGDHHTGSLMVTHDSTGVVIDFEFAFYGPMGFDSGAFIGNLILAFSGDGHADQANDRKYKVKWILKTTITETWLFHKKFLALWDEHKDPSGEAVLPEIYNNTELRLQVKKQYMKELFEDTLFGGAAMRIRRVGVVHVEDFESKDAAKRADGERLALNGAKLLKERRNFKBIDEVSTIEGVHLQI

NbL17g22800.1 uncharacterized_LOC104232799 [MW - SP = 22.74 kDa]

No. of times detected



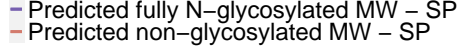
log(intensity)



Values from



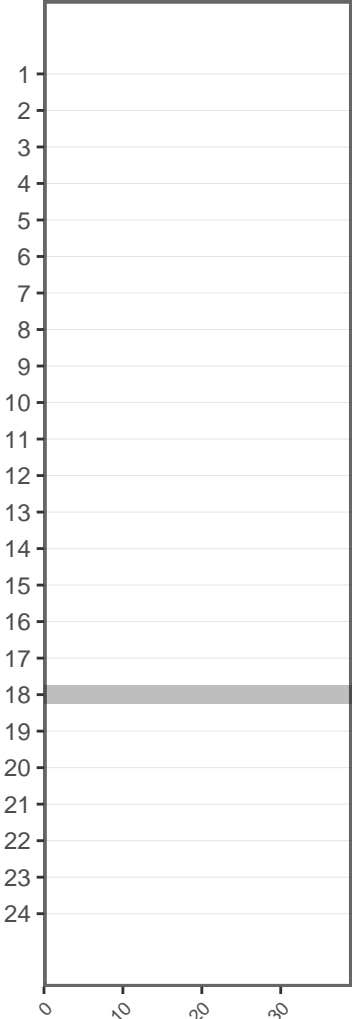
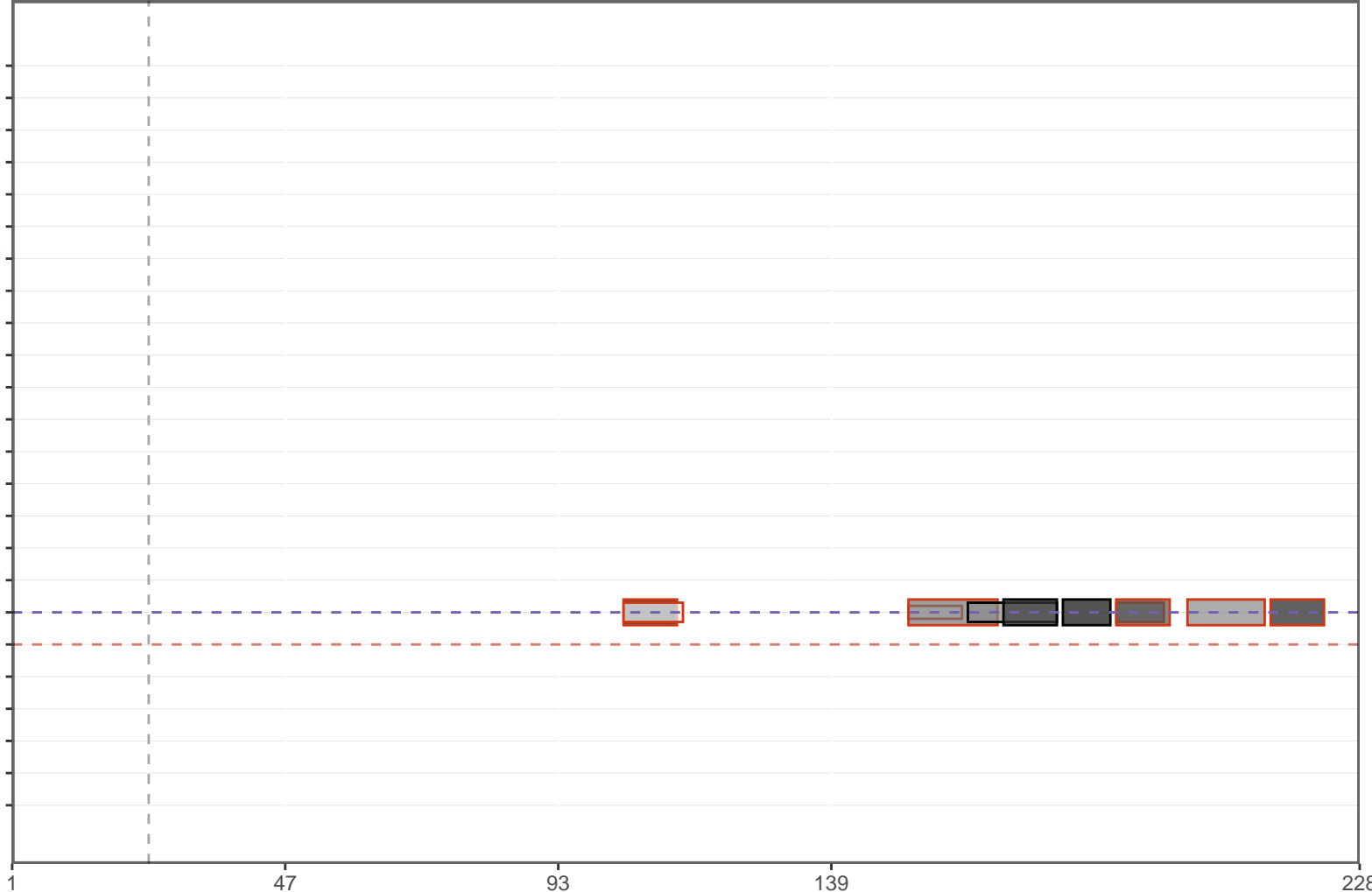
MW indication



Molecular weight

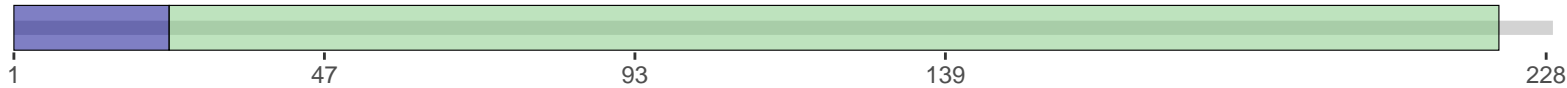


Gel Slice



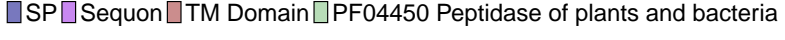
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

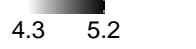
YIQGYSQDVRREITGVVYHESTHWGWNNGNGGAFQGLIEGIADYVRLKAGFGPSHWKPGGGDRWDGQYDVTARFLDYCNLSLNGFVGLNKKMRTGYSGNFFVLLGKTVQGLVNDKYKAFRA

NbL17g22790.1 uncharacterized_LOC101249214 [MW - SP = 23.22 kDa]

No. of times detected



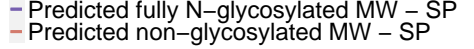
log(intensity)



Values from



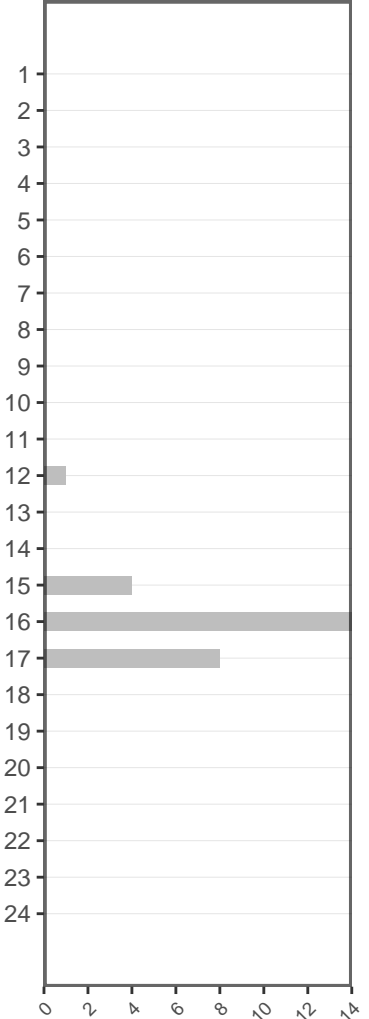
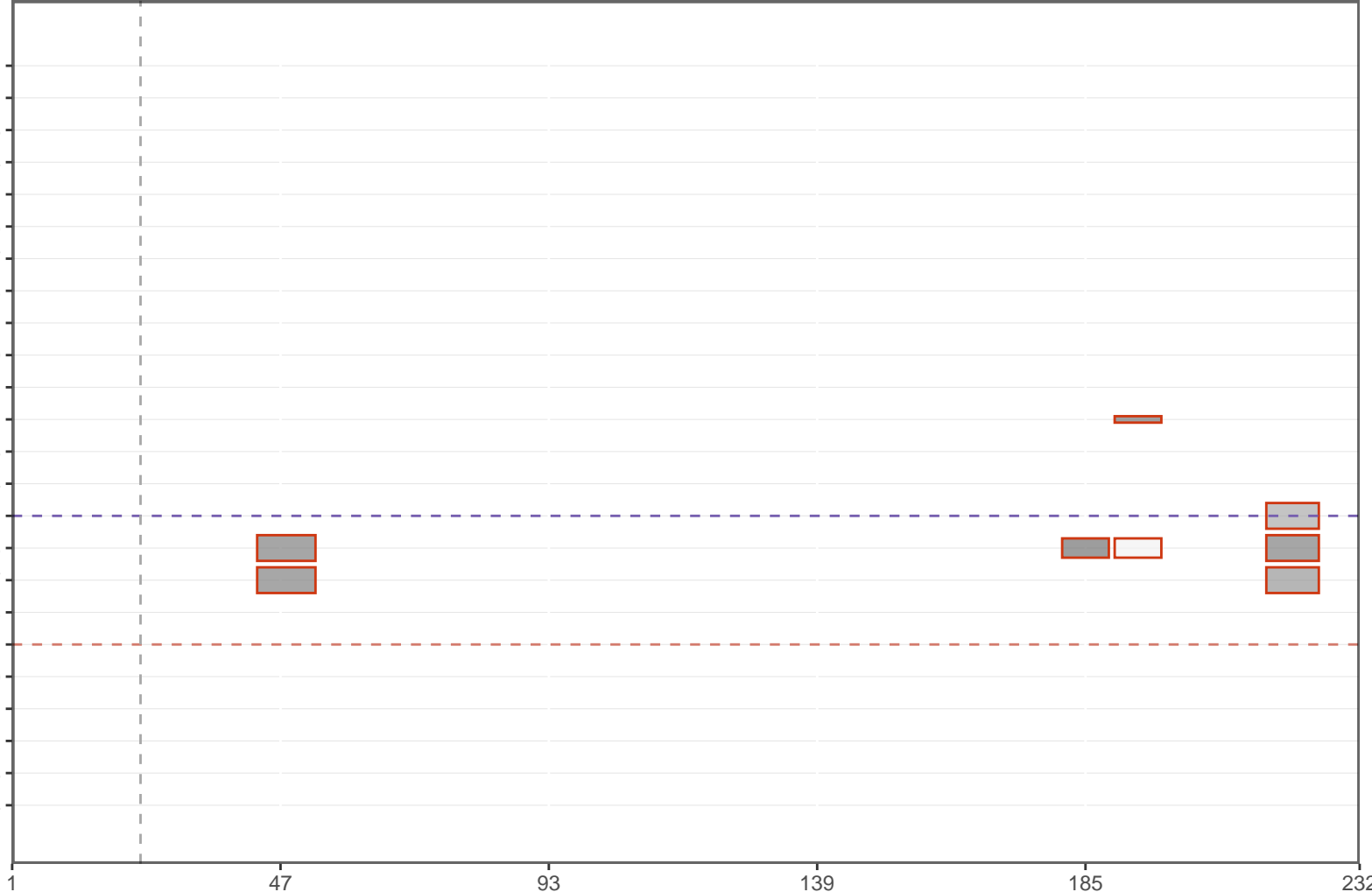
MW indication



Molecular weight



Gel Slice

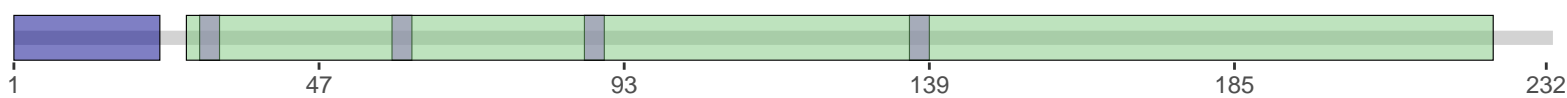


Protein length

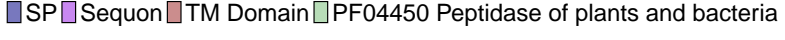


Peptide counts over 4 repeats

Pfam domains



Pfam Description

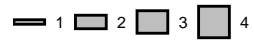


Protein sequence:

TSYIQSYSGNKTETLFGIFHEGVHWGFGNSPTPGSLIEGIADYVRLKADYAASNPQNGGGKWDGQVWYARFLDYGNLRFVAALNKKMRTGYSNFFVELLGGTPOOLFADYKAKYKTA

NbL17g22750.1 LYR_motif-containing_protein_At3g19508 [MW = 10.37 kDa]

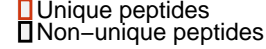
No. of times detected



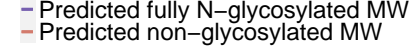
log(intensity)



Values from



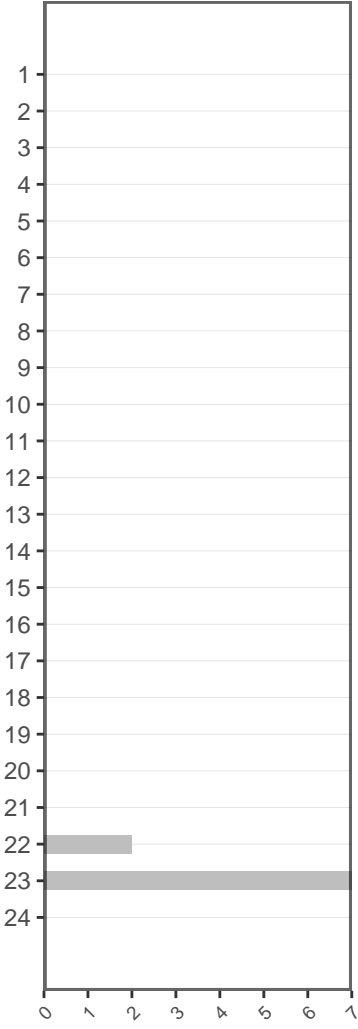
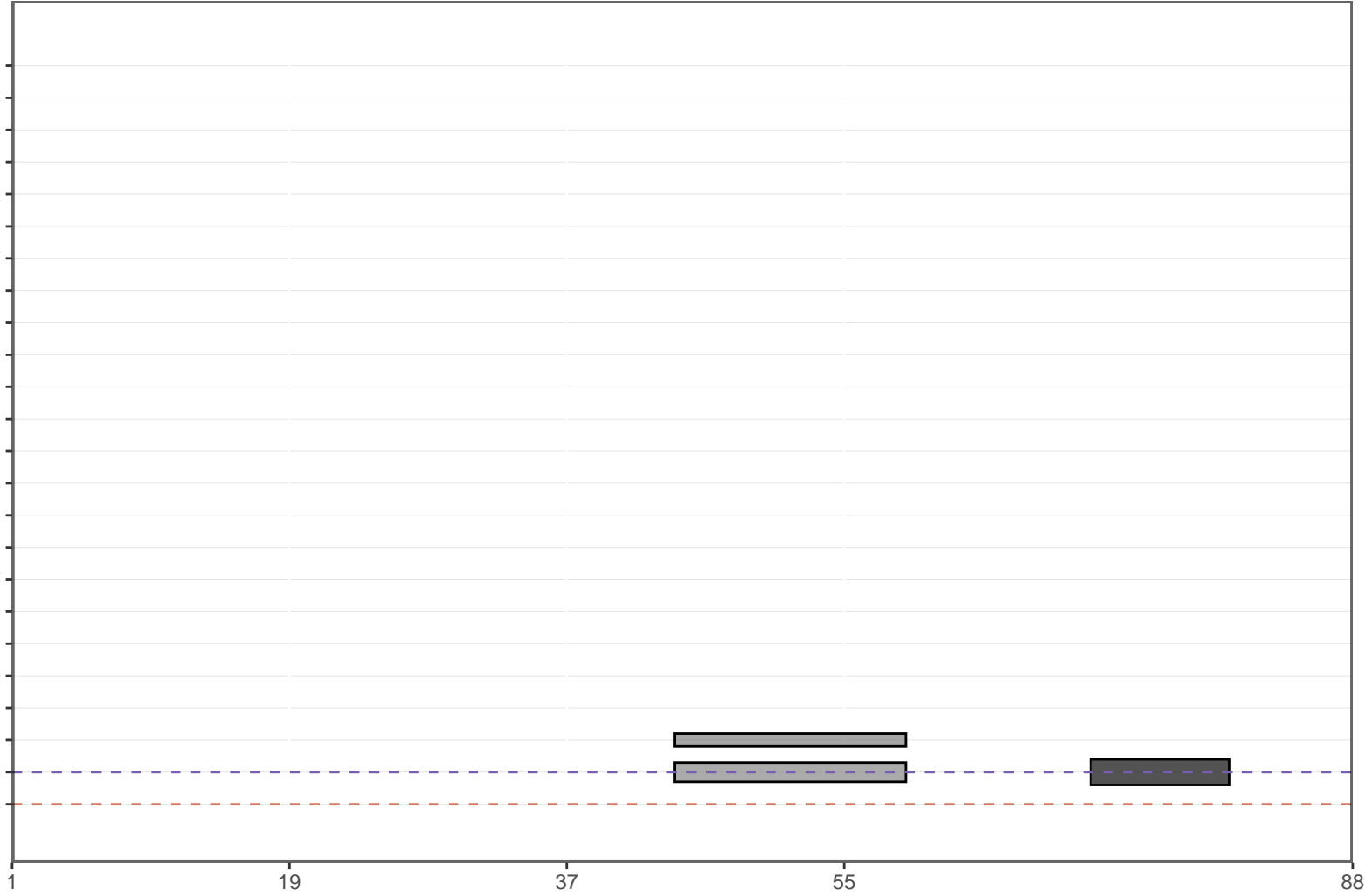
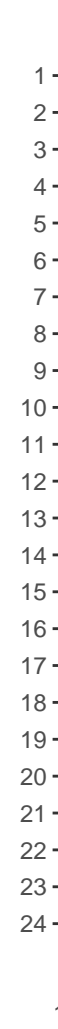
MW indication



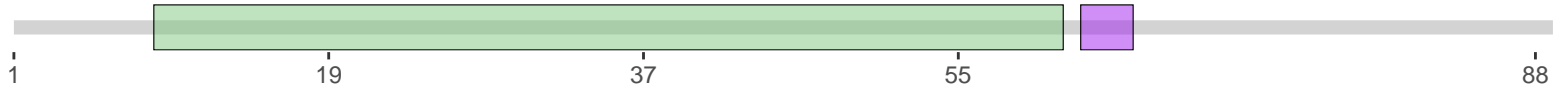
Molecular weight



Gel Slice

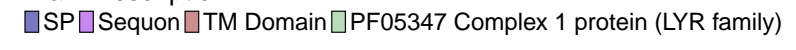


Protein length



Pfam domains

Pfam Description



Protein sequence:

AKYARENFNTRYREISDNDPNALGELLQRTYHNSLWLNKYSVDGSAADRLLKDMCTA

NbL17g22700.1 TIP41-like_protein [MW = 33.97 kDa]

No. of times detected



log(intensity)



Values from



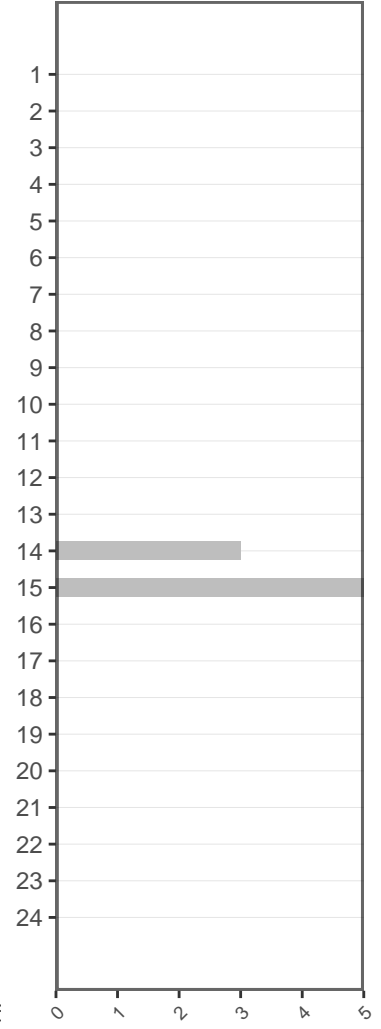
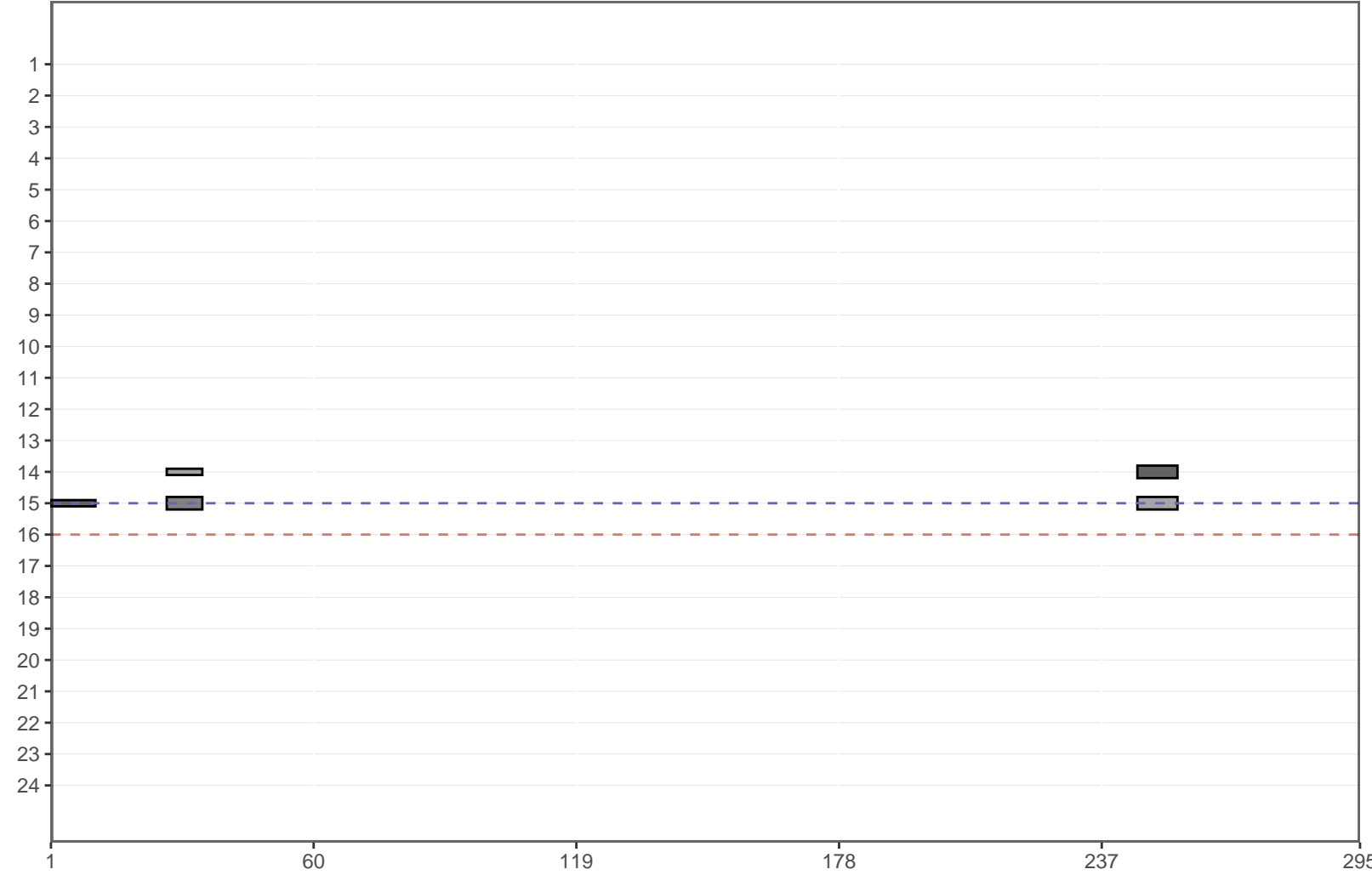
MW indication



Molecular weight

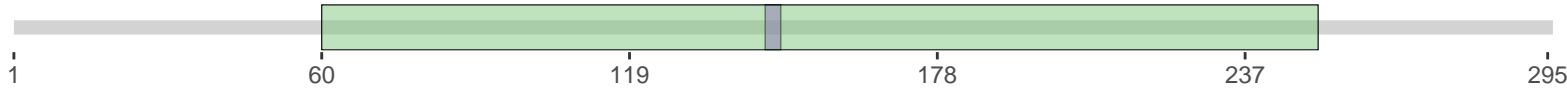


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TDTNAERVRLGSLNSES66GLGWEDDMEKIDLVALASKEPIFYDEIHLVEDELADNGSLITVWVRVMP66WFLLLRFWLRVDGVLMLRLDRTHLGLFGEHMKSVLRREGGWREATFOALS66KGFPSDCAAYSDPTSERLPIIMGKTKLSEIPCKWVLEI

NbL17g22490.1 mitotic_checkpoint_protein_BUB3.1-like [MW = 37.76 kDa]

No. of times detected



log(intensity)



Values from



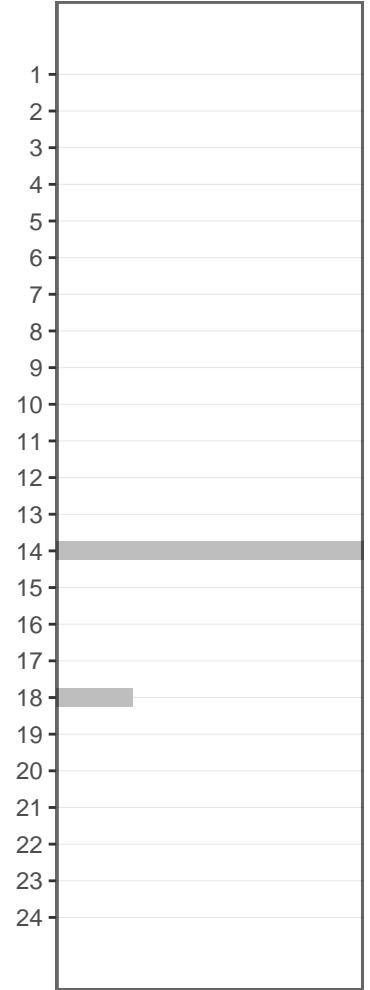
MW indication



Molecular weight



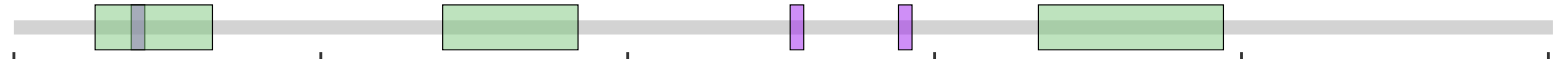
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description

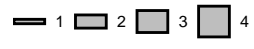


Protein sequence:

LVATAGRIHVNYYDLRNMSPQGRREBSLKYGTGRVRCYPTNGTGYVALLSSVEGRVAMEFFDLSEAGGSKKVFYKGRKTEAGRDIVYVVAIAHPHYGTATGGDDGYVNVWDGNKKKRLYQPKYPSIAALSFSDGRLALWASSVTFEEEGEKPEPDAIVRSVNEVEVKPKPKVLPNPTT

NbL17g22140.1 aspartate--tRNA_ligase_chloroplastic/mitochondrial [MW = 75.22 kDa]

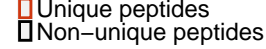
No. of times detected



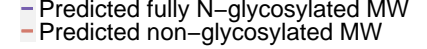
log(intensity)



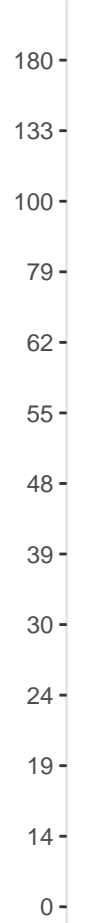
Values from



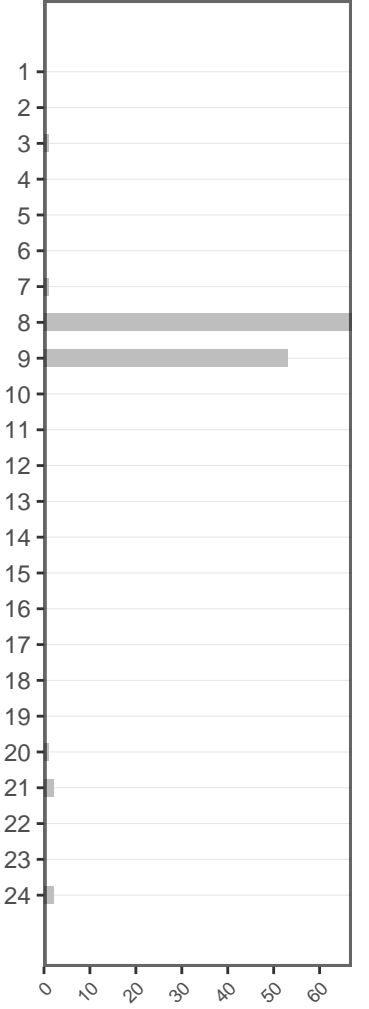
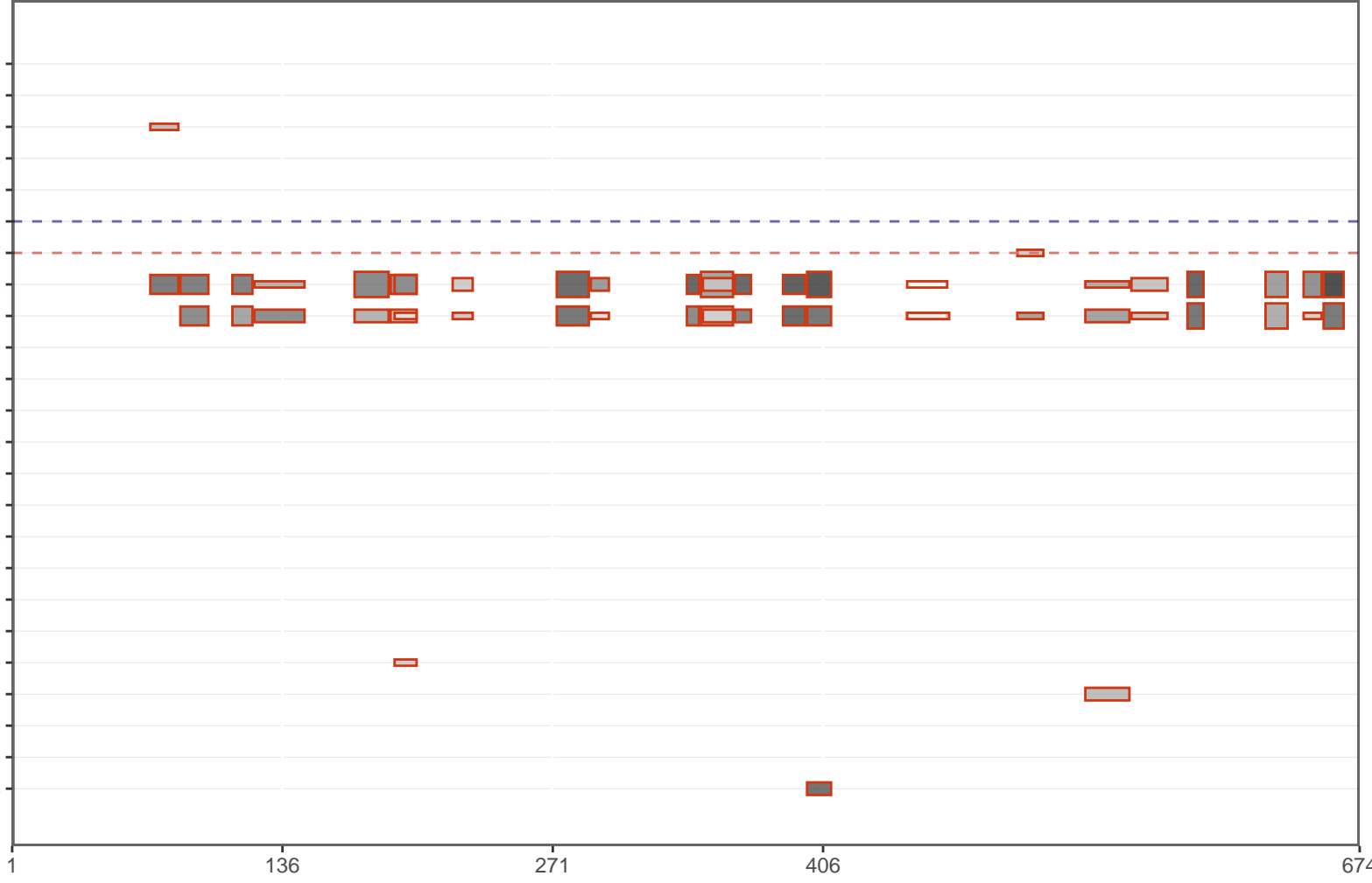
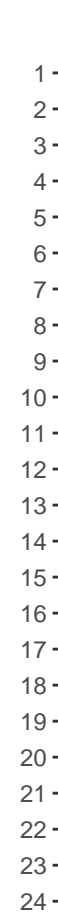
MW indication



Molecular weight

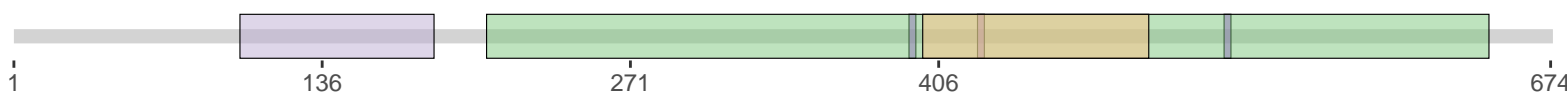


Gel Slice



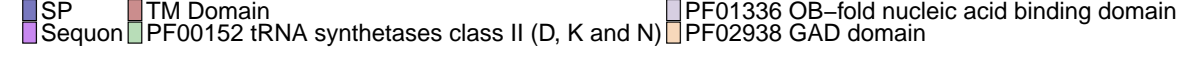
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

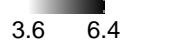
DMEMAFSTSMEDMLKLNEDLIRKVFGEHGGVGLNPNFPLRFLYAEAMSRYSRSDRPTDFVDELRLDVSQIFENSTFKVFDLALASGGIKALCVPSGDTKTVYNTSLKKGDIYKEAKGKGLPFLKVLNDDGSEIGPOLVSLDTEKKEELNQLSAVDDDLIFAVGHYAEVNIKLDRLRTYVADELGLDNERHBLWVTDFFMFEVNDSEGRFEALHHPFTAPNDDNDLSSARAWYDMVYNGVEKGGSLRIYKREVDKELVNVIGIRREGAEAKFQVYLLLEALDMGAPPHYGI

NbL17g21950.1 L-galactose_dehydrogenase [MW = 34.48 kDa]

No. of times detected



log(intensity)



Values from



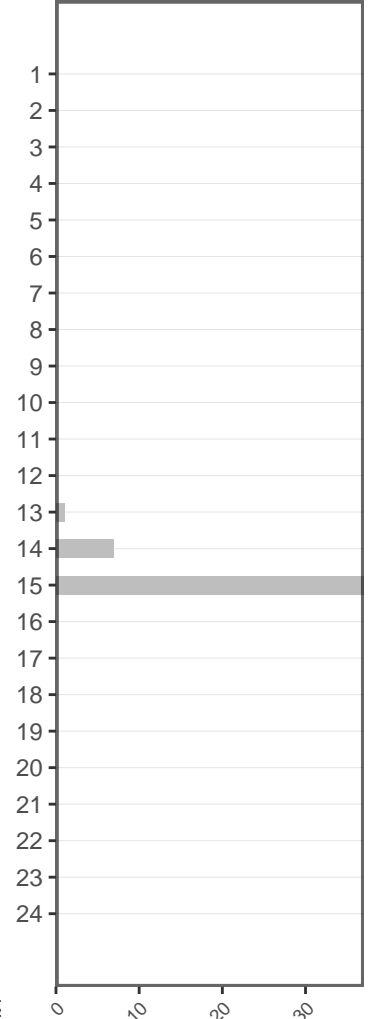
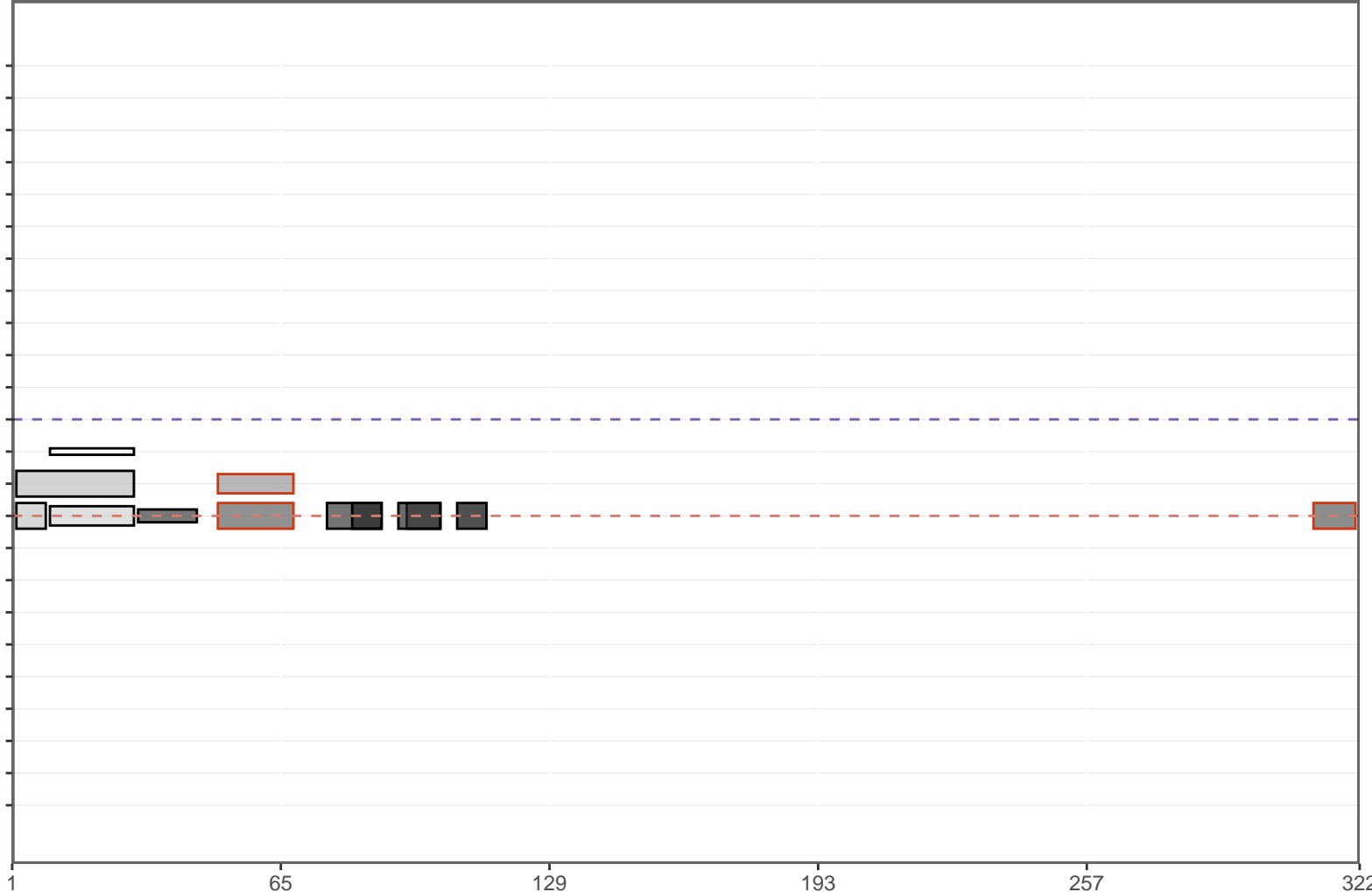
MW indication



Molecular weight

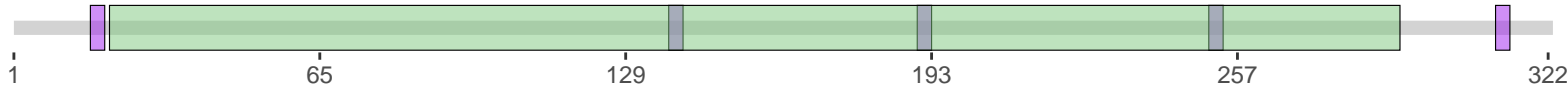


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LVKQAGKRFKFGITGLPLGIFTYVLDKRVPPGTVKDVILSYGHYSNDSTLEDLLPYLKSQKGVGVSASFLAMGLLTFEAGAPEWHPASSELKAAACRAAVDHCQKGGKGNISKLALGYSLANTGIVSIVLGMKSVKEVEENAAAELATAGMDEETLSEITDILKPKVKNQSWPSSGIGQS

NbL17g21930.1 soluble_inorganic_pyrophosphatase_6_chloroplastic-like [MW = 32.4 kDa]

No. of times detected



log(intensity)



Values from



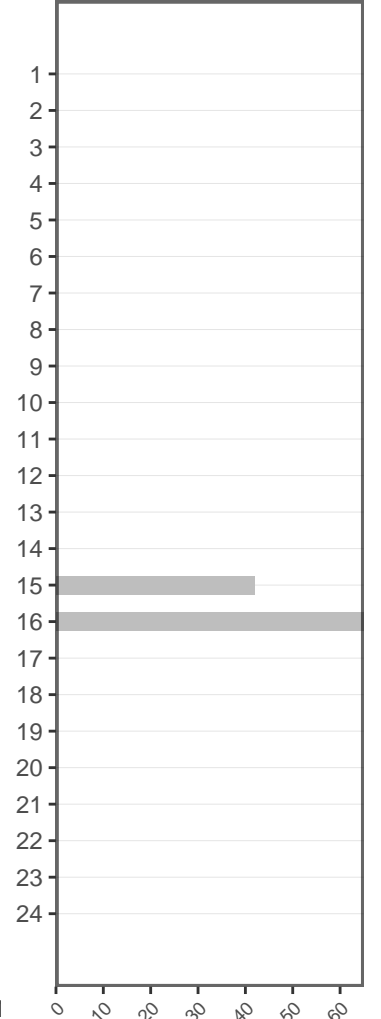
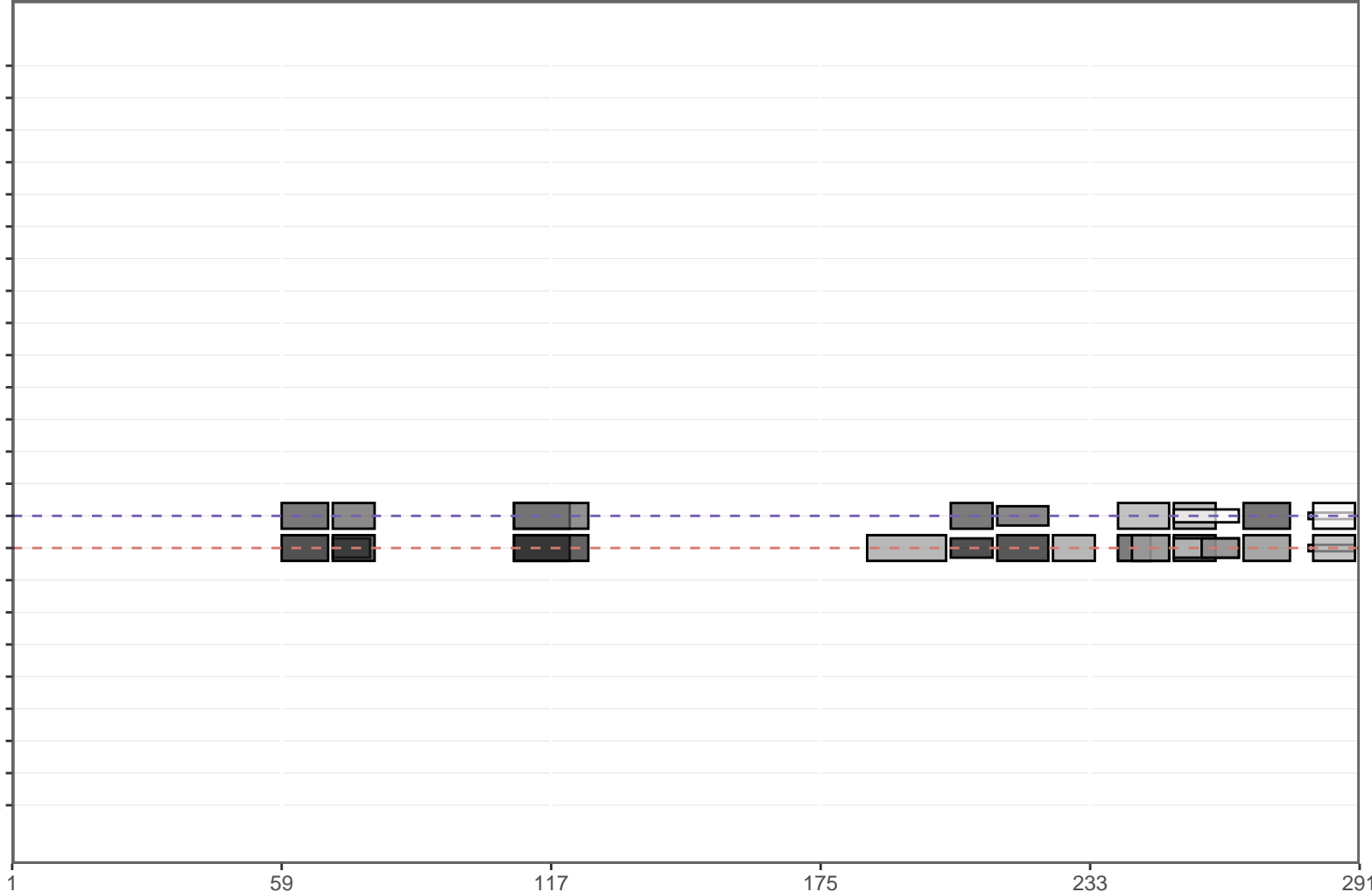
MW indication



Molecular weight

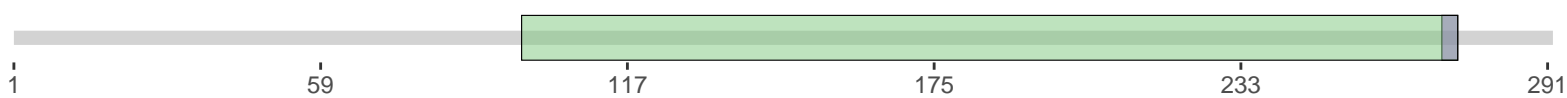


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

YPNYHWNYGLLPQTWEDPFPANSEVEGAFGDNIPVDVVEIGDSRGGKGVKXKPLAALAMDEGELEWVWVSLDPPRASLVNDVDDVEKHFPQTIAIRDWFRDYYKIPDQKPNRFAFGNPKANKDVALKVTETNESWAKLVKRSIPNGLELVLV

NbL17g21910.1 peptide_methionine_sulfoxide_reductase_B5-like [MW = 19.39 kDa]

No. of times detected



log(intensity)



Values from



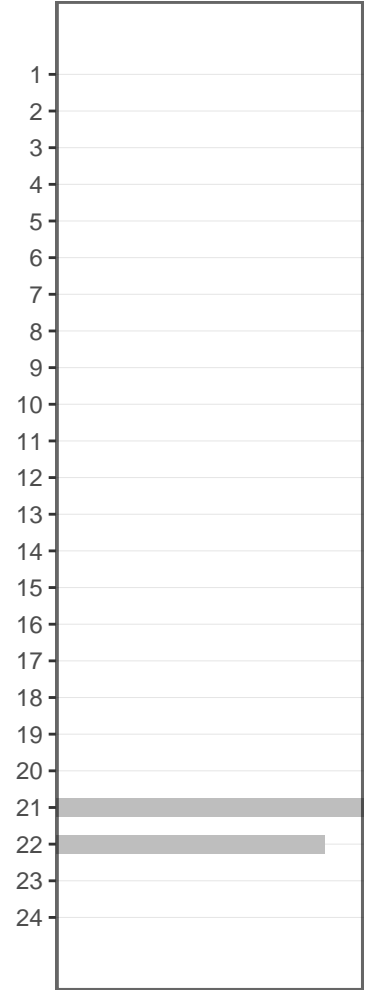
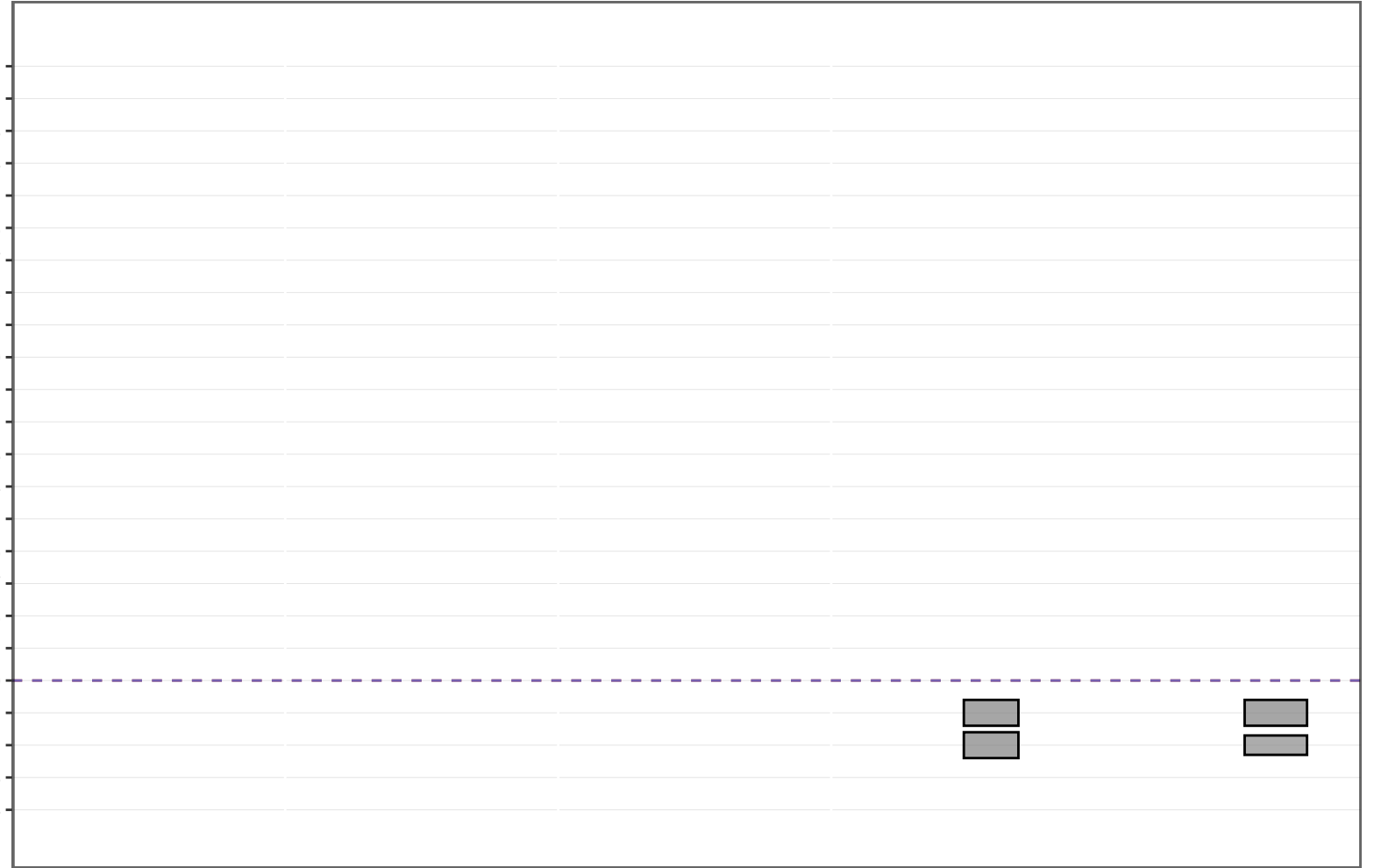
MW indication



Molecular weight

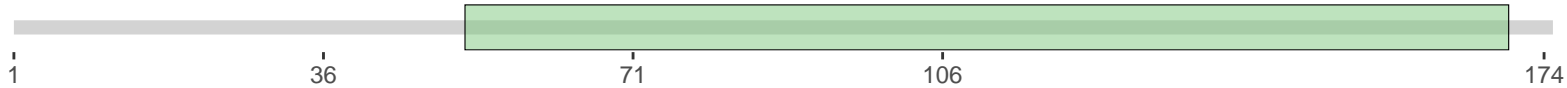


Gel Slice



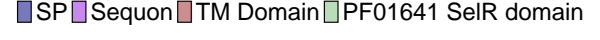
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IGENKFFGVGTYLCAAGGGTPVRSATKFNPCGWPSPFYEGLPAINRNPDPDGVMEFCAAGGGHLGHVFKGEGFRTPNERHGINSISLAKPKPNP

NbL17g21840.1 uncharacterized_LOC107824885 [MW = 53.39 kDa]

No. of times detected



log(intensity)



Values from



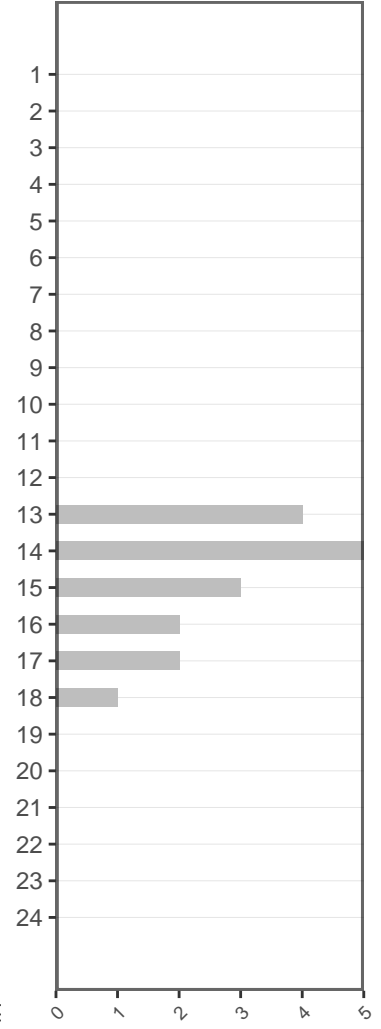
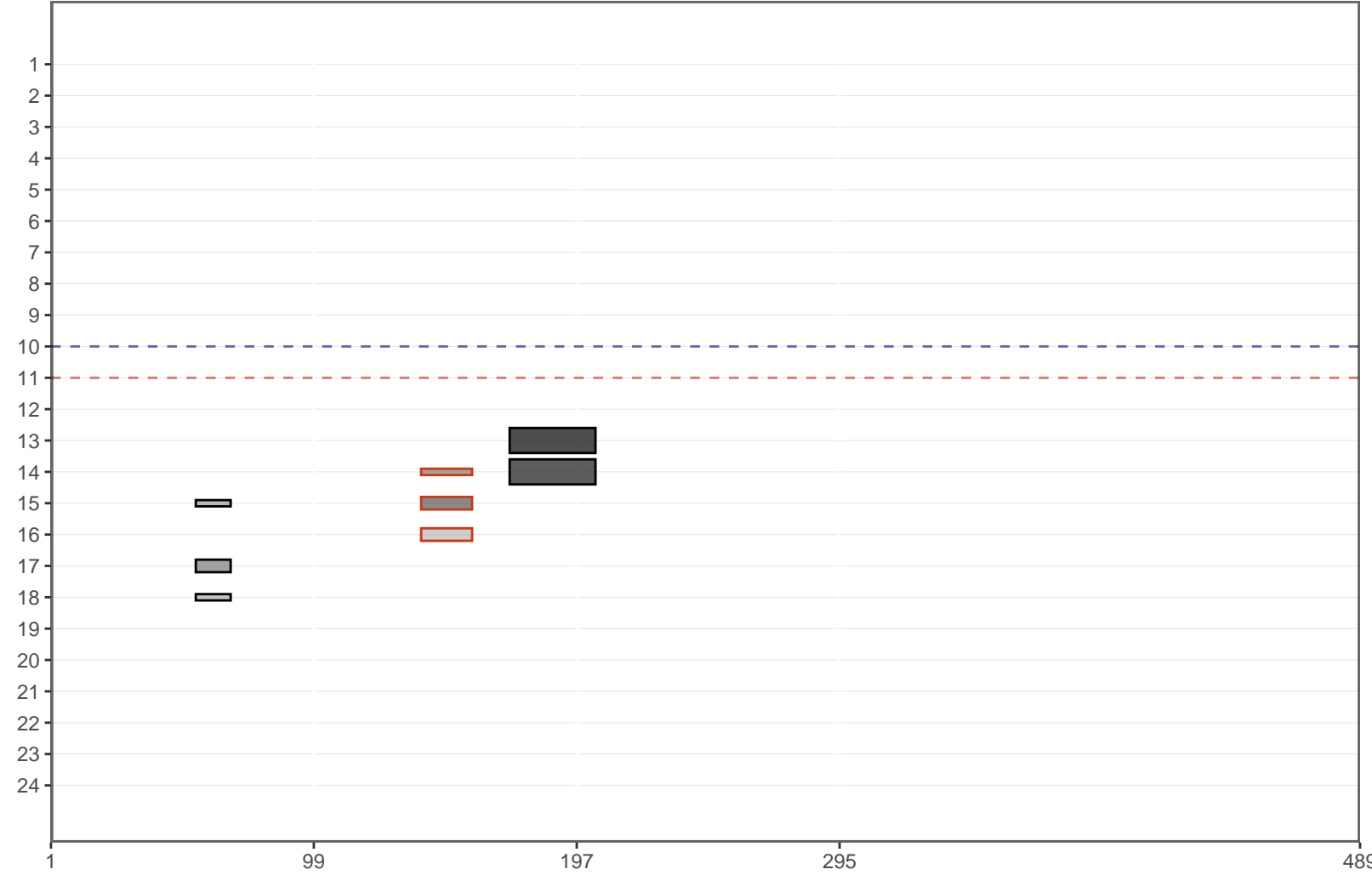
MW indication



Molecular weight



Gel Slice

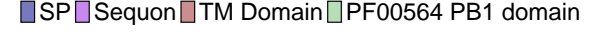


Protein length



Pfam domains

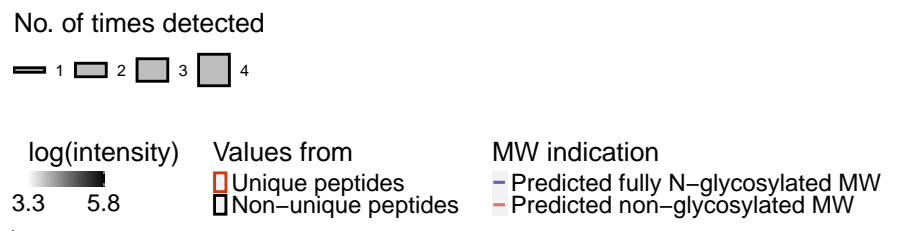
Pfam Description



Protein sequence:

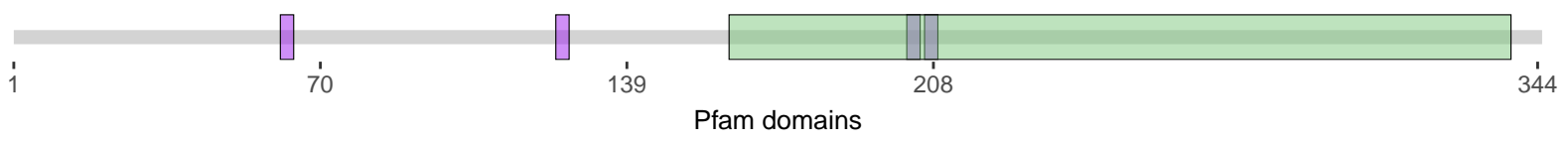
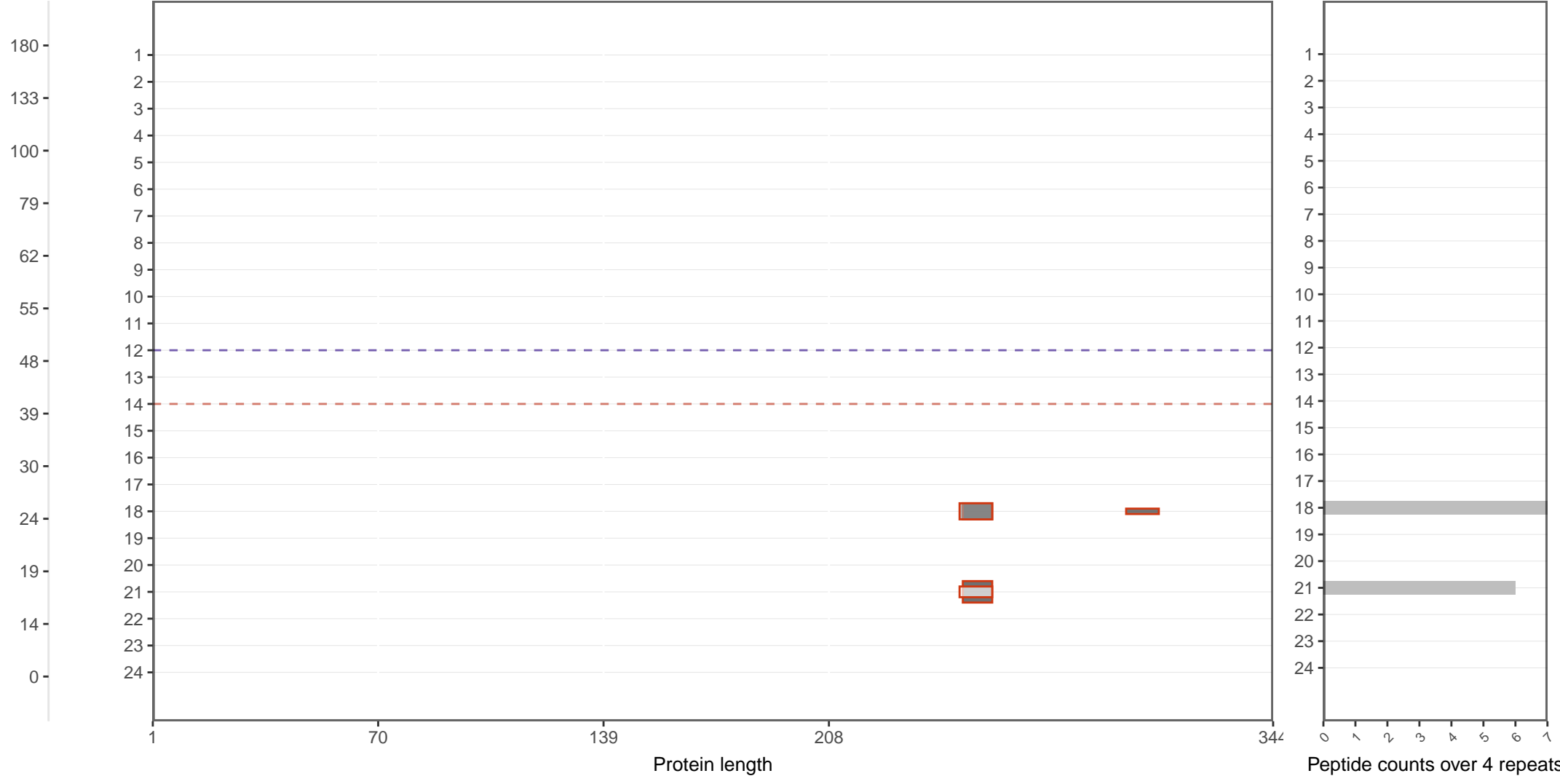
GTDPIQKHIDQLRLHLEEGQNMHLRKSDNLAFAATGGHDYVYKQKPEKIAKATVPGTVPAGVGVYDQENKQVPGGVHANSIGTEGPIVYMGAPKAYHGHQHPGFVRPMAGPPGGGYYAVGRMPQGEFVRDHPVYVNMPSVPGVAVPTVAATLPSGGGPKVAGYSEGYSMAVRATMTMGVGVADAGGYTGMVYDGGVGRGMVYPPGGGVMAPPDQPGVGMPPQAVVSSDMRTGEAAKVPKVKVNGNS

NbL17g21730.1 psbP_domain-containing_protein_1_chloroplastic-like [MW = 39.6 kDa]



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain PF01789 PsbP

Protein sequence:

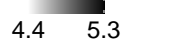
ISTEFREYDITDGYSEMYPRNMQVRSAGADIFFRDLVLDENLGMNHSFSSAYKRVKVEDLGPPEKAGKGVLRQVLTFFMSTRILGVRRESVLTSSFRVADGKLYVEVEVYKNSVANNELAVMPQGRVAVLEWDRRLYLVGVENNRVYELRIGTPEKTFADDEESDRAMDSEFRVYKVEV

NbL17g21710.1 methylmalonate-semialdehyde_dehydrogenase_[acylating]_mitochondrial [MW = 56.75 kDa]

No. of times detected



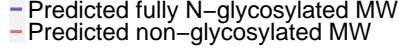
log(intensity)



Values from



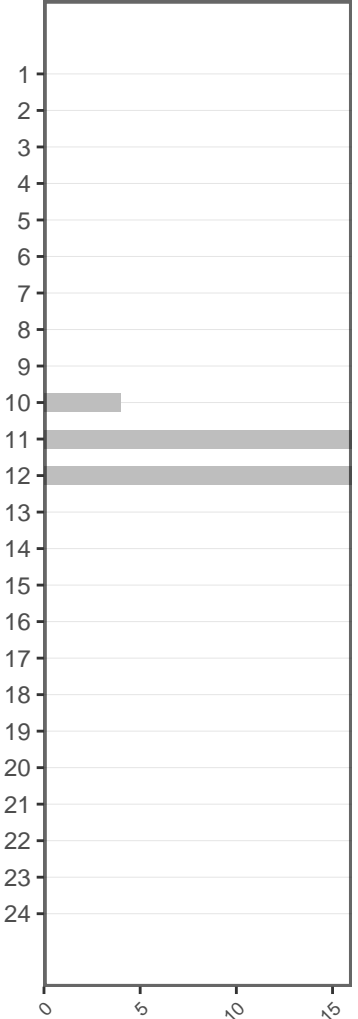
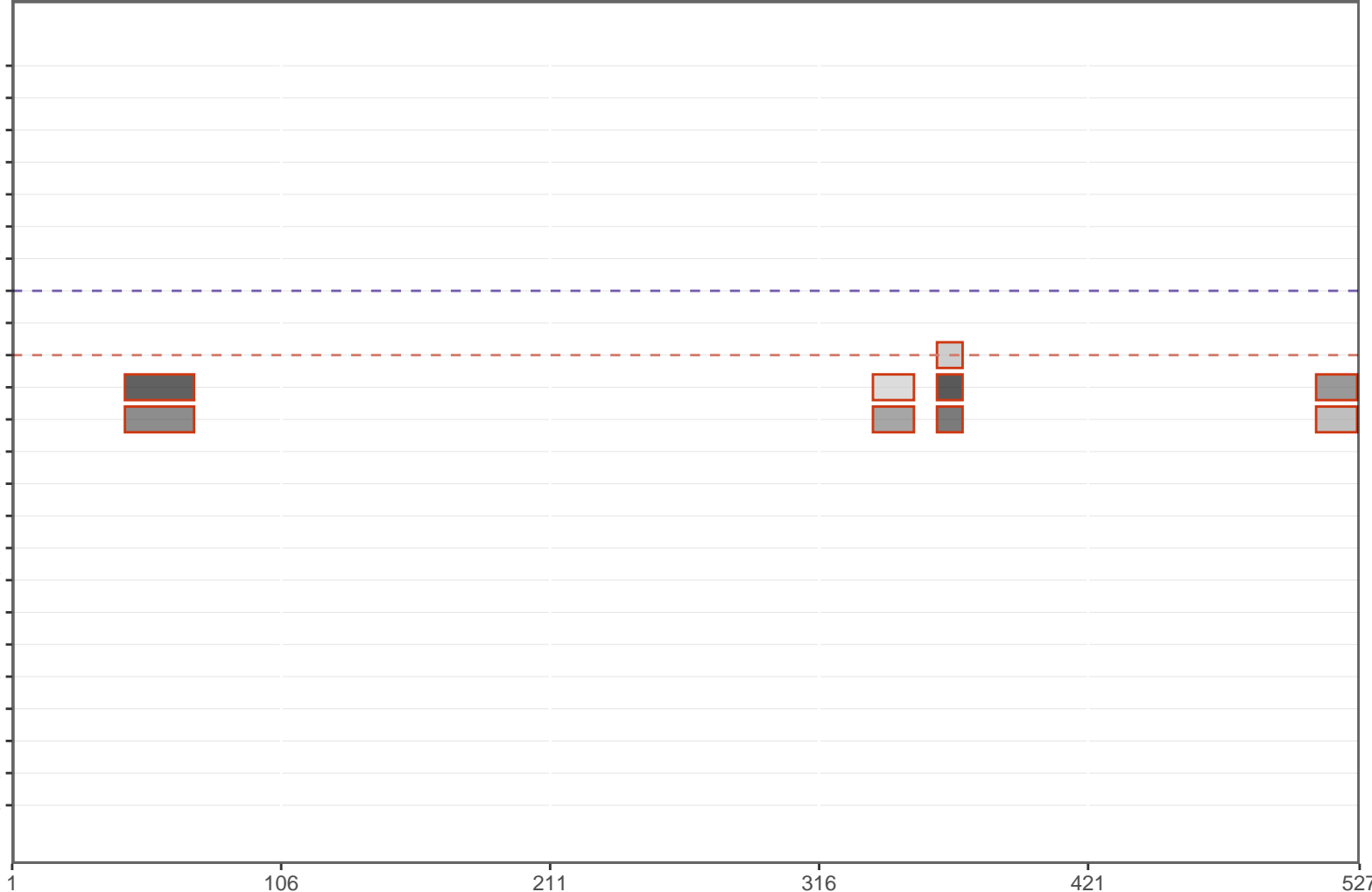
MW indication



Molecular weight

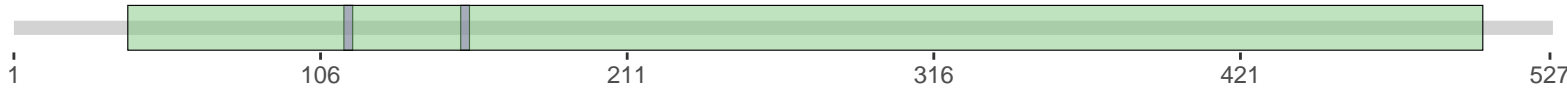


Gel Slice



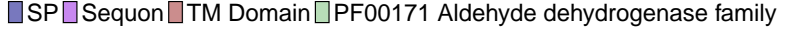
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VGSNQAQMRYARASANGKRVDENMGANNHGVWMPDANIDSTVNAVAAGFGAAGGROMALSTVYFVGDGKRWEEKLERAKALKVSGGTELDADLGPVWKAQKERVCRIVGSGVDGSAKLLLDGDRDVPVPGYEKGNFVGPTELSGVTTPDMEGKKEEFGVPLGMDQANLDEANVKNKHWGNGAAIFTTSGVAARKFQTEIEAGGVGNVPIVPLPFFSFTGSKAFAGDLNFGYKAGVDFYTKIKITFGQWKDLPGGGGSLAMPTSGK---

NbL17g21680.1 gamma-glutamyl_peptidase_5-like [MW = 27.3 kDa]

No. of times detected



log(intensity)



Values from



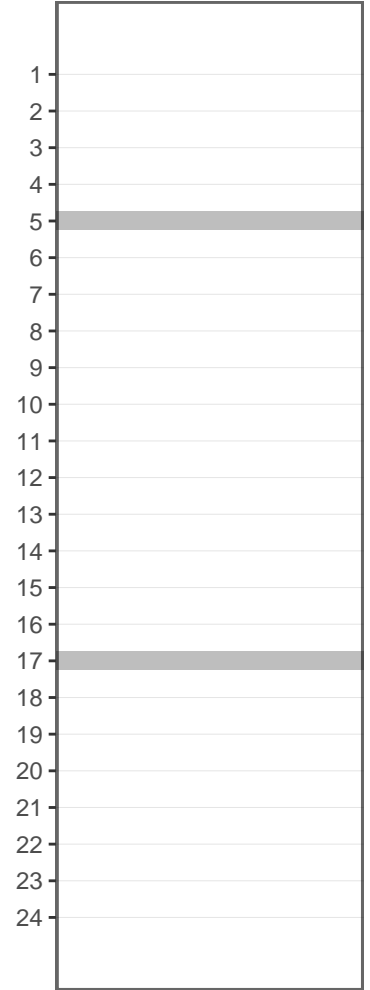
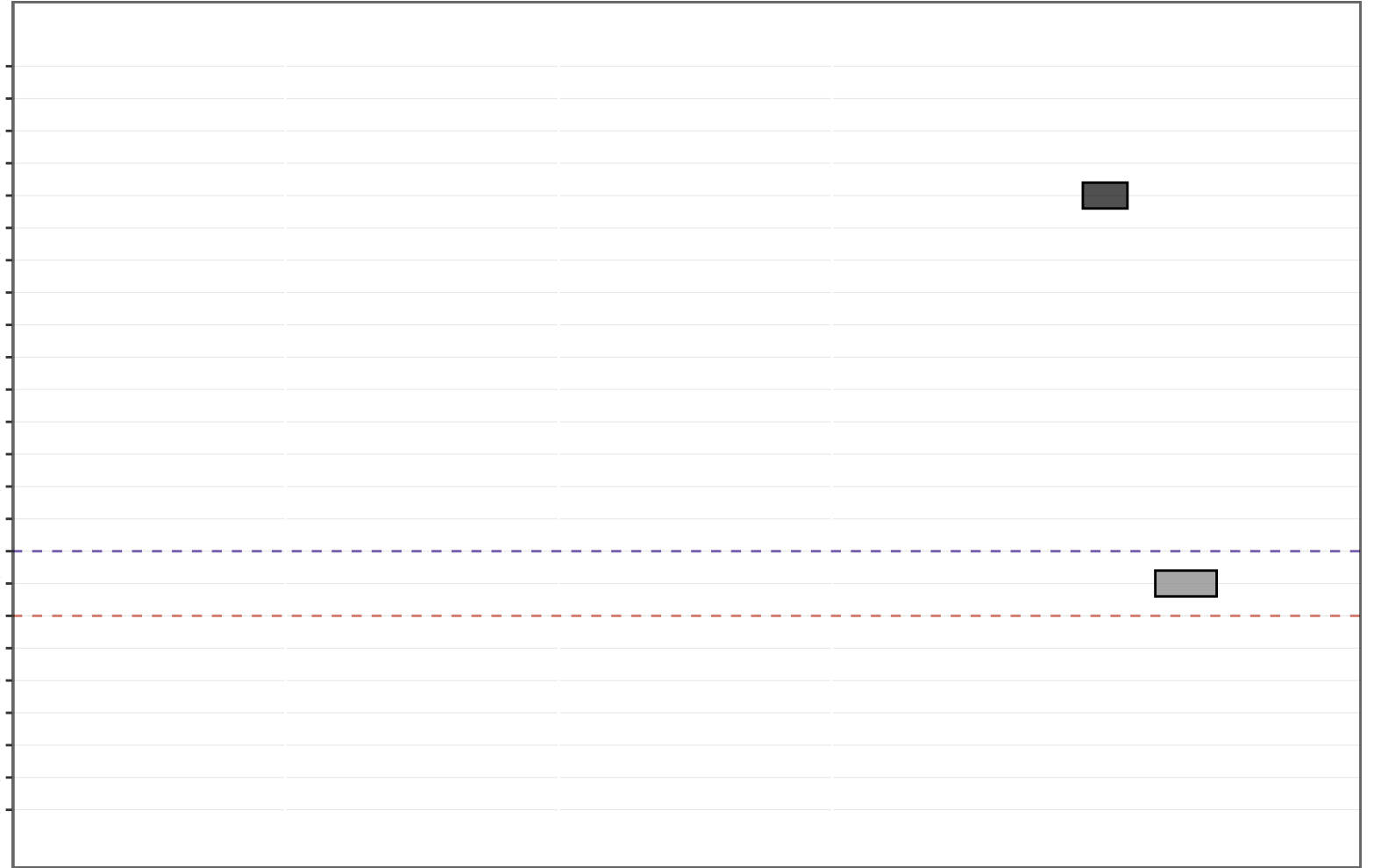
MW indication



Molecular weight

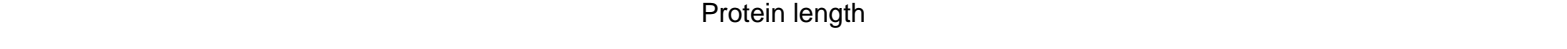


Gel Slice



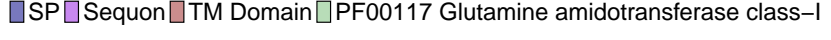
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ISLGGVIERATTGVDSVYTFVNLGTSKLFKTLNLPAFMGVIEGHRDEIRLPPKAEVMAVSNKGTGIEMFRYGNHMGIGQGHPEYTDLLHLIDRLGRNLEESIAADAKAKVEGCEPDREAWKKLGVSEFLKGRLE

NbL17g21630.1 magnesium-dependent_phosphatase_1 [MW = 21.52 kDa]

No. of times detected



log(intensity)



Values from



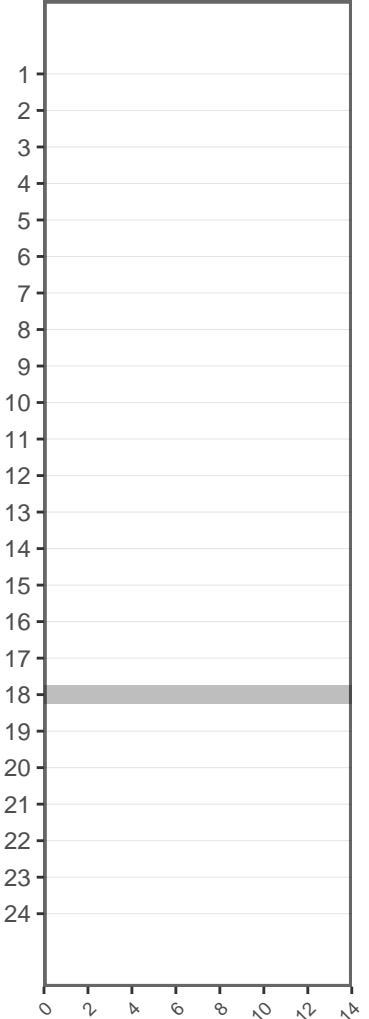
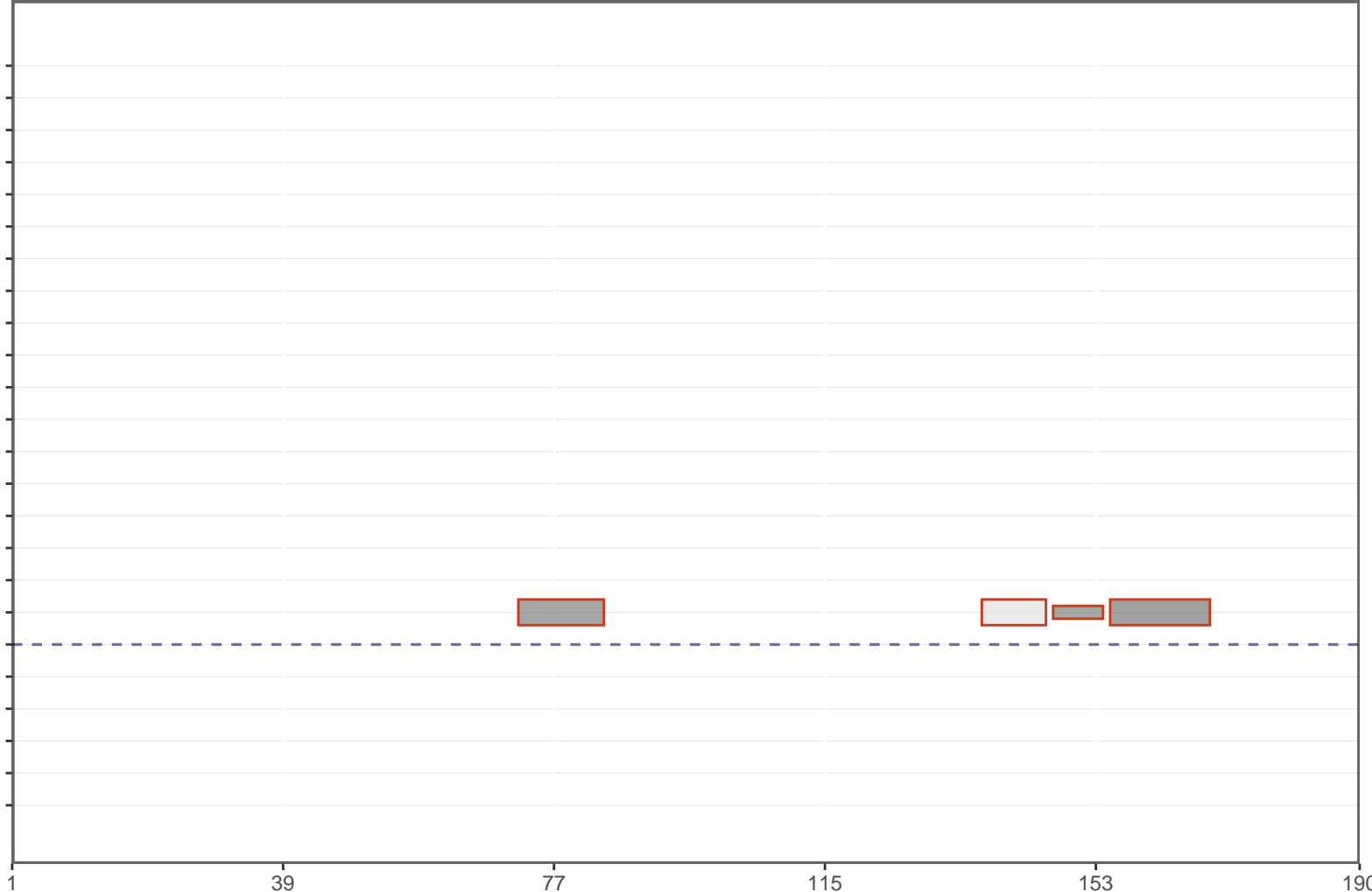
MW indication



Molecular weight

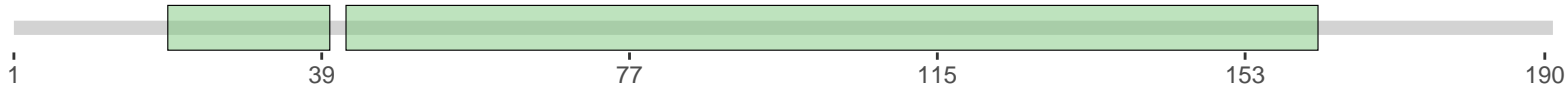


Gel Slice



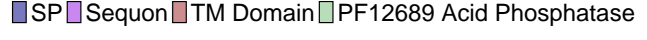
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LDKLEKSMFVQIEFSSWTHKTEHFGKINRKTAVPYSDMLFFDDENRNIGAVSKMGVTSILVKGKGVNIGAFROGLSEFVQNSASVEKNKERWRKFKEPGSKSDTQ

NbL17g21460.1 3-oxoacyl-[acyl-carrier-protein]-synthase_mitochondrial [MW = 50.01 kDa]

No. of times detected



log(intensity)



Values from



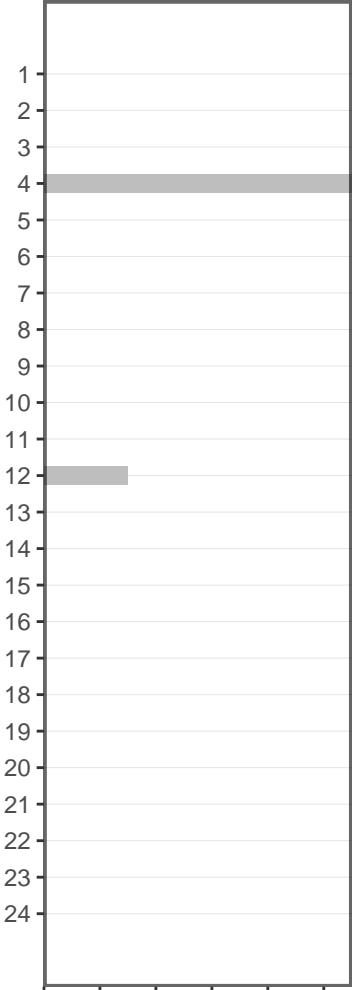
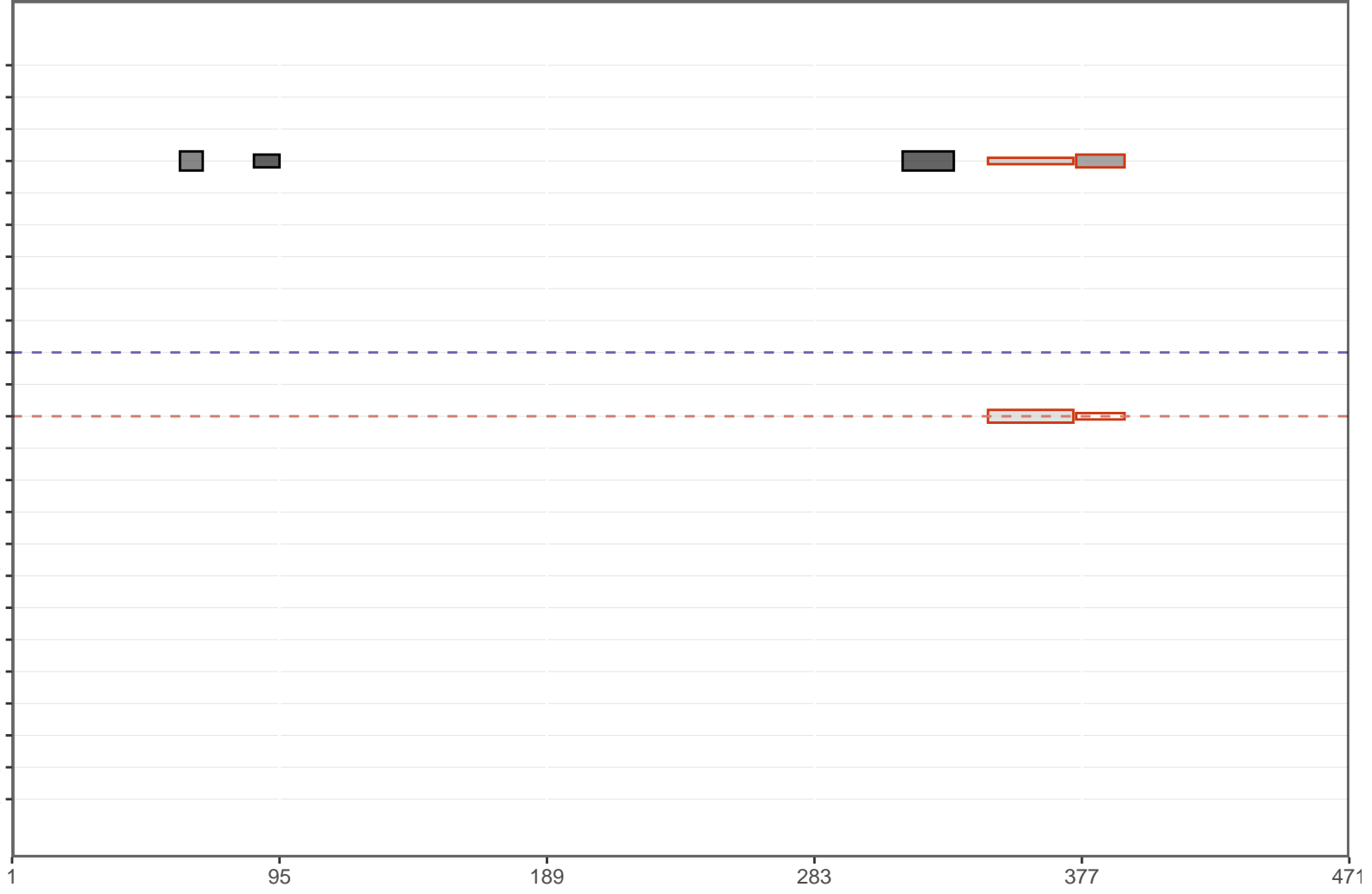
MW indication



Molecular weight

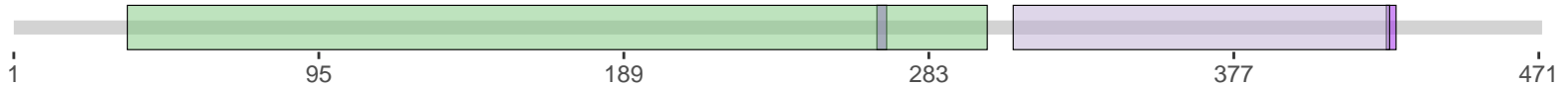


Gel Slice



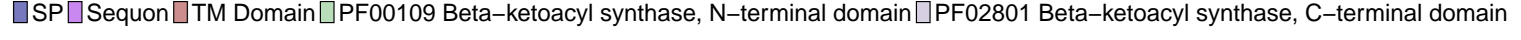
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

MHSVGDAAARMQFGGDADVAANAGGTEASIDALSIAQFORLRAITTKYNTSTPQEAASRFDCGRDFVYEGEGSGVMVLEELHARKRGAKEYTELKRGYGTGGDAHHITQPNIGRGAVALAMTRALKDGLHFNQVDVYNAHATSTPLGDAAEANAIAKHAFSDHATSGALSFSSSTKGAAGHELLGAAGAVEAIFTVLAHHGIAPLTLNISEPDPVFNFGFMPLTTSKEMAIAALENSFGFGGTSNGLLFTSIS

NbL17g21130.1 uncharacterized_LOC104219300 [MW = 71.17 kDa]

No. of times detected



log(intensity)



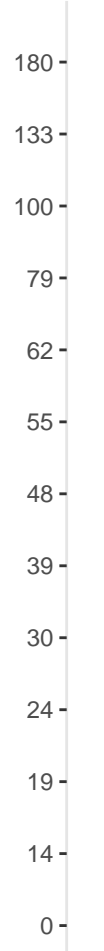
Values from



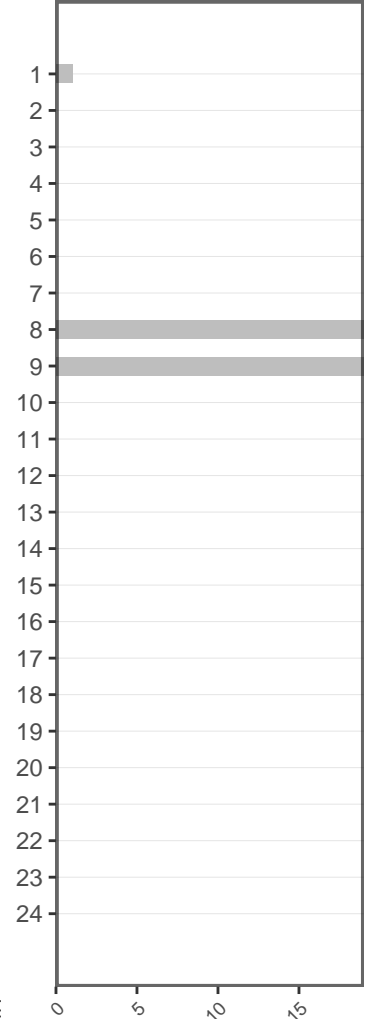
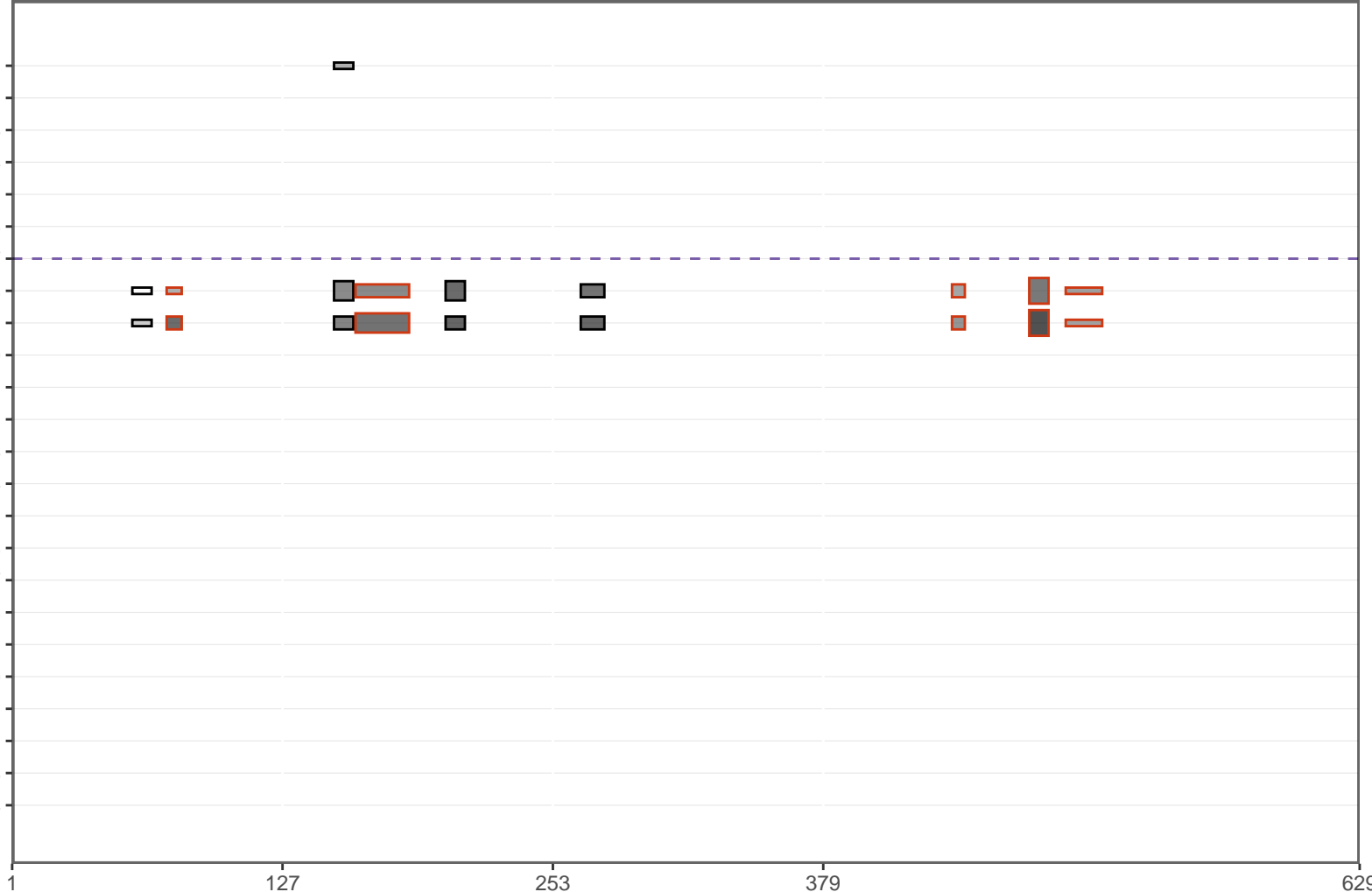
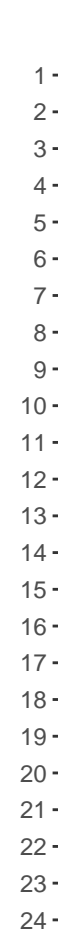
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

EHPDCVLLVFPDSDWNEFEVDYKELSGELSGLDWNGKPNVLSKEHGWDIVRTAEAAANKPLTFMNVSVVDPFGTSGTISESSYKDLRLRELVKRRSAVDMDFGTEMGSDTFYQLLHGMPSGSRDGEKVRQLALPFRSLAWDSIEHAAFLVHRVGLP6GLVFLVRNENHLDLKKKATRAEFKWWKPDGCPDPLVYELARGDGRELKRLSGHGDASDGCFLGMAHFEPTLRNKGSIWMYRPLFWETGVLGGVWLEAHAVG8ATGIGGFTDOPVHEVLGLKG

NbL17g21120.1 arginase_1_mitochondrial [MW = 37.13 kDa]

No. of times detected



log(intensity)



Values from



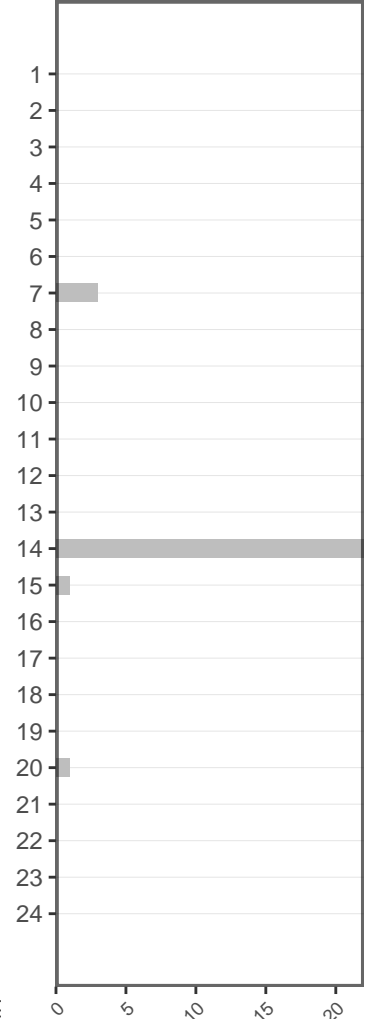
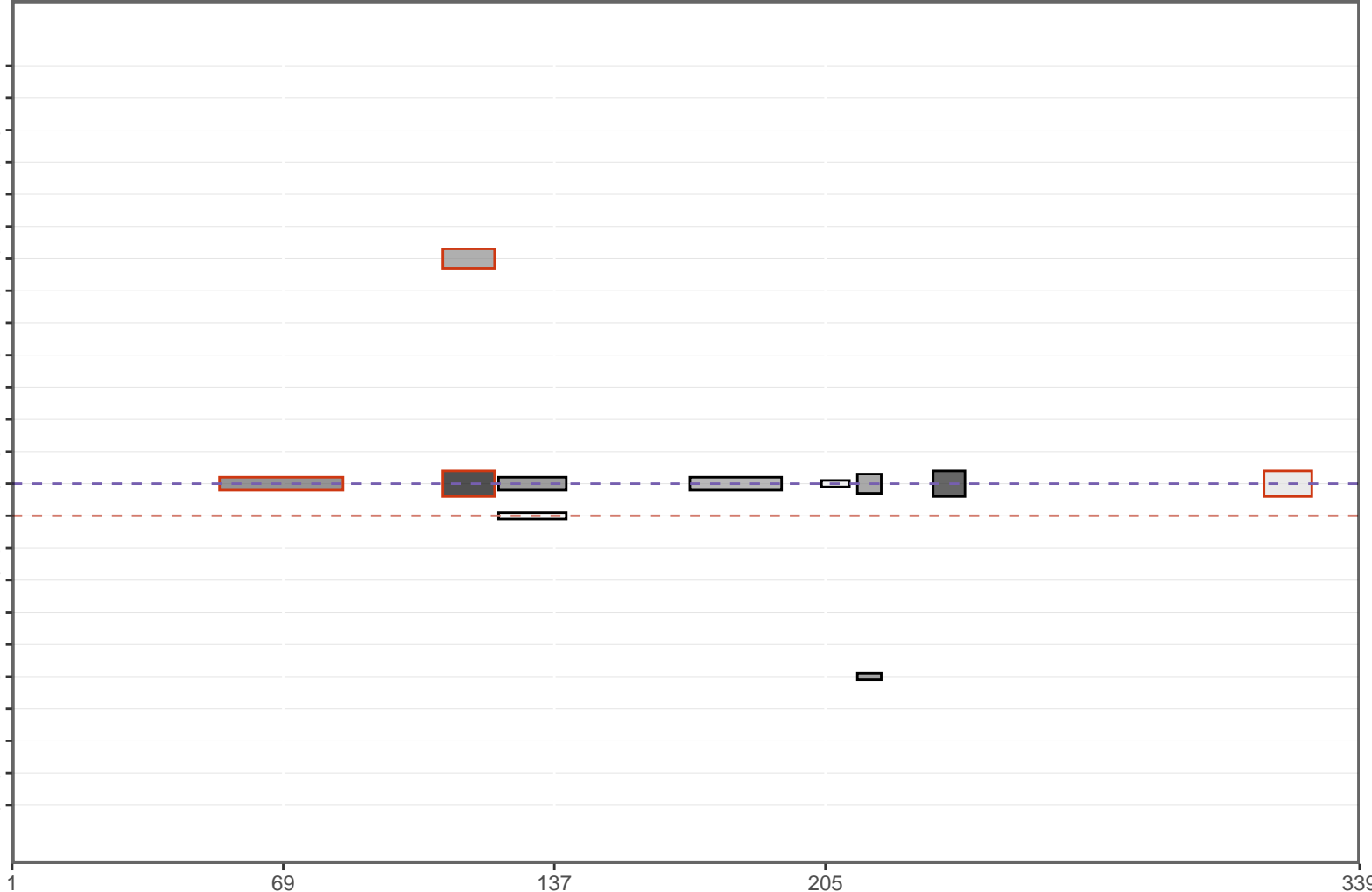
MW indication



Molecular weight

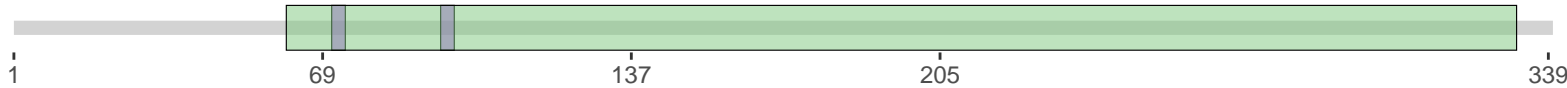


Gel Slice



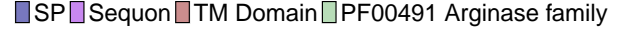
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MSISYTPVRAVISEKLGSPIDLLHDAHPDHYHSEFGNKYSHASGFARIMEGGVVRRLQVGRSITKEGREGGKRFVGEYEMRTFSRDRGFLENLKLGGVKGVYVSDIDCDMPFAPGVSHHEPGLSFRDVLNLHNLGADVGVADVVEFNPRQDITVDCMTAMAAKLVRELTAKIK*

NbL17g21090.1 3-phosphoshikimate_1-carboxyvinyltransferase_1_chloroplastic [MW = 56.45 kDa]

No. of times detected



log(intensity)



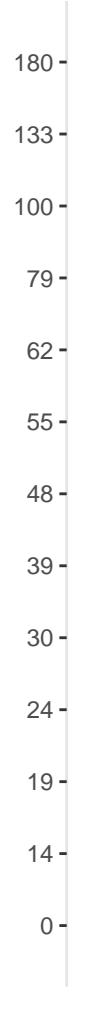
Values from



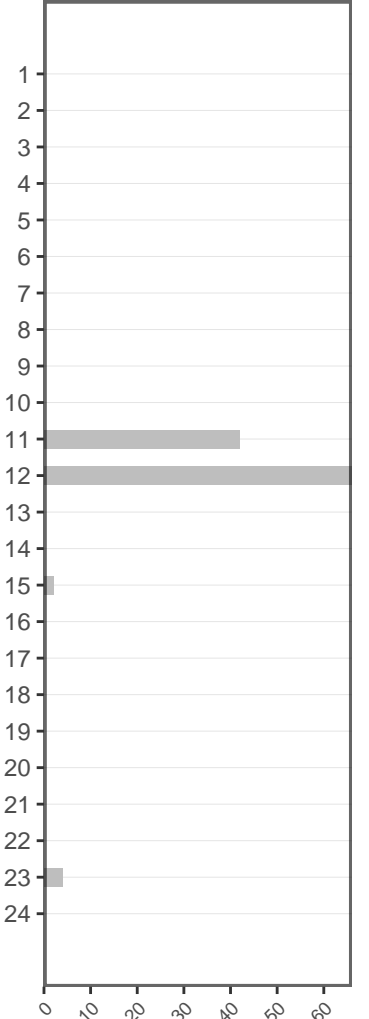
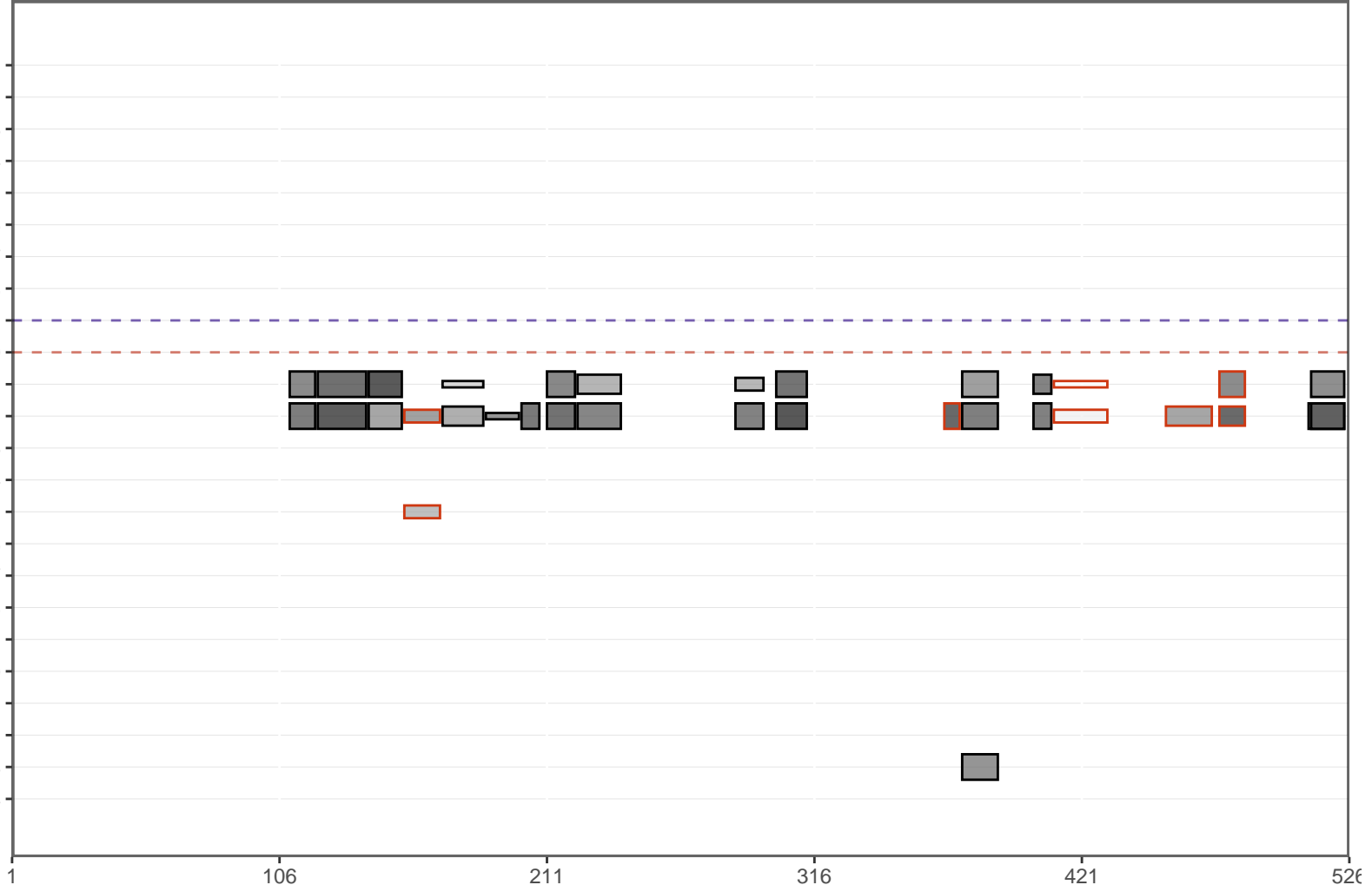
MW indication



Molecular weight

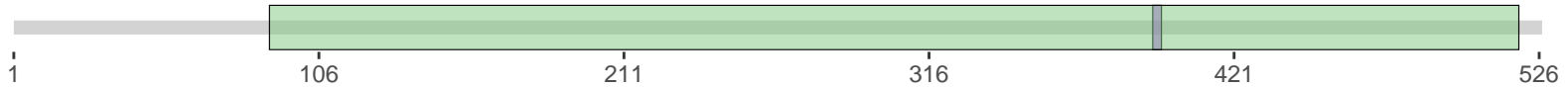


Gel Slice



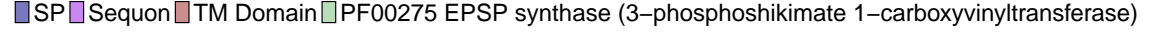
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KVPLSGSSISQYLTALLMAAPLAGDEVEIEHKLVSPVVEVTKLKERFGVSEHTSSWDKFLVRGGQYKSPGKAYVEGDASEASYFLAGAAVTGGTIVTEGGCGTSELGGQKFAEVLKMKGAEVTVTENSVTVKGGPPRNSGGMKHLRAVDNVMNKMPOVAMTLAVVAFADSPTAIRDVAVSWRKKETERMIAICTELRLKLGATVVEGPDVGIITPPEKLVKAEIDTYDDHRMAMAFSLAAGADVPVTKDPGQTRKTFNFDVLDGGYKHI

NbL17g21060.1 40S_ribosomal_protein_S13 [MW = 17.08 kDa]

No. of times detected



log(intensity)



Values from



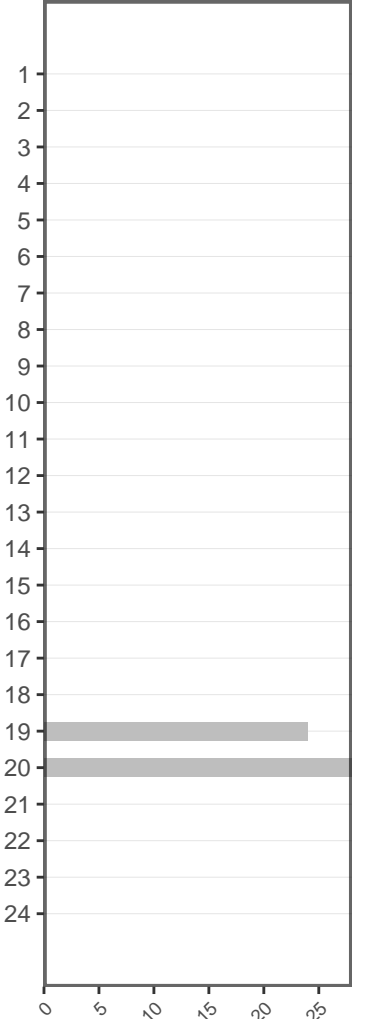
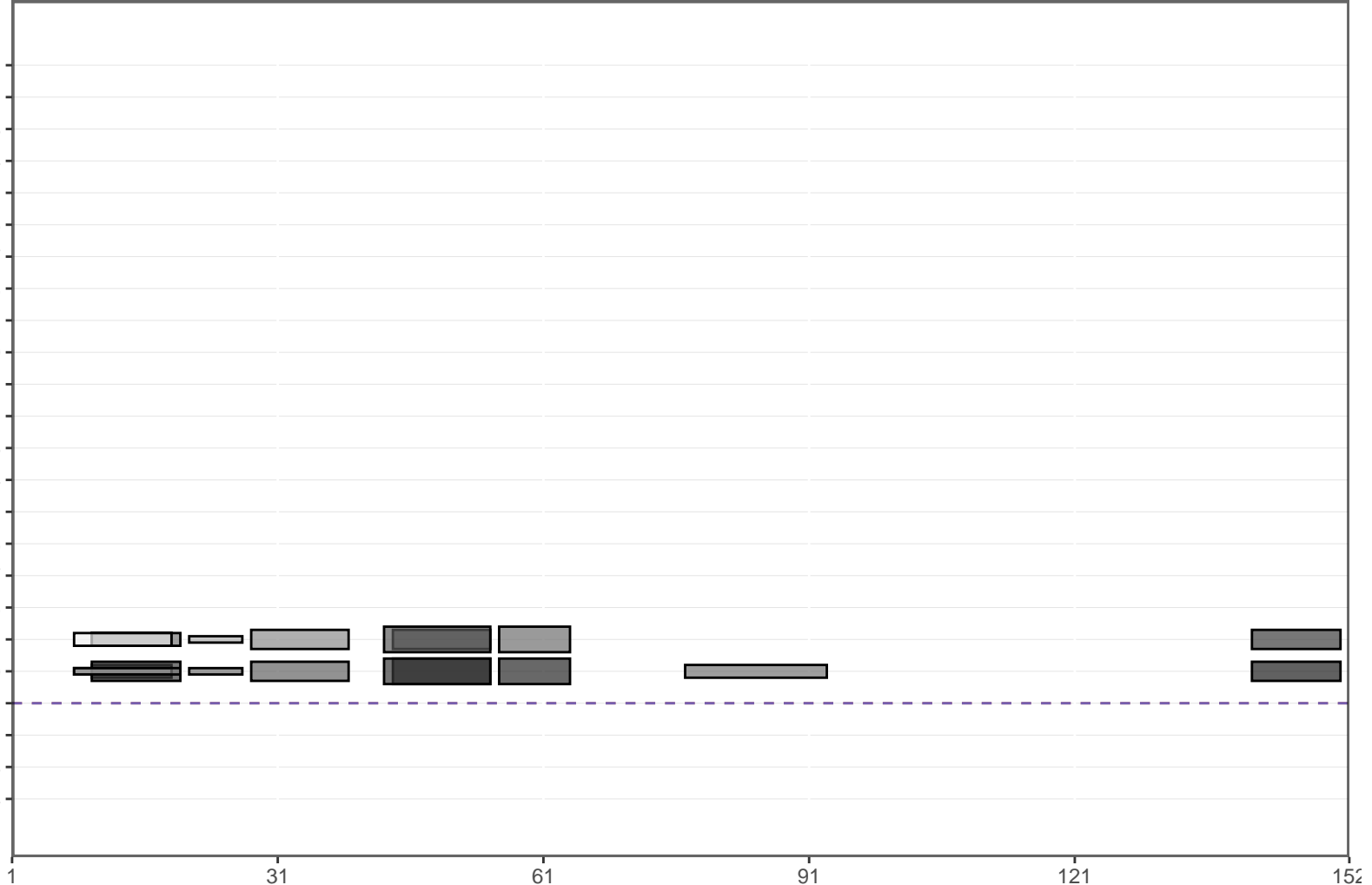
MW indication



Molecular weight

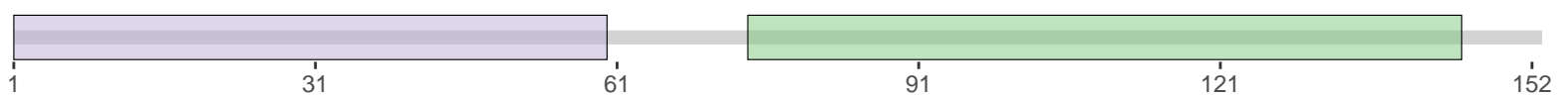


Gel Slice



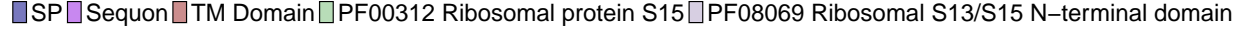
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IQVKSITGSKLRLLKAKHGLAPEPEEDLYHLKKAVARKHLERNRKDKDGSFRLLVESRIHLRLARYKKTKLFPWWYESTASTLVA*

NbL17g20970.1 transducin_beta-like_protein_2 [MW = 47.19 kDa]

No. of times detected



log(intensity)



Values from



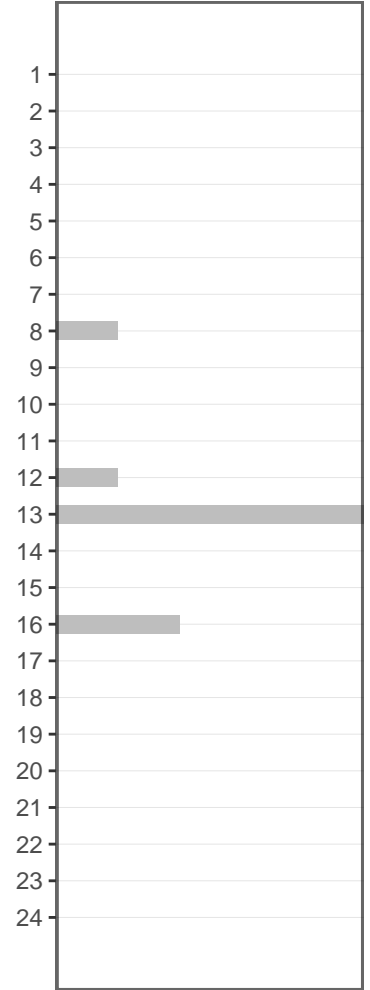
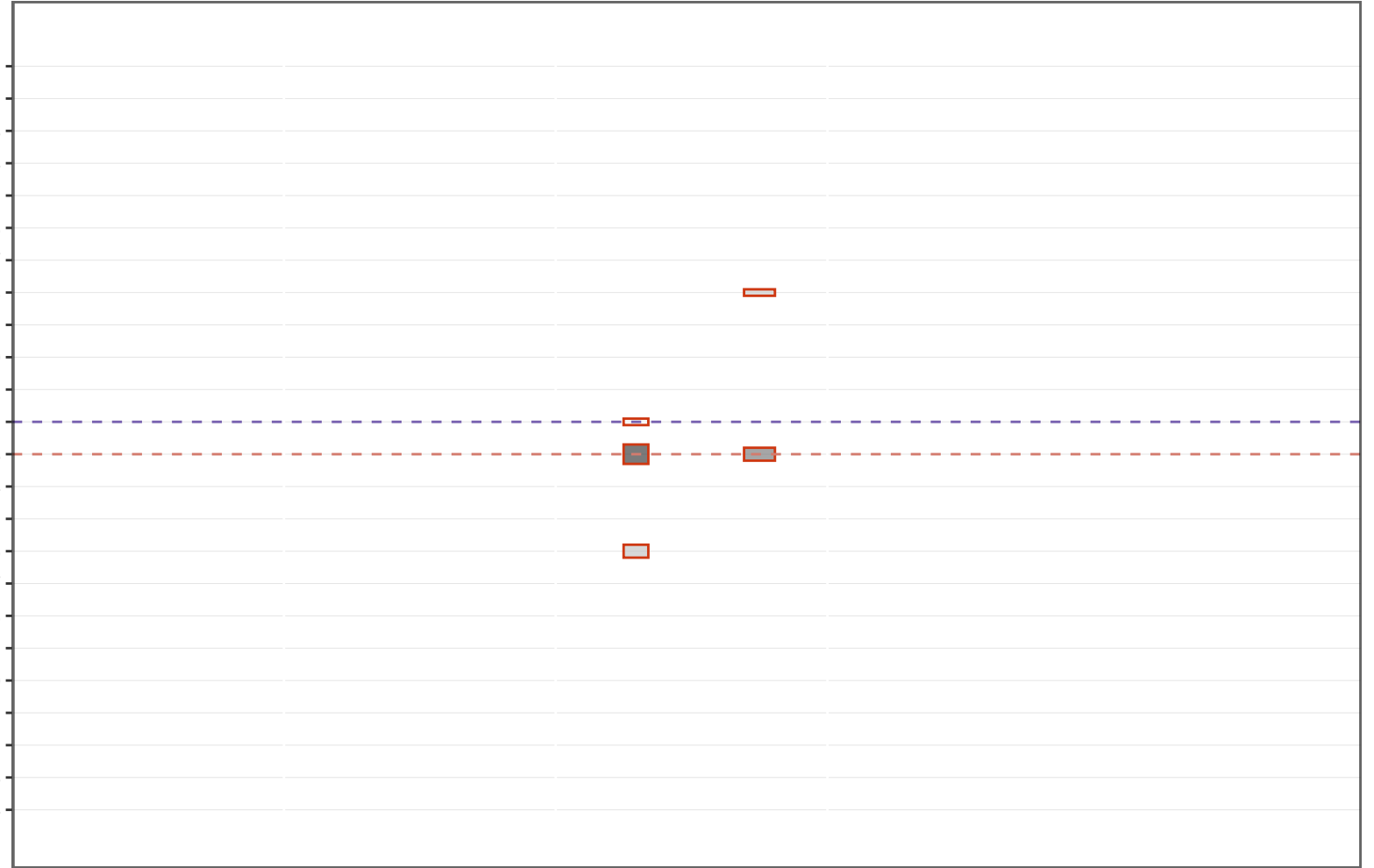
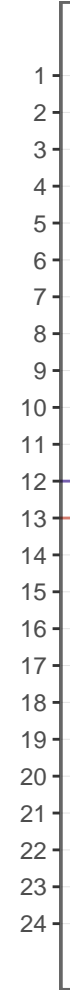
MW indication



Molecular weight



Gel Slice



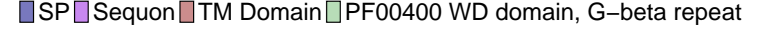
Peptide counts over 4 repeats

Protein length 1 89 177 265 438



Pfam domains

Pfam Description



Protein sequence:

ATYGSADGSIIVYSCSEGTDLVLFHGKSGHVGIVDTNGLKNNMAISPGRFIAAAAFADAVVWEIVYAKDGAWEKVRVIMELKHKSAVTGLGFTPNSEGITASKDGRVWVNNRYHLSSEDPKTLRVLPLPKDANGTILHYDRLLSPDGKILATTHGSMQGLCPENKVLKKAEKAKHDGDTDAWSPSPRPMGDKRVLATAVGVKRVKLVAAVPSFNPQ

NbL17g20730.1 fasciclin-like_arabinogalactan_protein_8 [MW - SP = 41.53 kDa]

No. of times detected



log(intensity)



Values from



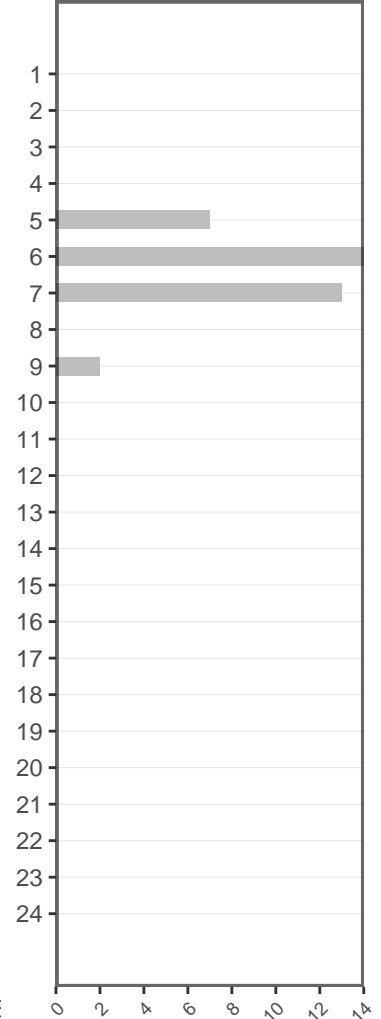
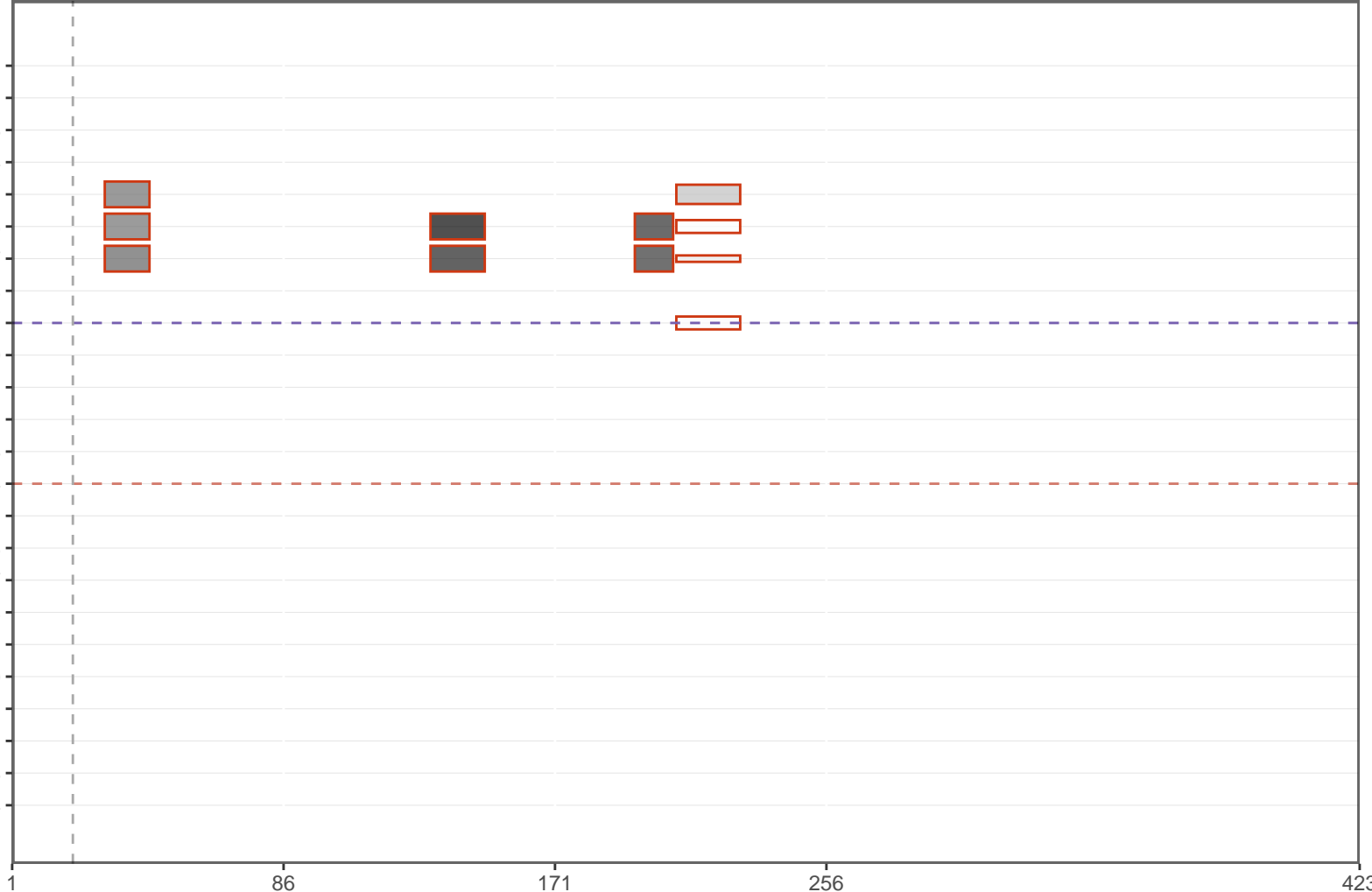
MW indication



Molecular weight



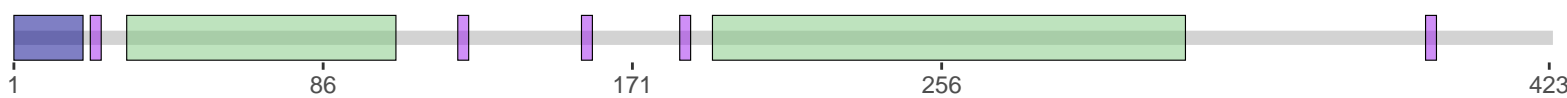
Gel Slice



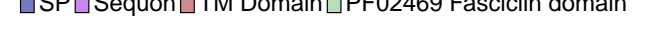
Protein length



Pfam domains



Pfam Description



Protein sequence:

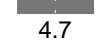
IQSGVLYKTYDTEIEFGILTVFAPNDEAFKGVKVPDLNKLKSAEIVSLLQYHAPSYTPIGTLKTKDRIETLATNGASKYDLSASTAGDQVFLDTGVDSRIASTVIDSTPFGIFTVDSVLLPEELFGKGSPPAPGAPETSPAPAFEGASPGVAPPEASGPEPMMSPPAPPTSSPAGAPADGPAADGENSTAKKNAGNANAPALLKVLFTVSDVGVIVSIVLS*

NbL17g20710.1 uncharacterized_LOC109229227 [MW = 18.6 kDa]

No. of times detected



log(intensity)



Values from



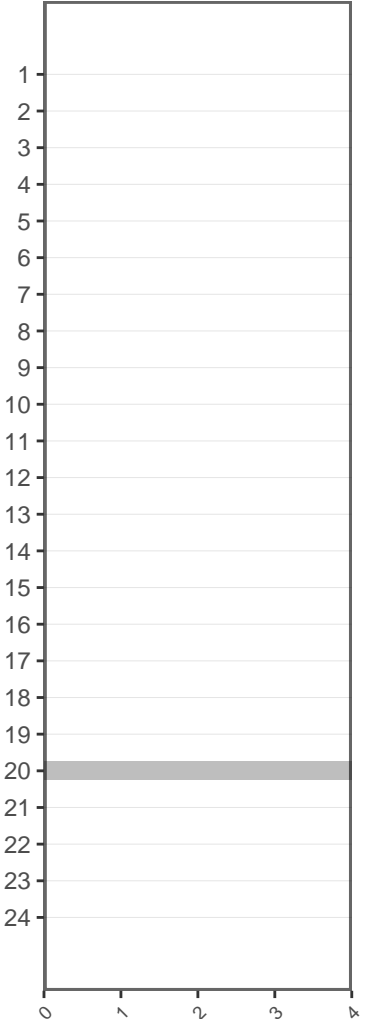
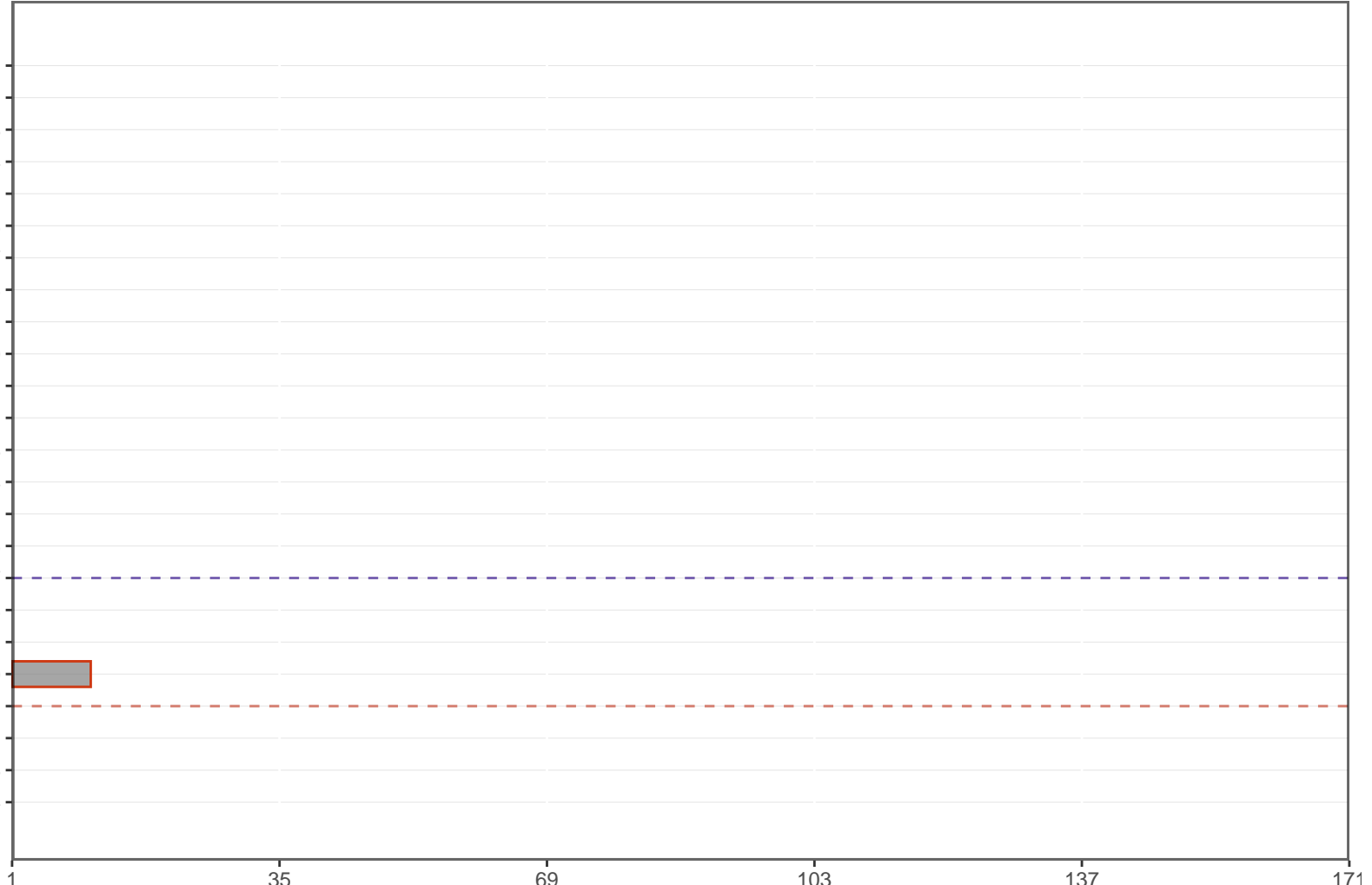
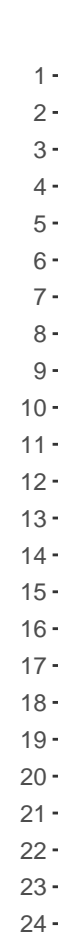
MW indication



Molecular weight



Gel Slice

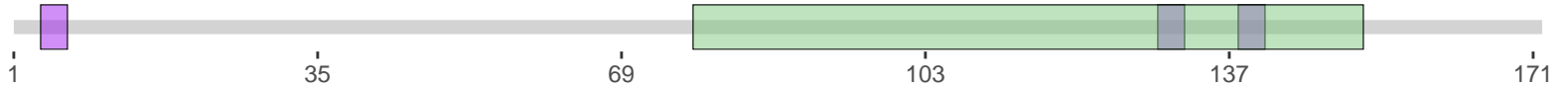


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

PMNYYGSLHGCAVGGVTVRIATAGARTIVGKDKKFLGELSEVLSGAPRPAEIVVNTAIRGRNLTVAWDFRIVKESEKLSYSHATFYHMPVAGL

NbL17g20460.1 protein-ribulosamine_3-kinase_chloroplastic [MW = 37.49 kDa]

No. of times detected



log(intensity)



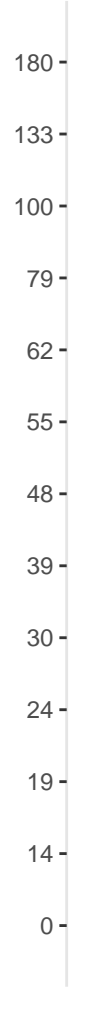
Values from



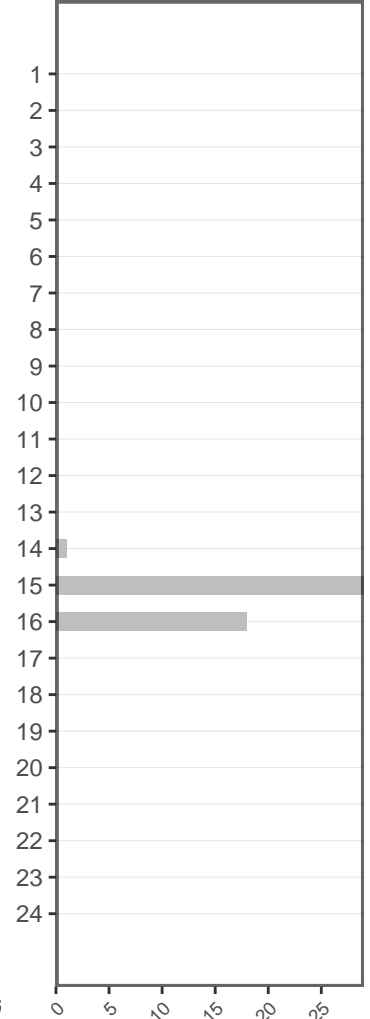
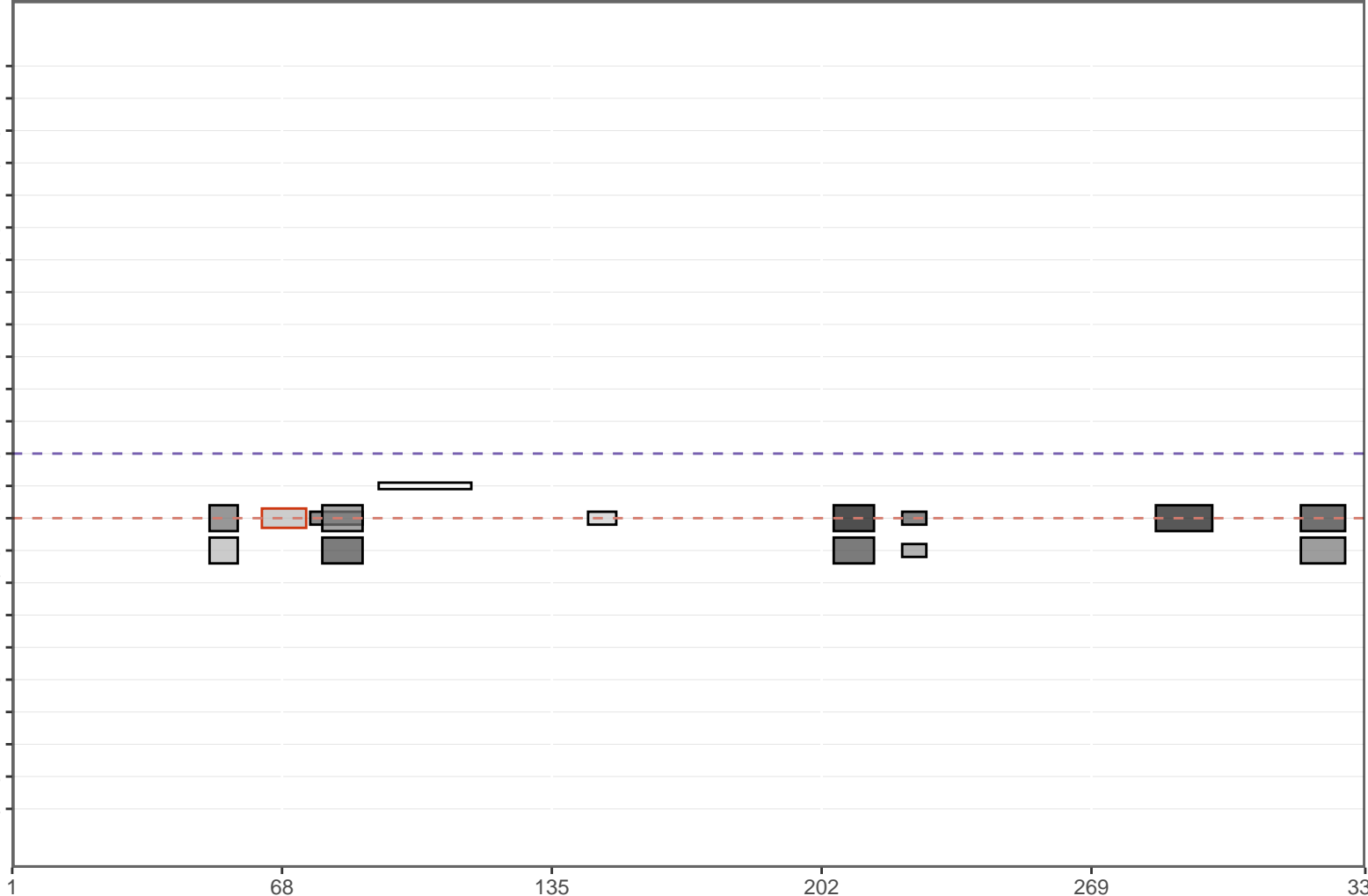
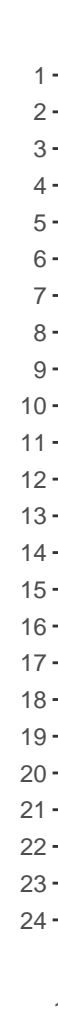
MW indication



Molecular weight

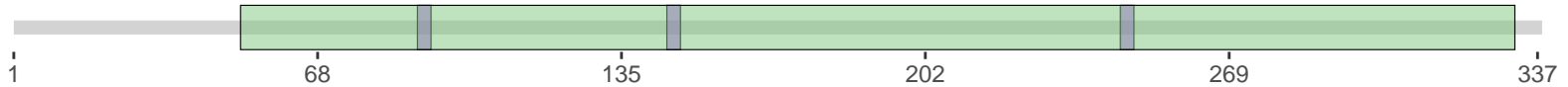


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KATKSEKGFVHIVENTIGSTPQNTWTSDFWIEFAELRLGVQLKLAREQVGDSTIYERGGRLAANLGLPKNAWIEPCLLHGDLWBSGNTYDQNGEPVLDPMQYYGHNEAFEGMHWGAGFGDFYKAYFQVMPGPGFQRRLMLYHLYLNHYALFGSGYRSAMSIDDYLRMLNVA

NbL17g20370.1 ATPase_GET3-like [MW = 40.49 kDa]

No. of times detected



log(intensity)



Values from



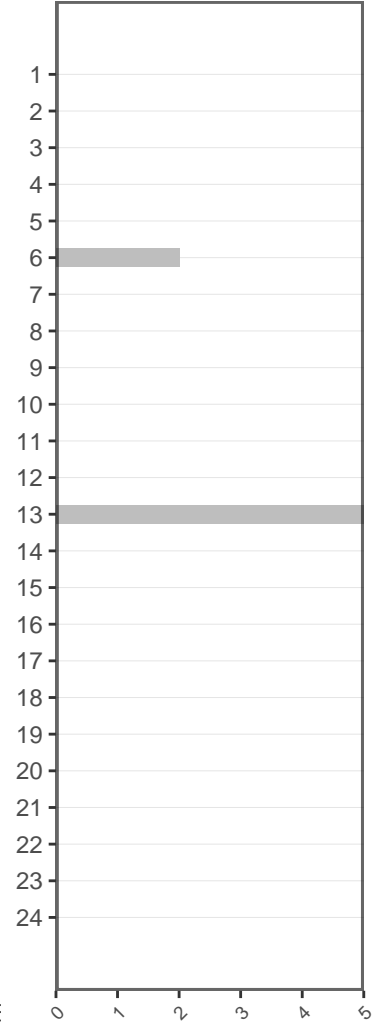
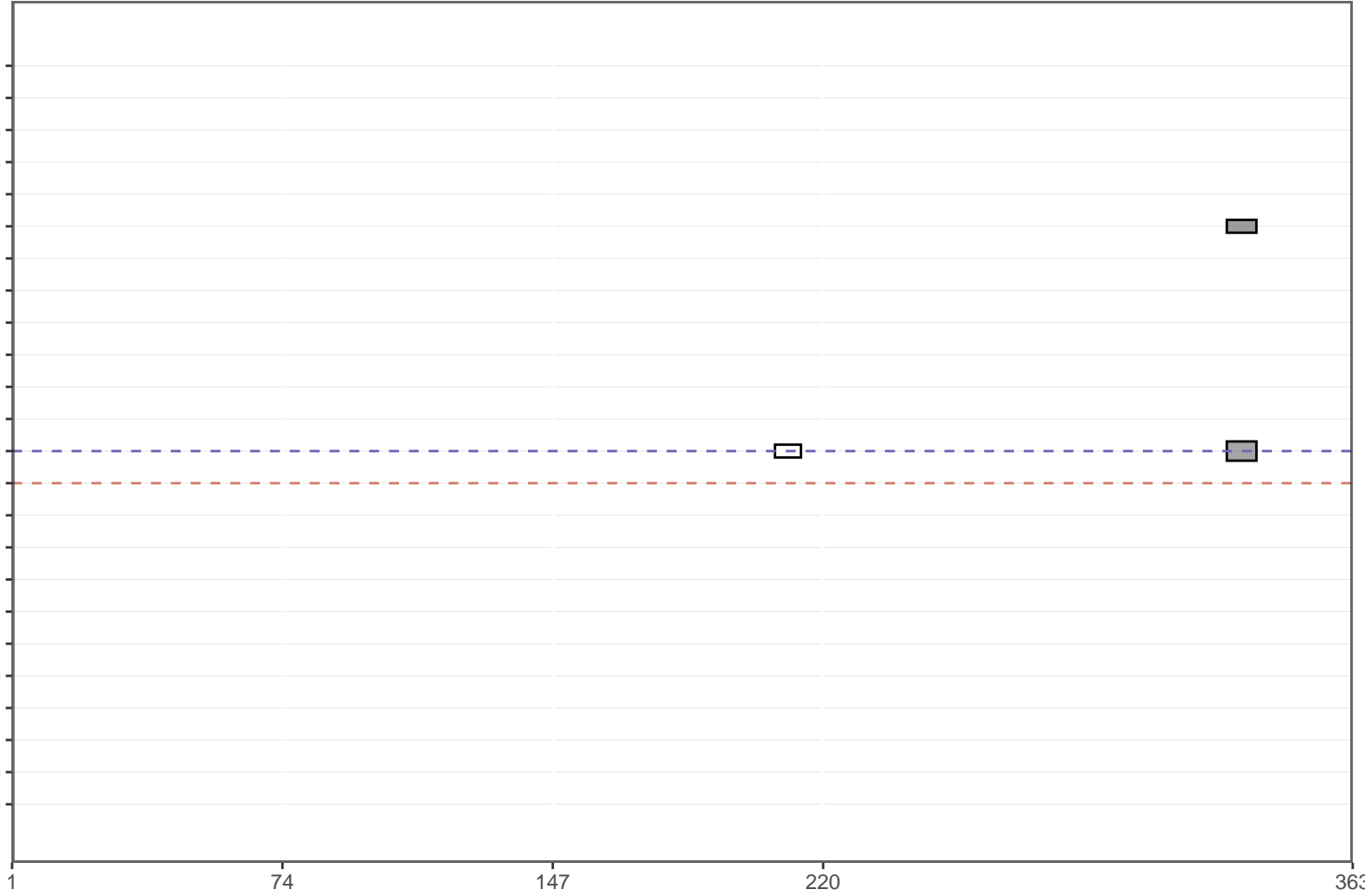
MW indication



Molecular weight



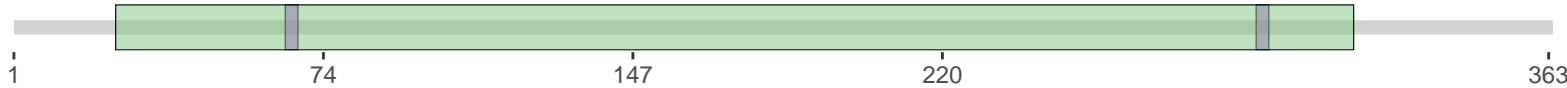
Gel Slice



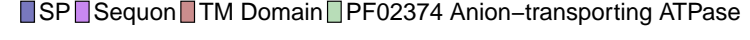
Protein length



Pfam domains



Pfam Description



Protein sequence:

KVMSLKSRFGGVLSQMTLLGVDDEFGAAALGKLEGMKEHEEVNKGFKDPLDTTFGVOPEFLSIVETERLVDELAKFEIDTHNLINQVIFDDEVESKLLKARMMGQKYLDFYMLYDDFNITKGLPLLPQEVGGVEALKGFSHFITPYKFLARGVSEELLENRVASLKEQLKDAEAELEKVRKGGKQV

NbL17g20360.1 ubiquitin-related_modifier_1_homolog_1-like [MW = 11.14 kDa]

No. of times detected



log(intensity)



Values from



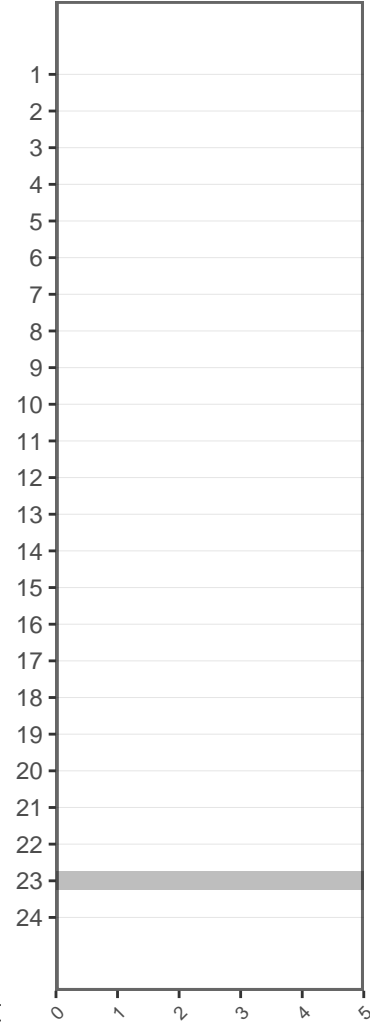
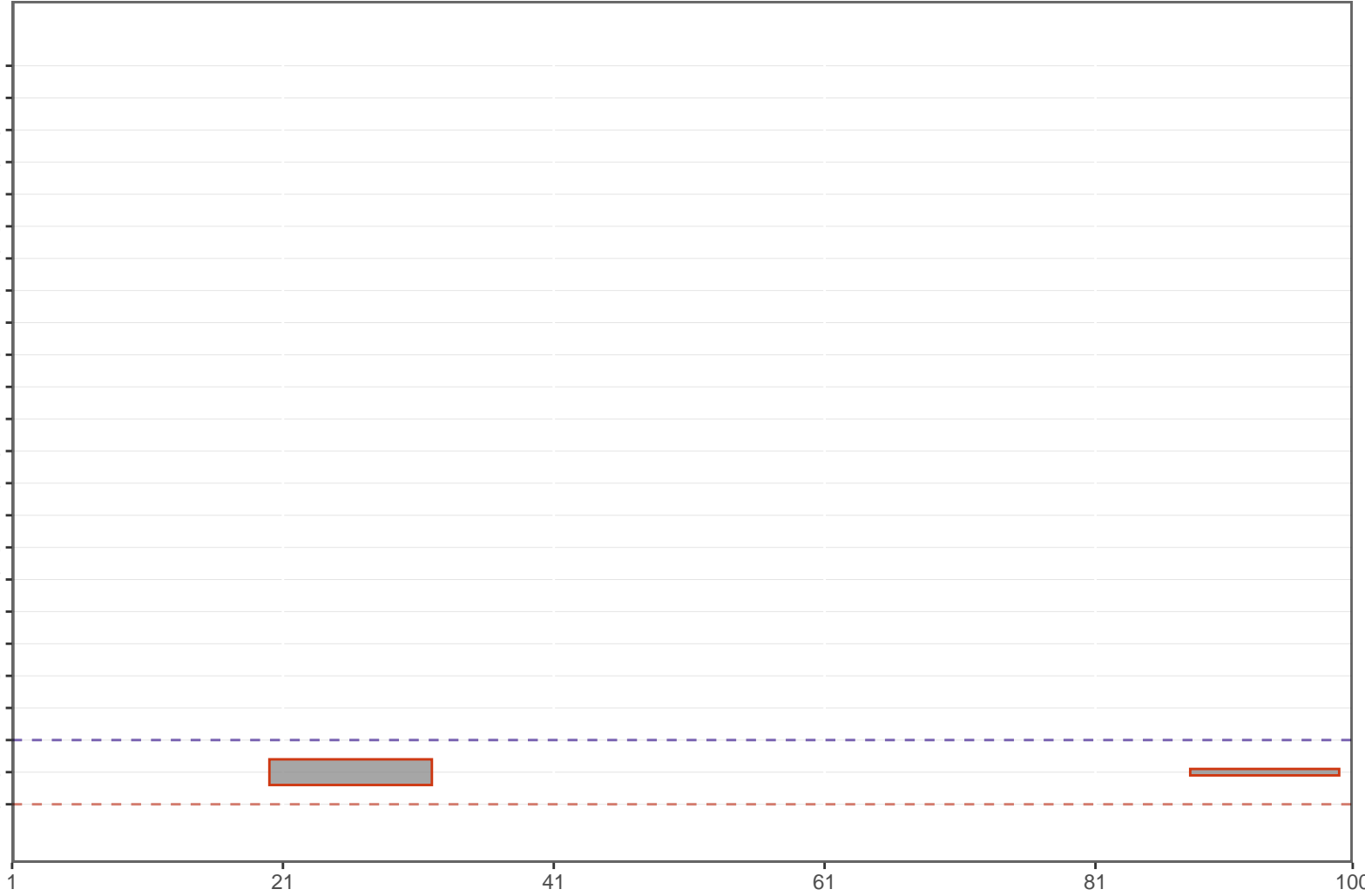
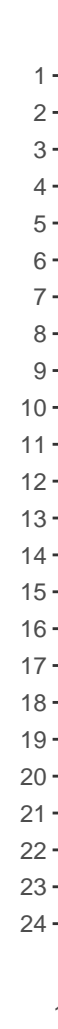
MW indication



Molecular weight



Gel Slice

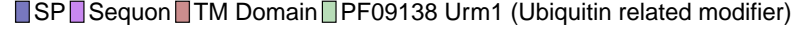


Protein length



Pfam domains

Pfam Description



Protein sequence:

NLLTWVRTNLKERPEMFMGGDSVRPGVLLVNDTFWELSGLETVALEEKDNNVFISTLHGGV

NbL17g20300.1 uncharacterized_LOC104238971 [MW = 66.74 kDa]

No. of times detected



log(intensity)



Values from



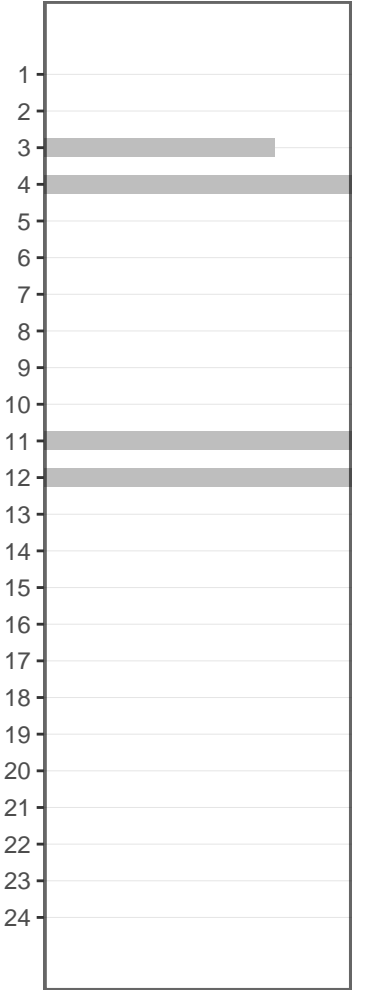
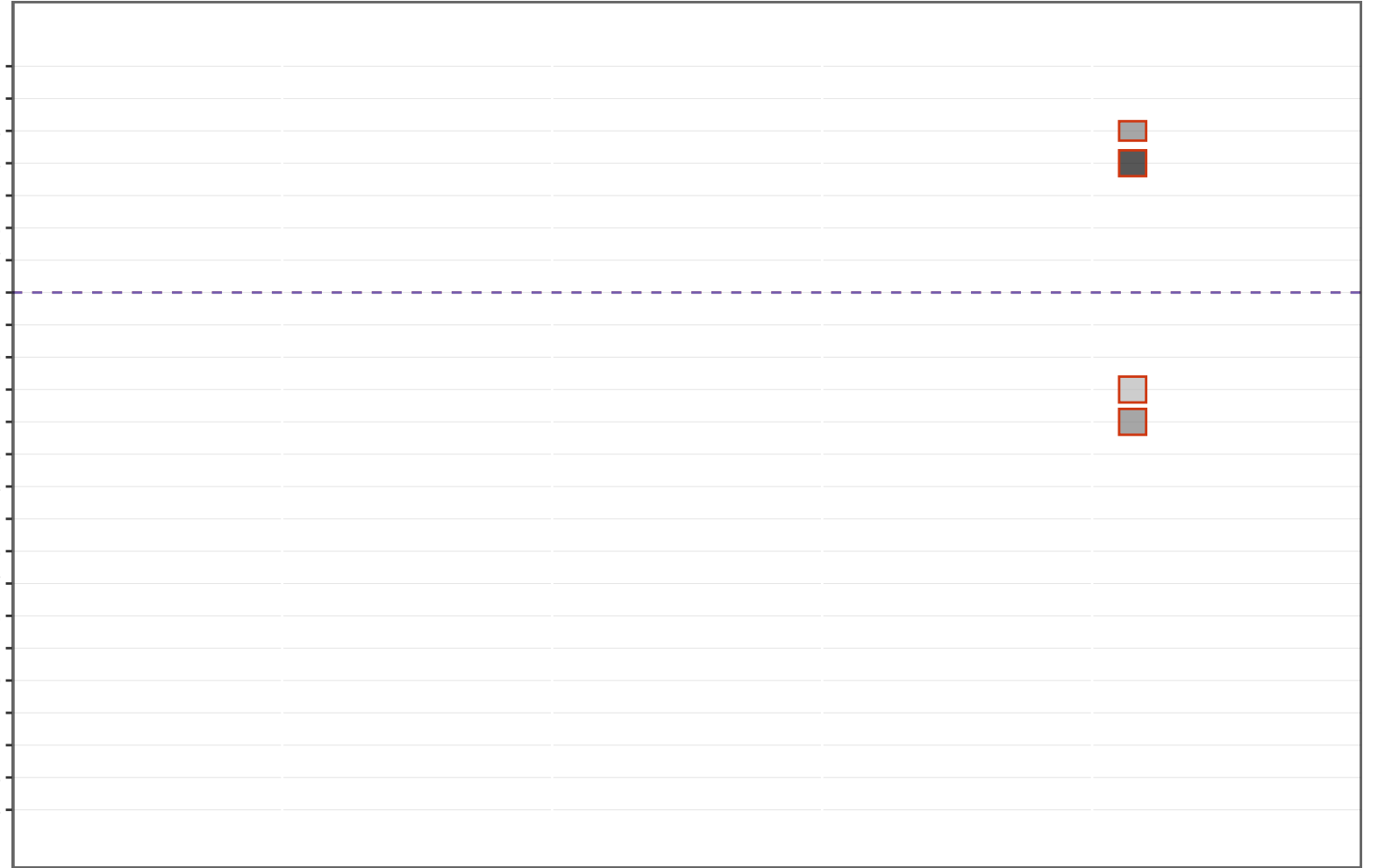
MW indication



Molecular weight



Gel Slice

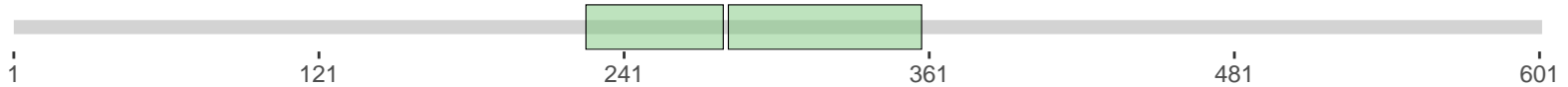


Protein length

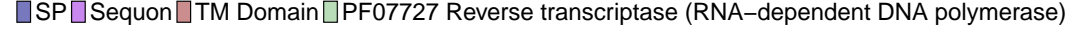


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VDDIVTGNDDQGSIFLKGHLFQHFQTKDGLGTLKYLFLGIEVAQSSGGVIGQRKYALDILEETGMGTGKPKVDTPMDPNSKLLPQHGELNDPERYRRLKGLNLTATRPDISFPVSVVSGDFMSSPCDGHWDVAVRILRYKIKSTPGKGLLFEDRGVEQIVGYSADADWAGSPDRRSTSGYCVLVGGNLVSSKKGKGNVARSBAEAEYRAMAITGELVWVKLLKELKFGDISGMGLVGDGQAAALHAENPVFHERTKHIEIDGHFIREKILSGDQATKFKVNSNDLADITFKSLT

NbL17g20230.1 glyoxylate/hydroxypyruvate_reductase_HPR3-like [MW = 35.7 kDa]

No. of times detected



log(intensity)



Values from



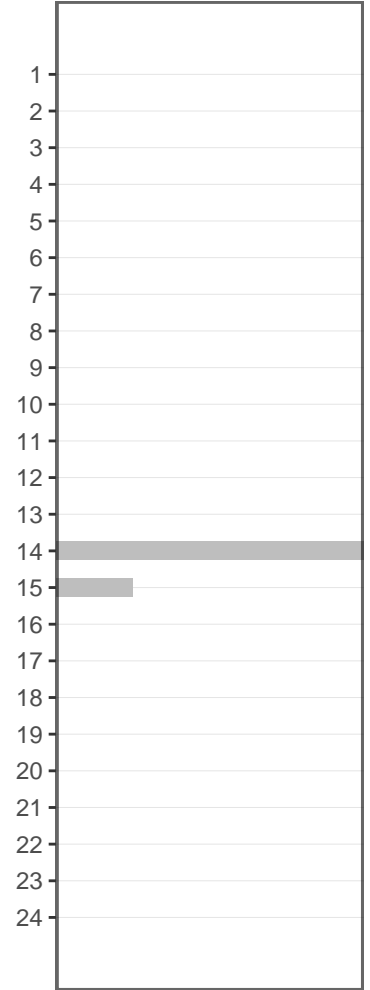
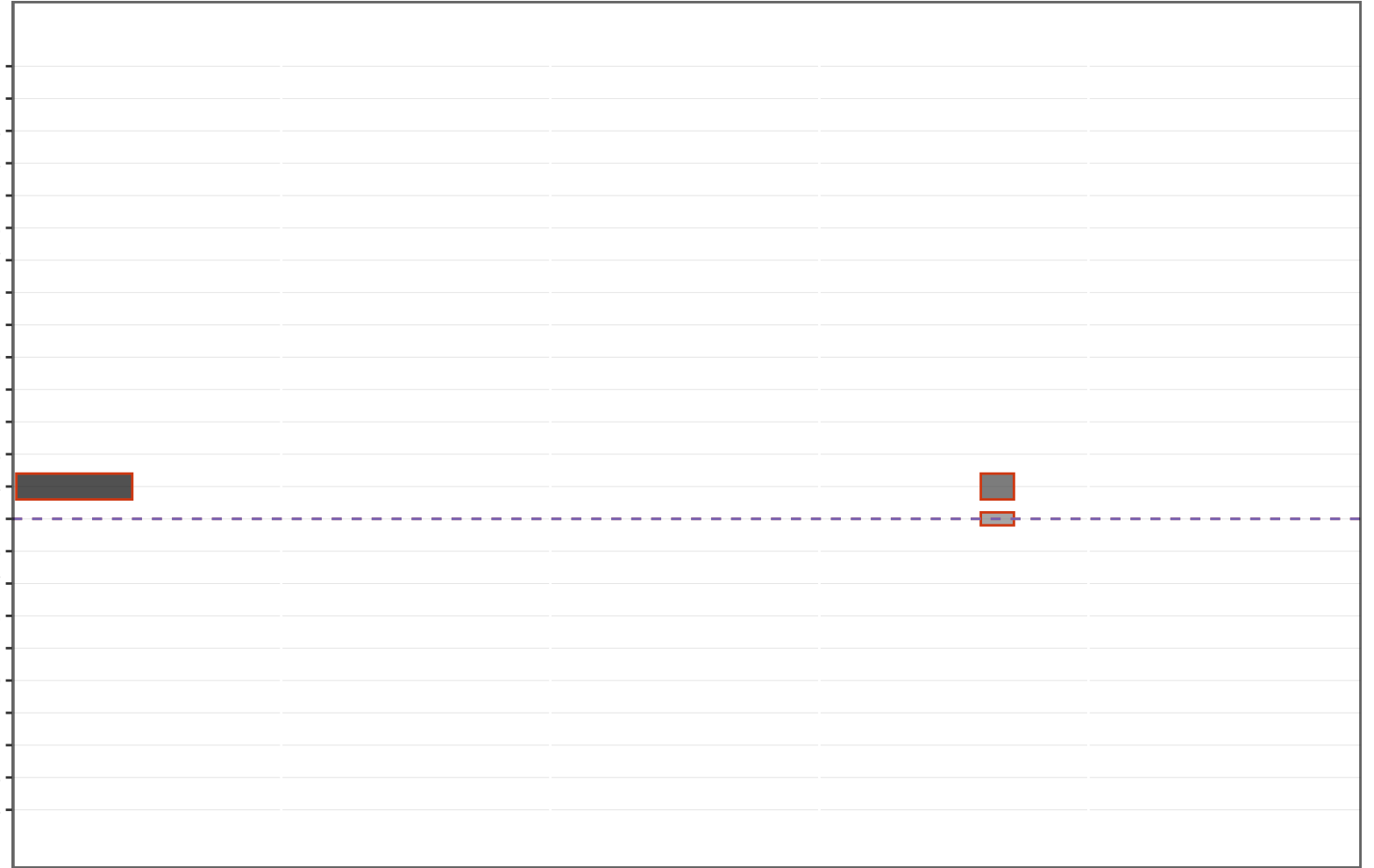
MW indication



Molecular weight



Gel Slice

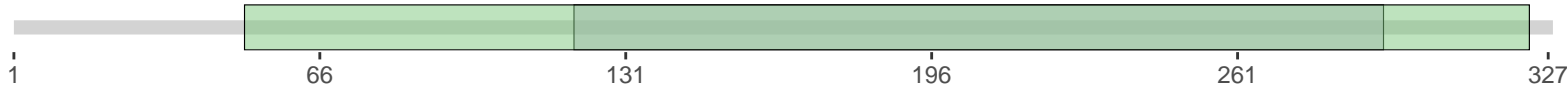


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

- SP Sequon
- TM Domain
- PF00389 D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain
- PF02826 D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain

Protein sequence:

CSKVGGRRKVGIVLGGSLKVAKRLKLEAFDGIHSYGRKKKPVYFPYFDHKLATKGDVLYGGALTEQTRHLINKEVLLALGKEGVINARGSVINEMELVGGVGGIAGVGLDFENEPNVPEDLFLDNLVLRHVAACTEDFRDLVELVSGNLEAFFLNKPLLSPVLDP

NbL17g20220.1 glyoxylate/hydroxypyruvate_reductase_HPR3-like [MW = 35.38 kDa]

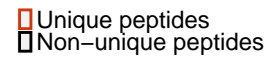
No. of times detected



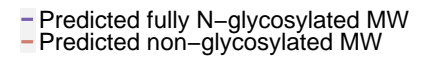
log(intensity)



Values from



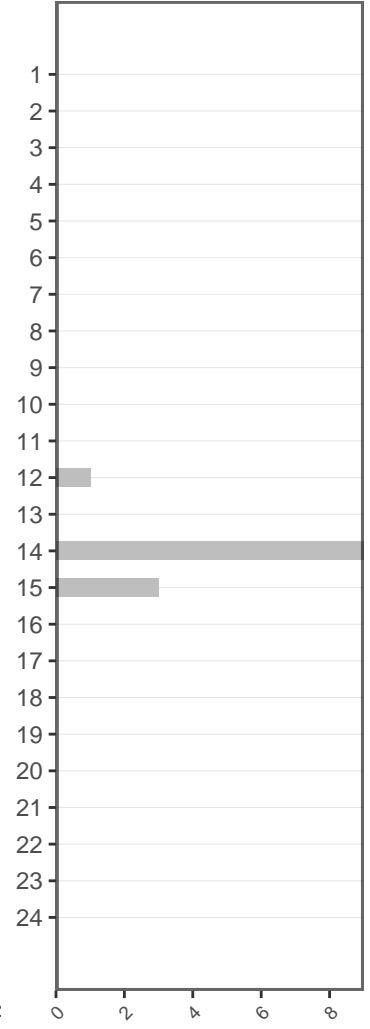
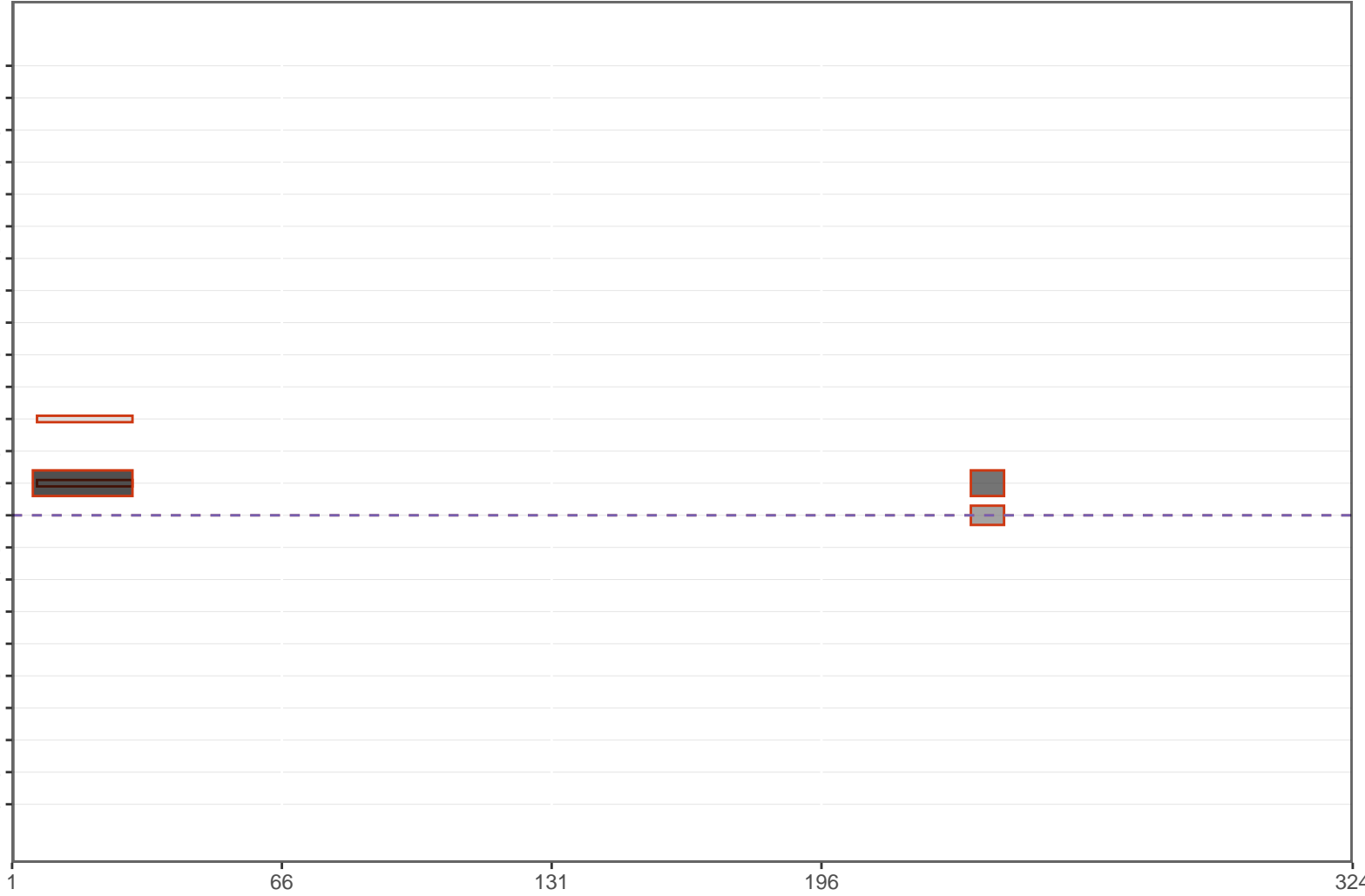
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

- SP Sequon
- TM Domain
- PF00389 D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain
- PF02826 D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain

Protein sequence:

LASKVGGRRKYGVVSLGGIGLEAVNRLEAFGGISYQGRKKKPVVYFYPDVELATKGVLVCCALTDGTHHLINKEVLLALGKEGIIINARGAIIINEMELVQGLVQGEIAGAGLDVFEIENPVPPEELLGLDINVLGSHVFLTEGDFRDLVELMGGNLEAFFLNPKLLSPVFDL

NbL17g20130.1 methionine_adenosyltransferase_2_subunit_beta-like [MW = 35.65 kDa]

No. of times detected



log(intensity)



Values from



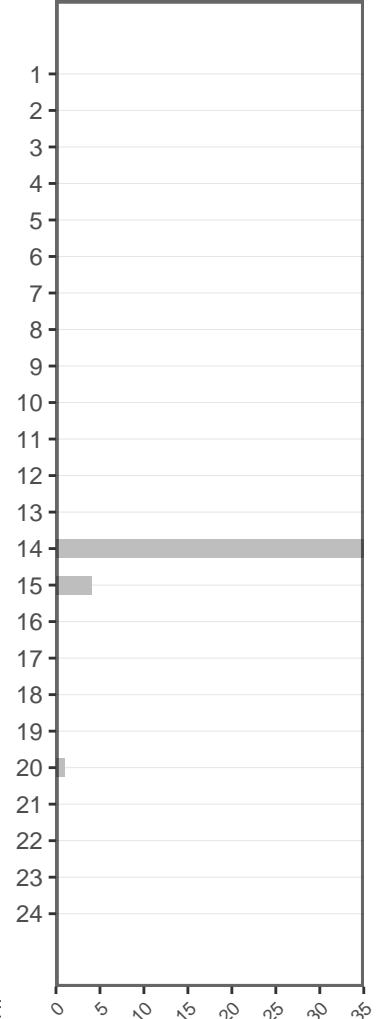
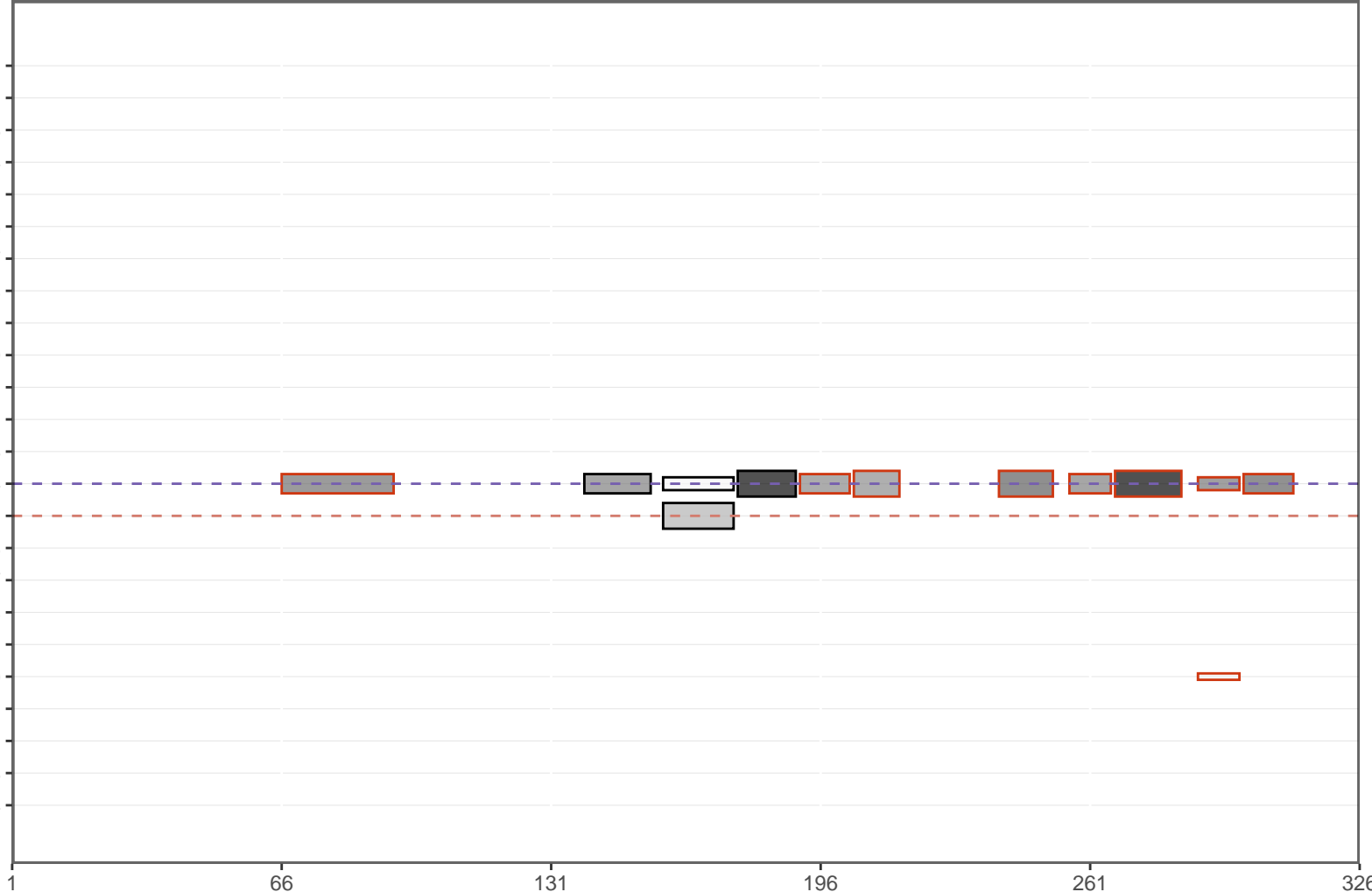
MW indication



Molecular weight

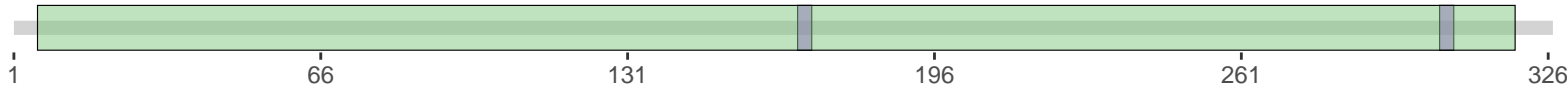


Gel Slice



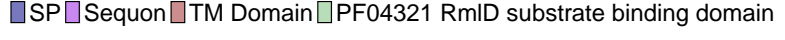
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NLYGRSKVALEGRISANYSNFAILRBSIRYVGPQTVPVFKSLPVQWMDVILAKGDAMEFFHDEFRCPIYKDLTVWTLTNRWISGREFPQLLLNVGGPDRVSRVQMAEAWHHRGYSLSLKPVSSTVNRGVKSPADISMDTRLIQITLMMSTTFFRDGKLTLEALELSTE

NbL17g20120.1 NAD-dependent_malic_enzyme_59_kDa_isoform_mitochondrial [MW = 66.34 kDa]

No. of times detected



log(intensity)



Values from



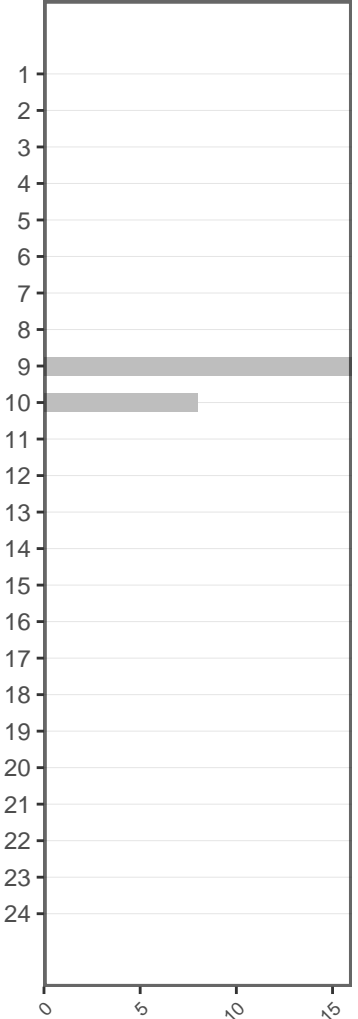
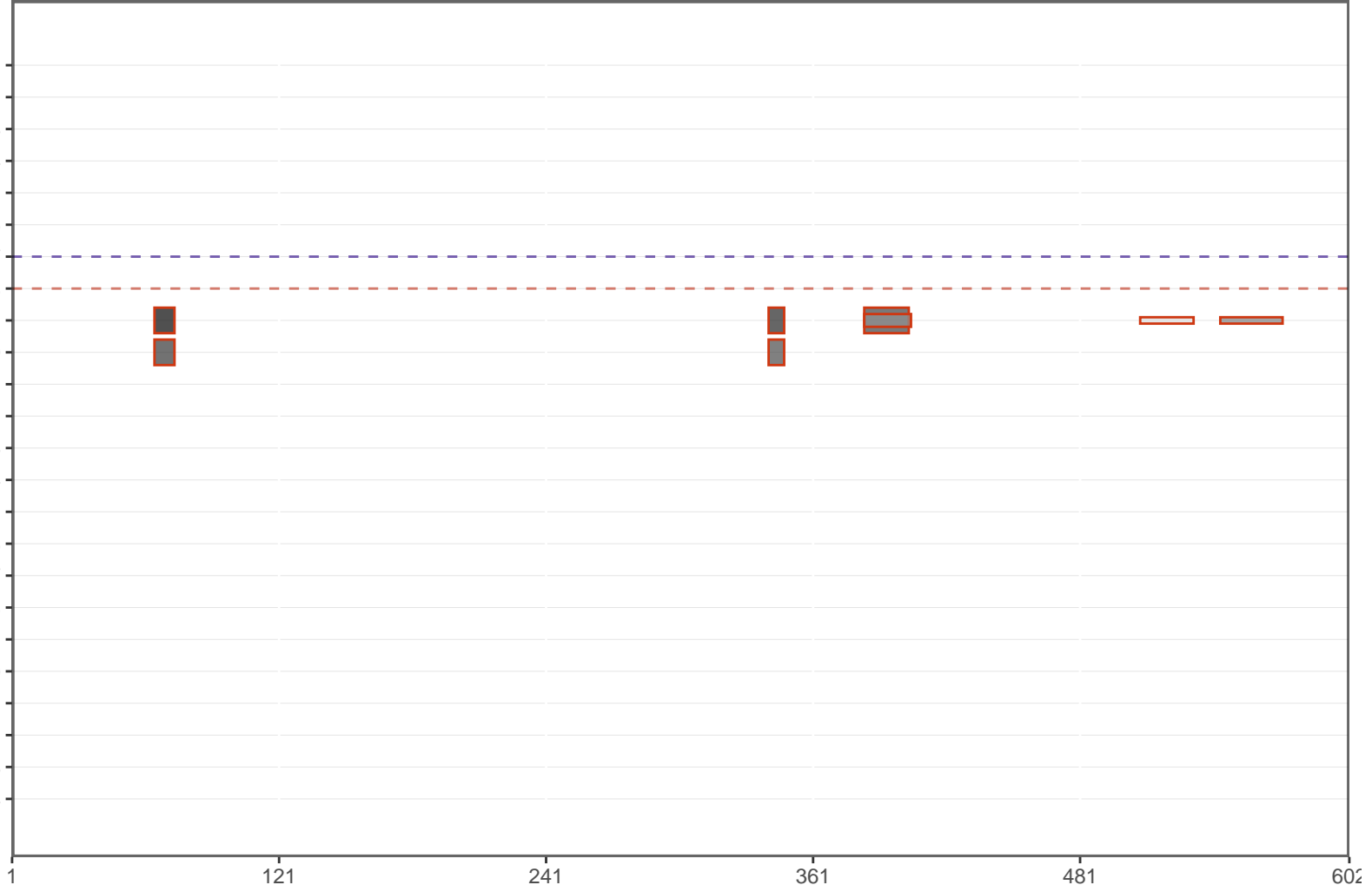
MW indication



Molecular weight

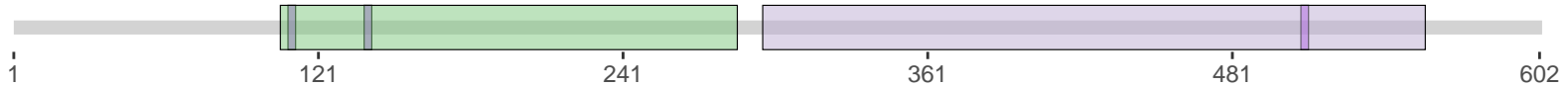


Gel Slice



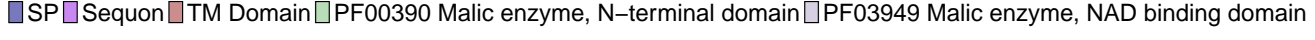
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KFCMFNDIOGTAAGVLAGLGLTVRAGRPPLTFANQKVVVAGAGSAGLVKMLALQTVSRMAGPSADPHFFLQKNGLTKHRKDDPALPFAKAQHEIEGLGLQEGAGLLEVVKKVPHVLLGLSDVGGDFHEEVLRRMREGSDVRRPFAFMSNPTNAEECPVDAPKLAGENIVFASGSPFENVDLGNQKIHVGNQANNMYLFPDGLGALLSGARNISDTMLEAAAEGLANVMSDDEIKRGLYPSINDRIDTAEVGAALGAAVAEDLAEGHGDVGAARELQHSKEE

NbL17g20110.1 50S_ribosomal_protein_HLP_mitochondrial-like [MW = 18.03 kDa]

No. of times detected



log(intensity)



Values from



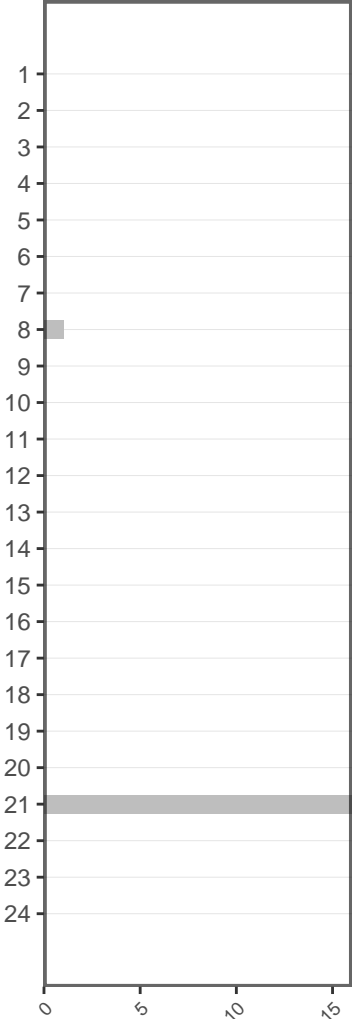
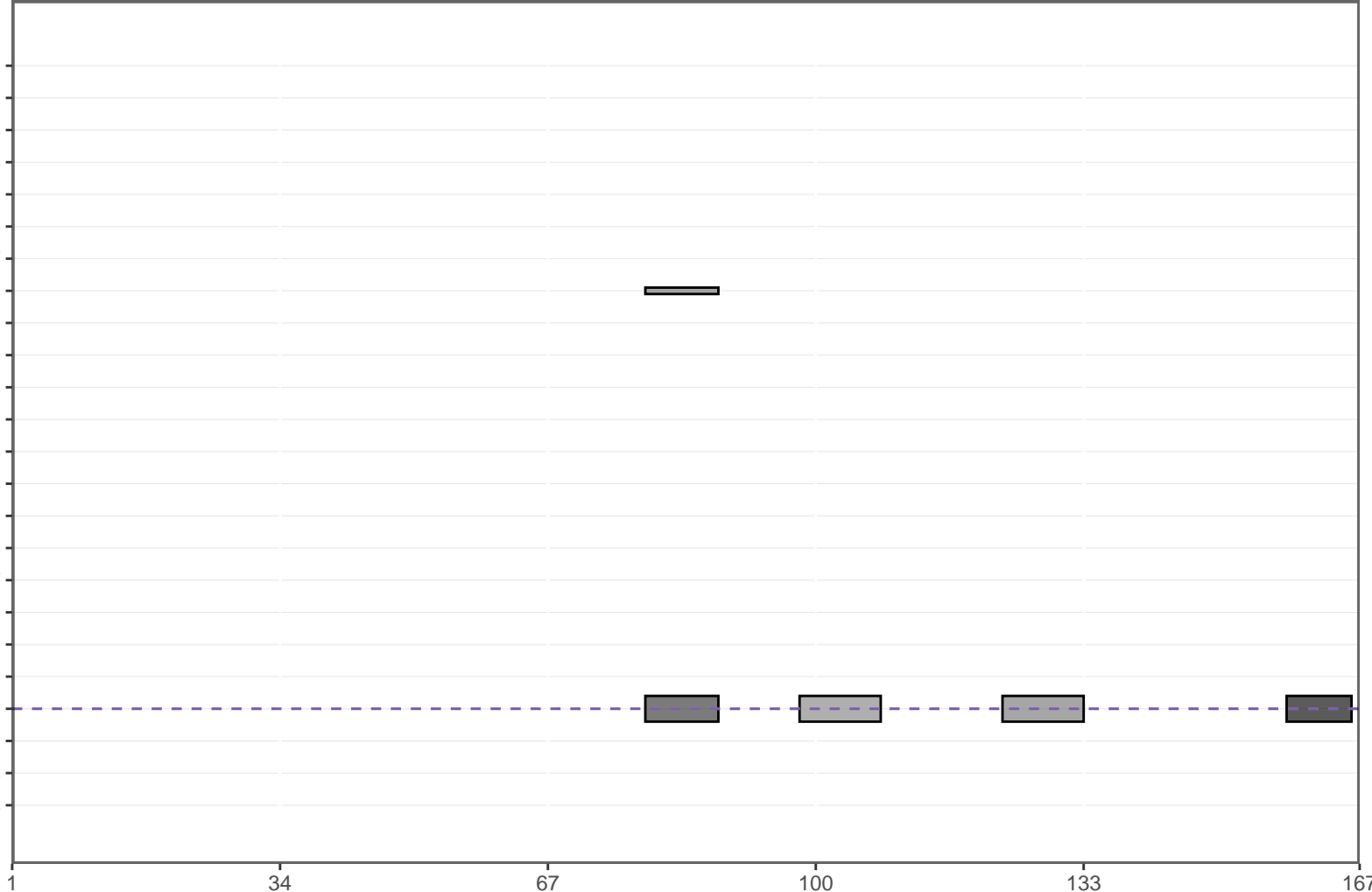
MW indication



Molecular weight

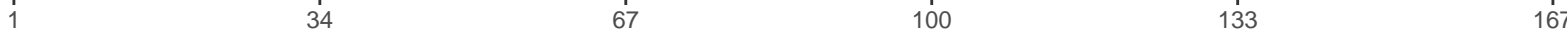


Gel Slice

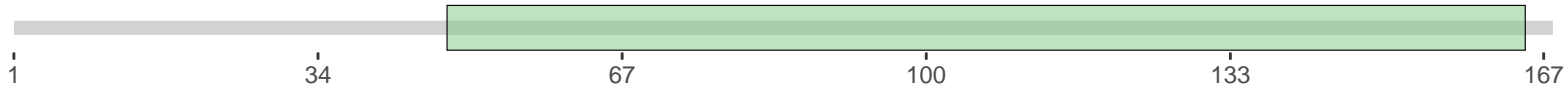


Peptide counts over 4 repeats

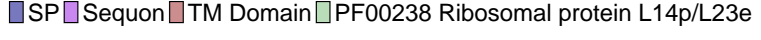
Protein length



Pfam domains



Pfam Description



Protein sequence:

LLKGGKGLRGLDTWQGVKKAQGGKVKKGGVHYGVVRAAMPKRGKGGSEVYKFDNNAVLNKHGEPGTRVFGPVPHELKPKKHVKILSLAEHA*

NbL17g20090.1 (+)-neomenthol_dehydrogenase-like [MW = 33.42 kDa]

No. of times detected



log(intensity)



Values from



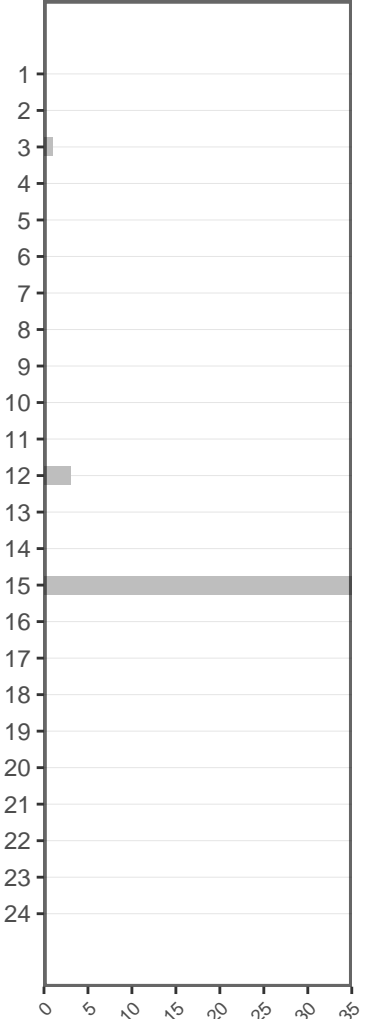
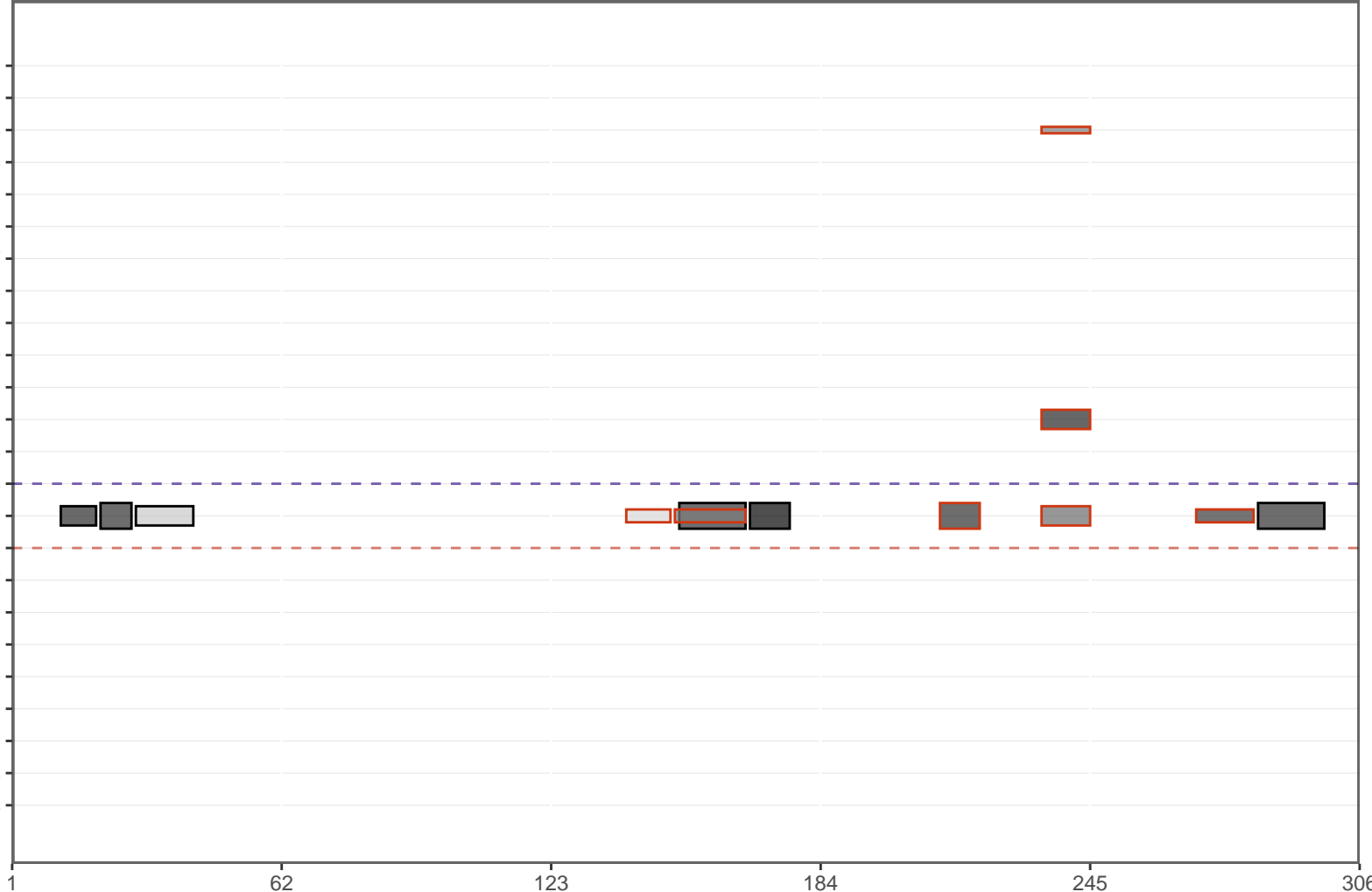
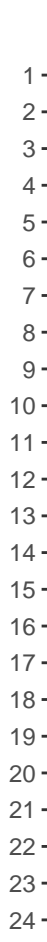
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

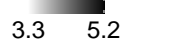
LETNYGVKRMTEAFIRLLQLSINPRINVSSSMGRRLRNKHEWAKGLSDSENLSSEKKEEVAAGYLDKDKEDSLGAKGWPSFLSAYTLKAAVNAVSTIMAKKHPSIQINGVCPGPKYKTMNMYRGLLSIEEGAESFVRLAMQPADGPSGLFFDRKEVSSFE

NbL17g20040.1 bifunctional_protein_Fold_4_chloroplastic-like [MW = 40.12 kDa]

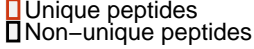
No. of times detected



log(intensity)



Values from



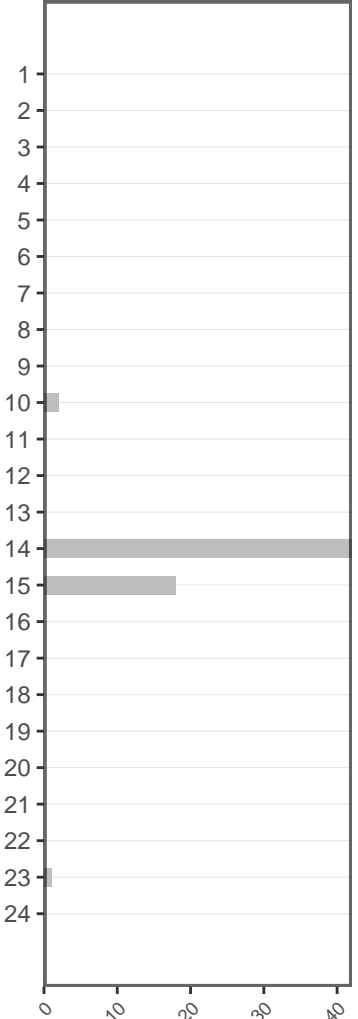
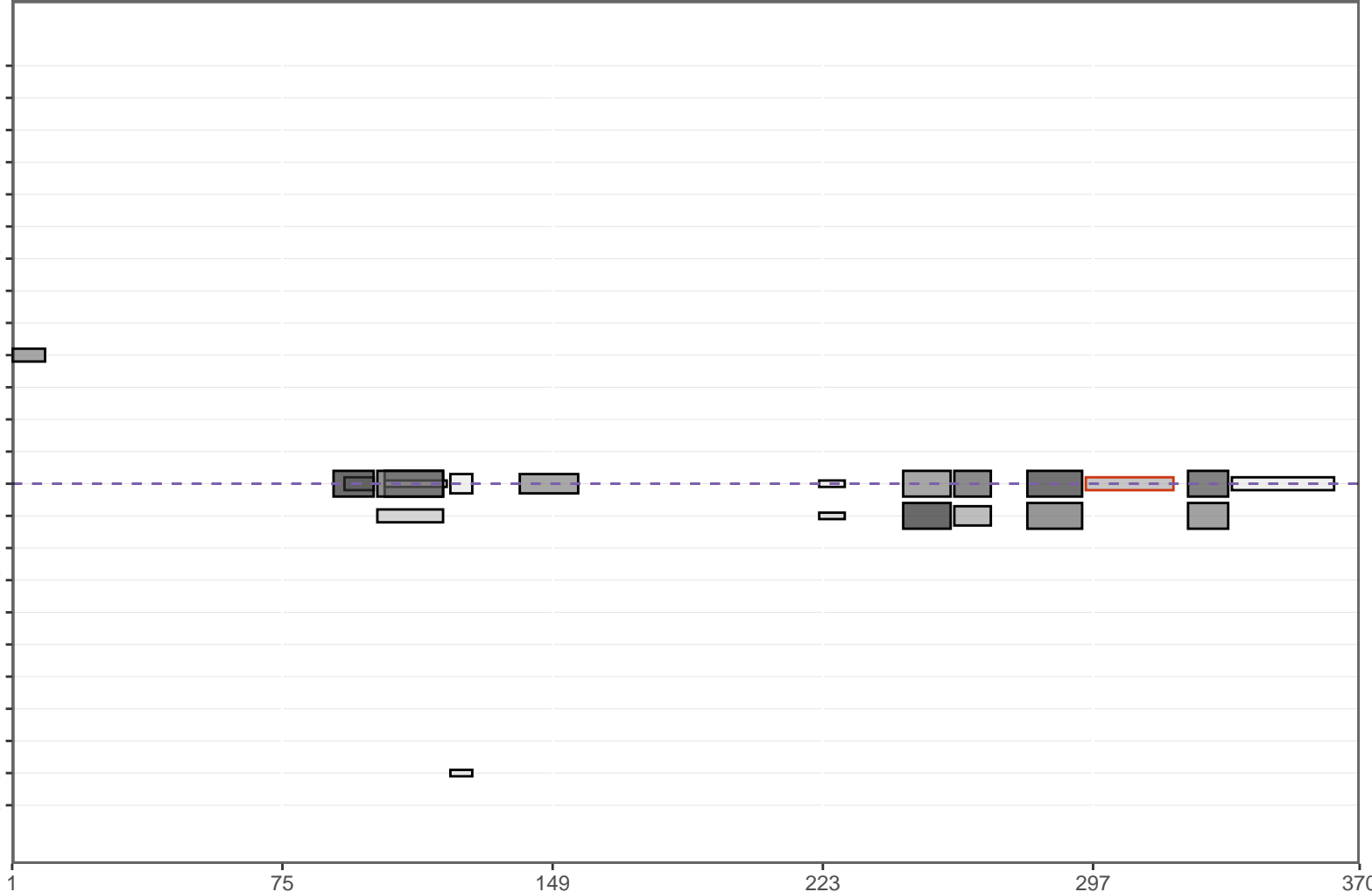
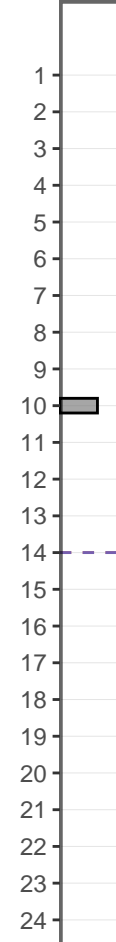
MW indication



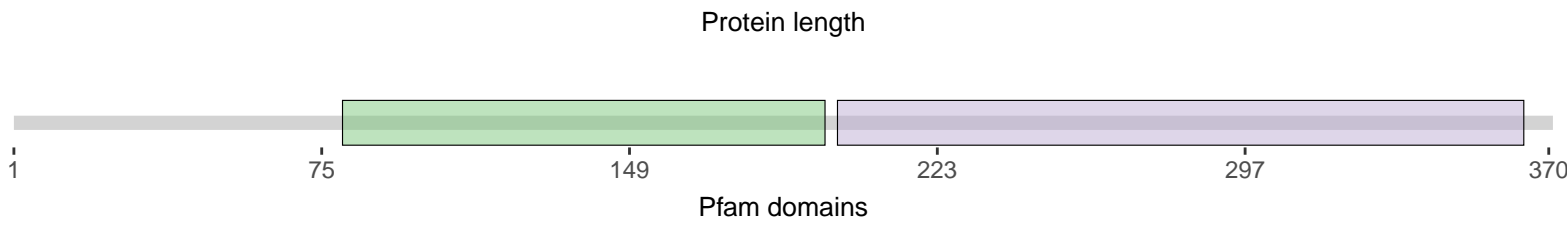
Molecular weight



Gel Slice



Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF00763 Tetrahydrofolate dehydrogenase/cyclohydrolase, catalytic domain
- PF02882 Tetrahydrofolate dehydrogenase/cyclohydrolase, NAD(P)-binding domain

Protein sequence:

.VQLPLPSHMNEQNLNANVGEKVDGDFPLNIGRLAMRGRPELFPVPTKPGDIELHRYNVEIKGRVAIVGRSNVGTPTALLLQREDATVSVHSRTKPEEITRQADHISAVGDPNMMVRGSKWPGAVIWDVGNFVEDATNTRGKRVLVDGVCYEEASKVASATPVPGGVSPTIALLSNTLLSAKRHNFN

NbL17g19770.1 small_nuclear_ribonucleoprotein-associated_protein_B'-like [MW = 33.61 kDa]

No. of times detected



log(intensity)



Values from



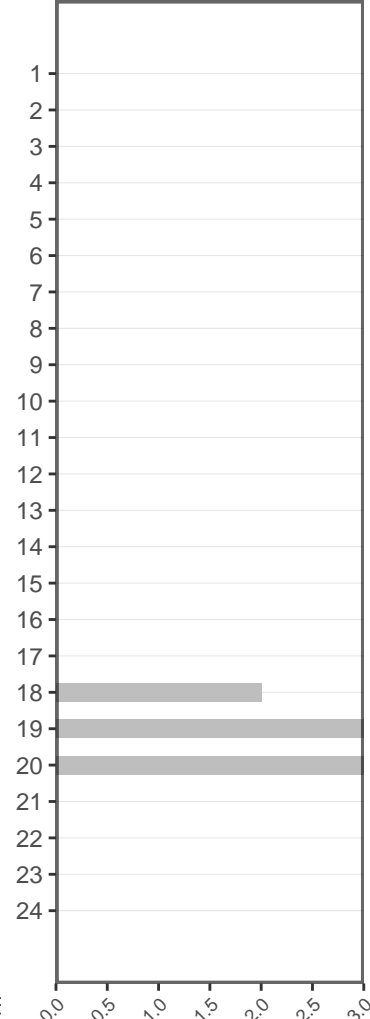
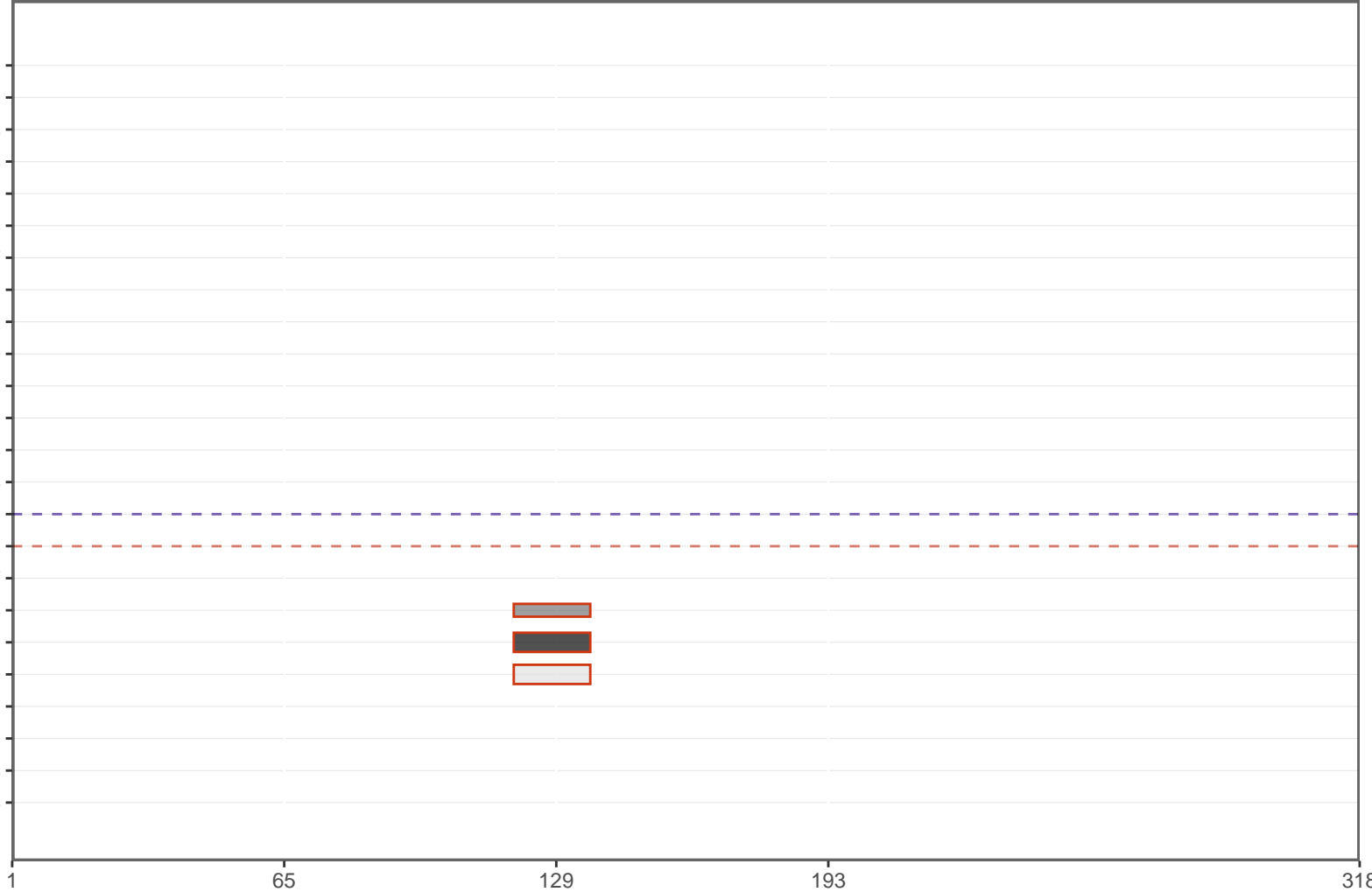
MW indication



Molecular weight



Gel Slice



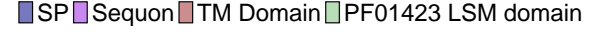
Protein length



Pfam domains



Pfam Description



Protein sequence:

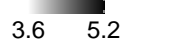
LGRAAGRGVPTGRLVHMQPLAGPVRVGGFAPGMQPGIQRPMNVSAFPMNYPFVMRPFGPPMMQMGQRPGFPPPMAPPQQRPRGGGPPQFPFGGRPMVPPFMMRGPFPFGAPRRPGMPPGPPGPPRRPMPPPPSGGGVPLVGGPRSGMPPPPNGG

NbL17g19510.1 uncharacterized_LOC104224003 [MW = 30.32 kDa]

No. of times detected



log(intensity)



Values from



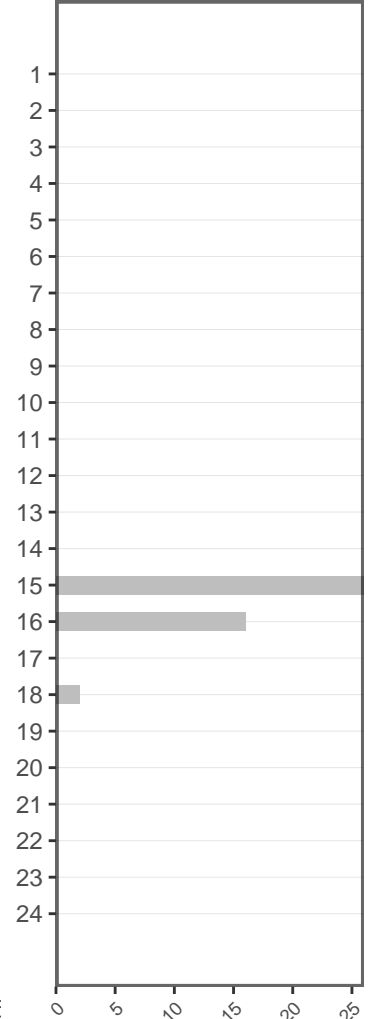
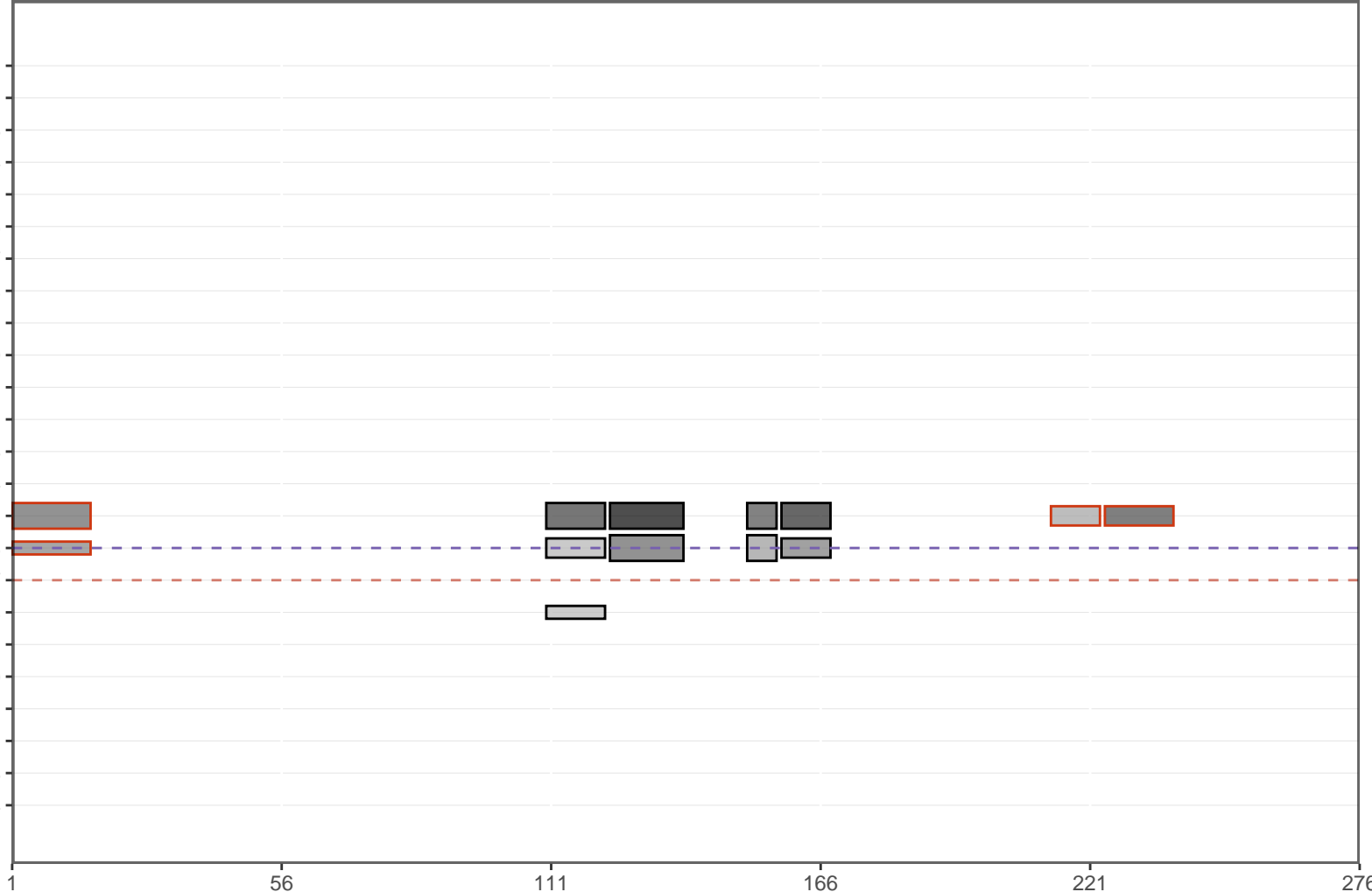
MW indication



Molecular weight

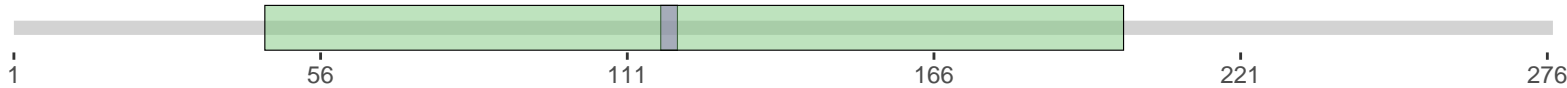


Gel Slice



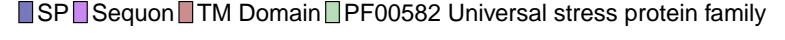
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

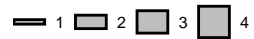


Protein sequence:

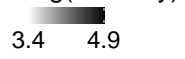
IQLVLDQIPYKHVWHDHMERLGLLEVERLGLBAMVMSGRGFGATKRGNDGRGLGSDVYVHHCACPVVVRYPDEKDGGMARKPVMSMASAKENEETATYHDAADDORGGKLRKNCNCFWVDSVYTNLLVSRKSLHERGKWLQ

NbL17g19330.1 reductase-like [MW = 42.98 kDa]

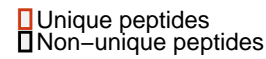
No. of times detected



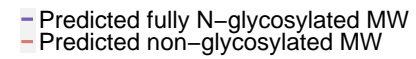
log(intensity)



Values from



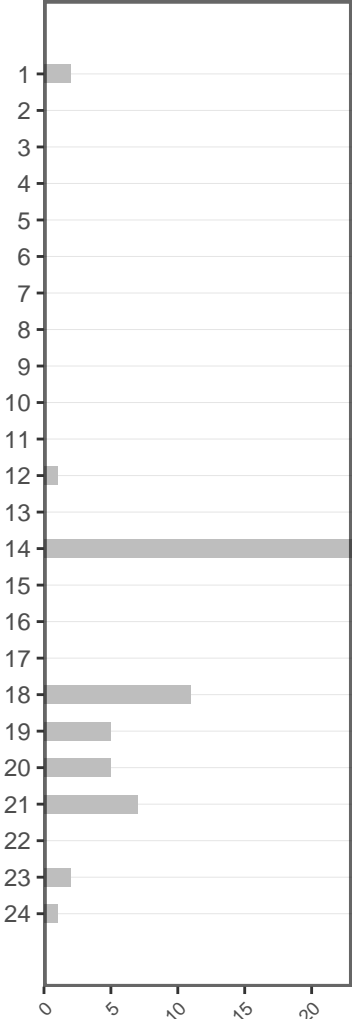
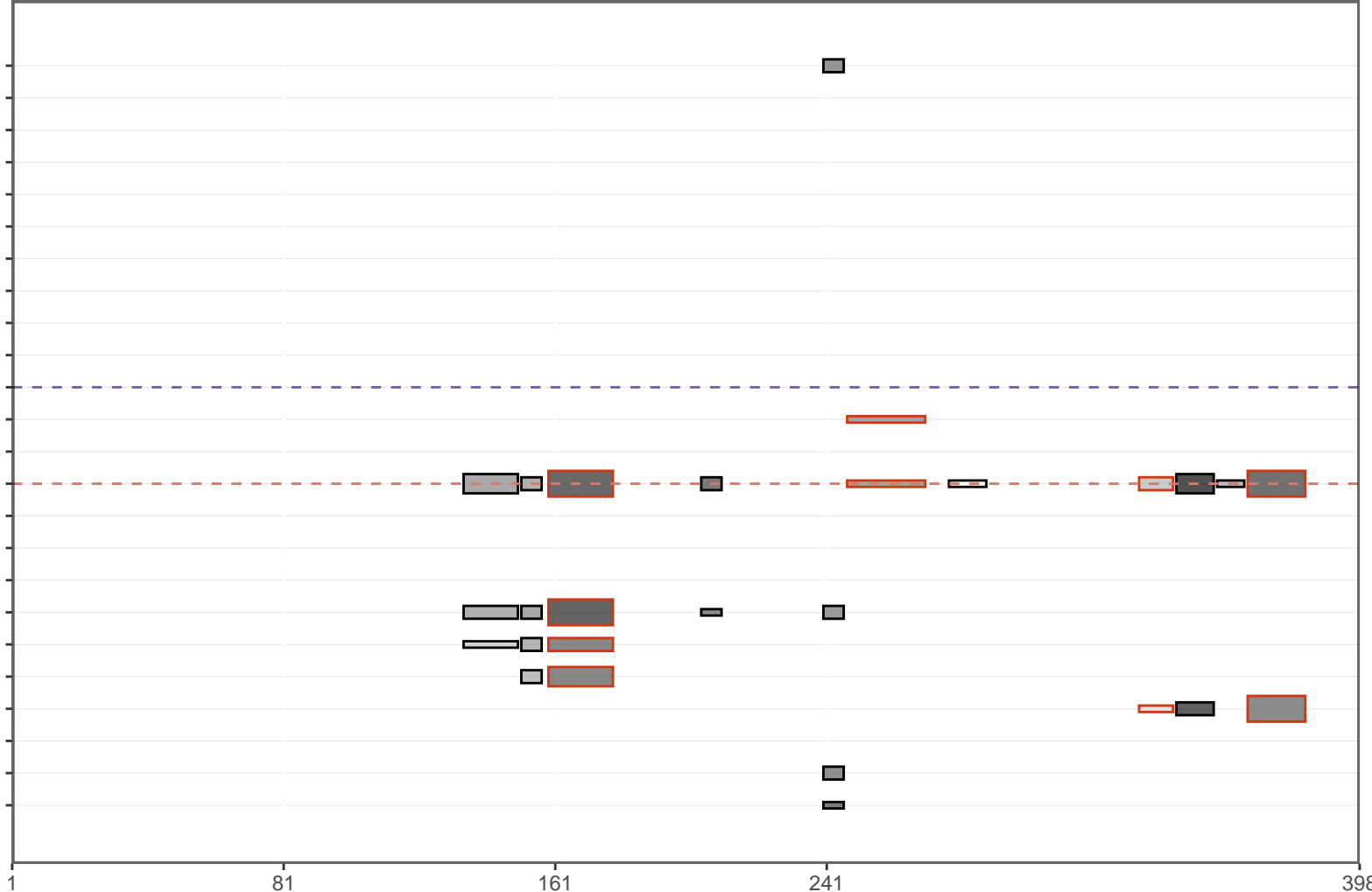
MW indication



Molecular weight

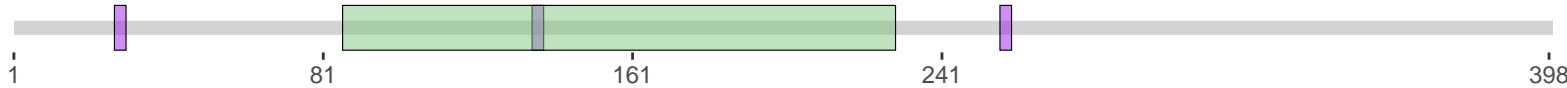


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GFELSVGTNLIKCHFLLEGRLLLEDLKDSDVPPKRLINGSGITNTLGNVFPKANKLGDLRGMAGLNGNSAMDDGGFDGAKAYKDSKVCNMLTMEQHRHRYHEETGTFGASLYPGCIATLGLFRHPLFRLLFFPFQKYTKGFVSETEAGKRLAQVSDPSLTKSGVYVSWNKGSAFENQLEESAEASDVEKARKVWEVSEKLVGLV

NbL17g19280.1 vesicle-fusing_ATPase [MW = 82.27 kDa]

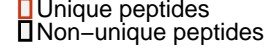
No. of times detected



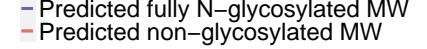
log(intensity)



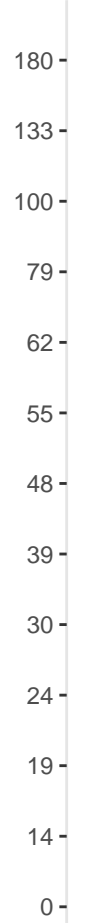
Values from



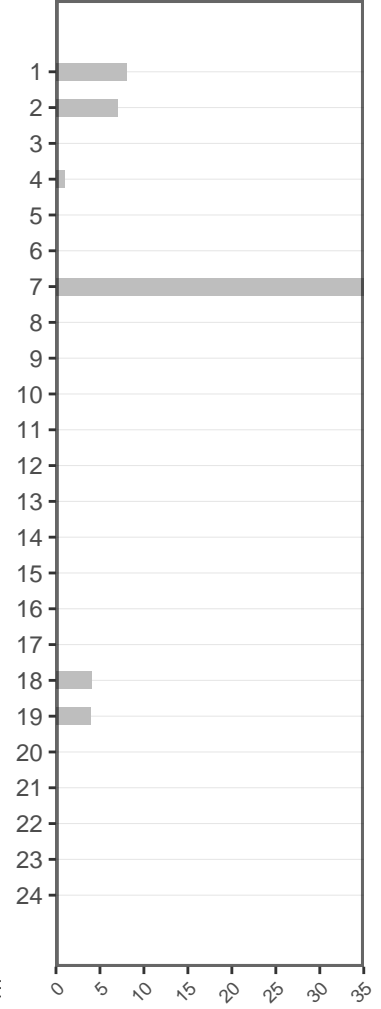
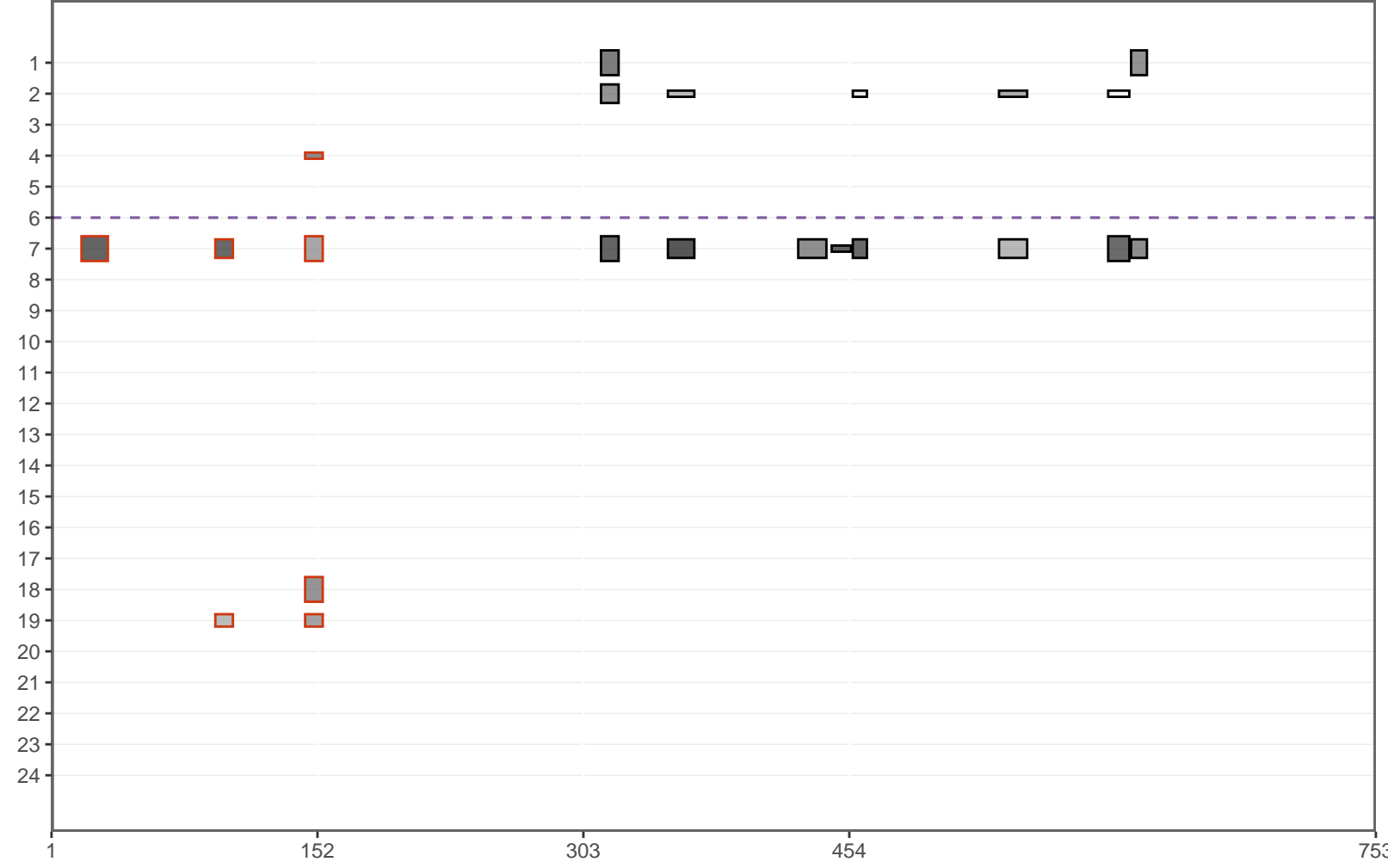
MW indication



Molecular weight



Gel Slice

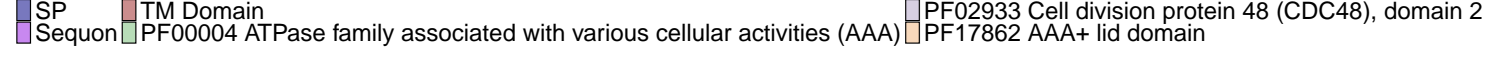


Protein length



Pfam domains

Pfam Description



Protein sequence:

LTIKDGVESLNNVLLIGMTNRKDLLEALMRPRLEVGVEISLPDENRGLGILGHTNOMKENFLSPDNLGEAAARTKHYSGALEGVVKSAVFALNRGLMDLTKPVDEESIKVTMDDFLHALGEVRFAGASTDQLERGLNGIVDGERHQHIVRRTMLLEQVQVVRGSPFLITGLLEGPSGGKTAAMAATVGIESDFPVYKHISAETMGLSESSKAGIVVYFEDAVKSPLEIVLDGIERLLEYVAIGRFRFNLISGTLVLLKRLPRKGLKILVQTTSEAGFLDSVG

NbL17g19230.1 probable_bifunctional_methylthioribulose-1-phosphate_dehydratase/enolase-phosphatase_E1_1 [MW = 58.16 kDa]

No. of times detected



log(intensity)



Values from



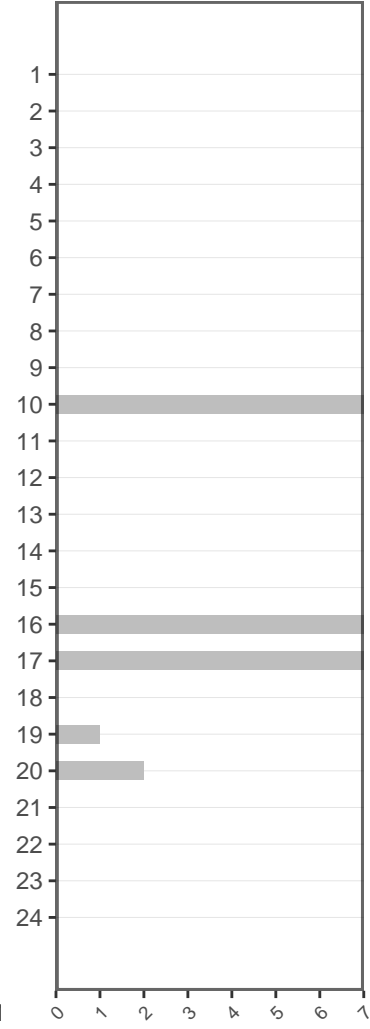
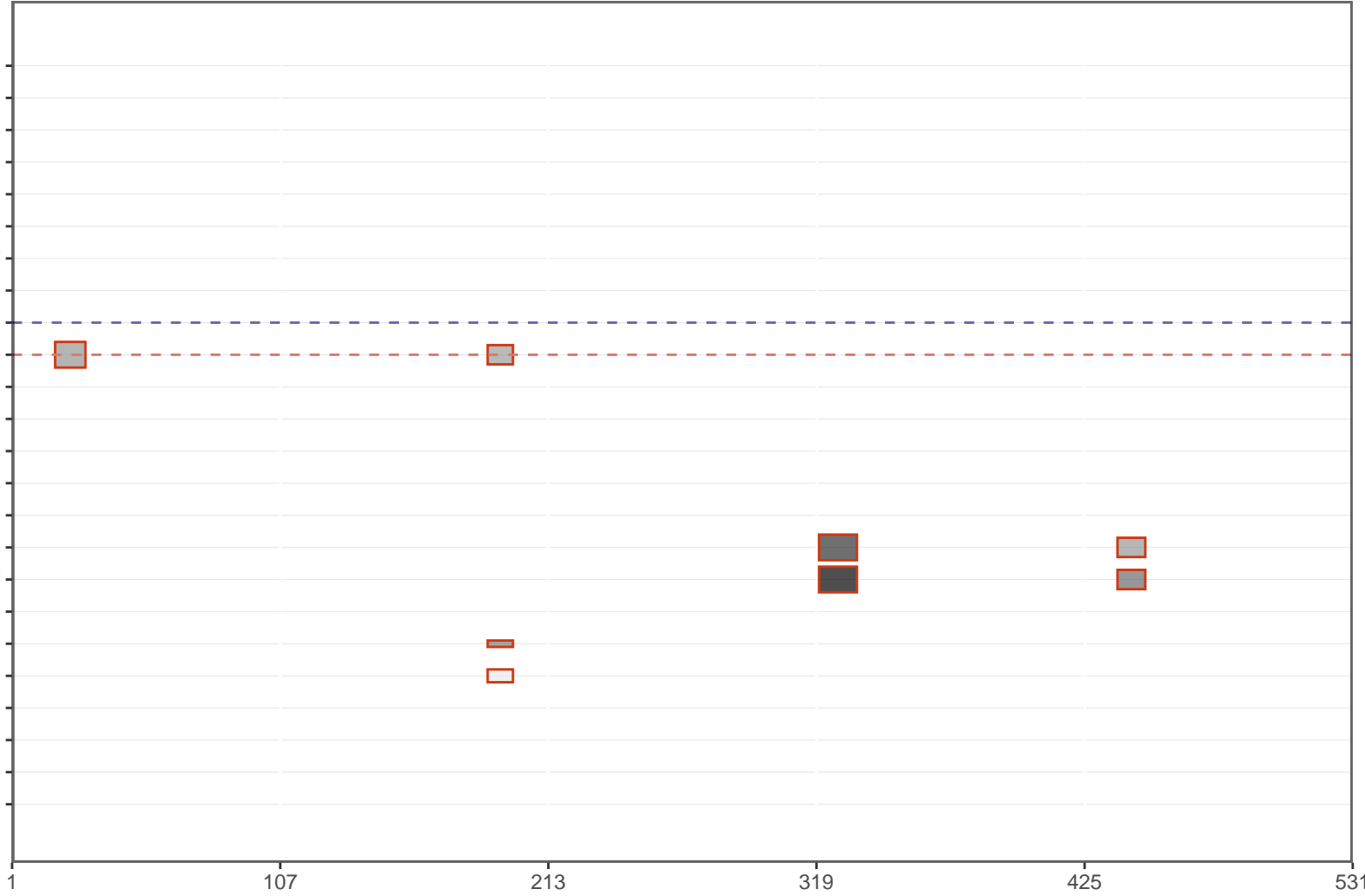
MW indication



Molecular weight



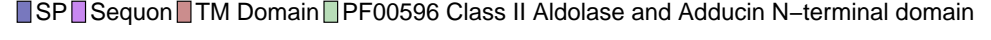
Gel Slice



Protein length

Pfam domains

Pfam Description



Protein sequence:

P*THGPIHNSNGALBITRNKTSAAKAGDLSLNGDNEPLRRGVLDEGTTTFPSFVTDVLPFYAFDNRHLDATYDSEATQEDKLLRAQVQEDLENGVGVAVPIPSDDAGKEEVIAALVTNVEAMKADRKITALKELGHWGTGFQNNLEAVVFDVPEALERWAALGLKVVYSSGSRLLAQLIFGVTNYGDLRKVLOGFFDFTVGNKRETKGKYTEITAGLVNPNSEILFVTDVYGEAAAKAAKLELVISVRPQNGPLPENHGFRITTSFSEI*

NbL17g19220.1 early_nodulin-like_protein_1 [MW = 24.18 kDa]

No. of times detected



log(intensity)



Values from



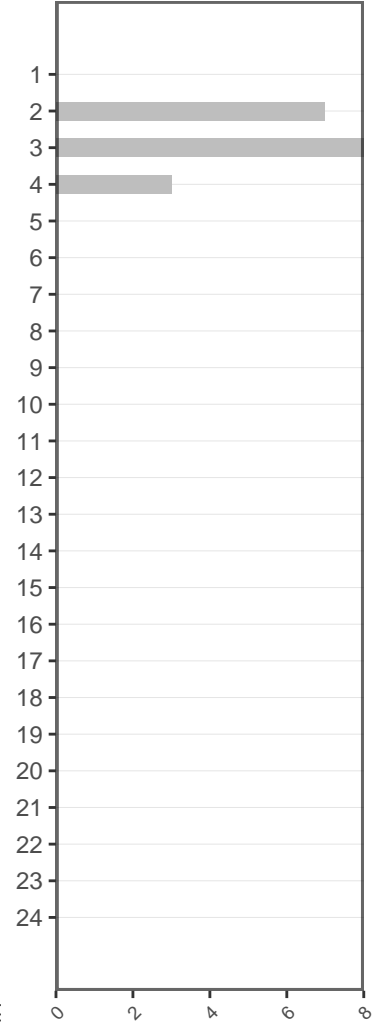
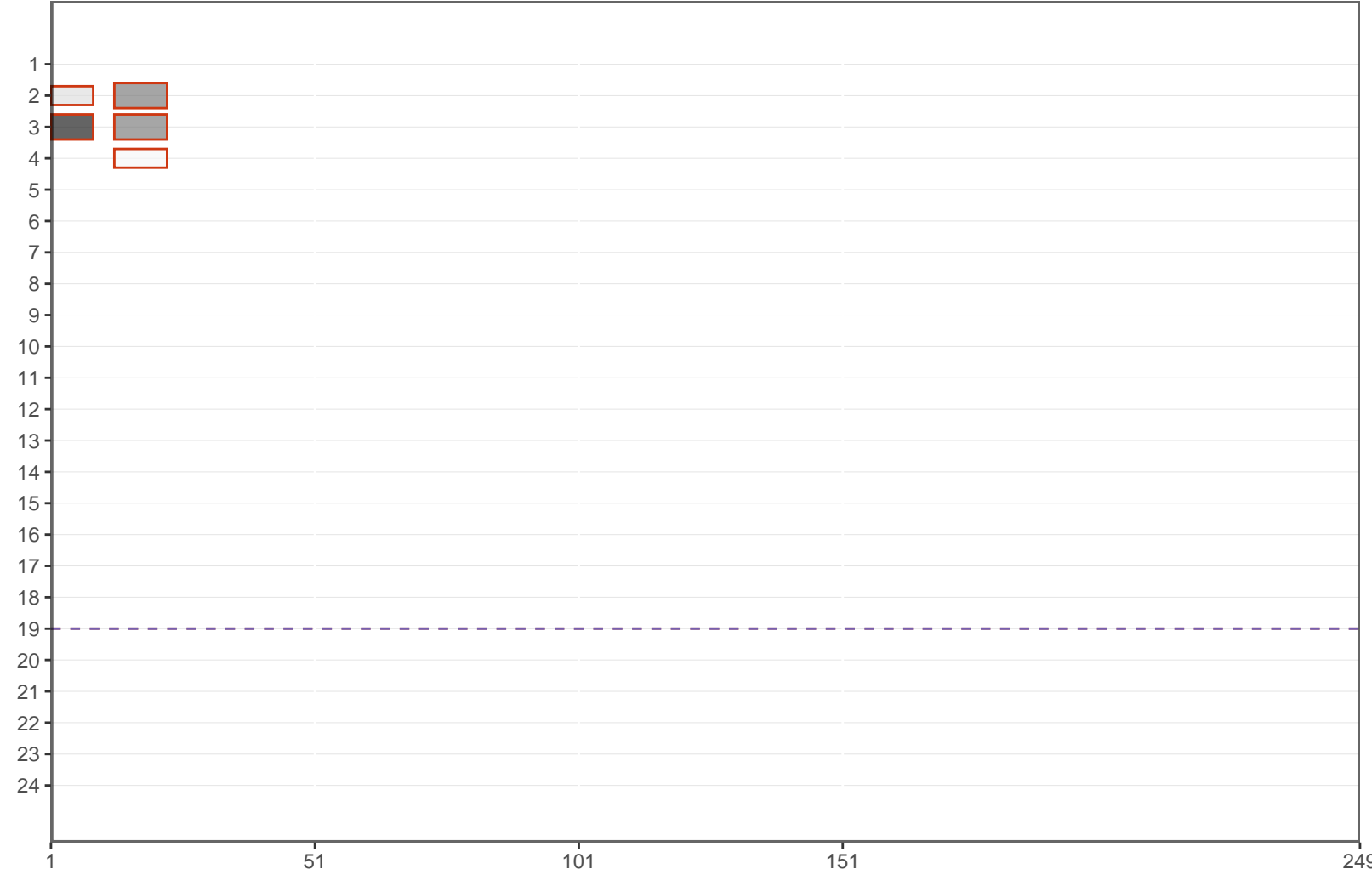
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



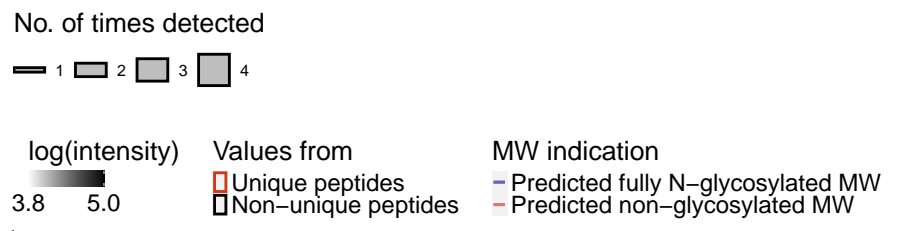
Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

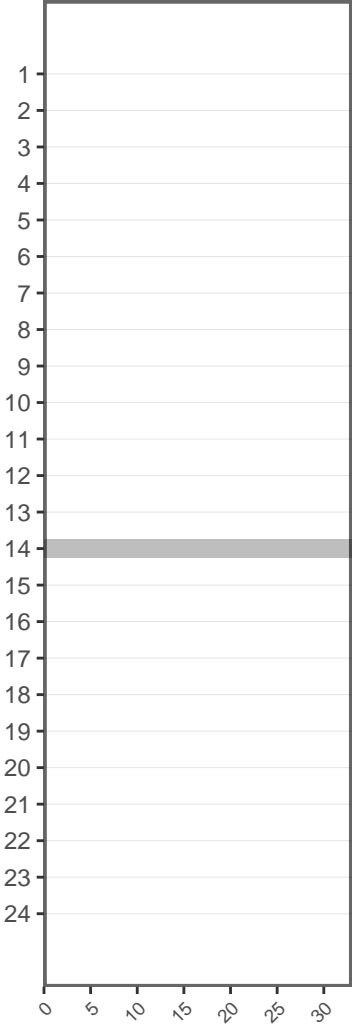
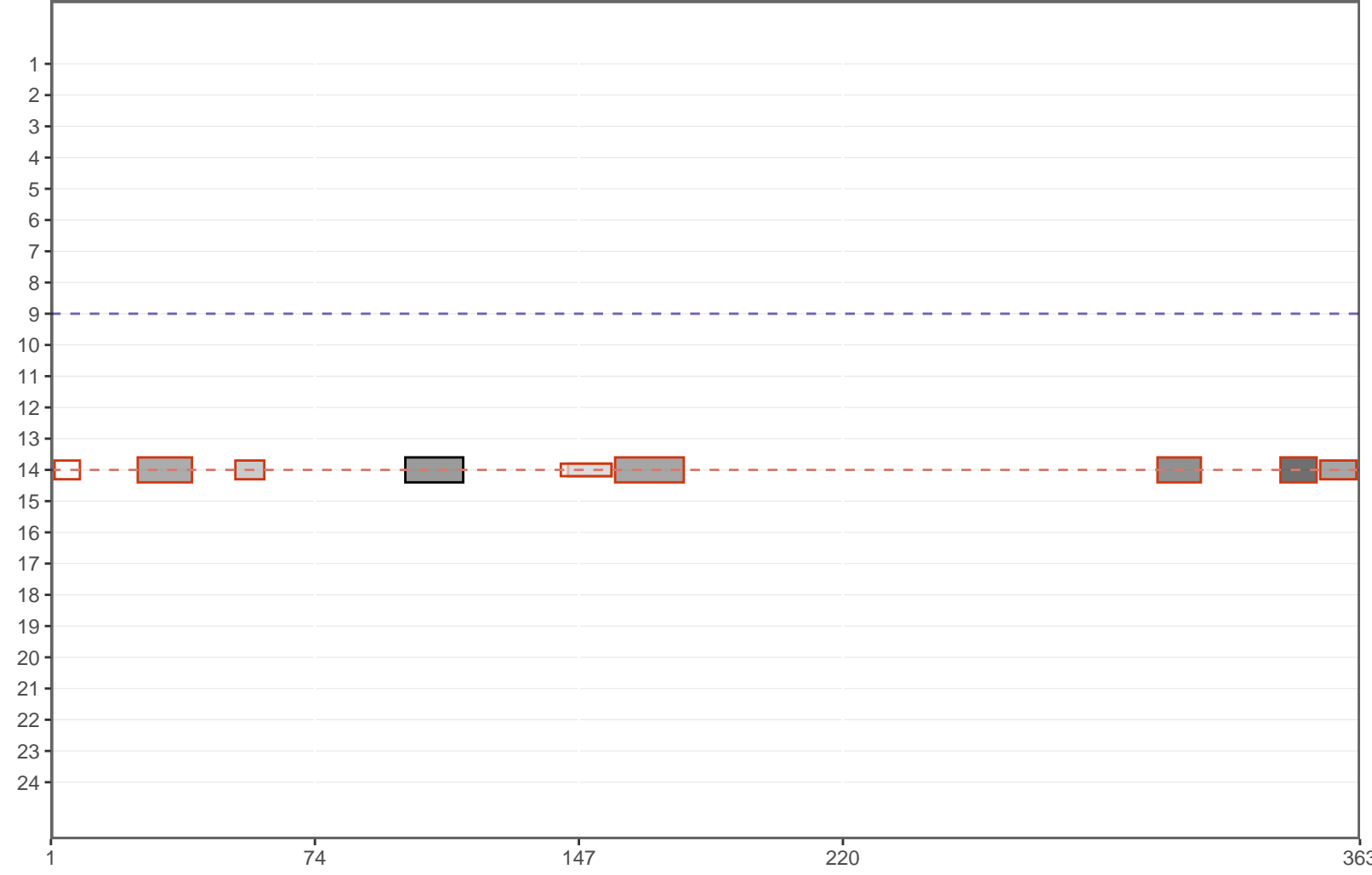
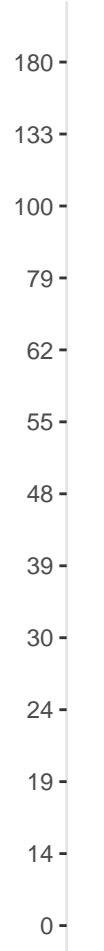
ISPQNAPTPANSPITSPFSTSHAPGINSPTSESPFATSPAPRIEPEGGDITAPSPSSGSSGSSSPTSEPPASGTPESPGKPTTPGSIAPATGGGNSPPVDIGSPTGSSSTNSKNAKAKFTPSAVLMLVLTIFLGGFVFP*

NbL17g19210.1 uncharacterized_oxidoreductase_At4g09670-like [MW = 40.46 kDa]



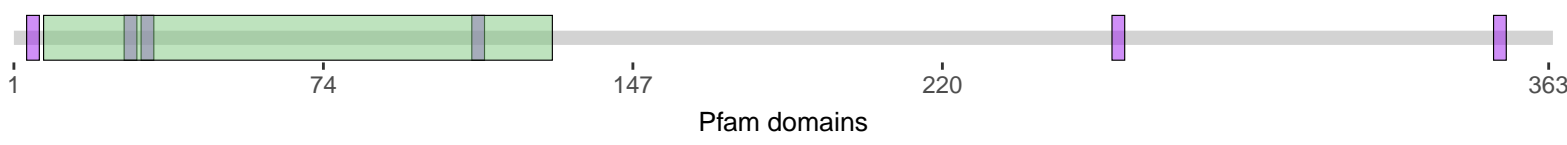
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam Description

- SP
- Sequon
- TM Domain
- PF01408 Oxidoreductase family, NAD-binding Rossmann fold

Protein sequence:

/FLENIRVKPDLDAIGALGGAGWYIGIGAILWAMNGNLPTTVALPTPTVARNISAGVLTGSASLHWKEETVATFVGFVSHETMDLIVYVSGNGTFLVYDFRHPMDENISAFSFTSGAKFVDRHIGWMMKPRAVEVTSKFPQEAEMIGEFGRLLWAEVSRKPKESKWPFHISRVTLQLVLDWANKSIDLGFQDPVH*

NbL17g19090.1 phosphoribulokinase_chloroplastic-like [MW = 45.15 kDa]

No. of times detected



log(intensity)



Values from



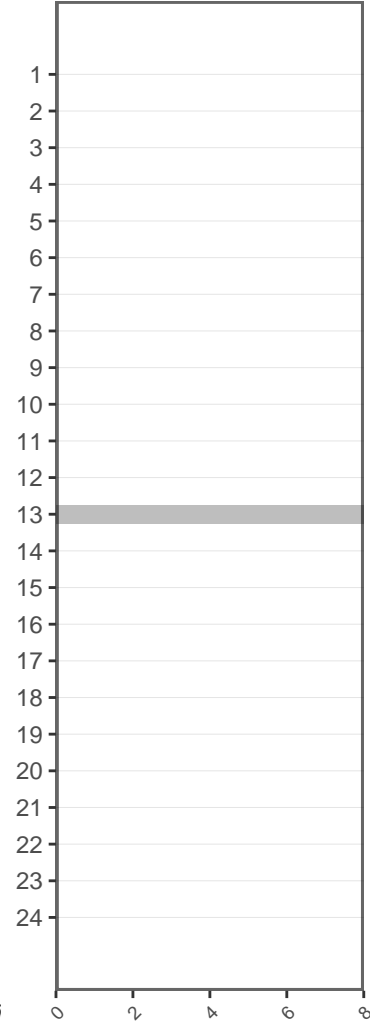
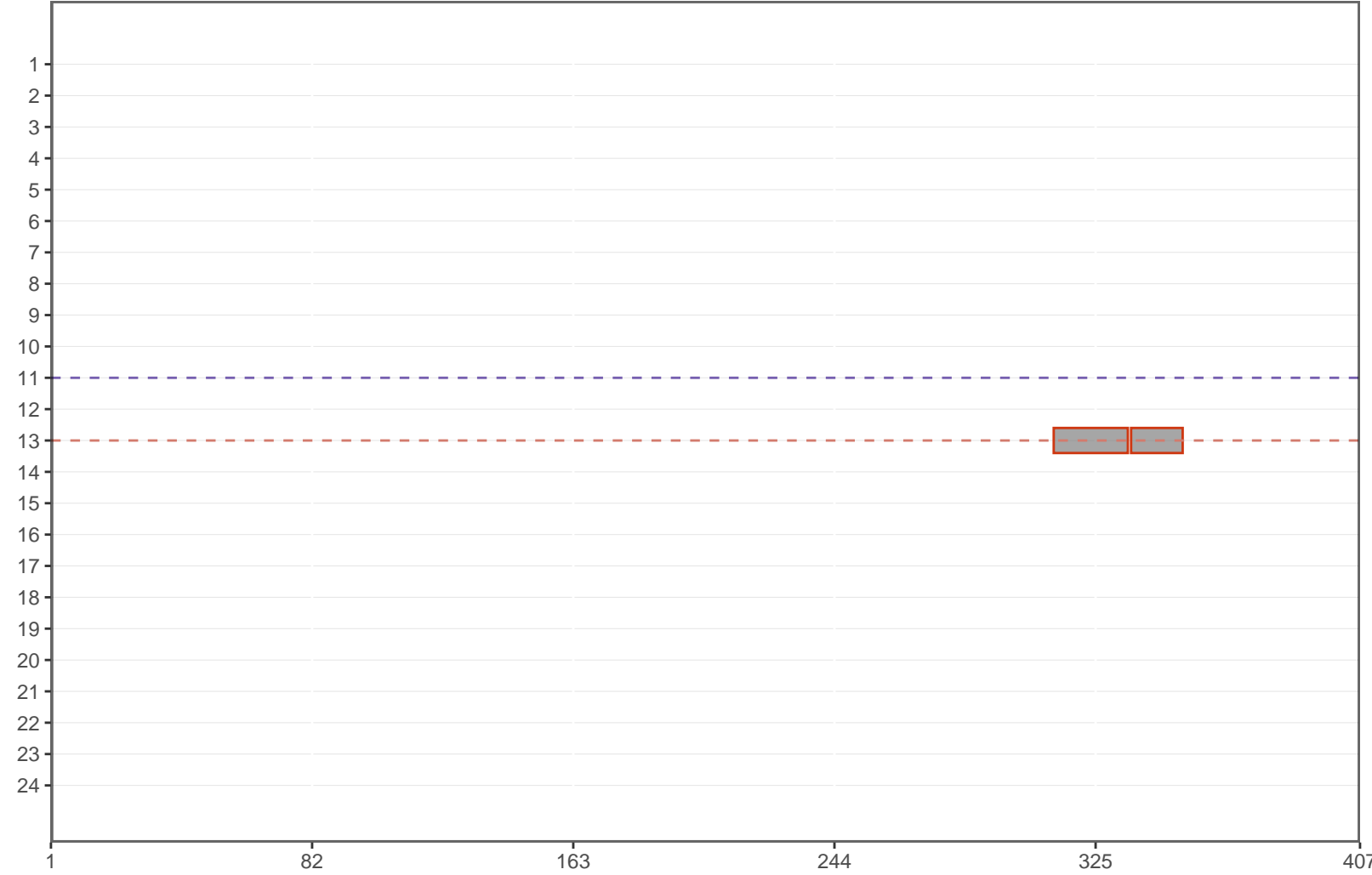
MW indication



Molecular weight

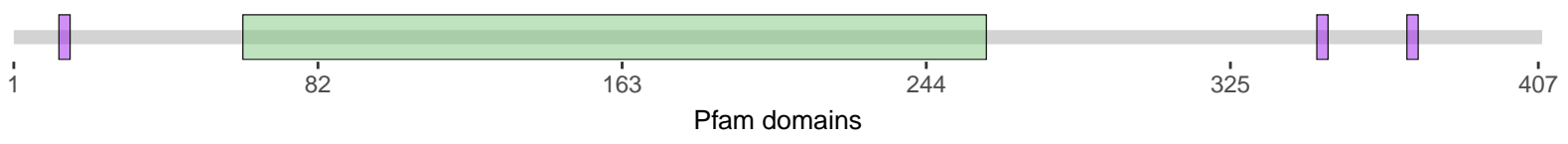


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam Description



Protein sequence:

RELLDFSYLDISNEVFAWQGRDMERGHSLSEKAEARKPQDFDAVIDPQKGVADAVIEVLPQIPDNEKGVLRVRLMKEGVNNFNPVYLFDEGGTISWIPGRNLTGSPKGFYFGDGYFGNEVSEVLEMGGQDFDRDLDELIVYVESHLSNLSKFKYGEVTDGOMLKHADFFQSNKGTGFFDTVGLKIRDLVEGIWASRAAAPVQAQA*

NbL17g18810.1 tocopherol_O-methyltransferase_chloroplastic [MW = 41.53 kDa]

No. of times detected



log(intensity)



Values from



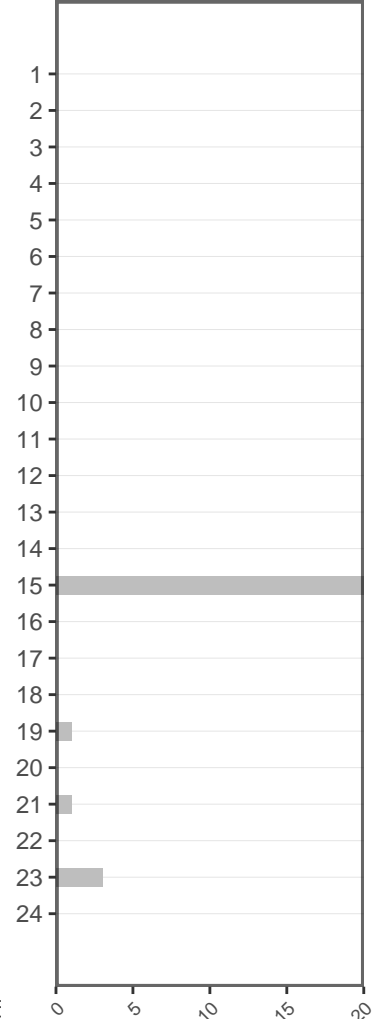
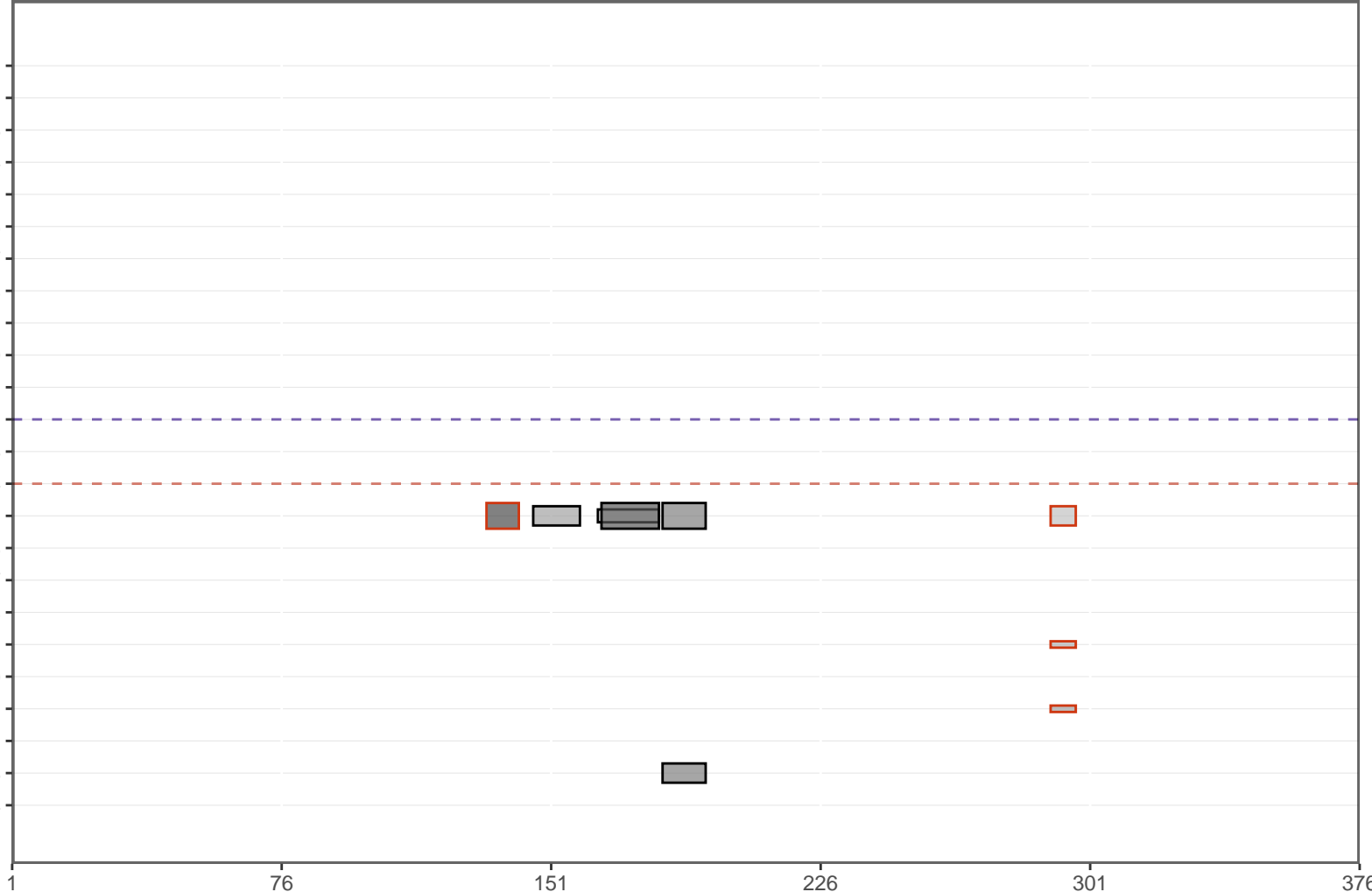
MW indication



Molecular weight



Gel Slice

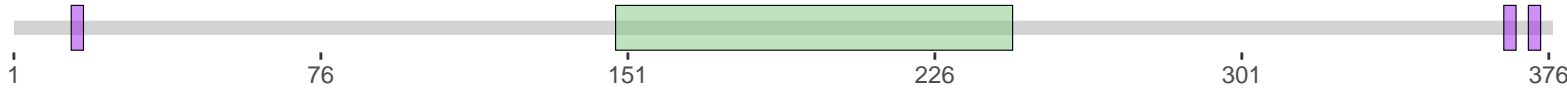


Peptide counts over 4 repeats

Protein length



Pfam domains



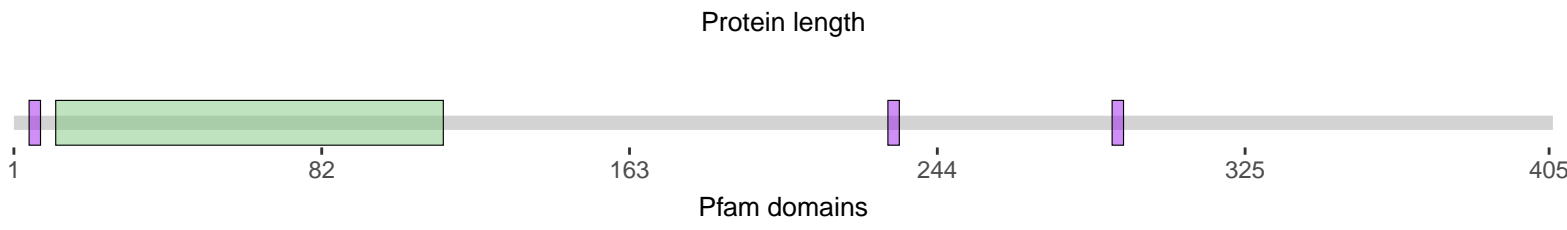
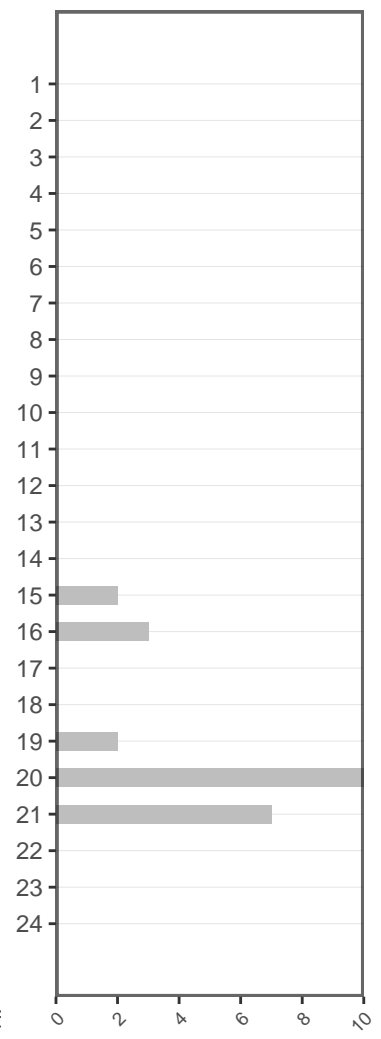
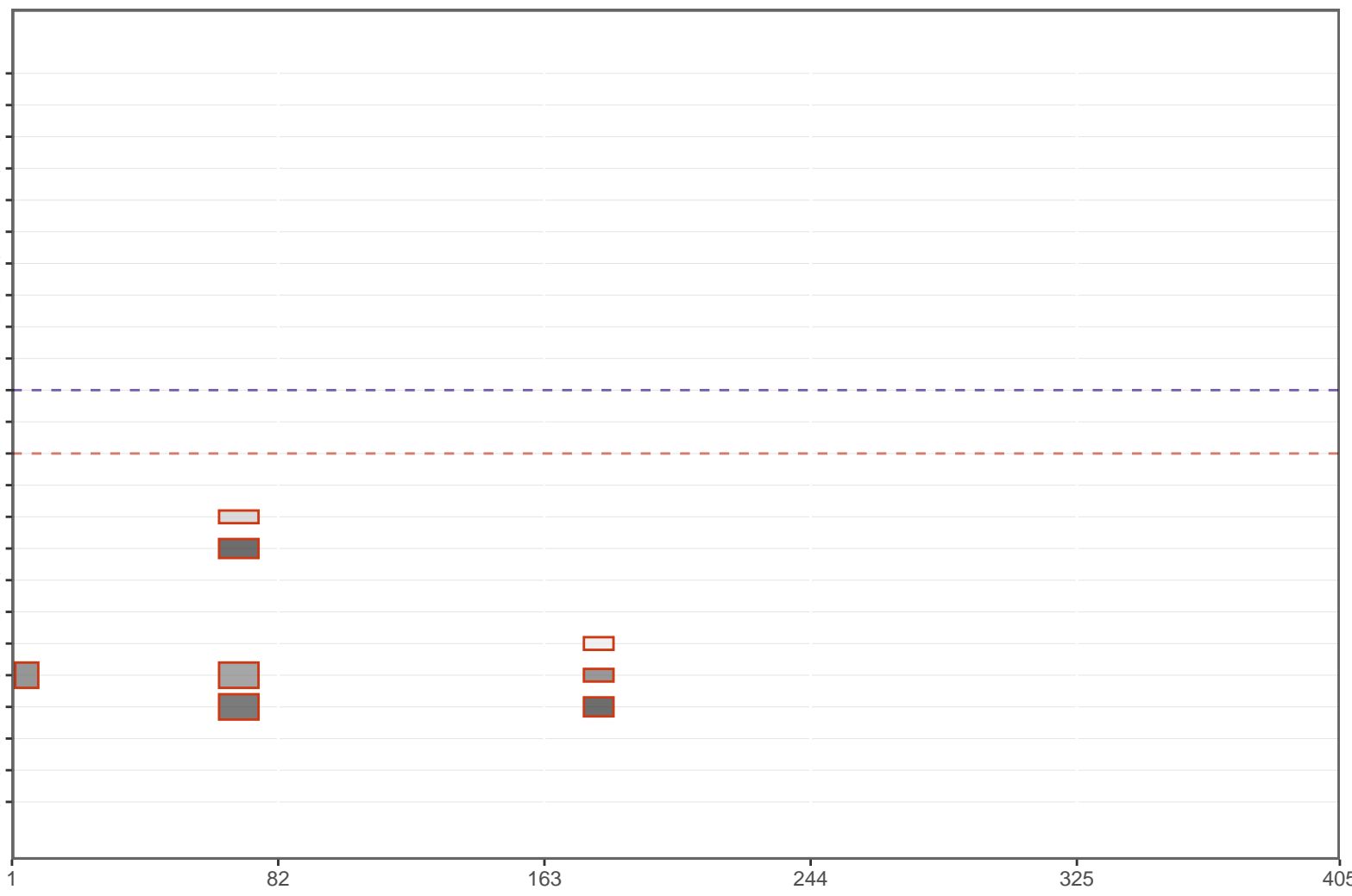
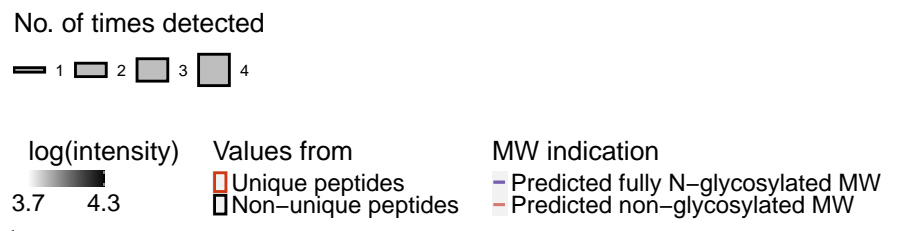
Pfam Description



Protein sequence:

IPVQAEARQAALAAADGLGDKAFQVADALNGPFPDGGDFLWVSMESGEHMPDKGKFLVGLARVAAPGDTLVTWCHRDLSPLEESLLFEENELLKIKGKSYLFAWGGSTADYMKLLGNSLRDKAAADWSENAPFVFWIKSALTWKGFSTLIRSGELCCAKIDVLLGHFGTFFGIDSSHYLRMEDNNGSGTGNATDD

NbL17g18710.1 probable_ADP-ribosylation_factor_GTPase-activating_protein_AGD8 [MW = 43.71 kDa]



Pfam Description

- SP
- Sequon
- TM Domain
- PF01412 Putative GTPase activating protein for Arf

Protein sequence:

YVAKKAGKSGGLGARKLTKKPKPEELYEKPEEPPHQISSSTANATTVGSSEFTSRFEYTDNIGPAETSFQGGPRVLAHVAAPKSSNFADYETDNGFTTKTKTNSNSKIQEETEDARKKFNNAKSSISADYFGDQSKTEMEASVSLQKFGSSAISEADLFGDDGGAFFDTAGELNRLSFGAQQDISEKNIAGETGKLTSLASTLMSLGDRIIP

NbL17g18440.1 phosphoglucomutase_cytoplasmic [MW = 63.29 kDa]

No. of times detected



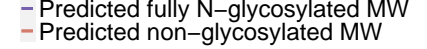
log(intensity)



Values from



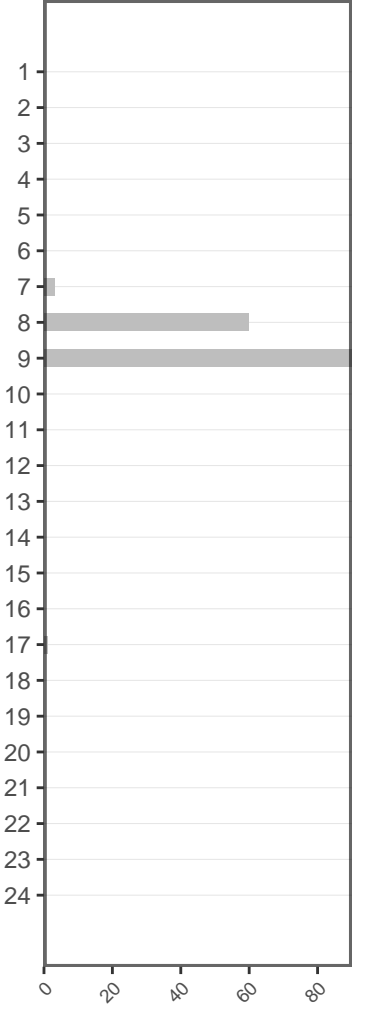
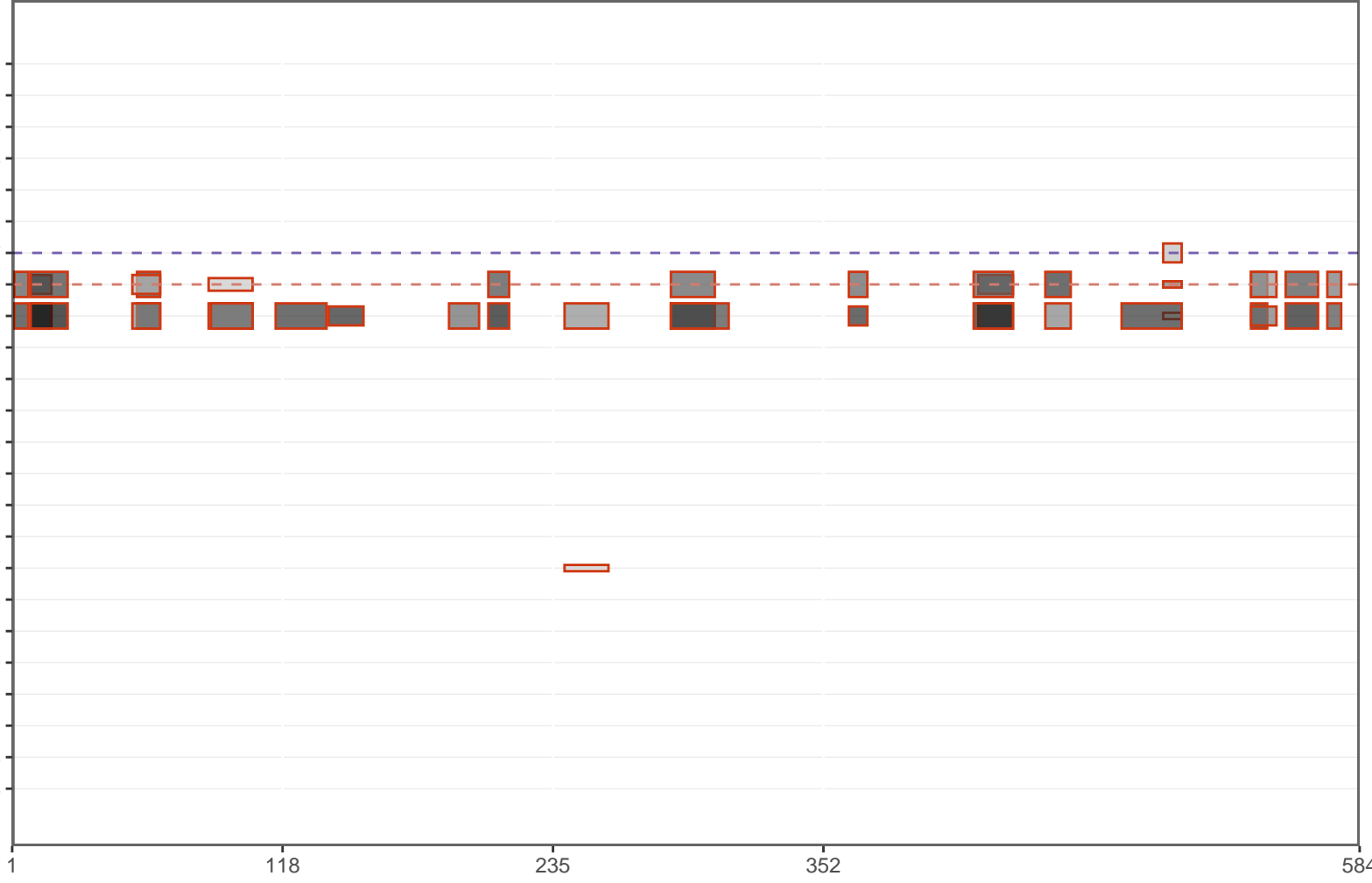
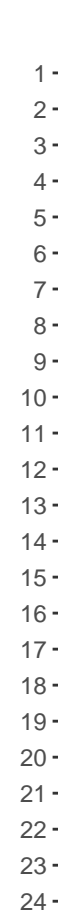
MW indication



Molecular weight

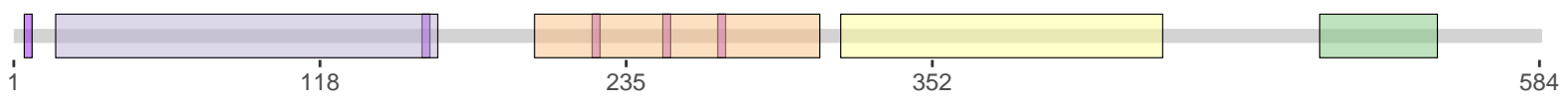


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

PF02878 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain I PF02880 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain II
 Phosphoglucomutase/phosphomannomutase, C-terminal domain PF02879 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain II

Protein sequence:

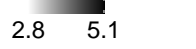
IMQLSKTHPEPNPPEFGAAGDGGDRNMLGKRFFVTPSDVAIAANVAEIPYFGGLKGVARSMPTSAALDVVAKHLNKKFVEVPTGKWFFGNLMQMGKSGCGEEFSFGTGDSDHIREKDGAWLAWLWLSILAVYKDKNLGGNLTVEDIVRQHWATYGRNYYTRVDYENVDAGAAKELMAHLVKGSSLDENVNKKIIGHSDVSVVVAHDEFYKDPVDDGSEKHOGIRVLFEDGGRLVFRILGDTGEGATIRLYIEQYKEDSKIGRDSGAEALPLVLEIALKLSKMOEY

NbL17g18180.1 villin-4-like [MW = 109.1 kDa]

No. of times detected



log(intensity)



Values from

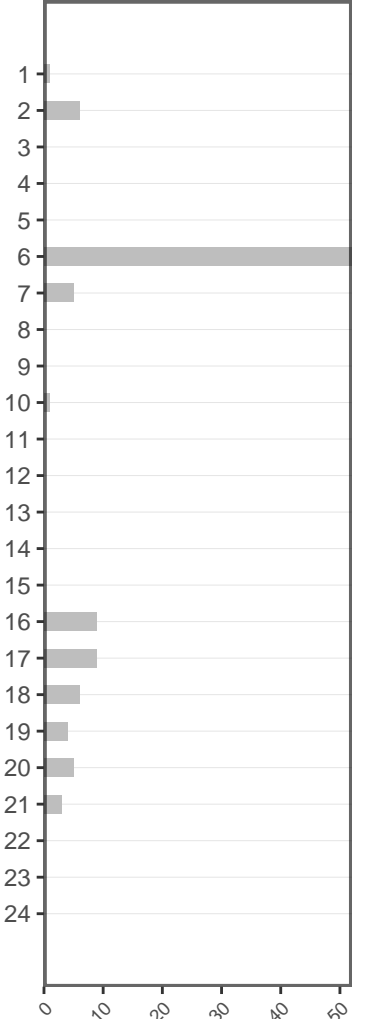
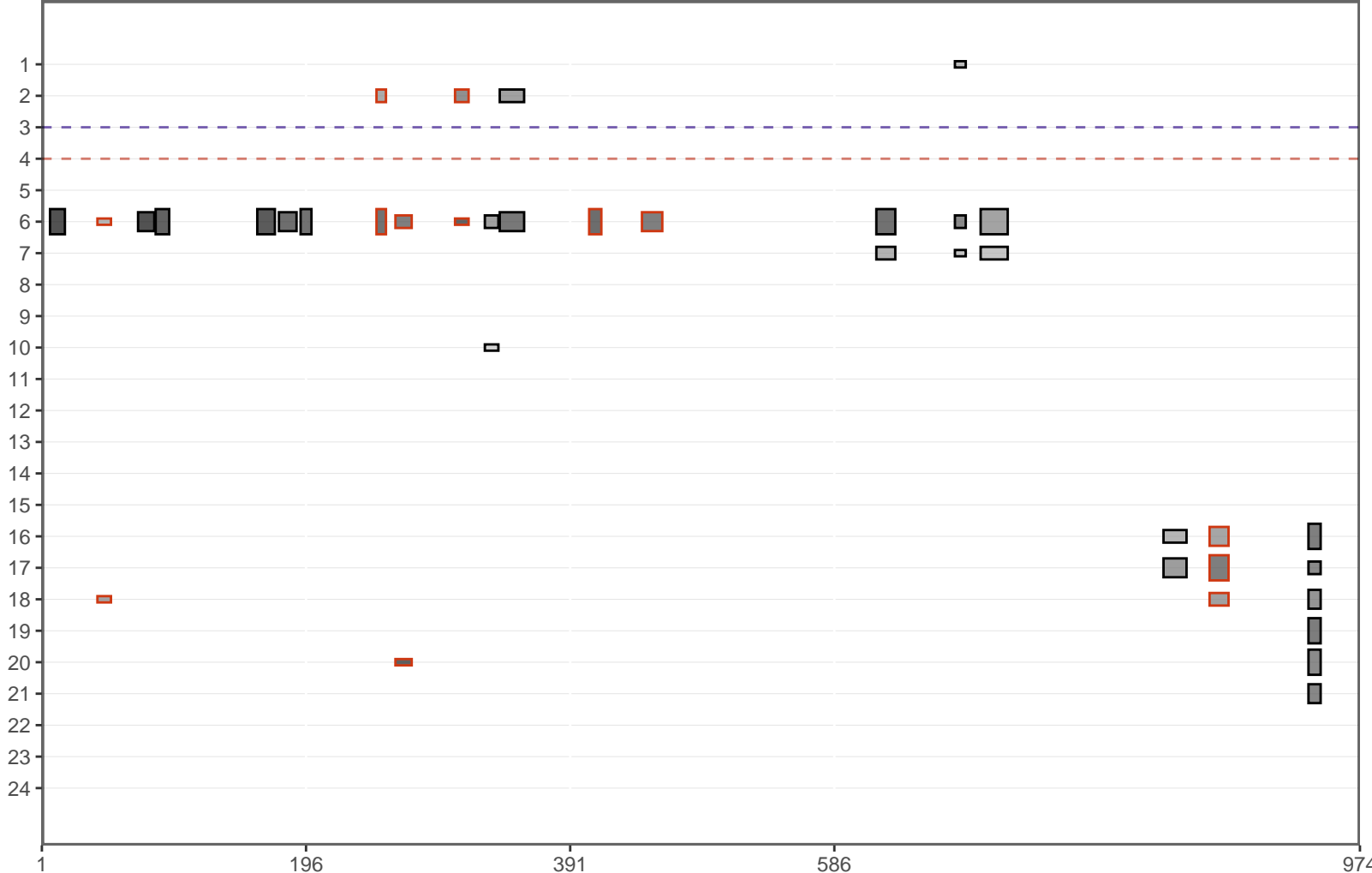
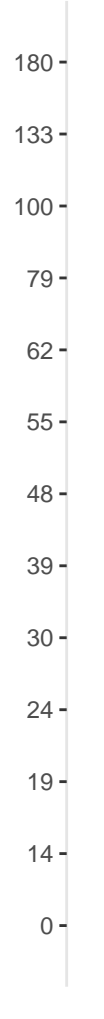


MW indication



Molecular weight

Gel Slice



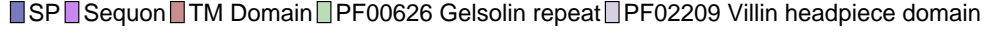
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

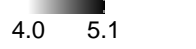
RVEYGEPLQFFVIFQGFVFRGDLSEGKHKRVEEELADDTYKEDGIALFRIGGTGPDNMQSGVEPVASLNSGSDYIHLHGSSVFTVTGSLTTSDEQDLVERQLDLKRPDMGSLKQEGAESEGFWEELGGKSEYPSKIGRDAE6DPHLF6CTFRKGDLYKTEYFNFGDGLMTEDFILDGHSDIYVWQDLVEYKNNKMAALSGKFLGDFLMEKLSHQAPHYVMEGSEPFPPFTRHFSWDSKSAAMHGNISFRKLTWVNGGPPPMKPKRRIPVSYGGRSAPE

NbL17g18130.1 thioredoxin-like_protein_Clot [MW = 18.85 kDa]

No. of times detected



log(intensity)



Values from



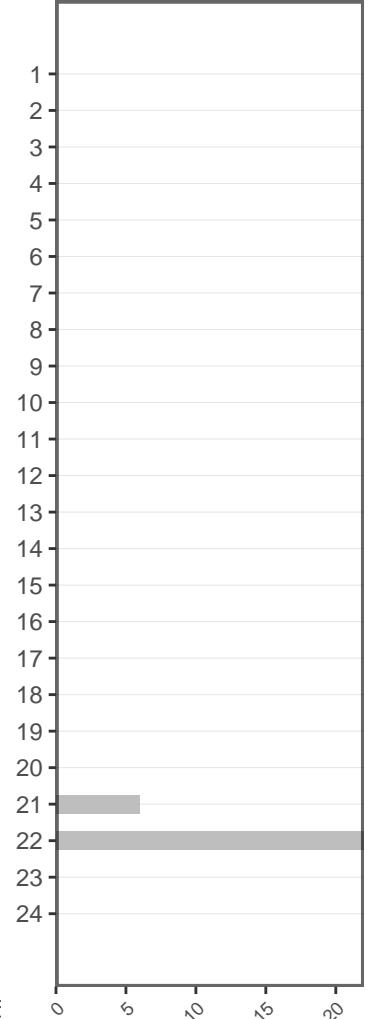
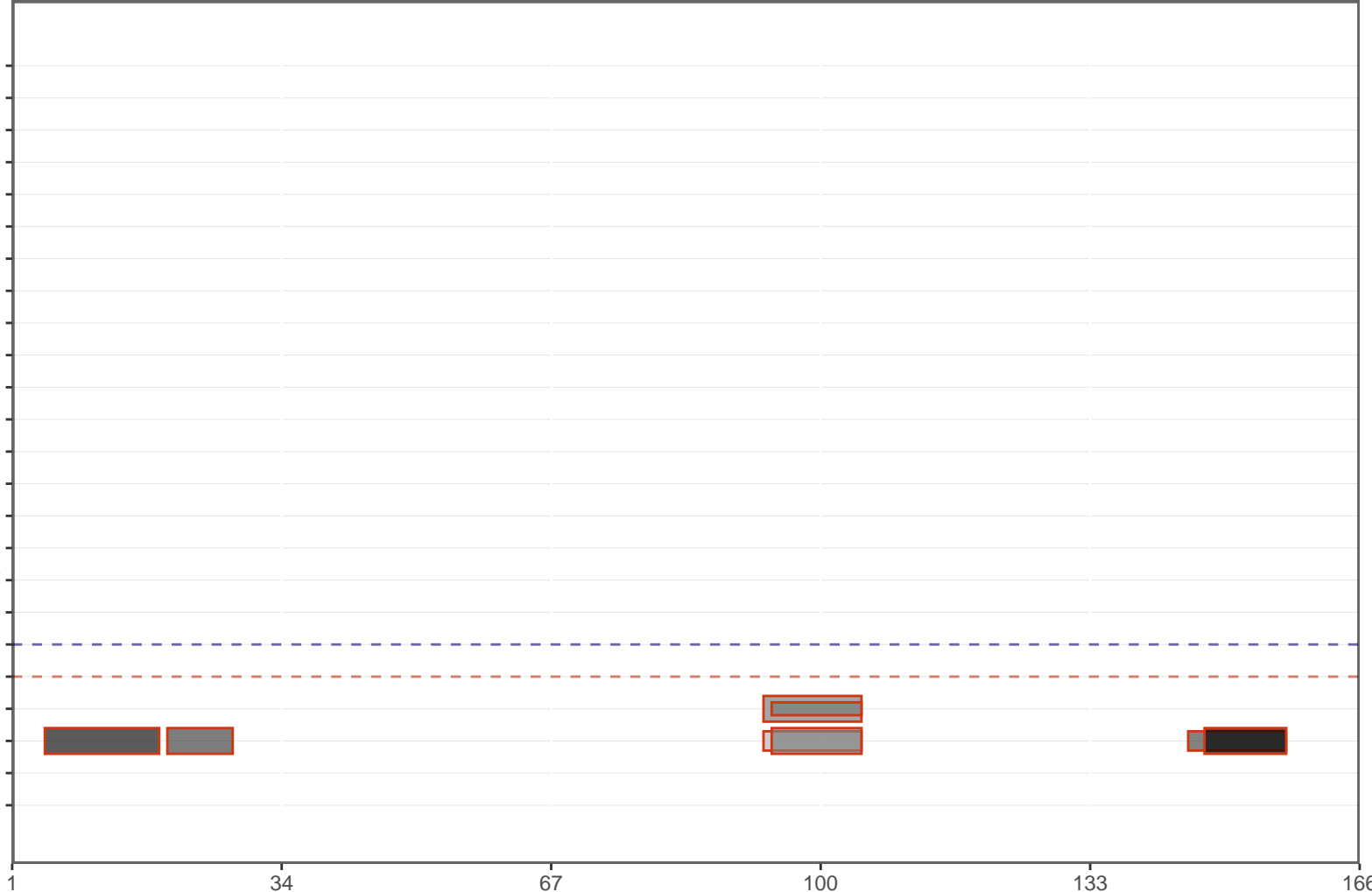
MW indication



Molecular weight

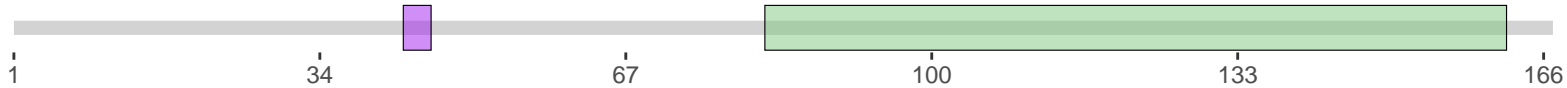


Gel Slice



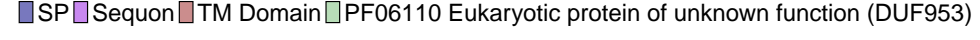
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LHLLQASRNTDCVRAEPVYKMKMEESAEEDALLRAYGDRPTWRTPQHPWRVDFRFLKGVPTLIRWENDATKGRLEDESAHLAKHIDSLIGN

NbL17g18120.1 30S_ribosomal_protein_2_chloroplastic-like [MW = 27.7 kDa]

No. of times detected



log(intensity)



Values from



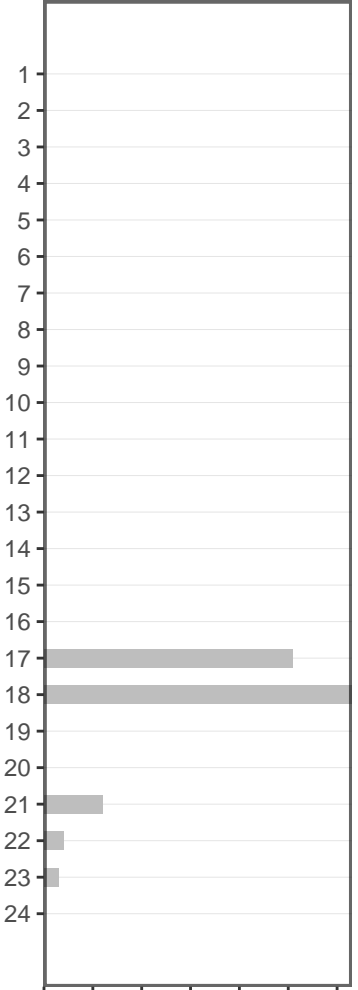
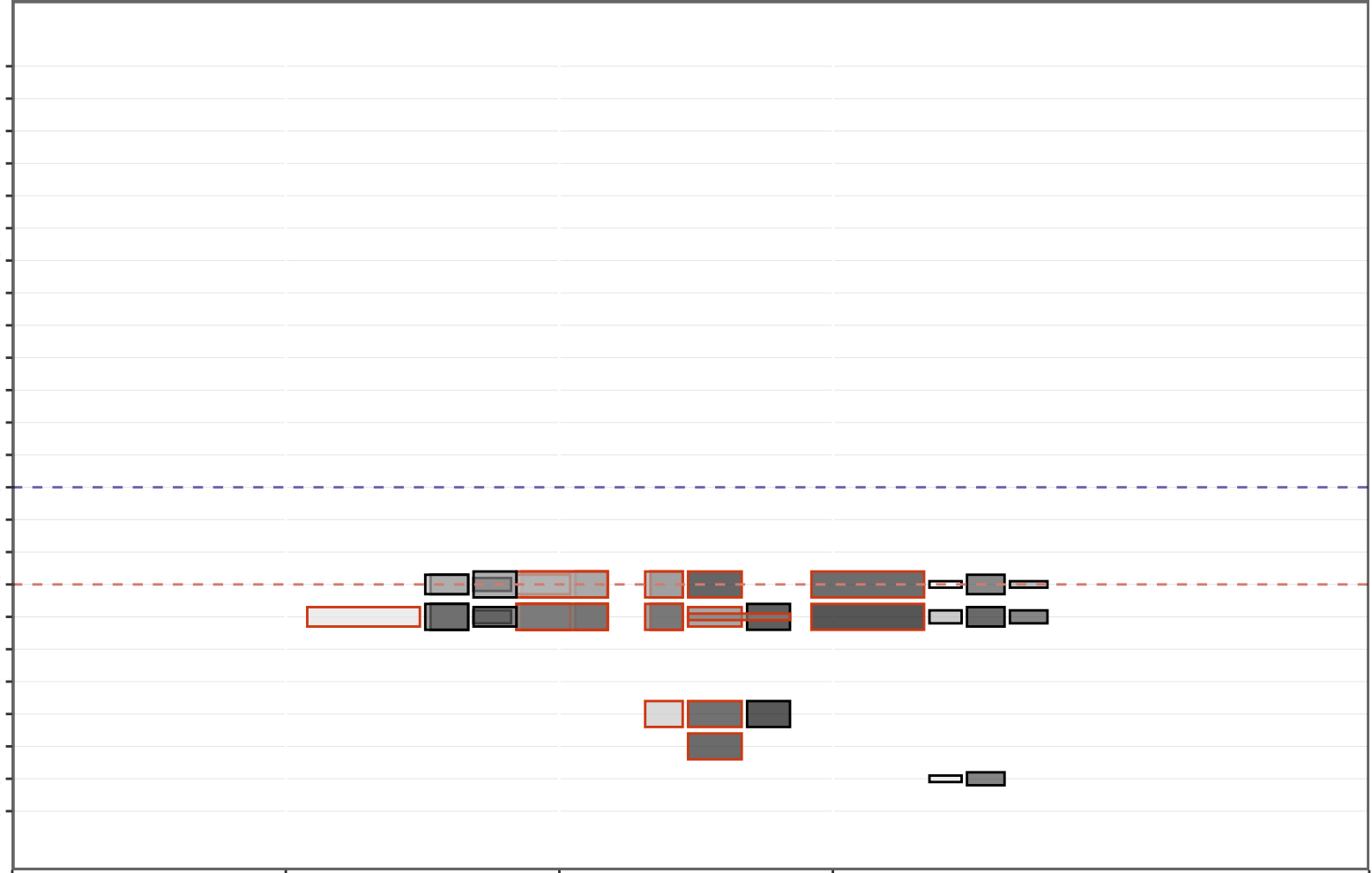
MW indication



Molecular weight



Gel Slice

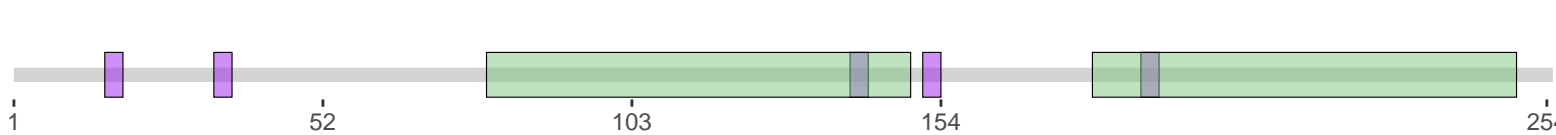


Peptide counts over 4 repeats

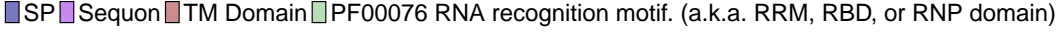
Protein length



Pfam domains



Pfam Description

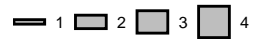


Protein sequence:

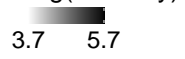
IRSRRFGVYTMKTVEDASAAVEKLNKTEIGGREIKWNTEKPLS6VGS6LLG6DDKFDSPHKYVYGNLAKNVTSESLNFFSEKGNVLSAKVSRVPGT8K66GYGFVFS6EEDVEAA6SLNALLDGGKIRVAKA

NbL17g18020.1 V-type_proton_ATPase_subunit_D-like [MW = 29.14 kDa]

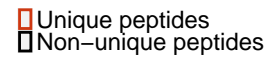
No. of times detected



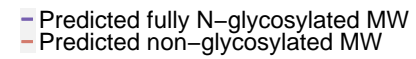
log(intensity)



Values from



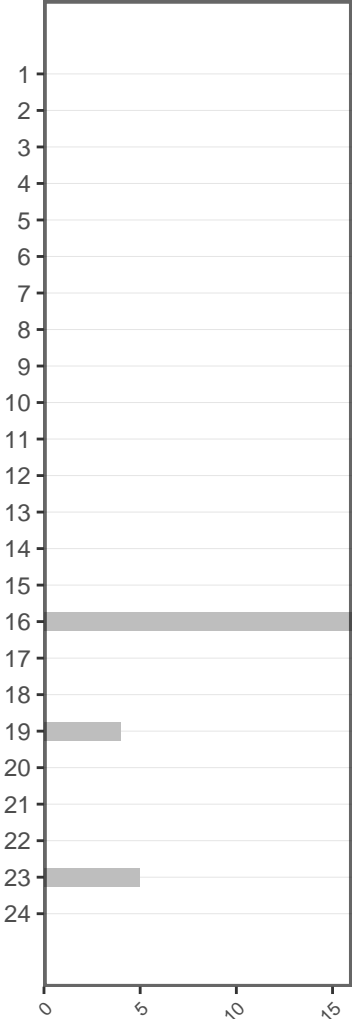
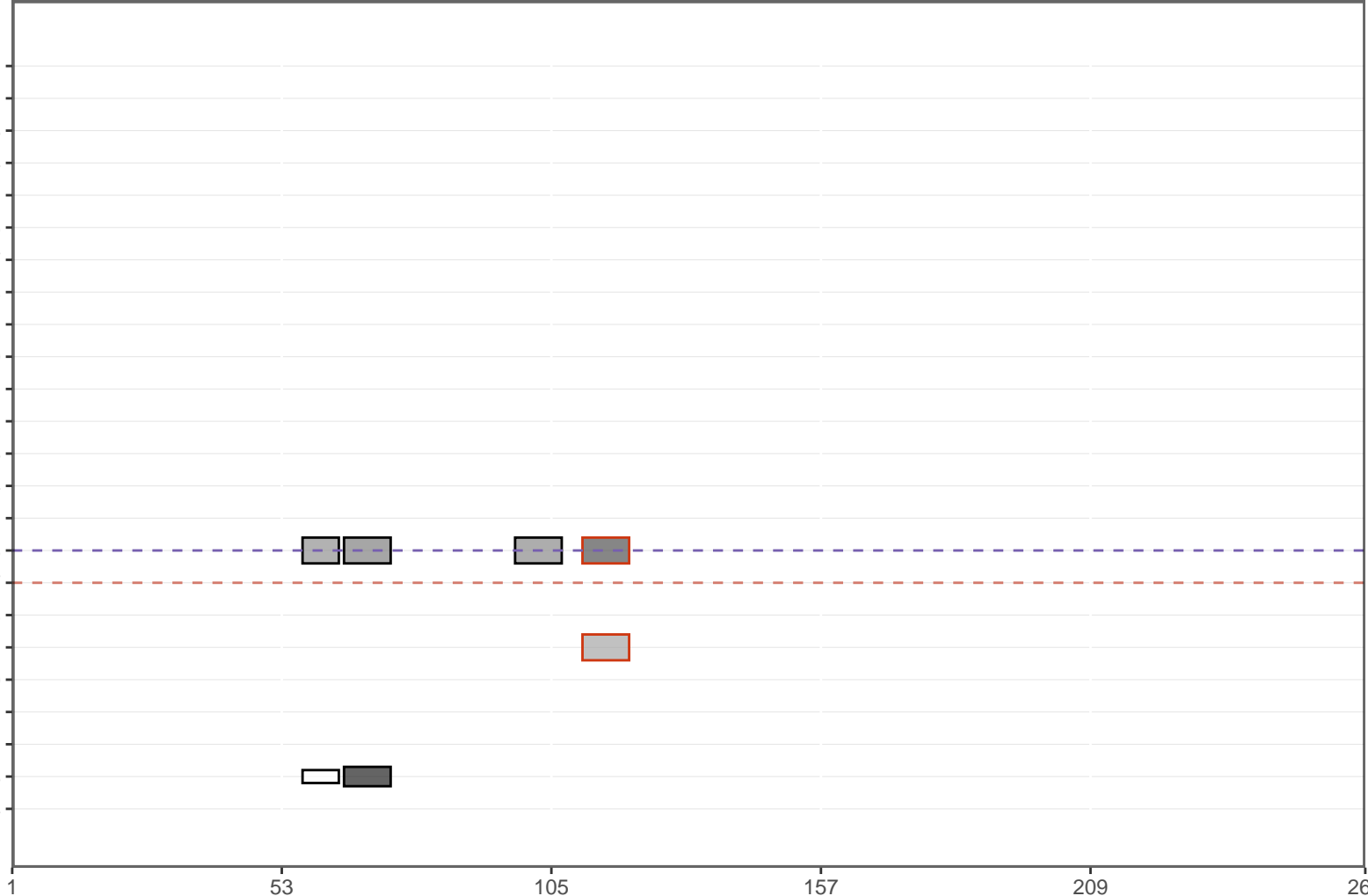
MW indication



Molecular weight



Gel Slice



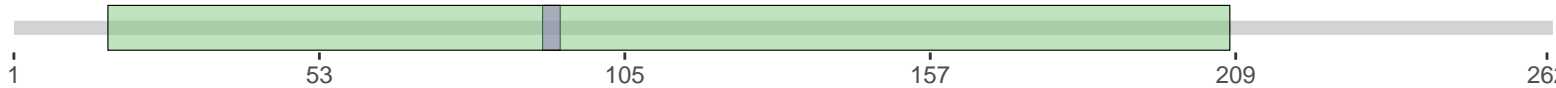
Protein length



Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

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NbL17g17800.1 ras-related_protein_RABH1b [MW = 23.11 kDa]

No. of times detected



log(intensity)



Values from



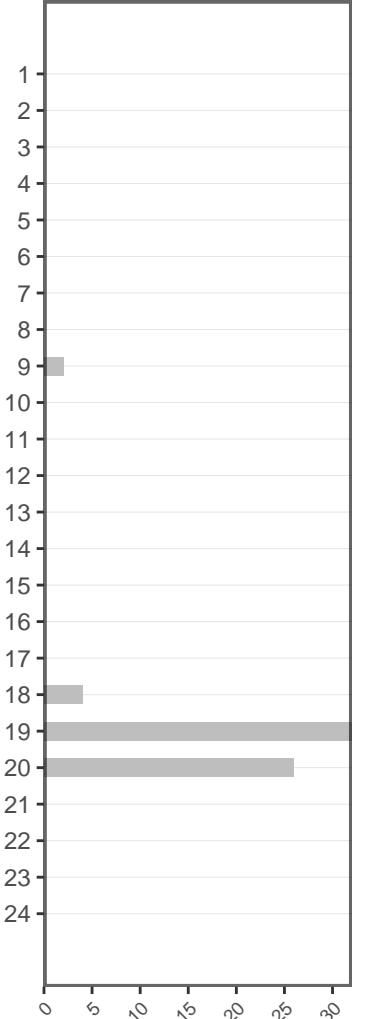
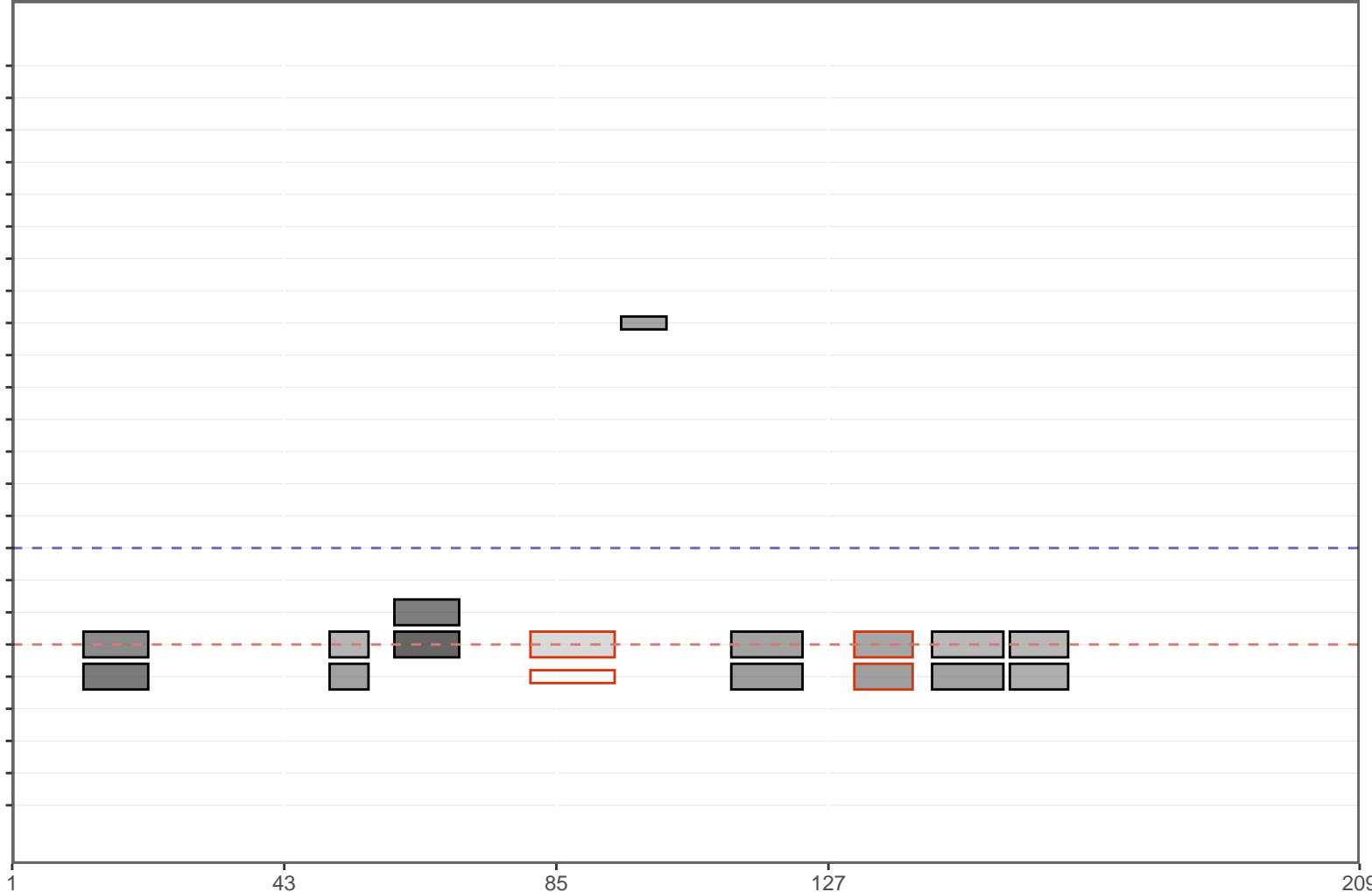
MW indication



Molecular weight

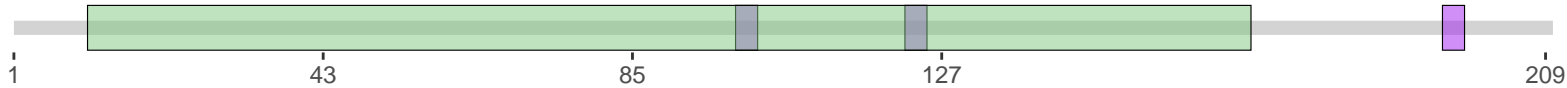


Gel Slice



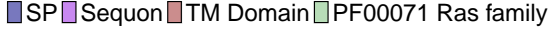
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SRSDFLNTSKWIEEVRTERGSDNVLVGNKTDLVEKRGVSHIEAEAKARELVNMFRTSAKAGFNKPLFRKIAAALPCMETLSSAKGEDMVDNLIKSSNNANASGSGAAGSGGCAE

NbL17g17730.1 heterogeneous_nuclear_ribonucleoprotein_R-like [MW = 88.06 kDa]

No. of times detected



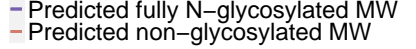
log(intensity)



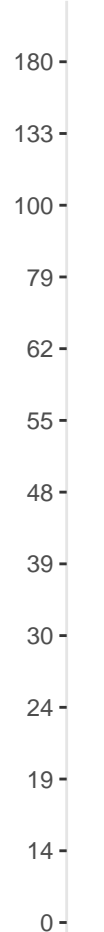
Values from



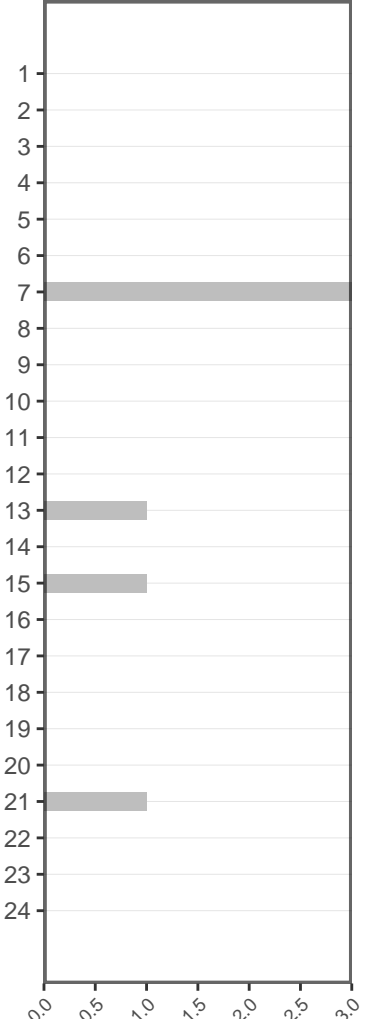
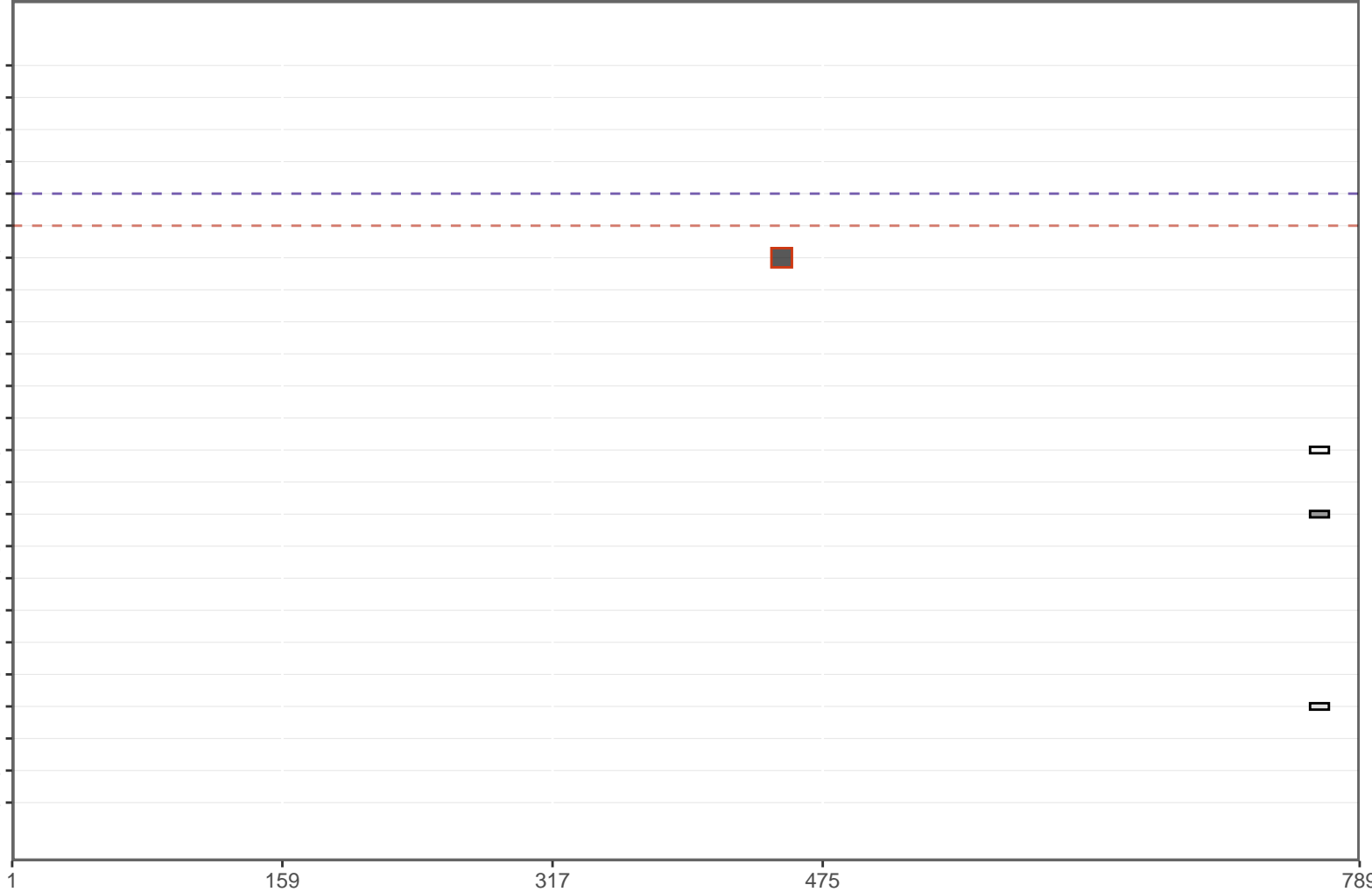
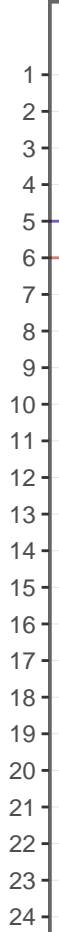
MW indication



Molecular weight



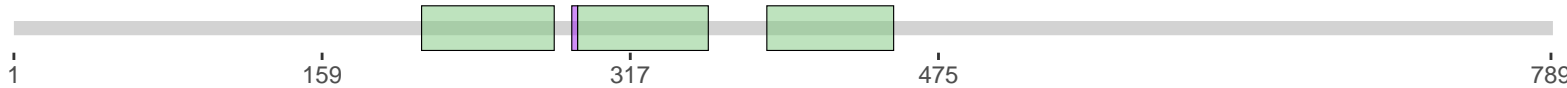
Gel Slice



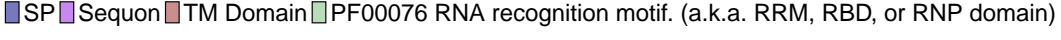
Protein length



Pfam domains



Pfam Description



Protein sequence:

VTVVVDGLSASVDEDRVQELLKEVYKIEKVELARNMPSAKRKDFGFVTFDTHDAVATCAKSNNEELGEGDNRYKVRALSRPLQRGRGKYGGRGDLRPHMPLRGLRAFVGRVTVGHSRPIGRTRVSTRLPPVGRGFKRPMLRDRRAVMALPPRGRFMAPPPSSRSYERRRPFPVSVAKSLKREYGRREEIPRRLALAEVPRVHSGRRAYSDVYSSRDGGVPEMPFRGTHSAGRRAYVDDGVGQRFERPPPSYRDRGRDREYVDSMGGSKRPPYSAVDDVHPR

NbL17g17700.1 nucleoside_diphosphate_kinase_1-like [MW = 15.41 kDa]

No. of times detected



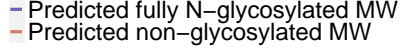
log(intensity)



Values from



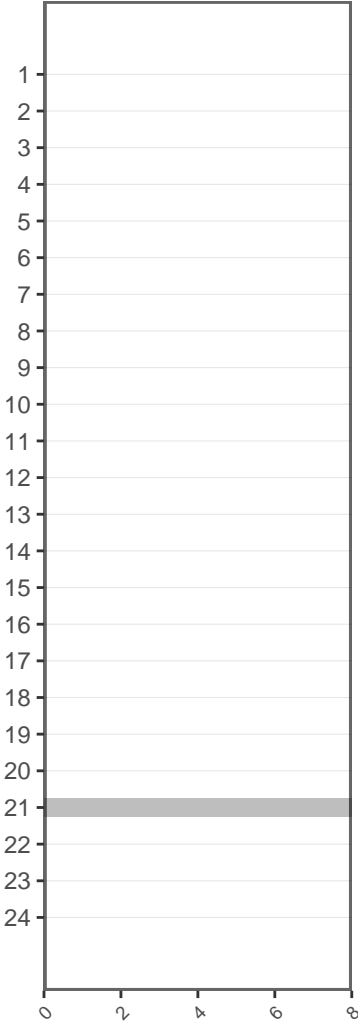
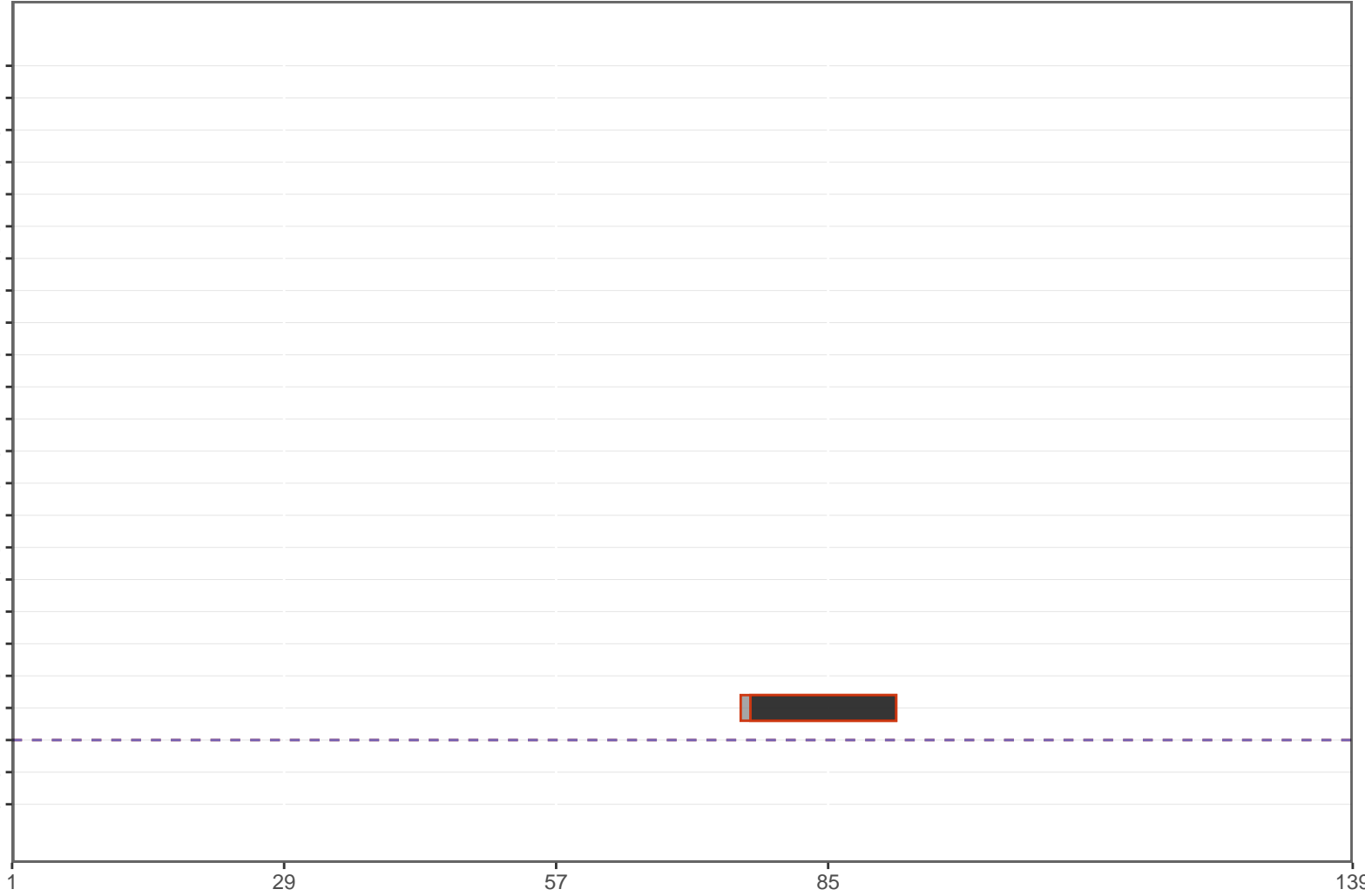
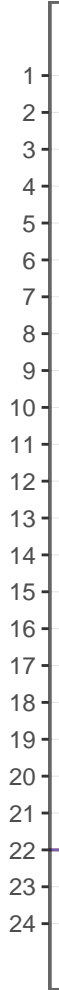
MW indication



Molecular weight

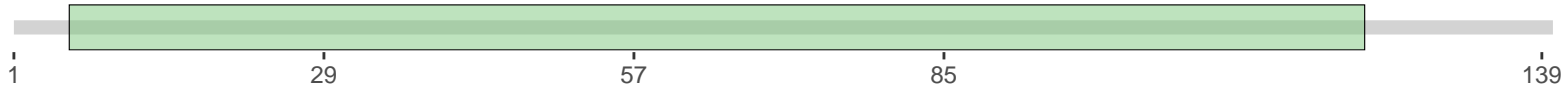


Gel Slice



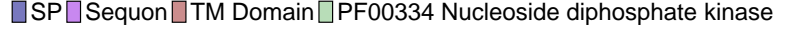
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGPVVAMIVWEGKGVWETGRKLGATNPLESAPGTRIRGDYTFIDIGRNVIHGGSDVDSAGKEKDLWFFPEGINWWRPESQHSWYE

NbL17g17680.1 uncharacterized_LOC107820933 [MW = 56.8 kDa]

No. of times detected



log(intensity)



Values from



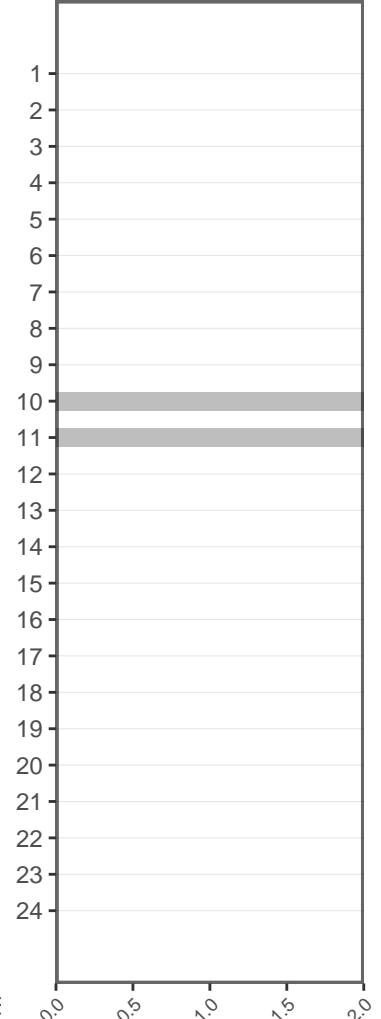
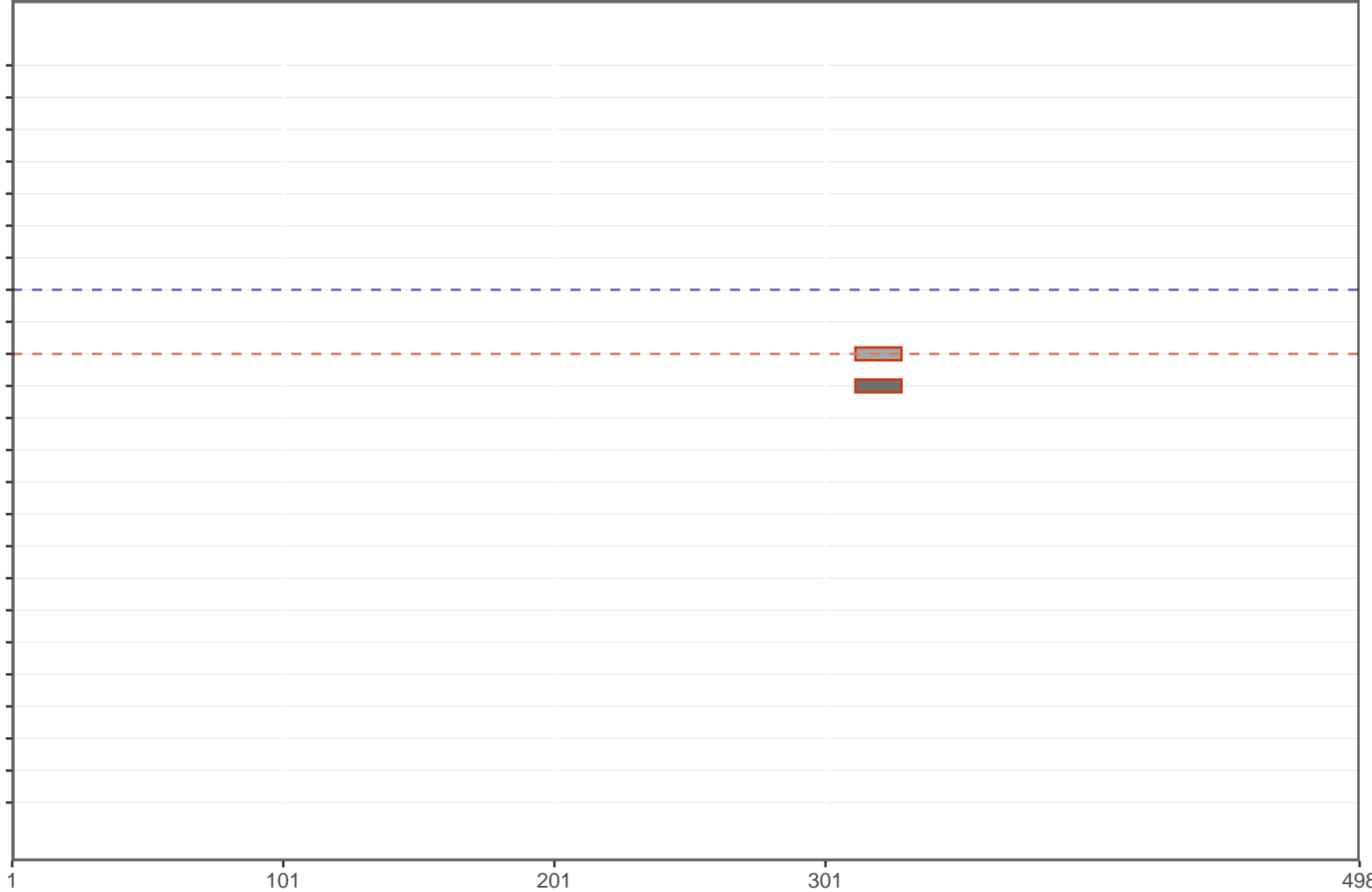
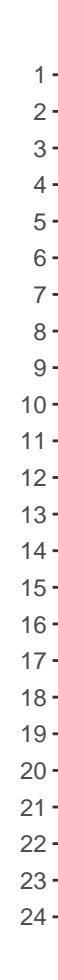
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

SRHQKLPKFSFDPEKSDMEEDMGMEKGLVFFEDGYSRGPVDPVIGELDESKYVISTFKFEQGLVKGCHKRLRIVHTDFSNFGGSDKQLRVAWVEEQWISPNLSDSESDTELDVLFGRRLRQPELAGSVAWVEMGATPHYSEEDVYQETDDVPIVYLLGTENKIKRLPENPWFYGGEEMLMDQDVTVLWLPGGVTSYVDNKKDGLGIGVGVWYDDEGVNLMERDYMEDGKKEVWVKSEMKRRWTFNPPMSLHL*

NbL17g17560.1 peptidyl-prolyl_cis-trans_isomerase_FKBP20-2_chloroplastic [MW = 29.24 kDa]

No. of times detected



log(intensity)



Values from



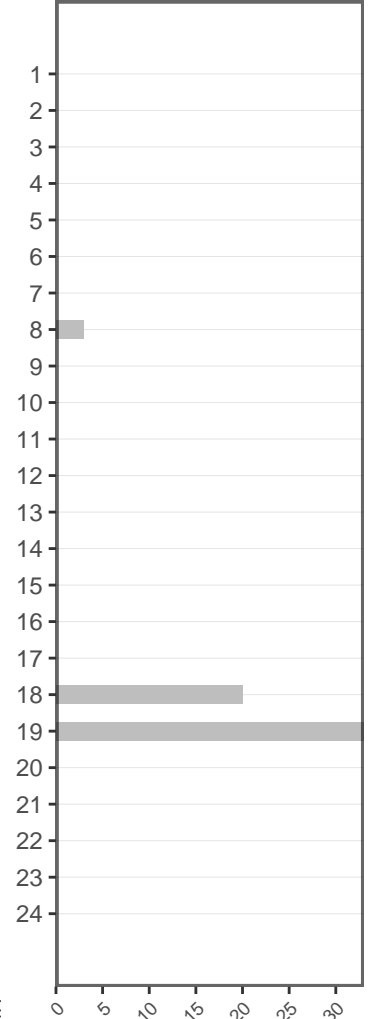
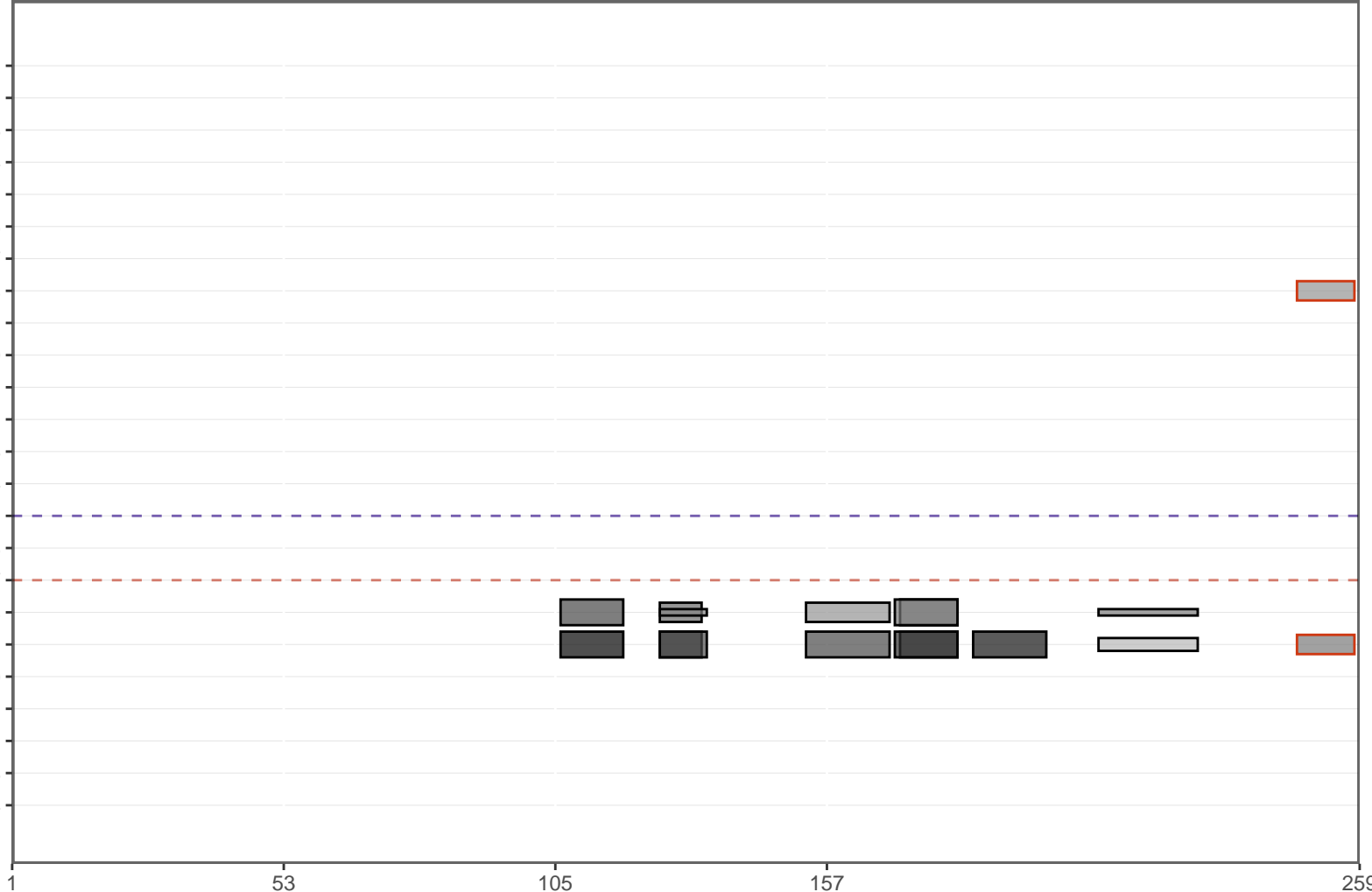
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

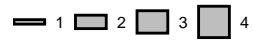


Protein sequence:

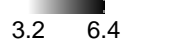
1REGFEVYVTSQNDNYKRDGSLGDLWDIAWEGEGDPRKDGQGVTFHVIQYNEGRRIDSTYLGQAPAWRMGTALVPGFEEGIRDMRPGGRRRIIPPELGGVPGPTFFSSKQGFVDFVLLSIGDCKRRTIAGFYSDVAVN

NbL17g17380.1 ATP-dependent_Clp_protease_proteolytic_subunit_4_chloroplastic-like [MW = 34.06 kDa]

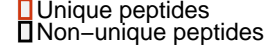
No. of times detected



log(intensity)



Values from



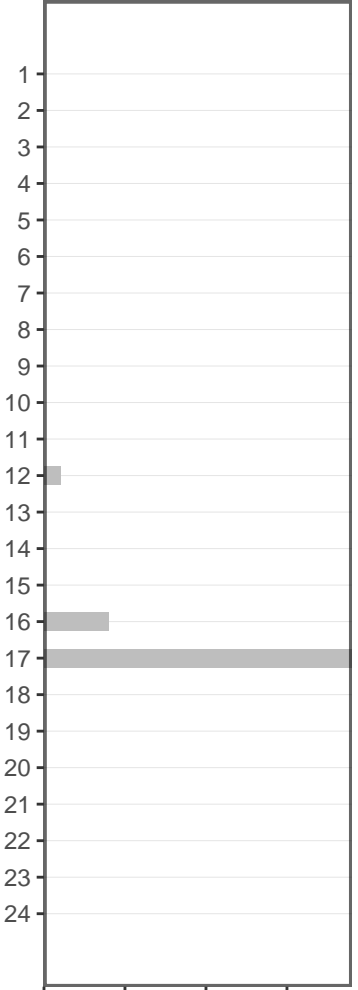
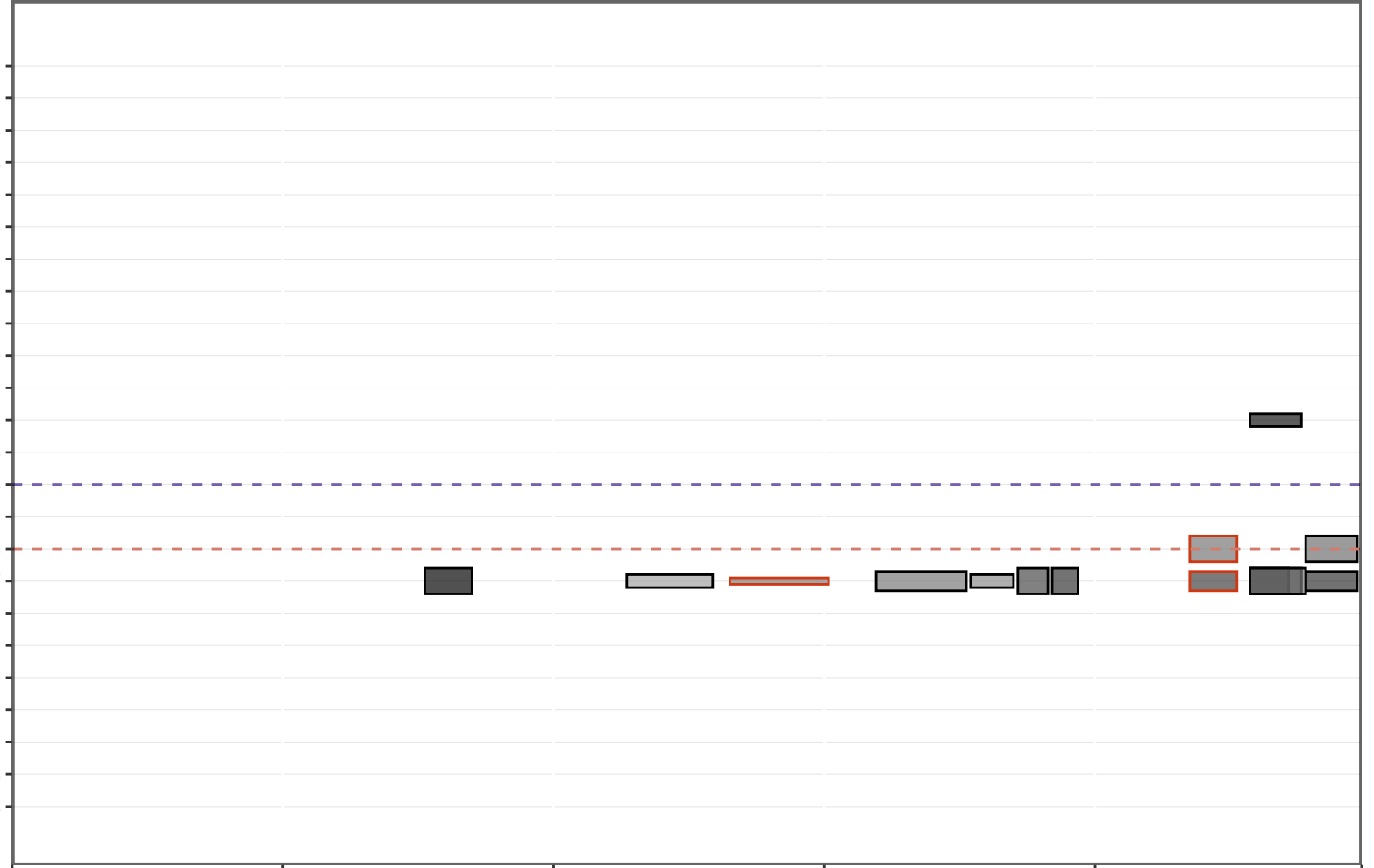
MW indication



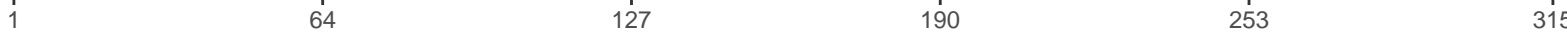
Molecular weight



Gel Slice



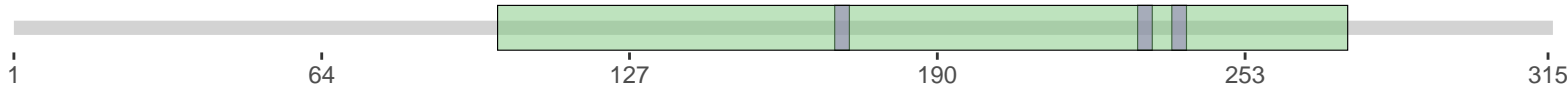
Protein length



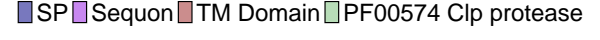
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

LFINSPGSLSATMAIFDVAALVFRANSTVALGIAASTASILGGGTGKGRFAMPNARIMHPLGGASGGADVEIQAREIMNKDNVTKIENGTGRSEYEQKDDRDVMSPEIAVEYGLIDGVIDRDSIFLELPVPERVKSTLVNQEIKDPKFLNPEIPDDEIV

NbL17g17340.1 60S_ribosomal_protein_L13-2 [MW = 23.58 kDa]

No. of times detected



log(intensity)



Values from



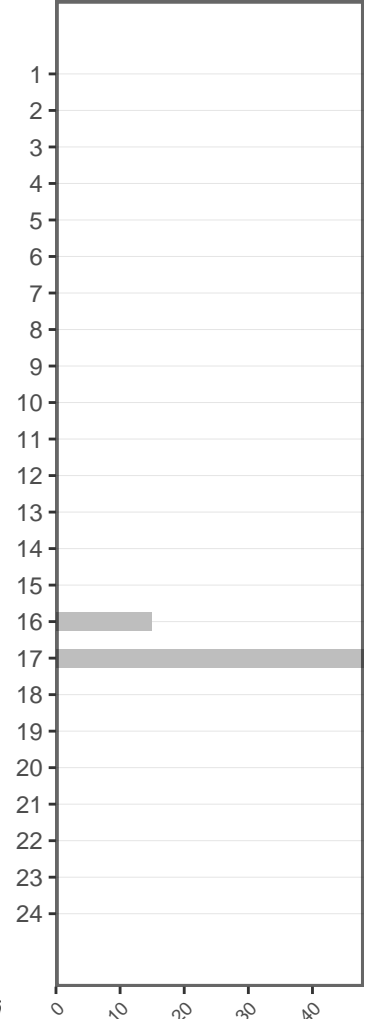
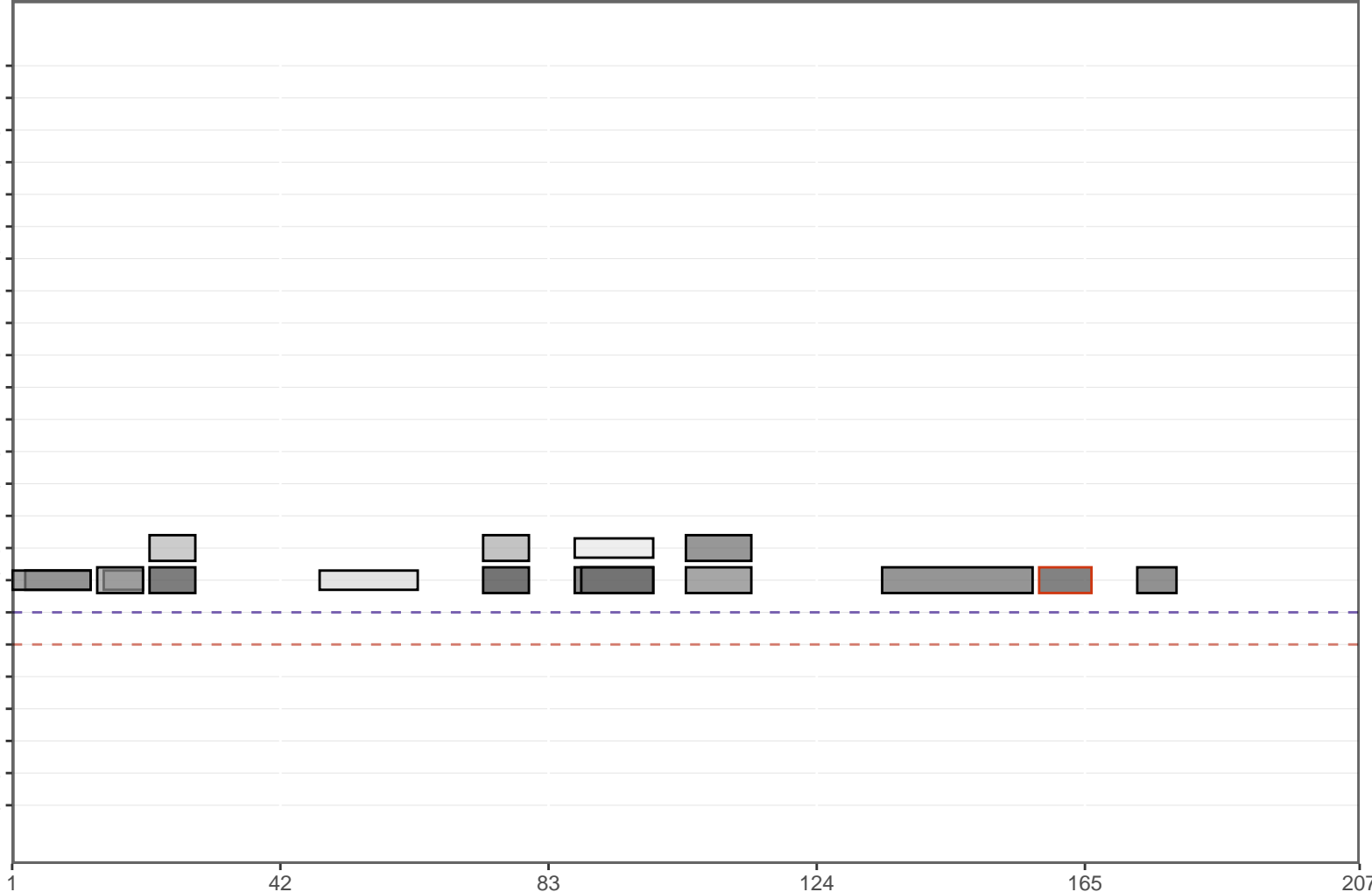
MW indication



Molecular weight

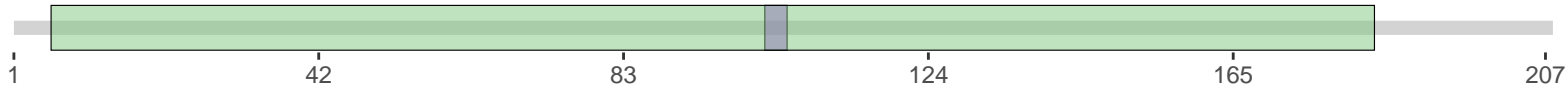


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

APTGIADVHRRNRRLSEGLGTNVRLLKTKYKALVIFRRRAKKIKAGDSBAEELATATQVQSGVYMPITREGPWDLVVRVTDKMFNFVNGKLIERTNARHGARKRAAEAEKEEKK

NbL17g17250.1 neutral_alpha-glucosidase_C [MW = 124.3 kDa]

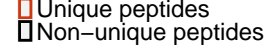
No. of times detected



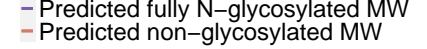
log(intensity)



Values from



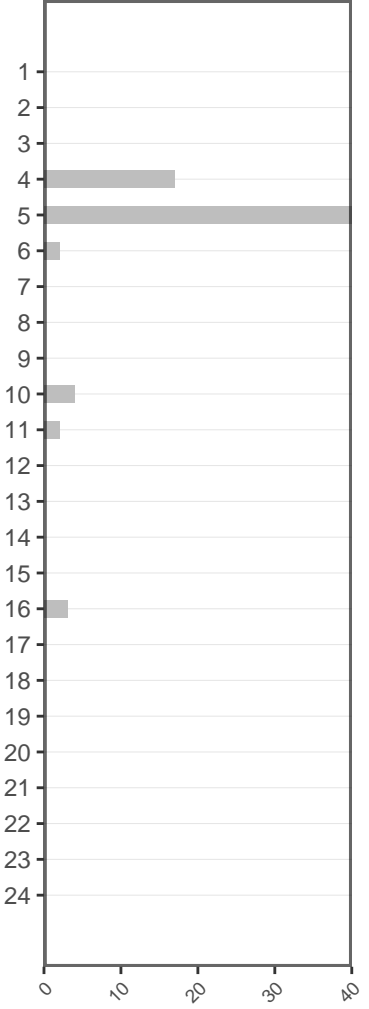
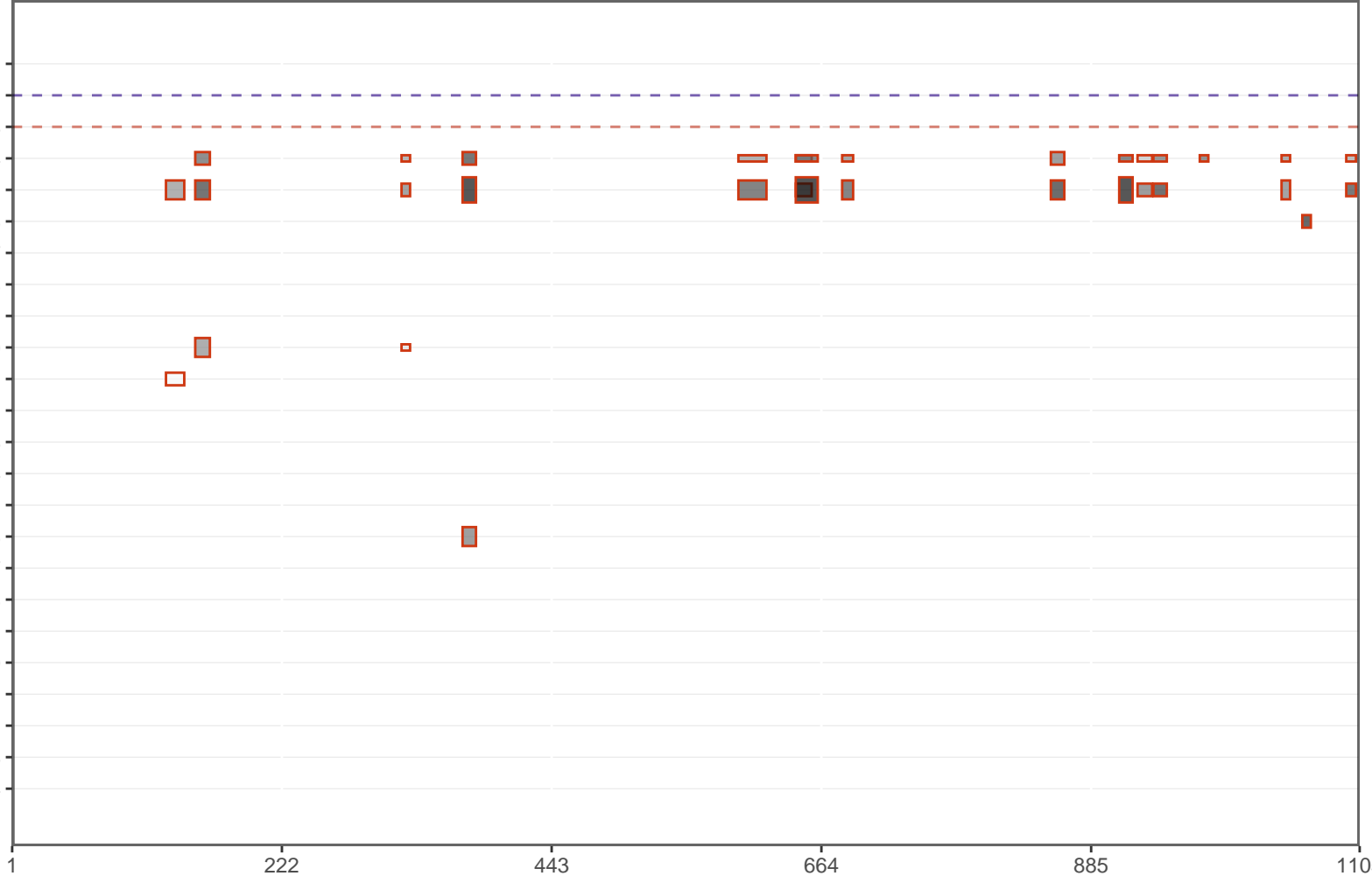
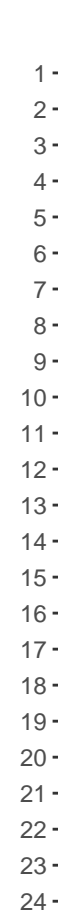
MW indication



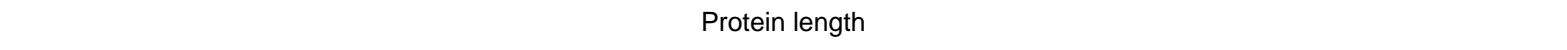
Molecular weight



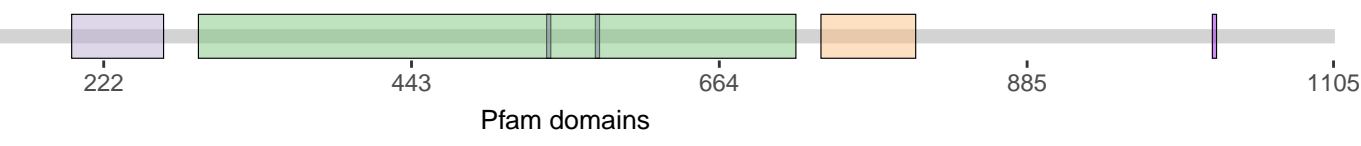
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam Description



Protein sequence:

NLSTWEHLHMSIPMLQLGLGGPLTGPDIQGFAGNATPRMFRMGVGVSLFPPGFRHSEAGTNDHEPWFSGEECEEVORLALERRVRLPHFYTLFYLAAHTRGTPTVATPTTFADPKDFELRKHENFSLLGPLVYASTQRGEEIGTQHKLPKGTWLSDFDELDHPDLPAVLLGGSIIPVGPLYGHVGNAPSDDLTLLVALDENKKAEGLLFEDAGDGYESEGGLLTTVAELQSSVTVTRISKTEGKWKRPNRRLHVRILLGKGMLEAWGSDGEIVQVAVPSETDV

NbL17g17190.1 probable_carotenoid_cleavage_dioxygenase_4_chloroplastic [MW = 65.96 kDa]

No. of times detected



log(intensity)



Values from



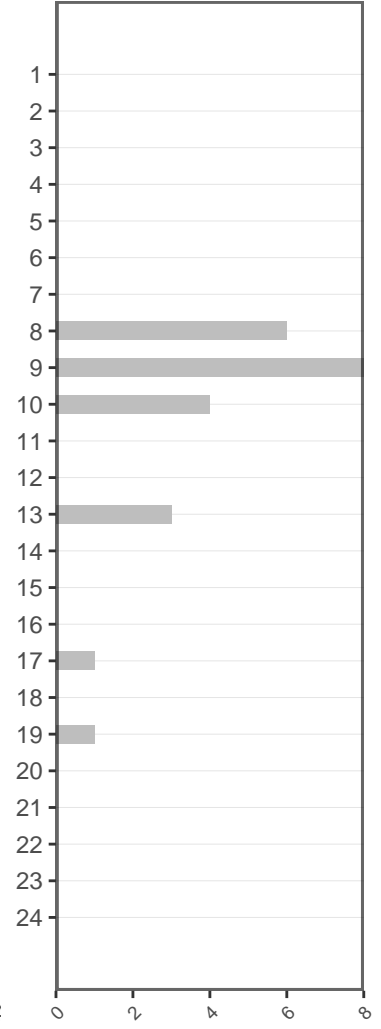
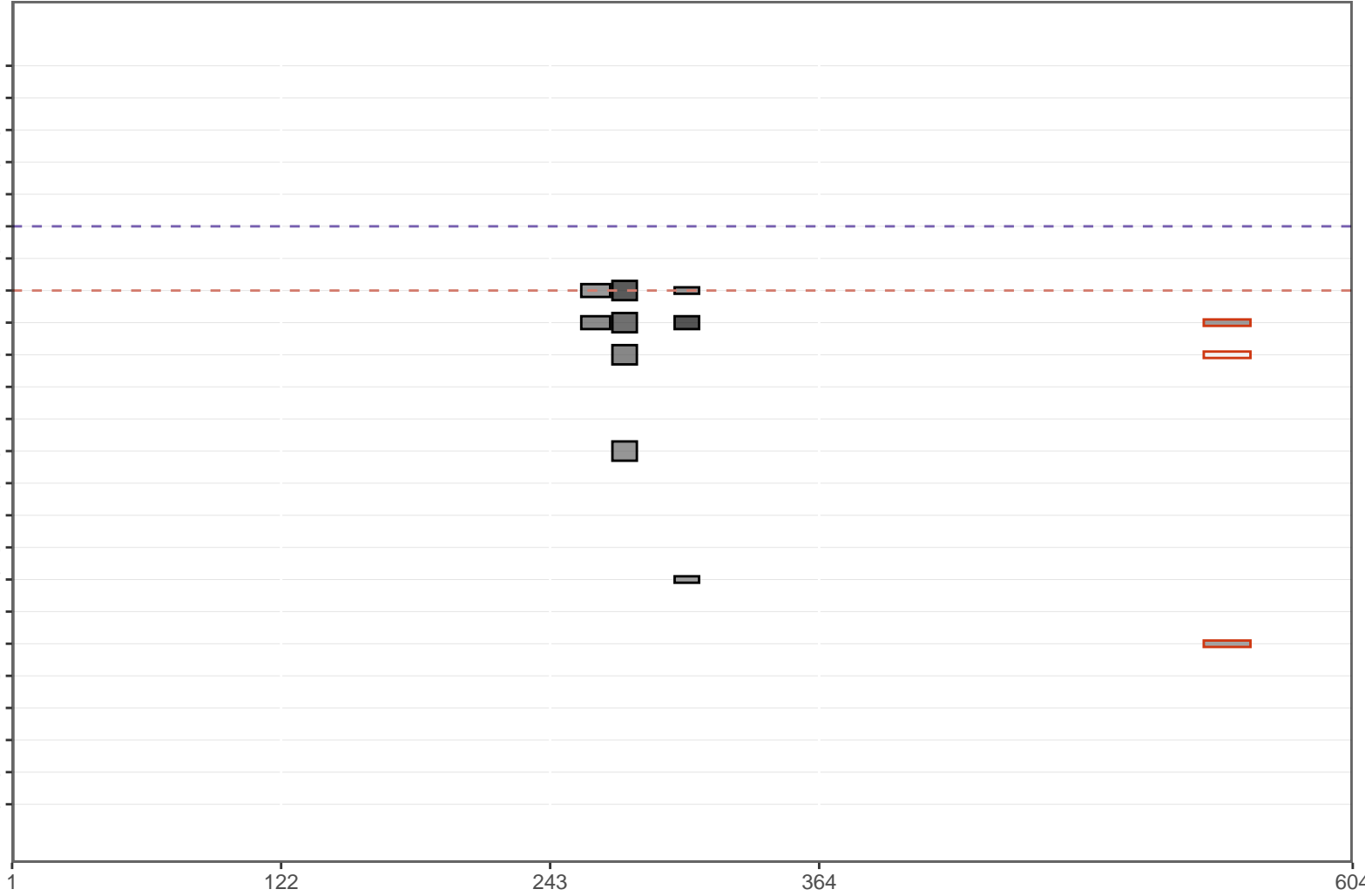
MW indication



Molecular weight



Gel Slice



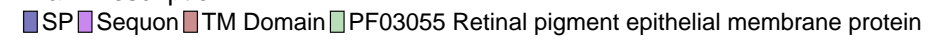
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

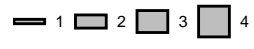


Protein sequence:

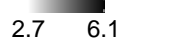
MSMTAIPKIDFDTNEAFARFRYGMPPLFLSYFRIEPNTKTPDVPFISMTLRFSLFDFAITKKYAFSDQIGMNPLEFITGGSPVSGDSGKIPRLGVPIDDADESKMKWFDPGFNIVHAINAWDEDDGDTVMVAPNLSVEHTLERVDIMHSAVEKWKIDLKSQGVSRHPVSTRNLDGVTNPAWYGGKKNVYAAIGDFMPRIAGIAKLDVSAETDRRDDVCGRLFGEGCFGGEPYFAKDPNPTADEDDGVVSVYHNEKTGESRFLVMDAKSPNLDVAAVXLPKR

NbL17g17060.1 ABC_transporter_E_family_member_2 [MW = 68.21 kDa]

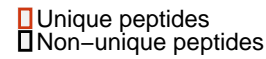
No. of times detected



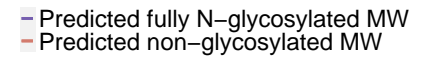
log(intensity)



Values from



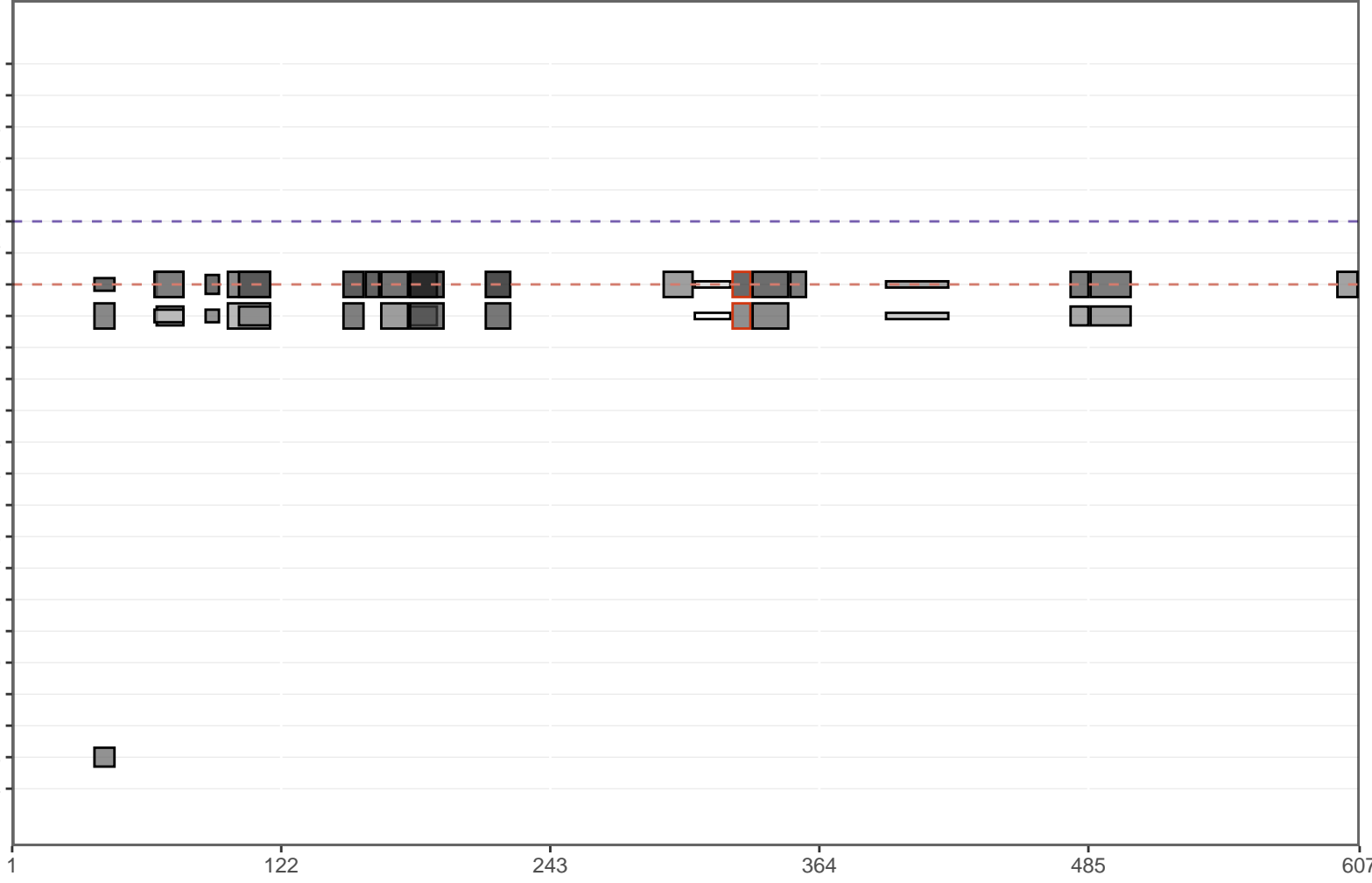
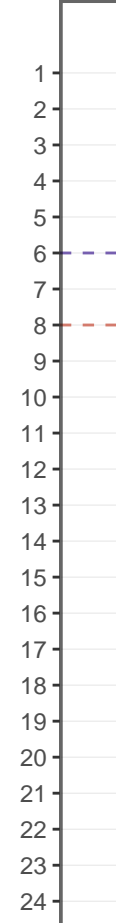
MW indication



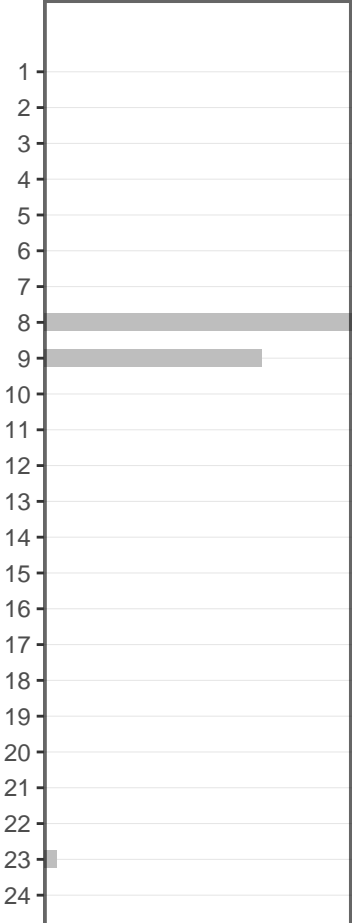
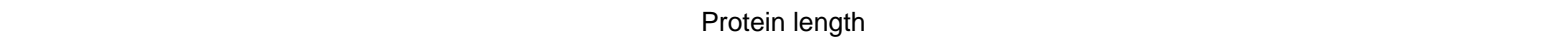
Molecular weight



Gel Slice



Protein length

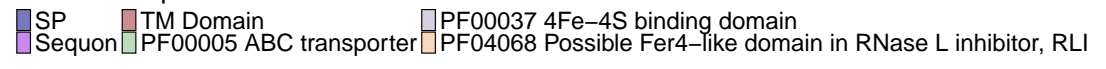


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

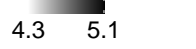
LYGKPGAYGVVTLDFSVREGINFLAGEVPTENLRFREESBLFRVAETPQEAEEETIYRVRVPTMTKGTGQNFKLVAEGEFTDSQVWMLGENGTQKTKTFRIMLAGLKPDDVVEGSDTDFEFNVSYPKQKISPKFQSTVRRHLHKGKRDVSYMHPQFSDVMKPLGIEQLMDQEVVNLGGELGRVALALGLGKPADYLIDEPSAVLDEGQRVAVSKVIRFHLHAKKTAFVHEHDFMATYLAGDRVIVVEGTPSIDGVANAPQSLTGMNLFSLHNTFRDPTNFRPRNKLES

NbL17g17000.1 AP-4_complex_subunit_epsilon [MW = 105.88 kDa]

No. of times detected



log(intensity)



Values from



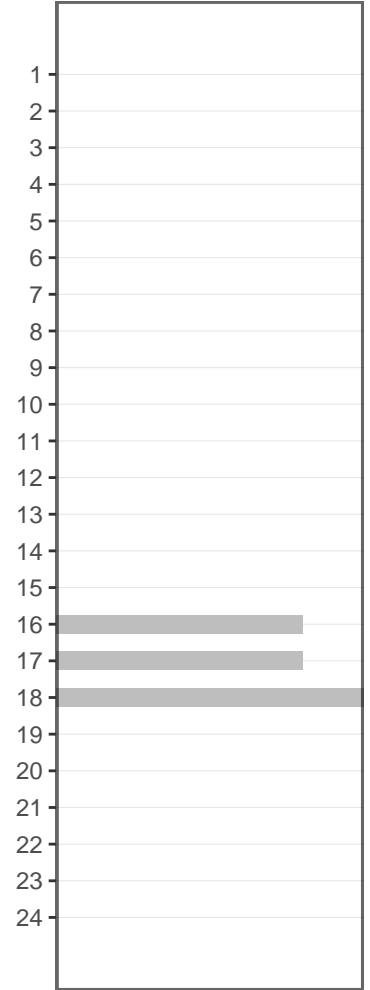
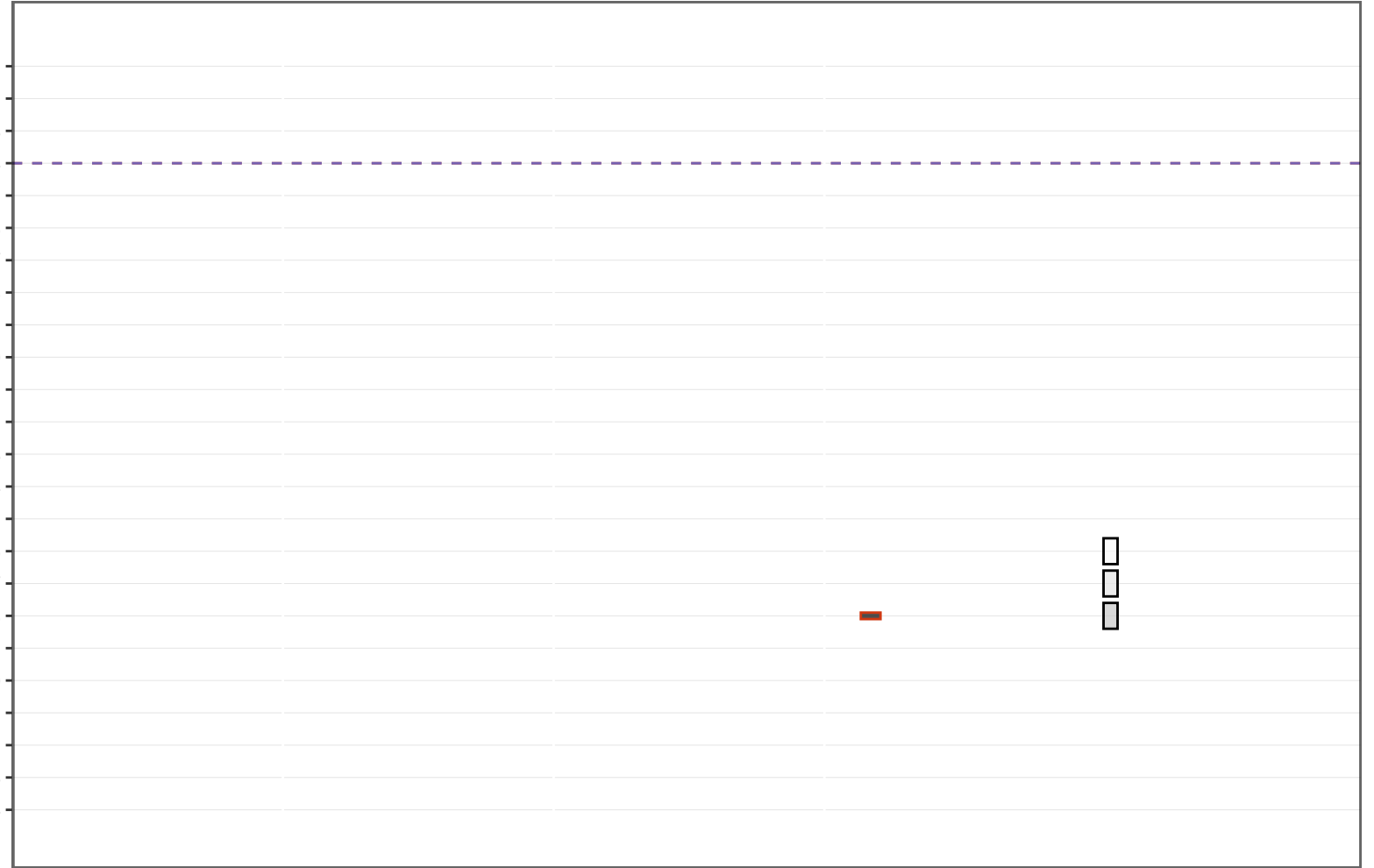
MW indication



Molecular weight



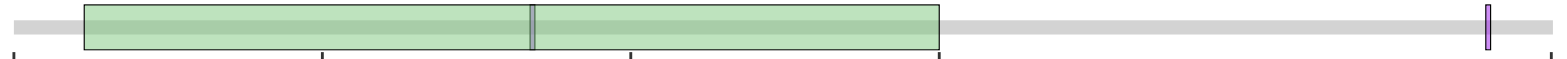
Gel Slice



Peptide counts over 4 repeats

1 194 387 580 963

Protein length



Pfam domains

Pfam Description



Protein sequence:

MGEPLPSAFLQVLDVWVLEGEYGTADGKYBASYFTGKICDIAEAHSTDDMKAYAVSALMKVVSFEIAGRKVDMLPEGESFIEELLASHSTDLQGRAYELQAVVGLDARAVENMPMDASGDEDEVDRELSFLNGYVQESLNGKAGPVPENARSGALTISGFRHEEGHGSSEGHSLRFEAYELPKPSPVSRPSPVPLVSTELVVPPEPTYHTEFHEAWAPKLSAEGTGSSEIKLRLLDGVQRKWKGTYS6666P6TSD6D6TYKTGNQVTRQRP6SL6SKTRD/SYESKROG

NbL17g16960.1 long-chain-alcohol_oxidase_FAO4A-like [MW = 84.84 kDa]

No. of times detected



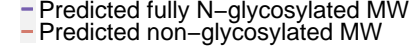
log(intensity)



Values from



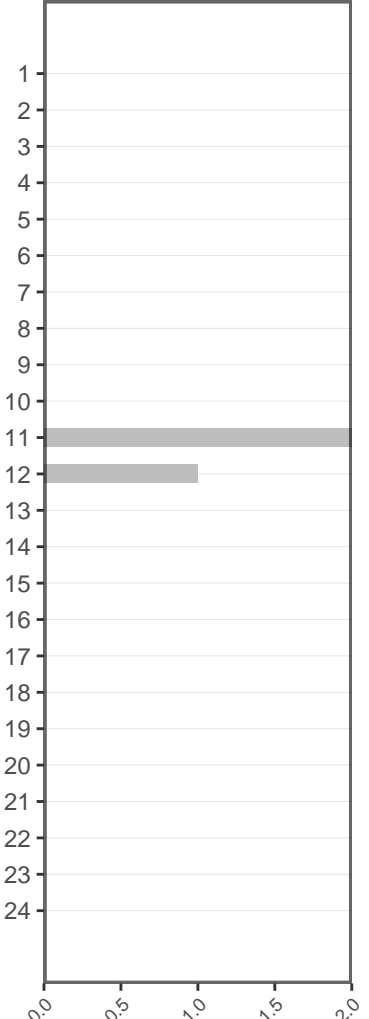
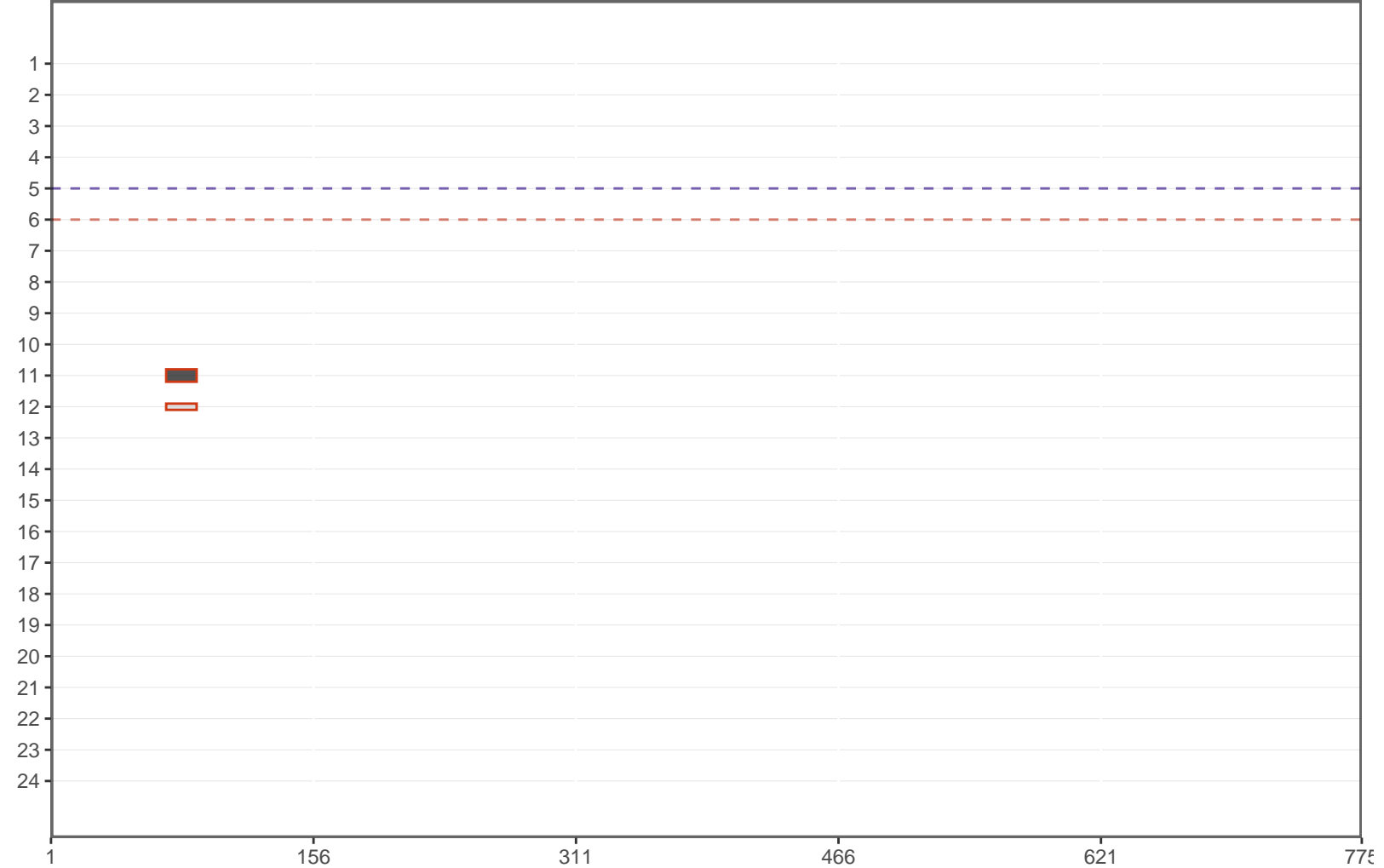
MW indication



Molecular weight

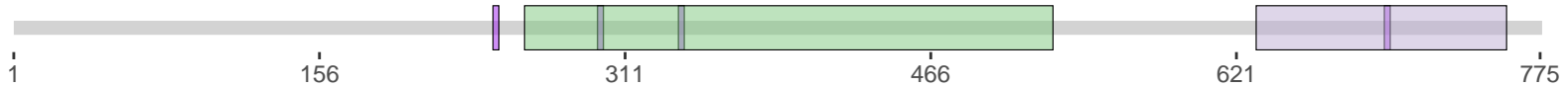


Gel Slice



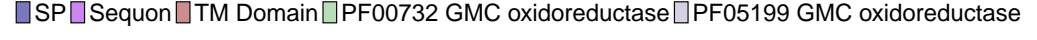
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MSVQSEIEDEGFQNMILRKGDELGYVETIPRNAGSDHYGGWDSMGCKDGGKKGTAETWLDLKBGNGAILPEGEALEVHVKKNDKSGSKAIGVAFAGFNQGVREICMKVKBKVTIAGGALSTPLSLKSGLNPNIGRNLLHPVVAWGYFFDTPSDSNVLPFADKKVYEGGIMTAMSKVWVFEGSGYGAIQTPGLHPCMFSAIMFWVSGLDKMRMCKYGRYALLALARDKGGSEAFSPYVYTKMDGIDEENKLGLEKMLRILAAAGAEIQTQHP

NbL17g16800.1 60S_ribosomal_protein_L7-2-like [MW = 28.74 kDa]

No. of times detected



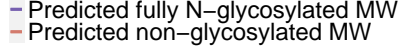
log(intensity)



Values from



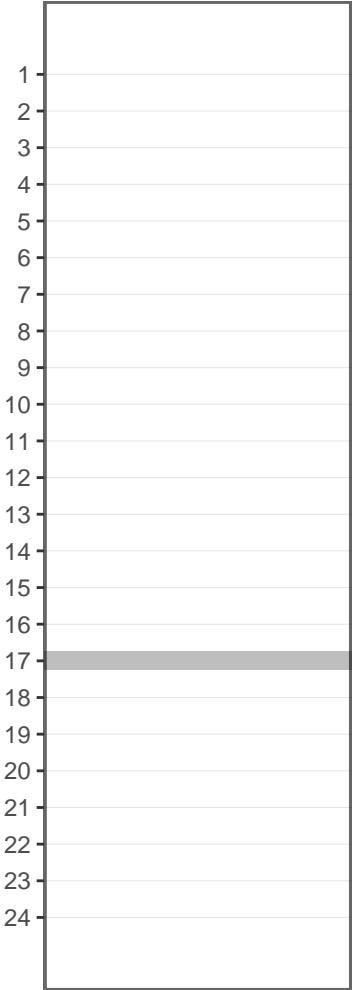
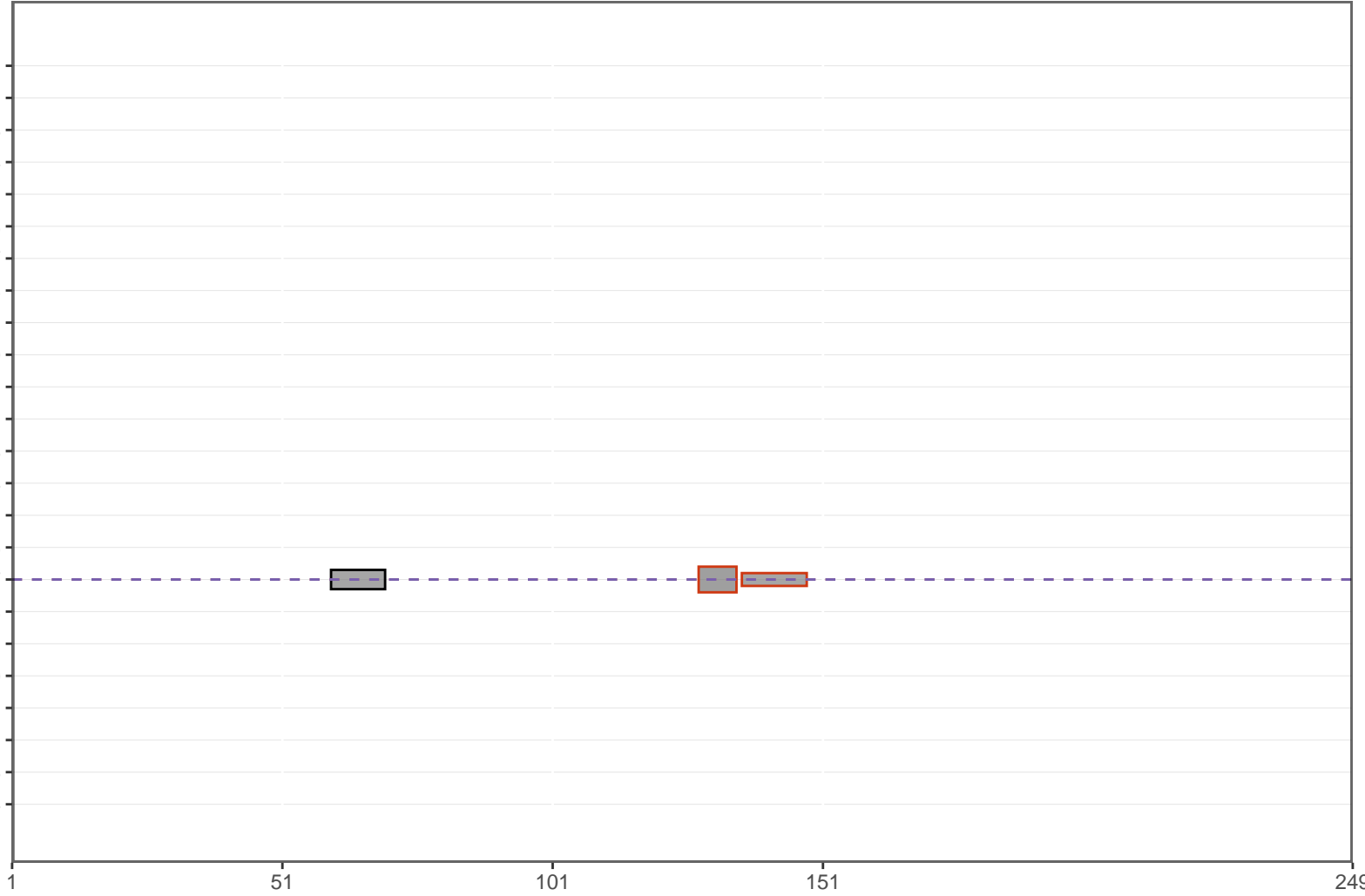
MW indication



Molecular weight

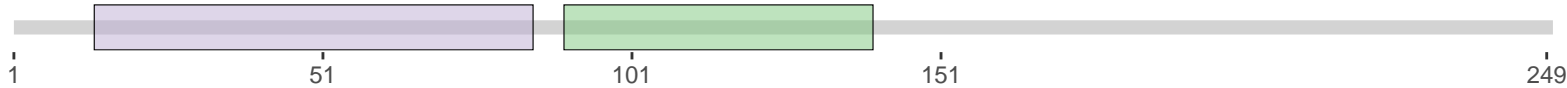


Gel Slice



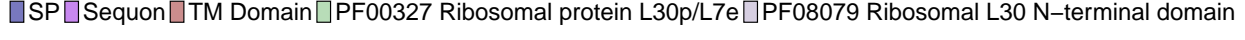
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LLRLRQIFNGVFLKWKATLNLMLRIEPIVTVYGYPNLKSIVRELIYKRFQKVDKQRIALTDNSVIEQVLRGHGIGMEDLVHELTVGFPHKEANNFLWPFQKAPLGGKQKRNHYVEGGDAGNRENYNEIIRRMN

NbL17g16680.1 carbon_catabolite_repressor_protein_4_homolog_4-like [MW = 43.19 kDa]

No. of times detected



log(intensity)



Values from



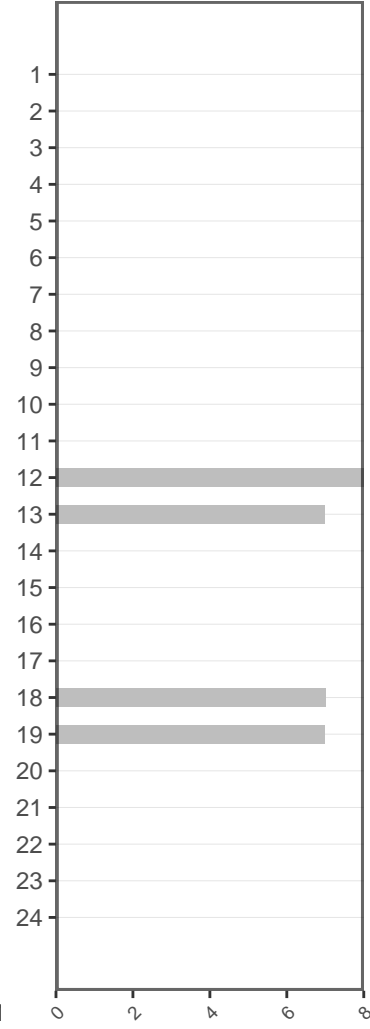
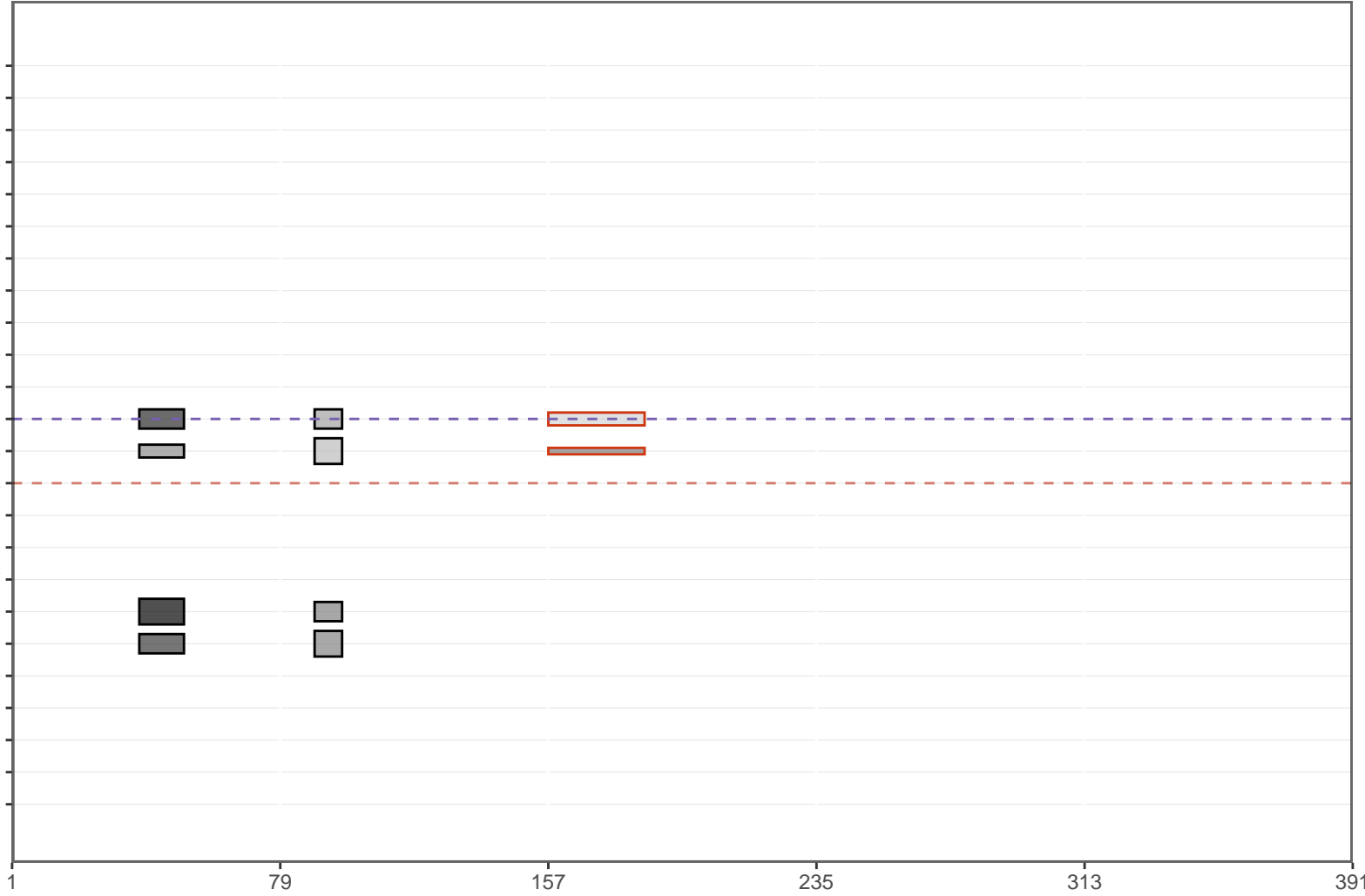
MW indication



Molecular weight

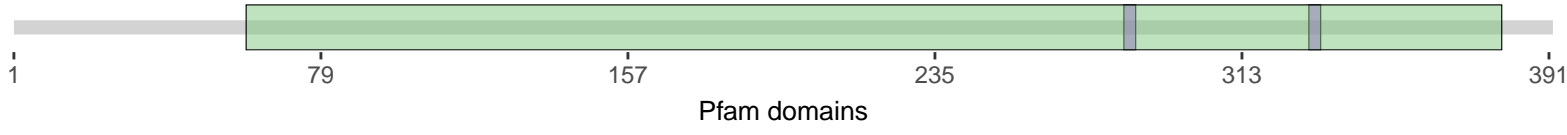


Gel Slice



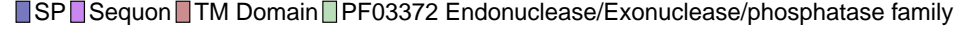
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKKLESKVSSKNSSQADHGDNDPRIRLKRDCVGVGMAARLKRDPDGLHVAETHYWDPELADNKLADARLLSRLAGFKLLVSDKFDGSPKVVAGDFNPTGGDGVVQHLGGSELVETLPESSNDMPRLGSAVASTKGEPHFTNCTPGFTGLDHLVFSPPGDKVIVLELPEPEASDVOGGLPNYYHPSDHLPGAEFIWH

NbL17g16660.1 pectin_acetyltransferase_8-like [MW - SP = 42.04 kDa]

No. of times detected



log(intensity)



Values from



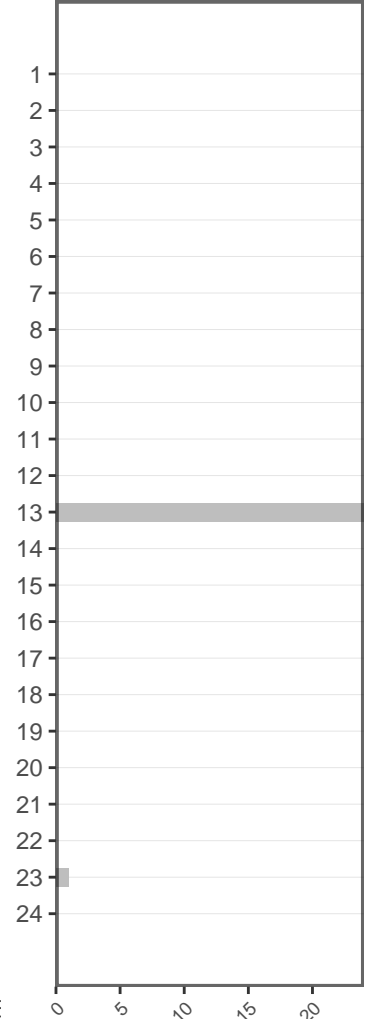
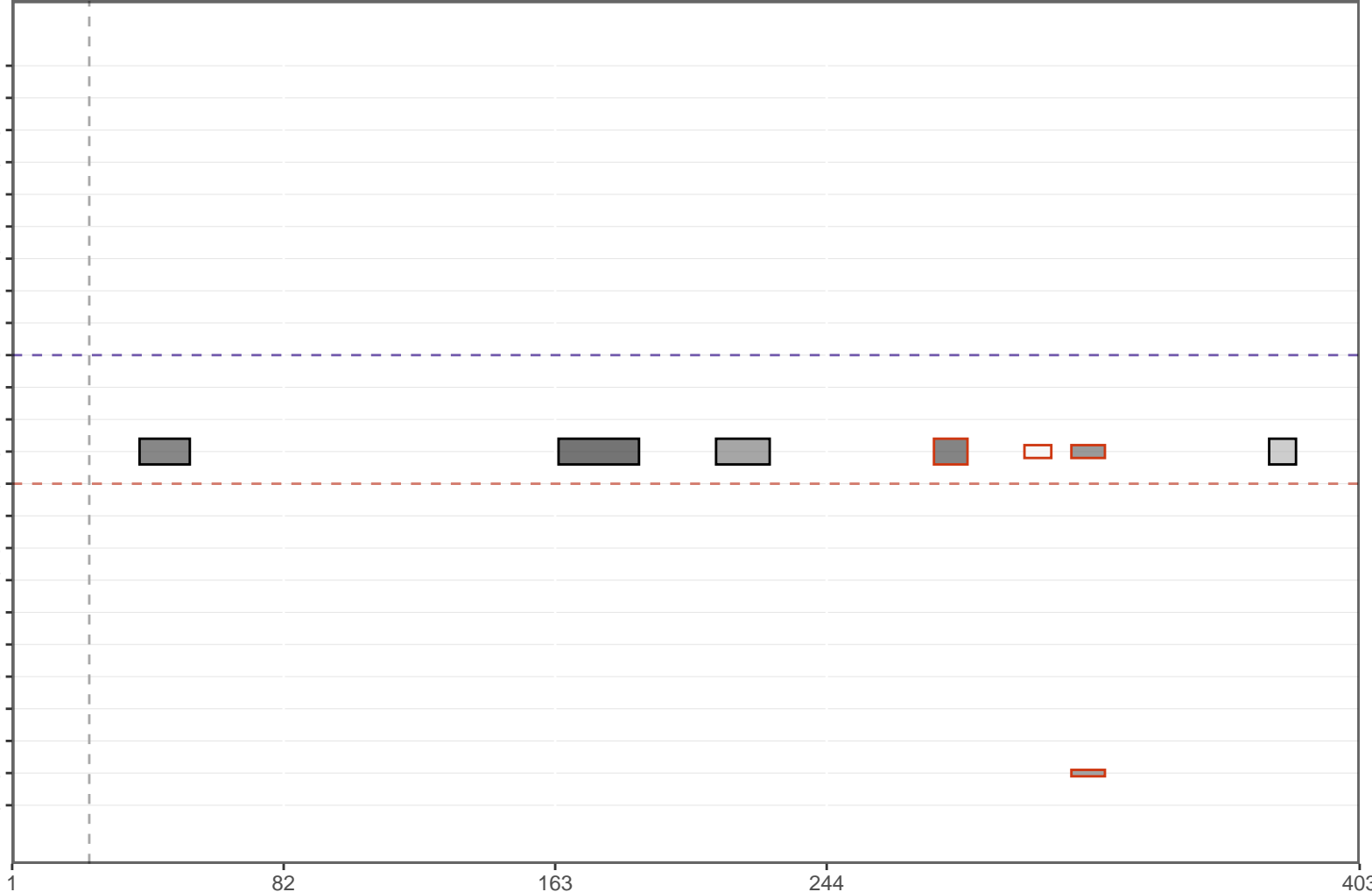
MW indication



Molecular weight



Gel Slice

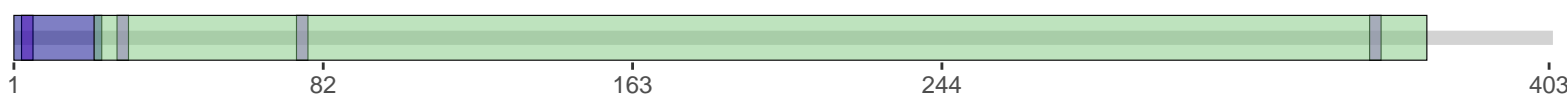


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description

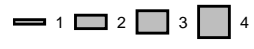


Protein sequence:

FKALLPMGAKVYKCFSDAGYFVNVKDSGAFHIEEFFGDVRLHGSAGKNLPLSGTSLKPNLGFPPQNVVYGHVTRPLFLVNAAYDSEWQIKNLAPEVADPRGVWRNKLDLIRGSSKQLGTMGFRLGLFRALMALGPSSSRGYFNSGVYHGGTEVGETWFRADSPKLANKTIAKALGDWFFDKNPFQKIDGPVCDKTCNHRIFNPVHHPFDIDM

NbL17g16590.1 eukaryotic_translation_initiation_factor_3_subunit_G-like [MW = 32.27 kDa]

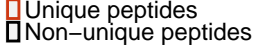
No. of times detected



log(intensity)



Values from



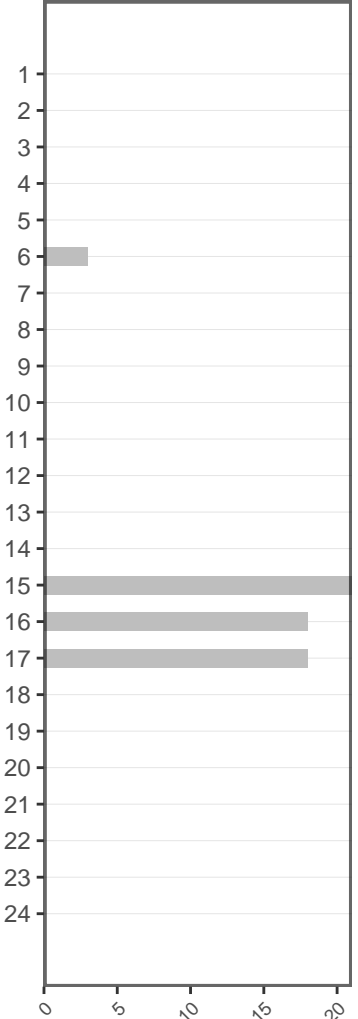
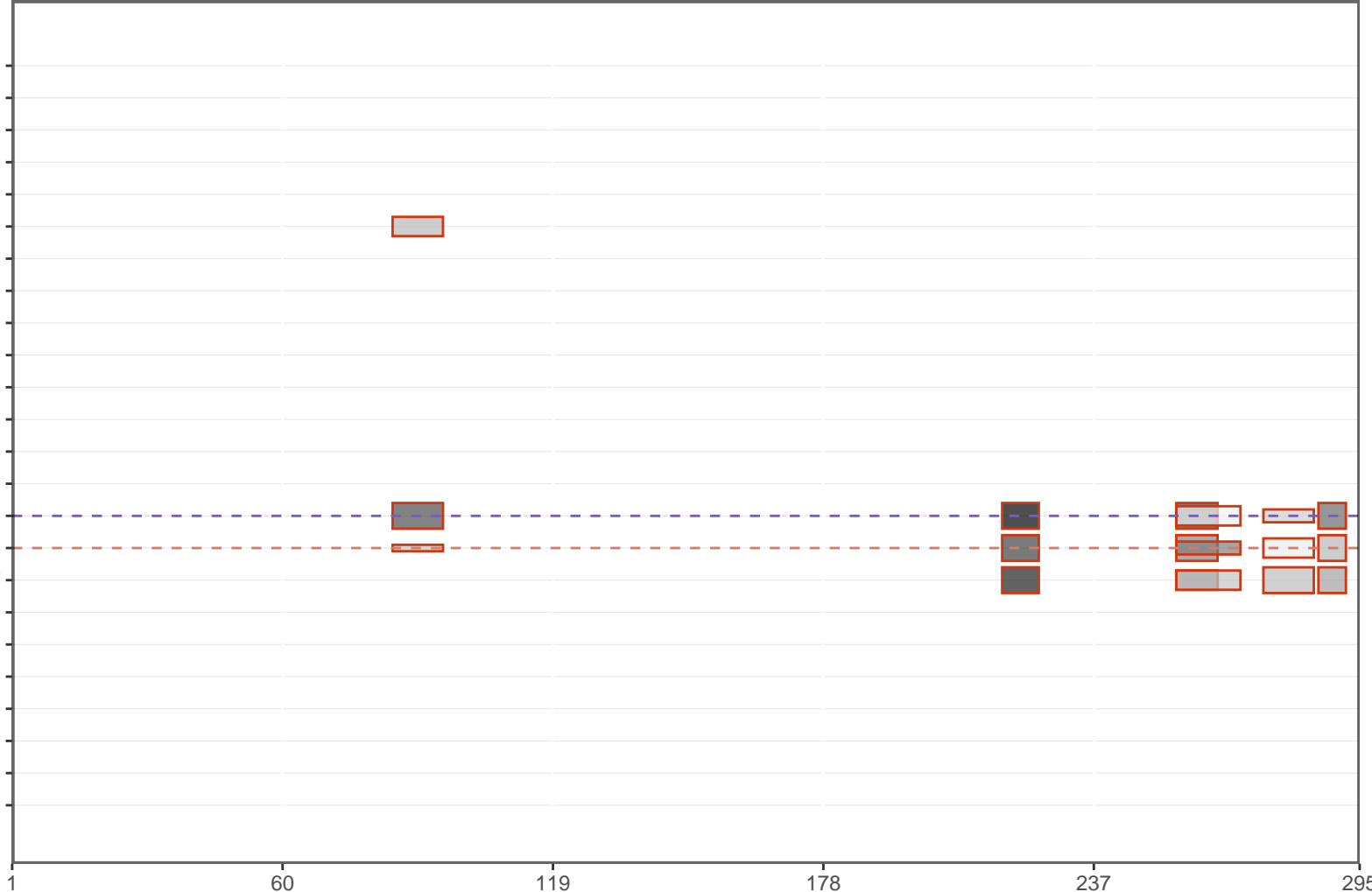
MW indication



Molecular weight



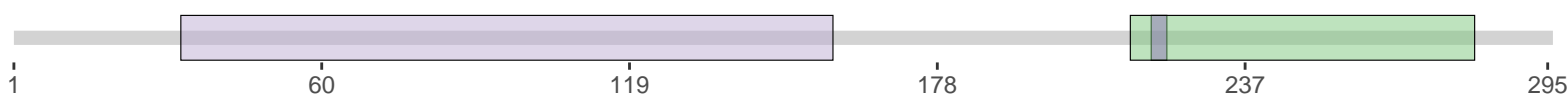
Gel Slice



Peptide counts over 4 repeats

Protein length

Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- PF12353 Eukaryotic translation initiation factor 3 subunit G

Protein sequence:

IIVCRCTCGKGDHIVTSKGFKDLAIPSDTFMDKPPSAEAPAGAGPKGAYVPPSMRGGGAERGGGGTEMRRRNEENBVRVFNLSGDTREADLLELHFPGHVSRVYVATDQIKTGMRFGRFVNFVNREDAERANKLNGYGVONLILRVEVAAPRTN

NbL17g16540.1 polyphenol_oxidase_E_chloroplastic-like [MW = 66.53 kDa]

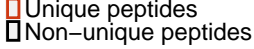
No. of times detected



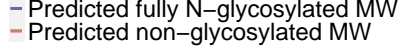
log(intensity)



Values from



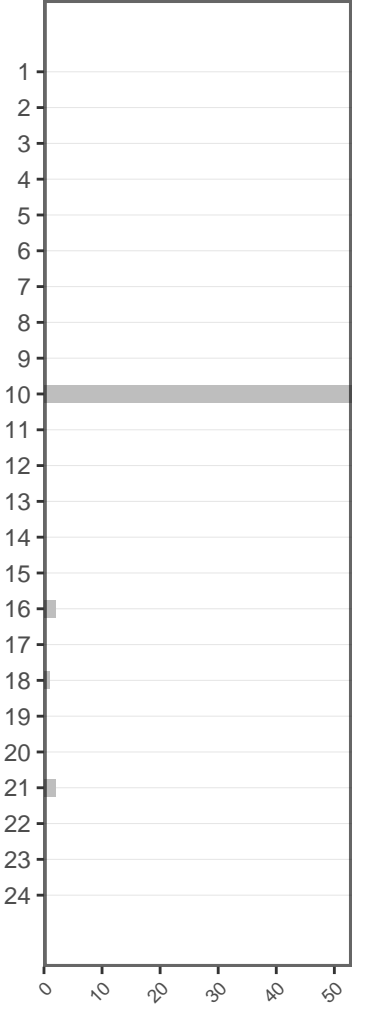
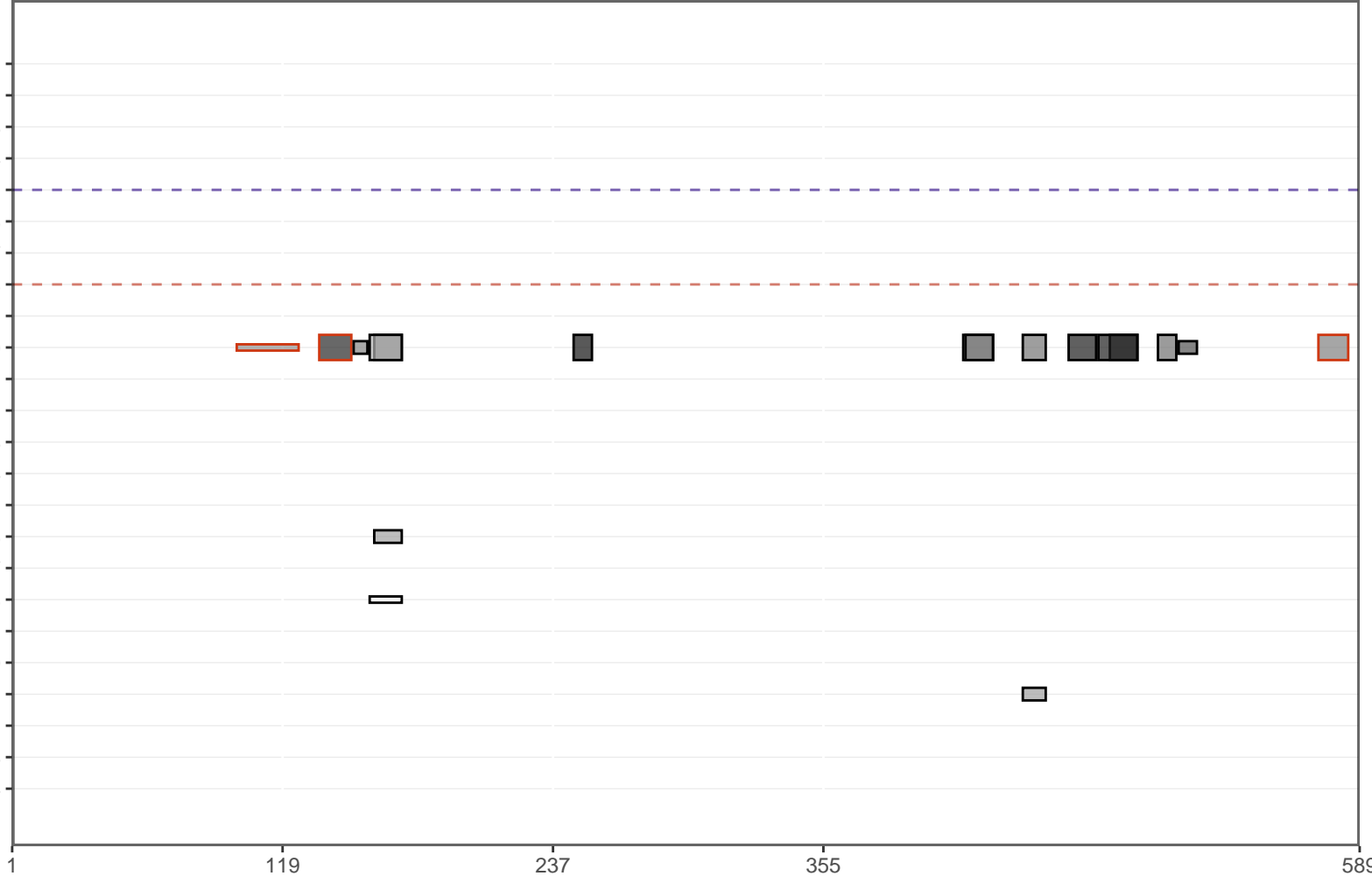
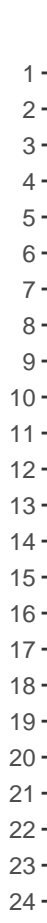
MW indication



Molecular weight

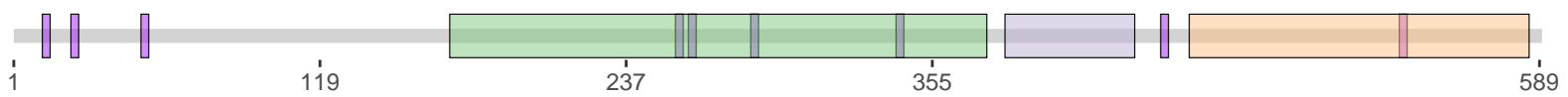


Gel Slice



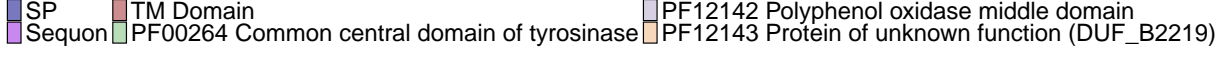
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

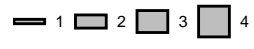


Protein sequence:

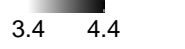
MATNLTMYRQMTNAPCPLLFFGGPYLGTDPSPGMGTIENIPHTPVHWVGGPRNENNVSHGEDMGNFYSGLDPLFYSHHANDRMMWBEWALGGKRRDLTKGDWLNSEFFFYDENRNPFRVKKVRDGLDQKMGDFWAPMPTPWRFKPKRISKDPKGNLGSVPPASKVFPIGKLDRAISFSDRPPSSSRGTQGEKNEQDEMLTFNNIKYDQSKYRFDFVFLNVDKTVNADELQKAEVAGSYTSLPHVHGDNATHVTSVTFQLATELLEDIGLEDEDAAVTVYPTG

NbL17g16350.1 L-arabinokinase-like [MW = 108.33 kDa]

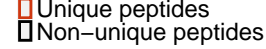
No. of times detected



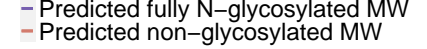
log(intensity)



Values from



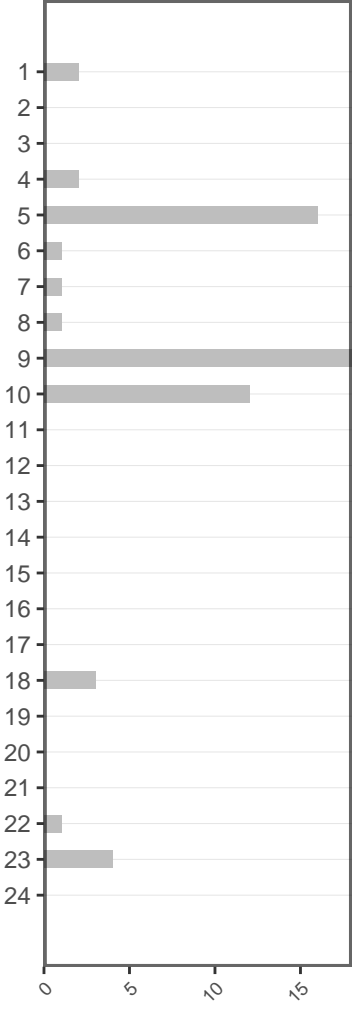
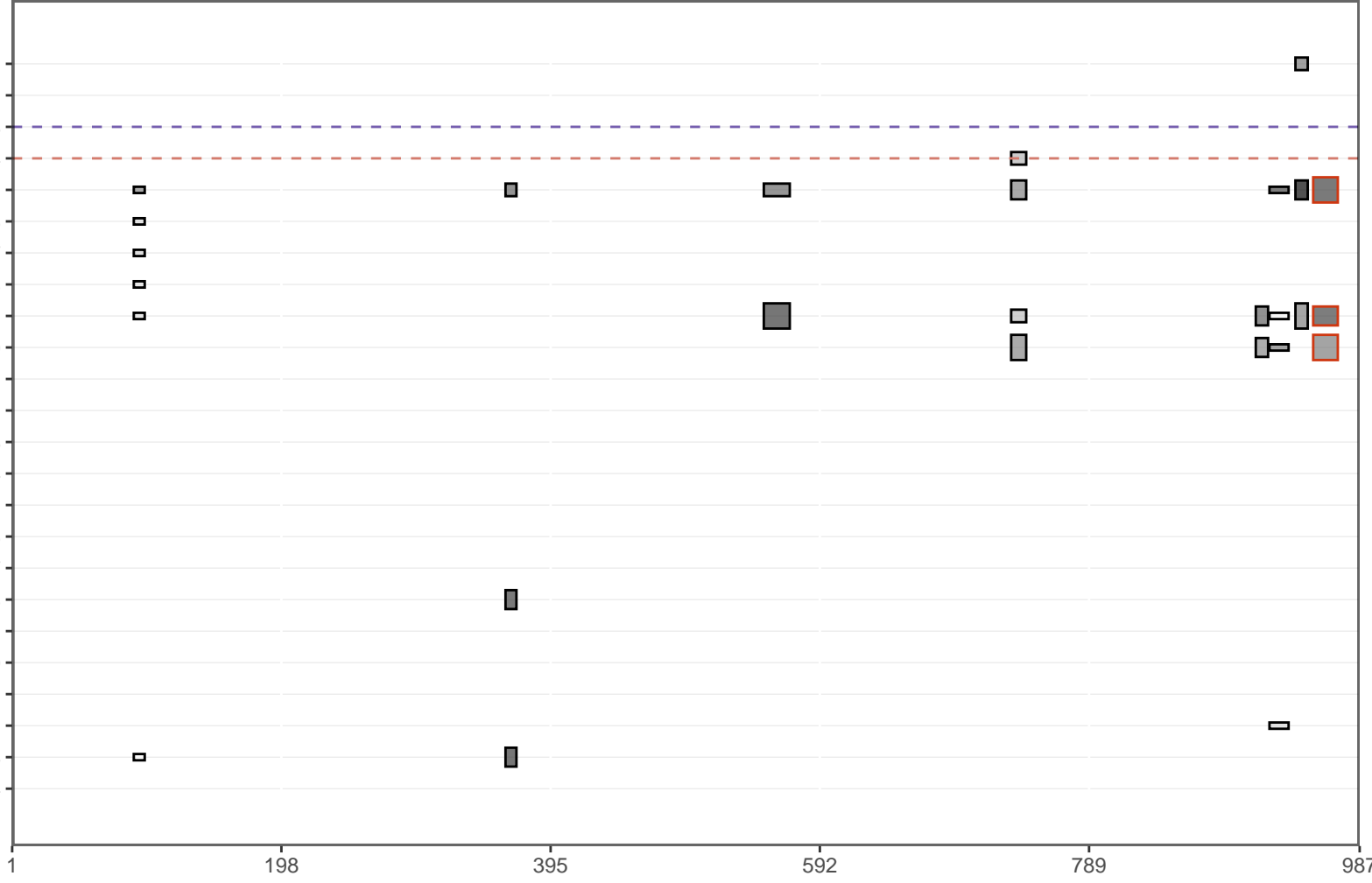
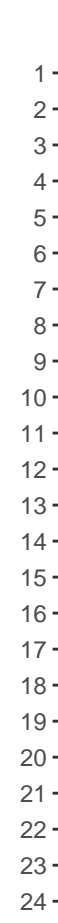
MW indication



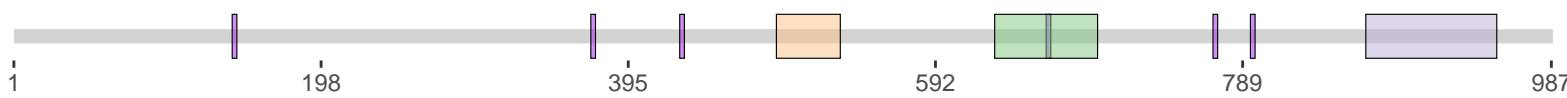
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

AAGLFNVEEDFVARAPGRLEVMGGIADYSGSLVLMPIREACHVAWQKHPKGRUWKHALRQDAKGGGPTFVLGVSYSGSELSNRGPTFMDLSDFLGDEPTTYEKGRQYFARDPGRWAAWVAGTVLVLMKELGIRFENKISGLLVESAVPEKGVGSSAEVEVASMIAAHHGLNPRELALLGKVENHVVSPAPGVMDQMTSACGEANKLLAMVGGPAEVLGLVDIPGHIRVWGDGSRHVEGADYGVGIRGAFMGRREIVAKSKLSQSLSTNGNHTDE

NbL17g16320.1 40S_ribosomal_protein_S6-like [MW = 28.29 kDa]

No. of times detected



log(intensity)



Values from



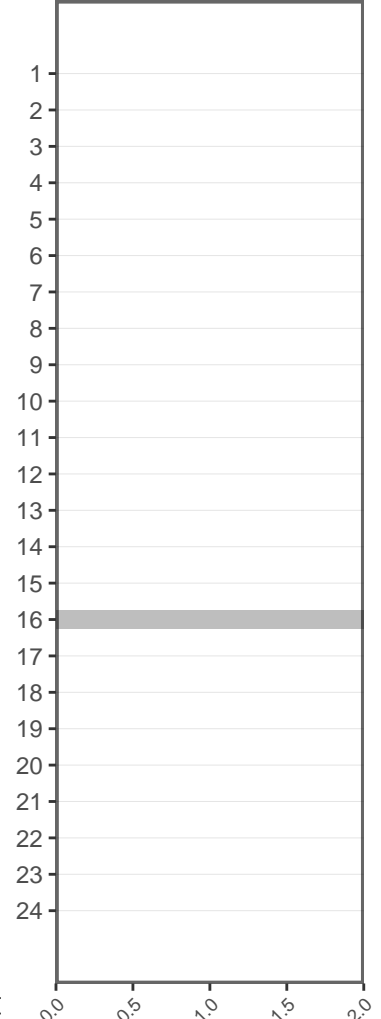
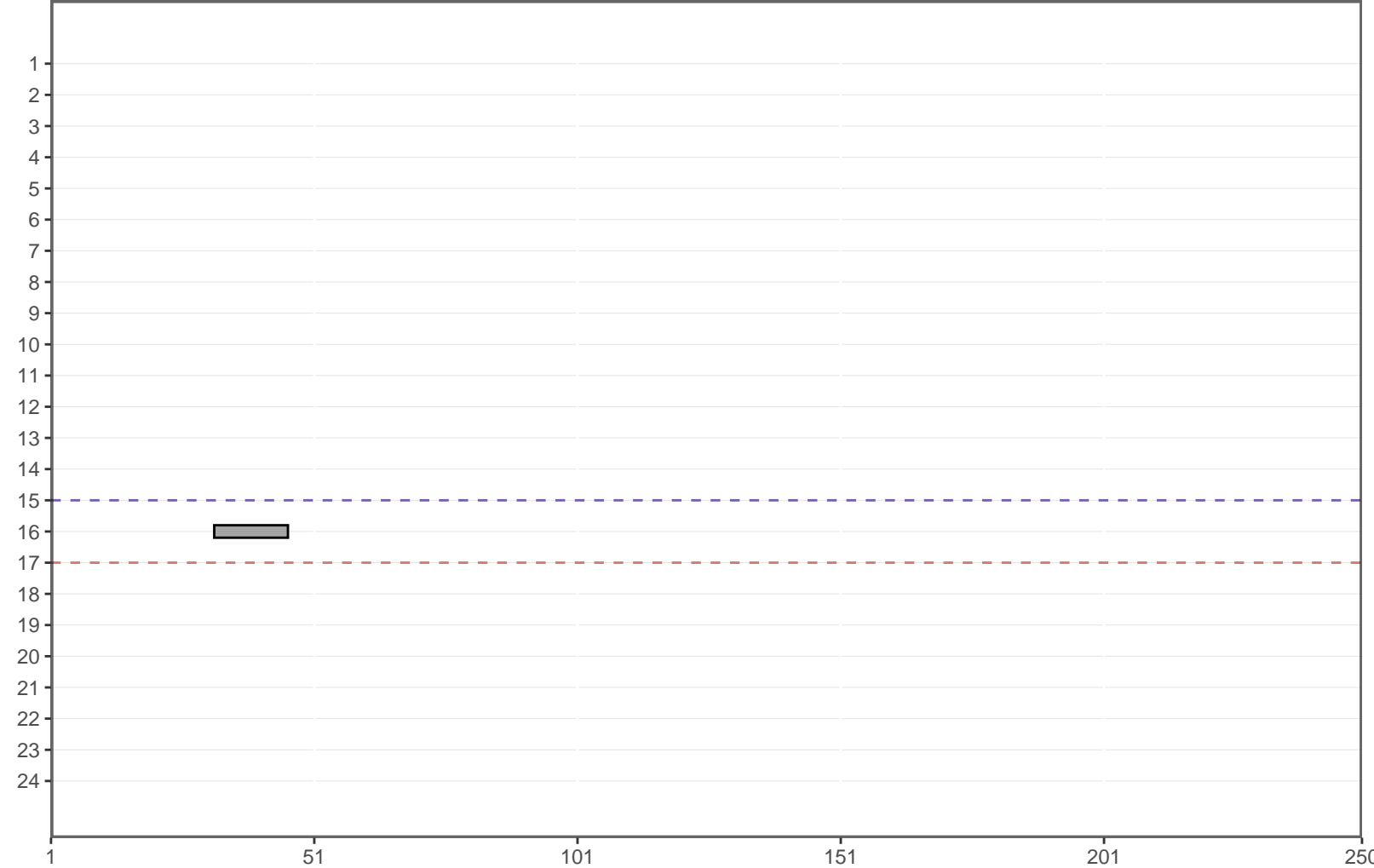
MW indication



Molecular weight

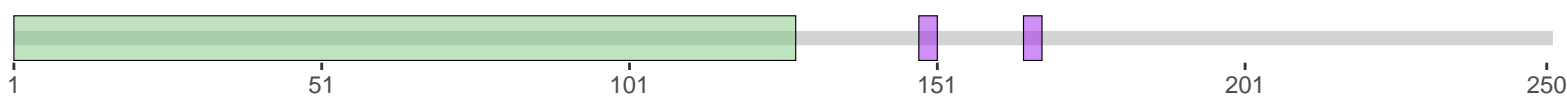


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

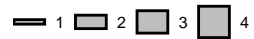


Protein sequence:

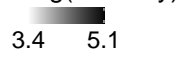
/LNLIYVKKGENLPGLTDFTEKPRMRGPKRASKIRKLFNLSKEDDMRKVYNTYRIRNFTTKTKKASKAPKIGRLVPLFLQRKRARIADKKRIAAKSAEAEYQKLLASRLKEQREKRESEGLAKKRSLSAASKPSIAA*

NbL17g16290.1 cryptochrome_DASH_chloroplastic/mitochondrial [MW = 66.82 kDa]

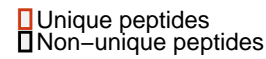
No. of times detected



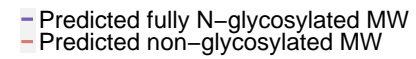
log(intensity)



Values from



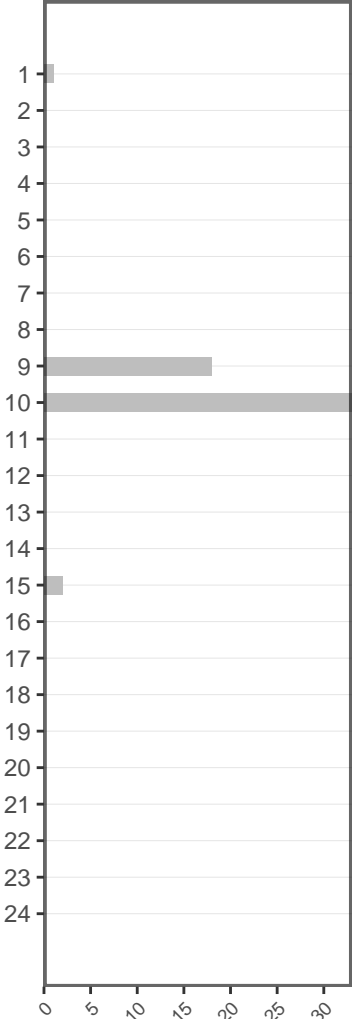
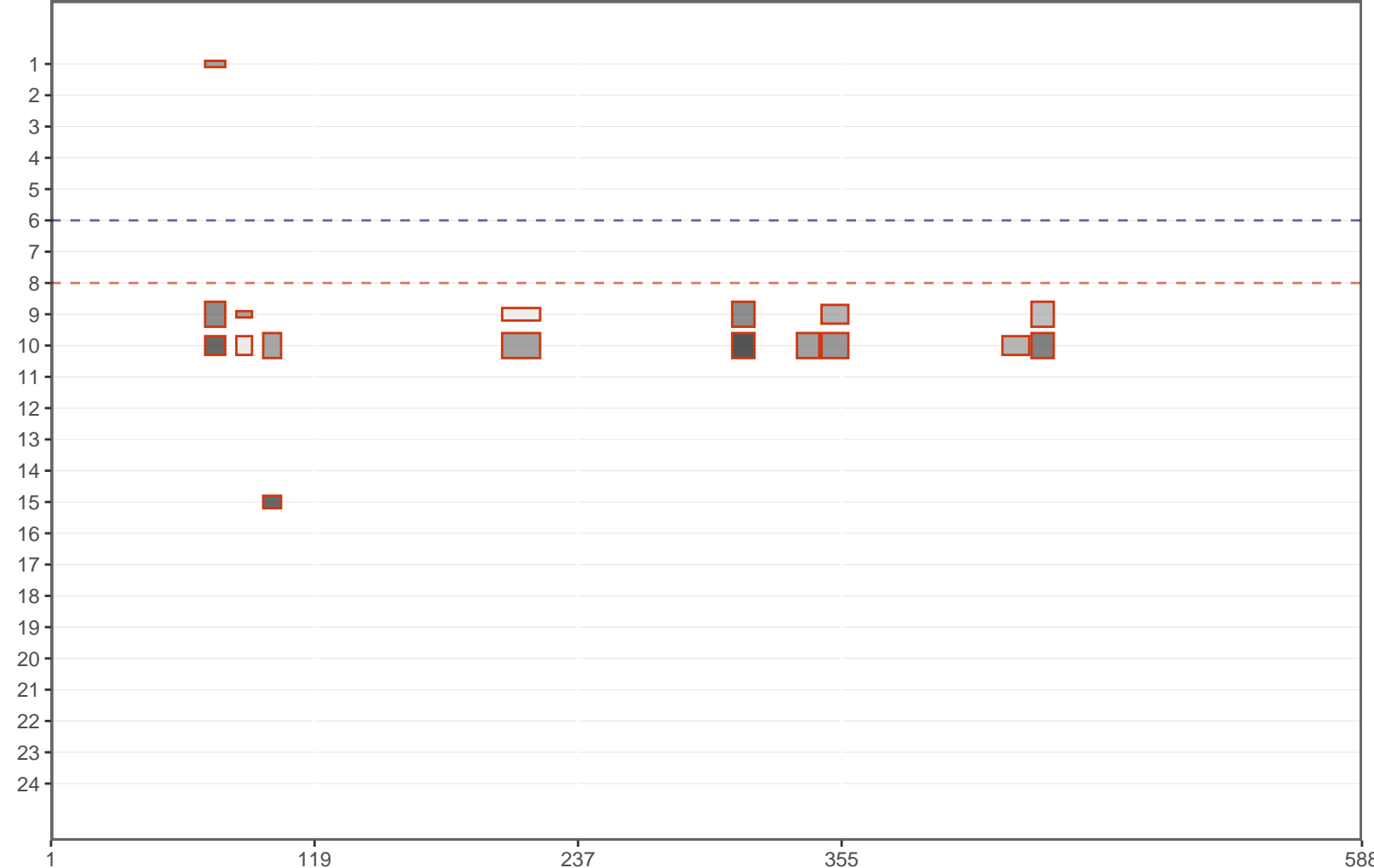
MW indication



Molecular weight



Gel Slice



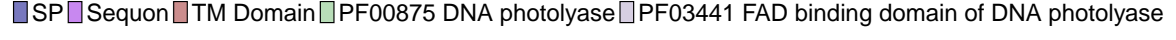
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CVPDYTELGLQSEKVKSGMFKFGESAAALGRVHDVFWKDKLKKVYKTRNGMLGPDVSTKFSFVWLAGSLSRFRFYEEVNRVEKERQSGNDSTVWLFELIWRDVFRLFSKGGNLFHAGSPKRVKVDNWSGDGTFMDAWRRGDTGTVPLIDANMKELDTTGFMSNRGRQVCGFLVRDMGIDWRMGAEFWTFELLDVYDPSNNGWNTFYAGVSGNDPRDRIYFSIPKQGMNDYDEGEFVWVWLFELRALPREKRHSFGMMYKPKVWLNHGVTRKTKGDSKMPYGSRR

NbL17g16230.1 glucan_endo-13-beta-glucosidase_5-like [MW - SP = 50.27 kDa]

No. of times detected



log(intensity)



Values from



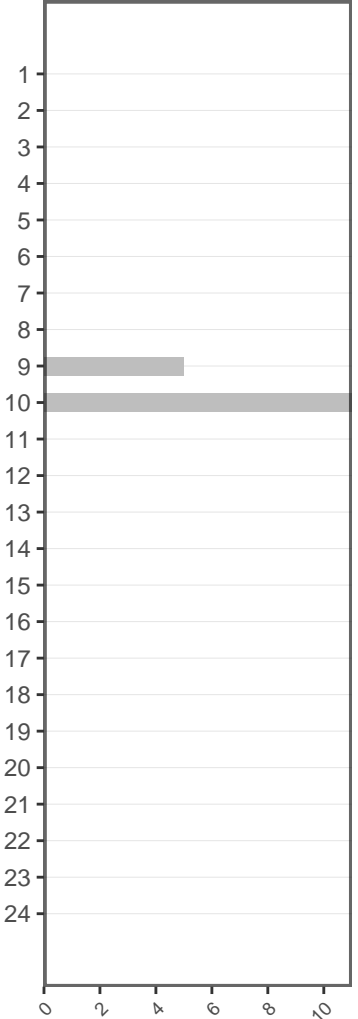
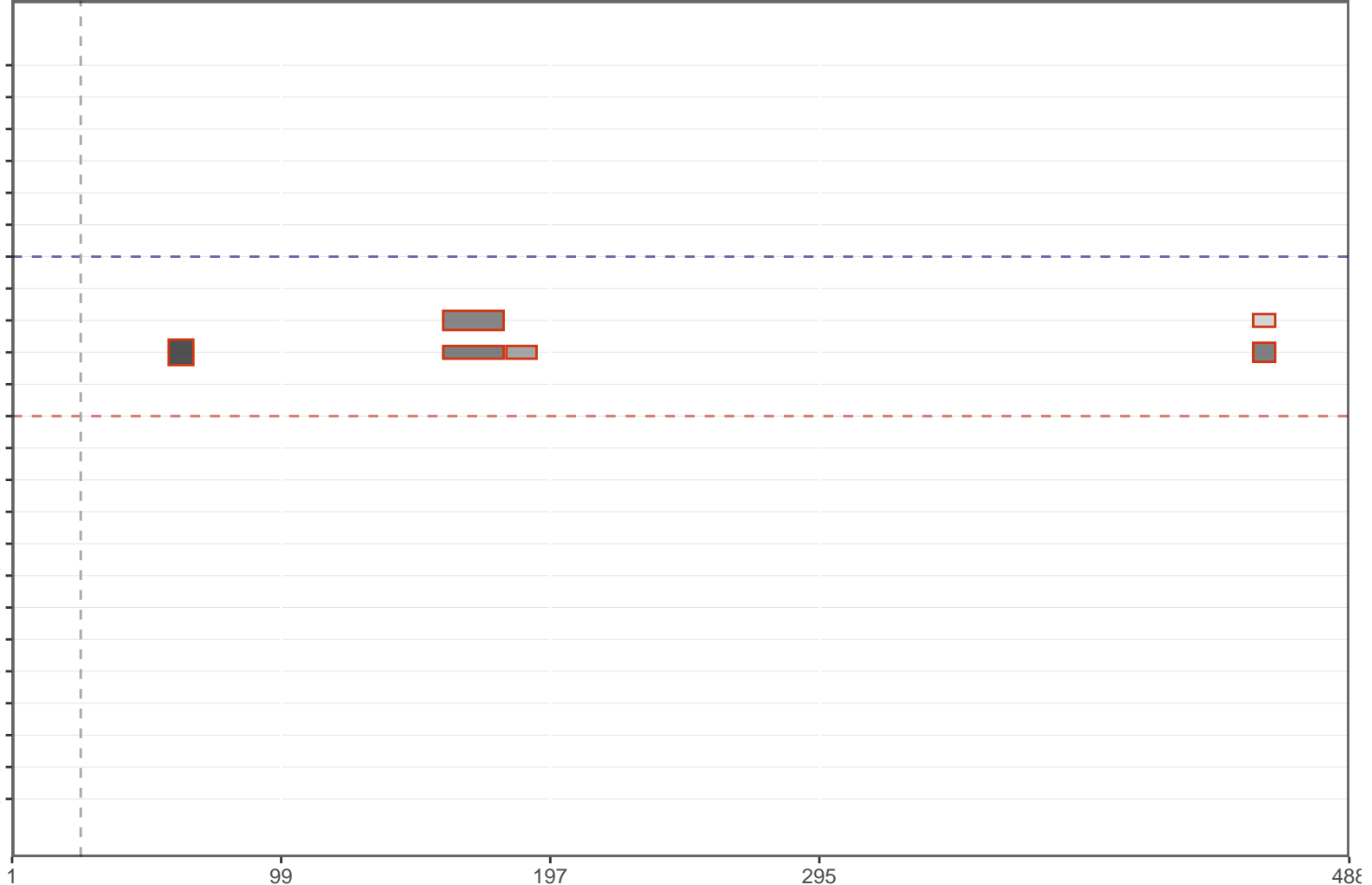
MW indication



Molecular weight



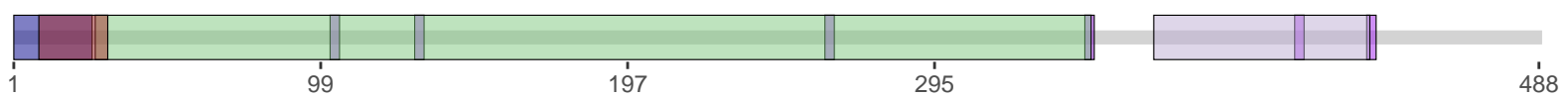
Gel Slice



Protein length

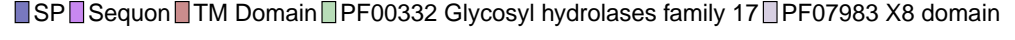


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGKTYNYVDANIGDRLWALQKNGYPMBSHIGEGWPTDGDNYANKAAGRFDNGVFMTHSGGKGTPMRPGIDAYLFLSDIEDAKSIGIQGNFERHWGIFYDGTGPKYVLLAANNKGLVPSGIVYRLARQWCVLLPESALDDPOLADSVGYAGSHADGTSLSGHETSADLDFRGNISYAFNSVYQENDQLPTACKFNLGMVNTNTDPSPPGGCKFKIMIGASSPKNHKGNFTSRPVMMLFLVHLLSLV

NbL17g16140.1 delta-aminolevulinic_acid_dehydratase_chloroplastic-like [MW = 46.71 kDa]

No. of times detected



log(intensity)



Values from

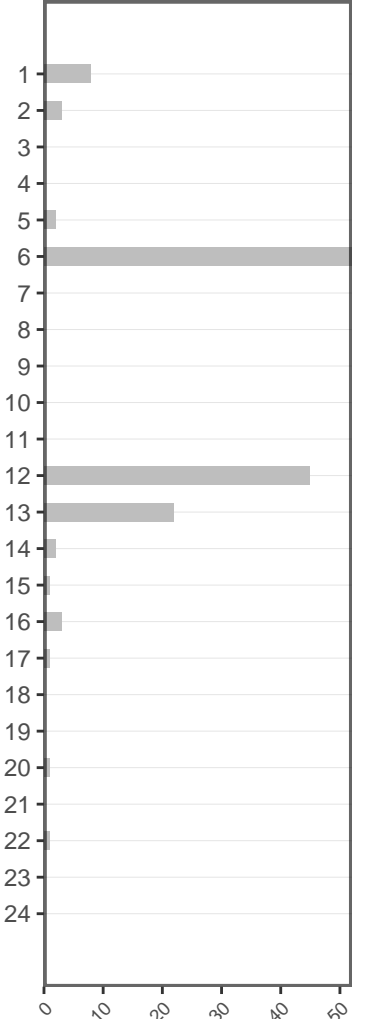
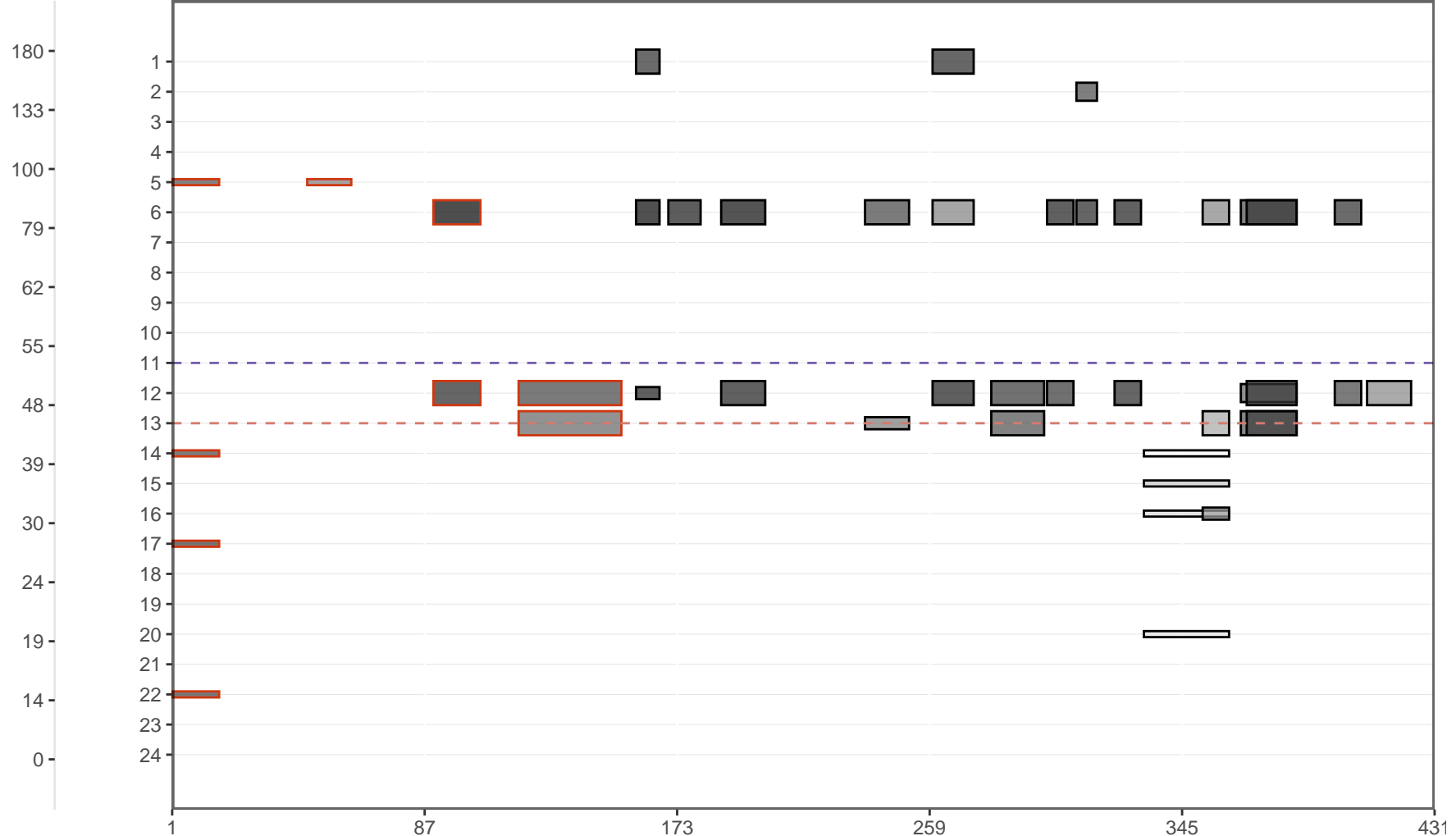


MW indication



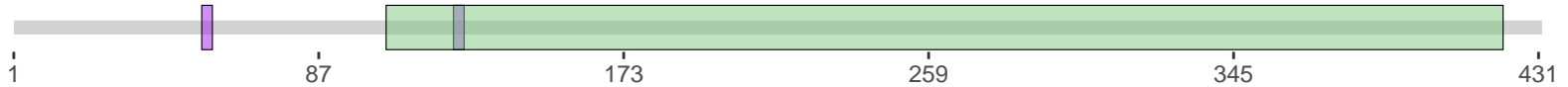
Molecular weight

Gel Slice



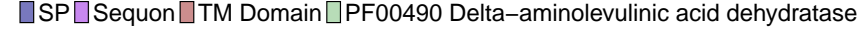
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL17g16130.1 peroxidase_16-like [MW - SP = 33.46 kDa]

No. of times detected



log(intensity)



Values from



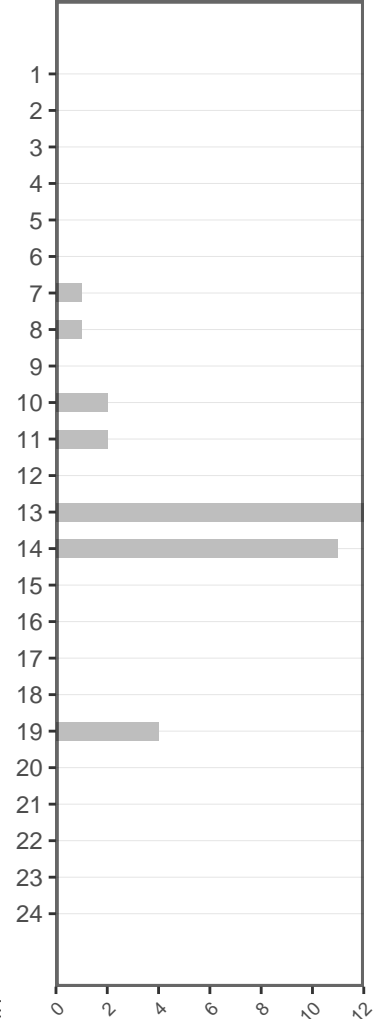
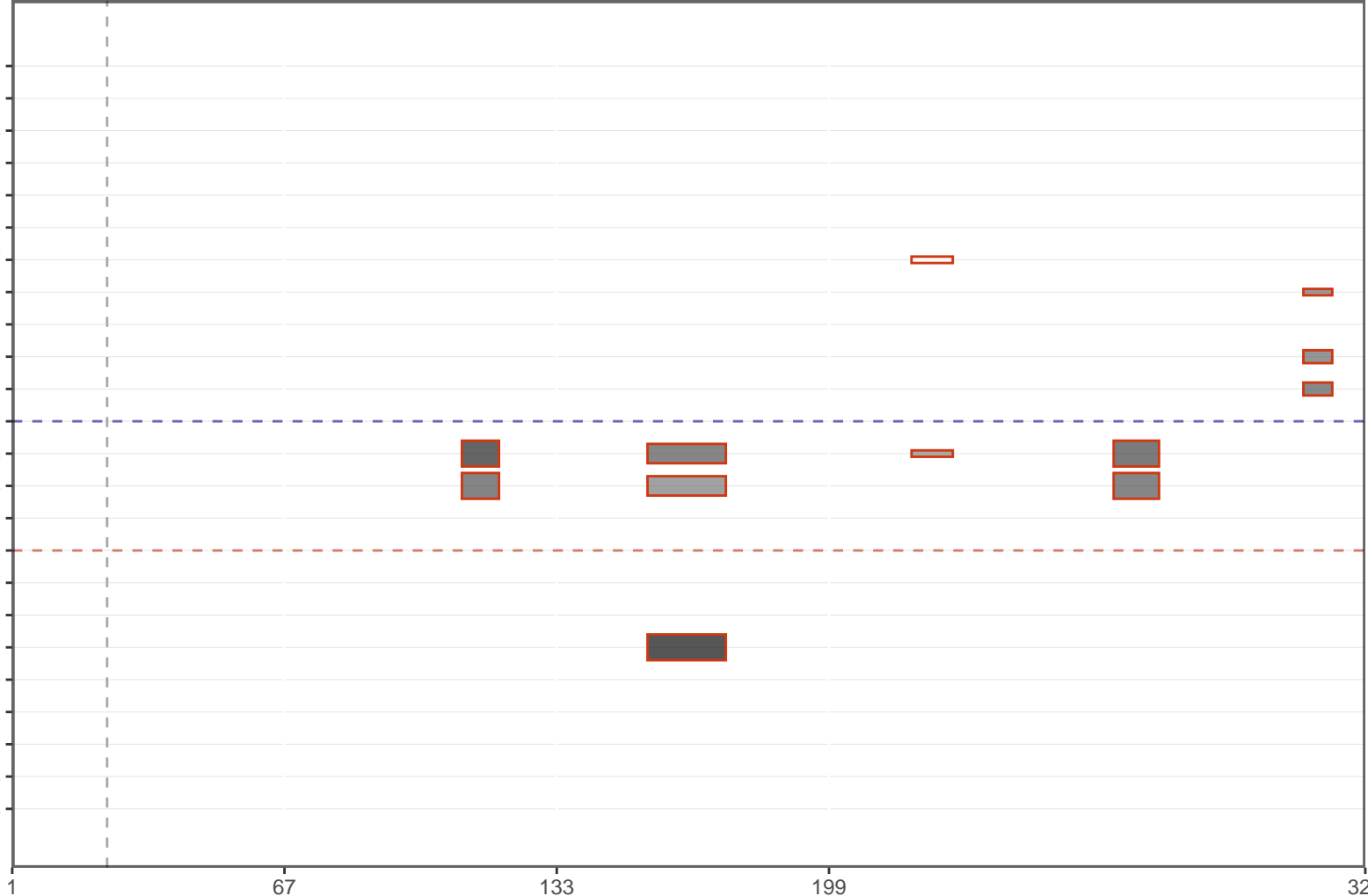
MW indication



Molecular weight



Gel Slice



Protein length

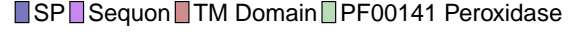


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGRMSSQTSVQNNLPHSNFDLQKLLPMFASRGLSIRLHLLGSAHTLGFSDHNGFSSRLVNFNETHKVDPTDVTYAKKLGEMCPQDALPGVVIPMDPDPQLFDNTYKNIQRGKGLFSDQTLVTKRGRSRIVNFAENKTAFERVFIAMMSKLRFGVTKGLGEIRKDGAVV

NbL17g15990.1 probable_plastid-lipid-associated_protein_10_chloroplastic [MW = 30.53 kDa]

No. of times detected



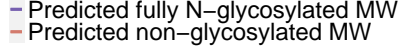
log(intensity)



Values from



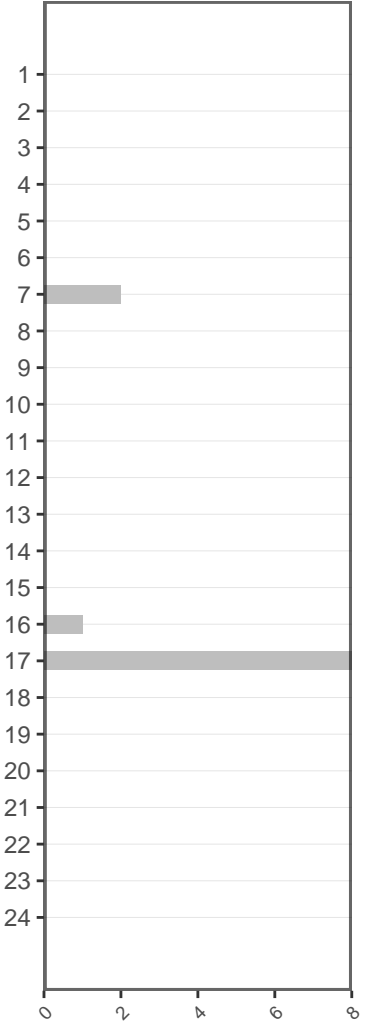
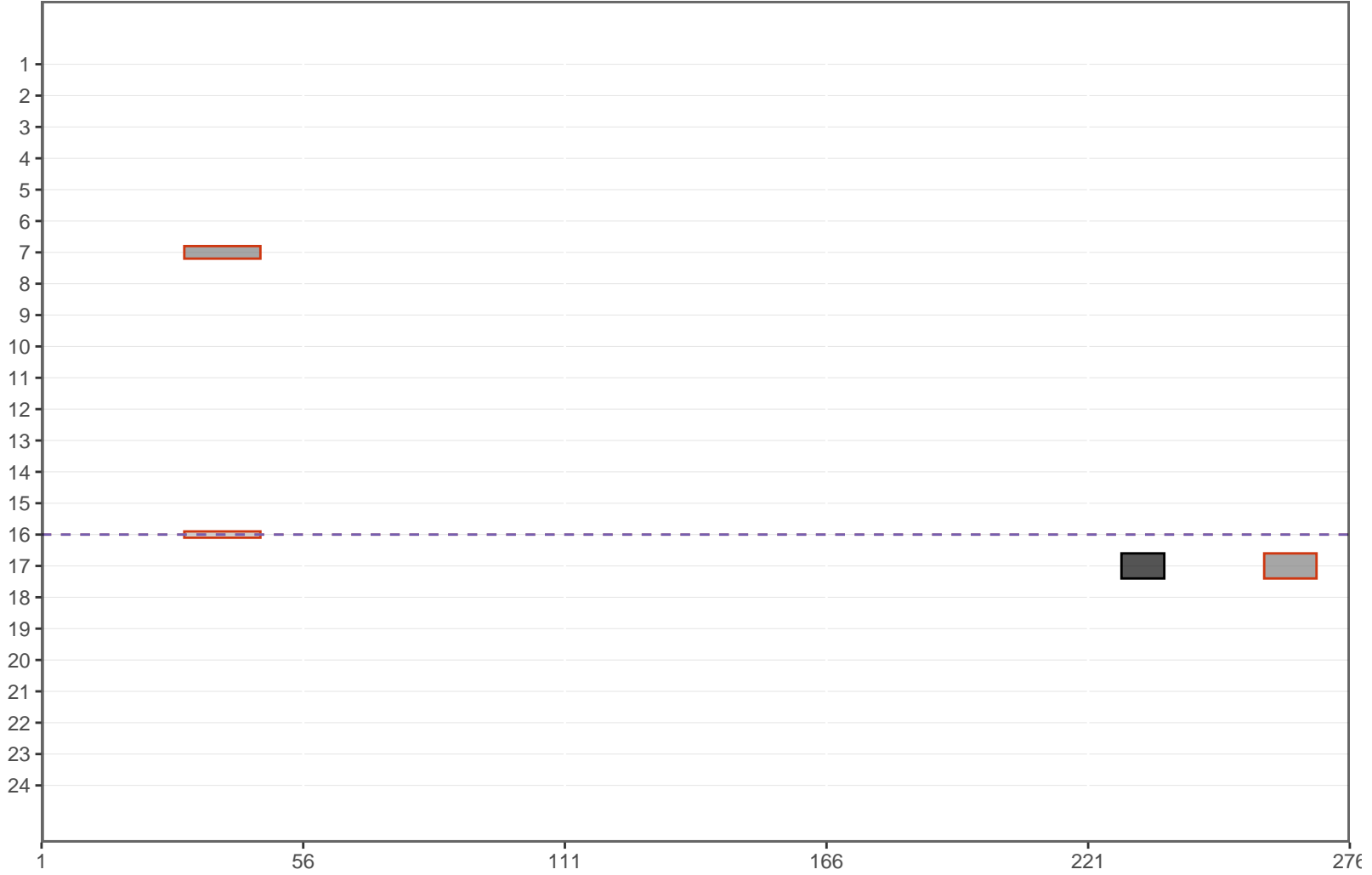
MW indication



Molecular weight

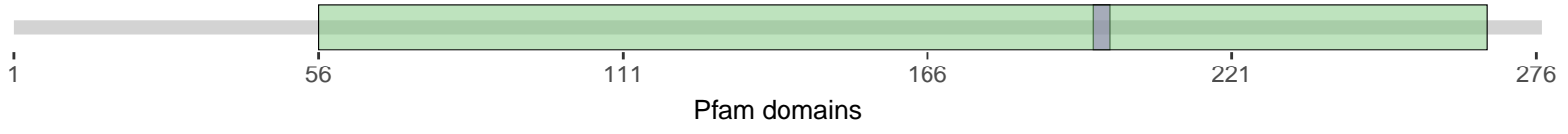


Gel Slice



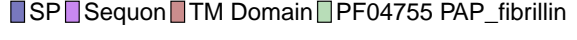
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SLPFFQVGGQFQKFEKBESEKGLRNVKIKWVPRLLKEEGATLVVSARFSDVBARNYLKFEEISLQNNISEDLGVAIPALPRFLSLQVLFIRFKAQVPTSPERRRSVGGGLYLYLVDNNMLLGRAVGGGGVFVTRAGSLT

NbL17g15960.1 probable_tocopherol_cyclase_chloroplastic [MW = 57.53 kDa]

No. of times detected



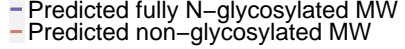
log(intensity)



Values from



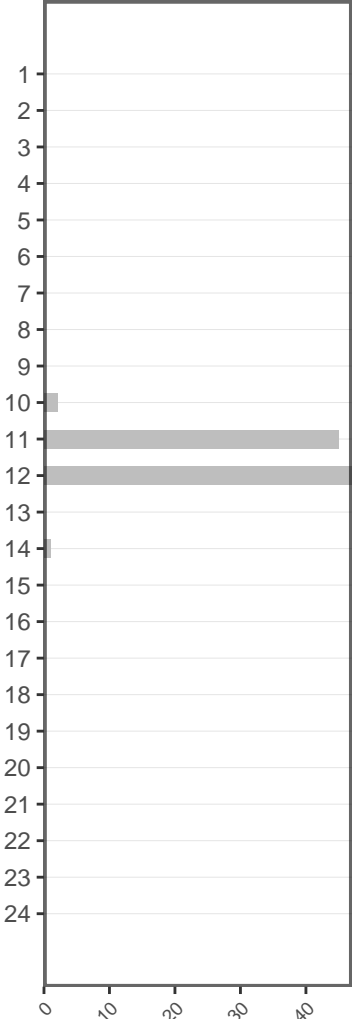
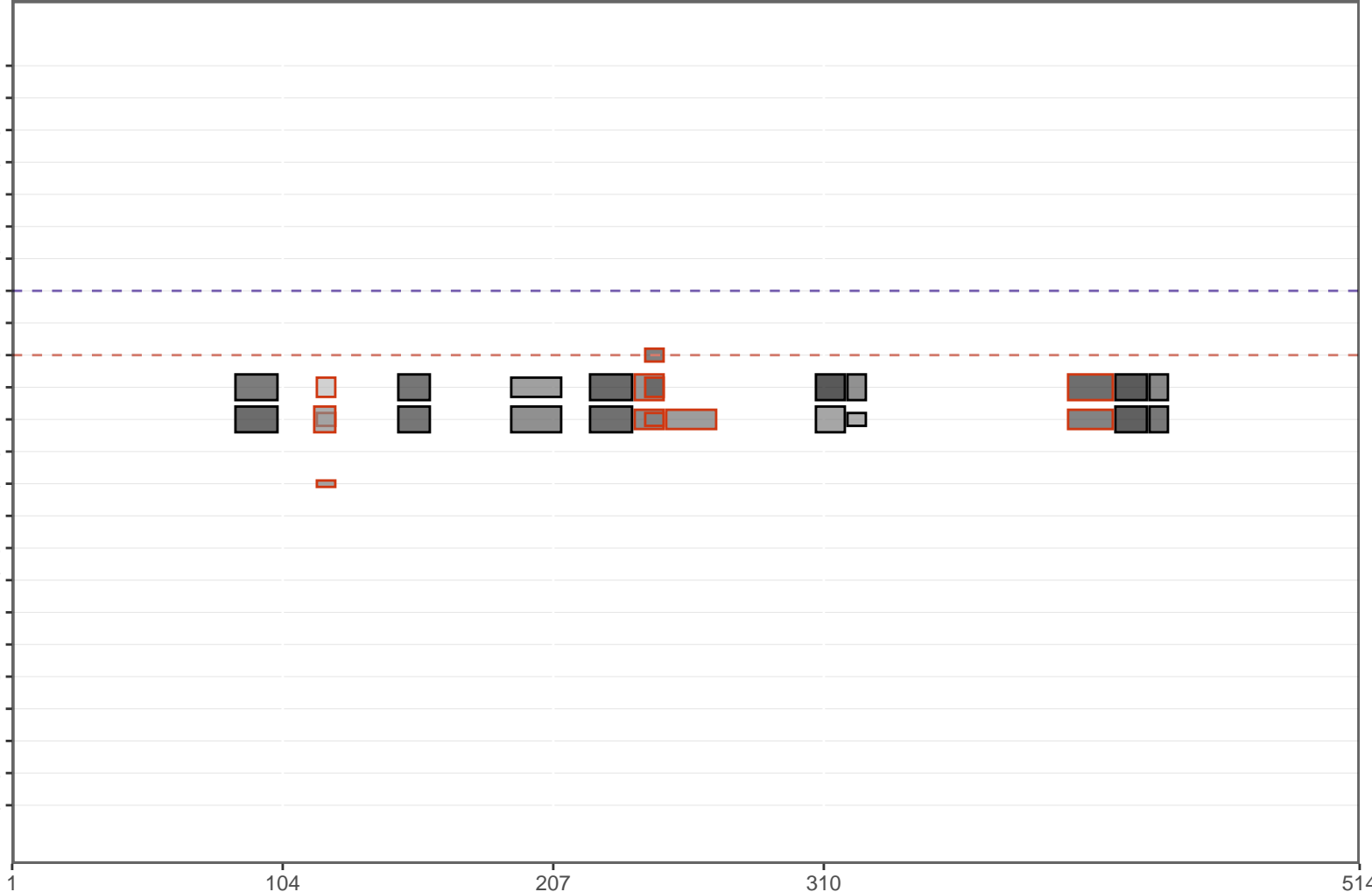
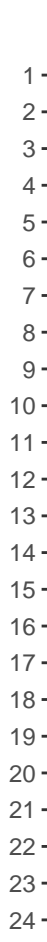
MW indication



Molecular weight

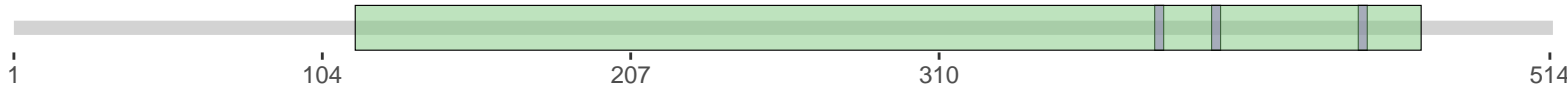


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

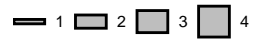


Protein sequence:

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NbL17g15920.1 peroxisomal_fatty_acid_beta-oxidation_multifunctional_protein_AIM1-like [MW = 76.11 kDa]

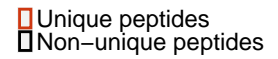
No. of times detected



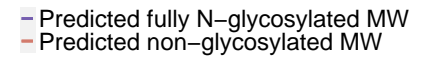
log(intensity)



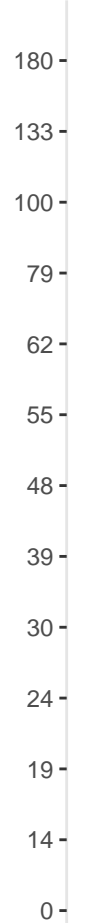
Values from



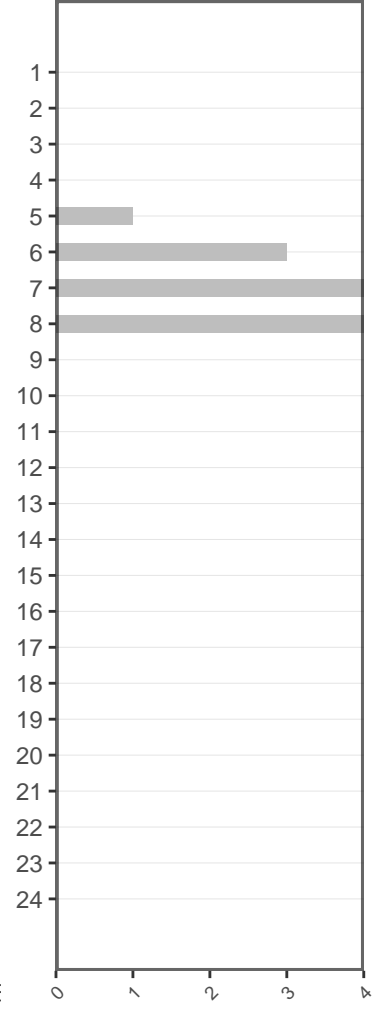
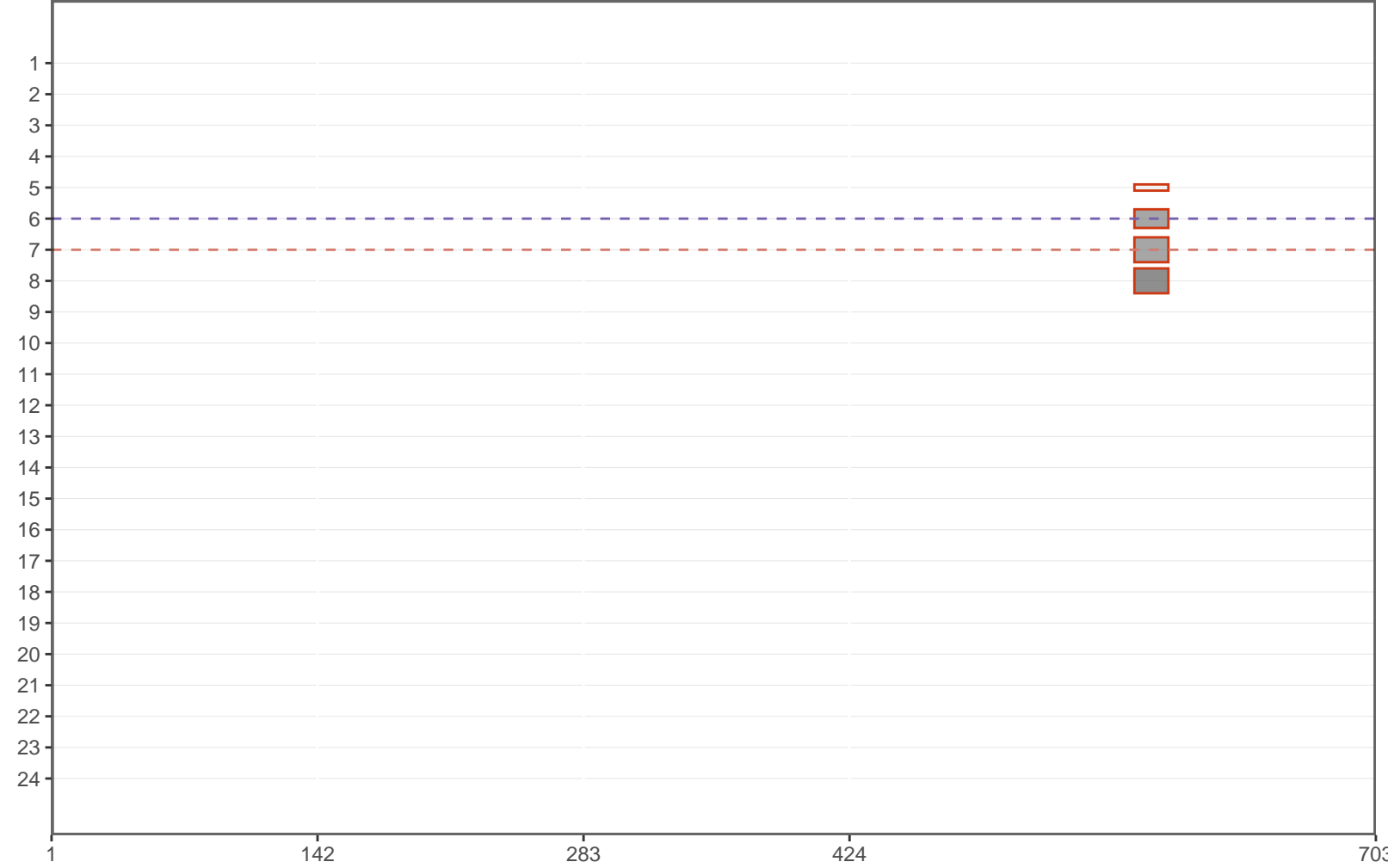
MW indication



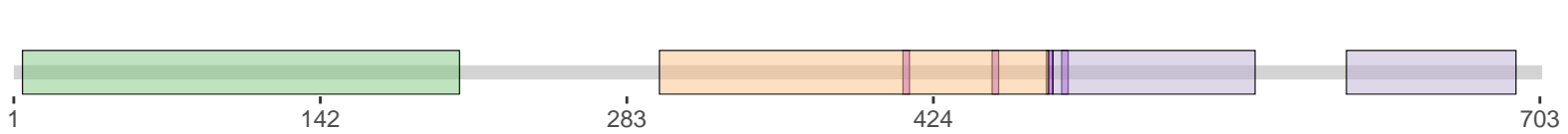
Molecular weight



Gel Slice

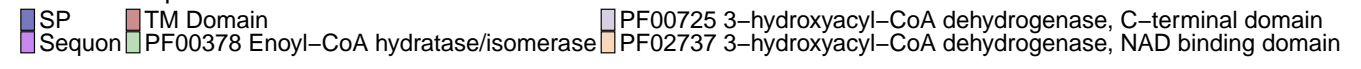


Protein length



Pfam domains

Pfam Description

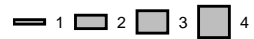


Protein sequence:

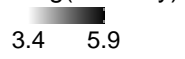
IEANLQGLVTRQGLNGDKMKTLALLKGLDLYEDLKDVMVEAVNEVVSLSKGSIFEDIKYSVSSDCIFASNTSTISLWIGERTSSQDRILGHLFSPAHMMLTVEIVRTEKTSQVIVDVFRTKTKMKKVPVYVYKNGTGFVAVRSEFFVYMGQDPLLANLGVDFRIDRVTDFGMRLGFPLQDLSDYGLFGLAVKKEVAAPDFRAFQSPVQLVMENGRREGKNGKGYTYTKKSGKPEADPVSQVVEESMRFTNAPGKPSVTDDEILEMIFFPVNEACRVIEEGIVRASD

NbL17g15860.1 eukaryotic_translation_initiation_factor_3_subunit_L-like [MW = 60.65 kDa]

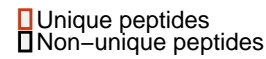
No. of times detected



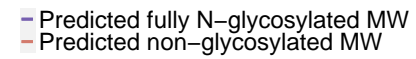
log(intensity)



Values from



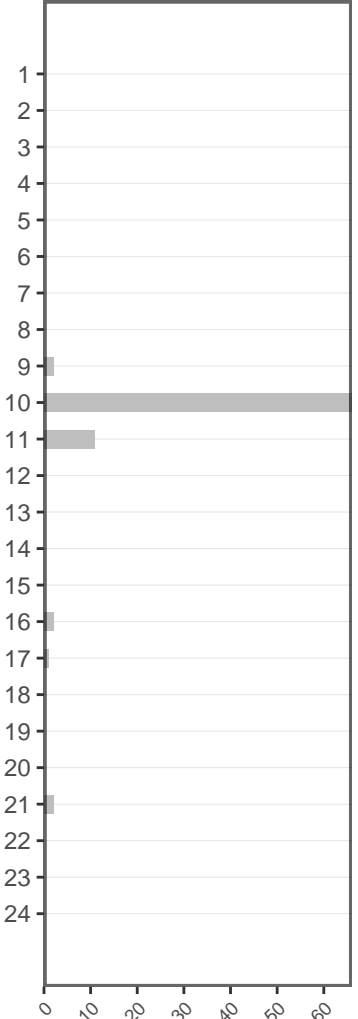
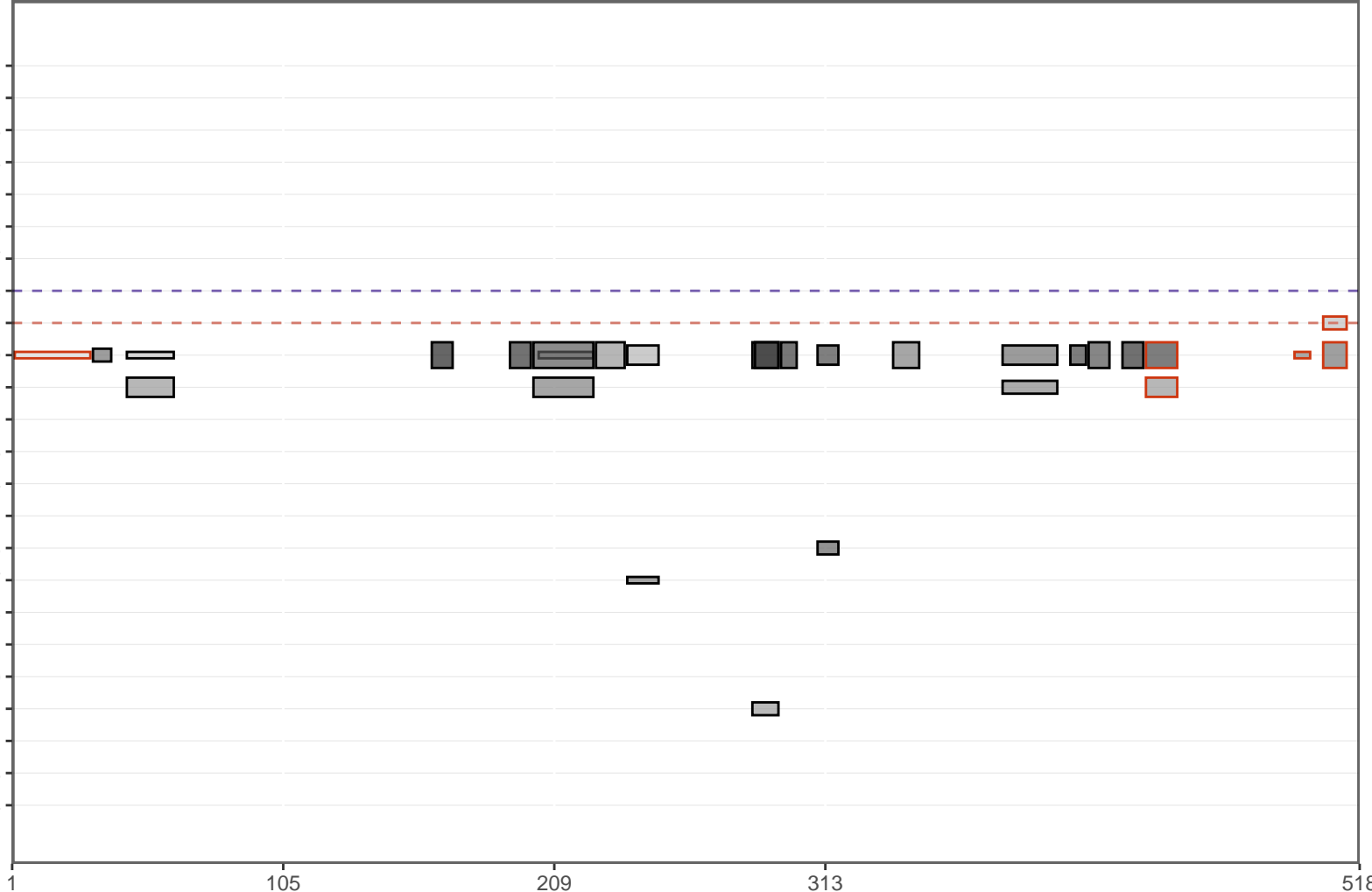
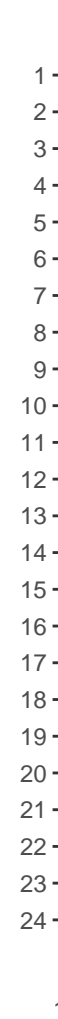
MW indication



Molecular weight

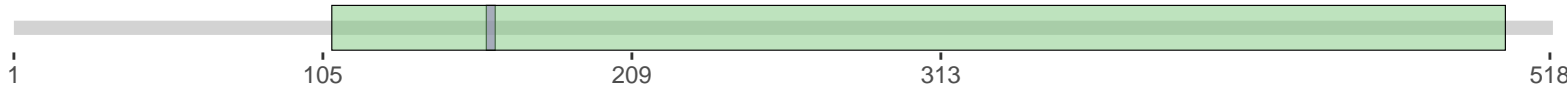


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LDGYHTGLKCLRNDITGGQVYFVSGSHTRHYHGFANLMRRVYDAIGEFNKILVYKTKGYHQKSPQVEGKQKNEGMVALLAISLGLPQVQLVEETVNSQLREKYGEMKARMGRVYDDEAFALYDELFSYAGFKFPTSPSAPSEEFPLVNYNGDAYRLGLKLFLEVKQGGQLLAGVRTLKVKYVSTISLGLKLANVMEVDEPTLRTLMTYKHKTHAVDDEGKFTSNADVDFYIDEEMRIVVESKPAKKYGDVFLRGIKLEGITDIDRIKLDI

NbL17g15850.1 aspartate_aminotransferase_cytoplasmic [MW = 49.32 kDa]

No. of times detected



log(intensity)



Values from



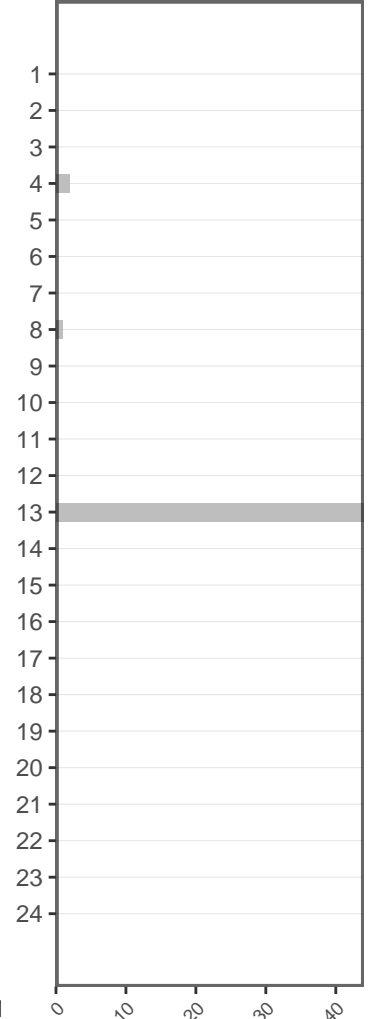
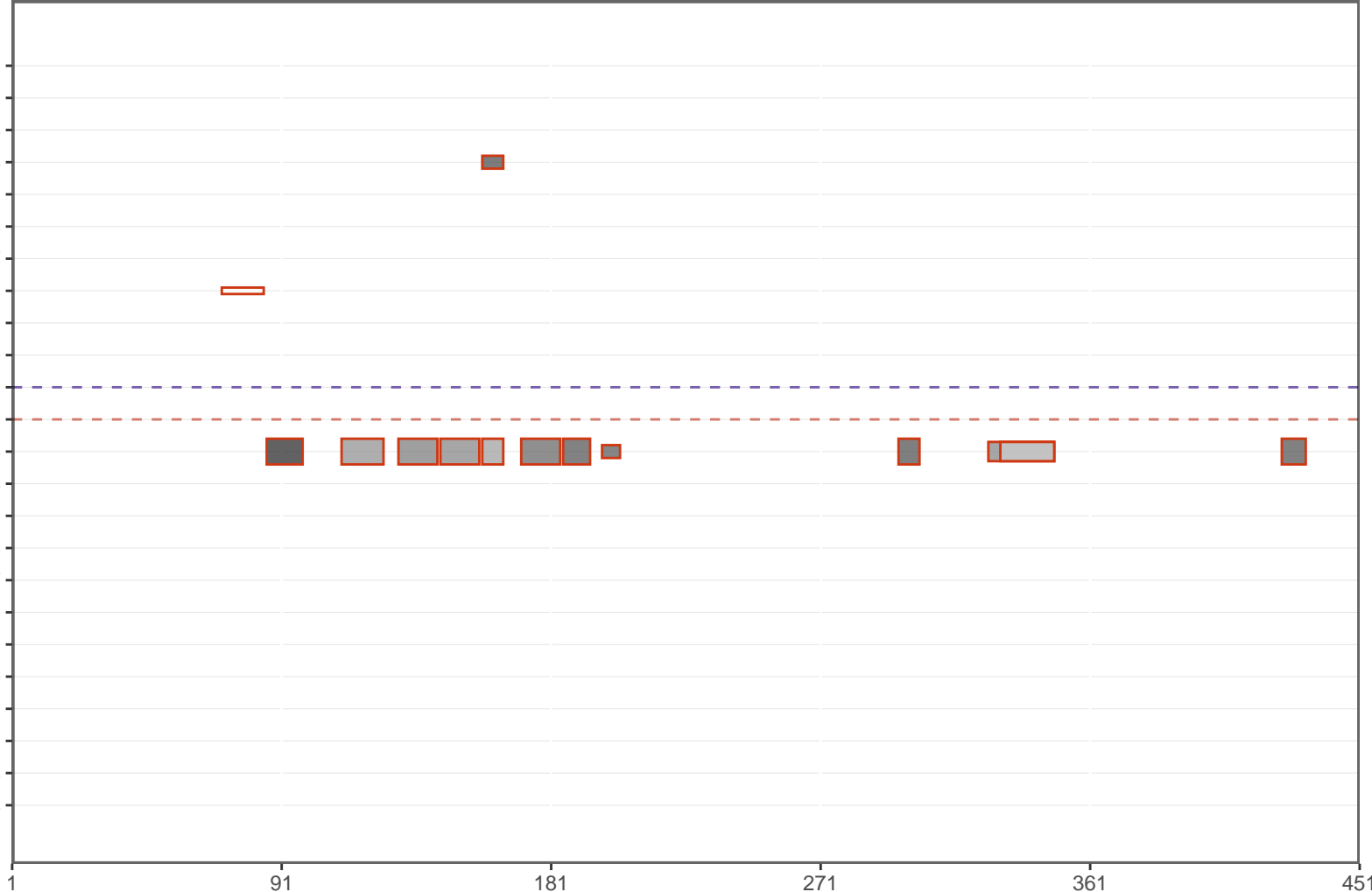
MW indication



Molecular weight



Gel Slice

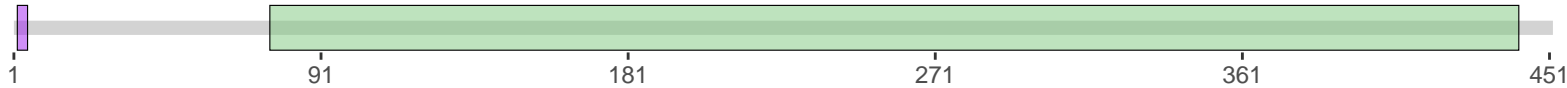


Peptide counts over 4 repeats

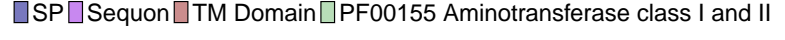
Protein length



Pfam domains



Pfam Description



Protein sequence:

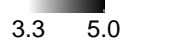
EDLGSAPSGAIVLLHADAHNPTGVDPDIDGWEQIRLMLRSRGLLPPFDSSAVGFGFASGLSDTDAGSVMFVADGGVLLVGSVYANNMGLYGERVGSALSGVRNADVASRVEGSLKLVIRPMYSNPPHSGASVATLKERMMYHEVTLKAMADRIRRMGOLFDFALRARGTQGDWSHIKGMFTFTGLNSEQVAFMKEYHYMTSDGRISMAGLSERTVPHLADAHVAVARAR

NbL17g15830.1 la_protein_1 [MW = 51.5 kDa]

No. of times detected



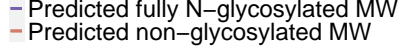
log(intensity)



Values from

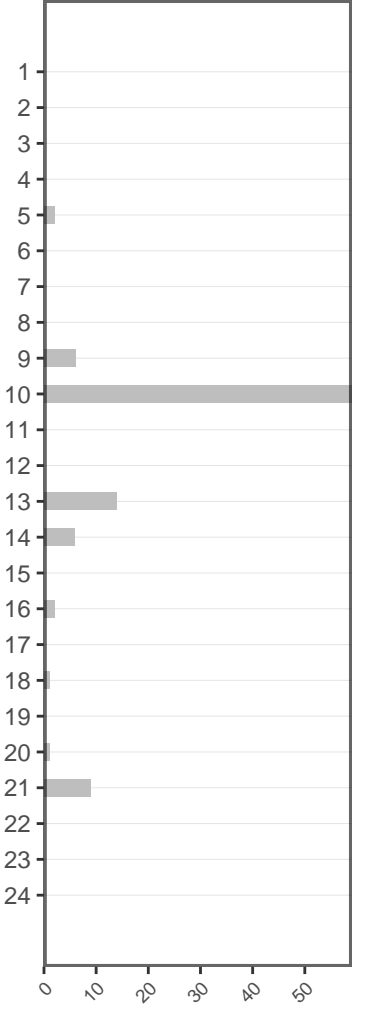
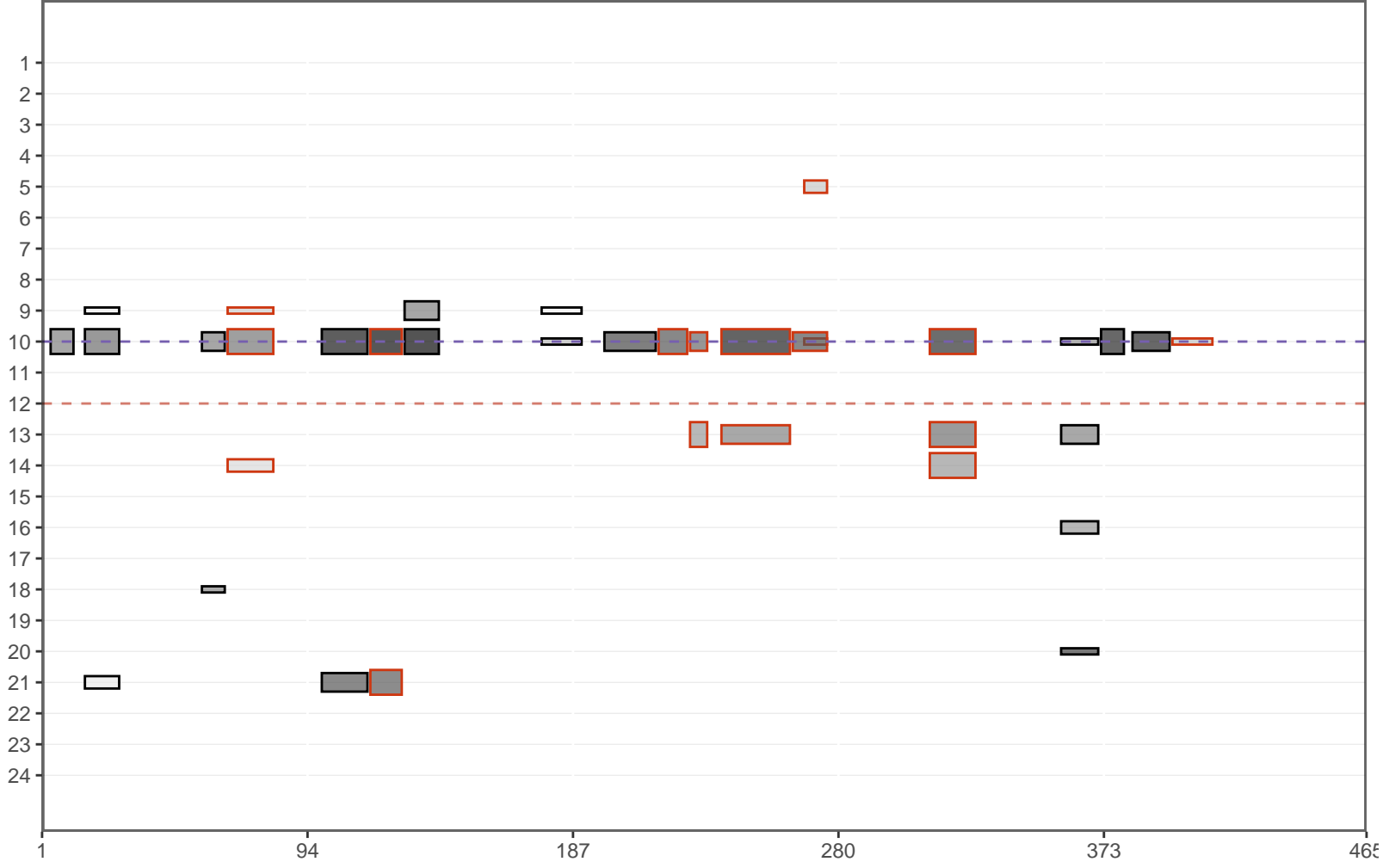
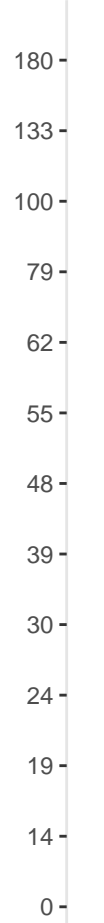


MW indication



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DYPKQLIAFLKLRKRSSTEGMGNHGAASASAPETGQNKETTKDKNVETEEKVSEDKDEEDNNEKGDKEKDAENGSGGETDVGMPPEAVENKSVESPTTEEDDGAPEAEKLSIAACKNDKQVAMREDLKVDFQKGTWVDFDTGSGEGYRIFENEGAAQKAAAGVLAEEGGLTKVNFALDPLVTDGAEKEYWEMFRNNGDKRDFNKNRGRGRYNRGGKHSRFRGNDSSGGRFNKFKQKVRT

NbL17g15800.1 coiled-coil_domain-containing_protein_25 [MW = 25.3 kDa]

No. of times detected



log(intensity)



Values from



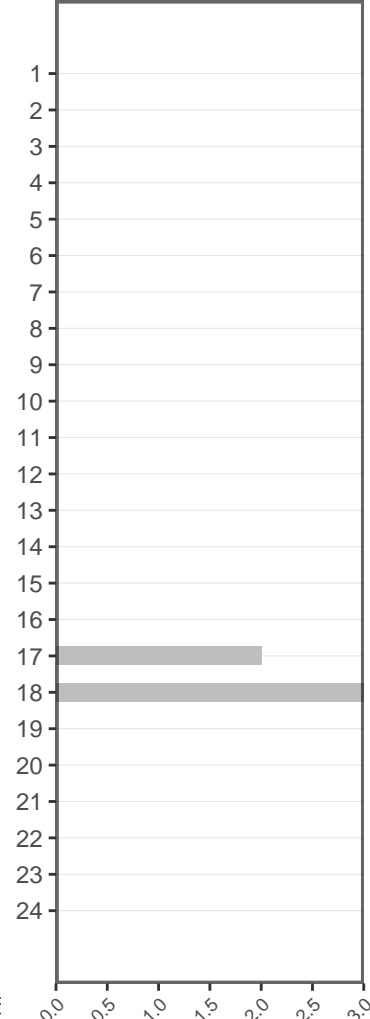
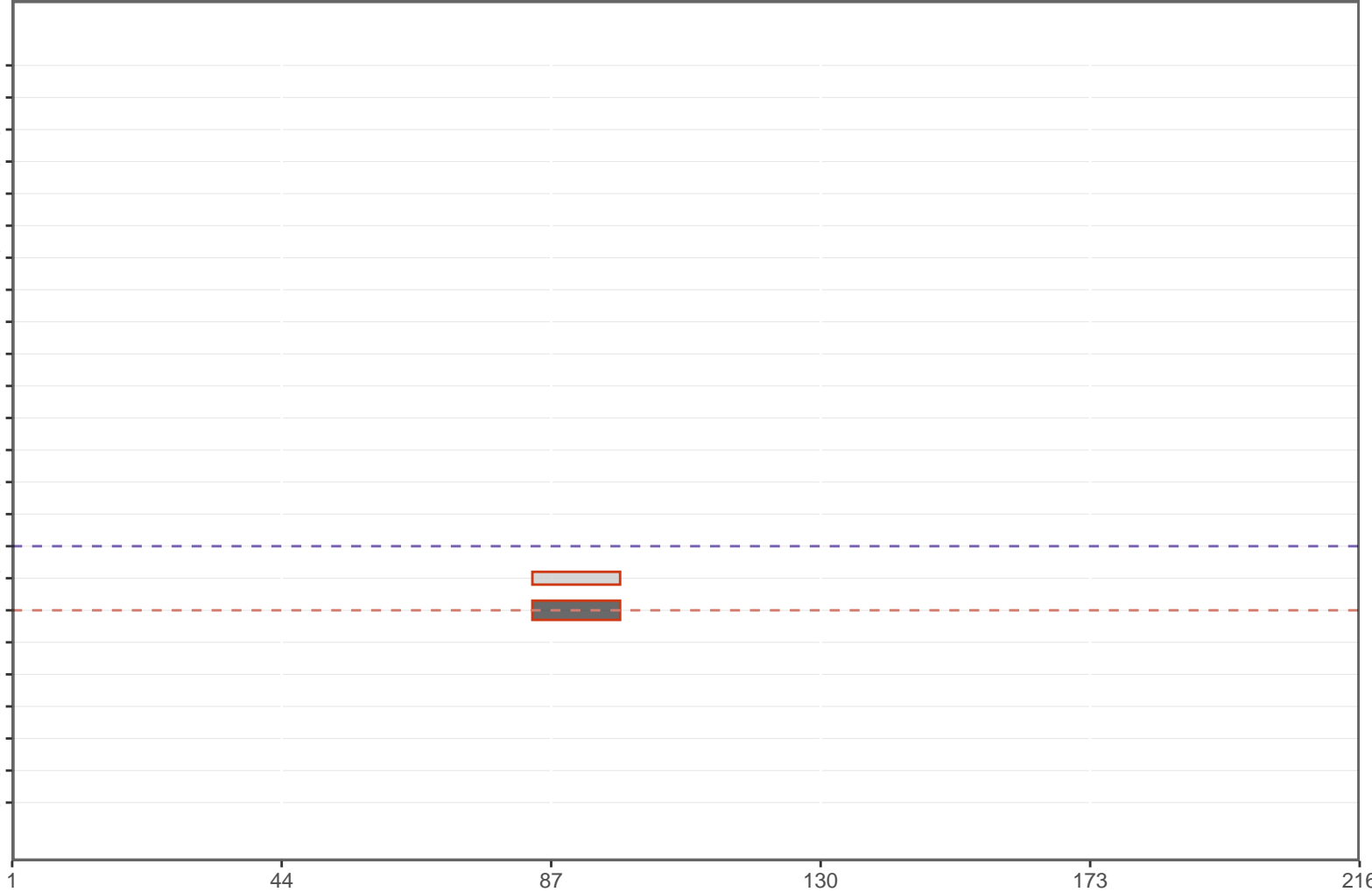
MW indication



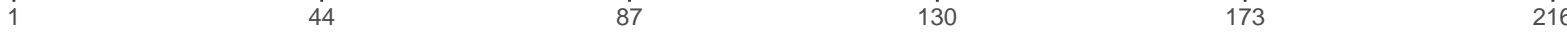
Molecular weight



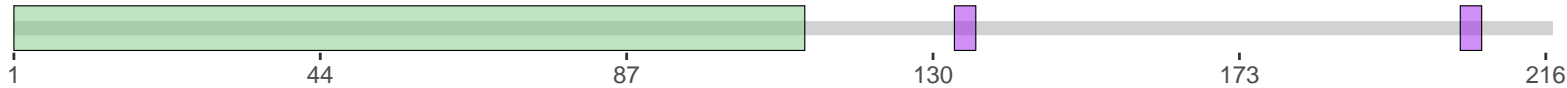
Gel Slice



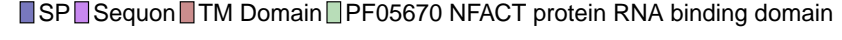
Protein length



Pfam domains



Pfam Description



Protein sequence:

ILKKTASMDVGVQVSPHNPKMVRTKVKVEKRINEIVNLRNRTKVKERKPKDLKAEREAVNAEAERKQDLREKKRREDMDRLEKERGAEMRISYKYLWADKMTSNKDIASNTKSLQEEEDFM

NbL17g15610.1 54S_ribosomal_protein_L24_mitochondrial [MW = 24.37 kDa]

No. of times detected



log(intensity)



Values from



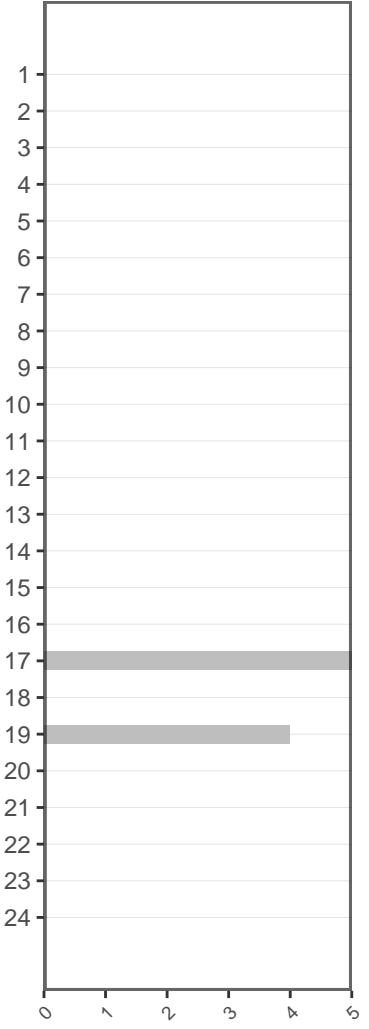
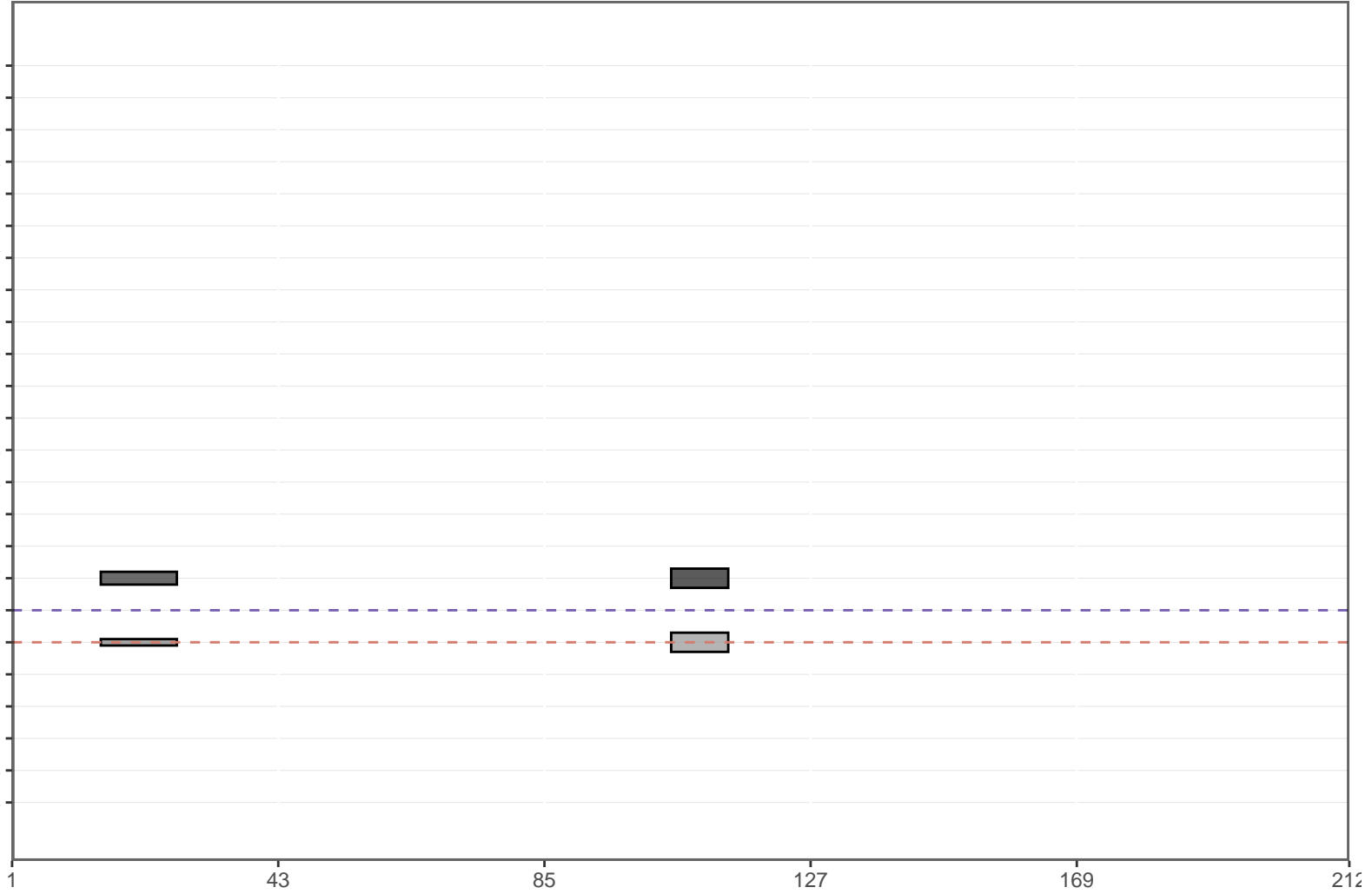
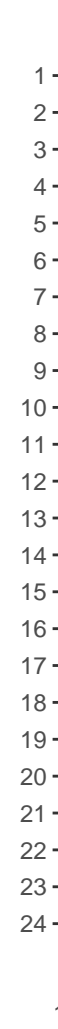
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

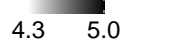
VYTHALRCIDKAGGIDVLLKTPYHEMDTEGLFWAKIKIYEELGKMEVVFPTPEAKLEEGFREVLEERAAARREARRKMYGWSFKSELKADSEGTDGEGVLOGDFHEGMVNAV

NbL17g15510.1 50S_ribosomal_protein_L17-like [MW = 18.46 kDa]

No. of times detected



log(intensity)



Values from



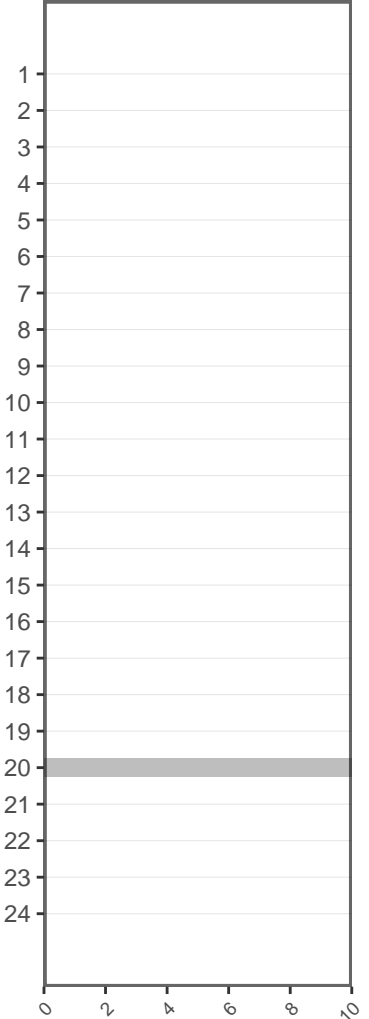
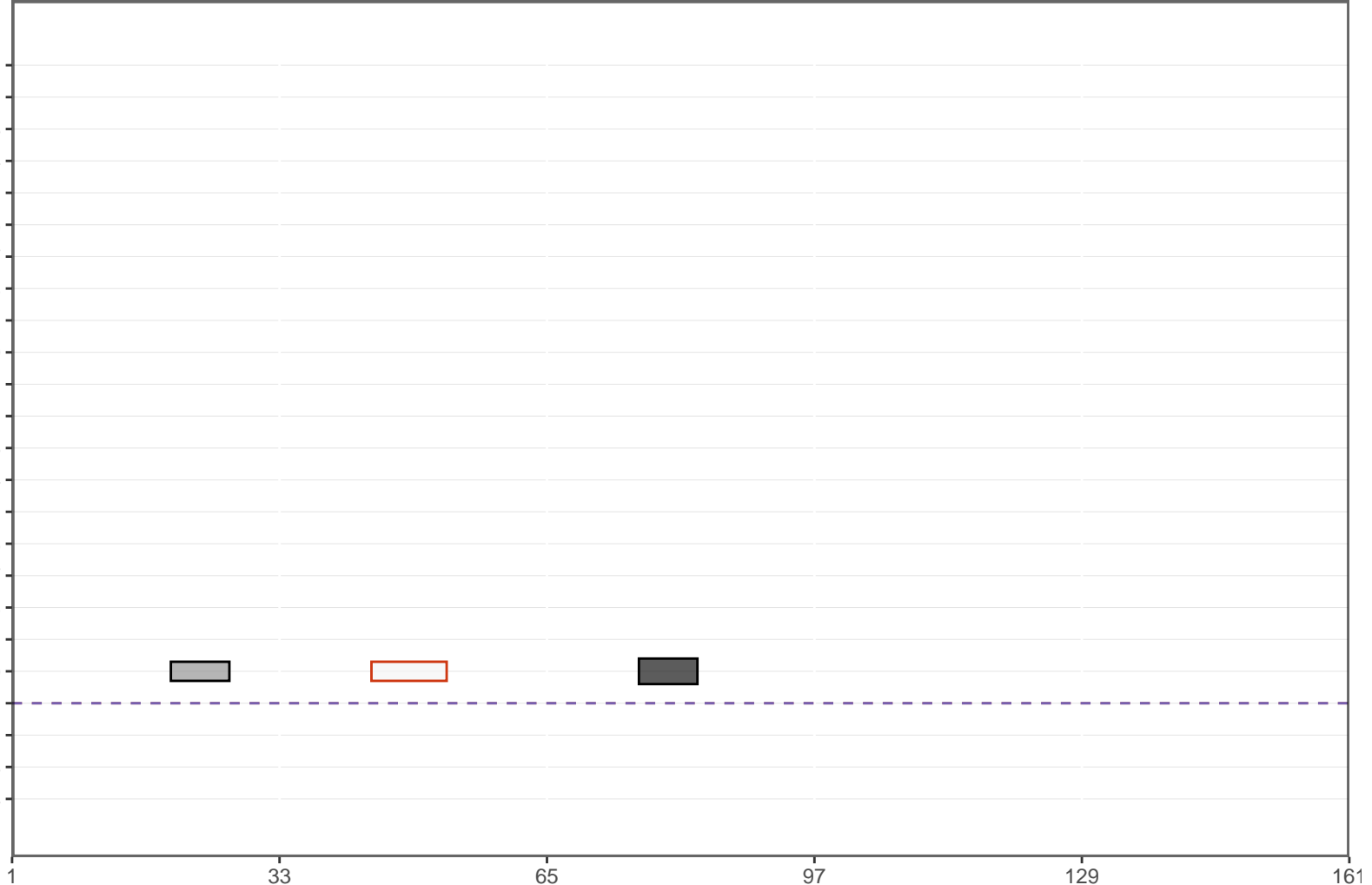
MW indication



Molecular weight



Gel Slice

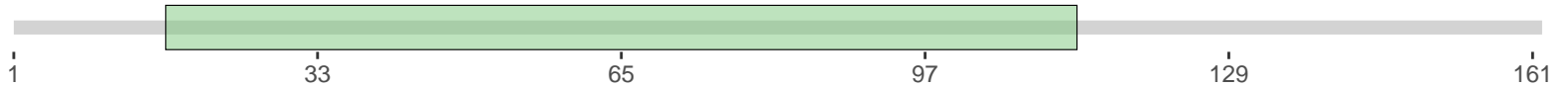


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

VRGDDVHKLFTLAWRYKDRAGGTRVLRTRIRRVGDAAPMAVIEFDRENELRQSKFPNPPQPRPMDPWTRELRGRGFAPPKKEEKSSDSDP

NbL17g15420.1 GDSL_esterase/lipase_CPRD49-like [MW = 29.06 kDa]

No. of times detected



log(intensity)



Values from



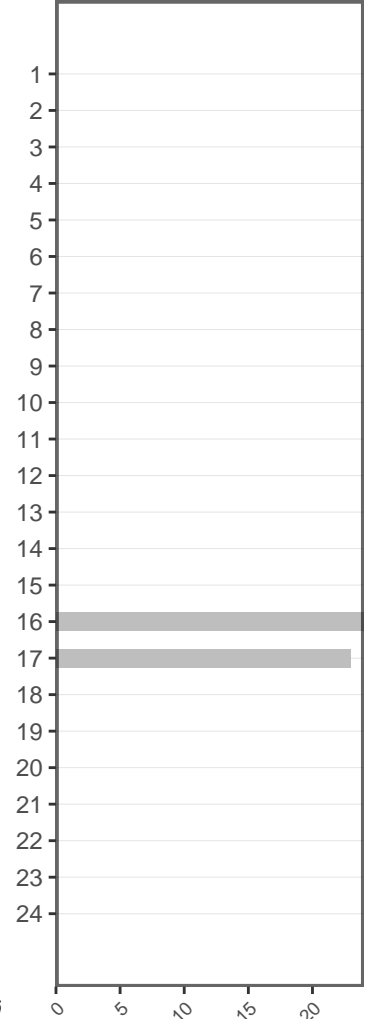
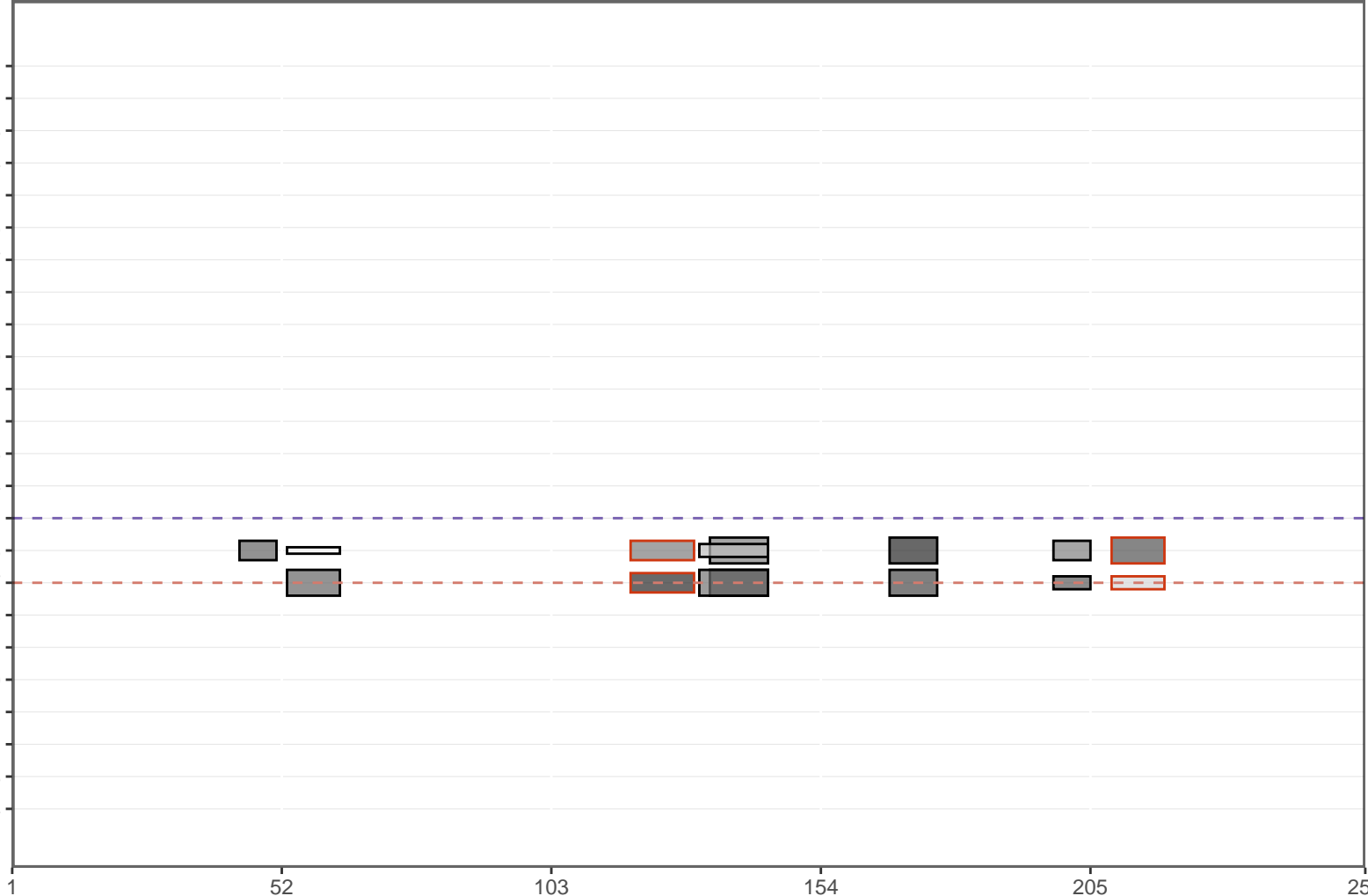
MW indication



Molecular weight



Gel Slice

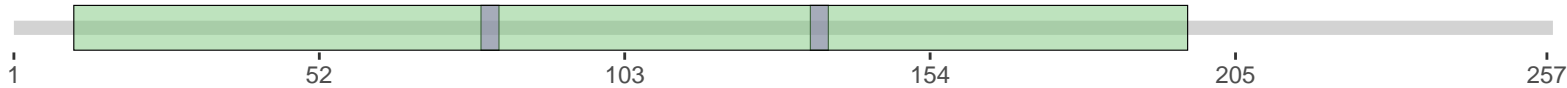


Peptide counts over 4 repeats

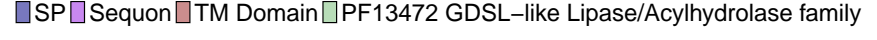
Protein length



Pfam domains



Pfam Description



Protein sequence:

INRIFLSCPVPYDEARVRENTSSYFSELRVITNELGRQYSDAGIELGNEMNLKVVLDLWALQKREDWLTSGFTDGHIAEAGSKIVVEEIKVLAKEAEVTPSLVWKSMPTEFAEDSSVLDVLDGKTTINPSEWYIHRGIQWDP

NbL17g15310.1 30S_ribosomal_protein_S31_chloroplastical [MW = 12.09 kDa]

No. of times detected



log(intensity)



Values from



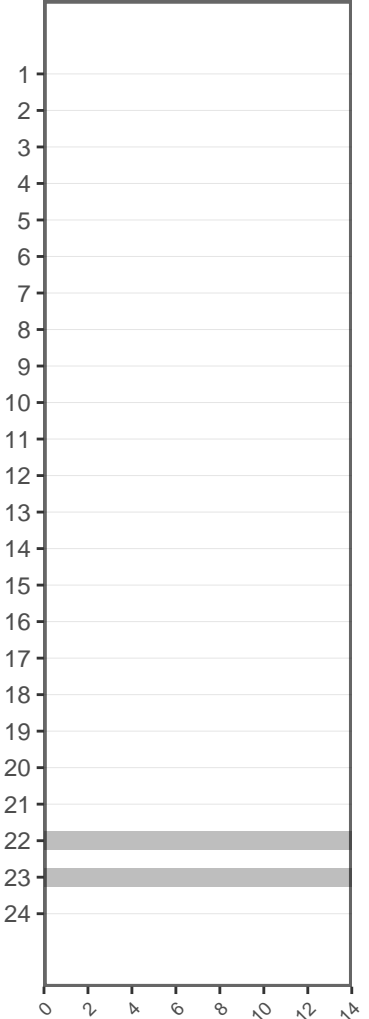
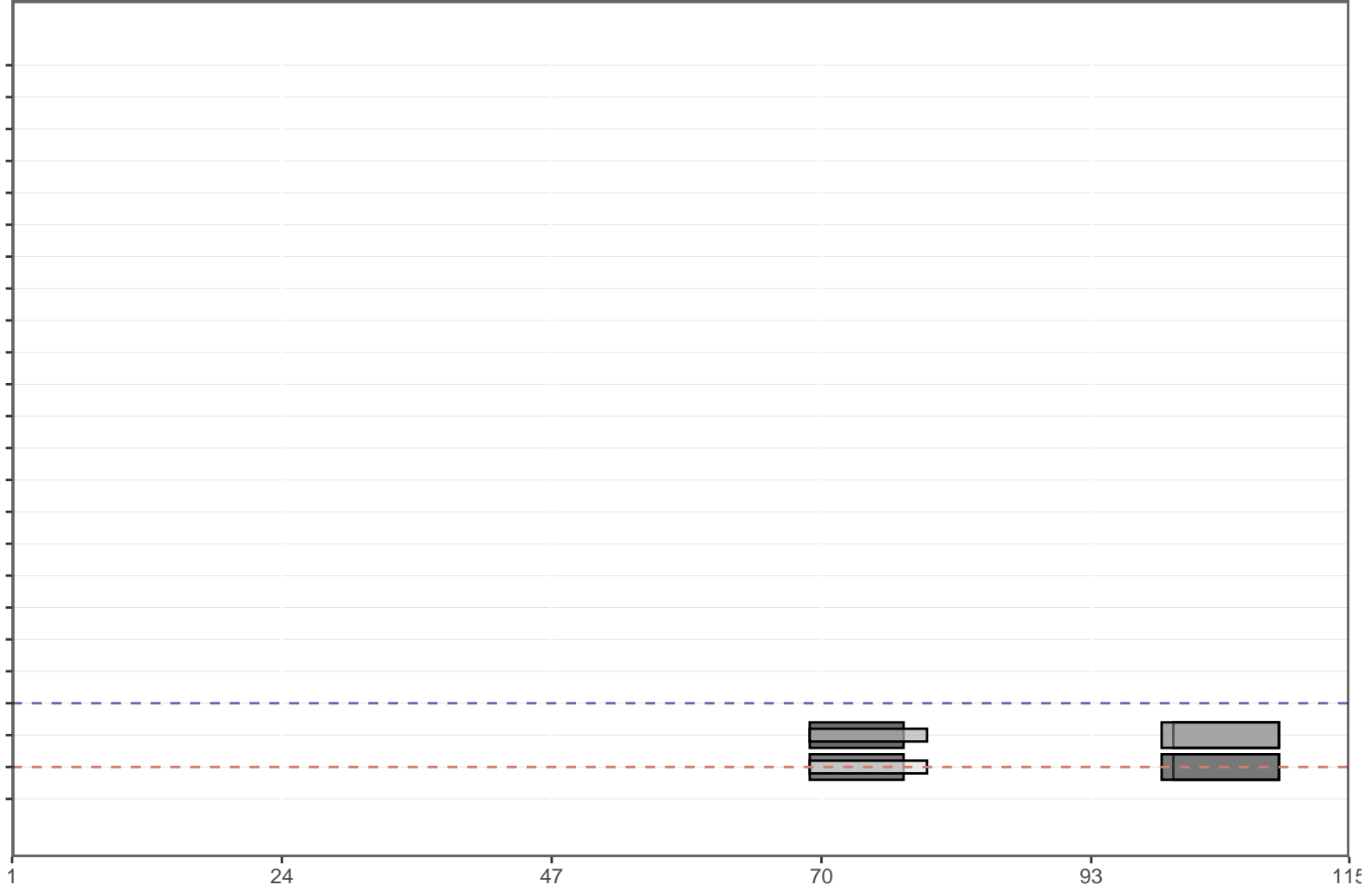
MW indication



Molecular weight



Gel Slice

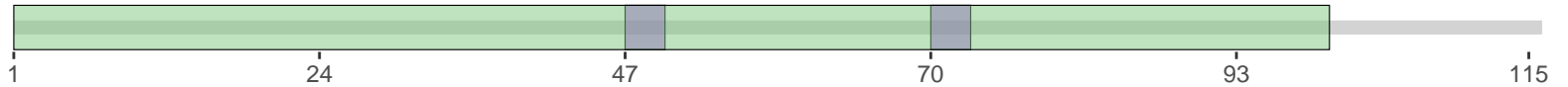


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

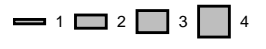


Protein sequence:

ANSSSLPLYCGRGGKKTAKGRFNFHSGNARPRNKKKGRGRPRVVAAPAPKRDPEDDGGVKEINE*

NbL17g15230.1 60S_acidic_ribosomal_protein_P0 [MW = 34.16 kDa]

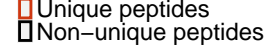
No. of times detected



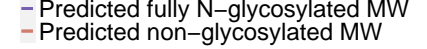
log(intensity)



Values from



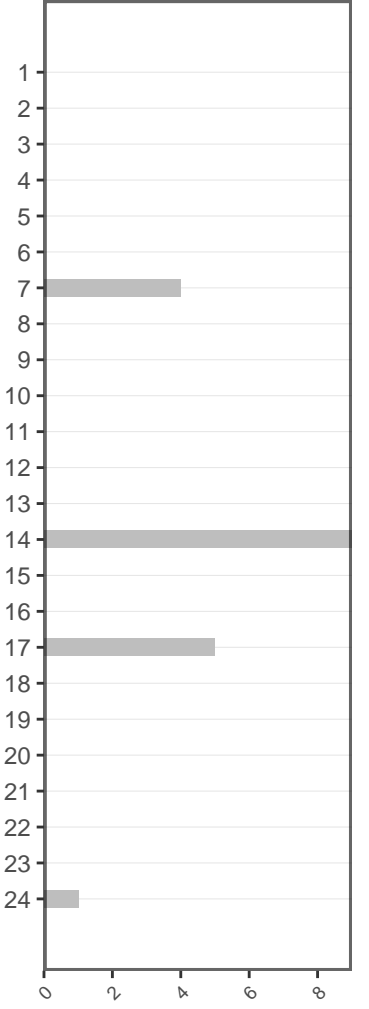
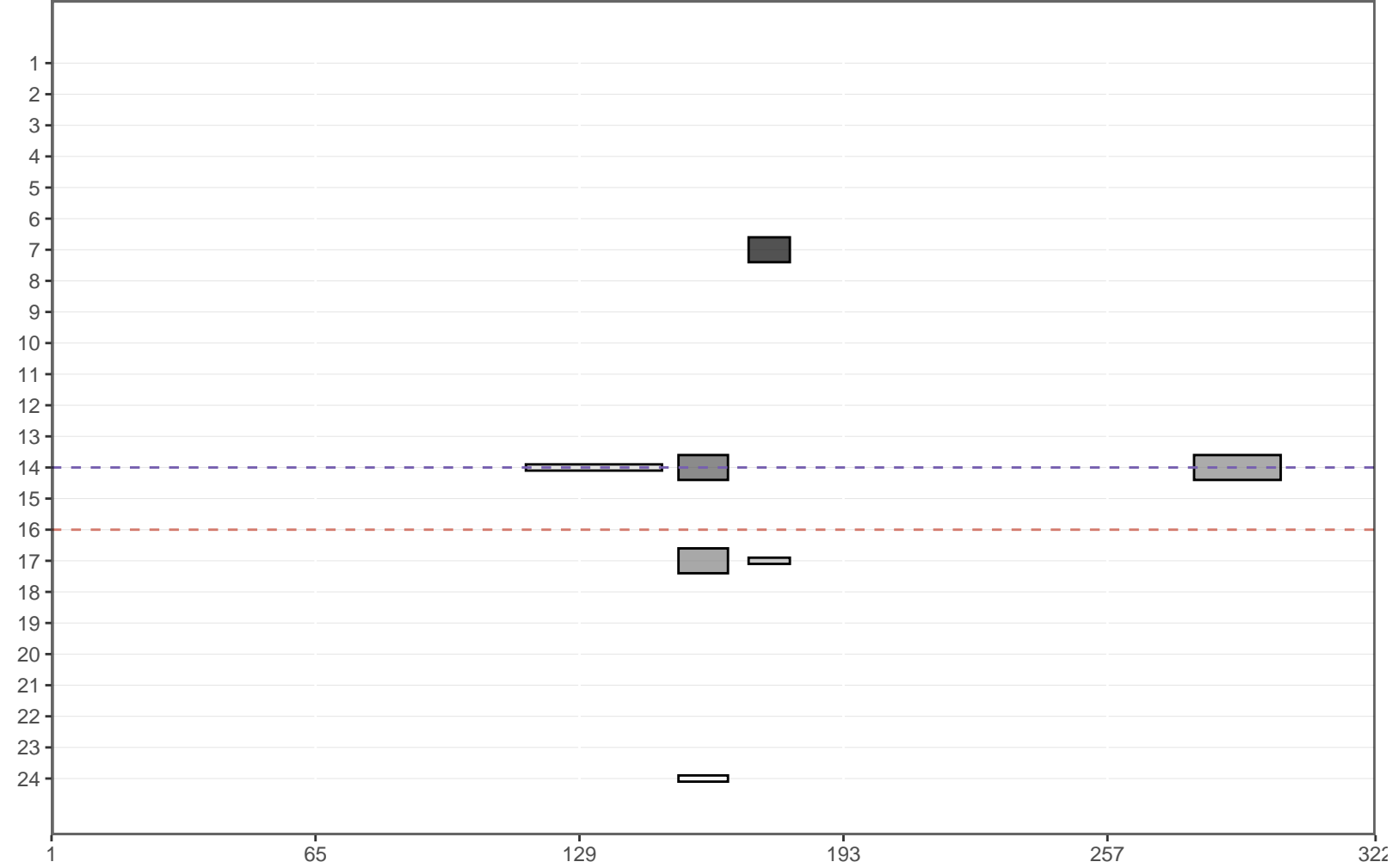
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

TKIKNGTVEIITPVELIKKGDVGSSEAAALLAKLGRPFPSYGLVLLVGVNDSVFSPEVLDLDTEDDLVEKFMGVSMVTLSLSLAISYPTLAAAPHMFTNAKKNVLAIAVETDYSFPLADKVKVEYLEDPSKFAAAVAAPVAAGSGAAPAAAKKEEKDEPEEESDDMGFSLFD

NbL17g15030.1 LIM_domain-containing_protein_WLIM2b-like [MW = 20.84 kDa]

No. of times detected



log(intensity)



Values from



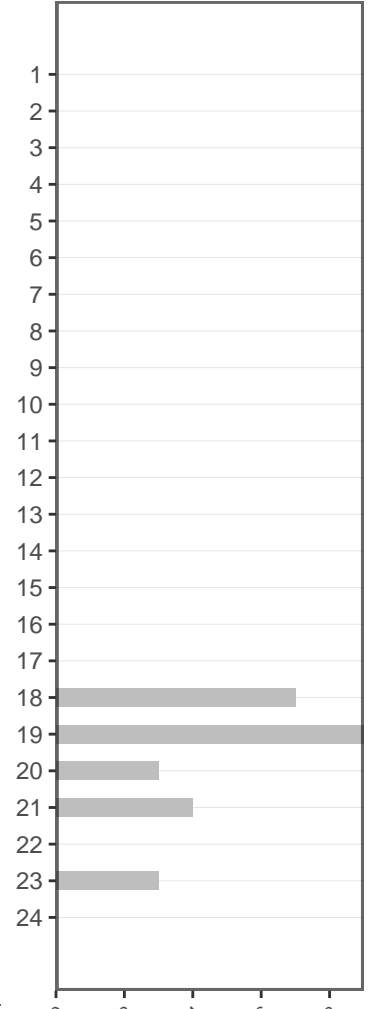
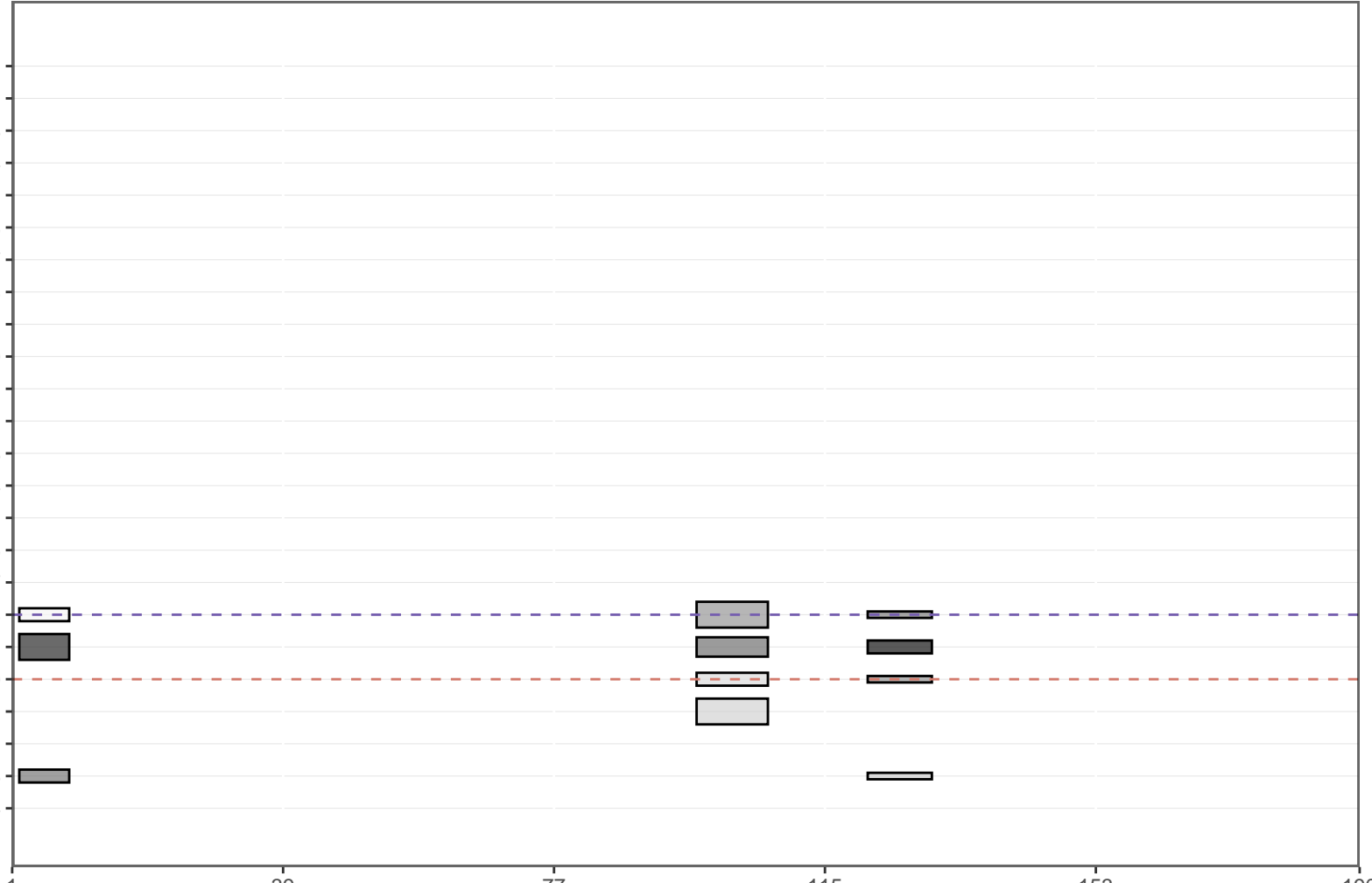
MW indication



Molecular weight



Gel Slice



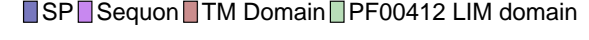
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISAEKLTPELTSRPSKAAAMFSGTDEKCATGKTAVPLEKVTVENGGYHKTFKSHGGGSLSPENVAALNGLYCKPHFSOLFKEKGGYHLLKSAAMKRPATVPSD

NbL17g14540.1 uncharacterized_LOC104238289 [MW = 81.41 kDa]

No. of times detected



log(intensity)



Values from



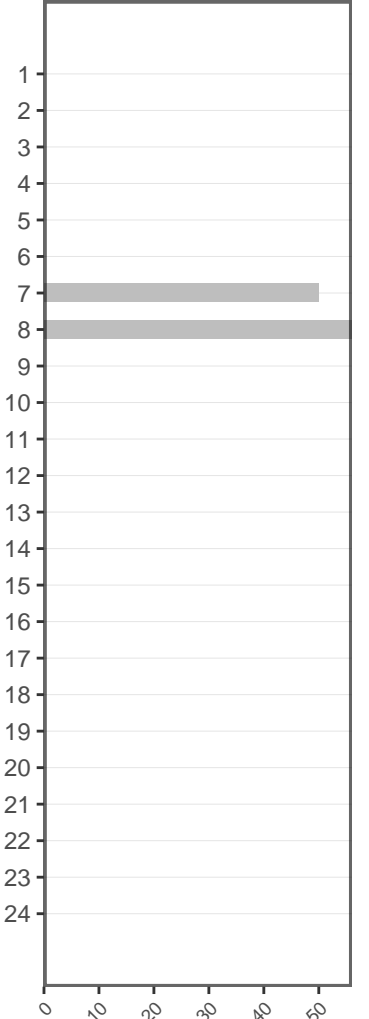
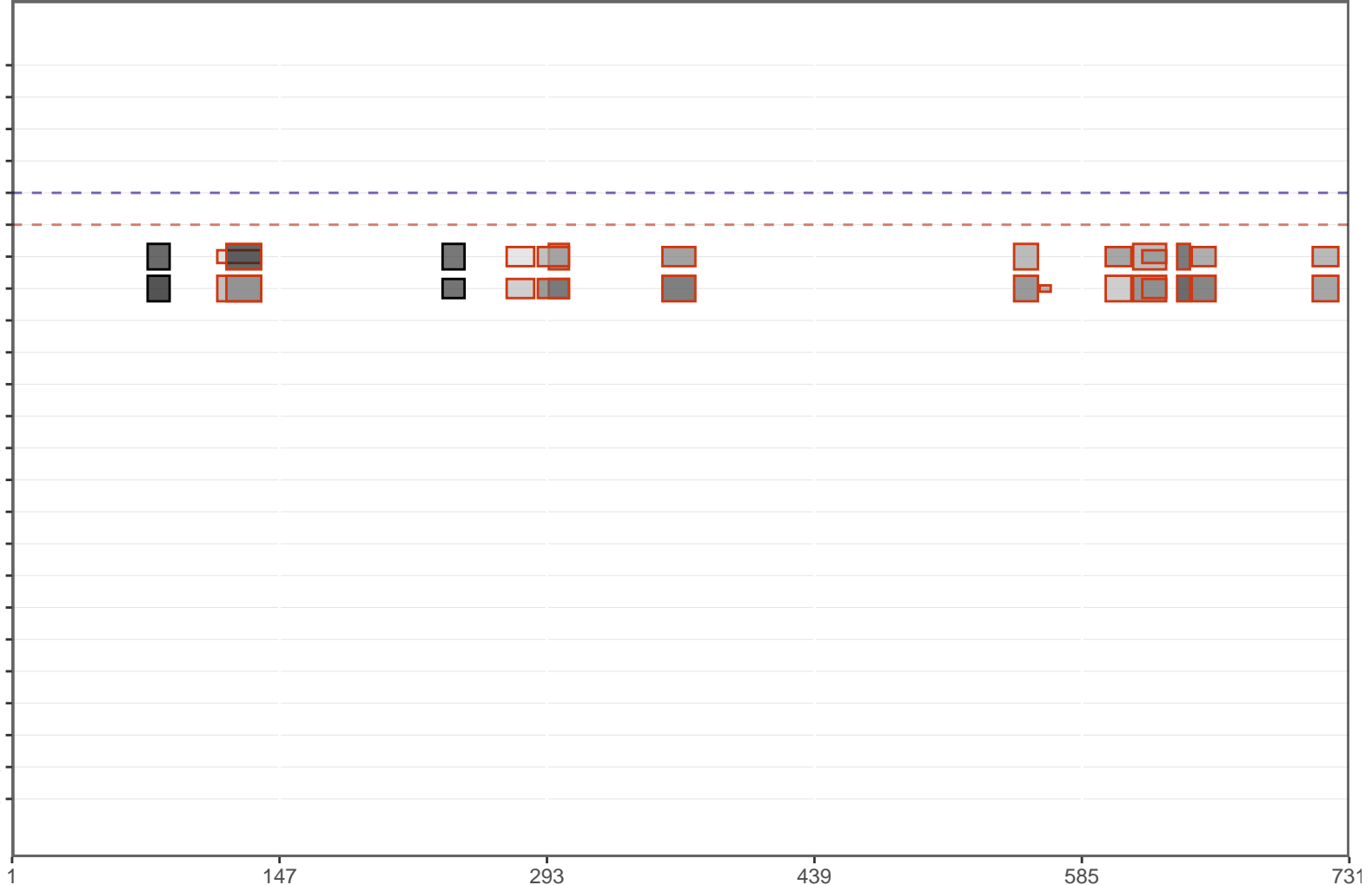
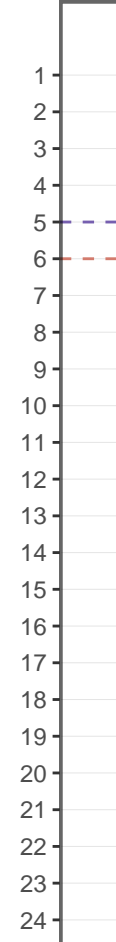
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

FGMKSYDFLEHPSQNTLHAGSYRENGNSYLVGLDLSLGHKIVLDIPFTDNNHSSGHHLYVEGSAVHPSSIAKTLDDQREKVIDFKMWSSSSISEMVTGYSWPELMMKFFTDIPQGSAYWFYPTTNPNYGASHGKPLLRHGHGPTAEARGLNLSVQWTRGWAYVDVNYGGSTGYGREYRERLLKHWGIVDNDGCGAKFLVDSGRVDRGLDITGSSAGGYTFLAALAFKDVFKAGASLYGGDLQLLRAETHKFESHYIDNLVGGKAYFERSPINVNR

NbL17g14340.1 jacalin-related_lectin_3 [MW = 71.29 kDa]

No. of times detected



log(intensity)



Values from



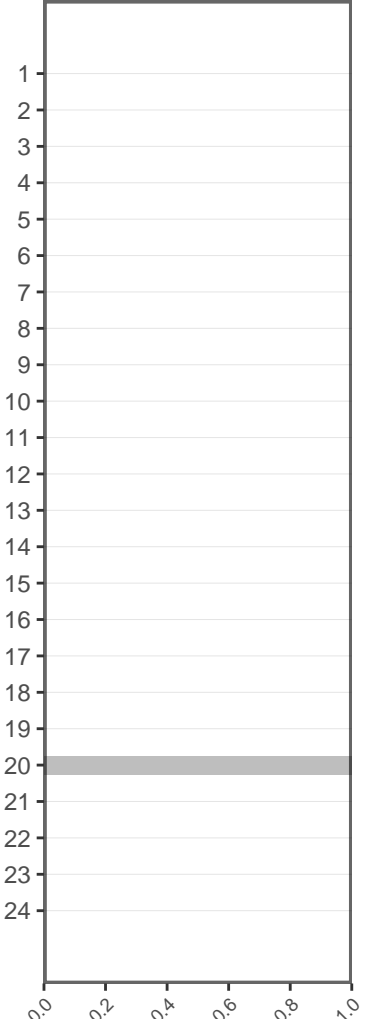
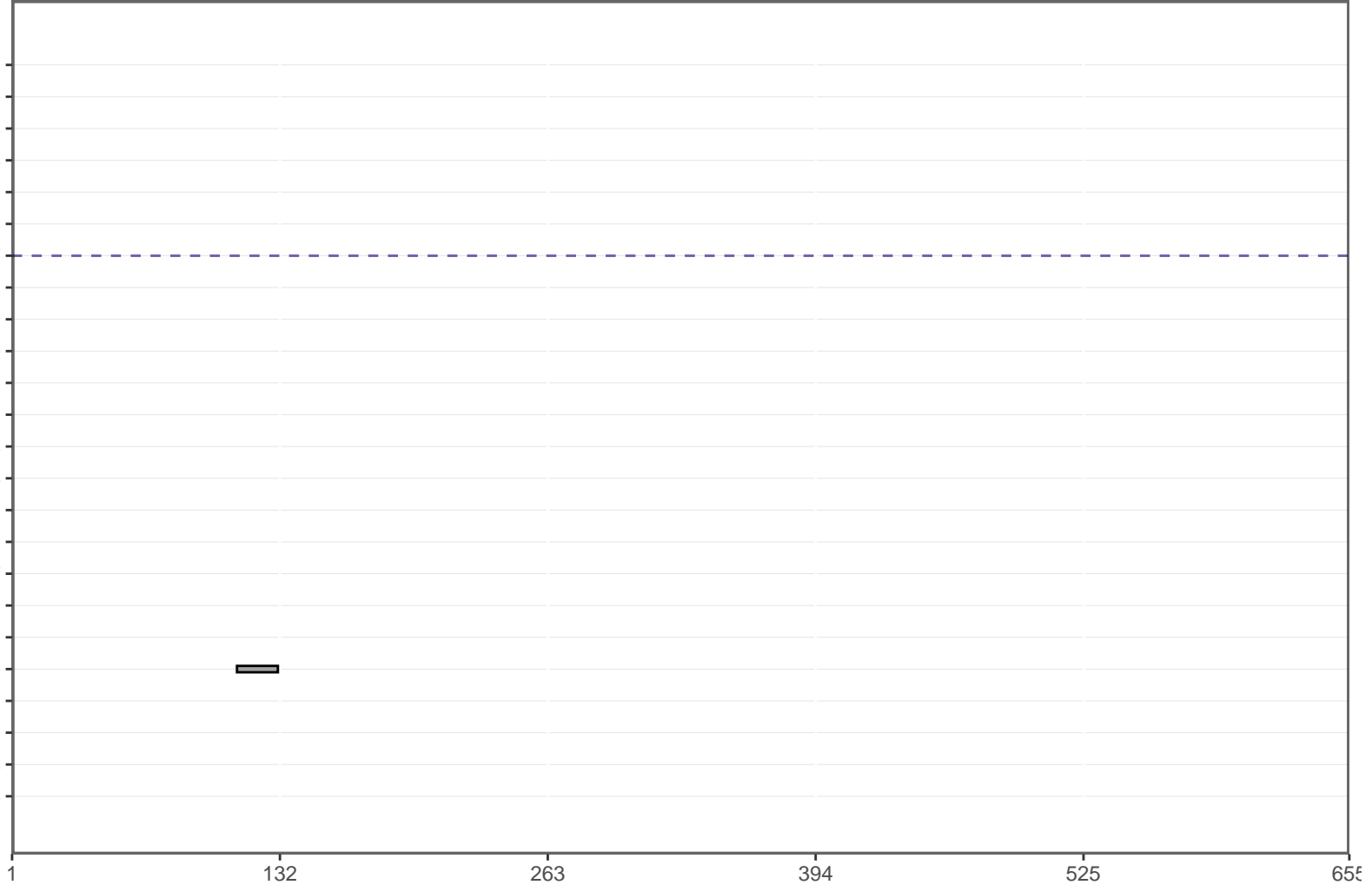
MW indication



Molecular weight



Gel Slice

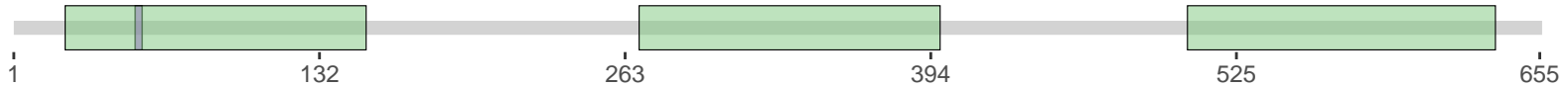


Peptide counts over 4 repeats

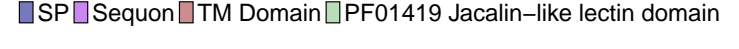
Protein length



Pfam domains



Pfam Description



Protein sequence:

GGTGGFKTEKIFDYPSEILTHFGYKGRMMGPNIGSLTRHTTKGKHGPIYGEEDGGDFSTRKLEKGIIVGPHGRKGLFLDALGVHVEGKVVSGLLPSPFTOTGKIPSAASVPSLPAAPFKPKSIPDAAVPSLPAAPFKPKSIEPKKPVTEVDDRPQWFSRLKGNLFTGEGVGRIVKDPAPYGPDPWGGDGGKPDWDDGVFTGKIKHLTQSSGEGICGIEIYDRNGGSAVWVWVHGANAGKGTNRVVKLEYRHEVLTGITGFEYGPISKDMGLKWKILTFHTTRKFGPTGEEELGYI

NbL17g14280.1 coatomer_subunit_alpha-1-like [MW = 137.1 kDa]

No. of times detected



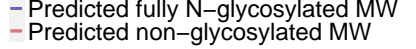
log(intensity)



Values from



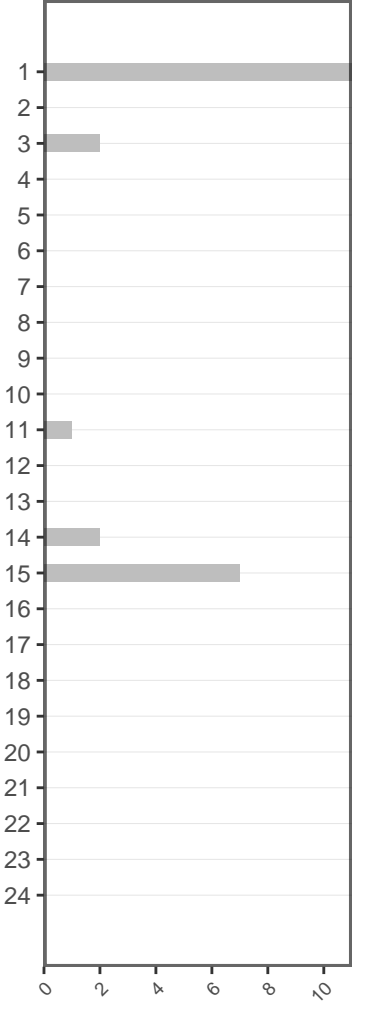
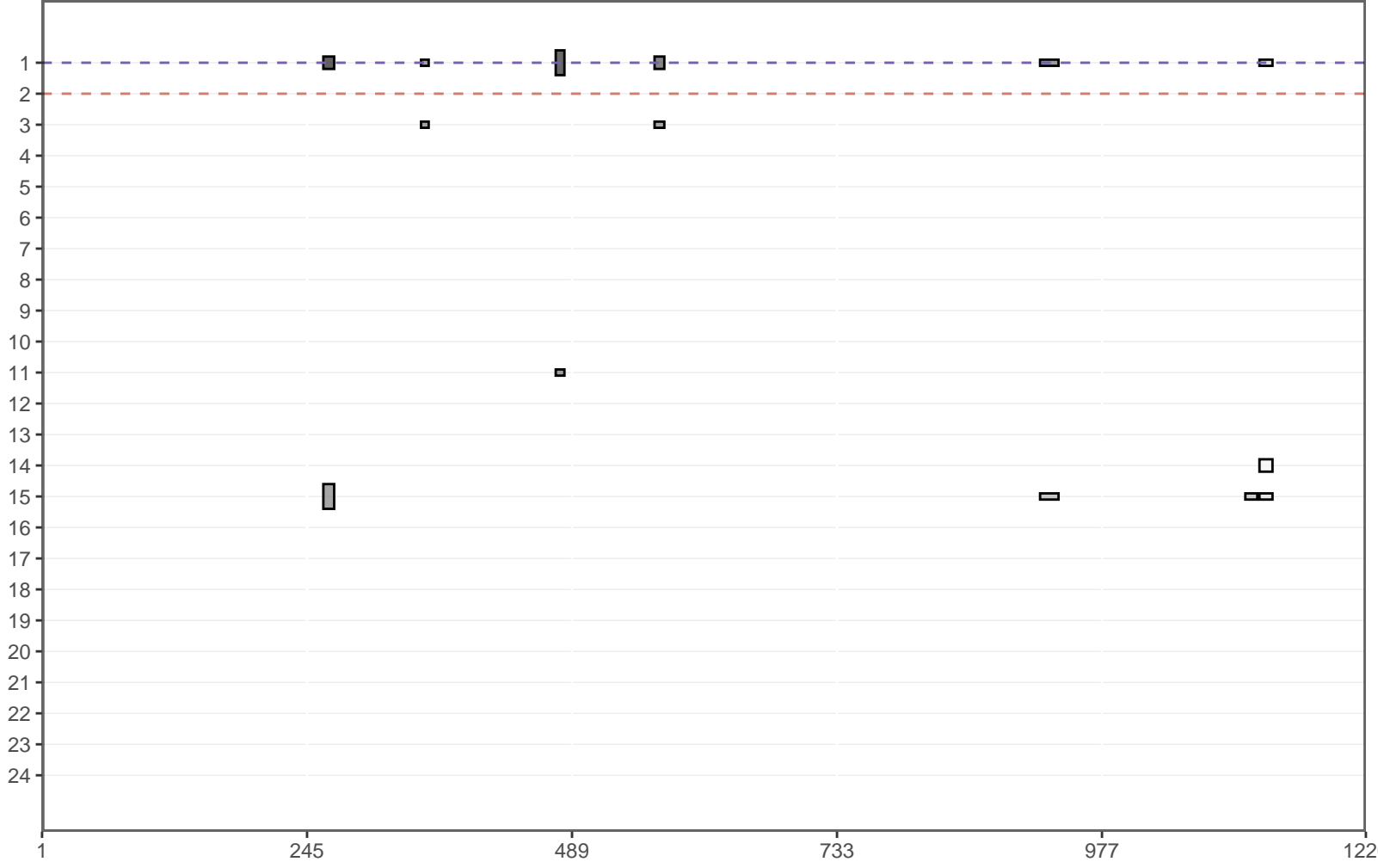
MW indication



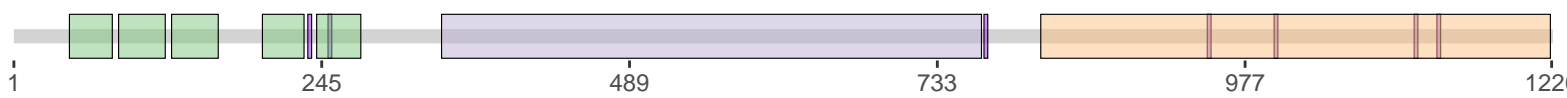
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

YYVFKLCLLRKRYDGVMSMRNSELGGAMIAVGGKGFPEVALHFVKDERTFRNLALESGNEIALESAAKIDKDHVYRVLGVLEALRGGNAGVYAWQTKNFERLSFLVLTGALKLEKSKMMKAAEVNNDVMGQPHDALYLVGDVRRERKILENAGHPLAVTATAGLNDTAEHLAEELGDNVPSLPGKAKASLLLPPTPLGGGDWPLMLMTKGFEGGLDAGRGGGDEEYEAADADWGESLDIGEVENLQNGDISMVLGDEEGGEGNDDEEVGWLELDLDPDQDT

NbL17g14160.1 peroxisomal_24-dienoyl-CoA_reductase [MW = 31.88 kDa]

No. of times detected



log(intensity)



Values from



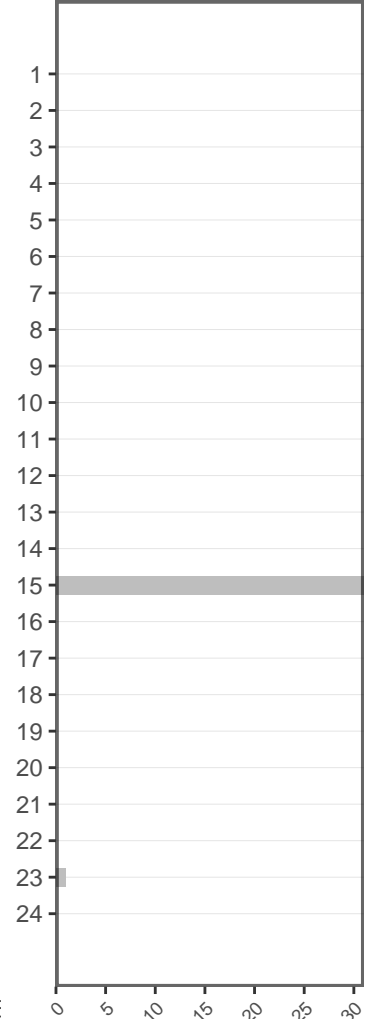
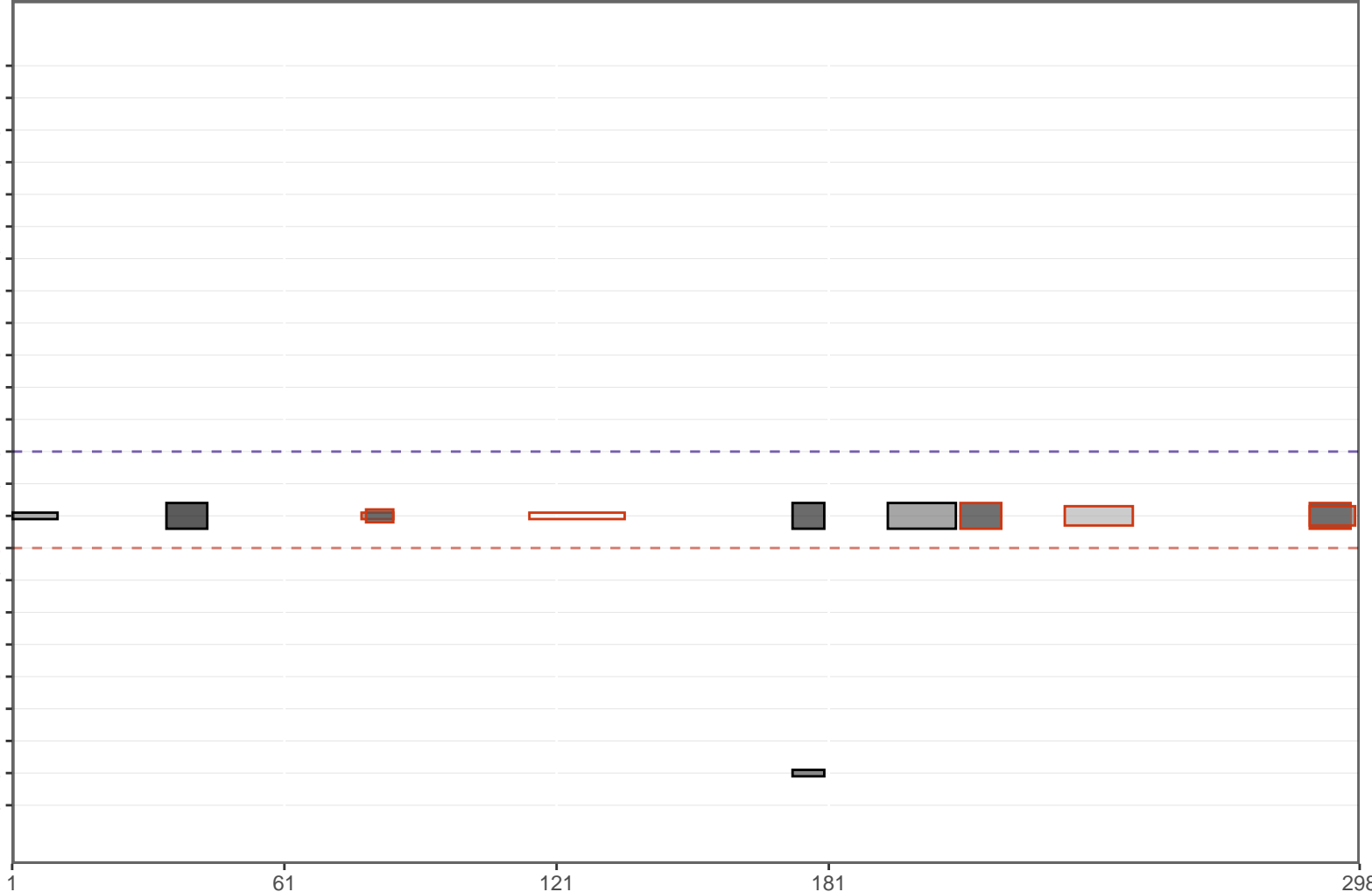
MW indication



Molecular weight



Gel Slice



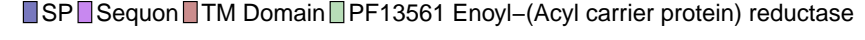
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

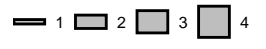


Protein sequence:

KGSLGRNSTGGHINBATLHYTASWYGHVAAAKAAVDVTRINLLEWGSTDYDIRVNGIAPGPGIDTAGMRKLVPEINNKTRVEMPLYKLGKDYDIAAMAALYASDAGKYNGTTTIVDGGUWLRPRHLPKDAVKELSRTEYKRRNAPVGVPSKLE

NbL17g14140.1 phosphoglycerate_kinase_chloroplastic [MW = 50.01 kDa]

No. of times detected



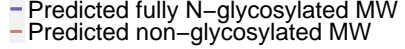
log(intensity)



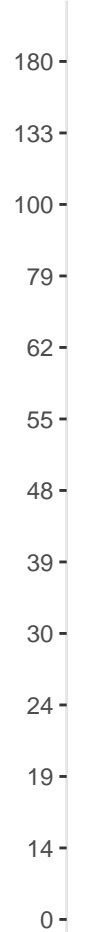
Values from



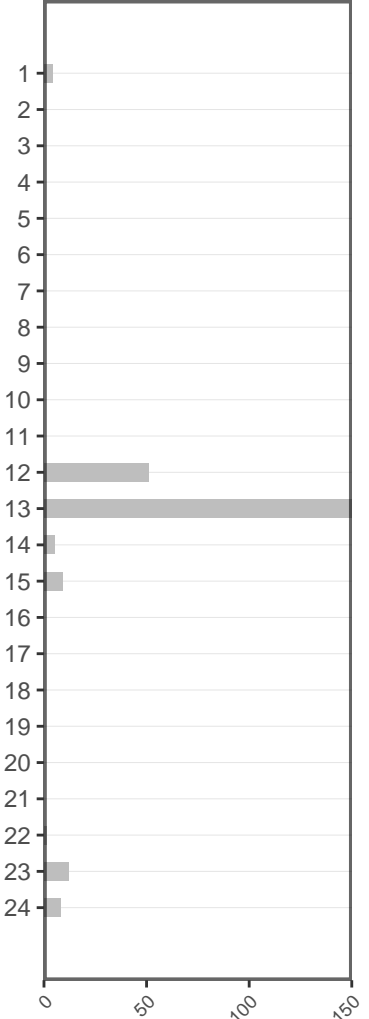
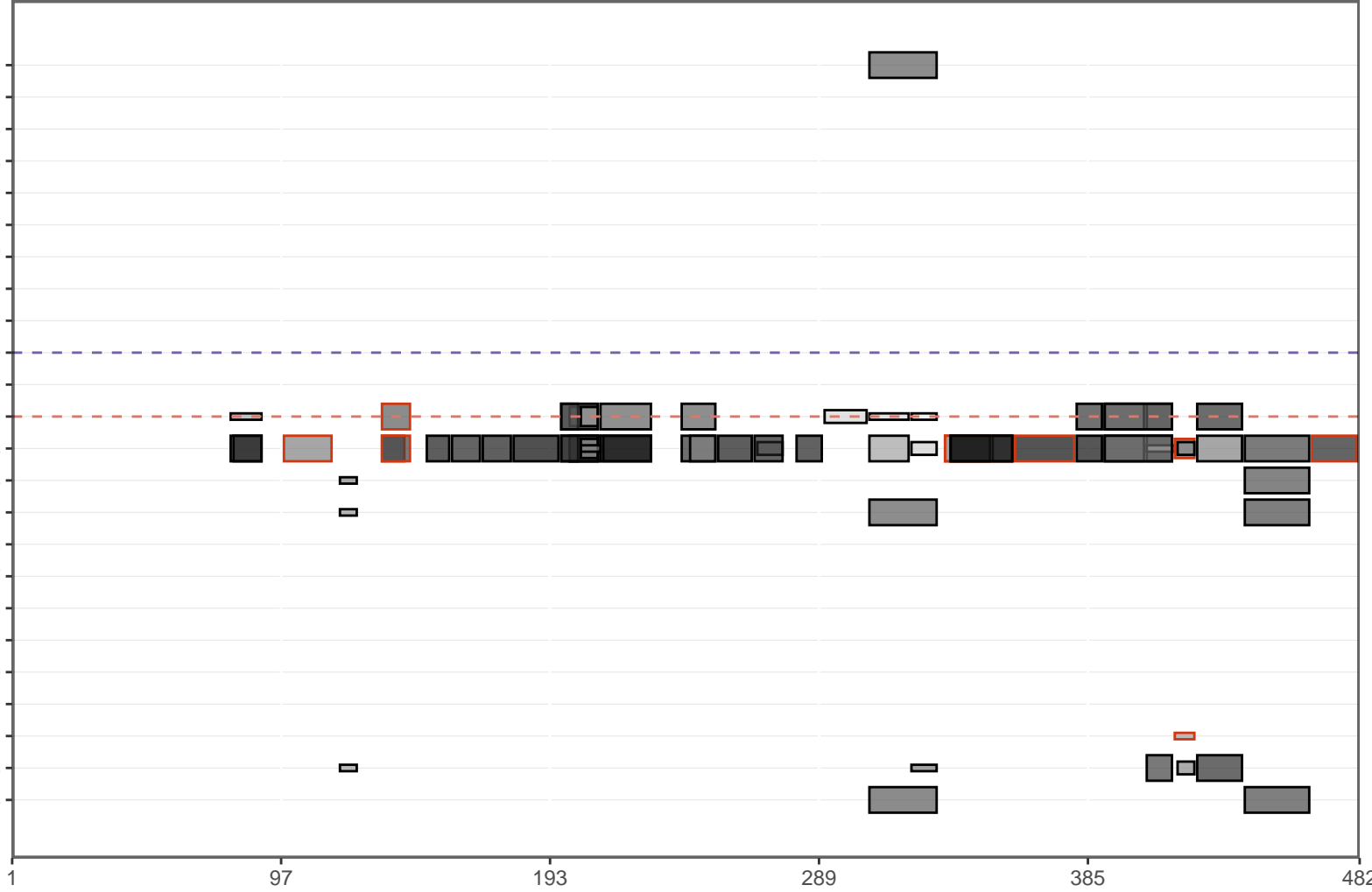
MW indication



Molecular weight

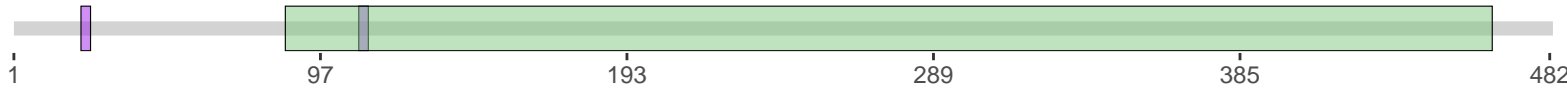


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

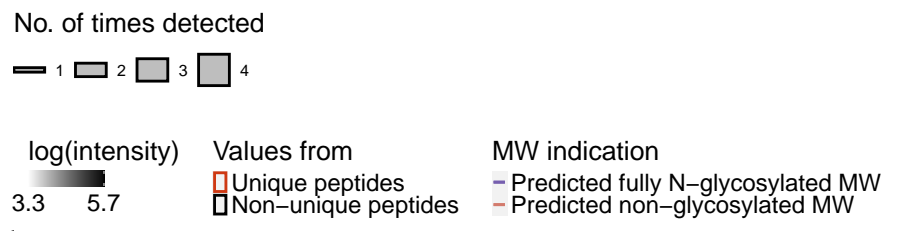
Pfam Description



Protein sequence:

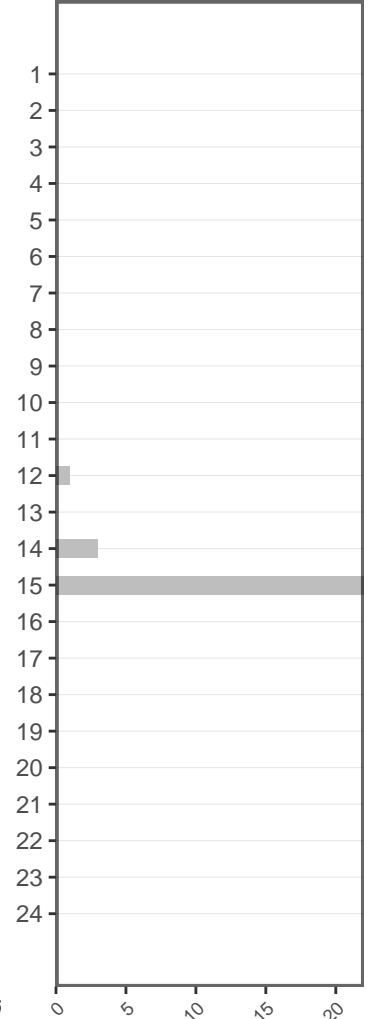
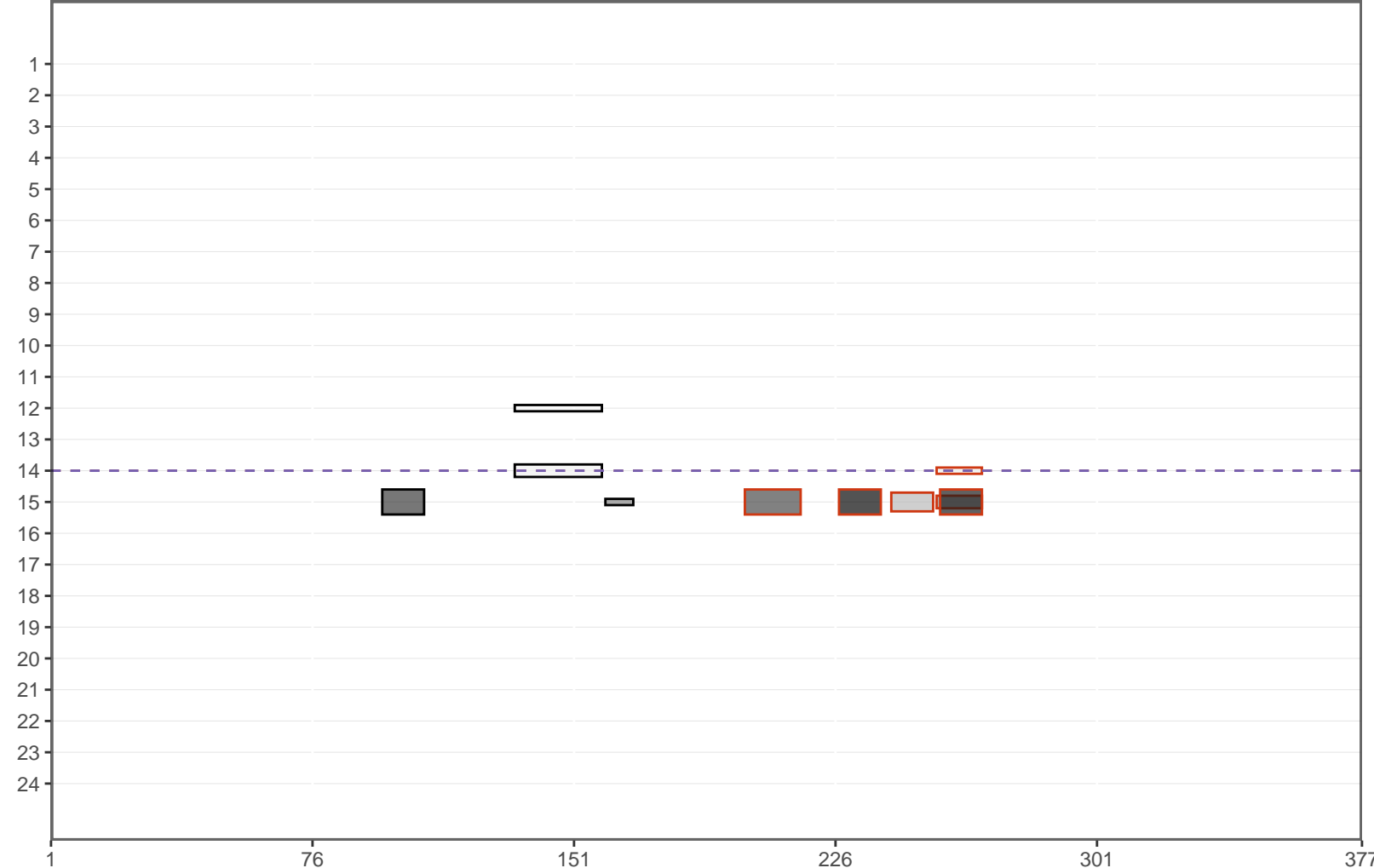
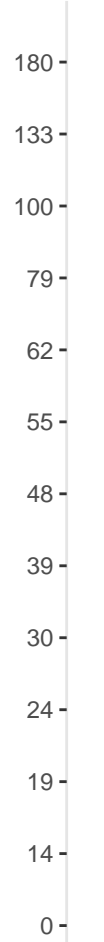
HRHAHSTEGVTKFLKPSVAGFLQKLEHLVGVAVSNPKRPFAMVGGSKVSSKIGVIESLLEKDKILLGGGMFTFYKAGLGVSSLSVEEDKLELATSLLEKAKAKGVSLLLPDSVVAADKFPADANSKIVFASIPDGMWGLDGPDEVKFTFDALDTTKTVWNGPMGVFEFDKFAVGTETAIKKLADLGGKGVTTIHGGDSVAVEKGVAVSMHSTGGGASLELEGGKVLPGVALDEADAPVAV

NbL17g14120.1 thiosulfate/3-mercaptopyruvate_sulfurtransferase_1_mitochondrial-like [MW = 41.38 kDa]



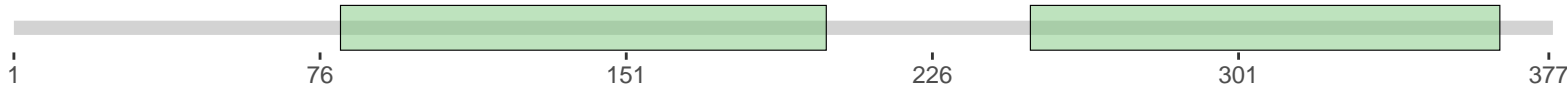
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

SP Sequon TM Domain PF00581 Rhodanese-like domain

Protein sequence:

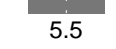
WWWLFRVYGHDRVWLLDGLPRWRASGYDVESSASGDALKASAAEAEKYYGGGTVAPTFRFKFQNLVWFLDGVRRKNIETTYQHIDARSKARFDGVAPEPRKIGRSHVPSGKGFPAQMLDGSYTLTSTDELKKKFFDQEGHLDKPKVTSGGTGTACILALGLHRLGKTDVPPVYDGSWTEWGAHPDTPVSTSEAV

NbL17g14000.1 porphobilinogen_deaminase_chloroplastic-like [MW = 39.26 kDa]

No. of times detected



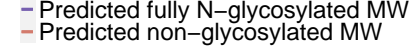
log(intensity)



Values from



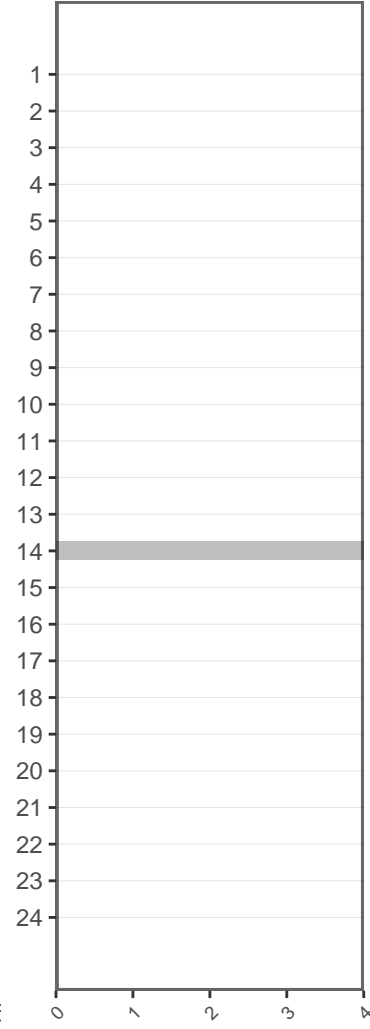
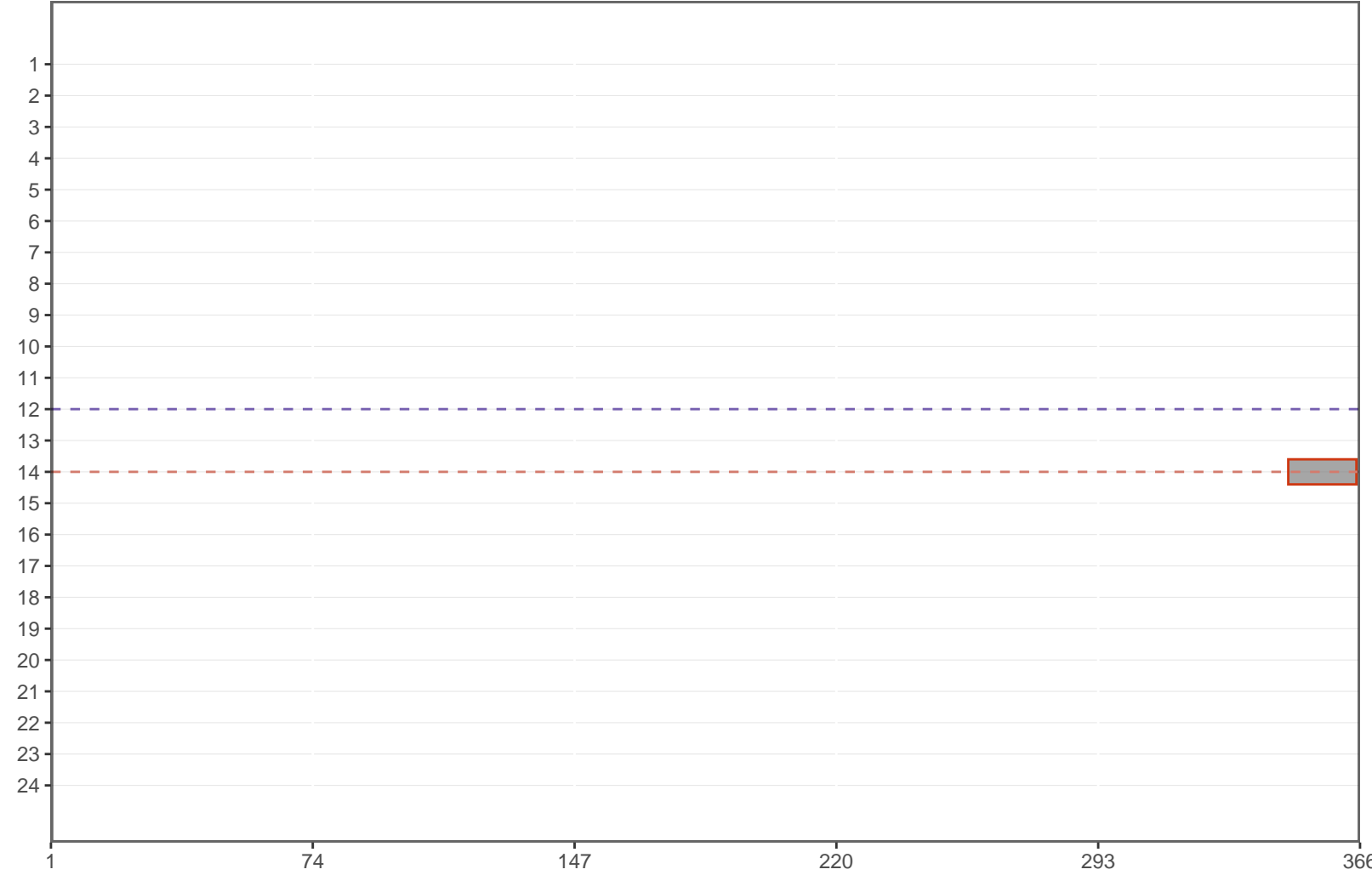
MW indication



Molecular weight

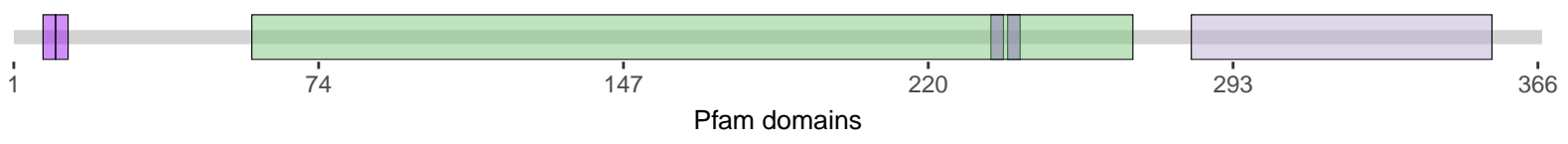


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01379 Porphobilinogen deaminase, dipyromethane cofactor binding domain
- PF03900 Porphobilinogen deaminase, C-terminal domain

Protein sequence:

IQLPSGGSTIGTASLRKRRKSQLHRYVPSLNLVLENFRGNVQTRLRKLNKGVVQATLLALAGLKRMMFTENVTSILPIEDMLPAVAGAGAGAGRTDDETMANYIASLNHEETRLAVACERAFKFLDSSGCRTPAGVACRGGEDGDCIFKGLVAVSPDGTTRVIETSRKGPVYTFEDMIRLGEDAGKELLAEGAPDFGN

NbL17g13990.1 protein_lojap_chloroplastic [MW = 25.89 kDa]

No. of times detected



log(intensity)



Values from



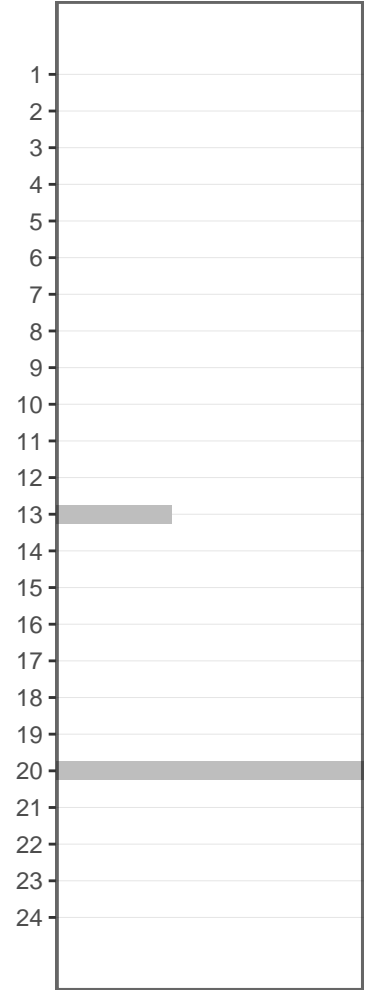
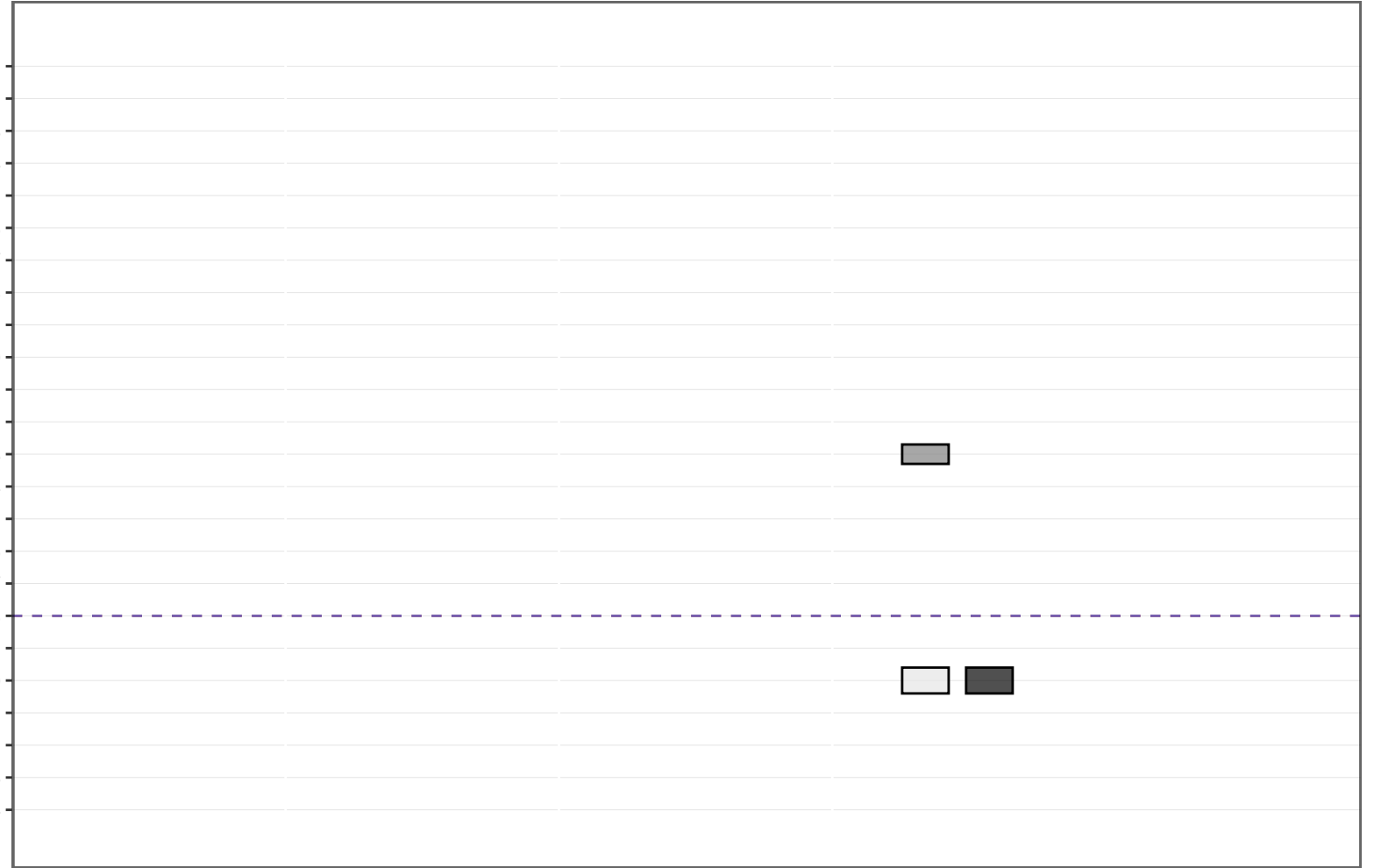
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length

1 48 95 142 233

Protein length



Pfam domains

Pfam Description



Protein sequence:

ITEIIDDAESLSFANWAKVASEWAGDKVLFVKPLVYVTRFFIATAFGRPGIDAGTRIRDMAEVQYGRVASGDFKPNWTLDFGDVVVHIFLPQGRYYNLEEFYGNAAPIELPFENGDLRSGKY*

NbL17g13950.1 ribosome-binding_ATPase_YchF-like [MW = 45.68 kDa]

No. of times detected



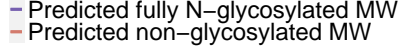
log(intensity)



Values from



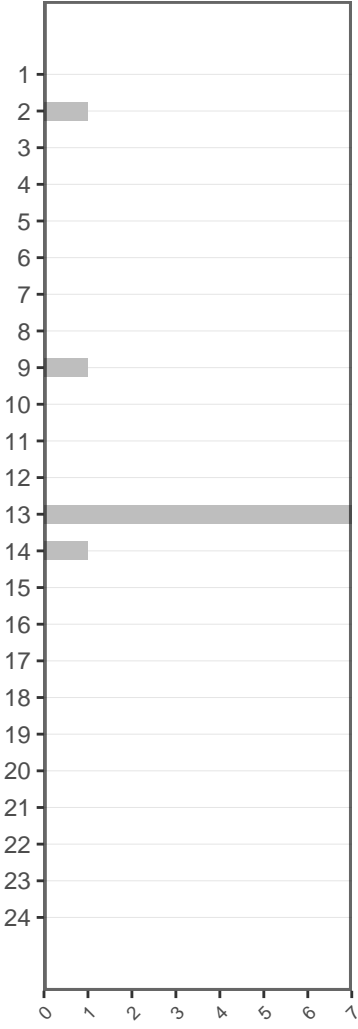
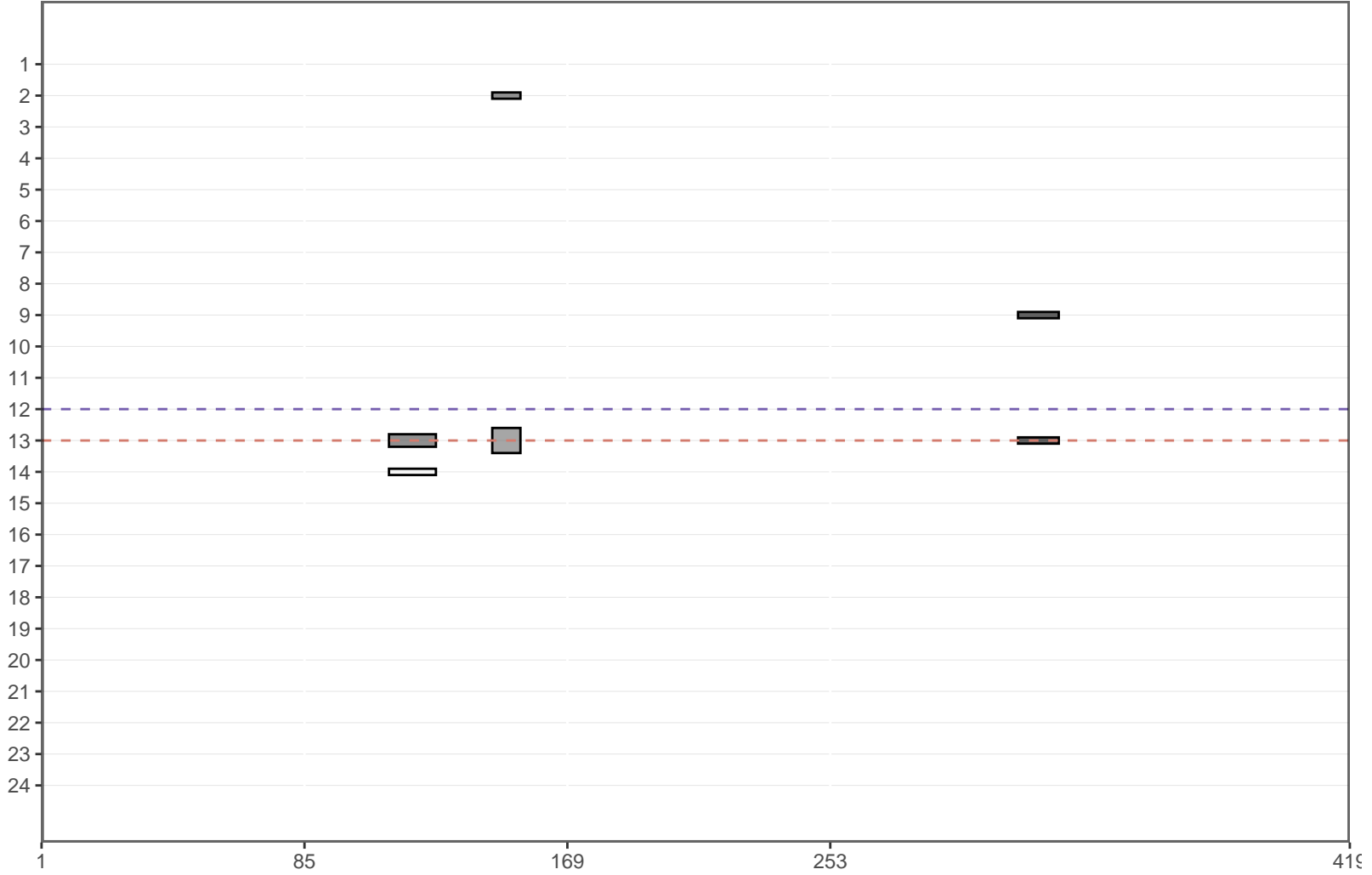
MW indication



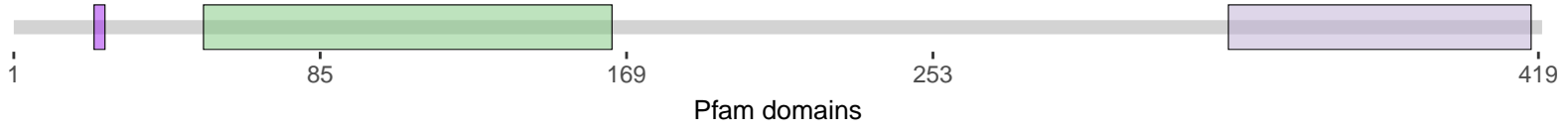
Molecular weight



Gel Slice

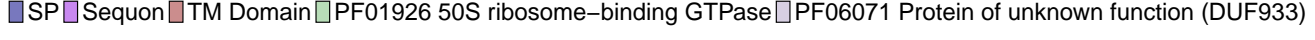


Peptide counts over 4 repeats



Pfam domains

Pfam Description

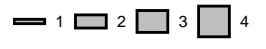


Protein sequence:

GRAKDSQAKYKEEAEKSALEKLPALMDGKPARSVLSSEFEKDKIKHLLGLTMRPVIFVAAVAESDVAEPENPHKVEVLTASELNSGVVTSAGVSELSLEPLEERIEYKLSLGVDESSGLNIRETYGLLGLRTYFTSGEKETKAWTILEGMPAQAAGVHSDFEKGRRAETVWVNDVVSAGSFAAAAREKGLLRLEGGKQVYVVEGDMIFRENY

NbL17g13940.1 peptidyl-prolyl_cis-trans_isomerase_CYP59 [MW = 69.17 kDa]

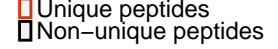
No. of times detected



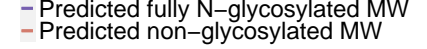
log(intensity)



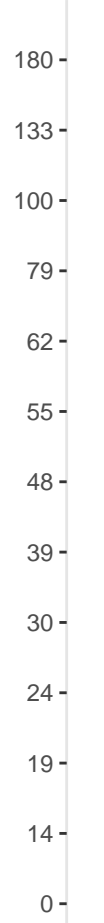
Values from



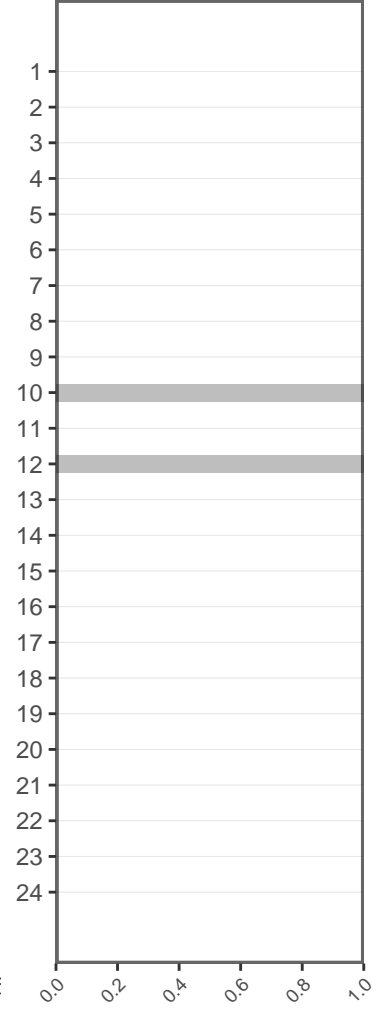
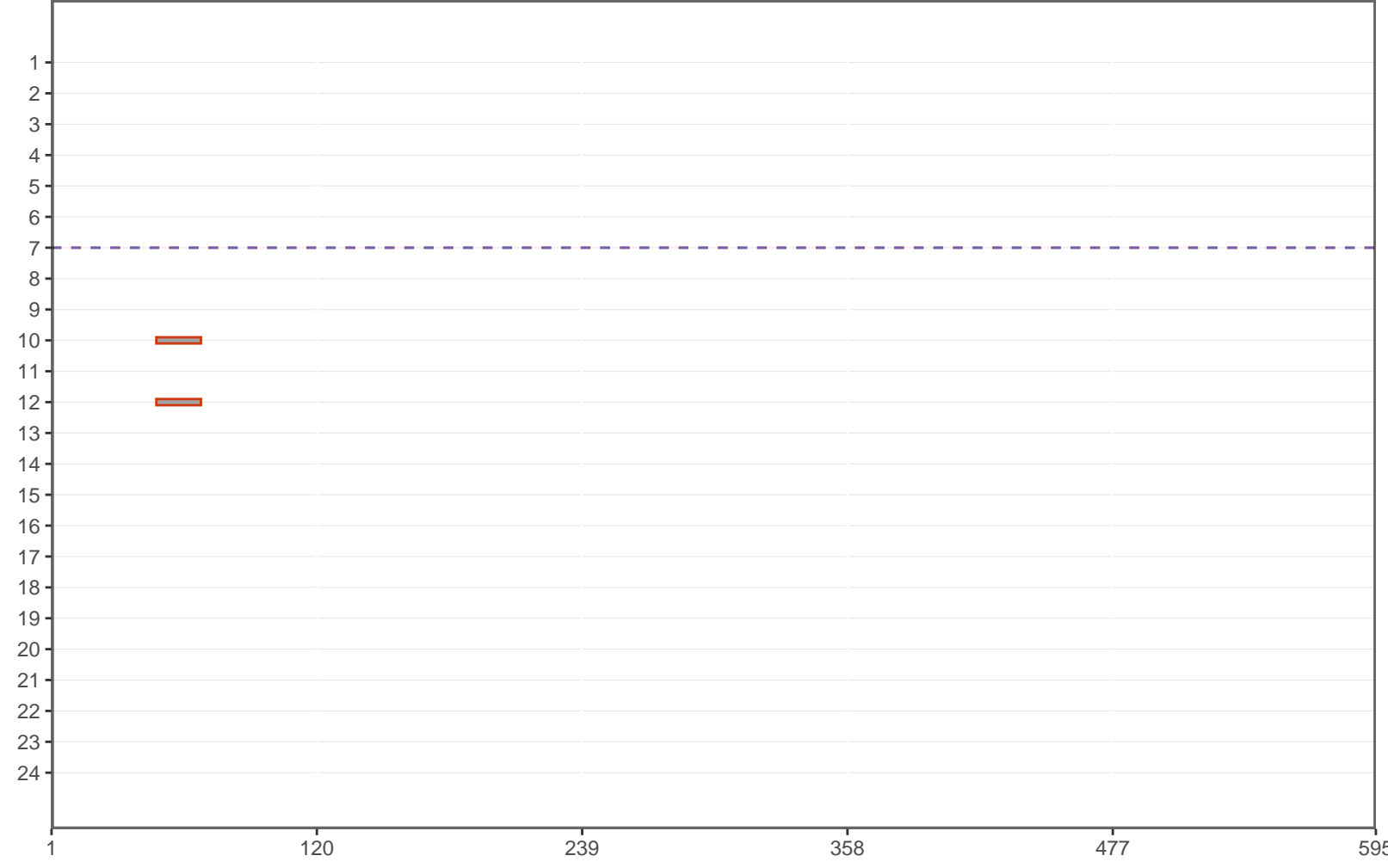
MW indication



Molecular weight

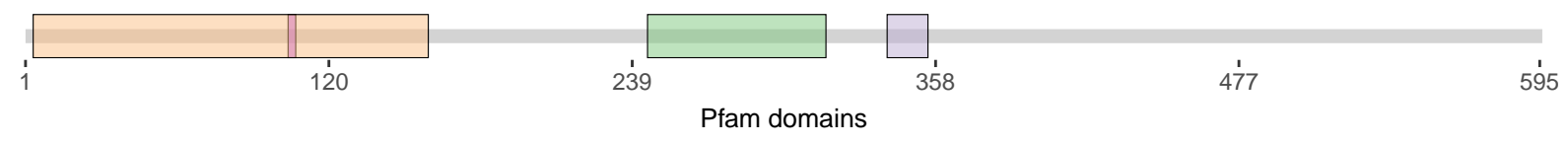


Gel Slice

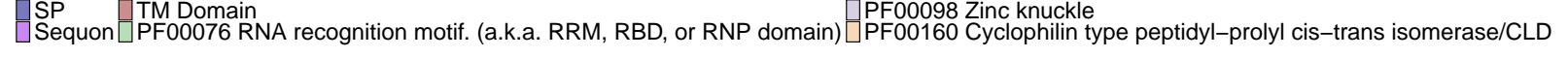


Protein length

Peptide counts over 4 repeats



Pfam Description



Protein sequence:

IACEQAYYMNTLHDDRRIHVDFSGVAKLWSGQYRRKDHMKGRGCGFKGSSLDHAKDCTVDATKQDSNYFLKQDNKGRGGDGNISRYEMVDFEDAWRSPKKNKRRYRYEDGKHENFNPKHRELEDDGVRKDRKRDGVERHRRGEERSKDYRTEERKRVGVARPSVEGERDVGGRNLDYRRNSDYDNHKGGRERPDHDKRHADKVRHRDKGNRRECEKRDQKDEVEVGGHMADEVRYRDKNRNEGQYERKQLDSNRGRGEEEDRQKRGLECDRAHDI

NbL17g13920.1 uncharacterized_LOC107785455 [MW = 17.95 kDa]

No. of times detected



log(intensity)



Values from



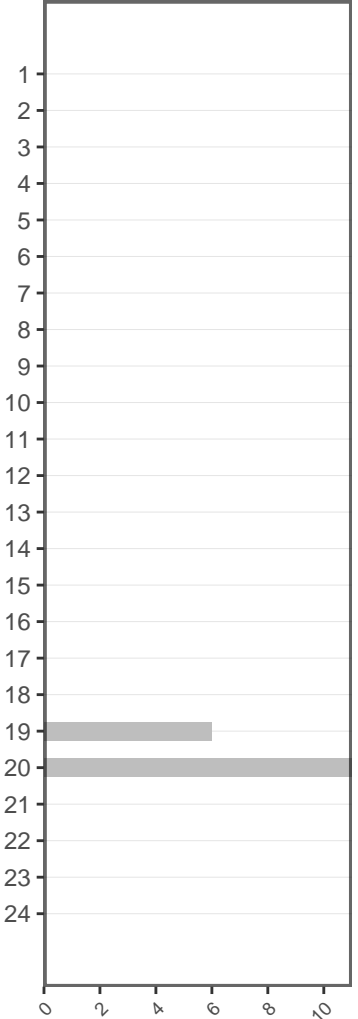
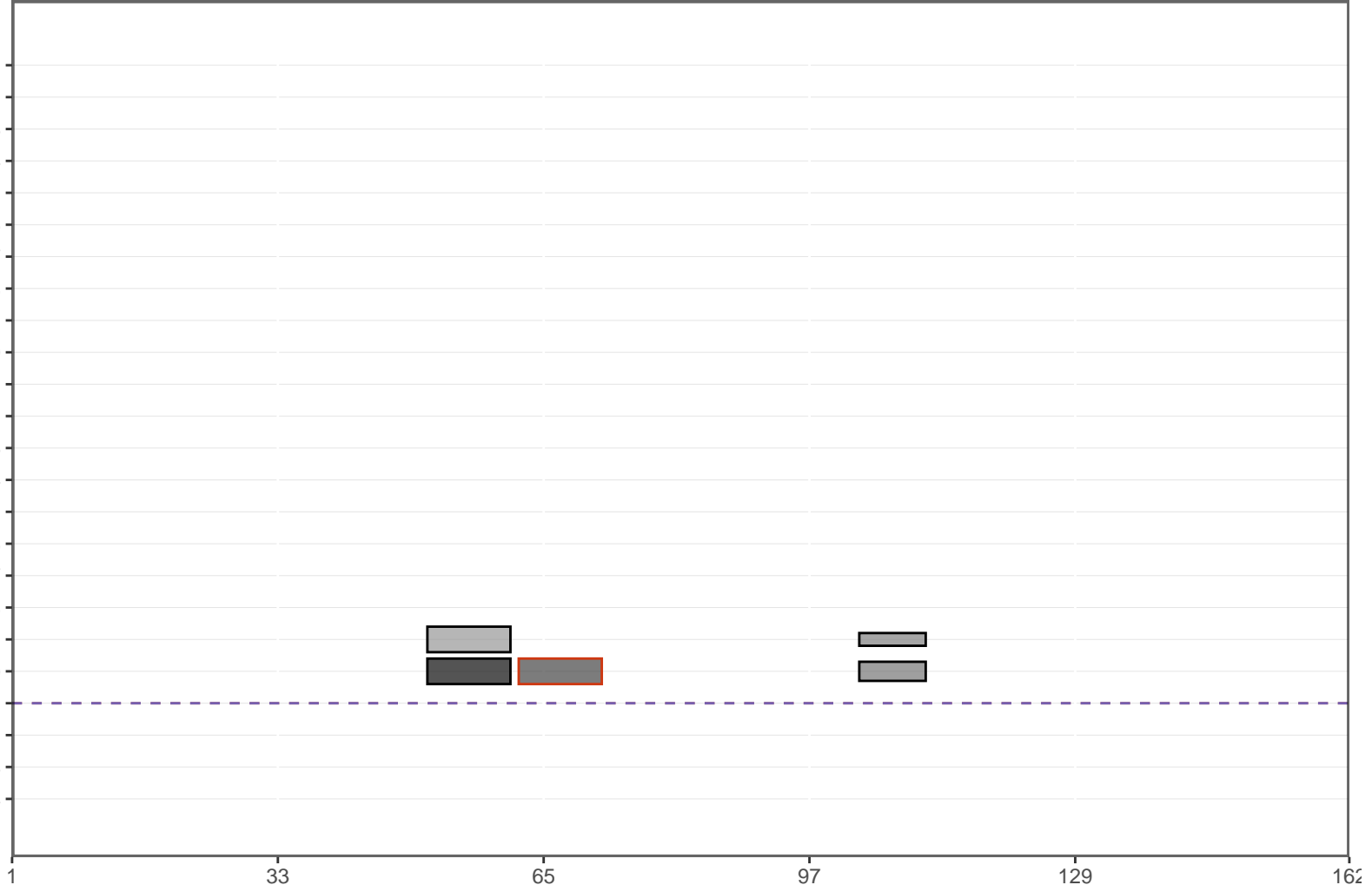
MW indication



Molecular weight



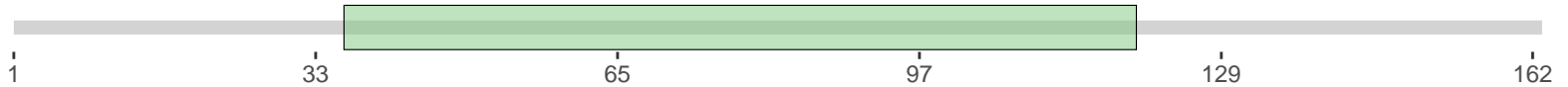
Gel Slice



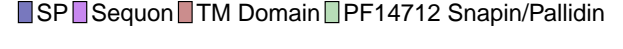
Protein length



Pfam domains



Pfam Description



Protein sequence:

ISLDRLTGELDKLLEDAPLFPIMQHAARIGGVKRRITSLNLSKIQRLDNDHTLSAGLHVRGWWARPRESKGSSLRGWRFRFKLSGGCQ

NbL17g13870.1 photosystem_II_10_kDa_polypeptide_chloroplastic [MW = 14.11 kDa]

No. of times detected



log(intensity)



Values from



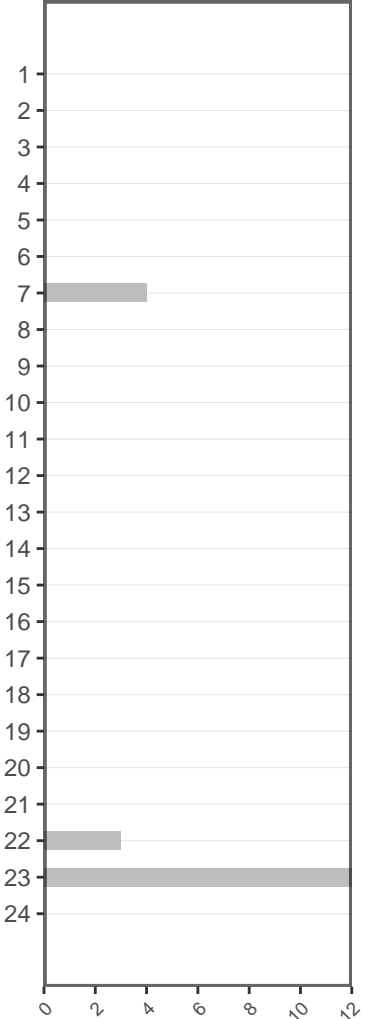
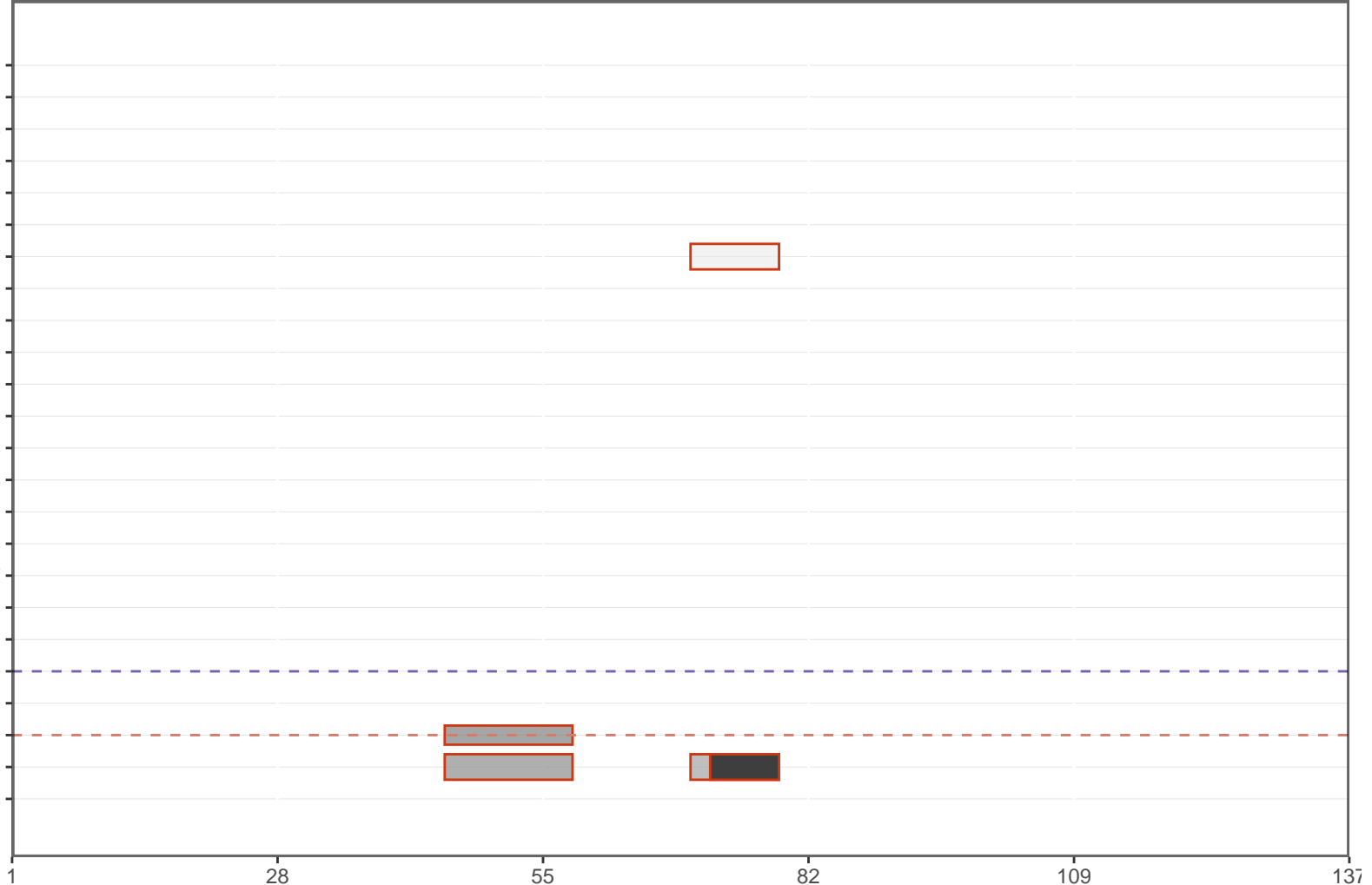
MW indication



Molecular weight

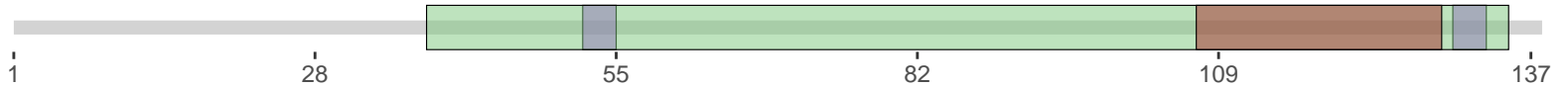


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SLRDDVDASGRKPKGKGVYGFVKYGANVDGYSPIVNTDDWSPSGDYYVGGTTGLAWVTLVGLAGGALLVFNFSALAQ

NbL17g13800.1 beta-ureidopropionase [MW = 46.58 kDa]

No. of times detected



log(intensity)



Values from



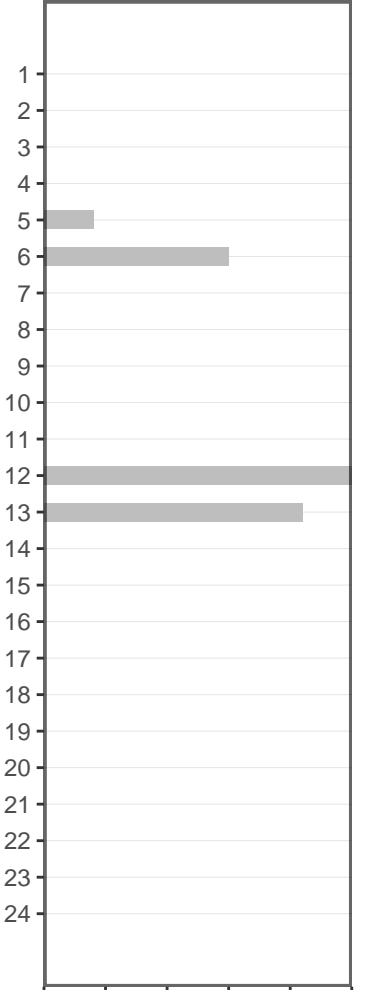
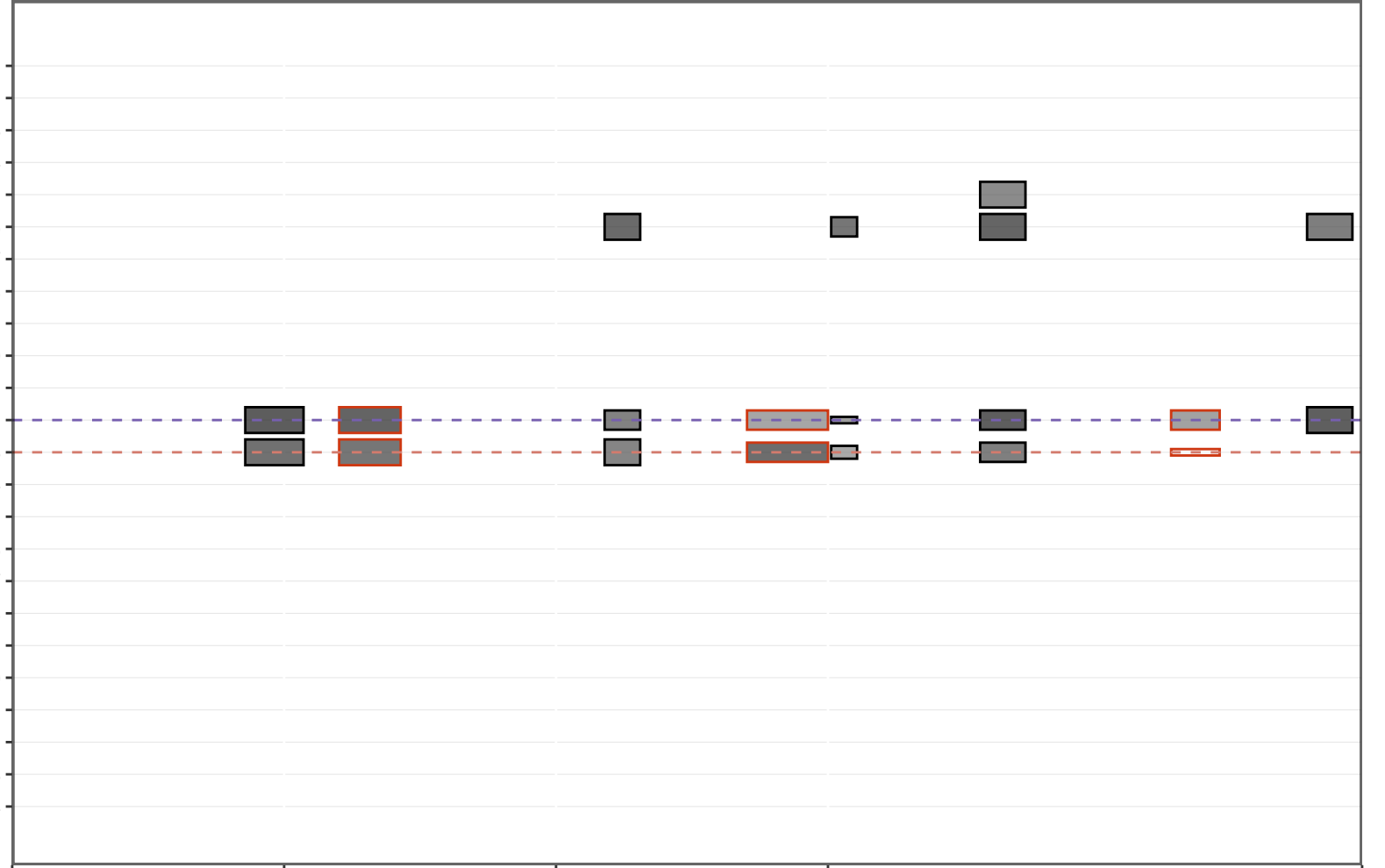
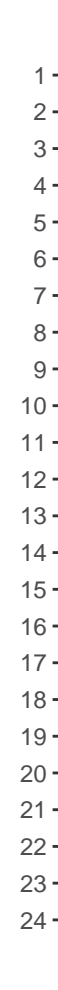
MW indication



Molecular weight



Gel Slice

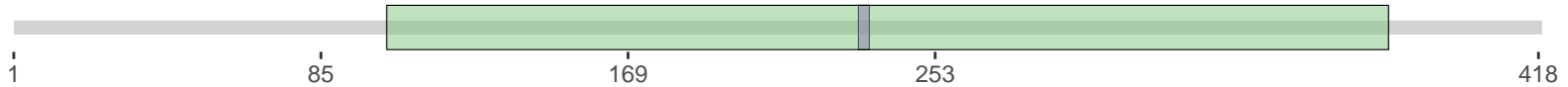


Protein length

Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

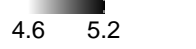
/HGETLLVNTAVIGNHNIGKGRKRNHPRVGDFFNESTYYMEGNTGHPVFDYAGKIAVNGYGRHHPLNALAFGLNGAEIVFNPEATVGLSEPFMWPVEARNAAVNSYFVGSINRVGTEVFNPFSTGGDKPKGHADFGHFYVGSIFSAFDSGGTPELSRHKDGLLSEMDLNLGRGLKEKVGFRMTARVEVYADLLARVVKHDFEPQVIGDPLLYKNA

NbL17g13780.1 uncharacterized_protein_C6C3.02c-like [MW = 14.27 kDa]

No. of times detected



log(intensity)



Values from



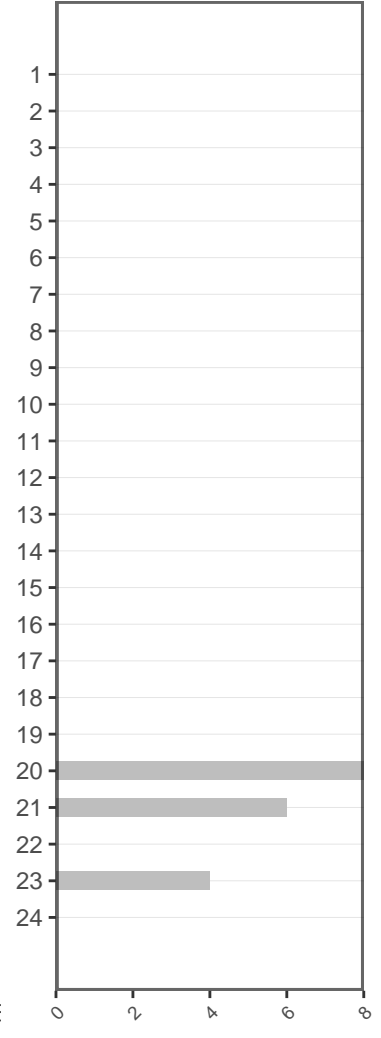
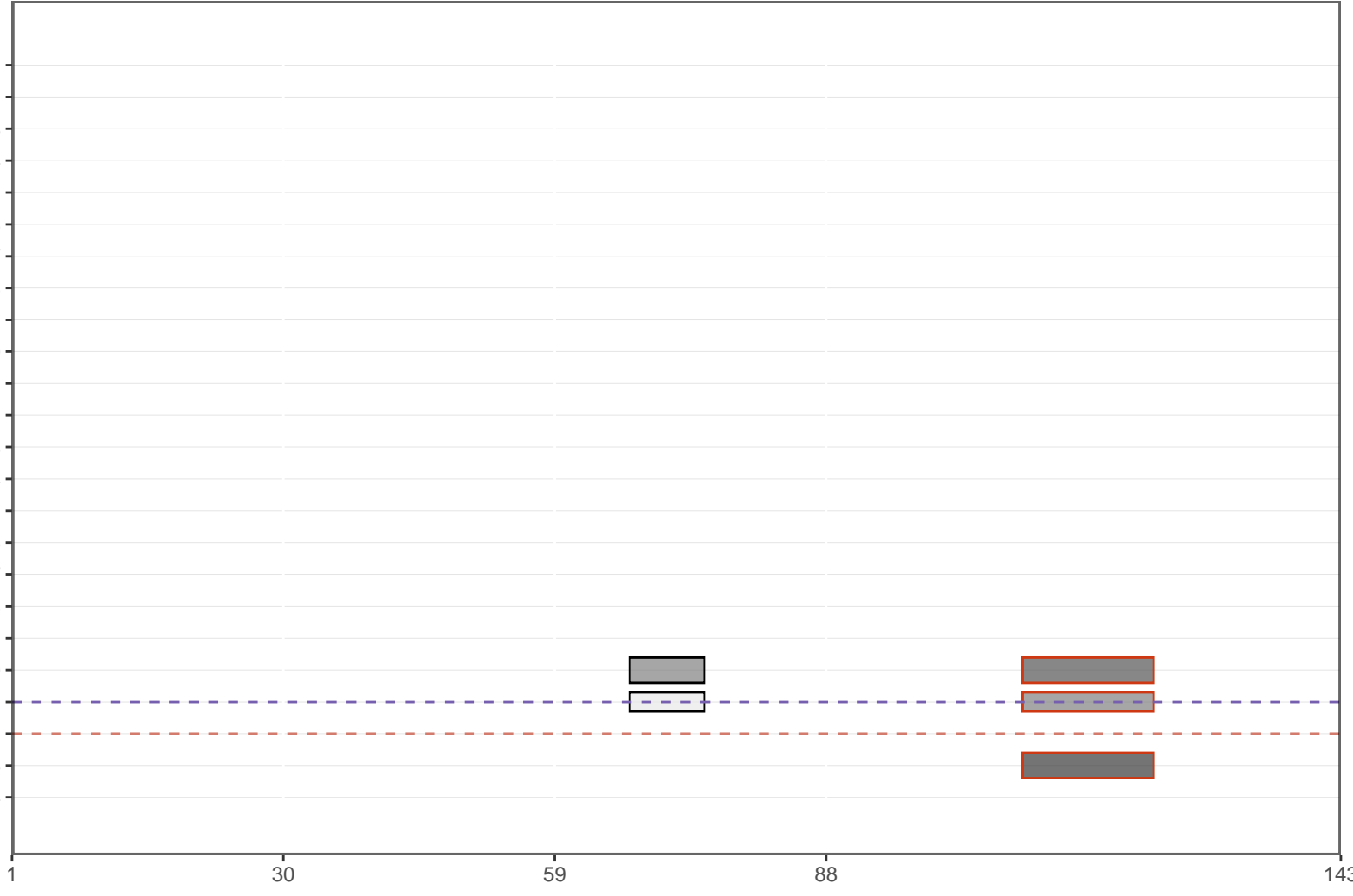
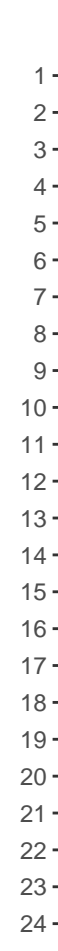
MW indication



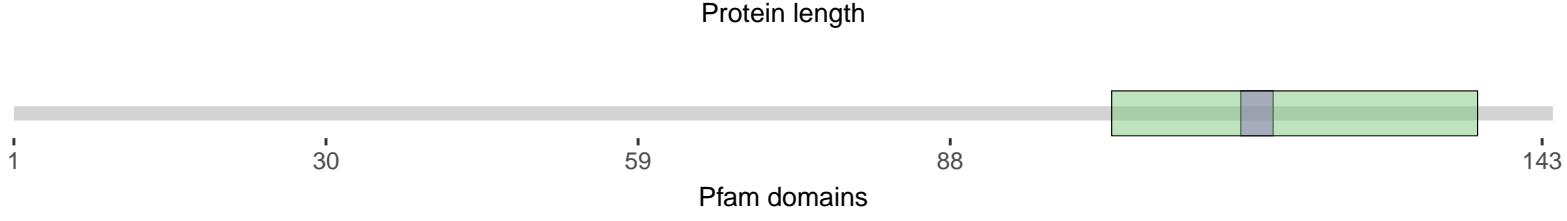
Molecular weight



Gel Slice

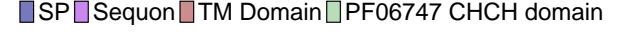


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ITGSVAHRAVDVIMGPRTIQHEIVASAVRAAAAPPTVGAABDAGMHSKAFQDCINSSGSDIGKGGFYMDMLSECRINEMLNAA

NbL17g13730.1 3-oxo-Delta(45)-steroid_5-beta-reductase-like [MW = 44.37 kDa]

No. of times detected



log(intensity)



Values from



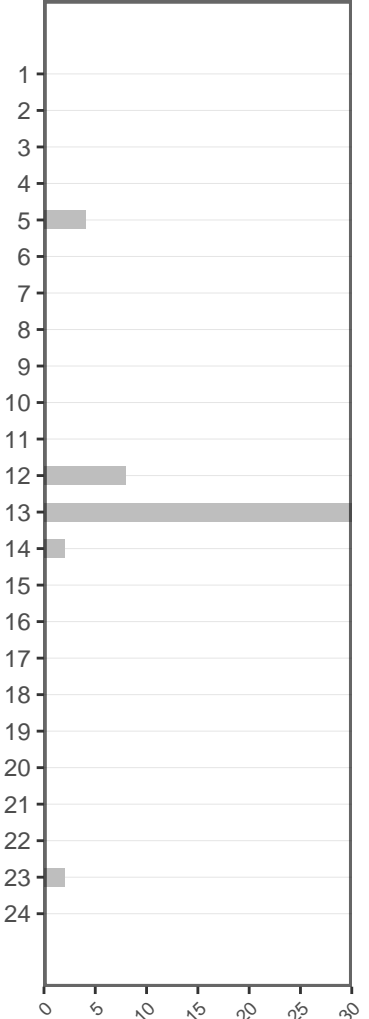
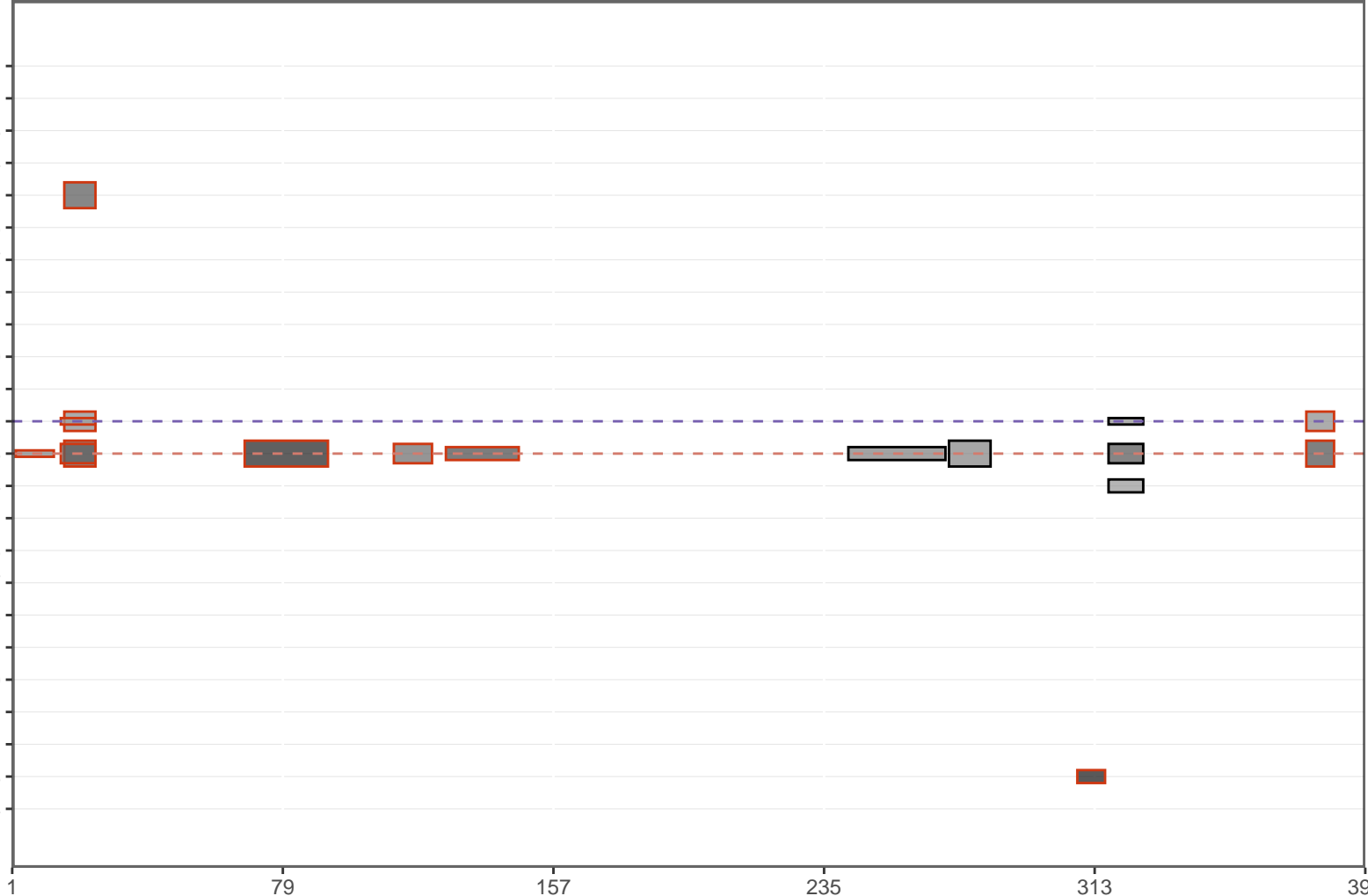
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

.EDILFEEVXXEKLTWWSVHRPLGIFGSPRYSLMNIASLGVAAIGKHGKLFKFPVWKAWDGYSDDSDADLAEHQWASVDPNAKNEAFDVSNGVFRKWHHLWGHLAEFEVEAEAFDENKKGWRLEEMMKDKGEIWDKIKENGLVFNKLEQVGGVWFADVLNDEGLPDTMKNKHEHGLGFRNKNVAFISWIDKIKAYKVP

NbL17g13720.1 3-oxo-Delta(45)-steroid_5-beta-reductase-like [MW = 43.71 kDa]

No. of times detected



log(intensity)



Values from



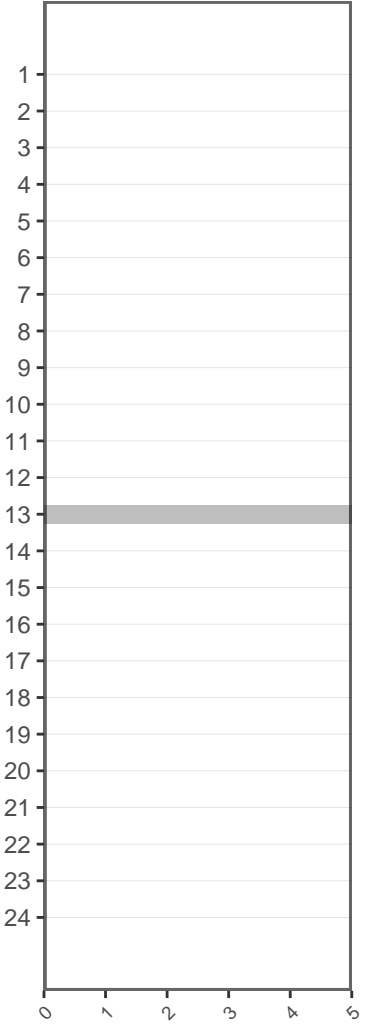
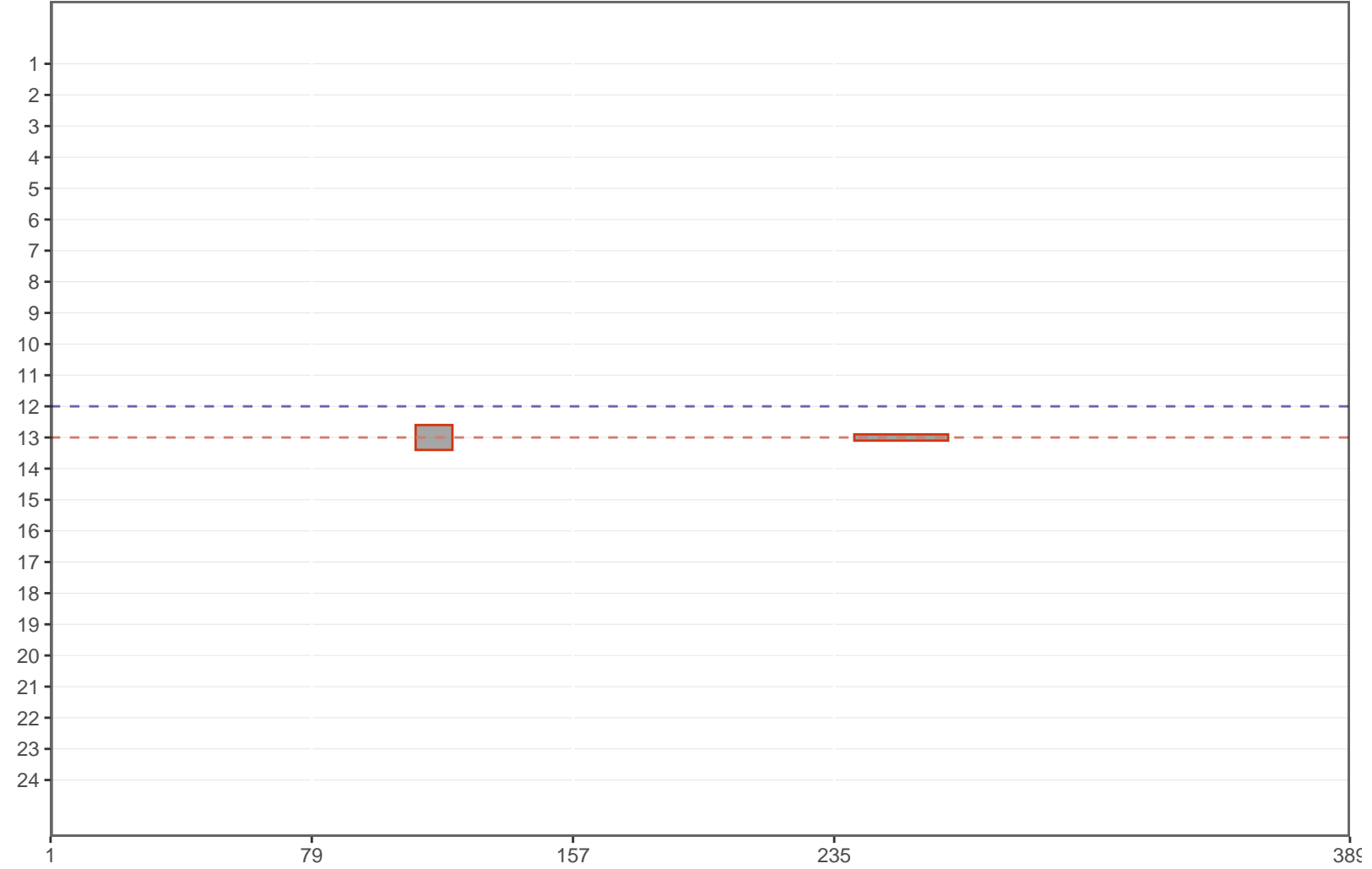
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains



Pfam Description

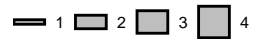


Protein sequence:

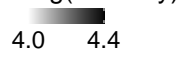
DILFKVEKEGLTWVHRPGTIFGSPVSLMNVGLGVAAKKGHEGLPKFPGVKKPWWGGVSDGSDADLAEHQHAAVDPYAKNEAFNVSNQGVFKWKHFVWYLAEGFGVEATEFDEVNRCLEAEMMKDKGPAWDEIVKENGKLTATKLEDDGVWVWFVLDLILAGDGLDTMKNKSEHGLFRNSGKAFISWIKVKAYKAVPI

NbL17g13670.1 ATP-dependent_Clp_protease_proteolytic_subunit-related_protein_1_chloroplastic [MW = 44.92 kDa]

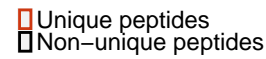
No. of times detected



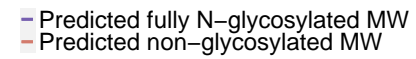
log(intensity)



Values from



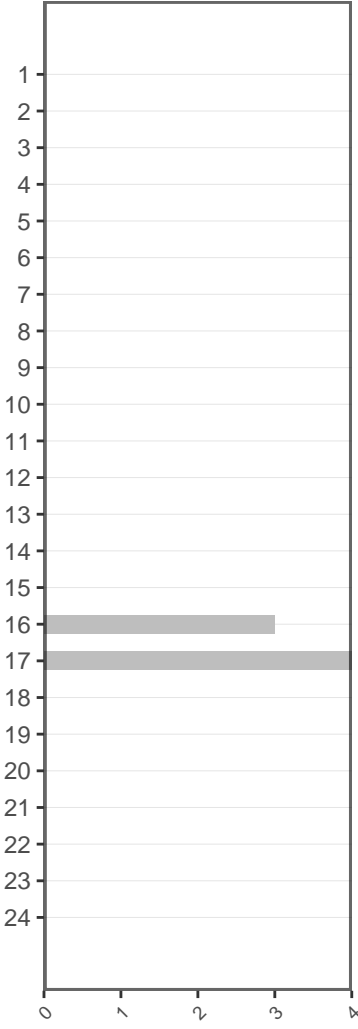
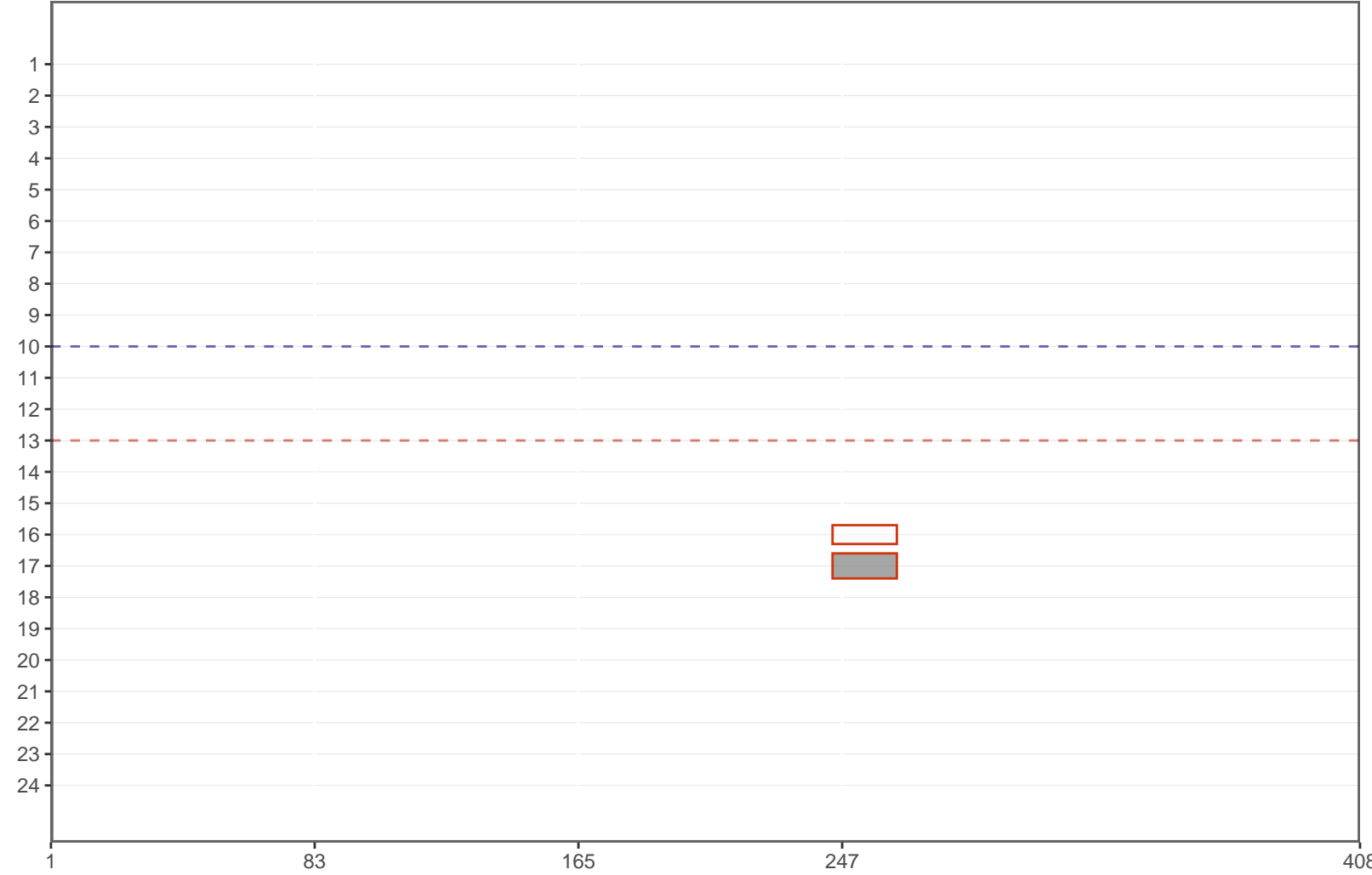
MW indication



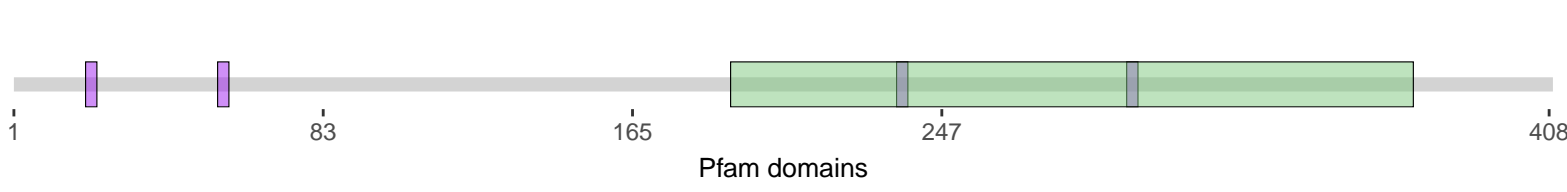
Molecular weight



Gel Slice

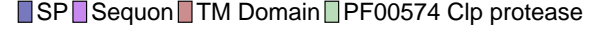


Protein length



Pfam domains

Pfam Description



Protein sequence:

PPDPLSLLLDARIVYLGMPVIVVTELLVAGFMFLVDVDPKPKVLYVINSSTGQNEKMETVYGSSETAVVAADTMAYGKSDIVTVNDGMAYGGSAMLLGLGKGRFRAMPQNSSTKLYLPKVKSSGAVDMVWKKAKELDANTEVYLELLAKGIGKPKVEIEKIDQRPKYLRYRAGEAIDYGIADKIDSRDIAFEKRYVDELAGSRAMRKAGPGCAAPSGFRV

NbL17g13420.1 pectin_acetyltransferase_10-like [MW - SP = 43.82 kDa]

No. of times detected



log(intensity)



Values from



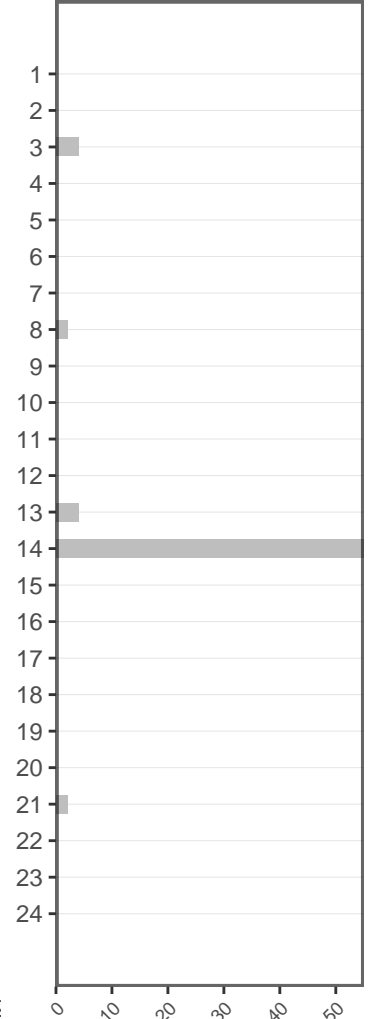
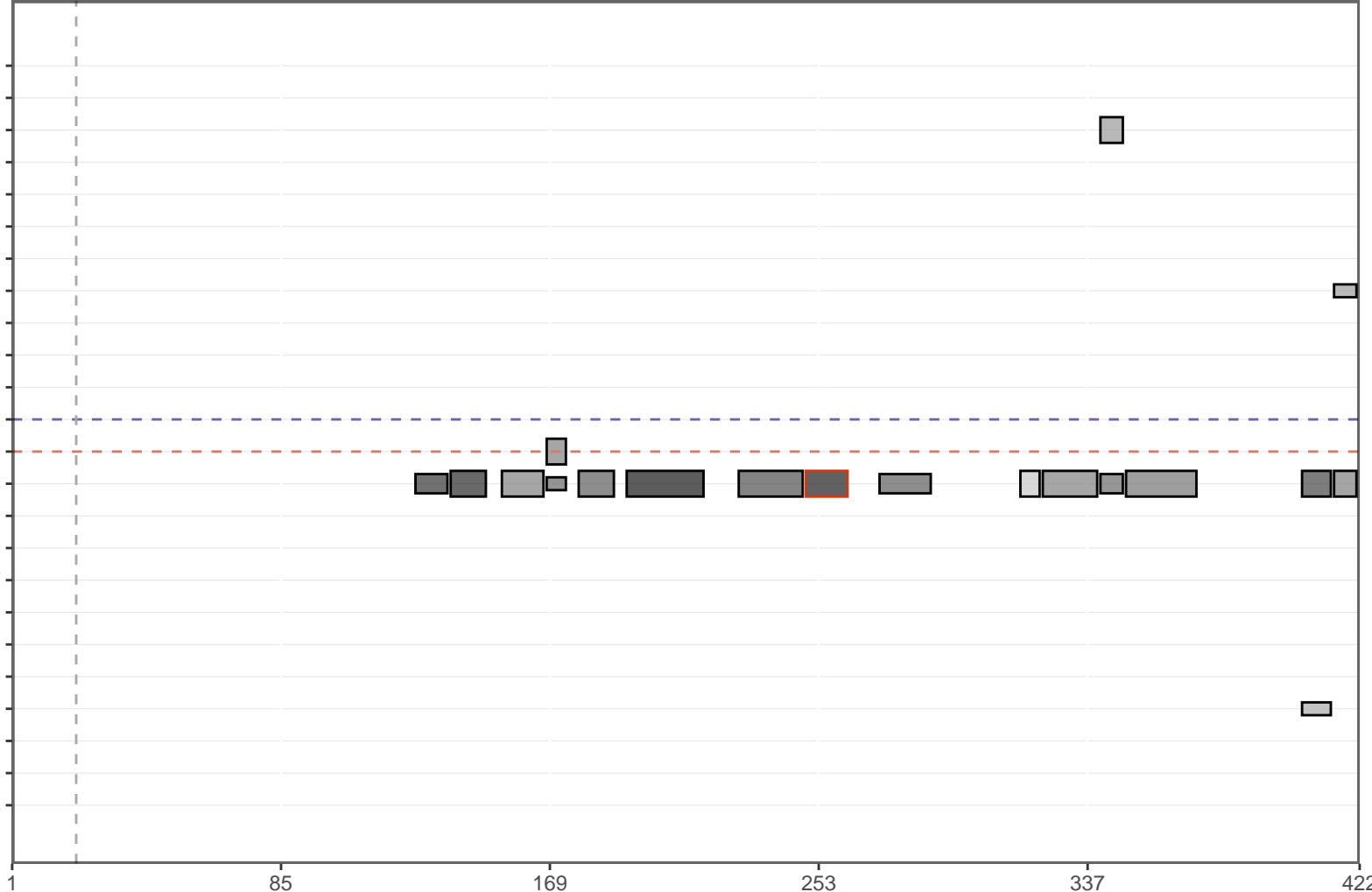
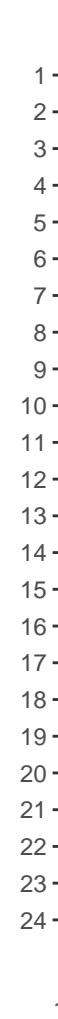
MW indication



Molecular weight

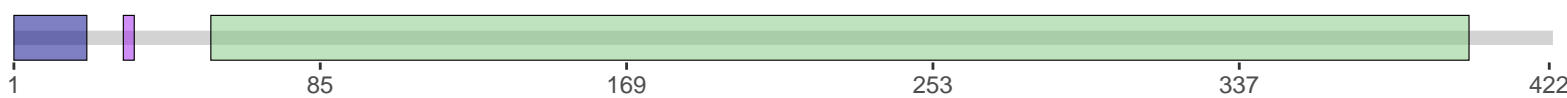


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ALLSGCSAGLASLHDCDEFRLFPPSPKWKGLSDAGLFMDATDVGSGHAIARNLYGGVNVVDGLGKTLFPTGKLNLDPTSGFFPNLIIGNIKTLFLFLNAAYDSWGVQGSLLAPPVADPKGLIWHDCIKLNEGGASAGIQFLGQFRNDMLNAWKGFAASTGNGLFINSGFAHQDSERQGTWTFADDSPLINDKPLVALVGDWVFDRAGVKSIDGAYPCDKTGHNLVFK

NbL17g13300.1 endoglucanase_25-like [MW = 76.89 kDa]

No. of times detected



log(intensity)



Values from



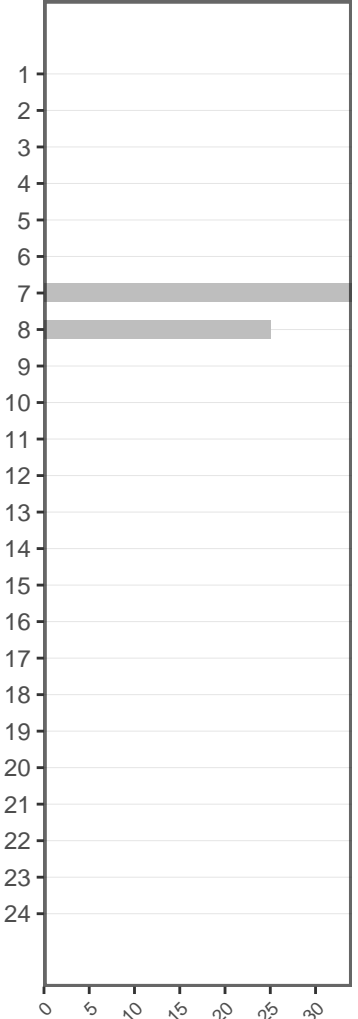
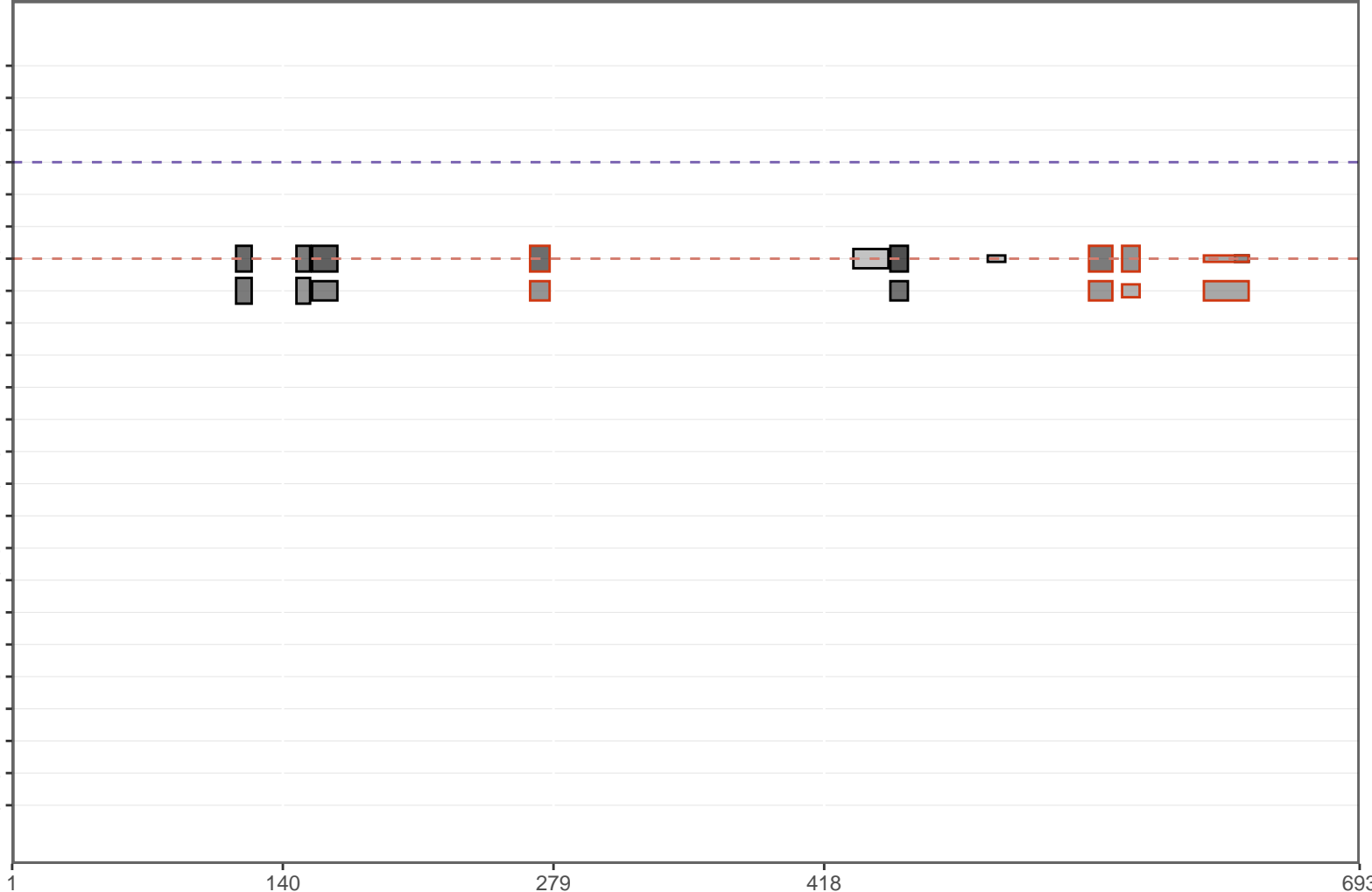
MW indication



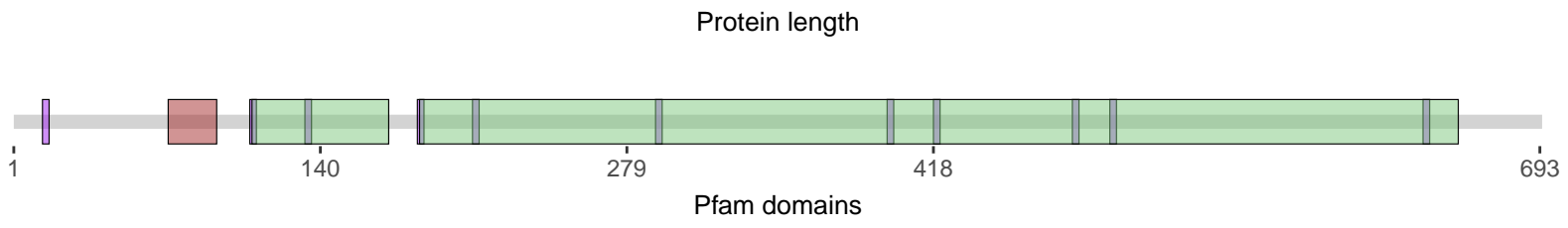
Molecular weight



Gel Slice



Peptide counts over 4 repeats



Pfam Description

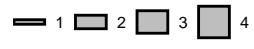


Protein sequence:

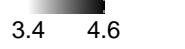
LVTECHSCSDLAEMAAALASASIVFKDKKVVGGKLVHGARTLRFKFRQGRGRYSSGNEAAIFNNTSYWDEFVWGAWLVYATGNTSYLGLATTTPGAKHAGAFWGGPDYGVLSWQNKLTGSDVLLSRLRFLFSPGYFVDELSTFHNGTGIMDFLFPVFSFNRTKGLGLKLNHGRPQPLGVYANAAFLATLVGDYLAADTPQWYGGPNFYSTDLREFALTGQVNYLGNPKRMISYVVGFGNRYPKRVHHRGASIPKPKVKNYNDKGGVWWRDSSKNPNTLVGA

NbL17g13110.1 microtubule-associated_protein_70-2-like [MW = 69.02 kDa]

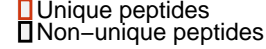
No. of times detected



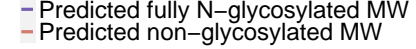
log(intensity)



Values from



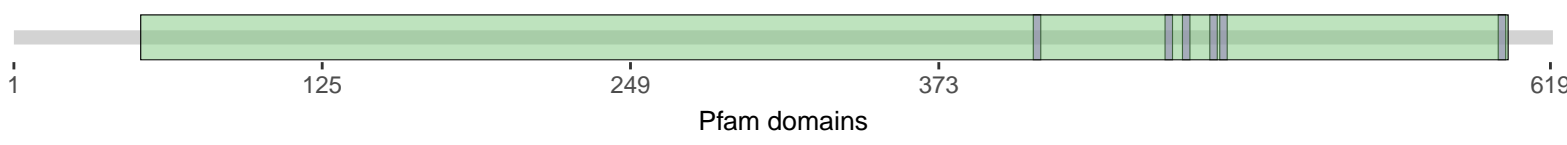
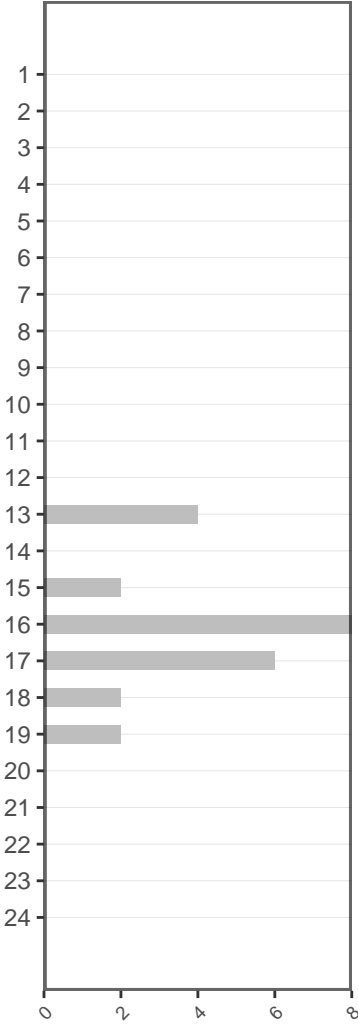
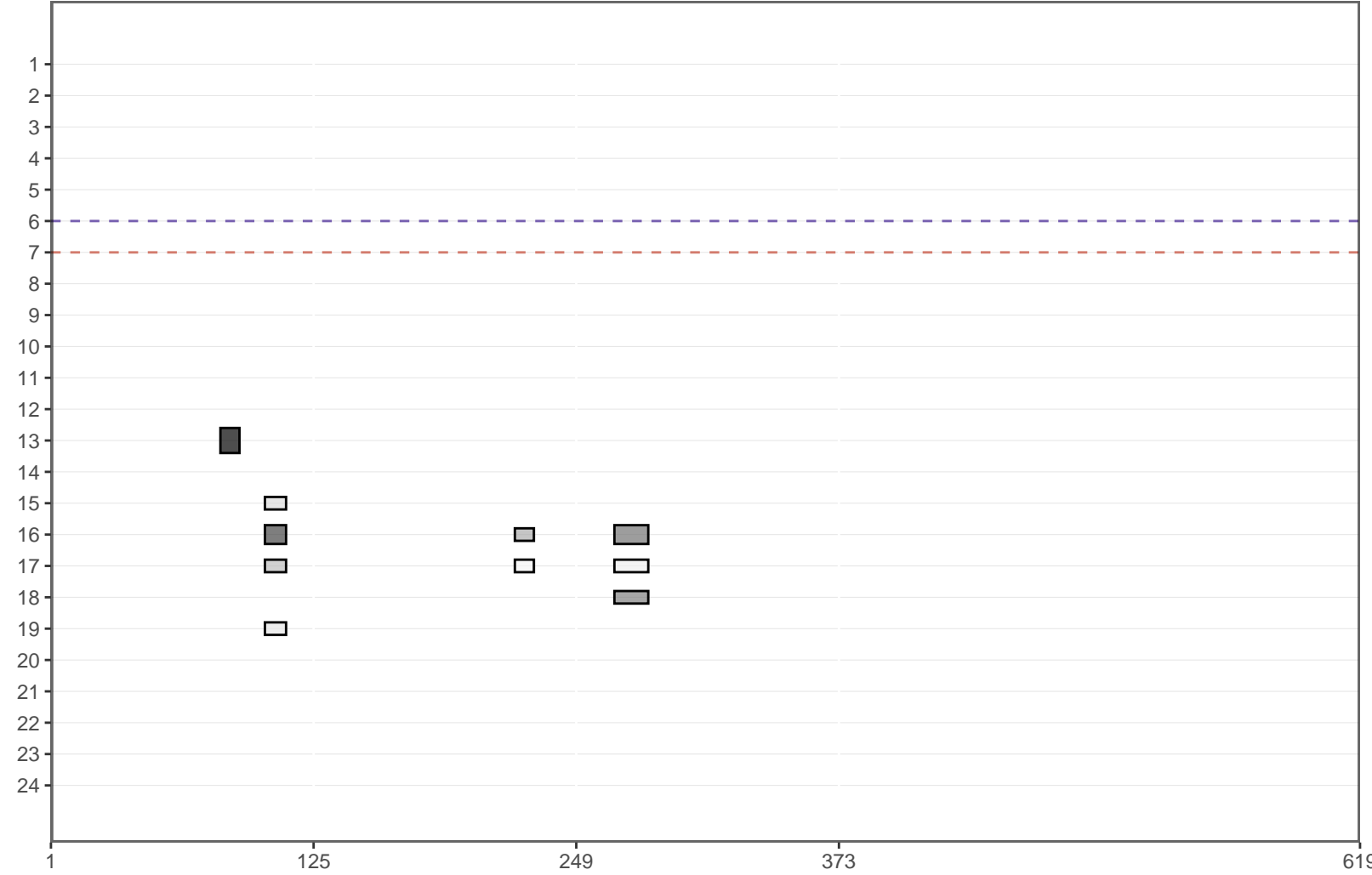
MW indication



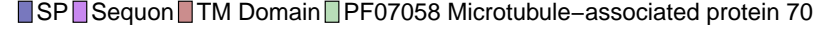
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

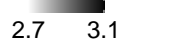
DRELARAKVTANRWATVAWNEWKDKANKMPPKQWLEERRFLQGMOTLRDLKAVTERAAKSEAMLKEKYQLRKLVEETLRSSSSATRTSPDGRSSSGNPARRRGLGGAENISKLTNGLPKRSPFQLRSSGSSFLVKNNAKGTSKSFDGSSRBLDKGNKLNLTGTFNFNSSKSGCDVANDNETENNNSWKSQVKEKNSDTQVTEREDSIPGLYDLKQKEVIALRKAGHEKDGSLKDKDDDAIEMLAKKVEFTKAMEVEAKKMRREVAAMEKEVALAIRVEKDHENRA

NbL17g13050.1 aspartate-semialdehyde_dehydrogenase-like [MW = 44.42 kDa]

No. of times detected



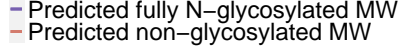
log(intensity)



Values from



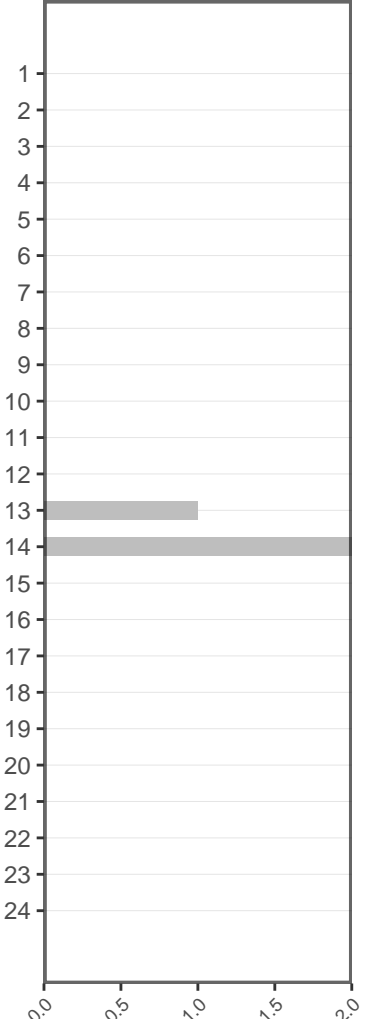
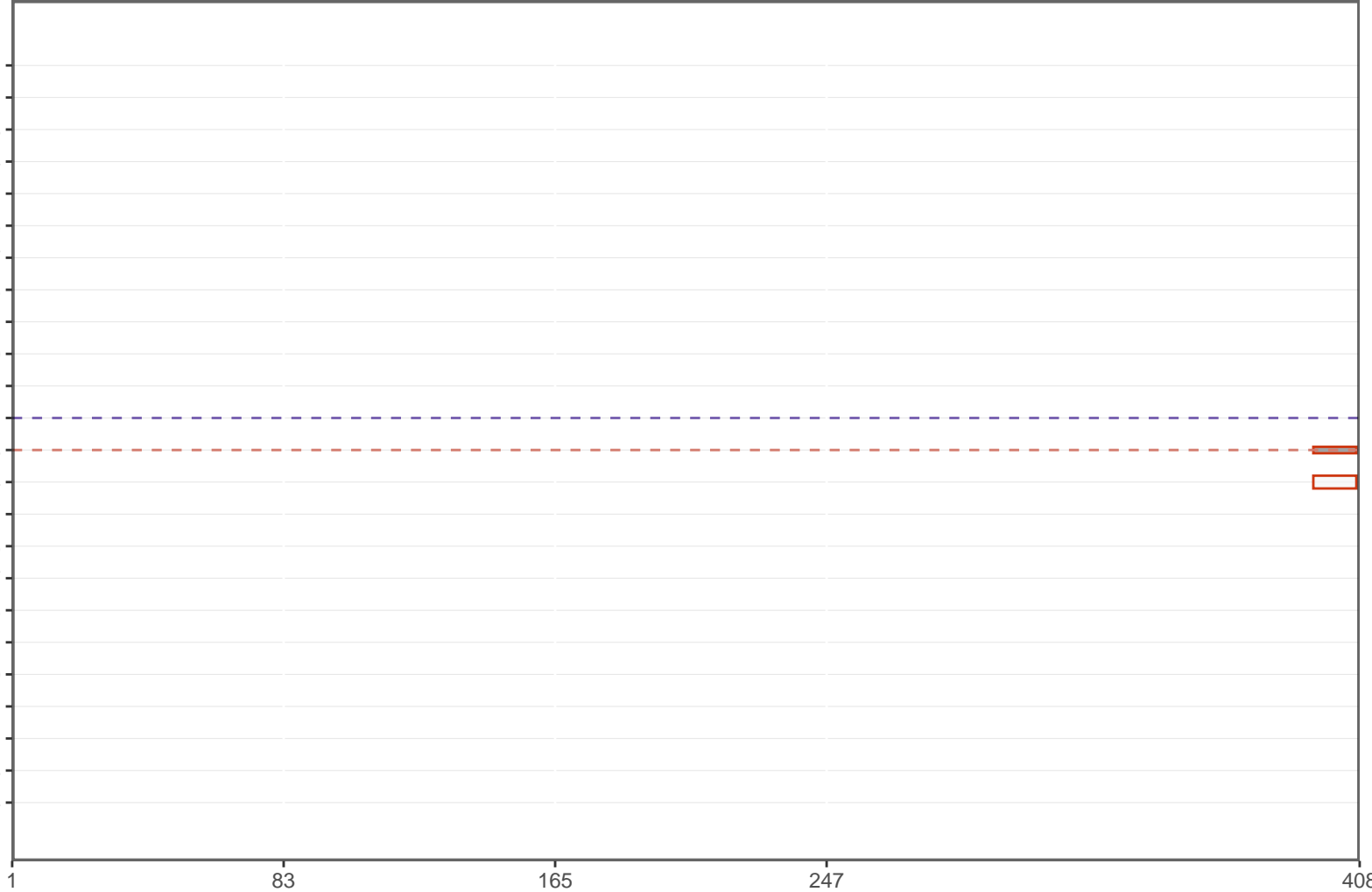
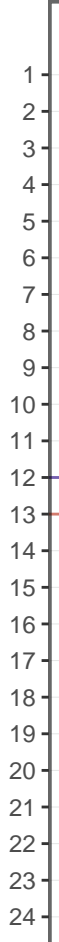
MW indication



Molecular weight



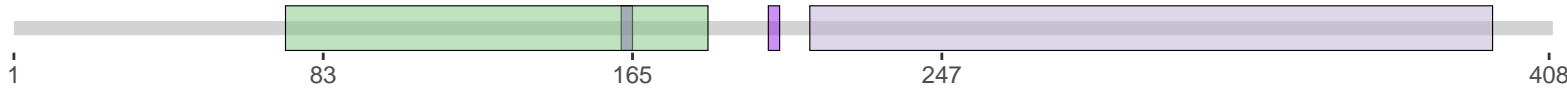
Gel Slice



Protein length



Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF01118 Semialdehyde dehydrogenase, NAD binding domain
- PF02774 Semialdehyde dehydrogenase, dimerisation domain

Protein sequence:

ISKGALLIAPNCSTHQLMVAITPLHRGAKVNRMMVSTYQGAASGAGAAAMEELVGGTREVLEGGKEPTQNFNGQVAFNLFQHNAPVQPNQYNEEEMLVKTRKRWKNDMDVAVTATGIRVPIVIRAHAESVNLGFKEPLDEDTARDILKNAPGHIIIDRASRFRFTPLLEVSNKDDVAVGRVRRDVSQGDGVDGLDFVGGDQIRKGAALNAVQIAEMLL

NbL17g12900.1 G-type_lectin_S-receptor-like_serine/threonine-protein_kinase_At1g11330 [MW = 94.54 kDa]

No. of times detected



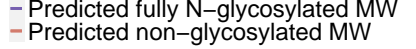
log(intensity)



Values from



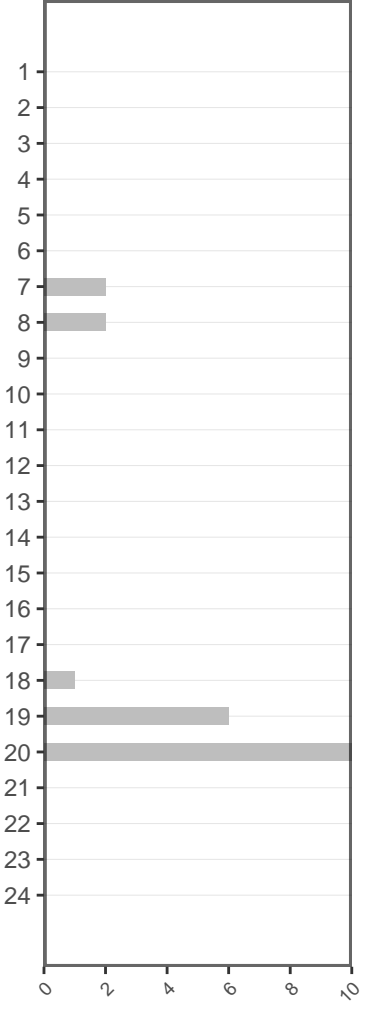
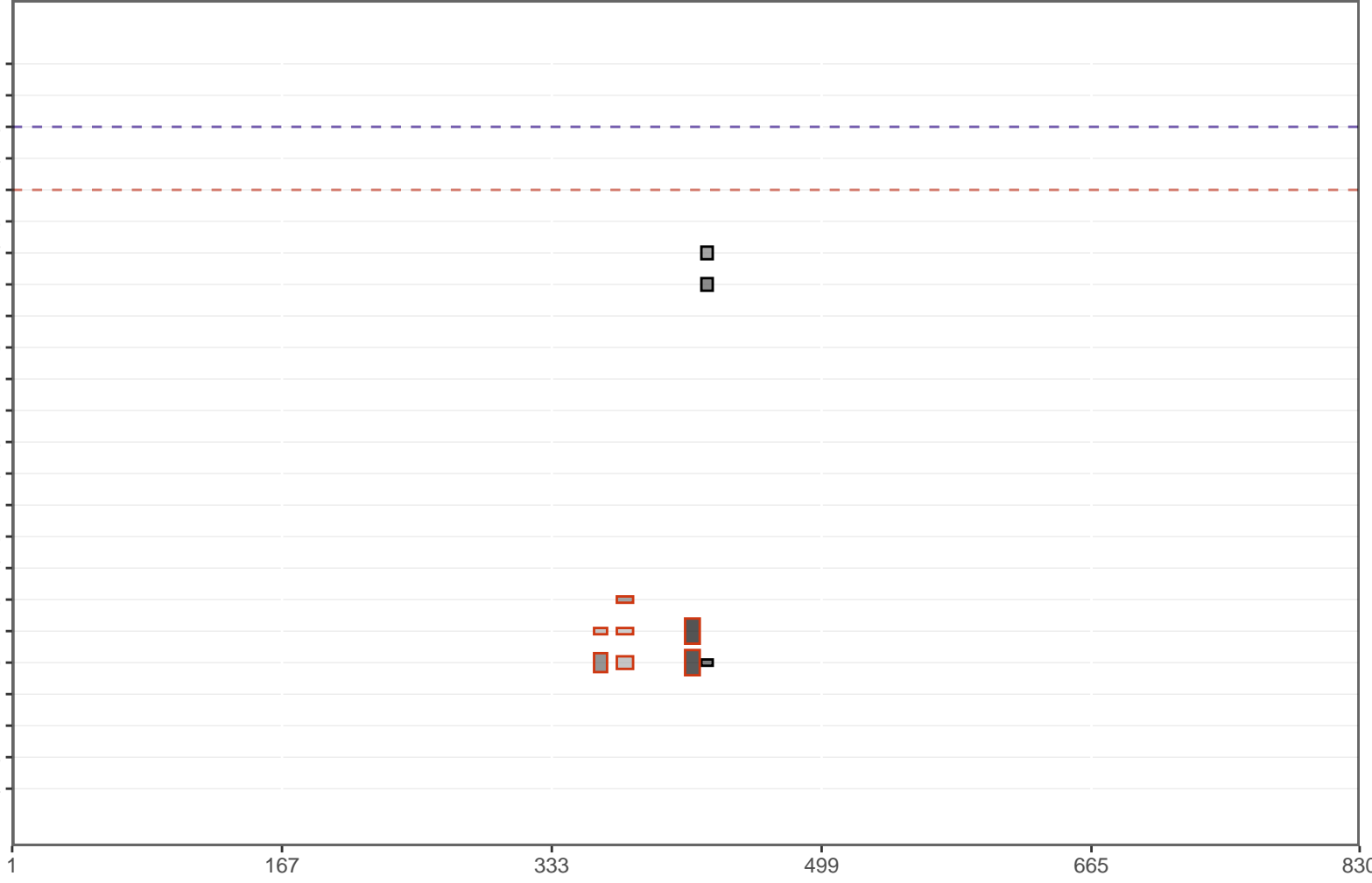
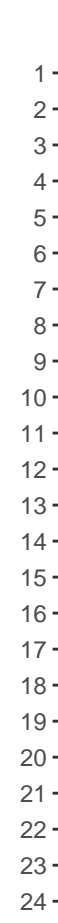
MW indication



Molecular weight



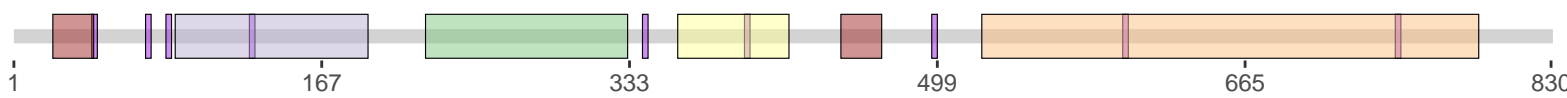
Gel Slice



Protein length

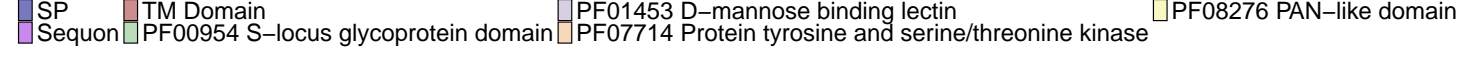


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NCSCLAYAFDAGIGCMWSRSLDGGQFORAGFTLNRWYSELDRPREIRLVAWLVVSLFVLCGIVFVCFWIPRRRGGIRFQKRNKQLDGGKSLKLEENFTTKVLDLDFMFKFVLAAMTDGFHENKLGQGGFGP/VYKGLADGKEIAVWRLESTASGGGMEFMEVNEVLVSKVQHRNLVLLGGCKEEMLYEVLNPKSLDVLFDPTHKRILDLKRLRHIEGGIGGLLYLHRDGRKIIHRDLKAPSNILLDNEFNPKISDFGMARIFKNGDGAETRAK/VAGTYGYMAPEYA

NbL17g12790.1 NADH_dehydrogenase_[ubiquinone]_1_beta_subcomplex_subunit_7-like [MW = 11.22 kDa]

No. of times detected



log(intensity)



Values from



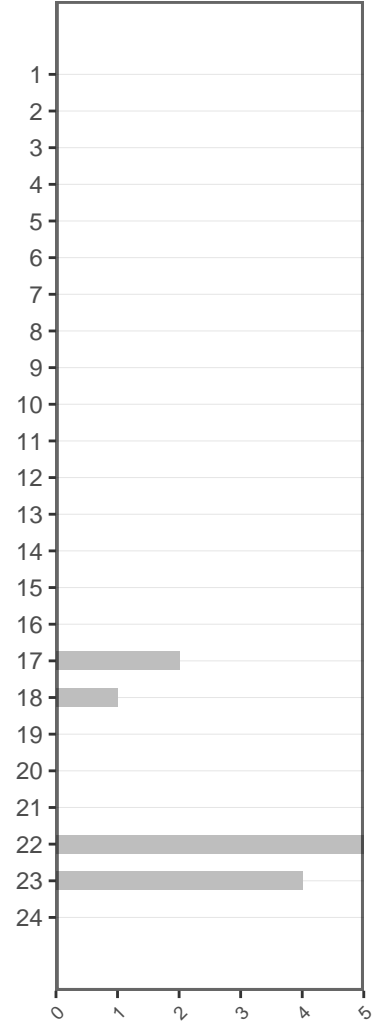
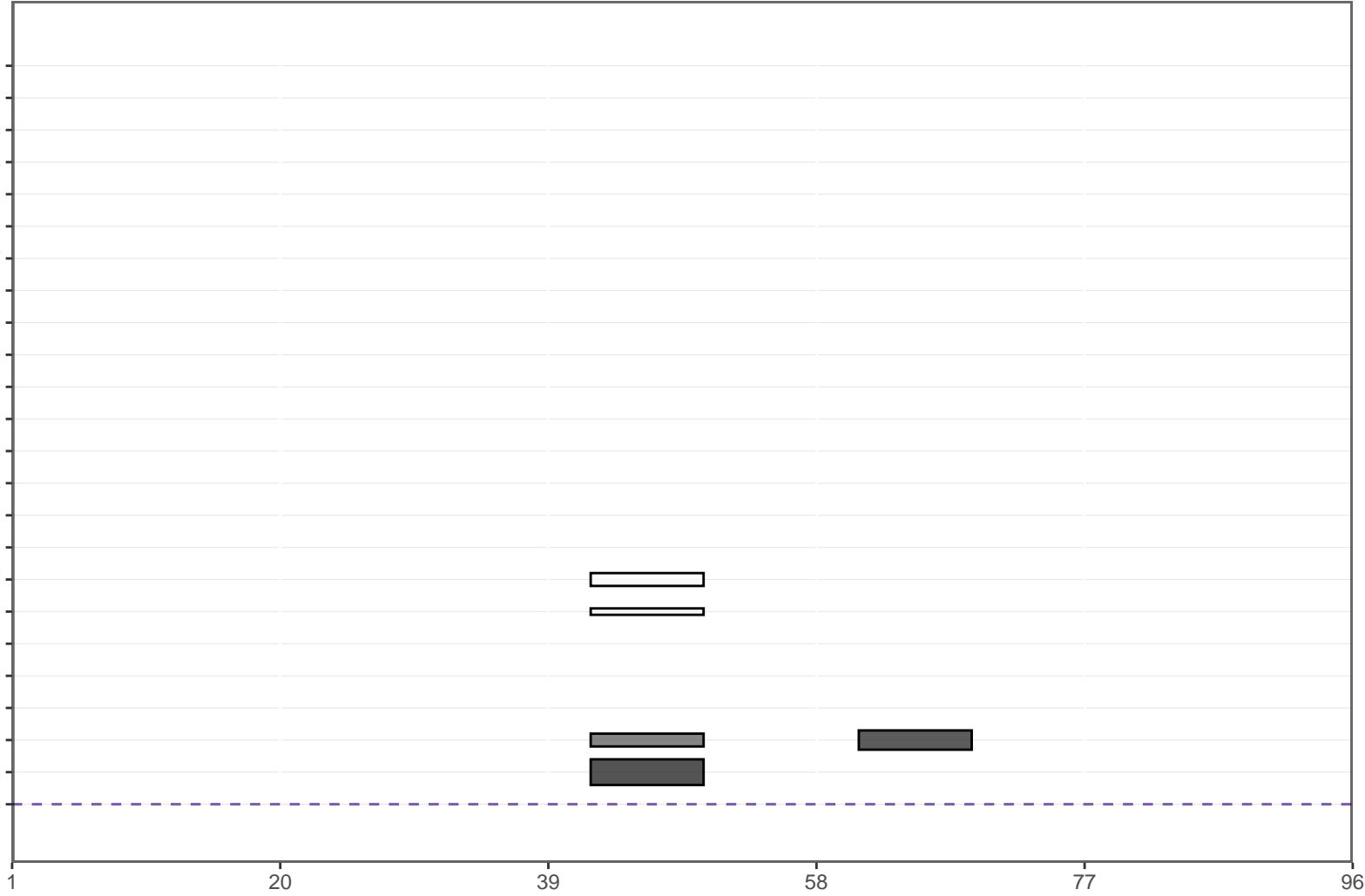
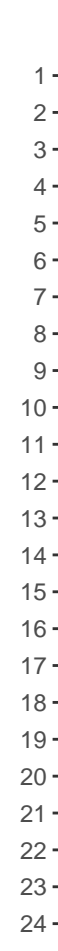
MW indication



Molecular weight



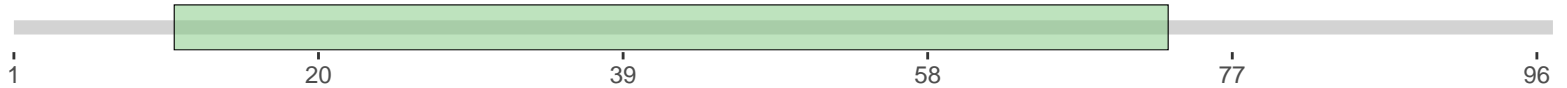
Gel Slice



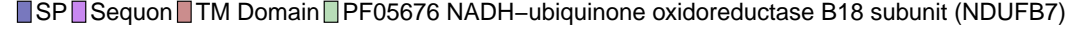
Protein length



Pfam domains



Pfam Description



Protein sequence:

PLNKCRCSEFYLPWKDEDERHSYKGEYELVMERMLGMQKIRGGQGGQGSPLFKTANA

NbL17g12650.1 uncharacterized_LOC109243108 [MW = 31.09 kDa]

No. of times detected



log(intensity)



Values from



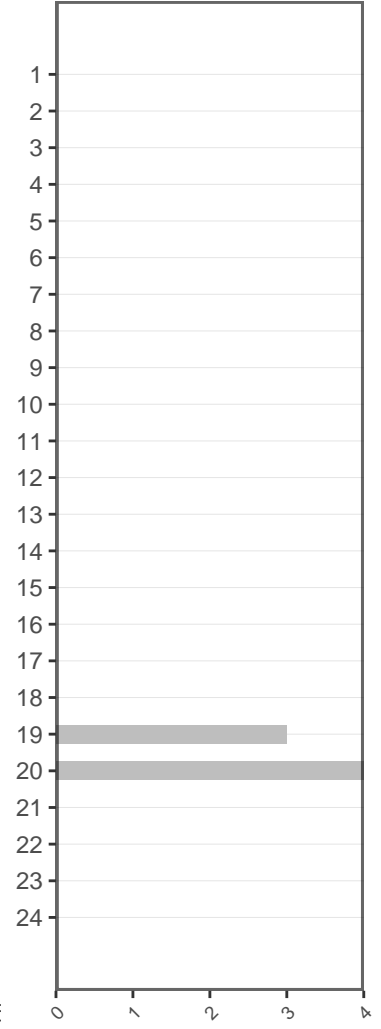
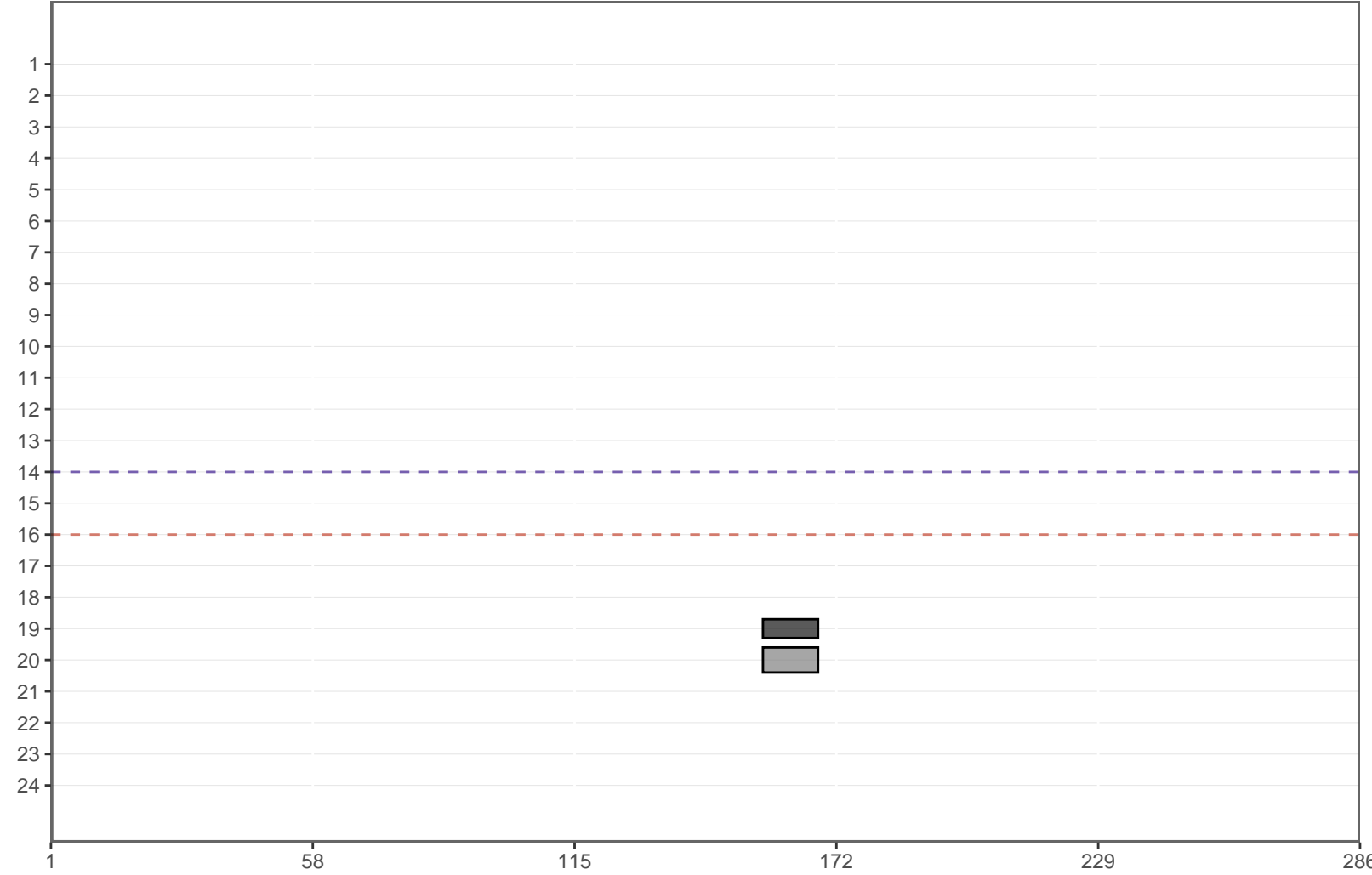
MW indication



Molecular weight

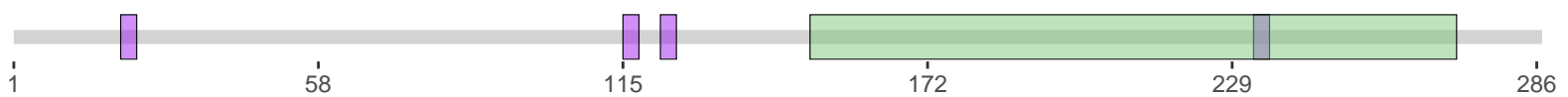


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

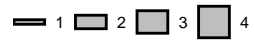


Protein sequence:

IKLIDLPKGDALSSGRBCTLEFDGASKGNPQDAGAGAVRRADDGSLKRLREGLGIAITTSVAEYRGLKRYAHKSGFTSIRAGDGSKLIVMGIQGLWVKNKNISTLFQDAKQKDRFLSFRHHVLRNSNGDADGGANLAVGLPDGHQEEIEK

NbL17g12600.1 ADP-ribosylation_factor_2 [MW = 19.5 kDa]

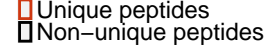
No. of times detected



log(intensity)



Values from



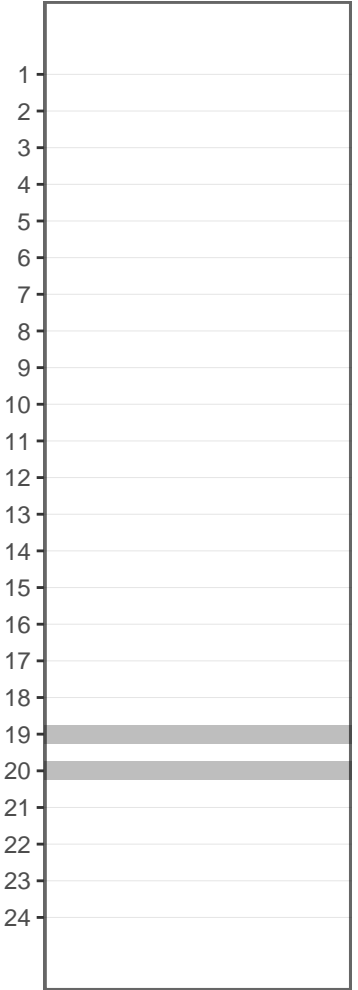
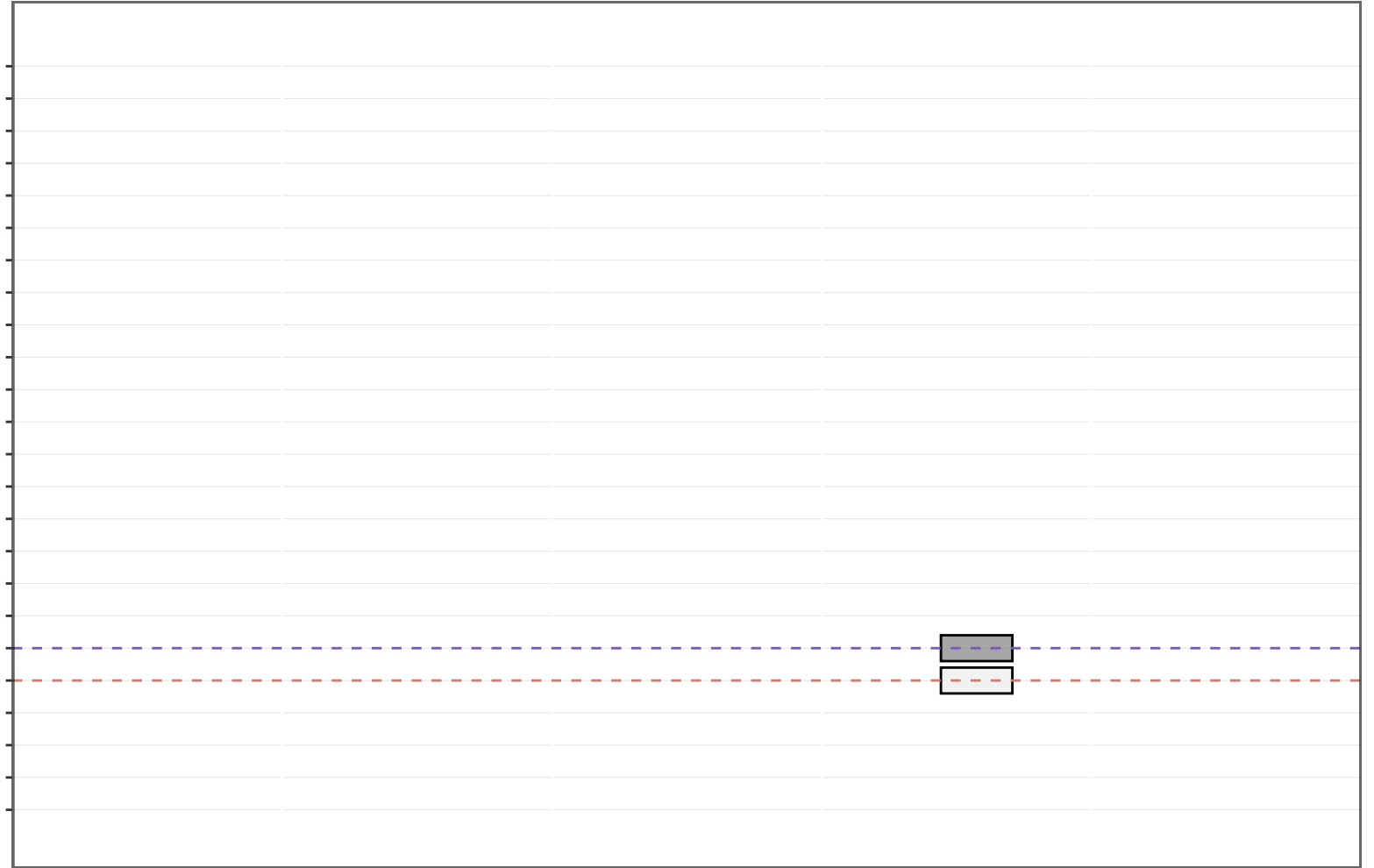
MW indication



Molecular weight



Gel Slice

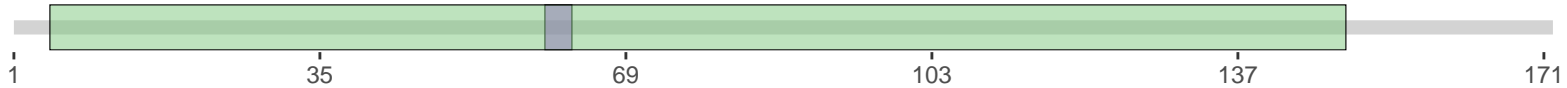


Protein length

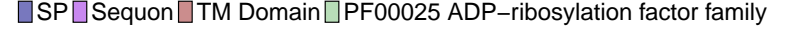


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

PLLVRSHYFQNTQGLFVVDNSDRDRVVEARDELHRLNEDELRDQVLLVFNKGGDLPNANNAEFTDKLGLHSRLRQLSLVHPPEHLGNFWRGTLRGA

NbL17g12510.1 succinate--CoA_ligase_[ADP-forming]_subunit_alpha-2_mitochondrial-like [MW = 35.19 kDa]

No. of times detected



log(intensity)



Values from



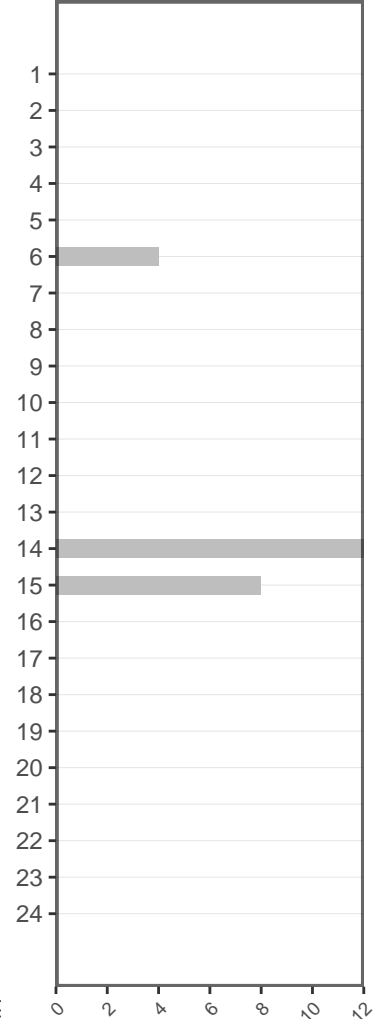
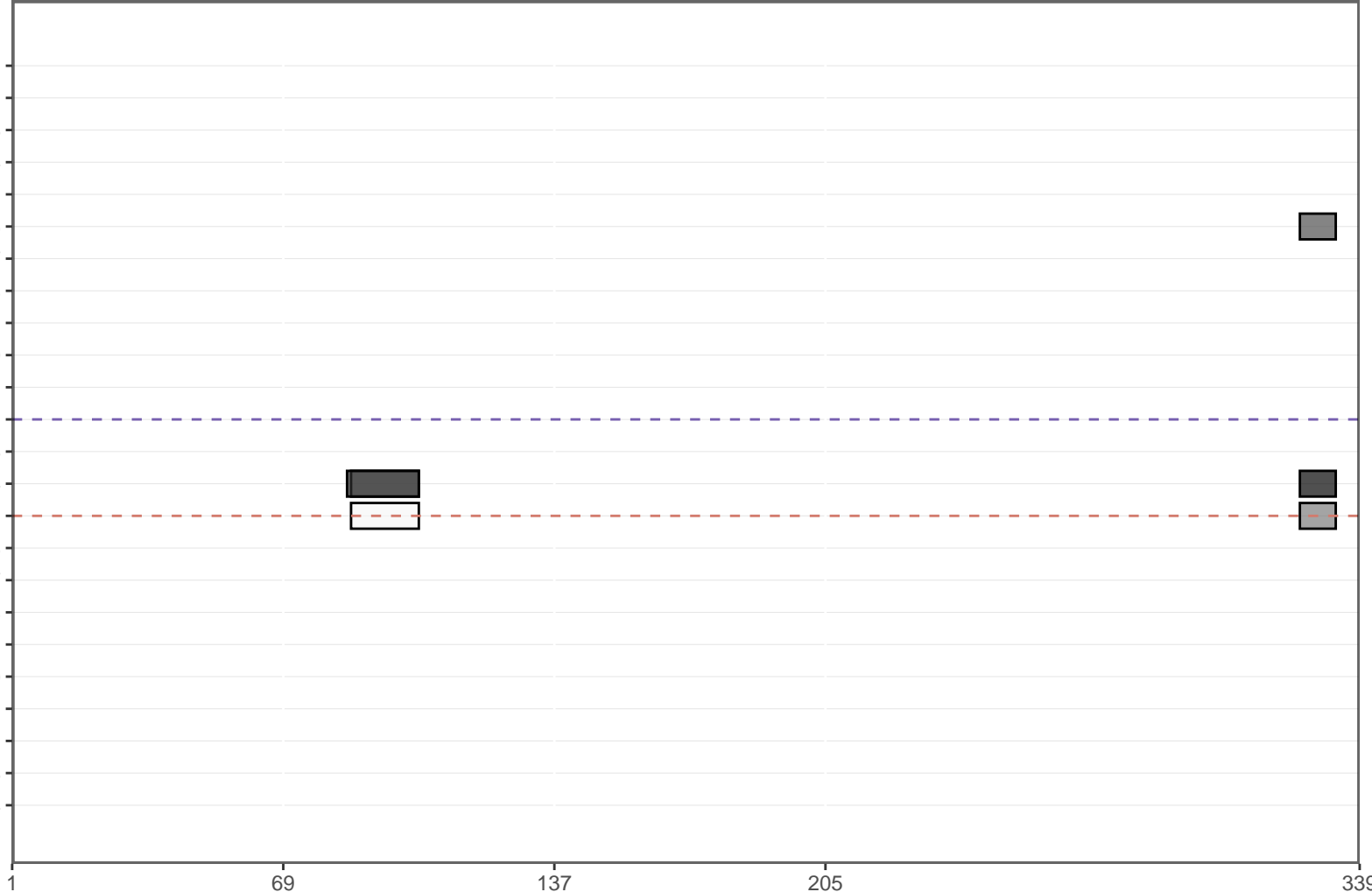
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

KKQSKTRLIGPNCPIKPKGEKGMPOYHKKPGRIGVSRSGTLTYEAVFGTTAVLGGSGTGVGIGDPPFNFTVVDLEKFAVDPQTEGIVLIGEIGETAEDDAAFIKESGSGKPKVVAFLAGLTAPPGRRMGHAGAVSGGKGTADDKKALKEAGVTVGESPAGKIGASMLENLFKQKGLV

NbL17g12450.1 thioredoxin_X_chloroplastic [MW = 20.73 kDa]

No. of times detected



log(intensity)



Values from



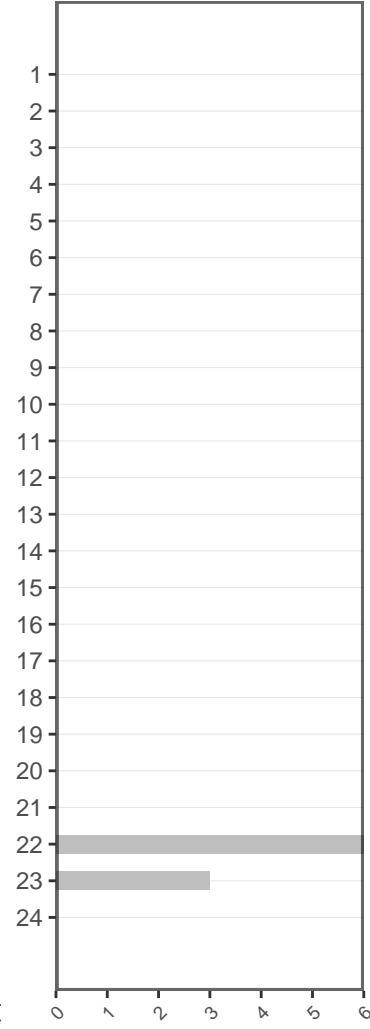
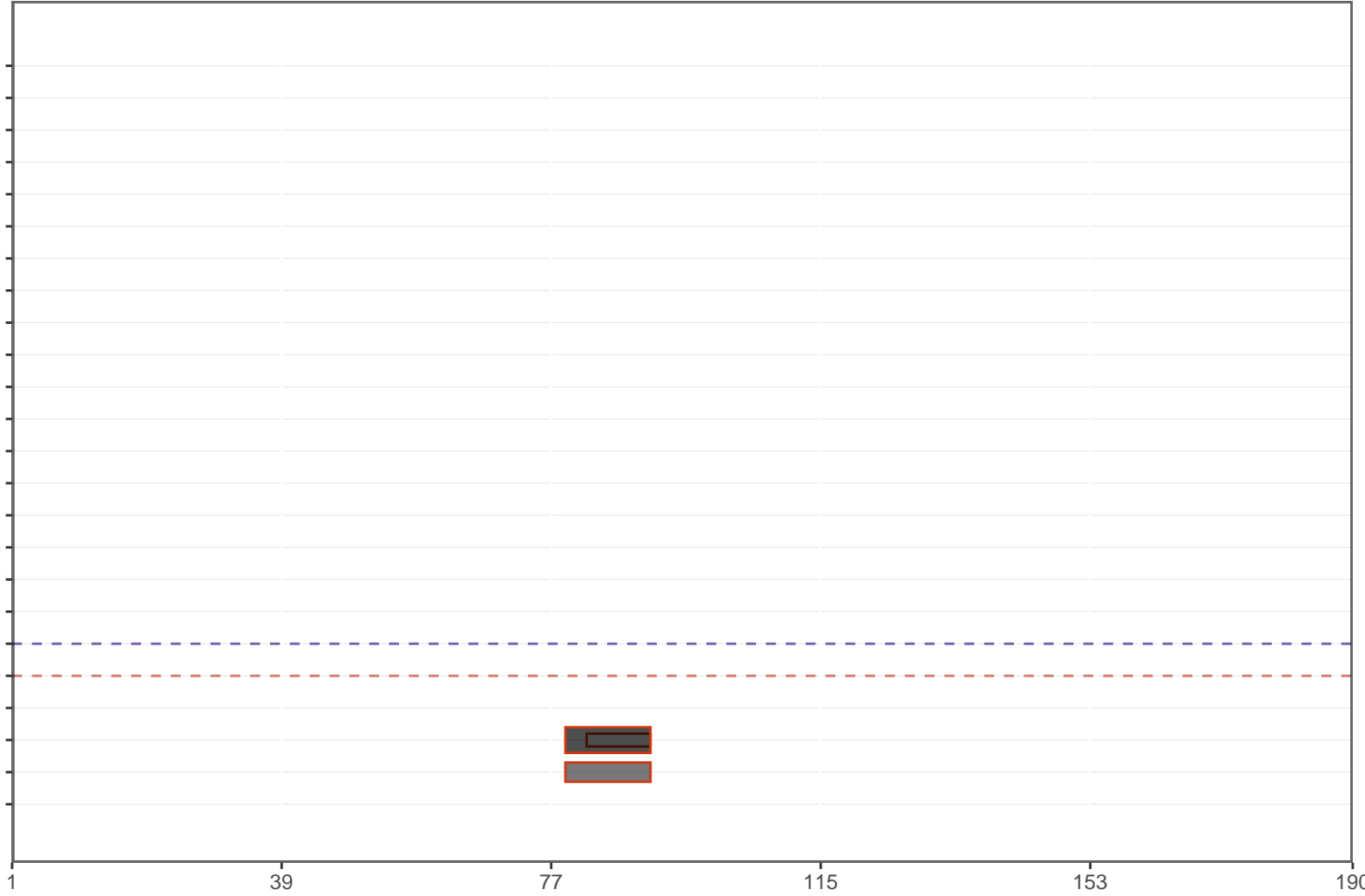
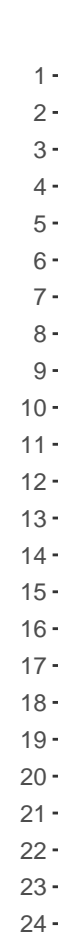
MW indication



Molecular weight

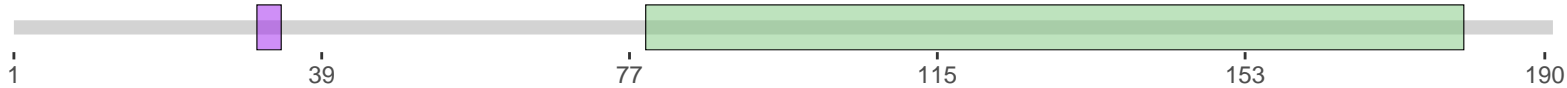


Gel Slice



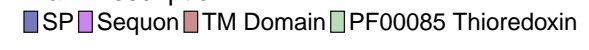
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

KEDEFSDVLLKSDRPALVEFVATWGGPCRLIGPAMESWAEVEYKEKIFVAKIDHDANPKLIEEFKYYGLPTLFLFKDQKEVPYKREGAITKWLKEYLIDGLLKTYSIA

NbL17g12420.1 probable_prefoldin_subunit_5 [MW = 16.62 kDa]

No. of times detected



log(intensity)



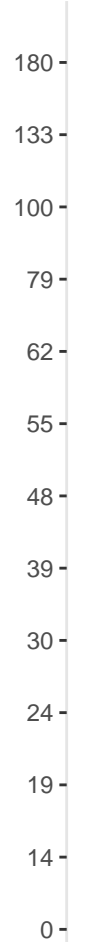
Values from



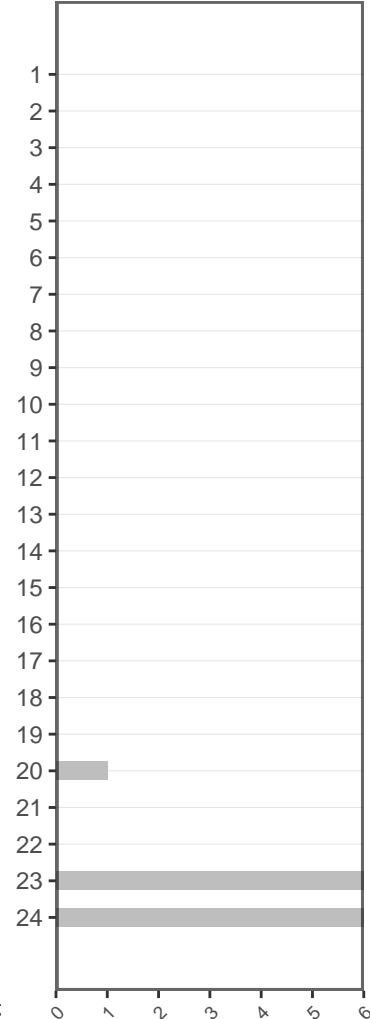
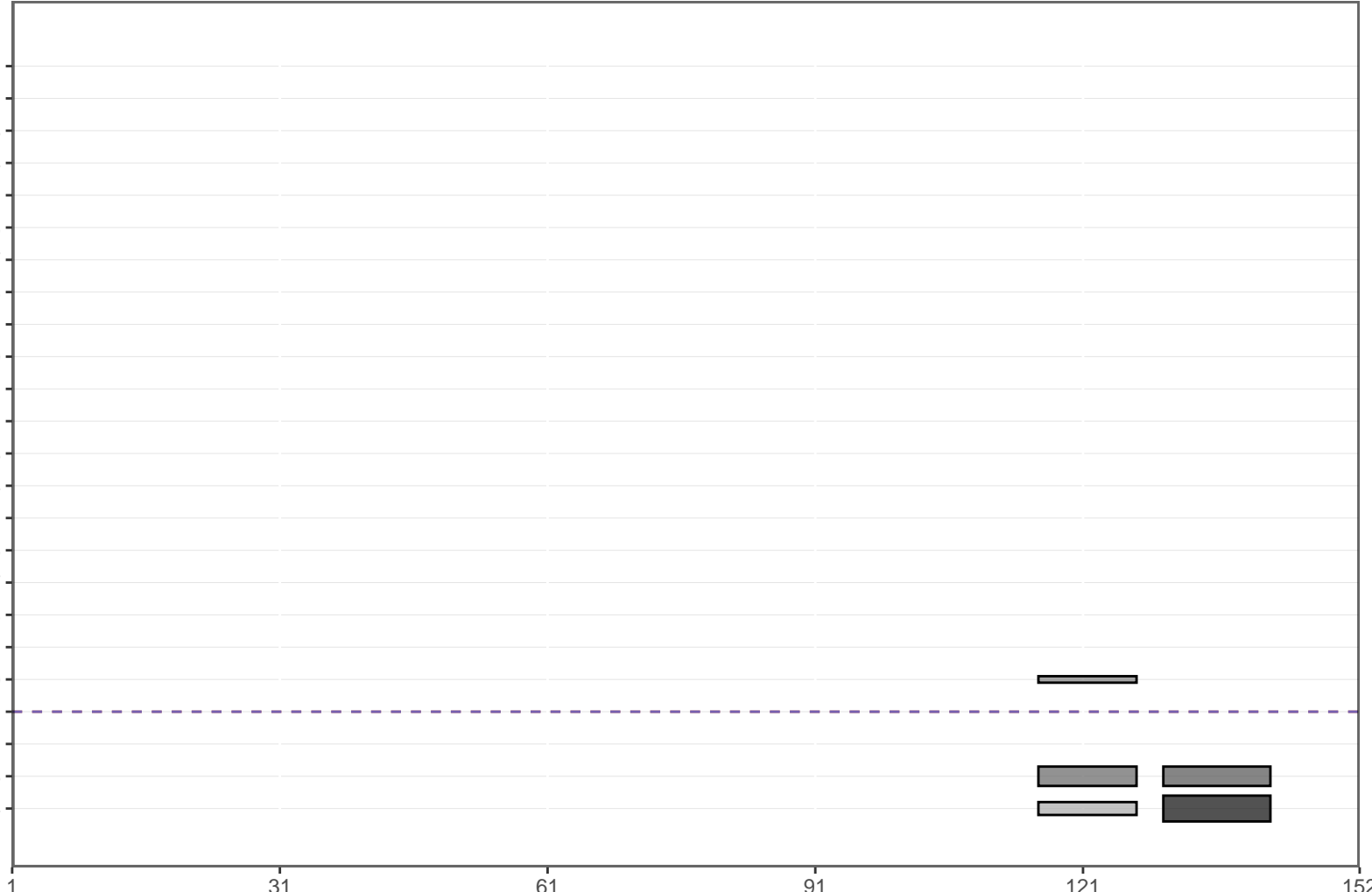
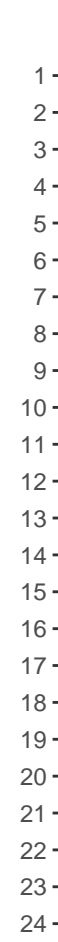
MW indication



Molecular weight



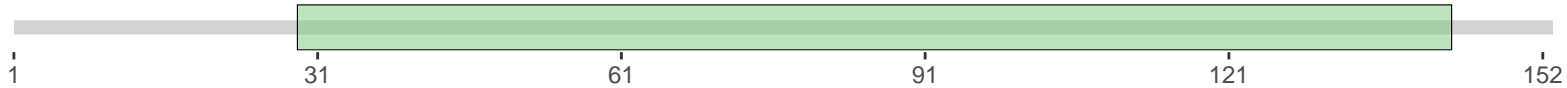
Gel Slice



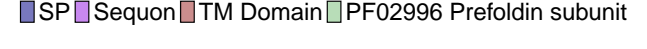
Protein length



Pfam domains



Pfam Description



Protein sequence:

IGKKMLVPLTASLYVPGTLEDDAKVLDVGTGYFIEKTMTEGKDYGERKNLLKSNVEGQLLDVATKXKXSADETGVILGAKLRLAPPAP

NbL17g12400.1 probable_leucine-rich_repeat_receptor-like_protein_kinase_At1g35710 [MW - SP = 34.6 kDa]

No. of times detected



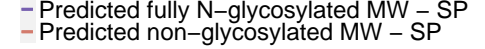
log(intensity)



Values from



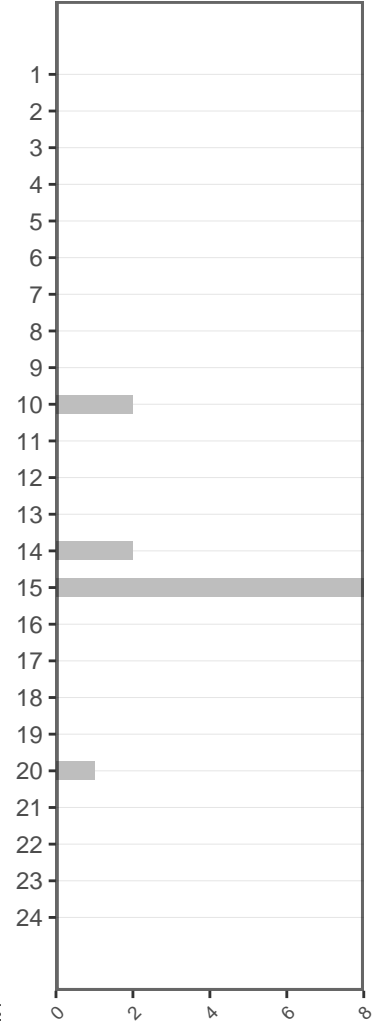
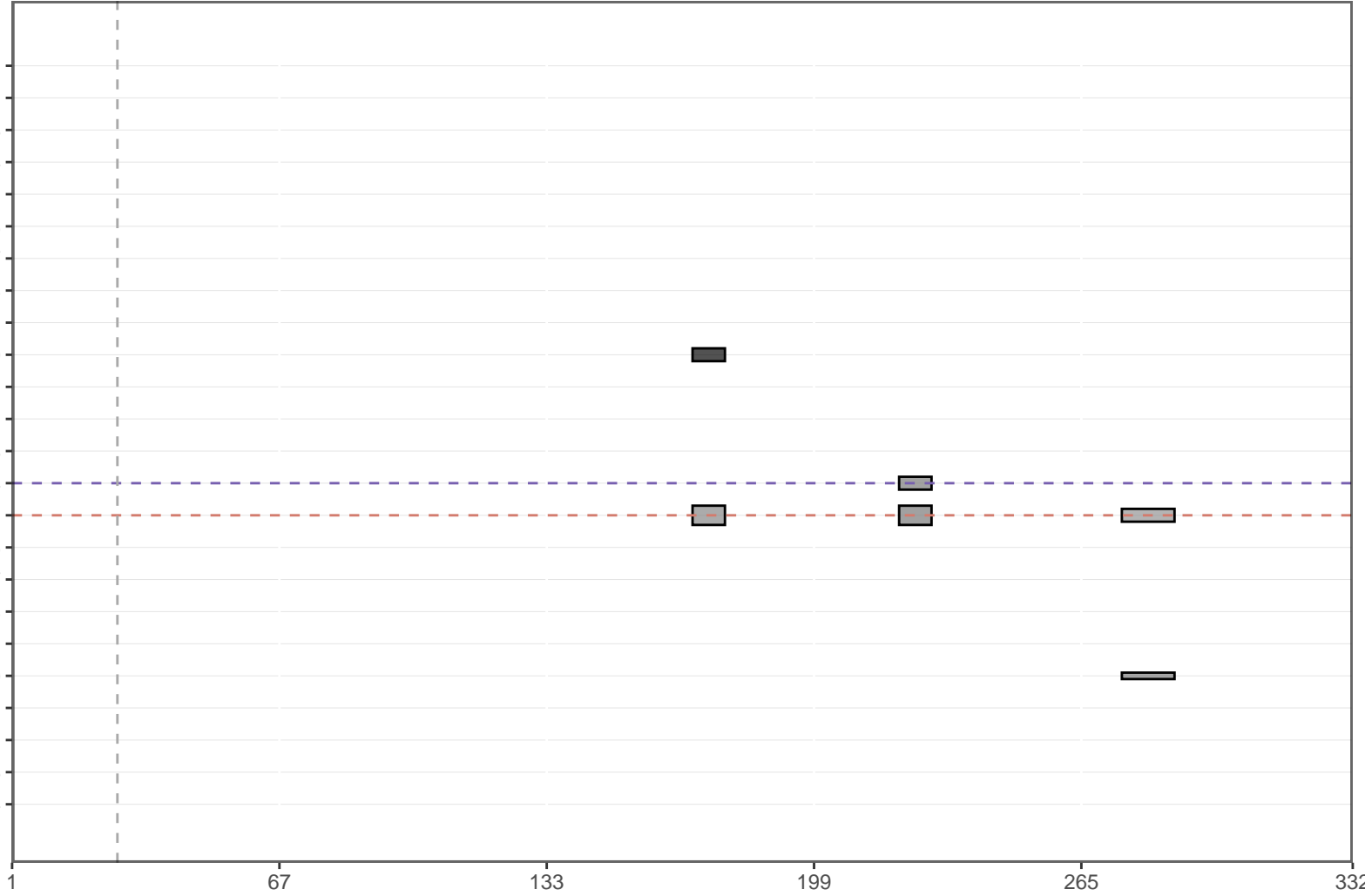
MW indication



Molecular weight

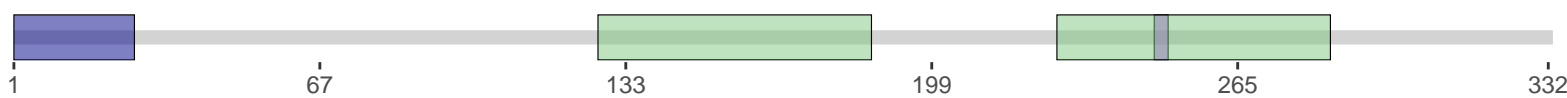


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DLTHLYLSFNFXGSEIPKELANPELRYLHLHENHFTGRIPPELGTLGHRLHLDVGNRNLVGTRELRIEGGFFVLRNLYLNHYLTGGIPAGLANLTNEELVLYNKMFGVPIYSIAHNPILTYLGHVQDFSGRIFAFYKHPFLKEMVIEENFRFGVKNPGLHEVLELTDADFLV

NbL17g12290.1 50S_ribosomal_protein_L19-like [MW = 29.01 kDa]

No. of times detected



log(intensity)



Values from



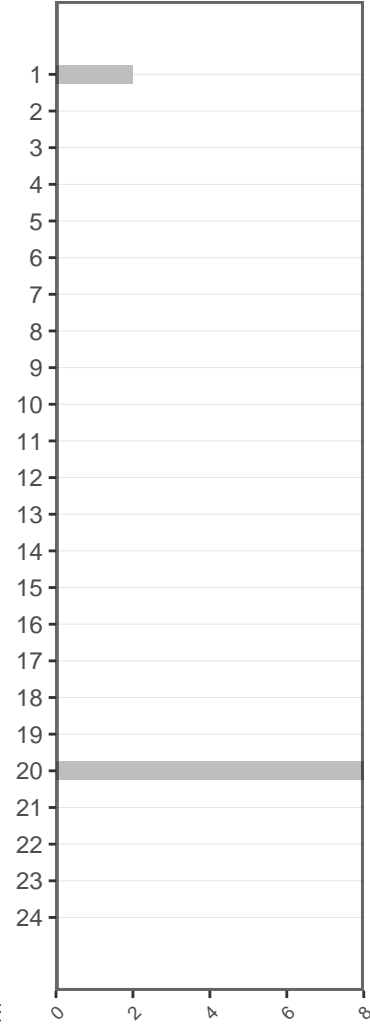
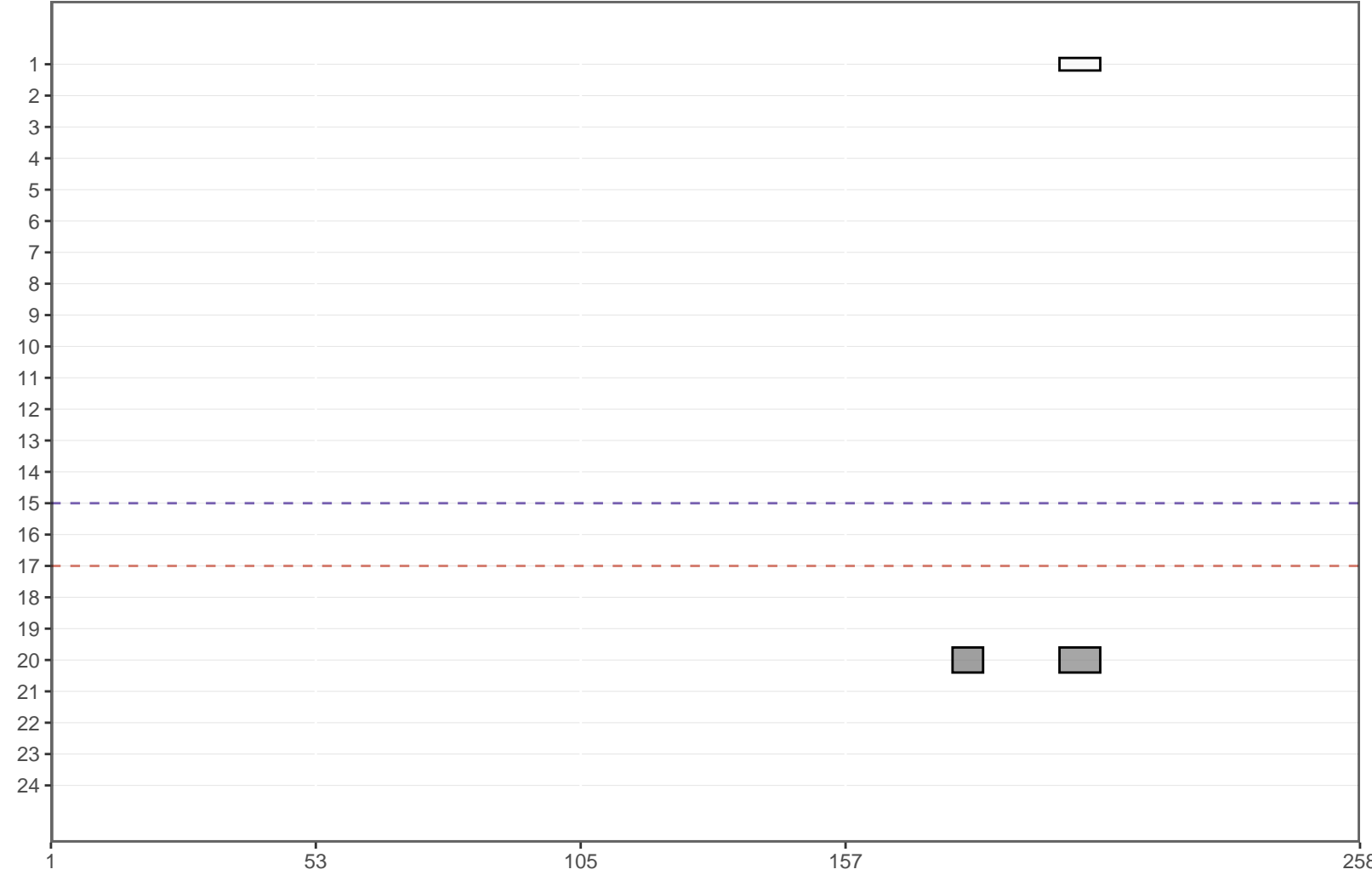
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

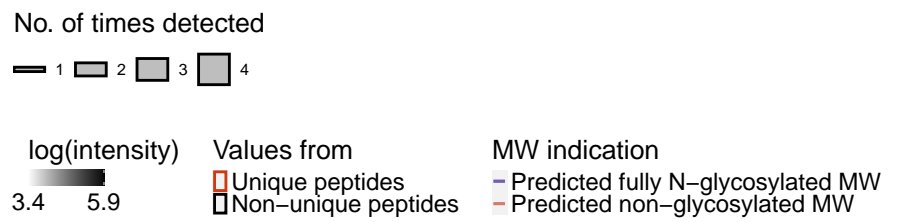
Pfam Description



Protein sequence:

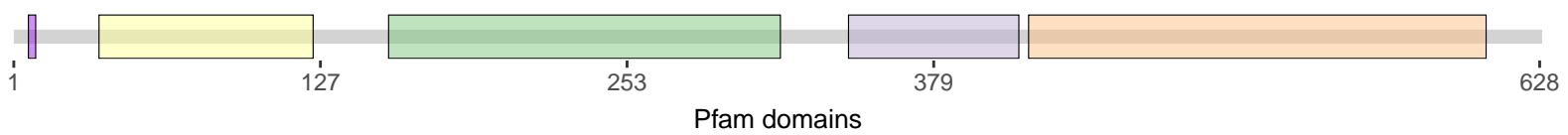
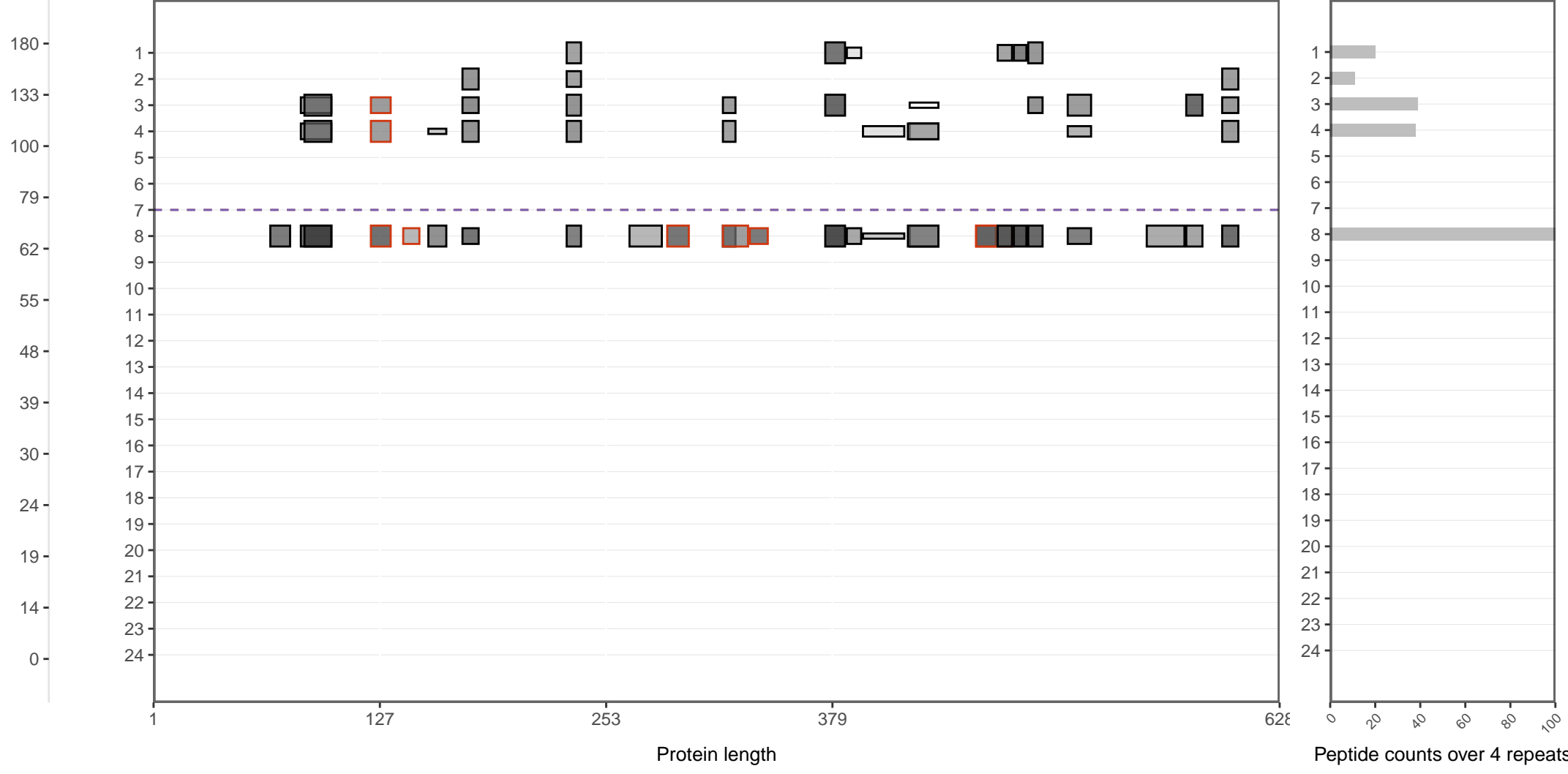
GATSYDVKYVPEDAASSSLATPRIKFRLDQAAHIMQLEKEAVEEVKAGSIPDKPGYVQLKVEVPEPKRRVSVVGVGVARRNAGLNTFFLRRLRVLVAGVGVENLFHLYSPNKEKMKVLDKDKKVRRAKLYLRLDKMNAKKH

NbL17g12260.1 phenylalanine--tRNA_ligase_beta_subunit_cytoplasmic [MW = 70.79 kDa]



Molecular weight

Gel Slice



Pfam Description

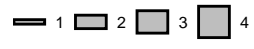
- SP
- TM Domain
- PF03484 tRNA synthetase B5 domain
- PF18262 Phe-tRNA synthetase beta subunit B1 domain
- Sequon
- PF03483 B3/4 domain
- PF17759 Phenylalanyl tRNA synthetase beta chain CLM domain

Protein sequence:

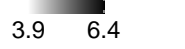
VLNTM/TMF/SY/CERKFEVEP/VWVYFDGKSFVYDLSIKYKMNPLGVITGIGVQLPENEVAELNKKMQLRAVESSENAEYKVFVSVPPTRSDVHPGDVAEDVAWGYNEIPKRRPASKPLPLSGFSDLRSEIAMAGYEVTEVTLWILGKKHESMLNSEEDKAVIADSRSTSEFEVVRTLMPGLLRTVGHNKDHPKPKMFEVGDVALLDGTKDVGVANRRHLLAALYCGANGSFELHGLVDRIKMEATGTFVSPGDGEGYHERSEEPFLGGRAKIVYKNGRIGT

NbL17g12240.1 eukaryotic_translation_initiation_factor_5A-2 [MW = 17.36 kDa]

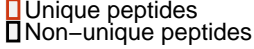
No. of times detected



log(intensity)



Values from



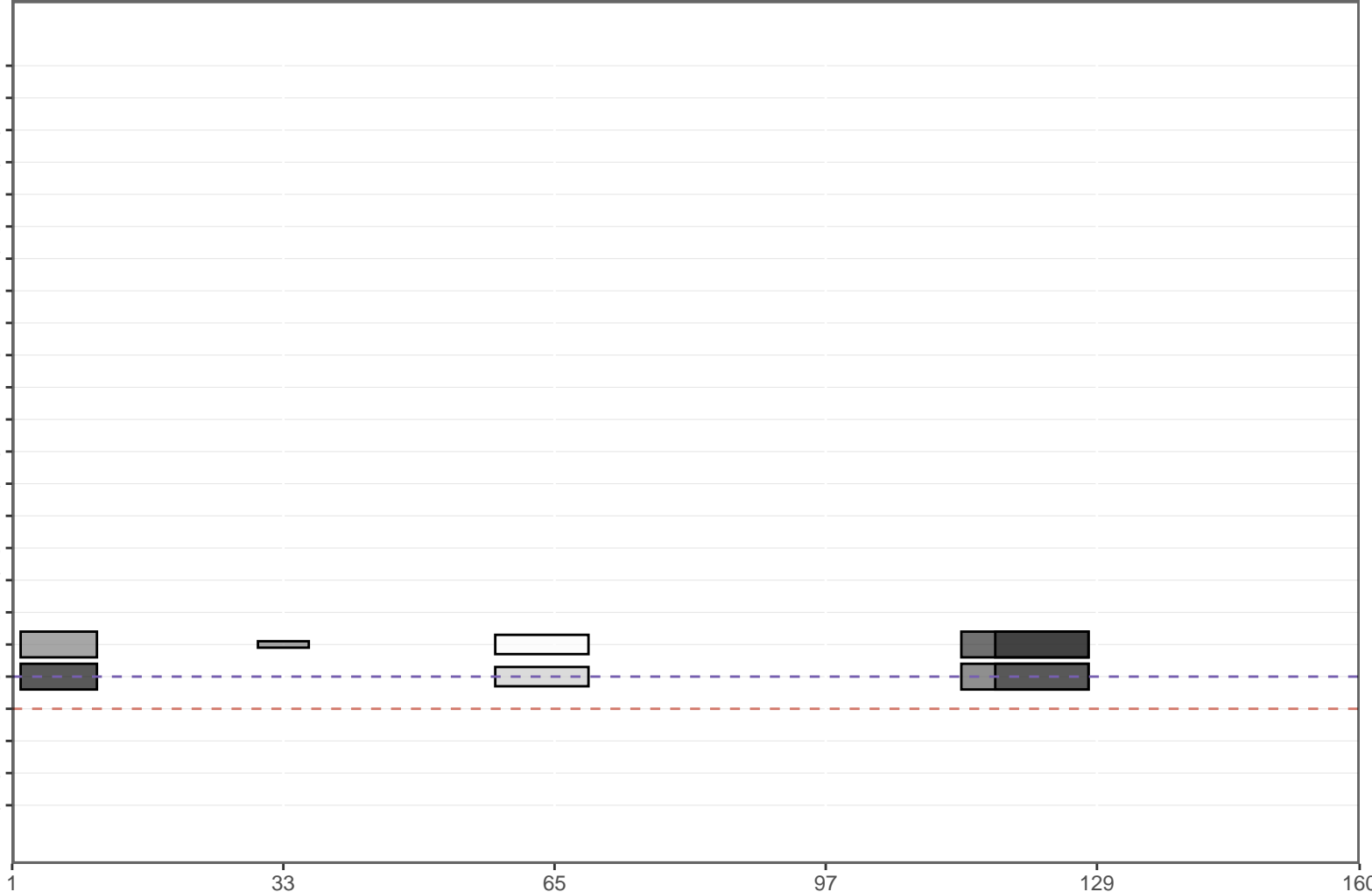
MW indication



Molecular weight



Gel Slice



Protein length

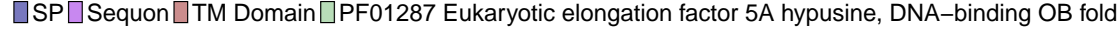


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

TGKLLDVPSSINQDVPVHNRFDVGLIDISGDFVLLTENGNTFKDQLRPTDQNLTKQKDFAEKGLVIVVMSAMGEEGIGALKDGGPK

NbL17g12070.1 40S_ribosomal_protein_S9-2-like [MW = 23.06 kDa]

No. of times detected



log(intensity)



Values from



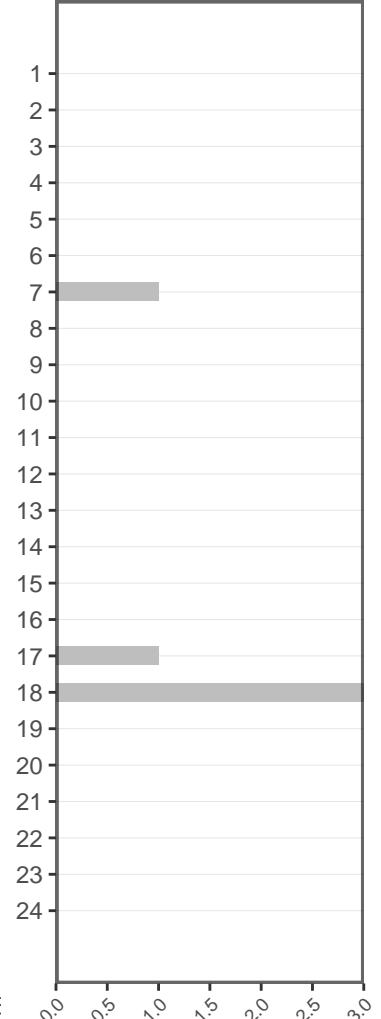
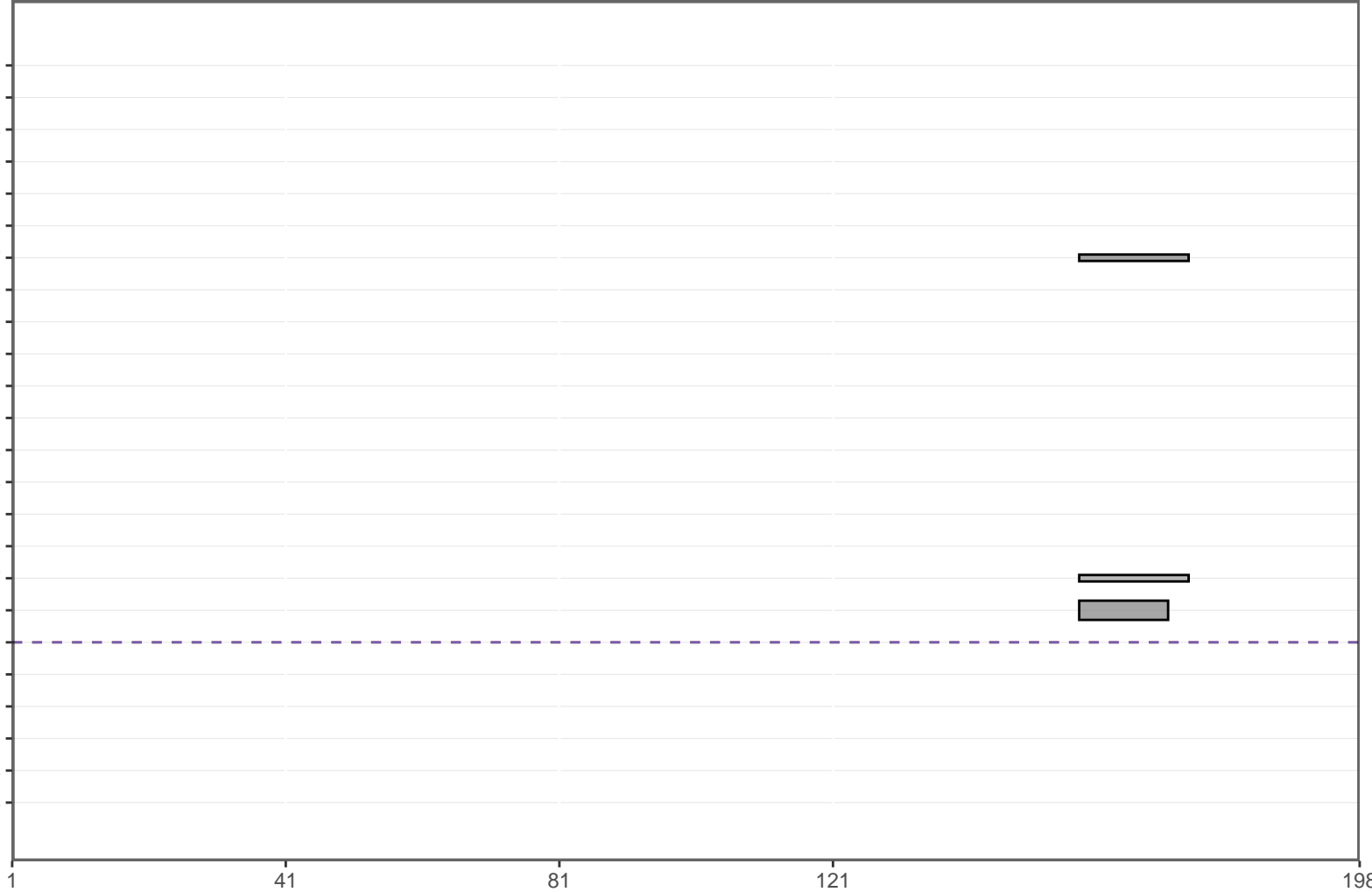
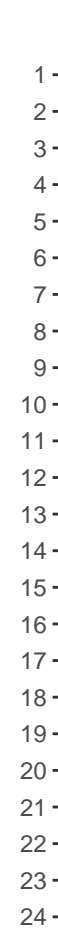
MW indication



Molecular weight



Gel Slice



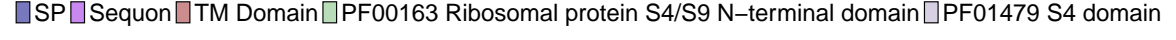
Protein length



Pfam domains



Pfam Description



Protein sequence:

SLLDESQKLDYVLSGVENFLERRLGTLVFKTGMAKSHHARVLRQRHVRGRQVWVPSFMVRLD5QKHDFLSIFFGGRRPRGRVKNKNGKAAAKKAGGGDDDEDEE*

NbL17g12060.1 peptidyl-prolyl_cis-trans_isomerase_CYP23 [MW - SP = 22.9 kDa]

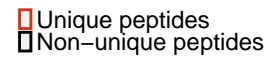
No. of times detected



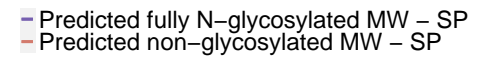
log(intensity)



Values from



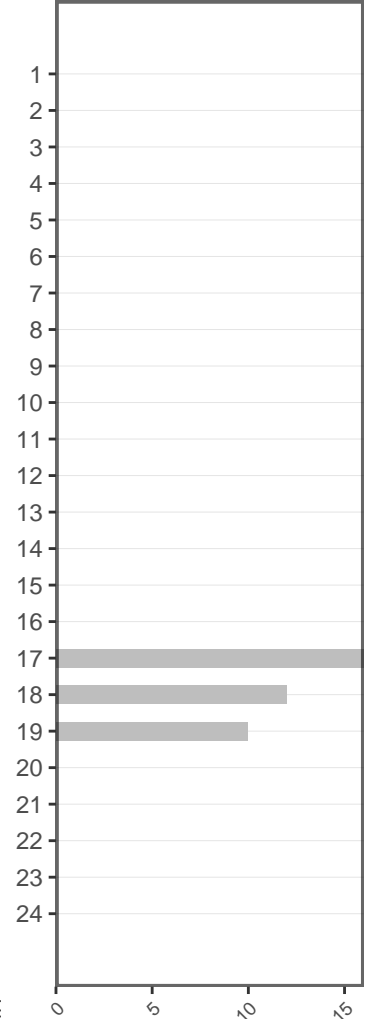
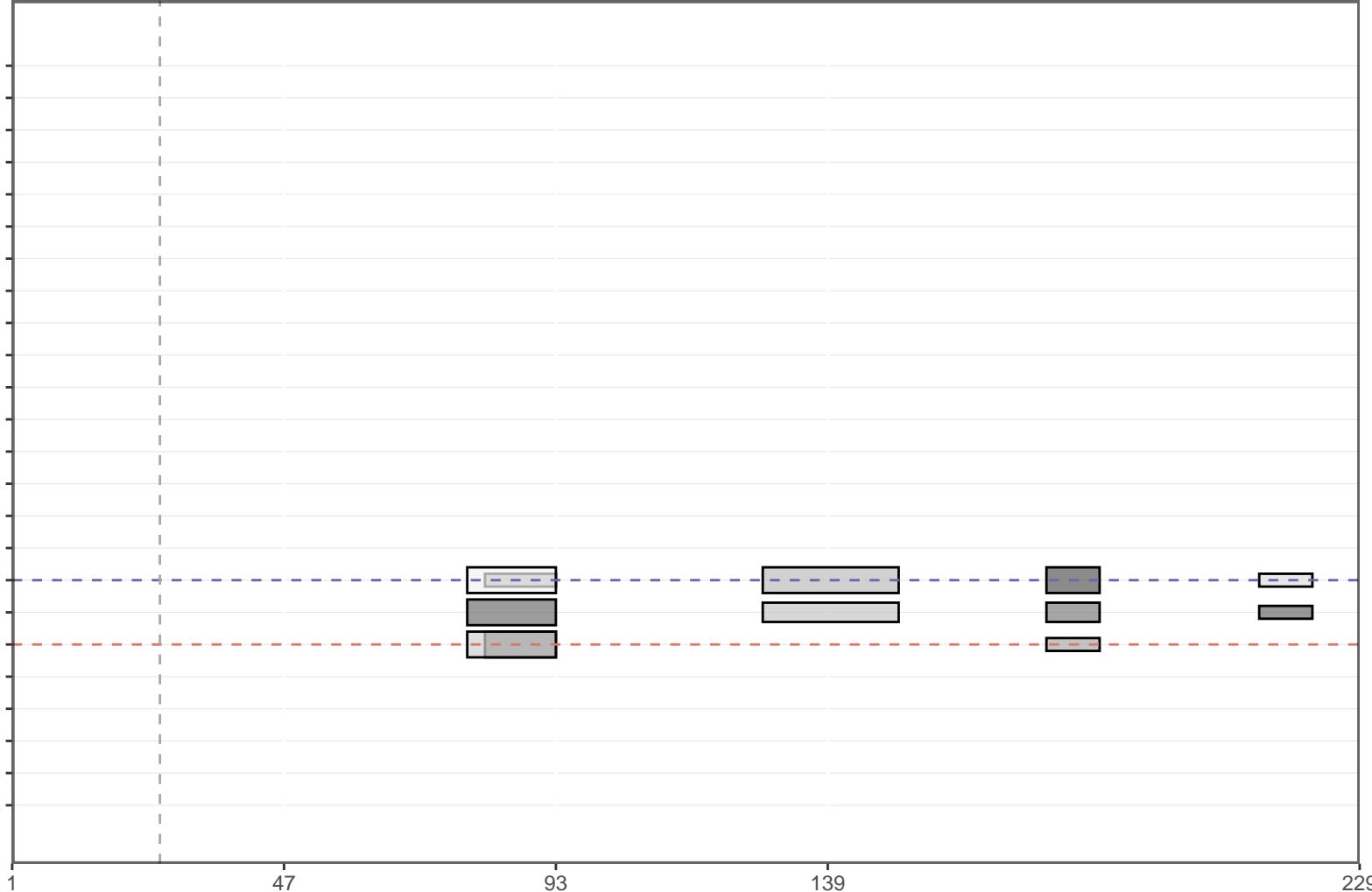
MW indication



Molecular weight



Gel Slice

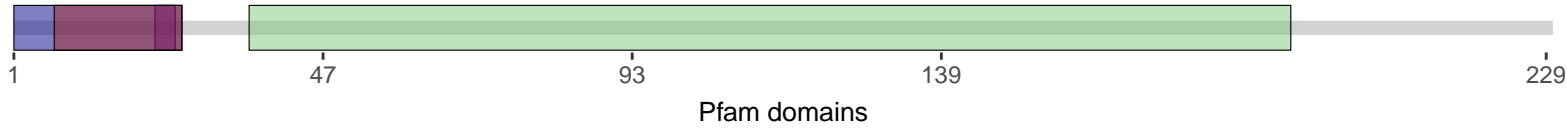
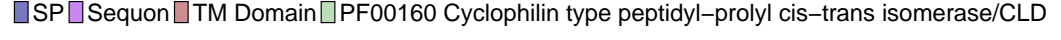


Protein length



Peptide counts over 4 repeats

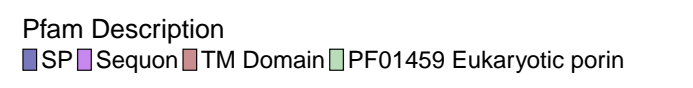
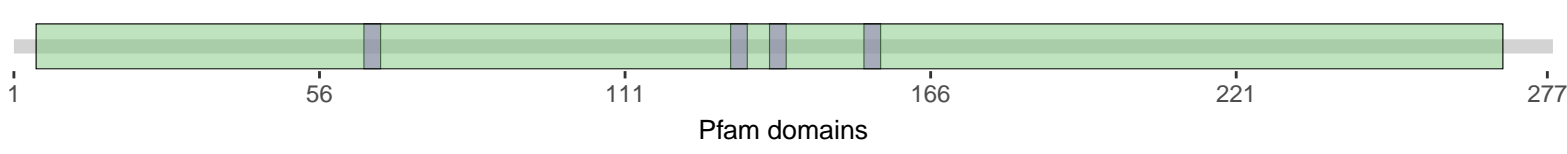
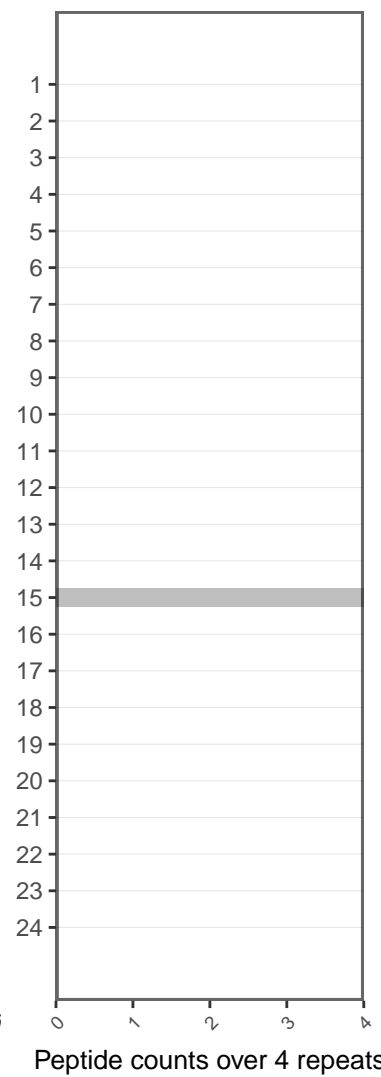
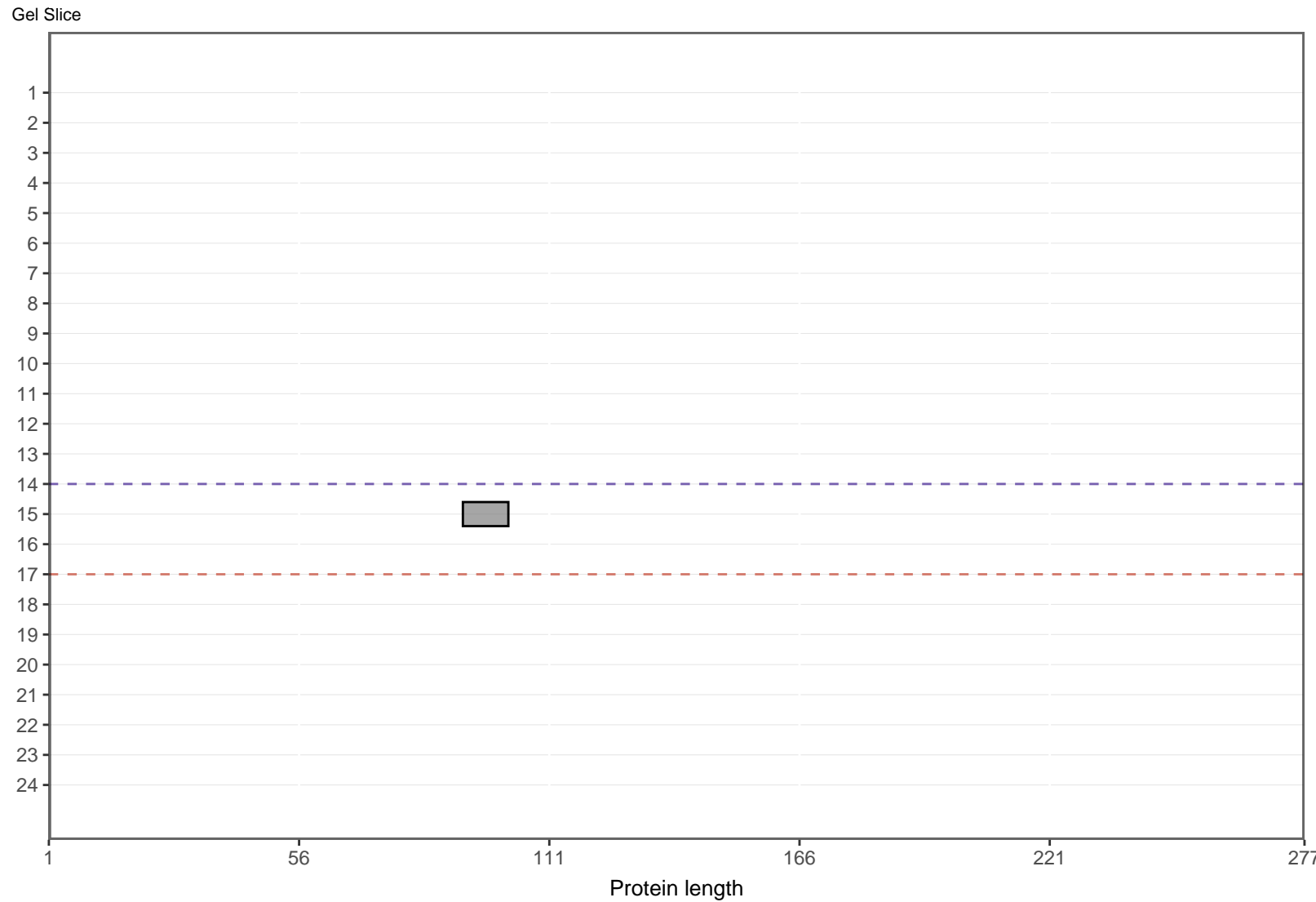
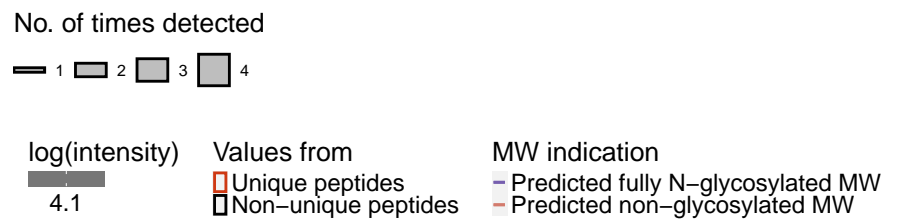
Pfam Description



Protein sequence:

RAEAEKTVYGLSEVHVRGLSMGRYDDPDSGTSF8F8MLGDAPHLDGKVAIFGKVTXGDETRKLEQLPTRREGFVMPTEKITGTYVYDITNMEICEEERSLLKRLGAAAVEIEKGRMKCFP

NbL17g12000.1 mitochondrial_outer_membrane_protein_porin_of_36_kDa [MW = 29.18 kDa]



Protein sequence:

SPLLYNFSGVAGNNTVALGTDLFDATASGNFTKGNAGLSFRTDLSLALNDKGDLSASYYHEWKPVTNTAWGAELTHFSFSENENTLITGTQHLIDPLFTTKARVNSYGGKASALQHEWRPKSLFTVSGGEVDTRAEKSAKIGLAWLKP

NbL17g11850.1 protein_SPIRAL1-like_1 [MW = 10.57 kDa]

No. of times detected



log(intensity)



Values from



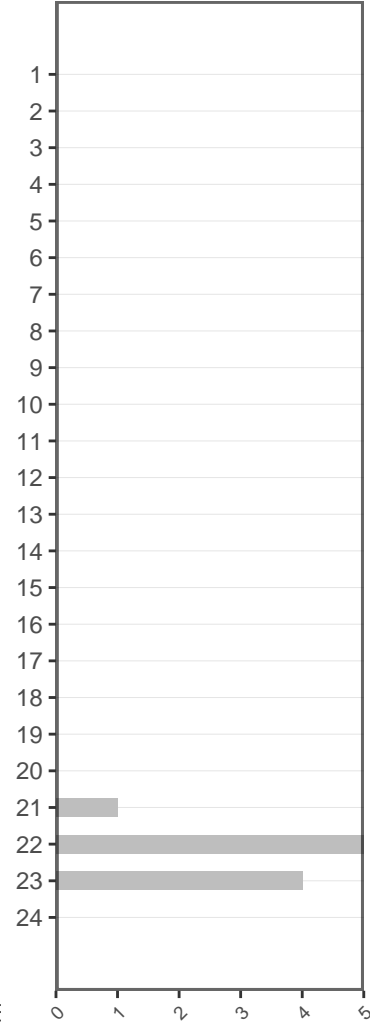
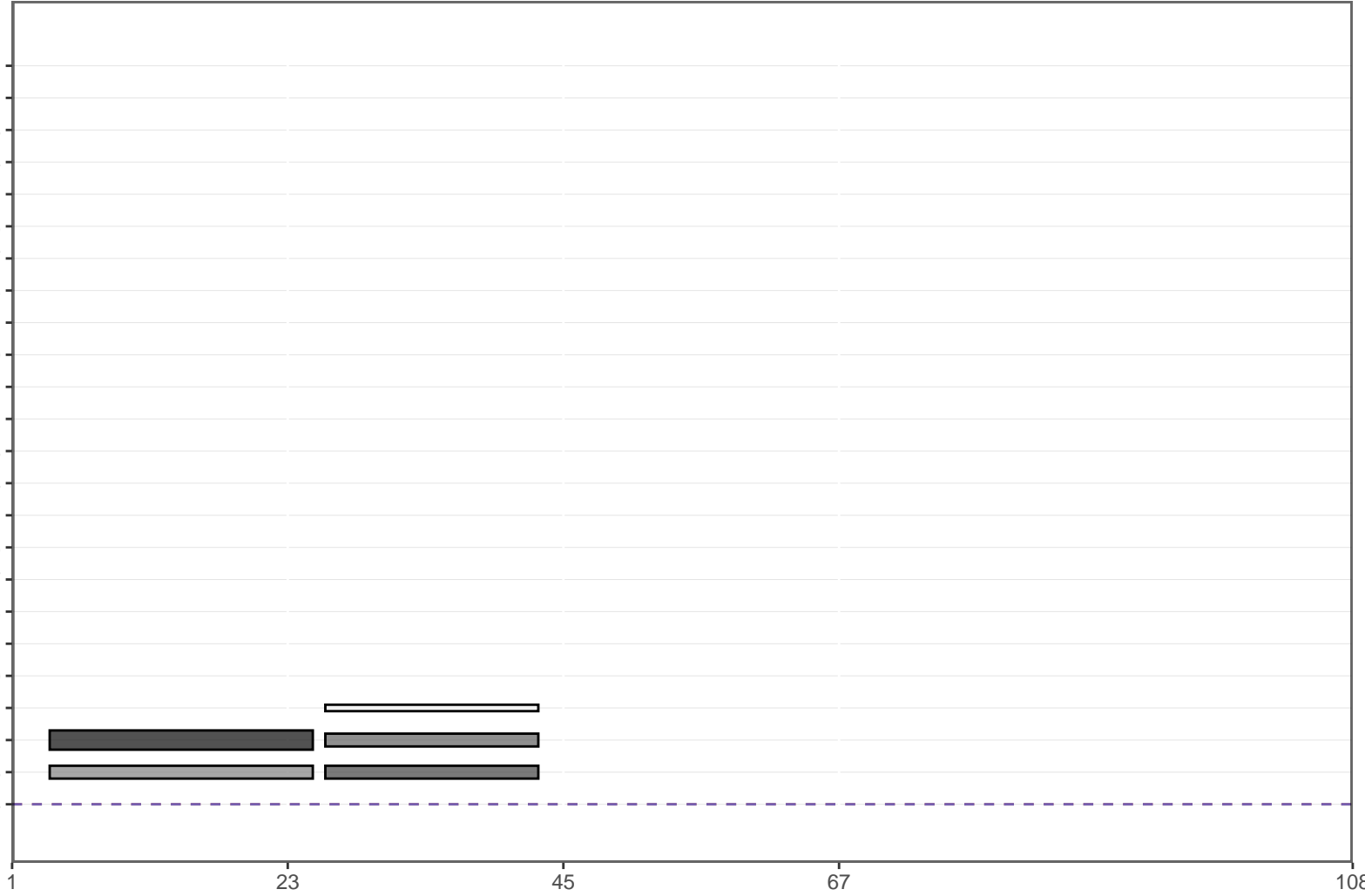
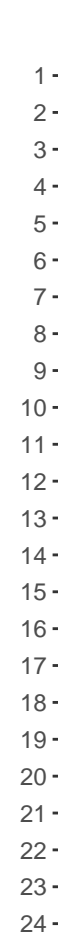
MW indication



Molecular weight



Gel Slice

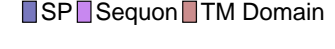


Protein length



Pfam domains

Pfam Description



Protein sequence:

IPINKEPSPKPVAAAPLADATKQIPAGIGIRADGGNTGNFIDRPSKIHAAAPGGGSLGYLFGGGSSP

NbL17g11810.1 peptidyl-prolyl_cis-trans_isomerase_E [MW = 18.12 kDa]

No. of times detected



log(intensity)



Values from



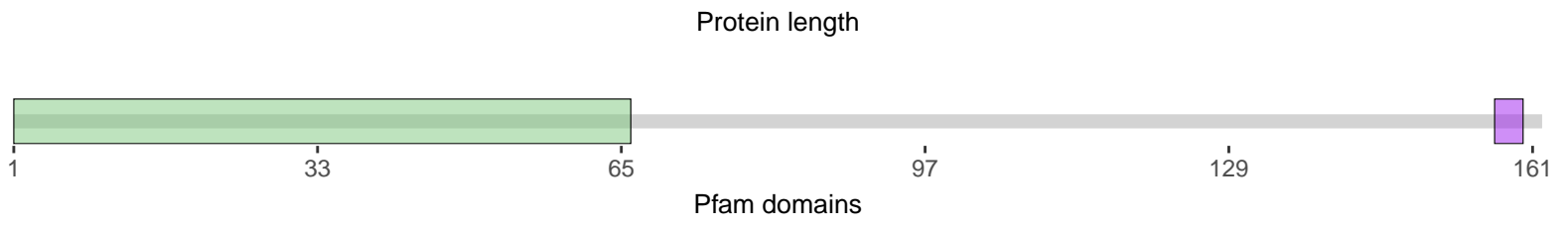
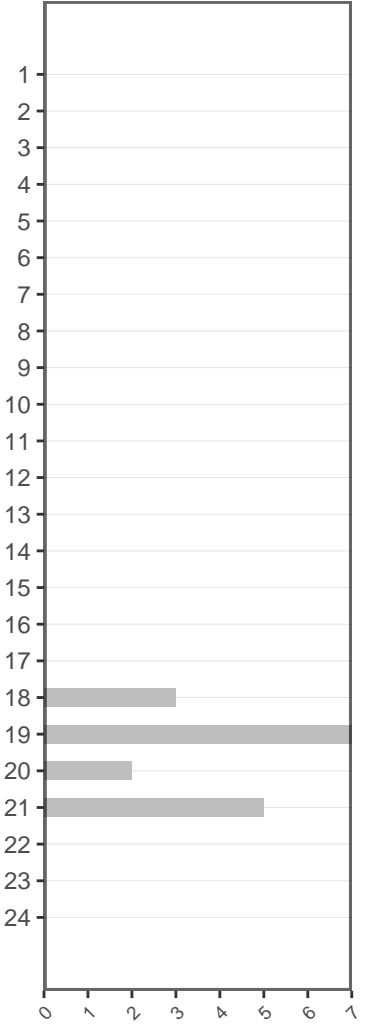
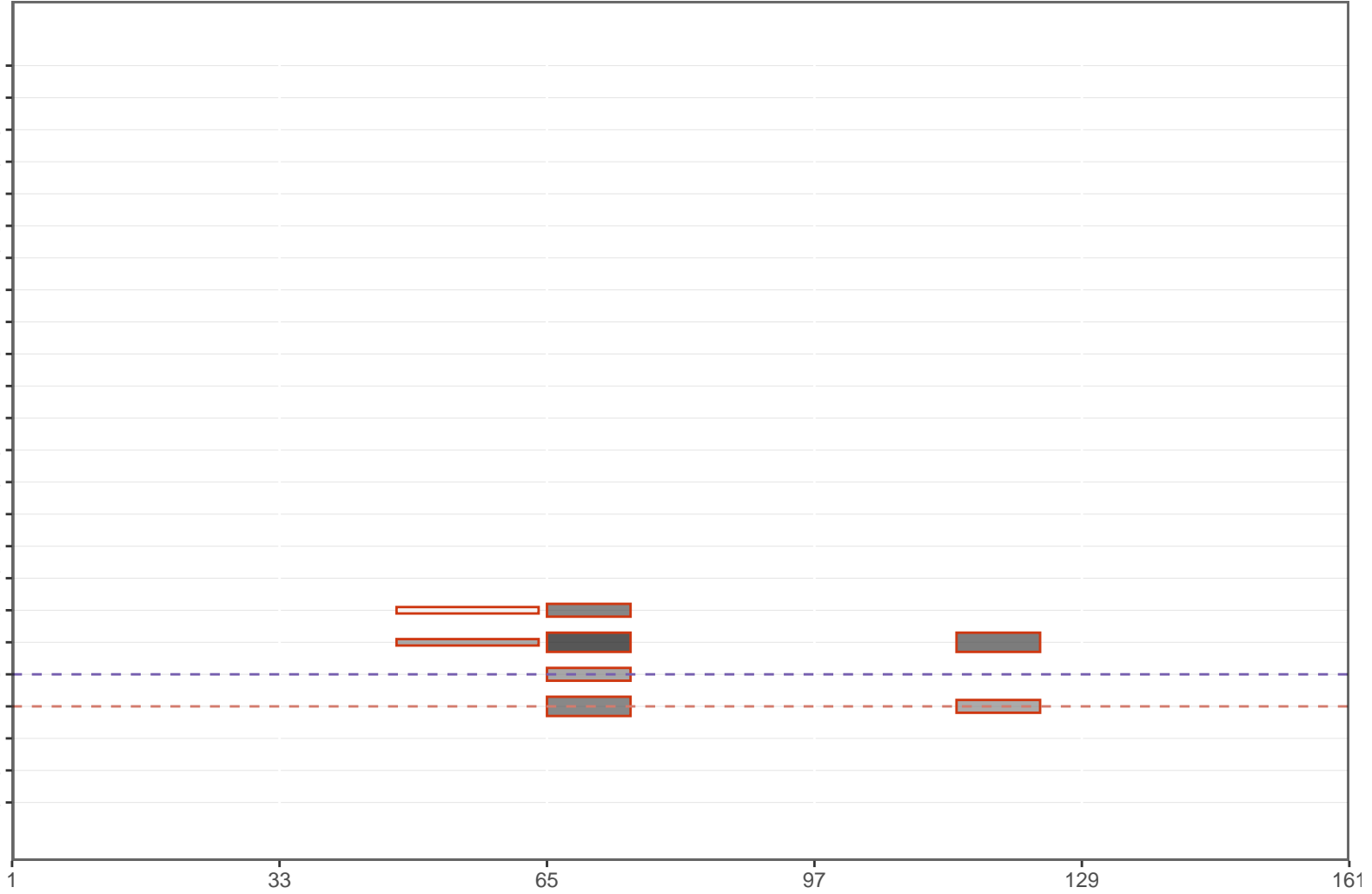
MW indication



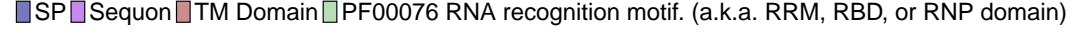
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

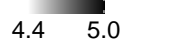
YALPEKIKGGEGWAGLWADFTWFERGGEEEMKRLGDEGRAAMGAEEELHRKXMAEERDGEKDEETNKGGDPMAMAEVLKGNATP

NbL17g11800.1 alpha-14-glucan-protein_synthase_[UDP-forming]_2-like [MW = 40.92 kDa]

No. of times detected



log(intensity)



Values from



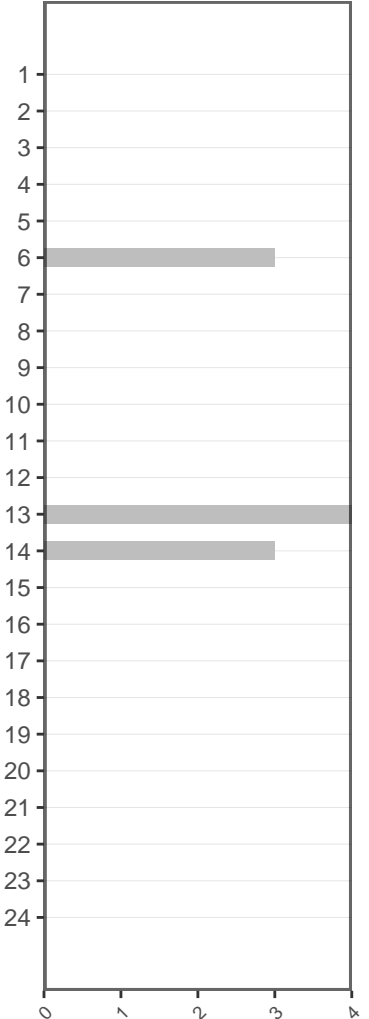
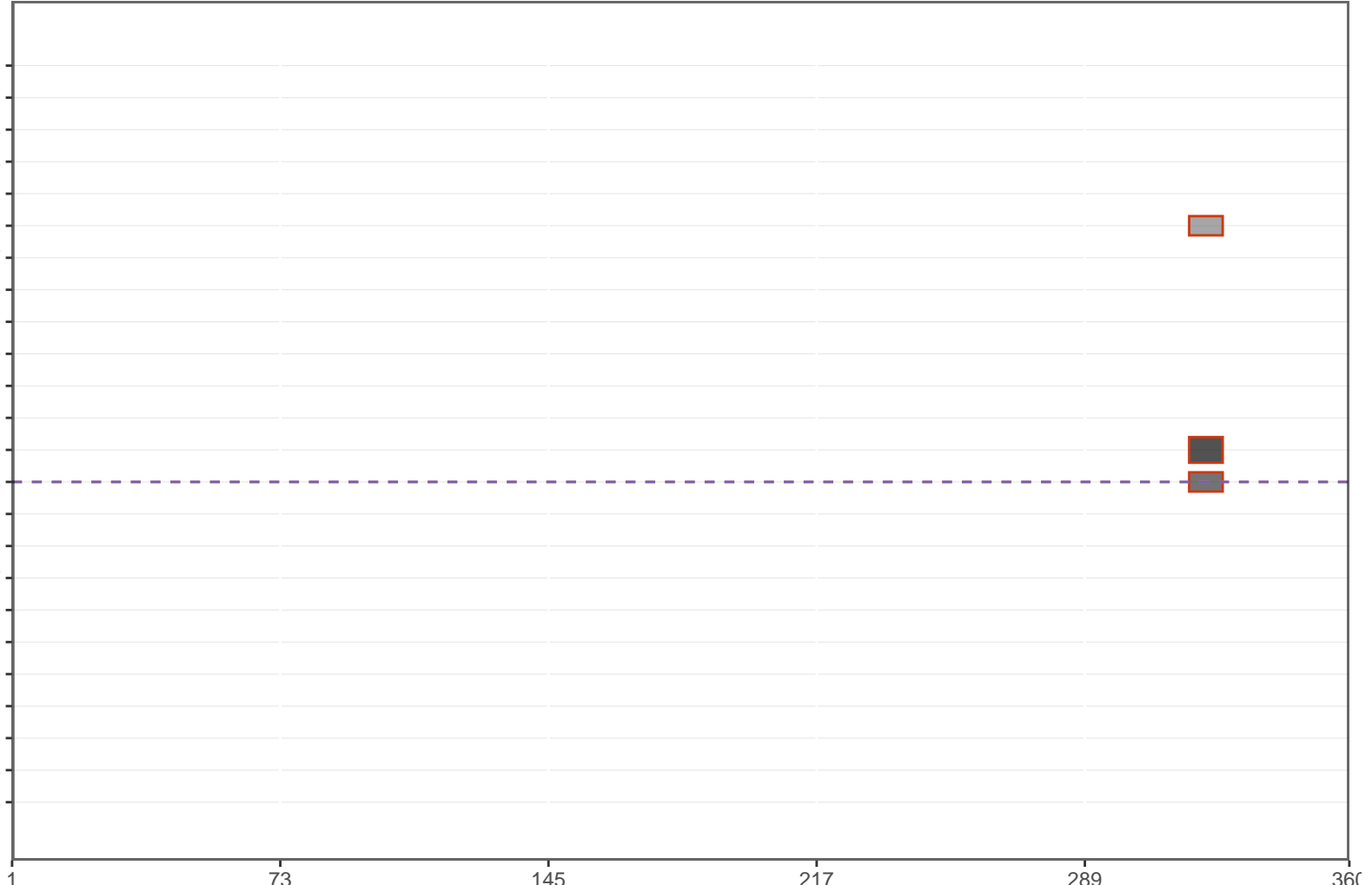
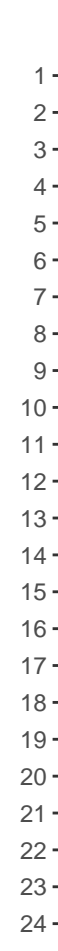
MW indication



Molecular weight



Gel Slice

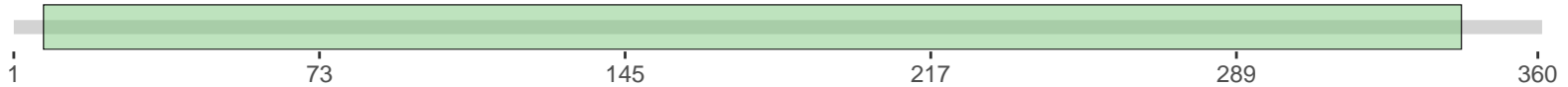


Protein length

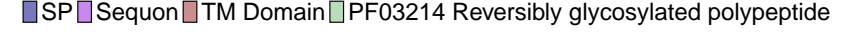


Peptide counts over 4 repeats

Pfam domains



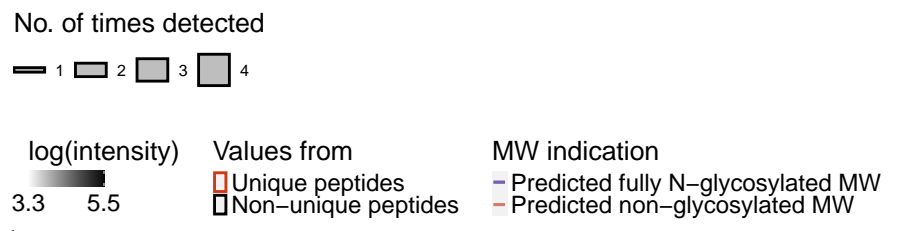
Pfam Description



Protein sequence:

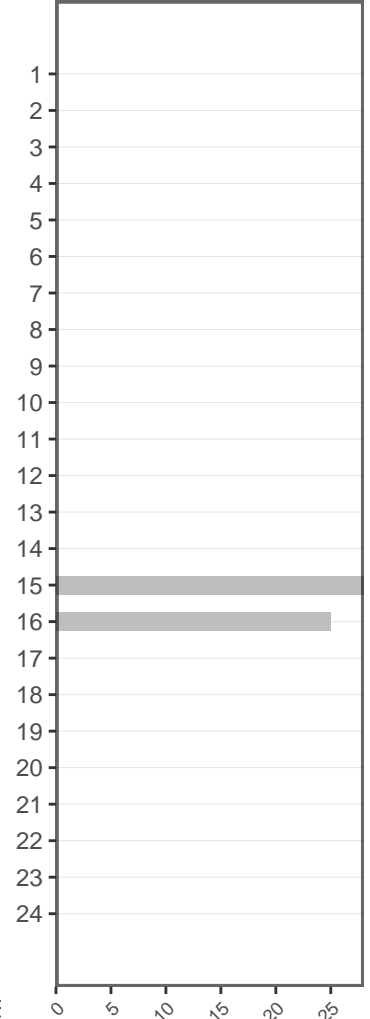
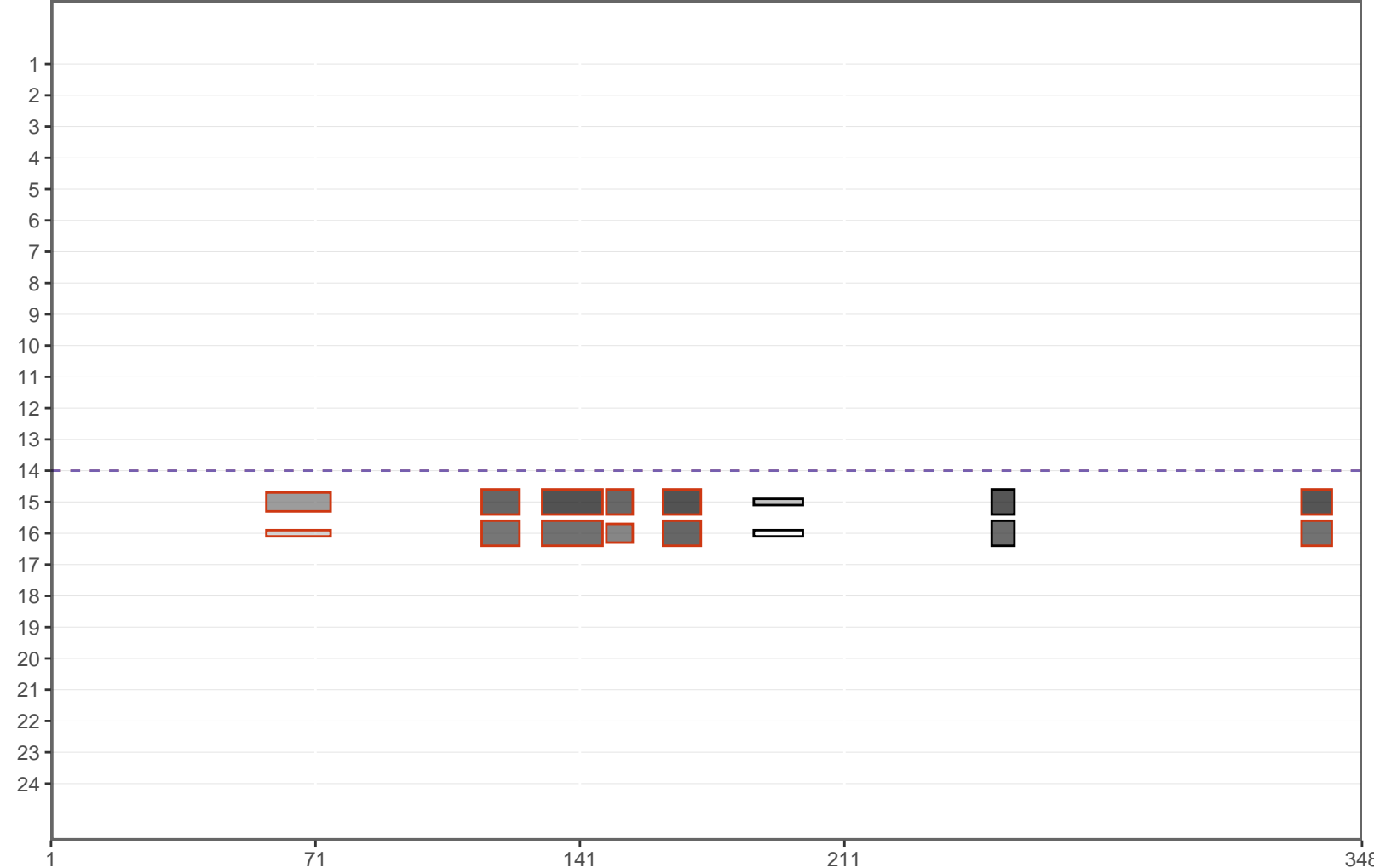
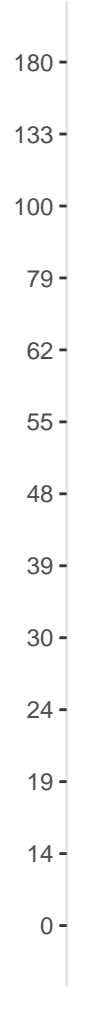
IFPDYDAPITQLVXKPRERNTRYVDAMTIRPKGTLFRMGMNLAFLNRELKGPAMFYGLMGDDGPIGRYDDMWAGWCTKVGDLGLGKTKGLPIYIWHSKASNPFVNLKKEYKGIYVQEEIIPFFQAVTLPKKCTTVGGQVVELAKGVKAKLSNVDGYFTKLAEMATWIEAWDELNPTGENLAKLSINDKTK

NbL17g11490.1 2-pyrone-46-dicarboxylate_hydrolase-like [MW = 39.06 kDa]



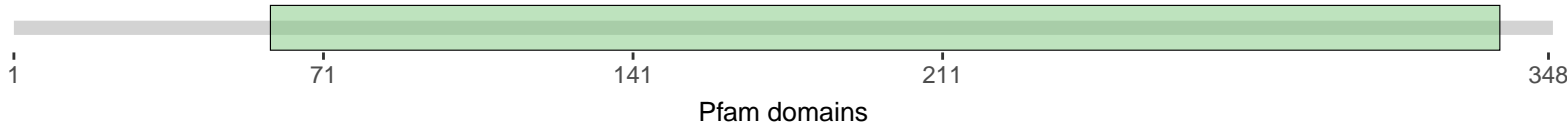
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:

RFNPNLYLPTGKQMTNEVSKALFKADELGVPPVGFPMKGLDHLHGEIEELGTEFFPTVLLDHLAFQKLPNNDEERPFSELLKLSRFPPQVYKFSALFRVSRNRPVYEDLSQVLAQLVSSVGAHRVMMVGSDFPYVPEGGYKEAREAVHLLANQGHLPSPATEWLGKTMQLFDGKWSVVTQI

NbL17g11450.1 short-chain_dehydrogenase/reductase_2b-like [MW = 41.54 kDa]

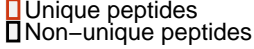
No. of times detected



log(intensity)



Values from



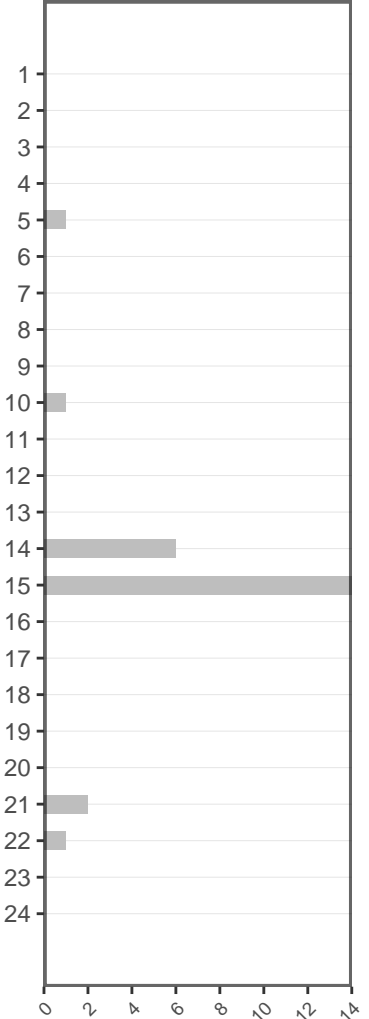
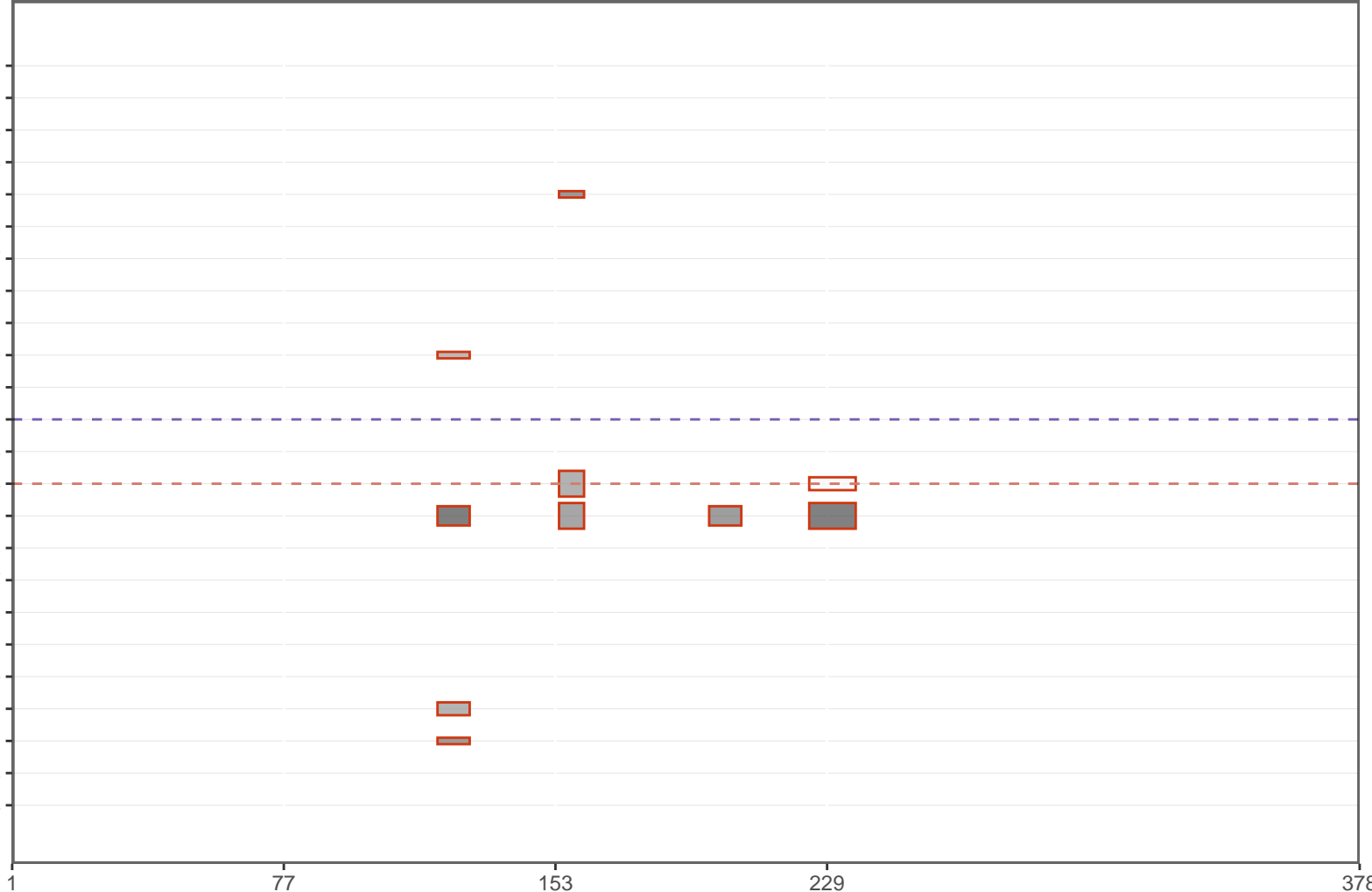
MW indication



Molecular weight

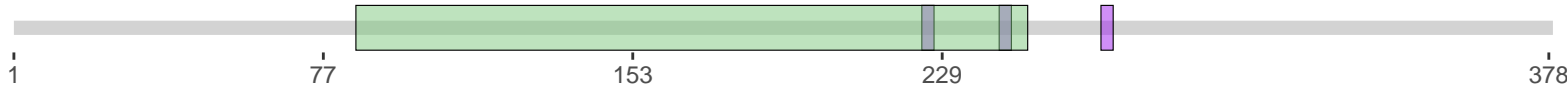


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

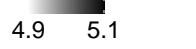
DEATLKAALNDIPYDWLAGKAANNVGMKTTYESAKLGLDTHYYGVKKNFEALLPLNGSRSAKIVVNSLRBELKRVFNEDRRKELGDENLEDTEKIEKIKGKFLHDKDADALEVNGWIMLPWYSISKVSLNAYTRVLRARRYPKIGKGVHPGVYNTDINWHITGMPVEEGAEGPVMALLPDDGPTGCVYFDRITVAQF

NbL17g11440.1 non-specific_lipid_transfer_protein_GPI-anchored_2-like [MW - SP = 16.91 kDa]

No. of times detected



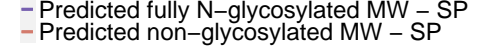
log(intensity)



Values from



MW indication



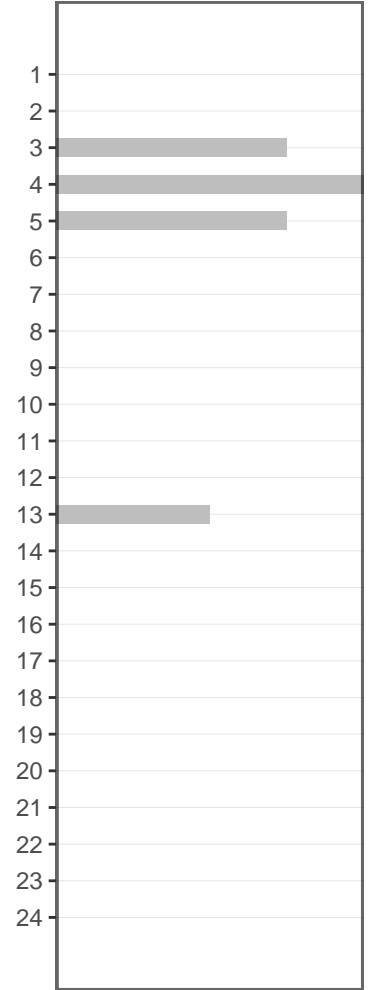
Molecular weight



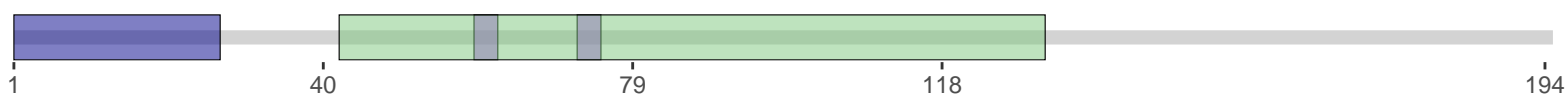
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ELAGLYDSNPICLGGGLGDPKLVGVDISRALKLNFGVETRPVSTGAALGIPWAPTADELAPALSPGLASSPTFENNKKNAQTMAFSKMNVLGFGIMFFTFIF

NbL17g11330.1 elongation_factor_1-beta-like [MW = 24.49 kDa]

No. of times detected



log(intensity)



Values from



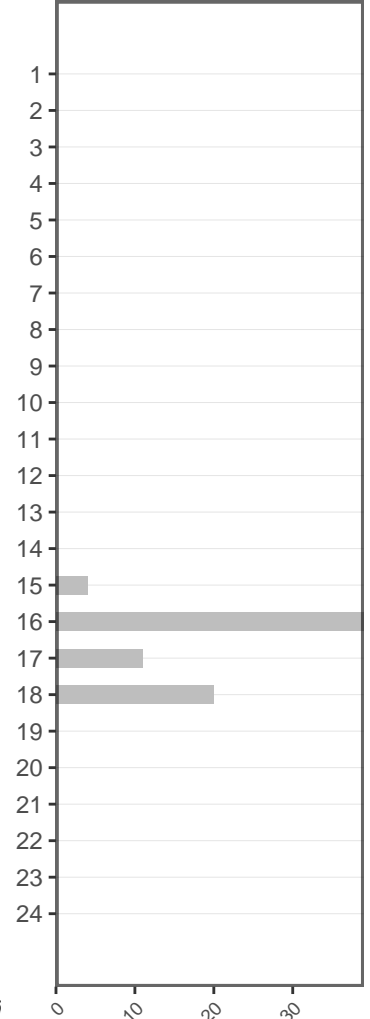
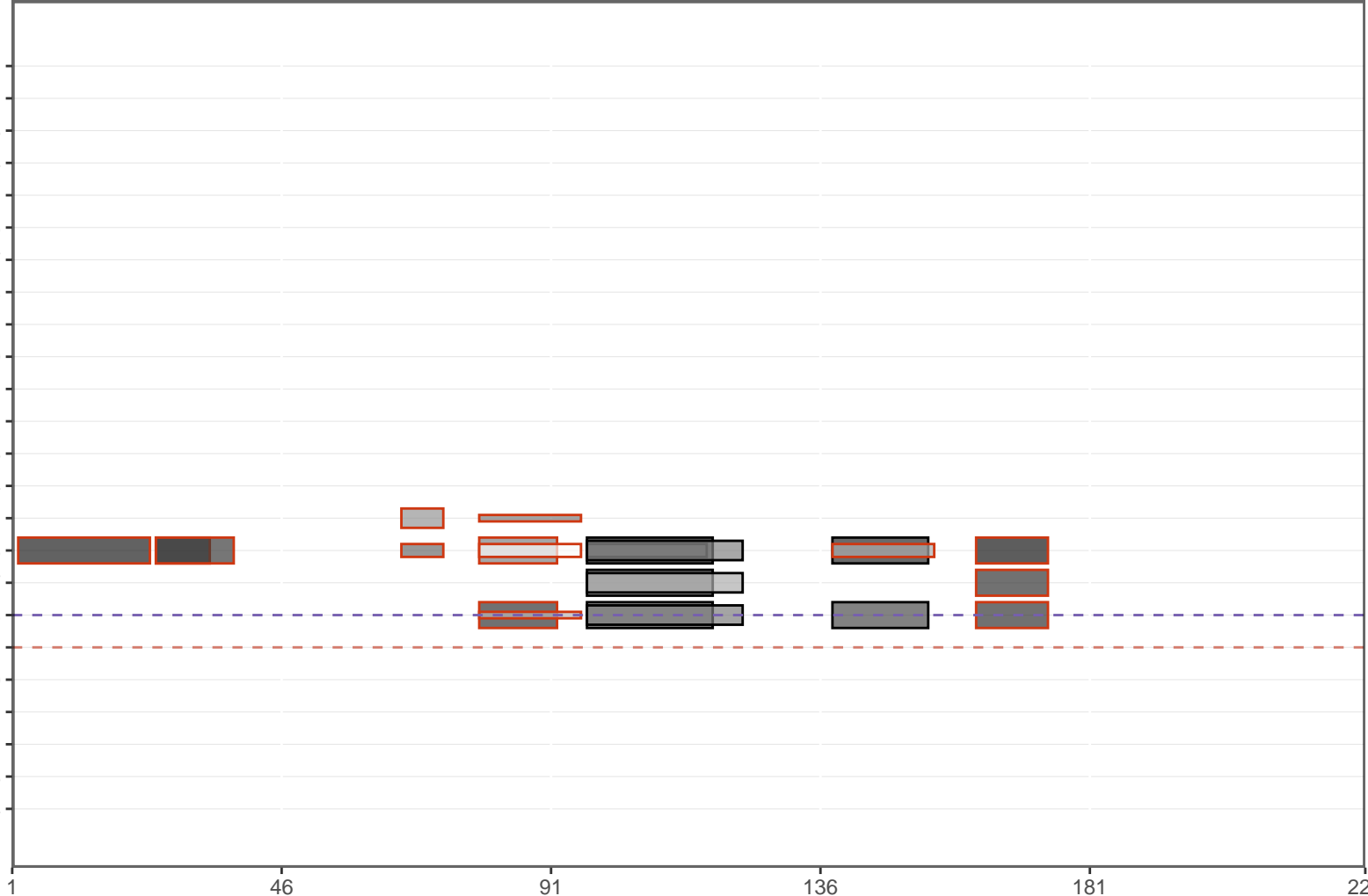
MW indication



Molecular weight



Gel Slice



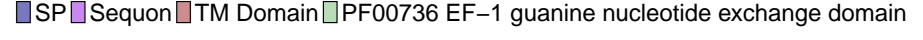
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

10000000DLFGEEETEENKKAEEAREATKASTTKKESGHSILLNKPWDDTDMKLEEAIVREVQDEGLTWGAELKLVVGVGKIKLQMLTVDLIVSVONLVEEHLTVPEINIEVYQSGCDVAFNKP

NbL17g11260.1 calmodulin-7-like [MW = 20.76 kDa]

No. of times detected



log(intensity)



Values from



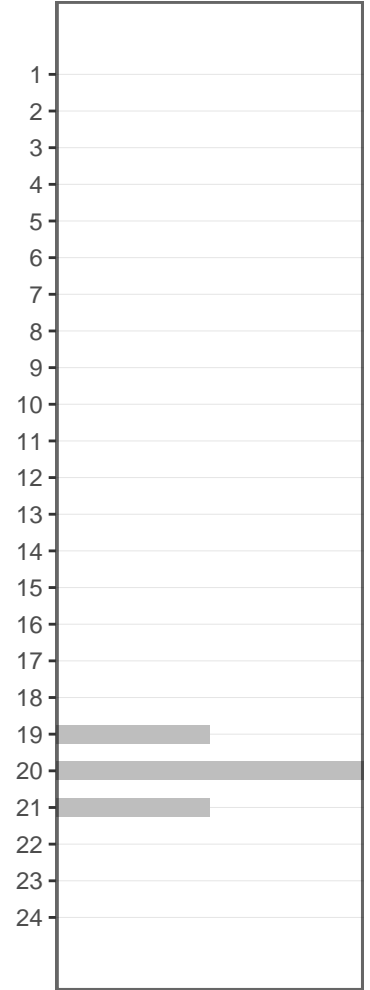
MW indication



Molecular weight



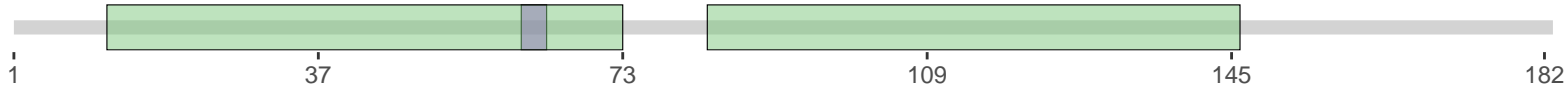
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

DTDSSEELKELAFRVFDKQNGFSAELRHVMTNLGKLTDEEVDDEMREADVQNGQINVEEFVWMMANRRRRRIEESKRGYSHGSGNKRKRDRGRTL*

NbL17g11170.1 uncharacterized_LOC104119948 [MW = 29.58 kDa]

No. of times detected



log(intensity)



Values from



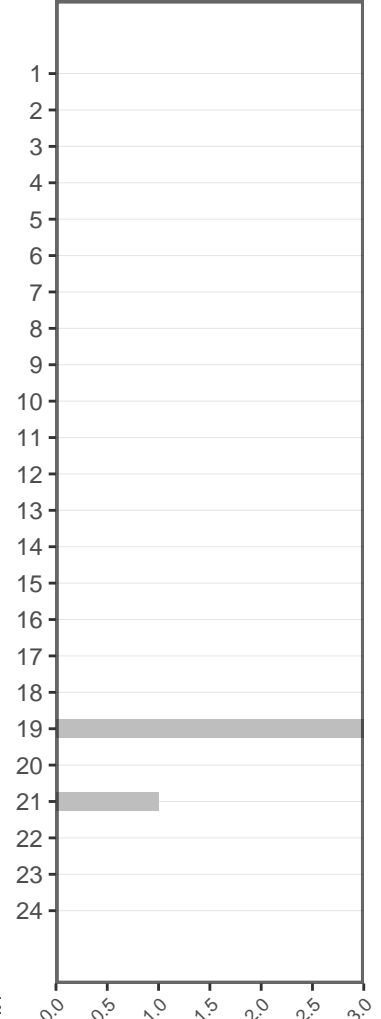
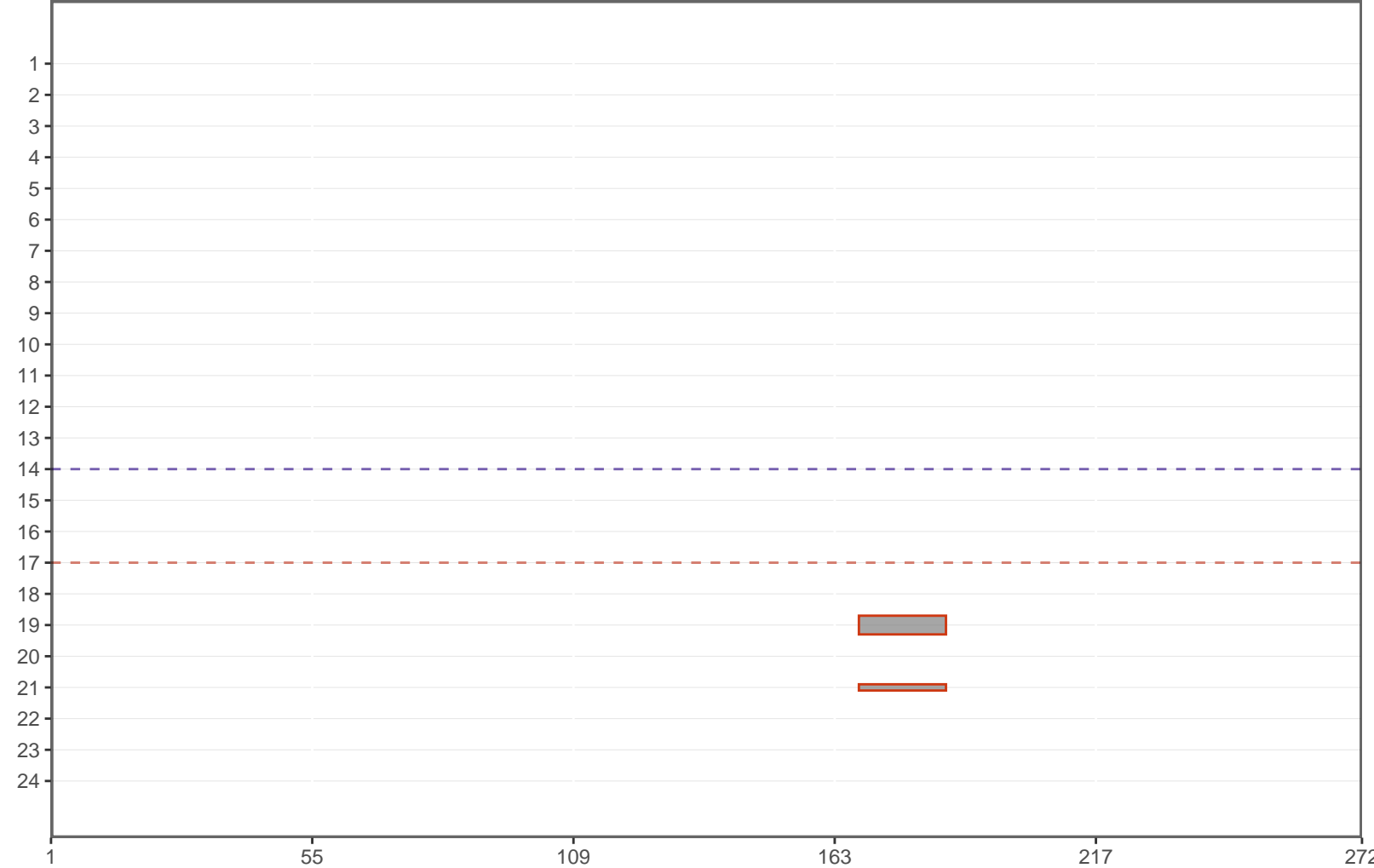
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

EEATKQKLCEDLNELVLESSNSGLARLEELKRRLAAMNPSRSTAPAPDQNPVPEVPGSSRTGQVSSVKDTPQPSGSSGNTSKEGNDRSBSGAENSGNGLPLSLAEARVKKKINLQGRGKGVPKGRGSTAPGWGTAGGFVDGRP

NbL17g10900.1 short-chain_type_dehydrogenase/reductase-like [MW = 28.07 kDa]

No. of times detected



log(intensity)



Values from



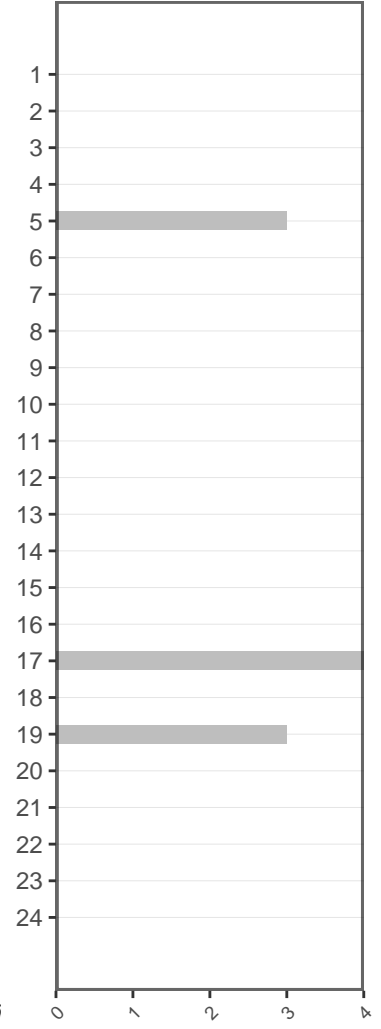
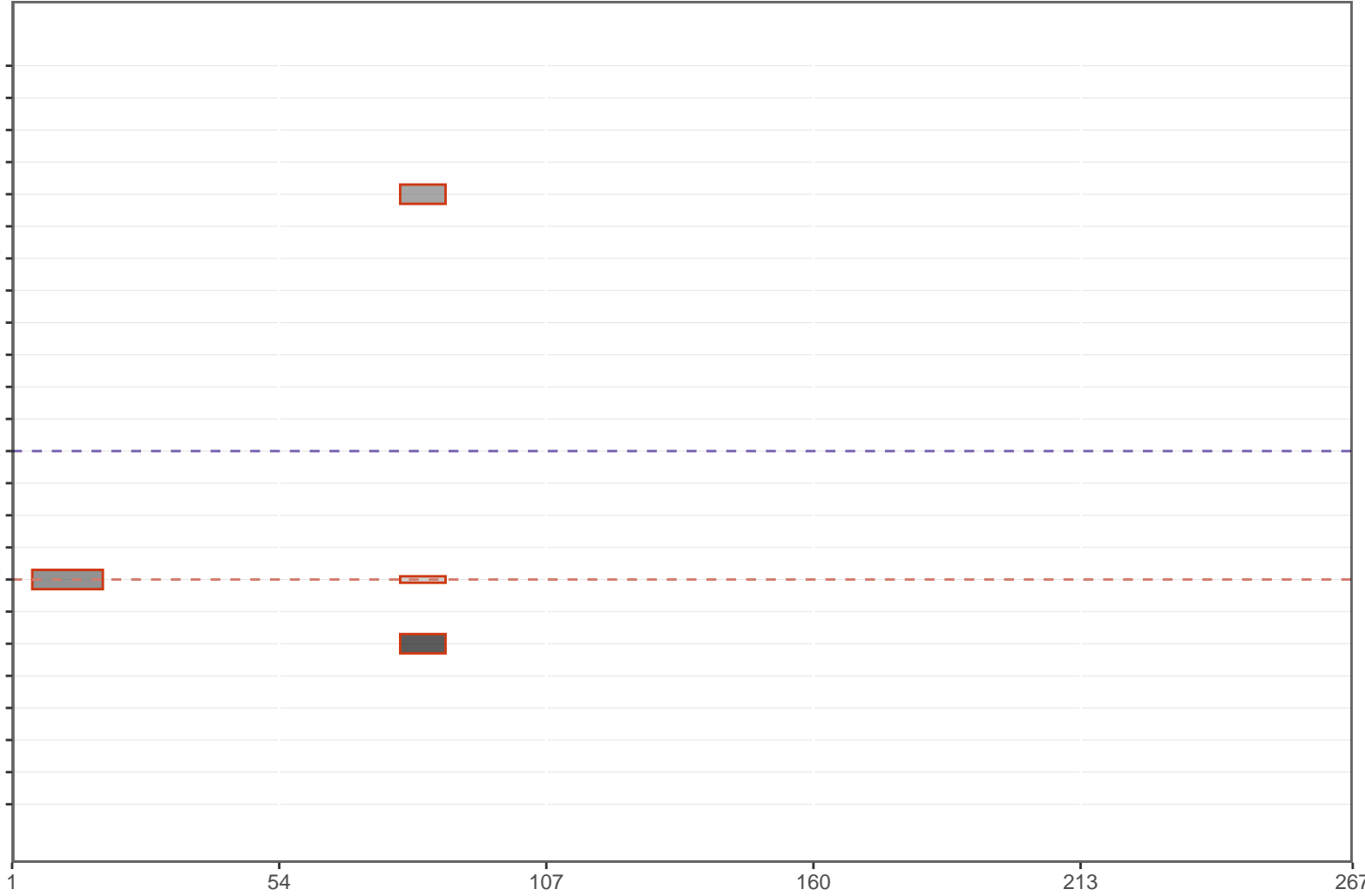
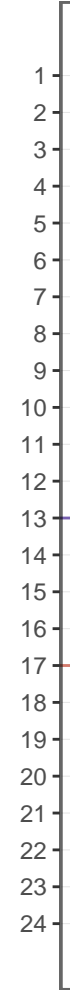
MW indication



Molecular weight

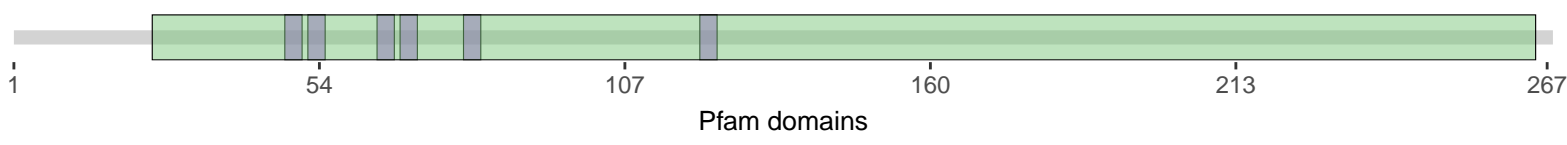


Gel Slice

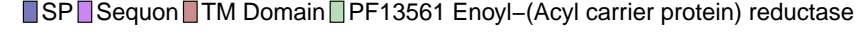


Protein length

Peptide counts over 4 repeats



Pfam Description



Protein sequence:

TTLEDFDRTFEVNRGAFICCKEGASRIKRGGGRIKLTSLAAAFRRPGYGYATASKAAVEAMVKILAKELKGTGTANGVAPGPIATEMFYDGKTEEMKRRVIDECPHGRLGOTEDVAPVVGFLAADAASEWVNGGIIKRVNGVYI

NbL17g10840.1 lysosomal_beta_glucosidase-like [MW = 63.72 kDa]

No. of times detected



log(intensity)



Values from



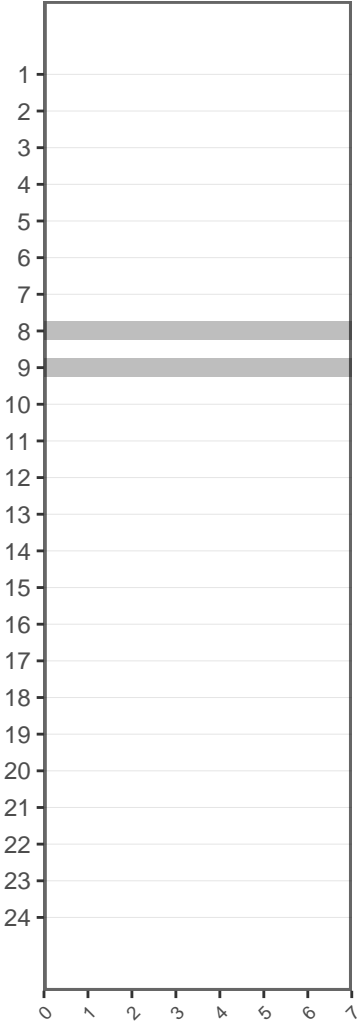
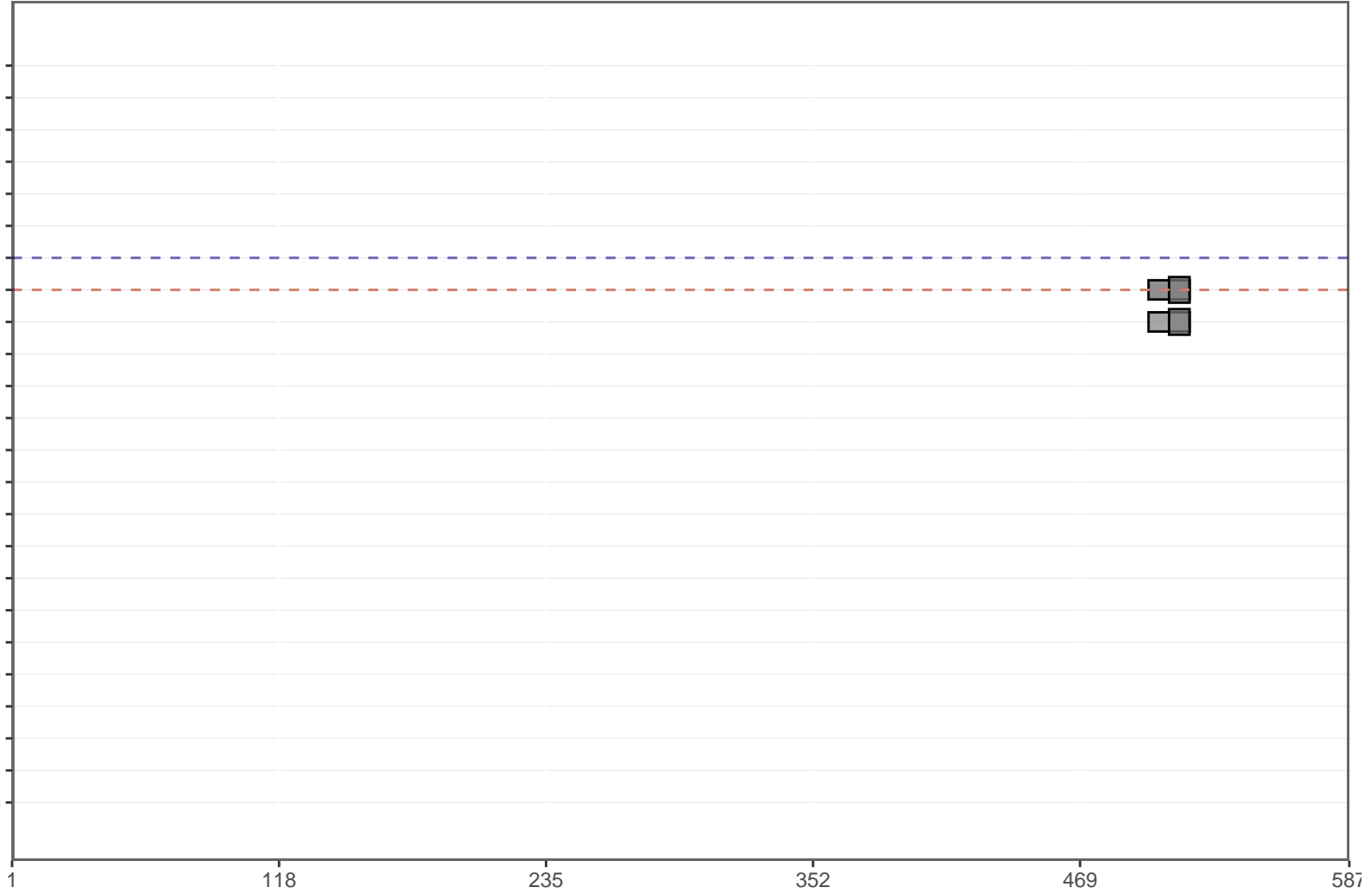
MW indication



Molecular weight

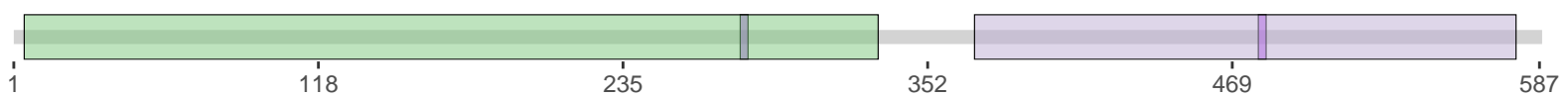


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00933 Glycosyl hydrolase family 3 N terminal domain
- PF01915 Glycosyl hydrolase family 3 C-terminal domain

Protein sequence:

YYSYSVQAGIMAGGEMMVPENYREFIDSLTSGVYKANIPMSRIDDAKRIILRVKFKVAGLFENPMEDPSLANLGGSGEHELAREAVRKSLVLLKNGKTPSGPLLPKAPKILVAGTHADNLGYGCGGWTRIEWGGVAGNDLITGTTLTAIKKTVDPSTGVVYQGNPDANFVSKNFSAVVVGEVPAEMFQDSSNLTAEKPGKSTINVCQAVKGVVAVVSGRPVLEPVIKMDALVAWLPCTEGGGADALFGDYGFYFTGKLARTWFRVFRVDFQFMNFDAAHYDPLFPI

NbL17g10520.1 GDP-mannose_46_dehydratase_1 [MW = 41.44 kDa]

No. of times detected



log(intensity)



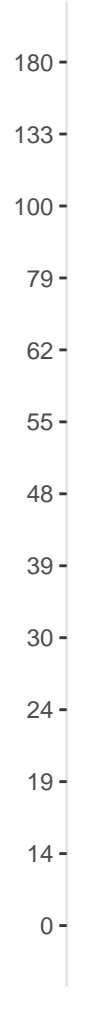
Values from



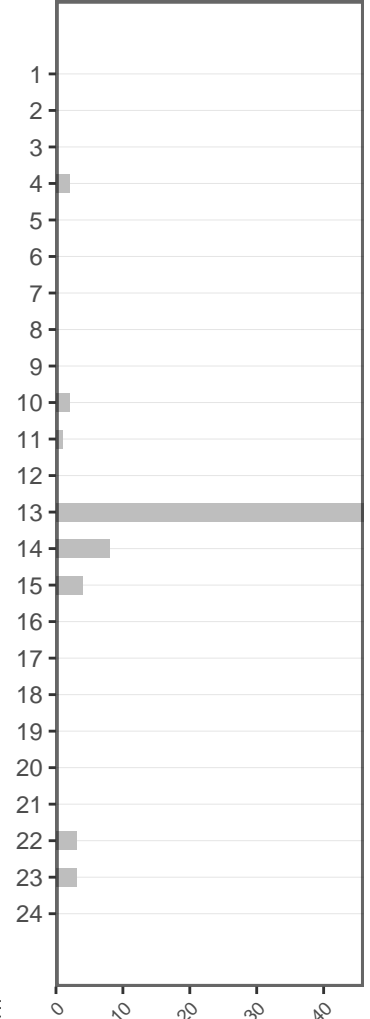
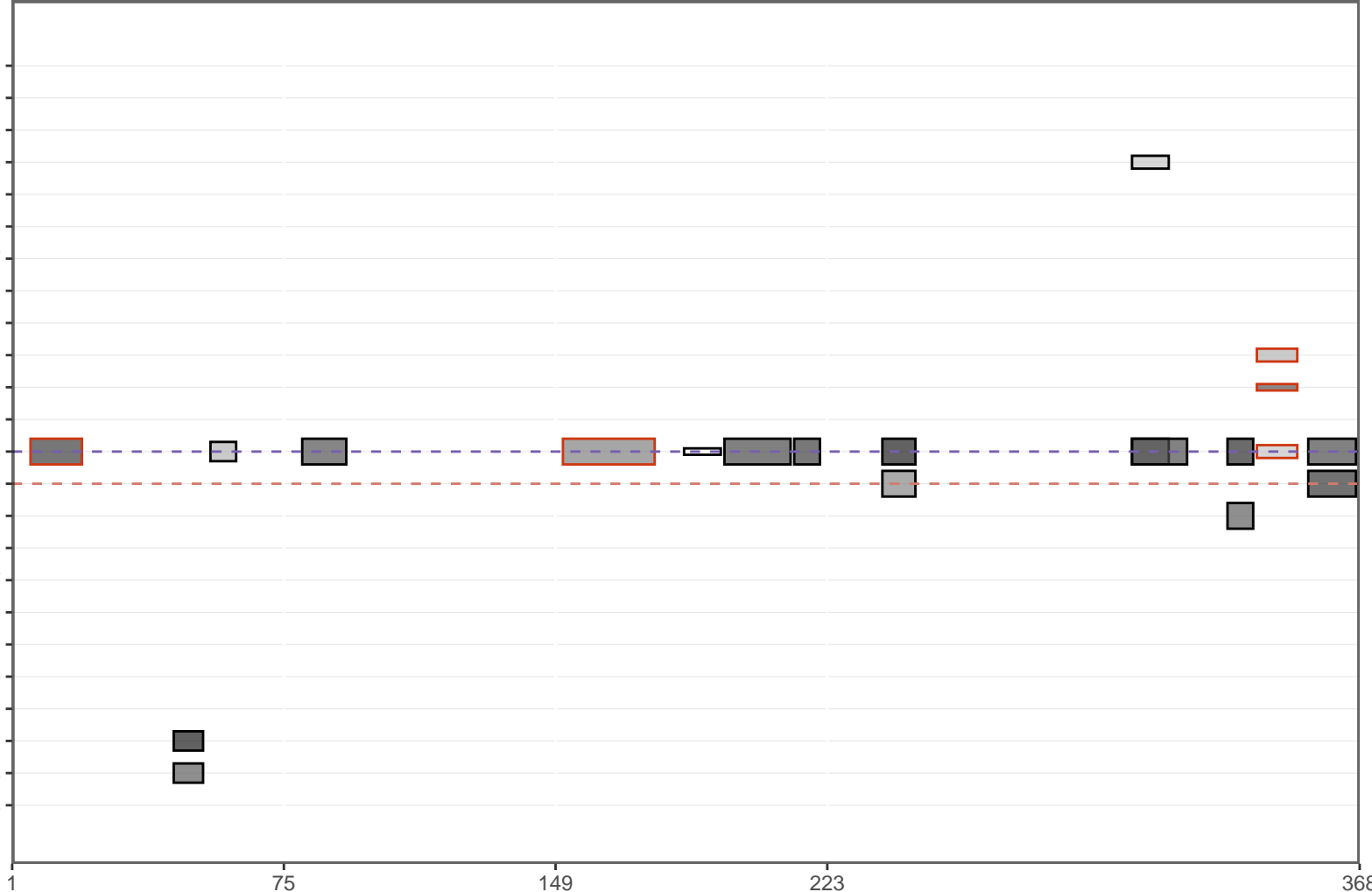
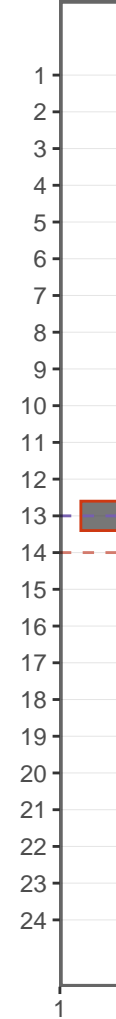
MW indication



Molecular weight

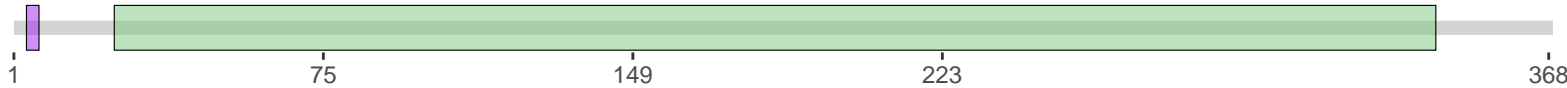


Gel Slice



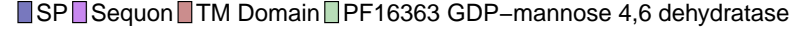
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

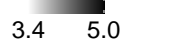
IPRSPYAVSKCAAHWYTVNIREAYGIFANGSLFNFHESPRRGENEVTRKTRAVGRIRKIGLQKFLFENLQASRDVDFAGDVEAMMMMLGQEKDDYVATEESHTEVEEFLEVAFGVGLNWKDHYVVDKRYFRPTEVDNLKGDSSKARKVLGWKPRVGFGLQVMMVDEDELAKREKVLVDAGYMDAQQGP

NbL17g10510.1 dihydropyrimidinase [MW – SP = 55.41 kDa]

No. of times detected



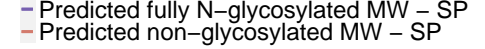
log(intensity)



Values from



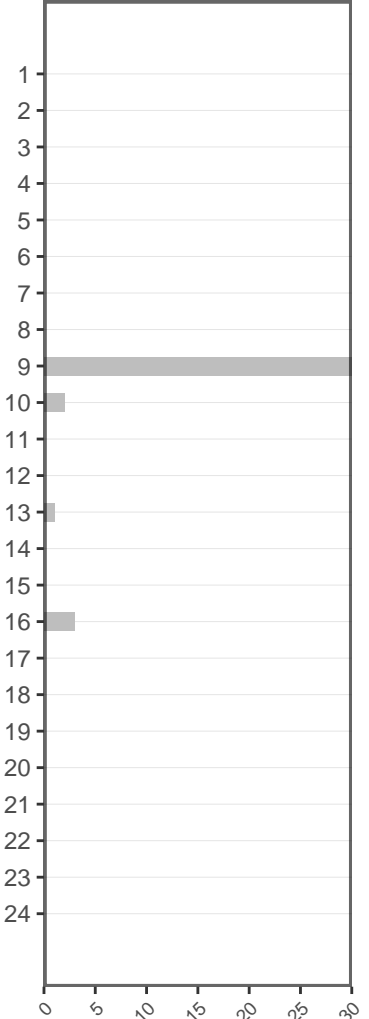
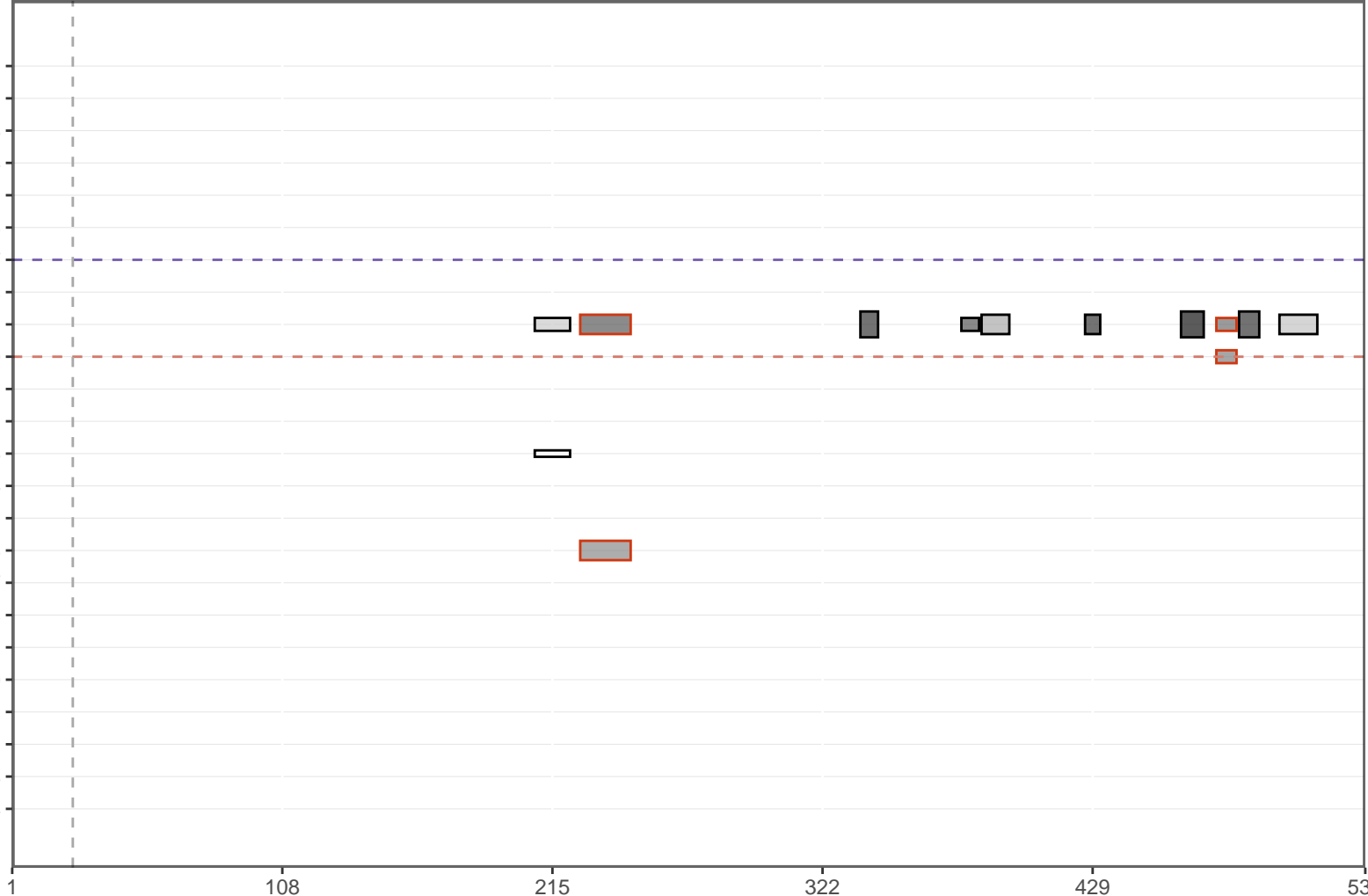
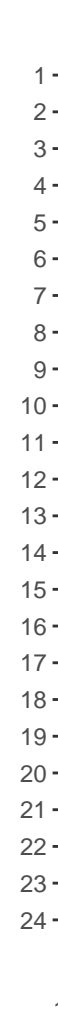
MW indication



Molecular weight



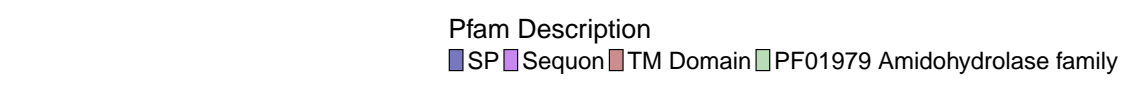
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

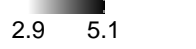
EGHTLSRPPVLEGEATARARLAGFVNTPLVAVHVMISIDAMEIARARKSGQRVVGEPVVGSLVNDSEVLWDFDFHFAARYVMSPPIRAAGHGTALGALMGLLGVVDTDHTCTFNTGKALGIGDFRKNPNDVNGMEERMHLVWDTMVASGGISVTDVYRITSTECARIFNFRKGAALVGSADHILNPNSSFEISKSHVYRTDTNVEGWRGKGVETIAGGRVWENDELKVPDGAKYEMPPFSVYDFDGIKADAKYLAFLAPVWRSTT-

NbL17g10120.1 glucosidase_2_subunit_beta-like [MW - SP = 64.28 kDa]

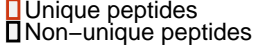
No. of times detected



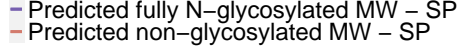
log(intensity)



Values from

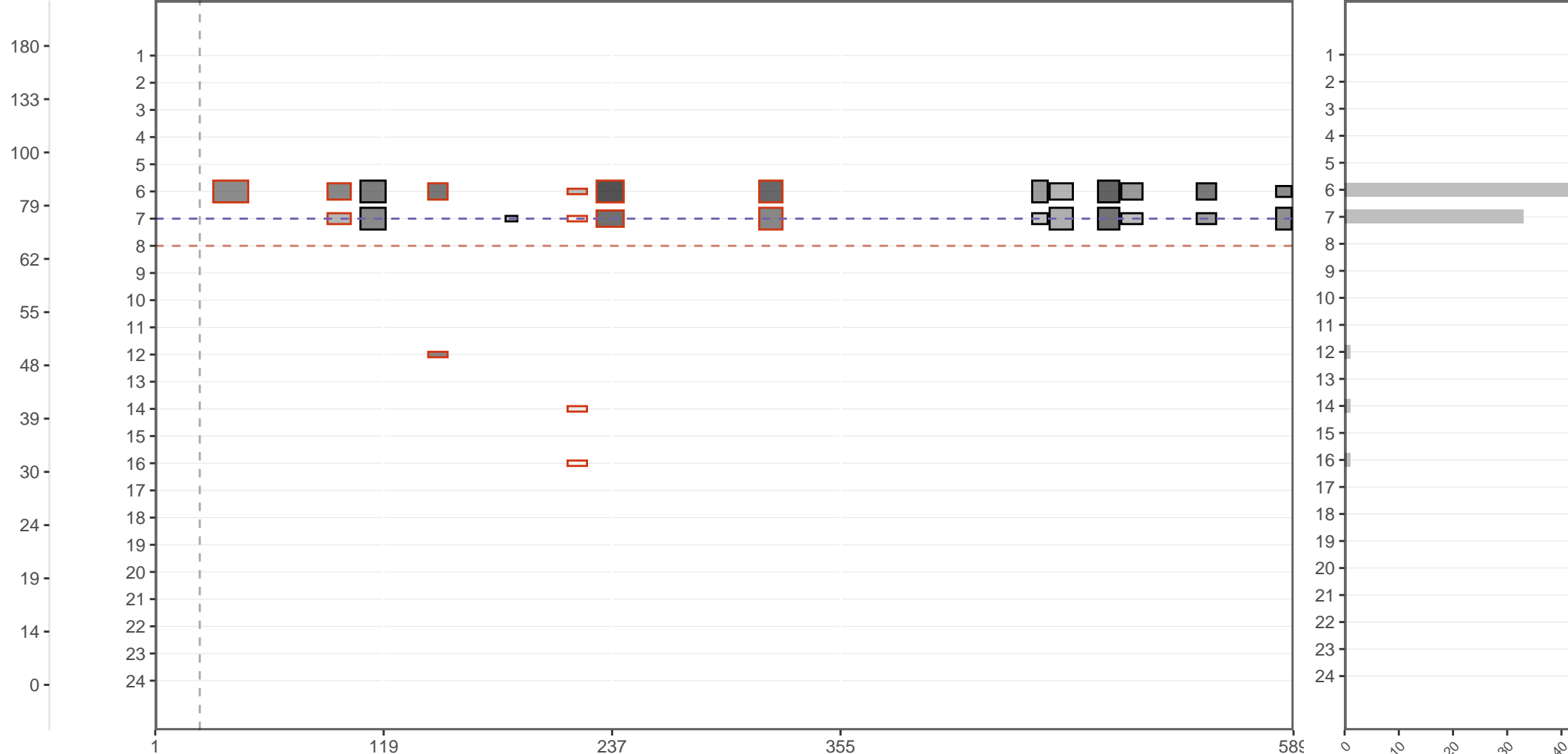


MW indication



Molecular weight

Gel Slice



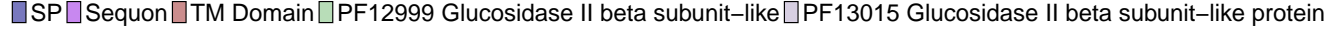
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

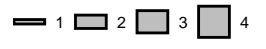


Protein sequence:

SEKDTENTESLSKEELGRVGRFRWLKKGEGQANEVEVDAGTKSNYDSSDEGPTDTHSEEVHGDDEDEDEHYEDDEDETPVEDLGGEDHDSSSSHYAESDDDDDFSDVATFQNPQWMEKIQRTMKGFHSVNLFGTPVNSDAAHRKEVDESSAKLGLKLSKSRLEKLLKGGDFPEKEFYGFYGGGFFESGKQNYTKYKGFPEATQVEGYSSTRLLGNWDFEDSVYRLLQFSSGDKWNGPDRSLKVKLLRGLKNEKLTVDPEPSRGEYMAFLSTYALCLEEKLEKLC

NbL17g10110.1 sulfite_reductase_1_[ferredoxin]_chloroplastic [MW = 77.69 kDa]

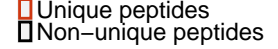
No. of times detected



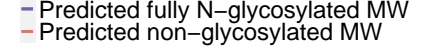
log(intensity)



Values from



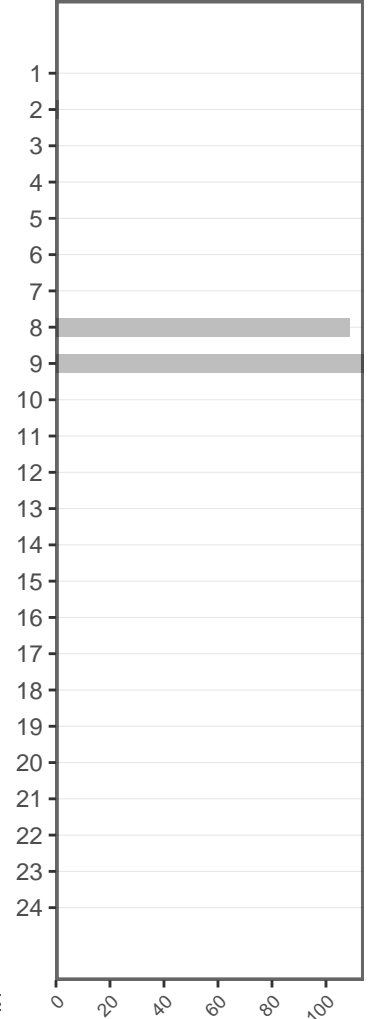
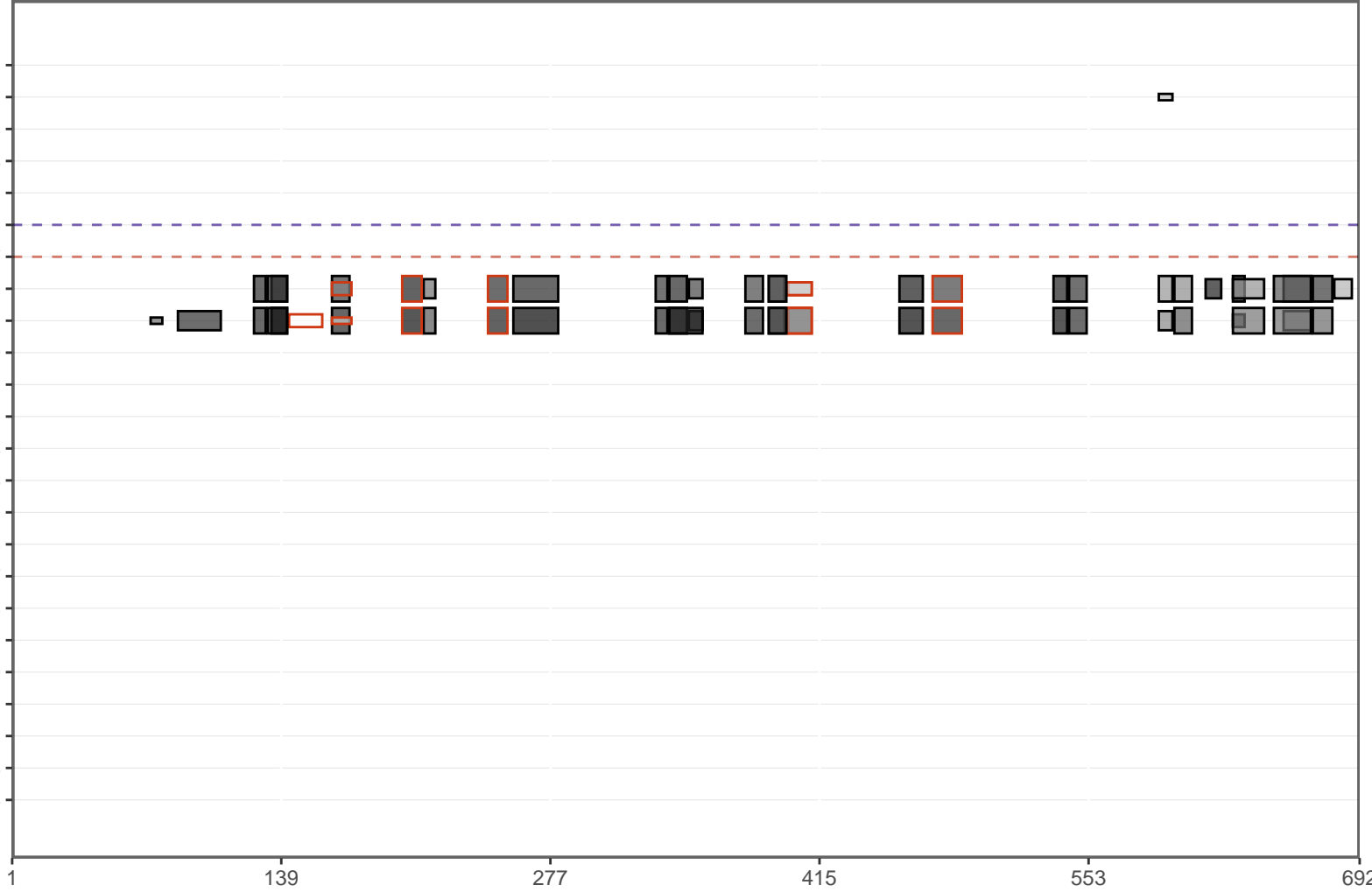
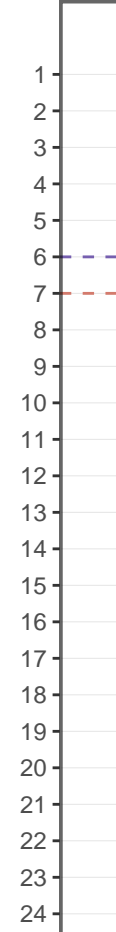
MW indication



Molecular weight

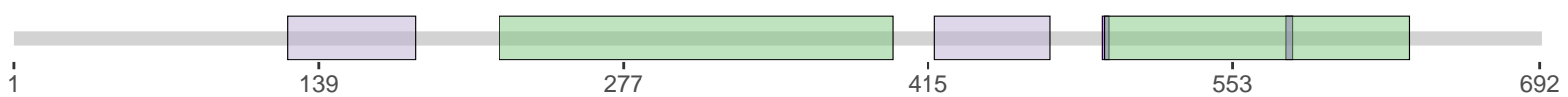


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

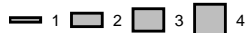
- SP
- Sequon
- TM Domain
- PF01077 Nitrite and sulphite reductase 4Fe-4S domain
- PF03460 Nitrite/Sulfite reductase ferredoxin-like half domain

Protein sequence:

FPRLAEPLOYYPKEDILWKAAYTQRENGRRDRRYSRLKYLSSWGIENFRSIVTEGYGKQKFEPCHELFEWEFKSVLGVHEAGDGLFGLHINRGRVKGAMKALREVEIKYLNVRILTPNQNILGNIRQAWKRPIITVLAGDGLLQPRVYDPLNLTAMAGPFLGPLATEAERGPDILKRVRAIFERVGLKYSESVWIRTGPGNGARPYMAELGLVSDGPNVQYWLGGTNTQTSLAKTFKDKVWVDLEKVLPLFPHWRKRQKESKESGDFTRMGSSEKI

NbL17g09950.1 THO_complex_subunit_4A-like [MW = 26.78 kDa]

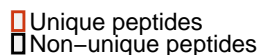
No. of times detected



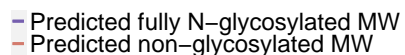
log(intensity)



Values from

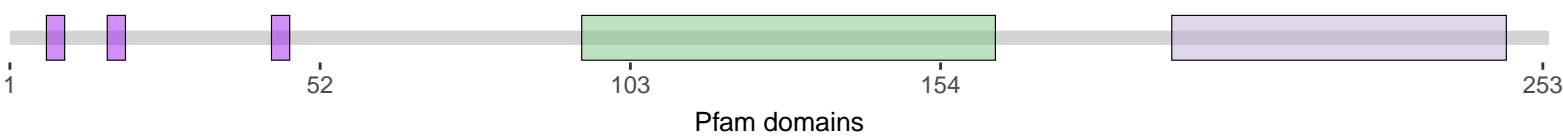
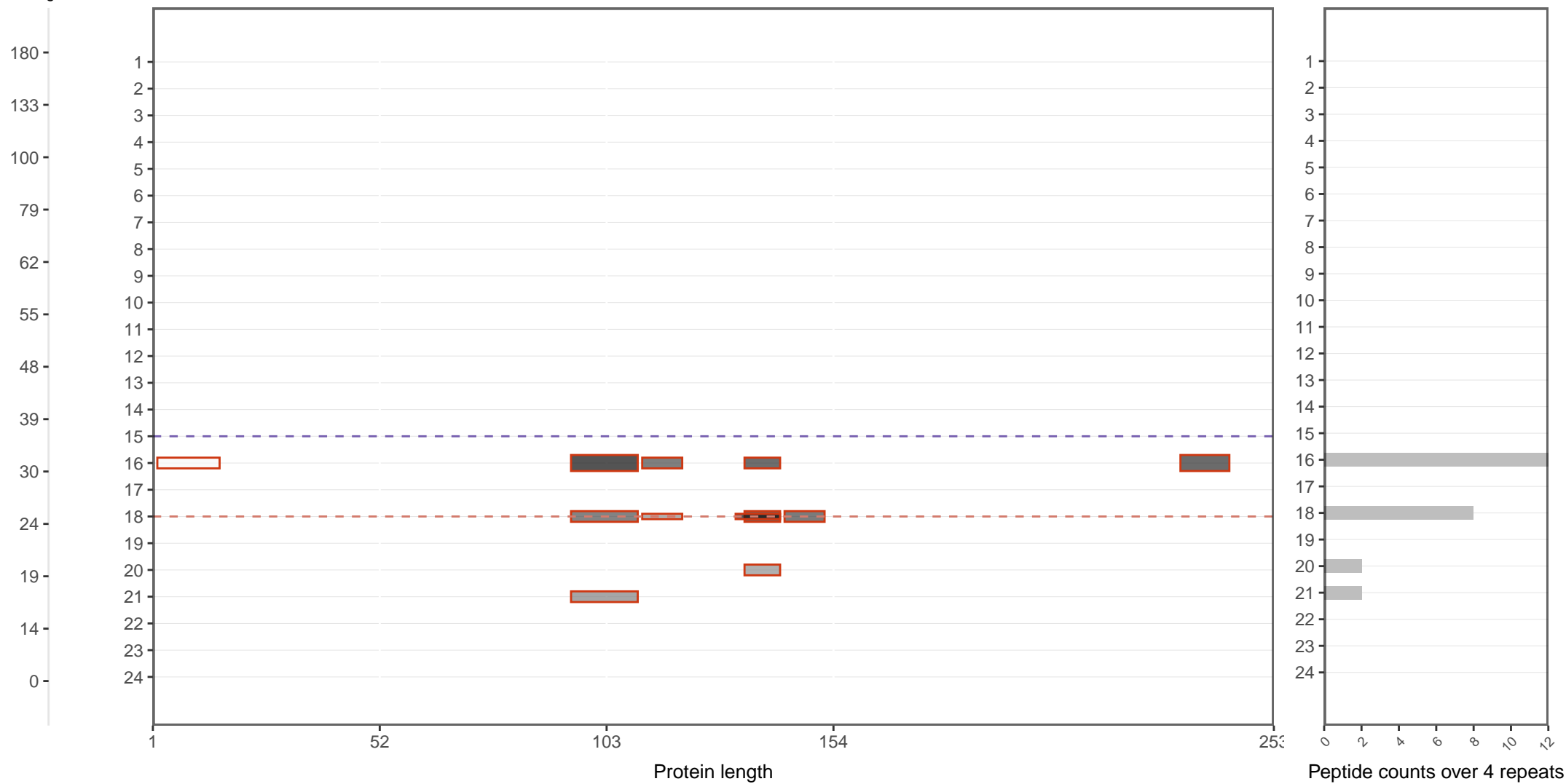


MW indication



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) PF13865 C-terminal duplication domain of Friend of PRMT1

Protein sequence:

EAGDLKRYAHHYDRSGREKGTAEVVFERRGGDAAWKRNNVQLDQKPMKIEVGTNATPAAFKFNCAFQFDGTNGGPRTDGARSGGFGRSRGGRGRGRFRGSGRGRGRGRGRGRGRGKVSAEEDLADLMKVHBEAMQTN

NbL17g09920.1 histone_H4 [MW = 11.41 kDa]

No. of times detected



log(intensity)



Values from



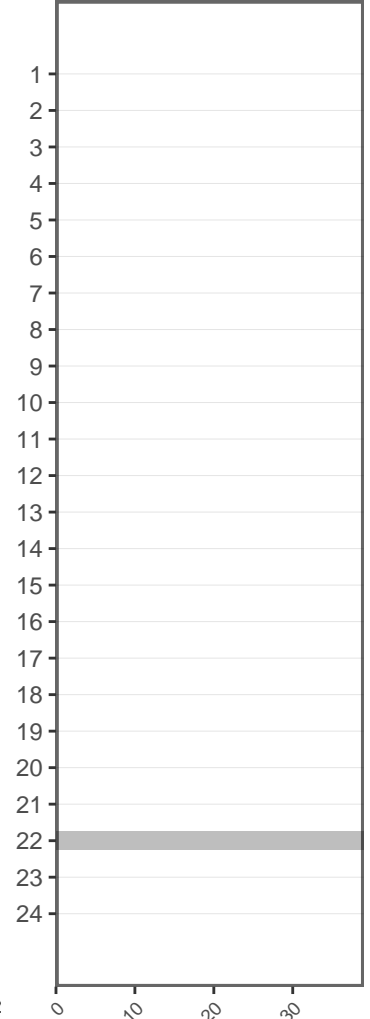
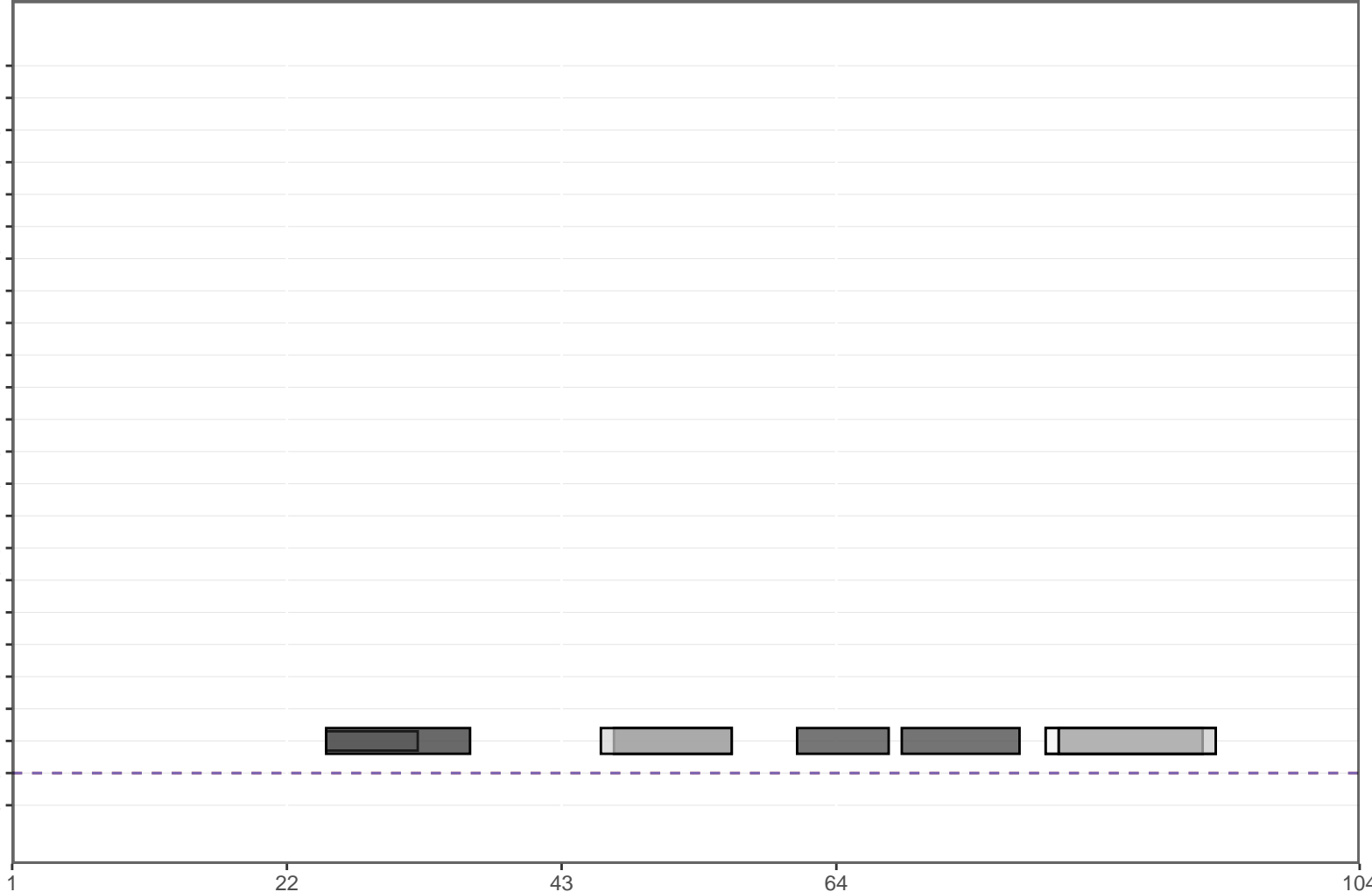
MW indication



Molecular weight

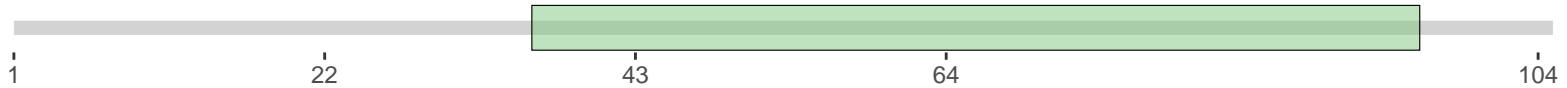


Gel Slice



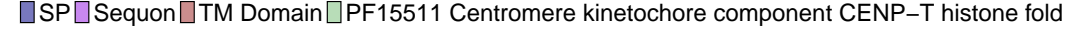
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

.ARRGGVKRISQLVVEETRGLVKIFLENVIRDVPTFEHARRKTVFAMDVVAALKRGRRLVGFQGI

NbL17g09880.1 osmotin-like_protein [MW - SP = 24.49 kDa]

No. of times detected



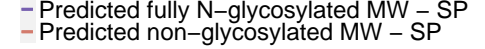
log(intensity)



Values from



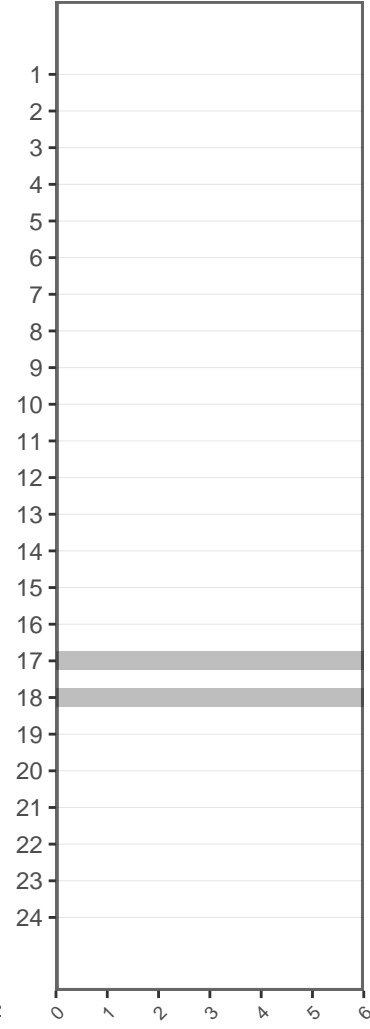
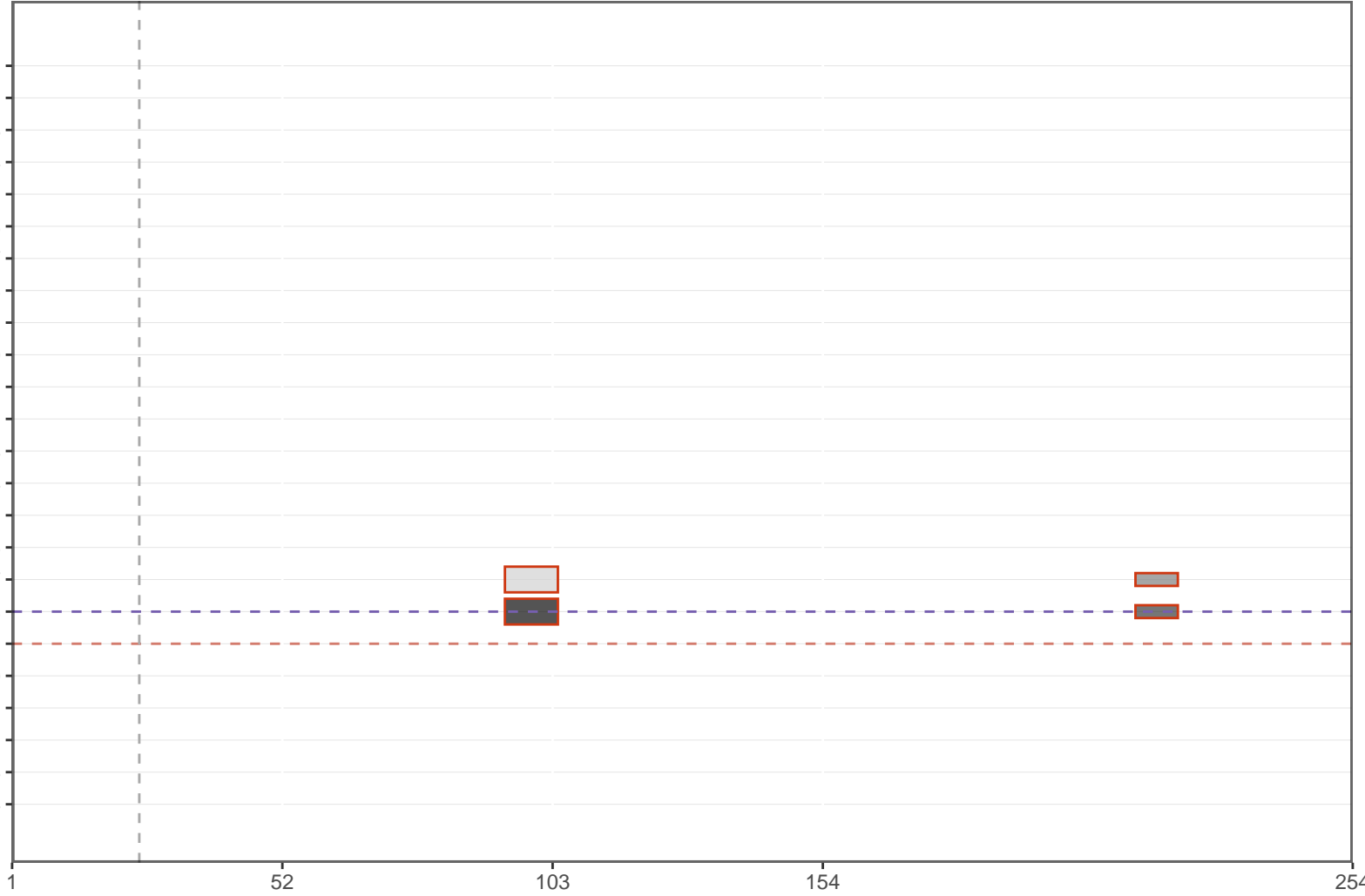
MW indication



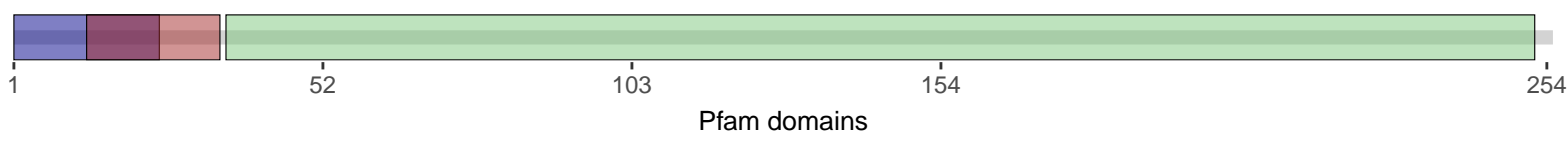
Molecular weight



Gel Slice

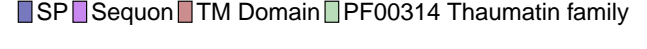


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YTLAQFALHIGHADDFSSYGVSLVDFGNIPVTPHHEGKGGCPVAGGRAELGTGPVWQLRSHGGHGAIVGCKSGGEAFKTDDELGGRHFNPSPTGCKGSSVSGDFKHAQRTFTFYVDRPFLMHEGSSPRELKVIFCH*

NbL17g09850.1 heat_shock_cognate_70_kDa_protein [MW = 52.43 kDa]

No. of times detected



log(intensity)



Values from



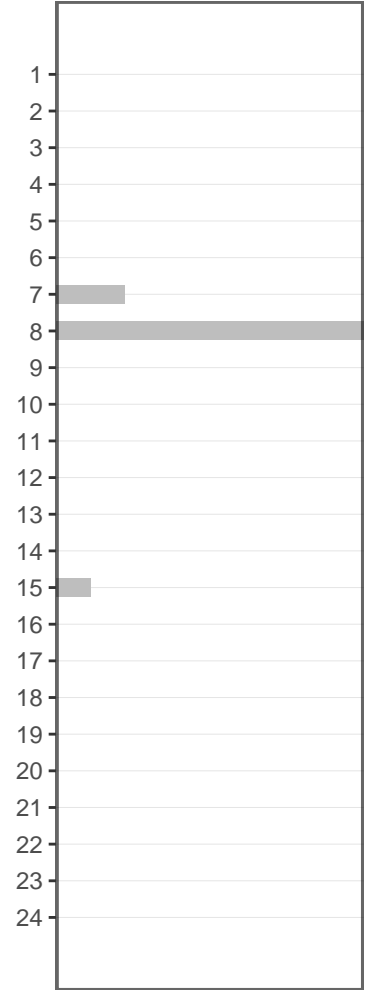
MW indication



Molecular weight

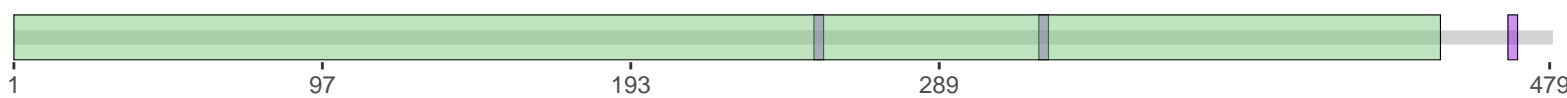


Gel Slice



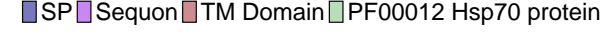
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DVITPLSLGLETAGGVMFLVLRNFTTPTKKEGVFSTYSDNPGVLIQVVEGERARTKDNLLGKFLSGSIPAPRGVPGQINVCFDIDANGLNVSAEDKTTGQNKITTTNKGRLSKEEIRMVGEAEKYSSEDEELKKVKAANLENAYWMRNTKDKKISSQLPAADRRKKEIDAIDEAKWLDNGLVAEDEFDQNKKELEGINPIAKMVGAGGAGGATMDEGSPVAGGAGNGSGAGPKIEVD

NbL17g09630.1 60S_ribosomal_protein_L35-like [MW = 14.2 kDa]

No. of times detected



log(intensity)



Values from



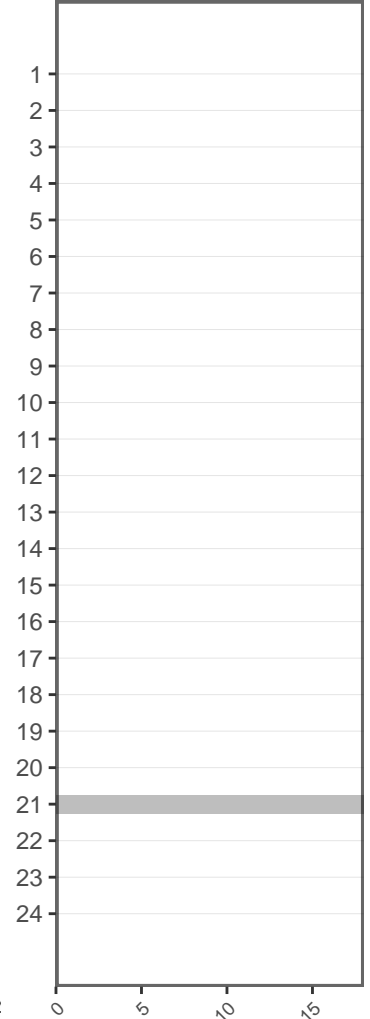
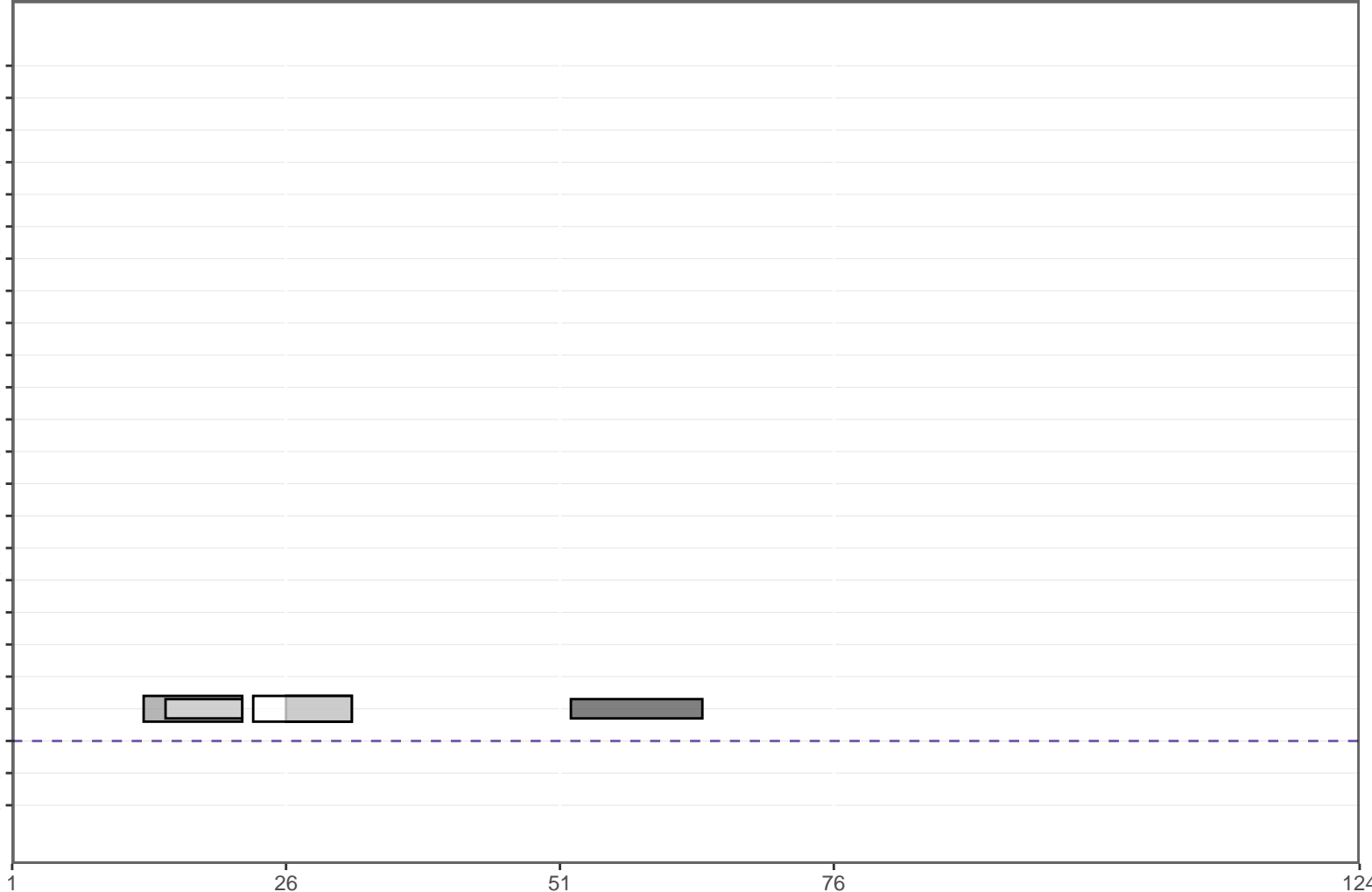
MW indication



Molecular weight

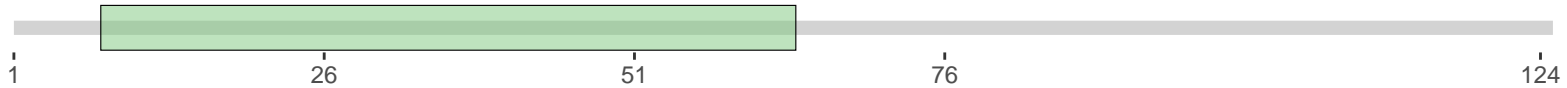


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

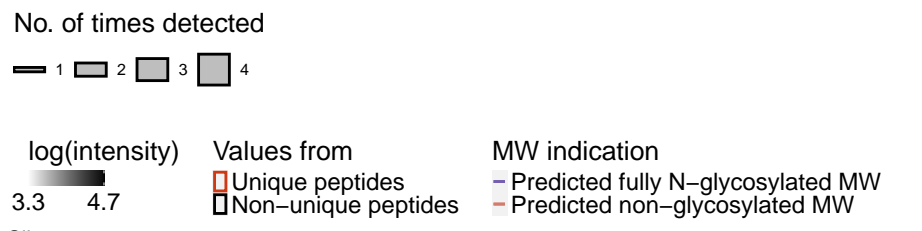
Pfam Description



Protein sequence:

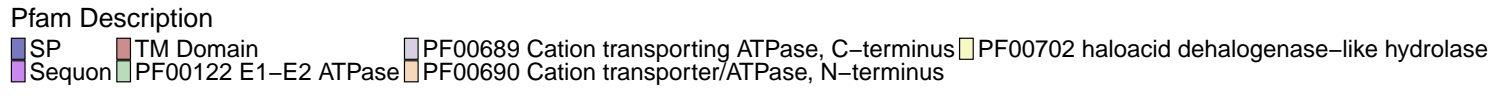
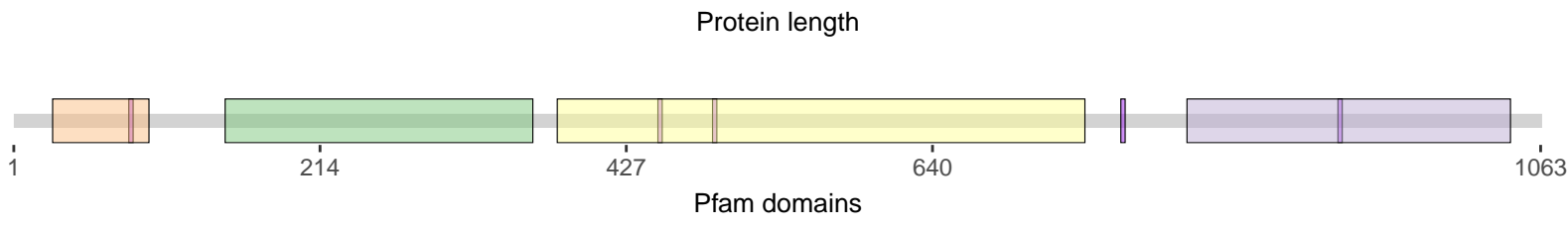
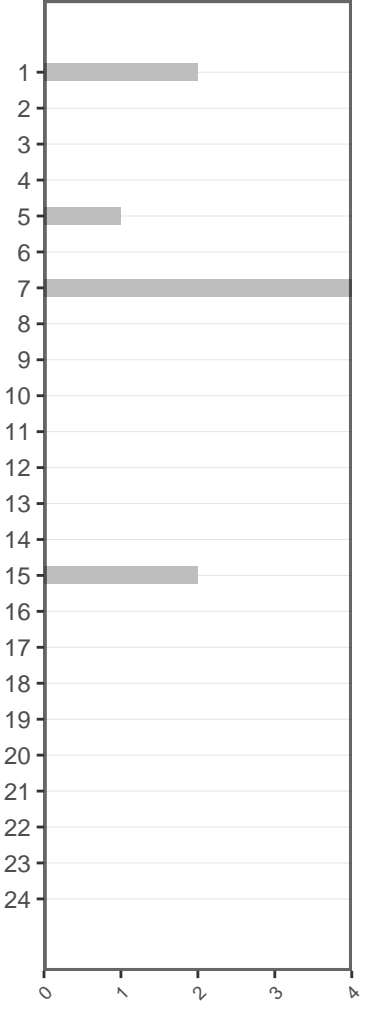
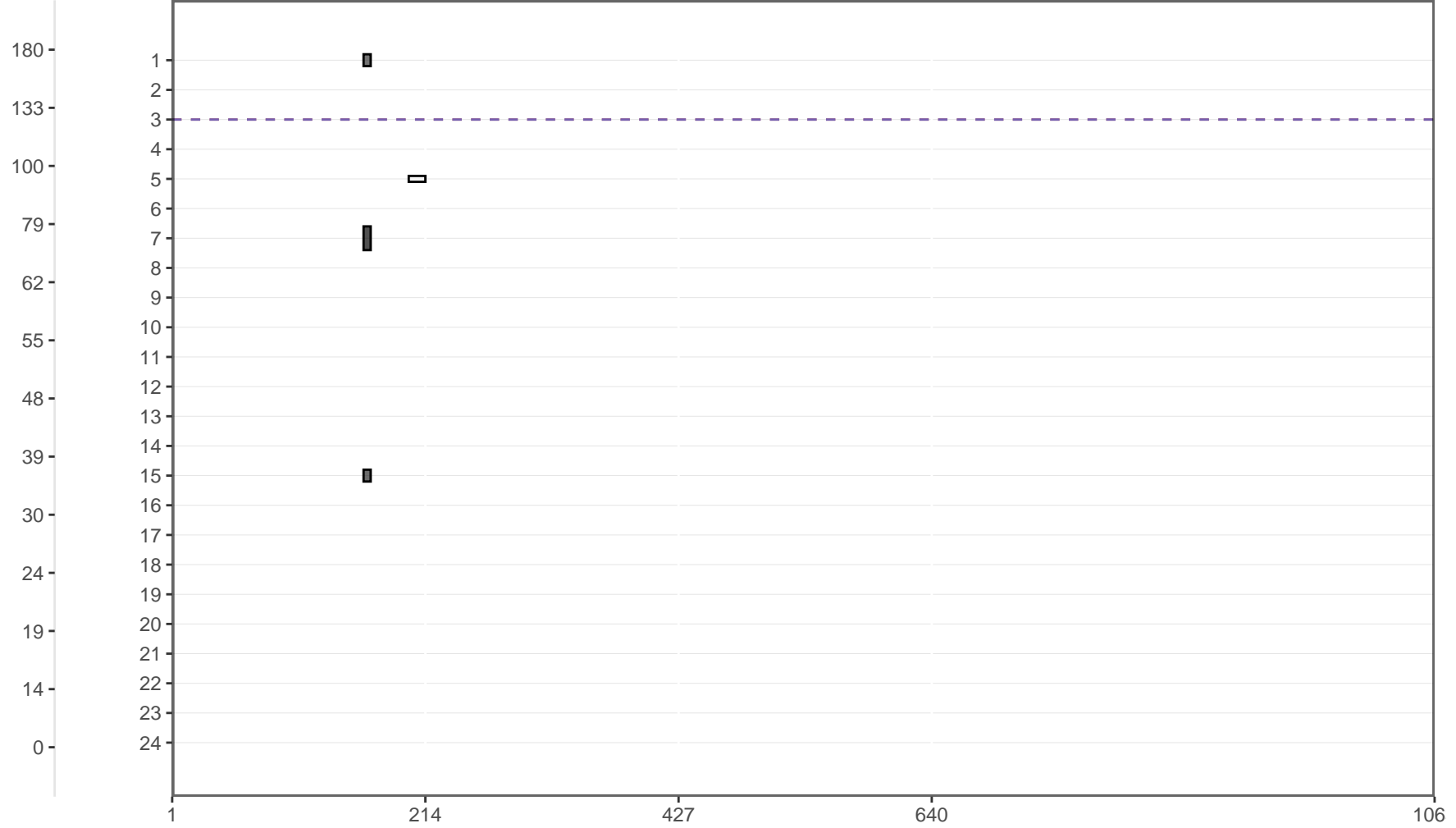
CVVRLSIAQVLTVISGKQKTALEAAYNNKYLPLDLRPPKTRAIRKRILTKHGASLTEREKKKEMVFPRIKVAIKV

NbL17g09530.1 calcium-transporting_ATPase_4_endoplasmic_reticulum-type-like [MW = 116.18 kDa]



Molecular weight

Gel Slice



Protein sequence:

LDKSMGVITISPSGRKLLWGAIVENLERSYVQLDGGVVELDLSRNHILQSLHEMSKALRVLGFAYKEDLPEFSTYNGDDEHPAHELLNPANYPSEKLIFFVGLAGIRPPPKVEVRAEDCCRRAGRVMVITGDNNKNTAEIAGREKIVFGSHEDISRLTQKEFMELANPKGHRGSGGLLFSRAEPRHKGIDVRLKEDGEVAMTGDGVDNAPALKLADIGIAMGIAGTEVAKEASDMVLADNINFTIVSAVGEGRSHNMKAFIRYMISSNICEVASIFLTAALG

NbL17g09400.1 phototropin-1-like [MW = 114.89 kDa]

No. of times detected



log(intensity)



Values from



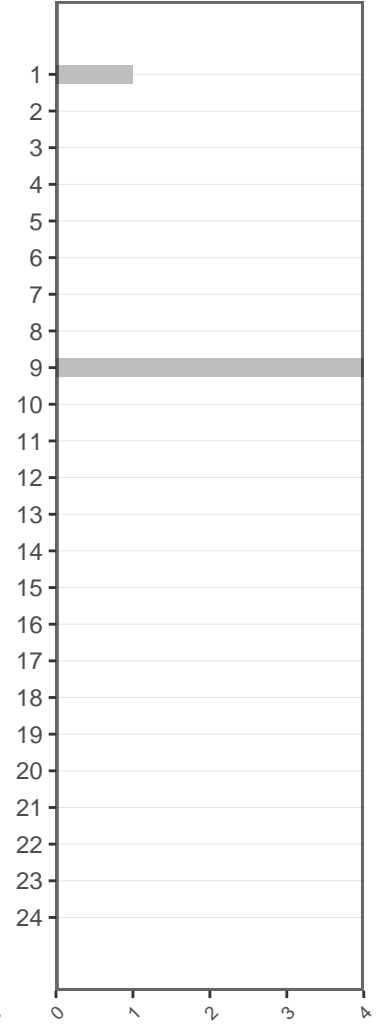
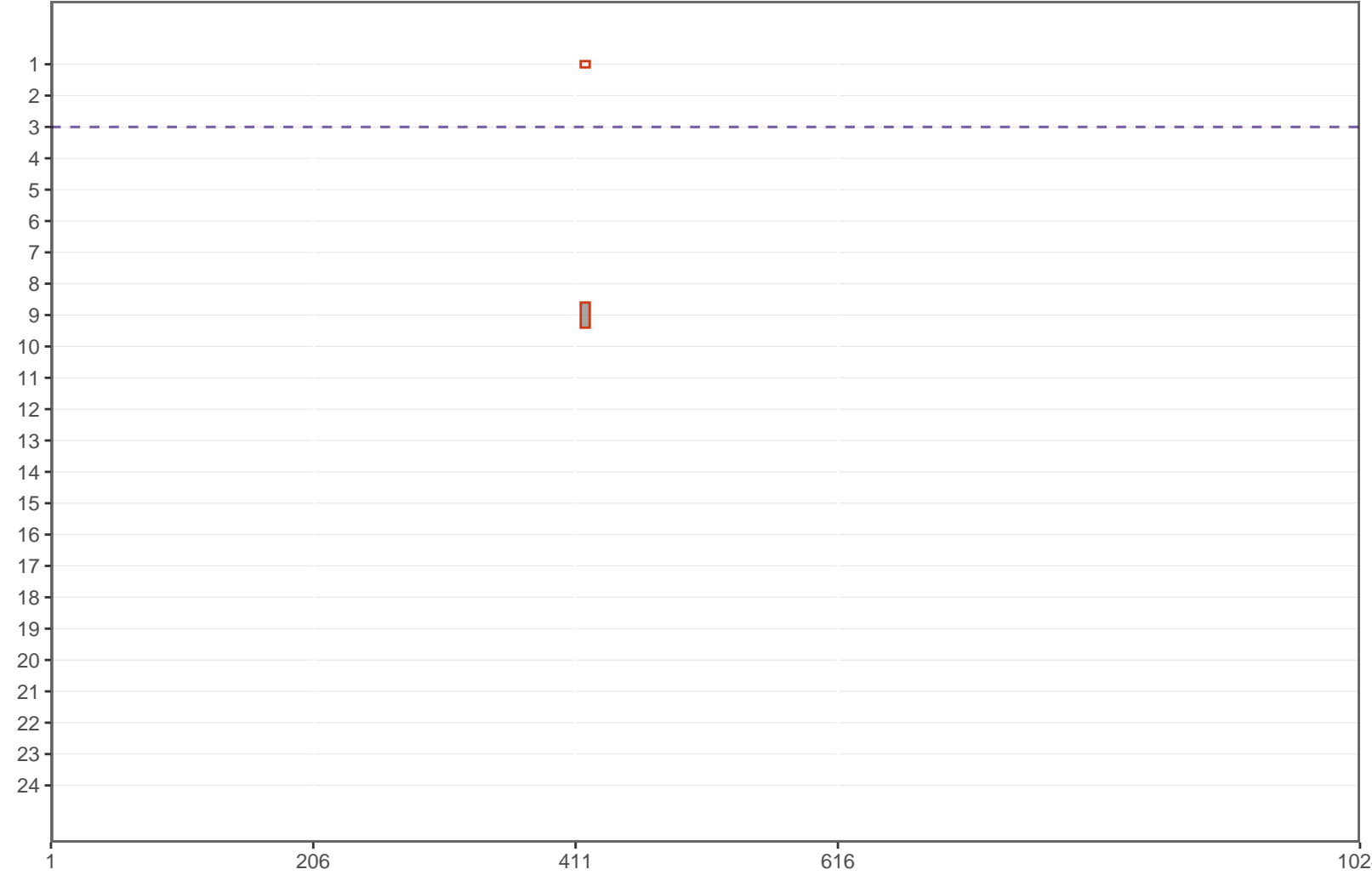
MW indication



Molecular weight



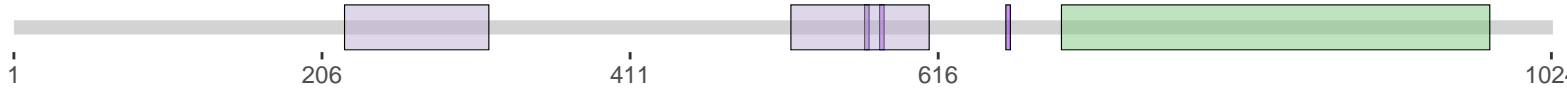
Gel Slice



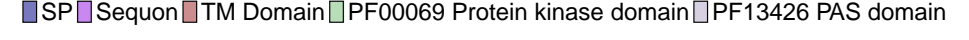
Protein length



Pfam domains



Pfam Description



Protein sequence:

GIDLATTLEIEKQNFVITDPRLPDNPFIASDSFLELFEVSRHEELGRNCRFLGGPEFDATVWKRQAIDNGTDVTVQLNRYTKTGKFWNLFHLGPMRDGKGEVGYFYGVDLDSGQVHPLHNSIPEDGKATESAKLVKETAENVDEAVRELFDANRNGKPEDLWRNHSKVVHAKPKRDKDSFWDVAIQKVLDSGEPKGLKHKPKPLGSGDTSQVHLVELOGTGGGFAMKMKEMLNRNKVVHRAGAEREILDMLDHPFLPALYASFGTKHGLTFDYYPGGELFLLLDRPTK

NbL17g09360.1 2-dehydro-3-deoxyphosphooctonate_aldolase_1 [MW = 32.79 kDa]

No. of times detected



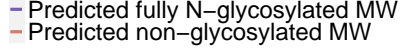
log(intensity)



Values from



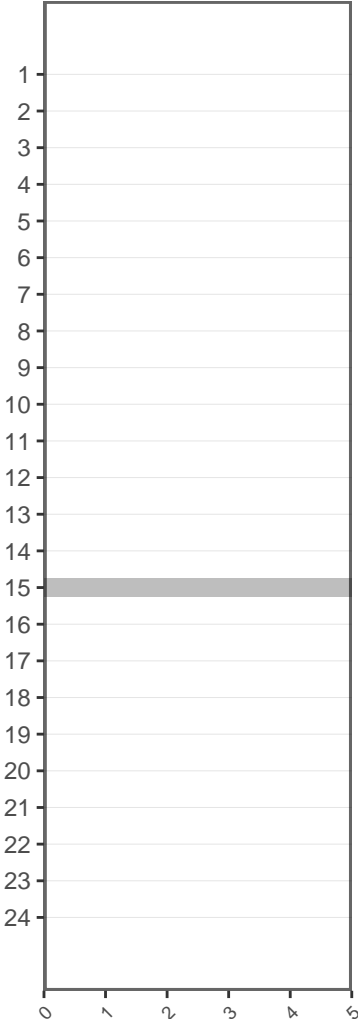
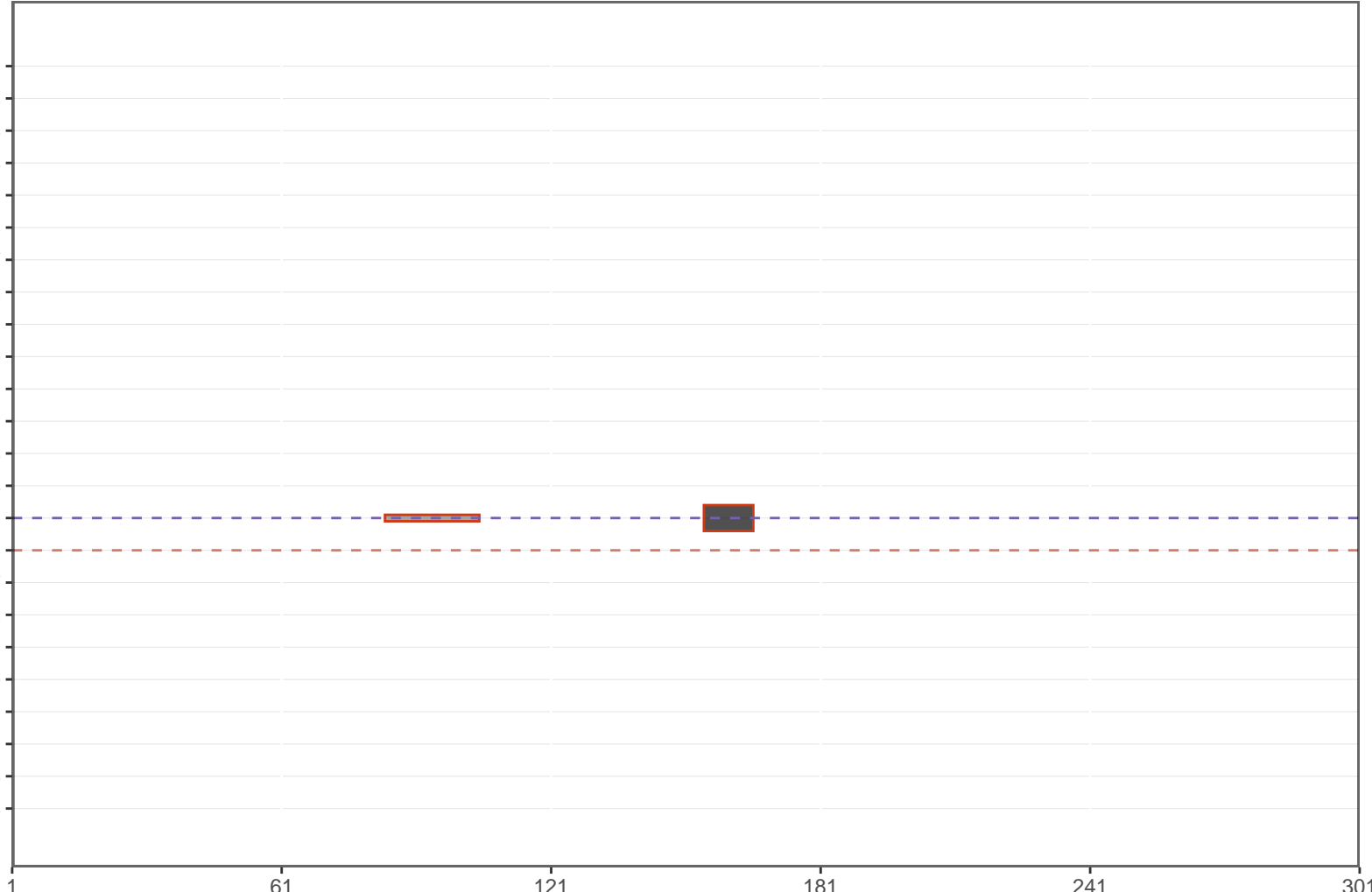
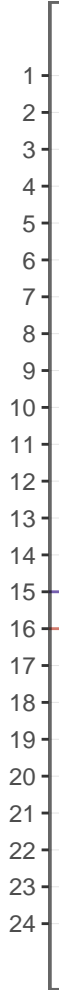
MW indication



Molecular weight

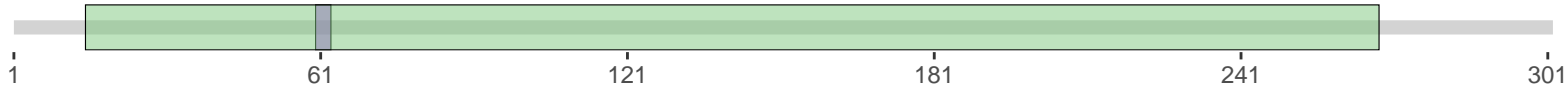


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MAPSVMANSAEKVRLAGNGNMVGERGTMFGVNDLIVDRNFEWMRKANCPVADITHLGGPAGKKEGGVABGGLRELPLCIARTAWAVGVDGIFMEVHNDPLSAPVDGPTQWPLRHLLEELLEELVTLGVRELKANGSSSKLISLHFVIRTQKFGYLV

NbL17g09290.1 probable_trans-2-enoyl-CoA_reductase_mitochondrial [MW = 41.16 kDa]

No. of times detected



log(intensity)



Values from



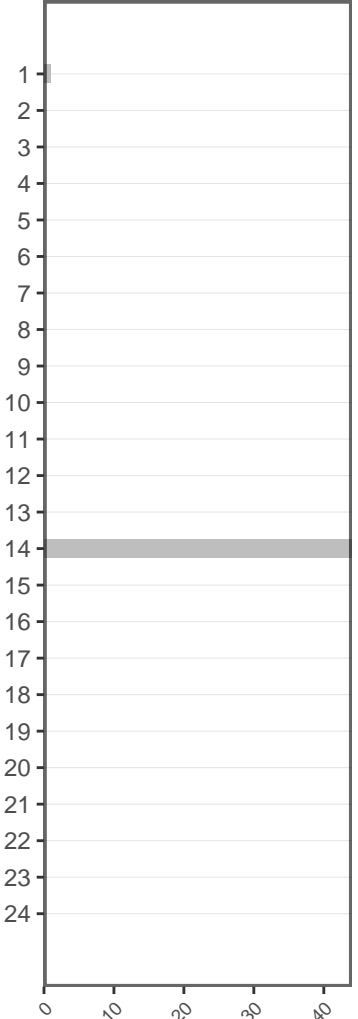
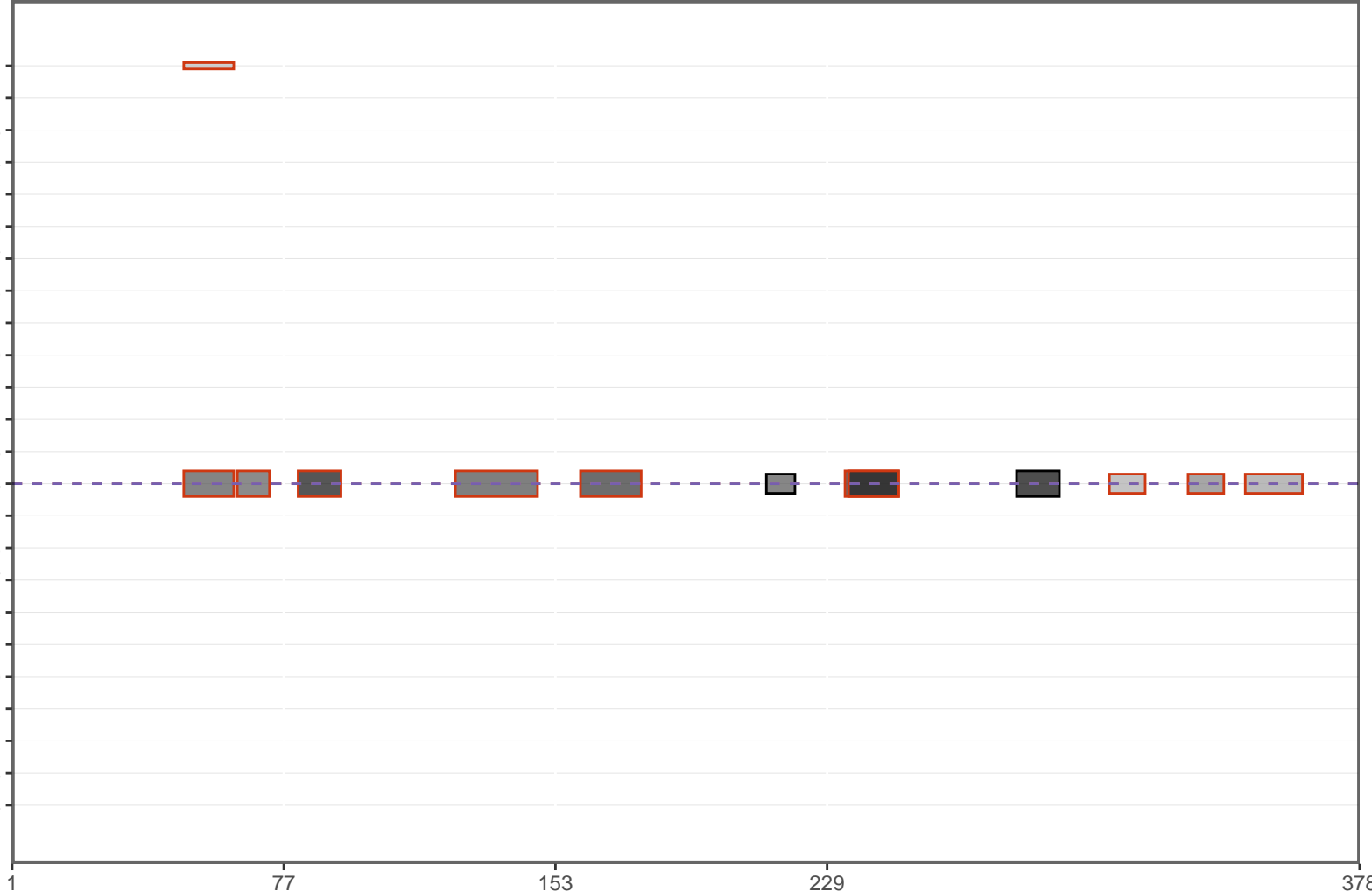
MW indication



Molecular weight



Gel Slice



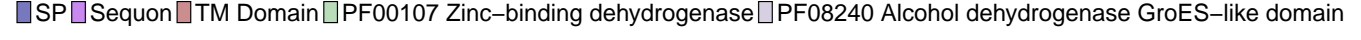
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

RMLEDFVTLKPGNSIVQNGATSMVGGQFGLARLRGHSINIRDRAGSDEAKEYKLLGADEVYTESQLEVNNVRGLLGSISERPALGFNCVGGNAALLVLRKFGDGTMTVYGGMSKRPTTVSTSSFFIKELTGTGFWLQRWMSSEKAEGRSMIDVLLGLGRDGLKYLELEVAFFDDFHSALEKAMGKRGSQPKQVLRP

NbL17g09070.1 ATP_synthase_subunit_d_mitochondrial-like [MW = 19.79 kDa]

No. of times detected



log(intensity)



Values from

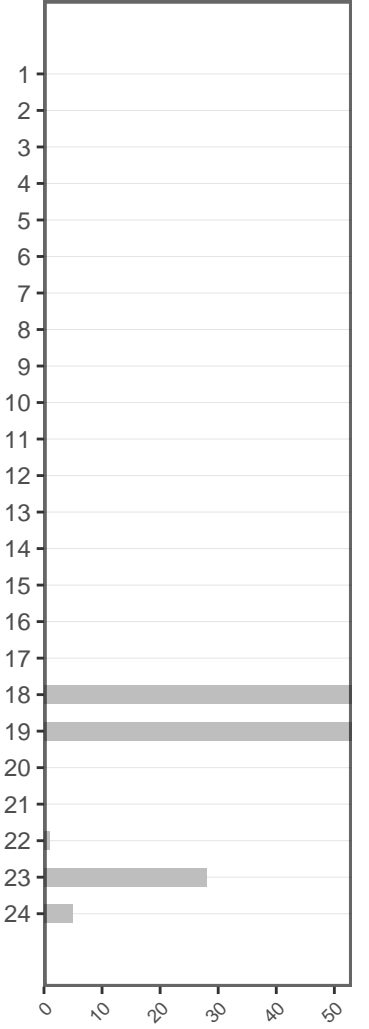
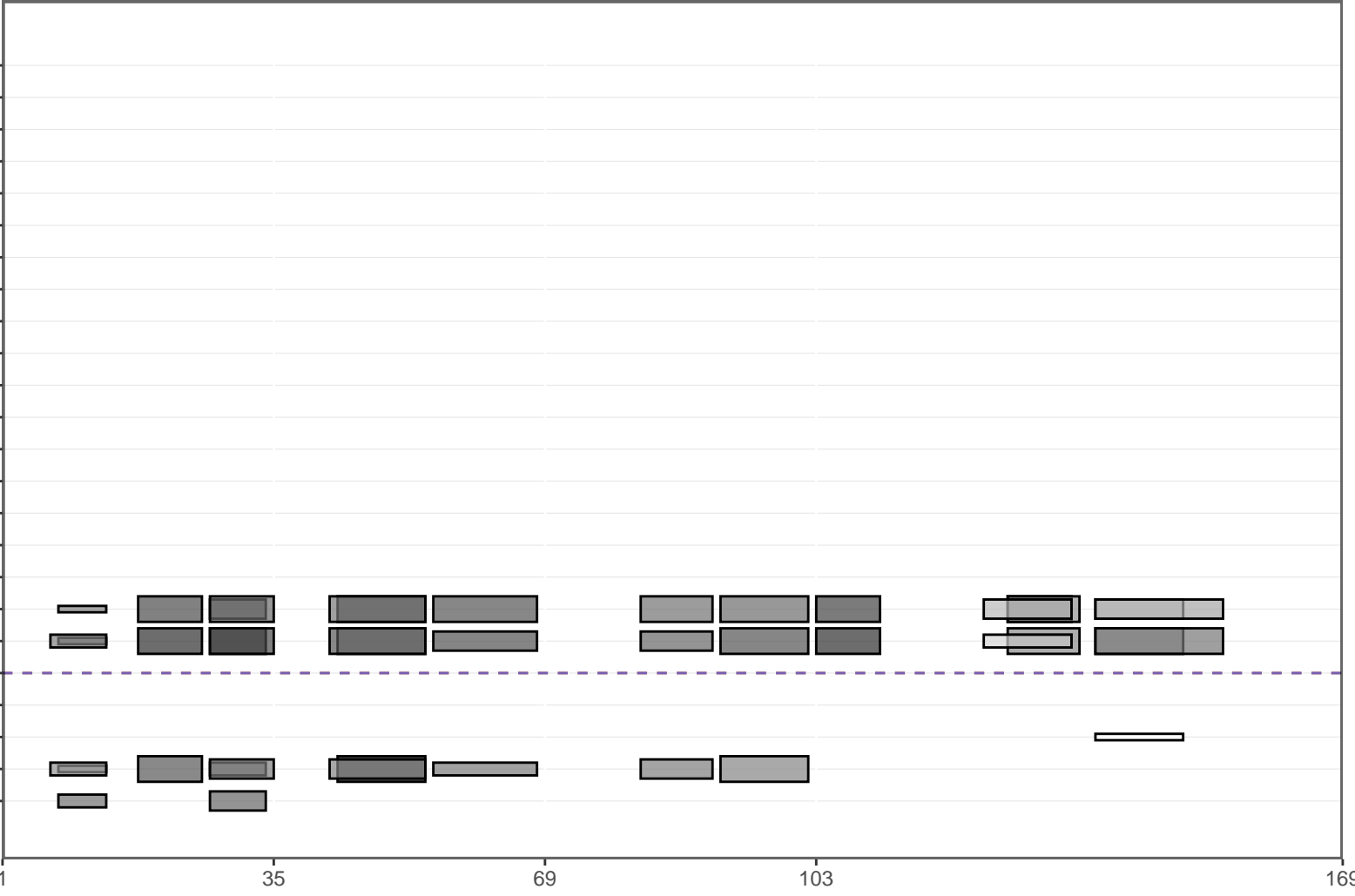
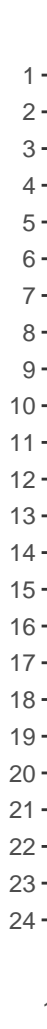


MW indication



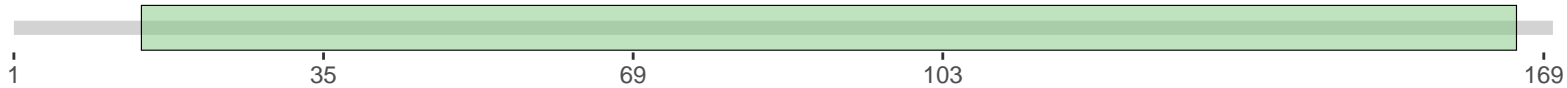
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IIGSRLLVDMYKAYAESIEIPKFDFTVTPQYKPKFDALLVELKEAEQKSLKESERLEKEVAEVOELKKKSLMTAAEYFKEHPELKKKFDDEIRNDYWGYP

NbL17g08990.1 elongation_factor_1-alpha [MW = 49.3 kDa]

No. of times detected



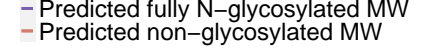
log(intensity)



Values from



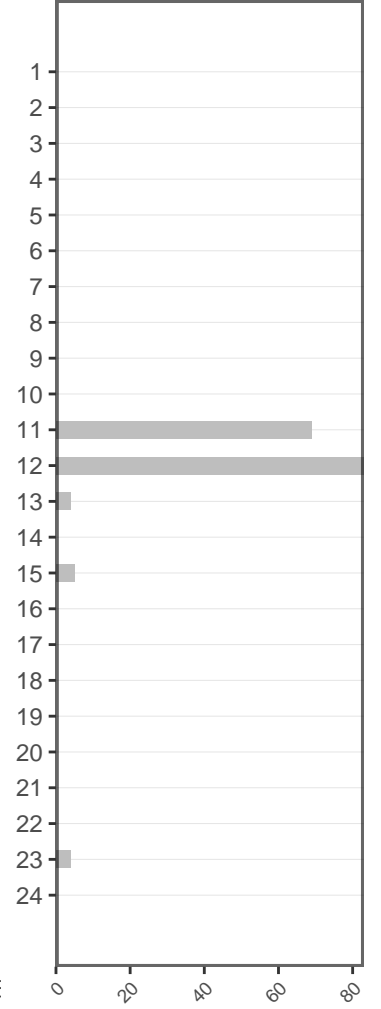
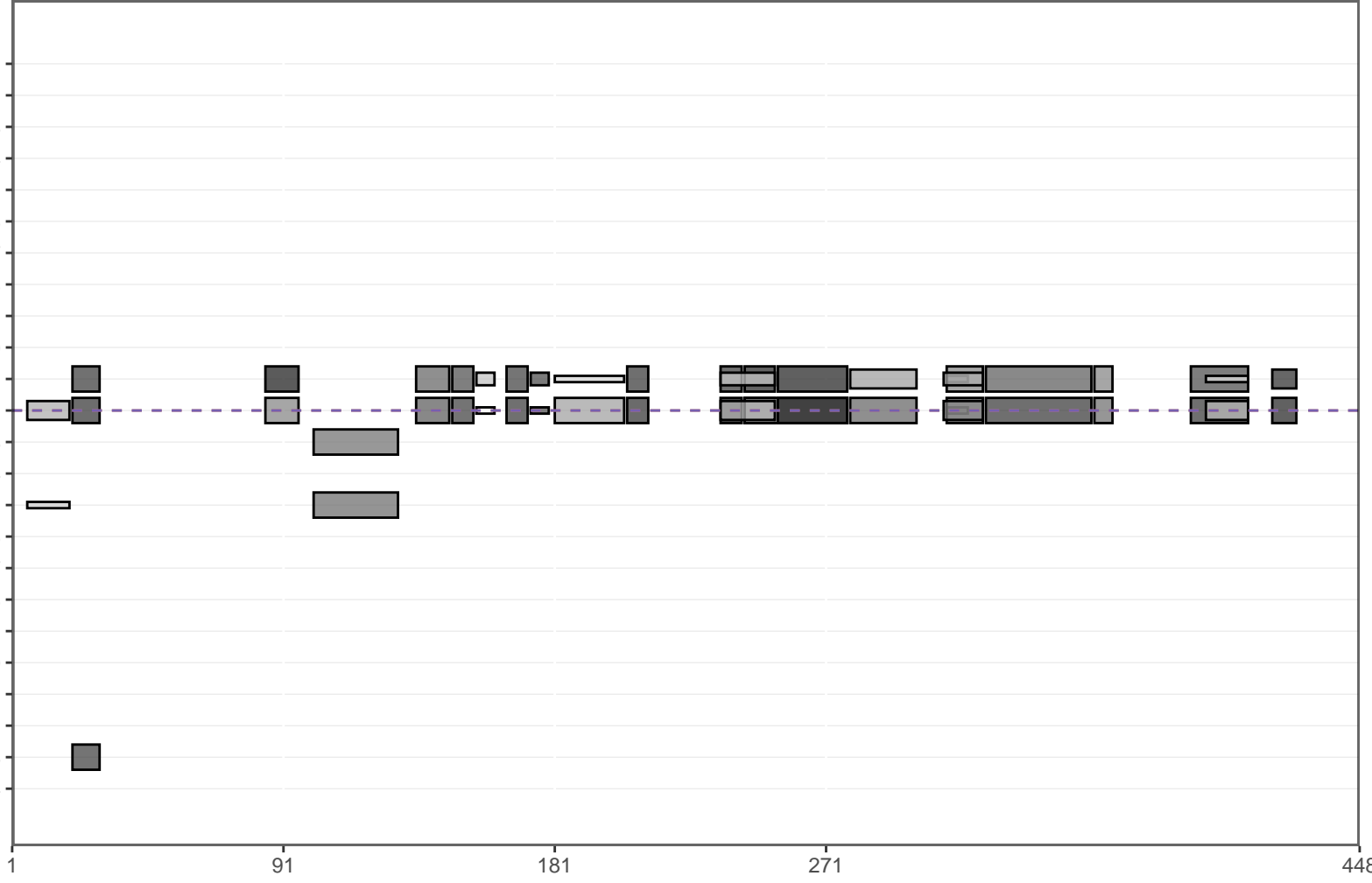
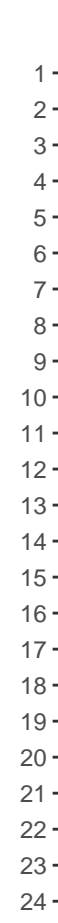
MW indication



Molecular weight

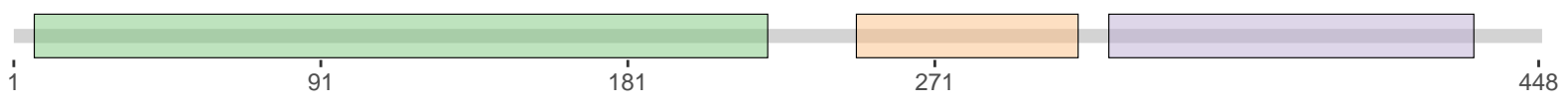


Gel Slice



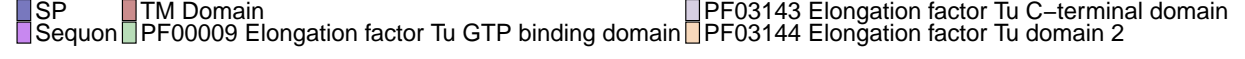
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SPTLLEALDQINEPKRRPSGKPLRLPLGQVYKIGGGITVPVGRVETGVLRKPGMVFYFGPTGLTTEKSEVEMHHEALGQALPGDNVGFNKNVAVKDLKRGFVASNKDDPAKGAASFSTGQVIMNHIPGGKGGVAPVLDGHTSHIAVKFAELTKIDRRSGKEKEKPKFKNGDAGMVKMLPTKPMVVFETSEYPLGRFAVRDMRGTVAWGVIKGVKDKKPTGAKVTKAAQKKK

NbL17g08980.1 protein_disulfide-isomerase_5-1 [MW - SP = 13.76 kDa]

No. of times detected



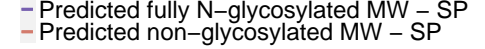
log(intensity)



Values from



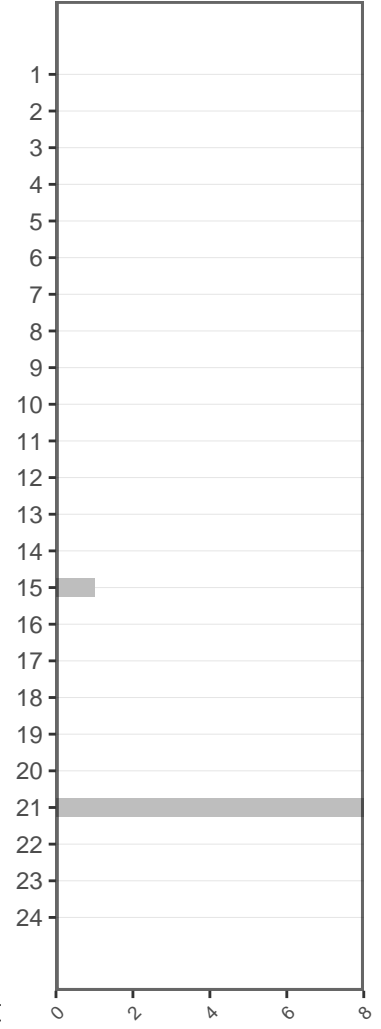
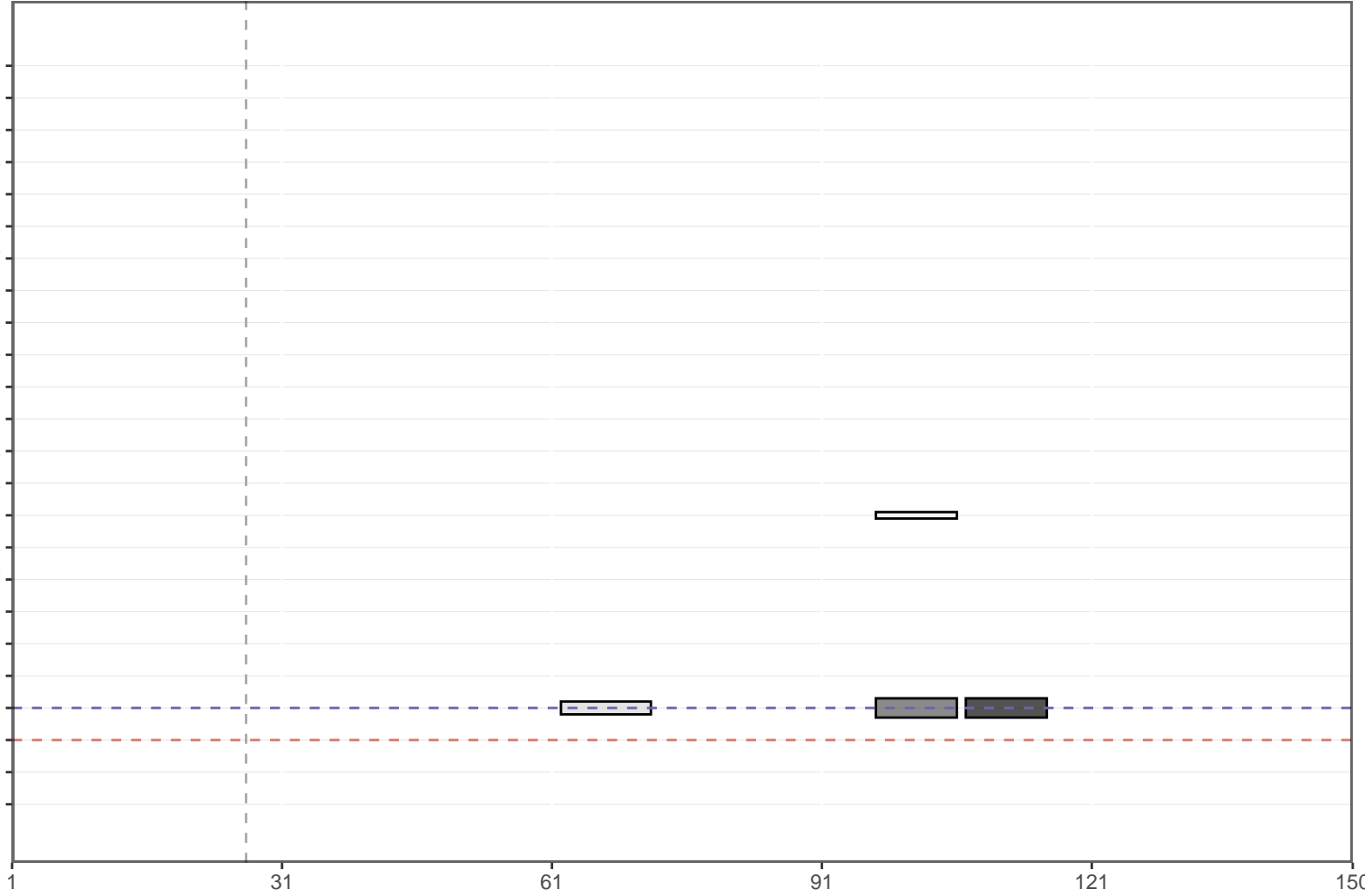
MW indication



Molecular weight

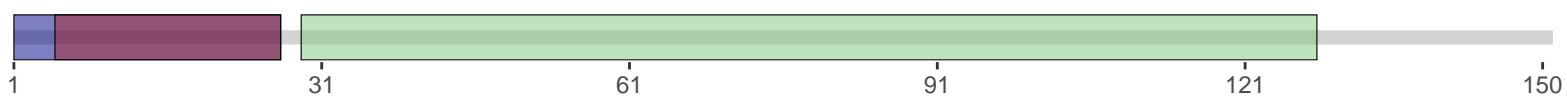


Gel Slice



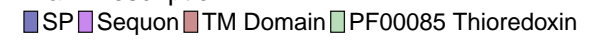
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

GTLVDDLGKAMEGEDEIEVGGVGGGTHKPKVGNKVDIHSYPTFKLFLYNGEEVAVYGGPRDIESLKFIALEEAEEKATKAEAGDDKEL*

NbL17g08910.1 ruBisCO_large_subunit-binding_protein_subunit_alpha [MW = 62.14 kDa]

No. of times detected



log(intensity)



Values from



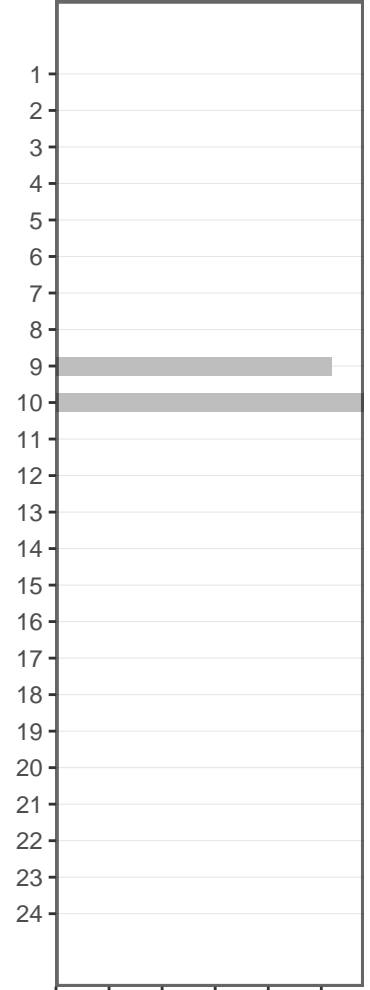
MW indication



Molecular weight

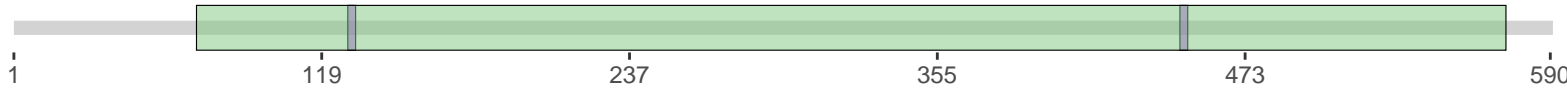


Gel Slice



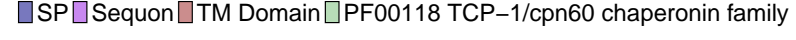
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IPLEKTTQLRSLIHAEDVTGEALATLVNKLRLGILNWKPKPGFERRKALLGDIAVITGAEYQATDLGLLEGITPVEALGIARKVITFKDSTTHADASKDEIGRIAGLKKELSETSDSYVDSEKLAERIAKLSGGVWIKVGAATEALEDRKLRIEDAKNATFAIEEGVPPGGGAAPVHLSTQVPAKDKLEDADKELGADIGRIQLVAPASLHAGNAGIEGVVVEKVRKAEAEWEMGVNMTDKYENLVDAQVDRPKVTRGALGNASAVAGMVTGQAVVEKAKPKYVAAPKPI

NbL17g08830.1 glutaredoxin-C4 [MW - SP = 12.08 kDa]

No. of times detected



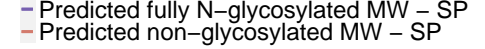
log(intensity)



Values from



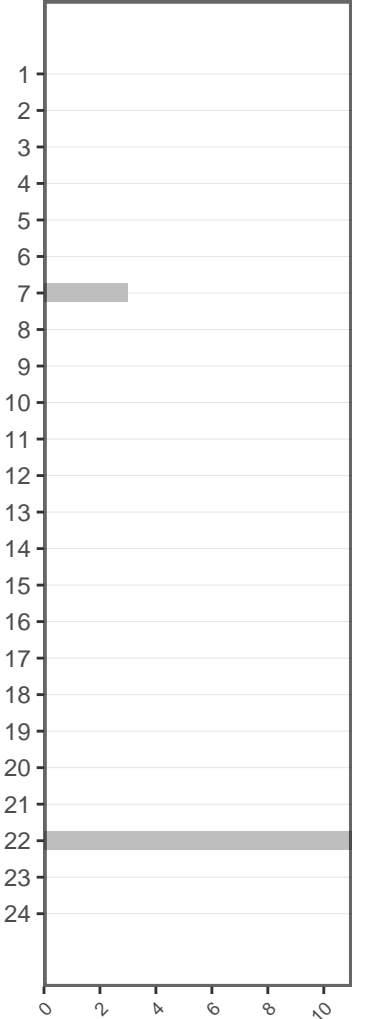
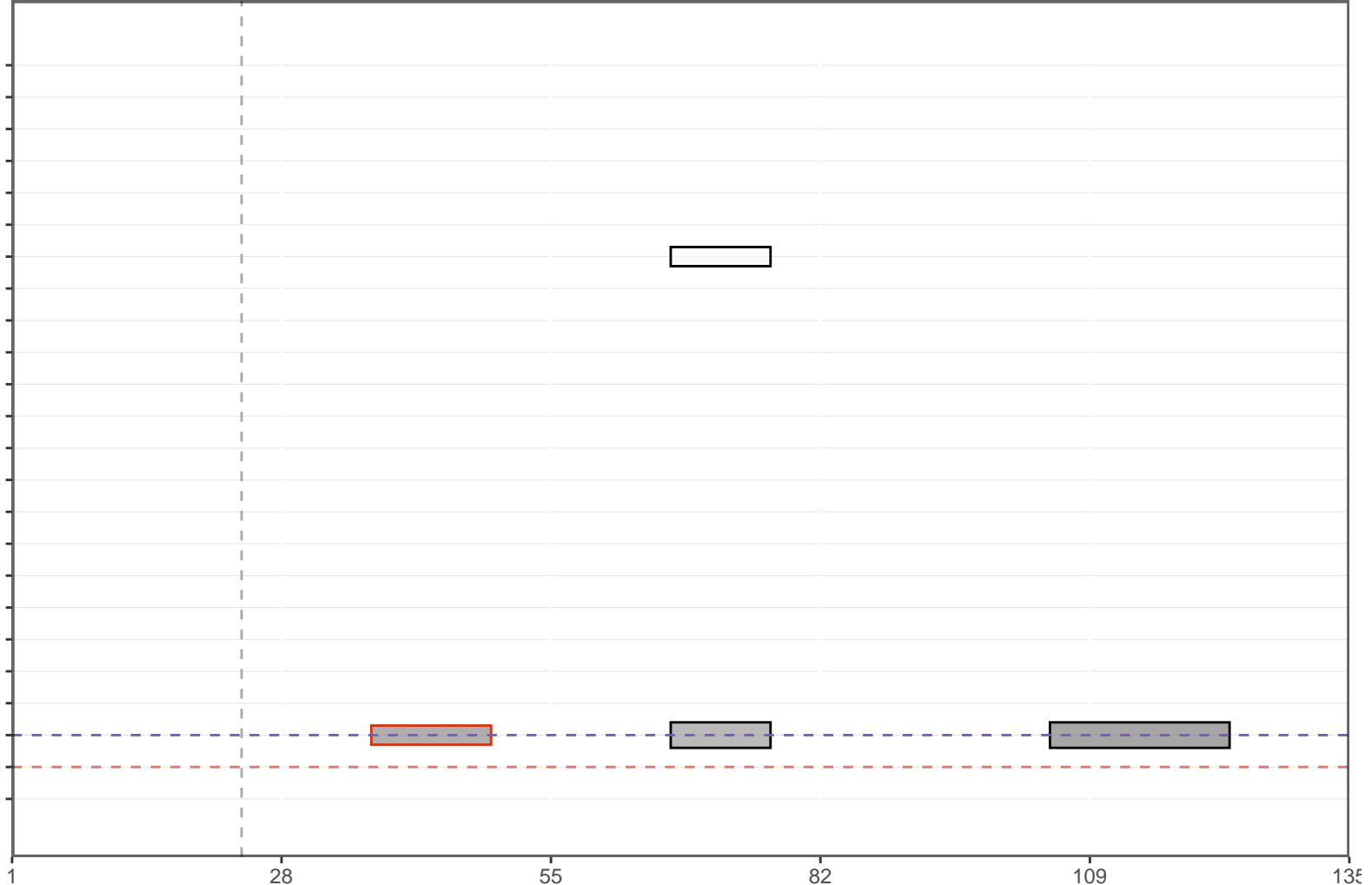
MW indication



Molecular weight

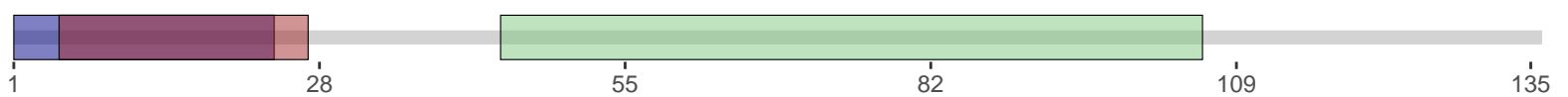


Gel Slice



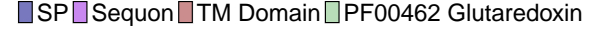
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IRKAKVFKELKOKPKFVVELDERDDGWSIQALSEVGRRTVPQVFNKIHGGSDDTVEAVENGELAKLLGLSANKDGL

NbL17g08820.1 cysteine-rich_receptor-like_protein_kinase_10 [MW - SP = 78.14 kDa]

No. of times detected



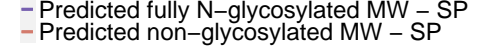
log(intensity)



Values from

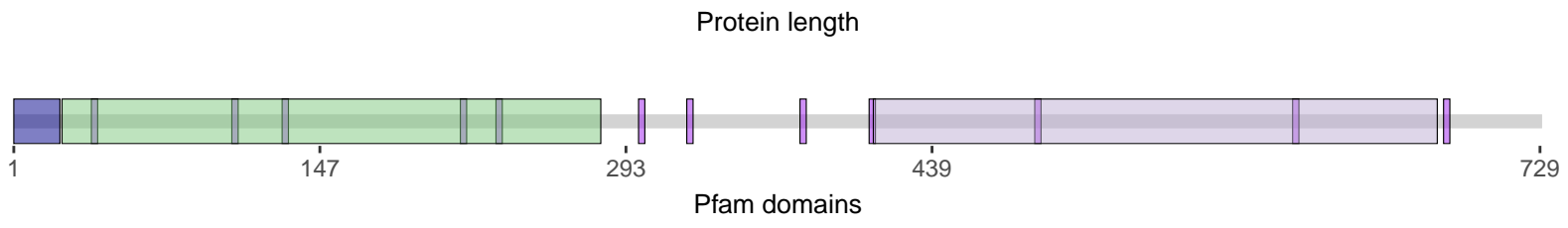
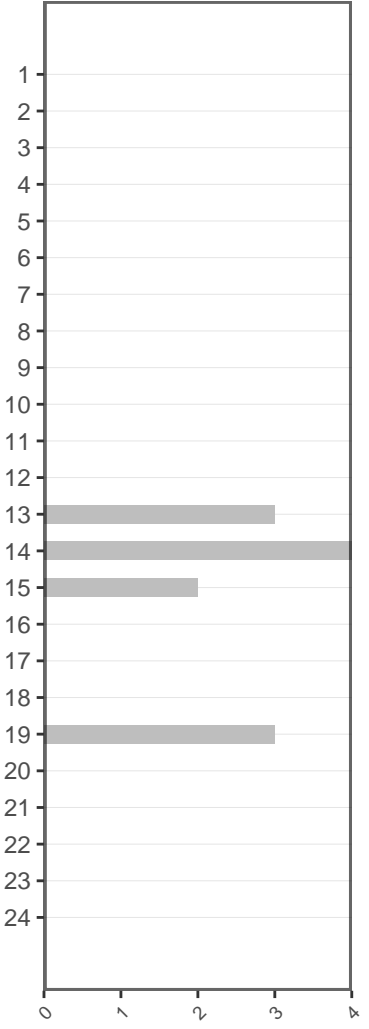
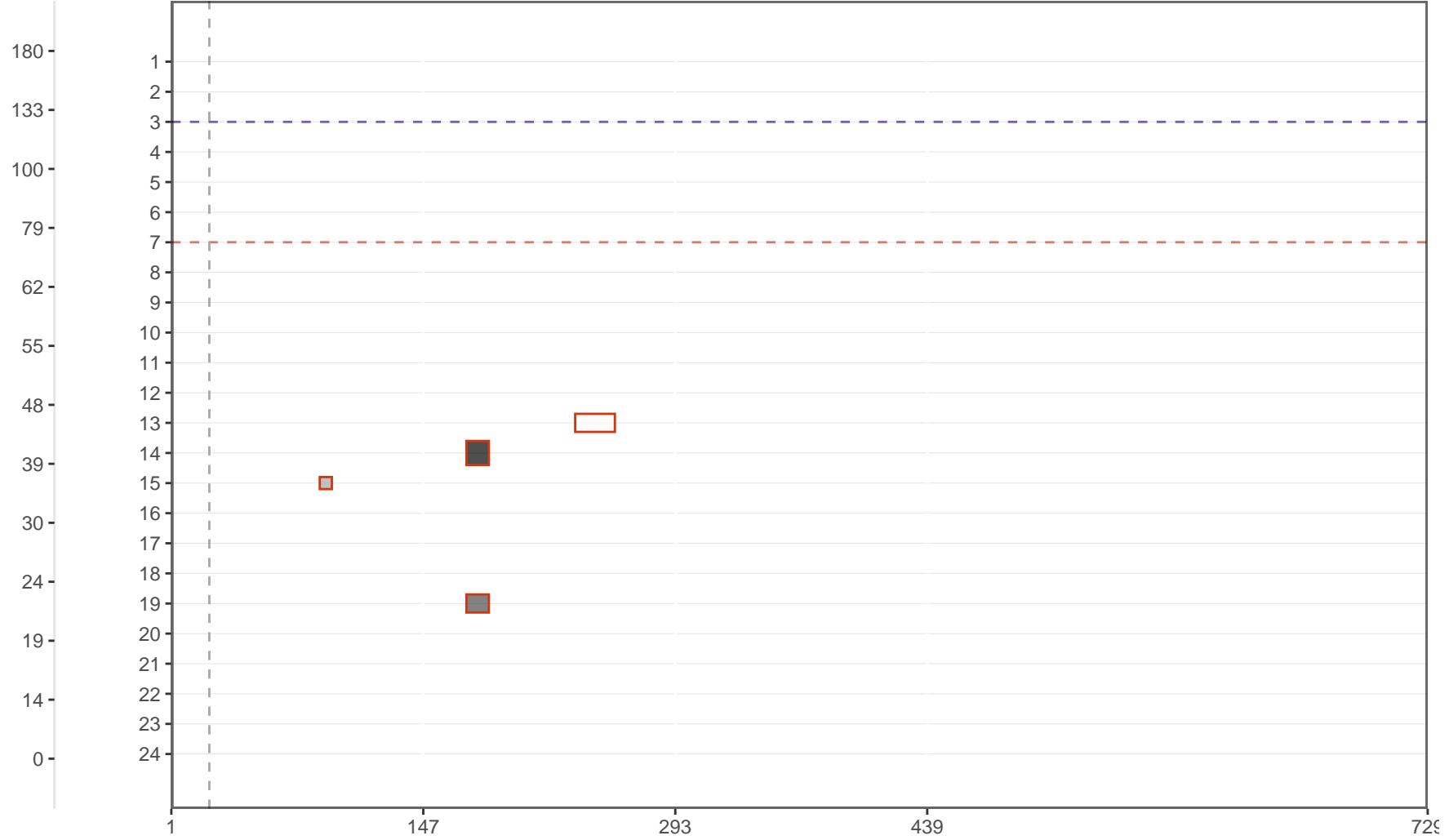


MW indication

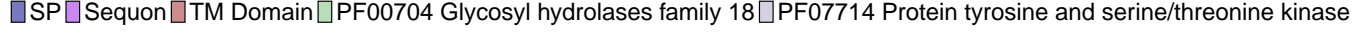


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

LSLSLCYLLLRKGGKAVTALLLLNGFTNRAARRRMDKMSSEEVQDFYFESLGIATNFSLGNKLGEGGFQPVYDQKFSDDGQVAKRLSTSSGGQVLEFRKNEILLAKLQHTNLRVLLGGVCTGQGEERVALVEYEMNKSLDFLLFDTKKERINWGTFRFRIEGWAGLLYLYKYSRLTVVHRDLKASNILLDNNMFKISDFGMARIFGGQGESEANTKRIVGTRGVMSPEYALRGIVSTKTDVFSFGVLLLEIVGKKNNSGVDSEHPLNLIGLAWELWREERALELLDGLTIESC

NbL17g08580.1 4-hydroxy-3-methylbut-2-en-1-yl_diphosphate_synthase_(ferredoxin)_chloroplastic [MW = 82.1 kDa]

No. of times detected



log(intensity)



Values from



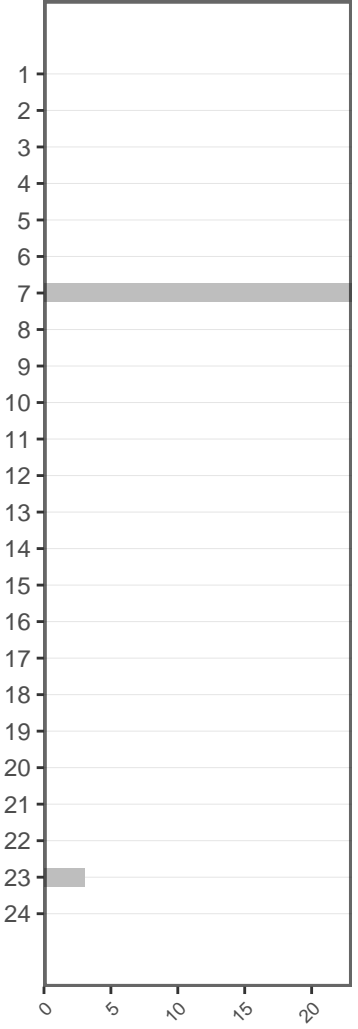
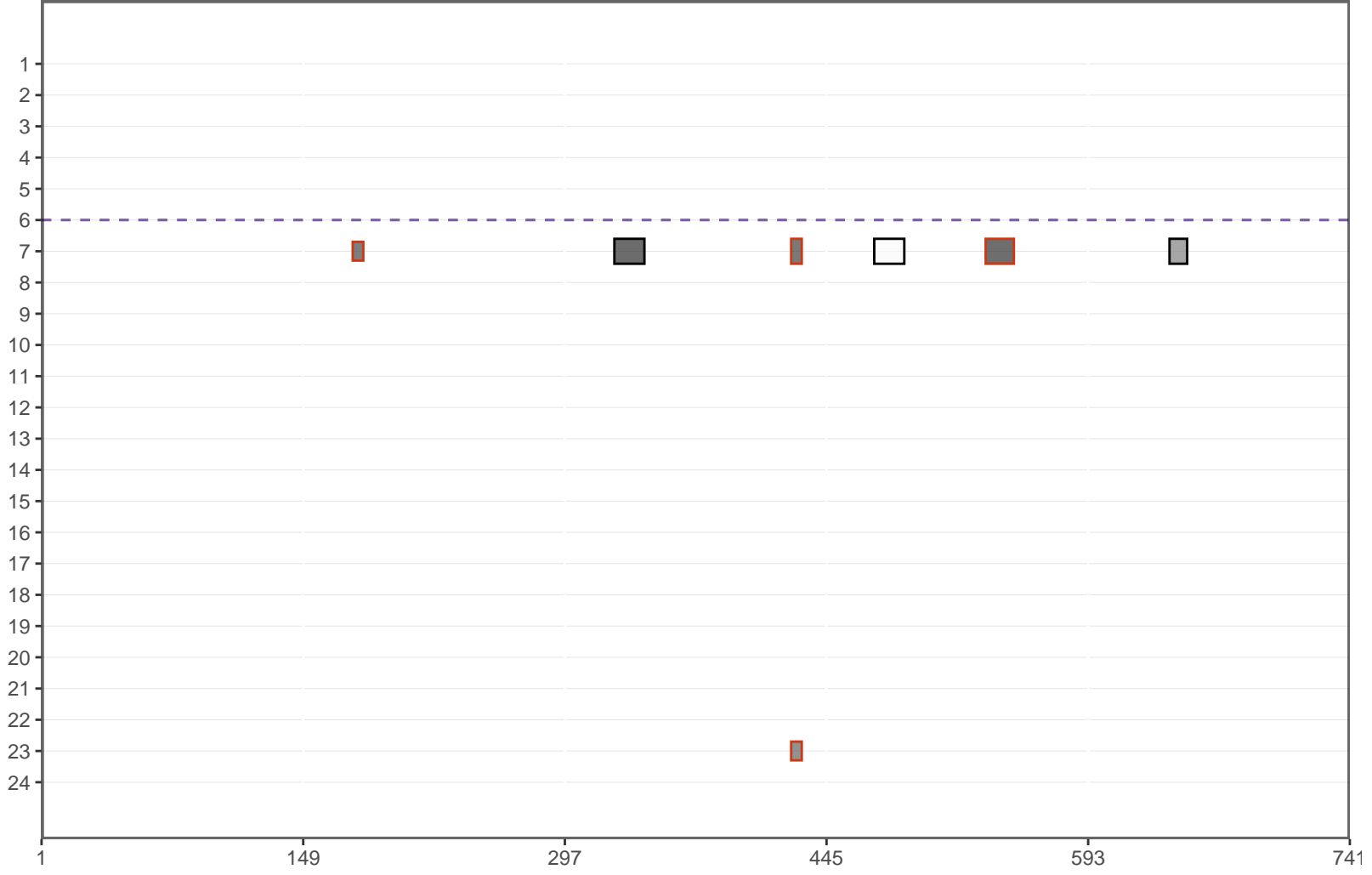
MW indication



Molecular weight



Gel Slice

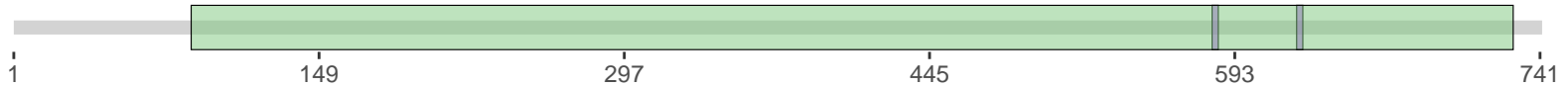


Protein length

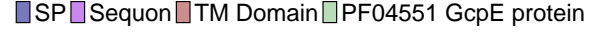


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

RLANLQKRAAEIQGGVAPFEENRVRVDFQRRSGELPMKKEGDEVYRGLVHRDGSVLMSEVLDQLKAPELLYRSLAAKLVGMPPFKDLATVDSLLRRLPPVDDKDRSLKRLVDSMDMGVITPLSEGLTKPLTNMVLVTLKELSGGAKLLPEGTRLVSVVRGDSKDELELKSTDTMLHLPLVTEEKGRVHAARRLFEVLSQNSLNFVPIHHHFFNDTHRDQLVIGAGANAGALLVDLGDGILLEAPDQDFDFLNRFSNLLGGCRMRNTRKTEYVSCPCSCRTLF

NbL17g08320.1 isovaleryl-CoA_dehydrogenase_mitochondrial [MW = 48.67 kDa]

No. of times detected



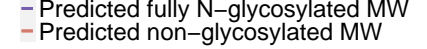
log(intensity)



Values from



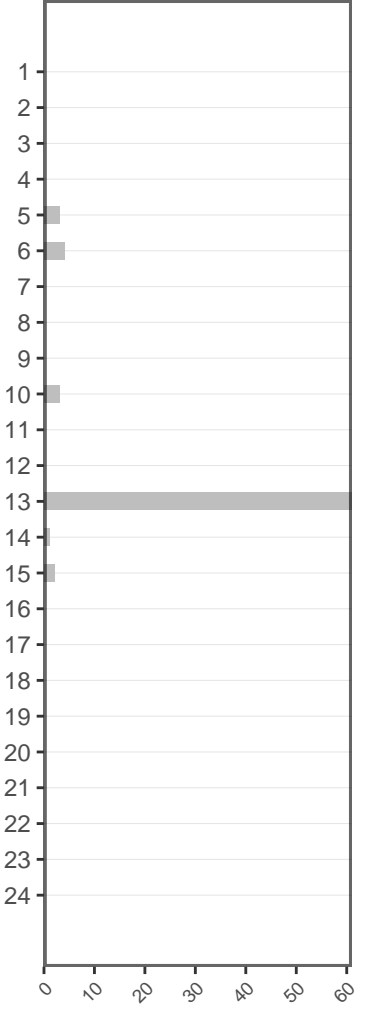
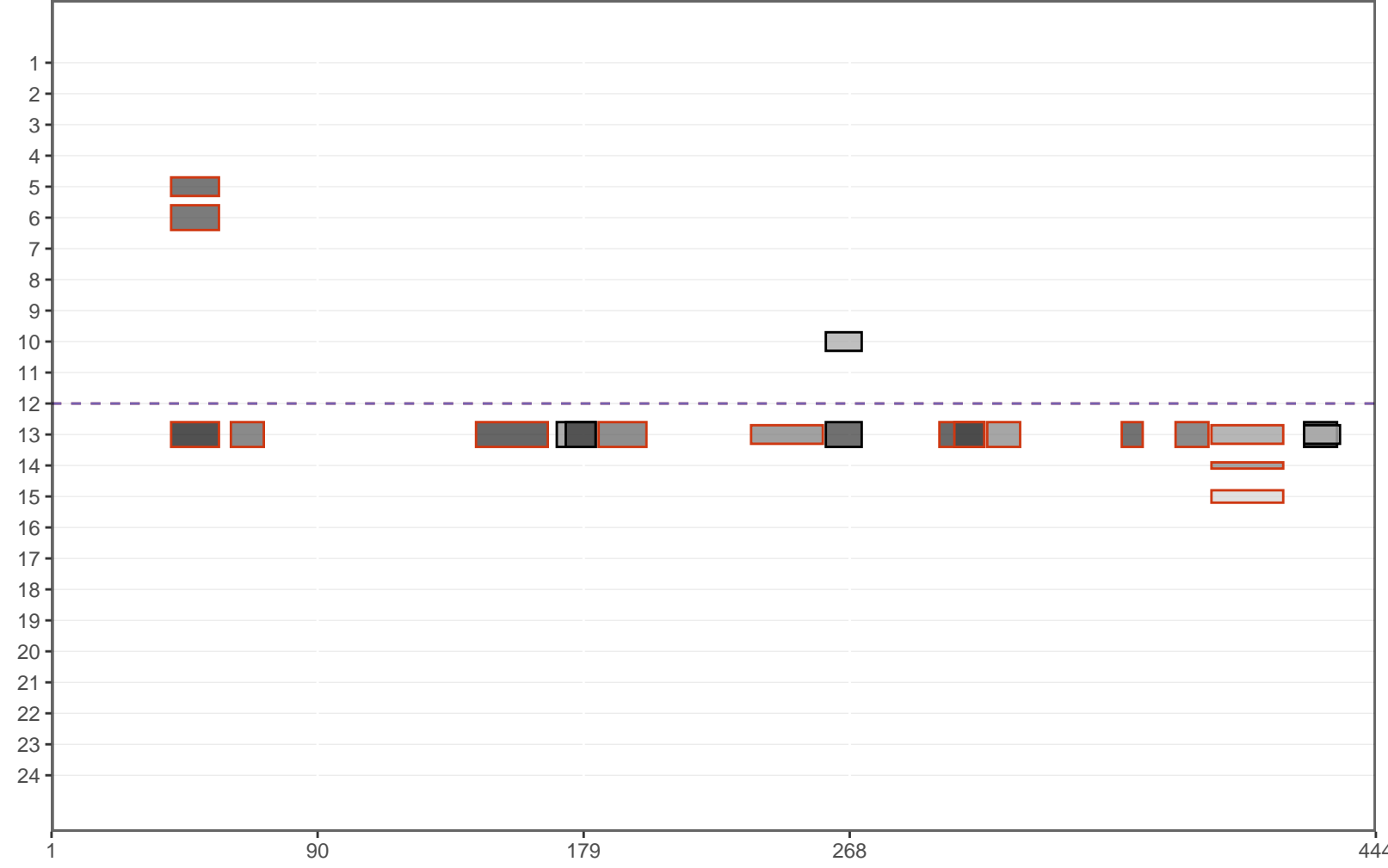
MW indication



Molecular weight

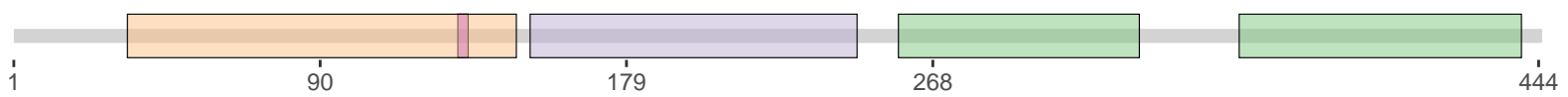


Gel Slice



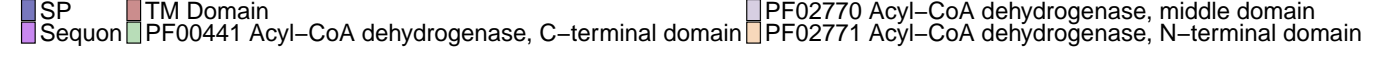
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISKGITAFIEIKGMKGFSTAGKLDKLGMRGSDTGEVFNFCFPEENLGGVYKGVVYVMSGLDLERLVLSGGPKVGLMGAGLKVLPVYKGRGFGFRPGEFGFQDKKADMYTSLGSSRSGLVCHTSSISFSLFLINNFMYLFFVFNHRAVYVSWAREGDSGNNTKDCAGVLAERATQVALGAVDGLGGNGYVNEYPTGRLLRDAKLVKAGTSEIRRMIGRELKPEQ

NbL17g08300.1 proteasome_subunit_beta_type-4-like [MW = 27.66 kDa]

No. of times detected



log(intensity)



Values from



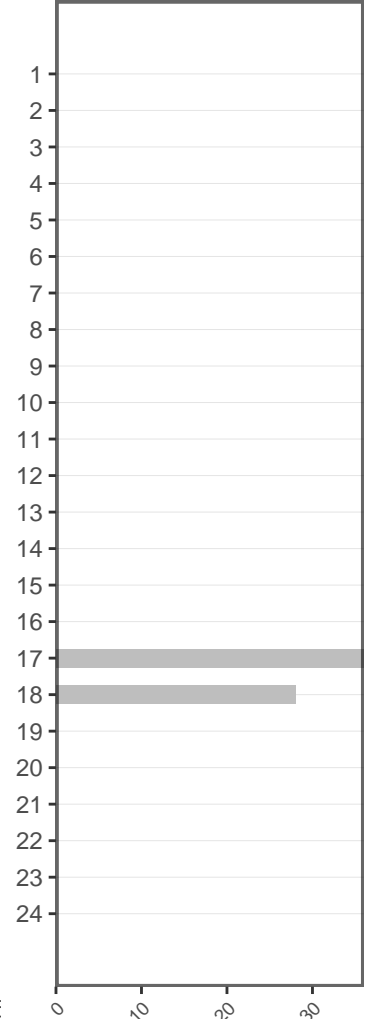
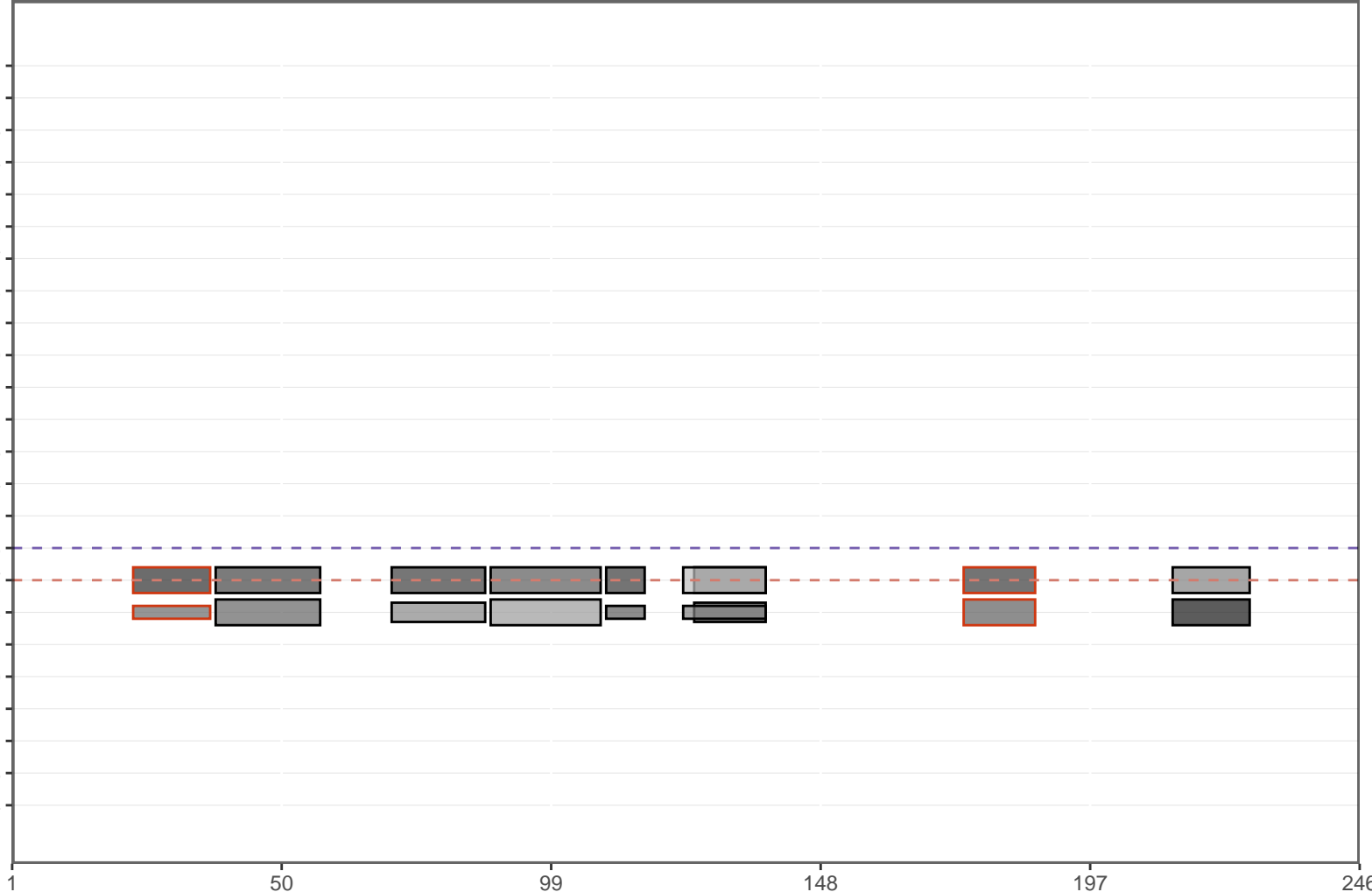
MW indication



Molecular weight

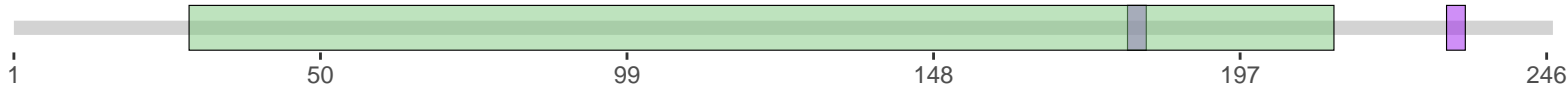


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

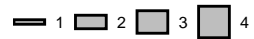


Protein sequence:

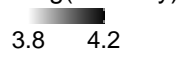
INLTLRMYYNRRNKNFPLWNLVLGGVKNQKYLGTVMIGVHYEDDHVATFGFNHLARPLREEWHENLVEEGVLLLEKCMRVLVYRDRSAVNLGIAKITEEGVTVSGPYSKTFVWNSAFQNPITVGAEGSW

NbL17g08290.1 ABC_transporter_F_family_member_1-like [MW = 67.48 kDa]

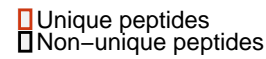
No. of times detected



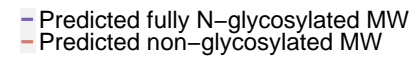
log(intensity)



Values from



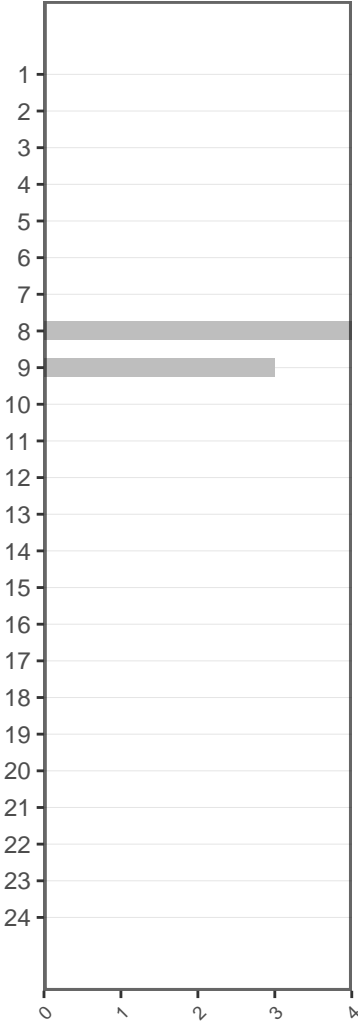
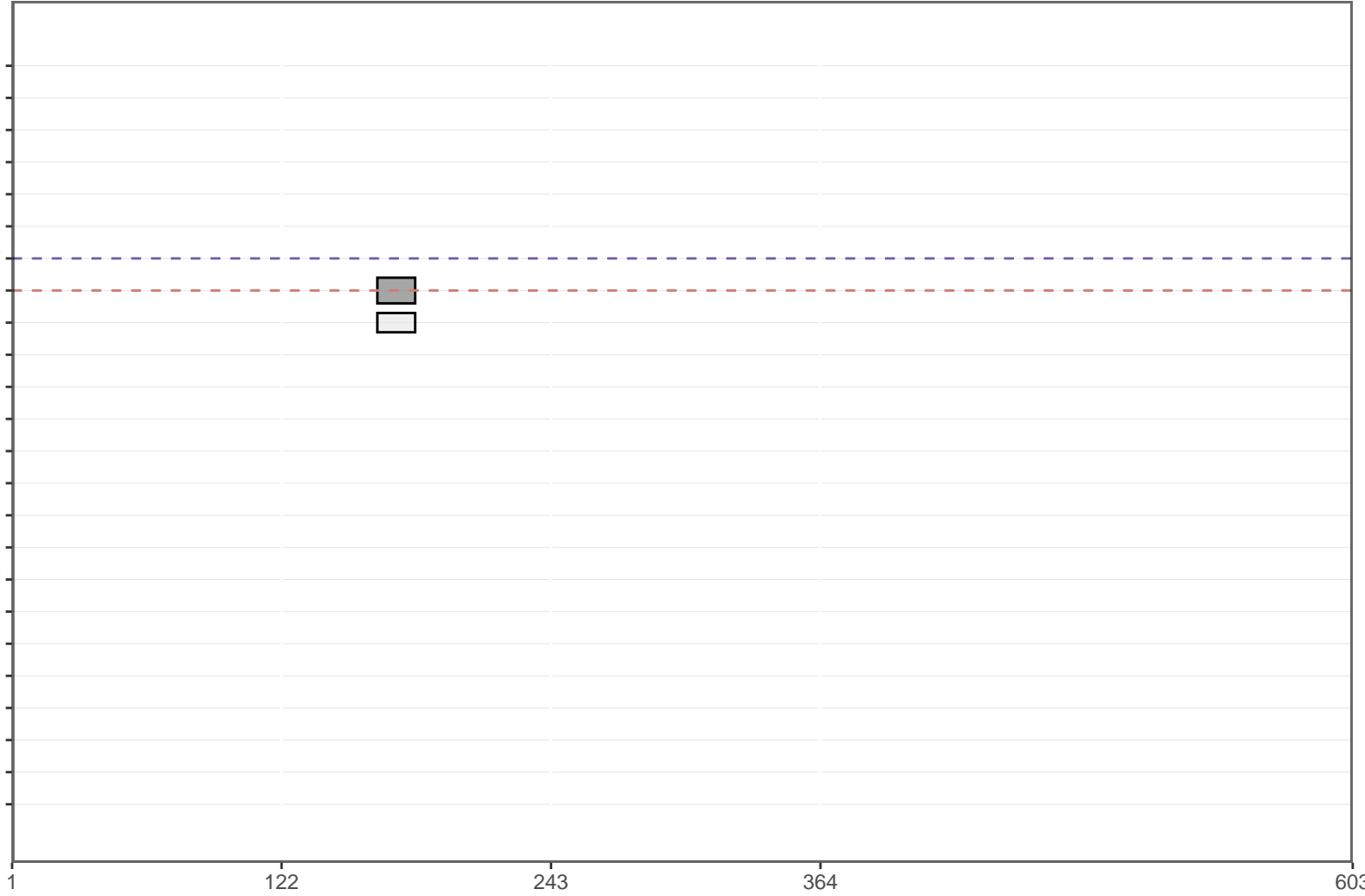
MW indication



Molecular weight

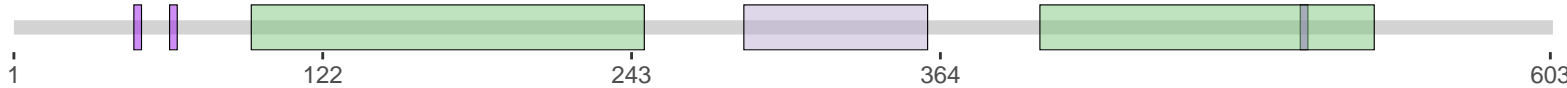


Gel Slice



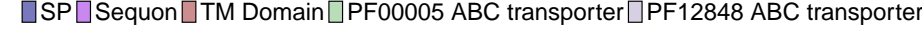
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KKLKYLTGNYDQYVGRSELEENGMQYKWEQEGIASMKEYARFGHGSAKLARGAGSKEKTLAMMERGGLTGKVSGRDSVLFVRFDTVGLKPPVLFQSEVAFGVTPELHYKSLDFGVDLDSRIALVSPNGACKSTLLKLMIGDLFFPTDGMVKRHNLKIAQVHGHLEAKLDMDSALGYMMREYPPGNEEEKMRAAIGRFGLTGKAGVMAAMKNSDGGRRSRVFAWLAVRQPHMLLDEPTNHLDIETIDLAELNEWDGGMVLSHDFRLNGVAHEIWCENQAV

NbL17g08240.1 4-coumarate--CoA_ligase-like_7 [MW = 58.9 kDa]

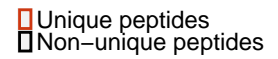
No. of times detected



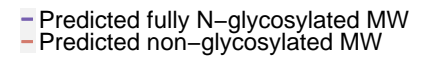
log(intensity)



Values from

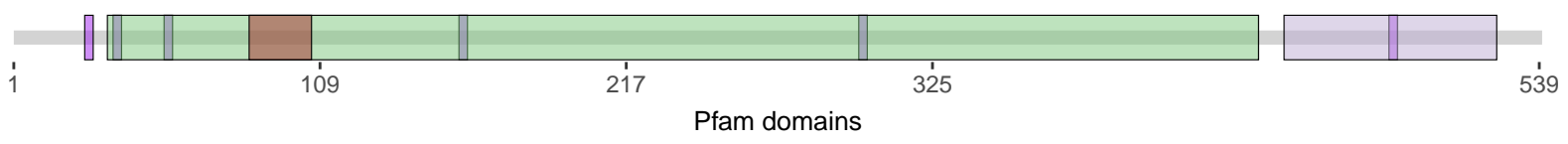
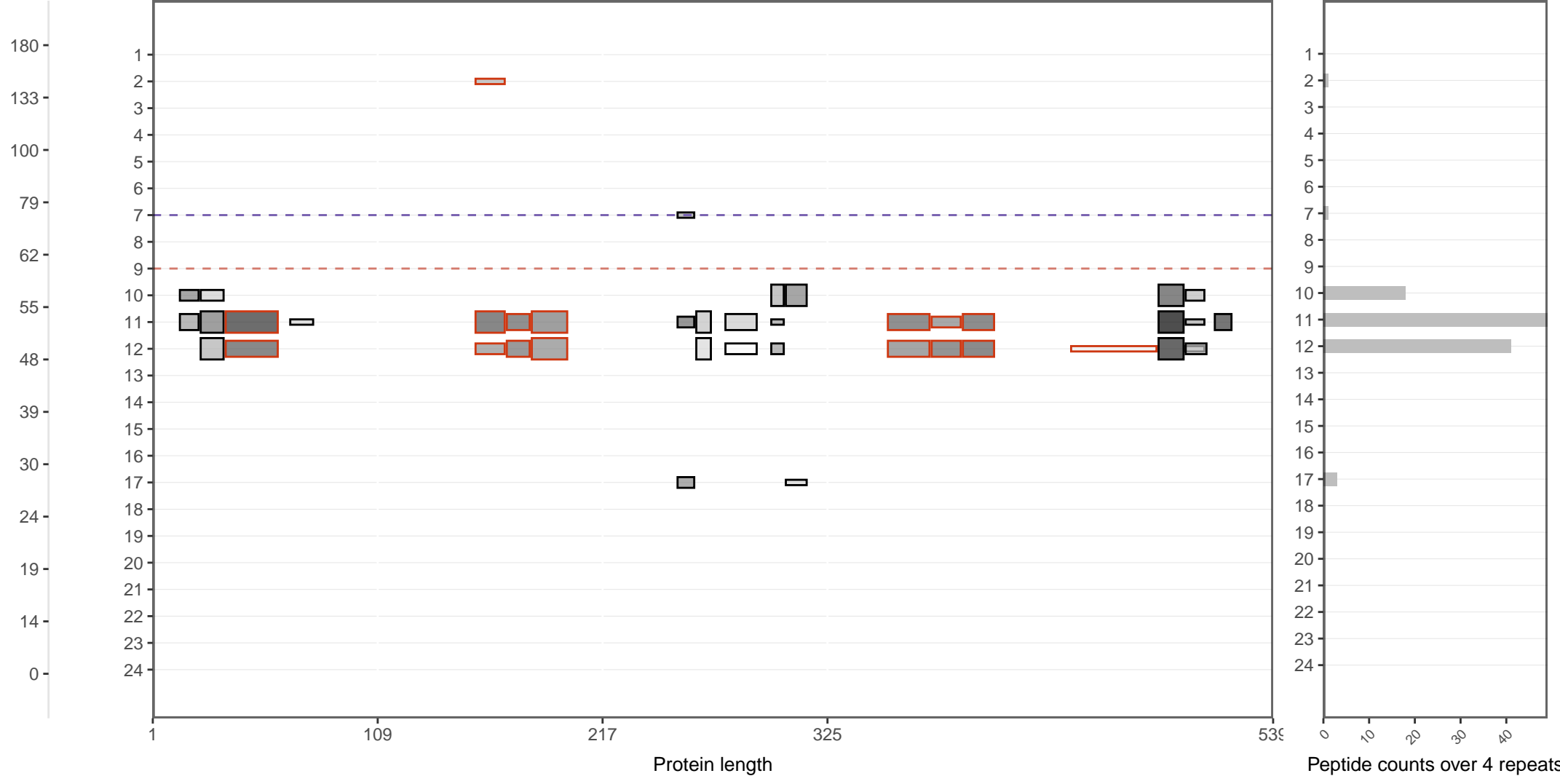


MW indication

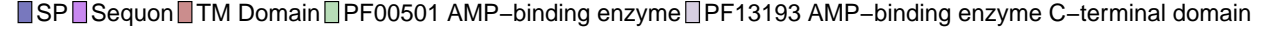


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

MAKFDLEMLKSVDRKRVTHLWVPPVLAALANPVRKYNLSTLRNIGSGAAPLGHKELMEEGAKNFPQVVVLOGYGMETETGIVWESPVYGRPHRTGAGTLVPGVEAGIVSDVKLKLPTPGDGLGEWVFRPNIMQGYFNPNPQATKLTIDNGGIVVHTGDLYFDEEGMLVYVDRKELRKYKGFQVAPAELEGLVSHPELDAVWIFPDAGEVPGHVVVRSFNSLSTEEQVQKFIADQVAPFKRLKRVTFVNSVPKSASGKLRRELIKVRKSL--

NbL17g08190.1 T-complex_protein_1_subunit_beta-like [MW = 57.01 kDa]

No. of times detected



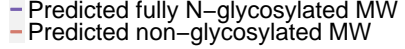
log(intensity)



Values from



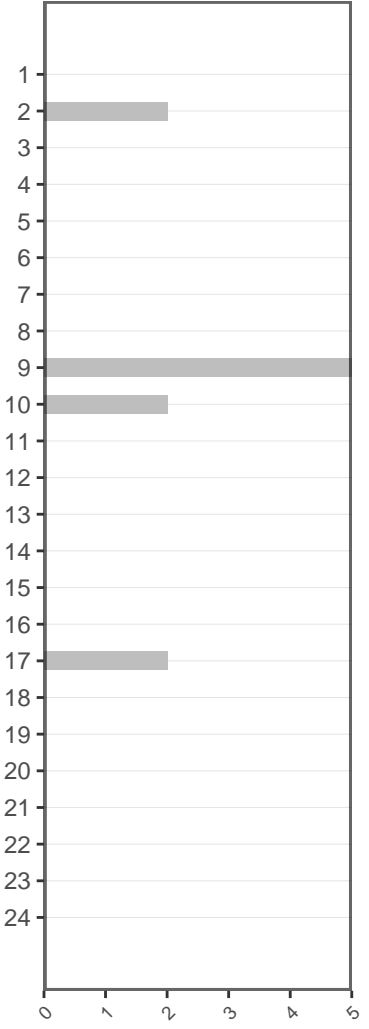
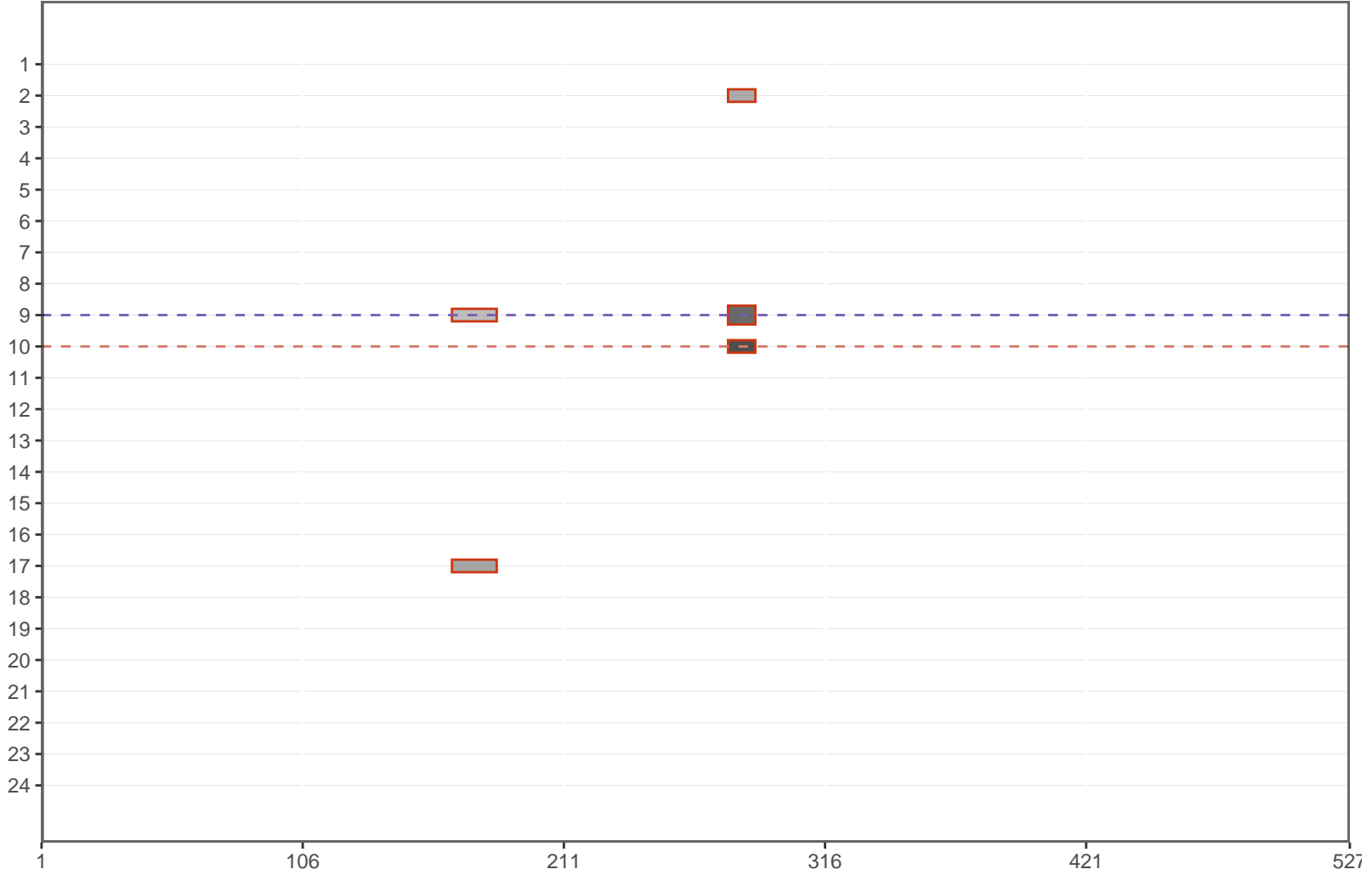
MW indication



Molecular weight

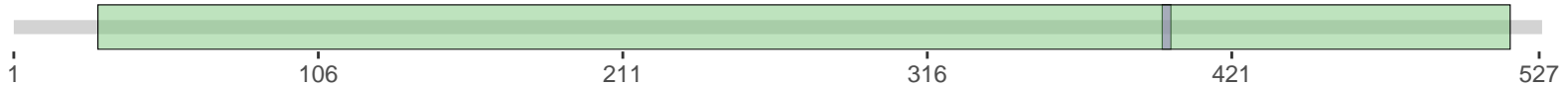


Gel Slice



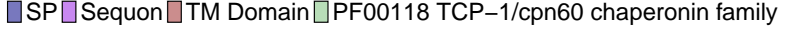
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

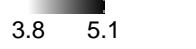
/R/VSMAKVALDEAAEKEMREKVKQKHSHGYNCFVNRQLVNFPEELFADAGLAEHADFDSGERLGLVTGGAEASTFDNPESVKLGHKQLEEMIGEDKLIHFGSGVEMGQAQCTVLRGASPHYLDEAERSLHDALGVLSGTVNDSDRVLVGGGWPEMVMMAKAVDELAKKTPGRSHAEAFTRALLAIPPTIDNAGLDSAEHLAQLRAEHLKKEESNAGIDVHSGVGMALGISESFKYKQAVLLSATEAAEMILRVDEITCAPRRREGM

NbL17g08130.1 xyloglucan_endotransglucosylase/hydrolase_protein_31-like [MW = 42.3 kDa]

No. of times detected



log(intensity)



Values from



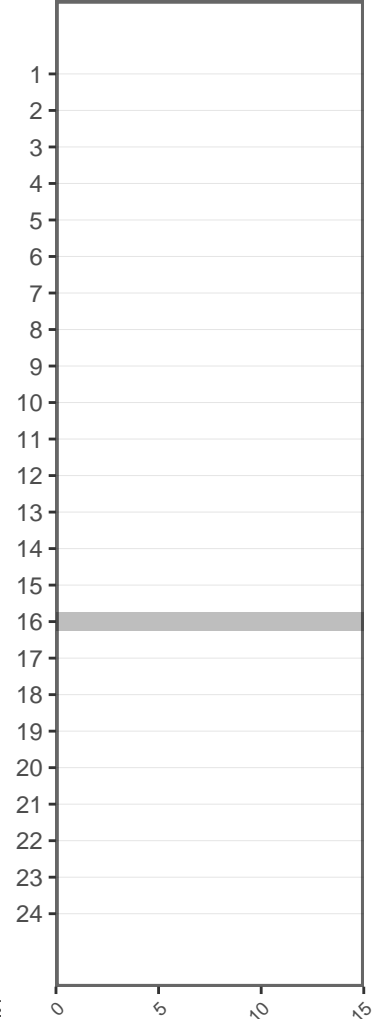
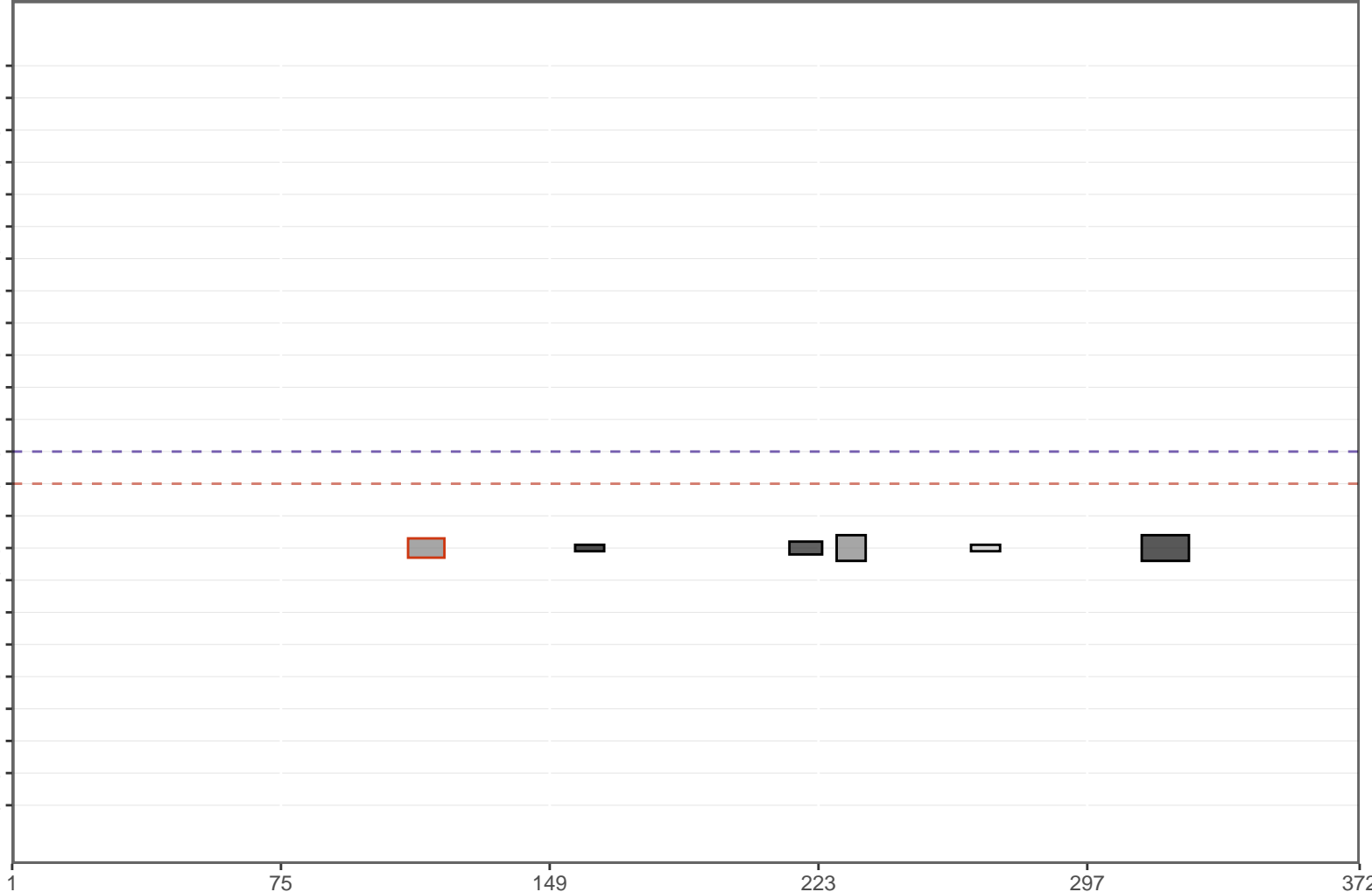
MW indication



Molecular weight

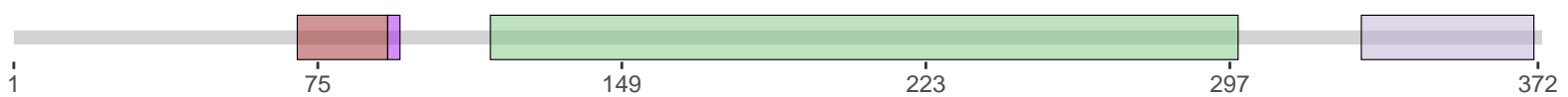


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00722 Glycosyl hydrolases family 16
- PF06955 Xyloglucan endo-transglycosylase (XET) C-terminus

Protein sequence:

IFYLSNQDYPGNHDEIDIEFLGTFPKPKYFLQTNVYIRGSGDGNIGREMPLHLWFDPTKAHNVAIWDNPEIFFVDQVPIRIRYPRKNDATFPQRFMYVYGSWDSBSEWATEEGRKADRYVQFFVQKYNFKIAGCTANENPWGSRPSGSPRAGGLSRQQAAMLVWGRNKKYVQVCRDPRRDHTHTPEQ

NbL17g07970.1 superoxide_dismutase_[Cu-Zn]_chloroplastic [MW = 29.56 kDa]

No. of times detected



log(intensity)



Values from



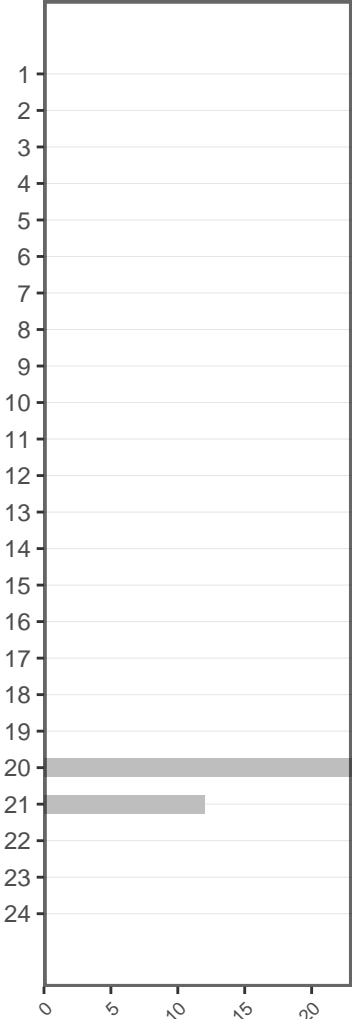
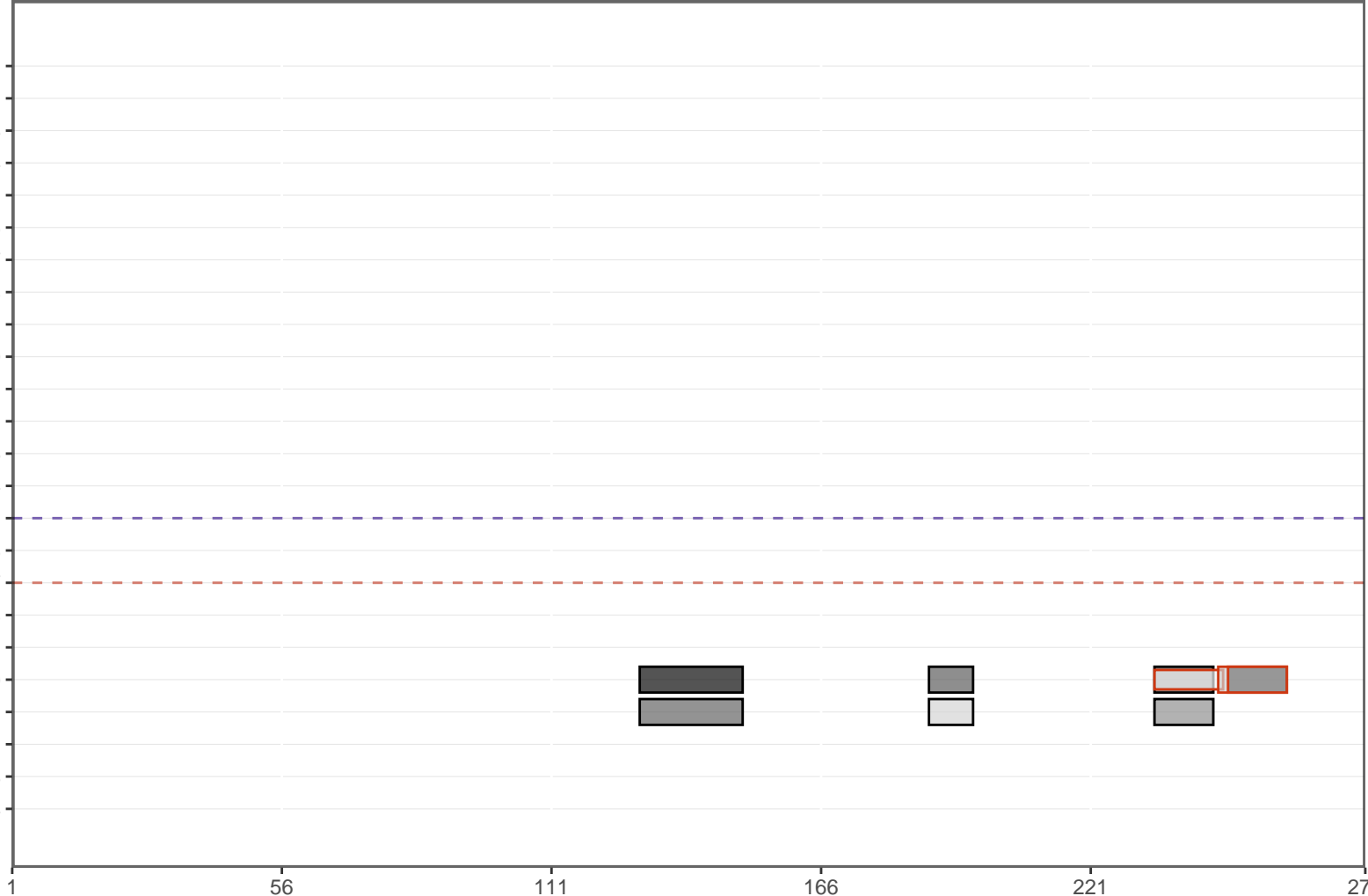
MW indication



Molecular weight

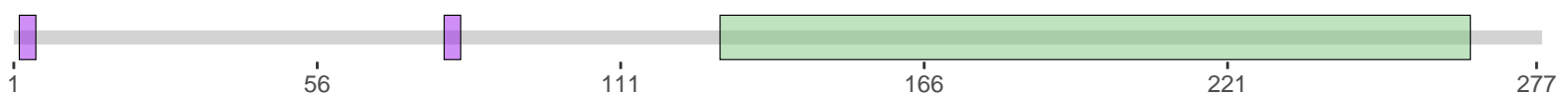


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

NSNVEGVTLSDQDDGGPTTKVRRIFGLTGLHGFHLHEYGDFTNGCMSTGPHFNPDGKTHGAPEDERIRHAGDLGNVANADGVAEATVVDNGIPLVGNPSVWGRALVHLELEDLKGKRGHLSLFTGNAGGRLAGDGKHTWFDENMK

NbL17g07960.1 50S_ribosomal_protein_L9_chloroplastic [MW = 21.64 kDa]

No. of times detected



log(intensity)



Values from



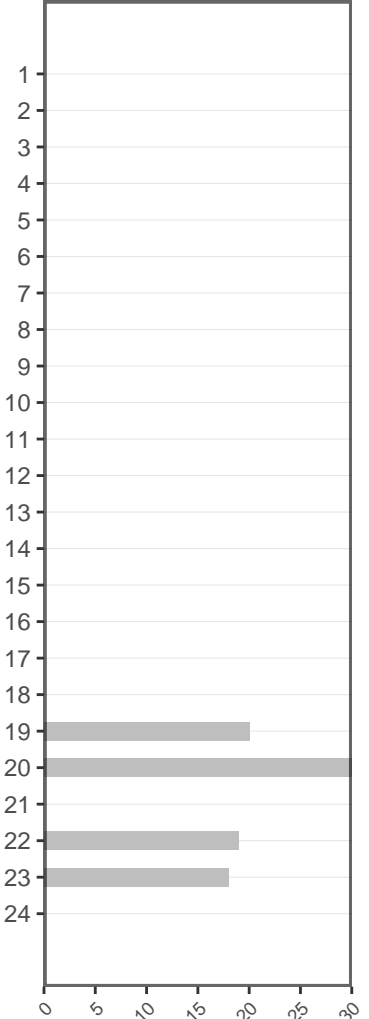
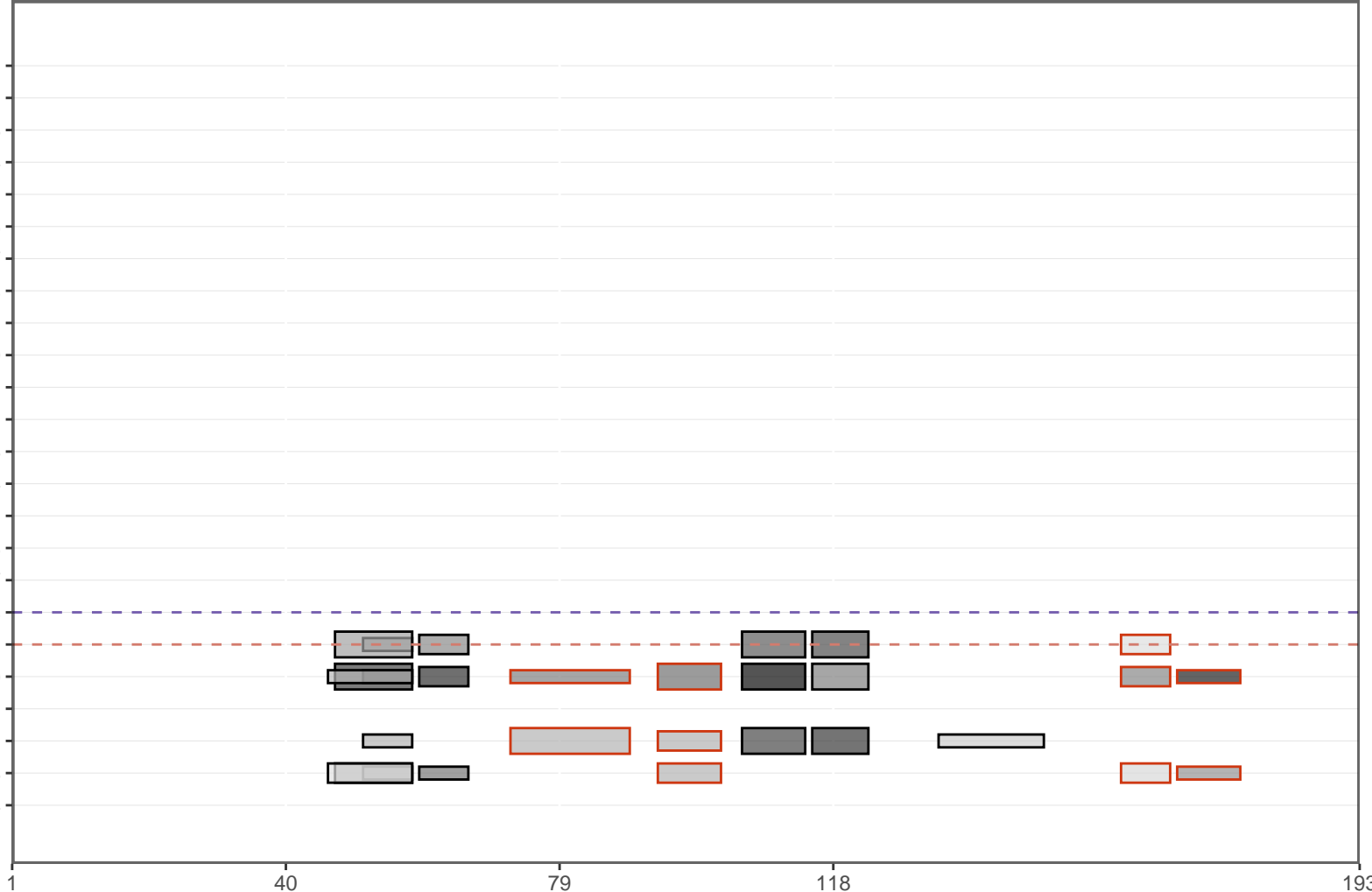
MW indication



Molecular weight



Gel Slice



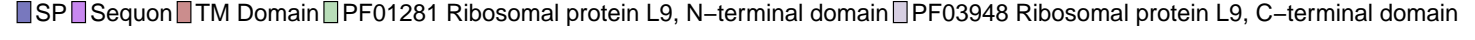
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PTLLKEMKMEDEIEAEKGRVKEEALQLARIFETVGAFAKVKRKGKGGKGFQGVTAQDLVDIKAGLQREVDKIKVYVPEIRETGEVVAELKLGQVTRARLRFVFN

NbL17g07940.1 histone_H2B-like [MW = 16.03 kDa]

No. of times detected



log(intensity)



Values from



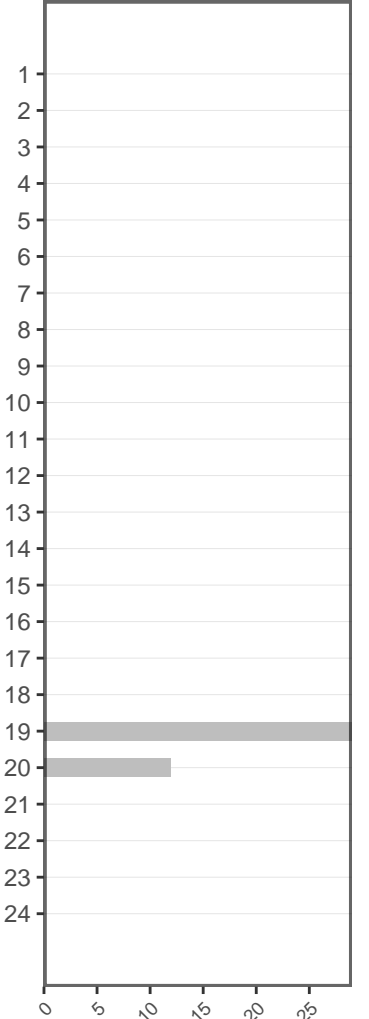
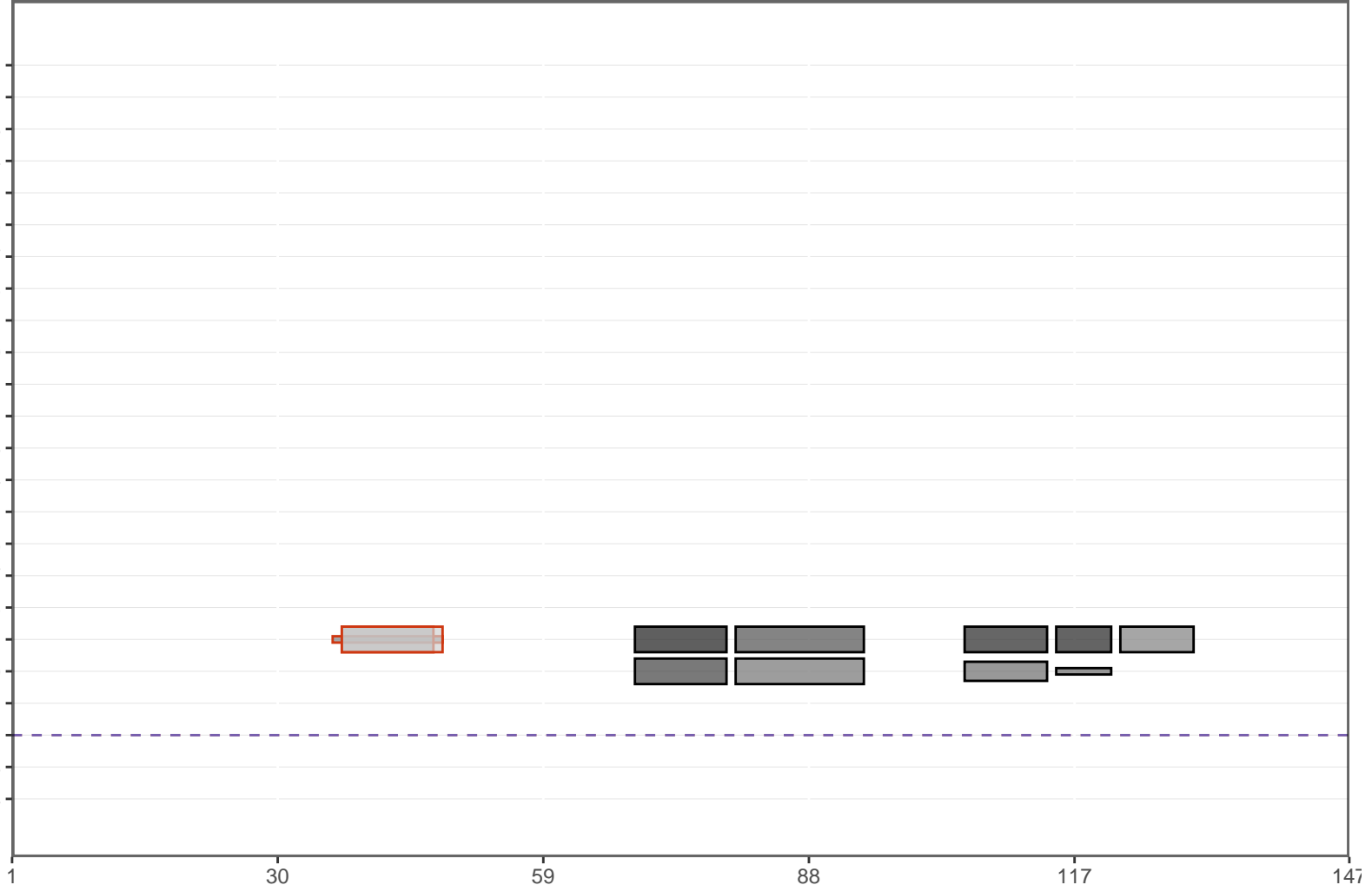
MW indication



Molecular weight

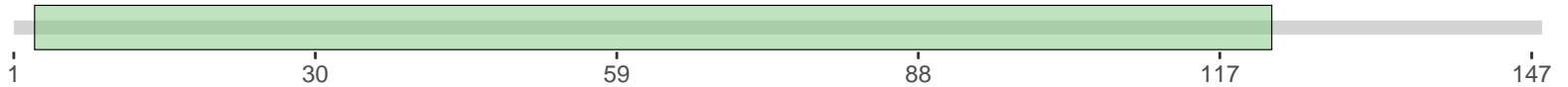


Gel Slice



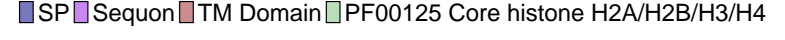
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TKYIKYFKVLLKQVYIPDGISSKAMGMSINFSINDIFEKLAGESRLRLARYNKKPITTSREKGTAVRLVLPSELAKHVAVEGSKAVTKTFSQ

NbL17g07830.1 aspartic_proteinase-like_protein_2 [MW = 32.86 kDa]

No. of times detected



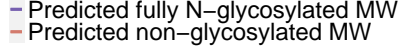
log(intensity)



Values from



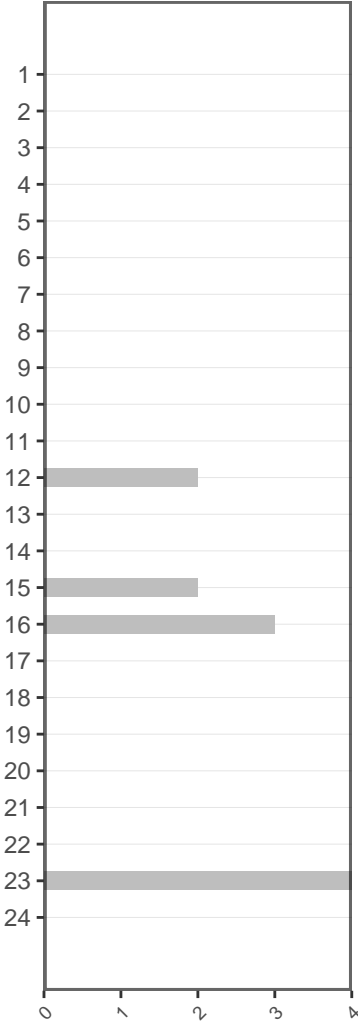
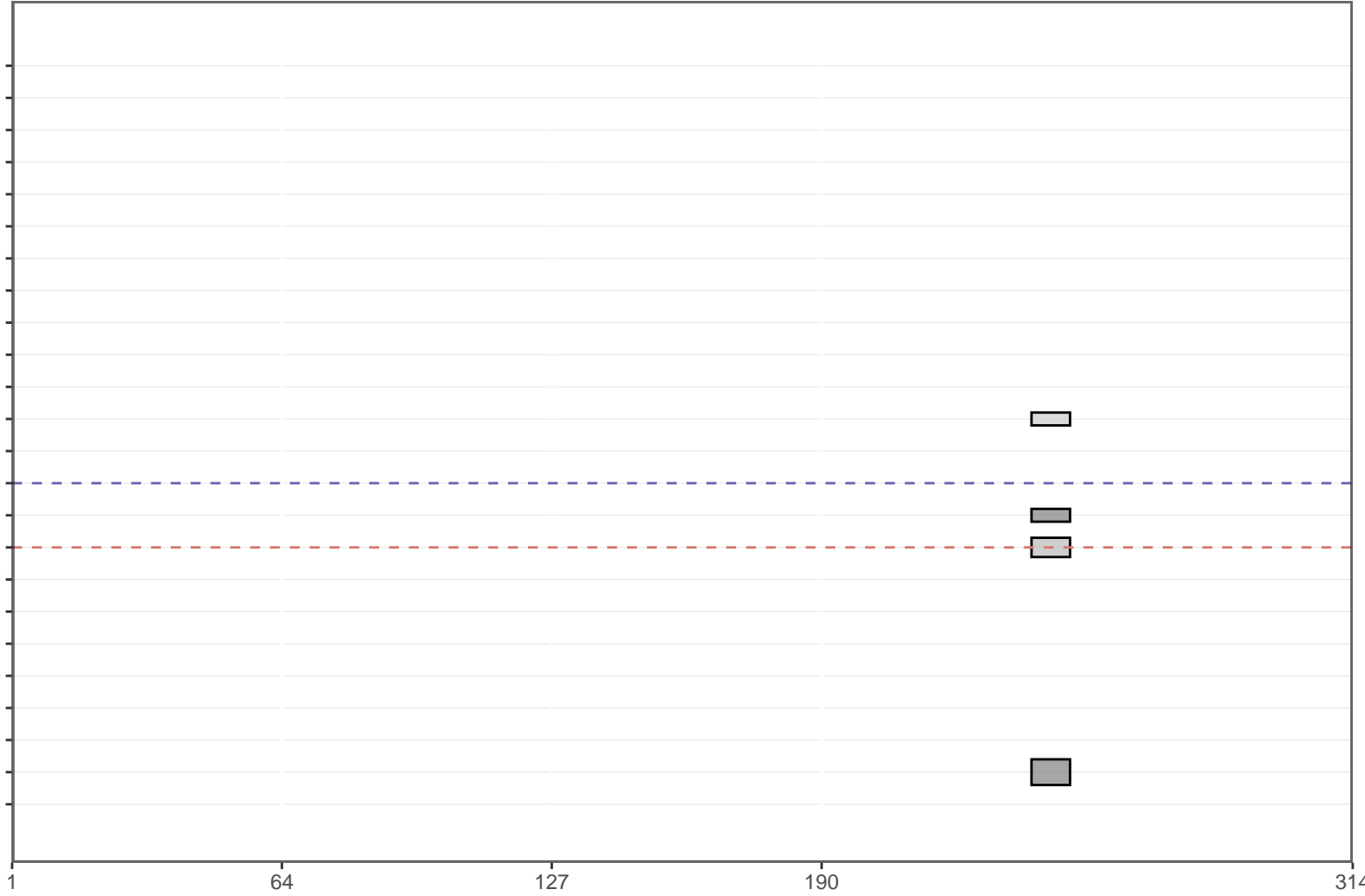
MW indication



Molecular weight



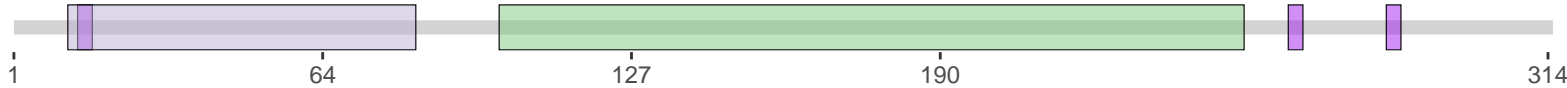
Gel Slice



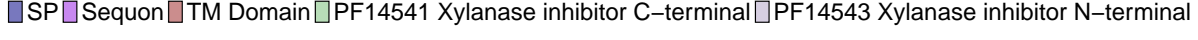
Protein length



Pfam domains



Pfam Description

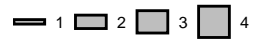


Protein sequence:

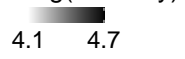
IEAYDFPFINANQAVSQNVRPLVTKNGCYLFTS6VGDFFPTVSLTFAGGATMVL6AADVLQGN6GGAAVWGMGFKIPGGGLTLDGLVLDKNIIVYDLAGGRVGVWVNYDGG6AVNV6ATT6RGTTEYVWAGQIGNNS6PG6D6YKLLLSFILT6VLHVLV6RGTNS6

NbL17g07680.1 UDP-D-apiose/UDP-D-xylose_synthase_2 [MW = 43.48 kDa]

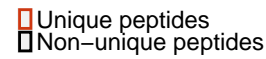
No. of times detected



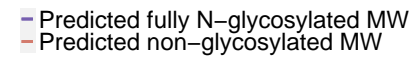
log(intensity)



Values from



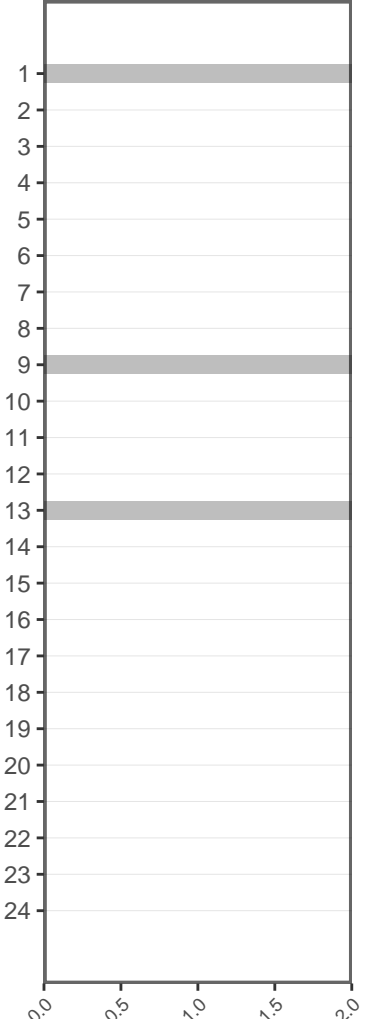
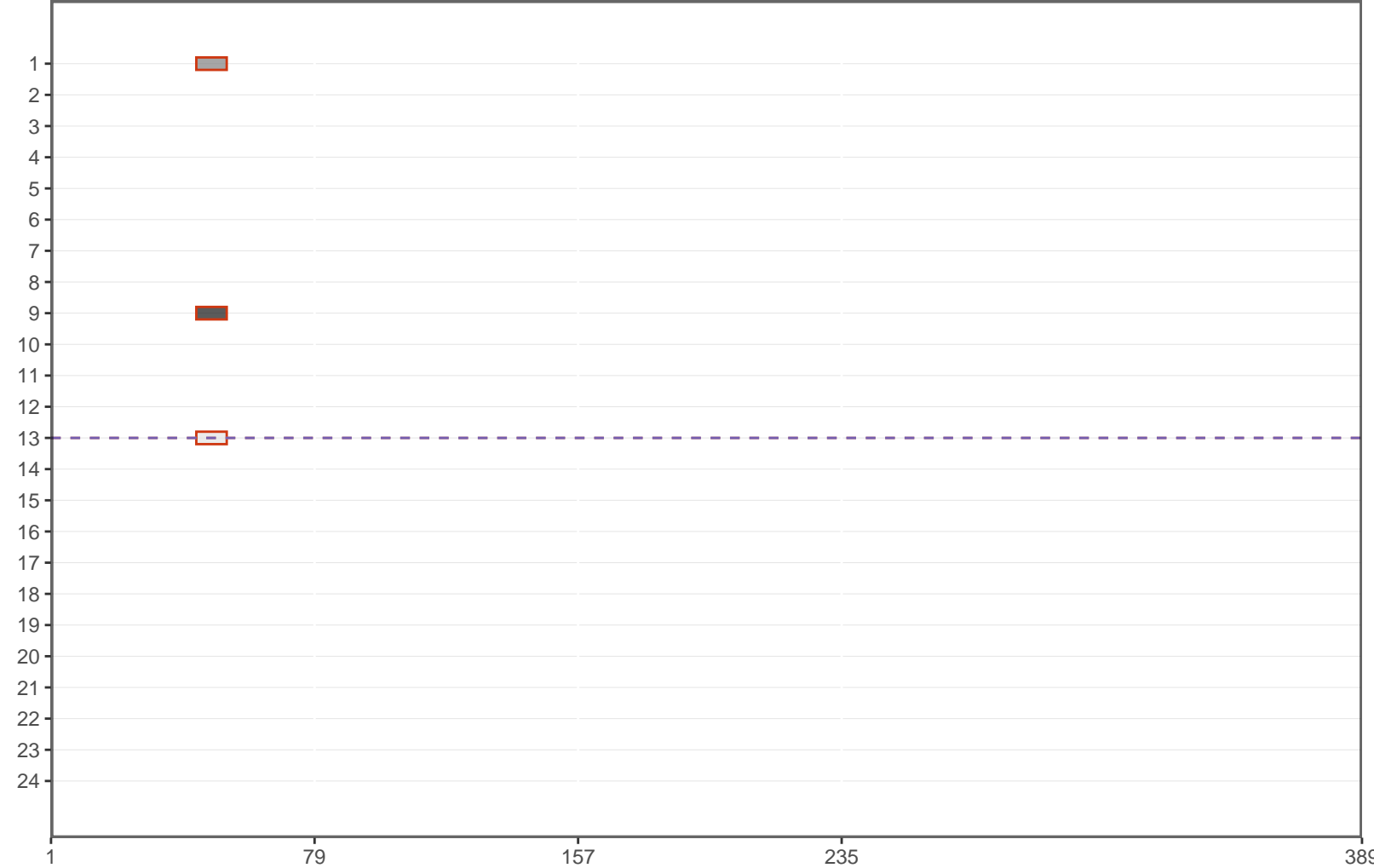
MW indication



Molecular weight

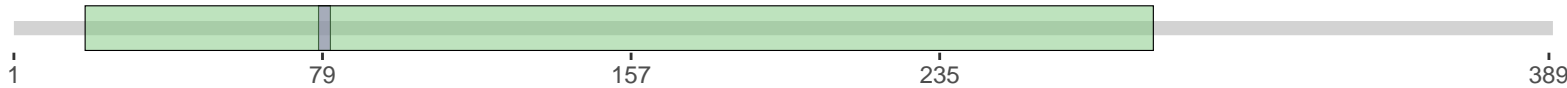


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

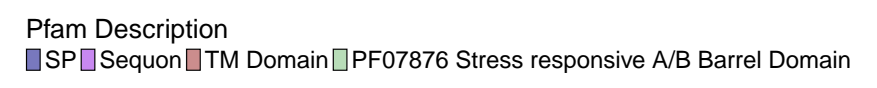
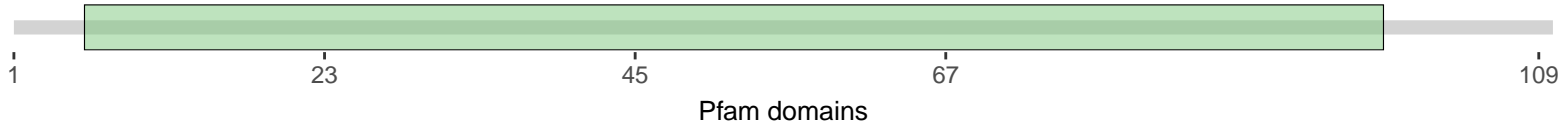
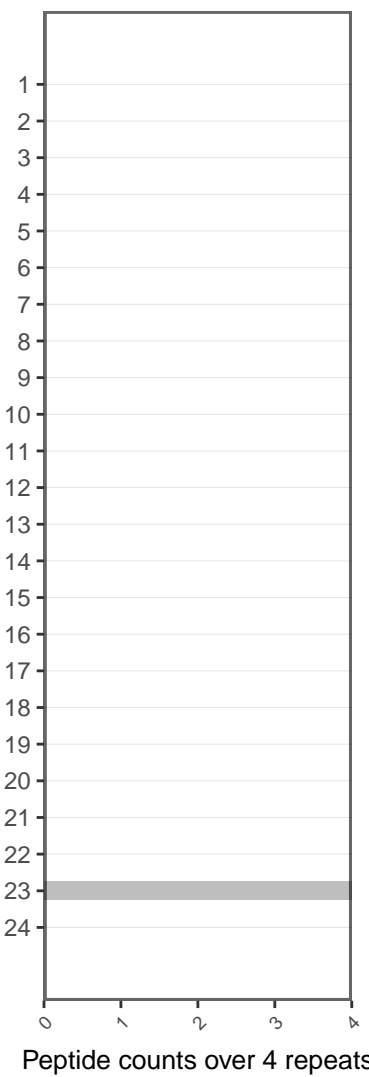
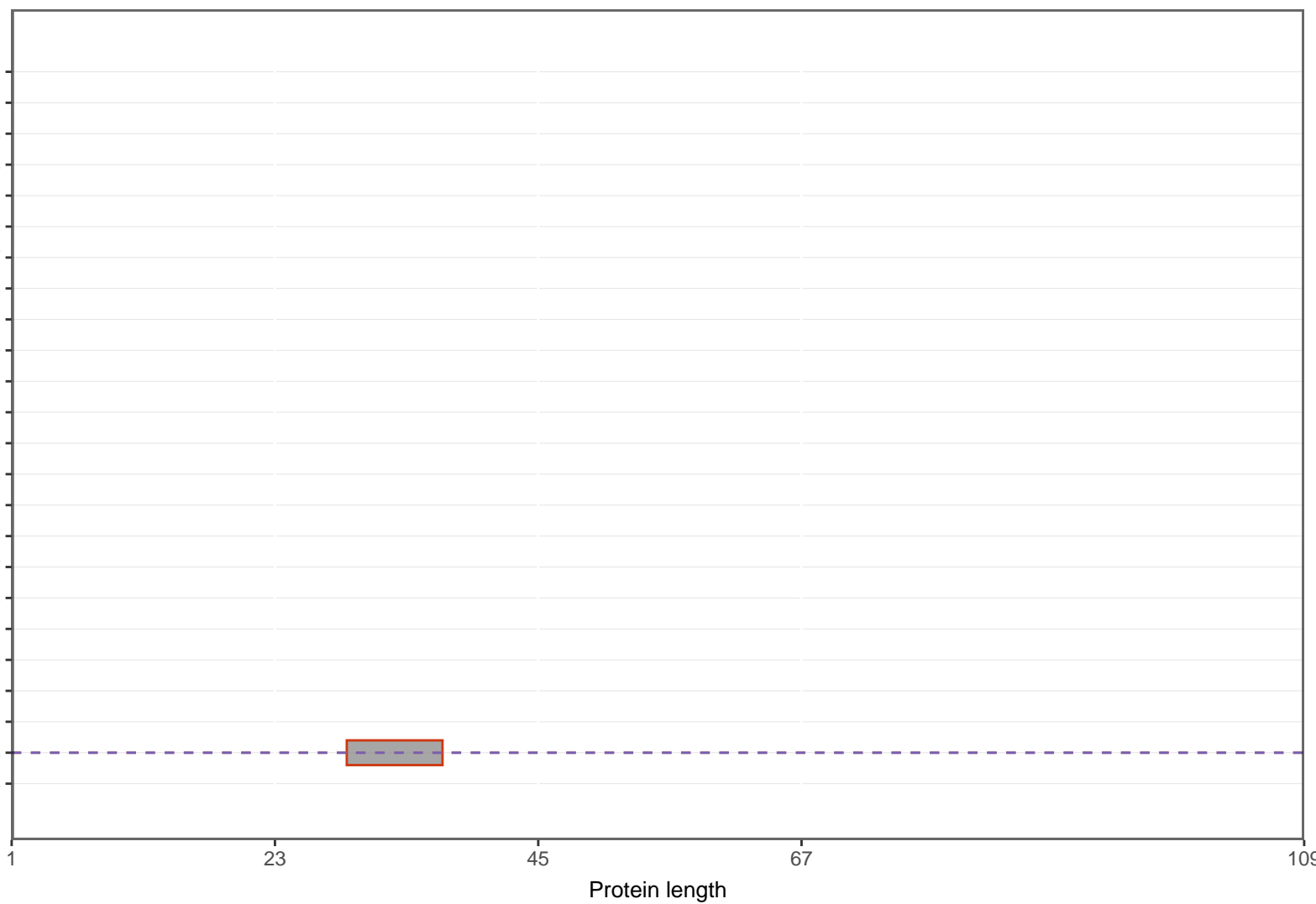
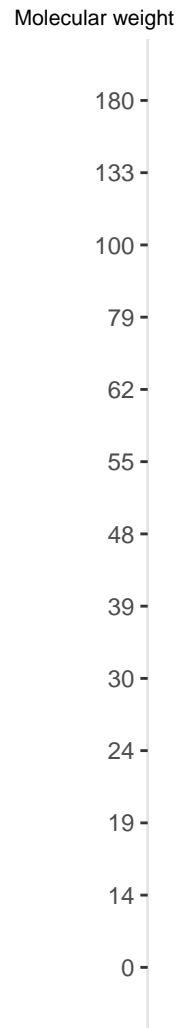
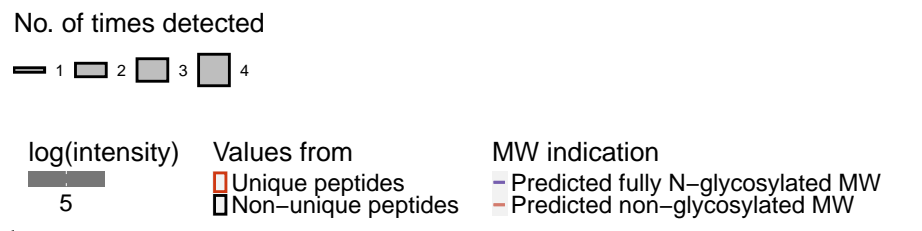
Pfam Description



Protein sequence:

YVACAKQLERLVFAEGAENGLEFTRPFWNIGRPMDFIPGIDGPGSEGVPRVLAGFSNLFRRPEPLKLVDDGESQRTFYVKDIEAVLLMIENPARANGHFHFNPNNEVTVRQLAEMMTQVYVKVSGESSEETPTDVSKEFYEGEGYDSDSKRIPDMFIRQLGWNPKTSLWDLLESTLYGHRVYAEAVKQAMKTTAN

NbL17g07450.1 stress-response_A/B_barrel_domain-containing_protein_At5g22580 [MW = 12.23 kDa]



Protein sequence:
 IGRDAESHMLRGGFTNIAFLMFTFNKDDYTFVSHPHNHFVFSATFSTVIDKAVLLDFRISVKAPLA*

NbL17g07340.1 peptidyl-prolyl_cis-trans_isomerase_CYP71 [MW = 70.48 kDa]

No. of times detected



log(intensity)



Values from



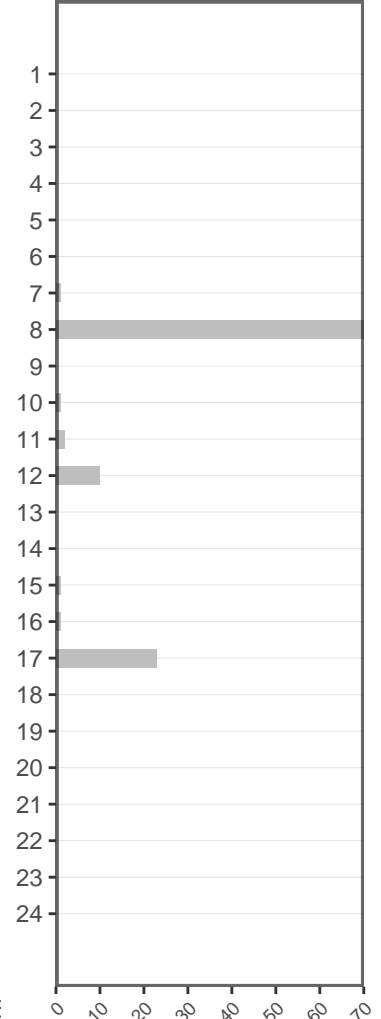
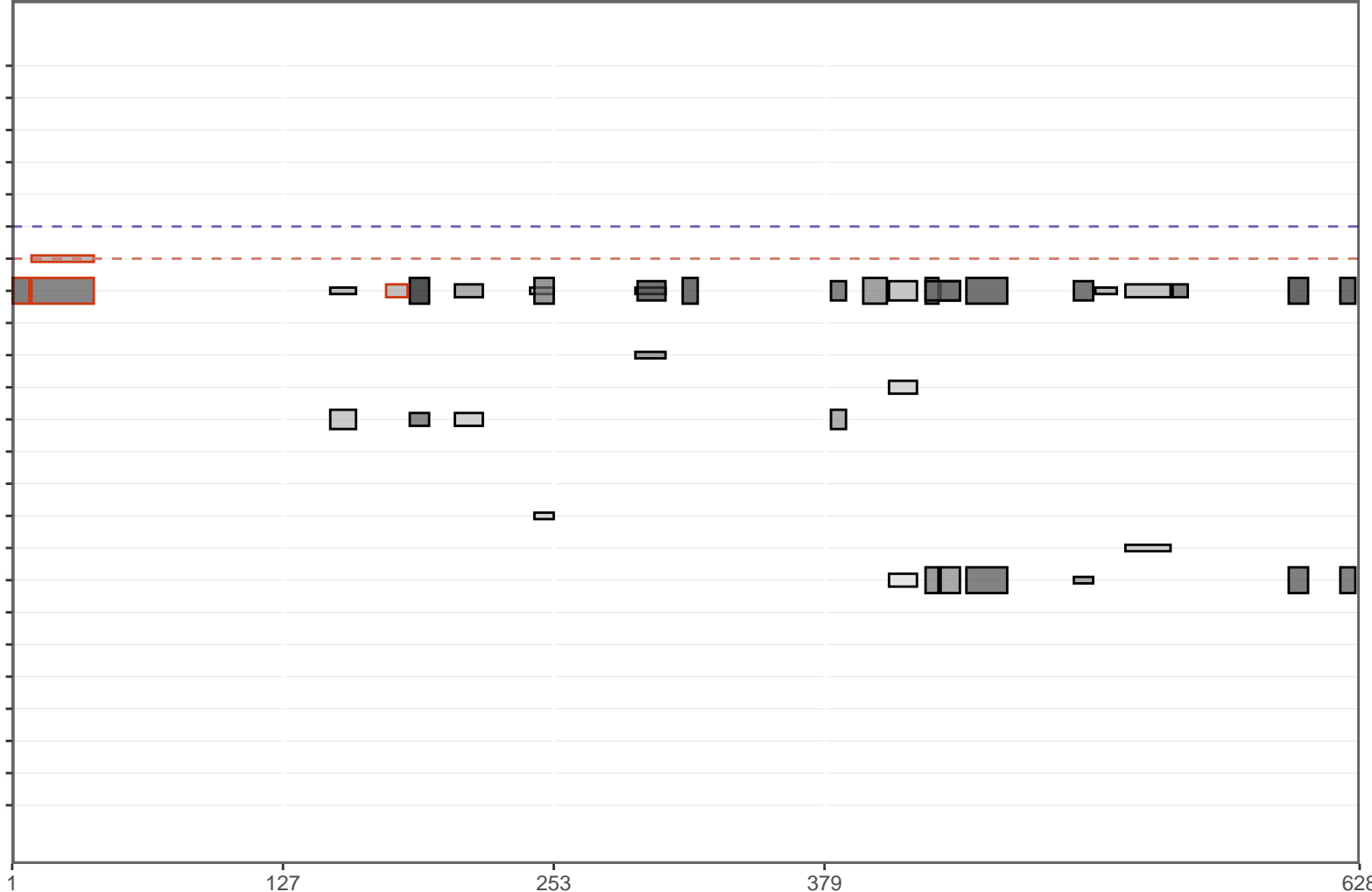
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00160 Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD
- PF00400 WD domain, G-beta repeat

Protein sequence:

DLQRTDVPVLYRLEADDFGRMAVEKEIEKEIHAAGPNAVDFDESSNFIIYATLLGKVVNLHTNKVSRILGKVESNDRLFRALYGGDRSSKKVRRKPAVAANANESKEPLIDPTLLCGAFKXKRRHLYFGQREPEEPDPTTKGRDVFNEKPSADELLAVSDIGKSVTTSLPDPAVLLHTSMGDHMKVYEECPKTKVENFTTHGRNGVYDNLIFHRVRFKFMVGTGDPDGGTGGGHWGREFEDEFKSLRHRDPETVGMANAGANTNGSGOFFITVATPWLGNKHITVYGRVYKGM

NbL17g07330.1 60S_acidic_ribosomal_protein_P2A-like [MW - SP = 9.72 kDa]

No. of times detected



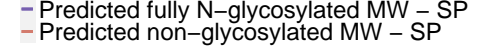
log(intensity)



Values from



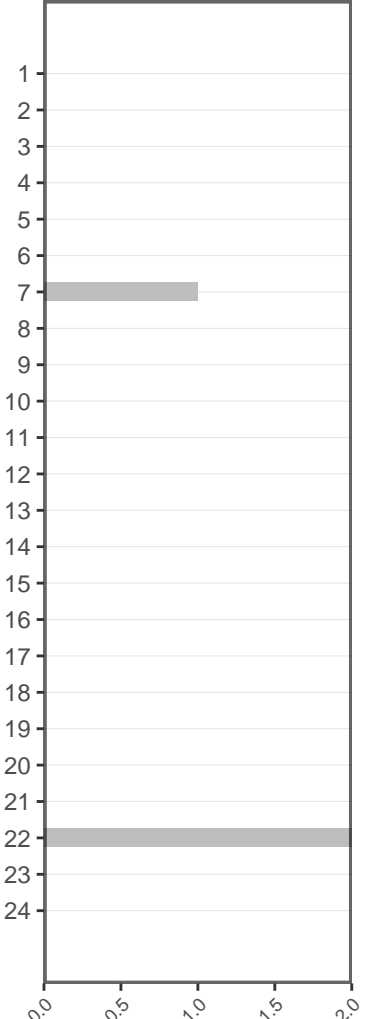
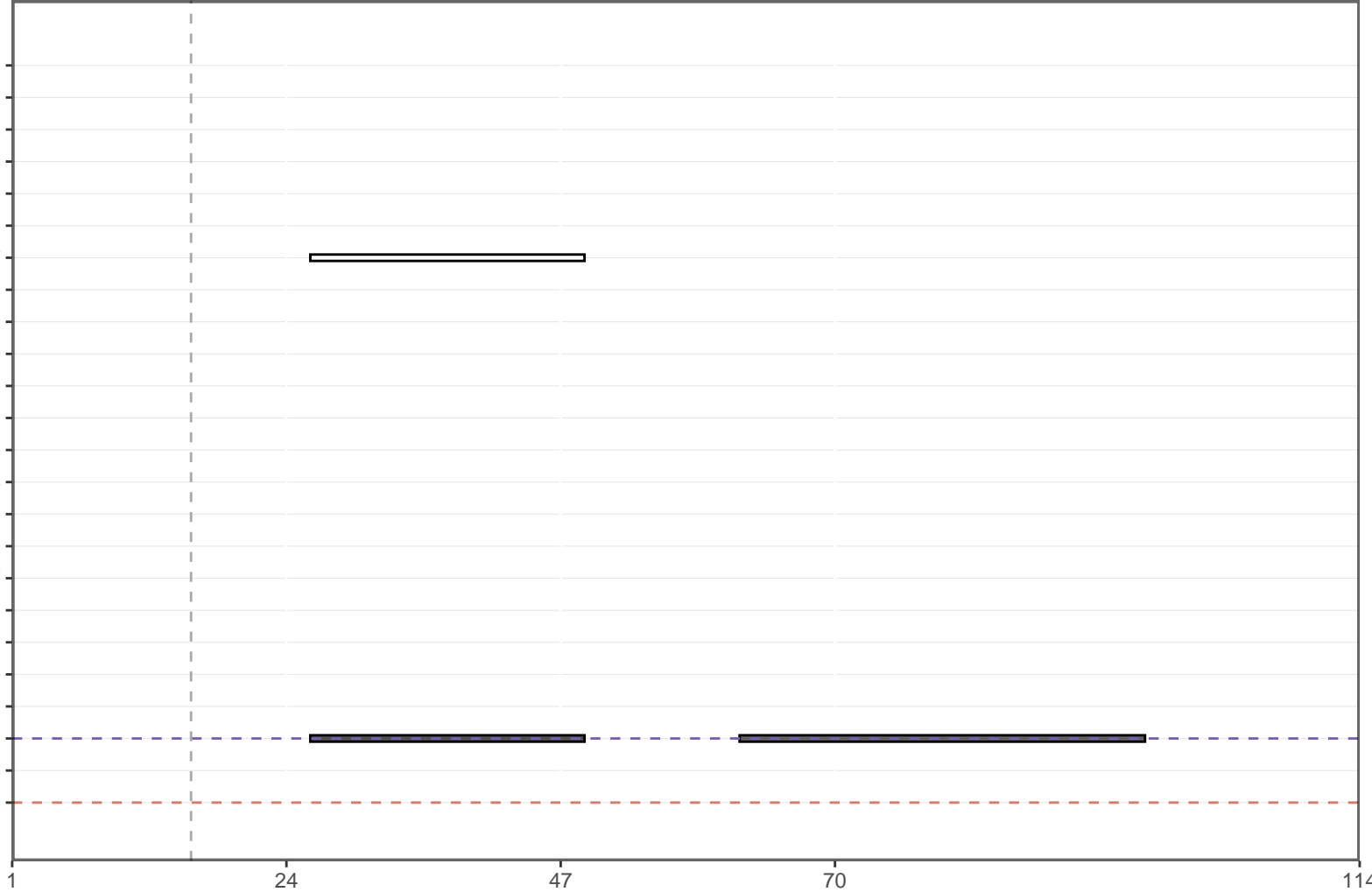
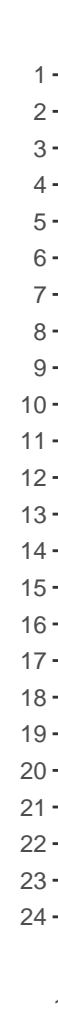
MW indication



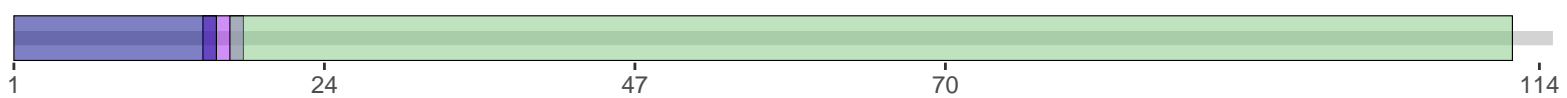
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

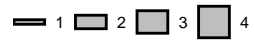


Protein sequence:

3VDDKDTLIAAGREKLAVPGGGGGVWAAKAGAAAAAPAAEKKKEEKKEEESDDDMGFLFD*

NbL17g07320.1 flagellar_radial_spoke_protein_5 [MW = 51.22 kDa]

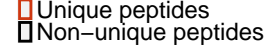
No. of times detected



log(intensity)



Values from



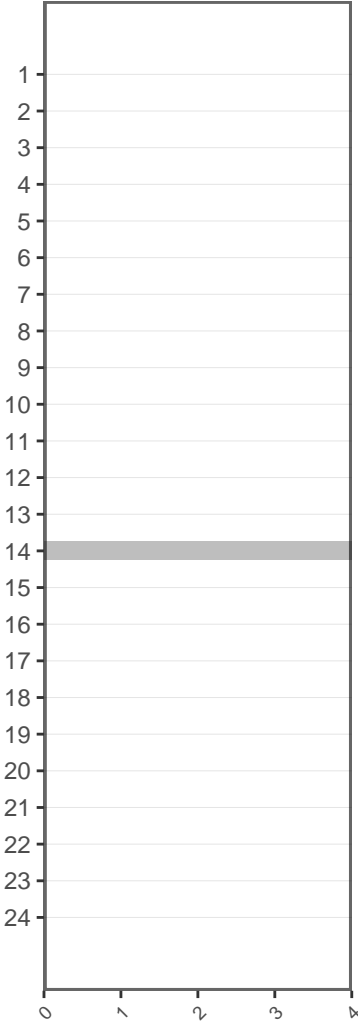
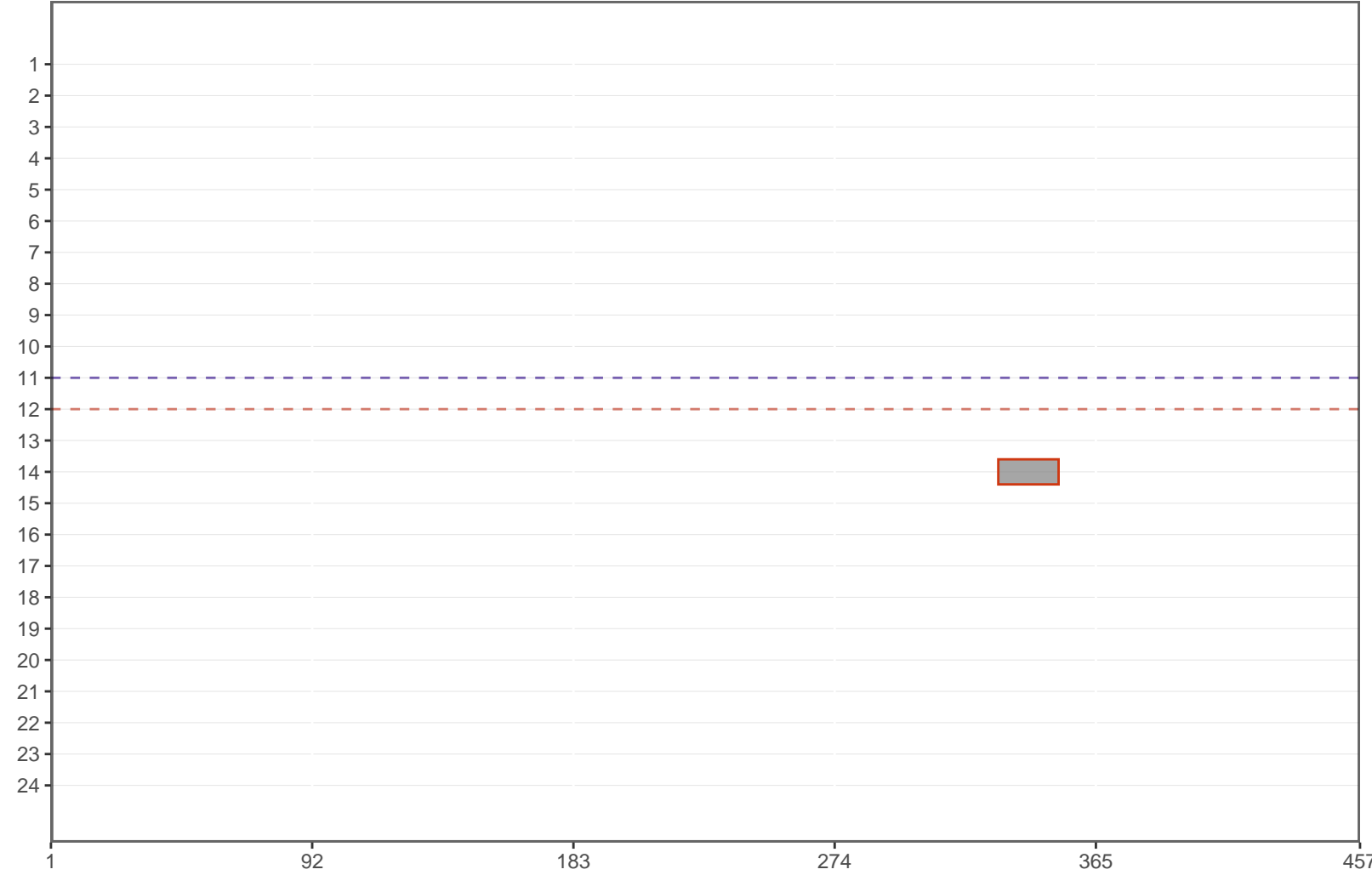
MW indication



Molecular weight



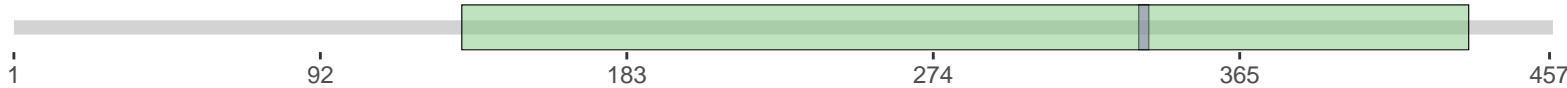
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

RSFVYQNDVSRKRMDVSLDMLGFHWWDYTNISGVLGALKHLTDLKEEGKKTALTNFDTERLRILENGIPVVSNGVGHSLVDMRPOGKMAELGOLGTGKLTGTVTVMGSLLEKFLGTLSPFAAPLNTPLSKQYKRMVDWAGGWSLFGELLRLTKTVANKHGVSPTWVWYLDQPTVAGSMVGVRLGLSEHIKVDNAVFSLLDEEDIRSLQVFNKPKDLQKIGDCGDEVRA*

NbL17g07310.1 uncharacterized_LOC109212815 [MW = 20.25 kDa]

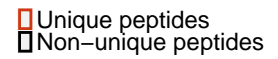
No. of times detected



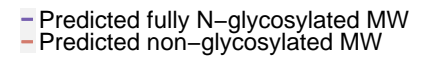
log(intensity)



Values from



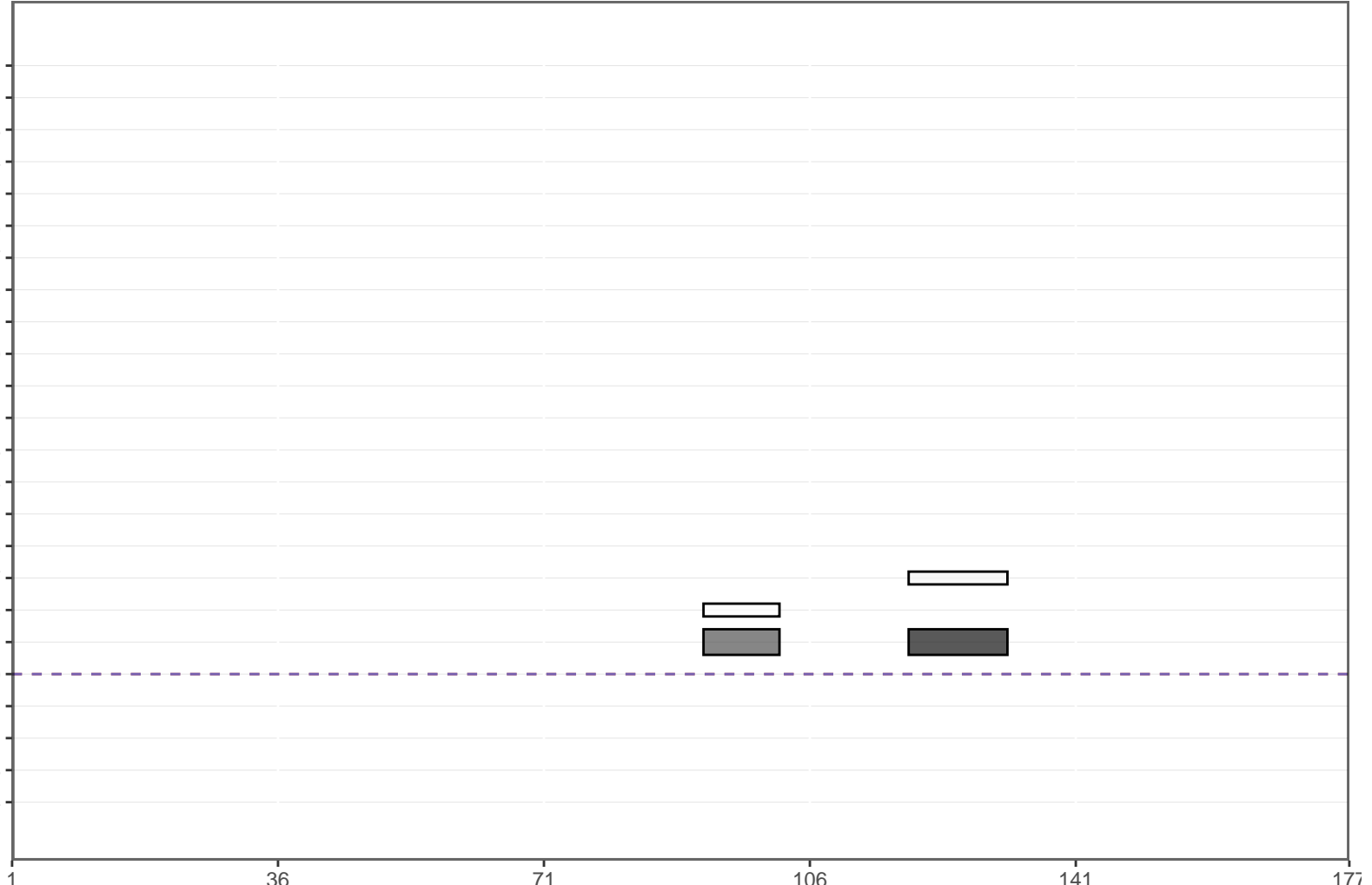
MW indication



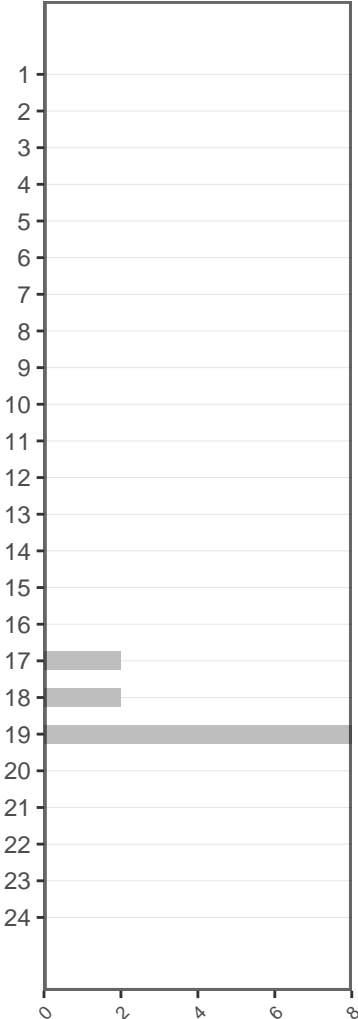
Molecular weight



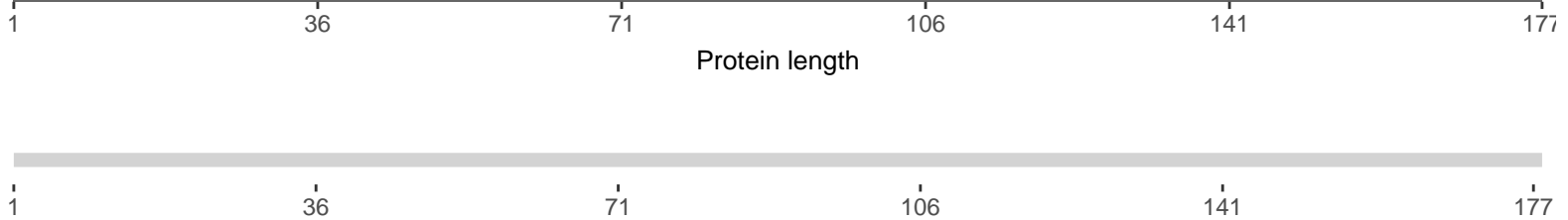
Gel Slice



Protein length

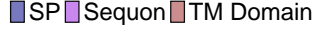


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DKELRDLRQDSEKALGLSMPLDGAKDRATQLESEVTLERRLLASGAEGMDGFRQRVSLHGRLLDTKRLLEALKGGEMENRKKDEPAIEPAAKKRWFVW

NbL17g07190.1 60S_ribosomal_protein_L10a-1-like [MW = 24.69 kDa]

No. of times detected



log(intensity)



Values from



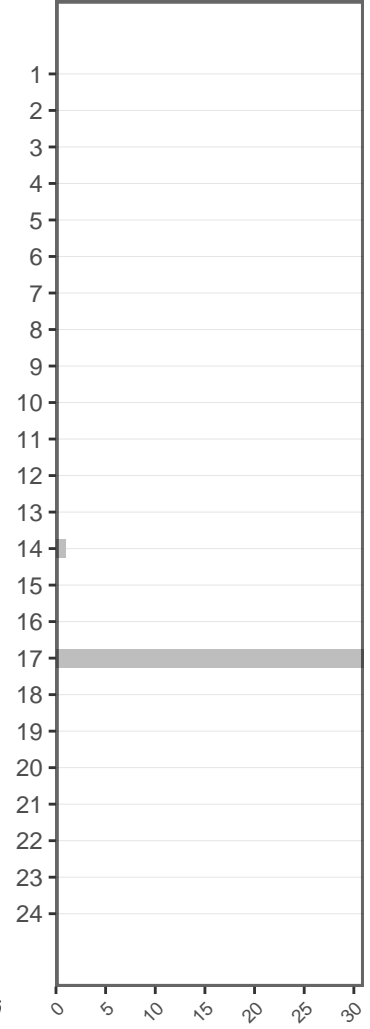
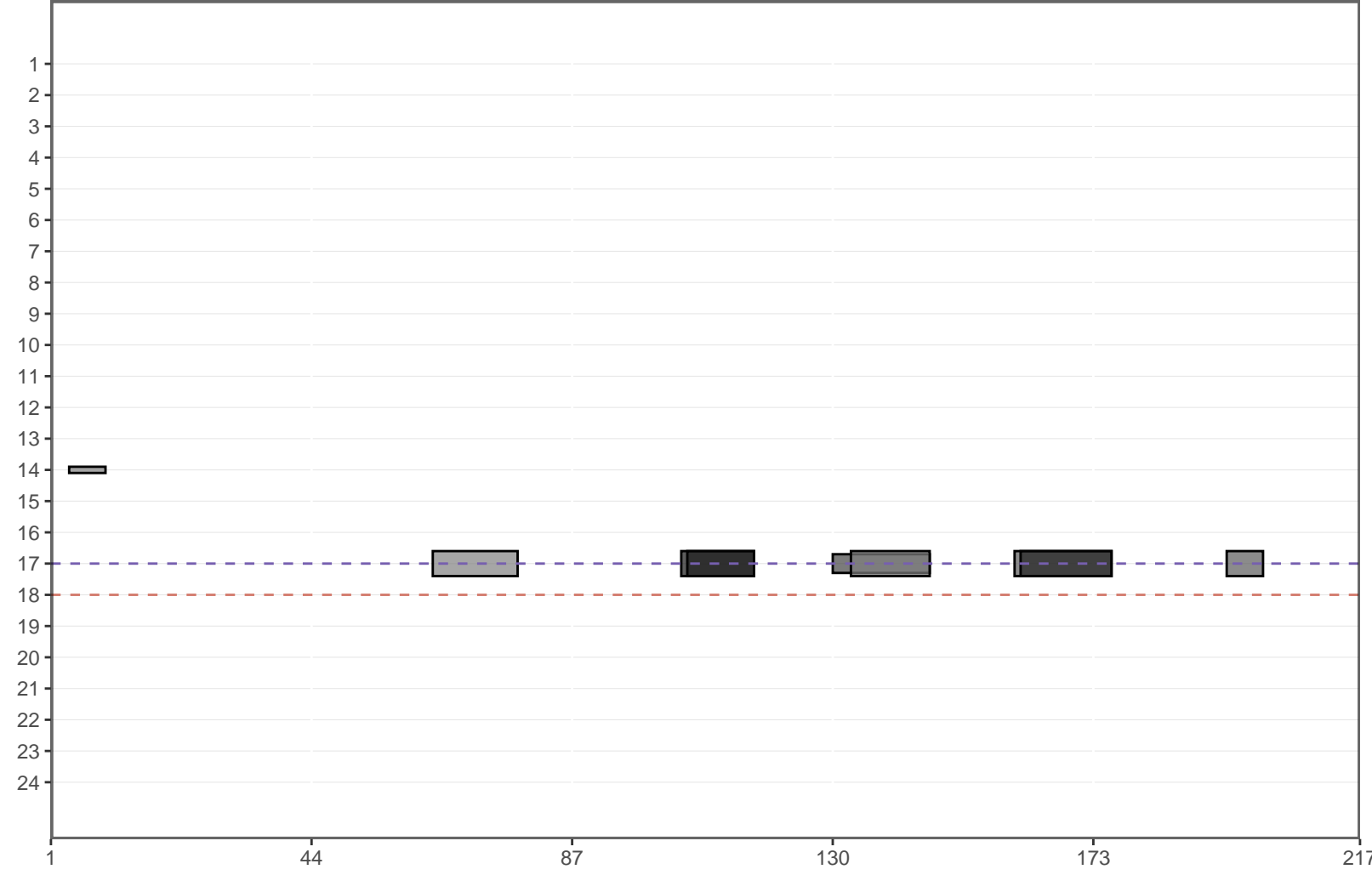
MW indication



Molecular weight

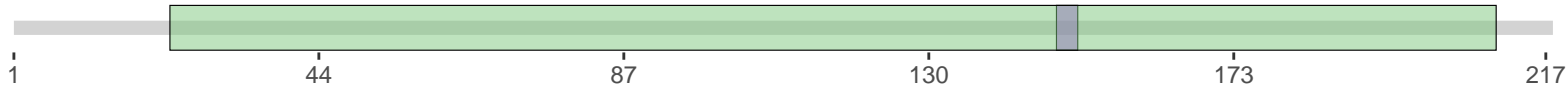


Gel Slice



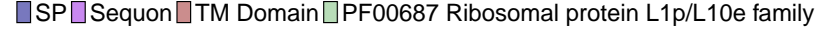
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KKLYKLAQKYYHFLASESVKQIFRLLGPGLNKAGKFPBLVSHQDESLESKVNETHKATIKFQKRVLGMGVAVGNLDMEEKQIFQNVQMSVNFVLSLLKKNWQVRFGLYKSTMGKTRQVF

NbL17g07180.1 ferredoxin_root_R-B1-like [MW = 16.1 kDa]

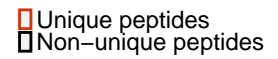
No. of times detected



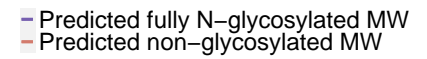
log(intensity)



Values from



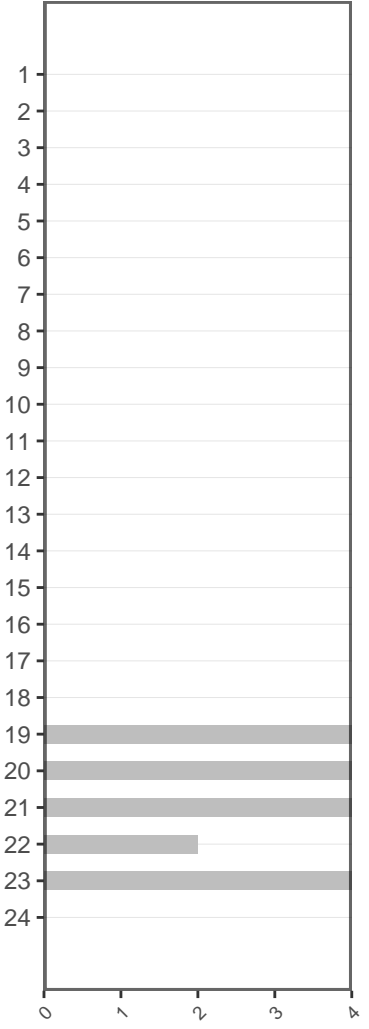
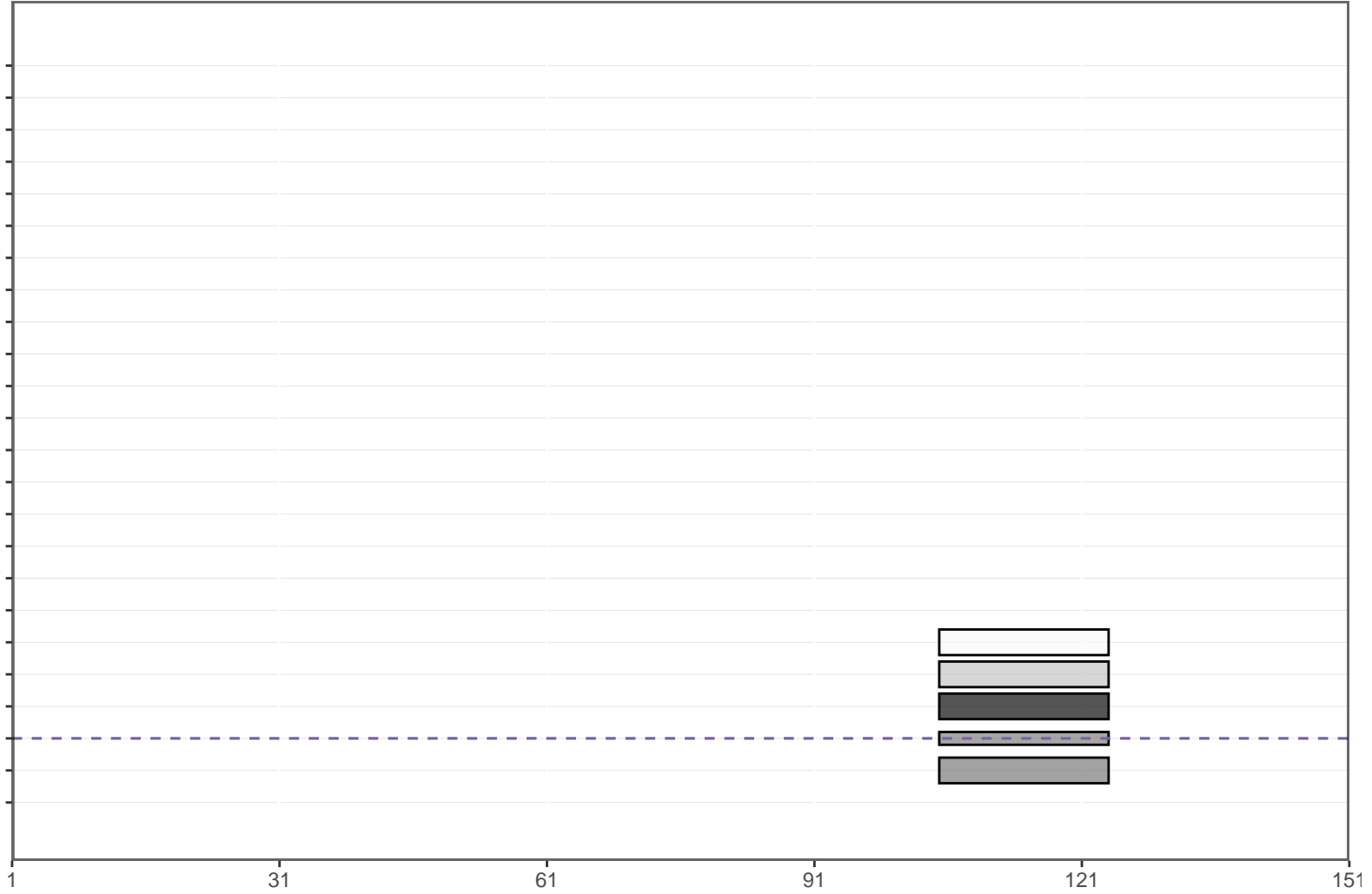
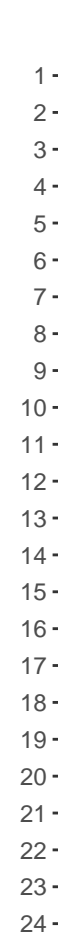
MW indication



Molecular weight



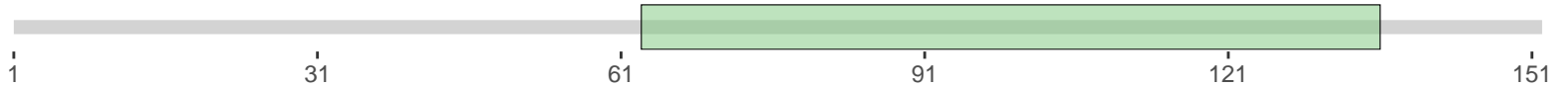
Gel Slice



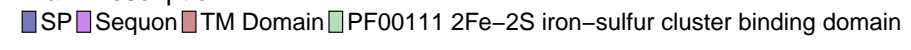
Protein length



Pfam domains



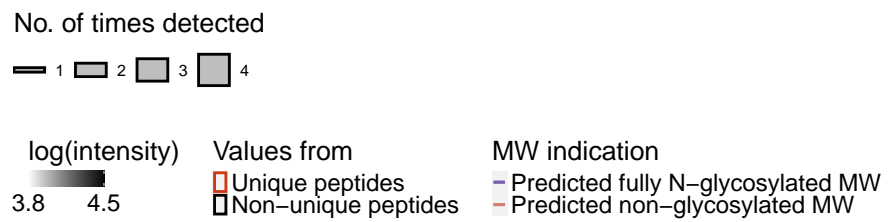
Pfam Description



Protein sequence:

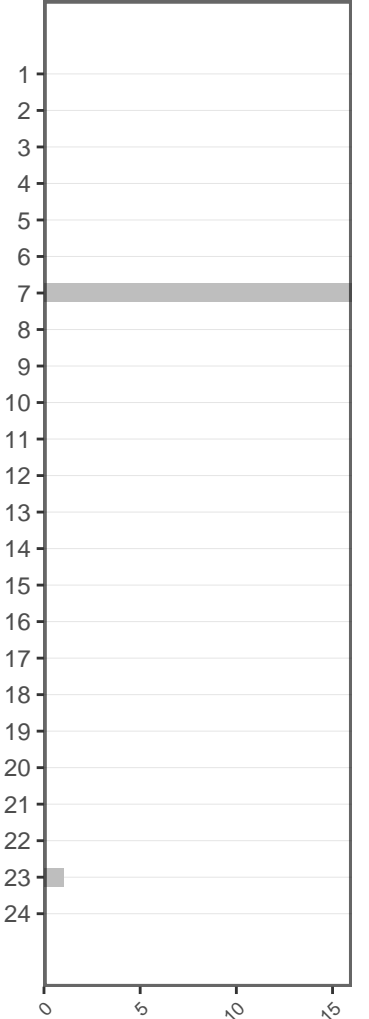
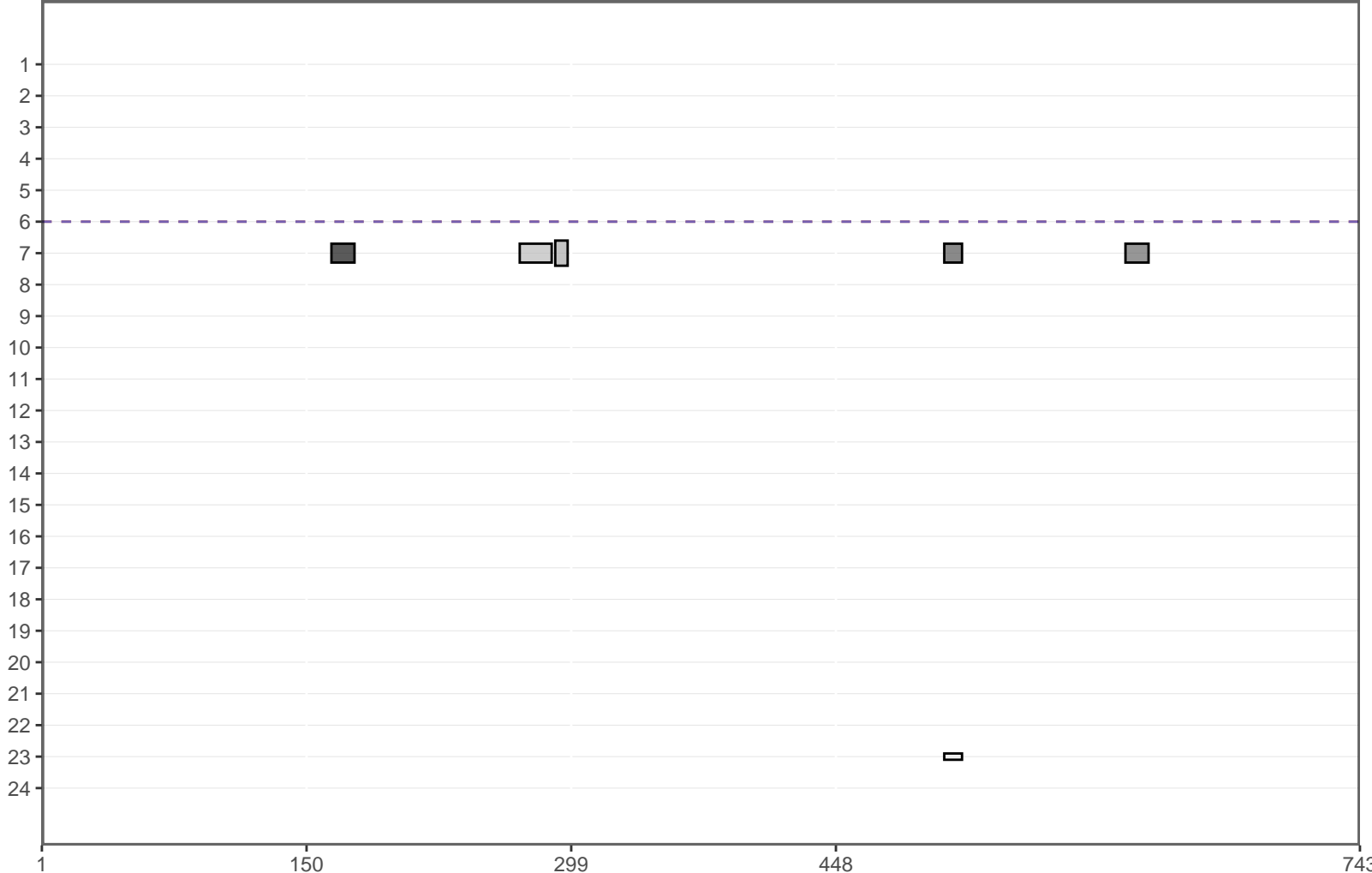
PDGTEHEFEAFSDTEVILDAEAEAGVELPYGCRAGADSTGAGKIEGGSDQDSDGSLDDNOMKEGYLTDVSEYPTSDGIVYTHKEGDLV*

NbL17g07110.1 protein_transport_protein_SEC24-like [MW = 81.99 kDa]



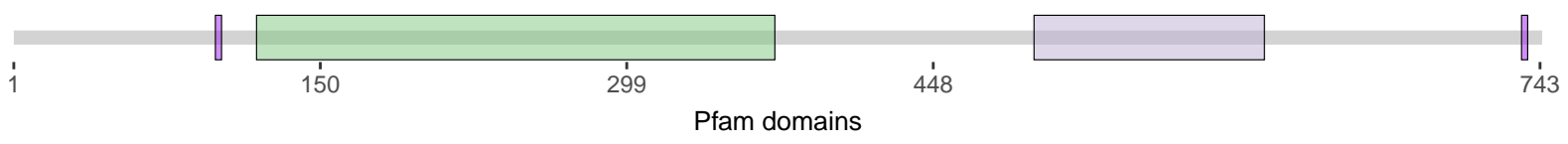
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF04811 Sec23/Sec24 trunk domain
- PF04815 Sec23/Sec24 helical domain

Protein sequence:

.FLYTSDDSTLPCGMVRLMLERPVAFNCLVLRRTSPEFQPSHVGCHFFPDQYENVQHICGDFATYAYDFEANNVGFSRHTSELPMAVQIAFQYTVVAPPDELANVGSSTTRTKHSLKRRRLRIRLQFGVWHSHEIVGDVDEVLGLLVHKVHLASLEGGVREGFMLLHWDVLLTQYNDACKLQSGHGGSTVHDAVAFSGGPGQLGRLPRVLRLLRPLRLLRHEEGVHPDWRVRYLQGLFSGLEPSSLNRAVPLTGVASPDKQAVPRHLSRAALITSGSPIFLDFT

NbL17g06950.1 DNA-damage-repair/toleration_protein_DRT100-like [MW - SP = 37.82 kDa]

No. of times detected



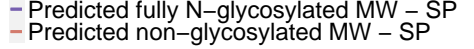
log(intensity)



Values from



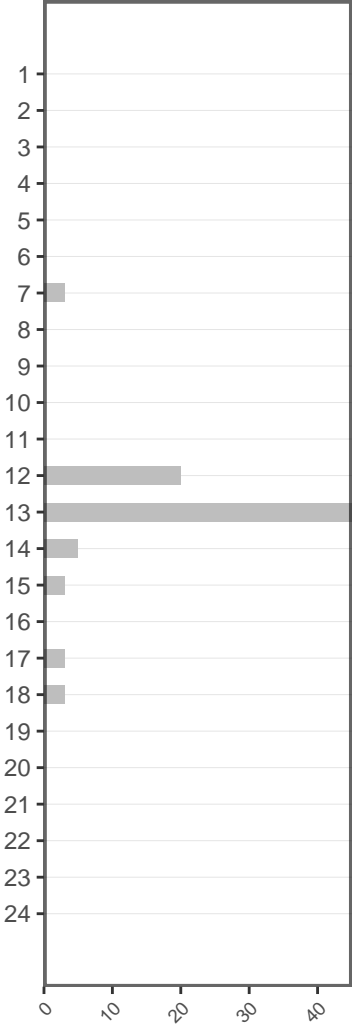
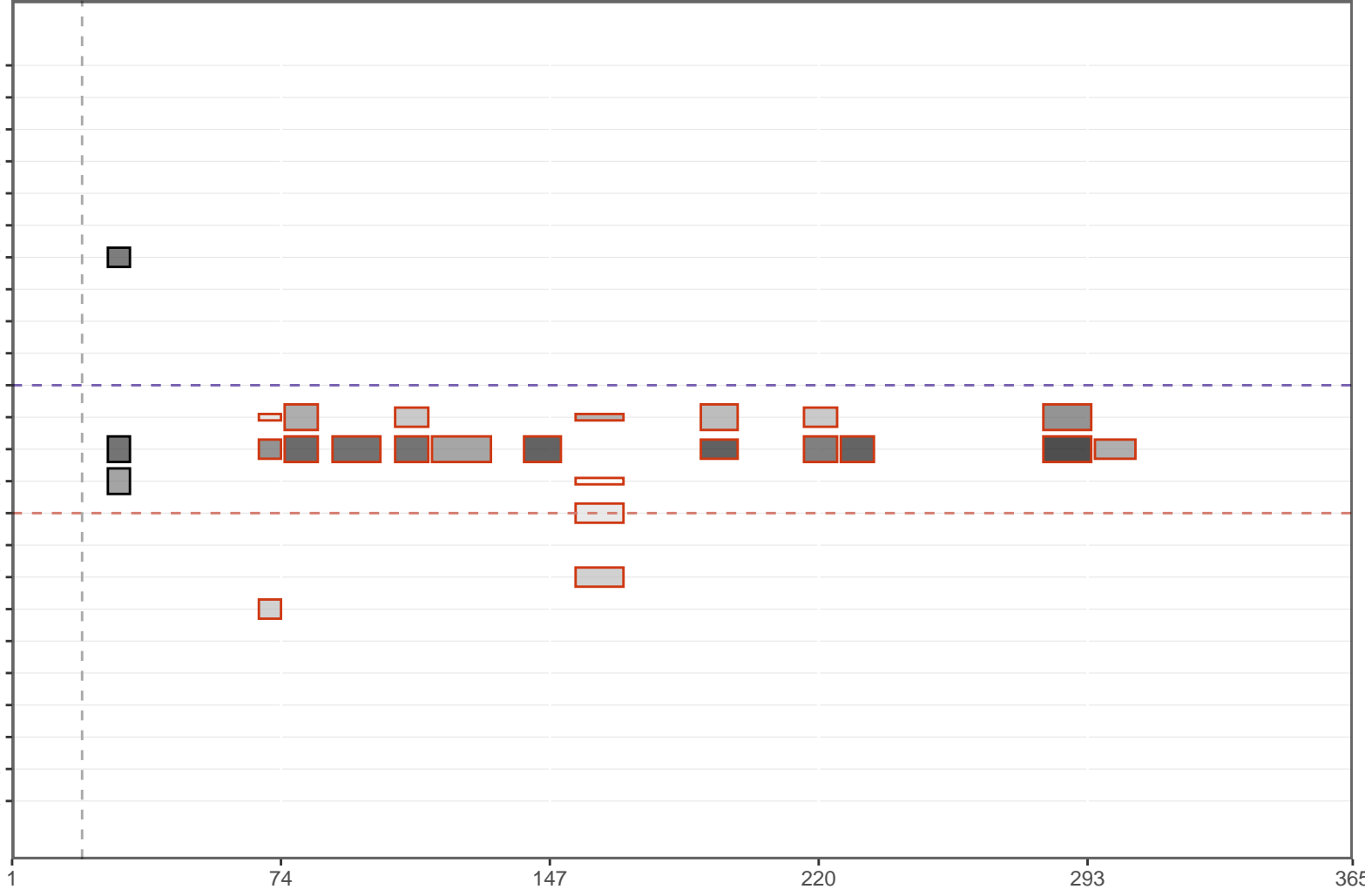
MW indication



Molecular weight

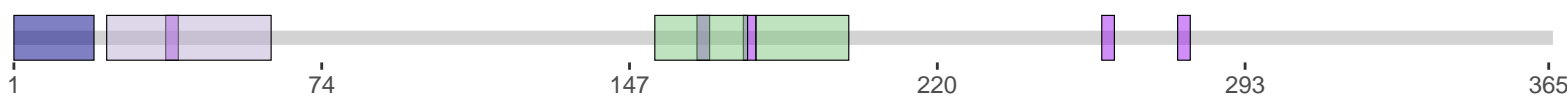


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

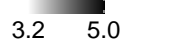
RSLTLLSLMLDLRNRNFRGFLPTNFQKLRMLRALLLGNRLGKIPYISYHFLSDLDLNLKSLGTFPPPLGKMRVLAFLNLGDNNGSGTPTLNRNRLNLSKNSIEGYIPDFDERSYFMMDLSEYKLRGKFKPKSISATFRIHFVDSHNLGGQFPAGSFPFDHLEASFTYNDLGGKPLKPCR

NbL17g06930.1 uncharacterized_LOC109227436 [MW - SP = 94.02 kDa]

No. of times detected



log(intensity)



Values from



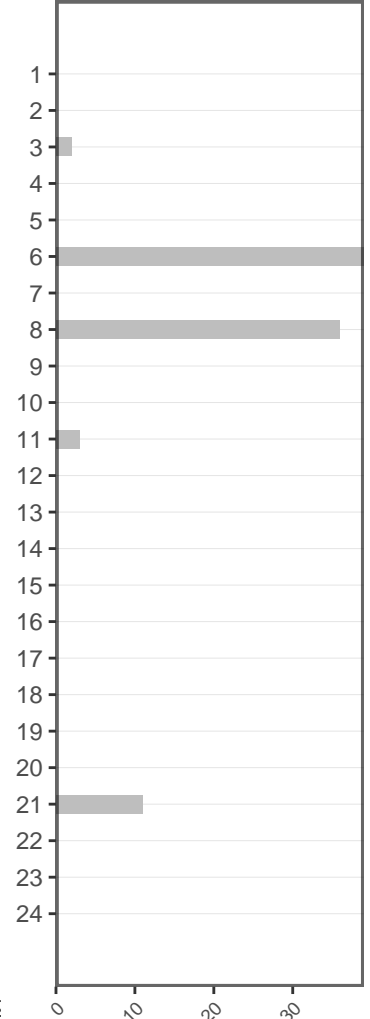
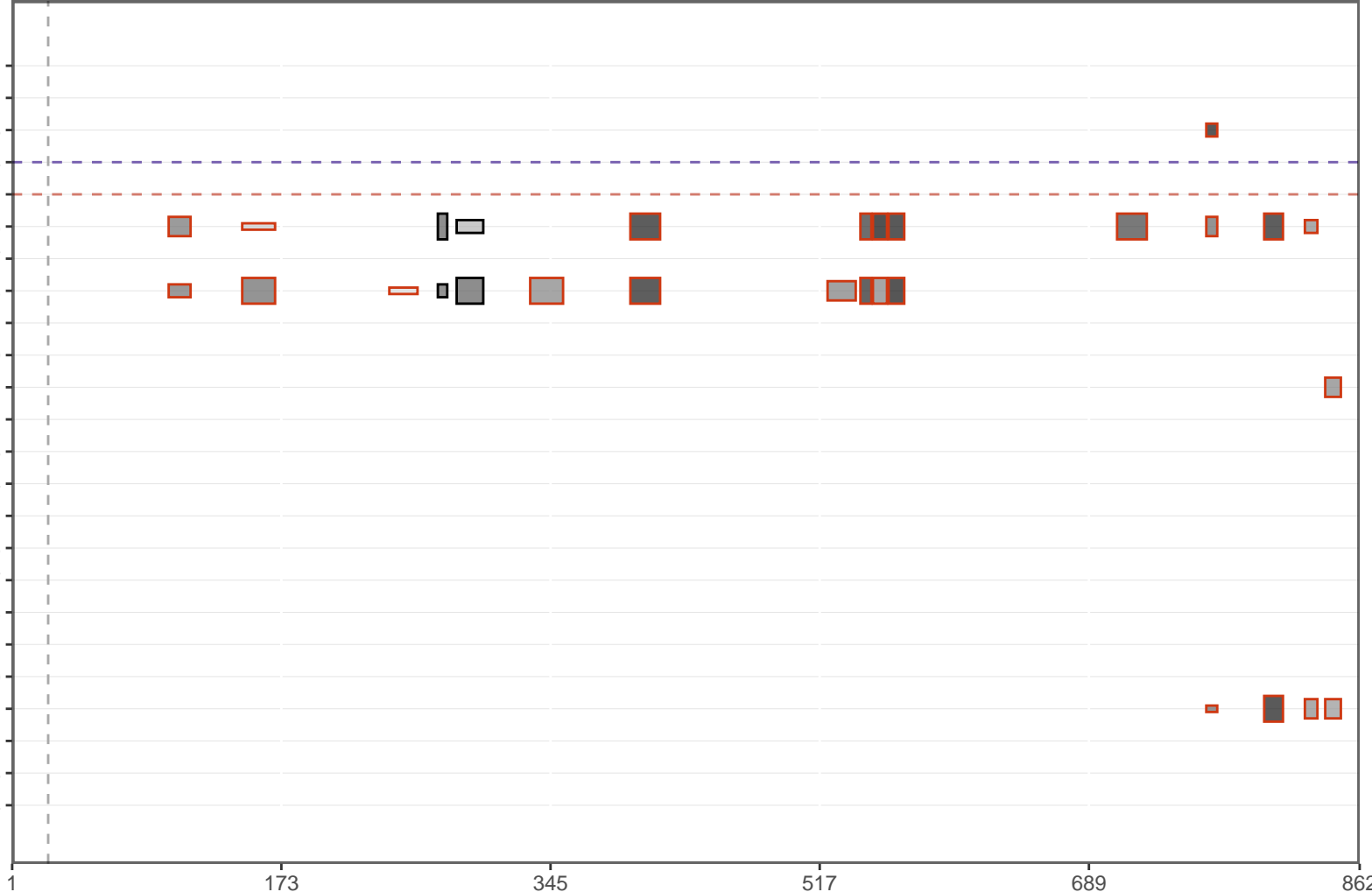
MW indication



Molecular weight



Gel Slice



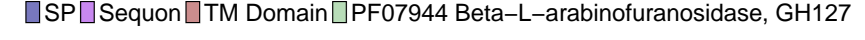
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SRHLFRVTKEMAYADYFYERALTNGVLEQRGRDPGVMYMLPLHRGGSKARBYHWGSPFNDFWDCYGTGIEFSLKGDGSHFEKGNPSGLVHQVHSSLDWAGGQVLYSGVEVPPVSWNDNRFRVTTVSSKGSASSTLNLRIPSWFDGTSKAKSLNGEDLSLPPPCNFLTITRWSVGGSDHTELEPMLRTEPKDWRPEVAKQALYGPVLLAGHSGGWDIEKSKASSLSDUTFPVADVNHHLBLAGEGNGTFLVSTNHQIMEMVPEPGTDSALSATTRLUSTDK

NbL17g06820.1 actin-104 [MW = 41.72 kDa]

No. of times detected



log(intensity)



Values from



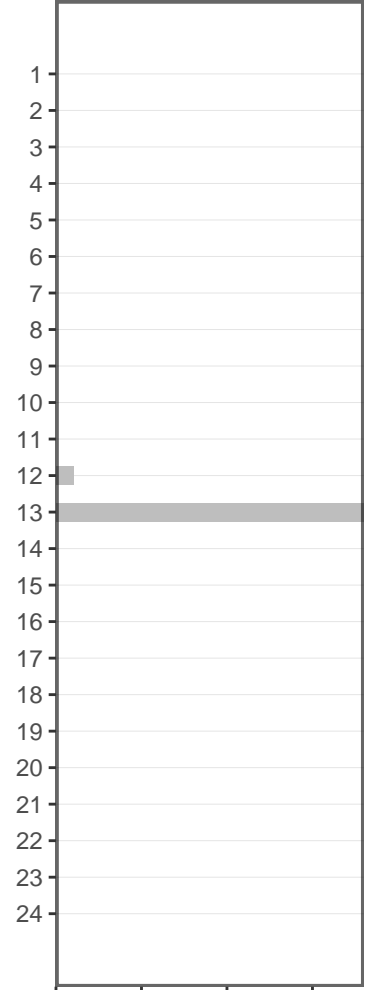
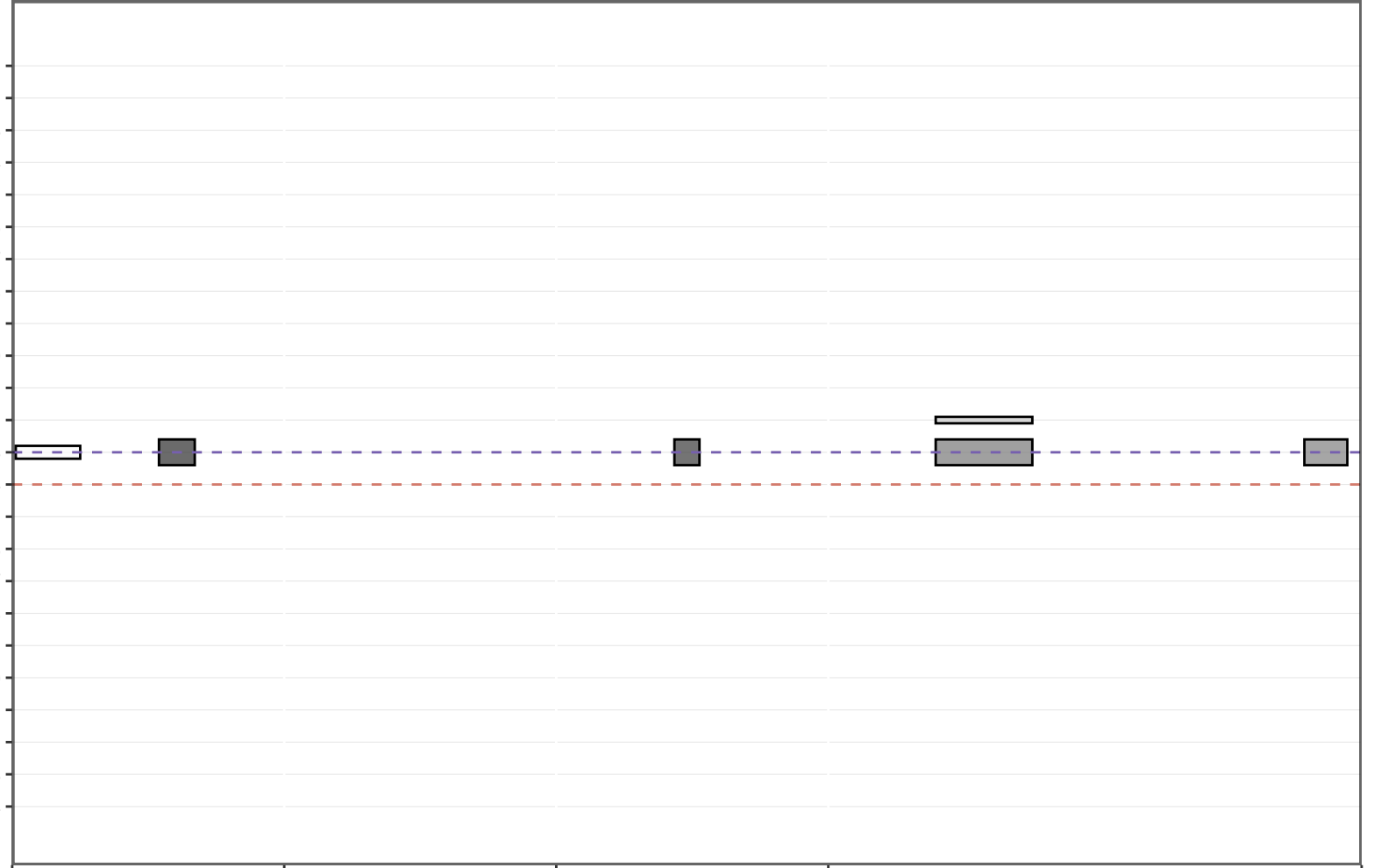
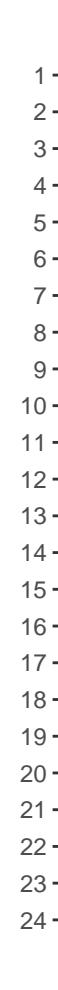
MW indication



Molecular weight

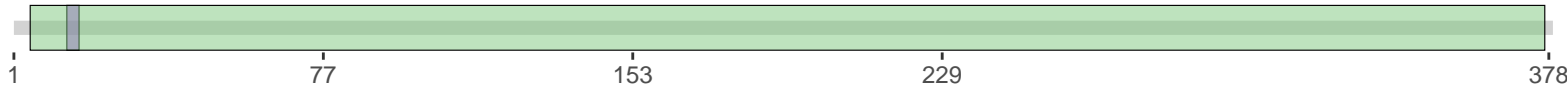


Gel Slice



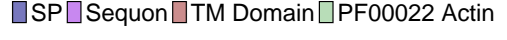
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

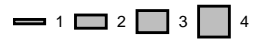


Protein sequence:

PHAILRLDLAQRDLSFDHLMKILTERGVHMTTSAEREIVRDKKELAYVALDFEGELETAKS66SVEKYSVELPDGGVITGAERFRGPEVLFQPLHGMEAAQHETTYNSIMKGDVDRKDLVGNVLSGGSTMFGIADRMSKKEITALAPSGMKIKVAVPPERKYVYVWGGSLASLSTFGQMMWIKAEYDESGPVAVHRKGF

NbL17g06660.1 signal_recognition_particle_subunit_SRP72-like [MW = 77.98 kDa]

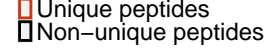
No. of times detected



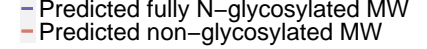
log(intensity)



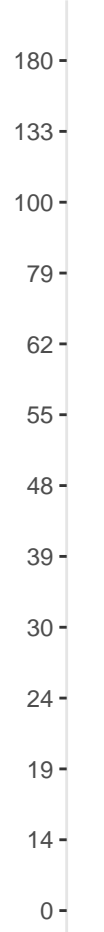
Values from



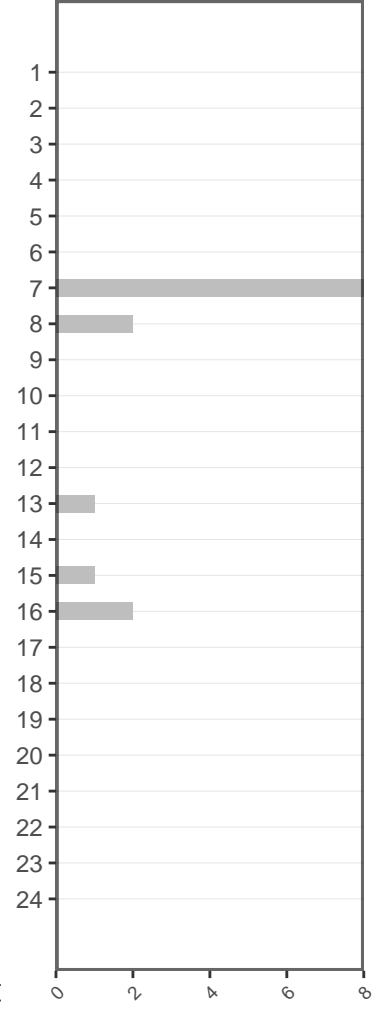
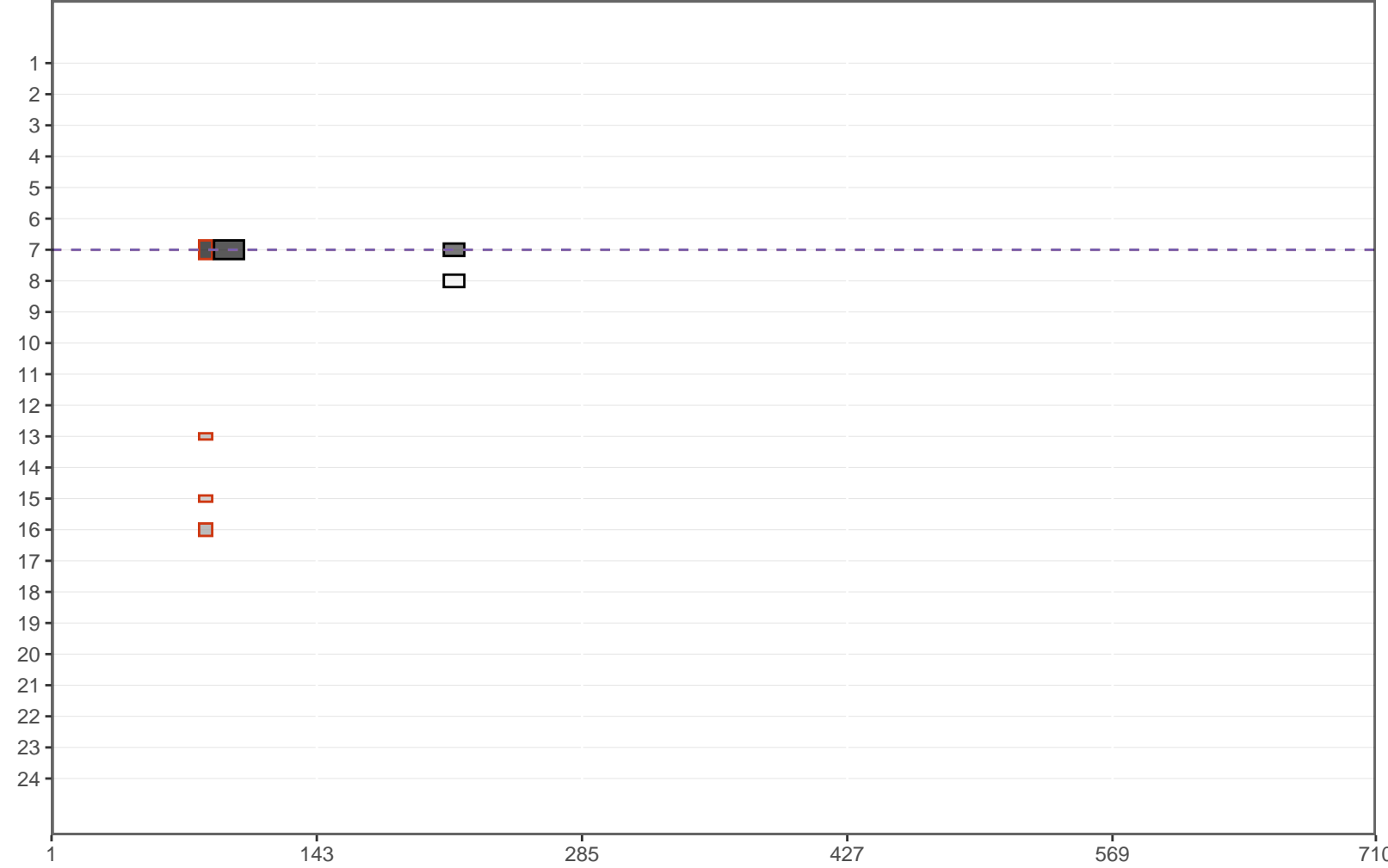
MW indication



Molecular weight



Gel Slice

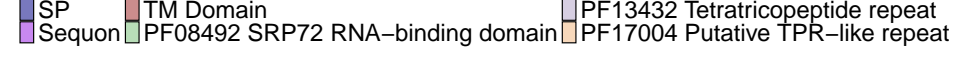


Protein length



Pfam domains

Pfam Description



Protein sequence:

IGPEKFLARGLDLKLSGKREAVYFNRIYLLLNHNKMDGARELVGALPGFIFSLMPVLLGAAHLYRENKAAAEELGGYADKFPDKSNILLARAGVAAAAGHPQAAADSLAKIPDGHKATVATLVSLKERAGDIDGADAVFDGCAIRWWSNAMTEDSKLNIMQEAFAFLRHGRKEDAAARLYEELVSKSHGSEIALVGLGTAHAGDVEKAEAEVKKLKLPLQLKAIDVDSLEKTSGAHAEKGPAAVTEIYEAKNKDKAKKRRKPKPKYKGFDFRANFGPPDPFERWLPKR

NbL17g06570.1 OTU_domain-containing_protein_6B-like [MW = 36.71 kDa]

No. of times detected



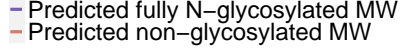
log(intensity)



Values from



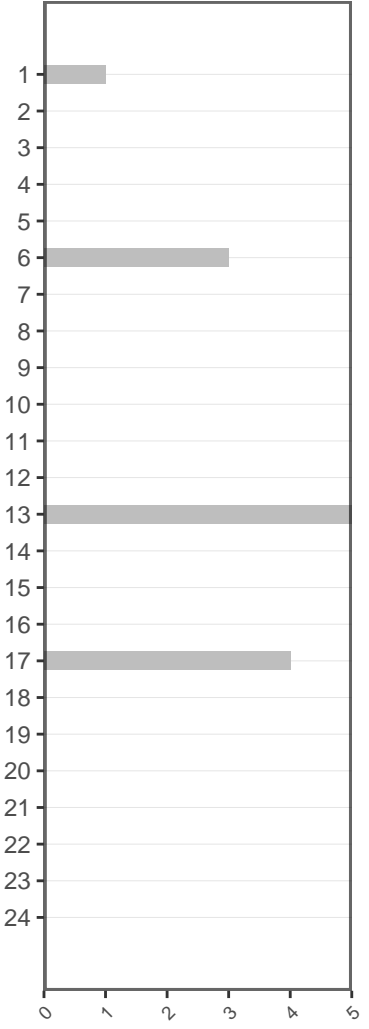
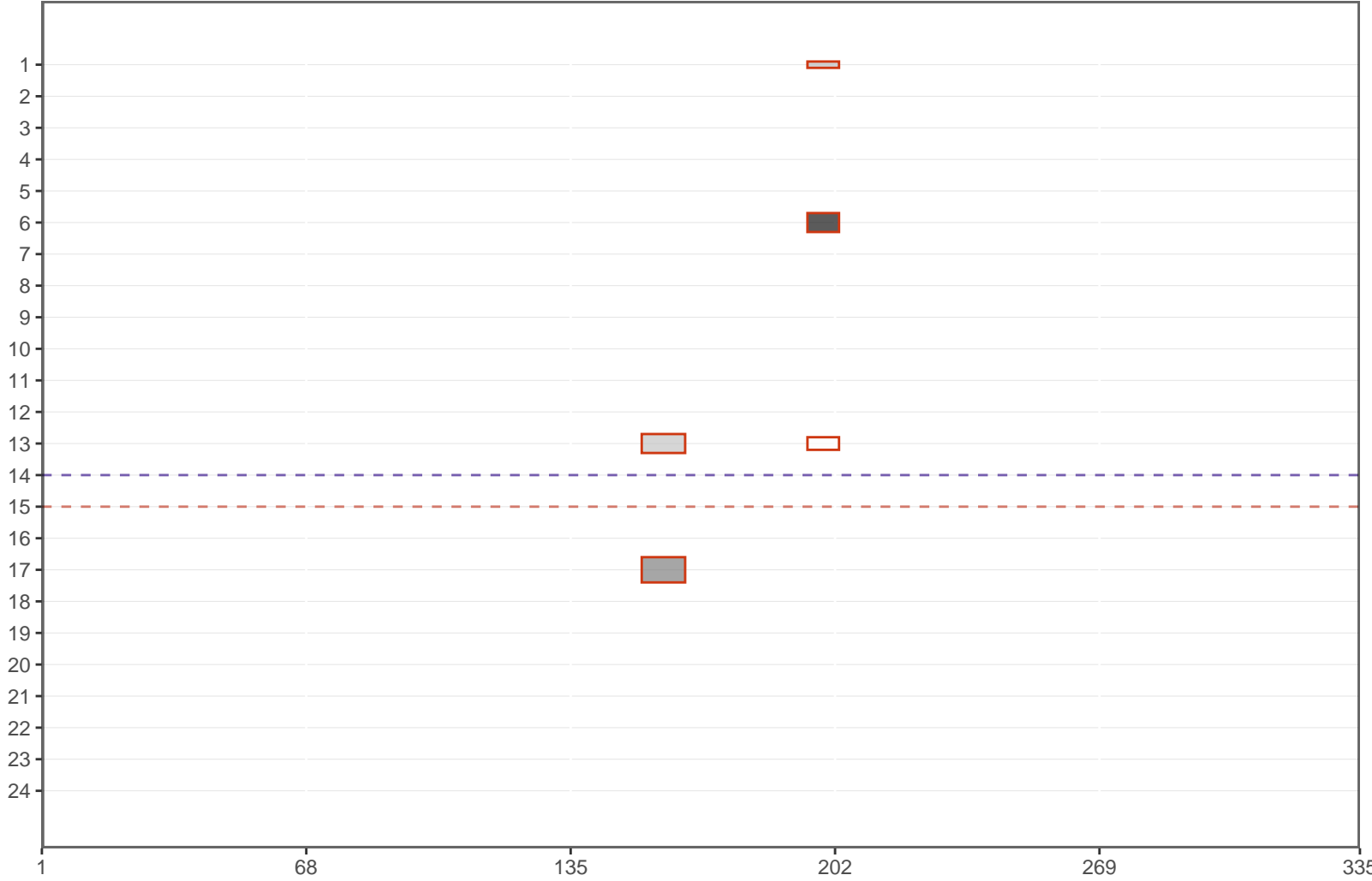
MW indication



Molecular weight



Gel Slice



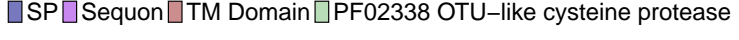
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

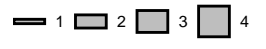


Protein sequence:

CEEQSSVSDRVIEKEKLDKLEFLGLMVAEKIKPDKGLYRAVENGLAIRSGSSPYTYLELRQMAVAVMRKQATNLFPPFLLENVEGGESDDGLVERFENYCGEVESTAWGGOLELGAETHLKKHMFSGSFFDVEEMKKEYKSDNSGGSGSSTSMILSHMHAFGLGEMHNSVFPSSA

NbL17g06500.1 probable_sucrose-phosphate_synthase_1 [MW = 117.24 kDa]

No. of times detected



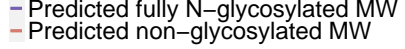
log(intensity)



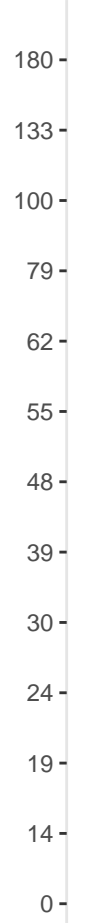
Values from



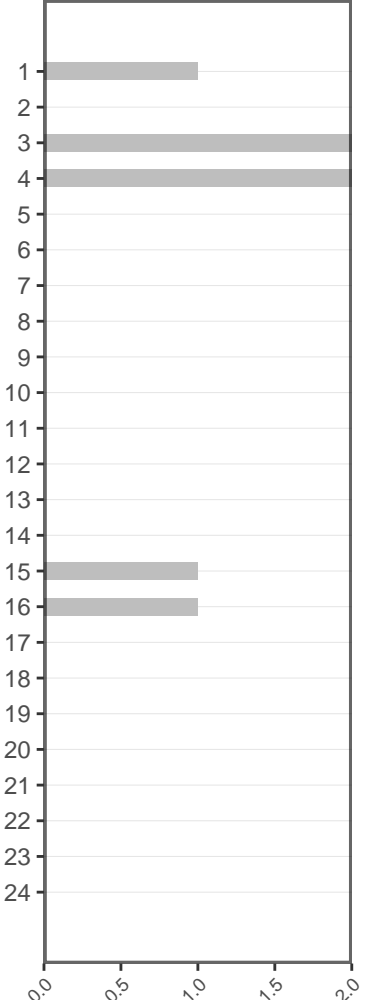
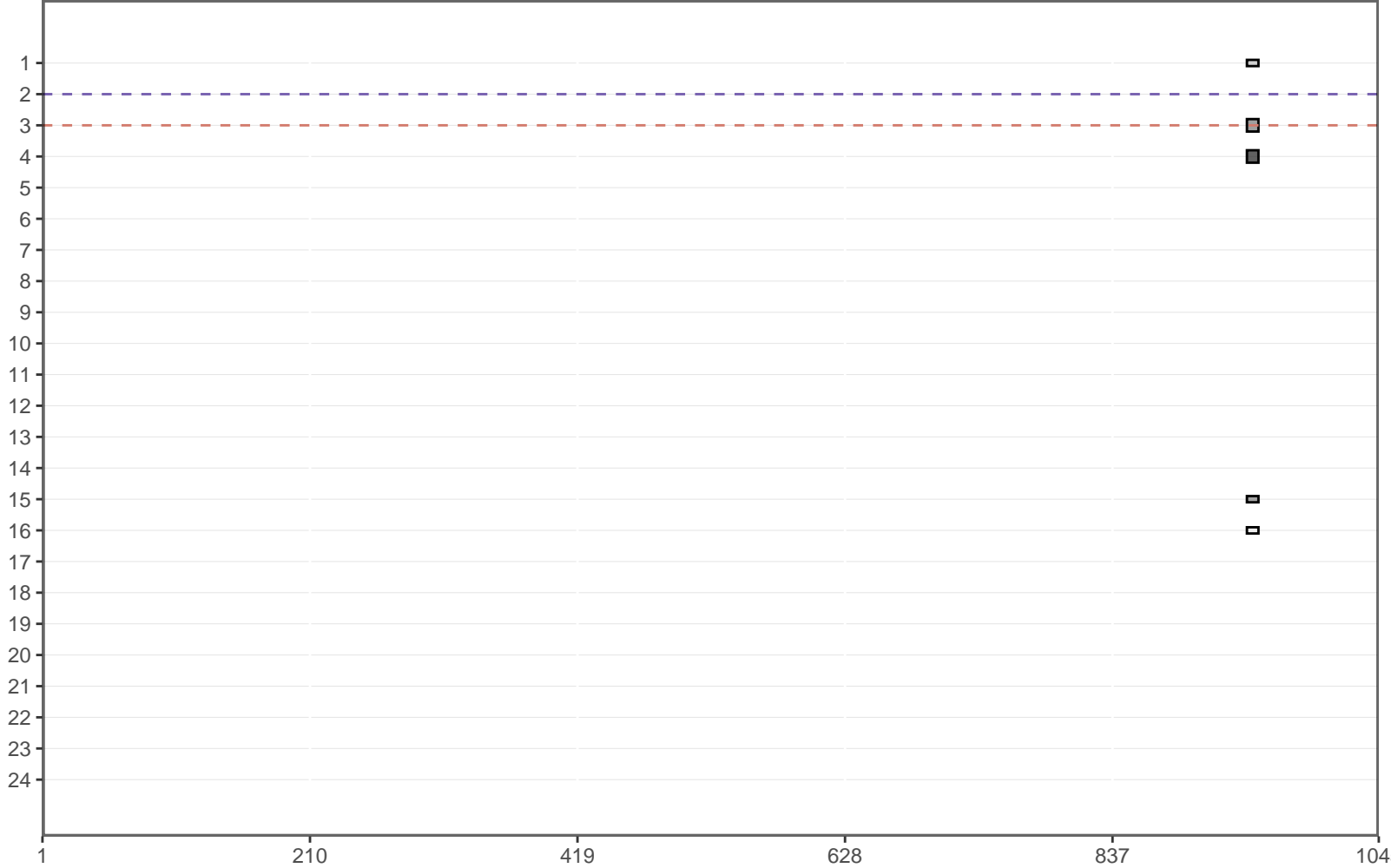
MW indication



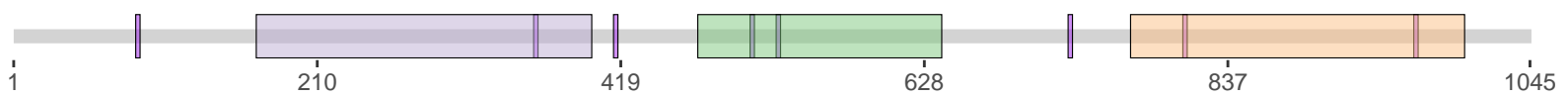
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

LRELANLTLVMGNRQVDEMSGTNSVSLVGLKLIKDYDLYGGVAYPKHFKGSDVPEIKYLAAKBKGVFINPFIPEFGLTLEAAAHGLPIVATKNGPDIHRVLDNGLLVDPHQDQSVADALLKLVADKLVWARGRGGGLRNHILFSWPEHCKTYLARVMGCKRQRPWRORNEDESSDSEPSDGLRDKDLGLSLKLSLDGDKNEKSGTSTALDFVENAKKSGLDGVAVPLFVSRMEKAEGSKFSLRRRRLVIAADGDTVAGLADTKIFETVYKKNDSOSHCC

NbL17g06470.1 vesicle-associated_membrane_protein_711 [MW = 25.21 kDa]

No. of times detected



log(intensity)



Values from



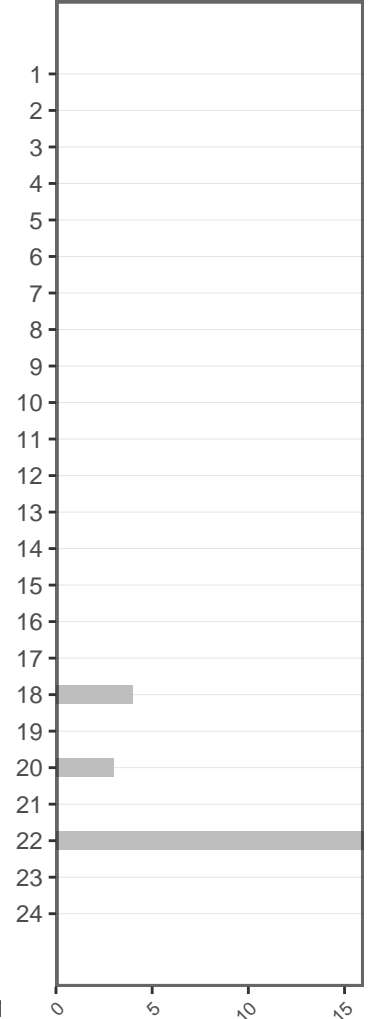
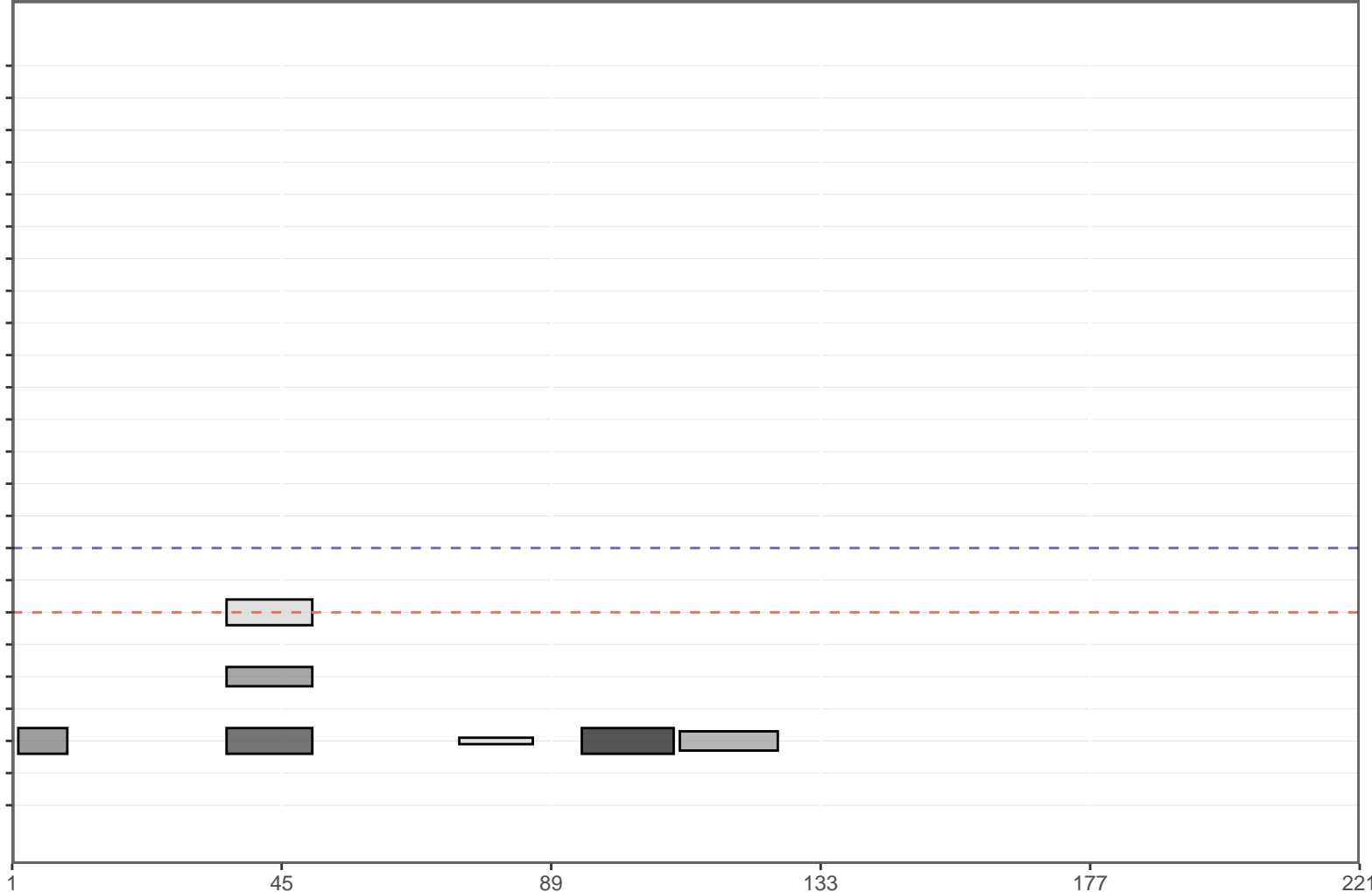
MW indication



Molecular weight

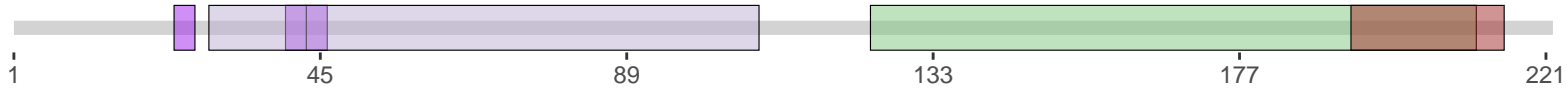


Gel Slice



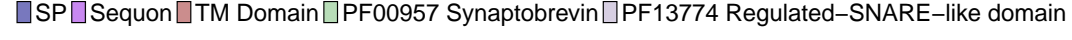
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

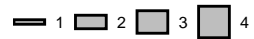


Protein sequence:

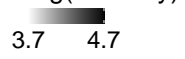
IQAYAMNDEFSRVLSGGIEYSSDPNADRINRLKGEISGQVRNMIENDKVLERGRDLELLVDKTTANMGNTFRFRKQRRFRSTVWWRNVLFTALFLLLVYVILAFVGHSLTPTGLK

NbL17g06440.1 adenine_phosphoribosyltransferase_5-like [MW = 20.64 kDa]

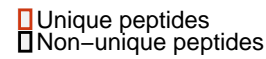
No. of times detected



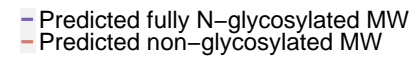
log(intensity)



Values from



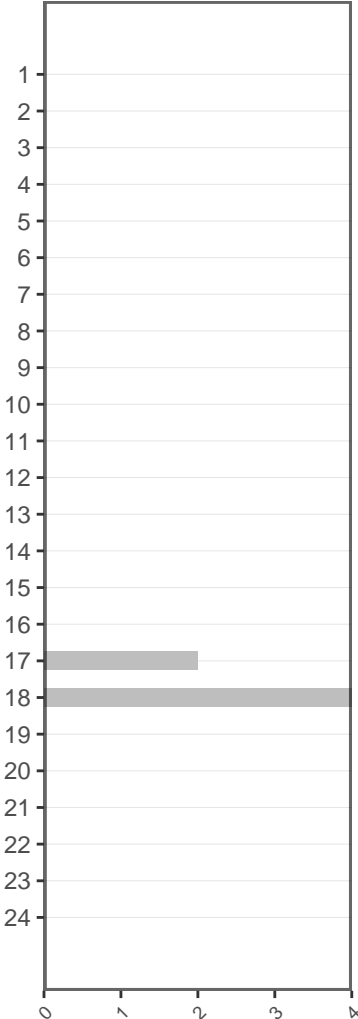
MW indication



Molecular weight



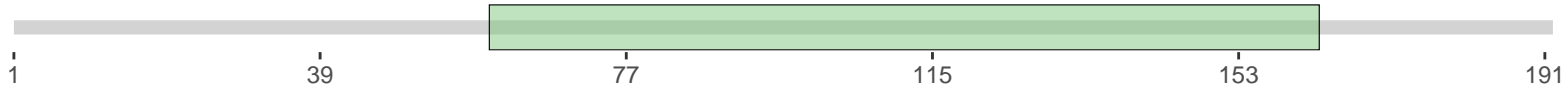
Gel Slice



Peptide counts over 4 repeats

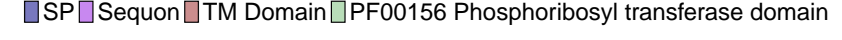


Protein length



Pfam domains

Pfam Description



Protein sequence:

AIGAKFVPLRKPGLPKGVVSEVELEYGKDCLEMHVGVAVQGGDKAVLDDLVATGGTLSAAIKLLERMGAIEVVEGGGVGLPEVKGQGRLLKPKPLVILVEPEEDF

NbL17g06410.1 ATP_synthase_subunit_b'_chloroplastic-like [MW = 23.98 kDa]

No. of times detected



log(intensity)



Values from



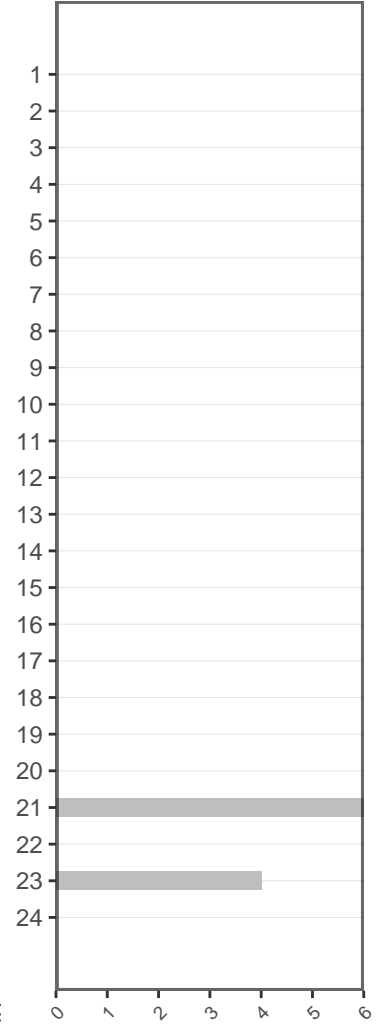
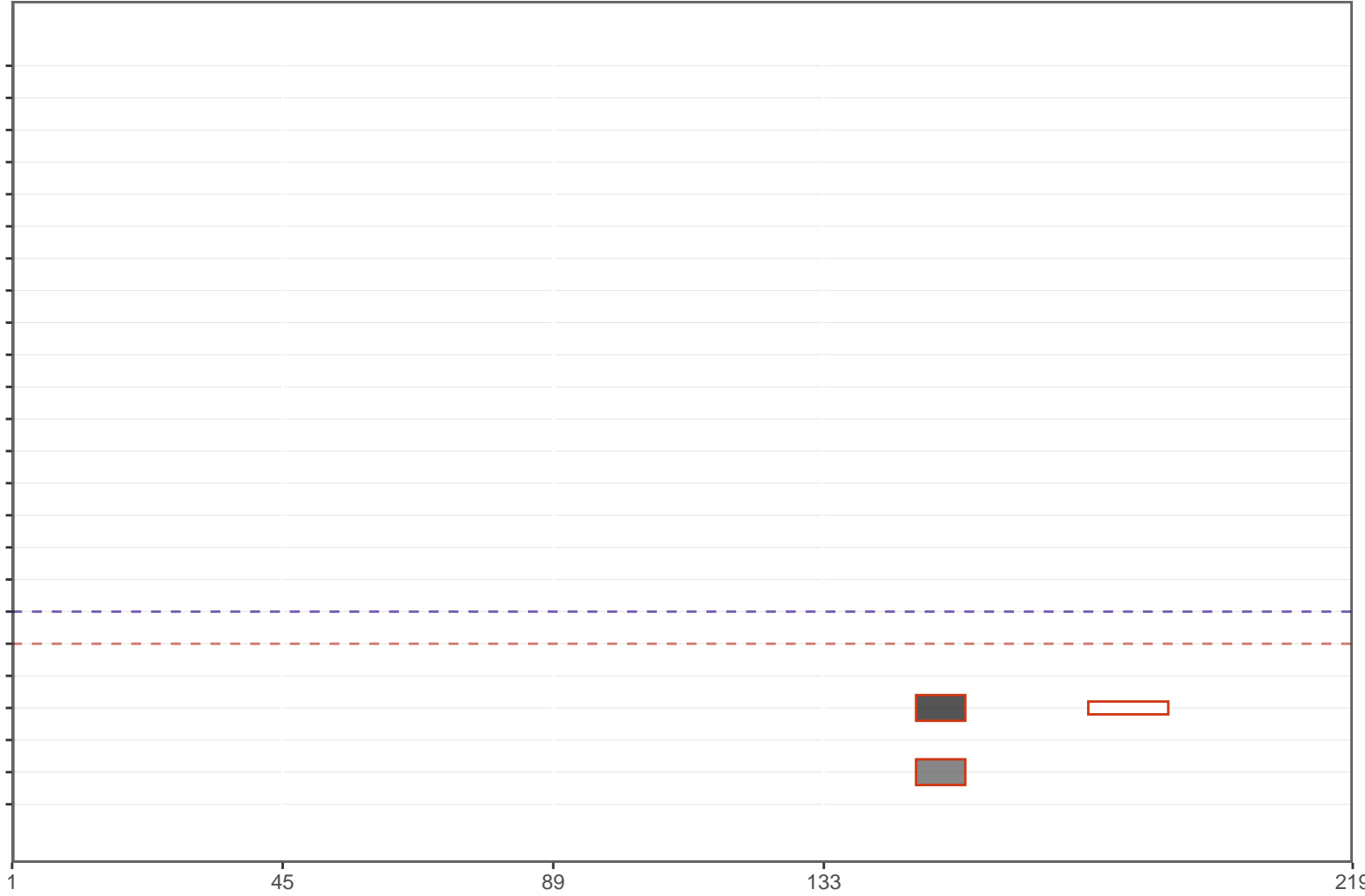
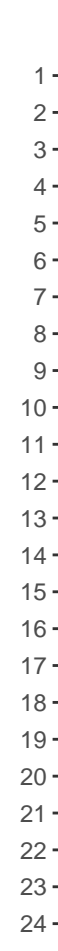
MW indication



Molecular weight



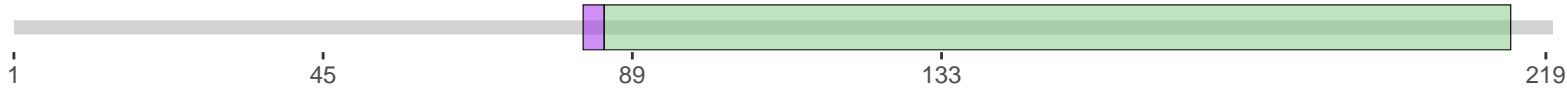
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

LDKLYTSPFGKFMIDERDAIKELNSVWDTSAEVKQLEDQAAAMKAAAEISAAANMKMKETQLEVEKQAEGRKKVEAELOEALASLDROKHEETKSLDSQIAALEDEIKKVLFPVSN

NbL17g06350.1 putative_clathrin_assembly_protein_At2g25430 [MW = 70.4 kDa]

No. of times detected



log(intensity)



Values from



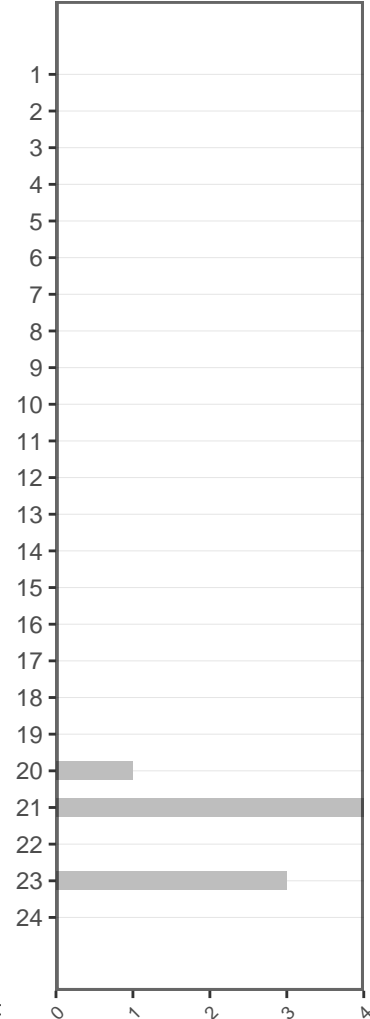
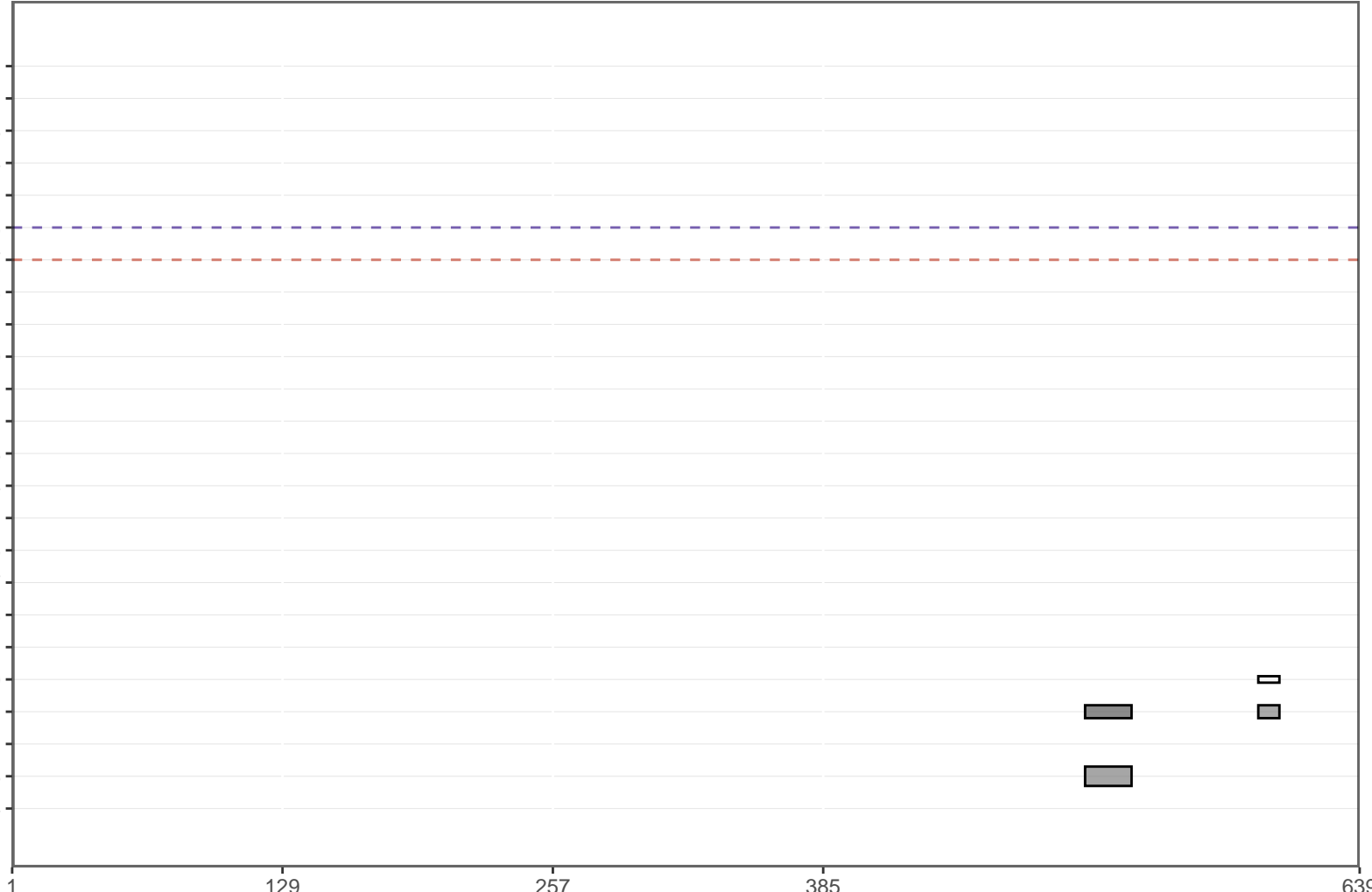
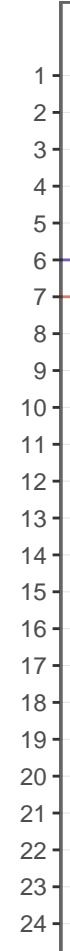
MW indication



Molecular weight

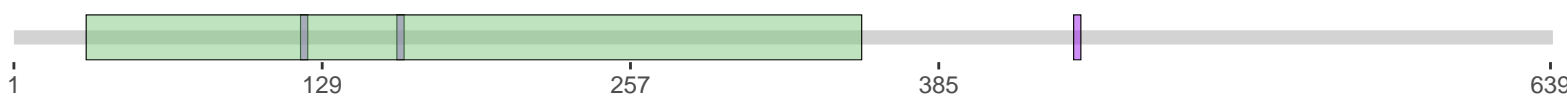


Gel Slice



Peptide counts over 4 repeats

Protein length 1 129 257 385 639



Pfam domains

Pfam Description



Protein sequence:

KQIDELVGFNWKDQGVARSSEYFVQRITSKLDTLEEFVDRRAKATKSPERKVEALPAPPEEPMDMNEIKALPAPEEYTPSPPEPERPKPVVQETGDVLDREEGVTDADDGKFKALFAGPQINNGSWEAFPGNGETQVTSAAWQNPAAEVKQADWELALVETASHLSNQAALGGGLPILLNGMYDGGIRRHVSTAGLGGGSAASVALPGPKKATPVLLPAPDGTVQTVGGDFFAASLTVPPDSYQWMADEFKKGQLLVGEGVWVWQYARDGMOGQTS

NbL17g06280.1 putative_L-ascorbate_peroxidase_6 [MW = 36.73 kDa]

No. of times detected



log(intensity)



Values from



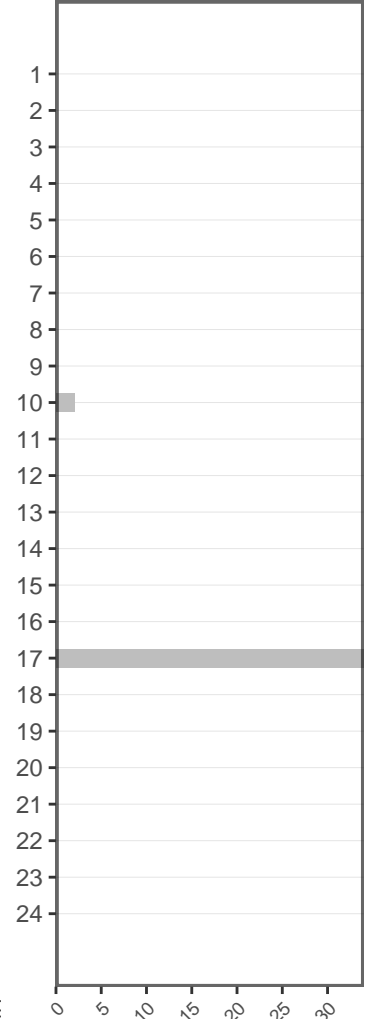
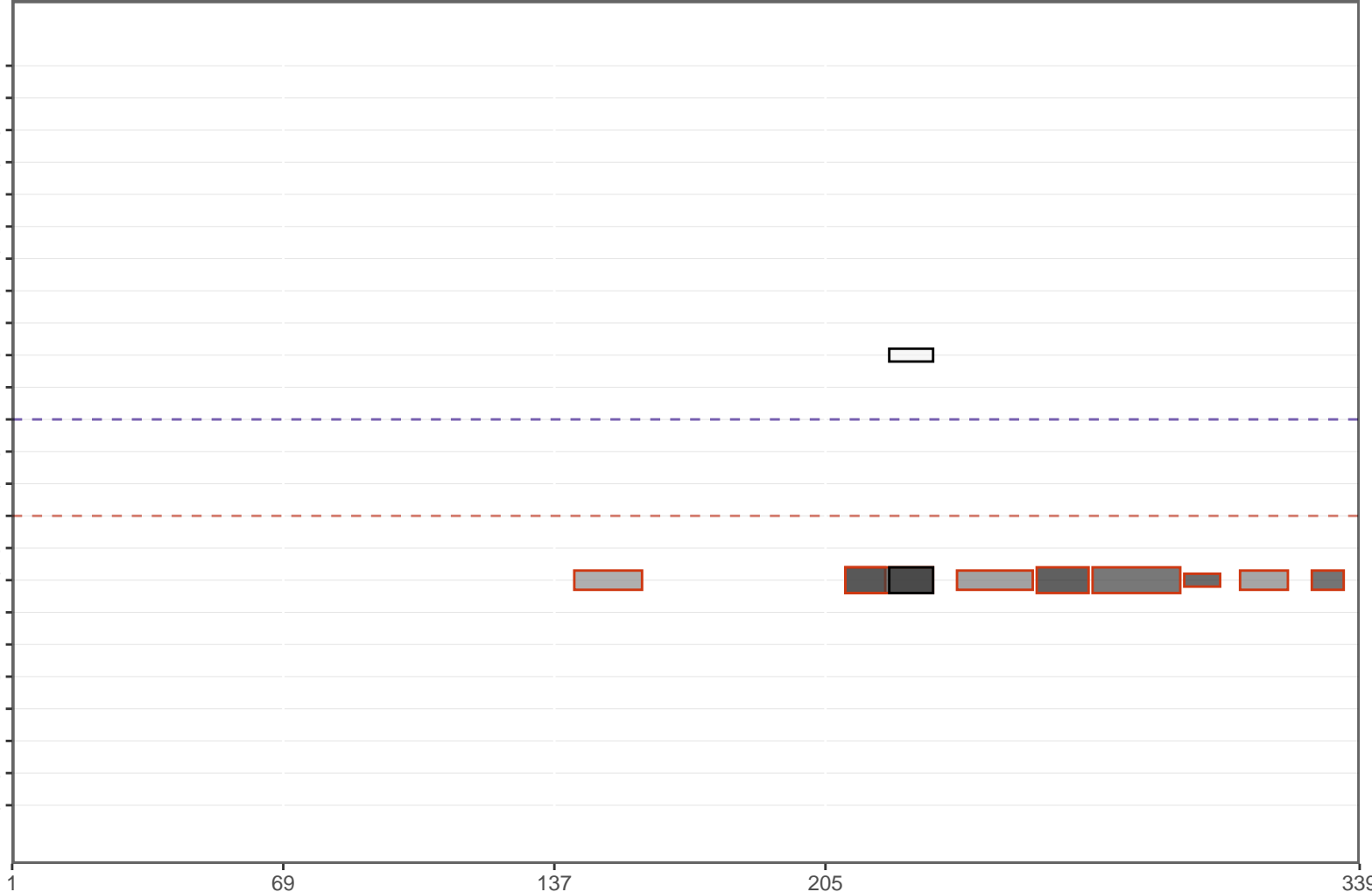
MW indication



Molecular weight



Gel Slice

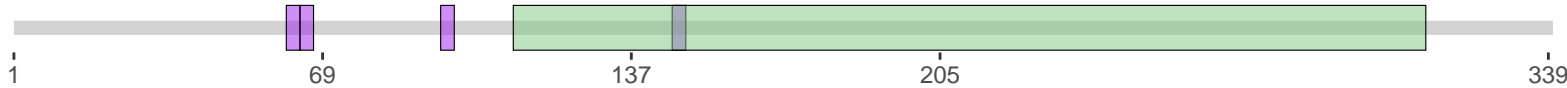


Protein length

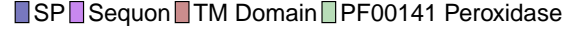


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ENKGLKXSVKLEKAKSGQIVVQPVSWADIALAGAEAVSLGGGPIPIQLGRDMSMPDPEKGLPEESLDATSLKGFERKGFSTQELVALSGAHTLGGKGFNPVVFQNAVFKILMEKPVWSSAGMTSMVGLPSDRALVEDEGCRVWISKYAEQDGLFFEDFKNATKQLVDTGATWQSL

NbL17g06180.1 RNA-dependent_RNA_polymerase_6 [MW = 135.65 kDa]

No. of times detected



log(intensity)



Values from



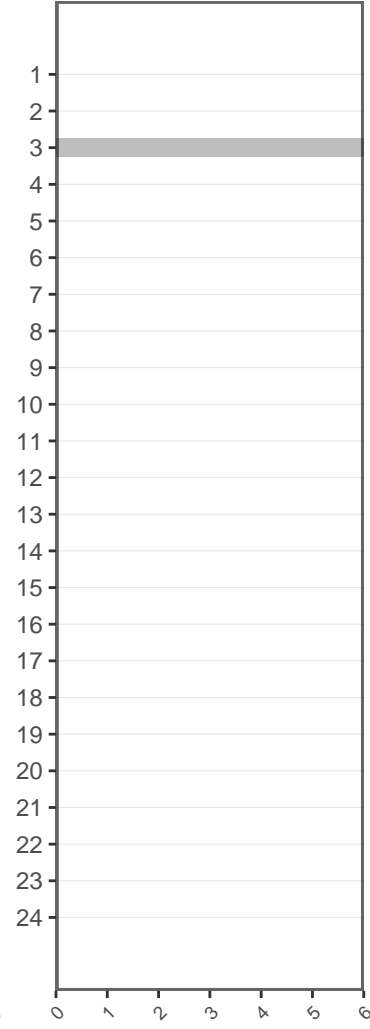
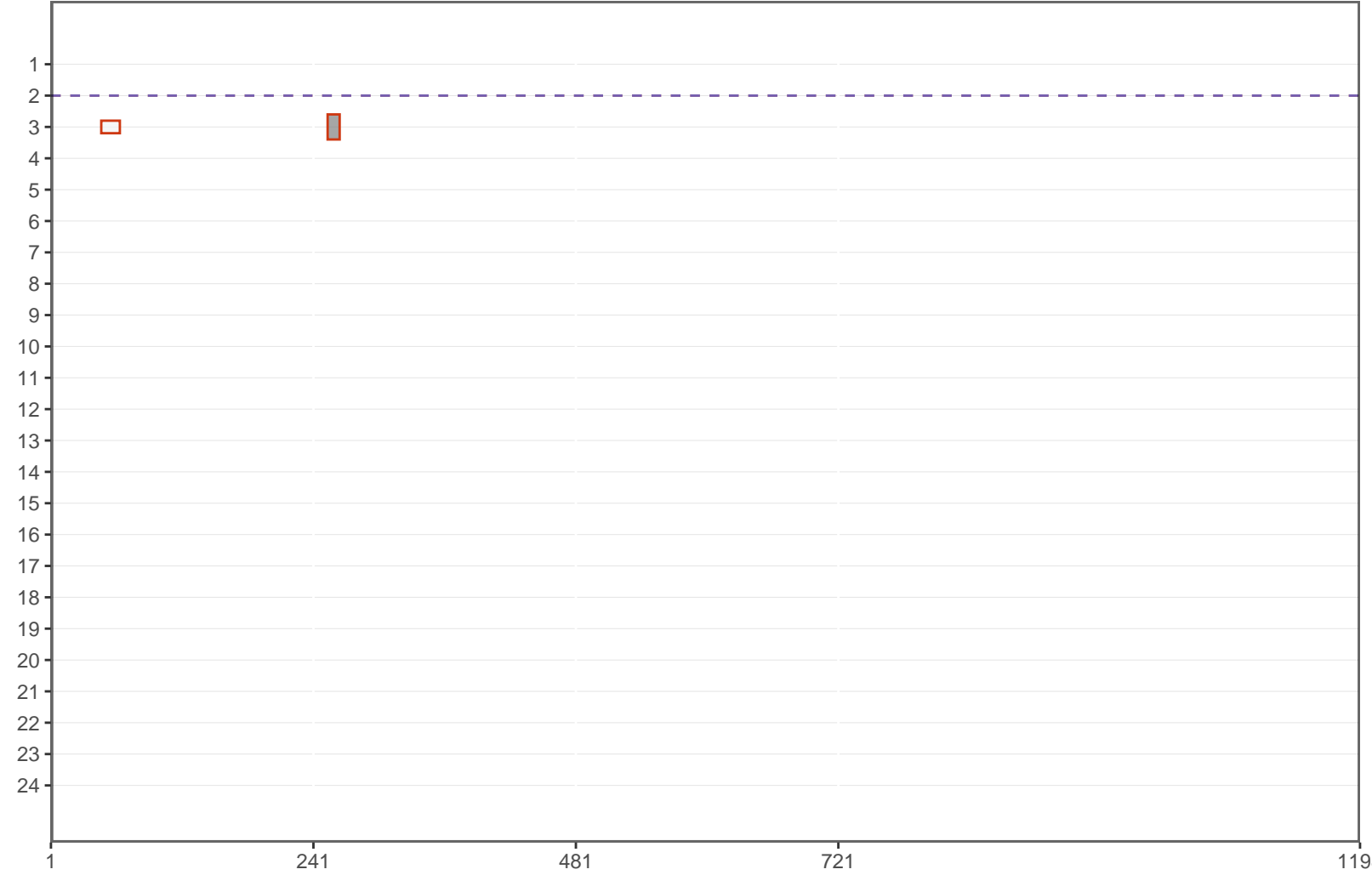
MW indication



Molecular weight



Gel Slice

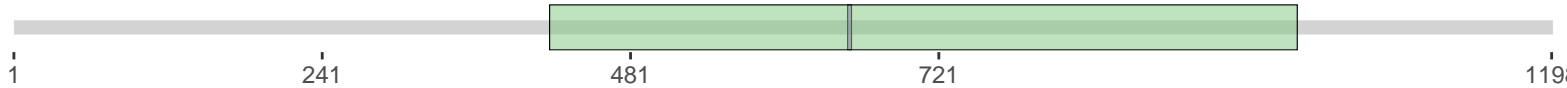


Protein length

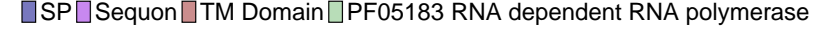


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

DDGIMISADLALLEVAEKJHLGVNPPSAYQIRYAGGKGVVAGWPTKNDGILLSLRPMKFDNHTLEICDWTFRFGPFLNRQIVTLLSGLDVKDQIFWEMQKEMISGLNKMILVDSDFVDFVITASCFAEAGNTAAMLSAGFKPQSEPHLRGMLSSIRASQIGDLRNRKARIFVPSGRWLMGCLDELGELEGGGCFQVSSPSELENCFRKHGPKFSDIKKNGVYKGLVIAKXNPKLHPGDVRIIEAVDVPGLHLYDGLVFPQKGRPHSEAEAGSDLDGLYFVTVYDLENLPPS

No. of times detected



log(intensity)



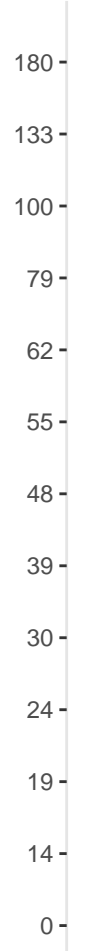
Values from



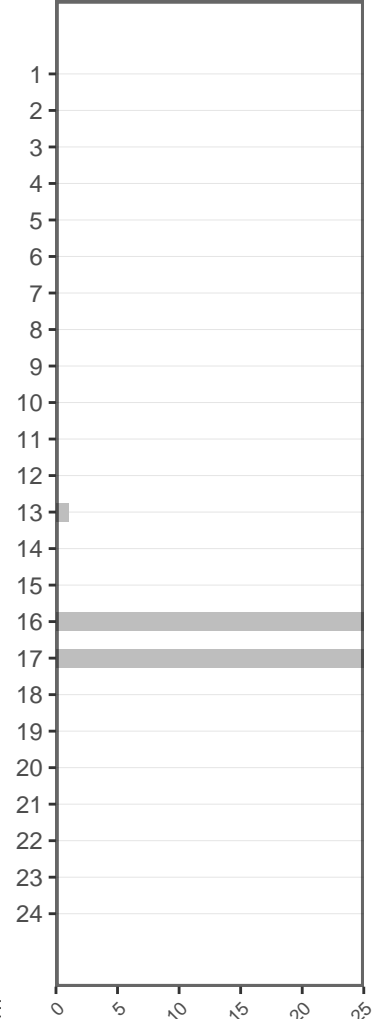
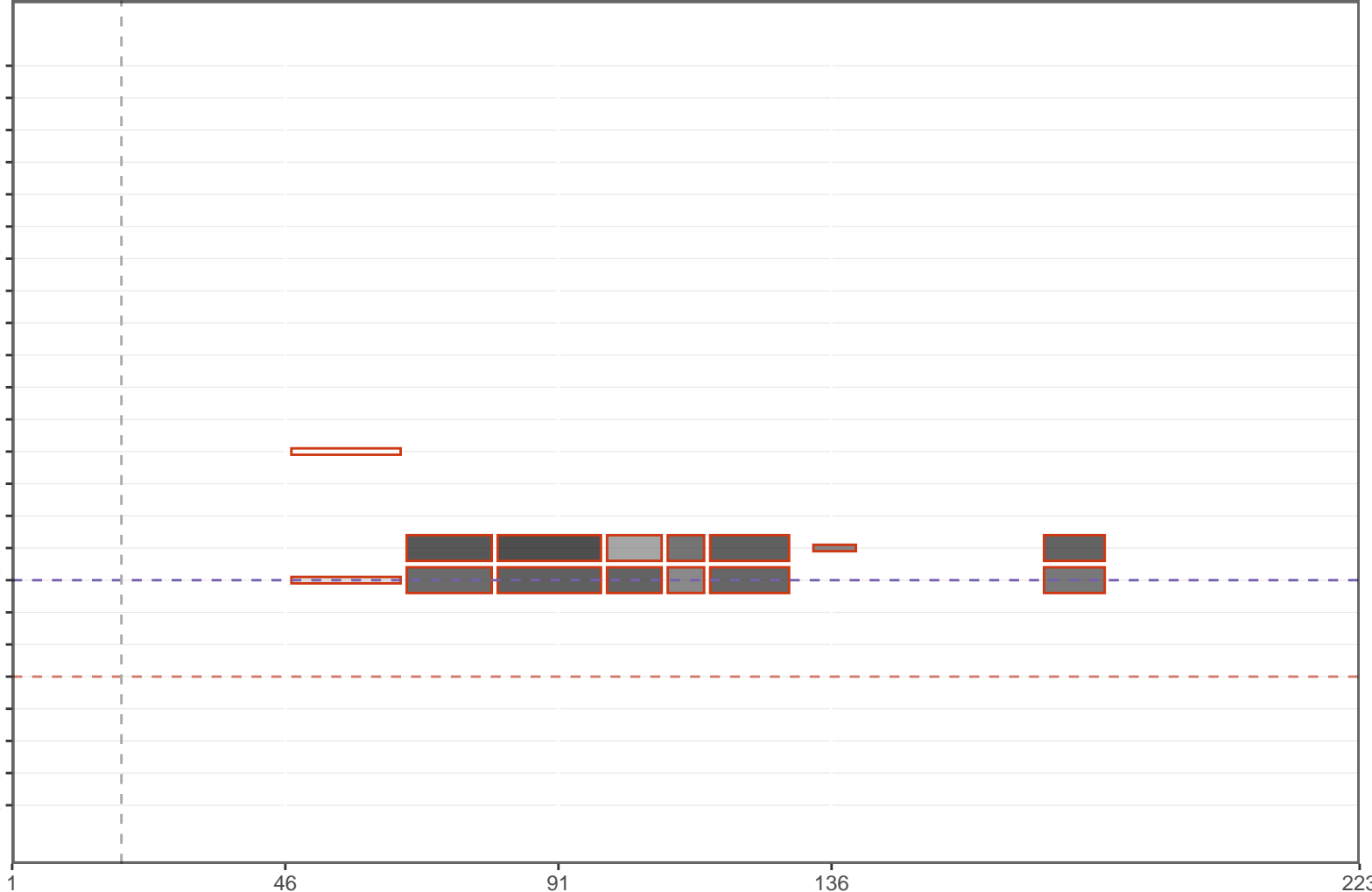
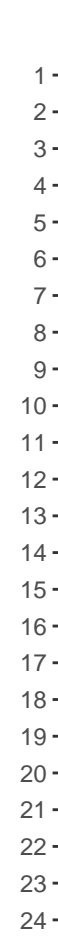
MW indication



Molecular weight



Gel Slice

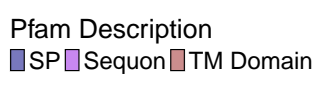


Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:

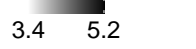
ASSLAQIGRFLACGKVAEPSEAFNDLIRNKRDLNLRNKHTEVGAAVSGDGGGPPYFWCVLFGNGKPKSFSVTEGGEPKVTIRPGCFSGANDGNGNLSRTHLWPTALGFAALLVAL

NbL17g05670.1 ADPATP_carrier_protein_mitochondrial [MW = 41.9 kDa]

No. of times detected



log(intensity)



Values from



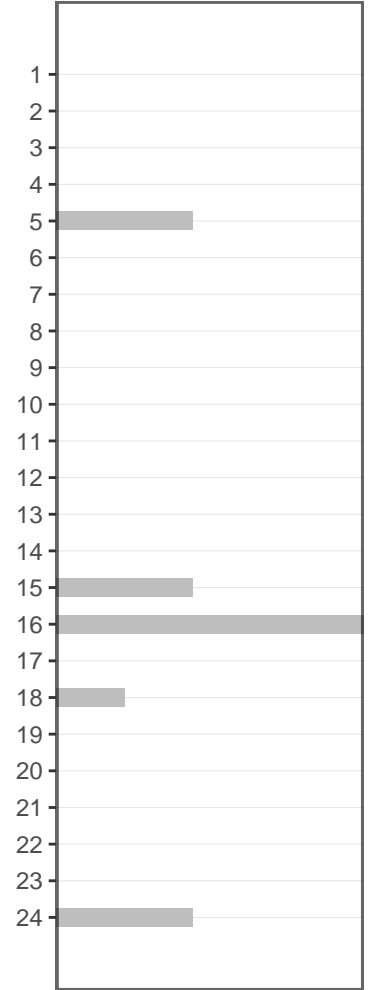
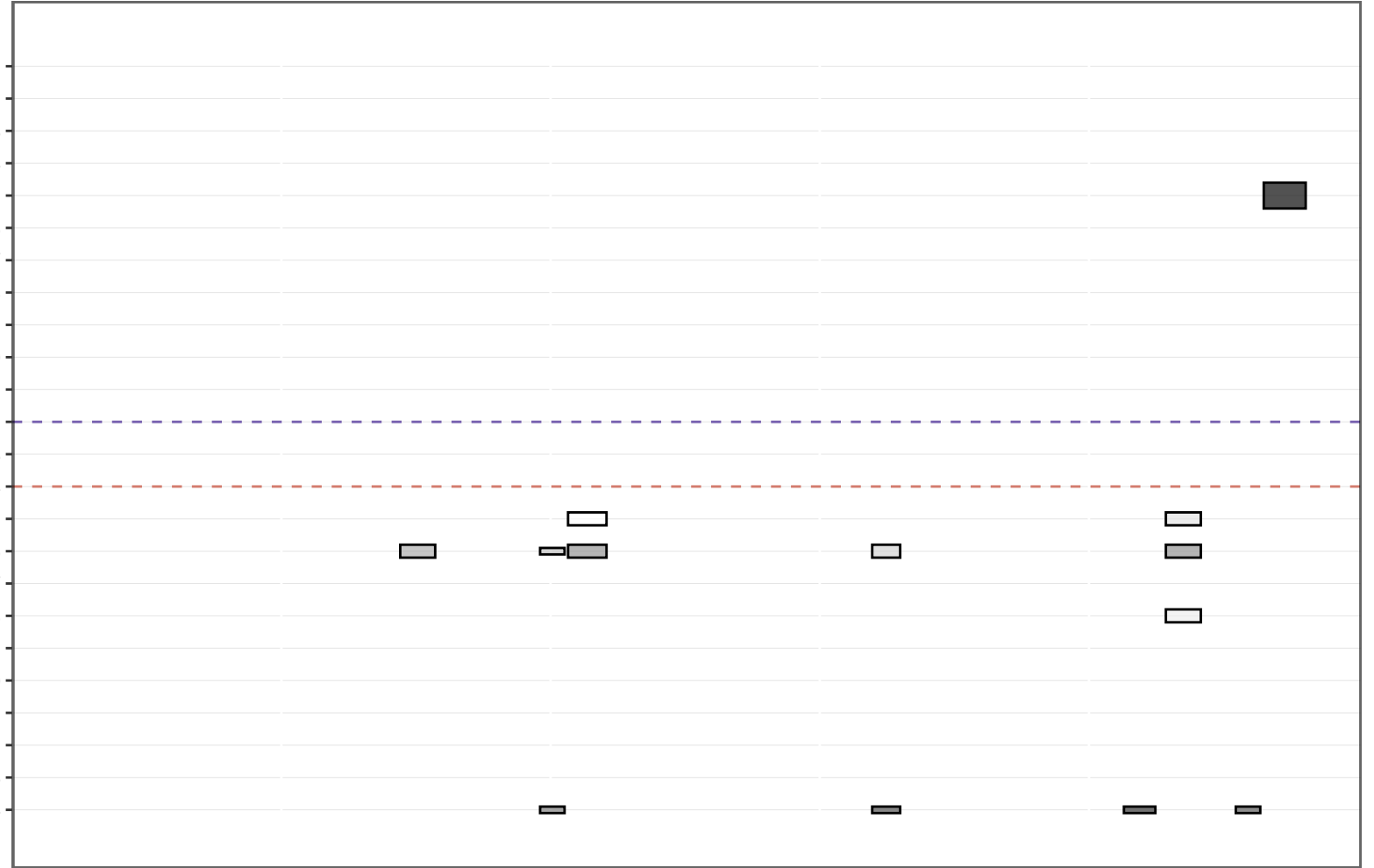
MW indication



Molecular weight



Gel Slice

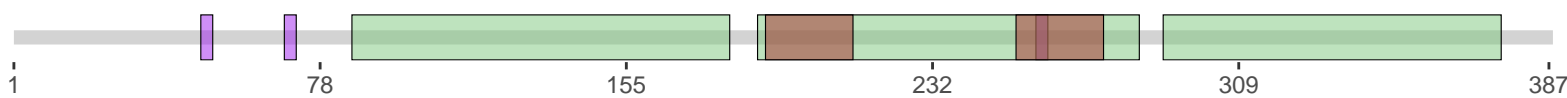


Protein length

Peptide counts over 4 repeats



Pfam domains



Pfam Description

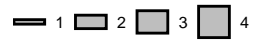


Protein sequence:

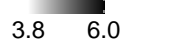
KKDRDGYWVWFAGNLSGGGAAGABELLFVYSLDWARLRLANDAKASKGGERDFNGLVDVYRKTLSKSDGAGLYRGENISGVGIIVYRGLVFGMYDGLKPLVLTGNLGDFFASFGGLGWLTNAGLASYPIDTVRRRMMMTSGEAWKYKSFDFSGNKNENPKSLFKGAGANLRAWAGAGVLAGYDGLGVVFGKYYGSGGA

NbL17g05660.1 omega-amidasechloroplatic [MW = 40.96 kDa]

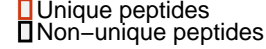
No. of times detected



log(intensity)



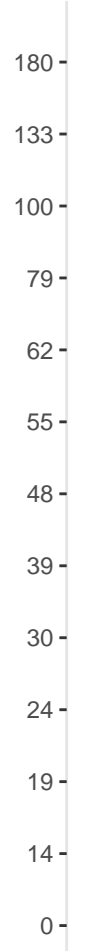
Values from



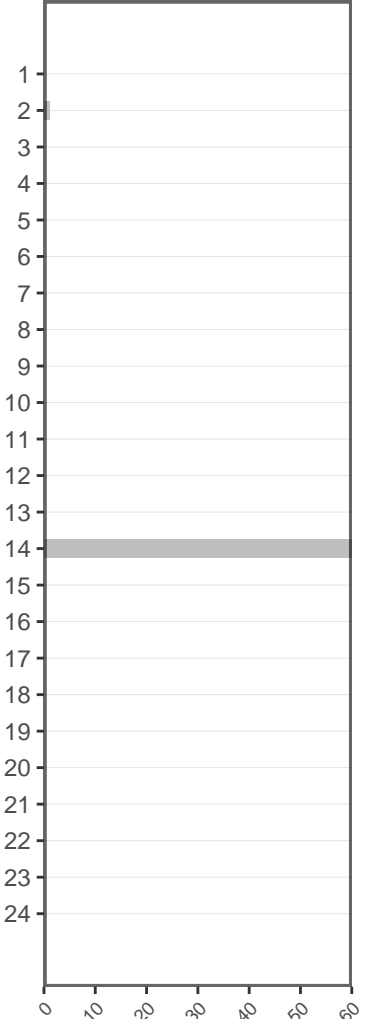
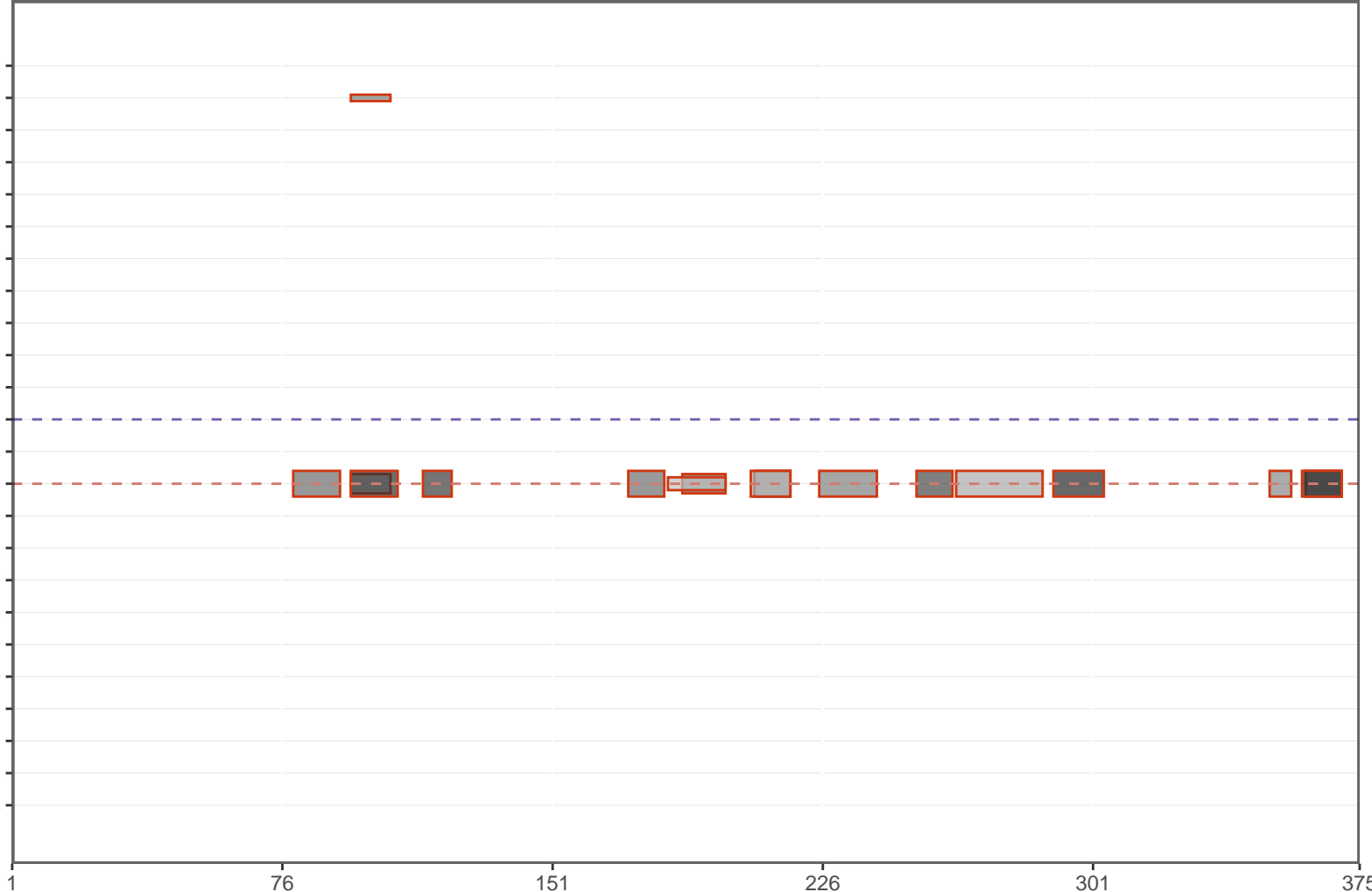
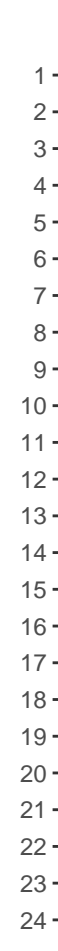
MW indication



Molecular weight

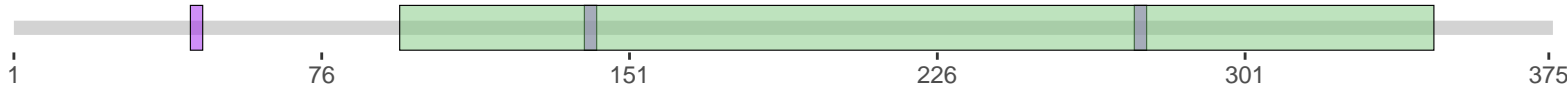


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

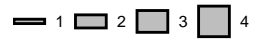


Protein sequence:

SGSIPERSGDKLYNFDGIFGVDGKAKHRKHLFDNDIPGKTFKESKTLGAGETPTTVYDTEVGRIGGICVDIRFQELMLVAARGAHLICYPGAFNMTTGPLHWELLRARAVDNDQLYVATGSPMRDAGAGVVAWGHSTLVGPFGEVLATTEHDEAIIHSEIDYSGIELRRTNLPLEKQRGDLVQLVDVQRNSGQ

NbL17g05460.1 aminopeptidase_M1 [MW = 99.18 kDa]

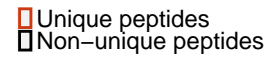
No. of times detected



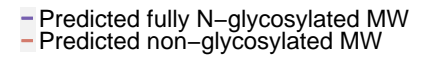
log(intensity)



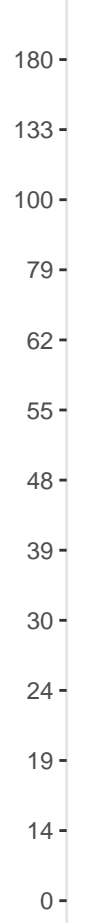
Values from



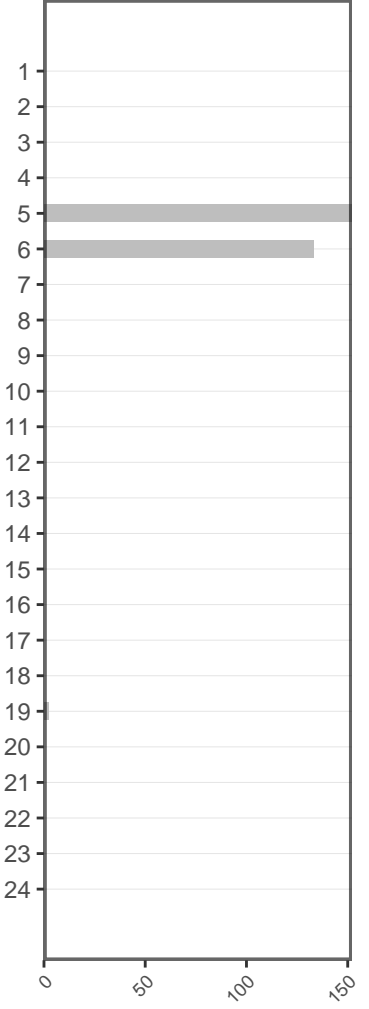
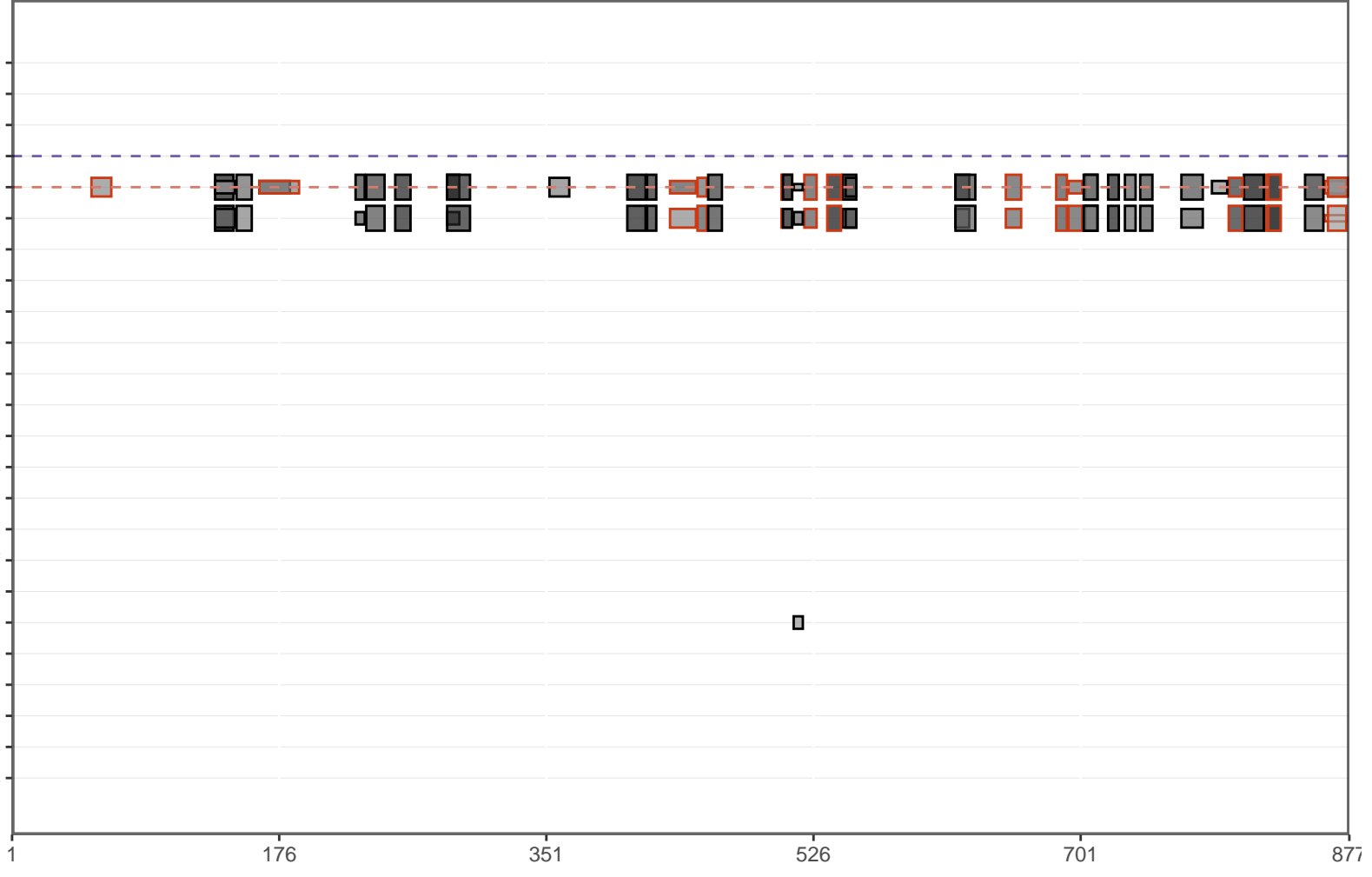
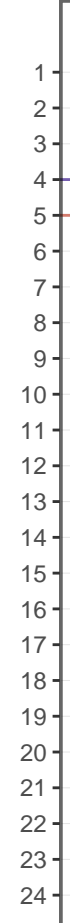
MW indication



Molecular weight

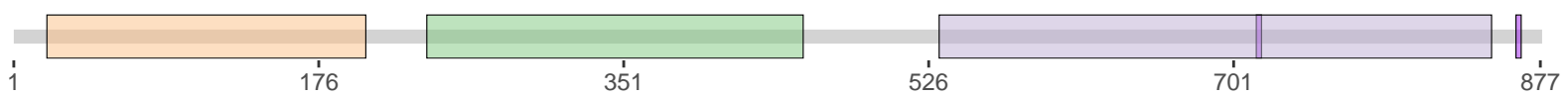


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ICSNAKTEDLVSYLQEEGGPYNKLMNSWTKGGGVPVWVKIKDKKLEGGDGTQFLLSGSHGGDQWVPLTLGGGVEARKFLMGEKBEALDVKGLLGSSESGNPKWIKVNDQGTGFRVRYVDDELSARLRVWESGKLGSTNDKYGLDSDVALSMACHQGLSLLALMASFREELDFTVALSNLSISGKVSRIAADAVPDKDKHKLFFINLQFSAERLQWDPKQGESHLDMALRGELLNLAALFGHDEITNEAIRRFYIFLDDRNTPVLPDLRRAYVWIMQRVNSDF

NbL17g05430.1 ran-binding_protein_1_homolog_c-like [MW = 24.49 kDa]

No. of times detected



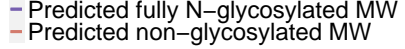
log(intensity)



Values from



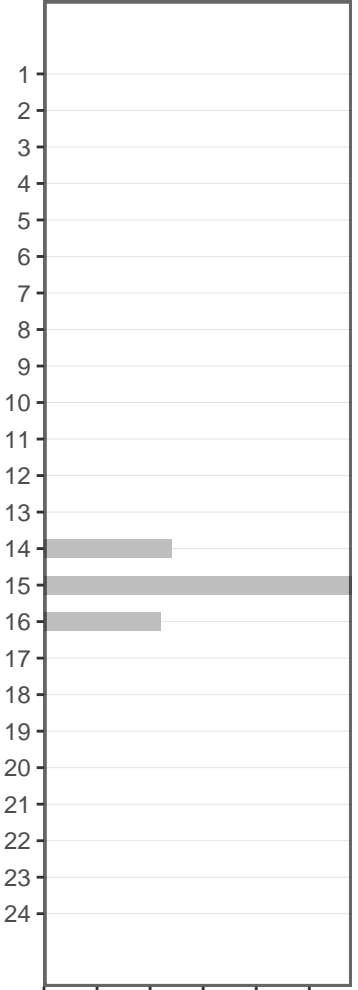
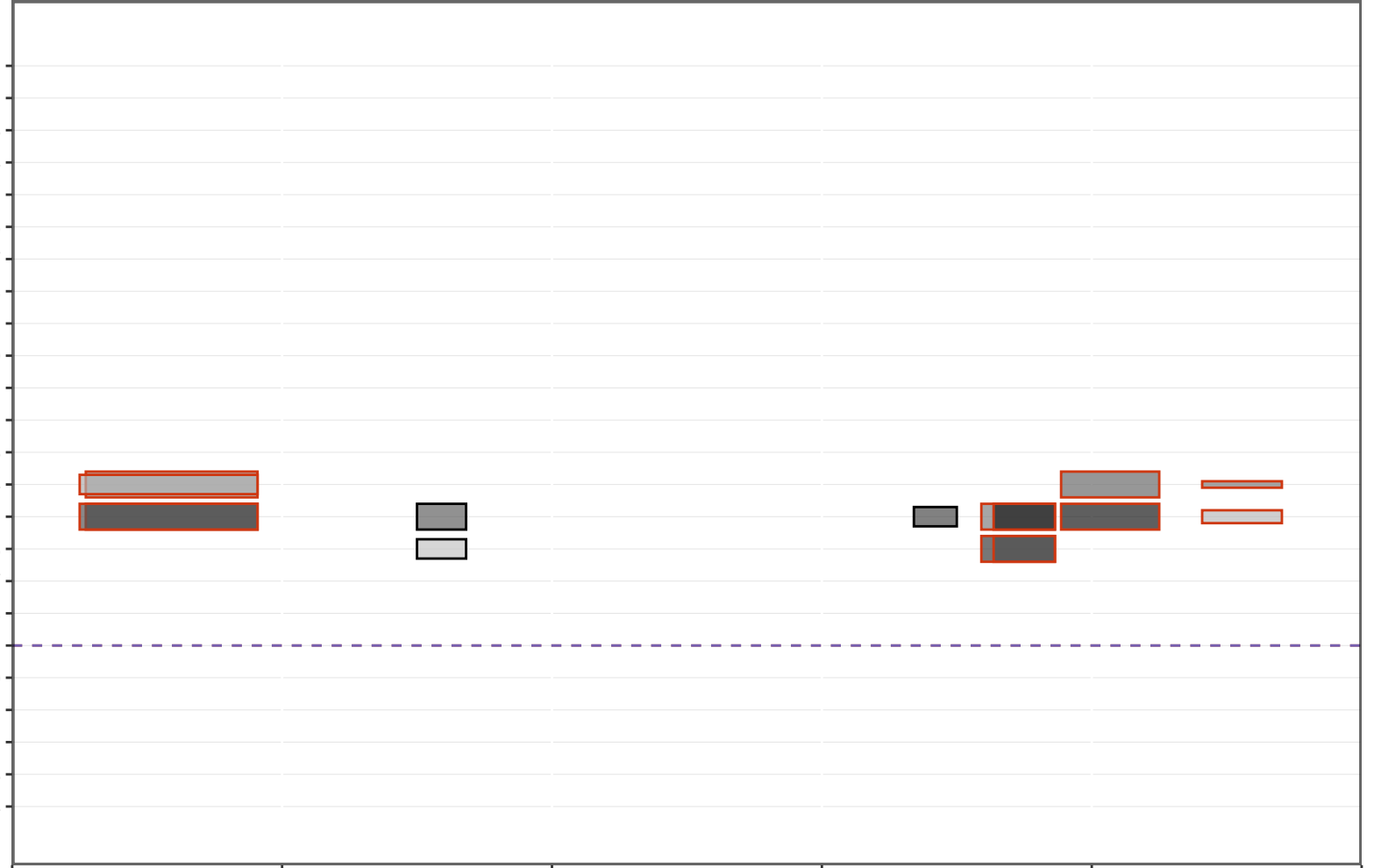
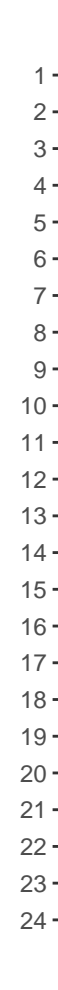
MW indication



Molecular weight



Gel Slice

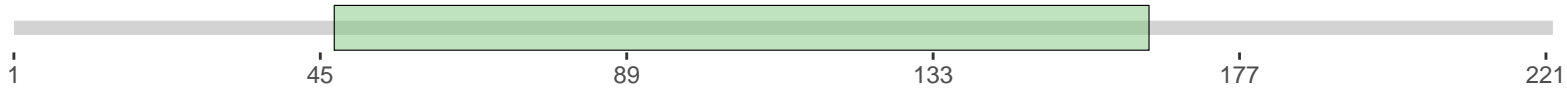


Protein length

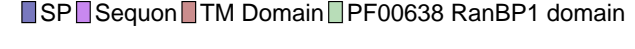


Peptide counts over 4 repeats

Pfam domains



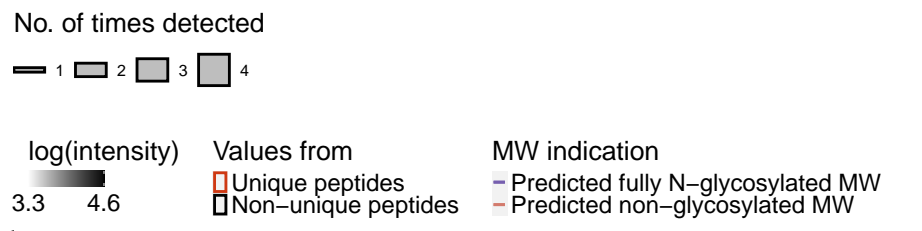
Pfam Description



Protein sequence:

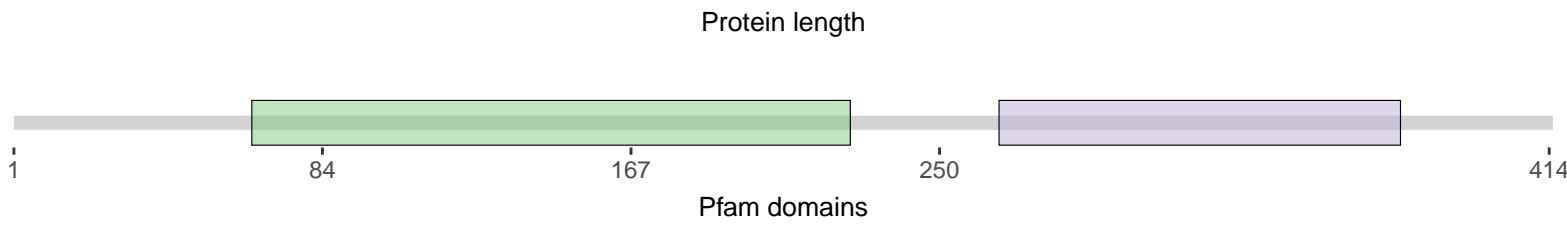
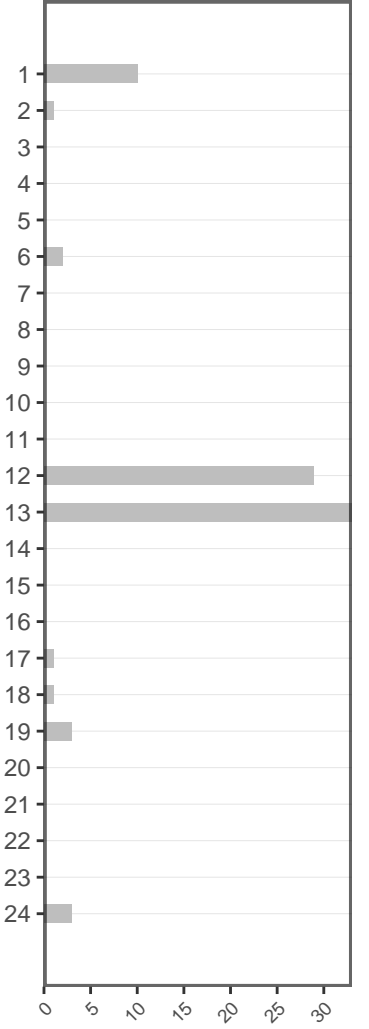
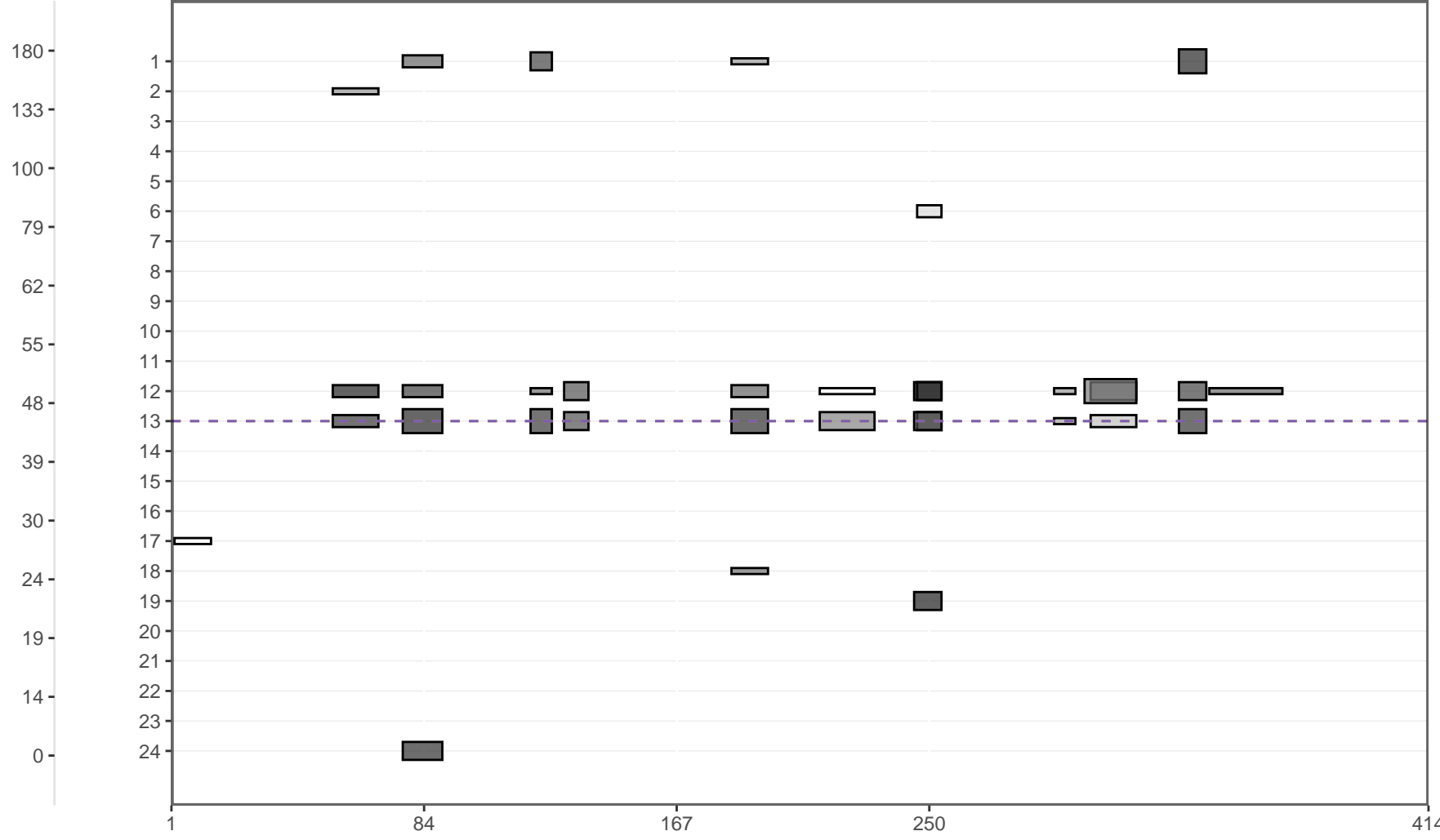
MRSQSKTLKICANILVLPMTDQEHAGNEKSGVWVAADFADGELKEETFGIRFASINDKSPKKEVEEAEAGGQTKSEEGEGAAAATELIEKLVESHKDKKEKSPMPTEKKEKNEEDENK

NbL17g05330.1 eukaryotic_initiation_factor_4A-14-like [MW = 46.93 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF00270 DEAD/DEAH box helicase PF00271 Helicase conserved C-terminal domain

Protein sequence:
 ADEMLSRGFKDQYDFQLLPKQGVGVSATMPPEALETRKFMKPKVRLVLRDELTELEGKGFYVWVQKEEWKLETGDDVETLATQGVVFNTRRKYDVLTKMRSRQHTVSATHGDMQDNTFRDMMREFRSGSSRVLFTDQLLRGIDVGGVSLVWVLDLFTQPEVYLRIGRSGRFRGKGVANFVTKDDERMFLDKQKEYVWVEELPANVADLL*

NbL17g05300.1 cytokinin_ribose_5'-monophosphate_phosphoribohydrolase_LOG8-like [MW = 23.27 kDa]

No. of times detected



log(intensity)



Values from



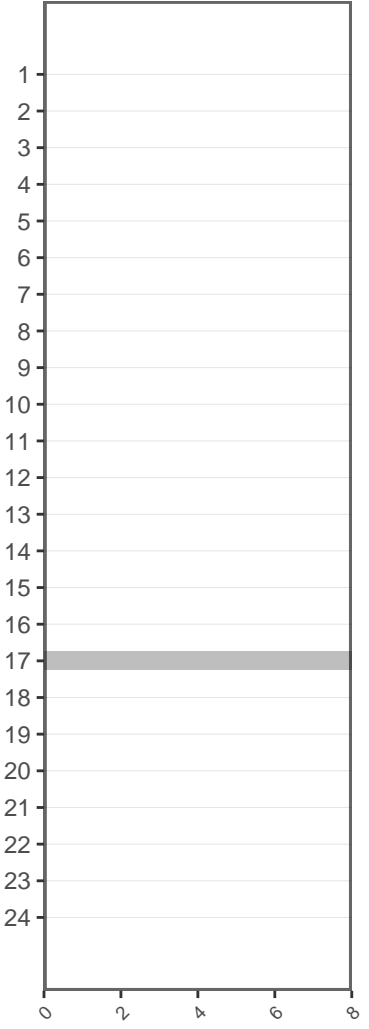
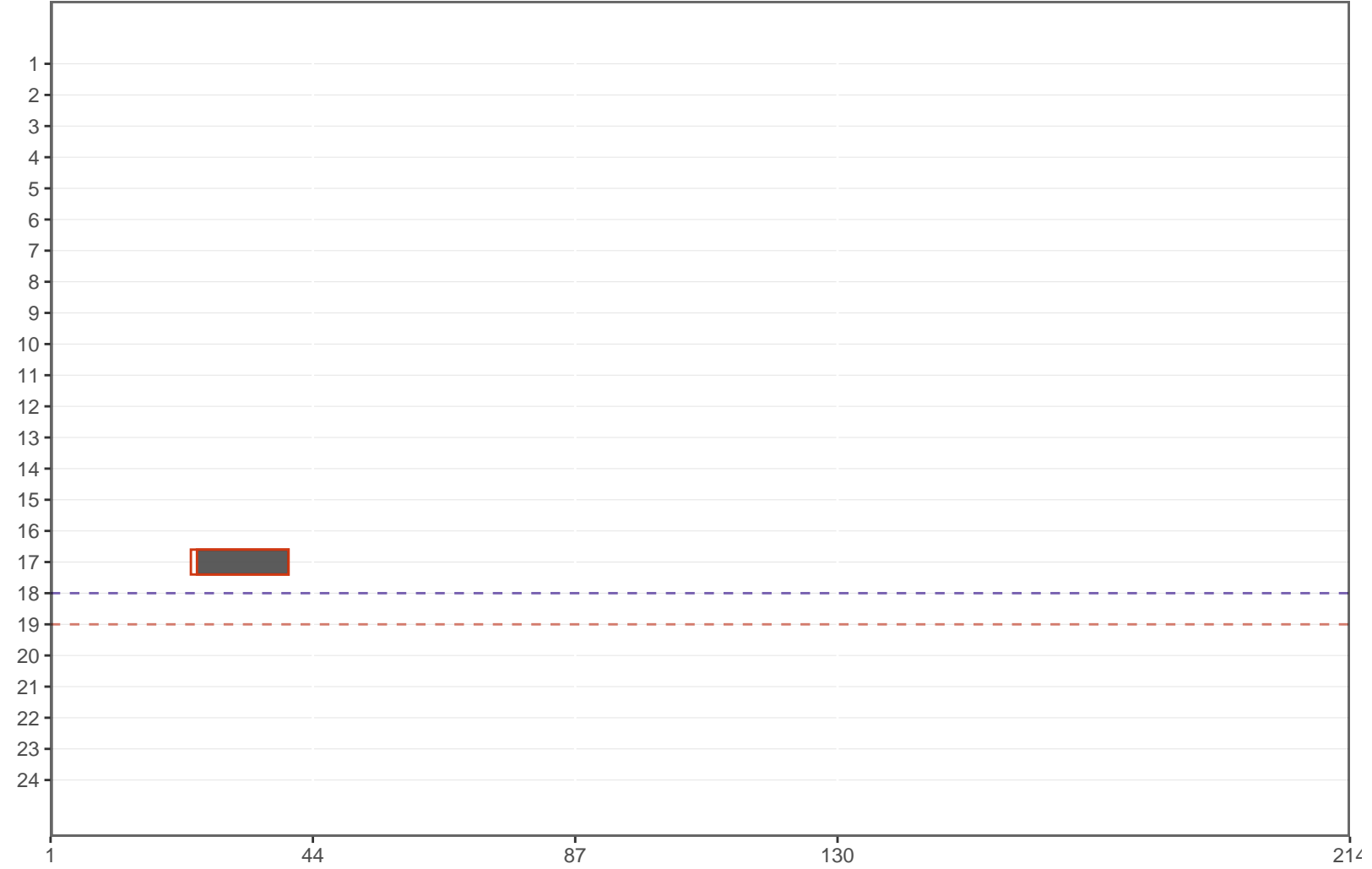
MW indication



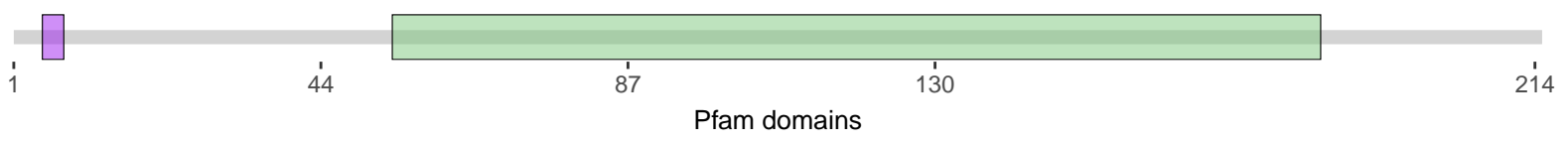
Molecular weight



Gel Slice

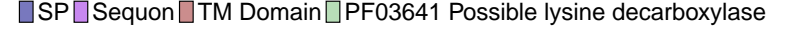


Protein length



Pfam domains

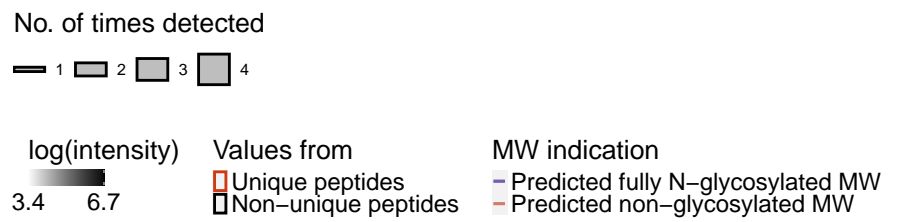
Pfam Description



Protein sequence:

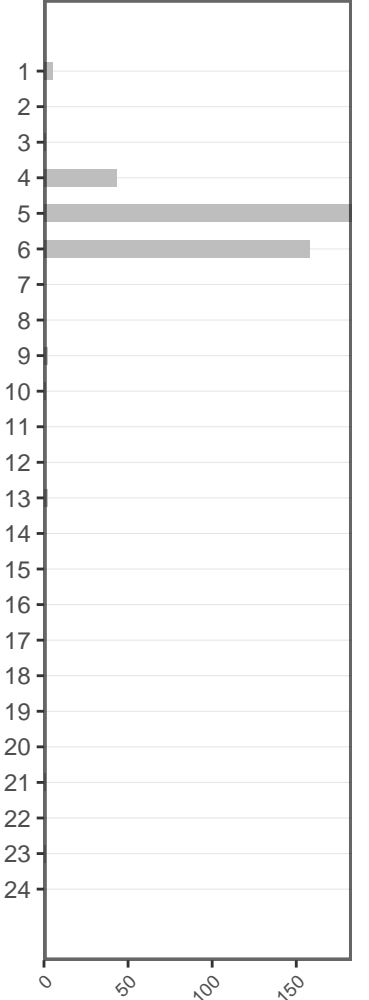
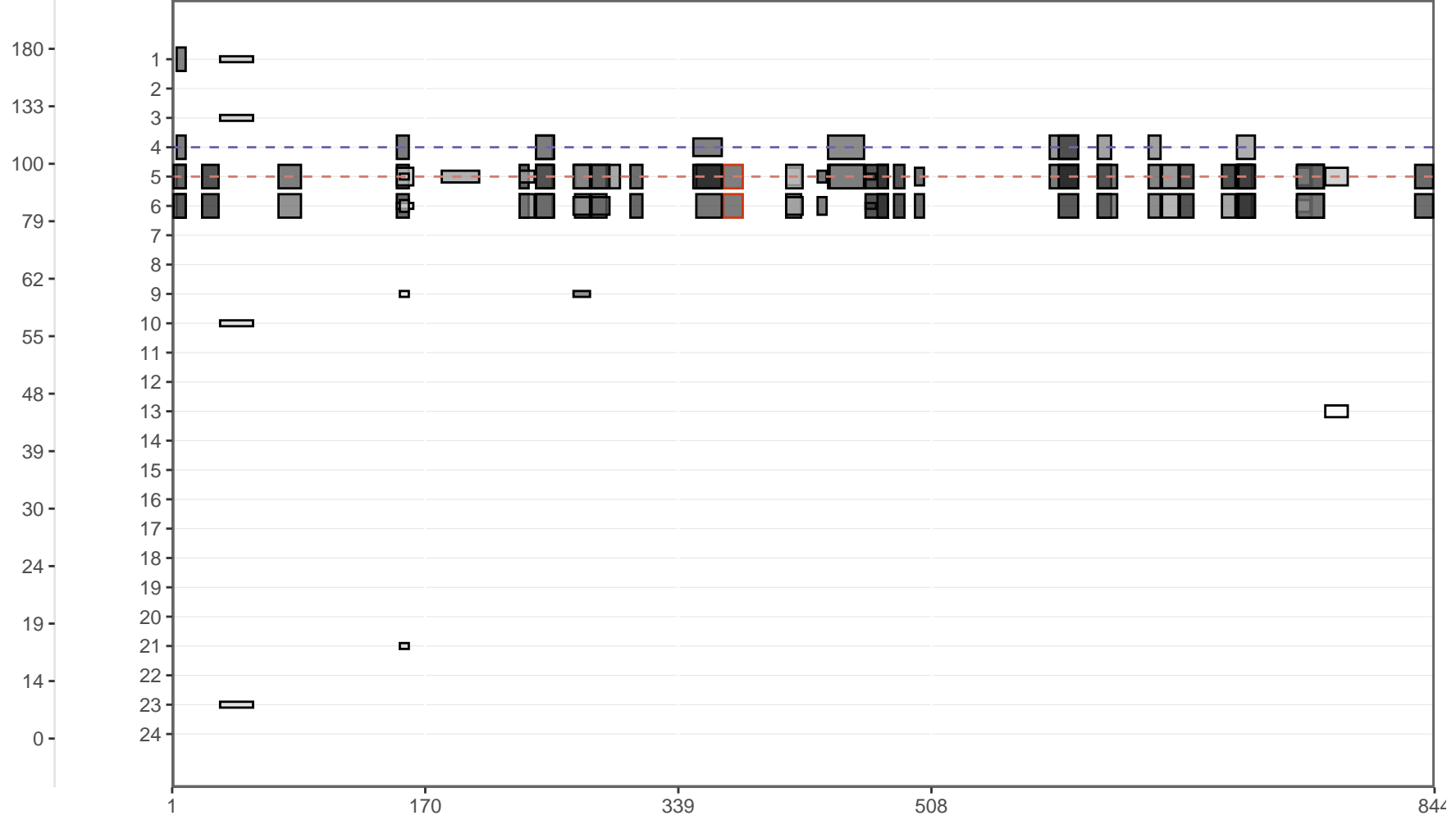
#HERKAEAMASQADAFIALPGGYGTMEETLEMTWQLGHHKIPVGLLNVEGYNSLTLFDNGVVEEGFRKPGARDIVLAAPTARELLSKMEGYTPSHDHPAPHEGWMEELAYKREGSP

NbL17g05280.1 elongation_factor_2 [MW = 93.97 kDa]



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

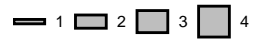
- SP
- TM Domain
- PF00679 Elongation factor G C-terminus
- PF03764 Elongation factor G, domain IV
- Sequon
- PF00009 Elongation factor Tu GTP binding domain
- PF03144 Elongation factor Tu domain 2
- PF14492 Elongation Factor G, domain III

Protein sequence:

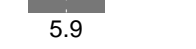
/RIMGPNYYPGEKXKDLVKNVGRRTVVMGKGETVEDVPCGNTVMVGLDFFTKNATLTNEKEVEAHPIRAMKFFVSPVVRVAVGKGLASDLKPKVEGLKRLAKEDPMVLSIEEGEHHAGDELHLEGLKLDQDDFMGGAEIIVSDPVVVFRETVLEKSGRTVMSKSPKHNRLVMYMEARPLEEGLAEIIDDGRIGRPDDPKVRSKILSEFGWDKDLAKKIWGFQFPETTGPNMVDVMCKGVGYLNEIKDVAAGFGWASKEGALAEENMRGIGFVCDVLIHADAHF

NbL17g05260.1 elongation_factor_2 [MW = 93.99 kDa]

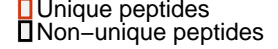
No. of times detected



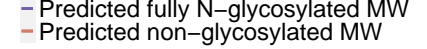
log(intensity)



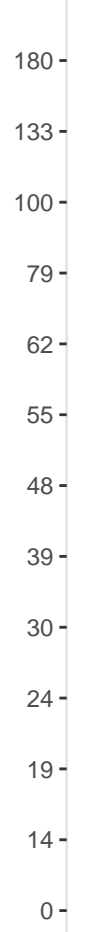
Values from



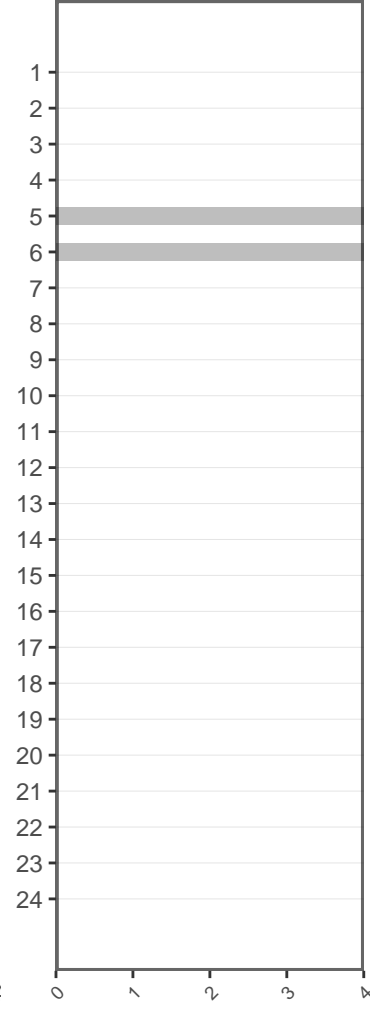
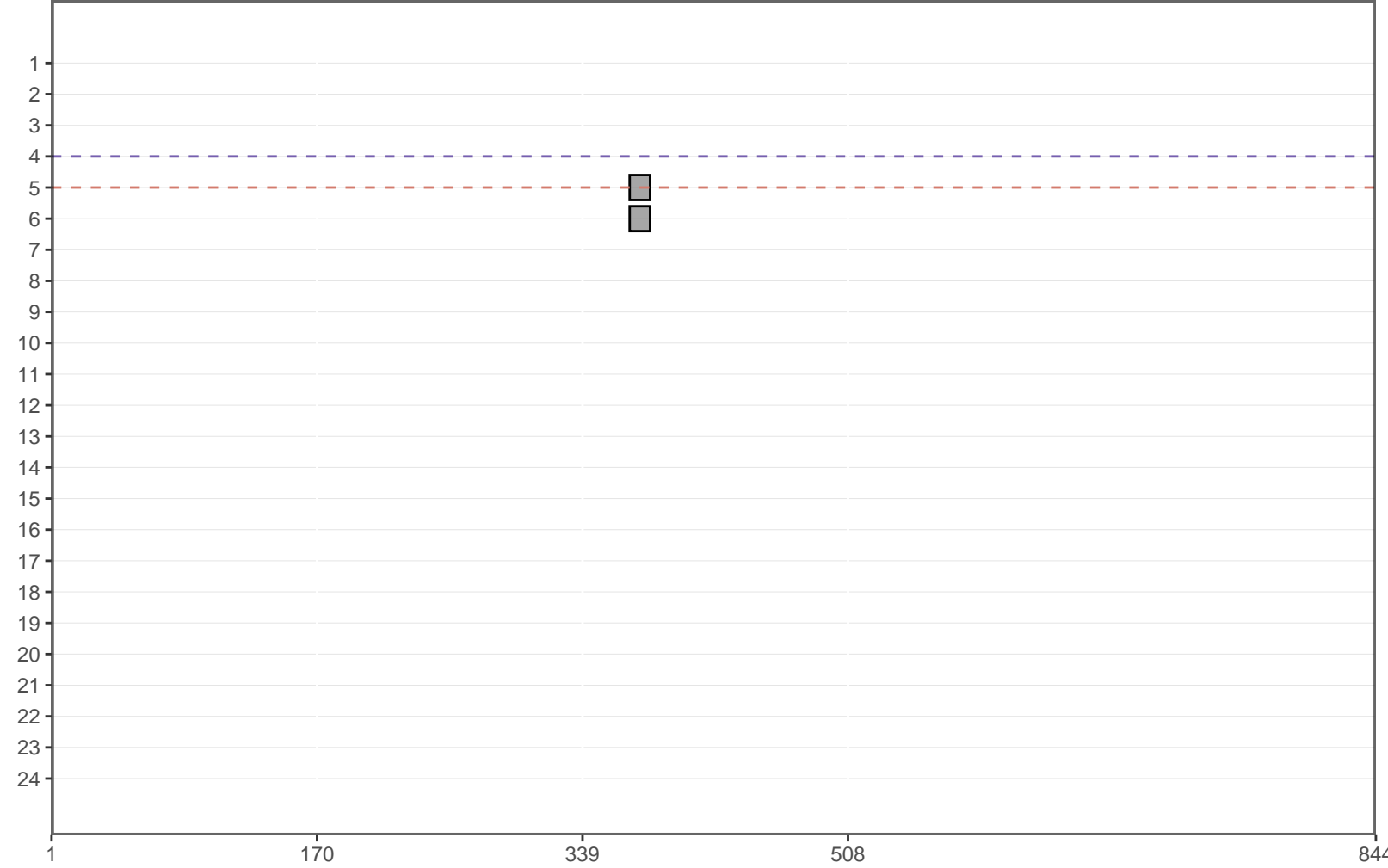
MW indication



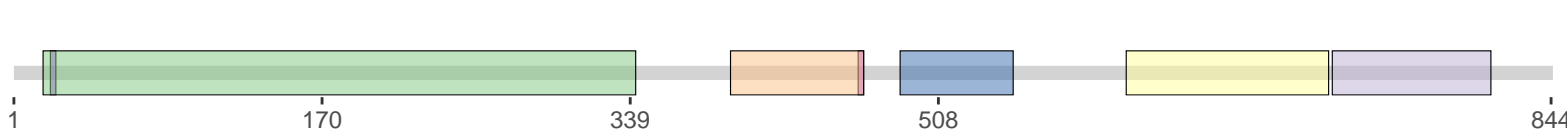
Molecular weight



Gel Slice

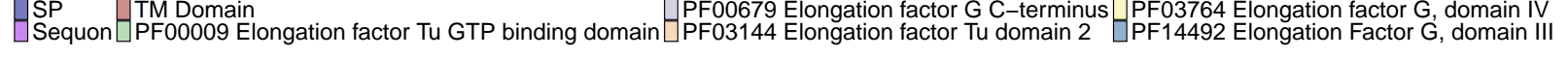


Protein length



Pfam domains

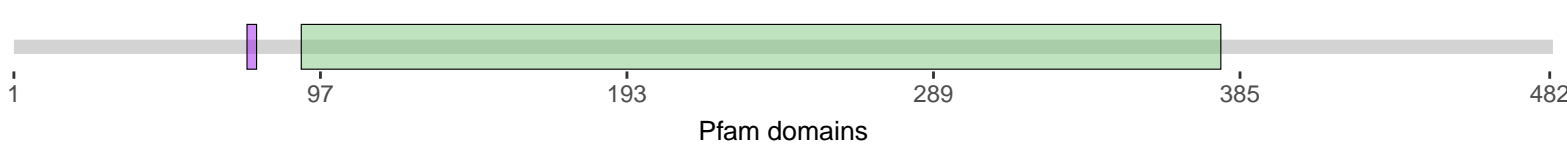
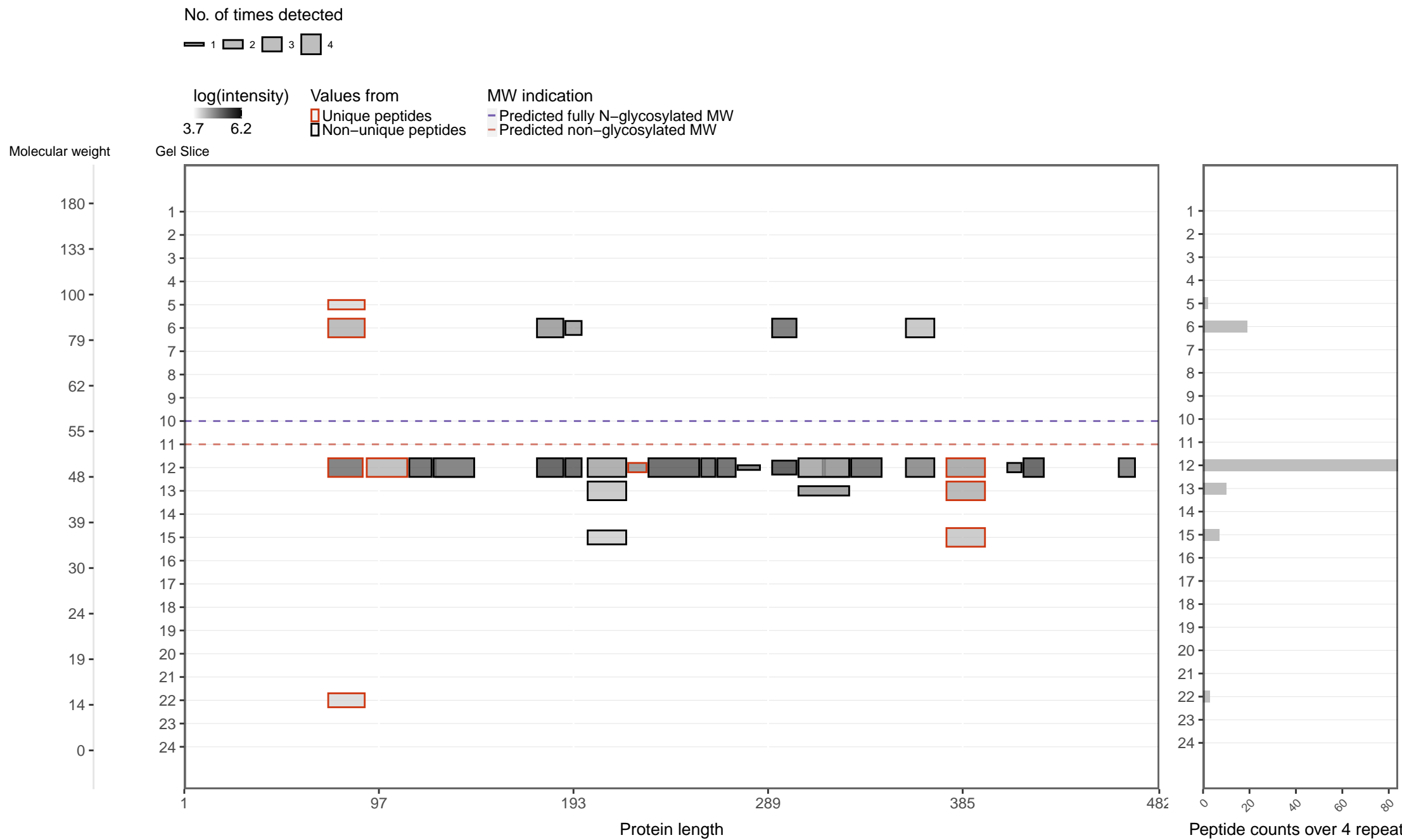
Pfam Description



Protein sequence:

/RIMGPNYYPGEKKDLVKNVGRVTVWVGKKGTEVEDVPCGNTVMVGLDQFTKNALFTNEKEVEAHPRAMKFDVSPVVRVWVGGKLABDLPLKLEGLKRLAKSDPMVLSGIEEGEHAGELHLEGLKLDLQDDFMGGAEIIVSDPVVFRFETVLEKSGRTVMKSPNKNRLVMEARPLEEGLAEDDGRIGRPRDDPKVRSKILSEFGWDKDLAKKIKWGFGETTGNMNVDMOKGVGYLNEIKDVAWGFQWASKEGALAEENMRGIGFEVCDVLIHDAIHF

NbL17g05150.1 UDP-sulfoquinovose_synthase_chloroplastic-like [MW = 53.39 kDa]



Pfam Description
 SP Sequon TM Domain PF01370 NAD dependent epimerase/dehydratase family

Protein sequence:
 VKLGTMSGEYGTPTNDIEEGFRITTHNGRTDPLPYPKQASBFYHLKVKVHDSHNAFTGKAWGIRATDLNNGSVYYGVRTDETAMHEDLVNRLDYDAVFGTALNRFQVQAAVGHPLTVYKGGSGTRGLDIRDTVQGVVEIAANPAKSGEFFRVFNQFTGEGFVNELAALVTKAGEKLGLEVKTEIVPNPRVVEAEHYYNAKHTKLELGLGPHLLSDLLSLLNFVAQYKDRVDTKQIMPVGVWKKIGAKPKTVAAL

NbL17g05050.1 glycine_dehydrogenase_(decarboxylating)_mitochondrial [MW = 113.92 kDa]

No. of times detected



log(intensity)



Values from



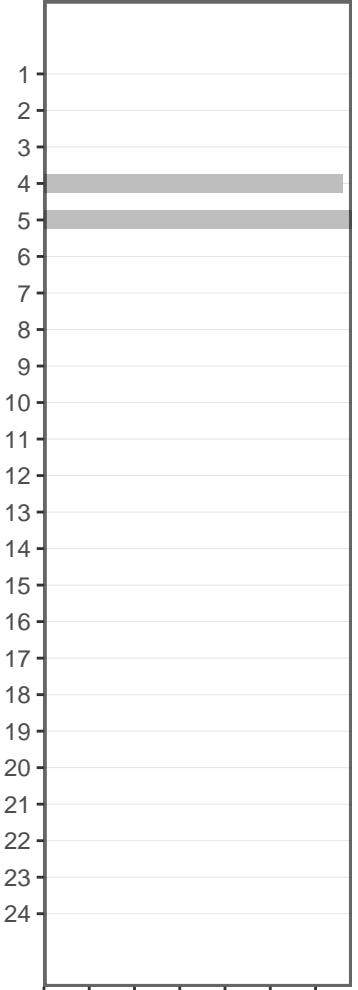
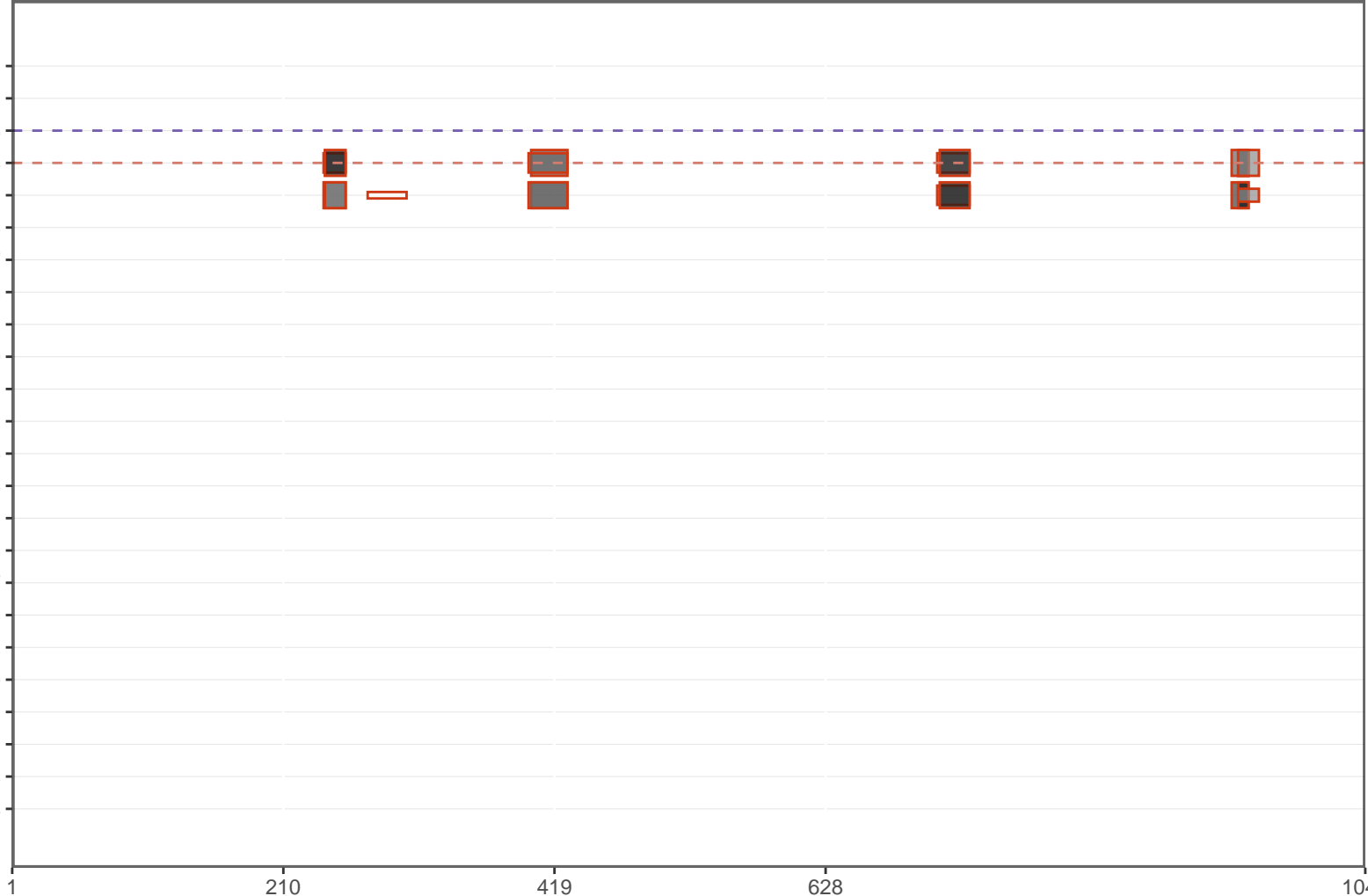
MW indication



Molecular weight

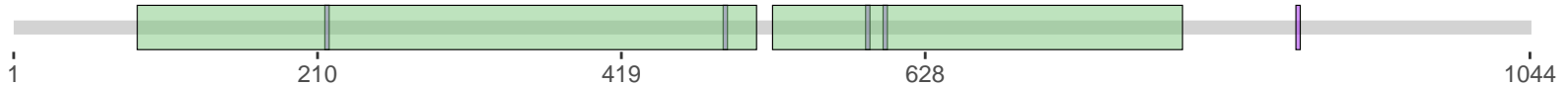


Gel Slice



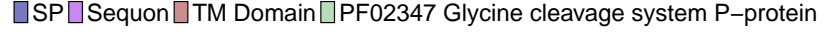
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LFKYFALGKPVTTTADSIAGEVENLPSGLVRETPVYTHQIFNSVYHEHELLRYLHKLGEKDLSLCHSMPLFSGSMTMLNATTEMMPVYTWPNFTNHPFAPEQAAQYQEMFNLDGLLCTITTFDFSLGPNAGAAAGEYAGLMVLAHYHMRGDIHRINVGHPVSAHGHTNPASAAAMCGMKIWWGTDAKNINIEELRKAAEANKDKLSALMVTYPTSHGVYEEGDEIKIHDNCGQVYMDGANMNAQVGLTSPQFISADVCHLNHLKTFGIPHGSGGPGMGPVGVKXKLAFL

NbL17g04950.1 abscisic_acid_receptor_PYL2-like [MW = 20.9 kDa]

No. of times detected



log(intensity)



Values from



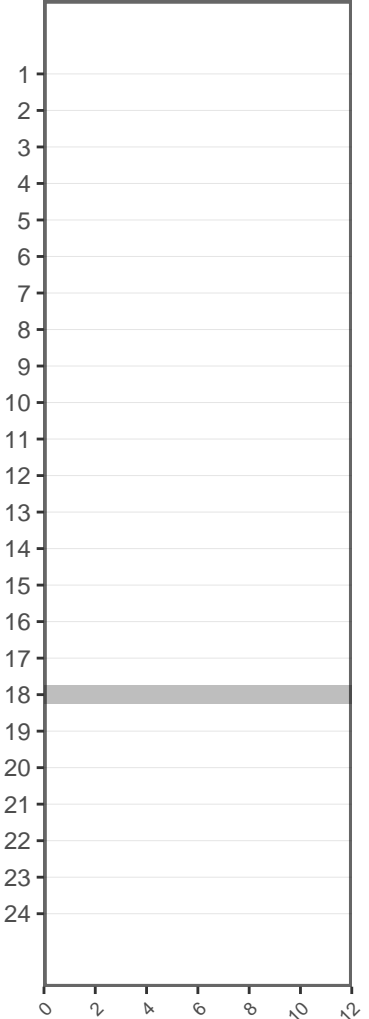
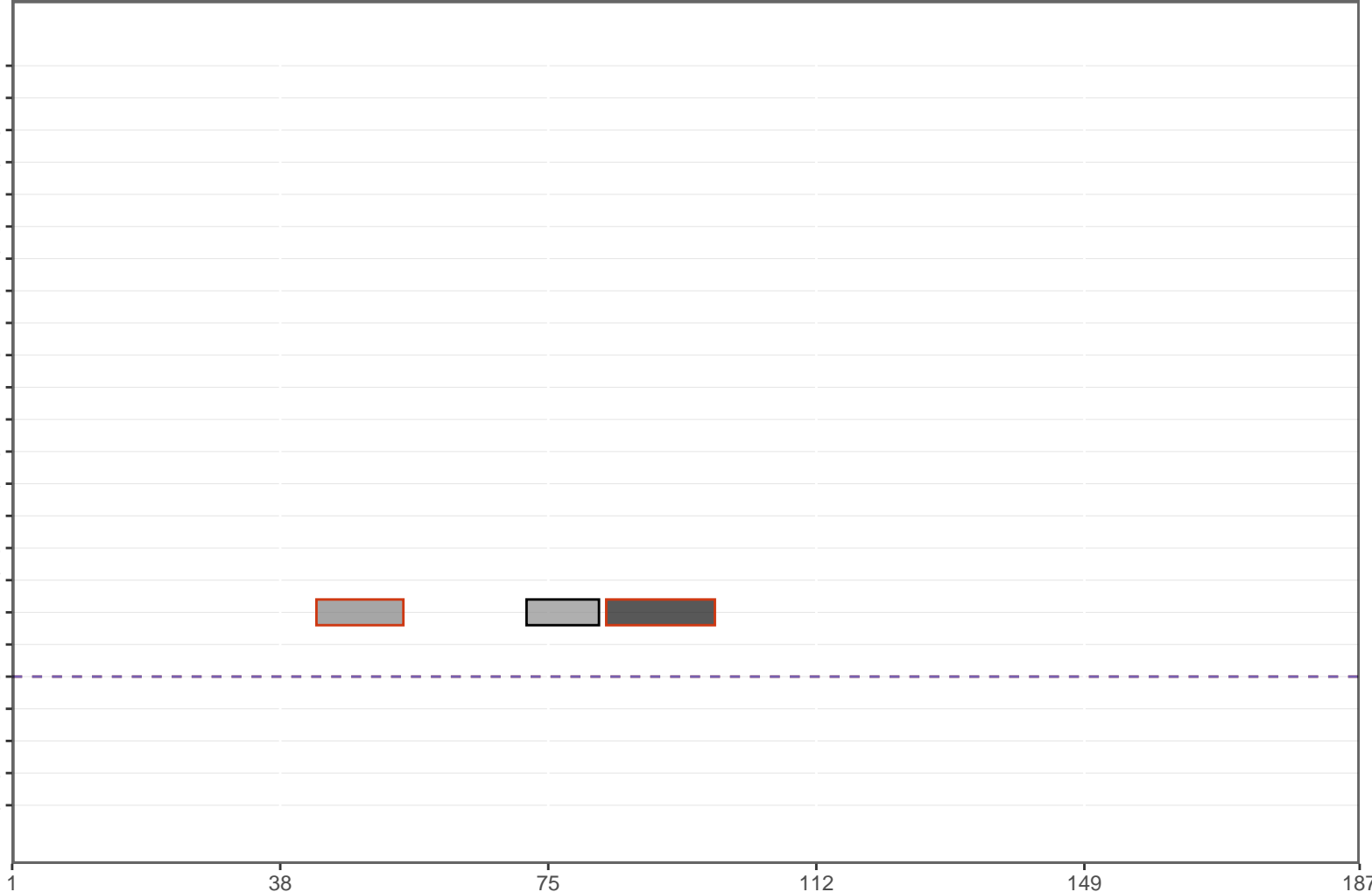
MW indication



Molecular weight

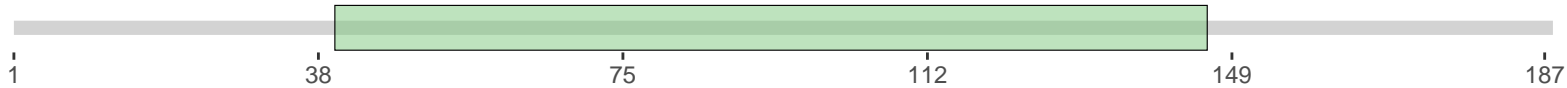


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

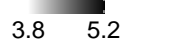
MSREVSVSGIPALSTFTELELDDDEKHLGPKVVGGEHRLNLYRIVTSVNEFRKNGKATVLESHYVDPEGNTGEDTKMFTDTVVKLNKQKLGVWMAALHGGD

NbL17g04900.1 NADH_dehydrogenase_[ubiquinone]_iron-sulfur_protein_7_mitochondrial-like [MW = 23.6 kDa]

No. of times detected



log(intensity)



Values from



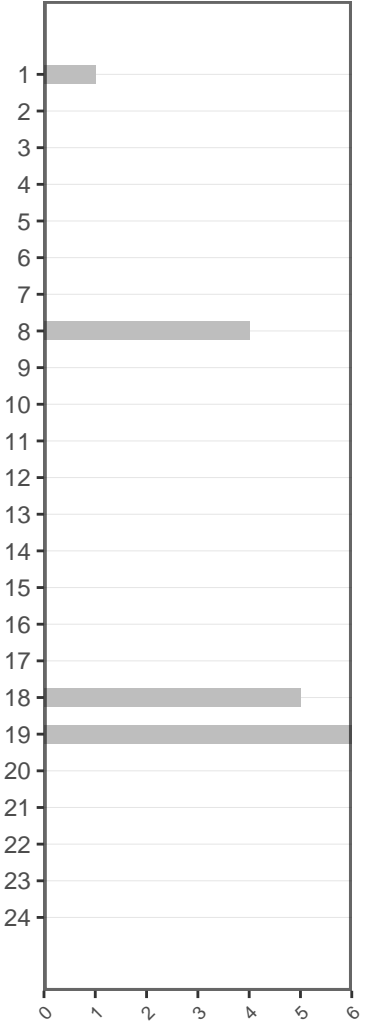
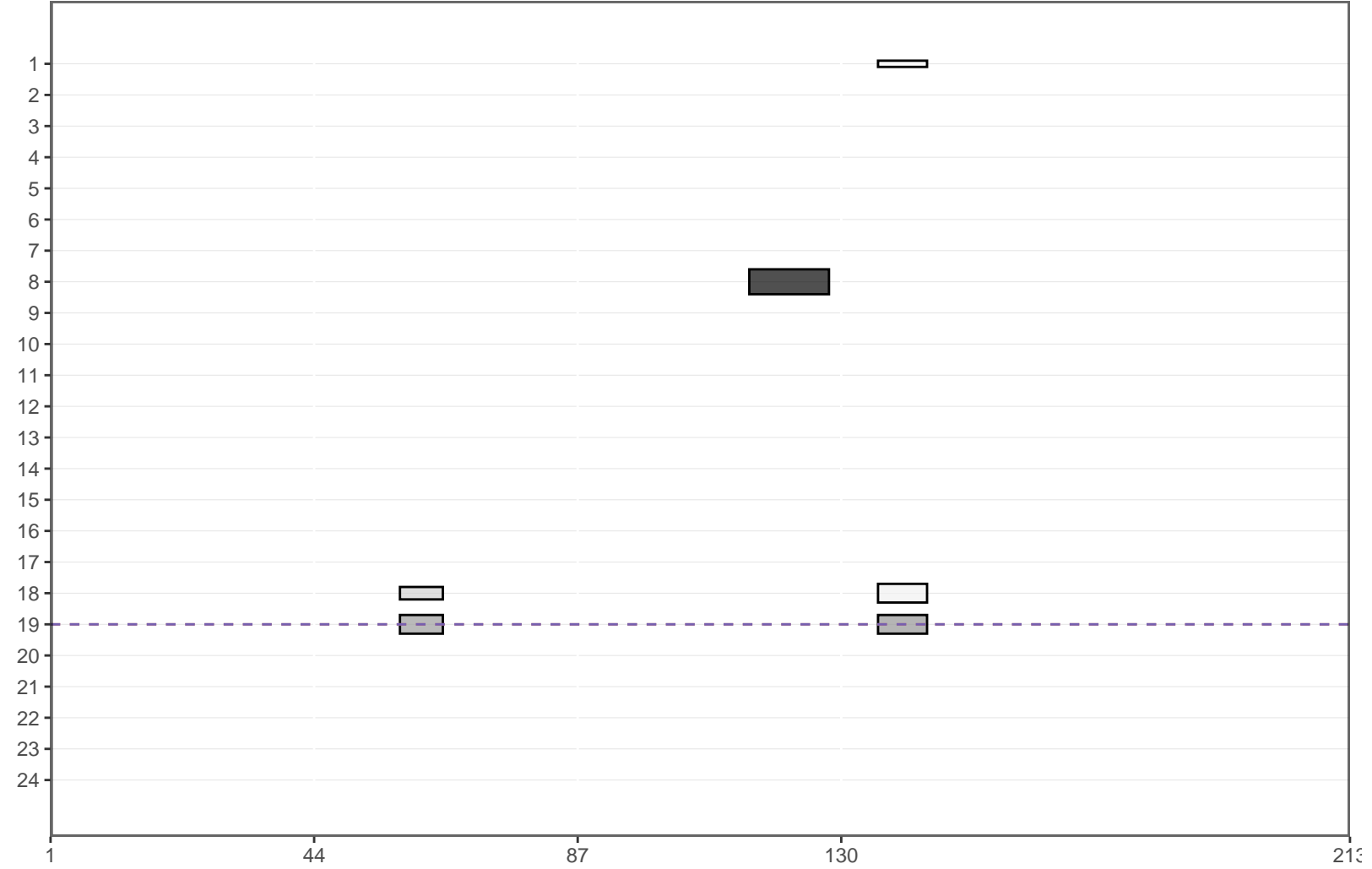
MW indication



Molecular weight

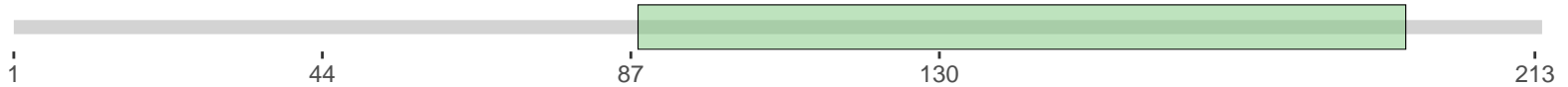


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

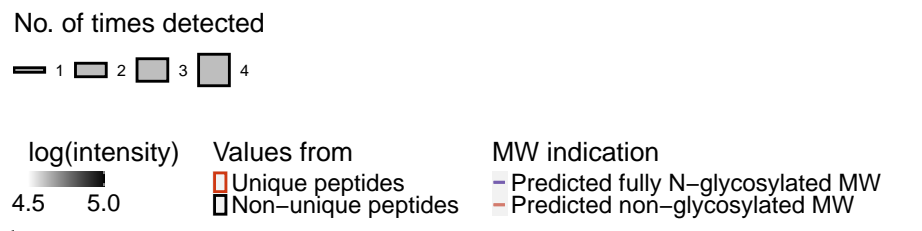
Pfam Description



Protein sequence:

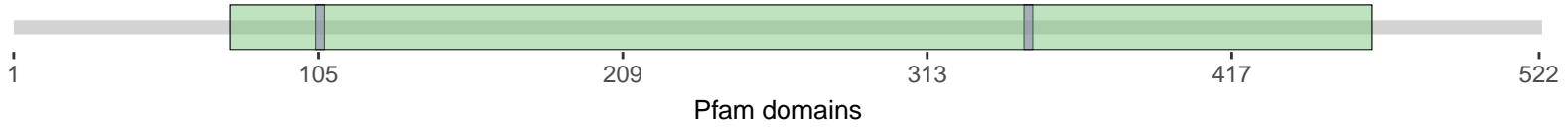
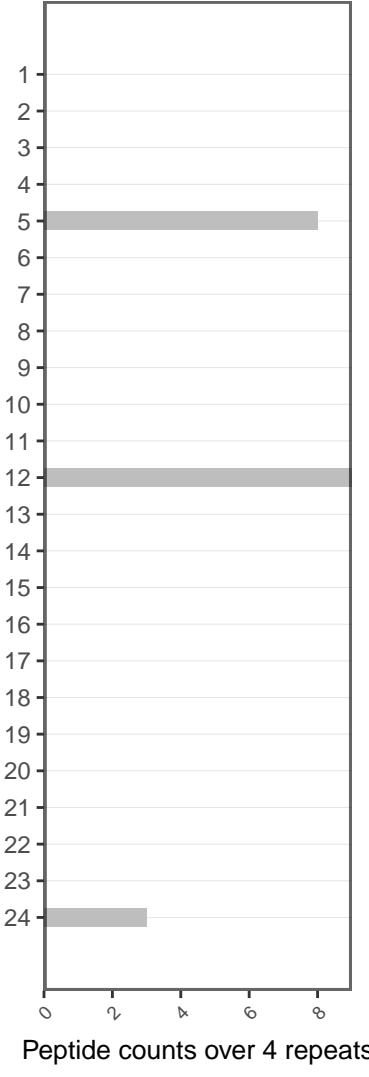
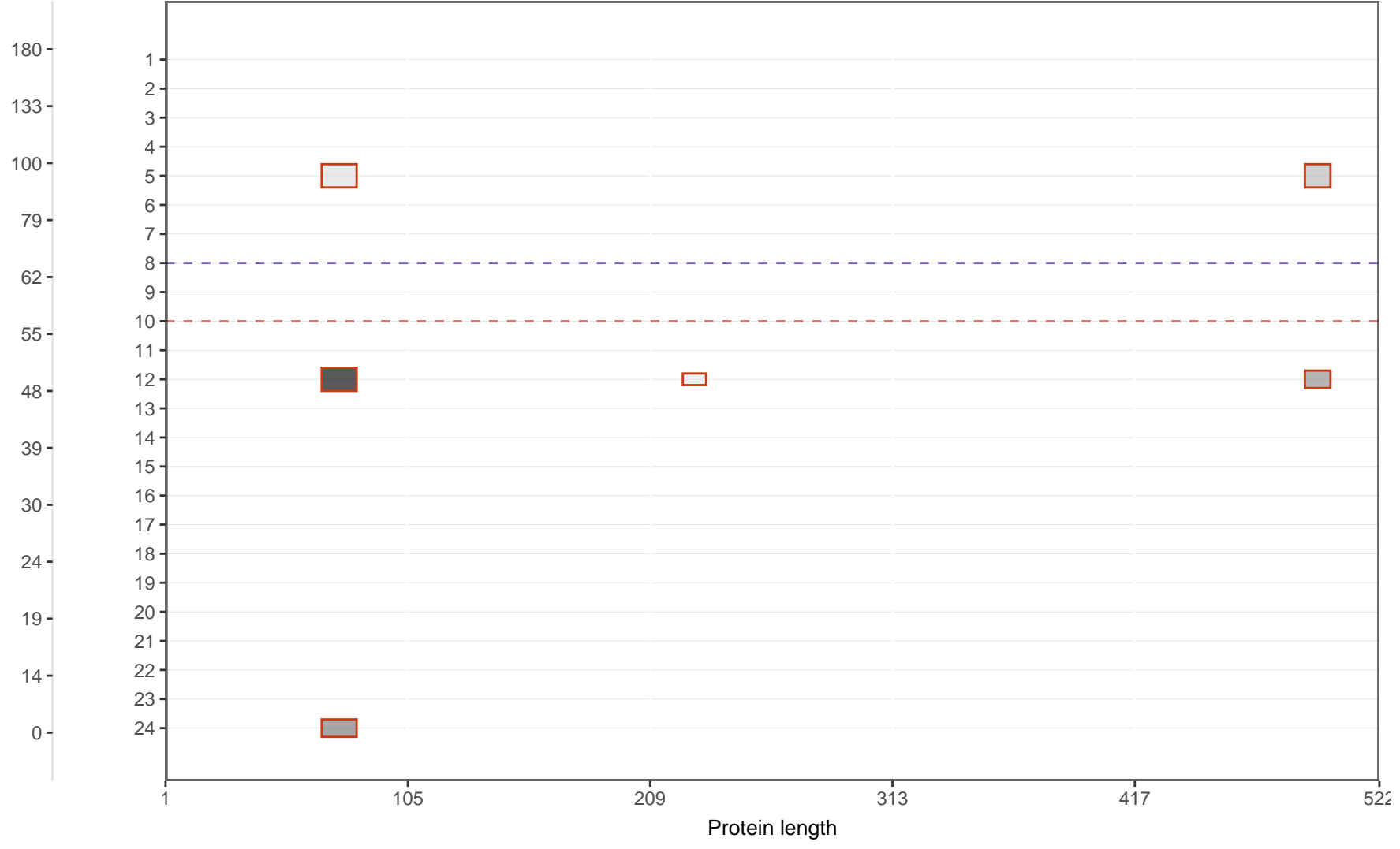
AGAARYDFDRFGVFRPFRPGSDCMVAGTLTKMAPALRKVVDQMPERRVVIEMGGGANGGGYHYHYVSVRGGCDRIVPVDIYVPGGPTAEALLVGLGLGKKNRKRDFLMWTK

NbL17g04850.1 serine_hydroxymethyltransferase_3_chloroplastic-like [MW = 56.36 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF00464 Serine hydroxymethyltransferase

Protein sequence:

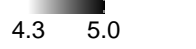
KLIIGASAYPRDFYVPLRLKADAVGAFLLMMDMAHSGVLAABVLANPFEYGDVTTTHKSLRCPFRGGMFFKDKDPLVGVDSLEAINNVPFGLGGGPHNFRIGGLAVLKLHAKSPFEKAYGNQVVENGRALASRLTELGYKLVGGSDNHLVLDLRPLGTGARVEKLDMASITLKNKNEVPGDKALVPGGRIGSPMTRFRGTEKEPVAWDFHEGVGDTLEAKKSVSSTKLDGFLKVFYTPADFNLDLDRVADLGRRVEAFTSGYPLPLGL

NbL17g04840.1 PITH_domain-containing_protein_1 [MW = 22.52 kDa]

No. of times detected



log(intensity)



Values from



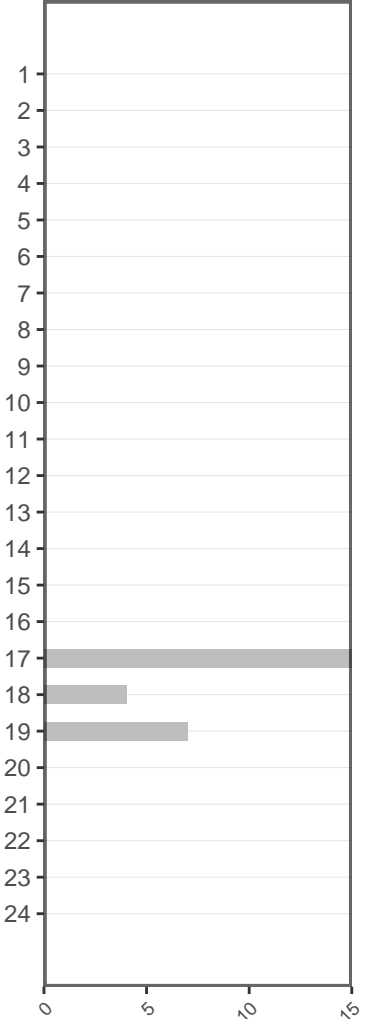
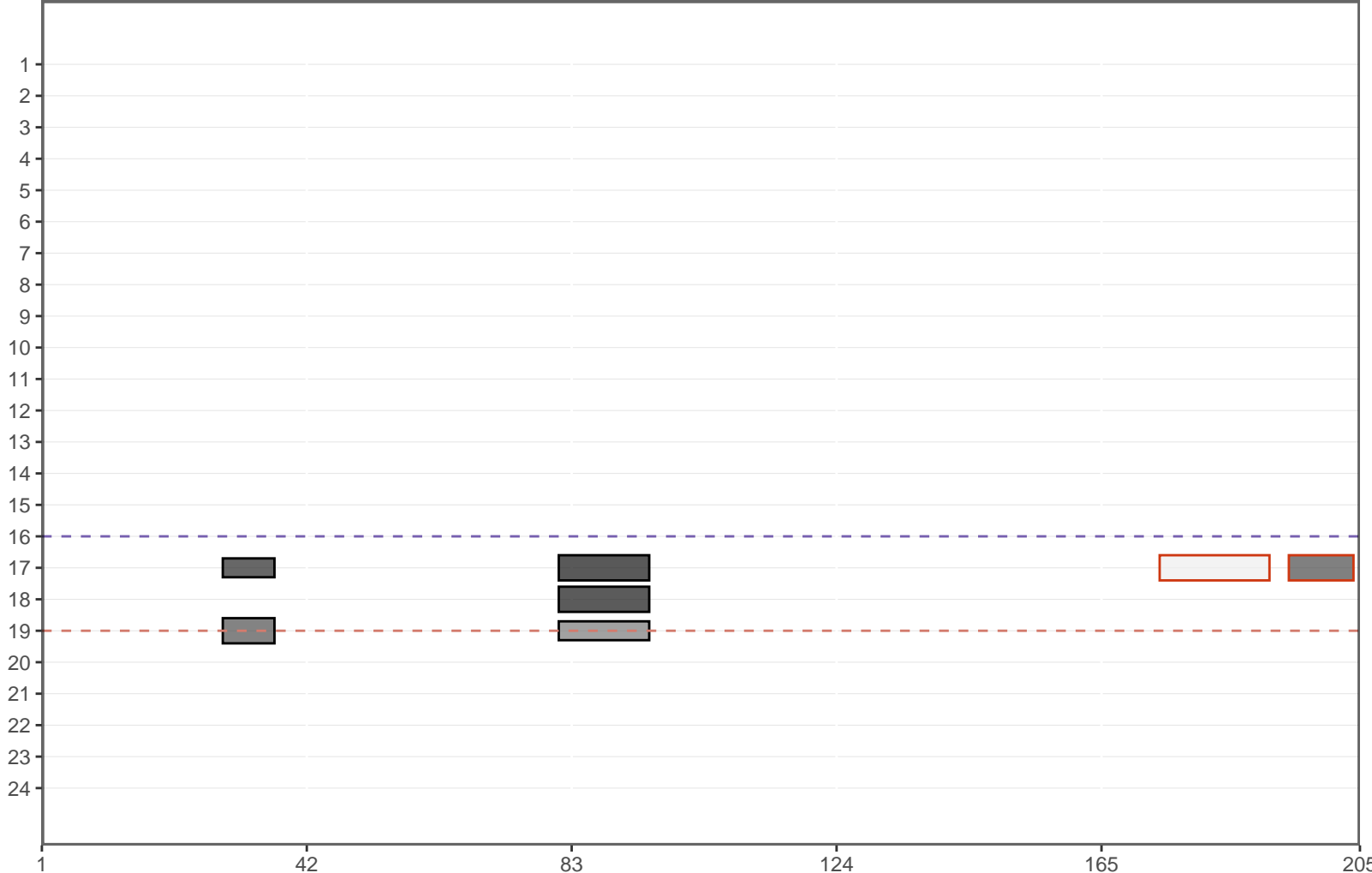
MW indication



Molecular weight

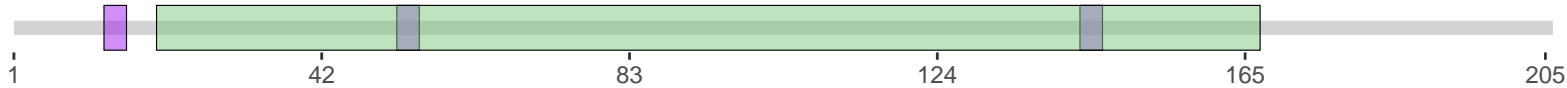


Gel Slice



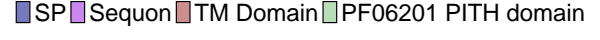
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TSPXVMRAFINRDSIGDFSDAGMGPVGEWDLAENLGGVLEYGTRYSRFQSGVSNITLHFFDNFGGDTTQHYHGLKGEATQMKREVVANVVEVVPNPSDKHKTAEAGGGGLSHVE*

NbL17g04760.1 vacuolar-processing_enzyme-like [MW = 57.08 kDa]

No. of times detected



log(intensity)



Values from



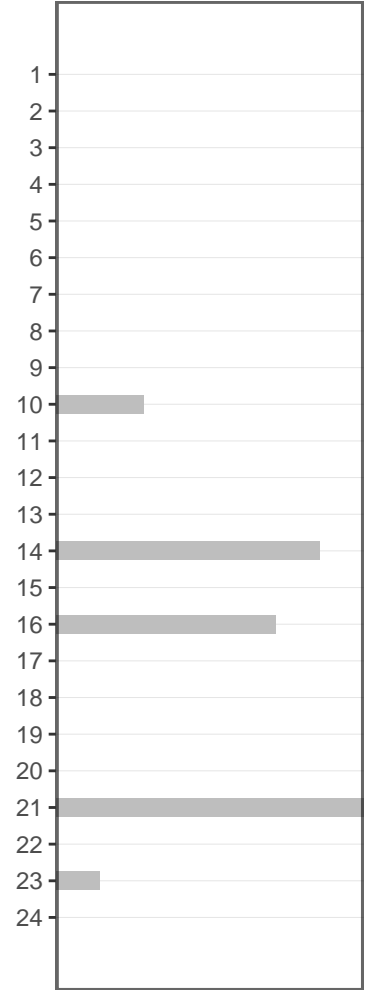
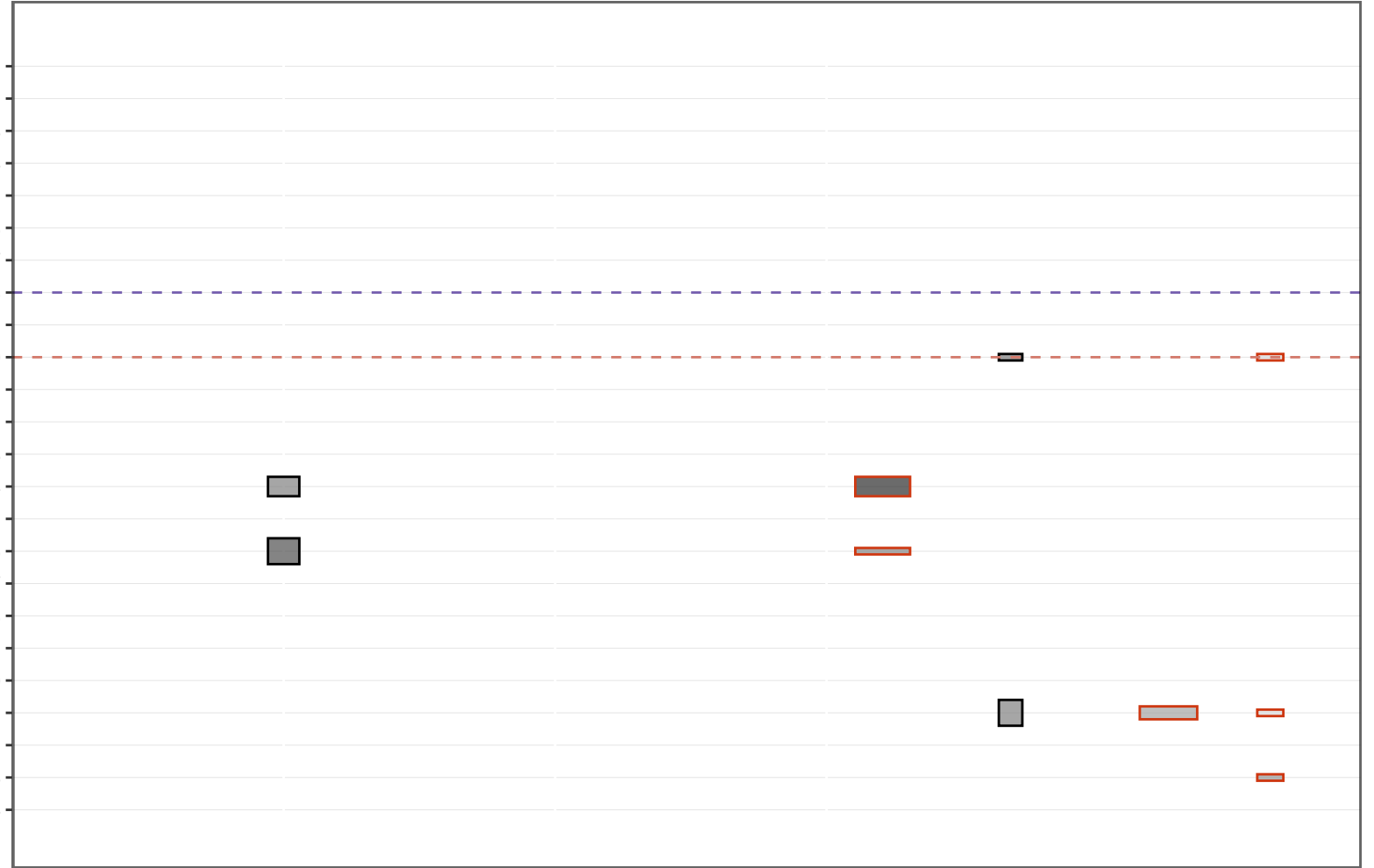
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

EGLLPEGLNYATASNAEESSWGTYPGDEVPSPPIEYMTCLGDVYSISWMEDELHNLRTESLKGQYHLKERTATGNPYYGSHVMGYDGLHLSKDALVLYMGTNPNANDNYTFMDGNSLIRVSTAINRRDADLLHFHWKFKAFEGEGRVKEAQQKLNKAISHRLHLDNSALVGLKLFGEIKGPEVLSVRRPAGPLVDDWDLKSPVRFKETHCGSLSGVGMKMRSEANICNVGKRMEGMVEASAGACPEVPSNTWSSLRGFSFA

NbL17g04650.1 uncharacterized_LOC109241480 [MW – SP = 151.69 kDa]

No. of times detected



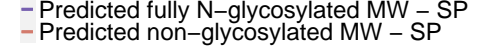
log(intensity)



Values from



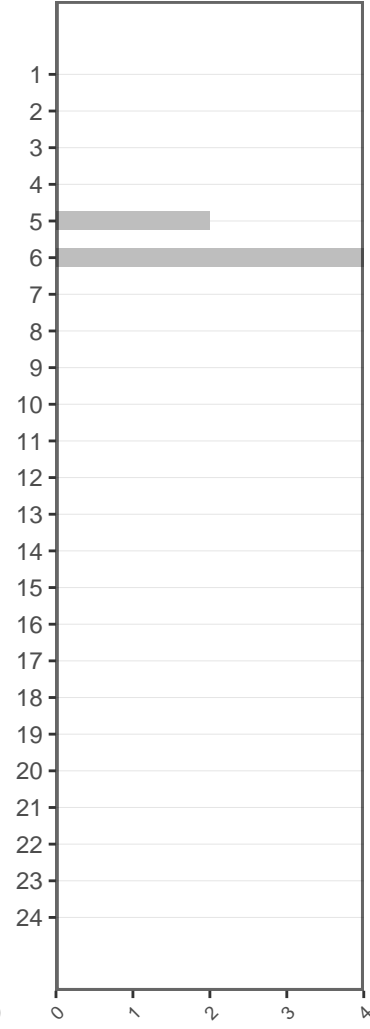
MW indication



Molecular weight



Gel Slice



Protein length

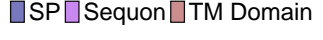


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IGSGSGSILLFLKSLHLGEGTMSLGGG6866GGGGGGRHIFHWSDIPTGDVYQPIATVNGSHTRGGLGGEGGGGGGGLSGKPKPKGKGFCECPFGTKFNVTGGDRALGVSDLDELPHRAVYISVRGQVTERPCPKVGVSEKRYHMPHCYTALEELYTFGGPWLFLVLLLLGLLALLLWARMKFKVGVDESPQNPATGGGQDHSFPFLESNEVLETNRVEEGSHVRLVFLGPNTFSEPHLHSHTPPQKIEVYEGAFNTFYDENTIAAYQW

NbL17g04640.1 glutamyl-tRNA(Gln)_amidotransferase_subunit_C_chloroplastic/mitochondrial-like [MW = 15.82 kDa]

No. of times detected



log(intensity)



Values from



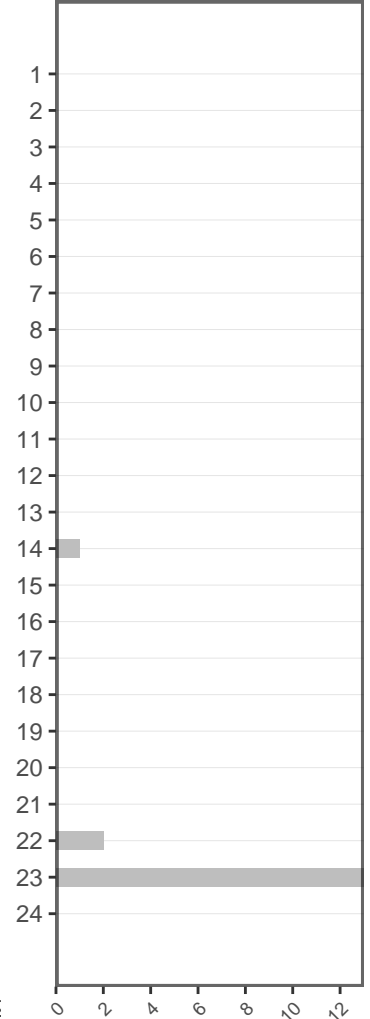
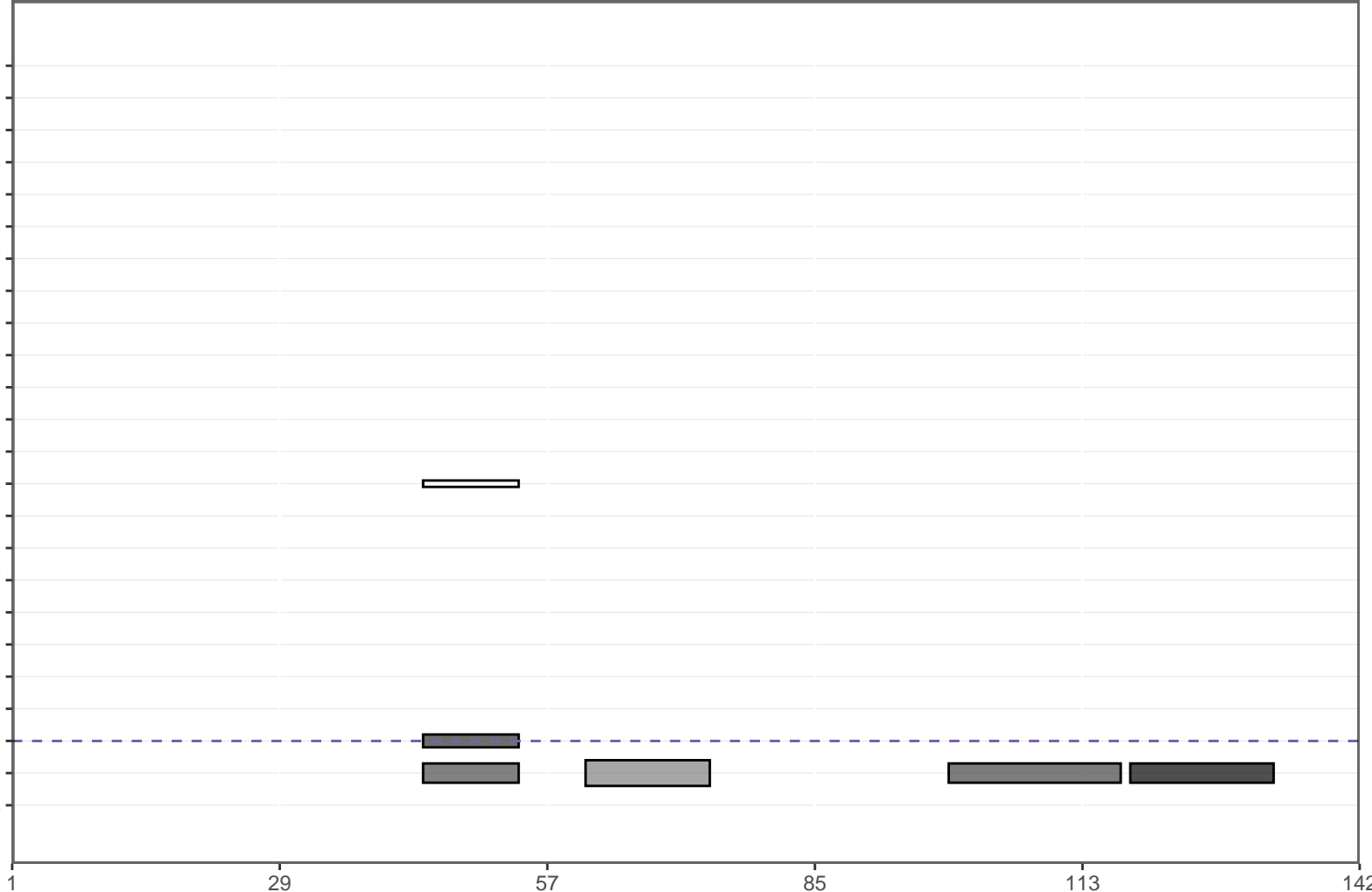
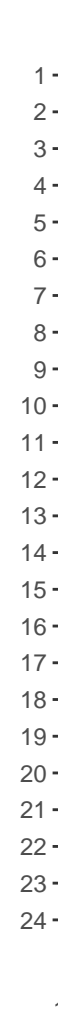
MW indication



Molecular weight



Gel Slice

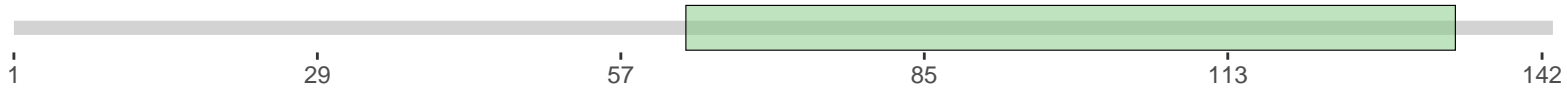


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

TARISLTPQOVEEFAPKIRQVDFWFGGLGAVDLOSIEPARADTEGQNLRDDVPEKFNREALISAVPSFEETPKVVKVNLKE*

NbL17g04560.1 profilin-2 [MW = 14.14 kDa]

No. of times detected



log(intensity)



Values from



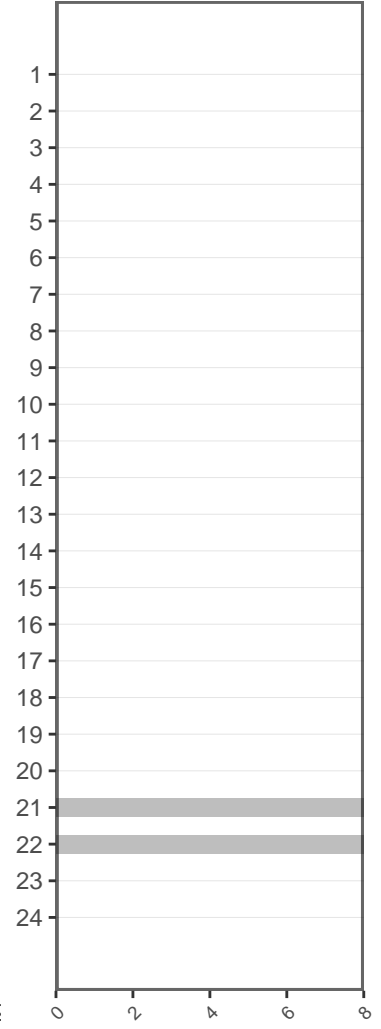
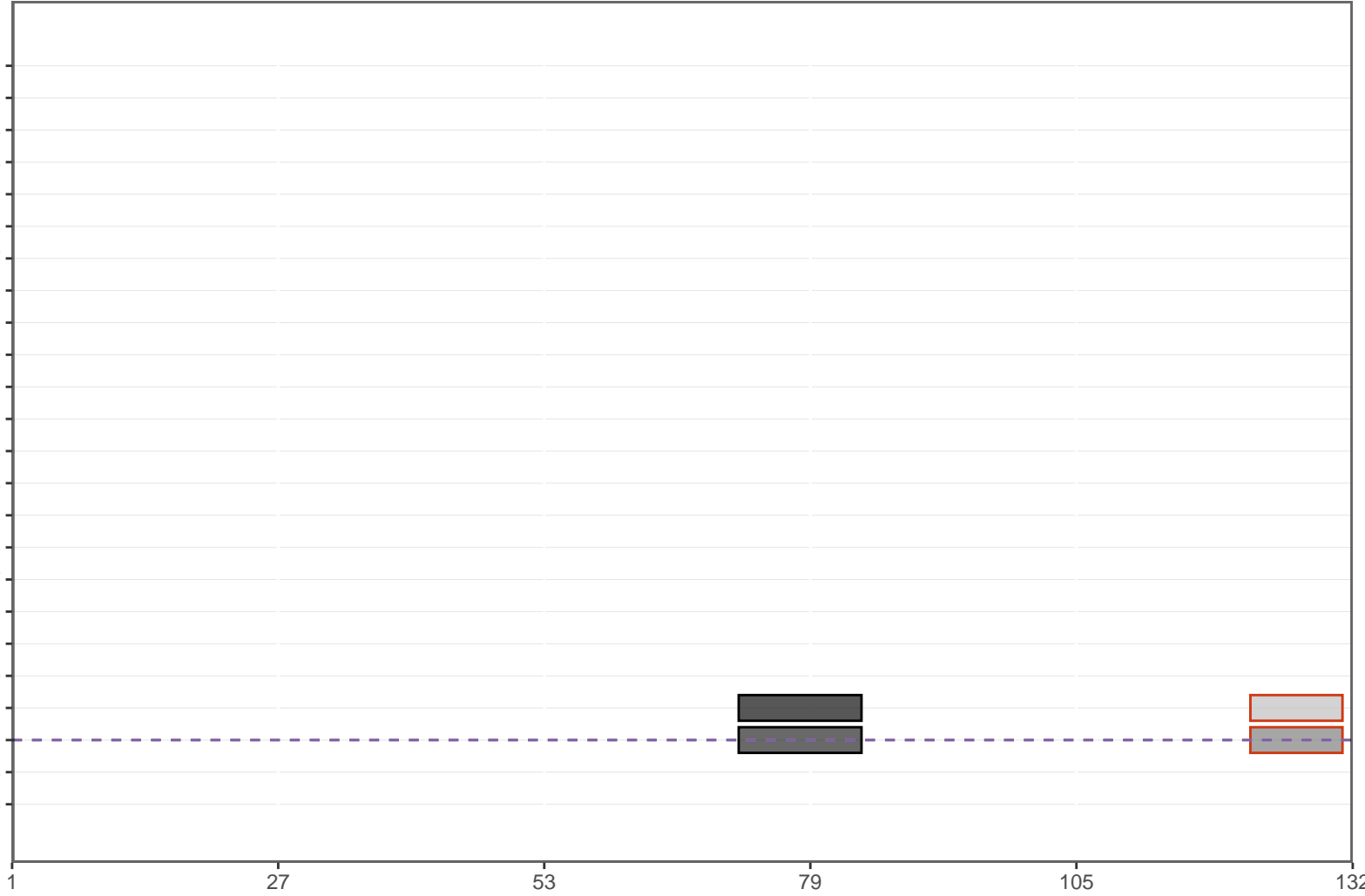
MW indication



Molecular weight

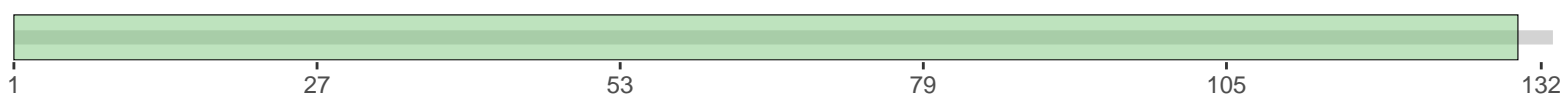


Gel Slice



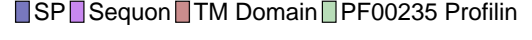
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IDFAEPQTLAPTGLVGGTKYMMVDSGEPGAVIRGKKPGGGFHKTKNGALRIGYDFEMTPGGQNMIVERLGGVLDQGL

NbL17g04500.1 NADP-dependent_malic_enzyme-like [MW = 69.39 kDa]

No. of times detected



log(intensity)



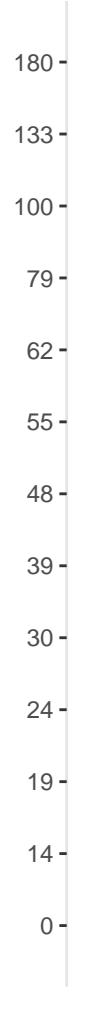
Values from



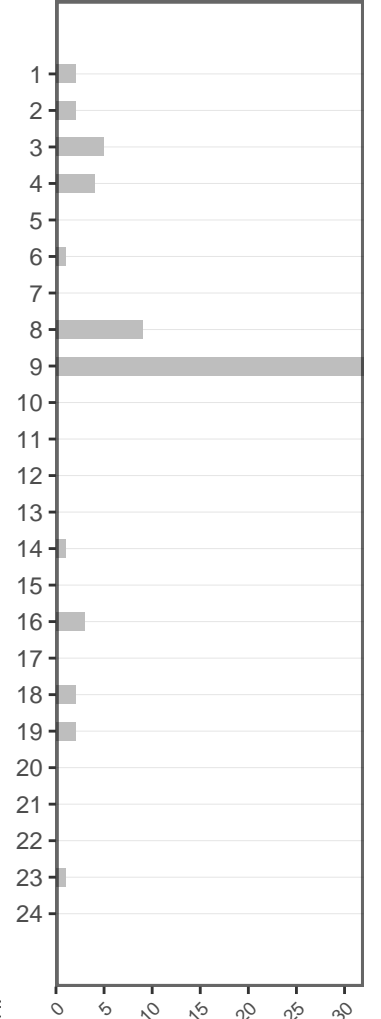
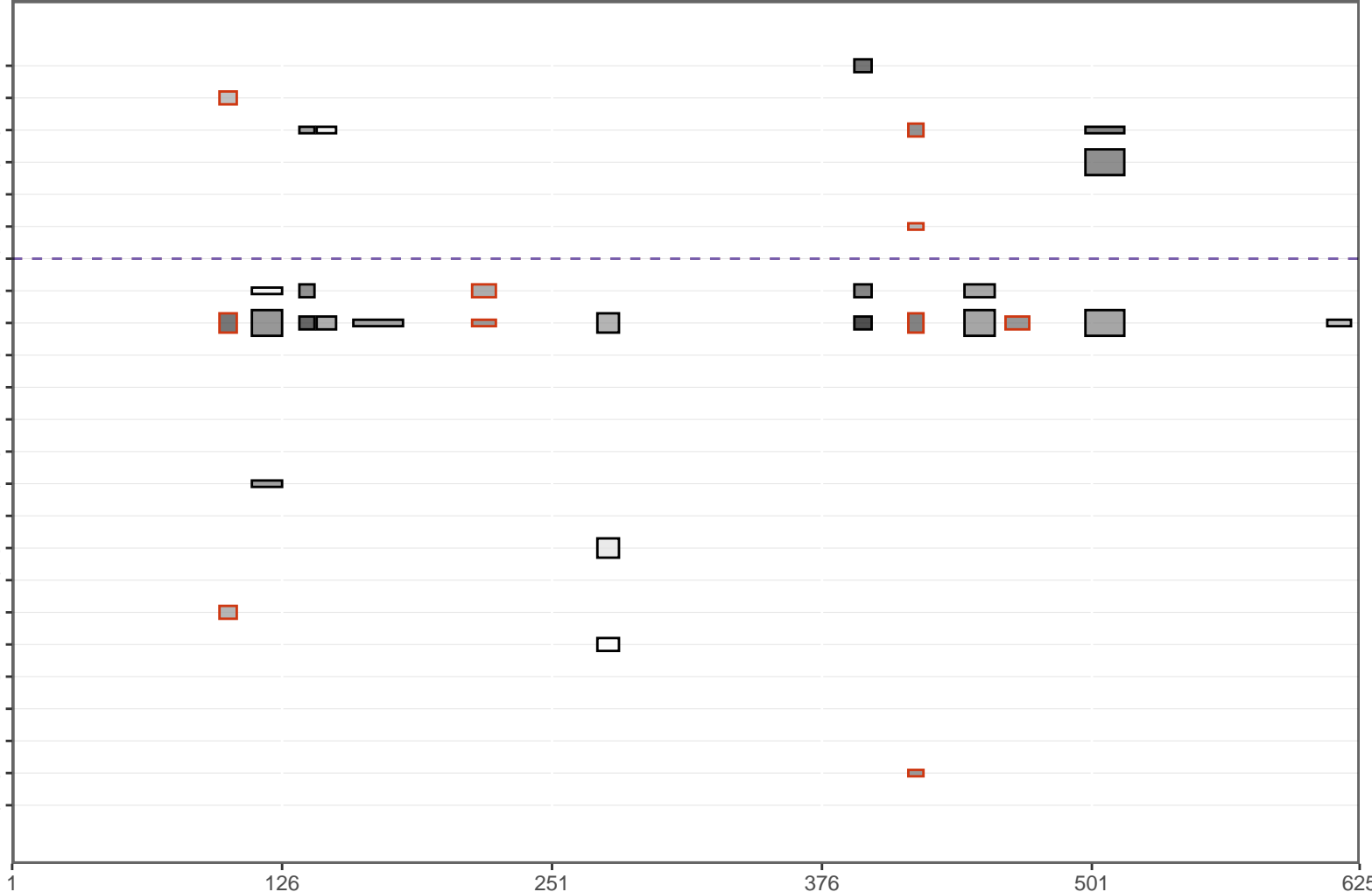
MW indication



Molecular weight

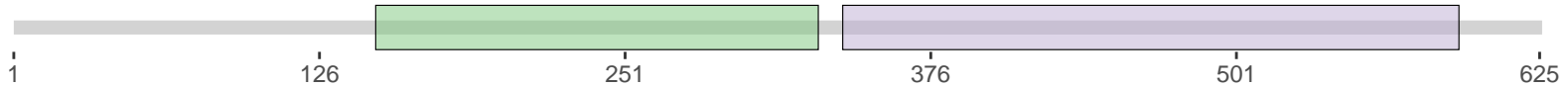


Gel Slice



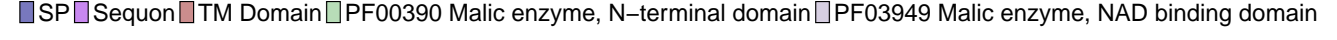
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IFMSAVKQNYGEKVLQGFEDFANINAFDLAKYRTHLVFNDDKGGTASVYVAGLHSLKLLGGTLDLADHTLFLFLGAGEAGTGAELALEIKRTPVLEEARKKIKVLDKDKGLVSSRLESLGHFKPKVAHIDHEPKVELIDVAKKPTVLLIGTSGVSKFTKEIVETMASLNPKPLIMALSNPTSDAECTAEAYTWSKGHAFASGGSPDFPEYEGRTFVSGQANNAYFPQGLGIMSGTIRVHDNMLLAASEALAGQVTEEDYLGKRVPPFTNIRKISAHAAEVAAKAYELGL

NbL17g04360.1 probable_transcriptional_regulatory_protein_At2g25830 [MW = 36.98 kDa]

No. of times detected



log(intensity)



Values from



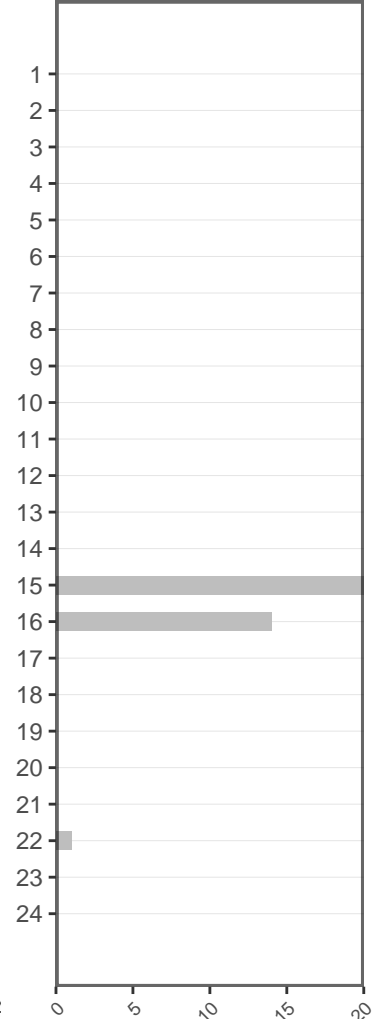
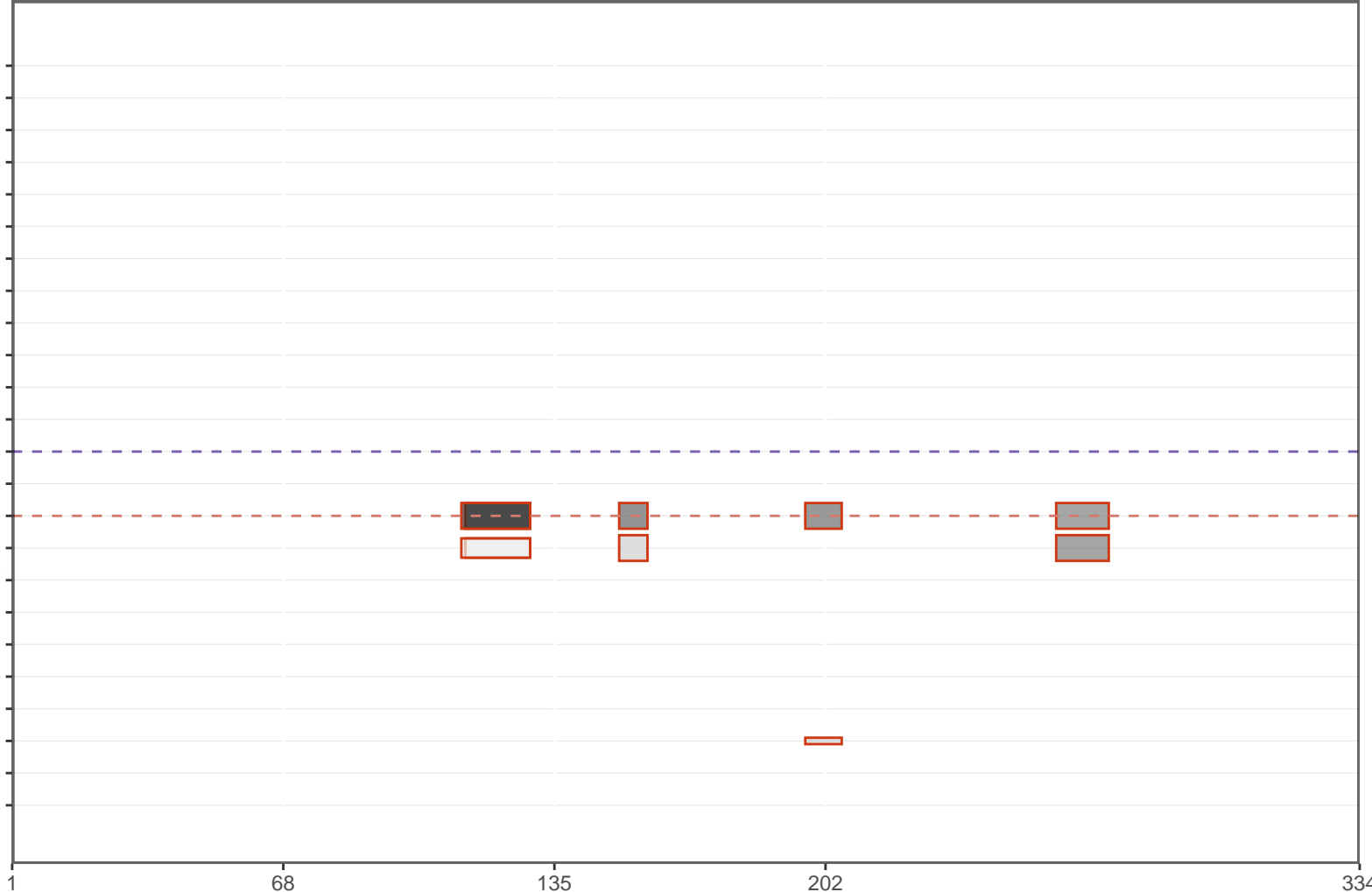
MW indication



Molecular weight



Gel Slice

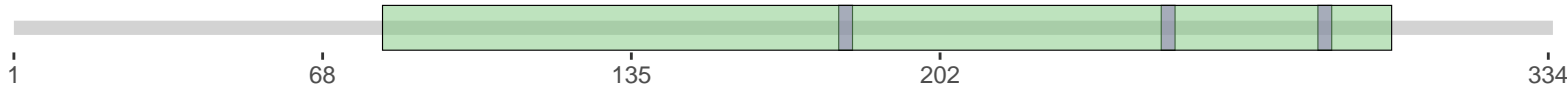


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IAFMKIKYEVYGYGGVSHVLTQKVNRSVAAVREVKKDDGGKMDAGSISMFKFRRARVANVYTDIDRDQLTALDAGAEHPSMDDYDTEANSSESRYKVVSSADNYPVLSKLGEEGKFEFGNSGELLPTTPIEVRKHSISEFYGSNLVALLRGEVYFNHEILQKFN

NbL17g04330.1 nuclear_pore_complex_protein_NUP85 [MW = 81.21 kDa]

No. of times detected



log(intensity)



Values from



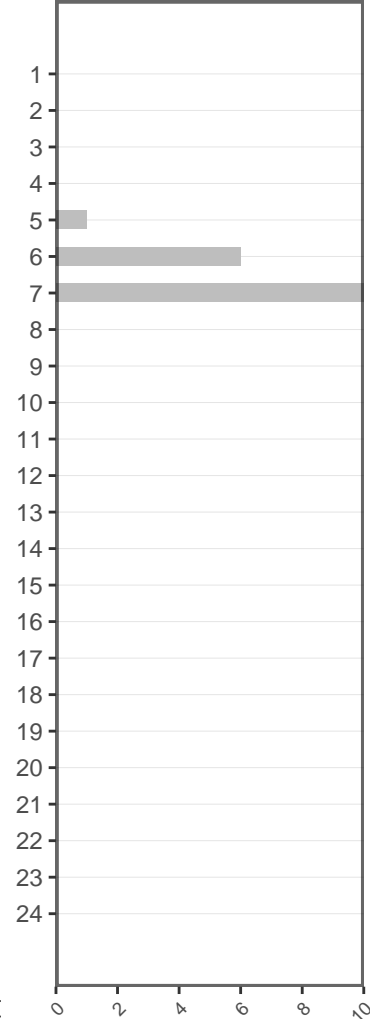
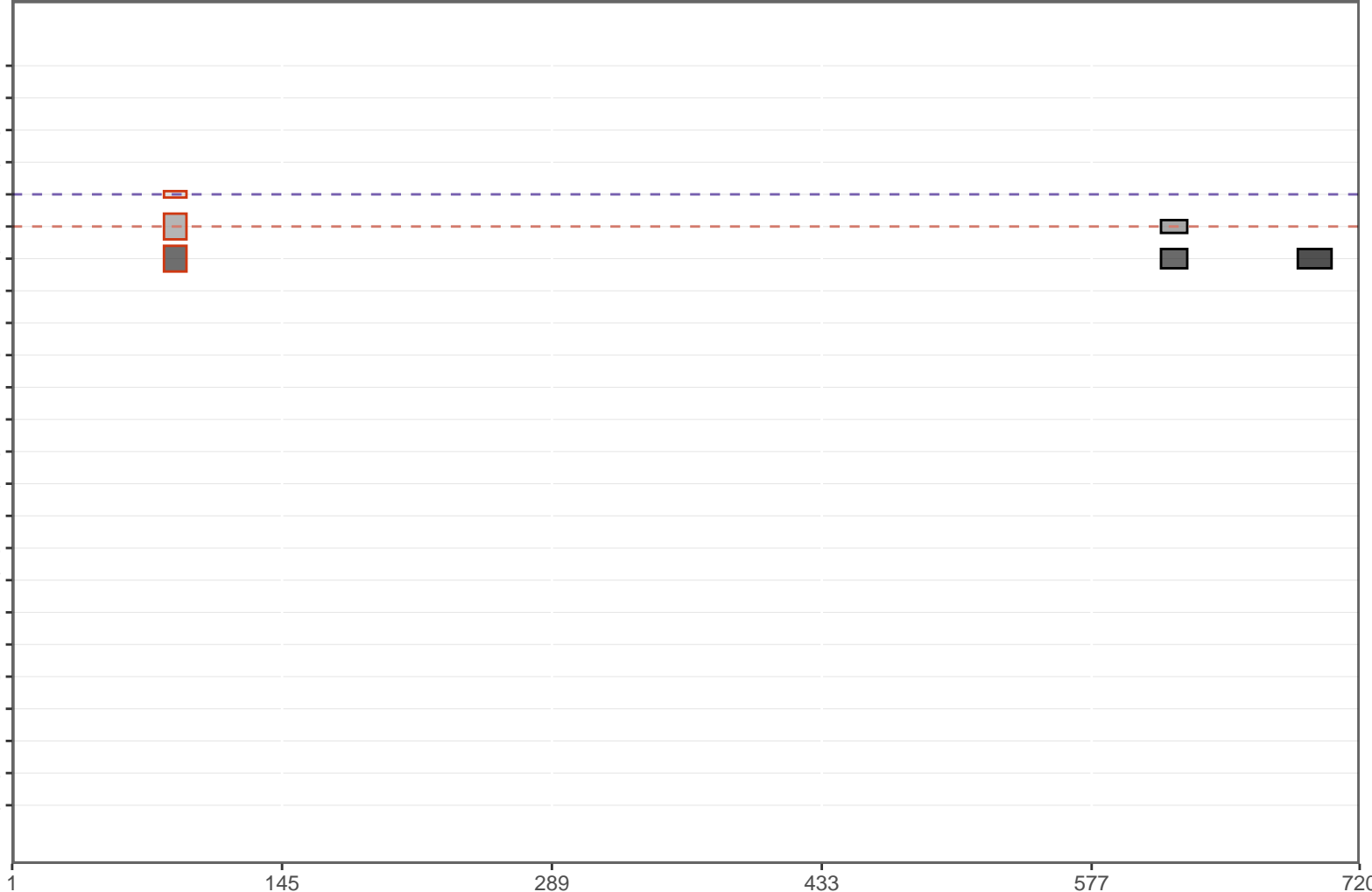
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

KNLIQIMLGSPVLSNATFNWMEIFISHFLVVRPFTAGLESMYNAQKMGKPKPSFPHKFLGLVILGILGENTEVYLAEGSRFQFVMMMAHVAVELLTAGSTHAEILLHEEGSKLGGISIEELKLVYAGVLSGHAFFTWQAPYKLTSCIKKGGILLENLFYKQPVQHSQILLKSEICRLEYLDTISSNMRIAGVHHWKGKRGKGGVFTVLQGARDEFRLNRAKQLDFVYKSVSDDEGFKQWEGLELLGSEERTAGGLEFLNKYRDFRRRLGLGVHGDPTPTDGRNAAEALVSLMKI

NbL17g04140.1 probable_lactoylglutathione_lyase_chloroplast [MW = 40.12 kDa]

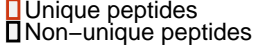
No. of times detected



log(intensity)



Values from



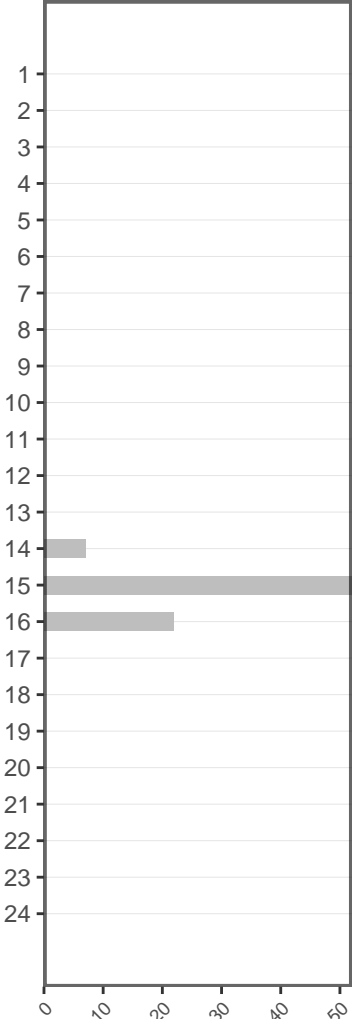
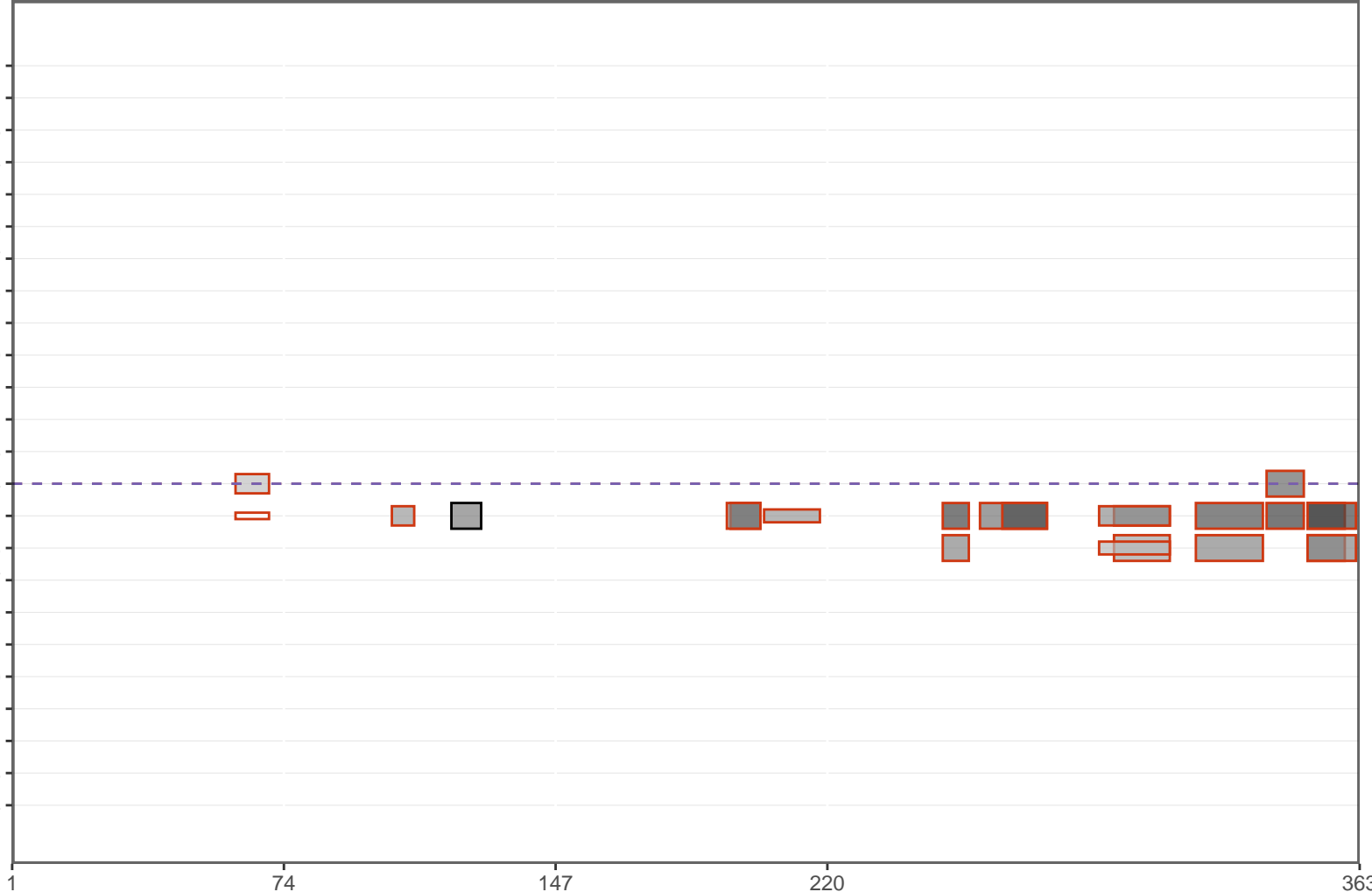
MW indication



Molecular weight

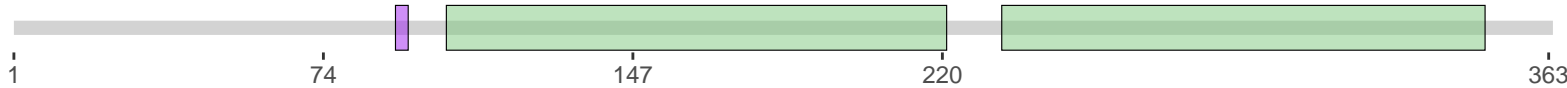


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TGFGHFGIAVEQIAKTVQDLWAKKRGSTWLNQSKVGGTIALVEDPDGKFKELLGRGPTPEFREVMLRIVGDLRSINFYKAFGMELLKRRNPNNNTAVLGVGPEDKNALLVLTFTYGVKSKYDKNGYAGIAGTDDVYKTAIAKLYGGIEVLEPGLPGRNTRKIMAGVDFDGVKTFVYQNAQFMKELE

No. of times detected



log(intensity)



Values from



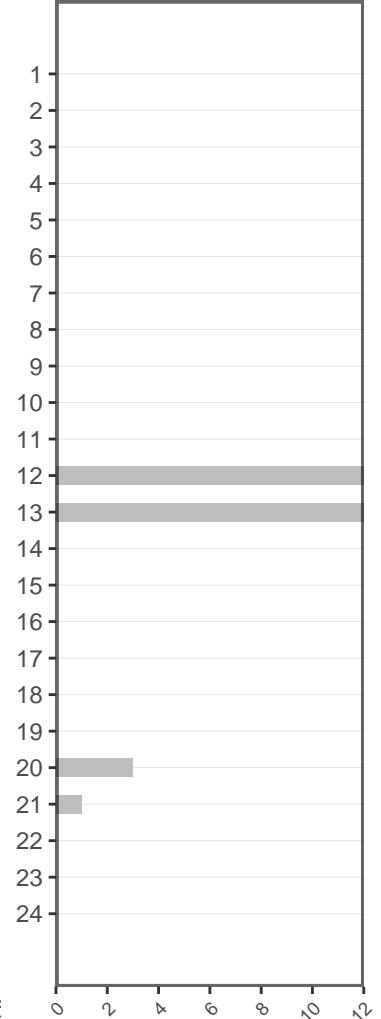
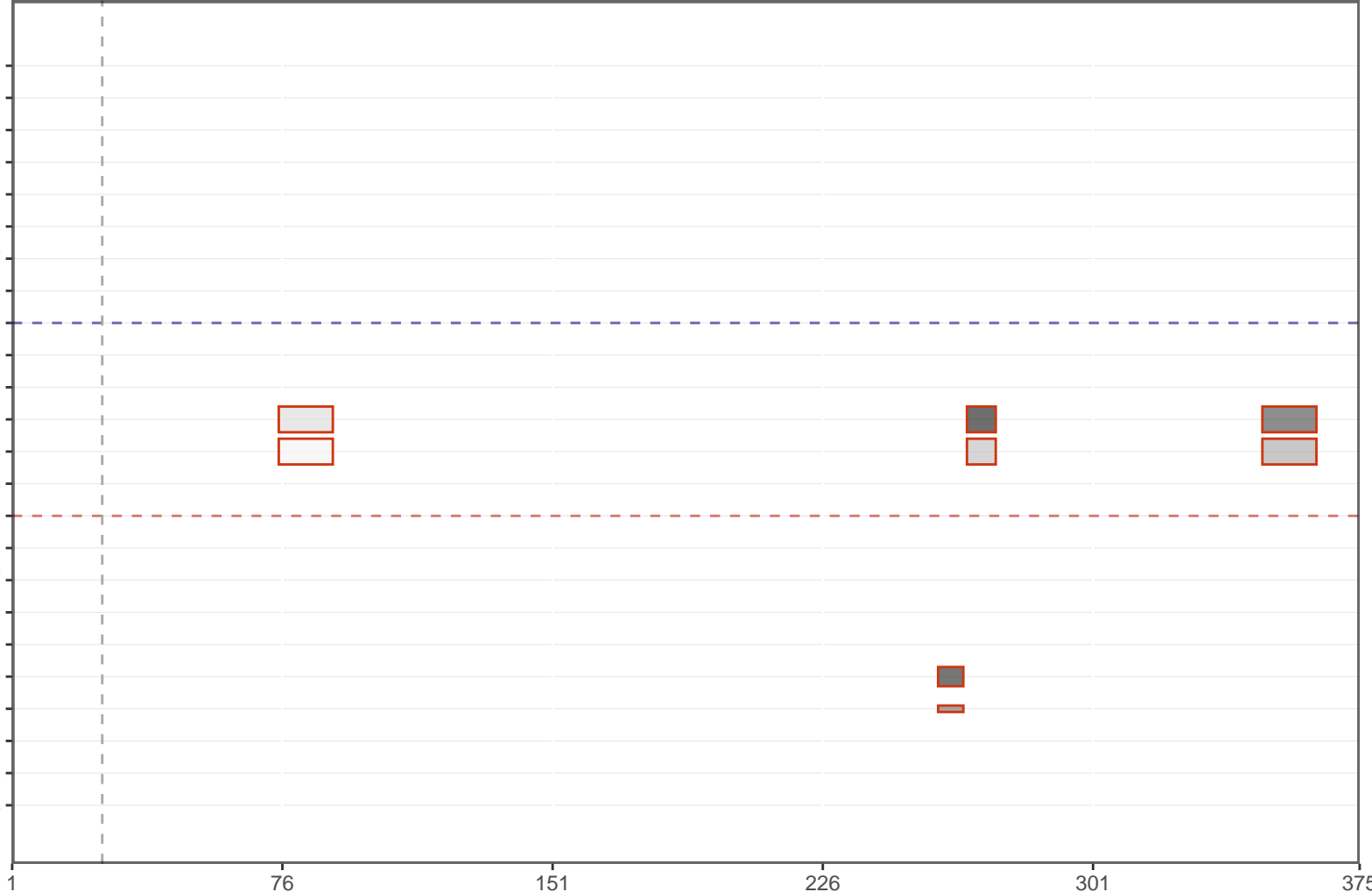
MW indication



Molecular weight



Gel Slice

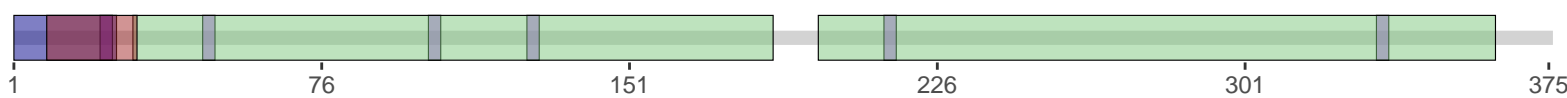


Protein length

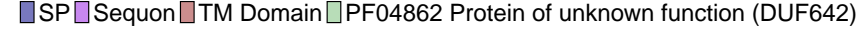


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

MCGLDIAIURLSLYPPKATNKLKNGDFEEGPIYFPNTSGVGLVPPNEDDHSPLPMMVVEGLKAVKYLDSDFEYVPOGKRAIELVAKESAAQVARTTIGMYELSPKVGASNSCEGEMIVEAFAGADTLKVPYEGKGGYKRAVLRFKAAASNRTRIMFLSTYYHTRSDDFVSLGCPVDDANLLGVRNPRFL

NbL17g04020.1 GTP-binding_nuclear_protein_Ran-A1 [MW = 25.02 kDa]

No. of times detected



log(intensity)



Values from



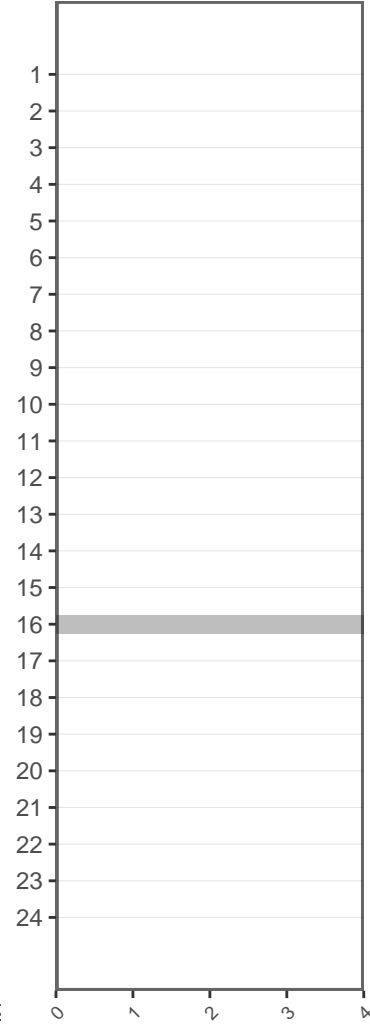
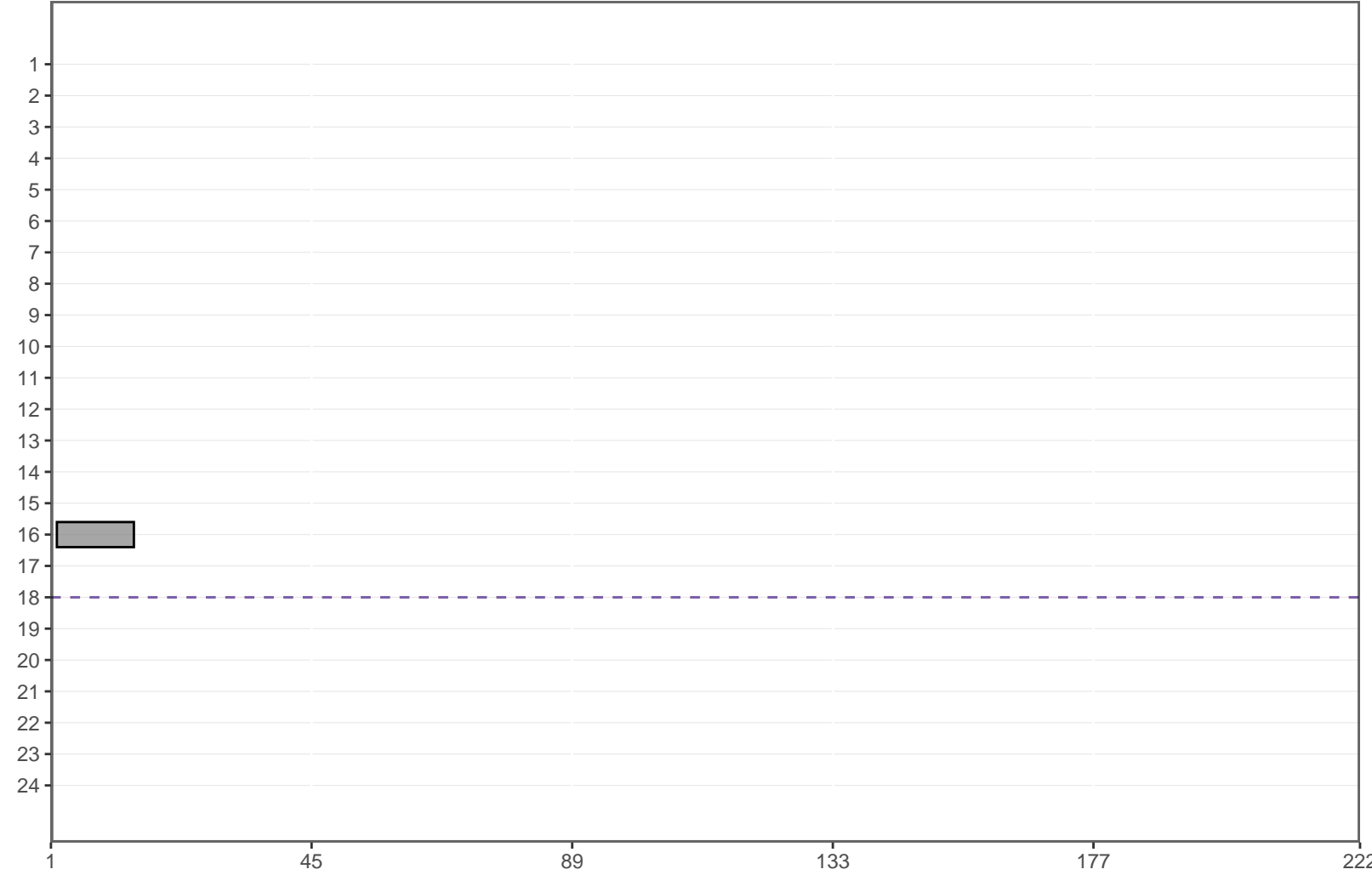
MW indication



Molecular weight

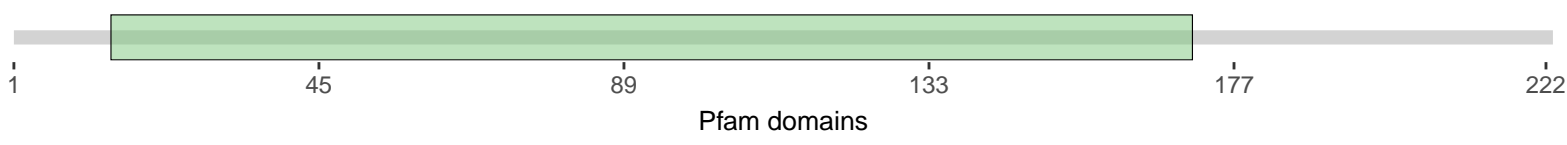


Gel Slice



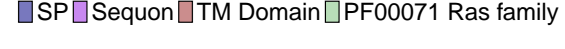
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

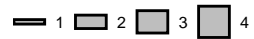


Protein sequence:

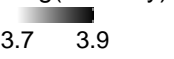
LTLYKVPVTHRDLDGRVGENPVLGGKVDKVRGKAKGVTFHRKKNLQVYEISAKSNYFEKPFVLRKRLAGDPLHFEVESPALAPREVQDLAQQGHEAELAAASQPLPDDDDDETFD

NbL17g03950.1 aspartyl_protease_family_protein_At5g10770-like [MW = 55.63 kDa]

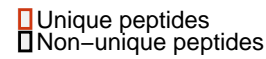
No. of times detected



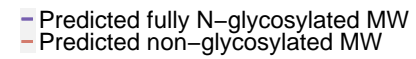
log(intensity)



Values from



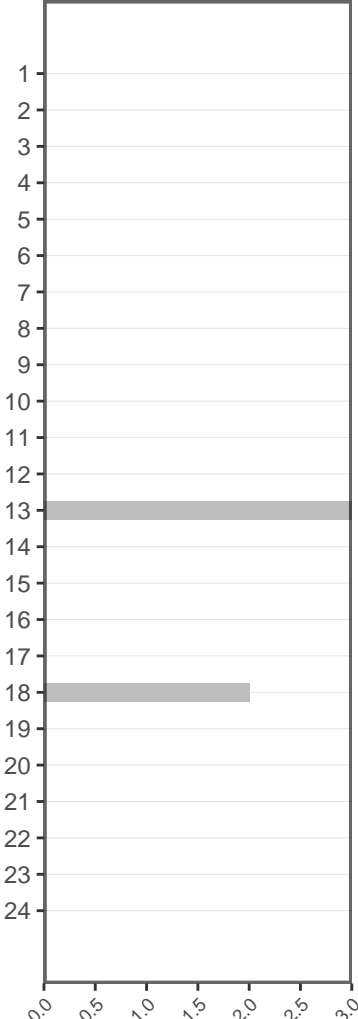
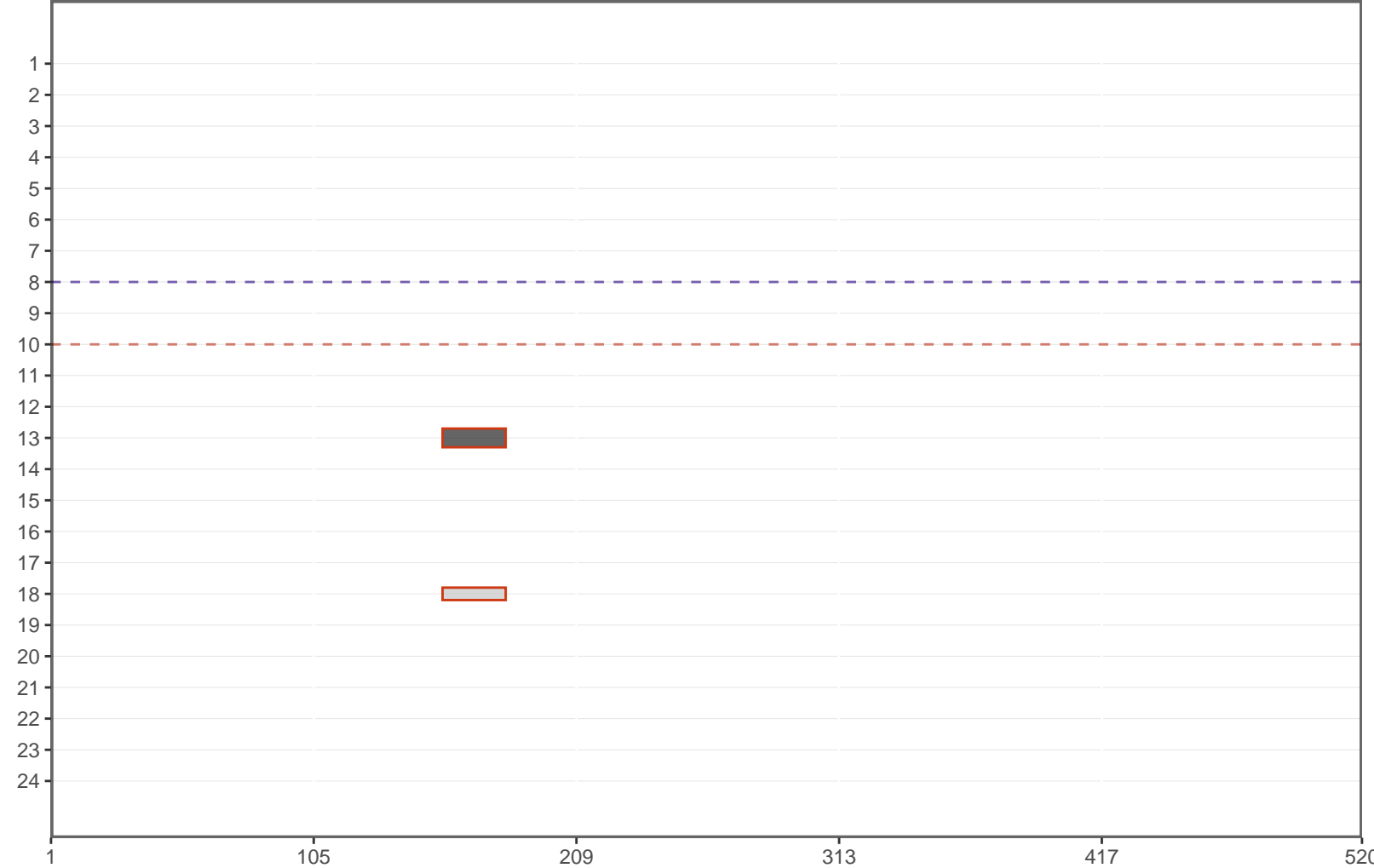
MW indication



Molecular weight

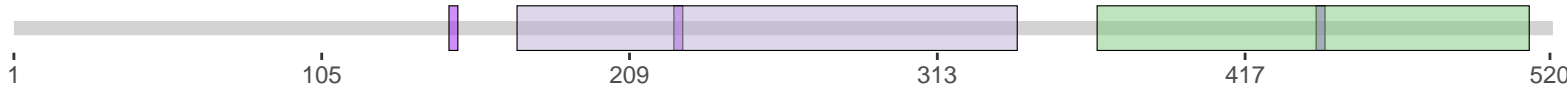


Gel Slice



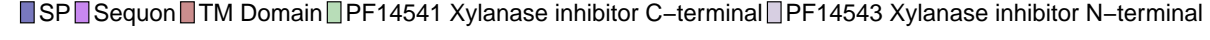
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

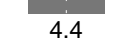
SSSNQVYGIQYGDTSFVGFVFFAKDKLTFKDFVDFGFMFGGGNNRGLFGKTAGLGLGRDPLSVGGTAKFKRYFSVGLPTSRGNGHILTFQNGNGYKSKAVNKHIFTFPSSGGATFYFDVLSGIVGGKALISPLFQNAHTIDSGTVITRLPSTAVSGLKTFKQFMKYPAPALELSDTCYDLNNTSBSIPKIFNFNSNANVLDLDRNGLITNGASQVGLAFAGNGDDDSIGFGNIQDGTLEWYVWAGGQLGFGVRRGS

NbL17g03930.1 acyl-protein_thioesterase_2-like [MW = 28.43 kDa]

No. of times detected



log(intensity)



Values from



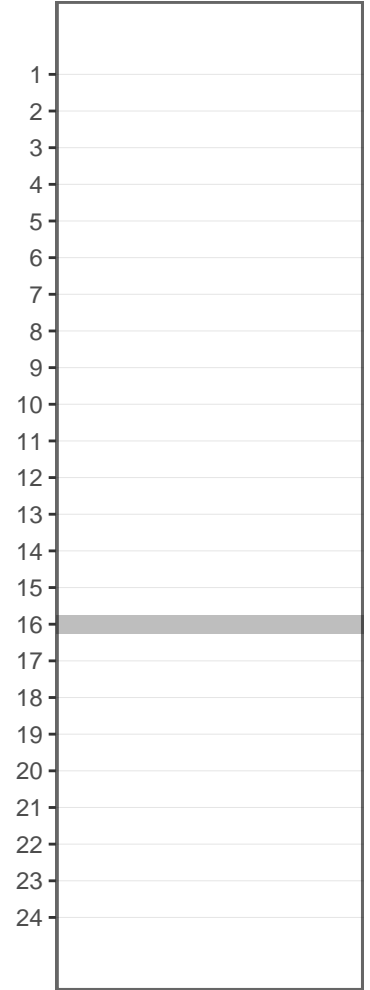
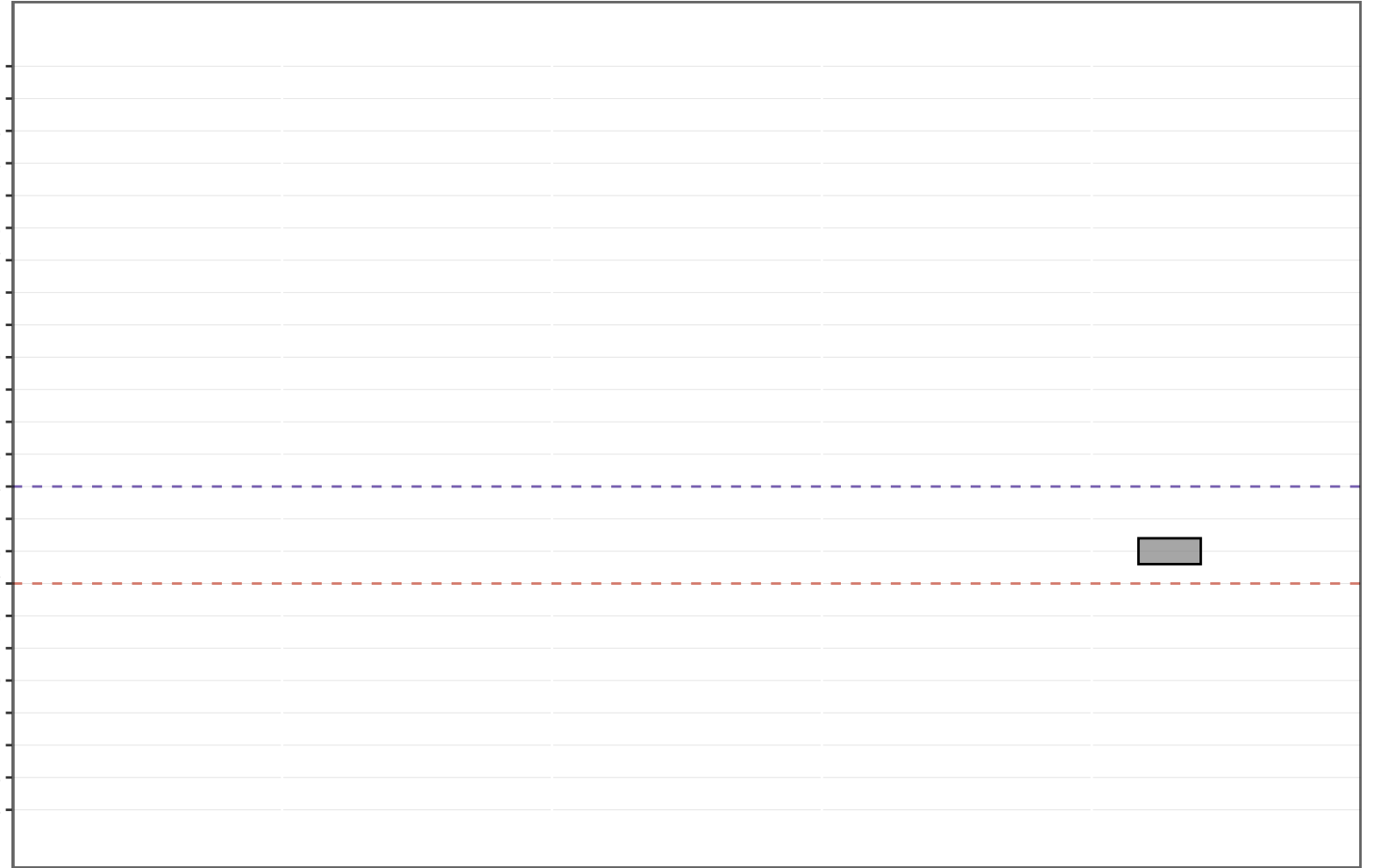
MW indication



Molecular weight



Gel Slice

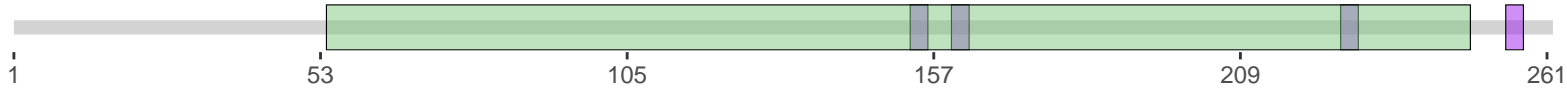


Protein length

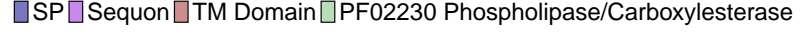


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

STEPADVLCVGGFEMGAAALYSATGAFKQYGNQSPYPLNSAVVGLSGWLPGSRFLNRMDGMDAGRRRAASLPILLCHGTGDDVWAYVHGQEKARILSSSGFQNLFRNYDGLGHYTIPEETDEVCGWLAANLSLGGT

NbL17g03820.1 E3_ubiquitin-protein_ligase_AIP2-like [MW = 35.71 kDa]

No. of times detected



log(intensity)



Values from



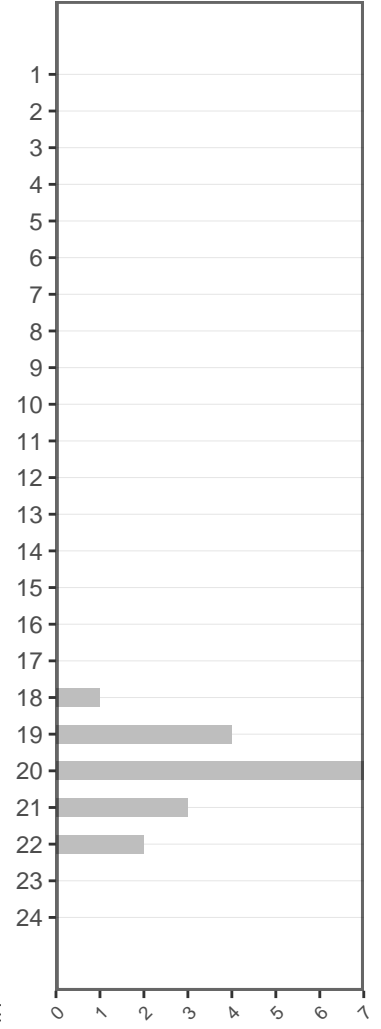
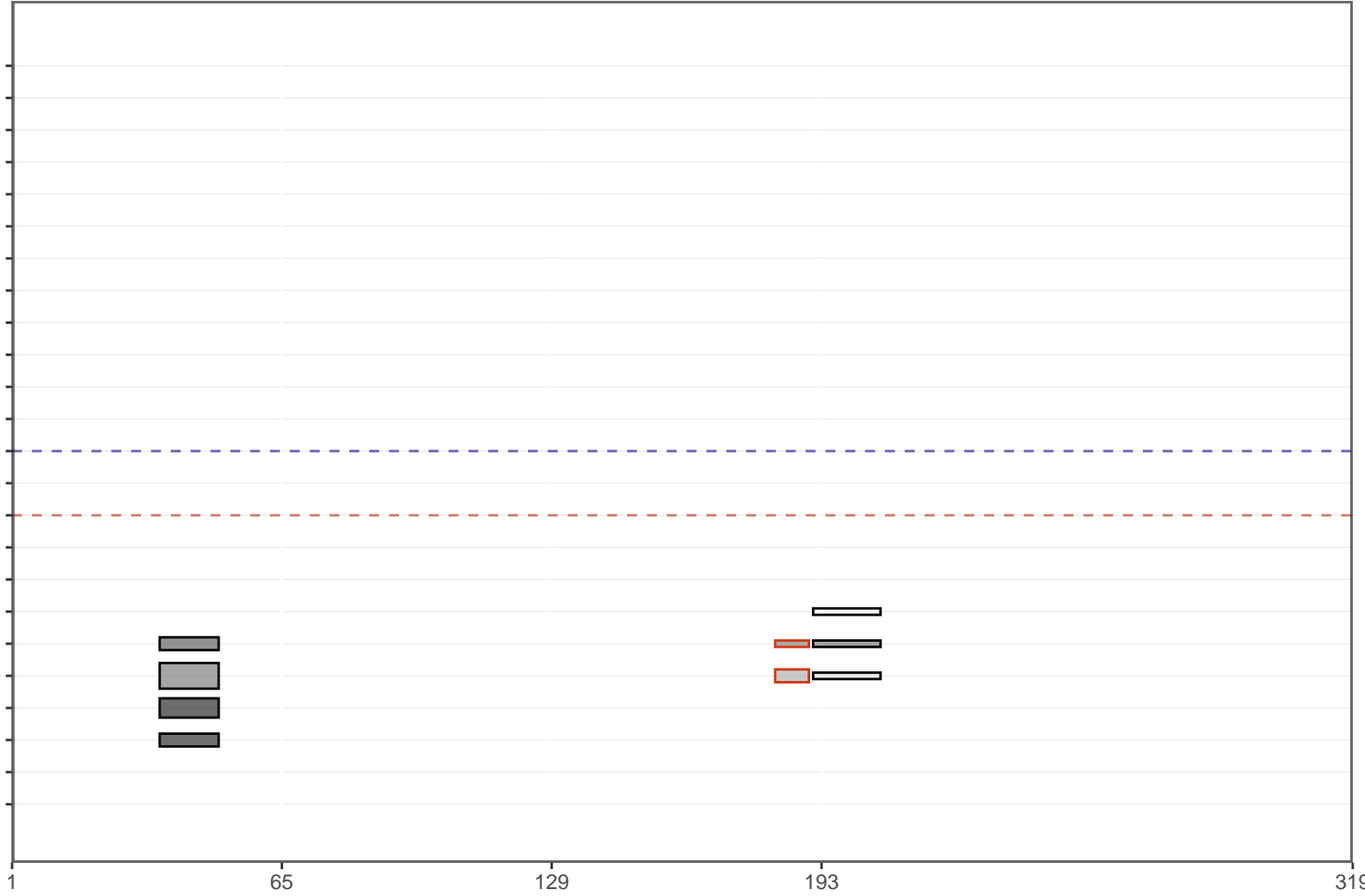
MW indication



Molecular weight



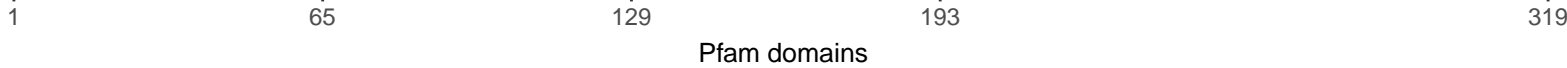
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

GWLQSNLLTAATLFAGESSEGLAGADASEGSRNILEELVRLDNIPELDDGPMARAPPASKKVVAALPVTVTDFELTKMGADAEAGICREVLVDDKMGELPKIMFHPCLKPKLDEHNSGPKRHELLTDHIIYESWKEREKEAEERKGAANAVREGEYMYV

NbL17g03660.1 photosystem_II_protein_D1-like [MW = 38.95 kDa]

No. of times detected



log(intensity)



Values from



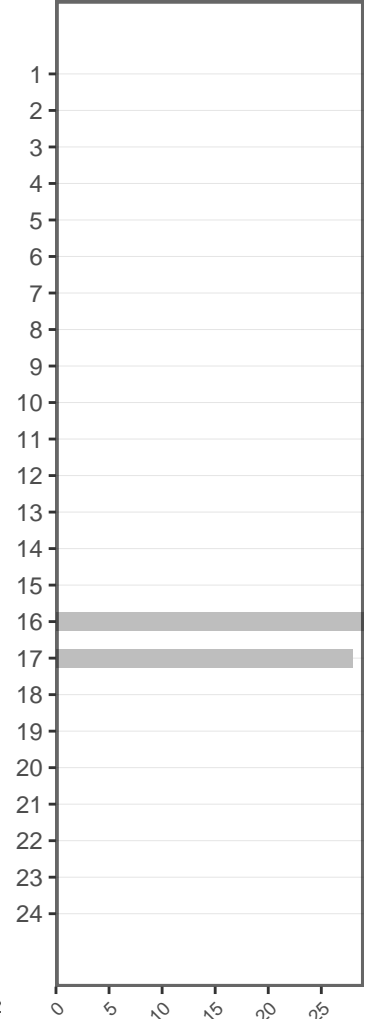
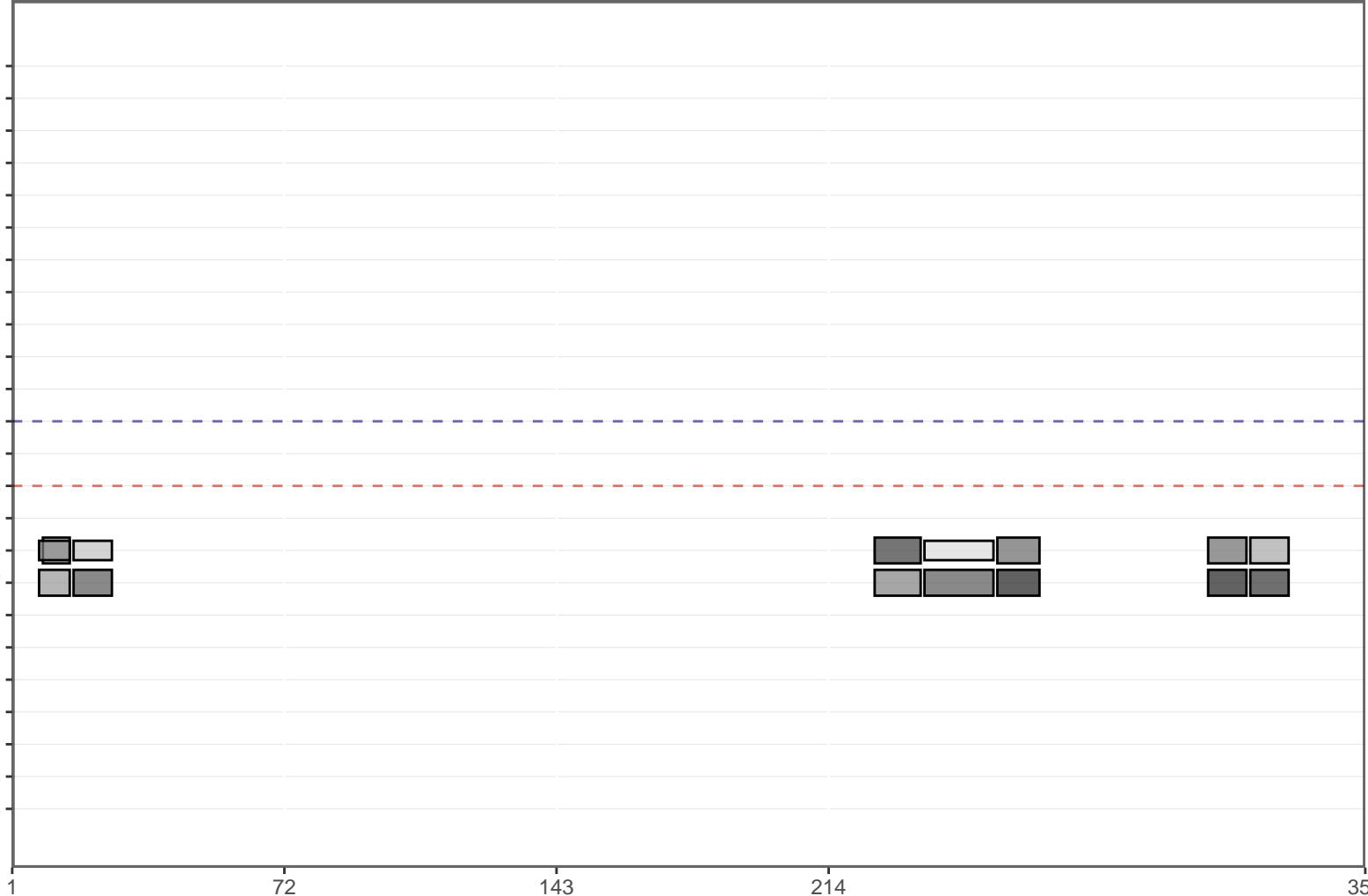
MW indication



Molecular weight



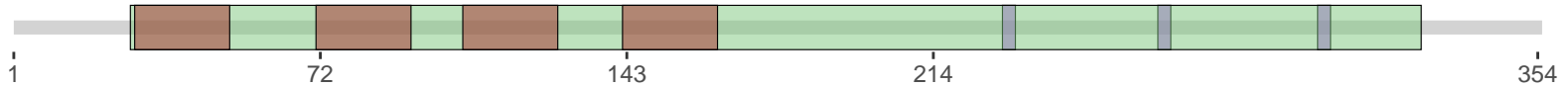
Gel Slice



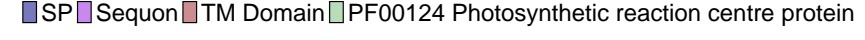
Protein length



Pfam domains



Pfam Description



Protein sequence:

FSDGMPLGISGTFNFMVQDAEHLMLPFLMGLGAGVFGGSLFSAMHGSLVTSLSLRRETTENESANEGYRFGDEETNVAAHGYFGRIFQYAFNRRSLHFFLAWPVAVGWETALGISTMAFNLFNGFNFGVSDGGRVINTWADINRANLGMVEMHERNAHNFPLDLAAEAPSTNG

NbL17g03500.1 psbP_domain-containing_protein_5_chloroplastic-like [MW = 33.34 kDa]

No. of times detected



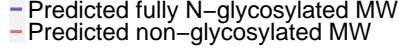
log(intensity)



Values from



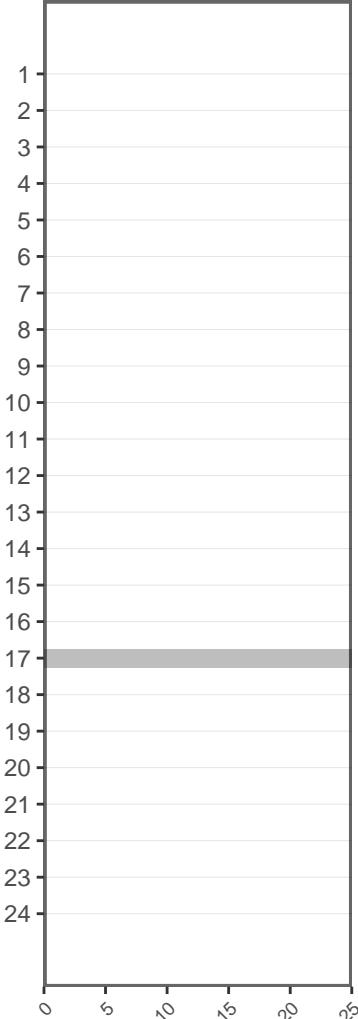
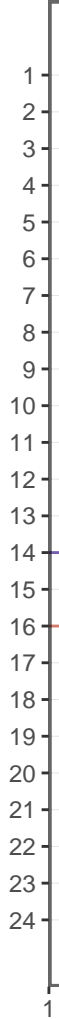
MW indication



Molecular weight



Gel Slice

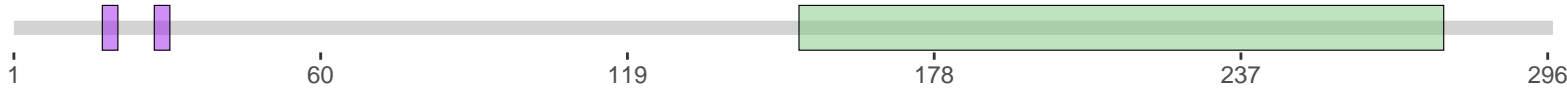


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

RLRIVSERVYDIDNLSBVSIGPPNSQFLKSKKSTWAKDVAQVSLSDKSLRVTSQNLAESSLDAHTSEIDGEPYVYVEYLVKRSPTKTAGETLFRHYAASAEKRDGVLVYTFASALGKQWDMKGFLEKSVASFRLLPPTESVVPYKDPWRFW

NbL17g03090.1 peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase_A-like [MW - SP = 62.44 kDa]

No. of times detected



log(intensity)



Values from



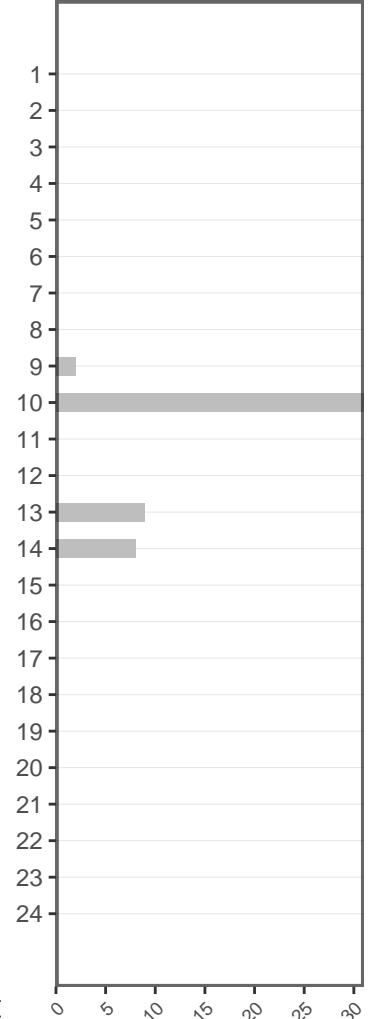
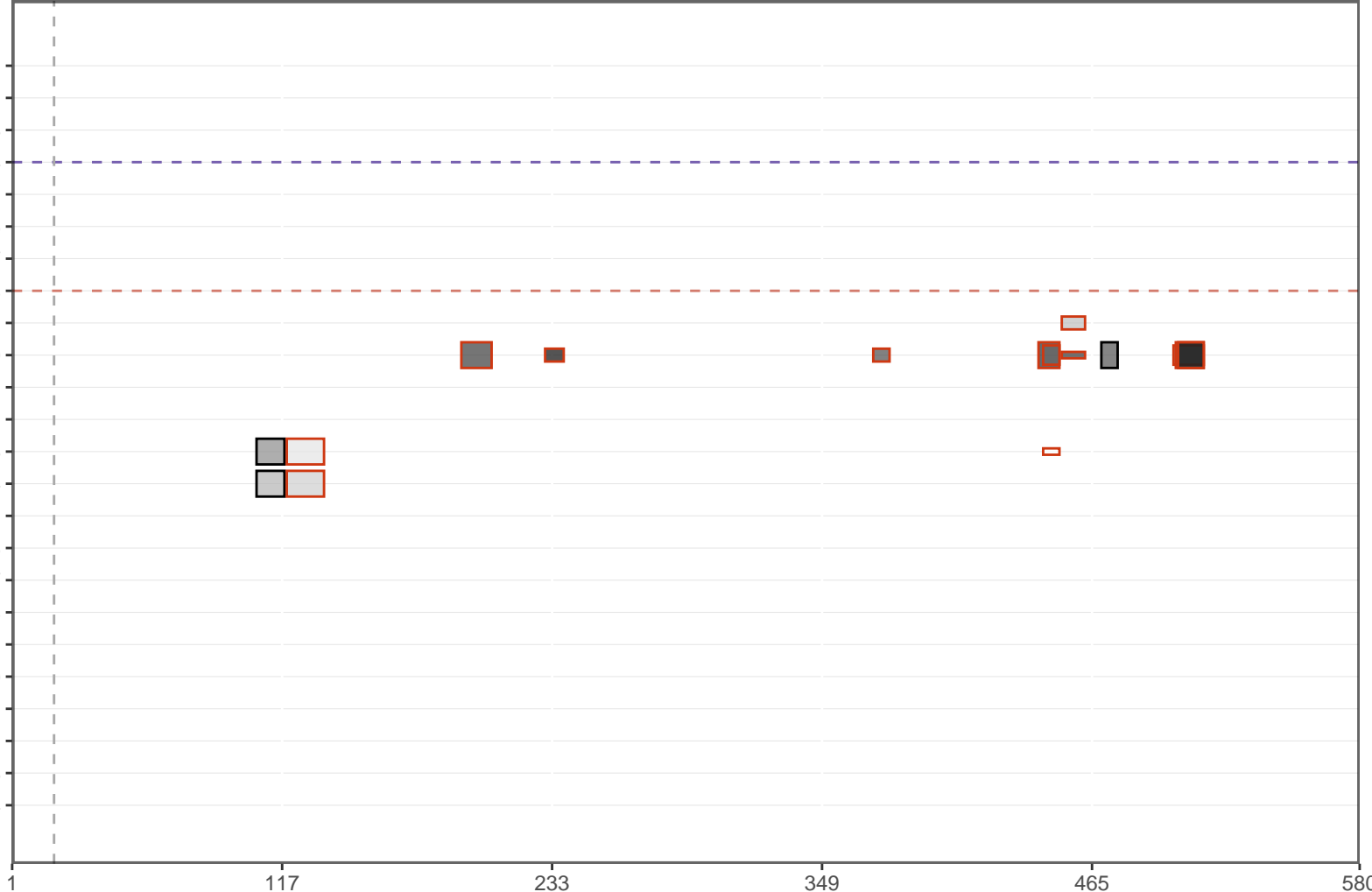
MW indication



Molecular weight



Gel Slice



Protein length

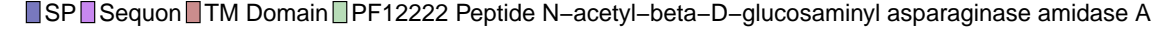


Peptide counts over 4 repeats



Pfam domains

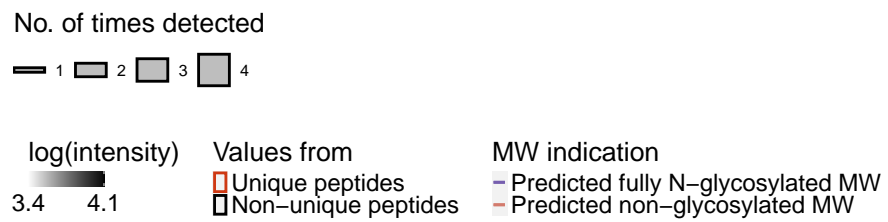
Pfam Description



Protein sequence:

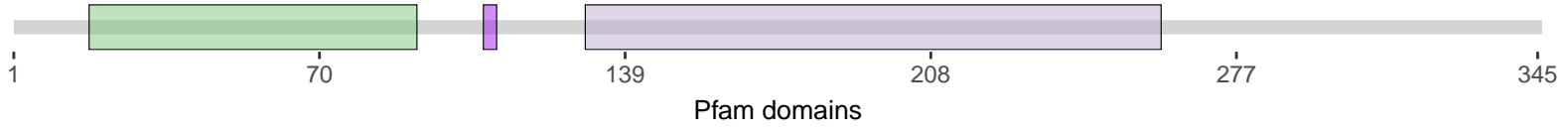
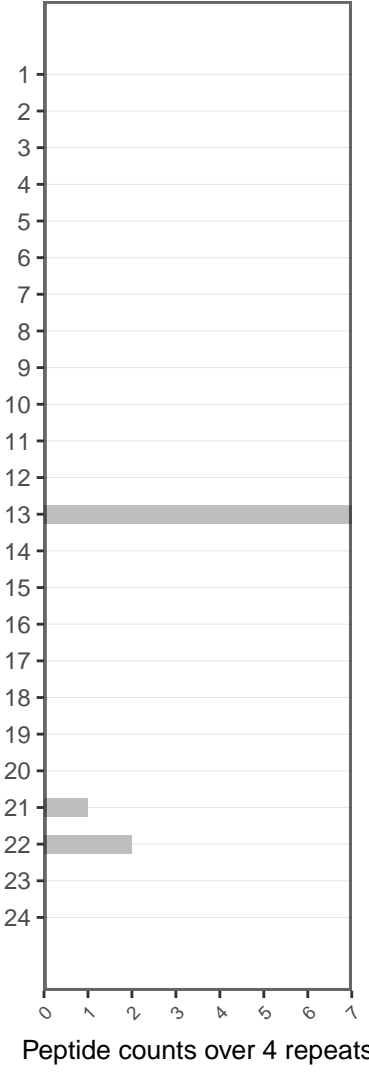
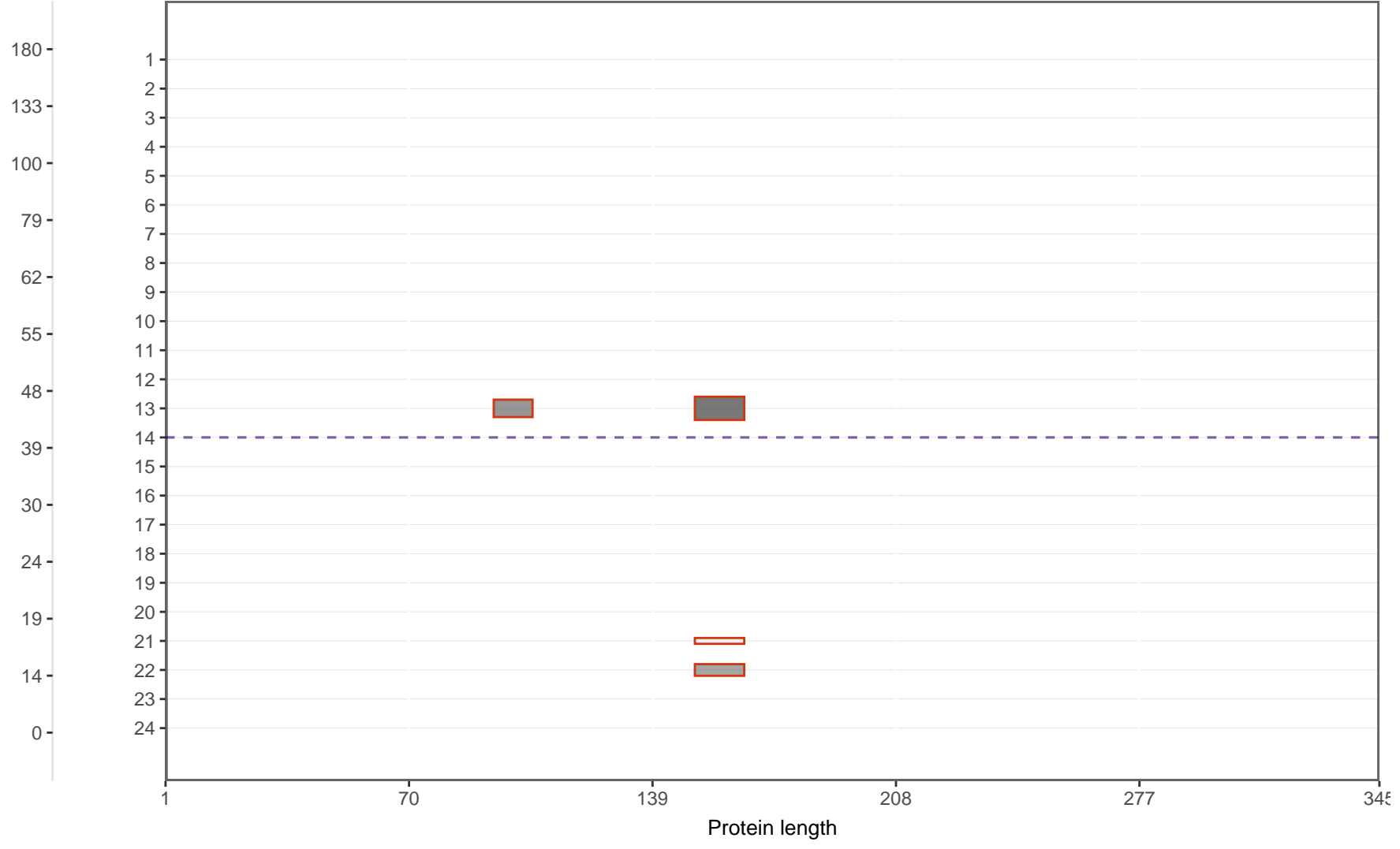
EVLLNIDENLAGSVPFPVFTGGNPLWYVLPVWVIGAFDLPVYDILTSFLGLLLDGGDHFVGLGVADSIPIWLVGANLHLWLASNEVDKATFDLGTKPKIERSSSIFLGDGSEFVLEKRIKSEISVWNSAGNLTLLVSRLEKFKQKINFYLNKTEKHKKGVKEEIEVRLVLSIGSSTIKTKVWRKYPLTITSKLPSTENGSTSLMLSDLDHEWKEKKKLDGSSSTLNRQGGNGWMAVGDHNVLYGGATTQGGVSYEGEAGGYSRSTANGKLMNDTANSLCAAPLKFQ:

NbL17g03070.1 eukaryotic_translation_initiation_factor_2_subunit_alpha-like [MW = 38.95 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF00575 S1 RNA binding domain PF07541 Eukaryotic translation initiation factor 2 alpha subunit

Protein sequence:
 .NSLTREKETGPDGSEVTKVVPALSEEVKDLVKNRRRMTFQPLKIRADIEKGFQFDGVIHKEAMRKAEEAANGDDGPKWIKLVAPPVYVLAQTLDKEGGIIVLSKAAIACTQIEIRHKGLTKVKEAPRAVSEREDKLLAEGMAKLGRENERRSGDDESEEEEDTGMGDELDKNSGTGTD*

NbL17g02910.1 PRA1_family_protein_B1-like [MW = 23.3 kDa]

No. of times detected



log(intensity)



Values from



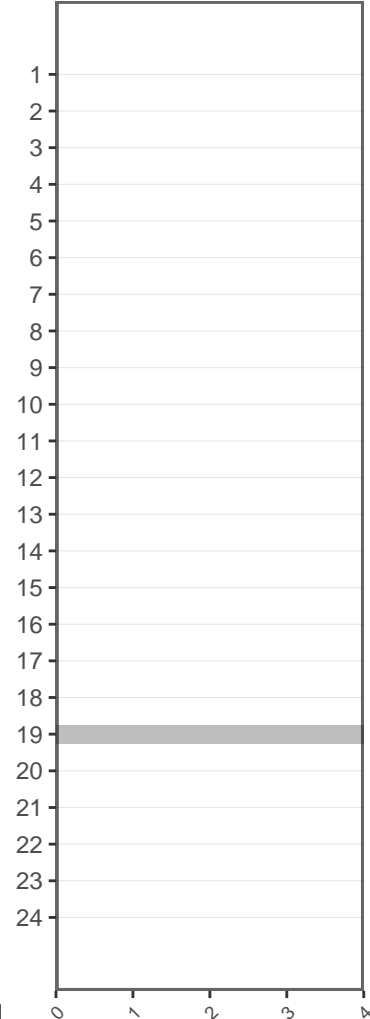
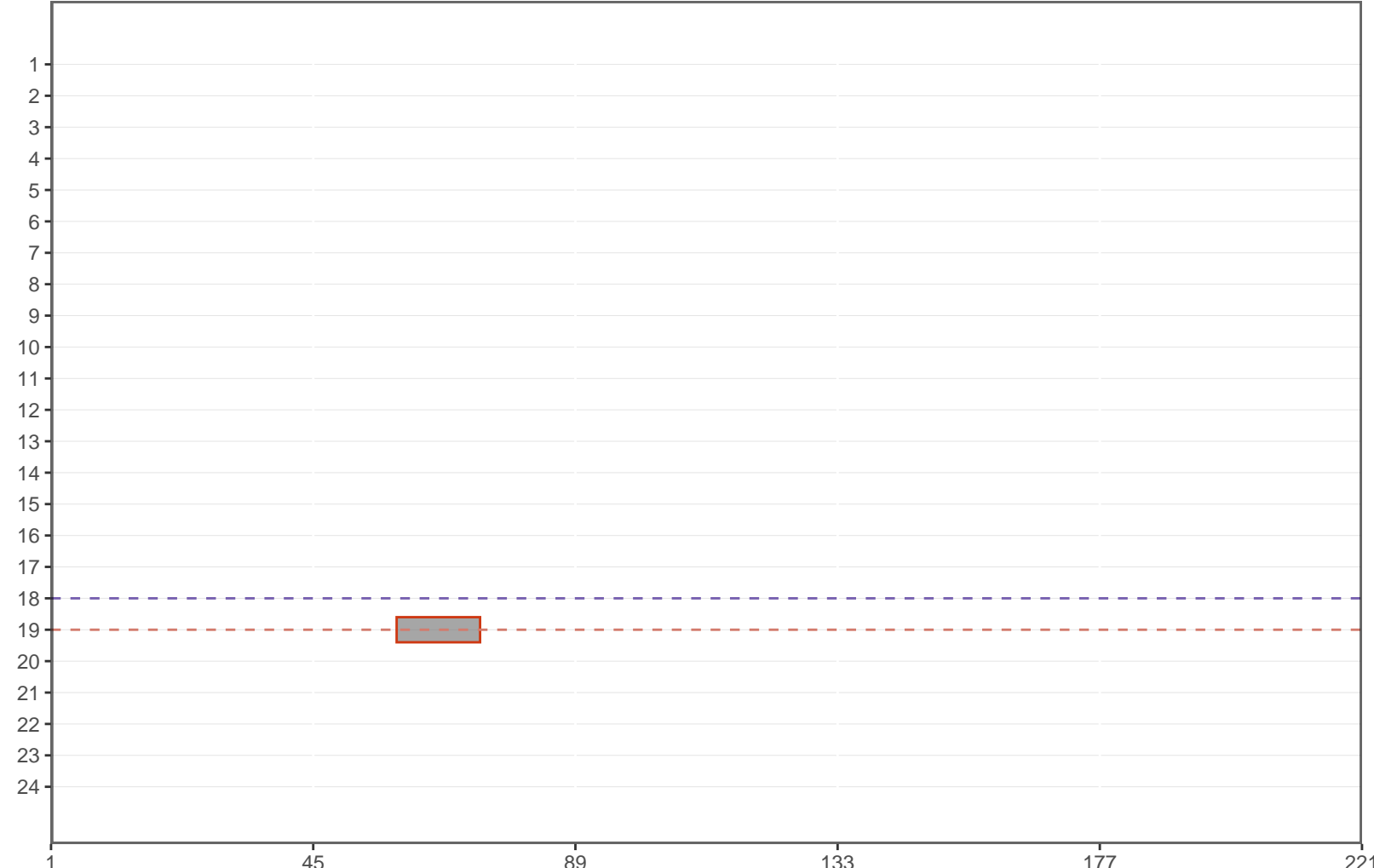
MW indication



Molecular weight

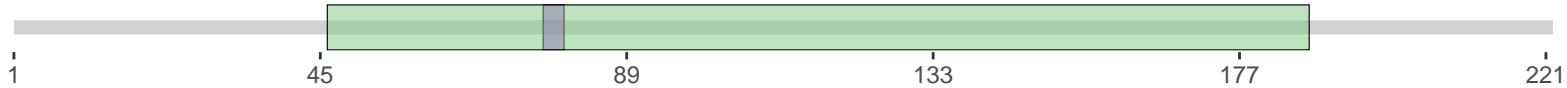


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

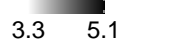
LLSHPFSLLLVLLALGGWFFLVLFKPSDQPVVILGRTFSDRETLGILVSTVWVFLTSVGLISALLVGLAVCAHGAFKRVPEDLFLDDQEPKVFGLSFLGGAASSAAAAADVAARV

NbL17g02890.1 uncharacterized_LOC104234041 [MW = 30.72 kDa]

No. of times detected



log(intensity)



Values from



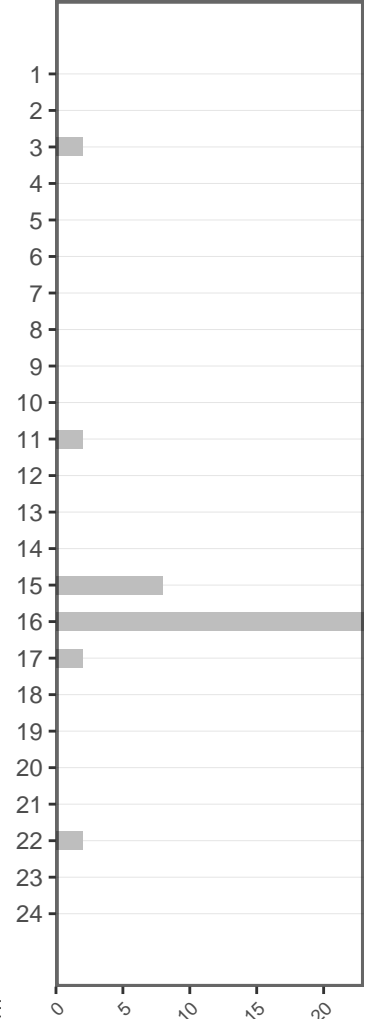
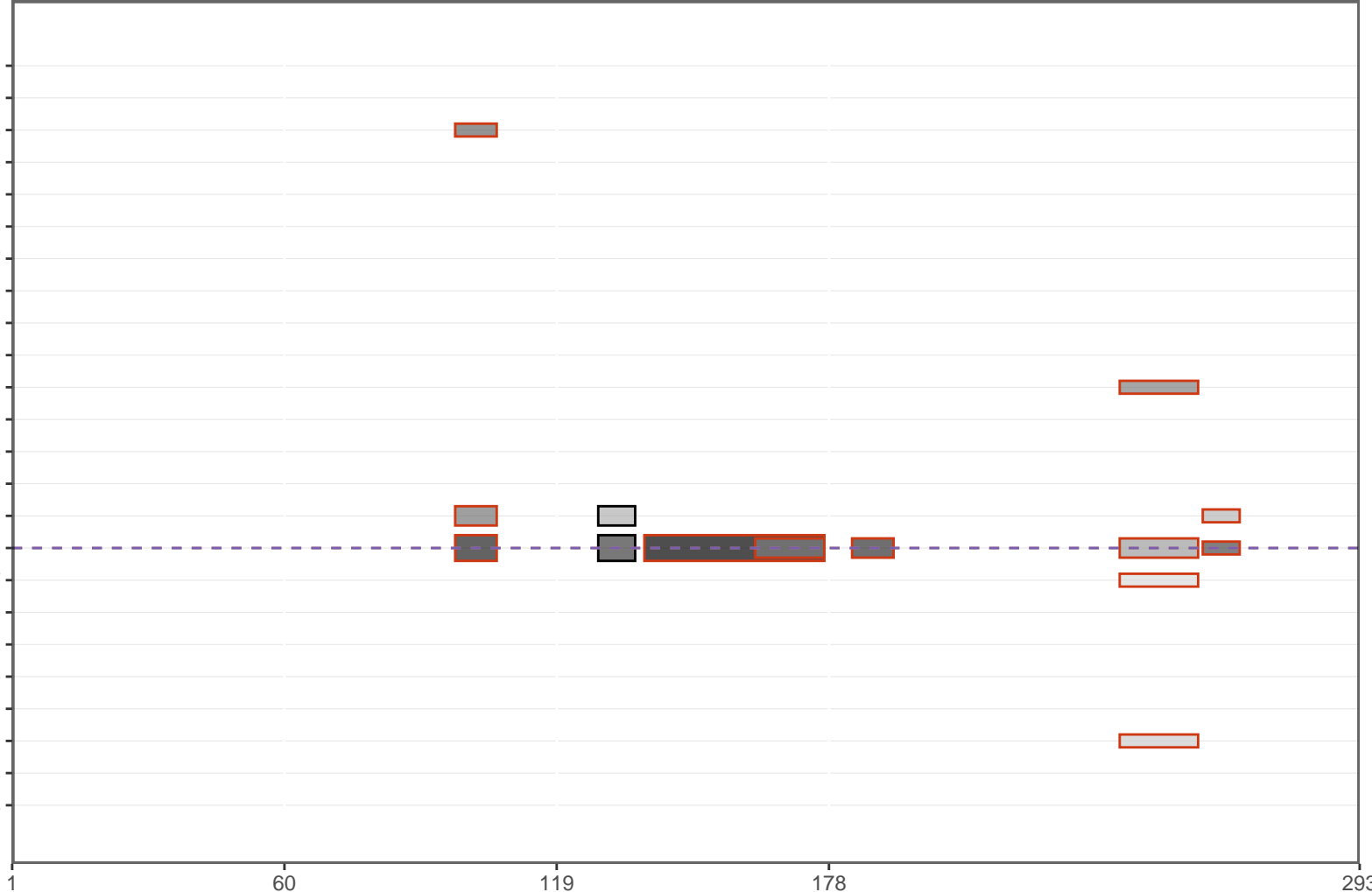
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LHLKRNIEAPVYLPFAVSTPTPTPPSAKPGTASTAAAPITSLGKSSSEKISPFITNAEKSAKLALETGGAGYVLVGPTVGSFRRAARTLKGKKQPPACKGEGVKEGGQIGFLDFGCTEHPVREDAAGEVAKILFNDGEAVGVGDRPLMVLPSFRGI

NbL17g02740.1 adenylosuccinate_synthetase_chloroplastic-like [MW = 55.02 kDa]

No. of times detected



log(intensity)



Values from



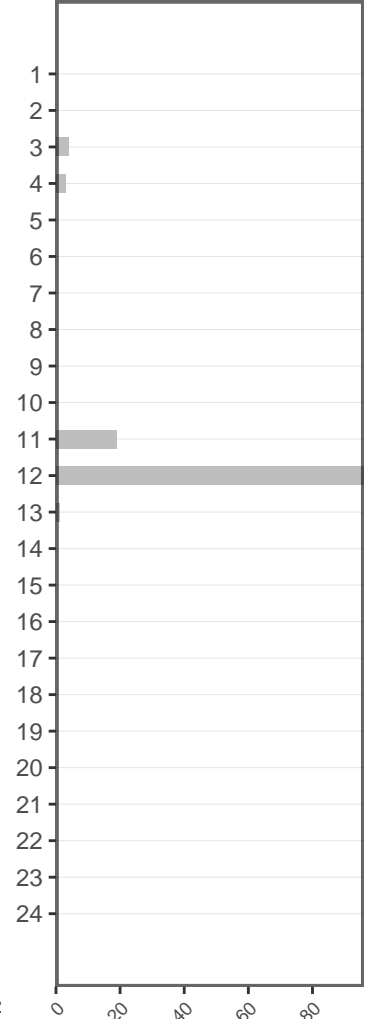
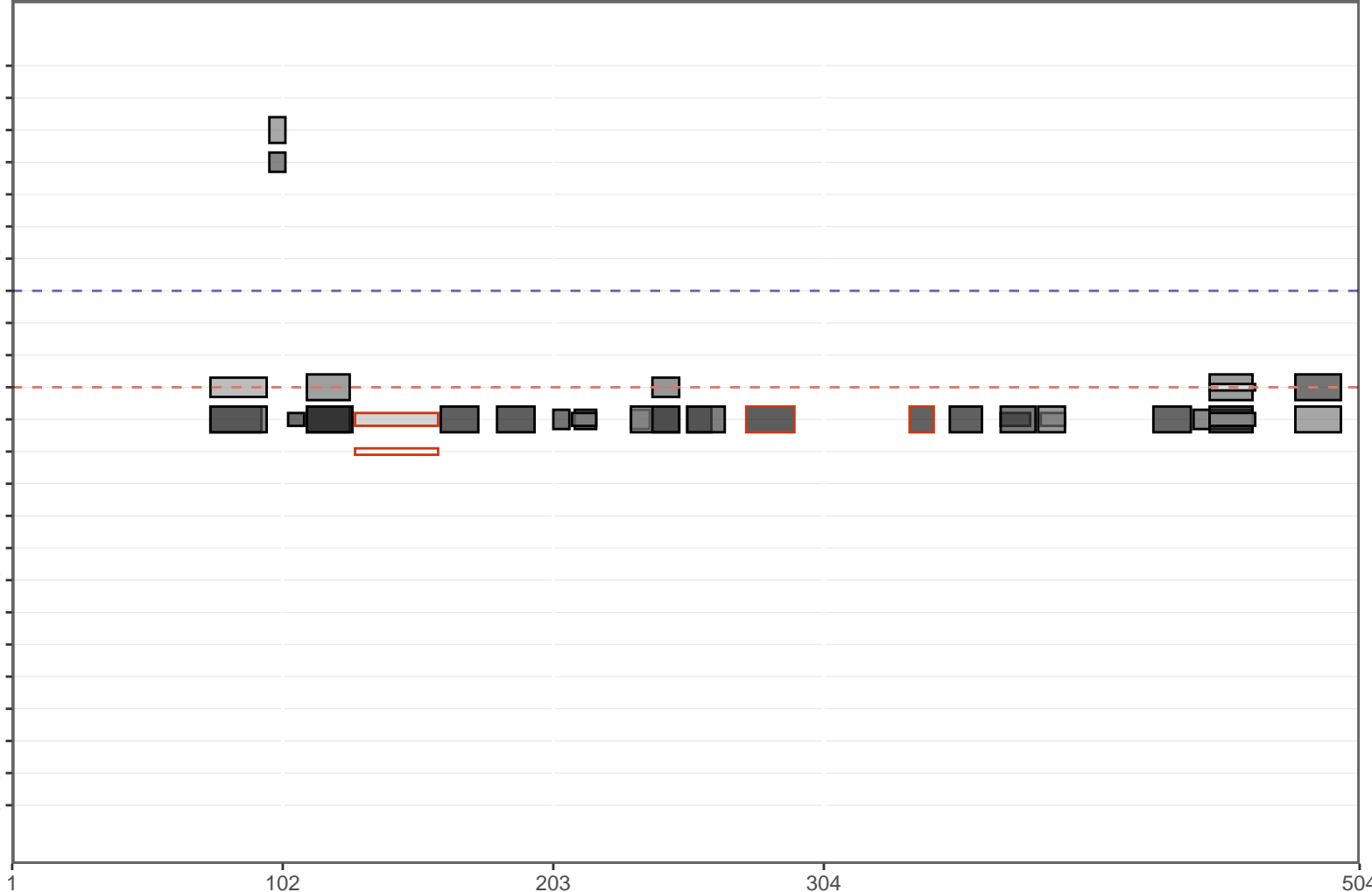
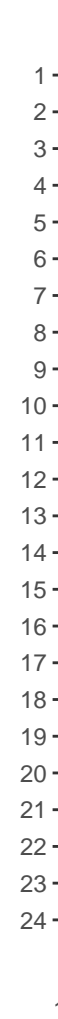
MW indication



Molecular weight

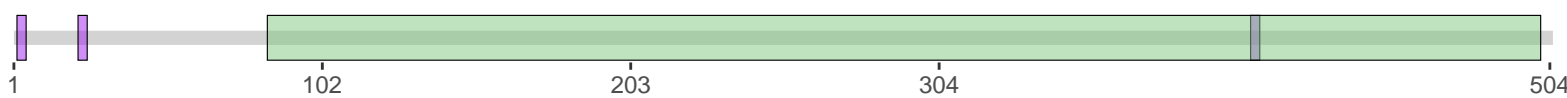


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

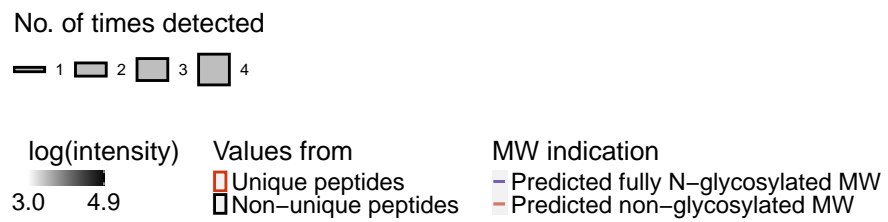
Pfam Description



Protein sequence:

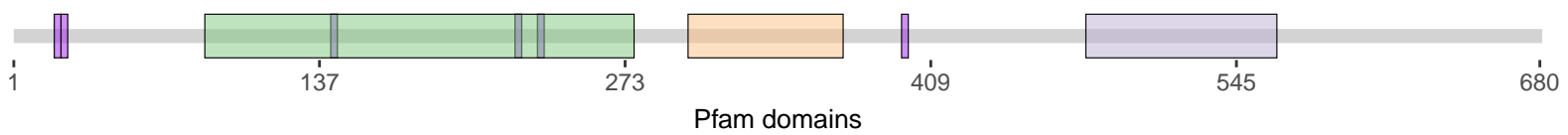
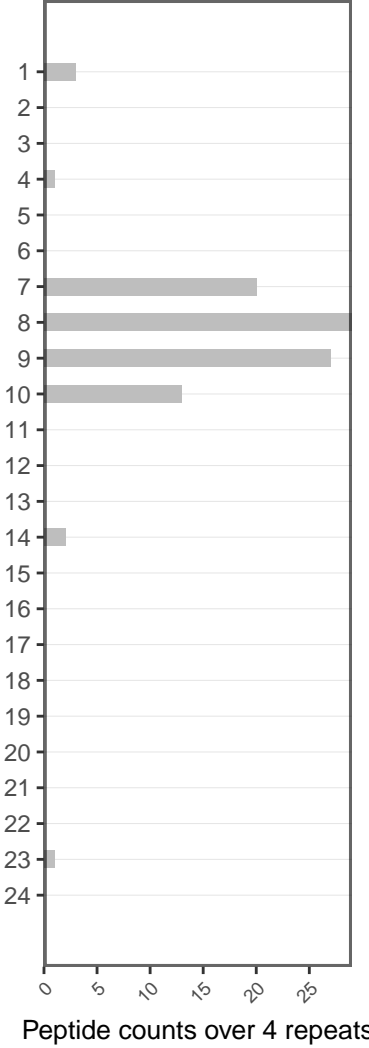
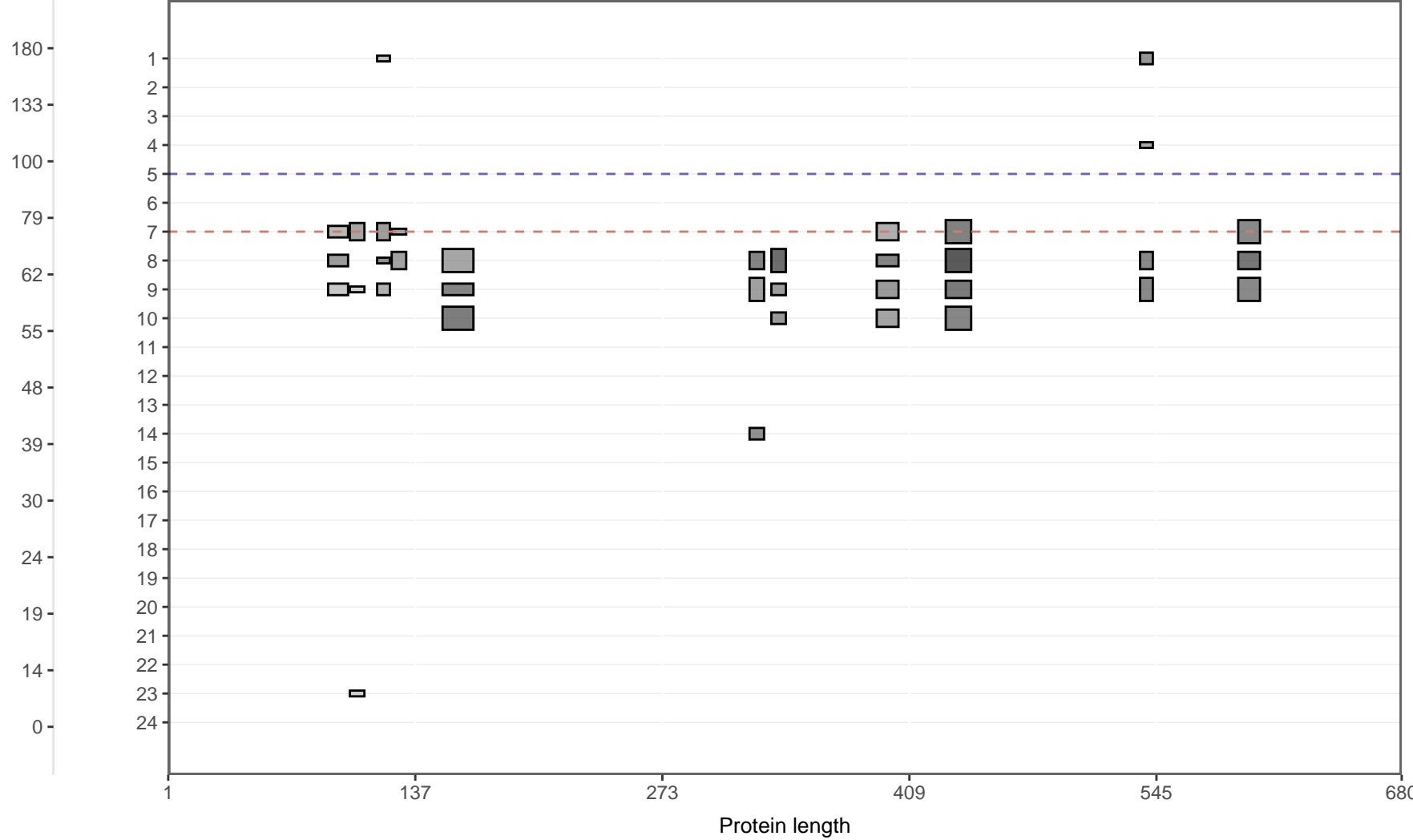
OKLDLLSDAASRFKGFNYPDMLEEEVERYYKFAERLEPFHDTVHFHNDALSGKHKLVVEGGGATMLDIDFGTYFPVTS66PEAGGIGCTLGIAPRVVGDVLGVKAVYTRFVGGGPFTELKGGKDLRFAGGDFGTTGRPRRCGLWLDVALRFCCGQNGFASLNLTKLDLVL6DL6EIEIGVSVRQPDGTPVESFSDLRLLDQIKVEYEVLPGWQTDSSIRKYSELFKAAAREVVERIEELGVPHYGVGPRDALNYK

NbL17g02570.1 GTP-binding_protein_TypA/BipA_homolog [MW = 74.93 kDa]



Molecular weight

Gel Slice



- Pfam Description
- SP
 - Sequon
 - TM Domain
 - PF00009 Elongation factor Tu GTP binding domain
 - PF00679 Elongation factor G C-terminus
 - PF03144 Elongation factor Tu domain 2

Protein sequence:

SRFGVSELYVEKFSRVPKMETVEAGDKAVCGIDDIDIGETADKBEQKPLPAKVEEPTVMMSFVNTSPFVREGKYVTSRNLDRILYRELEARNLAKMKEVDEGETADTFVSGRGLHTILLENMRREGVEFMGPKVNRKDGKLLPEVEIATVEVPEEIMGSSVELLGRRRGMDMDQGLSEGDTLLKVKIPTRGLLGLRNSLITASRGTALNTFDGVPWGGDSTRDLGSLAFEDGTSTFVYALMSGGDRGGLFIPGVGVYKGGVGHQRPGDALLNVCXXXA

NbL17g02560.1 aspartate_carbamoyltransferase_1_chloroplastic [MW = 45.42 kDa]

No. of times detected



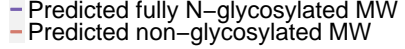
log(intensity)



Values from



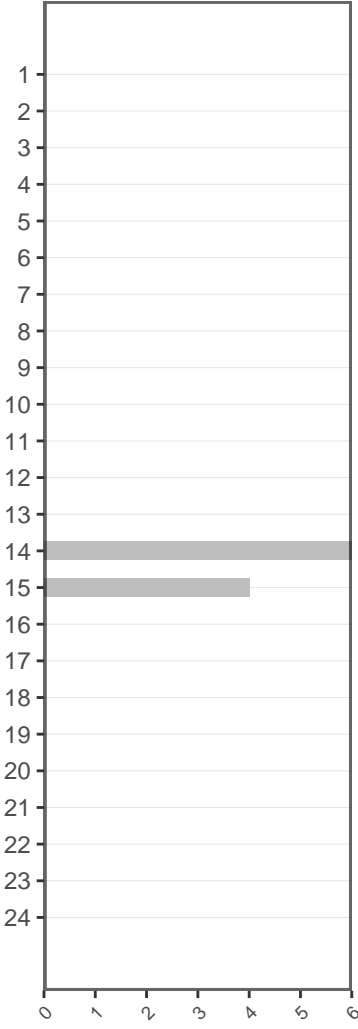
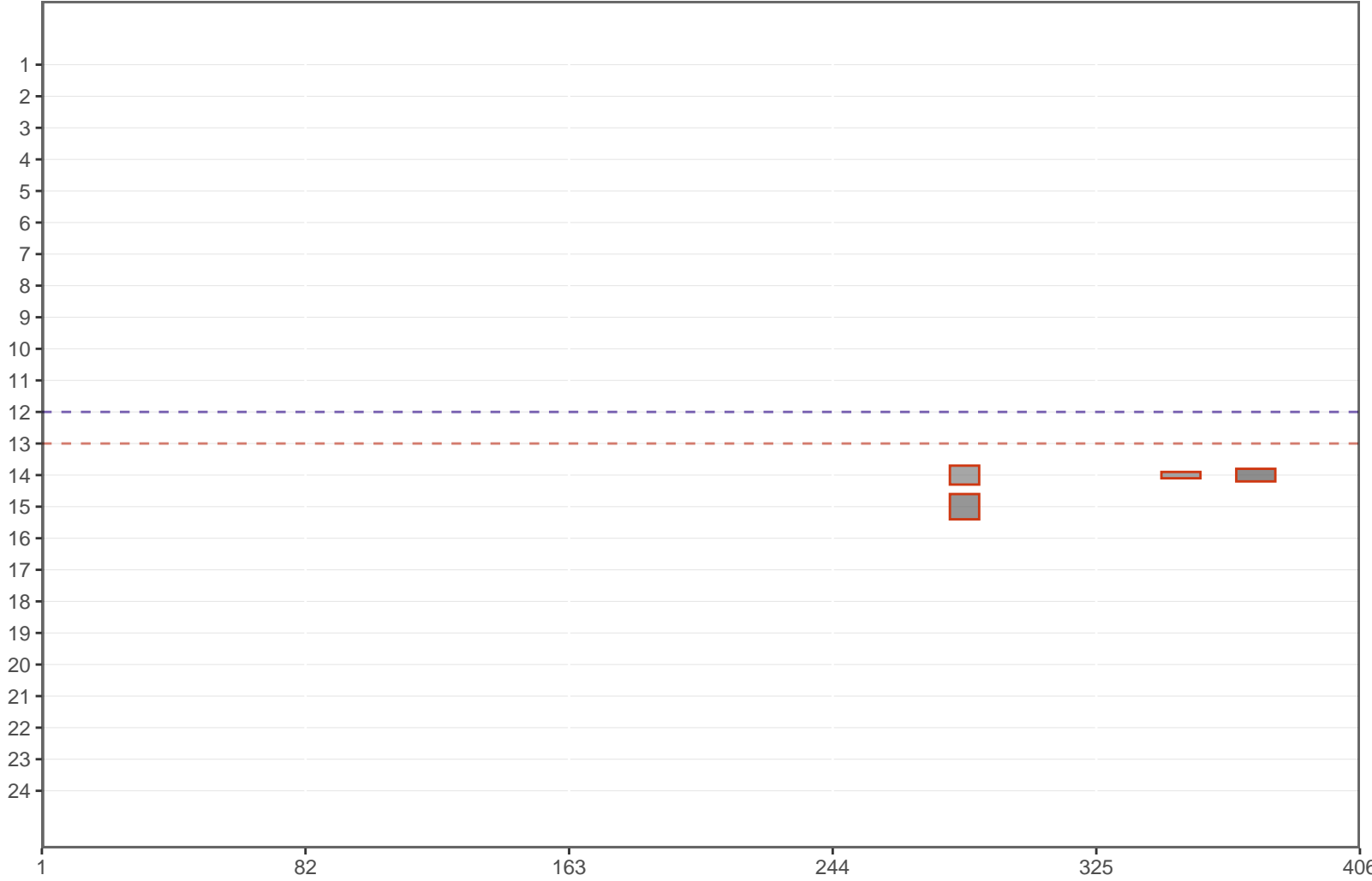
MW indication



Molecular weight

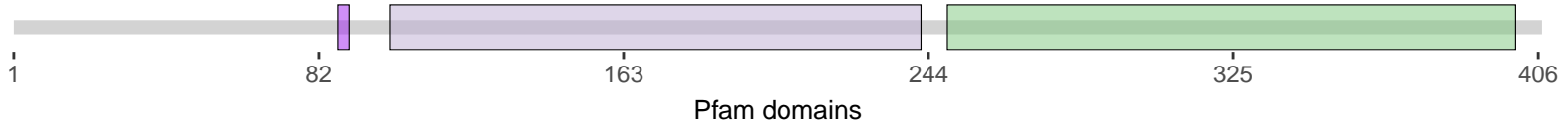


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00185 Aspartate/ornithine carbamoyltransferase, Asp/Orn binding domain
- PF02729 Aspartate/ornithine carbamoyltransferase, carbamoyl-P binding domain

Protein sequence:

ISIRTVKEYSDIVMRHFESGAAKRAAATASIPINAGDGPQGHPTGALLDVTYTEREIGKLDGKVALVGLAYGRVRLSLAVLLAKYQDVKYFVSPDVKMKDDKDYLTSMGVQVEESADLVVASKGDVYVQTRIGRERFGERVDLVEEARGKYVDLAVLNAHQHVAVMHPLRLDEITVDVDEDPRAAVFRQANGLYRMALLKLLGLGW

NbL17g02410.1 stearoyl-[acyl-carrier-protein]₉-desaturase_chloroplastic [MW = 44.78 kDa]

No. of times detected



log(intensity)



Values from



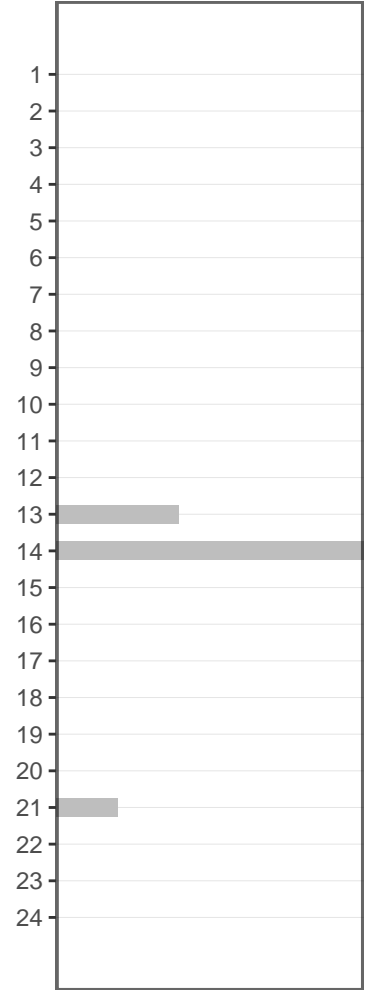
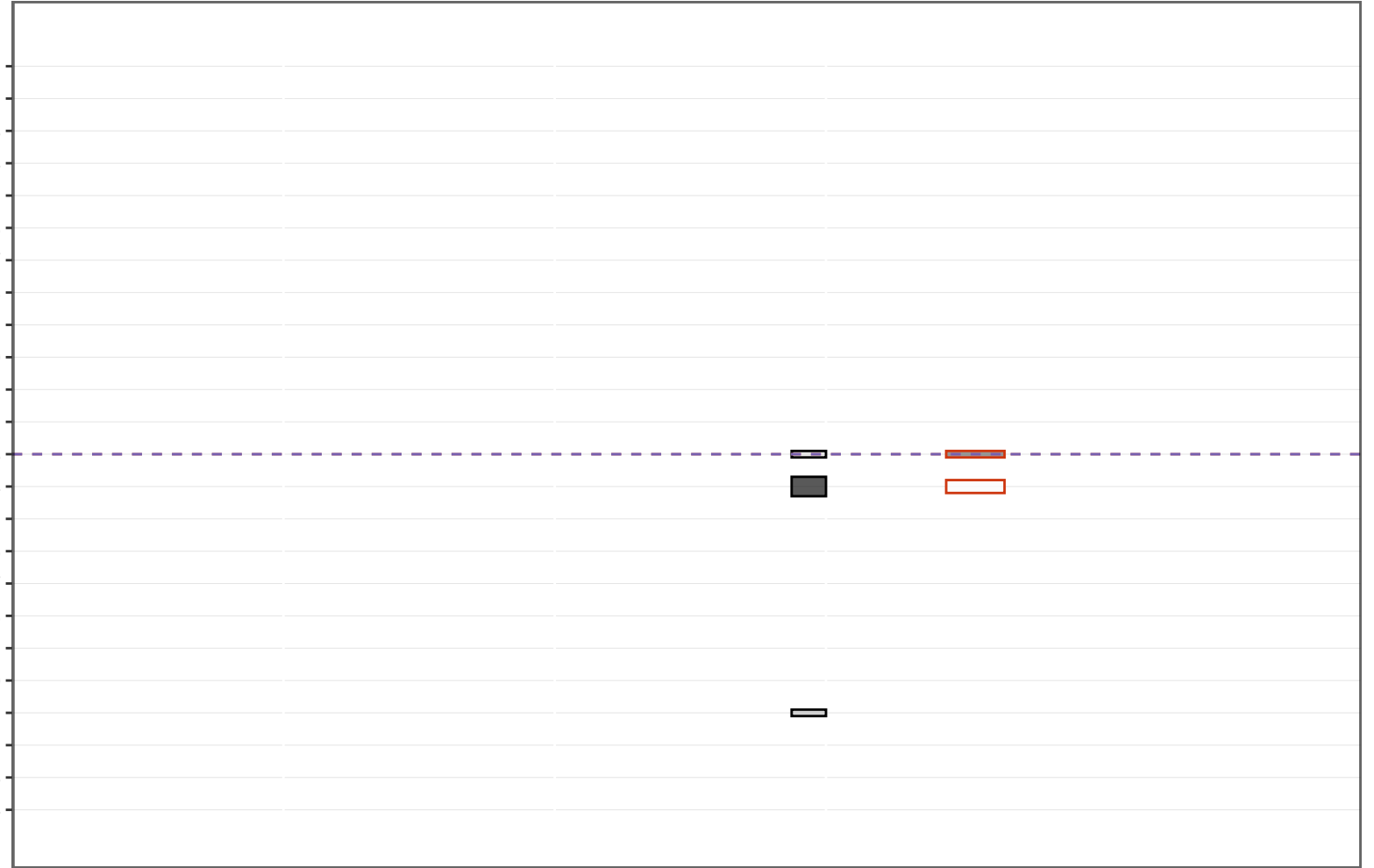
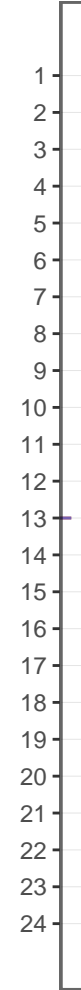
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

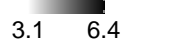
YLYLSGRVDMRQIEKTHGLKGGGMDPRTEFNFLGFIYTSFQERATFVSHGNTARHAKHEHGDGLKLAQVGGHAADEKRHETAVTRIVKELFEVDPDGTVGAVADMRRKIKSPHLMVYDGRDDNLFHFSAVAADRGLGVYATKADILEFLVGRWEKELTGLSGEGRIADGVVCGCLAPRIRKLEERADARAKGKAFVPSFWVDFGRIKL*

NbL17g02110.1 reductase_1-like [MW = 42.03 kDa]

No. of times detected



log(intensity)



Values from



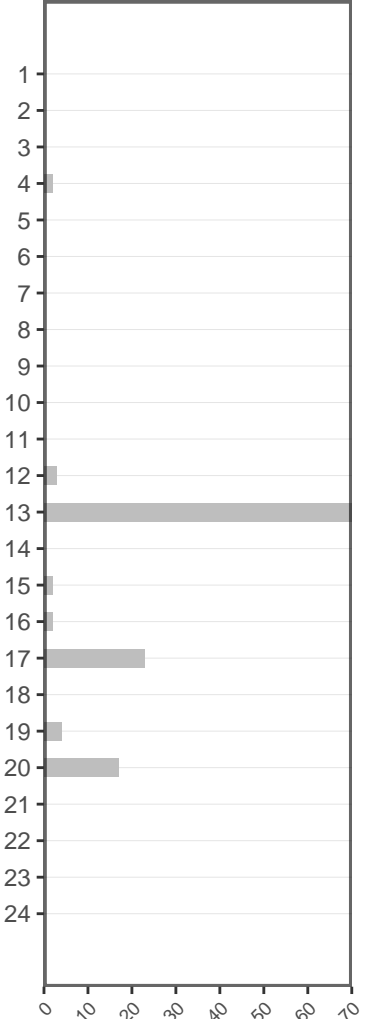
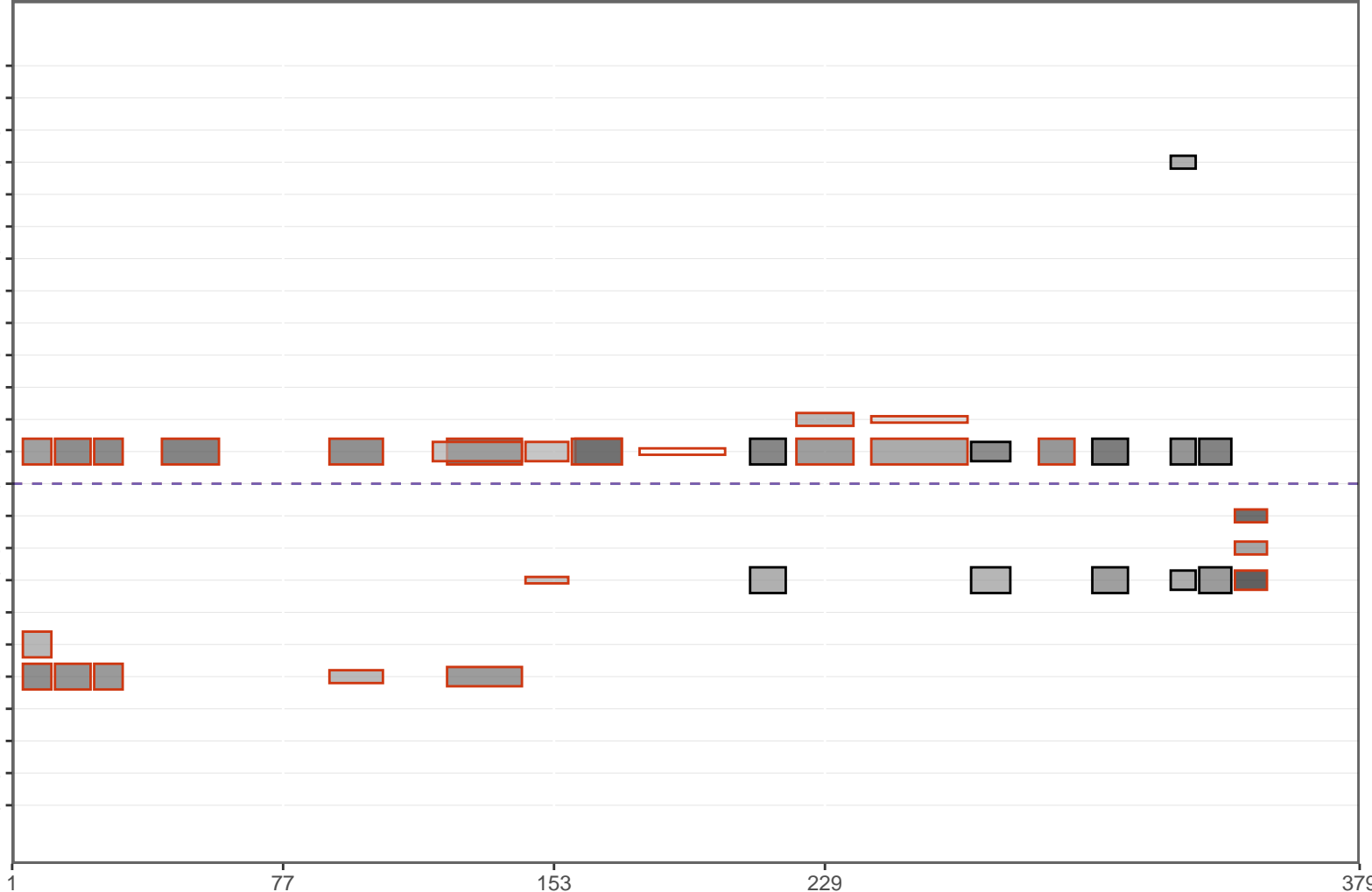
MW indication



Molecular weight

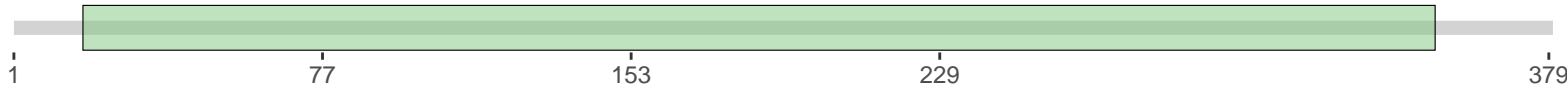


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

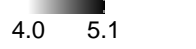
IAIEAGFDQVEIHGANGYLDGFMKDGINDRDTDHYGGSLNRCRFAHHEIVAVNEIGADRVGRILSPFASVMESSGDSNPSALGLYMAESLNKYGIAYCHVMEPRMKTVEKVEGSESLVPMRKAFTGTFMAGGYDRGDGNKAVVEDRADLWYGRFLANPDLPRRELEDFPLNKNRDTFYSDPVLVGYSDYFPLETAA

NbL17g02080.1 phosphoglucan_phosphatase_LSF2_chloroplastic [MW = 34.59 kDa]

No. of times detected



log(intensity)



Values from



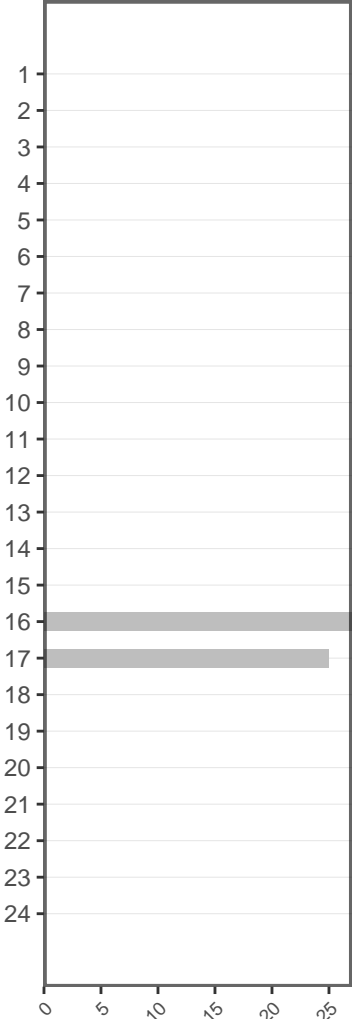
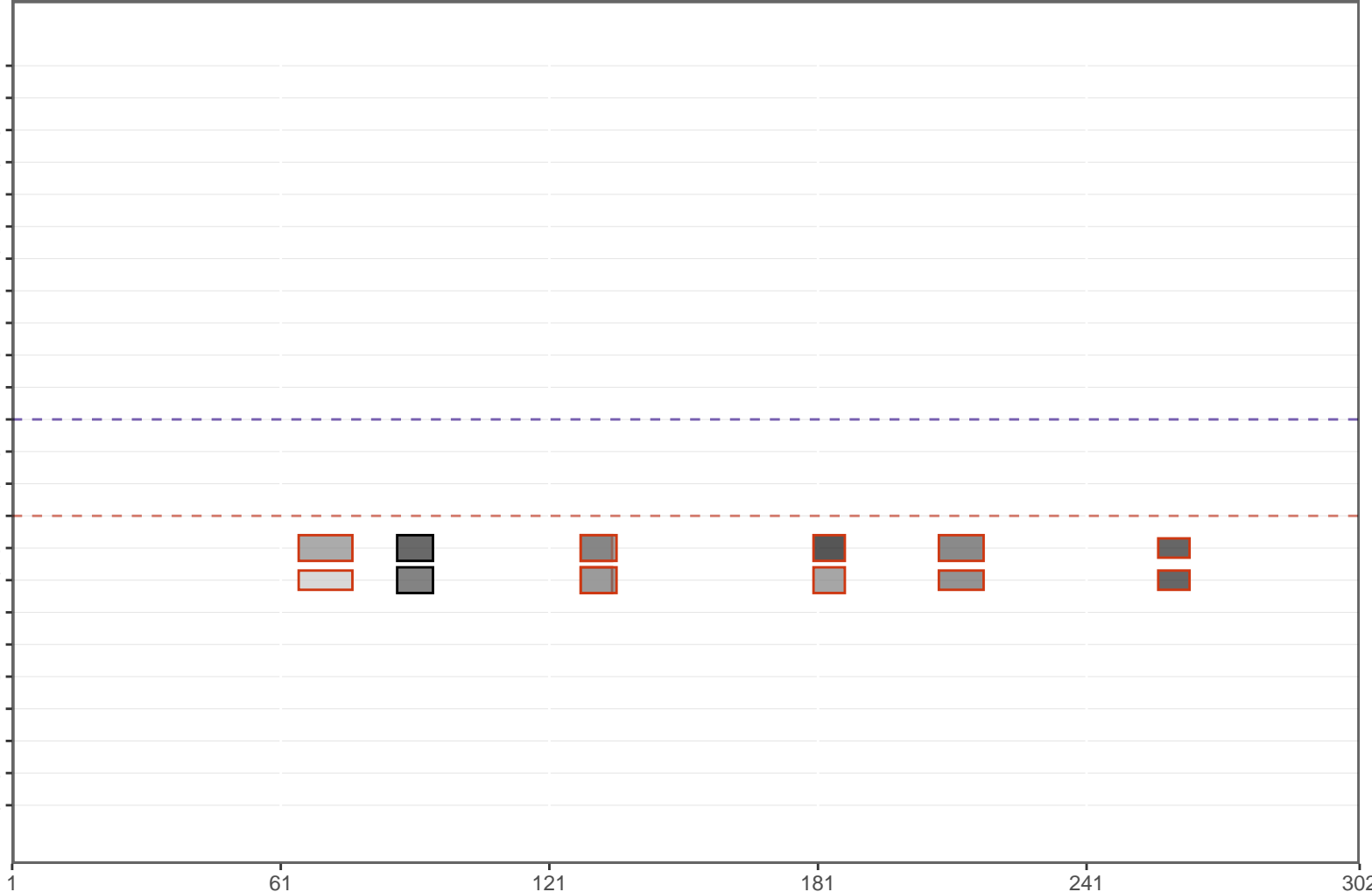
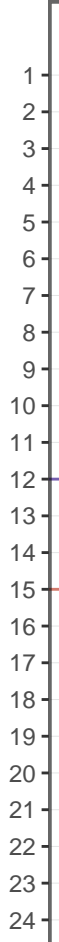
MW indication



Molecular weight



Gel Slice

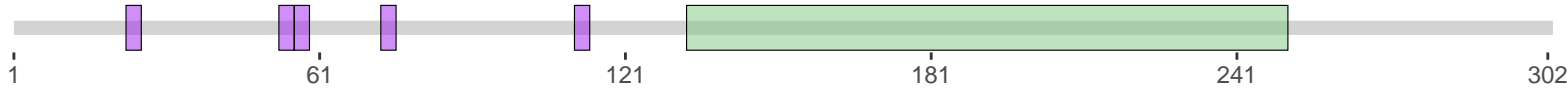


Protein length

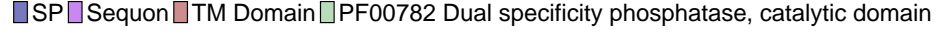


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ISENVAFILNLOOKDIEFWGIDLGSIVRRGELGIVHMRPKDFDPDELRLVLPFAVSSLEWASEGKGRVYVHCTAGLGRAPAVSIAMFVFGMDLNAAYDTLTKRPPCGPNKRIRAAITYDLAKNDHWKEPFENLPDVAFADADWERKLIQDRVRLINT*

NbL17g01880.1 protein_LST8_homolog [MW = 35.41 kDa]

No. of times detected



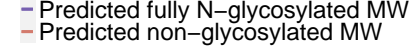
log(intensity)



Values from



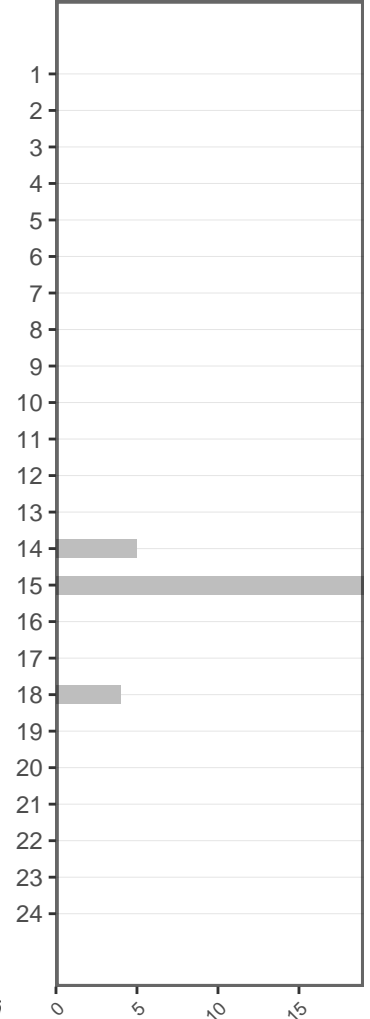
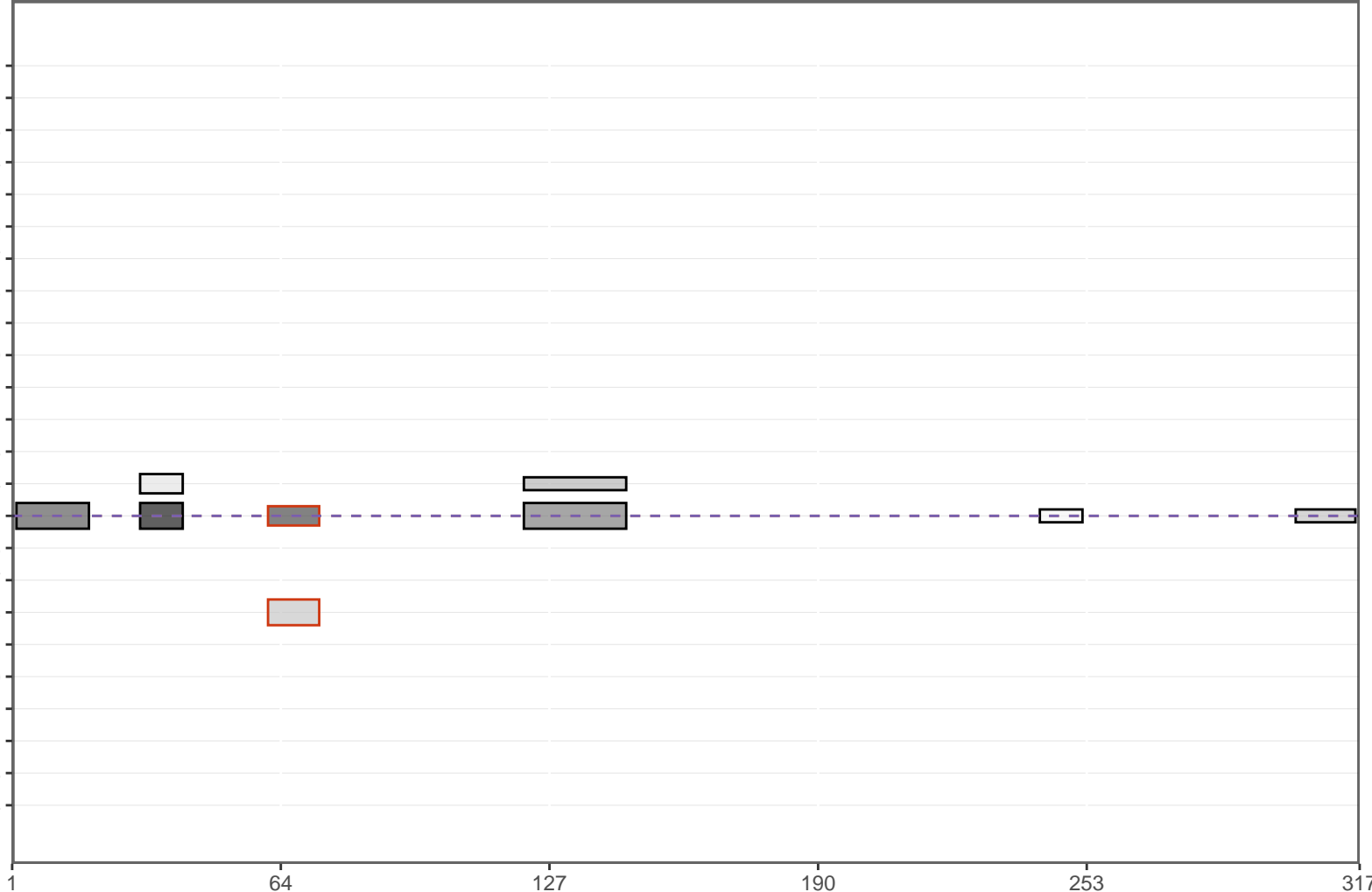
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

RVWDLRANSCSCELVPEVDIWRRLTMMWDGSLVAANNRGTGYWRRLLRGTETMTNFEPLKLGQHDGYLEKLLSPELCEPHRYLATASDDHTVWVWVDSFTLEKTLGHERWVWDCVFSVDGAFITASSDITARLWSTSTGDKIKVYGGHKKATVDGALHDGPEPSI

NbL17g01640.1 probable_polygalacturonase_At3g15720 [MW – SP = 50.29 kDa]

No. of times detected



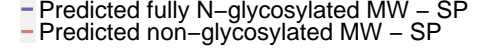
log(intensity)



Values from



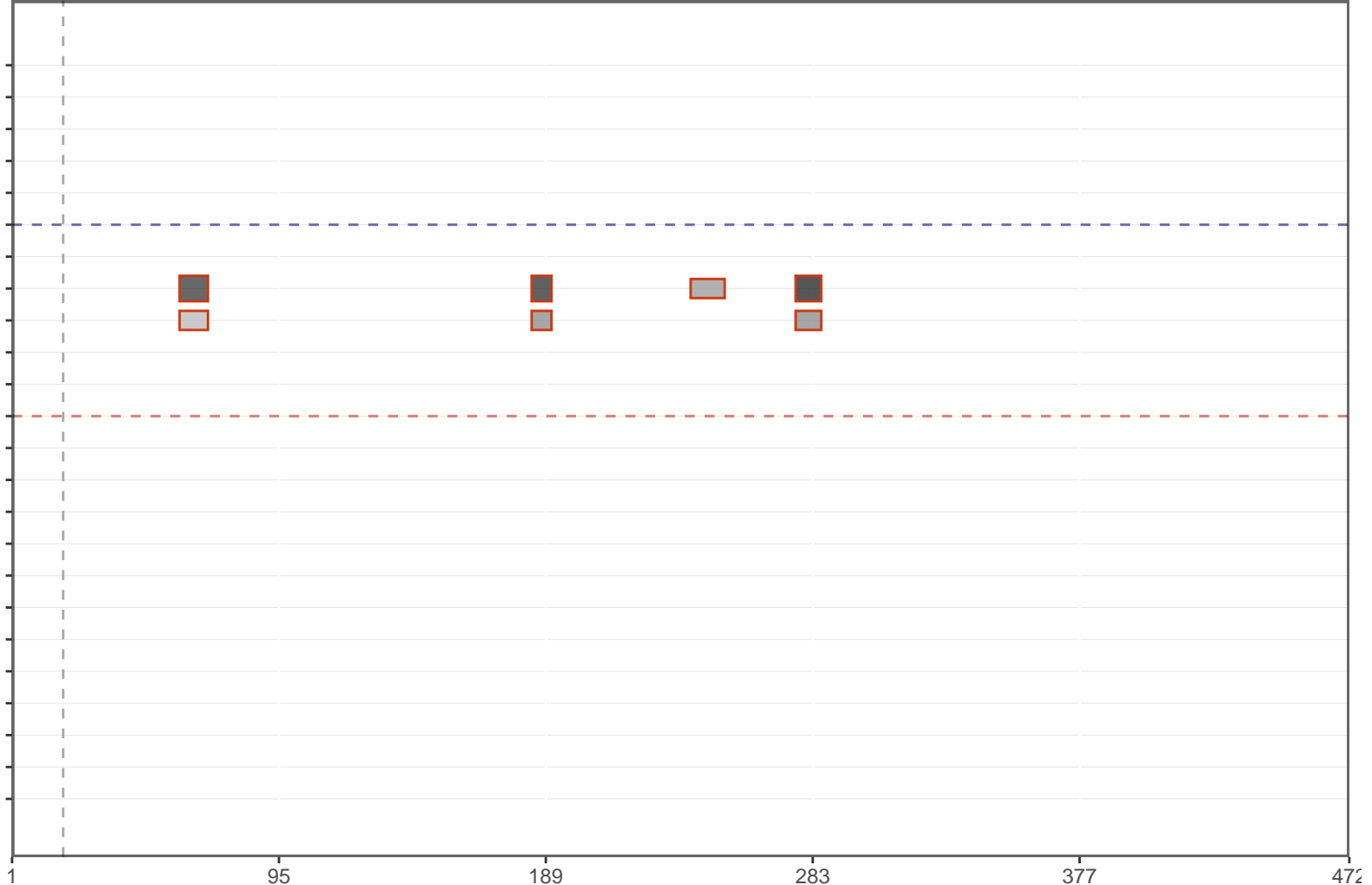
MW indication



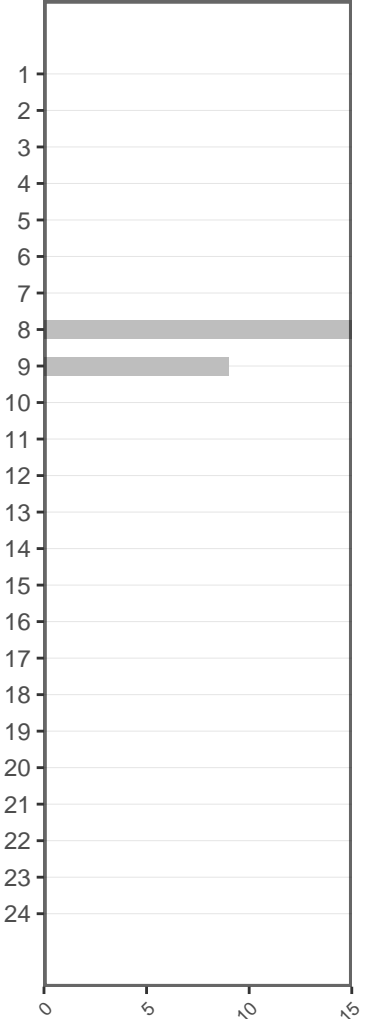
Molecular weight



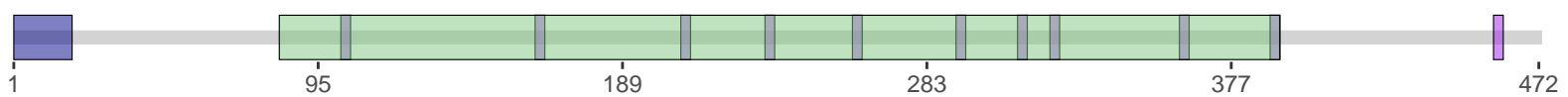
Gel Slice



Protein length

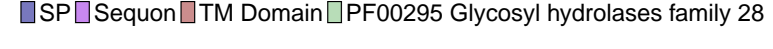


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DDIEDSNNTYITRDNNTGDDAICPKS6TGPVHNLTATNQHWRKTS6SAIKLGSASFYTFKFLFENTFESHRLGLALGRDGGVSDITFSNNTSTRIHYH6SWGRAEPIYVTTGPRDATEKAGSISNLLFVNTSTSENGIFL6SGGGVLESLKFNMLTYKRWTYKPDGWWGVRRPGGOELVKHQTAGFMMEHIDGLVFENVMKWSNDESMRWNNPLDFRPFSTVNNEMLNFYRSYGGQ

NbL17g01460.1 elongation_factor_1-gamma_2-like [MW = 47.67 kDa]

No. of times detected



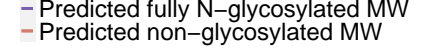
log(intensity)



Values from



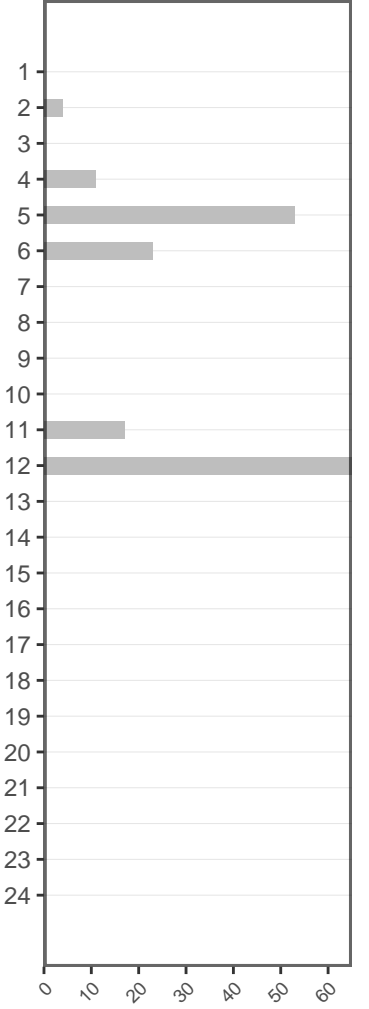
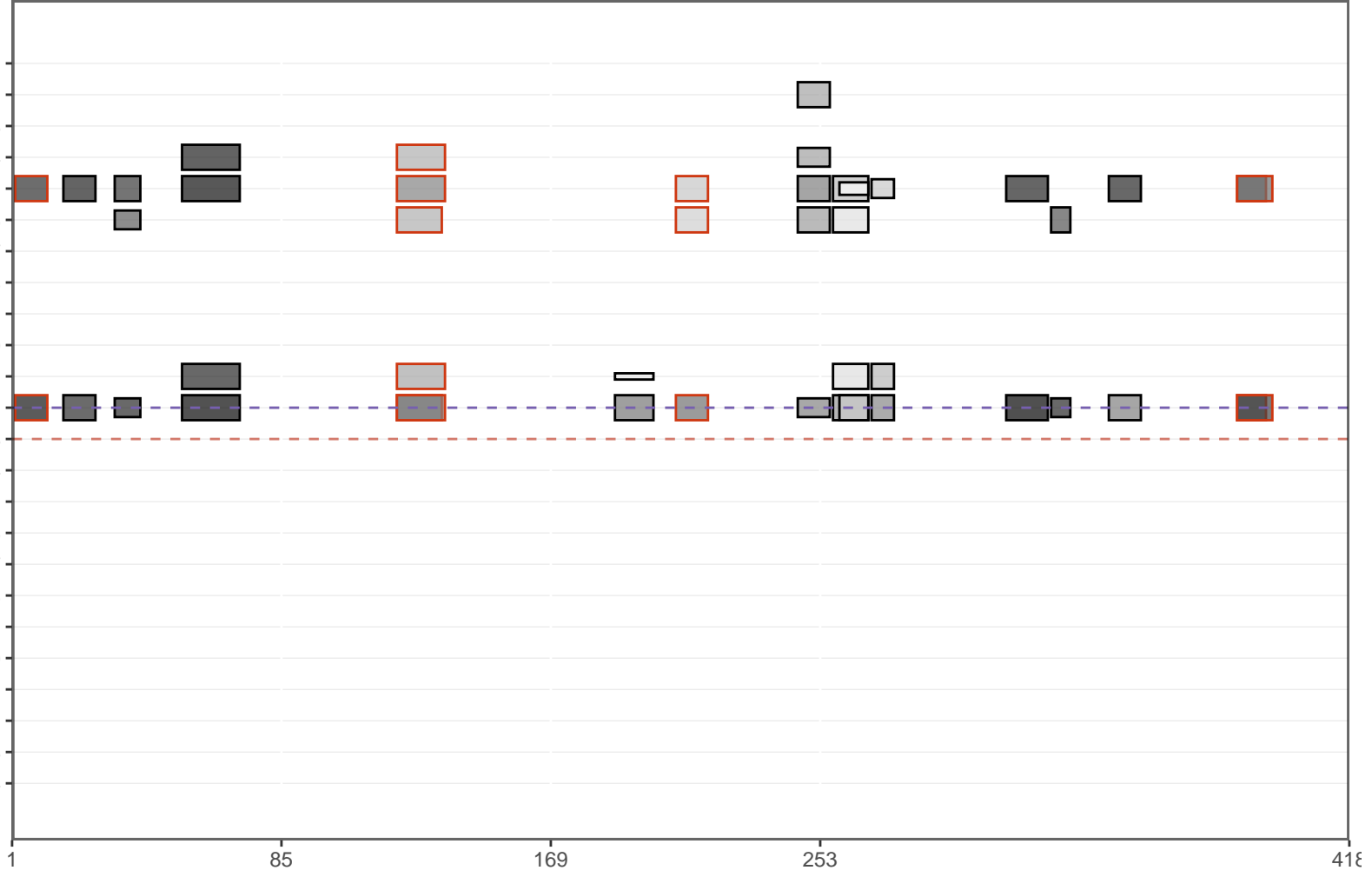
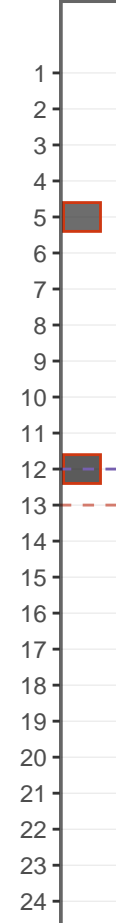
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- TM Domain
- Sequon
- PF00043 Glutathione S-transferase, C-terminal domain
- PF02798 Glutathione S-transferase, N-terminal domain
- PF00647 Elongation factor 1 gamma, conserved domain

Protein sequence:

FDKILGEVQDAESIAPDQSKKPKALAKEPKPKAKKEEFPKELKKEEPEEEEEAPKPKAKNPLDLPSPKMLDEWKRRLVSNTRKTFREVAIKGFVDMVDPQGYSLWFGDQKYGDENTVVFVTLNKVGGFLGRMDLARKYAFGKMLVIGSEAPKWKVGLDLVFRGKIKPKFVMDQCYDMELYEWKAVGNDDEAGKERVNGMIEDCEPFEGEALLDAKGFK

NbL17g01390.1 uncharacterized_LOC107819606 [MW = 19.86 kDa]

No. of times detected



log(intensity)



Values from



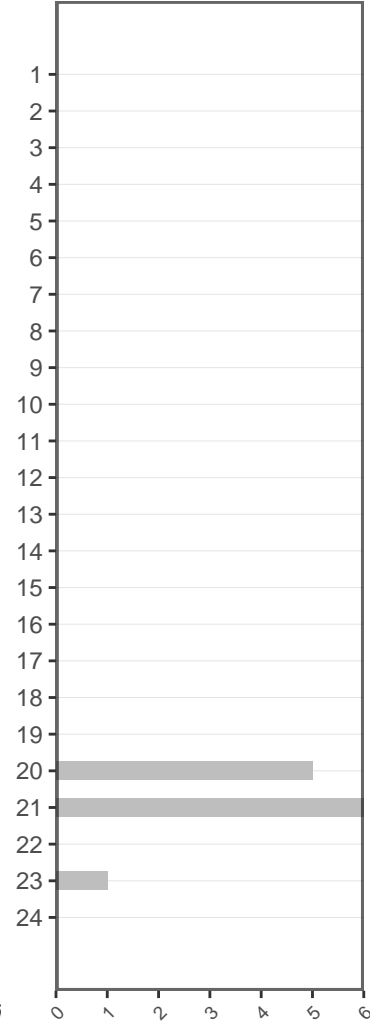
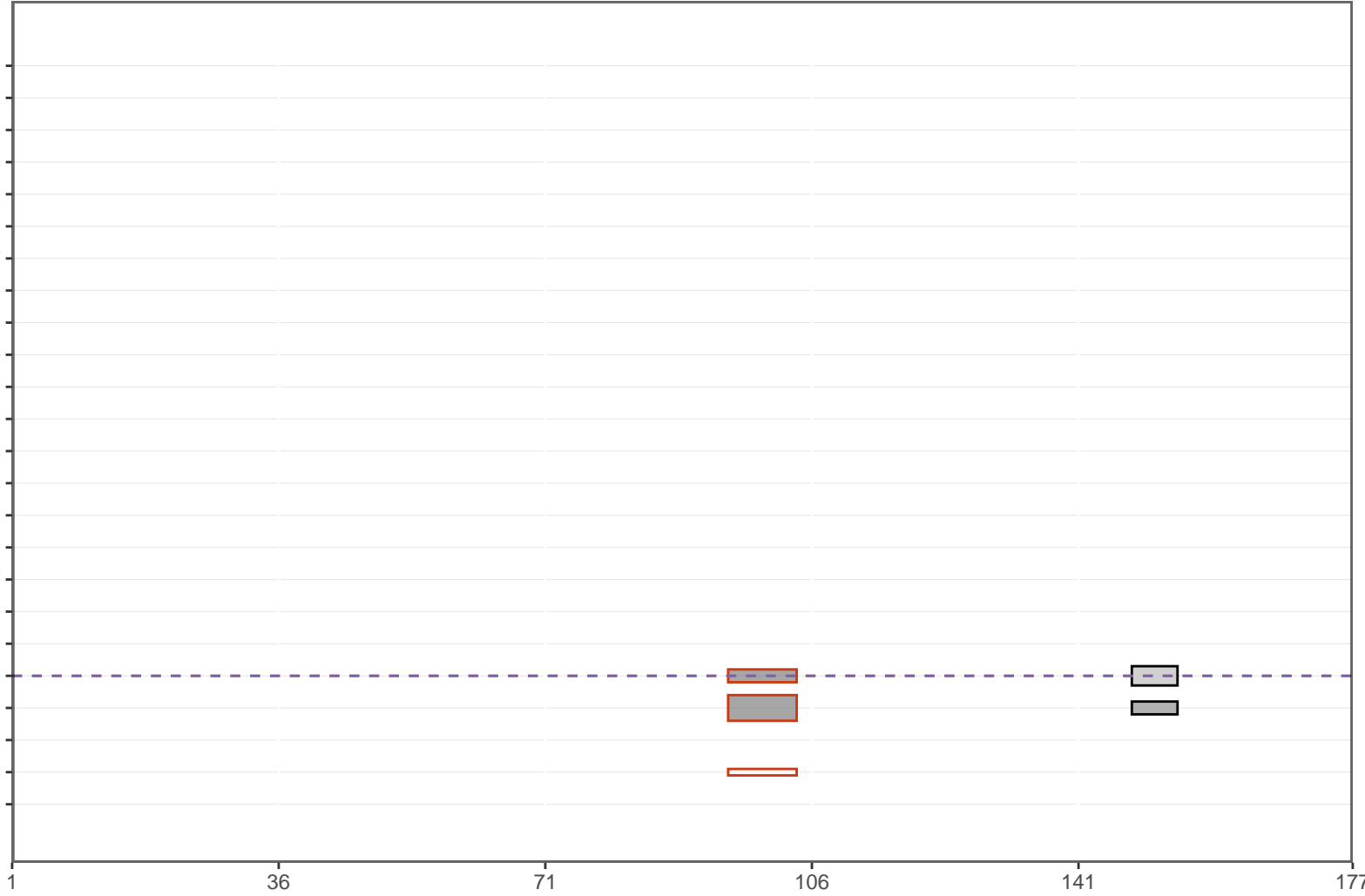
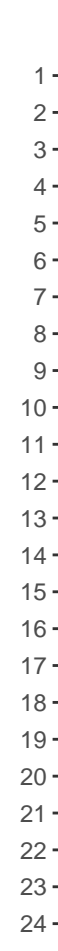
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



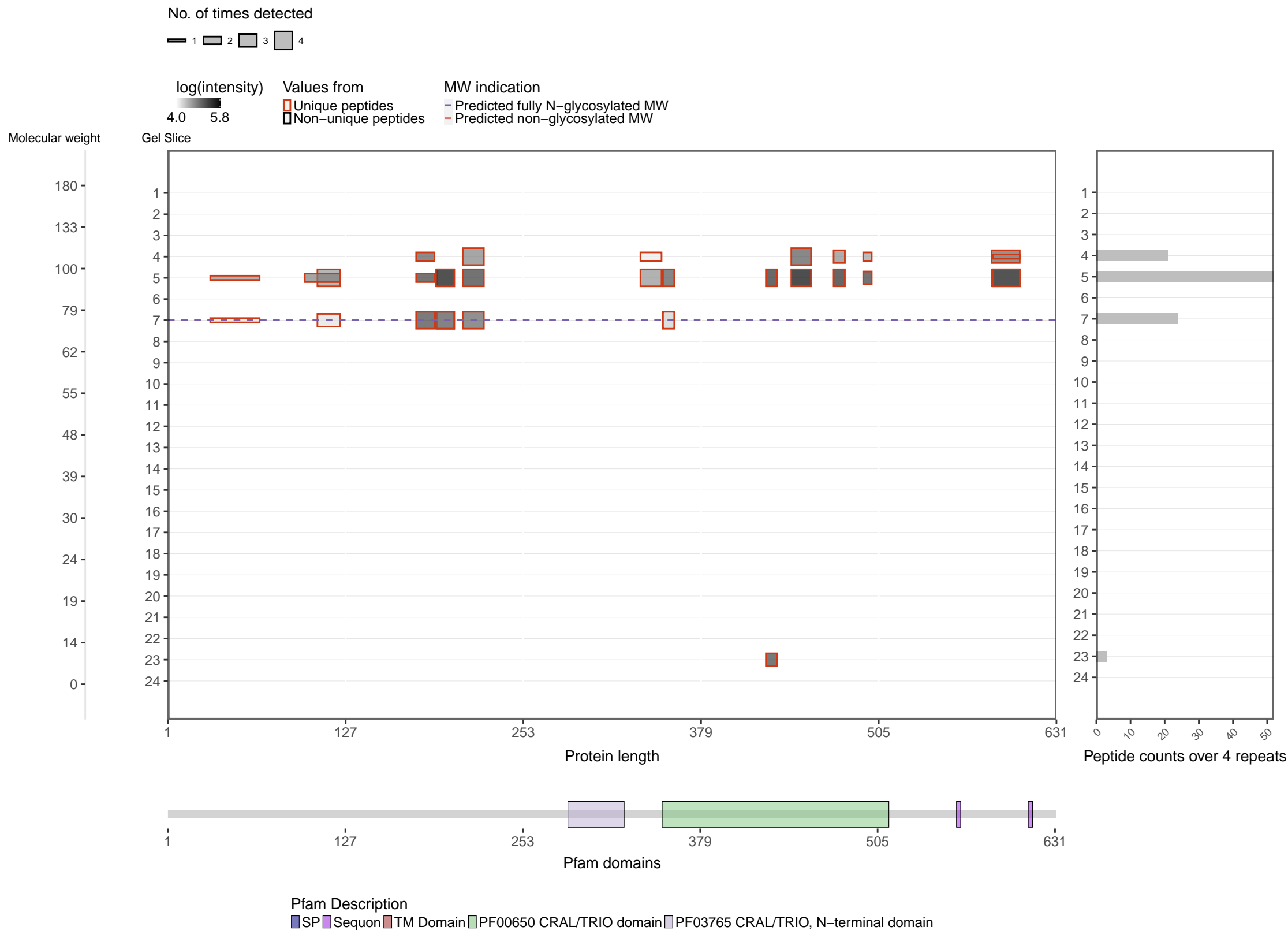
Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

KDAELIDKAREATOGGERMSSEGYGALRRKIGGTYNDFFPKSYVEVKGVEVVEEGWIDKTKGVCKKDRGEARQVQDFGRYAHWAGLENSKSGNFFTFNFR

NbL17g00940.1 patellin-3-like [MW = 69.35 kDa]



Protein sequence:

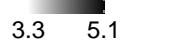
VILLFLRARDFKVWEAFAMLKVWVWRKFKIDELLVEDLGGLEGKVVYVHGVDKQHPVQYVAFGAFQDNLVQNTFADKEMKMKFLRWRIGRIFMEKSRNLDPSDQDCTFVQVHLKNSPGLYLFKKEIKRQATRAVQLQDNYPEFVAKQVFVYVWVYVYVYVMTNLFTRTKSKVYVAFGRRAETLKYVPEGVVQVGGLSREGEGETTAEAATEDTKPTSKVIEFFVTEKTSLVWEARVGGNVSYGAEFVPSAEGGYTIWVKSRRKVAADETVTNTYI

NbL17g00930.1 patellin-3 [MW = 59.8 kDa]

No. of times detected



log(intensity)



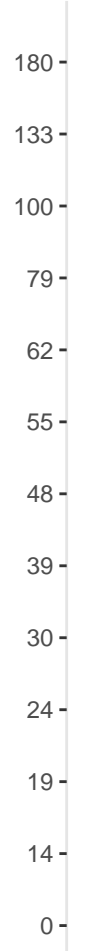
Values from



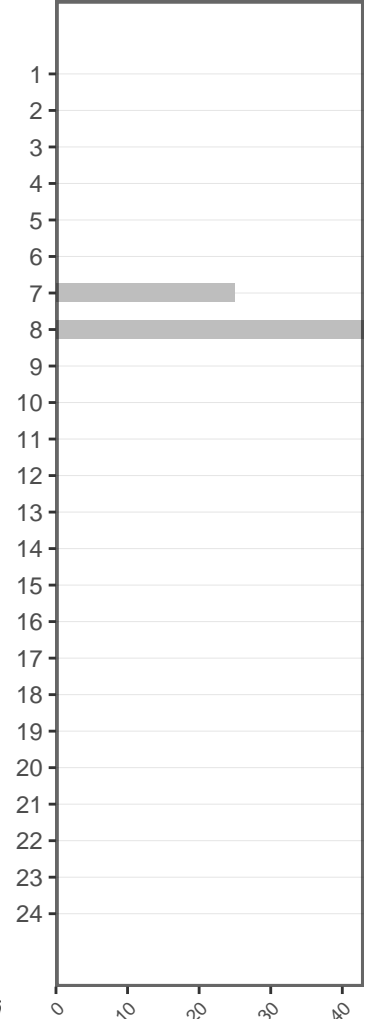
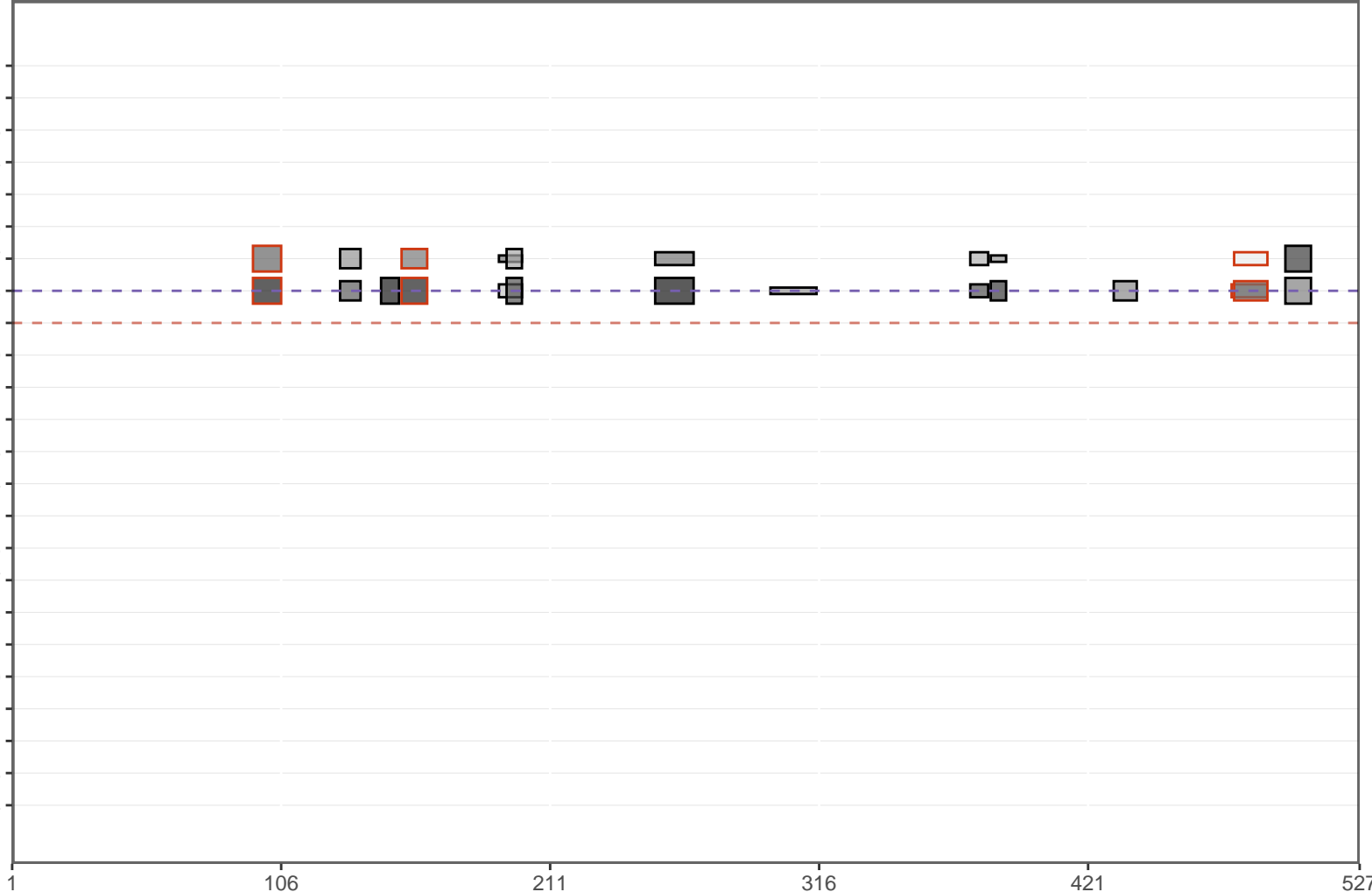
MW indication



Molecular weight

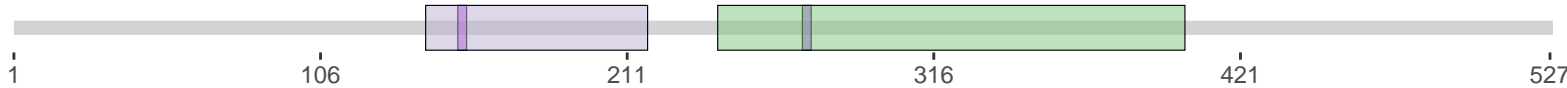


Gel Slice



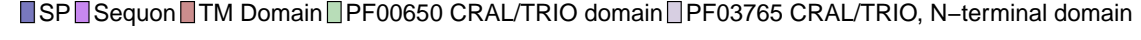
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

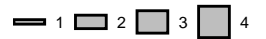


Protein sequence:

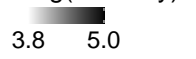
CEGHPVCYNYVYGEFGNKLKNTFGDEEKRNKFLRWIRIGFLERBIRKLDLDFNPGGNTIFQVSDLKNPSPGPKRELRLATRQAMHLGDNYPEFAKGVFINVWVYLAFTYTMISPFMTQRTKSKFVYAGPSKTAETLYKVVSPGQLPVGYGLSDVDYGECPNPTFTVSDPVEIVKPKTKGTVETVNEKGIKVELRVLGWDVLYSAEYVNPNTDGGVTVNKGPKRKMPTTDEPLVSSFRIVELGKILLETDFNPTSKKKLLVRYKDKKPYSTEHL*

NbL17g00900.1 carboxymethylenebutenolidase_homolog [MW = 33.5 kDa]

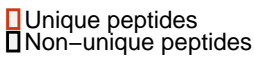
No. of times detected



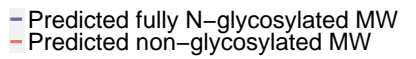
log(intensity)



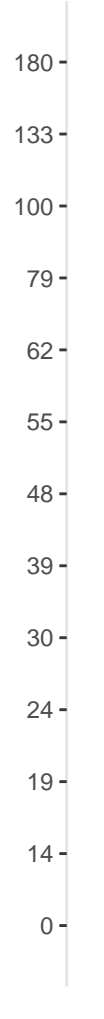
Values from



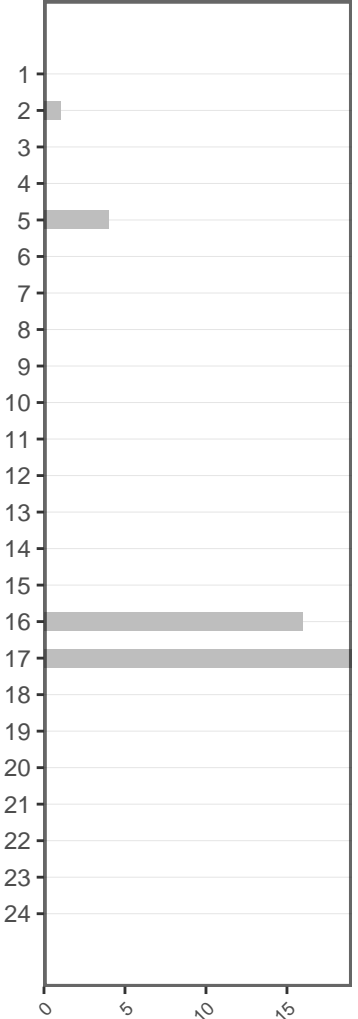
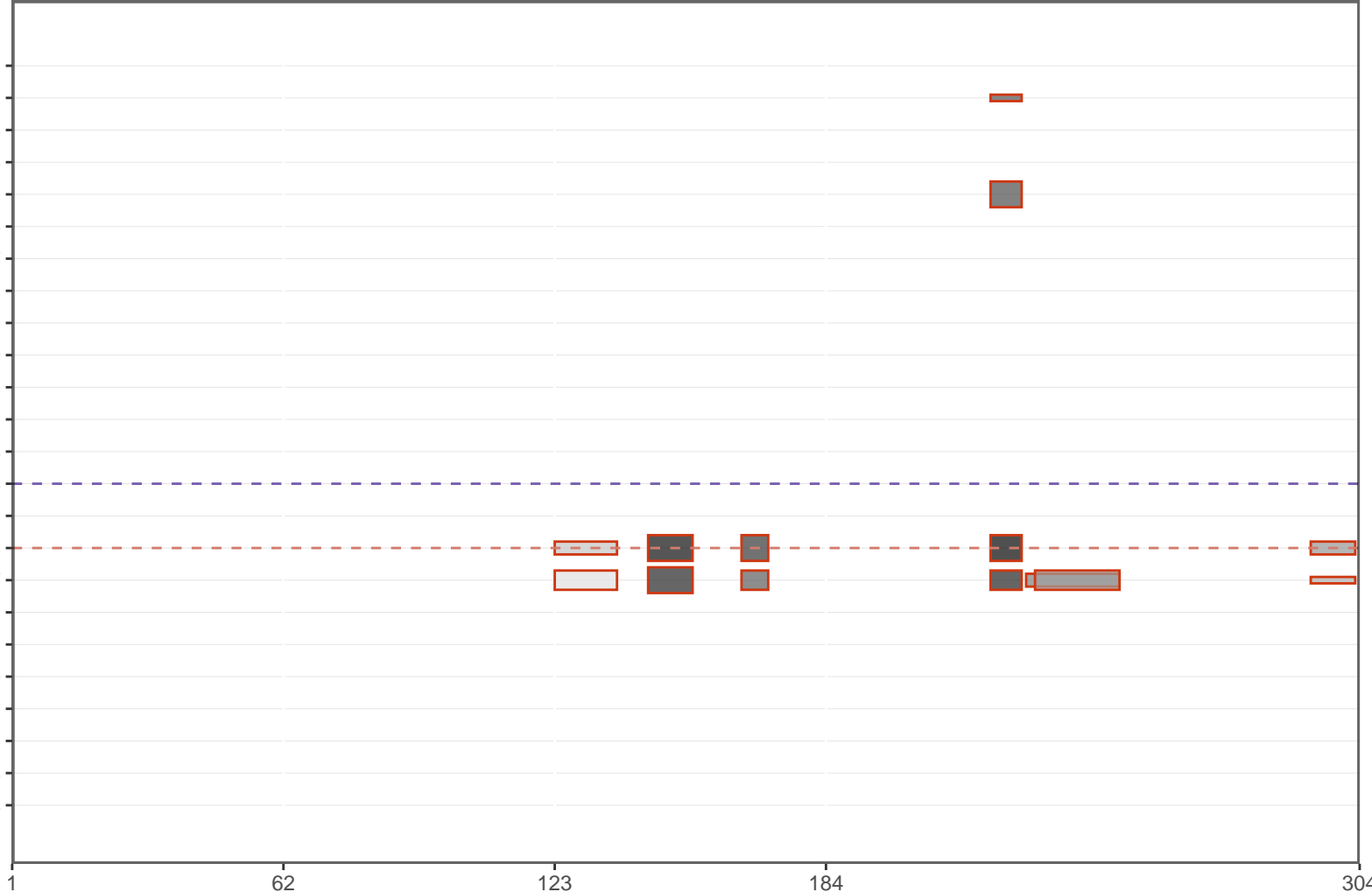
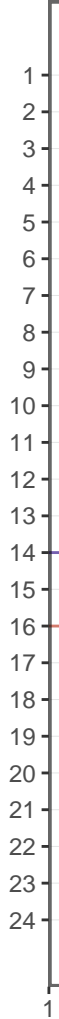
MW indication



Molecular weight

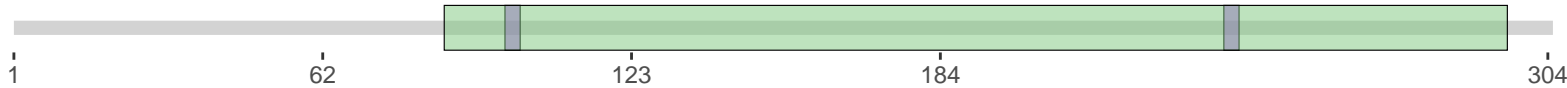


Gel Slice



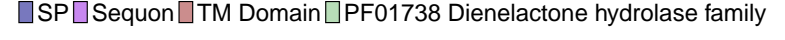
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

WGKDKPQASFEQWRGSLKGRVVRDIFSTKWMVDEFVAAGISKLGIVGDFGGLLHLLADOGSGFVGVISFYGTIRIVSVASKIKVPLLLIAGDNDLCPVWVNLKEVKNANGCKVVFEGRHHGFAHRPGLDDKDAEEAFLMMRNWLDHGLVSEY

NbL17g00510.1 uncharacterized_LOC104227417 [MW - SP = 27.62 kDa]

No. of times detected



log(intensity)



Values from

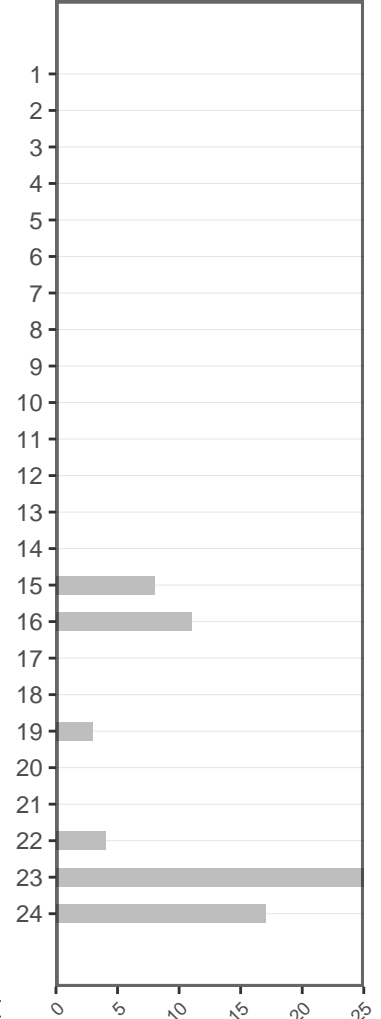
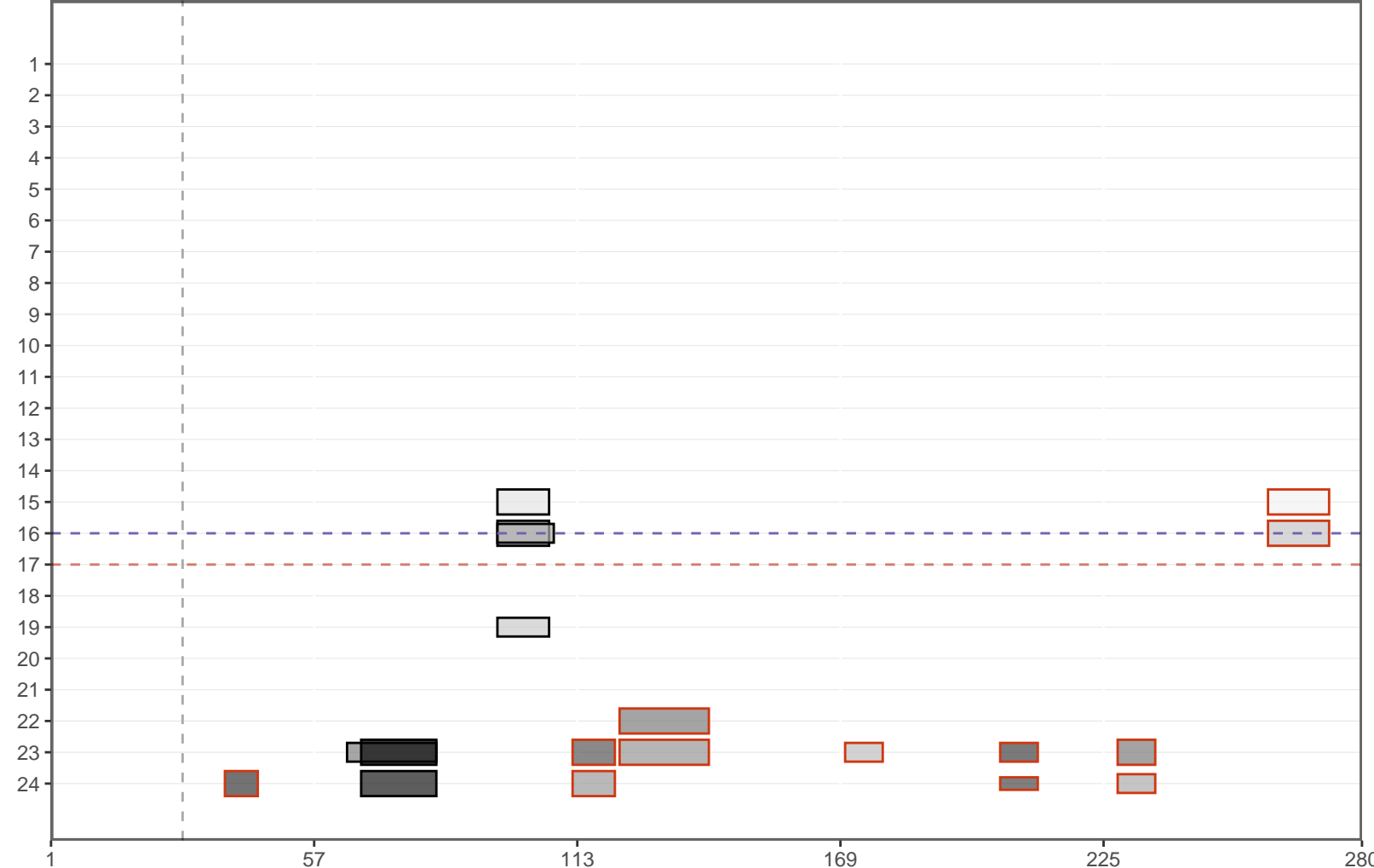
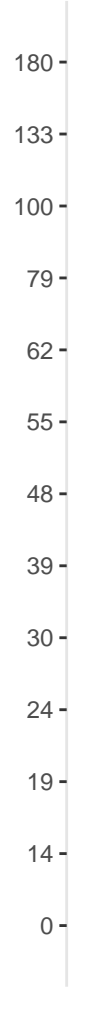


MW indication



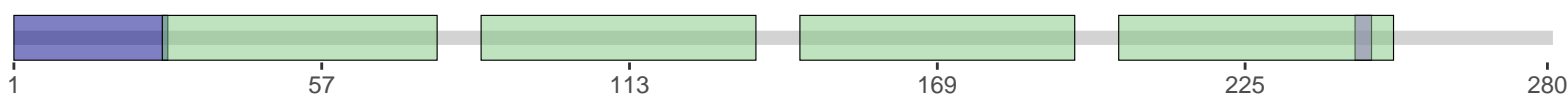
Molecular weight

Gel Slice



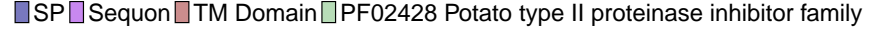
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LDGTFVCEGESDFRNPKACPRINDPRIDVCPREBEKKNDRICTNGGSGKGGKGYFSDGDTFVCEGESDPRNPKGGTFECDFRIVAGIKPLBEEKNNRLGTNCGAGKGGKGNVYFSSNGTFCDEGESEYGSKKVYEVYGEVEDDLGKSKVAVP

NbL17g00400.1 adenylate_kinase_chloroplastic [MW = 32.82 kDa]

No. of times detected



log(intensity)



Values from



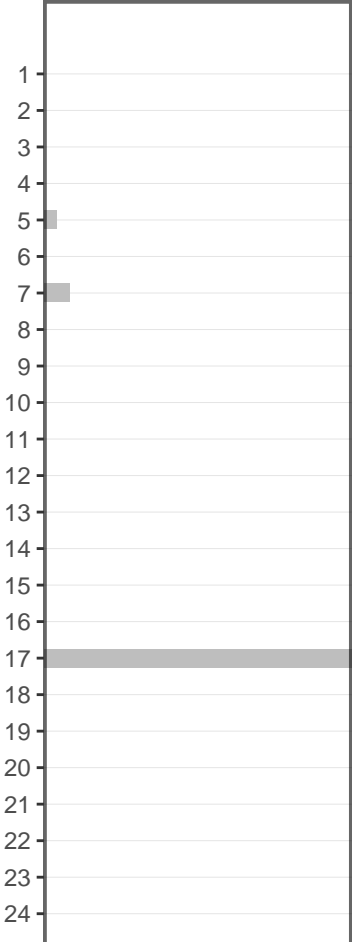
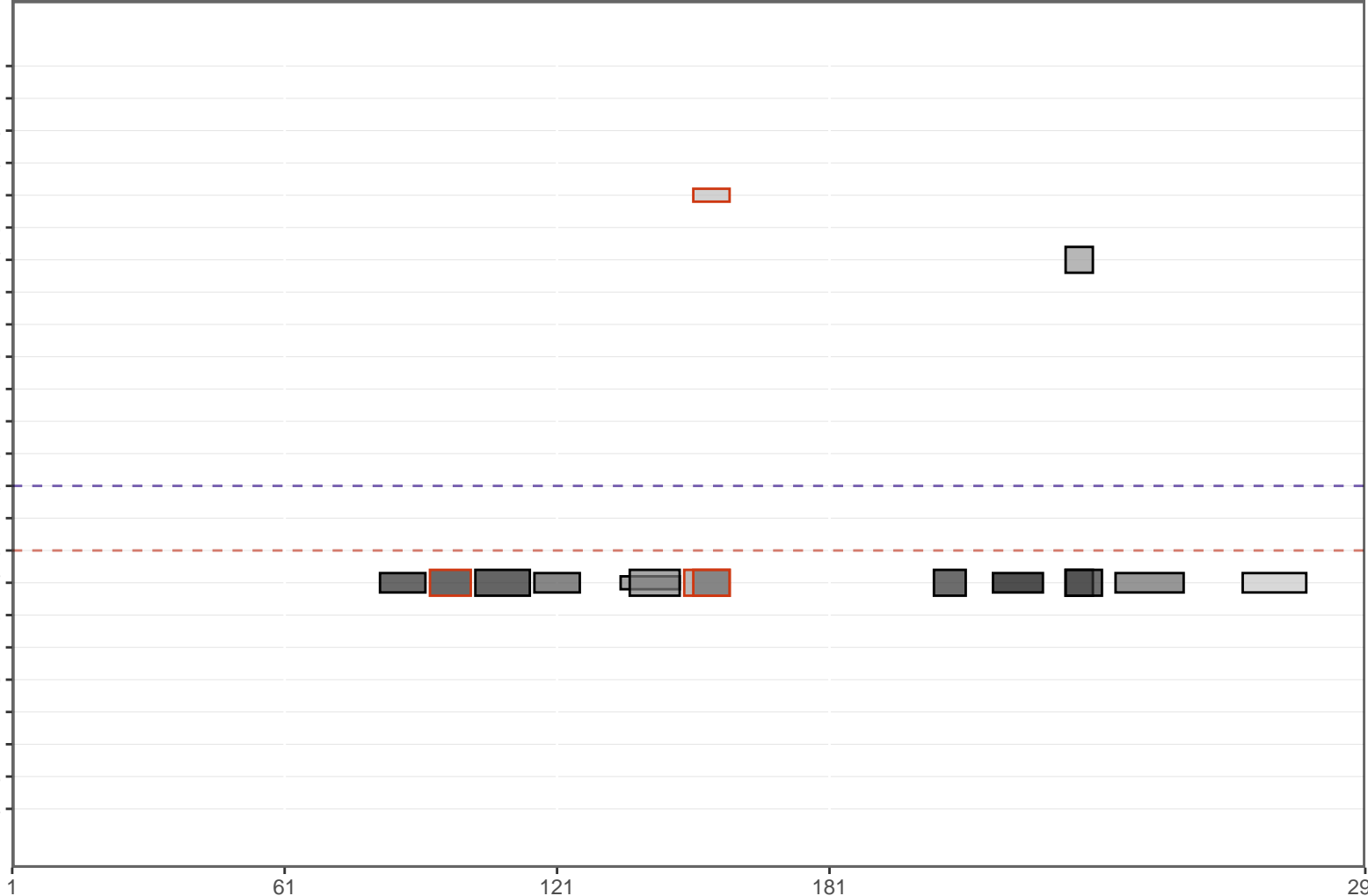
MW indication



Molecular weight

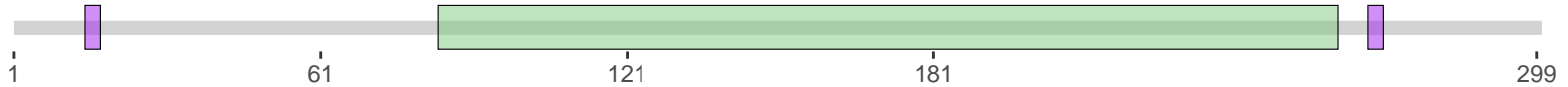


Gel Slice



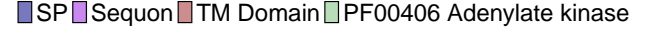
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

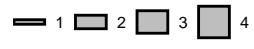


Protein sequence:

KLVPEIVTMYKERLNGPDDGKGLWLDGYPFRS66QAKLKEFGQFDLFILEVPEELVERVYGRRLDPVTGKYLKYSPPETEIAARLTFORFDDTEERKLRLLHTHHQNVEALSLYKDTIVKXNGSAEKDQVFAIGDDALTQLREGKGGKLGTVAA*

NbL17g00380.1 protein_TIC_40_chloroplastic [MW = 49.49 kDa]

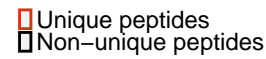
No. of times detected



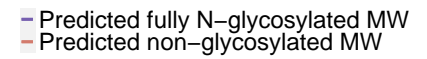
log(intensity)



Values from



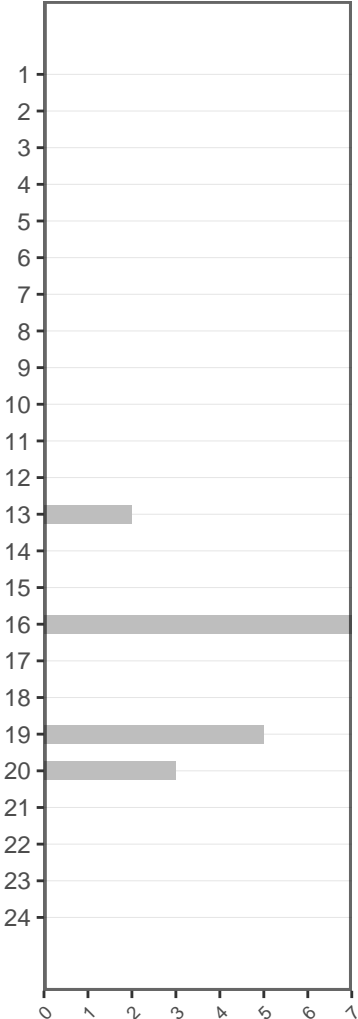
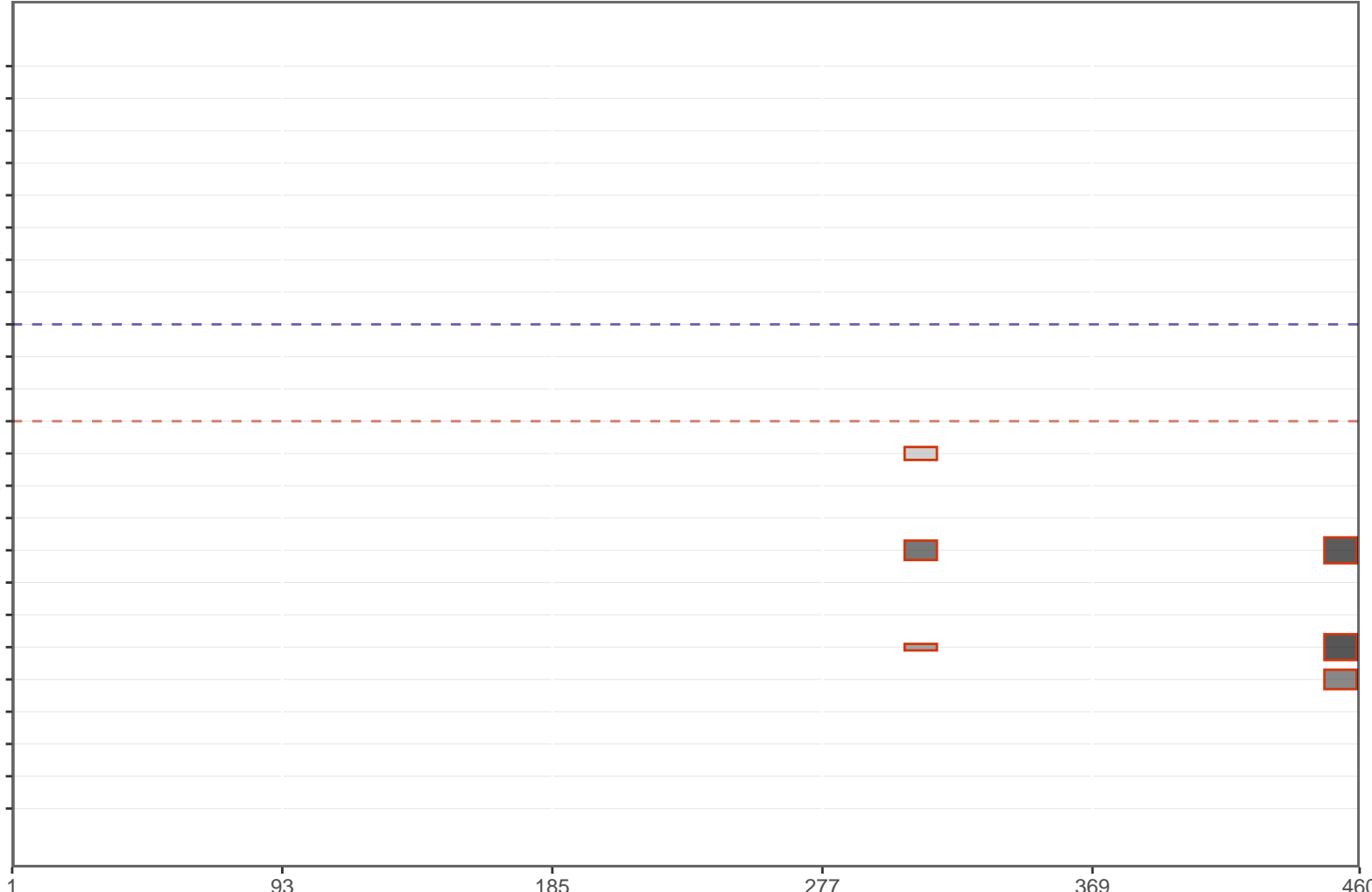
MW indication



Molecular weight



Gel Slice



Protein length

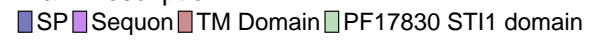
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

IAERVPKKNAFYDIDSPDETGGKAFEDGKESTETASVTVDQVYQNGAANKSGFGASTSDGTGFGAANTSNTTGFSGANTSGSTSTSEKSNPLMSVEALEKMMEDPTVQKMYVYPLPEEMRNPTTFKWLGNPQYRGGILGDLNLMNMGSNPEWDRNRMVDSLKNFDLSSPEIKGDFDQGLTPEEVISKIMANFDVAMAFQNRVQAAMDDSGNPLSAIKYQNDKEVMDVFNKISELFPQVSGSP

NbL17g00350.1 alkaline/neutral_invertase_CINV2 [MW = 62.69 kDa]

No. of times detected



log(intensity)



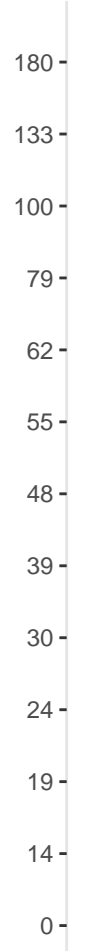
Values from



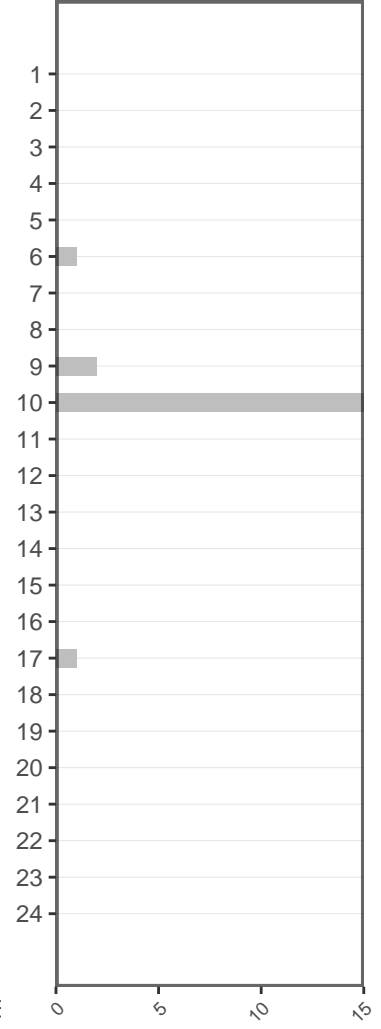
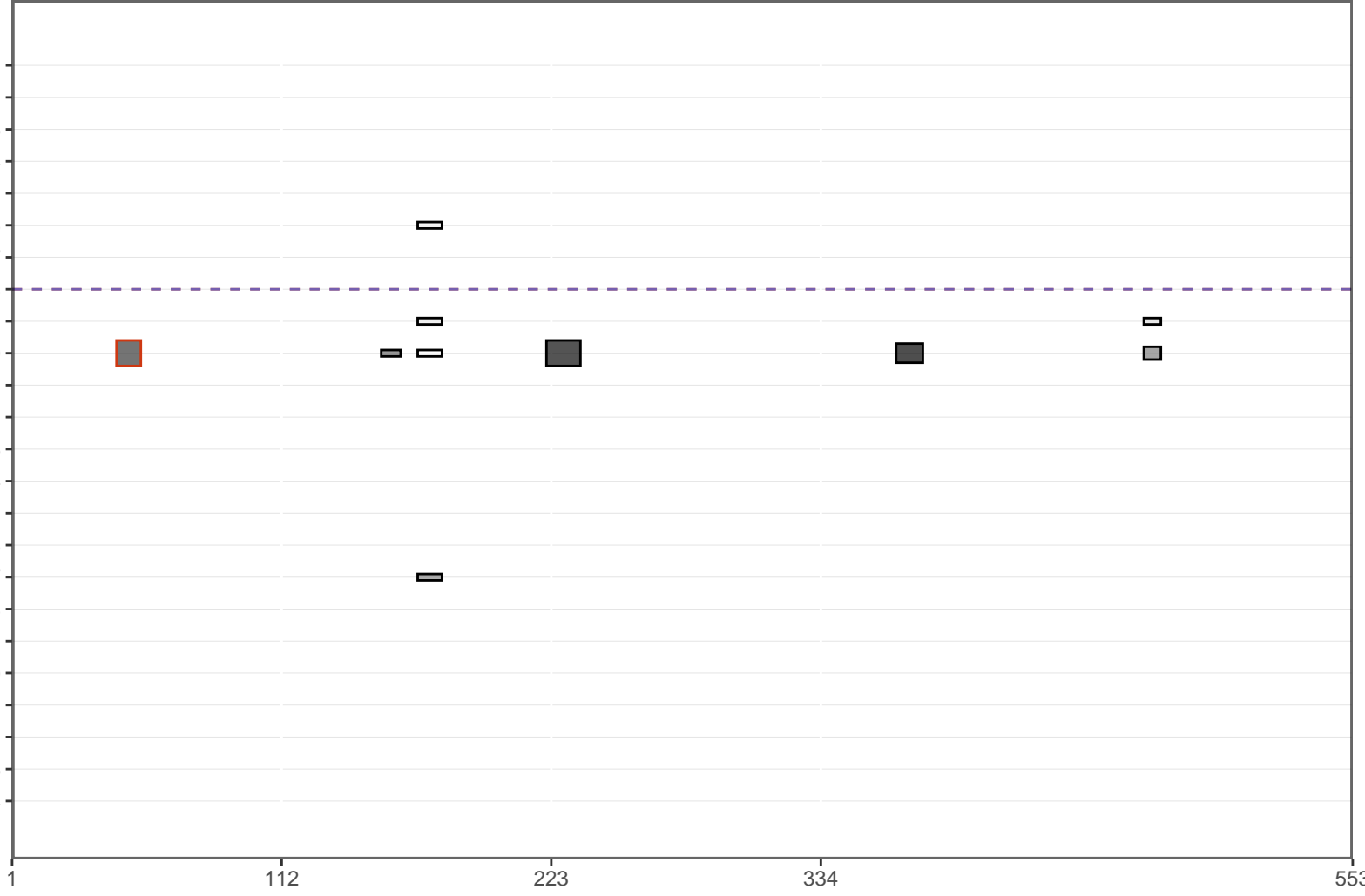
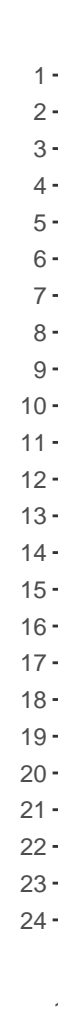
MW indication



Molecular weight

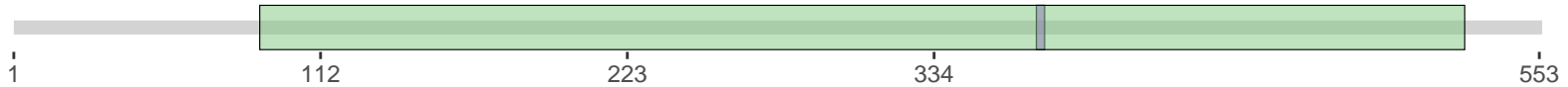


Gel Slice



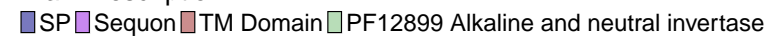
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SMIDRRMGVYGYPIEQALFFMRLSALMMKHDTGSESEFIERIVKRLHLSVHMRYFVLDFOGLNDYRKYKTEEYSHATANKFNVPDGIPEWFFEMPTRGQYFGVGNVSPARMDFRWFALGNCAISSLATPEQASAIMDLGARVDELVAEMPLKISYPALENHEWRLLTGCDDPKNTRWYHNGSGWVPLVLLVLTAACTGRPQIARRAIDLAEERLKDHWPEYYDQKVGIRVIGKQARKYGTWISAGVLYWAKMLLEDPHLLGMIALEEDKQMKPVIKRSASWTC

NbL17g00240.1 UPF0160_protein [MW = 42.3 kDa]

No. of times detected



log(intensity)



Values from



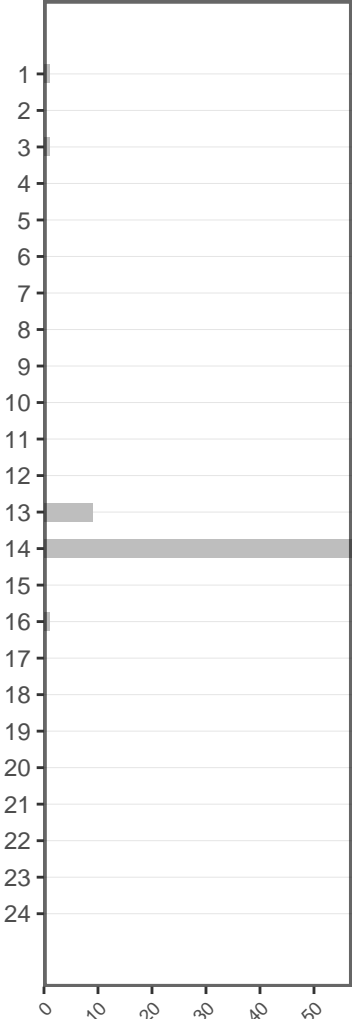
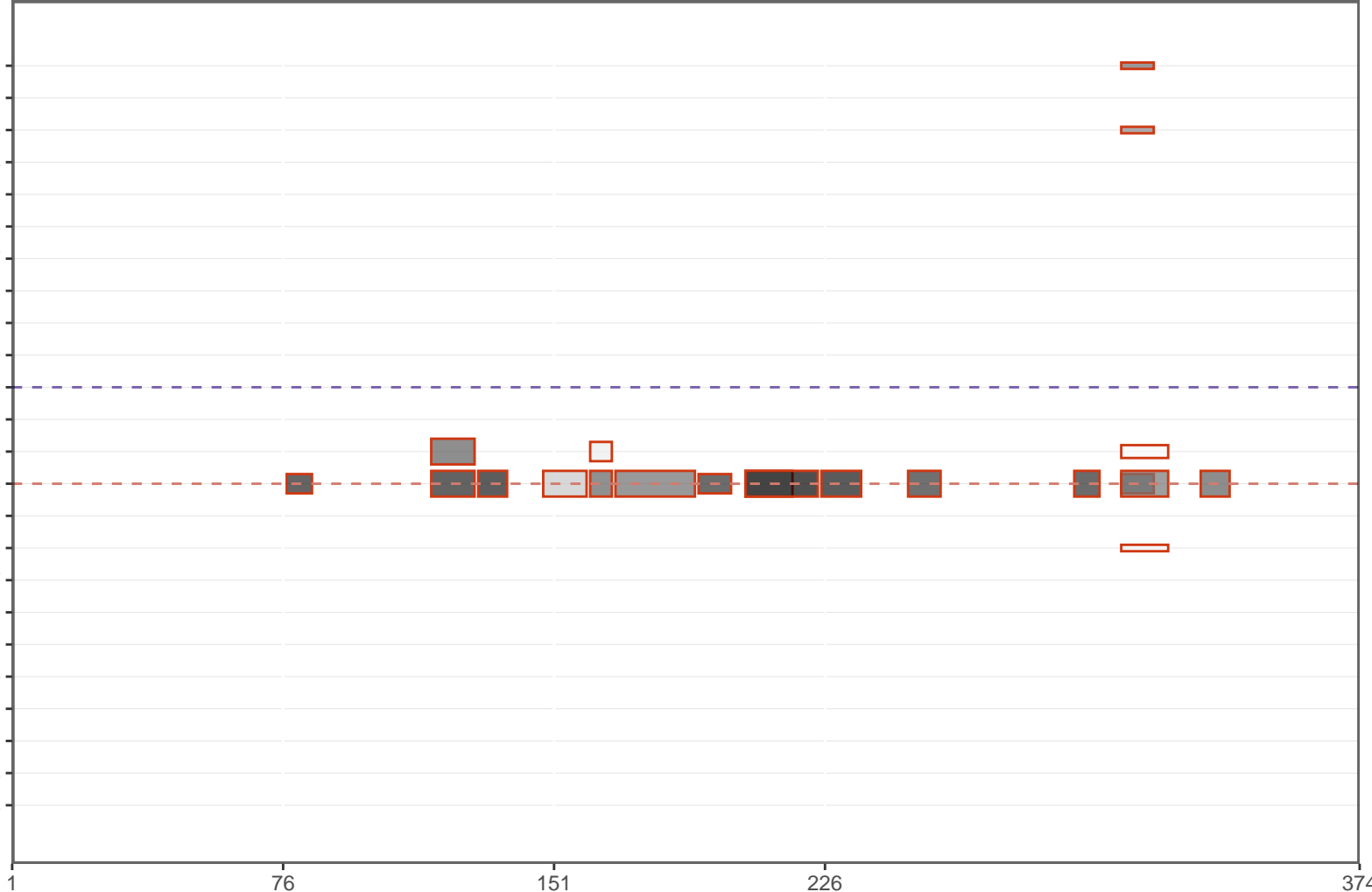
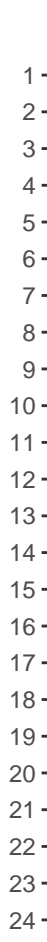
MW indication



Molecular weight



Gel Slice



Protein length

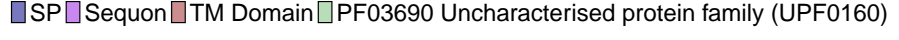


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VLDNGINQYDTDQPPRYVNTHLSSRVGRLLNDWEPDQSSSEKENEAFERAMNLAGSEFLDRVRFHVRBWLPARSIMMECLAARKKIDPQSGEIVFTFFQFPWKLHLELEEEKKIDPPKIVYVQDDRKDKGWRVQAVGVAPDRFESRWLPAQWIRGLRDELSKETGPGCVFHHMSGFIGGNGSYEGALAMRAALKV

NbL17g00170.1 hydroxypyruvate_reductase-like [MW = 43.93 kDa]

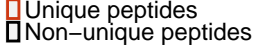
No. of times detected



log(intensity)



Values from



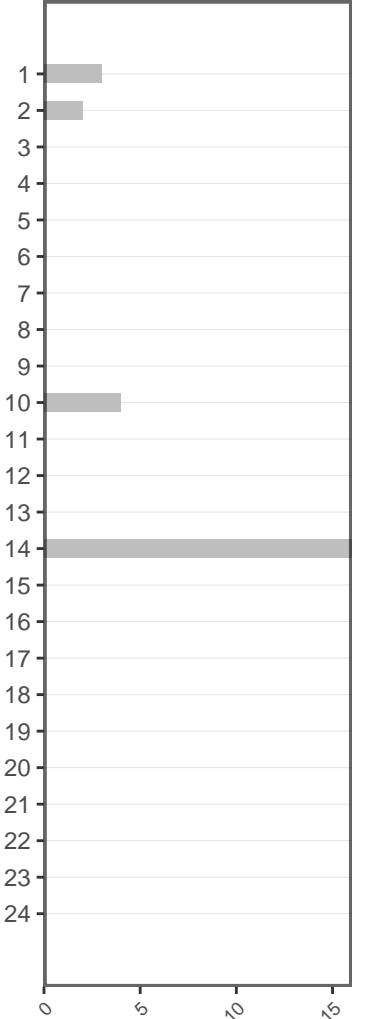
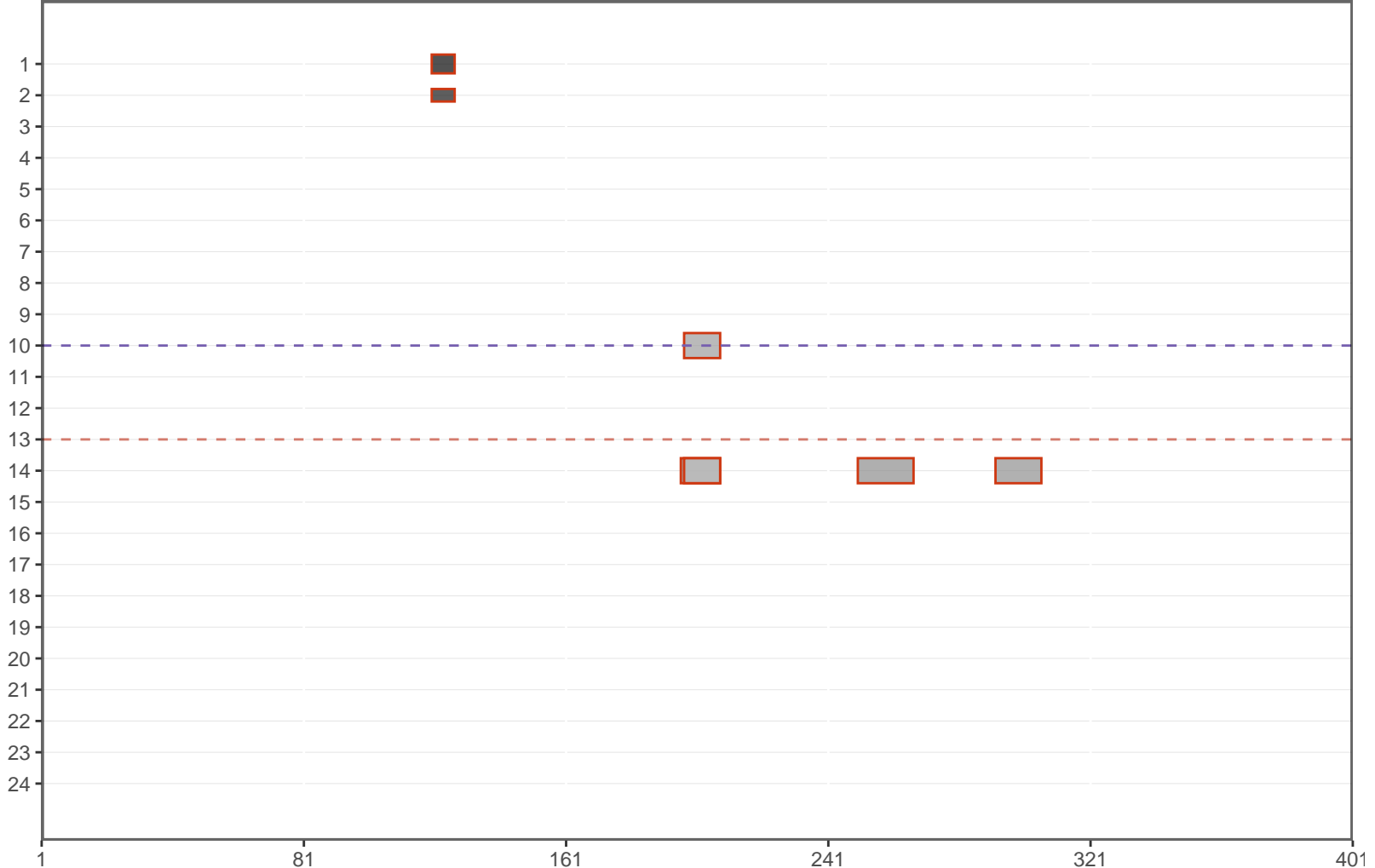
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF00389 D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain
- PF02826 D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain

Protein sequence:

3HQLKISVEORKLGEPISDNLGKTVILGFGNGIHLAKRLRPFDFVKLATKRISWRGADGDSKSEAPYVENSVDLVDKRNHDDILKFKASKADVICGLAMNKETAGIVNDFISAMKKGALINARGLLDYDAVPHLKSGLHGGIGIDAWAEPDPDDALIKFPEVITPHVAGVTEKSYRYMAKVVGDVALQLHAGEPFTGIEIWN

NbL17g00160.1 stromal_70_kDa_heat_shock-related_protein_chloroplastic-like [MW = 74.09 kDa]

No. of times detected



log(intensity)



Values from



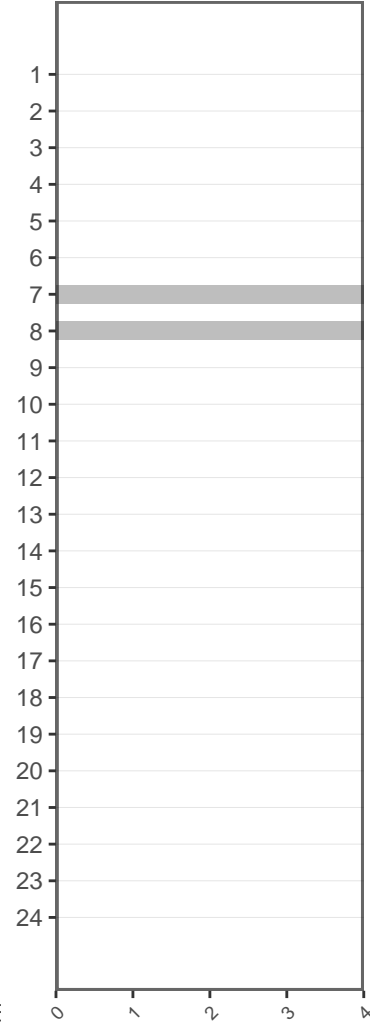
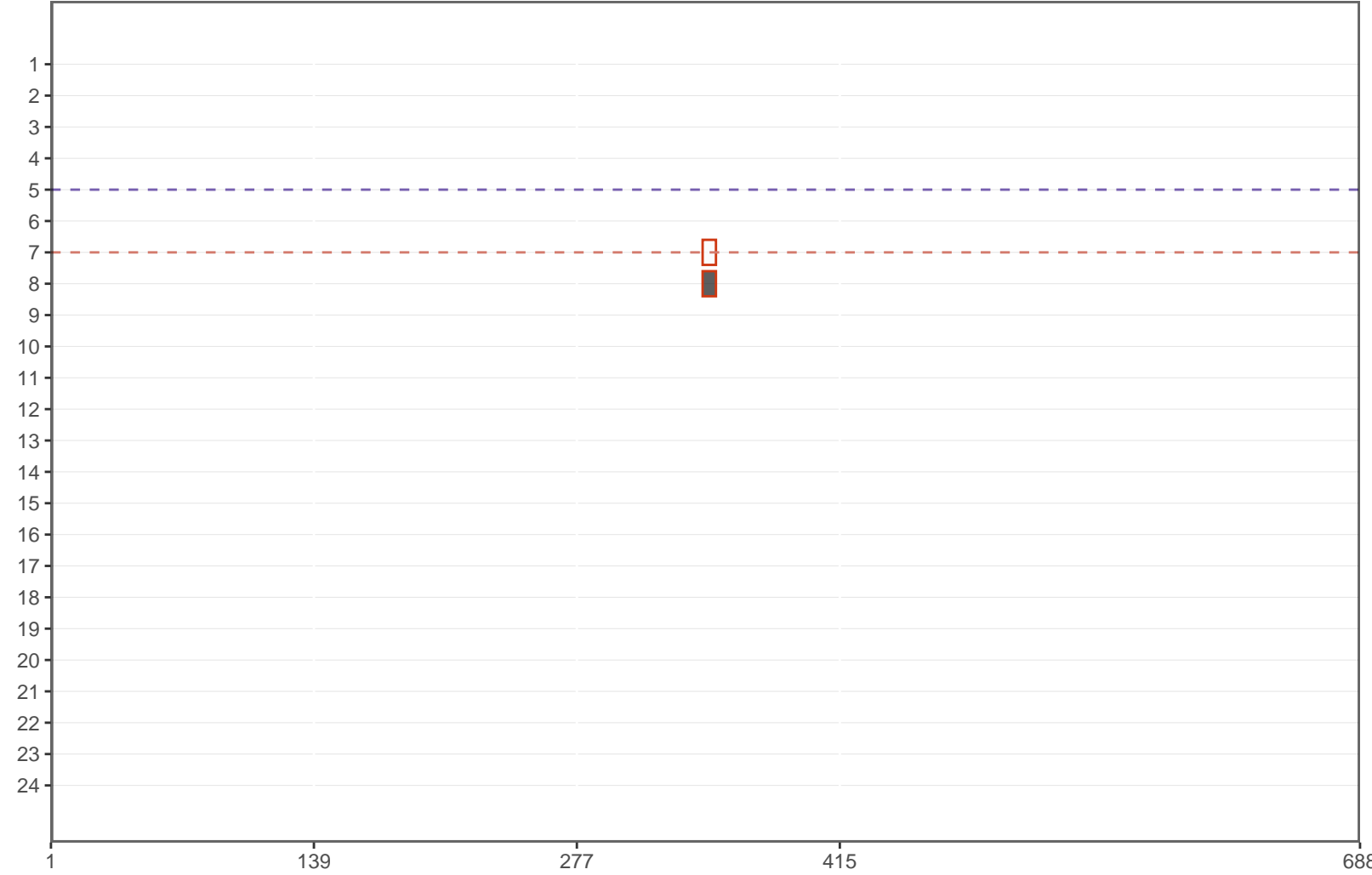
MW indication



Molecular weight



Gel Slice

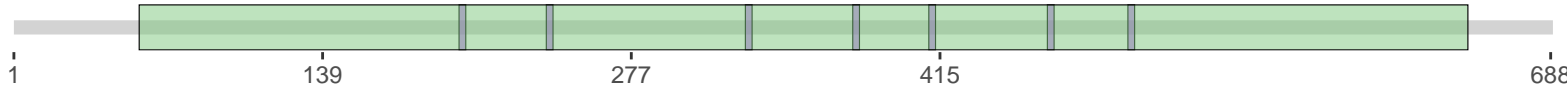


Protein length

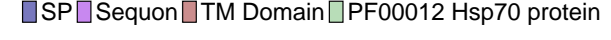


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LPFITADGPYHIEFTLRKFEELGTDLLDRKTPVDTALKKANLSPKDDDEVVAGSGSTRIPWQNLVRKMTGKPEPNVSNPDEVVALGASVQAGVLAGVSDVLLDVTPLSLGLETLLGGVMTKIPRNTPLPTSKSEVFSTADGGGTSVEINLQGEREFKKNKELGFRRLDGIPAPRGGVQIEVWFDDIANGLSVATDNGTGTGKQDITFGASTLKPDEVDIMVDEAKENFAKEDKEKRDGSDTKNGAESVYQTEKQLKELGDKVPAQVAKVSKLRLEKDAISGGSI

NbL16g27900.1 uncharacterized_LOC109206410 [MW - SP = 7.53 kDa]

No. of times detected



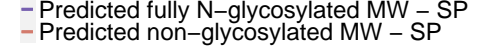
log(intensity)



Values from



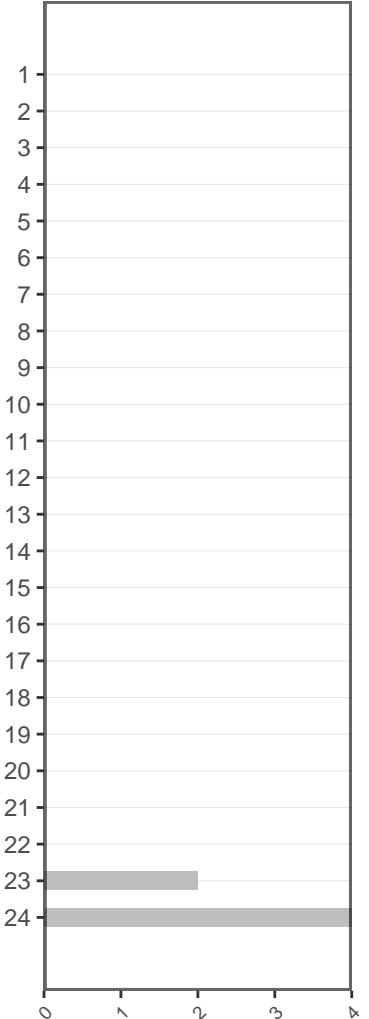
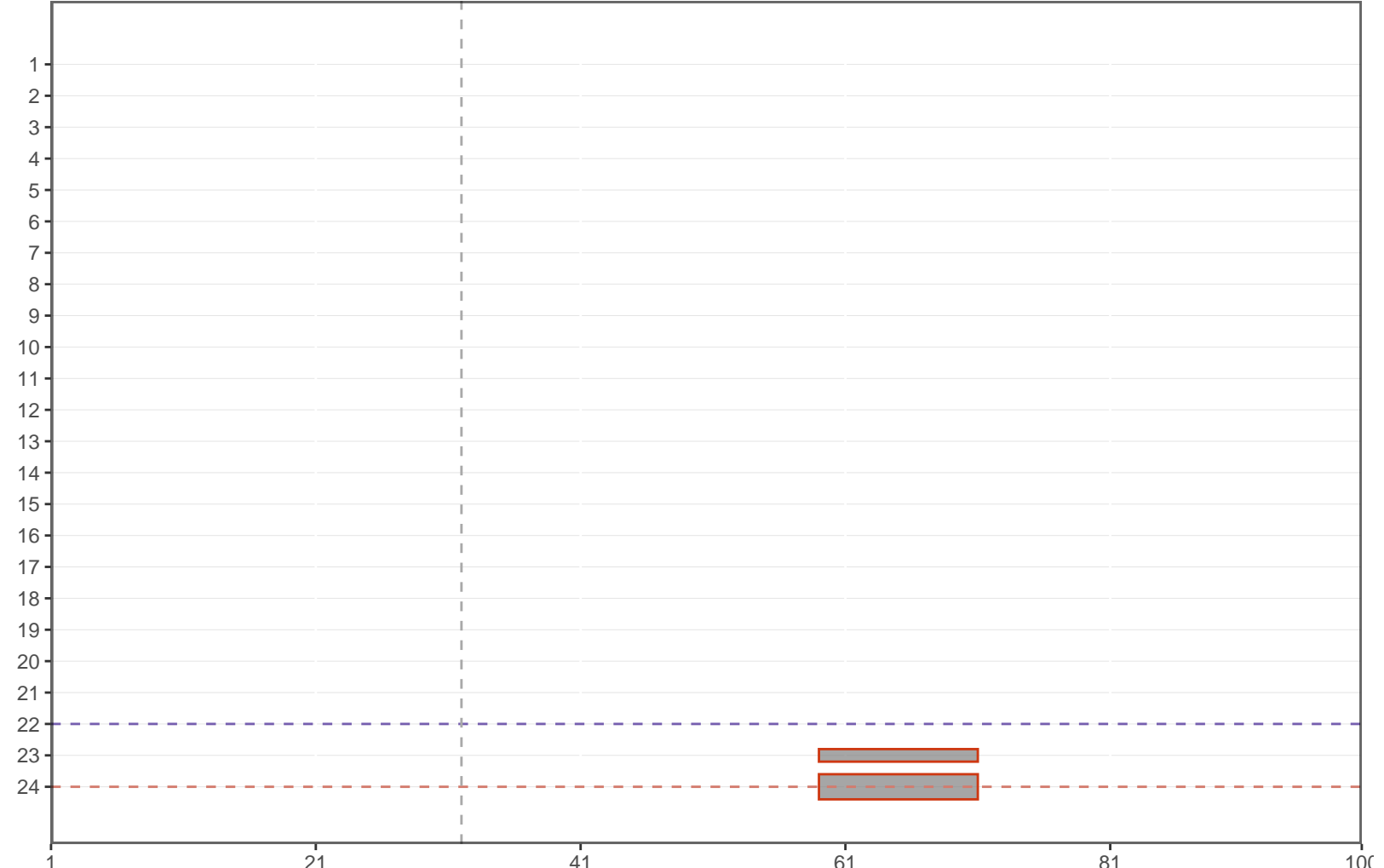
MW indication



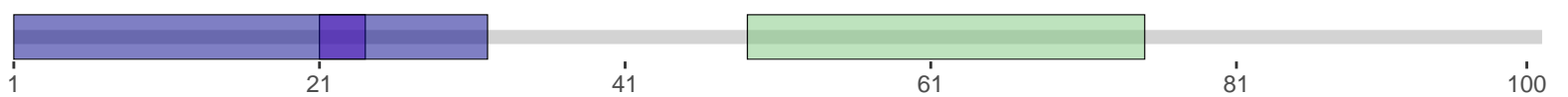
Molecular weight



Gel Slice

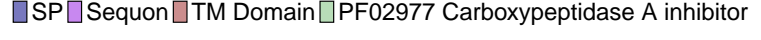


Protein length



Pfam domains

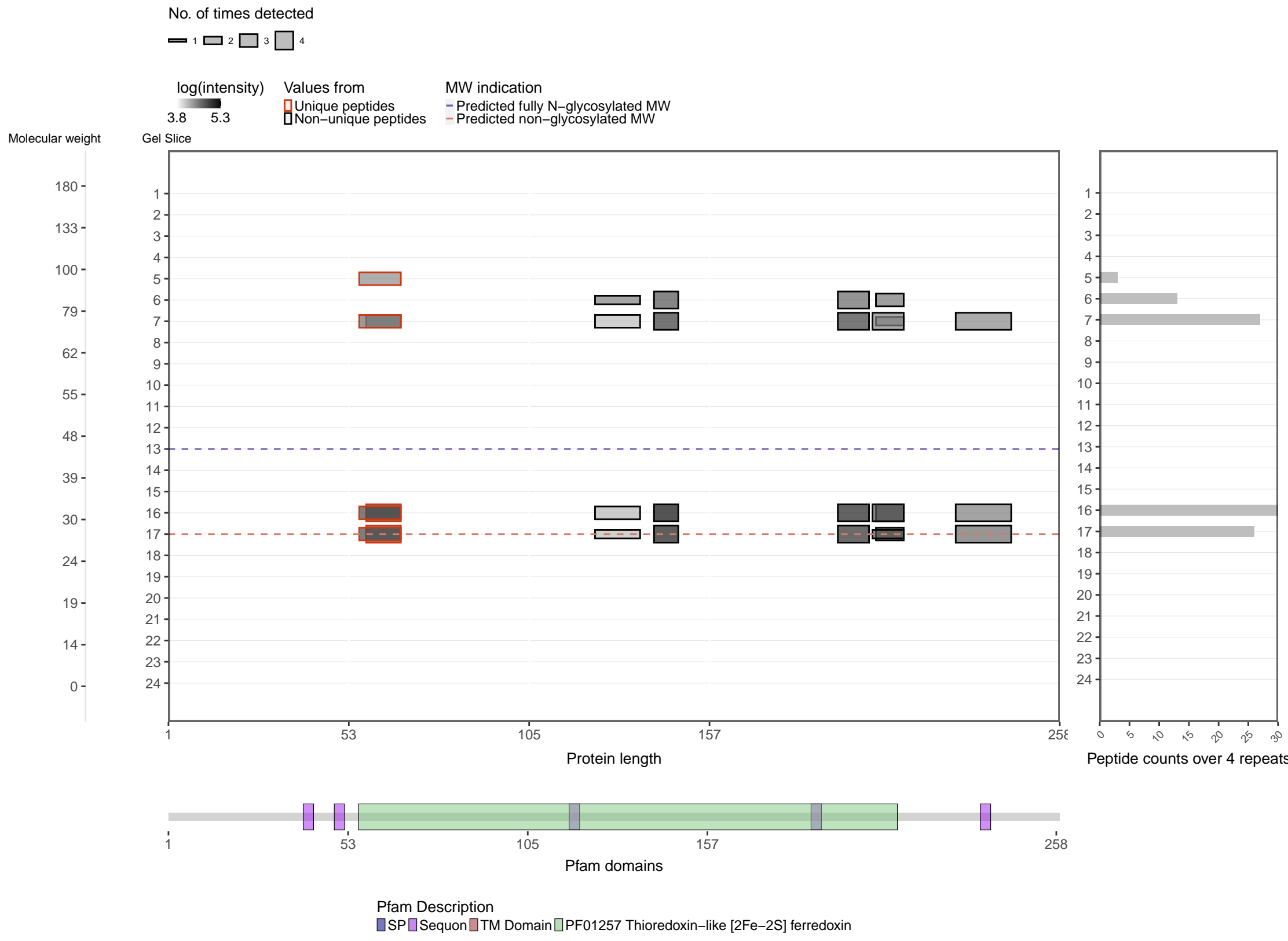
Pfam Description



Protein sequence:

DEIAMVKTLLPPLTDFITGKASSSDGSDGWRGTFYGIQNEIVIVSPVPIVRAAGYGES*

NbL16g27730.1 NADH_dehydrogenase_[ubiquinone]_flavoprotein_2_mitochondrial-like [MW = 28.59 kDa]



Protein sequence:

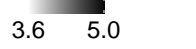
RTKVGKYLIVCGTTPGMIRGSRGIEAHLKHLGVKRNVEYTKDGLFSVGEEMCGGVDVADYNSGSEGKYNKYEDLTPKRAVEIYAFKGEKPGRTGTQNPGRINGPREGNFTLLGEPKAPPCRLDAGSAE

NbL16g27710.1 protein_OS2_chloroplastic-like [MW = 35.24 kDa]

No. of times detected



log(intensity)



Values from



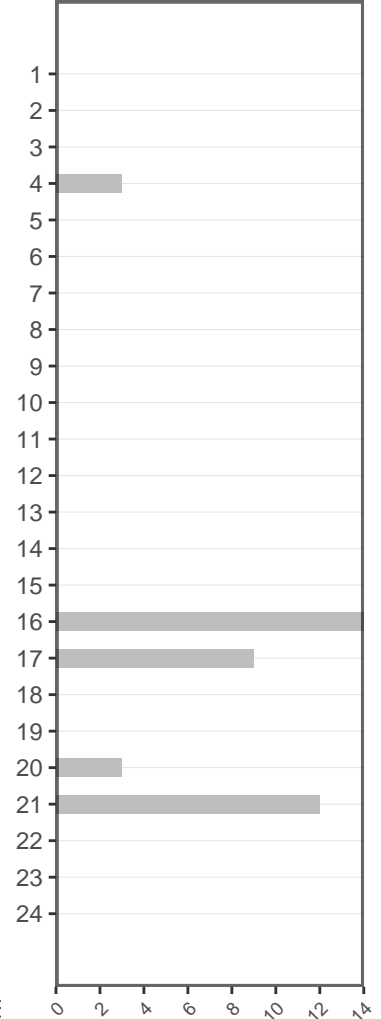
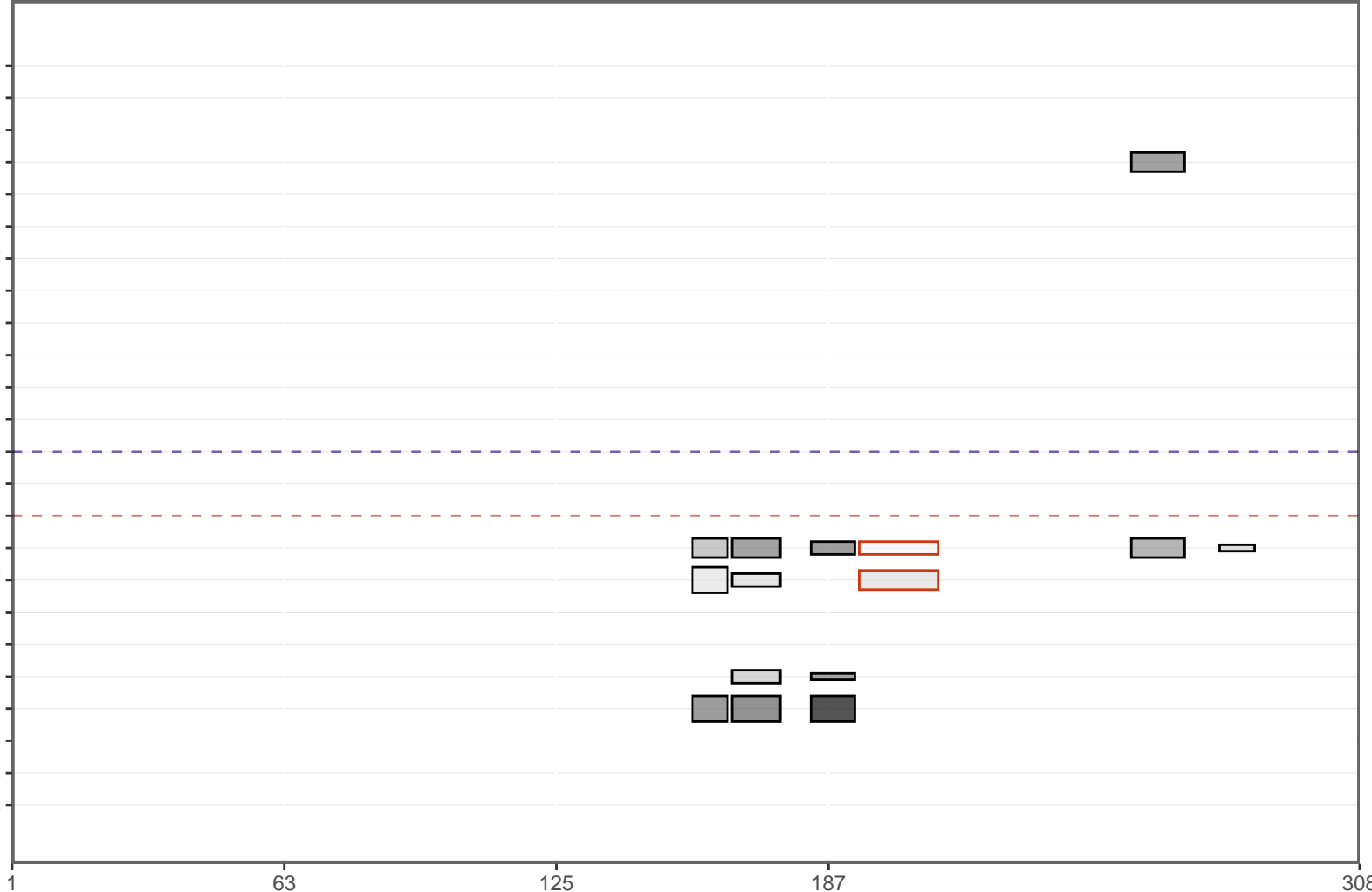
MW indication



Molecular weight



Gel Slice



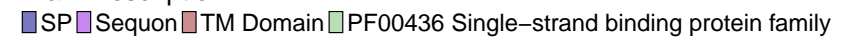
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILASVANDQYVEKHGQYVSGRLSDTVEGDGKQQTYYKVVVQGLNFVEKTSPEVAVNGSDNSMTFSRKNNYPMNTTGTTEELWGAFFANFLWWDNRKNNKRSFNPYDFKIKDTGEALWVEGRYNTVWVKSGLAVLDSKMESHFDGNGSANADFMEMENFGF

NbL16g27660.1 glutathione_reductase_chloroplastic [MW = 60.4 kDa]

No. of times detected



log(intensity)



Values from



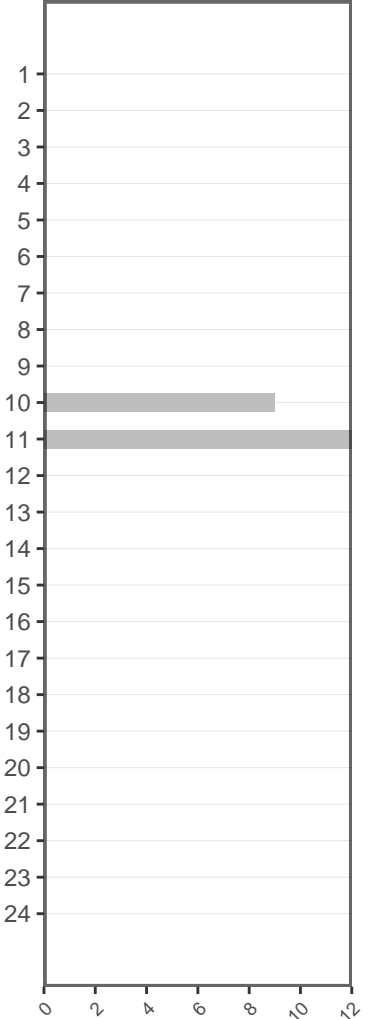
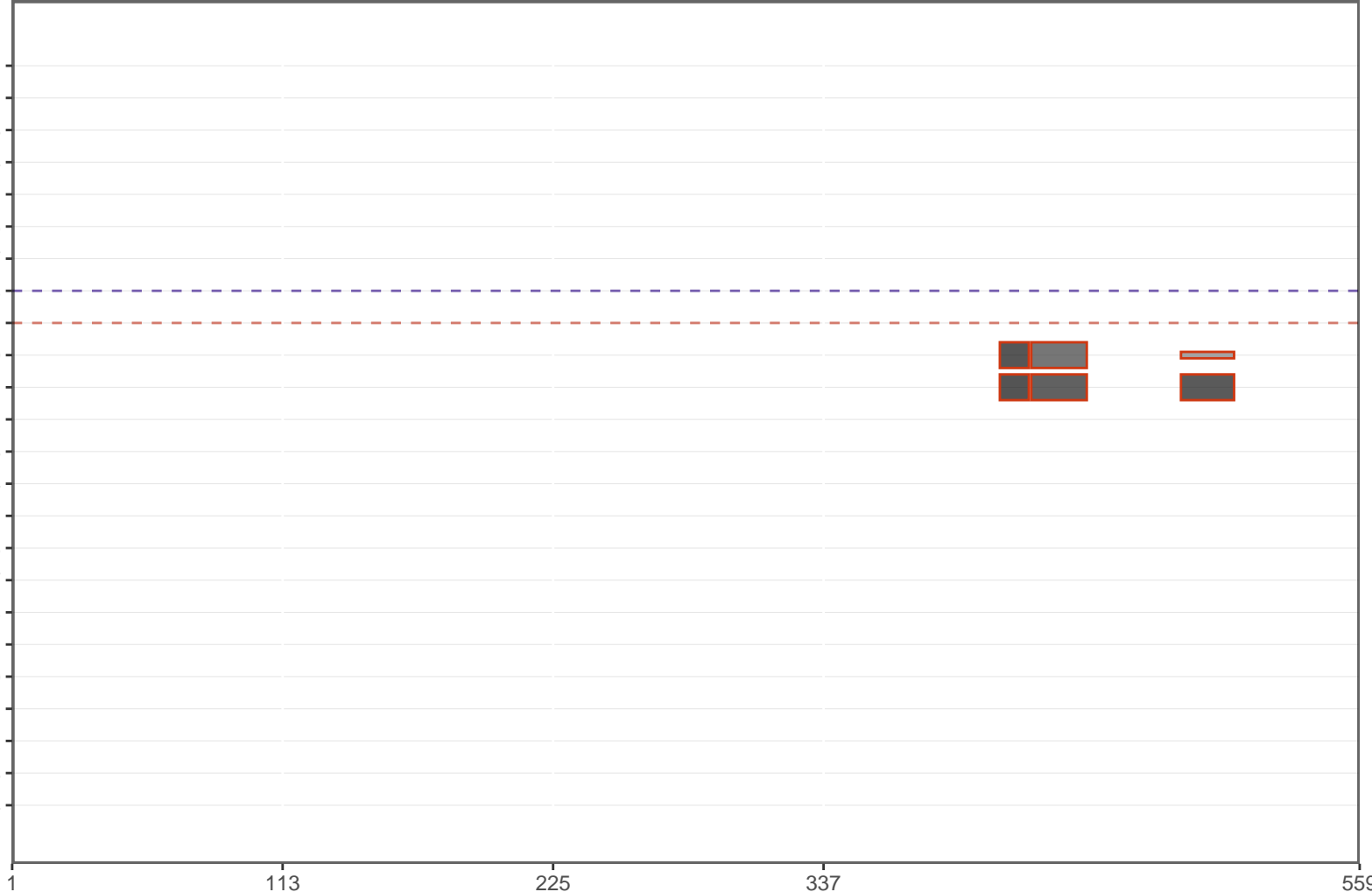
MW indication



Molecular weight



Gel Slice

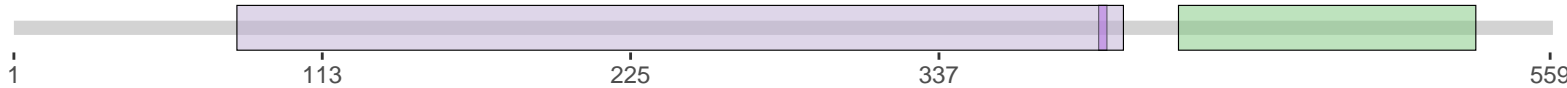


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

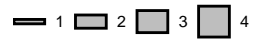
- SP
- Sequon
- TM Domain
- PF02852 Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain
- PF07992 Pyridine nucleotide-disulphide oxidoreductase

Protein sequence:

EFAGIFNGLKSEVHFRGKKVLRGDFEIRDFVGEQMLRGIIEFHTFEESPGQAVKSDGSLKTSRGTVEGFSHMFATGRRPNTKNGLETGVGKMTKNGAIEVDVSRVSPSWAVGDVDRINLTPVALMEGGALAKTIFAEPTKPDVRYVAVVFGQPPVGGVLTGEEQAKEYGDIDVYMANFRPLKATISGLPDRVFMKLVGAKTSKVLGLHMOGGDDAPEVVGQGFAMAVAGLTKADFDATVGHPTSAEEFVIMRTPTRKVRRSPEGKAEDIKAAAGV*

NbL16g27480.1 poly_[ADP-ribose]_polymerase_1 [MW = 112.03 kDa]

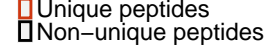
No. of times detected



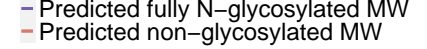
log(intensity)



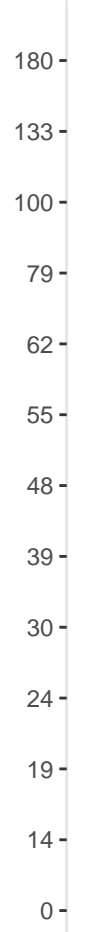
Values from



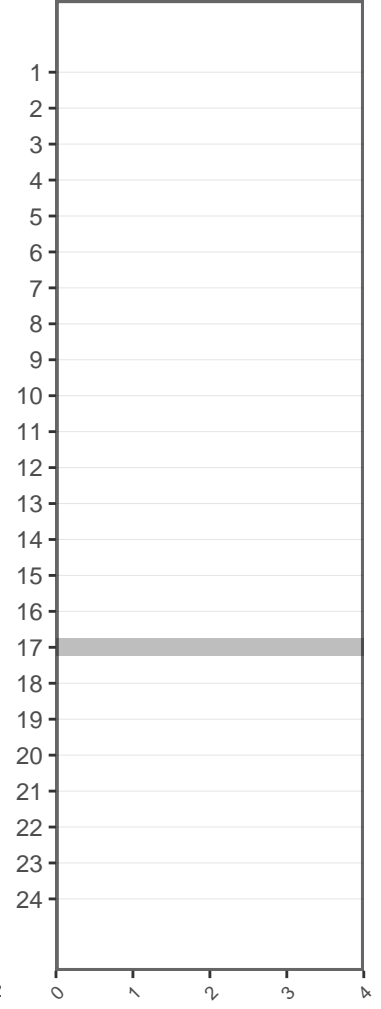
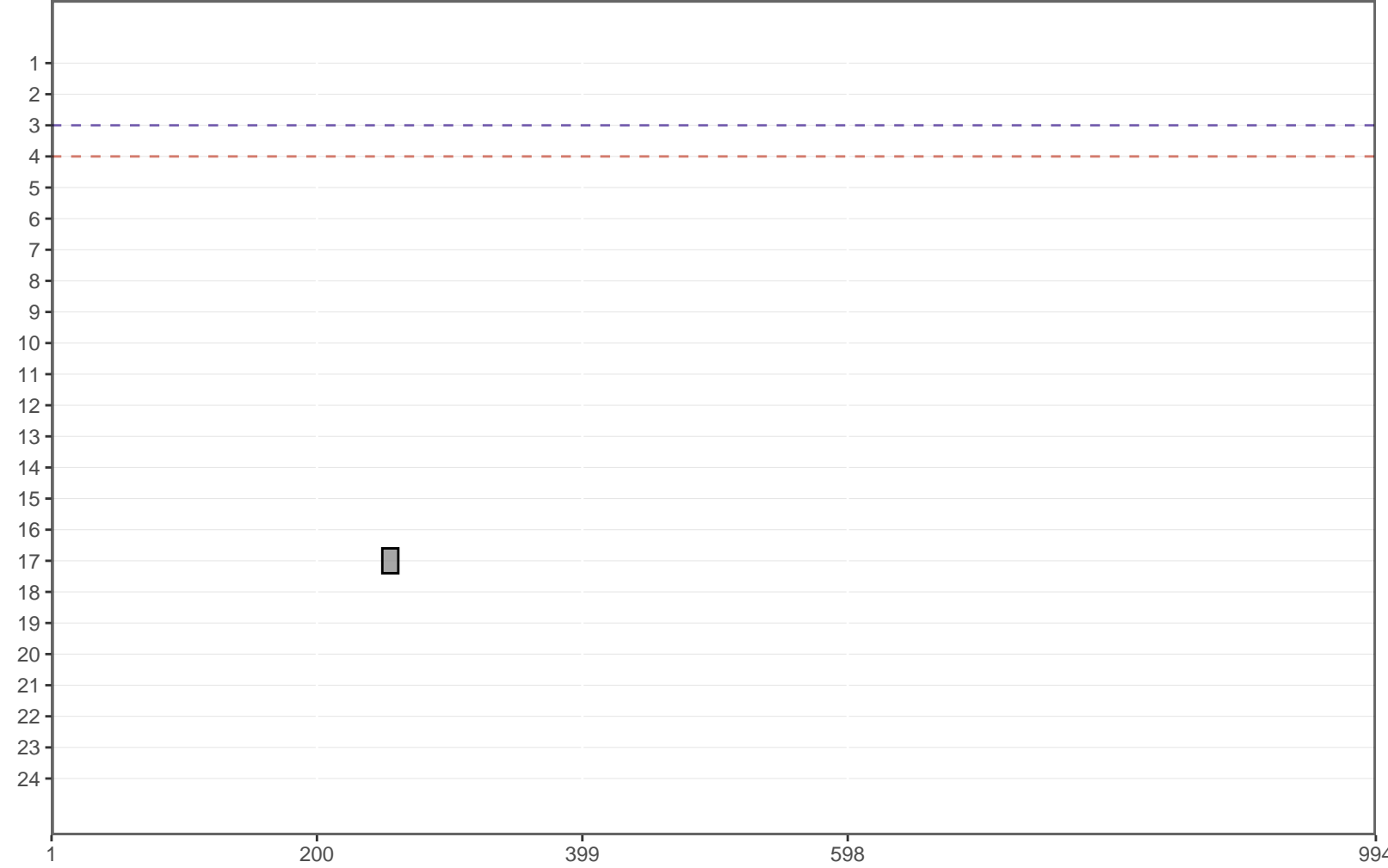
MW indication



Molecular weight

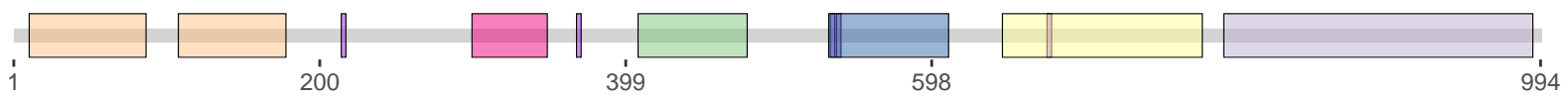


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Description

- TM Domain
- PF00533 BRCA1 C Terminus (BRCT) domain
- PF00644 Poly(ADP-ribose) polymerase catalytic domain
- PF00645 Poly(ADP-ribose) polymerase and DNA-Ligase Zn-finger region
- PF02877 Poly(ADP-ribose) polymerase, regulatory domain
- PF05406 WGR domain
- PF08063 PADR1 (NUC008) domain

Protein sequence:

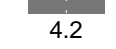
IERKKKLPFALYKLEAVEETGSMVTKWGRSAWHESSDLQDSGHLEDKTSVYFTLNMDSLSSGINSYVYLGHEEDKGBECYVFRKWRGRVGNKEKGGKLEEMSKSDAQDFKRLFLEKTCNSWEAWEQKTNFQKQGRFRYPLDIDYGVKDKNPPTKRNLENDANSKLAFLMELMAMKLFNVETRYRAMMEFEINEMSEMPKGLSKNKIKQKGFALTEIGNLLSGTNDPAKETLLVDAENRFFTHPSHHPHWKDEDDPKLHKIMALEALGDIEASRLVGFDDNDOSLDDKYK

NbL16g27250.1 TOM1-like_protein_2 [MW = 42.21 kDa]

No. of times detected



log(intensity)



Values from



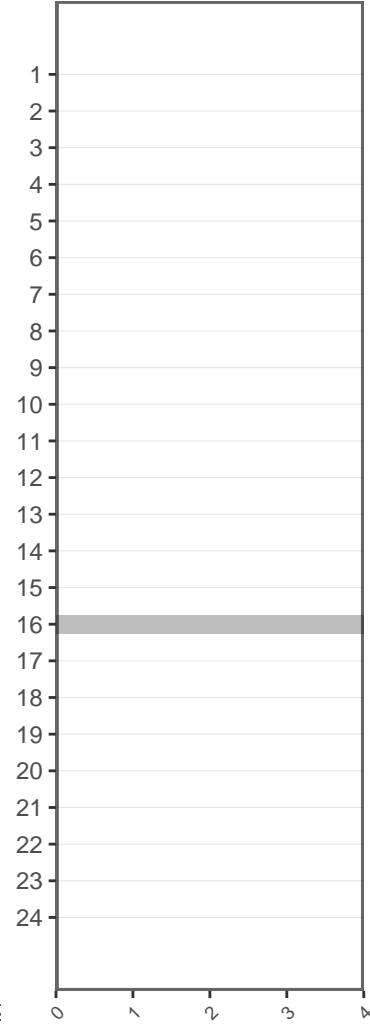
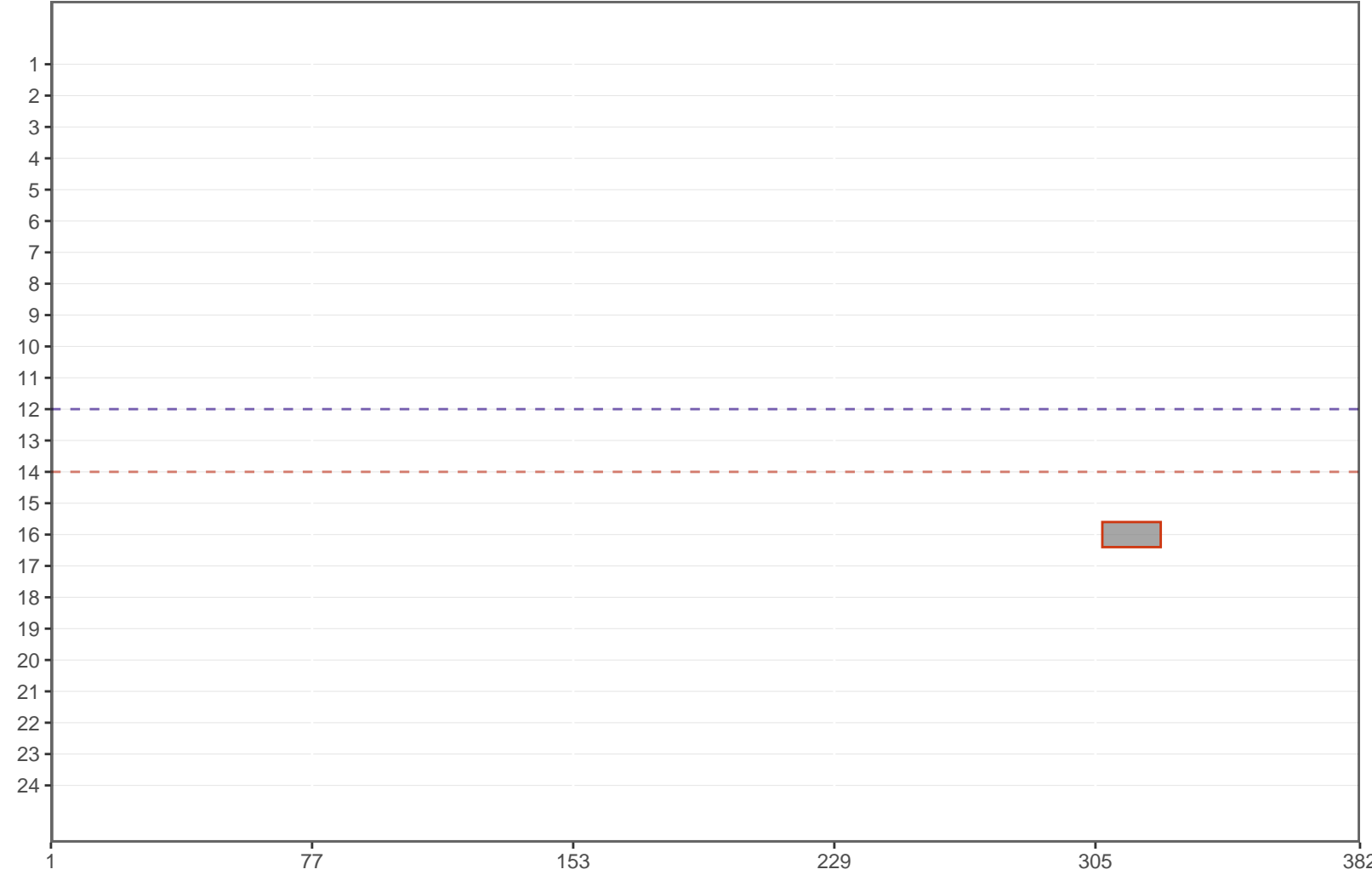
MW indication



Molecular weight



Gel Slice



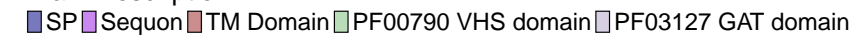
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LESHITNEQLLSPPEFYPHPHTGLRNHEHTAWIGESTEEKKEFLVTRNLEKLSLITSEVDPKPKDDLAVMLLENKKGELAWQRIVESTSGDEGLMFEALNLDLELRGVSKYEEEMEALESSEKLPKTRFDDGGSLNTPAPEAGEKLPKTRFKGGSLPNVADISGANLEKPSLNAGESHAWPTNEENNRHPEVWPKDNGE

NbL16g27240.1 putative_exosome_complex_component_rrp40 [MW = 26.14 kDa]

No. of times detected



log(intensity)



Values from



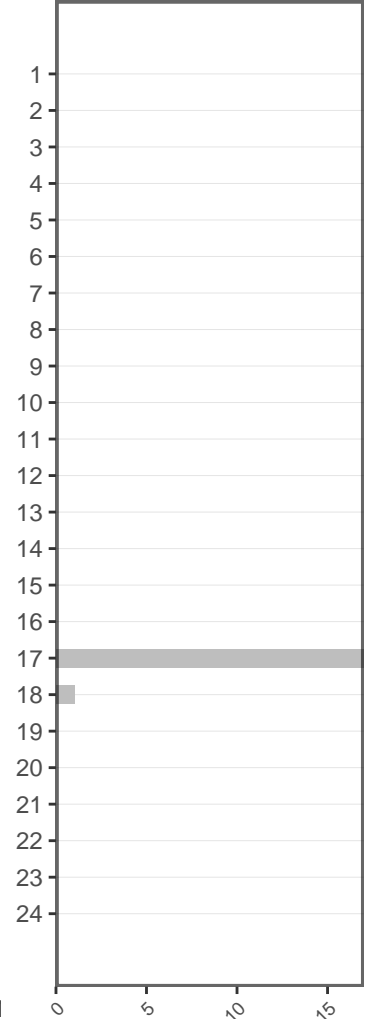
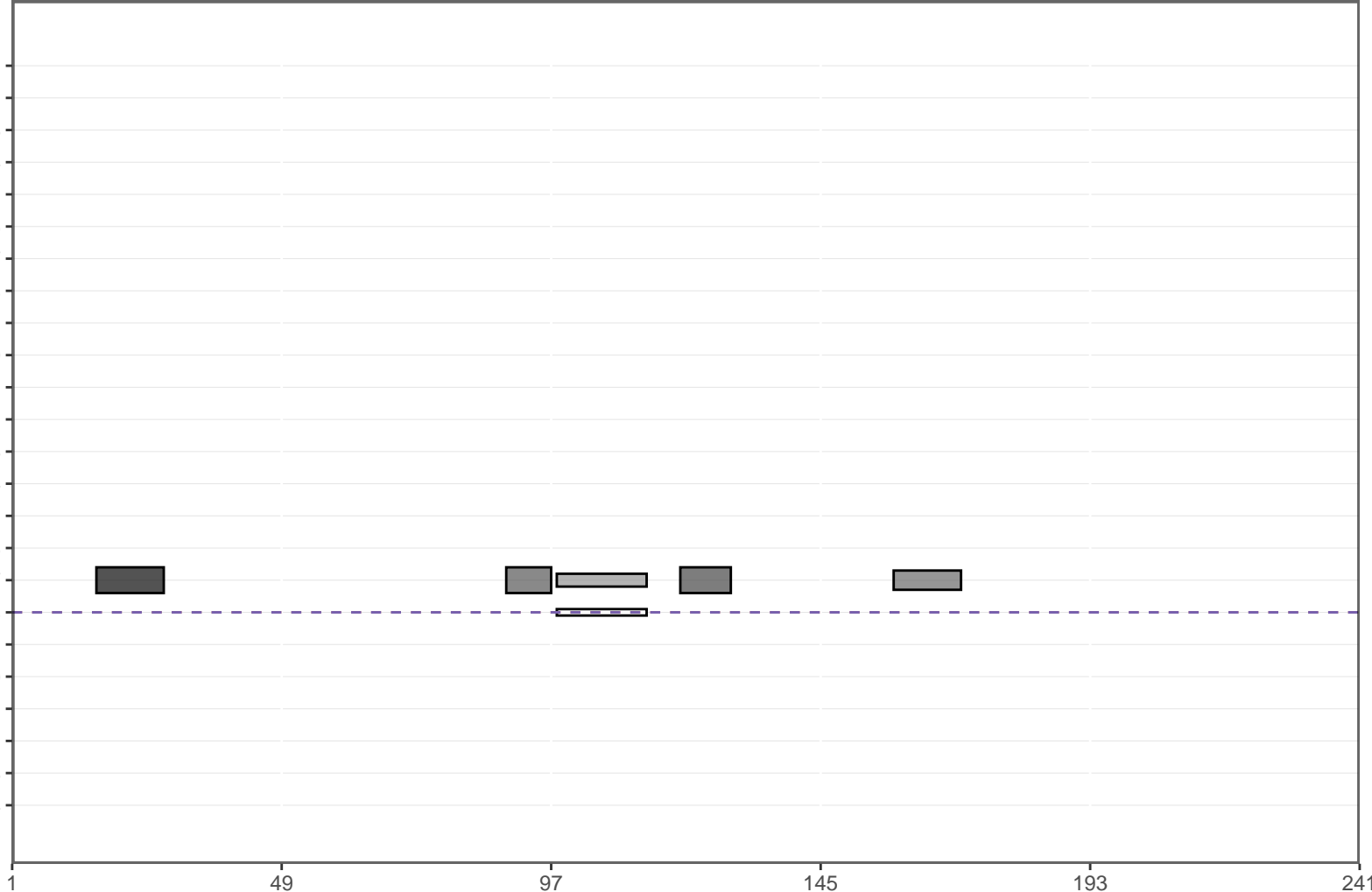
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

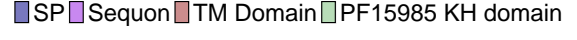
Protein length



Pfam domains



Pfam Description



Protein sequence:

FEQGTRRNIPKFEVGTLYHARVAKANTGMNPELSCMDASGKAAEGLIKDGYMFEESDTGLSRMLLSPTPTVLEGLGKLAFAEIVAGLNGRWWWNAEHQSTILVANAMNSELTPVQKIMVERLLDRVV

NbL16g27200.1 rho-N_domain-containing_protein_1_chloroplastic [MW = 42.71 kDa]

No. of times detected



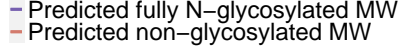
log(intensity)



Values from

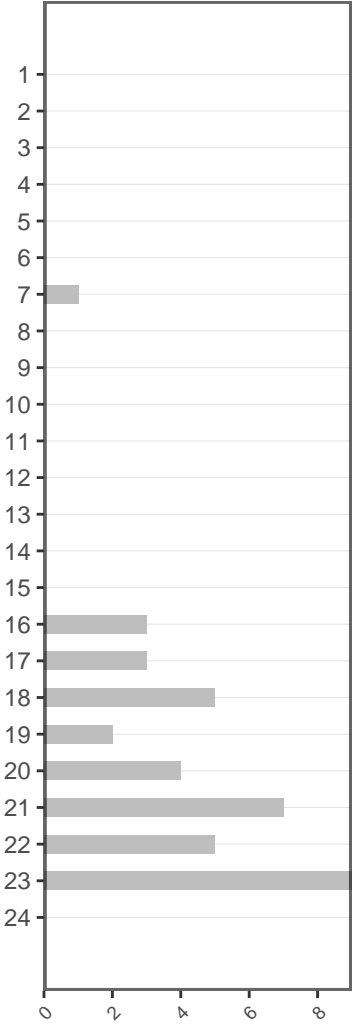
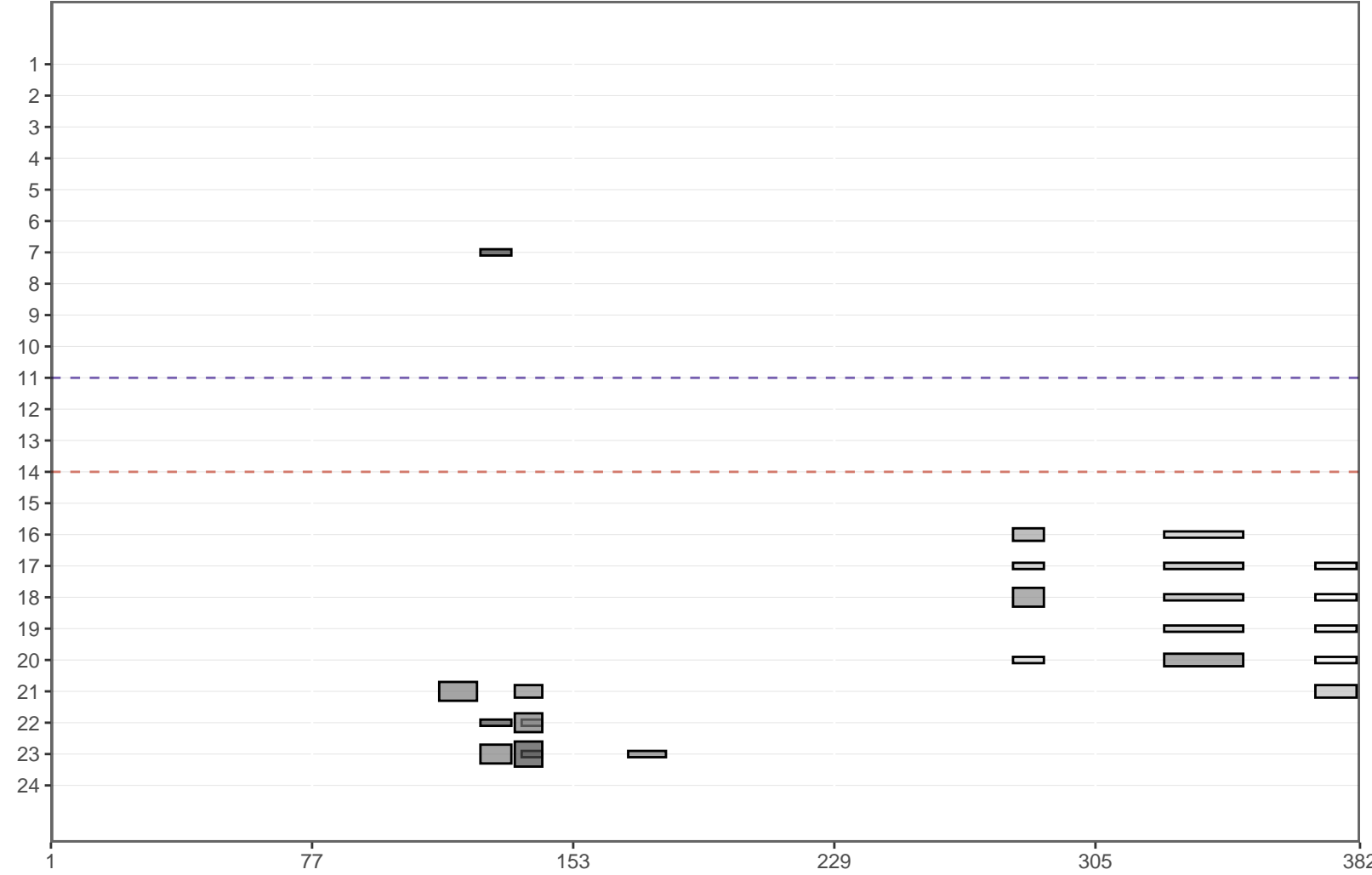


MW indication



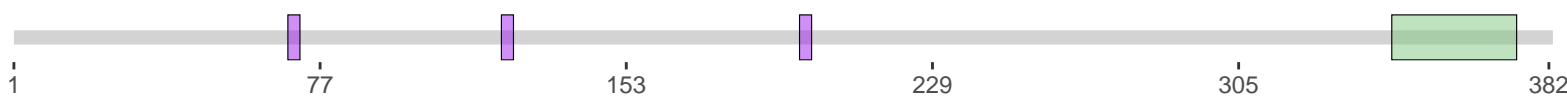
Molecular weight

Gel Slice



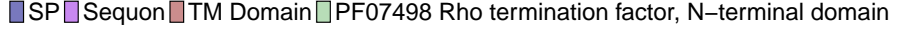
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

..LKLRLKISVQKGGKTKNENRISNFFLDQPDGNGVFFFEERAGSSTELNNDVNHVAGDGGTPIVNRPKSNFQRRSPVSRTKFQPIVYHEGDTNIVASTATDKTEKHLDPELGRTPKPKVDSTAHFDQIEPFSDQEDVDEMADDDTAKMFENVDANDDEEGHQVSEELAEMLKTELRAAKSRGLKGVSKLKKVLELLSADQV*

NbL16g27140.1 uncharacterized_protein_At1g03900-like [MW = 30.14 kDa]

No. of times detected



log(intensity)



Values from



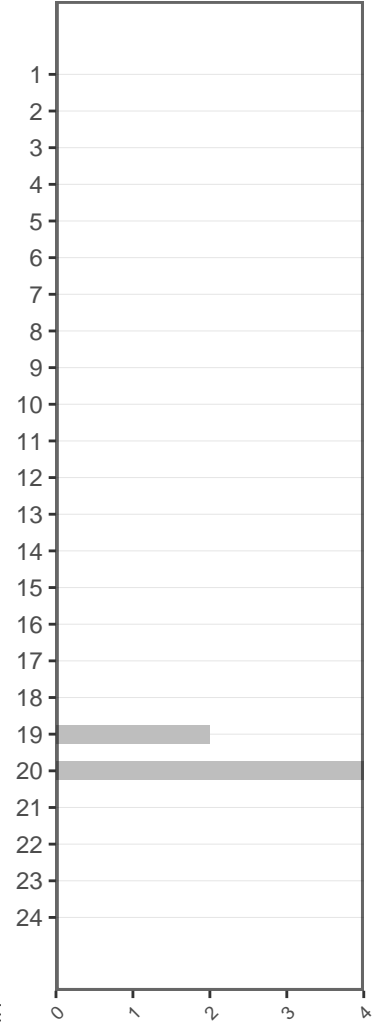
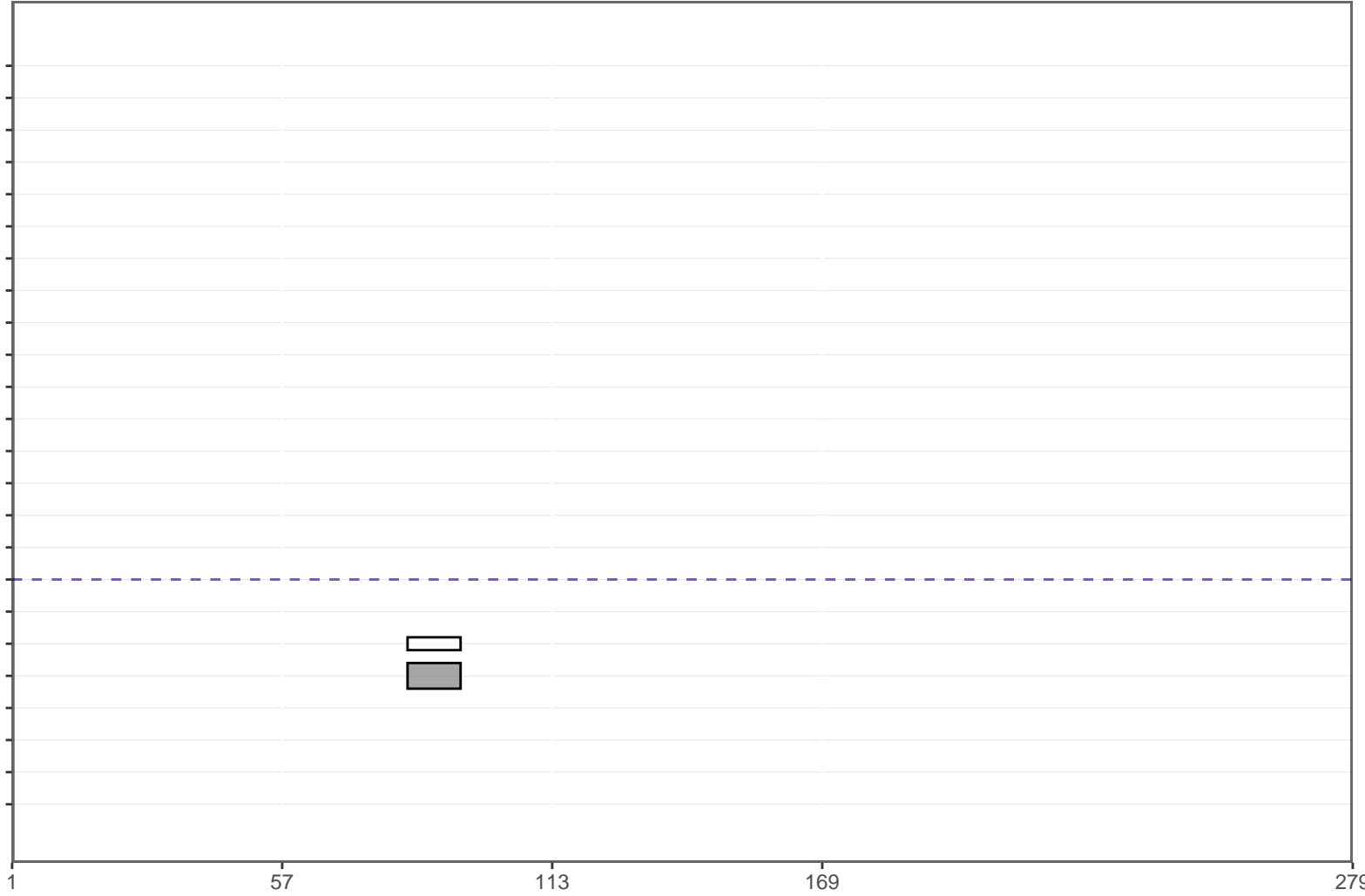
MW indication



Molecular weight



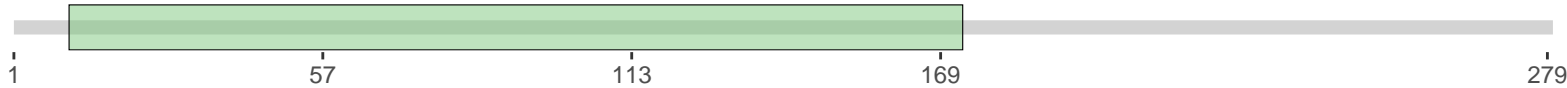
Gel Slice



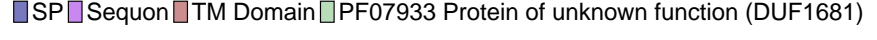
Protein length



Pfam domains



Pfam Description



Protein sequence:

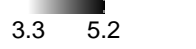
ALSDHDKYKRENEKEVGDGEAGDDNHIDHFWNHRUKEGETRISVKNKPSGGTQMLEAVGLMAGTTGAVKKTALAPPSPGGNKKISLPPRPNDPATARKTGTSTPSIALKENTKHSTDPLEDLAEIERGLPSAAGRSRSGKPTAAGWAAP

NbL16g27120.1 ABC_transporter_I_family_member_21-like [MW = 32.06 kDa]

No. of times detected



log(intensity)



Values from



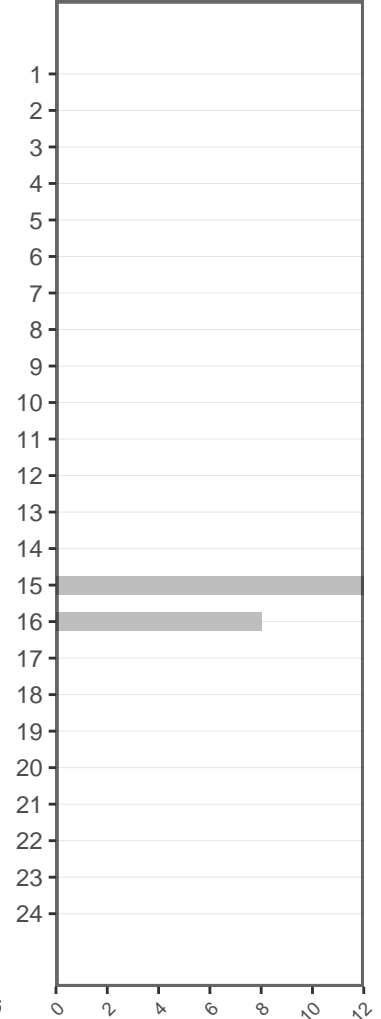
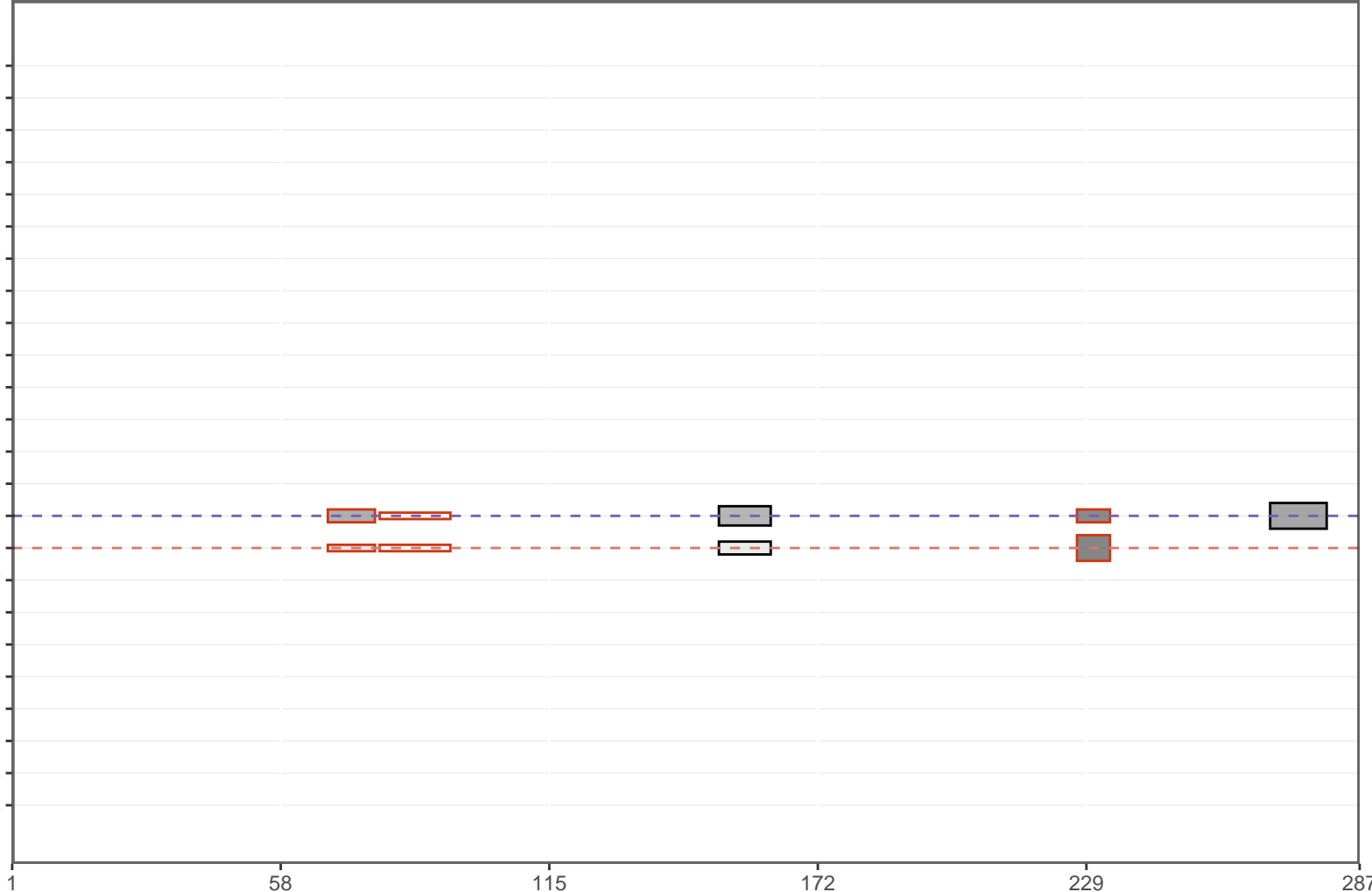
MW indication



Molecular weight

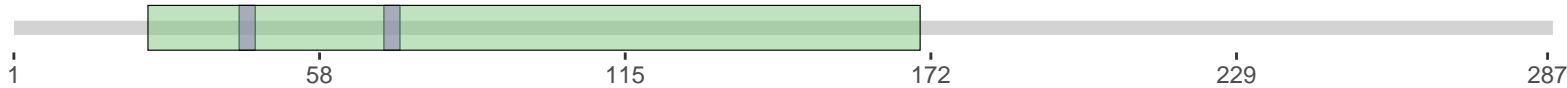


Gel Slice



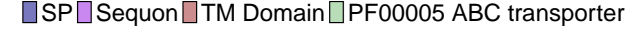
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

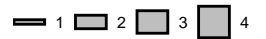


Protein sequence:

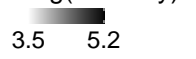
ELLNLDLQWRMFKVSDGRRRRVQKMGLLHPYKVLLEDVTVDLQVARMMLLDFKKEEGRGATIVYATHFDGLSEWATDLVYIGDGVLRKSEKLSGLPDKSPNLLSVENLWRSETTEKKKPVAPPKVKQKSSPFGSSPFGSRHMAYFR

NbL16g27090.1 probable_60S_ribosomal_protein_L14 [MW = 15.89 kDa]

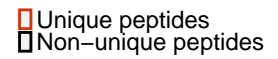
No. of times detected



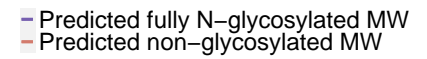
log(intensity)



Values from



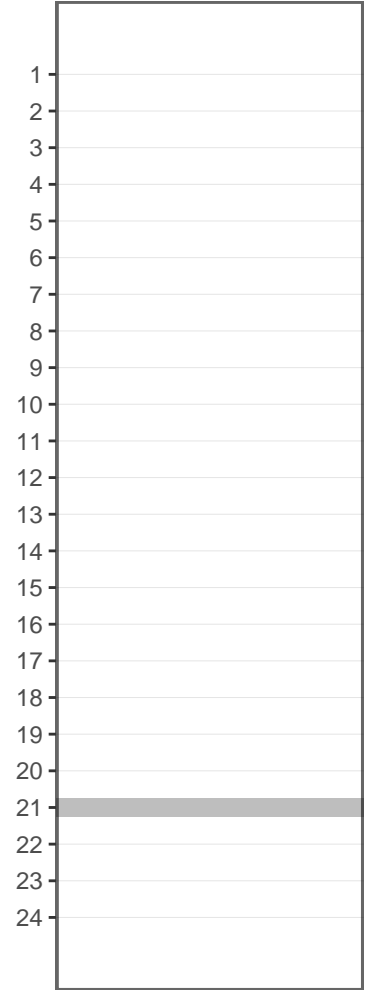
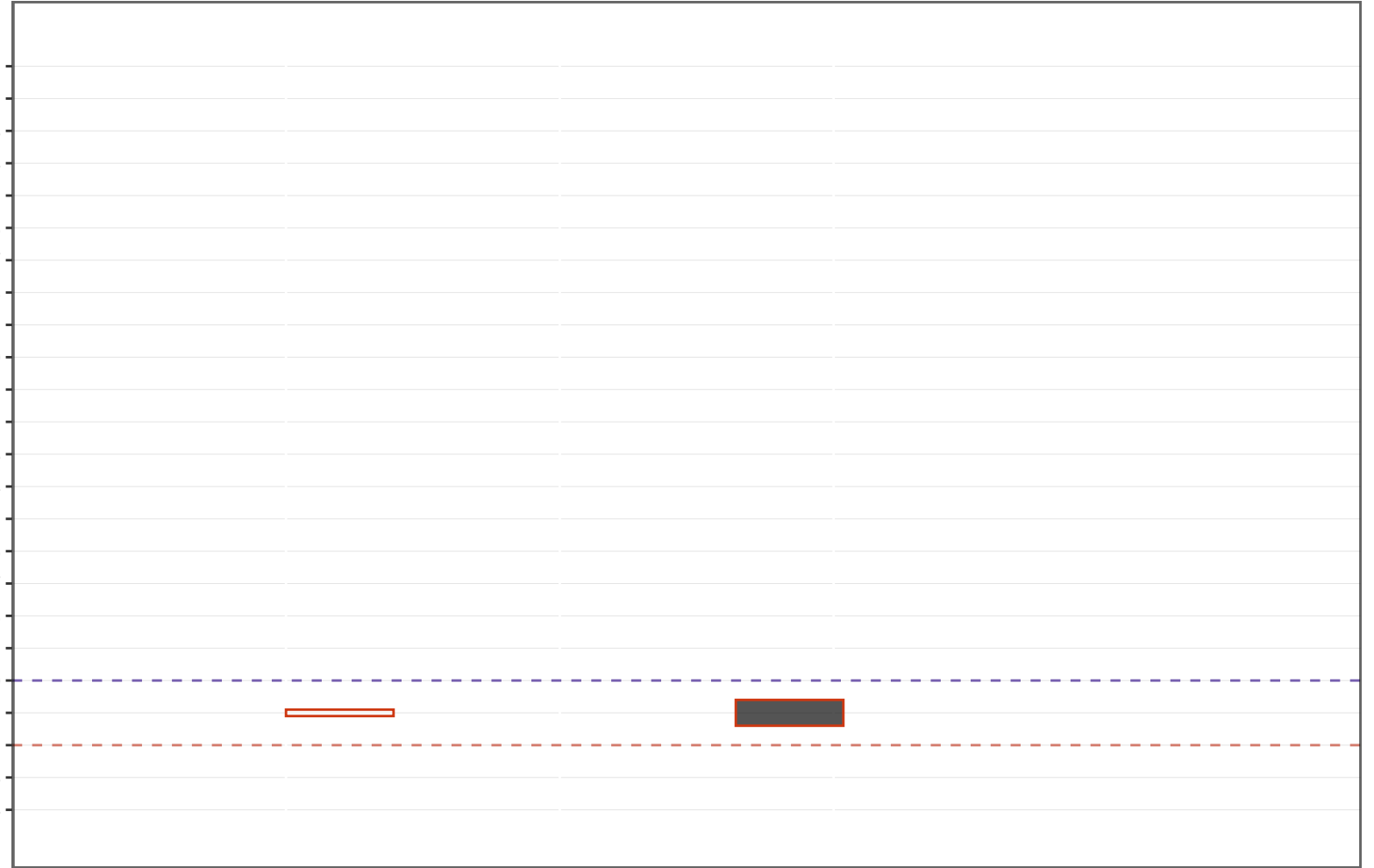
MW indication



Molecular weight



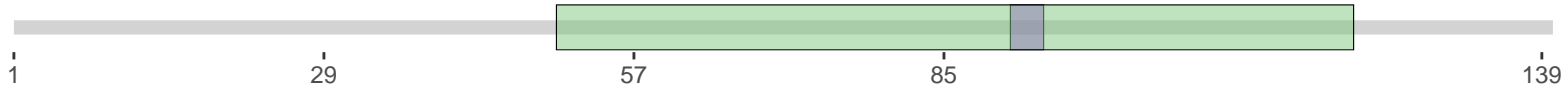
Gel Slice



Peptide counts over 4 repeats

1 29 57 85 139

Protein length



Pfam domains

Pfam Description

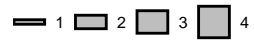


Protein sequence:

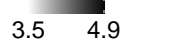
RLSLTDKIDKIRIPKQKTLVEAMEAADVKTWENSWGRKLVQKRRALNDFDFKMLAKKIRAGVVRGELAKLKTTAA

NbL16g27000.1 rho_GDP-dissociation_inhibitor_1-like [MW = 27.82 kDa]

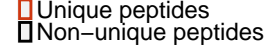
No. of times detected



log(intensity)



Values from



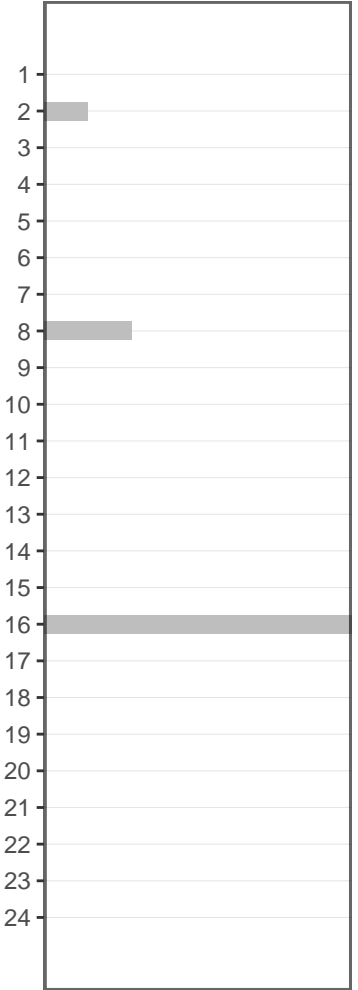
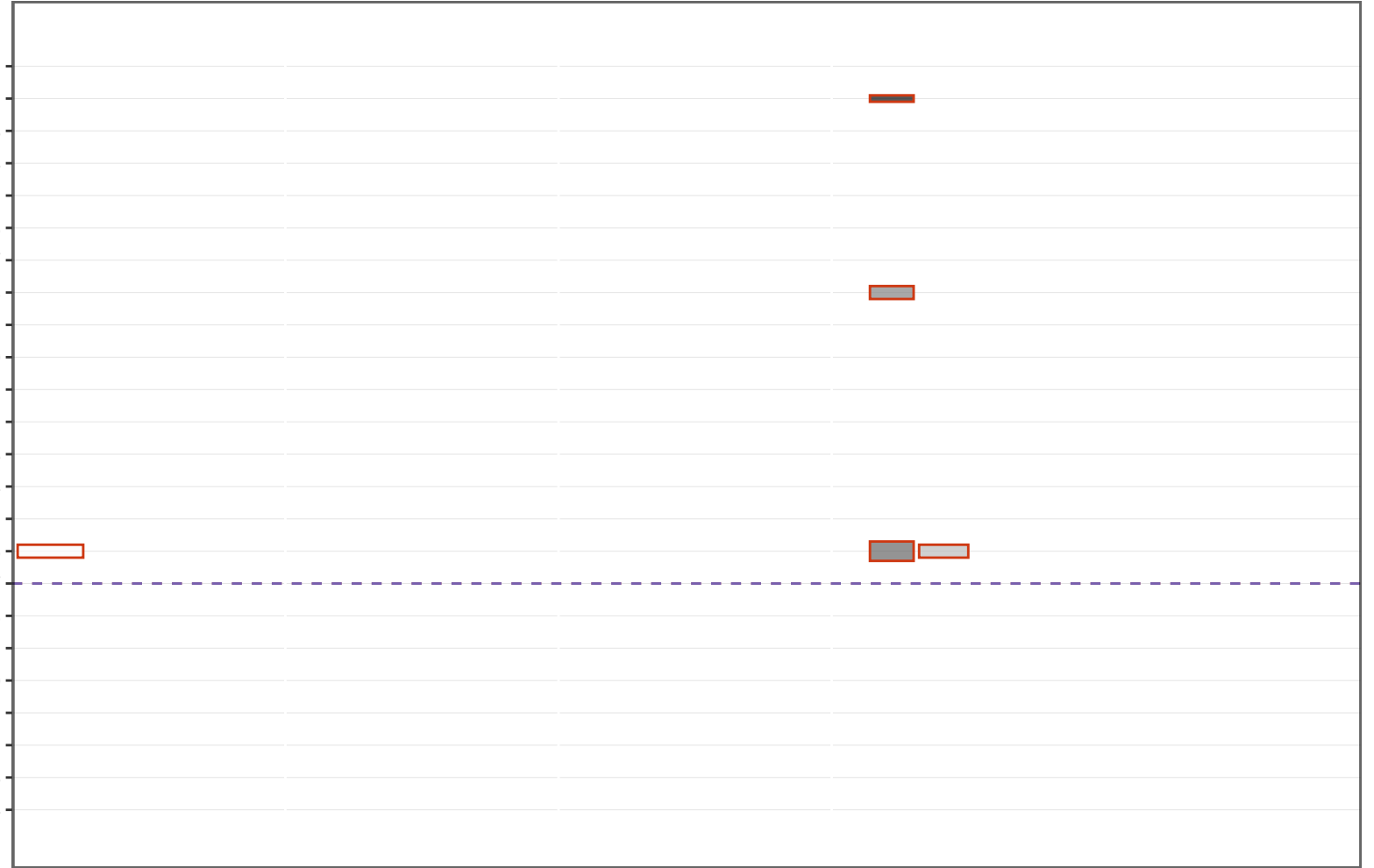
MW indication



Molecular weight

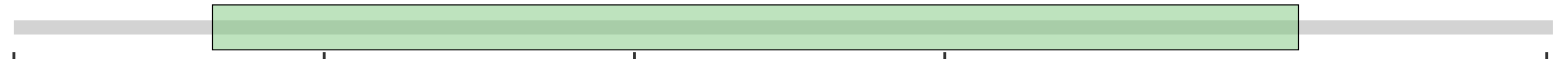
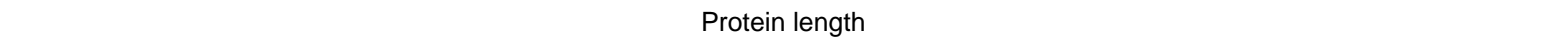


Gel Slice



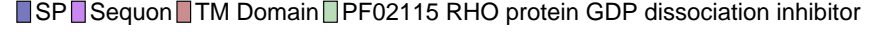
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

NTPLPIKEGQRKSVLFTLKEGSEYRLNLTFSVLHNIVSGLAYTNTVWKAGLGVDSKGMVGTAPGRFPVHMLEEETTPSGALARGTYTAKLMLDDIGETRIHLKNGKNSHRLIEVLVMMVHGVTLSNNGDLG

NbL16g26980.1 phospholipid--sterol_O-acyltransferase-like [MW - SP = 69.67 kDa]

No. of times detected



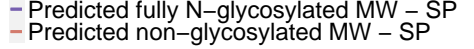
log(intensity)



Values from



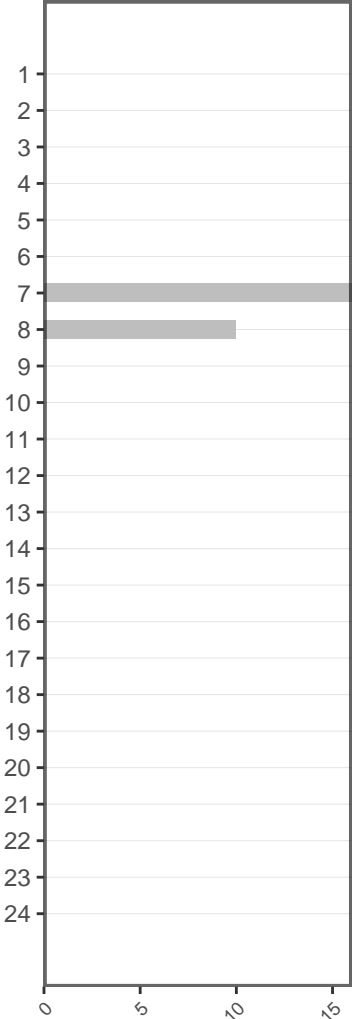
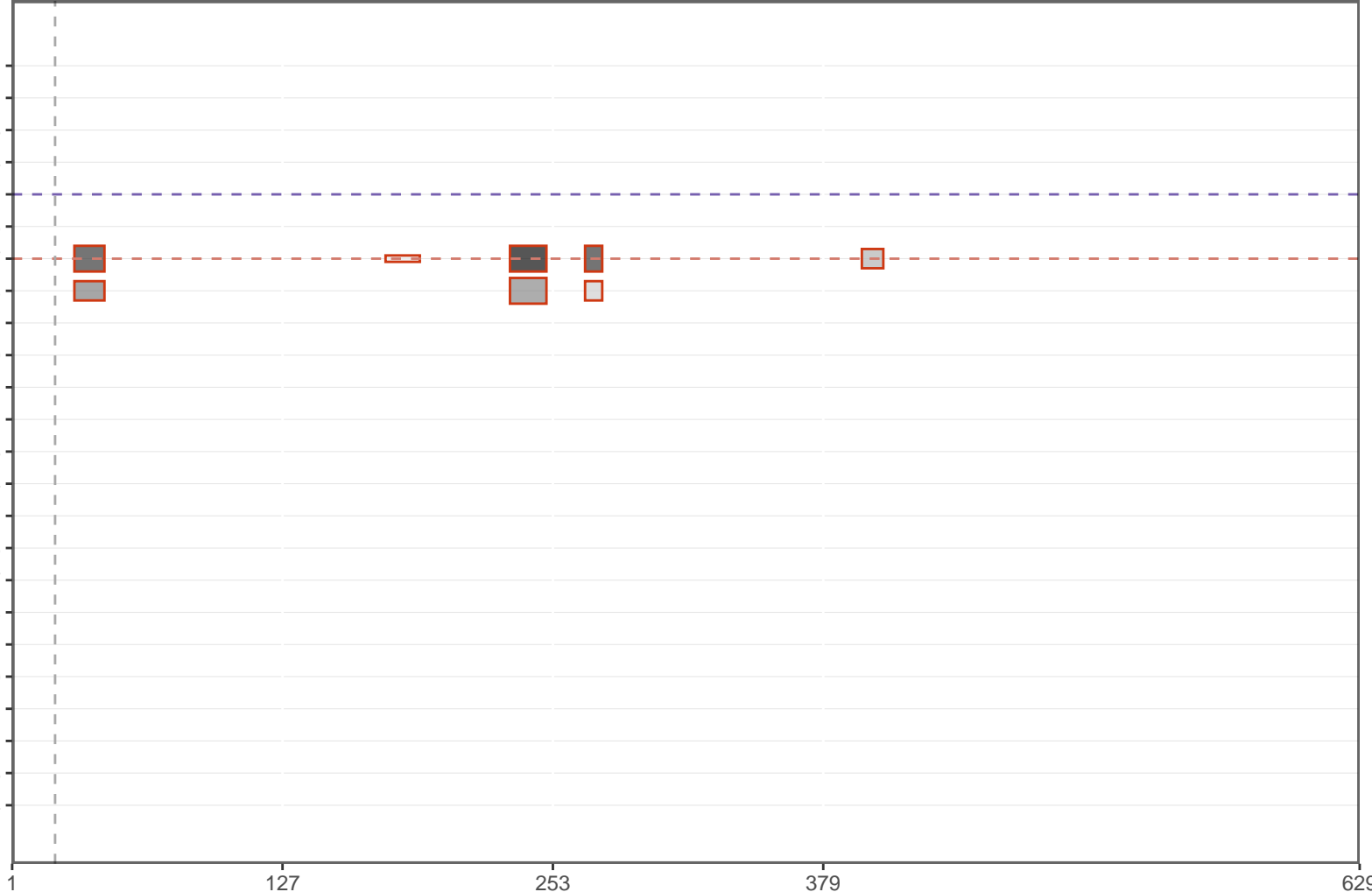
MW indication



Molecular weight



Gel Slice



Protein length

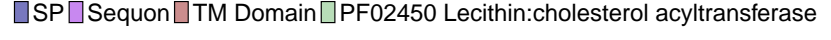


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GWPTNINEVPSIRGDKAVPSFVEIAGANLGGMEGCFPTQLSFSAREVSDGTFKAKDYDPSERLLYLLGKSYHADPLNPLTPWERPPLKFNDFYGDIKTEVGVYFAPGKPKYPPDNWITDVIYEIGSLYERSGNLVEGNPQATSGDETVPYHSLWCKNWLGPVYNTRTPQSEHDGSDVGVHGNIEHQHGDEHPNMTRLPTVKVYFVYEDSEFFPKRTAWWELDKANRRNVRSPVLMRELUWEMWHDHPDKGNFVTKAKRPLRDEDCYVDYQKRCAMV

NbL16g26880.1 60S_ribosomal_protein_L23-like [MW = 15.01 kDa]

No. of times detected



log(intensity)



Values from



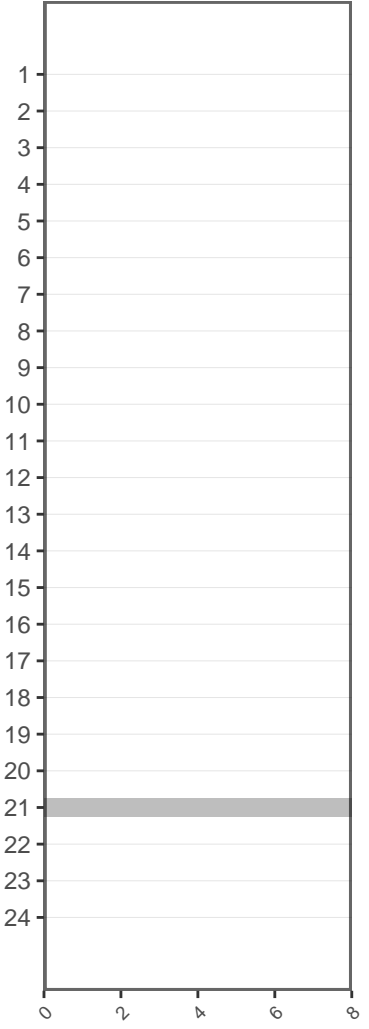
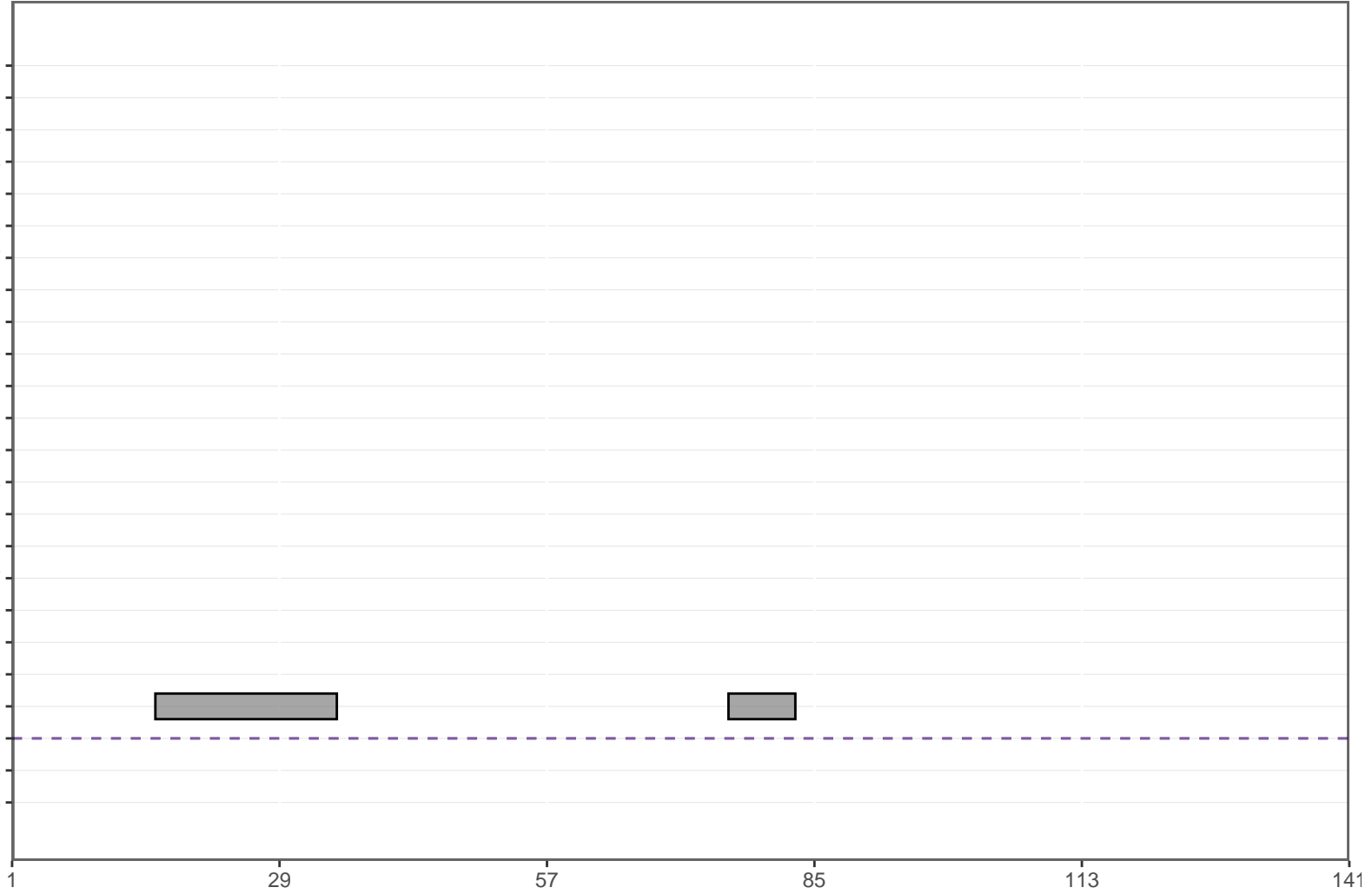
MW indication



Molecular weight

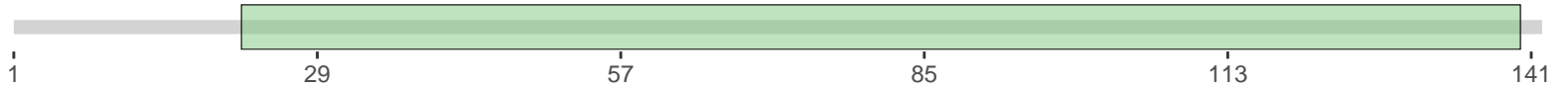


Gel Slice



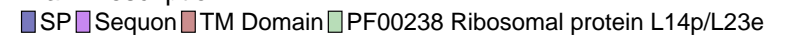
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SDMVMATYKKGKPKDLRKKVMPWVVRQRKPKWRKDKGVFMYFEDNAGVIVNPKGEMKGSATGPIGKEGADLWPRISAANAVV

NbL16g26760.1 NADH_dehydrogenase_[ubiquinone]_1_alpha_subcomplex_subunit_9_mitochondrial [MW = 43.45 kDa]

No. of times detected



log(intensity)



Values from



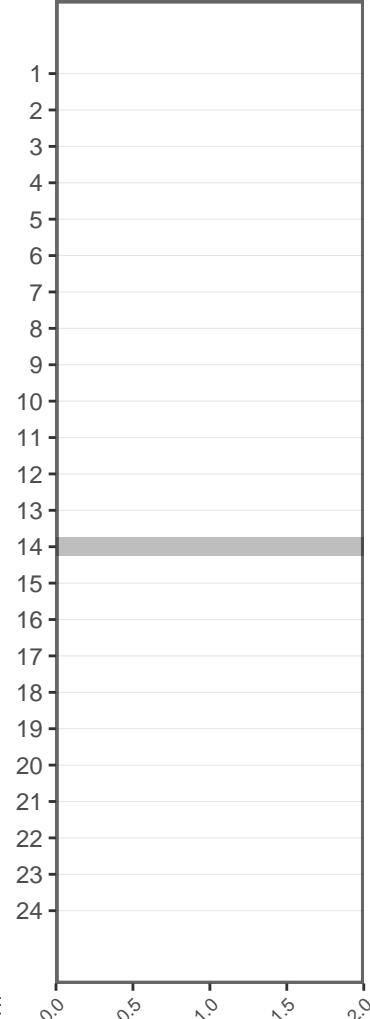
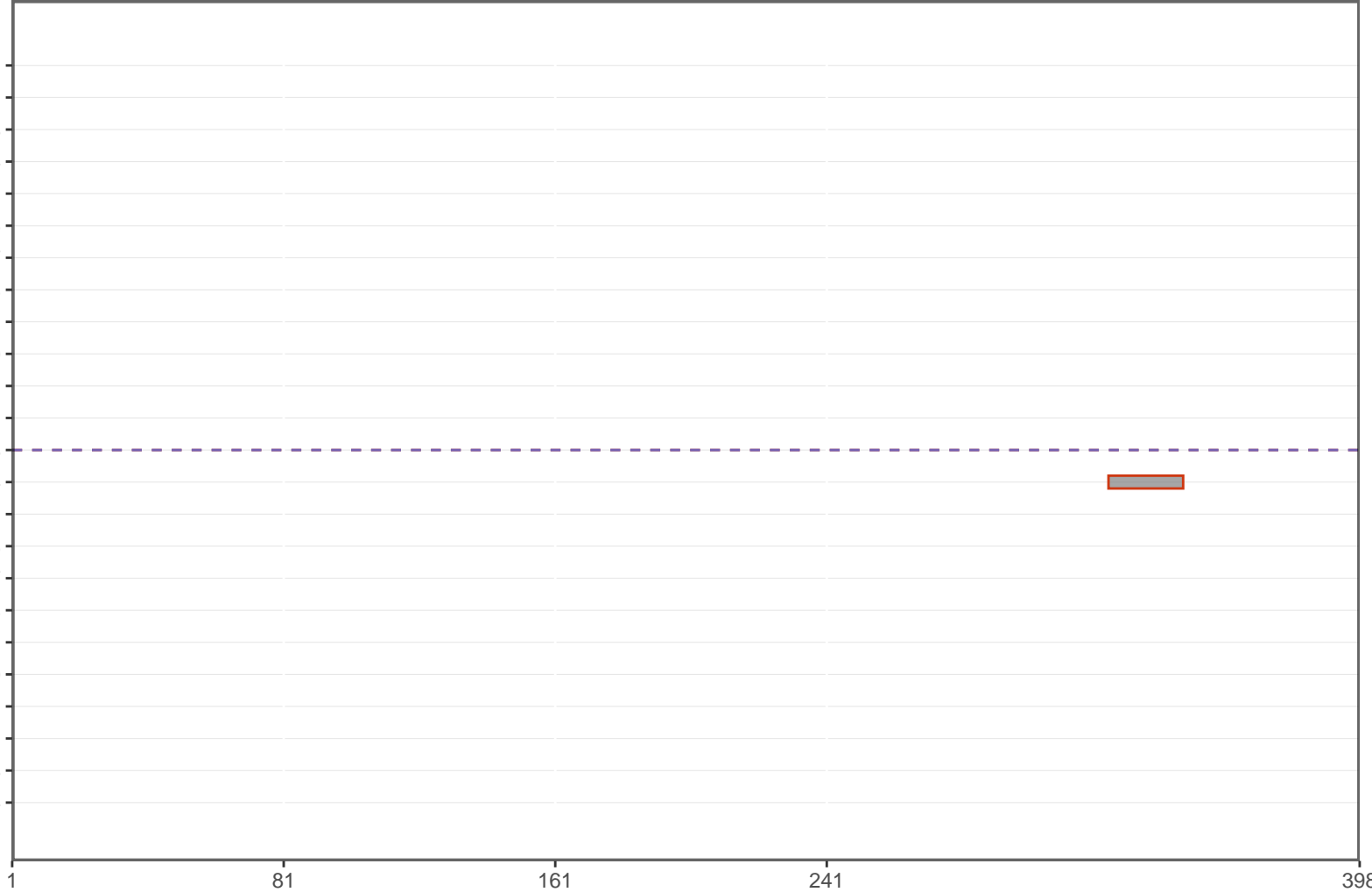
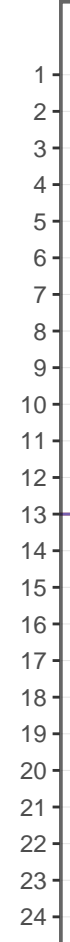
MW indication



Molecular weight

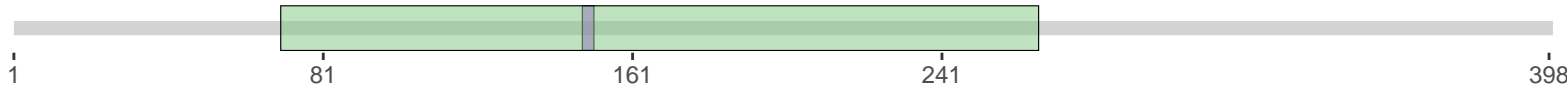


Gel Slice



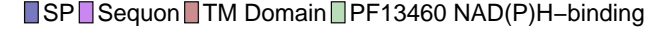
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SPTSPSRMLRAKAAEEAWHELPEATMRPVMIGTEDRLNPWAHFAKKYGFPLFGDGTGKQRFVADVASAVASLKDNGISMGKVELGGPDVYTHHELAELMDFMREWPRVYVYVFFPAKALASPREFLLNKVPMPPTPTTFINLDAIEALATDKVSKDALTFFEDLGLVPHKVGKGFVEFLIQYRKGGPNVGGSTVSEKRVSPGKYP

NbL16g26700.1 alcohol_dehydrogenase_class-3-like [MW = 25.78 kDa]

No. of times detected



log(intensity)



Values from



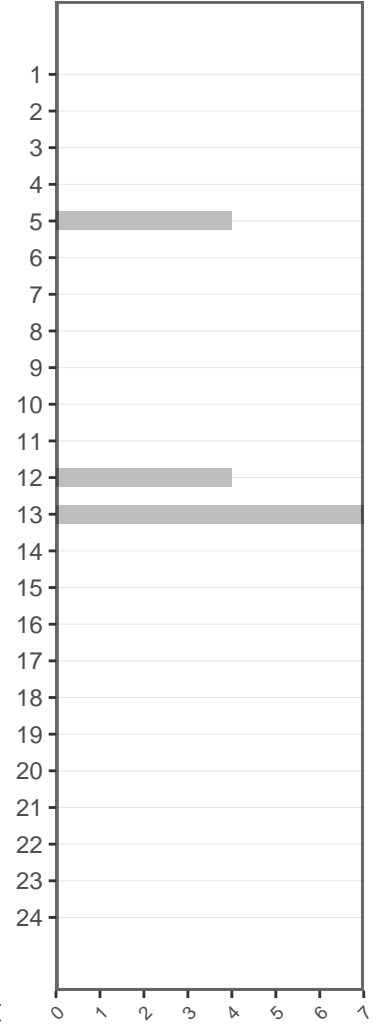
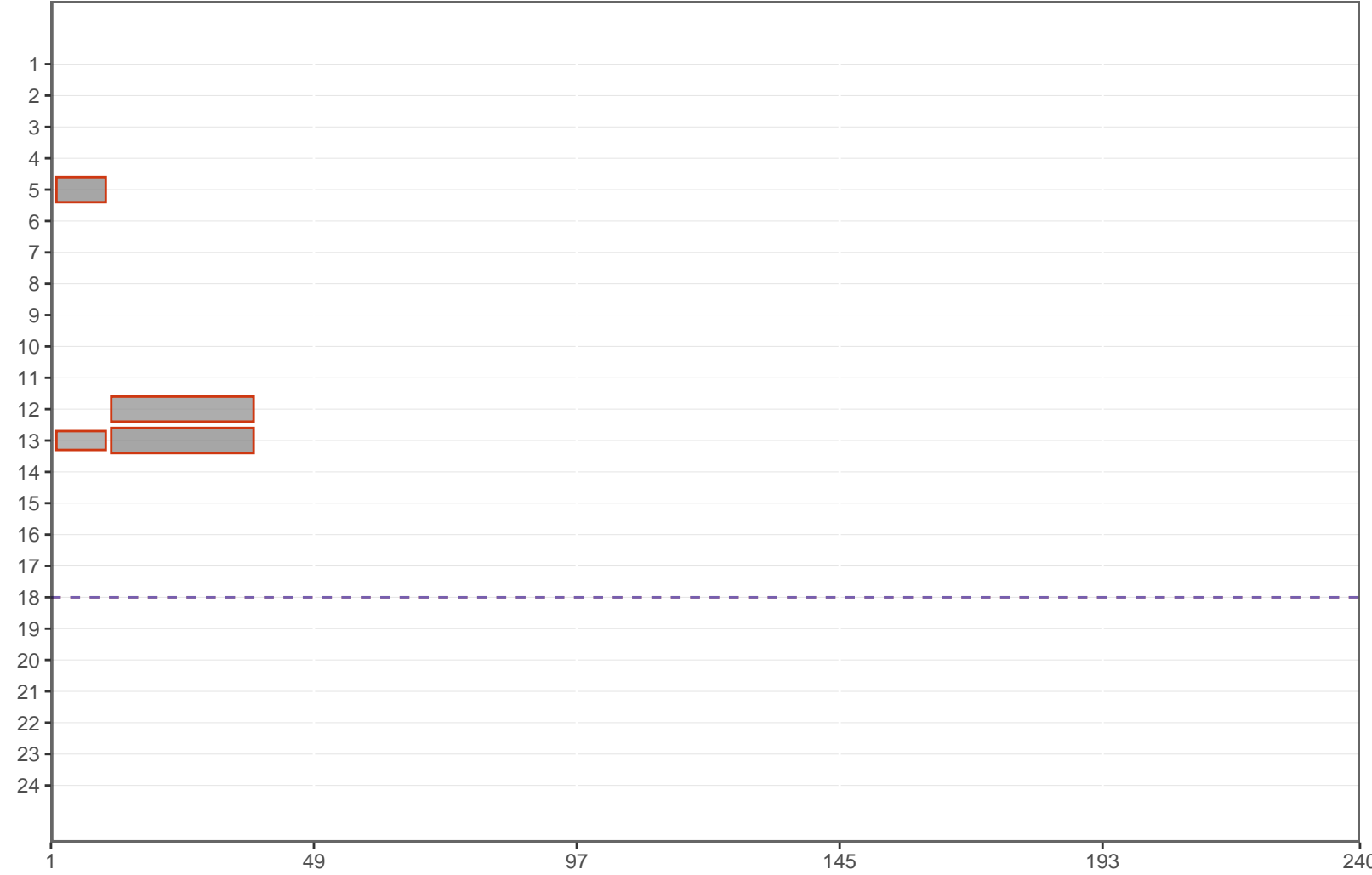
MW indication



Molecular weight



Gel Slice



Protein length

Pfam domains

Pfam Description

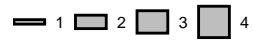


Protein sequence:

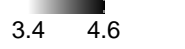
ISGKTNLGGKVRVAAATGGVMMNDGRGFRSNGKPIYHFMGTSTFFSGYTVVHEDVSWAKIDPAAPLEKVGLLGGVPTGLGAVWNTAKVPEKPLLSLAWAQLVLRVRRVQRLVLRRELLGLTANSLKPKLV

NbL16g26680.1 ribokinase-like [MW = 43.47 kDa]

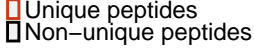
No. of times detected



log(intensity)



Values from



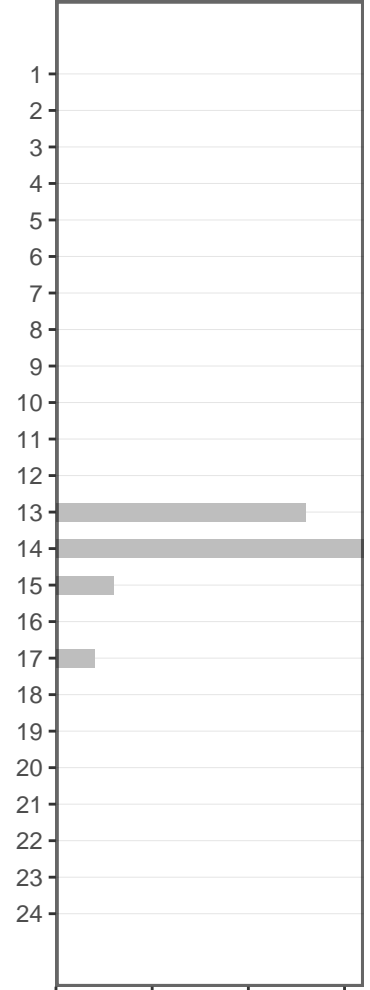
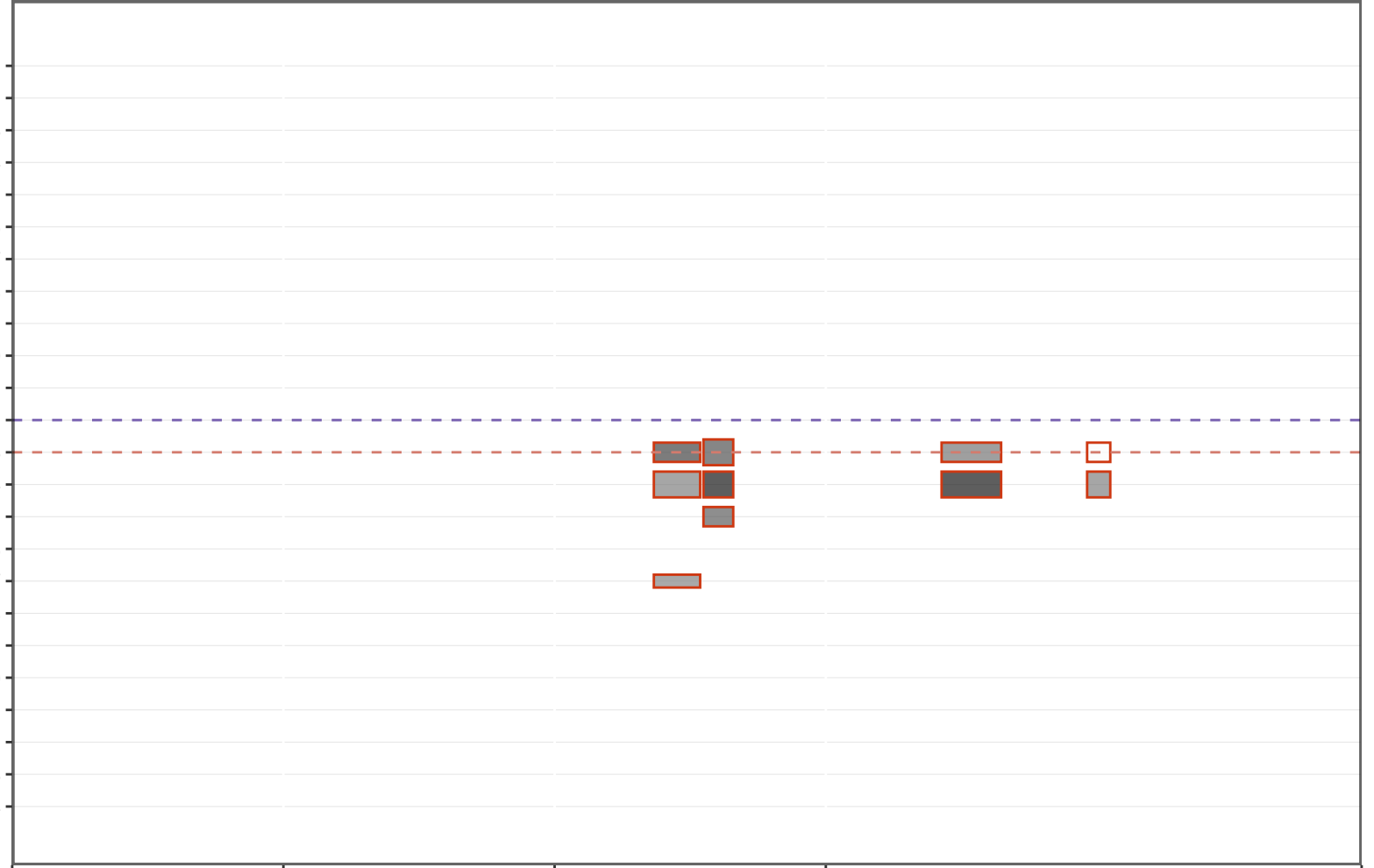
MW indication



Molecular weight



Gel Slice

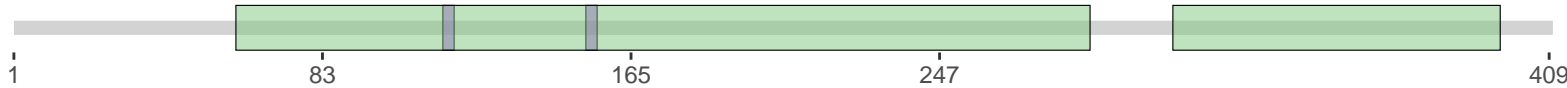


Protein length

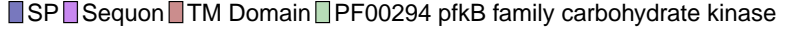


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

FDGRLLIETAIVVAEEANRRGPIIDTERIKREGLDHLLSFAVYVGGTKFQEWTEASSPVALVSMILRLPKAKFVIVTLGKDGGMQLQRTMEMVHSEEMDVNLFENLNGEKDTSATVFGGIGSNVYKLLHAKGIGTIGRLLVGTAEIPQTELDITFGAGDAFAGVLYGICANPFPEKMLPFAAGVAAIKRALGARAGLPHYTHRLRFLPLV

NbL16g26420.1 ribonuclease_P_protein_subunit_p25-like_protein [MW = 26.92 kDa]

No. of times detected



log(intensity)



Values from



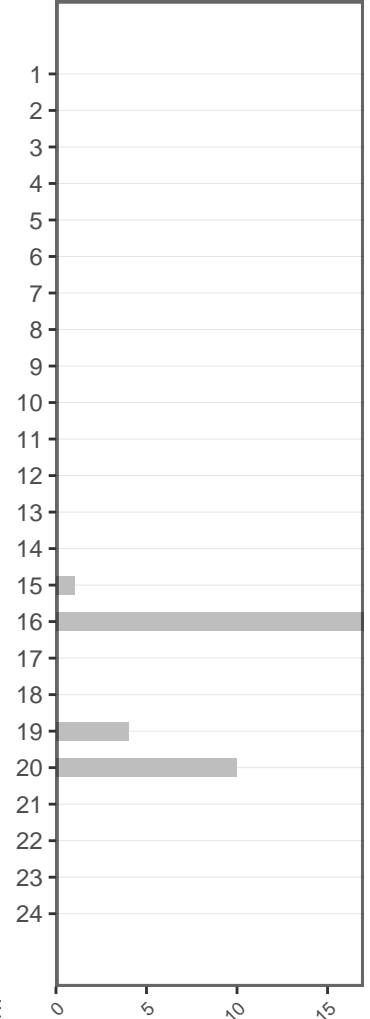
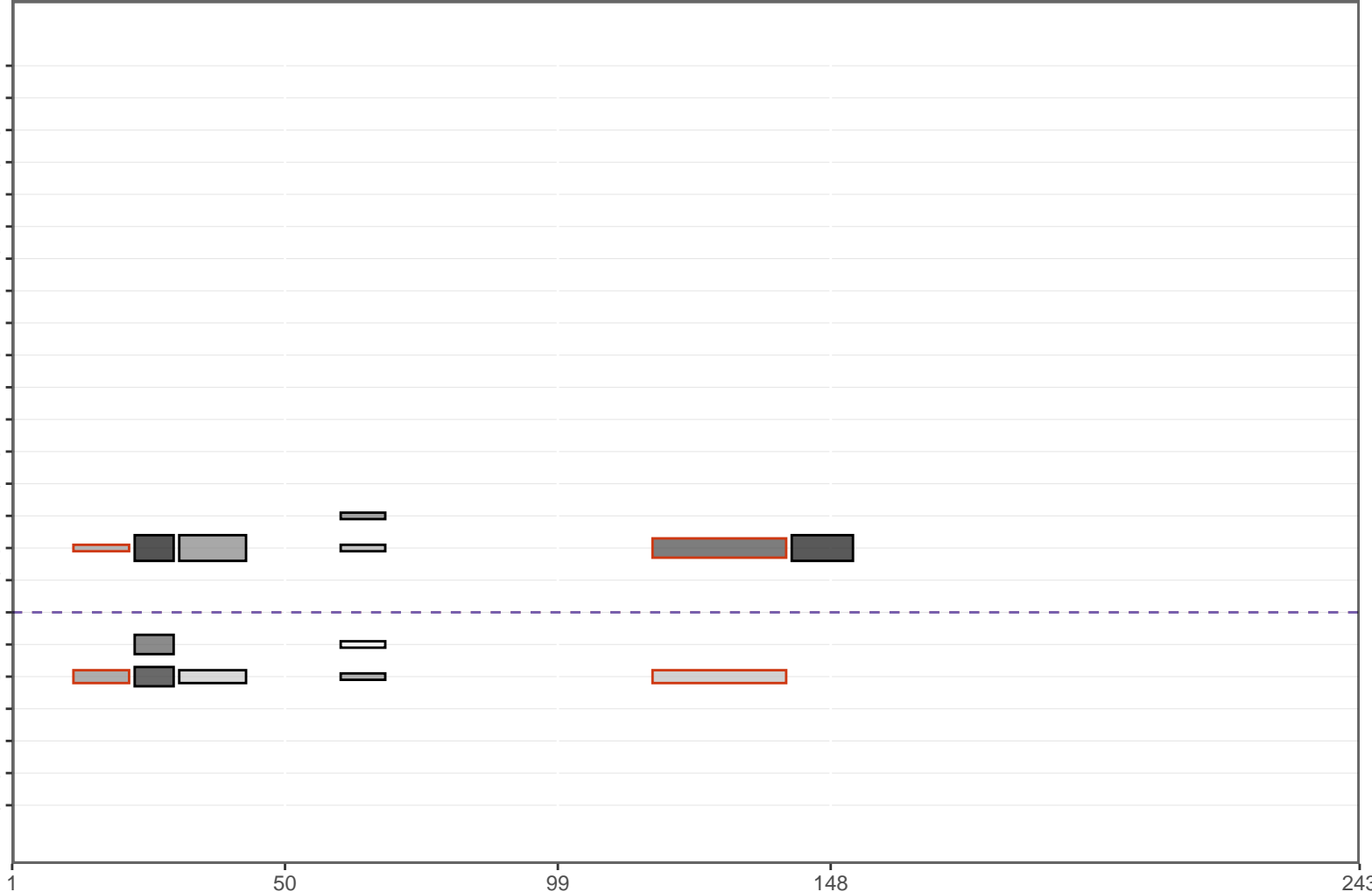
MW indication



Molecular weight



Gel Slice



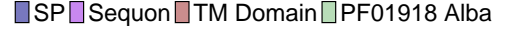
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IANSPGYQAPSQVEVEGKMPQYRNHPQLQGGPPRQTRAVYAGNEDSYGRGRGRGRGRGWSRGGYGNVQENGDSNWRGGGRGGWYDPSSEYGRGGGGGRGYGRGRGMGPRPRRGGGNAI

NbL16g26410.1 pantoate--beta-alanine_ligase-like [MW = 35.73 kDa]

No. of times detected



log(intensity)



Values from



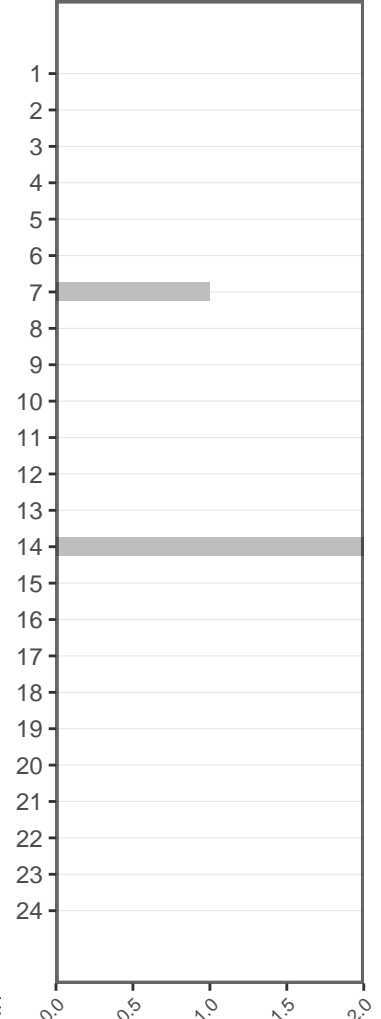
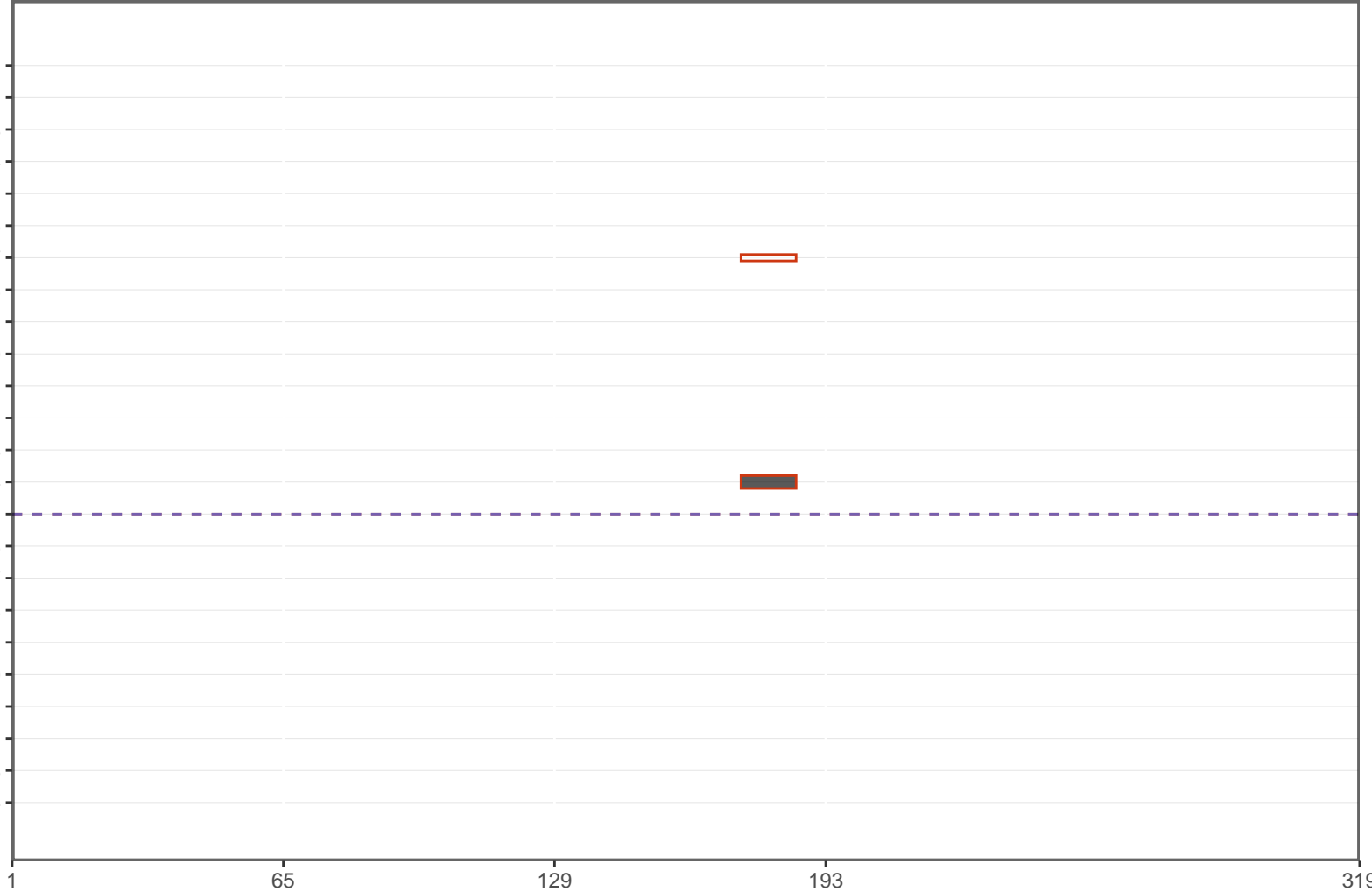
MW indication



Molecular weight

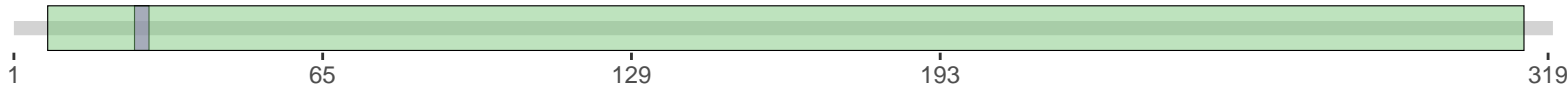


Gel Slice



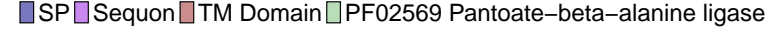
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

WVRVLEKGLCKGRPFVFRGVAIVTKLFLNVEPDIAVFGKKDYGQWRIRQRMVRDLDLGKIVGSDIVREHDLGLAMSSRNVKLLPEDRGKALSIRALSKAKVEAKGHVNGELNSAQTDEAGGRVDVAIEVHEHSLPETIKRPVVFQVAWFQKRVLDNMEIN*

NbL16g26400.1 vesicle-associated_membrane_protein_722 [MW = 24.77 kDa]

No. of times detected



log(intensity)



Values from



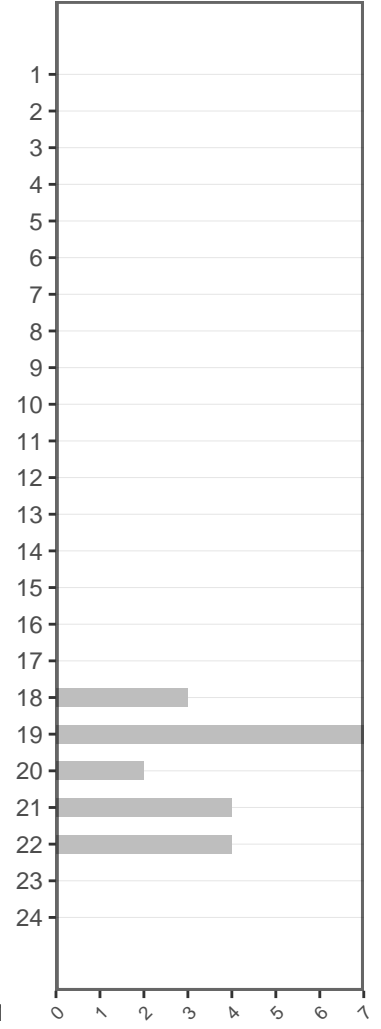
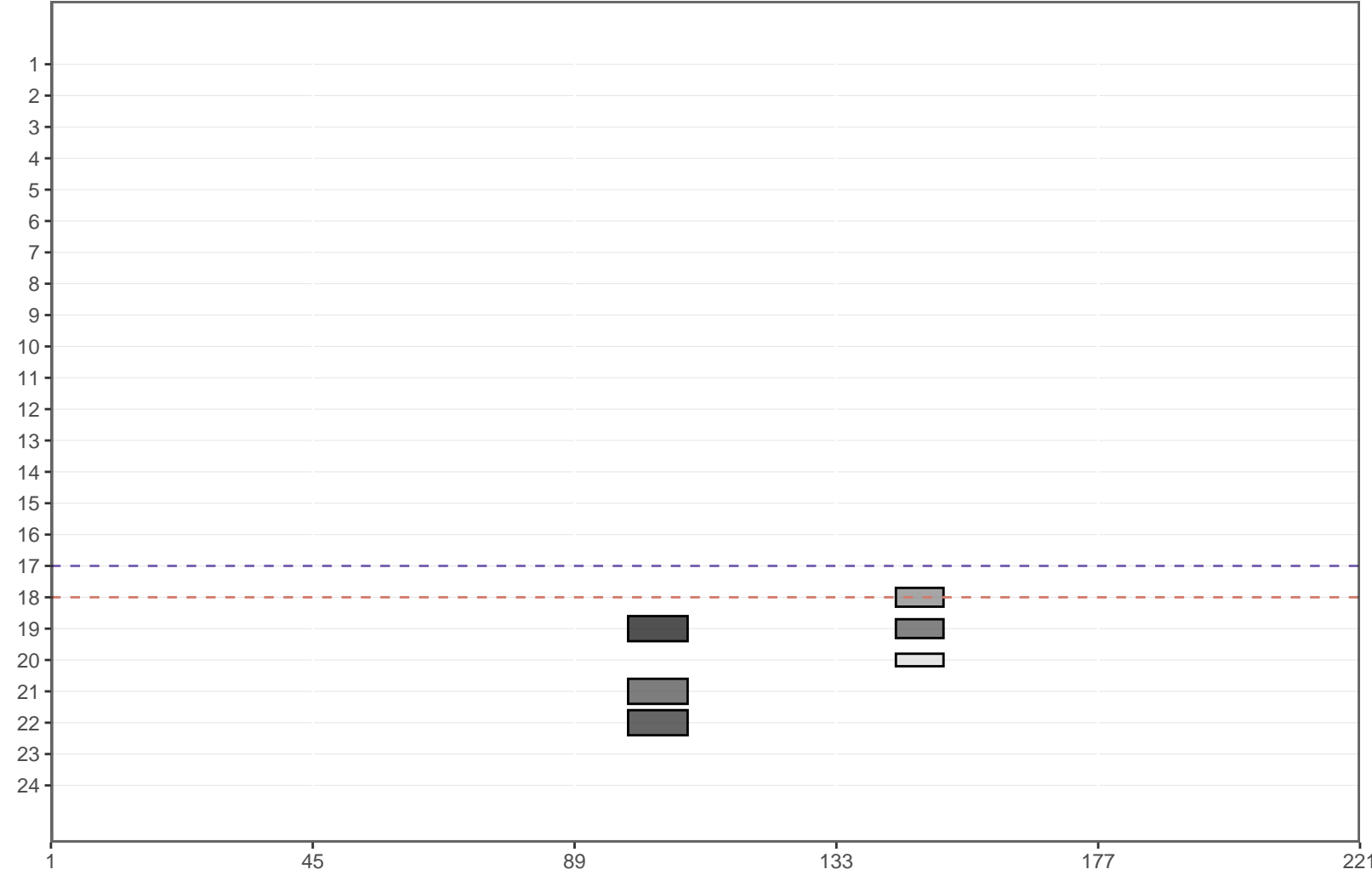
MW indication



Molecular weight

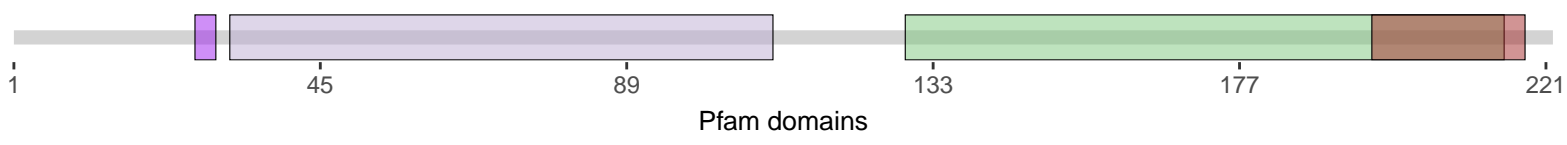


Gel Slice



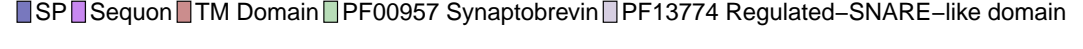
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KAATAVANSLSREFGPKLKEGMQGVYDHPFEIEIKLAKVKAQVSEVGVMMENIEKVLDRGEKELLVKTENLRSGAGDFRTGGTTMRKMAVLMKMKLIVLGHIALILVIVLVOGGFNGHF

NbL16g26330.1 desumoylating_isopeptidase_1-like [MW = 28.82 kDa]

No. of times detected



log(intensity)



Values from



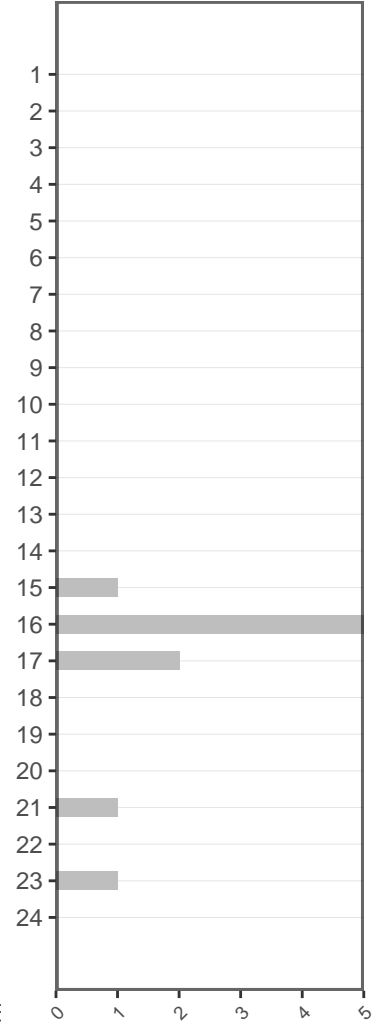
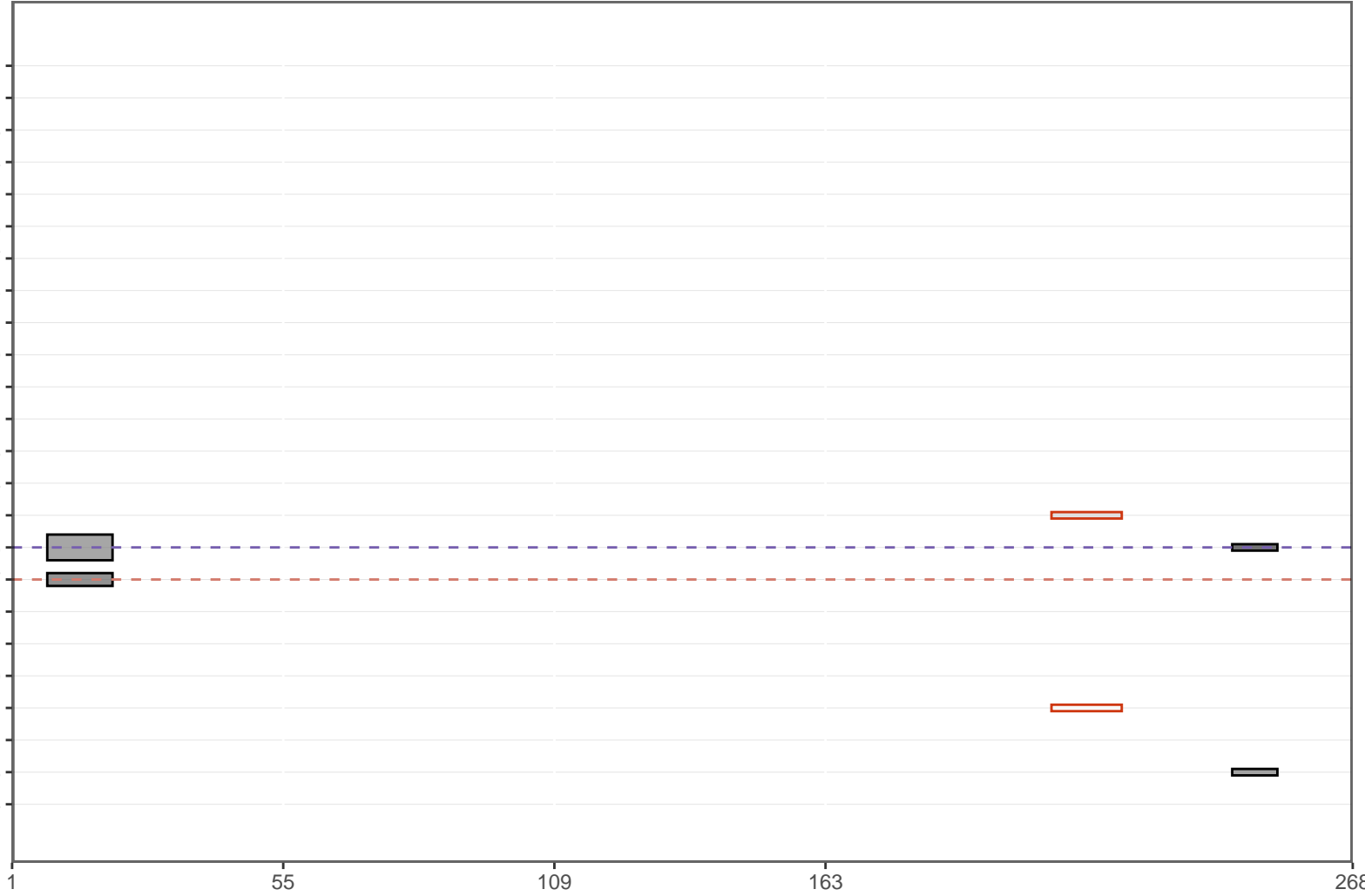
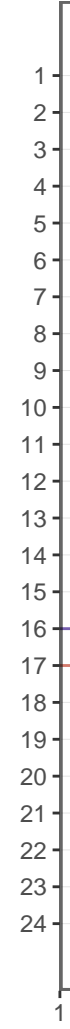
MW indication



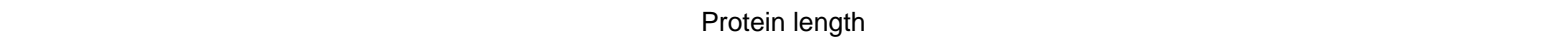
Molecular weight



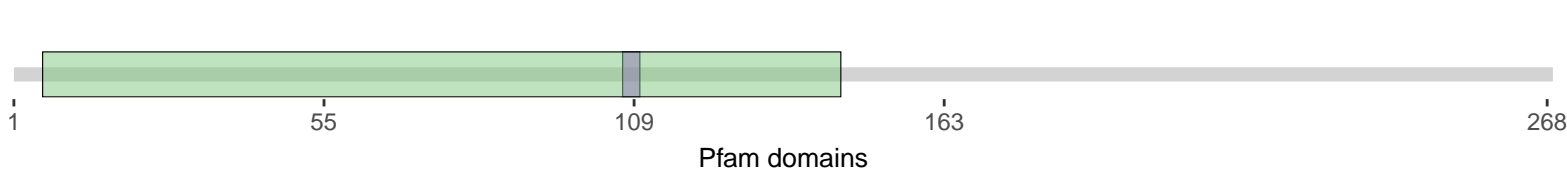
Gel Slice



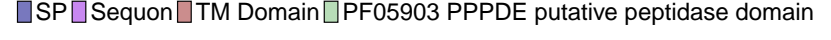
Protein length



Pfam domains



Pfam Description



Protein sequence:

MDLNLNLEVMNLSFMGALMPMIGQLESTRANAVGAPQDFRPFVVASAGQMVSQKSGVQGEKSGSVYKPKAKREKPFVGEKPTANTAVSDPLGDSRKRKQGEITREFAIMATGTLRASEAAALATKRMGRVGHHTAALN

NbL16g26250.1 cytochrome_b5 [MW = 14.98 kDa]

No. of times detected



log(intensity)



Values from



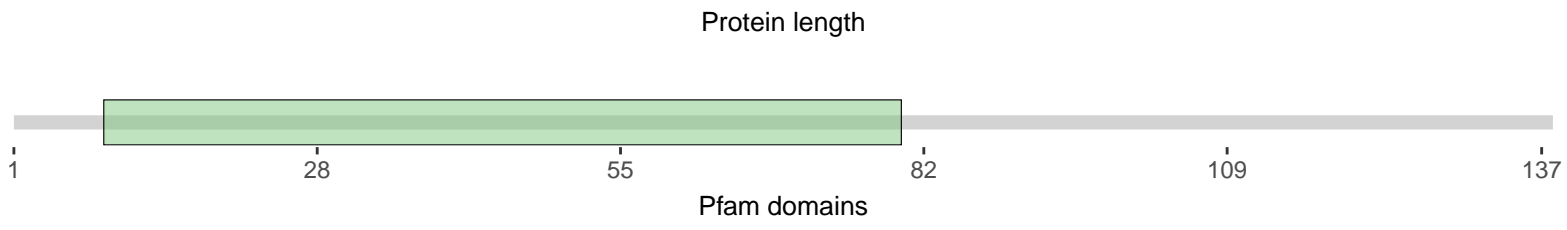
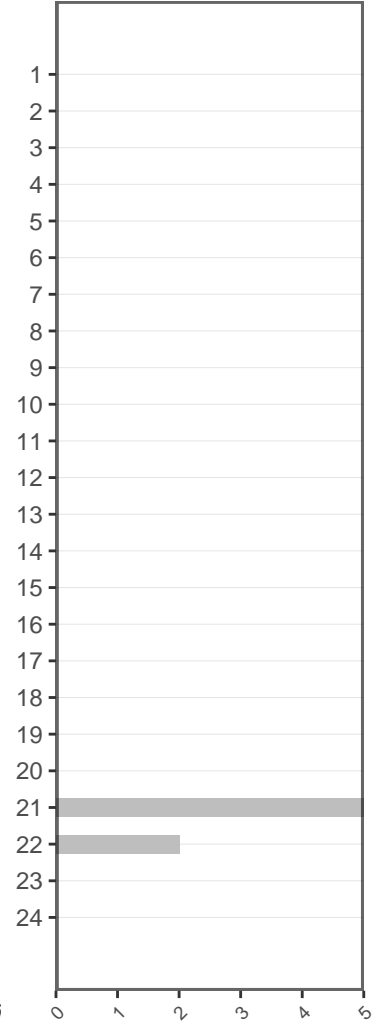
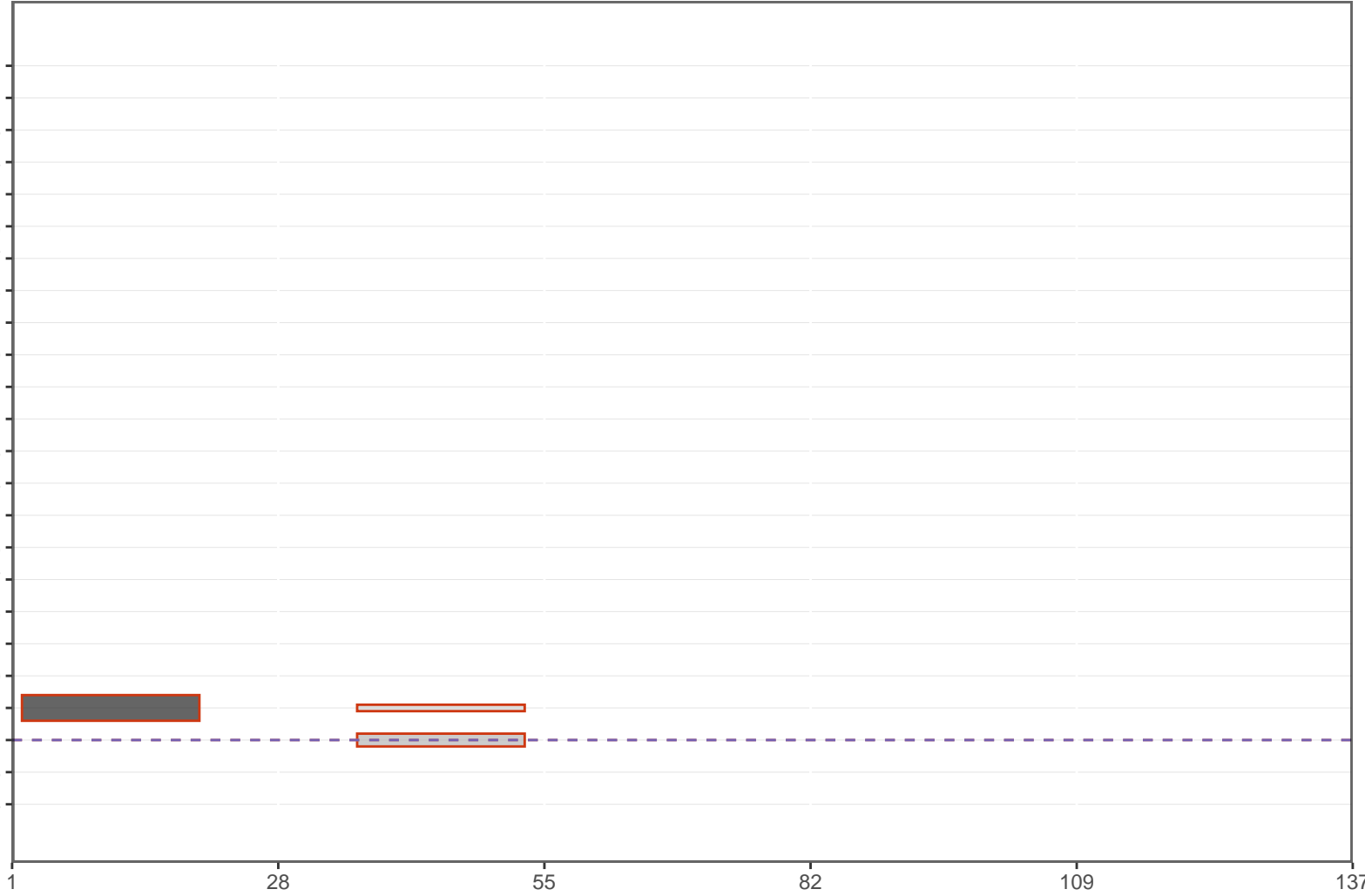
MW indication



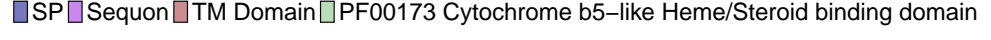
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

DATDDFEDVGHSSSARAMLDEYYVGDIDGATPTKTKYTPNNGPHVNDKTSFEVWLLGLVPLILGWAFGRFYKGSAA

NbL16g25980.1 putative_G3BP-like_protein [MW = 50.95 kDa]

No. of times detected



log(intensity)



Values from



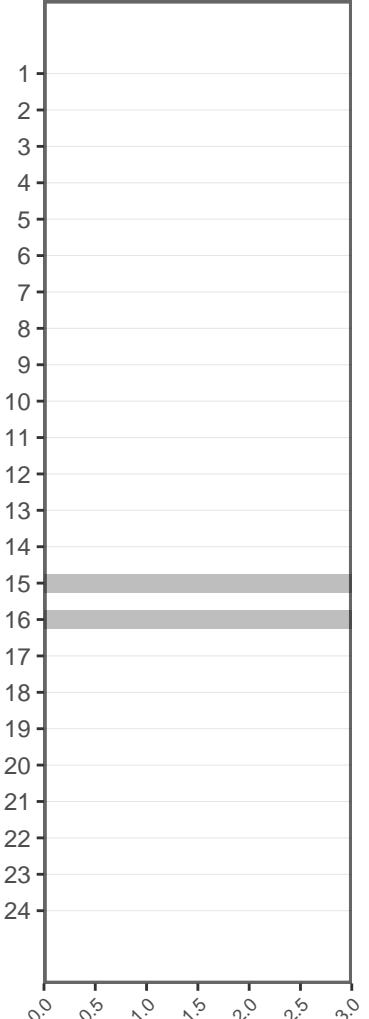
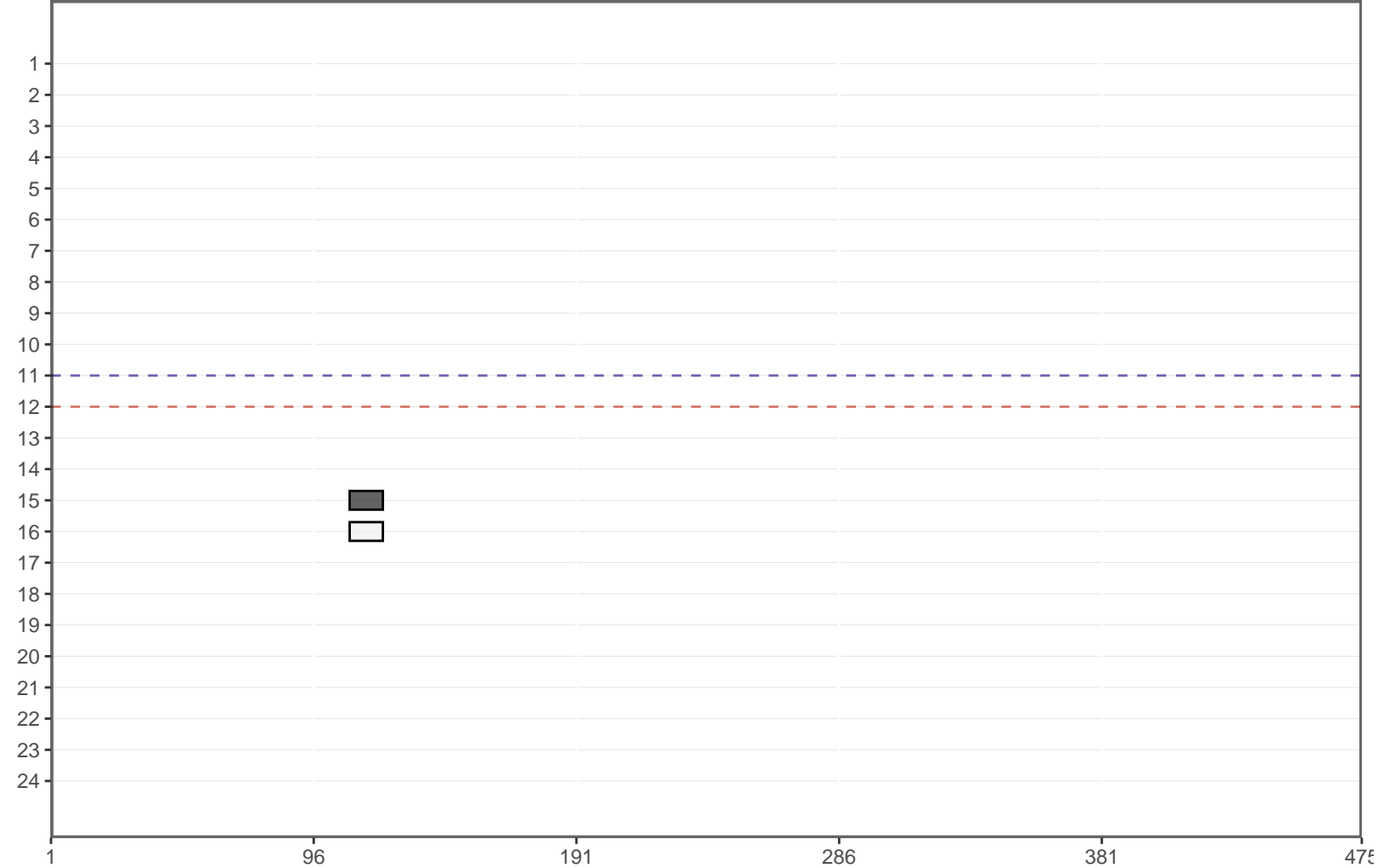
MW indication



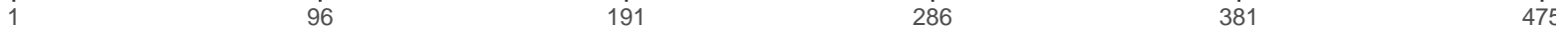
Molecular weight



Gel Slice



Protein length

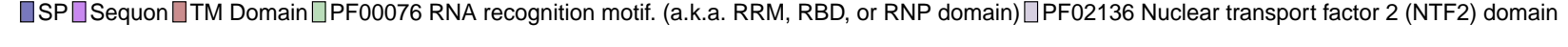


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IPKKSYSASIVMLIKESAITFSPFPAPRKRIVKPKVGMGSRPAAPADNPVLSSDFDNNVNWGEAGEADGYSYIKGLFMSATAAMLEDFRKFQPKNGGKIQVRSNRHGFCDFGFVEFEVLAQKVAIEASPLVIGGRQAAVEENKSTNSRGNTRPRYPGGRGGGFRNDGGRGRGNVGGGRGYSRGGDFNKRSEFNKNGRNGGSANRGGDGYLRTDNMGGNSGRMNHGGGMPNGAAKNMPRVSATV

NbL16g25960.1 anthocyanidin_3-O-glucosyltransferase [MW = 52.54 kDa]

No. of times detected



log(intensity)



Values from



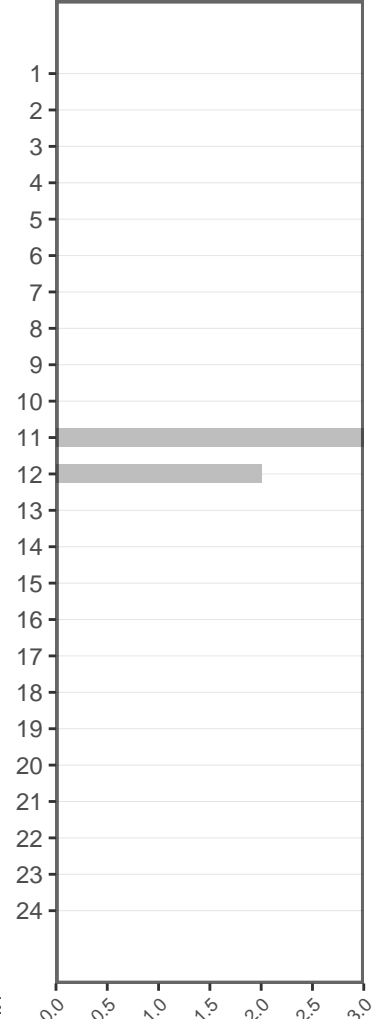
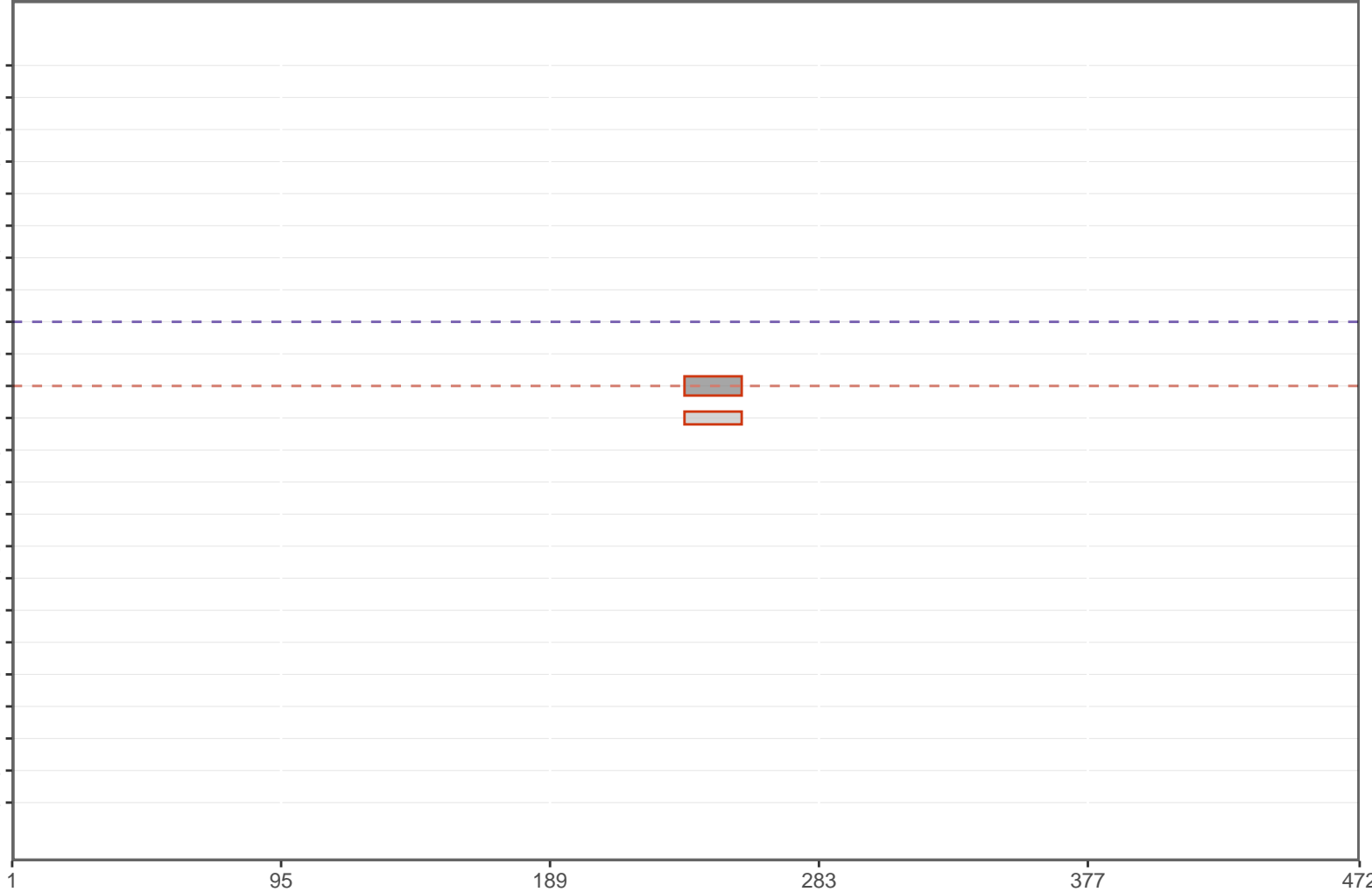
MW indication



Molecular weight



Gel Slice



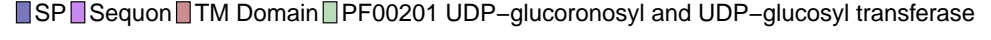
Protein length

Peptide counts over 4 repeats



Pfam domains

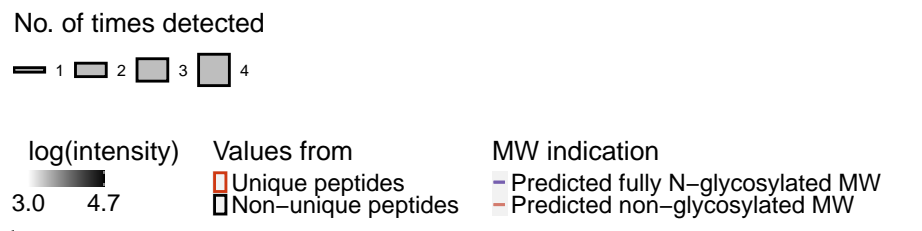
Pfam Description



Protein sequence:

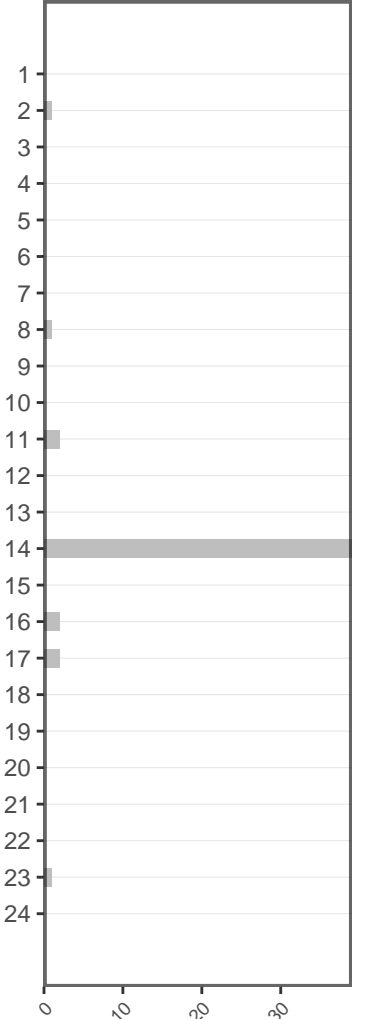
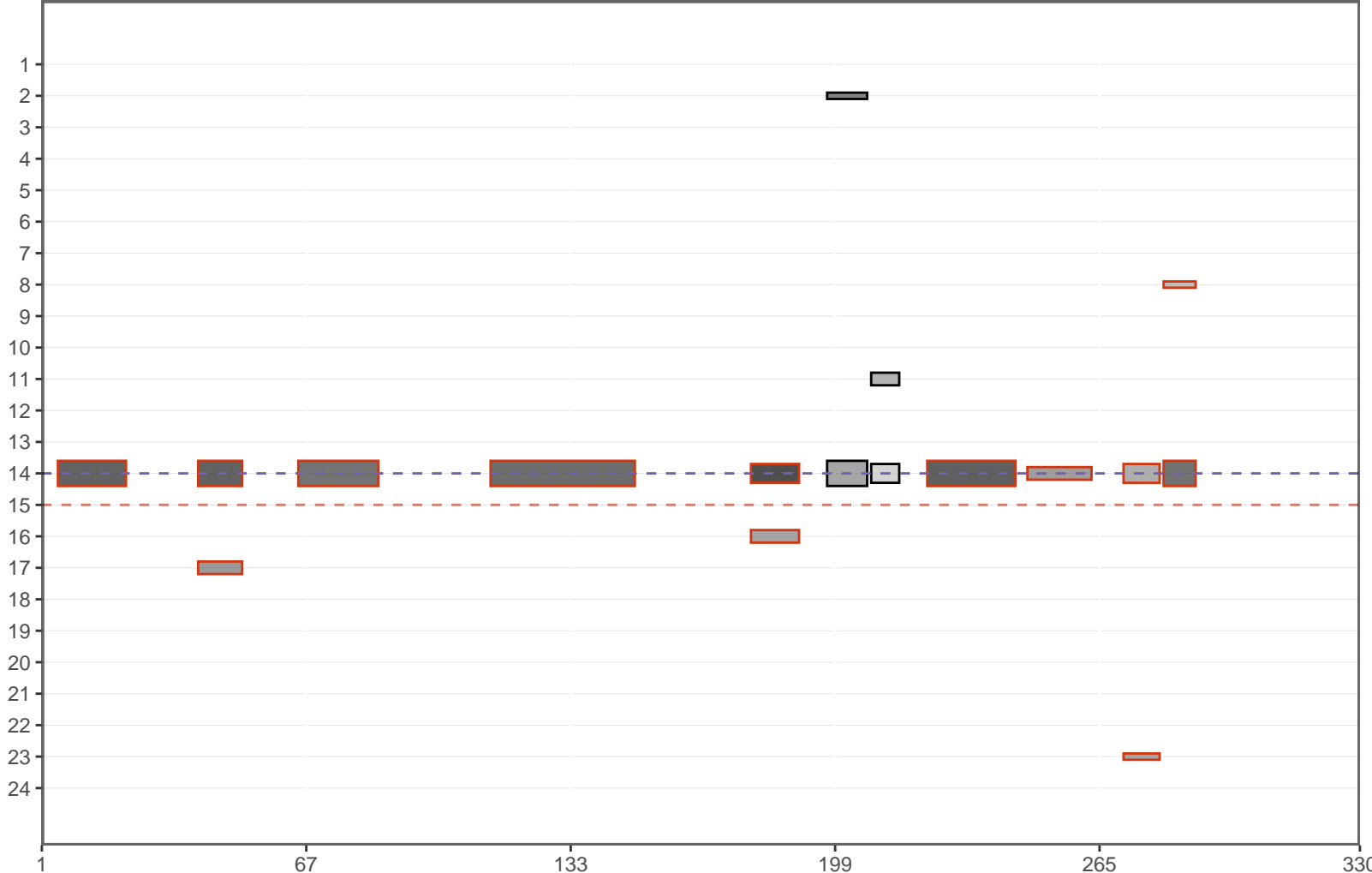
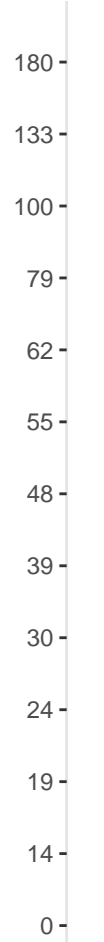
IMEGPIYEVYKADFNKPVFLVGPVDPDPGKLEERWBSGLNFKFAGTVYDGFSGSETFLKDEQIKELALGLEGTALPFFLILNFRANVNFVVELNRLPEGLFRVYDKGIHSGWVGGQHLAHSVGGVYVGHAGFSVIEALVDCQVVMIPKGGDFLNALVSGDMKAGVEVNRREDDGYYGKEDKEAVEMVMVEIDKPGELIRENGKWKKEFLLNKDIQCKFIEDLVGEMMAMTKVGS77

NbL16g25940.1 putative_quinone-oxidoreductase_homolog_chloroplasmic [MW = 34.65 kDa]



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:

DGSGPRKQNLVTAASGGVGHVAVQLGNTNVTATGGARNFDVYKLGDAEVLDKHTPEGAALKSPSGGKYDAVHCTTGIPWTFEPNLGAKGKVIDLTPGPSAMMTYAVKGLTFSKKQLVPLLLIPKKELDLVRRLVKEGLKKTVIDSKHPLSKAEDAWRSRIGDGHATGKIVP

NbL16g25880.1 peptidyl-prolyl_cis-trans_isomerase_FKBP15-1-like [MW = 21.89 kDa]

No. of times detected



log(intensity)



Values from



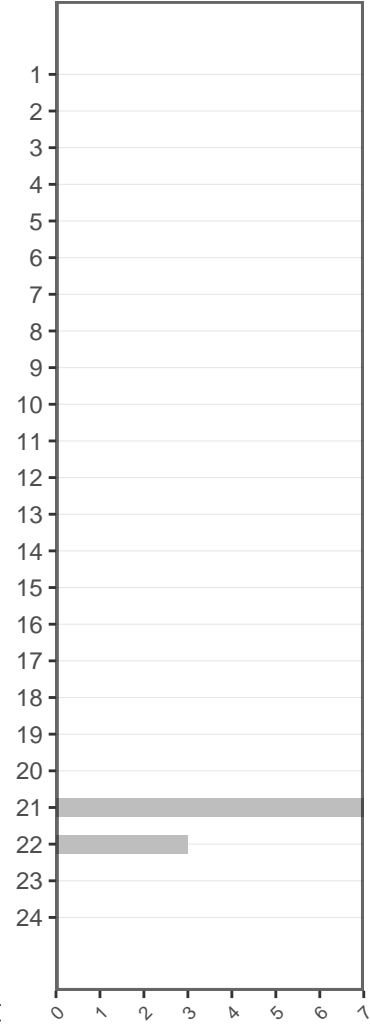
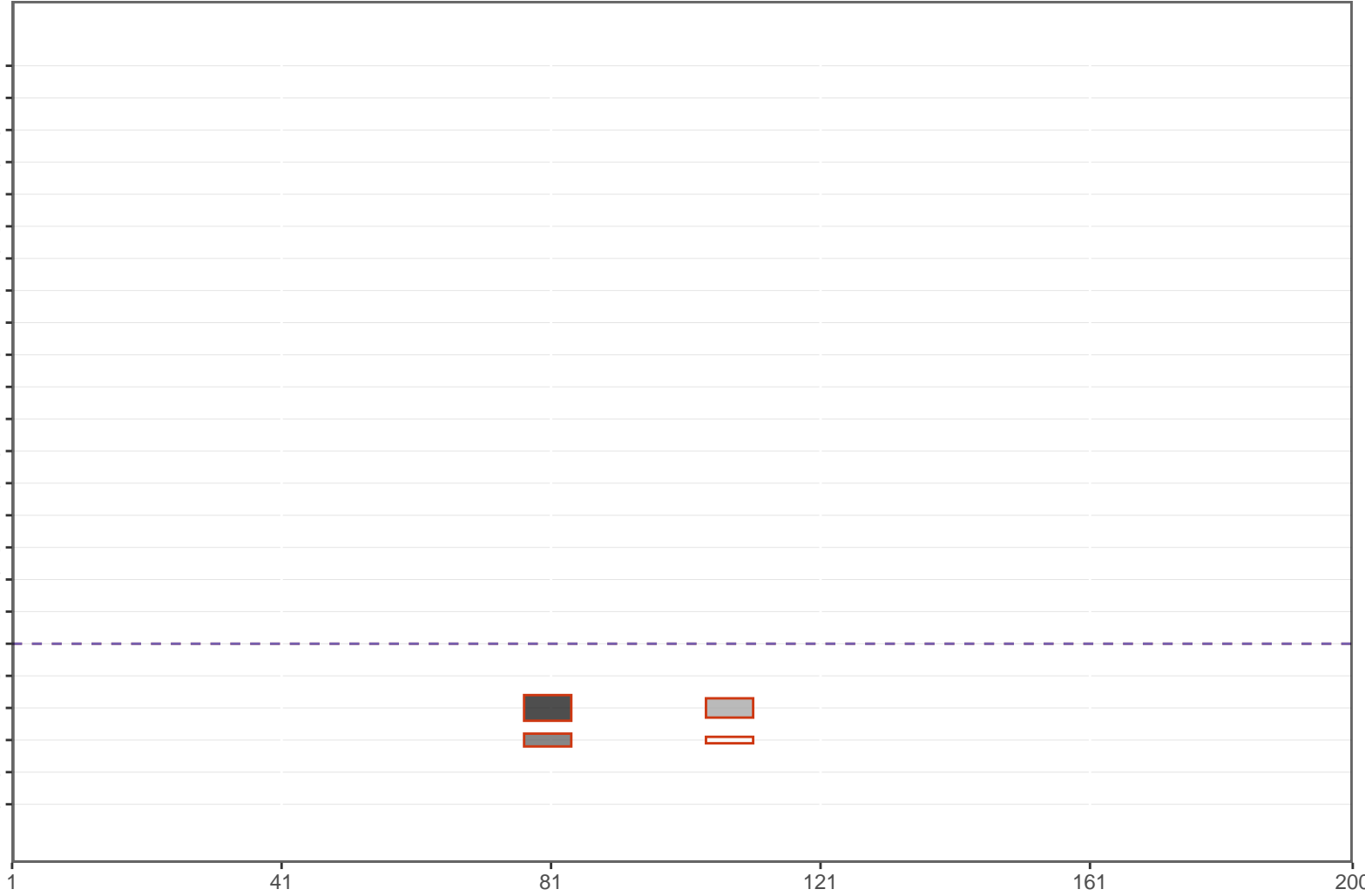
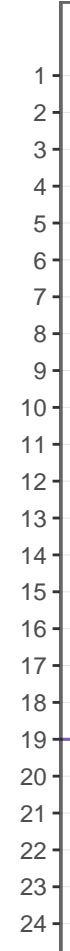
MW indication



Molecular weight

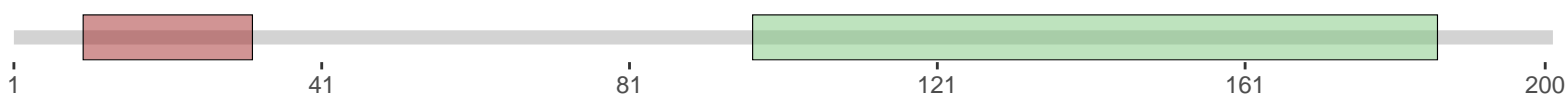


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KPKSCDLKAHKGRVSVHYSGALTDGTVFDSBYERNDRPEFELGSGGVKIGWDGDLGMCVGENRKLKIPAKLGYGEGSPFKPGGATLVFDTELVAWNGKKAADSEI

NbL16g25870.1 peptidyl-prolyl_cis-trans_isomerase_FKBP62-like [MW = 63.81 kDa]

No. of times detected



log(intensity)



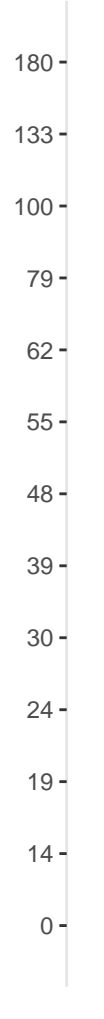
Values from



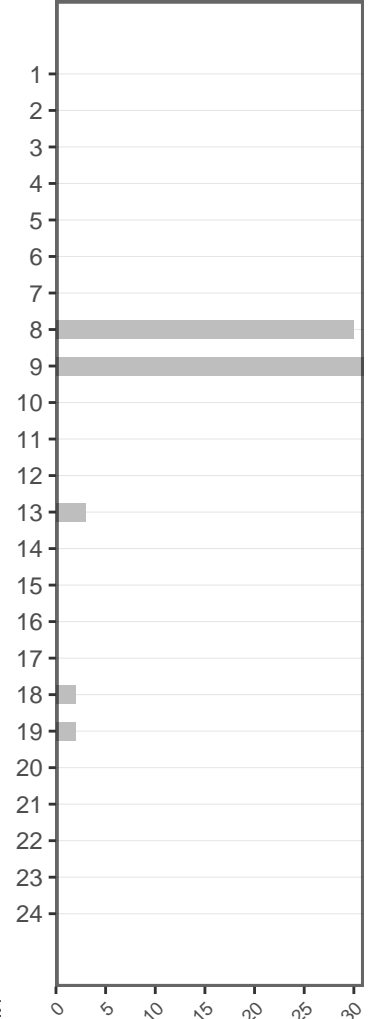
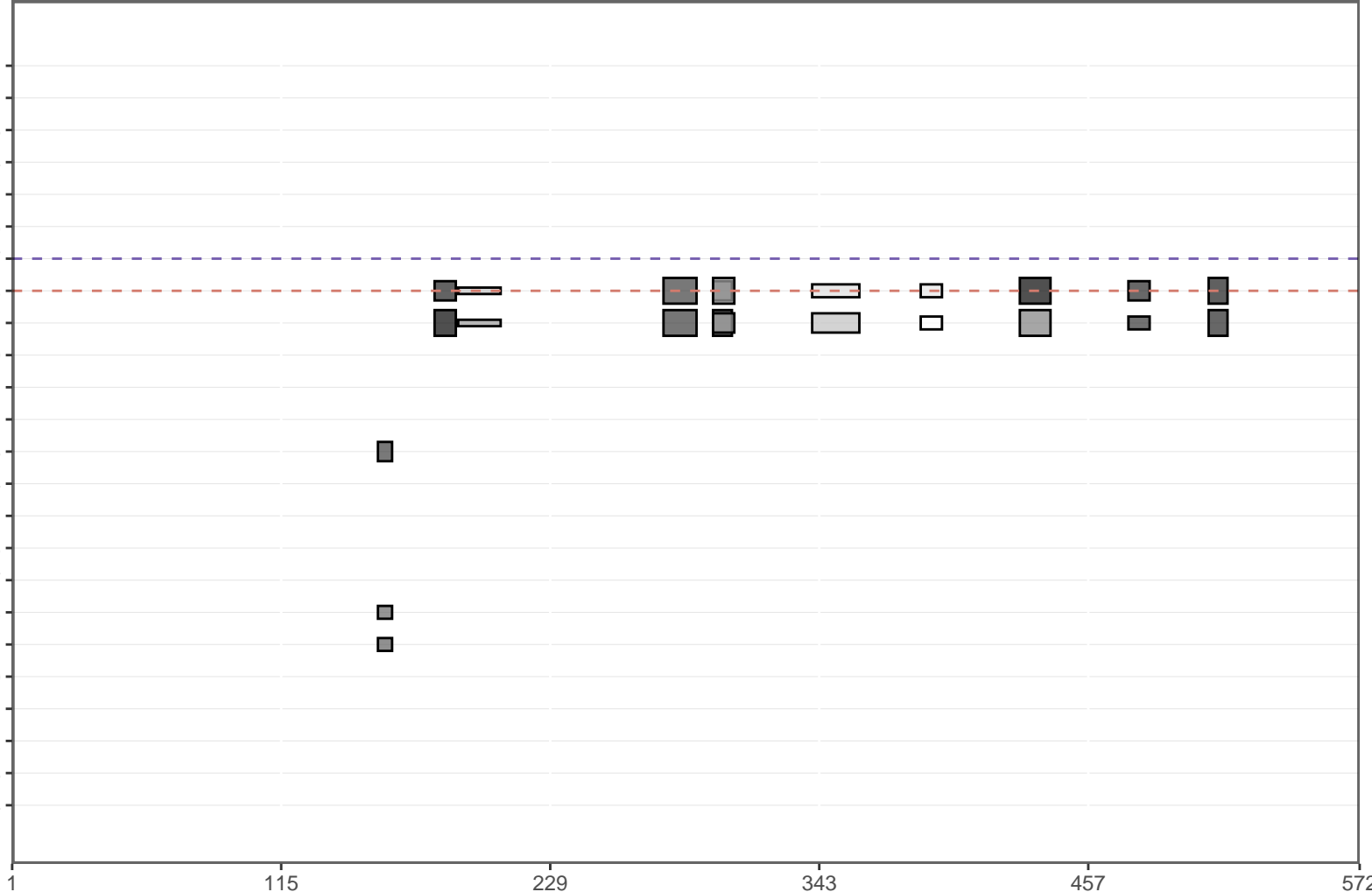
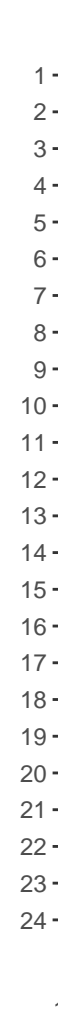
MW indication



Molecular weight

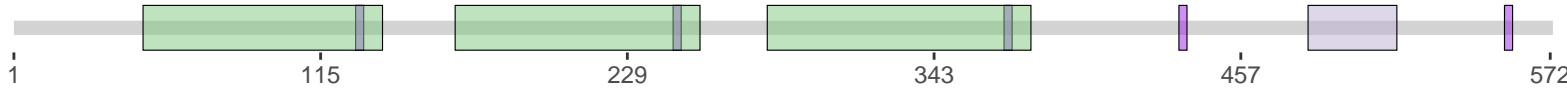


Gel Slice



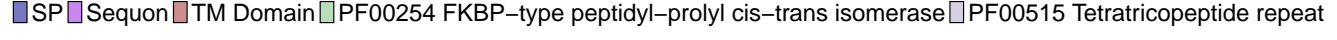
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

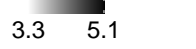
QLKEGEGYKFNIEGAMVVKLKLKGLGDSVFLKGGHDGNEEDDLFEFMTDEEGVVDGLDRAVMSMKKGEVALLHIAPEYAFQSSSEKQDGLVPPNSTVYVEVLFVFKKEGSDMTPEKIEAAGKKKKEGNALFKAGKYARASKRYEKAAKFIEYDTNFSEEEKKQKALKITGNLNNAAKGLKLVKQGAELGTVKLETETSNKALYRRAGAVINMVFDFLAEFDKKALEIDPARRKRVKLEYKALKKEKRVRYNRKDKAKFYGNMFSKLNKLDVNSNYSASKEPDM

NbL16g25810.1 adenylylsulfatase_HINT3 [MW = 22.35 kDa]

No. of times detected



log(intensity)



Values from



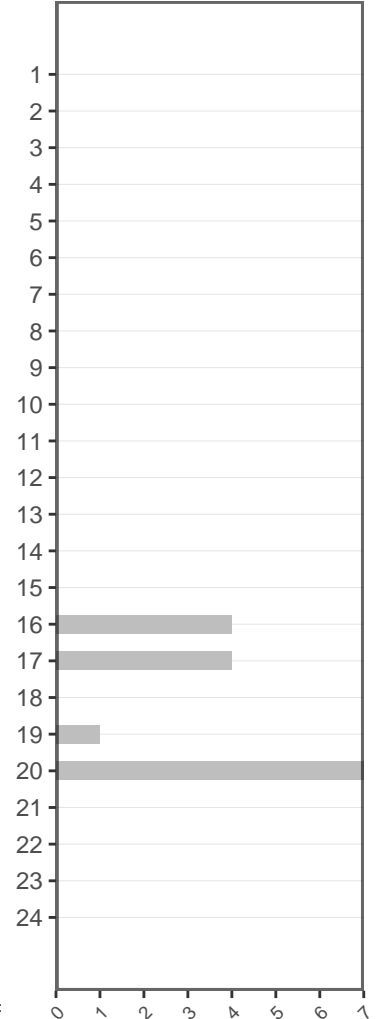
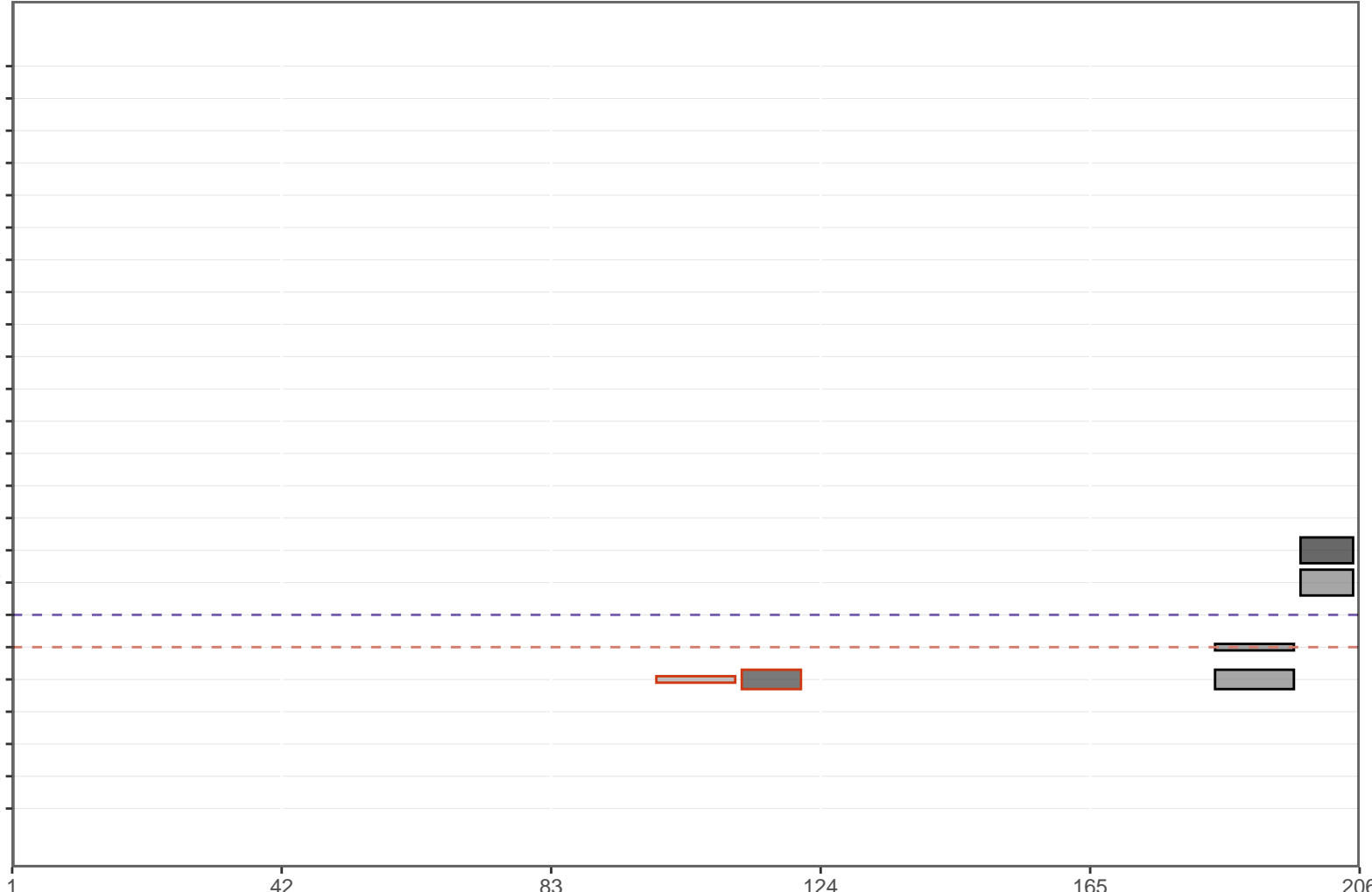
MW indication



Molecular weight



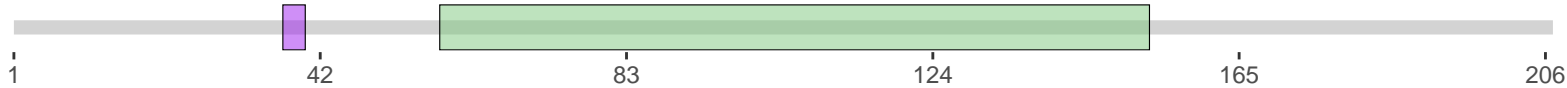
Gel Slice



Peptide counts over 4 repeats

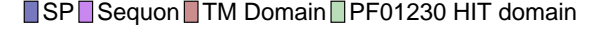


Protein length



Pfam domains

Pfam Description



Protein sequence:

KCHFSSLKETPPSWAAMFQKVPWISAVKATGVDSEFNLLVNGEAAAGVVFHTHIIPKASDGLWASESLRRRPLKLDGEAAKLGENRENLELGNIEDKGGVSDLGN

NbL16g25790.1 cytochrome_b561_and_DOMON_domain-containing_protein_At3g25290-like [MW - SP = 23.39 kDa]

No. of times detected



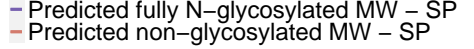
log(intensity)



Values from



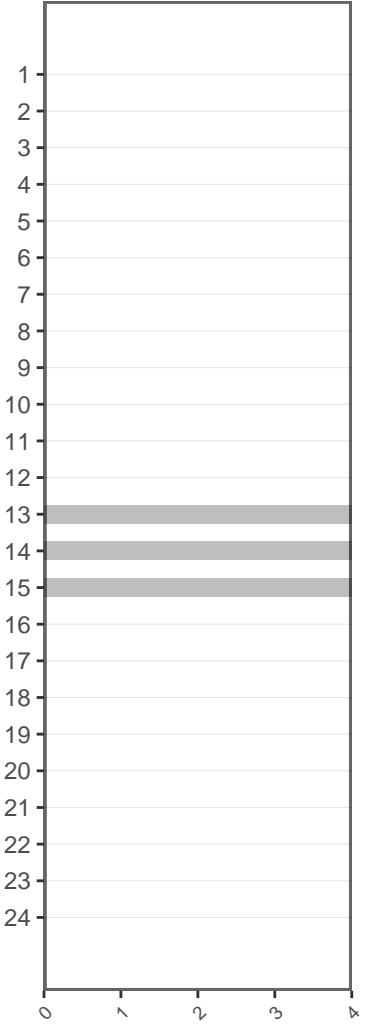
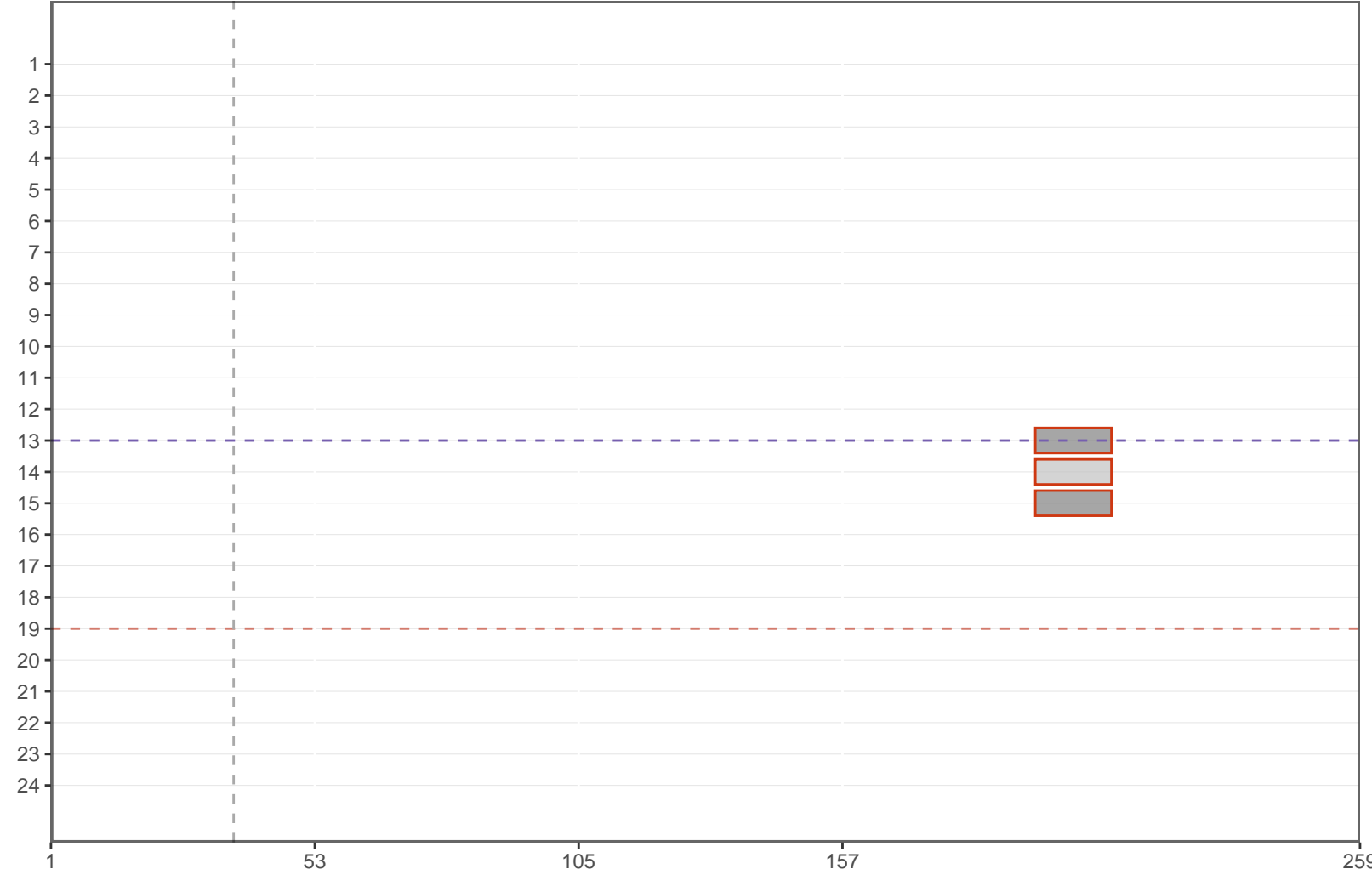
MW indication



Molecular weight



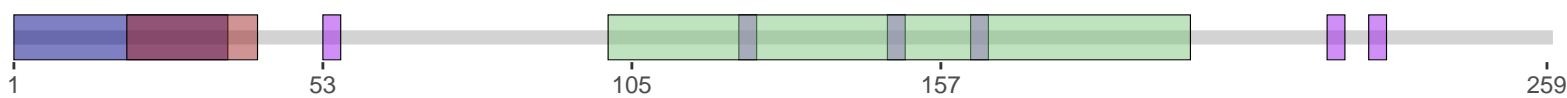
Gel Slice



Protein length

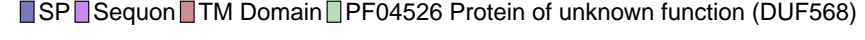


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VVYKTYNLTSYKSTFEKLLYVLDGKAESNGTMMKIFATLELPENTTTVNGVWGVGFVNDGKPVVHKFDTENLASKATLDLAATSSAGEGNKAGSSASNSNS650SGNETGSSRIKSENGIFAFLLGVLLQLL

NbL16g25770.1 cytochrome_b561_and_DOMON_domain-containing_protein_At3g25290-like [MW - SP = 39.66 kDa]

No. of times detected



log(intensity)



Values from



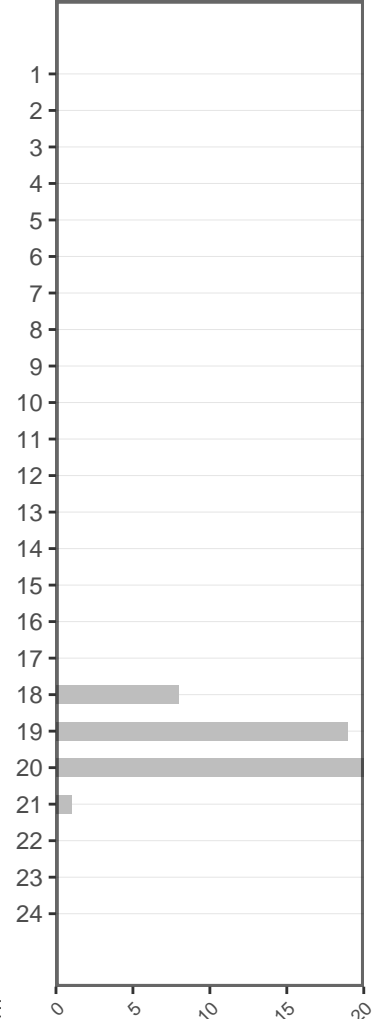
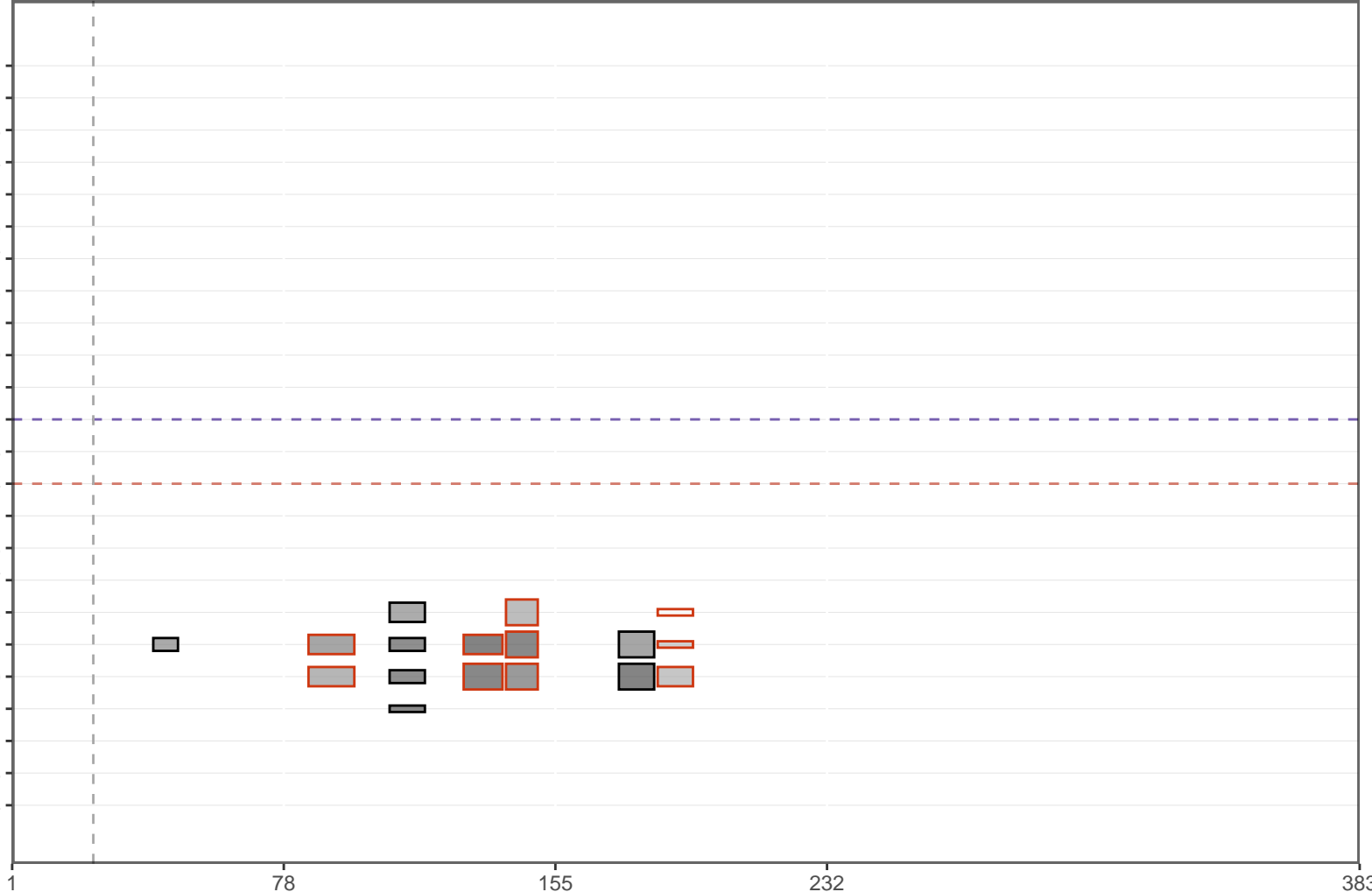
MW indication



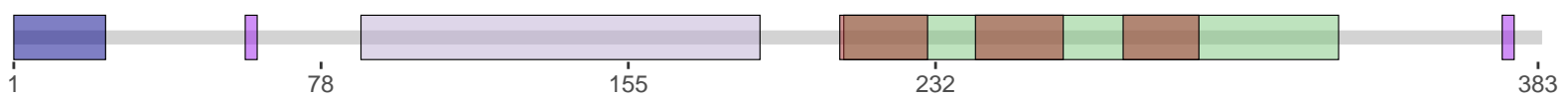
Molecular weight



Gel Slice

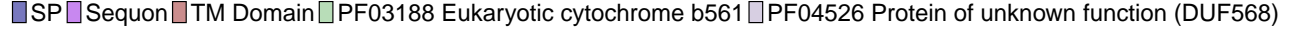


Protein length



Pfam domains

Pfam Description



Protein sequence:

FDPAFLNSKGTLDLVSGSEKTAASGNKWRKRNHGLNAISWGLFPIGHIAHYMRFTKSGADPAWFWLHVSDGCSAVHIGVAGWATGLKLGSESKGITYDTHRNIAGLFSFATLQVTFALLRPNKDKYRFYVWNYHHSVGVFTMLLSLNLVFKGLDILDPAKWRBAYKGLVVGAAVLLVETVWVWVLRKRNKSTKPYDGI

NbL16g25750.1 ras-related_protein_RABA5b-like [MW = 23.87 kDa]

No. of times detected



log(intensity)



Values from



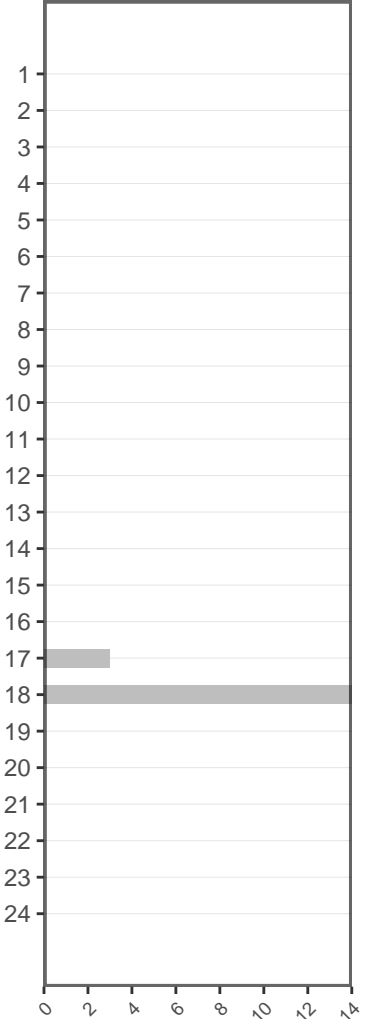
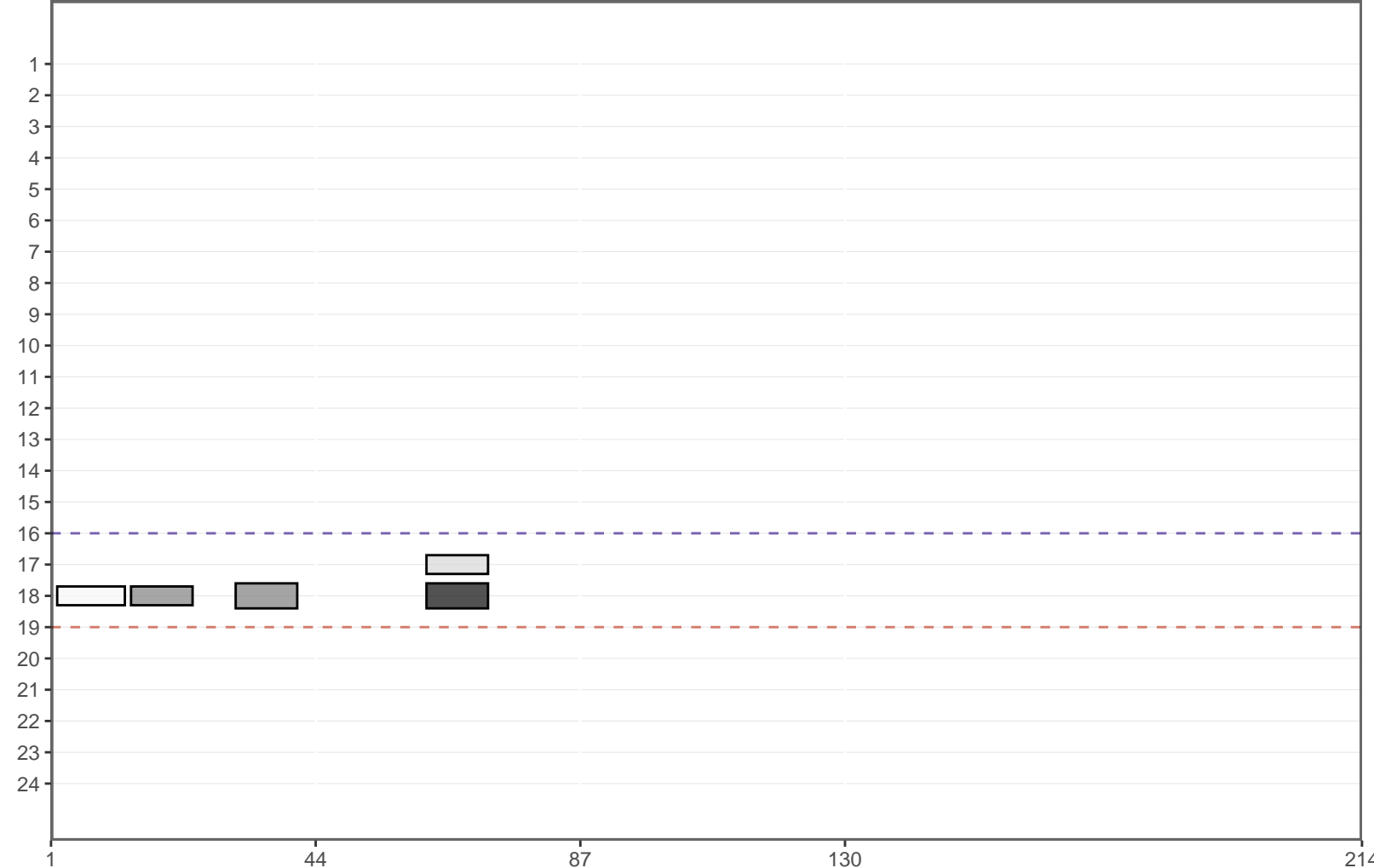
MW indication



Molecular weight

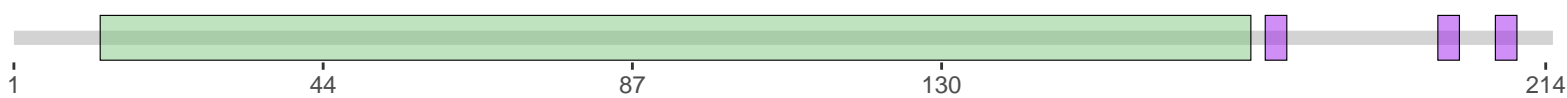


Gel Slice



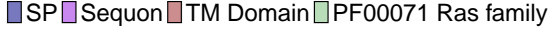
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RKTTFTENIKRIVLDELNTHGDTTFVARMVGNKGDLENIRDVSVEEGKNAEEEGGLFFIETSDLNNTAFEVVIREIYKNLSRKLVLNEDSVYKAEISVNRVSLANGTDMKQNASGGSR

NbL16g25740.1 cysteine-rich_repeat_secretory_protein_55-like [MW - SP = 27.18 kDa]

No. of times detected



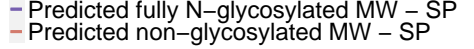
log(intensity)



Values from



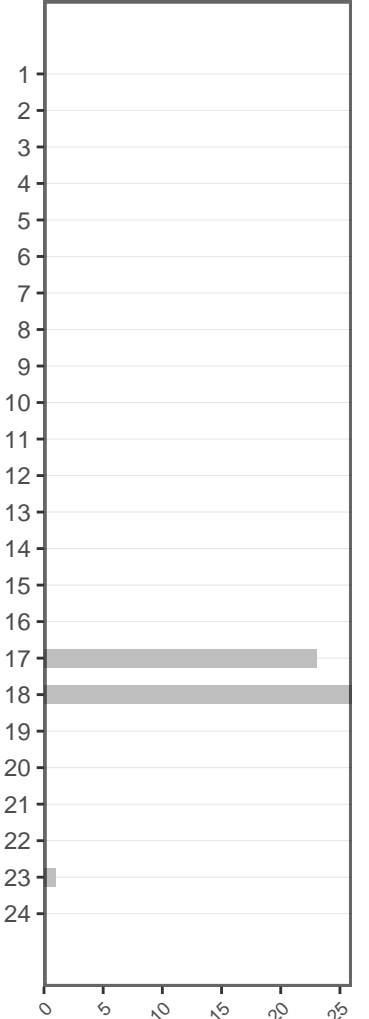
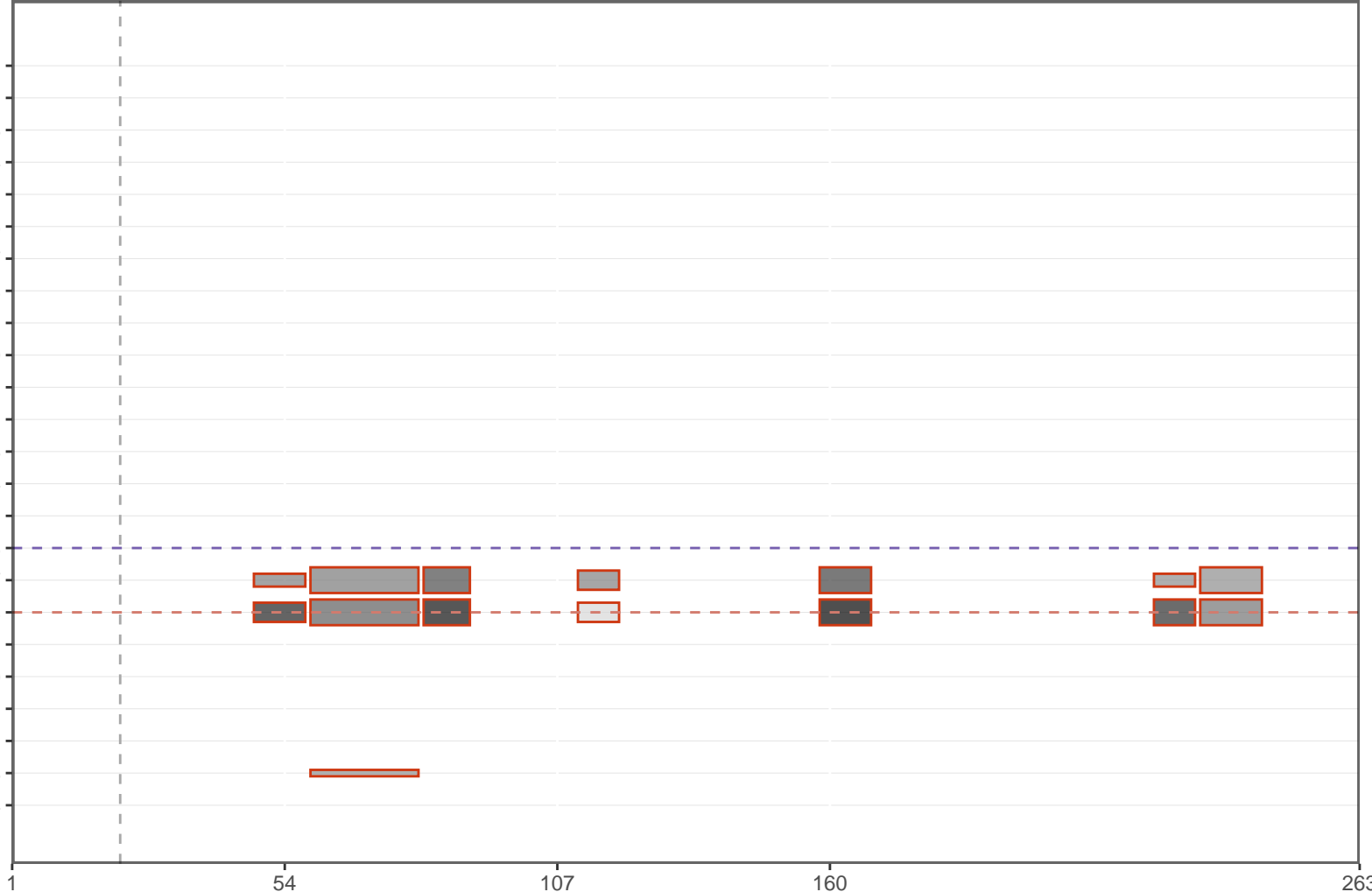
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

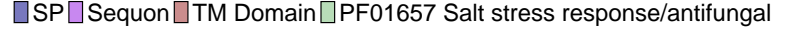
Protein length



Pfam domains



Pfam Description



Protein sequence:

LRVNTXNFLGGVETAPGIFVYVDFVSDTDFKFKKLVKLNQITAEATVPKNKGKGGKSGILSPFLVIALMDGTRDIPEDCAAGLIAVGNFPTQLNRRGRILVNSGIVRYELVPPFFPLDPKELANVSMNYYTMKISRPI

No. of times detected



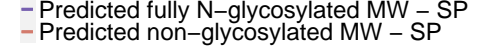
log(intensity)



Values from



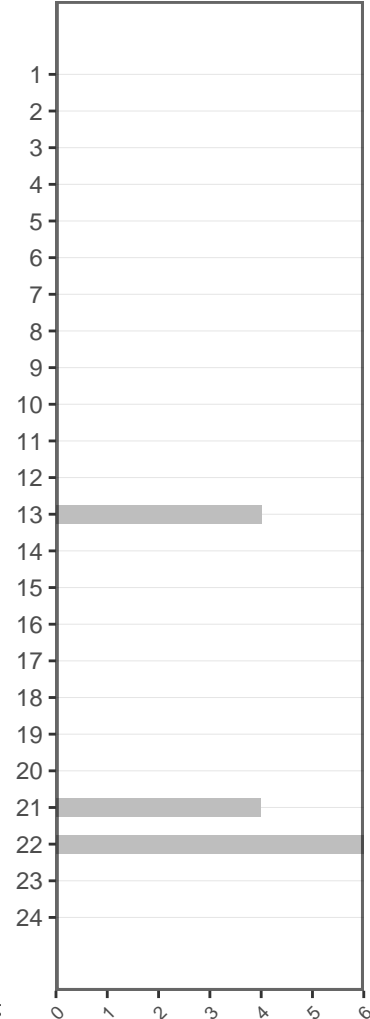
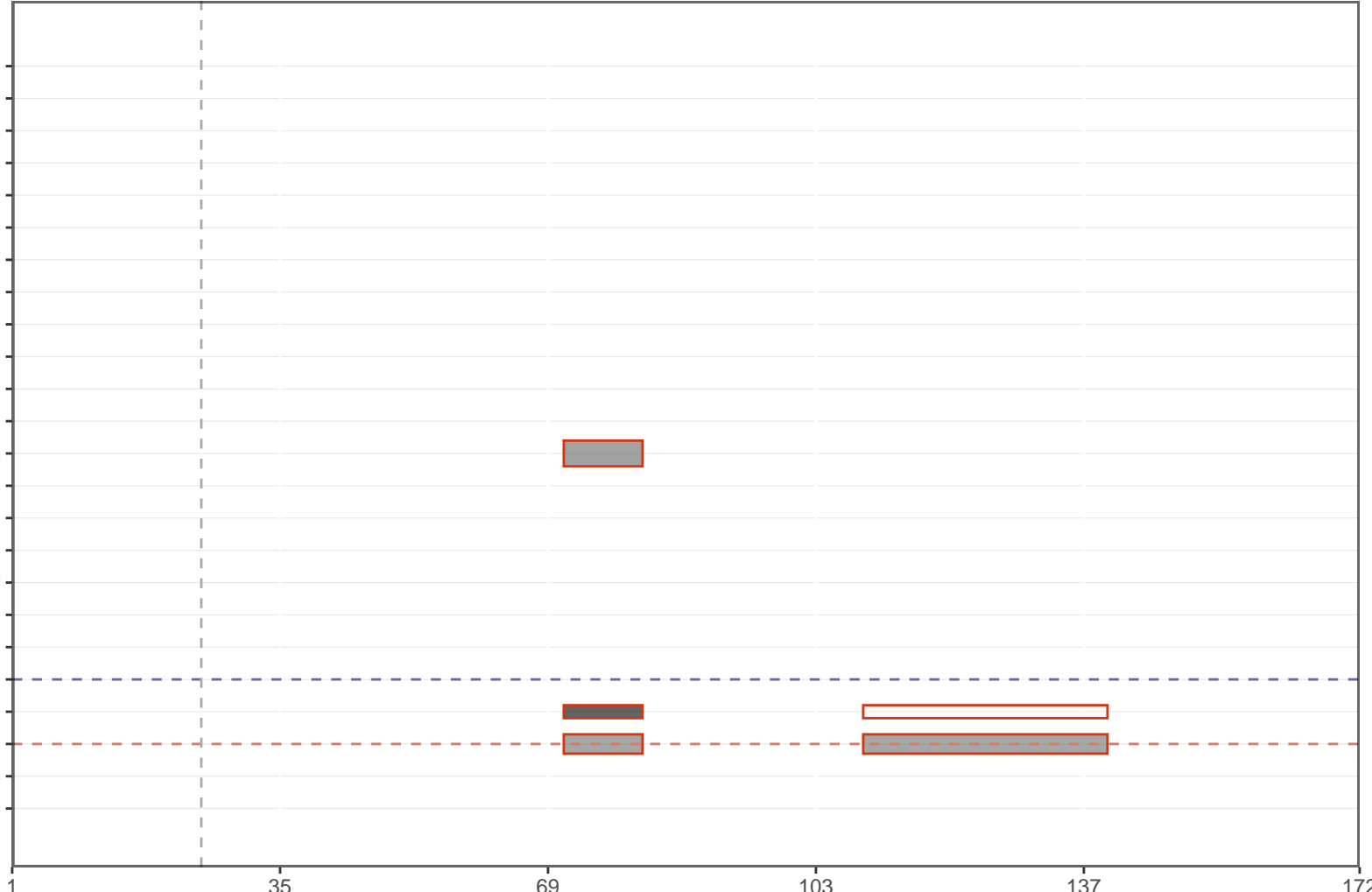
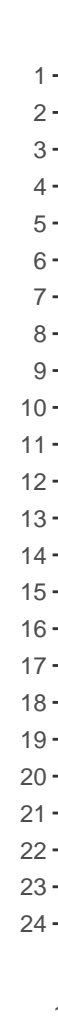
MW indication



Molecular weight



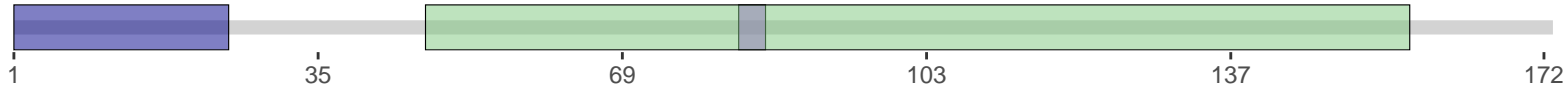
Gel Slice



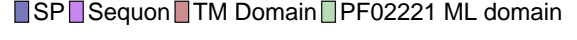
Protein length



Pfam domains



Pfam Description



Protein sequence:

FSISASTGNLITGGALVIVNLYLFFVHVEADLDKETSQPSAGDFLISHGDELPGFTPPGCVTLTMMVDDKNGQLSGISGFGSIFAEISGALAADE

NbL16g25650.1 33_kDa_ribonucleoprotein_chloroplastic [MW = 35.4 kDa]

No. of times detected



log(intensity)



Values from



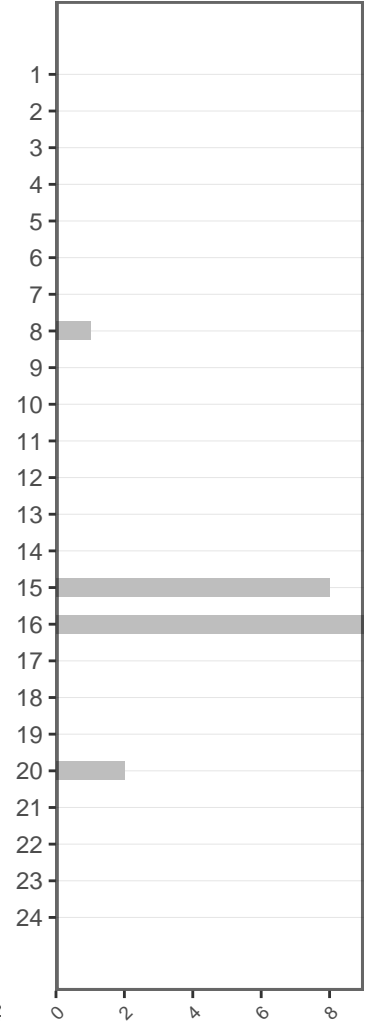
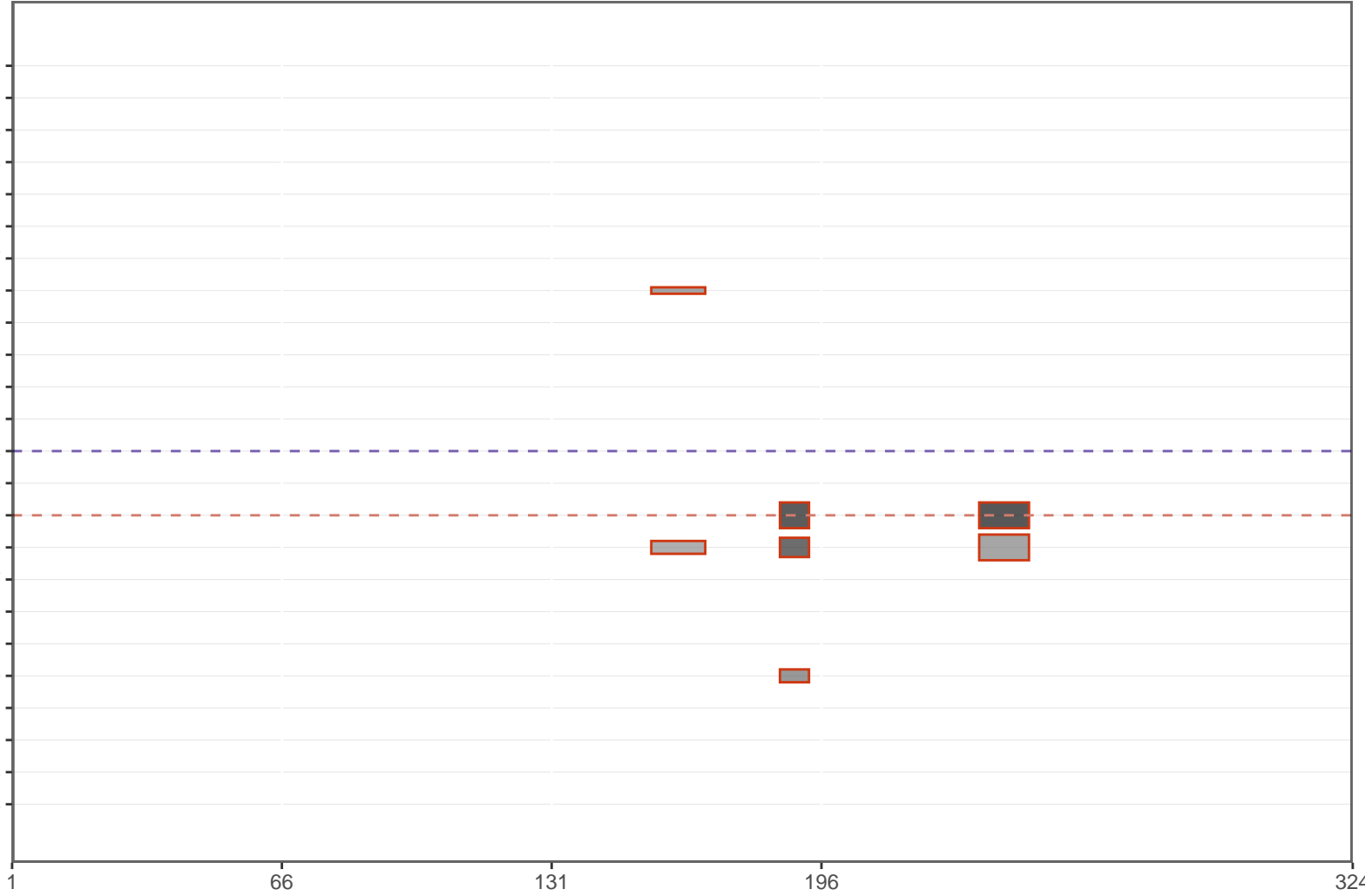
MW indication



Molecular weight

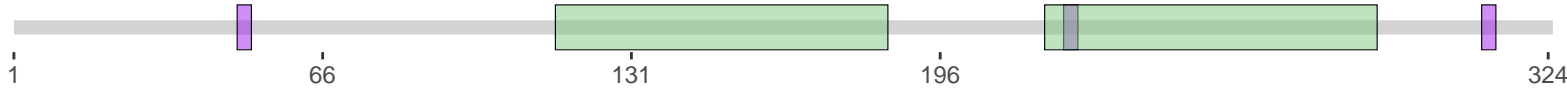


Gel Slice



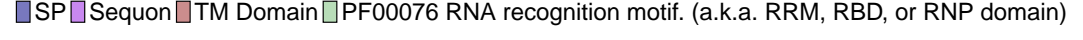
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SRGFAPVTMGSYEEAREAIRLFDGSGVGGRTKVKWPFPEVPRGGEREVMBKIRSTYGGFVDSPHKLVVNLISWALTDGGGLRDAFADQPGFMSAKVHYDRSGSRGRGFGFTTFSBAEAMESALDTMNEVELEGRLRLNWAGGKAPLSSPPVWETSPENDSENSELLSLSLSP

NbL16g25540.1 epoxide_hydrolase_3 [MW = 44.25 kDa]

No. of times detected



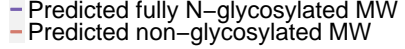
log(intensity)



Values from



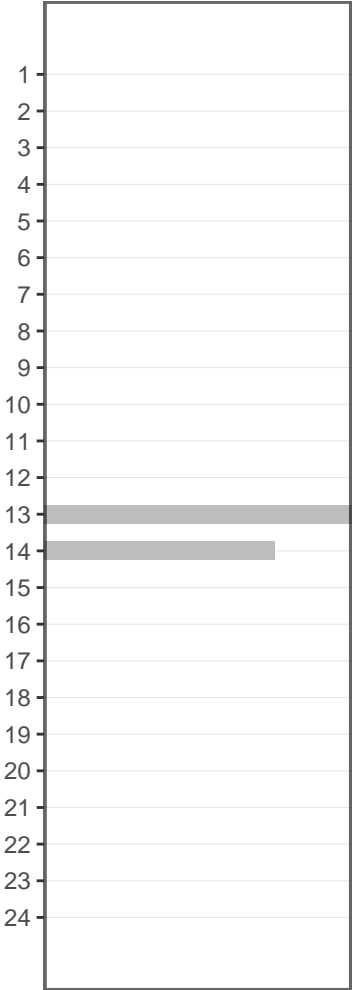
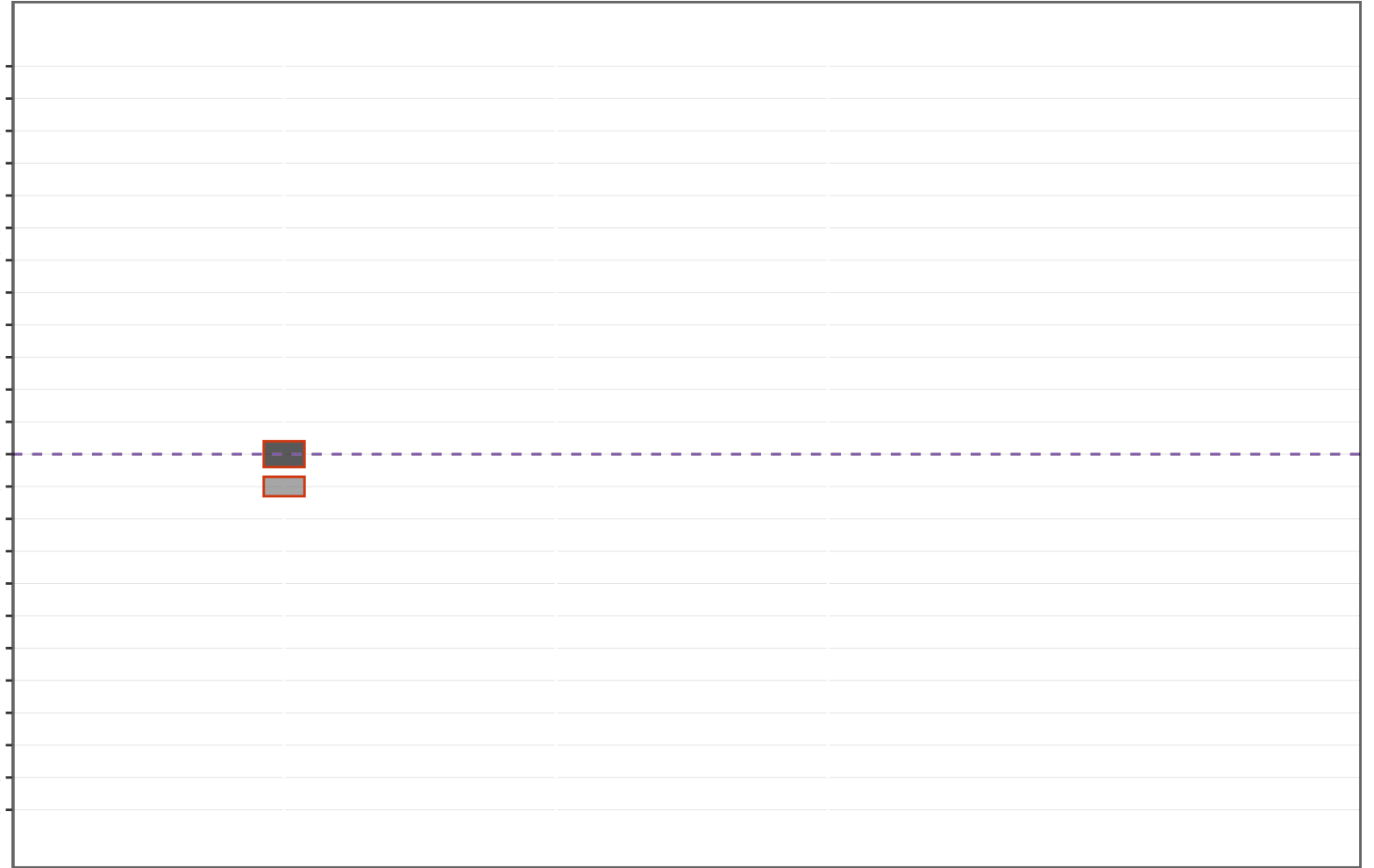
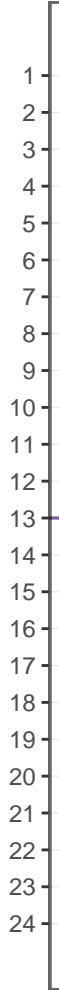
MW indication



Molecular weight

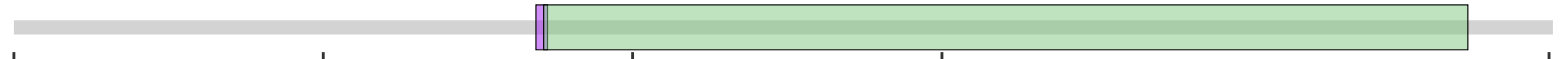
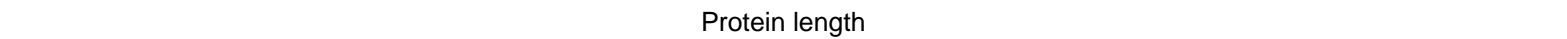


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

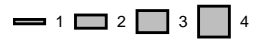


Protein sequence:

FDYTLDEYMASLEGINALTDKKVTLVGGYFSPIAKYASNHGKELNGLLNPLMTMGHANLPTSLVLENFLLGEIFDQDPLRASDKTMLSCGPVQIKEDVAMVYRRPYLFGSSAGFALNISKAMKQKLGKGVYEDGRAILMDNHNWVQTTVGVGQDRDLWLSFDGVEDFGKESKRLVLELPMGHHVQEDSGEELGQLLAGTVKES66L

NbL16g25440.1 monocopper_oxidase-like_protein_SKU5 [MW – SP = 64.22 kDa]

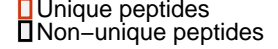
No. of times detected



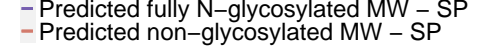
log(intensity)



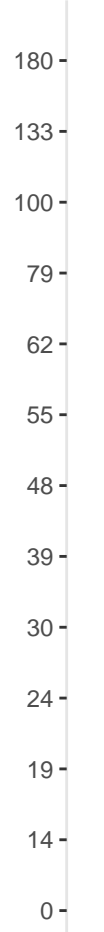
Values from



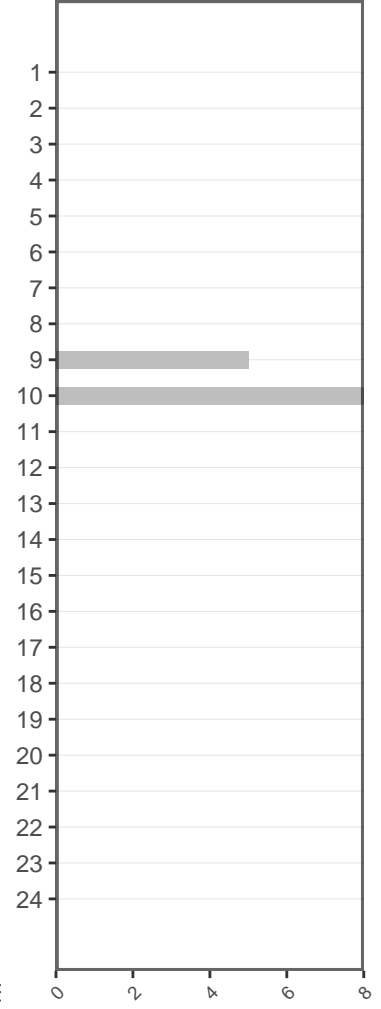
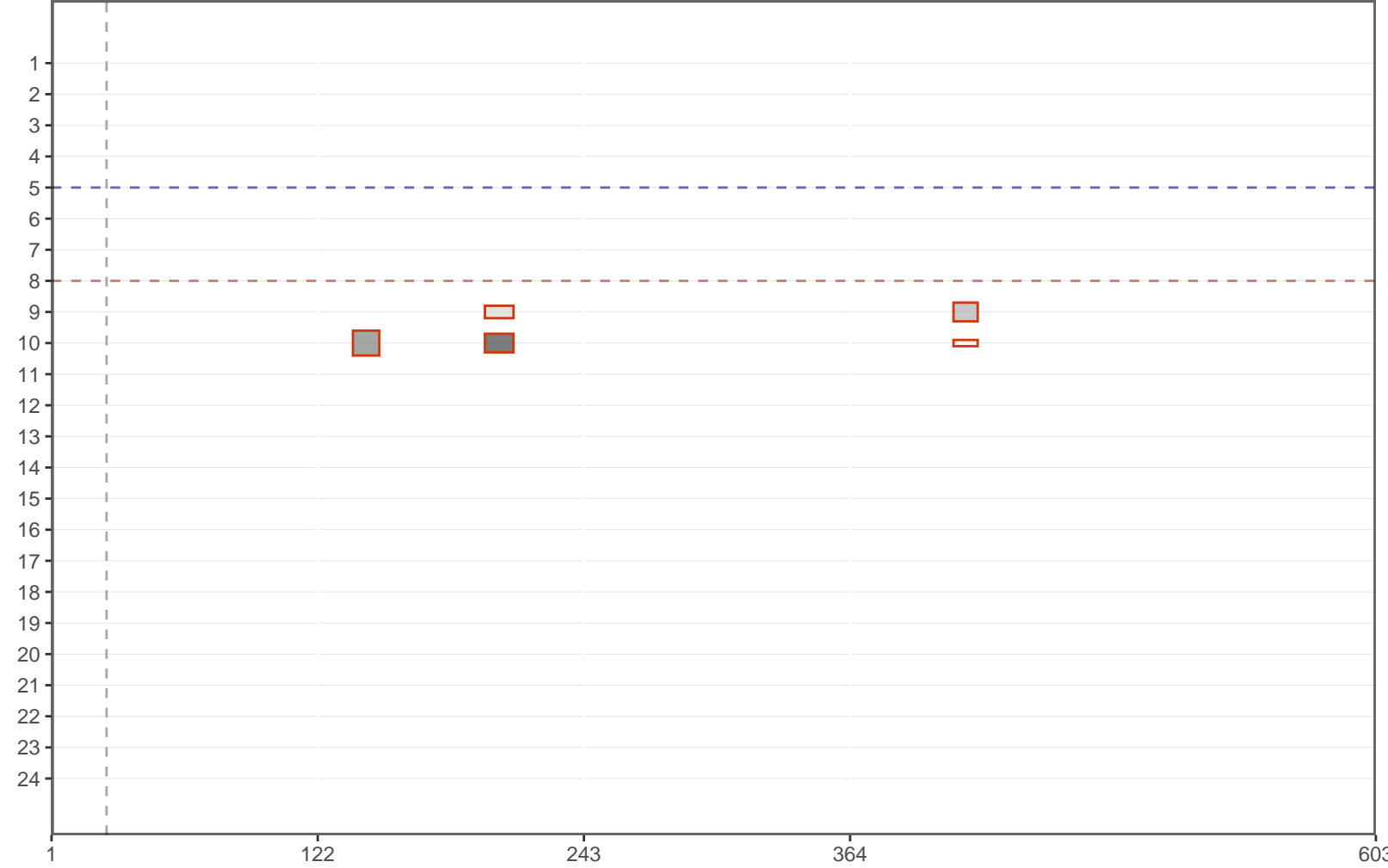
MW indication



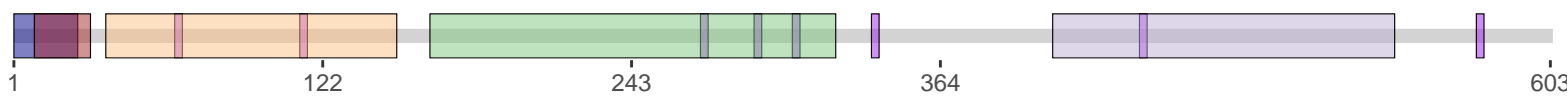
Molecular weight



Gel Slice

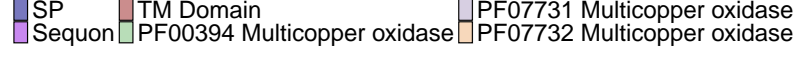


Protein length



Pfam domains

Pfam Description



Protein sequence:

DNASSDYIYLSRFVNSGGWSEKGVWVLYHNSGGPAGGLPDPNNEGDTFFSMGQARERWVDSASAARPNPQGGFRYGETVTDVFLVHNRPAELIEGKRRTLSGSIYAPSTPLKLAQGFNPGVFKLDFPNKMMNRPAKVDTSVINGTYKAFVEIFQNDITTVGSHLEDGVAFFVVGMDYGLWTEHSRSTYKWKVDGVARCTQVFPGAWTALVFLNDGHWLNRAGNLGQWYLGQETYSIVNPFETTKNDIPLFANVYGGALSPKQKQAHRYVNSGAPSL

NbL16g25360.1 uncharacterized_protein_At5g48480-like [MW = 16.93 kDa]

No. of times detected



log(intensity)



Values from



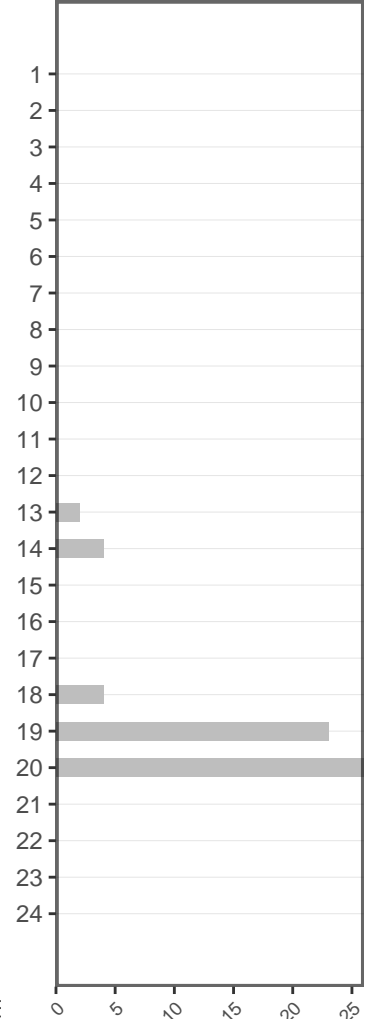
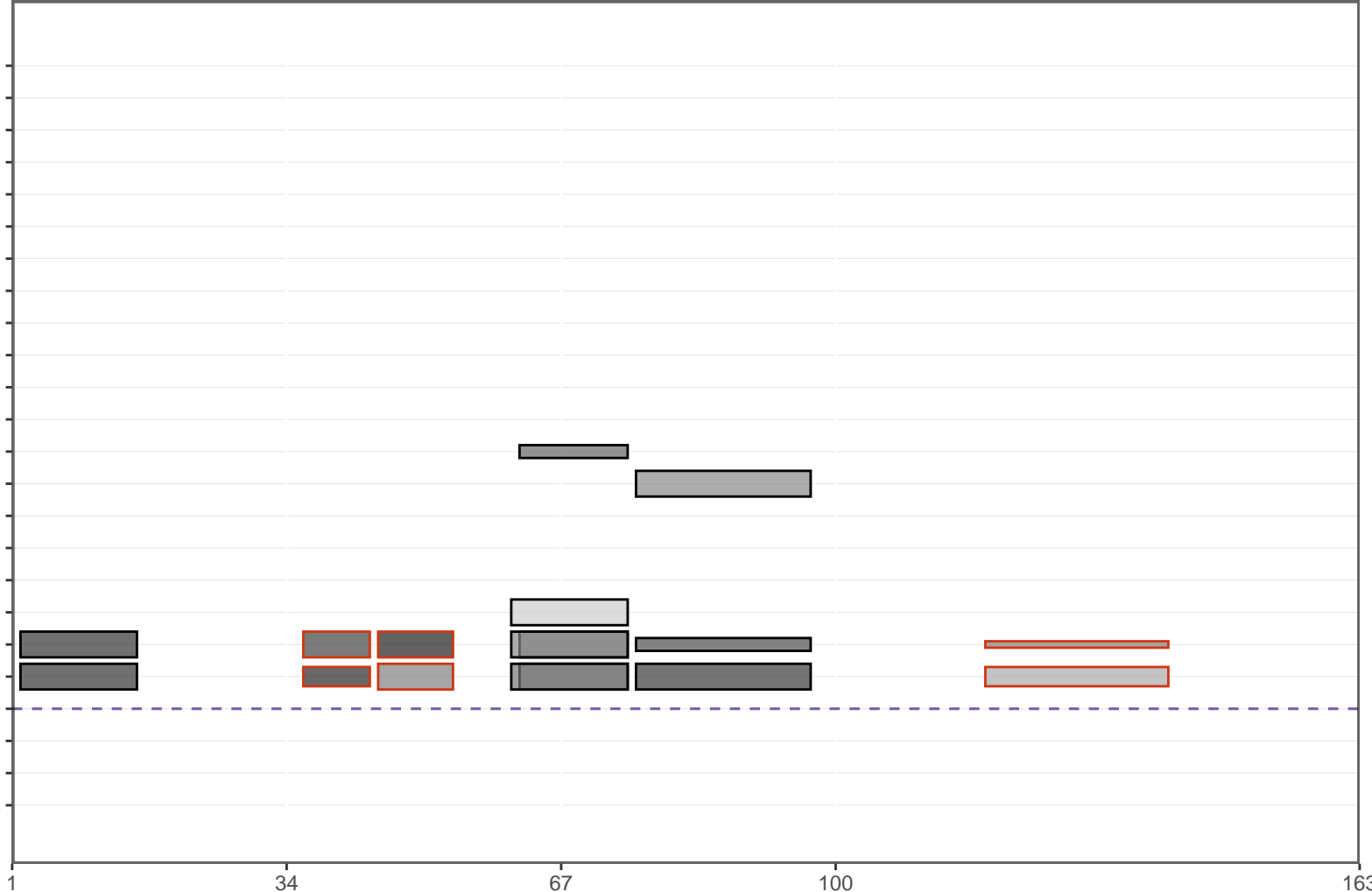
MW indication



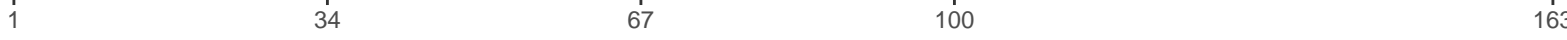
Molecular weight



Gel Slice

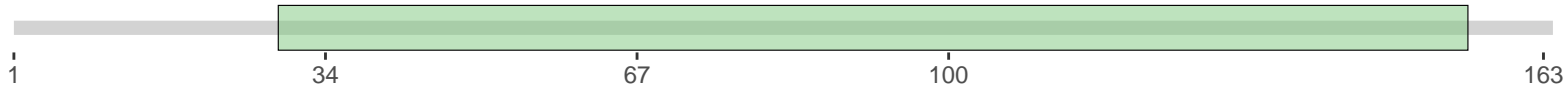


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

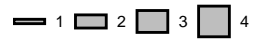


Protein sequence:

LLSAELKLGSTTFVSDSDLTDSDSAPVKTABGGIFGLETEDEVEGAAVAKA/TAGAVSEGEIAGEGDCAGYGRVGLKDPYGNVWLVGSPSKYK

NbL16g25210.1 ubiquitin_carboxyl-terminal_hydrolase_12-like [MW = 83.99 kDa]

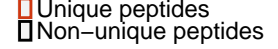
No. of times detected



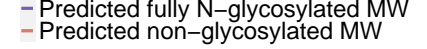
log(intensity)



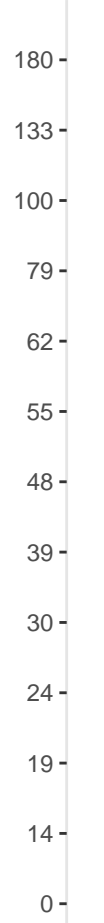
Values from



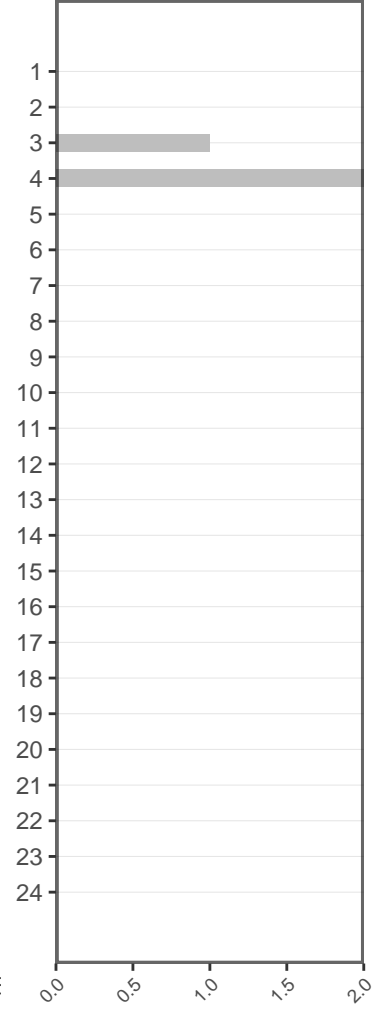
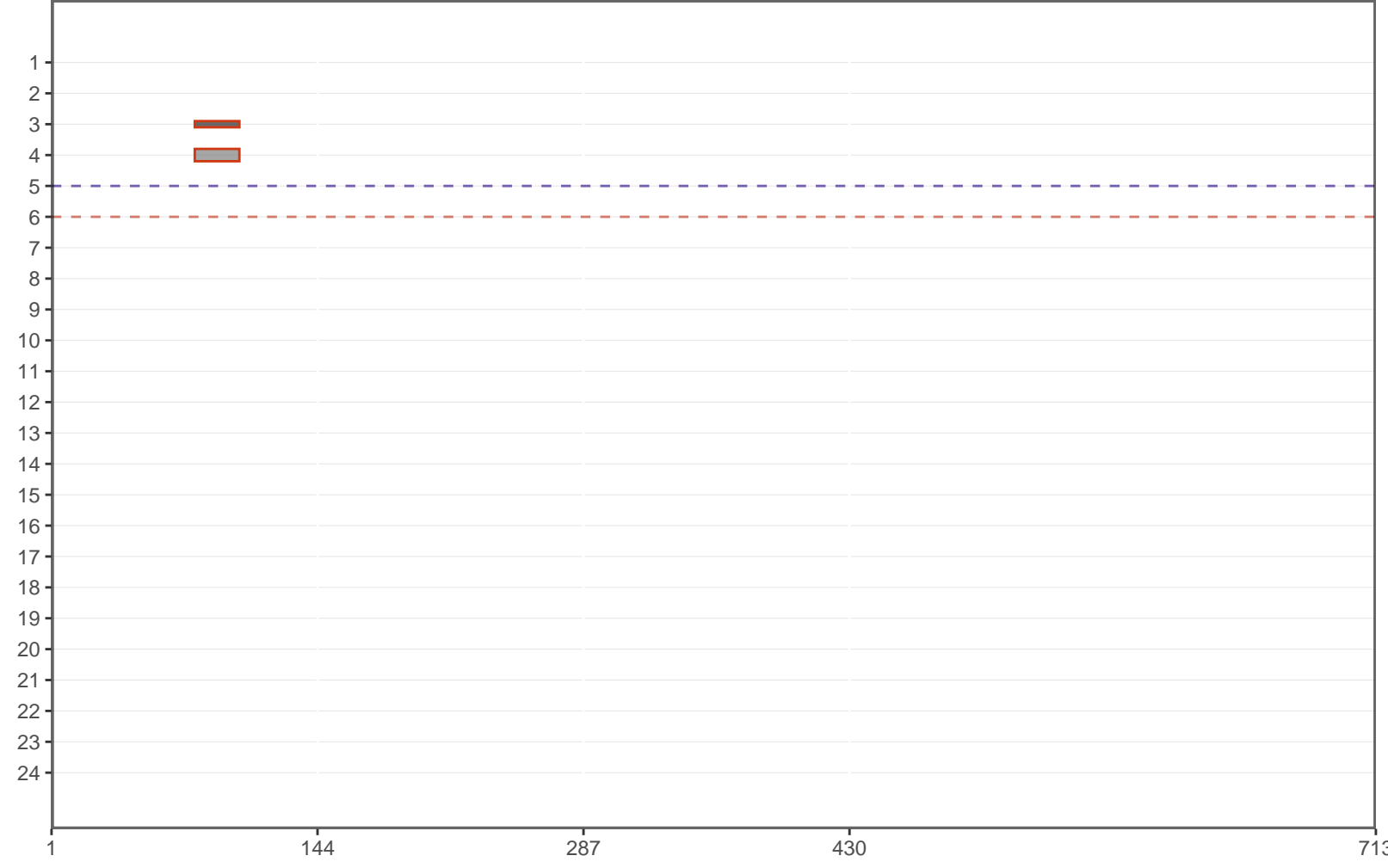
MW indication



Molecular weight

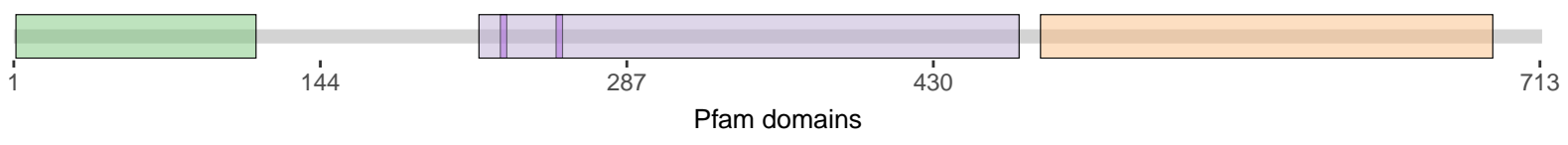


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

*SVLCEPLDXXKASFRFSQIEDGIDGICFKPSPEVEEGQVRYFDVSSFLFYVNRQIVHFRALFKPKVEVDFGLELAKNTYDEVVQKVAQRLGADDRPKIRLTPHNGYSGQPKPNPKYRSDVHLVDMLIHYNQSDILVYEVLDIFLPELQGLTKLVAFHHSKTKDEIEILNRLPKGTVGVVLEIKKVDLSRQDAELRLLLEVYHKYKIFLPEKIENINDGYWTLRAEIPPEEKNLGHDRLHVYHFTKETPQNGMGVQNGFPEFFLVEGETLAEIKVRIQKLOVDPDEF

NbL16g25200.1 ubiquitin_carboxyl-terminal_hydrolase_12-like [MW = 43.72 kDa]

No. of times detected



log(intensity)



Values from



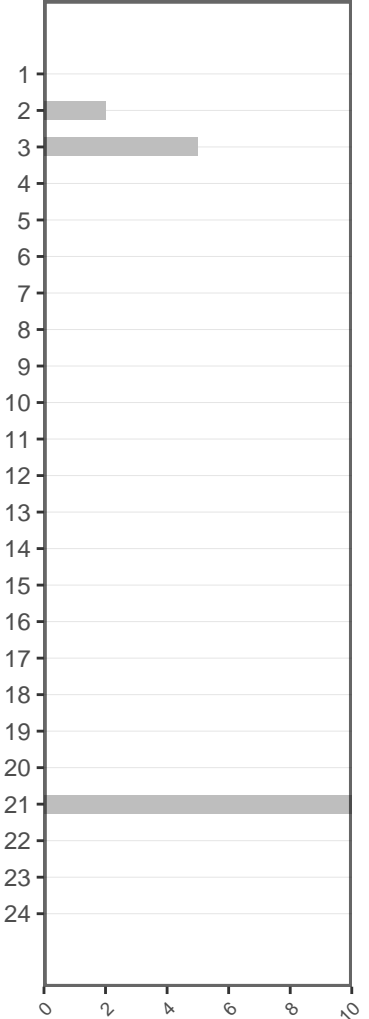
MW indication



Molecular weight

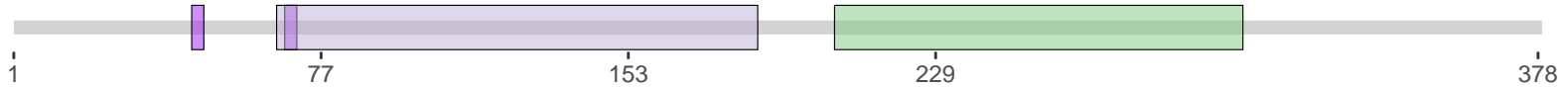


Gel Slice



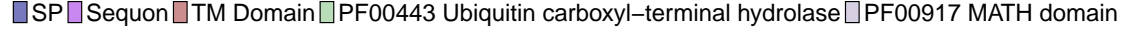
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DRVVEADVA/RK/VKHWTYDSKNETGVVGLKNGGATCYMNSLLGTQYHIFVRKAVVHMPITTEMDMPGSSPLALGSLFLYKLGYSKSVATKELTKSFGWDTYDSFMQHVDGELNRRVLGKLEDKMKGTAVEGTQKLFEGHHMNYIEGINVDFKSTRKESFYDLQLQKGGDRVYASFDKYVEVERLEGDNKYHAEHGLG

NbL16g25160.1 D-lactate_dehydrogenase_[cytochrome]_mitochondrial [MW = 62.77 kDa]

No. of times detected



log(intensity)



Values from



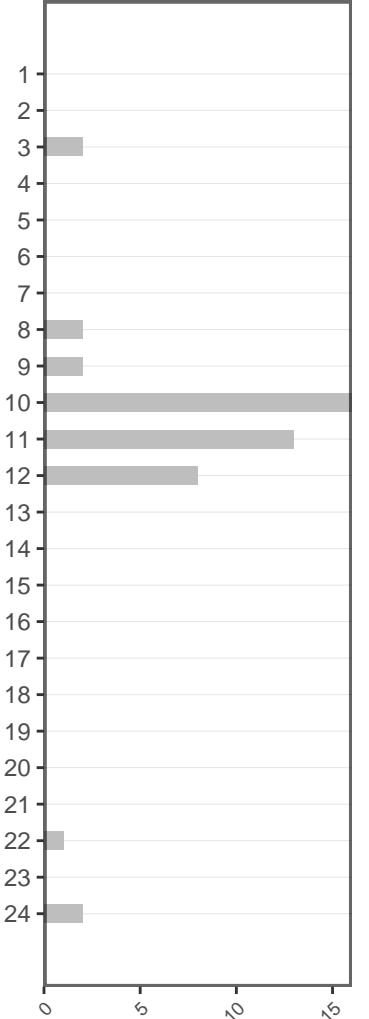
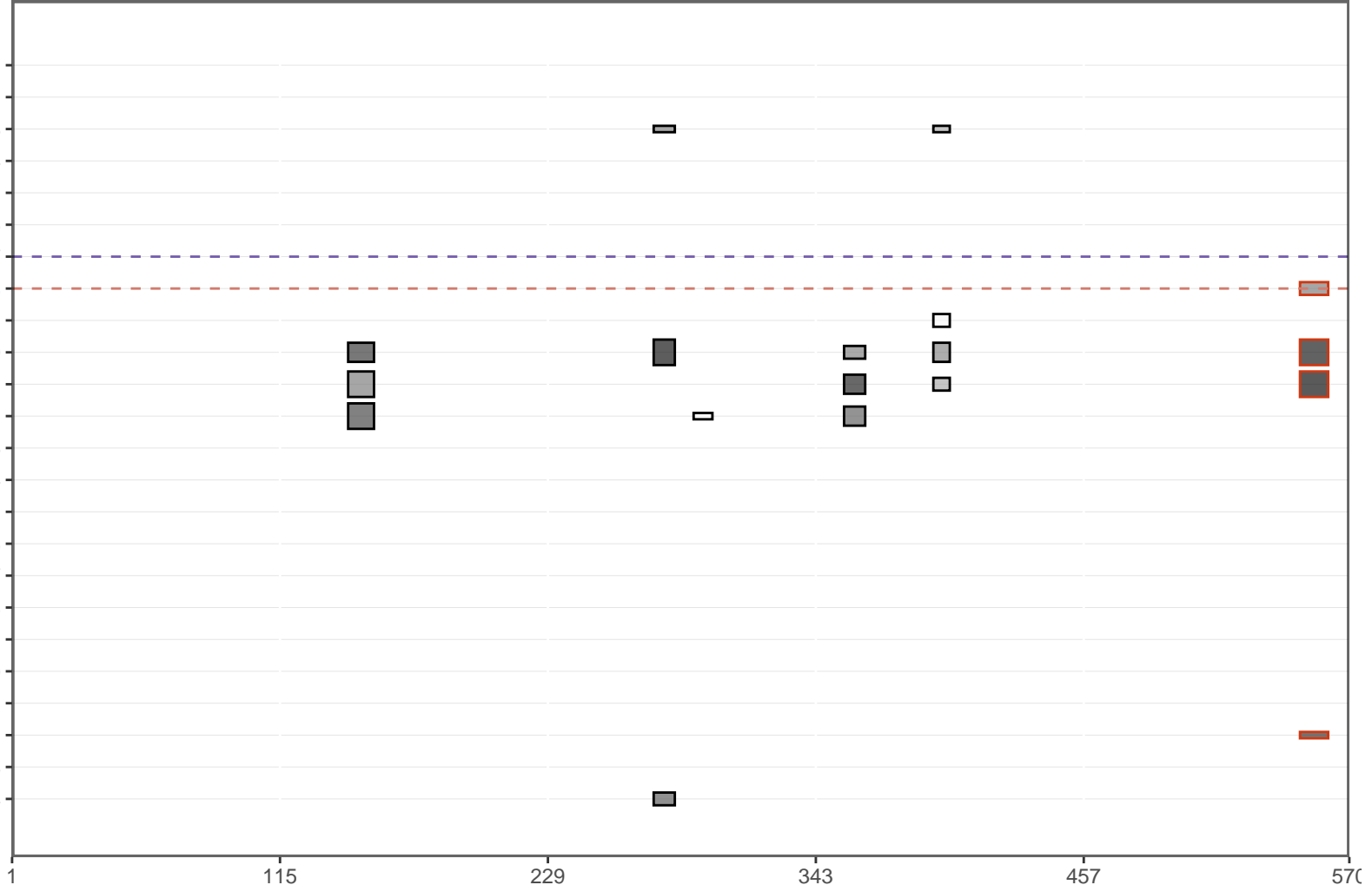
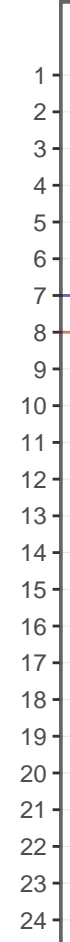
MW indication



Molecular weight

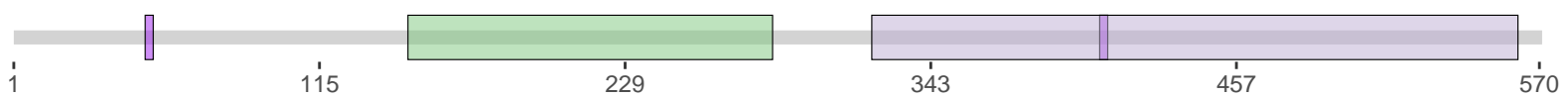


Gel Slice



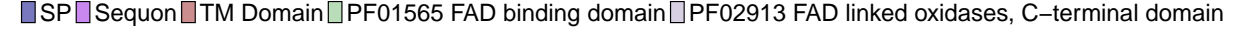
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LKVVLDAGEVMRTASARKSAAGYDTRLMIGSEGLGVITEIFLRLLGKLPESBVVAMNFTKDAADVAATMHSQIGVSRVVELLDEVGVRRAINLANDKLPVPTLMFEFVGTGAHSHREGTQIVQKIASQHNSSDFVFAEEPDEKELWKRKEALWAGFAMENPEAMITDVCVPLSHLAELISRSKQELDASPLTCTVIAHAGDGNFHTIVLFDPSKKEGRREAEERLNHLMHTALSMEGTGTGHEGVGTGKMKYLEKELGMENLRTRMKKIKVALDPNINMNPGLKLPPI

NbL16g25090.1 sucrose-phosphatase_1 [MW = 52.67 kDa]

No. of times detected



log(intensity)



Values from



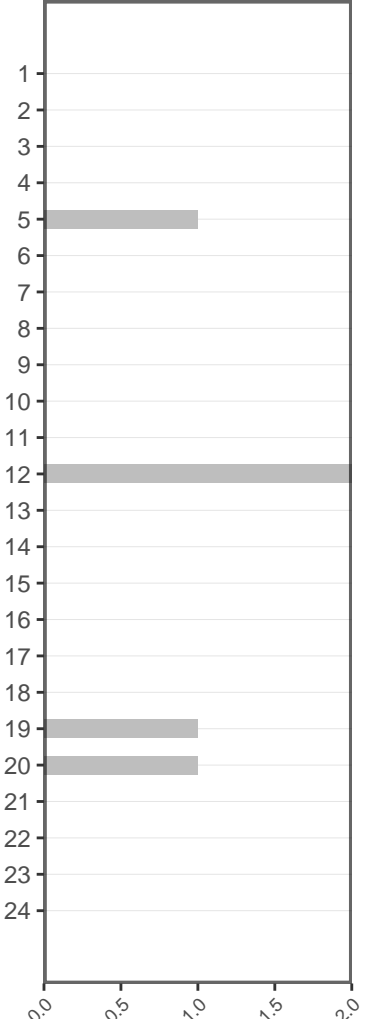
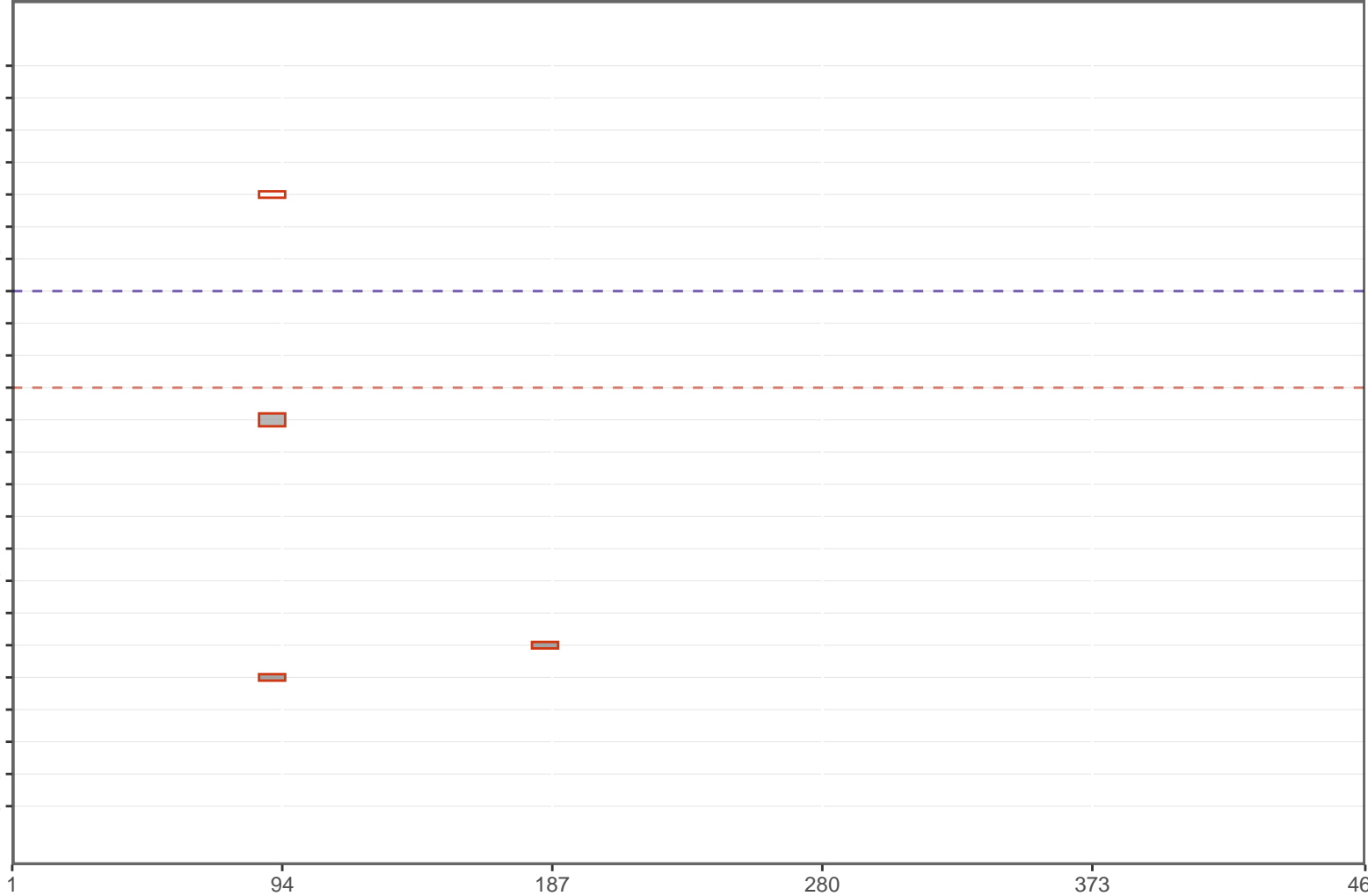
MW indication



Molecular weight



Gel Slice

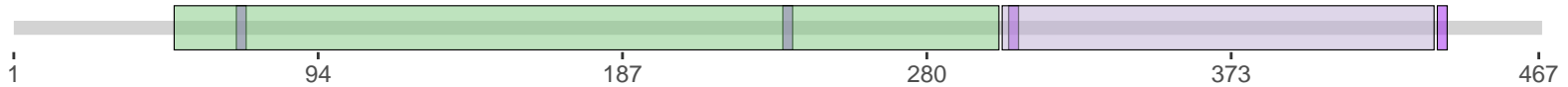


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF05116 Sucrose-6F-phosphate phosphohydrolase
- PF08472 Sucrose-6-phosphate phosphohydrolase C-terminal

Protein sequence:

YLLKLIKSEDKLPNNTLAGGDSGNDALFSPDQYGVGMVANGDELLQWRANAKNDPKVHATERGCAAGIQAGHFNLGPTSPRDFDTMEDGCKMENFVWVEVYKFFFEKWRIRGEIENSDJLHNLKAVGRPSGTFVHPGVEKLEDCINTLRTHGDKGKGFQVWDDGLPTDQVSDSDWLVSRKKWELGGEERGGDITFLLSKSLTVADGLTWHVHQTWMDGAAATDEAAWFF

NbL16g25060.1 methionine_aminopeptidase_2B-like [MW = 48.7 kDa]

No. of times detected



log(intensity)



Values from



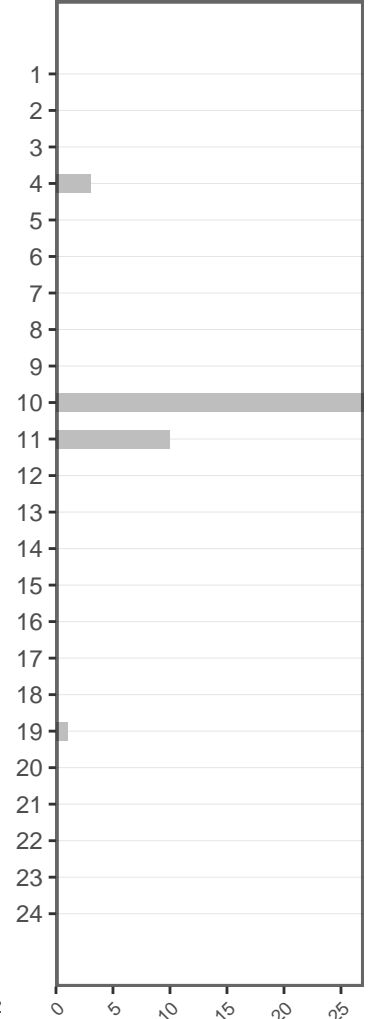
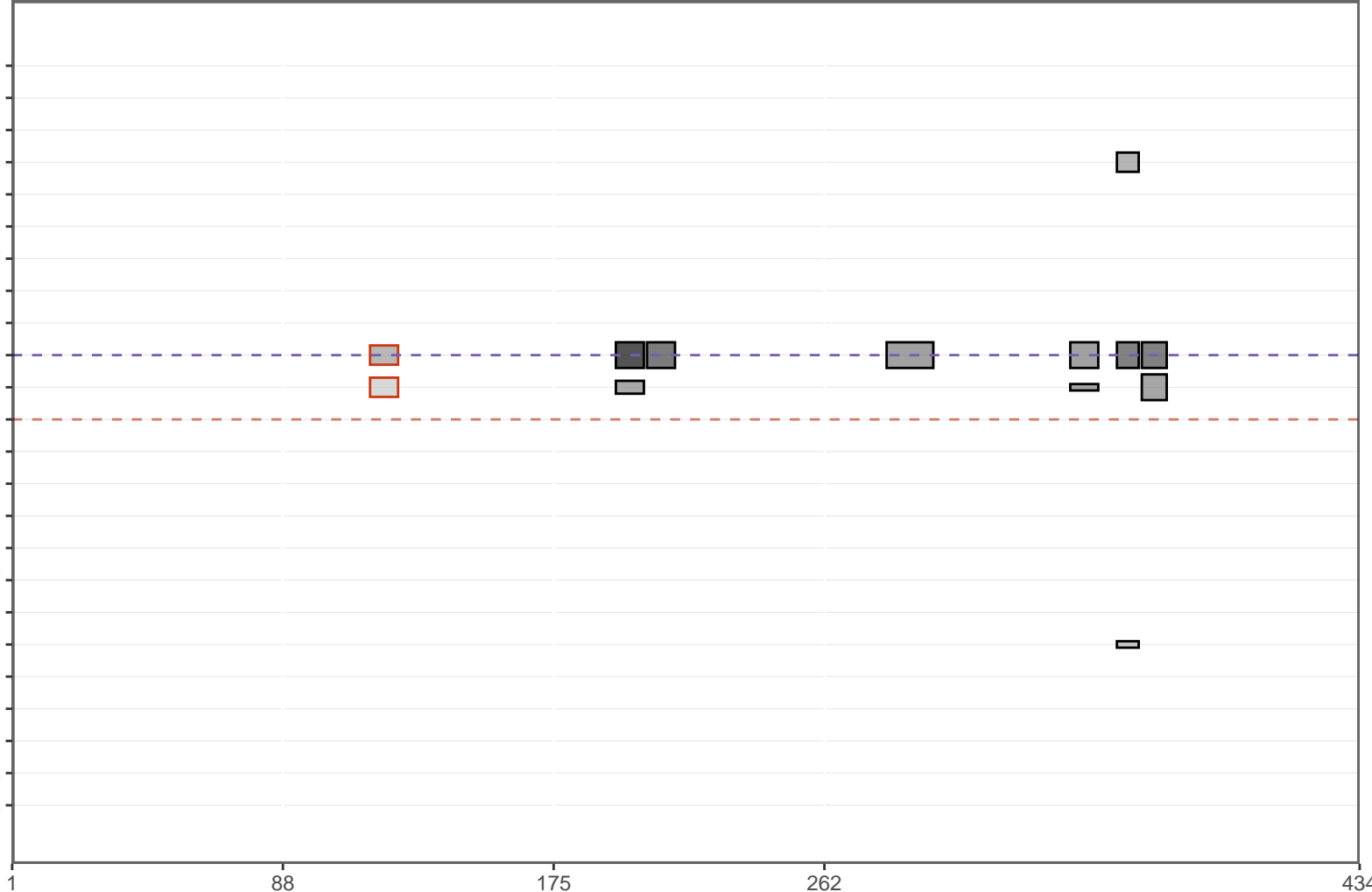
MW indication



Molecular weight

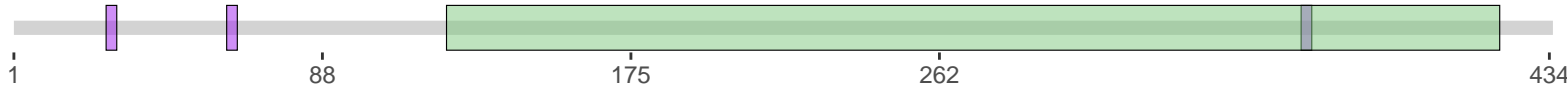


Gel Slice



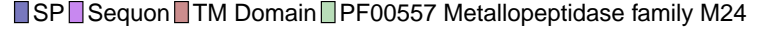
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

M/KLDFGTHDGRVDDGAFVAFNFMFDPLLEASREATNTGKKEAGIDHRLGDVGAAGVEVMESYEVEINQKVFQVKSRLNLGHSIGQYQIAGKSVPIVKGEGQTMEEGEFYAETFGSGTGKGVYREDELEGSHYMKNFIDGHPRLRPRAKQLLATINKNFSTLAFORRYLDRLGETKYLMLAKNLGDAGVQVPPPLGDKGKGVYVSGFEHTLLRPTCKEYVSRGGDY*

NbL16g25050.1 fasciclin-like_arabinogalactan_protein_17 [MW - SP = 47.11 kDa]

No. of times detected



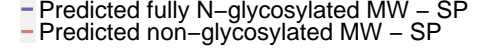
log(intensity)



Values from



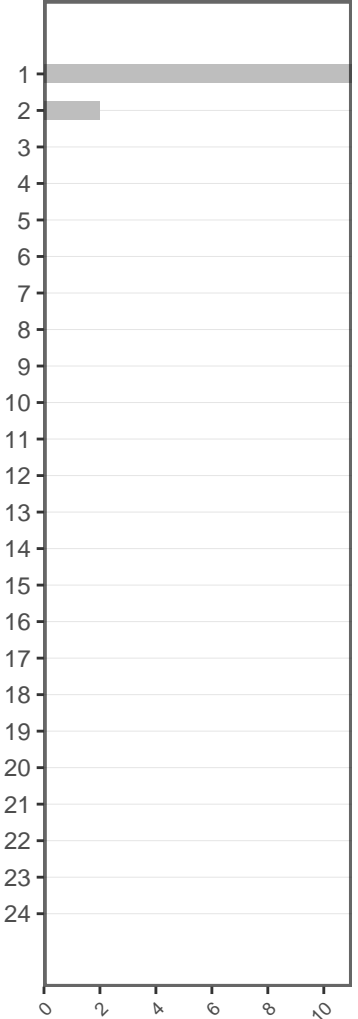
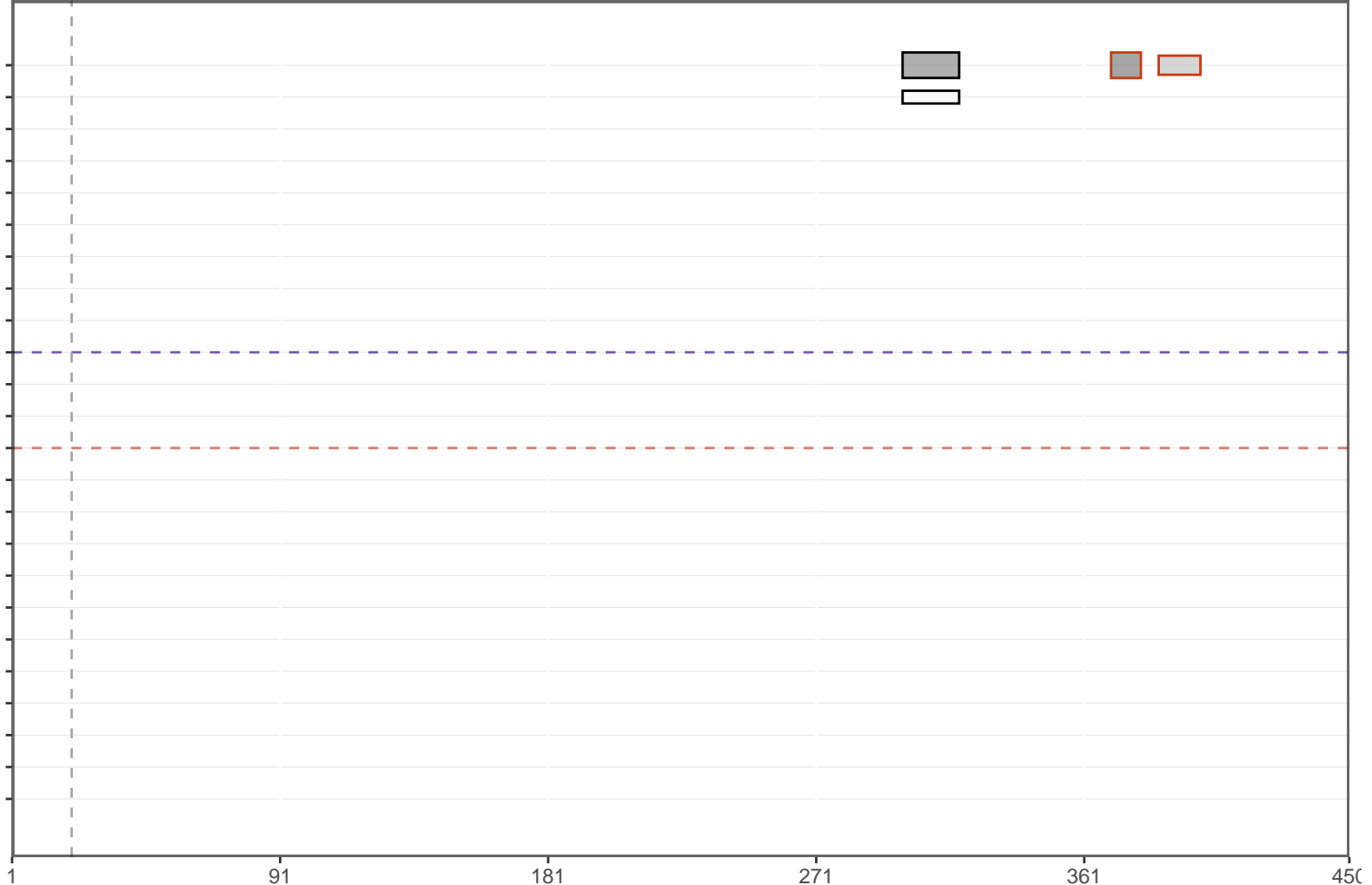
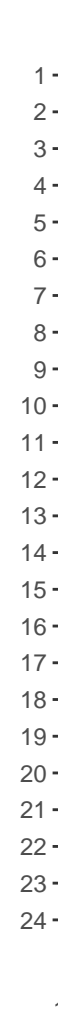
MW indication



Molecular weight

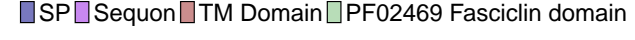


Gel Slice



Pfam domains

Pfam Description



Protein sequence:

TNRLLKXKPTLTPVAGAPPVLPVLSAMAPGRLAPAPAPCPGPGPHHFDGEGVNDFTGLLHYGGVNEFADILVNTSLATEMGRRLVSEGIVLTVLAPNDEAMAKLTTDGLSEPGAEGIMFYHLPEVYQTEESMYNVAVRFRFGKVKYDTRLRFKVVVAGEADSGSKVFGVAKGSAYLFDPRDVTGDRISVGGIDGVLPFVPEEKAAAPVAPVAKVWAKPRRGLMEVAGSVLGSFC

NbL16g25020.1 iron-sulfur_cluster_co-chaperone_protein_HscB_mitochondrial [MW = 30.39 kDa]

No. of times detected



log(intensity)



Values from



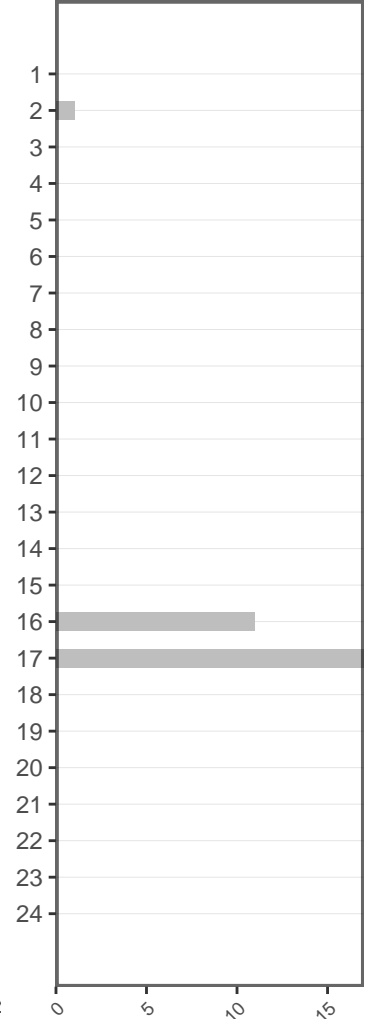
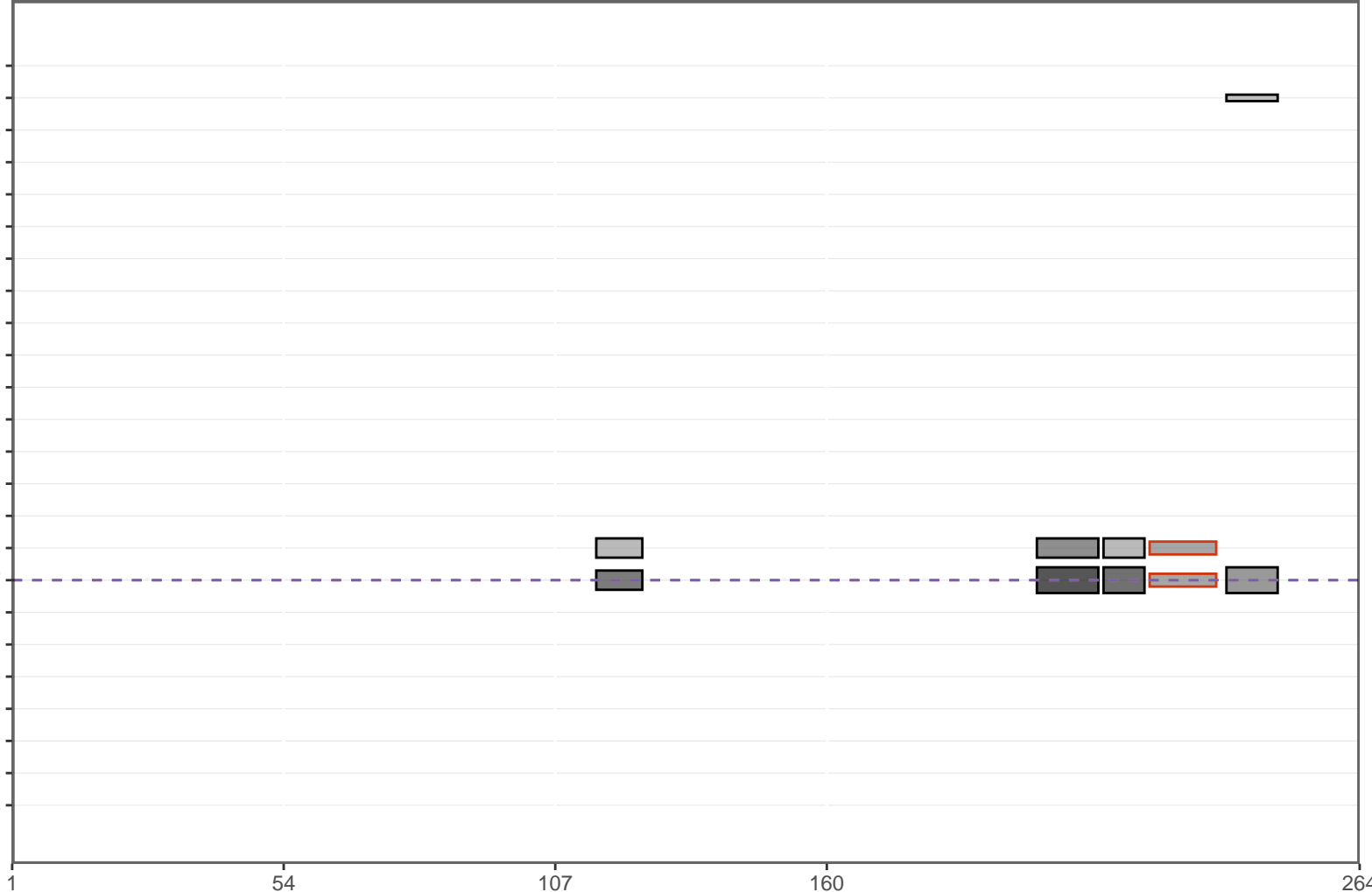
MW indication



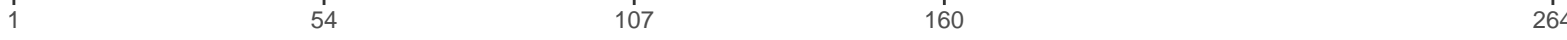
Molecular weight



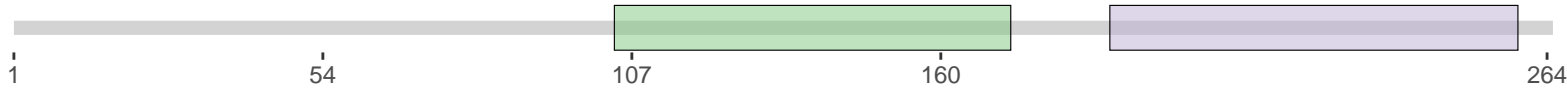
Gel Slice



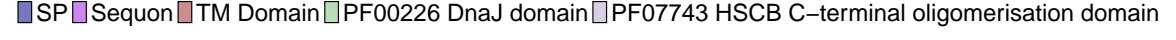
Protein length



Pfam domains



Pfam Description



Protein sequence:

EGENLERKYDWRKLPDLVHTKSEKEREYVAEGSARVIDAVRTLSPLGRAIYKLEGVHYDEEERIDDELLLAEMELRETVEEAAANAGALKGIQGEIQGKFEQSSISFANALQKRIKRYEEAAWATQRTMYKIRANEKVKLL*

NbL16g24920.1 5-methyltetrahydropteroyltriglutamate--homocysteine_methyltransferase [MW = 84.58 kDa]

No. of times detected



log(intensity)



Values from



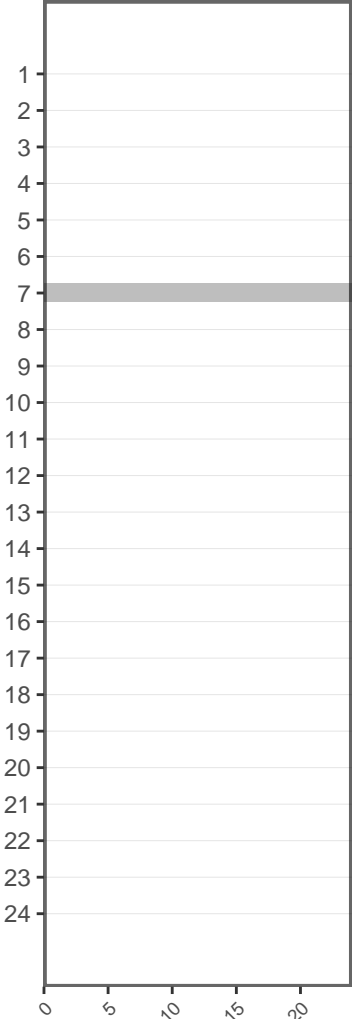
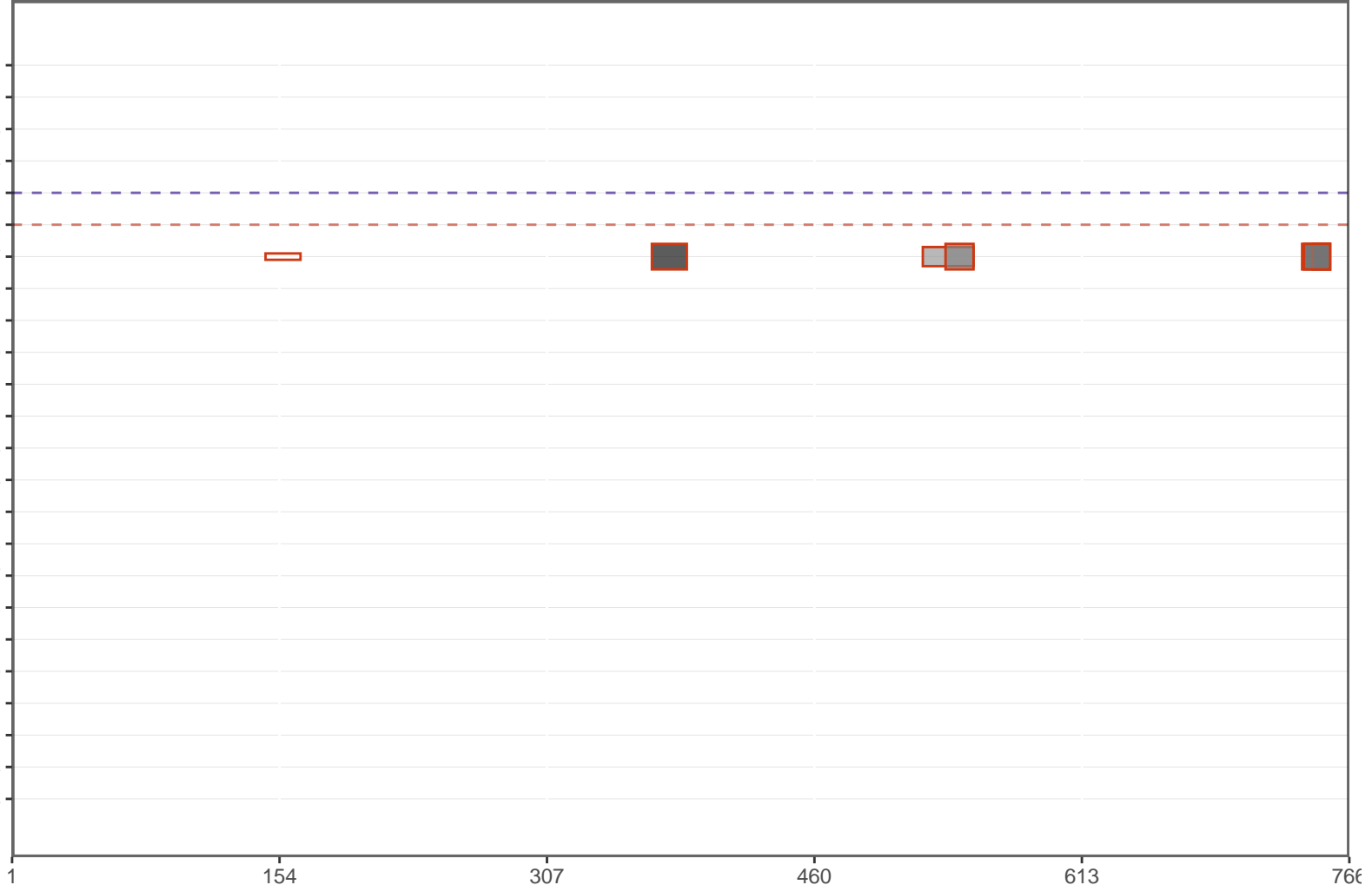
MW indication



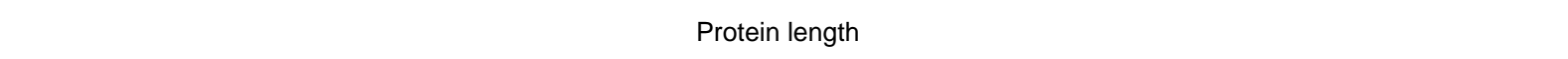
Molecular weight



Gel Slice



Protein length

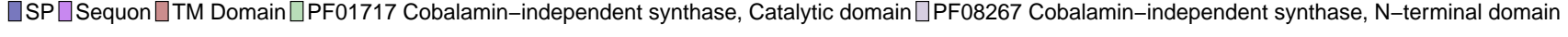


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SHKDEAFFSANAAGASRKSFRVTEAVQKAKATALKGSDHRRATNVSARLDAQGRKLNLPVLPFTTGGFPQTVELRRVREYKAKKISEEYVYKAIKEEKVYVLEQELDIDLVLHGFPERNDMVEYFGEQLSGFAFANGWVWVGYGRCVYKPPHVGDSRPNMTEVFWSTTQDSMTKRPKGMLTGPTILNWSFVRNDQPRFETGVQIALKDEVELEKAGITVQIDEAALREGLPLRKAHAPELWVWHSFRFTNIGDQTTQIHTMGSYFNFDIHSIDMDI

NbL16g24840.1 NADH--cytochrome_b5_reductase_1-like [MW = 31.08 kDa]

No. of times detected



log(intensity)



Values from



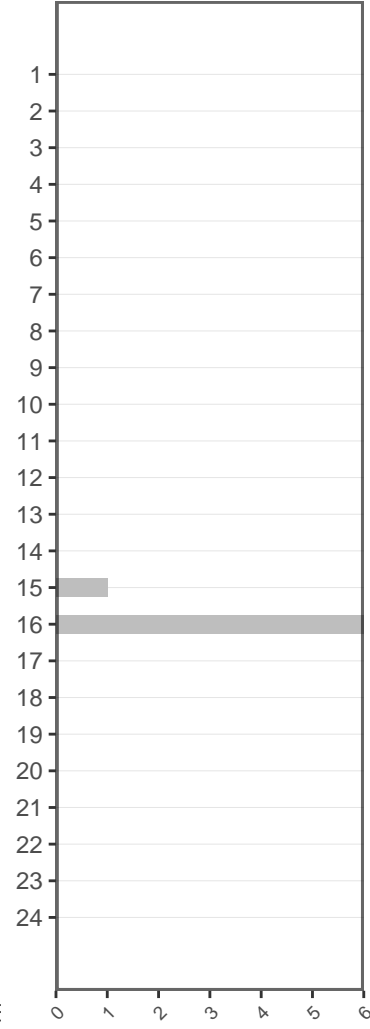
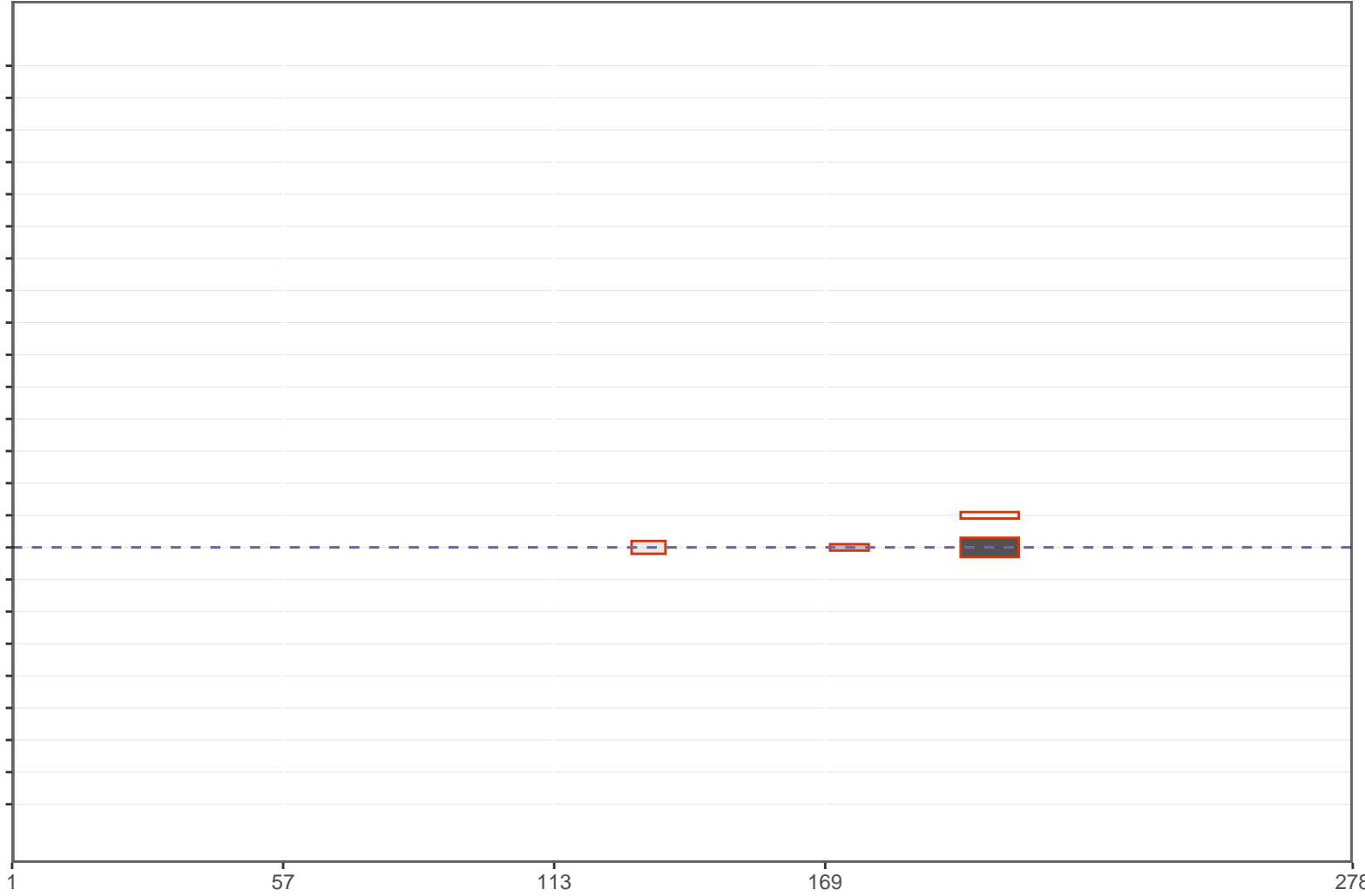
MW indication



Molecular weight



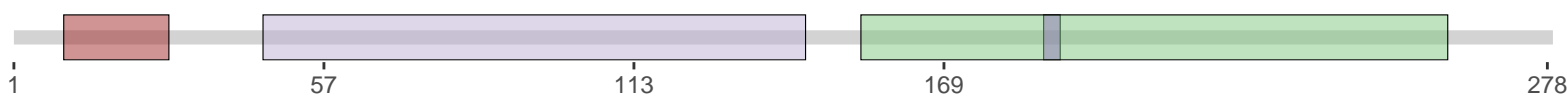
Gel Slice



Protein length

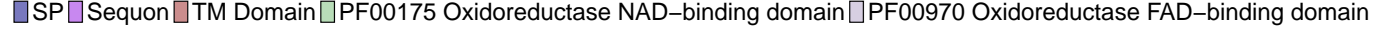


Peptide counts over 4 repeats



Pfam domains

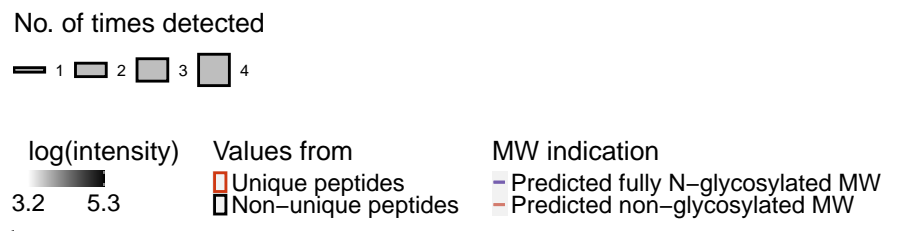
Pfam Description



Protein sequence:

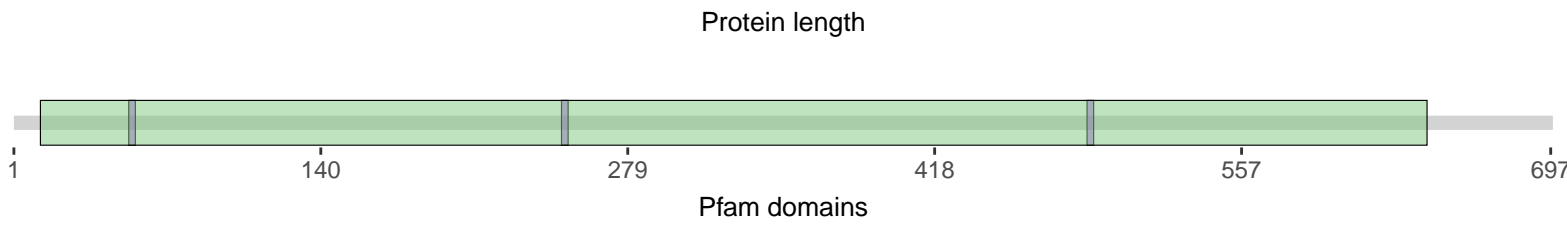
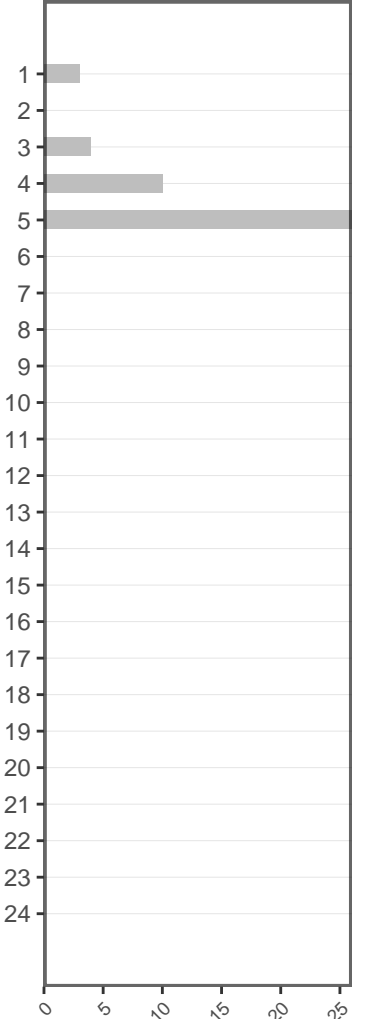
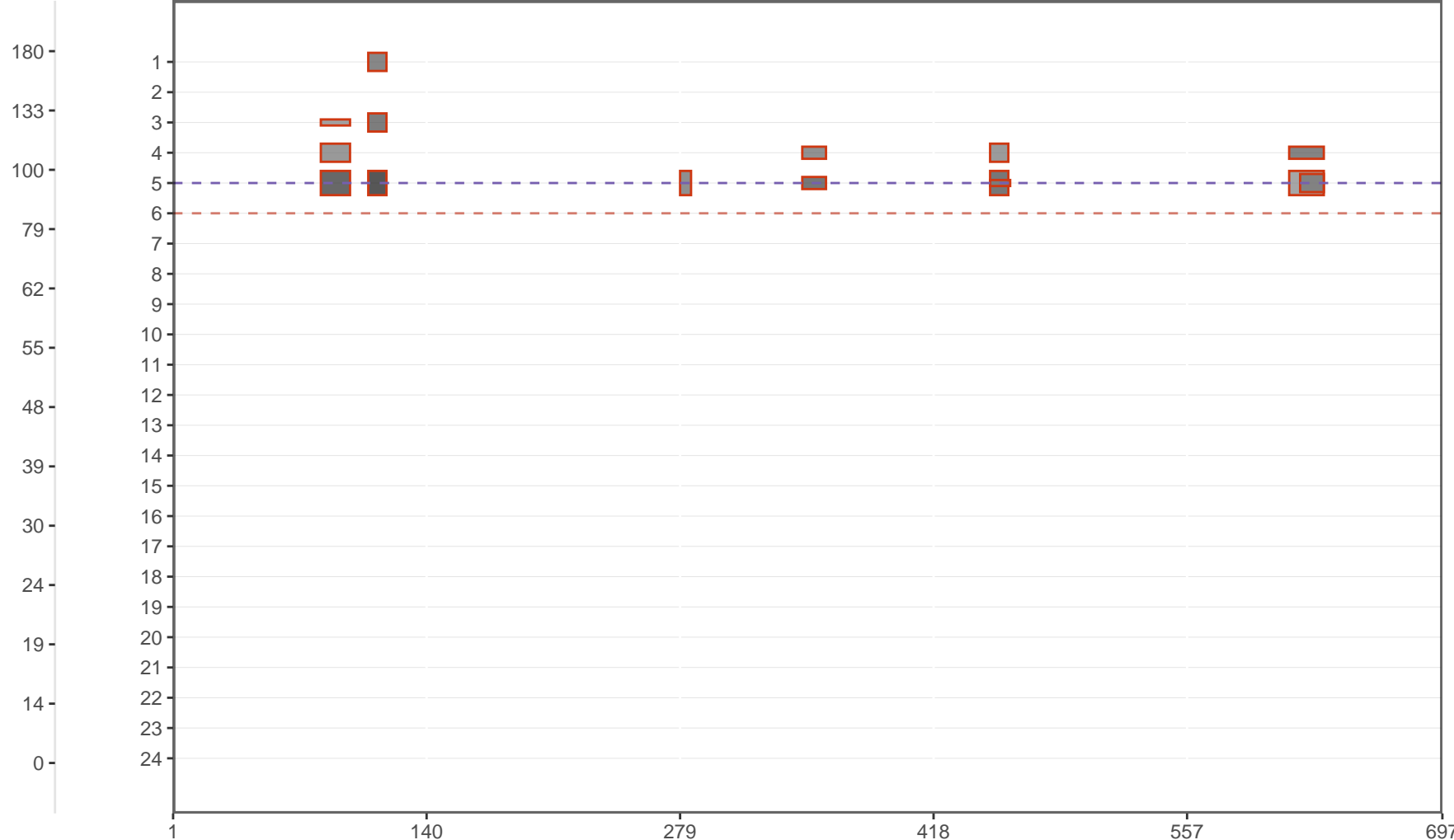
REGDYMAYVKGPKGRFKYQGGVRAFGLMAGSGGTFMFQVRAILENPNDKTKVHLIVANVTYEDLLKELDGLAANYPDFRKYVYVLDNPPFVWGGVGVSKEMIGNHCAPASDQILRGGPPPMKMAHALEALGYTPMGGFQ*

NbL16g24700.1 4-alpha-glucanotransferase_DPE2 [MW = 81.21 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF02446 4-alpha-glucanotransferase

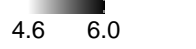
Protein sequence:
 ESDGLWDFNRLTFPIVGHHELLGKFGASWTAASTFLNEYRKLKLYEFKKECENTEKKIABVLSKFLKTEMLVESEKLRRLKLFLLGNVALKIDPELRFKYPFRFNEIDTTSFKDLDHSGNVLKRLYYDYFFQRGEGLRGNALKTLPLVLSNSSLACGDEGLGPSQVHPVMOELGLVGLRQRMPSPEPLGDFGIPGQYGYMTVGPASCHDCGTLRAWVEEDEERRHRLFGAVVGSDELPPDQCTFEIVHFVLRQHVKAPSMVSIIFRAGLLALKEDYVTRPAVEETNDP

NbL16g24500.1 oxygen-dependent_coproporphyrinogen-III_oxidase_chloroplastic [MW = 34.51 kDa]

No. of times detected



log(intensity)



Values from



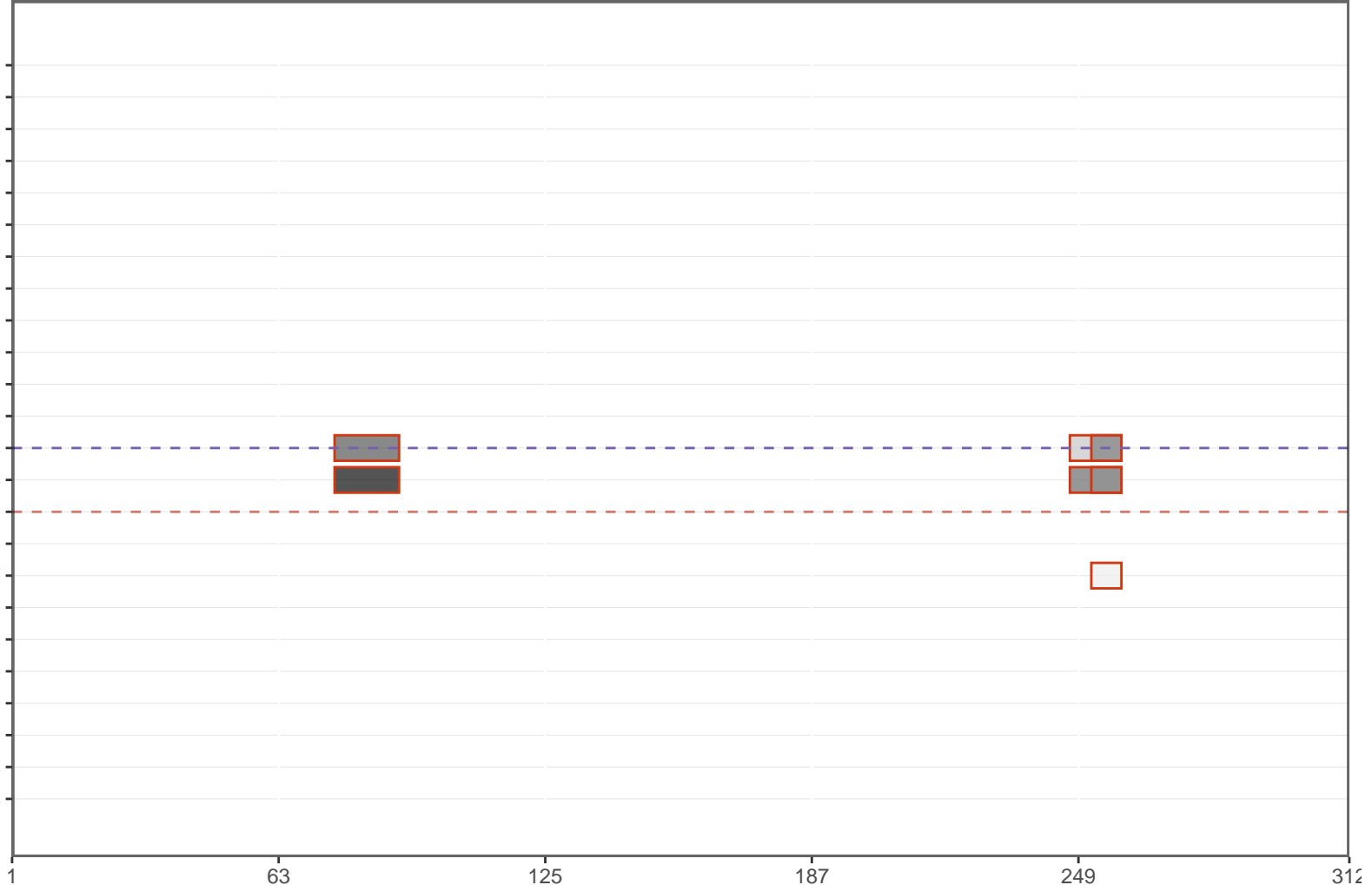
MW indication



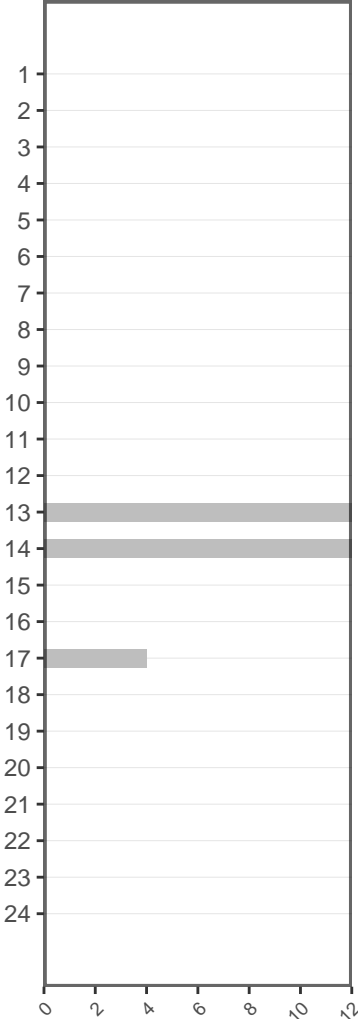
Molecular weight



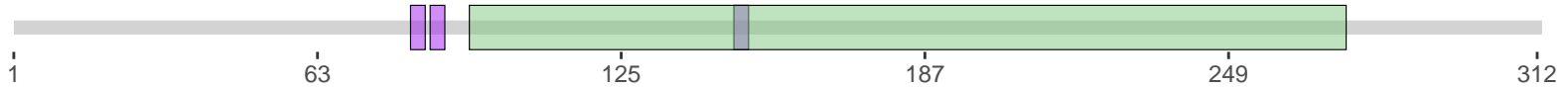
Gel Slice



Protein length

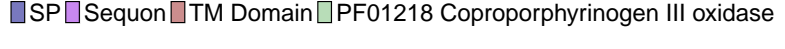


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKAGLVNIVYGVMPPEAVRAARPTDNGNKKPGRIPIFAAGVSSVLRHPKPFAPLTHFNRYRYFETDAPKIDAPGAPRQWVFGGGTDFTRWIFEEEDVKHHSVQKAAAGDFASFYRFRKRWDDNFKYKWKASVPLETGFQWLELAIESKILAFLLKYLGLFTSHP

NbL16g24490.1 alpha-ketoglutarate-dependent_dioxygenase_alkB_homolog_6 [MW = 28.34 kDa]

No. of times detected



log(intensity)



Values from



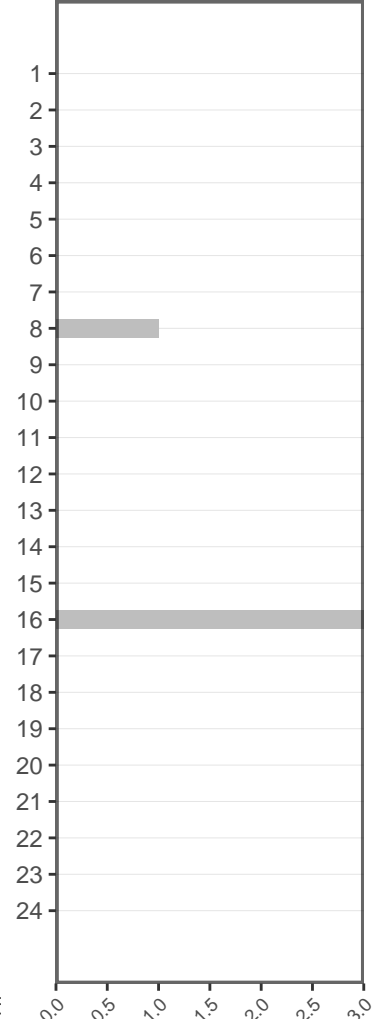
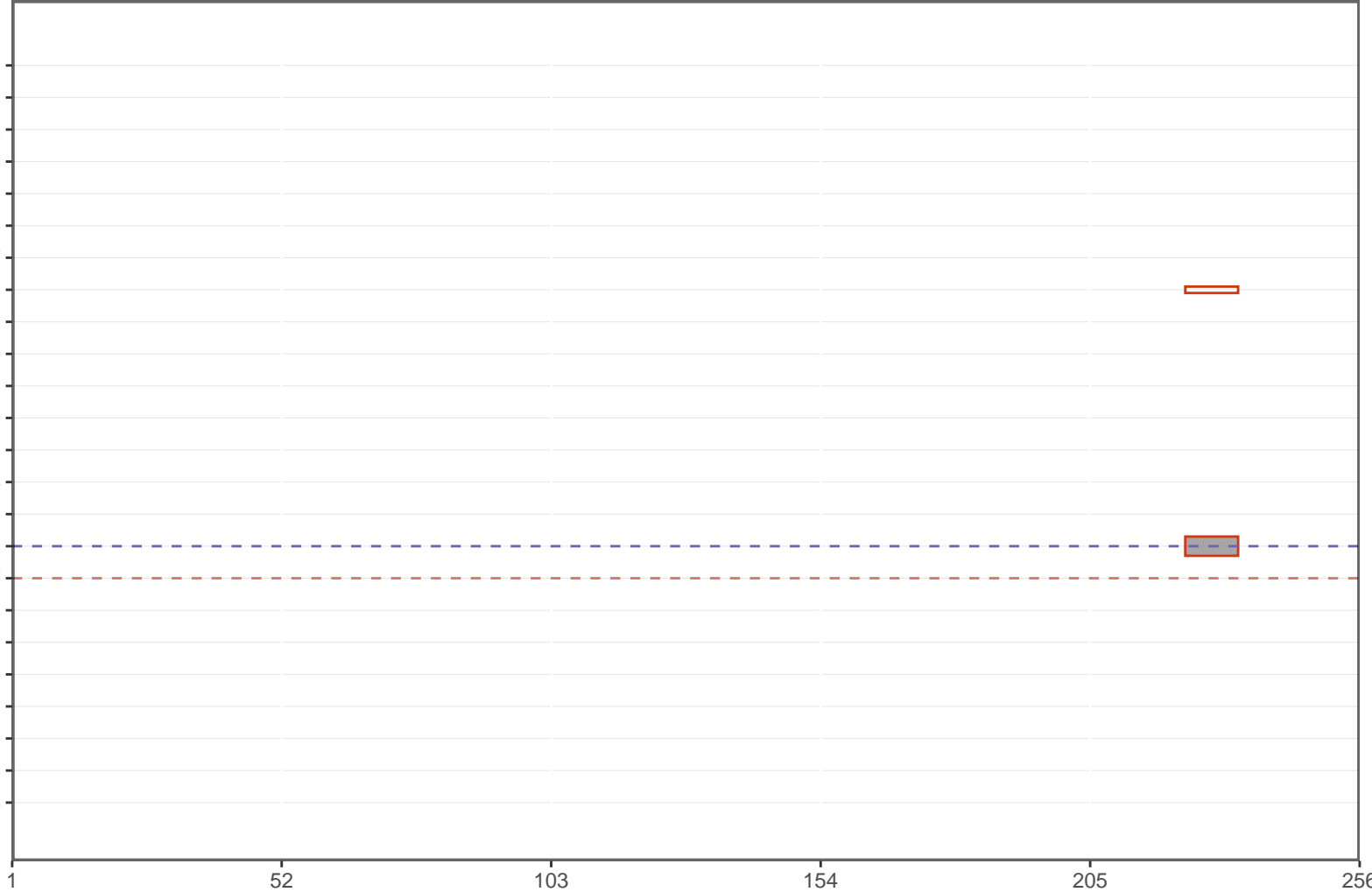
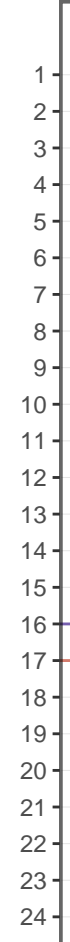
MW indication



Molecular weight

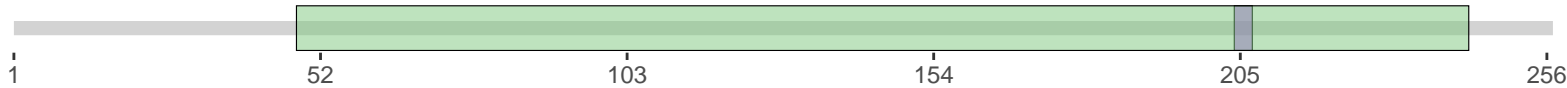


Gel Slice



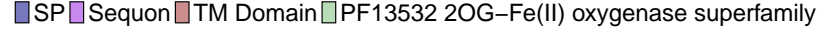
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LSLGGSPVVMDFTPRPNLRGCVGTHGNGVDEKEDPEAAVMMNSGEQLNGLPFQVLMRRELLFKDLVYSDYLGKIKDEVEVGRGNEAVNLTNAQNGDGVVQVHLSGSGKALDQDETVYRANTRVSLTGRVYTKVCKNIFKL

NbL16g24470.1 transcription_factor_Pur-alpha_1-like [MW = 31.78 kDa]

No. of times detected



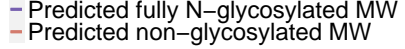
log(intensity)



Values from



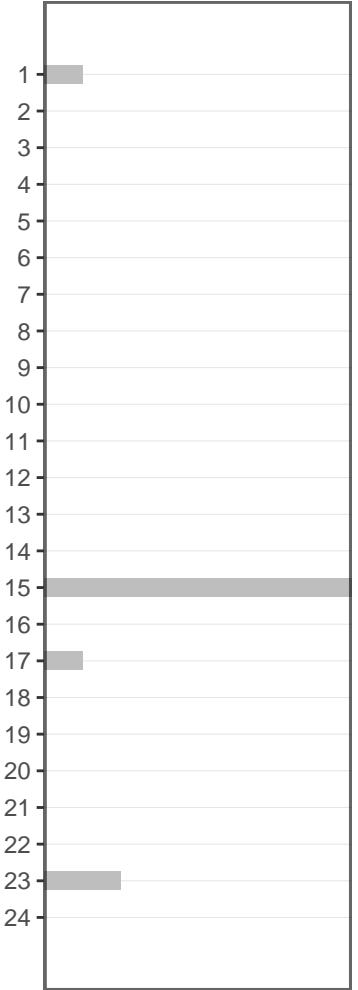
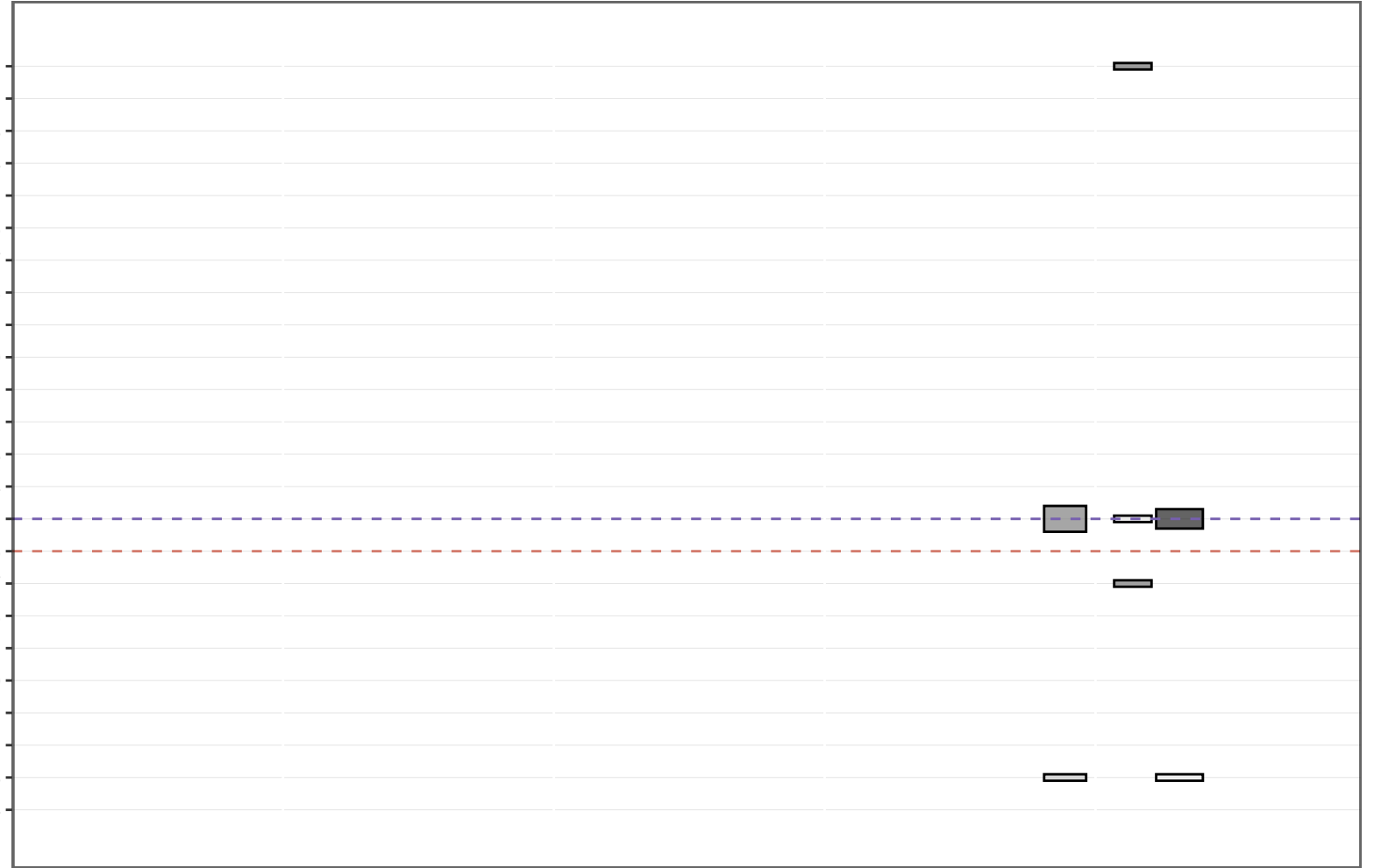
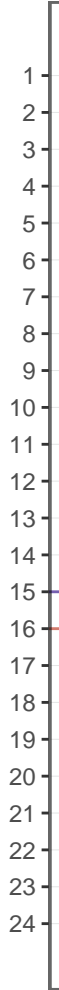
MW indication



Molecular weight



Gel Slice

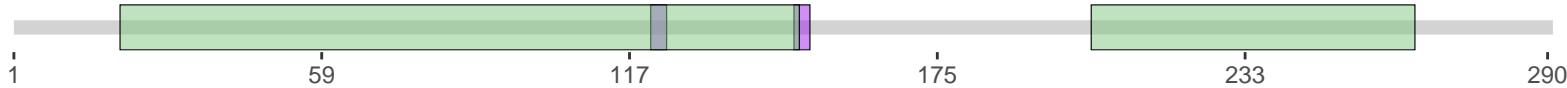


Protein length

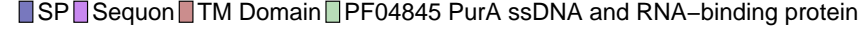


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SAQDGGWAAFRNLAENETSLRFSFNGGTSEPSDRLLGLSDVVGAGFSSHS6G5GPTADLGVERTIDLPAADEVNLSGVSKVIRADQKRFFFDLGENNRGHFLRISEVAGDSR6SILPLSGLKGFHEMVGHFVEISKDRLEGITGANVRTIDSPQR

NbL16g24360.1 pyruvate_kinase_cytosolic_isozyyme [MW = 55.03 kDa]

No. of times detected



log(intensity)



Values from



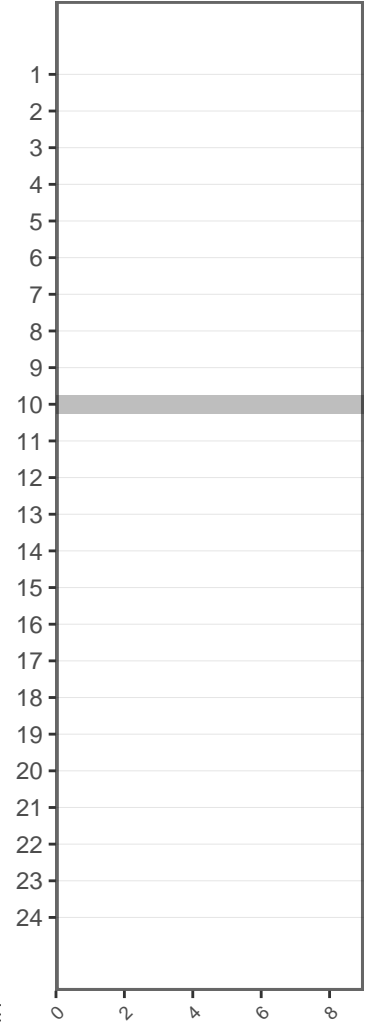
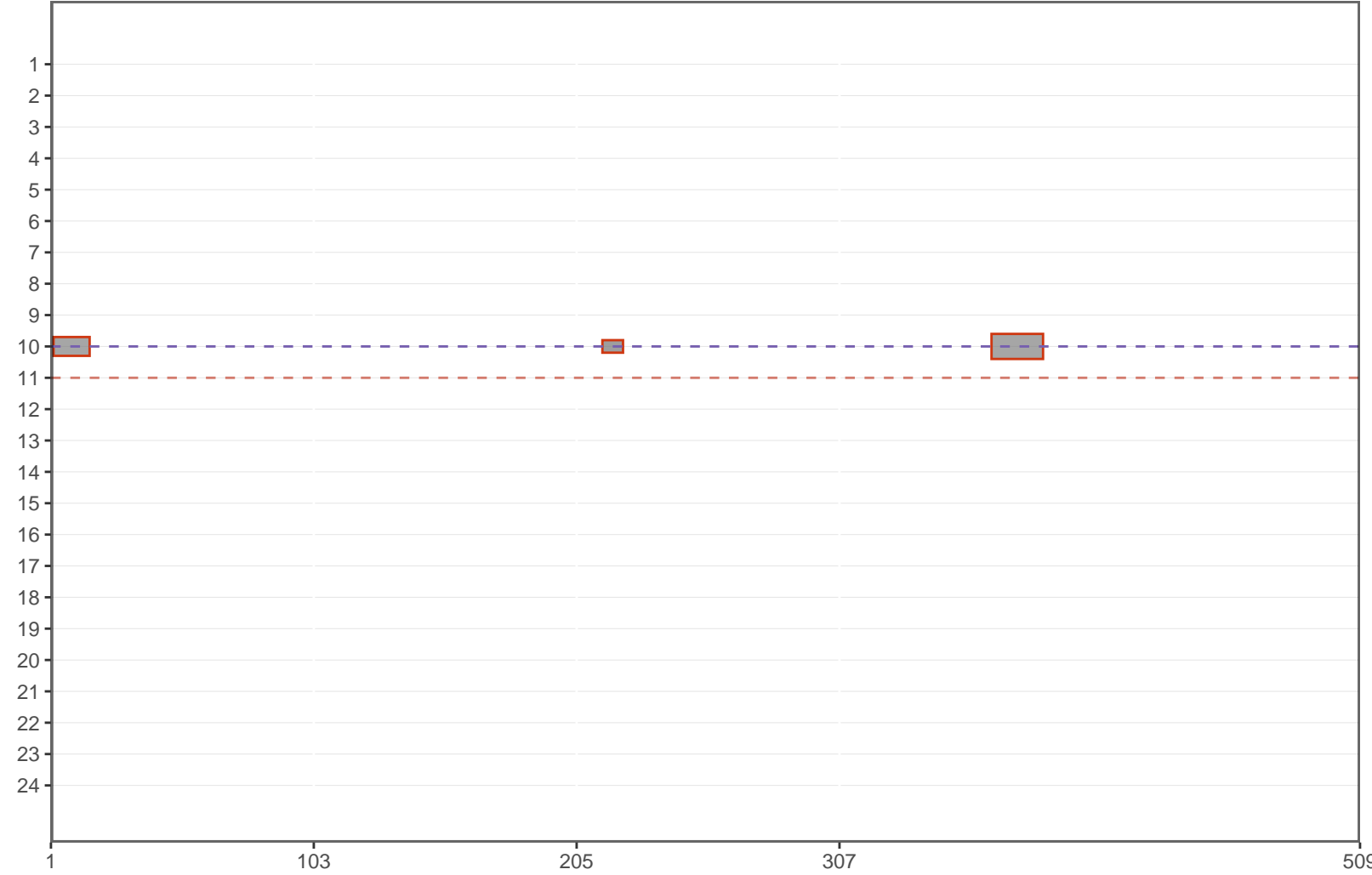
MW indication



Molecular weight

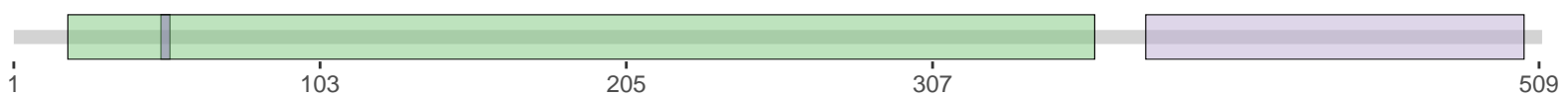


Gel Slice



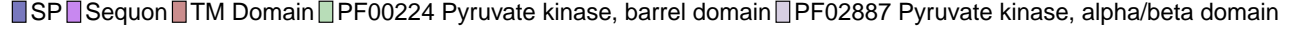
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ENQEGVAFNFDDLLNSDFMVRGDLGMEPIEKIFLAGKVMYKNGIGKPFVVTATQMLEMKRSPRTRAEATDVAANAVLDGTDGCVMLSGETAAGAPDLAVGTMAKIDIEAESTIDHPDVKRIRMSNAPVPMSEPLESLASSAVRTANSKAAALHLLVTRGGSTAKLVAKYRPGMPLLEVYVPEIKTDFDFTGSDSPARHSLIFRGLVPLVHAGSARASHHEESTEEALDFALGHAKTKGLGKGGDSVVALHRVGTASVIVKIVK

NbL16g24300.1 2-oxoisovalerate_dehydrogenase_subunit_beta_1_mitochondrial-like [MW = 39.6 kDa]

No. of times detected



log(intensity)



Values from



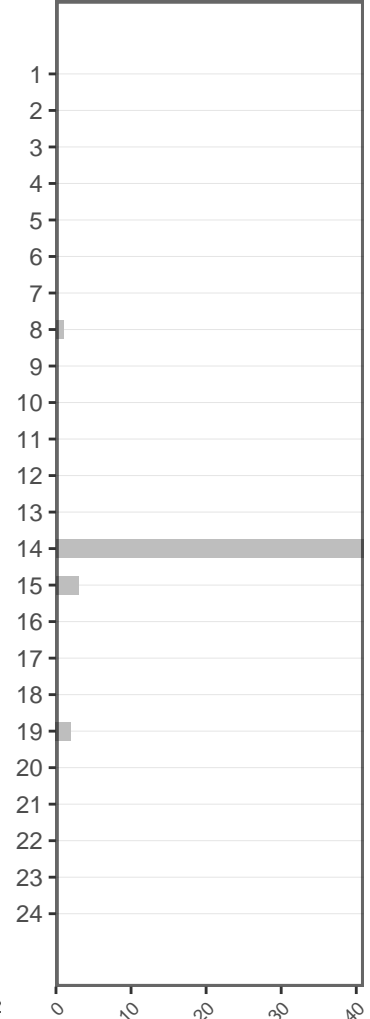
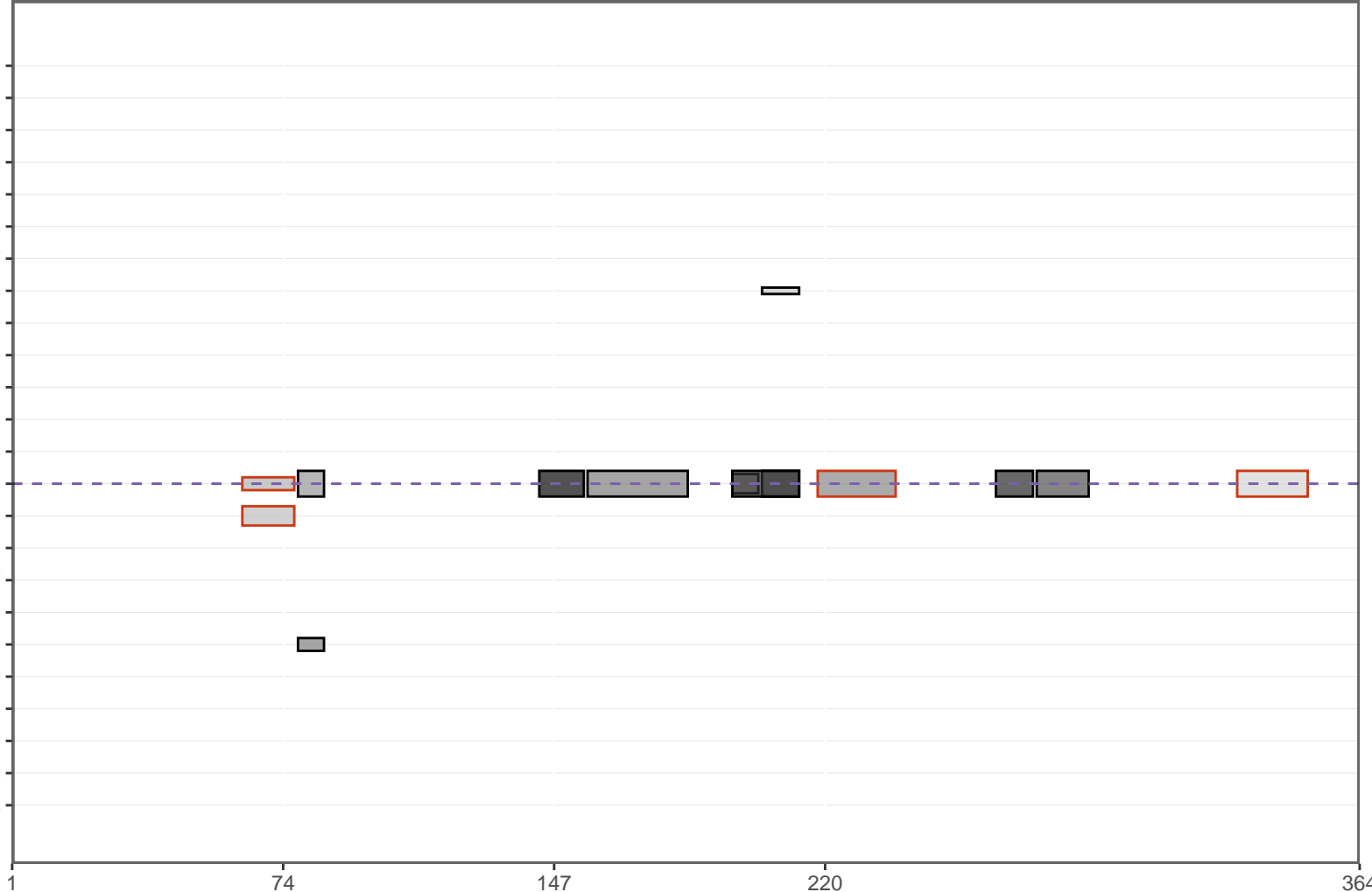
MW indication



Molecular weight

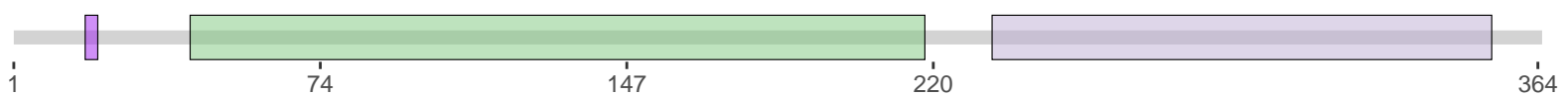


Gel Slice



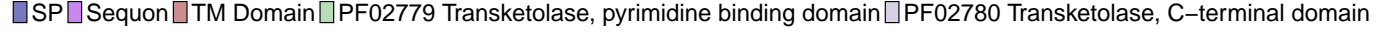
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISQSPESFFCHVPGIKVIRPSPHQAKGLLSSIRDNPVVFPEPKMLYRMVAEEVPEDDMLPLSEAEVREGSDITLVGWGAGLSTMEQAGCAEAAKIGISGELIDKLTLPDKETVEASVKKTRLLVSHAPVTFGFGAIEISASIVERGFTRLEAPVARVCGLDTPFLVFEFPVLPFNKILDAKSTNVY

NbL16g24290.1 protein_kinase_and_PP2C-like_domain-containing_protein [MW = 72.07 kDa]

No. of times detected



log(intensity)



Values from



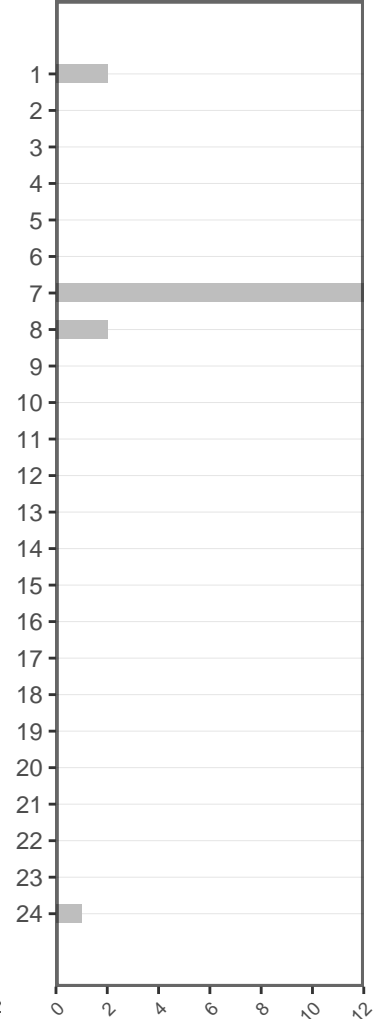
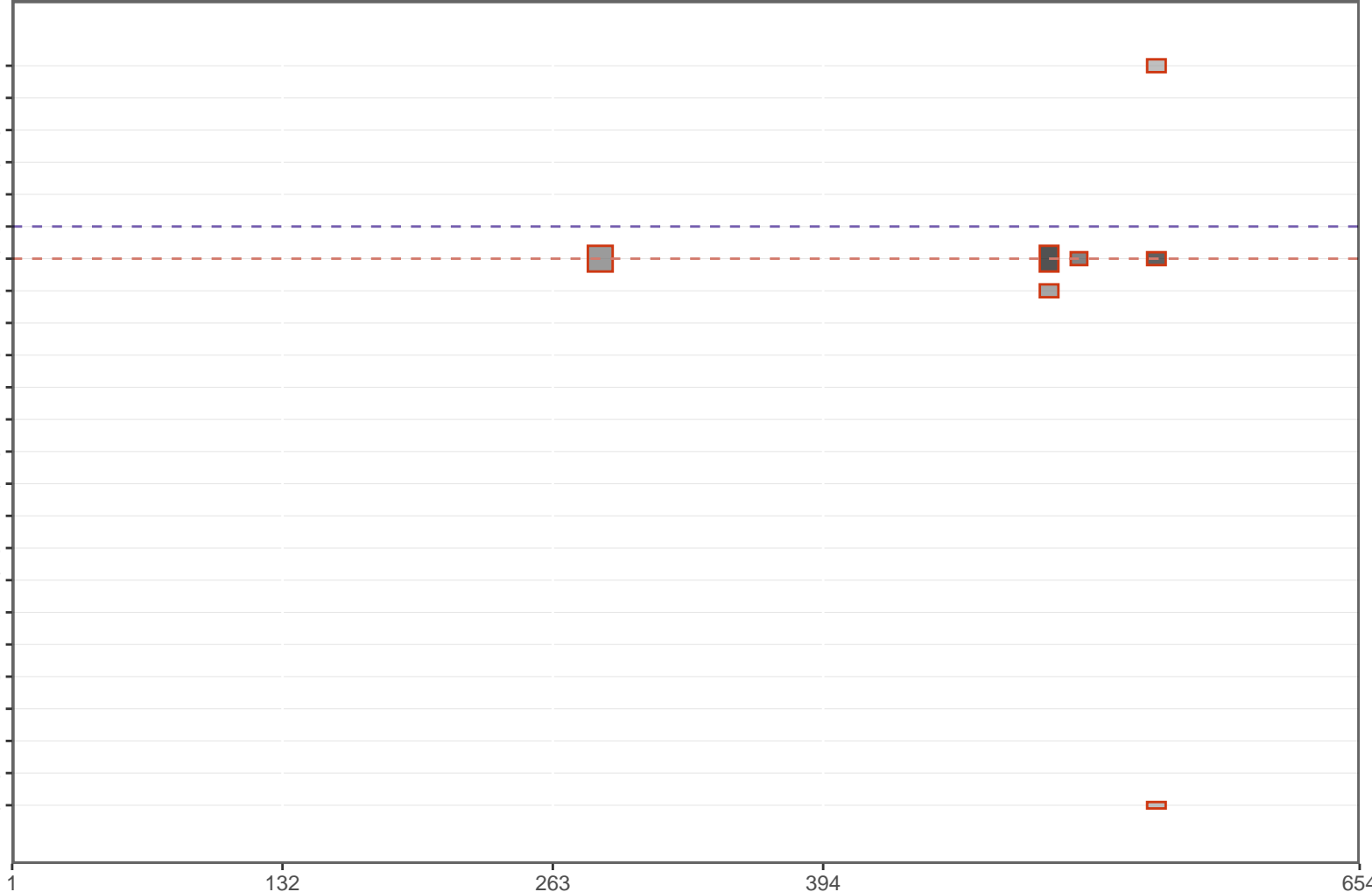
MW indication



Molecular weight



Gel Slice

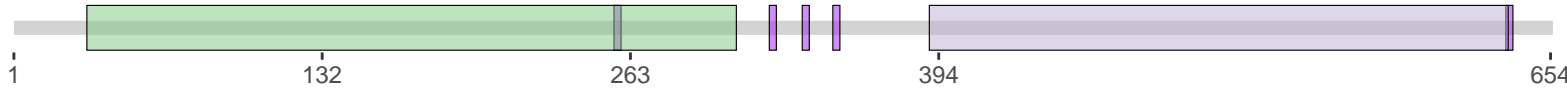


Protein length

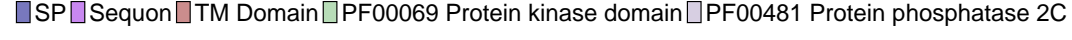


Peptide counts over 4 repeats

Pfam domains



Pfam Description

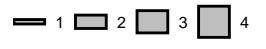


Protein sequence:

EDEIGTNHTEMASADDFISNNGSDGANIGYGENISWFGGGEKFSKRPVTAALASAWLDYSDQGVYFPAIGWGFASGGRRRETMDRHFLMPQLGDEKDHVFAFDGHRGSAAAEFESAGALPCFLQNLGSISSPQDALFEAFIKTDVAFRTGLDSCRNRKGAIGKDWHPGCGTAAALVKNKLVANAGDCRITLGRAGNYPALGRDHVASCHHEERERIRAGGLVKKWQVDTWRVGDALGVTRBIGDDDLKPAVTAEPETLITLSAEDEYIWMASDGLWVYSETDVTNIF

NbL16g24250.1 chaperonin_60_subunit_beta_2_chloroplastic-like [MW = 63.31 kDa]

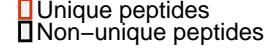
No. of times detected



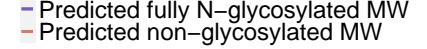
log(intensity)



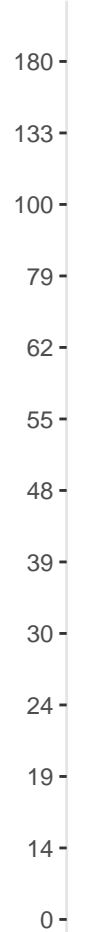
Values from



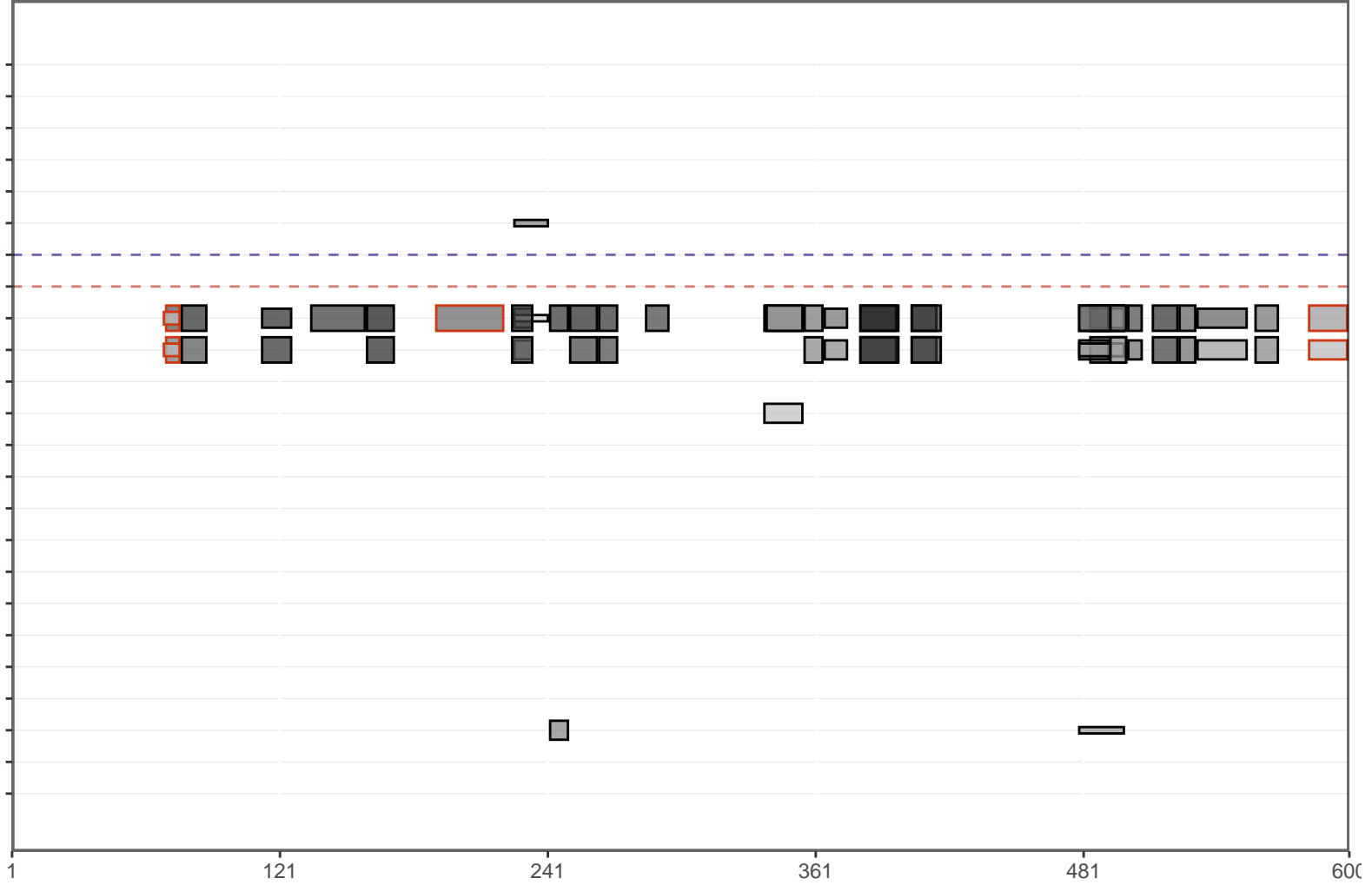
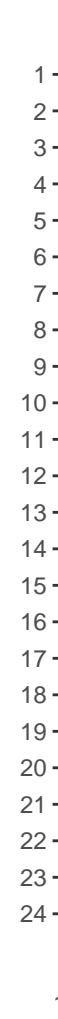
MW indication



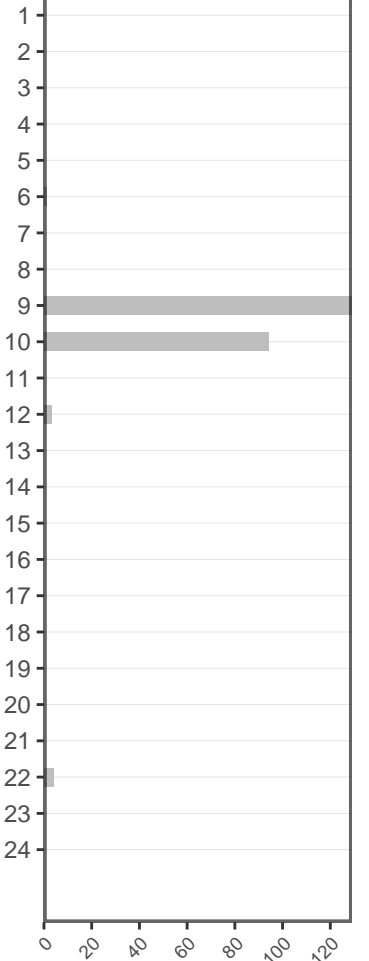
Molecular weight



Gel Slice



Protein length

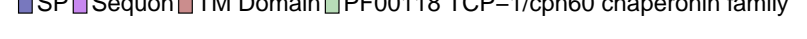


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

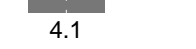
RDLVGLVLEDAIRNIGYRPLIHAEDIEGELATLVNKLKRGALKAALKKAPGFERKSGVLEDDIATLTGGTVIRDELGLTLKADKEVLGHASKVVLTKDATTIVGGSGTGDVANKRVIQKINLEAAGDQVEKELNERIAKLSGGVAVIQVAGTETELKEKLRVEDALNATKAAVEEGIVYGGGTLRLRASKVDAKETLENDEEKVADIVKRALSYPLKLIKAKNAGVNGSVSEKVLSSDNPKFGVNAATGNVEDLMAAGHIDPTKVVRRGLEHASSVAKTFLMSDCVVVEIKEPE

NbL16g24010.1 uncharacterized_LOC107786789 [MW = 27.48 kDa]

No. of times detected



log(intensity)



Values from



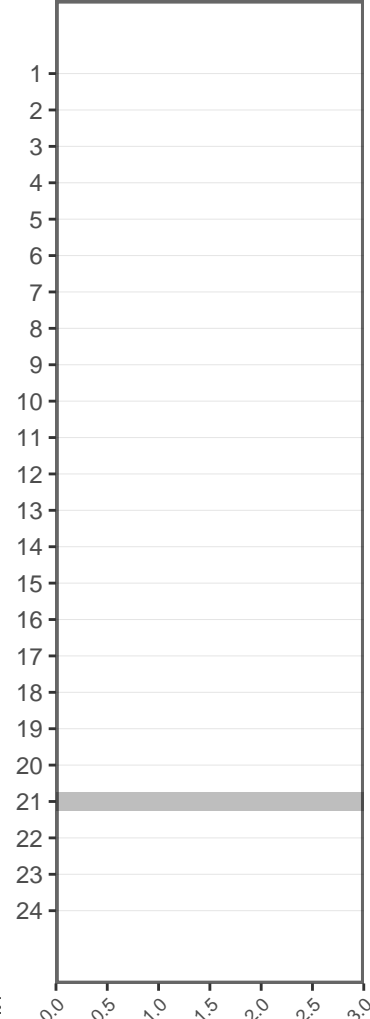
MW indication



Molecular weight



Gel Slice

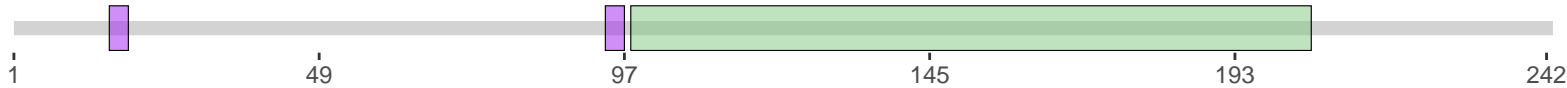


Peptide counts over 4 repeats

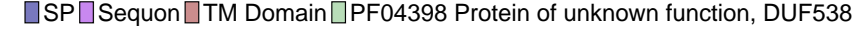
Protein length



Pfam domains



Pfam Description



Protein sequence:

GLLPDSVKSYSLSKIDGNFEVELEKPGVVEFEVLYVYAEKITGKLBIGSITDLEIGIQKRFLLWLVNNEIRVDFPSGGHYFQVGINKKLDMNQFETVHSGRDNALOGVSLRQVQLFNPVNDMPMLITE

NbL16g23980.1 dirigent_protein_22-like [MW - SP = 18.57 kDa]

No. of times detected



log(intensity)



Values from



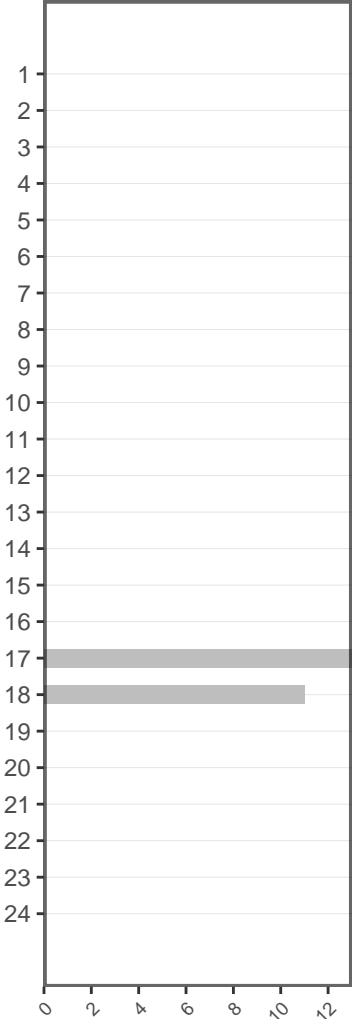
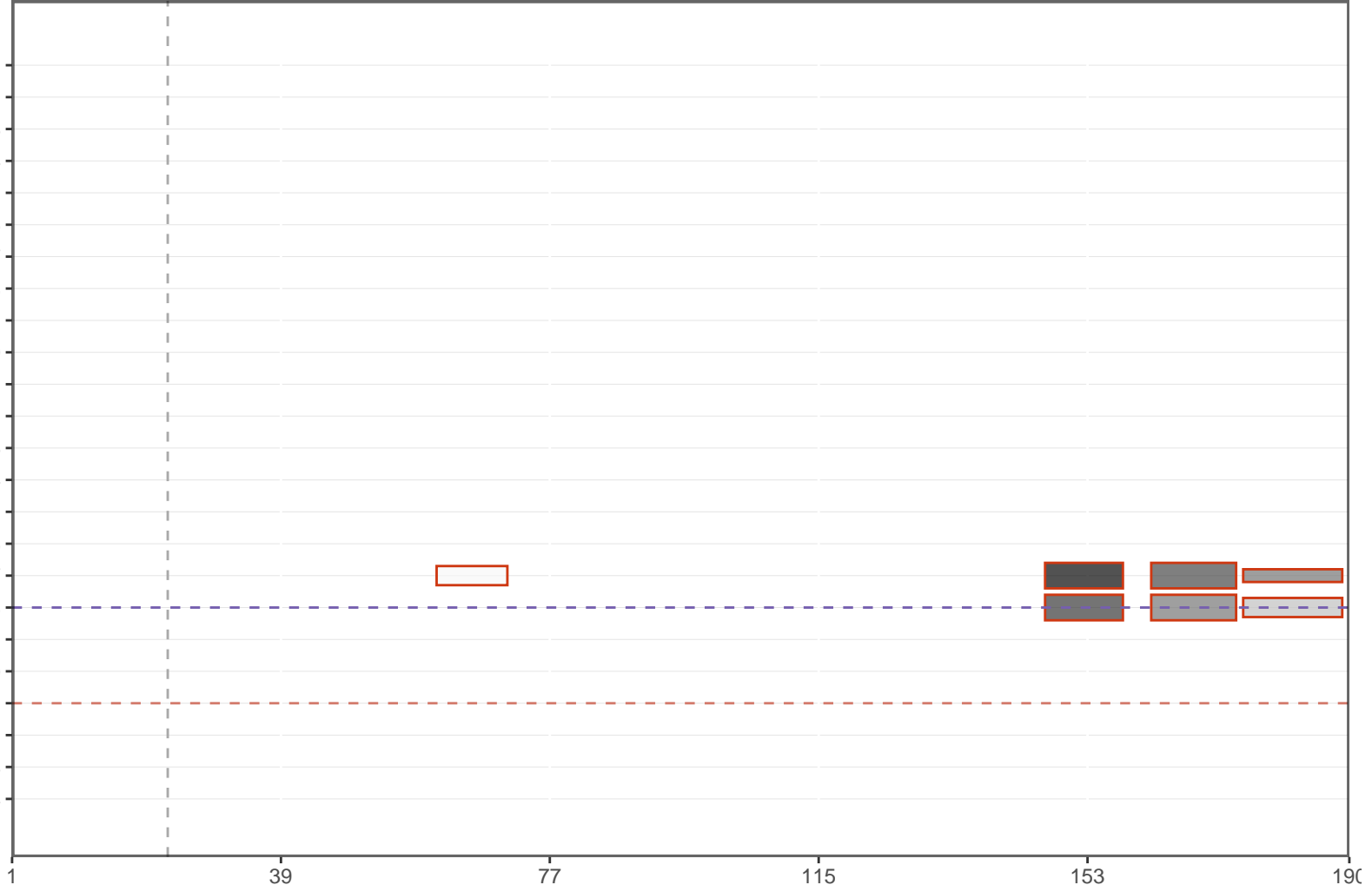
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

NALTLGPELSSKIVGRSGGFYASAGNDVGLMMVMNFAPVEGKYNGSTFTVLGRNSVFEKVRREMAVIGGSGLFRFARGYVQASTHSWDMKTGDTVQYDVAVLHY

NbL16g23540.1 glucan_endo-13-beta-glucosidase_acidic_isoform_GI9-like [MW = 38.99 kDa]

No. of times detected



log(intensity)



Values from



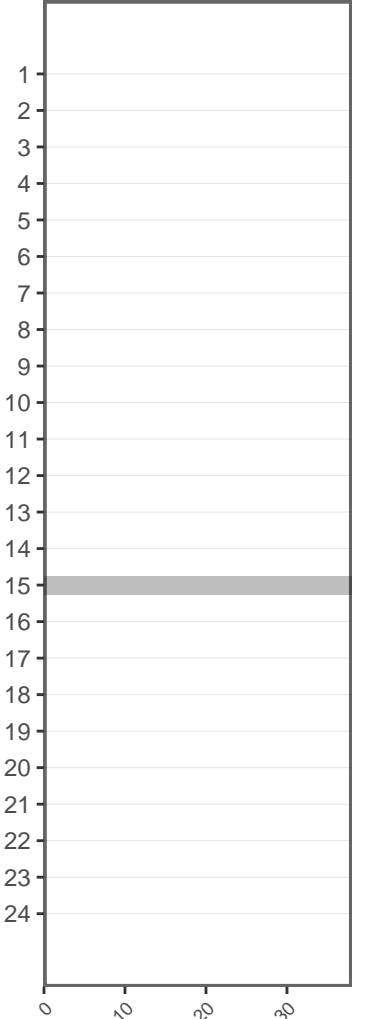
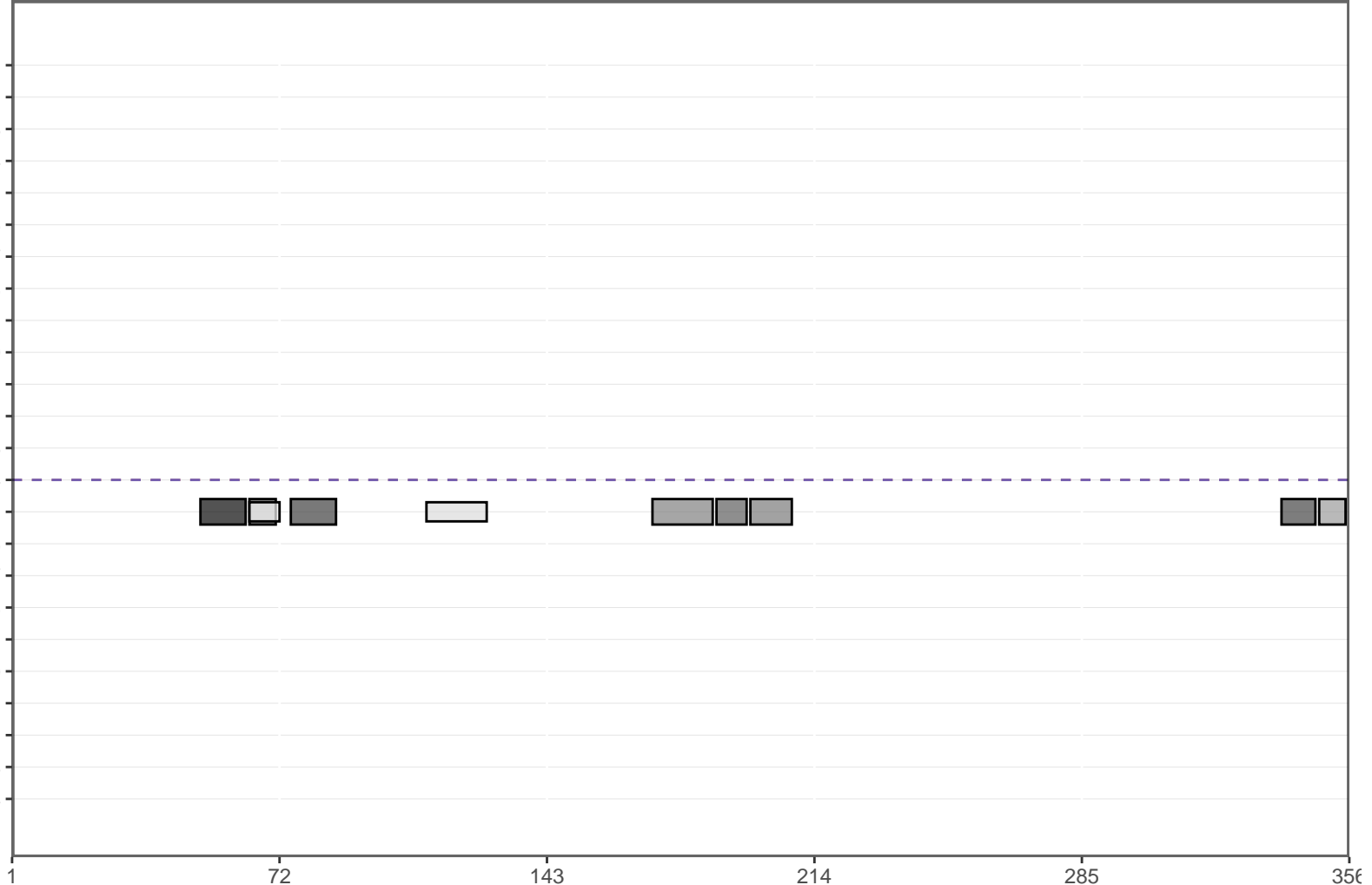
MW indication



Molecular weight

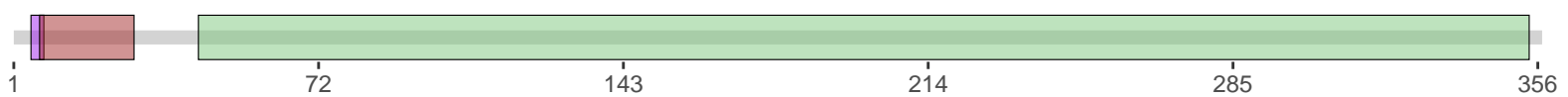


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

...DDQIKVSTATYSGLENTYPPKDFIFREEFNSTNPHQFLARHNLPLLANIYVFGCHYHSADVSLGVALFTQQGTNSAGYQNLFDALLDSMHFAVEKAGGQNVIEIVSESGWPSSEGNAAITENAGTYTINLNNHVKSGAGTKPKIPGKTETLYLFAIFDENNKEGDVTEKHFGLFSPDQRAKYQLNFN...

NbL16g23410.1 CBL-interacting_serine/threonine-protein_kinase_3-like [MW = 50.02 kDa]

No. of times detected



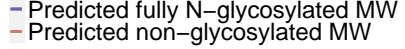
log(intensity)



Values from



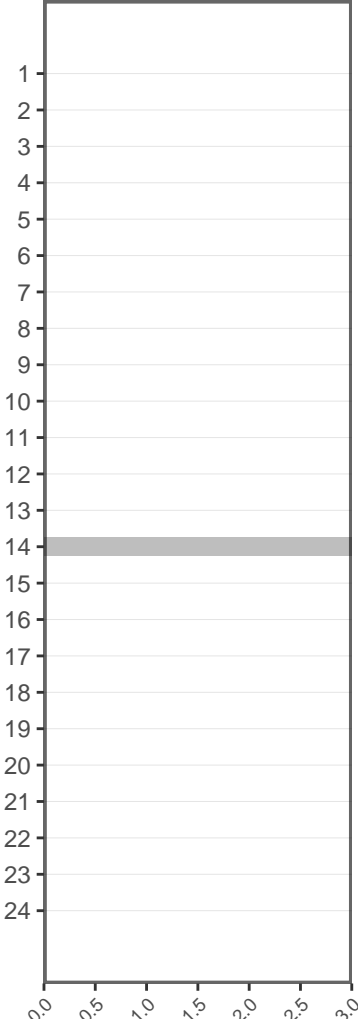
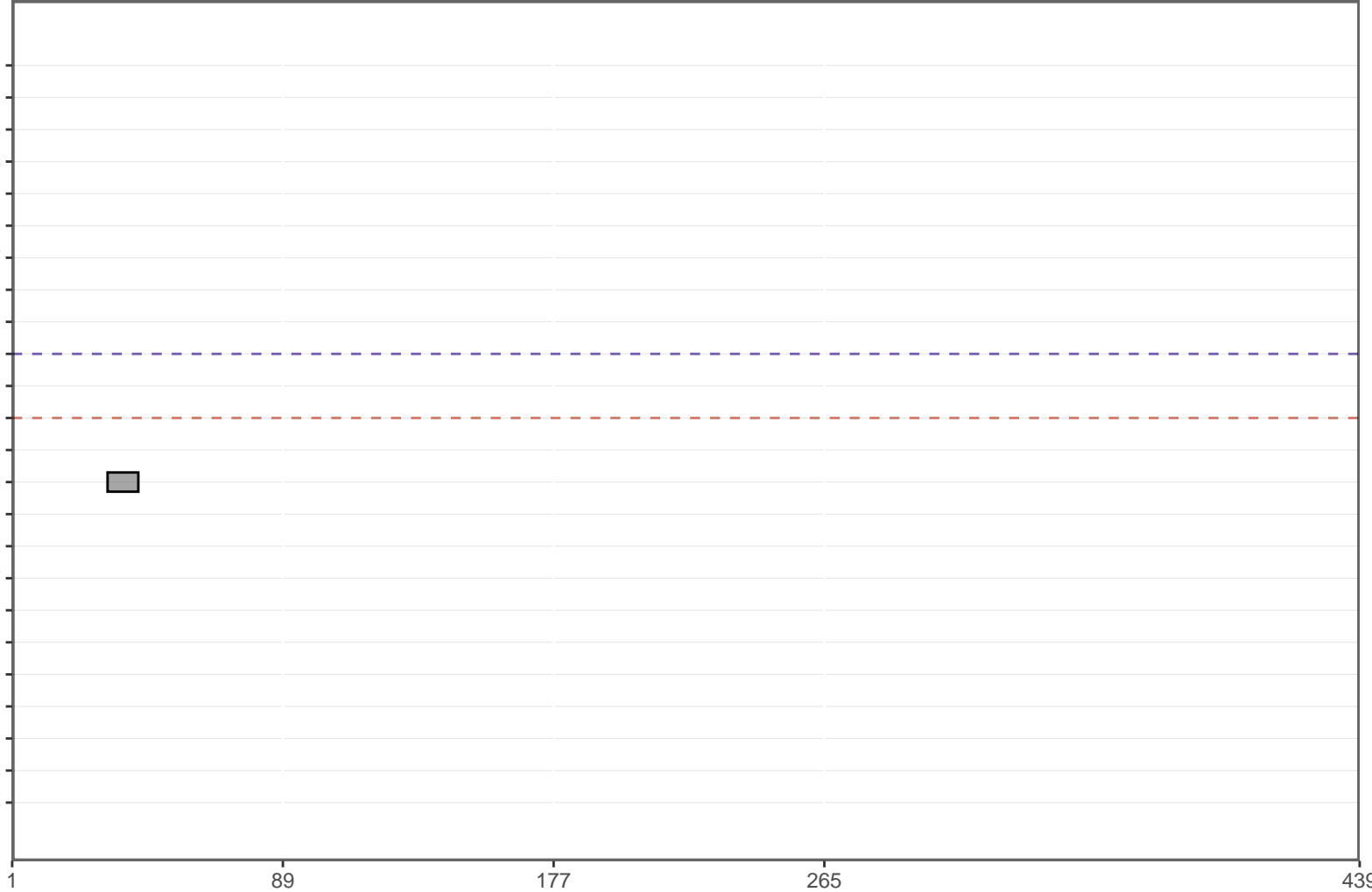
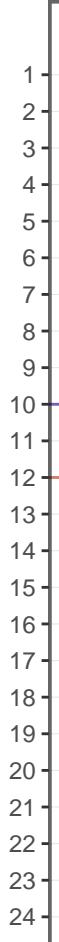
MW indication



Molecular weight

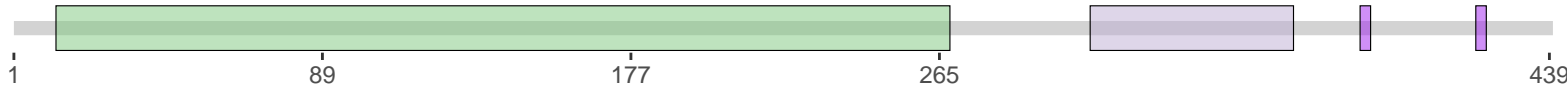


Gel Slice



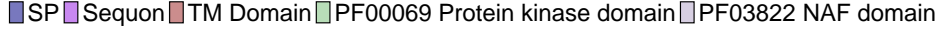
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

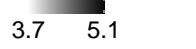
LLAGLYLFDOSNLMLNLYKISAAEFTGPPWIFSAAMKILTRILDNPPTTRITAPLELDEWFKKDYRPPVFDIEIDANLDDVEAVFKDSEEHYTEKKEKPTSMNAFELISMGGGLNGLNLFDEQGFKRFTRFTSKPASEIKSIEEAAKPLGFDVSKKYNKMRLLGNLAKGRKGNLNVSTEVFQWAPSLHMEVEKPKAKAGDTLEFKHYKYNLSTLSEDEVVWKTTEEMKKKK

NbL16g23370.1 uncharacterized_protein_At2g37660_chloroplastic-like [MW = 36.74 kDa]

No. of times detected



log(intensity)



Values from



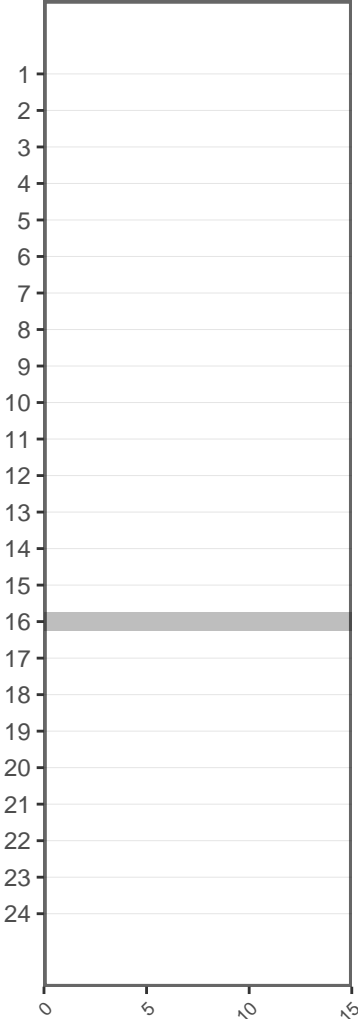
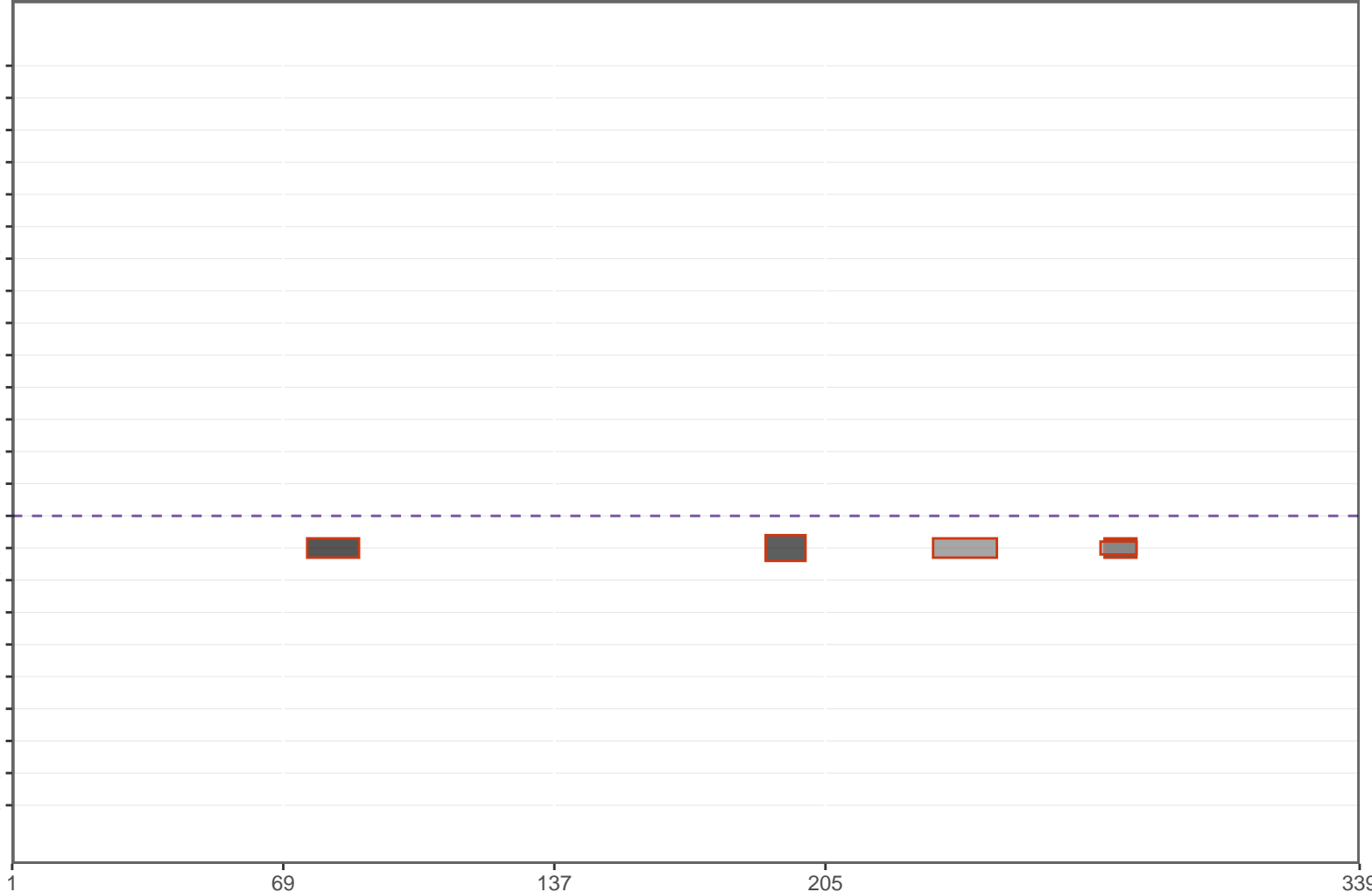
MW indication



Molecular weight

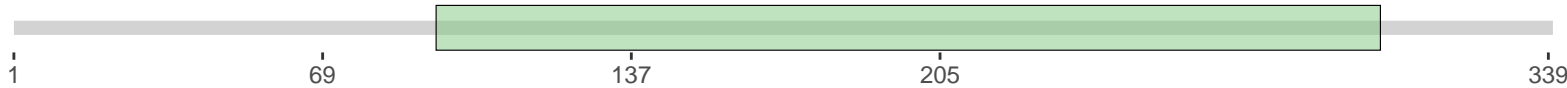


Gel Slice



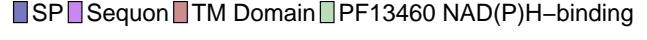
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SVTHVICCTGTTAFPSRRWDGDNTPERVDWEGVSRNLVSAIPQSLKRLVLSGIVTKFNELPWSIMLFGVLKYYKMGEDFVQNSGLPFTIRAGRLTGGPYTSYDLNLLGATAGERRAVLGGGDKLVGSEVSRLLVWEACIGALDVFDTGGOTYENISPIGGDGTDLKAWGELFRASHNNV

NbL16g23330.1 UBP1-associated_protein_2B-like [MW = 52.03 kDa]

No. of times detected



log(intensity)



Values from



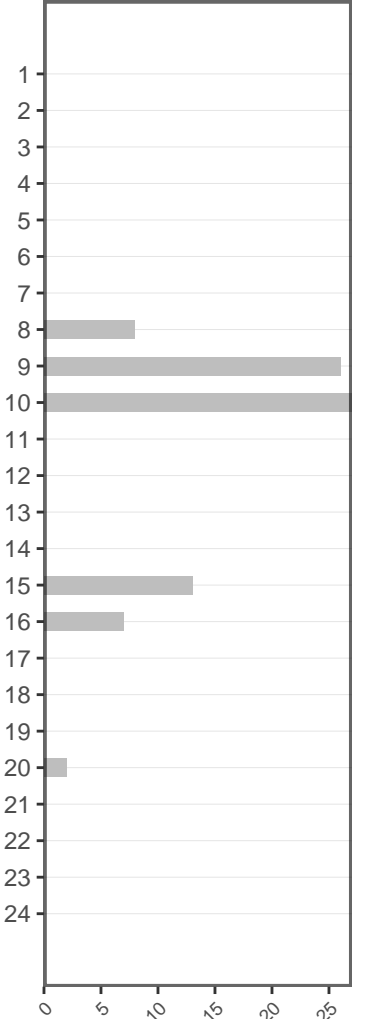
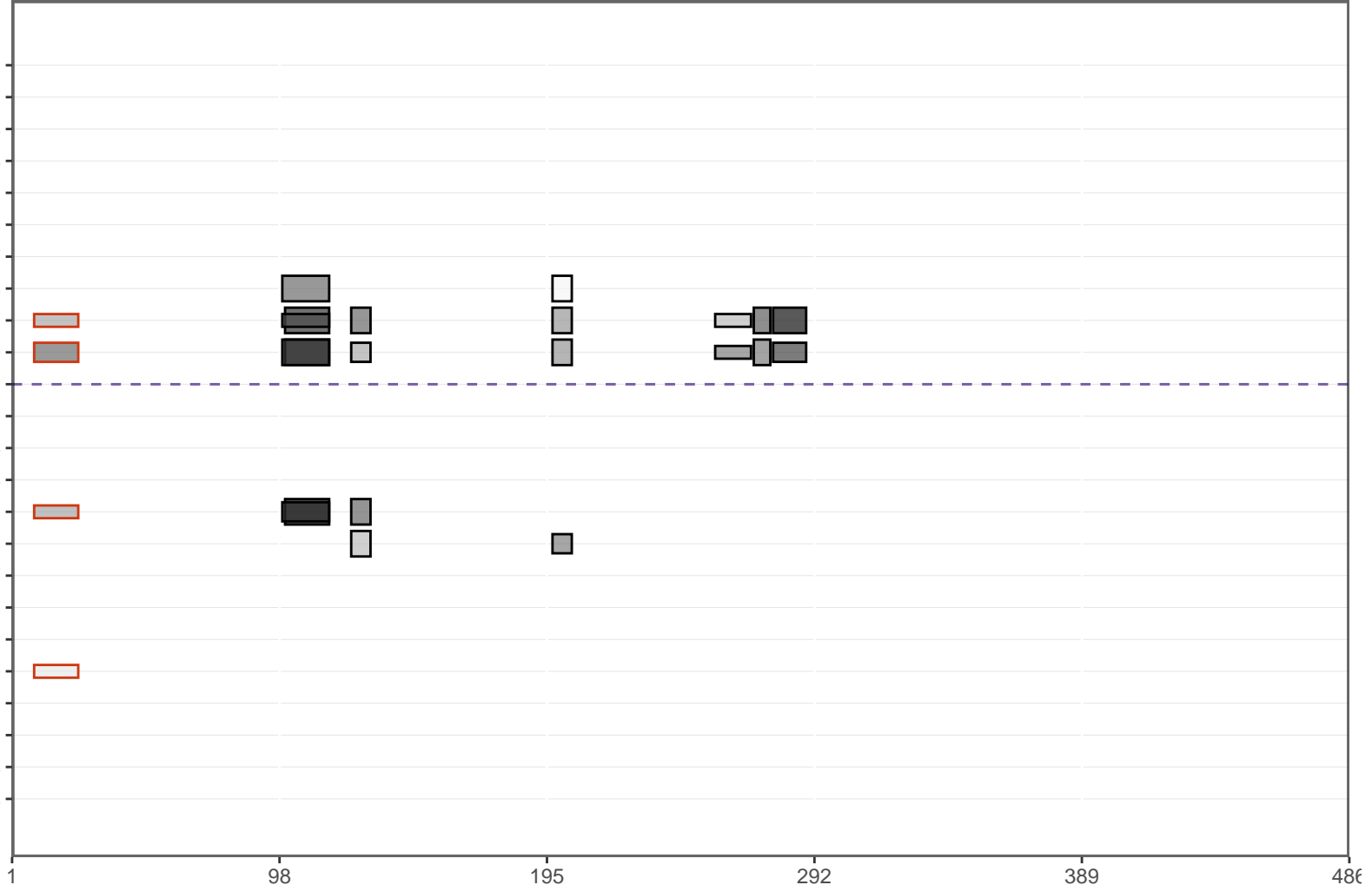
MW indication



Molecular weight



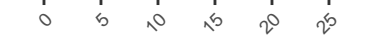
Gel Slice



Protein length



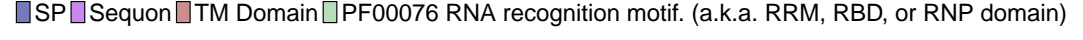
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

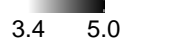
YKAPPPPTAAVPPVSEYTRGRKIFVSNVAADLDPKHLEFFSKFGEVEEGPLGDKGTGKPKGFCLEFYKSVESARKALEEPKHFEGHTLHGQKAVDGPKNKNNYHQHGGPQGHYPQHQHGGHQQYHQHPKKGKYSGGSGSAAAGAGHLMAPSGPMPGPNFPAWAFALGQALLTALQTGAGLGGKGLLGGFSGPVNHQGGVPPVMNNAAGGYGAGGAAGGYGAPRMQYGNFQMGGARGPQGGAPYRPGYGL

NbL16g23230.1 molybdopterin_biosynthesis_protein_CNX1-like [MW = 70.28 kDa]

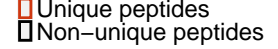
No. of times detected



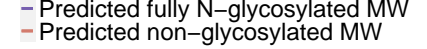
log(intensity)



Values from



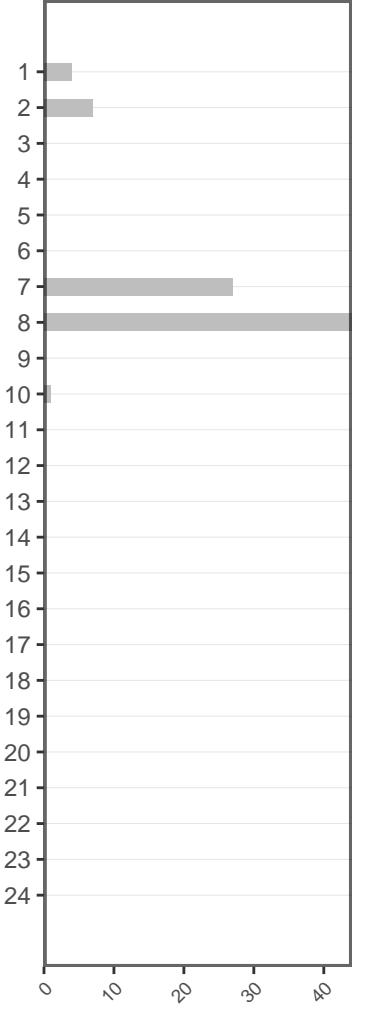
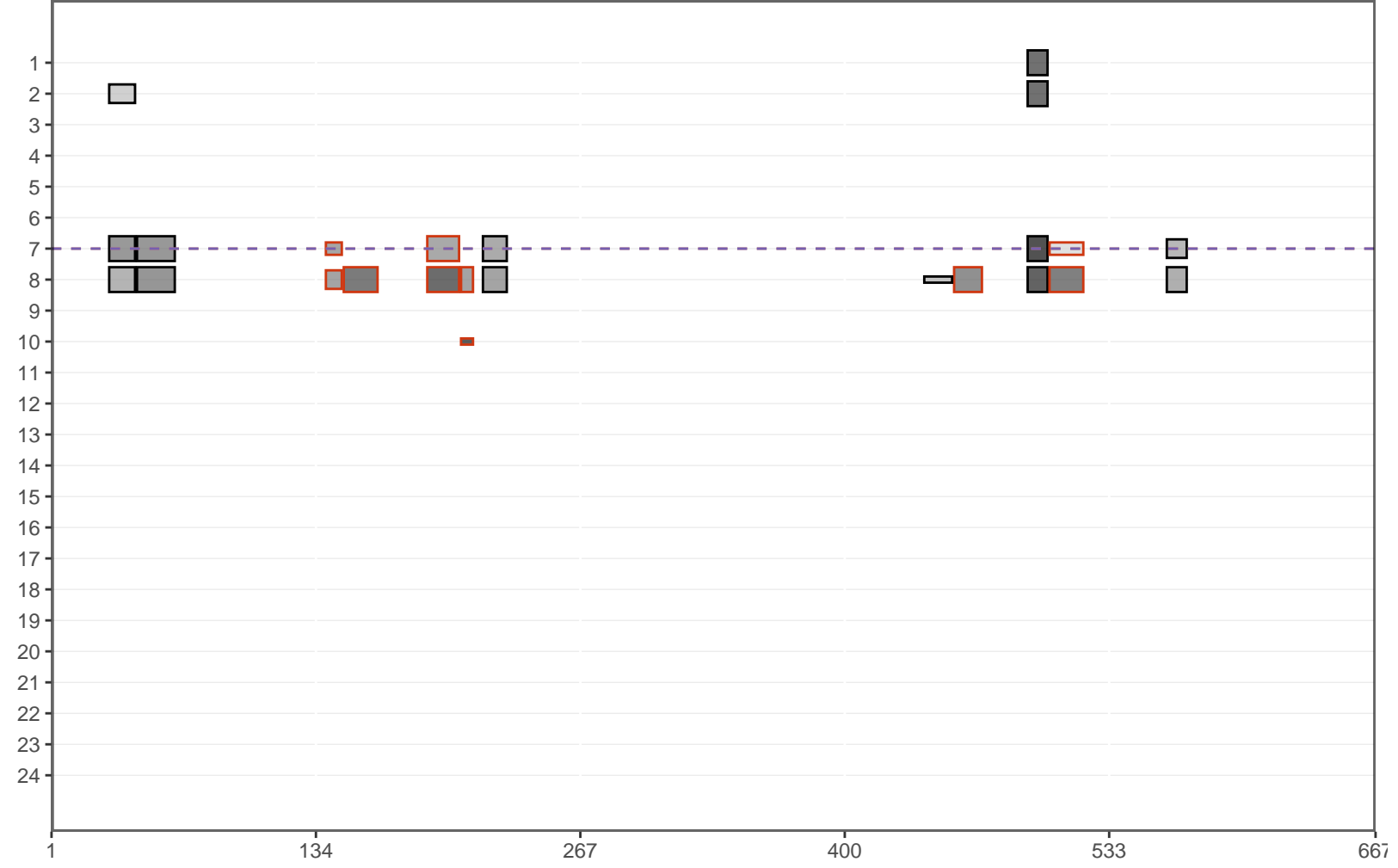
MW indication



Molecular weight

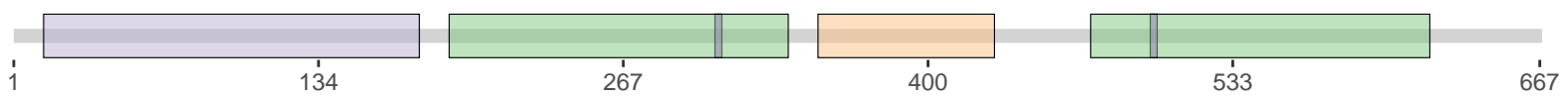


Gel Slice



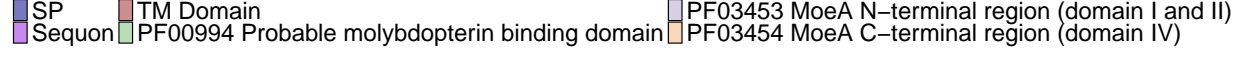
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISLVCFYLFVVAIRHISGWANPHLPRVQARVHKSHKTNFFRPEYHRAIHQWLNDSGGSGGFMAEESTGGGSRLLSMKSNALLELPASDTSLPAGALVSAHLSIDISNPGSRSLQLPLDSVVOGDKLAAANTGSCDESEFRVAILVSDTVAAGLGPDRSGPRAVSVNNSSESLGGTSEVAVAVVPPDDEGKIKNMLQMWSDVDKVDLHFLGGTGTTPRDVTPKATKSMQKETPGLLYVMMREGLKVTPEAMLSRAAAAGIRGDTLIMPGNPNVAIECEMALLRLKH

NbL16g23040.1 kirola-like [MW = 16.8 kDa]

No. of times detected



log(intensity)



Values from



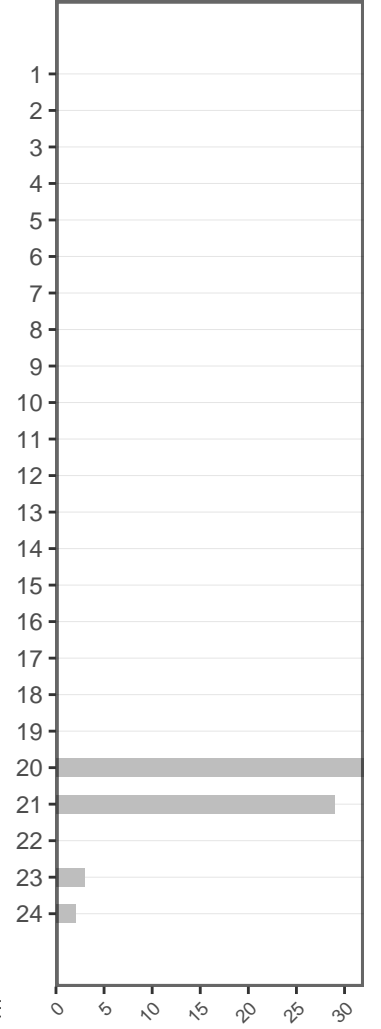
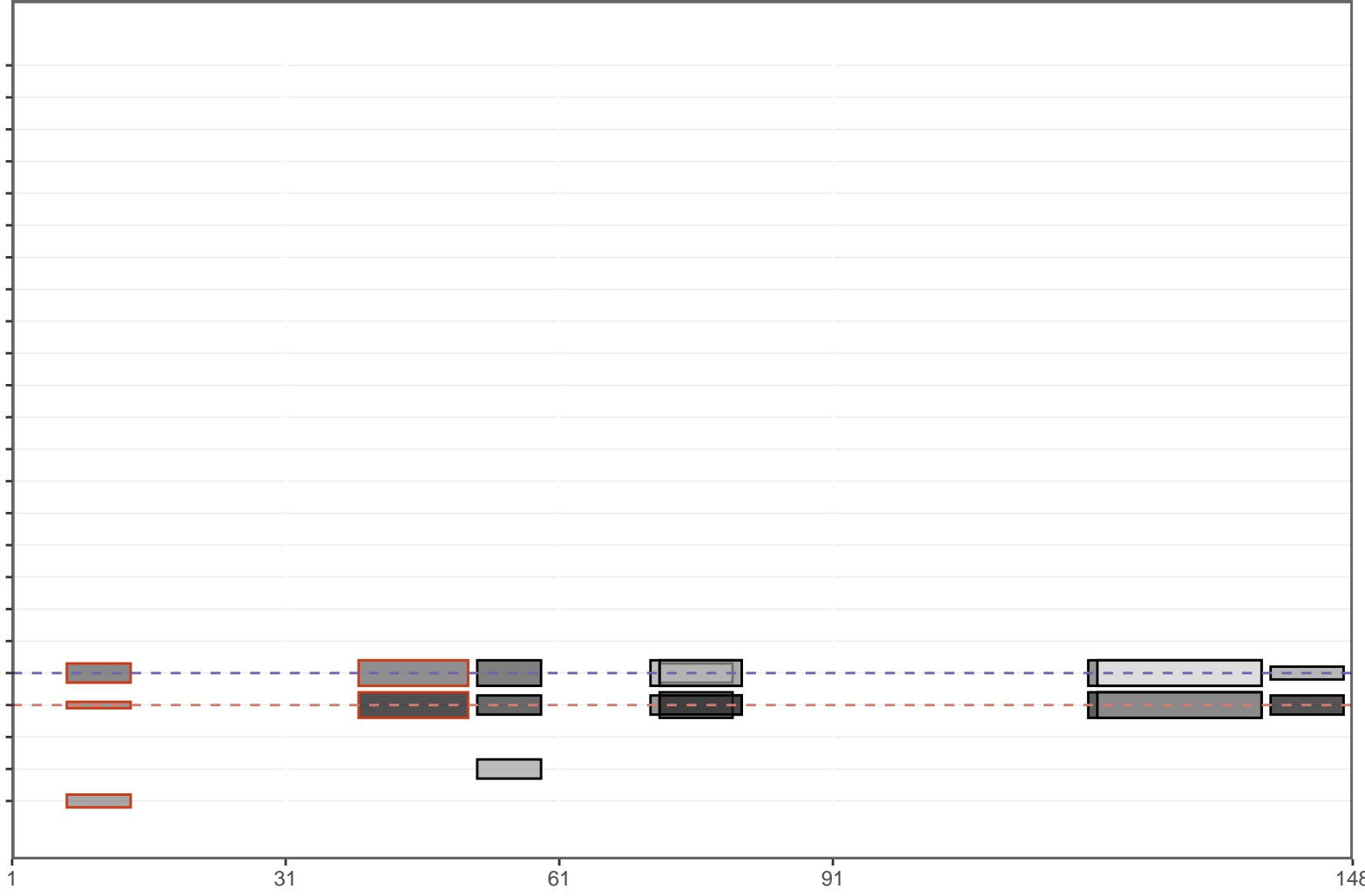
MW indication



Molecular weight

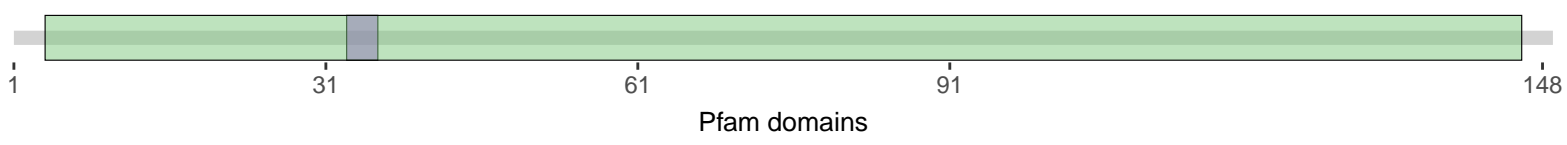


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEDGKEKTVKXVIEAFDPQKQKSVTWKIVDGDLLLELYNYFTIHSSEDDQWTFWTIMYEKKTEDTPEPLASMGVLLVTKDIDSHLLMK

NbL16g23010.1 indole-3-acetaldehyde_oxidase-like [MW = 149.36 kDa]

No. of times detected



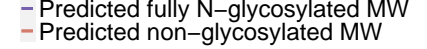
log(intensity)



Values from

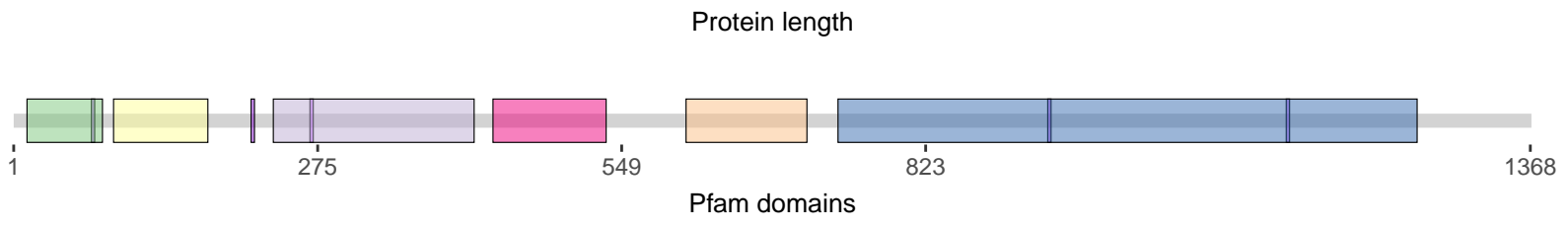
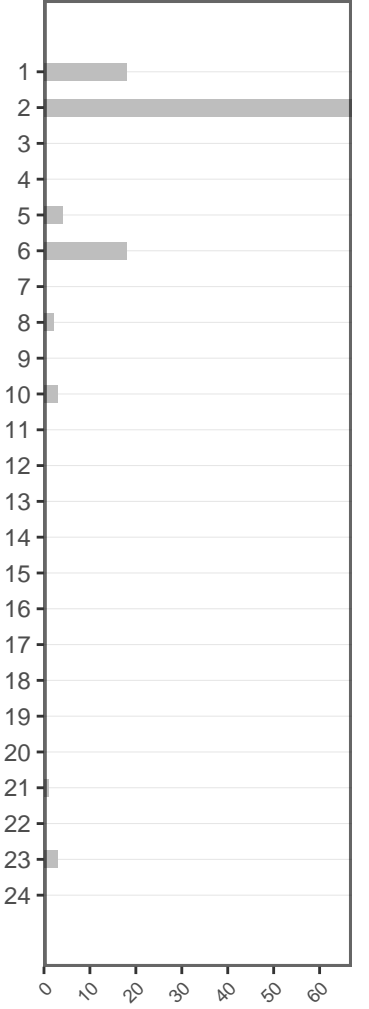
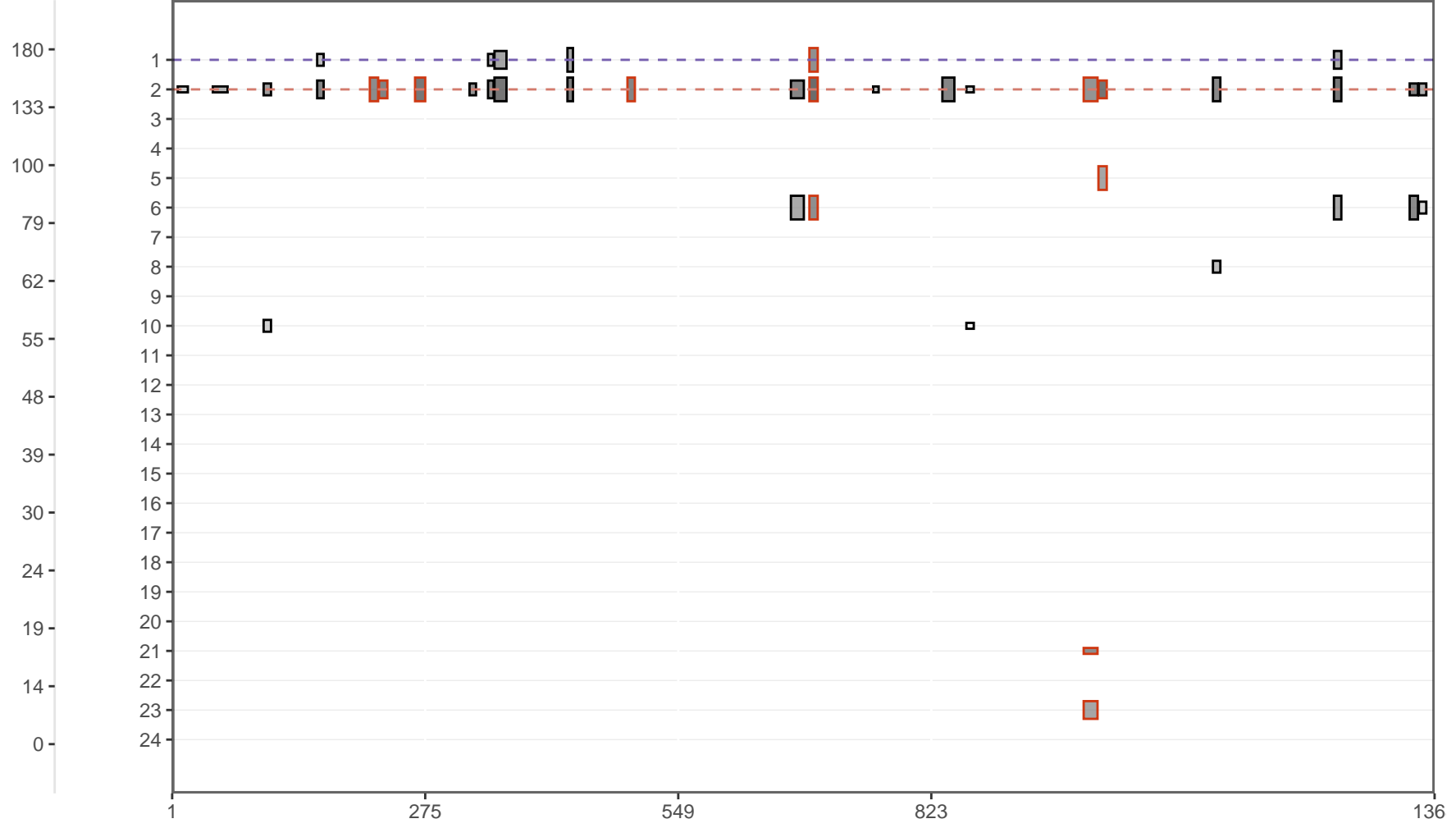


MW indication



Molecular weight

Gel Slice



- PF00941 FAD binding domain in molybdopterin dehydrogenase
- PF01799 [2Fe-2S] binding domain
- PF03450 CO dehydrogenase
- PF01315 Aldehyde oxidase and xanthine dehydrogenase, a/b hammerhead domain
- PF02738 Molybdopterin-binding domain of aldehyde dehydrogenase

Protein sequence:

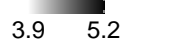
IGPEPLFADDLARVAGDRIFAVAESGRSADVAANMAVVEYDTEVDSEPTLTVVEEAVKSGSFFQVPPFLVYKRVGEFSKGMAEADHKILSAEMRLGGQYFYVMEQTALAVPDEDNGMVAVYASGGQPEVAGSVAAGLGVPEHNIRVYTRRVGGFGGKAVRAMPVSTACALAAFLQRPVRYVNRKTDMMAGGRHPMKITVYVGRKSNKGTALHLEDVLINAGIEDVSPISPFNGFALKKYDVGALSFDKVKTKLNTSKSAMRGGPEVGGSHAEAMEHVAISVLSSEVI

NbL16g22990.1 uncharacterized_LOC107782810 [MW = 13.57 kDa]

No. of times detected



log(intensity)



Values from



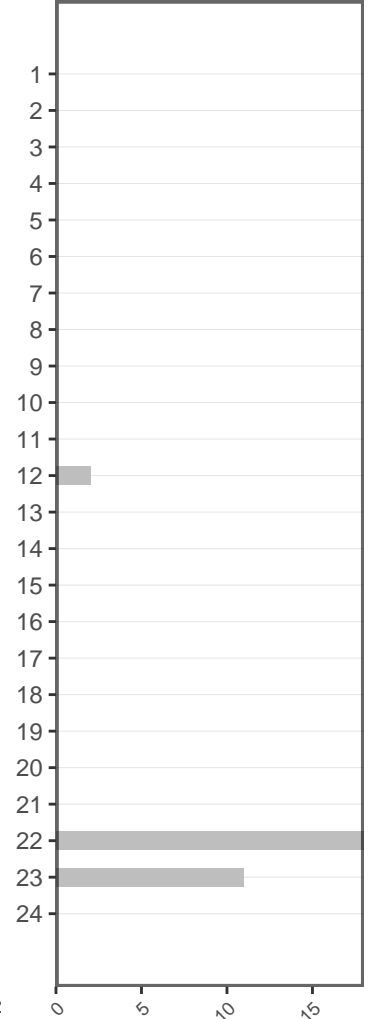
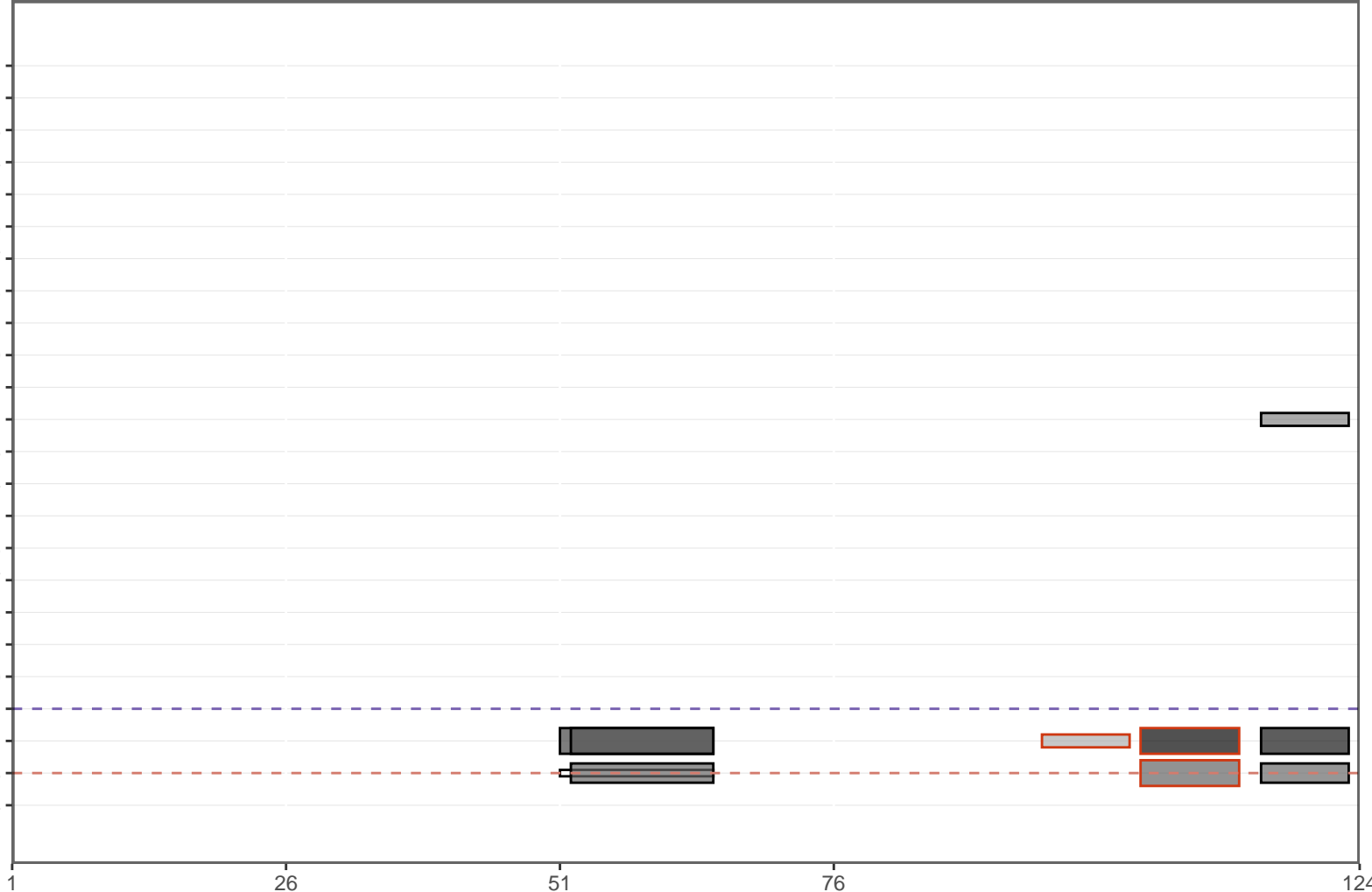
MW indication



Molecular weight

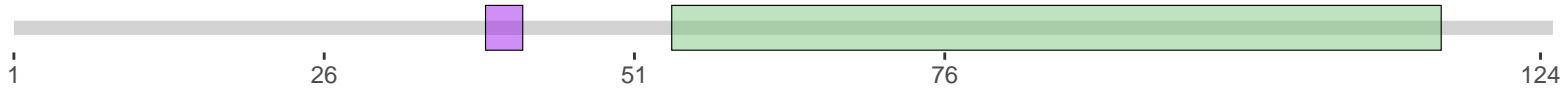


Gel Slice



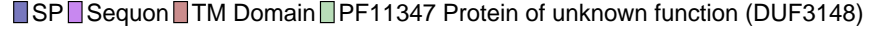
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DSKLGIGSPITVEAPKLLKTAASVPLRLPNDGLKPGDNGRIVSRKPMDDWAIRLGGTYLDRKYRPLELEN

NbL16g22950.1 serine/threonine-protein_phosphatase_BSL3-like [MW = 104.34 kDa]

No. of times detected



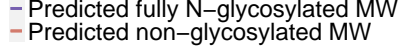
log(intensity)



Values from

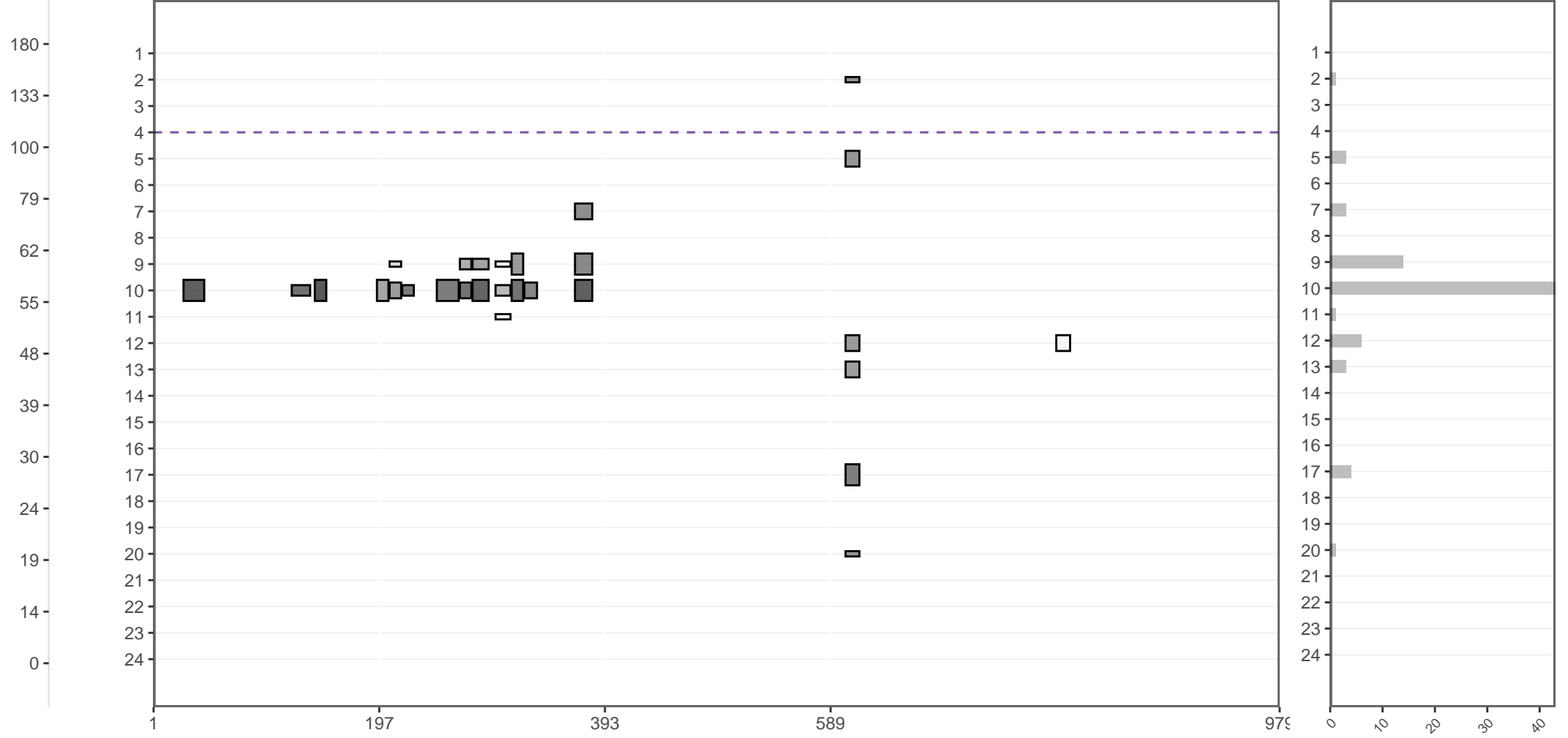


MW indication



Molecular weight

Gel Slice



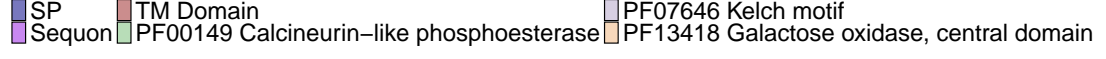
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VAPPVNGDMFTDIDSTENAVLGGSRKLGKGVVEVLSASAAEAATAALAAKARQGGNGEVELPDRDRGAETPSSGGASTLKPDSNNETSAGVRLHRRAVVAETGALGGMVRLGSLDGFENEGRRVYVGTPEATAARLLDRQGMVSNVSPKVAIAHLKPRGWKPPVRRGFFLDCNEIADLGDSEARIFSSSEPSVLQLRAPKIFGDLHGDFGDMRLFDEYVGSPTAGDAWIDVFLFGDYVDRQGHLEMTLLLAKVVEYVPHNHLIRGNIEAADINALGFR

NbL16g22940.1 protein_CLP1_homolog [MW = 48.01 kDa]

No. of times detected



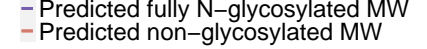
log(intensity)



Values from



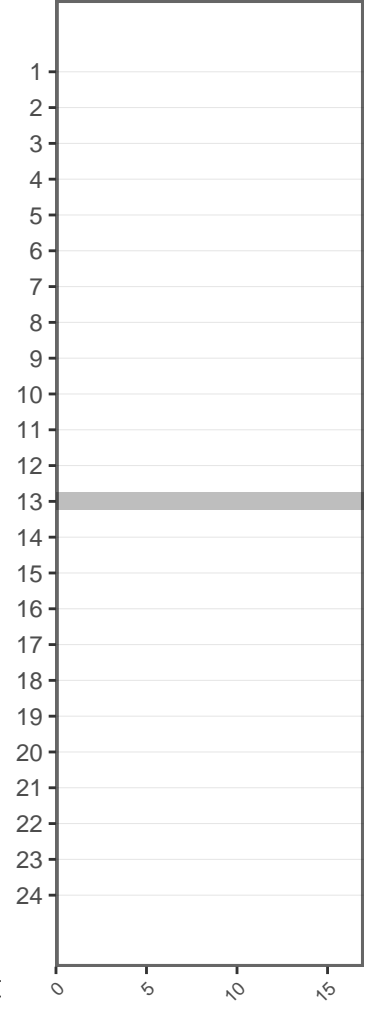
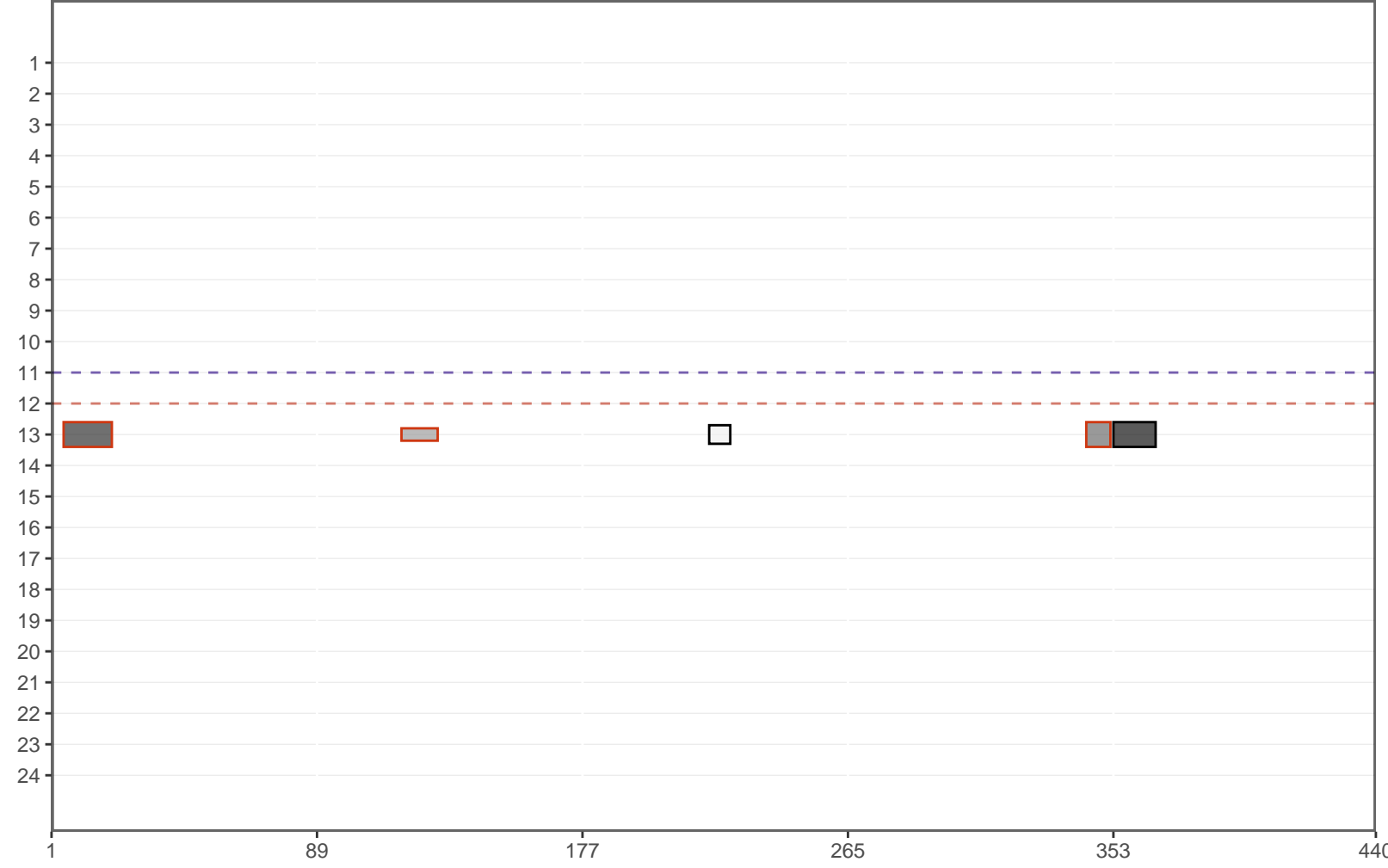
MW indication



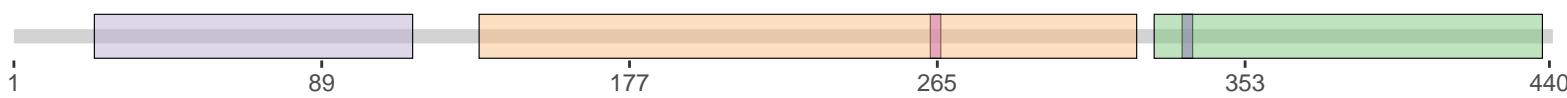
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

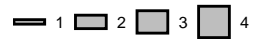


Protein sequence:

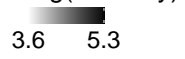
'SANDHYKLVKELAQTLERQFSNAESRASGMVNTFMQWIEGQYELLHIAIDFTNATVILVLDGKLGSMKDKVILKRNRPVDAVKLQKGGVSRNAKVRQKARGYRREYFYGFSDNLSFHSNVAVNFSDLFYRIGGGPAAPRSALPFAEPAADPTRLVLSINRDLHLVAVSWNEPDQIISNVAQFIYTDVDMHRKKITFLAPCAGELPSKYLVTETWEN'

NbL16g22840.1 UDP-D-apiose/UDP-D-xylose_synthase_2-like [MW = 43.32 kDa]

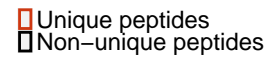
No. of times detected



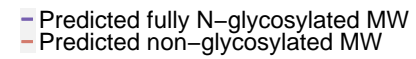
log(intensity)



Values from



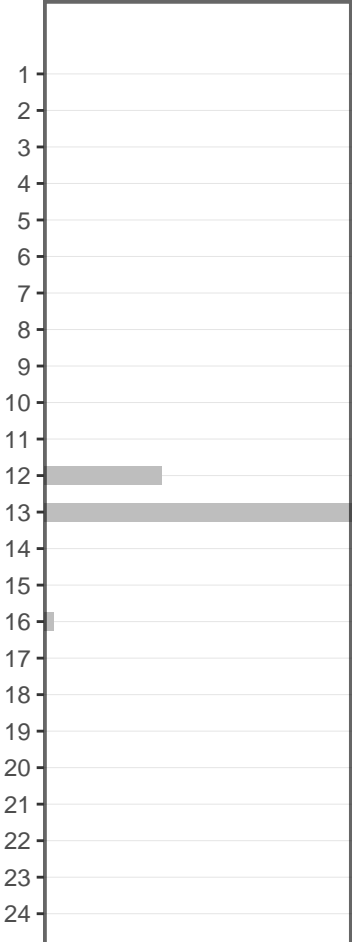
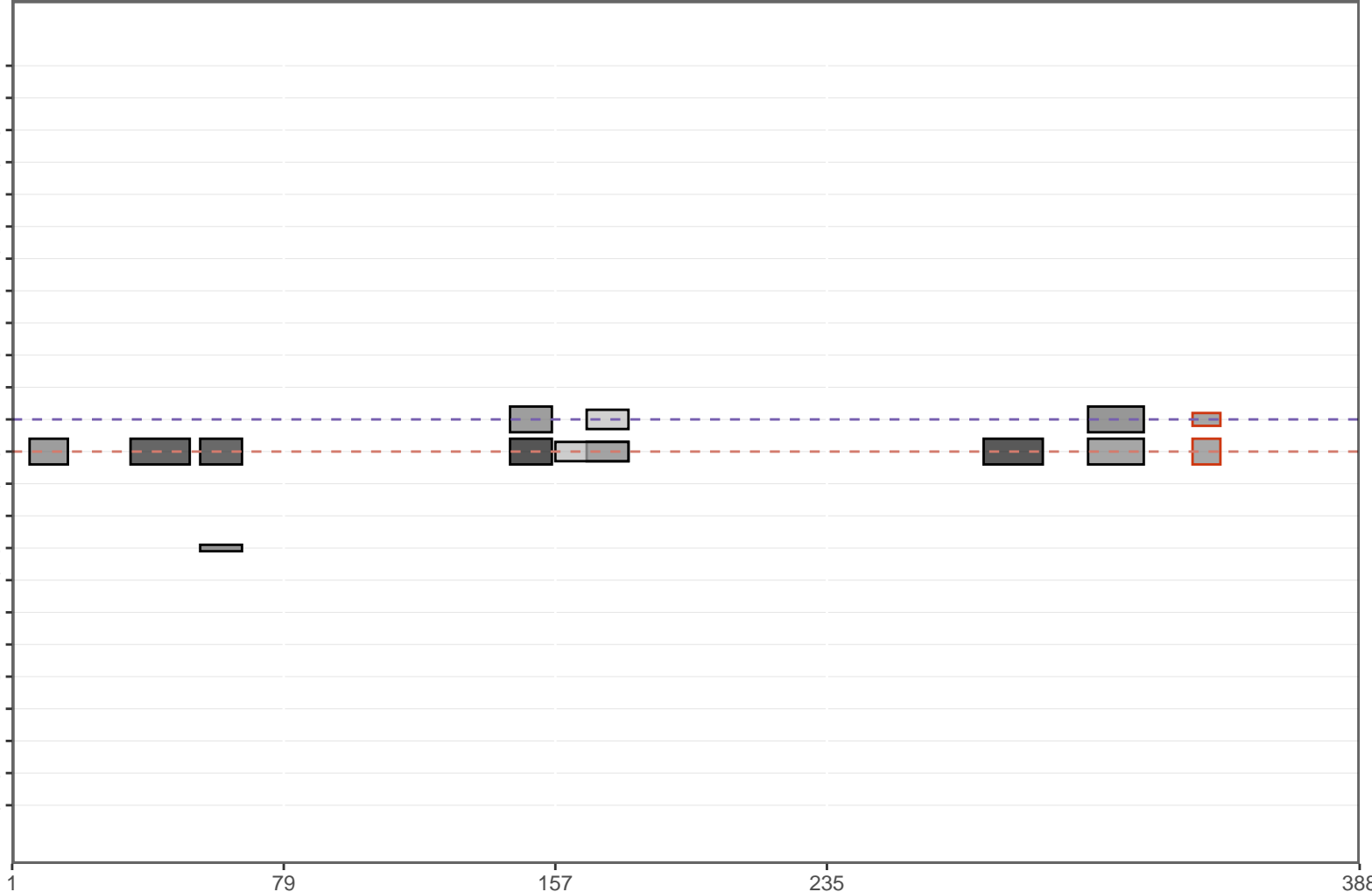
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SYACAKQLERLIYASGAENGLLEFTIVRPFNWIGPRMDFPQIDGPGEGVPRVLACFSNNLLRHEPLKLVDDGHSGRFTFYKDAIEAVLLMIENPARANGFNQVNPNNNEVTVRGLAEMMTQVYKVKVGGESPPETPTDVSSEKFEYVGGEGVDDSDKRIPDMFLINRQLGWNPKTSLWDLLESTLYGHRTYAEAVKQAMSKTIAN

NbL16g22720.1 60S_ribosomal_protein_L10a-1-like [MW = 24.61 kDa]

No. of times detected



log(intensity)



Values from



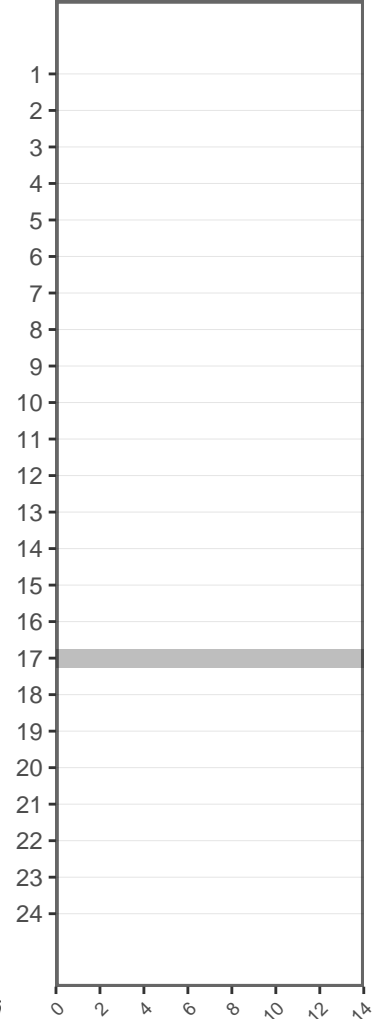
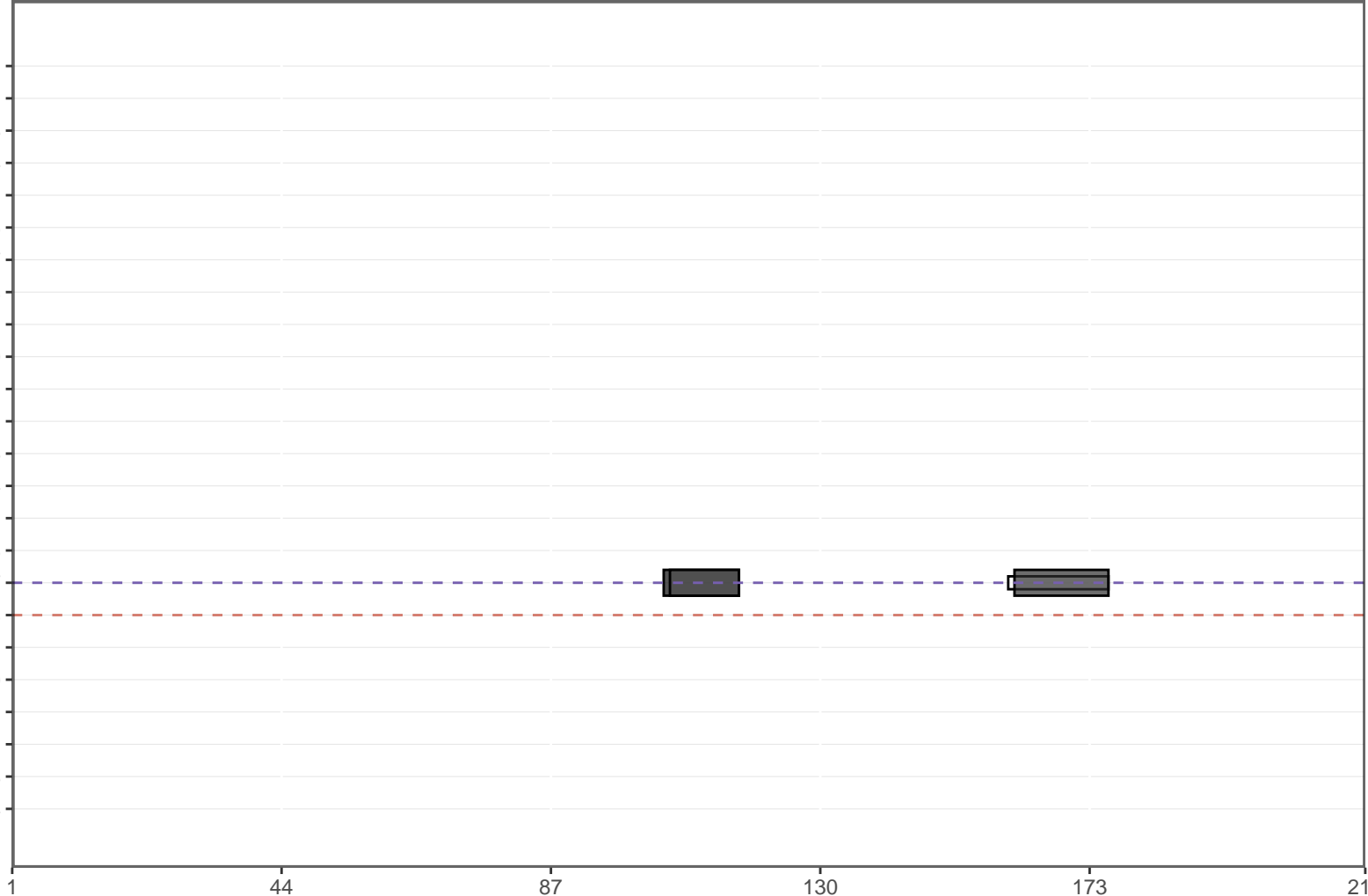
MW indication



Molecular weight



Gel Slice

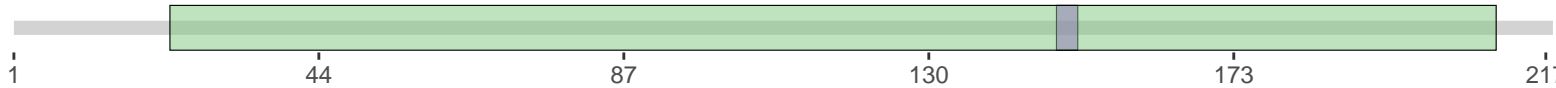


Protein length

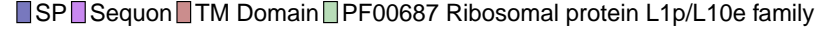


Peptide counts over 4 repeats

Pfam domains



Pfam Description

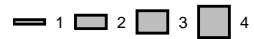


Protein sequence:

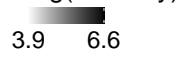
QLLVKLLAKYIYHFLASEAVIKQIPRLLEGPLNKGKGFPSLIVSHQESLEEKVNETKATKIFQLKKVLCMDVAVVGNMDMEKQIFQNVQMSVNFVLSLLKKNVQNVRLGLYLKSTMGKTRVF

NbL16g22580.1 proteasome_subunit_alpha_type-3-like [MW = 27.22 kDa]

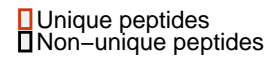
No. of times detected



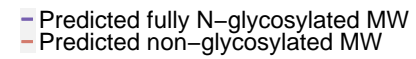
log(intensity)



Values from



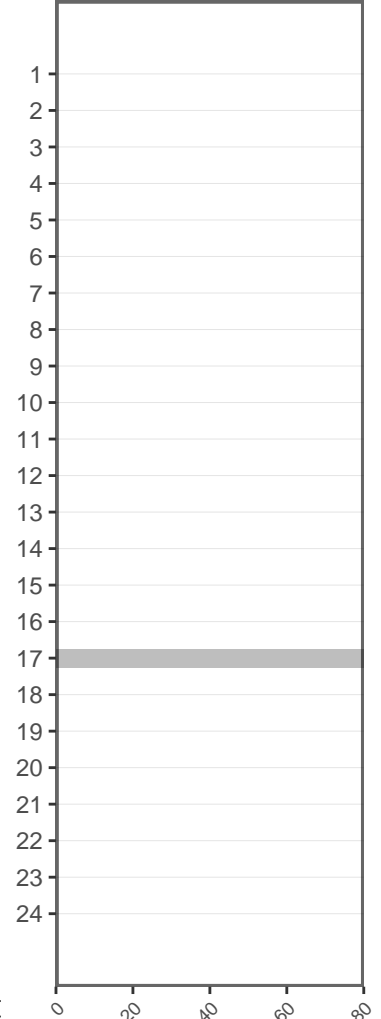
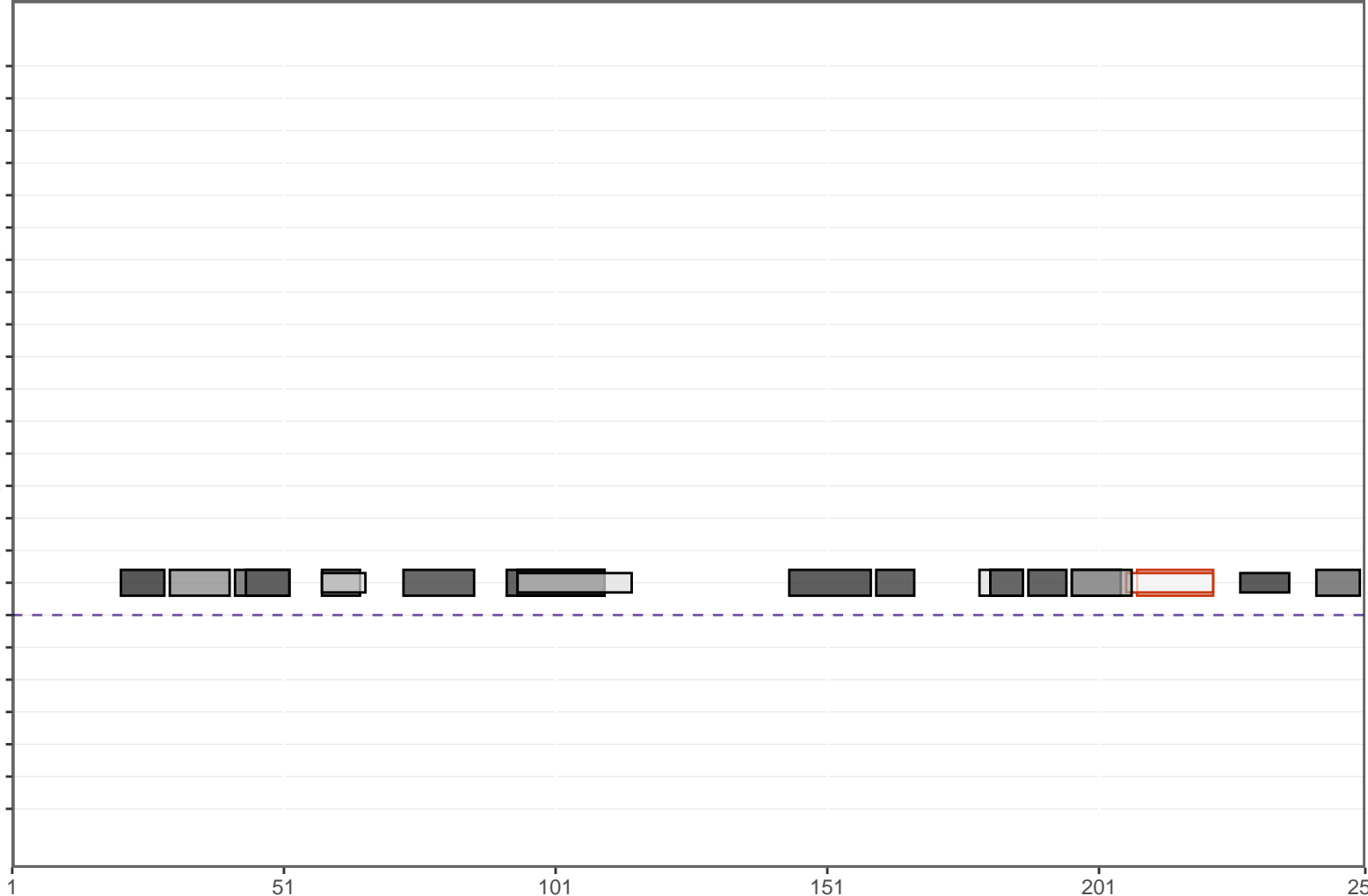
MW indication



Molecular weight

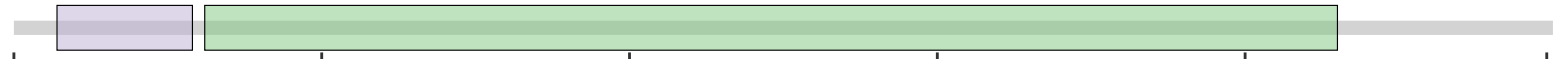


Gel Slice



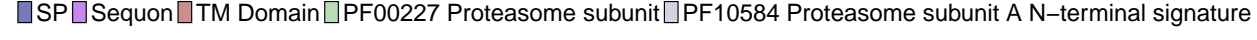
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

AERVASVYHLCTLYWALRPFGGGVILGGYDRDPQLYLVFPGVYRFRFGAANGKGRGAAKTEIEKLLSEMTRGGVIEVAKIHYGVHDEAKDKAFELMSWDCESNRHQKVPDILEEAKTAAKAALEEMDAD

NbL16g22570.1 magnesium-protoporphyrin_IX_monomethyl_ester_[oxidative]_cyclase_chloroplastic-like [MW = 47.3 kDa]

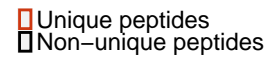
No. of times detected



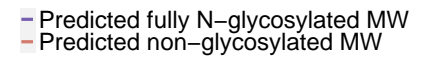
log(intensity)



Values from



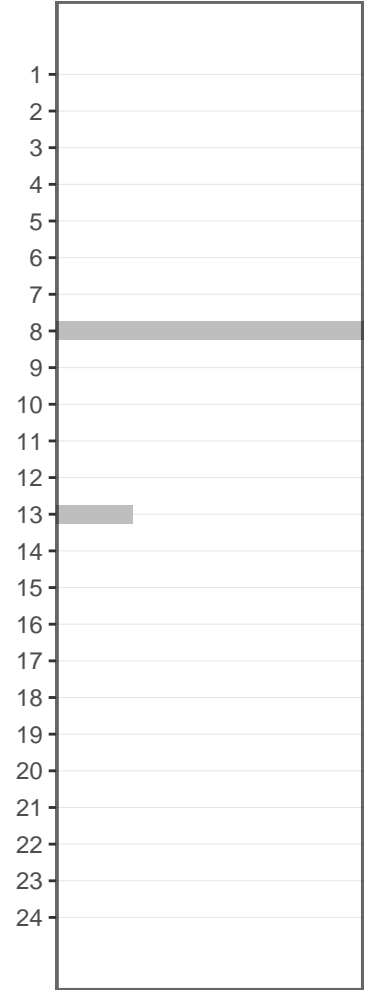
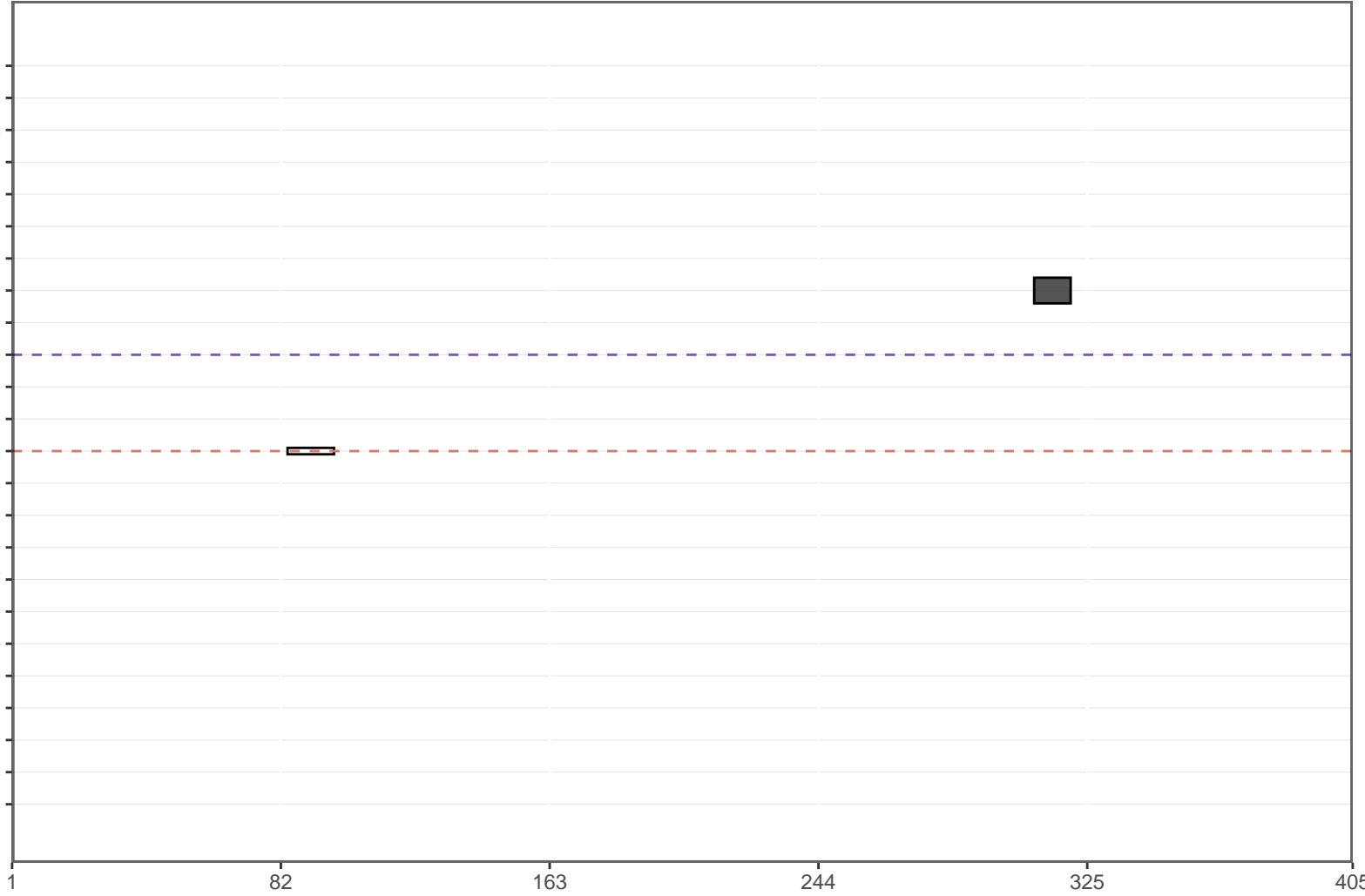
MW indication



Molecular weight

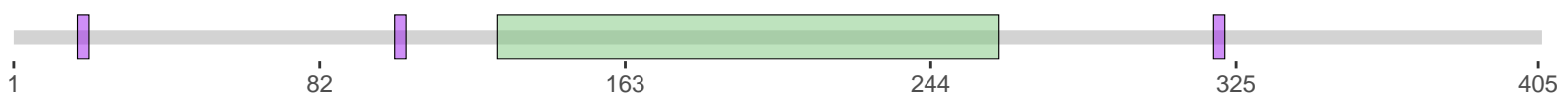


Gel Slice



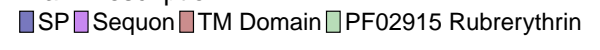
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

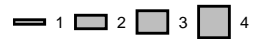


Protein sequence:

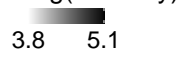
DLGLTKARKYTFKPKRFVATYLSKIKGIYRWITRHLKAMPVYGVPIKRYFENWGDENRHGDFSSALMKAGPQFLNDWKKLWSRFFGLSVVITMYLNDGQRDFYEGIGLNTKEFDMVVIETNRITARIKFWLVDVNPFRKRLDRMVEIKILAVGETDDPLVNFKRIFLAALASELLAAVLMKPIEGGSVDFAEFEPQLVY

NbL16g22490.1 nascent_polypeptide-associated_complex_subunit_alpha-like_protein_1 [MW = 21.45 kDa]

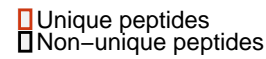
No. of times detected



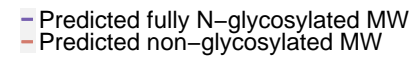
log(intensity)



Values from



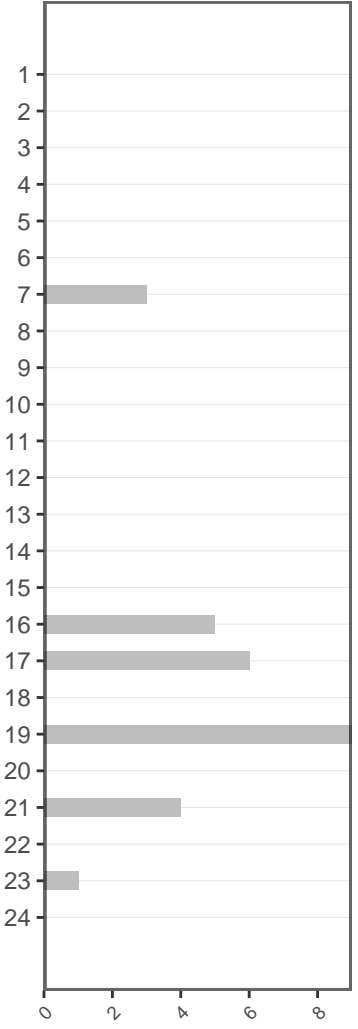
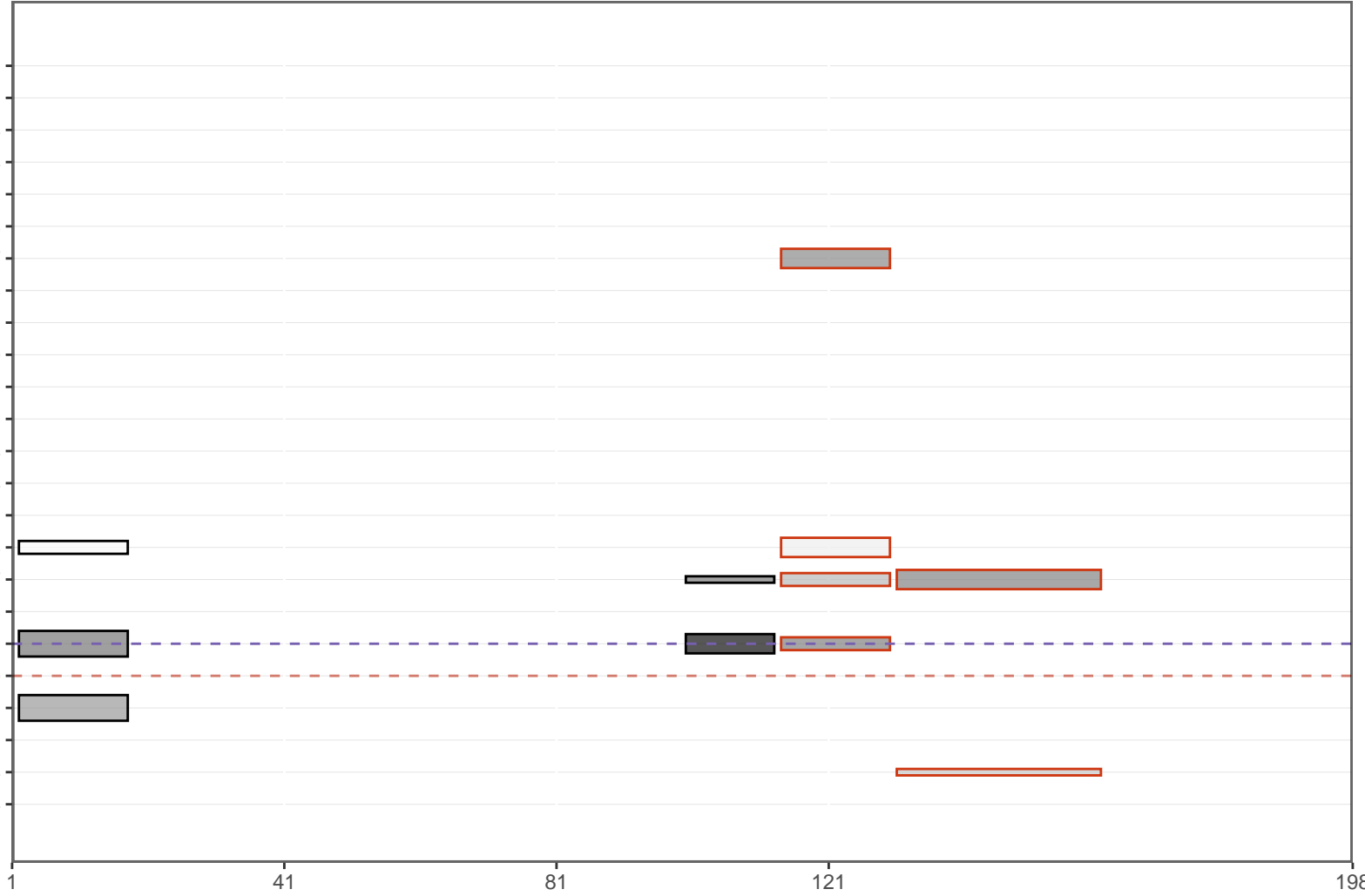
MW indication



Molecular weight

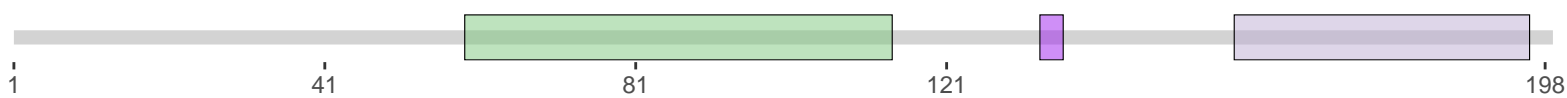


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

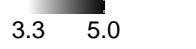
ISKILFVISKPDVFKSPASDFTYVFGAEAKIEDLSSQLQSGAAEGRKAPLNLSNVISKPEPPTVAGDDEEDVETGIEPKDIELMTQAGVSRKAKKALKGADGDVSAIMELT

NbL16g22420.1 vinorine_synthase-like [MW = 50.77 kDa]

No. of times detected



log(intensity)



Values from



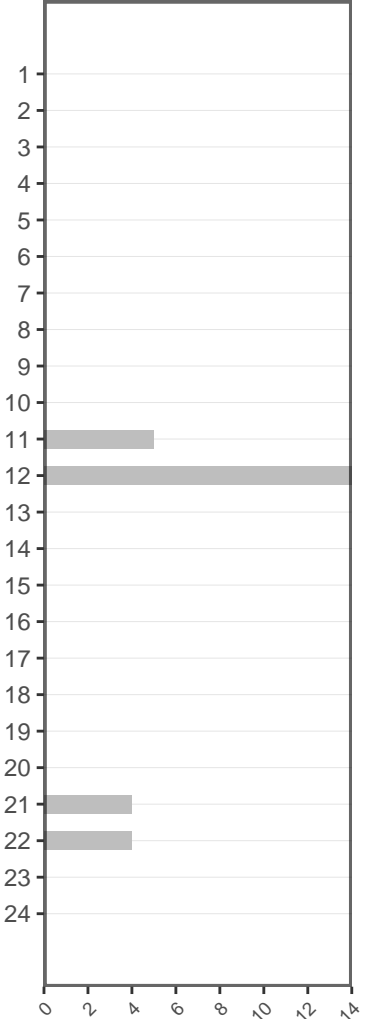
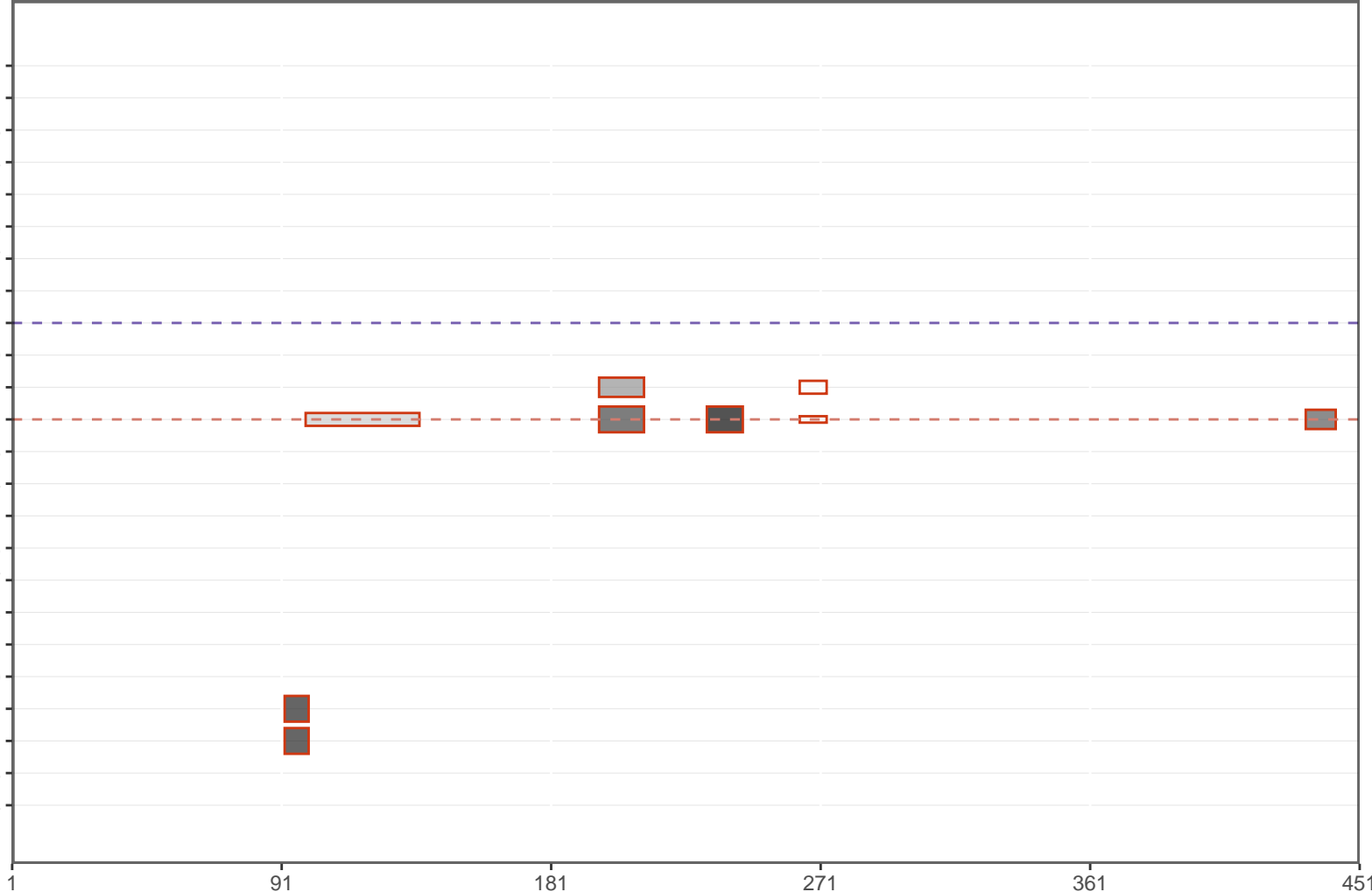
MW indication



Molecular weight

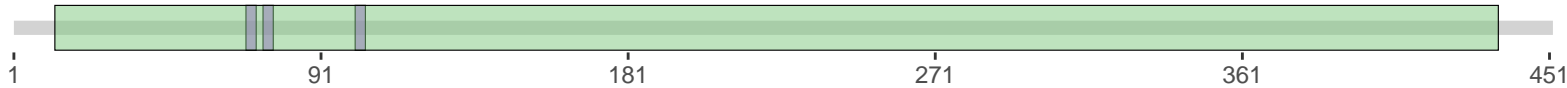


Gel Slice



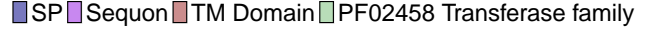
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PRNECPSPSHSTEGAFSRGALTYVDENPRVIAFLKTKAASENPKPRRVNVVTSVWVWGLTAHSEKRPSTLVHLVNMKRVDPDMHDHYIGAFVGFSEASKDENKEIANNMVALMRKGLAKFDNDCKVRLKGDGAEAGTLEHVKDAVDLNSRKGVDLYYFTSWGGYGFYDVFQWGNPKFSTTEGKFNMMIMLMDTKDGGVEAWVTLSDDMEIFENNELTLYATLKASFPDRE

NbL16g22270.1 tubulin_beta-2_chain [MW = 50.21 kDa]

No. of times detected



log(intensity)



Values from



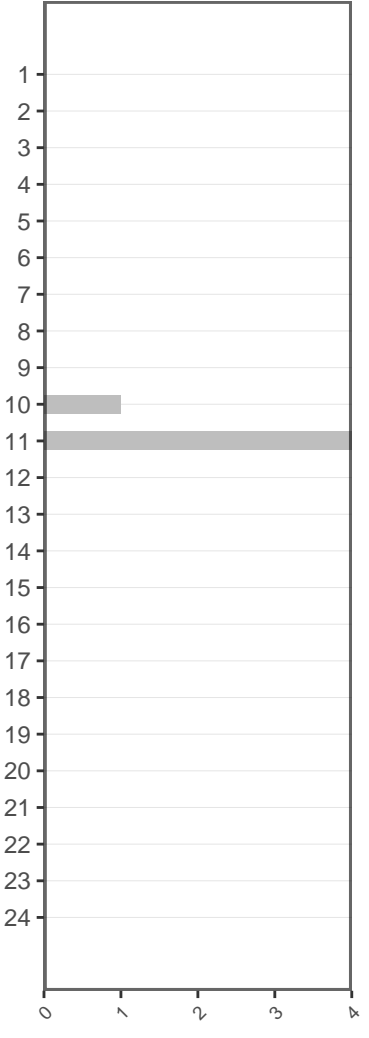
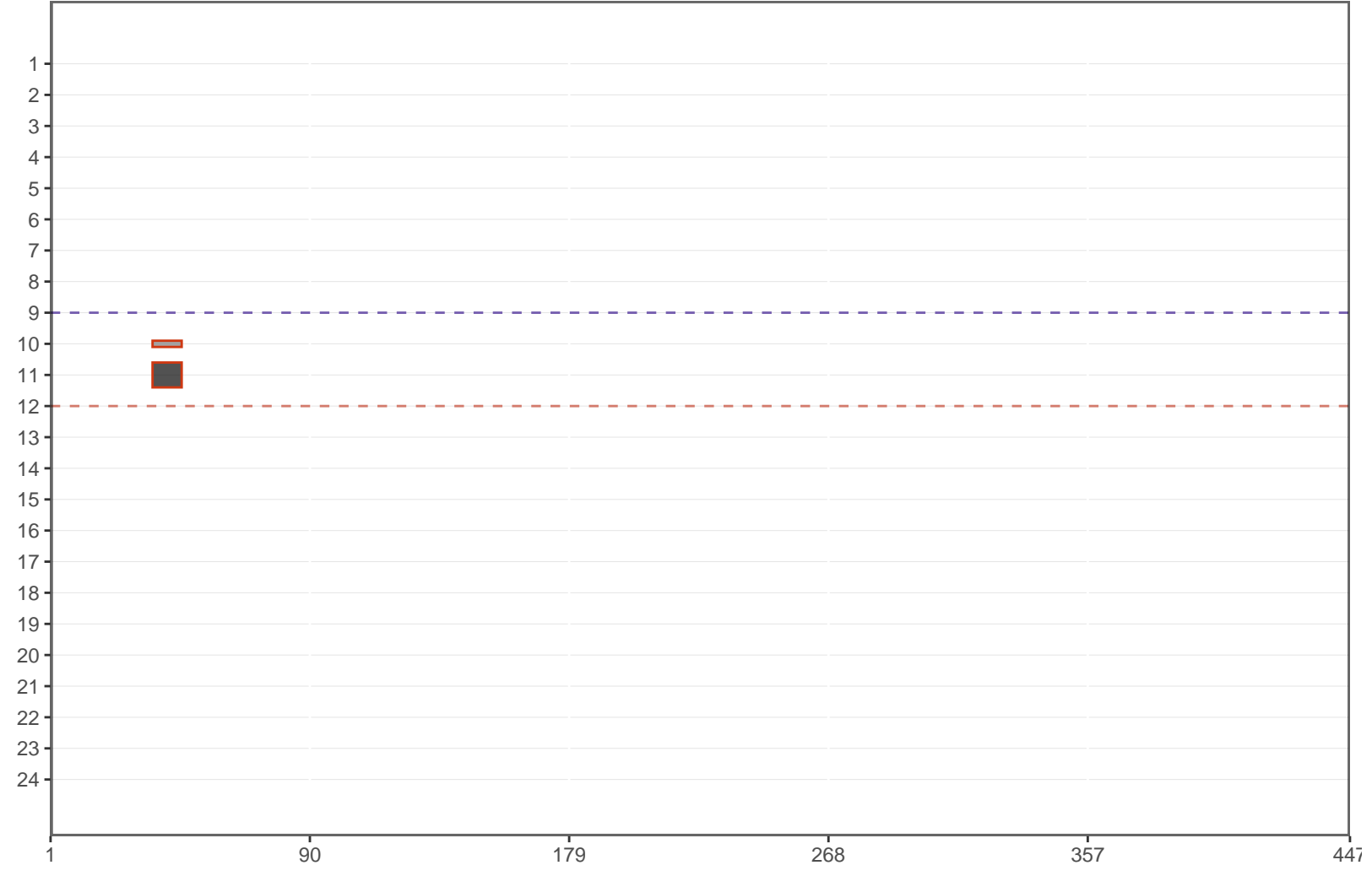
MW indication



Molecular weight



Gel Slice

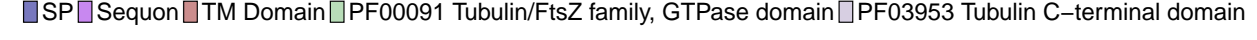


Protein length



Pfam domains

Pfam Description

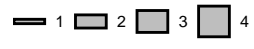


Protein sequence:

MFRTLLKLTTPSGDINLHLSATM5GVTCGLRFPQGLNSDLKRLAVNIPFPRLLHFFMVGAPLTSRGGQYRALTVPFLTQGMWDSKMMGAAADPRHGRVLTASAMFRGKMKSTKEVDEGMALNVGNKNSYFVEVWIPNNVKSFLVGDIPPTGLKMASTFIGNSTGIGEMFRFRVSEQFTAMFRKAFHWHVYTGEGMDMEFTFAESNNNDLVSEYGGYQDATADEEGEYVEDEEADED

NbL16g22210.1 laccase-4-like [MW - SP = 58.62 kDa]

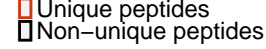
No. of times detected



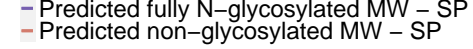
log(intensity)



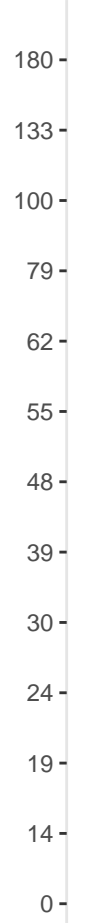
Values from



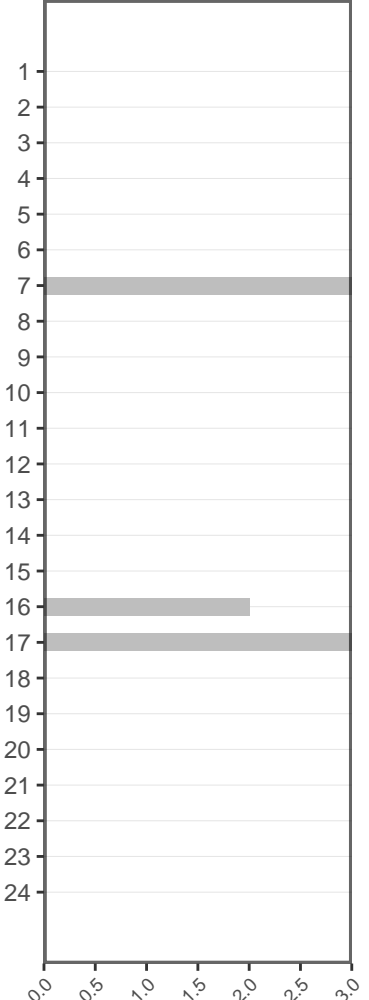
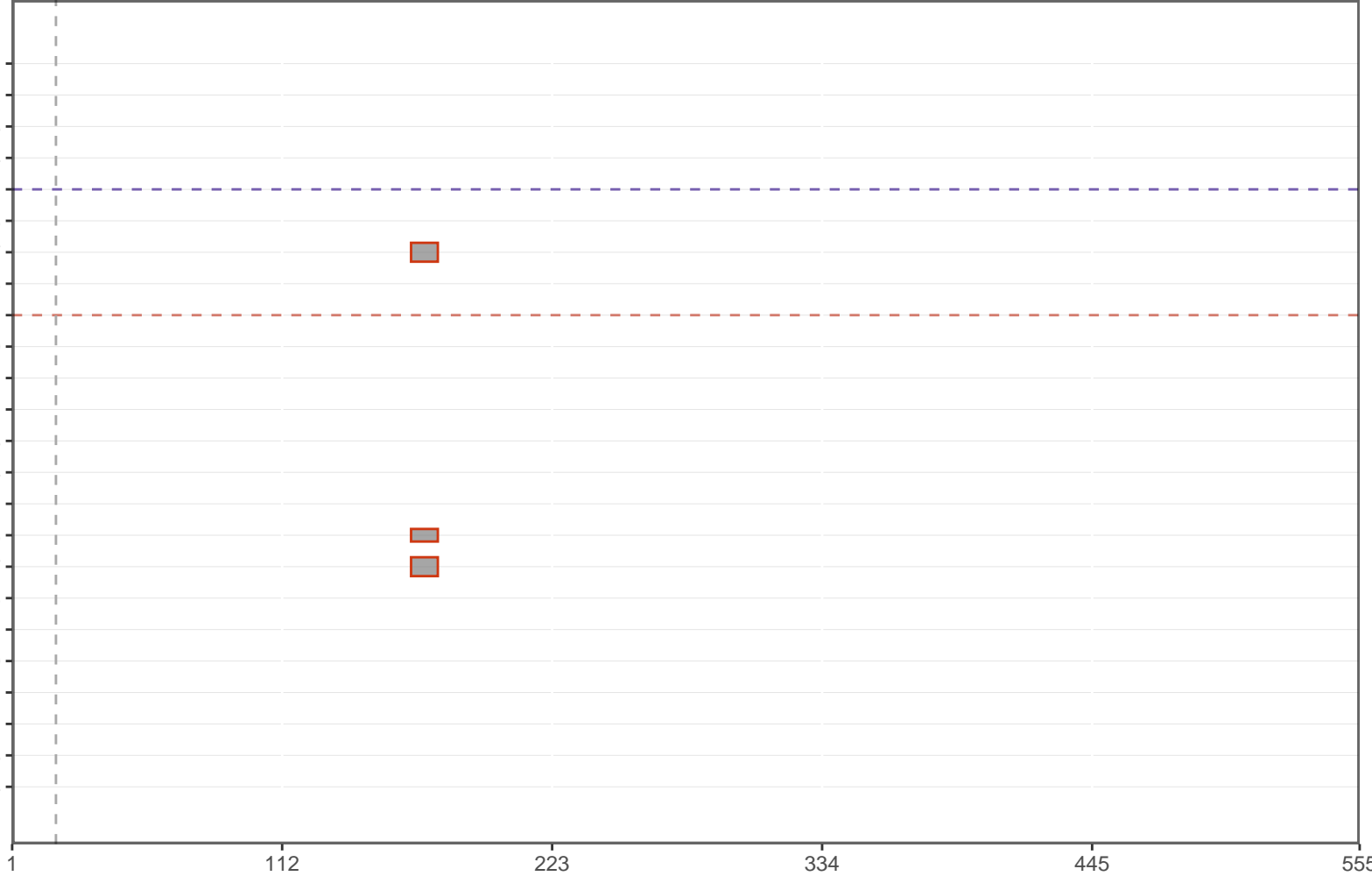
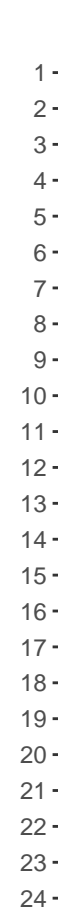
MW indication



Molecular weight



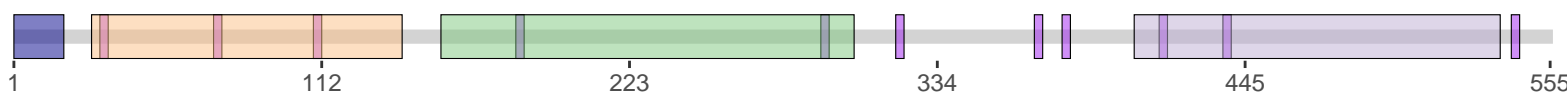
Gel Slice



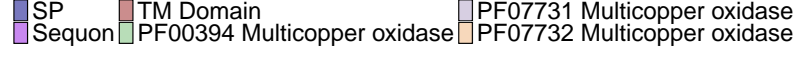
Protein length



Pfam domains



Pfam Description



Protein sequence:

NIIVTADQSFQKYMVAASPFEMDAPIAWDNTATATLHYSGALGSSPTLITSTPPQNAISVANNFLDALKSLNSKYPKAVPQTVDRSLFFTVGLGNGPQTGGKANGSRVAEAVNNTFVMPFTVALLQAMFFGNGVFTTDFRANPPFVFNVTGTSTPTNLATKGTIVYRFLPNATVQLVLDGTGIAFENPHILHGFNFFLVGKGLGNFNKSTDPKNFNLDPVERNTIGVPSGGWVAIRWRADNPGWVFMHGHLEVHTTWGLKMAFLVNDKNGKPNESLLPPPKLKYC

NbL16g22110.1 oxysterol-binding_protein-related_protein_3A [MW = 52.17 kDa]

No. of times detected



log(intensity)



Values from



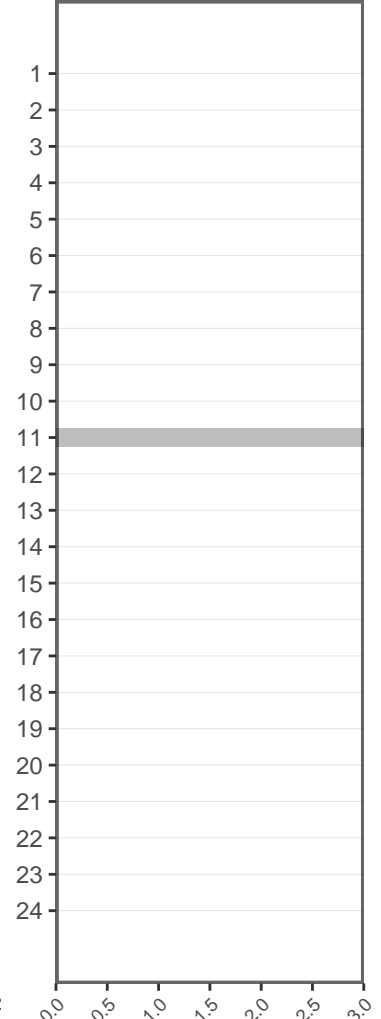
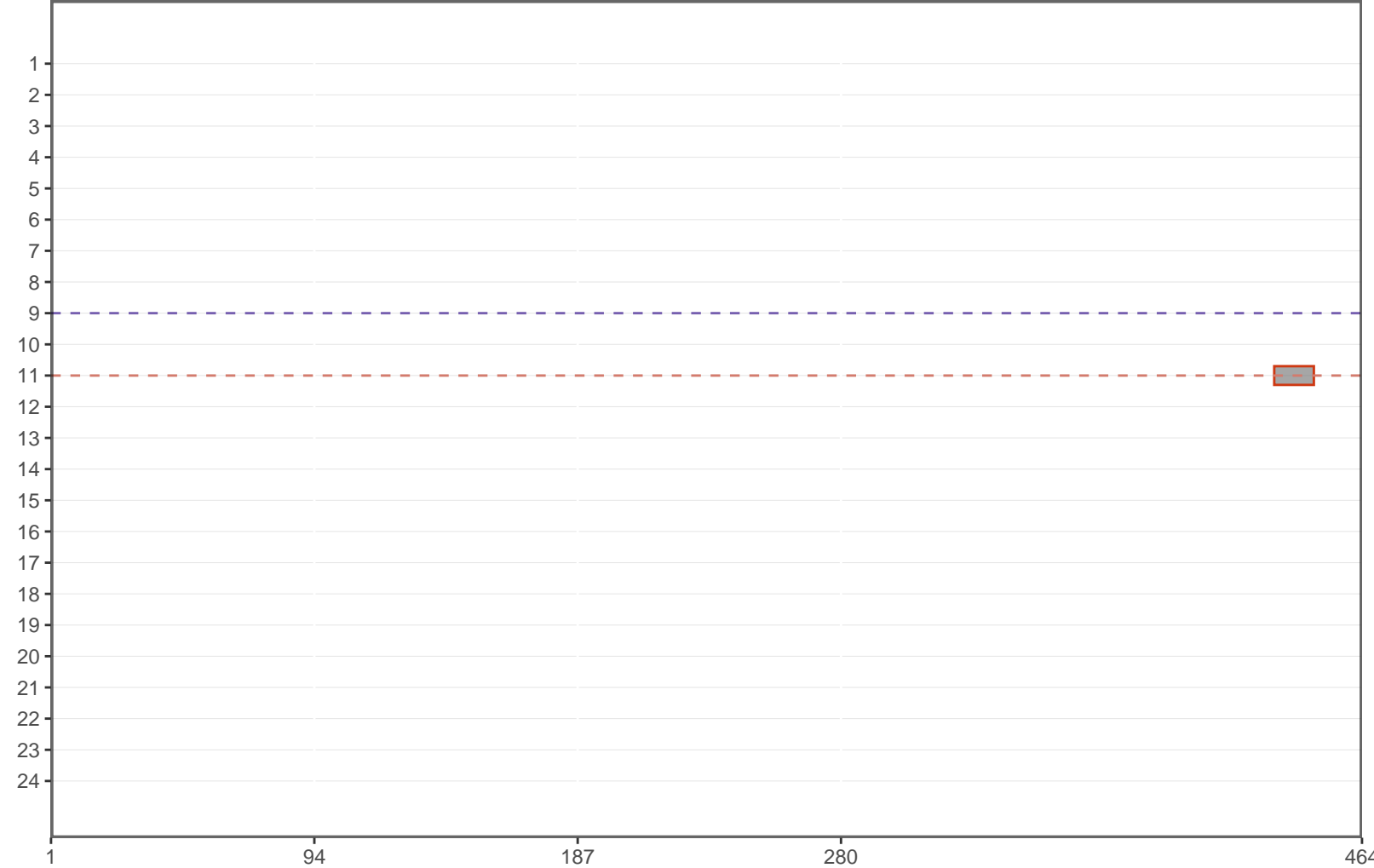
MW indication



Molecular weight



Gel Slice

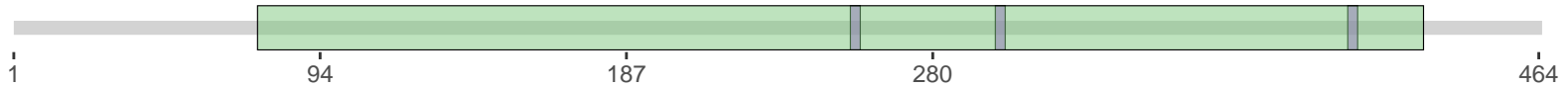


Protein length

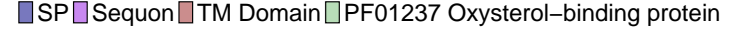


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KKSGVLDLVPPTKVNHLFGRTWIDSPGEMILNTLTDGKLVLYFQDGFWDGAGRYEVDGYYNSEEPEKILMTGKWNESLGYQPDLEGEPLDQSTKKEVWRITADAPKNDKFGYTFYFAHKINSEFDLTPKLLASDRLRDPDYALEKGDLSKASSEKRLLEERGRADRRTRREAKGDEFKPKWENLSEVGTPTPWGDLELVYENKGYHEHRAIDSGSHAEADKITEFNPWQYEDSVSAI

NbL16g22070.1 tyrosine_aminotransferase-like [MW = 46.52 kDa]

No. of times detected



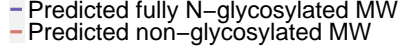
log(intensity)



Values from



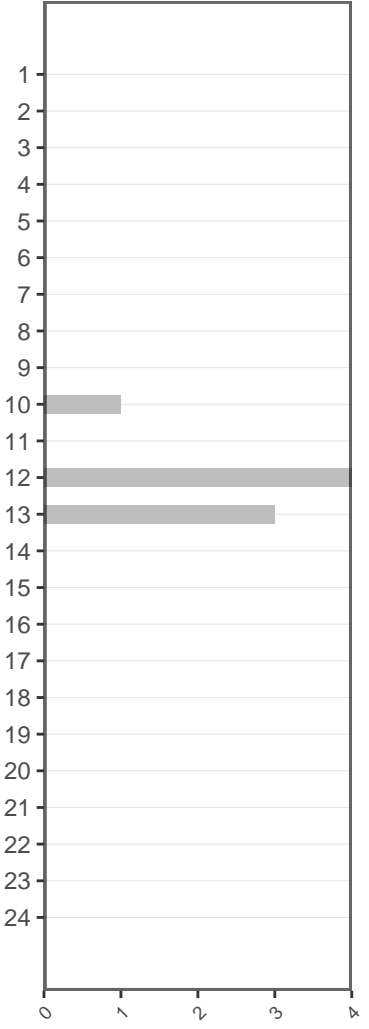
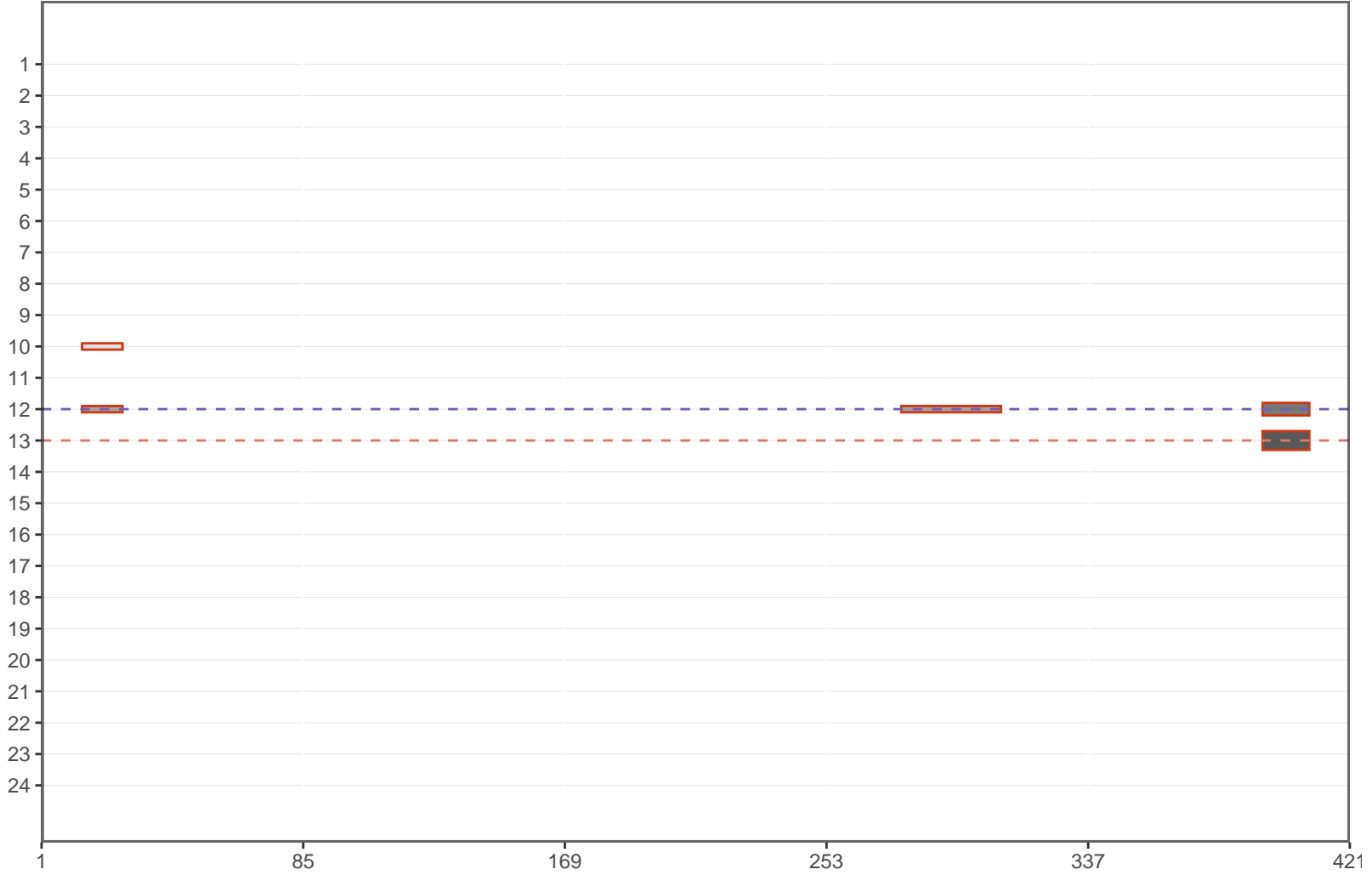
MW indication



Molecular weight

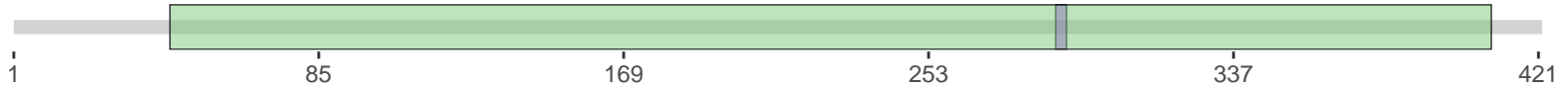


Gel Slice



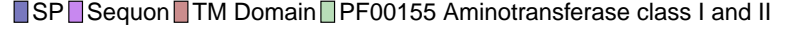
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

INVTYQHLEVAEMARKLGLVADEVYDHLTFQSKPFPVPMGIFGSIAPVFLGSGIKRWVPPQWRRLGWLVTNDPNGLKHKGVDSIRGFLNISHPATFQGAIPQIKTKDDFFKIVANMLRETADICYDRKDPICFQPEKSGSGSMFVAVLHNLVDEDDLDFGLKLAKESLHPGVAVGLNWLRFSSAGEPSLEDGLKRLNAFYGRHAKKQ*

NbL16g22030.1 probable_ADP-ribosylation_factor_GTPase-activating_protein_AGD6 [MW = 49.18 kDa]

No. of times detected



log(intensity)



Values from



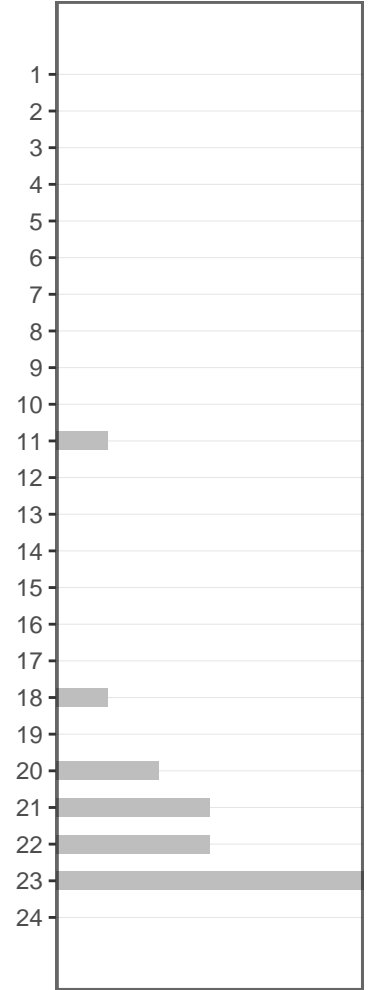
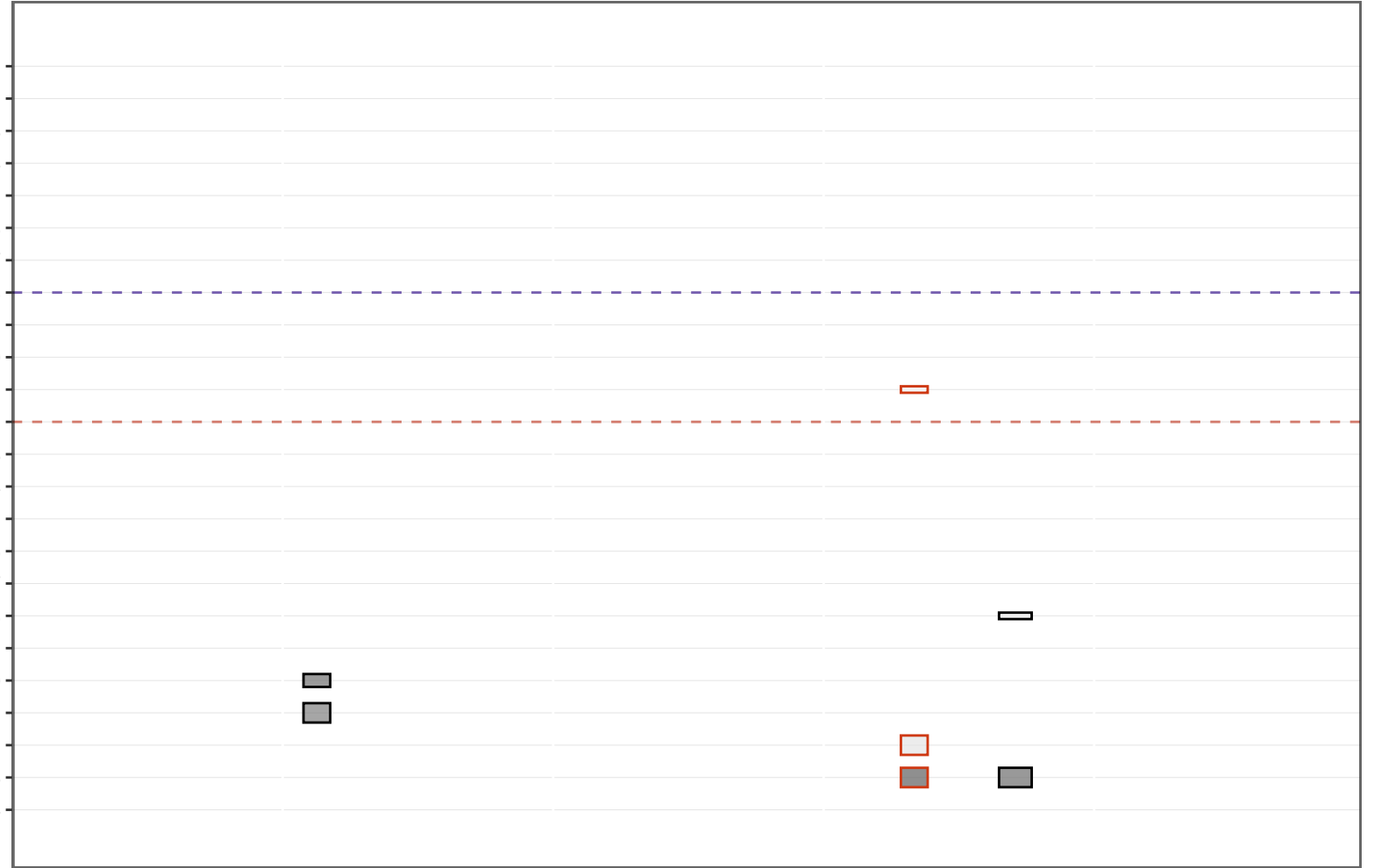
MW indication



Molecular weight



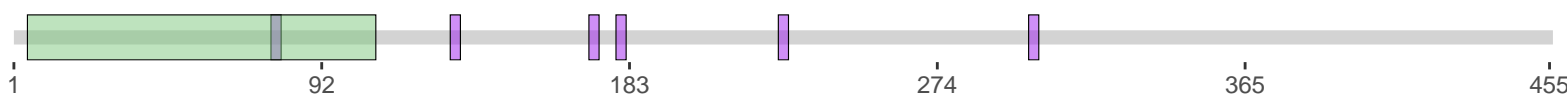
Gel Slice



Protein length

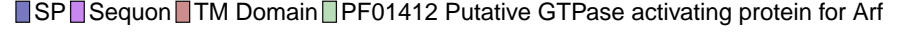


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IDNFTARKMAENE SRPDGLPPSGGKRYVFGSPPAPMPRNINNNLGGDVL SAVTQFGFRLSMAASAAGELGKRVKEGGYDNKNVNETVNVARKTTVIGGKGVGIMKGVLAALASGKVEEYAEGGPNKDNWRSNGNGQNYYPEFSKESKGVNFPQGAQSSGRHSNENVSQSGVDDWVSKDKNRKGTSTKGTATSNDDGAGWAGWDDGKDDGVDNFDQASANNKHVSYGGKSEKWTDRGL*

NbL16g21970.1 60S_ribosomal_protein_L23a-like [MW = 17.24 kDa]

No. of times detected



log(intensity)



Values from



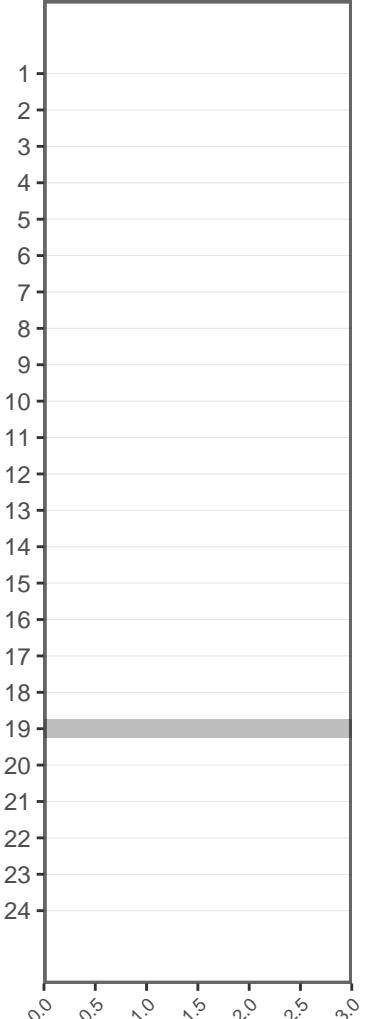
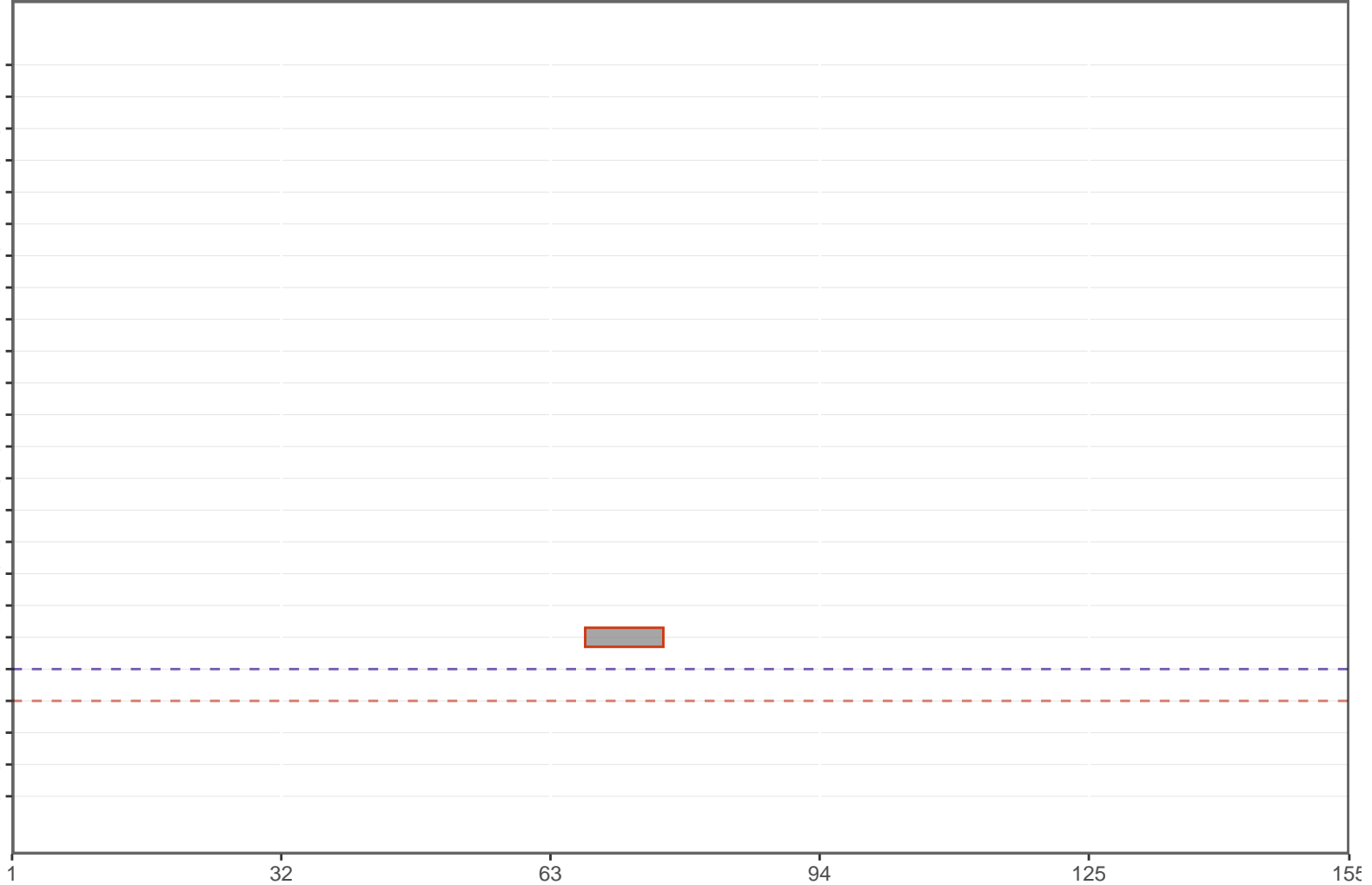
MW indication



Molecular weight

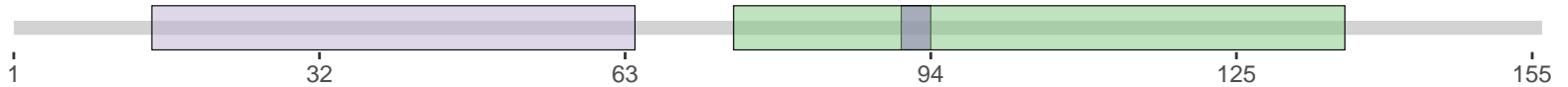


Gel Slice



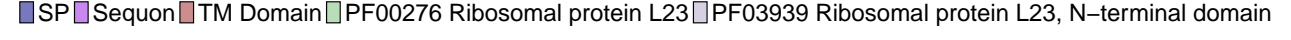
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IAPGRNKLDRHYGLKVPFTTEBAMMKIEDNNTLVFVDRKADKKKKDVAKKMYDGTGKVNFLRIPDGTGKAVVRLTPDYDALDVAANKIGP

NbL16g21880.1 TIP2-1-like [MW = 10.04 kDa]

No. of times detected



log(intensity)



Values from



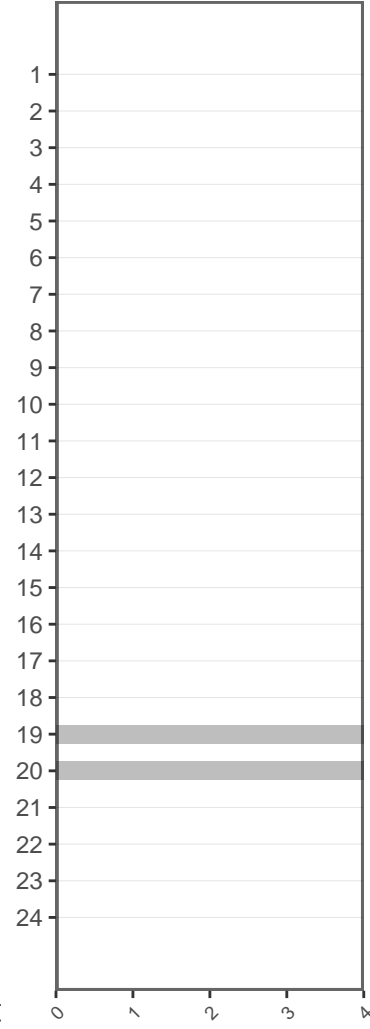
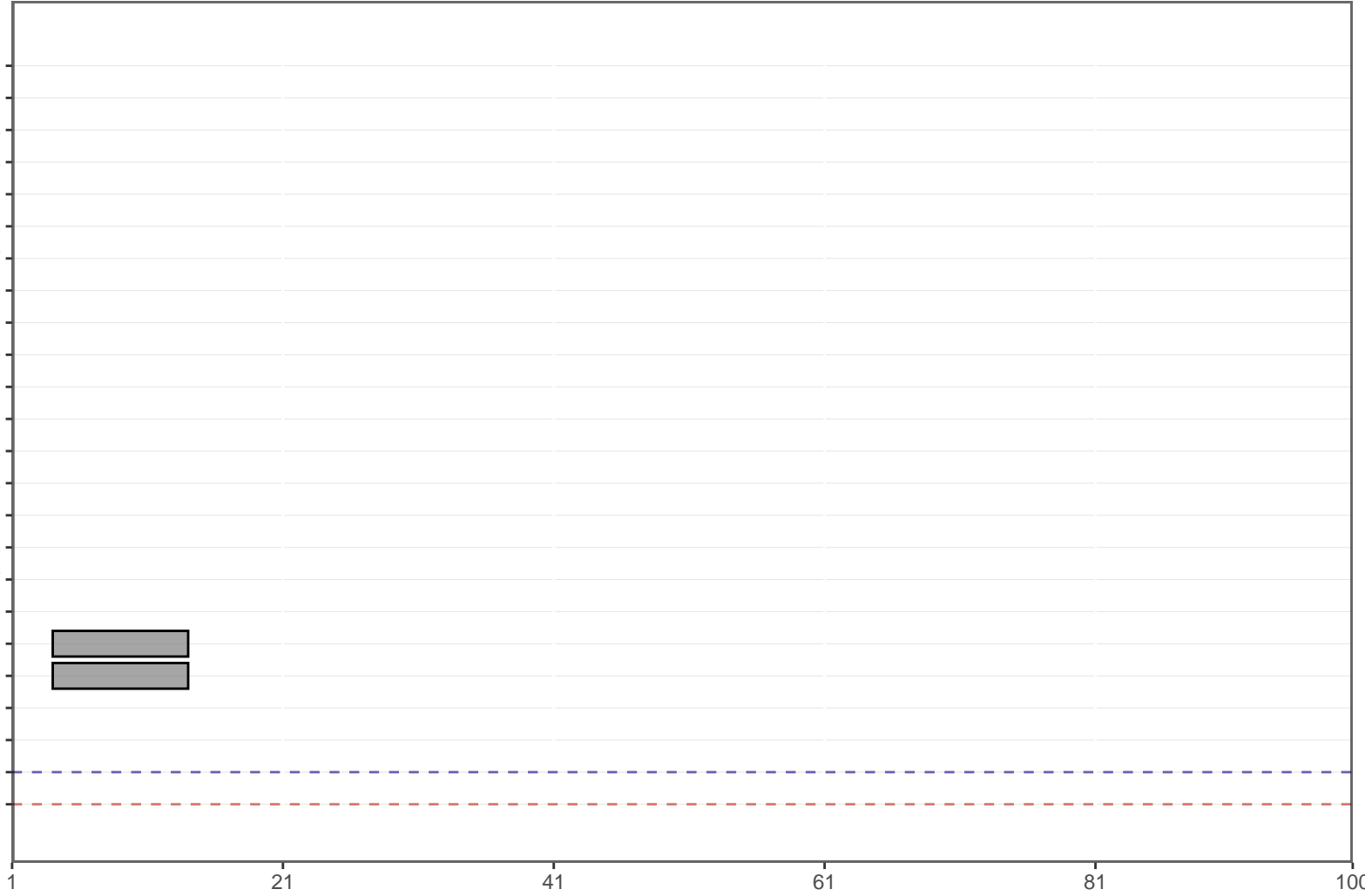
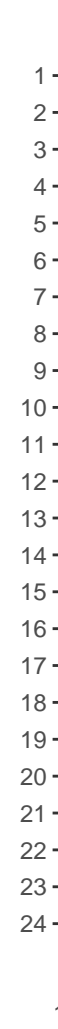
MW indication



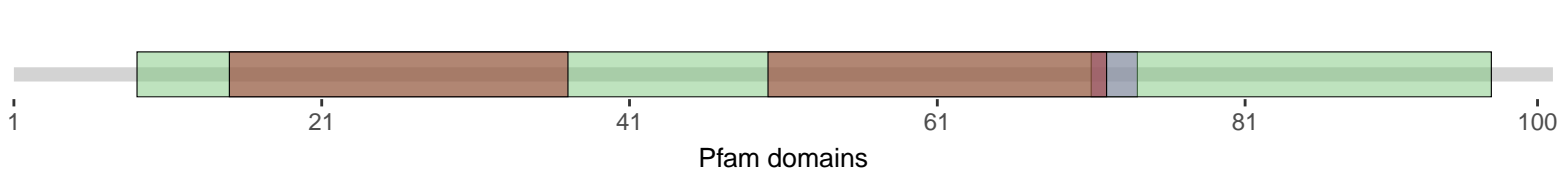
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

YNKLTADAALDFKGIWVWVGHGFLFVWVAVGANISGGHNPVTFGLVGGGDFITGLFLH

NbL16g21800.1 60S_ribosomal_protein_L4-1-like [MW = 44.61 kDa]

No. of times detected



log(intensity)



Values from



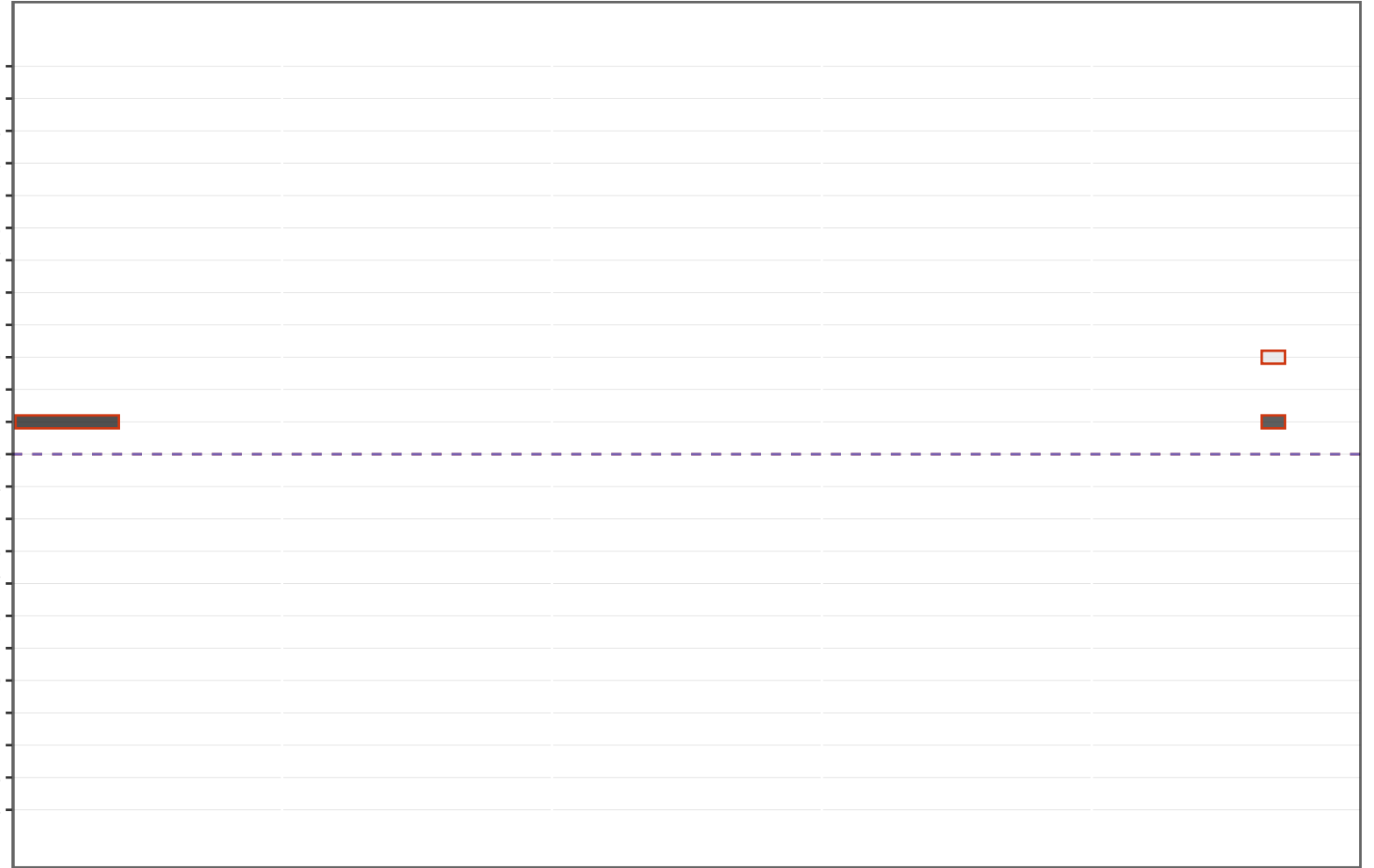
MW indication



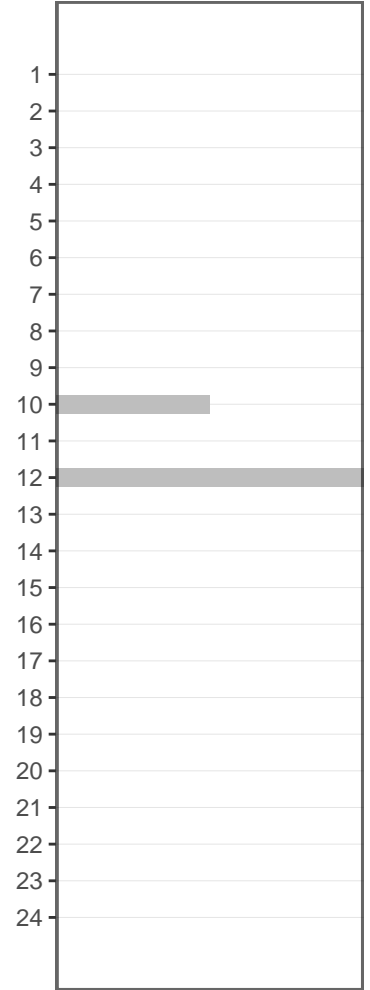
Molecular weight



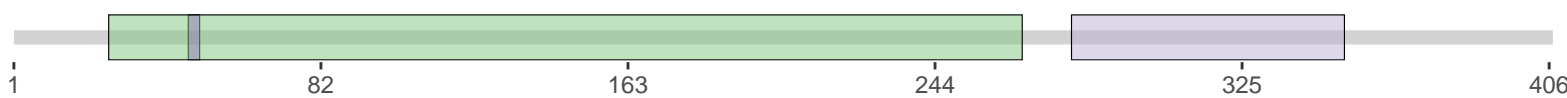
Gel Slice



Protein length

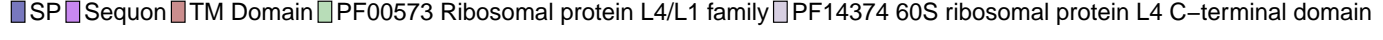


Peptide counts over 4 repeats



Pfam domains

Pfam Description

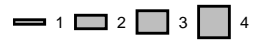


Protein sequence:

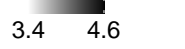
SHAIRPGGKMRNRRYHSKGPLVYGTGEGAKLKAFRNIPGVEICHVERLNLLKLAPOGHLGRFVAWTKSAEKLDEHYGFDKPSSEKKGYYLPRAKMWNADARINSEDEVGIVRRPIKQDVKRATLKKNPLNLLKLNIPYAKTARRMSELLAEAGRVKAKKELDKKRHDVTKKEEASAIRBSEAWYKTMISDSDVAEFDVFTKWLGVSGQ

NbL16g21520.1 tyramine_N-feruloyltransferase_10/30 [MW = 25.97 kDa]

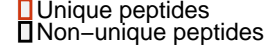
No. of times detected



log(intensity)



Values from



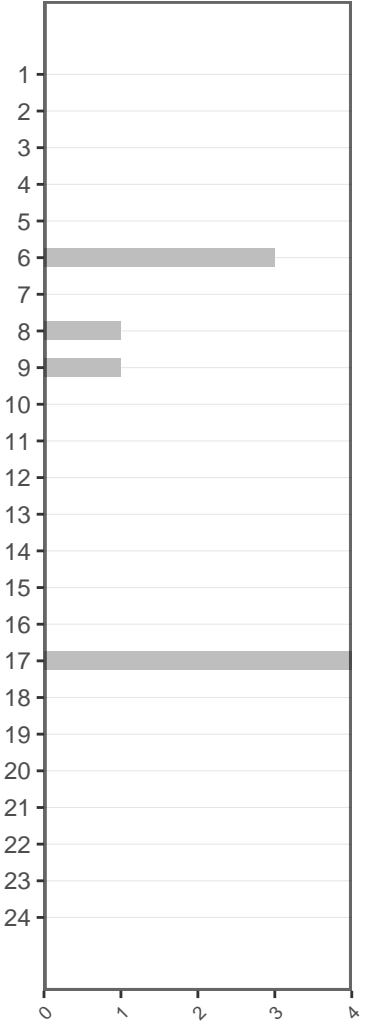
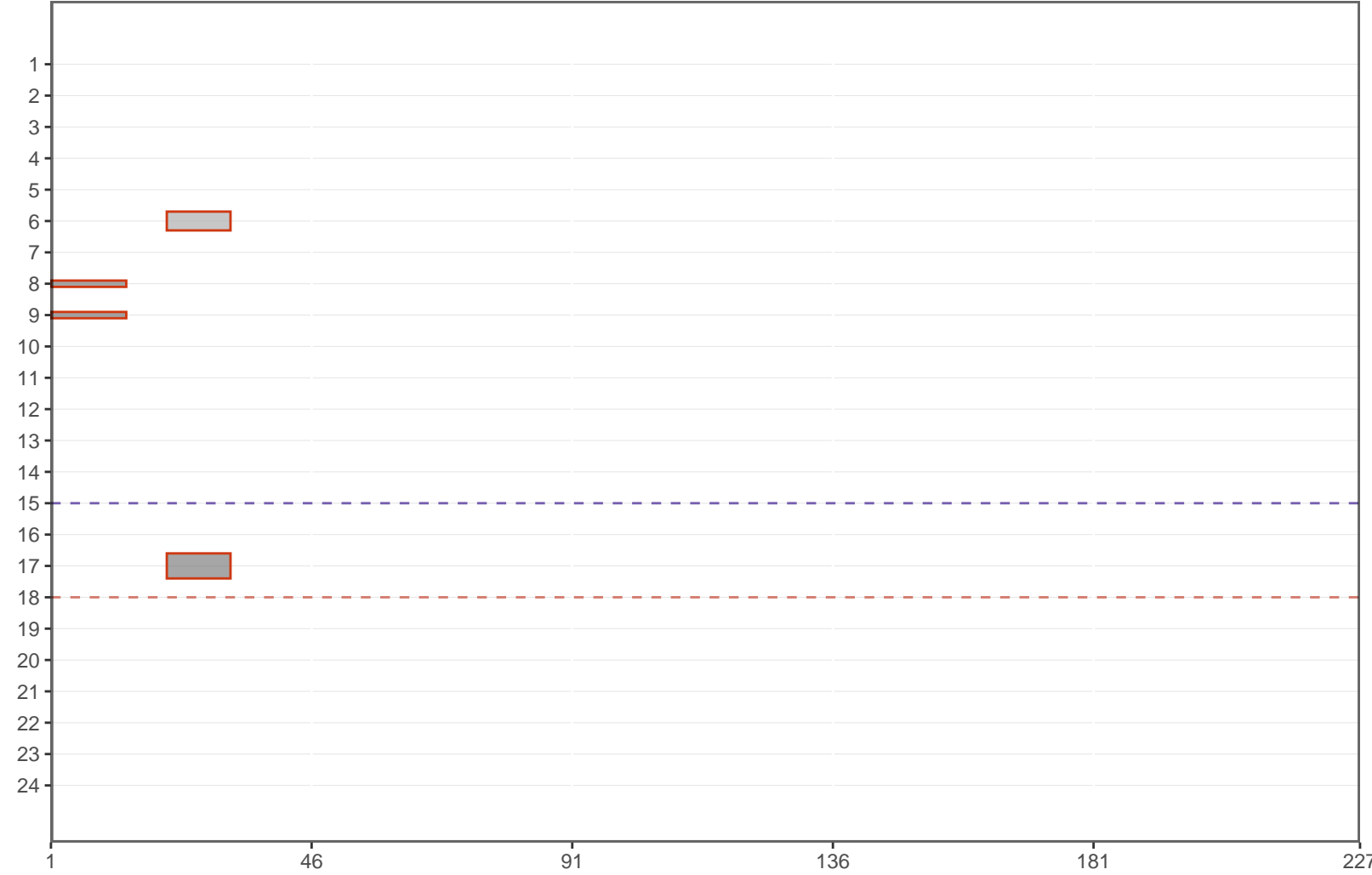
MW indication



Molecular weight

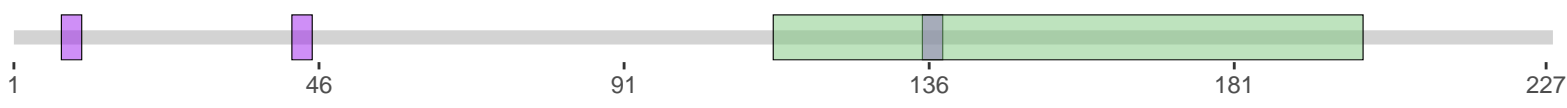


Gel Slice



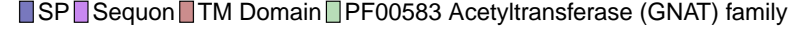
Protein length

Peptide counts over 4 repeats



Pfam domains

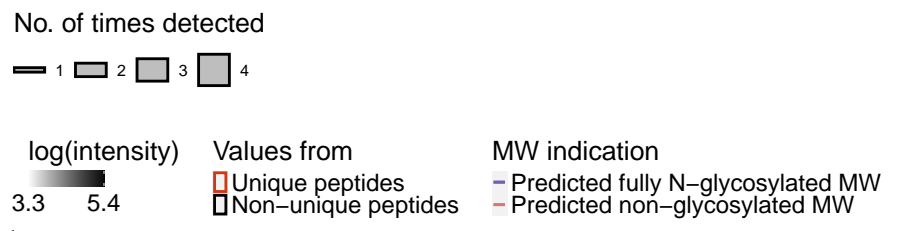
Pfam Description



Protein sequence:

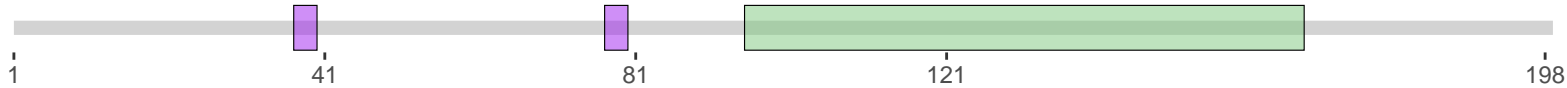
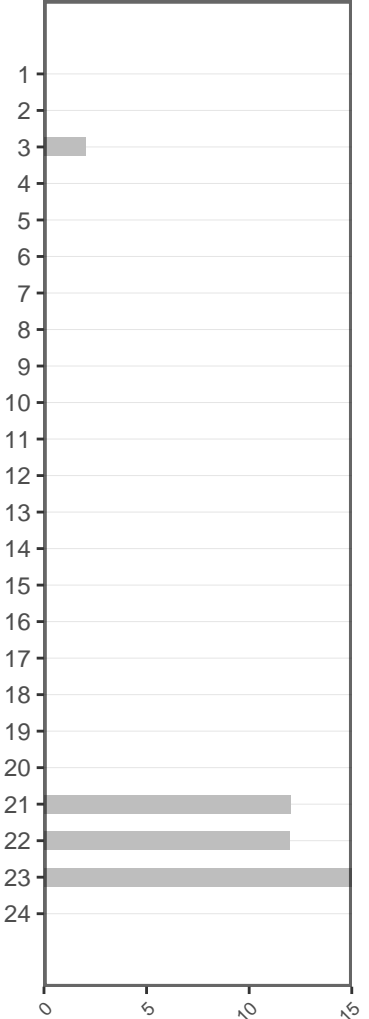
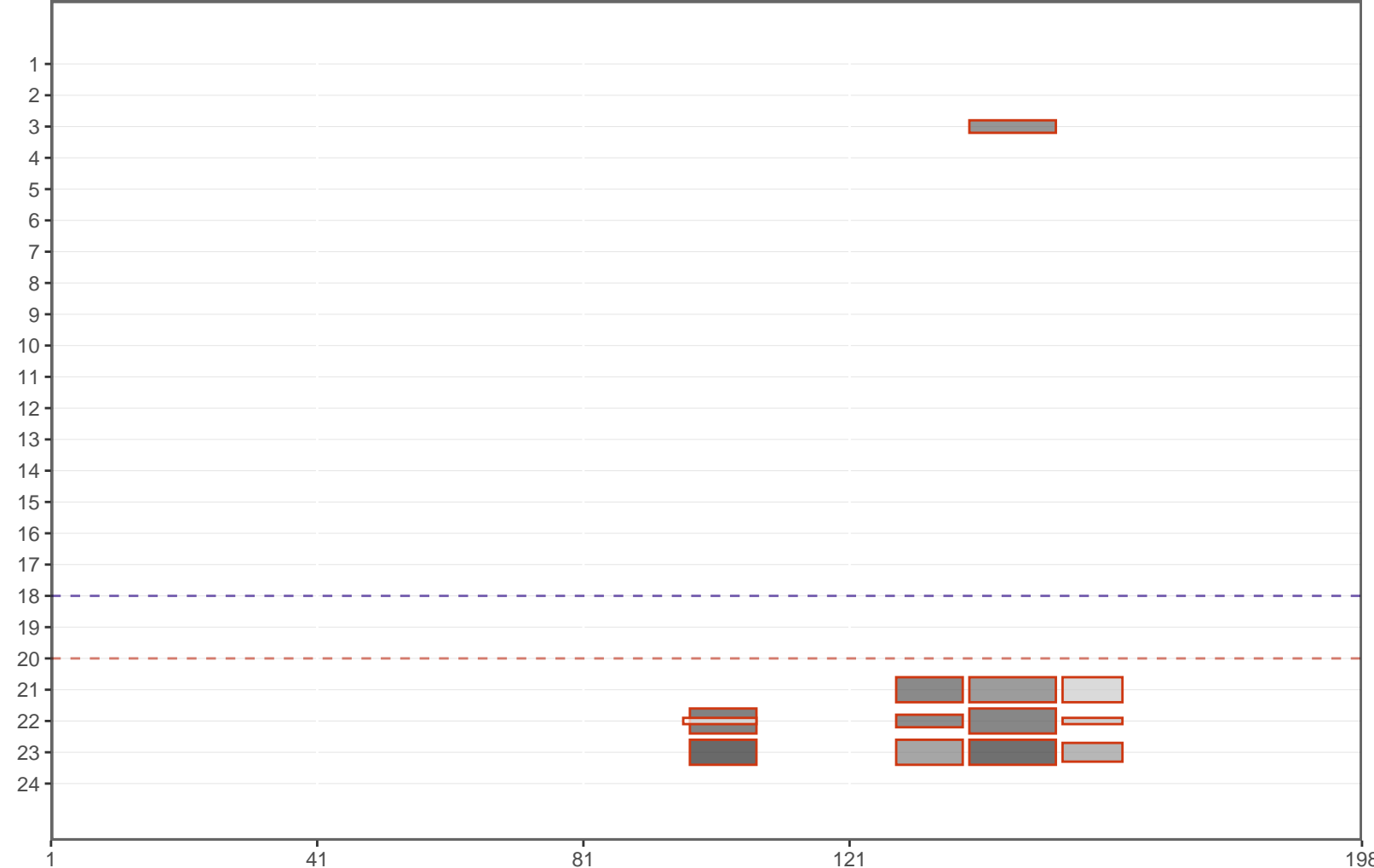
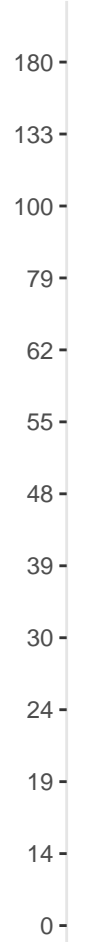
ITVEDKEAEFEKSKGGGDEKEDVFAGVAFYFVWYSGFYDKAGIYFESLYFRFQYRKLGMGLLFGTVASIAAANGFASVEGIVWVWNNKSYDFYVNMGEVDFDFRYGKLVGDALQKADKEKV

NbL16g21460.1 nucleoid-associated_protein_At4g30620_chloroplastic-like [MW = 21.48 kDa]

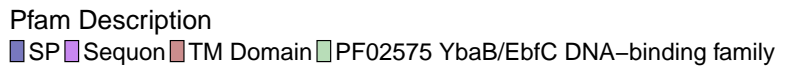


Molecular weight

Gel Slice



Pfam domains



Protein sequence:

INMNLVETVKKQGMVQGVAVRVKELAAAFDGYCEGELIKATLSGNGQPPVRIETDAAMDLSPEKLSLVTAAKDAHQNSVLRRTIKLAGRMVAFDHLVSTFLLRFFVT

NbL16g21420.1 early_nodulin-like_protein_1 [MW - SP = 17.53 kDa]

No. of times detected



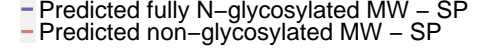
log(intensity)



Values from



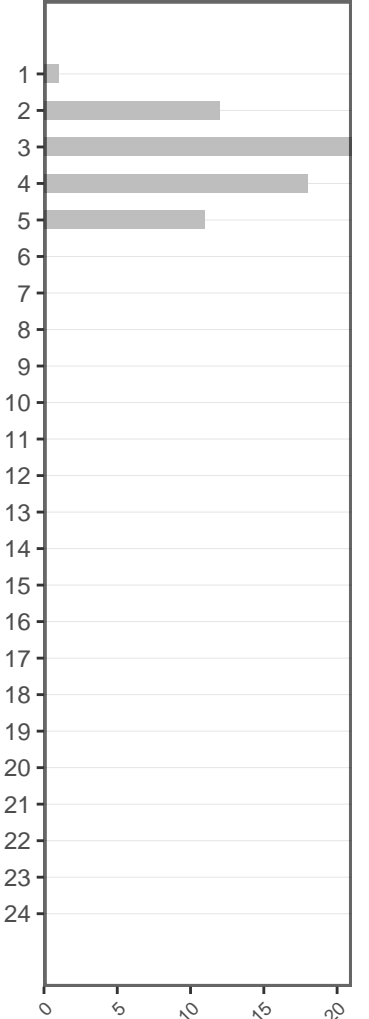
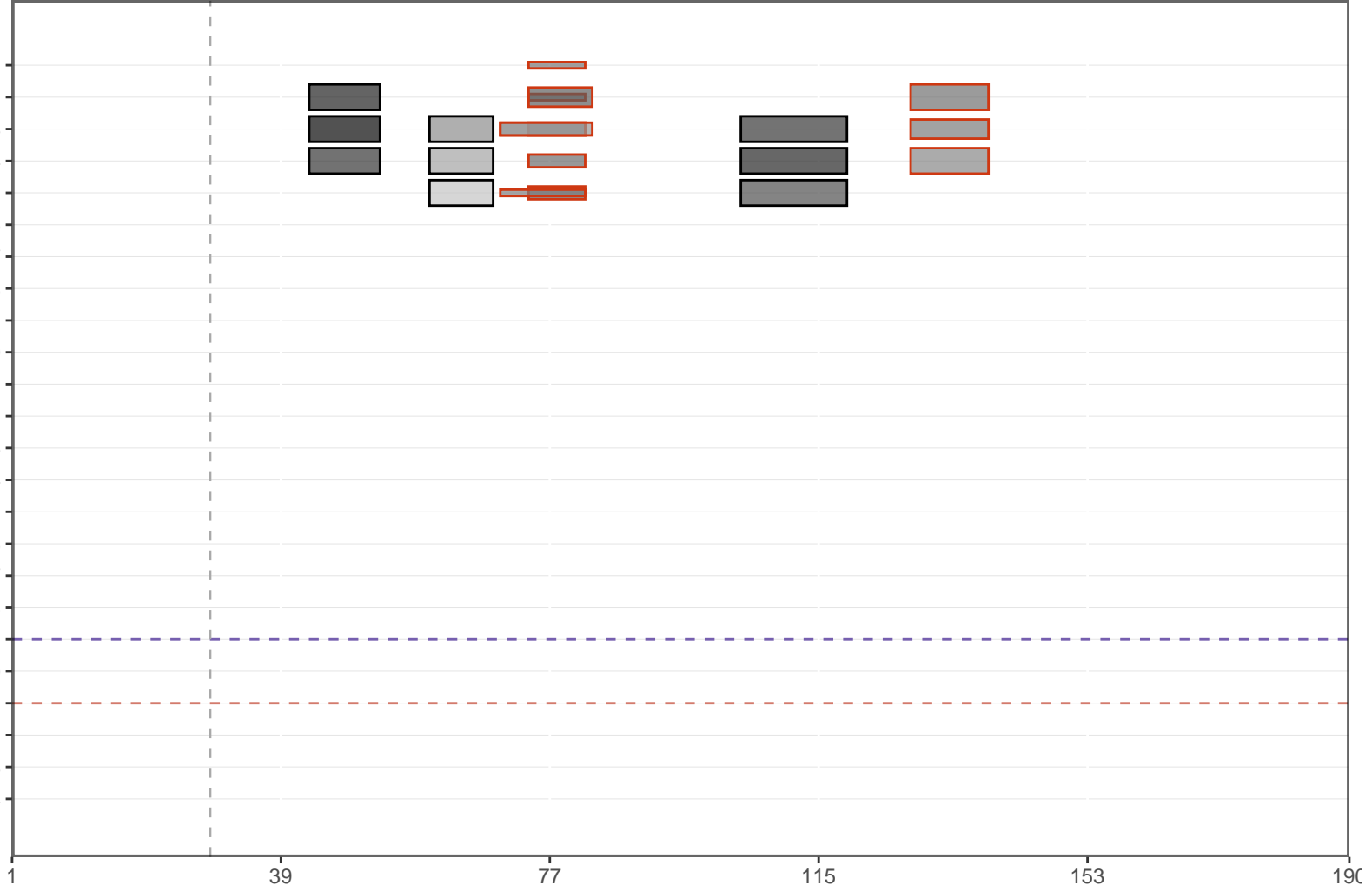
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

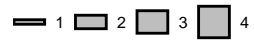


Protein sequence:

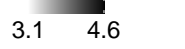
IRDVYTCNTSSPIAHHNDGNTKIELTHSGAVYRISGAKGHGEGGGKLIWVFLSESNMRRFMGAPAPGQTEFDPMAMPTSGNSATLAKGLVMAFGVLMGFFFLNEGYSHT

NbL16g21370.1 DNA-directed_RNA_polymerases_II_and_IV_subunit_5A-like [MW = 20.14 kDa]

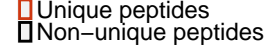
No. of times detected



log(intensity)



Values from



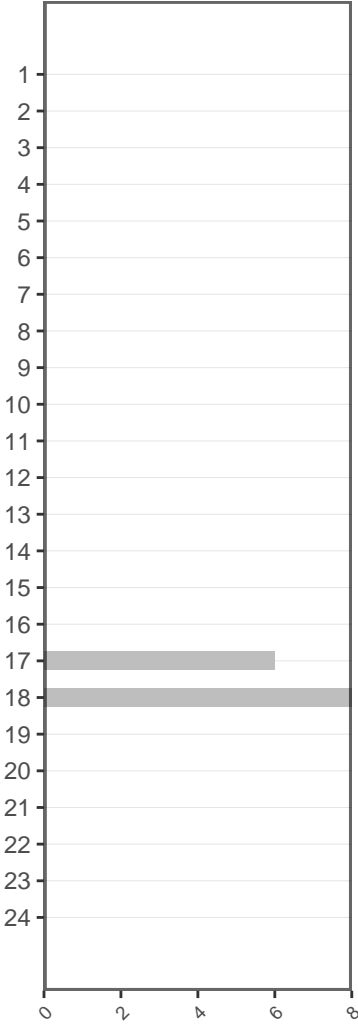
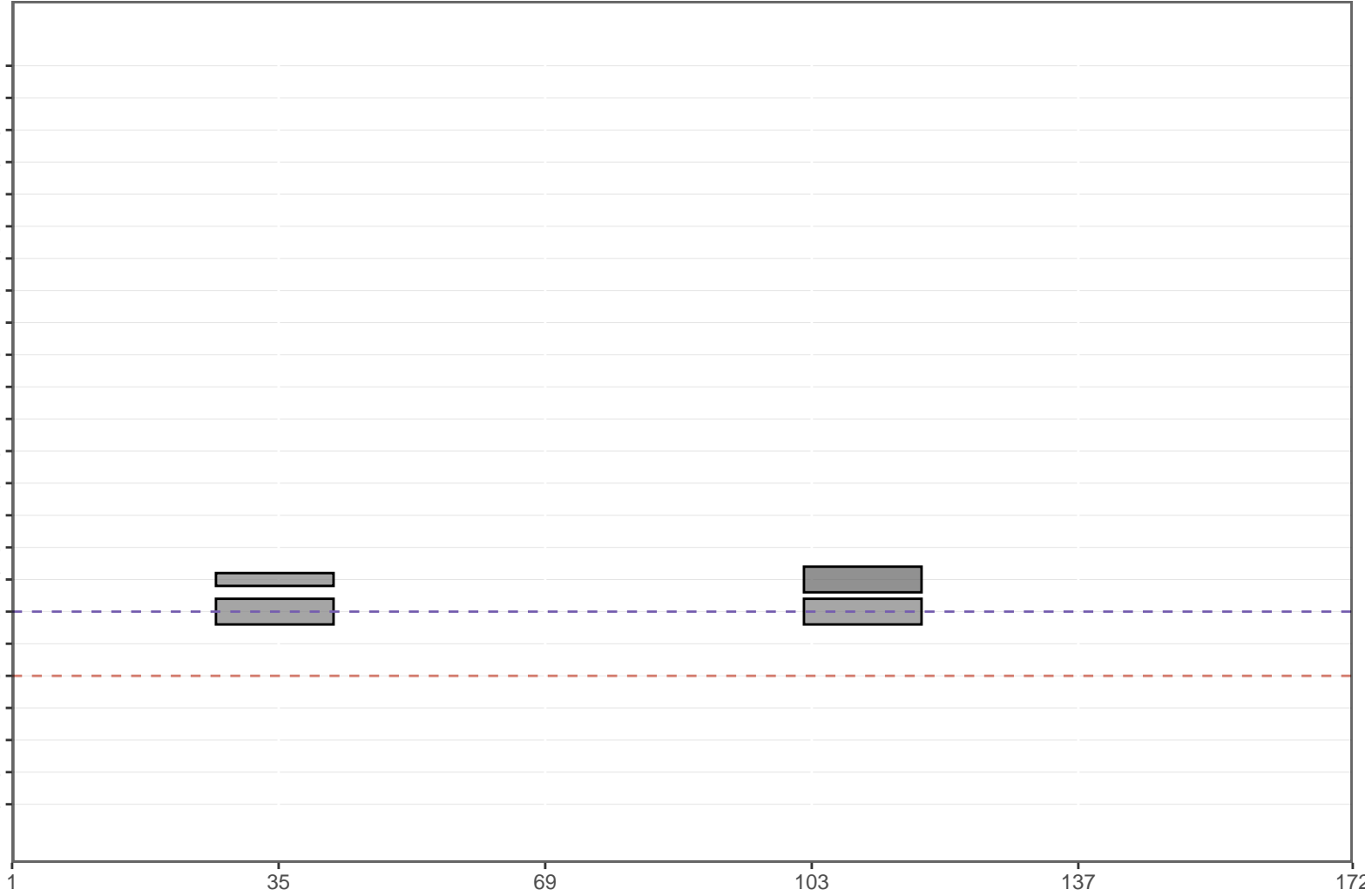
MW indication



Molecular weight

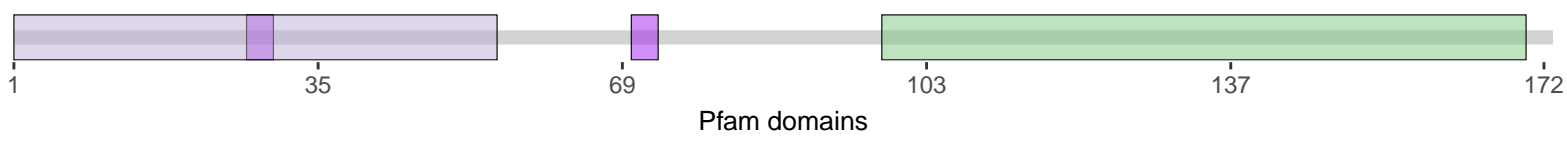


Gel Slice



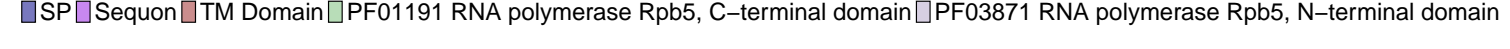
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILTPFARTCISESTKFKLEVFQEAELLVNKNHVLVEKHGKLPFEENKTLLEKRYFVKETQLPRIQTDPIARYVGLKRGDVKIKRPSSETAGRYVTVRVVV

NbL16g21360.1 uncharacterized_LOC104225434 [MW = 48.02 kDa]

No. of times detected



log(intensity)



Values from



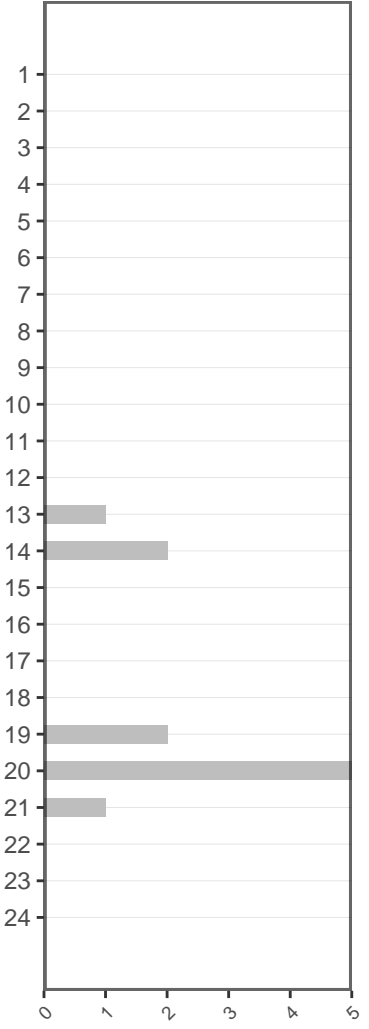
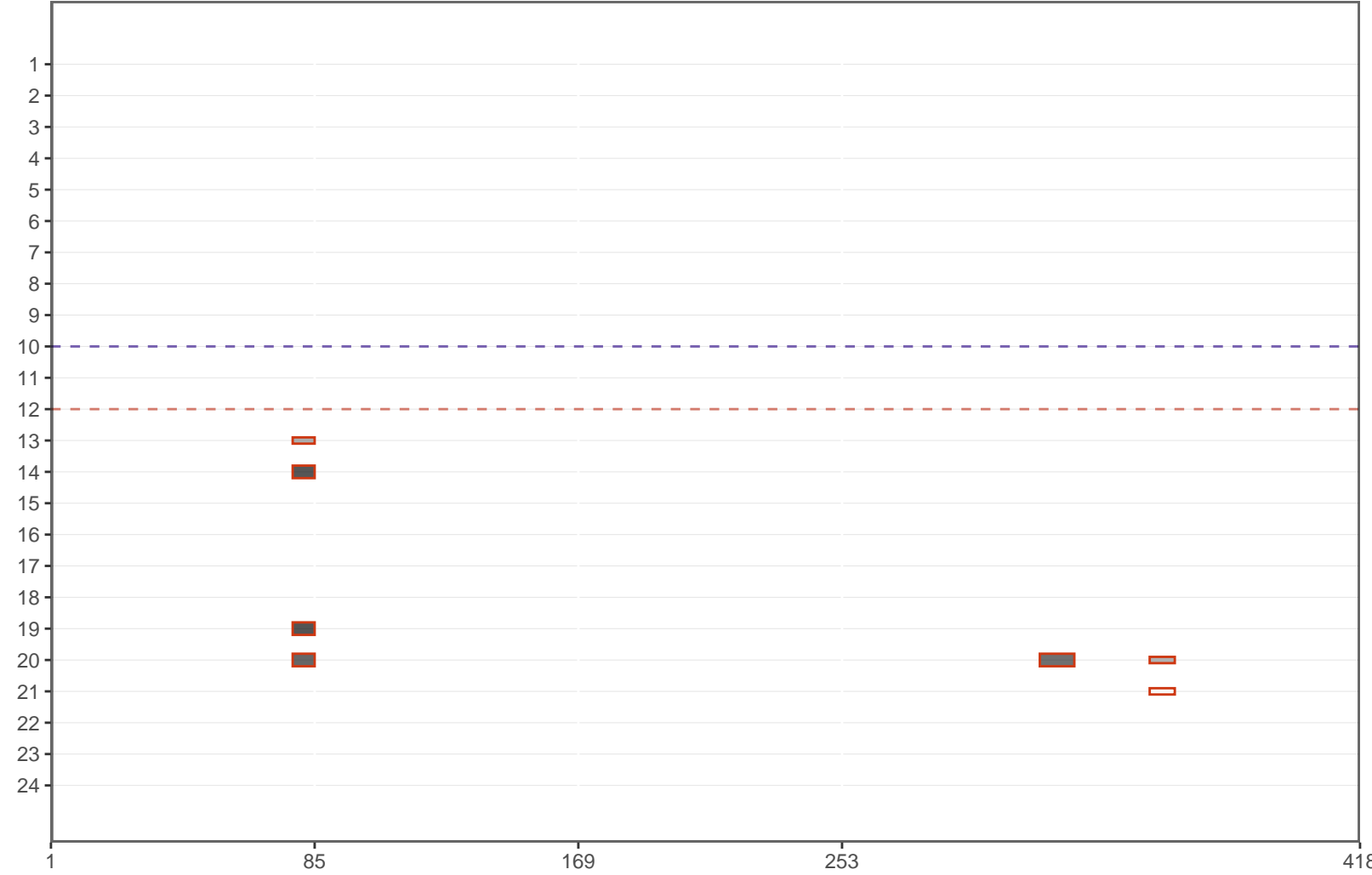
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

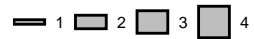


Protein sequence:

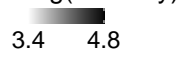
GDKEGMRPEFVRMYSHGELGELKMLRFRKKKEGEGKGFSLKELNDRILAKLRTEKESESRRMADSVFSEKIKSLWMSTDDDEEKAKRTMGRILDVGLGGLGTPSPFMLHPKPEELVEKYFHPDNMSSEENMKLELQKVRDEFKMSSESDGGSRVQVAGLTTKKHLSVLLHKDKHSRKGLOAMVQKRKLLKYLRTFDWDVYGLVLEKLGRLNPKKE

NbL16g21340.1 ABC_transporter_C_family_member_2-like [MW = 180.89 kDa]

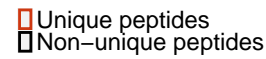
No. of times detected



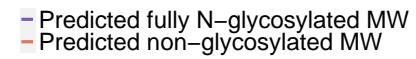
log(intensity)



Values from



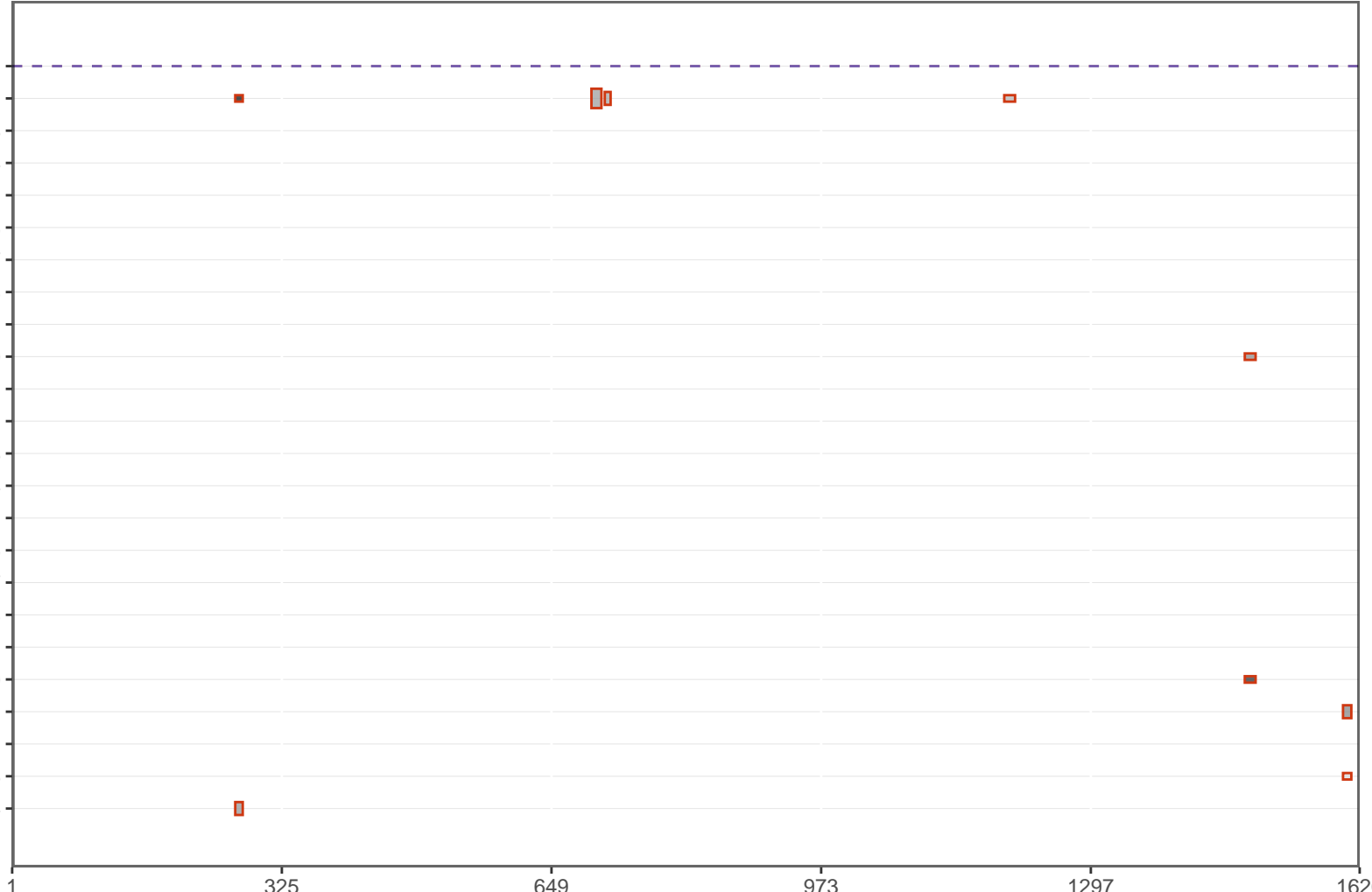
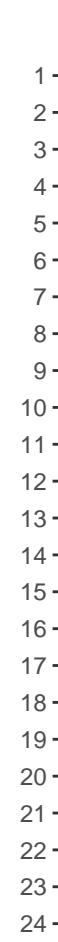
MW indication



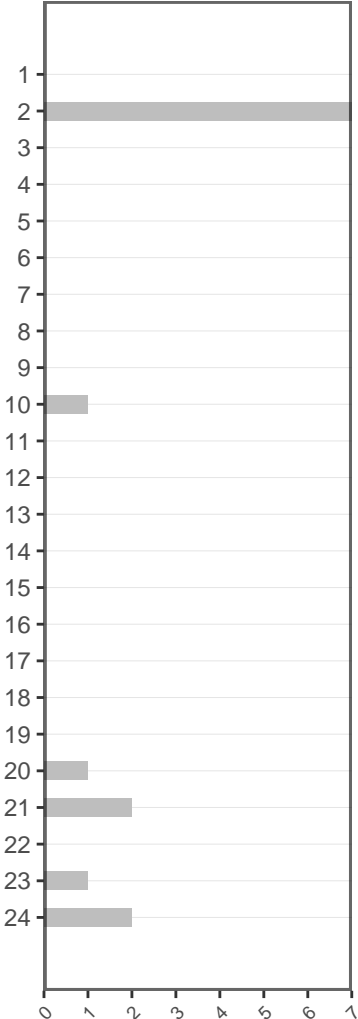
Molecular weight



Gel Slice



Protein length

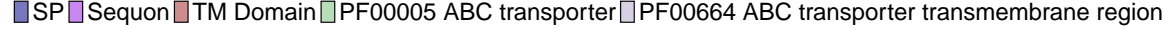


Peptide counts over 4 repeats



Pfam domains

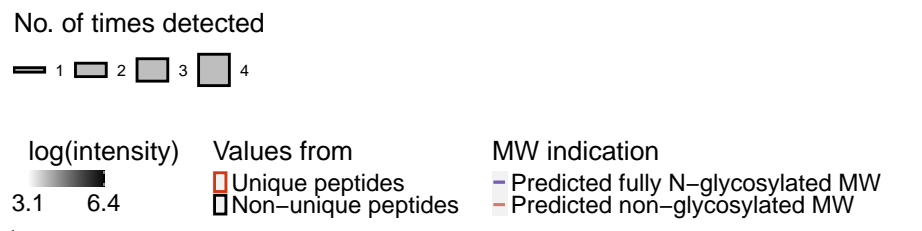
Pfam Description



Protein sequence:

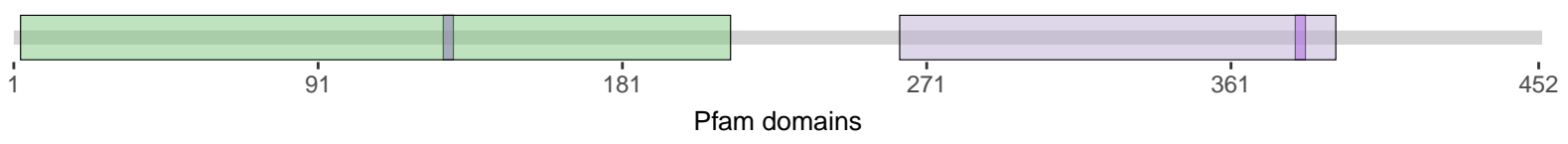
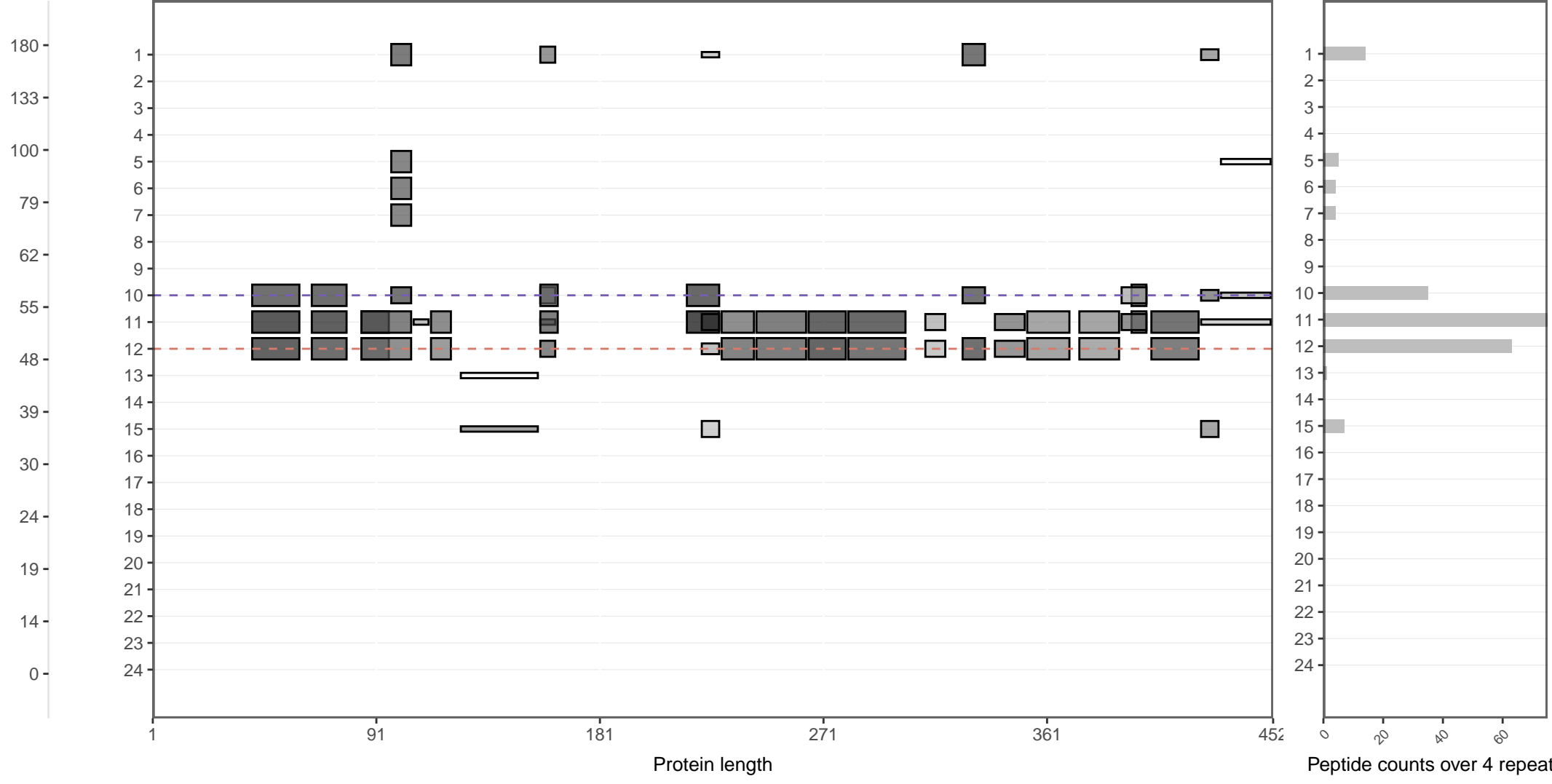
IQLIFLSQVDRILVHDGMKKEEGTFEGLGNNVLFQKLMENAGKMEVTEEEKENDNDKSSKPIANGSETNGVSKVKGDKKGGKSVLKGEEERETGVVSWNVALRYKNAKGGSSWVVVFLFGVLEALRIGSSTWLSFVTDQGSSTRTYAGFYNLVSLLSGGVMMVLTNFSFWLITSSLVAAKRLHDMNLNLRAPMVFHTNPLGRINRFADLGGDIDRTVAPFVSMFLGGVFDLSTFVLIGVSTMSLWIMPLLVEFGAVLYYQGTAREVNRLLDSISRSPVYAQFI

NbL16g21330.1 tubulin_alpha-2_chain-like [MW = 49.77 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF00091 Tubulin/FtsZ family, GTPase domain PF03953 Tubulin C-terminal domain

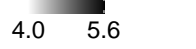
Protein sequence:
 IRSLDIERPTYTLNLRLLSGVSSLSASLRFDGALNVDFNEFGTNLVYPRHFMLSSVAPVISAQKAYHEGLSVAETNSAFEPSSMMVWGDPRHKGVMAGQLMFRGDVWPKDQVNAWATIKTKRTIGFVDWVPTGFKGGINYGPPTVVPQGDLAIVGRVADMIENSTVAEIVSRDKHFDLIVAKRAFHVWYVYEGEMEEGEFSEAREDLAALAEKDYEEVGAEGDDEGEDEDEY

NbL16g21320.1 60S_ribosomal_protein_L32-1-like [MW = 15.56 kDa]

No. of times detected



log(intensity)



Values from



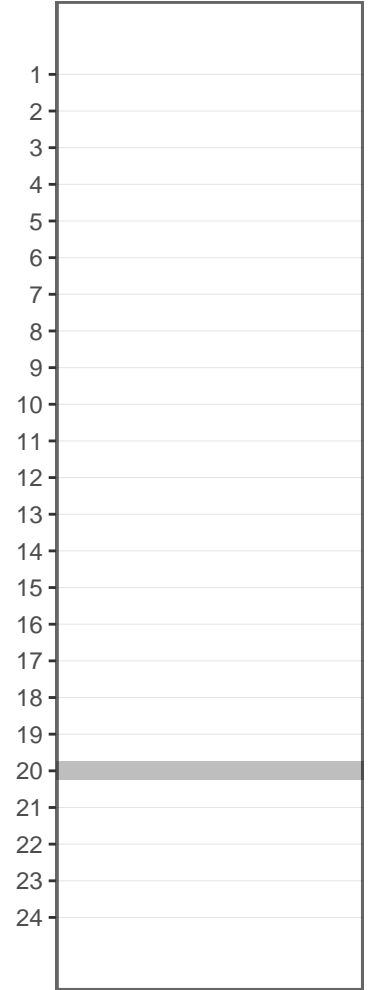
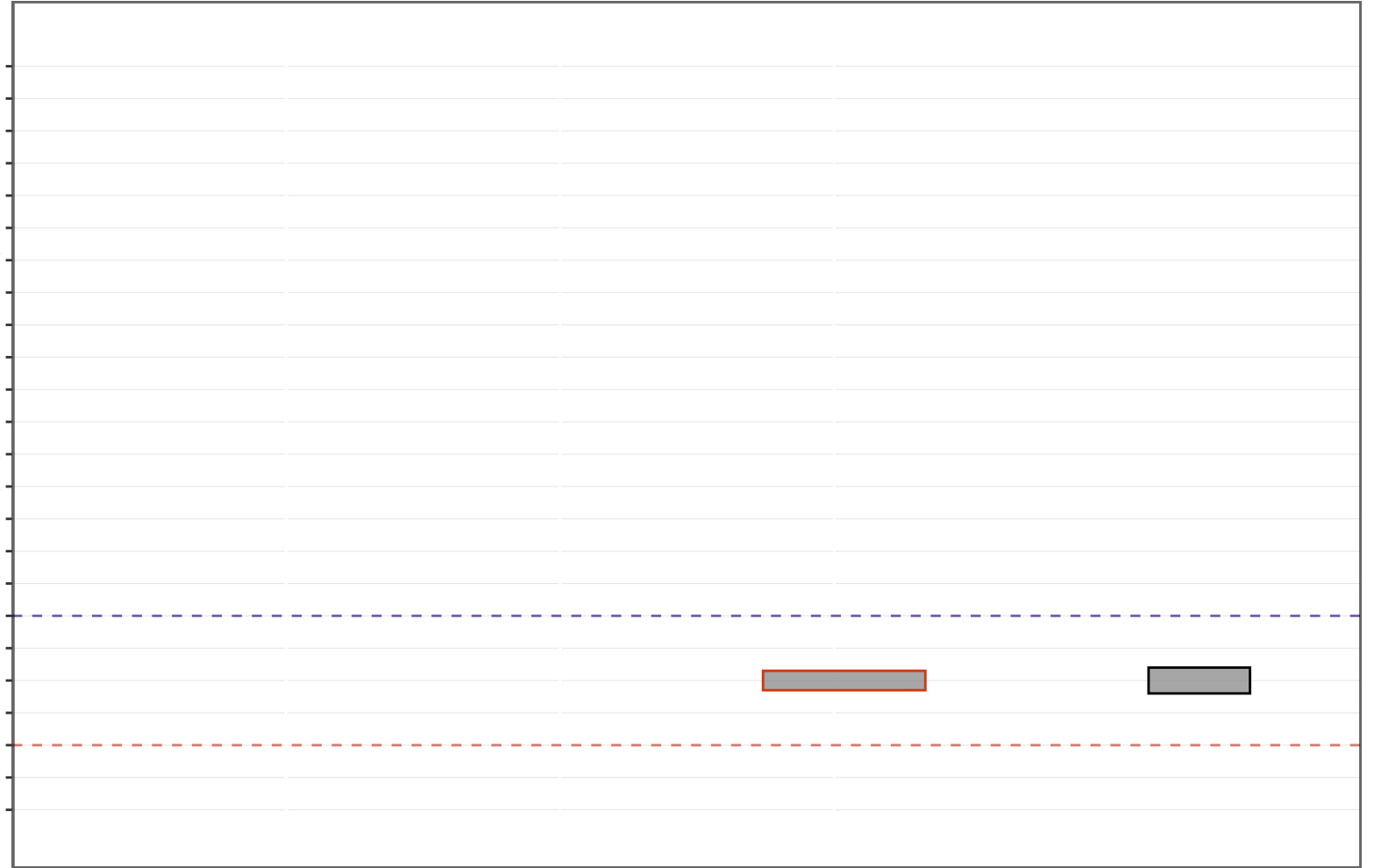
MW indication



Molecular weight



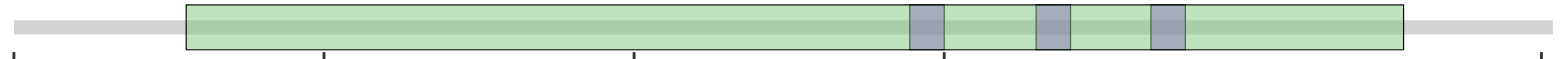
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

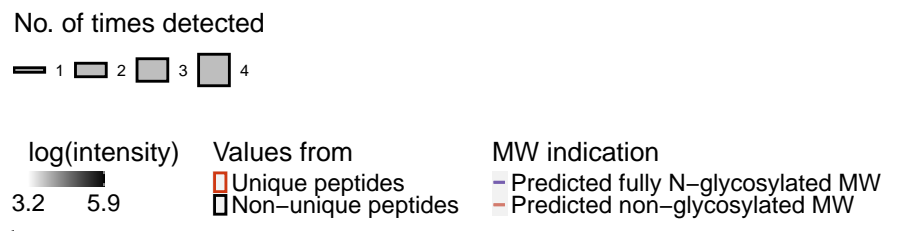
Pfam Description



Protein sequence:

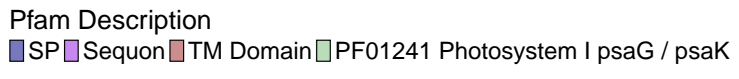
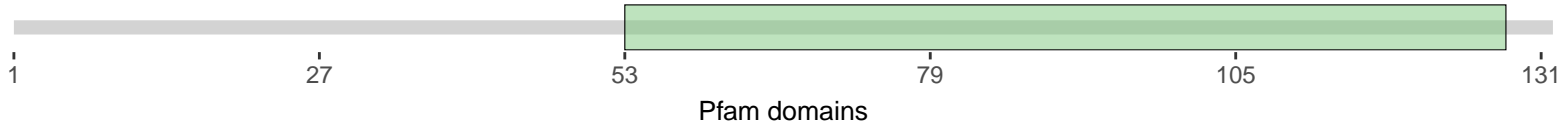
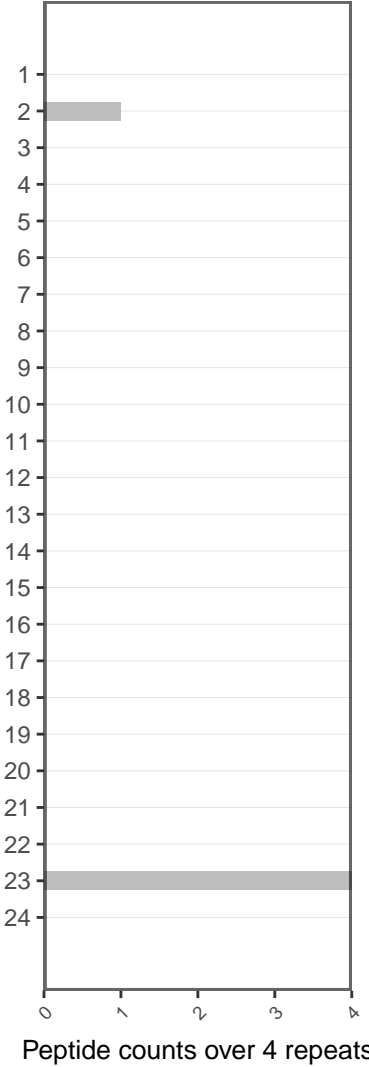
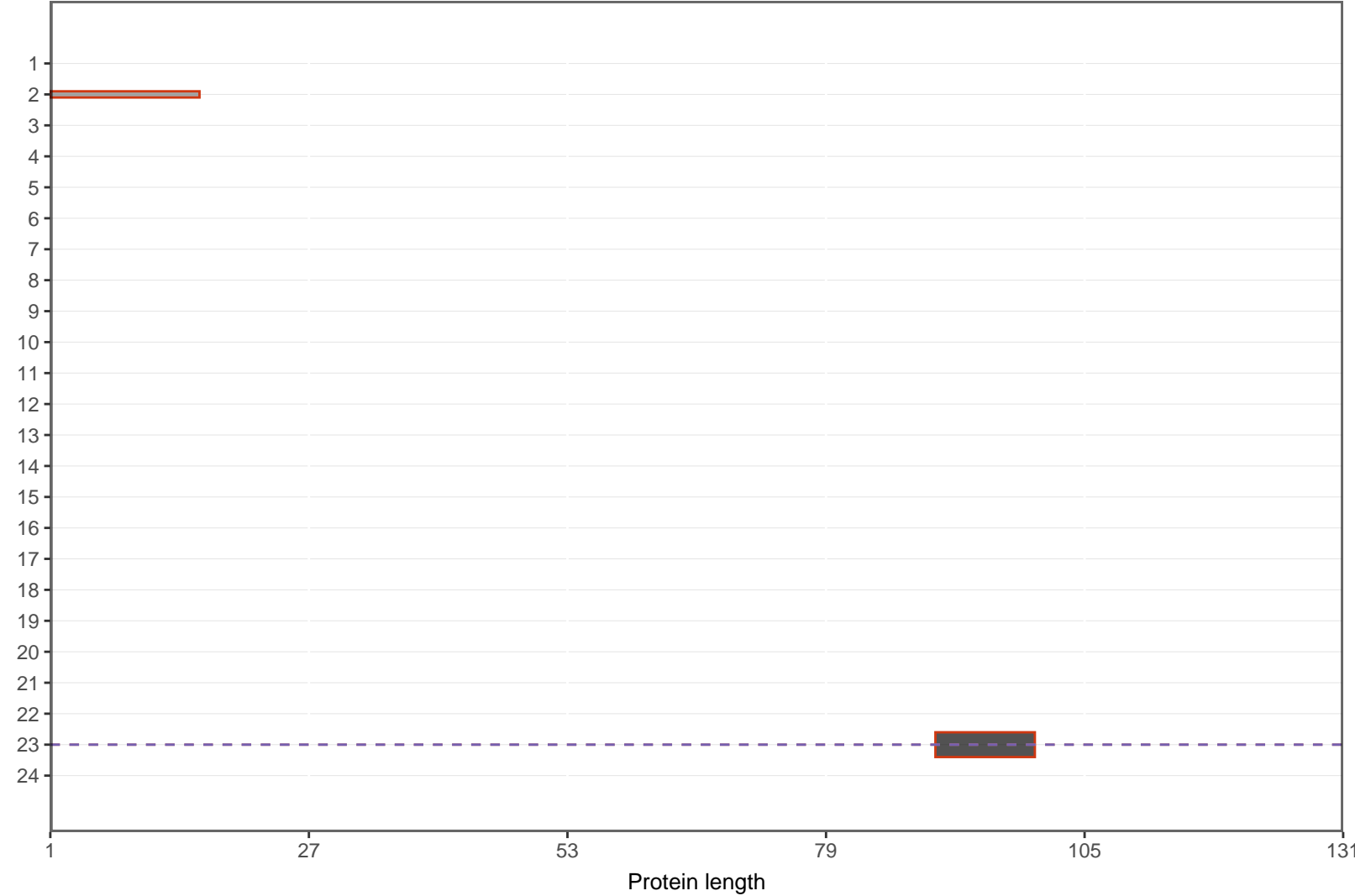
NIGYSDKQTRHYLPNGFKFVHNASELDVLMHNRITYGAEIAHNVSTRKRKEVERAAGLEIVVVTNKLARLRGDEE

NbL16g21290.1 photosystem_I_reaction_center_subunit_psaK_chloroplastic [MW = 13.4 kDa]



Molecular weight

Gel Slice



Protein sequence:
 SPTNLMVTSTSLMIFAGRFLGAPSNRKAATAGLKEIVRDSGLGTGDRPFRFLADTLAAGVYGHIGVGVVGLKNGAL

NbL16g21230.1 3-isopropylmalate_dehydrogenase_2_chloroplastic-like [MW = 43.43 kDa]

No. of times detected



log(intensity)



Values from



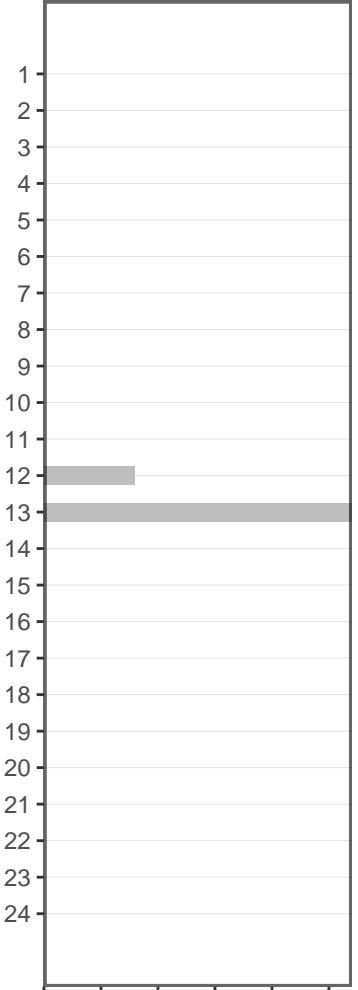
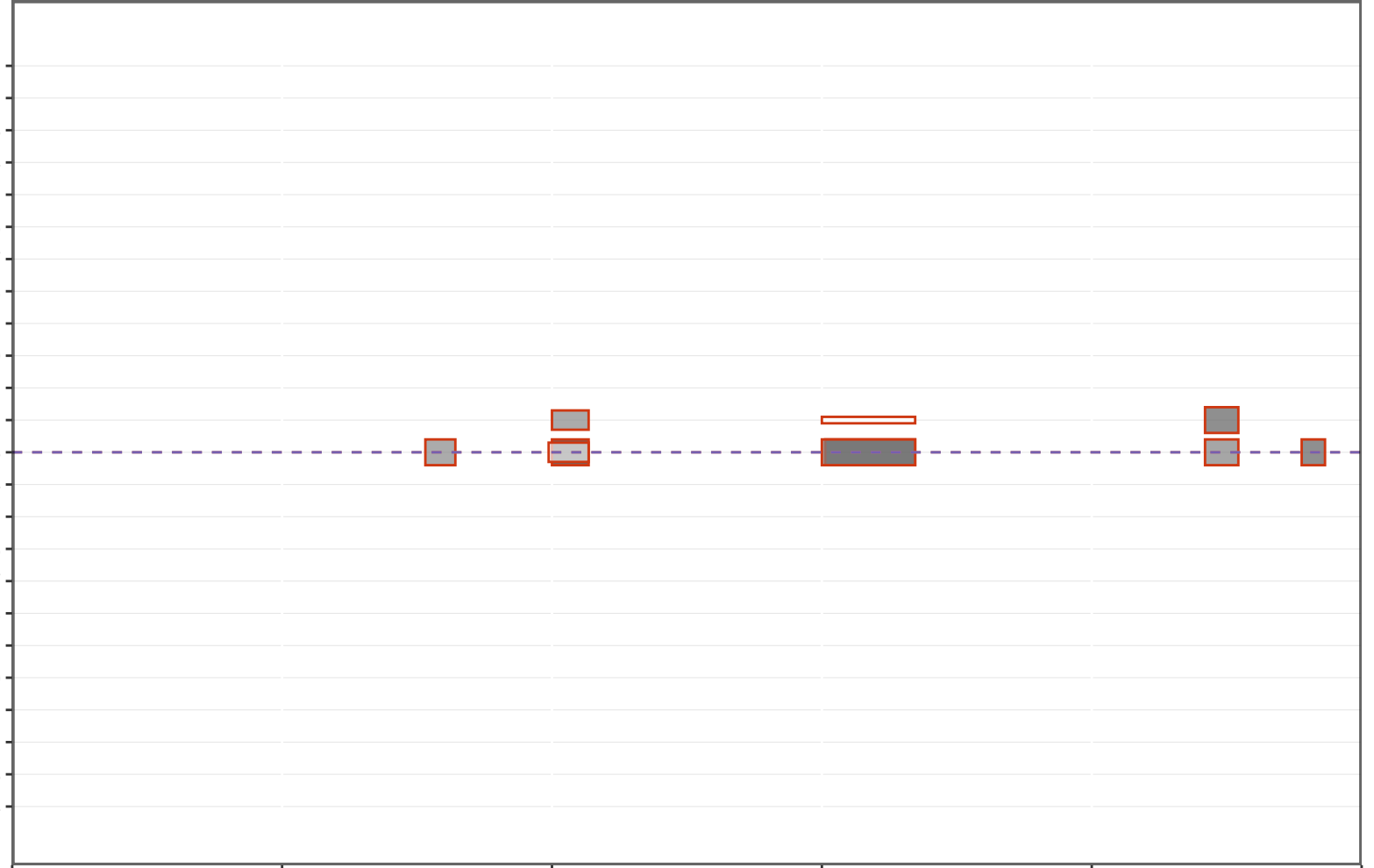
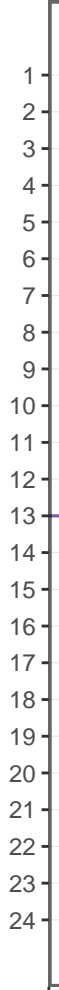
MW indication



Molecular weight

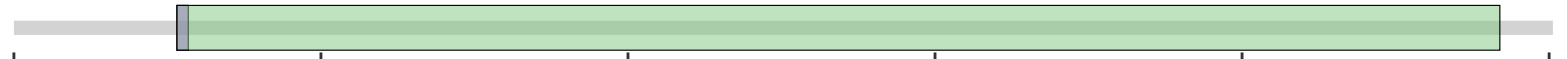


Gel Slice



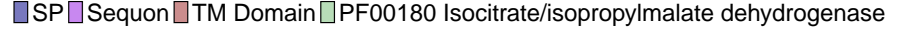
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TNENGQIEGFNTEVVAWEIERIARAFETARKRRKGLGSDVKANVLEASMLWRKIVTALASEYDPVELSHMYVDNAAMQLVRRPKGDFVTWTFNFIQDILSDEASMITGGIGALPEASLGETGPGLFEPHIGSAPDIAGDDKANPLATVLSAAMLLKYLIGEKAAGRIEAVALDALNRGFRFGDHSAGHKLVGCKEMGEELVLSIDSKTPAV

NbL16g21110.1 putative_hydrolase_C777.06c [MW = 35.9 kDa]

No. of times detected



log(intensity)



Values from



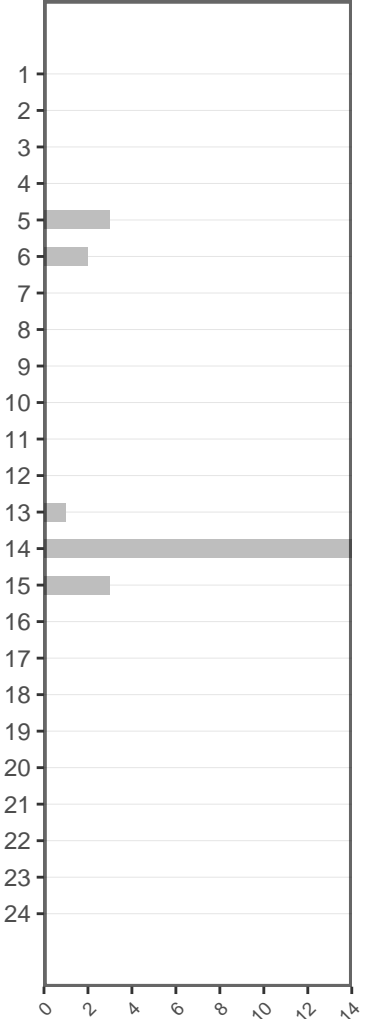
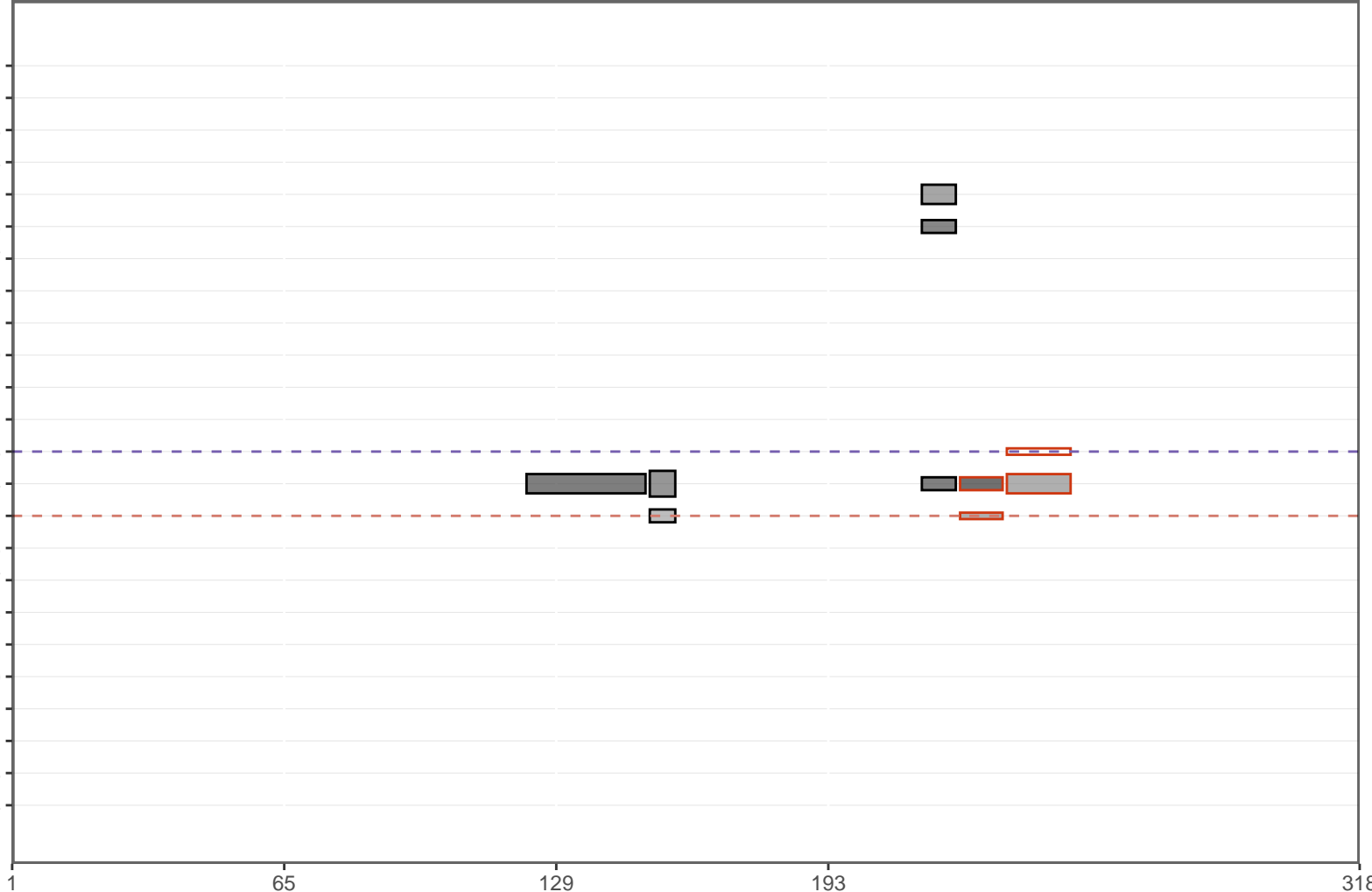
MW indication



Molecular weight

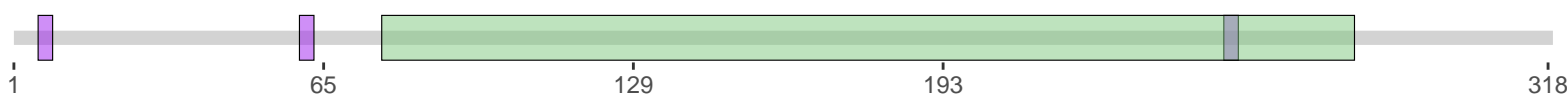


Gel Slice



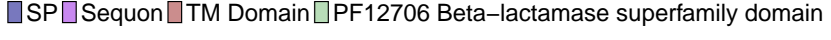
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

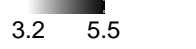
IDQKFPYLVQKLEKGGQIRRVAGLDWGHENDGCTPFVAGLEFVFLPVMHGEDYVGLGFLGKFRVAVSDVSRFLPTTVSHYKHSQGLDLLLDTLYKNGSHNVHLGLTGLEALKMLGPKRALLIGMTHFDHKKDNEFLVWESRRREGIEVQLAHDGLRVPVDL

NbL16g21000.1 ornithine_aminotransferase_mitochondrial-like [MW = 53.43 kDa]

No. of times detected



log(intensity)



Values from



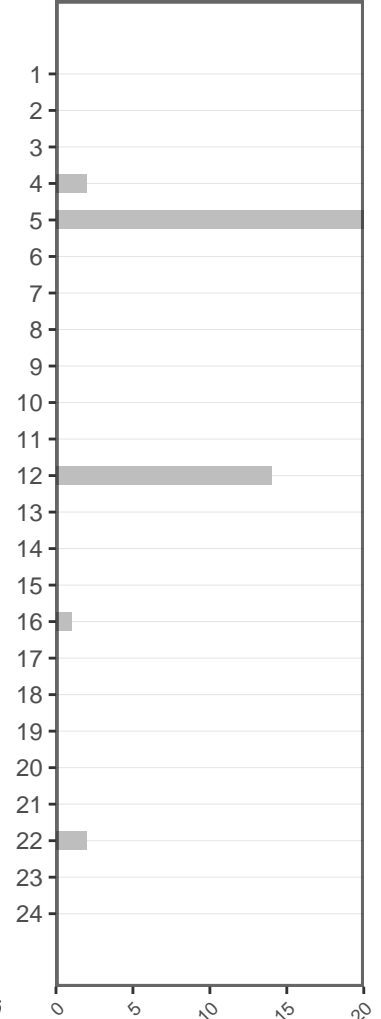
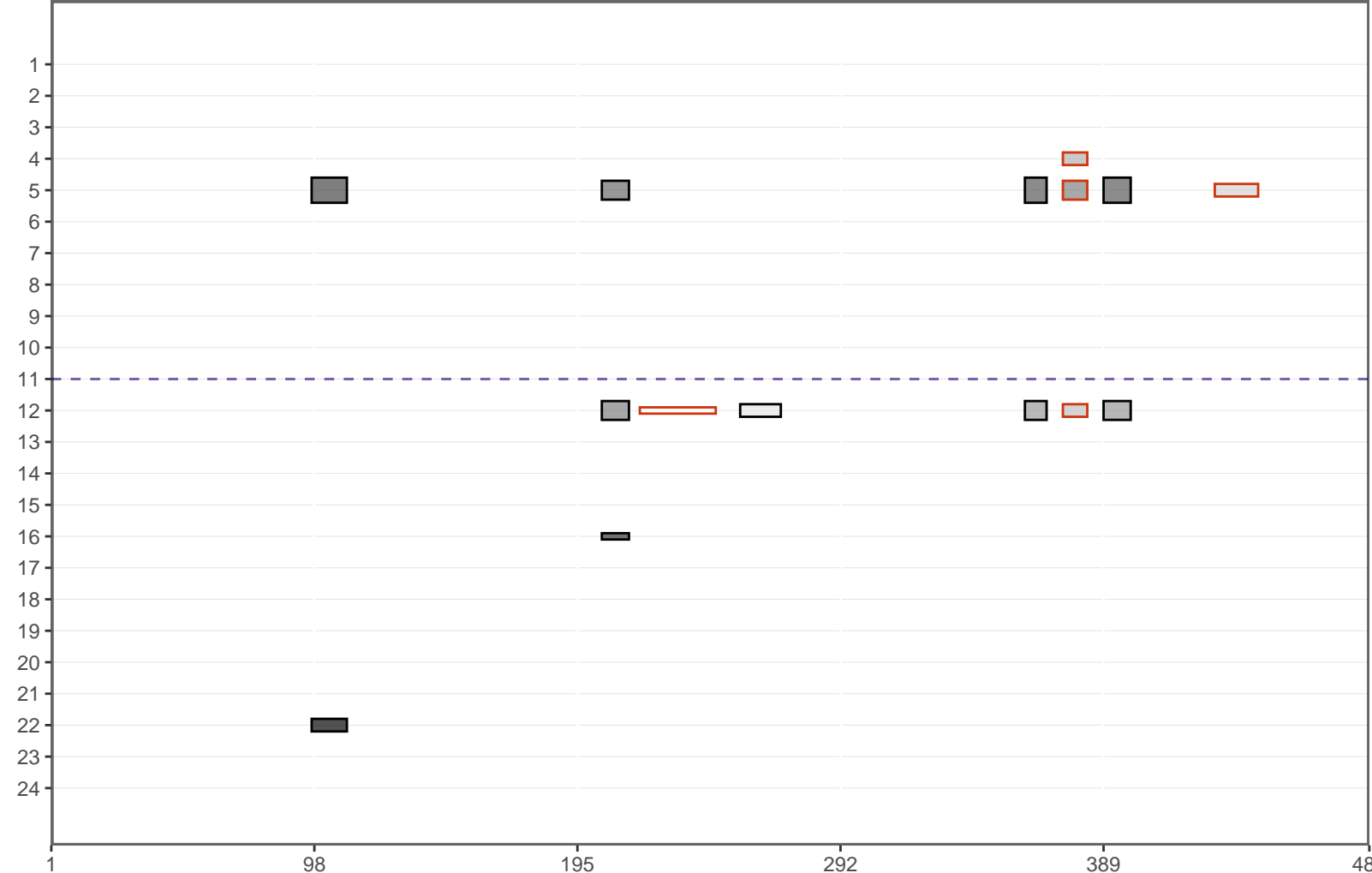
MW indication



Molecular weight

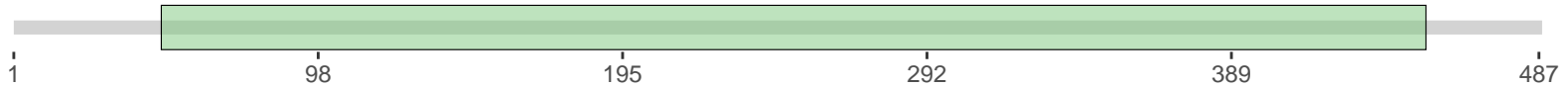


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

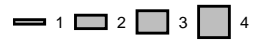


Protein sequence:

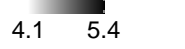
EPIQGEAGVIVPEGLKAVRDHDSKYNLMADEIQSGLARGRLLAGDGEVFRPDIKLGKALGGVLFVSAVLADKVMKIQAGHGSTFGGNPLASAWAIAASLVRDEGLAERYGLLWSKLIDERSAQMGEGQLRHLMKYGQGFNFKIKVRGKGLFNVELNSKALLPVTAVDICMKLKERGLAKPHTDSIRLTPPLSMLSEELQEGSKALHDFELDLPMQKEKPTVSHATSSFGDRGGRNLYGSS

NbL16g20970.1 protease_Do-like_5_chloroplastic [MW = 32.64 kDa]

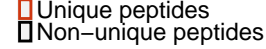
No. of times detected



log(intensity)



Values from



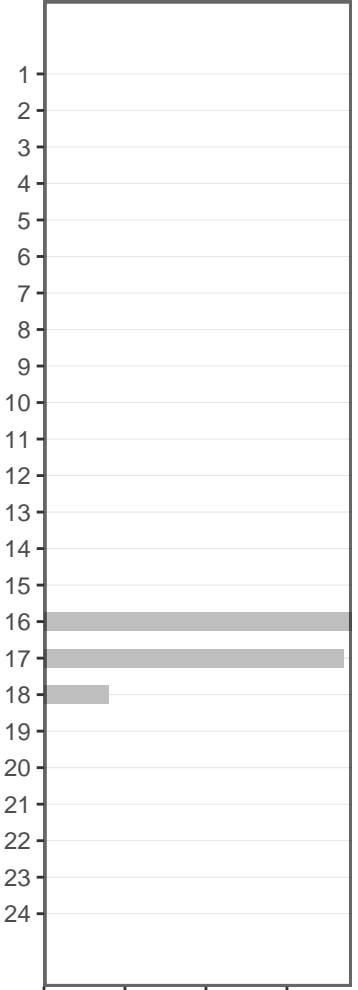
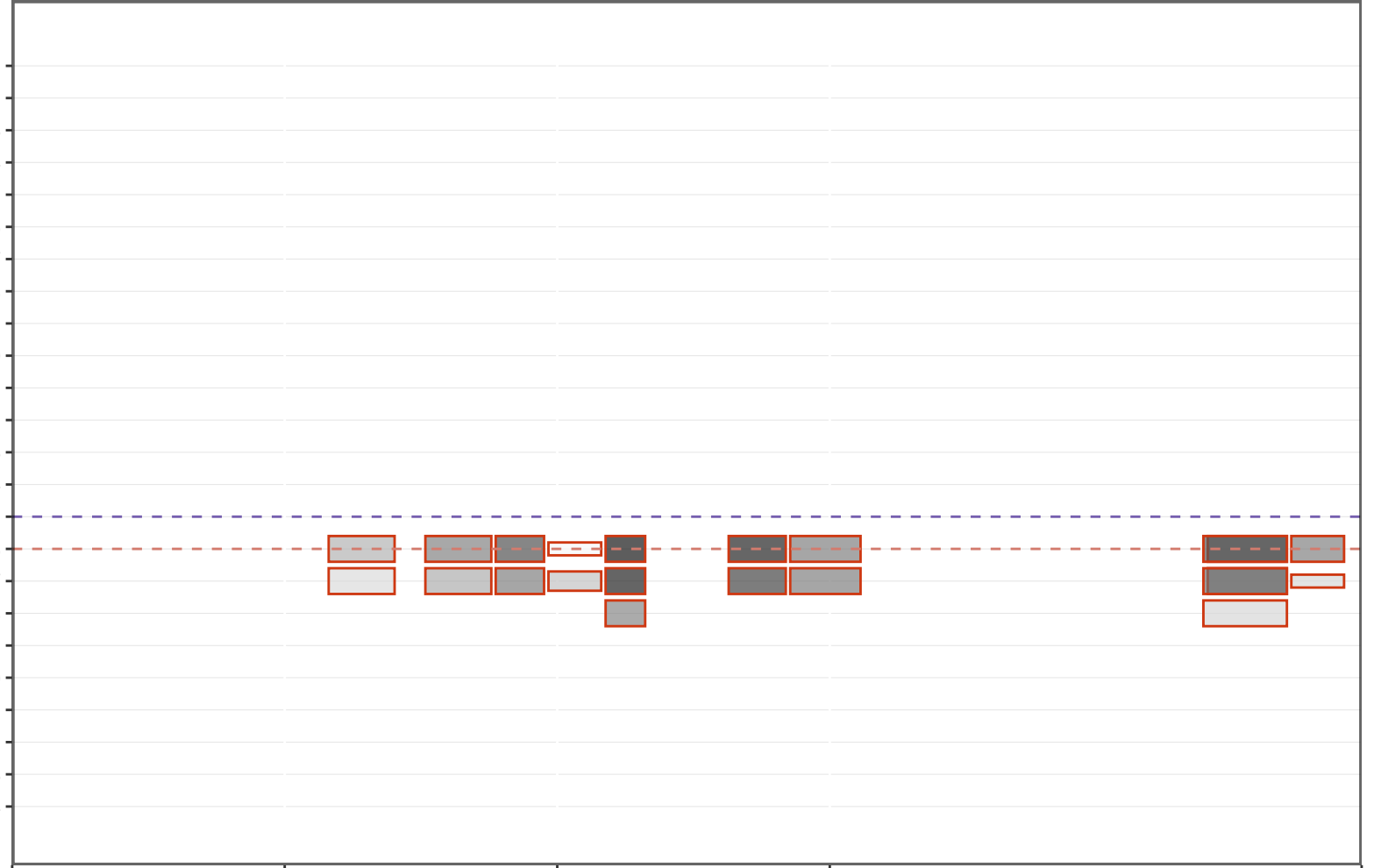
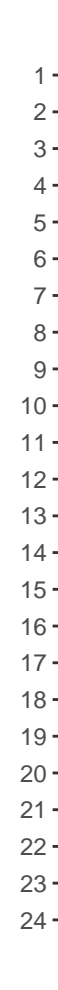
MW indication



Molecular weight



Gel Slice

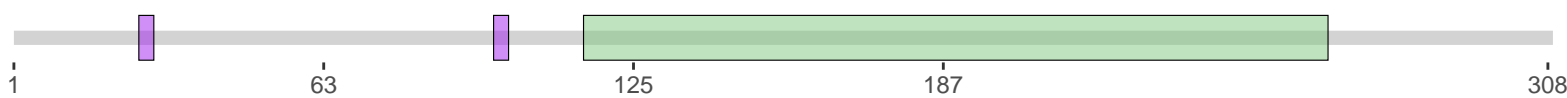


Protein length

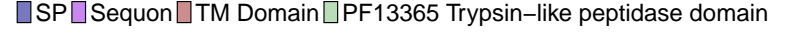
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

SGLQRCYKSLVNAKGESEAKKIVGVDPLVDLAVLKVDEGDEVKPIBVGTSRGLRVGQSGFAQNPYGFENTLTGIVVSGLGRIPAPNGAAIKGAQTDAAANAGNSGGPLIDSSGHVIGINTATFTRRGGSGMSSGVNFAIPIDTVRTIPYLVVGGTQKDRV

NbL16g20800.1 prefoldin_subunit_6-like [MW = 14.9 kDa]

No. of times detected



log(intensity)



Values from



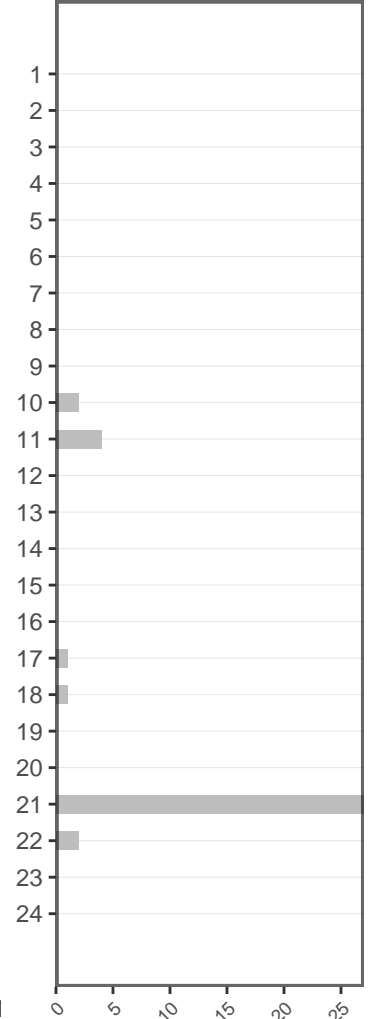
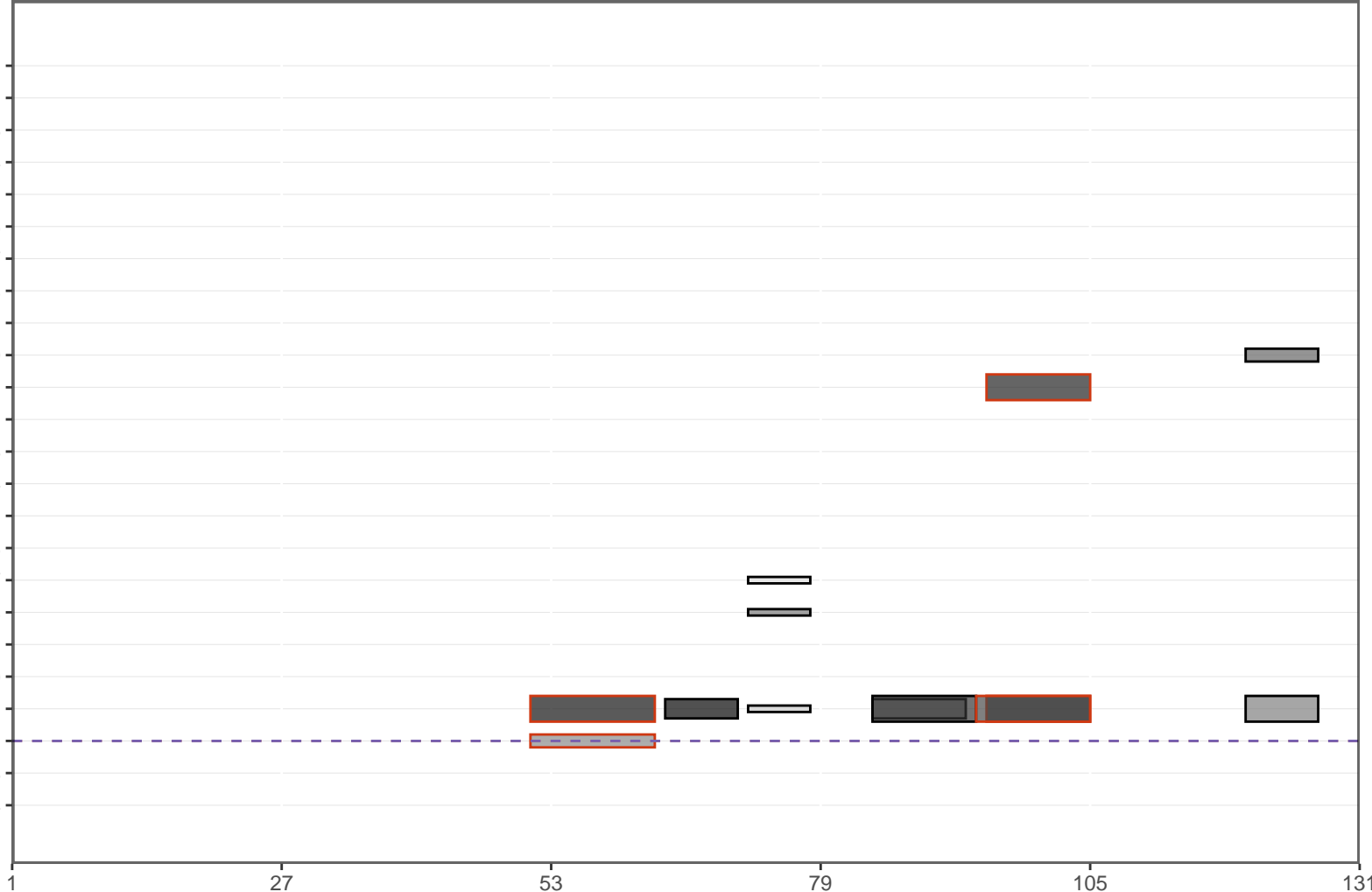
MW indication



Molecular weight

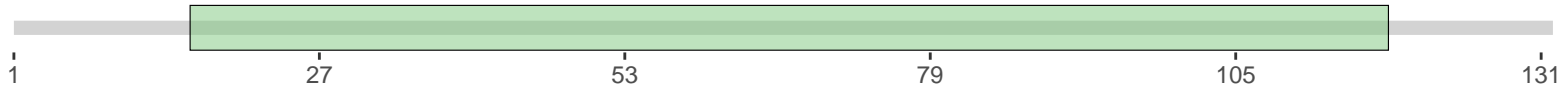


Gel Slice



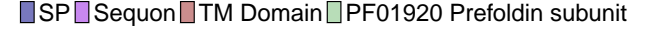
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DLLNEDANVYKLGPIVWKGDLAEARANWKRREYISAELEKRLDGLDLEEEKNSKRKRILKFGQKIGSLGAGKGA*

NbL16g20750.1 60S_ribosomal_protein_L18a-like [MW = 21.45 kDa]

No. of times detected



log(intensity)



Values from



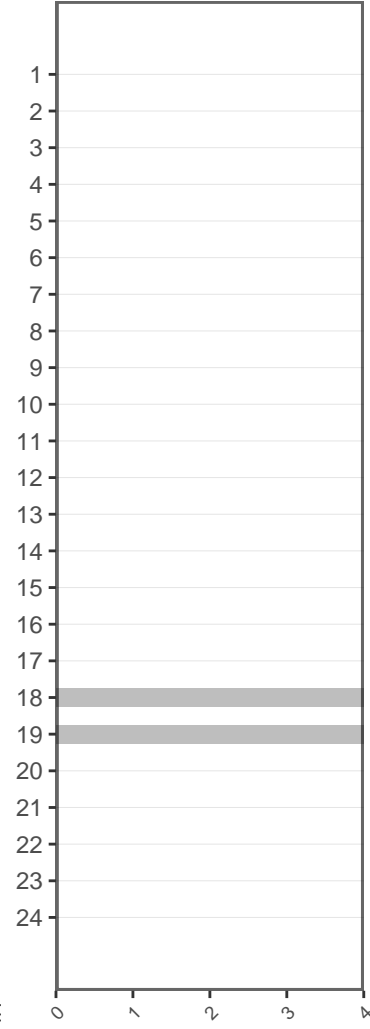
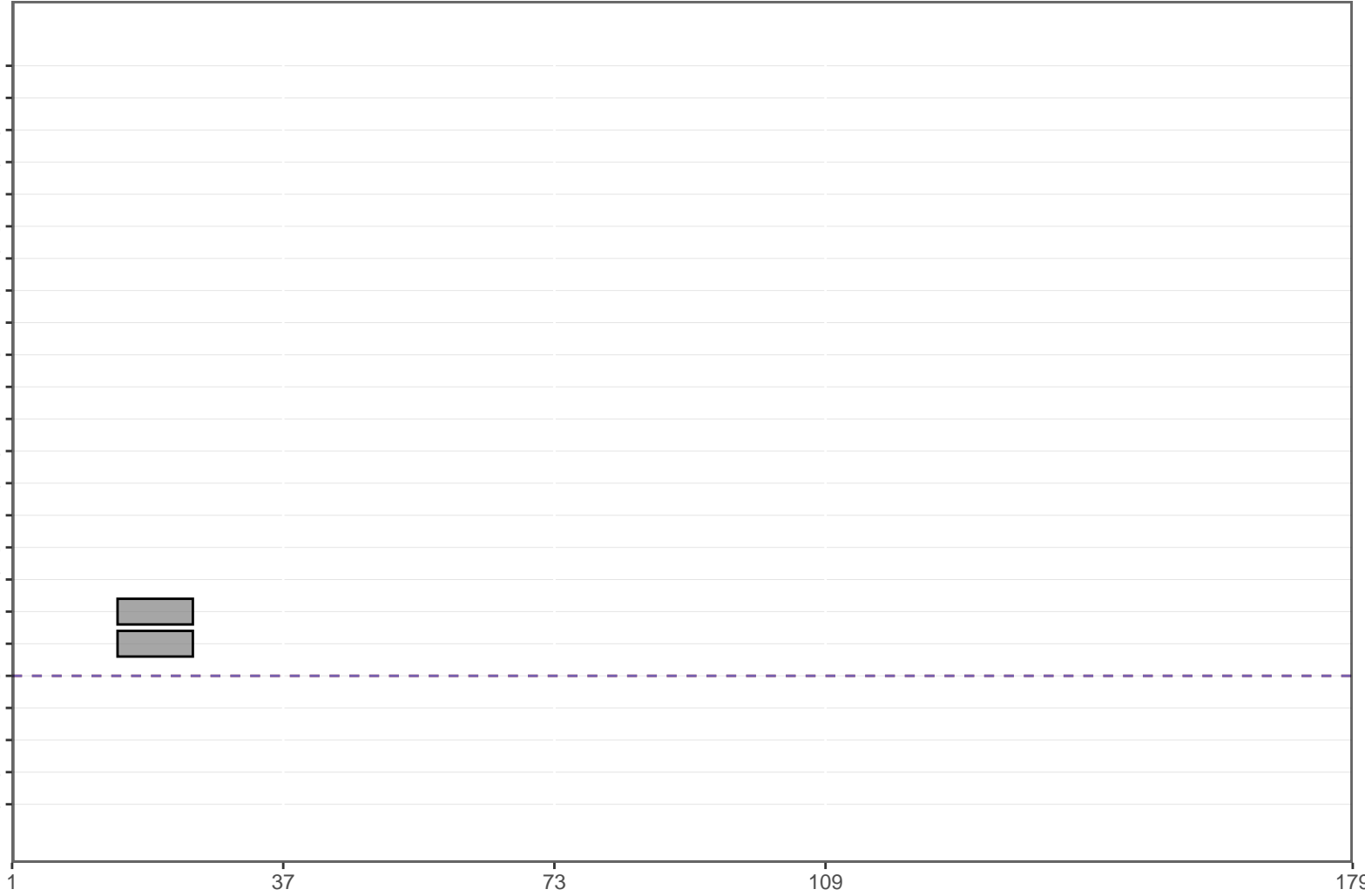
MW indication



Molecular weight



Gel Slice

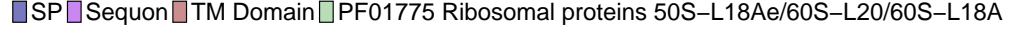


Protein length



Pfam domains

Pfam Description



Protein sequence:

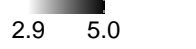
YVGIWLRYSQRTGYHNMVKEVRDFTLNGGVEQMVTETMASRHRVRRHHCIGIKTATIRAKLQKRESTNGFHDGSKIFPLVFKKVRPPSRALKTTFKWATRNLFM

NbL16g20710.1 uncharacterized_LOC109214655 [MW = 66.18 kDa]

No. of times detected



log(intensity)



Values from



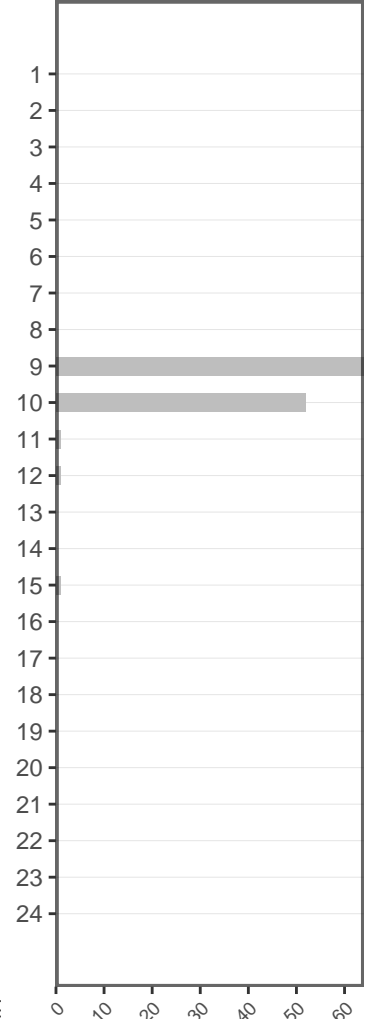
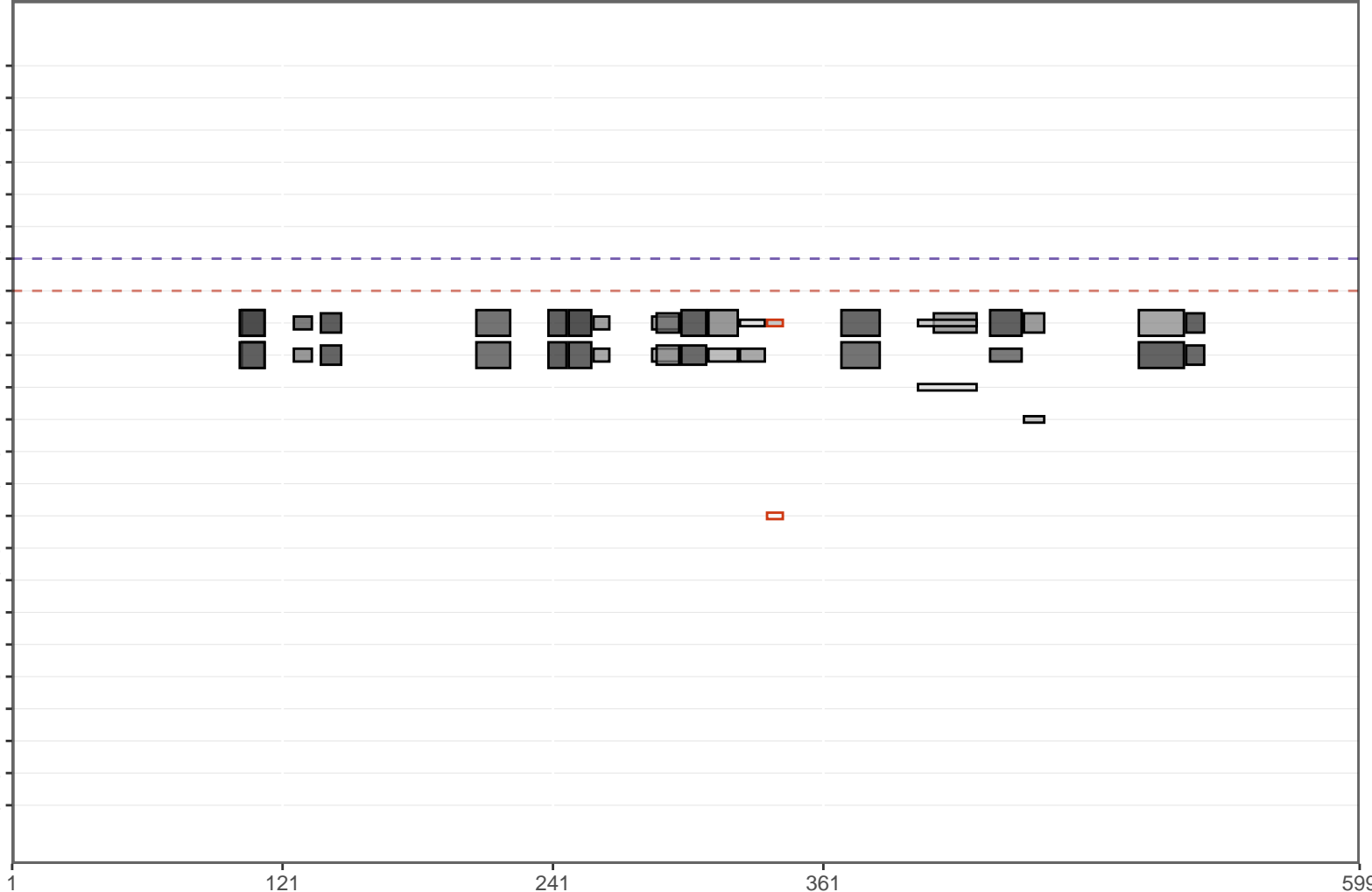
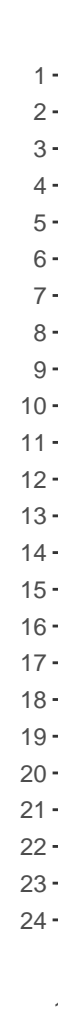
MW indication



Molecular weight



Gel Slice



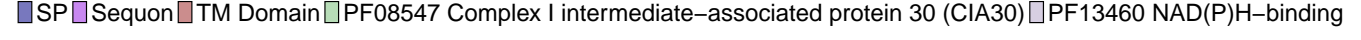
Protein length



Pfam domains



Pfam Description



Protein sequence:

SEDSLNGVEVROGTYFDQVASKYDQGMDFEFERGEAFSGVYFRGGYVELSRKLSPLGYLDRYEGLVFVGGNGSRVYVLEAGPSADTQKYLFRISTKAGFCRVRVYFSSFRVYFDDPLDFLVHLTRIFRPRRPPIDGPGVNDLIRFQIMEYKALPTGGEDFVILVSGTGGSEPTREGLVRAKRAGEDSLRRLGLGYTHRPGPLMEEPGGQRALFDGGNRISGGSGADVADGVKALHDSIARNKSFDFVGYEVAEPGKELYELVAHP

NbL16g20690.1 Golgi_to_ER_traffic_protein_4_homolog [MW = 37.07 kDa]

No. of times detected



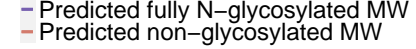
log(intensity)



Values from



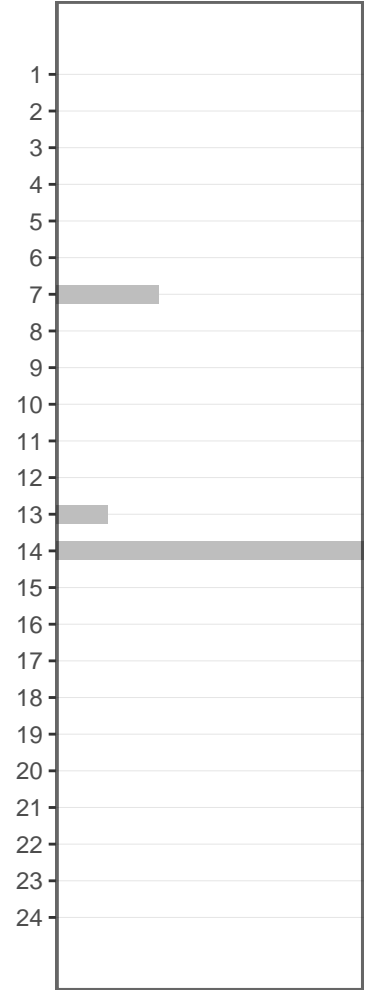
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

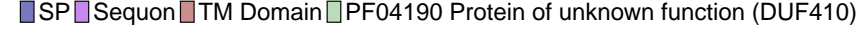
Protein length

66 131 196 261 327



Pfam domains

Pfam Description



Protein sequence:

SAIEFGAHRKIQSSPELHEMLADHYSGSTEVDMKVVGFHFVIRGRNLKFFASTINFMGKDYVGEDDLAARALMNYLELGNLRDANKLMEVEVEKEMEAHHLGFPQSELMGFVNYLLLTQLRQDALPLFNMLRQSYKSSDRDPLLNELLDEIAKFKYGVQRKNPLGGIFGDFKMMGGE

NbL16g20680.1 aminoacyl_tRNA_synthase_complex-interacting_multifunctional_protein_1-like [MW = 30.46 kDa]

No. of times detected



log(intensity)



Values from



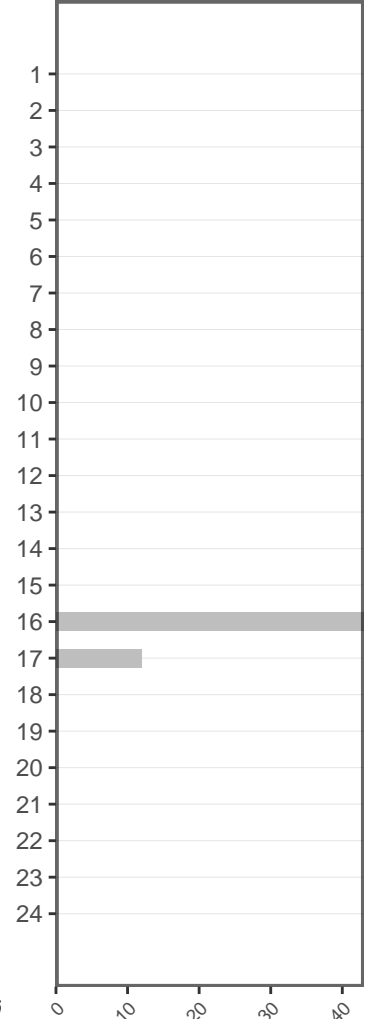
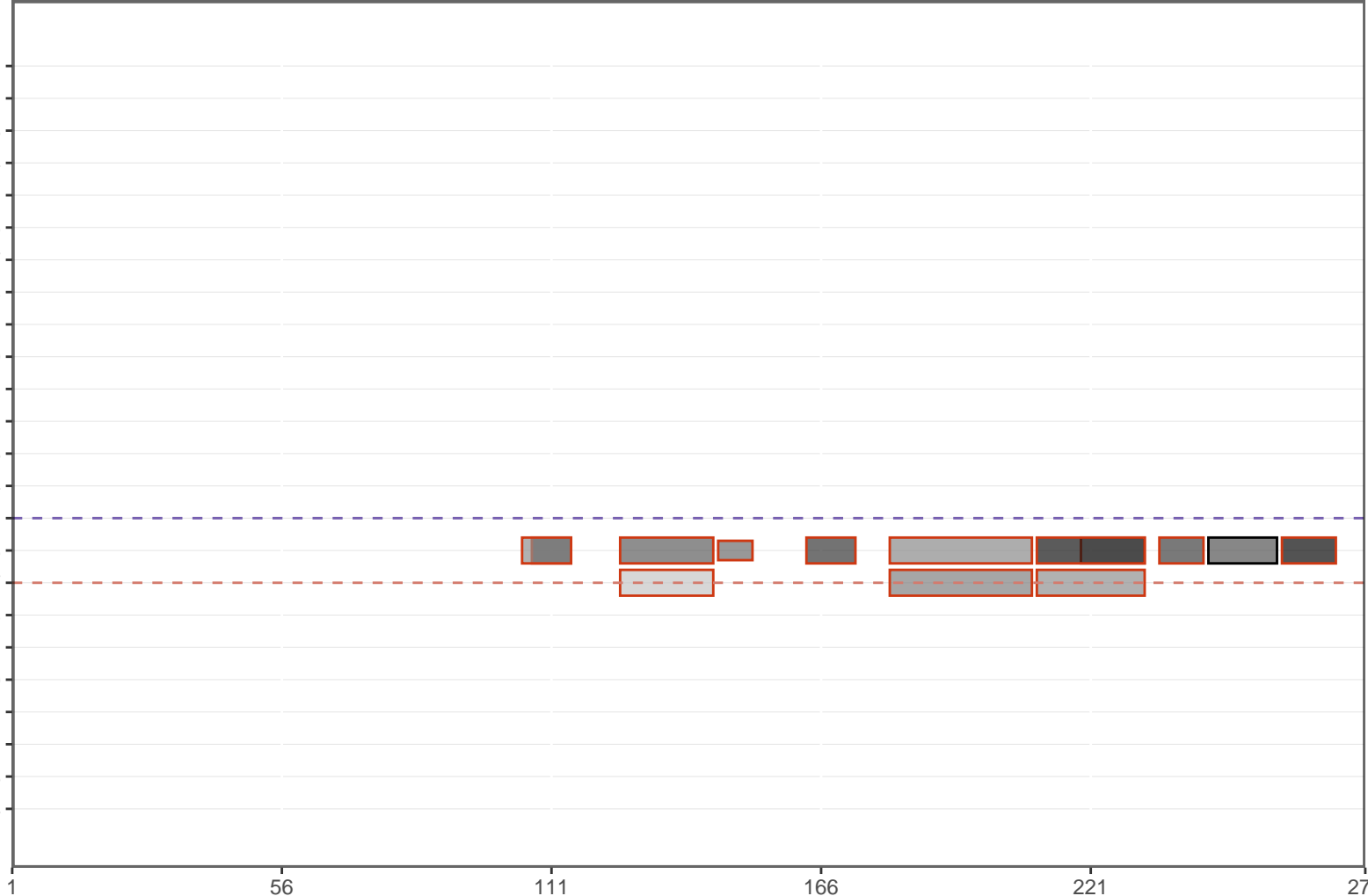
MW indication



Molecular weight

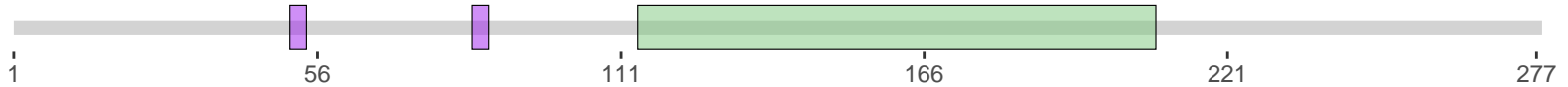


Gel Slice



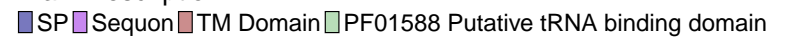
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

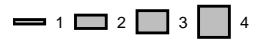


Protein sequence:

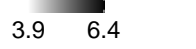
IEADSLYEEVDVGEVEFRIGSLGKLYPLDHLGQRNIVLANKRPNMRGKSGNGMLMAASDASHENVELLEPPGEGVPCRNIWFQSADEKENLPEWTPNQVAKKIWEVGPNIKTDGACVAALGMHSMRTSTGVAVSGSLKDAKRIQ

NbL16g20660.1 guanosine_nucleotide_diphosphate_dissociation_inhibitor_2-like [MW = 49.68 kDa]

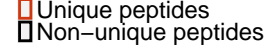
No. of times detected



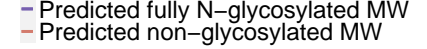
log(intensity)



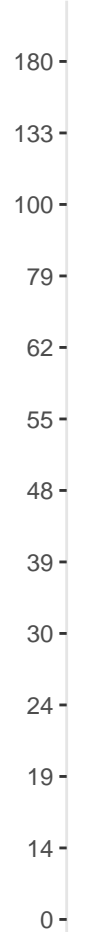
Values from



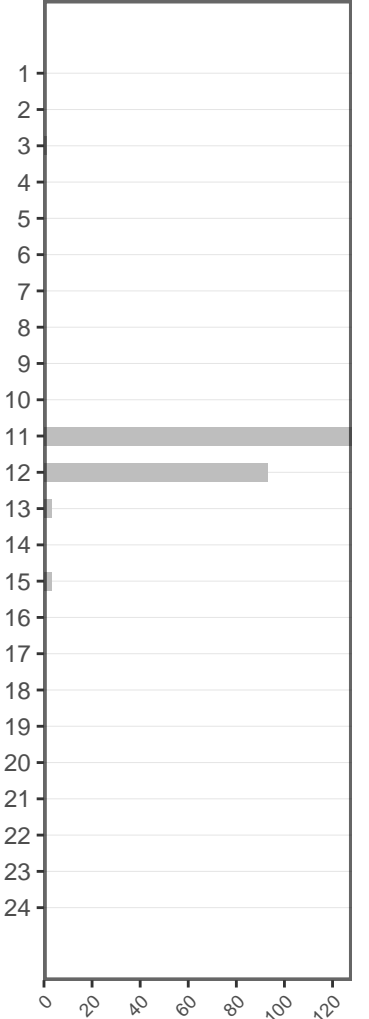
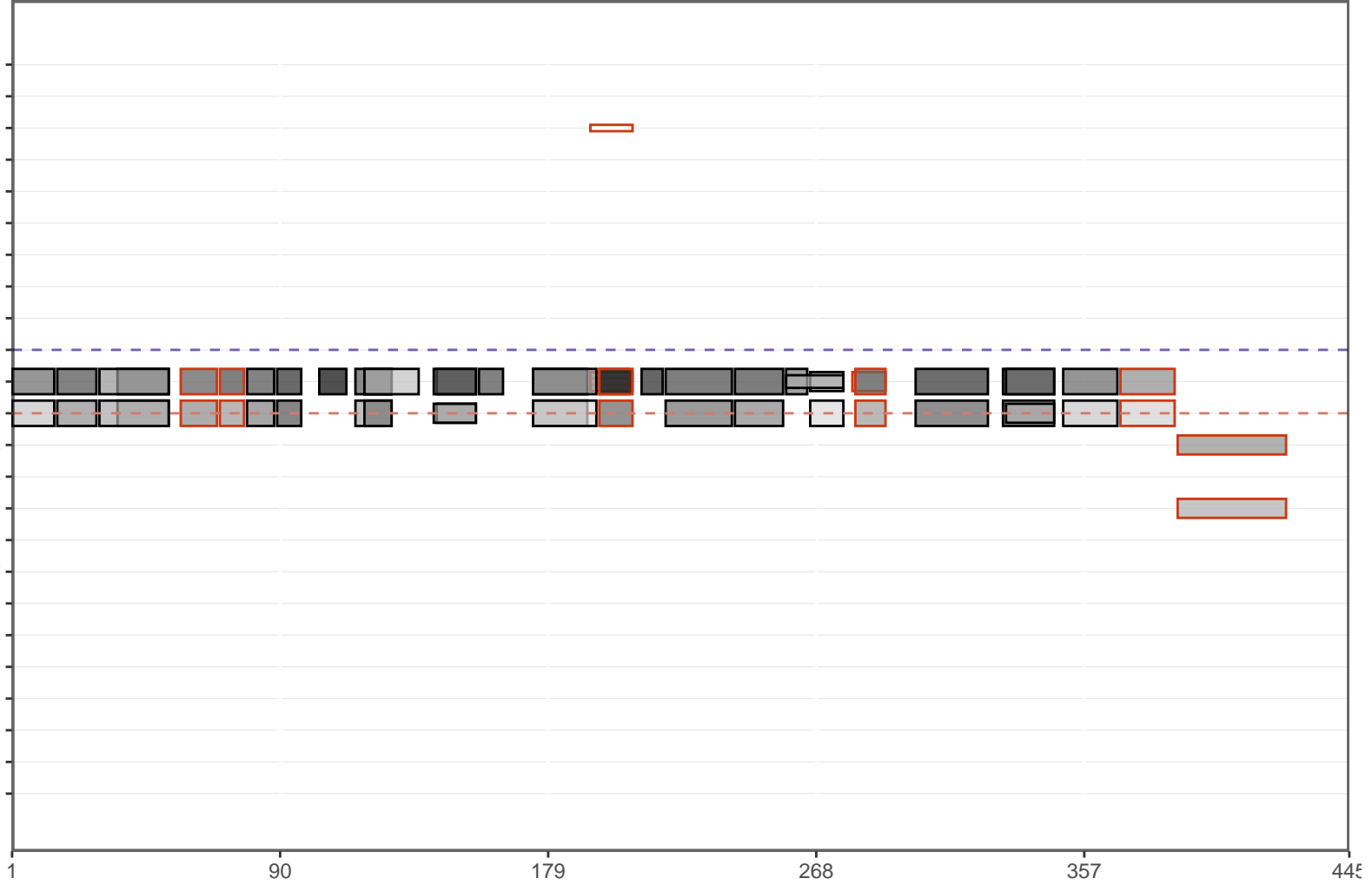
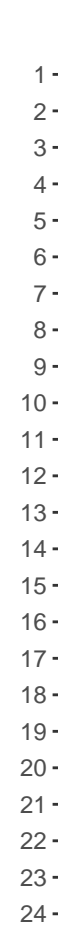
MW indication



Molecular weight

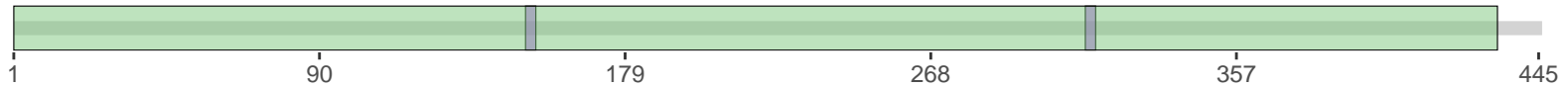


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

KLYAESLARFOGGSPYVPLVGLGELPQAFARLEAVYGGTYMLNKPGEKVEFDEEGKVCVGTSEGETANGKRVVGDPEYLPKRVKRVKVARAIAIMSHPIPTNDHSVGHLPQKLGGRKSDMYLFGCGVYTHNAPKGFIAFVSTEAEITNFESELKGGVNLGPVDEIFVETVDRSEPVNEPDLNGFISTYDATHFESTVDVNLNLYTKTKGLDLNVDLSAASAAEE

NbL16g20610.1 pyruvate_dehydrogenase_E1_component_subunit_beta-3_chloroplastic-like [MW = 44.46 kDa]

No. of times detected



log(intensity)



Values from



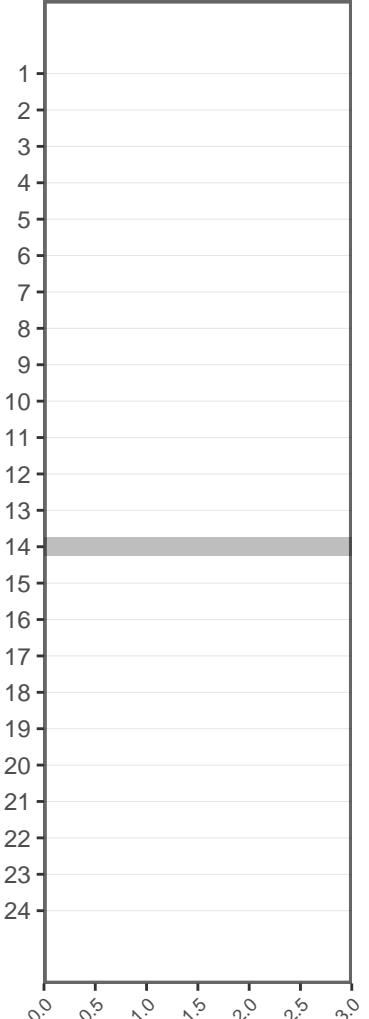
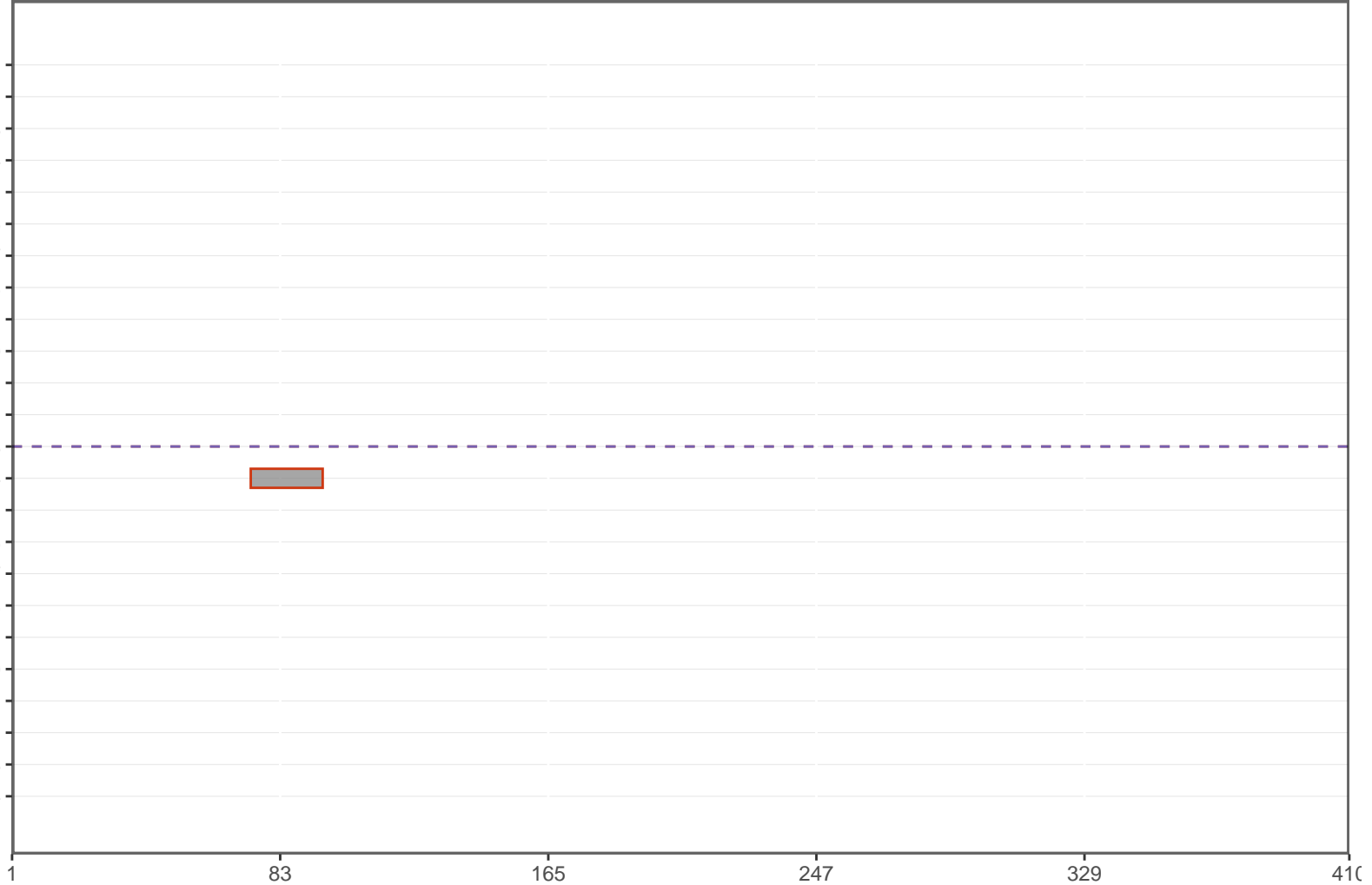
MW indication



Molecular weight

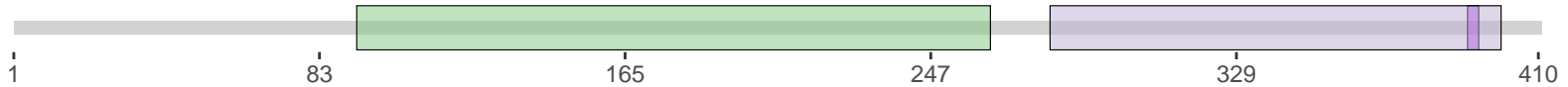


Gel Slice



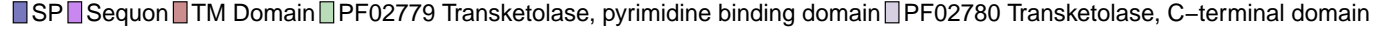
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SGGQFKPVIIRGPGGVGRGLGAEHSQRLESEYFQBPISGIMWAGSTPYNAKGLMKAARSDNPIVLFHVALYLNKERPDSEYVNLLEAEAMVRPGEDTILTYSRMRVHVMGAAKTLVDKGYDPEVIDRSLKPFDLHTIGNBNKTKRHWVVEECMRITGGIGASLTAIFENFHDVLDAPVQLS66DVPPTPVAGTLENVTVGPPQIVTAEVQLQI

NbL16g20560.1 vacuolar_protein_sorting-associated_protein_25-like [MW = 20.85 kDa]

No. of times detected



log(intensity)



Values from



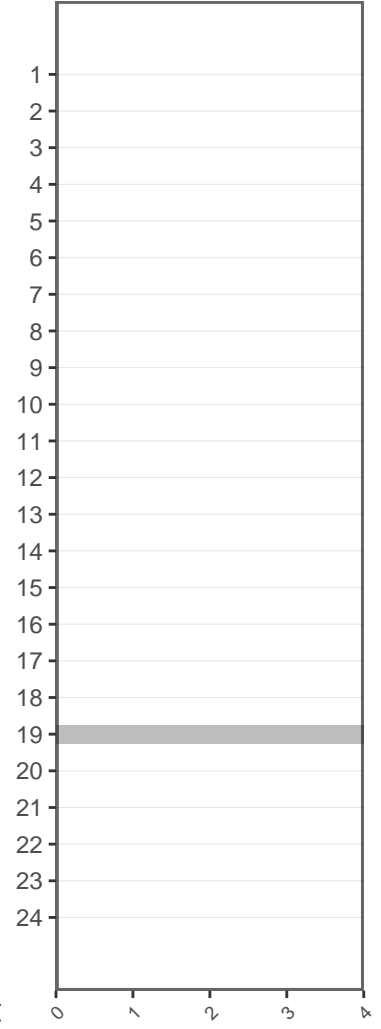
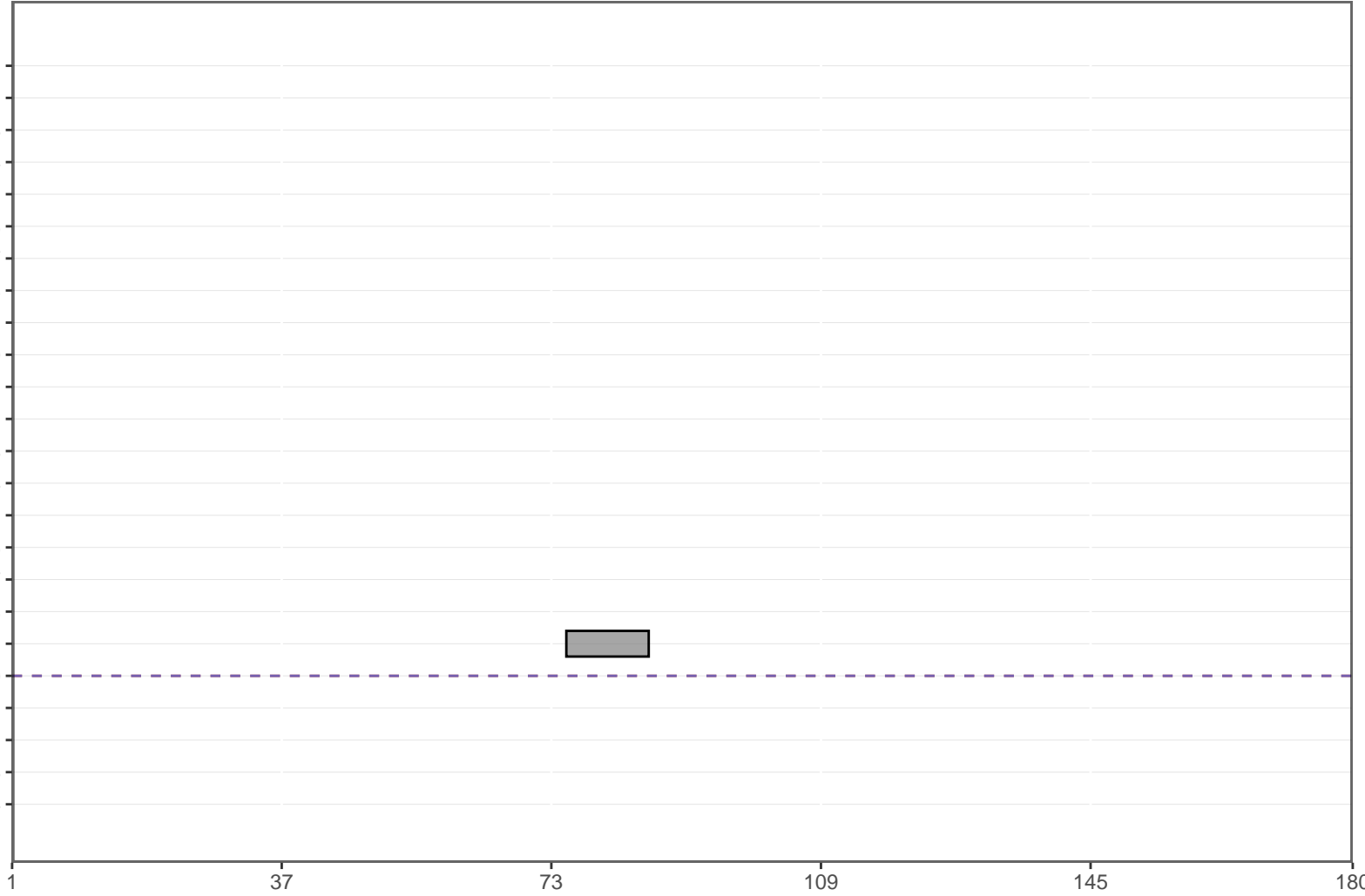
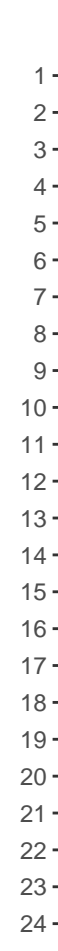
MW indication



Molecular weight

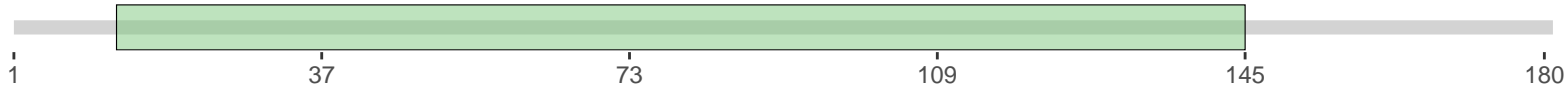


Gel Slice



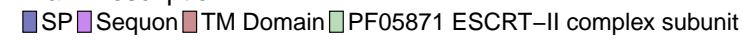
Protein length

Peptide counts over 4 repeats



Pfam domains

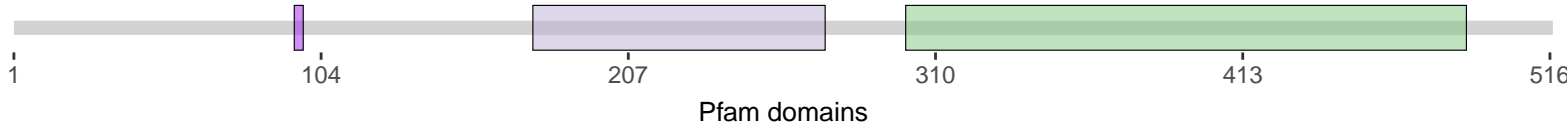
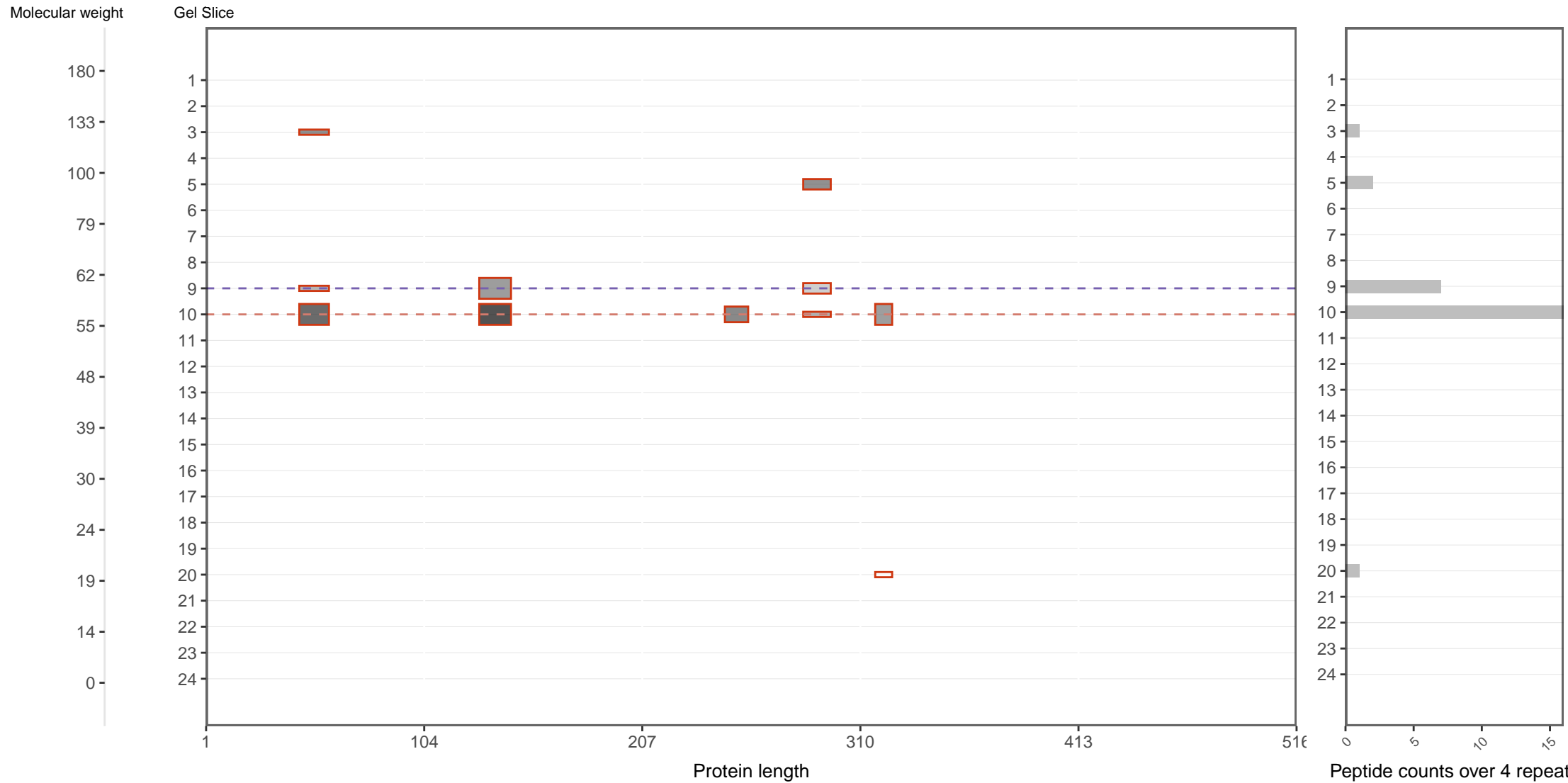
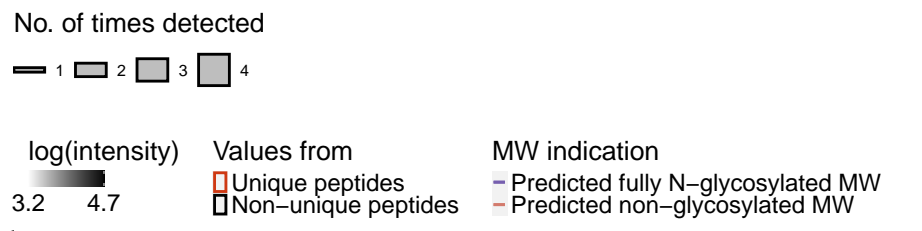
Pfam Description



Protein sequence:

.SALVSDGRAEVMDKGRKGLWHRIGDQWADLVNFMVKEYGLEDSVMTVEEIGSGTESRGTTELVGMDRTVLMRAKLLKLEHKGLAIFKGTSDADDEGVKFSL

NbL16g20540.1 inositol-tetrakisphosphate_1-kinase_4 [MW = 57.81 kDa]



Pfam Description

SP Sequon TM Domain PF05770 Inositol 1,3,4-trisphosphate 5/6-kinase ATP-grasp domain PF17927 Inositol 1,3,4-trisphosphate 5/6-kinase pre-ATP-grasp domain

Protein sequence:

INKVTYTEGMEQLGRVIRCHPDCGVDFPNSVPLDLRKLKIGILGGLLENLTKSGSKIRGPHFLKLVDFRPEKLEMLADAKLSLNPVQVAGGVSDAHSMVAVKADSVKDLNPLPFAVGVDFVDSHSTMFKFYVGGKFFAANKSTPNADILKLAEEKLPLFLDLSLSPVQKDNQGGKSGHQHEQNDRIDQELVTDAAVWLRVRLDLMFGFVWQEGTGDHVVQVWVNYLPSFKFVPEVAIPTFWEAKELTKGKSTEAAILV

NbL16g20470.1 60S_ribosomal_protein_L9-1-like [MW = 21.99 kDa]

No. of times detected



log(intensity)



Values from



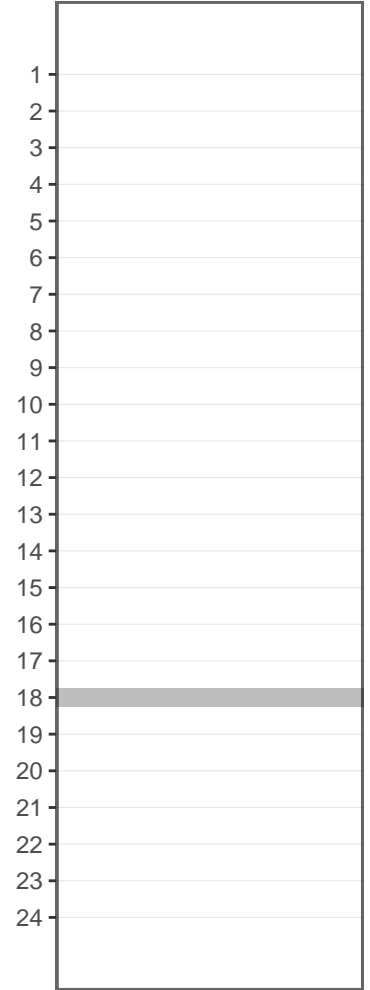
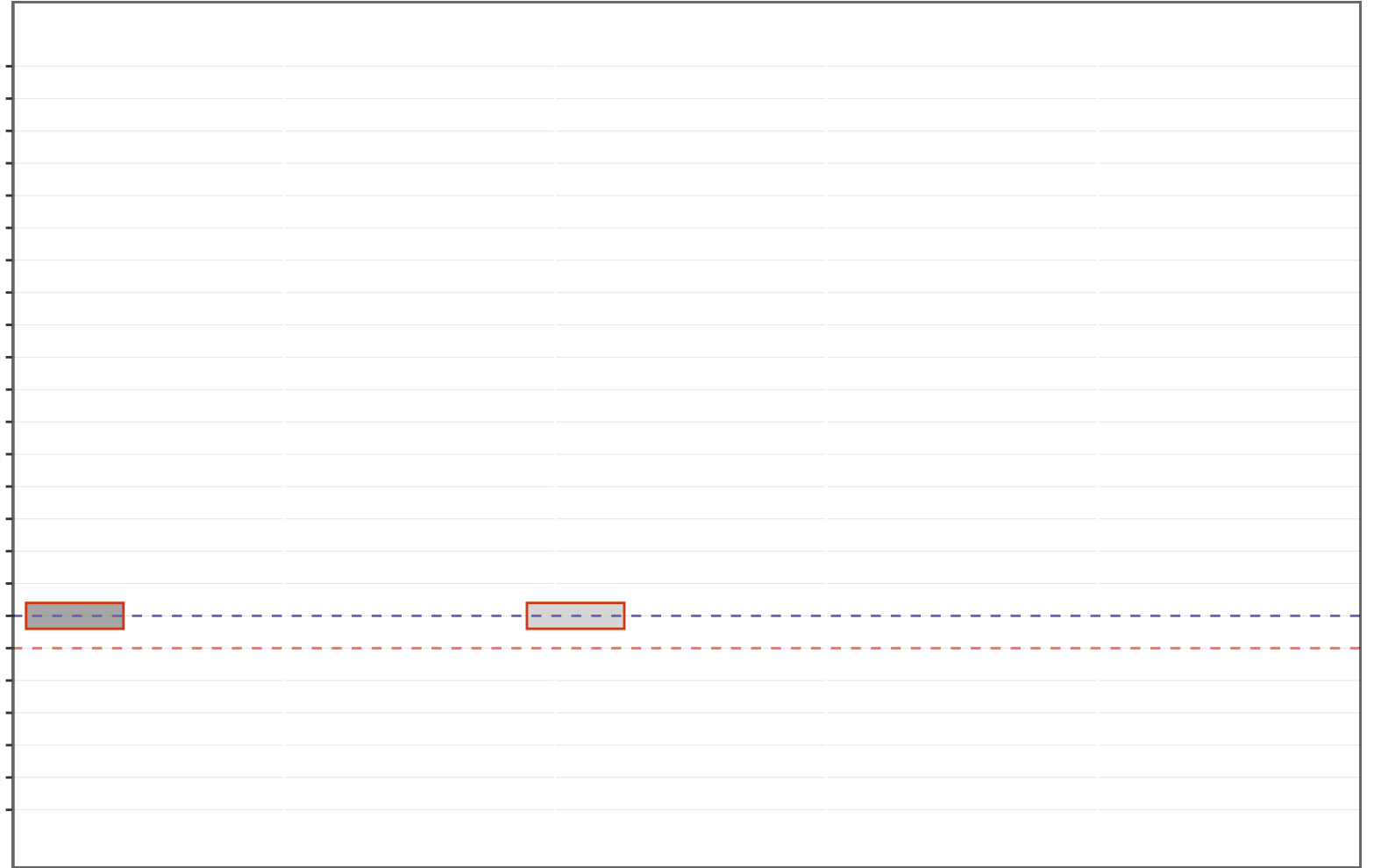
MW indication



Molecular weight

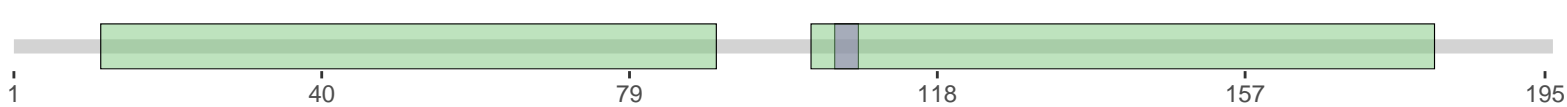


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

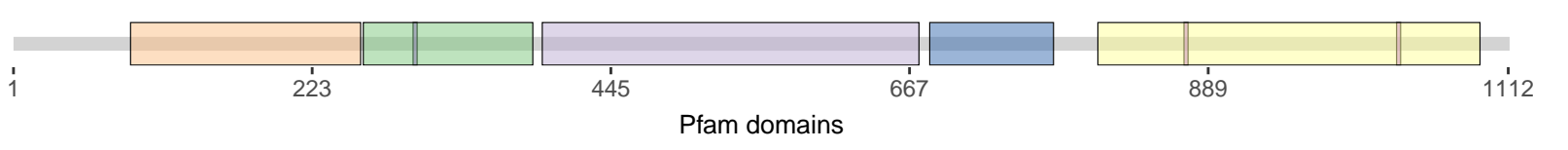
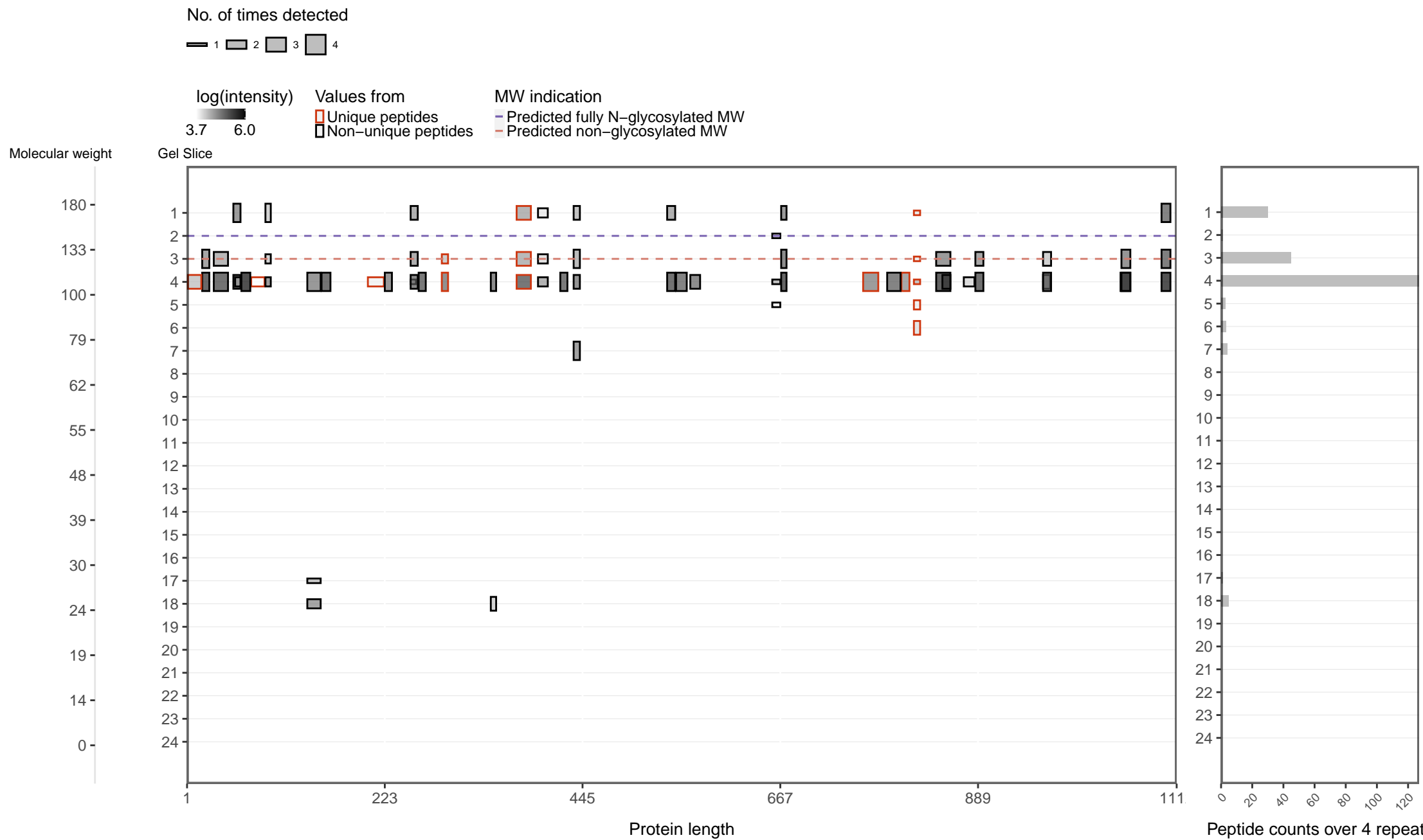
Pfam Description



Protein sequence:

IGVTKGYRYKMRFYVAFHFNASITGNGKAEIRNLFGEKRVKVDMLDGVTYVRSSEKVKDELVLDDGNDIELVRSAAALNGKHVKNKDKRFLDGIYVSEKGRIAEE*

NbL16g20450.1 beta-galactosidase-like [MW = 125.88 kDa]



- Pfam Description**
- SP
 - Sequon
 - TM Domain
 - PF00703 Glycosyl hydrolases family 2
 - PF02836 Glycosyl hydrolases family 2, TIM barrel domain
 - PF02837 Glycosyl hydrolases family 2, sugar binding domain
 - PF02929 Beta galactosidase small chain
 - PF16353 Domain of unknown function (DUF4981)

Protein sequence:
 /H YEGGARTSSTDNVCPMVARVSKVEIANDPTEGRPLHLGEYSHAMGNSNGLHKYWEADSTFGLGGDFIWDWADGGLLKEGPRGKMCWAYGGDFGDPINDLNFOLNGLVWVPRSPHPALHEVKFLVGPVKVFKEGIVKTNMFFDITQALEFNWILHGDGDELGGGLFLPVEPQRSHETKWEVSGDFVFSAWTSSAAEIGLITAKLHLHTRVWANGHLISSTQVLLPNRRRVVPRIKGTDTALLGEVLDMMIKLGGNGWELKFNKRTGGIEGVKWKGVSYMNC

NbL16g20410.1 mitogen-activated_protein_kinase_homolog_NTF4 [MW = 45.23 kDa]

No. of times detected



log(intensity)



Values from



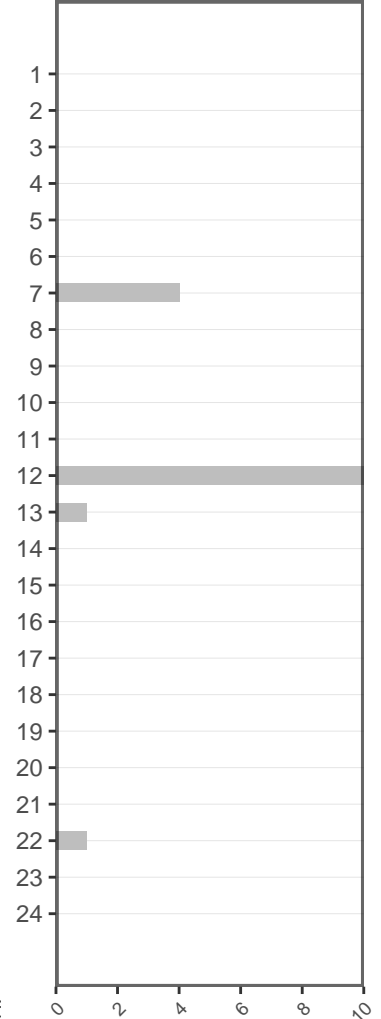
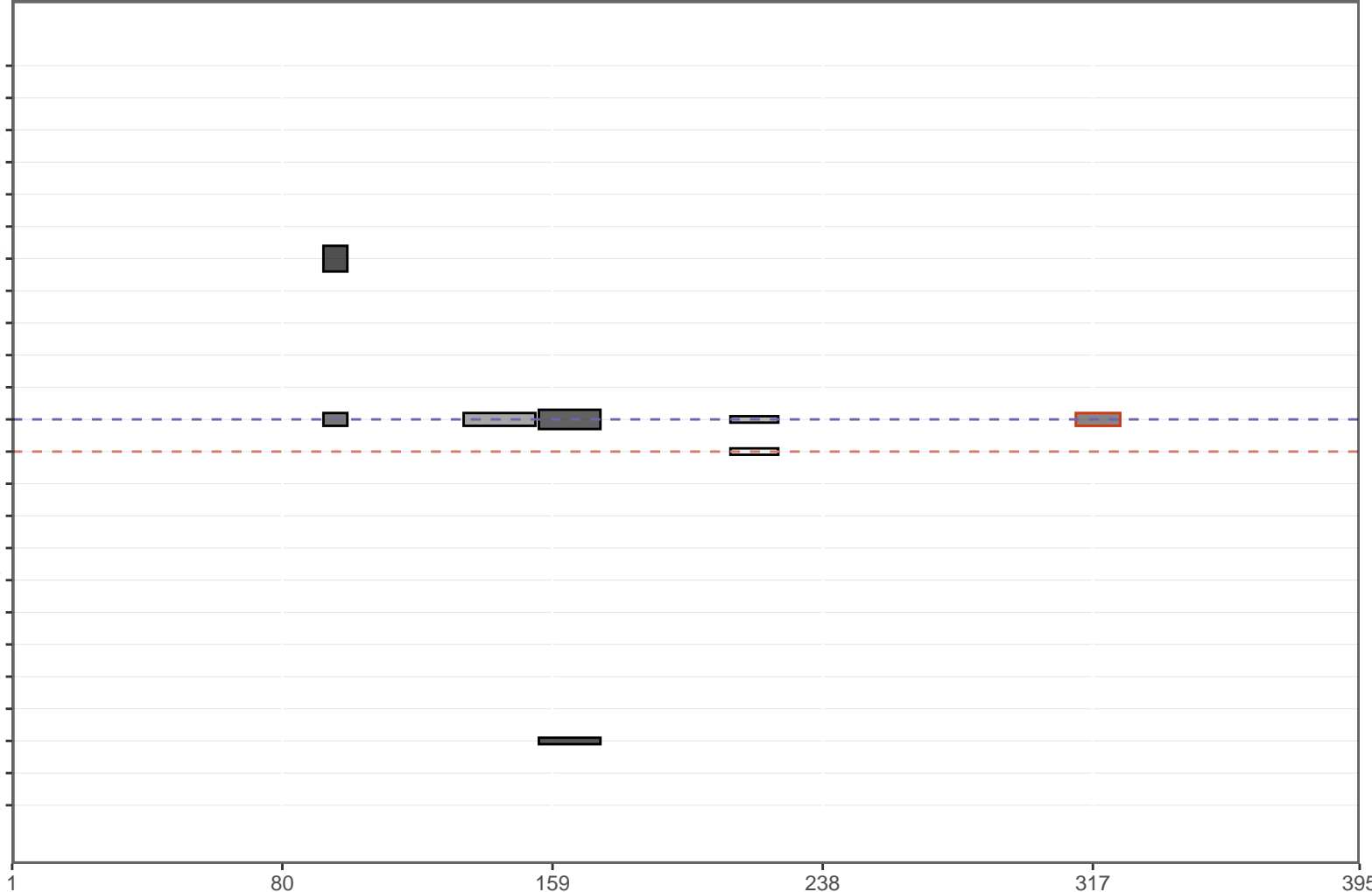
MW indication



Molecular weight

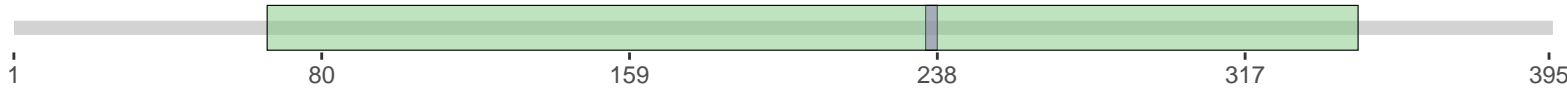


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILKPSNLLLNANDKIDGFLARVTSDFMTEYVYTRWYRPELLNSGDTAIDWVWGGFMELMDRKLFPGRDHYHQLRLLELIGTSPSEAEMLFNENAKRYIROLPLVRRQSFVEKFPNINPAIDLVEKMLTFDPRRRITVEDALAHPLYLSLHDSIDEPVCMTPFNDFDFEQHALTEEQMKELIYREGLAIFNPEYGHM

NbL16g20390.1 cysteine_synthase_chloroplastic/chromoplastic [MW = 41.26 kDa]

No. of times detected



log(intensity)



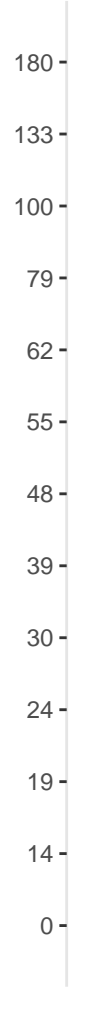
Values from



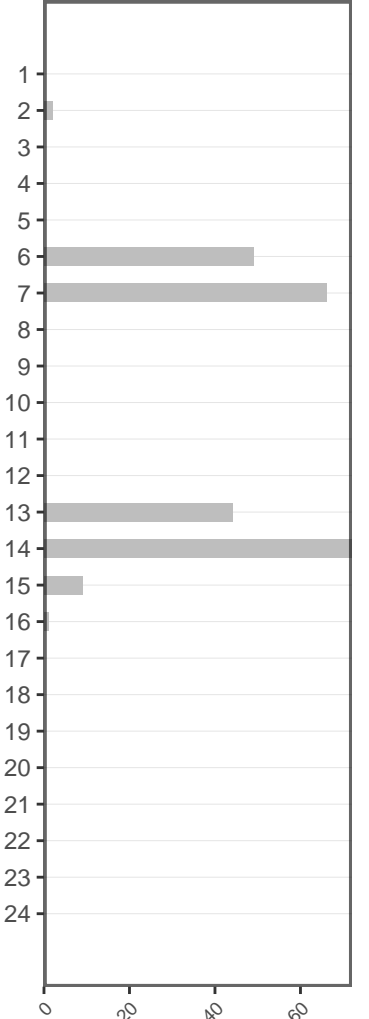
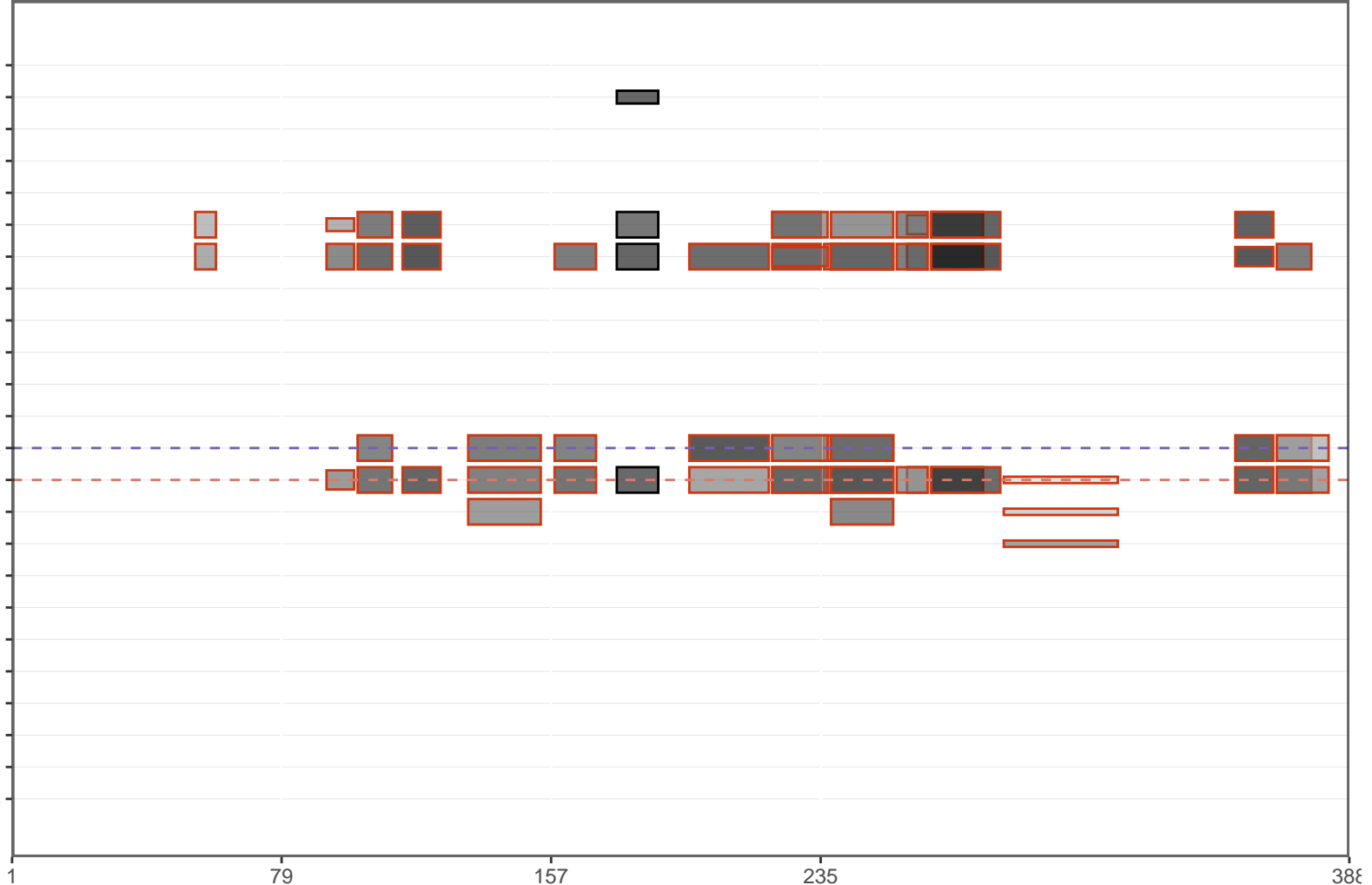
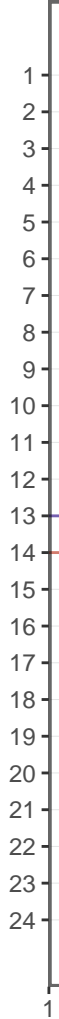
MW indication



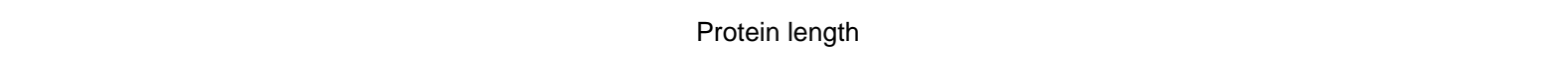
Molecular weight



Gel Slice

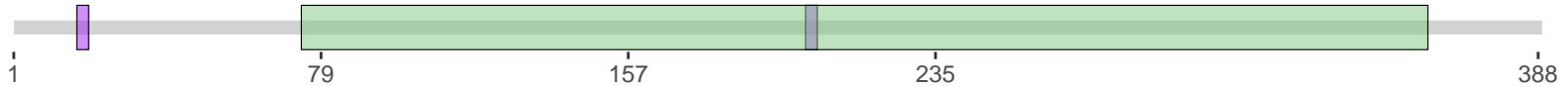


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

.VLTDPAGMKGLAVSKAEELNTPDAVLGGFDNPNPKHYETTFGPEIWEEDTKGKIDILVAGIGTGGTISGAGRFLEQNPNNKIKIVERTESNVLGGKPGPHKIGGIGAGFIPGNLDDGMDEVEISSDEAVETAKQLAQEGGLVIGSSGAAALAAIQVGRKRRENGKLIWVFPFGERYLSTLFGBIRECEKMQPES

NbL16g20370.1 uncharacterized_LOC107775190 [MW = 16.8 kDa]

No. of times detected



log(intensity)



Values from



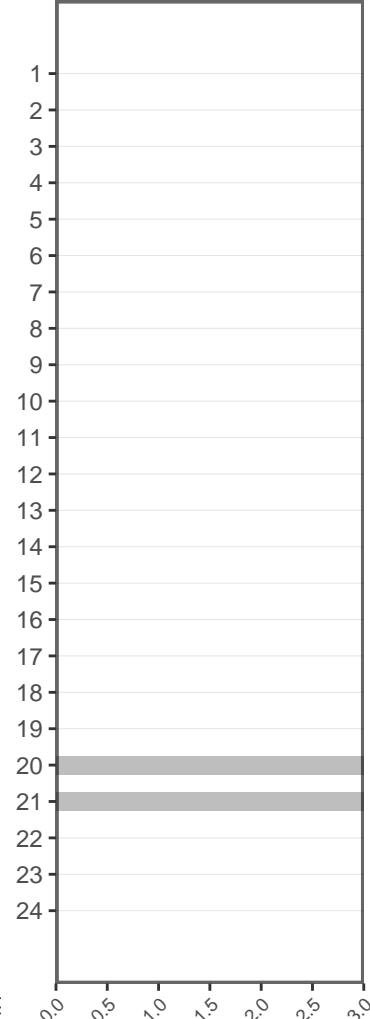
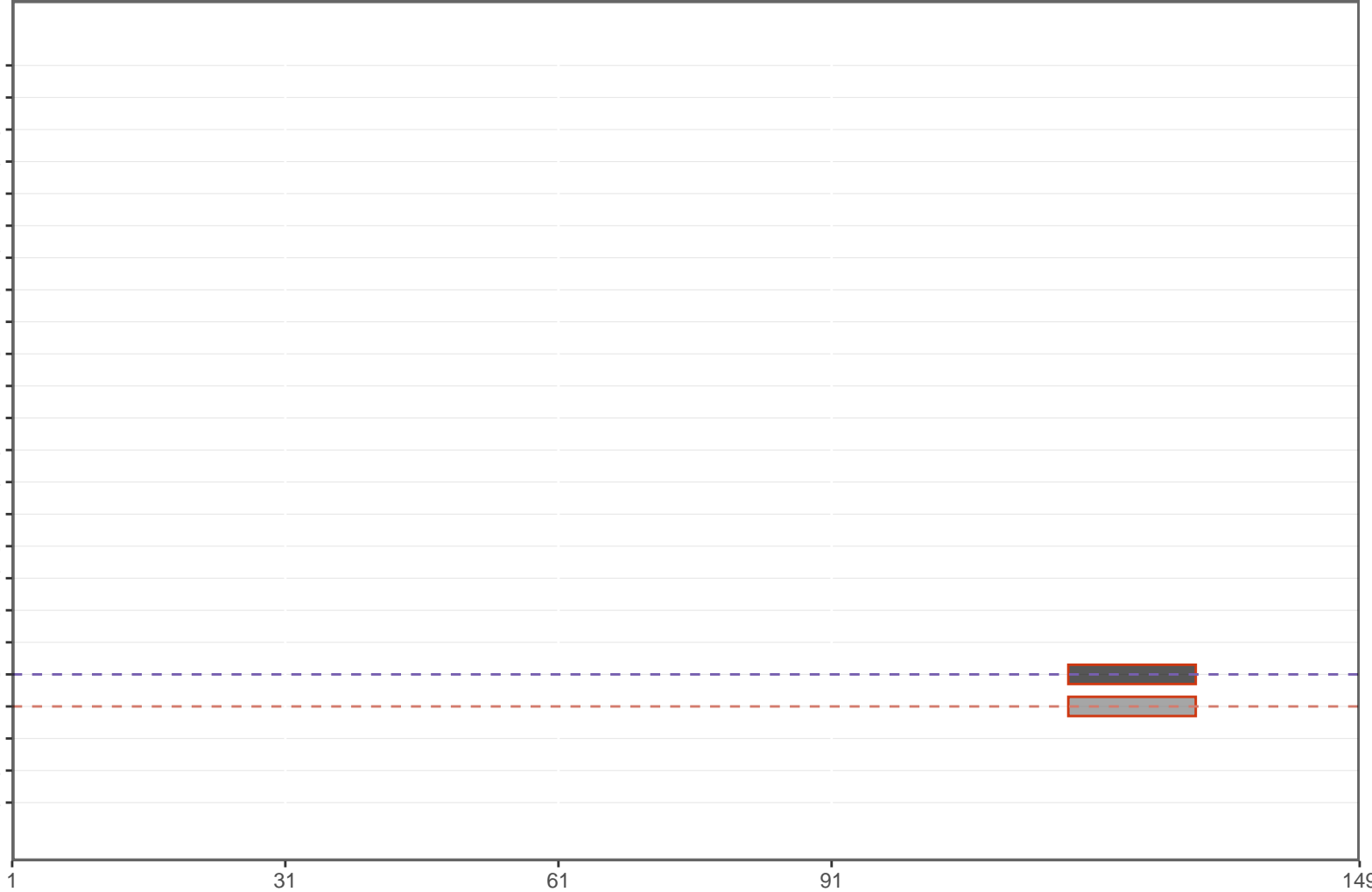
MW indication



Molecular weight

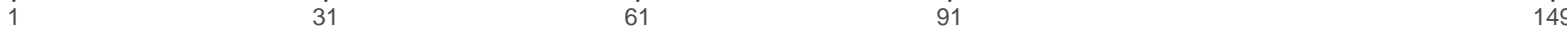


Gel Slice

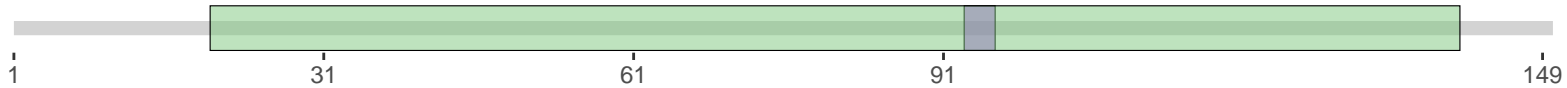


Peptide counts over 4 repeats

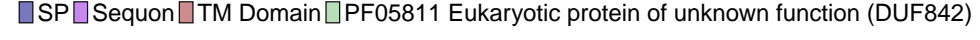
Protein length



Pfam domains



Pfam Description



Protein sequence:

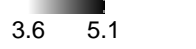
EIDNCVEYCSVPVLDAGNIVENEMANFGEKMMRSLRVRGDDKYETAKLQK66DATKVEEGVDG5VDD6IKTLPHLVGKLVKSLGVTD*

NbL16g20300.1 2-isopropylmalate_synthase_A-like [MW = 59.88 kDa]

No. of times detected



log(intensity)



Values from



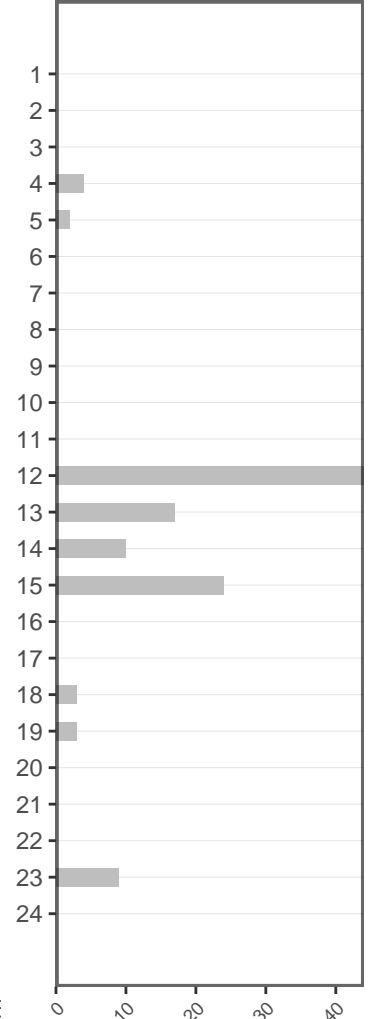
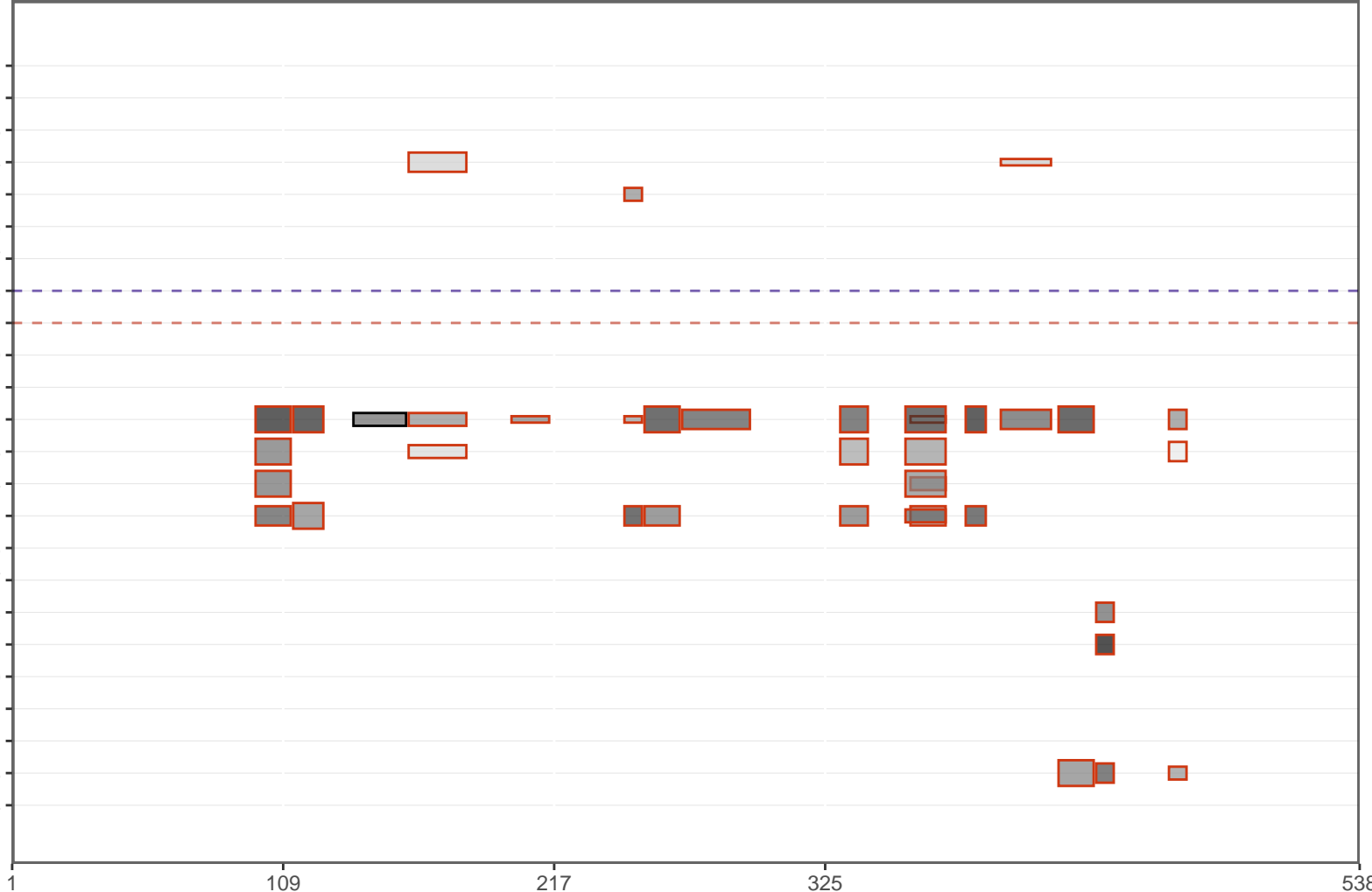
MW indication



Molecular weight



Gel Slice



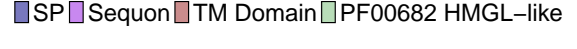
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

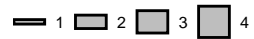


Protein sequence:

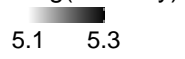
KEFLYHLEGGKAGATASLGDYVSNLPEYVAQLSDIKANTPGIGGVNHTGHDDLLGLATANTLAGICAGARLVNVTMNGIGERAGNAGLEEIVMALKYRGEQVLGGVYGTNKHVFMFSKMYEYVSLKLGAKKAVGANAFSGHESGHODGVLKNRGTVEYVSPEDVGFQREHGGISLGRLLSRRHALSKMLELGFEGEKELDDDFWRPKSMAEKKKVNSISDSIMOGSNLLFLMLFVQVFFGFFDINMFWLWLVLPGLYSENVRGRPKSTQ---

NbL16g20000.1 probable_U3_small_nucleolar_RNA-associated_protein_7 [MW = 19.07 kDa]

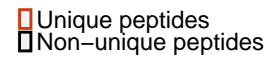
No. of times detected



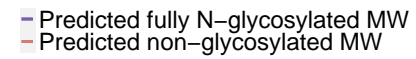
log(intensity)



Values from



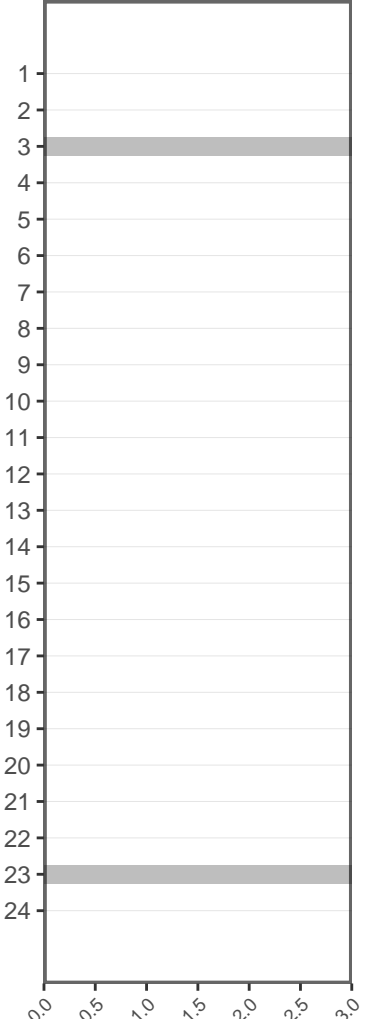
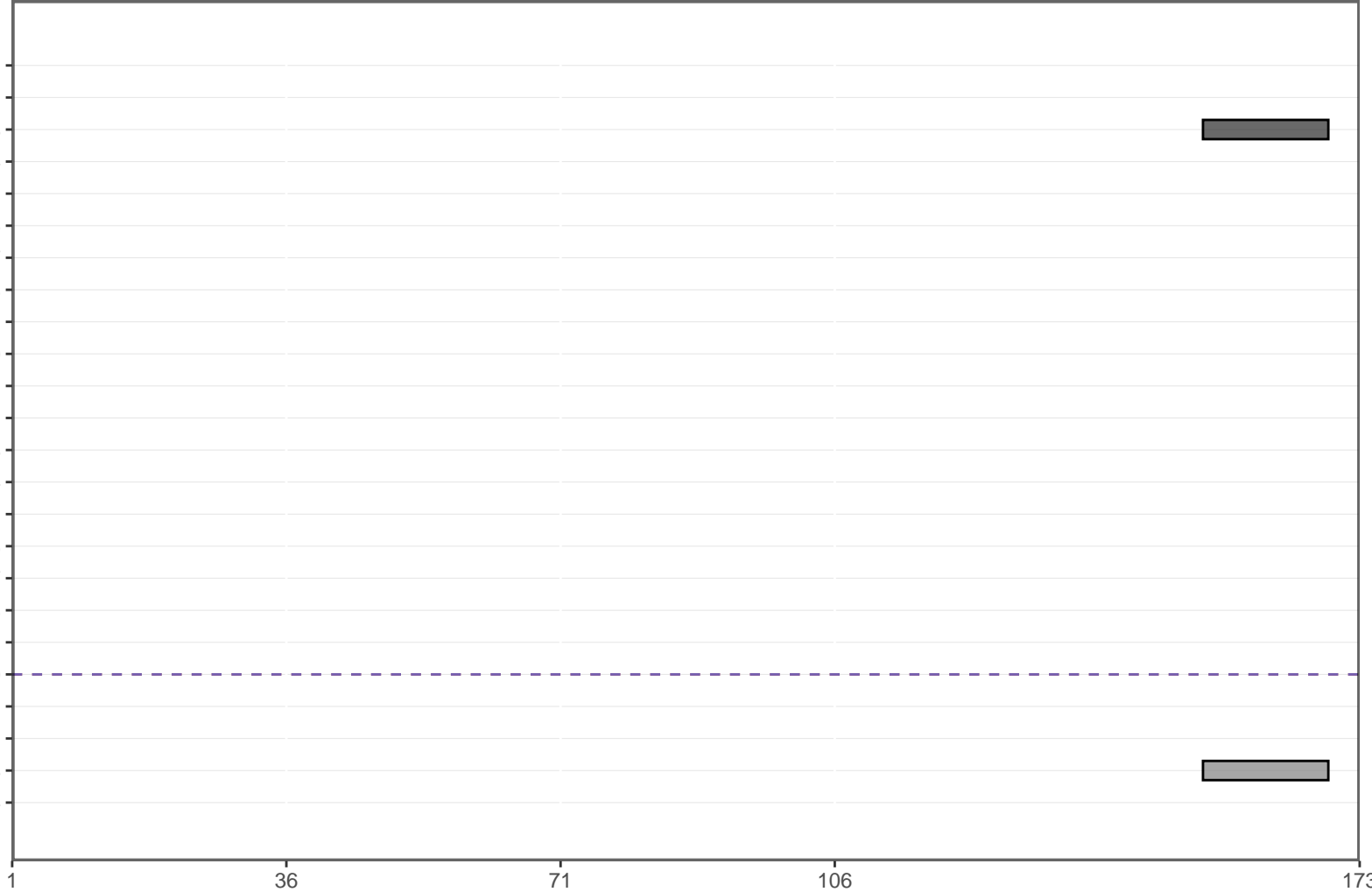
MW indication



Molecular weight



Gel Slice



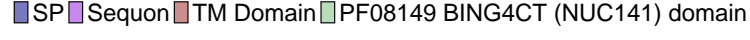
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DVLLGIGHSMGVSYFIIIPGSGEPNFDSEWASPFETSKGRREKEVRSLLDLPETMLDPTKIGTVRSTRKKEQPTKDDKEAEMEAIEEAKSMPIKAVV

NbL16g19980.1 50S_ribosomal_protein_L3_chloroplastic [MW = 29.99 kDa]

No. of times detected



log(intensity)



Values from



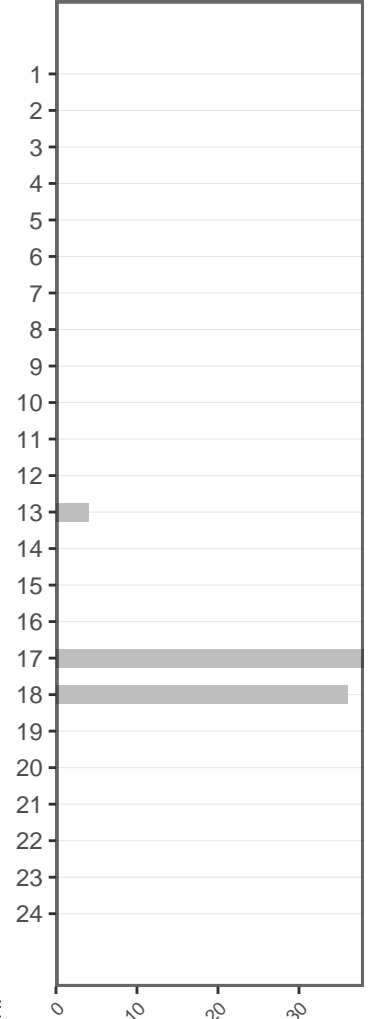
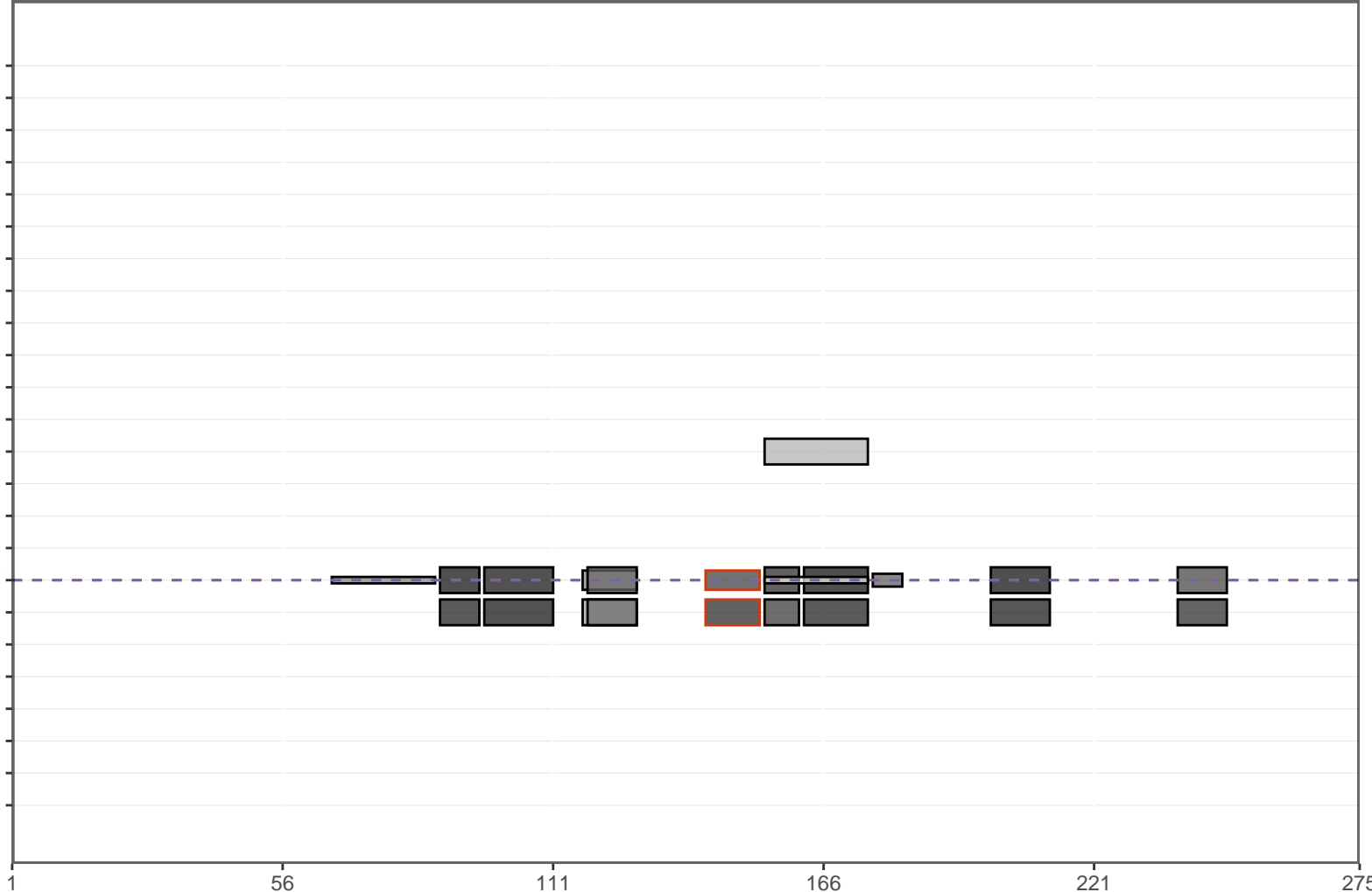
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IHLKSGIPLRHLQEFRLQSDGFVETKLDGELFKREGDLVDVSGTTIKGDFGGIKRHFNRKRGMTGHSKSHRQLGSGAGTTPGRVYKGNKMPGRMGSTKRRKRLKLVKIDDLNIMIKGALPGKPSGLLRAPAKIVGNPKPS

NbL16g19800.1 DNA-damage-repair/toleration_protein_DRT100-like [MW – SP = 36.8 kDa]

No. of times detected



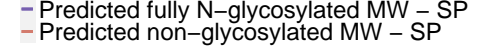
log(intensity)



Values from



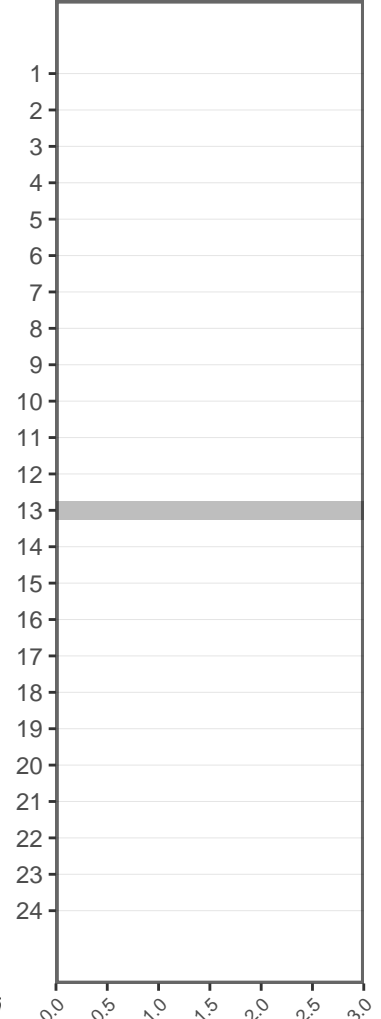
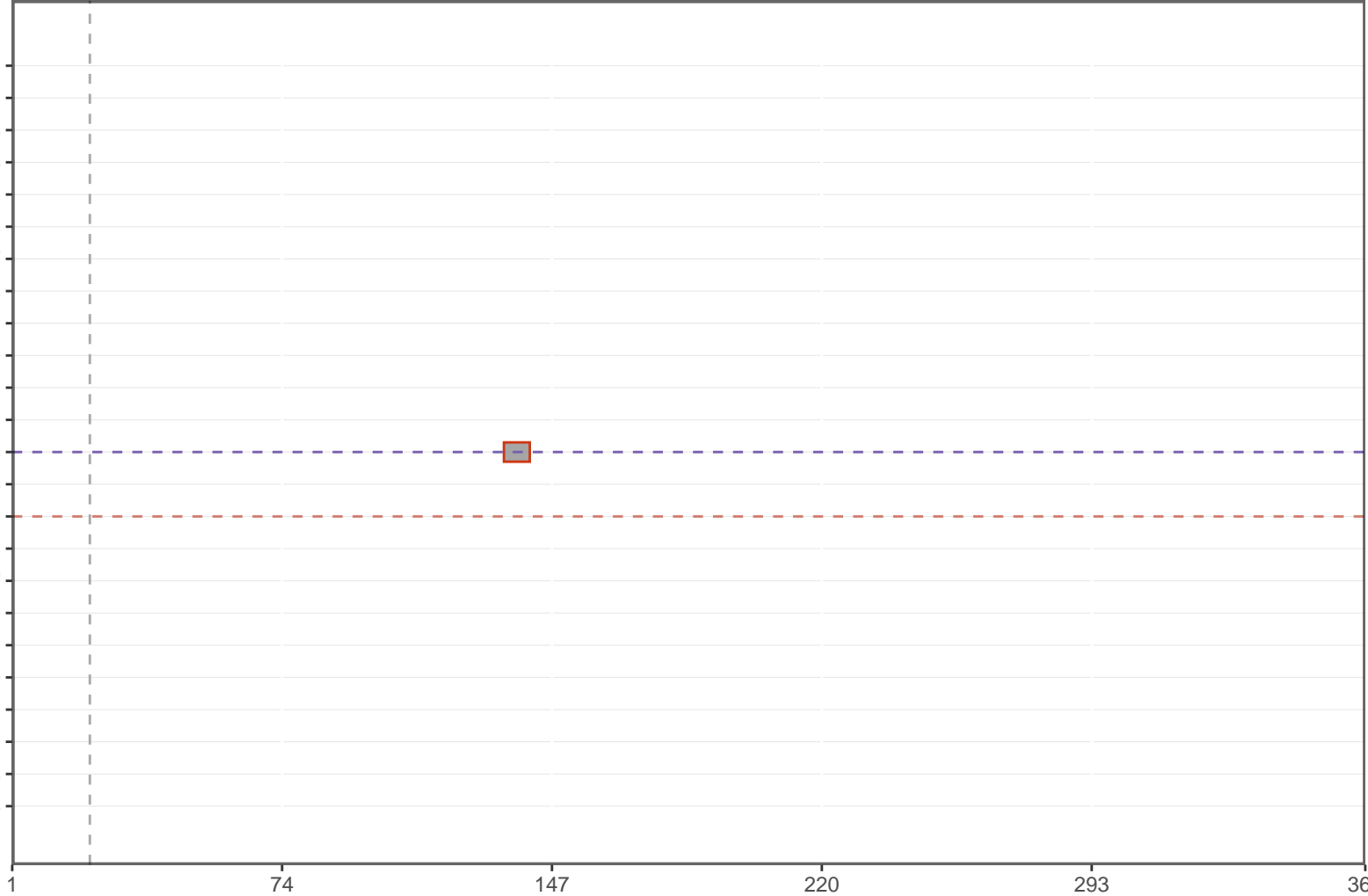
MW indication



Molecular weight



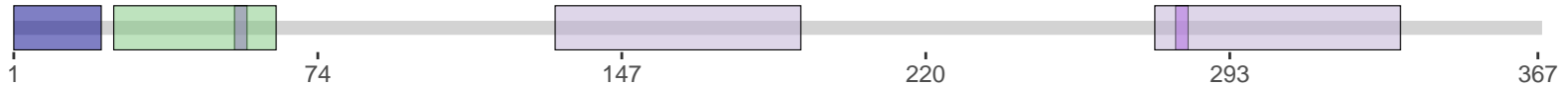
Gel Slice



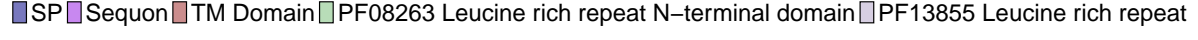
Protein length



Pfam domains



Pfam Description



Protein sequence:

IPSSVTLGRLLHLDENMLTGEIPSDGKMSMLSRAMNNNGIGSIPPTSAKLYRVLVLDLDMNGIGSIPAEI GSNMPLVTLVNLDSNGIGSIPPTNLTSGLNLNLGRNLEGLPDFVPTTYFTHLDLDSYNNLGGSPKTLSSAKYVGHLDLNNHGGIPGGFFNLSLEASSFENNDLGGSPLLGCD

NbL16g19660.1 40S_ribosomal_protein_S16-like [MW = 16.93 kDa]

No. of times detected



log(intensity)



Values from



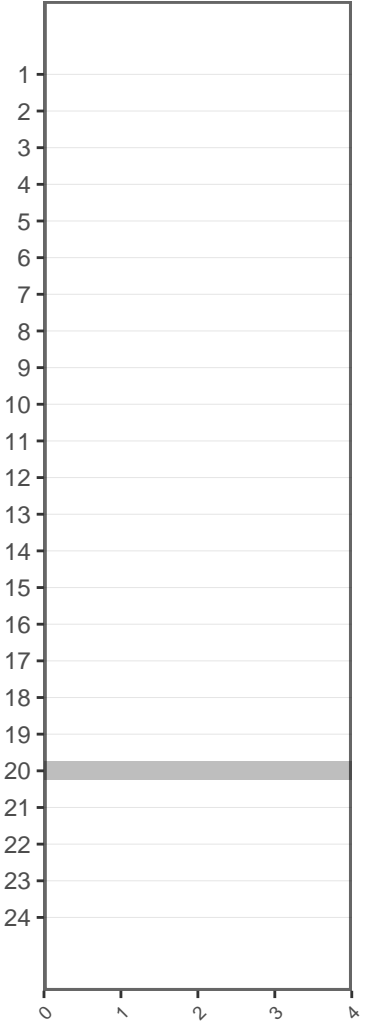
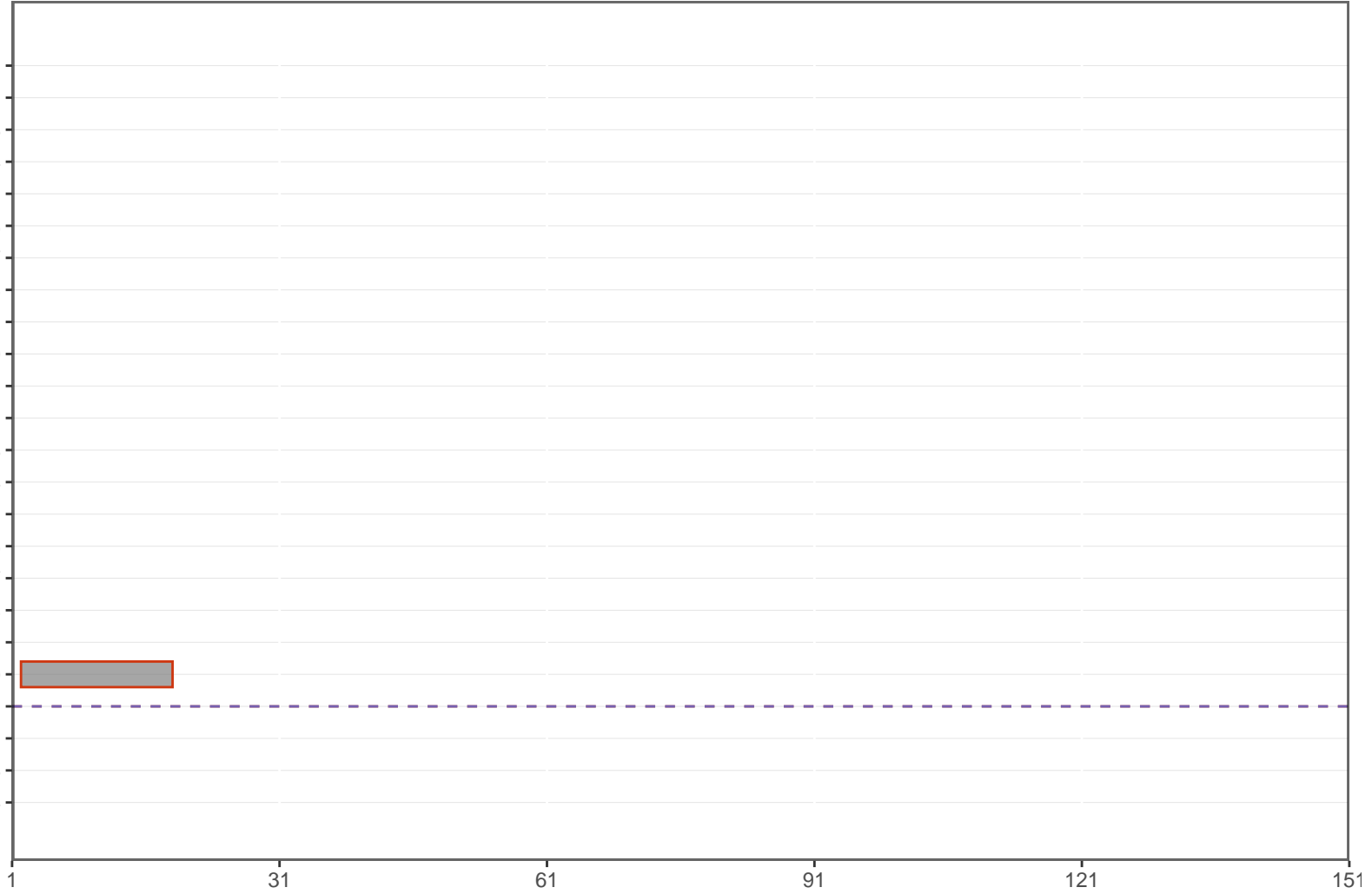
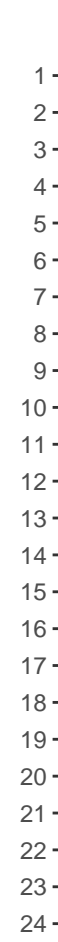
MW indication



Molecular weight



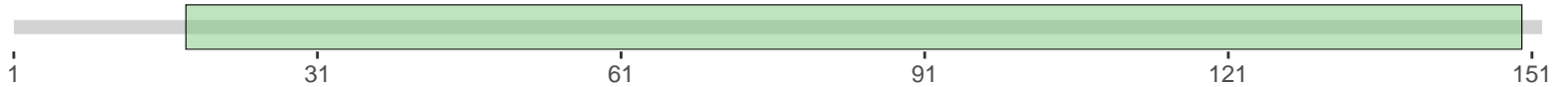
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

IRHRFAGVDMRIRWGGGHTSGYAIRGSAKALVAFYQKVKVDEGSKKEIKDLVRYDRLLVADPRRCEPKKFGGRGARARFQKQYR

NbL16g19620.1 uncharacterized_LOC107811196 [MW = 25.56 kDa]

No. of times detected



log(intensity)



Values from



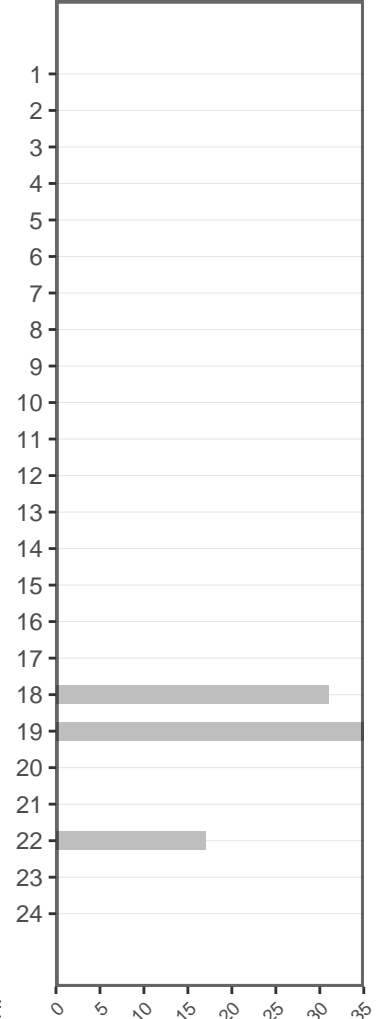
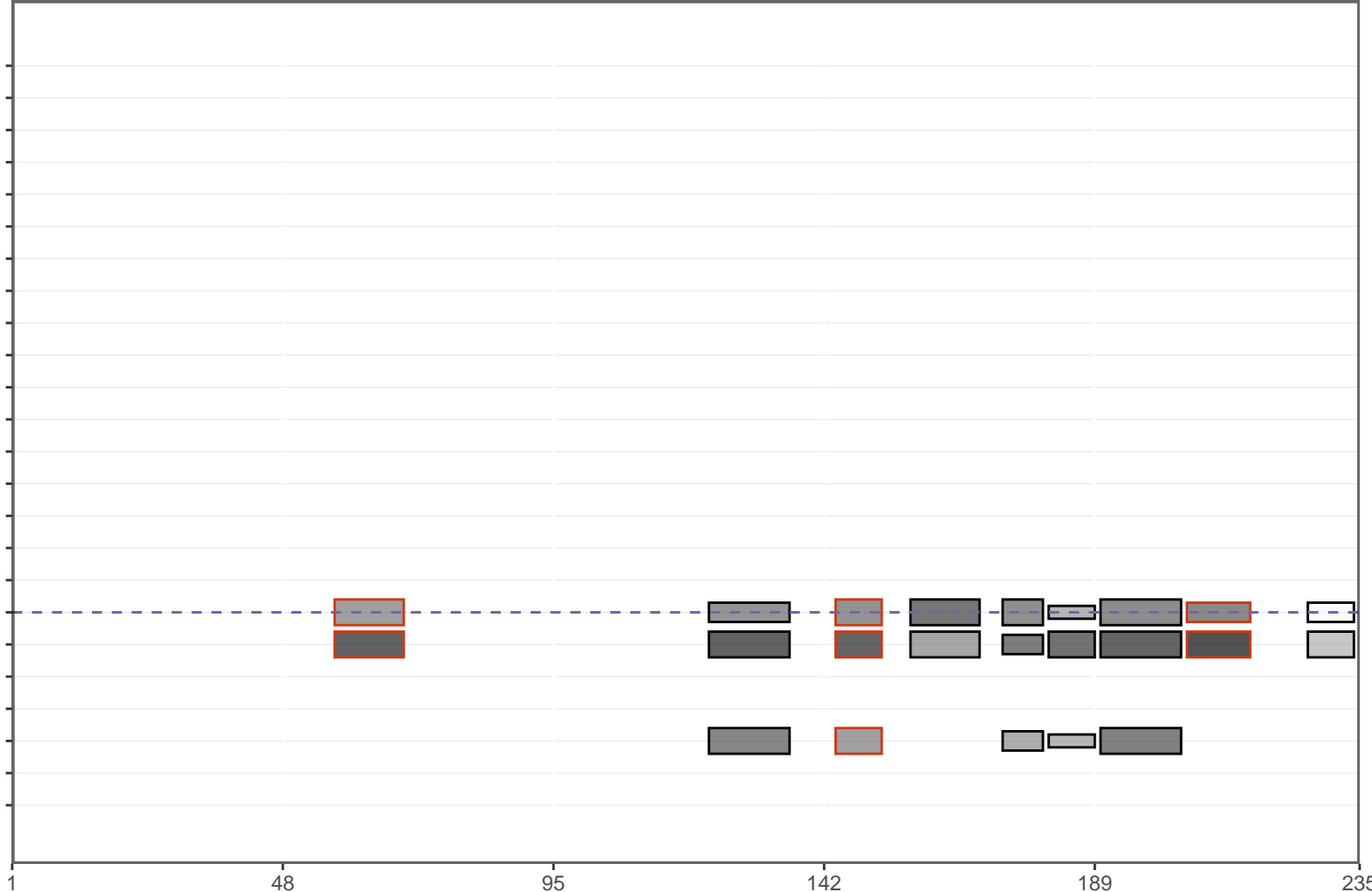
MW indication



Molecular weight

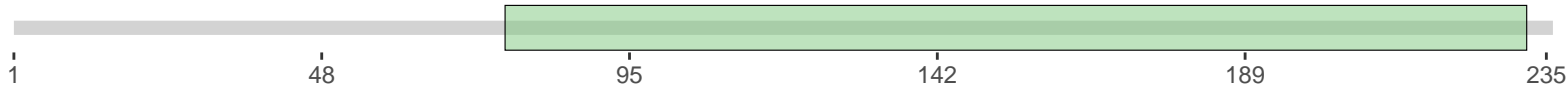


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SDKAKPKKFAARFASDRRGEVLGVIRPSPNQLKITFLKAKDITDLGSLKEAANIFVPGATLVSGRSIKIKEDGFRYYFYEFARDEGHVLAVWNSGKAYAAATAPESKWNDDGKLRSAVSLMVL*

NbL16g19580.1 linoleate_9S-lipoxygenase_6 [MW = 97.25 kDa]

No. of times detected



log(intensity)



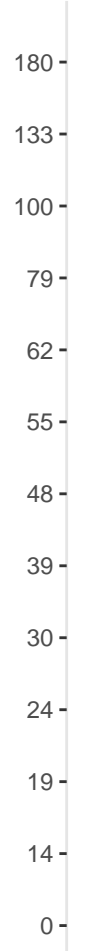
Values from



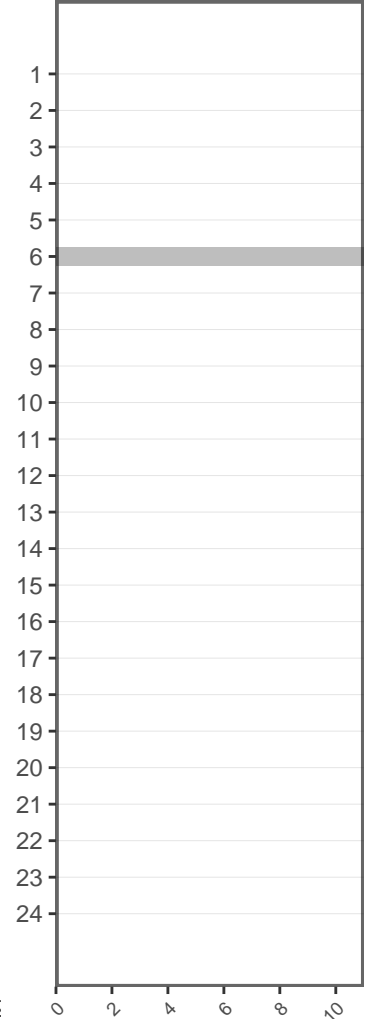
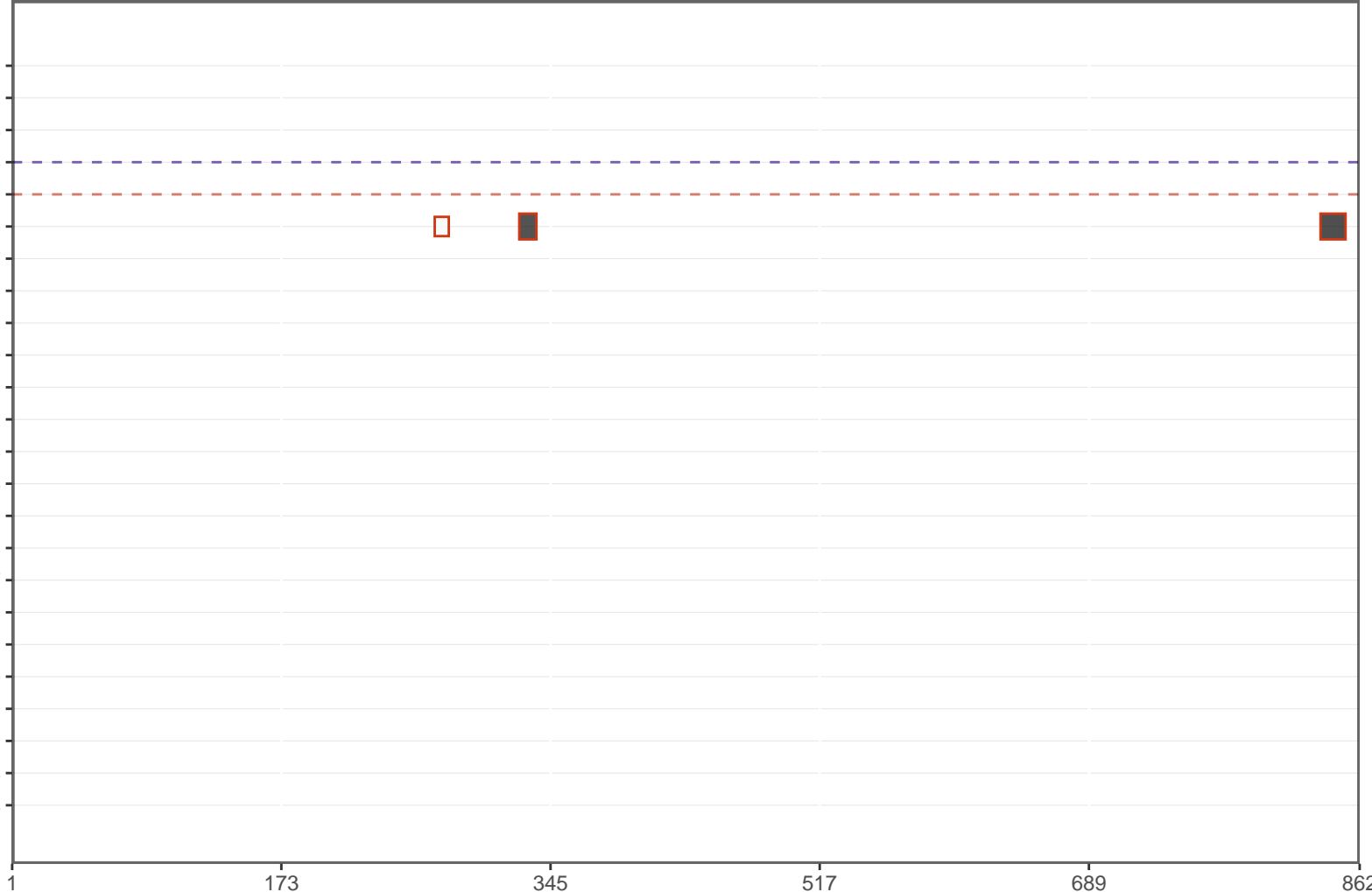
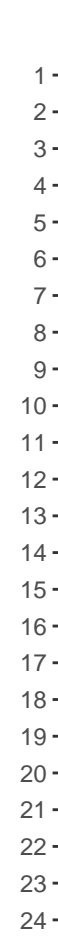
MW indication



Molecular weight



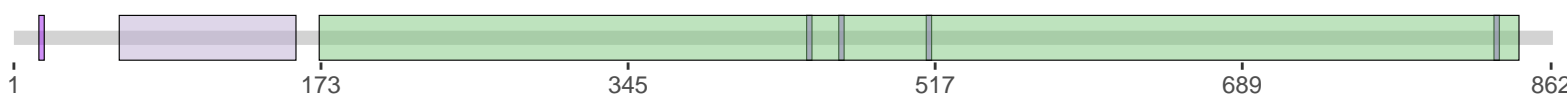
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TIDAEAKSNRLFILNHDITMPLRRINNTTFTKTYASRTLLFLDQNGSLKPLAIELSLPHDGGDFGAISKVYTPADEGVEGSIWELAKAVAVNDGQVHQLSHLNTLHAEPEFYATNRQLGSLVHPHKLHPHFRDITMNNAMARQLNAGGVLESTVFPKIAMEMSAVYKXWIFDQALPTDLVKRGMVAEDSSPHGRLLIQDVPYAVDGLIWSAHSWTEYGSFYKSDSILKDELQAWWKELREEGHGDLDKDEPWVWPKMENSQELIDECTIIIVTASALHAA

NbL16g19540.1 delta-1-pyrroline-5-carboxylate_synthase [MW = 77.79 kDa]

No. of times detected



log(intensity)



Values from



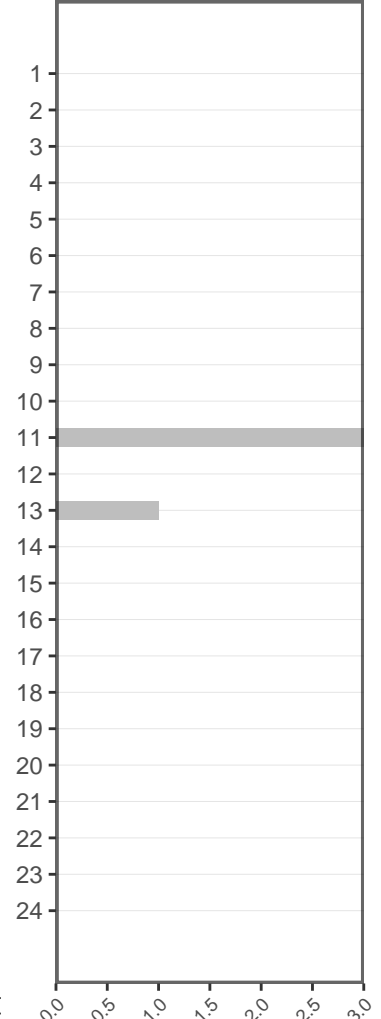
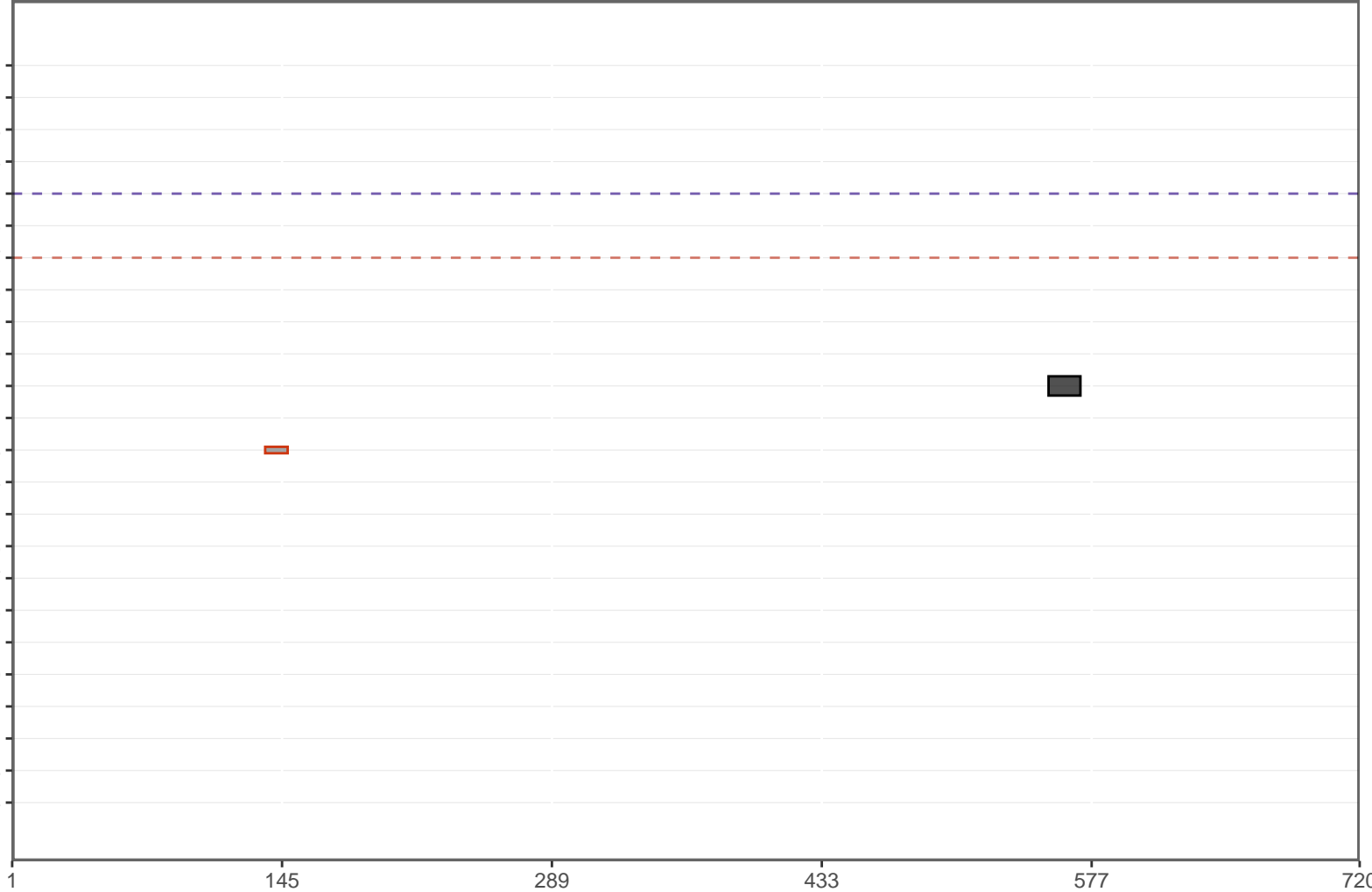
MW indication



Molecular weight



Gel Slice

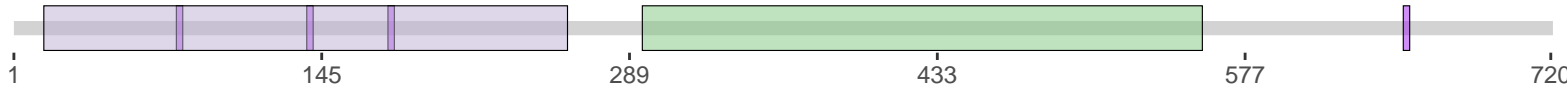


Protein length

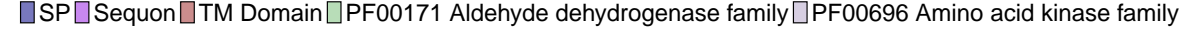


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

AAQQAQYEKLSLSRLALPKPKKSNLAKGKRVRLANMDEPKRILRRTVEVADGILEKSSPLGLVLIIFESRPDALVQIASLAVRSQNGLLKGGKEAKRGNAILHKVITSAPDGTVGERLIGLVTSEEPPELLKHDDVDLIPRGSNKLVSQIKASTKIPVLGHADGGICHVYVDKESADMMAKRVVYDAKTDYPAACNAMESLWHKDLAAGNGLNDLVELGQTKGVSLSVGGPKASLLKPEARTFHHEVYGLACTIVEVEDVYAADHIIHQHGSAAHTDSHTKQDEAAEFLRQVDSAA

NbL16g19530.1 uncharacterized_protein_At2g34160-like [MW = 14.5 kDa]

No. of times detected



log(intensity)



Values from



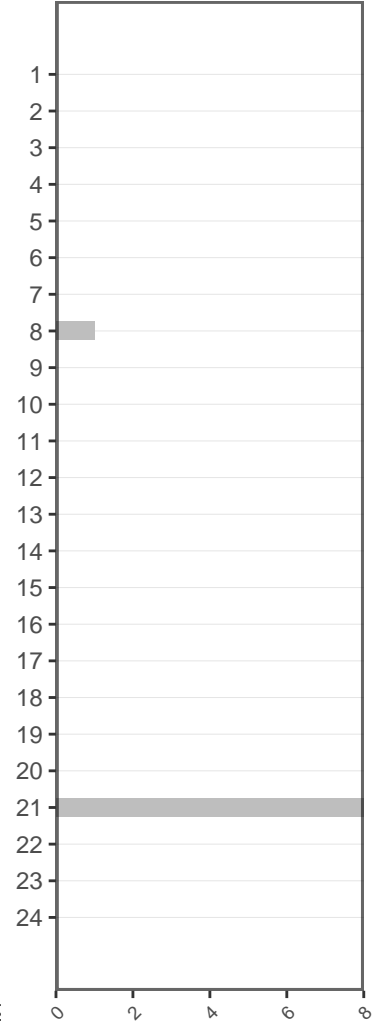
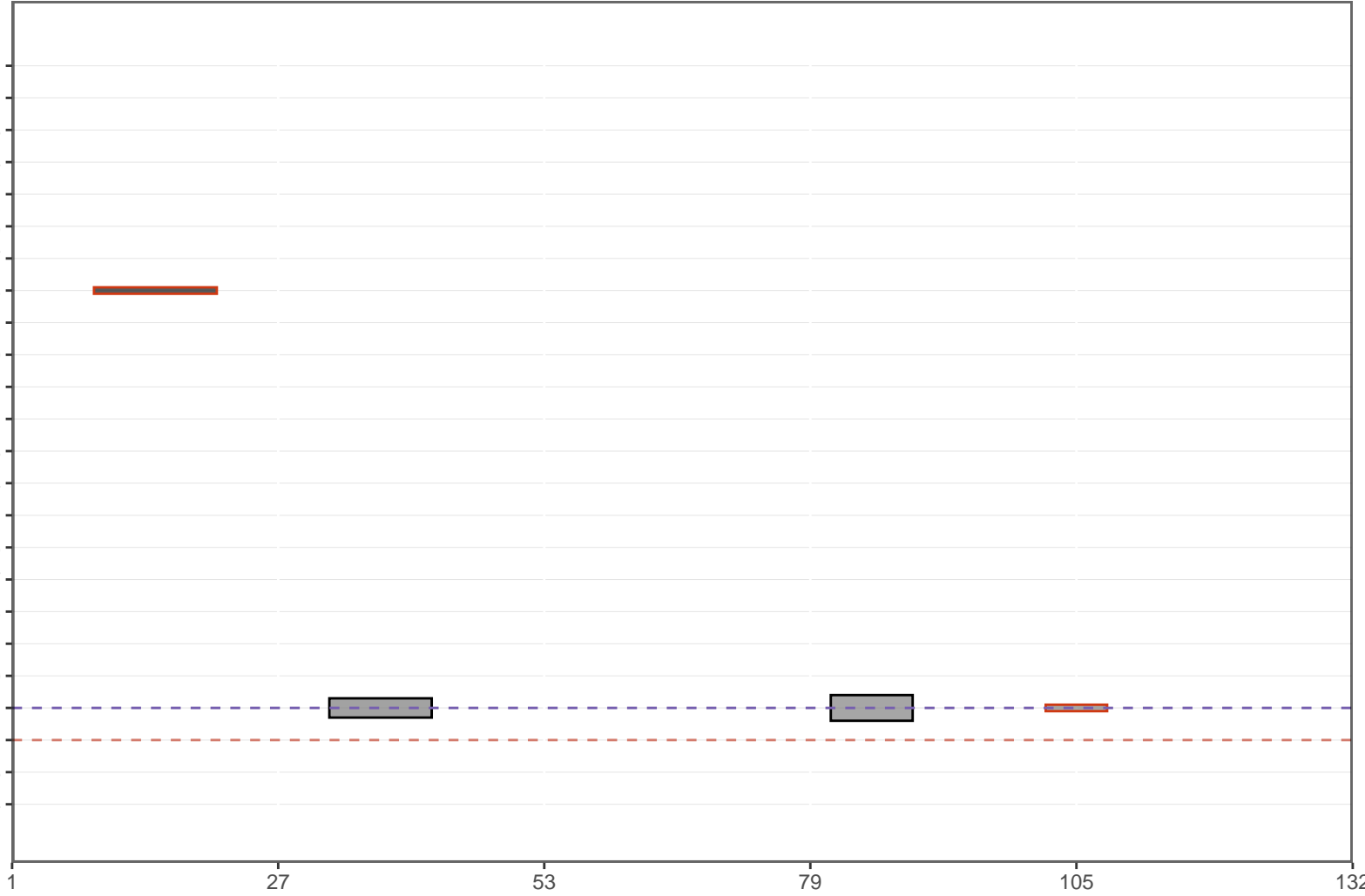
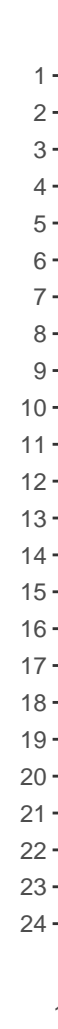
MW indication



Molecular weight



Gel Slice



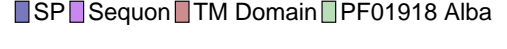
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

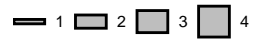


Protein sequence:

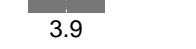
ELSLGMAUTVYSIAELKSNFVAVKIMFSTVDVNDGSRGRPVSKAKIEVLLGKSEKFDNLMAAAARELGDGEEQS

NbL16g19450.1 importin_subunit_alpha-2-like [MW = 58.48 kDa]

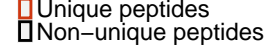
No. of times detected



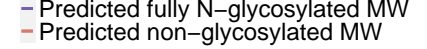
log(intensity)



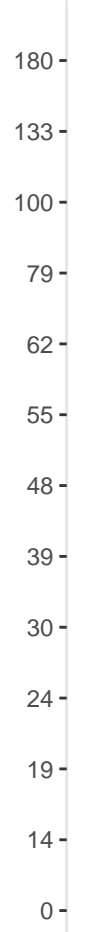
Values from



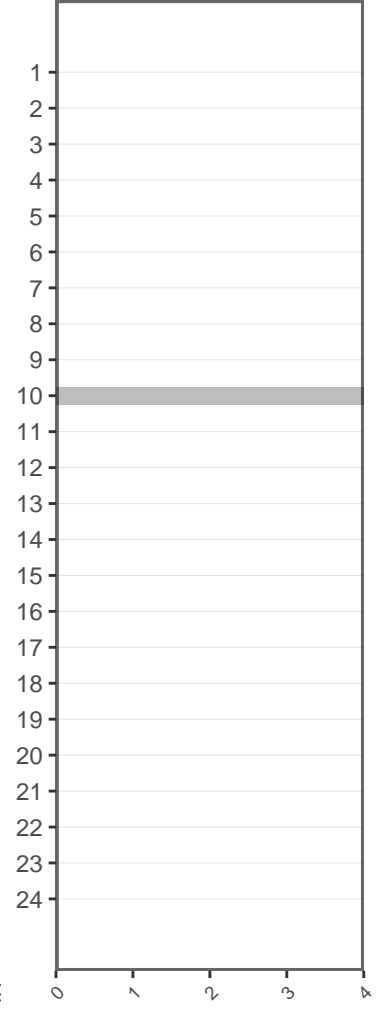
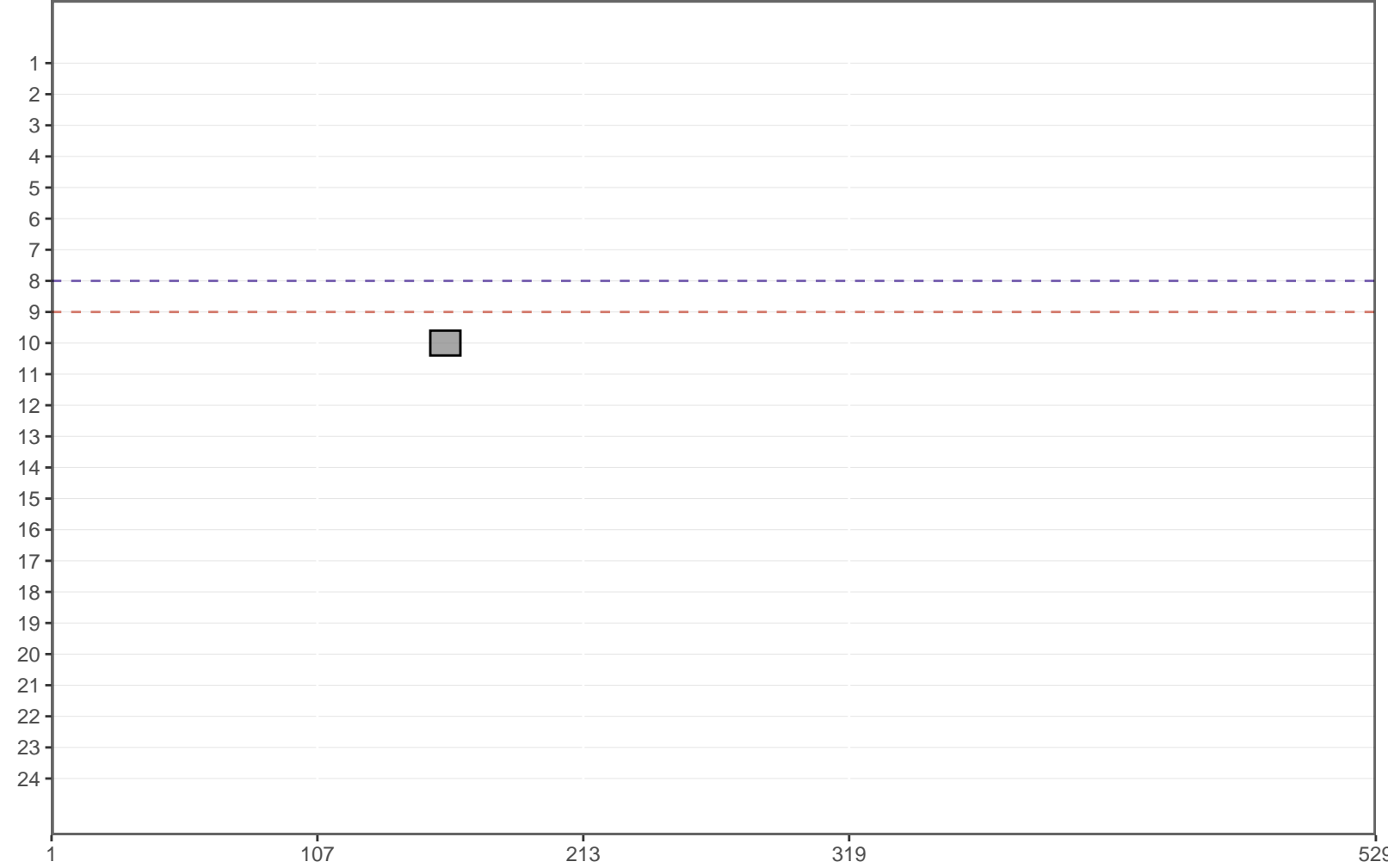
MW indication



Molecular weight

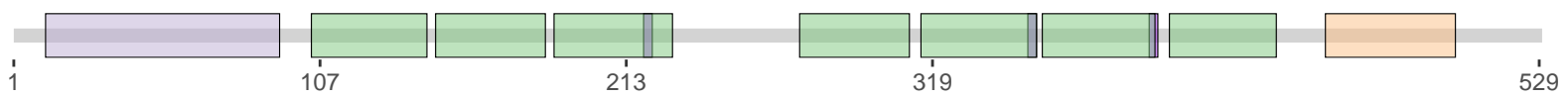


Gel Slice



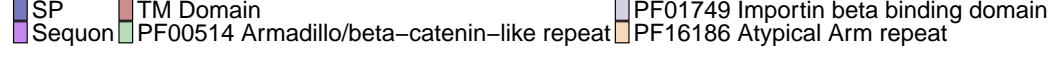
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

COQLHLDDEEVLTDAQWALEVLEDDGTNDKKGAVDSDGCRRLHELLLHPSPSVLIPALRTVGNVFTGDDMGDTGGINHGSLPRLLNLNGNKKSKKKEACWTISNITAGNREGIGSVEAGIGPLNLLGNAEFDIKKAAWAINATSGSGSHGKIKYLVSGGCKPLGDLICPDFRIVTVGLELENLKYVSEAEKNGRTADVNLVAQLDDAEGLEKIENLGSNDGEVYEKAWILETYWLEEDDEKLPPGDAPOGGGFGDGDGVVPSGGGFSN

NbL16g19390.1 40S_ribosomal_protein_S20-2 [MW = 13.63 kDa]

No. of times detected



log(intensity)



Values from



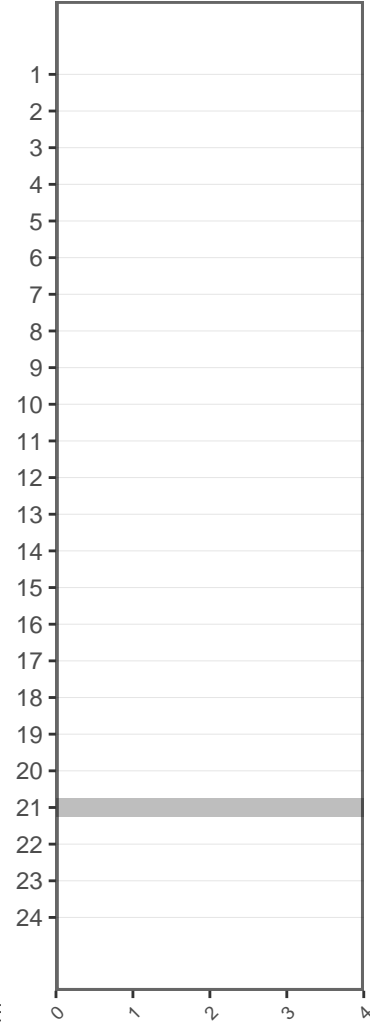
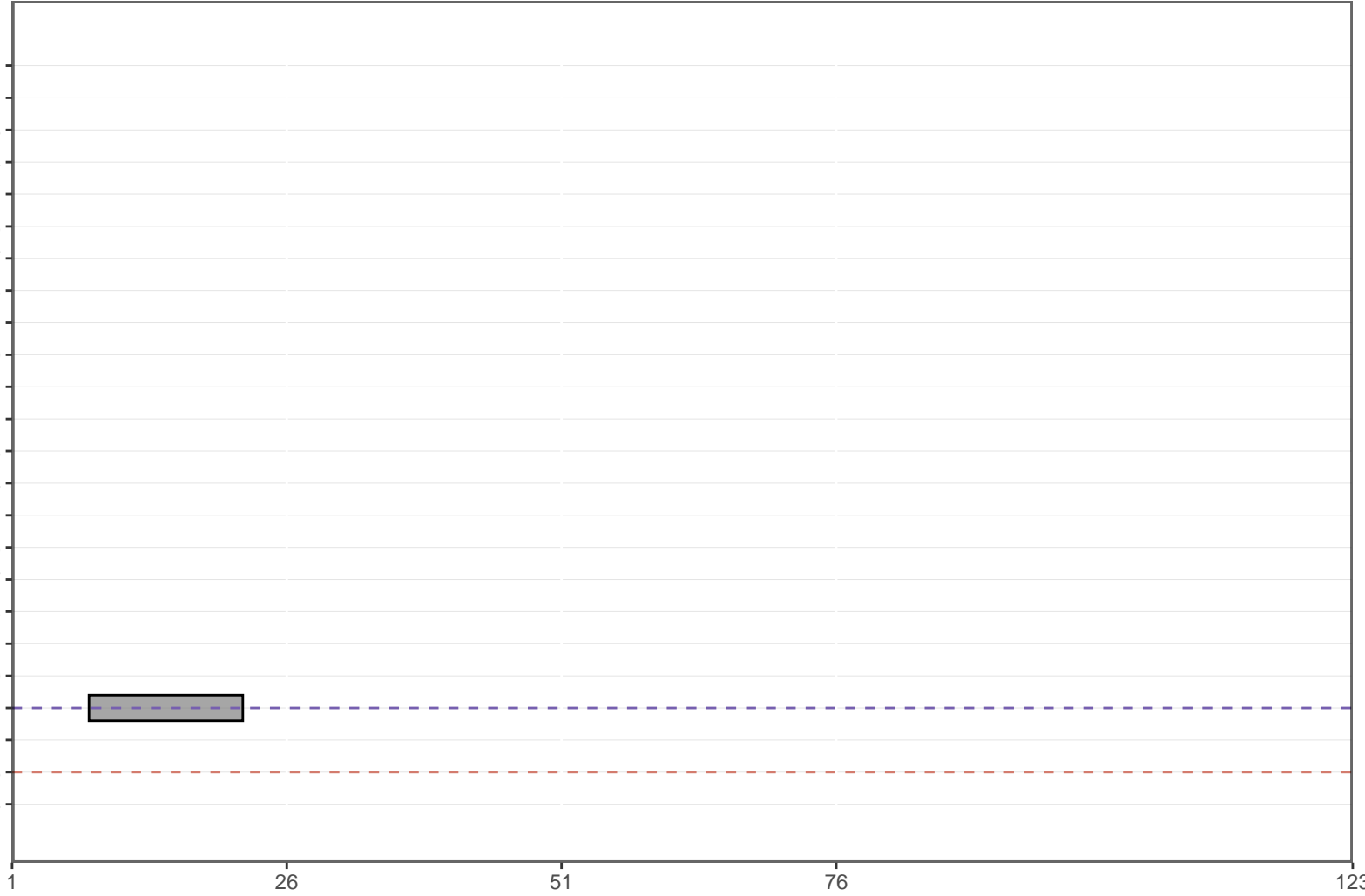
MW indication



Molecular weight

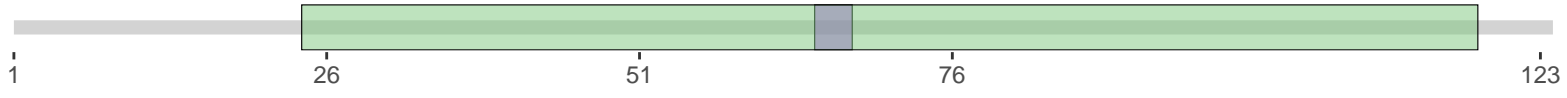


Gel Slice



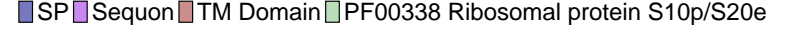
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

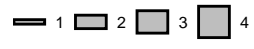


Protein sequence:

IKRLRVKGPVIRMPFRVNLNITTRKSPCGEGTNTWDRFELRVHHRVDFSSADVVKGITSTHEPGVEVEVTADS*

NbL16g19360.1 nudix_hydrolase_16_mitochondrial-like [MW = 20.43 kDa]

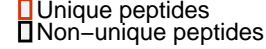
No. of times detected



log(intensity)



Values from



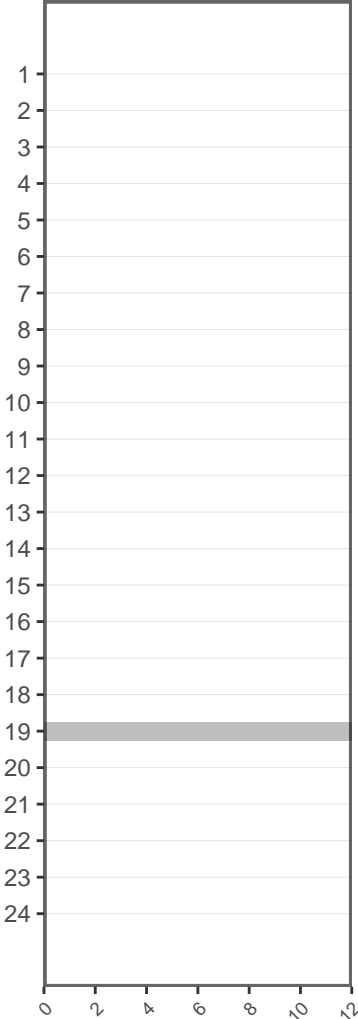
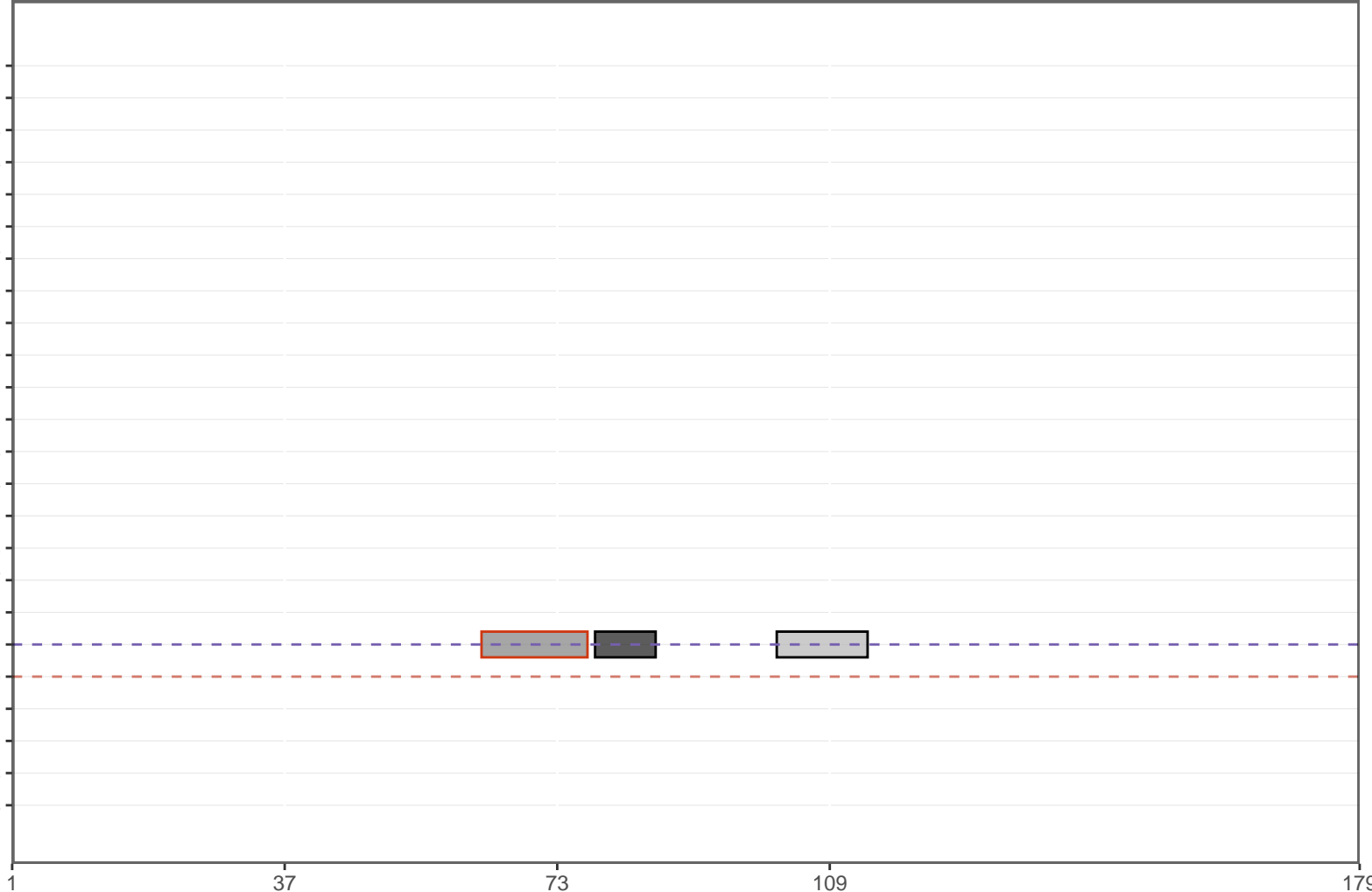
MW indication



Molecular weight



Gel Slice

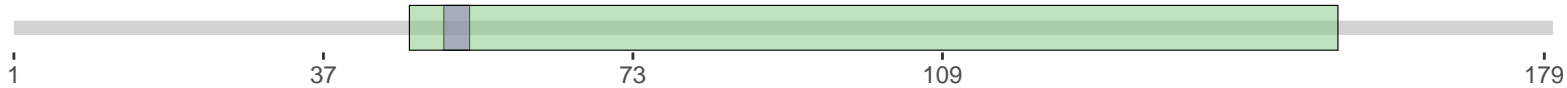


Protein length



Peptide counts over 4 repeats

Pfam domains



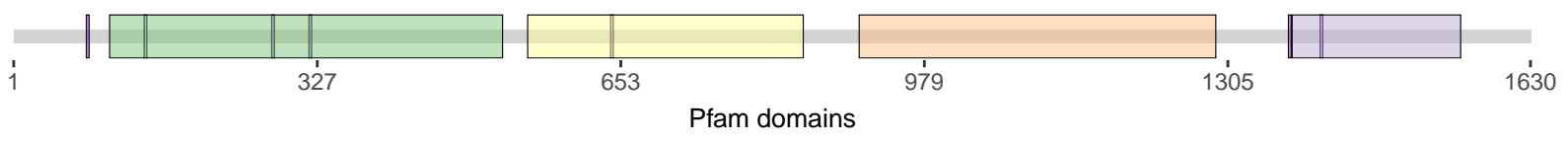
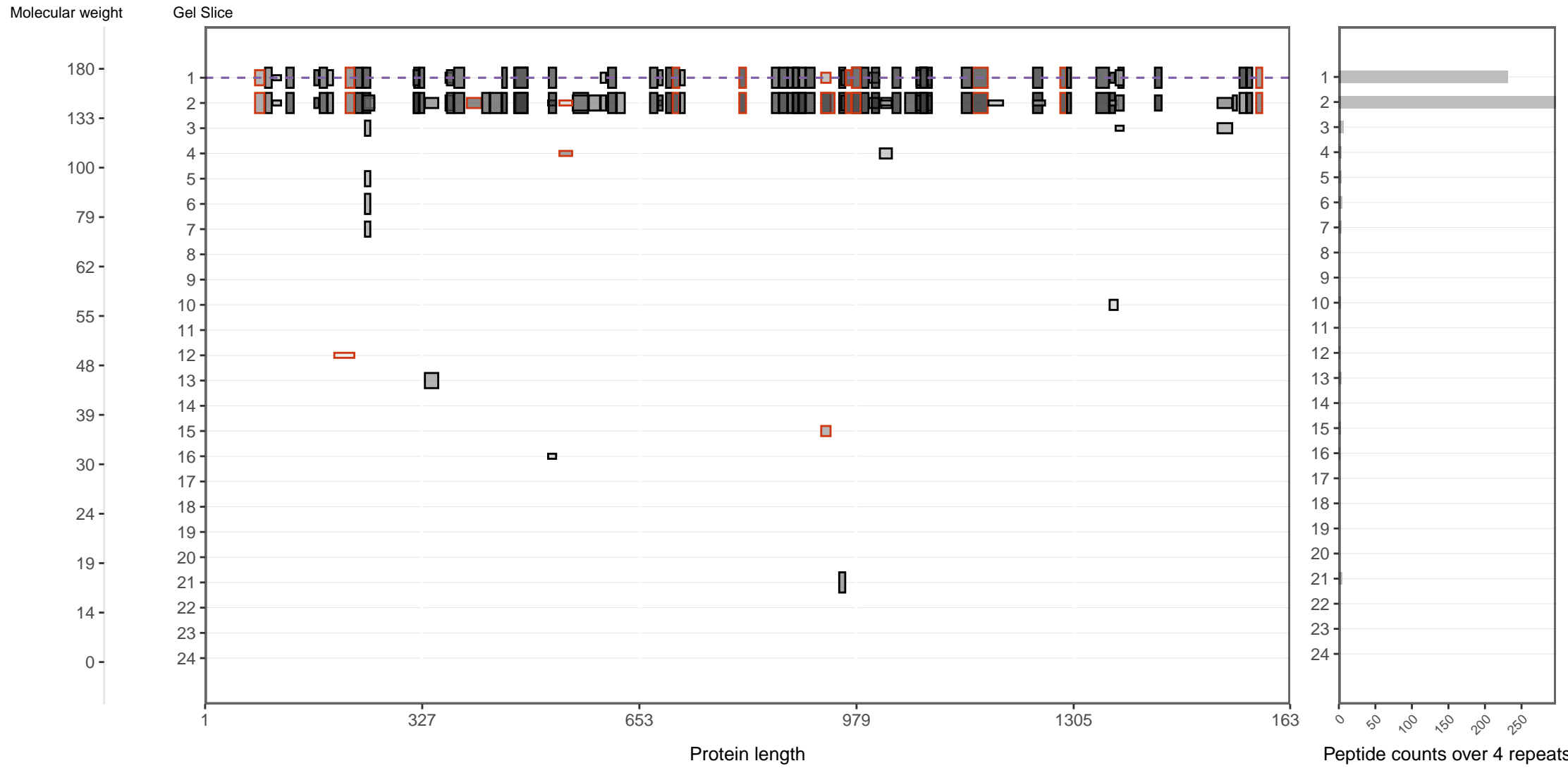
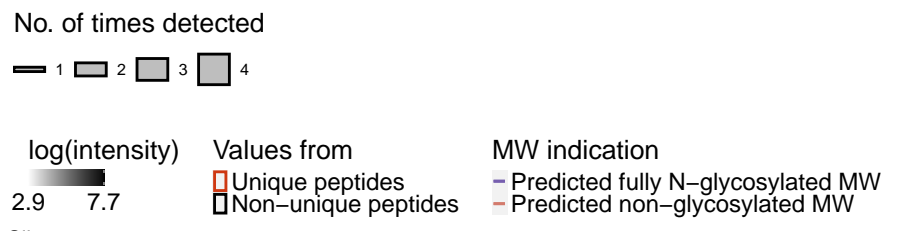
Pfam Description



Protein sequence:

EAIEEAGVRCGLVHFLGYFFKSKTLQDEYSPGELGRAMFALLVKEELEGWPEGRLLRRRSLWTPAEAGCRHPVMRGALEEGFSKWHDSGMATMNNED

NbL16g19330.1 ferredoxin-dependent glutamate synthase chloroplastic [MW = 177.69 kDa]



- Pfam Description**
- SP
 - Sequon
 - TM Domain
 - PF00310 Glutamine amidotransferases class-II
 - PF01493 GXGXX motif
 - PF01645 Conserved region in glutamate synthase
 - PF04898 Glutamate synthase central domain

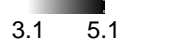
Protein sequence:
 IGMKPTVTIEQADKNFKAVNSGLLKLKMKMGILLSSVYGGAGIFVYGLGKEVVDVAFQGGKSGISGLTLDLARELTSFVWKAQFSDTAKRLNENYGFQFRGGSEYHGNNFEMKLLHKAVRQKGGSAVSYQQHLNRPVNVLRDLLEFKDRSPVIGRVEPASAIVRRFQTGMMLGSAISRETHEAIAAIAAMNRLGGKSNSEGGEDPRRWKPLTEVVDGVSFTLPHKGLGNQGDATSAIKQVAGRFGVYPTPTFLANADLEIKIAGGAKPGEGLDPLGKVSAYIARLI

NbL16g19310.1 ultraviolet-B_receptor_UVR8-like [MW = 47.44 kDa]

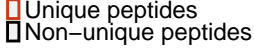
No. of times detected



log(intensity)



Values from



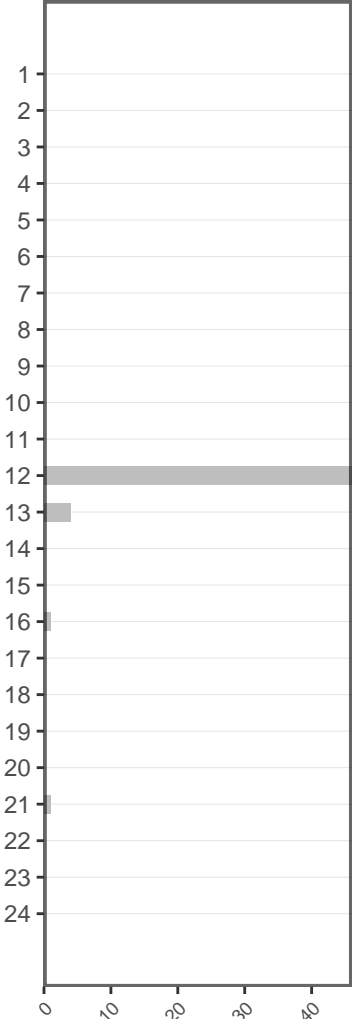
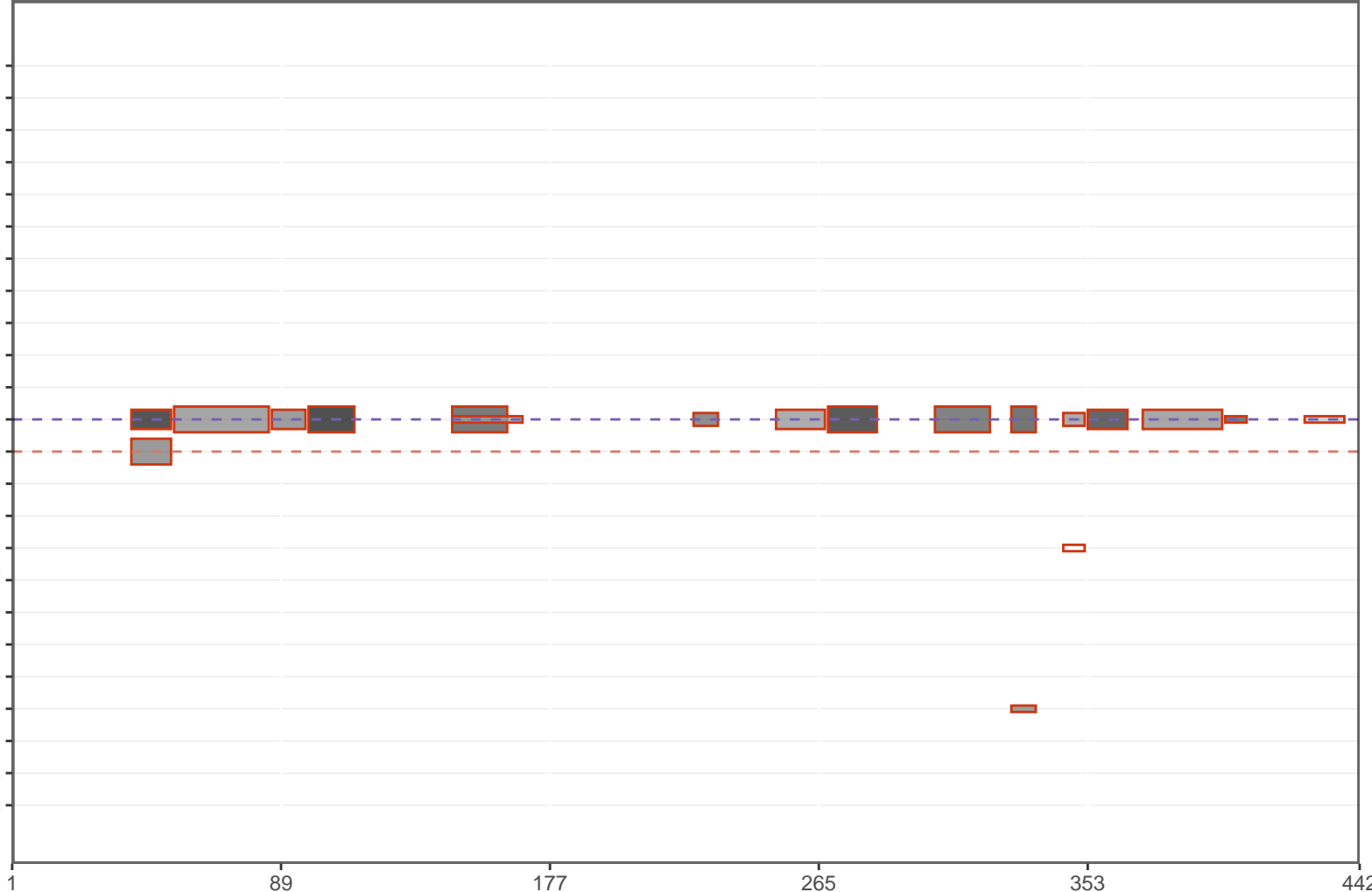
MW indication



Molecular weight

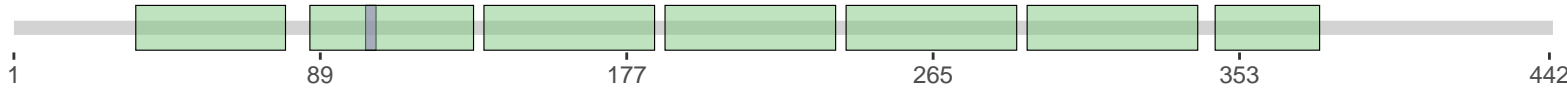


Gel Slice



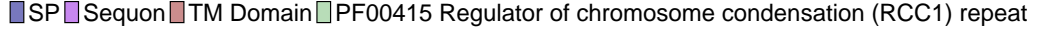
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DRLVPLVYKYSATYGEKMMVADGWRRHTKCVSSSGALTYFGWSKYGQLGHGDFEDHLPFKVQALHDFSTSGISGGWRHTMALTDGELYGWGWNKFGVGVGDVNDVHSGPVGWVFFPHDQKVLHSGCWRHTLAVTERGNVFSWGRGTNGQLGHGSEVDVNPRIEALVDGSSGGQIGS6TFDPSAAEKSWSPTEYAVVFNENVPKGTVTSVKGNGNDVNPENDKRIRL

NbL16g19100.1 glucose-6-phosphate_1-dehydrogenase_chloroplastic [MW = 67.31 kDa]

No. of times detected



log(intensity)



Values from



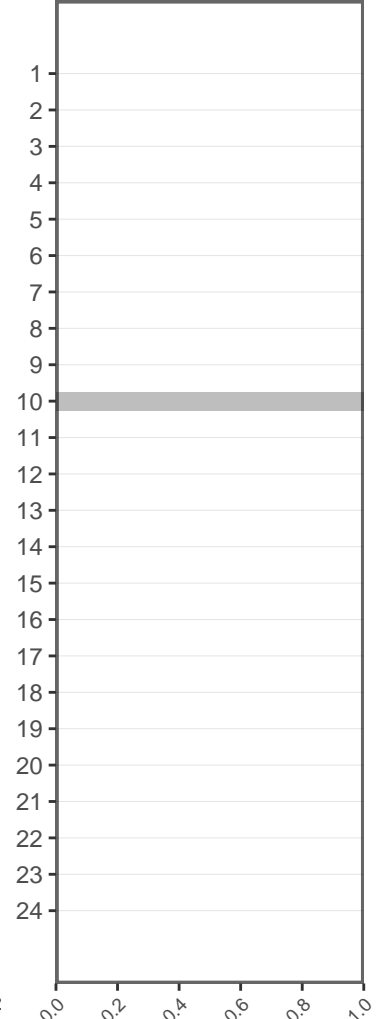
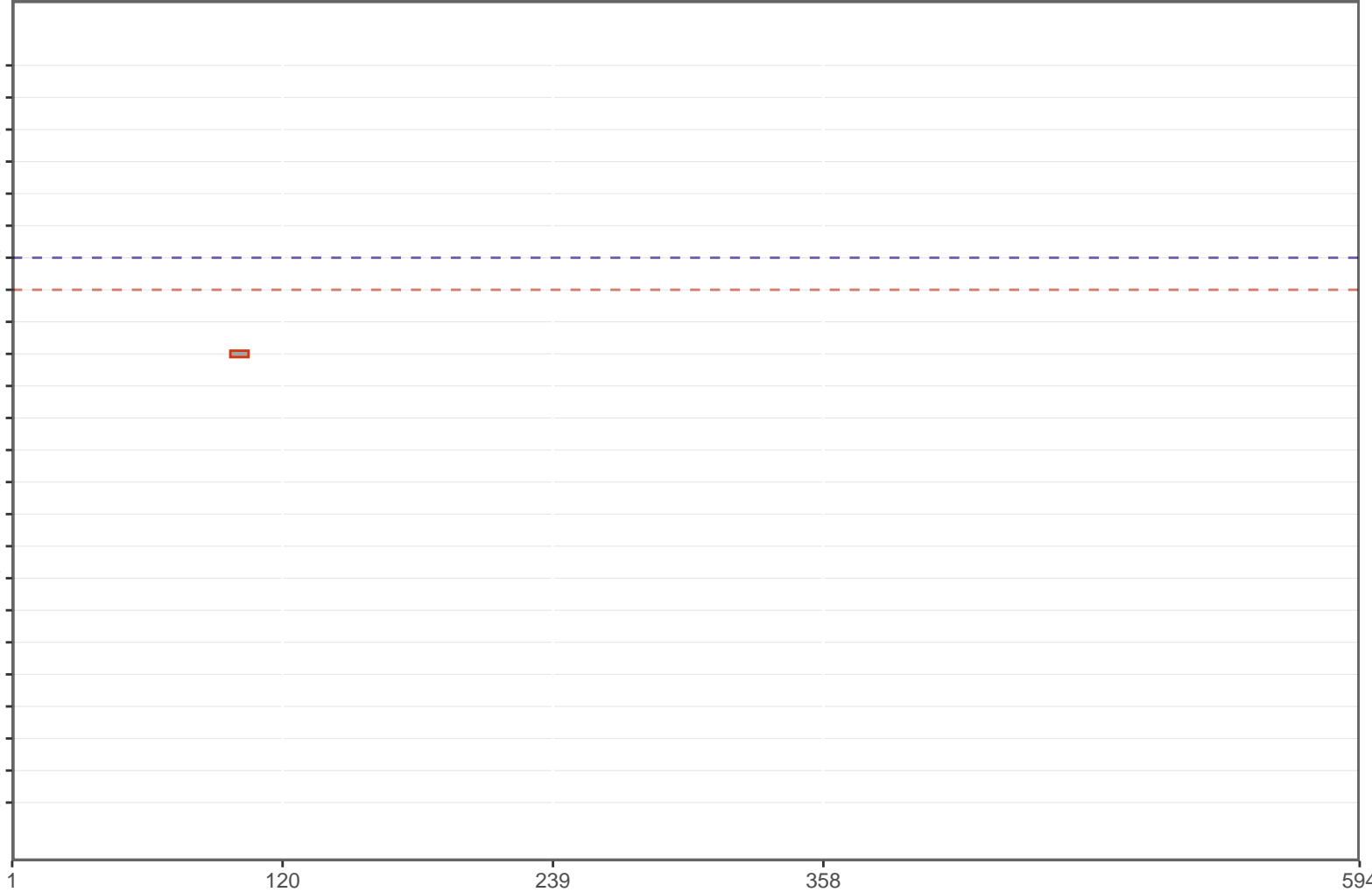
MW indication



Molecular weight

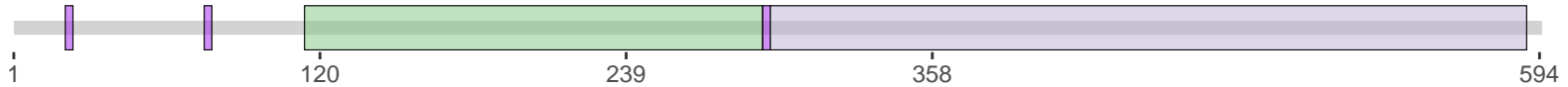


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

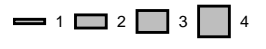
- SP
- Sequon
- TM Domain
- PF00479 Glucose-6-phosphate dehydrogenase, NAD binding domain
- PF02781 Glucose-6-phosphate dehydrogenase, C-terminal domain

Protein sequence:

YLQKELVNLVLRFSNLIFFPLWIRGVRINVGIFSEDFOTEGRGVYFDHYGIRDMQNHLLQLALFAMETPVSLDAEDIRNEKVKVLRMRPLGLDDVIGQYKSHTKGQVTPYDGYDDKTKVLDLTPFAAAALFDINARWQVDFFLMKAAGKALHTRBAEIRVQFRHVPQNLNKNKNGGSDLDGATNELVIRVQPEAYLKNKKNKVPGLGMRDLDRSNLNLVSARYSKEIPDAVERILLDDIEGERLRFIRSDDELDAWVSLFPLVKELEDKKNVPEYKPYGSRGPVGAHYLV

NbL16g18660.1 NADH_dehydrogenase_[ubiquinone]_flavoprotein_1_mitochondrial [MW = 56.6 kDa]

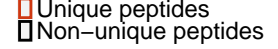
No. of times detected



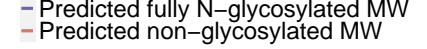
log(intensity)



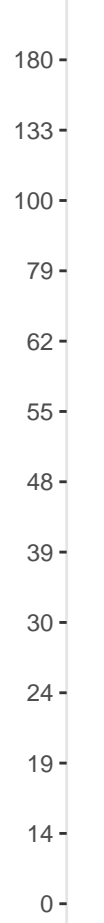
Values from



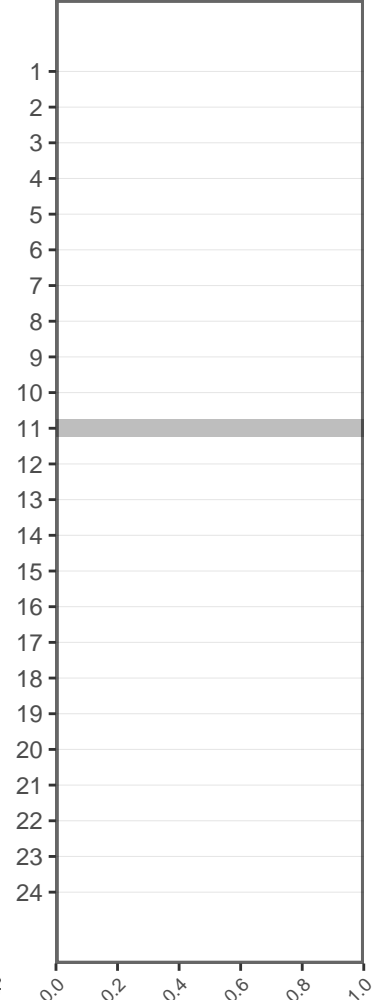
MW indication



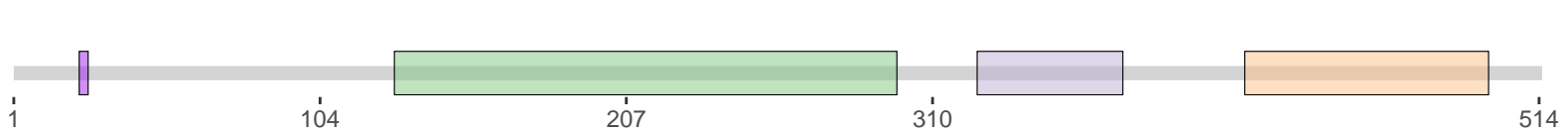
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

TDVYHFAGAGYCGEETALLELEGKQKPKLKPFPANAGLYGGPTTVTVNVEVAVWSPFLRRGPEWFAFGKRNKNGTKLFGISGHVKNKPTVEEEMSIPLKEIHERHGGVRRGGWQWNLAWPQGGSEVPLPKNICEVLMDFDALKAVQSGLGTAAVVIDKSTQVDMARLSVYFKHEGGGCTPCREGTGWLWMMERMKVGNAKLEIEIDMLQEVTKGIEHTICALGDAAAWVQGLRHFRPELEIRRIREHADRELQHAATAA

NbL16g18640.1 adenylate_kinase_4 [MW = 26.49 kDa]

No. of times detected



log(intensity)



Values from



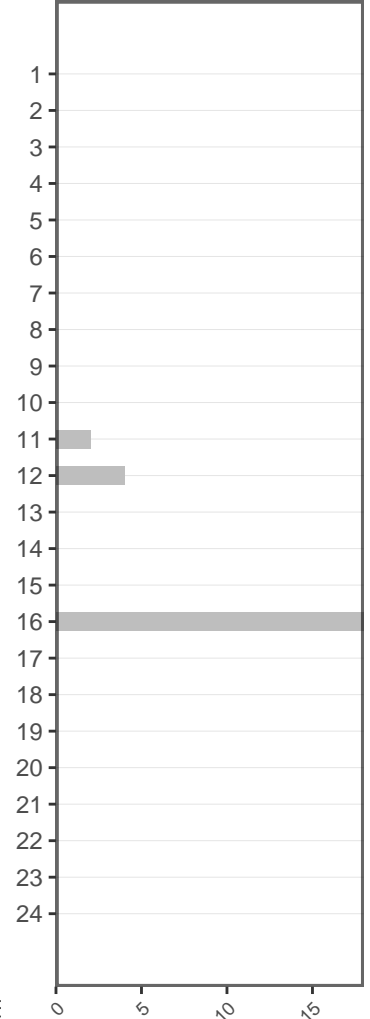
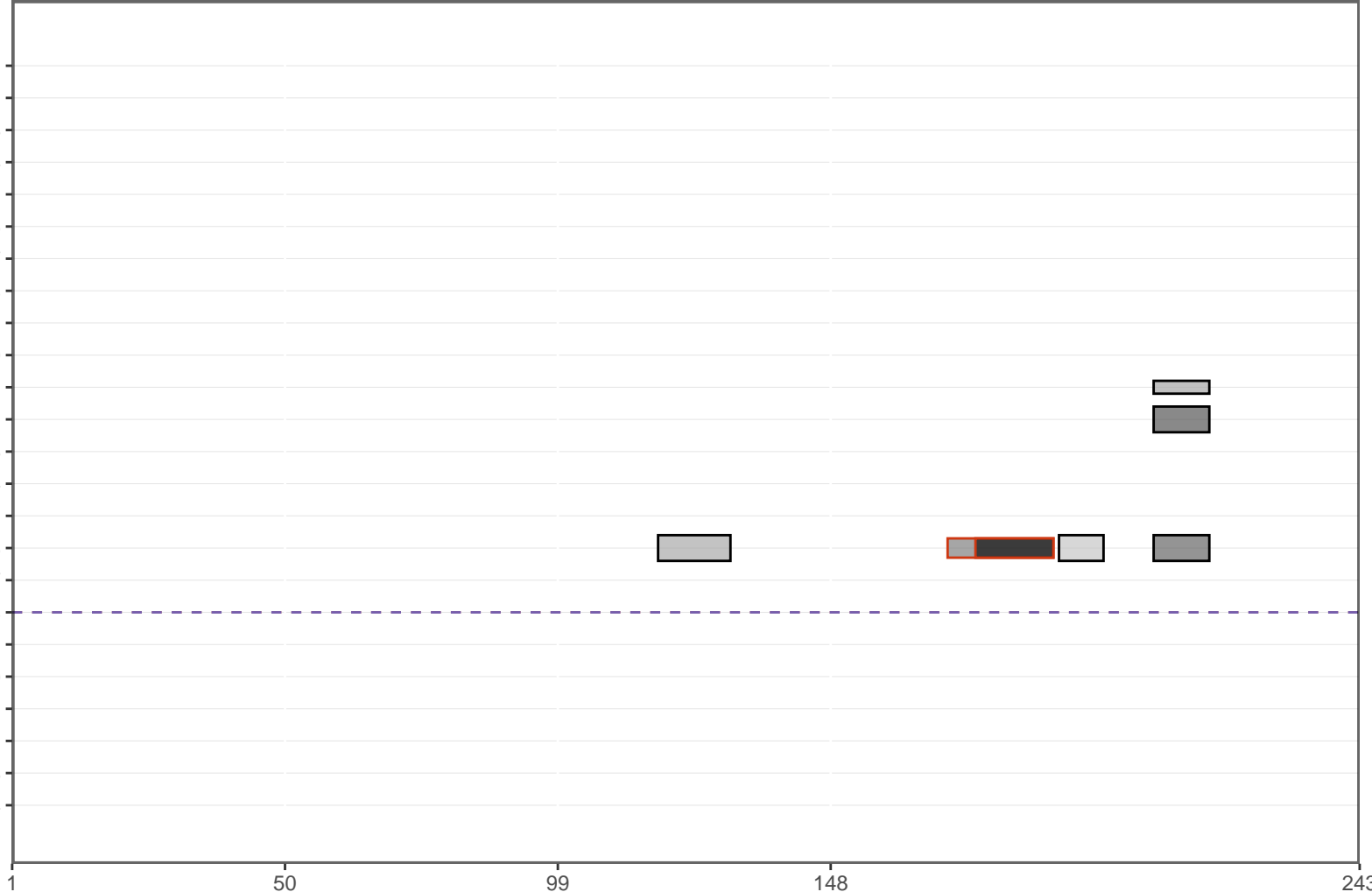
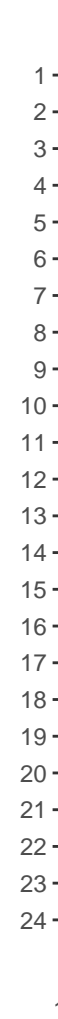
MW indication



Molecular weight

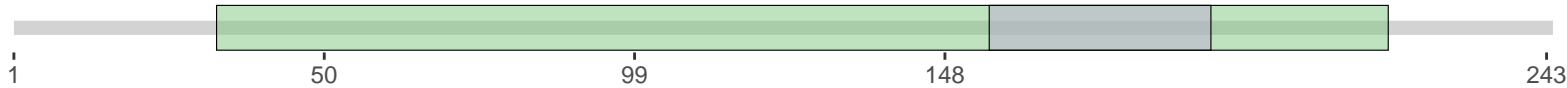


Gel Slice



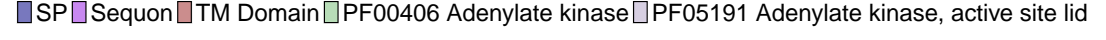
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SFILDGFFRRTVQAASKLDEMLQKGGTKIDKLVNFNFAIDDALEERTGRWHPSSGGRBYHTKFPFKPLPGVDVDTGTEPLIGRDKDTAEVLKRLDAFHRGTETPVINYYGKGGVAASLHAEKPKPEVTSEWNVLSG

NbL16g18420.1 glyceraldehyde-3-phosphate_dehydrogenase_cytosolic [MW = 36.99 kDa]

No. of times detected



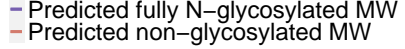
log(intensity)



Values from

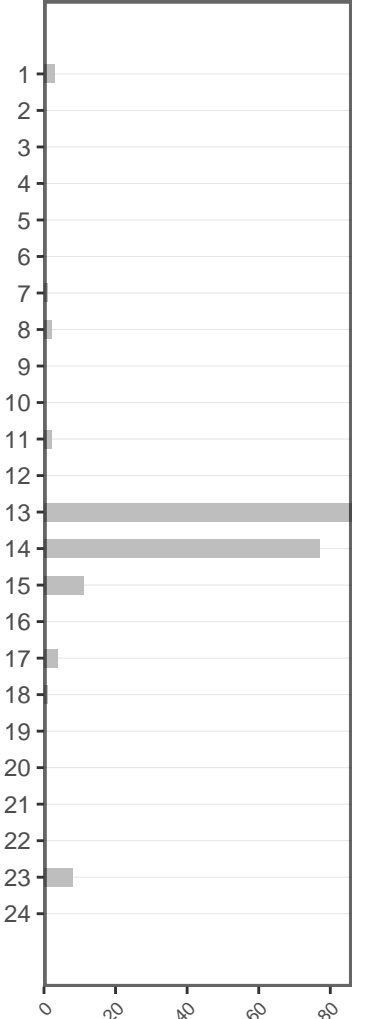
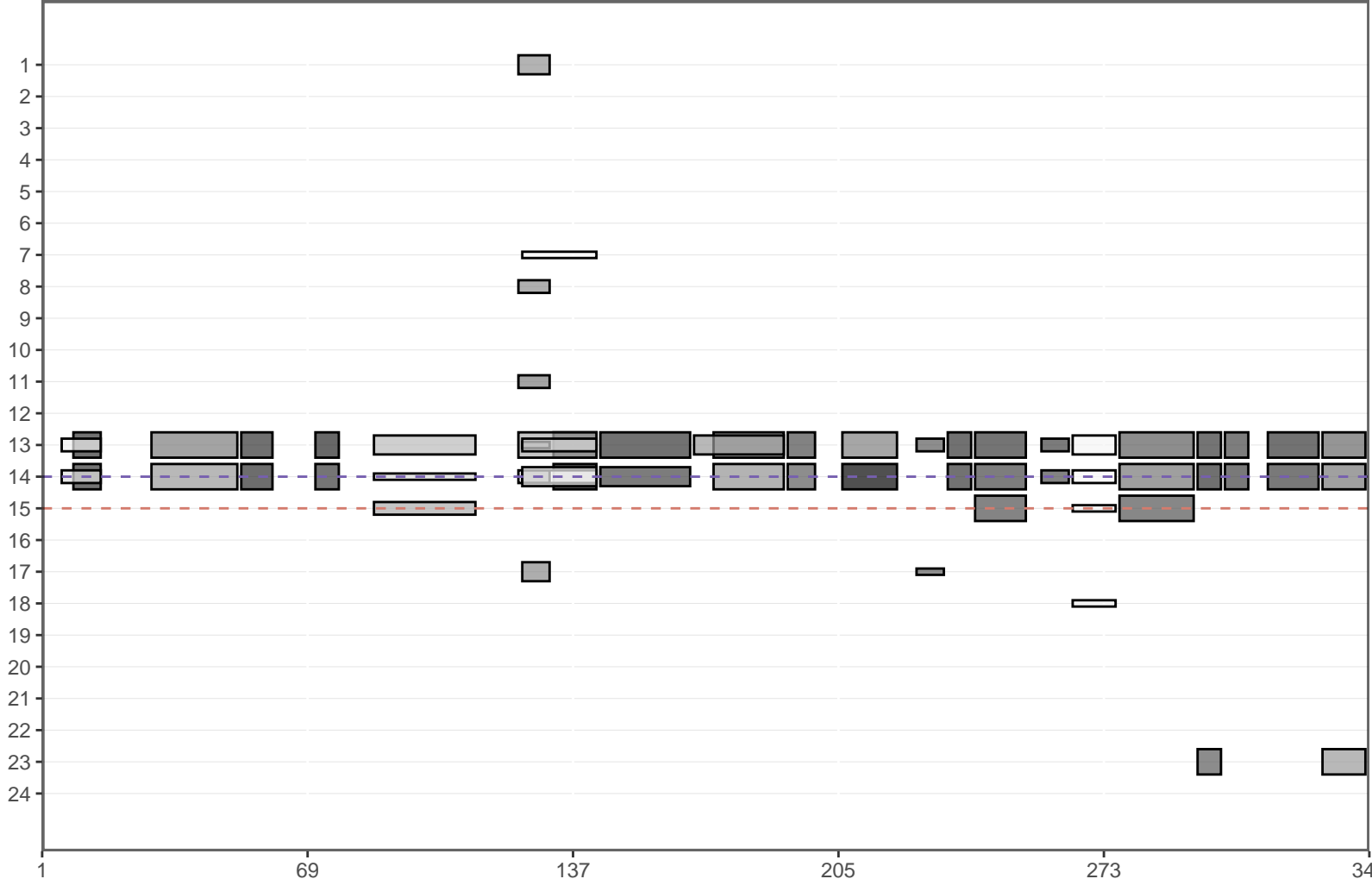
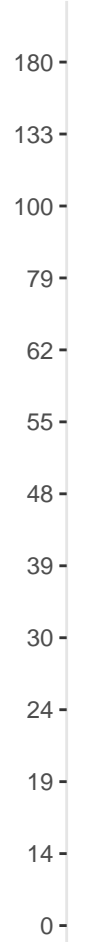


MW indication



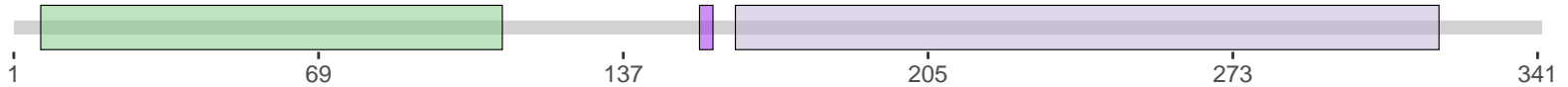
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon TM Domain PF00044 Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain PF02800 Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain

Protein sequence:

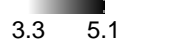
CTTNCCLAPLAKVINDRFQVIEGLMTFTVHSLTATQKTVDDGSPMKDWRGGRRAAFNIPSTGAAKAVGKVLPAALNGKLTGMFRVPTVDVSVDLTVRLEKEASYDEKAAKEESEGLKGLGFTFEDDQVSTDFVGDGRSIFDAKAGIALSKSFVKLVSWYDNEWGYSRIVDLGHMAVA*

NbL16g18340.1 protein_HHL1_chloroplastic [MW = 25.92 kDa]

No. of times detected



log(intensity)



Values from



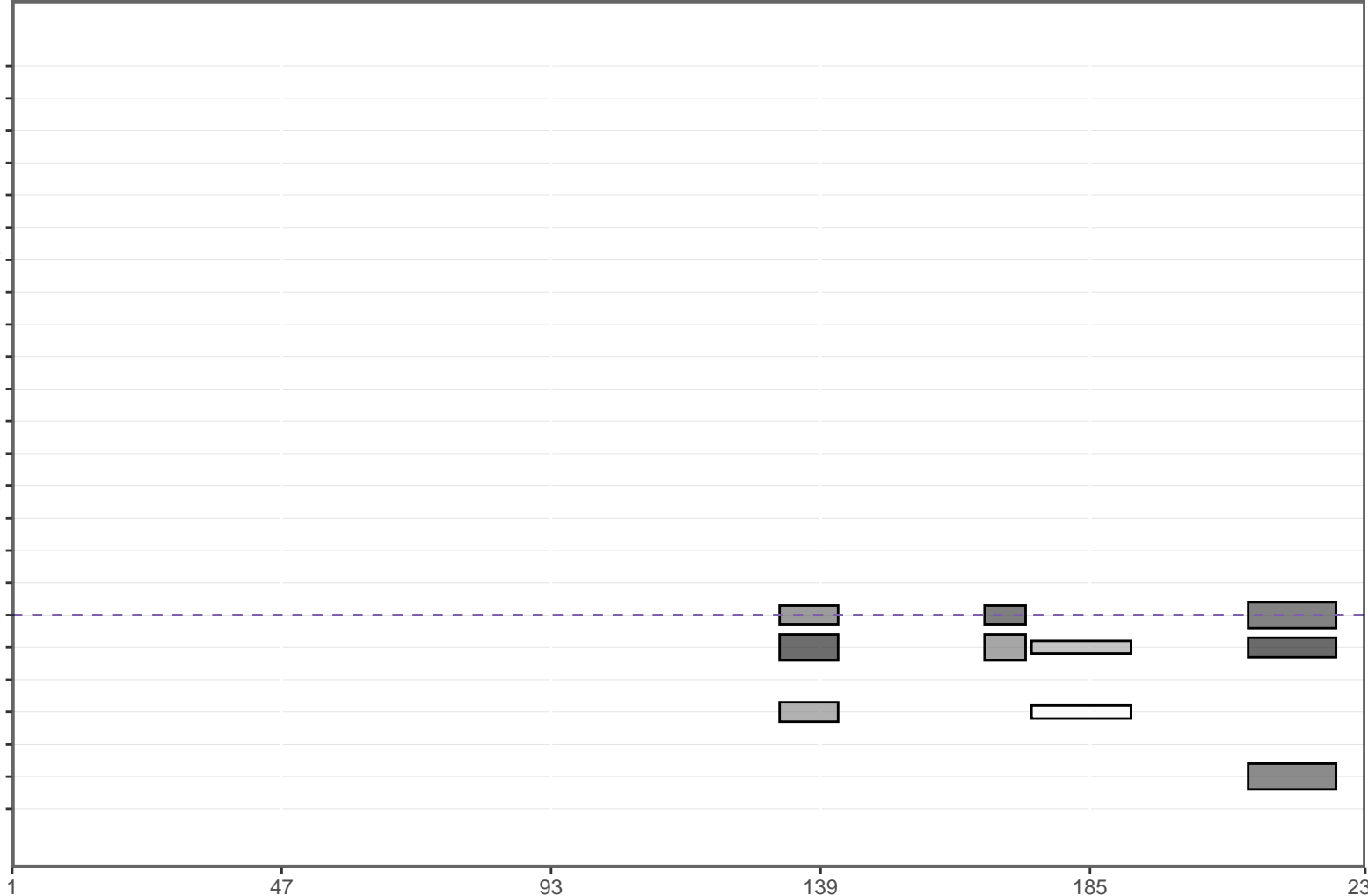
MW indication



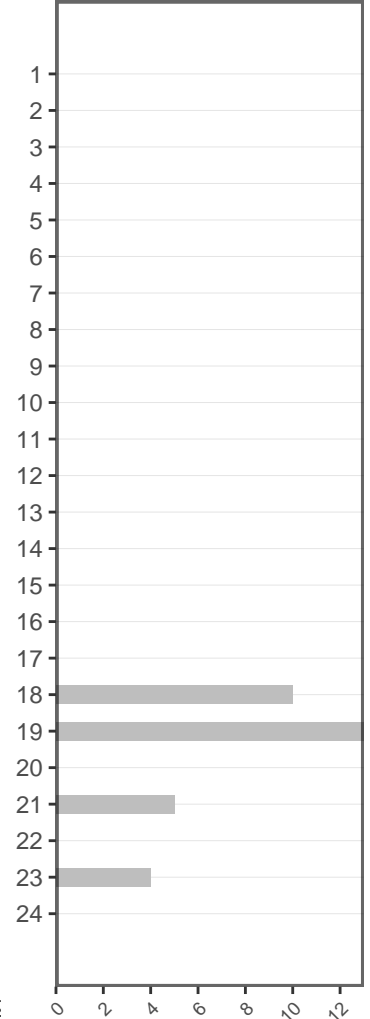
Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description
 SP Sequon TM Domain

Protein sequence:

IIVTGGTTAKIMIAAKDNFLGKYYKDLARNLAAVYINDEKNKKIAMKQHRVLSKATEFRYGYKLVENNLRAALSTFDVIELPTDGLKTVVDKVKDFGDAKESFGKLTALPTSESSSEEDSPKGGPKI

NbL16g18190.1 probable_pectate_lyase_5 [MW – SP = 42.53 kDa]

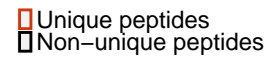
No. of times detected



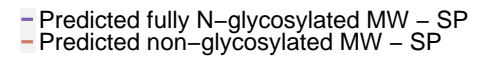
log(intensity)



Values from



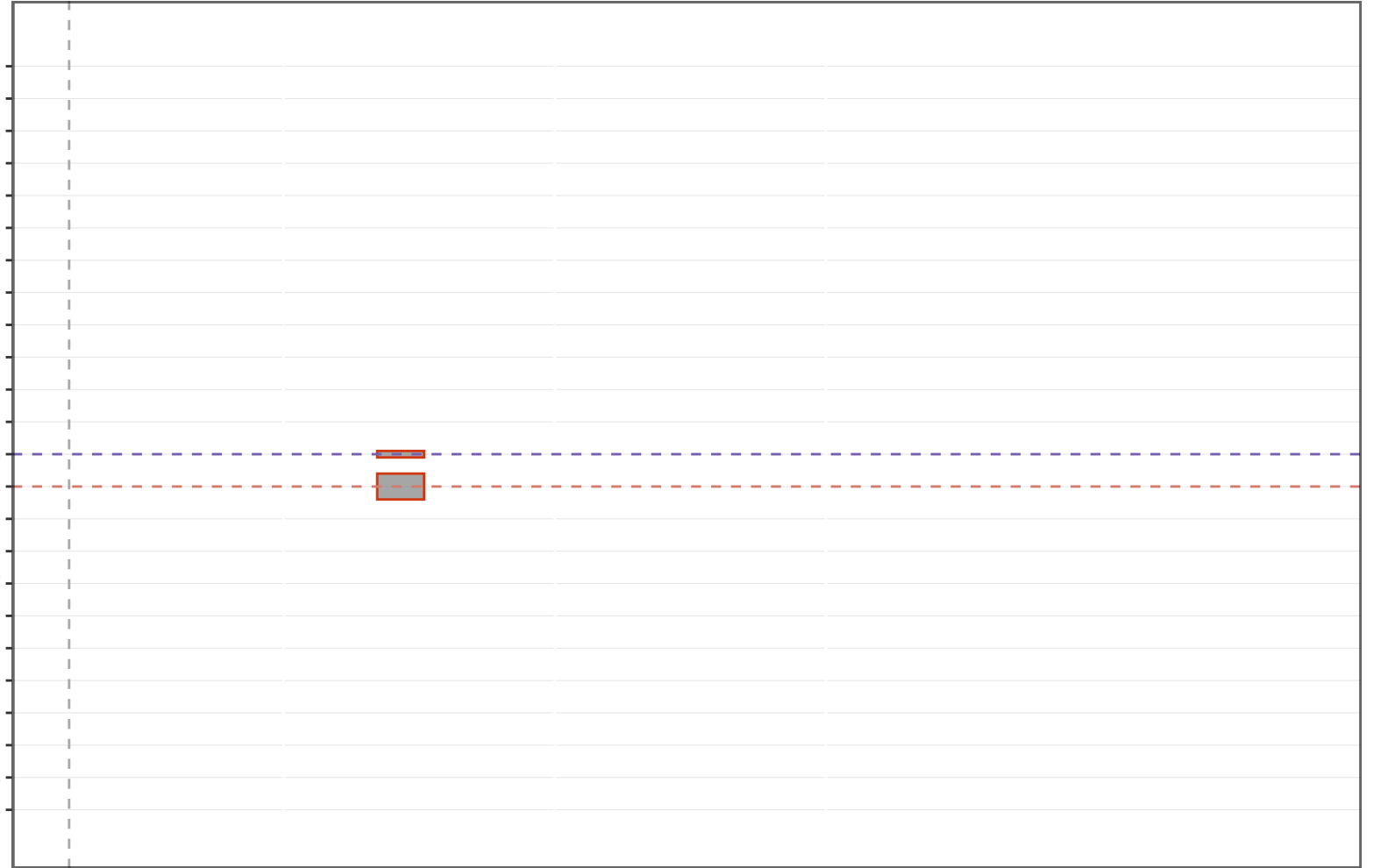
MW indication



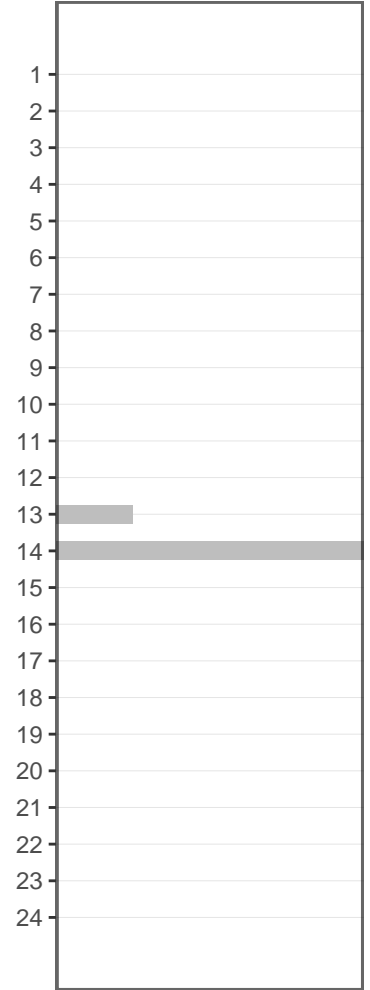
Molecular weight



Gel Slice



Protein length

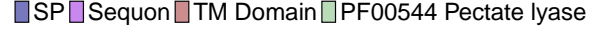


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ITLSDGQVSIFFGGGHVWVDHCSLENGRDGLDARIGSTATITENNYMTHHNKVMLLGHSDSFTDRKMMQVTFANIFGEGLVQRMPSENGRCRGRHYFVYVNDYTHWEMVAWGGSASPTINSQGNRFLAFNDFNKEVTRHEDAAESEWKNWNRSEGDDMLNGAFFTRISGAGASKEVAKASELSARPSTLVSSFLNAGALGCKKARRG

NbL16g18180.1 T-complex_protein_1_subunit_epsilon-like [MW = 59.04 kDa]

No. of times detected



log(intensity)



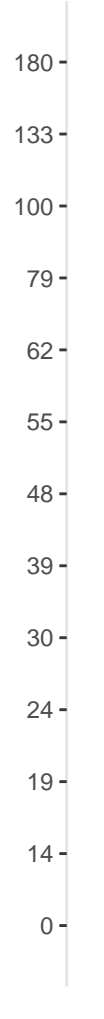
Values from



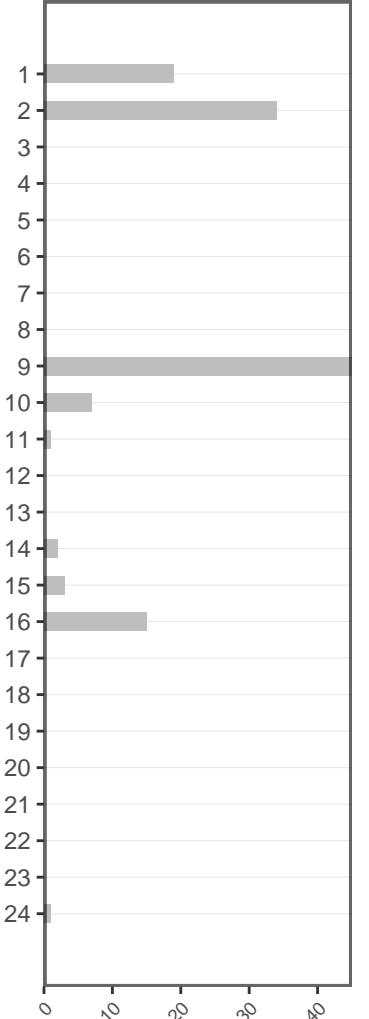
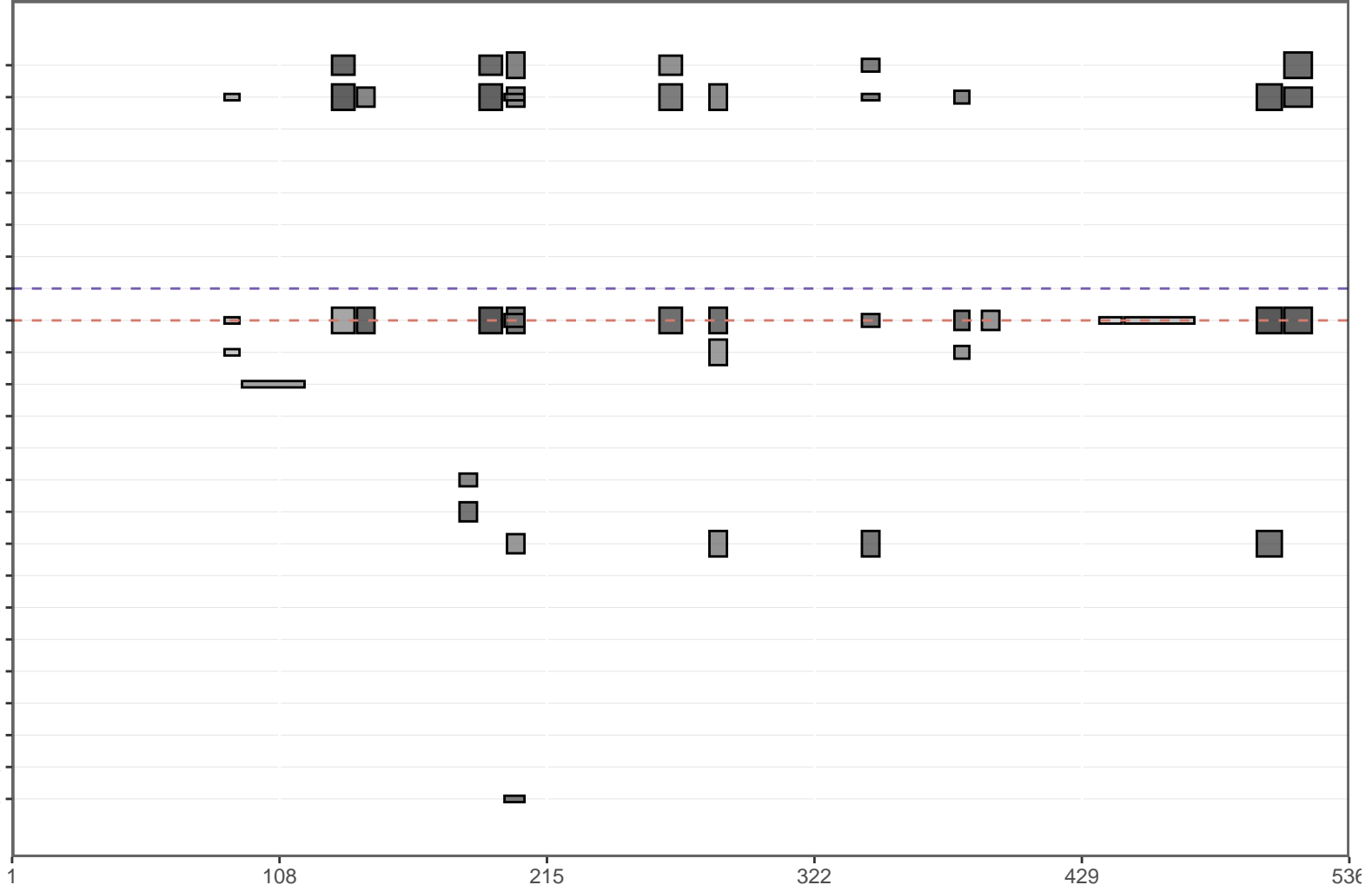
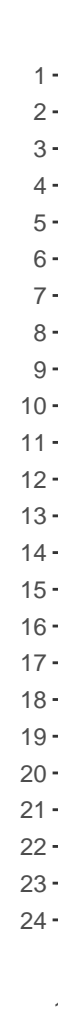
MW indication



Molecular weight

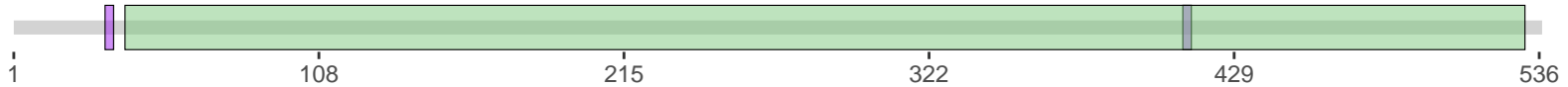


Gel Slice



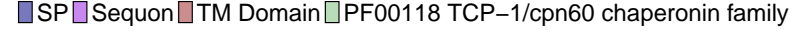
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PXTKHVYDSDVEKFGTLRGGEGKVFDDMVGKGDVGFATLVGQVGFDEANHLMLRNLRNLRVRRVGGVELELIATGGRIVPRFQELTPEKLGKAGVYRREKSFQTTKDRMVEHCANSEKAVTIFRGGKMMIEETRSHIDALGVARNLIRNNSAVGGGSAEISCSIAVEAAADKHPGVEQVIRAFADALDVPMLAENSGLQPIETLSAVKAAQIKENPCCGGIDCDNDVGTNDMREQNVFETLIGKQQLLATQVVKMLINDVVISPEYV

NbL16g18060.1 60S_ribosomal_protein_L18-2-like [MW = 20.86 kDa]

No. of times detected



log(intensity)



Values from

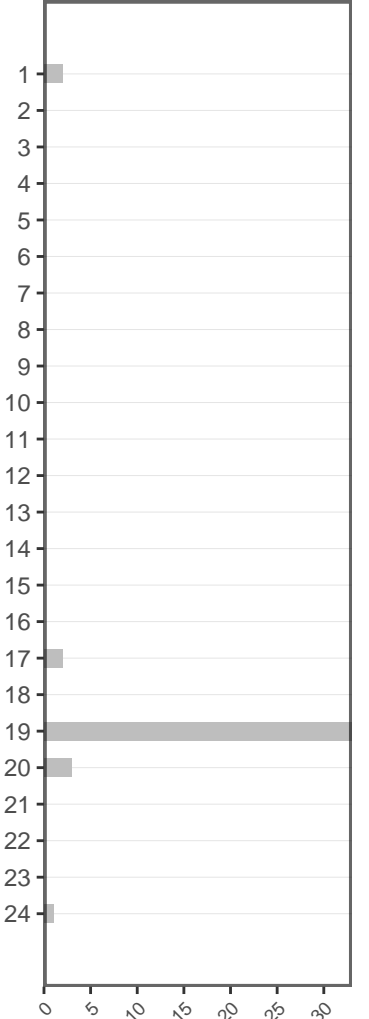
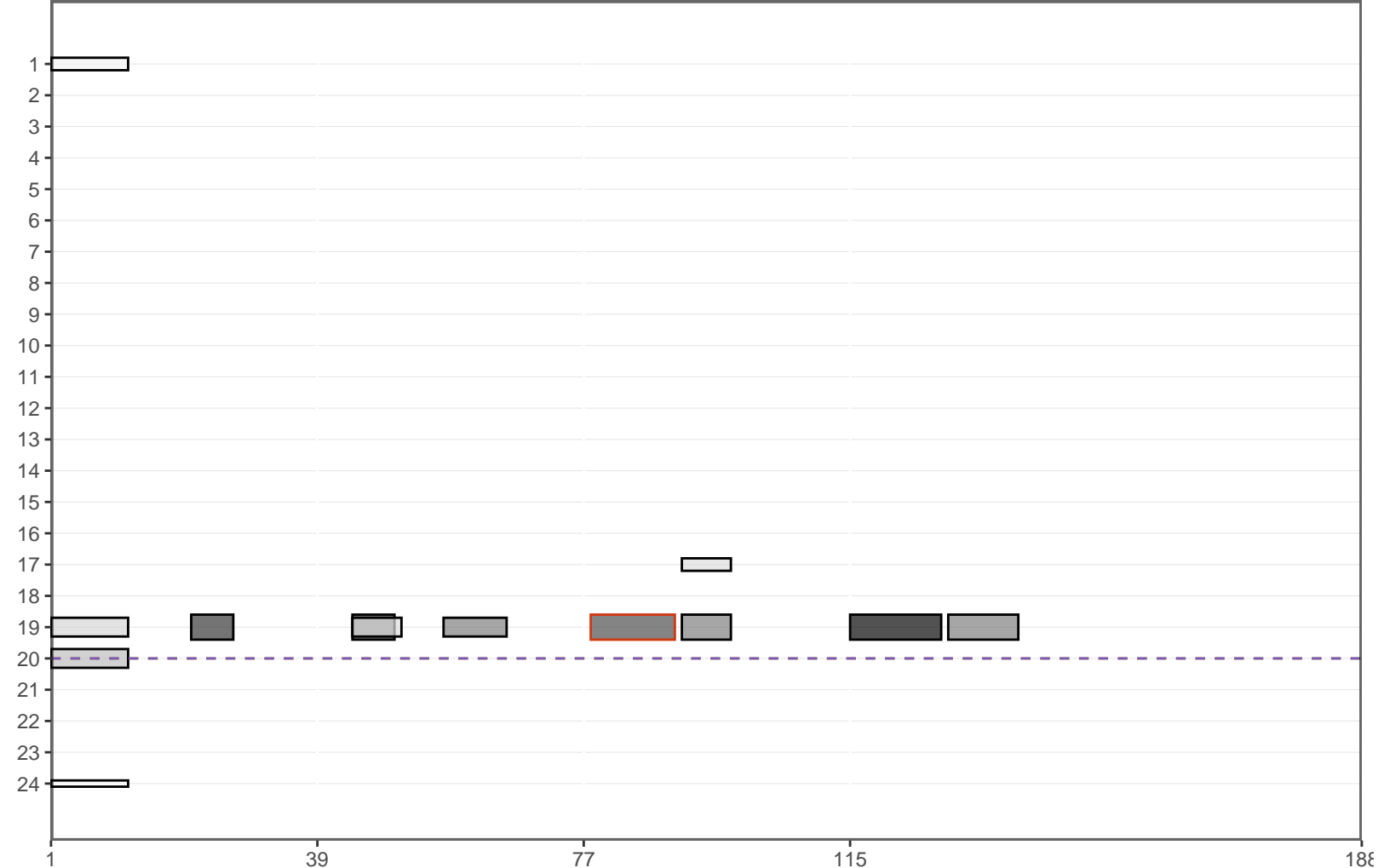
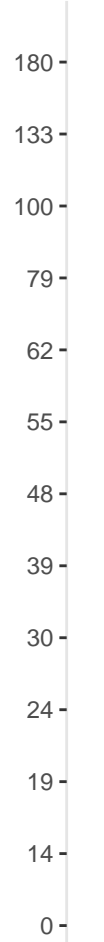


MW indication



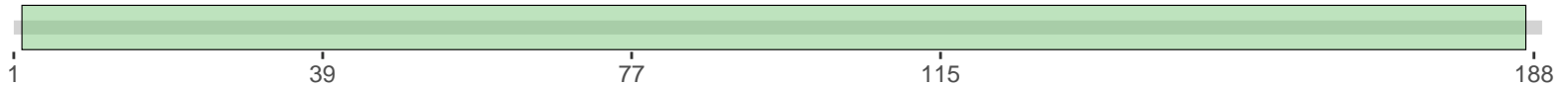
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

STITDDVRAYDVPITMVGALREFIKTARARIEKAGGEGELFDGLALRAPLGNNTLLLRGPKNAREAVKHFQAPGVPVSHTKPVPVRSKGRKFERARGRNRGRGKYV

NbL16g18040.1 probable_pectinesterase/pectinesterase_inhibitor_41 [MW – SP = 54.26 kDa]

No. of times detected



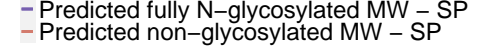
log(intensity)



Values from



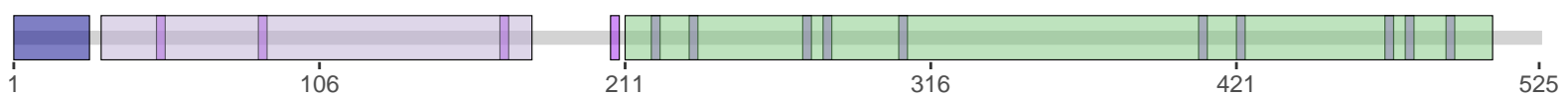
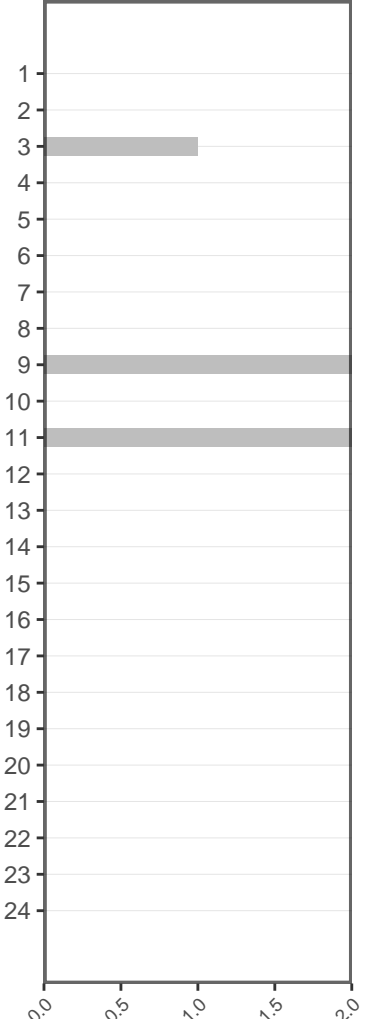
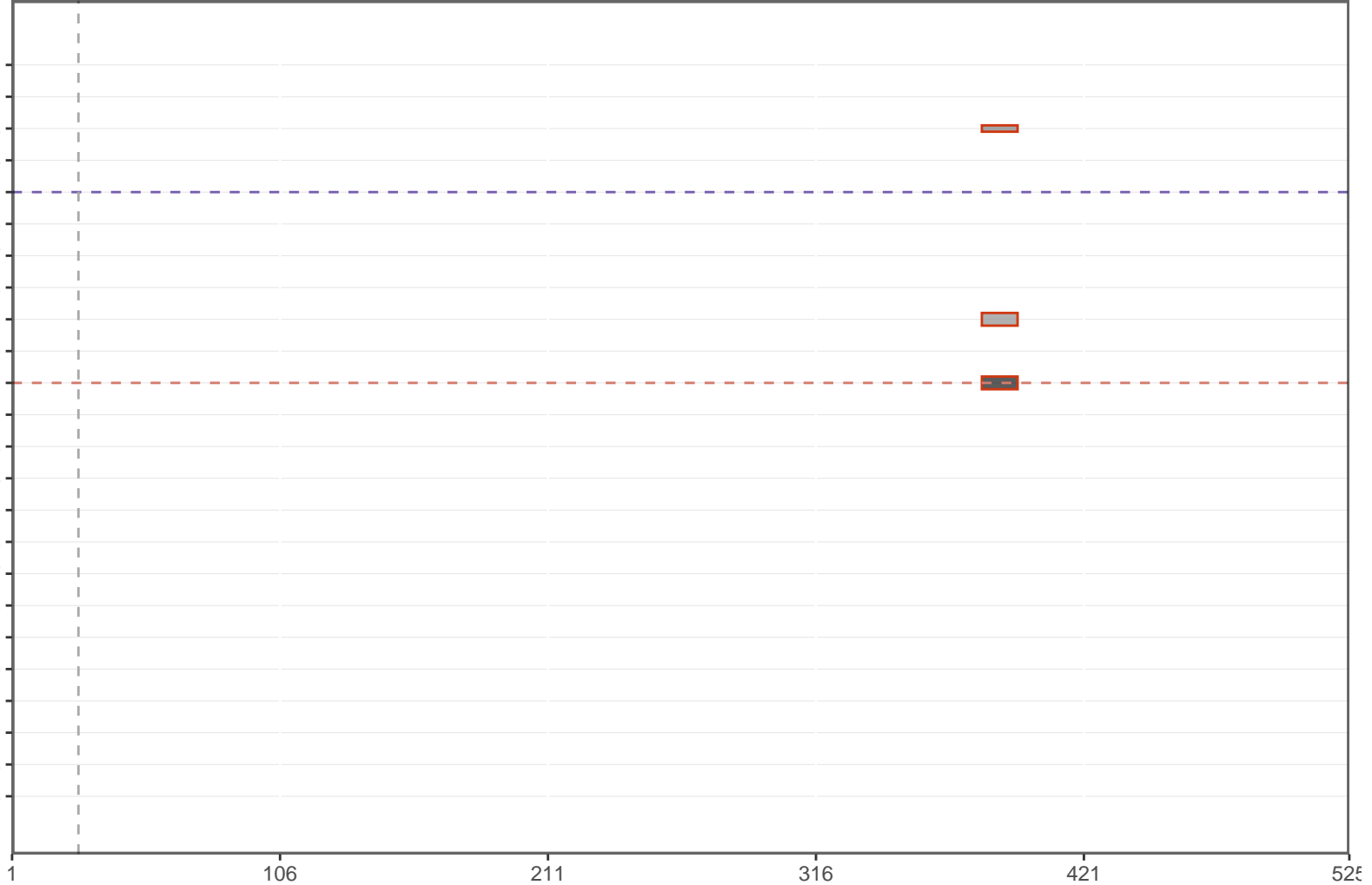
MW indication



Molecular weight



Gel Slice



Pfam domains

Pfam Description



Protein sequence:

DEYYVSPSNKKYLLMVGSDGINKTIFGNHSVVDGWTFFNBATFAVGEGLMANNITGNTAGAKHQAIAWRNGADLSTFYSGSFEYQDITLTHSMRQFYREDQYGTDFIFGNAAVVFGNQNVPRLPLOGGFNPITAGRTRDINQNTGTSIHNCTKAAAPDLSSNGTGTGLGRPAKEYSRVLYMGSFMDLNPAGVAWAWSGDFALSTLYAEVYNTGPGSNTSSRVTWPGYHWNSTDAISFTVSNFIAGDFALPATGVPVYTGDLI

NbL16g18030.1 uncharacterized_LOC107803223 [MW = 33.57 kDa]

No. of times detected



log(intensity)



Values from



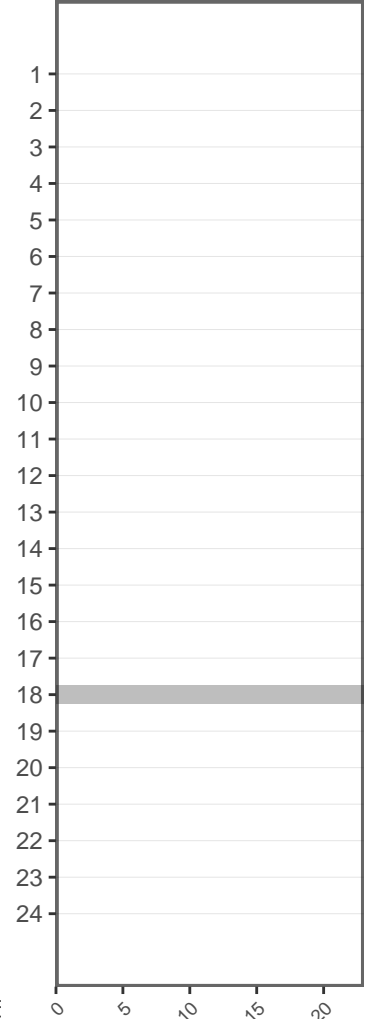
MW indication



Molecular weight

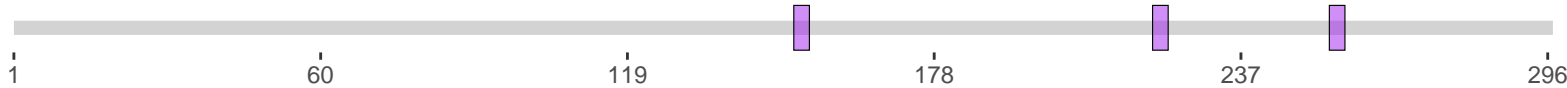


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

IGAEQFRLDVACNPNDTEESGWFLGEAGLVGVGEARKRYLELMGVGVGRDRPVMREAVNMFNDGGNPEKLVWRIFSLTNYSLIKLVAFFSSGGPNEYFYASLVAGLYYESQNESSDAKRVHIAAGQSAVGSRSDDYMAALAKVHGKGRNWNLY

NbL16g17960.1 dihydrolipoyl_dehydrogenase_2_chloroplastic-like [MW = 60.26 kDa]

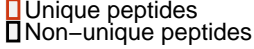
No. of times detected



log(intensity)



Values from

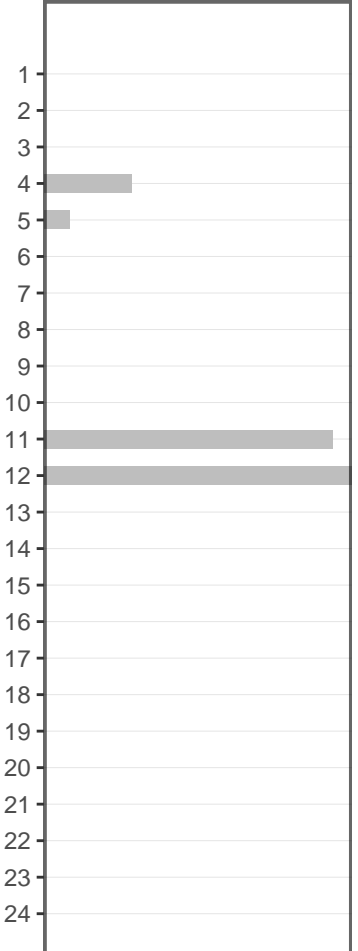
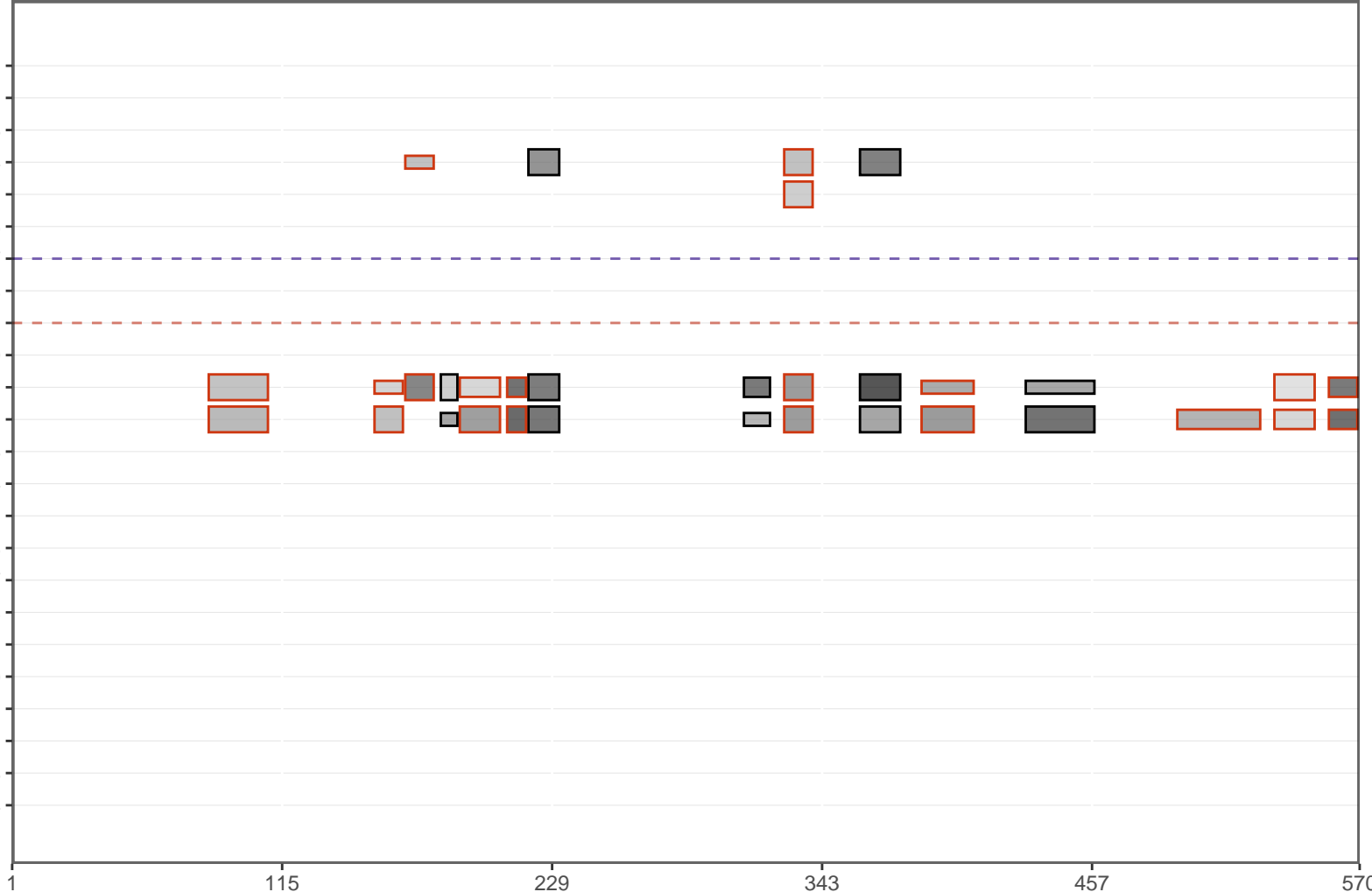
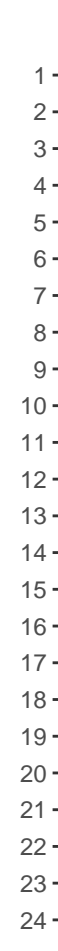
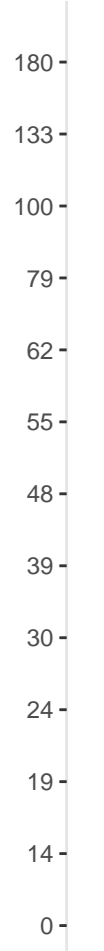


MW indication



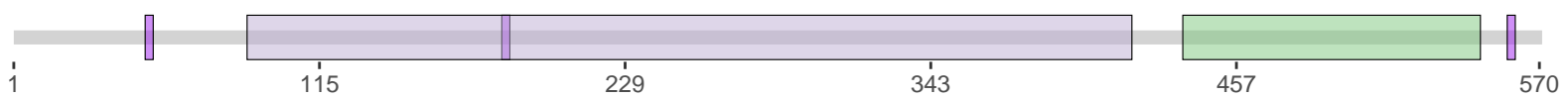
Molecular weight

Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

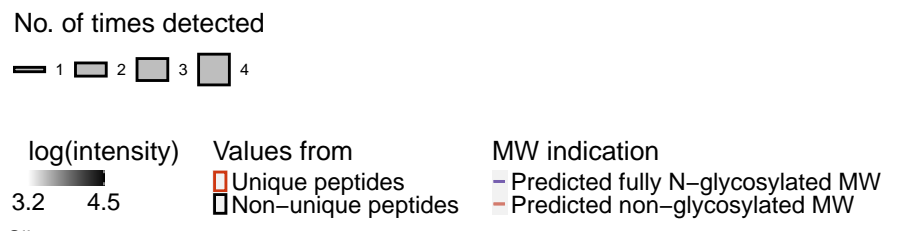
Pfam Description

- SP
- Sequon
- TM Domain
- PF02852 Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain
- PF07992 Pyridine nucleotide-disulphide oxidoreductase

Protein sequence:

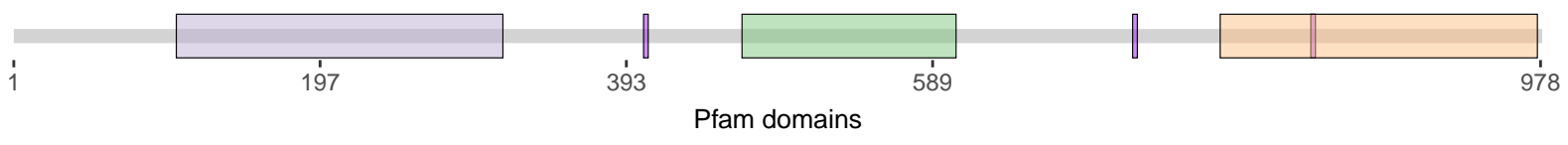
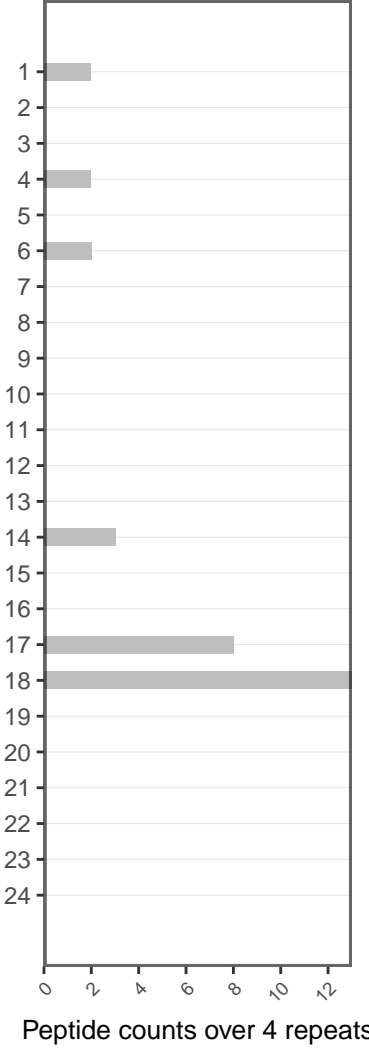
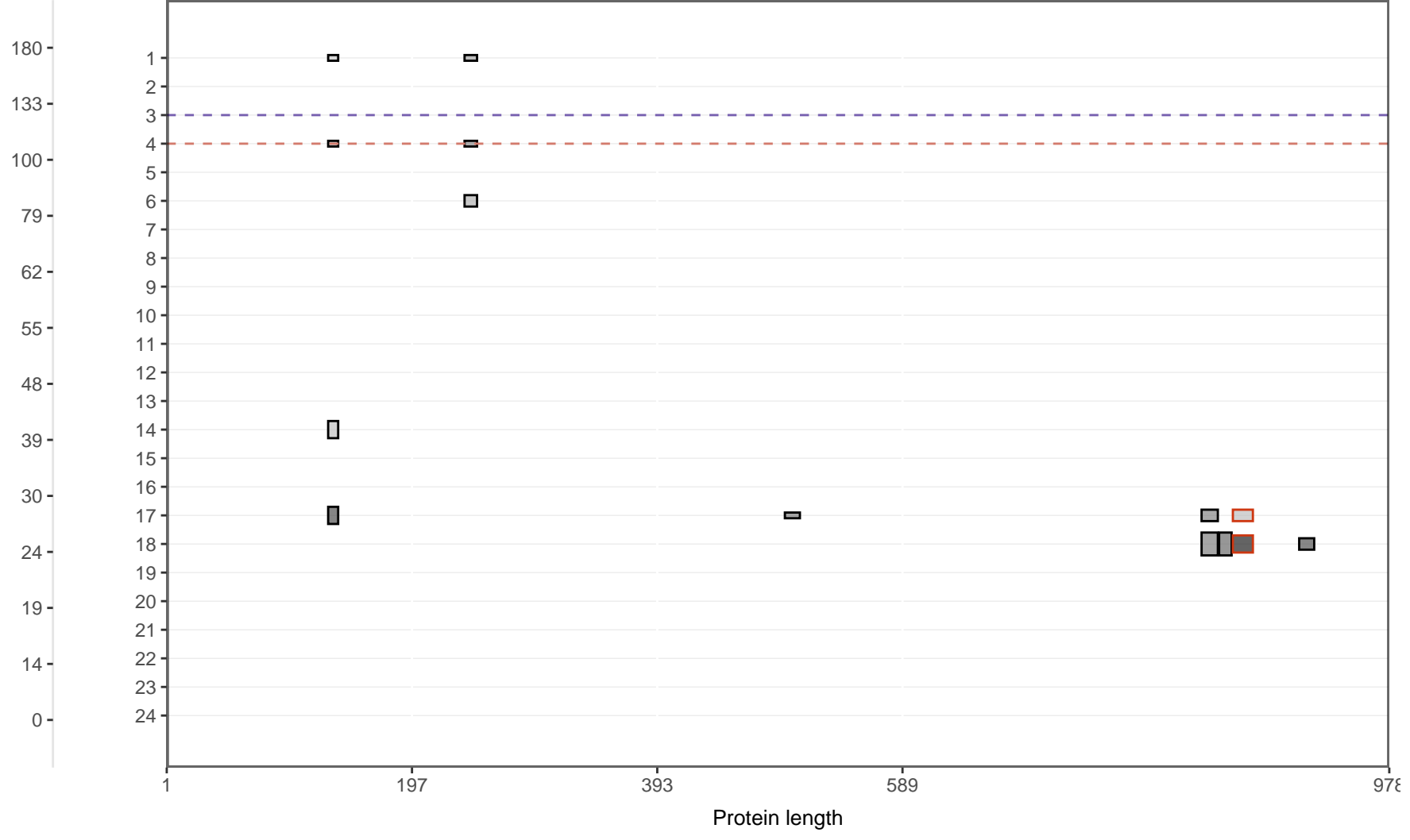
DVYTLGSEVTFVYALDQLMPGDFEIKGLAGRVLNRPKIDYHTGVFASKITPARDGKPVVLELDANKTKPKDTLEVDMAALATGRAPFTQGLGLENVVGTRGFVPIVDERMVDVANGELVPLVYIGDANGKMLLAHAASAGGIVVEHVTGKHLNLHLSIPACFTHPFESMVLGTEPQAREKAEKEGFEISIAKTSFKANTKALAENEGLKALVYRPDNGELGVHFGMHAADLHEASNAALGSRIGDKYVAHAPRTLSEVIDELFKSAWKTRNASRPAEPVAA

NbL16g17940.1 Ion_protease_homolog_1_mitochondrial-like [MW = 108.13 kDa]



Molecular weight

Gel Slice



Pfam Description

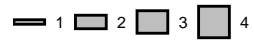
- SP
- Sequon
- TM Domain
- PF00004 ATPase family associated with various cellular activities (AAA)
- PF02190 ATP-dependent protease La (LON) substrate-binding domain
- PF05362 Lon protease (S16) C-terminal proteolytic domain

Protein sequence:

IKTSIGRSIARALNRKFRFSEVGGLESDVAEIKGHRRTYIGAMPGKMGVGLKVGSTANPLVLUDEIKLGRGHAGDPMASMLELLDFEQNAFLDHYLVPIDLSKVLVCTANVEMINPFLDRMEVSGIAGYITDEKMHARDVLEKATRETGGKPEQVEVITNSALLAIENYCREAGVRLNGKGEIKYRRIKALKVIREDDGIEFPQNTVEVDEVKAEGHLESDERKSKGEEIQAGAESANGSSDDDEASENNAEAEAEAGENGMKGSANEDTGLQHTGTEKATESEASKTVNKVV

NbL16g17920.1 ATP-dependent_Clp_protease_proteolytic_subunit_5_chloroplastic-like [MW = 31.63 kDa]

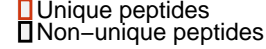
No. of times detected



log(intensity)



Values from



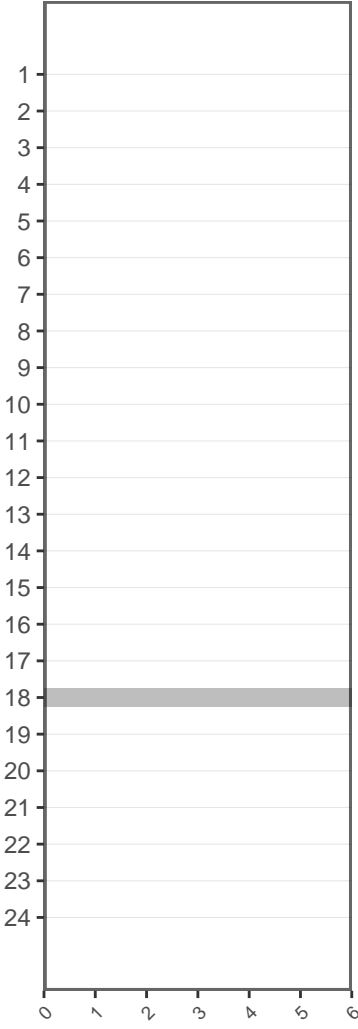
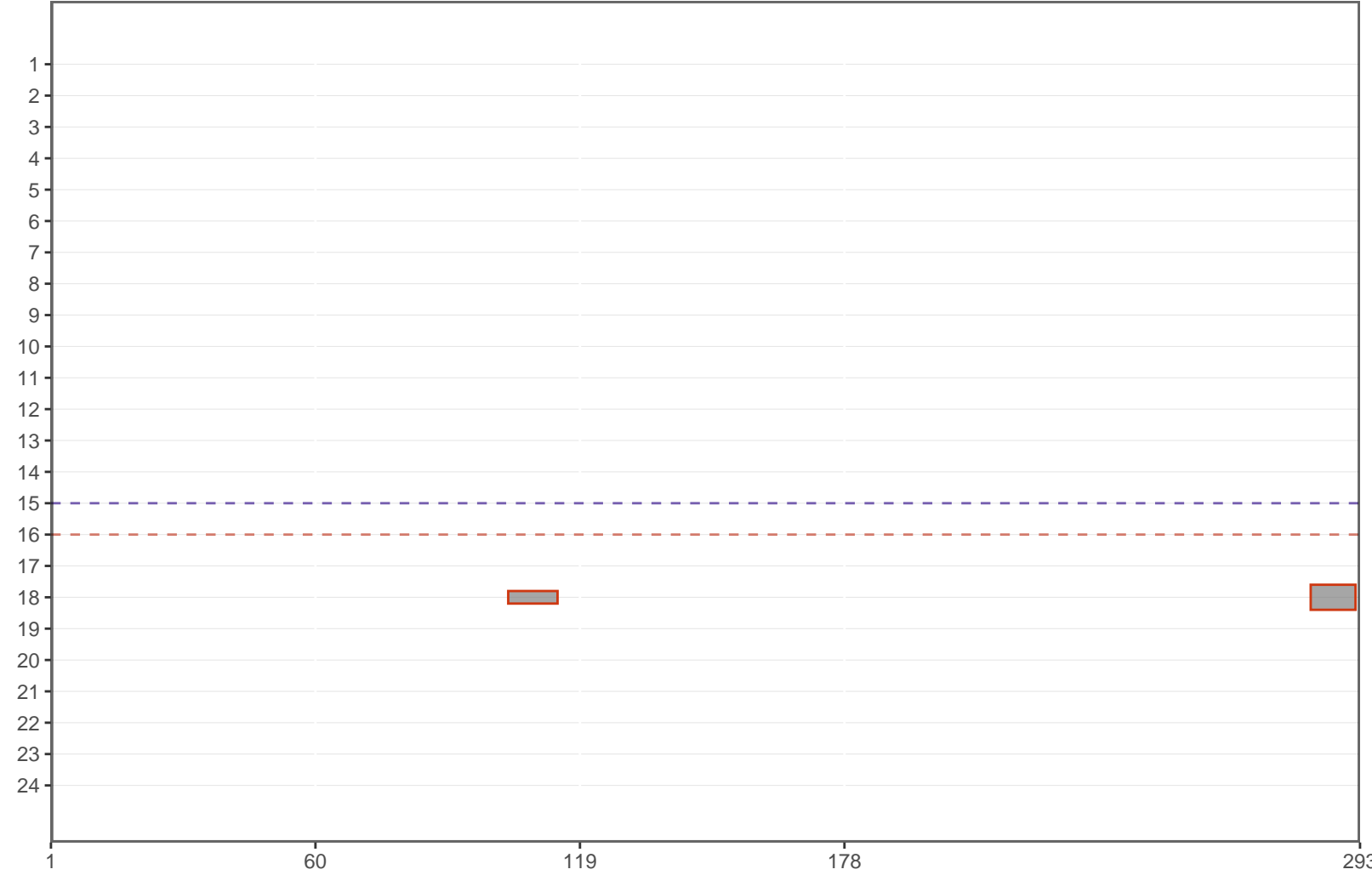
MW indication



Molecular weight

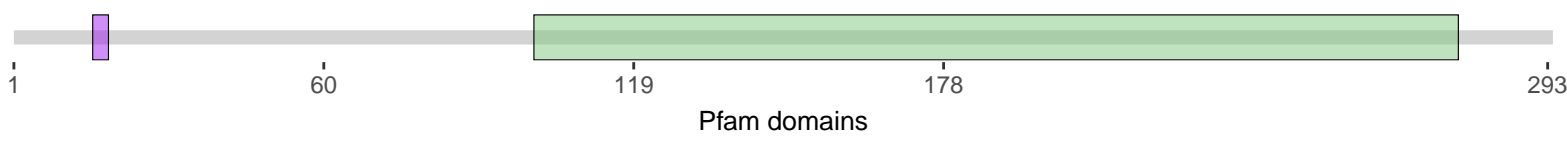


Gel Slice



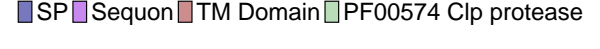
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

..LYLDVDPDKDVIIVYVNSPFGGVTAGMAIFDTRMHRIPDVTGCVGLAASMGAFLLSAGTKGRYSLPNERIMHQPGLGGAGGGDTDDIQANEMLHKHAKINGVLAHYHTGGLEKNGDTRDRDFMSAKEAKEYGLDGVILNFMKALGPIAAAEQ*

NbL16g17830.1 uncharacterized_LOC109210602 [MW = 27.17 kDa]

No. of times detected



log(intensity)



Values from



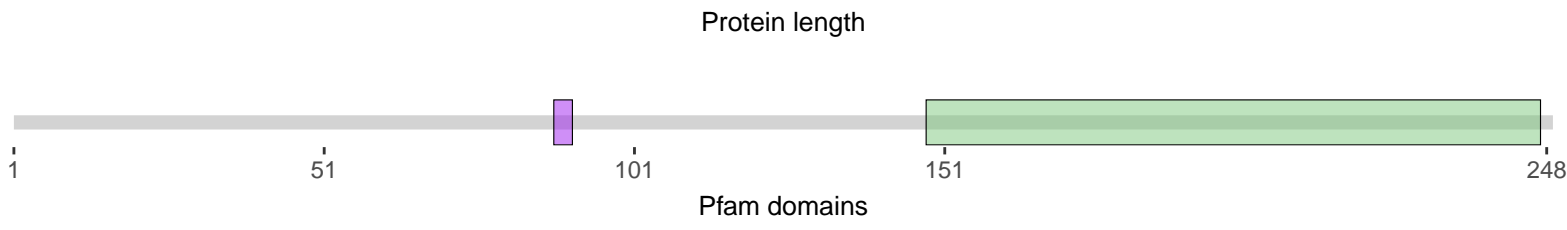
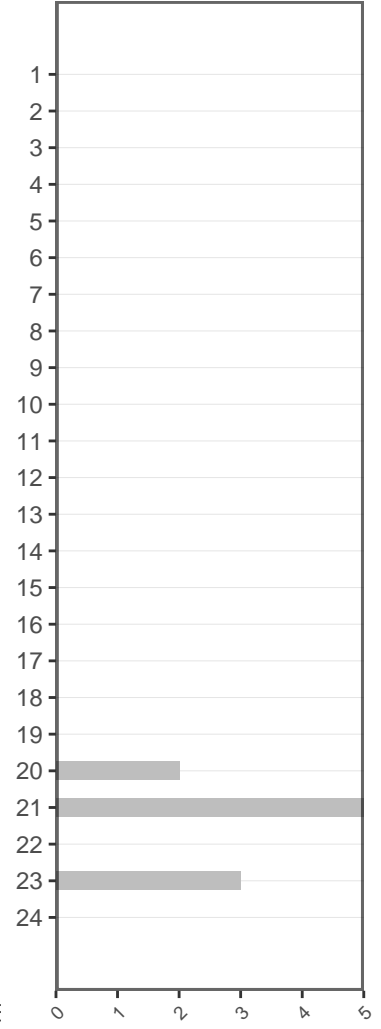
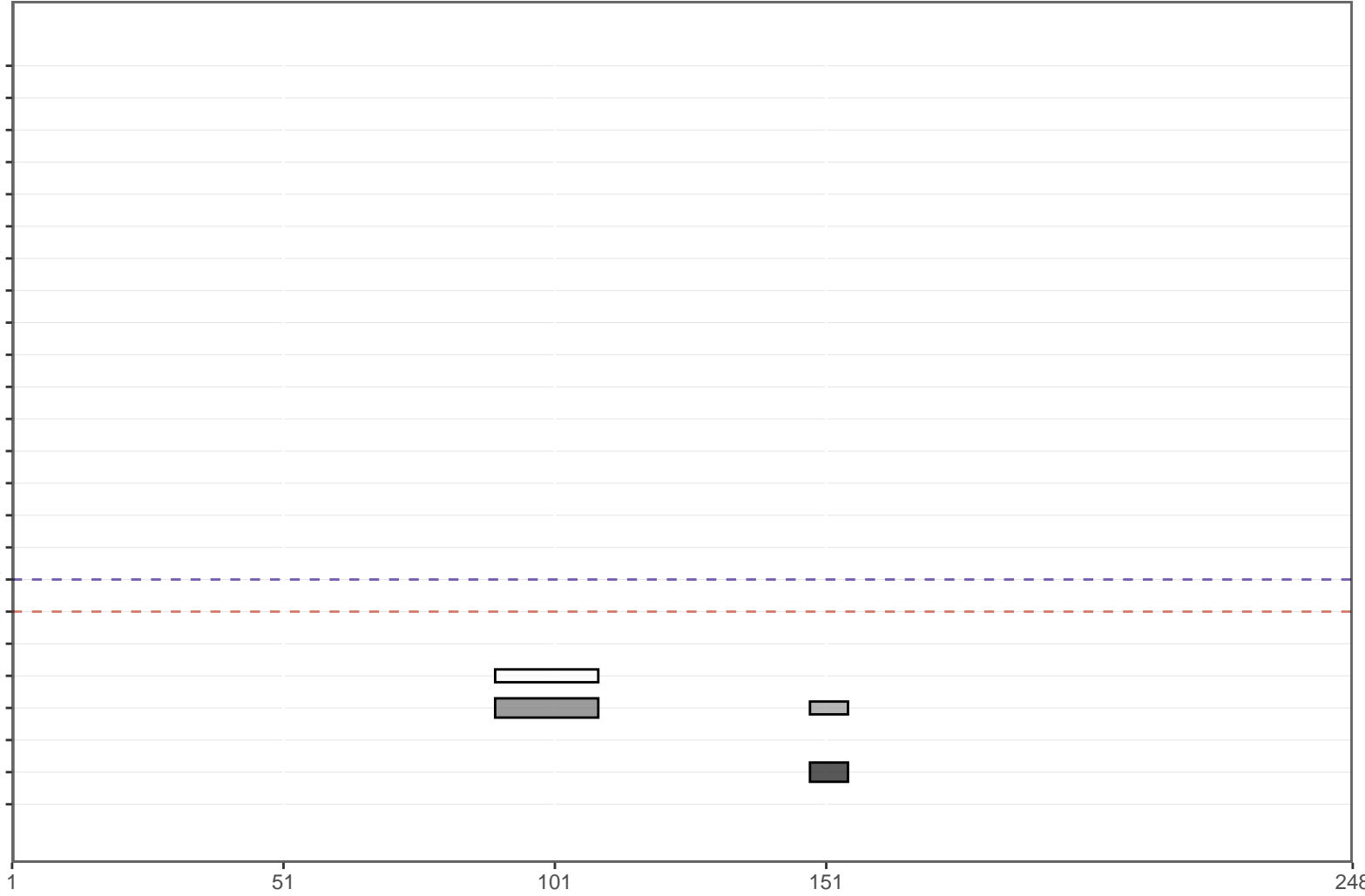
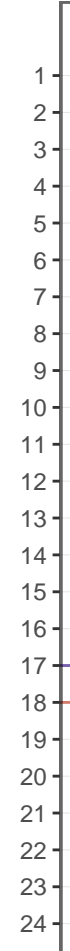
MW indication



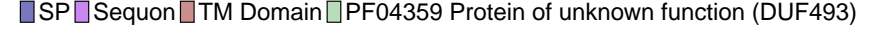
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

SEVSKSEGRVGGTTFNVIIGGTGGDDATNEWALADKKNVNYPTERGFITAIGTGGDFVQAMVAVESVGGPBEAEVDPDPVHDDVDFVGVKRGKLSGGGKVVGVNIGPEVVSSEGVAVVYAMRKKDORMKYFL

NbL16g17670.1 sm-like_protein_LSM36B [MW = 11.89 kDa]

No. of times detected



log(intensity)



Values from



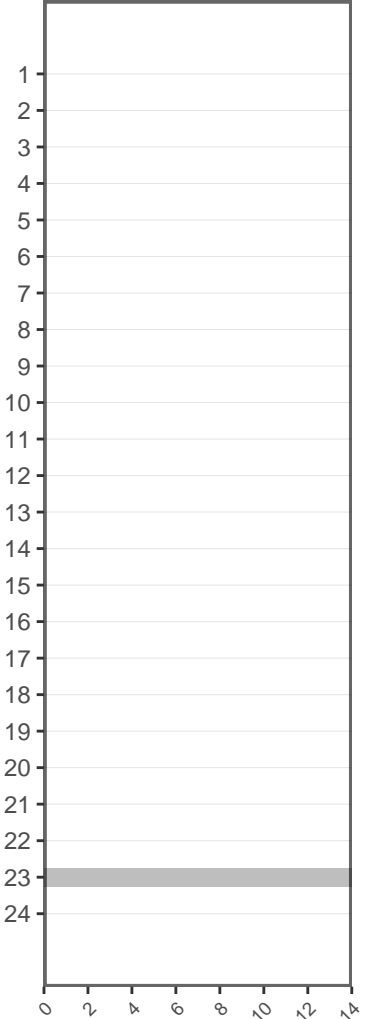
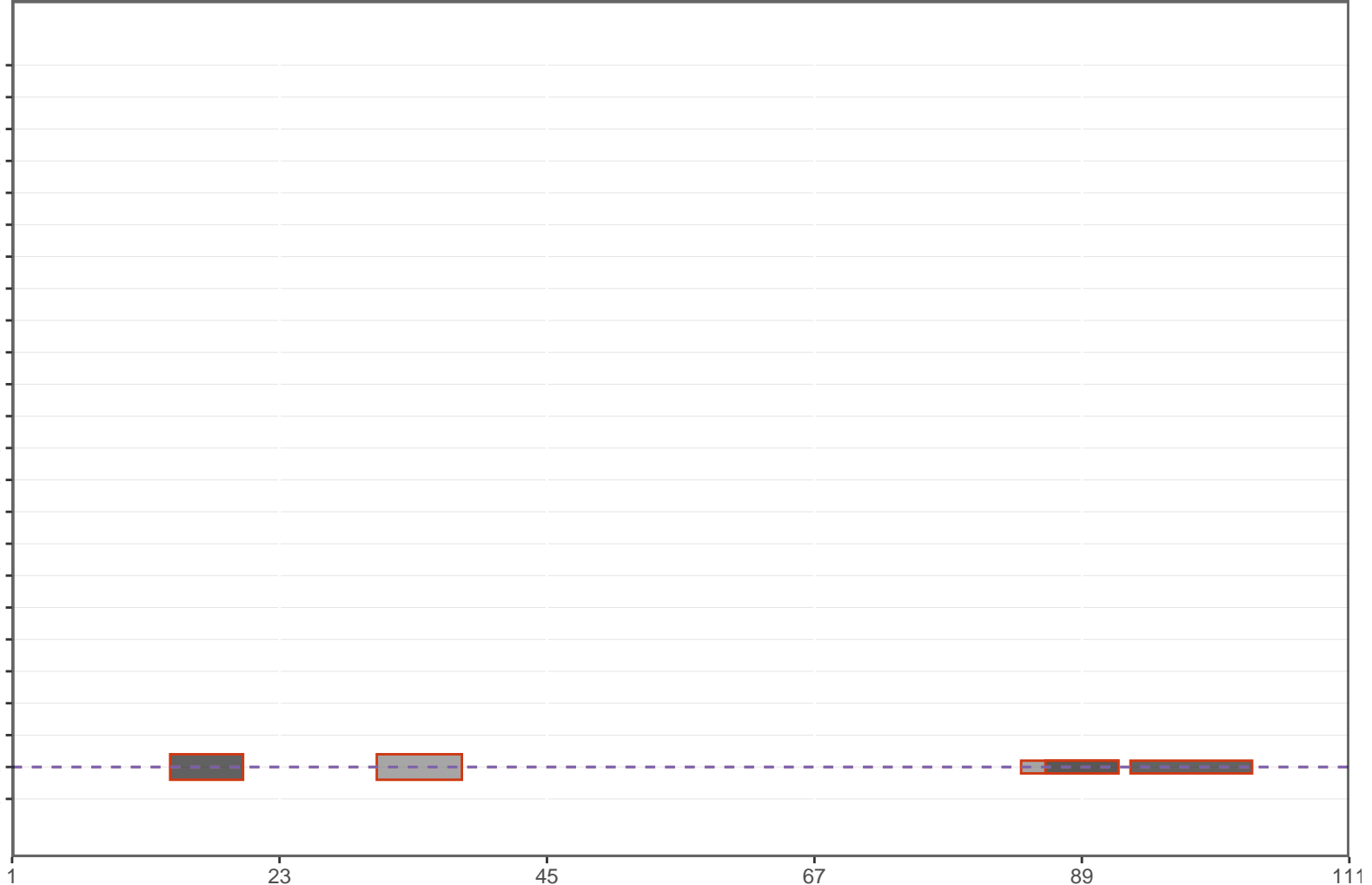
MW indication



Molecular weight



Gel Slice



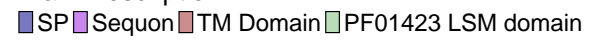
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SATLLSRIHIGFSSSBLAAGDGYMNAMEGTEEVVNGLKNKYGDFAIRGNVNVHSTKRTGEGEA*

NbL16g17620.1 glucan_endo-13-beta-glucosidase_8-like [MW - SP = 51.13 kDa]

No. of times detected



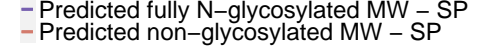
log(intensity)



Values from



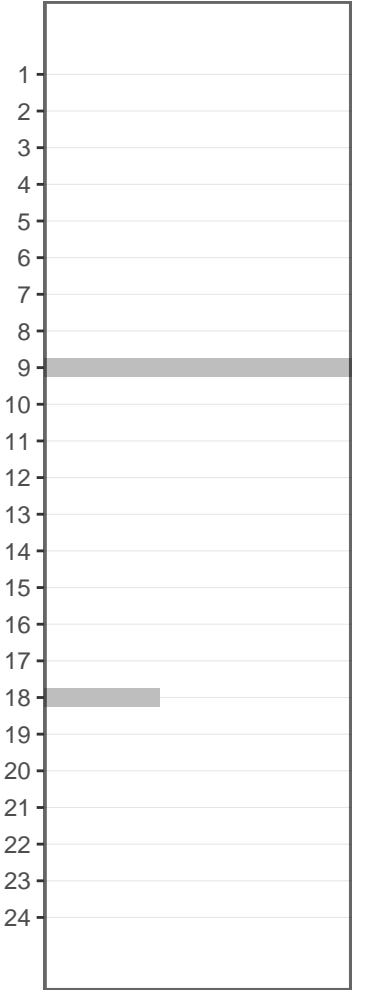
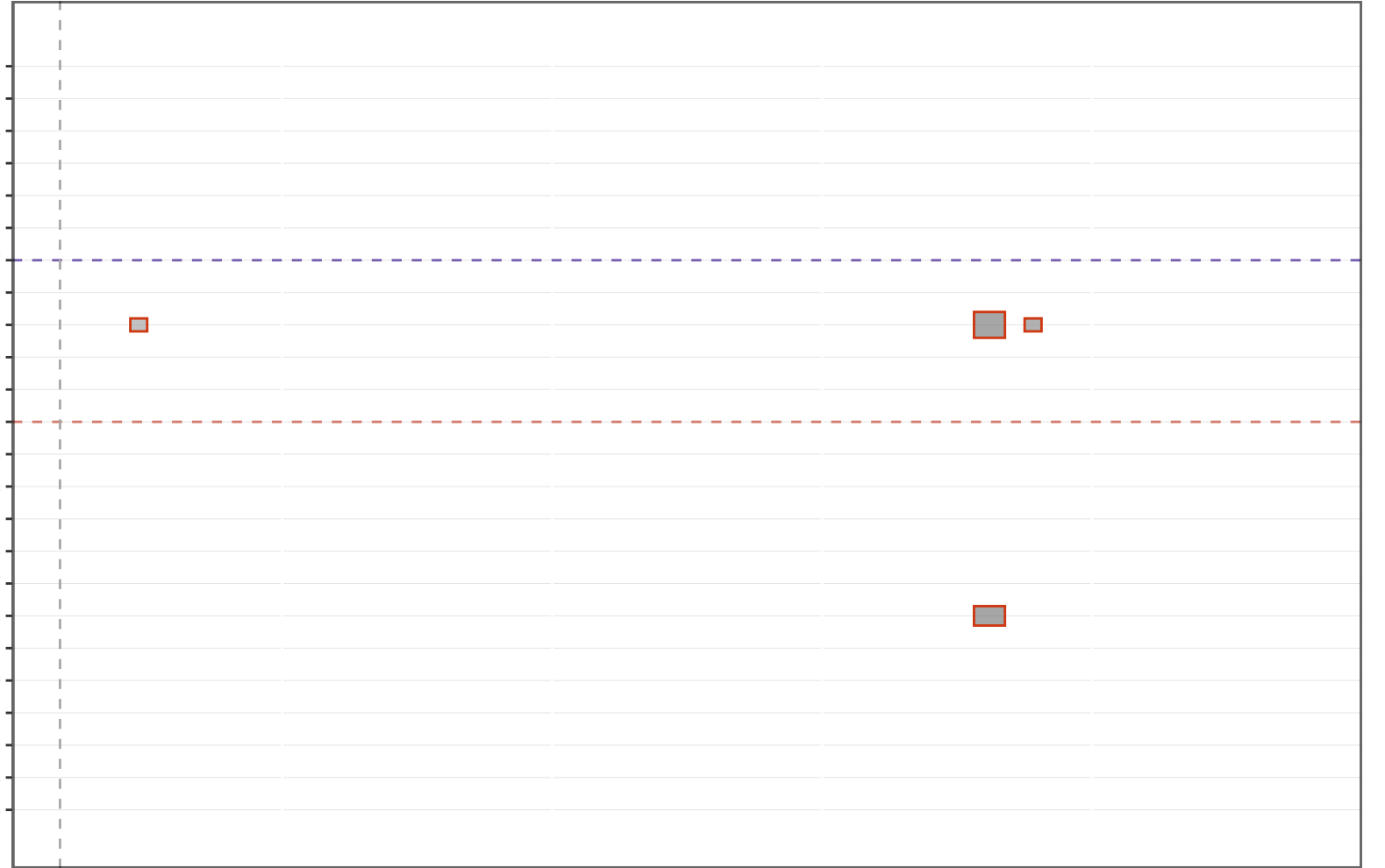
MW indication



Molecular weight



Gel Slice



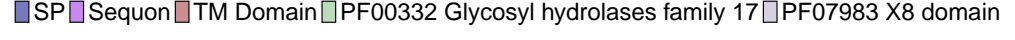
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SNPVDNGVEYTNFDANFDLYSALKAVGVGNMILVGEVGVWPTDGDKNANNSNNAVRFYKGLFSRLAANKGTLPDPQYIEVYLFGLIDEBAKSIAPNFERHWGIFRRYDGGPKFAMDIDGGGDDKHLVAANKVGVLFKRWCKMLNPNANLGLANNIDVACTFSDCTALGVGSSCNLELDANGASVAFNMYGVQVGNLDELSDDFGLAMVTDKNISDGTGCFNFIQTGIVSVSSKVLPGIVLLSGFTFLLL

NbL16g17580.1 glutamate_dehydrogenase_B [MW = 44.52 kDa]

No. of times detected



log(intensity)



Values from



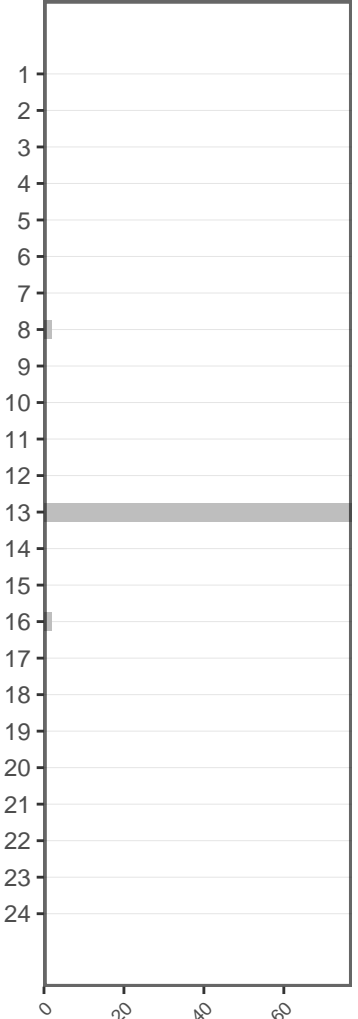
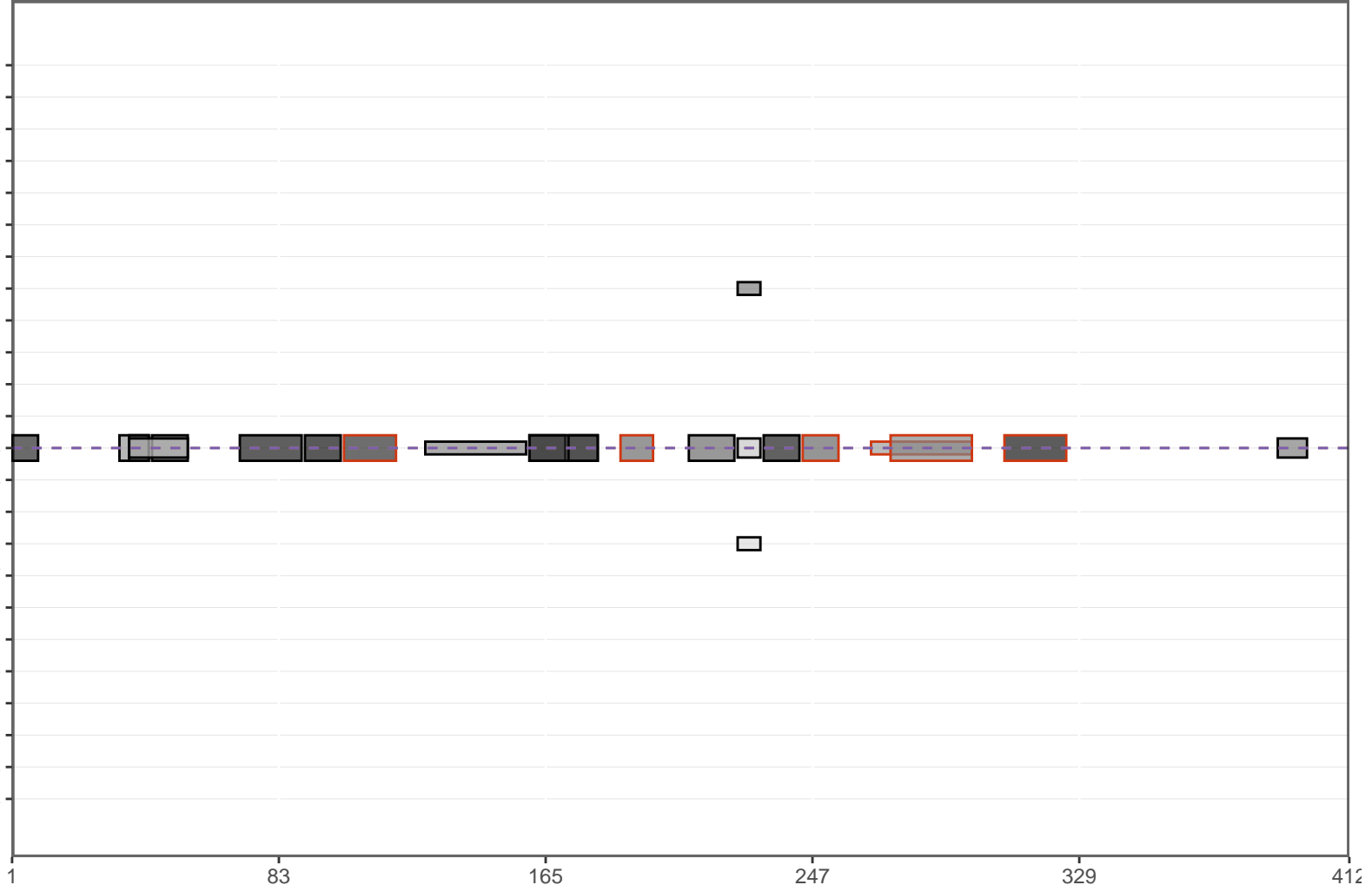
MW indication



Molecular weight

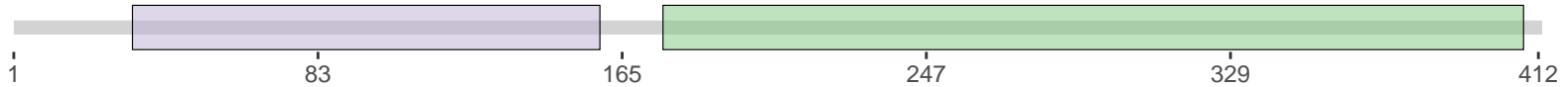


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00208 Glutamate/Leucine/Phenylalanine/Valine dehydrogenase
- PF02812 Glu/Leu/Phe/Val dehydrogenase, dimerisation domain

Protein sequence:

ITALLKEHGKSIAGORFVIGDFGNVGSWAANKLINEGGGKIVVSDITGAKNENGLDASLKHVKENRGVKGFDARFIDPHSLVEDGCVLIPALGGVSRDNRANDKAKYIEAANRPTDEADELAKKGVVLPDYANSGGVTVSYFEWVQNIIGGFMAWDEEKVNAELKTYMIRGFKVDKDMCKTHNGDLRIMGAFTLGVNRRARATVLRGWEA

NbL16g17540.1 40S_ribosomal_protein_S28 [MW = 11.97 kDa]

No. of times detected



log(intensity)



Values from



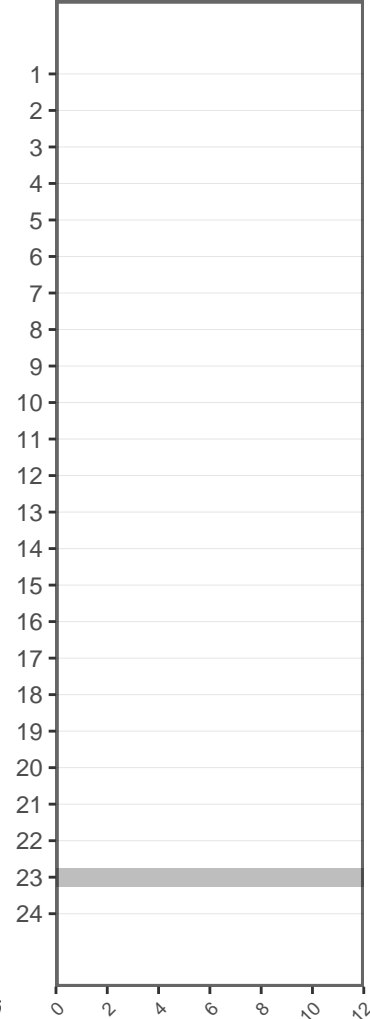
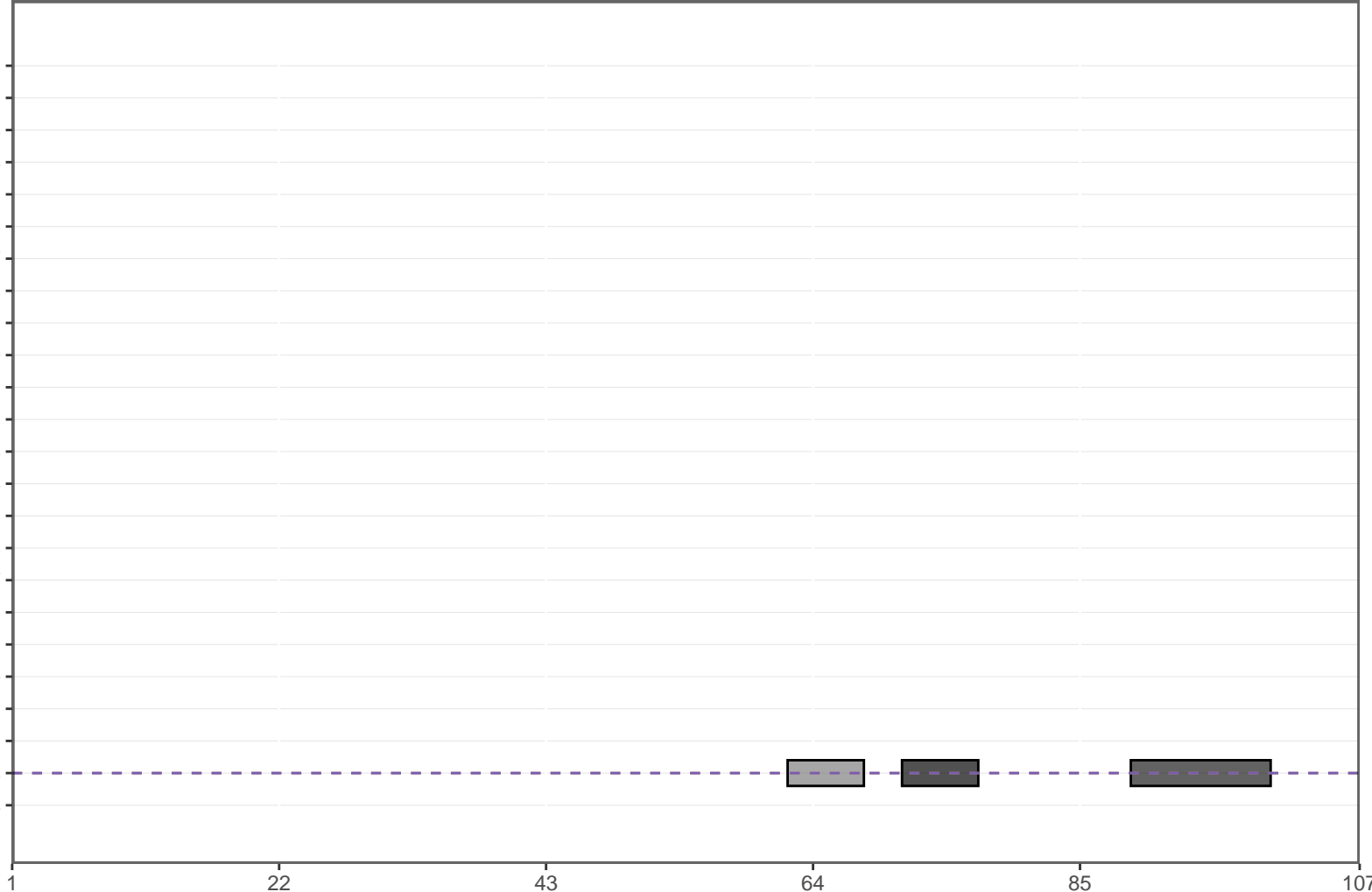
MW indication



Molecular weight

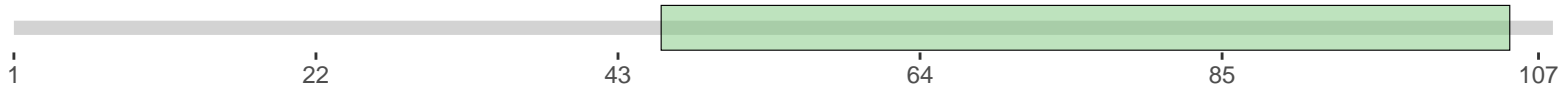


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

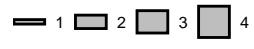


Protein sequence:

IESATKHAIIVKVMGRGTGSRGGVTVQVWVFLDDGNRFIMRNWVKGPIREGDVLTLLEGEREARLR*

NbL16g17380.1 protein_trichome_birefringence-like [MW = 76.6 kDa]

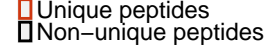
No. of times detected



log(intensity)



Values from



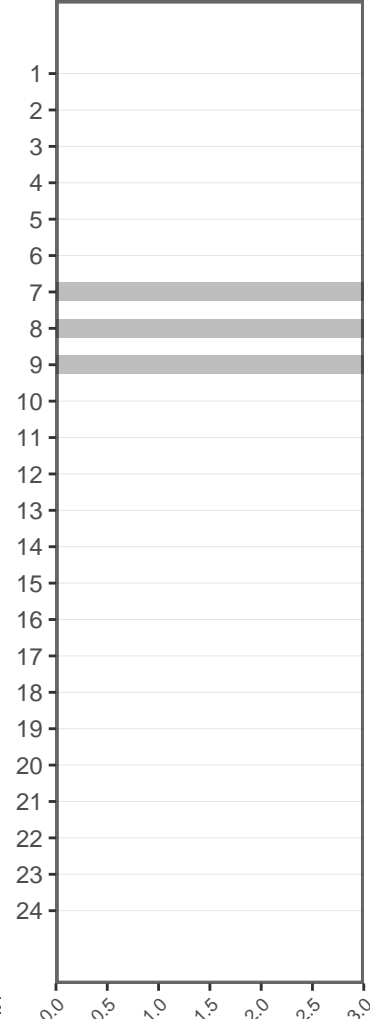
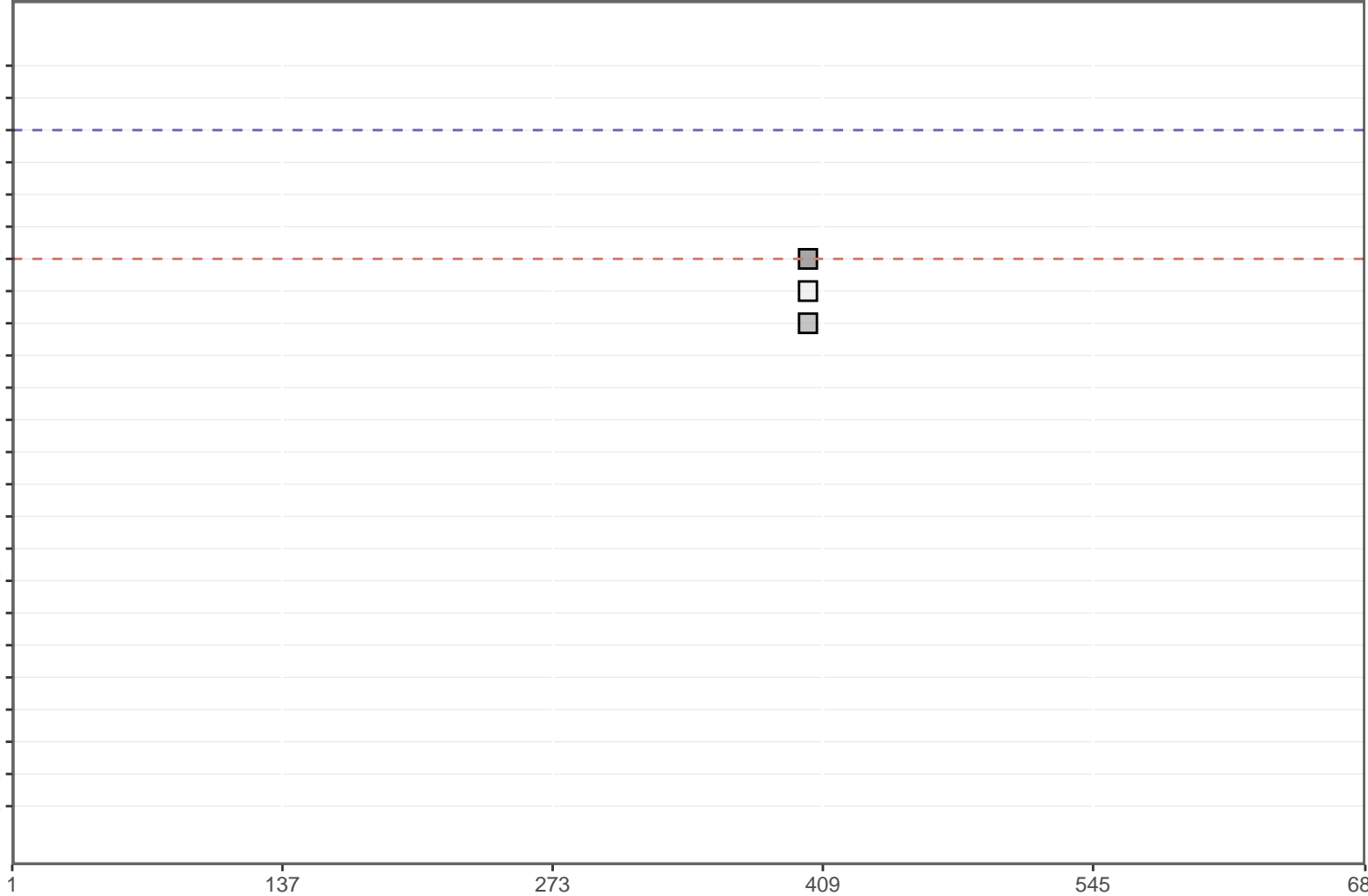
MW indication



Molecular weight

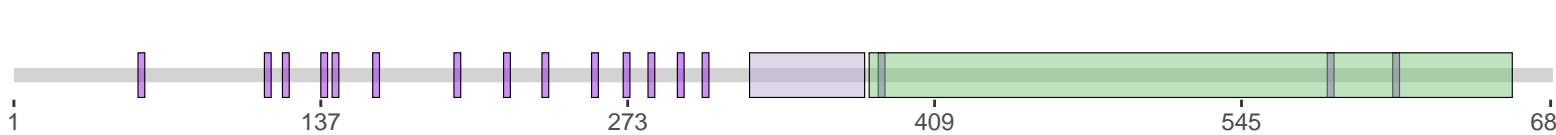


Gel Slice



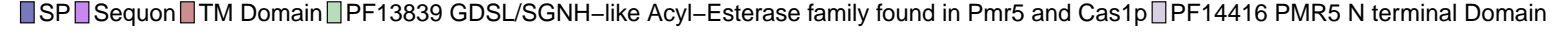
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

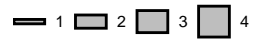


Protein sequence:

DFDDKWKYKDESYPKPKPGGGSLDEGFNGLNGRPSDNYKMKWPKNACTLPRLNGTHMLELLRGRKRVFVGDGLNRNMWESLVGLRNSVEDDKKYYEEFGRHHFRTEASYSFLFEEVNGRVEFFVSPFLVGEVWEFADKKGAKKELRLDLIGOSADGYSADILFNGHWWTHEKTSLSGKDYVQEGSHVYSELDVLEAFRKALTYWGRWIDSHVNHKTFVLRFGYSASHFSGGGWNSGGACDHETEPKNNTYLPYPKMNVLERVLRGDMETQVSYLVNTRV

NbL16g17260.1 DNA-directed_RNA_polymerase_III_subunit_2 [MW = 129.89 kDa]

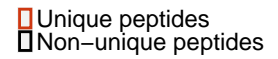
No. of times detected



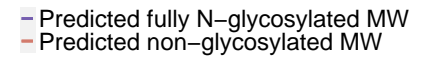
log(intensity)



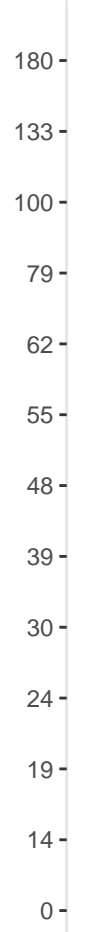
Values from



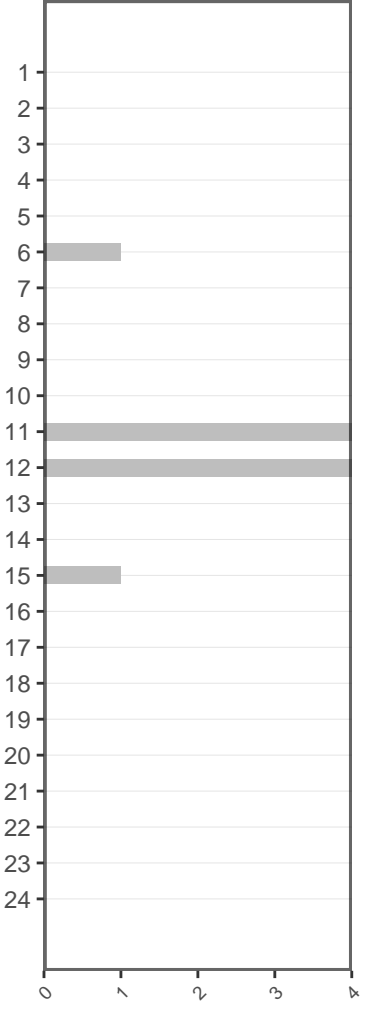
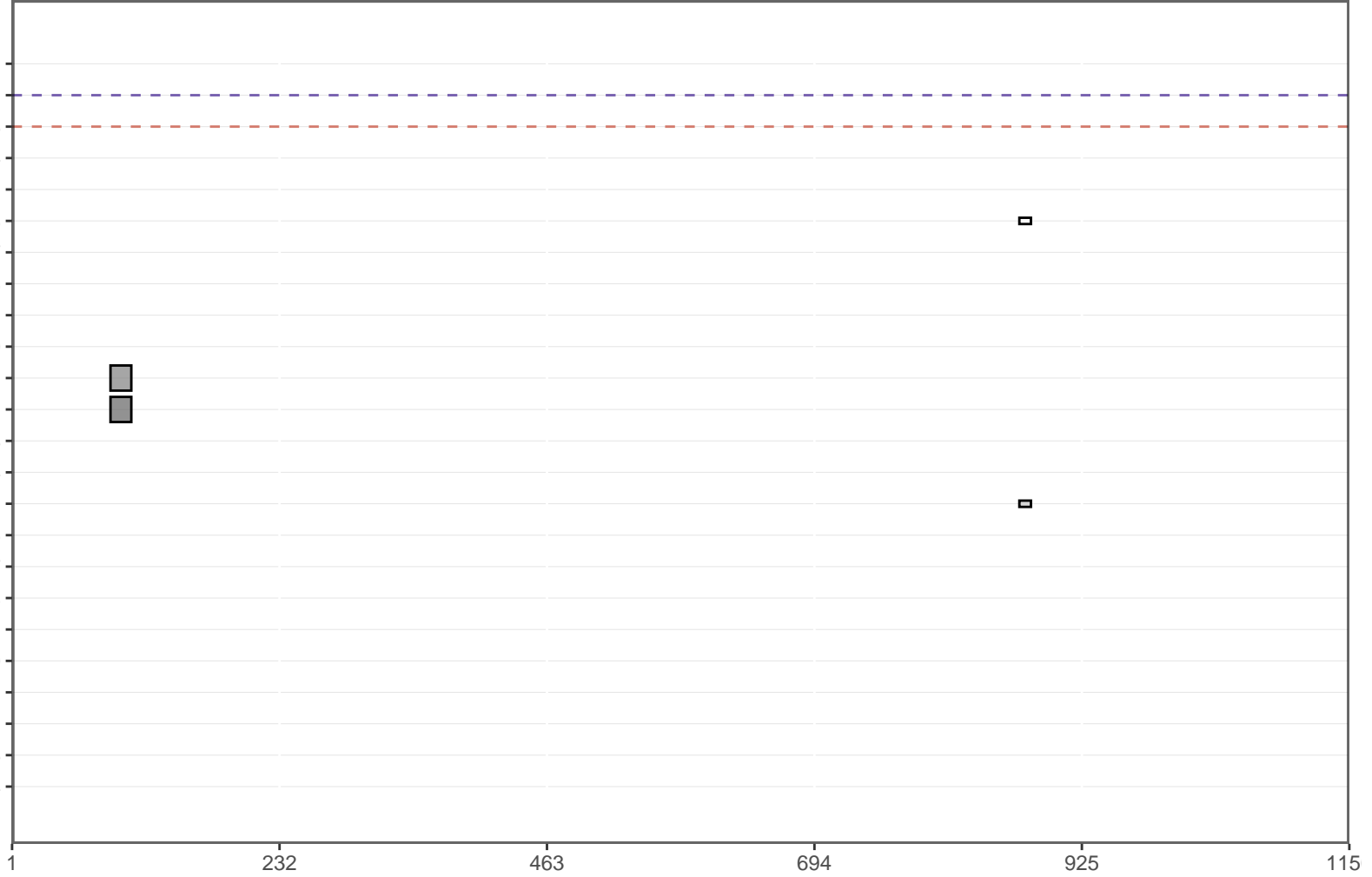
MW indication



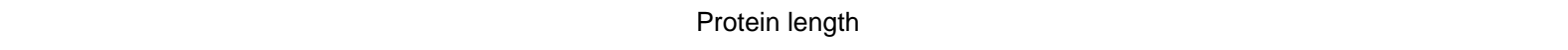
Molecular weight



Gel Slice

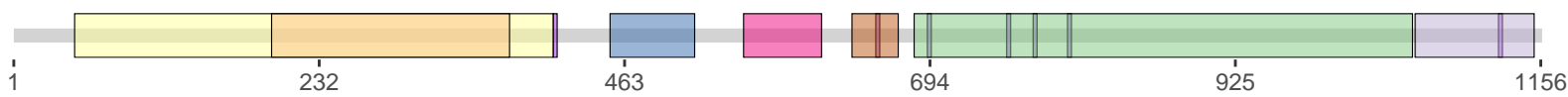


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

- SP
- TM Domain
- PF04560 RNA polymerase Rpb2, domain 7
- PF04563 RNA polymerase beta subunit
- PF04566 RNA polymerase Rpb2, domain 4
- Sequon
- PF00562 RNA polymerase Rpb2, domain 6
- PF04561 RNA polymerase Rpb2, domain 2
- PF04565 RNA polymerase Rpb2, domain 3
- PF04567 RNA polymerase Rpb2, domain 5

Protein sequence:

IPHRFANAMRLRRGGKVFGEFISFVNEKGRGVYIADDGGRRVCRPLVIADKGVSRIKEGHMKELRDGVRNFDLFRDGLIEYLDVNEENNLIAYEKEATPETHIEIEPFTLGVCGALIPYFPHNGSPRINTYGCAMKQKAMGNIAVNLRSMDTLLVLYPQRPLLTTRTIELVYDKLGAAGNATVAWMEYSGYDIEDAIAMKSLDRGFGRGVIMKMYSATLKYENNTSDRIKPGRGGVEAERMQLDEDLGASPGIEIRPHDIVNKEEPTVTRTPVSSPMSLPSDAY

NbL16g16760.1 glutamine_synthetase_chloroplastic [MW = 47.51 kDa]

No. of times detected



log(intensity)



Values from



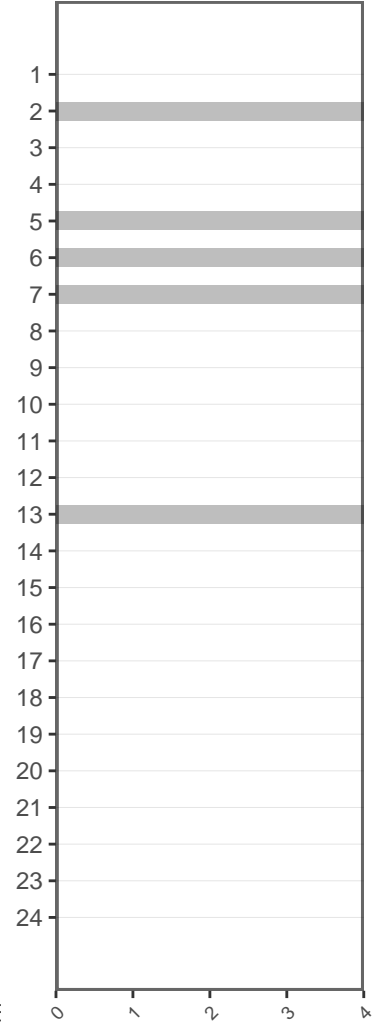
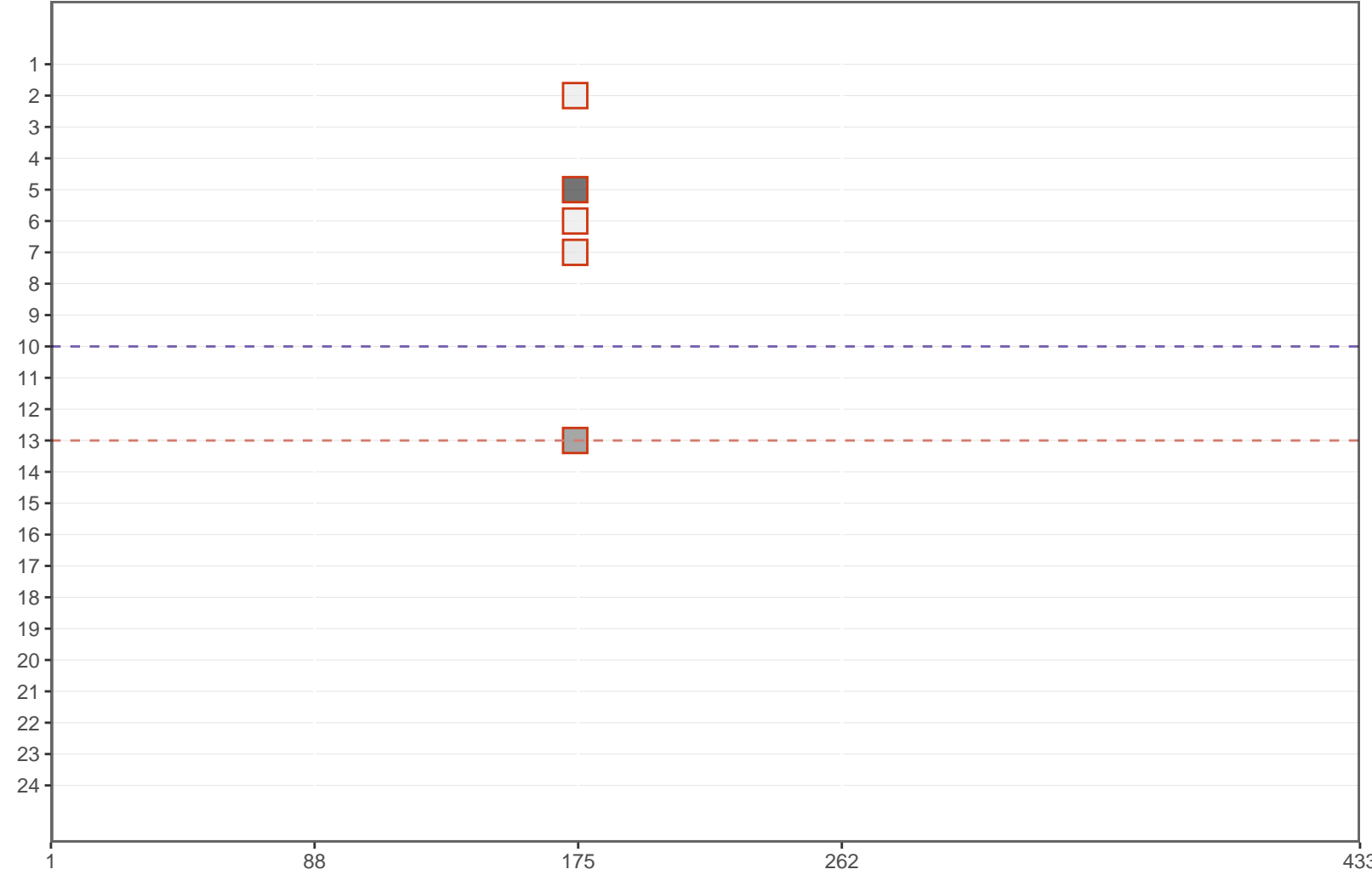
MW indication



Molecular weight

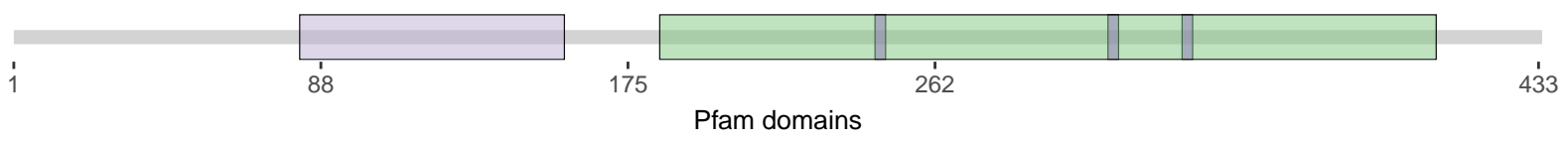


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

WVPLGGYPOGPPHYGGAGADKSGFRDISDAHYKAGLYAGINISGTNGEVMPPGQWFEFQVSPVGVIEAGDHWGARVLERITEGAGVVLSDLPKPIEGDNGAGCHTNYSTLSMREEGGFVKKKALNLSLRHKEHSBAYGEGNERRLTGKHETASIDKFSWGVANRGCASIRVGRDTEKGGKGLYLEDKRRPASNMDPVVVTGLLAETFLIWEPTLEAEALAGKLANV

NbL16g16660.1 UPF0613_protein_PB24D3.06c [MW = 37.07 kDa]

No. of times detected



log(intensity)



Values from



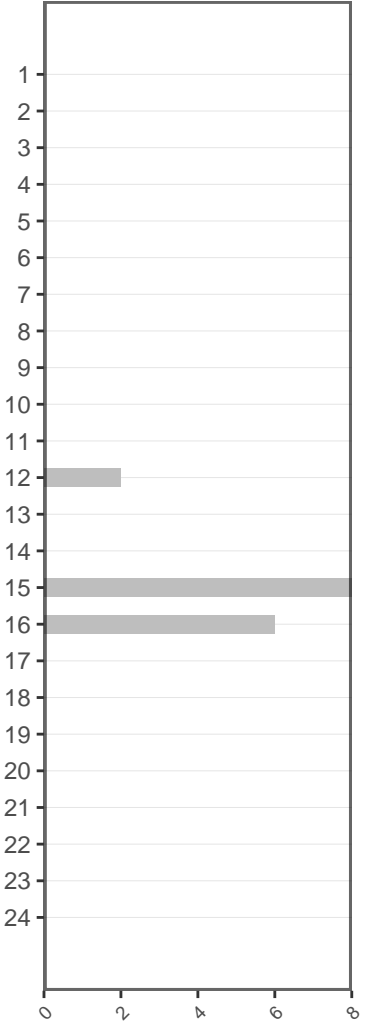
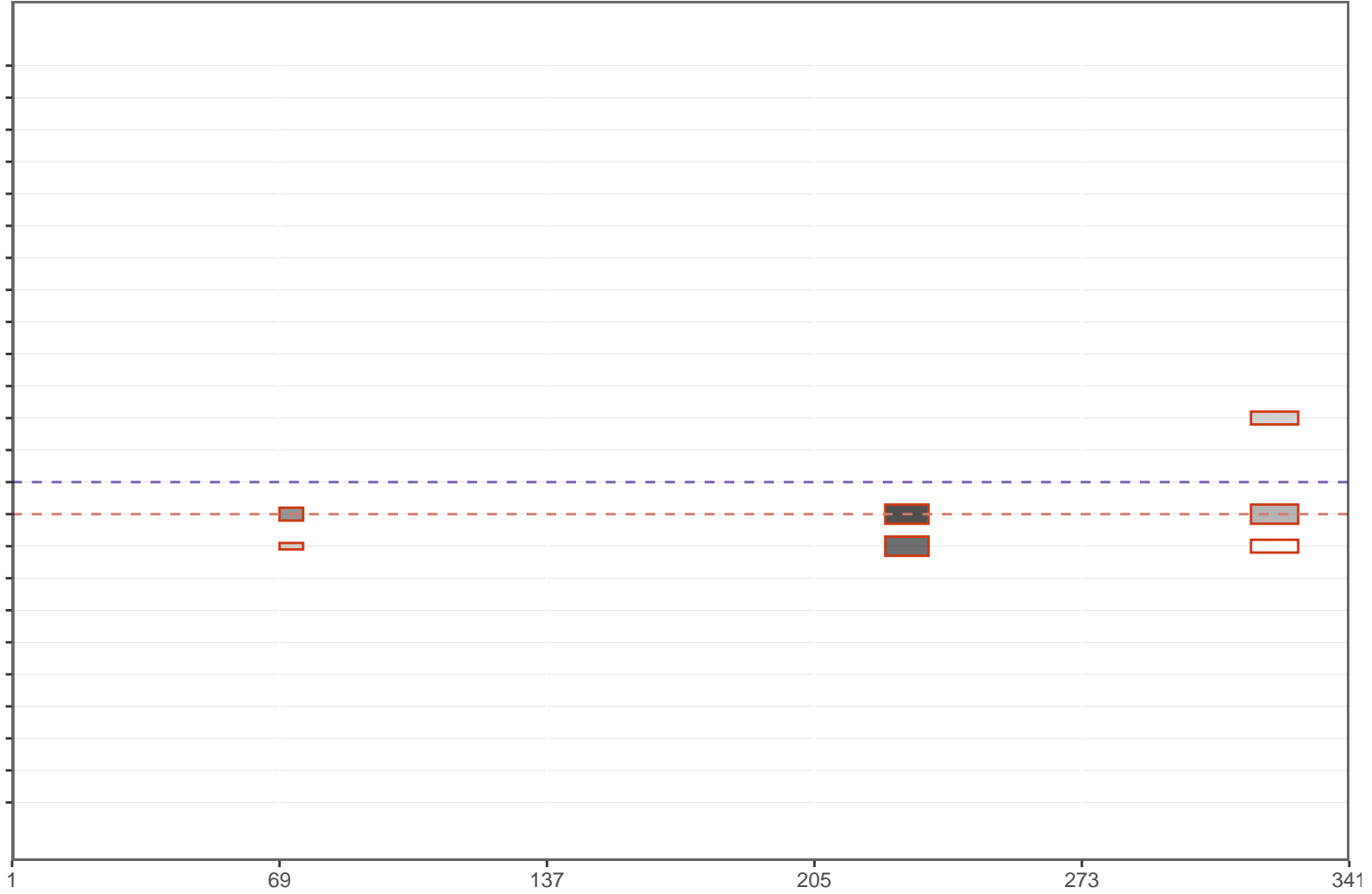
MW indication



Molecular weight

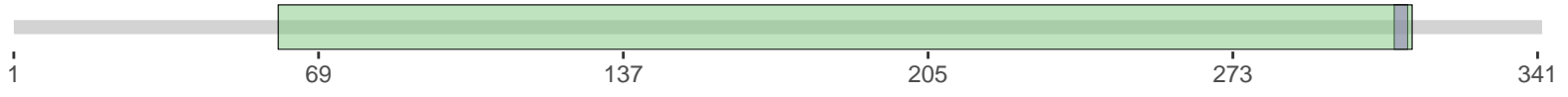


Gel Slice



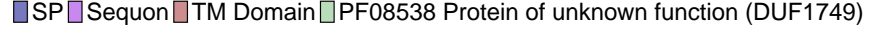
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

STGGCDIYYMRTNAAGSRAVRAALGAPVSDREYKATLPDTASMDLANSMISEGRESELMPRDANPAPPTAFRRHSLGAYNGEDDLFSDDFDLQKRLGHMSNTPGQVIFSMGDEYVDPVYDKKALVDRLGRAMGGAERKVEIEHGNHSLNRRVAEAEIMFVWRREGPFGWDDPWN

NbL16g16530.1 basic_7S_globulin-like [MW - SP = 44.81 kDa]

No. of times detected



log(intensity)



Values from



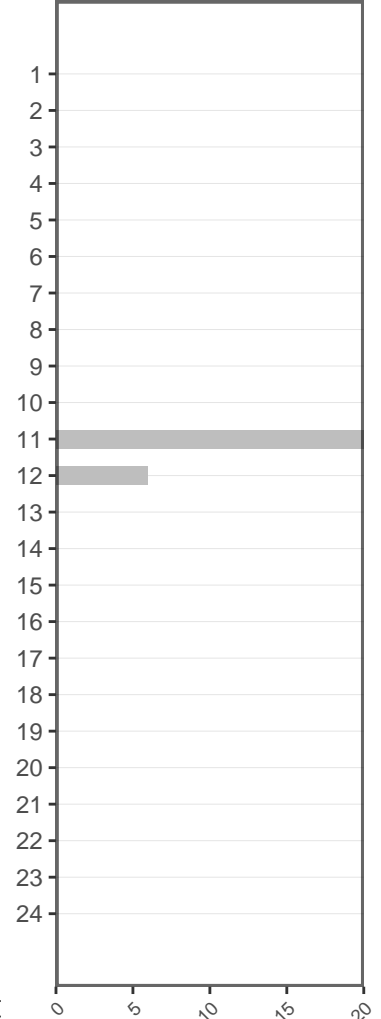
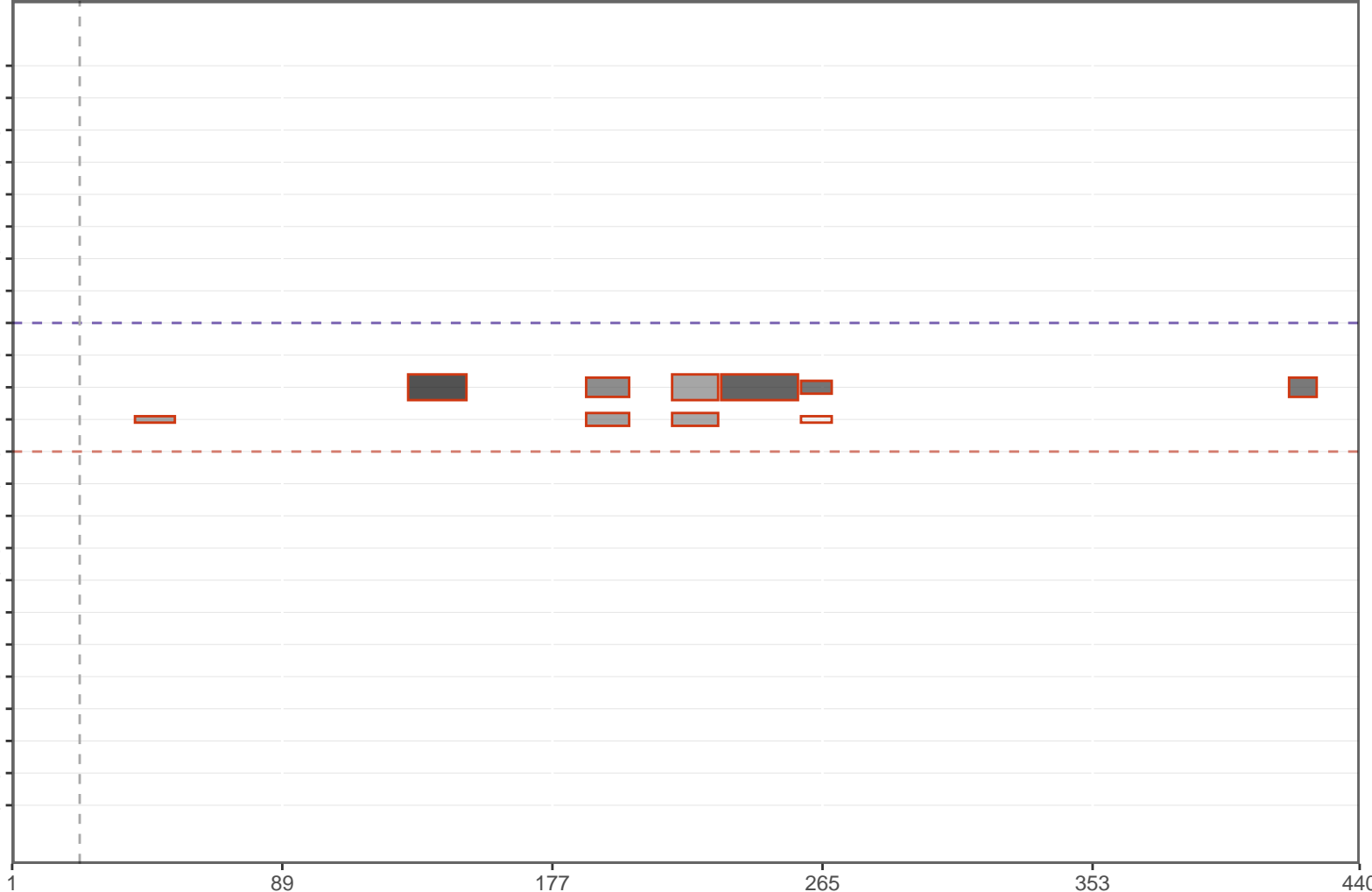
MW indication



Molecular weight



Gel Slice

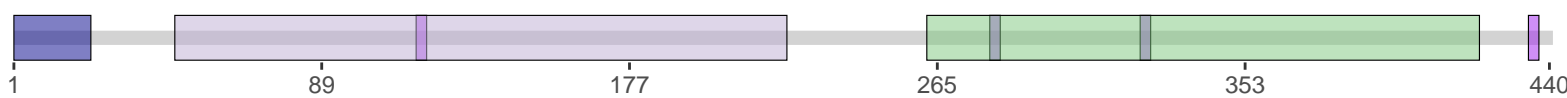


Protein length

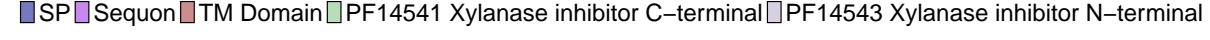


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

FAVCLSSSTNSKGVVAFGGDGPYFLPNREFANDFEYTPFLFINPVGTAFSAPGSRPESEYFQVYKSIKNEKVPINTLLSDIDNGGVGKTKISTVNPVYLETSTVNPVAVTFFVKELVNTIRVAGVAFRAFDFSRNIASTRVGVAVPSIDVLAQENEFVRFVIGANSIMVGVSENVLGLGFVGGVSPRTSIVVGGYTEDNLLGFDLARGLGFTSSILFRGTTCANFNFTSIA*

NbL16g16480.1 ammonium_transporter_1_member_3 [MW = 50.05 kDa]

No. of times detected



log(intensity)



Values from



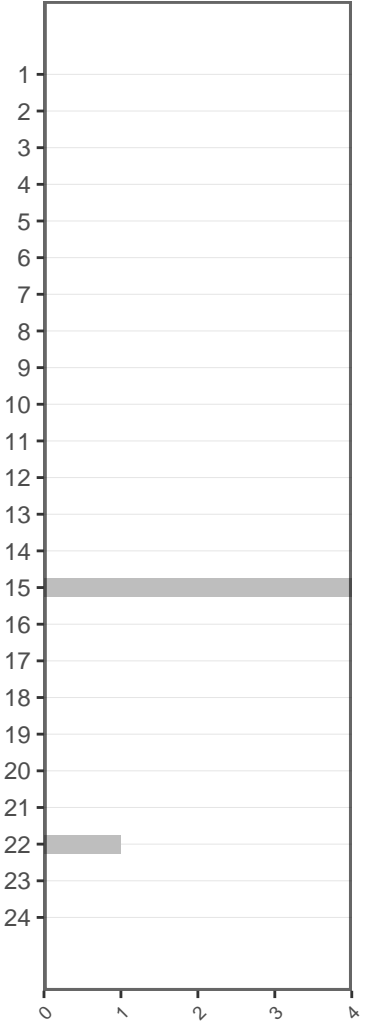
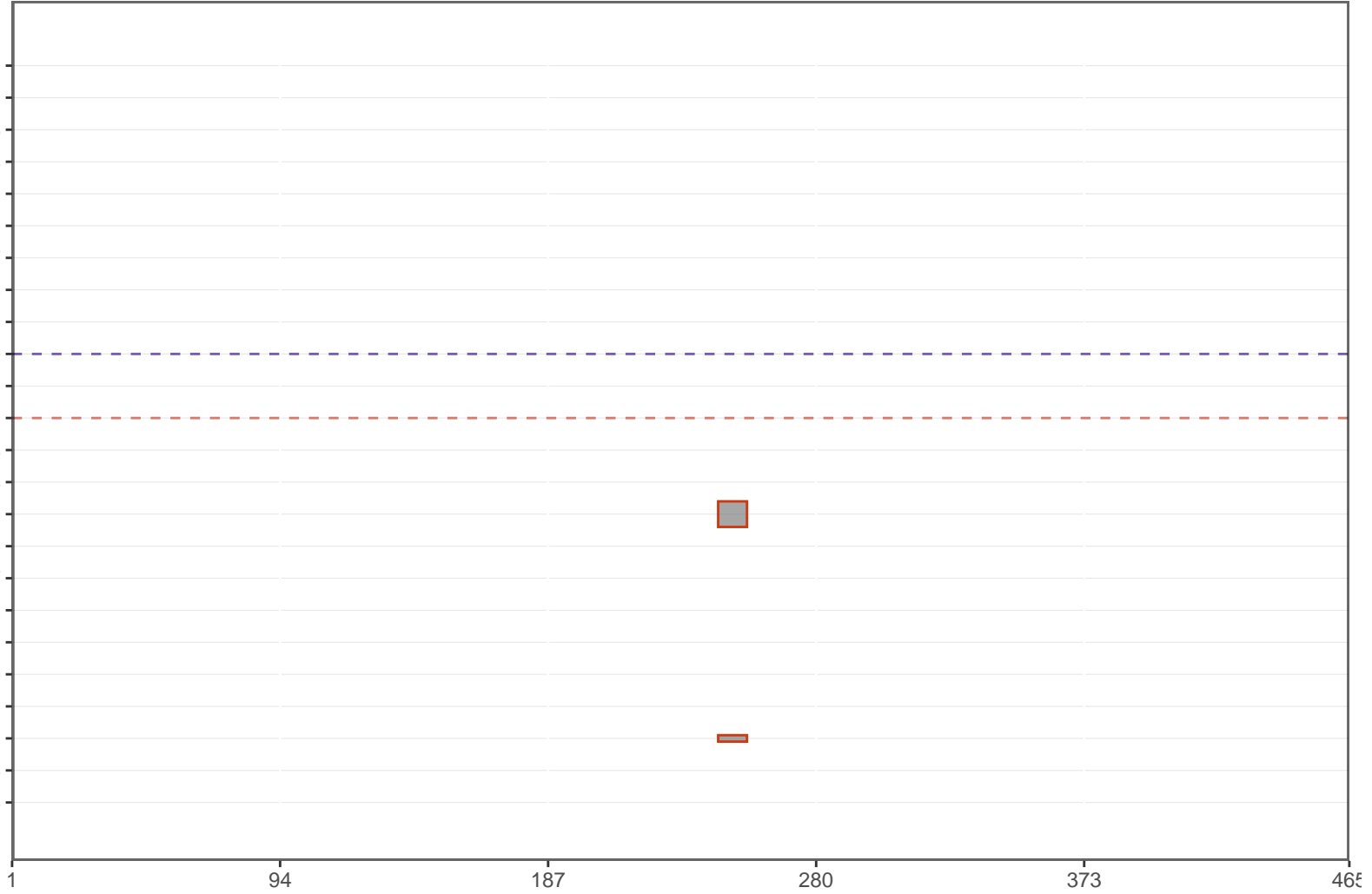
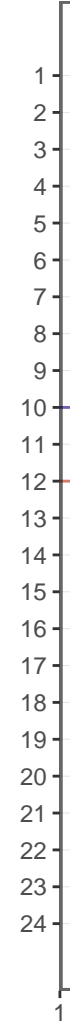
MW indication



Molecular weight



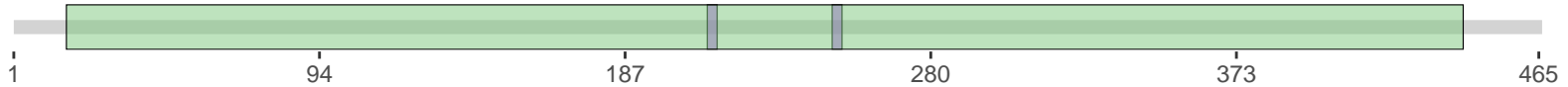
Gel Slice



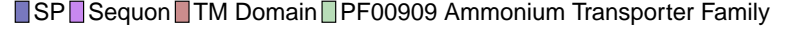
Protein length



Pfam domains



Pfam Description



Protein sequence:

LLLVFGWFGFNPGEFDKLVPPFNKIDQGNWTSVGRATVTTLAGSTAGVTLFGRRLVGHVWDATDVCNGLGGFVMTSGGSVEFVPAWAVCGFCAWVLLGLNLAKLKFDDPLEAAGLHGCCGAWGLIFFTGLFAKEEFLVGVNKGKTVWRVRYGLLGGGWGLFGAQVVELLSVAVVSLTMGPLFTLQKLGILRITADEEAVGLDISHGGWYEAANGDEESGPRFYGEYLRMQHQS

NbL16g16470.1 stem-specific_protein_TSJT1-like [MW = 28.11 kDa]

No. of times detected



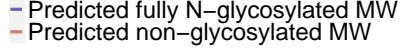
log(intensity)



Values from



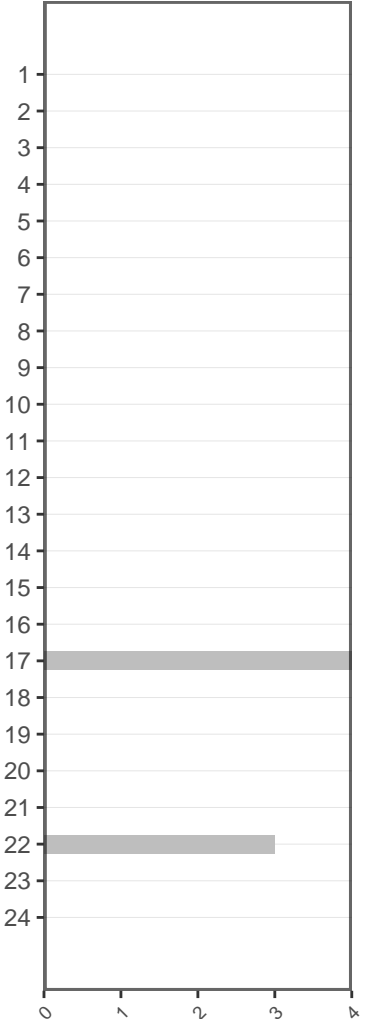
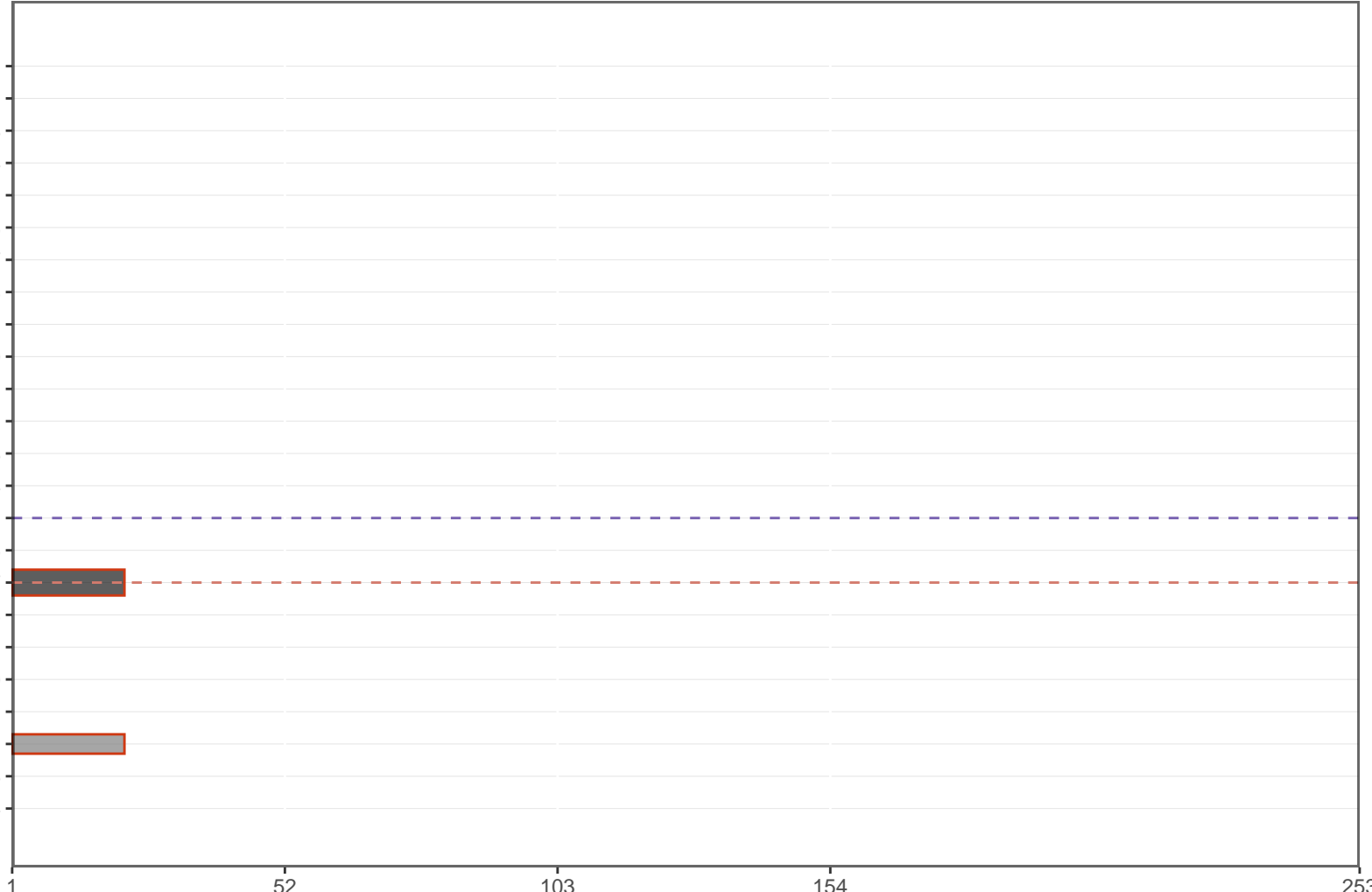
MW indication



Molecular weight



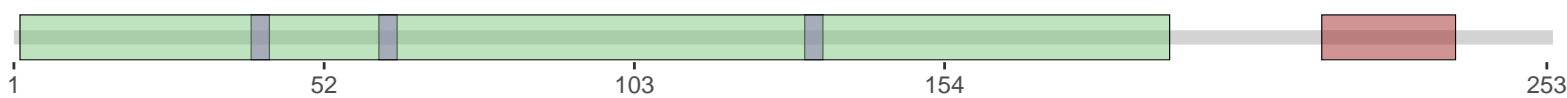
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

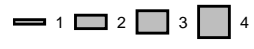


Protein sequence:

ALRDRAFYPPNHYVGHLEGNFTTFVFDKSTSLFVTDGIVGKIPVWGGITADGYVAFANDADLLKAGCGKSLASFPQGWFDRLFFFRGSDLSGGTREGIMLVFVLYLFLNSISFVCFIRVFLYHWRIEKLREPQK

NbL16g16450.1 ATP-dependent_(S)-NAD(P)H-hydrate_dehydratase [MW = 34.29 kDa]

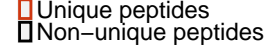
No. of times detected



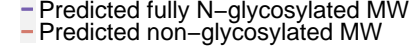
log(intensity)



Values from



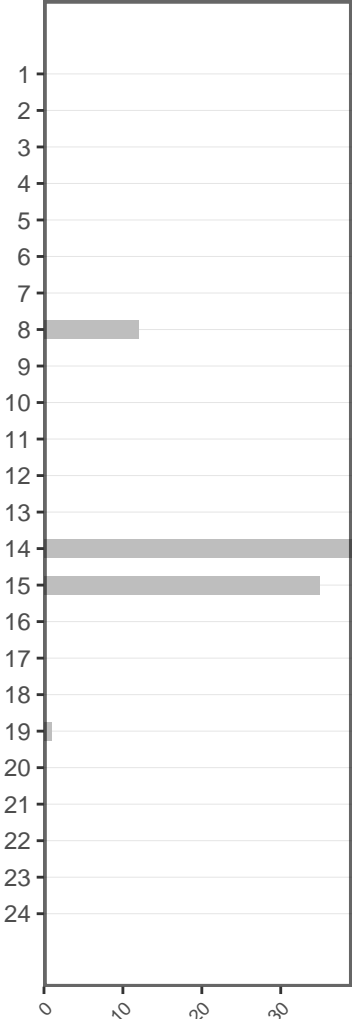
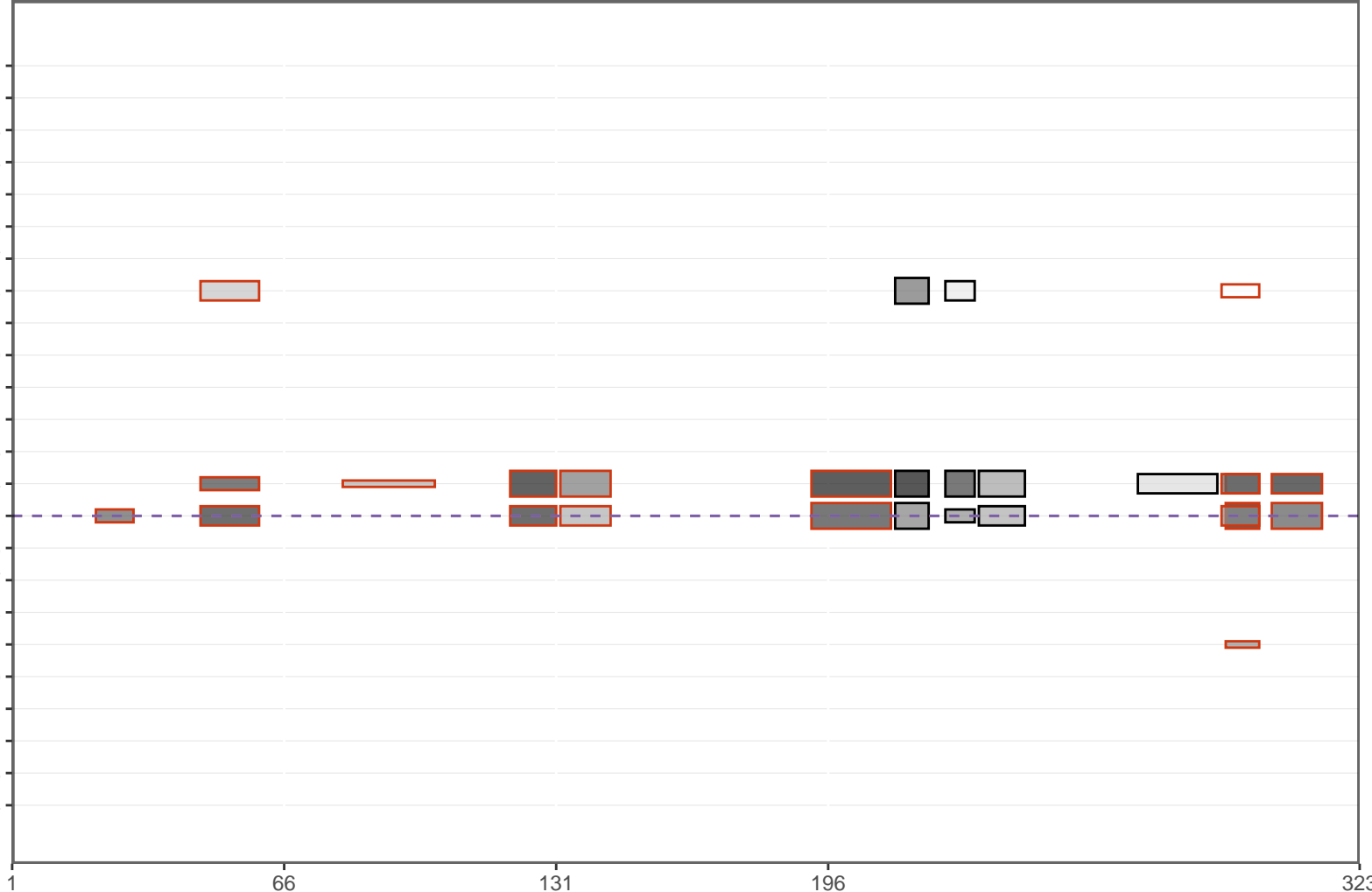
MW indication



Molecular weight

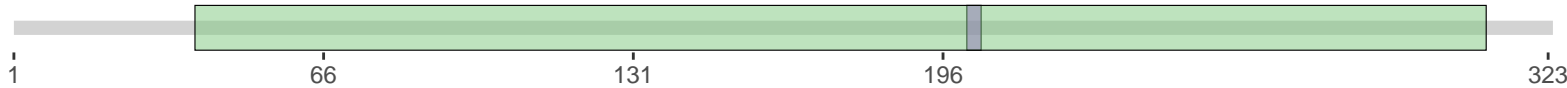


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

INPMMVDDGDLFLVNNGLKLVGGYFLAVLTPNNEVYKRLVQKLVNSEVNDGNGTNGLLSLAKGIGGVTVLRKGGKDFRSDGKTACAVSYGSPRRCGGGGDLGGVAVFLGWARQGAAXGVEVMPNPTLGGVAGSALLRRAASLAFESKRRSTLTDGDIKGLRSLQKQKPLV

NbL16g16350.1 COBRA-like_protein_7 [MW - SP = 68.92 kDa]

No. of times detected



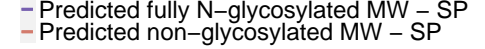
log(intensity)



Values from



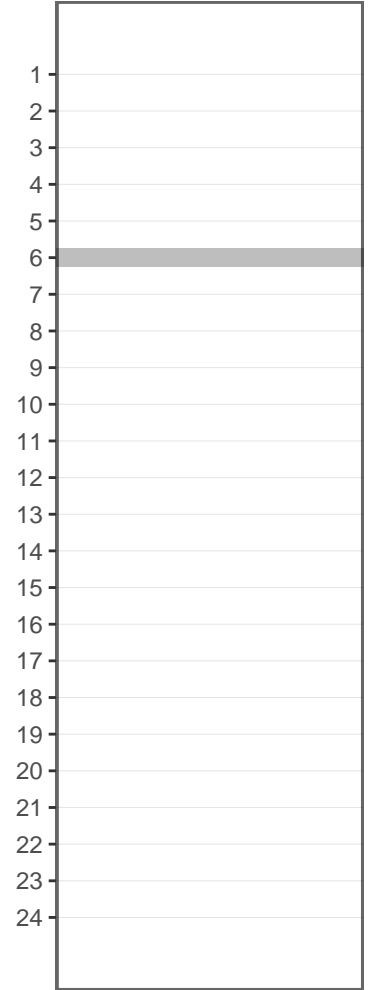
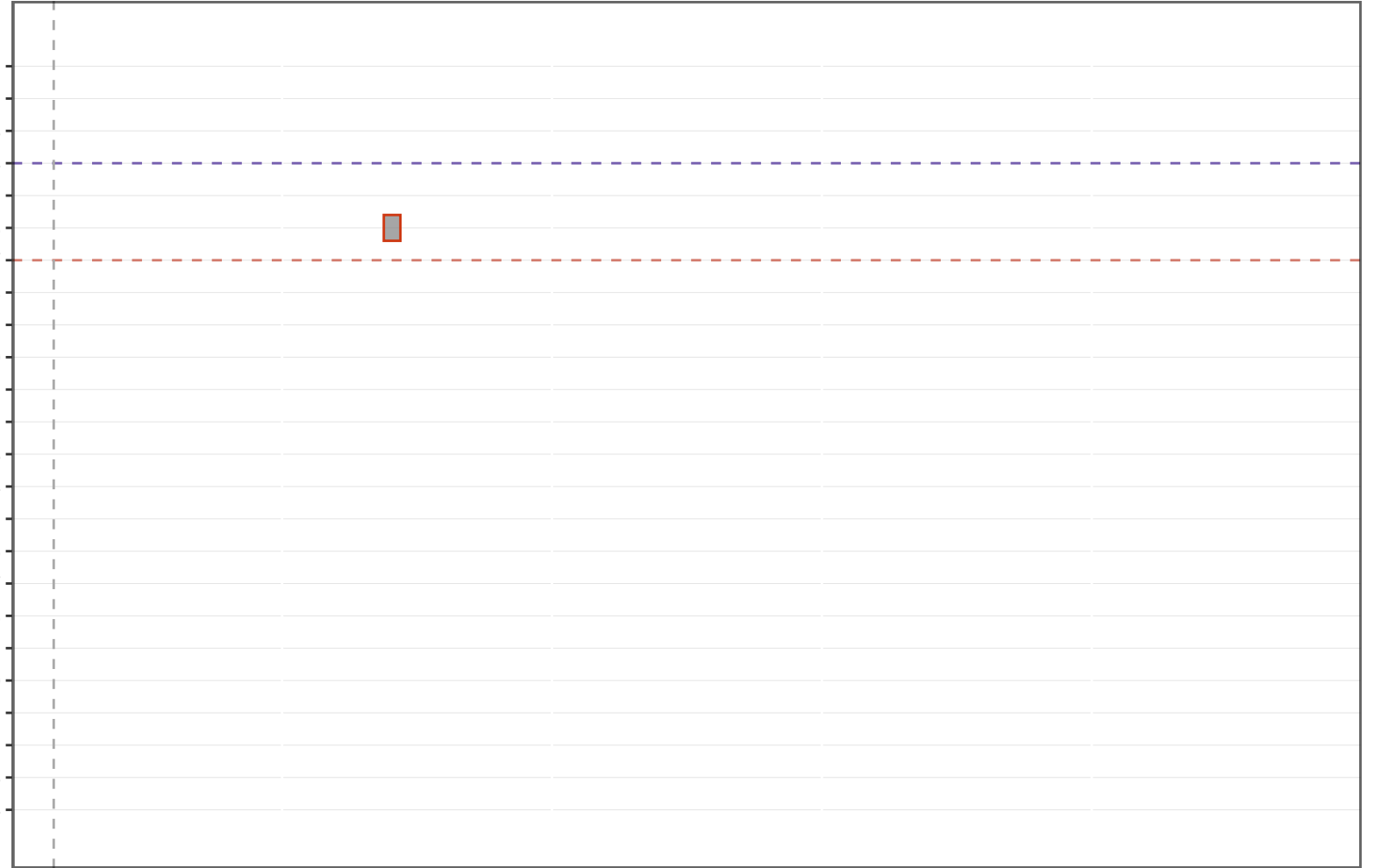
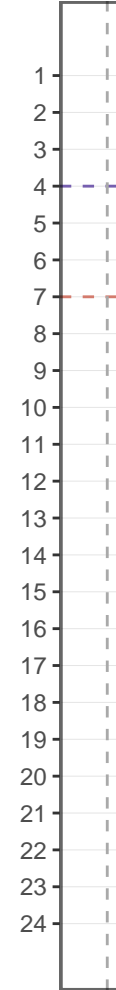
MW indication



Molecular weight

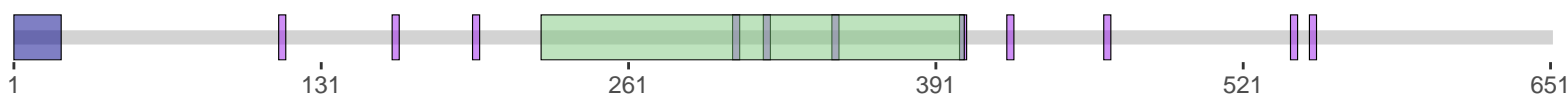
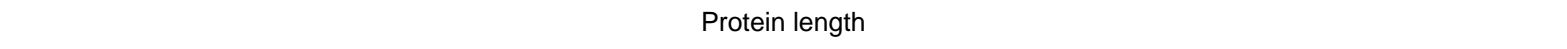


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

*FCCRNGLTLPAMDPSKASAFQNVKMPDNLNRSFTRPQNWKIEGRINPQVKGKPPVRSVPSGQFDPDPSGLLPDTAAFAVWQVGNITQPKGASPRGCVSFAFYNEIHPGPTGSGGGPNTARTDSAKARALLPSGALLVFNENRTKMSVAVADNHLPVENPLPGGNGGVSINWHLFTDPRGGWSEARITLNNWDTGSDADWFTAWGLDKAALGFDAVYFNGTLDGWNNTLFMGGLEGLNLYVAETDGNPEKDRPVKGGQVHFTKNIKPGINPGDGF

NbL16g16320.1 importin_subunit_alpha-2-like [MW = 58.5 kDa]

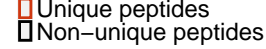
No. of times detected



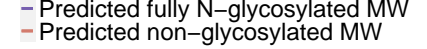
log(intensity)



Values from



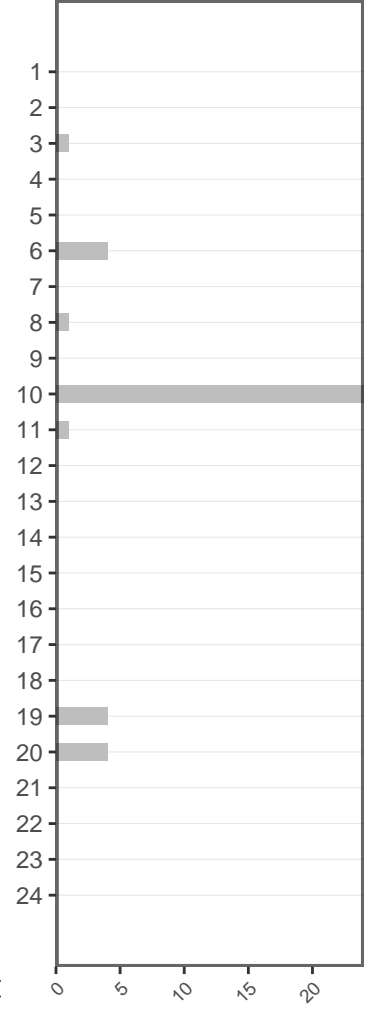
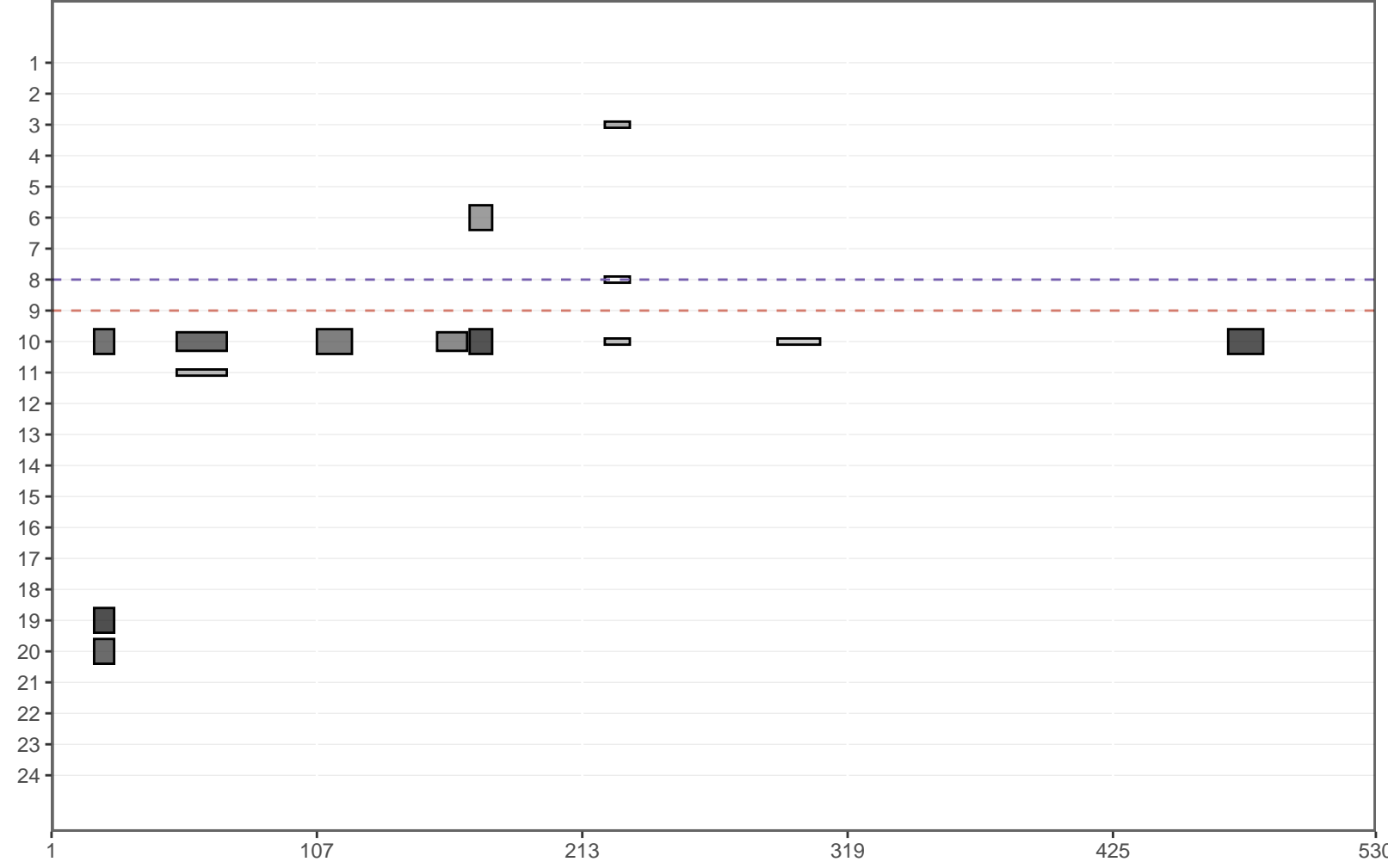
MW indication



Molecular weight

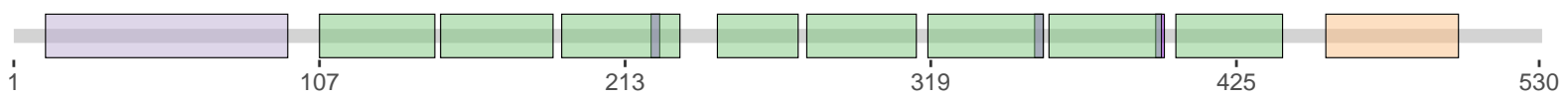


Gel Slice



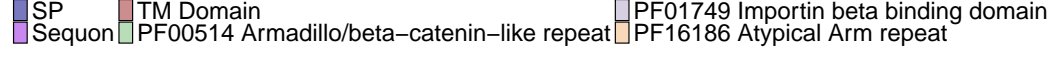
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

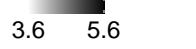
SALQRLVHSDNEEVLTDAQWALSYLSDGTNDKQGVAEAGVSPRLVELLMHPSPVLPALRTVGVNVTGDLGTFQCHENGALACLLSLTHNHKKSRKEACWTSNITAGNKEGQVAEAGLAPLVNLLGTAEFDKKKAAMVAISNATSGGTHGKIFLVSGGCKPKLGDLLVCFDPFRNFTVGLGLENLKVKSEAEKANTGGINYYAGLTDQAEGLKNIENLQSHDNNNEKAVKILETFWLEEEDETLPMGDETQAGFNFGGNDQVPSGGKFKQI

NbL16g16250.1 acetate/butyrate--CoA_ligase_AAE7_peroxisomal-like [MW = 62.53 kDa]

No. of times detected



log(intensity)



Values from



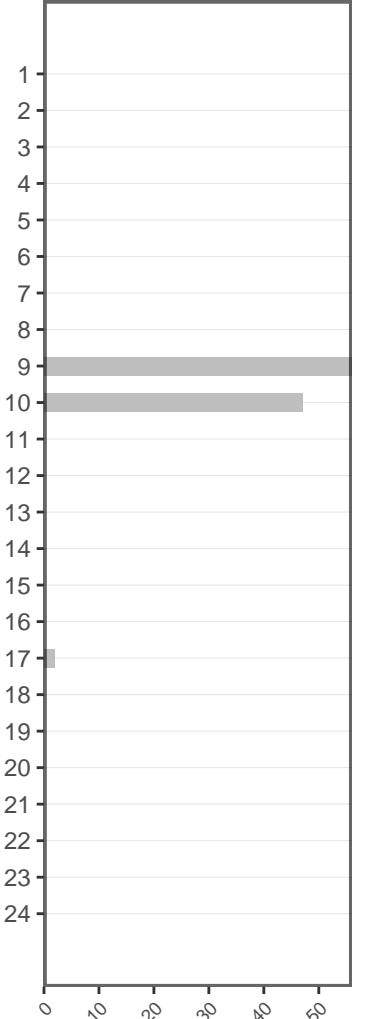
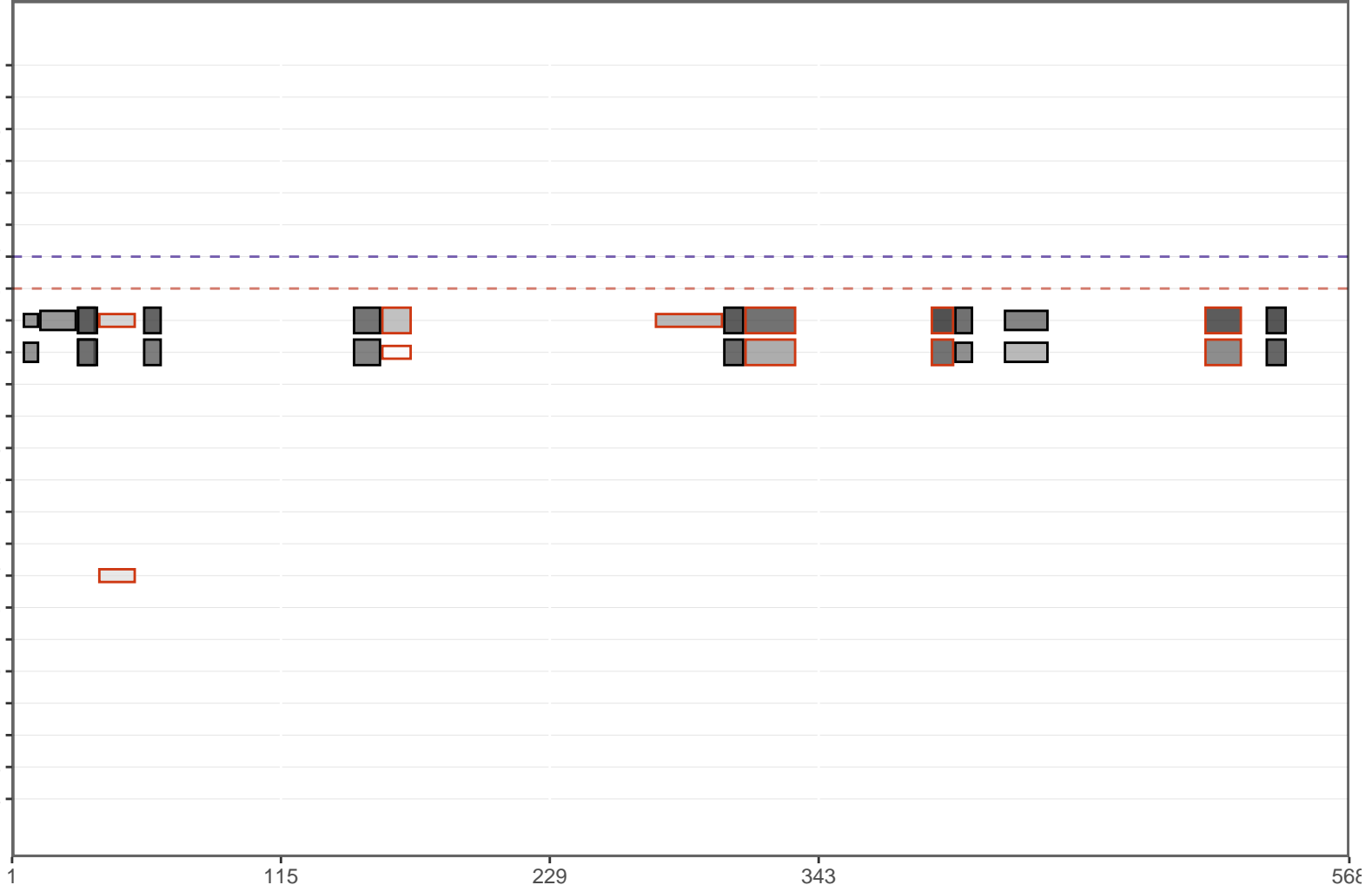
MW indication



Molecular weight

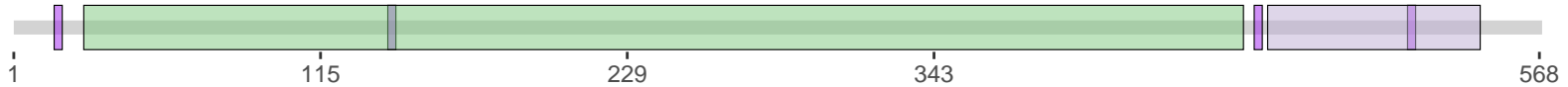


Gel Slice



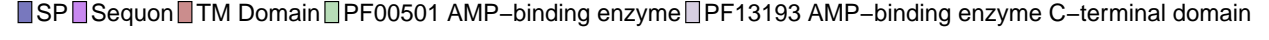
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VTKAVYSATHLGVTHFSAAPVAVLNTVWAPKKEETILFLRLLVQVSTAGASPPSPVLAAMTGRGRFRVLYHTYGLSETYGPDTGCTWKPEDLLPDIGARLNARQGVYRYSLEKLVVNSKDMTPVYKDGKTMGEIVFKGNVYMKGVLNPKNAEAFAGGVIYHSGDLAVKHDPGYIEKDKRKHIIISGGENISEVEVENILYGHPALEIVYVARDDEGWGSEPCAFVTLKPNVKKETDQGGSAEDIMNFRSKMPRYWYFKGVVFGPLFKTATGKQKHLRKAQAKEMGPGV

NbL16g16230.1 GTP-binding_protein_SAR2 [MW = 21.94 kDa]

No. of times detected



log(intensity)



Values from



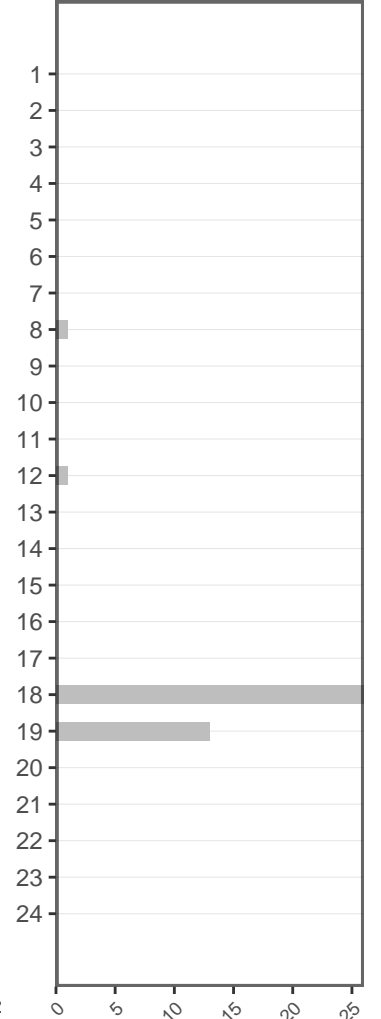
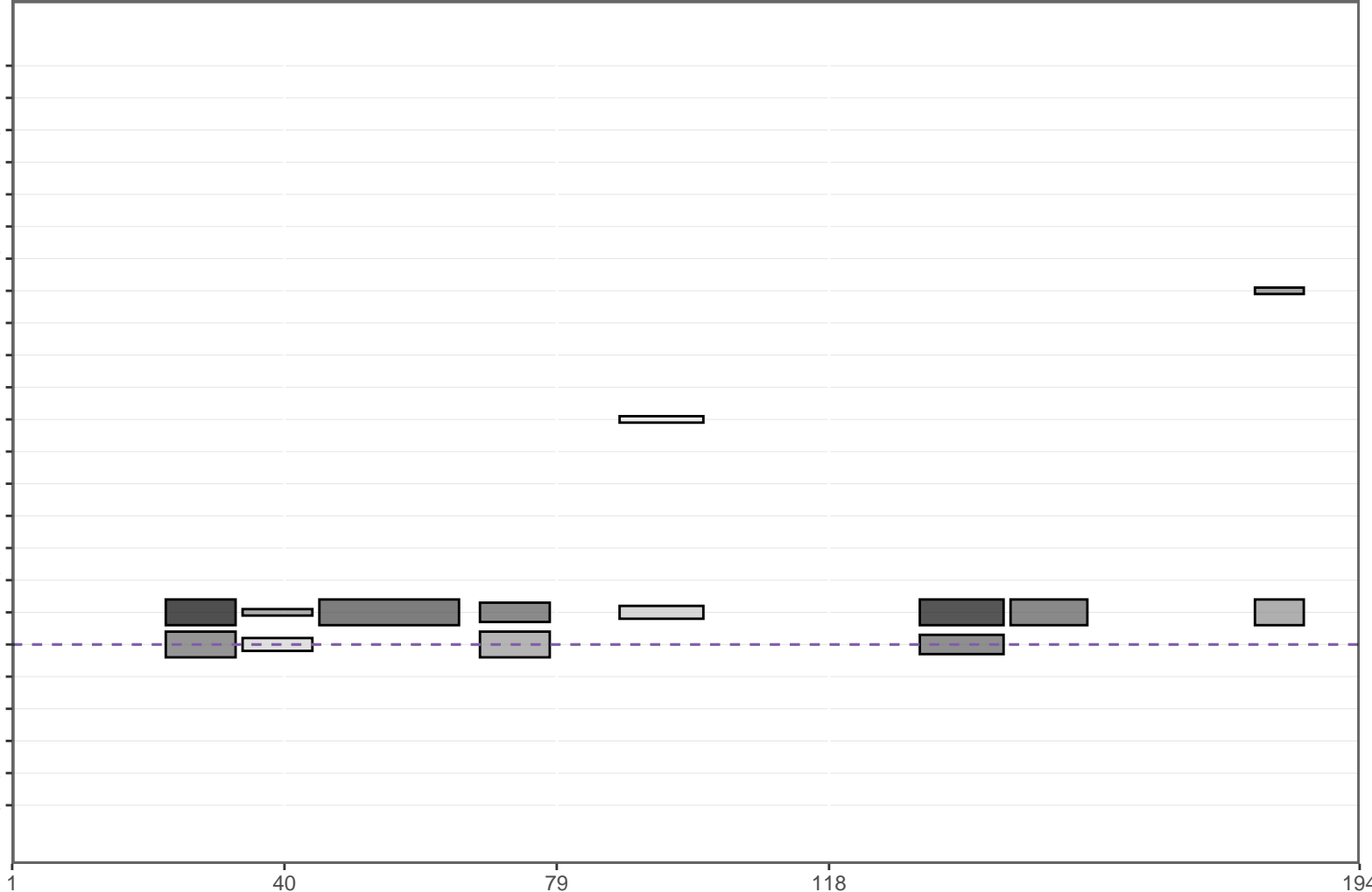
MW indication



Molecular weight

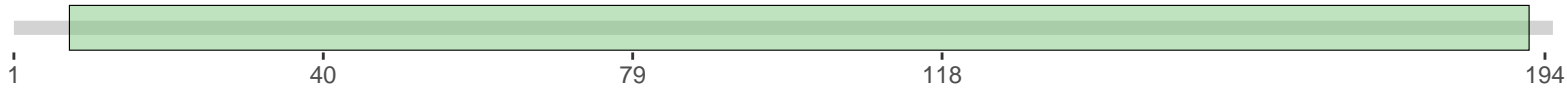


Gel Slice



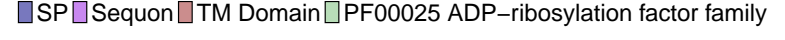
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YYAKYDAVYLYLDVDRERFPEGKELDGLLSDGLANVFFLILGNKIDIPWASEDELRHYLGLTGVTGKGNVNLAGTNVRIEVMGSRKMGVYEGEGRKWMGQYK

NbL16g16190.1 uncharacterized_protein_C167.05-like [MW = 17.84 kDa]

No. of times detected



log(intensity)



Values from



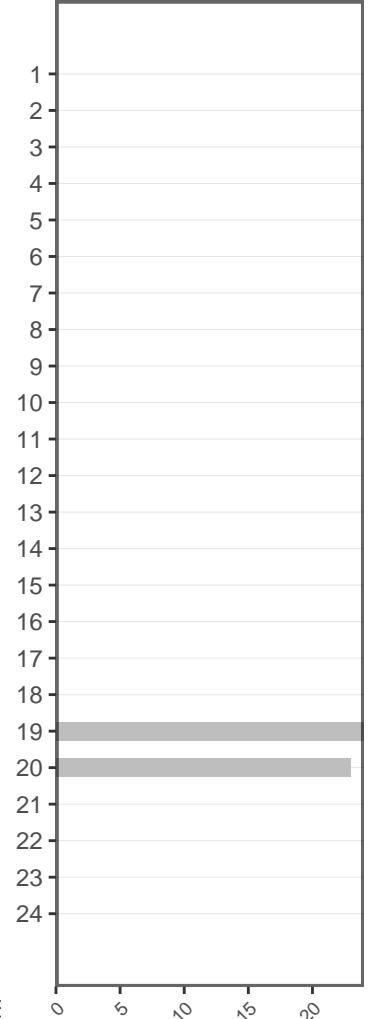
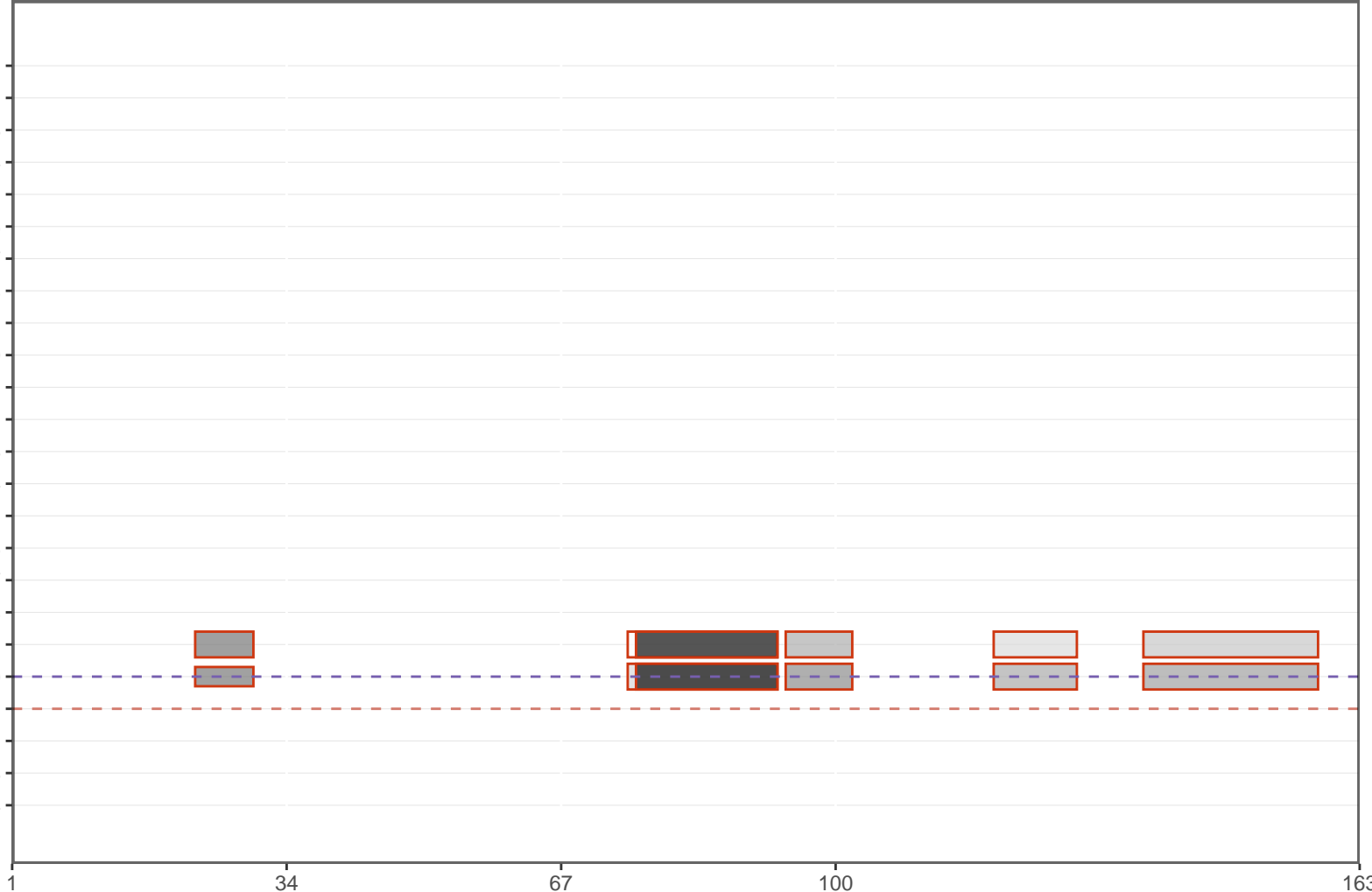
MW indication



Molecular weight

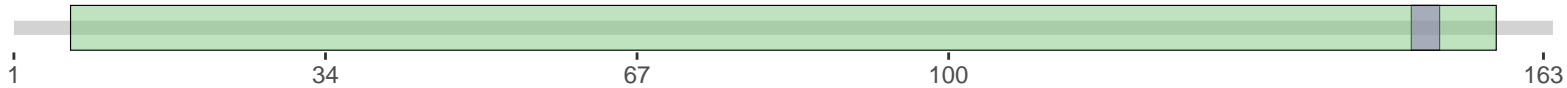


Gel Slice



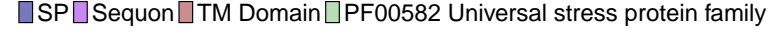
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

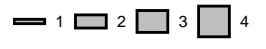


Protein sequence:

DAHTMKYGVNFDPELEDMVTLAARGKEIMVVKRYWGDAREKLGAEIDKTPLEGLVGNRGLGKIKRAMGSEVSNVYVNNATGPVTVKHDV

NbL16g16150.1 phytochrome_B-like [MW = 125.82 kDa]

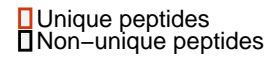
No. of times detected



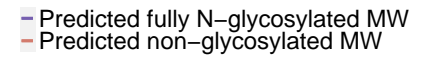
log(intensity)



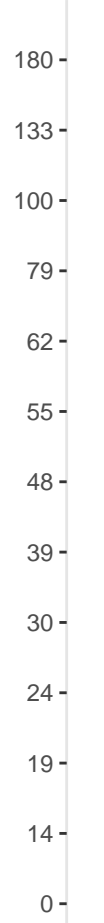
Values from



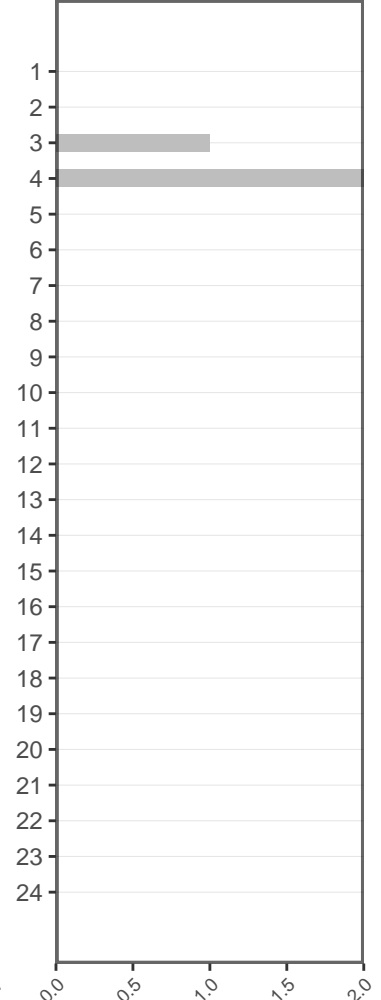
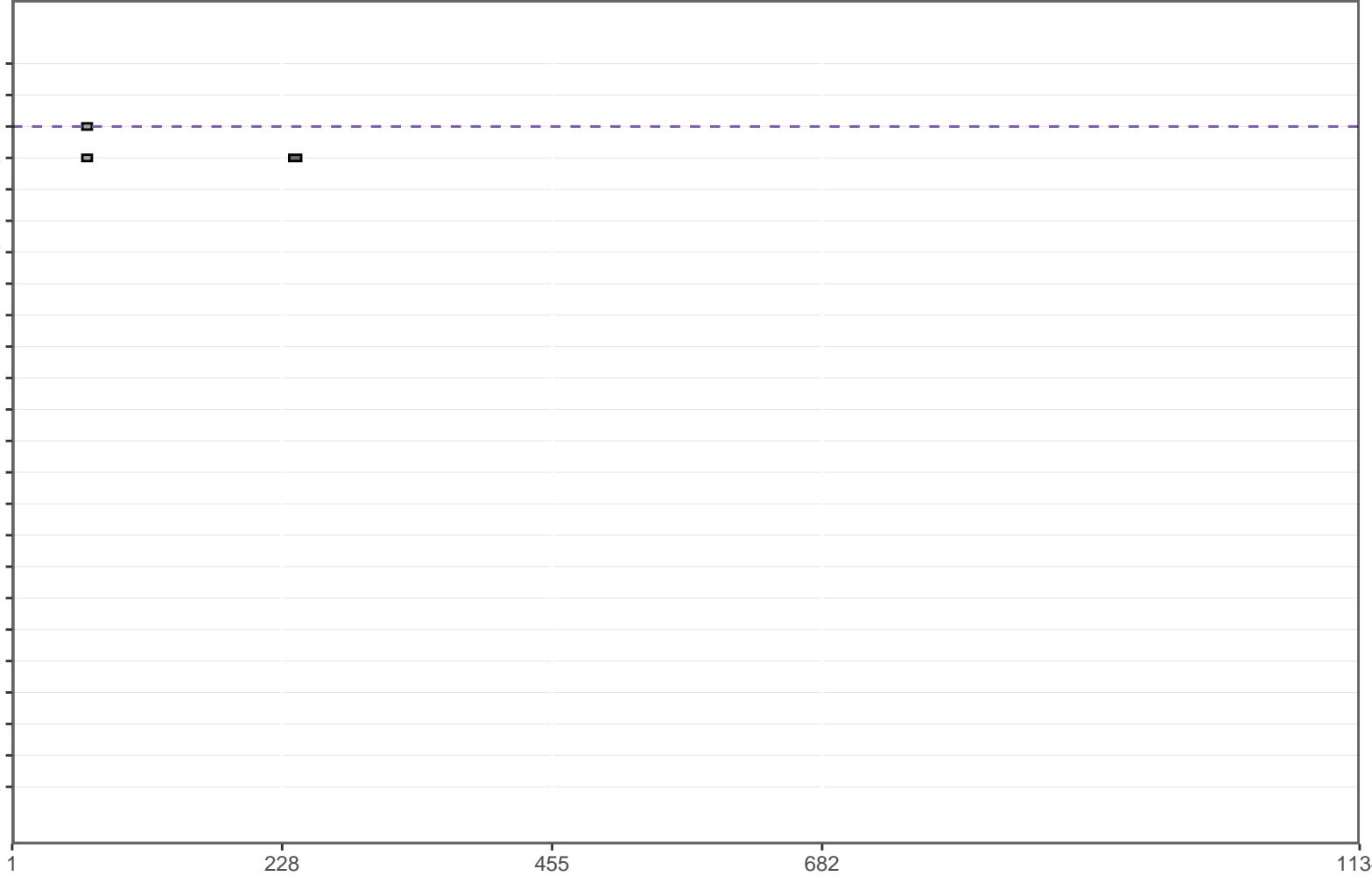
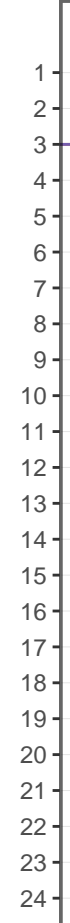
MW indication



Molecular weight



Gel Slice

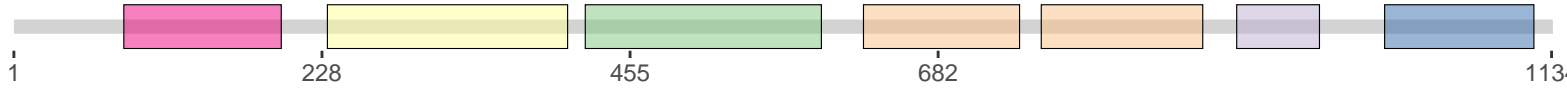


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

- SP
- TM Domain
- PF00512 His Kinase A (phospho-acceptor) domain
- PF01590 GAF domain
- PF08446 PAS fold
- Seuon
- PF00360 Phytochrome region
- PF00989 PAS fold
- PF02518 Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase

Protein sequence:

QRMHPRSSFKAFLEVVNSRSLPWENAEIMDAHLSQLLRDFKDAEASNSKAVWHAGLGEMLGGIDELSSVAREMVRLETATAPFAVDVEGRINGWNAKVELTDLSEVEATGKSFVHDLVHKKEGGETAELKLFNALRGEEDKNVVEIKLRTFGSEQLKKAVFVVVNAAGSSKMDYTNINVDVCFVGGDVTGGKVVMDKFIHQGDYKAAHNSPNLPIRFASDENTCCSEWNTAMEKLTGWSRGEIGKMLVGETTFGGCGRLKGPDAKTRFMVLVHNAAGGETDKFPFFFD

NbL16g16030.1 galactokinase-like [MW = 54.53 kDa]

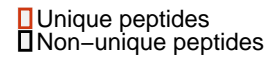
No. of times detected



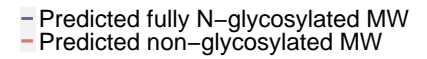
log(intensity)



Values from



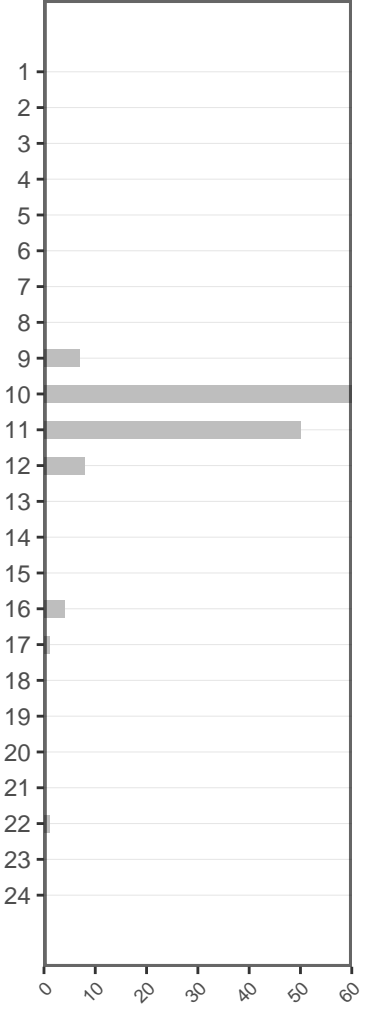
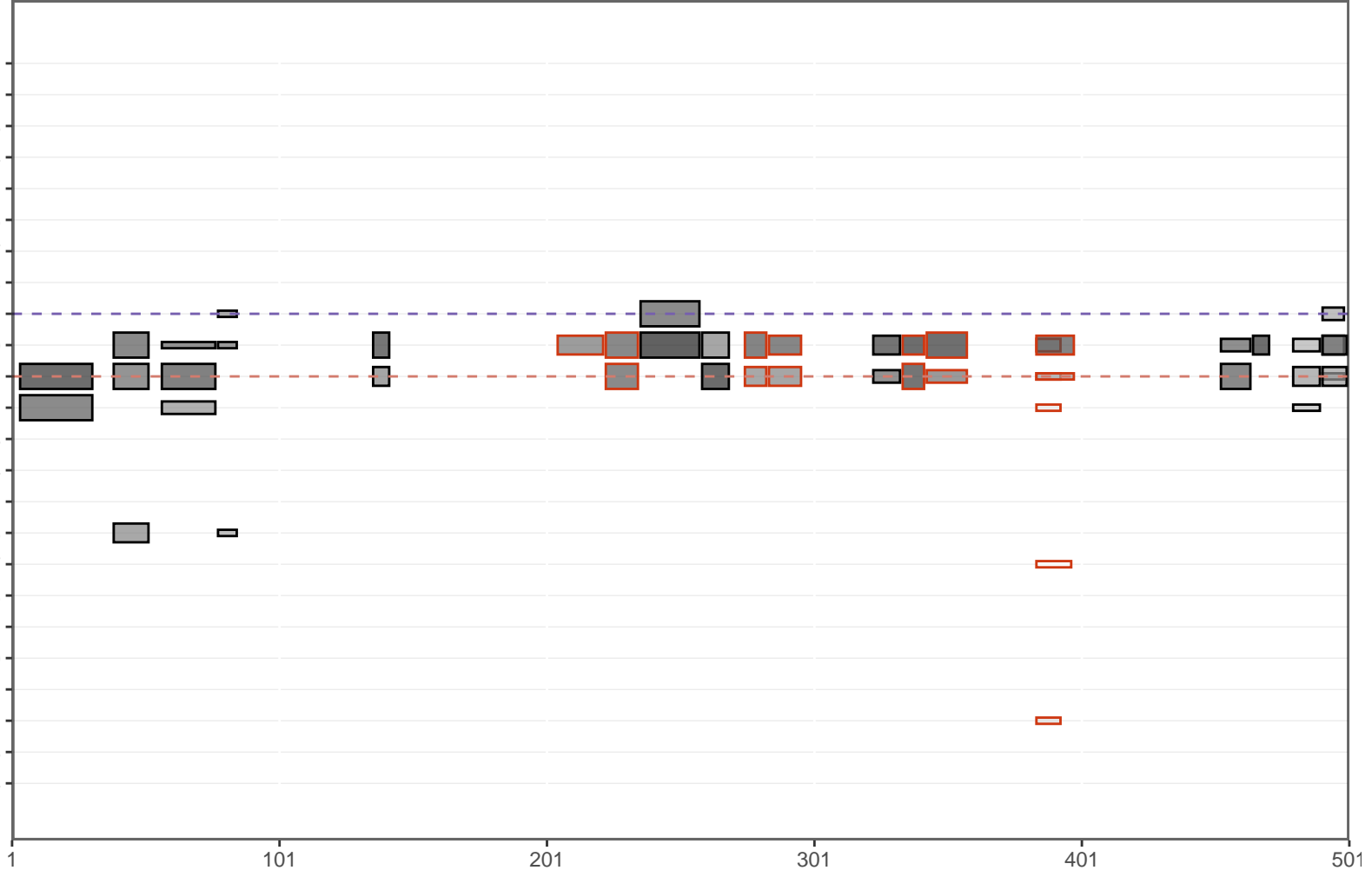
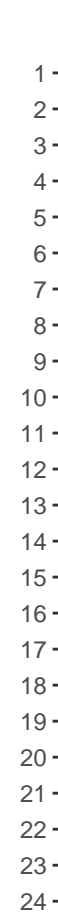
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

3VQLPAGGTFTVIAHSLAESGKAVTAANNVNRVVEGRLAAMVLRGRLGMEPEHAEINWRTLSDEVEGLGIFAGTHSGSDPFLAVKELLHEEPYTSKEIENAGQKLESVFAASPTSLDLVRAAKDQYKLRGAAHYVSETKRVHAFKDTVSGELSDKMLKLGDLMNEGHNSGSLVYEGSGPELLEELVKICRDNALGARLTGAGWGGCAVALYKELVPOFLNLEKQFYQSRDKGTINKNDLGLYFASPKPSGSAIKF

NbL16g15970.1 30S_ribosomal_protein_S1_chloroplastic-like [MW = 45.59 kDa]

No. of times detected



log(intensity)



Values from



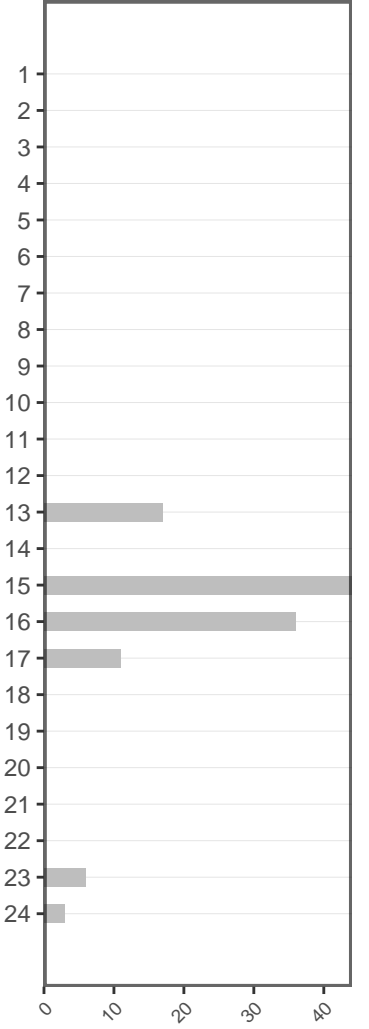
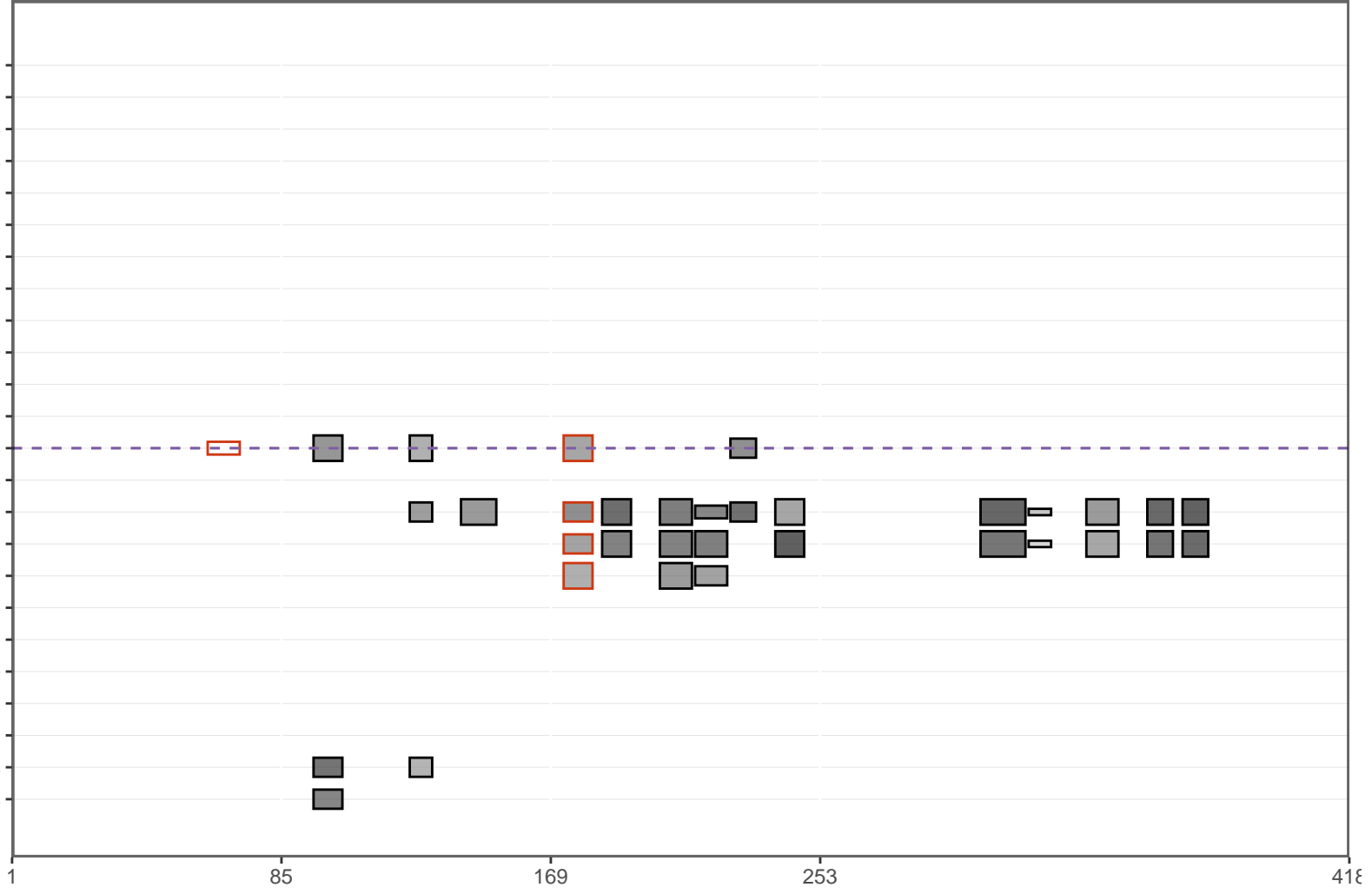
MW indication



Molecular weight

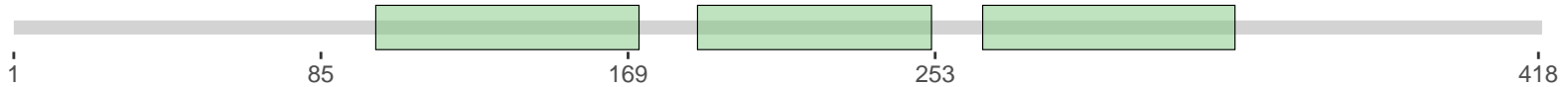


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

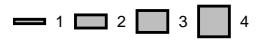


Protein sequence:

KVYGANKGGVVALVEGLRGFVPSGISTKSTAEELLEKELPKFVEVDEEGRIVLGNRKAMADSDGQLGGVVLGTVGSKPKVYGFADIDGINGLLHVSQSHDRVSDIATVLPDGDITLVKMLSHDRERGRVLSLTKLLEPTPGDMIRNPKLVFEKAEAMQTFRRRIQAQAEAMARADMLRFQFESGLTNSDGLGPTLSLPEDGLDLSEPPAEDL

NbL16g15950.1 DEAD-box_ATP-dependent_RNA_helicase_40-like [MW = 125.02 kDa]

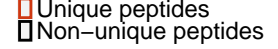
No. of times detected



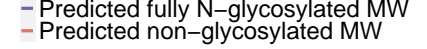
log(intensity)



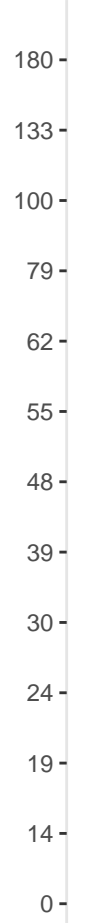
Values from



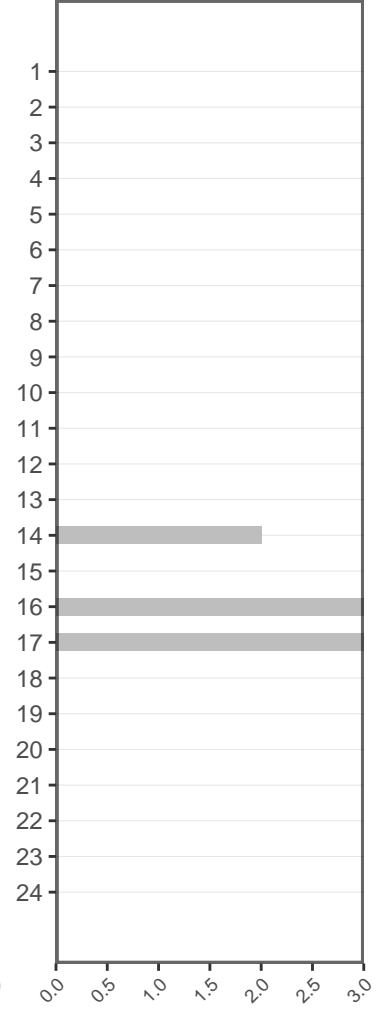
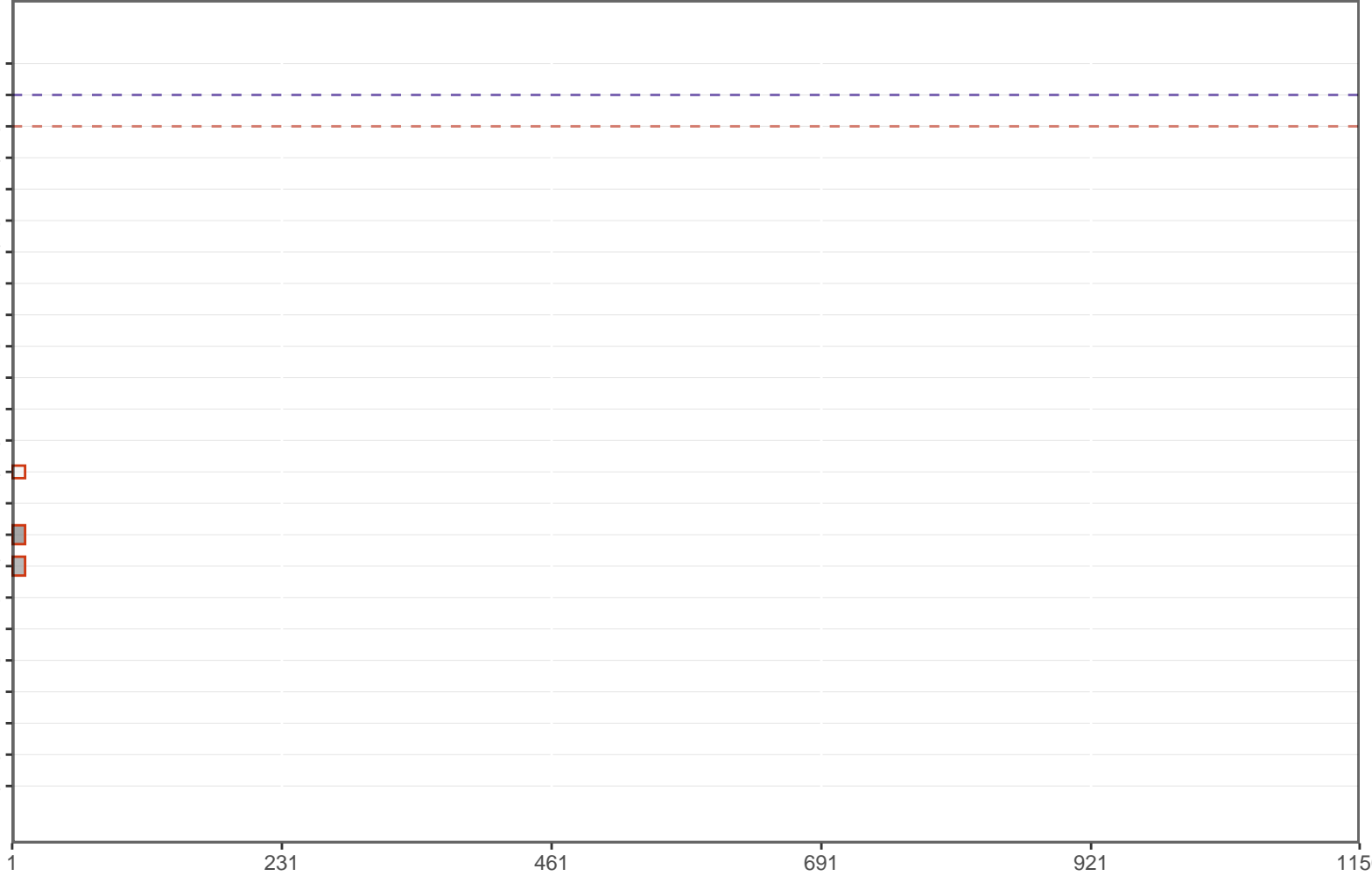
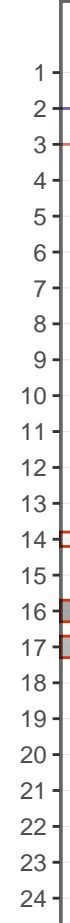
MW indication



Molecular weight

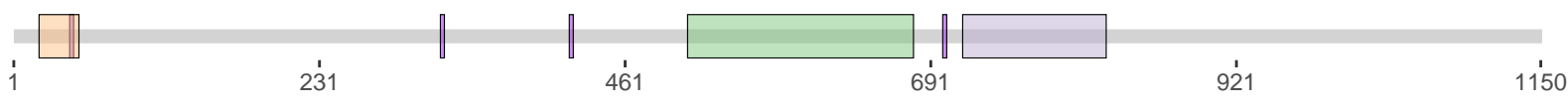


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

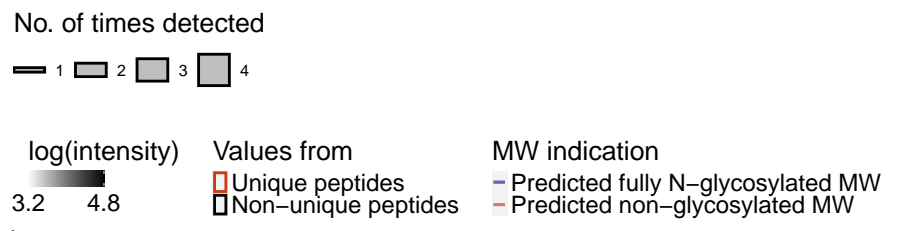
Pfam Description



Protein sequence:

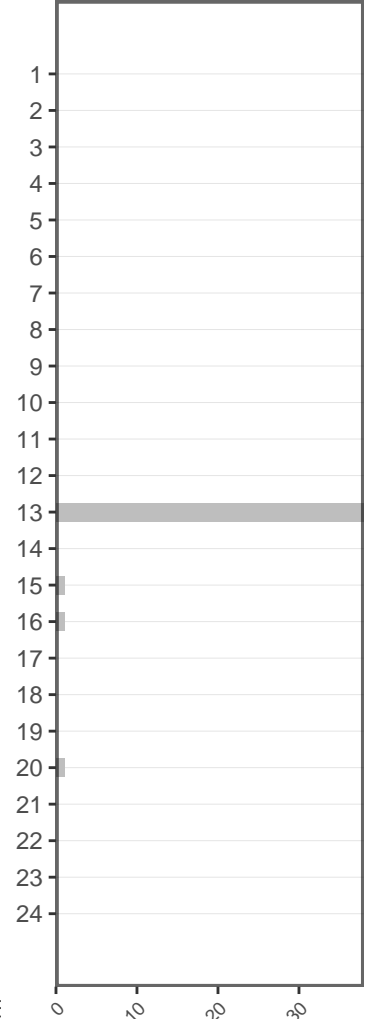
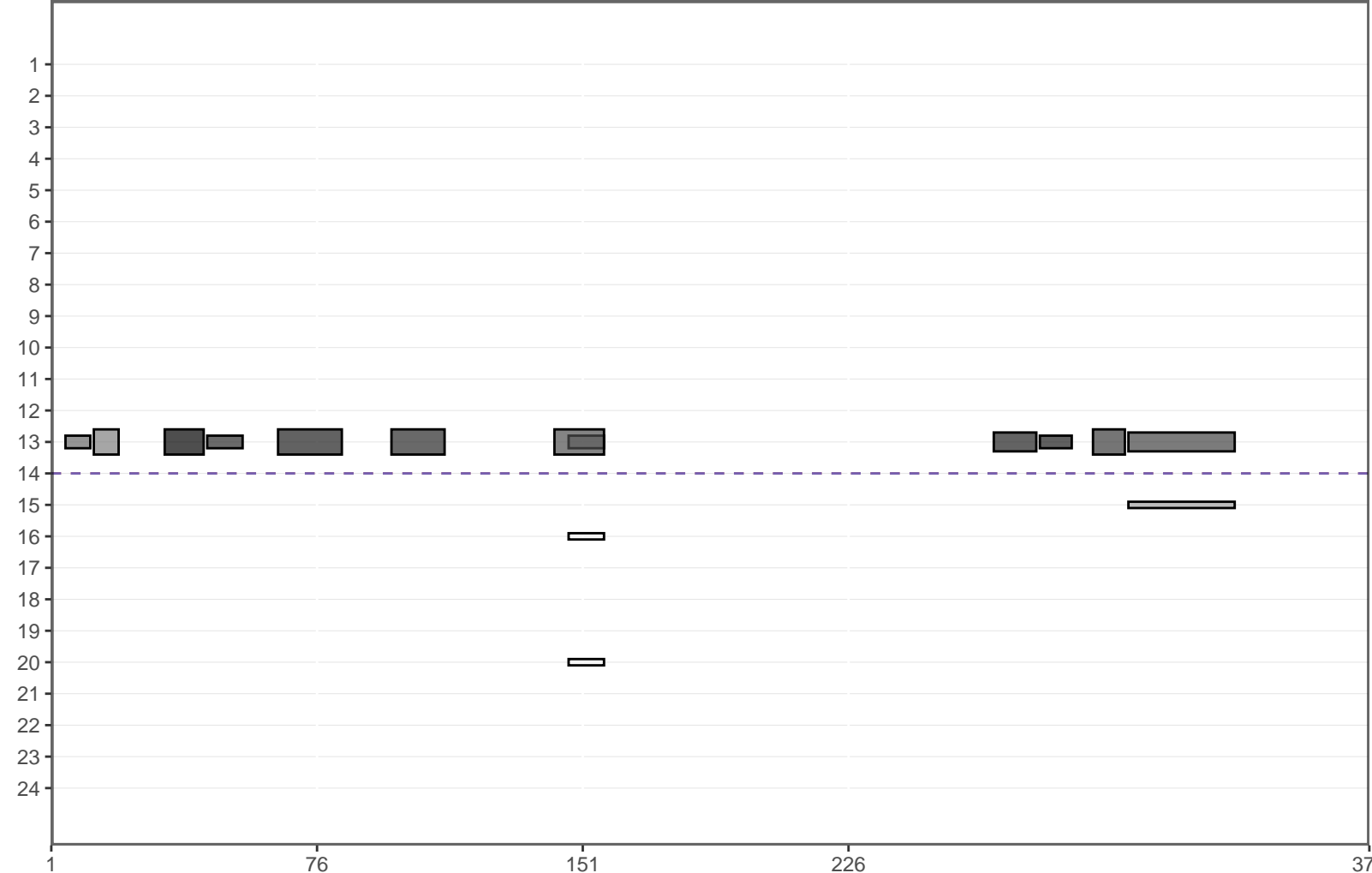
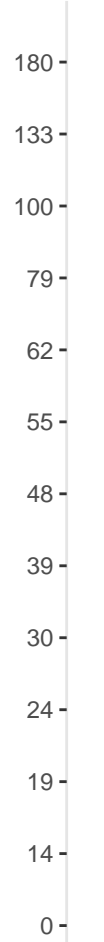
APTRELATQIDCALKFGRAIRVSGTGLYGGAPKVVHQLKELEGADVVATPGRNLNLEMKRDFRQVSELLVLEADARMLDMGFEPQIRKINVEIPRGRGLMYTATWFKVEVRIKAGDLLRSPVQVNGVNDGLAANKSTQYVEVVPQMEKQRRLRGLRSGERGKAIIFDSTKGLCDGLARSGRFGAAAHGDKSGGERDWWLNGFRSGKTPHVAEVAARGLDIPDIRVAVNYDFTQIEDVYHRIGRTGRAGATGSHYTFLDGGDMKVPDLVWLEGANQIHVPPNVI

NbL16g15820.1 pyruvate_dehydrogenase_(acetyl-transferring)_kinase_mitochondrial-like [MW = 42.26 kDa]

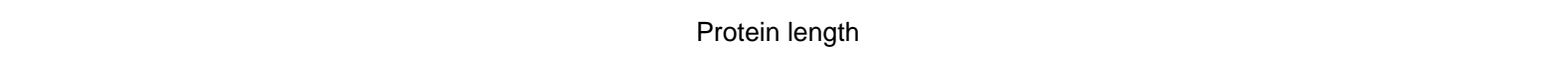


Molecular weight

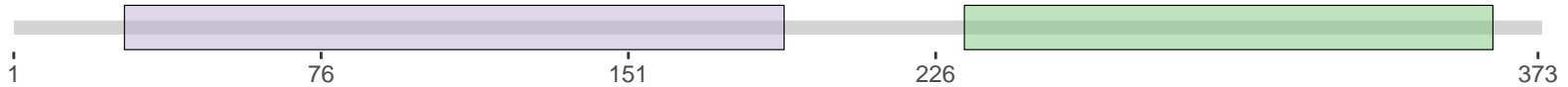
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF02518 Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase
- PF10436 Mitochondrial branched-chain alpha-ketoacid dehydrogenase kinase

Protein sequence:

IVALIDPNPPPCDGVYRHTKMSPLEVARISASEDARGICGREYGSAPDNVHYGDPDFFTFVYPLHGLMVFELVKNLRAVEERFMDSDKVARPRIRIVADGLEDVTRKYDDEGGGPRISGLPKWIFTYLYSTARNPLEDHSDLETTDVAFLSTLAGYGVGLPISRLVARYFGDGLQHEMEGVGTDAVLSRLGDSGDEPLP

NbL16g15720.1 photosynthetic_NDH_subunit_of_luminal_location_1_chloroplastic [MW = 25.81 kDa]

No. of times detected



log(intensity)



Values from



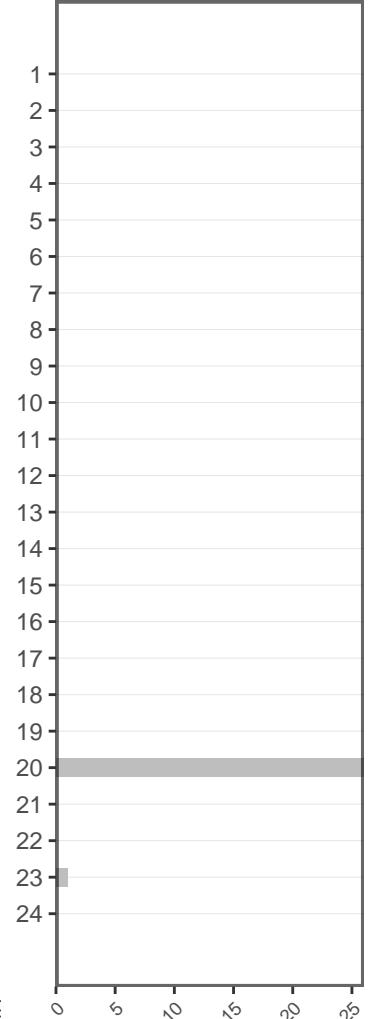
MW indication



Molecular weight



Gel Slice

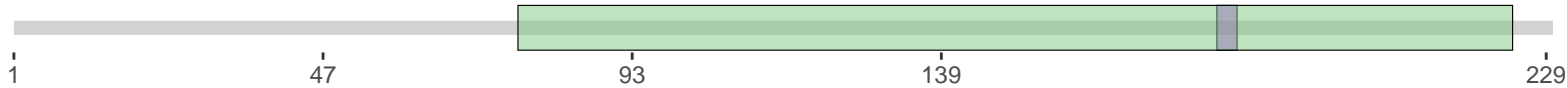


Peptide counts over 4 repeats

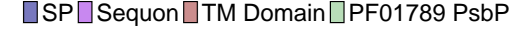
Protein length



Pfam domains



Pfam Description

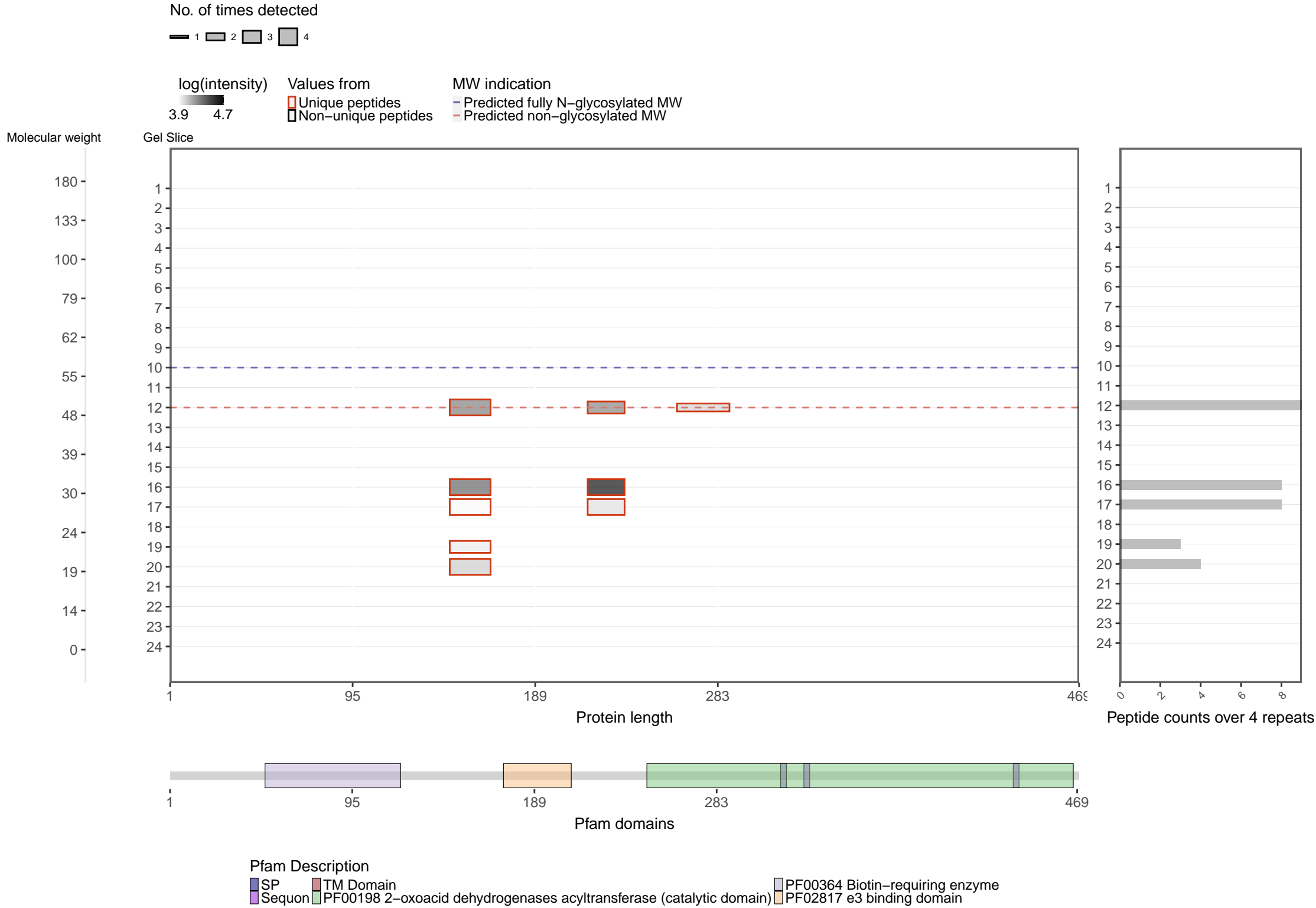


Protein sequence:

IGHDSAFKDRYLQGNVRLSFIPTKSDIHLGPMEEVAVNLVKKHVSAPNQVANMEMERBSTNGKNYCTFEYVLTSPNFSRAAFATAIGNRGVYTLVIGANERRWRKFRNKKVVAISDFQLDMP

NbL16g15670.1

dihydrolipoyllysine-residue_acetyltransferase_component_4_of_pyruvate_dehydrogenase_complex_chloroplastic-like [MW = 48.99 kDa]



NbL16g15340.1 anthranilate_phosphoribosyltransferase_chloroplastic-like [MW = 38.74 kDa]

No. of times detected



log(intensity)



Values from



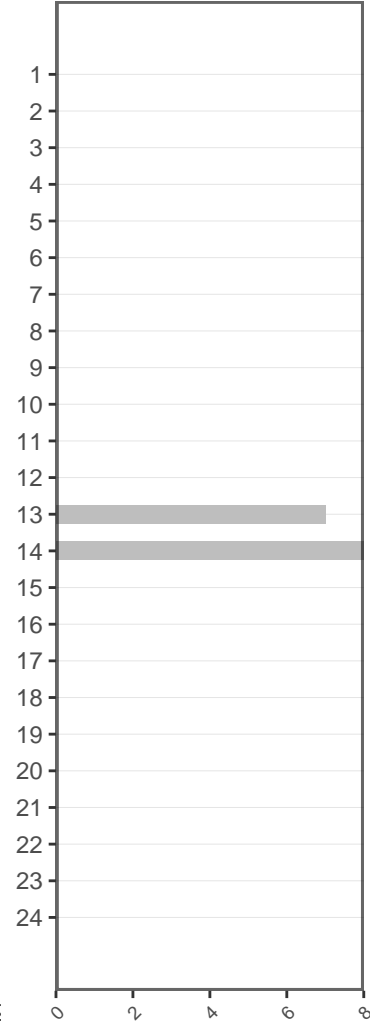
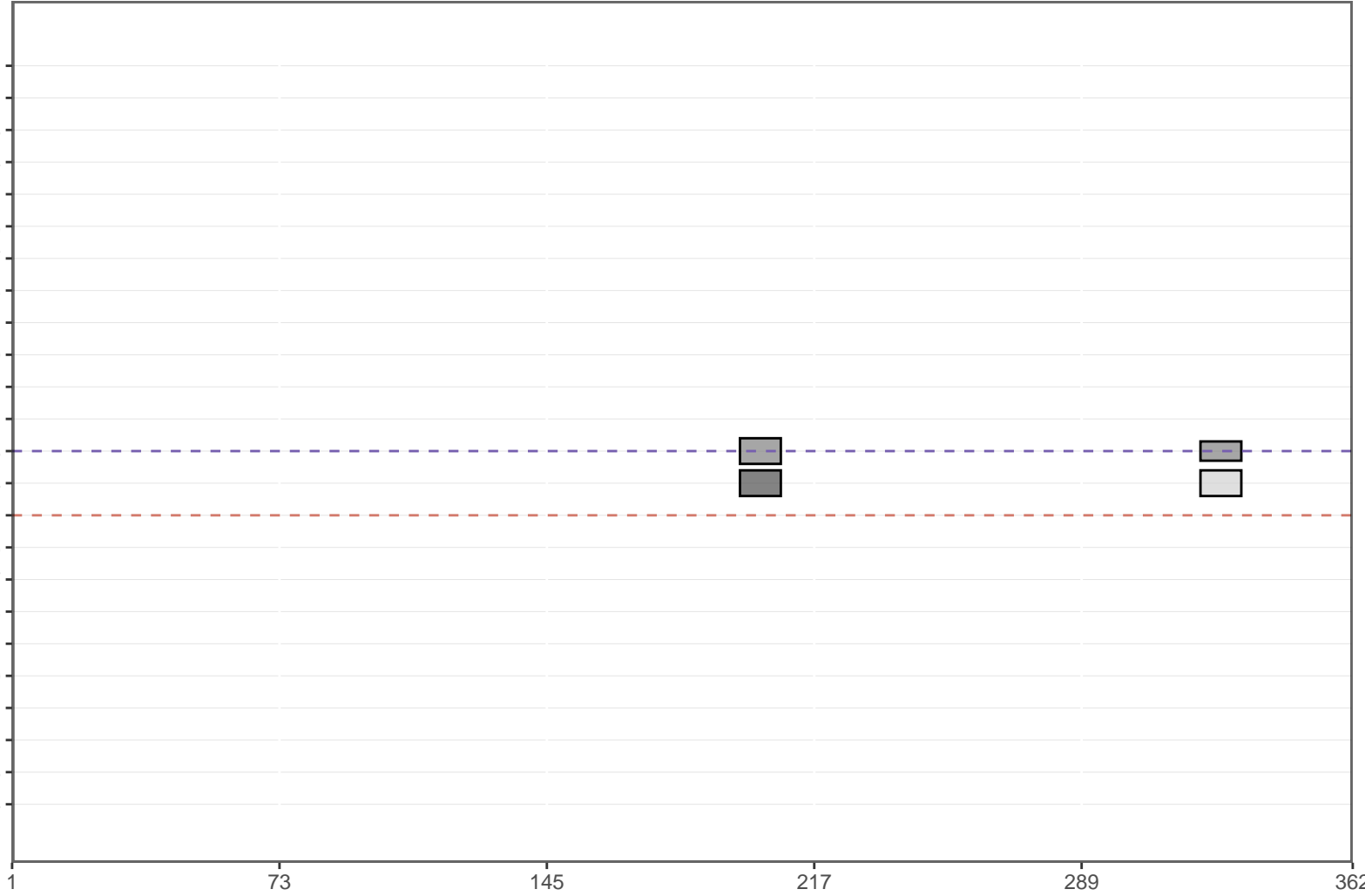
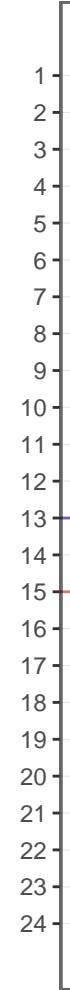
MW indication



Molecular weight



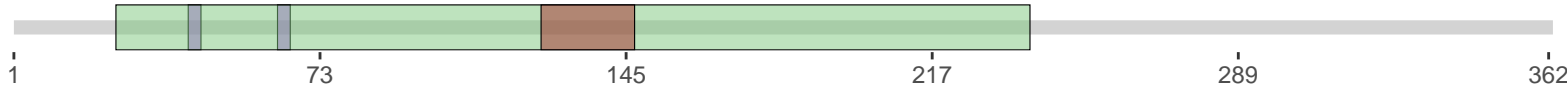
Gel Slice



Peptide counts over 4 repeats

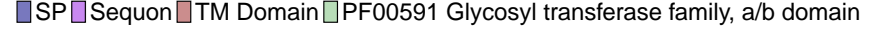
1 73 145 217 289 362

Protein length



Pfam domains

Pfam Description



Protein sequence:

.FVHSEGLDEMSPFGPGVAVLDVTAEKIKFDFPLDFGIPRCTLGDLRGGGPEHNAGVLRRLVSGETGFMAADLDIATLVKTYDICHHSLSAGRWRHKNMLLGLLLHSFGCLASKDLVQNLVSHSDVALHHYKHMLPLMLNAAAAALLVRRVGNLAEQVAVRTHHSGKALDTLNHWMMFQVHMLLEVRG'

NbL16g15300.1 universal_stress_protein_A-like_protein [MW = 21.16 kDa]

No. of times detected



log(intensity)



Values from



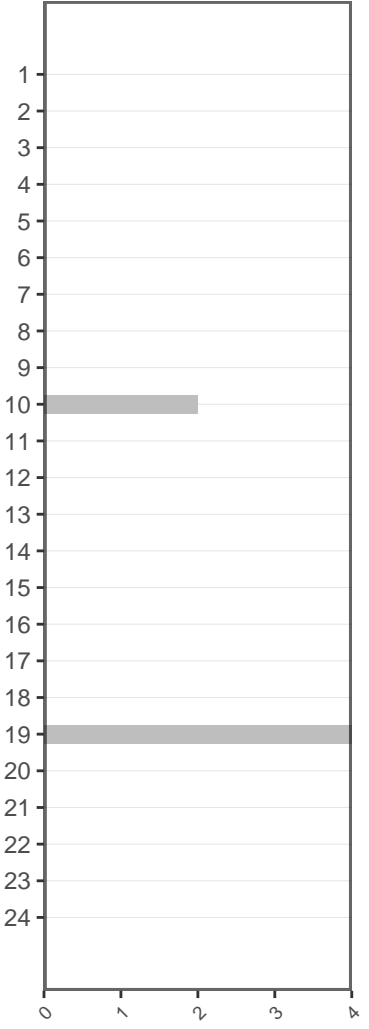
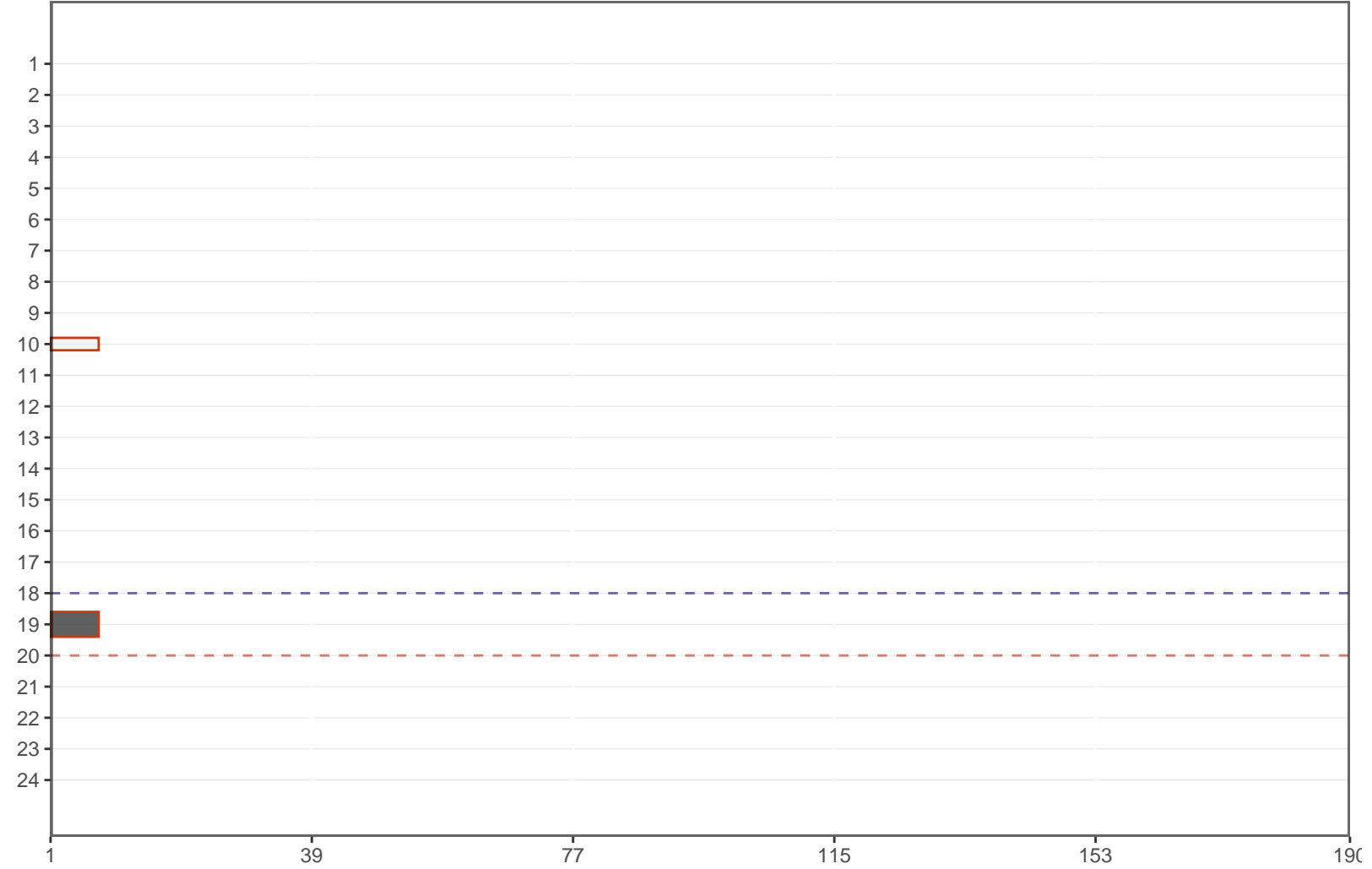
MW indication



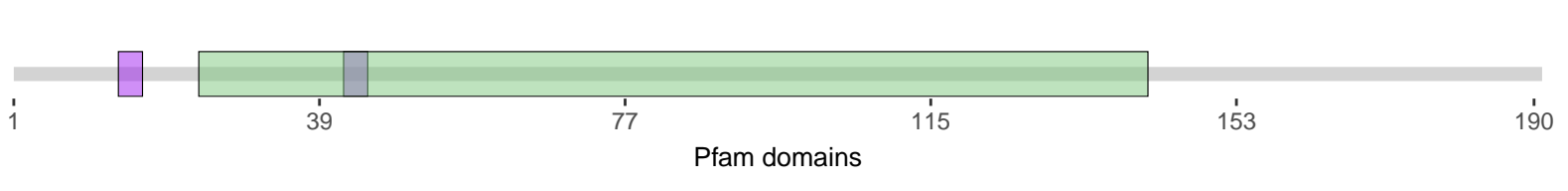
Molecular weight



Gel Slice

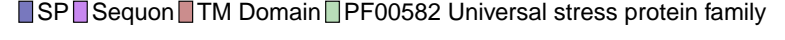


Protein length



Pfam domains

Pfam Description



Protein sequence:

LDKIRGLHLLFCFVNRGHEIGVPEAWIKGGDPKEVVLGVKRVGPDLLVVGRLGPFQRIAKRLPFDFGRSLRLEFGSGVSTGLQLVIEVSRISKAYFRGEITPELD*

NbL16g15290.1 50S_ribosomal_protein_L12_chloroplastic-like [MW = 19.68 kDa]

No. of times detected



log(intensity)



Values from



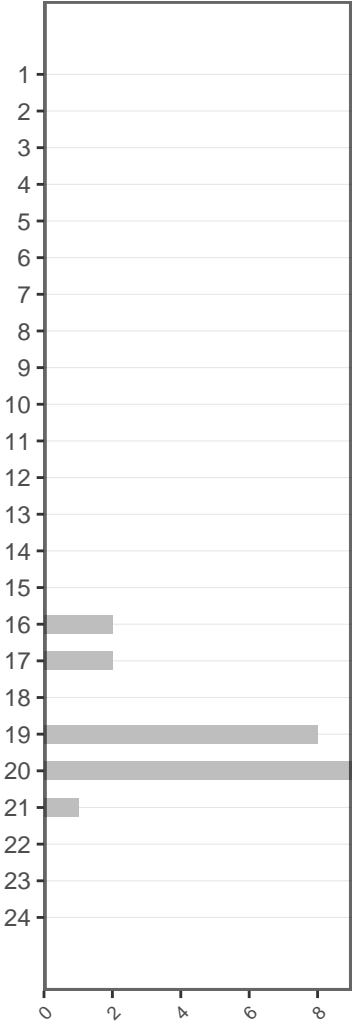
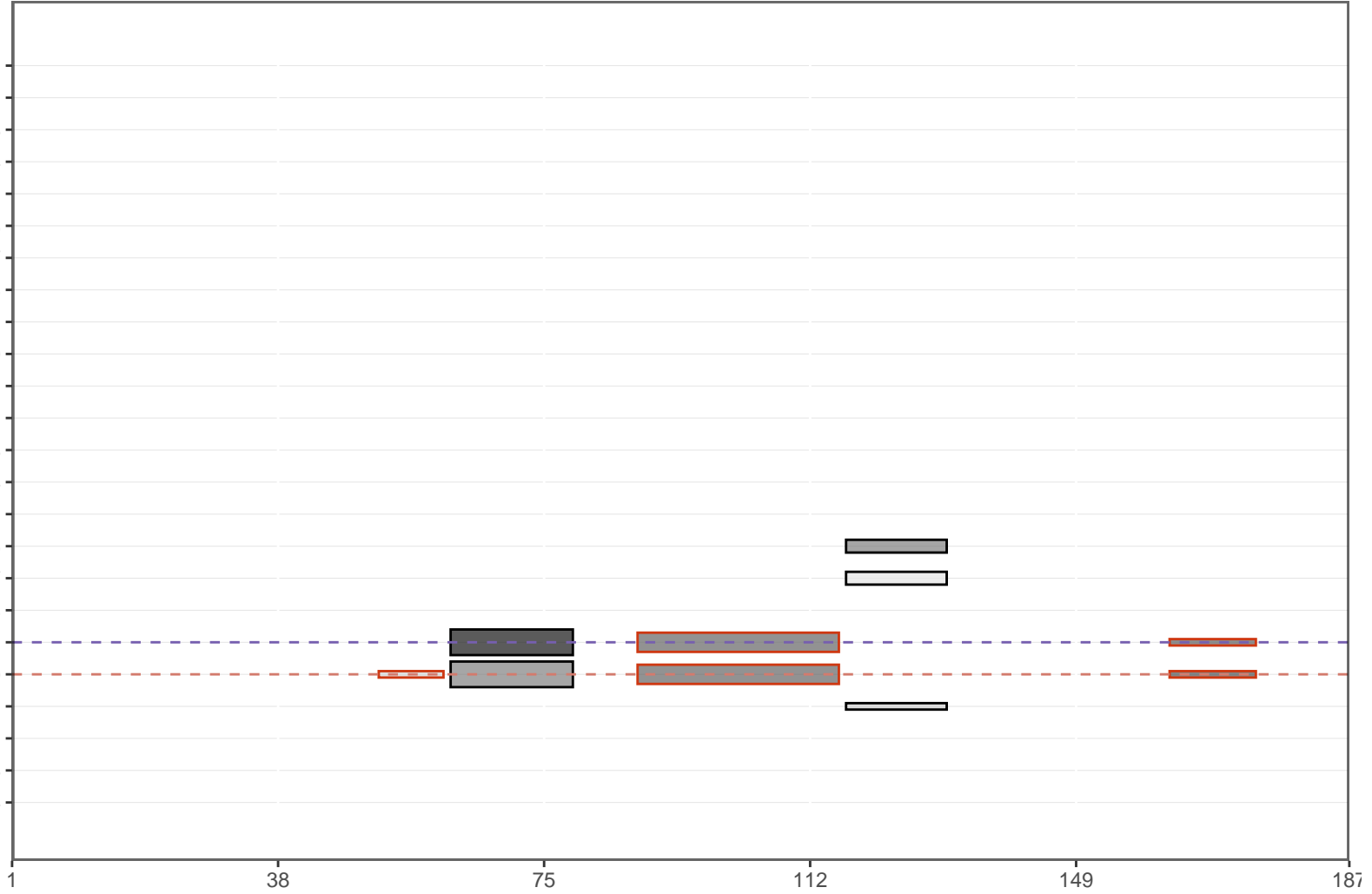
MW indication



Molecular weight

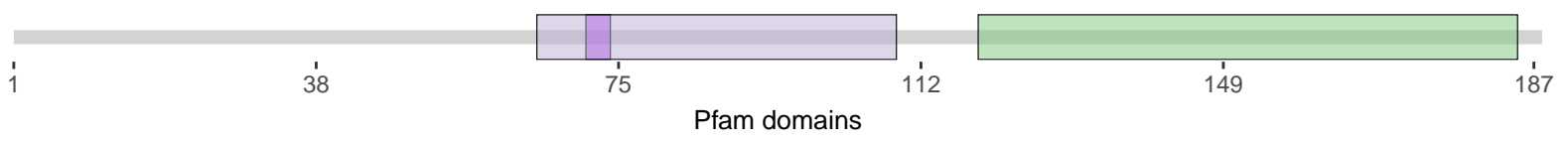


Gel Slice



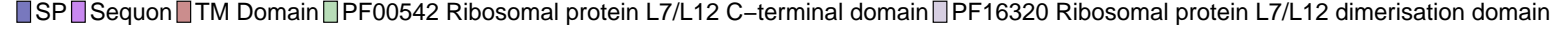
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

.VEYLQDKLGVTAAGFAPAAVAVPAAAEAPVVEEKTEFDVIEEVPNSRMAAKAVRALTNLALKEAKEIEGLPKPKFKEGISKDEAEADKKKOLEEAGAKVSIAT

NbL16g15050.1 3-dehydroquinase homolog [MW = 43.91 kDa]

No. of times detected



log(intensity)



Values from



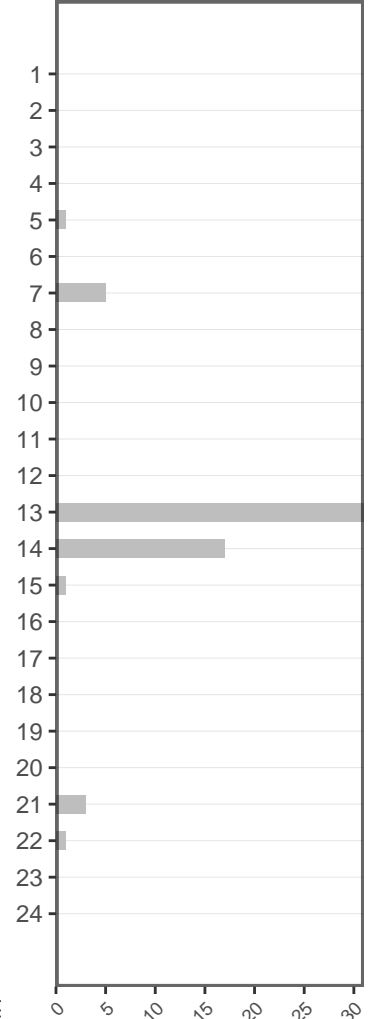
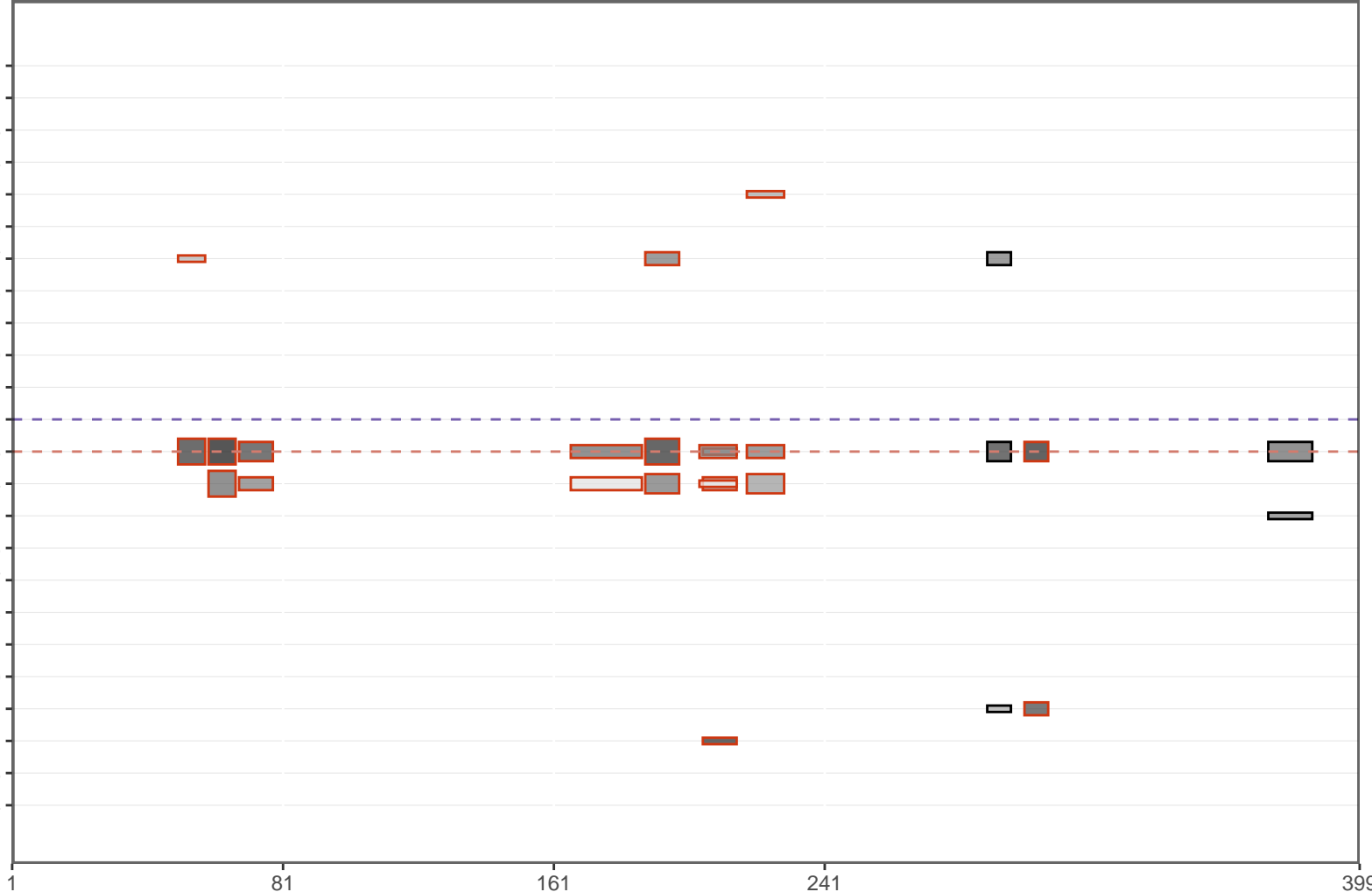
MW indication



Molecular weight

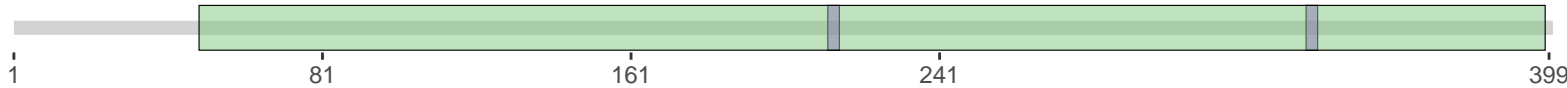


Gel Slice



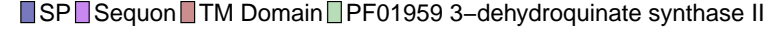
Protein length

Peptide counts over 4 repeats



Pfam domains

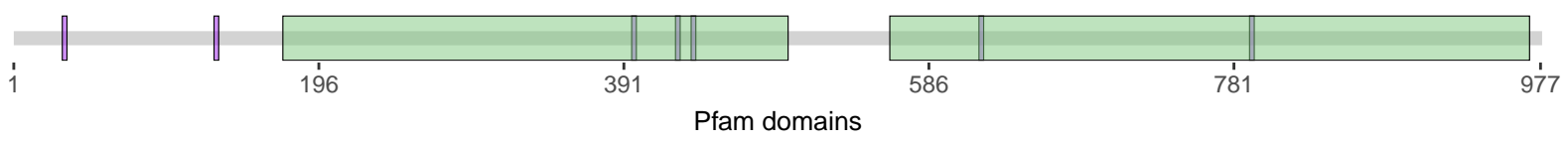
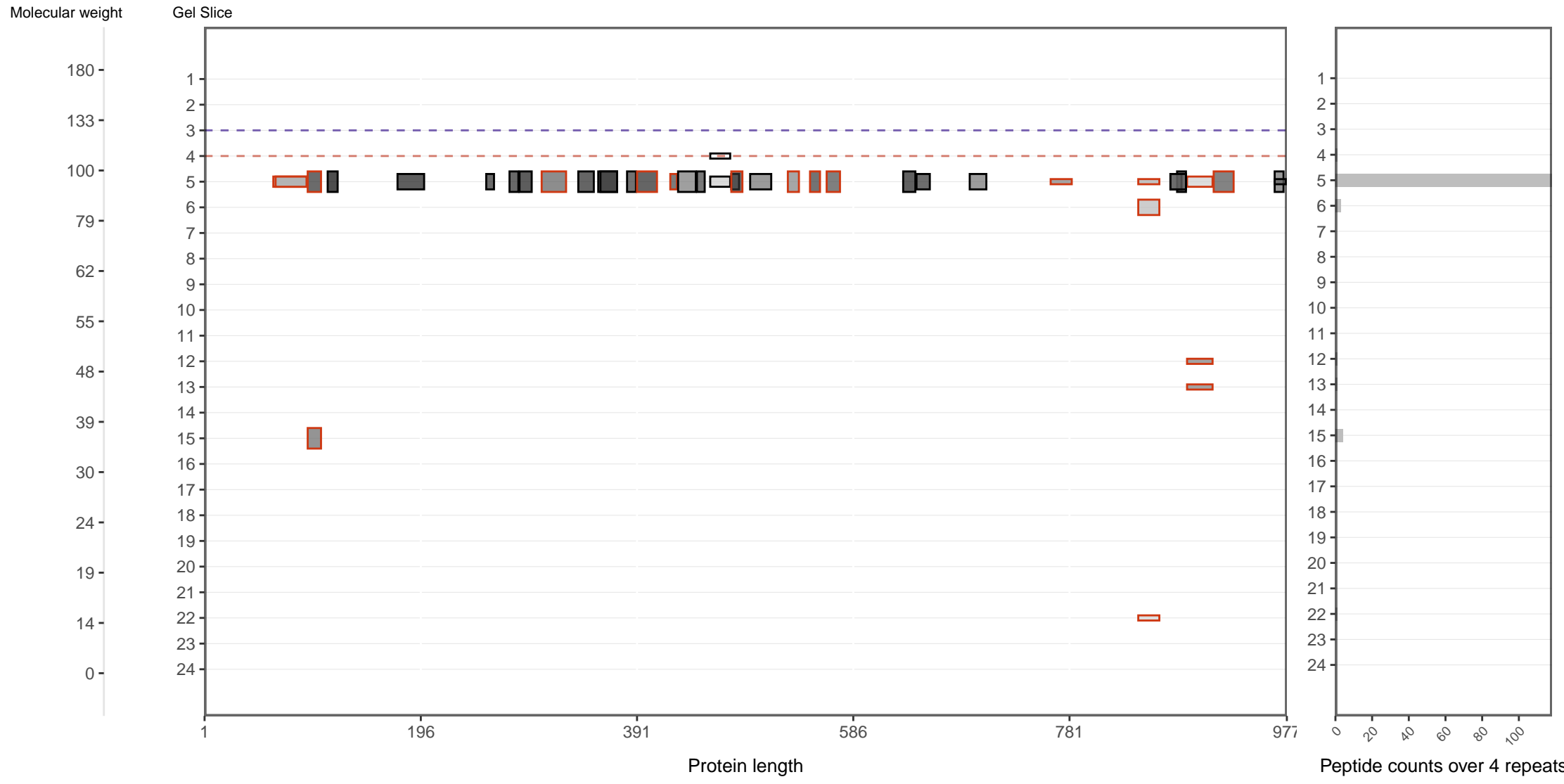
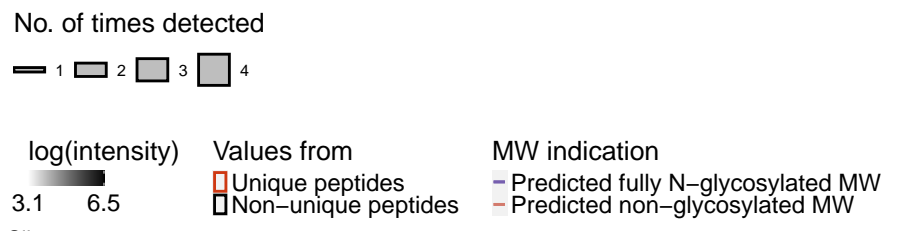
Pfam Description



Protein sequence:

/MKVEDV/GALDLKGYFDRRNEEDSLLNFKAKITHVQSTGMGDRVCDVIGSLMRPGEGLLVGSFARGLFLVHSEGLESNHSSRPFRVNAQPHAVVAVPGKGTSLVSELKSGKEIVVDGRGMQRTAVGRVWETRPULVEAEVESKNEEYVILLQNAETVGLVSPLQEEGYQRITFPVTLKLVGDEVCLLVGGGARHTGIEKEFVEK

NbL16g14910.1 alpha-14_glucan_phosphorylase_L-1_isozyme_chloroplastic/amyloplastic [MW = 110.39 kDa]



Pfam Description

- SP
- Sequon
- TM Domain
- PF00343 Carbohydrate phosphorylase

Protein sequence:

KYVGSLELDKLEKXAMRLENFDPSSWADLFTKPERLVDADTFEVSQKVEVVTNDELKNGEYDTEKKTSTVPELGAKDIDKKTMTMPEPVAIPKQVIRMANLGVGGHAWNGVAEHSSEVKEEYFNEFYELWPEKFNKNTGVTRRRWRIFQCNPLPSSITKWTGTEDWLNTEKLAELQGFADNEDLQIEWREAKRBNKIKAVSLKKEKGTQYVVPDAMFDQVWRHIEYKRGQLLNFGVAVRYKKMKEMTAERKAKYVPRVGFGGKAFATYVQAKRIVKFIADVGI

NbL16g14470.1 nicotinate_phosphoribosyltransferase-like [MW = 62.82 kDa]

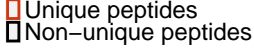
No. of times detected



log(intensity)



Values from

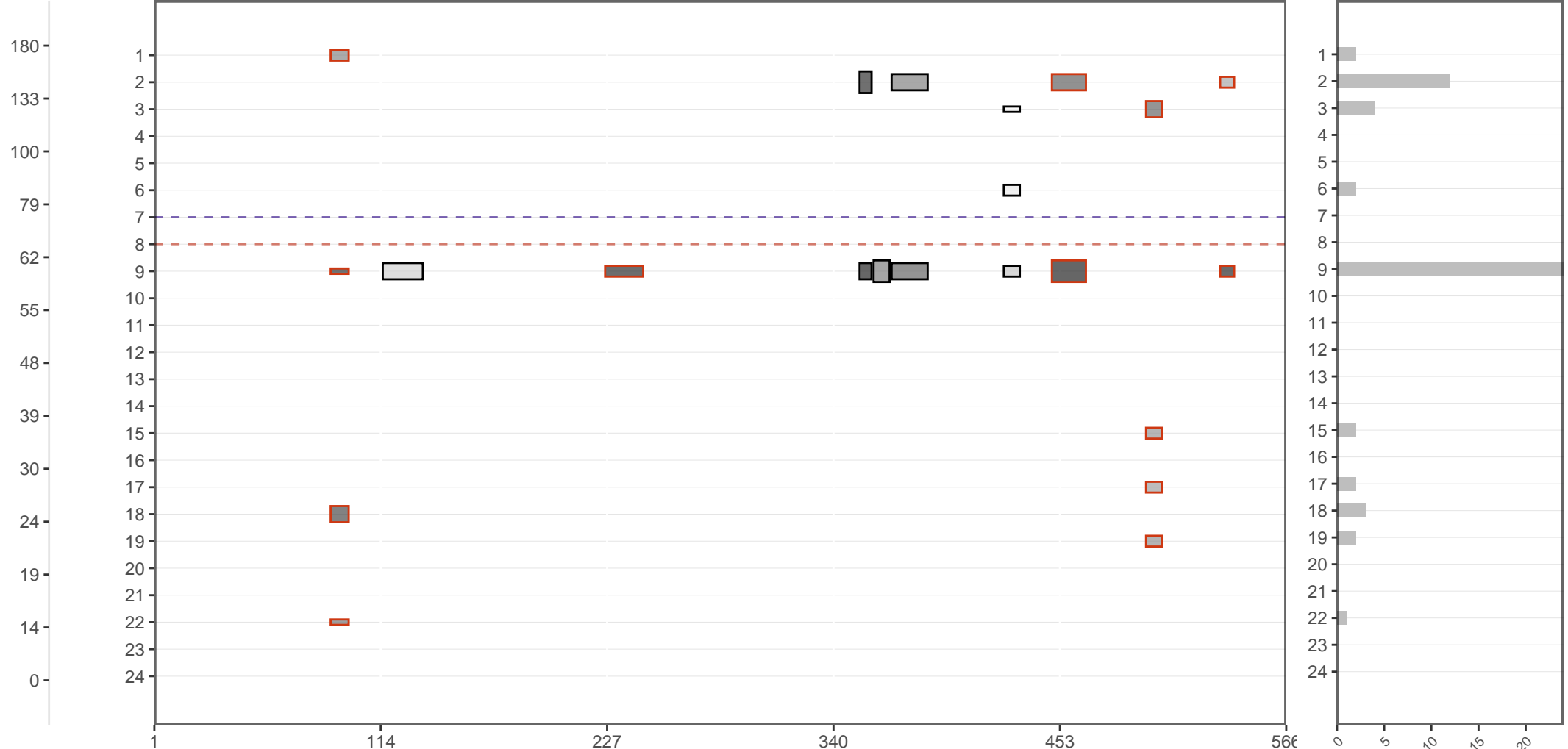


MW indication



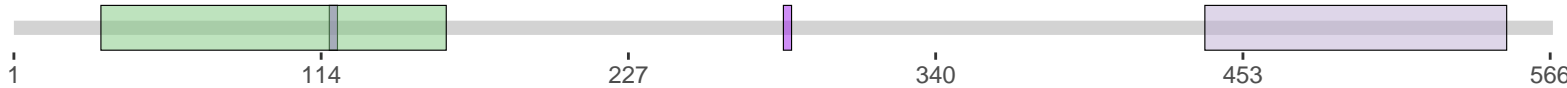
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

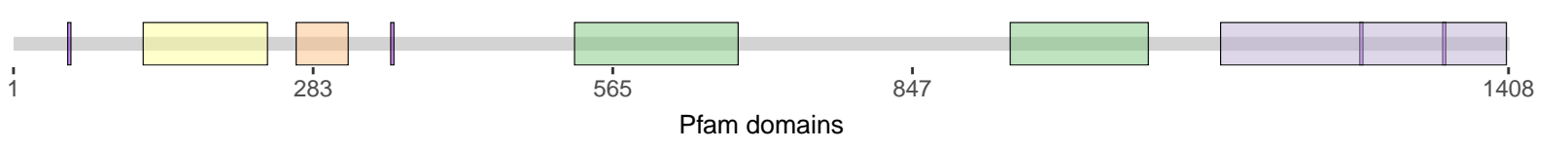
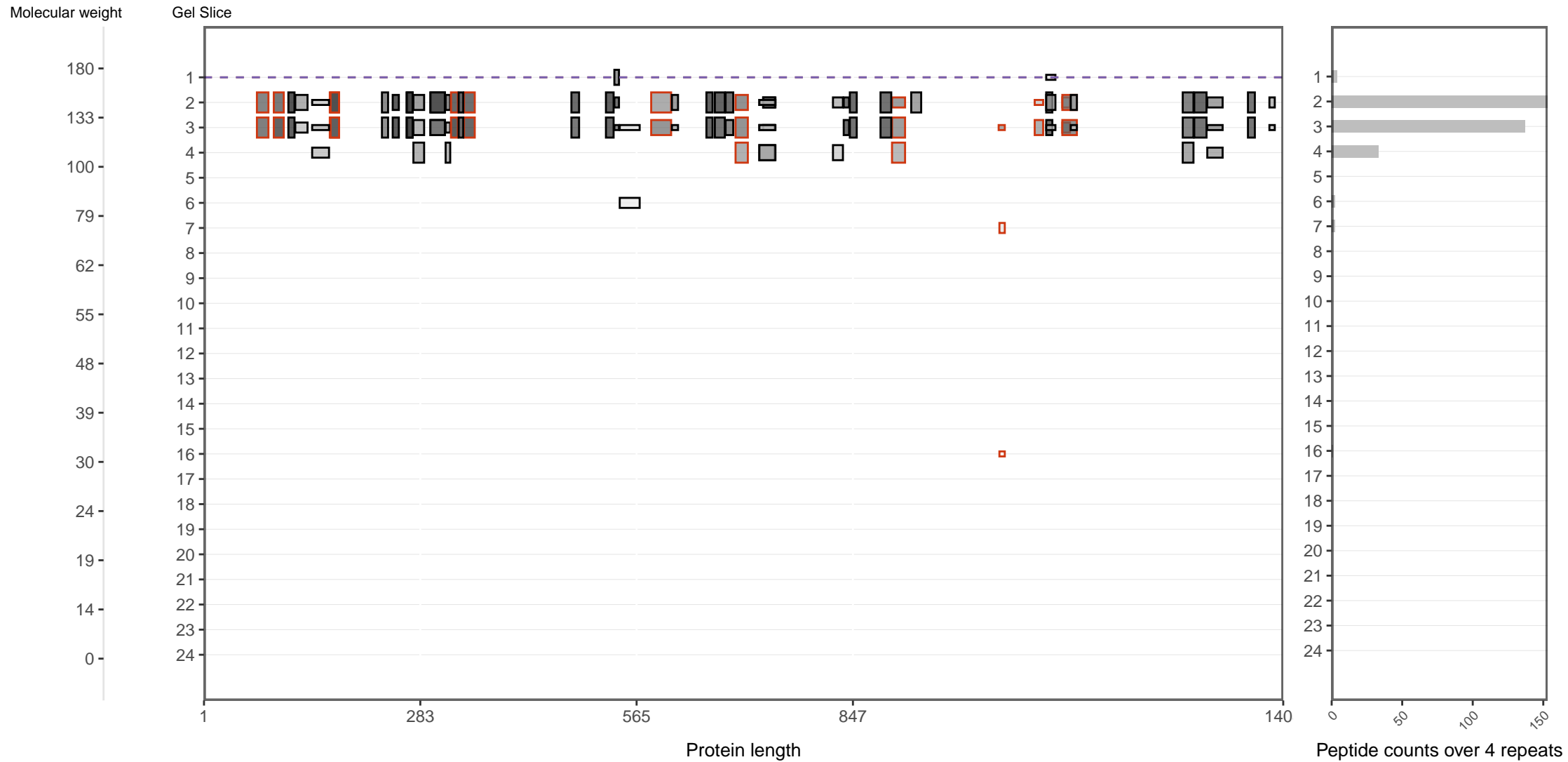
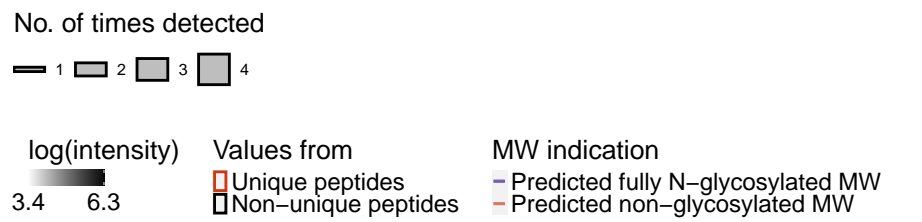
Pfam Description

- SP
- Sequon
- TM Domain
- PF17767 Nicotinate phosphoribosyltransferase (NAPRTase) N-terminal domain
- PF17956 Nicotinate phosphoribosyltransferase C-terminal domain

Protein sequence:

IGSHLGGIFSETNGSELAAFTSYGLAFAGFLALVDYDVMRSGVNFDAWALALNDLGVRAVGRILDSGLAVGSGEARKFFQTIKEFGVSGFGKMSITASNDLNEETLDALNKGQHEVDFSGIGTHLVTCYAGRALGVVFKLVEINNPRIKLSDDVTKVSIPOKRRGFLRYLKGEGFFLVDMAGENEPKPKVGERILGRHPFSESKRAVAVPQRVEELIKGFWPGSSDKKREDLPLPKIEIRERCQKLEGMRPDHRMRLNPTPKVYVSAALYDFIHFLLVLEAPVGELO*

NbL16g14460.1 probable_phosphoribosylformylglycinamide_synthase_chloroplastic/mitochondrial [MW = 154.18 kDa]



- Description
- TM Domain
 - PF02769 AIR synthase related protein, C-terminal domain
 - PF13507 CobB/CobQ-like glutamine amidotransferase domain
 - PF18072 Formylglycinamide ribonucleotide amidotransferase linker domain
 - PF18076 Formylglycinamide ribonucleotide amidotransferase N-terminal domain

Protein sequence:

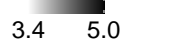
LPFPPIVLDLEKVAQDMPIKTFEFRFRMNLEPLDIAPATVLDLKLRLPLPVGSKRFLFTKVDRCVTGLVAGDQTVGLGDLADVAWIAGTYTDFFTGGACISGEGPKLGLDLPKAMARLAVGEALTNVWVKYTSLSLVDKASGNMVAAKLDDGEGAMVDAAVASEAMELGIANDGGKDLSSAAHSSGGLVAKAPGNVISTYVTCDFDITKTVTSDLKLGDDGVLLHDLAKGKRRLGGALAGVFDGIGDESPDLDDVYKTVFNEVGNISGELISAGHDSIDGGI

NbL16g14390.1 putative_oxidoreductase_TDA3 [MW = 44.35 kDa]

No. of times detected



log(intensity)



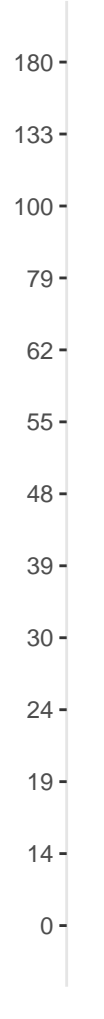
Values from



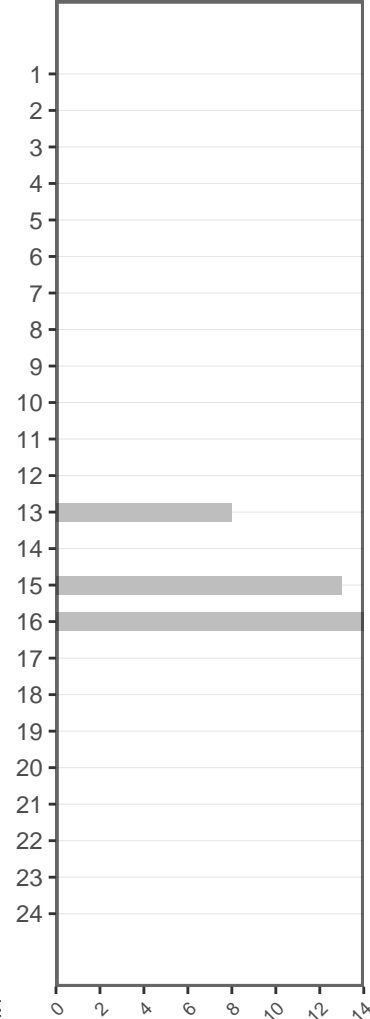
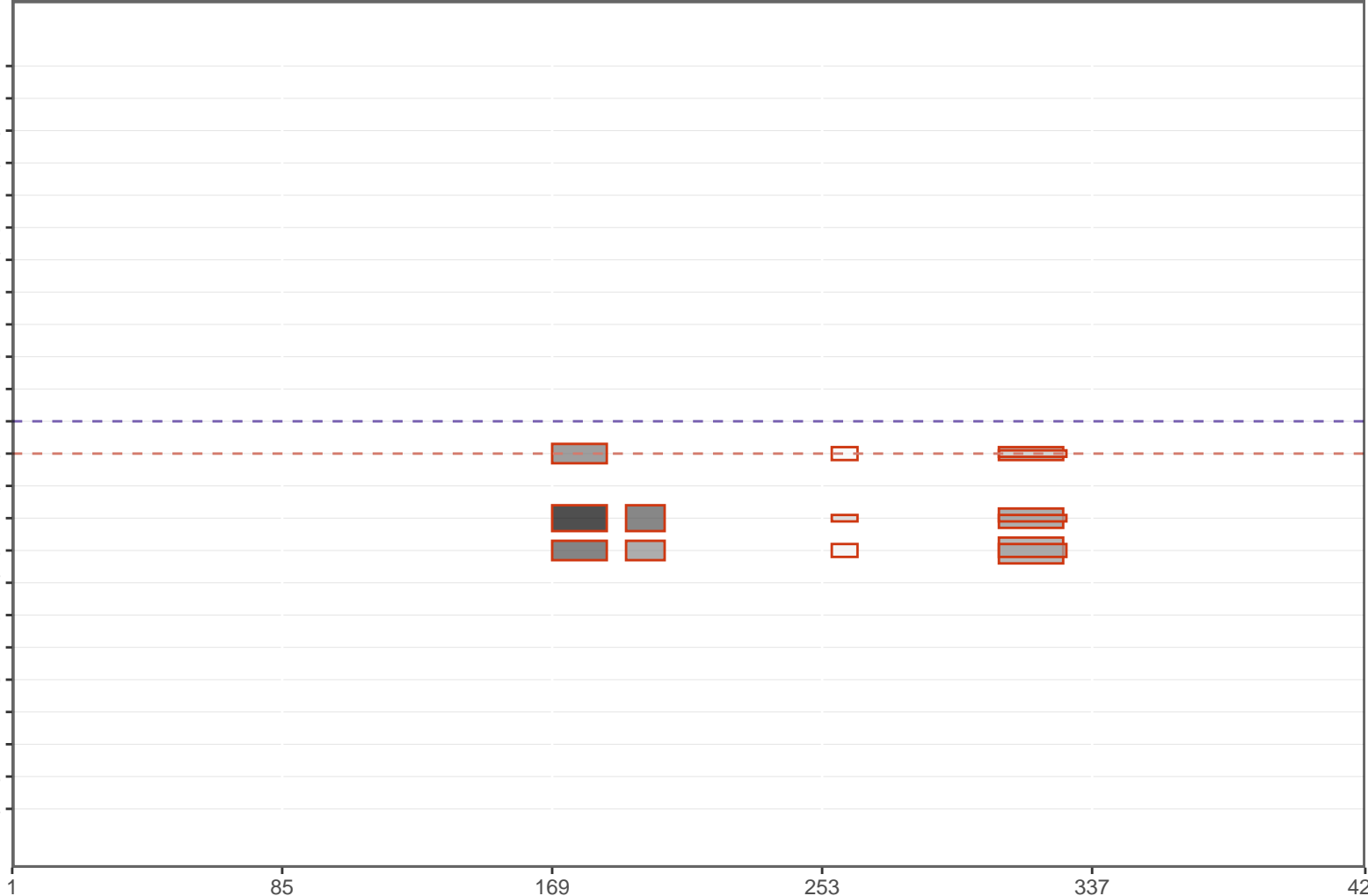
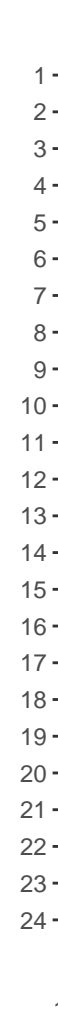
MW indication



Molecular weight

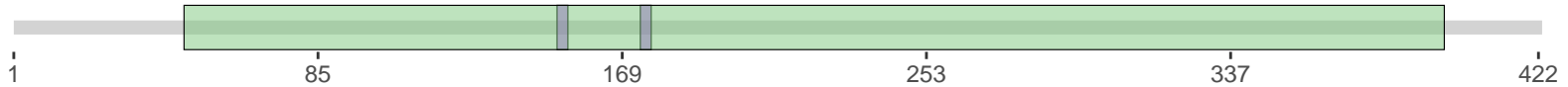


Gel Slice



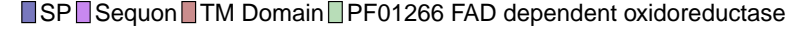
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGVEVVGKAEKRVEMAEKTKNGVLEDDGREVADAVLALGPWTKRFSILGSLFGVYQKAKHSVLEPKENRTPHALFLTYYPHSGKPMDEPVVPRPTGVEVYVIGCMSAREEVPDDPGQVPIVPESSINALKRWAAQVSSHLVEGAAVTEAQGLPGSEDDVPIGEVPGIKGCVYATGHSQWGLNGPATGAAMAEILDGGANIVDLGGFTPRRFASLKKI

NbL16g14350.1 subtilisin-like_protease_SBT1.7 [MW - SP = 78.77 kDa]

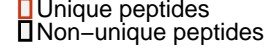
No. of times detected



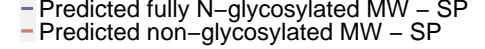
log(intensity)



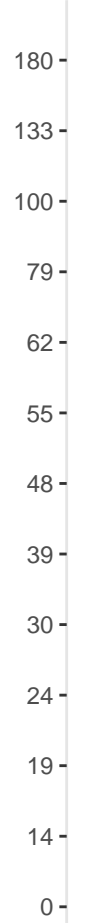
Values from



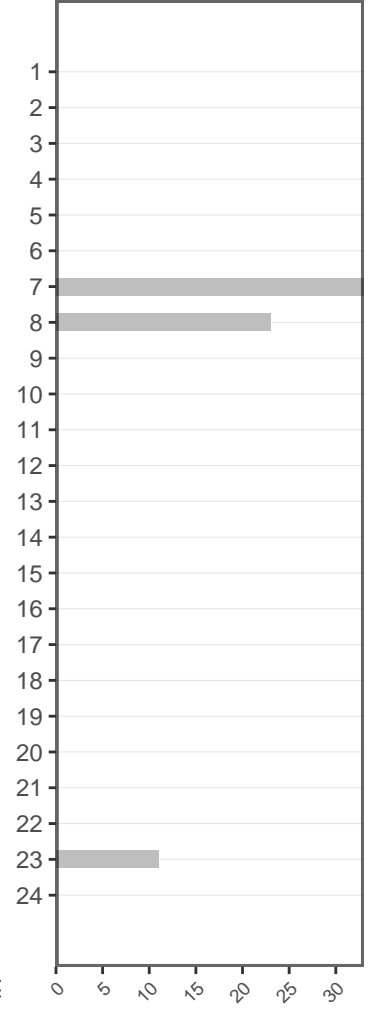
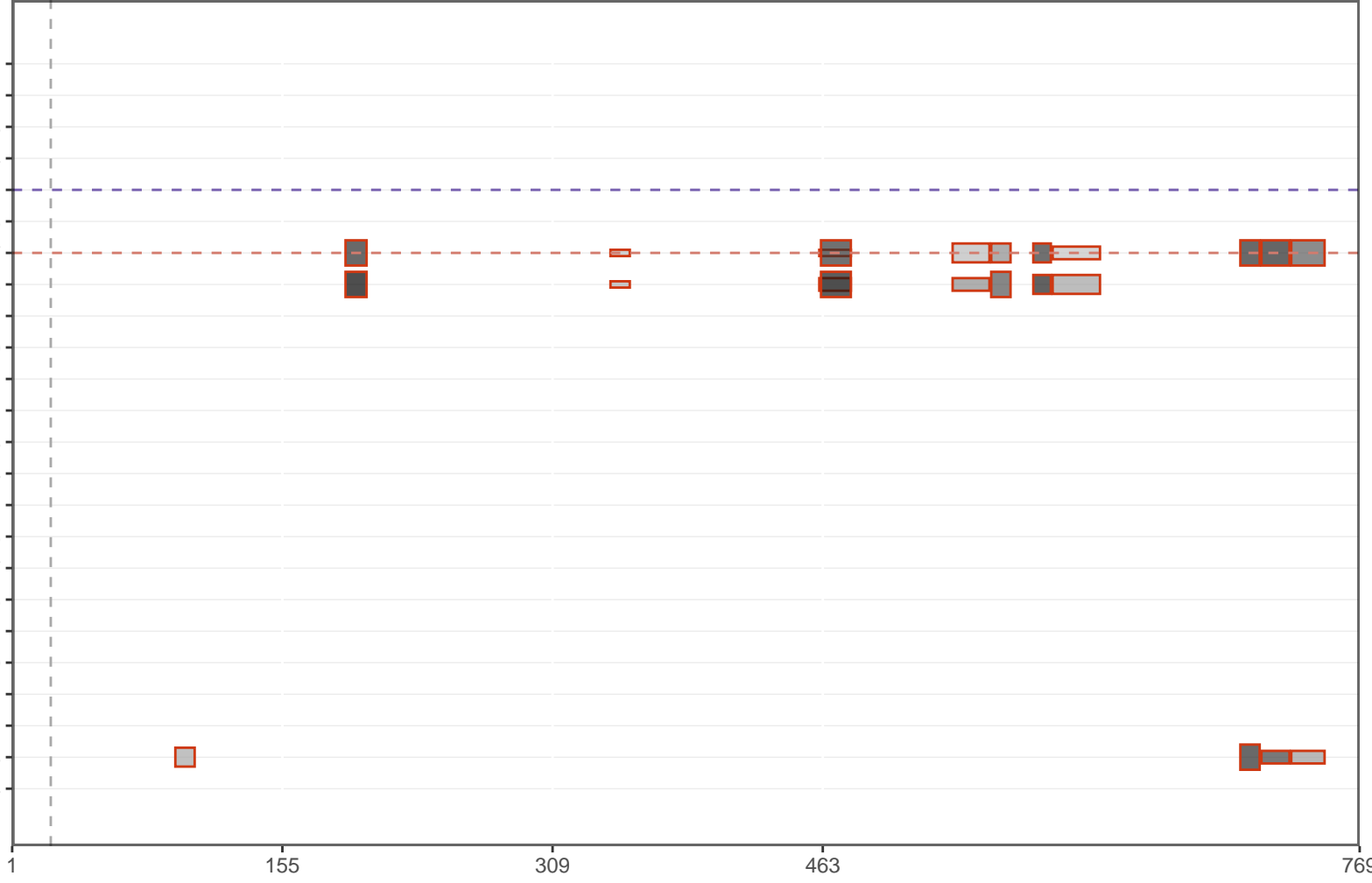
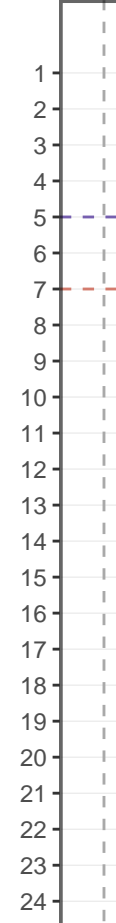
MW indication



Molecular weight

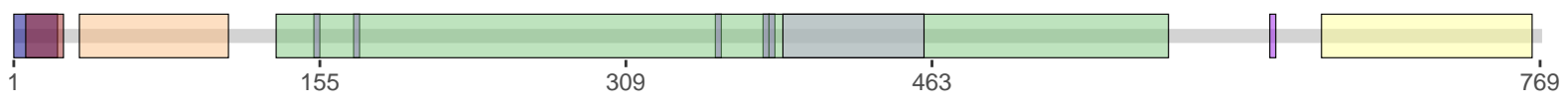


Gel Slice



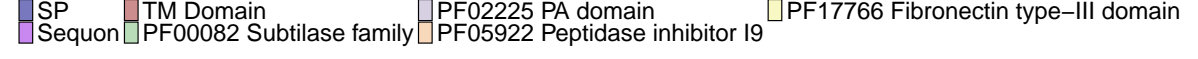
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KMLPFVYAGNASFTNGNLGMDTGLPEKVKGKVLGDRGINPRVKGVAKEAGGVMLANTAANGDELVADHLLPATTVGDMTGEANKYLAGDPNPTATLFEKTVKGIKPEPVAFAFSSRGNPNSTQELKPDIAKPVNLSGGWTGAAGVPTGLAEDTRRVRFNISGTSMSGPHVGLAALLKGAHPDWSPAIRRSALMTTAVTVYKNGGALGDVSTRKPTPEFDKAGHVDVVAALNPLGVYDLRADDHNLFLGALNYTSQINSIARRNVCETSICKYSYVDLNYPSF

NbL16g14340.1 casein_kinase_II_subunit_alpha-2 [MW = 39.35 kDa]

No. of times detected



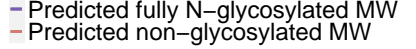
log(intensity)



Values from



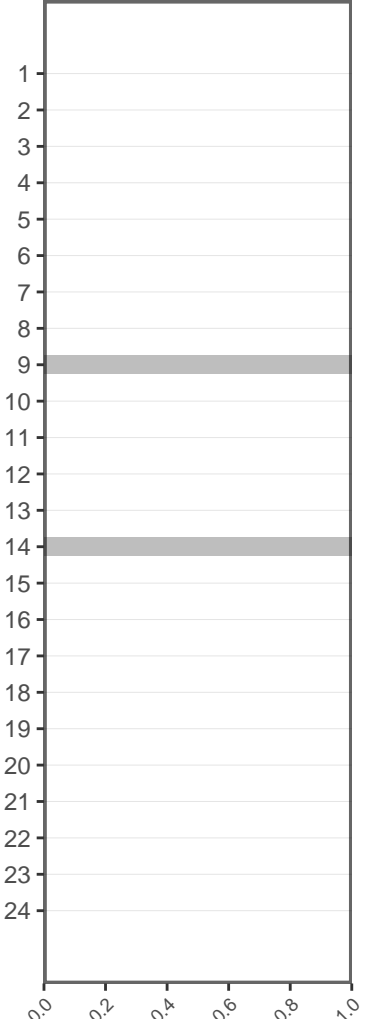
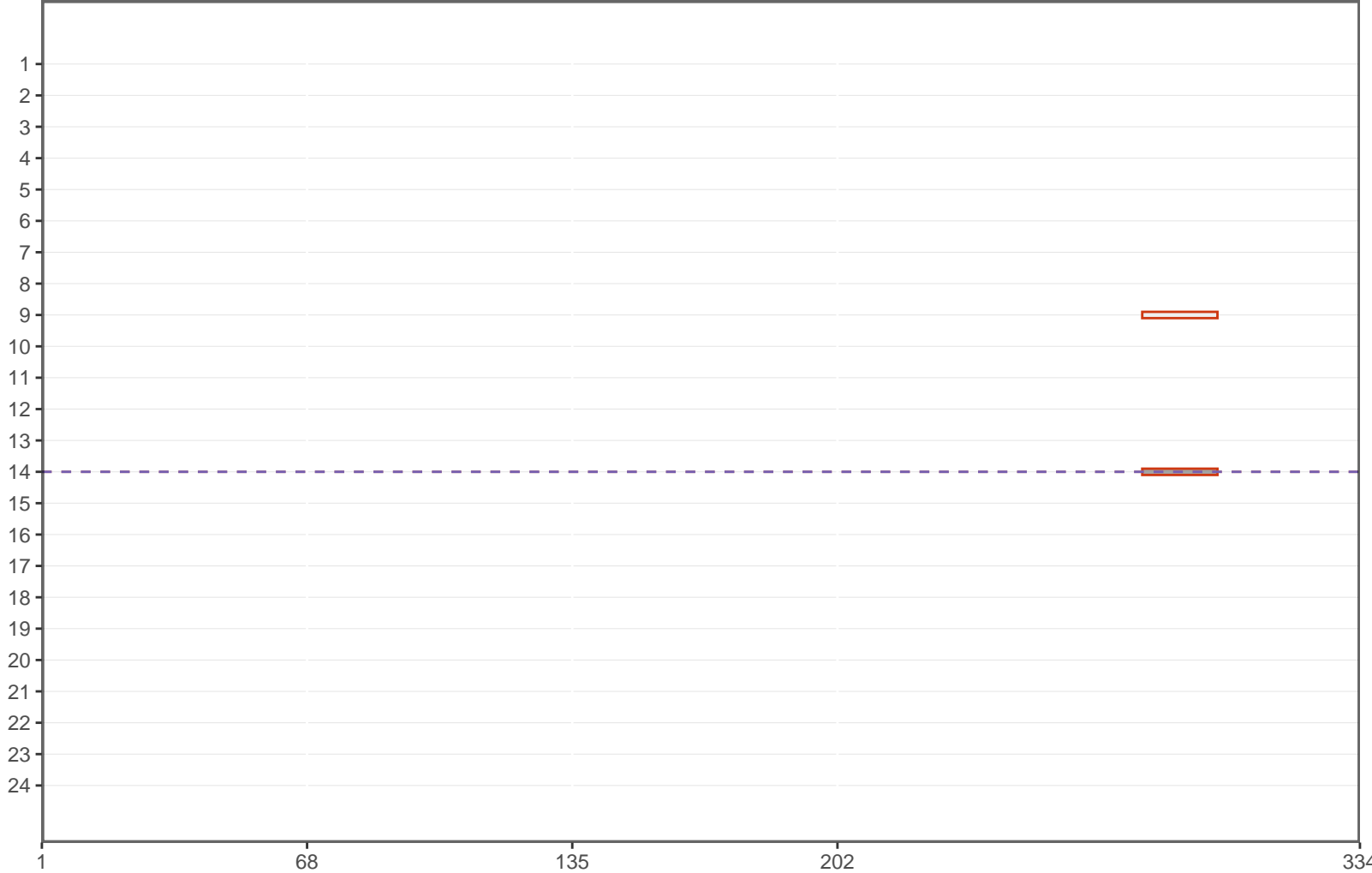
MW indication



Molecular weight



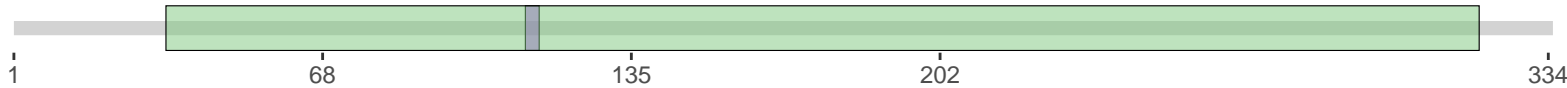
Gel Slice



Protein length



Pfam domains



Pfam Description

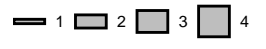


Protein sequence:

VMDHELKRLLDWGLAEFYHPGKEYNVRVASYFKGPELLDQDYDYLDMWISLGGMFAKFRKEPFYGHNDQDLVKAIVLGTDELNAVLYHKYQLELDPQLEAMVGRHSRKPWKFNFNADNGHLVSEIDFLDKLLRYDHDQRLTAREAMAHPIYFLGVRAENSRMRTQ

NbL16g13950.1 protease_Do-like_7 [MW = 57.84 kDa]

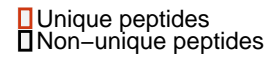
No. of times detected



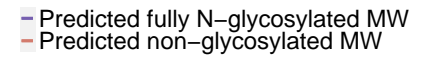
log(intensity)



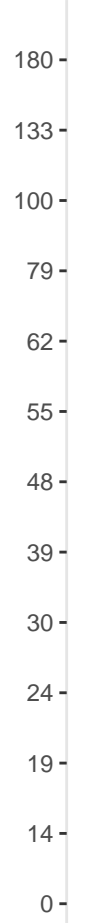
Values from



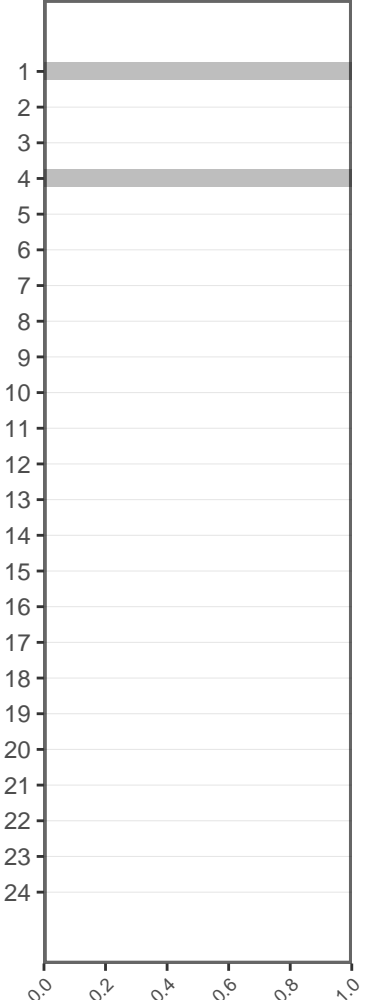
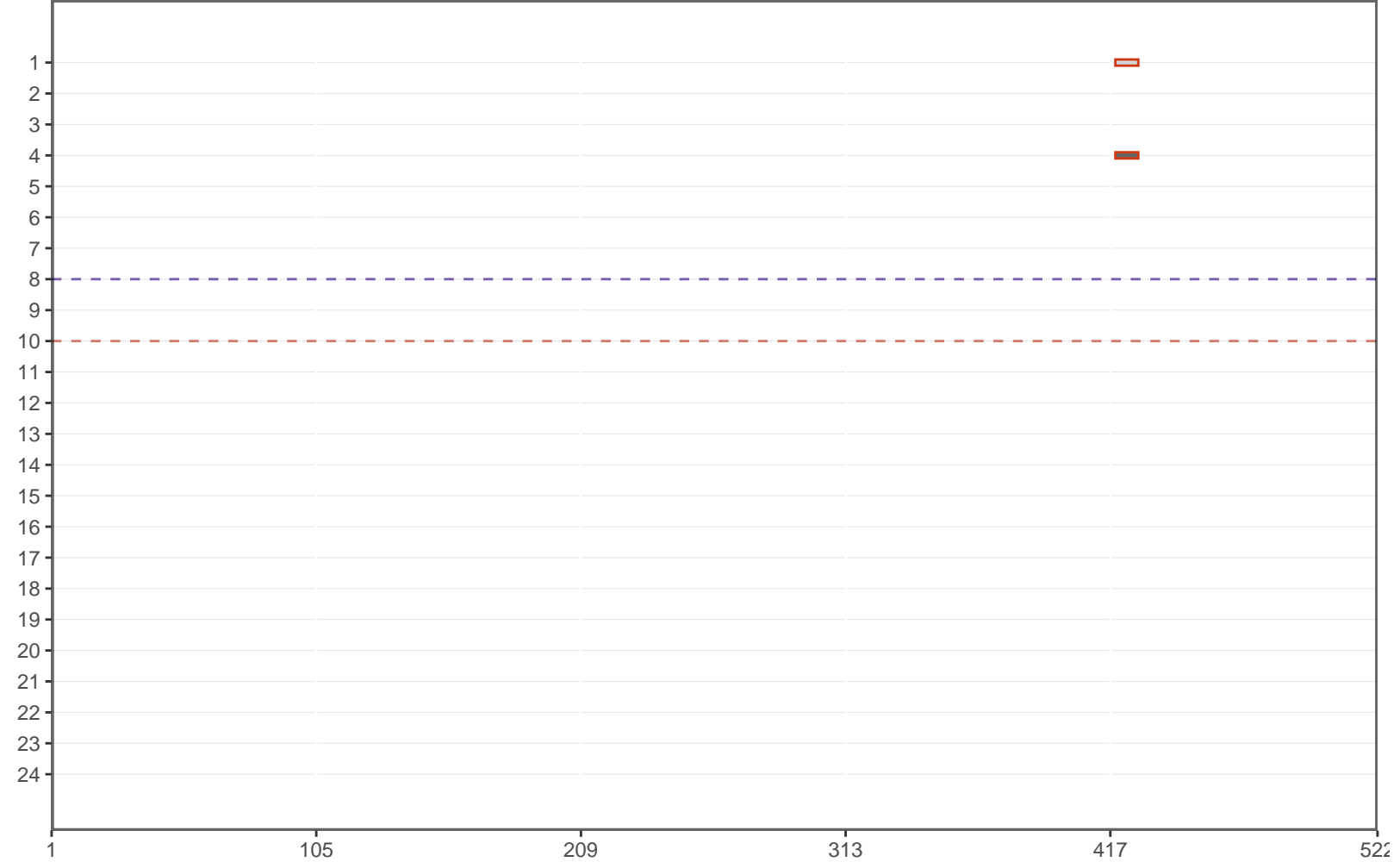
MW indication



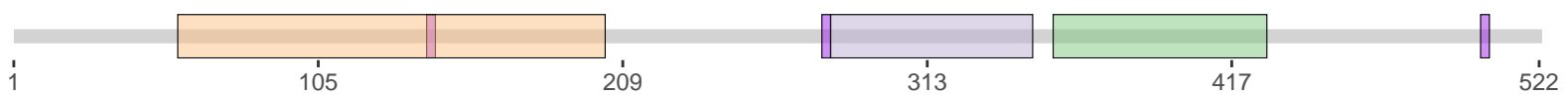
Molecular weight



Gel Slice



Protein length



Pfam domains

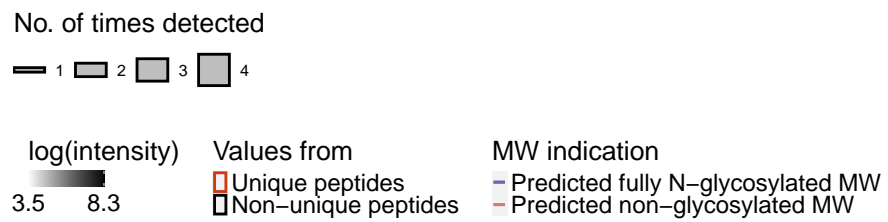
Pfam Description



Protein sequence:

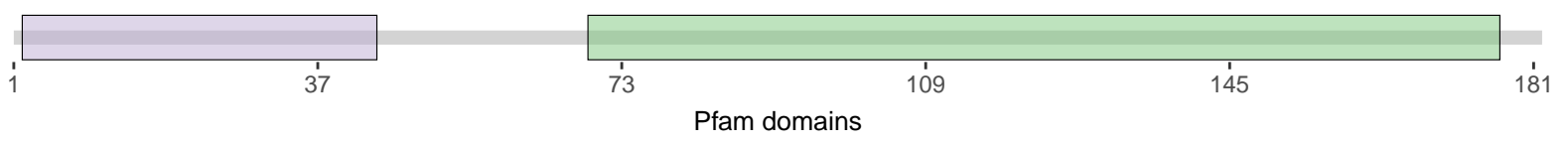
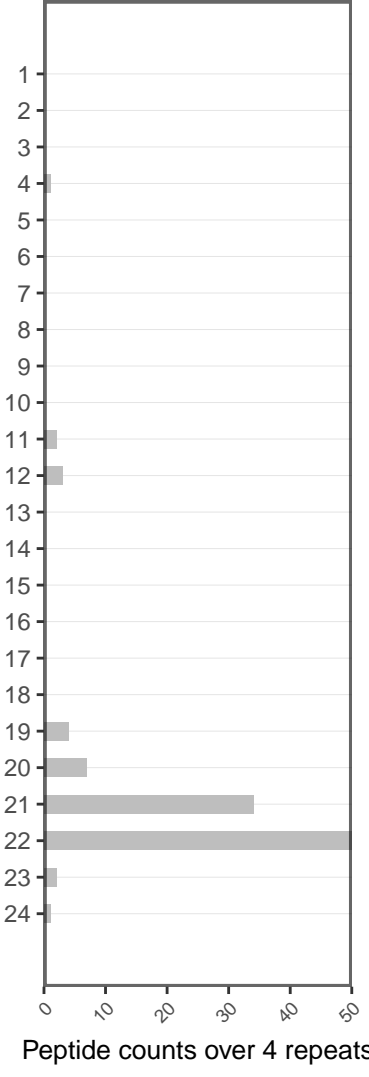
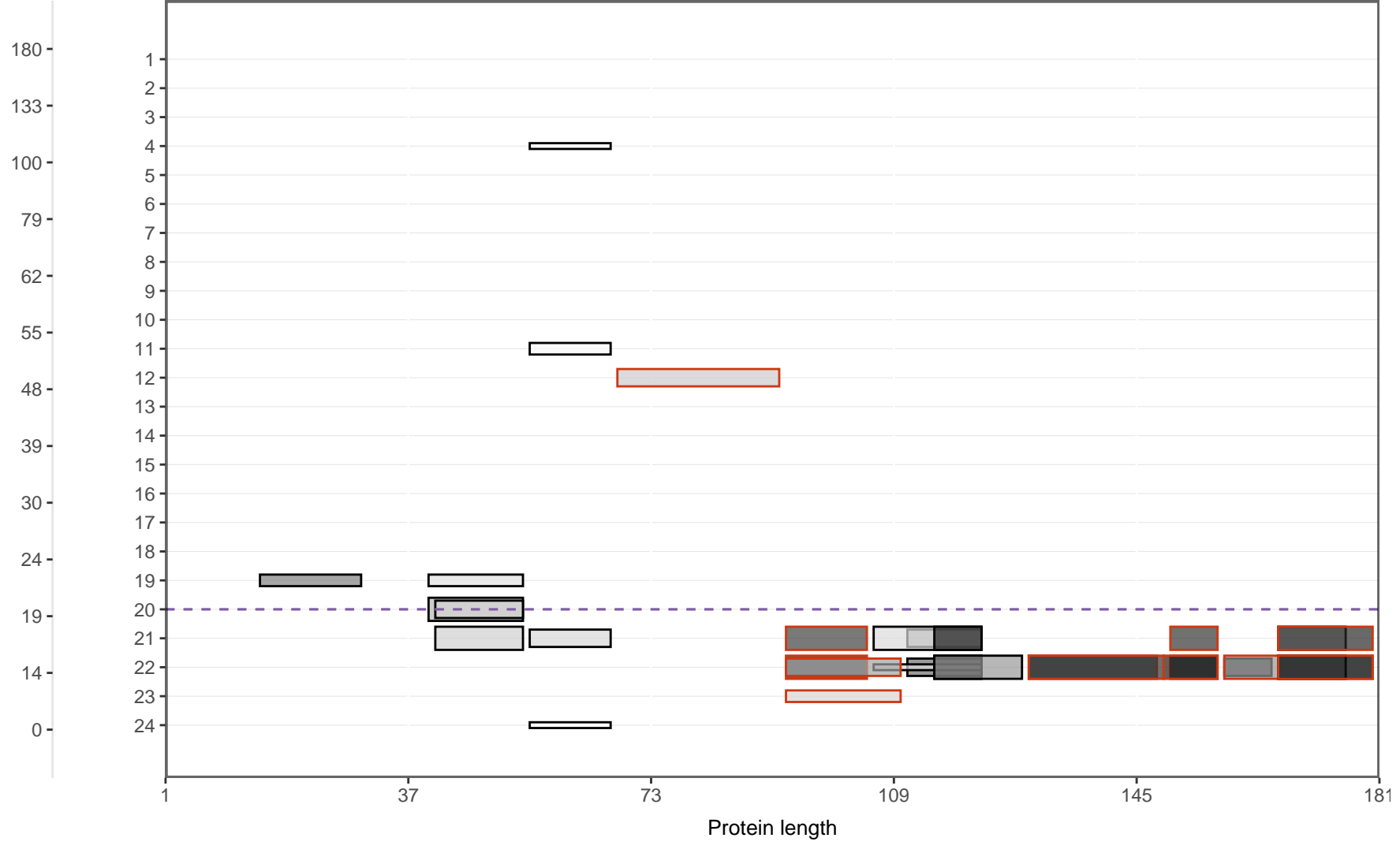
GTLOVTFLLKGFDETRRLGLGHETEGLVRNSTPPSETGMLVDDGVVPGGFGMHLKPCGDVLRMMGEVVTGFLKMETLLDSDVEKIEIQIERSSTPLVDLLVGLHSITPRHFLVLEVGAVHPLSYGGARNFRFNGDLYVVAEPGVMLEFRAGVPRHSIKKFFAGEGSRLEEDLSVLGKMERGARVPLEYISYKERHQRKSVLVTDRHEWVAPPQYKRRDSSGLWTVLALRQESPLLGGYPPVEGDLNHTGSGIGGVKDYPEGVSGE

NbL16g13890.1 ribulose_bisphosphate_carboxylase_small_chain_chloroplastic [MW = 20.25 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00101 Ribulose bisphosphate carboxylase, small chain
- PF12338 Ribulose-1,5-bisphosphate carboxylase small subunit

Protein sequence:

.SDEQLLSIEYLLKNGWVPLEFETEKGFVREHHKSPGYDGRVYTMWKLPMFGGTDATQVLAEVGEANKEYPQAWRIIGFDNVRVQGGISFIASKPDGY

NbL16g13840.1 14-3-3-like_protein_E [MW = 31.39 kDa]

No. of times detected



log(intensity)



Values from



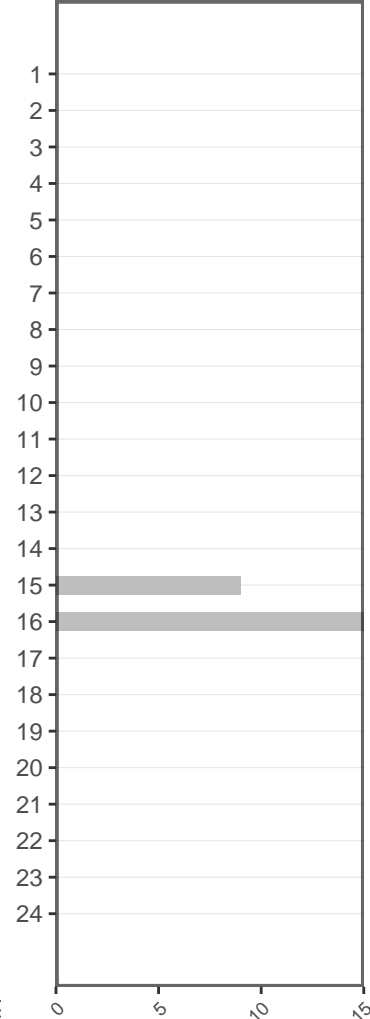
MW indication



Molecular weight



Gel Slice

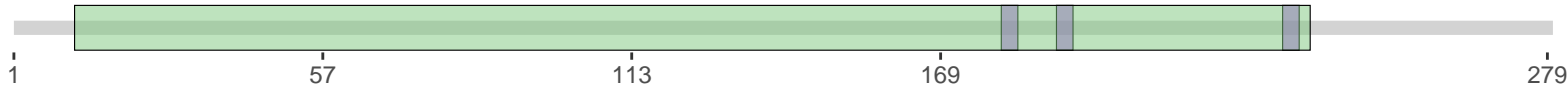


Protein length

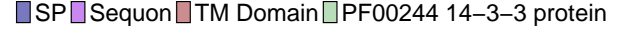


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KMKGDYIRYLAELFKTGAERKEAEMNTLLAYKSGAGDIALAELAPTHIRLGLALNFQVYFYEILNSSDRAGNLAKGAFDDAAELDTLGEESYKDTLIMQLLRDNLTLWTSDDTVLSLFLPPLPRLALSHTEKYKPTNADAPTHKHCYAH

NbL16g13610.1 proteasome_subunit_beta_type-1-like [MW = 24.61 kDa]

No. of times detected



log(intensity)



Values from



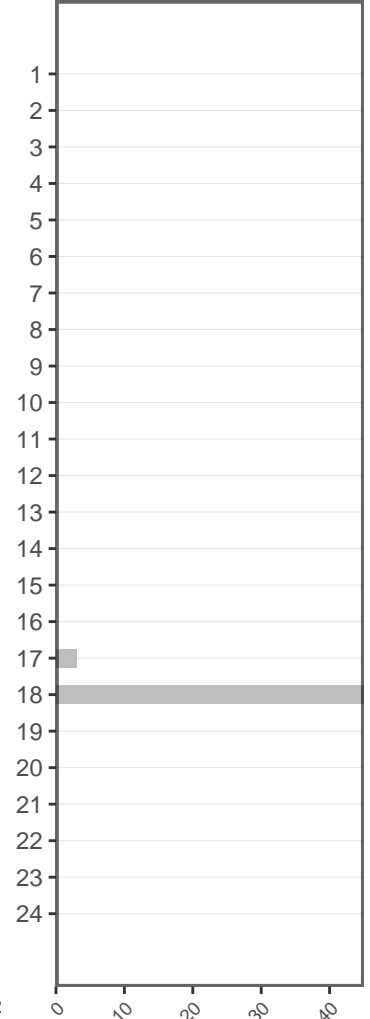
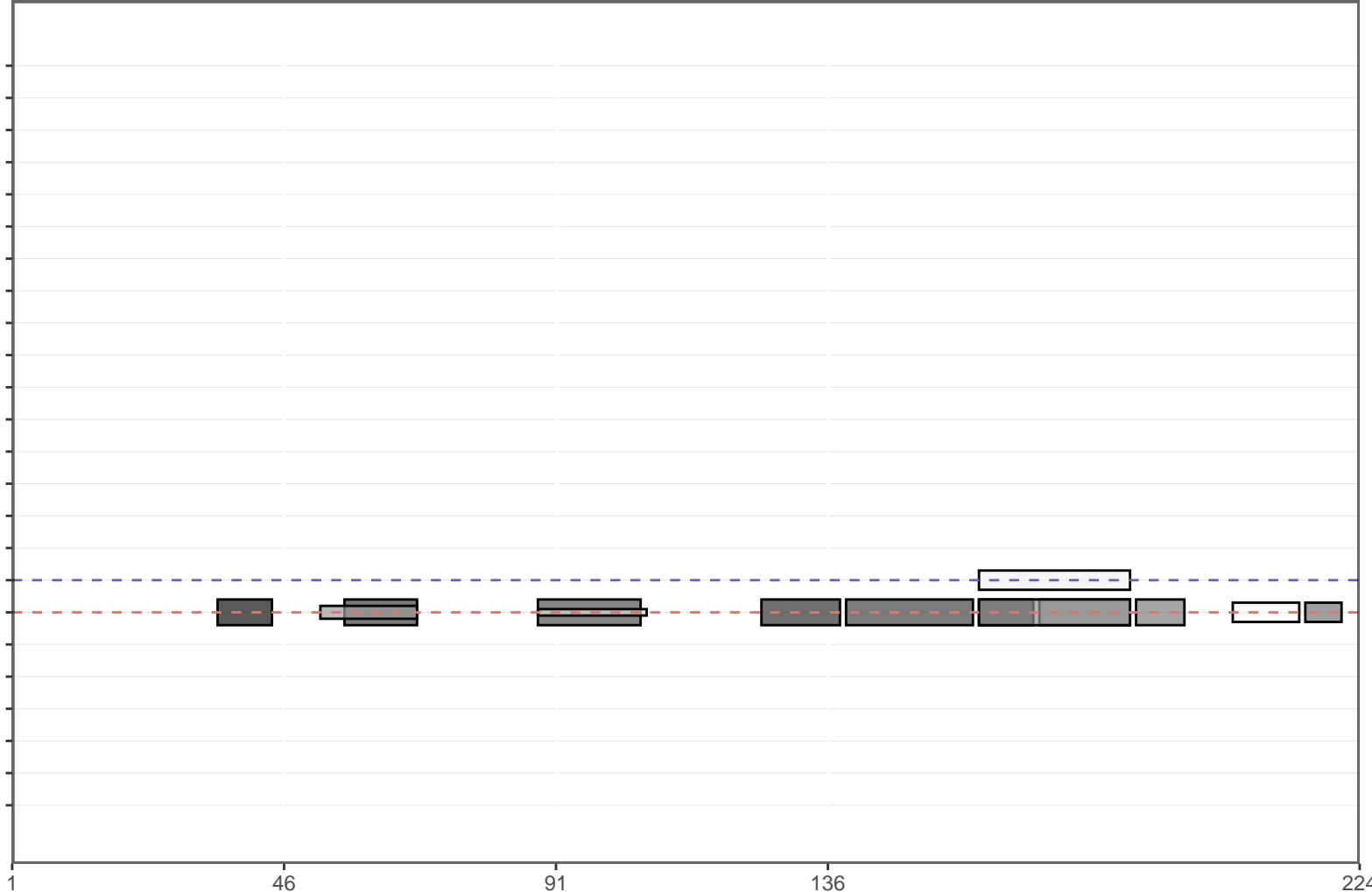
MW indication



Molecular weight

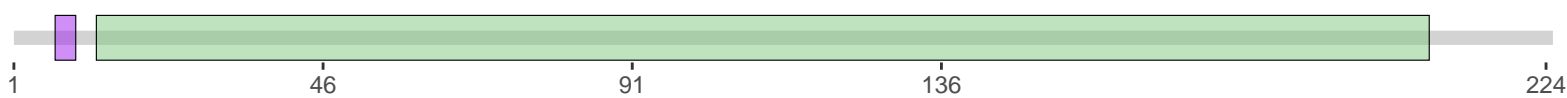


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LSNTLYKRFFPYAFNVLGGLDNEGGVFTYDAVGSYERVYSGGGSGSTLMPFLDNQKSPSPLLLPAKDAVTFLSESEANDLWKTGFASATERDVTGDKLEIVLNADGVRRREEMDLRRD

NbL16g13590.1 inosine_triphosphate_pyrophosphatase [MW = 22.67 kDa]

No. of times detected



log(intensity)



Values from



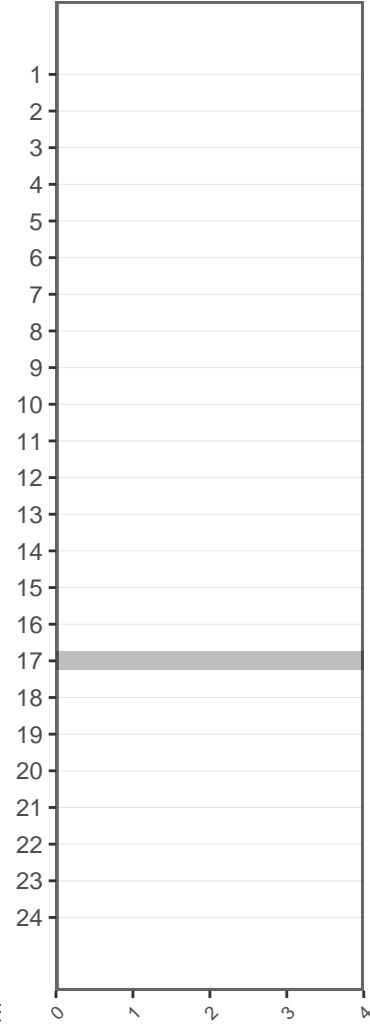
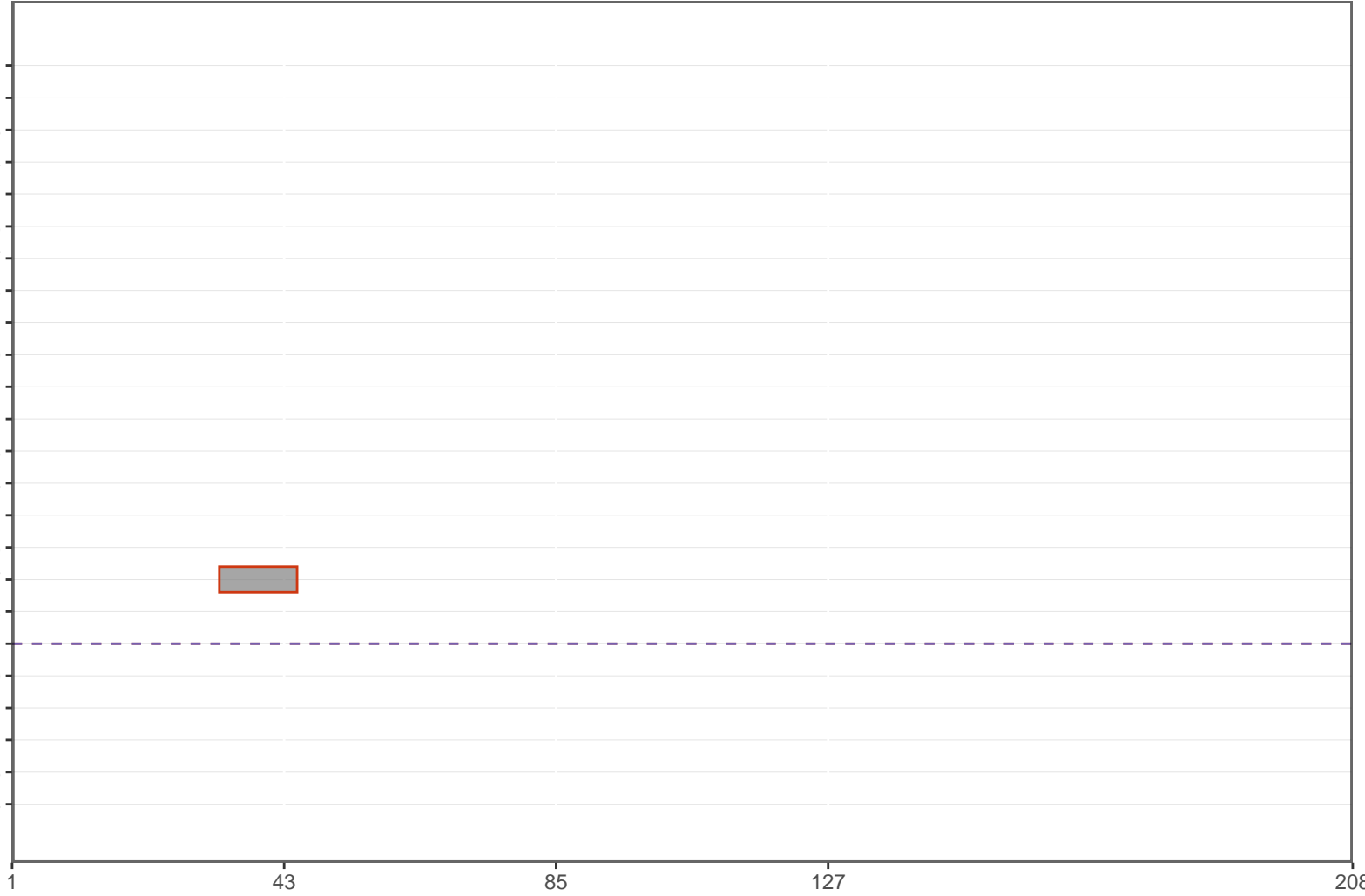
MW indication



Molecular weight

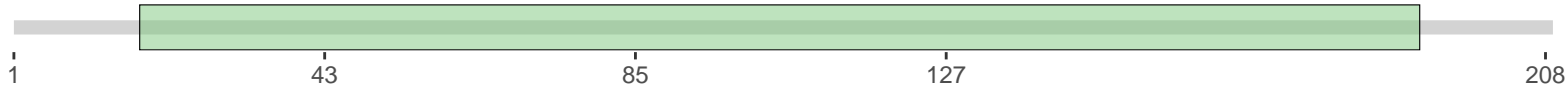


Gel Slice



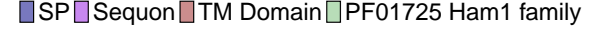
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

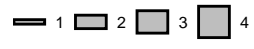


Protein sequence:

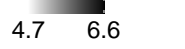
SPYIKWFLQIKGHEGLNLLLAYEDKTAAMQVFLALGPNSEELTFVSKTLGRVWPARGPNDFGWDPIFGPHGVDQTYAEMPKEGKNKISHRGKALELWKSFAEARVTFQTDITA

NbL16g13290.1 chaperonin_CPN60-2_mitochondrial [MW = 61.38 kDa]

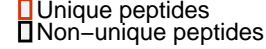
No. of times detected



log(intensity)



Values from



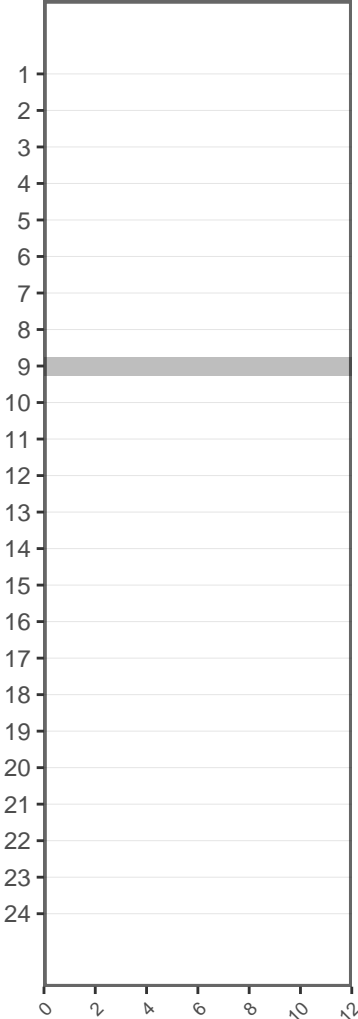
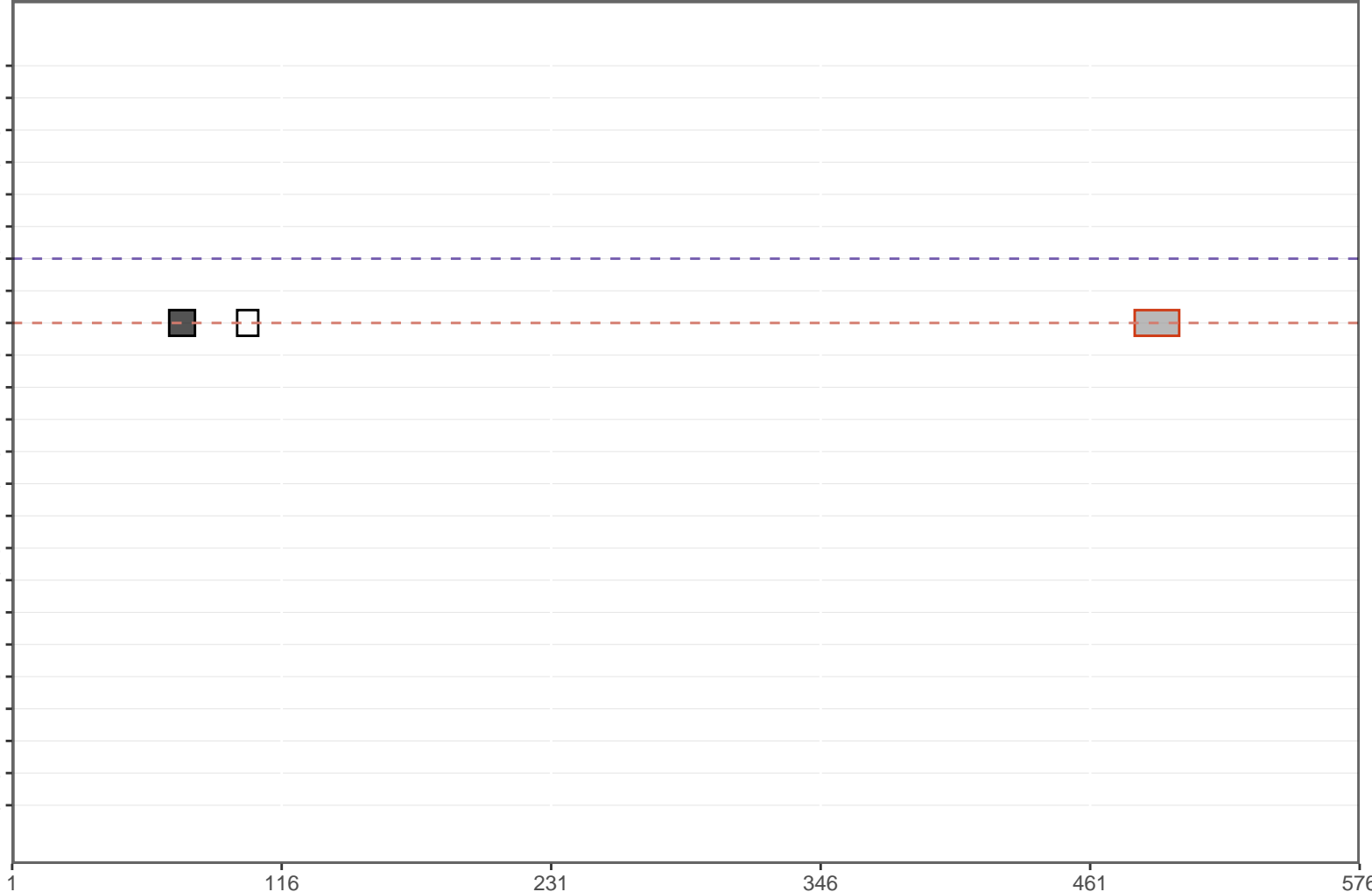
MW indication



Molecular weight

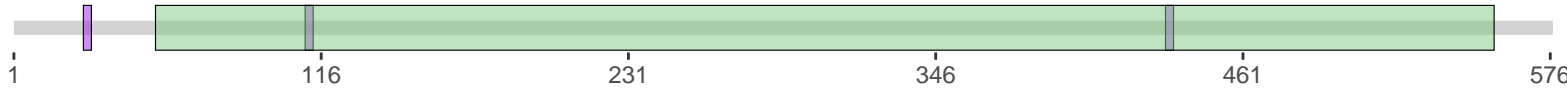


Gel Slice



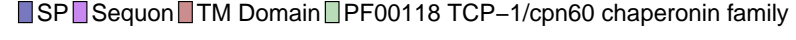
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KRORPLLVIEDVDSSEALATLILNKLKAGIKVCAIKAPGSGENRKAAGDLALTGGQVYVEELGLNIENVELEMLGSCKKVAIKDDTVILDGAGEKKISIEERGEQIRTEIESTSDYDKEKLEERLAKISGGVWVKIKIGGABAEVGEKKRVRTDALNATKAAVEEGVPPGGVALLYAAKELDKLETNFDQKIKGKIQKALKTPVHIASNAGVEGAVVVKLLEGGDTLGLGYDAKGEYVDMKAGHIDPLKVRTALVDAASVSLFTTEAVVVELPKDEKETPMGGMGGI

NbL16g13240.1 7-hydroxymethyl_chlorophyll_a_reductase_chloroplastic [MW = 50.46 kDa]

No. of times detected



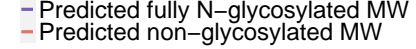
log(intensity)



Values from



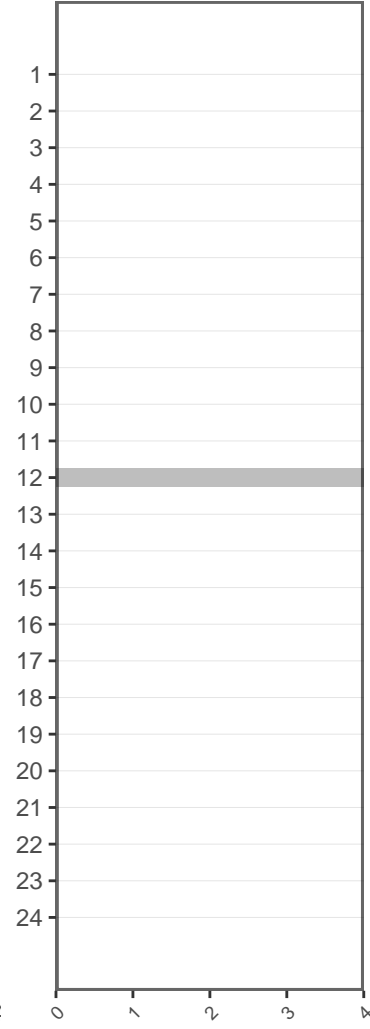
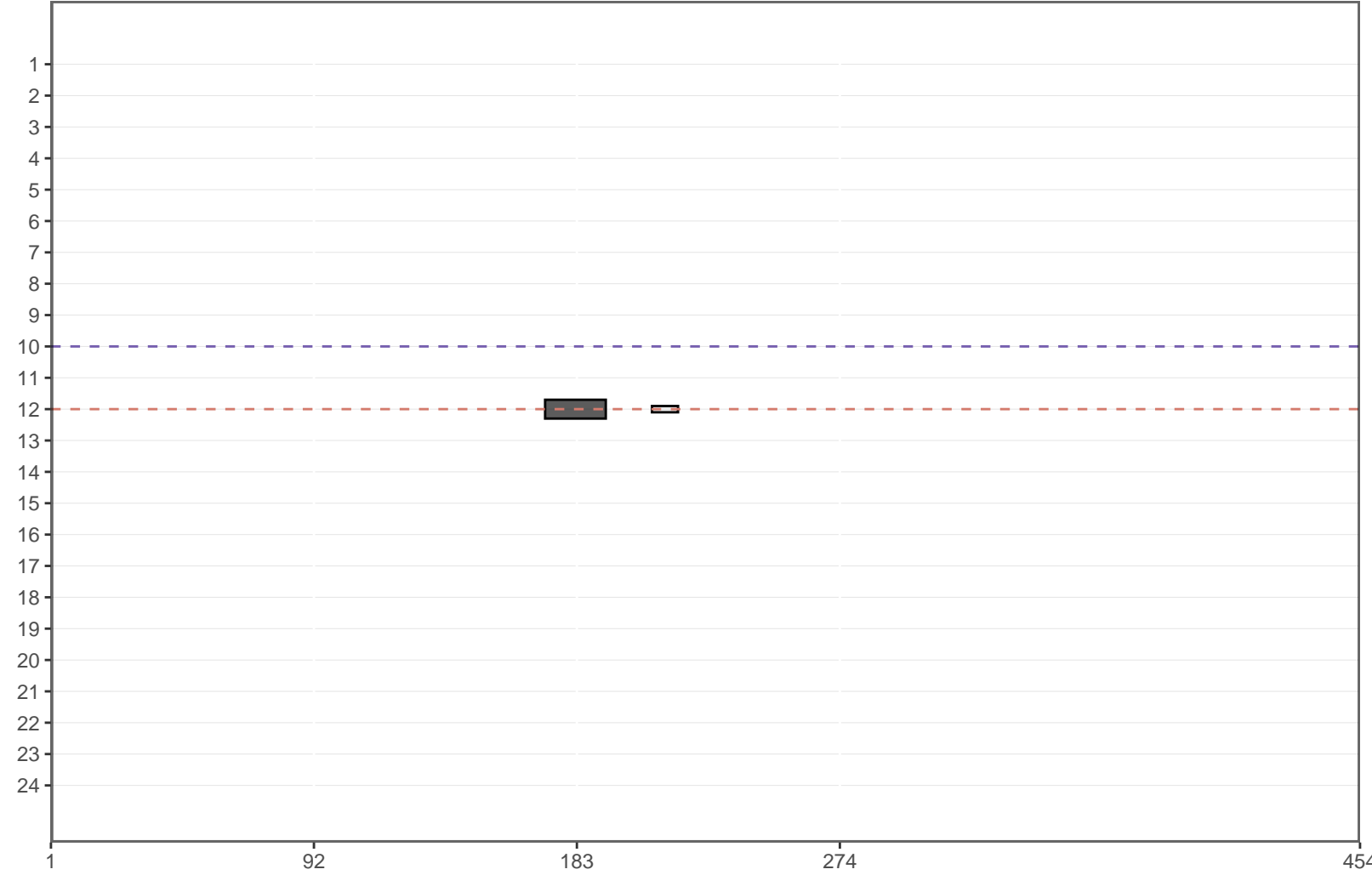
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF04422 Coenzyme F420 hydrogenase/dehydrogenase, beta subunit N-term
- PF04432 Coenzyme F420 hydrogenase/dehydrogenase, beta subunit C terminus

Protein sequence:

LNLEKLYLGTNCVQNGKREGLDKFLKAASBPETVLHYEFMDQYKHLKHLDDGHIEEVVFGLPANELVDVIAFSGYSGFDYTNGLADLVGVYMGVYSGISMMQHPQYVTVRNERGREMLSELVENLEITPTISSGNRRPFVETVKADDEAKFGRGAPGAPKPKVGNLIJFFLNIVGPKGLEFARYSLDYHTIRNLIHVVVRKWKGERADRHMPAWAKKIVSMYNGSGEIDQMLESK

NbL16g13200.1 malate_dehydrogenase_chloroplastic-like [MW = 43.93 kDa]

No. of times detected



log(intensity)



Values from



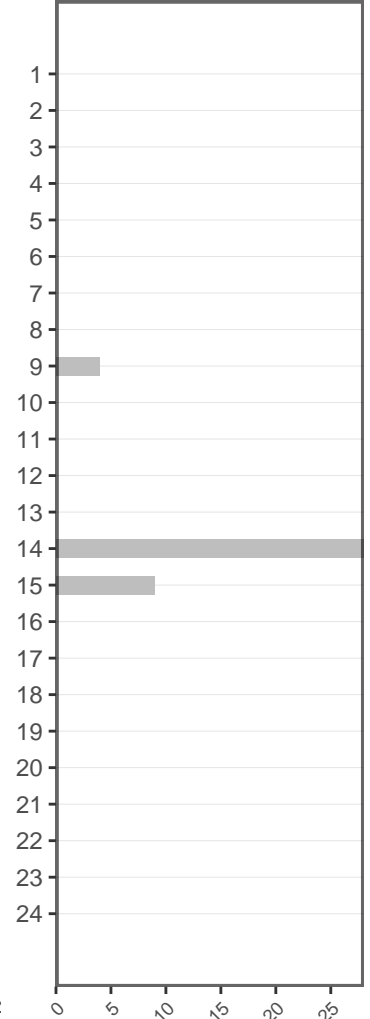
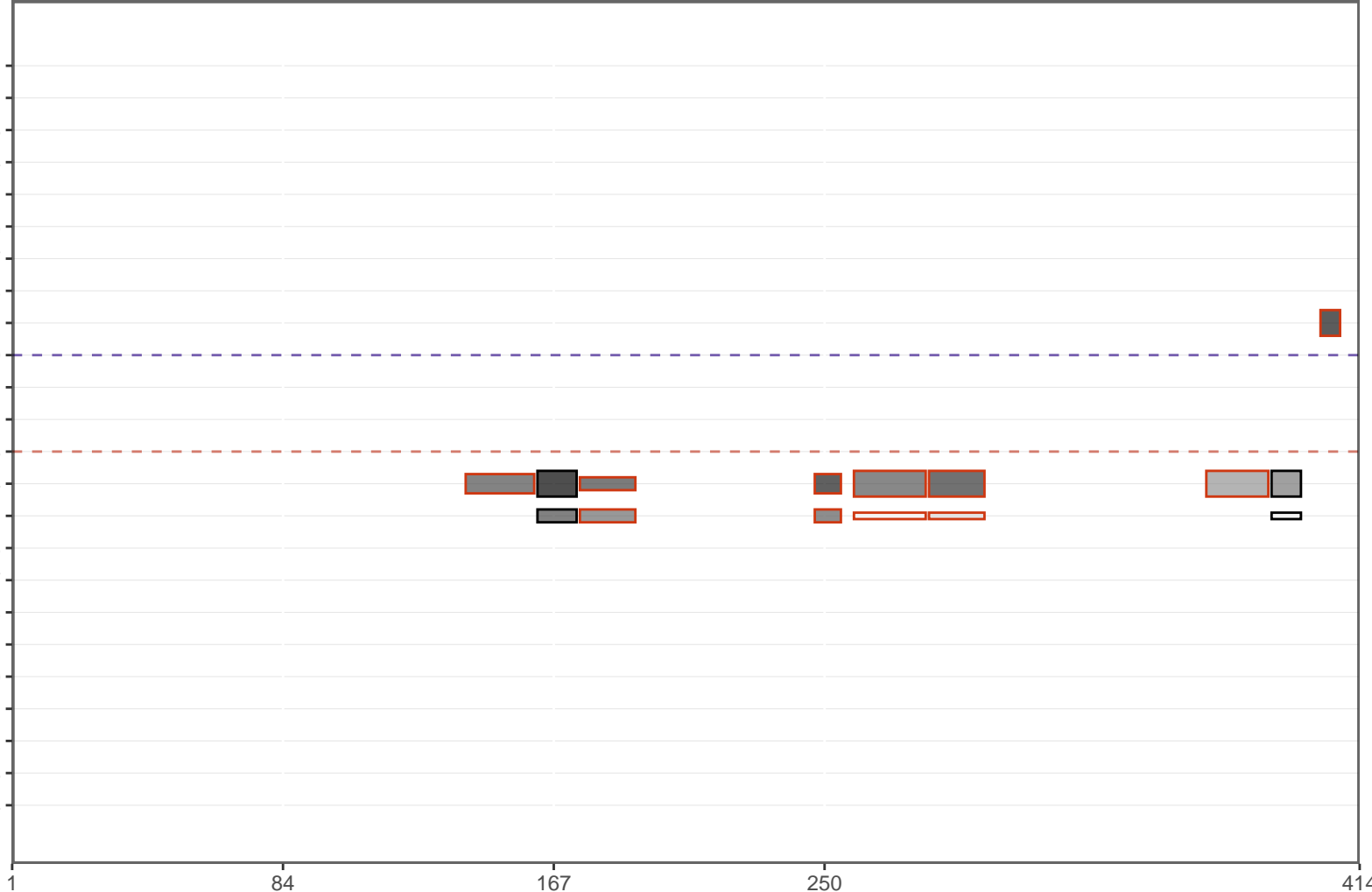
MW indication



Molecular weight

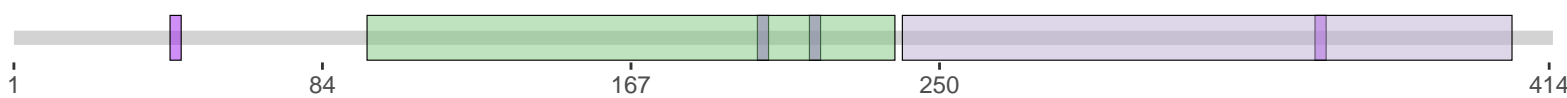


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00056 lactate/malate dehydrogenase, NAD binding domain
- PF02866 lactate/malate dehydrogenase, alpha/beta C-terminal domain

Protein sequence:

GLLVEAVADNCSDAFHSENPVNSTVPIAAEVLKQKGVYDPKILFGVFTLDVVRANTFVTGMKKLRLLIDVDVPIVGGHTGRTLLPKLSTPTFTTQKVEGLTVRIGNAGCTVEEAKAGAGSATLSMMAAAARFVVESSLRAIDGDADVYEGTYVEENLTELFFAFSRWLGRNGVEALISSDLNGLTYEQKALEAKPELKAIEKGVAAQKETVTA

NbL16g13130.1 haloacid_dehalogenase-like_hydrolase_domain-containing_protein_At2g33255 [MW = 28.46 kDa]

No. of times detected



log(intensity)



Values from



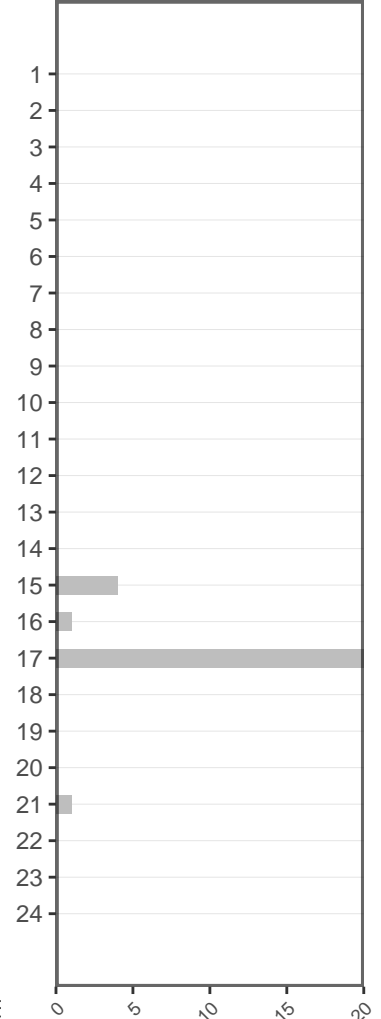
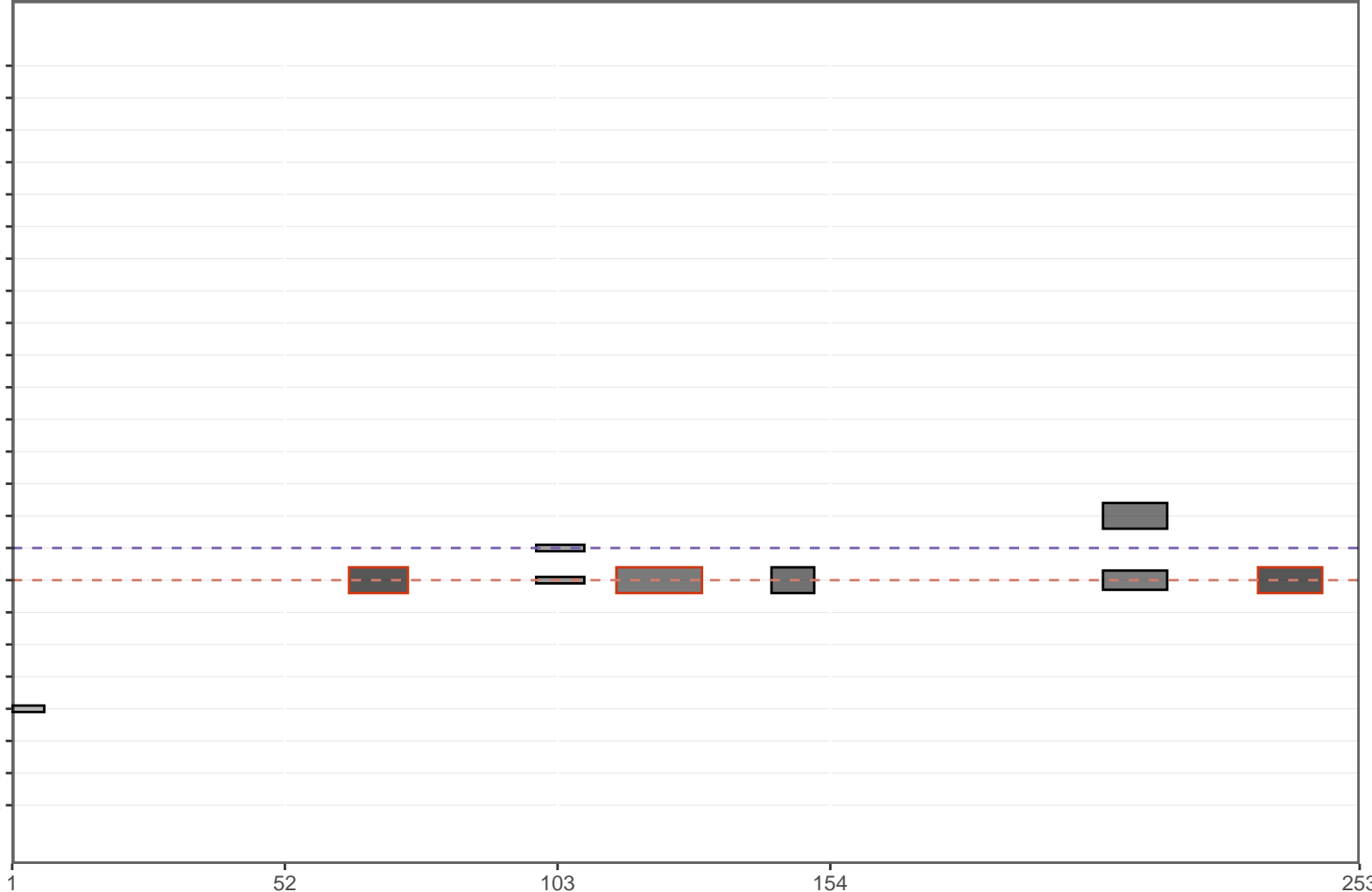
MW indication



Molecular weight

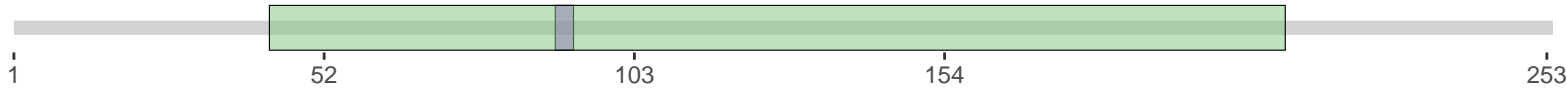


Gel Slice



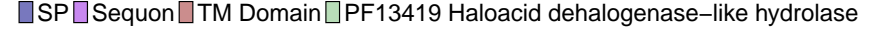
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

.QIMPQTAELCSFLDSKNIIRRGILTRNRYKDAVDLPHVRFQGVKFSPLSRFRFPYKDPAPLLHGISTWVQVNEVMMIGDSLKDDWAGGKRAGFTGLLDETRGVDAPEYANVHEHQPDKYKVSLSVEIGSLERHFELAS

NbL16g13010.1 glutamyl-tRNA(Gln)_amidotransferase_subunit_B_chloroplastic/mitochondrial [MW = 60.6 kDa]

No. of times detected



log(intensity)



Values from



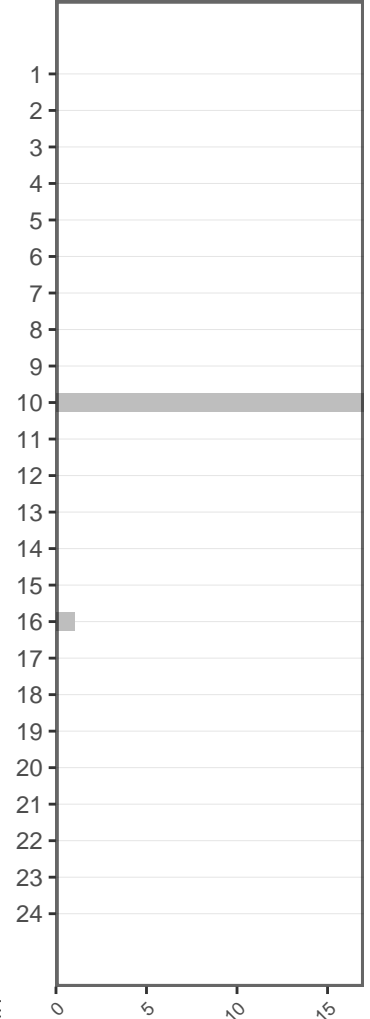
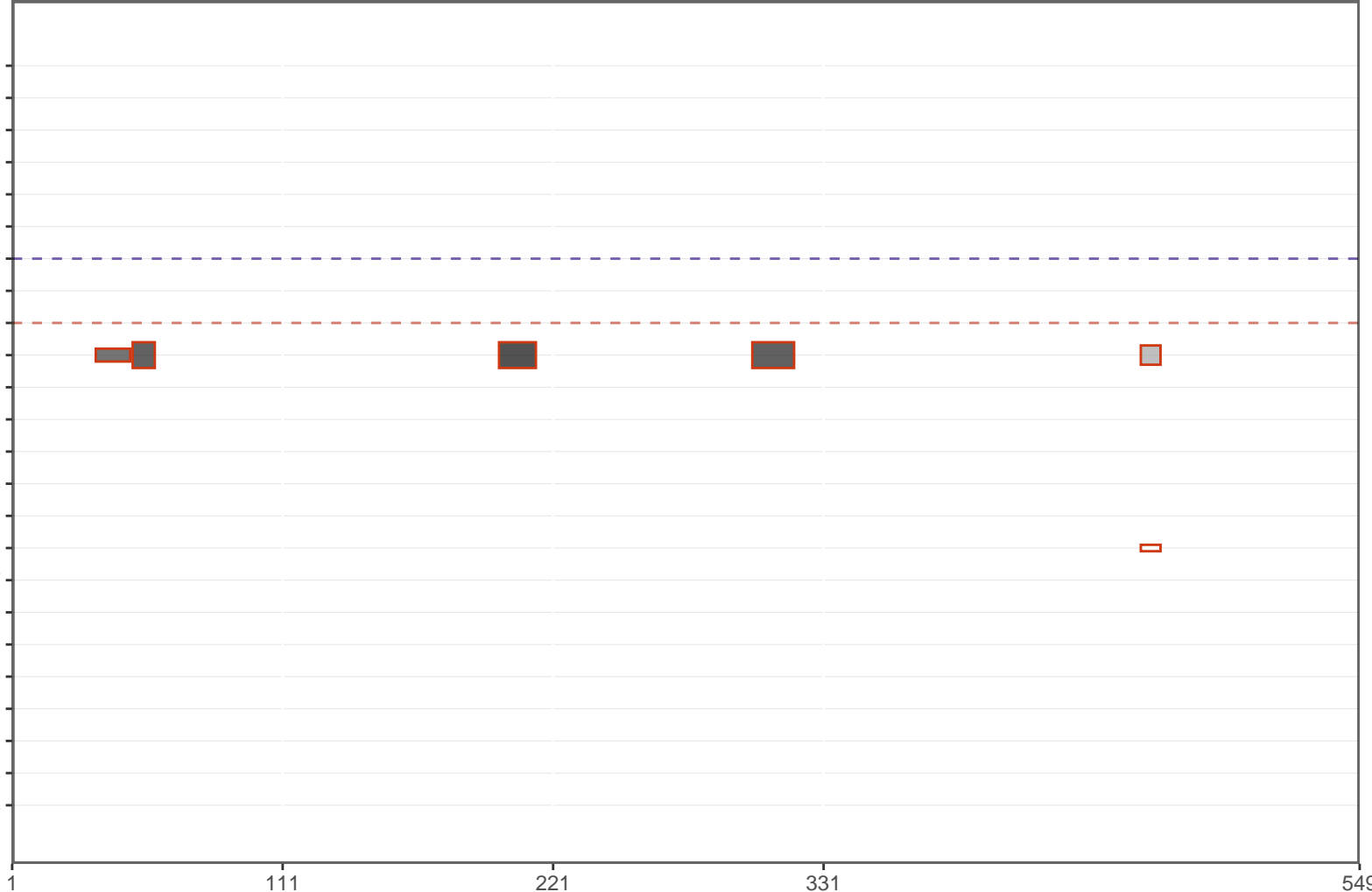
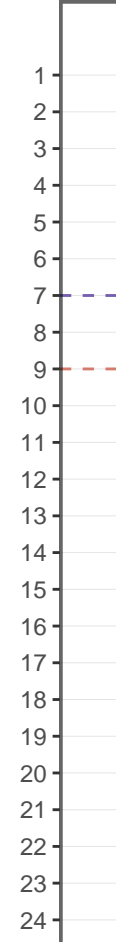
MW indication



Molecular weight

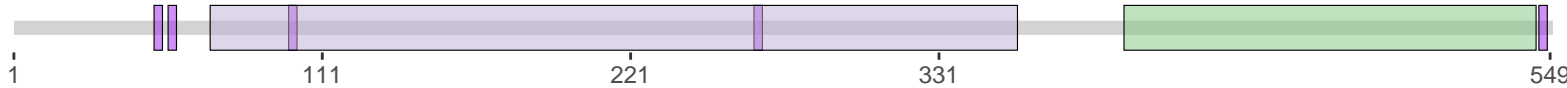


Gel Slice



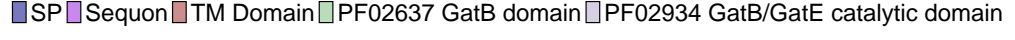
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ISLRCDVNSVSRPIGQLEFDGTRVYKKNLFSFVSRADYKSRQVLLHSGGQGVDEVPETRLWEEGAGKTVTMRKKEGLADRYFFPEPDLPSVLTTEVYENIRELSEVPEAKRRRYEDMGLSMGDLVFLANDMNAIEEFDATAAGADVKLANWIMSDIAAMKNEKVTINEIKLSPQELGELASIKDGTISGKIKELFELMAGKGTVYKGLIKEDLVGVDTAEIKMMYKVAADNPKQLEQYRGGKTKLOGFFAGGVKESKSKANPKLLNKLLEKLNATS

NbL16g12970.1 3-isopropylmalate_dehydratase_large_subunit_chloroplastic-like [MW = 55.43 kDa]

No. of times detected



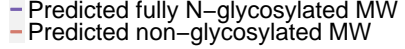
log(intensity)



Values from



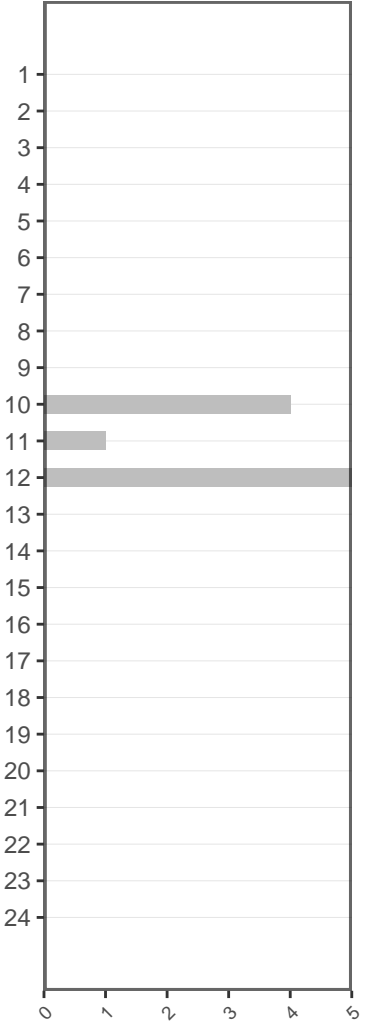
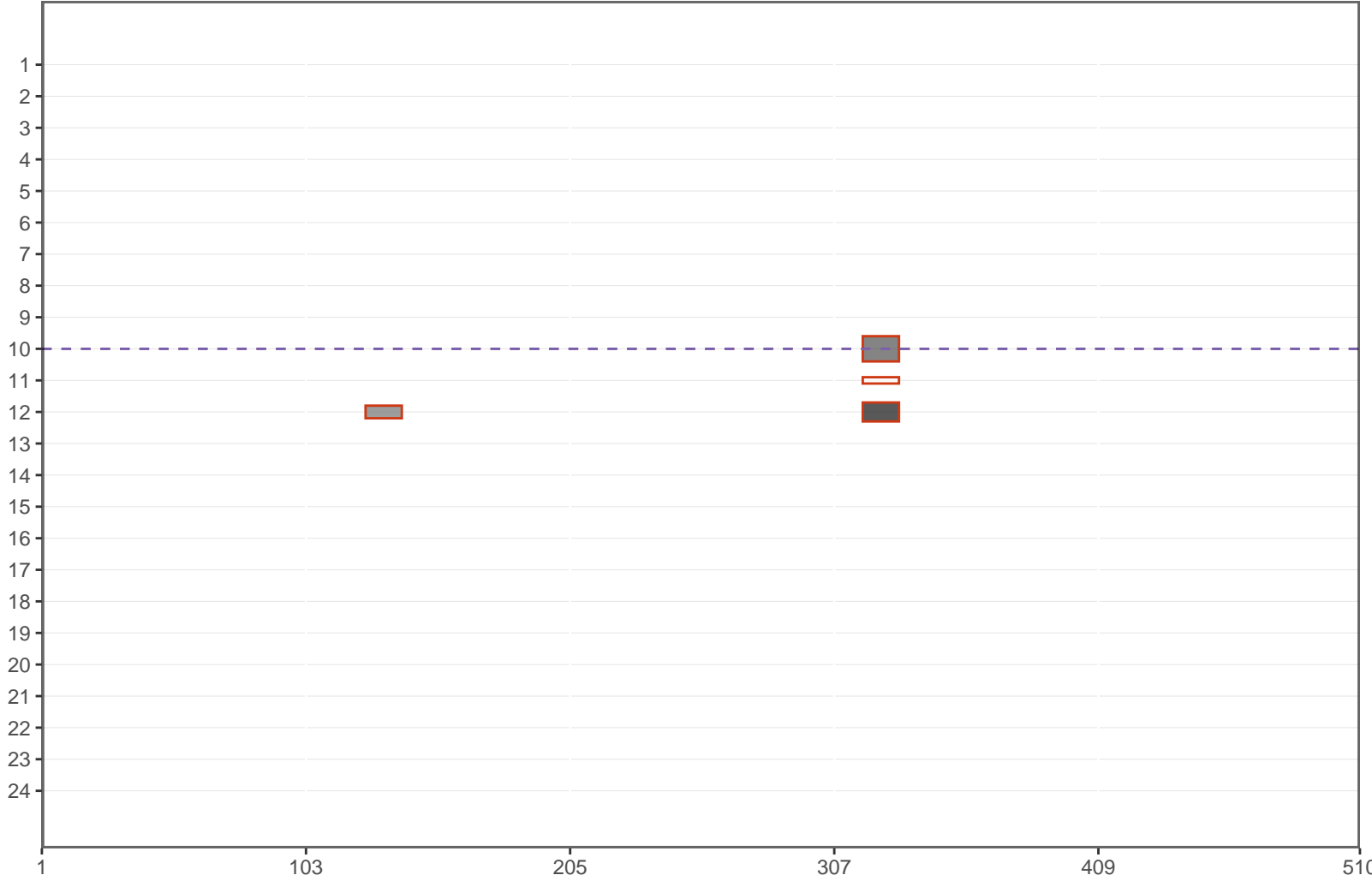
MW indication



Molecular weight

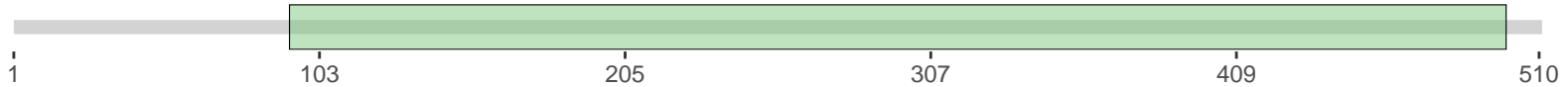


Gel Slice



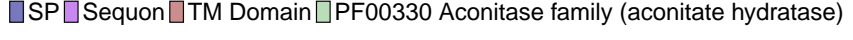
Protein length

Peptide counts over 4 repeats



Pfam domains

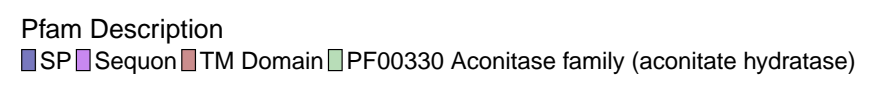
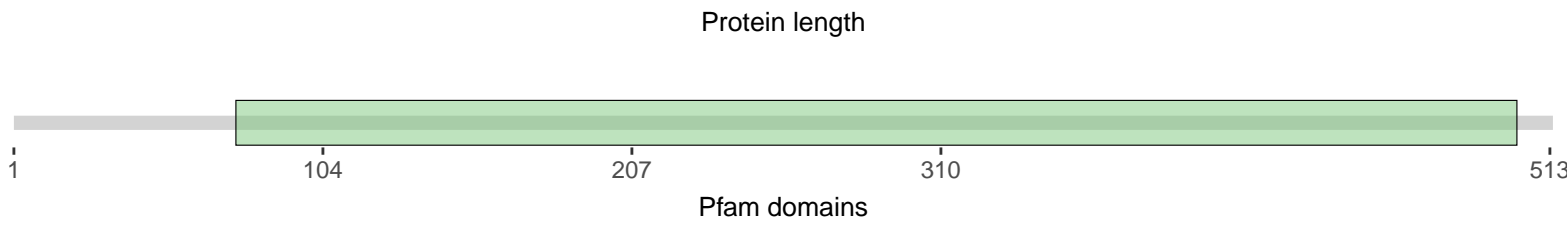
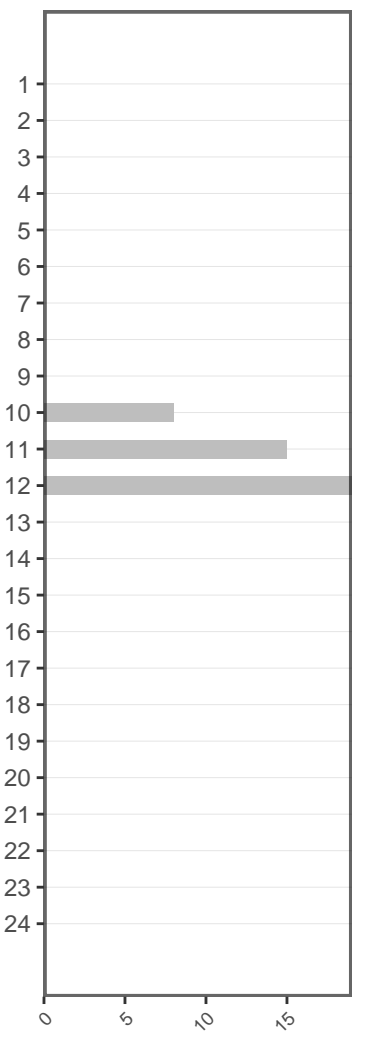
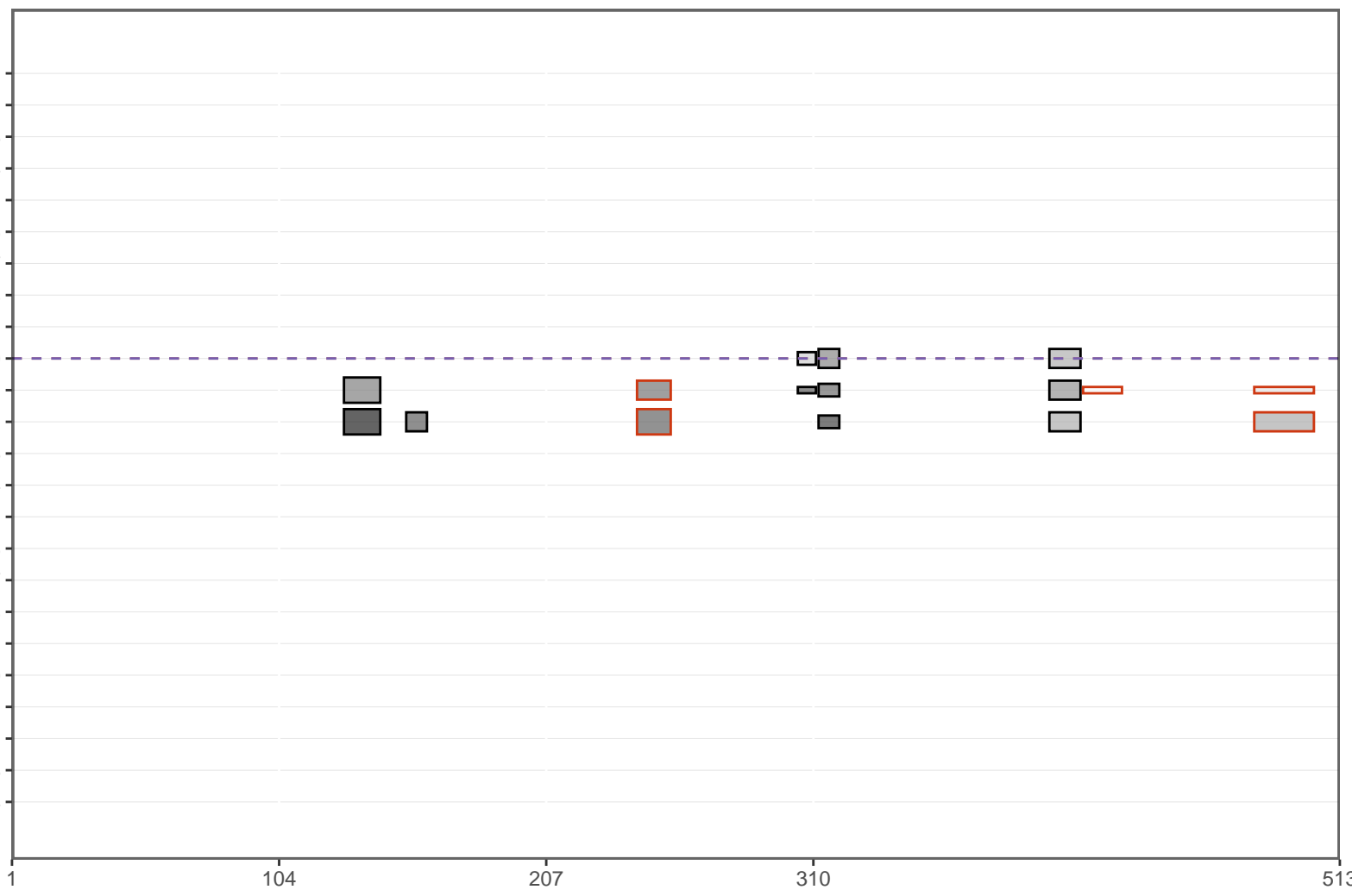
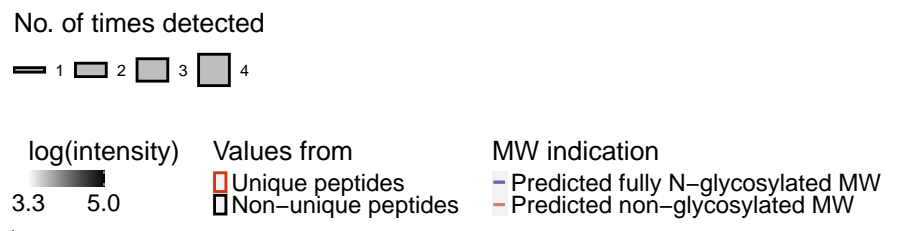
Pfam Description



Protein sequence:

GEMPNYLLAKDLAQHGSEISVAGATYKTMFEAGTTAESLHMEERMFLGNMVEAGGKNGVFPADKTTYDYLKDKTKTVPYEPVYSGDGGARFLKEYRIDISKLEPLVAKPHSPDRALARECKDVIDRIVYSGSGTGKTEDFMBAALFQAHGKHKVYPTFLVATREVMMDIYSLFVPGSGGKTCGGIFDEAGDGYEPASPSGGAGPGLPDTYGRLLNEPKVCVSTTRNFPGRMGHEGGVLAHPYTAASALTYVTDPREFLM

NbL16g12960.1 3-isopropylmalate_dehydratase_large_subunit_chloroplastic-like [MW = 55.75 kDa]



Protein sequence: MDGQMPSYLLAKDLMLGIGSEIVSGATYKTMFVGTTFVSLMEERMTLGNMVEAGGKNGVPTDKTTFYKLNKTSVFPVPSYDEGARFLKEVRIDISLFLVAKPHSPDRALARECKNVDIRVYHGSGCTGGKTEDFMAAAKVFASGKKKVPFTLVATQKVMMDKYLTPVPGGGKGTGQDFQEAAGDETPMSFQAACLGPPQDITYARLNKPKVGVSTTNRNFPGRMGHEGGYLLASPYTAATSALTGKITDPRFLM

NbL16g12910.1 putative_G3BP-like_protein [MW = 52.34 kDa]

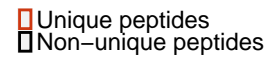
No. of times detected



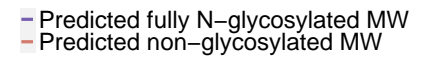
log(intensity)



Values from



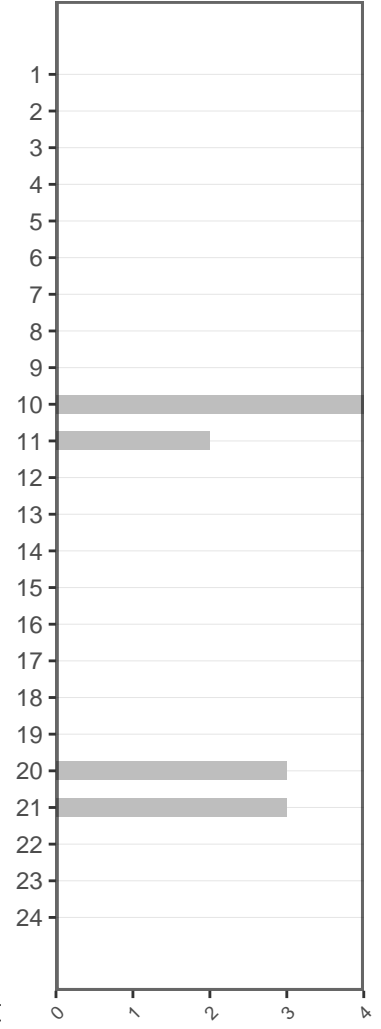
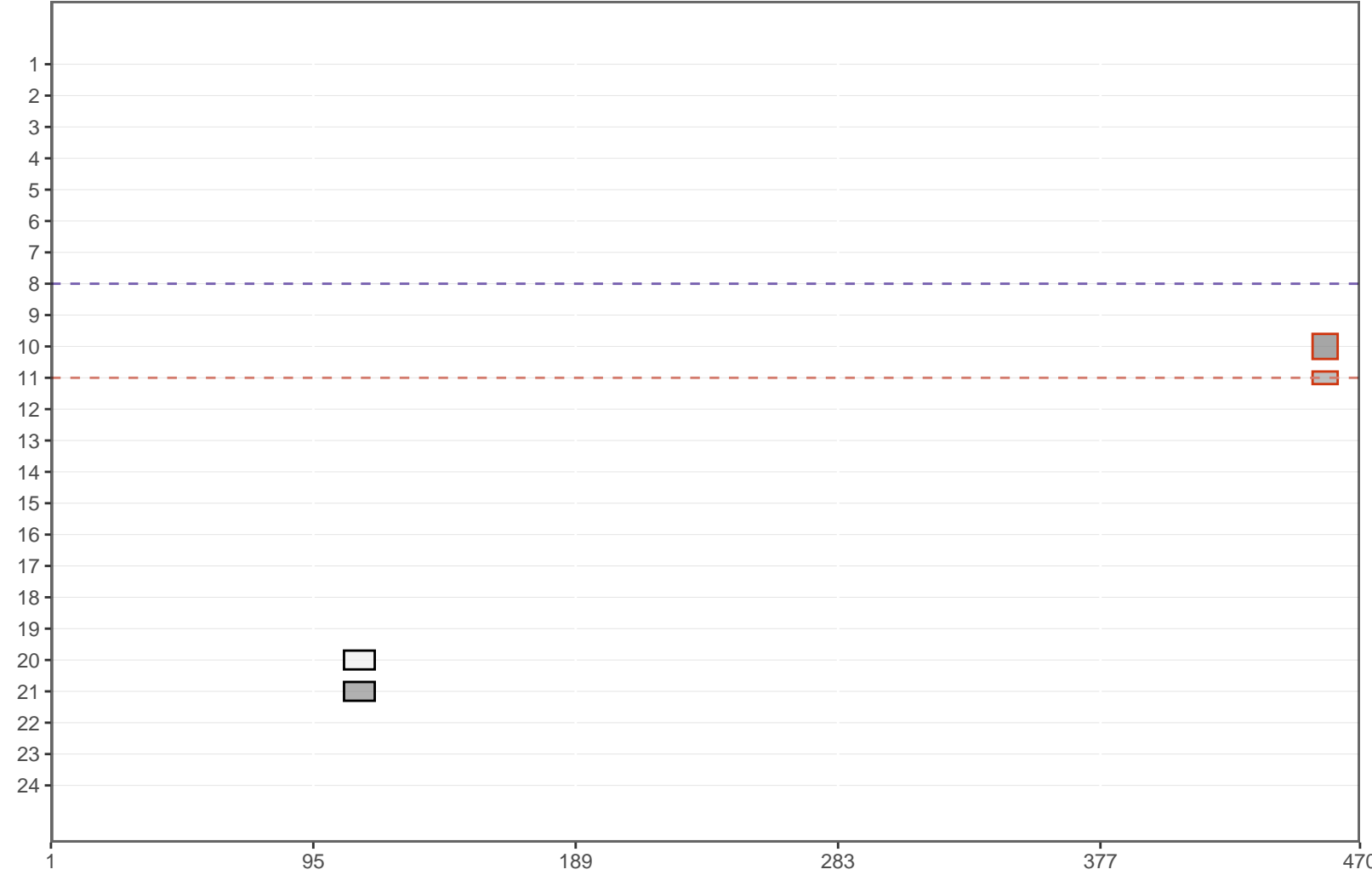
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

SP Sequon TM Domain PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) PF02136 Nuclear transport factor 2 (NTF2) domain

Protein sequence:

VQEI LSSPIIEPVAEPKQHTYASIGLVTKGPRMGGPMGSSFNKPTLPPSEWGHVSEPPSLGVPSTNAIERSTFATEEASAVEDEVKSVYKVVPTTMAVVEIEEFKFKGLKPDVAWRTRKDDVCFVFEFEDVTGVQNAIEASTVQGGHLYEGRRPNRNLIJRGRRGRGRVSVMDGRGRVGRGFRGGDDGDDRDYGRGRNGYVRQAPRGERAVSGNQGSLRNEQVWE

NbL16g12900.1 RNA-binding_protein_CP33_chloroplastic [MW = 32.42 kDa]

No. of times detected



log(intensity)



Values from



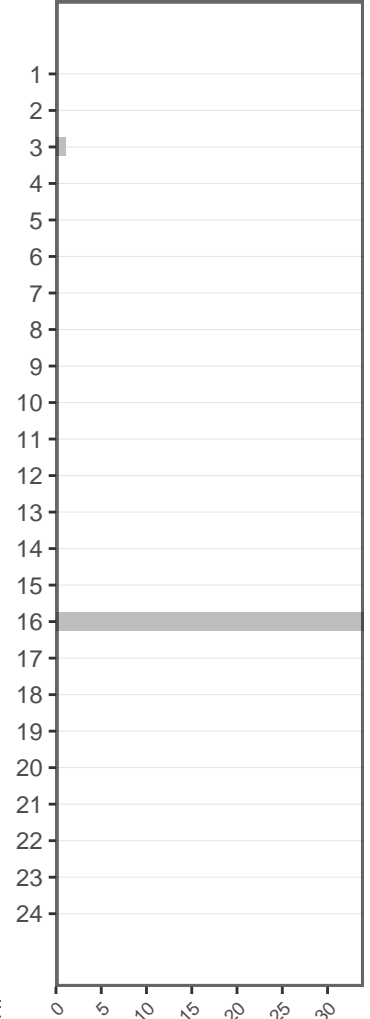
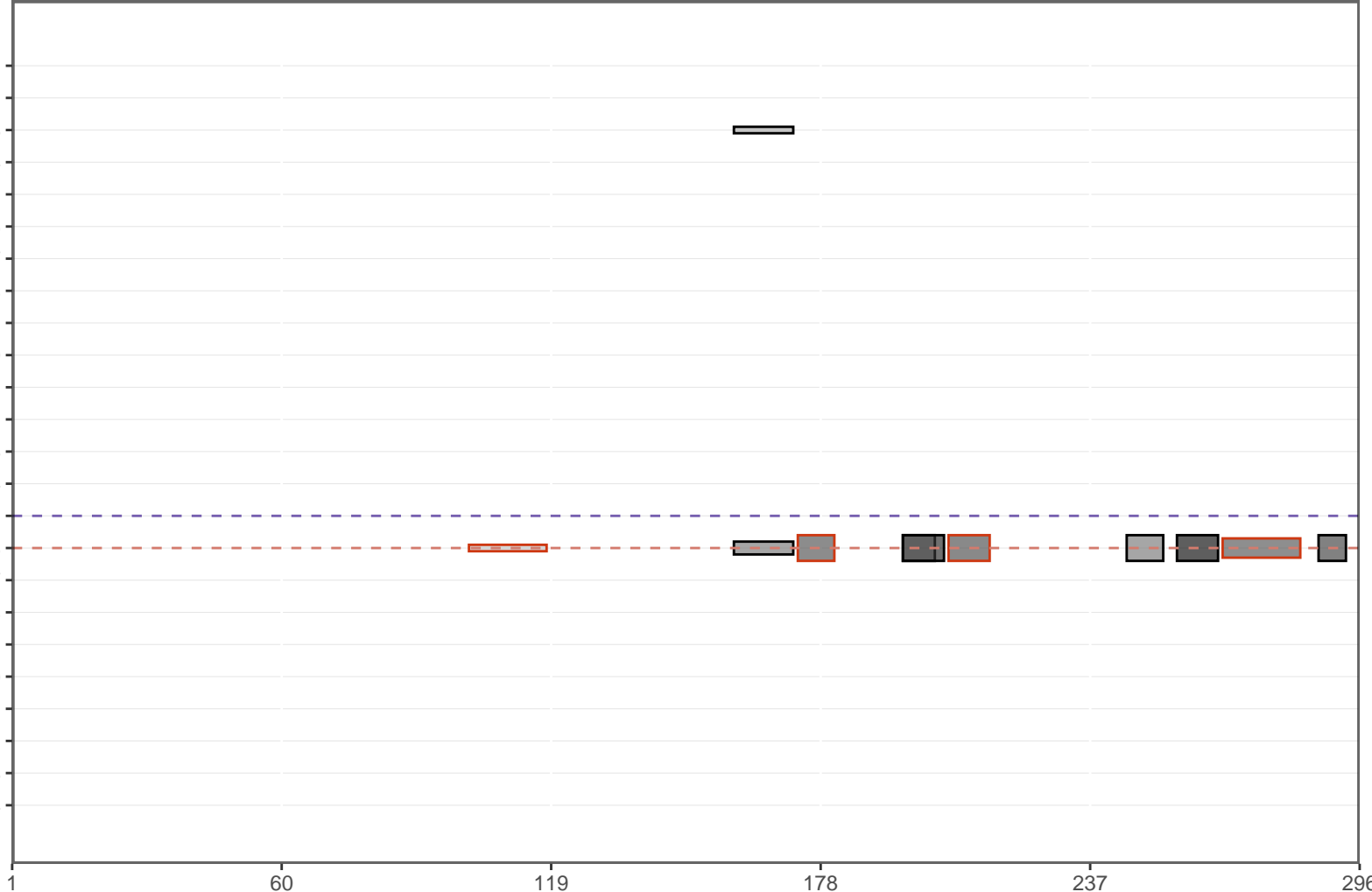
MW indication



Molecular weight



Gel Slice

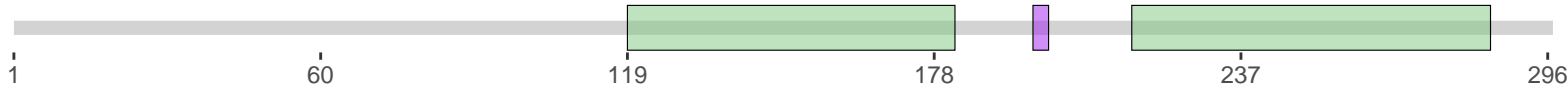


Peptide counts over 4 repeats

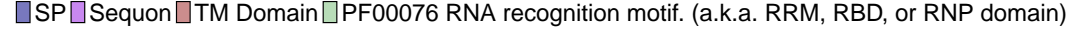
Protein length



Pfam domains



Pfam Description



Protein sequence:

VQDYATPELVLYDRETFKSRGFVFTMSLEDCKTVENLDGRGDLTSGVWGRTRLRVNFSDKPKPKPEFLYPTETKLVFNGLAWSVTSLSLQAFQEGYGVVGARVLYDGETGRSRGFGFVEYENREQQENALGNLNGVELDGRAMRISLAGGKKQ

NbL16g12820.1 glucose-6-phosphate_isomerase_cytosolic [MW = 70.28 kDa]

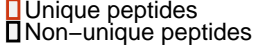
No. of times detected



log(intensity)



Values from



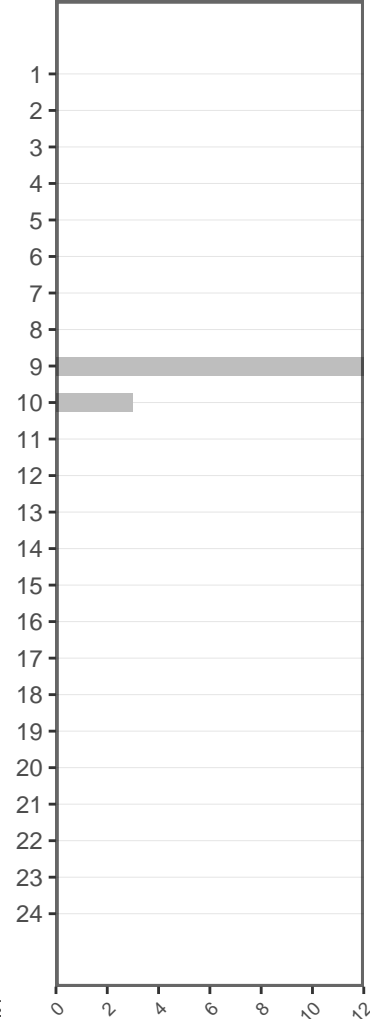
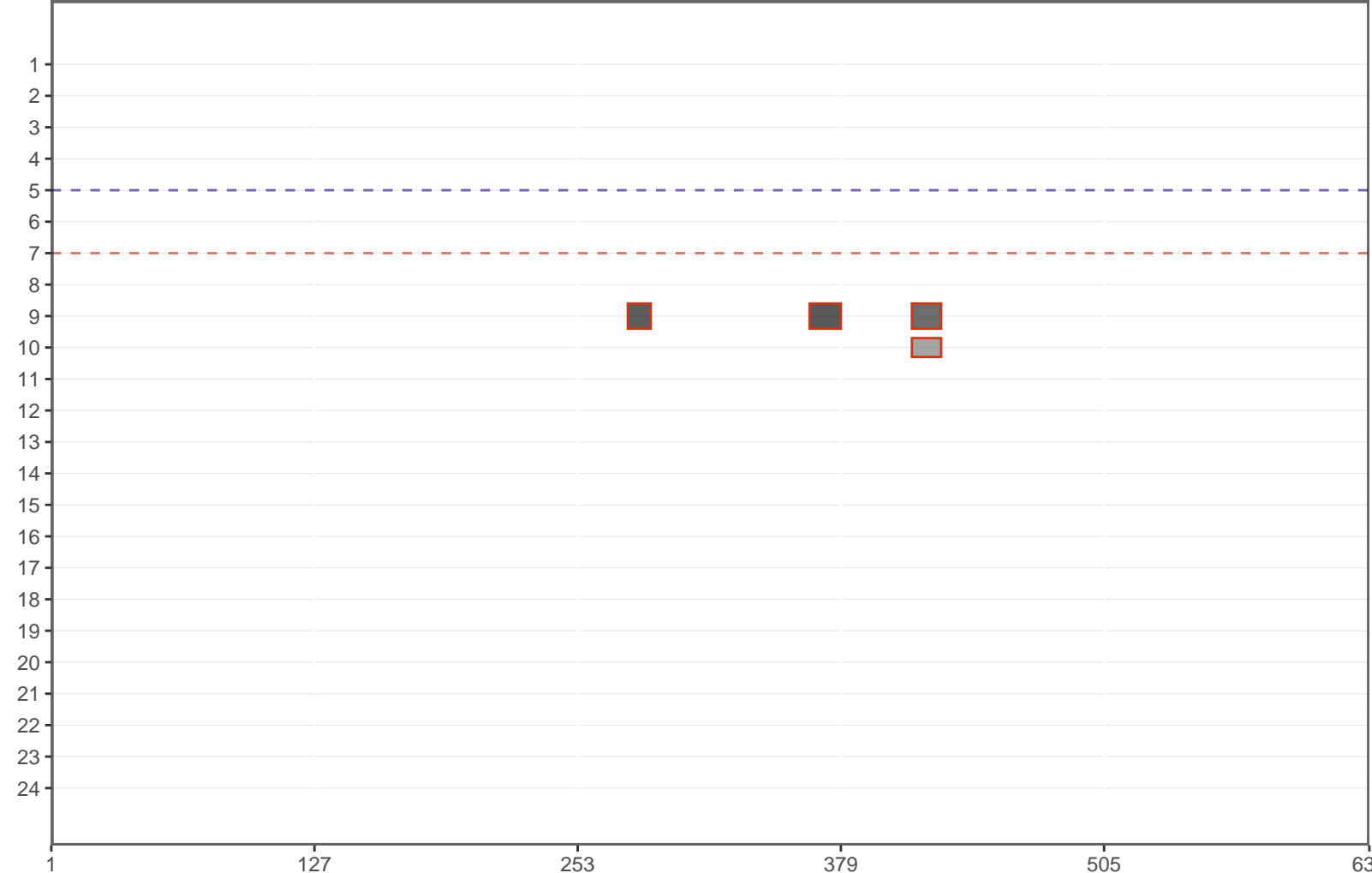
MW indication



Molecular weight



Gel Slice

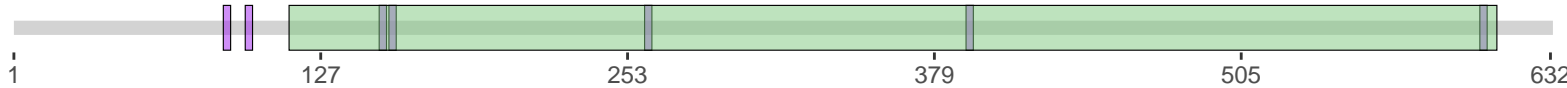


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KHIMVAVSTNLLKLVESGFDIPNNAFKFDWVGGGRVYVGSVAVGVLPFLGKYGFFIVEKFLKGAASEVDQHFYSTPFEKNFVLLGLLSVWVNSFLGYSARALPYGDALEKTFPHQDQVSMESNGKGVSDGVPFVETGEIDFGEPTNGQHSFYQLHOGKRVPCDFGIVYKSGQPVLYLKDDEVSNHDELMSNFFAGPDALAYGKTFPEGLQKSNVAEHLVSHKTFSGNRPFLSILLPLNAYNQGQLLAFYEHKRVAVGQFVWGINSDGQVVELGKLSASQVIRKQLIHASRQK

NbL16g12780.1 pathogenesis-related_protein_STH-2-like [MW - SP = 16.93 kDa]

No. of times detected



log(intensity)



Values from



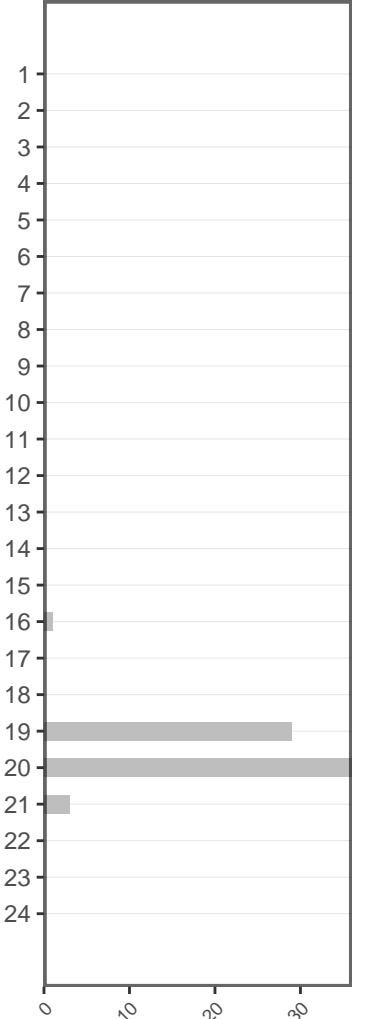
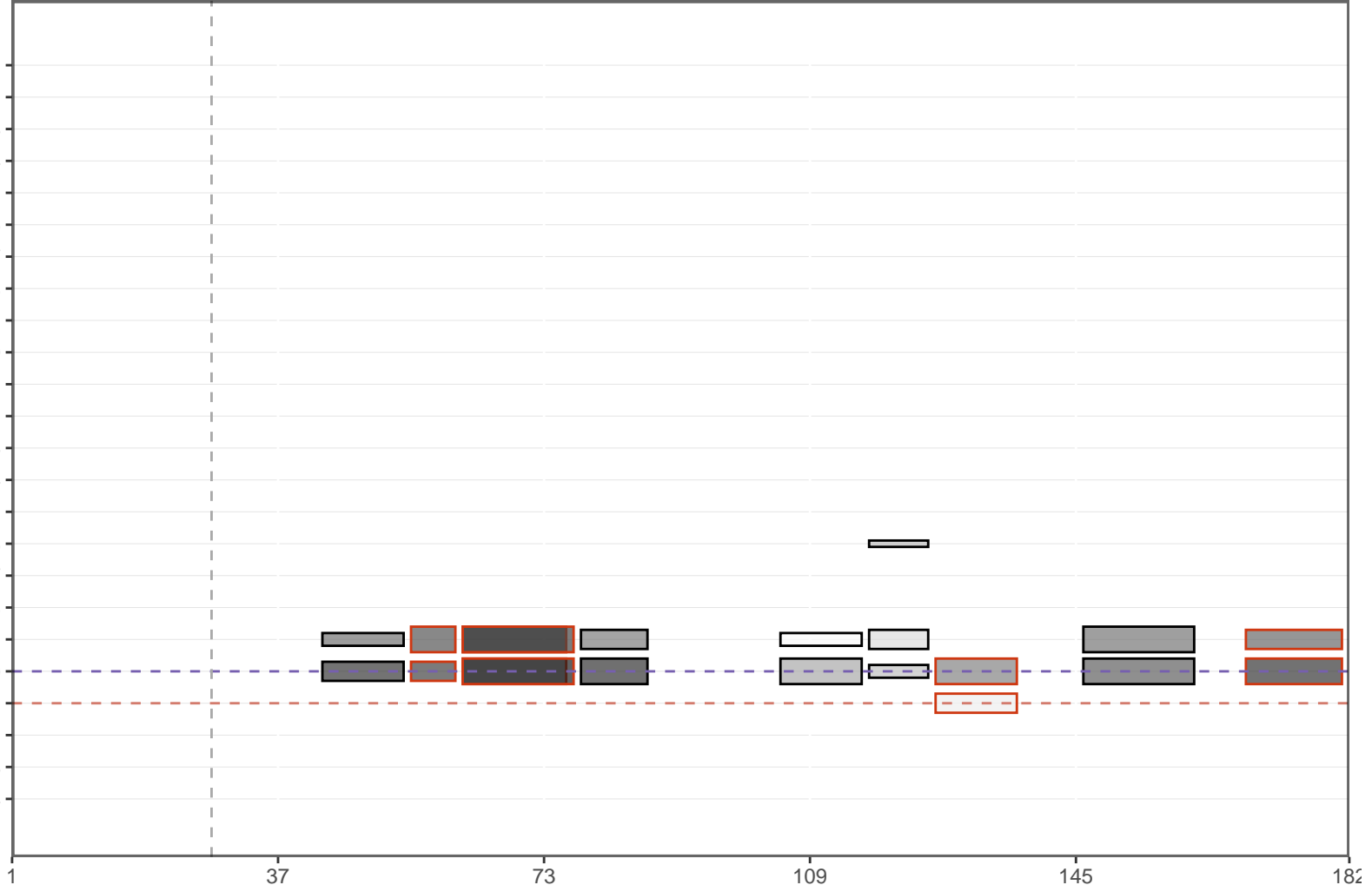
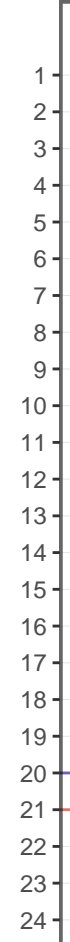
MW indication



Molecular weight

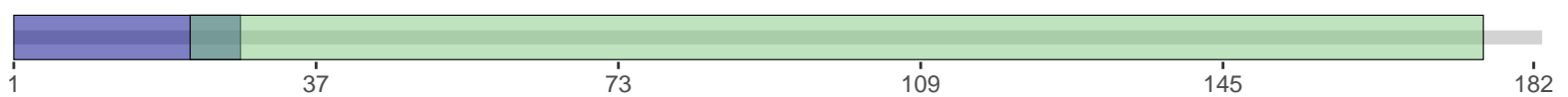


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

INFVEGGPKYLYIKLHLWIDNKNLTKYSLLEGDLGDKLEIFDYDKFETSAANGGDKTSTEHYHTKGDVFKKEEHNKGGKAMELFRKAVEDYLLANPTVAI

NbL16g12770.1 pathogenesis-related_protein_STH-2-like [MW = 17.81 kDa]

No. of times detected



log(intensity)



Values from



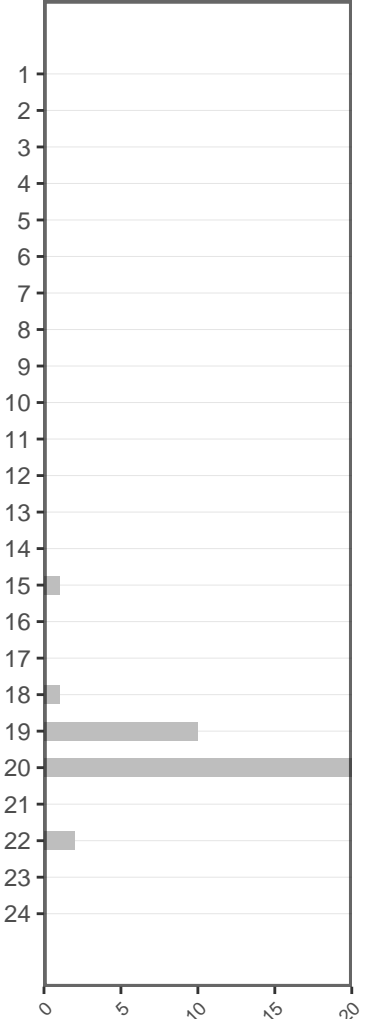
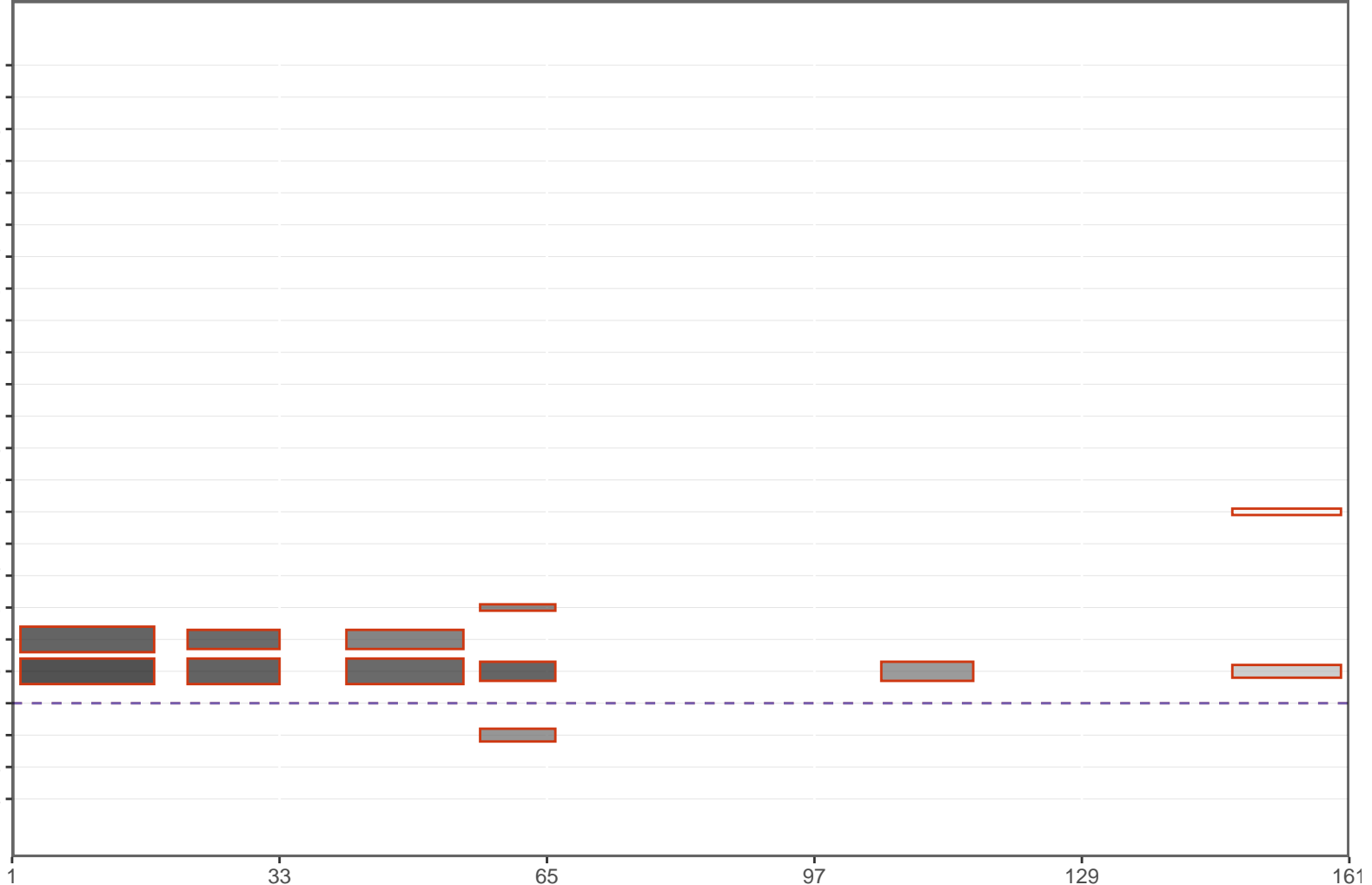
MW indication



Molecular weight



Gel Slice

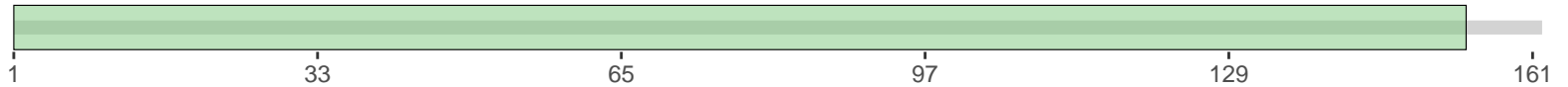


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

/LQIKKHVDDKLNLRKYSLIEGDAIDKLEFVYDIKFEASNGGGICKTSTEVHTKGDVYFKKEEHSEGGKDGAMELFKTVEDYLIANPLVV

NbL16g12620.1 cyanate_hydratase [MW = 18.58 kDa]

No. of times detected



log(intensity)



Values from



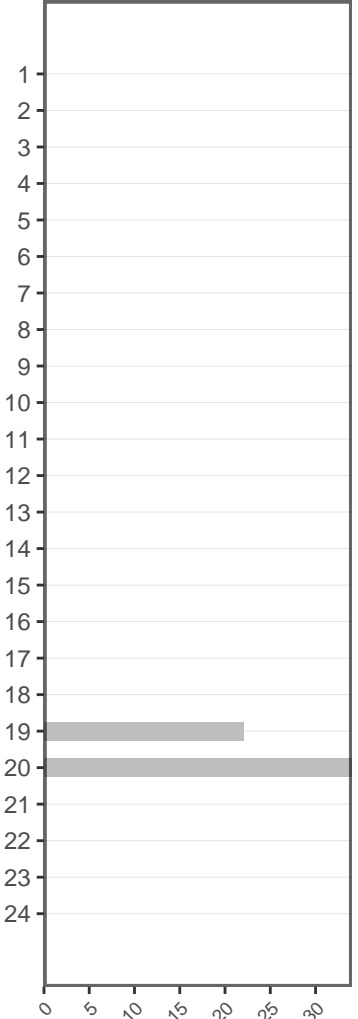
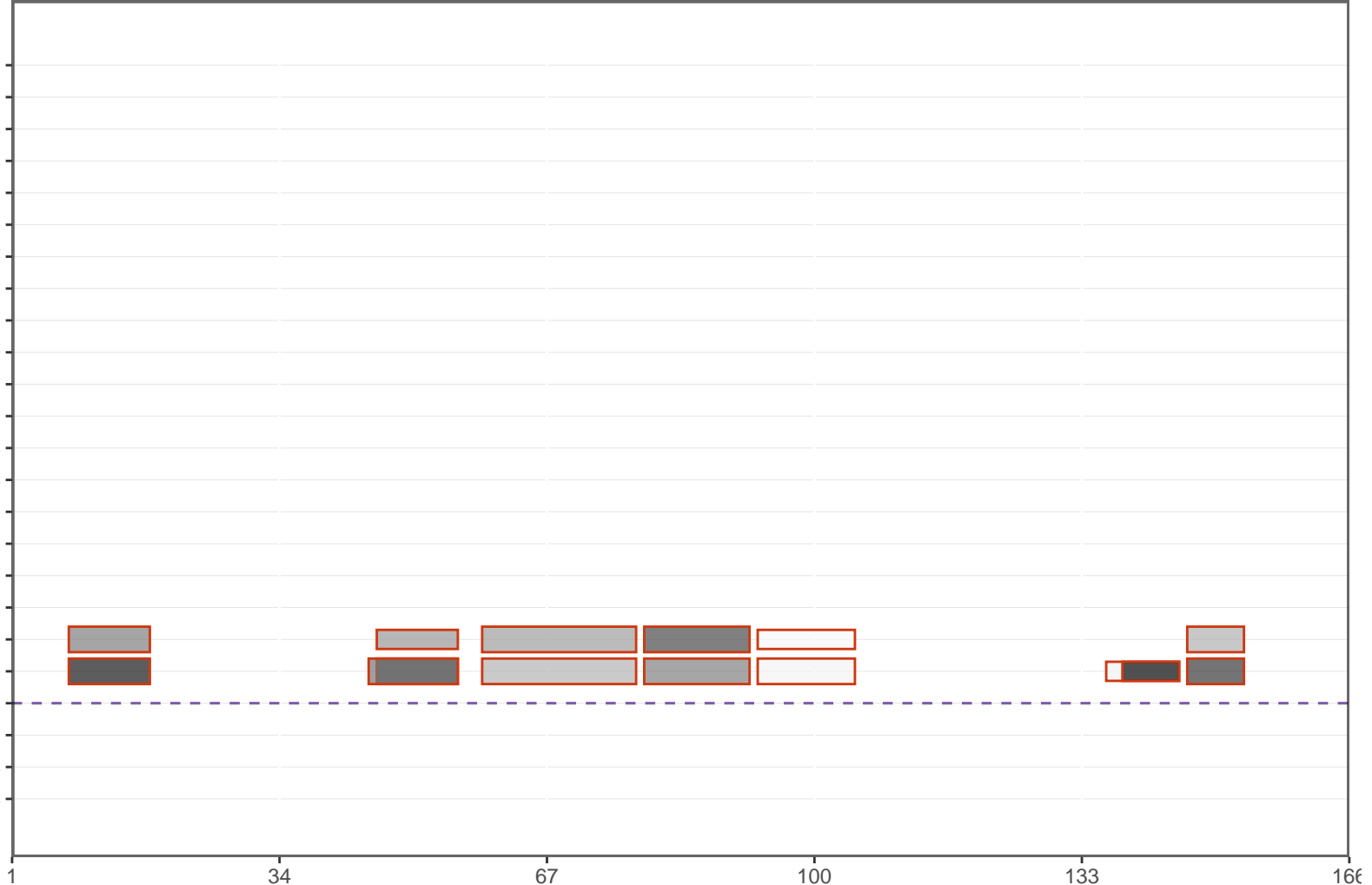
MW indication



Molecular weight

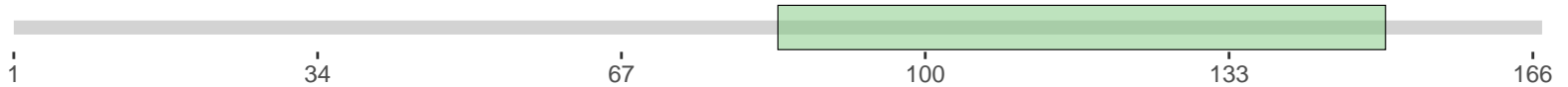


Gel Slice



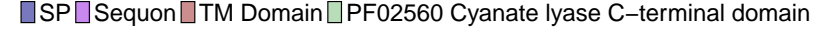
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IDMMEAPLRSYDPLNIGDPTVYRLNEAVMFMGGGSIKEINEEFGDGMIAIDFFGSDVKVKGVDGKDRVAVTFDQKYLPHTEQKSEHMVSRLLMRKE

NbL16g12590.1 50S_ribosomal_protein_L28_chloroplastic [MW = 16.34 kDa]

No. of times detected



log(intensity)



Values from



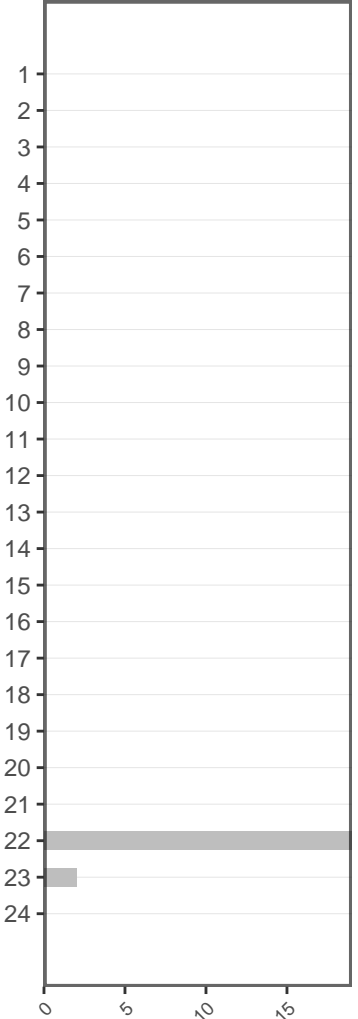
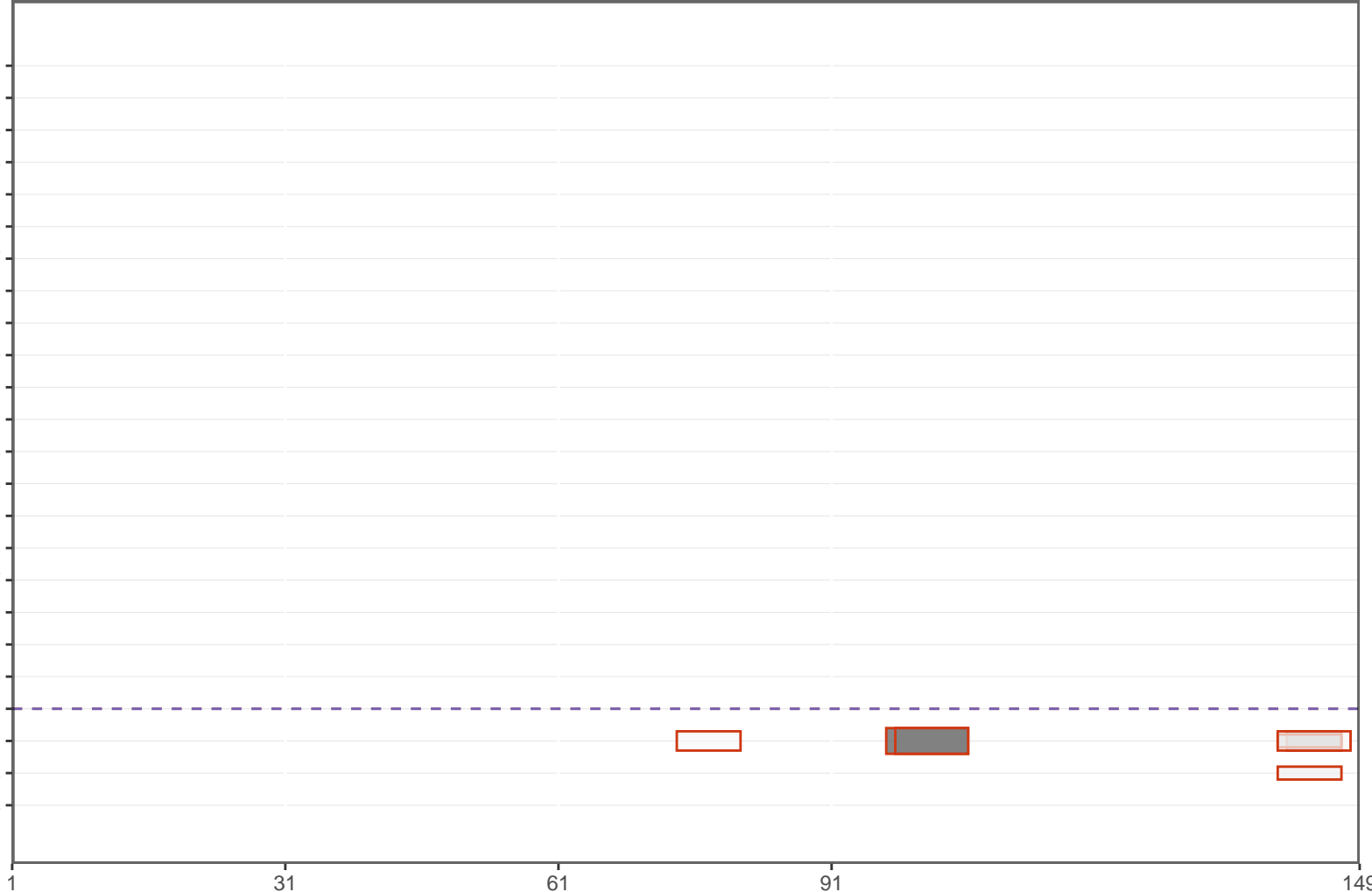
MW indication



Molecular weight



Gel Slice

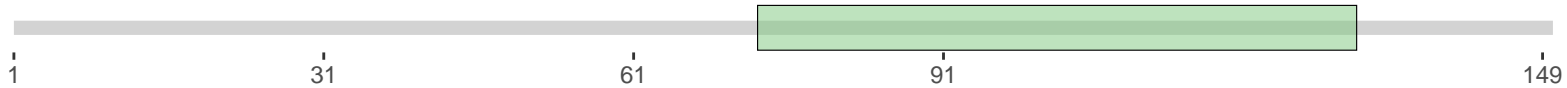


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KPSLQPVARRICPFETGKGNRANKVSHSHNRKTKLGFVNLQYKRIWWEAGKRYVYLRLETKALKTIENGLDAVAKKAGIDLK

NbL16g12530.1 probable_plastid-lipid-associated_protein_6_chloroplastic [MW = 30.17 kDa]

No. of times detected



log(intensity)



Values from



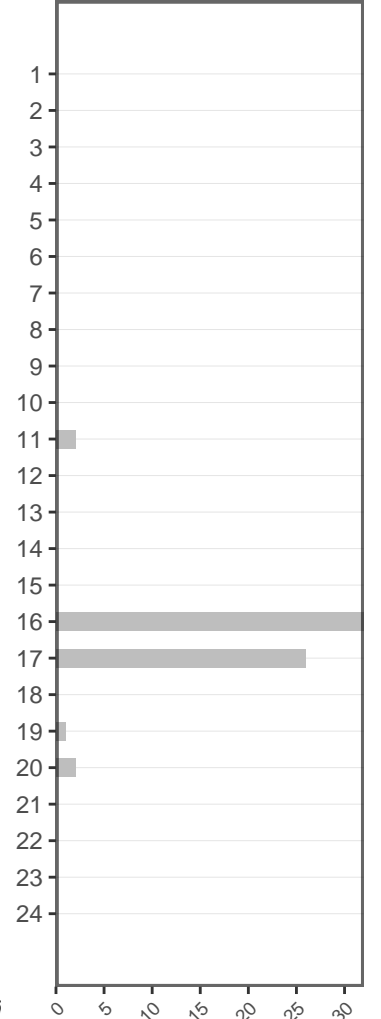
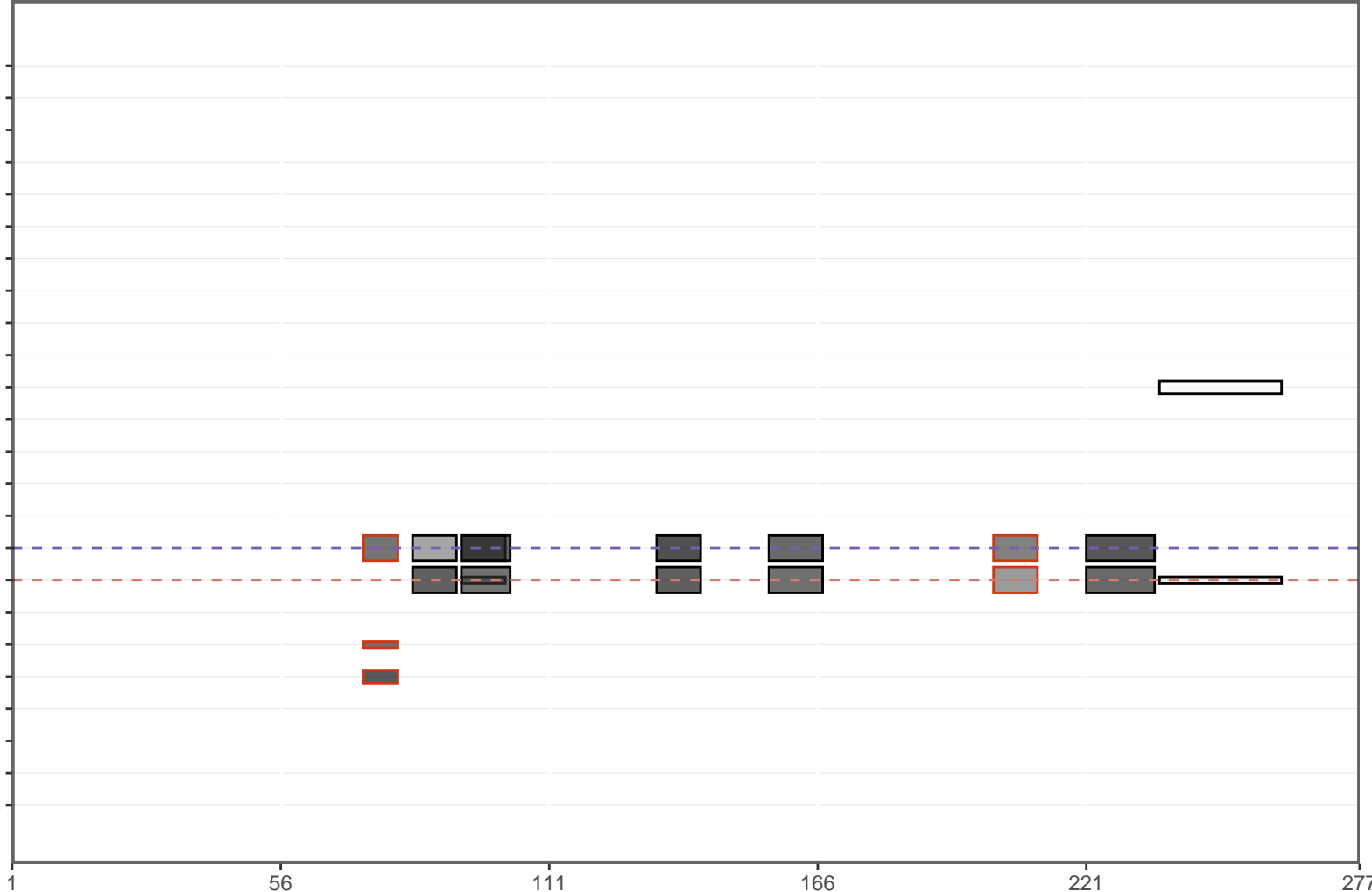
MW indication



Molecular weight

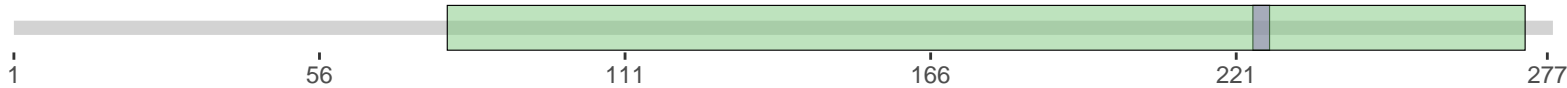


Gel Slice



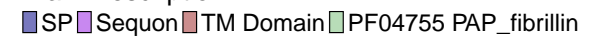
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

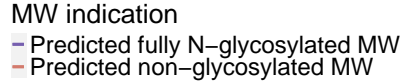
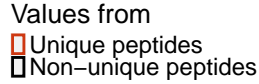
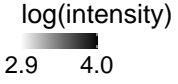
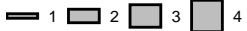


Protein sequence:

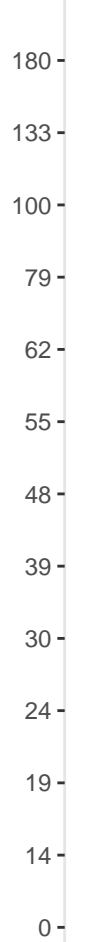
DKLQGRWKLKLYSSAFSGRLLGSGRPGPTGRLLPFLTGQVFORIDVLSKDFDNVELELGAIPWLPPELTLAHLKFKELSGSTNITFEKTTIKTTGNLSGLPLLEVPRIPOQFRPPSNTGSGGEFEVTVIDSDTRVTRGDRGELRVFVIG

NbL16g12430.1 probable_methyltransferase_PMT3 [MW = 70.25 kDa]

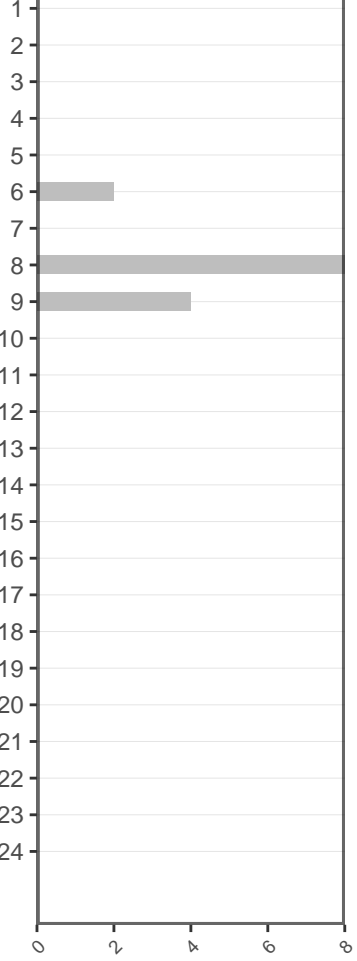
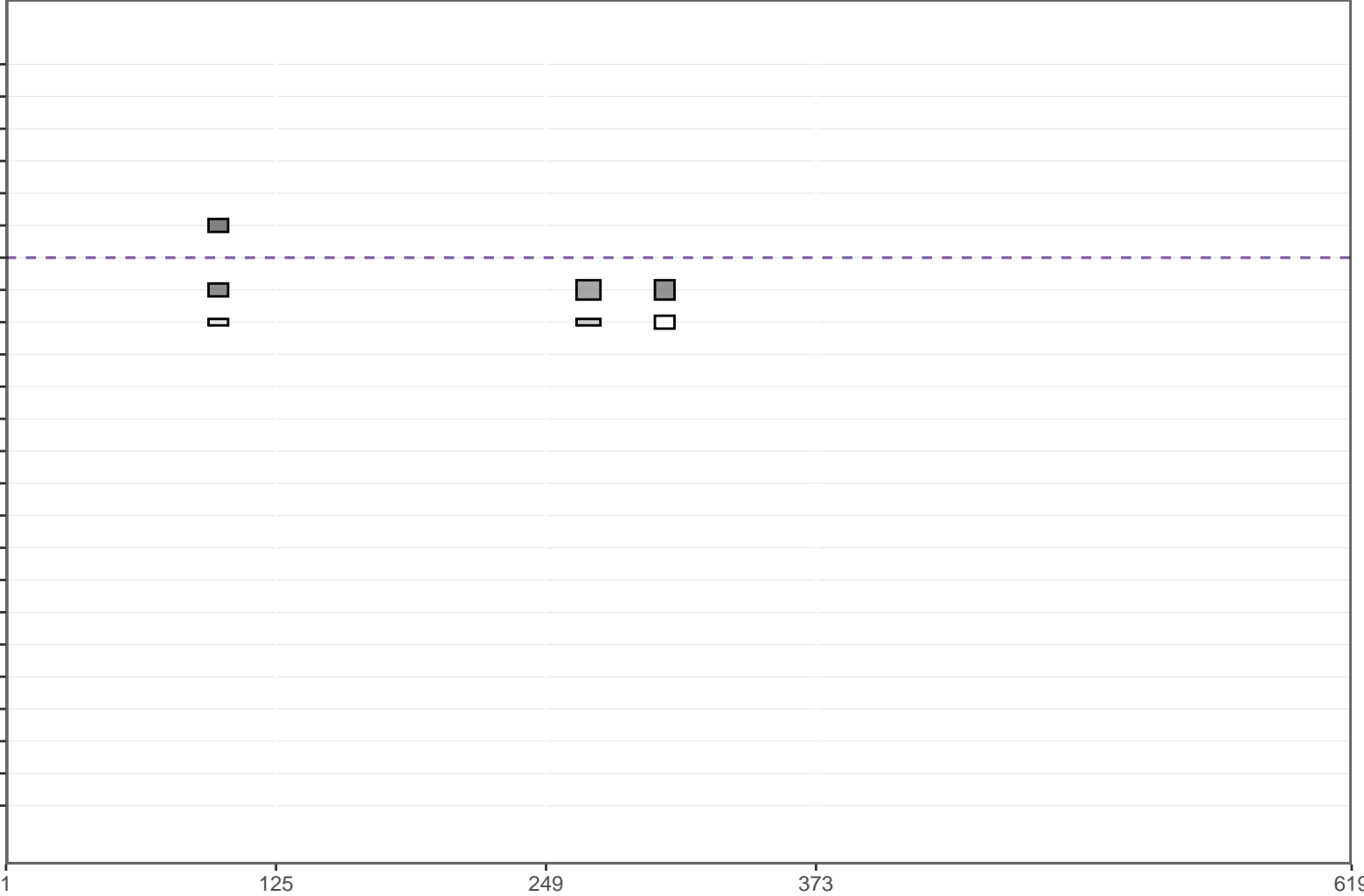
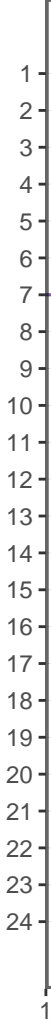
No. of times detected



Molecular weight

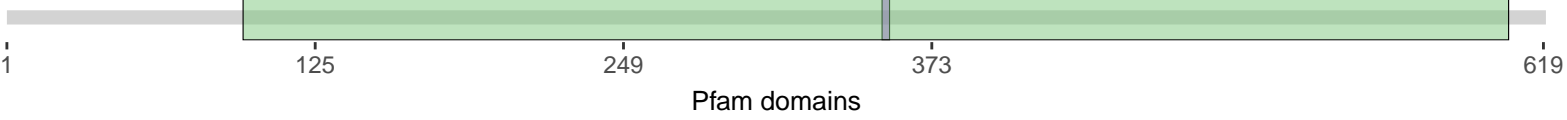


Gel Slice



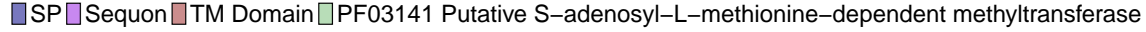
Protein length

Peptide counts over 4 repeats



Pfam domains

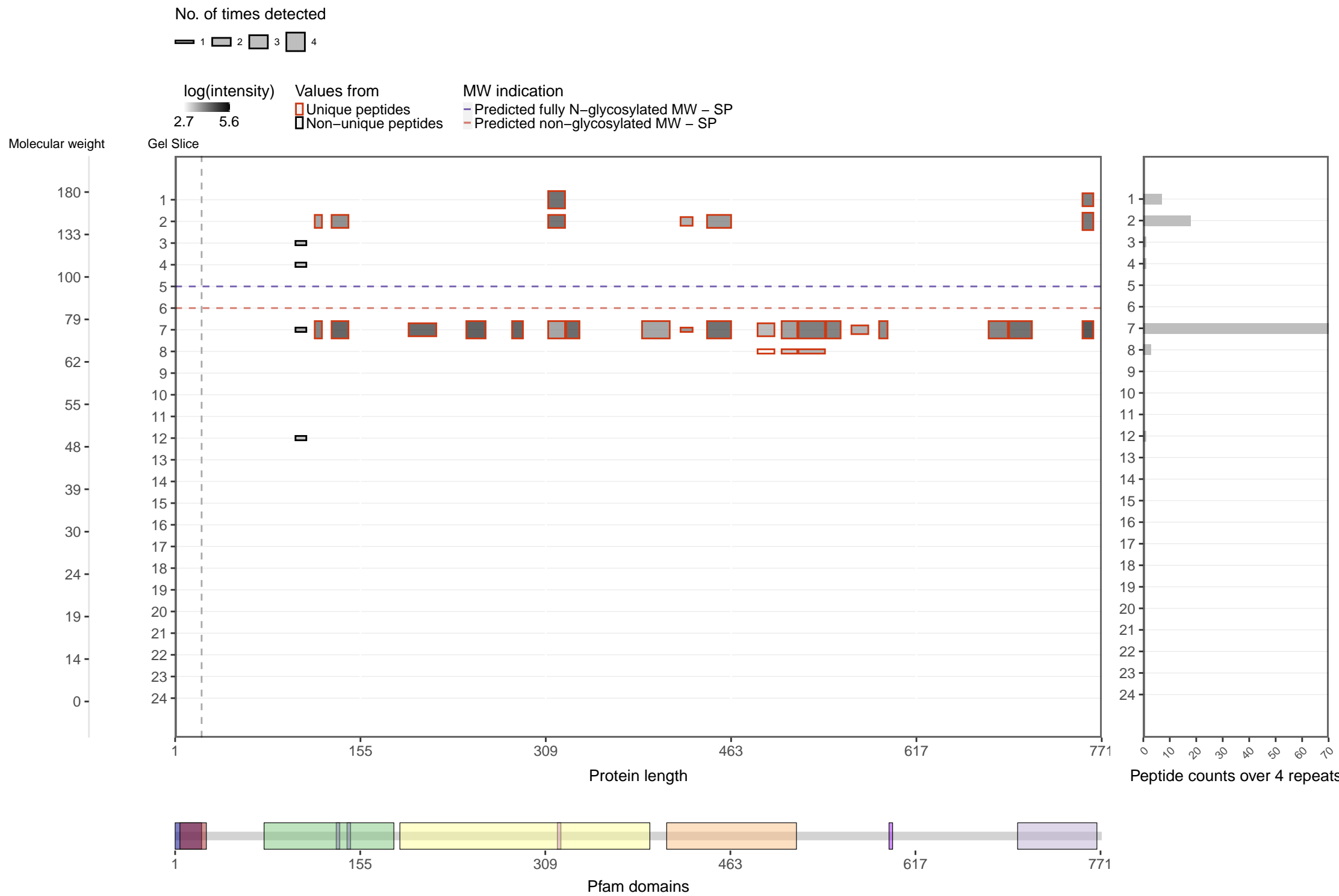
Pfam Description



Protein sequence:

SRDGLLLELDVLRPQGYFYSSPEAYQDEEDLRWRMSALVERMCDWMAEKRNQTVHWWKPLNNDGYMERPKGTDPFLCRSDDDPDVAVGWVMEACITPYSEHDKVSGSGLAPWPARLTSPFPRLADFGYTTMEFEKDMELIWRVREHVVWLLLEPKISSDSLNRNMDAKANLGSFAALAKDKDWWMMVVSKDGNFLKVVYDRGLGTTDHWCEAFSTYPRTYDLVHAWVDFSDIEKKGSGEDLLLEIDRIIRPQGFVFNKDKGHDFVKKYLISALHWEAVAI

NbL16g12270.1 methylcrotonoyl-CoA_carboxylase_subunit_alpha_mitochondrial [MW - SP = 82.29 kDa]



Pfam Description

- SP
- TM Domain
- PF00364 Biotin-requiring enzyme
- PF02786 Carbamoyl-phosphate synthase L chain, ATP binding domain
- Sequon
- PF00289 Biotin carboxylase, N-terminal domain
- PF02785 Biotin carboxylase C-terminal domain

Protein sequence:

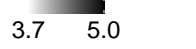
I/VGQDLVEVQIRVANGSEPLPLTQSEVFFSGHFAEARVAENVPKGFPLPATGVLHRYRQVPTVTSARVRETGVVEGDTVSMHYDPMIAKLVWGGDRLAALIKMKDCLKFKQVAGLPTNDFLKLASHRAFQNGEVETHFRERYKDDLFIDGANSISGAEAGVAKHAASIVAGCGKELATLRDKAAGGLHLWYGNPPFRVHIFAKRQVLEWENKYNNGSDDLTVSITFLPDGKYLVEETGEENSPGLEIGVYQLSNNDFRVEVNDLSLVGLAAYKDDIEHHTWQNGCOH

NbL16g12180.1 ETO1-like_protein_1 [MW = 100.22 kDa]

No. of times detected



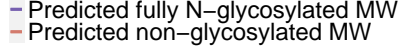
log(intensity)



Values from

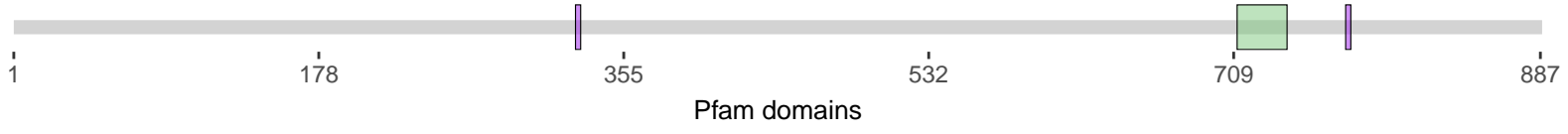
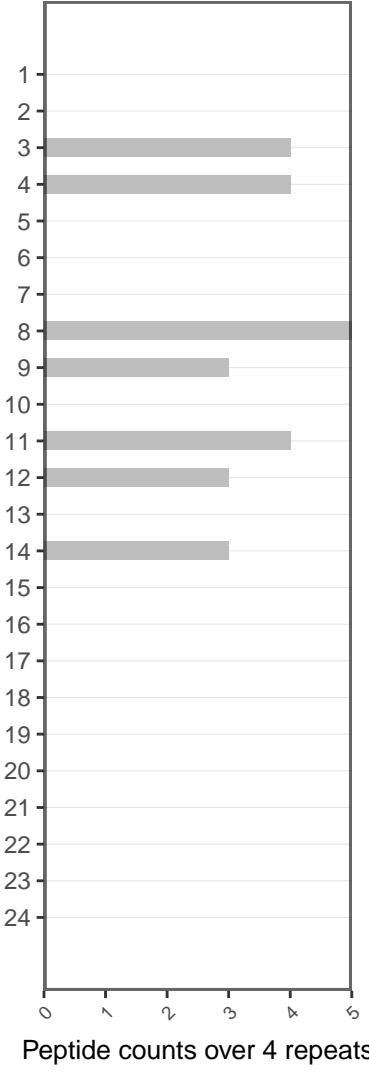
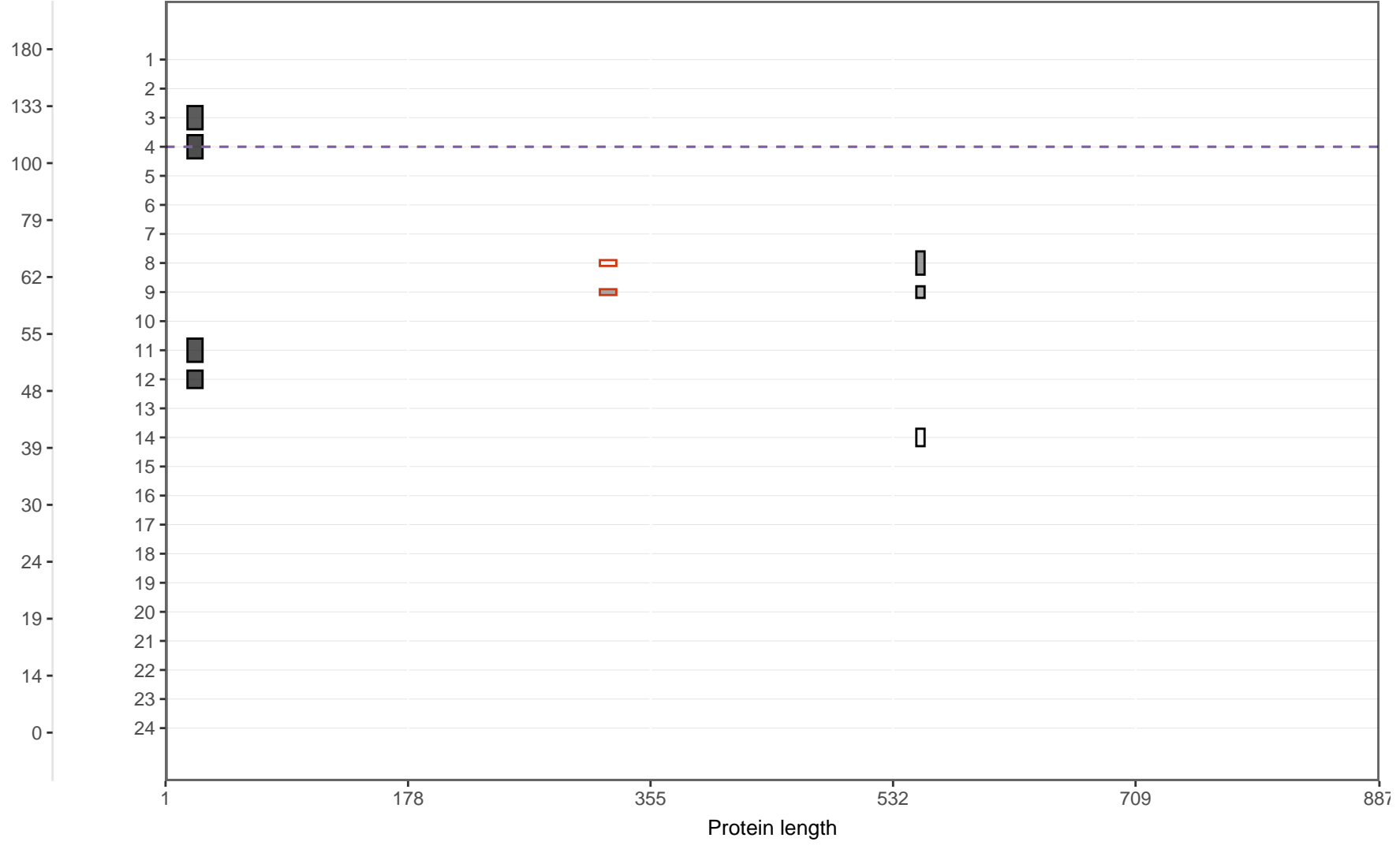


MW indication



Molecular weight

Gel Slice



Pfam Description
 ■ SP ■ Sequon ■ TM Domain ■ PF13374 Tetratricopeptide repeat

Protein sequence:

EKLSSVSSSTPLGWMYDGGSLVDDGKRLDDLGKATELDPFLVYPMYRAASLIRKGNVYGAALSENIRLGFKLAEGLLELRFGFLALEDRYLAIGDQALTLCPDQVYFEGRWALQLRLLREHVEGWTEDADWLGLYDRWBSVDDIGSLGVYQMLSDAAGKGLVYFRGSLLLLRNGPDAMRSLHARQHASSEHERLVYEGWLYDTGHCCEGLQKAEESIKRISFEAVFLKAYALADSPDASGSGSTVISLLEELRGPDRLRKGGALNLSGVYYDCCGLDAV

NbL16g12050.1 probable_histone_H2A_variant_1 [MW = 14.67 kDa]

No. of times detected



log(intensity)



Values from



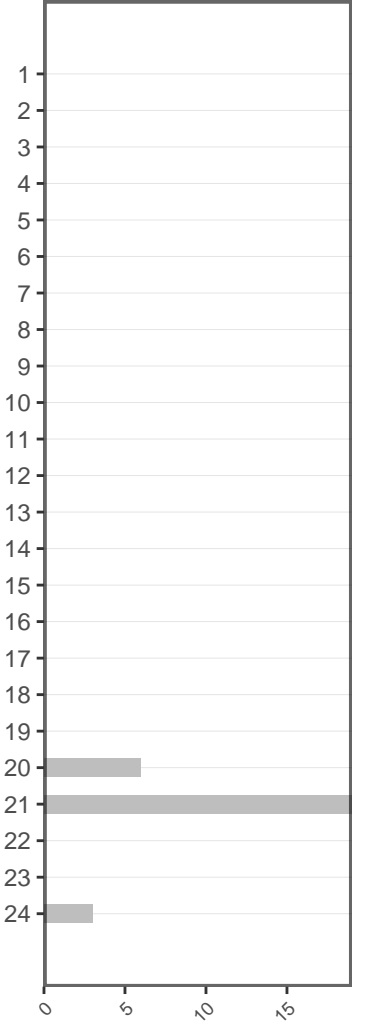
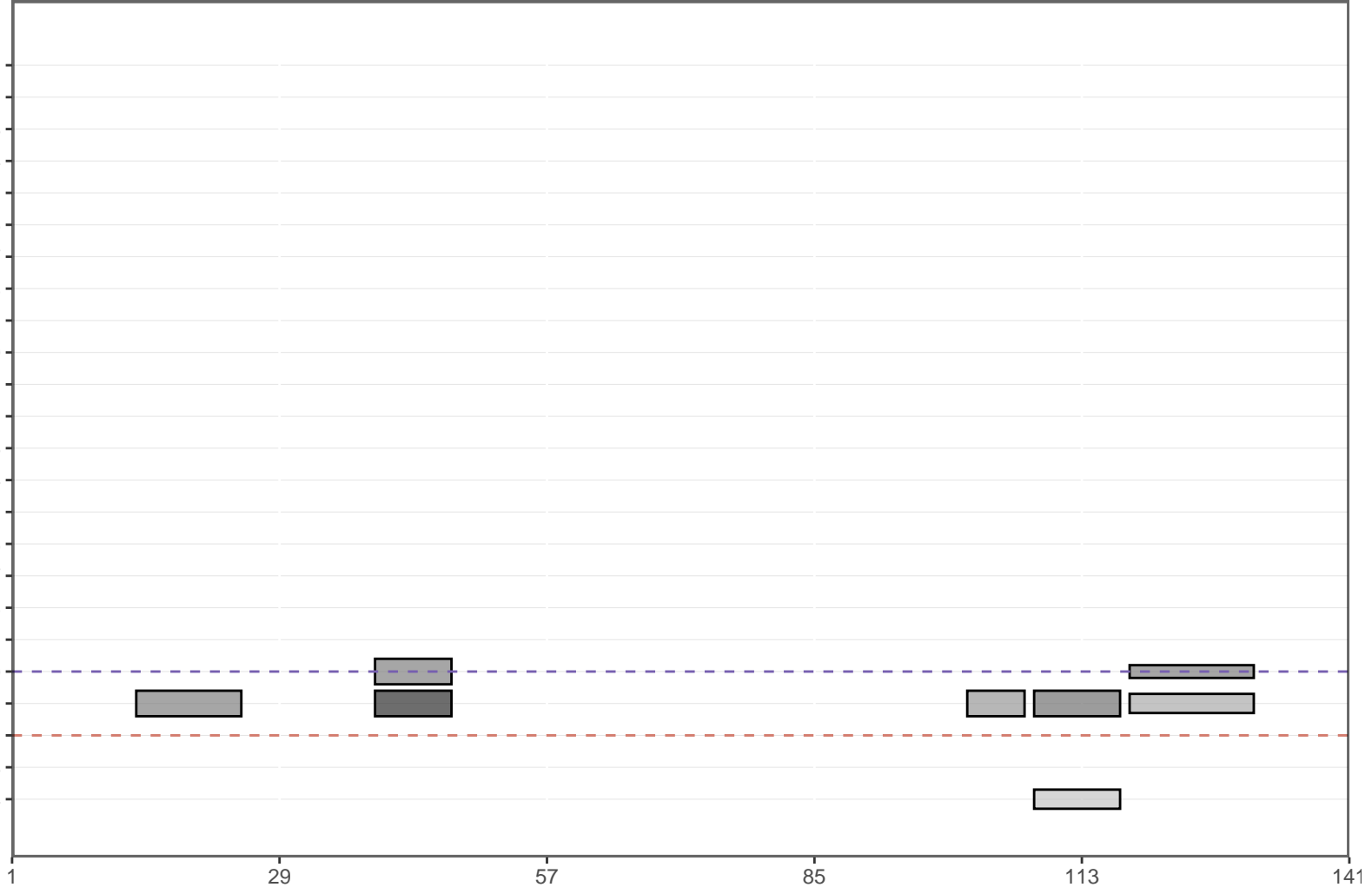
MW indication



Molecular weight



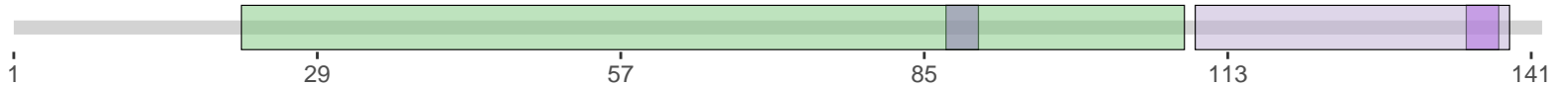
Gel Slice



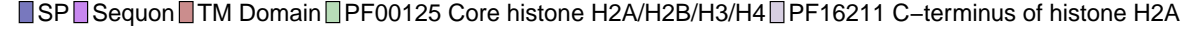
Protein length



Pfam domains



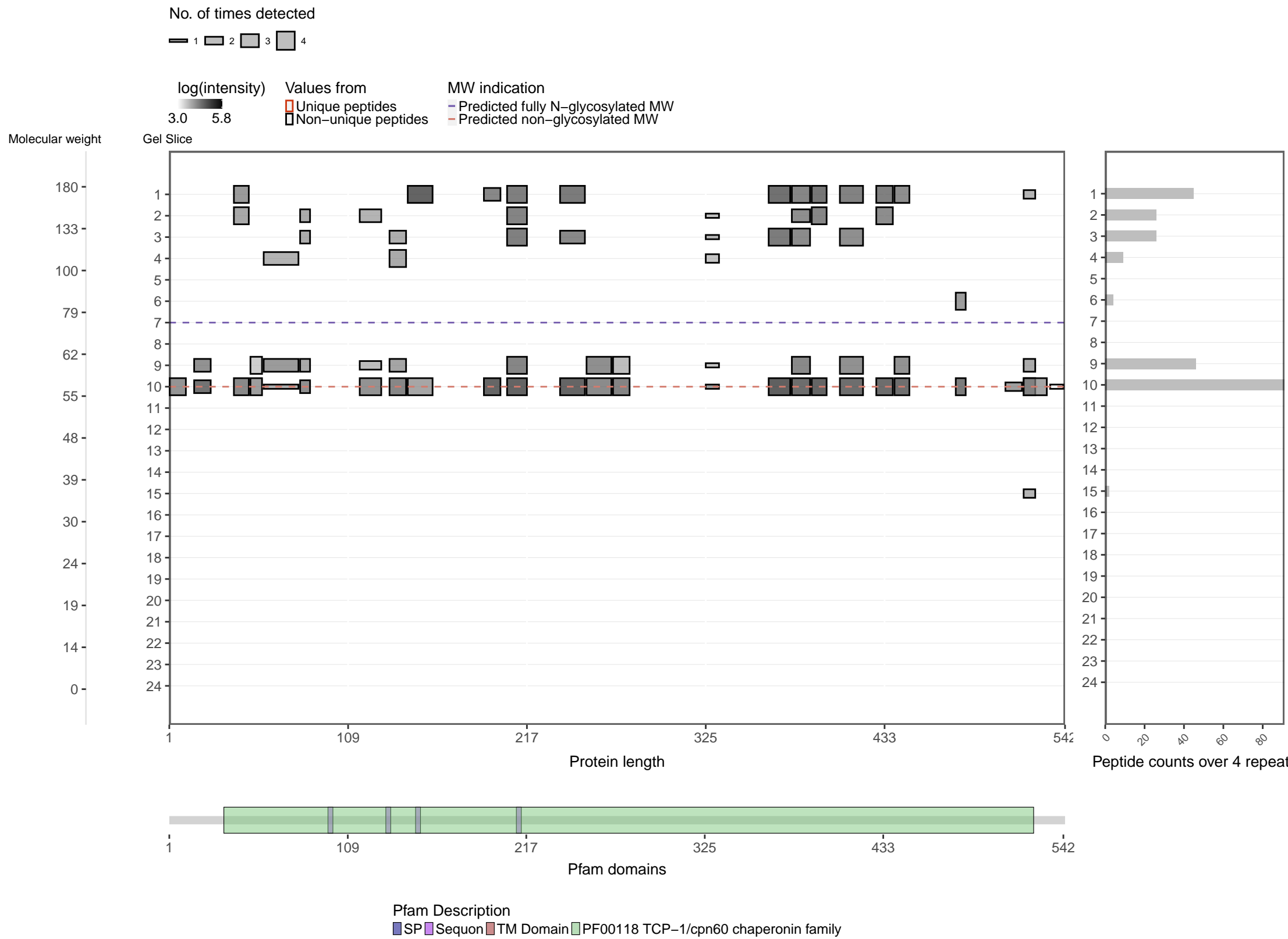
Pfam Description



Protein sequence:

RTSAHGKRVGATAVYVSAILELTAELVLELAGNARKDKVKRTRPRHLGLAIRGDEELDTLTKGTAGGGVPIPHKSLNKTAKE

NbL16g11980.1 T-complex_protein_1_subunit_theta-like [MW = 58.15 kDa]



Protein sequence:

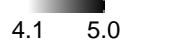
IAEQLENYAKTEEARVVEELKAWADGSAKVVGGAVGEMALHFCDERYKLMVKIKSDFELRRFRTTGAVALLKLSQPNADDLGYVDSVSVVEEIGQVRVTVRNEEGGNSVSTVYLRGSTDLSLDDLERAVDDGVTNTYKAMDRDRVPGAAATEIELASLKEFSFKETGLDQVAAKFAEAFEMVFKTLAENAGLNAMIEISLVAEHAQNTKVLNLEKGAAGEDELSLWDLVYTKFFALKYAADAVCTLRVDDQIMSKPAGGSPRRDQFAGMDEP

NbL16g11520.1 protoporphyrinogen_oxidase_chloroplastic [MW = 59.8 kDa]

No. of times detected



log(intensity)



Values from



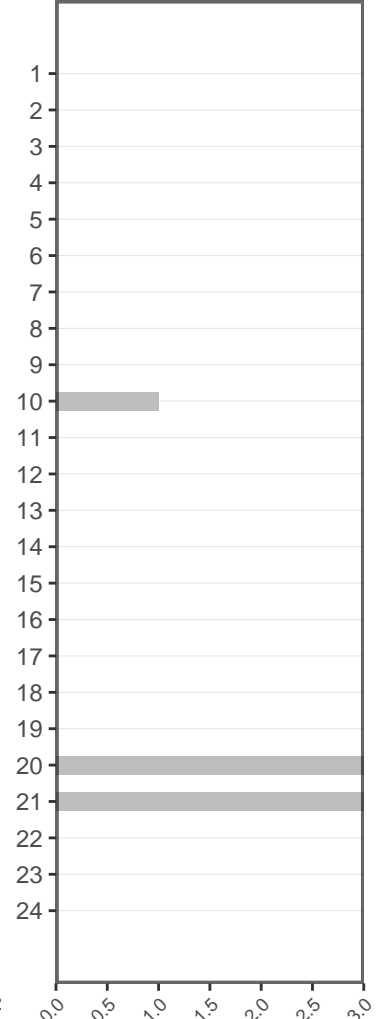
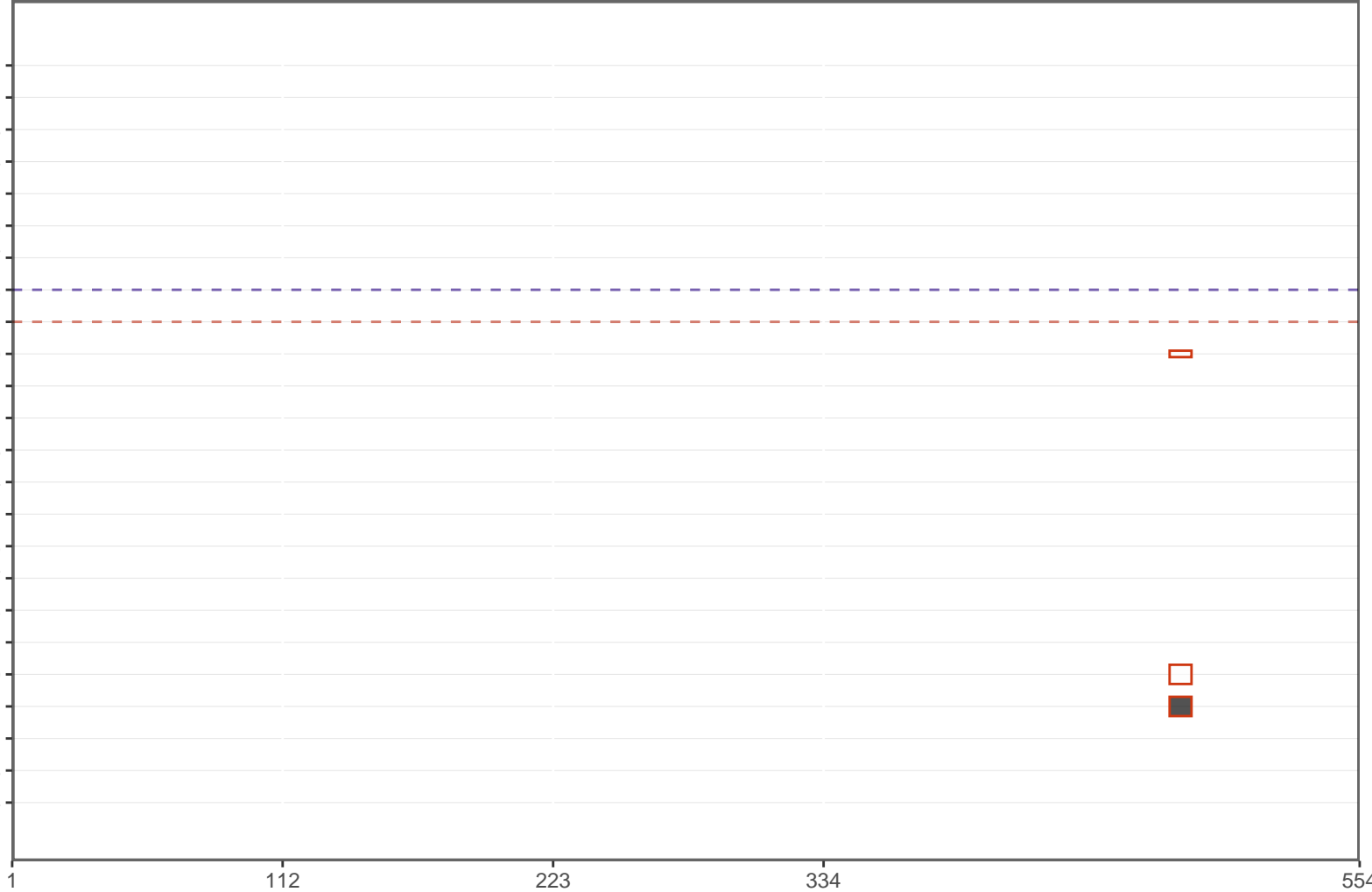
MW indication



Molecular weight

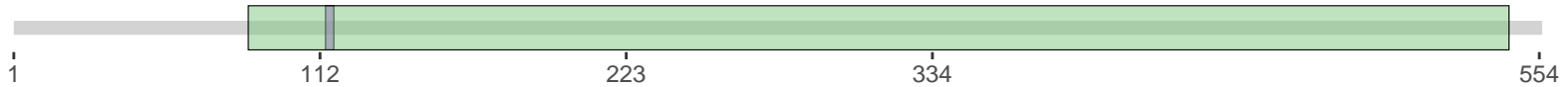


Gel Slice



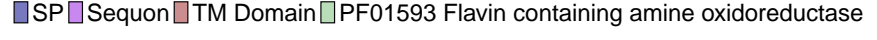
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

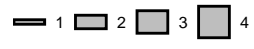


Protein sequence:

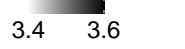
IGGTFKAIKERSSTPKAPRDRPKPKGGTGVGFRKRLMLPDAISARLGSKLKLSWKLSSITKSEKGRVRLTYETPEGVVBLGERSIVMTVPSYVASNILRPLVAAADALSNFYYPVPSAVTISYVQEARDELRVDSGLKGFGLHPRTGQVETLGTIY66SLFFNRAPKGRVLLNHYGGAKNPEL8KTESGOLVEVVDRLDLRKLKPKAGDPVAVVGVRRVWPAQDFLVGHLDTLSTAKAAMSDNGLGLFGGNVYSGVALGRGVEGAVEVSEVTGFLSRVAYK

NbL16g11450.1 protein_trichome_birefringence-like_42 [MW = 42.53 kDa]

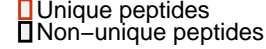
No. of times detected



log(intensity)



Values from



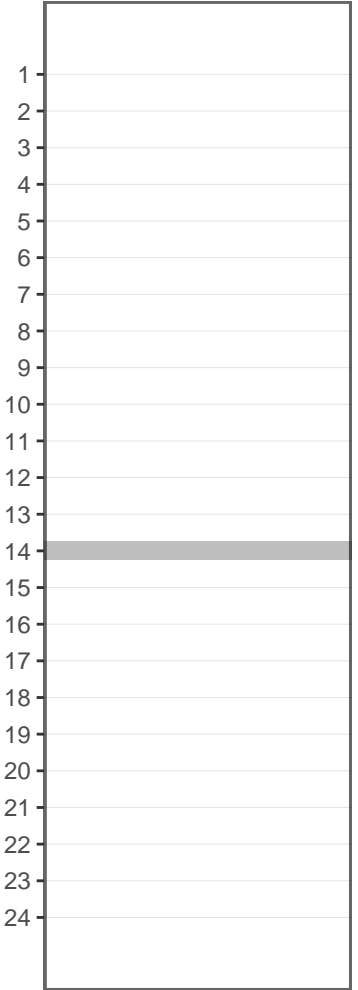
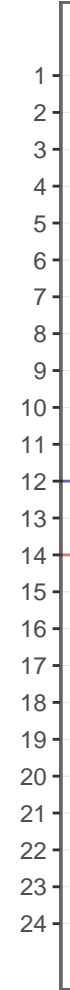
MW indication



Molecular weight



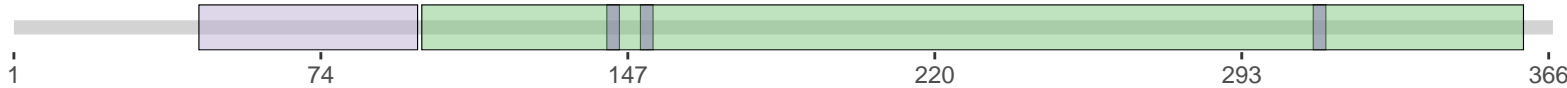
Gel Slice



Protein length

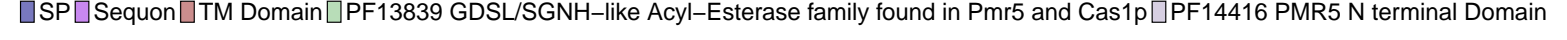


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LIDLVEETGRVLYKLDLSLRSDQWKGVDLNFYHWIHTGNLGTWVDFQVGDKYKEMDHMEAKKALTTAAWVDSNIDRMTRVFFQGGSAVHYHGKDWNEPMVGGDRGGTKPIEGSNYPGDRYPGEAVKKNLSNMTKSVYLLDITLTLQLRKDGHPSPRYANGETDCGSHWQVAGVPMWVWELLTYLLGK

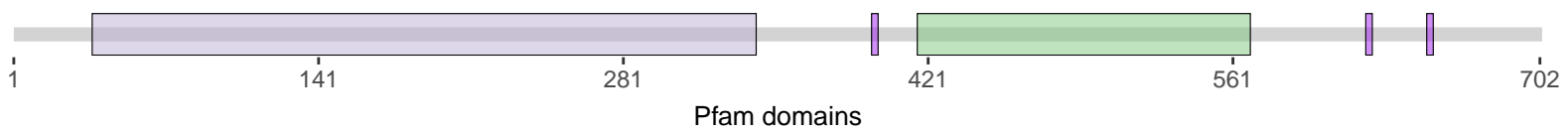
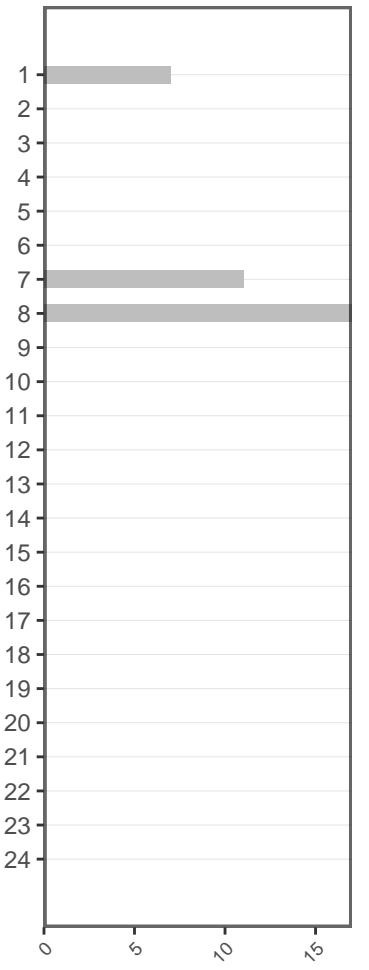
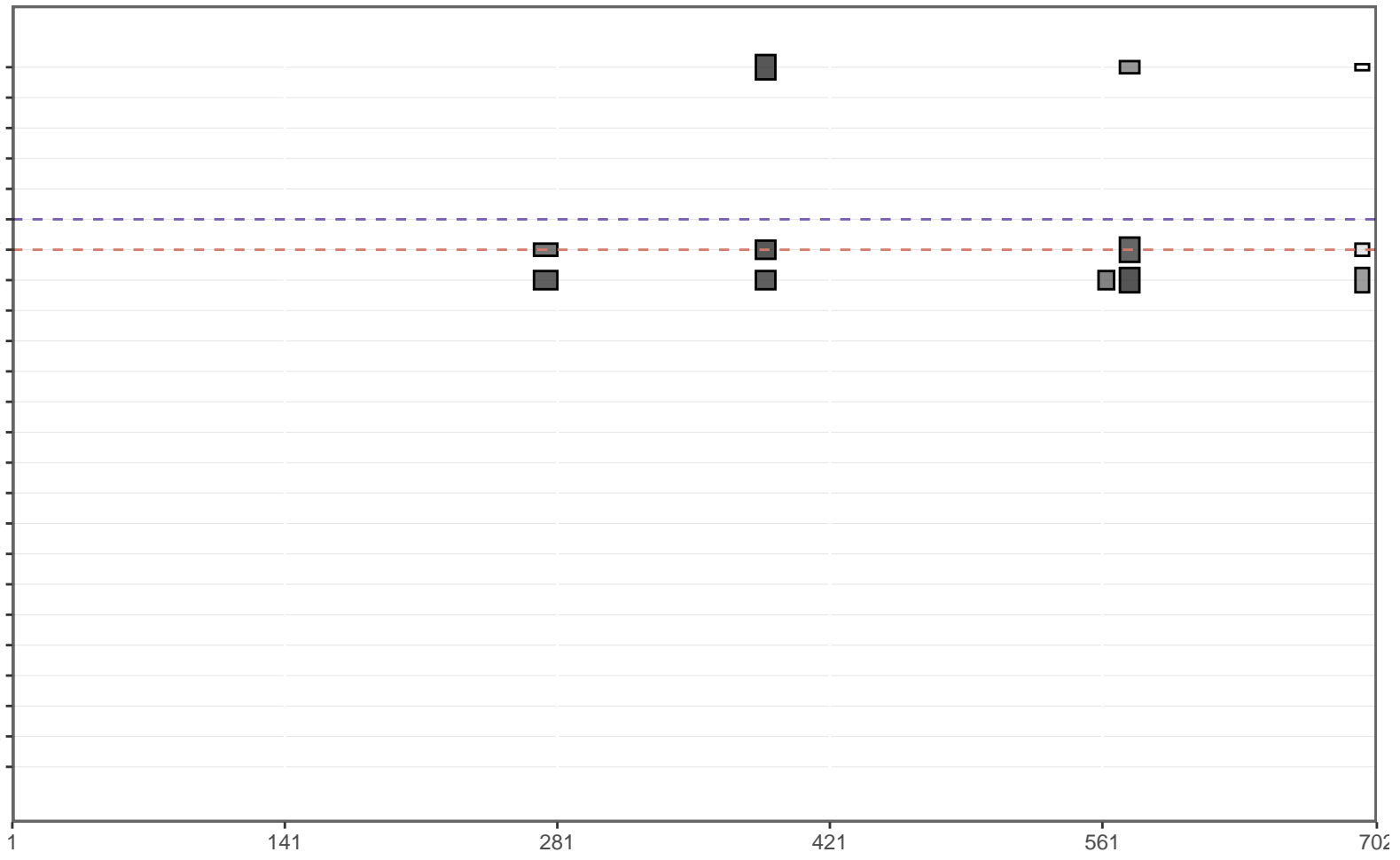
NbL16g11430.1
 trifunctional_UDP-glucose_46-dehydratase/UDP-4-keto-6-deoxy-D-glucose_35-epimerase/UDP-4-keto-L-rhamnose-reductase_RHM1
 [MW = 78.93 kDa]

No. of times detected
 1 2 3 4

log(intensity) 3.3 4.6
 Values from Unique peptides Non-unique peptides
 MW indication Predicted fully N-glycosylated MW Predicted non-glycosylated MW

Molecular weight
 180
 133
 100
 79
 62
 55
 48
 39
 30
 24
 19
 19
 20
 21
 14
 22
 23
 0

Gel Slice
 1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24



Pfam Description
 SP Sequon TM Domain PF04321 RmlD substrate binding domain PF16363 GDP-mannose 4,6 dehydratase

Protein sequence:
 KTEIYWTNPNQVWGDVSGALLPHPRMLMMPGGERHLDGAKEYDSSSEFSAKSNETKTVAPKPKSSEMPQKSPFKFLYGRIGWIGDGLGKLCCKGQIPYEVYKGRLEDRKLLADNALKPHTYVFAAGVGRPNVYDWCESHKPKETIRTYAGTLNLADYCREHGLLMMNFATGCFEYDMKHPGGSGQKPEEDTPNFAQGFYSKTKAMVEELKEVDNVCTLRVYRMPISDLDNPRNFTKISGVNRYVNPMSITLDELLPISIEMAKRNLEKDWNTFPGVGSIN

NbL16g11330.1 peroxisomal_(S)-2-hydroxy-acid_oxidase [MW = 40.52 kDa]

No. of times detected



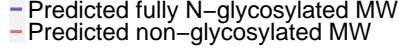
log(intensity)



Values from



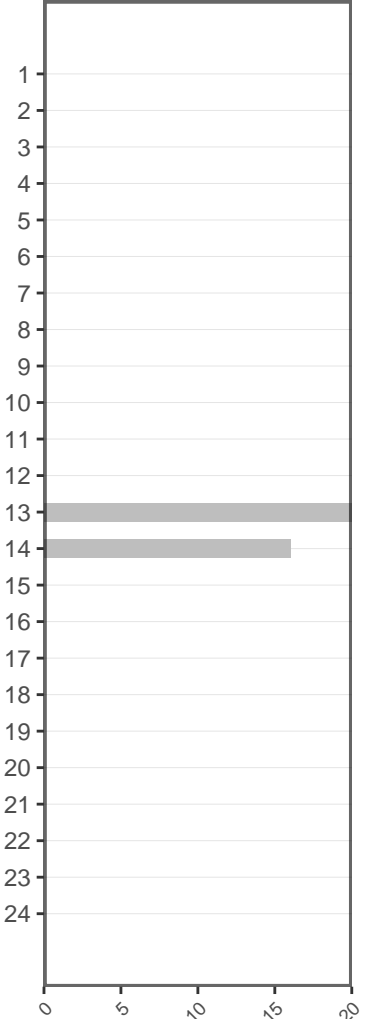
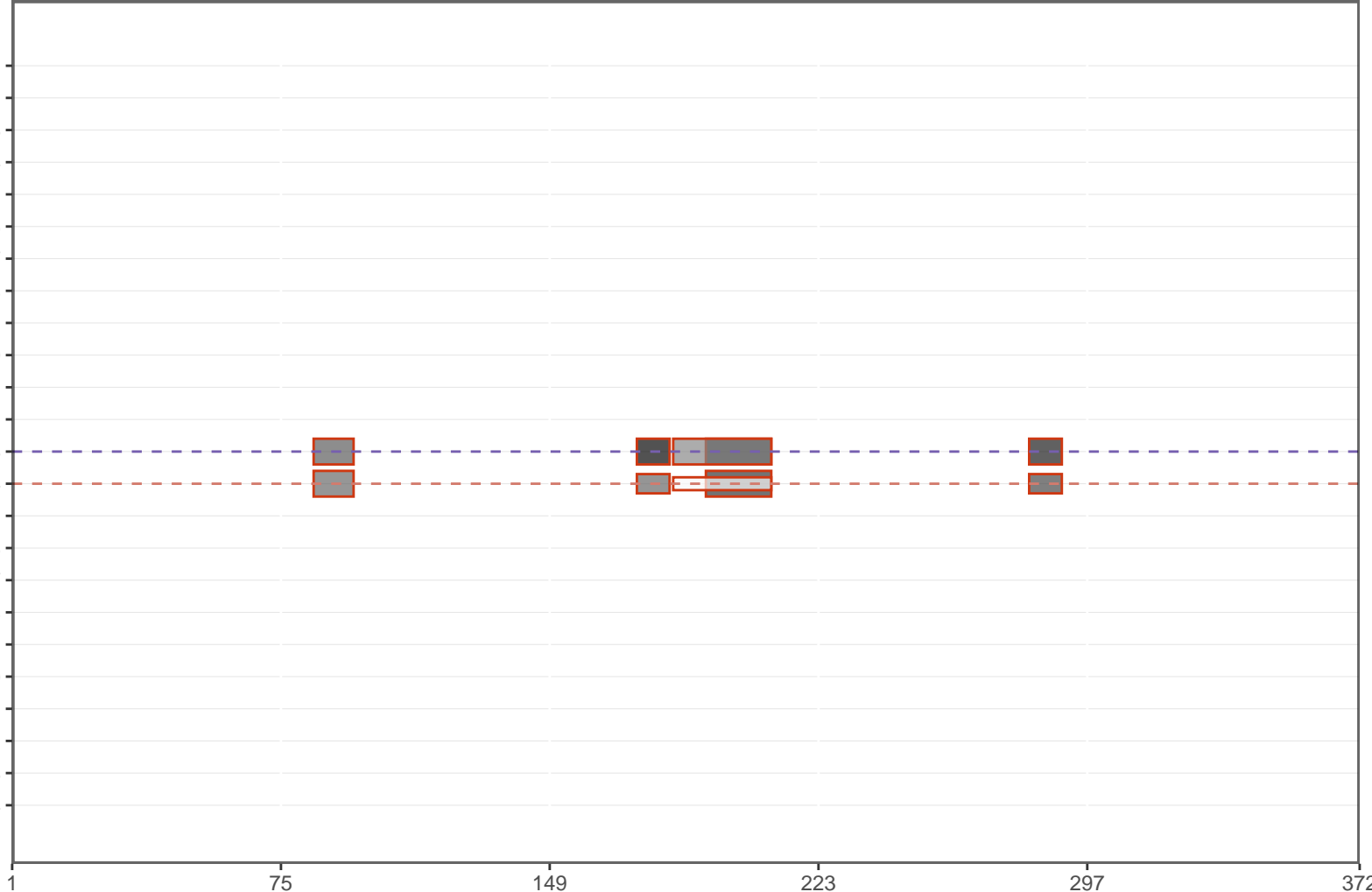
MW indication



Molecular weight

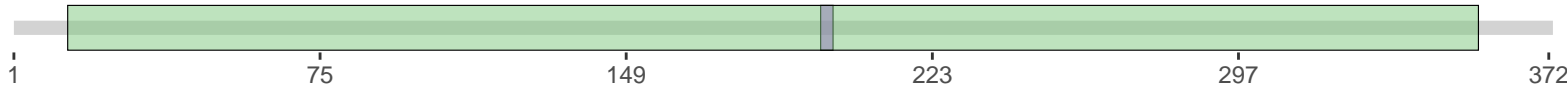


Gel Slice



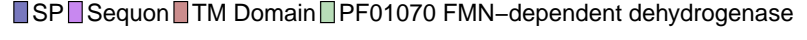
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TLPPFLTKNFEGLDLGMDEANDSGLASYVAGGIDRSLSLWQVWLGTTTSLPILVKGVLTAEDARIAVQAGAGIIVSNHGARGLDYVPTIMALEEVKAAAGGRVVFVLDGGVRRGTDFVKALGASGVFGRVVFVSLAEEGAGIRKVLGMMRDEFELTMALSGGRSLKEFRINHWADWDAPRAALPAPSL

NbL16g11260.1 chlorophyll_a-b_binding_protein_8_chloroplastic [MW = 29.37 kDa]

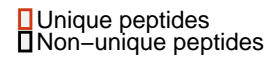
No. of times detected



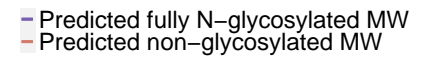
log(intensity)



Values from



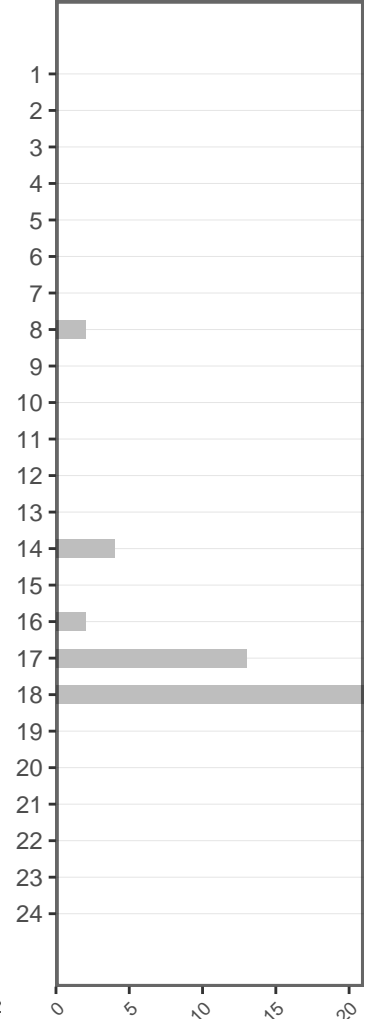
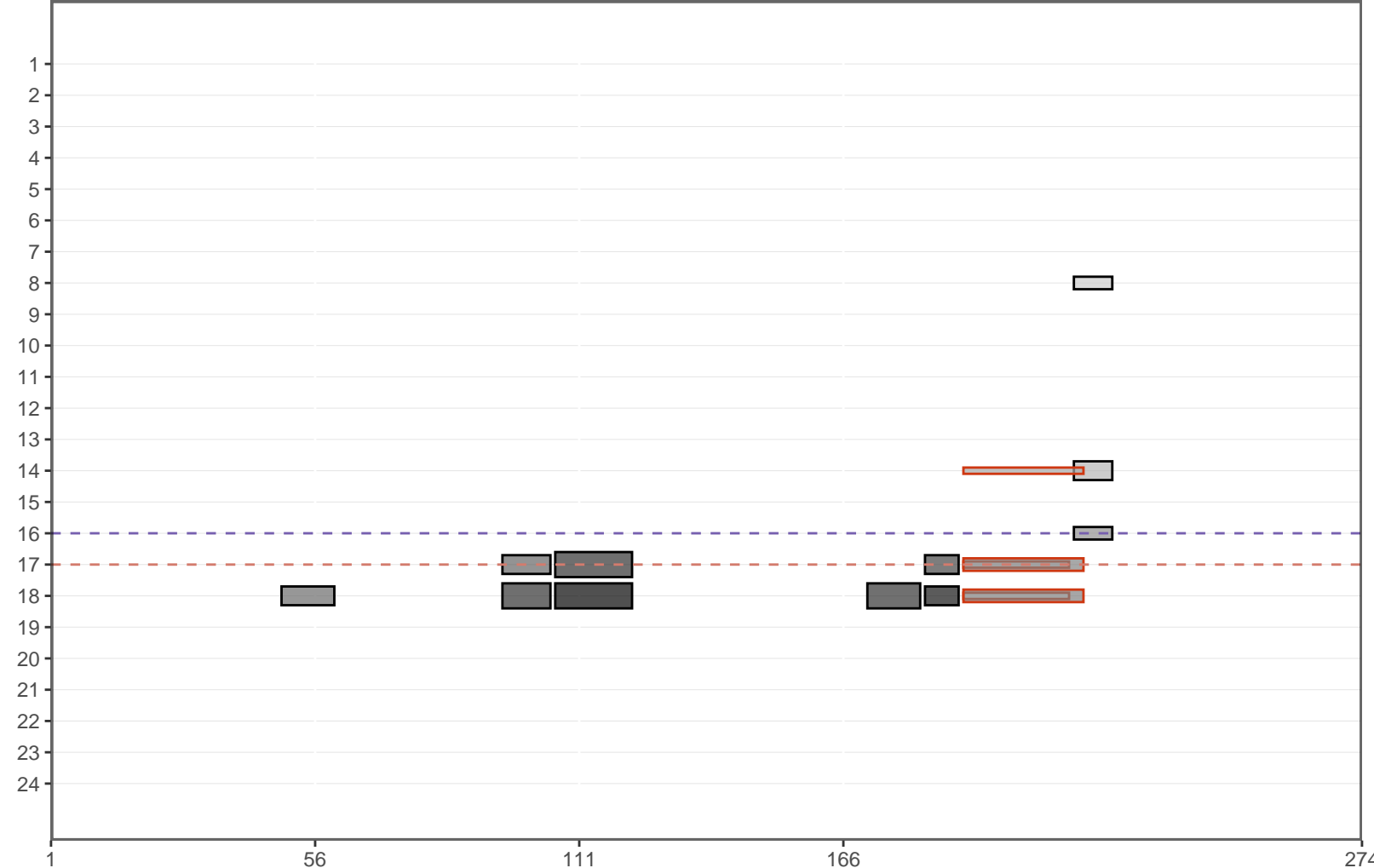
MW indication



Molecular weight

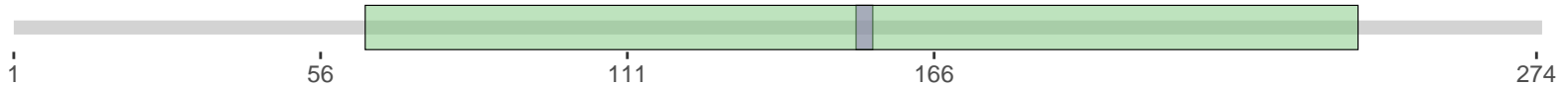


Gel Slice



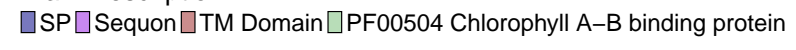
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

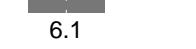
IIPPETALPWFOTGVIPDAGTNYWADNKTFLVLEMLMGFAEHRRFQDWAKPGSMGKGYFLGKLGKGGSEPRVPGSGFFNPLGFGKDEKSMKDKLKEVKNGRLAMLAALGYFIQGLVTEGVSPIYQNLIDHADPVAANNILTNKPH

NbL16g11160.1 60S_ribosomal_protein_L11-1 [MW = 20.74 kDa]

No. of times detected



log(intensity)



Values from



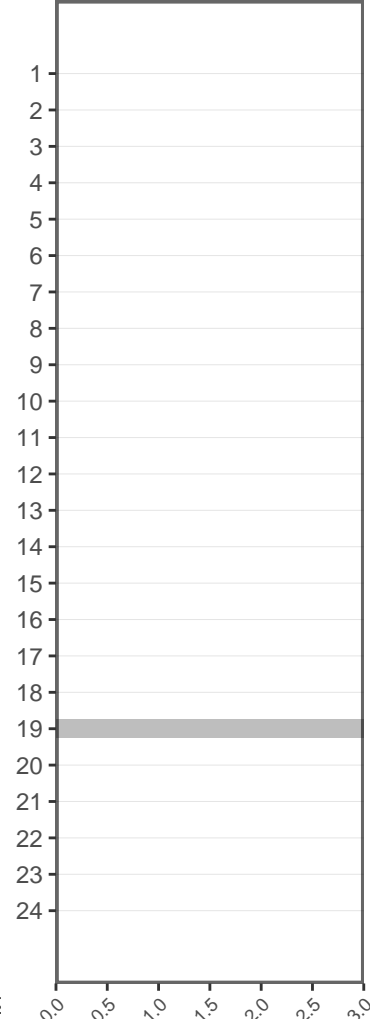
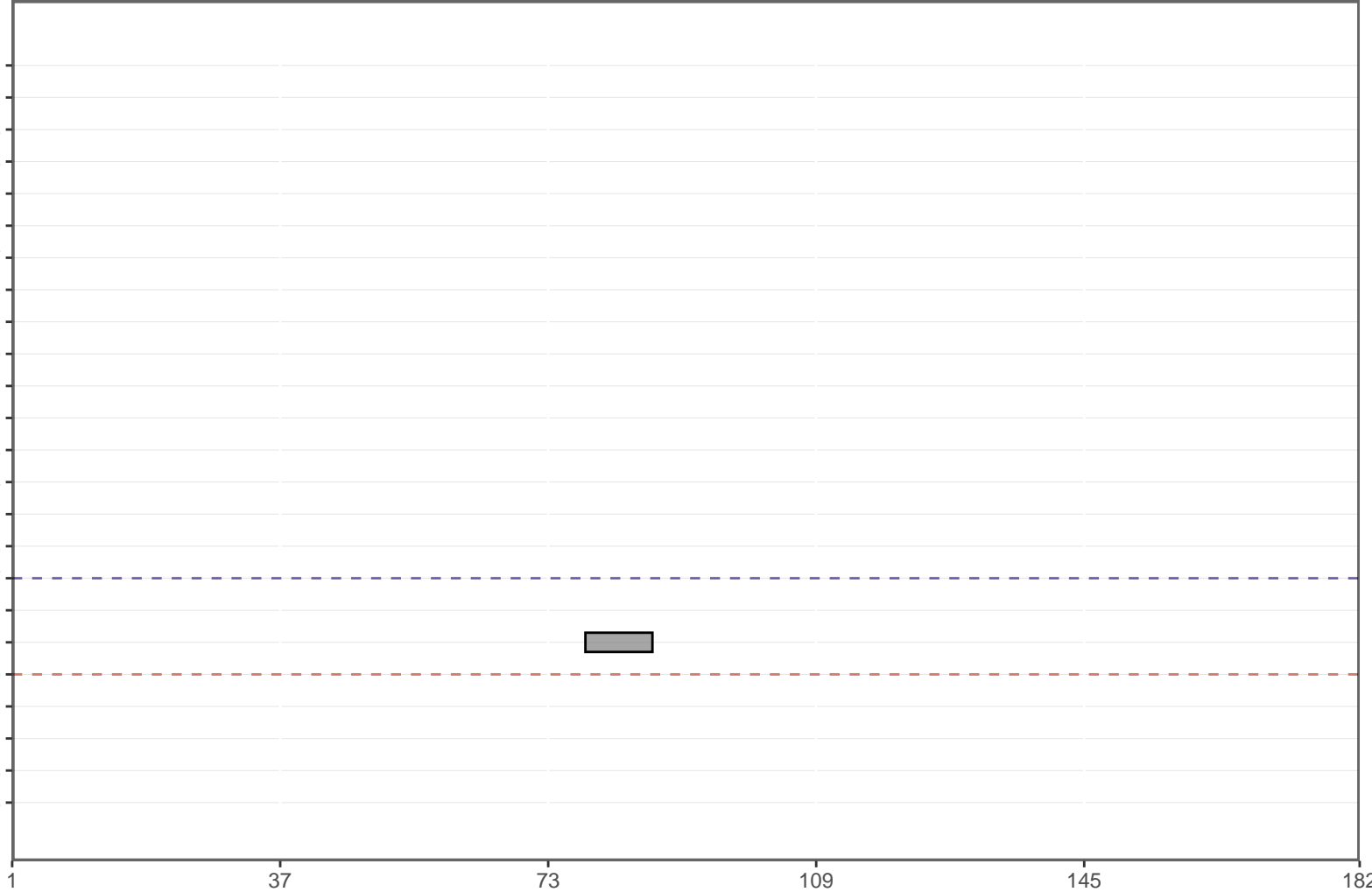
MW indication



Molecular weight

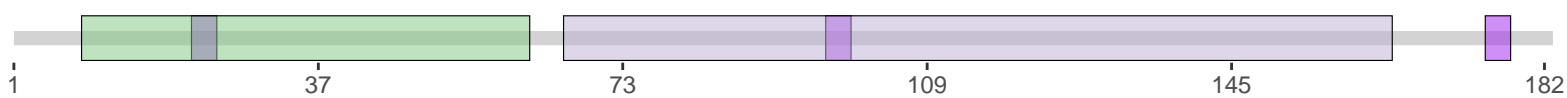


Gel Slice



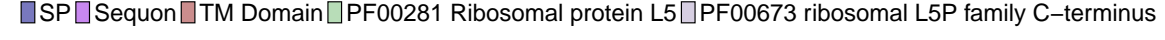
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

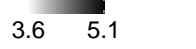
MOLLESGLKYEYELLRRNFSETGCFGFGDGHDLGKHYDPTGIVGMDFFVALLERPGYRVARRRRCKARVIGIHRVTKDDAMKWFQVYKYEGLNKSNDI

NbL16g11070.1 uncharacterized_LOC107795773 [MW - SP = 9.99 kDa]

No. of times detected



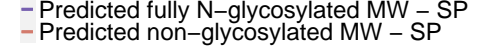
log(intensity)



Values from



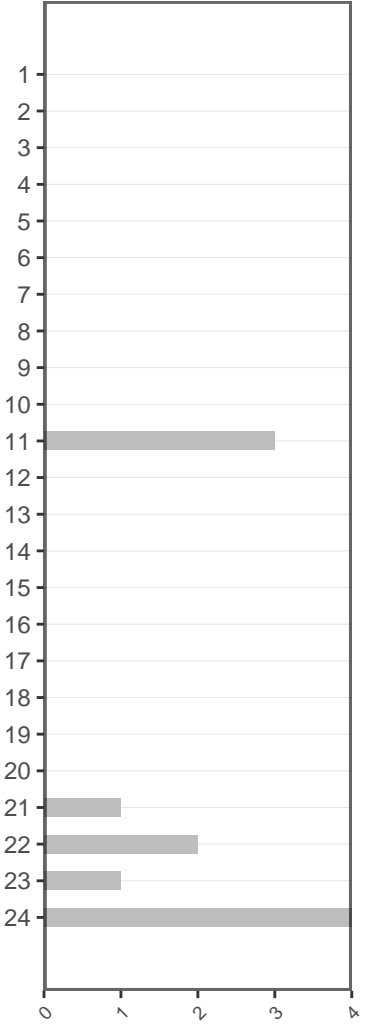
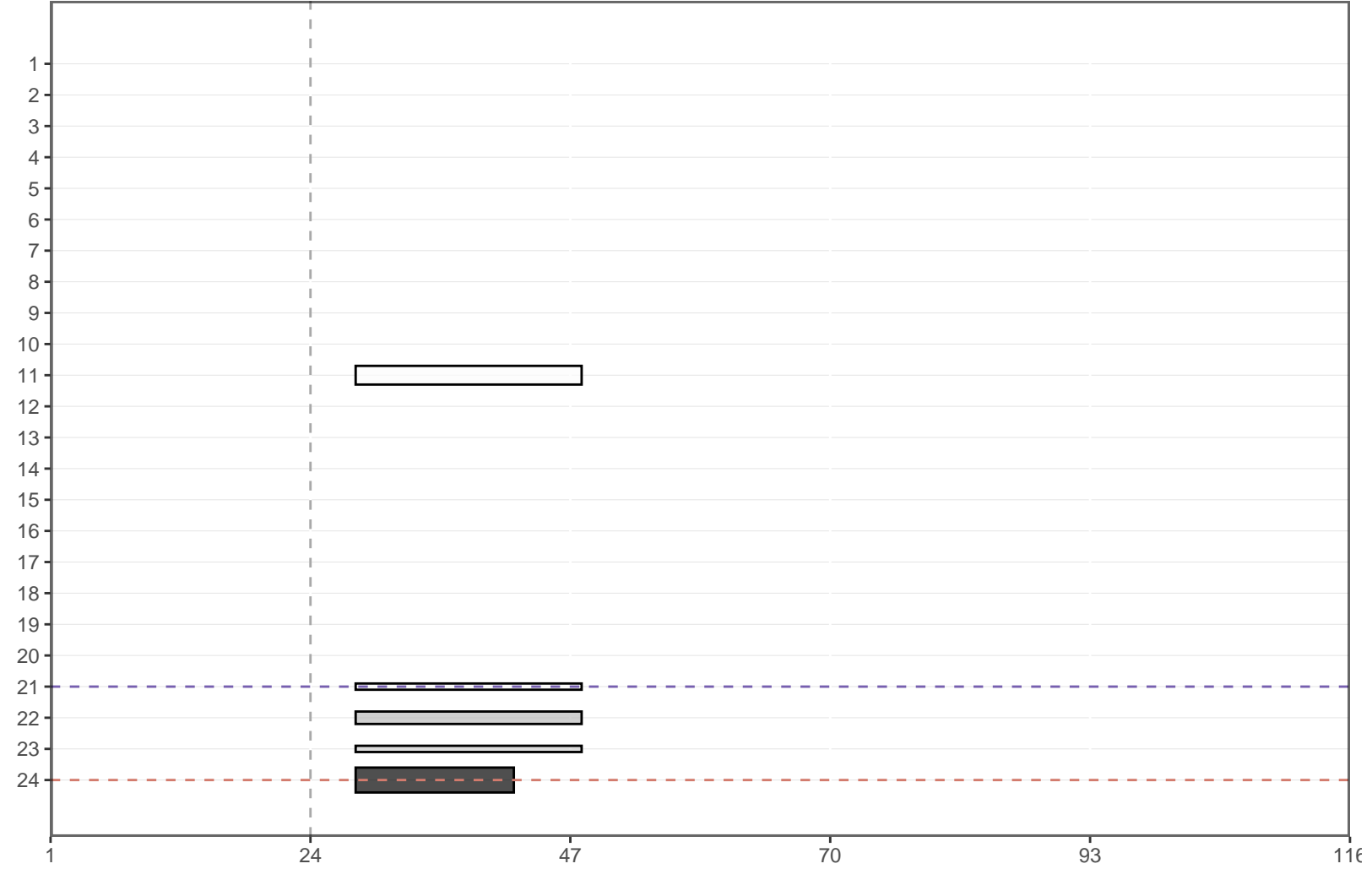
MW indication



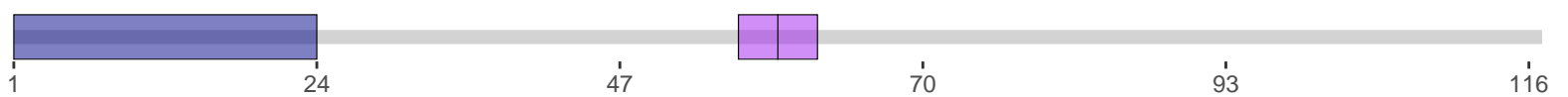
Molecular weight



Gel Slice



Protein length



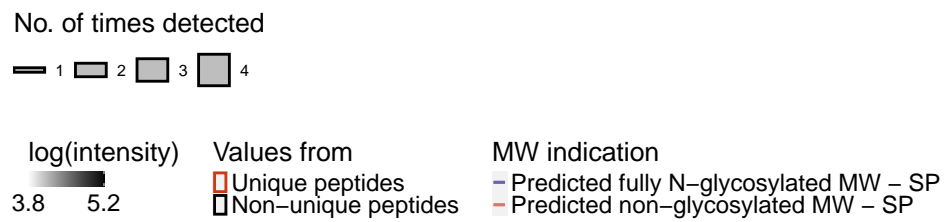
Pfam domains

Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

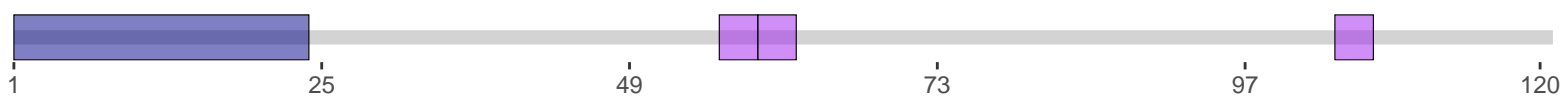
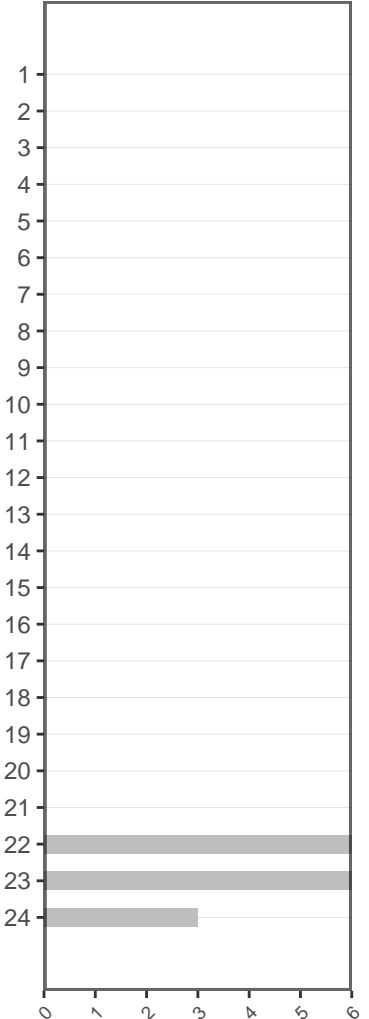
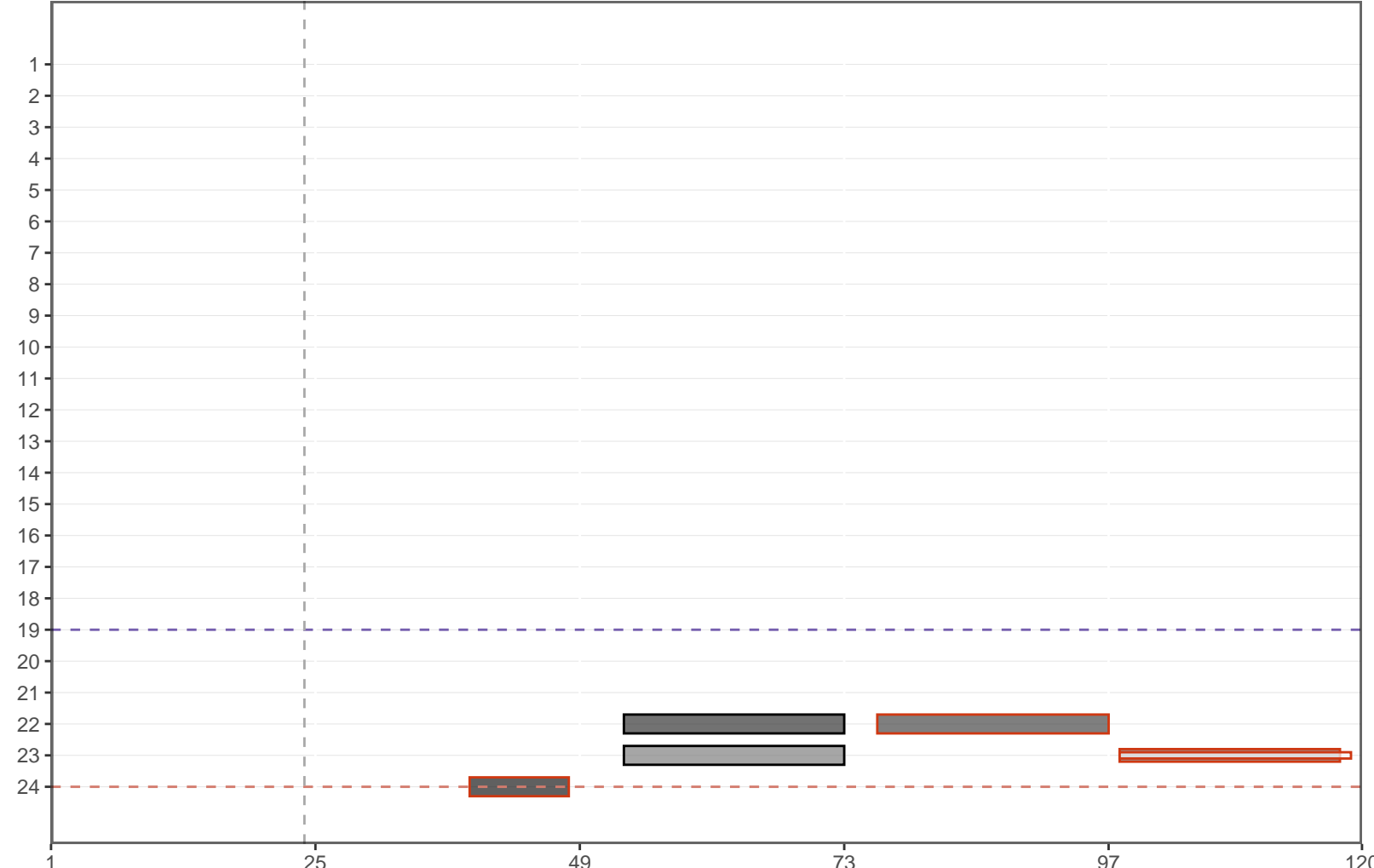
CLARCIMARCFLENAENDTLDSEHSSTLEARNRNVGNVGGSLGHCSEFLQYVTRSLLELAGQTAVRTIIVATML*

NbL16g11060.1 uncharacterized_LOC107795773 [MW – SP = 10.45 kDa]



Molecular weight

Gel Slice



Pfam domains

Pfam Description

SP Sequon TM Domain

Protein sequence:
ICMARCFUNASNDTLDSEHSTLEARNRVQNVGGDLGHGSEFLFQYDNEKFGTGMNGSENYCMGNNALEKA

NbL16g10770.1 probable_plastid-lipid-associated_protein_11_chloroplastic [MW = 19.66 kDa]

No. of times detected



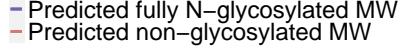
log(intensity)



Values from



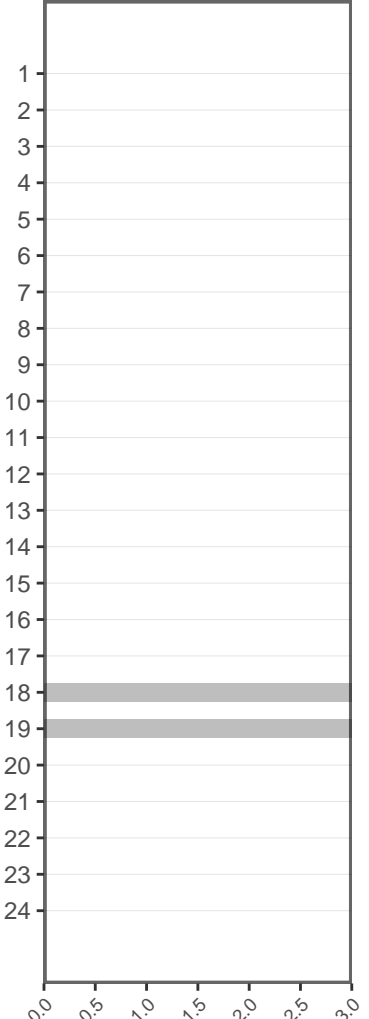
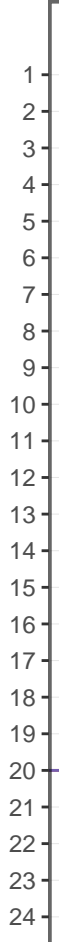
MW indication



Molecular weight



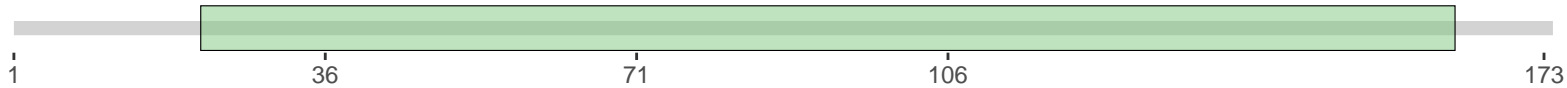
Gel Slice



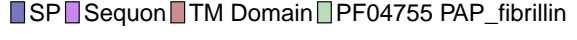
Protein length



Pfam domains



Pfam Description



Protein sequence:

SDVLDVDEKGTLLNNVTFPPDGGVFFVRYTIDVASSGRVNFRTSVALRGNKWEFLPPFGDGFETVLDDEIRVVKDIRDYLVERAPYTKKE

NbL16g10490.1 peroxisomal_membrane_protein_11C [MW = 25.73 kDa]

No. of times detected



log(intensity)



Values from



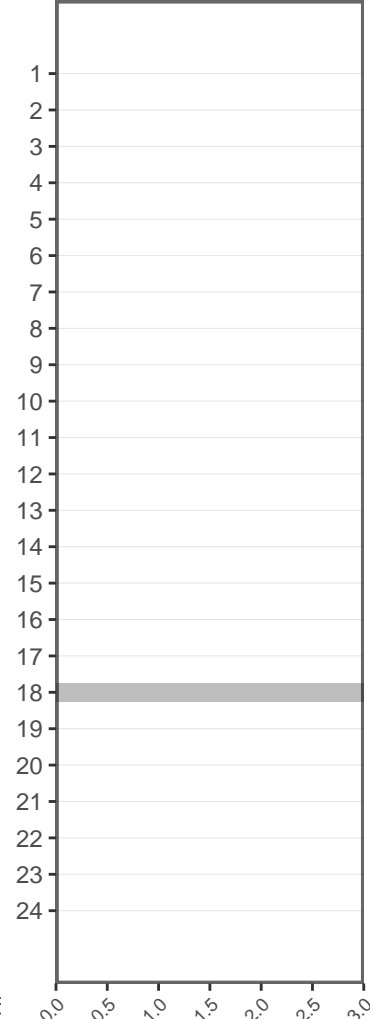
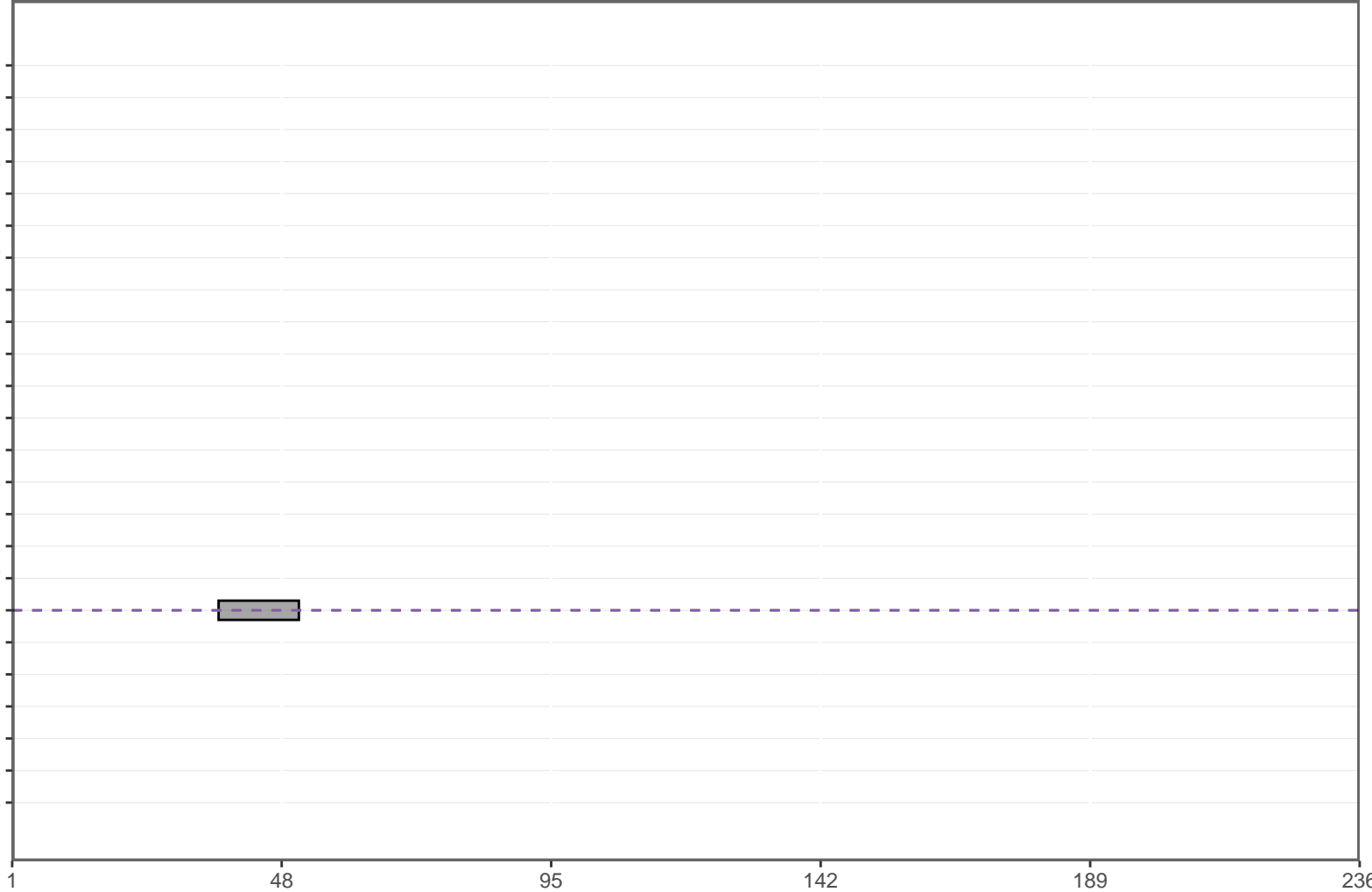
MW indication



Molecular weight

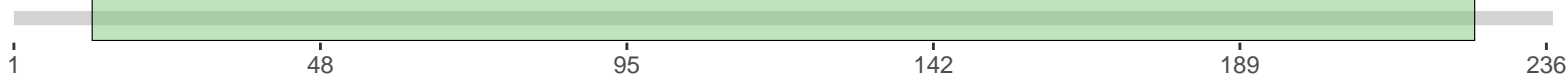


Gel Slice



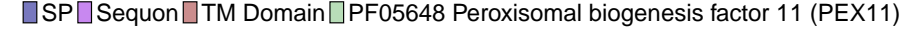
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

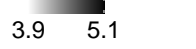
MLGRTGYDKERTELGRISLFGWMGSSIGTALVEIGELGRIGSGLKLEKLNNTDKHKNEQYQSGKQKSNERSLAIKAGMDIVVWGLLQLAPKVTPTVGTGAFGFVSSLSISYQLLPEPPPKAS

NbL16g10300.1 uncharacterized_LOC109231095 [MW = 30.26 kDa]

No. of times detected



log(intensity)



Values from



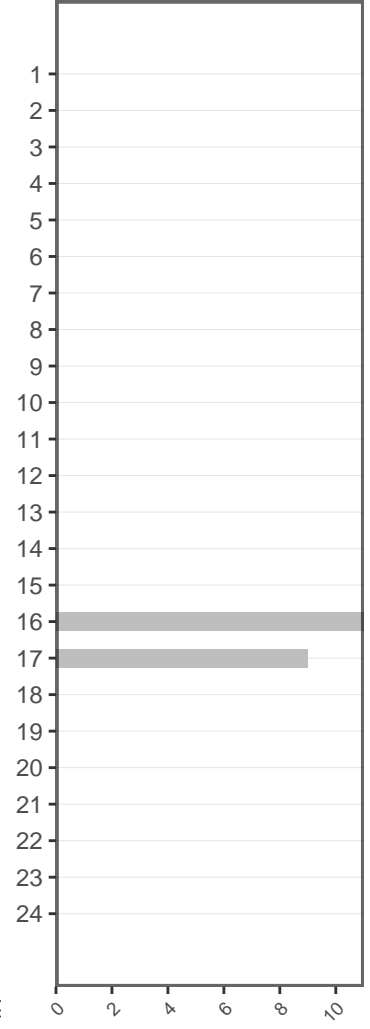
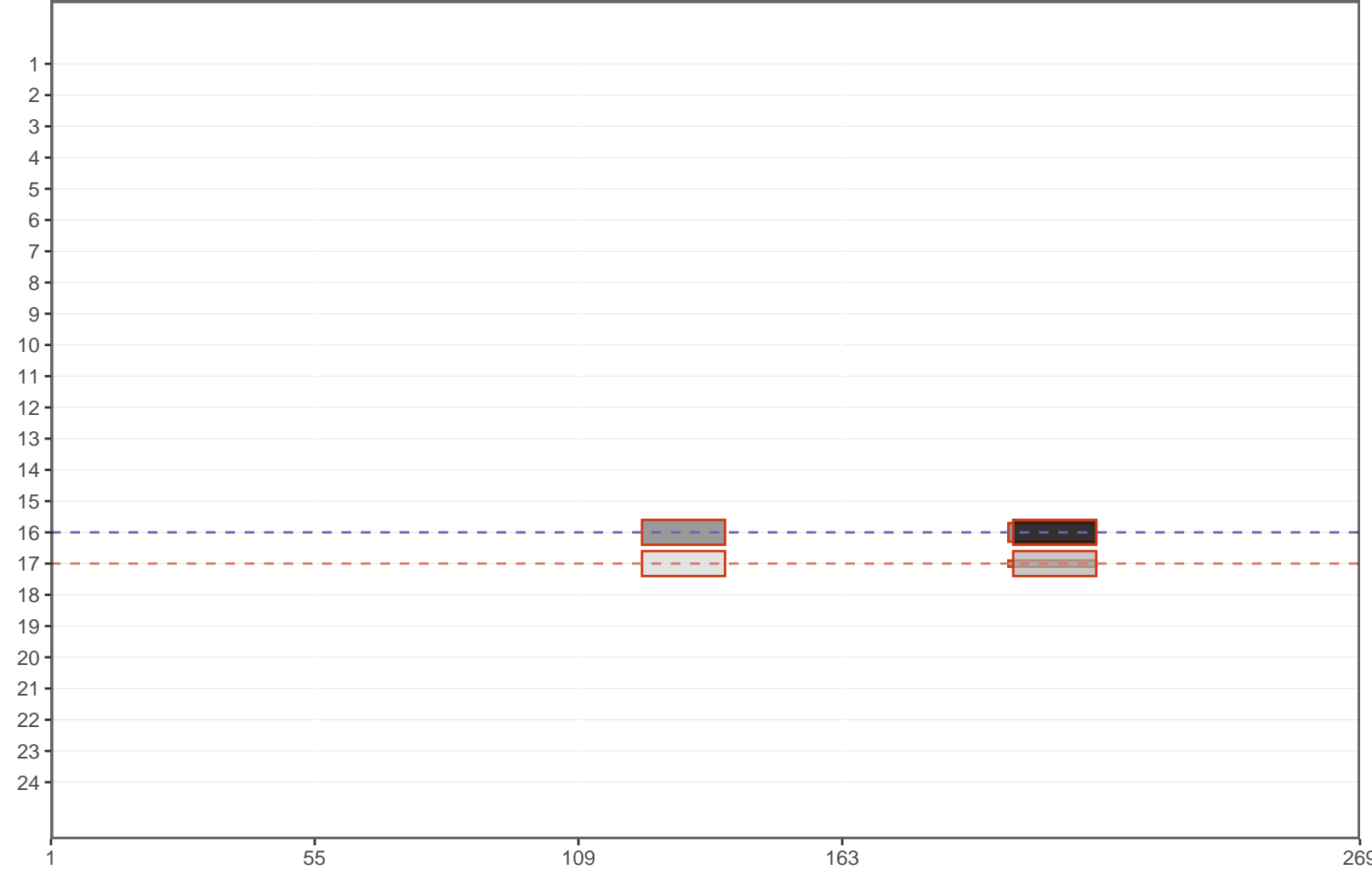
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



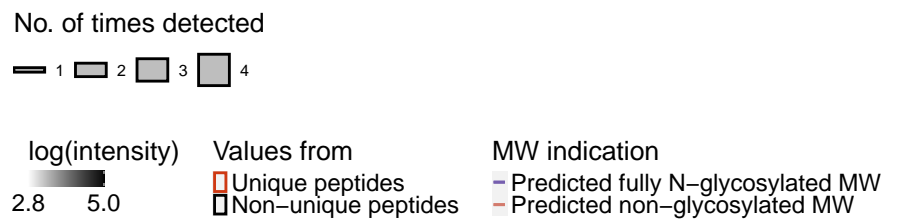
Pfam domains

Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

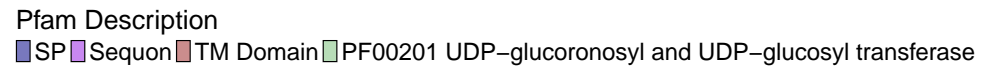
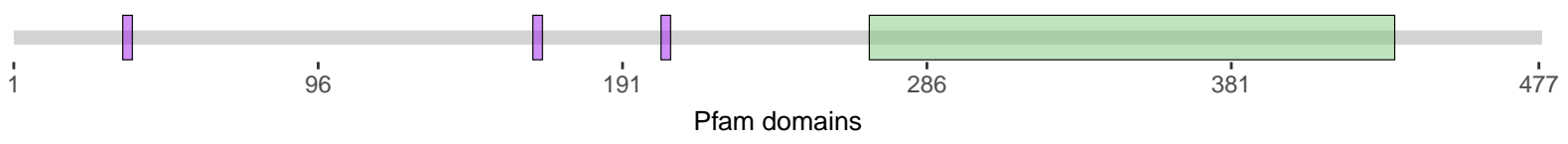
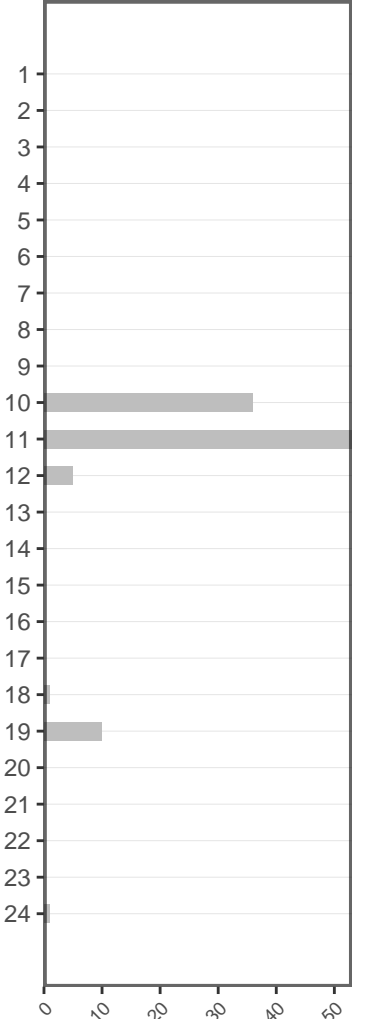
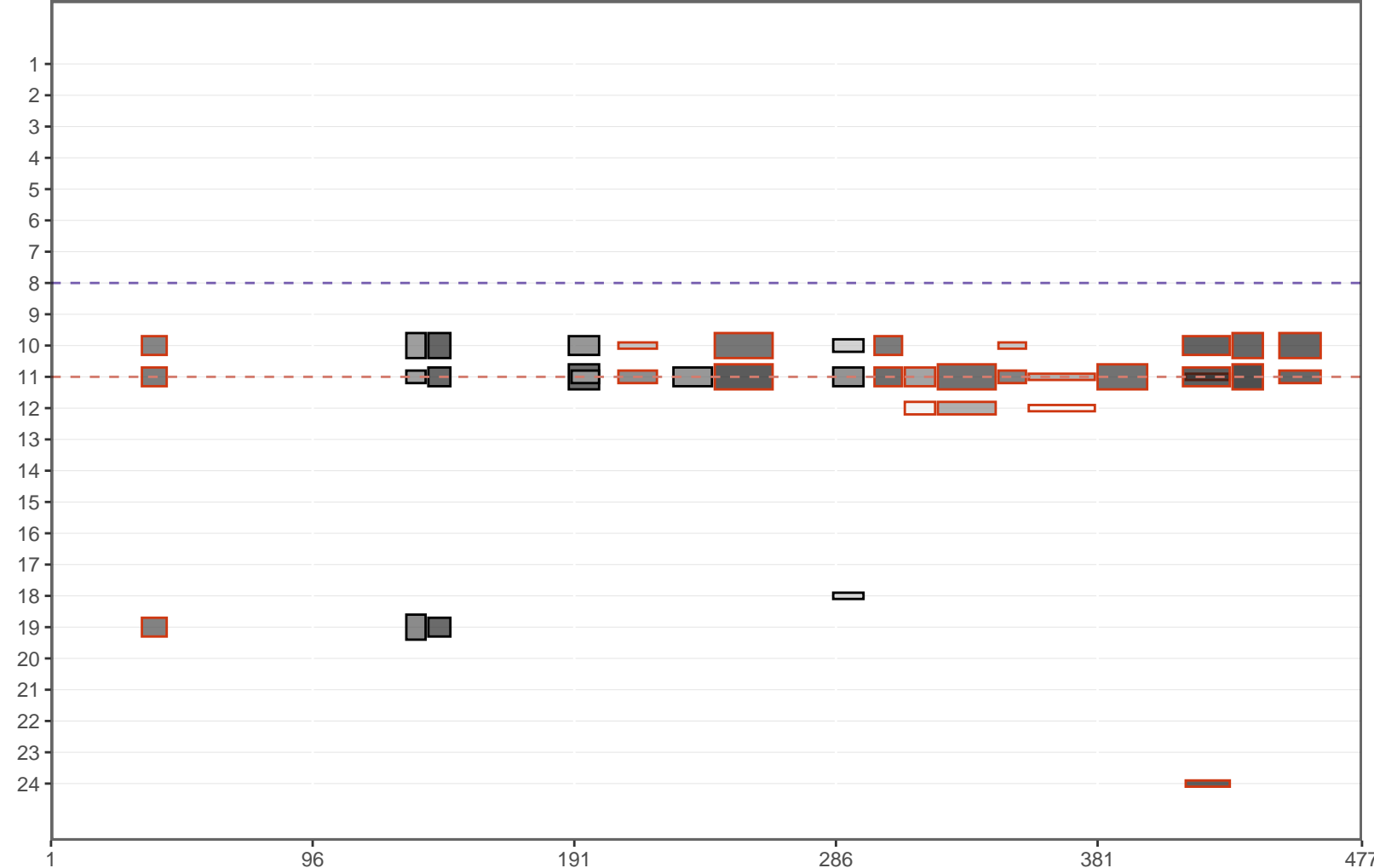
LVKDEWMDNDLATWIGANRFYGPVDAIKFASGKLVVITTKGSRFADALLRELAGITFRERIKYGLGTPKVKVLYKXGQEMPEHQGLTLHFVEDRLATLKNVKESELDGWNLYLGDWGYNTQKEREEAASIPRIILLGLSDFSNLKY

NbL16g10200.1 putative_UDP-rhamnose:rhamnosyltransferase_1 [MW = 52.96 kDa]



Molecular weight

Gel Slice



Protein sequence:

MEFEGEYLDITYNKAGKPVIPGILLPEELPADERTLDGPNWQKIKWLDGKPRVLPVGFSGSEKLSKNDVYEIMANGVKLSGLPFFWILGRPSWALNDLPSGFGASTEGRLVHGHWAPQKEILHPSIGGSLFHGHWGSTIETLRVGHVAVLPLVFDGGLNARLLVKGKVAIEVYKRNEDDSFGSNDIATSLREAMVSEDDGELRARGAKDGIFGDQNLHDSVYVNFVEYMRINGEMKV

NbL16g10190.1 UDP-glycosyltransferase_91C1-like [MW = 52.56 kDa]

No. of times detected



log(intensity)



Values from



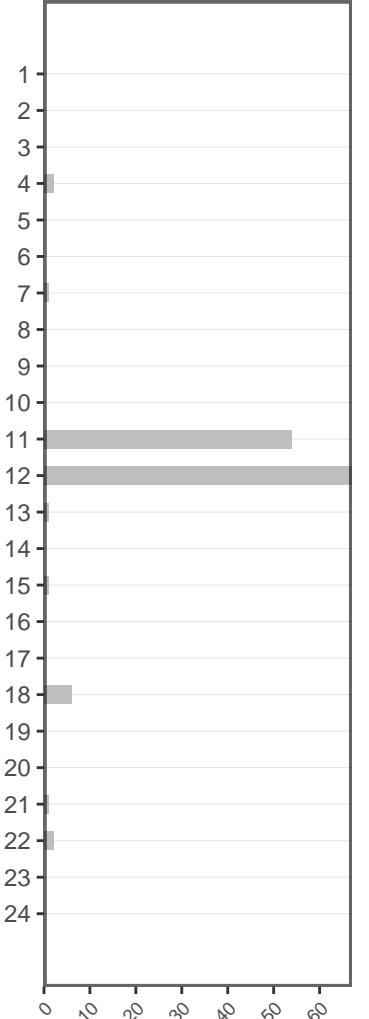
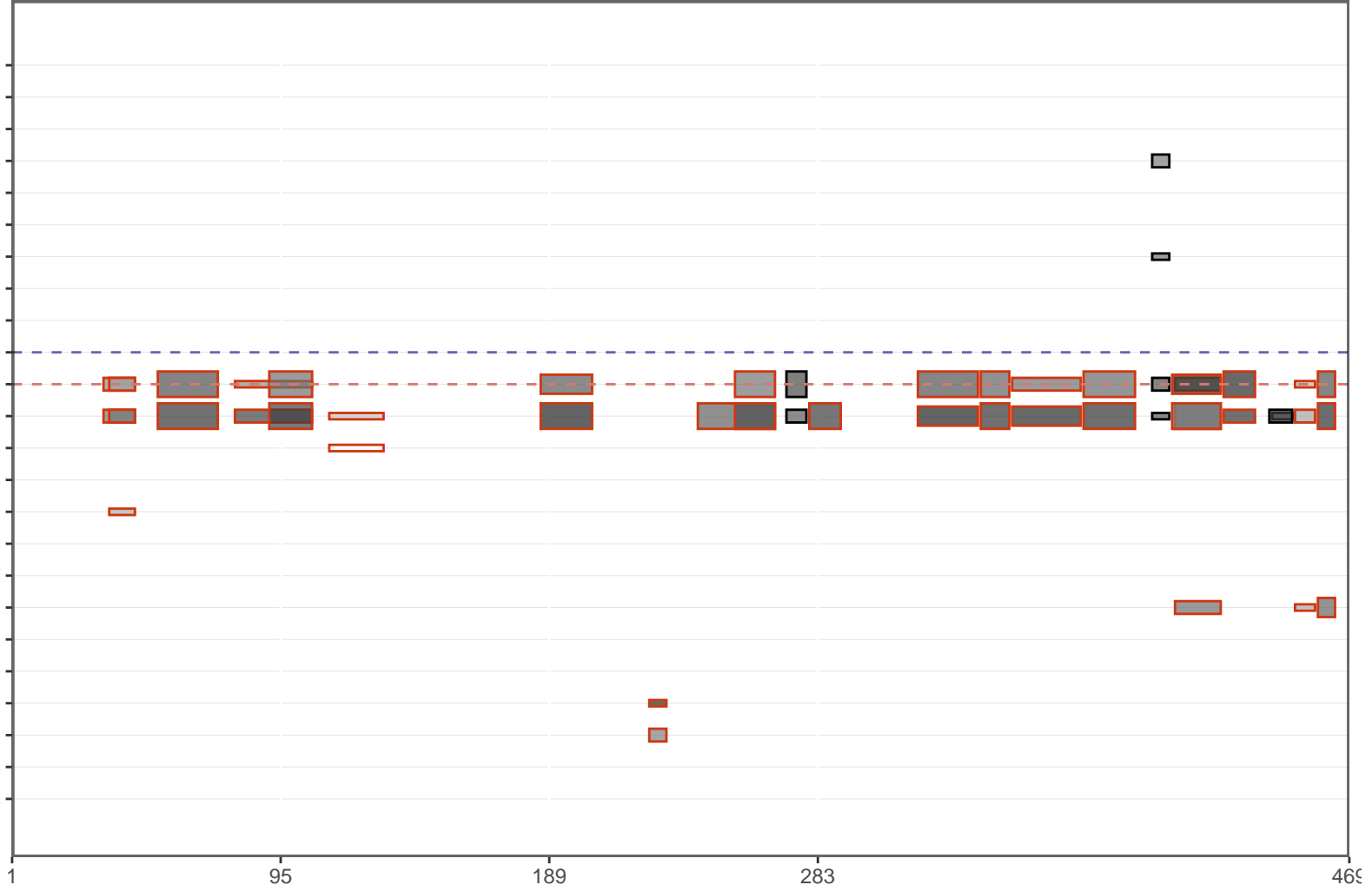
MW indication



Molecular weight



Gel Slice



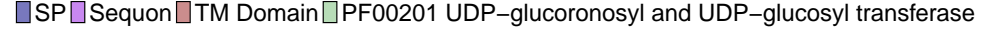
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL16g10160.1 uncharacterized_LOC109218791 [MW = 12.48 kDa]

No. of times detected



log(intensity)



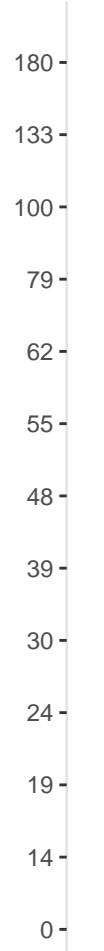
Values from



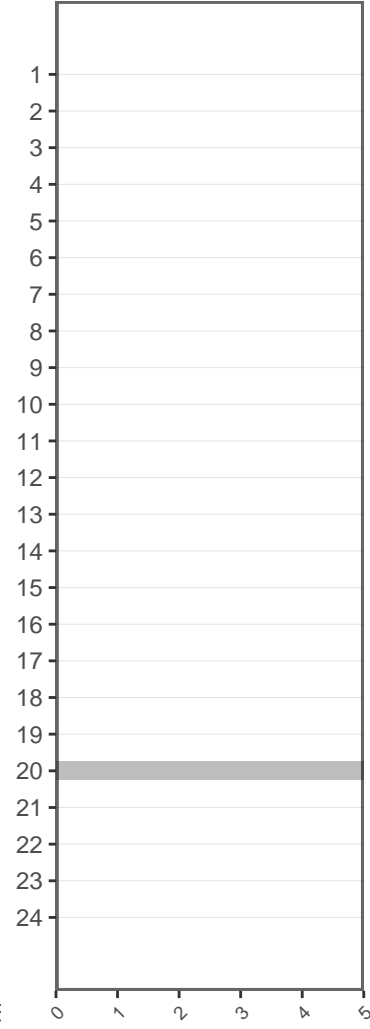
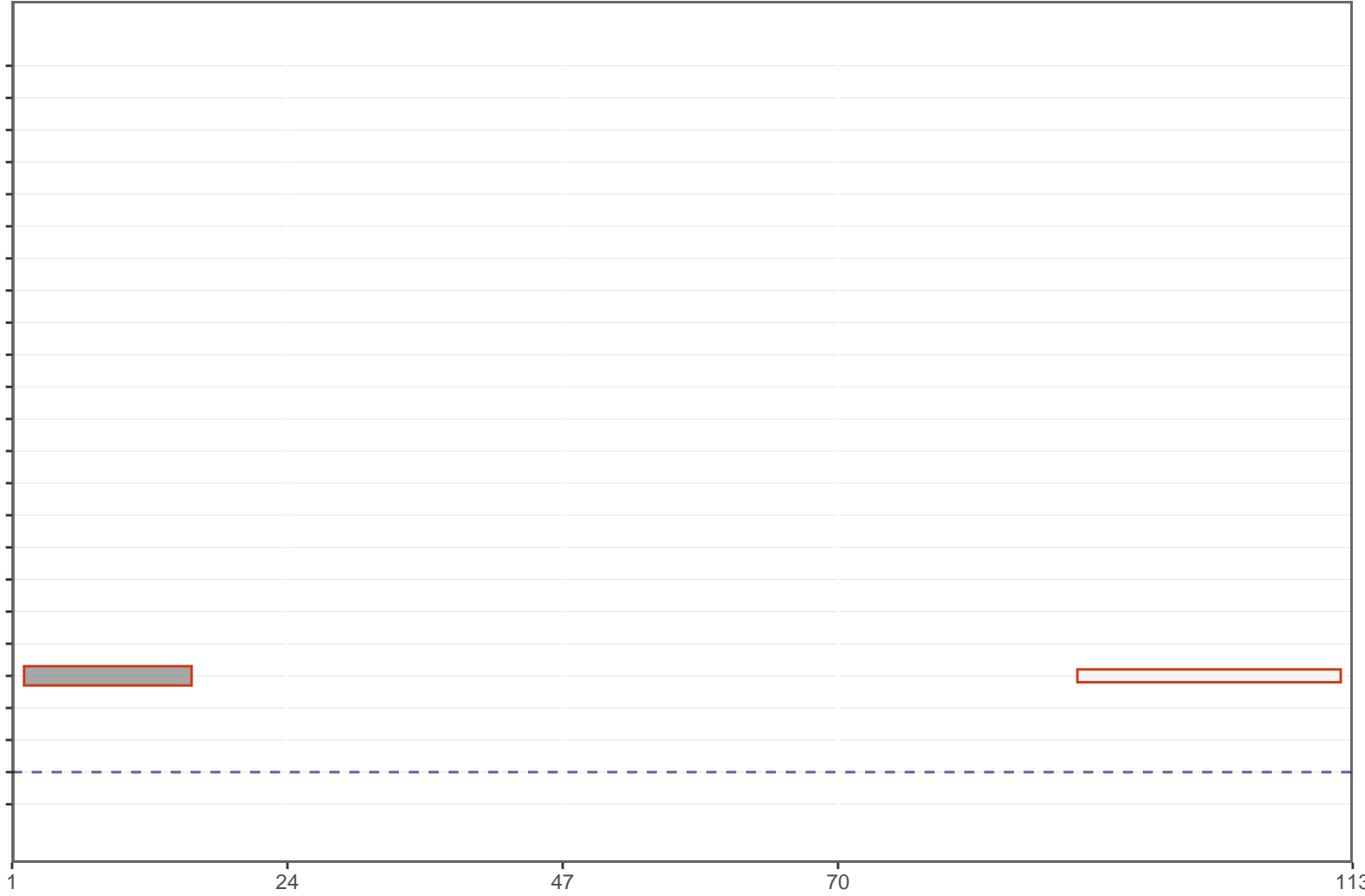
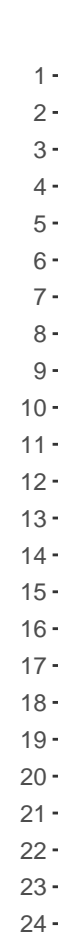
MW indication



Molecular weight

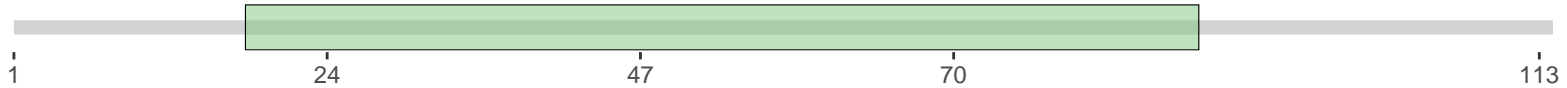


Gel Slice



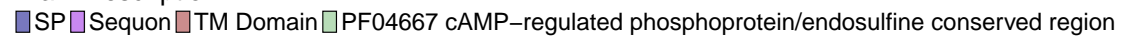
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

KDHERAYFDSADWALGKGGVAKPKGPLEALRPKLGPTNGQTRVYRKGSPYAPSEGEDGSNAPPEDPTANE

NbL16g09900.1 rhodanese-like_domain-containing_protein_4_chloroplastic [MW = 50.87 kDa]

No. of times detected



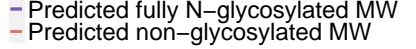
log(intensity)



Values from



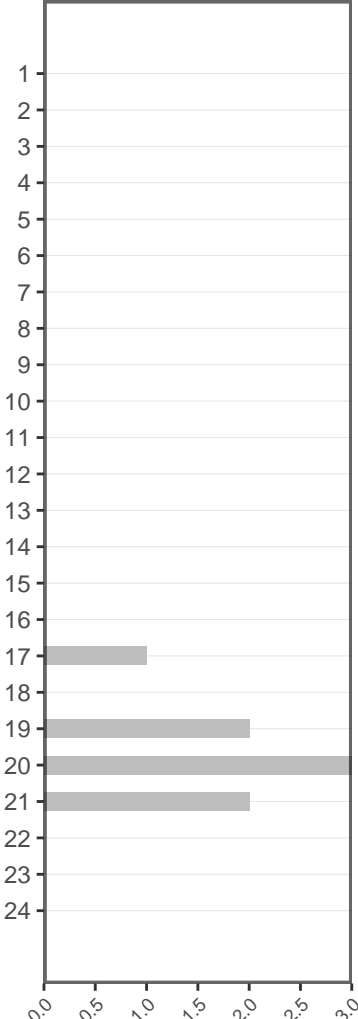
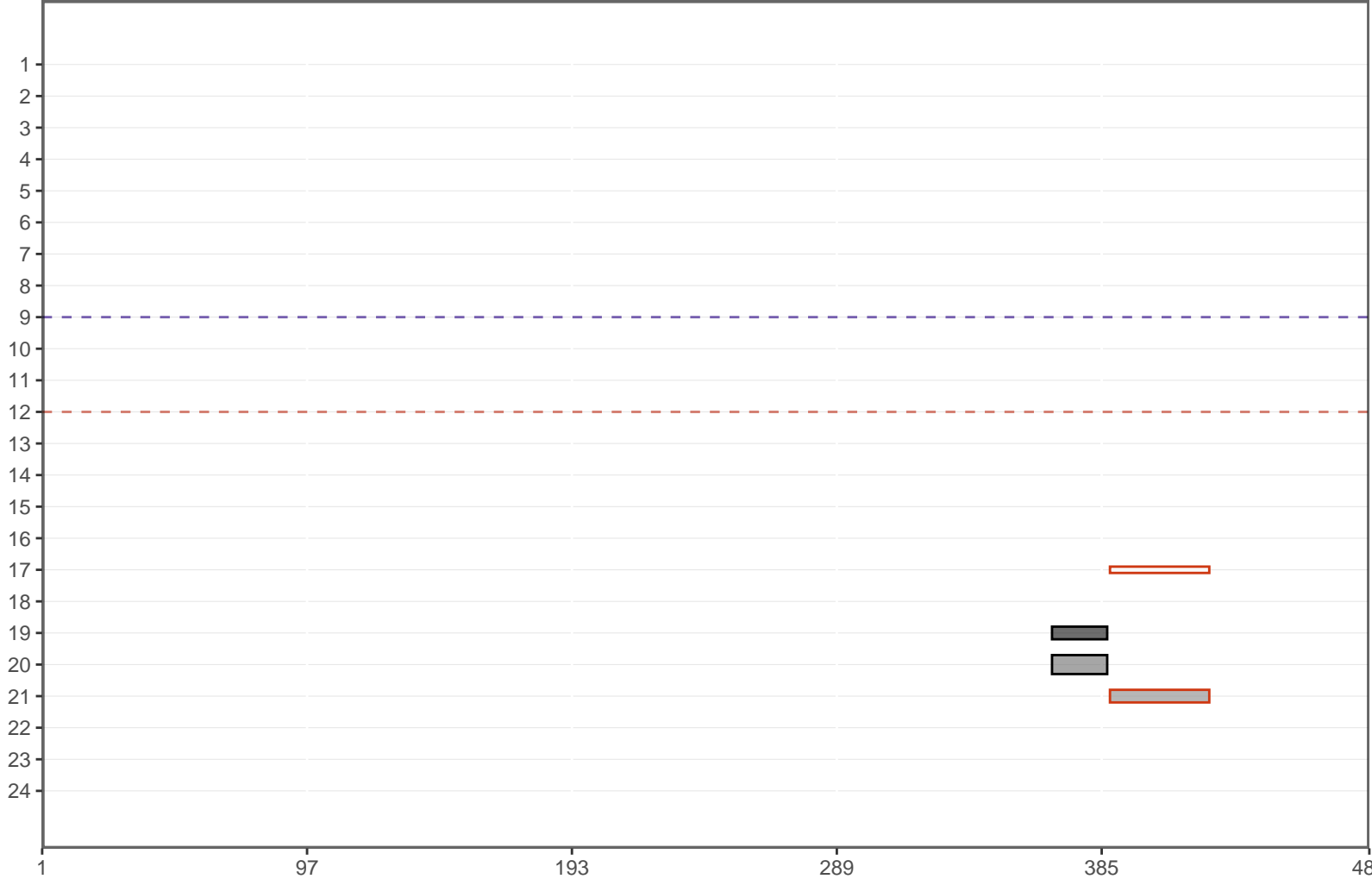
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

IGFKAAAYAKDGAEGPRGWKNSGLFWLPHKTKLRLDLGNLSDALDGVFVDDGSDMAVGLGVAATVLFGLVFEVETLGVLGSAALQQLVSTLKLFAEVRKTKLQGVDAFVFTTNAFKKELVGDQIKGMALLPTPVTSKSLPAAPAEETFEINSPKPKPEVKVEALTGISKPLSPYPSYDLKPKPTSPMPSQPSGSAEKTEAVSKVELSAESTFEINSPKLEVKAEALAGSSKELSPYPNYFDLKKPPTSPTPSGA

NbL16g09580.1 serine/threonine-protein_phosphatase_2A_65_kDa_regulatory_subunit_A_beta_isoform [MW = 65.57 kDa]

No. of times detected



log(intensity)



Values from



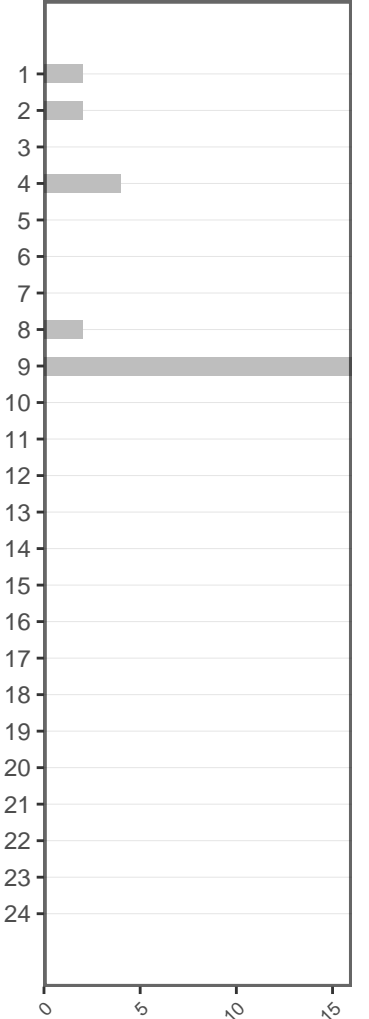
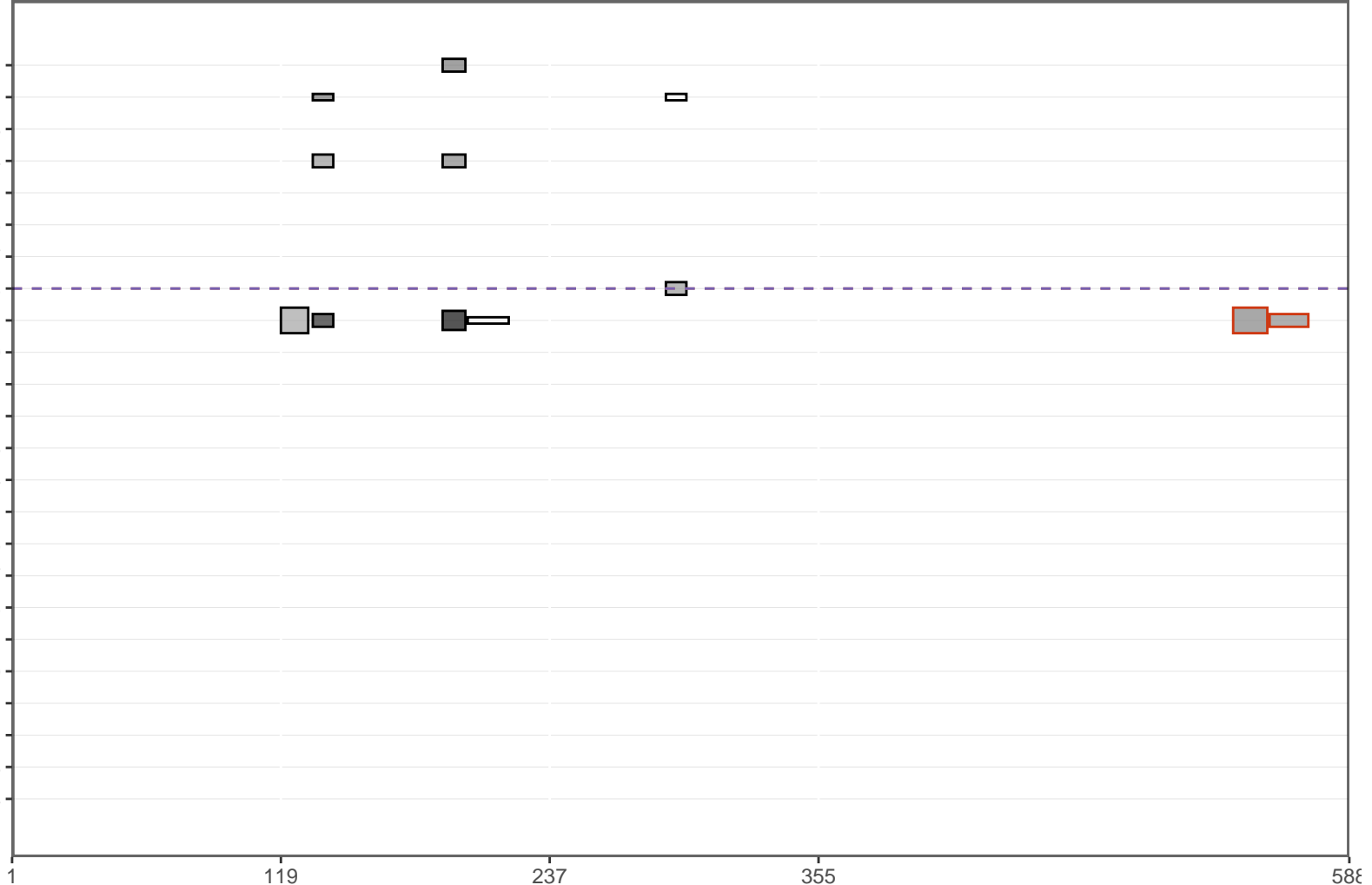
MW indication



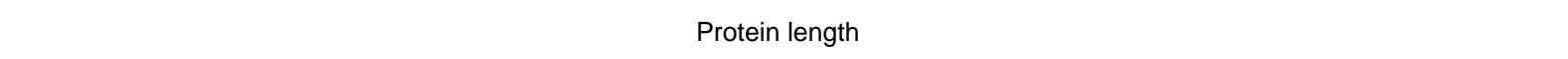
Molecular weight



Gel Slice



Protein length

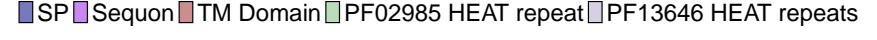


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

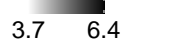
RTDLYPYVYRLLRGNAEVRIIAAGKVKTKFDRILSPRLAQHILPCVKELSSDSGQHYRSALASVIMGMAPVLGKDATEIHLPIFLSLLKDEFPDRLNHSKLDQVNGVIGIDLSSGSLFNIVELAEDRHWVRLIAIEYIPLASQLGIGFFDDKLGALCMQWLGDKVYSRDAANLNKRLAEFGPEVWAMQHIPQVLDMTTSPHYLYRMTLRAISLLAPVMSSEITGSKLLPVITATKDRVFNKFNWAKVLSLPIVDHSMVEKTRPSLVELAEPDNDVRFYANQALQSID

NbL16g09440.1 pyruvate_dehydrogenase_E1_component_subunit_alpha_mitochondrial [MW = 42.95 kDa]

No. of times detected



log(intensity)



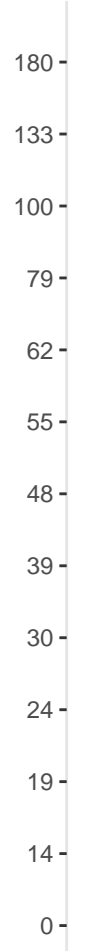
Values from



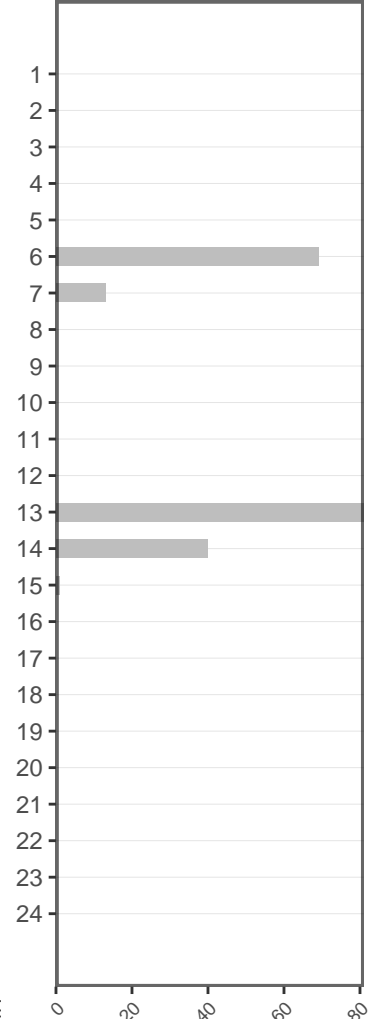
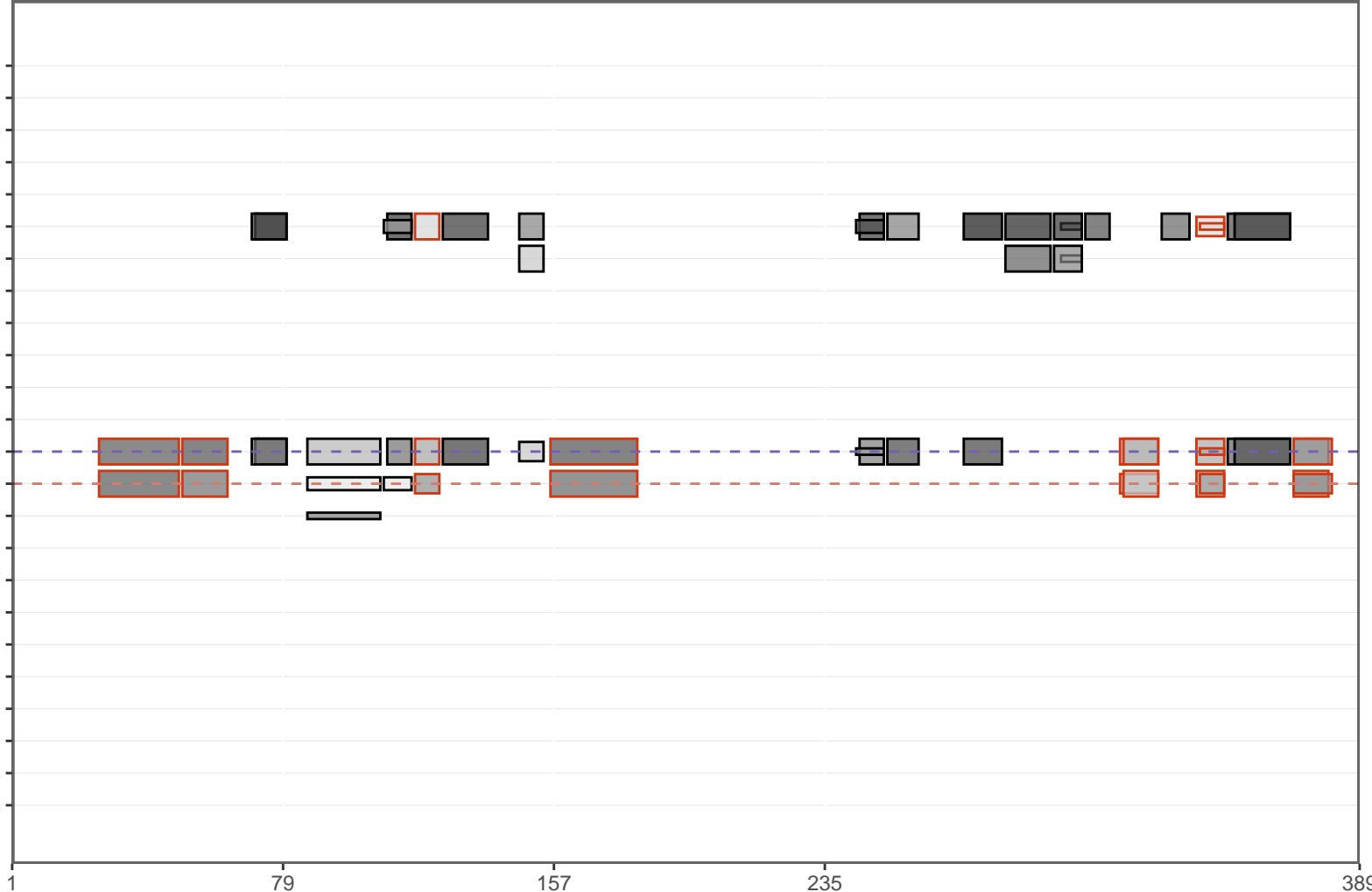
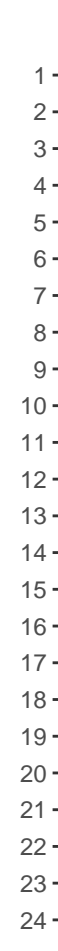
MW indication



Molecular weight

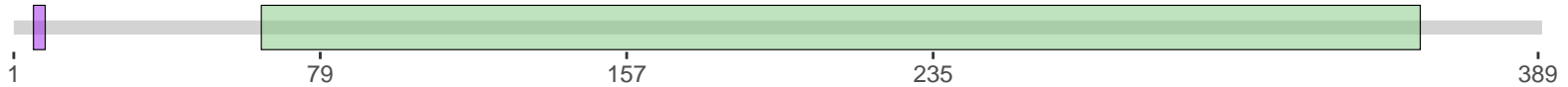


Gel Slice



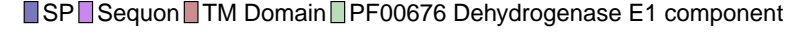
Protein length

Peptide counts over 4 repeats



Pfam domains

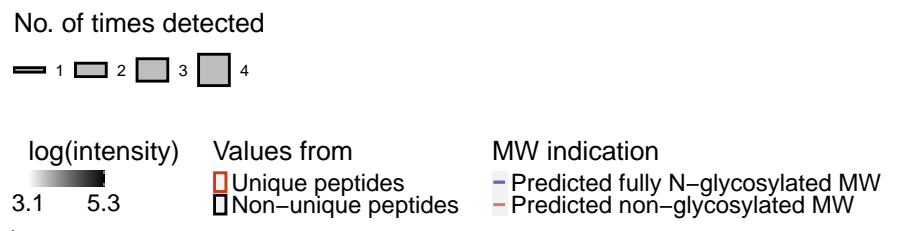
Pfam Description



Protein sequence:

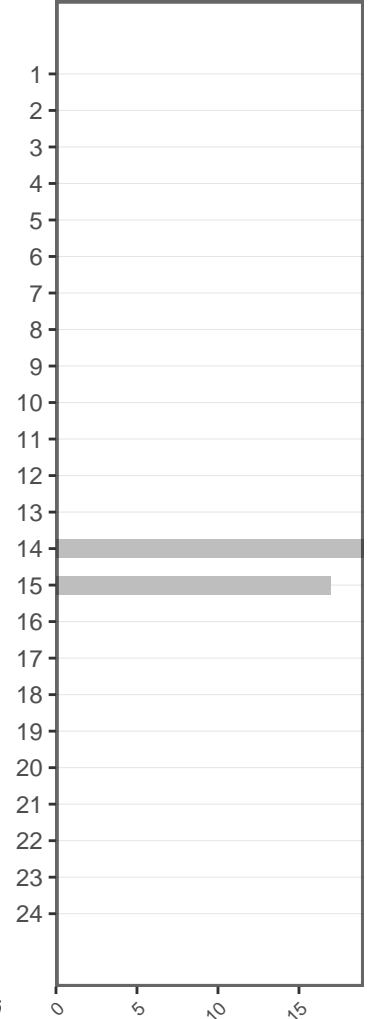
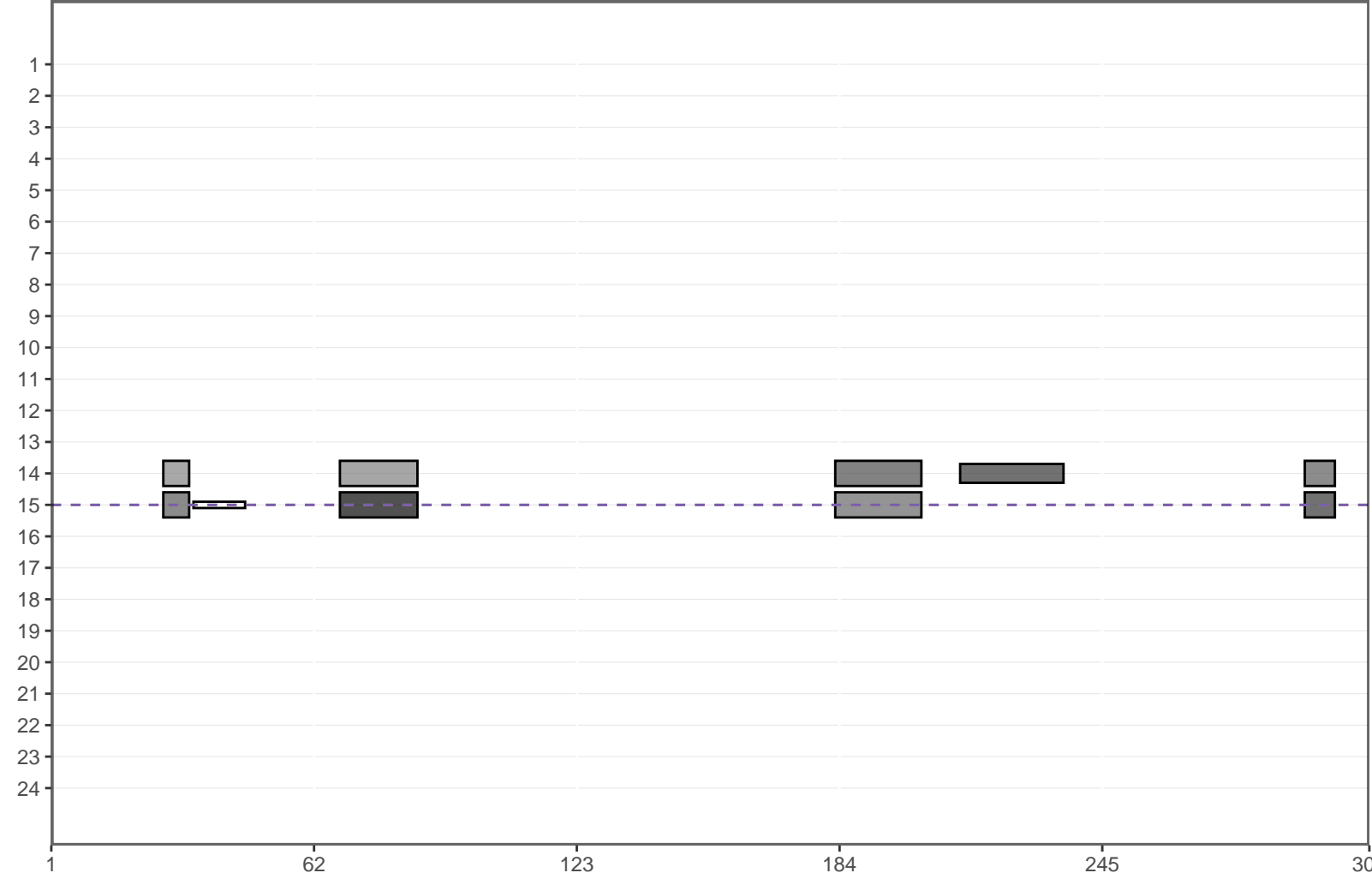
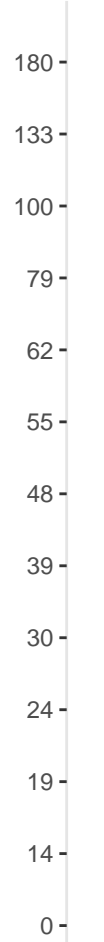
SKEEHVTAMYGDSAAANGOLFEEALNMAALWDLFALVGENNHYGMGTAEWRAAKSPWYKRGDVFGLKVDGMDALAVKQACKFKHEHALKNGPILEMMDTVRYRHGHSMSPGCTGYRTRDEISGVQRGERDPIERIRKLVLAHDIAEKELKDIEKERKVVDEAAKAKESPMFDPPELFTNYYWGFQVESFGADRKEVRTALP

NbL16g09420.1 serine/threonine-protein_phosphatase_PP2A-2_catalytic_subunit-like [MW = 35 kDa]



Molecular weight

Gel Slice

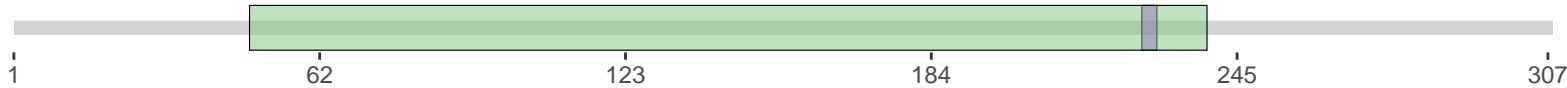


Protein length

Peptide counts over 4 repeats



Pfam domains



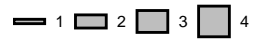
Pfam Description
 SP Sequon TM Domain PF00149 Calcineurin-like phosphoesterase

Protein sequence:

KYVTDLFDYLPILTAIEGQIFGLHGGSPLEDTLDIRSLDRIGVEPHGPMGDLIWSQDPRGGWGISFRGAGYTFGGDASGFNFTNGLTISRRAHQMLMEGFNWDGDKNVTTFSEAPNYGVRGGNMAAILEIGENMEQNFLOGDPAAPRQIEPDTTRKTPQVFLV

NbL16g09180.1 26S_proteasome_non-ATPase_regulatory_subunit_11_homolog [MW = 47.13 kDa]

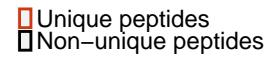
No. of times detected



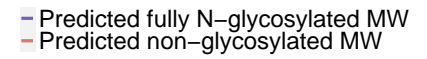
log(intensity)



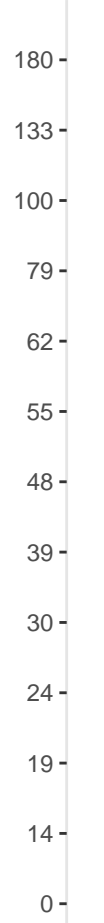
Values from



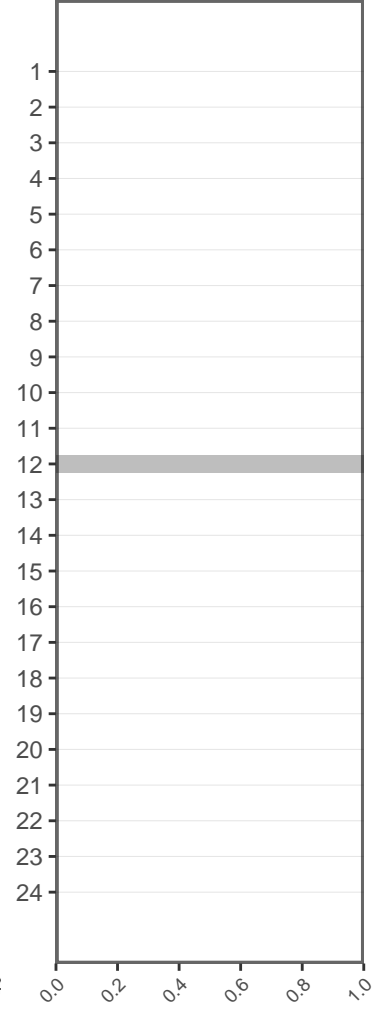
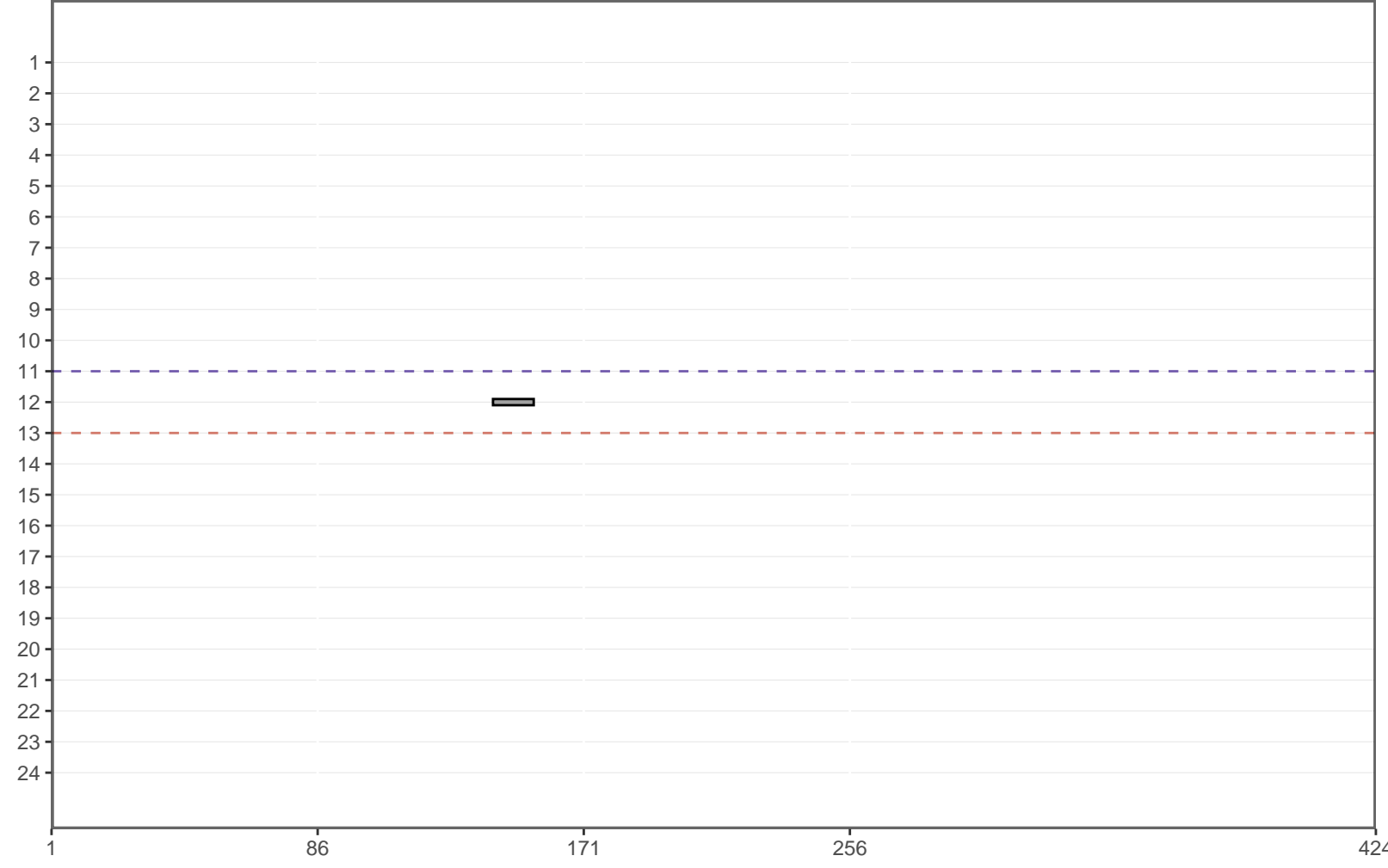
MW indication



Molecular weight

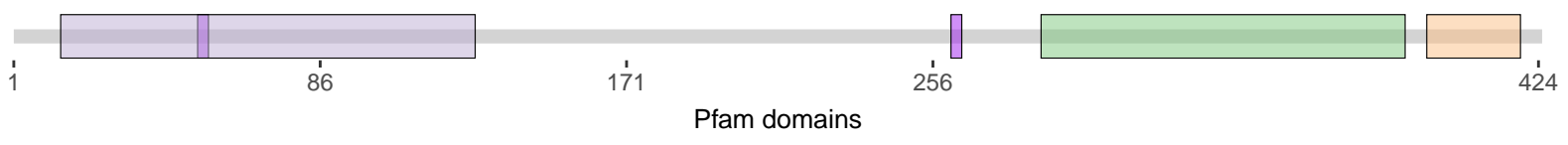


Gel Slice



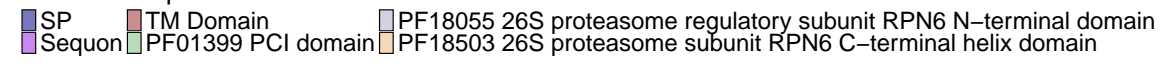
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

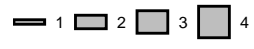


Protein sequence:

VPRVQGGSDLDLQSGILHAEKNDKTKGVSYEYEAFAFNALDEPQAYSLKYMLLCKIMVNGSDQVAGITSSPKVGLGVGGPEVDAMKAVADHSHKRSKLFETALRNFKAGLDEDPVHRHLLSSLYDTLLEQNLRLIEPFRVIEIAHMAELIELPGDHVEKLLGMLLKKFKAGTLDQDAGGLIFEDPKPDAIVPATEVSNMGKVVDSLFRSSRIIA*

NbL16g09160.1 eukaryotic_translation_initiation_factor_5A-2-like [MW = 17.35 kDa]

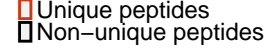
No. of times detected



log(intensity)



Values from



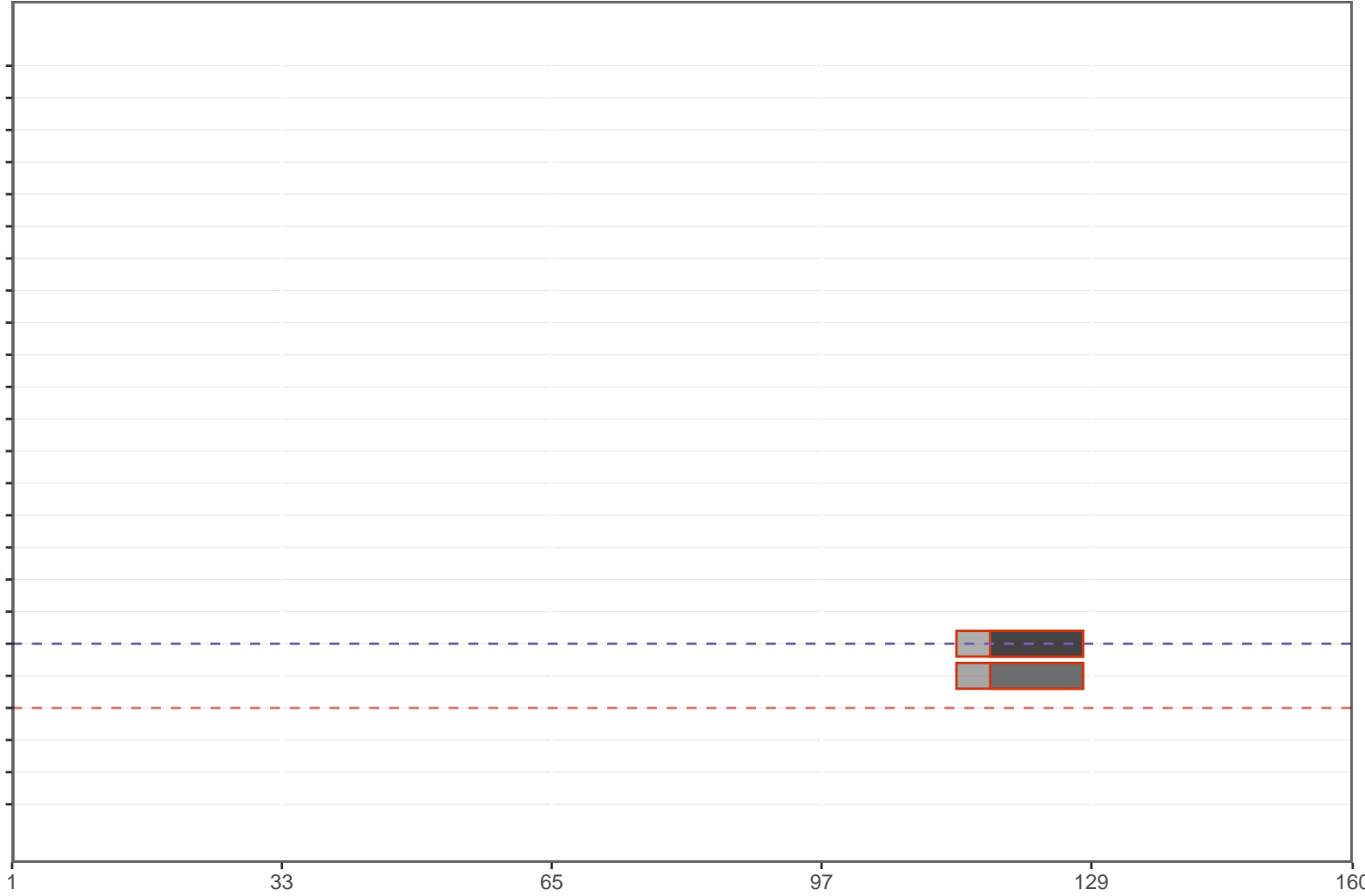
MW indication



Molecular weight



Gel Slice



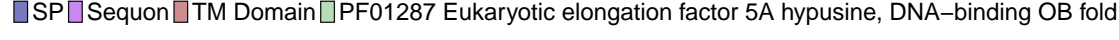
Protein length



Pfam domains



Pfam Description



Protein sequence:

TGKKLEIVPSSINIGDGFYVNRFDYGLIDHSEDGFRVSLTENGSTKDDLRPLPTDENLLTQKDGFAEGKDIYVVMAMGDEEGICALKDQPKK

NbL16g09020.1 alpha-14-glucan-protein_synthase_[UDP-forming]_2 [MW = 41.36 kDa]

No. of times detected



log(intensity)



Values from



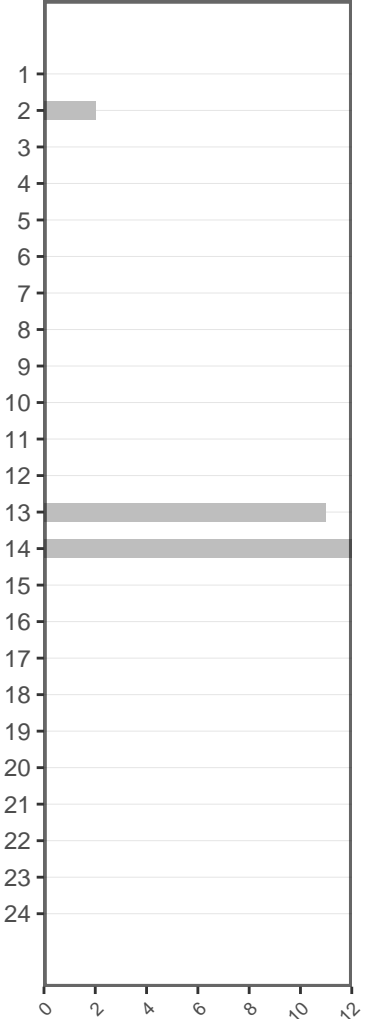
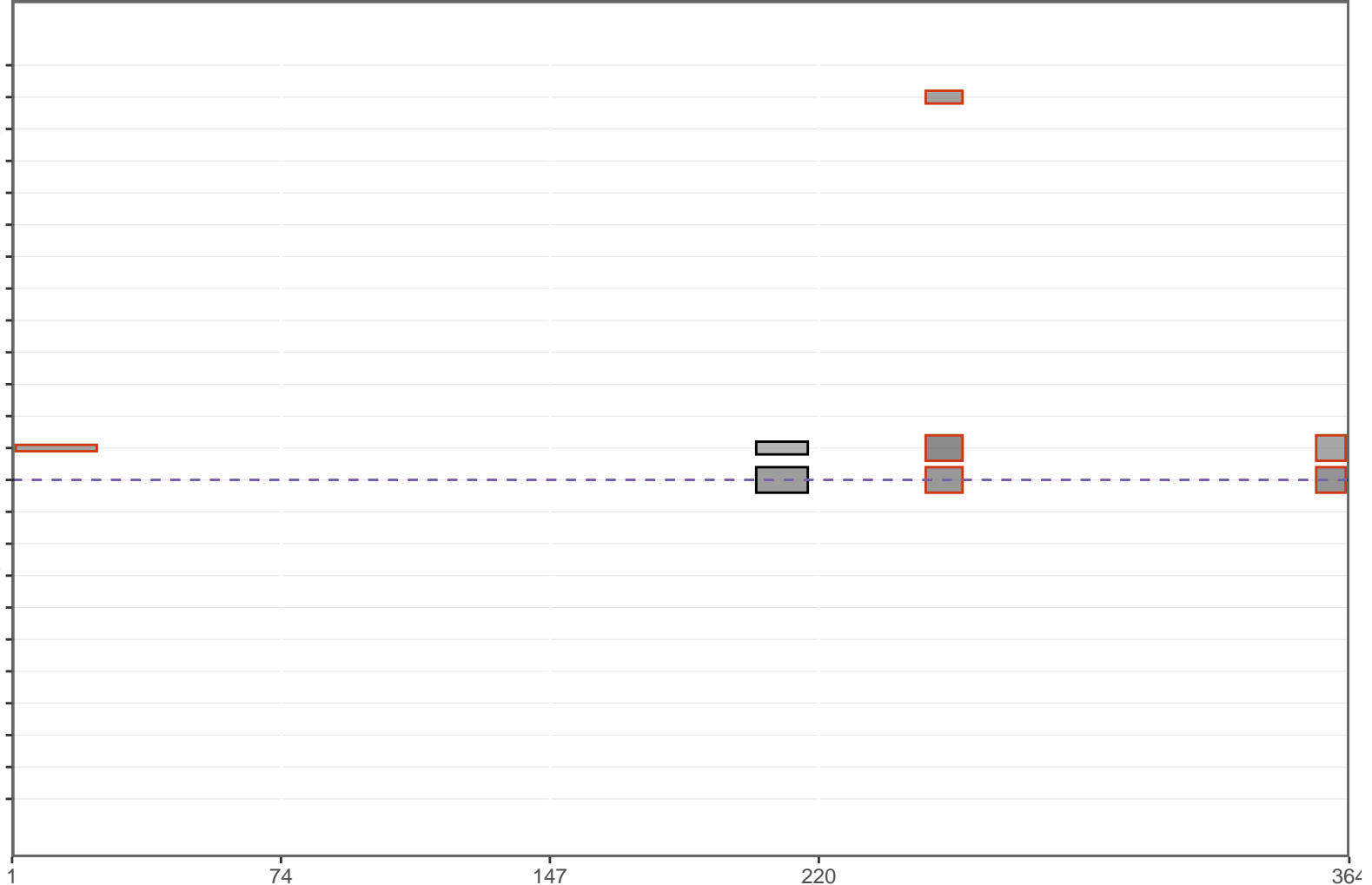
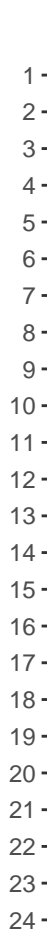
MW indication



Molecular weight

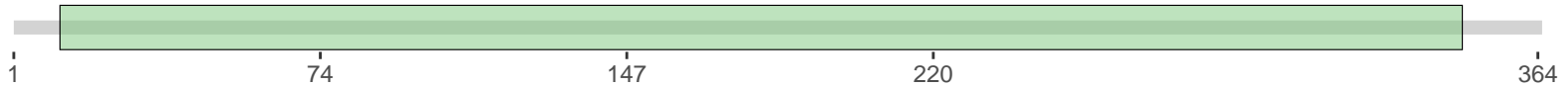


Gel Slice



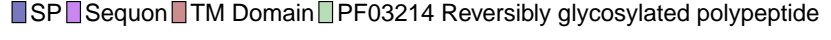
Protein length

Peptide counts over 4 repeats



Pfam domains

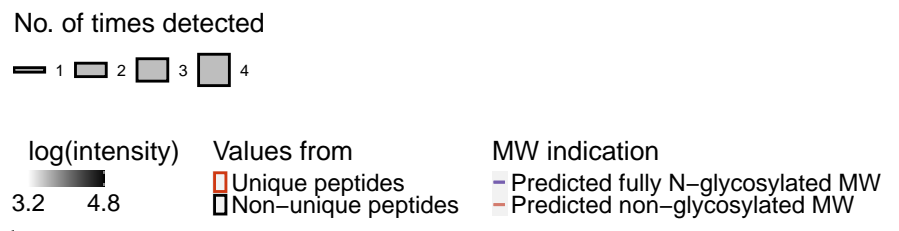
Pfam Description



Protein sequence:

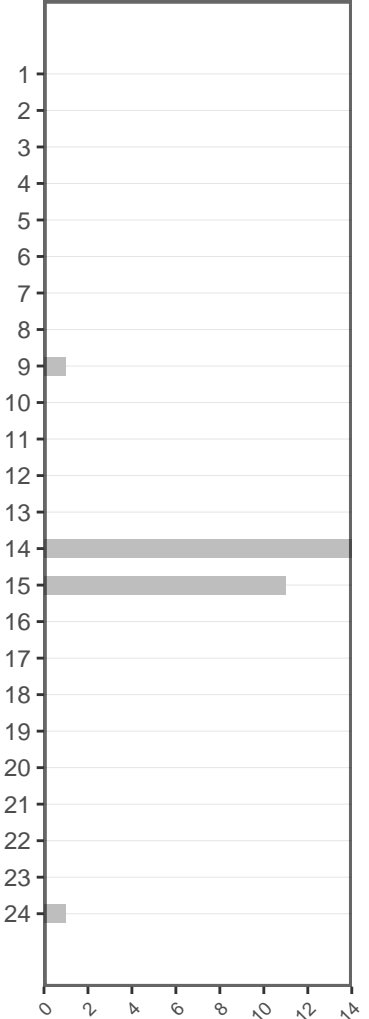
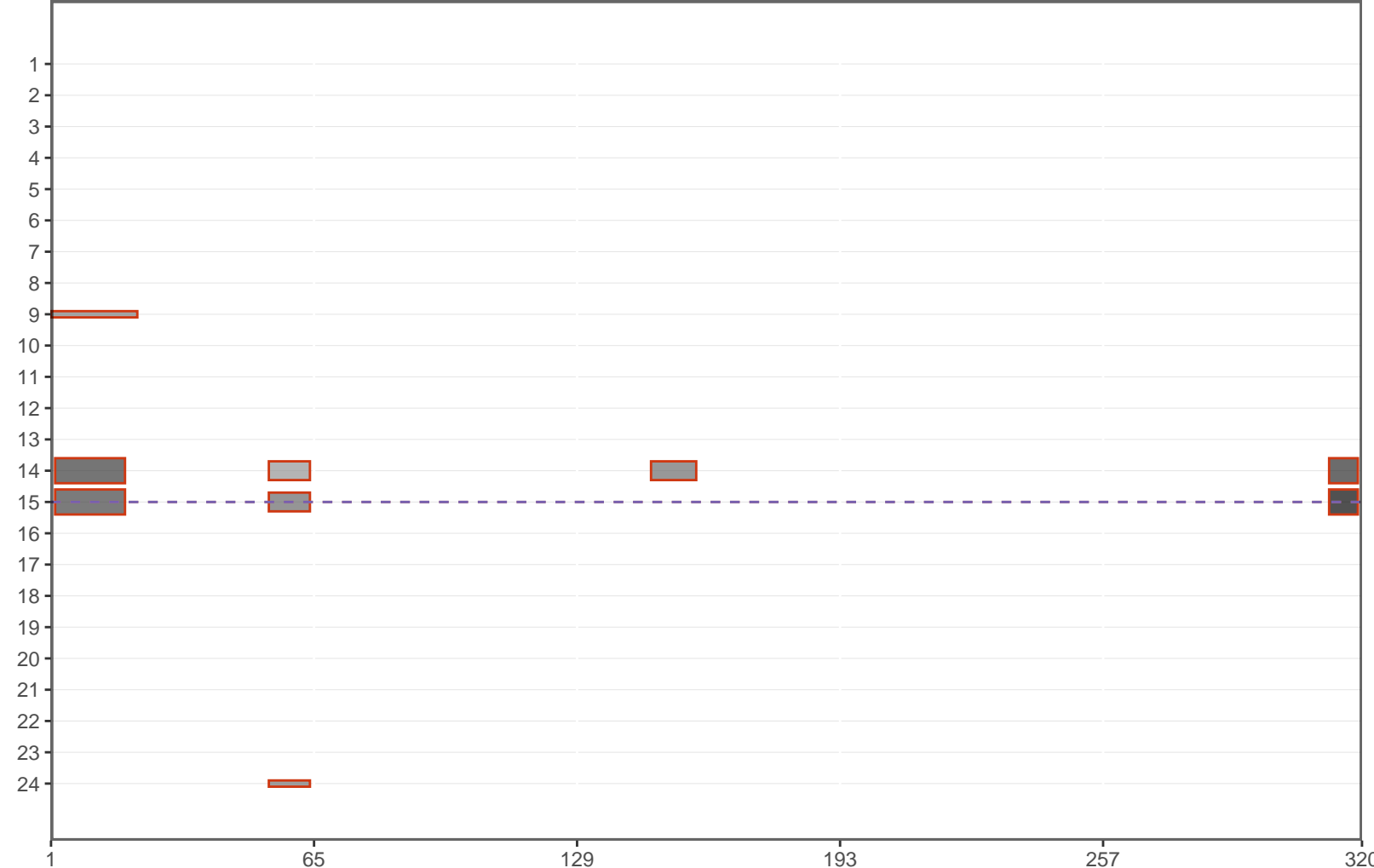
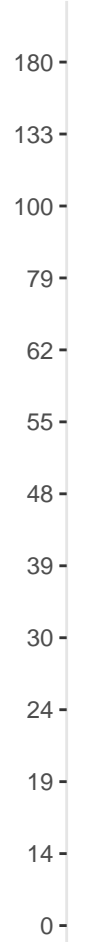
VLNIPDYDPTQLVNPBRNTRYVDAMITPKGTLFPMAGMNLAFNRELIGPMMYFGLMSGGPIGRYDDMAGWCTKIVGDHLMGKIKTGLPIYVHSGKASNPVNLKKEYKGIYWGEEIPFFGSAFLPKDCTEVGGCYIELSKGVKDKLKVDPYFTKLADAMVTEAWDELNPTGEGLANLSGNVYK

NbL16g08920.1 2-hydroxyisoflavanone_dehydratase-like [MW = 35.75 kDa]



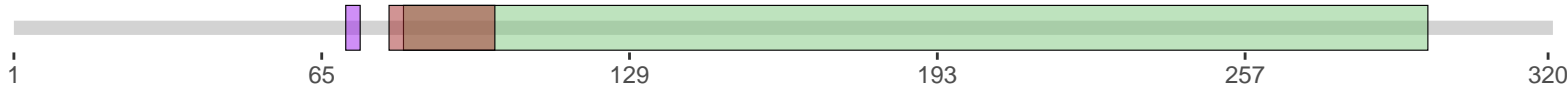
Molecular weight

Gel Slice

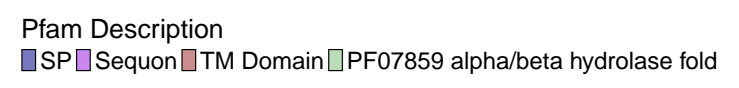


Protein length

Peptide counts over 4 repeats



Pfam domains

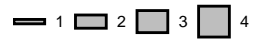


Protein sequence:

LVLTNYGDFNKFVSGEGGANIVFVVRAGREKLNQGVNIGGSLACPGFLFPHENVDVKLDMAYKLLTIVGPKWIEFLDGPMINPLCKMAPSLGSLGGSKLFLVGLAEKDEWVDFGEMELQFVEGVKSGWNGEFVFFVVEGEGHSFFILDPETEKARDLKRFRANFIQWV

NbL16g08900.1 protein_PHYLLO_chloroplastic [MW = 150.95 kDa]

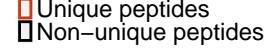
No. of times detected



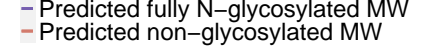
log(intensity)



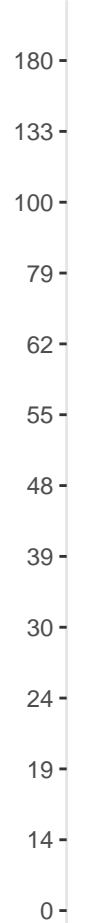
Values from



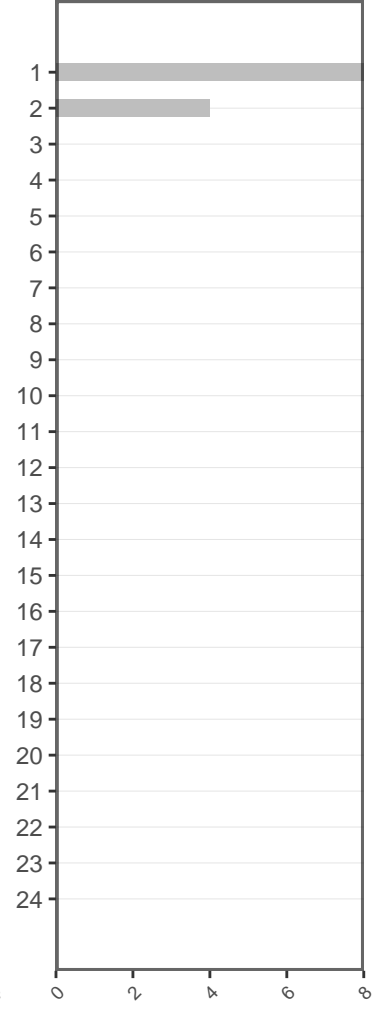
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Domain Description

- PF02776 Thiamine pyrophosphate enzyme, N-terminal TPP binding domain
- PF12697 Alpha/beta hydrolase family
- PF13378 Enolase C-terminal domain-like
- PF16582 Middle domain of thiamine pyrophosphate
- PF02775 Thiamine pyrophosphate enzyme, C-terminal TPP binding domain
- TM Domain

Protein sequence:

RIQLSSPTSSSATHISTYQREGFISLFLEDGNTGVGEVAPLEIKENLLENVEEQLGFLMHVYVEGVYDHFLLKLGDFRVLWQSLGQIPNSIFPVRFGLEMLNVAIAAAREGSLNLVYGGQTVESGGSLGVKVCALLEENGGPYEMALLATLWKEGFTAKLKVARGADPTVDAIKERIKKVGWEIELRADANRISWNYDEAVKFGSLGVKDSGLQVHEEPVNDDEDDIKFCGEETGLEVALDETINSIRKHLKVLAKYTHPMVAEYVKKPQVGVGFENALLARVAHQGGK

NbL16g08880.1 6-phosphogluconate_dehydrogenase_decarboxylating_1 [MW = 53.31 kDa]

No. of times detected



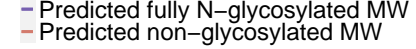
log(intensity)



Values from

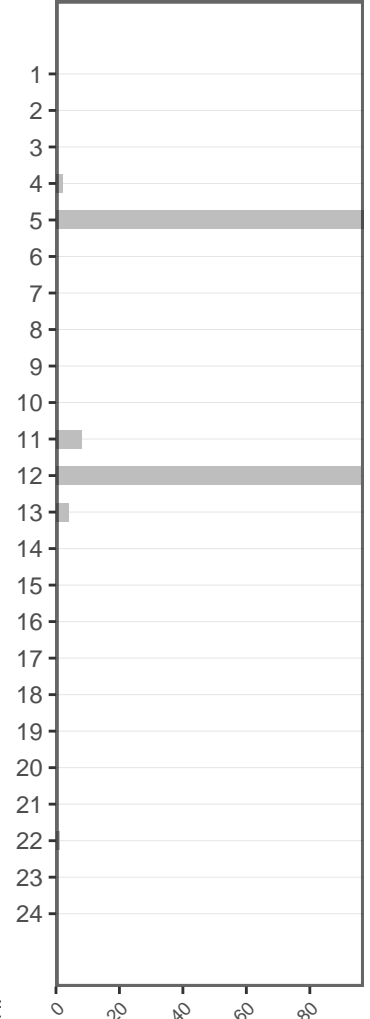
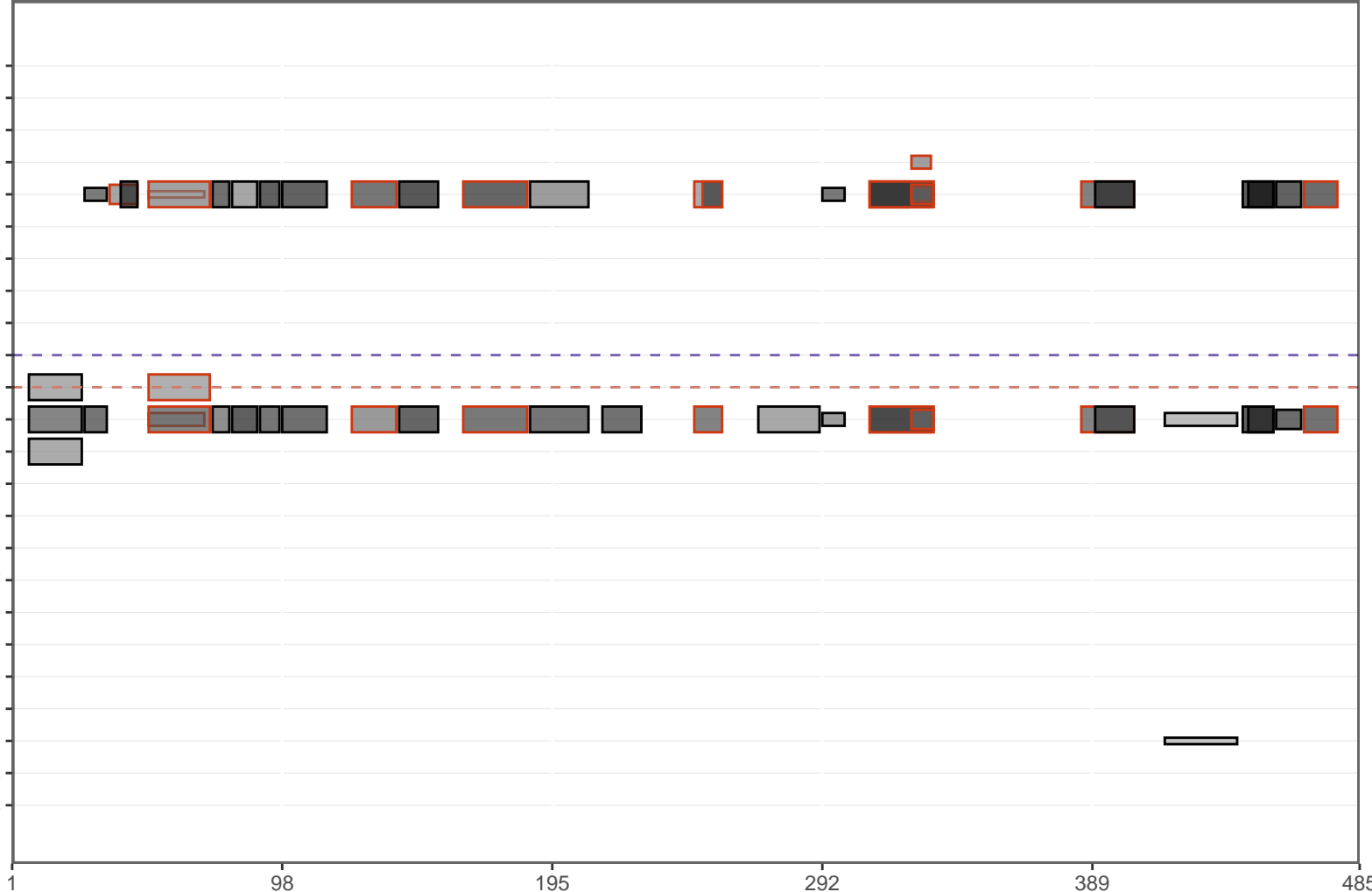


MW indication



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

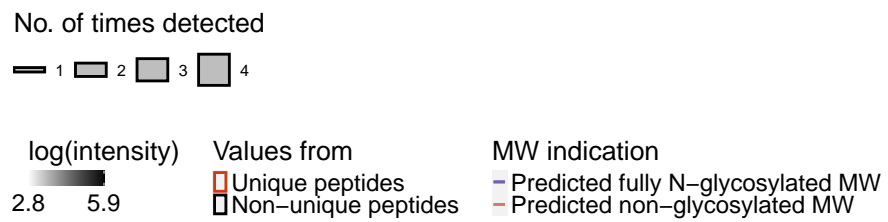
Pfam Description

- SP Sequon
- TM Domain
- PF00393 6-phosphogluconate dehydrogenase, C-terminal domain
- PF03446 NAD binding domain of 6-phosphogluconate dehydrogenase

Protein sequence:

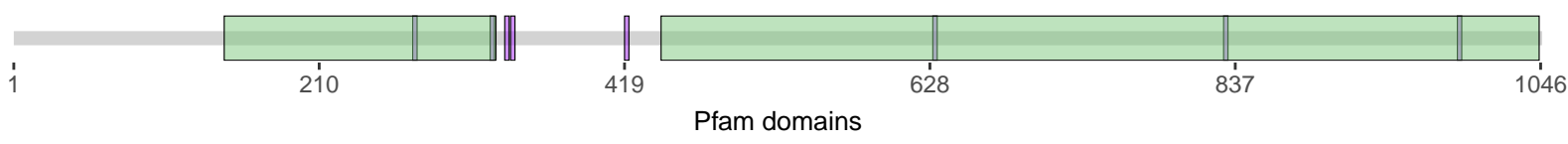
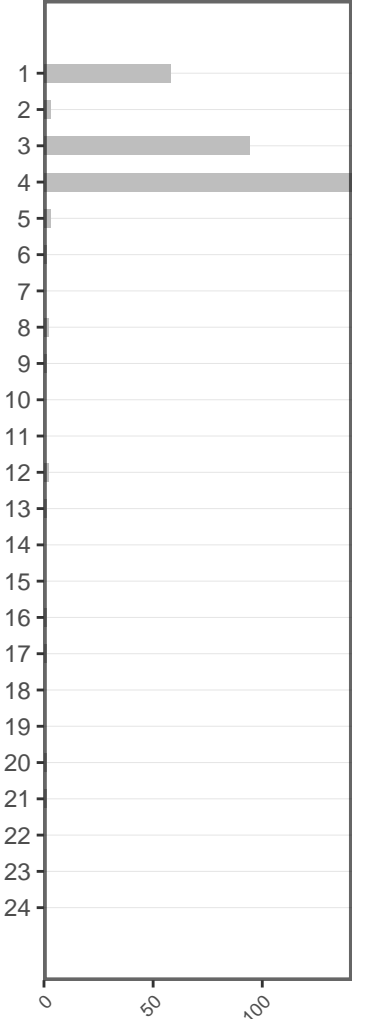
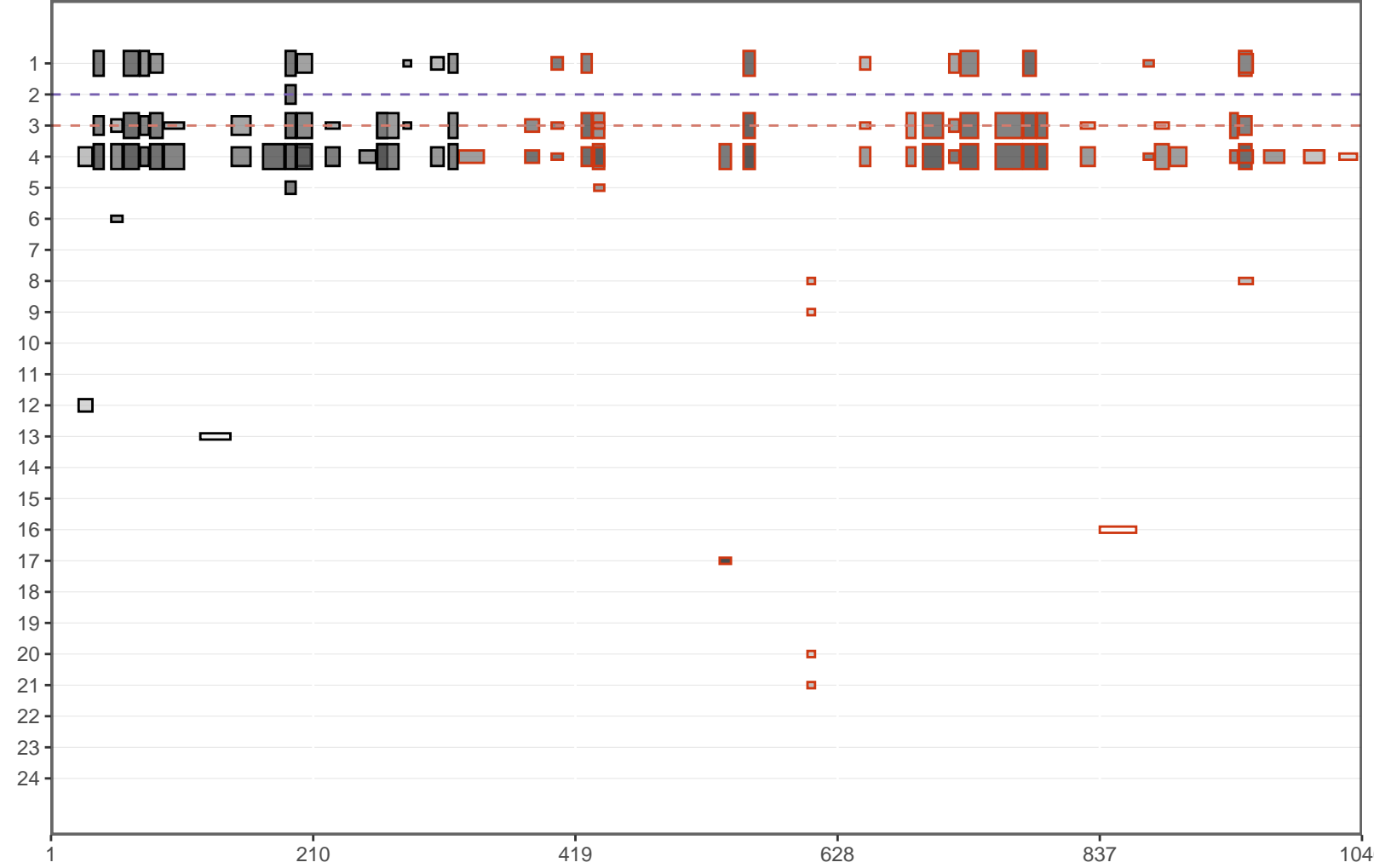
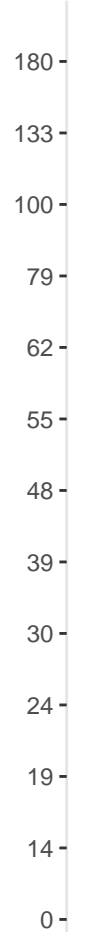
IELLSFLIETADIFGKDDKGGDGLVQKVLDKTKMGTKGKWTVQGAALSLVAPTIASGLDSRFLSGLKDERVGAAYFKASGVSDLVQGSVDKNGLIDVIRKALYASKGCVAGGMNLRKAKSEKGVGDKLGLGARVWGGGRRIFLDRIKGAYDRNPDLANLLVDEEFKEMVERGSAWRRVGLAINGISTPDMSSSLAYFDVYRRERLPAFLVQAGRDYFGAHTYERTDVGSGVHTEWFKIARGKIN

NbL16g08690.1 phosphoenolpyruvate_carboxylase_4 [MW = 117.38 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF00311 Phosphoenolpyruvate carboxylase

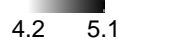
Protein sequence:
 CYDSLSCGSGVLDAGRLADLRIRRWTFGMVLMKLDLRGEGSRHSEALDTRKYLDMGTYSSEWDEEQKLDLKEKKGKRPVFPPTIEVPPDKVEVLDTRKVAELGSDSLGAYVISMNASDVALELLKQKRLAAGELGRPCPGGTLRVLVPLFETVKDLREAGSVIRLLSGDWYREHKKHHDGHGEVMMGYSDSGKDGRTVAWELLYKAGEDVVAADNEYGRVTLFHGRGGSGRGGGPTVLAQGGPPGSGVMGTLRSTFDGEMVQAKKGLPOMAVRQLEYI

NbL16g08610.1 ubiquitin_receptor_RAD23c-like [MW = 41.22 kDa]

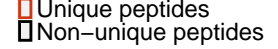
No. of times detected



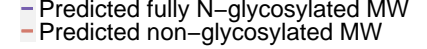
log(intensity)



Values from



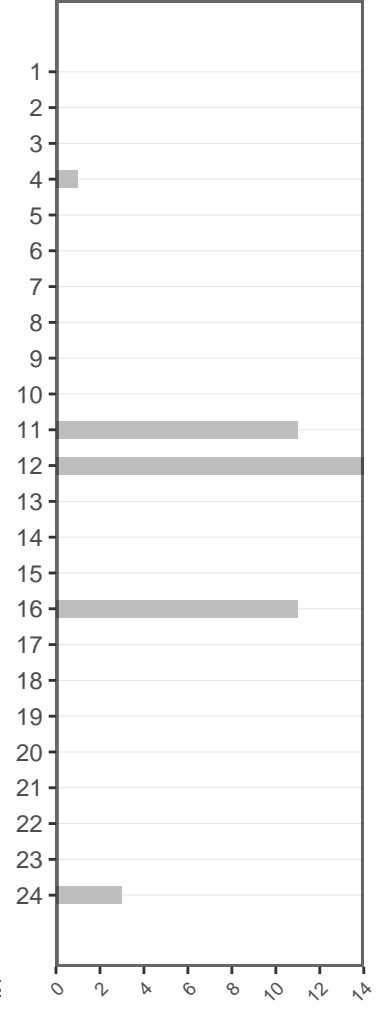
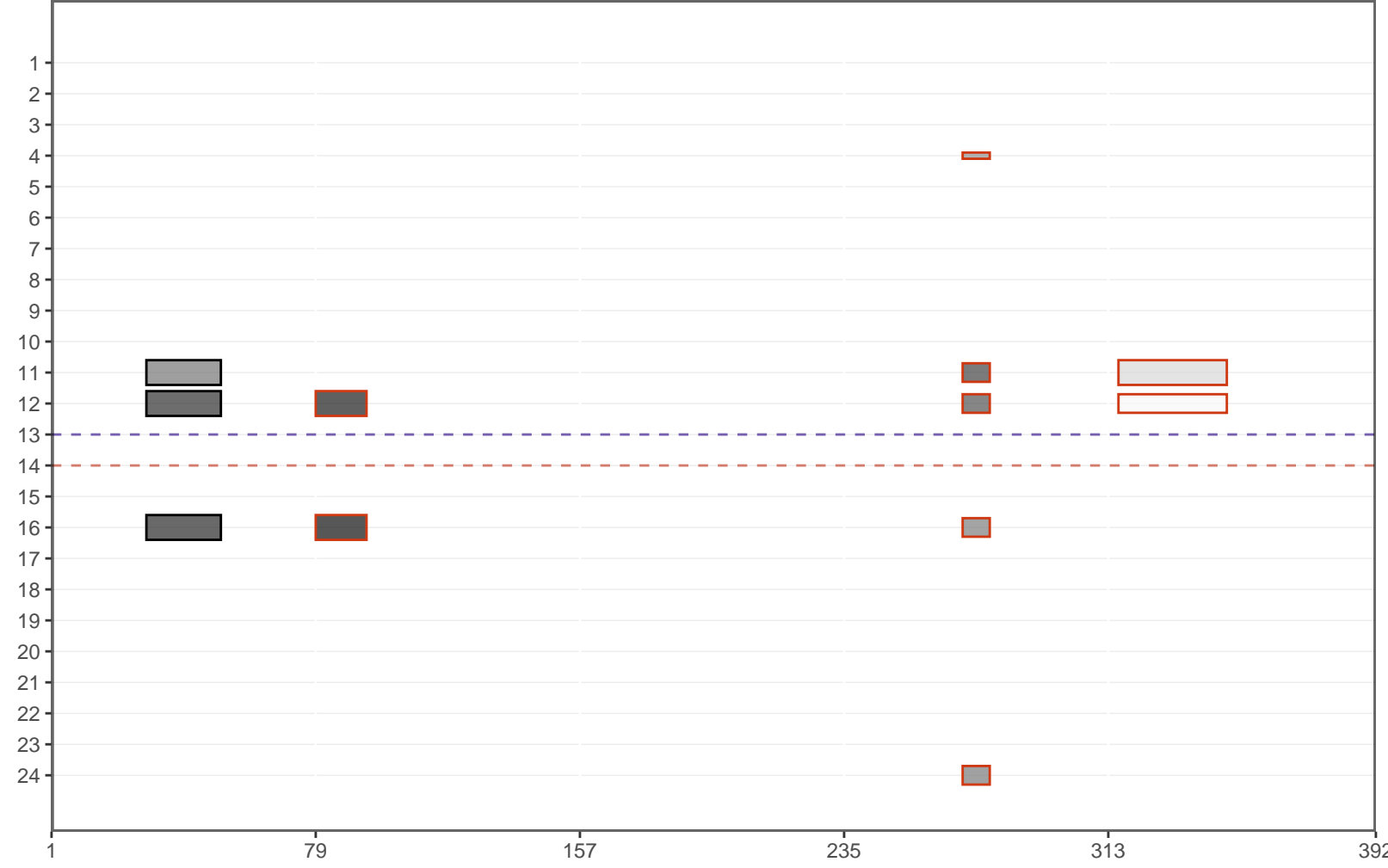
MW indication



Molecular weight

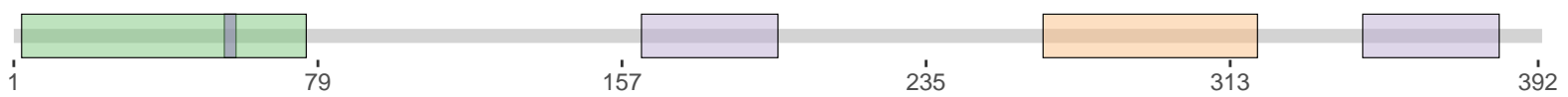


Gel Slice



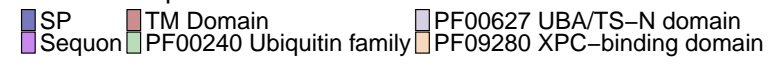
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AAFNPERAVEYLGGIPETAEVPPVGGGSPSAGAGNGRQPLMAGRPVPPAGGPNADPLNLFPOGLPSLGGNTGGANTLDFLRNNGQGFALRAMVQANPOLQPMELGKGNQPLMRLQEHQADFLRLINEPVEGGGEGNLGGAAAMPQAGVTPREERAEIERLEQMGFDHDLVLEVFACNKNNEELAAANYLIDHMHEFEE*

NbL16g08600.1 alpha-xylosidase_1-like [MW - SP = 101.62 kDa]

No. of times detected



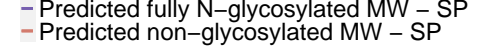
log(intensity)



Values from



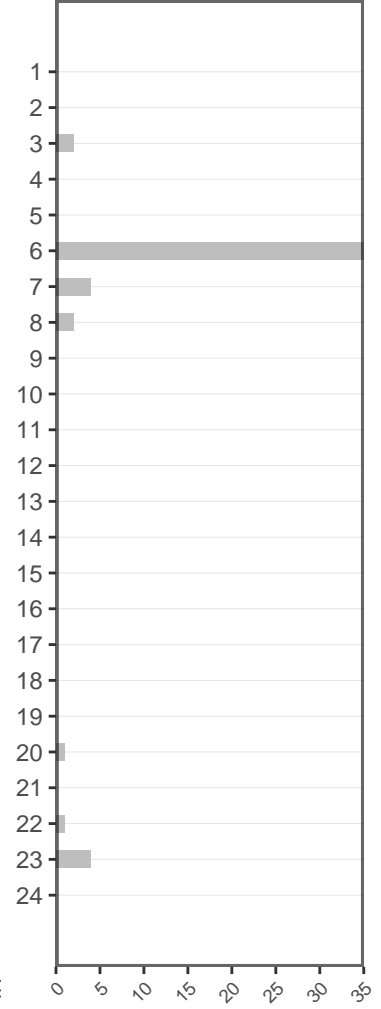
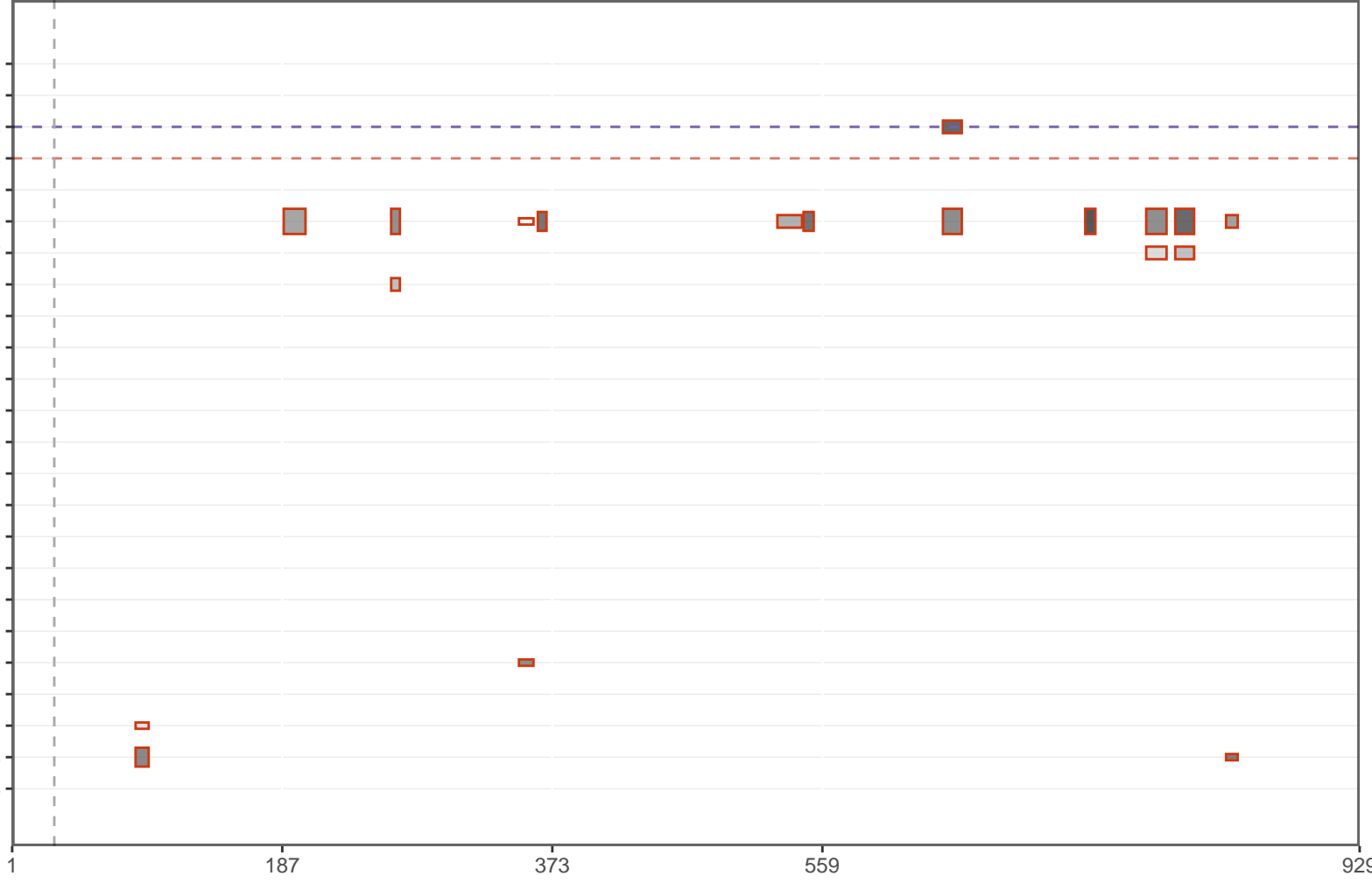
MW indication



Molecular weight

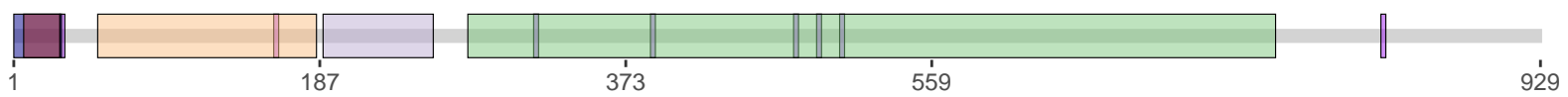


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MNEVSNFCSSGLCTFENRIGPNGTGPGWIGLGDKNITNTRKWDPPYKINAGIGAPGKYKTSAAVHYNGVREYDAHSYGFDSQSIATHKALQGLGKRPFLSRSTFVGGSHYAAHWITGDKNATWDDLRLYRISGTMNFGLFQVPMVGGDGGYKPAFTEELNRRWIEVGAFYFSSRDHANYSRQGLGQWESGVAESARNALGMRVYKLLPFYTLNVEAHTTGAPAPLFFSFFNLPLQYDVTGQLGSGSVAASPVLDGKTEVKALFPPGTWYDFDMTRAVITPEP

NbL16g08500.1 acyl-acyl_carrier_protein_thioesterase_ATL3_chloroplastic-like [MW = 24.14 kDa]

No. of times detected



log(intensity)



Values from



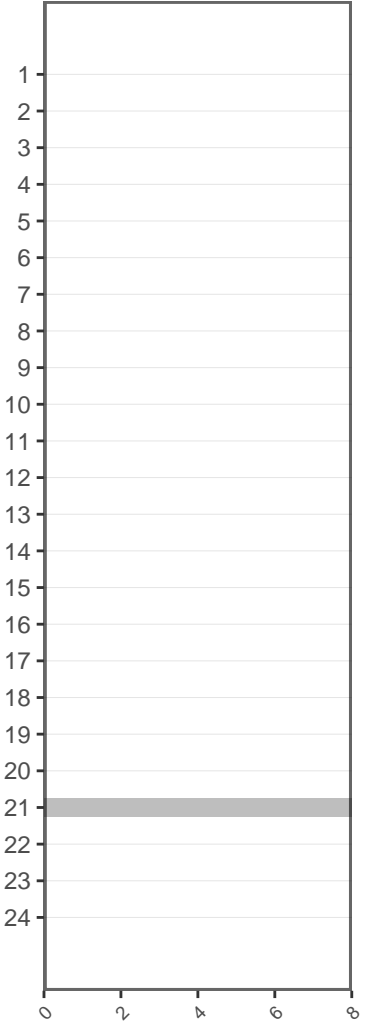
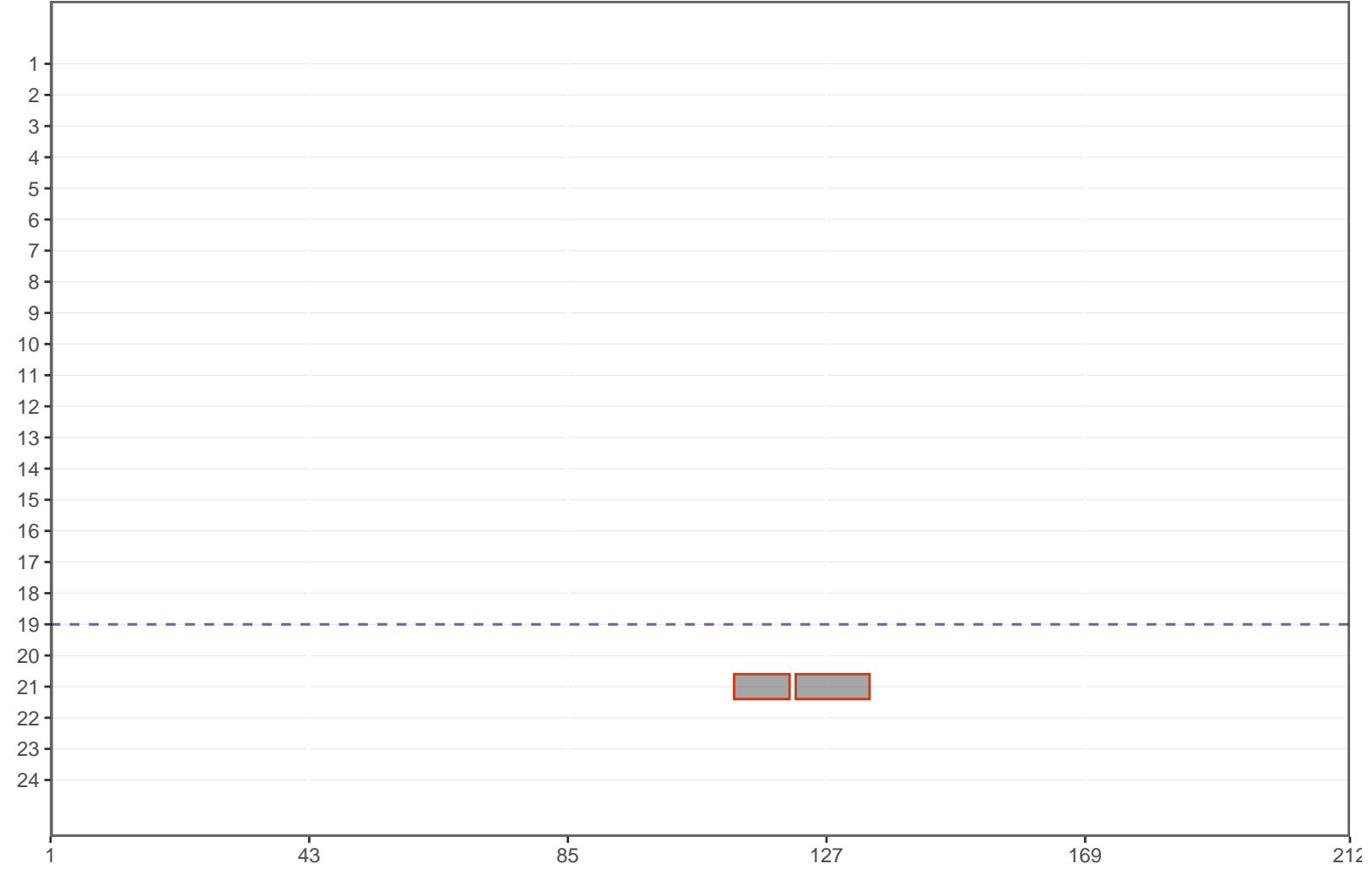
MW indication



Molecular weight



Gel Slice

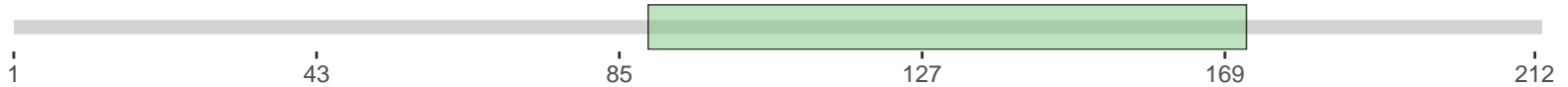


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

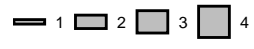


Protein sequence:

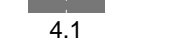
INNAIYASYCICRHELLERLGISADTVARDGDALATELSKYLAPLRSGDRFVYKVRISDSSVRLFFEHFIFKLPDGEPLAETGTAWLNKMYRFRIPRSEFRSKYVQFLRGEASK

NbL16g08230.1 DNA-directed_RNA_polymerases_II_IV_and_V_subunit_10-like [MW = 11.84 kDa]

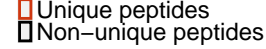
No. of times detected



log(intensity)



Values from



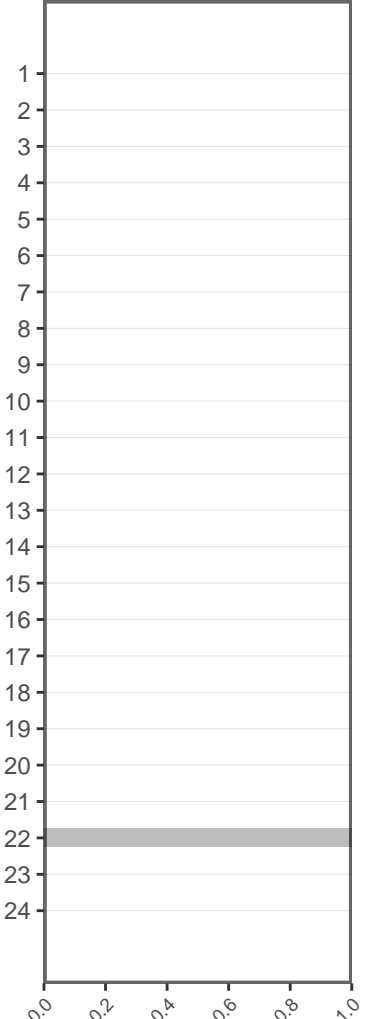
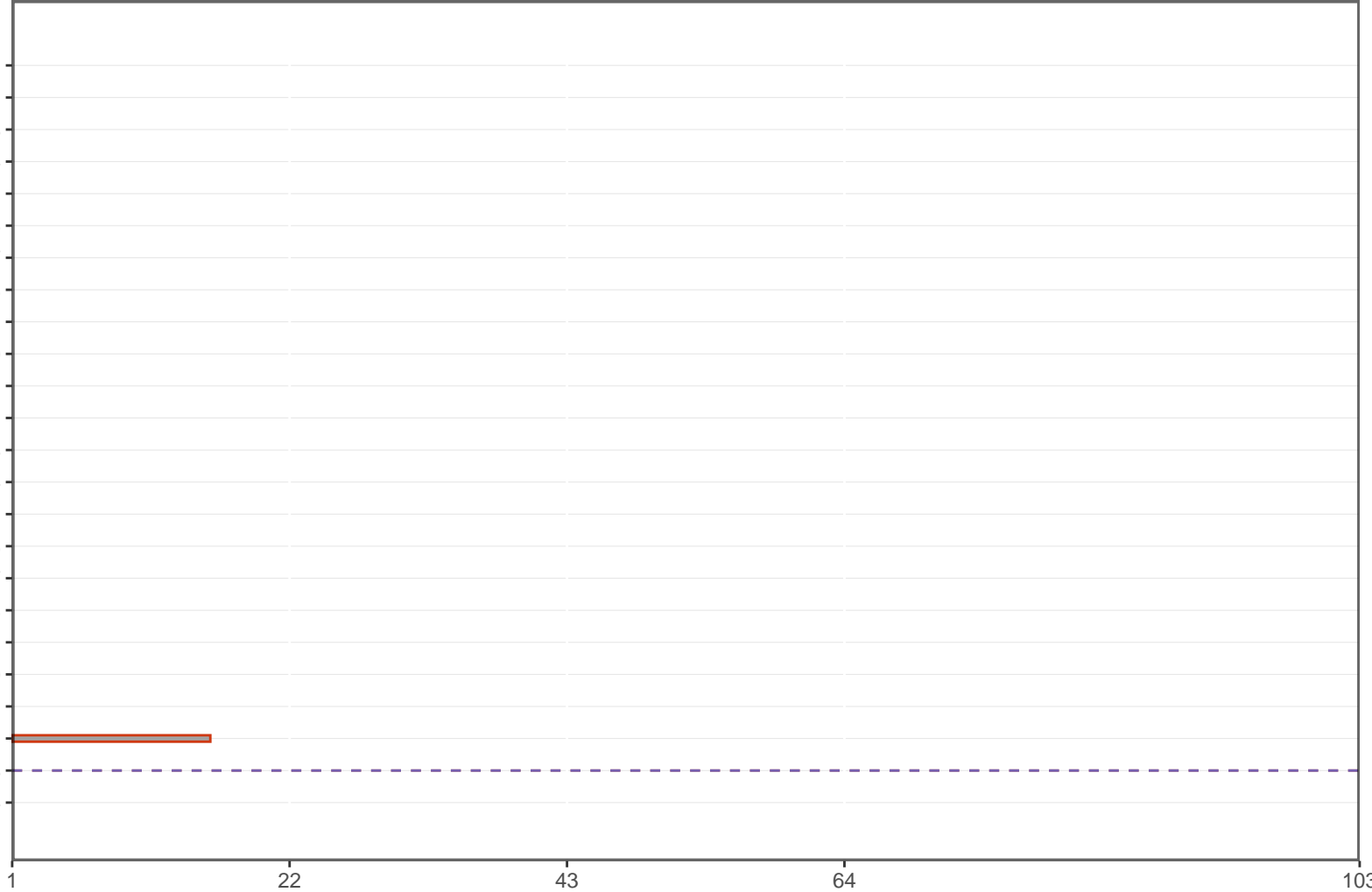
MW indication



Molecular weight

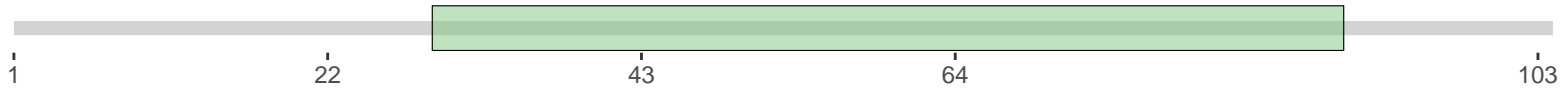


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GNKWDQYLDLVLASVDKDKGGTAEAEALDGLVRYGRRMLMTHVDLIEKLLNNTLGSSEGS*

NbL16g08210.1 ALG-2_interacting_protein_X-like [MW = 97.97 kDa]

No. of times detected



log(intensity)



Values from



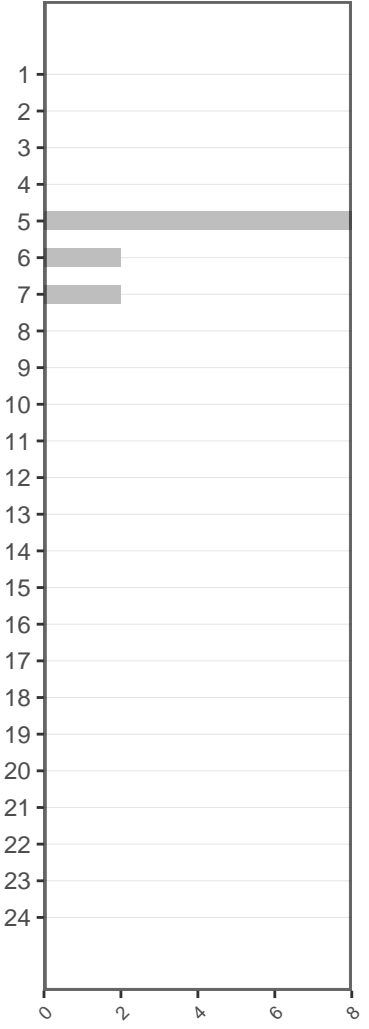
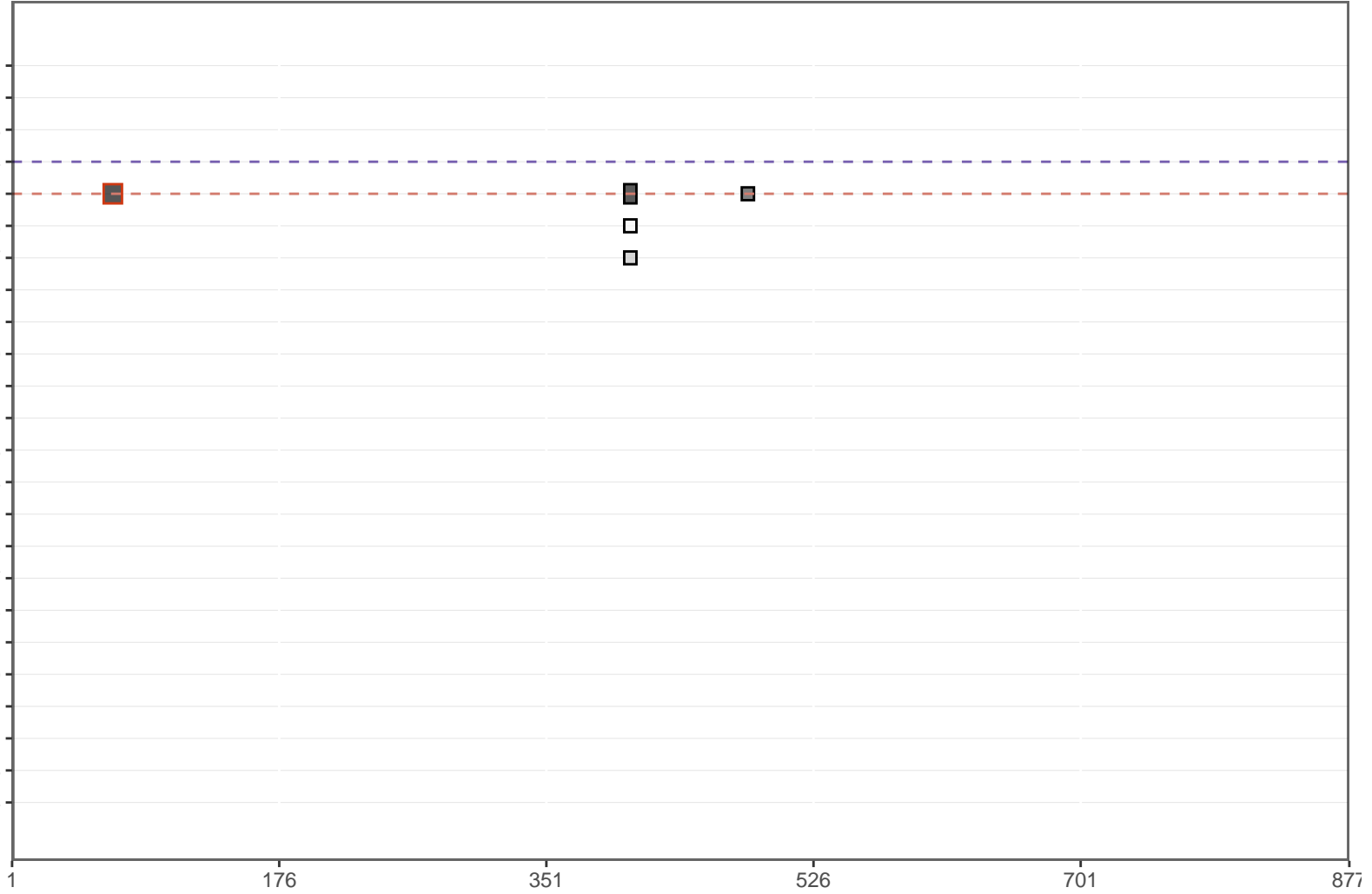
MW indication



Molecular weight

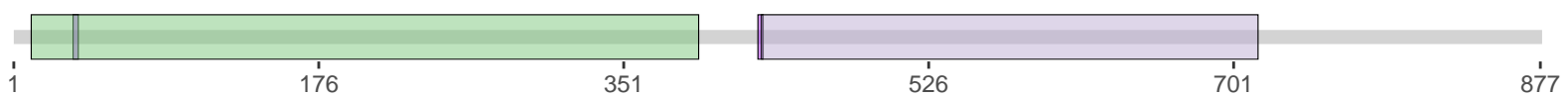


Gel Slice



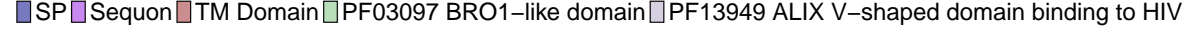
Protein length

Peptide counts over 4 repeats



Pfam domains

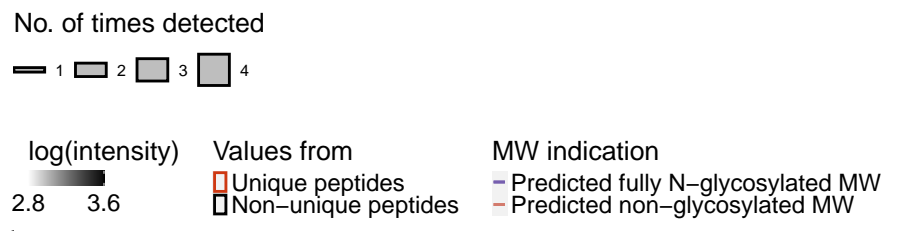
Pfam Description



Protein sequence:

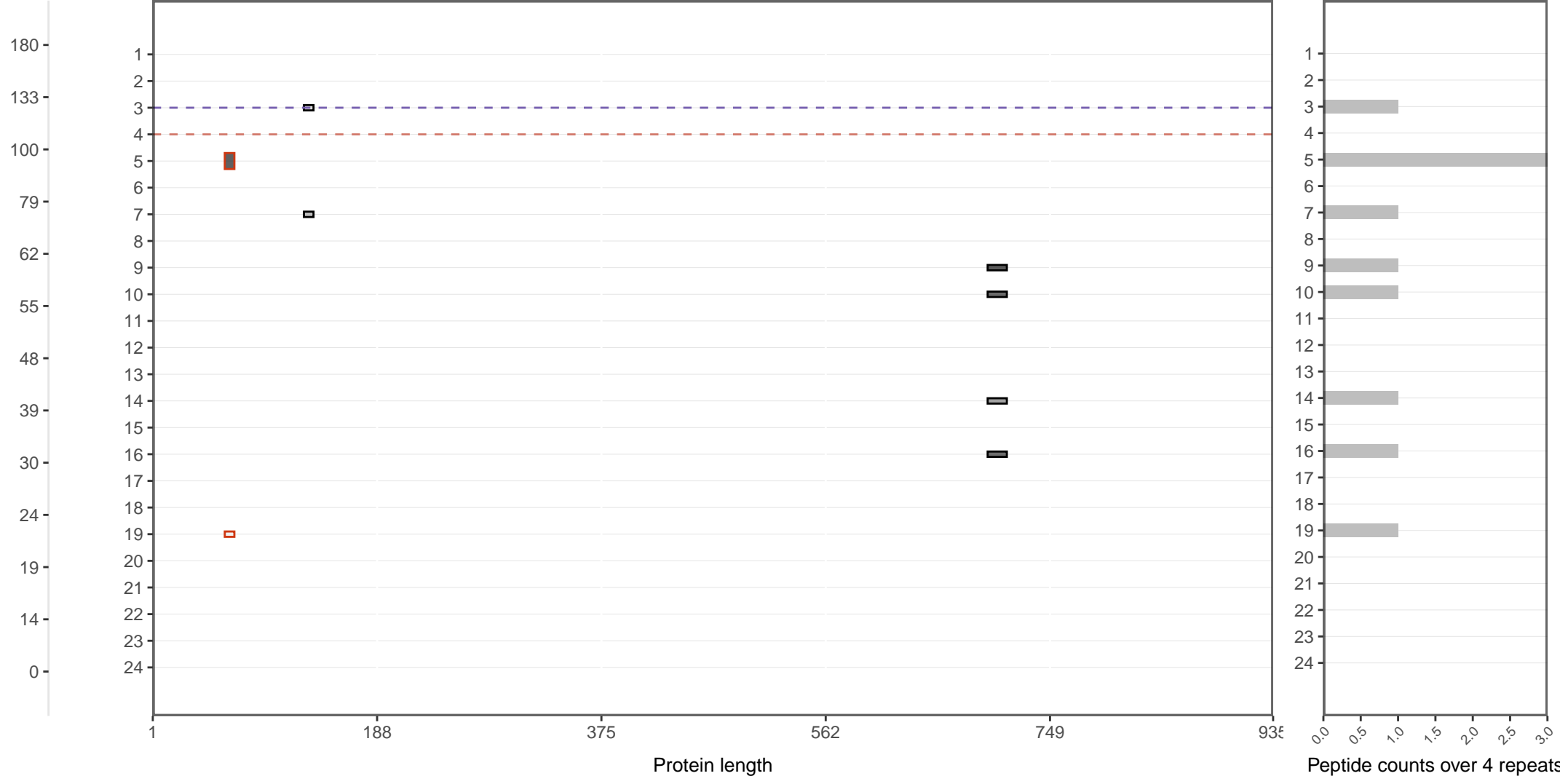
SNLSLPVALKEDV EAVVQGGGPAAGLAELGQLRDLKRVNDELVGTTEHLGKEATEDAQFRFGFTRWTRPQSTTLTKNLDLRLNRFANLKGAAESDARIERSVRDHALMSLDLRHPIESALPTLARPIMSLDATEDAVVGALKQSLRHLETGAGRAGLEMDLKEKRRKDDLPKLMSTGSHEDLFRKEIAYVDHICEEIAQNLAGEQILLGQAQNEEFASIFNLEDYKASRERYKQIEAASIKYREIKENIEGLKFKVYTLQEAITNVKGGGSDFMTRSIQCEEMEE

NbL16g08100.1 neurofilament_heavy_polypeptide [MW = 101.32 kDa]



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain

Protein sequence:

EAIVYAPSSVTLSPGSEAPKGGKGRKEDLNQEECVSEKESSEATSDLELVKQVRPQKAKAPKPEPKHKEKNEGGSTSDVEANKGKSKDKKIDKTKNKNQVPSVRNKEDEKGRGRGKASPETAAPPPEPDDSAKHEGNEEDIPKTSANKKRPSSGKGRERVPSPPEPDSNAKHENNEEETPRTSAKRKRSSGKDKVSGTVGHGELVIGKKIKVWVPLDKFEYEGVVEKFDANKKRYAVYTDGDVEINLFEERWKLVEDDPMSEGEQIASADAASERKQKXPRNAESL

NbL16g07920.1 probable_N-acetyltransferase_san [MW = 18.41 kDa]

No. of times detected



log(intensity)



Values from



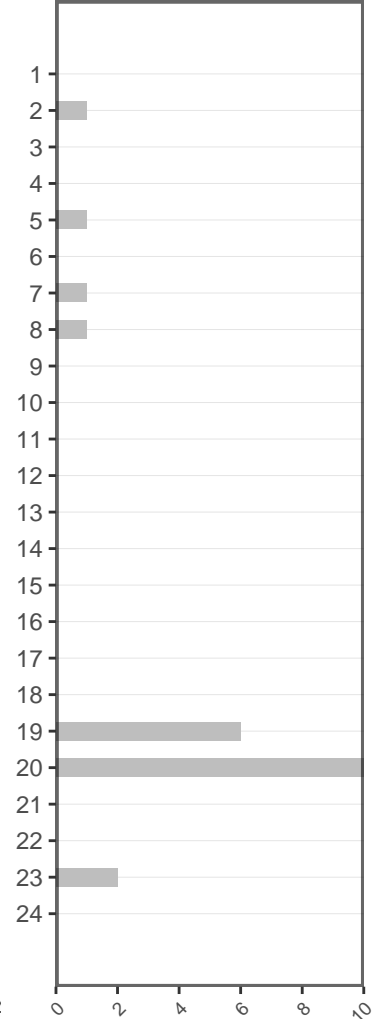
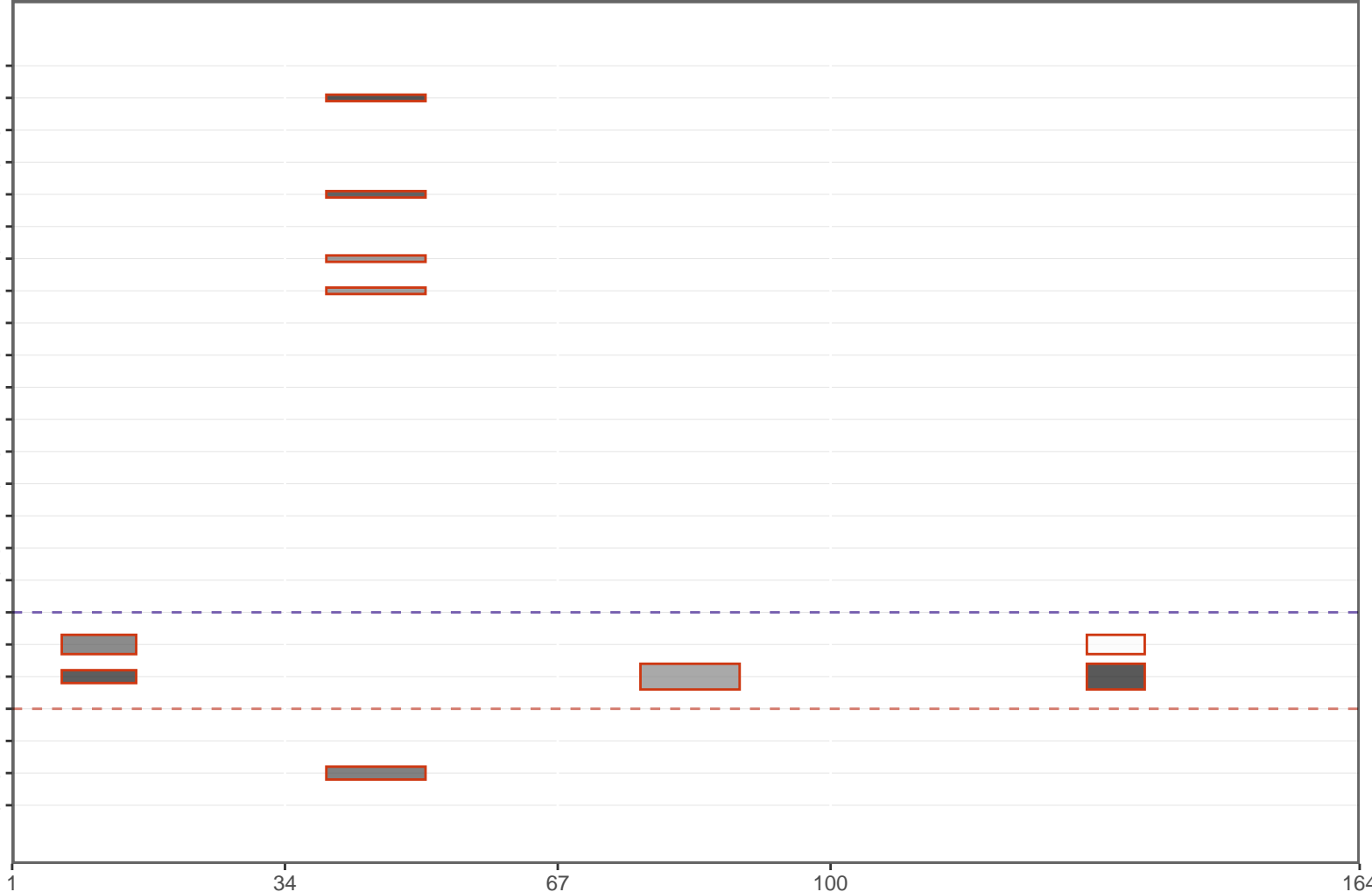
MW indication



Molecular weight



Gel Slice

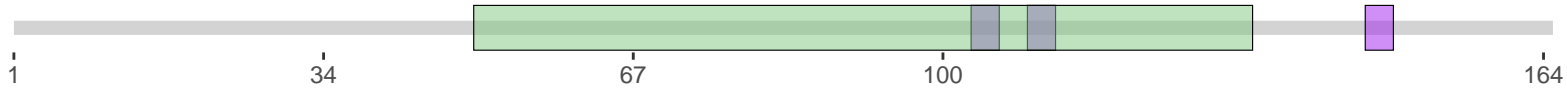


Protein length

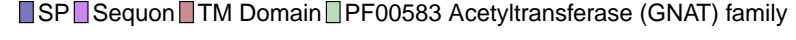


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

EKEGGAVRYIMTLGLVLPYRGLGIGKMLLNHLNLSAKGNVSEIHLVHFTNEDALNFYKFGFEVTDKIGNVYTNITPPDGFVLTQFTQKK

NbL16g07840.1 psbP_domain-containing_protein_6_chloroplastic-like [MW = 28.21 kDa]

No. of times detected



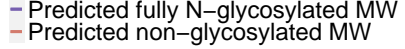
log(intensity)



Values from



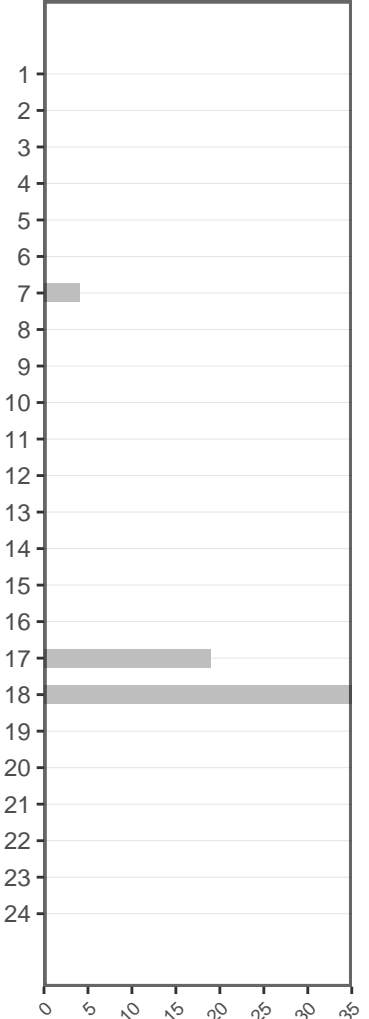
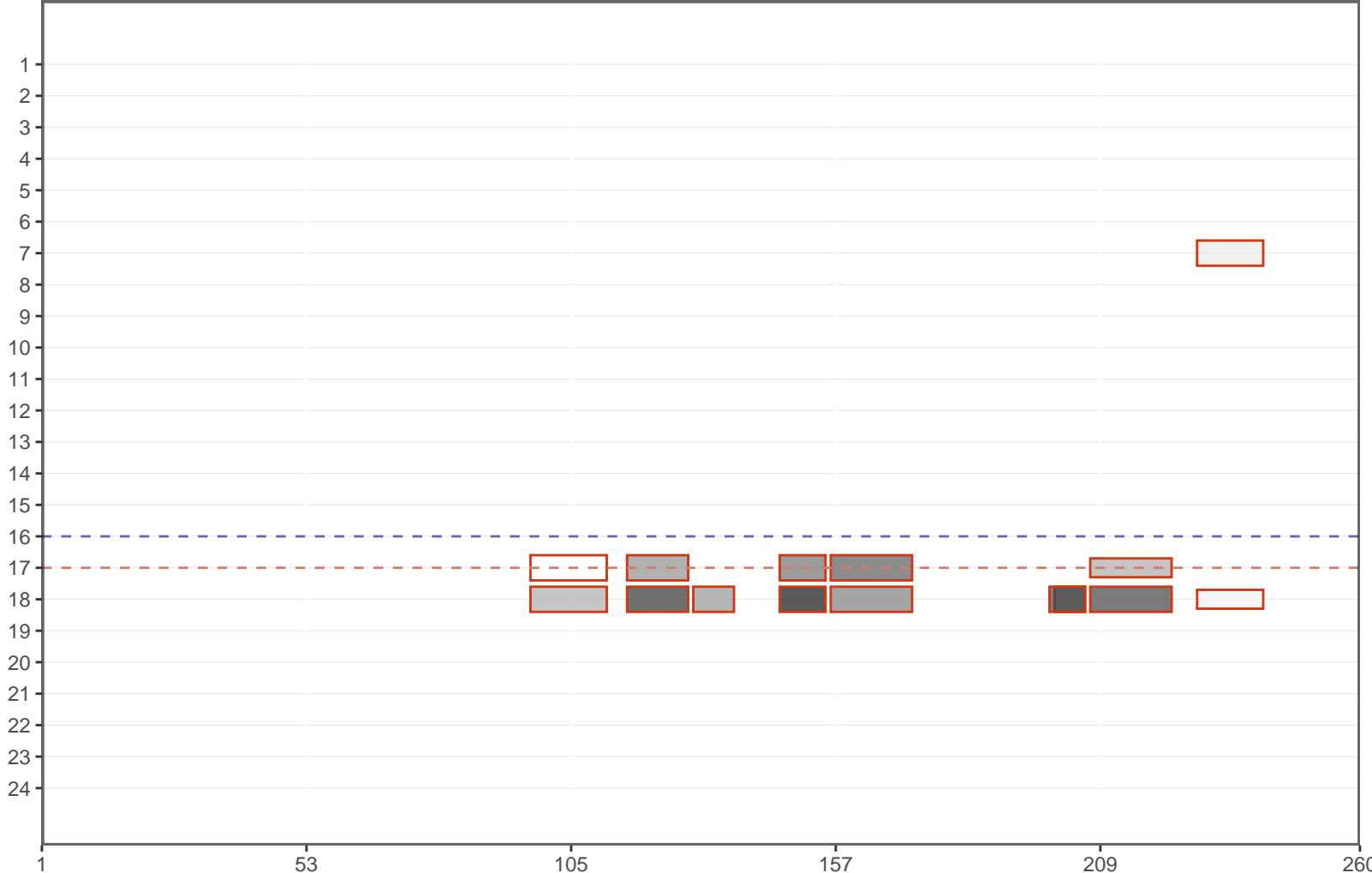
MW indication



Molecular weight

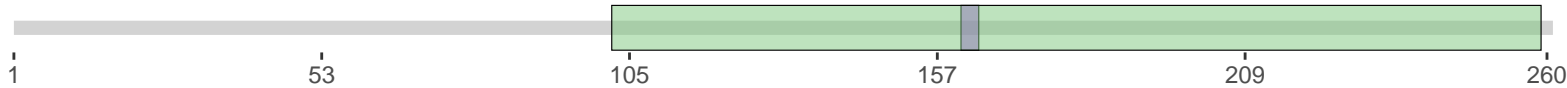


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ANILSQNYCQPKCAEPWVEVFEDEKGGKGVVASPLRLRFLNKPNTIEDDGTPEKVIASLGFVGTNLDPELLQTAIEKRGLTFYKYVLETPVALTGHINLAKATKGNFTVFLFVVSANDKGVSSGKLTLEALDSEV

NbL16g07410.1 poly(rC)-binding_protein_3-like [MW = 57.37 kDa]

No. of times detected



log(intensity)



Values from



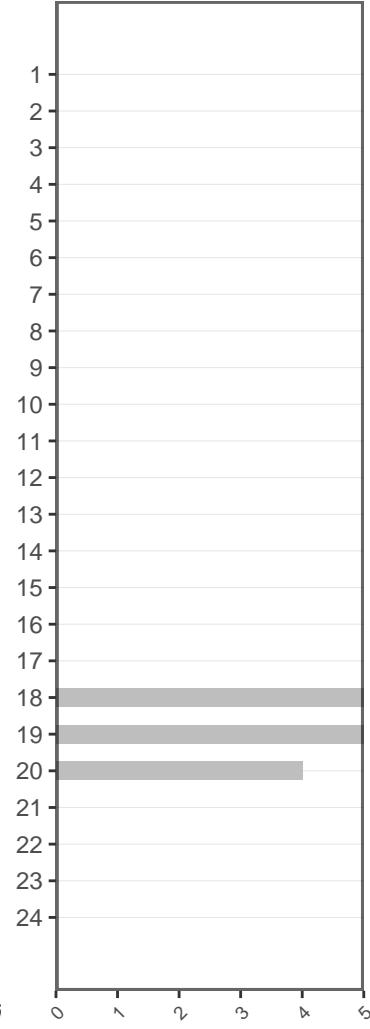
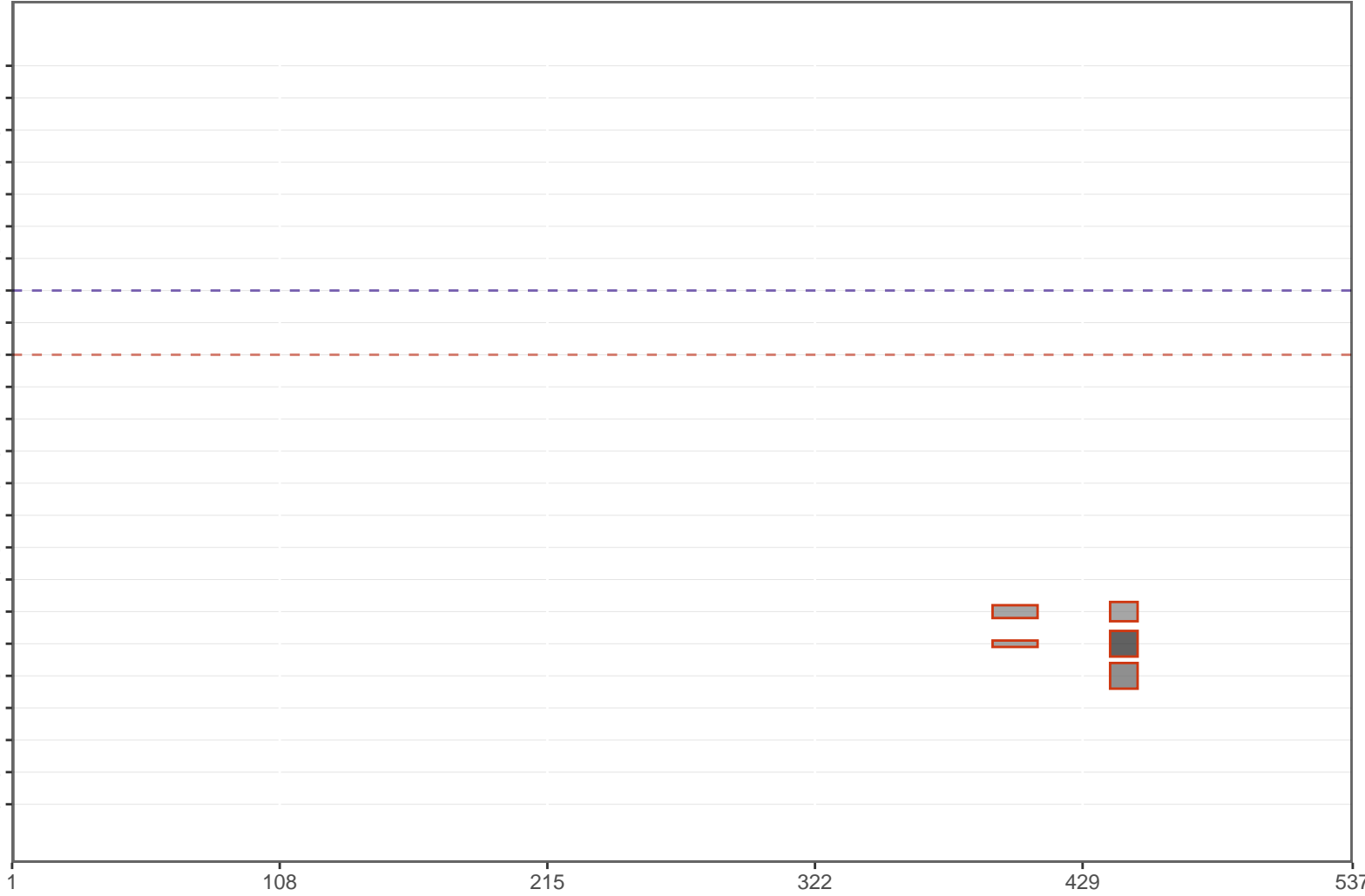
MW indication



Molecular weight



Gel Slice



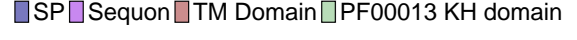
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DESHCTIRLGGELSPFALPDDSEVIEGDFGIVKAVEMIAHLRKLFLVDRBRVIGVFEKLMQMFNARAHQNMPLFGSTEPWGPSPSFLSAGGPFQGANPQVMPFRQYDNYFFRDRPLDMGPHKAPFVYGRDNVSGHMANVQPGQSLKVTQNGIPLSYADAVIGASGSEVYRRTSGATIAVGETRGVPEMTVEINGASGAVLTAGQLQNSIADATNSMGNAAAAGPPSGGYNPYPGQVFPVYSSGSSATGHAGQAPADYGSVYGGSYG*

NbL16g07280.1 EKC/KEOPS_complex_subunit_bud32-like [MW = 33.54 kDa]

No. of times detected



log(intensity)



Values from



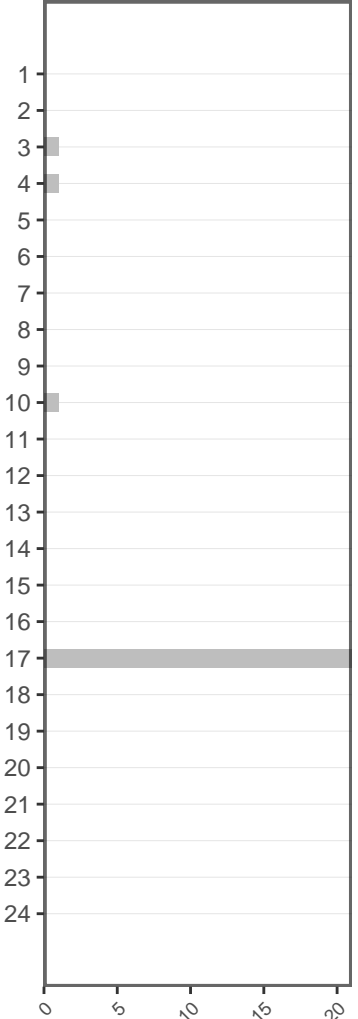
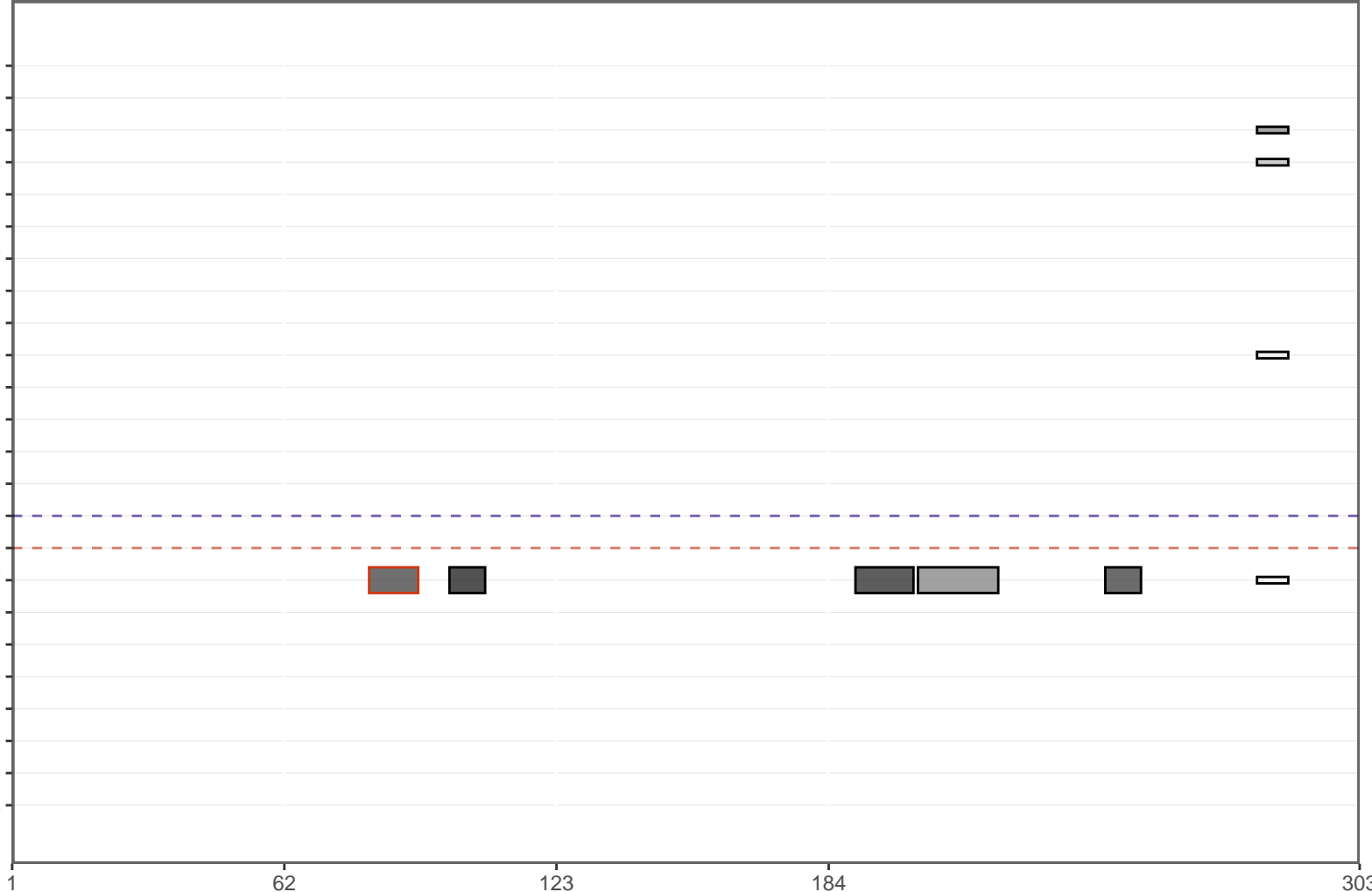
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

CAARLQVITTPVLYAVDPVTHLTFEVEVGGPKVDFLFGGLGVGDDERMFDATQGNAGKLDHGGVHGDLTFSNMLMRSSANQLVLIQDFGLSFTSTLPEKAVDVLVLERALLSMHSSGGNVMDQILAGYKSKSGVSSFTFNKLAGVQRGRKRTMVG

NbL16g07220.1 40S_ribosomal_protein_S24-1 [MW = 15.39 kDa]

No. of times detected



log(intensity)



Values from



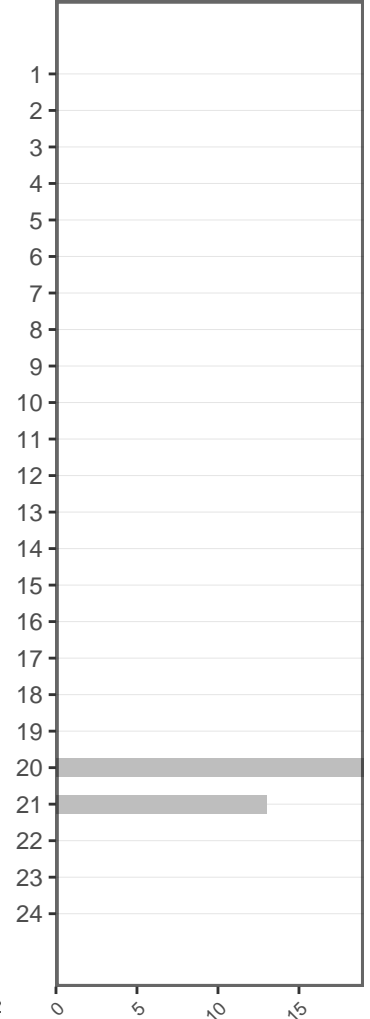
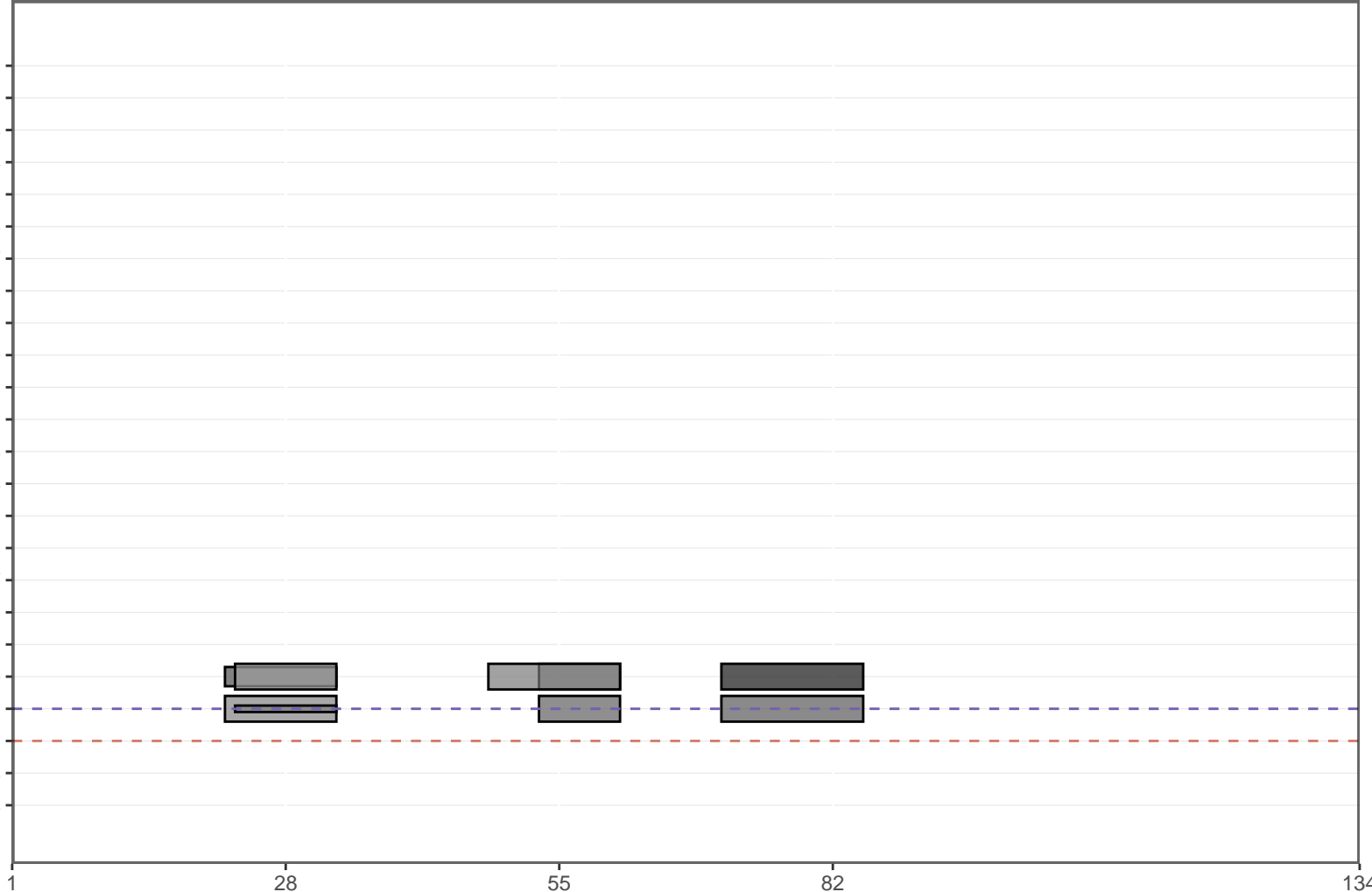
MW indication



Molecular weight



Gel Slice

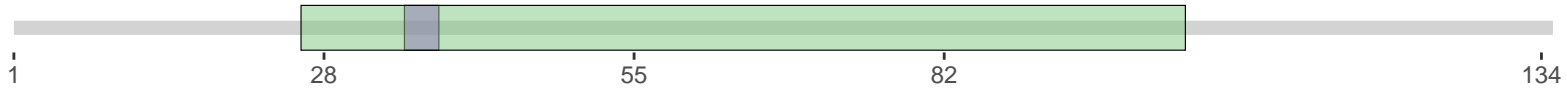


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

NAIFVYKFRTHFGGKSTGFLYDVENAKYKPKVRLIRNGLDTKVEKSRKGMKERKRAKKVIRGVWTKTAGDAKKK

NbL16g07120.1 probable_glutathione_peroxidase_5 [MW = 18.91 kDa]

No. of times detected



log(intensity)



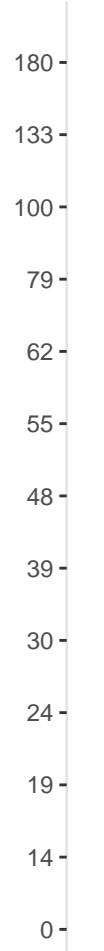
Values from



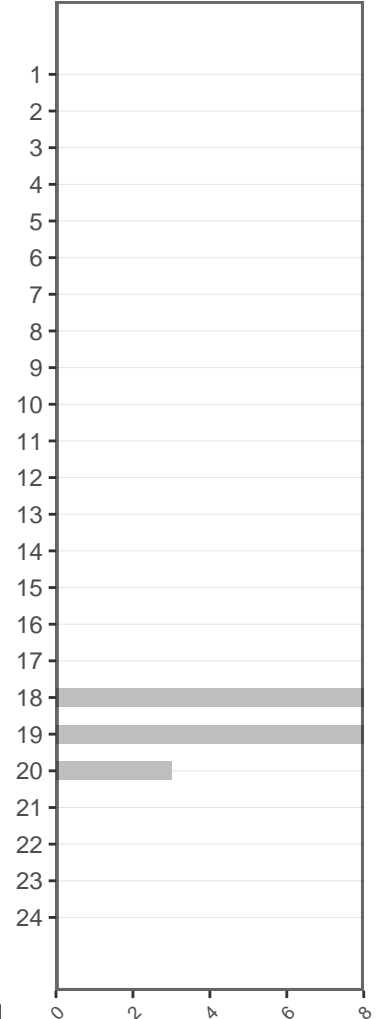
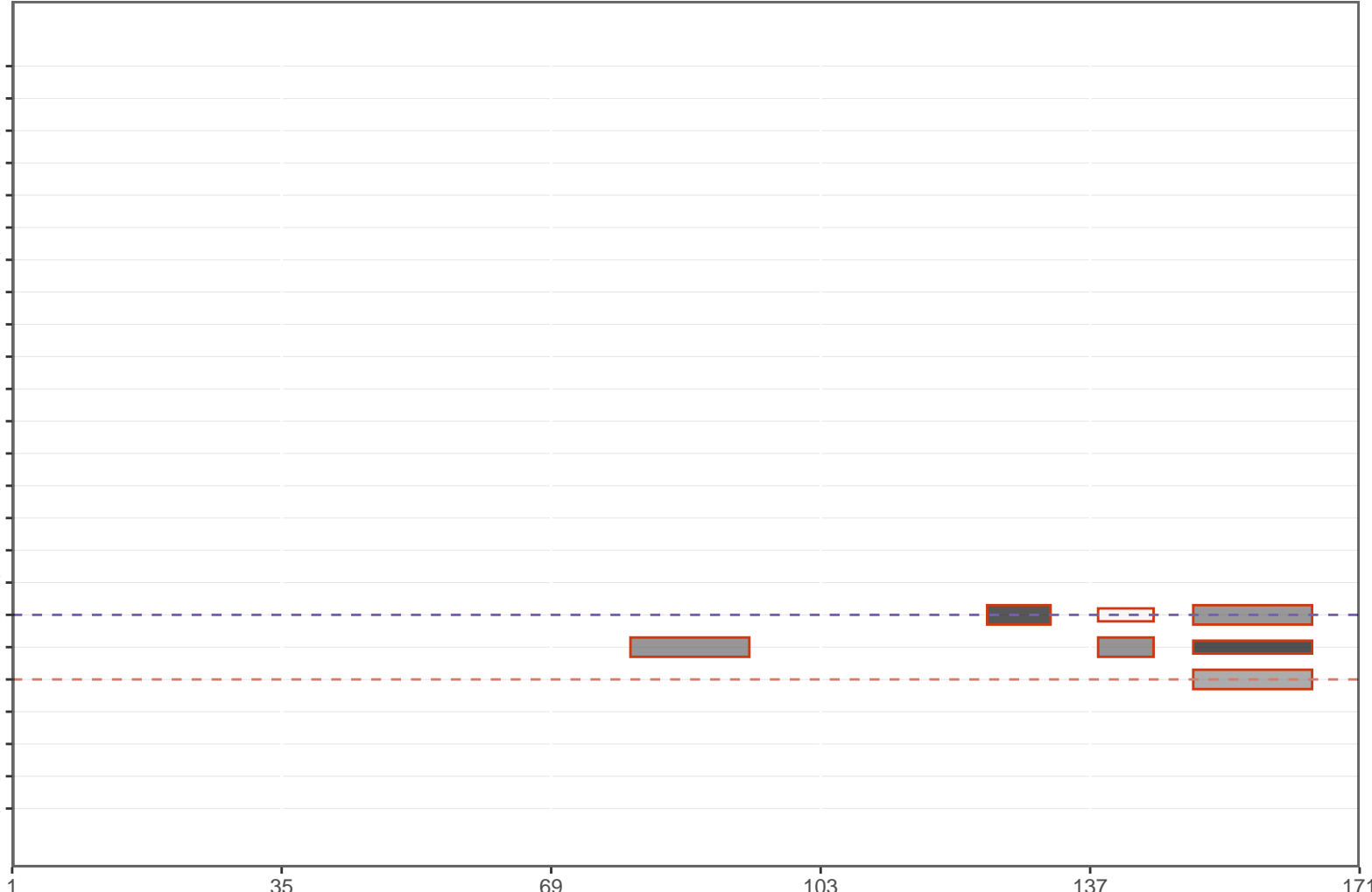
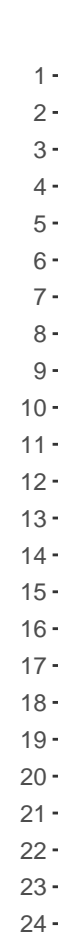
MW indication



Molecular weight

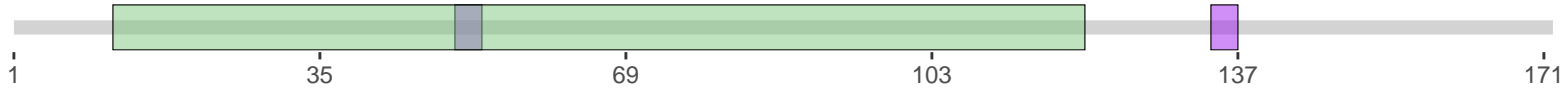


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CSNDFLKEPPTSEADGQFACFRFAEYFHFQKVRVNGPDAAPVYQFLKSKGGFLGSSKWNFTKFLDKKGGKVRKRYGSDTTPLAEADIKALGEV

NbL16g07060.1 auxin-binding_protein_T92 [MW = 26.21 kDa]

No. of times detected



log(intensity)



Values from



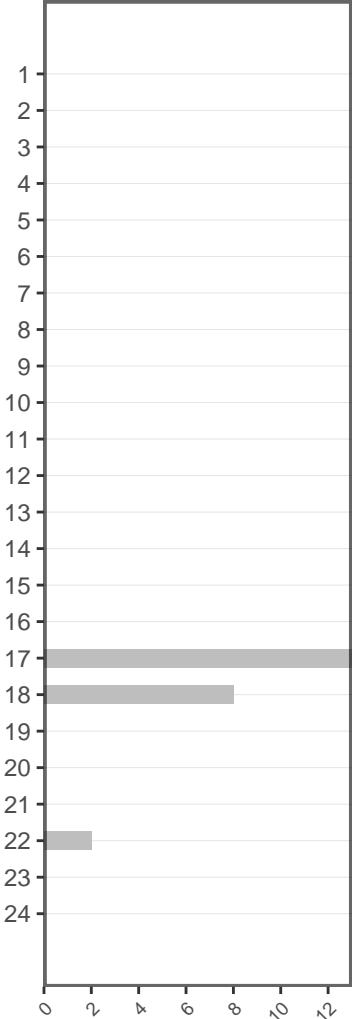
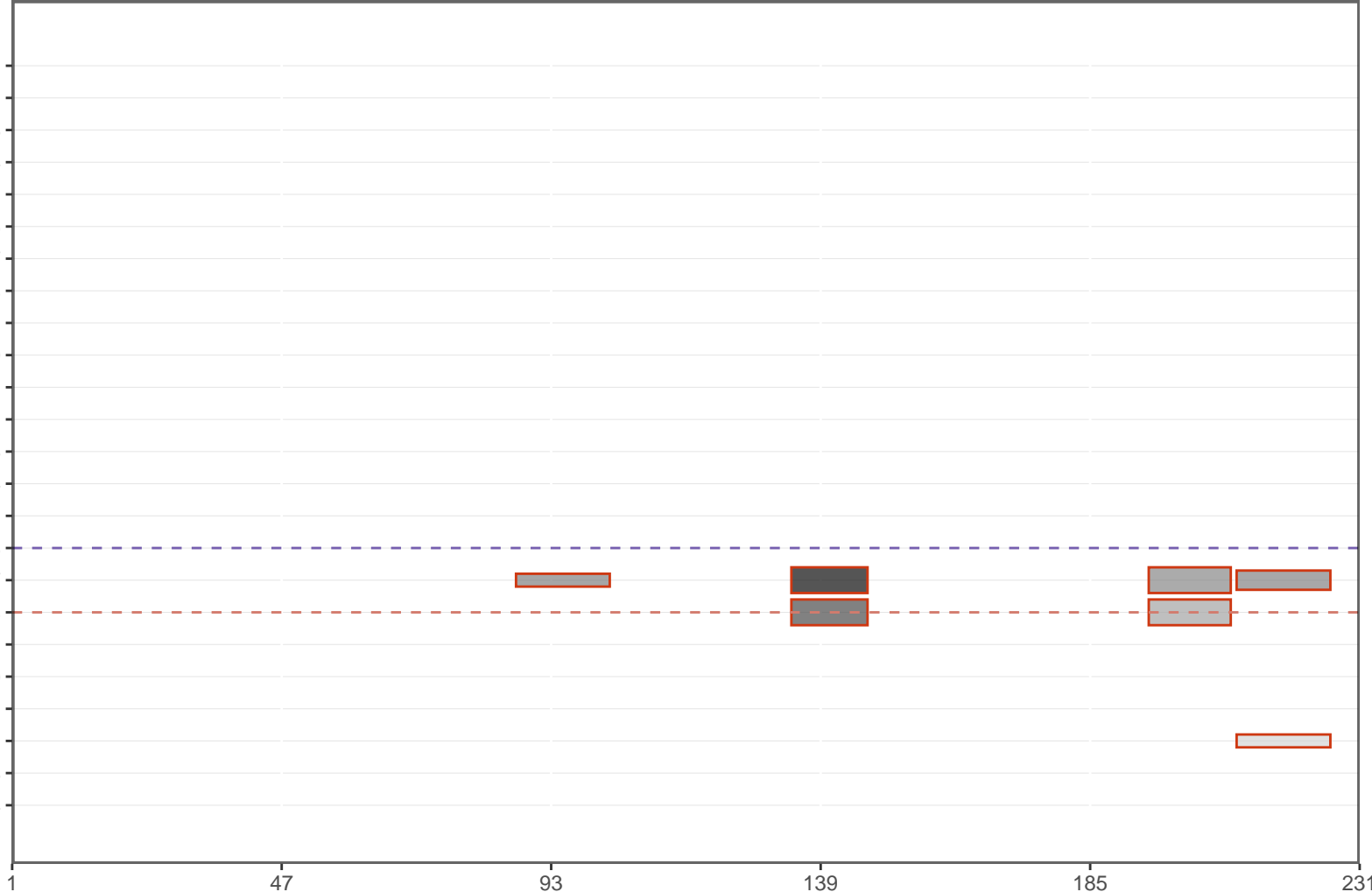
MW indication



Molecular weight

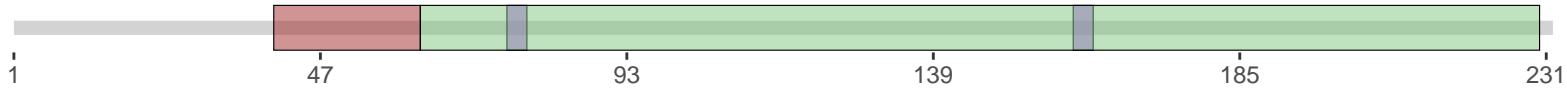


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEIYVLOTFAFGSRTPHRHSGEELKLGKGGTLVLPSSHSKYKGNPQERHIFPNSTVHPVNDVHQVWNTGHEHEDLQVLLVSRPPKVFMYDDWSMPTAANKLFPYVWDEECYQTTSRANDEL

NbL16g06970.1 histone_H2AX-like [MW = 15.22 kDa]

No. of times detected



log(intensity)



Values from



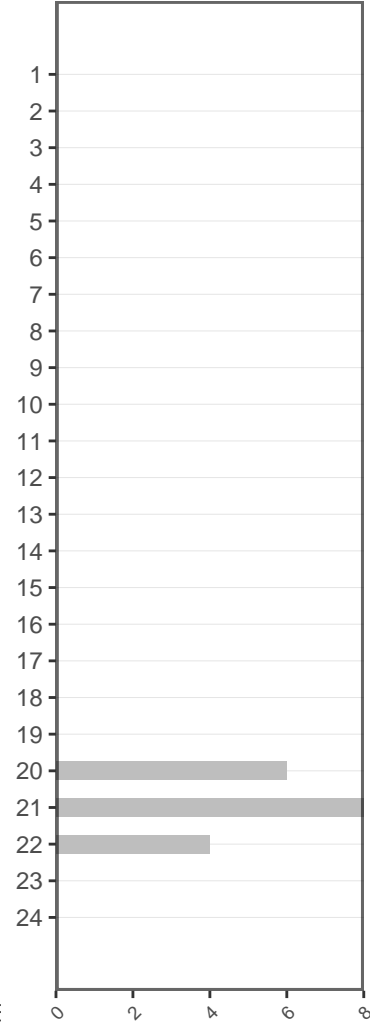
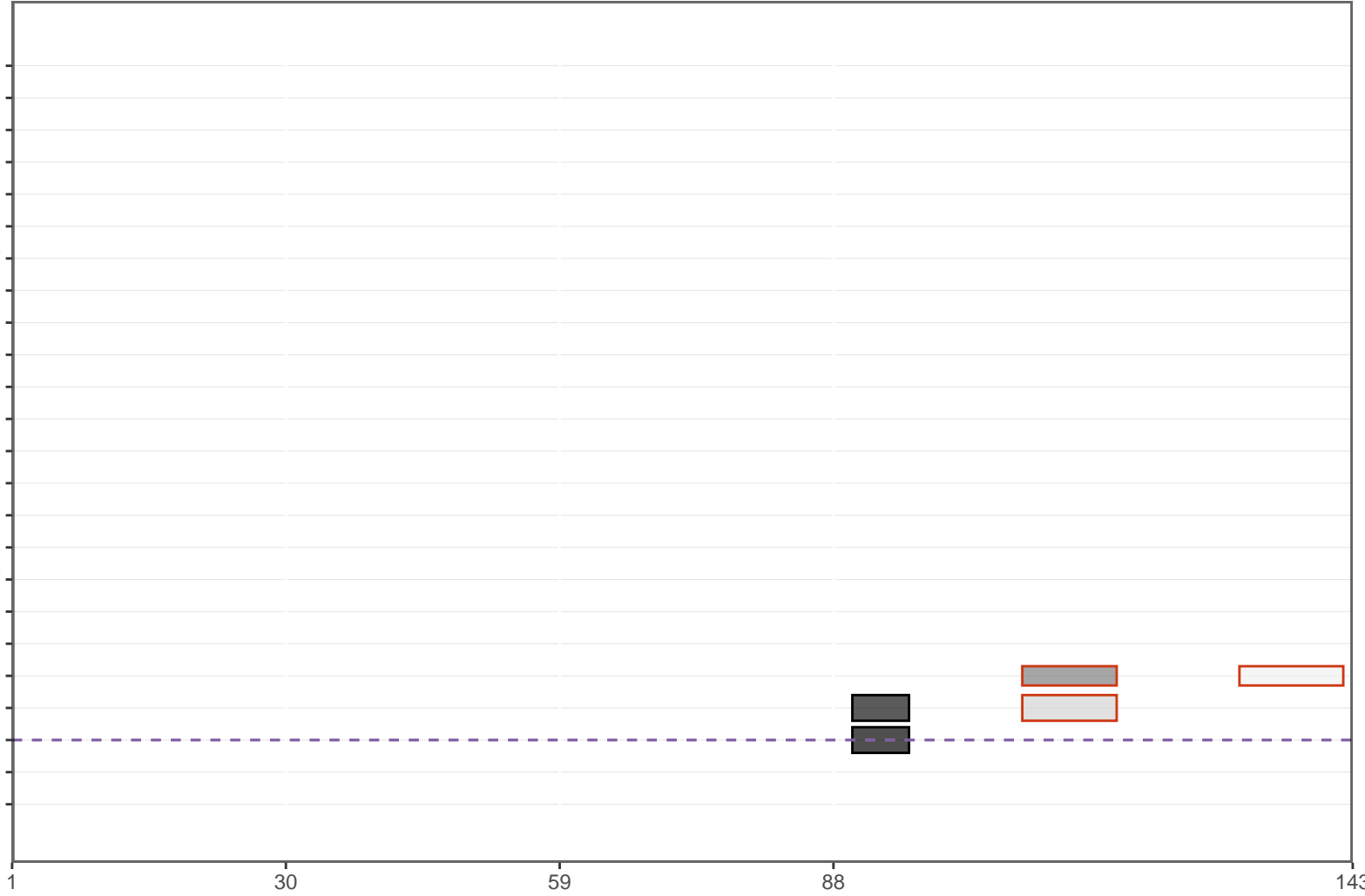
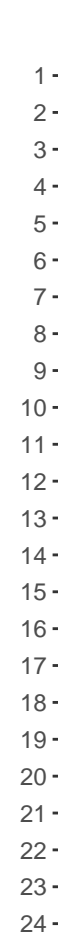
MW indication



Molecular weight

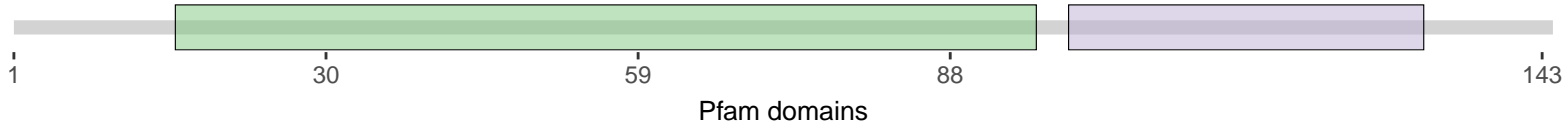


Gel Slice



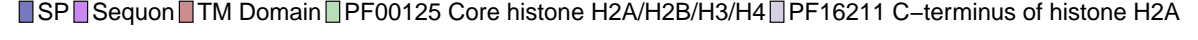
Protein length

Peptide counts over 4 repeats



Pfam domains

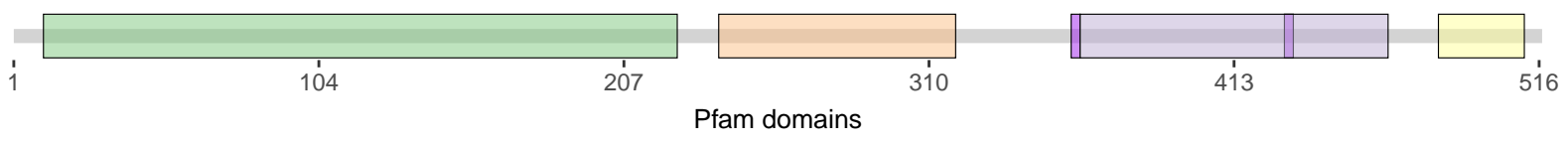
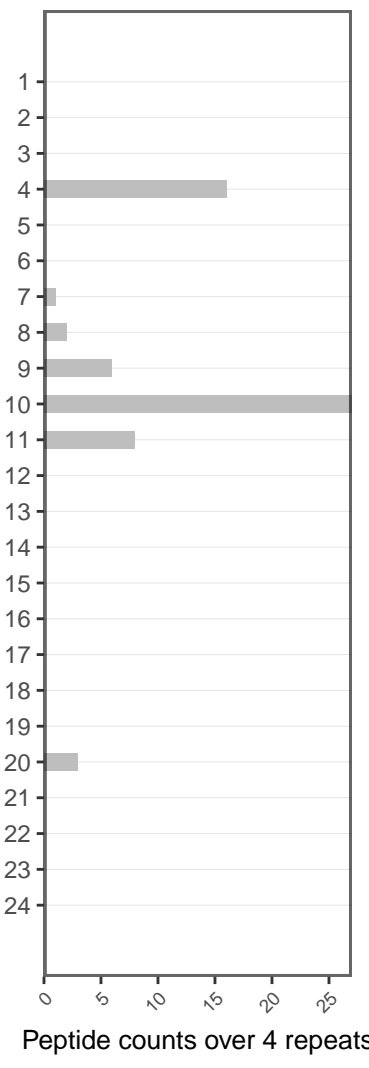
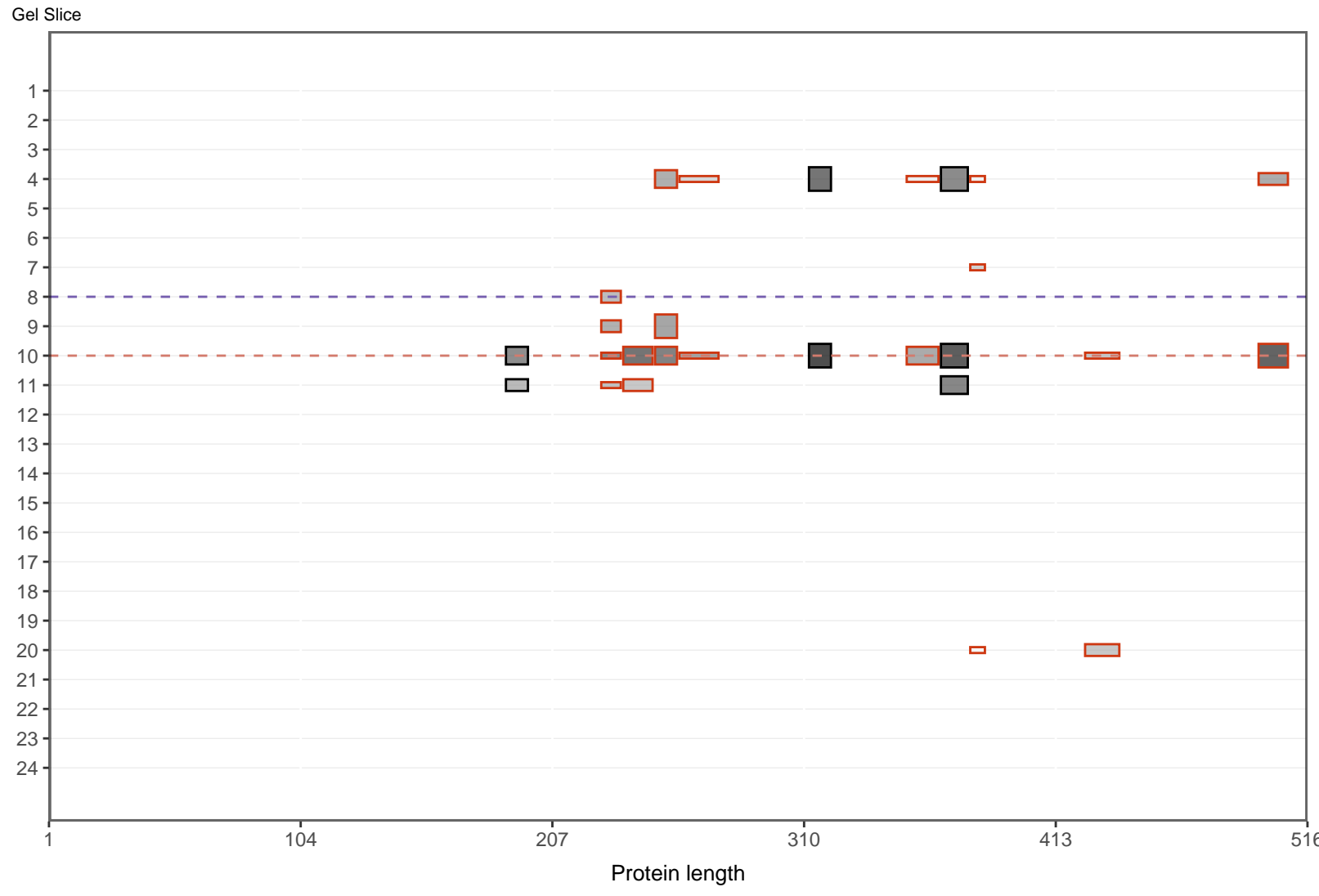
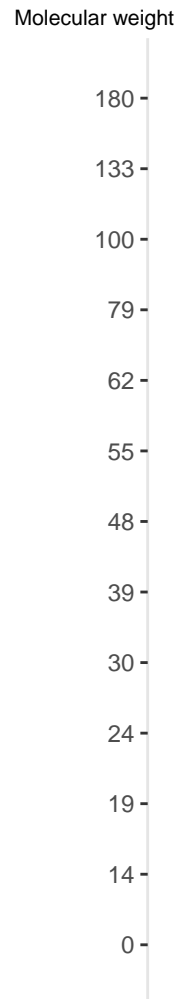
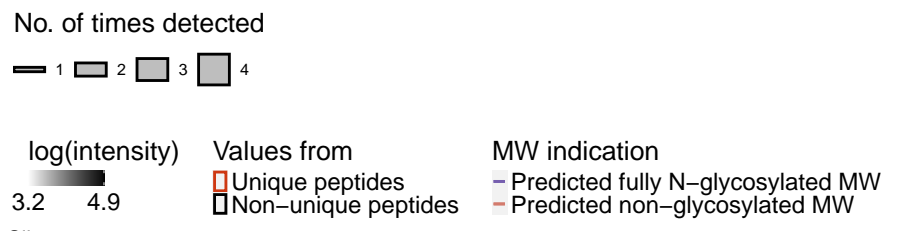
Pfam Description



Protein sequence:

YLSAVLEYLAAEYVLELAGNAARDNKTRIVPRHQLAVRNDEDELSKLGKVTIANGDVLKPKHPALFPRKNGKGLKLEAGTQSGDF

NbL16g06920.1 bifunctional_3-dehydroquinase_dehydratase/shikimate_dehydrogenase_chloroplastic-like [MW = 56.48 kDa]



Pfam Description

- SP
- TM Domain
- PF01488 Shikimate / quinate 5-dehydrogenase
- PF18317 Shikimate 5'-dehydrogenase C-terminal domain
- Sequon
- PF01487 Type I 3-dehydroquinase
- PF08501 Shikimate dehydrogenase substrate binding domain

Protein sequence:

ISKGPLLIINPFRIRHFGYNGHYVPLLVLDNIKEFFRVFSDNDVAGFSVGLPHKEAAVRCGDEVLDPLAKSGAANTHRRPDSGKLGVNTDCEAGVTAIEEALRERQKTNHSHASNPVIAKGLFVIVGAGGAGRAAFVKSRSRGAHVIFNKRKYERAKALAAVSGEALPYEQLNDFCPKGMILANASAVGMQPRTDQTFNKEALSKYELVFDVAYTPRNTRLRLLGAEATVGAAVVGGVEMFVRGAIGQKLFETNGLAPEDFMRRIVVEGE

NbL16g06900.1 protease_Do-like_2_chloroplastic [MW = 66.9 kDa]

No. of times detected



log(intensity)



Values from



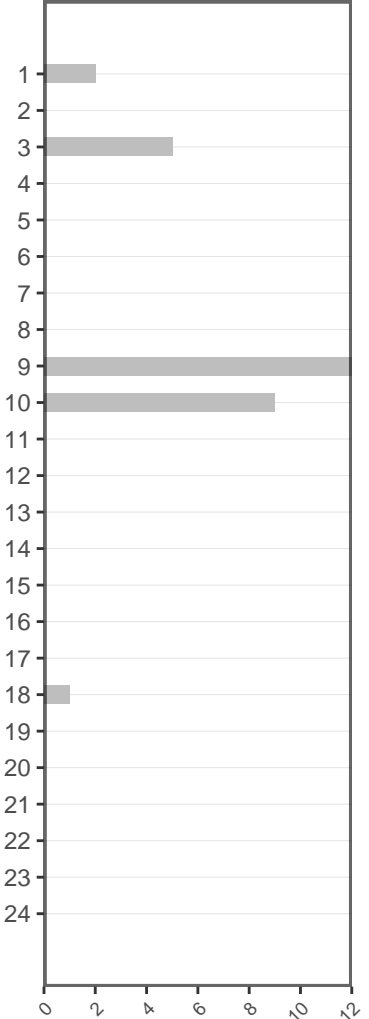
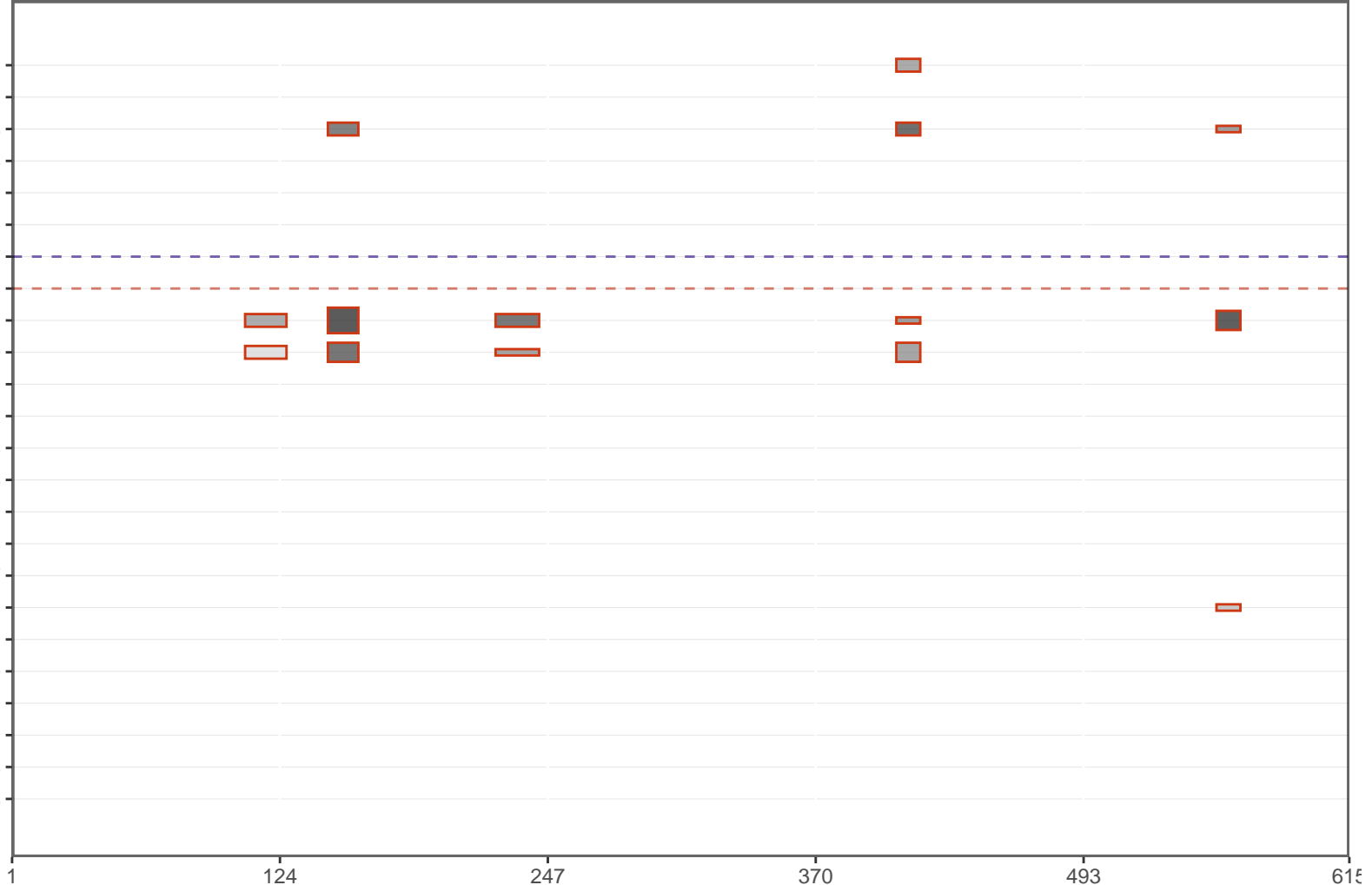
MW indication



Molecular weight



Gel Slice



Protein length

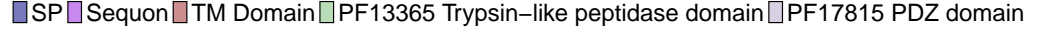


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

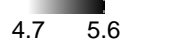
IQVYRSDDAENIGYVPTTVVSHFLEDEVRNGKYGFFPLGLVLLGKLENPLRAGLKVPSNEGVLLRVKVEPTSDVSNVLEKGGVIVSFDGVHVGSEGTVFRFRSERIAFRYLISQKVFSGDSEVLRAGEFMKVGAVLKPRVHLVFPVHIEGGQPSLVAGLVFTPLSEPLEEEEEESIGLKLTKARYSLAKFEGGQVLSQVLANEVNIGVYEDMSNEGVLLKNGTRIKNHHLAHLVDSCKGKYLVEFEEDNFLVLEREAALDASBIKDYGPFAERSSDLMGAYVDSIEQSEI

NbL16g06810.1 universal_stress_protein_PHOS34-like [MW = 17.5 kDa]

No. of times detected



log(intensity)



Values from



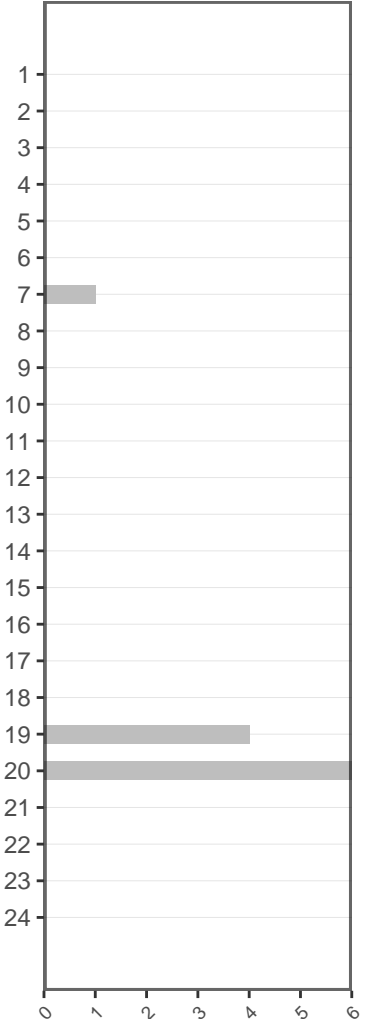
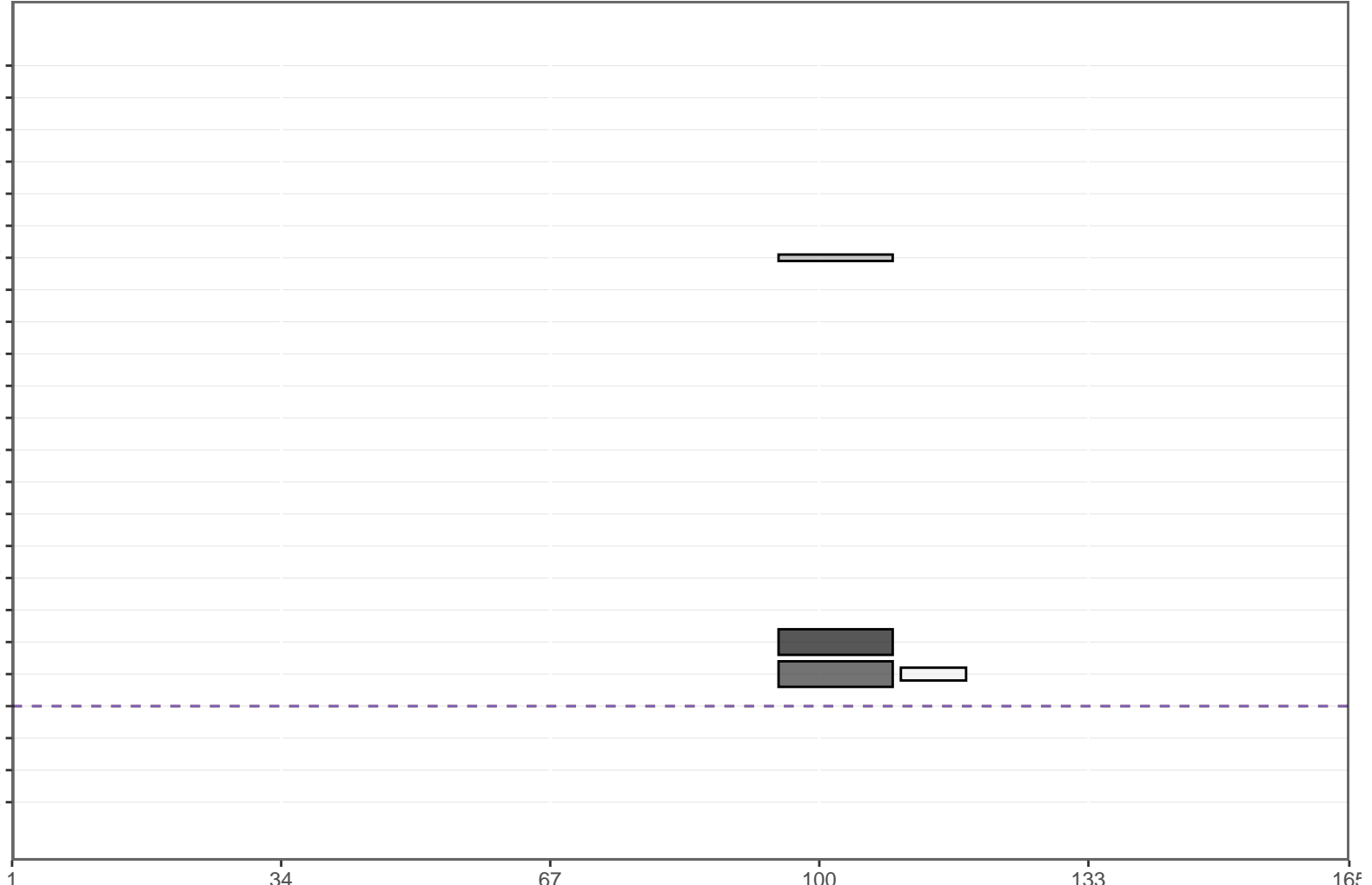
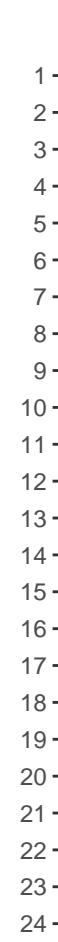
MW indication



Molecular weight



Gel Slice

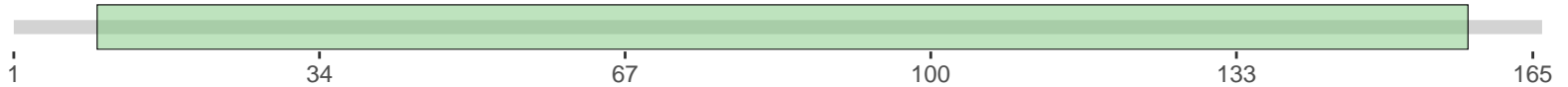


Protein length

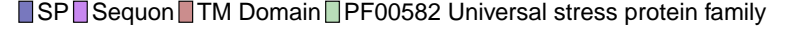


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

YYEADLRKISSRVAEKAKGIGSAKSVNDVVEVMEGDARNVLCDAVEKHASILVGGHGGYGLKRTVLSGVSQYCAHHAGSVMVRRPKVKA

NbL16g06800.1 beta-glucosidase_11-like [MW - SP = 55.64 kDa]

No. of times detected



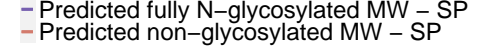
log(intensity)



Values from



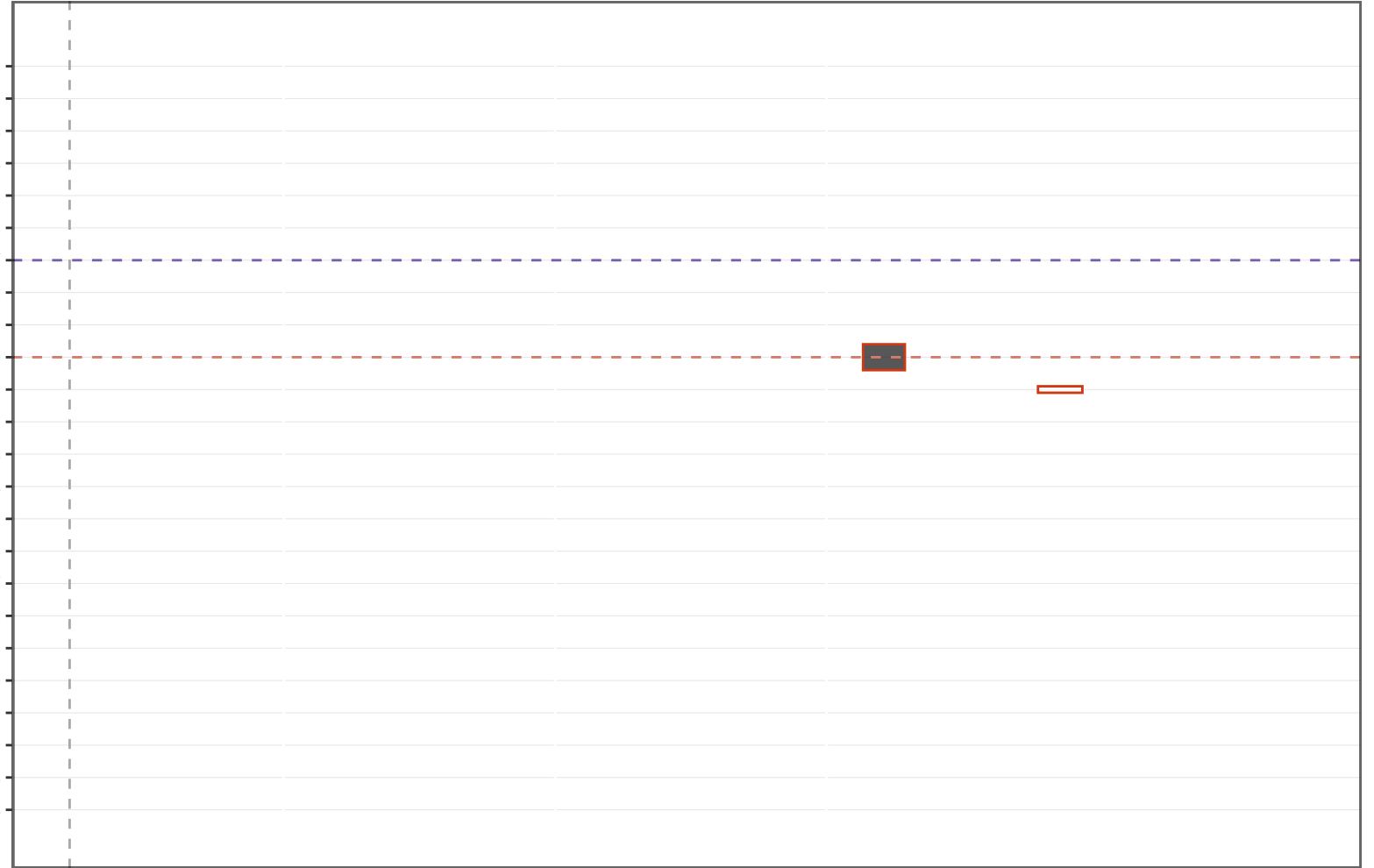
MW indication



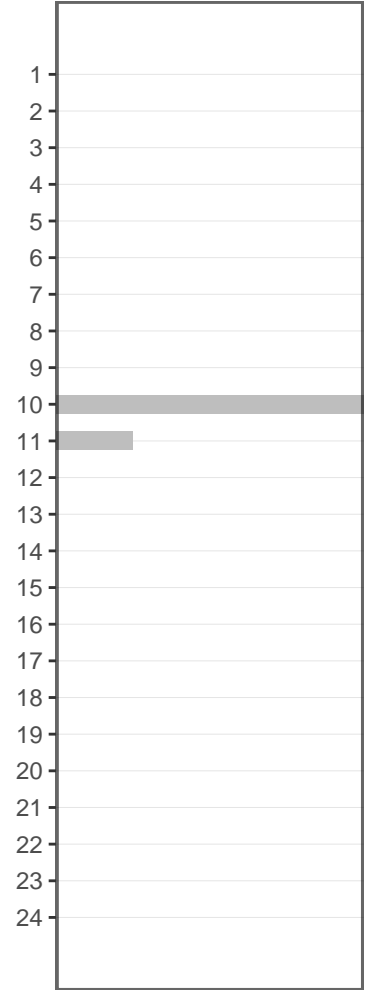
Molecular weight



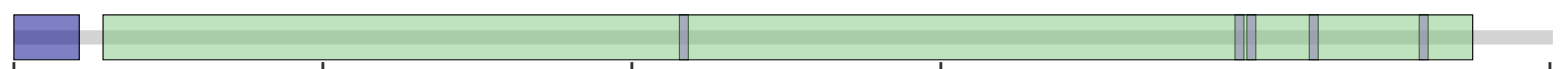
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

RLLYKRYKSIQIGFVGLNFARFIRPTNAKADGATLRWAFYLGWFMPLFGDVPYTMKDRVGSRMPTFTRQESGQVGAIDFGLNHWTLPVNDRPSAFERDFDSTDAKDLVFEQGGVTRPKGEVPTWQPLRAVLEVPKTYGALPIWHENGQTPRNATLNDTGRVEYLVHAYIRNLLDAMRNGSNVRGFFBWSFLDGLLELLDGYKSGVLYVLDLDDENLTRYPKLGGHYSNFKLGGKRNKSGVDLVKKEVSHSSEKFFSS

NbL16g06720.1 60S_ribosomal_protein_L19-3-like [MW = 27.35 kDa]

No. of times detected



log(intensity)



Values from



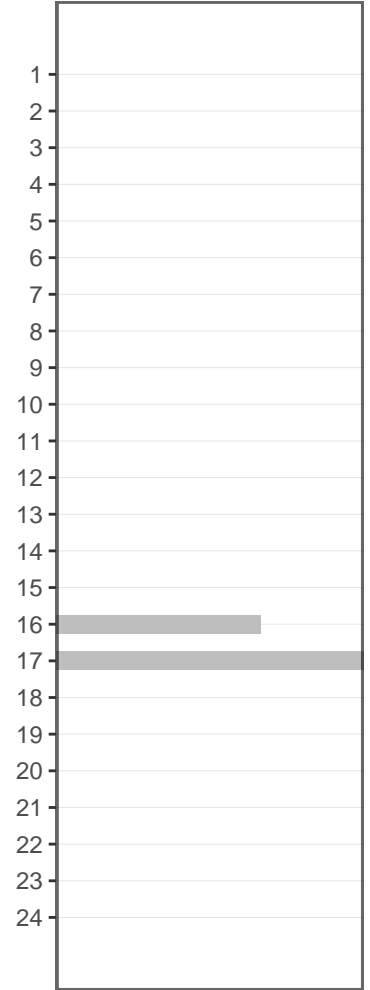
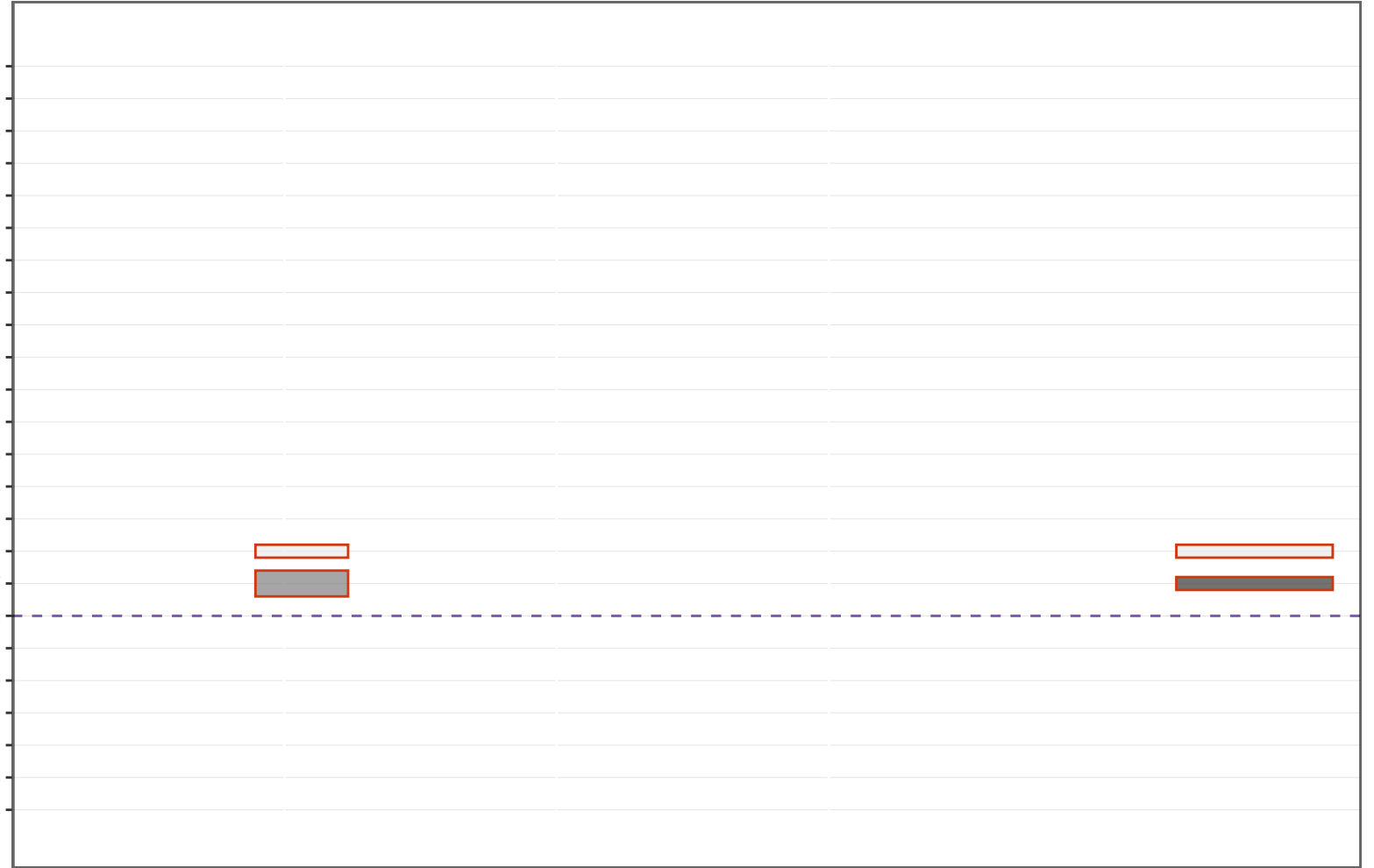
MW indication



Molecular weight



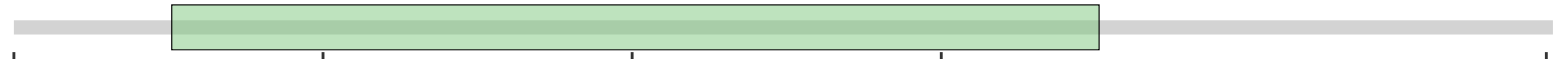
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

ITREARLPTXVLMRRMRVLRLLRLKRYREKKIDRHMHDMYMKVKNVFNKRVLMENHRTKAEKAREKTLSDQFEARRANKKASREKFKARREERLAGGPGSERPIQPAATATPQAGPMGGKSKK

NbL16g06700.1 methionine_aminotransferase-like [MW = 44.94 kDa]

No. of times detected



log(intensity)



Values from



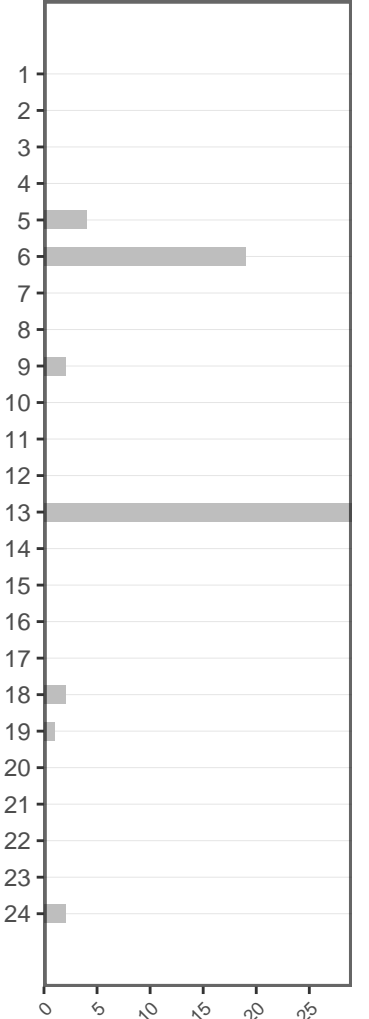
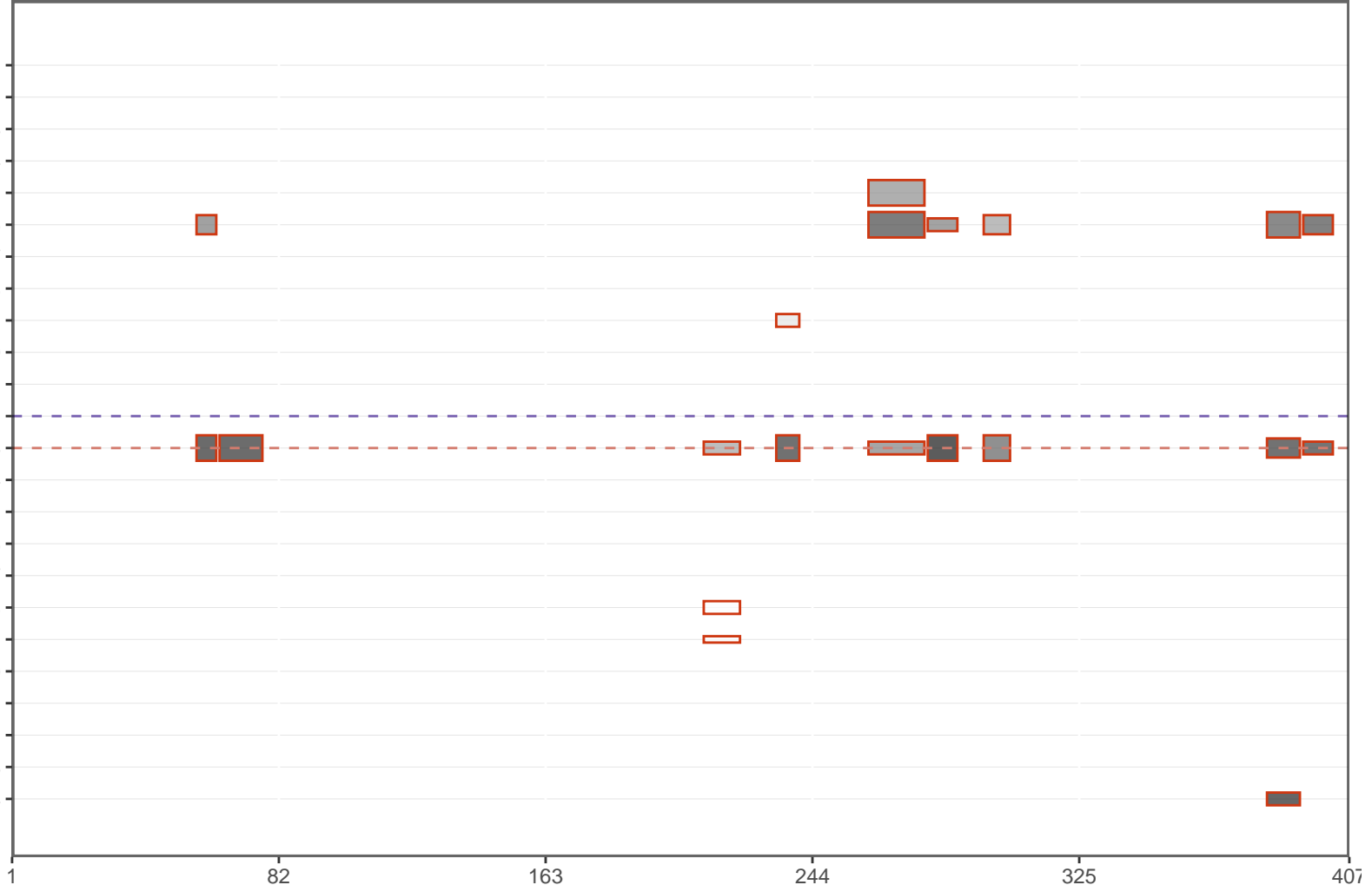
MW indication



Molecular weight

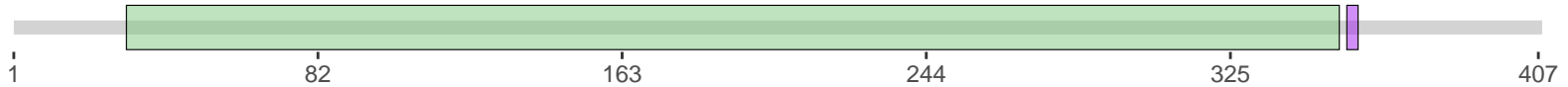


Gel Slice



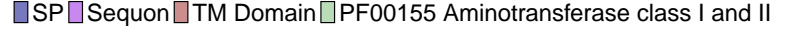
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RTLDLAVTDEVYEHITFDGERHTSATFPGMQKRHTTSLSLKSFSFVIGWRIGWAGPAGFASARINHHXITDSAPMPFGEAALTALRSGPEYFDALRQGVESKRDYLTQVLTQVGFQVFPMPKGGFFLFMELPSTGLSDVFEVVEELKQAGVAVVPGHVFFHTNLSLLEDFSTASVYHRRYRFAFKBEETLAAASQKTELVDGSGRLKLF

NbL16g06670.1 CTP_synthase-like [MW = 67.33 kDa]

No. of times detected



log(intensity)



Values from



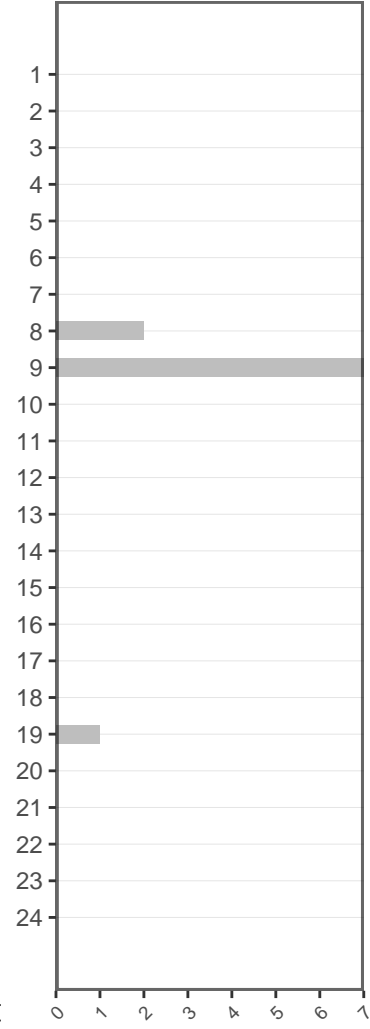
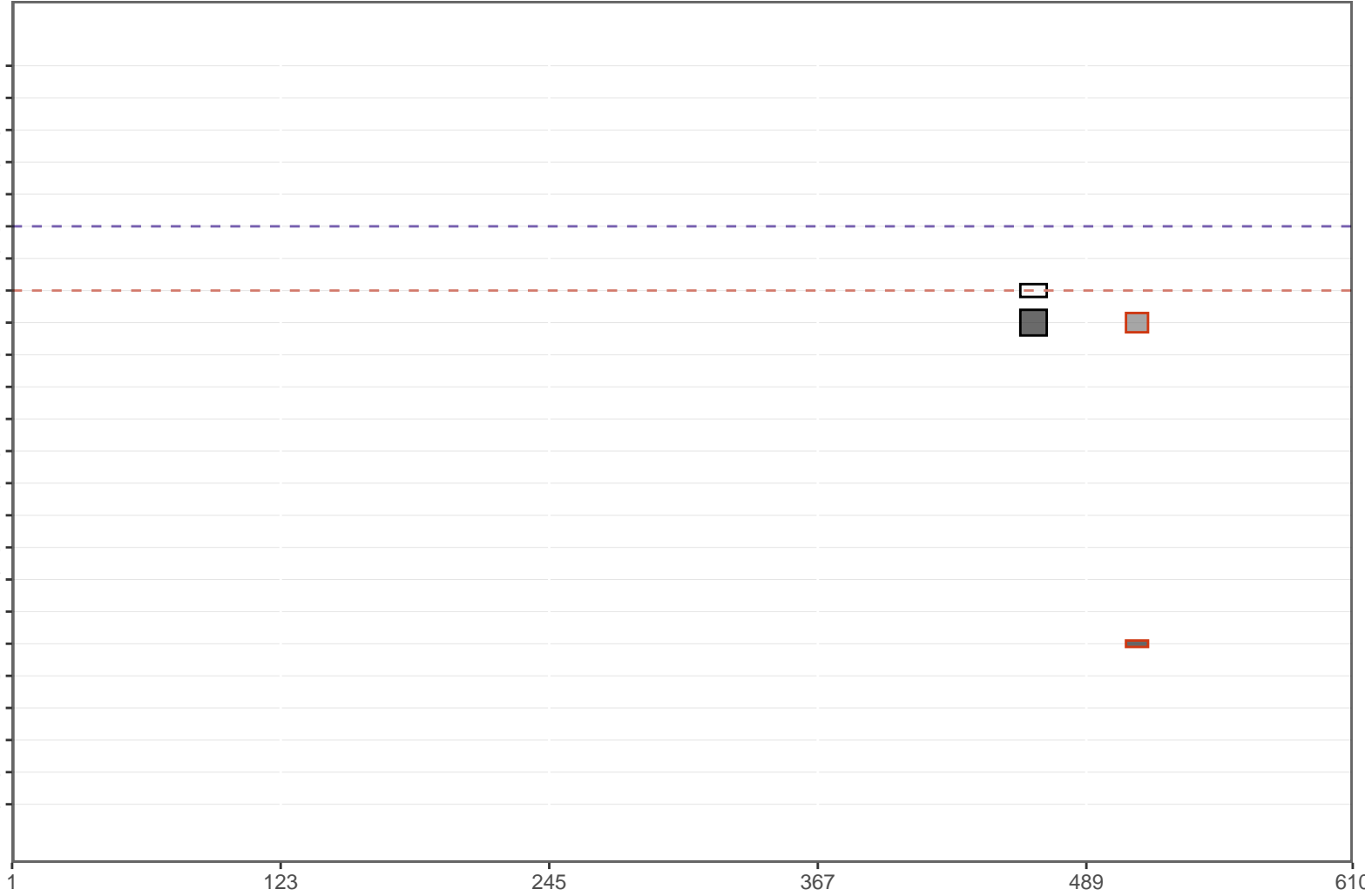
MW indication



Molecular weight

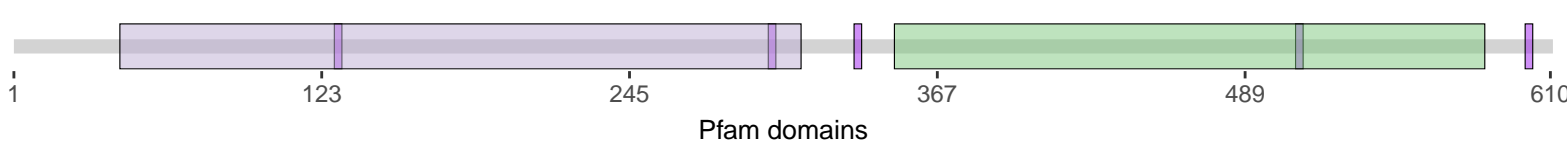


Gel Slice



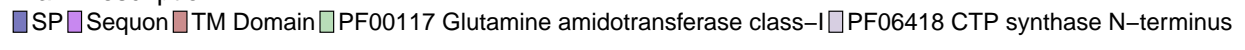
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IPLLLNQSAIDAAKGLDLSVAHWYDLGEWTRRAETSNDITKSVSIAMVGYKGLTDEYLVVKKALMKADIAGSLKPSIDWAAASDLEDDTANLPEAHAAAWKTLRGAAGLVLPGGFDGRGVKGMMLAARVARENSVPIYLGIGLGMQGVIEFARVSLHLEKANSEEFDPQTFVRFVFMPEQSKTHMGSTMRLLGSRRTLFRTPDGTALNLYNSEVYDERHRRHYEVNPEVGSLEEAGLKFVGRDESGNRMIELELPHDPFYGVGQHFPEFKRPRGRPSAPFLGLVLAJ

NbL16g06550.1 glycolipid_transfer_protein_1 [MW = 22.34 kDa]

No. of times detected



log(intensity)



Values from



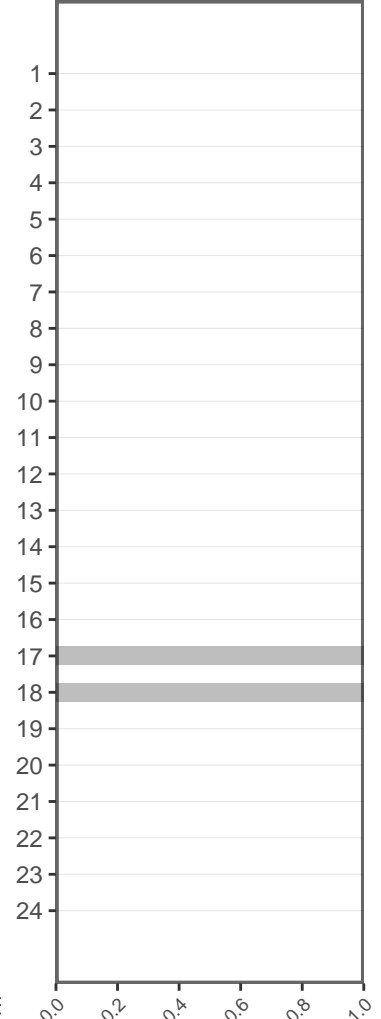
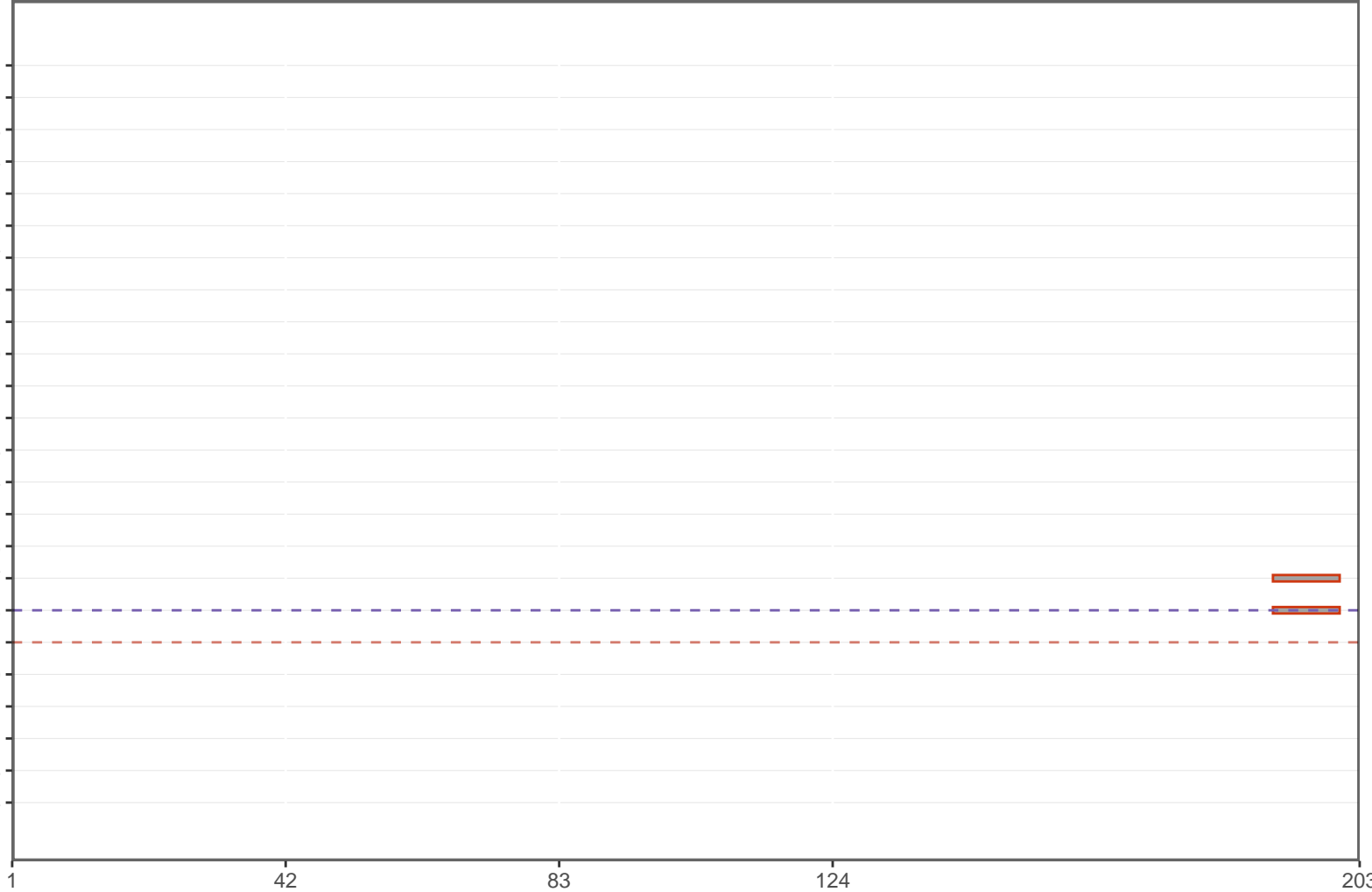
MW indication



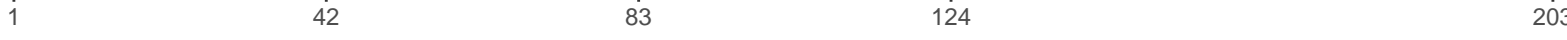
Molecular weight



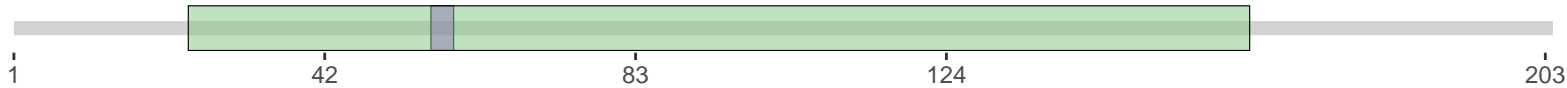
Gel Slice



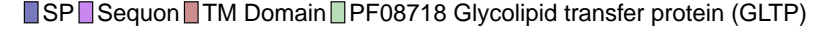
Protein length



Pfam domains



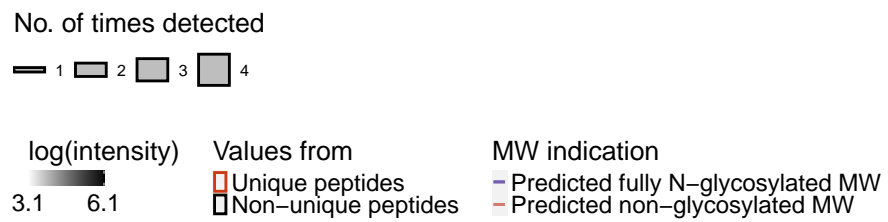
Pfam Description



Protein sequence:

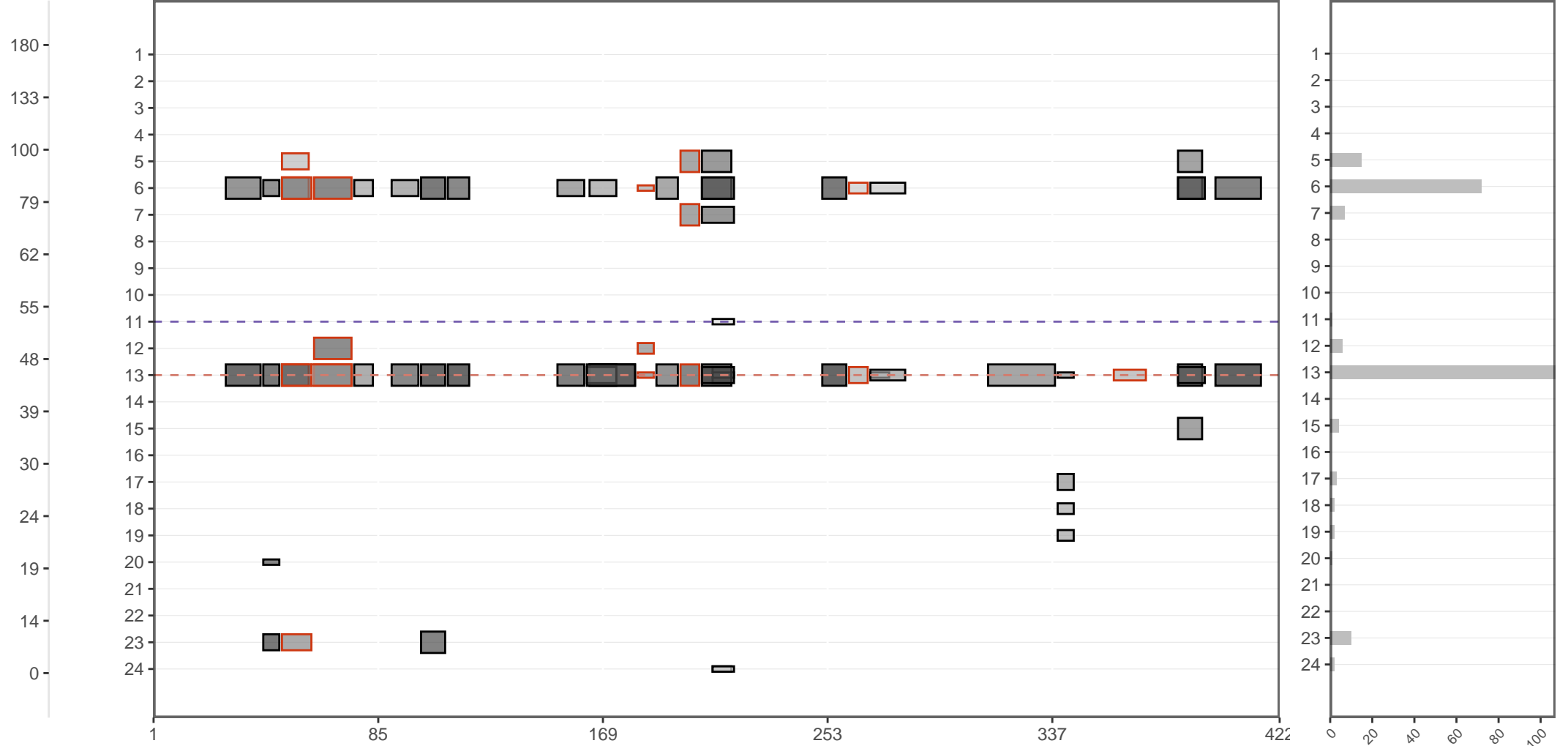
SCTCTGLLWLRAMDVFLVFRINLLEHGDAWAMGAGSDSIVKTLKFKHGWLABSSFSVAMKLPDRKRFMEVIGTGDSDMGQFCITTFSPLEENHKFLAVGMDDLKAS

NbL16g06530.1 succinyl-CoA_ligase_[ADP-forming]_subunit_beta_mitochondrial [MW = 45.15 kDa]



Molecular weight

Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description
 SP Sequon TM Domain PF00549 CoA-ligase PF08442 ATP-grasp domain

Protein sequence:

KVYDGLSPKVAIDRNDSEGVKLYLKFQESDCTMLEINPLAETSQNKLVADAKLNFQDINAAYRQKDFSLRDSGGEDPREVAAKADLNHYGLDGEKGMVNGAGLAMATMDIKLHGTRNFVLDVCGNATEGQVVEAFKLTADKVKAILNFGGIMKGVFIASGIANAAKGAQKVPVVRLEGTNVEQGRILKEGGMTLTAEEDLDAEKAVKALV

NbL16g06510.1 60S_ribosomal_protein_L23 [MW = 15.01 kDa]

No. of times detected



log(intensity)



Values from



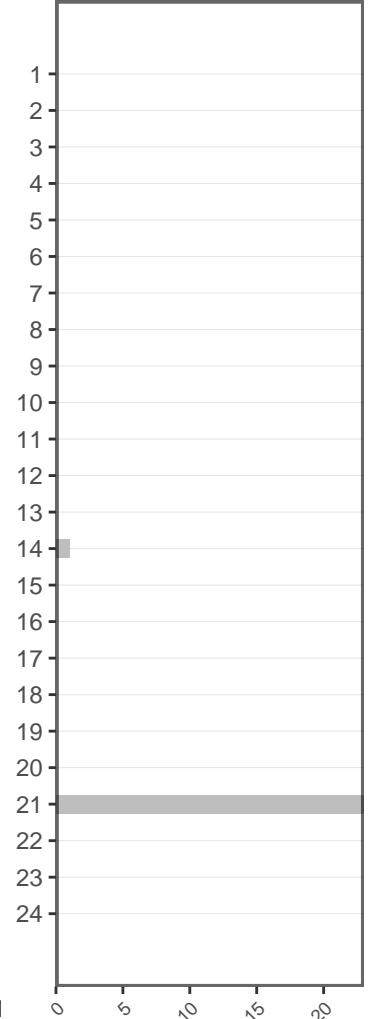
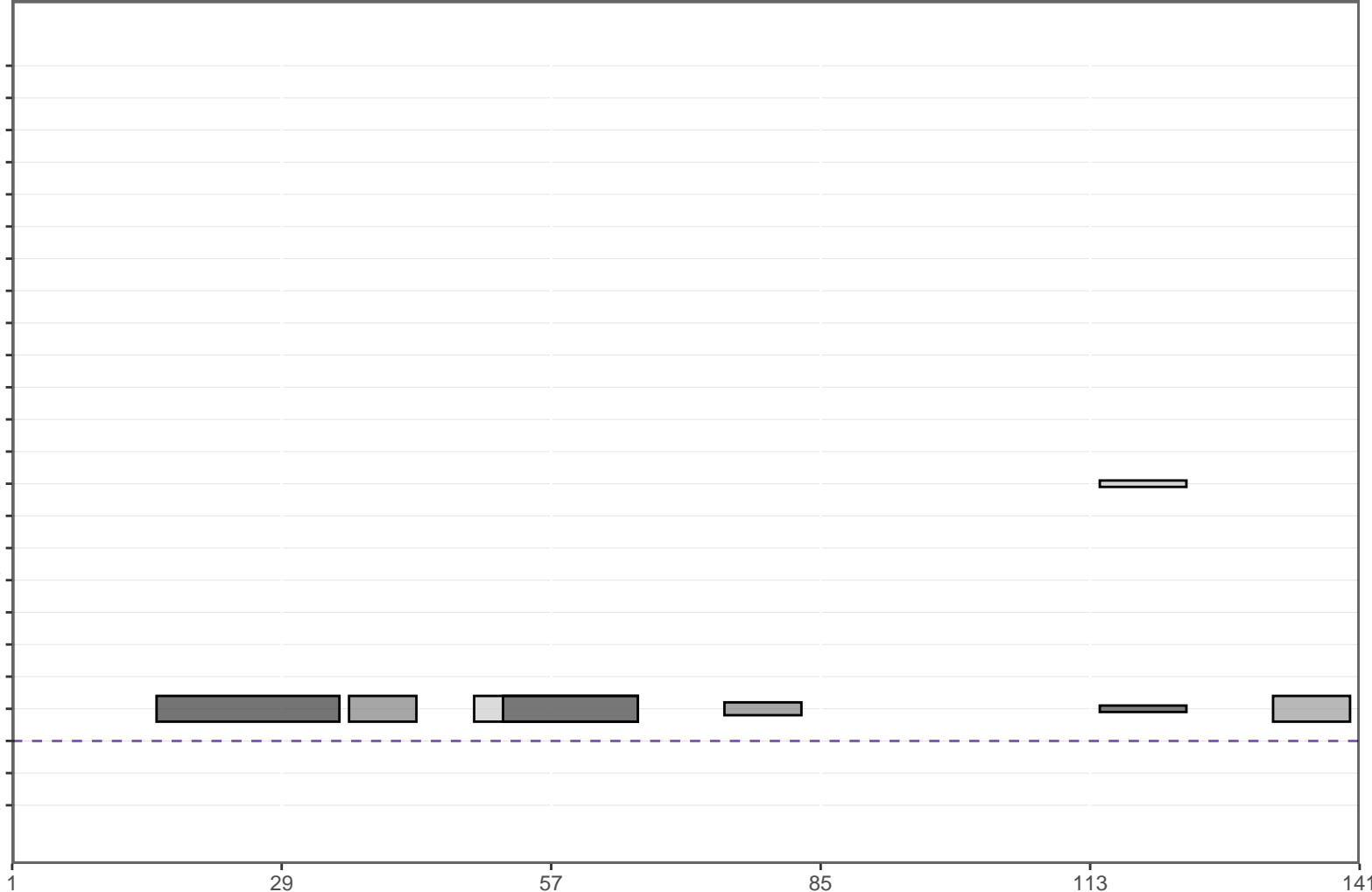
MW indication



Molecular weight

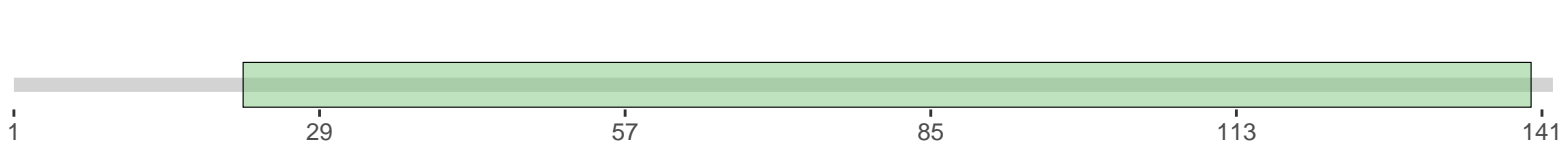


Gel Slice



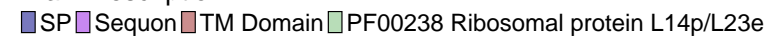
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DMVIMATVYKGGKPLRKKVMPWVVRGRKPKWRKDGVMYFEDNAGVIVNPKGEMKGSATGPIGKECADLWPRISAANAVV

NbL16g06460.1 putative_G3BP-like_protein [MW = 49.47 kDa]

No. of times detected



log(intensity)



Values from



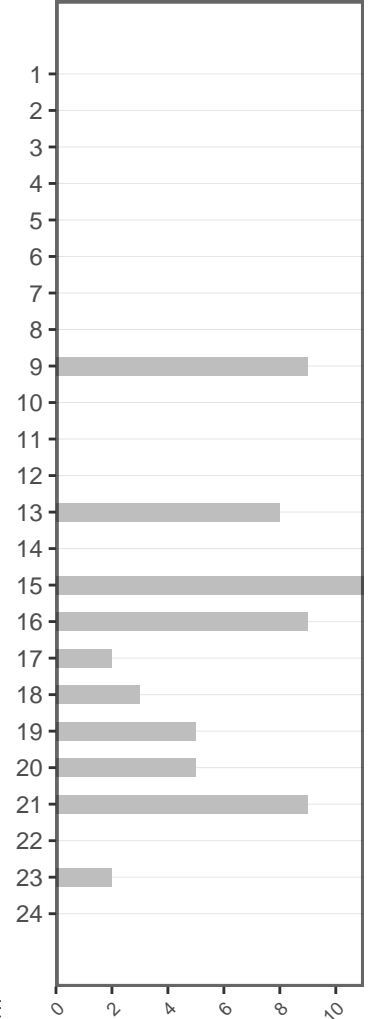
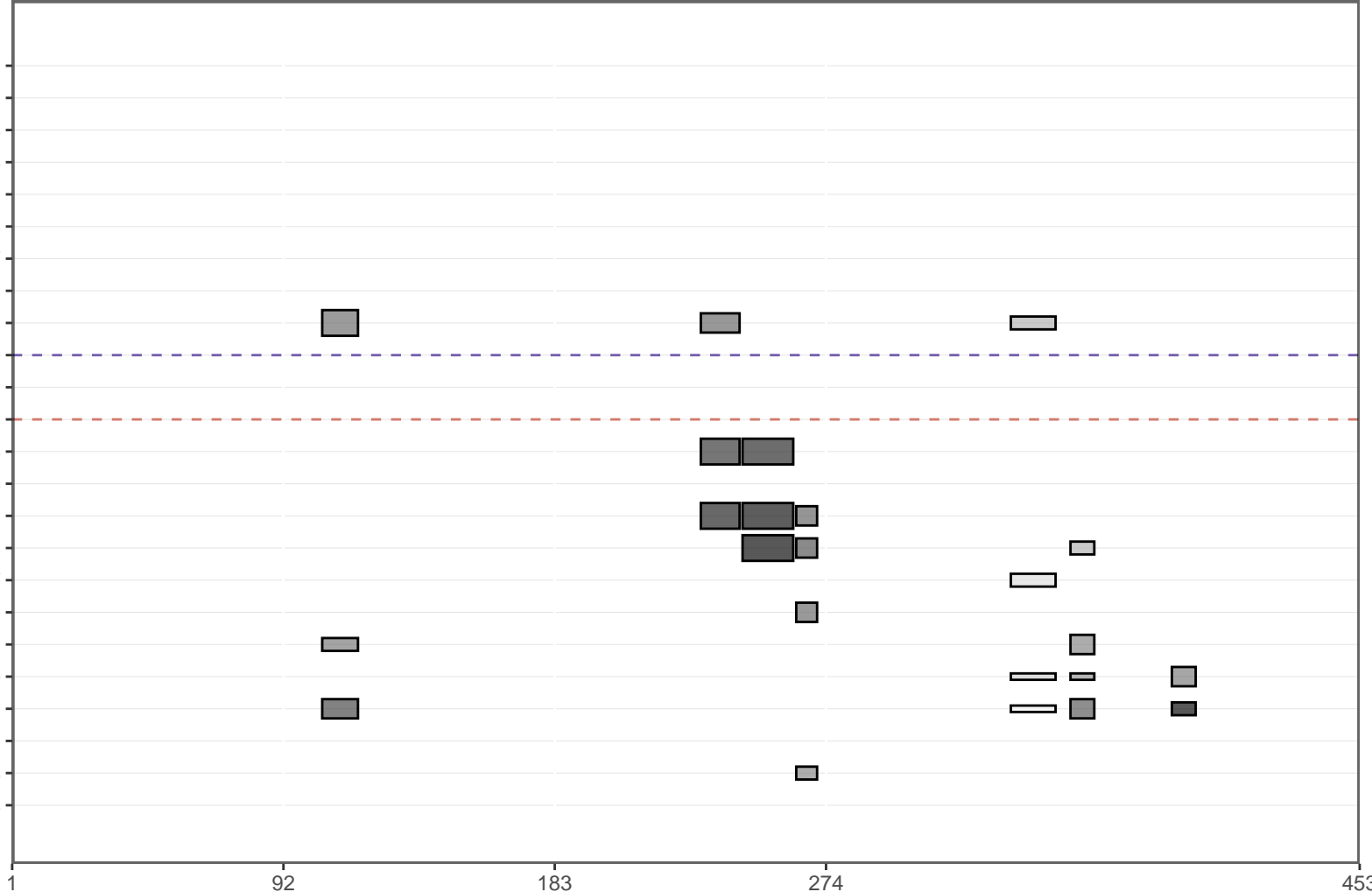
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- PF02136 Nuclear transport factor 2 (NTF2) domain

Protein sequence:

IEAEVPEAAHLREFTTQVRISLEESTALPNVAVVPEPEPAAEPEVGEPSKFSYAAIARAFKPKAFPSIRIQPSTYKTAAPPVSEWQPPVGEQSHMPAAVAVSLDTEEGSSGEGEPKSYVYRNLPSTVSLDLGERKFKGKIDGVFLRNRTDGVGVAFVFEVEVGVQNAKASPIQLAGROVYIEERRPSHNGISRGGGRSGSGRGRGPRGGRFTFGAGSNPDDRWNSNGFRGI

NbL16g06390.1 photosystem_I_reaction_center_subunit_IV_A_chloroplatic [MW = 15.05 kDa]

No. of times detected



log(intensity)



Values from



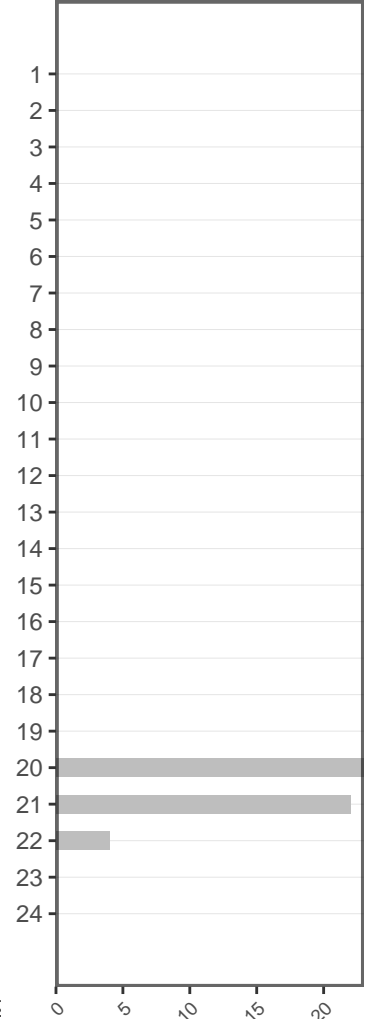
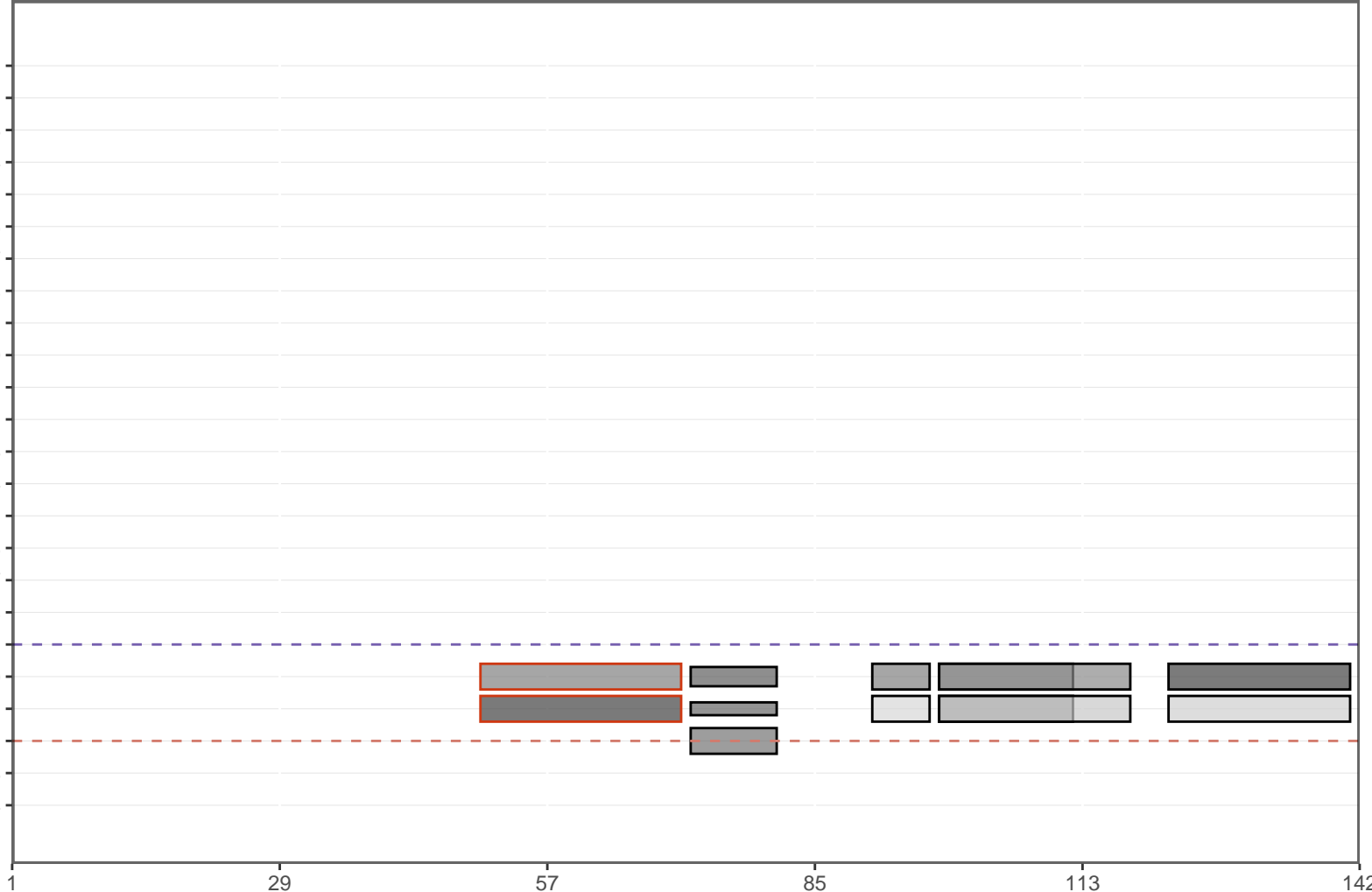
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LAATAEPAEAPYKAAKPPPGKRGTRVRLRKEEYWKGTGSVAGDGDPNTRYFVVRFNKVNANVSTNNHALDEIEEKV

NbL16g06360.1 GDSL_esterase/lipase_LTL1-like [MW - SP = 36.96 kDa]

No. of times detected



log(intensity)



Values from



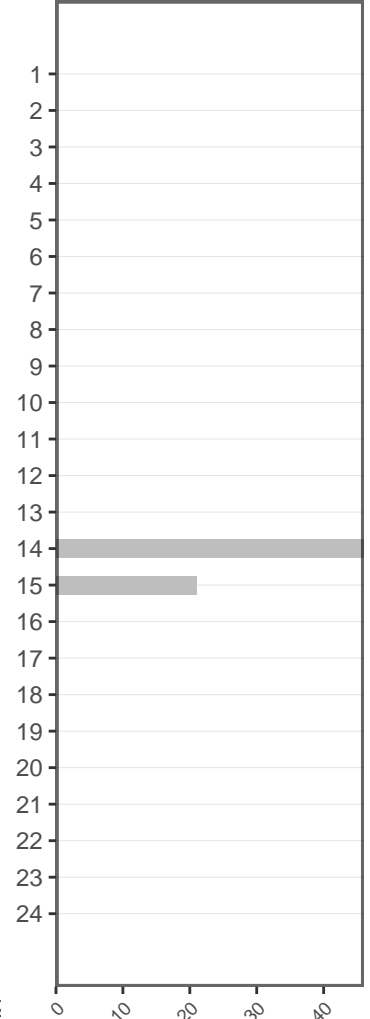
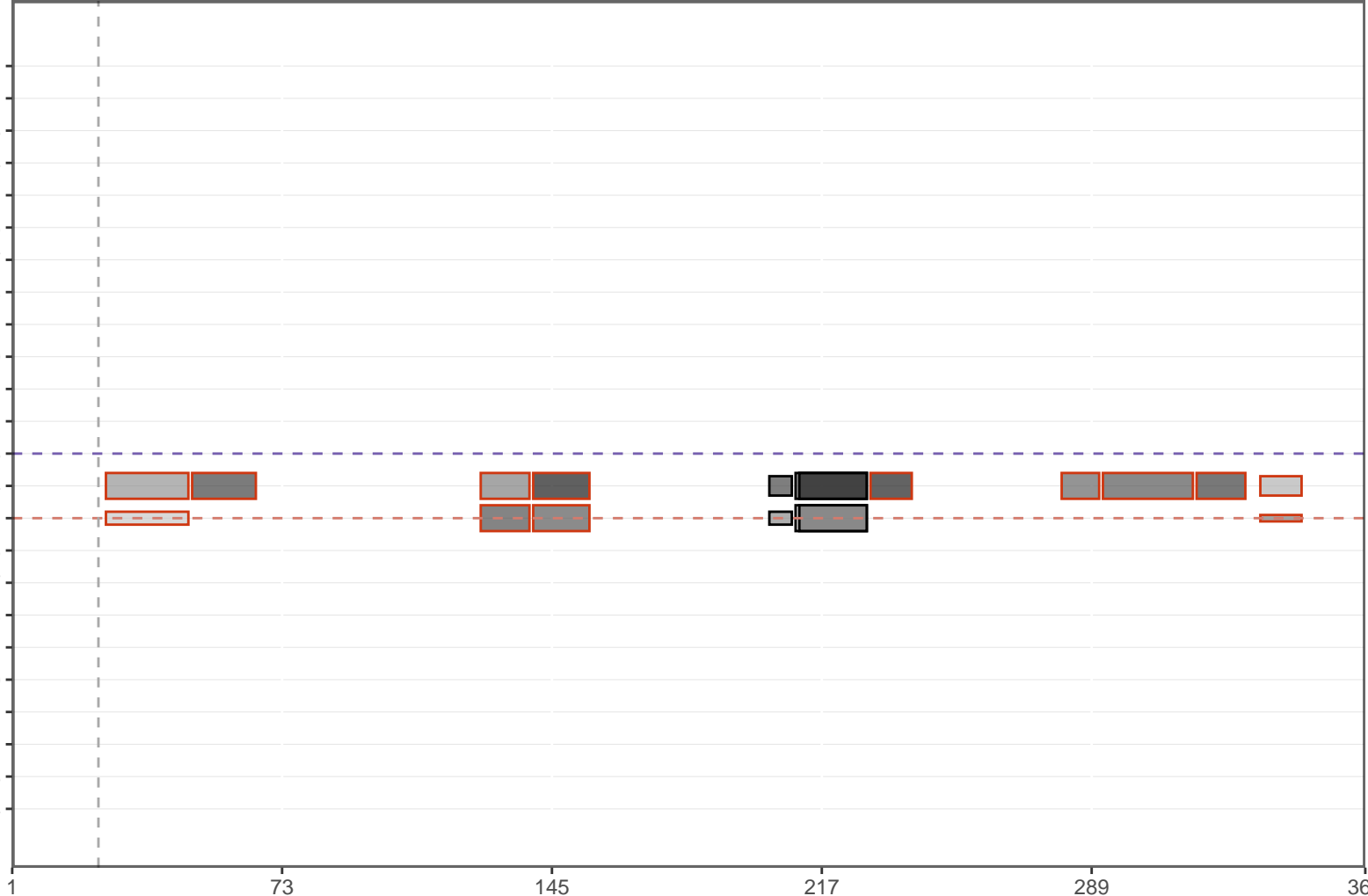
MW indication



Molecular weight

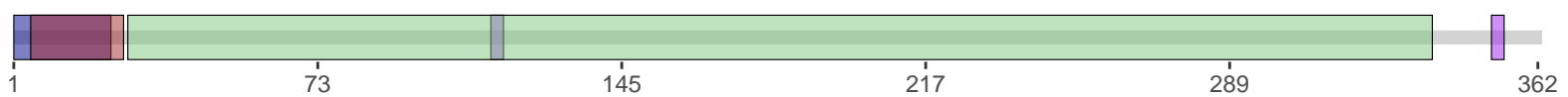


Gel Slice



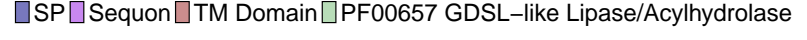
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NYFFTPV[SARRLQWLNLEDVSVHSEYKILMRVLDGARRVAVTGGPLGQVPSLARSNSGCEAEEPRGRASAFNPLVEMIGSLNGELGSDVFAANAVDMGNDHFRDPQAFGFTTSKVAAGCGGQPNYNGVGGSAANLGNPRDVAFAFDWPHPTERANKIVQFTFTGSDKYMTFMINLSTIMADSL

NbL16g06330.1 26S_proteasome_regulatory_subunit_4_homolog_A [MW = 49.5 kDa]

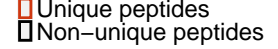
No. of times detected



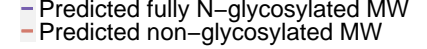
log(intensity)



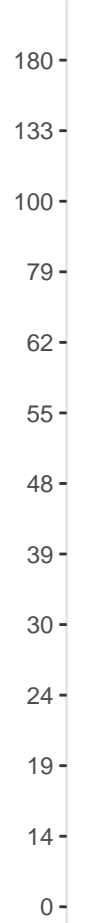
Values from



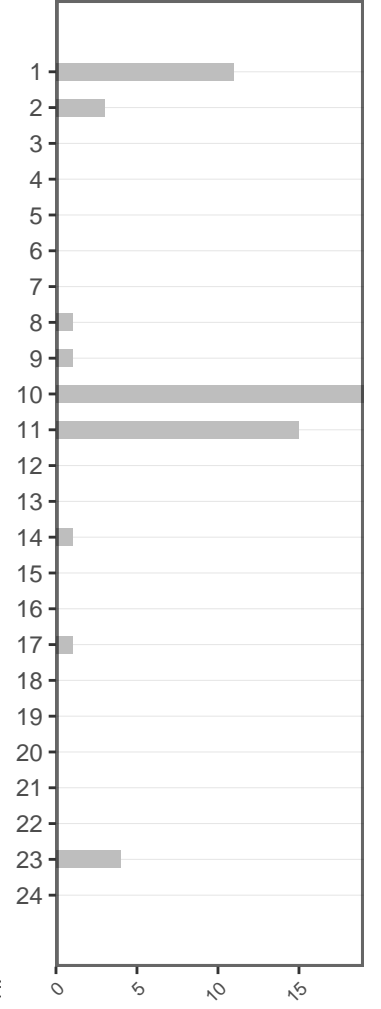
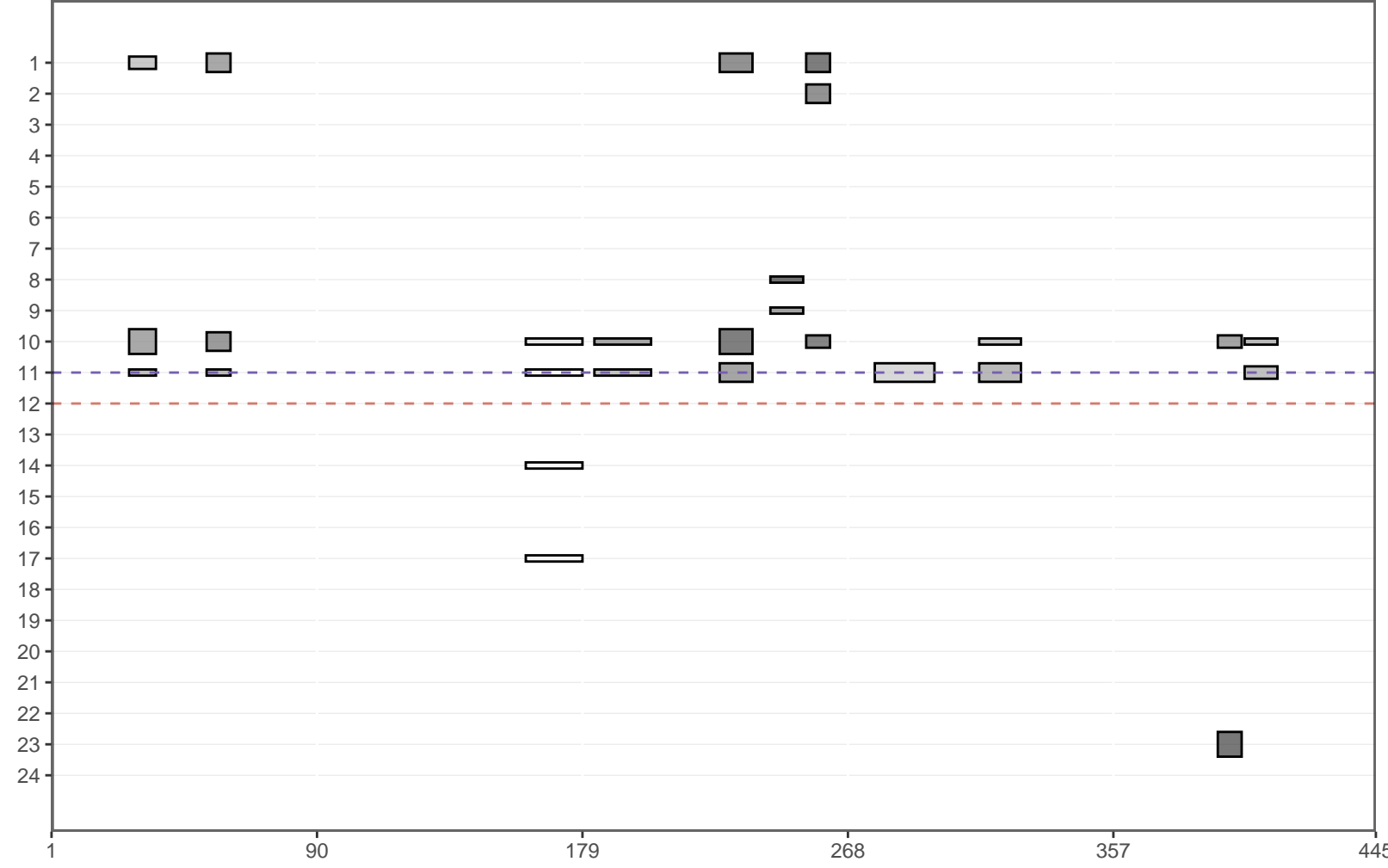
MW indication



Molecular weight

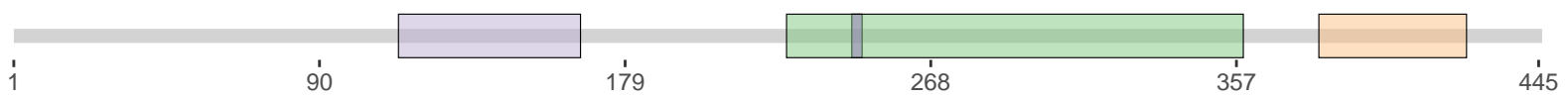


Gel Slice



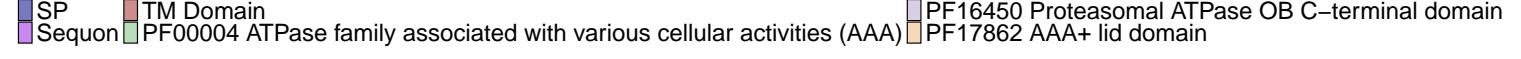
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

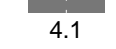
[ELPLTHPELVEDIGKPPKGVILVGEPTGKTLAKAVANSTSATFLRVVSGSELQKYLGDGPKLVRFLFRVADLSPSIVFIDEIDAVGTRKYVDHSGGERIKRTMLELNLQDGFSDRSQVVLATNKIESLDLALLRPGRIDRKIEFLPKTKRRRFQIHRTARMLADDVLEEFVMTKDFEFGADKAICTEAGLLALRRRMKVTHTPDFKAKDKVMFKKKEGVPEGLYM

NbL16g06310.1 probable_pectate_lyase_8 [MW - SP = 46.38 kDa]

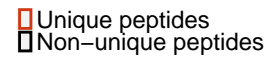
No. of times detected



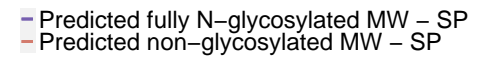
log(intensity)



Values from



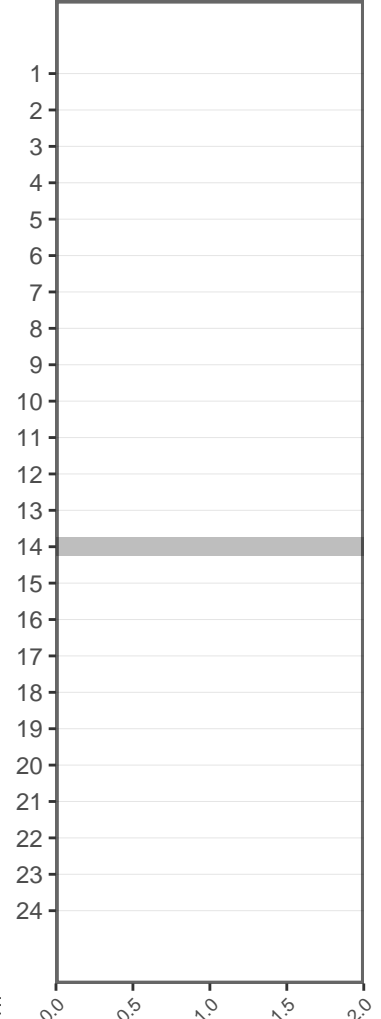
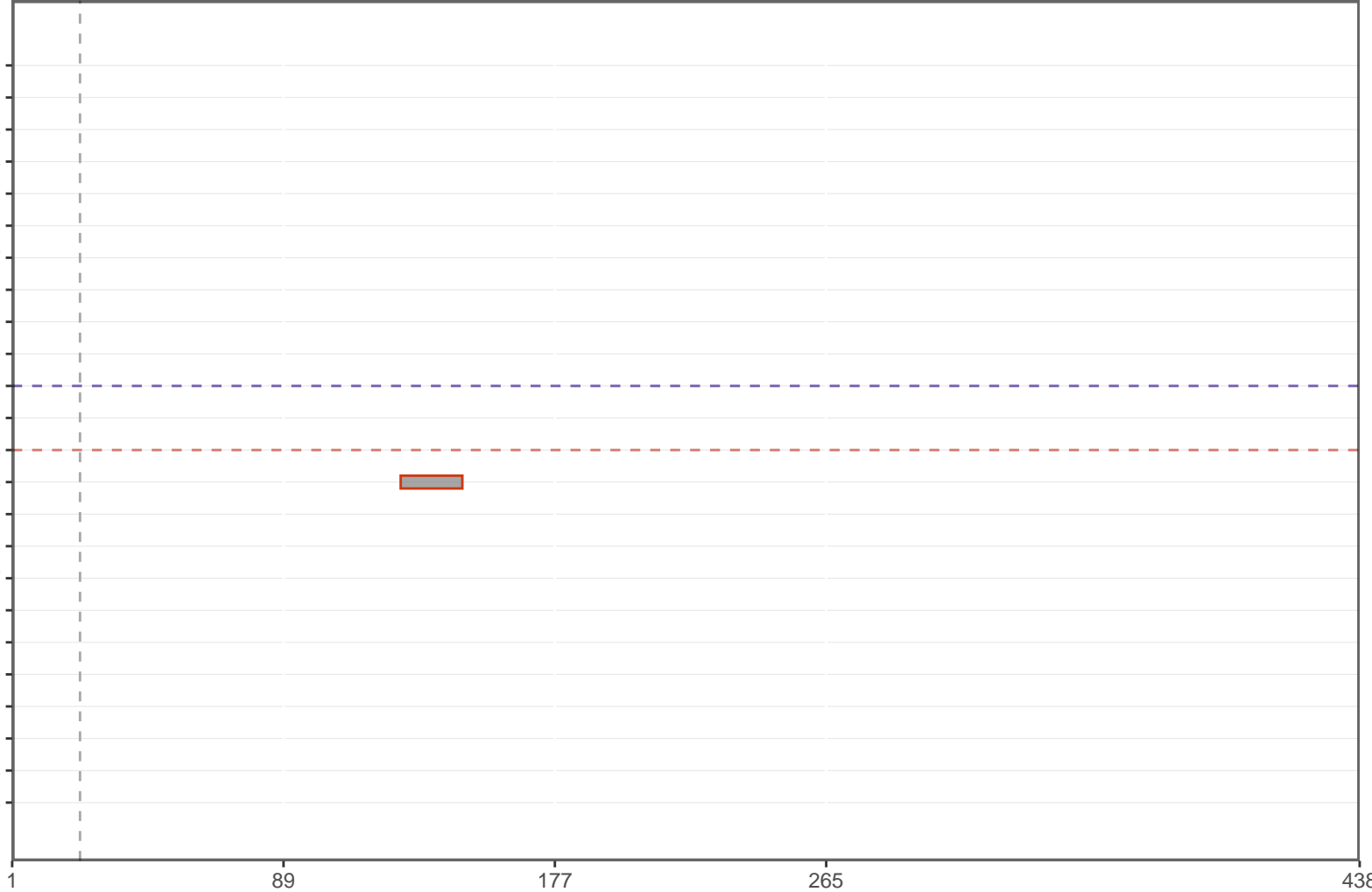
MW indication



Molecular weight

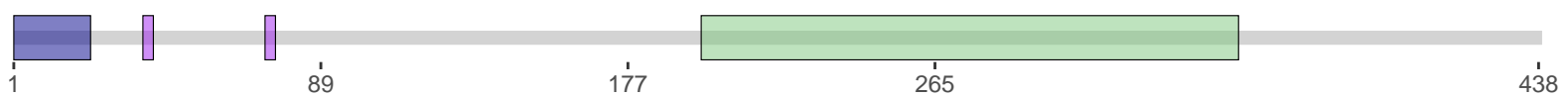


Gel Slice



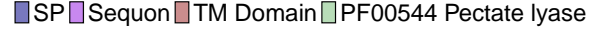
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

HHDCCKPTQNAMVRIKNSPSHYGWRITMADGGDGHIFGGSHHWIDHNSLGNACDGLDAMGSTATISNNVFTTHNEVILLGHSDSYHRDKVMQVTFANHFEGELGQRMPRRRHGDFYHVVNDKTHWEMVAIGGSADPTINSQGNRYLAPVNPFAKEVTKRIVPEPWEGSWKHWNVRSQGLMLNGAYFTASGRAAPRBYARASSLAAKGSSMVGSTITSNAGALSCHHGFC

NbL16g06060.1 oleoyl-acyl_carrier_protein_thioesterase_1_chloroplastic-like [MW = 42.06 kDa]

No. of times detected



log(intensity)



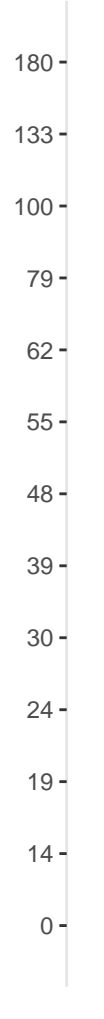
Values from



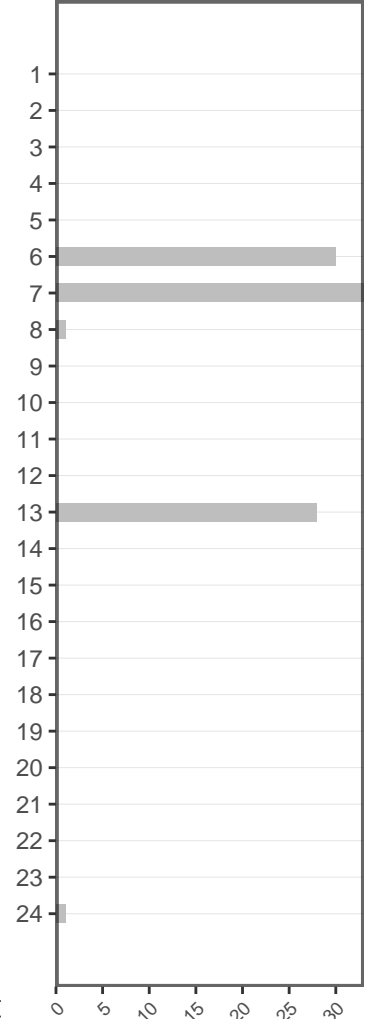
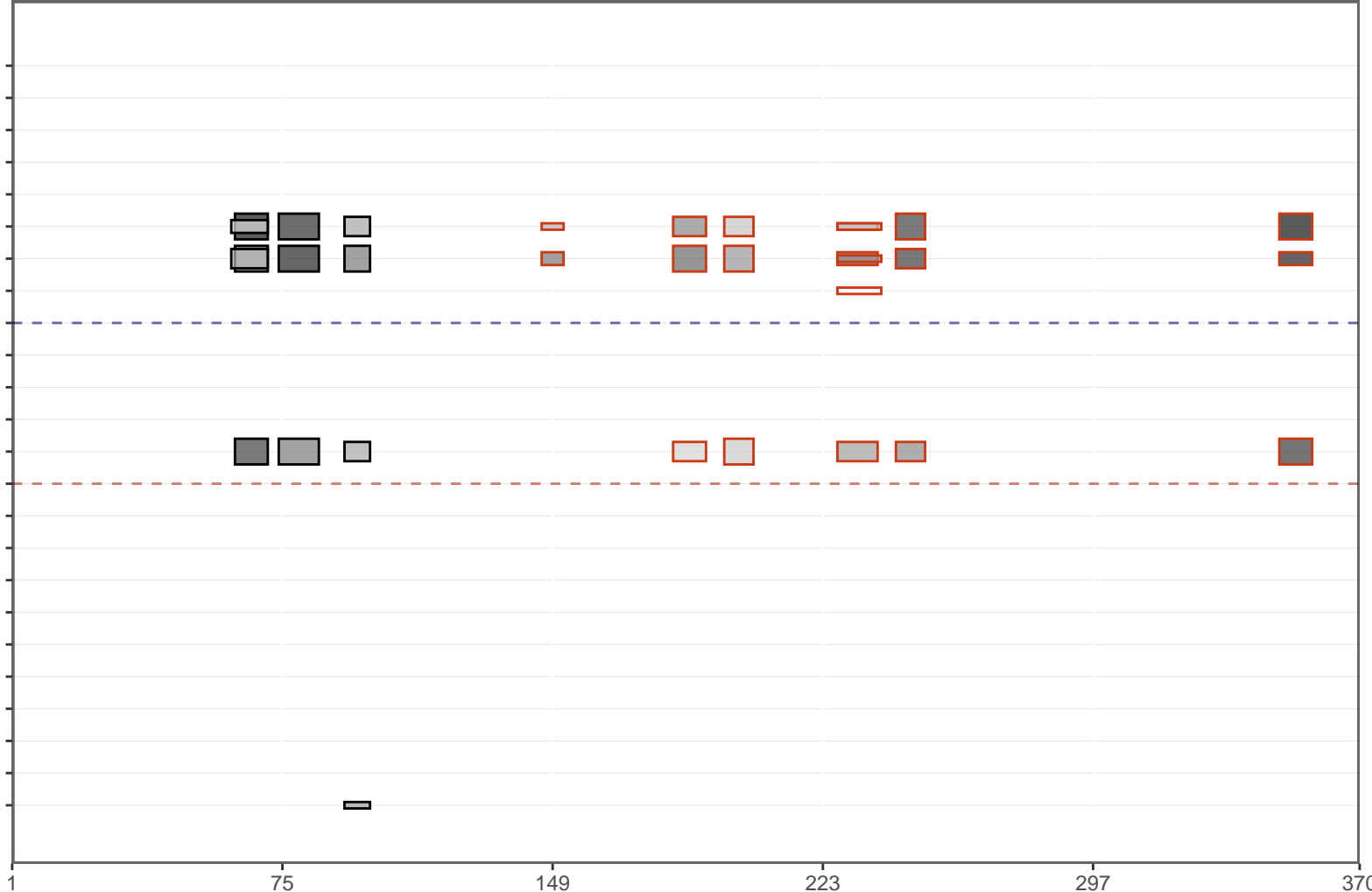
MW indication



Molecular weight

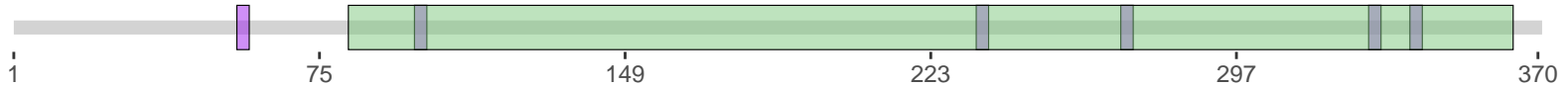


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

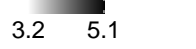
IGTRRDVILRDCATGSDVGRATSKWMMNGDTRRLRGLQVADEVREDELGYFFKELRLAFPEENNGSLUKKAKLEDPEYSGKGLVPRRADLMMNGHVNNTYVIGVWLESMPGEIDTHELETTEDVYRREGQHDVVVDSLSTVEPEIDAAASLEGAANGSGTAPKDKLNKFLHLRLLSDDGLENRGRTEWRKKPARI

NbL16g06030.1 galacturonosyltransferase_8 [MW = 65.39 kDa]

No. of times detected



log(intensity)



Values from



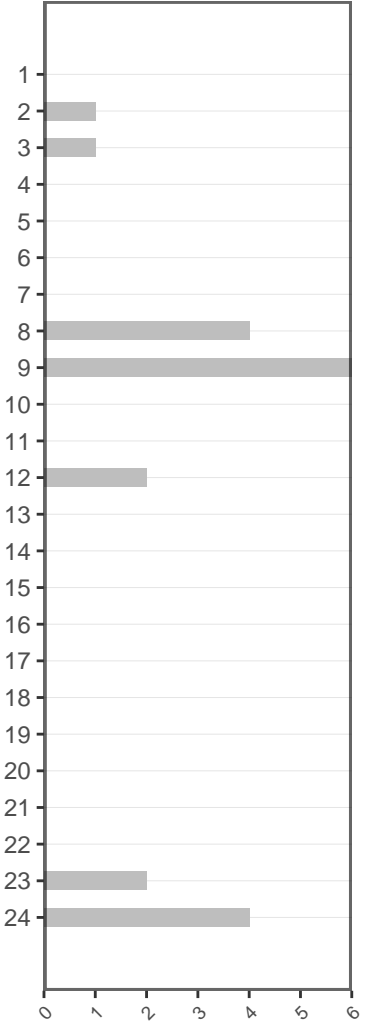
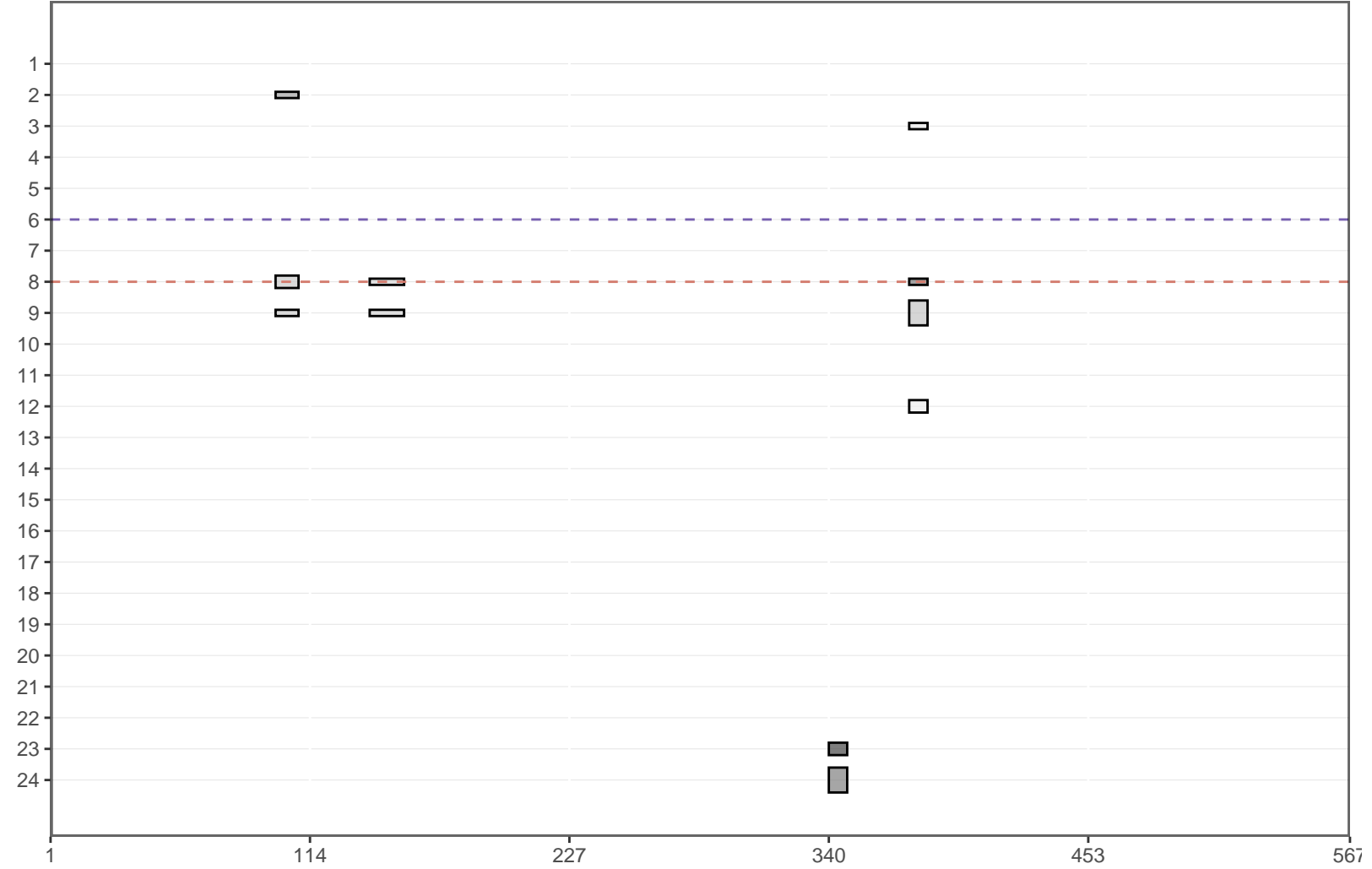
MW indication



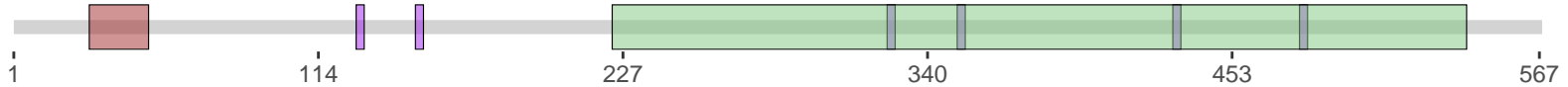
Molecular weight



Gel Slice

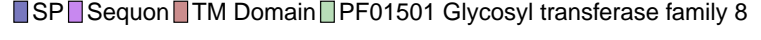


Protein length



Pfam domains

Pfam Description



Protein sequence:

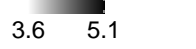
IAVHSHKDPKSYVFNHYTDKMLNGAMQVAFKMKDYNGAFIEKVEDEYKFLNSVYPLVKGLESALGGFYFENKLENATKDTTMMKFRNPKYLGINHRYFLPELYPKLHLRILFLDDVVYKDLTGLWIKIDMDGKVNQAVETGFGSFRHYAGYMNFSHPILKEKFKAGAWAYGMNFFDLDAWRREKLTETEEHYWQSLNENRLLWKLGLPLPLGLTYSTTKPLDKSWHVLGLGYNPDSMDEINAAVYHFNENGMKPKLDIAMNNGFRPLWTRKYDYENEYQACNF

NbL16g06020.1 putative_G3BP-like_protein [MW = 50.43 kDa]

No. of times detected



log(intensity)



Values from



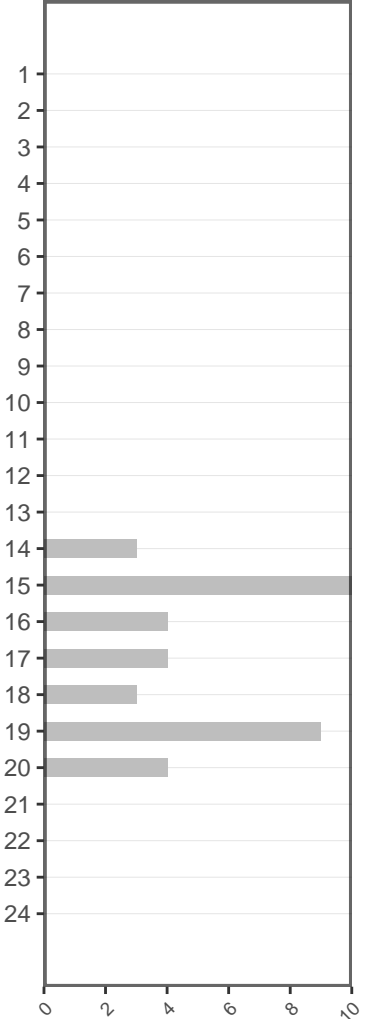
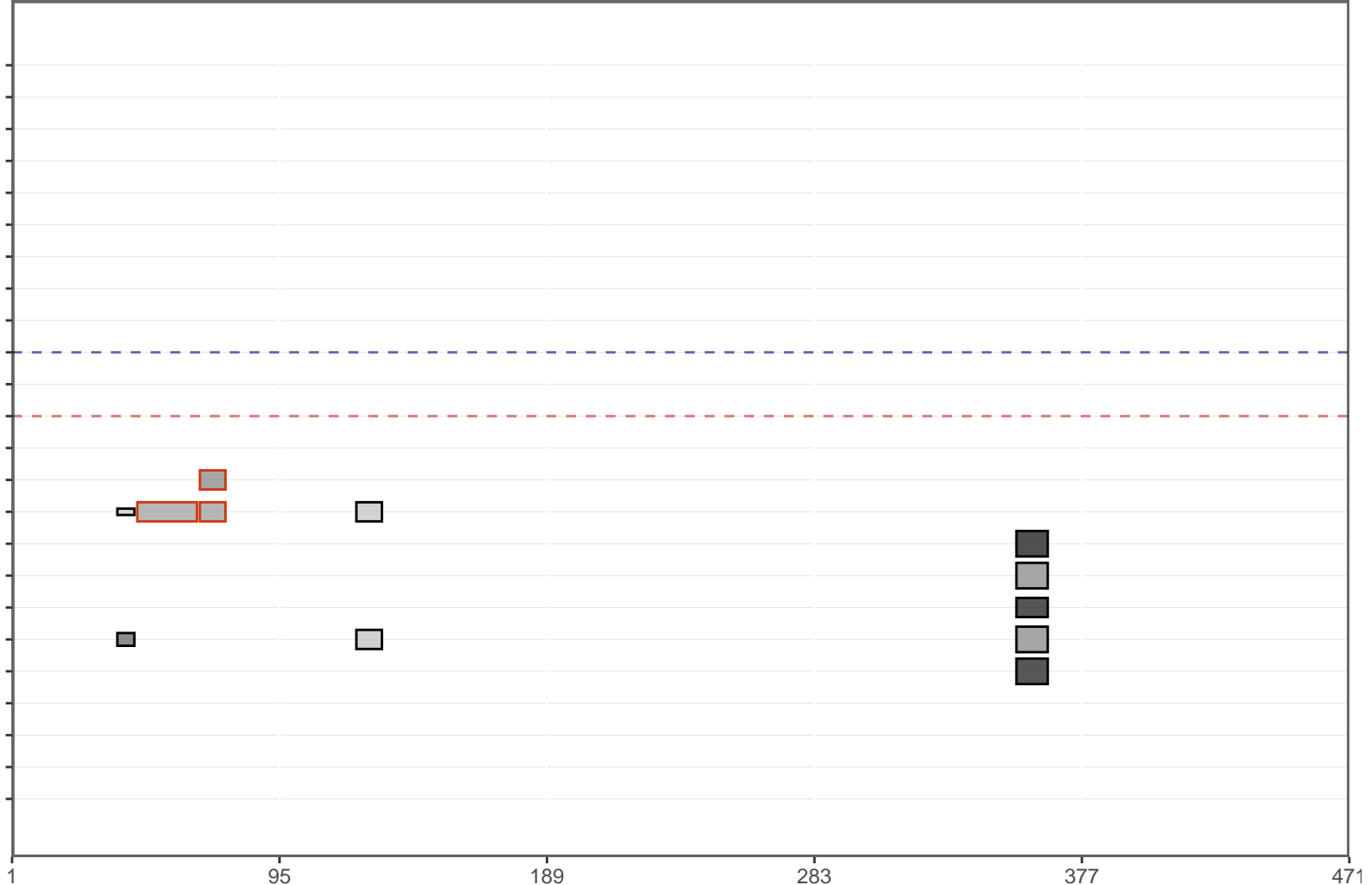
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- PF02136 Nuclear transport factor 2 (NTF2) domain

Protein sequence:

SEVPKKSYASIVMHLKESAAATFSPPAPBRKPMKRIEQVNGPDATDGPVSSSDVYNNDFEGEAADGYSYIKGLPMSATVALLADEFKKFGPKNGKQVRSNRNGGGFCGFGFVEFEVESAVQKAEASPLUGSRQAVVEEKRTNSRGNTGRGFRGSGRAGFRINDGGRGRGTYYGGRGYGRDDFNGRNEFRNRGGGRGSSNRGGDGYRRDNTDGRMNHGGGVNNGTAAAPRYSAAA

NbL16g05940.1 peptidyl-prolyl_cis-trans_isomerase_FKBP62-like [MW = 64.08 kDa]

No. of times detected



log(intensity)



Values from



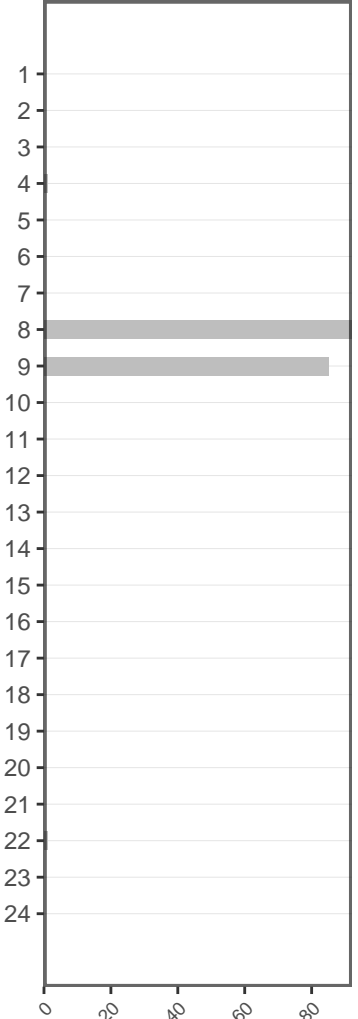
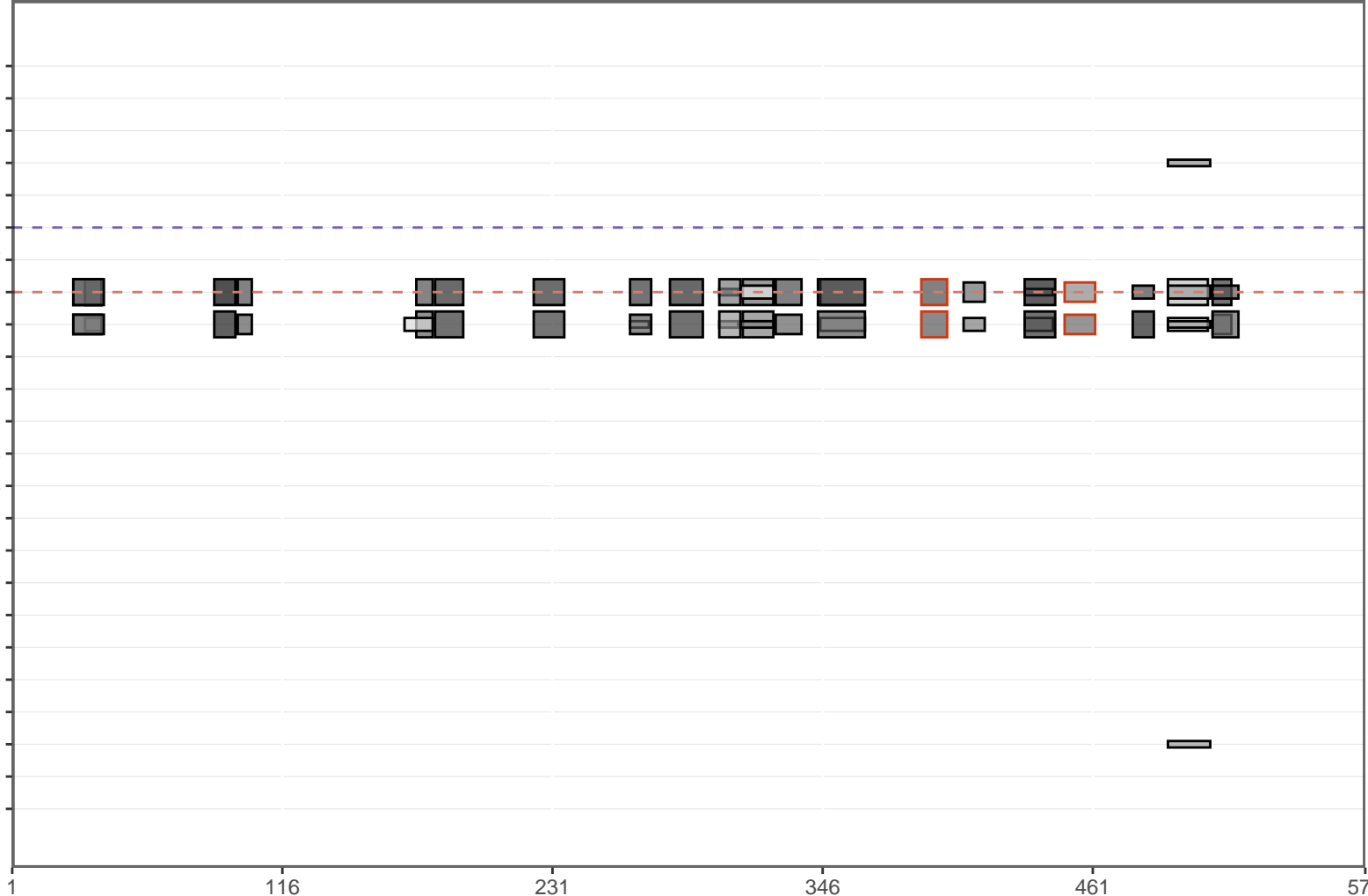
MW indication



Molecular weight



Gel Slice

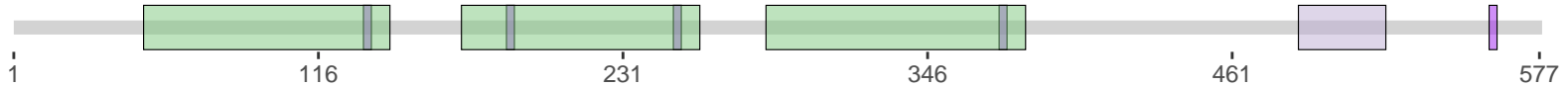


Protein length

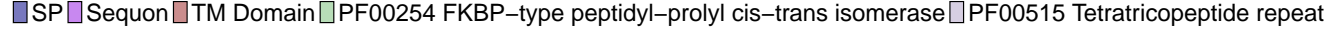


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VVKLKEGEYKPNEGAVKLLKGLGDTVFIRKKGHDGENEDELFEFKTDEEGVIDGLDRAVMTMKKGEVALLTAPEYAFGSSSEKGLDLVFPNPTVHYEVELVDFVNDKESWDMNTQEKIEAAGKHKKEGNALFKAGKYTRAKRYEKAANKFIEYDTSFSEEEKGSKALTSIGNLNAAGKLLKLDKPYGAEKLGCTKVALEESTNWKALYRRADAYINMADLDLAEFDKKALEDPPDRNRDKLEYKALKDKVYKFNKDKDAFYGNMFAKLNKLETANSKSAKPEPE

NbL16g05930.1 40S_ribosomal_protein_S8 [MW = 25.02 kDa]

No. of times detected



log(intensity)



Values from



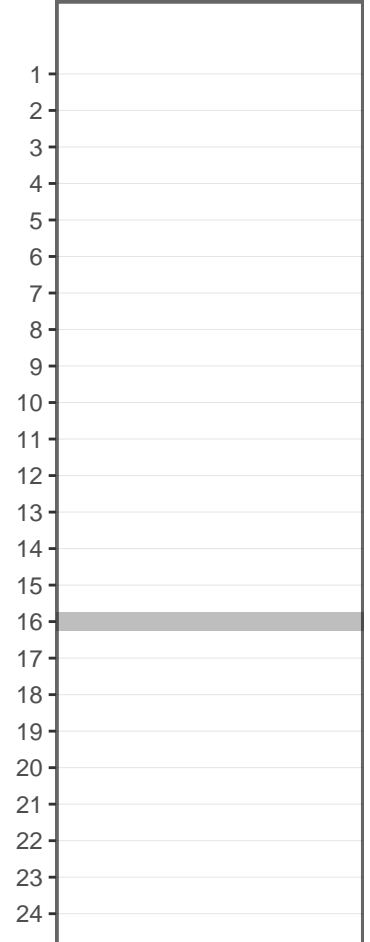
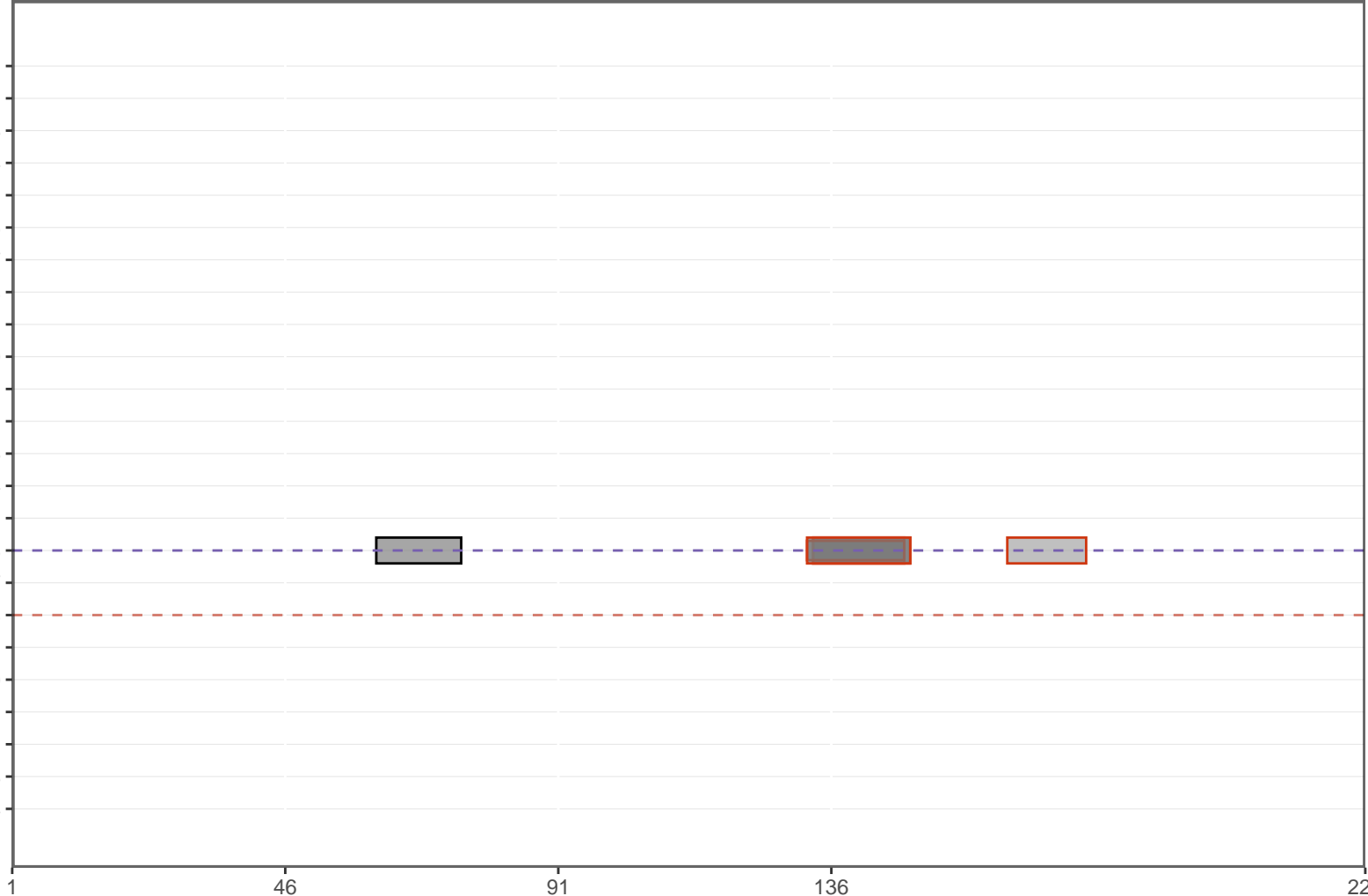
MW indication



Molecular weight



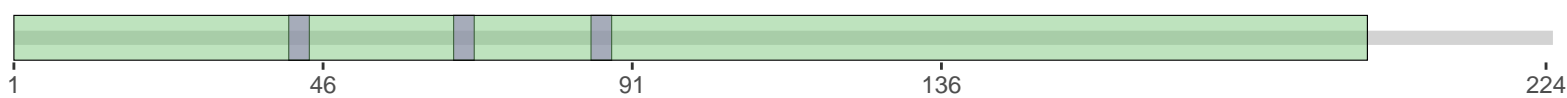
Gel Slice



Peptide counts over 4 repeats

1 46 91 136 224

Protein length



Pfam domains

Pfam Description



Protein sequence:

SAIVQVDAPFKQWVLFQHYGVDRKHKGAANKKETAEEEGEGAAAAEETKKNHVARLKRQKDRKLDHLEEGFGAGRLADISRPGQRGRADGYILEGKELEFYMKLGNKKKAGAGAA

NbL16g05790.1 protein_AE7-like [MW = 17.72 kDa]

No. of times detected



log(intensity)



Values from



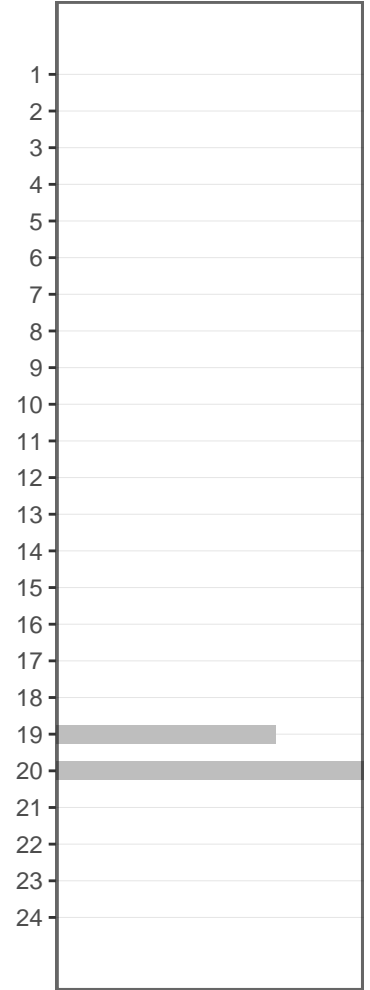
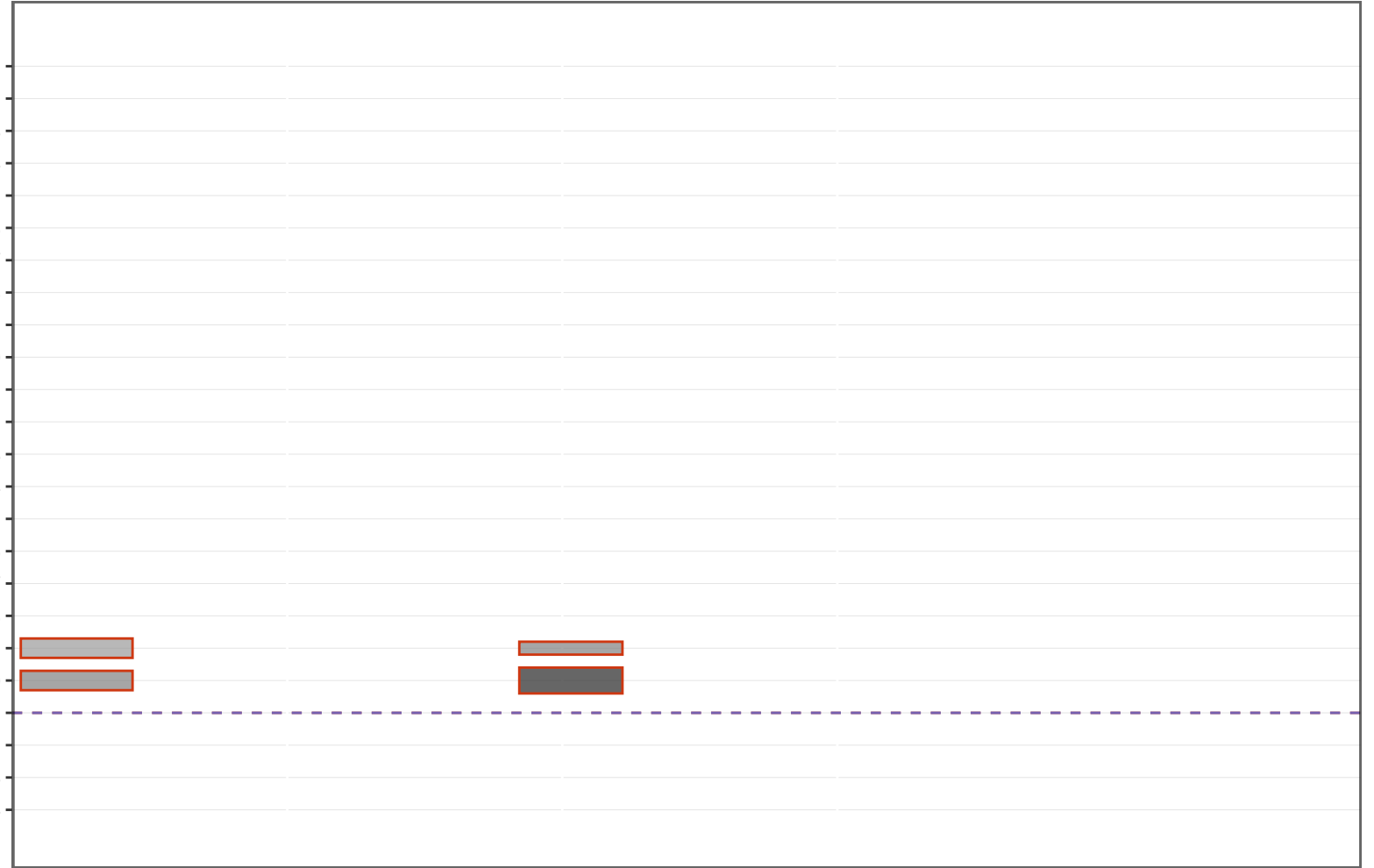
MW indication



Molecular weight



Gel Slice

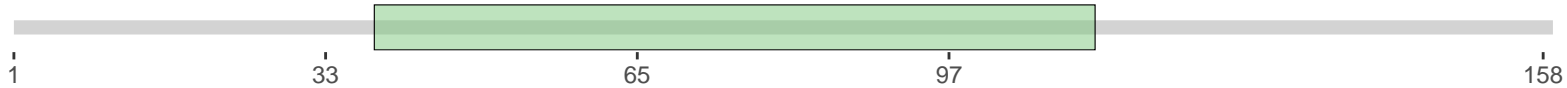


Peptide counts over 4 repeats

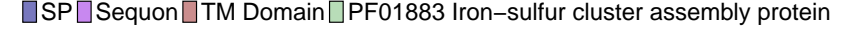
Protein length



Pfam domains



Pfam Description



Protein sequence:

VDDEKSYR/TFPTVEHDEMATVIGLGRVQLMRSLPRWYVDHVPQTHATEAAWKNGLNDRKRWAALENPLVDMVDGGLARFE

NbL16g05780.1 serine_carboxypeptidase-like_20 [MW - SP = 53.01 kDa]

No. of times detected



log(intensity)



Values from



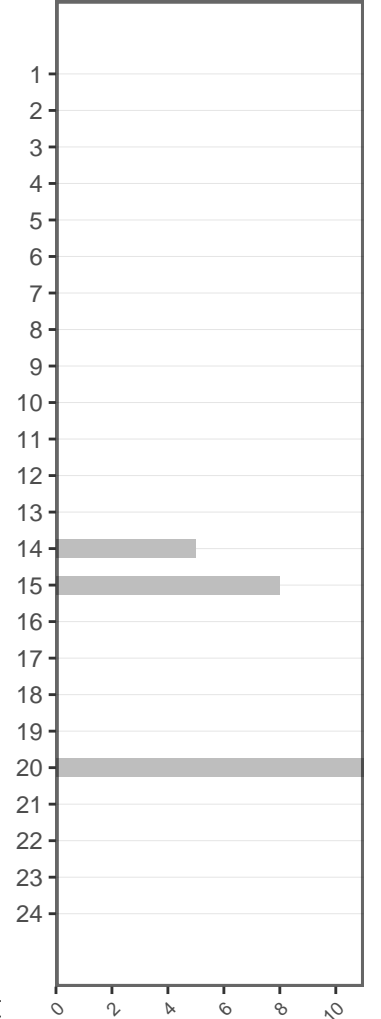
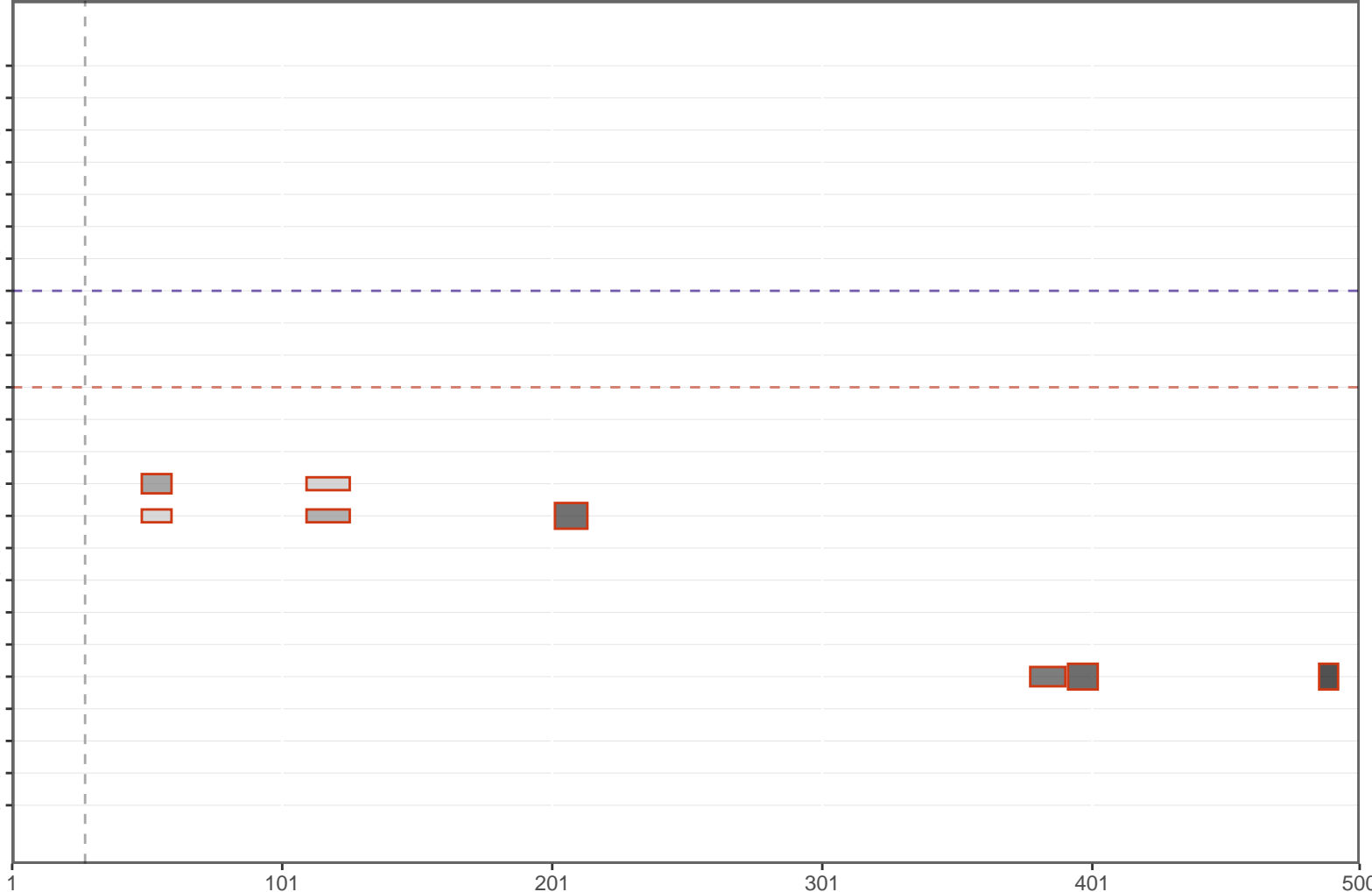
MW indication



Molecular weight

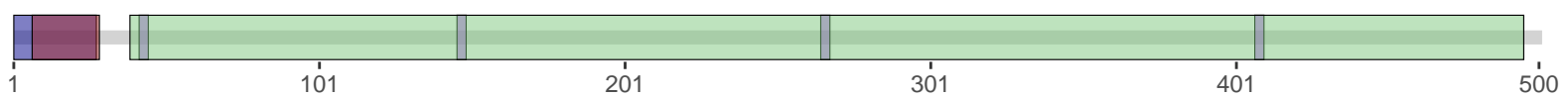


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

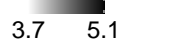
MGLSDELFEVYTLTGNGNFPANNGSDKLSGVDGQWADLNLYDILEFCYHSKSDSTVSTGNRLPMSFRKLGETERLPVRRKRMFGRAWFFRAPVREGHVPTWPELNGVDPVPCGTDORWATAWLNNEEVKRAIHKETTIVGIPWELGTGKHLHDSGSMIKYHKNLTARGYRALYSGDHDMDVFPFTGSEKWTRSLGYYWVDWRPWWVEGVAGYIGGYDNNLFLTWKAGHTVPEYKPREALAFYARWLEGKN

NbL16g05660.1 60S_ribosomal_protein_L5 [MW = 34.67 kDa]

No. of times detected



log(intensity)



Values from



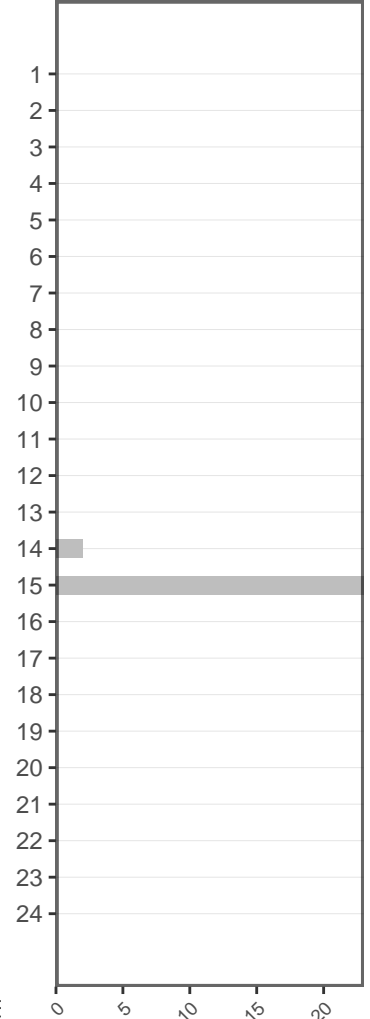
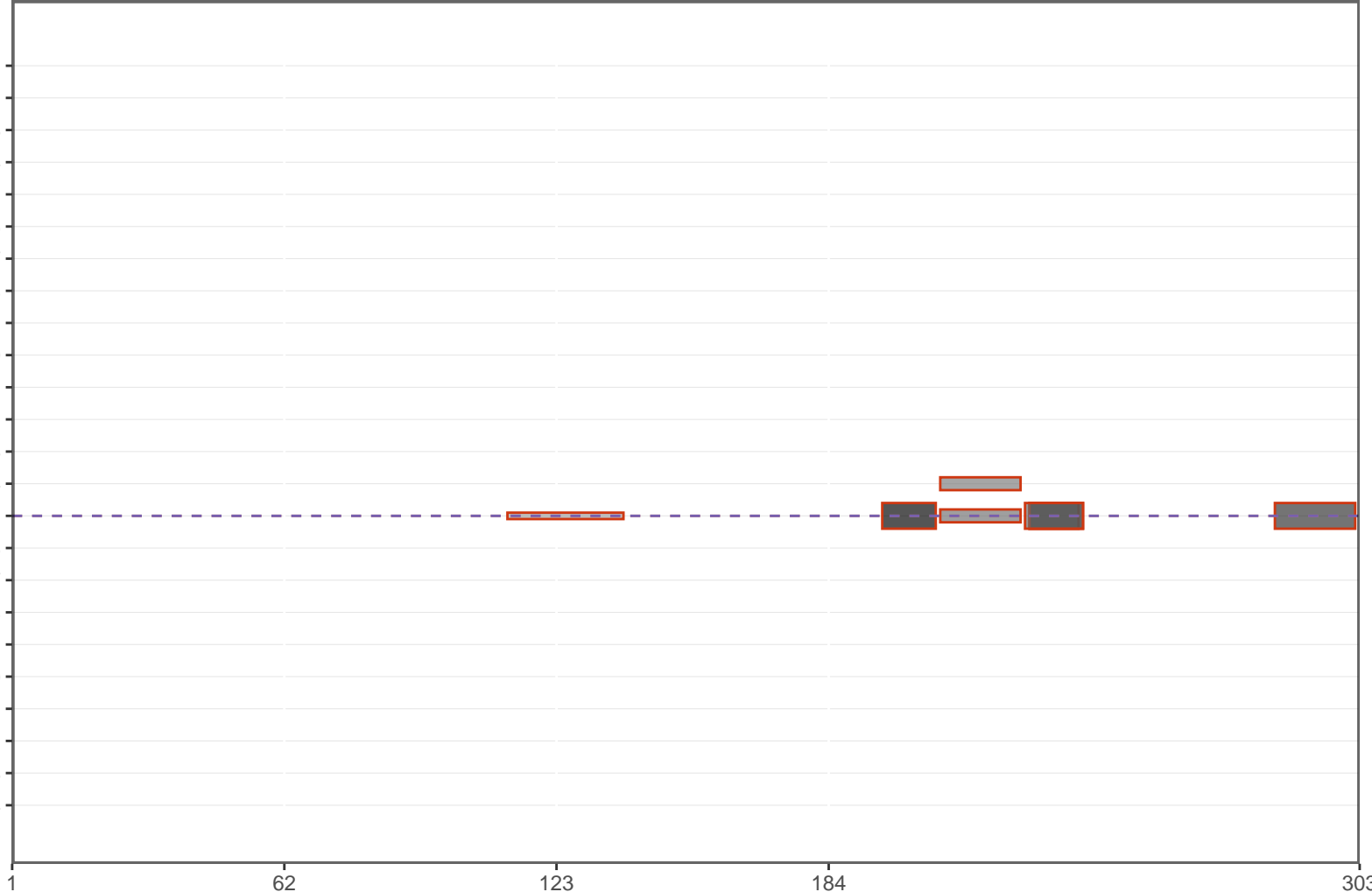
MW indication



Molecular weight

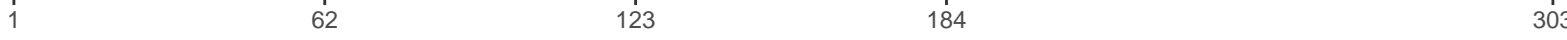


Gel Slice

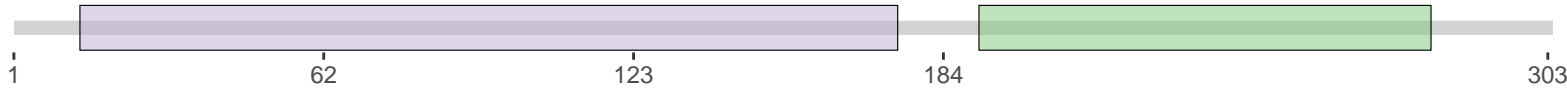


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

IPFRALLDGLRITTSGNRVFGALNGALDGLDIPHEKRFAGFSKDSKQLDADNHRNYYGGHATYMKTLLEDEPEKYGSHFSEYKKGLEADGLEEMKKYKHAARADPTFKKSDKQFPKQKRYNKKLTYEERKAKLIERLNALNSAAGNDNDDEDEDEE

NbL16g05560.1 50S_ribosomal_protein_L17_chloroplastic [MW = 23.16 kDa]

No. of times detected



log(intensity)



Values from



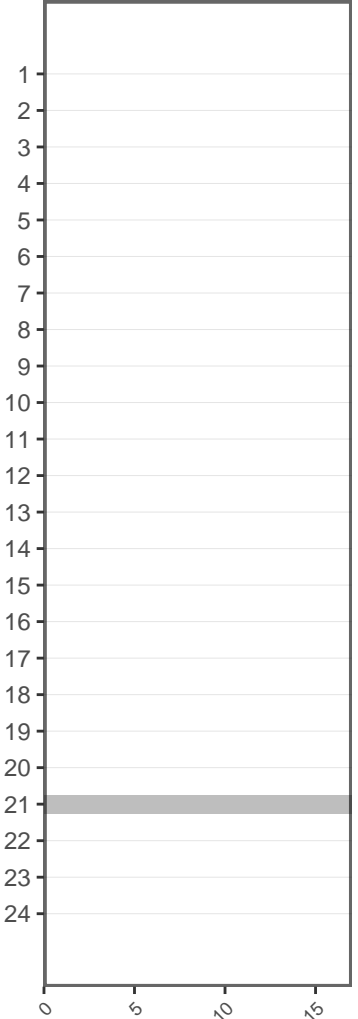
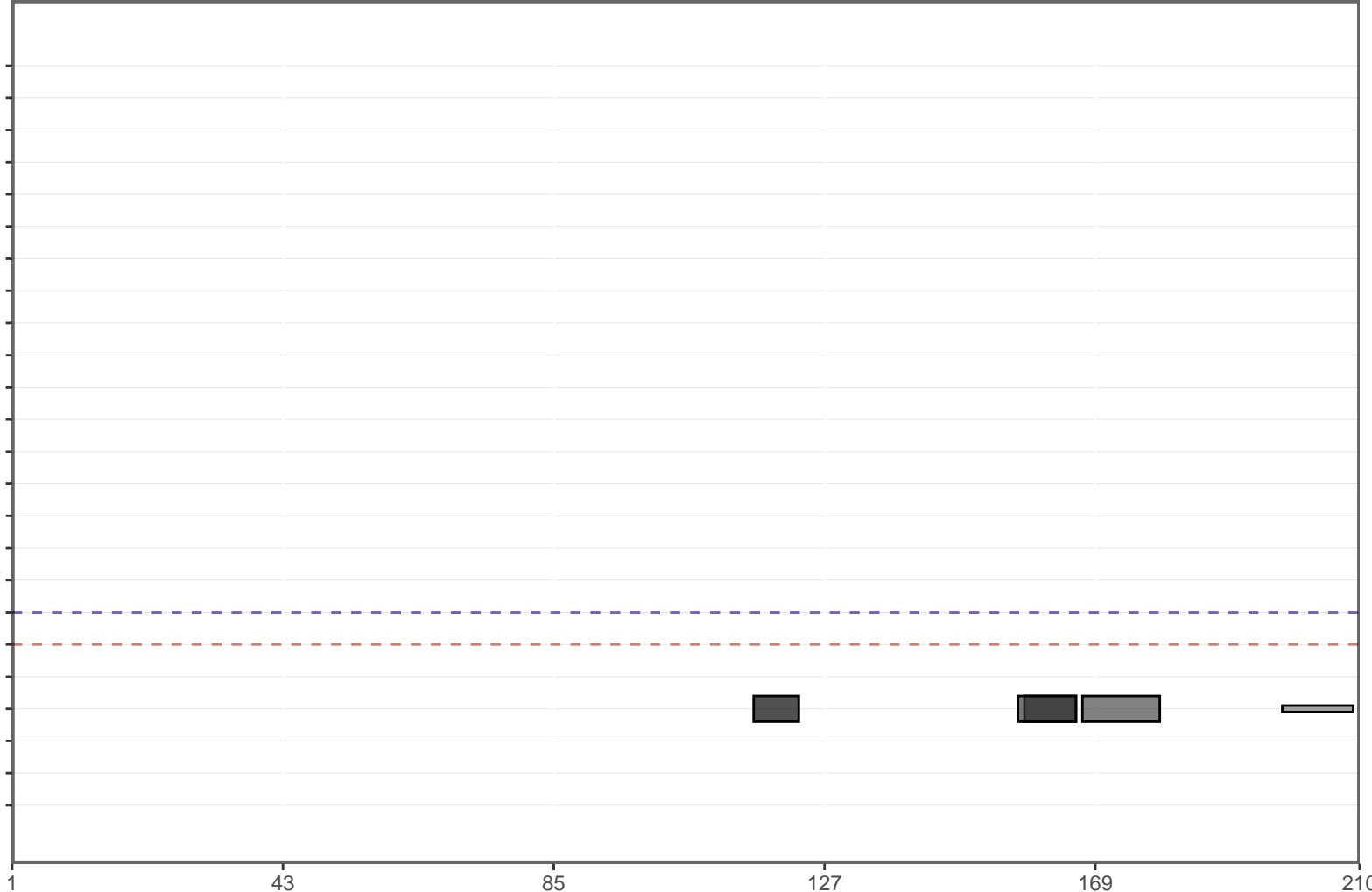
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

MRRHGRKVPKLNRFPPDQRRLRLGLTQLLKHGRKTKARARAVRKVVDKMTMAKDGSLHKRRQALGFYEKQVHALFAEVPDRYGERNGGYTRIRFLPRRGDAPMAHIELV

NbL16g05490.1 pathogenesis-related_genes_transcriptional_activator_PTI6-like [MW = 29.68 kDa]

No. of times detected



log(intensity)



Values from



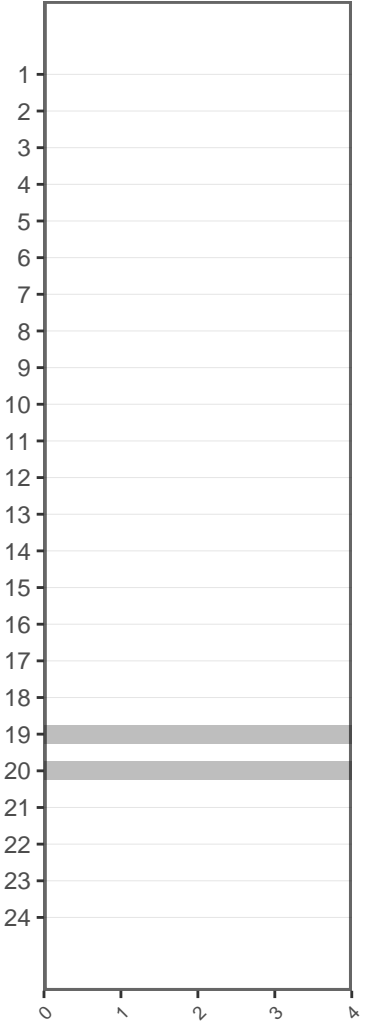
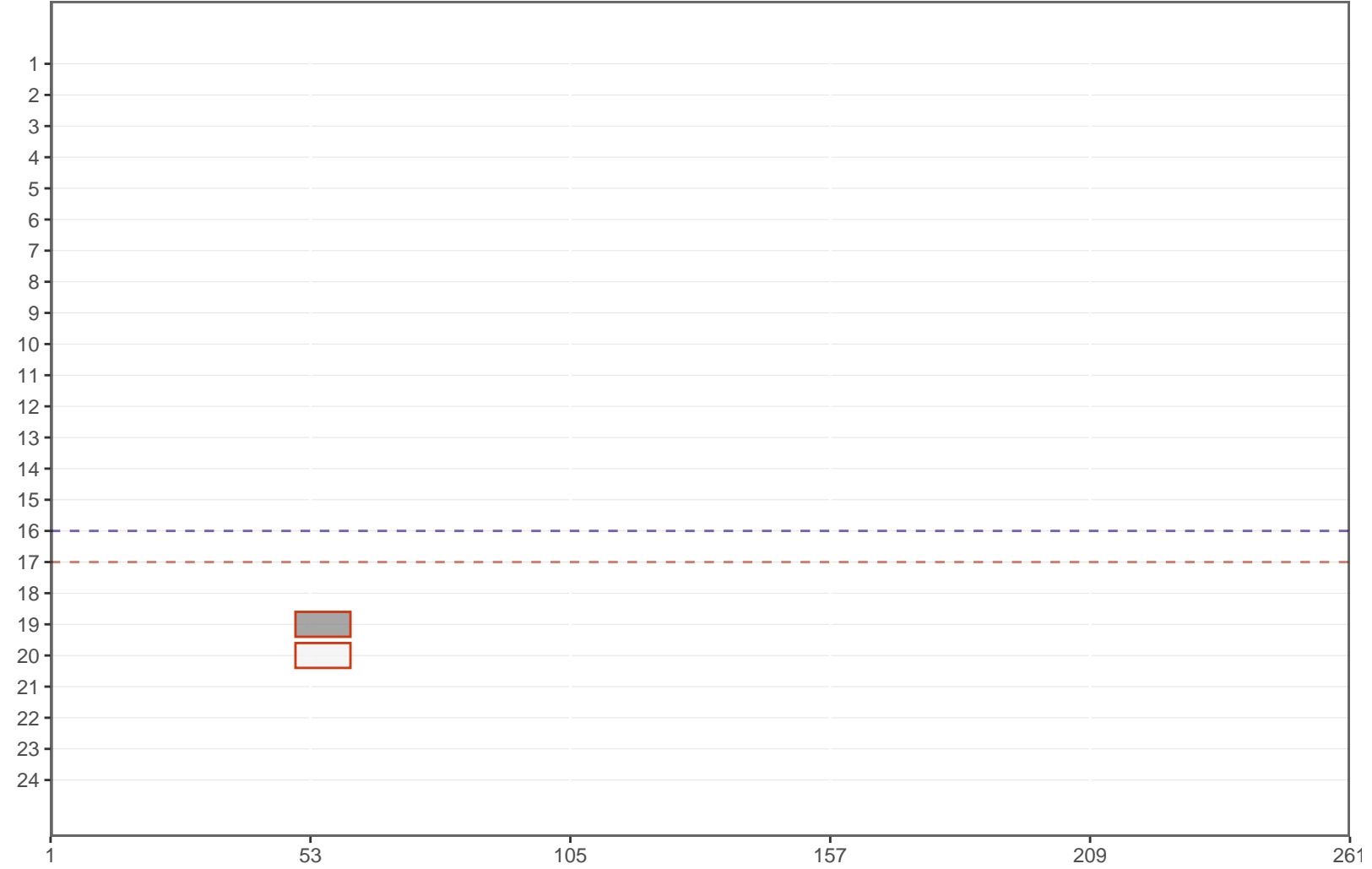
MW indication



Molecular weight



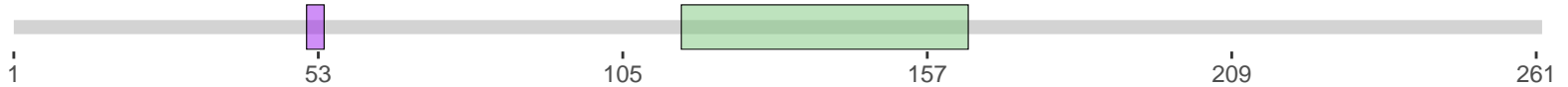
Gel Slice



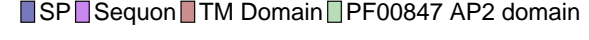
Protein length



Pfam domains



Pfam Description

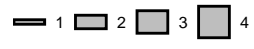


Protein sequence:

/RQRPWGRWAAEIRDPTRGKRWLGTYDTPPEAATVYDEAAVKLGPDAVTFNPKVITADITETESVTDGGEKSENDFLSPTSVLRNDVYTFPFDLGFGEVDAFGFDVDFLFRQPEFGMSEKYDEEFGDFDQFALEAR

NbL16g05480.1 eukaryotic_translation_initiation_factor_2_subunit_beta-like [MW = 35.55 kDa]

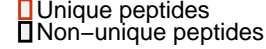
No. of times detected



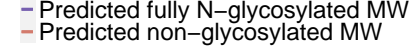
log(intensity)



Values from



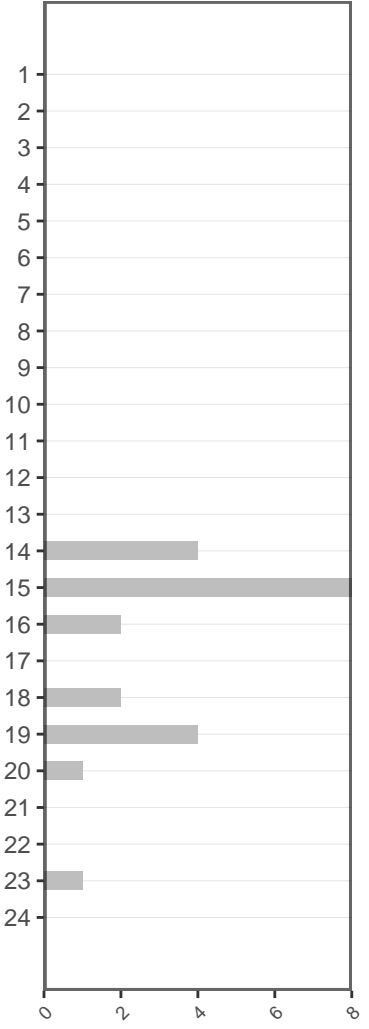
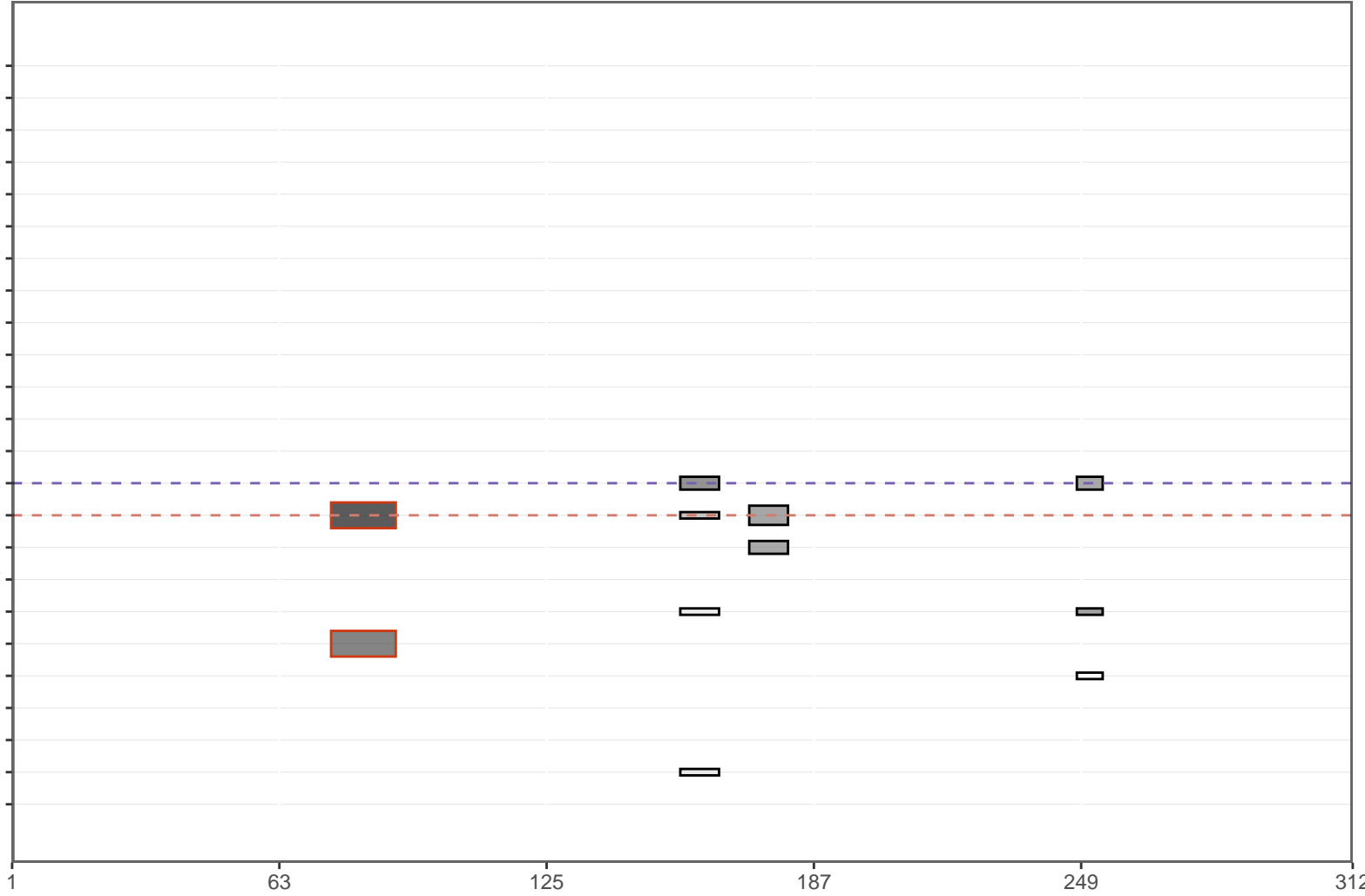
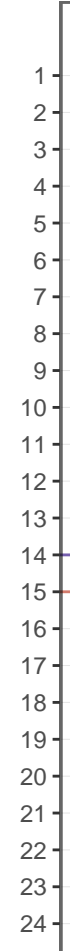
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

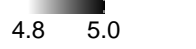
VLDQYPTVEGTDRDVEYEELLGRVFNILRENNPELAGDRRTVMRRPQVLRGKTKVTFVNFMDLCKTMHROPEHVMFTLLAEMGTSGSLDGGQRLVWGRFAPKFNFEGLRRVYNEVYVNGGKPEPTILSKENRFLFLRCEKGGSGREAVPKAGFVAVRGRKAGT

NbL16g05410.1 40S_ribosomal_protein_S26-3-like [MW = 14.59 kDa]

No. of times detected



log(intensity)



Values from



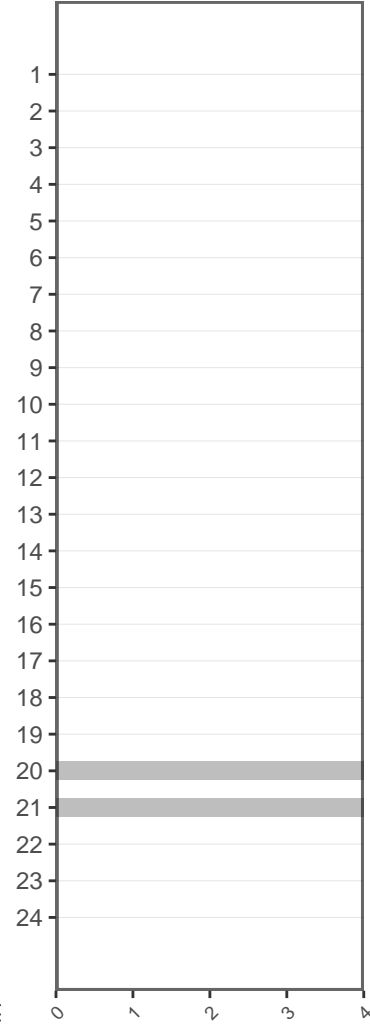
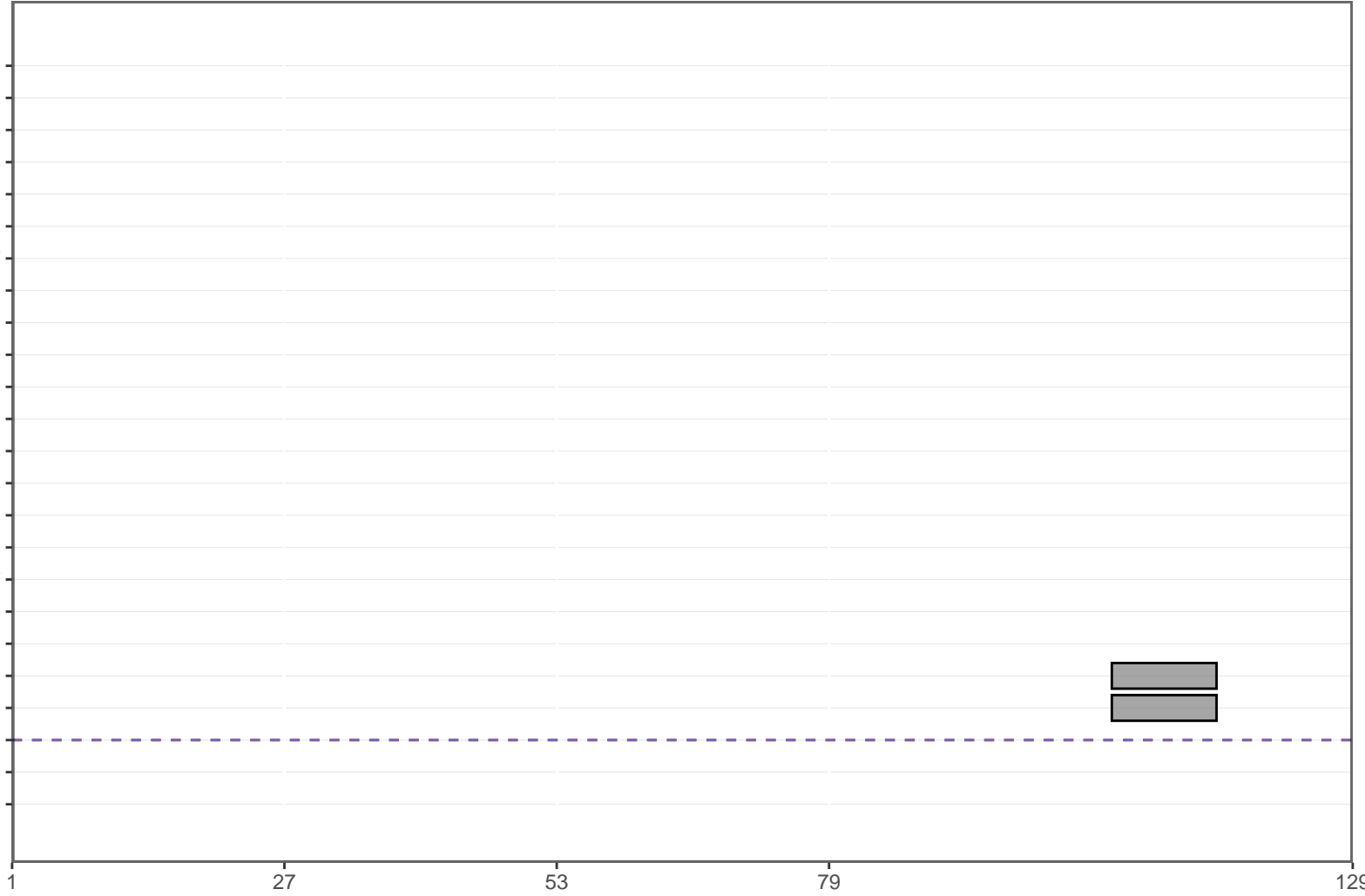
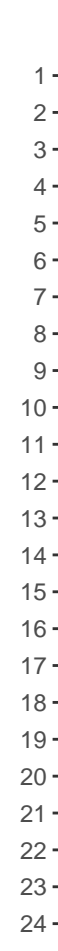
MW indication



Molecular weight

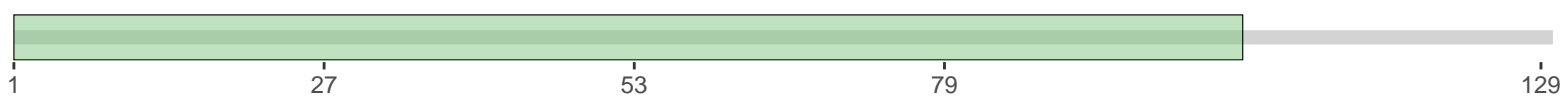


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LDVQEACAFETYTLRKLKLMGKGVGSAHKKVWRVRSRTRRRVREPPQFRFRFRDPAKPGQAPRVGAAPTAAART

NbL16g05260.1 alpha-galactosidase_3-like [MW - SP = 48.93 kDa]

No. of times detected



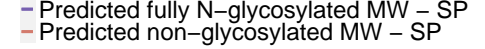
log(intensity)



Values from



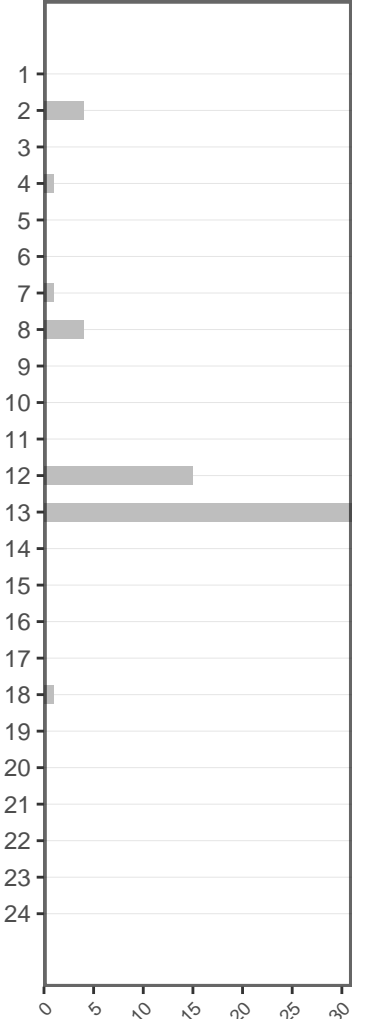
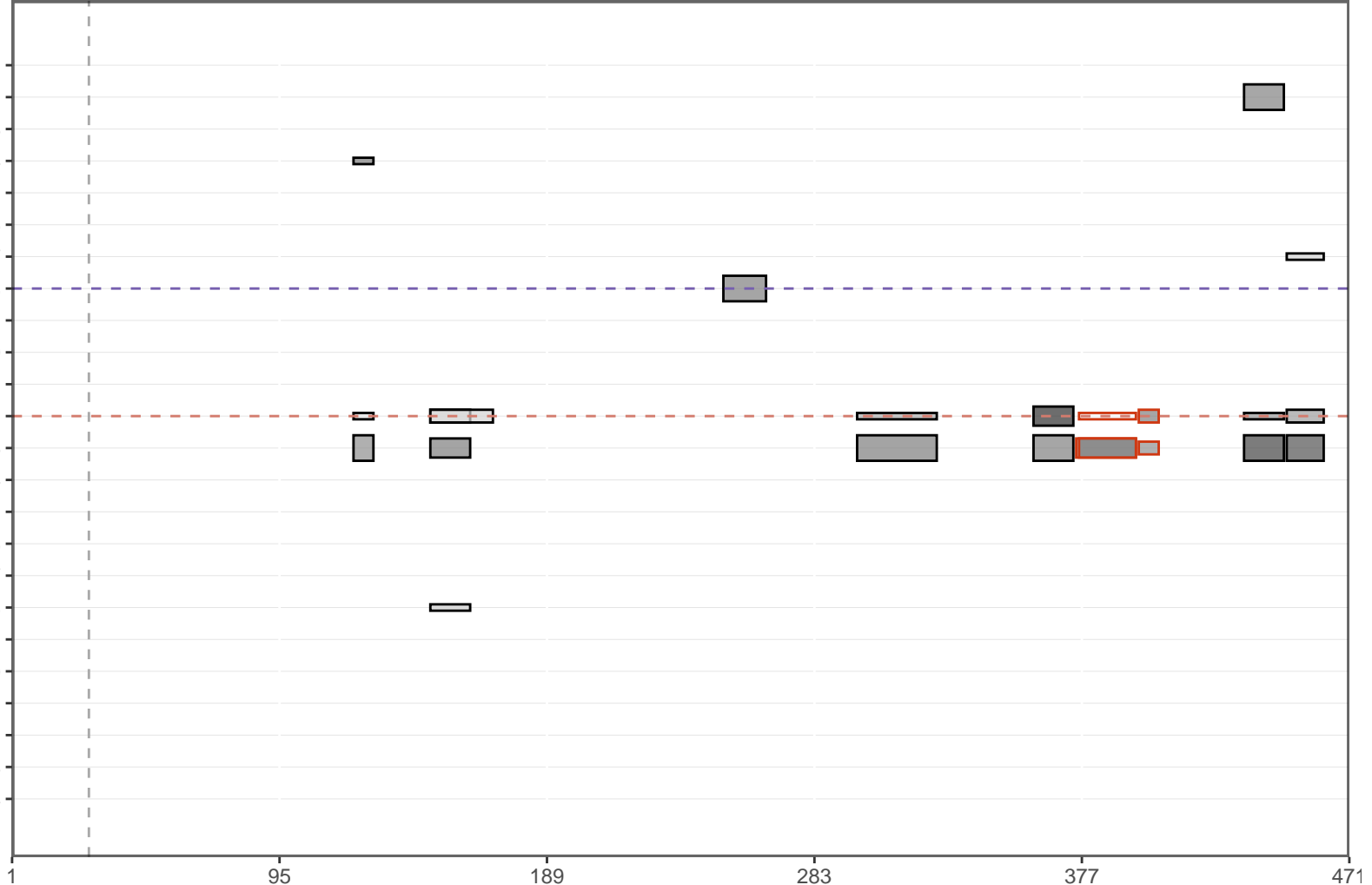
MW indication



Molecular weight

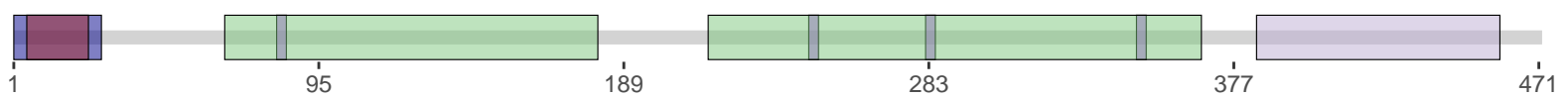


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

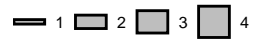


Protein sequence:

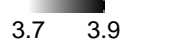
INCFNLGLPPOKRYPPMRDNLNATGRIFVALGEVGVDDPMMWAGKIGNSWRTTDDINDTWASMTTADINDKWAASVAGPQGWNDPDMLEVNGGMMYHEVYKGFSAWLMKAPLIGGQVRRITAELELSEKENVAVDDQPLGVGGRVYVAGSGDQEGWAGPLSGNRLAVLVNRCNSAATITAKWBAIGLESBKGVSFRLLWKEVVGENTVGFSAKRVDAHGGEMVLTPKRETLASKP

NbL16g05170.1 transcription_initiation_factor_TFIID_subunit_15b [MW = 44.63 kDa]

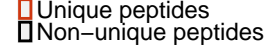
No. of times detected



log(intensity)



Values from



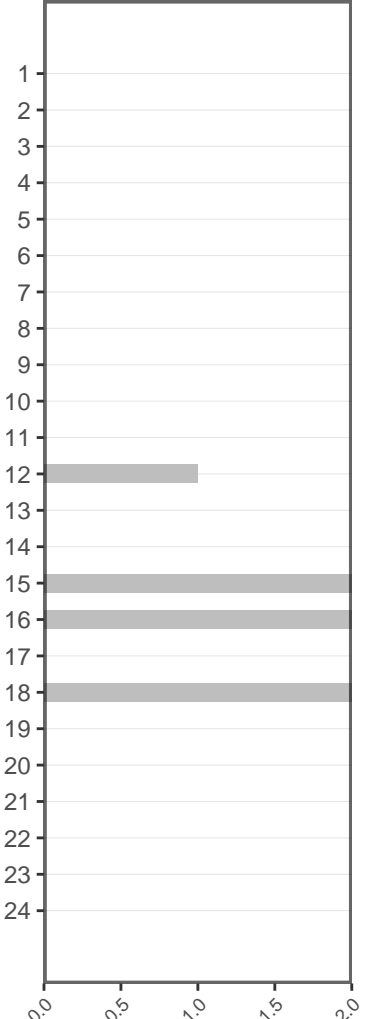
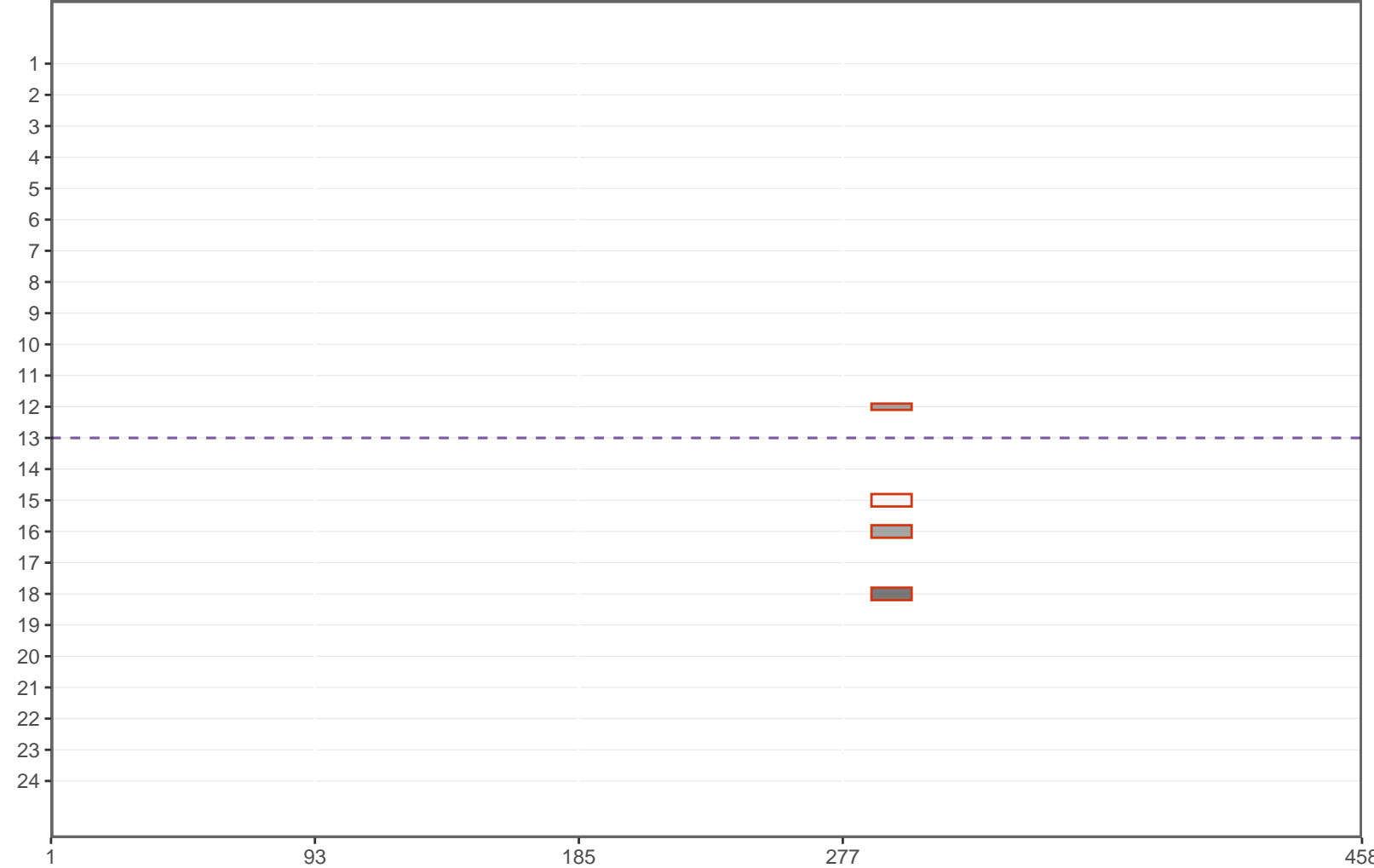
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- PF00641 Zn-finger in Ran binding protein and others

Protein sequence:

PPSYGAADSNYPSPNTYGRNFDVAPPPFTSYVGGPASYPPSVYGAPGGYGGDKTANRGGGRGGPPGGYDGGYGGGGRNAGGVDISPAEAPKVKKCDCTGGDFDNRHISALPPDVTIEELRELFGSGGVARIKKGKRGYKDDQWPWIKLYTDEQGNKGDALSYEDPSAAHSAGGFFNHFDRGKVKISVMAEKSAPKAPAFGSGRGGRGYGGGGRRDNRDGGGGGPPDRGSHGGRNRPV

NbL16g05080.1 protein_DCL_chloroplastic-like [MW = 26.02 kDa]

No. of times detected



log(intensity)



Values from



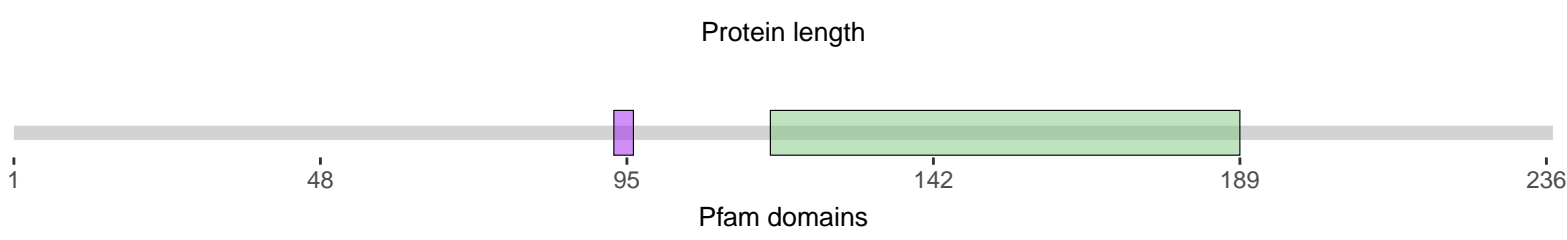
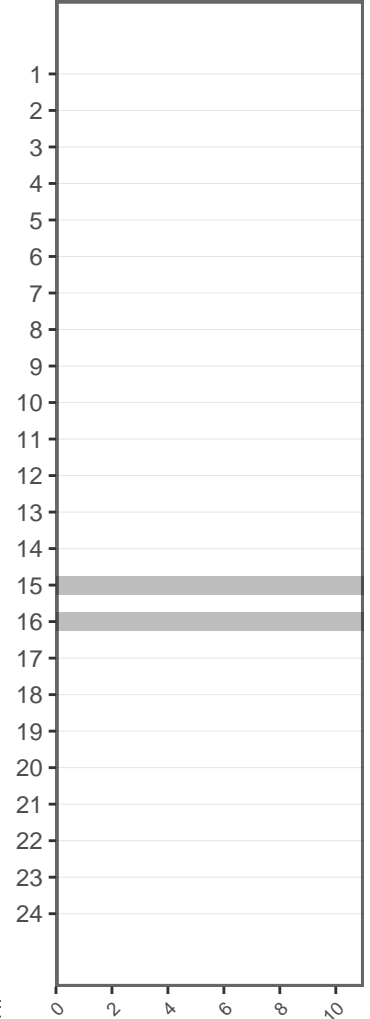
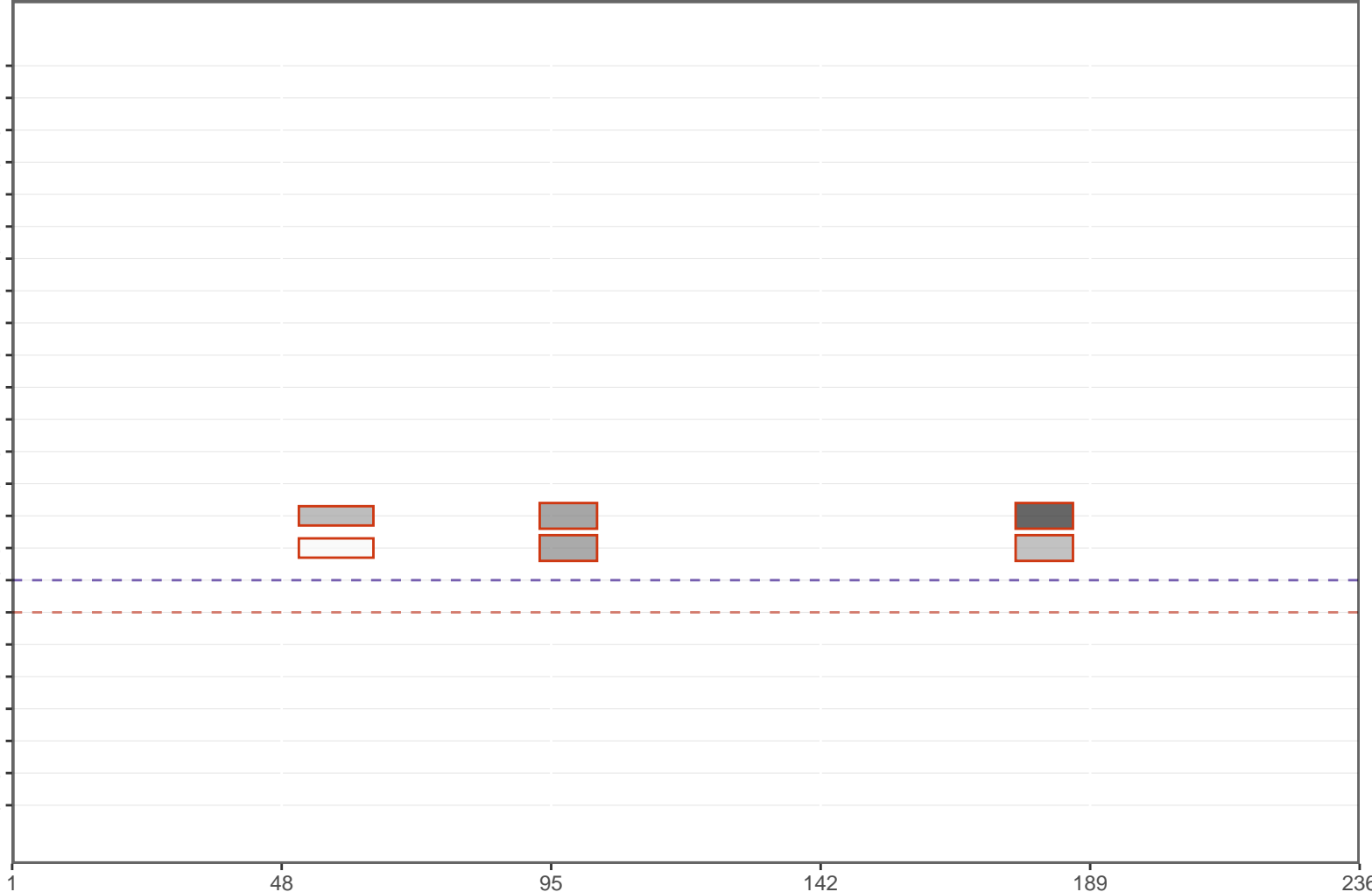
MW indication



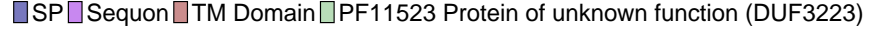
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

FGSSVEMFDYFYKLLHSWSPNLSNKYEHVLLDLLKKGHLERPERKIGTGRAFGQIRFHPQFKSRGCFVIREDDGSDVDFSRFKVDHLLPLPENMQVWHHEANKGLAHSQKGGSRKGGHGRDRGNGGKERY

NbL16g05060.1 chlorophyll_a-b_binding_protein_4_chloroplastic-like [MW = 27.6 kDa]

No. of times detected



log(intensity)



Values from



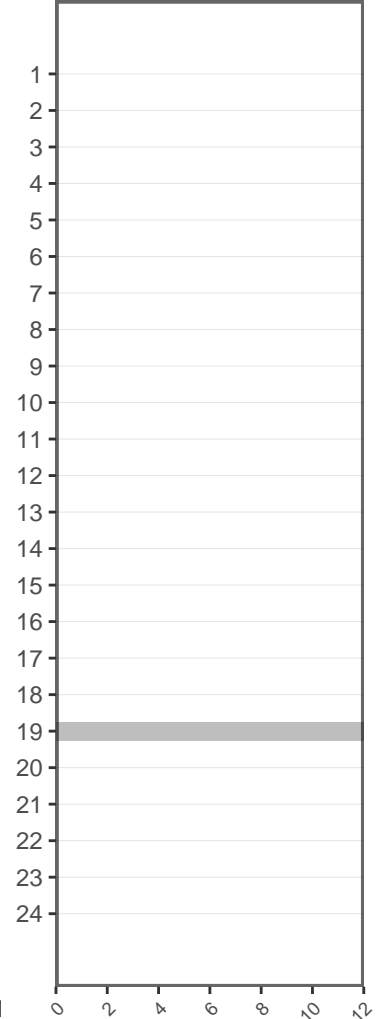
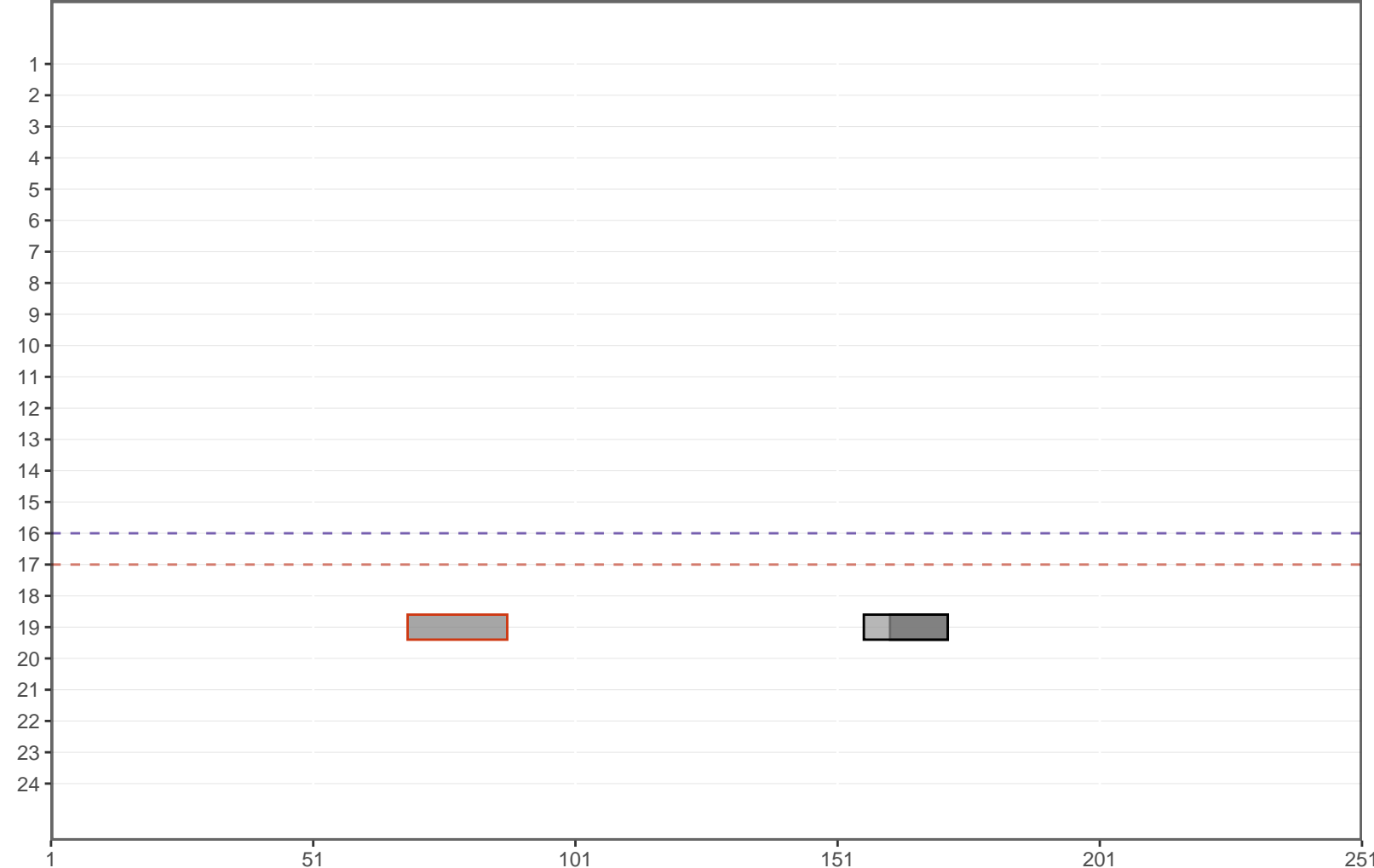
MW indication



Molecular weight



Gel Slice

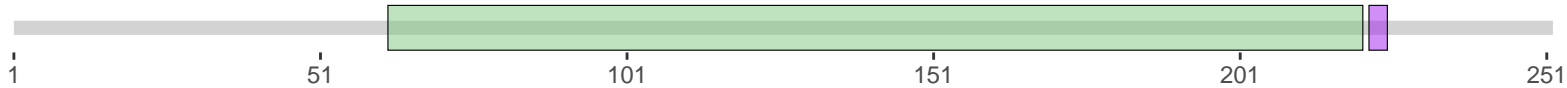


Protein length

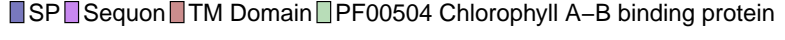


Peptide counts over 4 repeats

Pfam domains



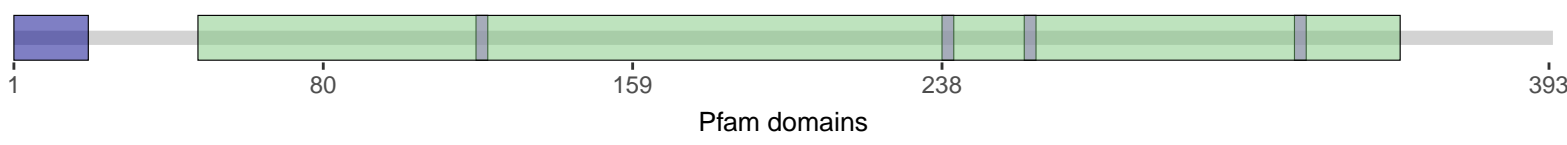
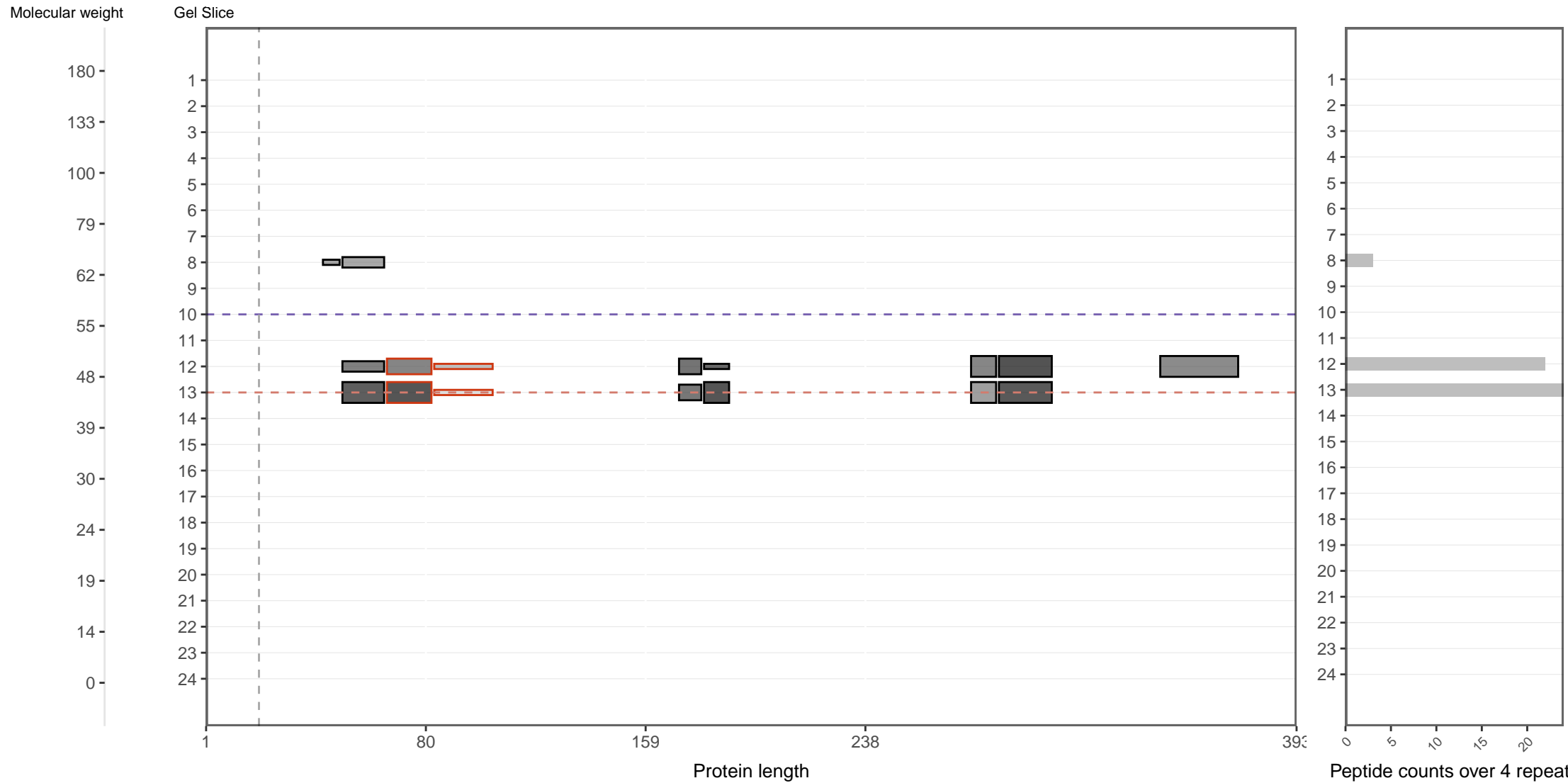
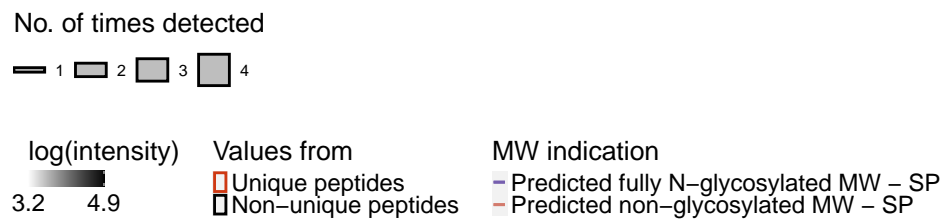
Pfam Description



Protein sequence:

PEVLTSAQLLVKRWYDAGKSEYFASBSLFLVIEFLFHYVEIRRWQDKNPGSVNGDPIKSYSLPPEVGYPGGIFNPLNFAPLLEAKEKEIANGRLAMLAFLGFLVGHNVYTKGKGFENLLQHLSDPWHNTHQTFAN

NbL16g04760.1 glycerophosphodiester_phosphodiesterase_GDPD6 [MW – SP = 43.5 kDa]

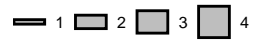


Pfam Description
 SP Sequon TM Domain PF03009 Glycerophosphoryl diester phosphodiesterase family

Protein sequence:
 DQVWVPGGRFEDKDFVETLNKYGYRGSYMSKQVWLGKQPFQISFAPTSLSYHNGTDLKPKFLIDVDMPDQDTNGSYYWEITSDSYLDFKEYVYVGGPFWKDNIPVSNYLGTPSDLVARAHANLGVHPYTFRRNENKFLHFNFSSEDPVNEYDYYWIKNGVDGLFDFDTGSLHHYGEWTFNPFASGKEATRLLHKEIEMLSKPKYFN

NbL16g04660.1 D-aminoacyl-tRNA_{deacylase}-like [MW = 40.79 kDa]

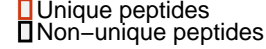
No. of times detected



log(intensity)



Values from



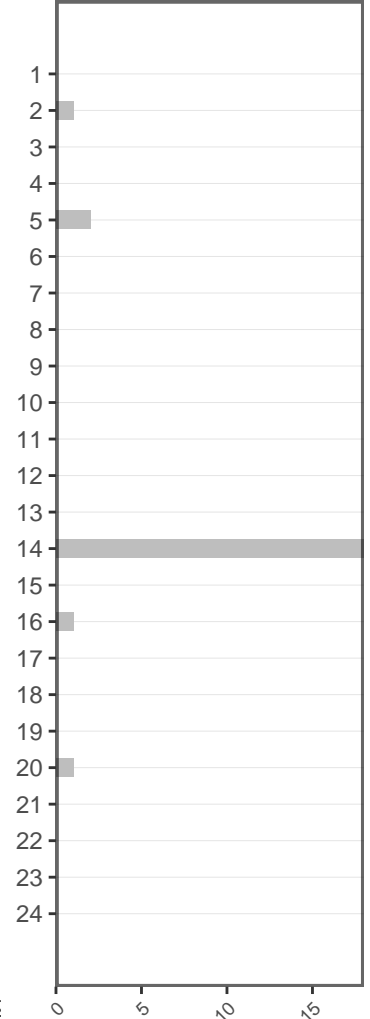
MW indication



Molecular weight

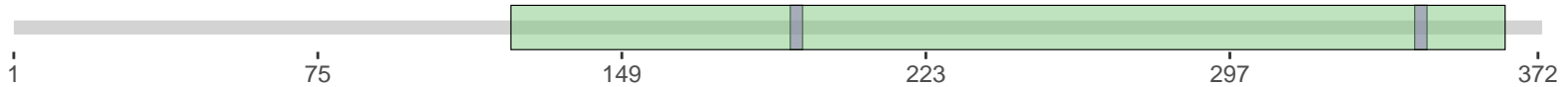


Gel Slice



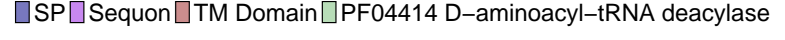
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

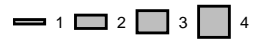


Protein sequence:

IGPWFRLLKSAIESGNLTPREFEVLTEATHHGPLTNPATMFMVEIGSTEEYWKRRGDAAGMALLVWEGGLNGGAAVGDWGRFRFRYSGGQKILLGGGGHYVPRHMDLKDGVVYGHLLAGYSLFMEQPGPTKAPALVGGTWRQARVAFDTRAAFPKGEVLAHIDNKSKFGWQKQANGLAEQNKIKVQKPSDFY

NbL16g04550.1 ribulose_bisphosphate_carboxylase_large_chain [MW = 53.68 kDa]

No. of times detected



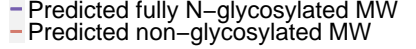
log(intensity)



Values from

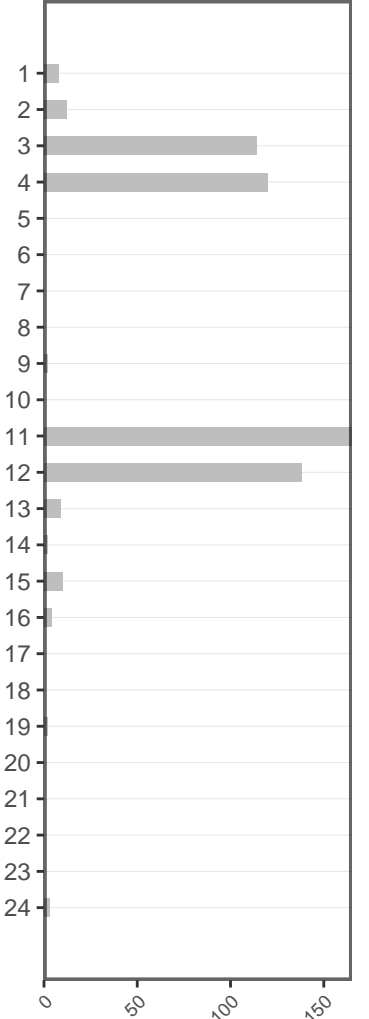
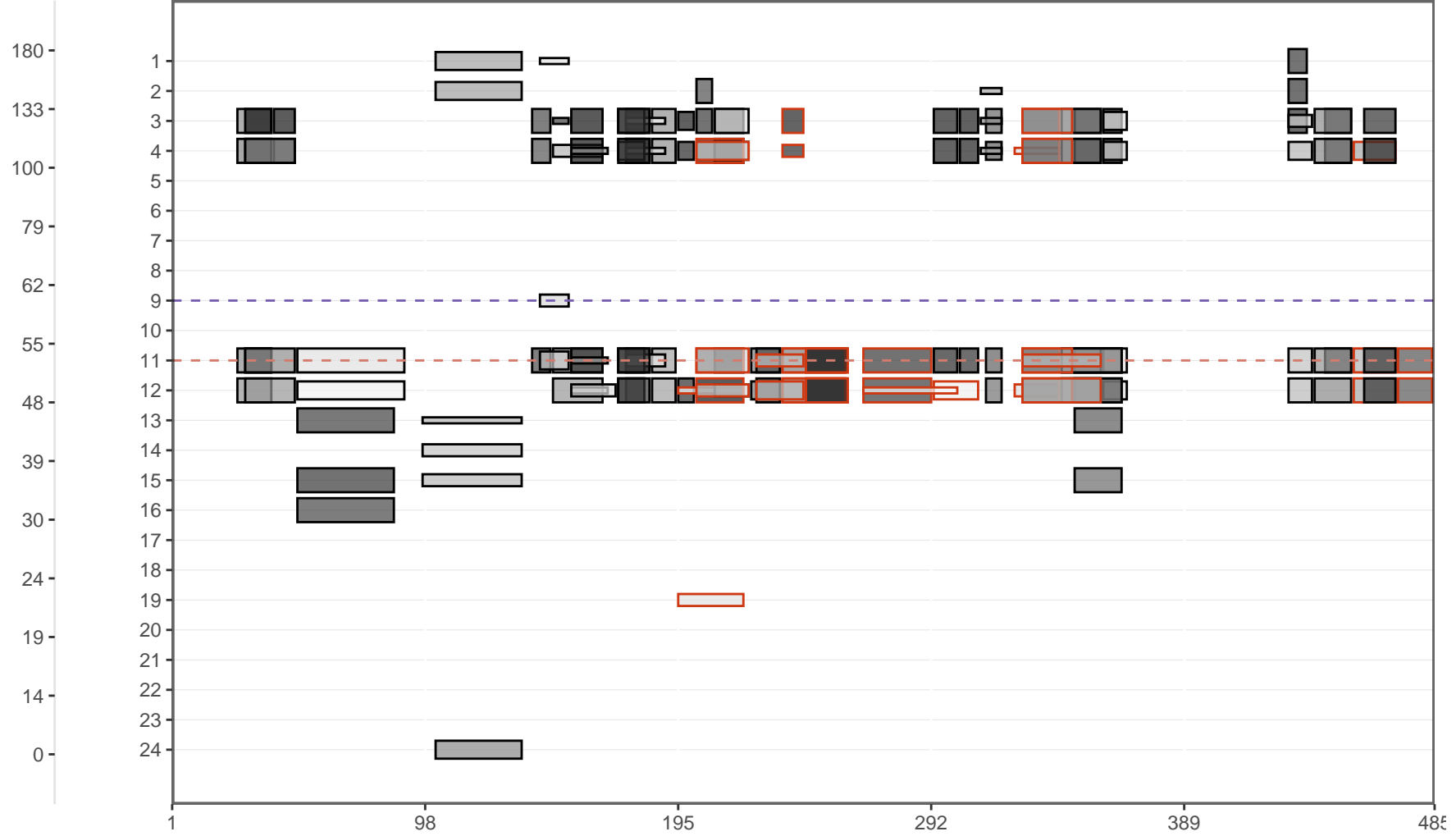


MW indication



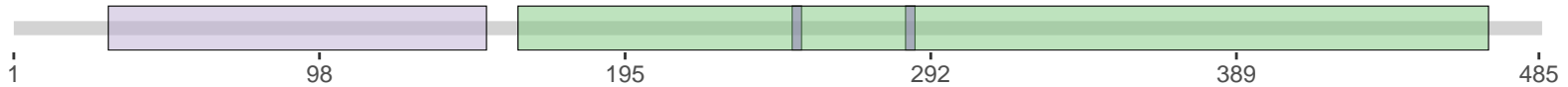
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00016 Ribulose bisphosphate carboxylase large chain, catalytic domain
- PF02788 Ribulose bisphosphate carboxylase large chain, N-terminal domain

Protein sequence:

KEALFKAQSETGEIKGHYLNATAGTCEEMIKRAVFARELGVPMVHDYLTGGFTANTSLAHYGRDNGLLLIHRRAMVAVDKQKNGHIFRVLAKALRMSGGDHIHSGTVYVGLKEGERDITLGFVLLLRDDPFVQDRSRGIHFTQDWSLPLGVAHVASGGHVVHMPALTEIFGDDSVLQFDGGSTLGHWPQAPGAVANRVALEAGVKARNEGKRLDAGEGNGIHEAKKWSPELAAACEWKENFNAAVDVLK*

NbL16g04540.1 ATP_synthase_subunit_beta_chloroplastic [MW = 25.73 kDa]

No. of times detected



log(intensity)



Values from



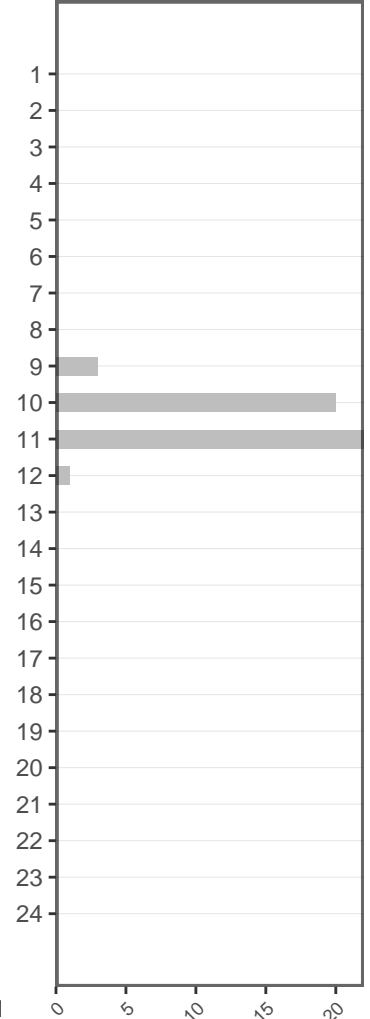
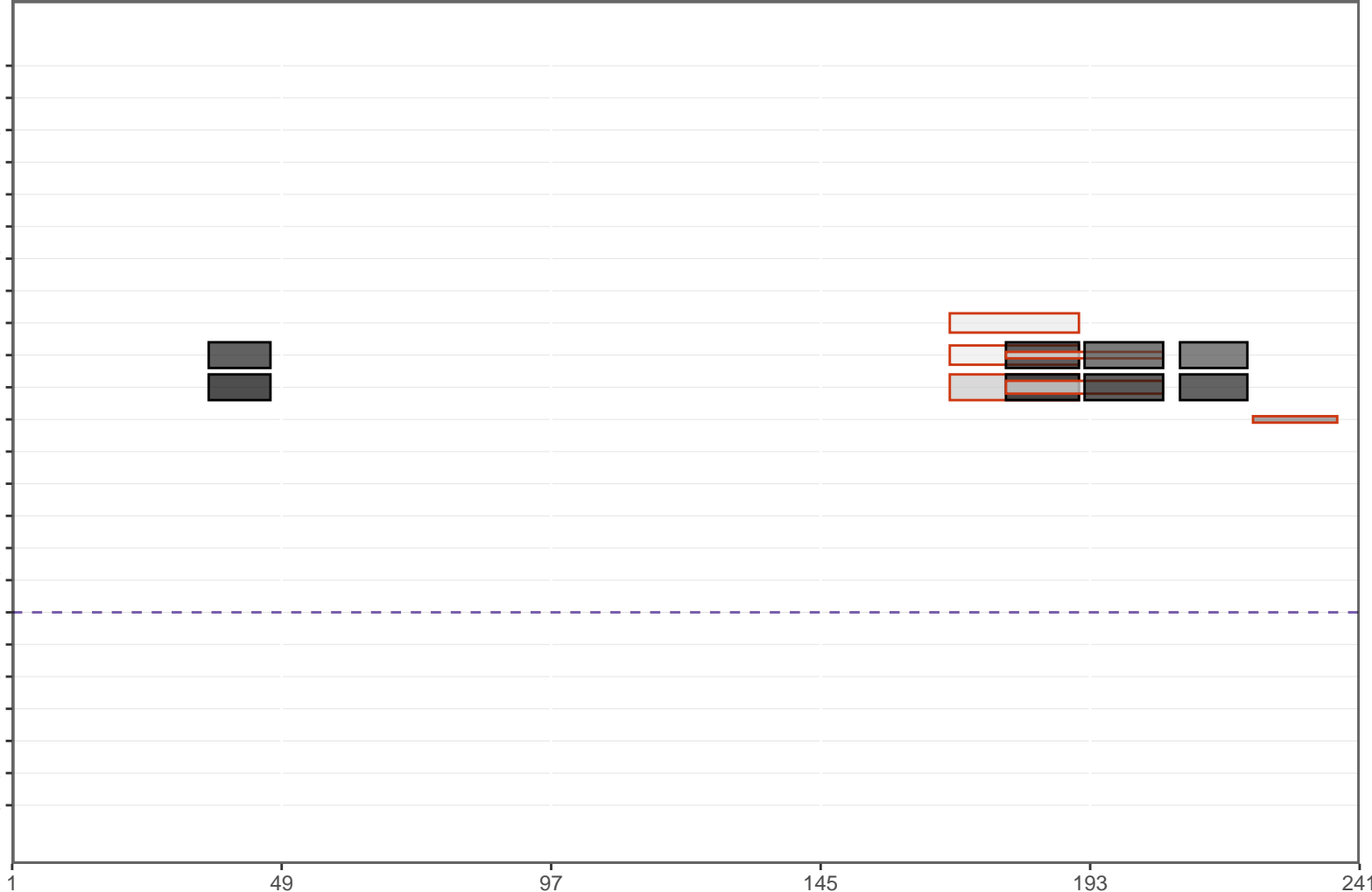
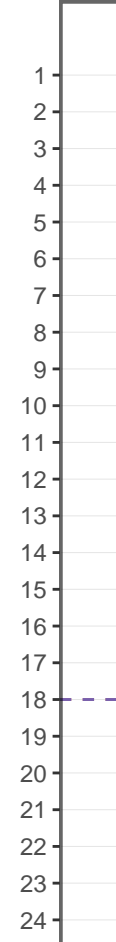
MW indication



Molecular weight



Gel Slice

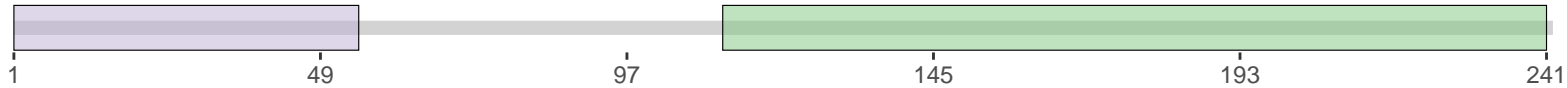


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description

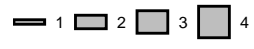
- SP
- Sequon
- TM Domain
- PF00006 ATP synthase alpha/beta family, nucleotide-binding domain
- PF02874 ATP synthase alpha/beta family, beta-barrel domain

Protein sequence:

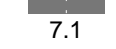
IFETGKVVOLLAPVRRGGKGLFGGAGVSKVLMELINNAKHHGVSVFSGVGERTRREGNDVLMEMKESGVINEENAEKVALVYQGMNEPPGARMRVGLTALTAEYFRDVEQDVLFDINFRFVQA

NbL16g04530.1 ATP_synthase_epsilon_chain_chloroplastic-like [MW = 14.61 kDa]

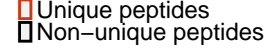
No. of times detected



log(intensity)



Values from



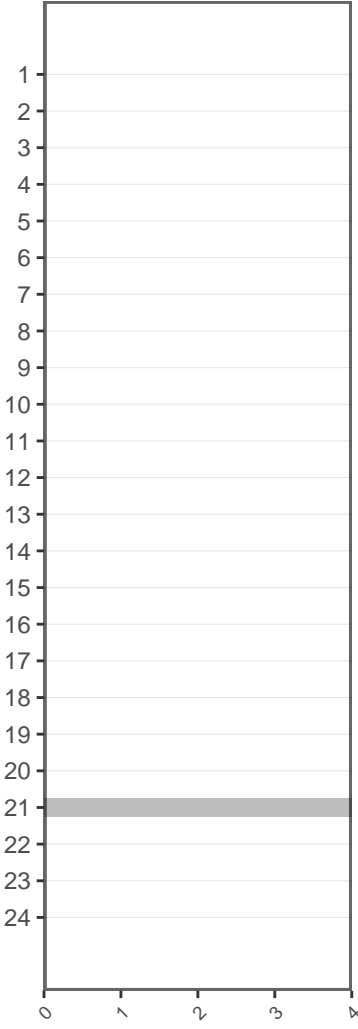
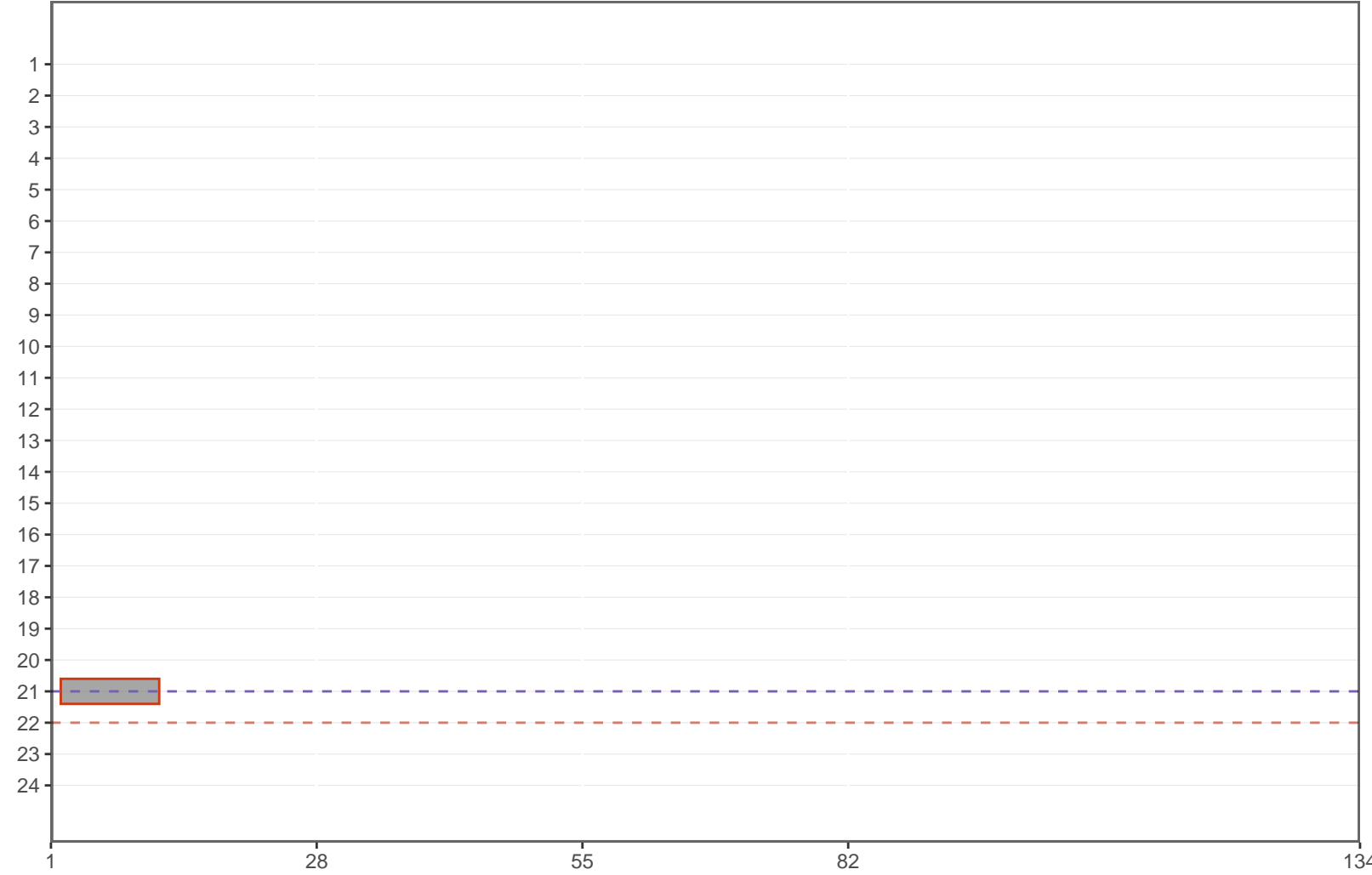
MW indication



Molecular weight

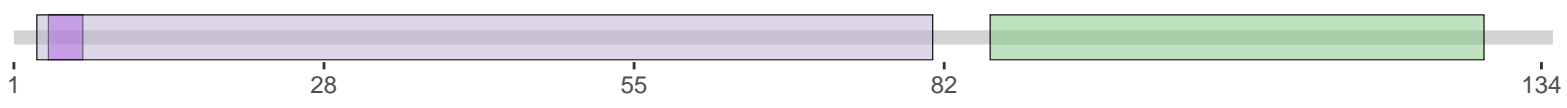


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00401 ATP synthase, Delta/Epsilon chain, long alpha-helix domain
- PF02823 ATP synthase, Delta/Epsilon chain, beta-sandwich domain

Protein sequence:

QWLTMLMGGFARIGNNETVAVLNDAEKGGSDIDPQEAQGTLELAEANVKKAEGRGRKIEANLALRRARTRVEANPIE*

NbL16g04380.1 ribosomal_RNA_small_subunit_methyltransferase_NEP1-like [MW = 31.39 kDa]

No. of times detected



log(intensity)



Values from



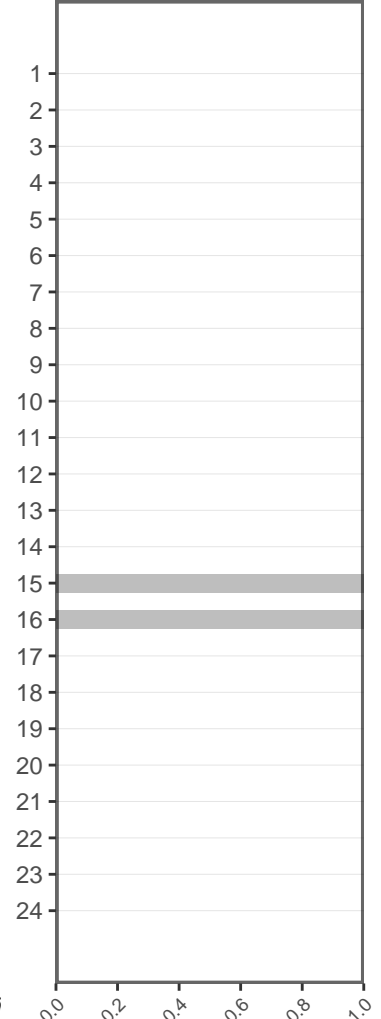
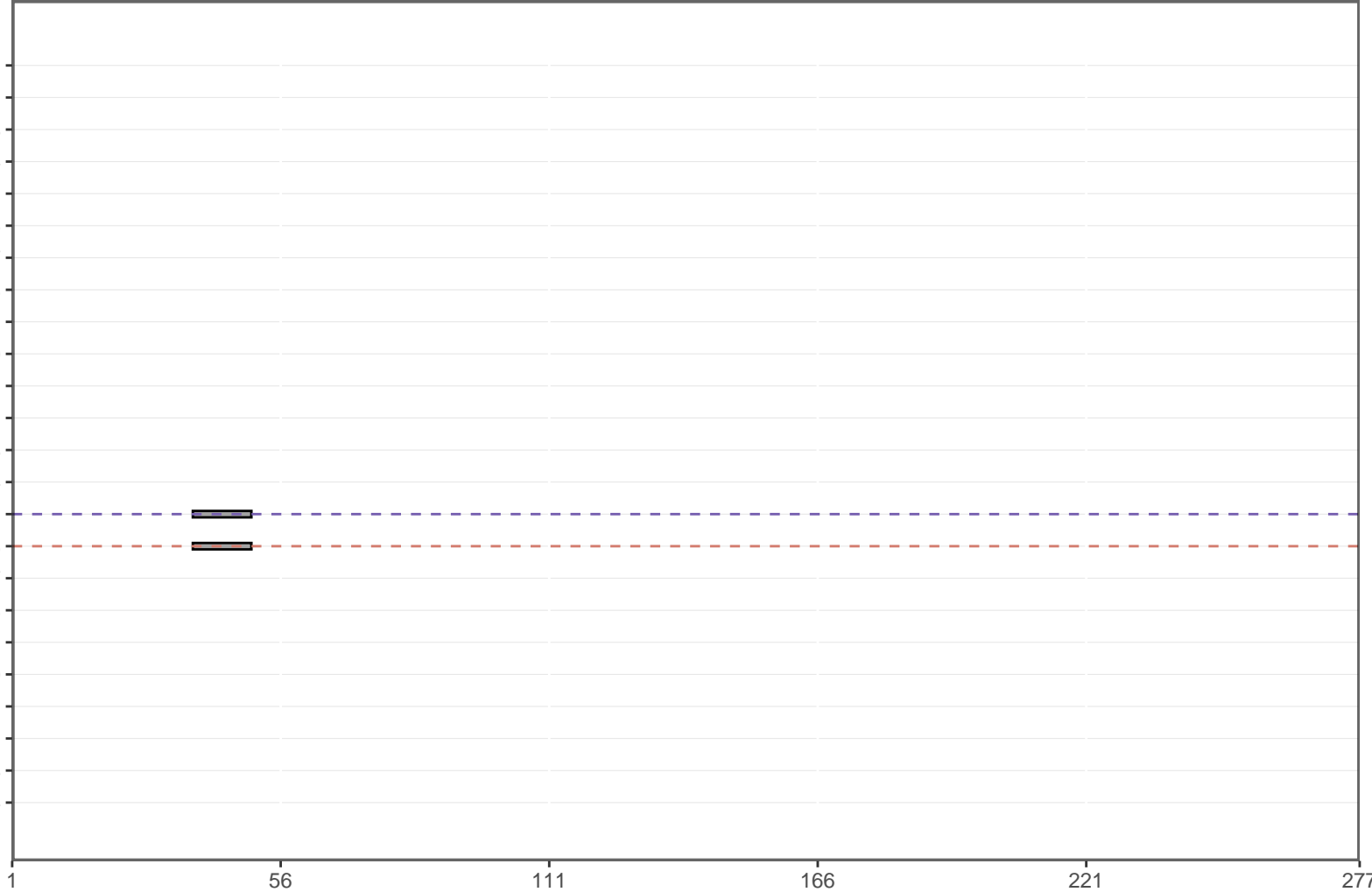
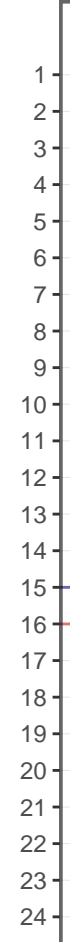
MW indication



Molecular weight



Gel Slice

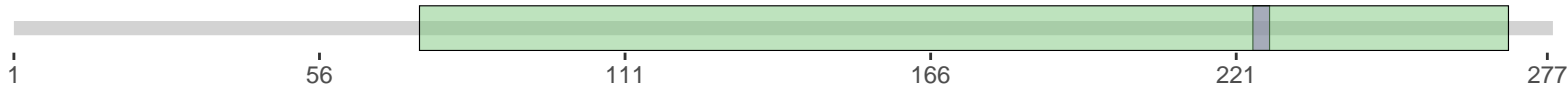


Protein length

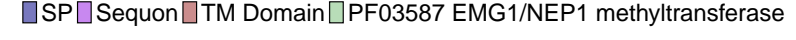


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

DSRYNKARRLKALVYKTEKGLVEKVPKVRIPRTFRFAGIMQLLQKLSITAVGKREKLLRVIKINPVSDYLPIDCRKIGFSHSEKHLVDIGDYVNGINNETNLVFFVGGAMAHKIEKDYVEDHISVSDYPLSAAYGISMVINAVERKWKIL

NbL16g04330.1 40S_ribosomal_protein_S7-like [MW = 22.06 kDa]

No. of times detected



log(intensity)



Values from



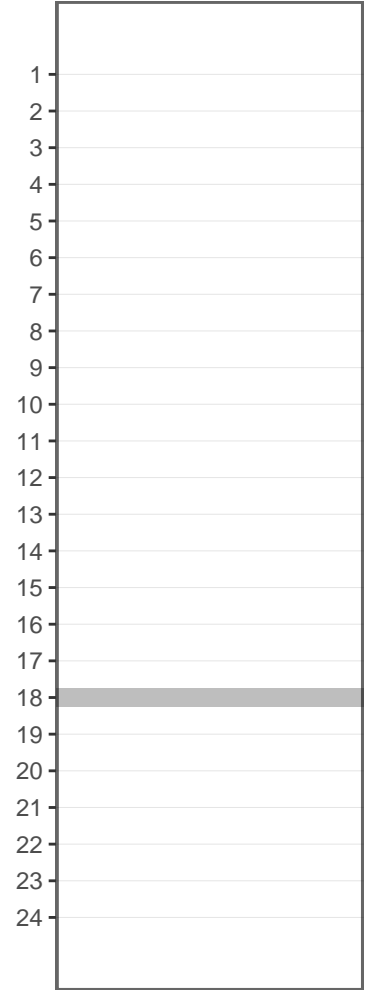
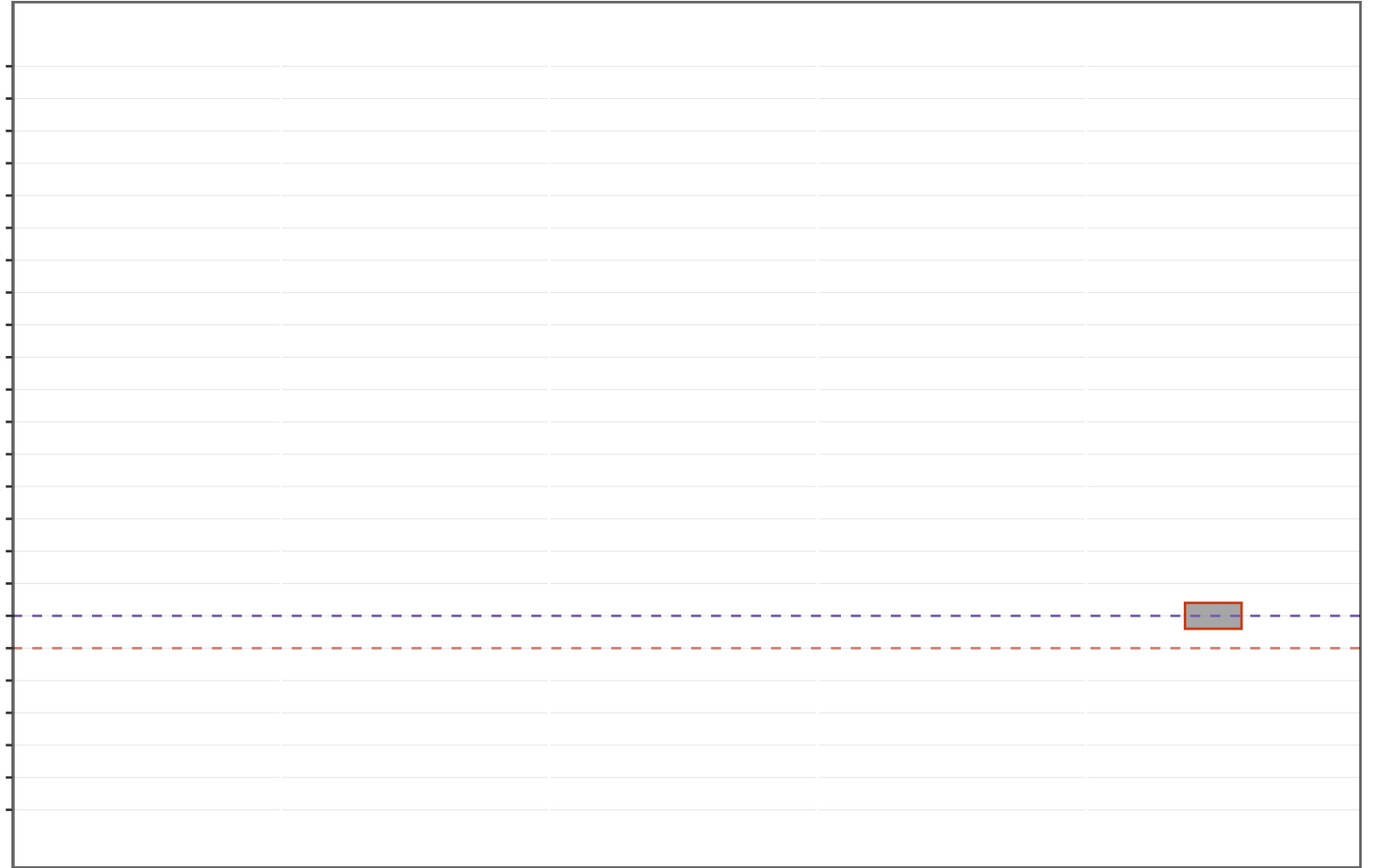
MW indication



Molecular weight



Gel Slice

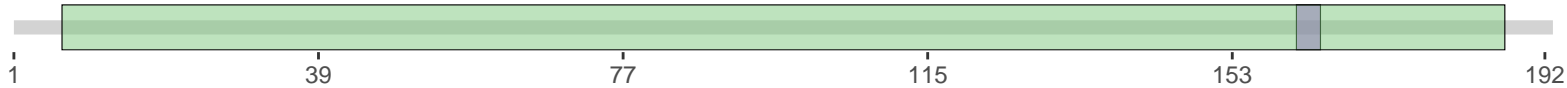


Protein length



Peptide counts over 4 repeats

Pfam domains



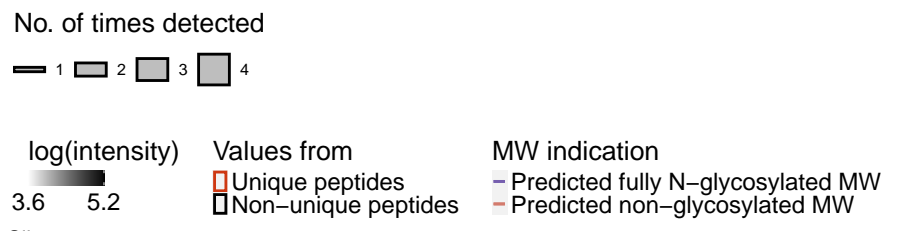
Pfam Description



Protein sequence:

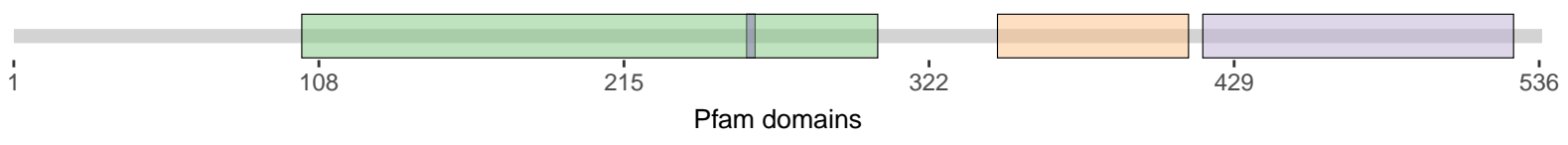
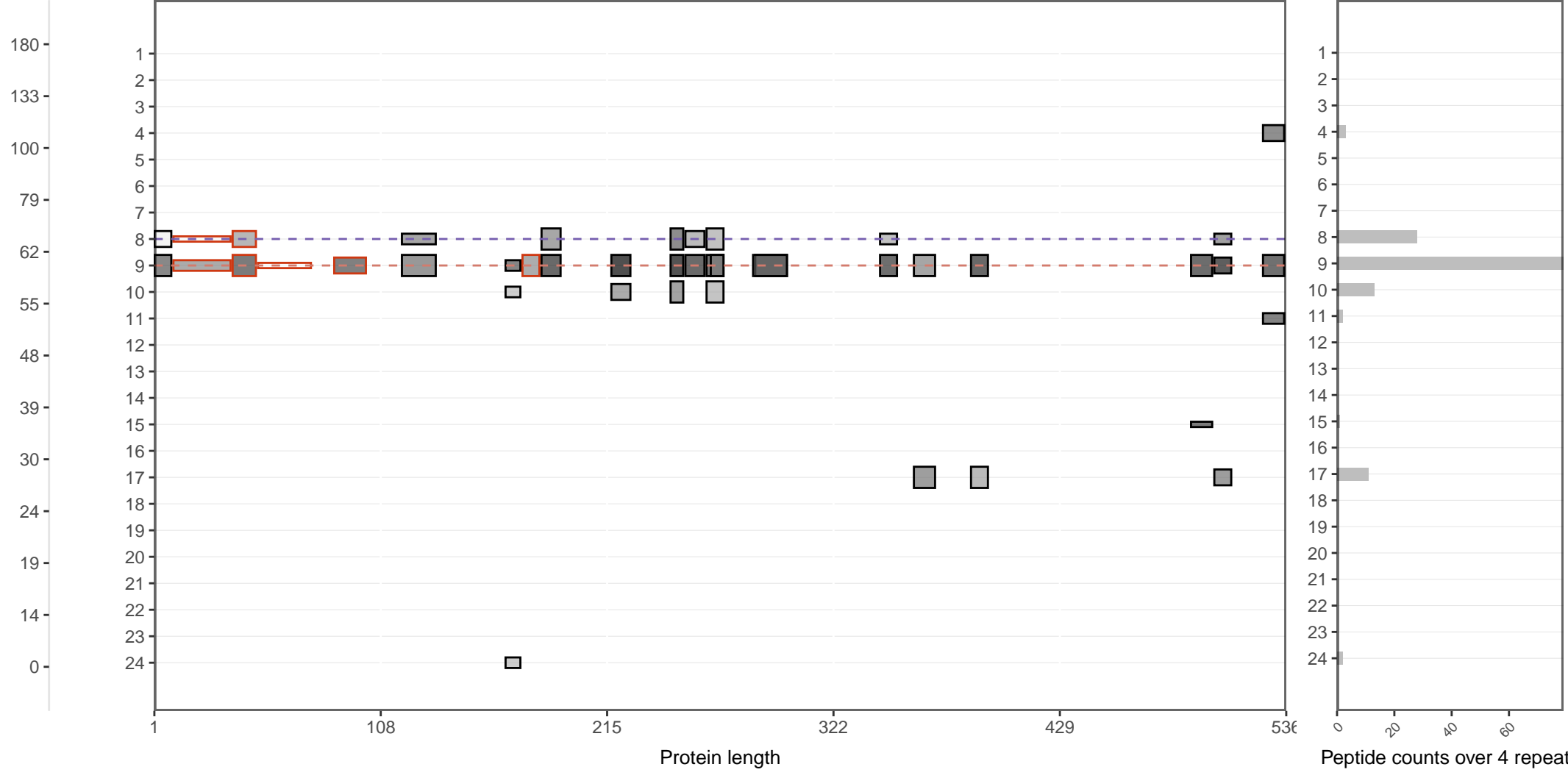
RELEKXFGKDVIFATRRRIARPPNRGSAAGRPRSRITLGVHDAILEDVVAEIVGKRTIRYIDGSKIMKVFDPKERINTEYKLEIFSAVYRKLGGKGVFEYPTEA

NbL16g04290.1 eukaryotic_peptide_chain_release_factor_GTP-binding_subunit_ERF3A-like [MW = 59.34 kDa]



Molecular weight

Gel Slice



- Pfam Description**
- SP
 - Sequon
 - PF00009 Elongation factor Tu GTP binding domain
 - TM Domain
 - PF03143 Elongation factor Tu C-terminal domain
 - PF03144 Elongation factor Tu domain 2

Protein sequence:

DDPTVNSKERYDEIEGKAVPFLRSGYNNKDDVQLFPIBGLLGENLKRMEKGVCPWWNGPCLFETLDAVEVPRDPNGLPLRPIDKFKDMGTVMGKSGSIREGDNLLVMPNKAQKYLAFCDQKVRHVGPGENVRVRLSGVEEDDLSGLVGVAKPHAVTEFVAQLQLELLDNIFTAGYKAVLHHISVVEEIEVLMGGDLTKPKMKKKPLVYKNGAVLGRVDVNNLIGVEKFSDFAGLGRFLRTEGKTVWKGITALPTVADNA*

NbL16g04260.1 guanine_nucleotide-binding_protein_subunit_beta-like_protein [MW = 35.72 kDa]

No. of times detected



log(intensity)



Values from



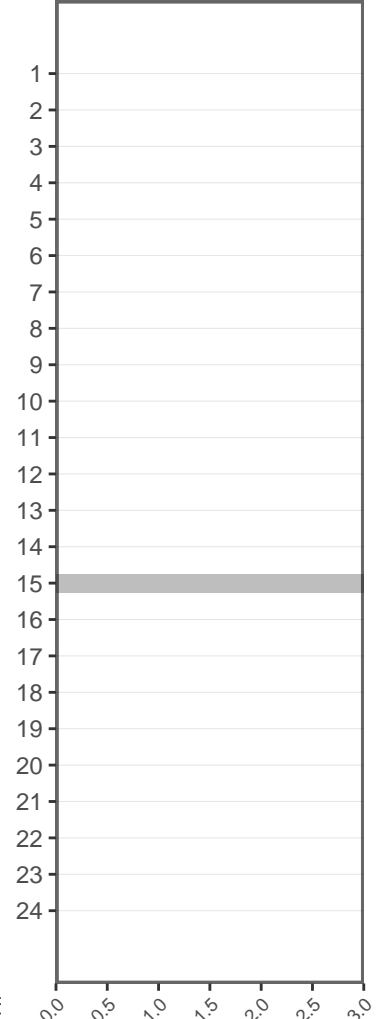
MW indication



Molecular weight

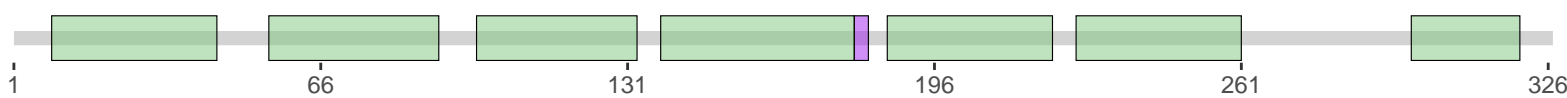


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

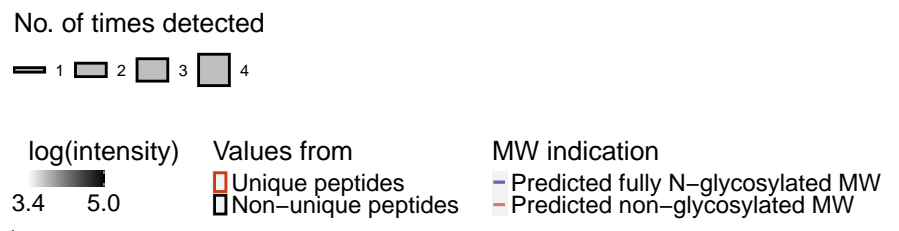
Pfam Description



Protein sequence:

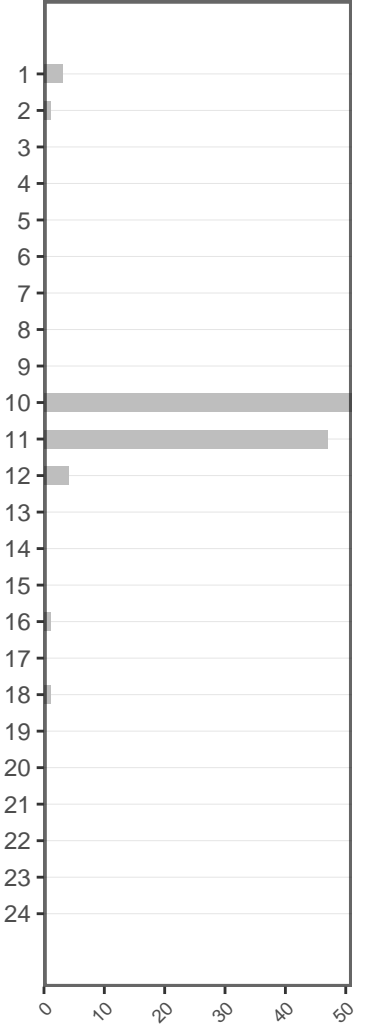
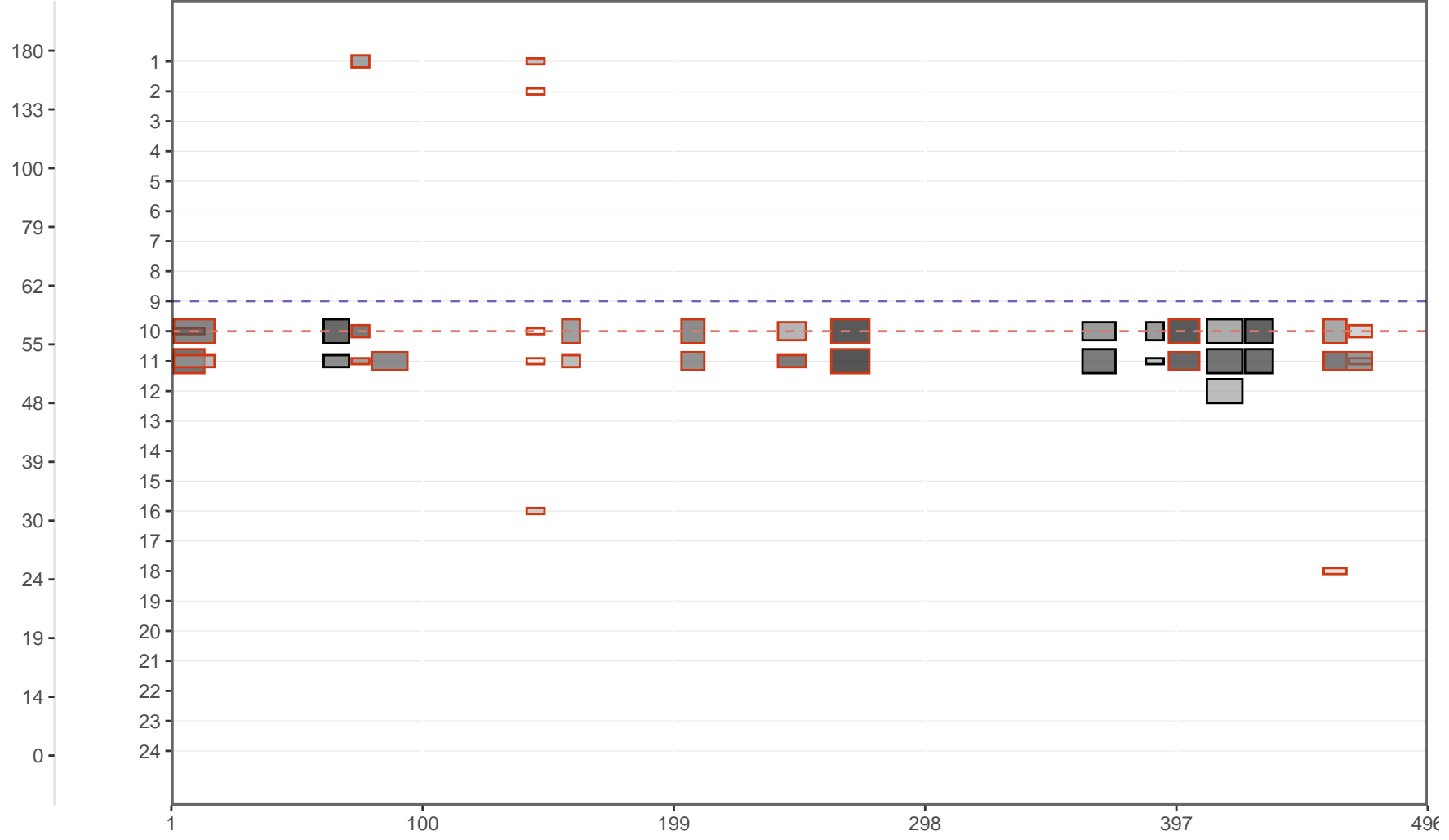
DWVSCVRFSPNQLQPTIVGGWDRTVKWNLTNGKLRRTLAGHSGYVNTVAVSPDGLGASGGKDGVLWDLAEGRKLVLEAGSIHSLGFSNRYVWLGATESCIRKVDLESGKSIYDLKVDLQGESEMCAEGTAAANKKIYCTGLSWADGSLFGGYSFDGLRIRWGIQRY

NbL16g04140.1 phosphoethanolamine_N-methyltransferase_1-like [MW = 56.19 kDa]



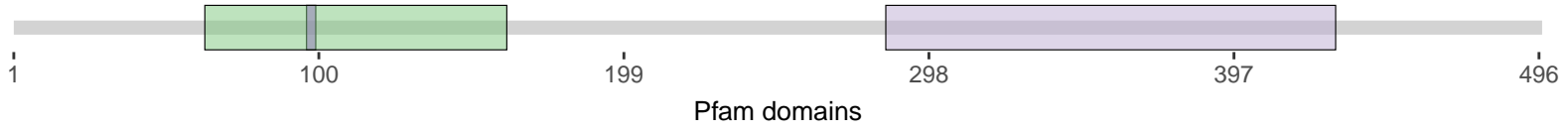
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

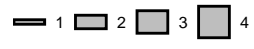
SP Sequon TM Domain PF08241 Methyltransferase domain PF13489 Methyltransferase domain

Protein sequence:

SADDKGFQFLDITVGHKSNGLRFRVFGHGSFVSTGGIDTFRFVAMLDLQPGKVLSDVGGGIGGGDFMAEKVEVYVGDLEVNMIQLAFERAVGRKGAVEFEVADCTTKTFPEGTFRVYVSRDITLHQDKPALFRFVYWLKPGKVLSDVGGKAGPASEEFAEYKGRGVYDLDVEVAGOMLRDAGFNDAEEDRTEQFKVLOKELDTVEKERESFQGFSEKDYNDVGGWAKLRSTSSGGEQRWGLFIKKY

NbL16g04130.1 calcium-binding_allergen_Ole_e_8-like [MW = 17.28 kDa]

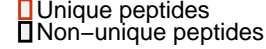
No. of times detected



log(intensity)



Values from



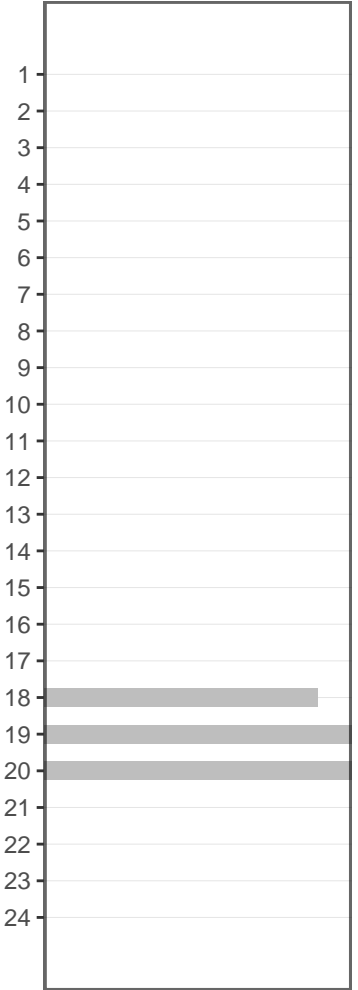
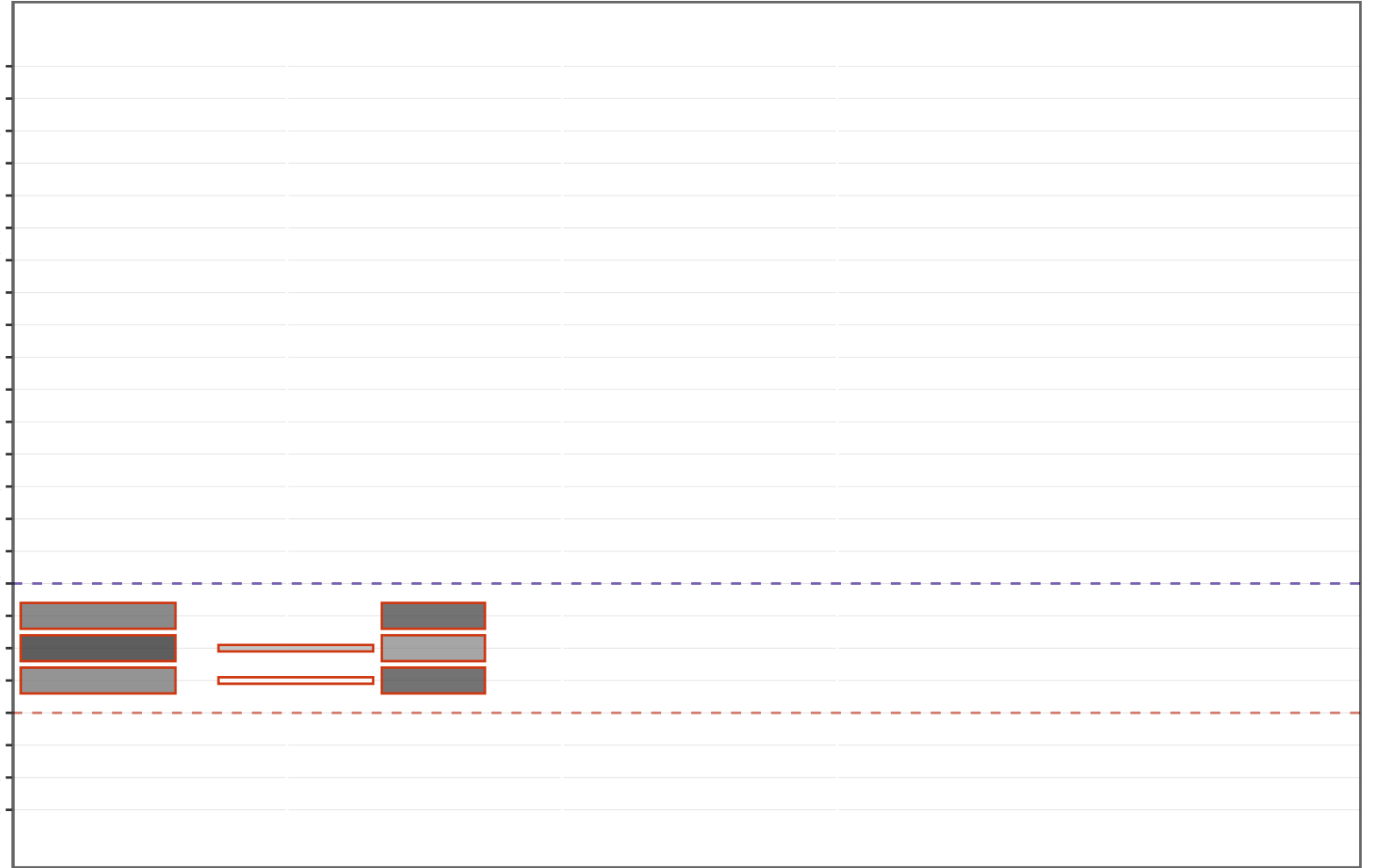
MW indication



Molecular weight



Gel Slice

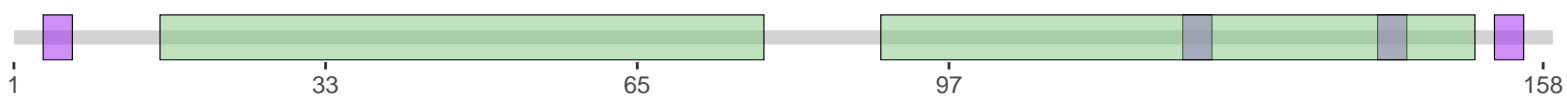


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

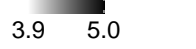
DGCLNLEEFADFCR66DDEVDGAKELKEAFDLYVDGNINGLISAELHQLNRLGGNGTVDGCTRMITSVDADGGDNVSEFEFKQMMNNNSKI

NbL16g03910.1 60S_acidic_ribosomal_protein_P2A-like [MW - SP = 9.84 kDa]

No. of times detected



log(intensity)



Values from



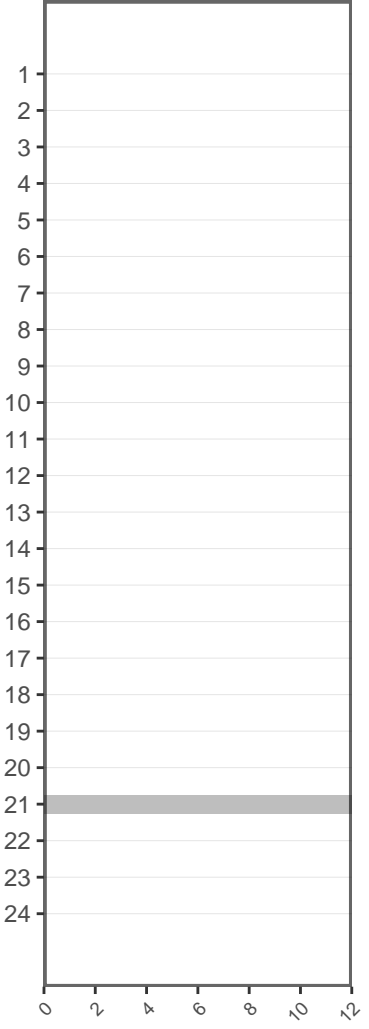
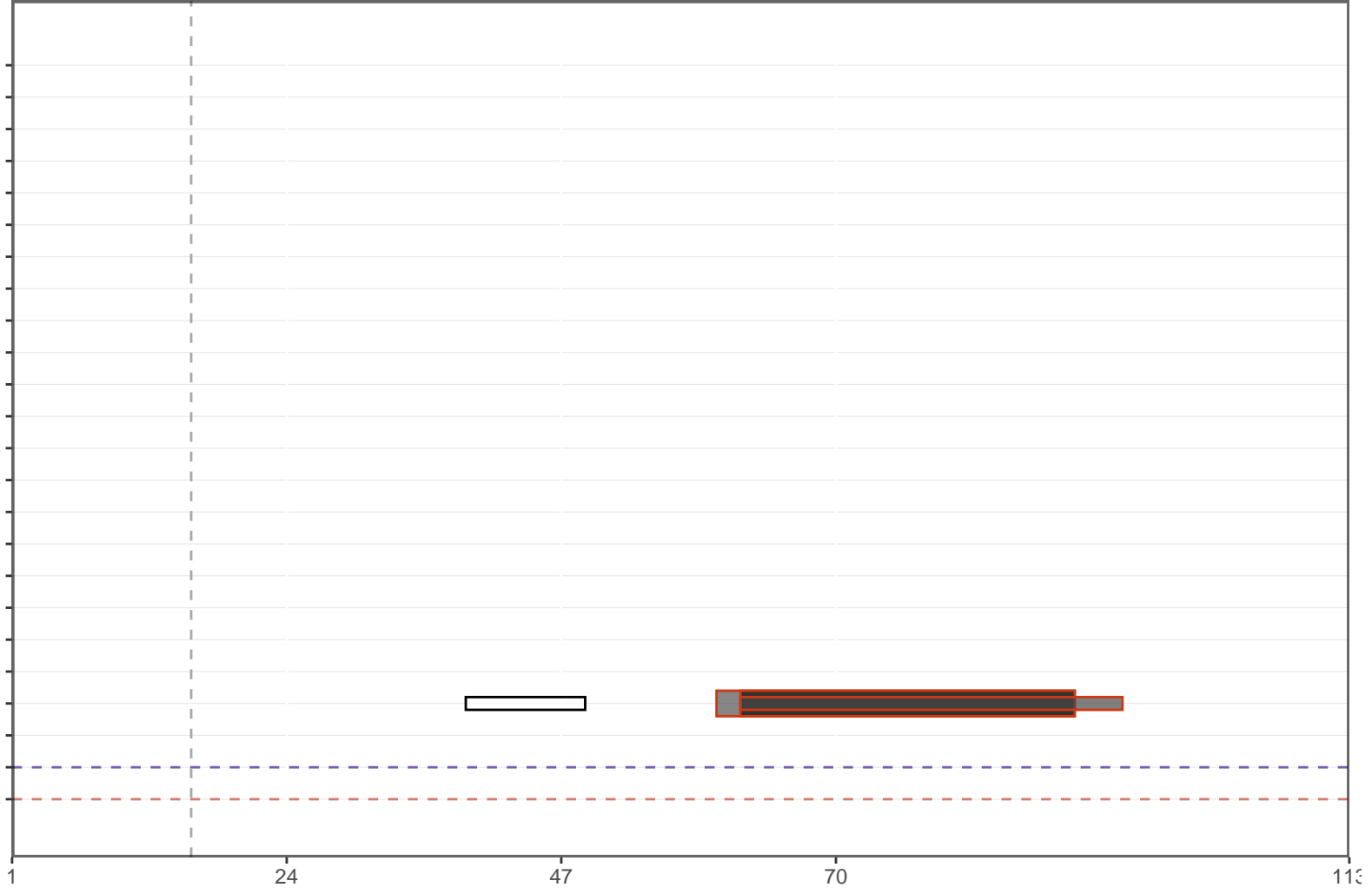
MW indication



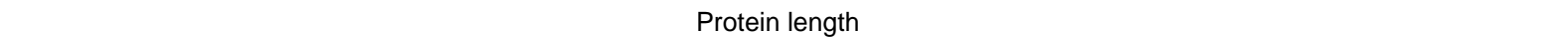
Molecular weight



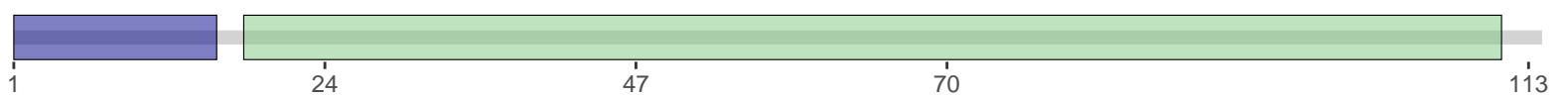
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IQVEGKDTLLAAGREKLABVPAAGAGVAAAPTGGAAAAAPAAEKKKVEEKEEEDDDMGFLFDI

NbL16g03870.1 60S_ribosomal_protein_L27-like [MW = 15.69 kDa]

No. of times detected



log(intensity)



Values from



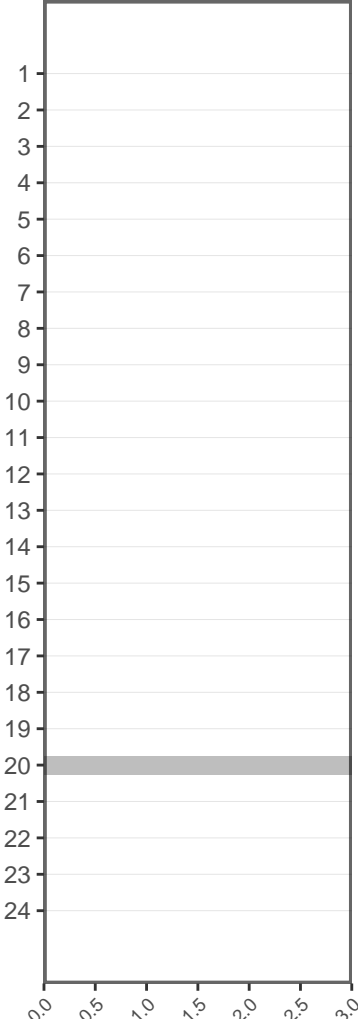
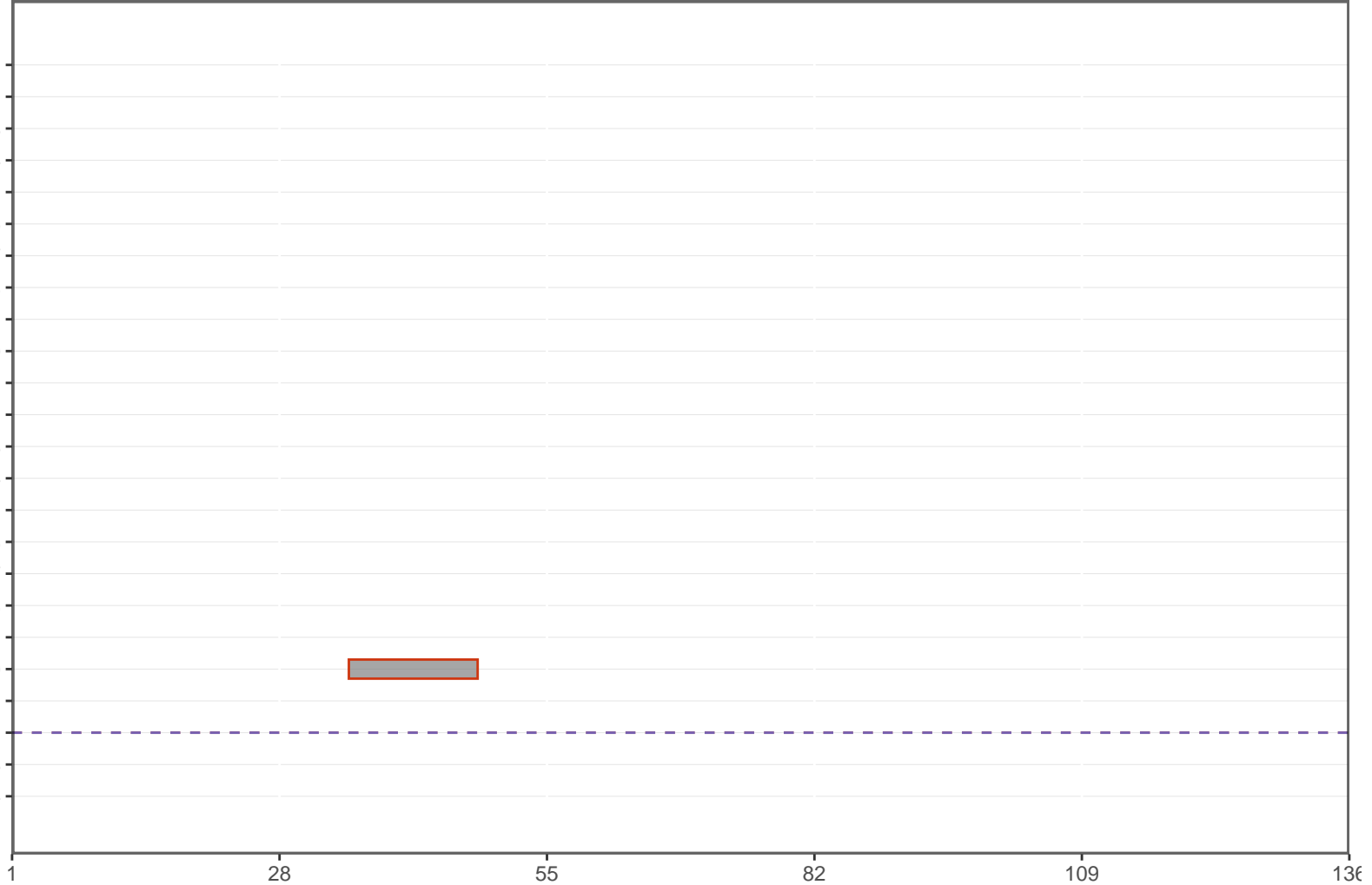
MW indication



Molecular weight

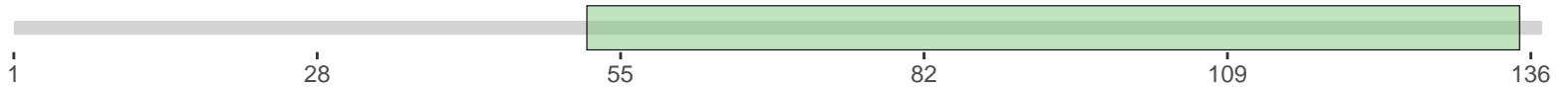


Gel Slice



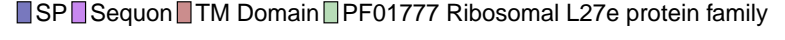
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

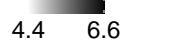
QSAKKGAKSRVNAFRLNLYNHMPRTYFLDVLKDVANNVDLQGRDKKVTAKAEAKARLEERFKTKGNRWFTKLRP

NbL16g03830.1 chloroplast_stem-loop_binding_protein_of_41_kDa_b_chloroplastic [MW = 42.14 kDa]

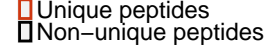
No. of times detected



log(intensity)



Values from



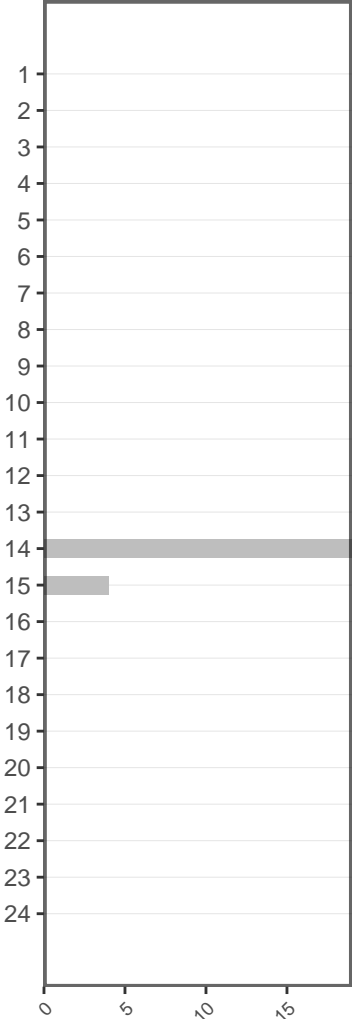
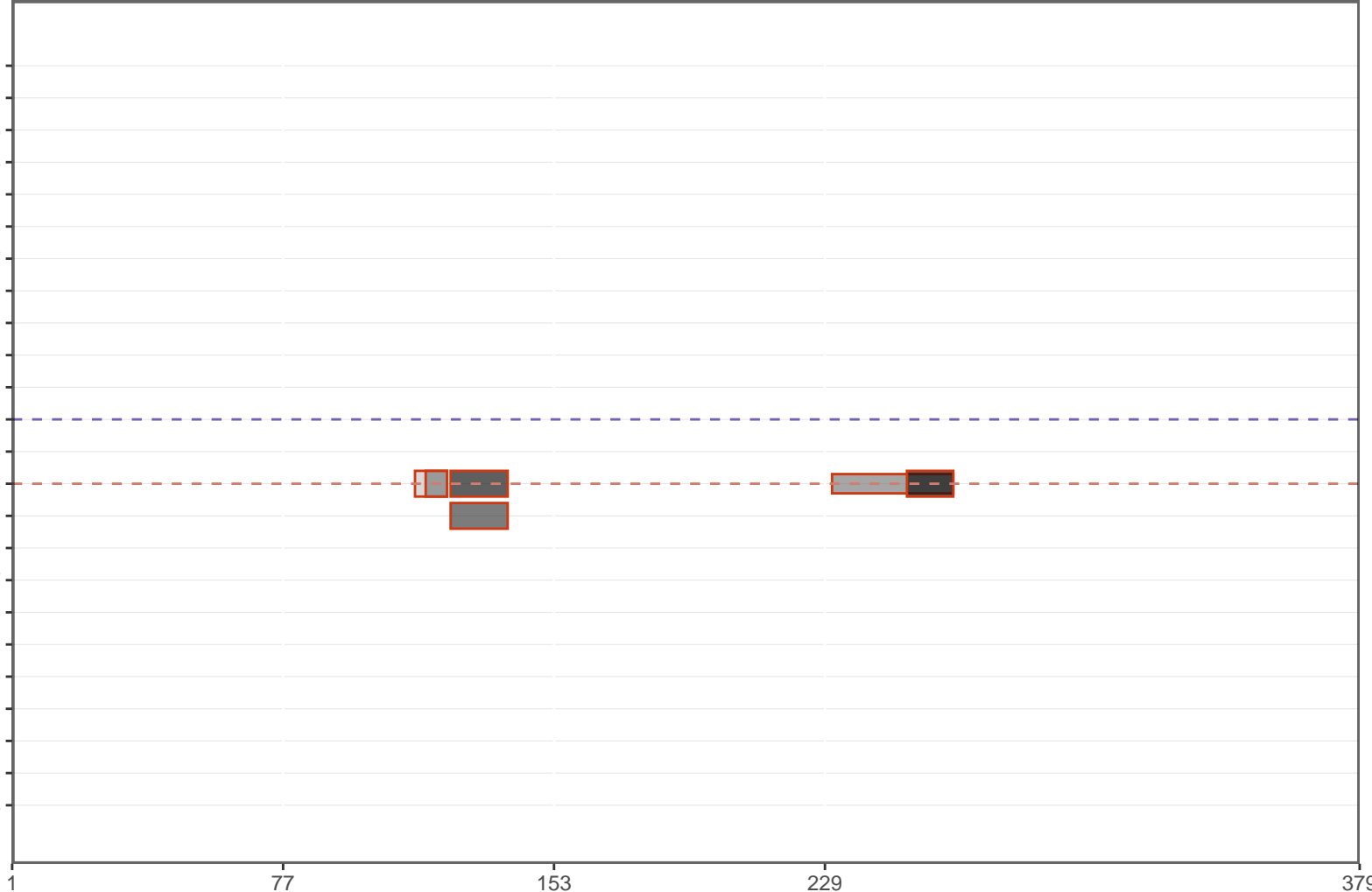
MW indication



Molecular weight

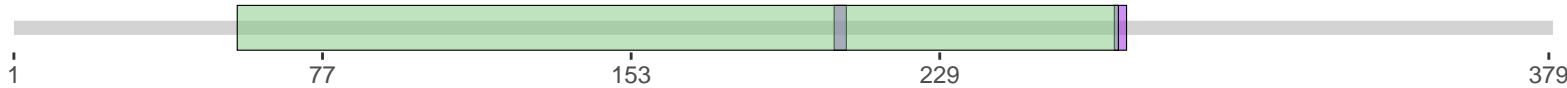


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IADAVDPKSRHKGKLETESELLESRDWNVTVSRPVYVYIGPLNPNVPEEWFHRLKAGRPINPNSGLQITLGHVXKDLATAFIQVILGNEKASKQVFNISGKRYVTFDGLAKAGAGGFEPEVHYNPKFDFGKKAFFPRDQHFHFAIVEKAKAVLGLWKPFEFELVEGLTDSYVNLDFGRTYRKEADFSTDDLLGKGLVLAN

NbL16g03810.1 probable_carbohydrate_esterase_At4g34215 [MW = 27.62 kDa]

No. of times detected



log(intensity)



Values from



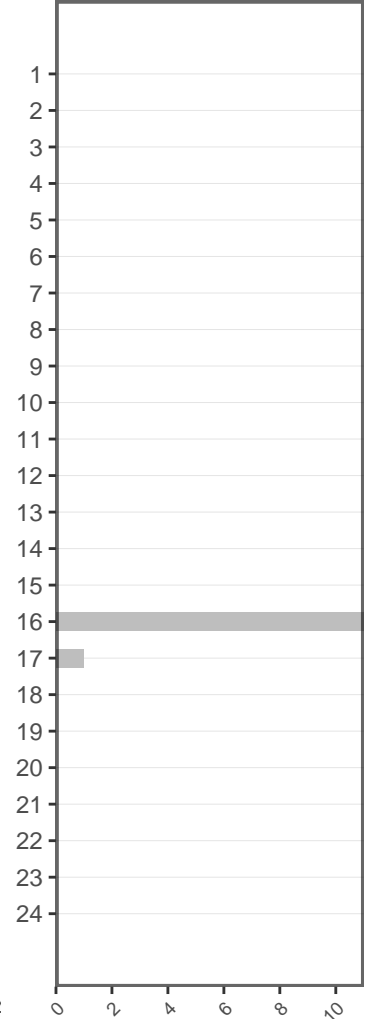
MW indication



Molecular weight

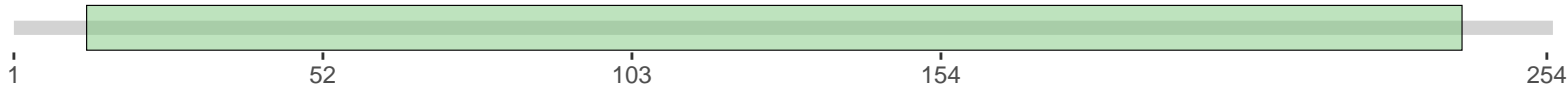


Gel Slice



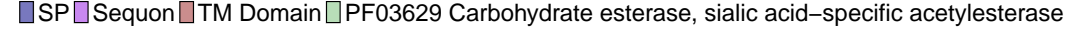
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IGEHLYENMKRARASVHGGDEKALWYGGESDTLSGHCAETFKANIEKLIHNVKADLDLPLPIQVYVHSGDDKYIEKIREAGMVDLPNVCVDDAMGLQKEDNLHLCTEAGVKKLGGMLADAVLTHFAPGQPEVASSP

NbL16g03800.1 tRNA-dihydrouridine(20)_synthase_[NAD(P)+]-like [MW = 36.06 kDa]

No. of times detected



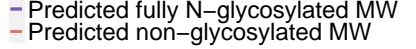
log(intensity)



Values from



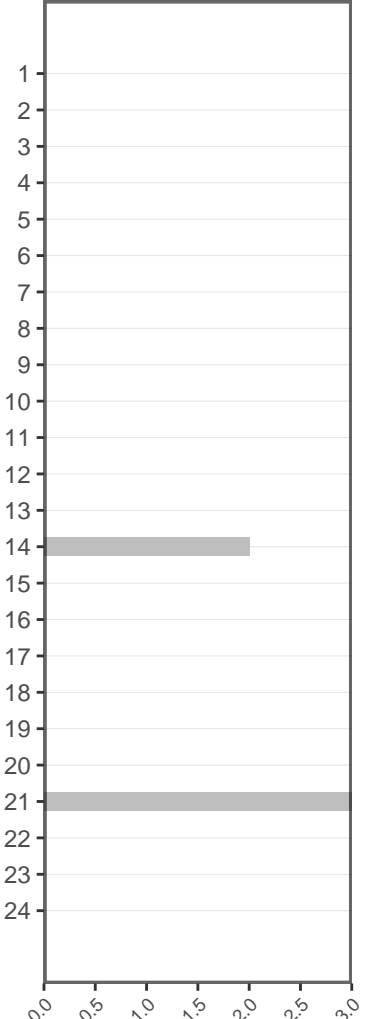
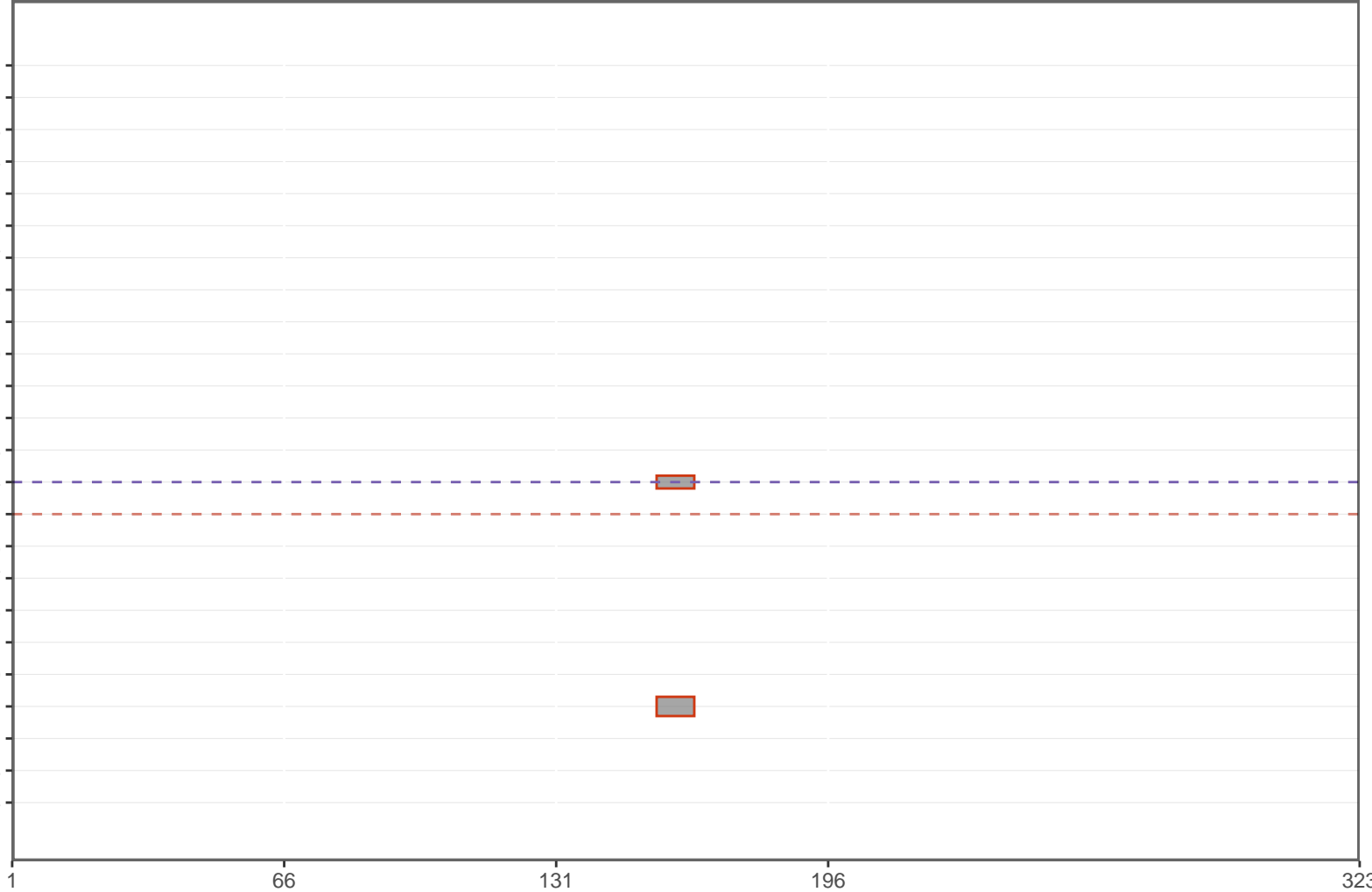
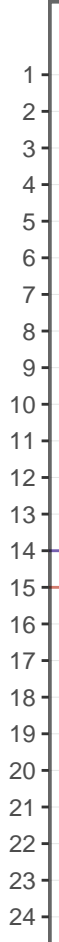
MW indication



Molecular weight



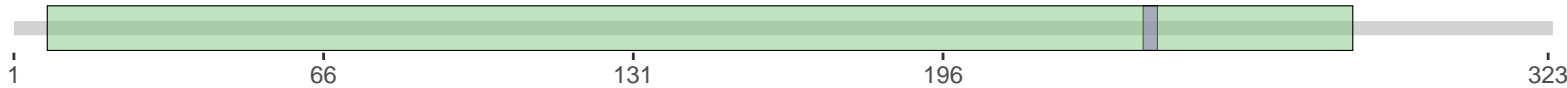
Gel Slice



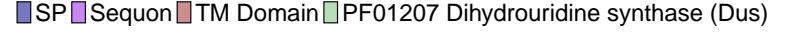
Protein length



Pfam domains



Pfam Description

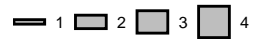


Protein sequence:

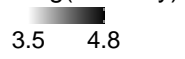
IRLLKSPDQTVLARRIERTGVSAVAHGRKVDPRPRPAKWSEIADVAASLSIPVANGDVFVEYDFQMRDQTGASGVMMVARGAIVNASIFSSEGGKIPREDVYRKRKISILWQNDIKSTKHTLKEMMQYSSGLLPEGGAVKSDTLADLQGLYGEKKYVEYVTEGWRSAI

NbL16g03740.1 fructokinase-2 [MW = 34.78 kDa]

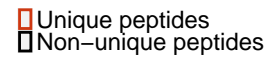
No. of times detected



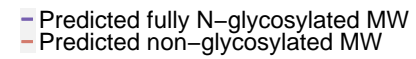
log(intensity)



Values from



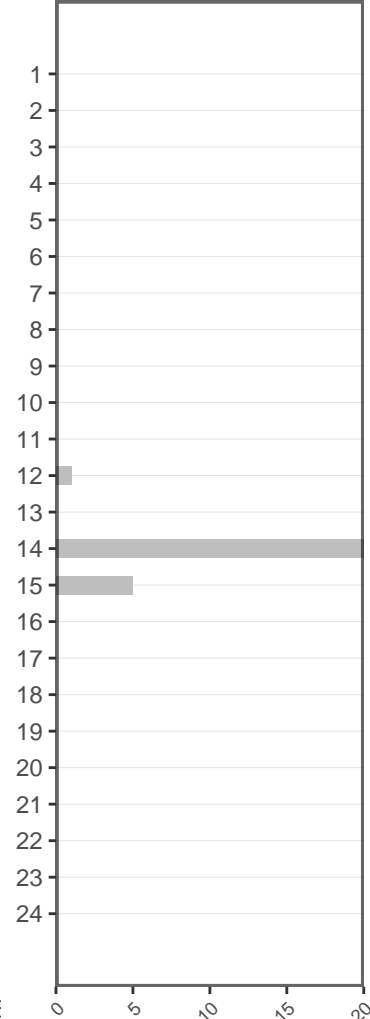
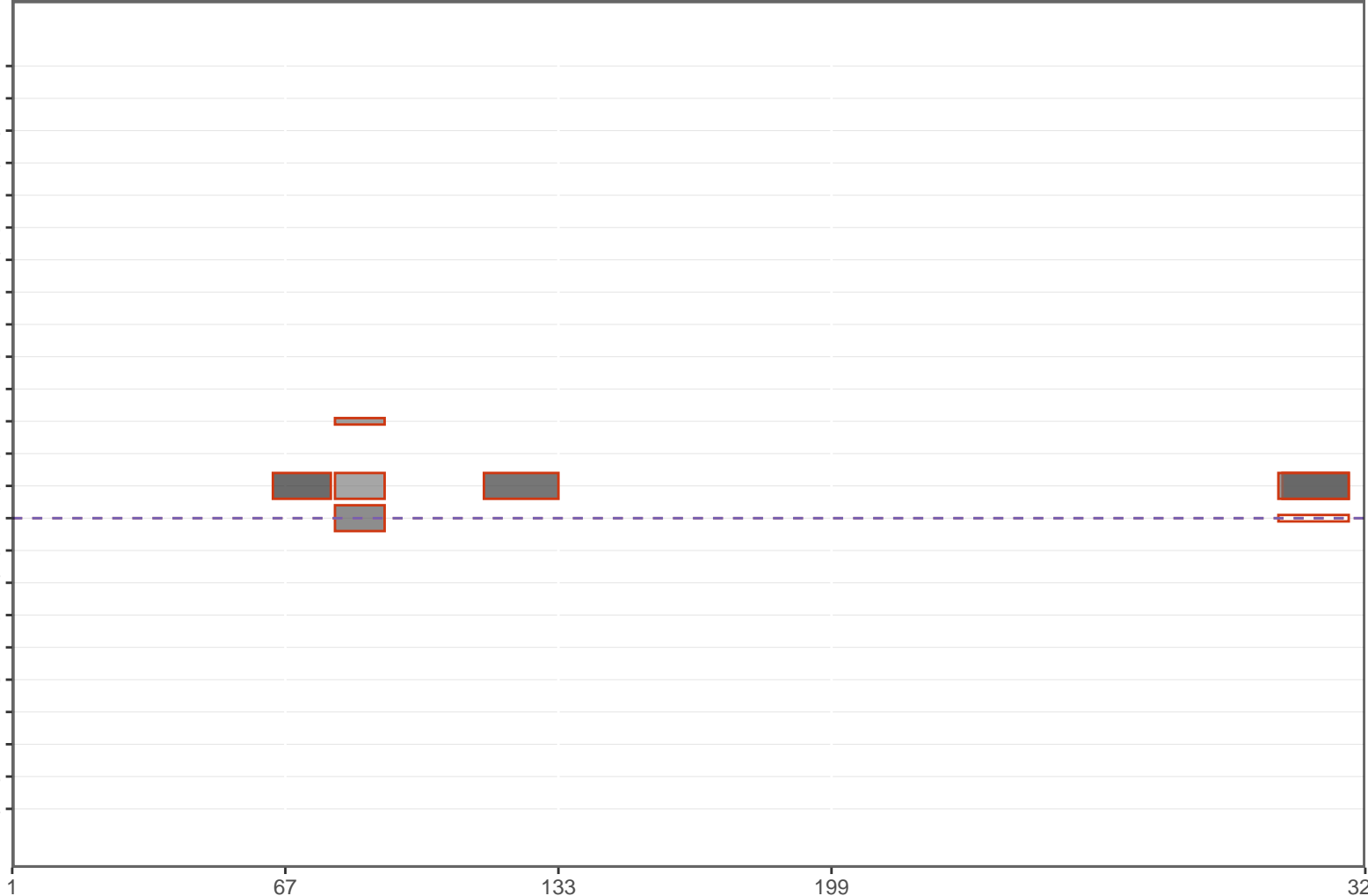
MW indication



Molecular weight

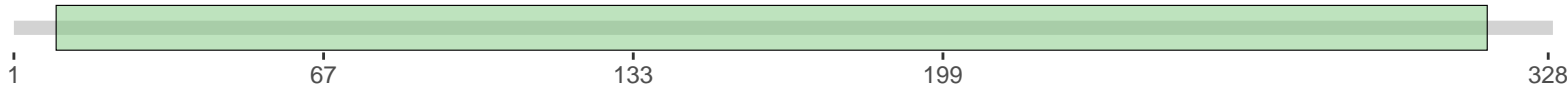


Gel Slice



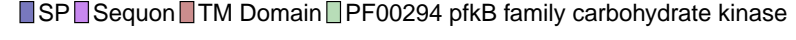
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RSAAHLKAMEVAKGAGALLSYDPNLRLLPLWPAEEGARIKGKGIWIKADVKKVSDVELEFLTGSDDKIDDESAMSLWHPNKLKLLVTLGKGGNYYTKNPHGGVEAFHVKVDTTGAGDFVGLTKIVDDGILEDEARLKEVLRFAAGAGATTTKGAIPALPTESEALTLKGGAV

NbL16g03630.1 haloalkane_dehalogenase-like [MW = 47.36 kDa]

No. of times detected



log(intensity)



Values from



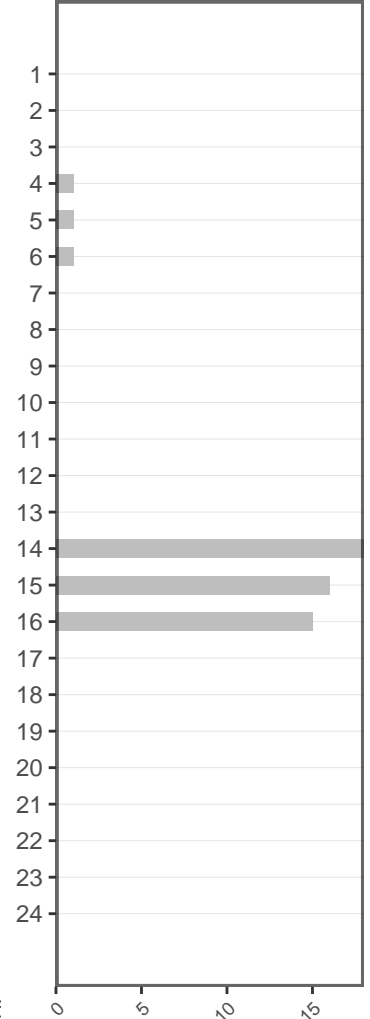
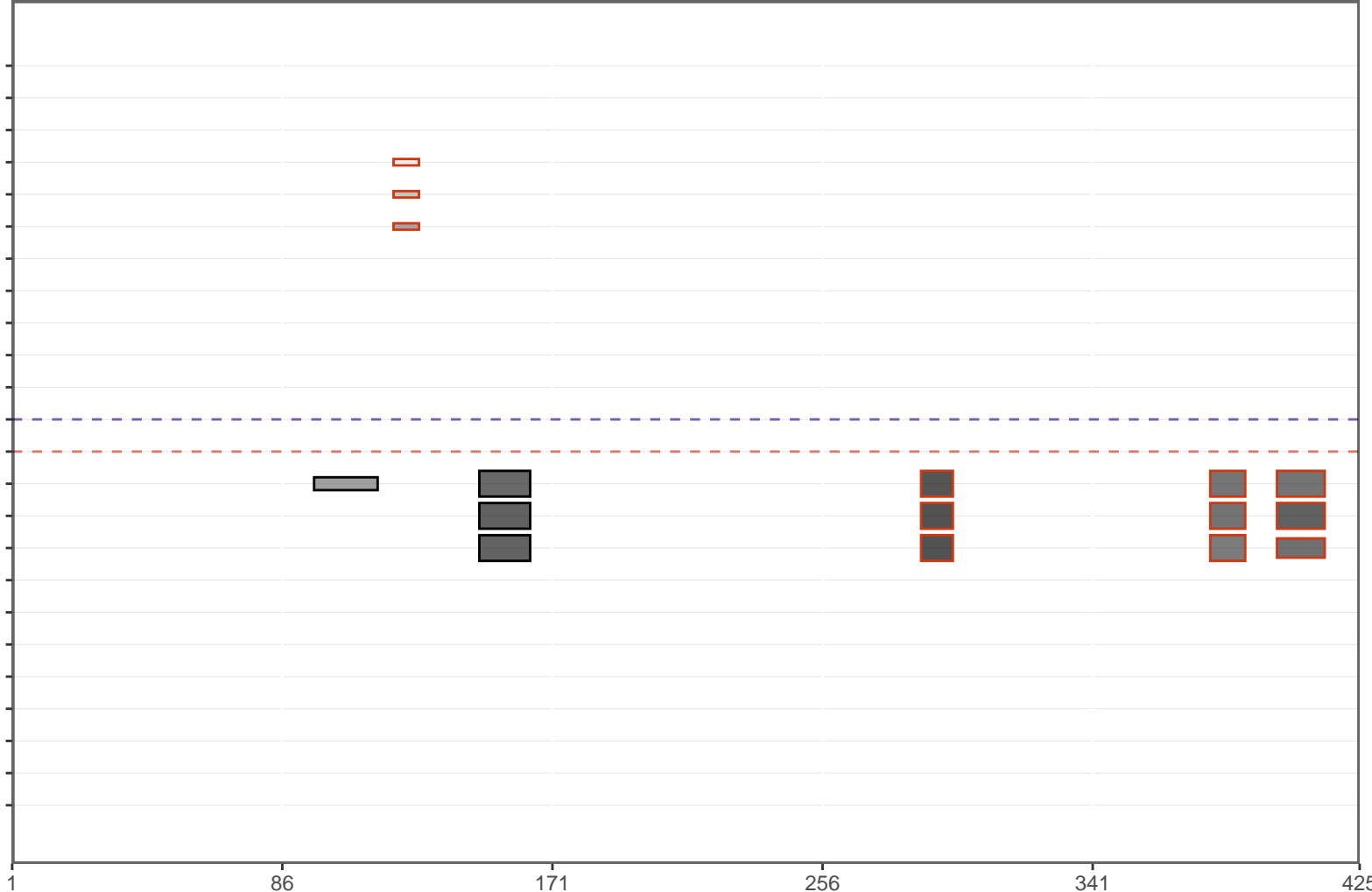
MW indication



Molecular weight

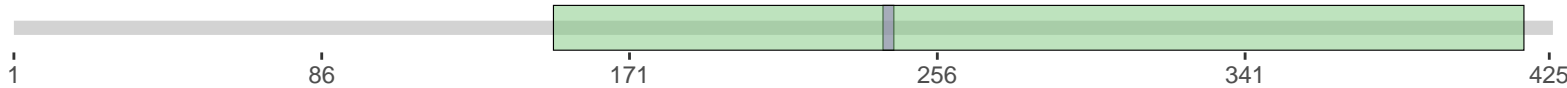


Gel Slice



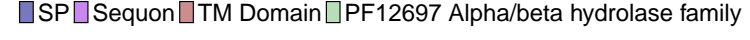
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

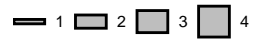


Protein sequence:

FDYTEKEFHIEEFENKLELVGVTSFFFLVVGGLVGSYGLTWTLKNKSKIKLALNPLTVSSPFGDFGDLRIPFFGFEFTGQNAVMAERFIEAGSTVYLLKLEKADVYRILPYLAGSGPFGFSGVYRILRERPGSPHLSDLPRALLEETARKAKFNEIASQISGSGFASGSDWKPIILWVGISDXYLPQSIIEEFQKANKPDSVKLKLIEGAGHMPOEDWPEKVVDAIRMFFR

NbL16g03620.1 clustered_mitochondria_protein_homolog [MW = 188.94 kDa]

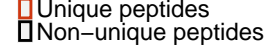
No. of times detected



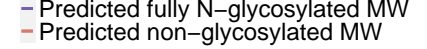
log(intensity)



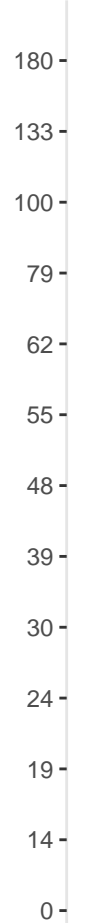
Values from



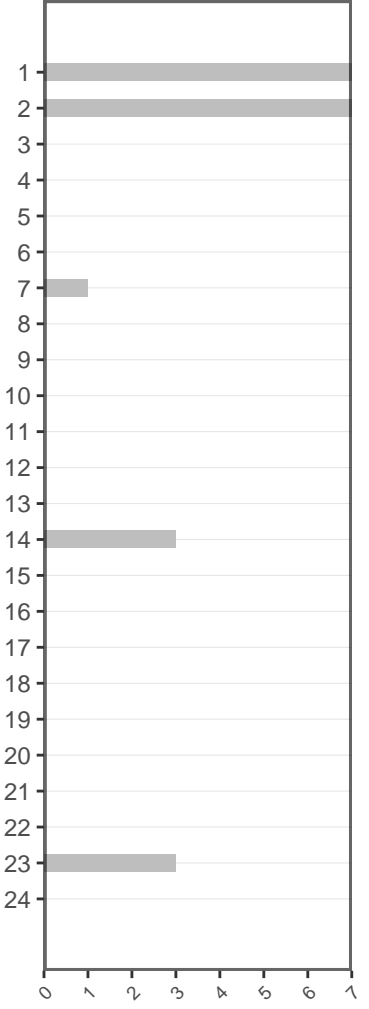
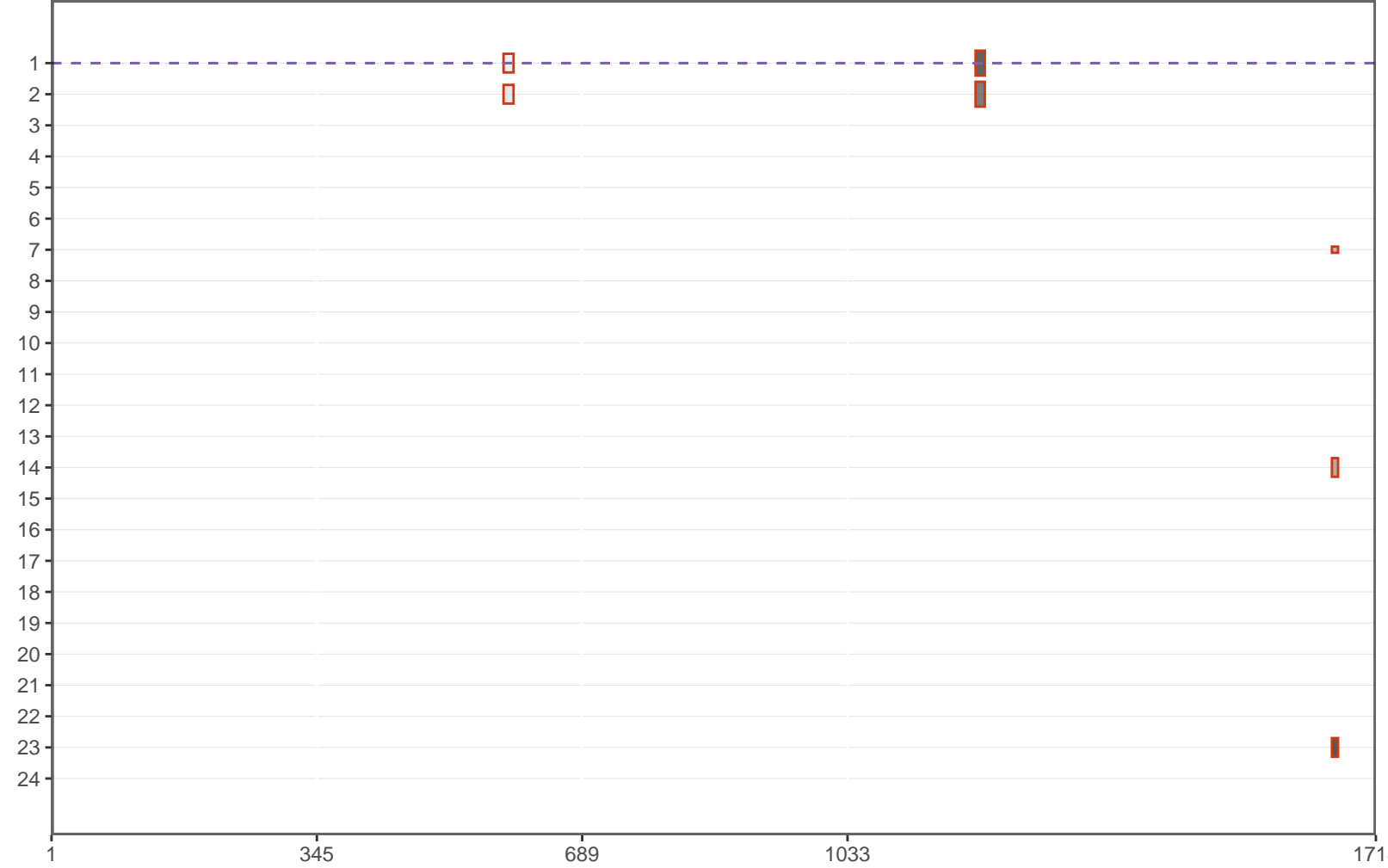
MW indication



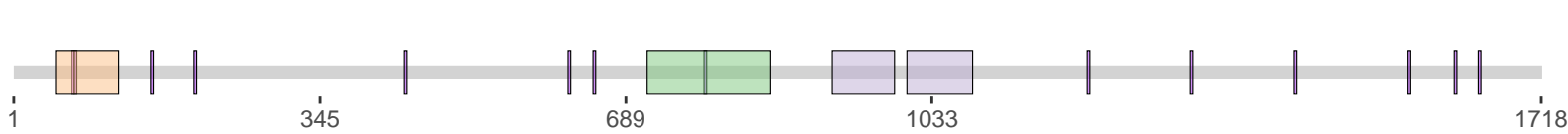
Molecular weight



Gel Slice

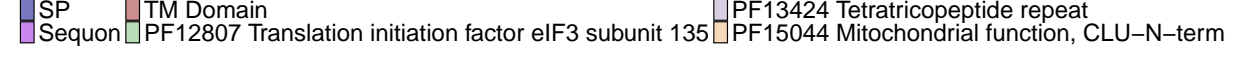


Protein length



Pfam domains

Pfam Description



Protein sequence:

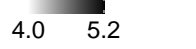
PKYDMESEPPYFPSKTDVTSWPLCKHVGGSADGRITLESKVALDKGKLEDAWVYGTAKALAKLAVGGPVRATASVSLAVVLYHTGDFNGATVGGKALDINERELGLDHPDTMSEYGGDSVIFYRRLGHELAALKYVNRALFLHFTGGLSHPTATVYINAMMEEGMGNVHALRVLHEALKGNRLLGVDHQGTAA5YHAAALSLMEAVSLGVQHEGTTLQILGAALGAEDLRTGDAAWALEYFESKALEQQEAAARTGAPRLDPAASKGHL6VSDLLDYISPSOGSI

NbL16g03600.1 triphosphate_tunnel_metalloenzyme_3-like [MW = 28.08 kDa]

No. of times detected



log(intensity)



Values from



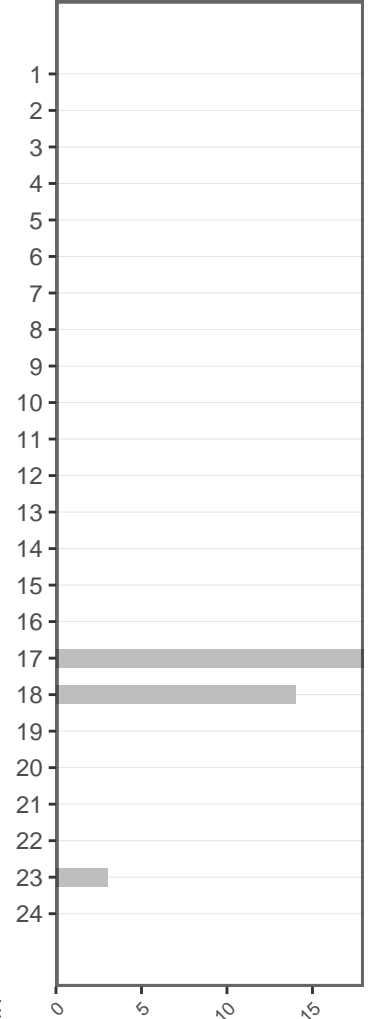
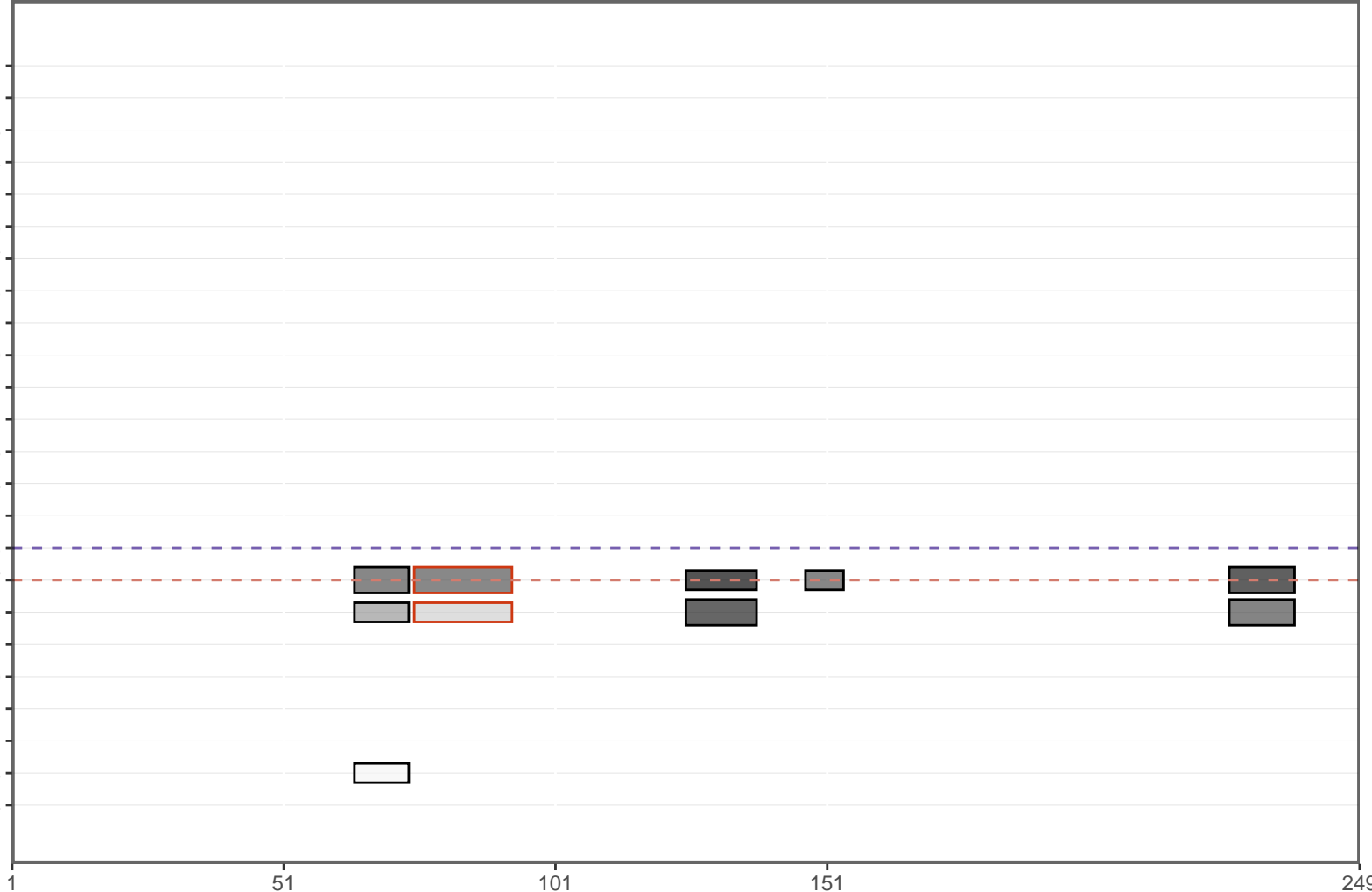
MW indication



Molecular weight

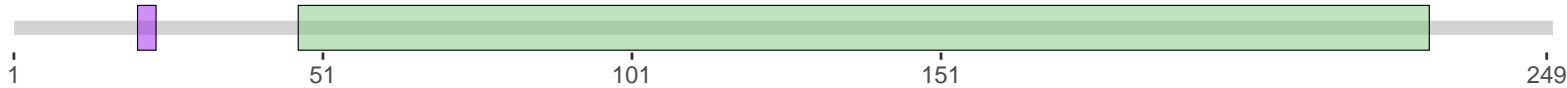


Gel Slice



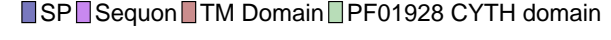
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KAKPYSNGISRIEEDDEPDPGRACVSDPWRLLLDSSRVQRWRDEVGDKGLVGLGFRNRAVYEWKGLKLELDETHYEFQMNYYEIEGSSDPERAKMDLEELKSHGIEYSYSTVSKFAIFRSGKLPQ*

NbL16g03580.1 proline--tRNA_ligase_cytoplasmic-like [MW = 57.03 kDa]

No. of times detected



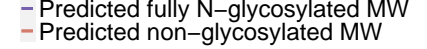
log(intensity)



Values from



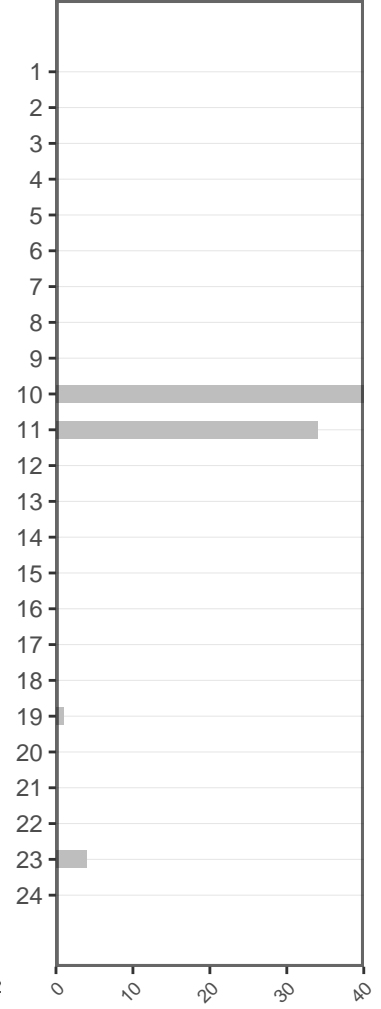
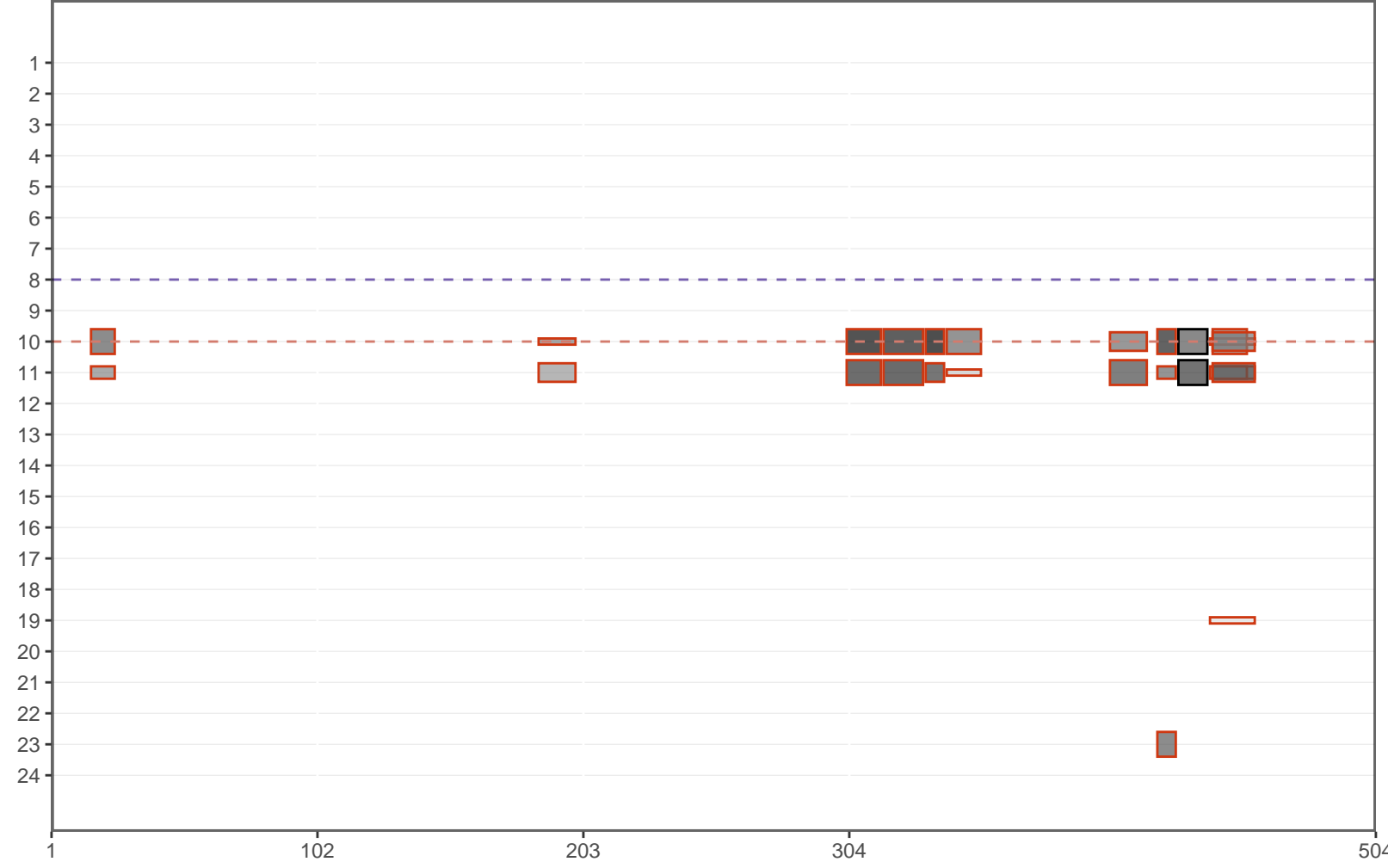
MW indication



Molecular weight

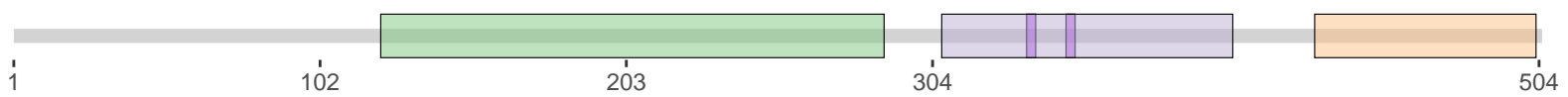


Gel Slice



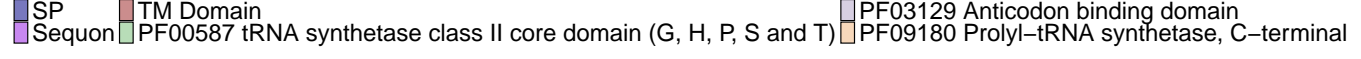
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IQGATSHICLGGNFAMFEINFEENEKEMAVVQNSWYTRTRIGVMMVHGDDKGLVLPKVAATQVIVIPYKIDANTGGFDACAATVKNLNEGGIRAEADVRDNYSPGWKYSHEWEMKGVPLRIEIGPKDLANNQVRAVRRRDNGAKADIPVANIAEQVKNVLAISGQNLFDVAKGRDAGVQVYKWTWDFAEALSQKLLIAPVWQDEEDVEKDKVARTKIGEMGAAKTLGSPFDQPELPEGLTLCFASGKPKMKWTYVGRGVY

NbL16g03320.1 aconitate_hydratase_cytoplasmic-like [MW = 105.48 kDa]

No. of times detected



log(intensity)



Values from



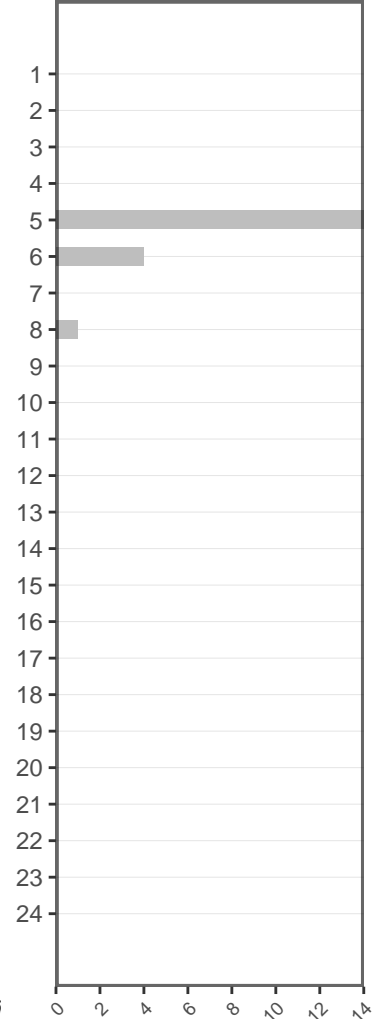
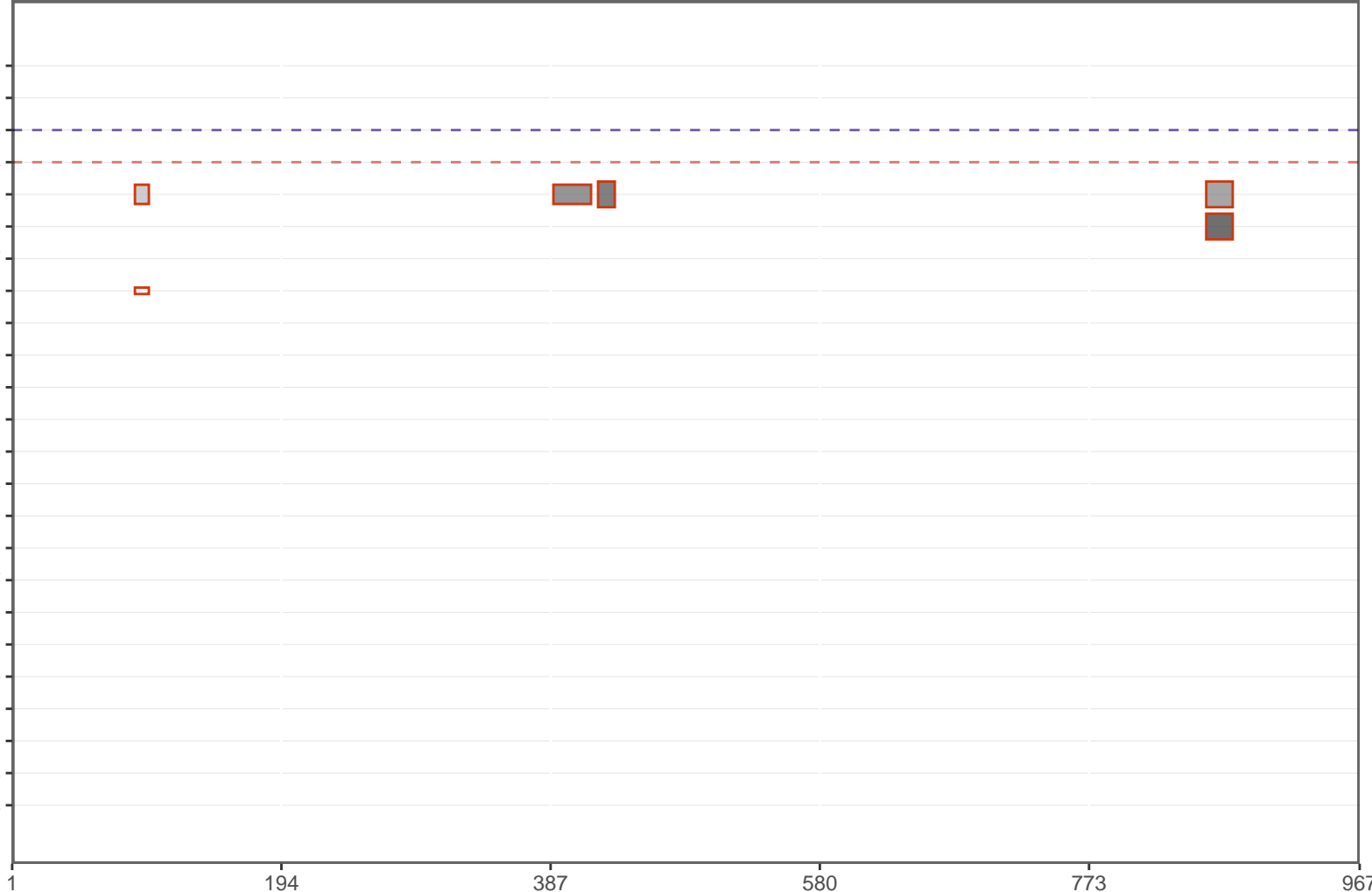
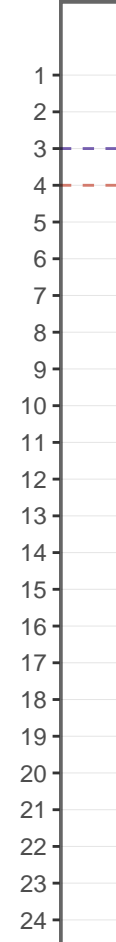
MW indication



Molecular weight



Gel Slice

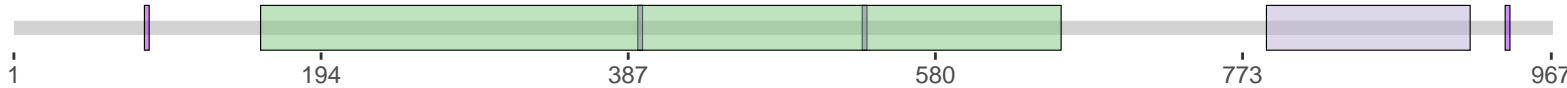


Protein length

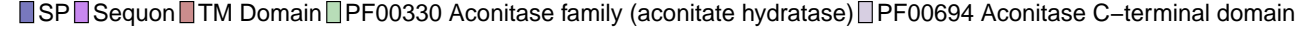


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

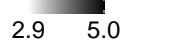
IPHDRVPLKEMKSDWHSGLNKKVGFKAVPKDAGEKVKKFSFHGDQDELKHGSVVAATSGTNTSNPVSMLGAALVAKKACDLGLHKPWTKTLAPFGSIVTKYLLGGGLKYLNGGGFHVGVGGTTCIGNSGDLDESVAISENDVAAVLSGNRNFEGRVHPLTRANLALAPPLVVAALAGTVDDIFEEEPKGVNDGKSVFFKDWIPSTEEIAEVVQSSVLPDMFKSTYEATKGNMWNQGLSVAAKLYSWEPSSTYHEPPYKDMTMDPPGPHGVKDAY

NbL16g03310.1 NEDD8-activating_enzyme_E1_regulatory_subunit_AXR1-like [MW - SP = 60.43 kDa]

No. of times detected



log(intensity)



Values from



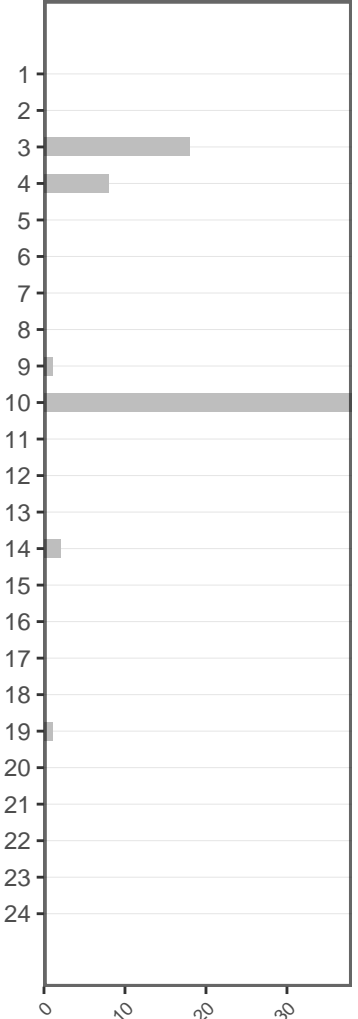
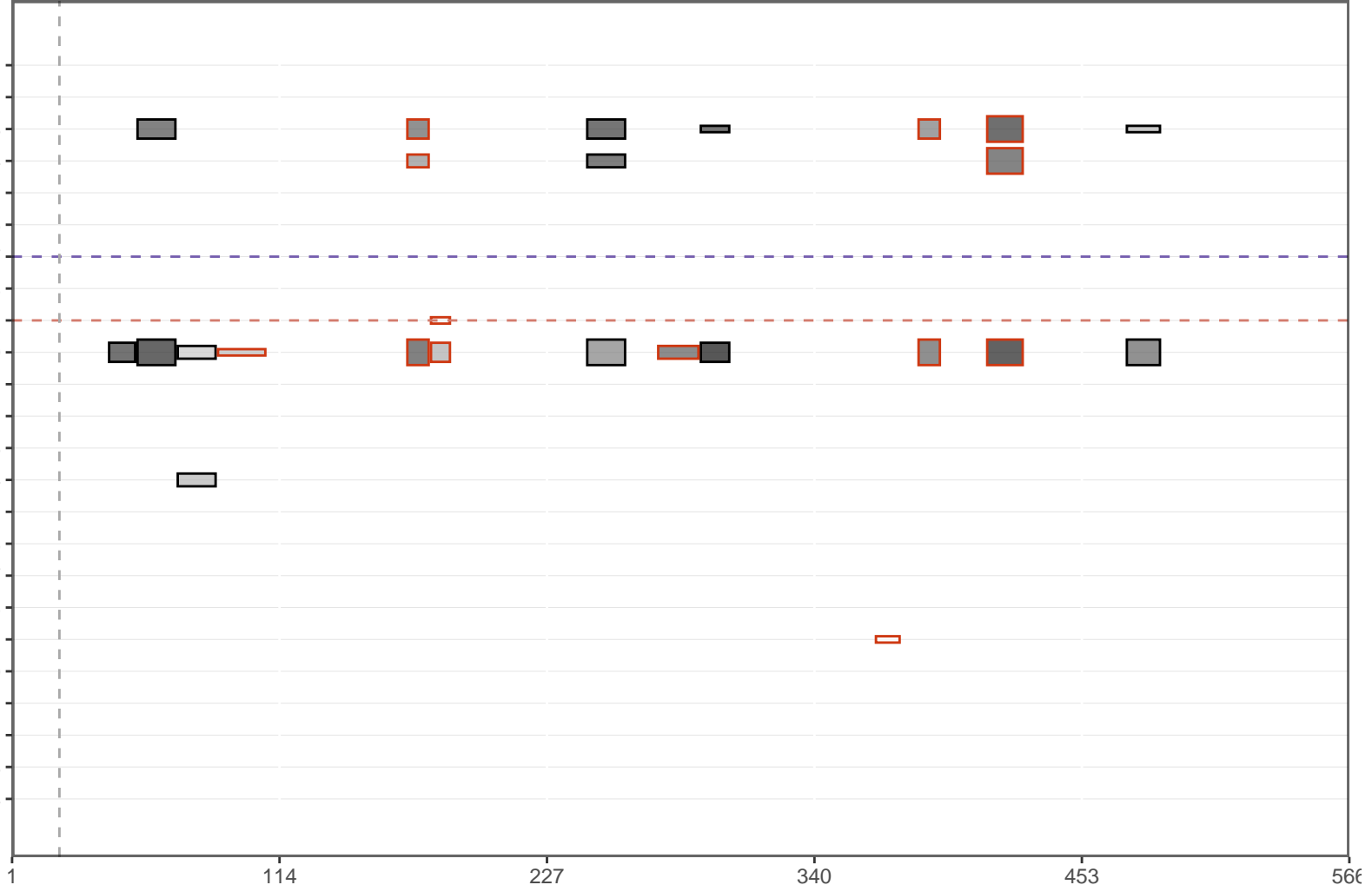
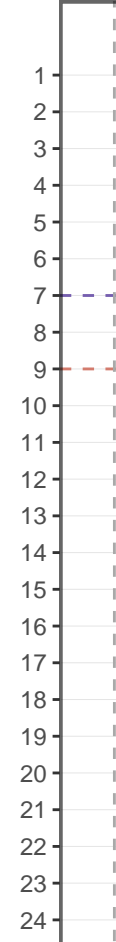
MW indication



Molecular weight

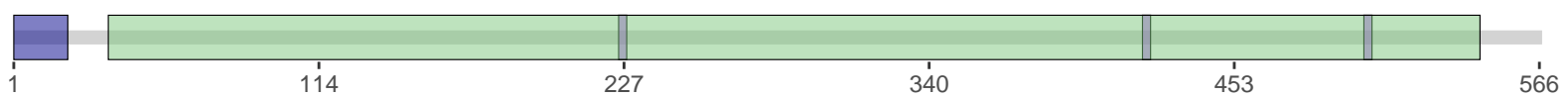


Gel Slice



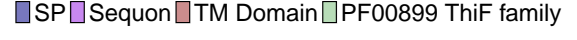
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKSKMTADEENYKAEVAYKLFSPGGTGNLQKHDDGCTEVDS66SDFWVVAALKEFIANEGGSETPLEGSPDMTSGSTELVNLQKTYGAKAEADFLVMEQKVRNLLKIKIGDRFASISKANKISFGQNAKRLAVCRVRLIEDEFNS6VQPELQKYLIDEDYGLTQEAANSLKVPENTAVGLVLLRAADRFAANYKFFQGFDMGEMDEDIRLKTAVGLLNDLGGNSGALSSEDLINEMCRVYGASLHWAAPVGGVAGQEVKILFRQIRPIMSGTFRFNGIDLKSLLLL

NbL16g03230.1 1-aminocyclopropane-1-carboxylate_oxidase_1 [MW = 36.05 kDa]

No. of times detected



log(intensity)



Values from



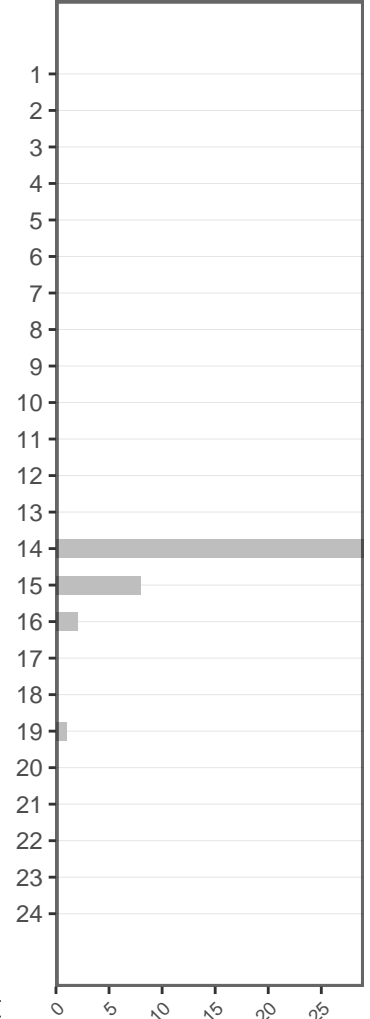
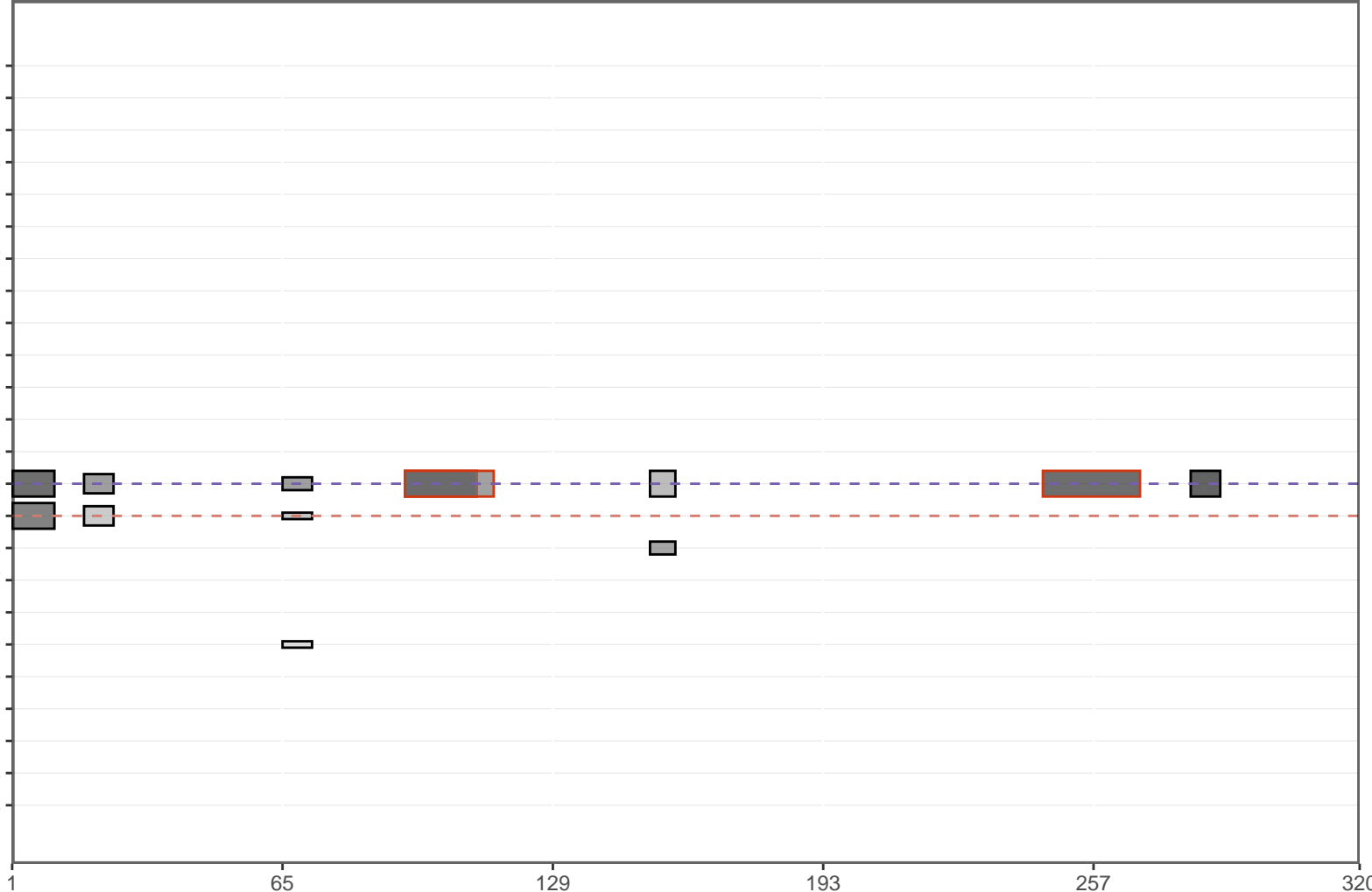
MW indication



Molecular weight

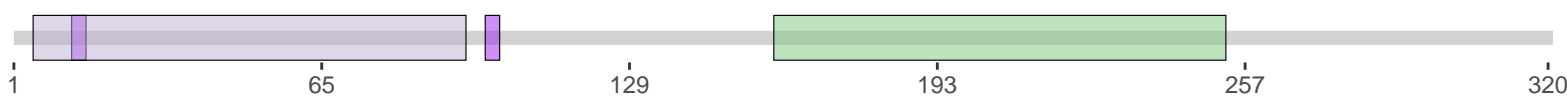


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF03171 2OG-Fe(II) oxygenase superfamily
- PF14226 non-haem dioxygenase in morphine synthesis N-terminal

Protein sequence:

VFYSGKGFNFCTKWSNYPGPKPDLKGLRAHTDAGGILLFDDDKVSGGLKDKGGWIDVPPTRHSIVNLDGQLEVTNGKYKSVMRHWIAGKDGTRMBSLAFYNGSDAVYPPALVAEKEAVESKGVYPKVFDDYMKLVAGLKFQAKEPRFEAMKBIESDVKMDAATAV

NbL16g02880.1 acylsugar_acyltransferase_3-like [MW = 46.42 kDa]

No. of times detected



log(intensity)



Values from



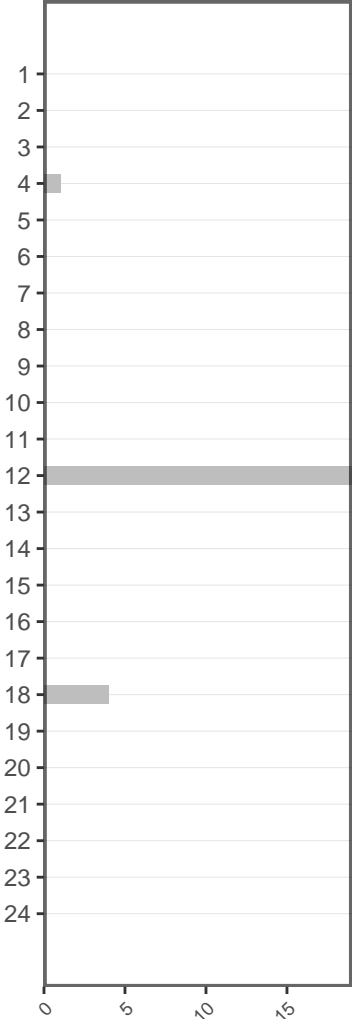
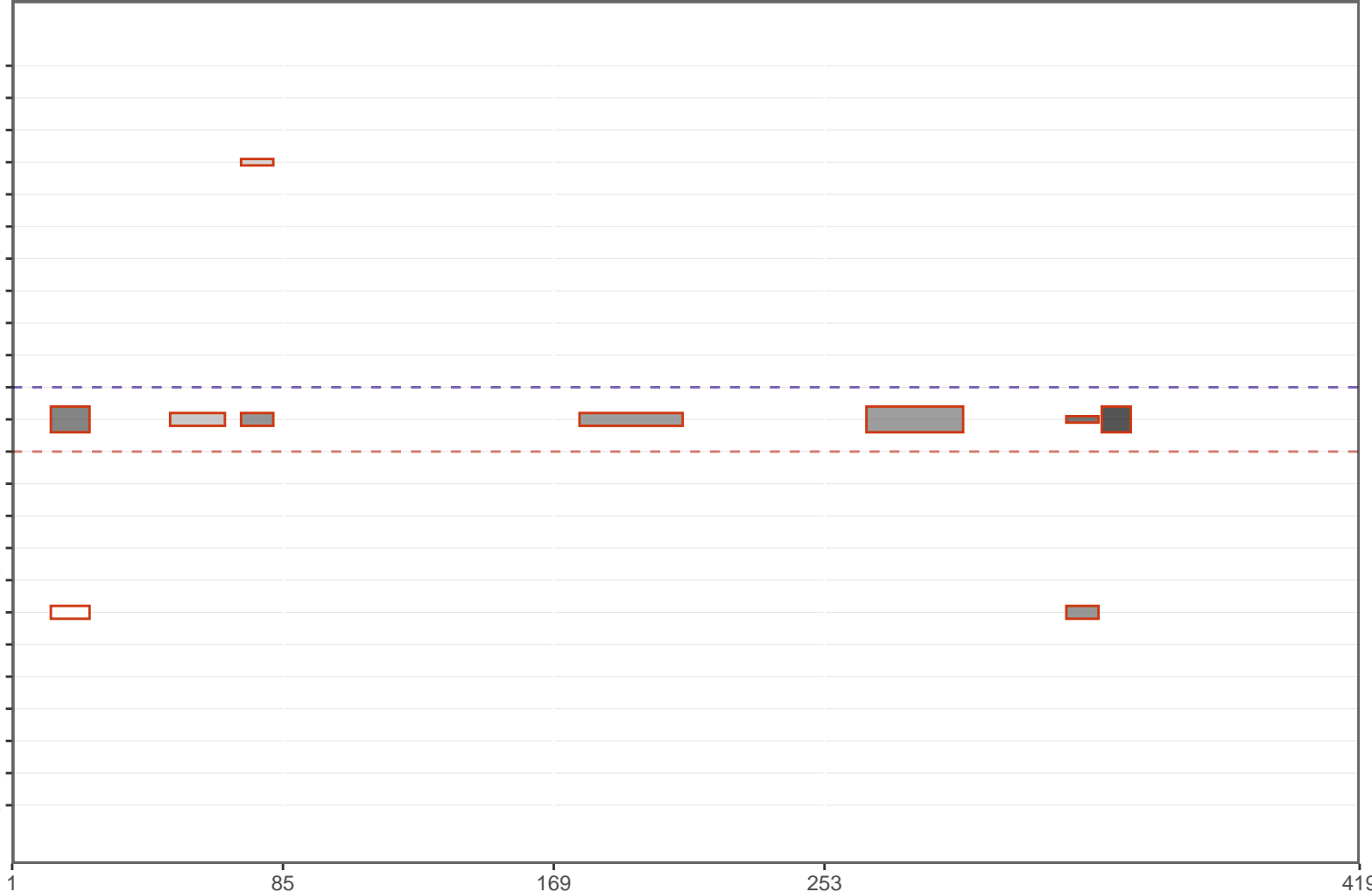
MW indication



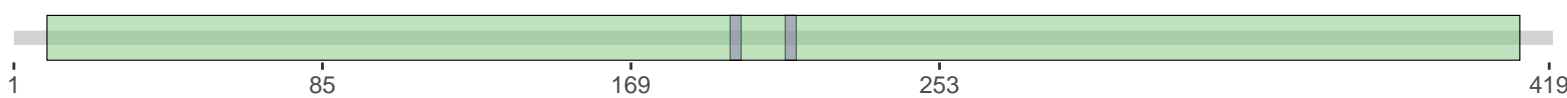
Molecular weight



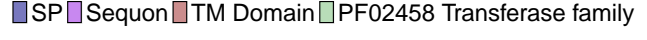
Gel Slice



1 85 169 253 419



Pfam Description



Protein sequence:

/SAPPLVADPSPKQNASRHYHFSASGLKALKARSGIPPTTVEAVTAFKCGKANTPTFKPBLLDGAWHLRGTNDALVPAGLVGNVLPYLVSAANEEDKLGRLGELREGKEKVRHMLKDKKSEEDLVSRVSELTQINERTSSNDFSIYRFSSLRKLPFHDLNFGDWGRPKIVDITSPMNMFYLENNONGDGDVLLVNL EEGEMSLFESNEELLOFASLQ

NbL16g02770.1 pyruvate_dehydrogenase_E1_component_subunit_alpha-3_chloroplastic-like [MW - SP = 51.45 kDa]

No. of times detected



log(intensity)



Values from



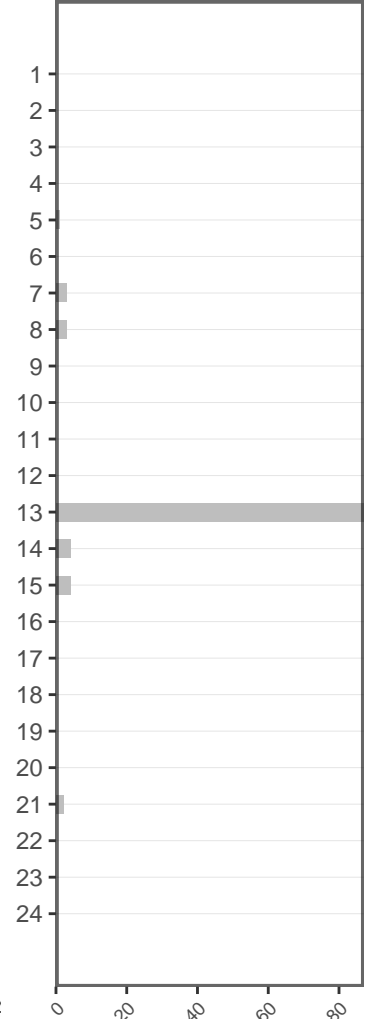
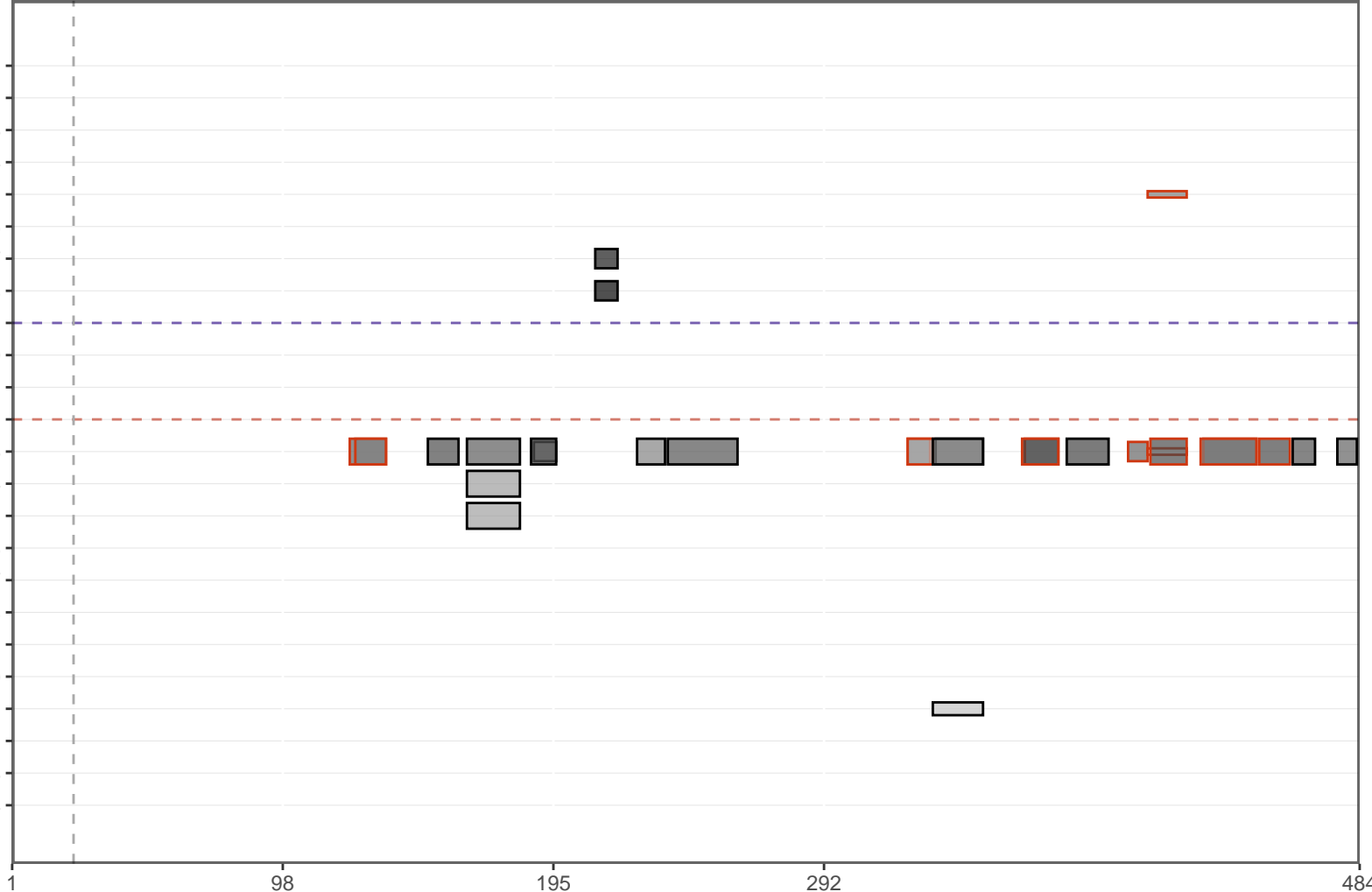
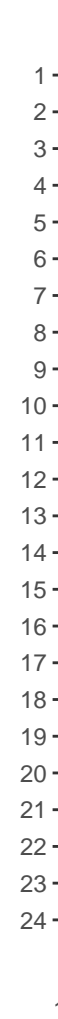
MW indication



Molecular weight

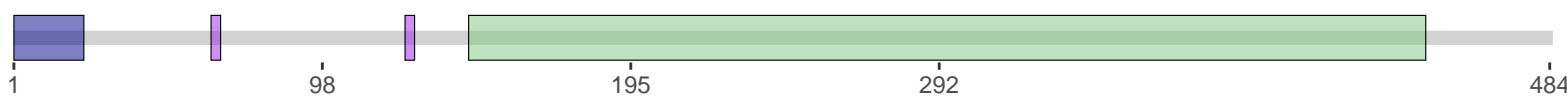


Gel Slice



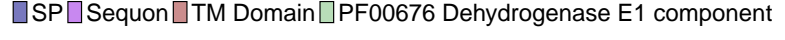
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IHMFSKEINVLGGFAFISGEGIPVATGAFTSKYKREVLKEADGDHVTMAFFDGDGTGNGOFFECLNMAALWKLPIHFVVENNLWAGMSHLRATSDPEIKWKKPFGMPCGVHVDGMDLVKRVKAEAVARARRDGDPTLVEGETYRFRGHSLADPDELRPKKNHYAARDPSALKKVMFENNLVNEALKAIDKIDDELVEDAVEFADSPHPVRSOLLENVFAIDPRFGFGDGRVRCEDPKFTEGTAHV

NbL16g02690.1 20_kDa_chaperonin_chloroplastic-like [MW = 31.85 kDa]

No. of times detected



log(intensity)



Values from



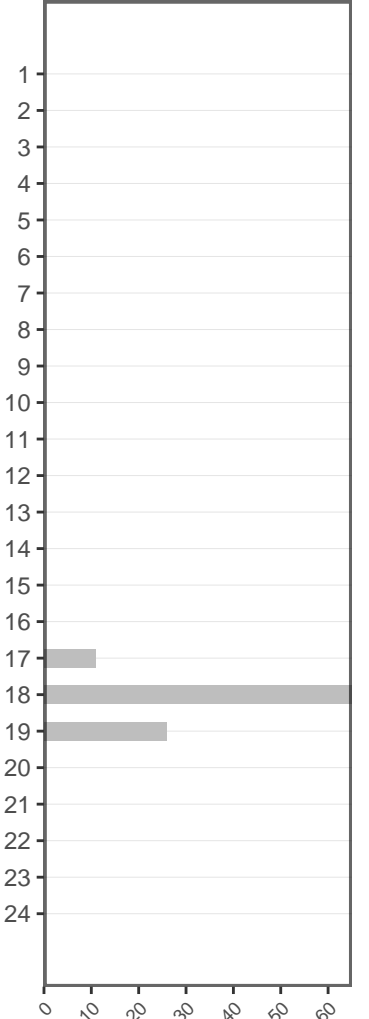
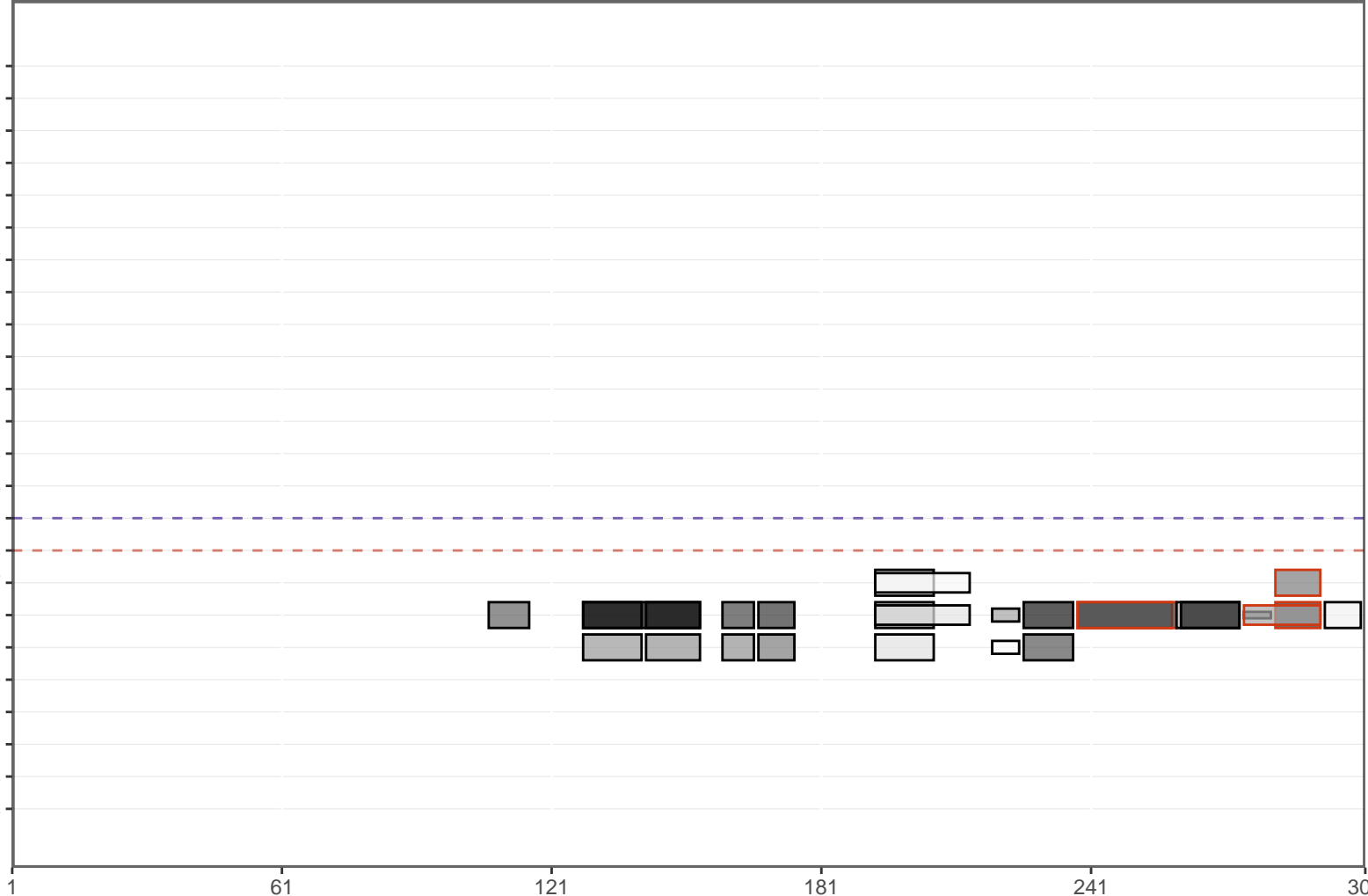
MW indication



Molecular weight

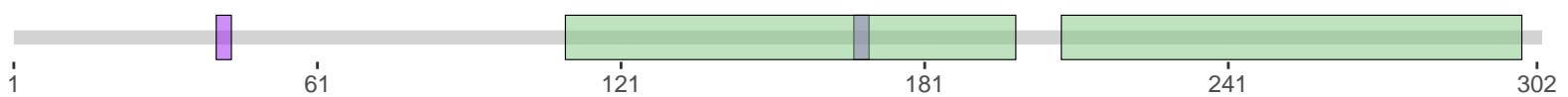


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IQSKPQGGIEIWAIGEGRSIGKTRKVEISVNGTGVLYSKYAGTEVLFDFGSHLILKEDDIVGILETDDKDLGFLNDRILIKVAEVEKTAGGLFLSEAAKEKPKSIVIAAGPGLDEEGNRKSLVSPGNTVLYSKYAGNDFKAGDGEDVYTLRASDVAIWLK

NbL16g02640.1 probable_polygalacturonase [MW = 55.1 kDa]

No. of times detected



log(intensity)



Values from



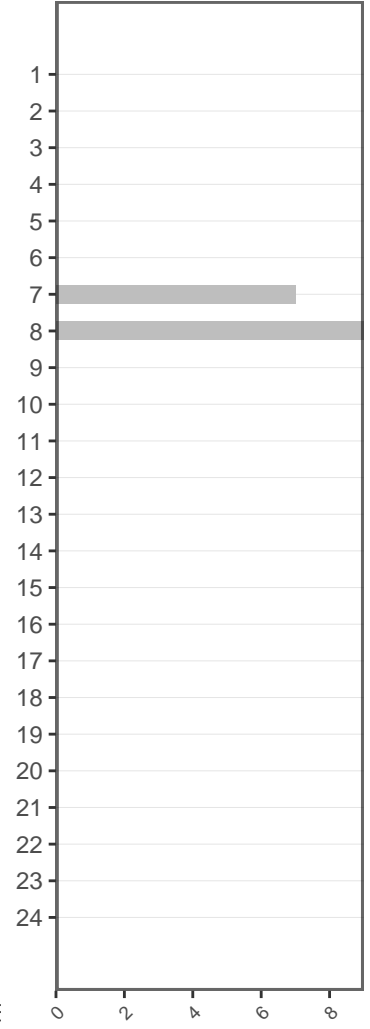
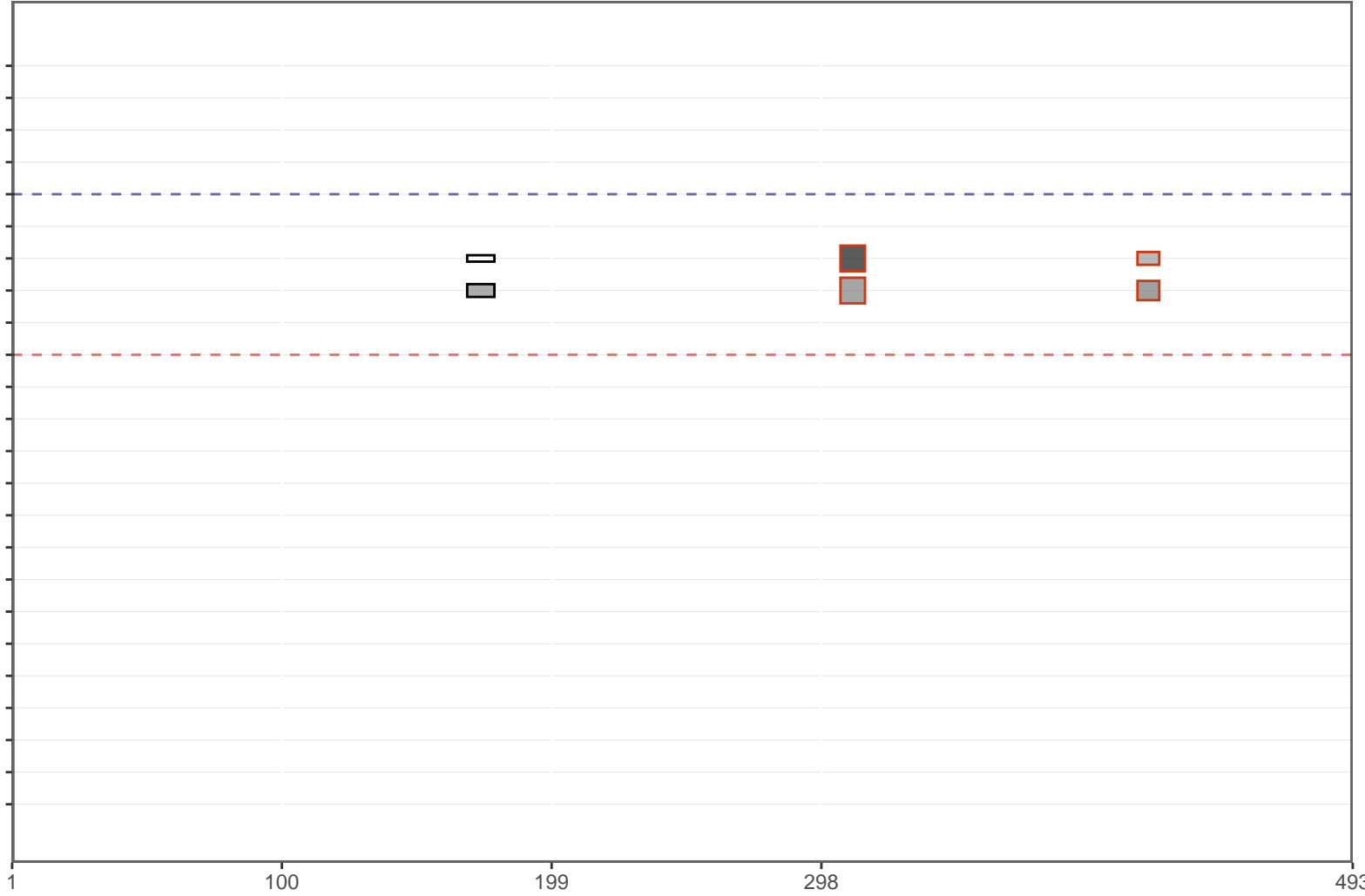
MW indication



Molecular weight

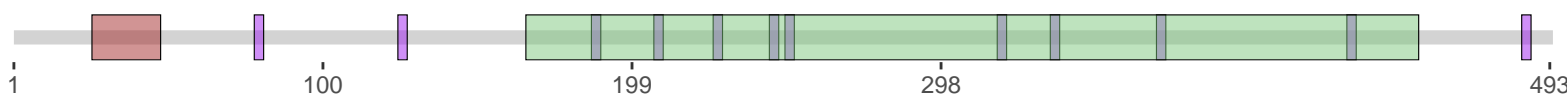


Gel Slice



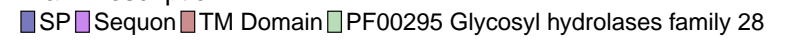
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SPFVTLIPYDCKNTRIRNNTILAPAGAPNTDGDIDPDSGEDVLIENGYISVGDGDIKAGGWDGYSIAYGRPSKNIILGNLIVIRNVSAGVSGISEMGGVSNVTVENLWNSRRARIRKTAIPGRGGYVRDYSYRNLTFENVRVGVIKTDYNEHADEKFDPKAVPLKDISYTSIHGEGVRRVPLVGHGSKPEPWNVYTRFDMSEVGLYKHKHIFGCAFVGGRRVGTTFPAPCENLDLYDEQGLIRRDGSDGNATDIDVQI

NbL16g02600.1 uncharacterized_LOC107785378 [MW = 21.73 kDa]

No. of times detected



log(intensity)



Values from



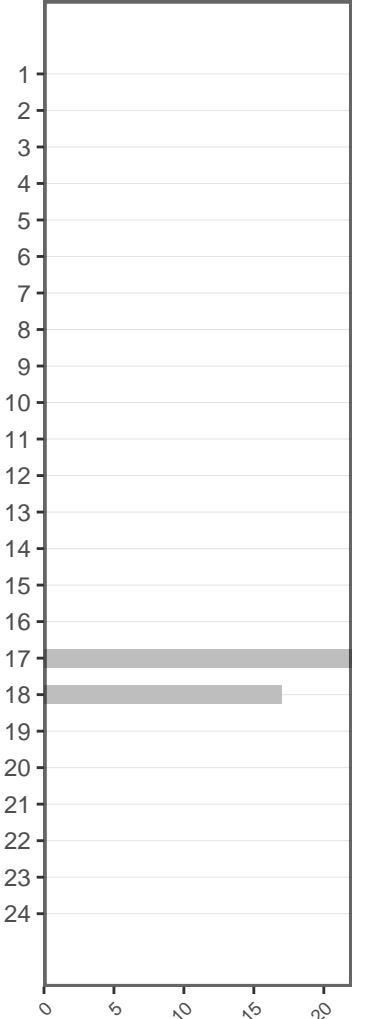
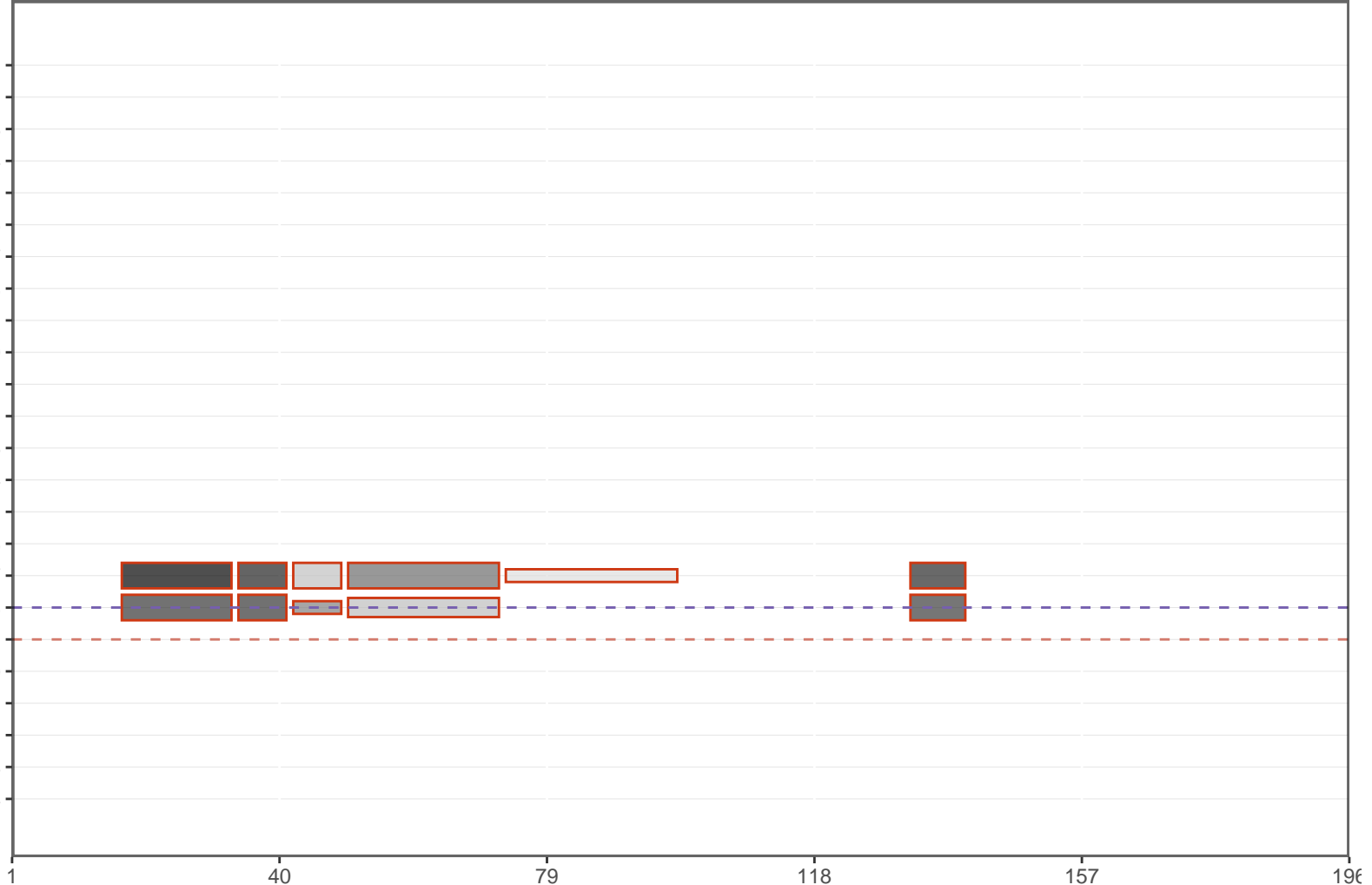
MW indication



Molecular weight



Gel Slice

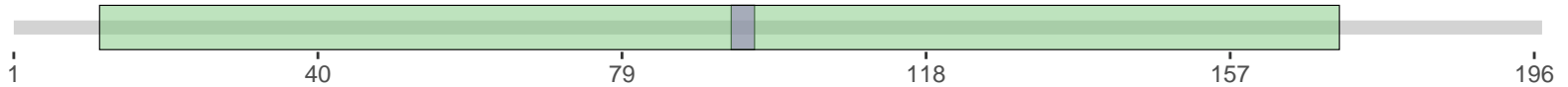


Protein length

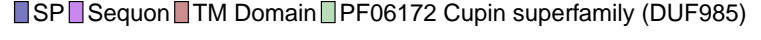


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

EPLTVMEINETDGGKALTGIGPDLADGGVGVYVFPNWWFGAFPTDFSSISADMKYTKAPARDGEKHFSLVGGTCAFNFGFEDFELAKRSELVRFPMHESLSLTFLE

NbL16g02550.1 subunit_alpha_type-6 [MW = 27.29 kDa]

No. of times detected



log(intensity)



Values from



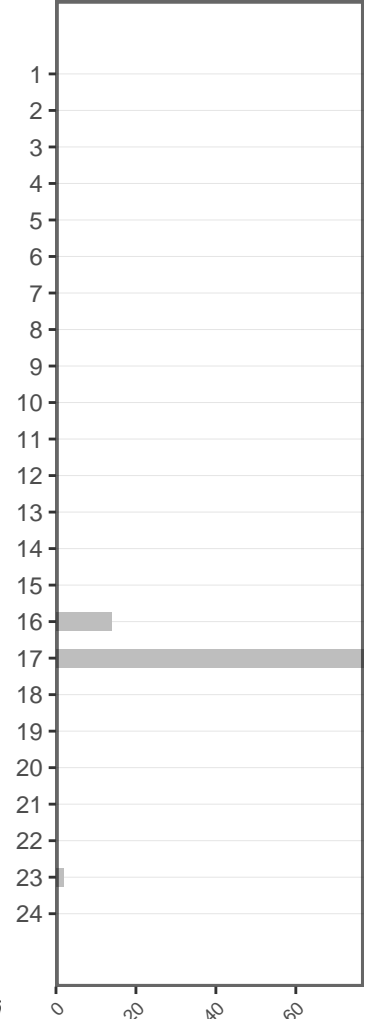
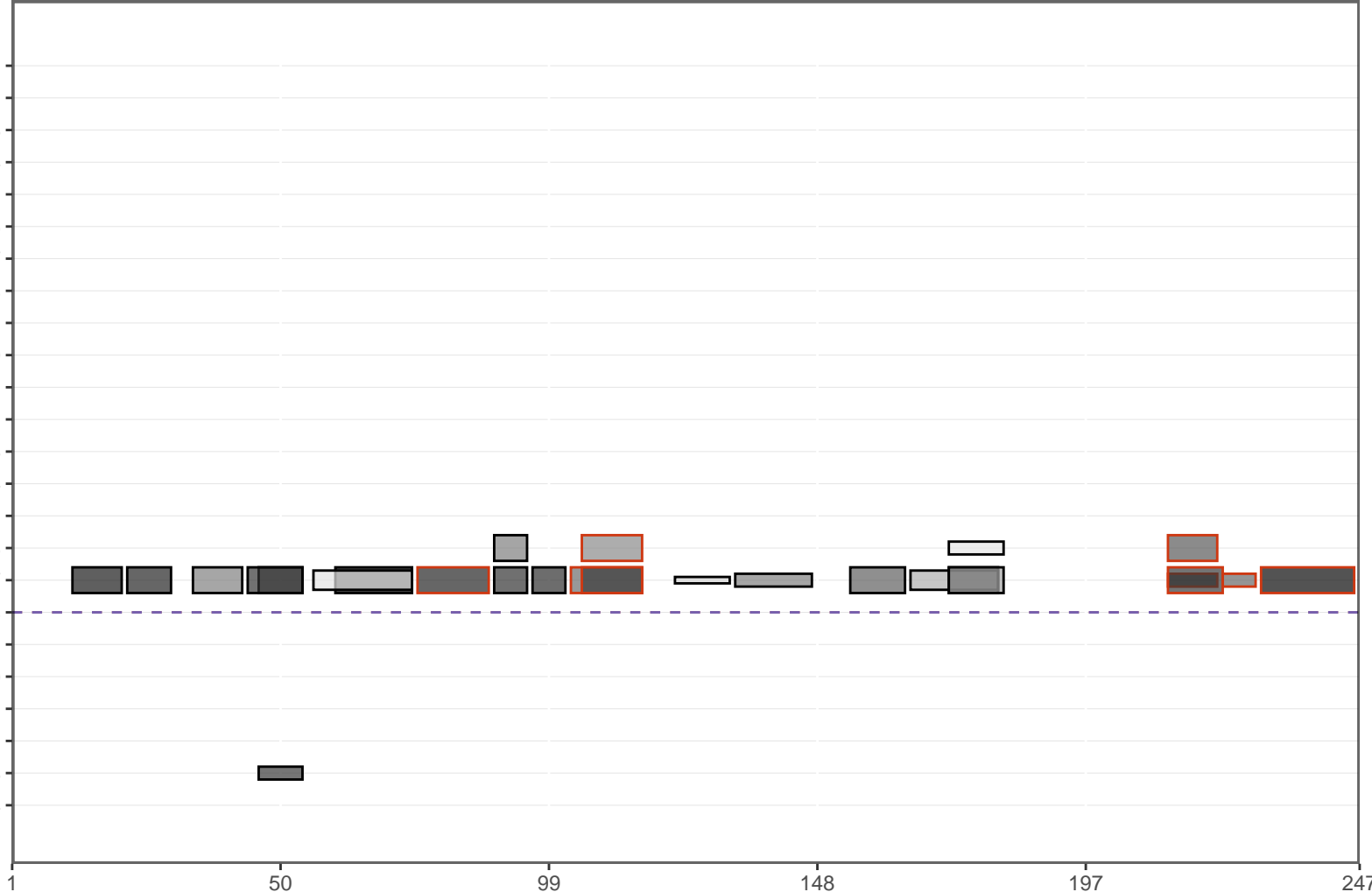
MW indication



Molecular weight



Gel Slice

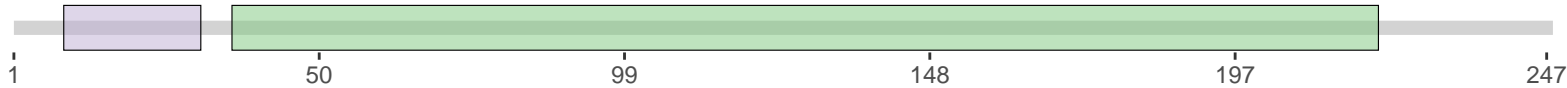


Peptide counts over 4 repeats

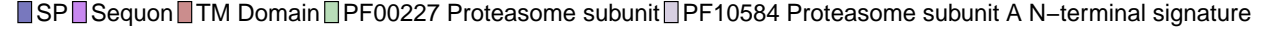
Protein length



Pfam domains



Pfam Description



Protein sequence:

IPVDYLSKWADKSGVYTRHAMRPLGVVAMILGIDEKGGPOLFKCDPFGHFGHKATSAGSKGEGEINFLKMKMNDPFSYEETVQTASALQSLVGEDFKASEIEVGVVKKKEDIPFRVLTTEEIDELTAISERD

NbL16g02480.1 40S_ribosomal_protein_S3-2-like [MW = 31.13 kDa]

No. of times detected



log(intensity)



Values from



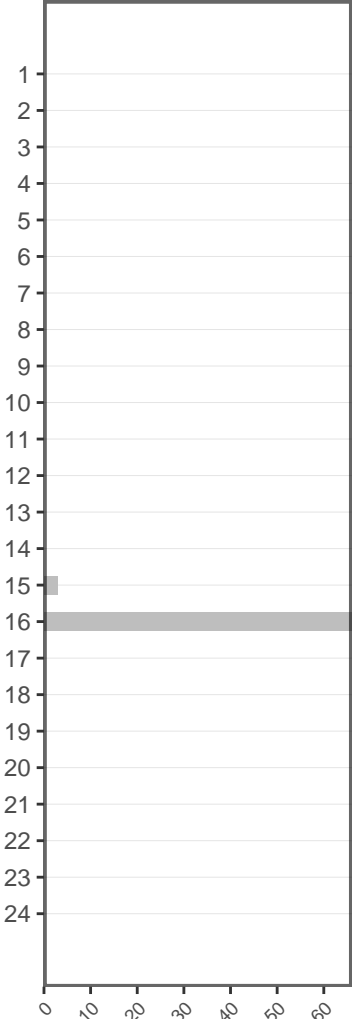
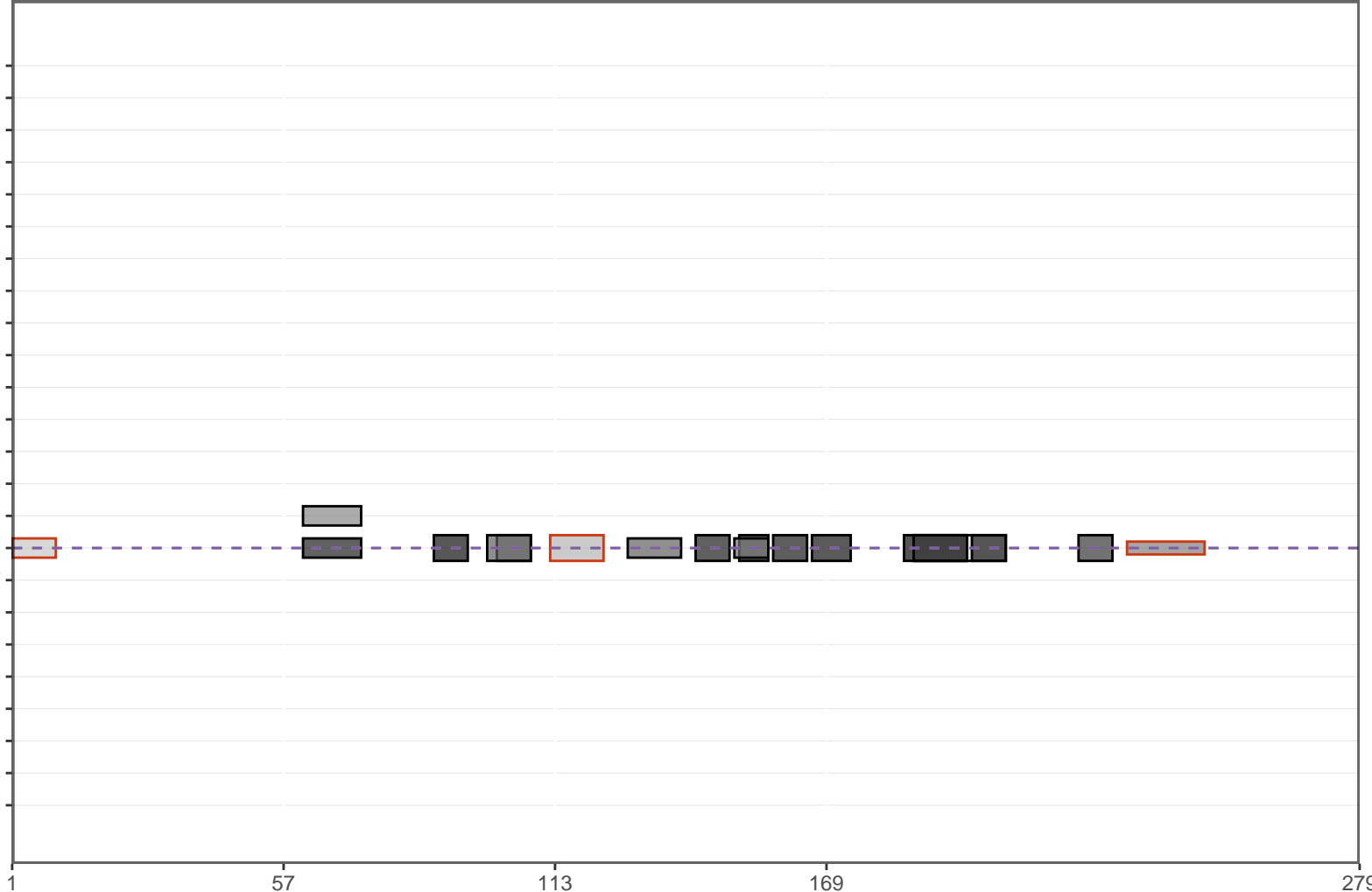
MW indication



Molecular weight

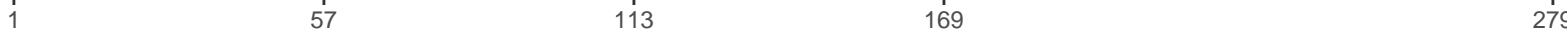


Gel Slice

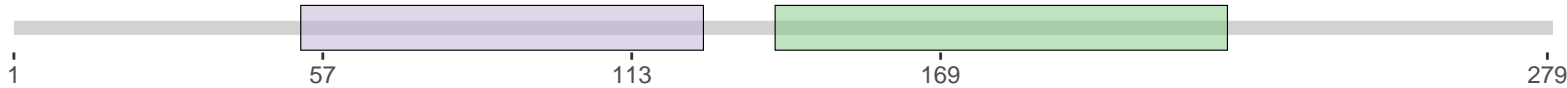


Peptide counts over 4 repeats

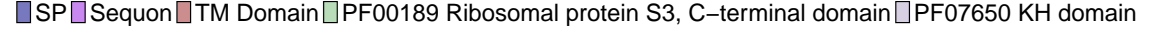
Protein length



Pfam domains



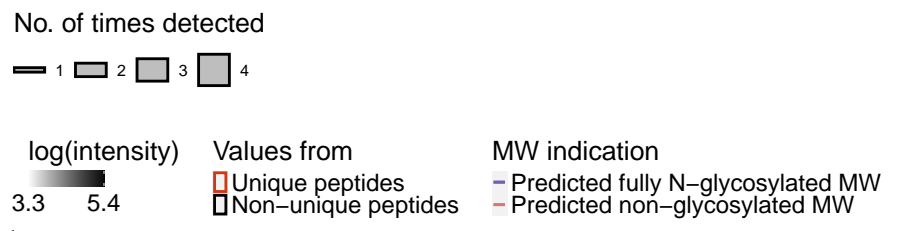
Pfam Description



Protein sequence:

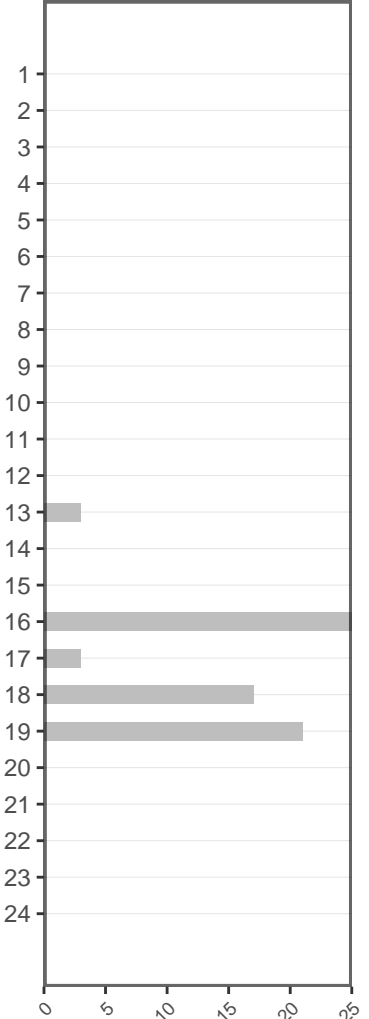
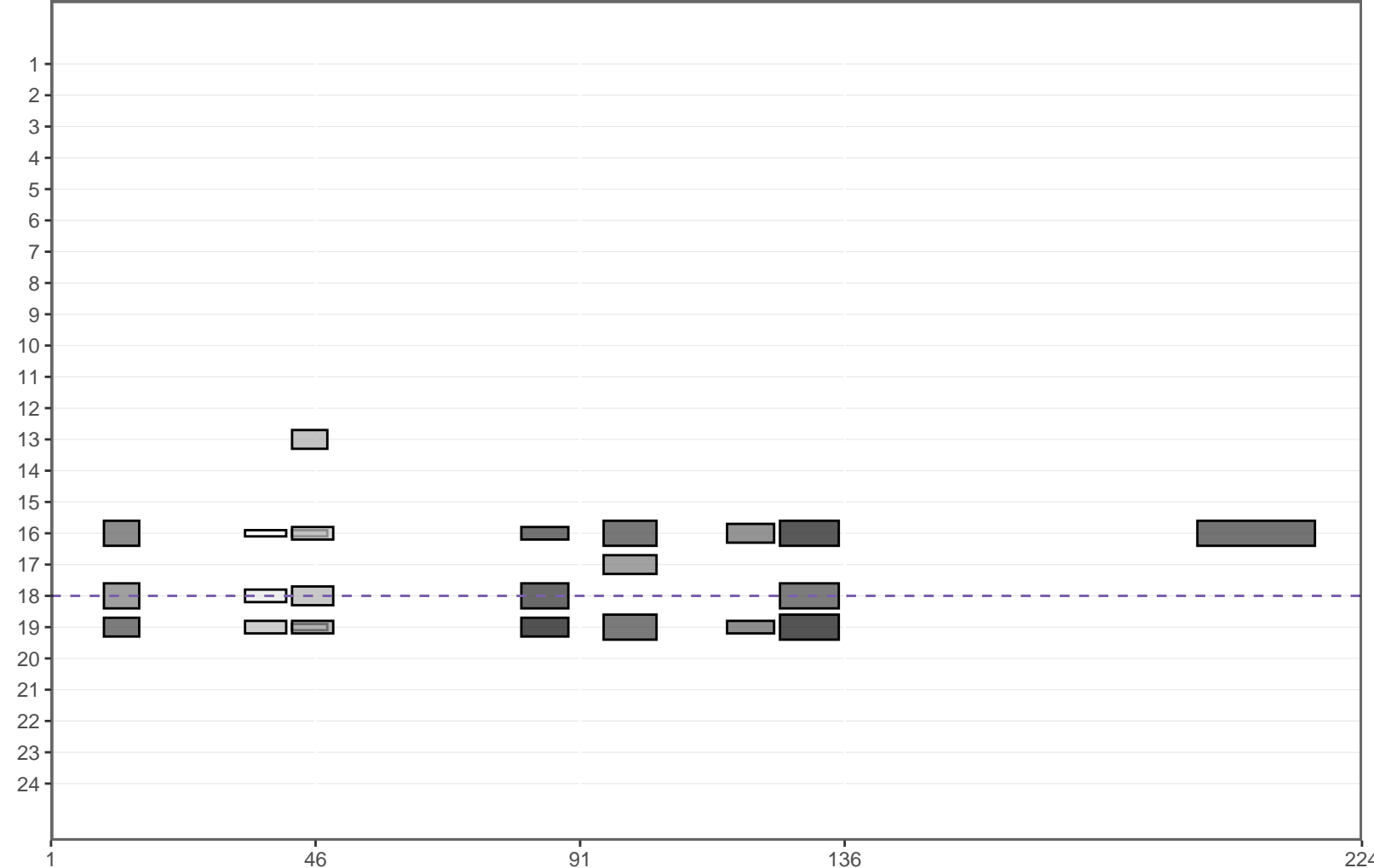
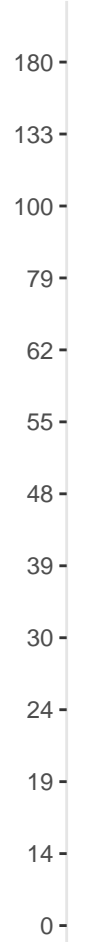
ISLCAVAQAEISLRYSKLLGGGLAVRRADYGVLRFMESGAKGCEVIVSGKLRAGRAKMKFKDGYMISGGGPVKEYIDSAVRHLMRGGVLGKVMILDLWDPKKGKGGPTTLPPLVTHSPKEEKQARTSVVVPDVAFTMLPTDIPRPVAVV

NbL16g02460.1 vacuolar_protein_sorting-associated_protein_2_homolog_1-like [MW = 25.12 kDa]



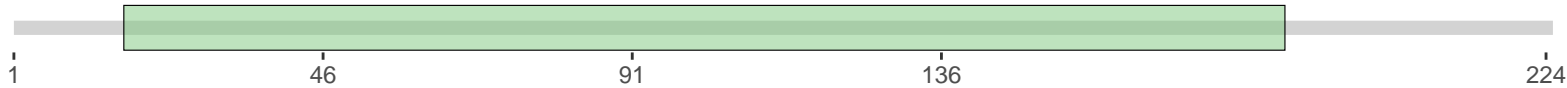
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

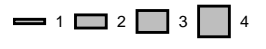
Pfam Description
 SP Sequon TM Domain PF03357 Snf7

Protein sequence:

EAMKGVTKAMGQMNIRGNLPLGRIMQDEFEMQNEKMEMVSEVMGDAIDDALEGDDEEEETEELVNGVLDIEIGISMNKLINAPSEAAVAPAKNKNVAGAEASEHDDGGDSDLQARLDNLRKM

NbL16g02390.1 probable_inactive_receptor_kinase_At2g26730 [MW = 77.45 kDa]

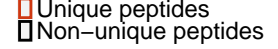
No. of times detected



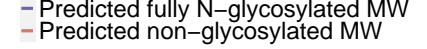
log(intensity)



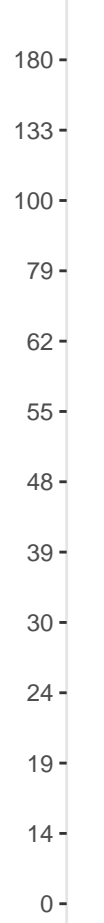
Values from



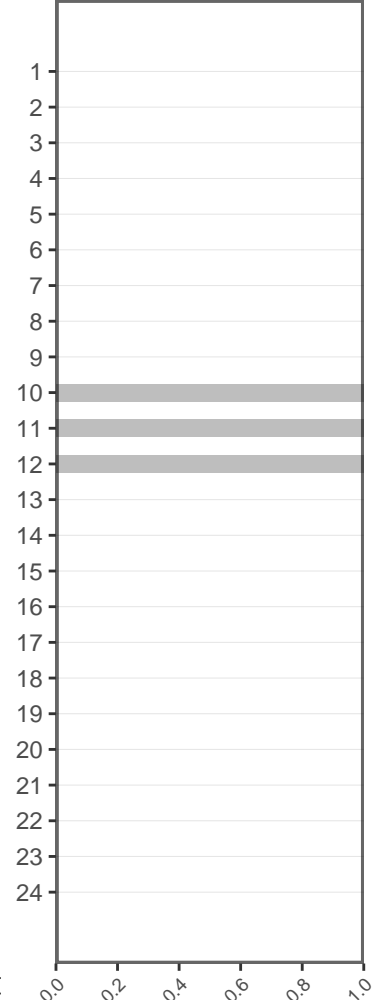
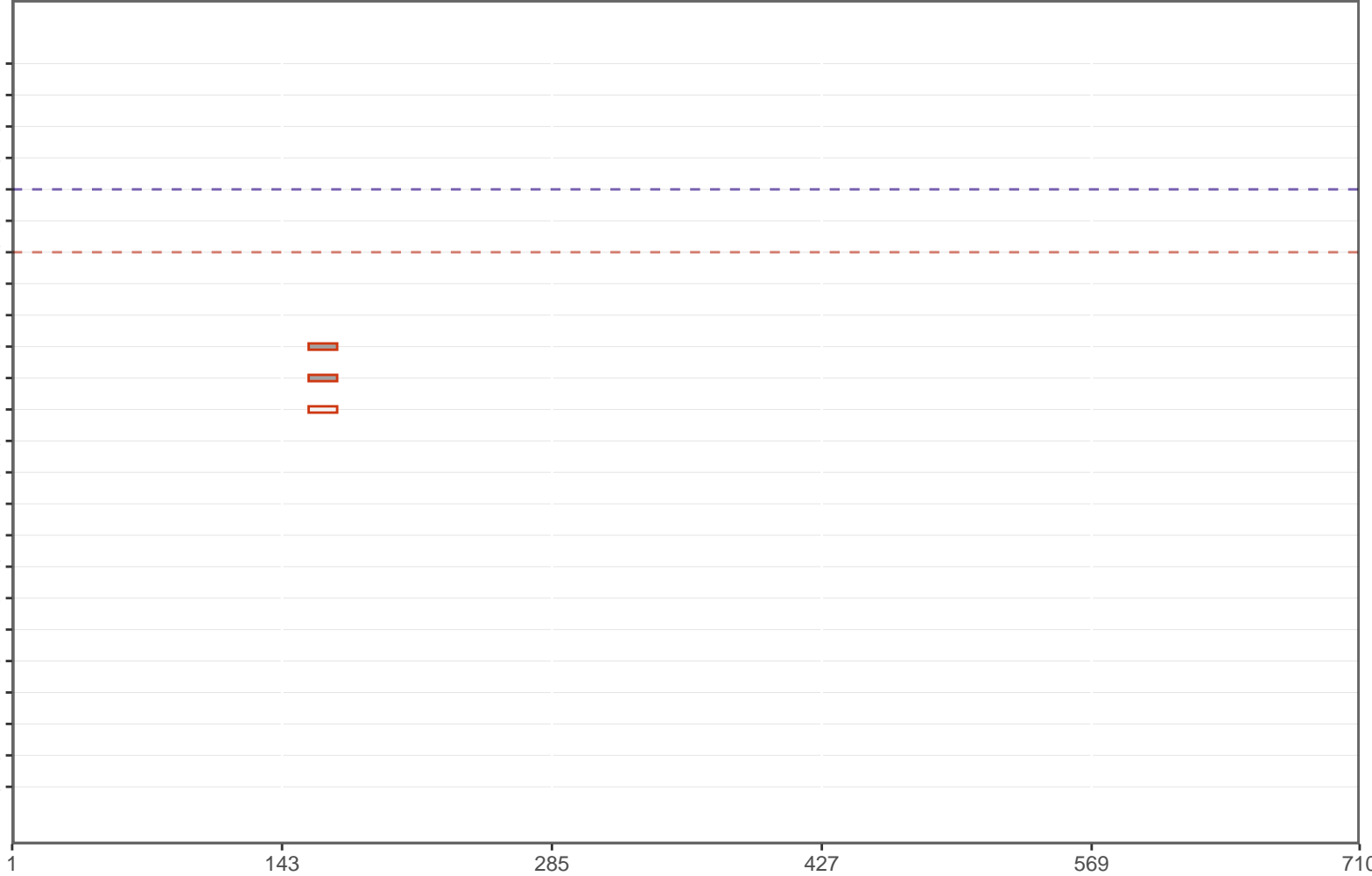
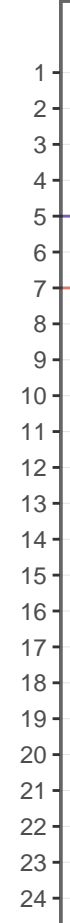
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IKPPTTAAFTGAGEAGTSSKDDLTAEGERNKLFFNGGGYGFQLEDLRLRBAEVLGKGVGTSYKAVLEEGTIVVVKRLKDVVTRKEFEQGMVLDGKMKHENVLRAPFYKDEKLLVSDVVPAGSLGSLHSGRSRGRFLDWDSDRMKIVLSAARGISYLHSGIKVHGNKASNVLKGDNDGDVAVSDVGLNPLFSTATPYNHHRVAGYRAPEVLETRKIVFKSDVYDFGVLLLELTGKAPNGASLGEEGDLPKRWVGVVREEVTAETFDVLELMRYINVI

NbL16g02310.1 translation_machinery-associated_protein_22-like [MW = 20.71 kDa]

No. of times detected



log(intensity)



Values from



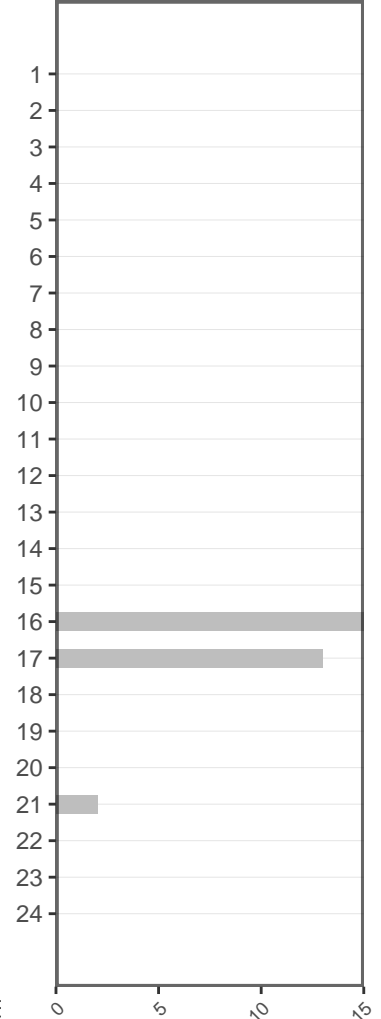
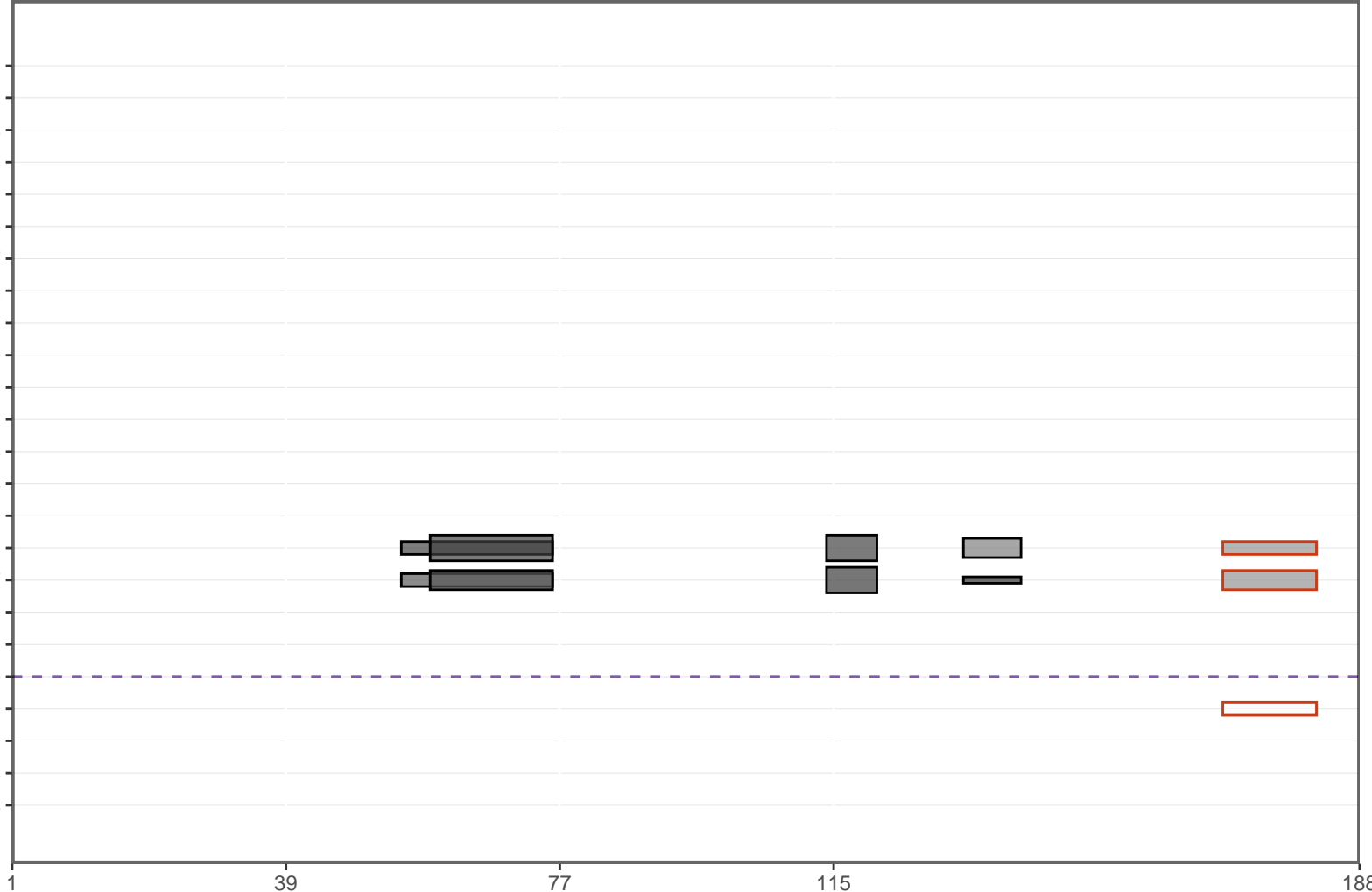
MW indication



Molecular weight



Gel Slice

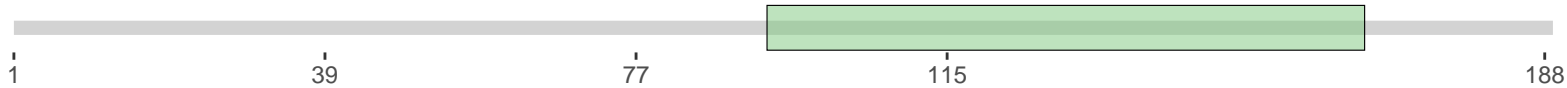


Peptide counts over 4 repeats

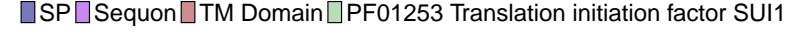
Protein length



Pfam domains



Pfam Description



Protein sequence:

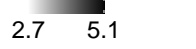
EVKRLPGGKIKKIKERQGEIVKTRNRKRKISITIKGLDLDFGVKLGDAKIKLGGKFKATGABVVKGFTEKEQGVGGDEVDVDFITETWRDVPASVFFIEDGKKVPMI

NbL16g02290.1 carbamoyl-phosphate_synthase_small_chain_chloroplastic [MW = 47.18 kDa]

No. of times detected



log(intensity)



Values from



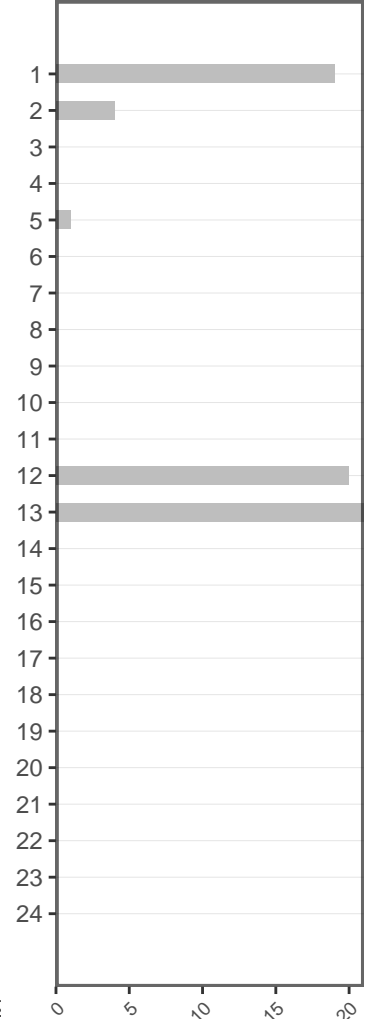
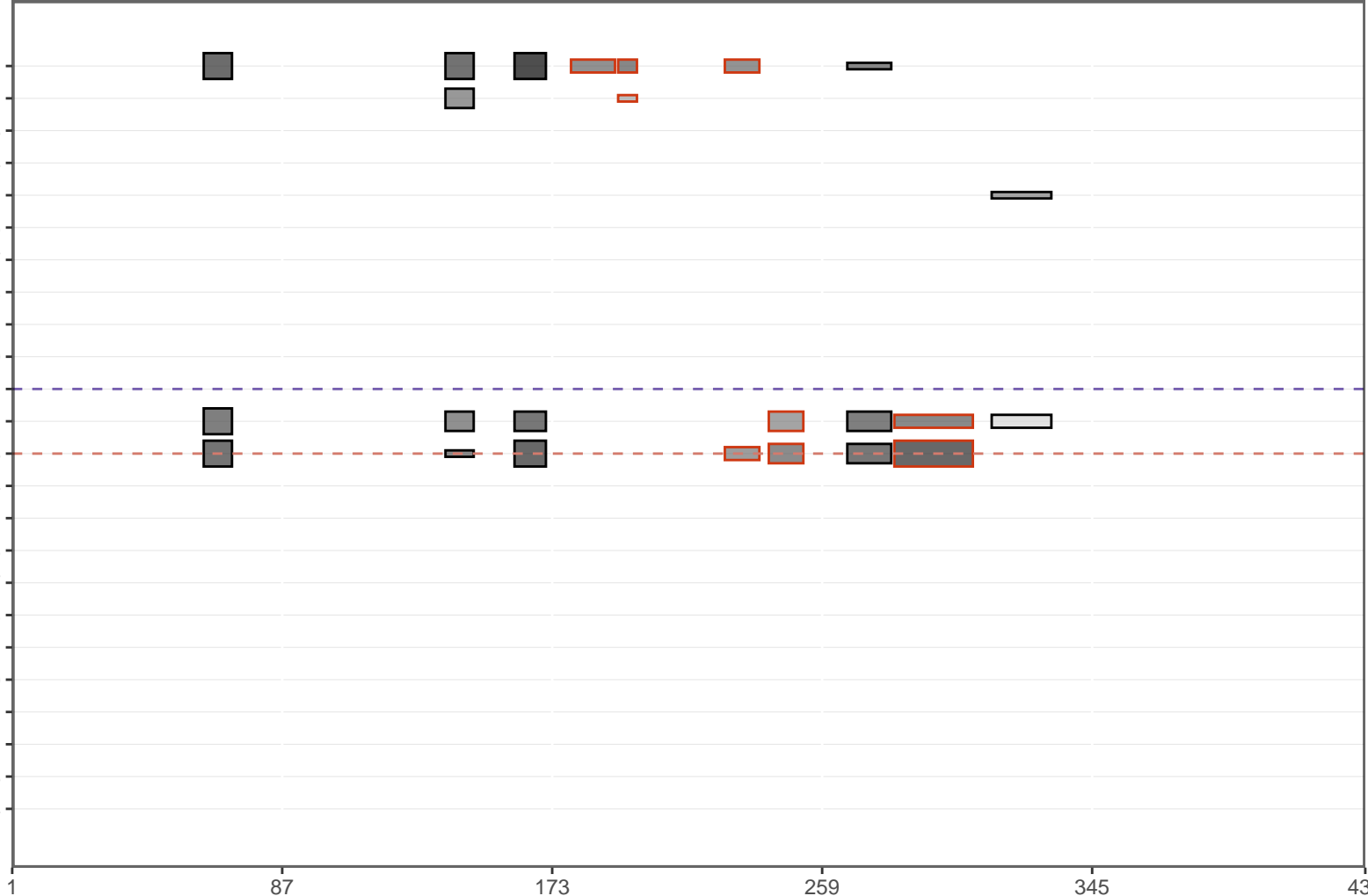
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00117 Glutamine amidotransferase class-I
- PF00988 Carbamoyl-phosphate synthase small chain, CPSase domain

Protein sequence:

VDIVGVDLSGVSCKSPYEWDRITASDWEFNVNGRNKTFNVAVDFGKINILRRLASVGGKTFVVPSTWPASETLKMKPDGVLFSNGPGDPSAVPVAVETKVELGKIPVFGFMGHLLGGALGGKTFKMKFGHHGGNHPVRNLRNGDVEISAGNHNVAVDPEGLPEGVETHVNLNDGGCAGLASSMKMLSLGYPHPEASPGPHDSDPVAEFLMKDQKVA*

NbL16g02270.1 beta-galactosidase-like [MW - SP = 78.3 kDa]

No. of times detected



log(intensity)



Values from



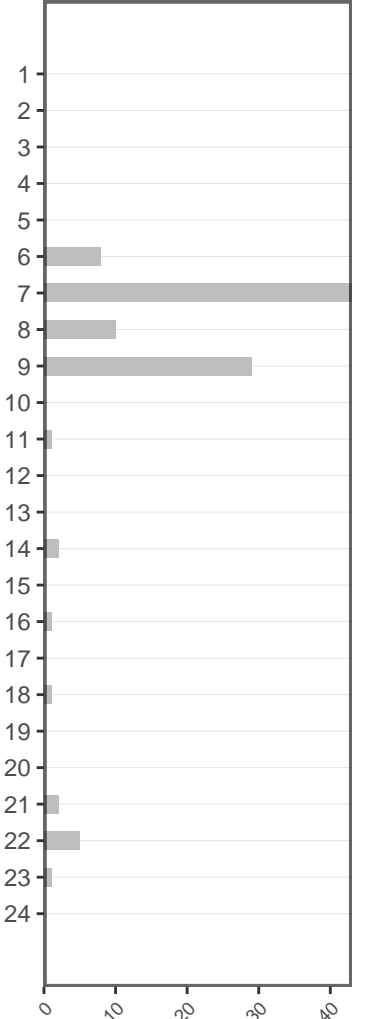
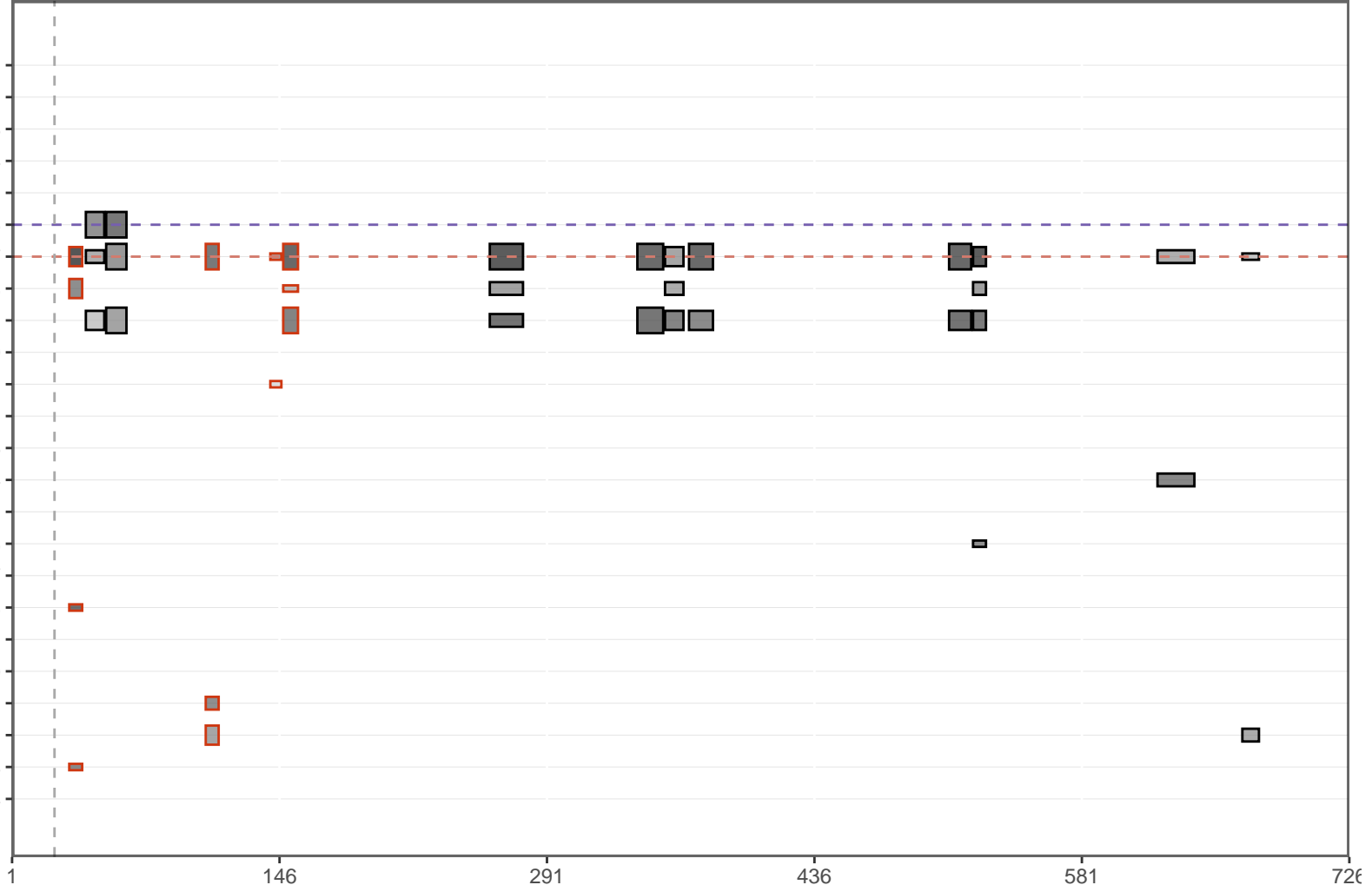
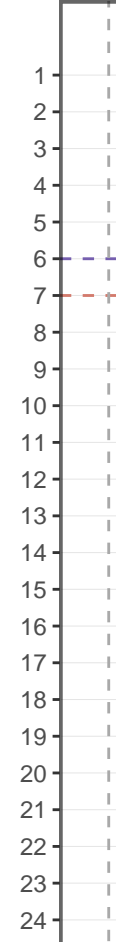
MW indication



Molecular weight

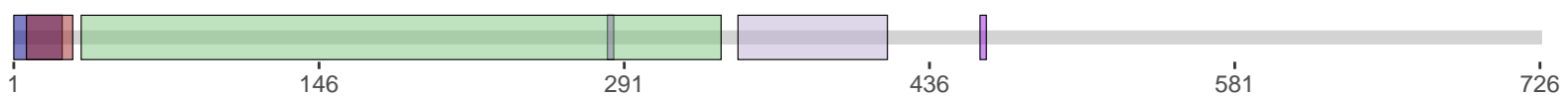


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01301 Glycosyl hydrolases family 35
- PF17834 Beta-sandwich domain in beta galactosidase

Protein sequence:

CGNNDGEAHHYRSKSGNGAAFLSNVDSKVKVYFDQNKPYDLPFWISILPDCCKTAVYNTAKVSTRSSSKMTSTGGSLGWDVYNEETPTADDSDTLSANGLWEGKHYRSDKPYLTVMSAGHVLHFVINGKLSGTVYGLDNPKLYTSGNKKLRAGINKLLELVVGLFPNVGVHFDFTWVAGVLPVTLGSLNEGKRDITGRVWYKVKLKGESLSLHTLGGSSVEWIKGSLVAGKGLPTWYKATFNAPGGNDPLALDMASMGKG

NbL16g02040.1 IAA-amino_acid_hydrolase_ILR1-like_4 [MW - SP = 46.43 kDa]

No. of times detected



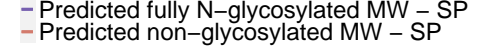
log(intensity)



Values from



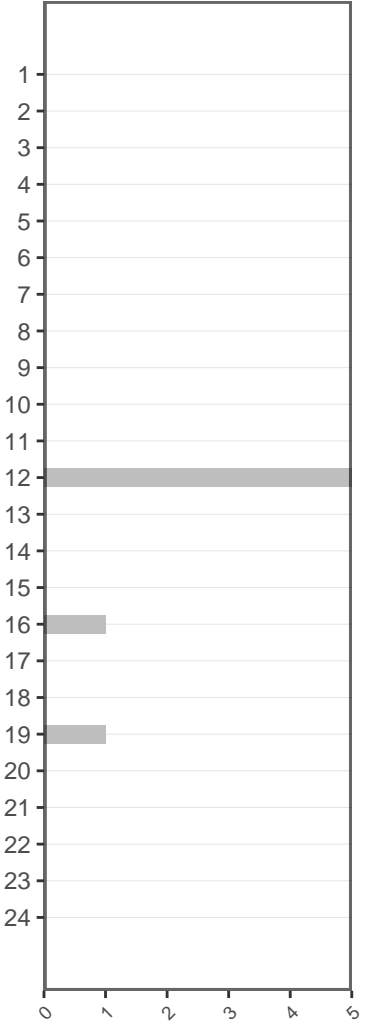
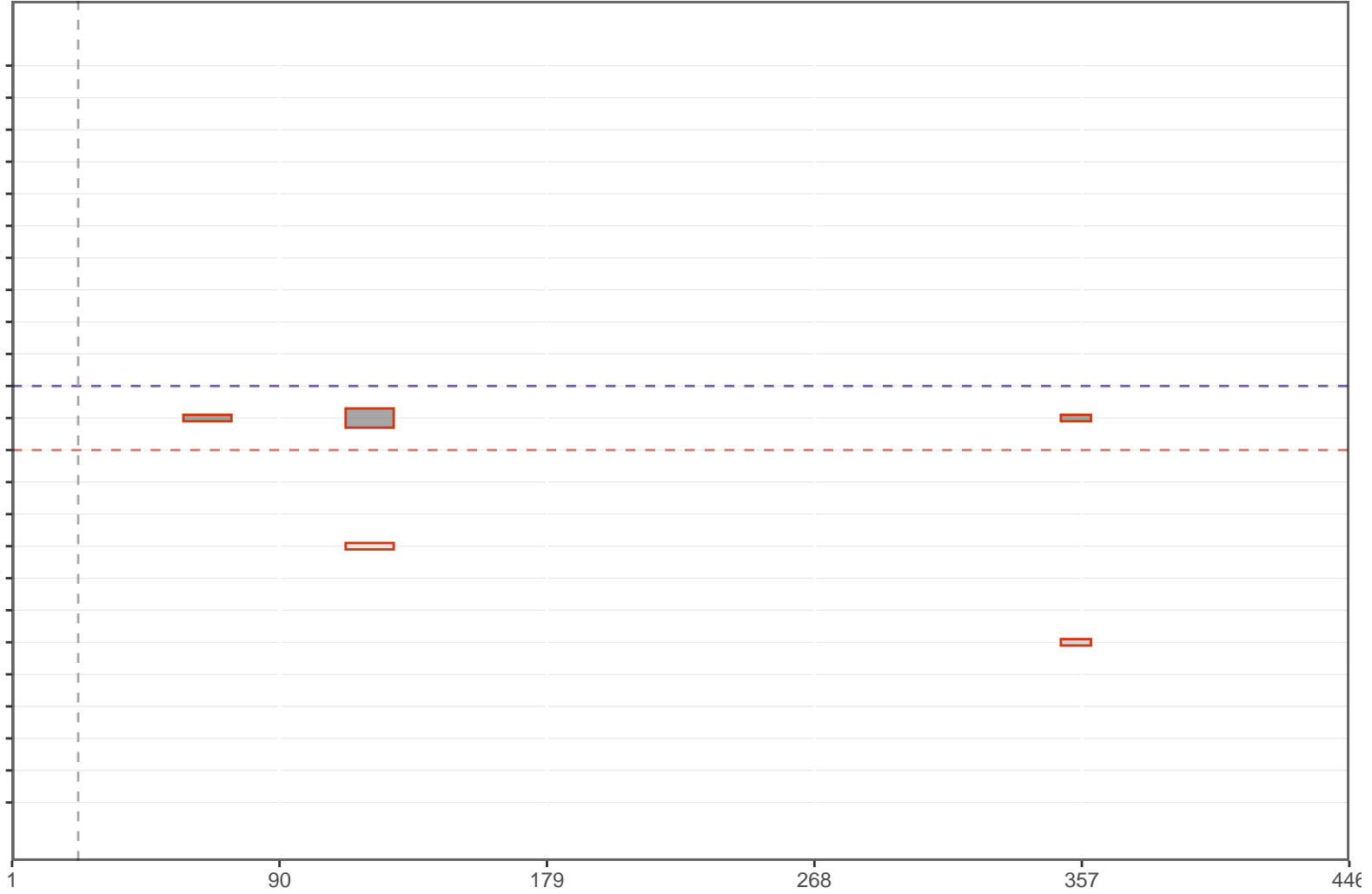
MW indication



Molecular weight



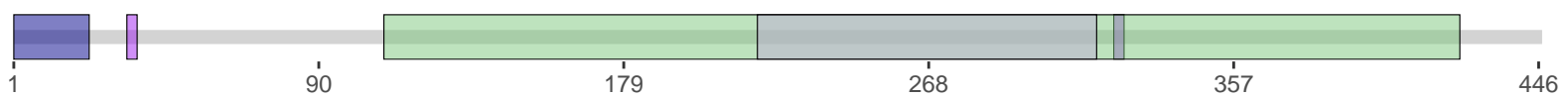
Gel Slice



Protein length

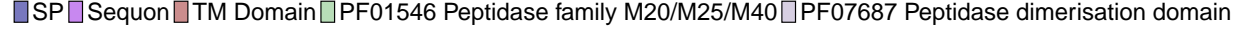


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KSGPLAGSGFEEAWINGKGGHAIPIQHTDPLAAGNIVSLGHLVSRREADPLDGGVTVYVKFKGGGAFNVPDSEVTIGGTFRAFSEKSFOLKGRIVEVTRGAAVGRGNATVFDFTNKKFFVTVNDKTLHEHFKNWAGMLGTEKIRELKLPMSTEDFSFPAEAPGYFYFVGMTEDETKGRFESGHNPLVRRNEDALPYGVALHSLATFYLLDHLKVTQDRNKHDEL

NbL16g01990.1 mitochondrial-processing_peptidase_subunit_alpha [MW = 54.81 kDa]

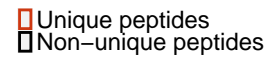
No. of times detected



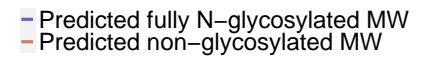
log(intensity)



Values from

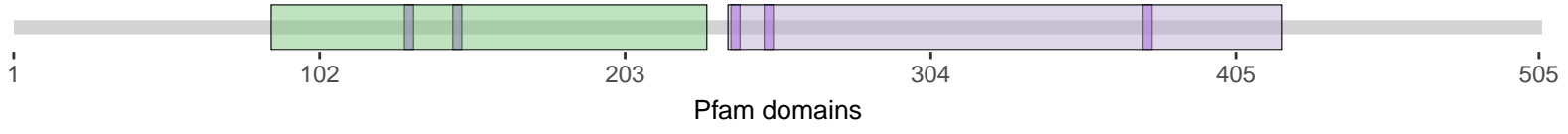
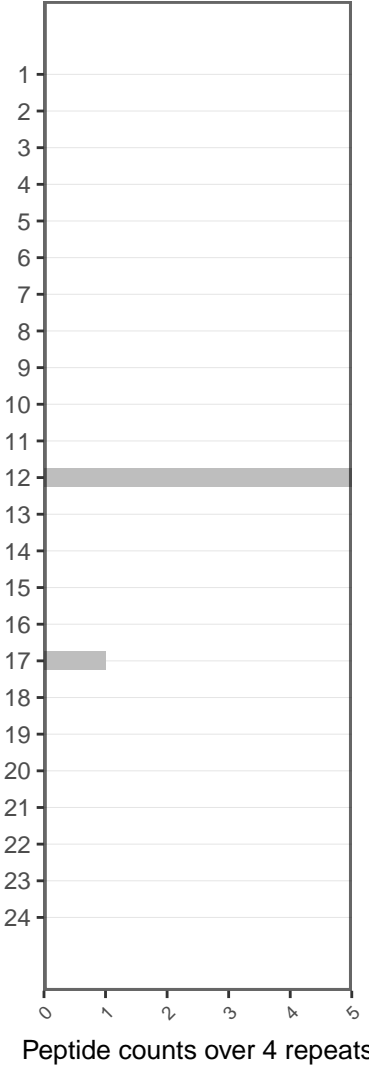
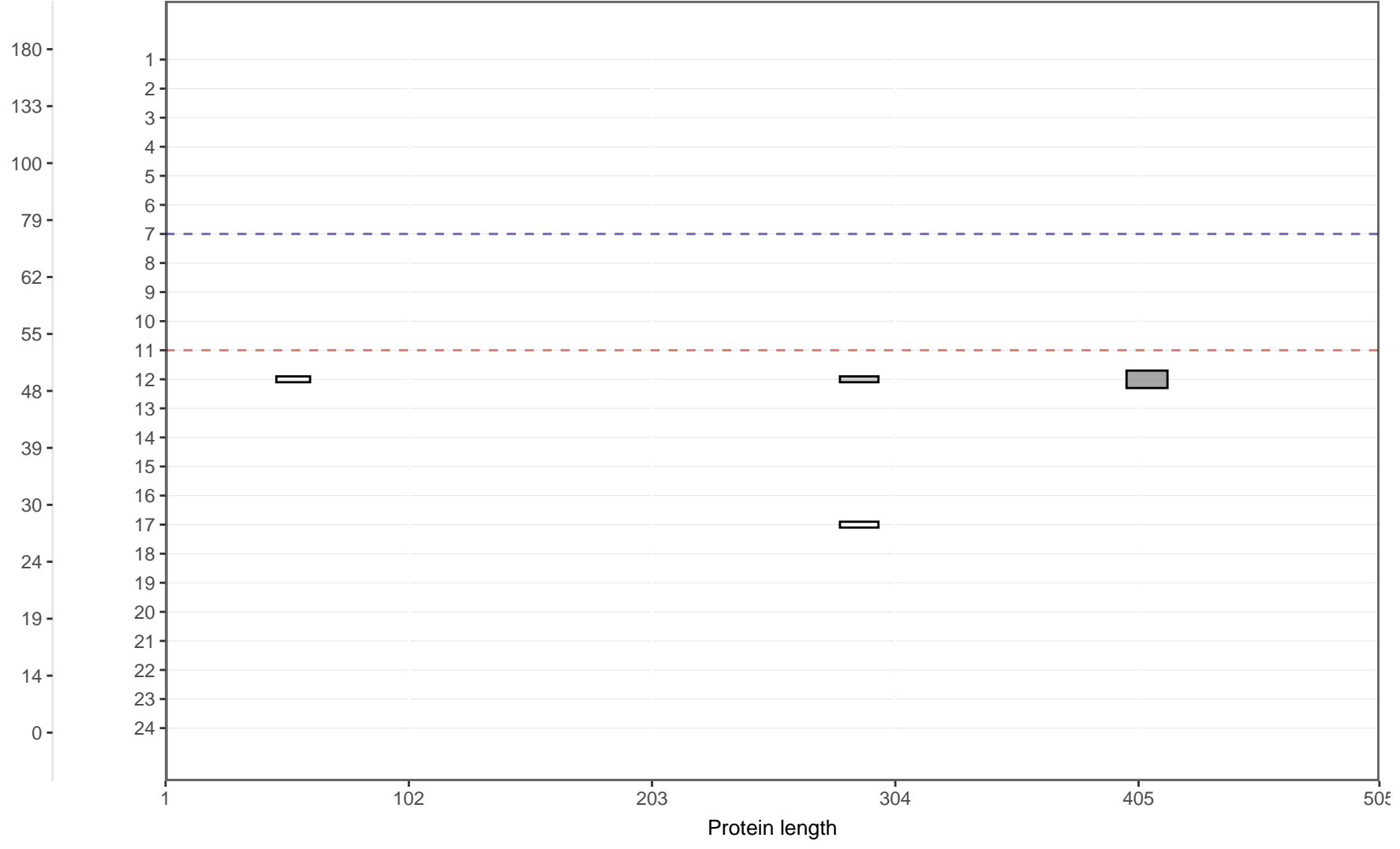


MW indication

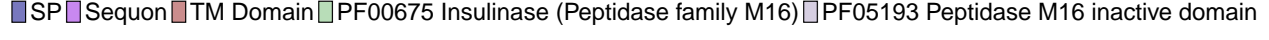


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

VLEEFVAENYTAPRMVLAASGVVEHGKLNIAEFLIGDLPKVATSEVFKPVIYVGGDPRRQADAEMTHFALAFEVPGGVMSEKESMTLVLQMLMGGGGGFSAGGPGKGMYSRVLRLVNLNGHPQIQGAFSAFSSVNDTGLFGIGATTTDFGPGQAVDVAWVELIAANPGEVDDVQLDRAKGSTEKSAIIMNLESRMVA SEDIGRQLTYGERKPKVEHFLKAIIDVASAKDIASVADKLISSPLTMAKYGDVLSLPEYDVAISNRFHKV

NbL16g01960.1 profilin-1-like [MW = 17.27 kDa]

No. of times detected



log(intensity)



Values from



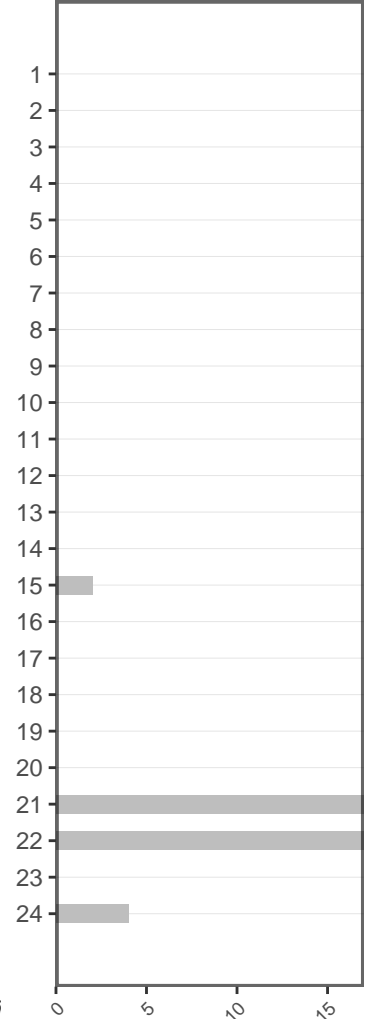
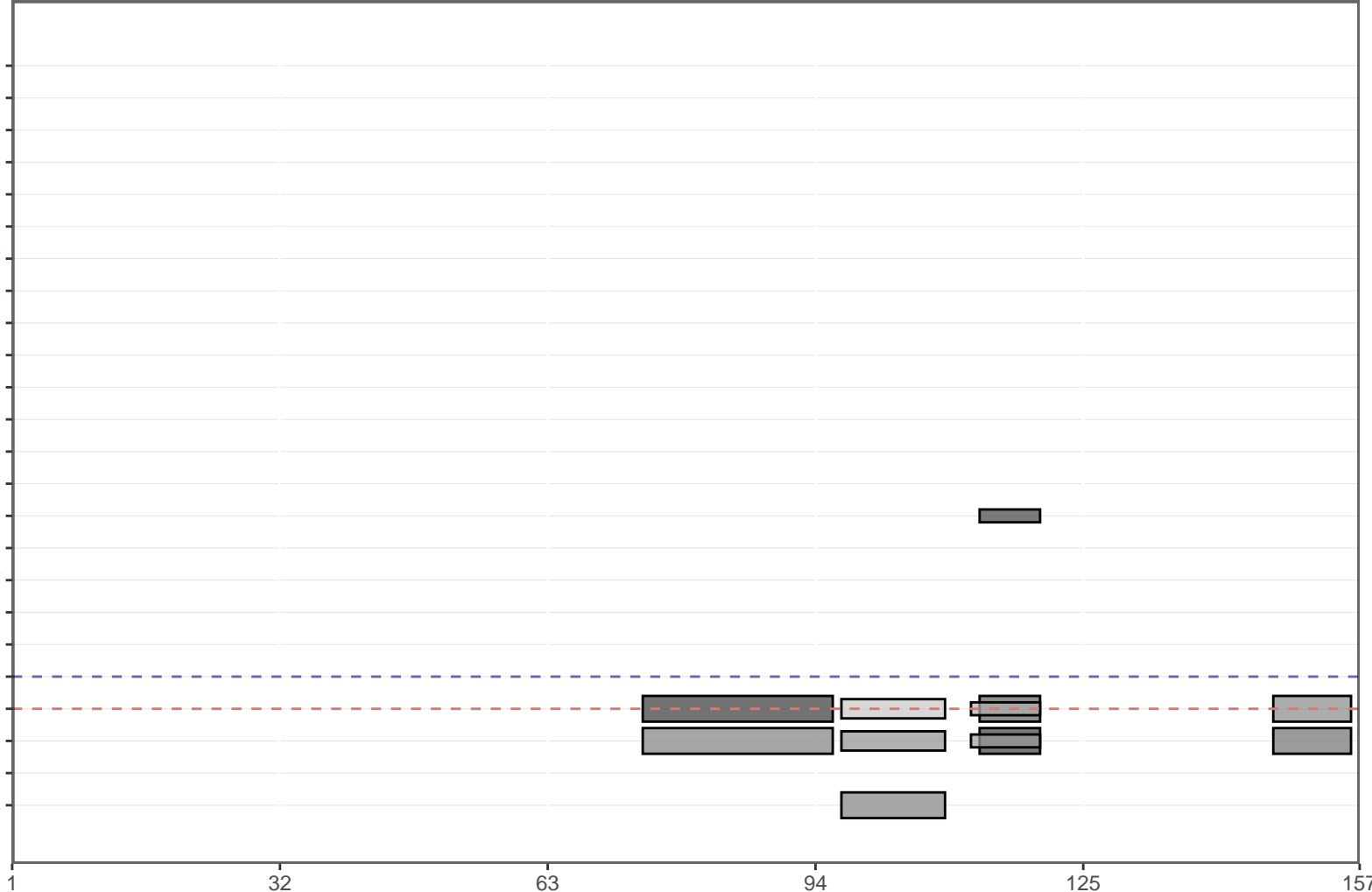
MW indication



Molecular weight

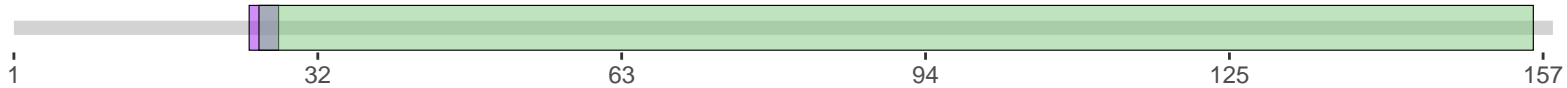


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IQFKPEEKAMNDFEETGTLAPTGLHGGTKYMWLVGEGAGVIRGKKGPGGFTIKTNMALLGIHDEPMTPGGCNLVVERLGDVLLDGGP

NbL16g01950.1 glucan_endo-13-beta-glucosidase_13-like [MW - SP = 51.37 kDa]

No. of times detected



log(intensity)



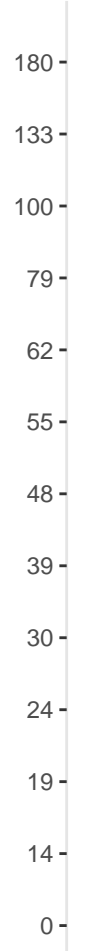
Values from



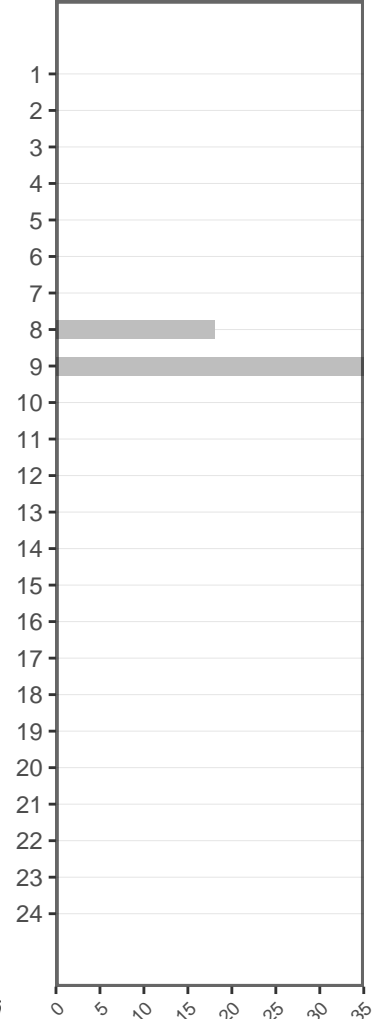
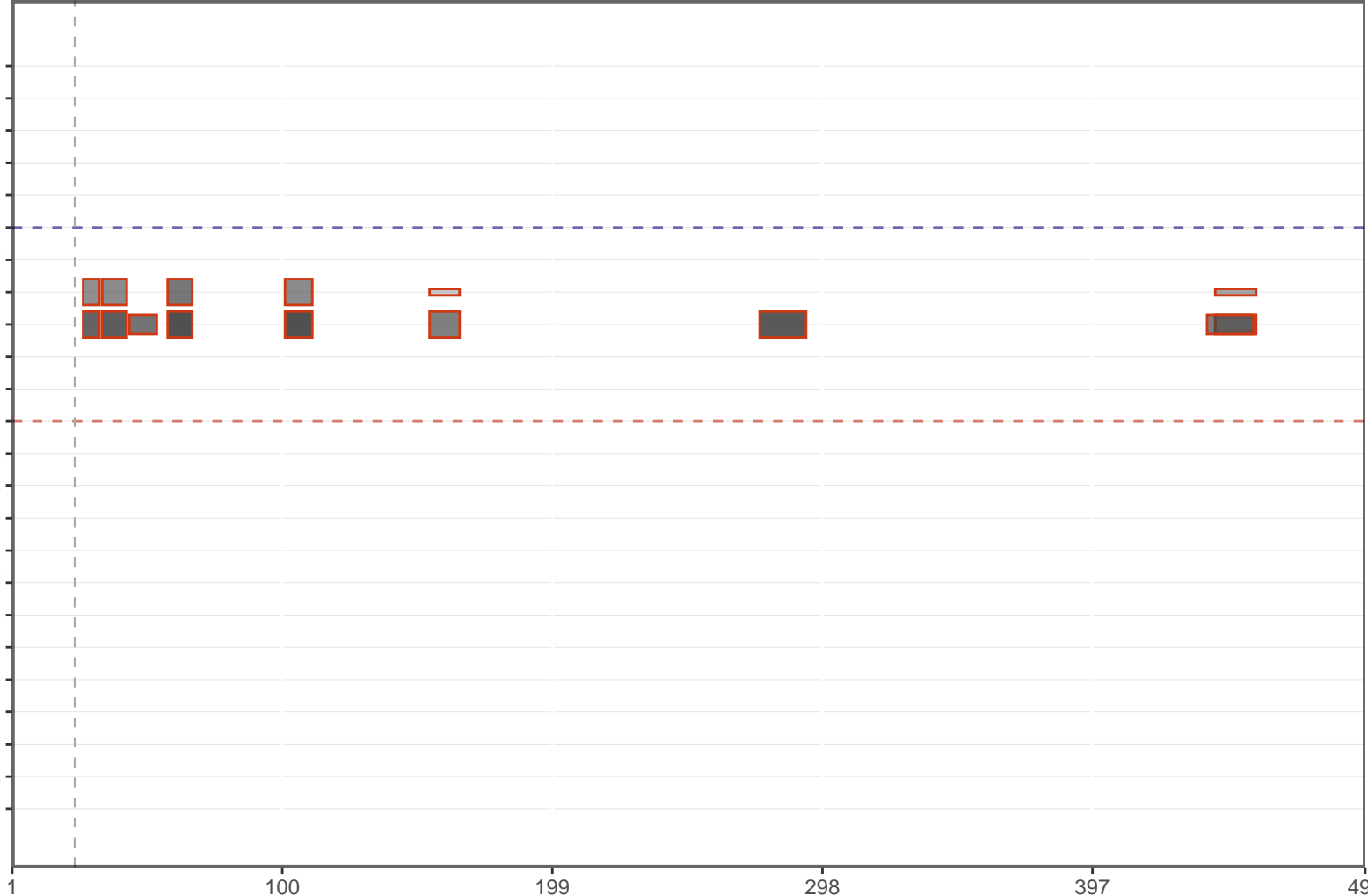
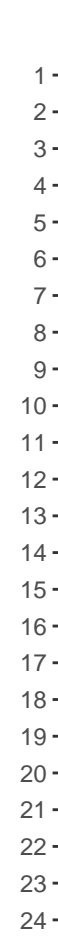
MW indication



Molecular weight

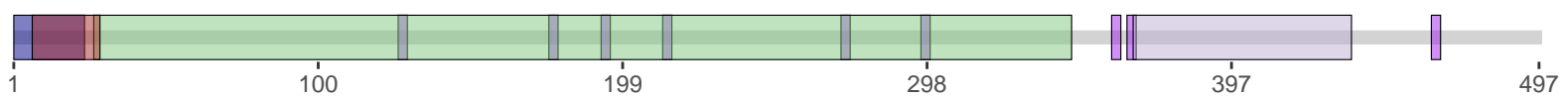


Gel Slice



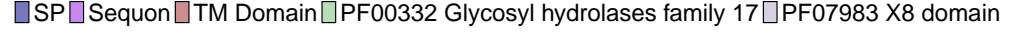
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

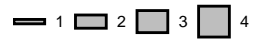


Protein sequence:

JAQLDARYALMLGNLRFKTVNIMVTEFGWPSNGSPKETAATPDNAGTYNTNLRHWVNTGTAKPKGVADITVYVFSLFNENRKPGLASERNWGLFPDGTGTVVNLDFTGKGAIDVTTDGNATSGNFTWCIASSVSEADLGNALSWACSGGNVVDGSAIGPSPGCFEPDNASHASVAFNBYKGNAGTADAGSFGGVGIRTKNKPQVNDGLYETTGGKKAATNATASPTKSSSSHRR66QWQGHLLAFPLFLVLF

NbL16g01930.1 arginine--tRNA_ligase_chloroplastic/mitochondrial-like [MW = 73.29 kDa]

No. of times detected



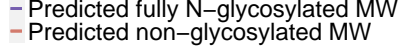
log(intensity)



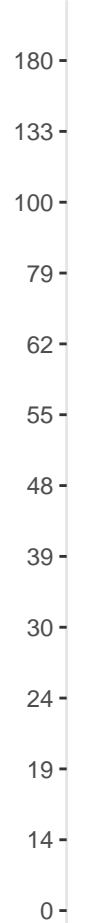
Values from



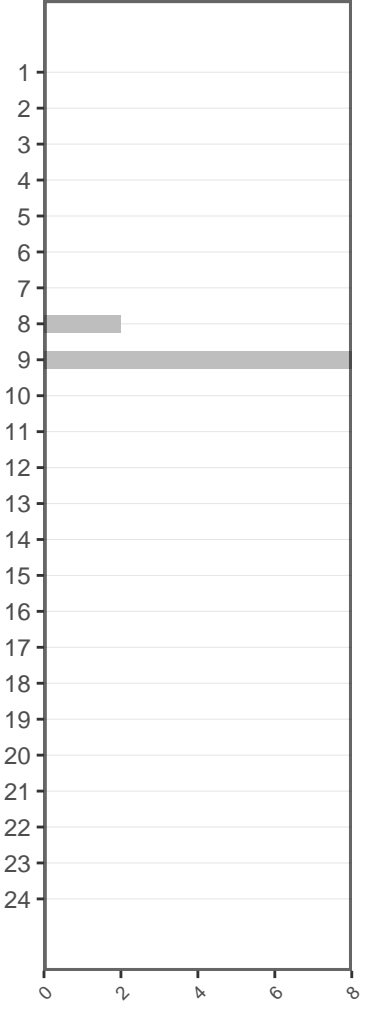
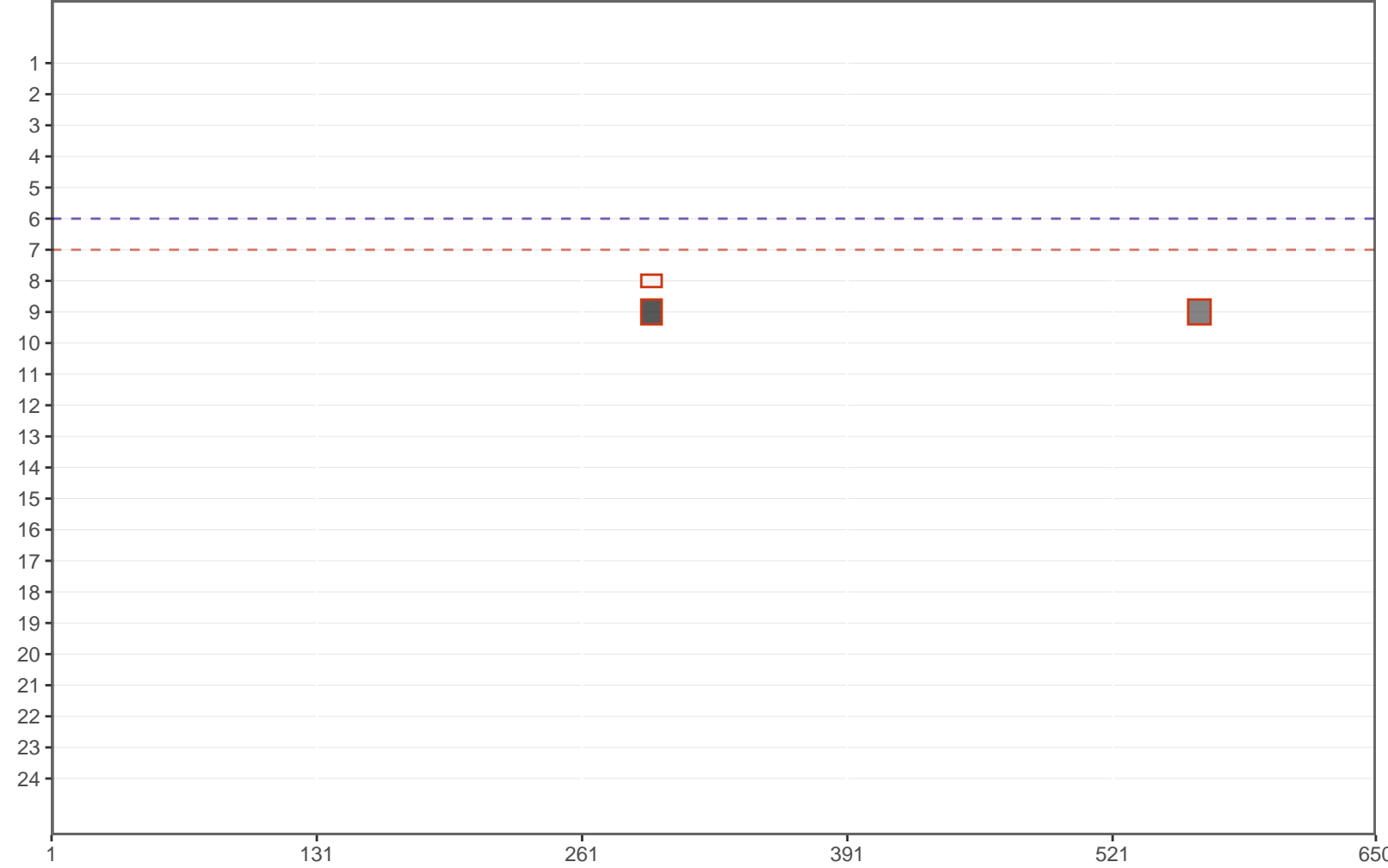
MW indication



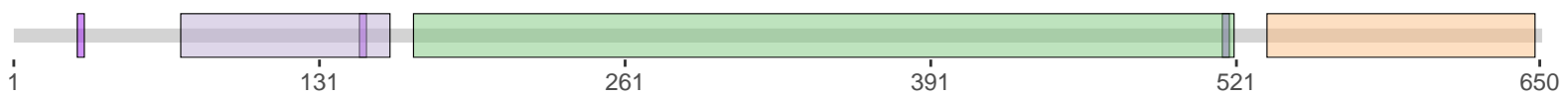
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

RKKEFKYVYERLQVHLLEEKGESEFNPWPKALELLNEKGLIEESEGARVFIERKPKLIVVKRDGGFNASTDLTALWYRLSEEKADVMKIVTDDGQREHFEMFFSAKRAGWLPQNEENDPKASHVYFGVLVGEDGKRFRTRSTEVVYLVLDLDEAKSRKLALEERGAKEWTAEEELDQTAEVGVGAVKYADLKNRNLNYTFNFDQMLSDKNGTAVVLYVHARIGSIRKSKDIEELKKGAMGLAHGDERMLGLHLGFPFIVEEAGTNLPLNLCYLYKLSDFTKI

NbL16g01910.1 probable_glutamate_carboxypeptidase_2 [MW = 79.91 kDa]

No. of times detected



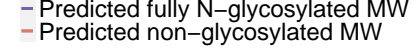
log(intensity)



Values from



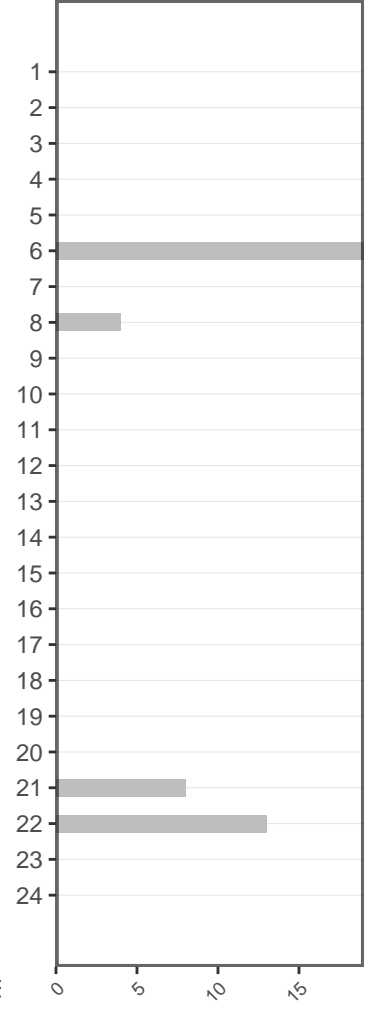
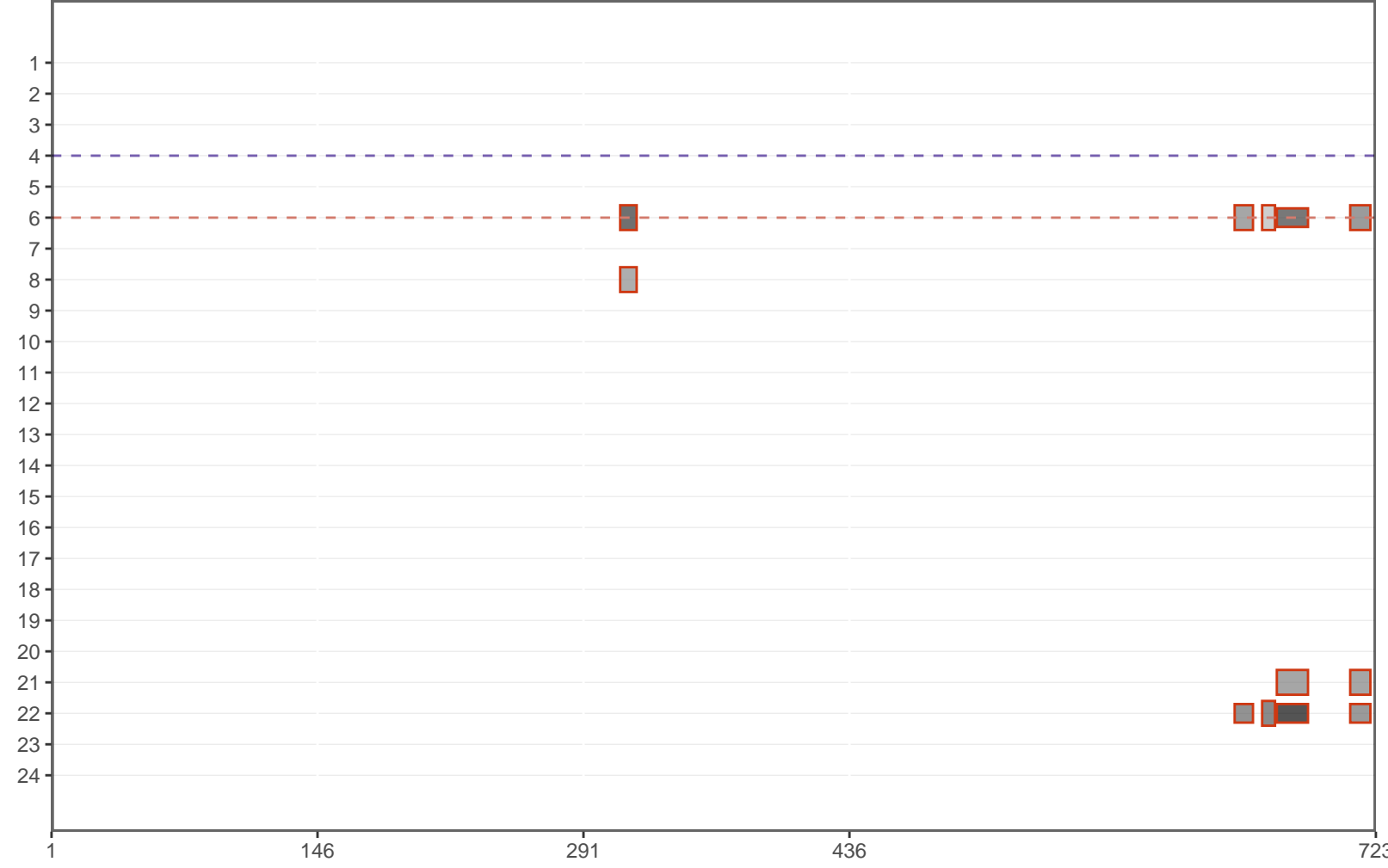
MW indication



Molecular weight

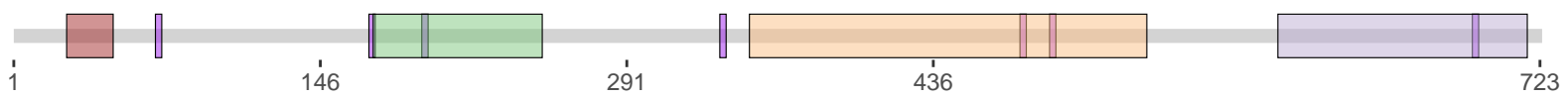


Gel Slice



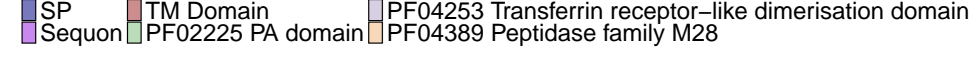
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VIEGEEEPDRFVILGNIRDAWTFGADPNNGSTAALLEIEMRLKLRKRGWRPRRTVLGNWDAAEYGLIGSTEWEEENREMLASRVWAYLNVDAVQGGHFRASANPOLDELHGVSGQKDPDSSGTVQSWLDSGNDTTVNLGRLLGGAGSDVAAFVQHGIPALDLDFGDCVYVYHSMYDDFVWMKFGDPMFHRHWAVASFWGLLALRLADDELPFNLYTAVELQKSAVQLEAEISENGKIVPLVYSEKFRKAARIEDDVKAVAKRQSWESLRELDRLMTERA

NbL16g01720.1 probable_lactoylglutathione_lyase_chloroplastic [MW = 40.2 kDa]

No. of times detected



log(intensity)



Values from



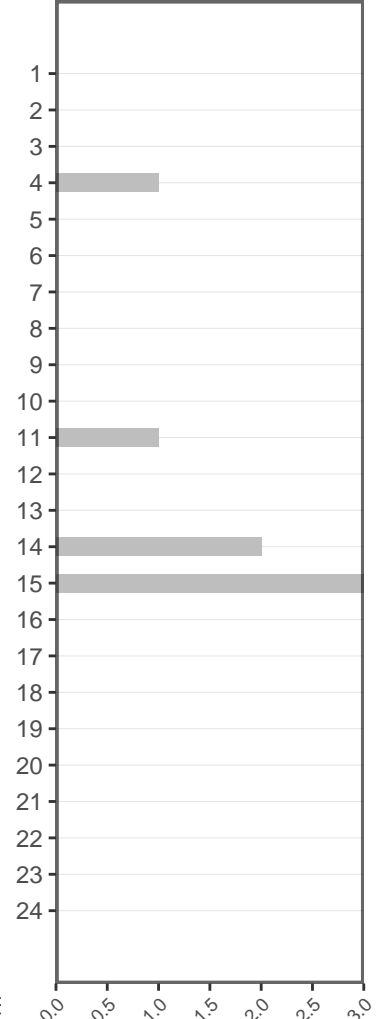
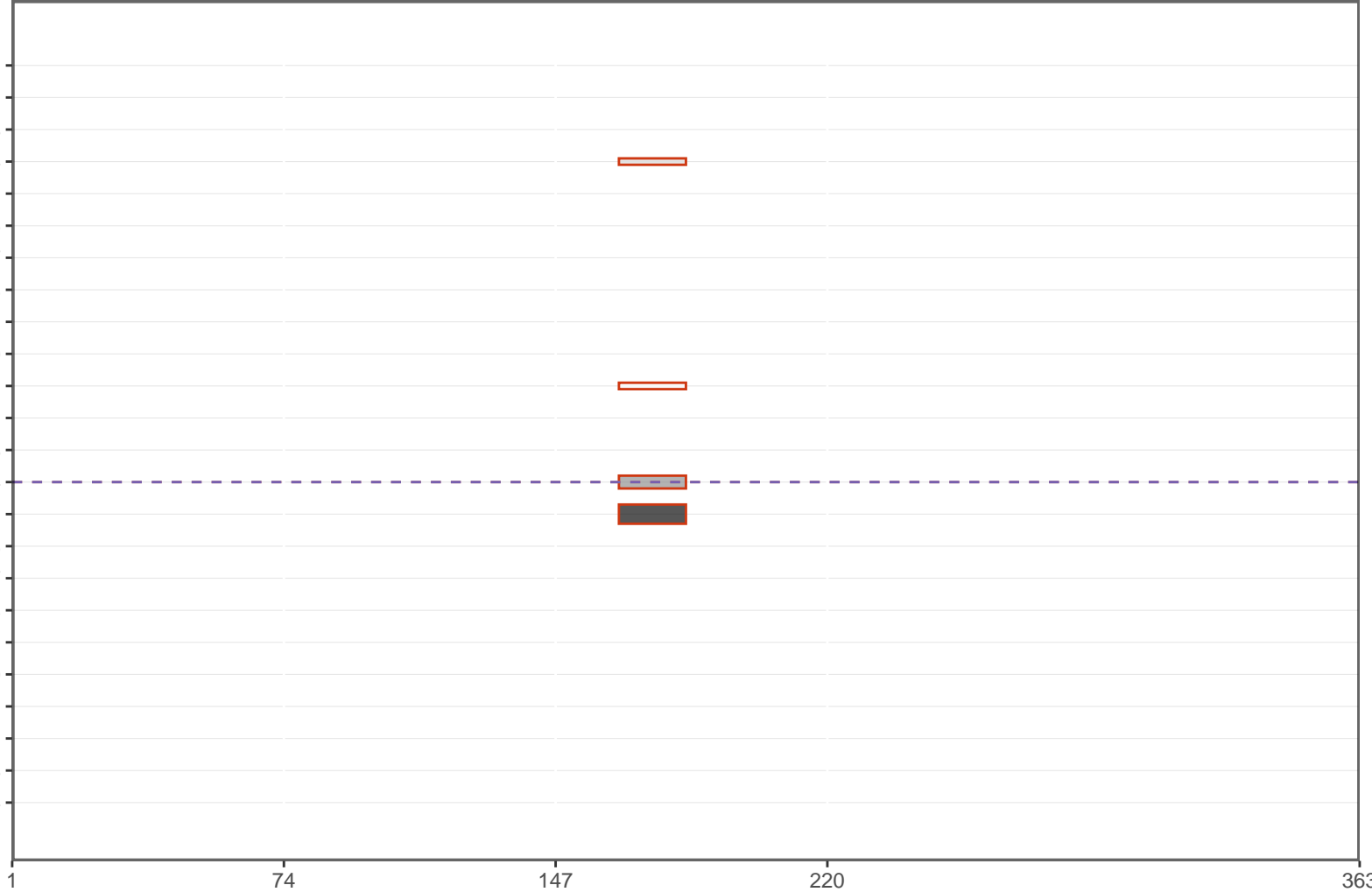
MW indication



Molecular weight



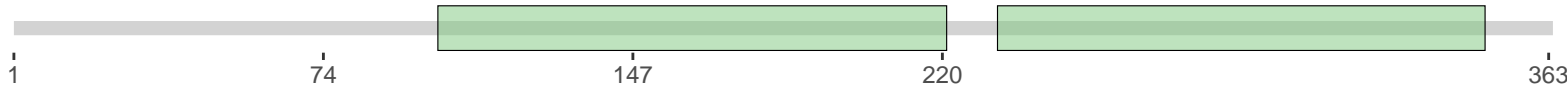
Gel Slice



Protein length



Pfam domains



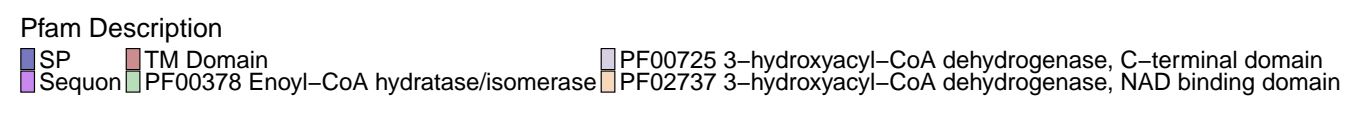
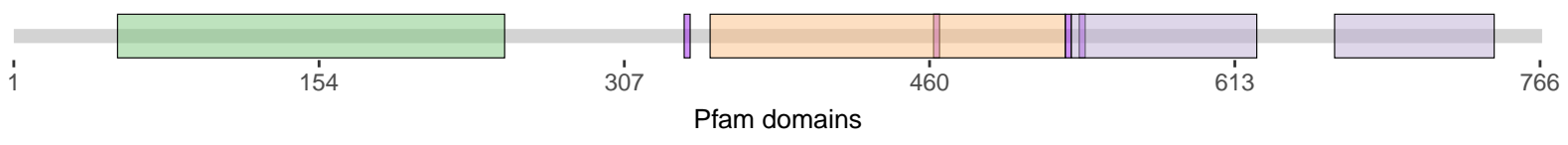
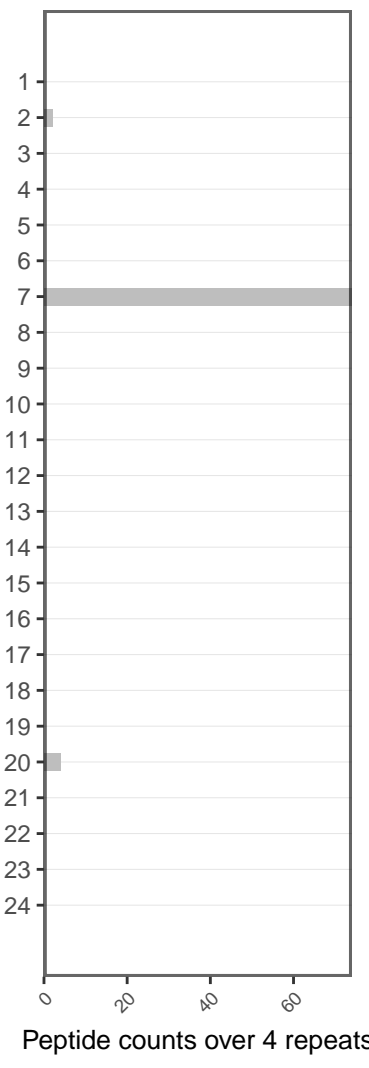
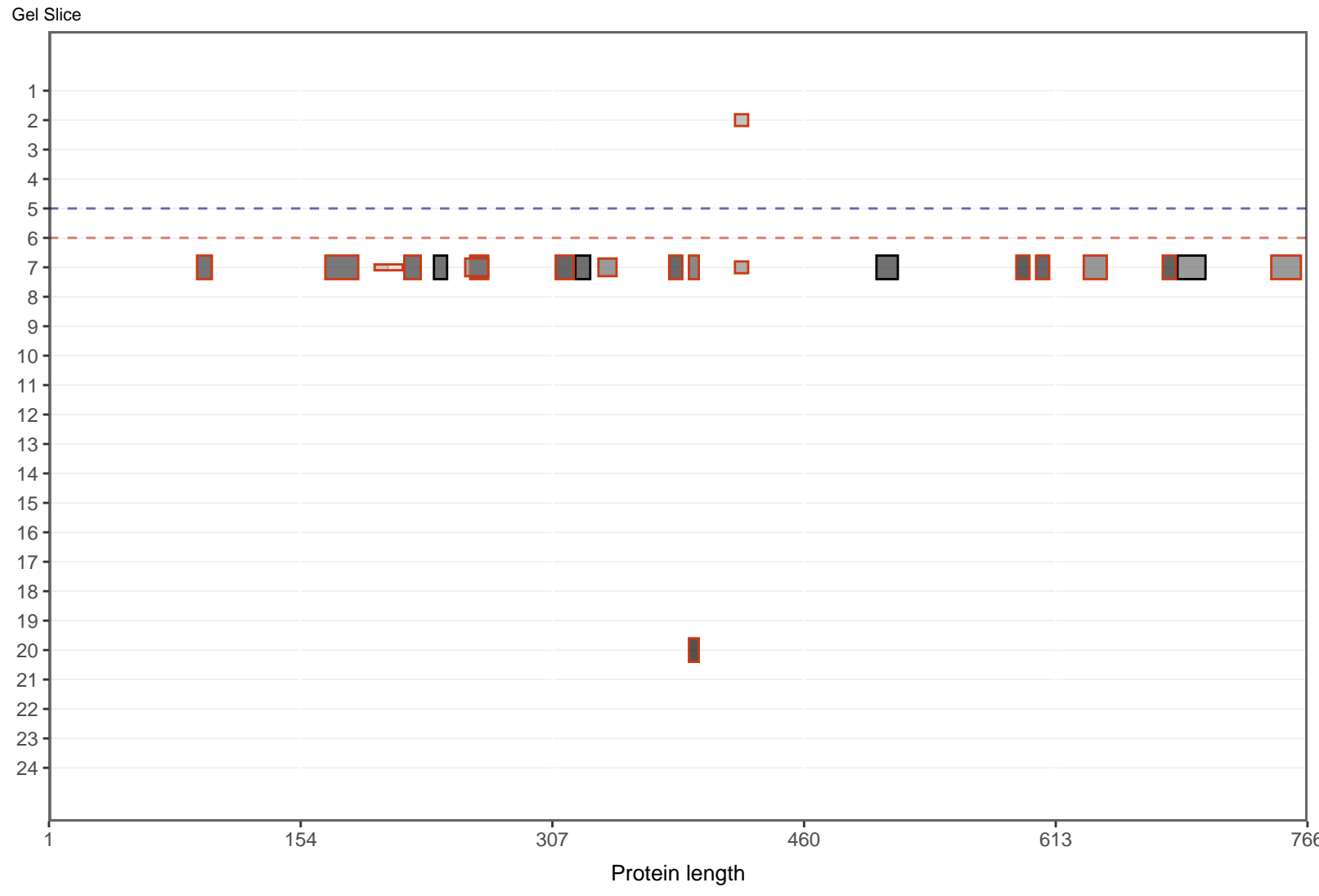
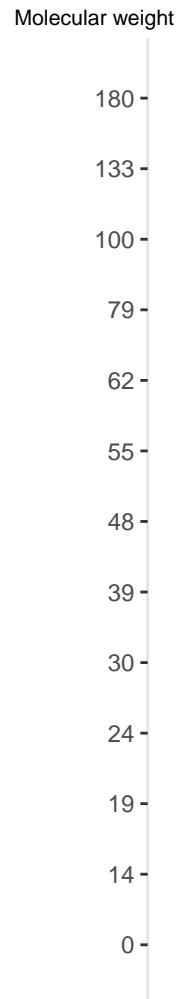
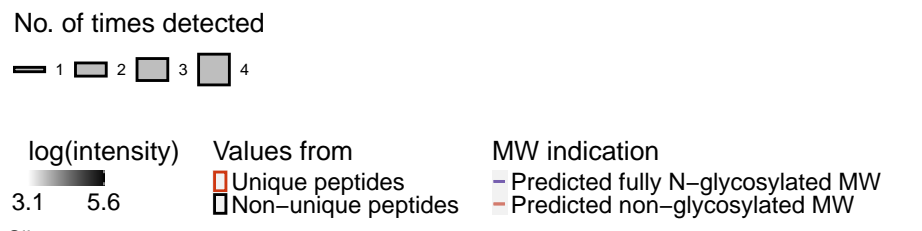
Pfam Description



Protein sequence:

SGFGHFGIAVEDYSKTVELVWAKGGKVSREPGPKVGGKTVARIEDPDGYNFELLERGGPTPEPLGGVMLRVGDLDRAINFYEKAYGMRLLRTRDNPYKYITAMLGGYGPEDSSAVMELTYWYGVTEYDKGNWAGIAGTDDVYKTAEARLGGGKTRREPGLPGISTKWAGLDPDGWYKVFVNDVDFLKELEI

NbL16g01600.1 peroxisomal_fatty_acid_beta-oxidation_multifunctional_protein_AIM1 [MW = 82.66 kDa]



Protein sequence:
 LVLNPFYLNKFNPEYLGKGRKAVEANRGLVARKKLGDDKASKALSIVKGLDYSSEKNDVMVEAVENVPLKQDFSDIEKVPDPHGLATNTSTDLNLIGEKTRSDRRIGSAHFSPAHMPLLEVRTEKTSADAILNLMAVGGKIKKVPVAVVNGTGFVAVRFFFPVQDSAHLANLGVGVYRIDSGITSFGLPIGIFQLGDLADYGVAVATGKEFASAFPDRTFKSPDLLDLKSGRNGKNNKGYVYVYKKGKPKPDRVLPPIEEGRRLTNMPPGKPKISVTDQEVEMLFPV

NbL16g01450.1 aldehyde_dehydrogenase_family_2_member_C4 [MW = 54.59 kDa]

No. of times detected



log(intensity)



Values from



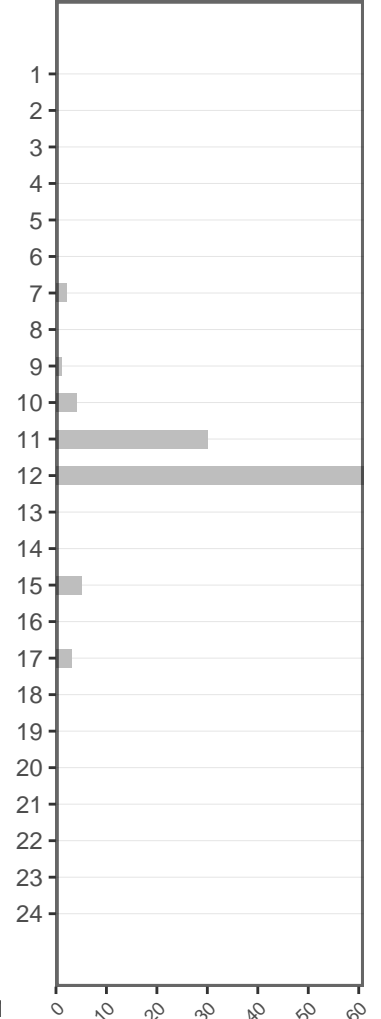
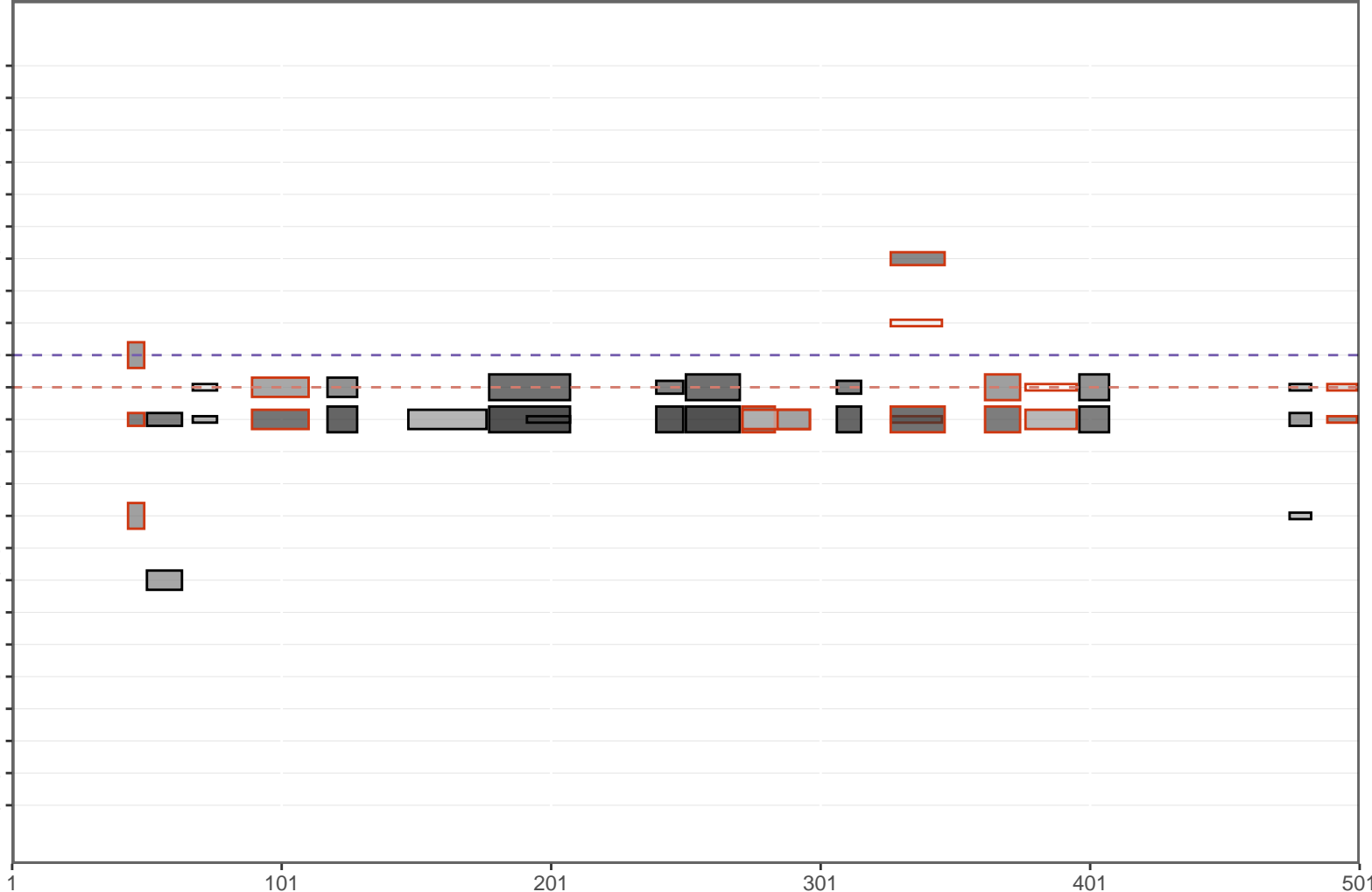
MW indication



Molecular weight

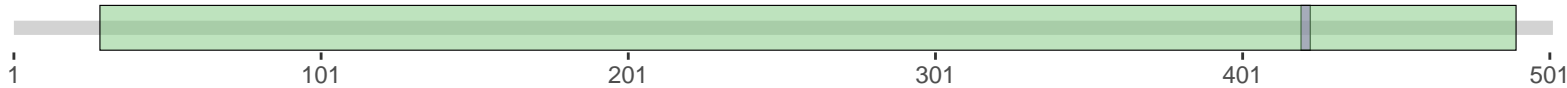


Gel Slice



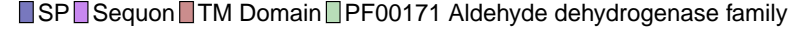
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

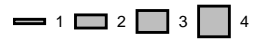


Protein sequence:

KSISFTGSTEVEGRLLVMQAAALSLNPKVLELGGKSPFIVFDNDVQKWLAPLAMIGLYNKGEVGVAGSRLEFDGGYDKFVKKLVEITKTWVYGDPPDPNSHGQPKVQKKGFERVLSYEHGKREGATLLTGGNTLDRDKYFVEPTIFADVDHMIKAEKIFGSPVLEVMKFKTVEEVKRNCTQYGLAAGVMTNLIANIATVSRKIRAGVWINDYFAFDPCPYGGYKSSGFERDLGMEGLHKYLGKSWATPHNSPWL

NbL16g01430.1 fe-S_cluster_assembly_factor_HCF101_chloroplastic-like [MW = 57.03 kDa]

No. of times detected



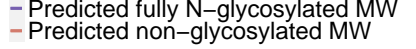
log(intensity)



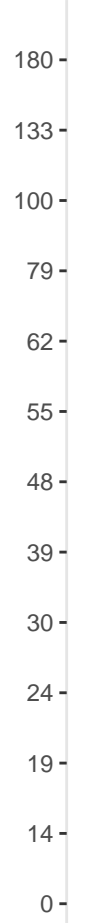
Values from



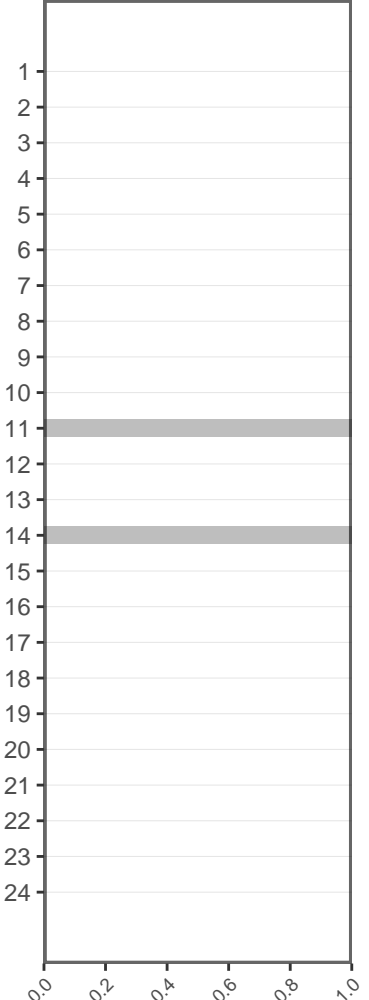
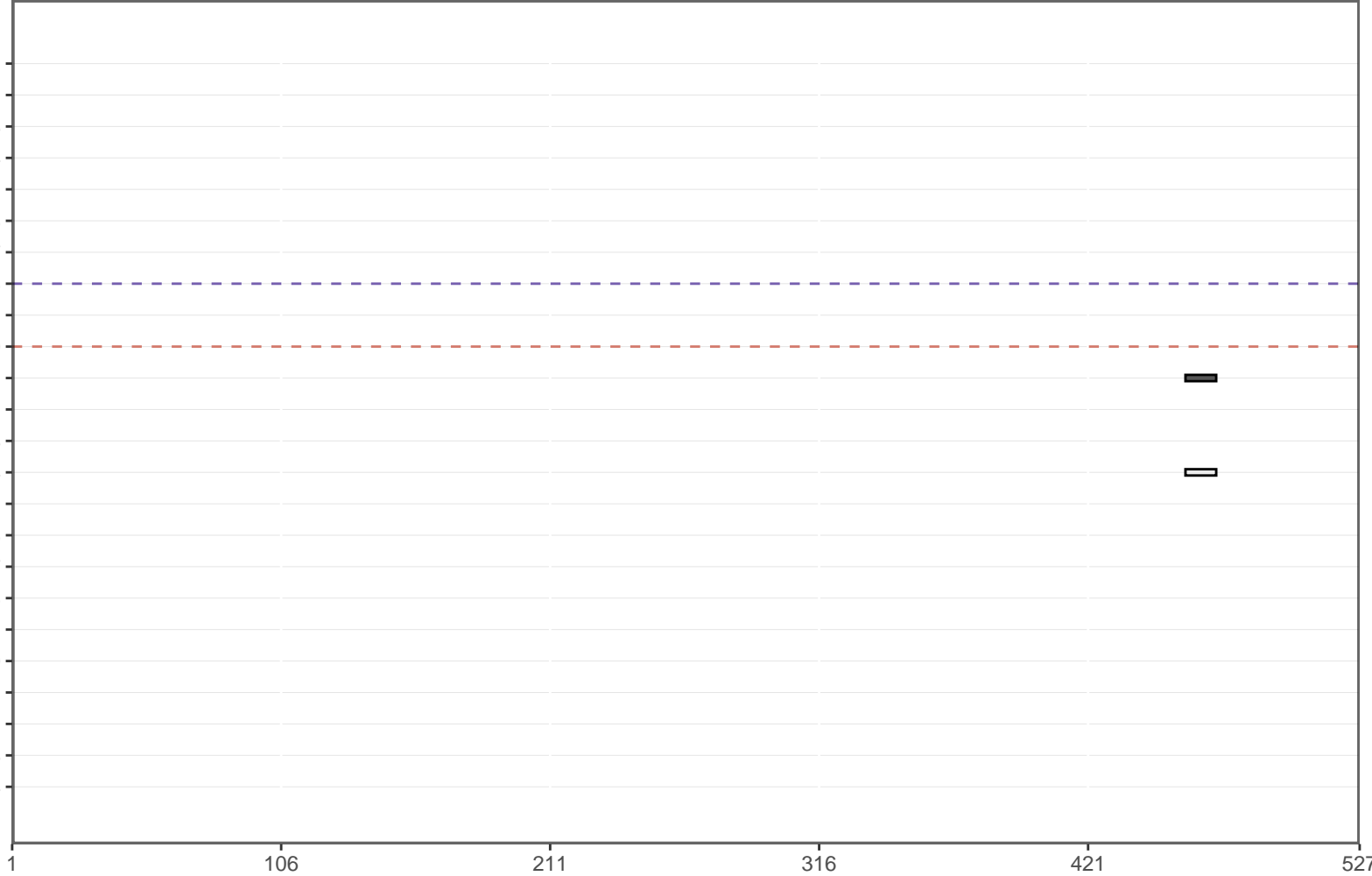
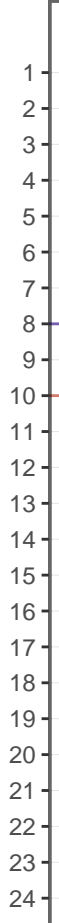
MW indication



Molecular weight



Gel Slice

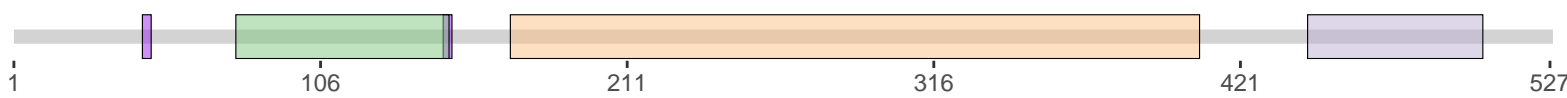


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

AGQGRAMRGPMLVSGVINQLLFTTEWGELEHYLVDMPPGTGDKQLTGGVPLTAAVIVFTPKLAFIDVAKGVRFMSKLVPCVAVVENMCHFDADCKRYYPGRGSGGGVVGQFGIPHEFDLPIQPTLSASGGDSGMPEVADPQGEVSRTFQELGVCIVGGCANIRGGVSTAVSYDRSKAAKVKVPSDDEEFLHPATVRRNRDSAGSDVEVTGEKIQIYSDIPDDEPEEIRPLGNVAVETWPDGFGNIAPIYDQLGMMERLVEVPQLTPA

NbL16g01420.1 uncharacterized_LOC107801219 [MW - SP = 14.23 kDa]

No. of times detected



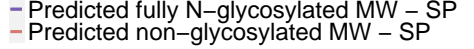
log(intensity)



Values from



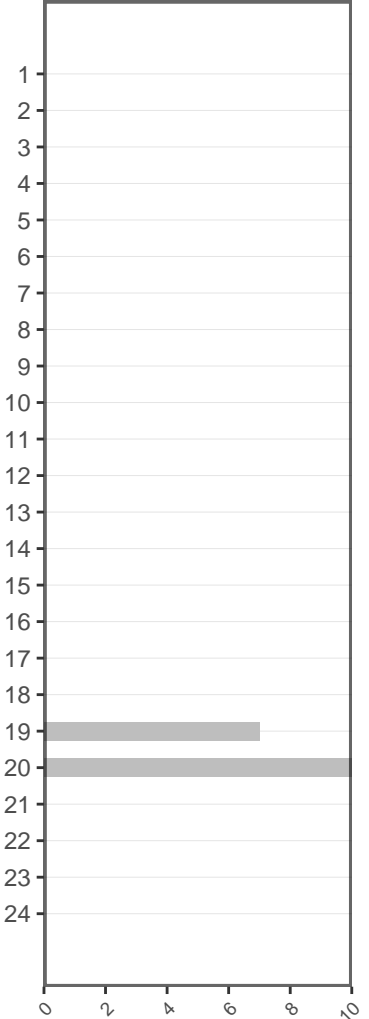
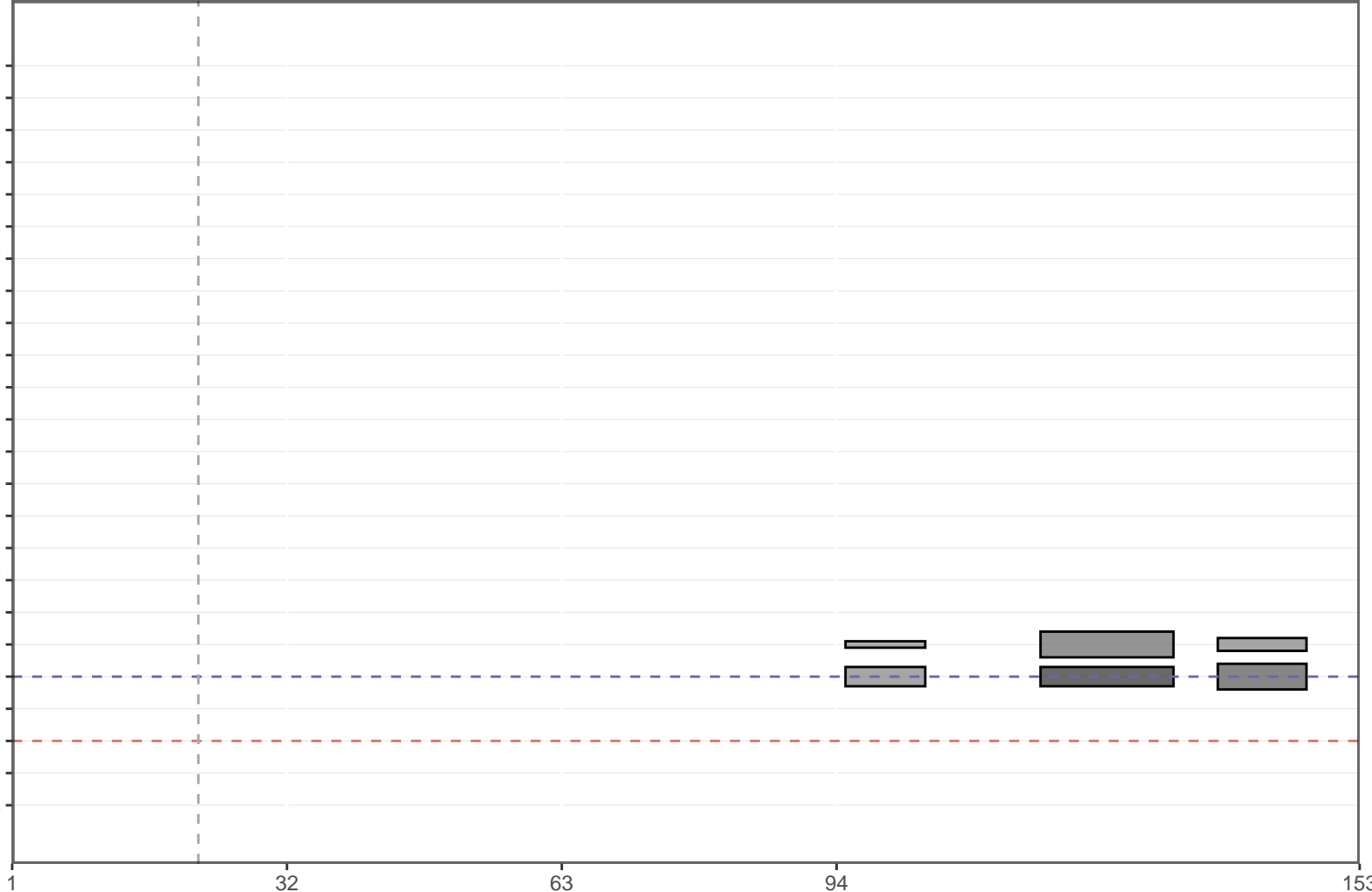
MW indication



Molecular weight

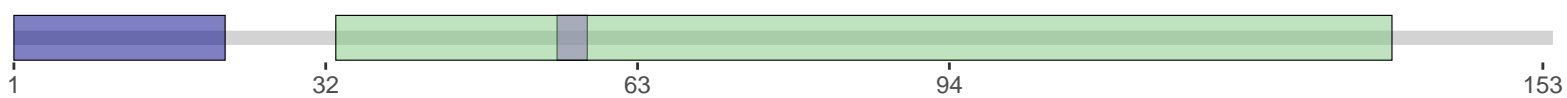


Gel Slice



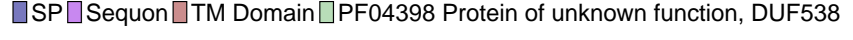
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILGATCKITLPPDNVLAFTYKIKITGKIVENRIALDGIIVRAFFRWGGITGIRSGGENLVFEVGMVTANYPKNFDESPECEGKHKH66S

NbL16g01390.1 leucine-rich_repeat_extensin-like_protein_4 [MW - SP = 47.34 kDa]

No. of times detected



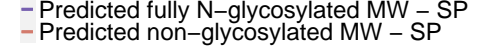
log(intensity)



Values from

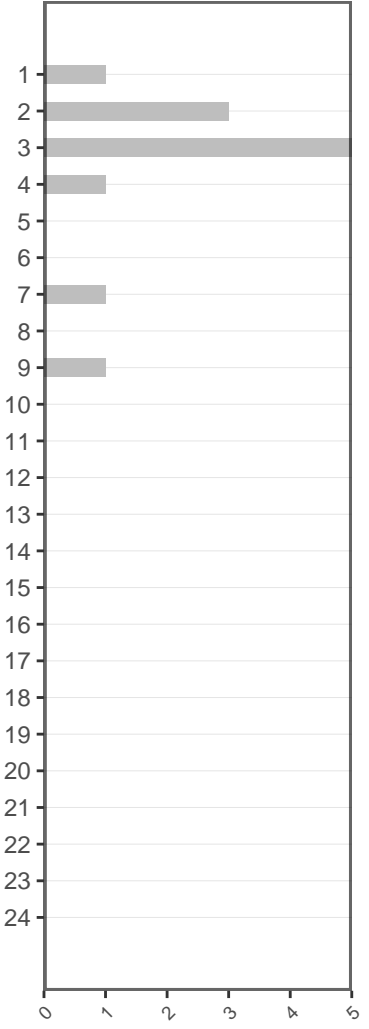
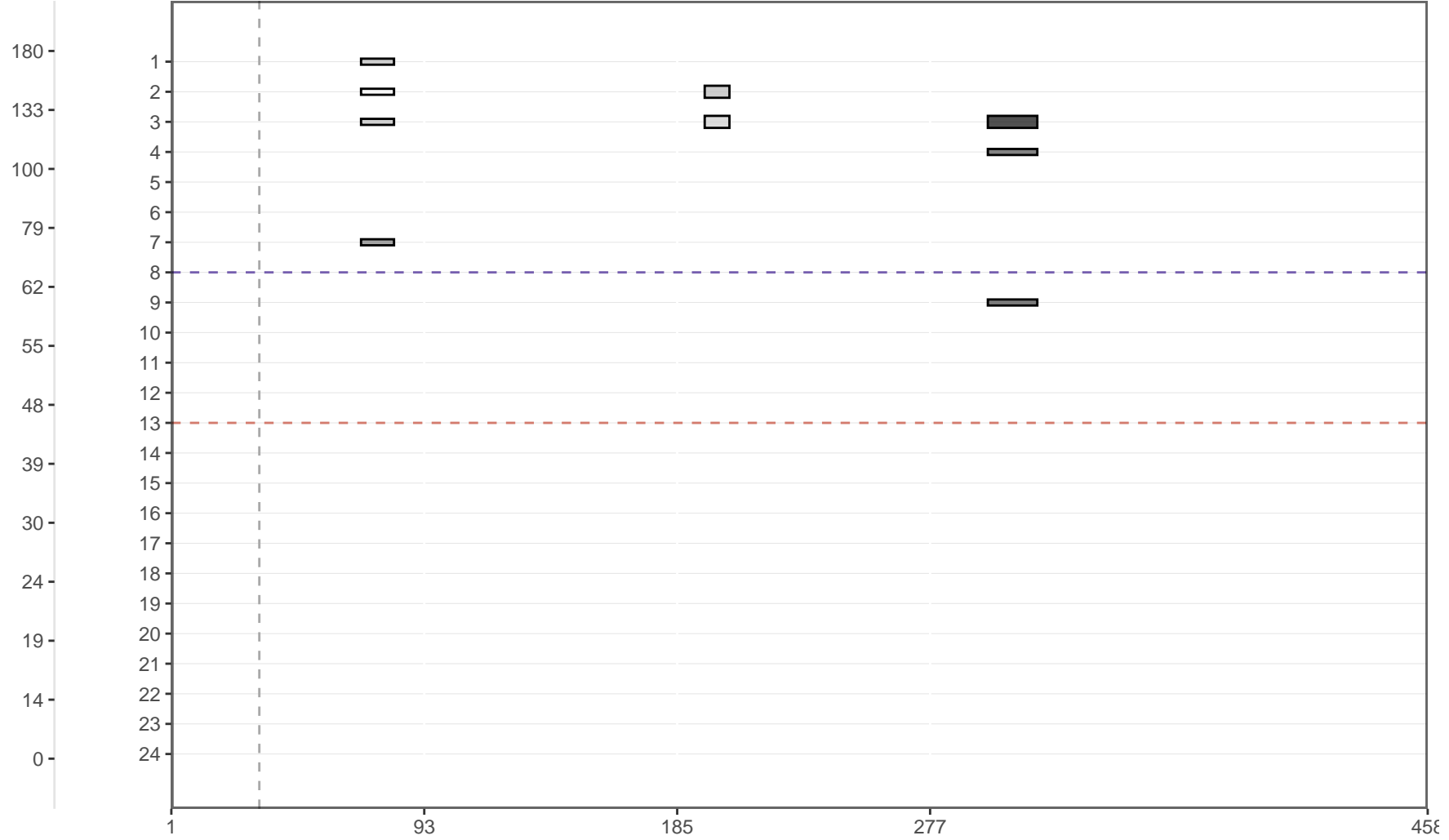


MW indication



Molecular weight

Gel Slice



Protein length



Pfam domains

Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

/PSOLFDKPLDAIFNHNRFMEFSPDFNGSPVSVIVLANKFKGGLPABIGAMSNLNEVIMMNNGLRBSQLPTEIGMLKNTVDFVGFNLQMLKPLPEKFGVLEQLGNVHNMVGGSPKSGQLKLENTFYGVNFTTGEPPVGLGLFEFDGDRNGLINRIPVGRSPAGCKAFKSKRKHGAFKCHKRIPALPPPLLSPLLPAPPPVVVHPSPSPVLSPPPPPPSPPPPVVSPPPP

NbL16g01280.1 GTP-binding_nuclear_protein_Ran-B1 [MW = 25.19 kDa]

No. of times detected



log(intensity)



Values from



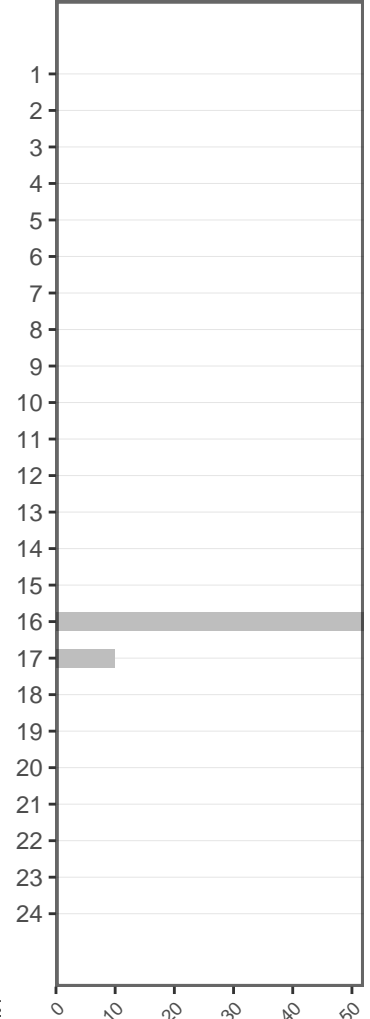
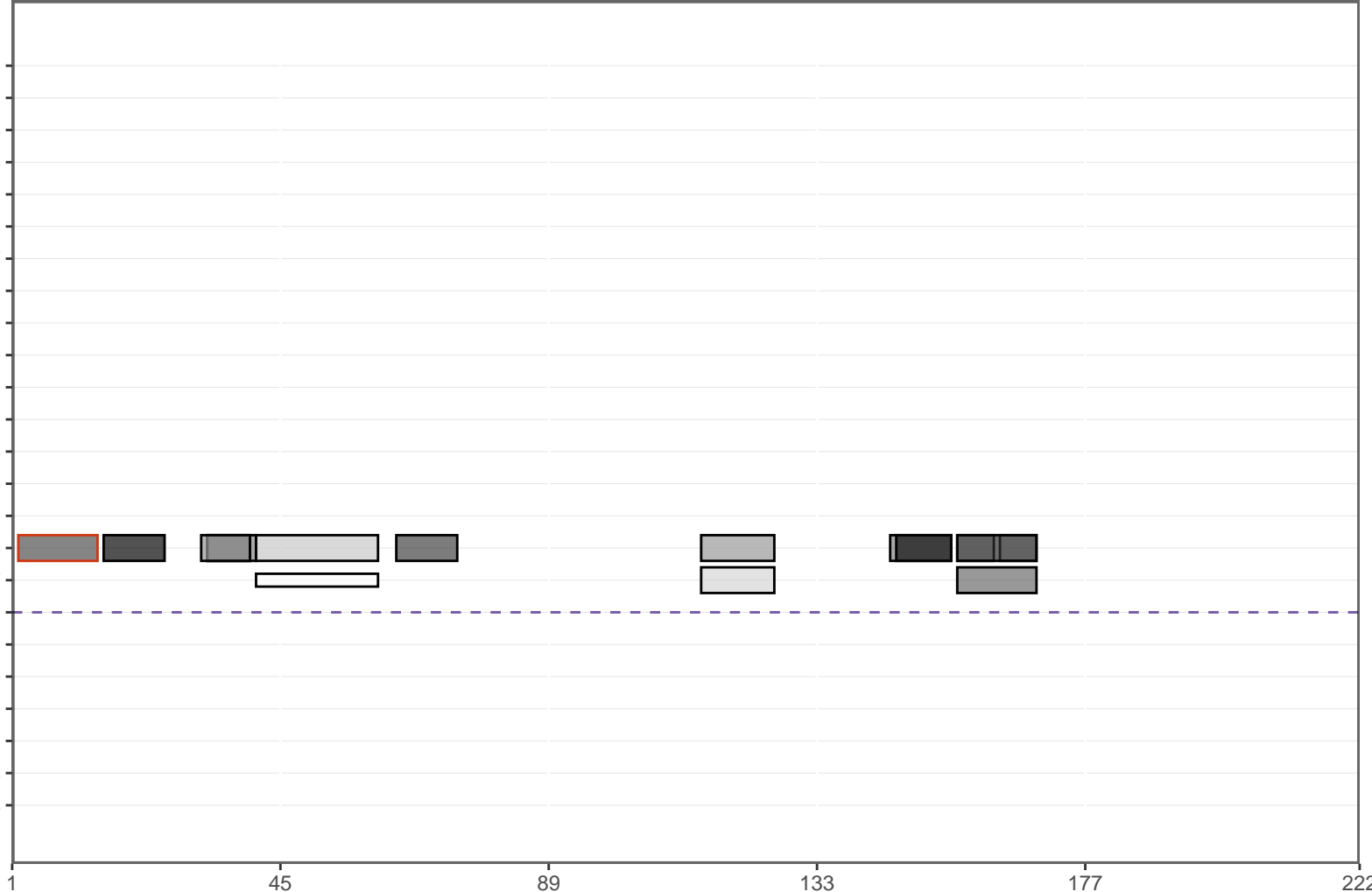
MW indication



Molecular weight



Gel Slice

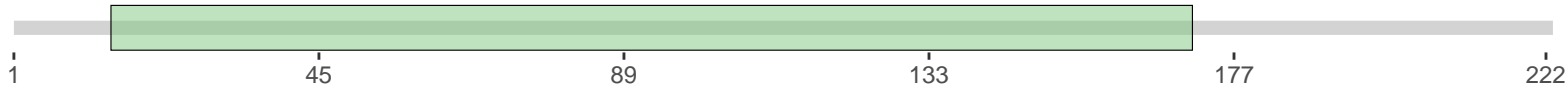


Protein length

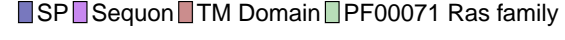


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ILTYKNVPTWIRDLGRVGENPVLGGNKKVQKRGVKKAGVTFHRKKNLGVYEISAKSNYFEKFPVYLARKLAGDNLHFVESPALAPREVQIDLAQQLHEGELLGAAAGLPDQDDSEAFE

NbL16g00840.1 oxygenase_1_chloroplastic-like_(LOC107792958)_mRNA_HQ690822.1_Nicotiana_tabacum_heme_oxygenase_1 [MW = 32.13 kDa]

No. of times detected
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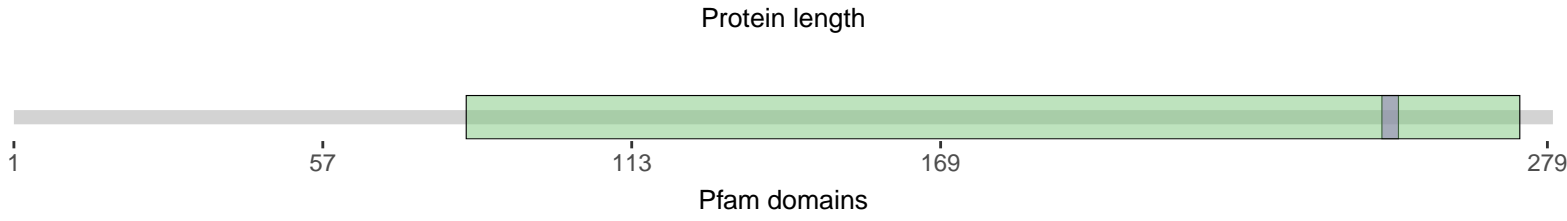
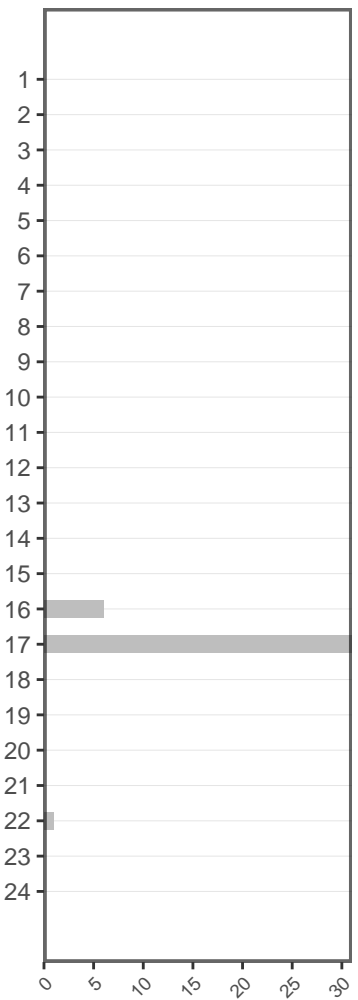
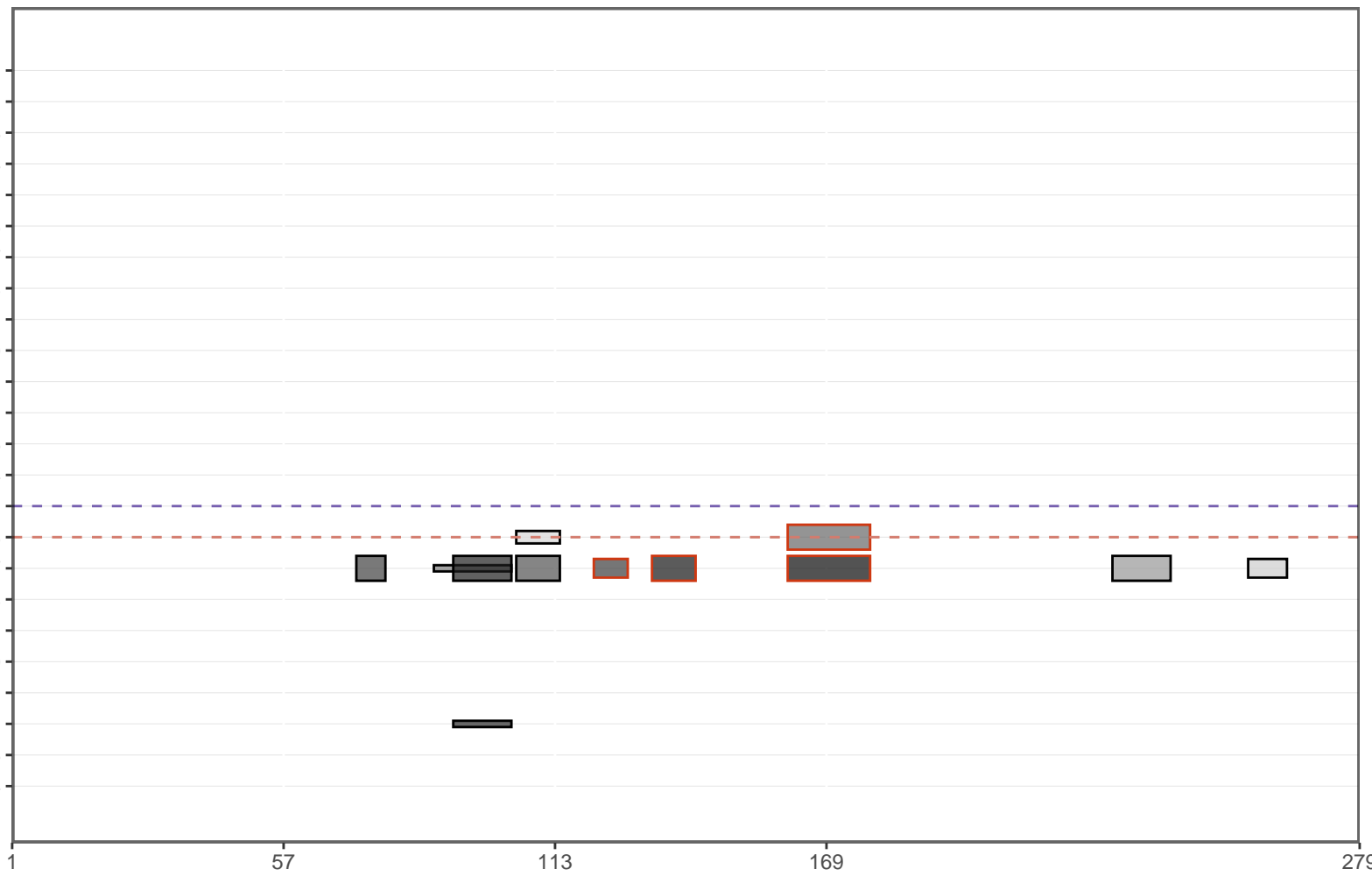
log(intensity)
 4.0 5.8

Values from
 Unique peptides
 Non-unique peptides

MW indication
 Predicted fully N-glycosylated MW
 Predicted non-glycosylated MW

Molecular weight
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 133
 100
 79
 62
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 23
 24

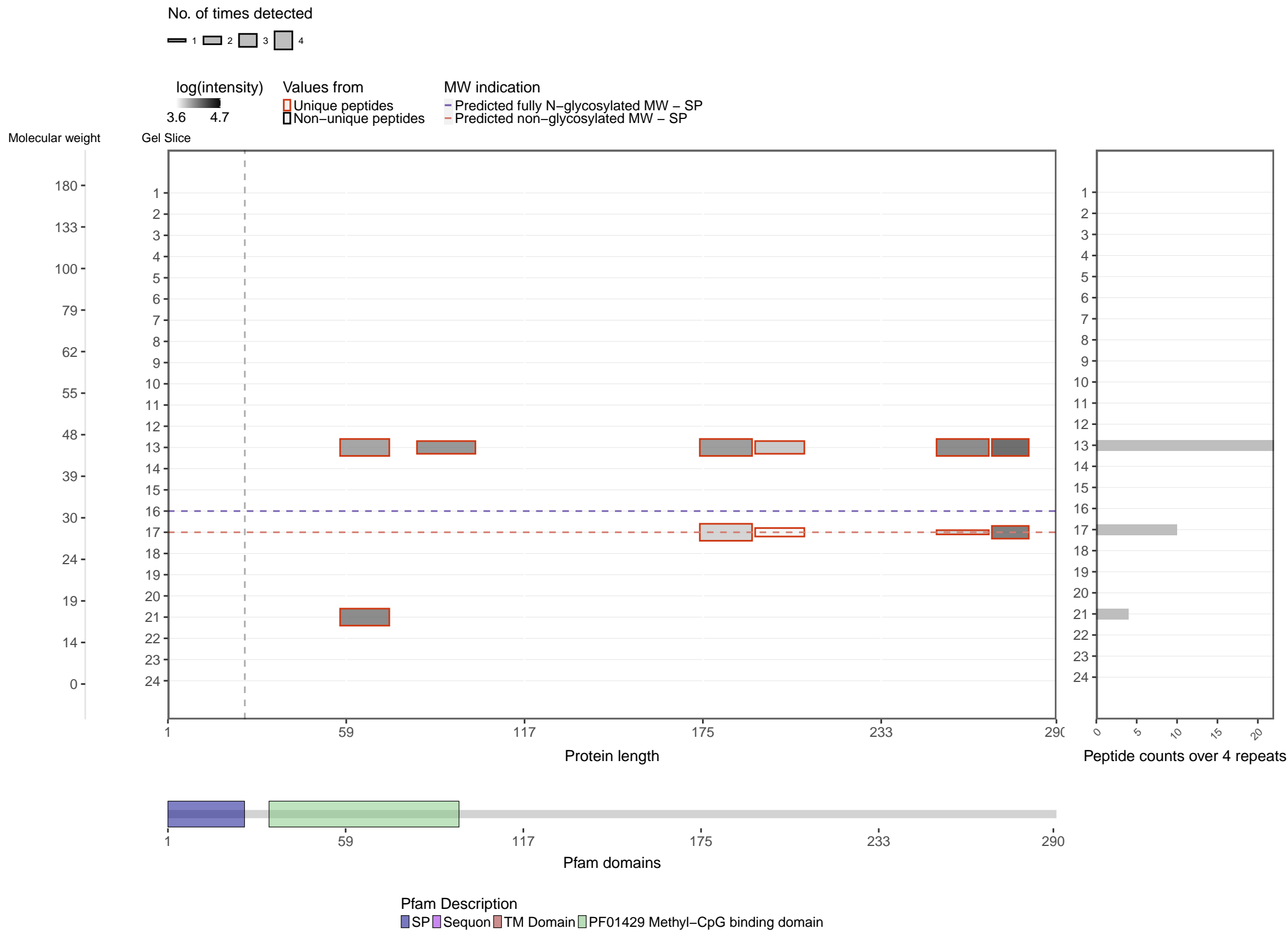
Gel Slice
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 22
 23
 24



Pfam Description
 SP Sequon TM Domain PF01126 Heme oxygenase

Protein sequence:
 LKIKMKAPFSEYAEFRNTGLERSEALKDLEWFRLLGGVAIPERAPGLNVAHYVLEELSEKDPQAFCHFNNTYFAHSAGGRMIGRWAEKLNKKELEFYKWDGDLGQLGNVREKLNKVAENWTRREKNHGLEETKSPKFSGEILRLILS

NbL16g00780.1 methyl-CpG-binding_domain-containing_protein_11-like [MW - SP = 28.99 kDa]



Protein sequence:

KDSDNEVPEETEAAKDDDDMEAEAEHEKDKTVAIVEAEKIVKVEKQKQDENGQDETQDGESELEKKEAEAEATEKIVSEKDKIKSSSENDGKQKDESNADGKIVEDAPSEETQVEKIVKQVEMADNVGHSHKIVKVEEAFQDKVADDDLEATKTNEEKKIVFVEEKVANLLKQI

NbL16g00770.1 thylakoid_luminal_16.5_kDa_protein_chloroplastic-like [MW = 24.27 kDa]

No. of times detected



log(intensity)



Values from



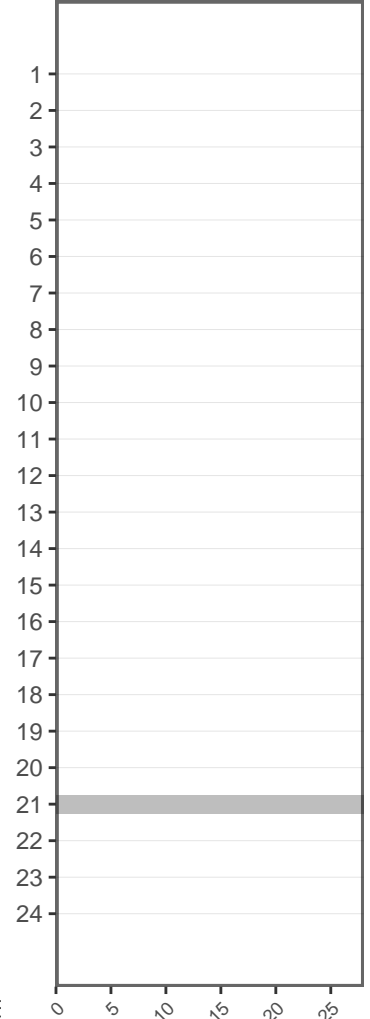
MW indication



Molecular weight

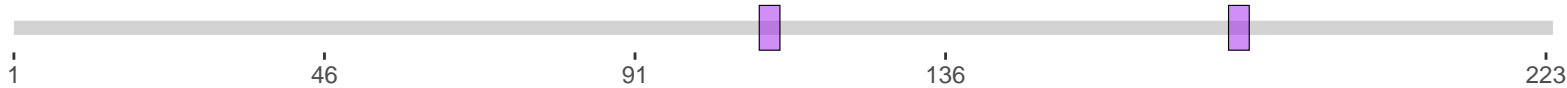


Gel Slice



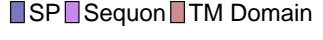
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KKRLERGGINSSTKEKGVLDLVYKLBIVGDAIEKNDLSAASVLYGGSDMDWQKVNISAFNKFSGSDEEKTEIDSFNSLFLVSVTKNDIEGKTAFASASAFKWTTLTGLIEELKGL*

NbL16g00730.1 repetitive_proline-rich_cell_wall_protein_1-like [MW = 32.45 kDa]

No. of times detected



log(intensity)



Values from



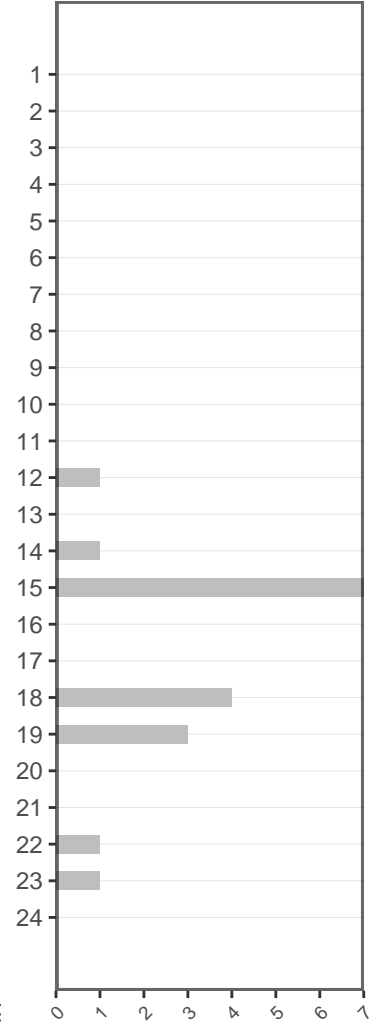
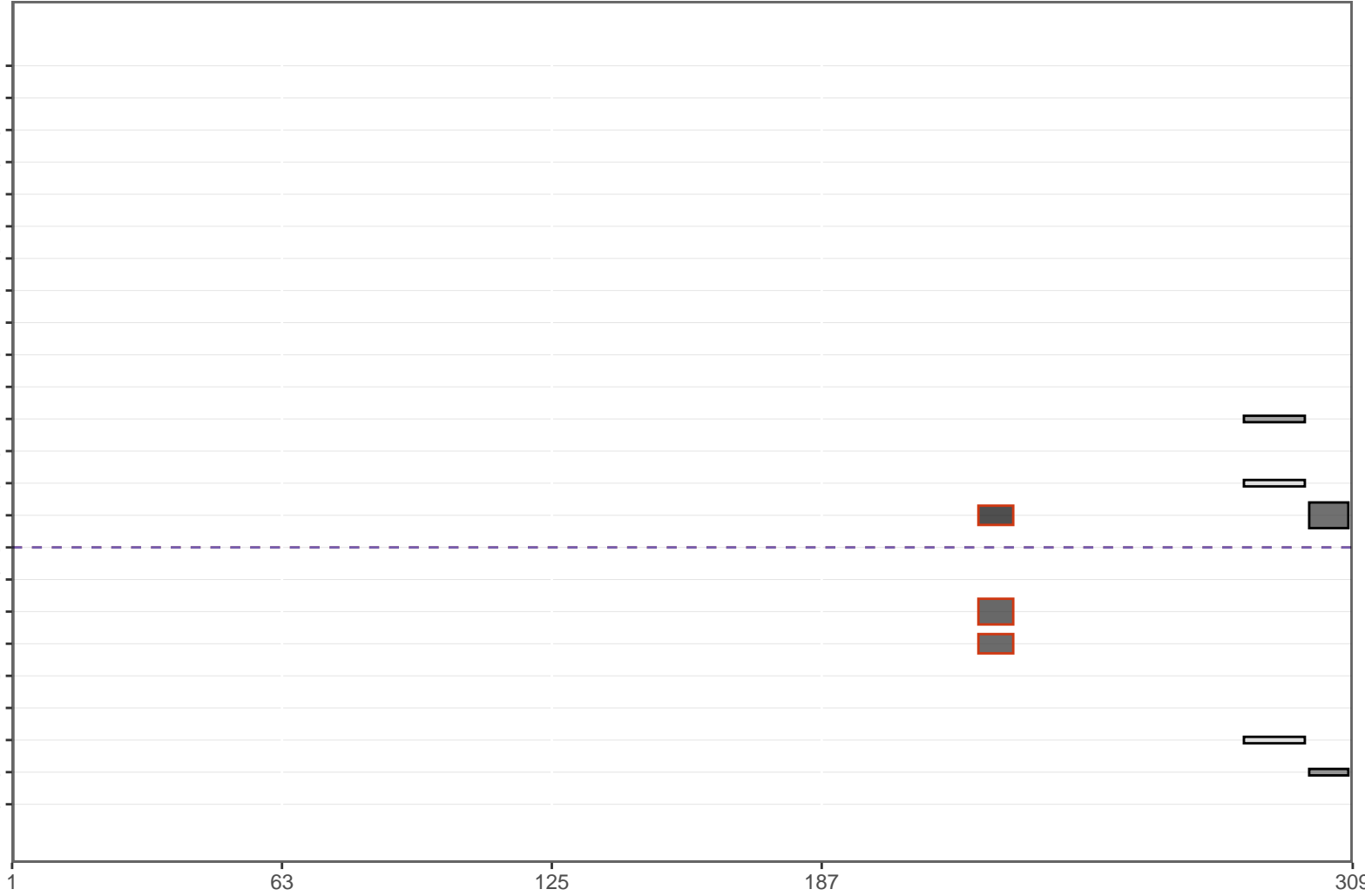
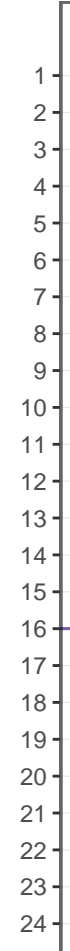
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGIPPVYKPPINFPVPPVFKPPKIPGIPVTVPPVLPKPIGLPPVPPKPNLPPKIPGIPVTVPPVLPSPKGGKPCPSPPPTTKATCPINTLKLGAQVDLLGGLMHIGIGDPVNECCGPIHLSGLEAAAGLCTFLKILLNKKIFVPLALQLLVTCGKTRPPPGVTCGL*

NbL16g00670.1 bifunctional_purple_acid_phosphatase_26-like [MW - SP = 52.61 kDa]

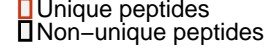
No. of times detected



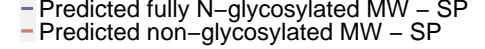
log(intensity)



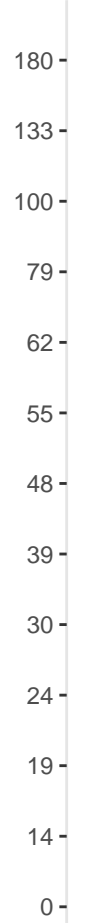
Values from



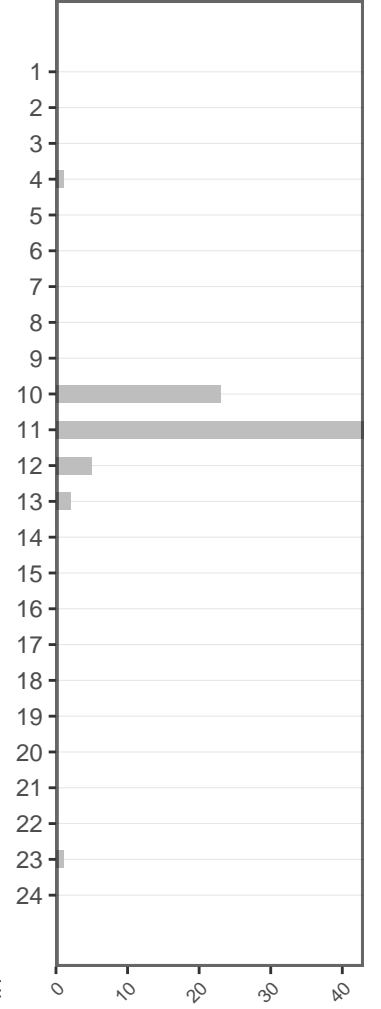
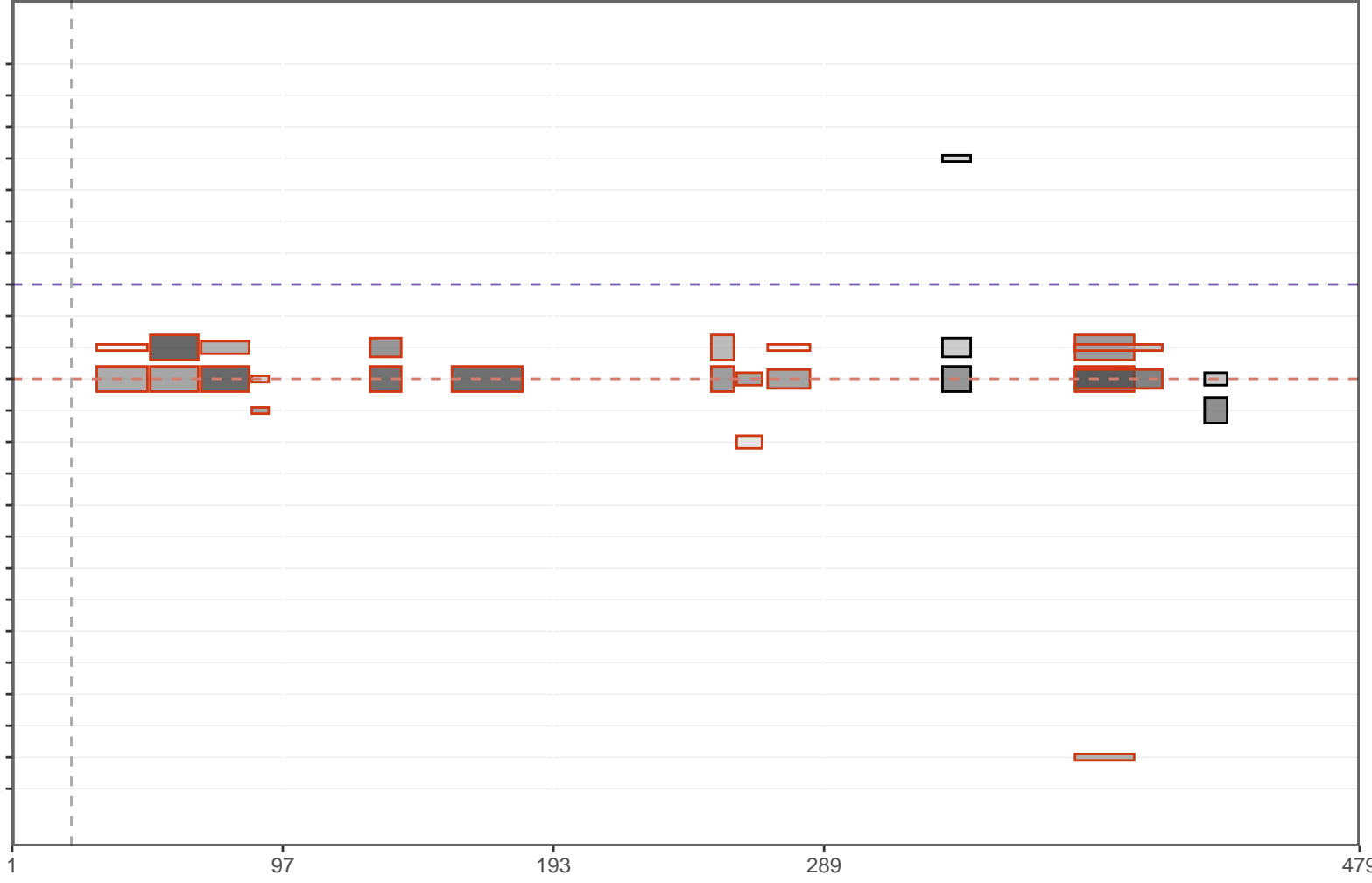
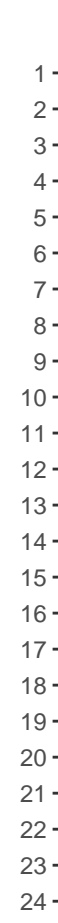
MW indication



Molecular weight

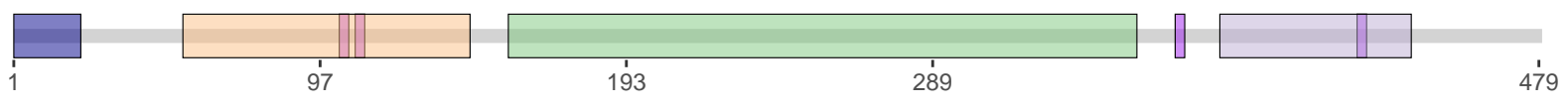


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IHEIEMPMGEVTFPKKLYRPTPYGASKSSPLWYGIIRASAHIVLSTYSPFKYKTPQWKLREELKNVDREKTPVLVLMHVRYNTNAHFMEGSMRVSFEGVFEHKVDFIFAGHVAVERSYRVSNIHYNVSSGDPYVPDKAAFPVYTVGGGGKGEGLASTFRDPQDFVSFAFREASVGHSTLEIKRTHALVHWNRNDGKVKVSDSVLHNGVYVGSNHQRRLKQKHLHSEVILNRASTAGL

NbL16g00610.1 pyrophosphate-energized_vacuolar_membrane_proton_pump [MW = 80.02 kDa]

No. of times detected



log(intensity)



Values from



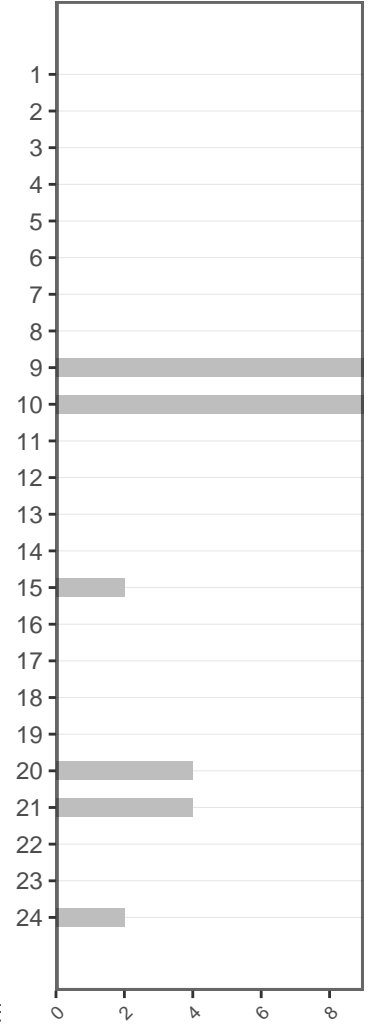
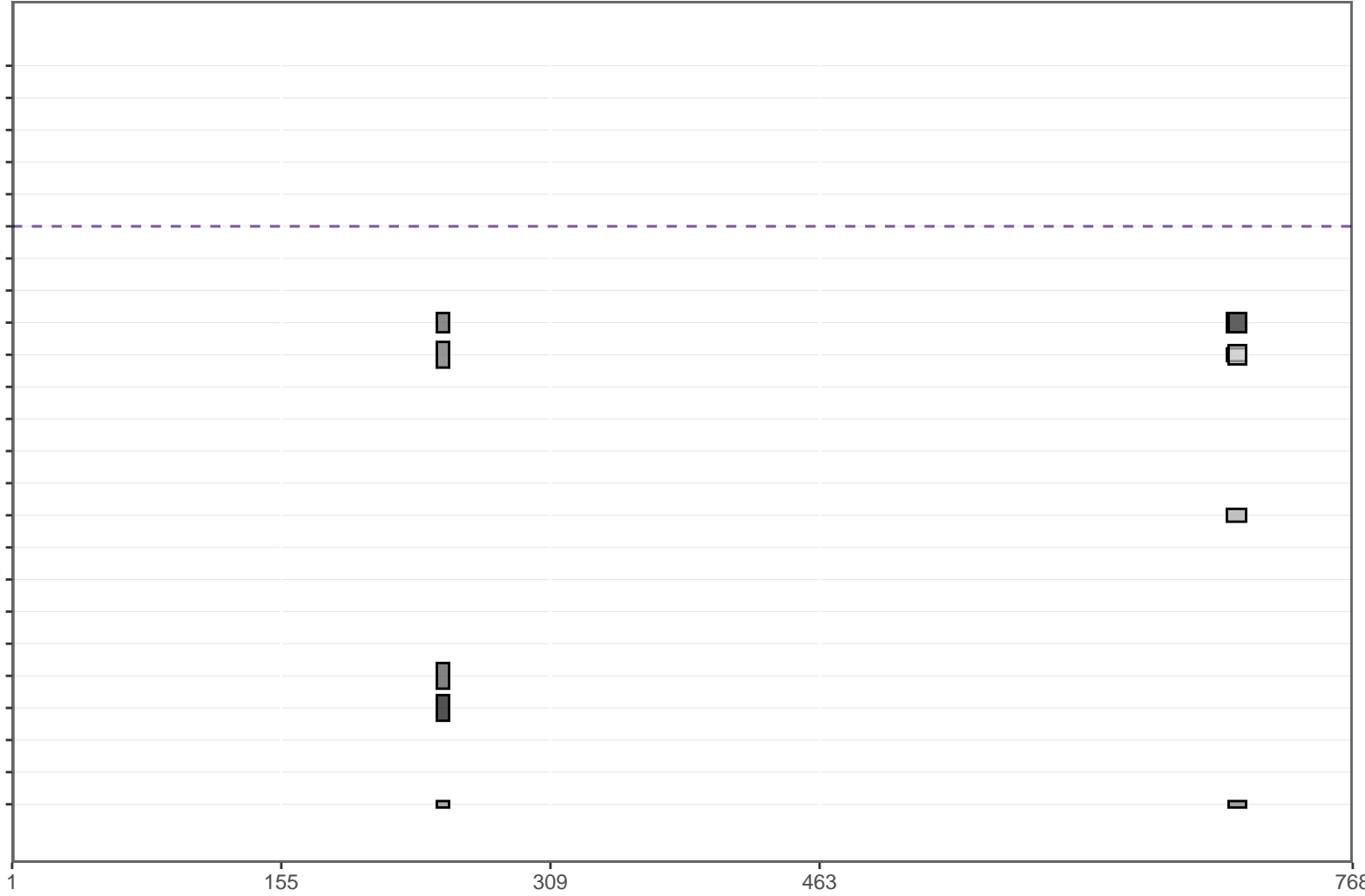
MW indication



Molecular weight



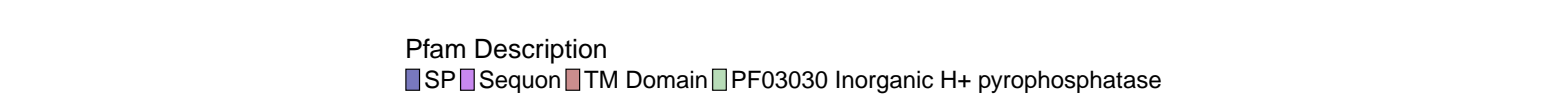
Gel Slice



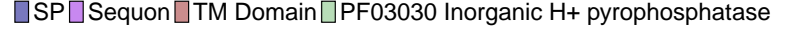
Protein length



Pfam domains



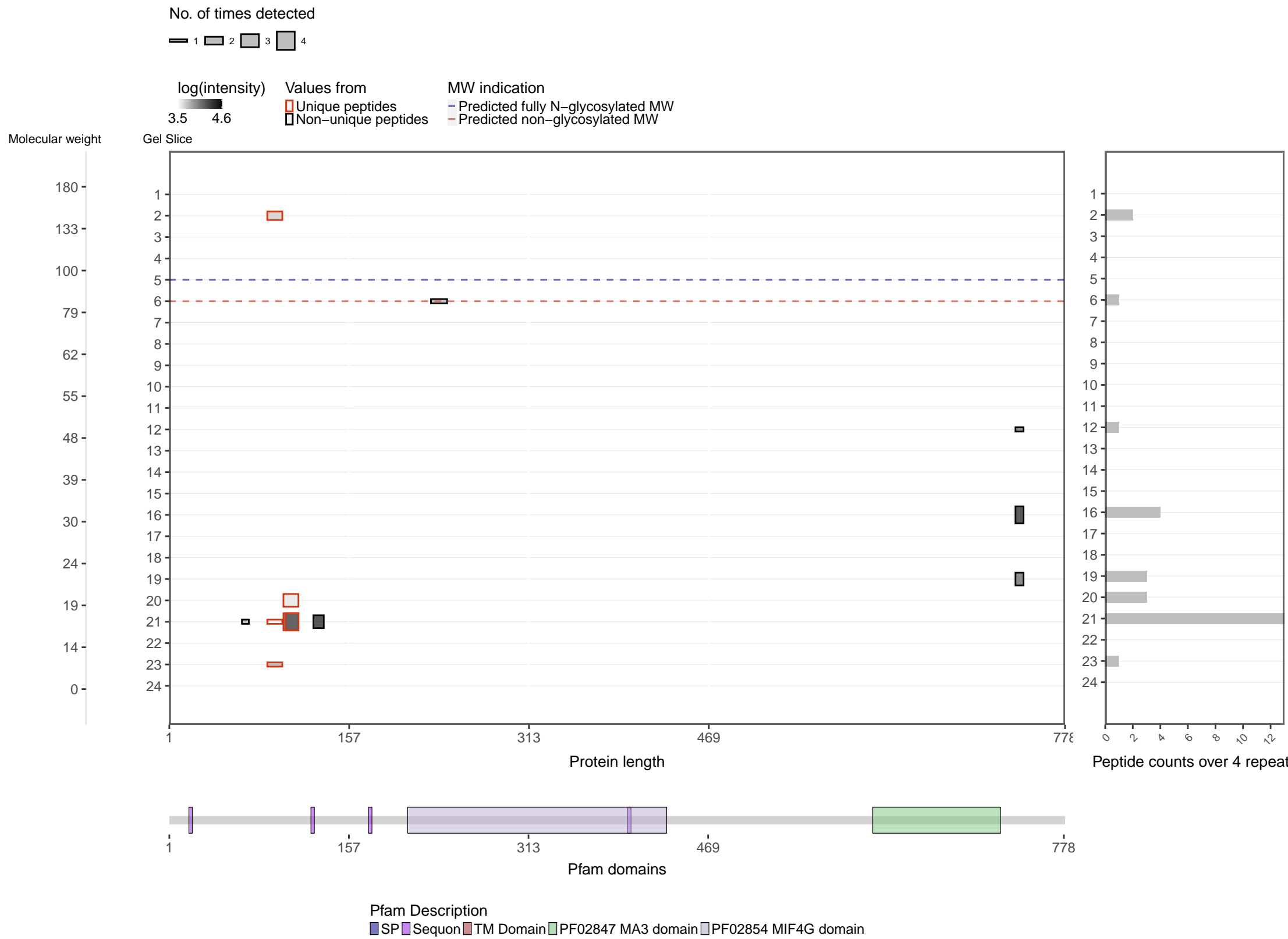
Pfam Description



Protein sequence:

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NbL16g00550.1 eukaryotic_translation_initiation_factor-like [MW = 86.03 kDa]



Protein sequence:
 VEACDFNTGKQKLDKQSRHNDYFNRLKELSTNPQLASRLRFMVRDVLDRANWVPRREYKAKTNEHWEAEKEMGLRPGATASIRNARIPGAGGNLAAVGRPGTGMMPGPGVYKMPGMPGMDNDNWEVQRSRMPRPGVOPPLUGKPSLNRQLPQGGGGHIGRSEALQGGGGPPRIPSGVASAMEPVPQVPGVPRPSPATTVPSVAEKPRAPRARSNPEELKRTVSLLEEYFNRLRLLDEALGGIEELKSPDFYEVVKETISLGLDKSPPR

NbL16g00540.1 shikimate_O-hydroxycinnamoyltransferase-like [MW = 49.28 kDa]

No. of times detected



log(intensity)



Values from



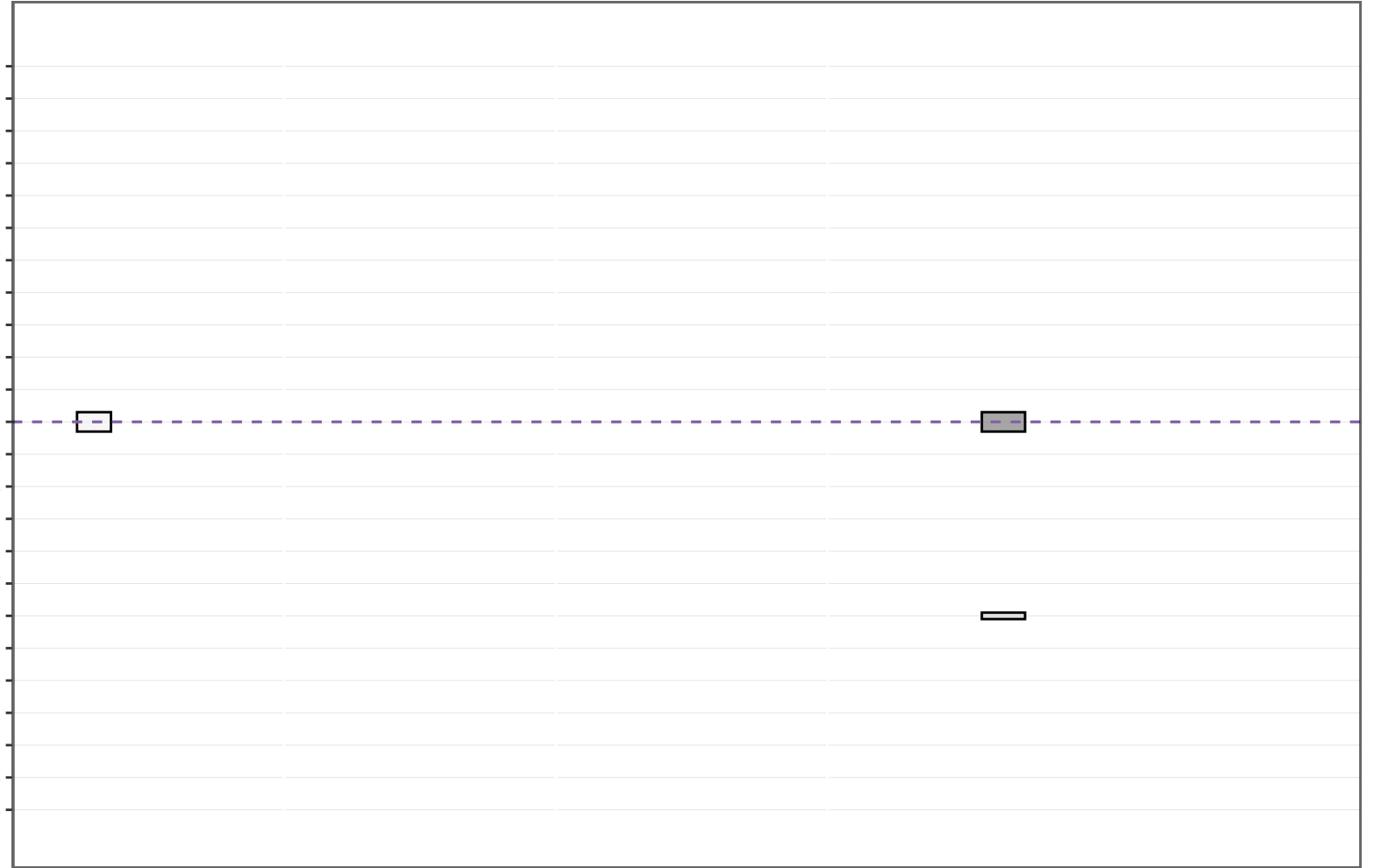
MW indication



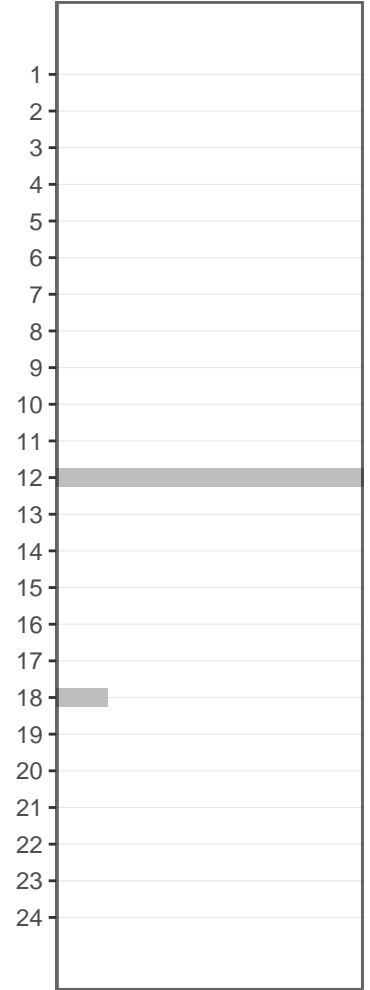
Molecular weight



Gel Slice



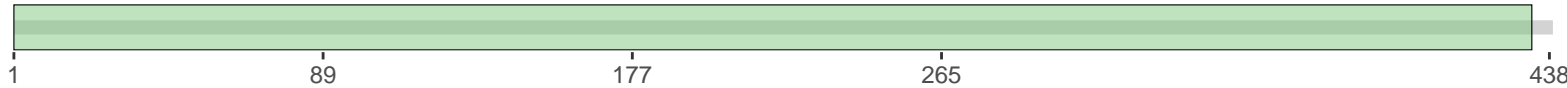
Protein length



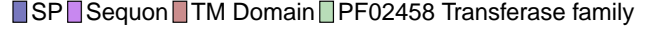
Peptide counts over 4 repeats



Pfam domains



Pfam Description

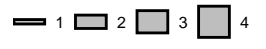


Protein sequence:

YIHPPTLKSSEIHHGQVNGPKFSTTAMFKITSDQLLKTGKHGEGRYEVLAAHWRCGKARALDDQLTKLHWTDGRSLFFPLPPGVLGNVVFATPIANSGEILSEPLMNTAGRIHTALARMDDLYLRSADIKLELGTDLKLRGPTVYFASPLNINSWTRLPVHDSDFGWGKPVHMGPAKILVEGTVYLPSPSDDKNLRLAVGLDADHMFLEKYLVDI

NbL16g00490.1 leucine_aminopeptidase_2_chloroplastic [MW = 60.87 kDa]

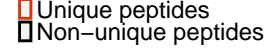
No. of times detected



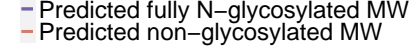
log(intensity)



Values from

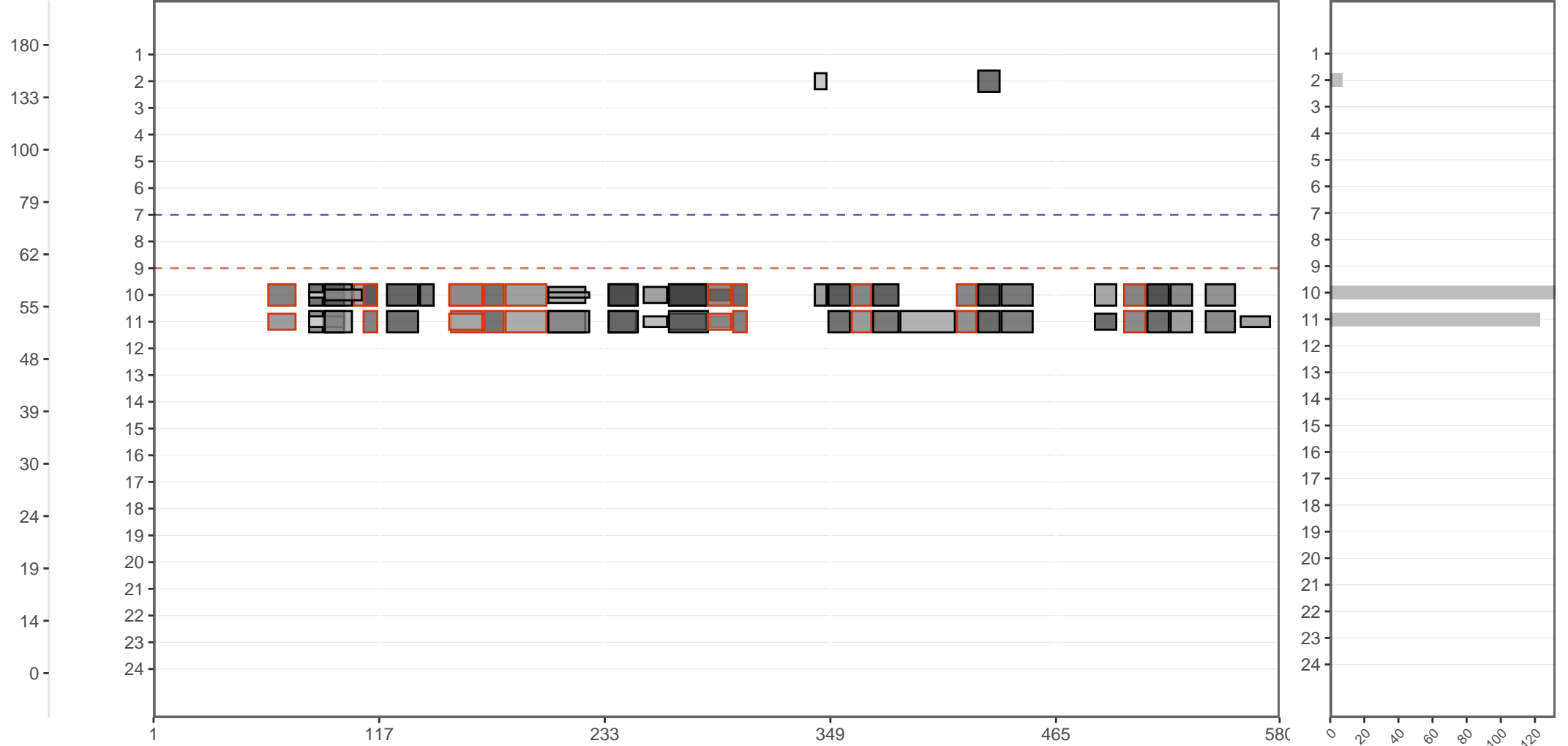


MW indication



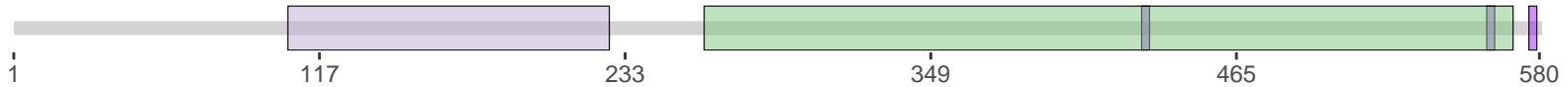
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00883 Cytosol aminopeptidase family, catalytic domain
- PF02789 Cytosol aminopeptidase family, N-terminal domain

Protein sequence:

LAEEAKKASTYSYDVLBAKILNVEGCKELKMGSYLAWGEASANPPHRIHLGYKPTDGEKRLALVGLKLTDFDGGYNIKTGPGCLIELMKFDMGGSAVLSAAKALGGKPKGVVHFVAADENMISGTGMRRPGDVTASNGKTEVNTDMEGRLLADALVYAGNDGVEKVDLALTLTGAGIVALGPIAGVFTFSPDOLAKEVAAAEVSGEKLWRRMPLFEEGYWETMKSGVADMVNTGGROGGAAVAAFLKGFVDEKVGWVHDLAGPVAWDDKKKKNATGFGYSTLVEW

NbL16g00460.1 eukaryotic_translation_initiation_factor_5A-1/2 [MW = 17.48 kDa]

No. of times detected



log(intensity)



Values from



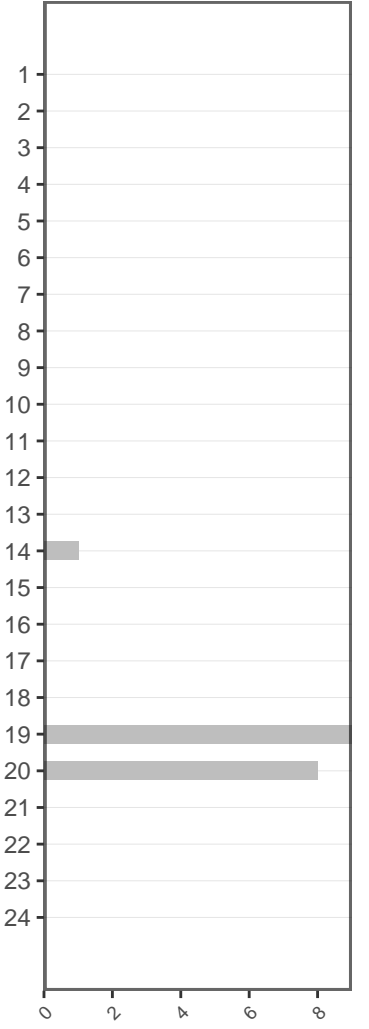
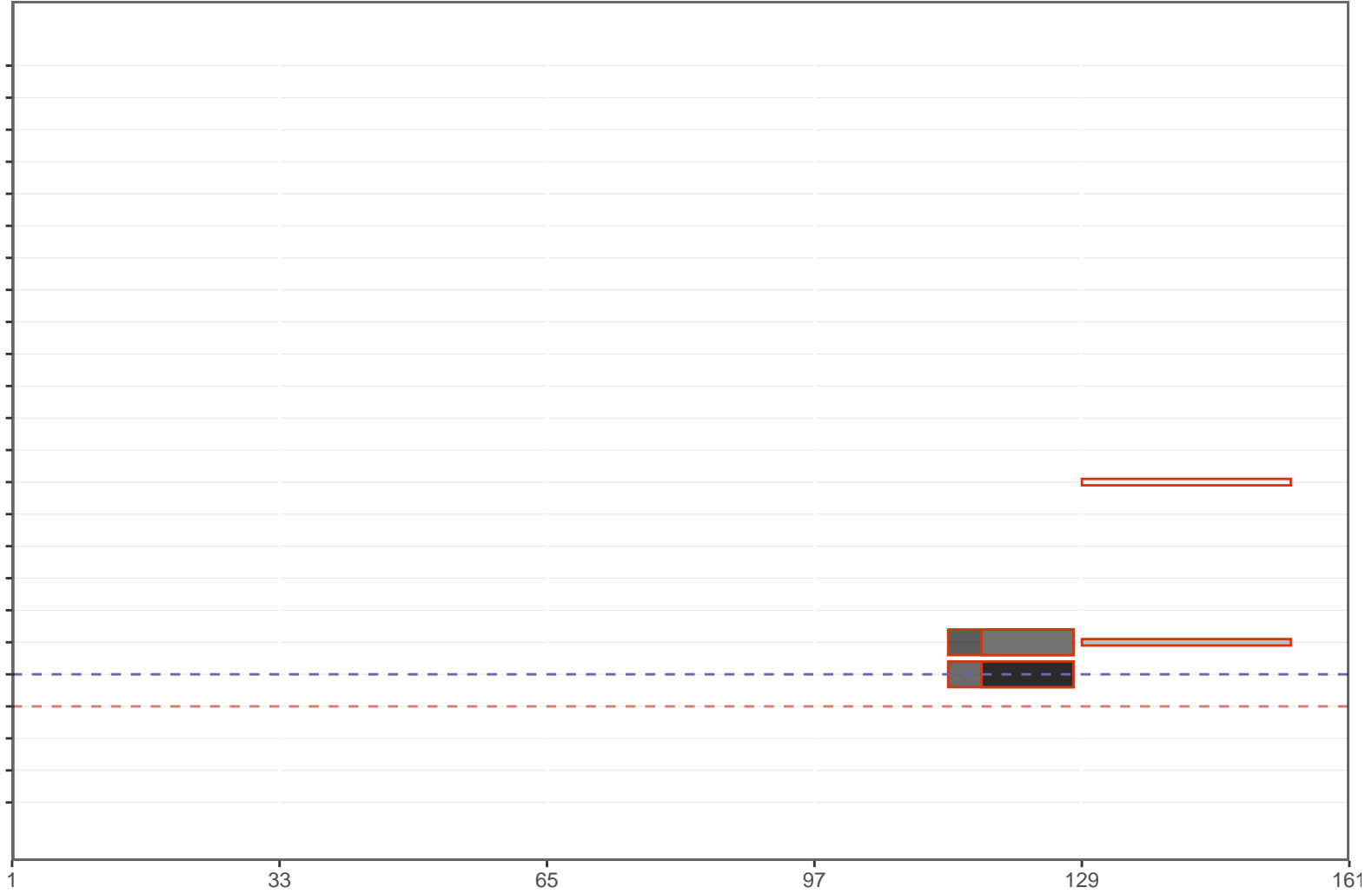
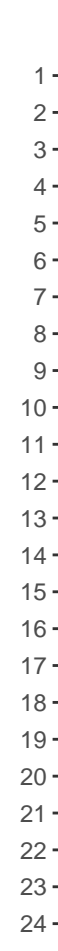
MW indication



Molecular weight



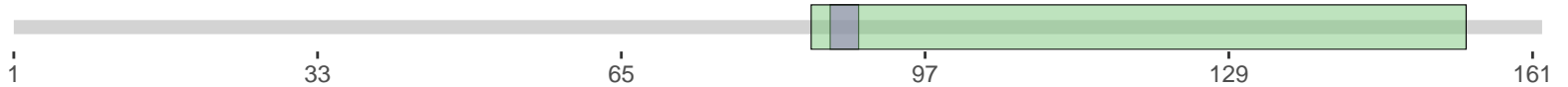
Gel Slice



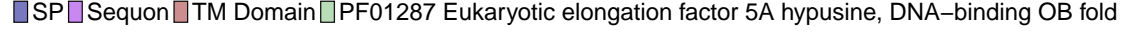
Protein length



Pfam domains



Pfam Description



Protein sequence:

IGKKLEIDVPSHNGDNPHVNRITDYLQIDISEDFVSLTENGNTKDDLRPLTDEALLSGVWGGFEFGKDLVLEVMAMGEEGINWKKDGTKN

NbL16g00370.1 anthranilate_synthase_beta_subunit_1_chloroplastic-like [MW = 31.26 kDa]

No. of times detected



log(intensity)



Values from



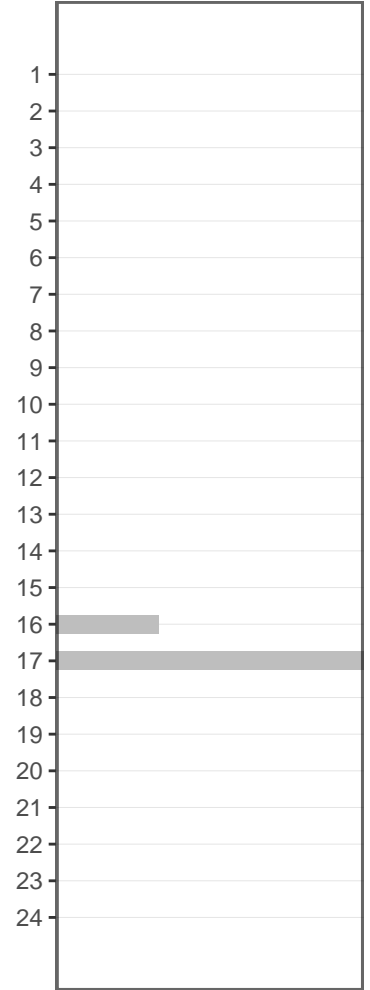
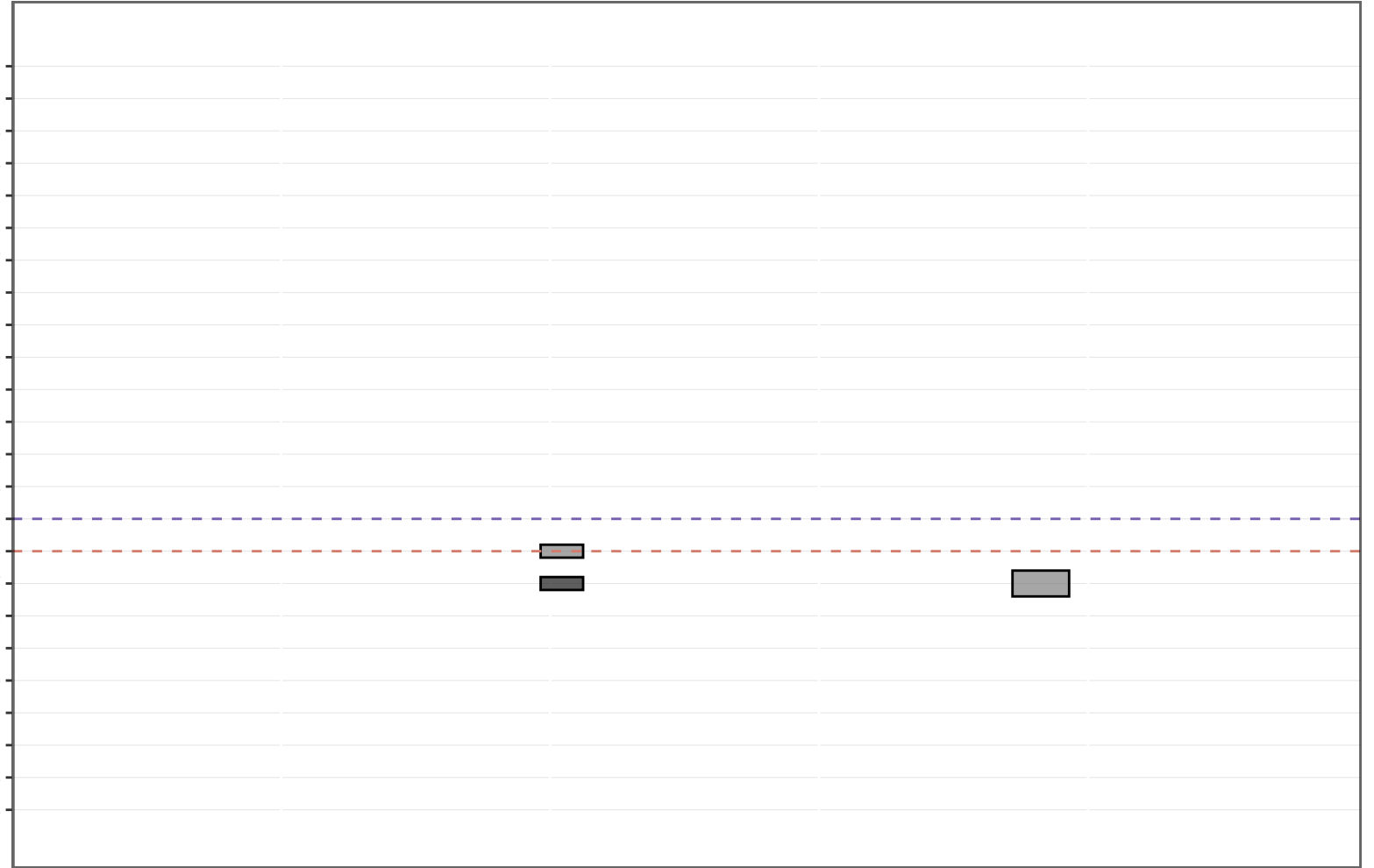
MW indication



Molecular weight



Gel Slice

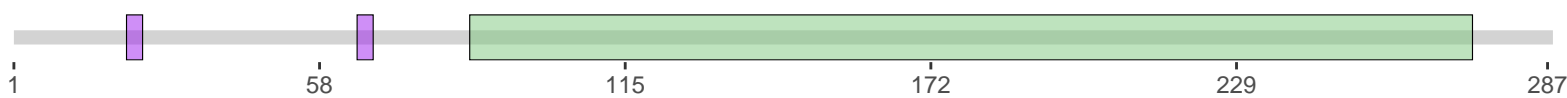


Protein length

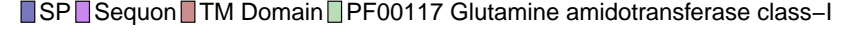


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

GPGAPDDSGISLGTVLELGPTVPLFGVCMGLGCGEAFGGKIVRPVGVVHGKSSPVVYNEGDEGLFAGLSNPFRTAGRVHSLVDKDFPFKGALEITAWTEDGLUMARKHKVYRHGGVDFHPESITTEGMTWRNFKMERKEEAEDQ

NbL16g00260.1 temperature-induced_lipocalin-1-like [MW = 21.48 kDa]

No. of times detected



log(intensity)



Values from



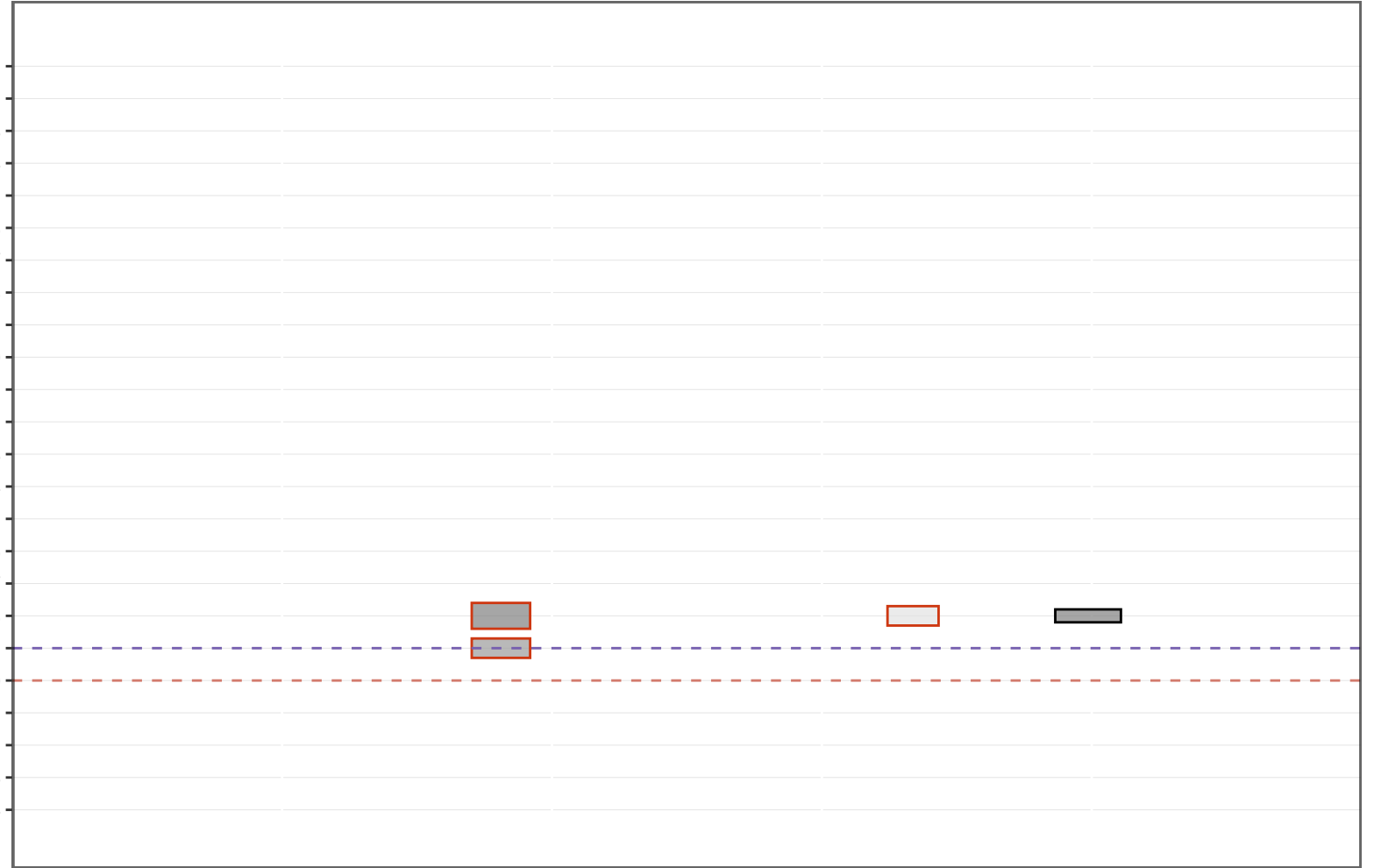
MW indication



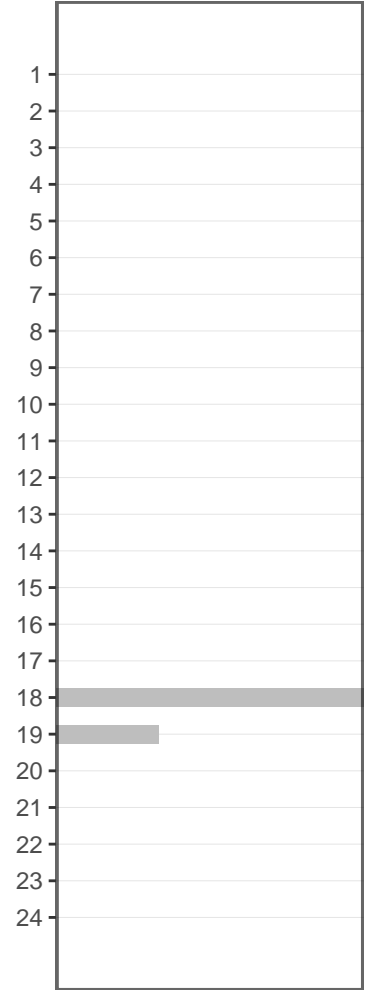
Molecular weight



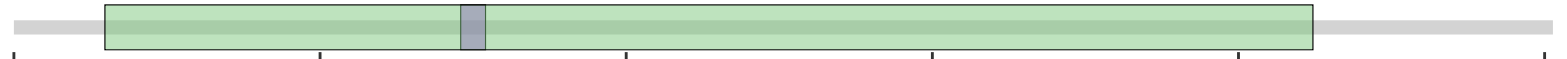
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

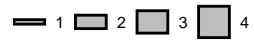


Protein sequence:

EAALKLVKFKYVPPFLNPVPTGDVWVHIDENHYALIGPGRNLYLWLRGNVLDDEMYNQLVEKAKEEGYDVKLHKTRHTNPPPEDDDAKDKTKGIWIKLGVK

NbL16g00210.1 adenylate_kinase_5_chloroplastic-like [MW = 70.68 kDa]

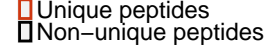
No. of times detected



log(intensity)



Values from



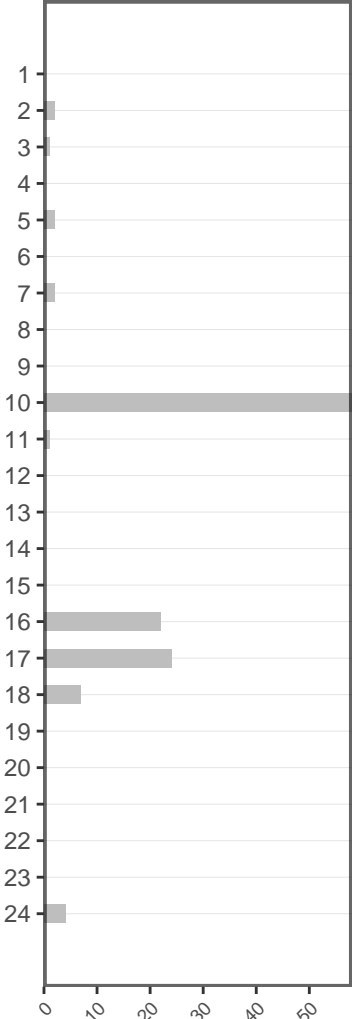
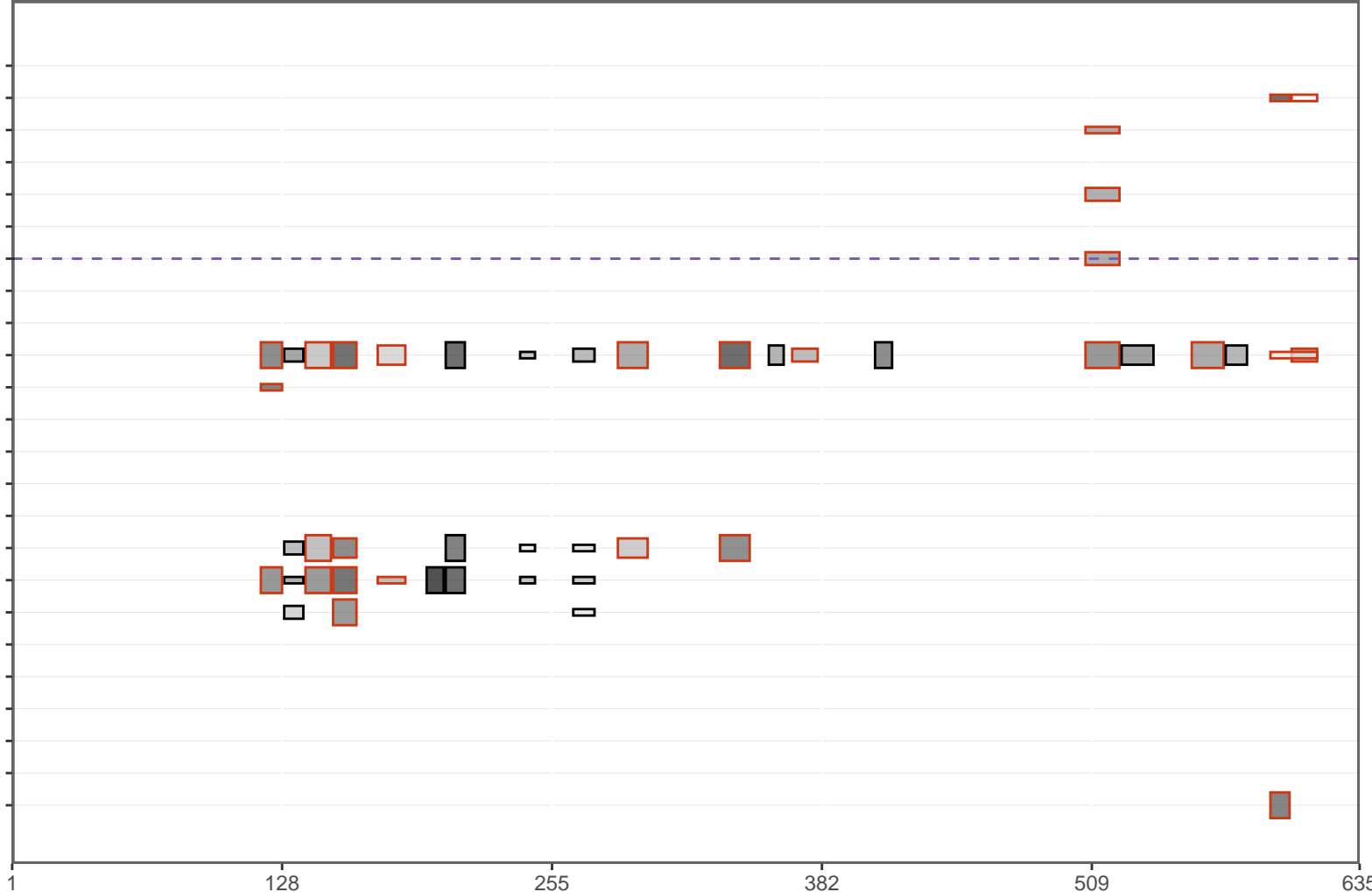
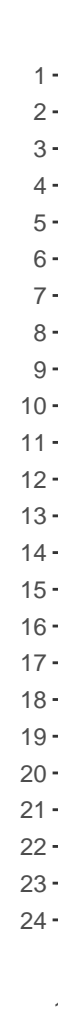
MW indication



Molecular weight



Gel Slice



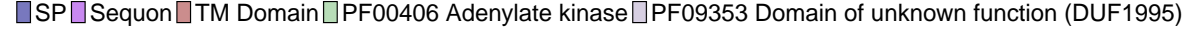
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KDAVFEEDSLLSVQKEEDANKLEKSEFTSTQVDMASGGKDWRGIPTRLNPHSREREYFTEVLGATGRAVNDGKTRLKEISPELNATVYRIGTLMELRVLALSFADDDKRVKVCVGGSMGDGALAGMPLGLAGSRKILEYMDVGDVYALGTFVNISSGGKVEKQDDLFILVAPQNAVNGIHDDMRAMTDAAAGSRPVLNPKLKDLPSSGSMGTMRGRDKLEYAASFICYHFRLLYVAGTQYPIMLGRMSYPPYVELNKRVDSPGKEYVALATFASR

NbL15g25260.1 zinc_finger_CCCH_domain-containing_protein_11-like [MW = 42.98 kDa]

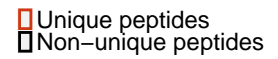
No. of times detected



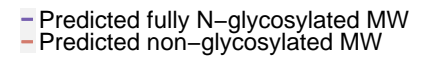
log(intensity)



Values from



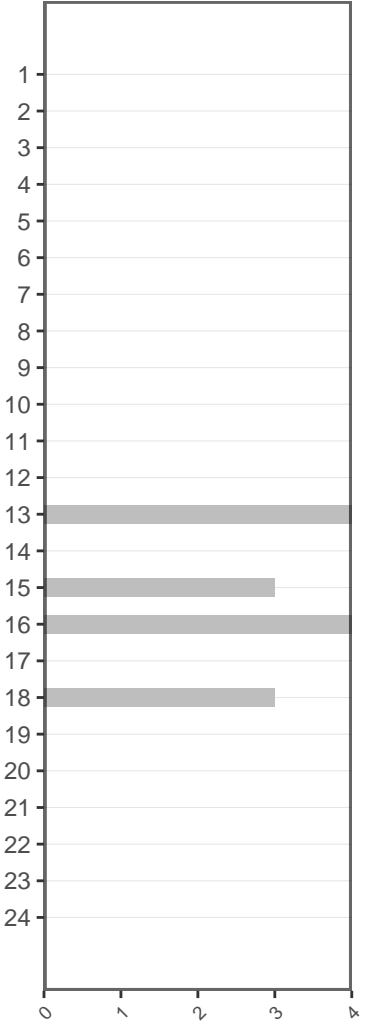
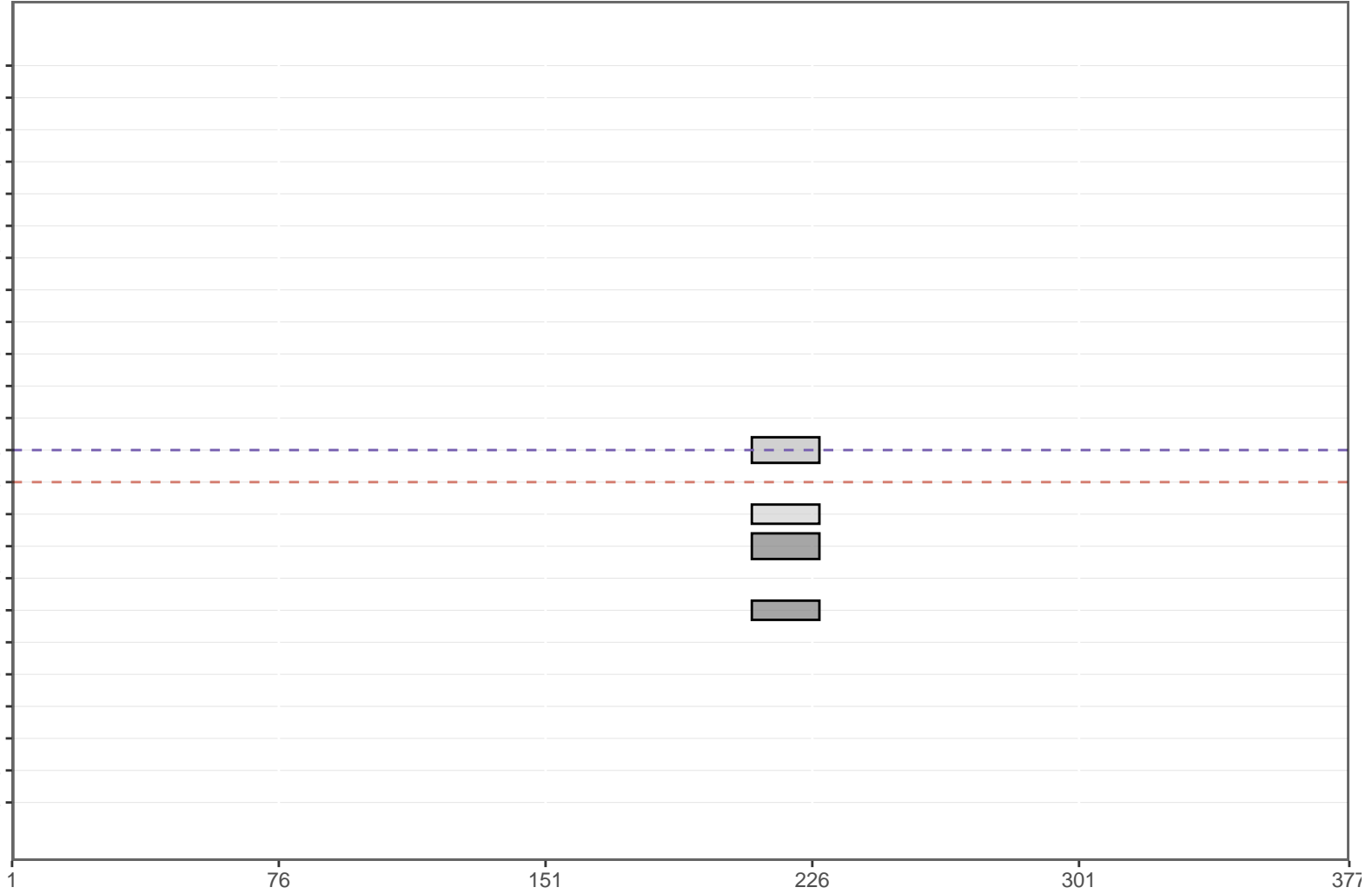
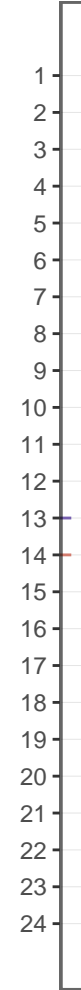
MW indication



Molecular weight

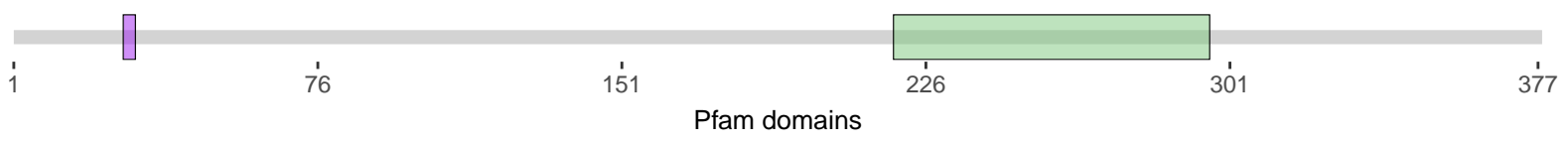


Gel Slice



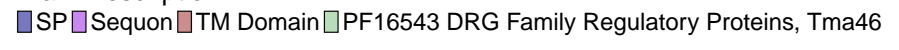
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

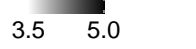
YIGWFWVCPNGGKEHYRHALPPGVLKSGMKALLGEEADKMPHEEIEIDQRALKTASTPLTTELFMEWXXXXXMEEREASLAKGRADRAKNDNRMSGRFLFMSDASVFWVDVGVAYDKYERDEESGEPKDTARDEASSMPARNIDDDGGEASHHNEVNDNYDDDDDDDDDDDDDDDDDELVDLNELEATLSKTSLSQINEPGGHV

NbL15g25240.1 60S_ribosomal_protein_L4-like [MW = 44.83 kDa]

No. of times detected



log(intensity)



Values from



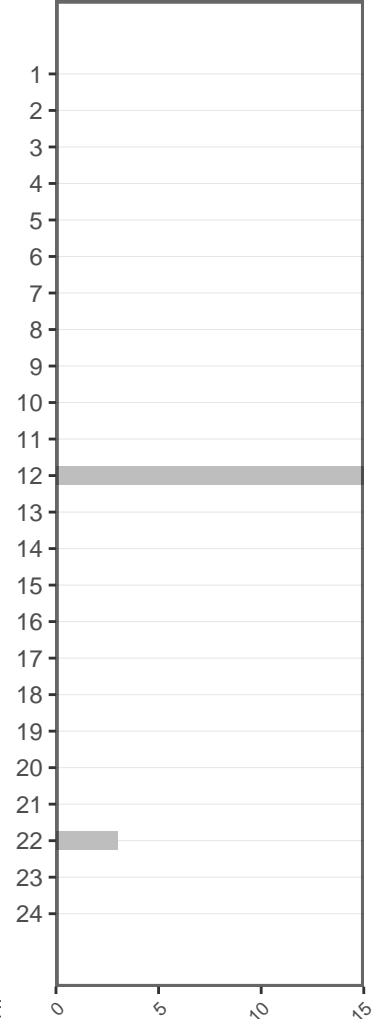
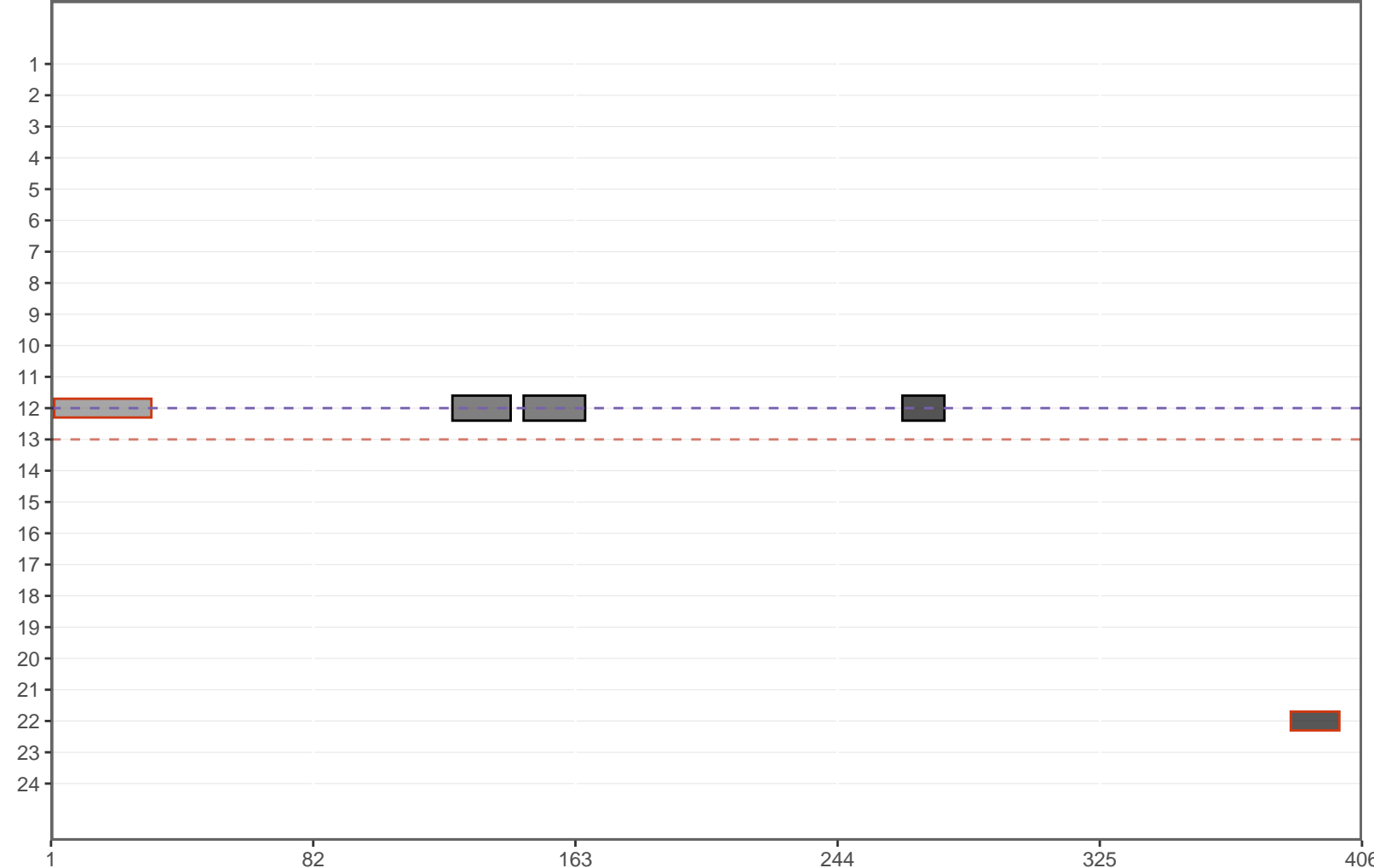
MW indication



Molecular weight

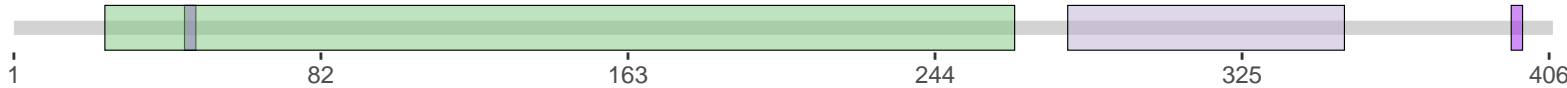


Gel Slice



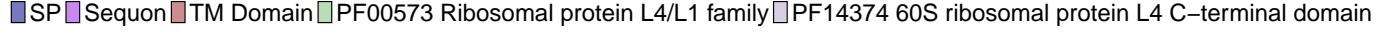
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

HAIRPGKGMNRNRRVFCRKGPLAVVGTETGAKLVKAFRNIPGVCHVDRLNLLKLPQGHLEGRFVWTKSAVEKLDVSGVDFKPKSEKKGKYLRLRPKMNADLARINSDVGVVFRPKKQVNRKATLKKFNPLNVLKLNLPYAKTARRMSLLAEAGRKAKKEKLDKRRHQDTKEEASAIRBASHSWYKTMISDSDVAFEDNFTKWLGVSDI

NbL15g25210.1 probable_LRR_receptor-like_serine/threonine-protein_kinase_At1g67720 [MW - SP = 100.36 kDa]

No. of times detected



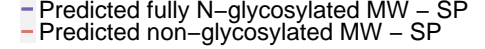
log(intensity)



Values from



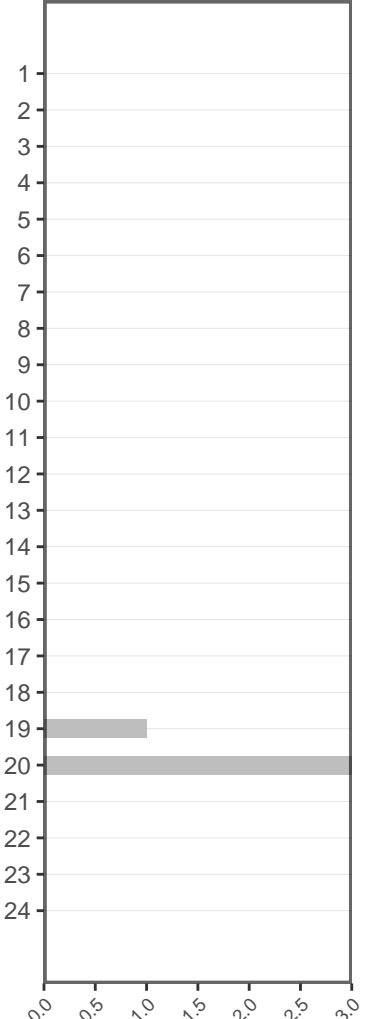
MW indication



Molecular weight



Gel Slice



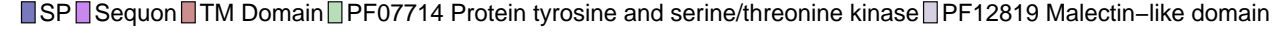
Protein length



Pfam domains



Pfam Description



Protein sequence:

IGPDPDTCPCNLOIHFENNQLSGELFSPGLEGLTSLKEVYQNNRLTGVSPGGLLNGVILNYTGNINLRKGDNNHRRKIKGISTVGAEBALLLATAISGLLQKGGKSPKQGLQGNLPPQRVFSFGDAATEAAHQFTLAELEAATRFENKYGSGGFGVYVYKGLKDGKEIWKVLTNNSFGQKRFESNEVALLSRHHRNIVQFLFGQGEDGKSLVYEFMHNGLTKEHLVYGPQLPDRSINWRRLEIEDAAGKIEVLTGGVPSIHRDVKTSNLLQKNMRAKYSDFGLS

NbL15g25120.1 40S_ribosomal_protein_S23 [MW = 15.73 kDa]

No. of times detected



log(intensity)



Values from



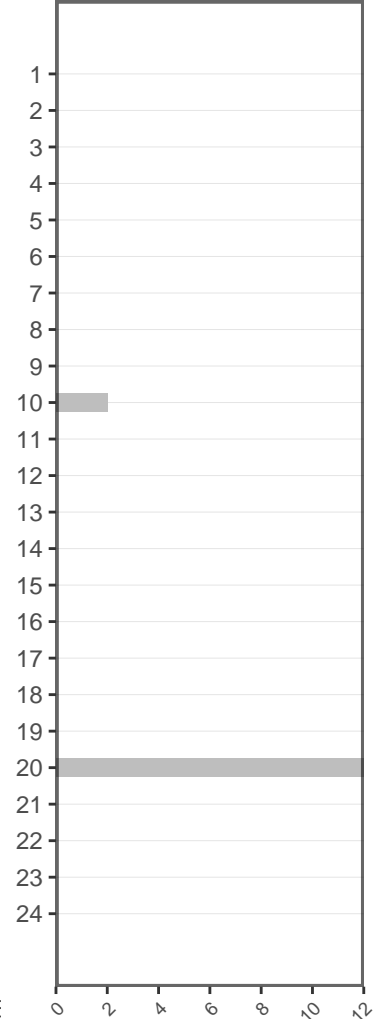
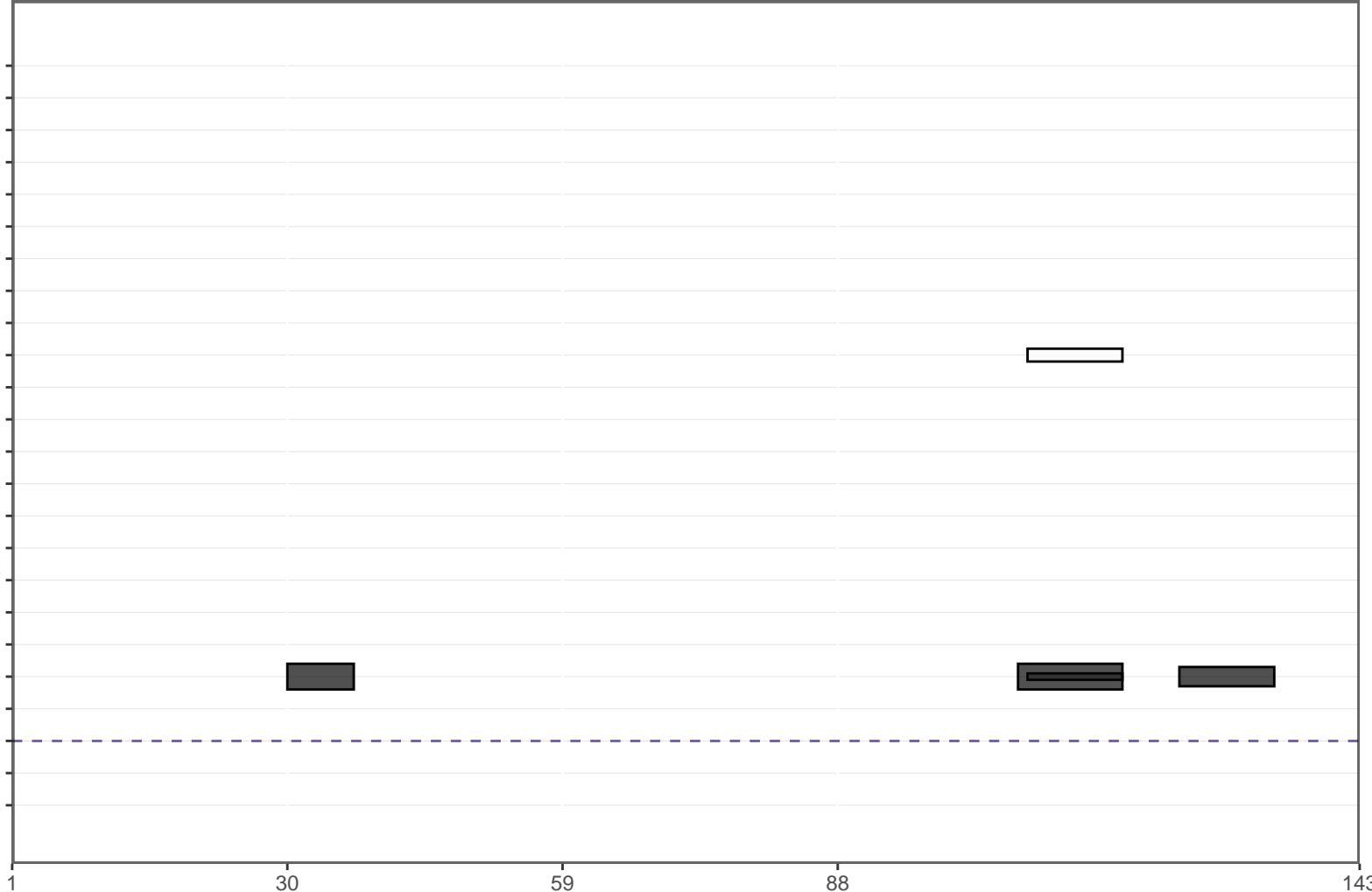
MW indication



Molecular weight

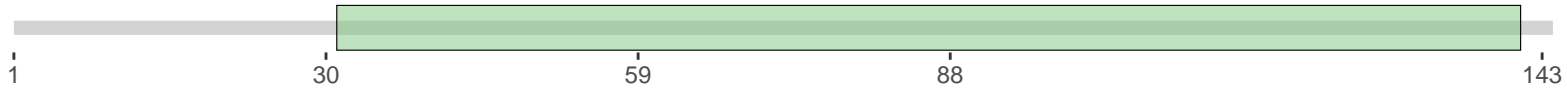


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

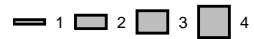


Protein sequence:

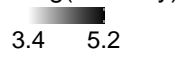
IAKQPNLSAIRKCARVQLKNGKKAIFVNDGGGLNVEENDEVLAGFGRKGHVAVDIPGVRFKVVYSGVSLALFKKKEKPRR

NbL15g24940.1 peroxidase_21 [MW - SP = 33.75 kDa]

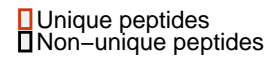
No. of times detected



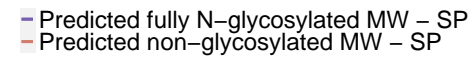
log(intensity)



Values from



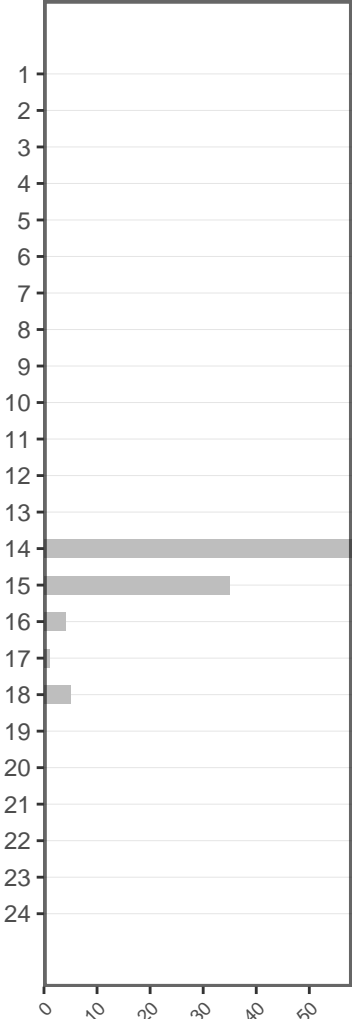
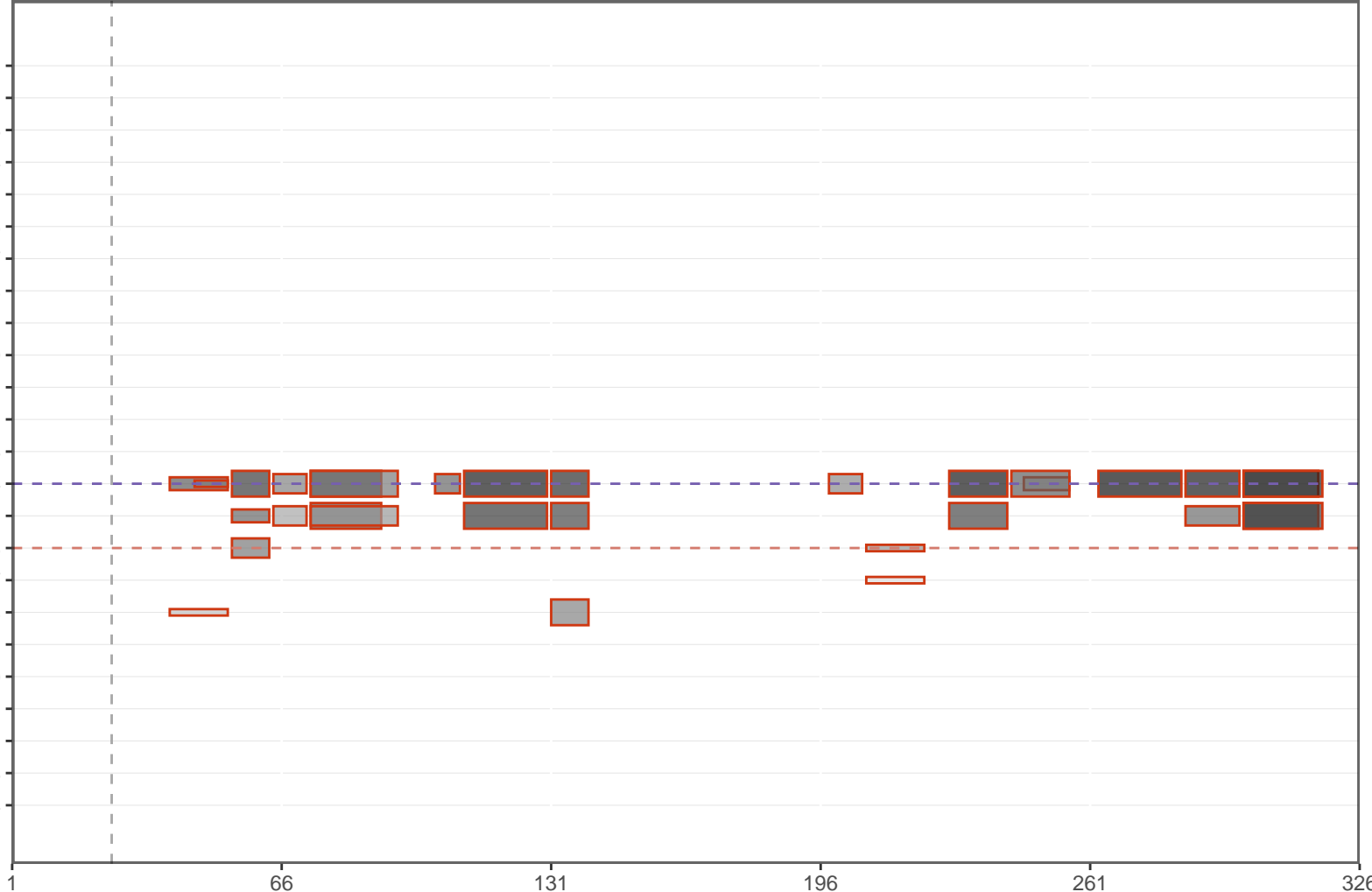
MW indication



Molecular weight



Gel Slice



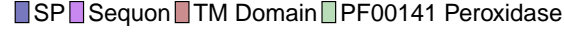
Protein length

Peptide counts over 4 repeats



Pfam domains

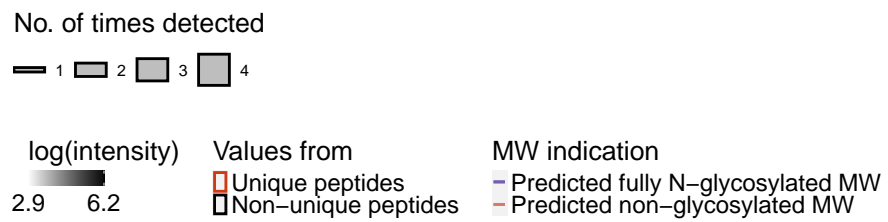
Pfam Description



Protein sequence:

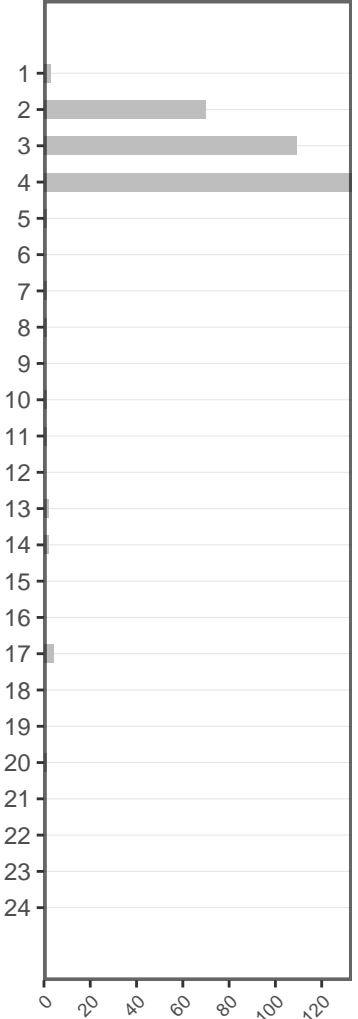
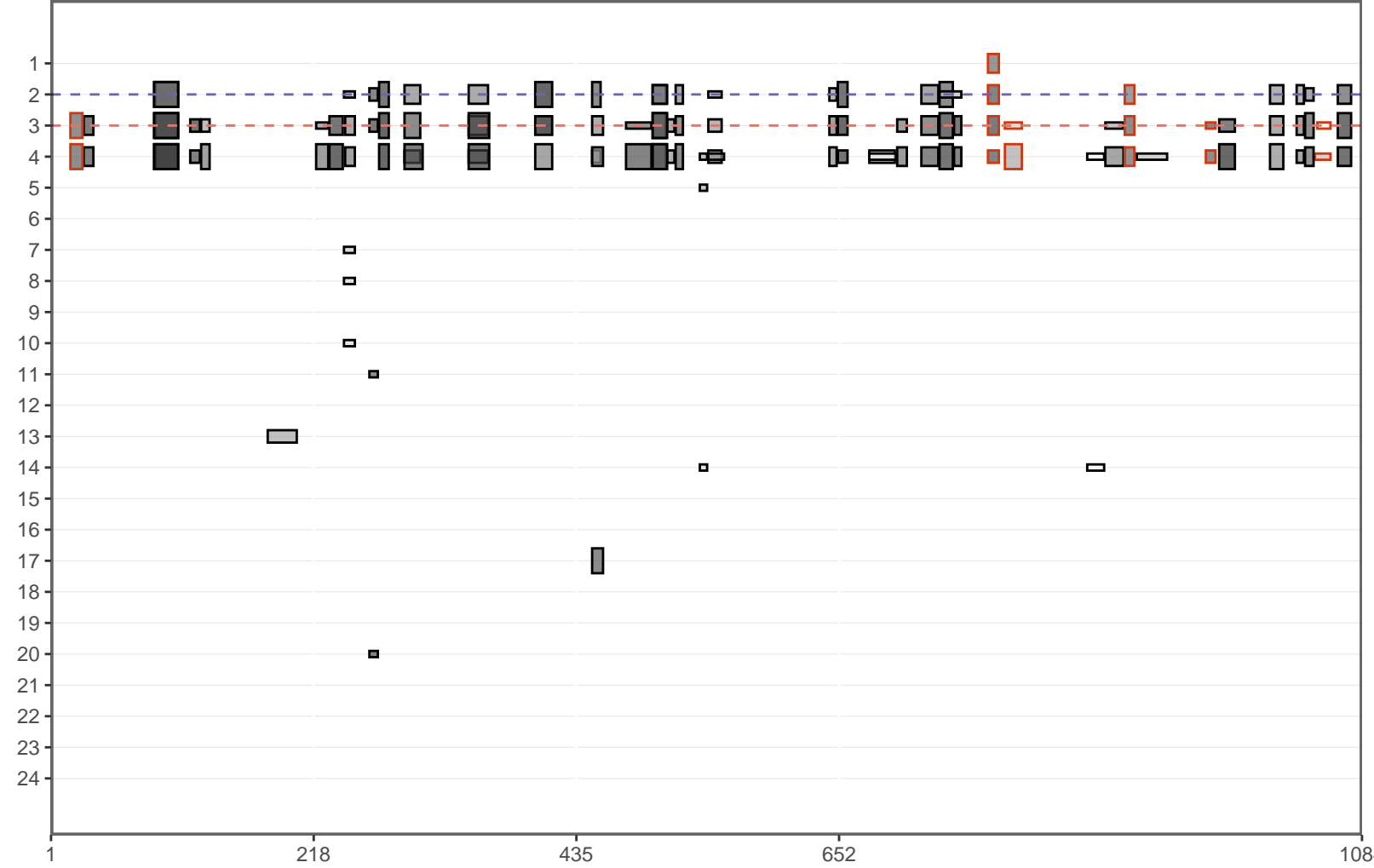
SKESYLAEVENSIPNINDGMSVLRFRFGQGVDFEGTVALFGAHSVGRVHCNVLNHLVFTVDPLDPDAKYLKGRGPTPNPDEAVLYSRNDRETTMLDMMYYKNLHKGLLVGGELVSDPNTSFFPEKMAADNGYFHDGAFARALVISENPLTGDGGEIRKVGKRVNSA

NbL15g24920.1 valine--tRNA_ligase_mitochondrial_1-like [MW = 123.32 kDa]



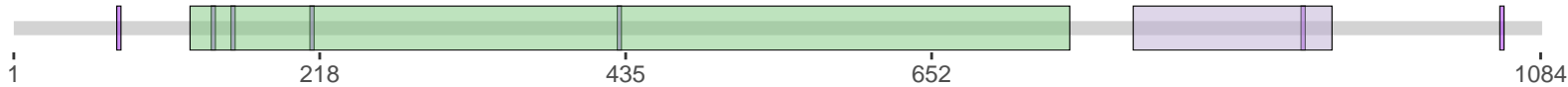
Molecular weight

Gel Slice

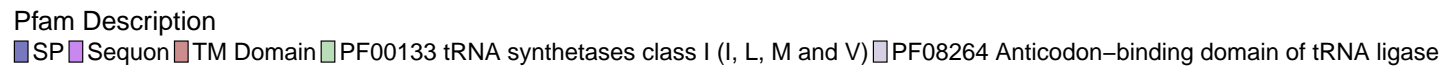


Protein length

Peptide counts over 4 repeats



Pfam domains

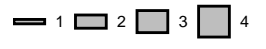


Protein sequence:

NIRDVICSRQLVWVGHRIPIWVYTLHDDKQKEFGVDDHWHVWNRNEEARDLAKRFSGKEVGLTDDPDLVDTWFSGLFPLSLVGLWPDPTADTKFTYPTSLVLETHGHLDFLWARMVMLGKLGDDVPTFYVYHPMRDHAHGRKMSKSLGNVDPLEVINGLIAGLHKRKEGNDAKEFERAKEGGAKDFPFGPEGADALRALFVYTAGSDKINLDRVYVYRQWGNKLNWNAIRFAMSKLGEDYTPAWIVREMPFSGGWISALNKAIKATVSSLESYDFSDA

NbL15g24890.1 dnaJ_protein_P58IPK_homolog [MW = 53.82 kDa]

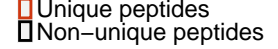
No. of times detected



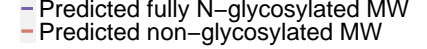
log(intensity)



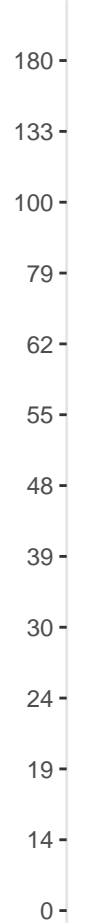
Values from



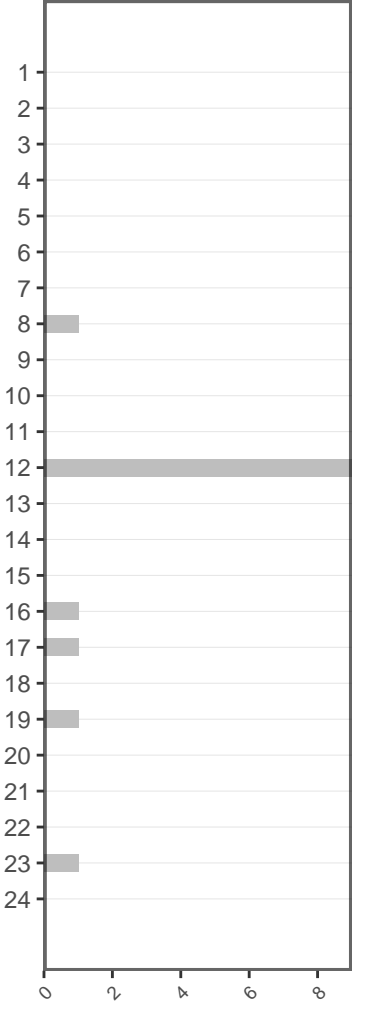
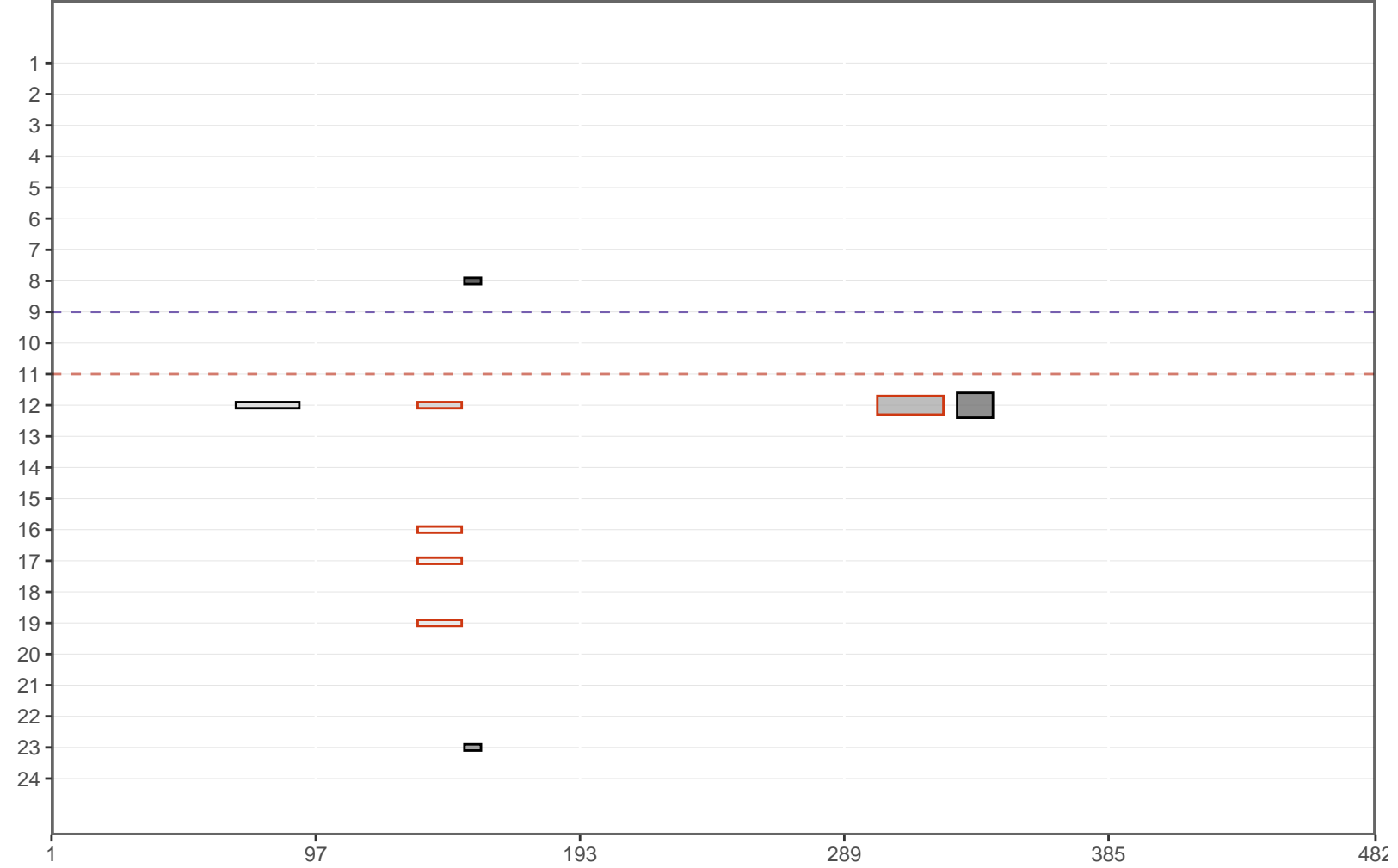
MW indication



Molecular weight

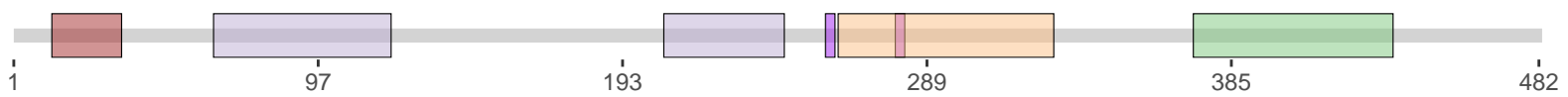


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PEHGELXXAYFGLKSLKTKSAEDNNAKGGKLRVAVEEYKAALMDPNHSAHNVNHLGLKRVLVKGRKDAISSCTEALDGLDIALVQRGEAKLTFDEWEGAVLKEAAEKSPQDRNREALMRAERSLKLSGRKDWYKILGVSKTASVSEKKAYKQLQWHPDKNVENEREAENKFRKIAAAVEVLGDEDKRTRYDGGEDIDDMGSGMGGGGFNPFGGGGGGQYTFHEGGFFGGGFGGFHPI

NbL15g24880.1 serine_carboxypeptidase-like_50 [MW - SP = 47.61 kDa]

No. of times detected



log(intensity)



Values from



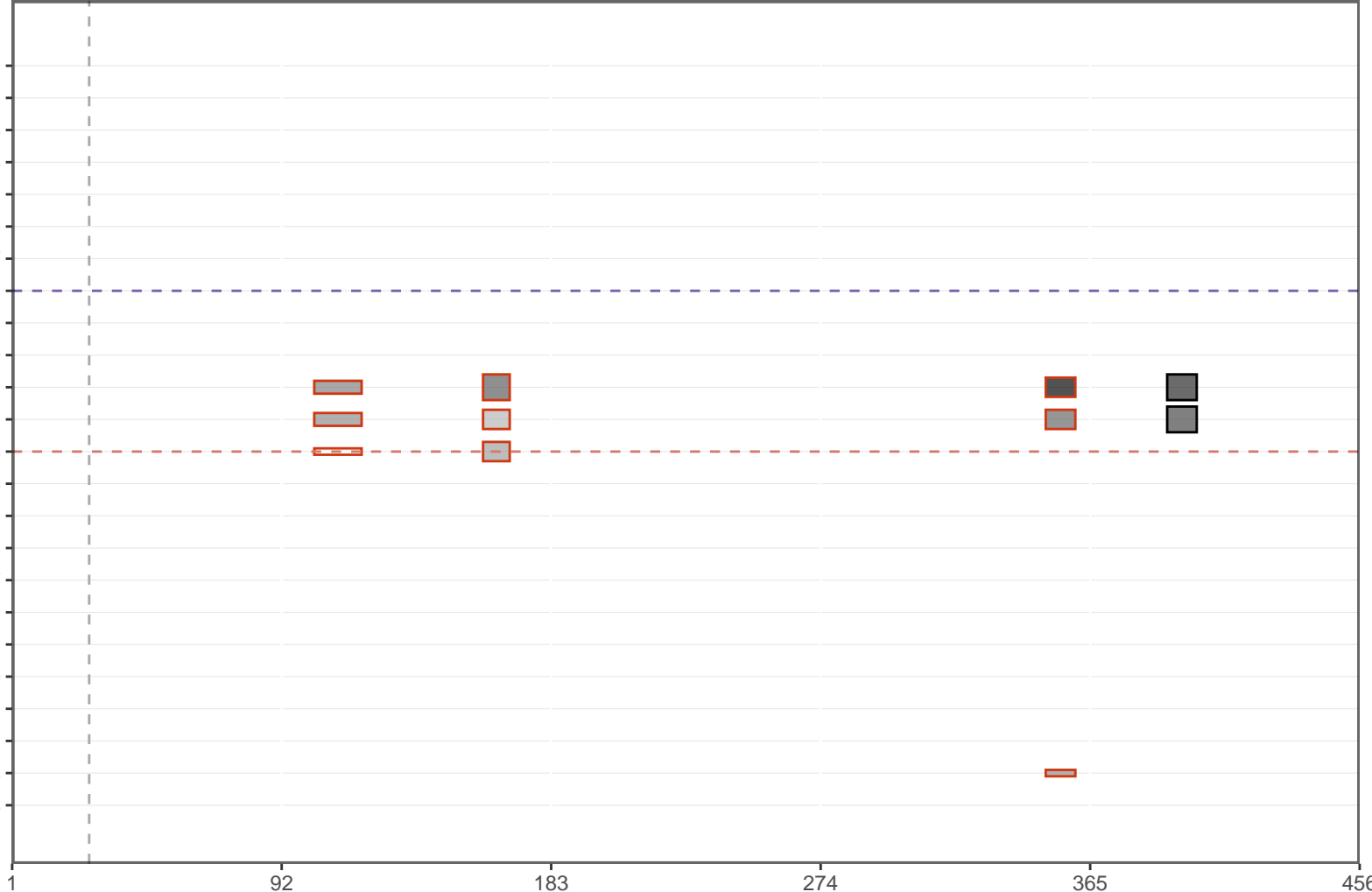
MW indication



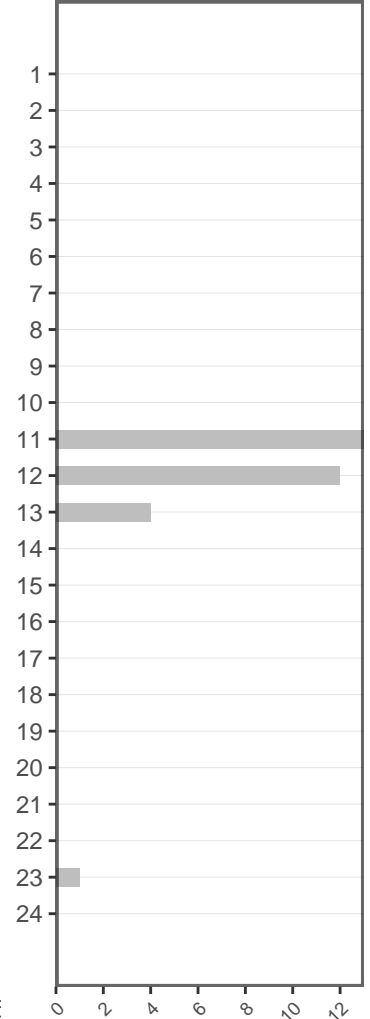
Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PETQVGTALSAAYVGLNEKQKTMESLQKEAQLAKNGNWSEATGARSKVLGTLTMMAGLATLYDFRRLKPYEDELWAKFLSNVEIKRALKANESIVFEVGSGLKALHEDVAKMSERYMVEFLVNTKRVLLYGGGCDLRDGVVSTEAWMKMKWDDGIEKFLAERKVVRRVNDGLAGYVQKRWESLSHYVVMNAGHLVPTDQAVNSQVMIEDVLEKGLFATGGKQKPKENIGKSLV

NbL15g24820.1 PIP2-1-like [MW = 31.22 kDa]

No. of times detected



log(intensity)



Values from



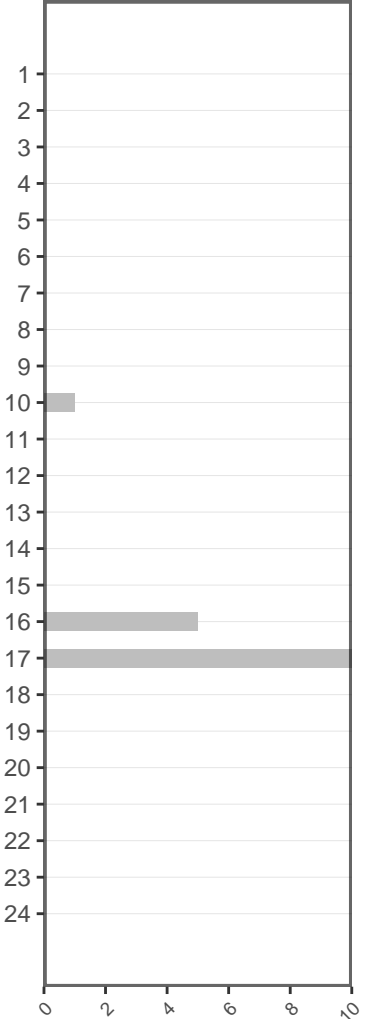
MW indication



Molecular weight



Gel Slice

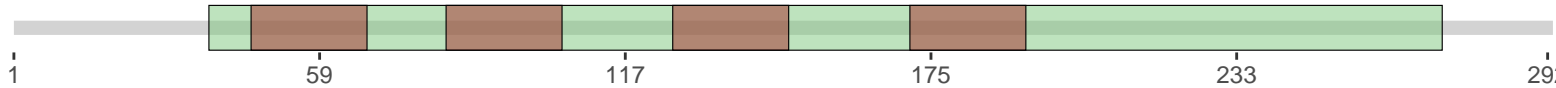


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

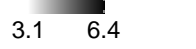
MLAACLGLAICCCGSLKAFKQKAVYKYGSGGANTLNDGYYTGTGLGAEHGTFLVYTVFAATDKPRINARDEHVPVLAPLPFGFAVFMHLLATPVTGTGINKPISFGAAVYKDKAWDDQWFFWVGFPGMAAAAFYHDFLRAGAVKALGSRNVA

NbL15g24670.1 29_kDa_ribonucleoprotein_A_chloroplastic [MW = 35.71 kDa]

No. of times detected



log(intensity)



Values from



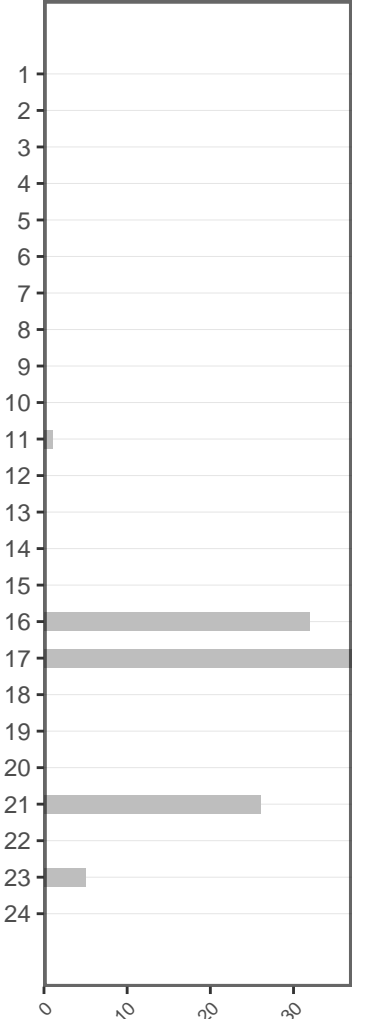
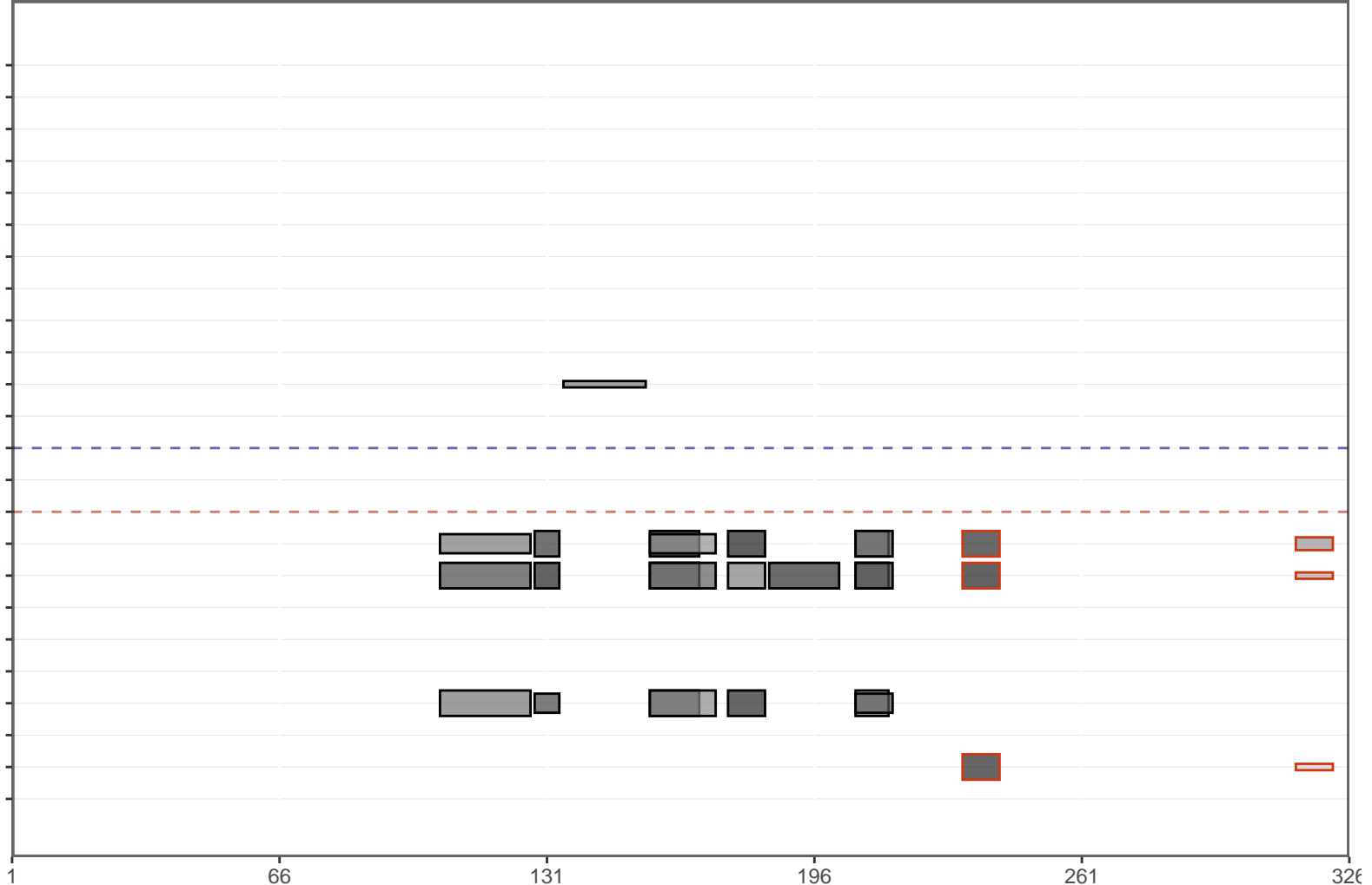
MW indication



Molecular weight



Gel Slice

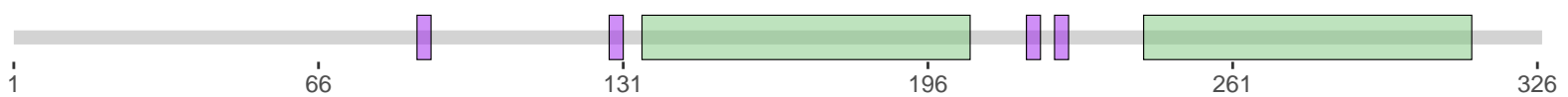


Protein length

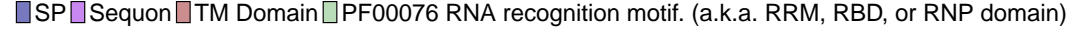


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

RAGNVEVVEVYDKLGRSRGFGFTMSKKEVEAAGQGFNGVYELDGRALRVNSGPPKRENSFRFNSFRGGSGSFDSPNRYVGNLAWGVDDGDALETLSFEGGKVVDAKVVYDRDGRGRGFGFVYSSAEVNVNIEGLDGVLDNGRAIRVSPAEARPPRRGF

NbL15g24630.1 ammonia-lyase-like [MW = 78.15 kDa]

No. of times detected



log(intensity)



Values from

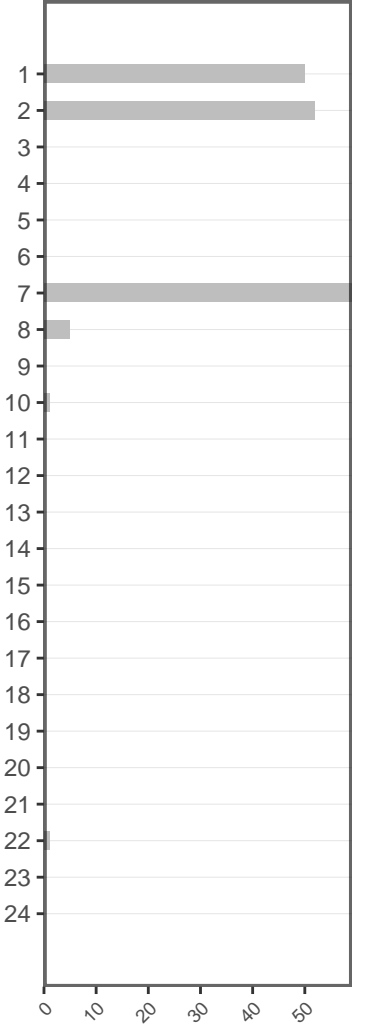
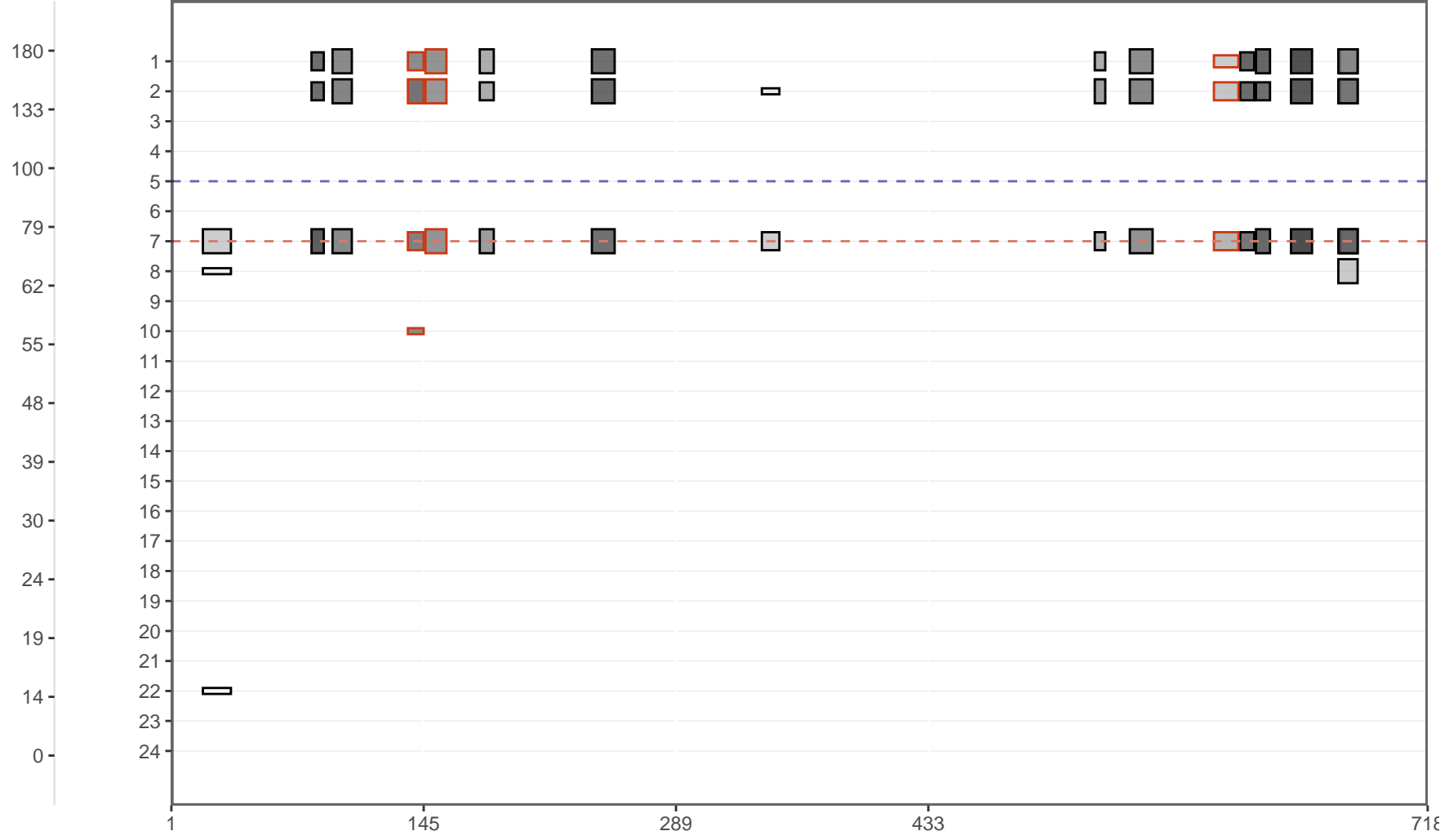


MW indication



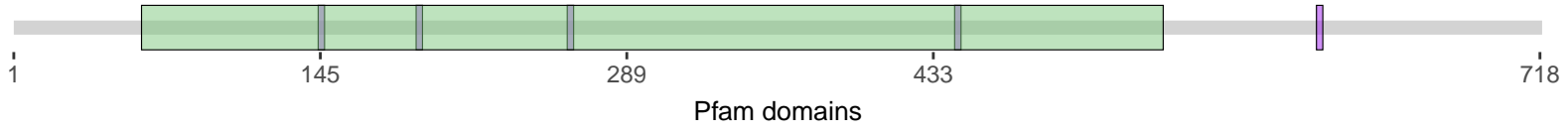
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DKPKDQRYALRTSPQWLGPDQEVRSATKMERIEINVDNDPLIDVSRNKALHGGFGFTGPGVSMQNDARLALASIGKLMFAQFSELVNDYYNNGPLSNLTAQRNPLDYGFGKAEAMASVCESELQFLANPVTNHVQSAEQHNQDYNLGLIGARKTAEAVDILKLMSTYLVWALGQADLRHLEENKNNVKNVTVSGVAKRRLTITMGANGELHPRFCEKELLRVDRVYLFVAVDDPQSGNYPMLQKLRQVLDHAMNNGESEKNNVNSFGKIGAFEDLXAVLPKEVESA

NbL15g24610.1 adenosine_kinase_2-like [MW = 37.48 kDa]

No. of times detected



log(intensity)



Values from



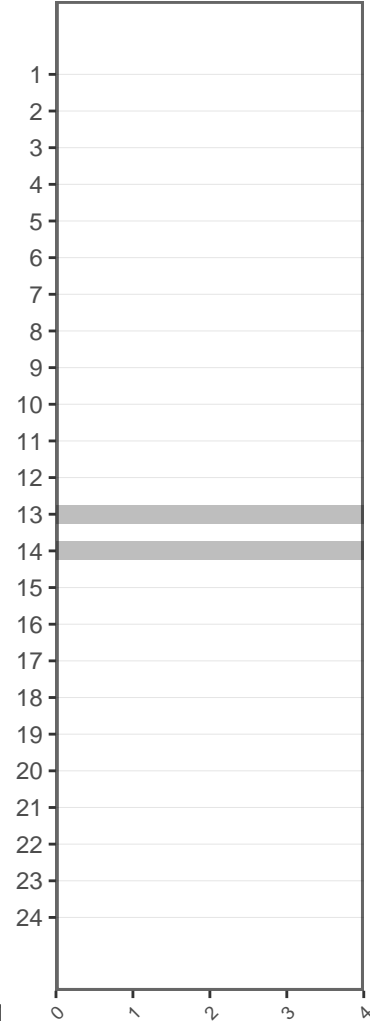
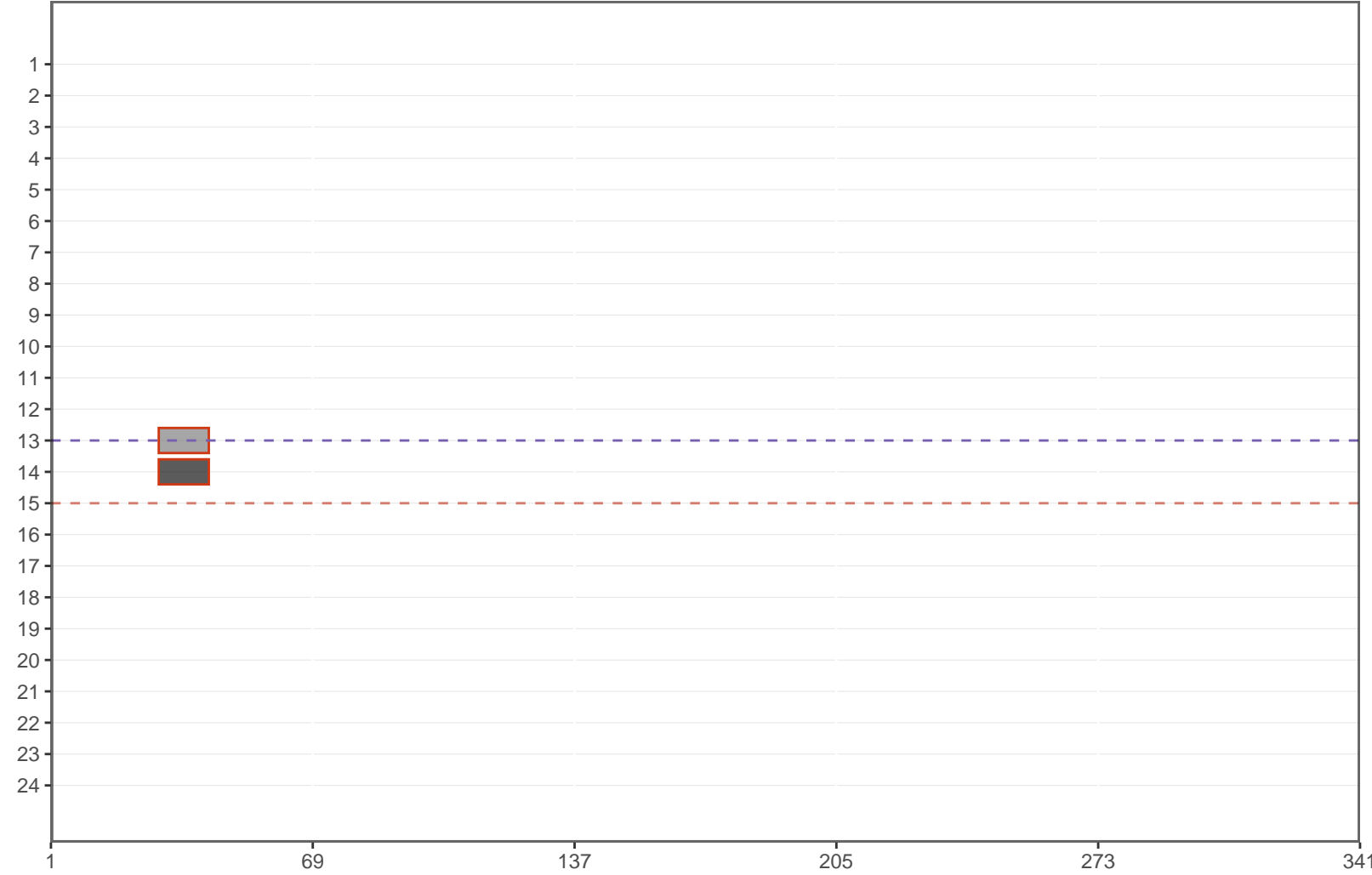
MW indication



Molecular weight



Gel Slice

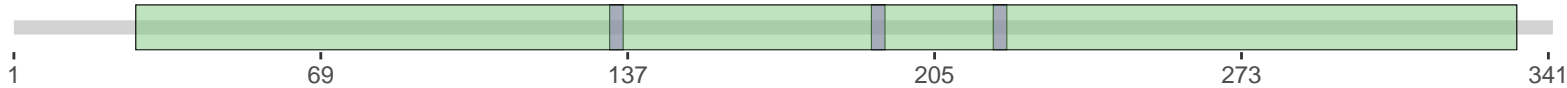


Protein length

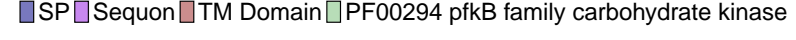


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KAQFYIAGFLTYSPESIQIAEHAANNKIFSMNLBAPFCIEFFRRDPQEKALPYMDFVFGNETAARTFSKVIHWETDNVEEIALKISEWFKASETHKRITVITGADPPVAENQKWLFFVPLPKKELVDTNAGADAFVGGFLSGLVQKPFVFDGVRAGCYASNVIQRSGCTYPEKPDFV

NbL15g24490.1 cell_division_cycle_protein_48_homolog [MW = 91.74 kDa]

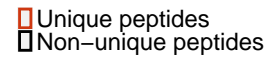
No. of times detected



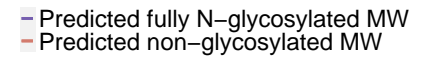
log(intensity)



Values from



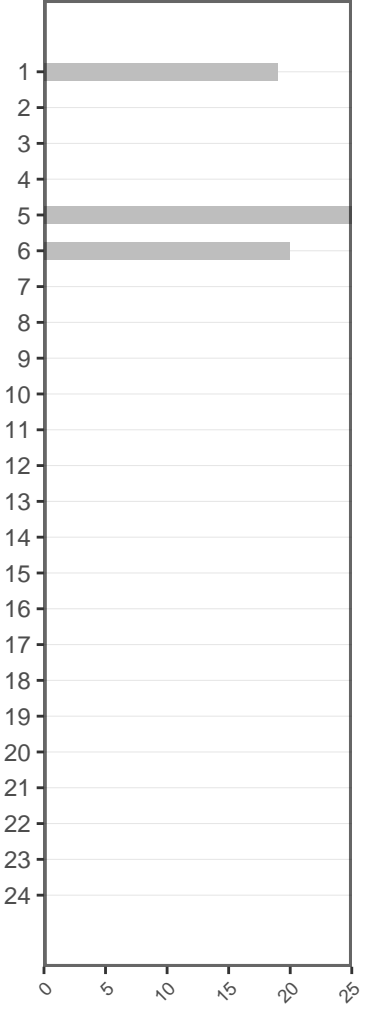
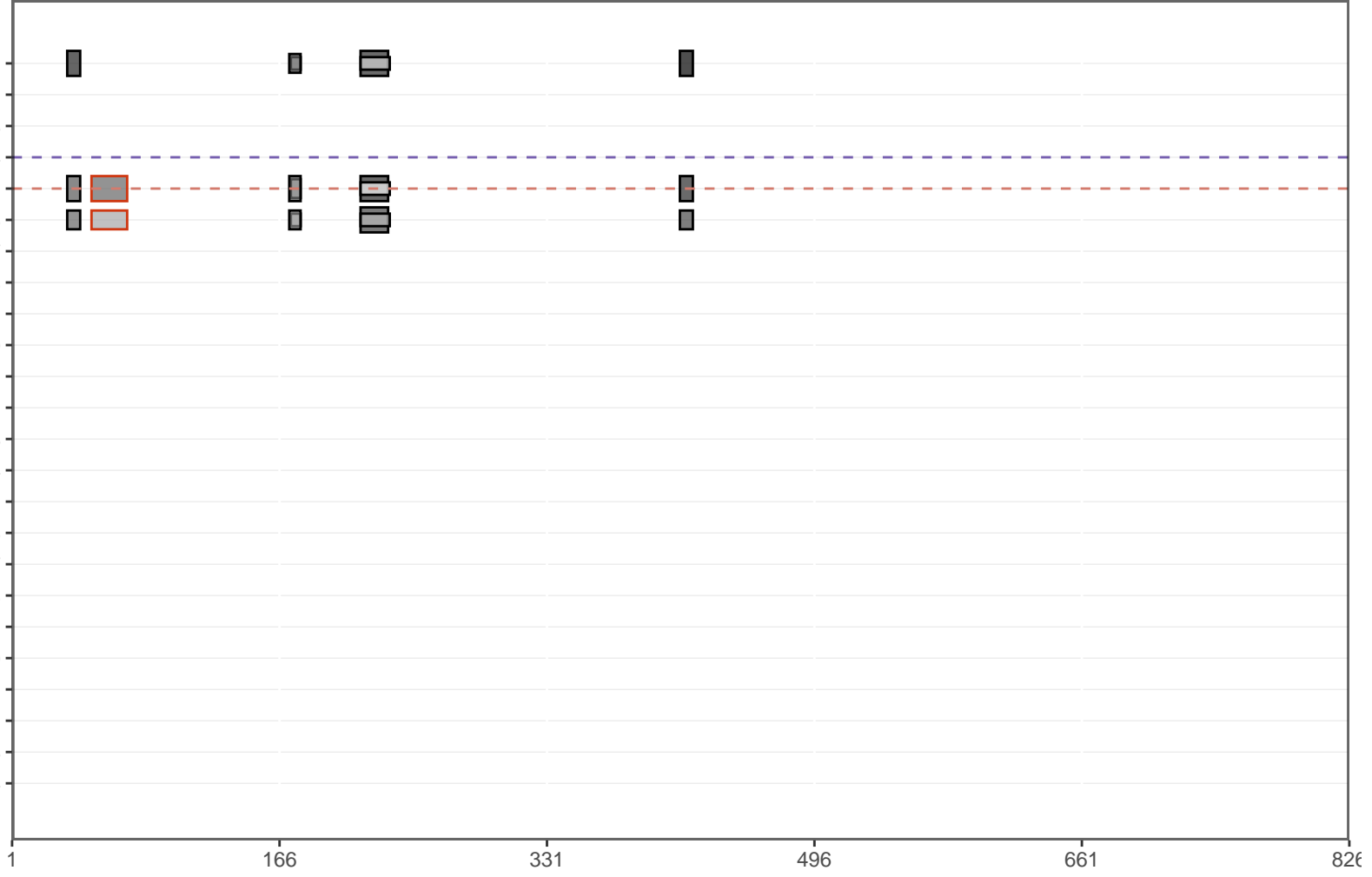
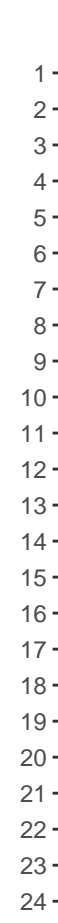
MW indication



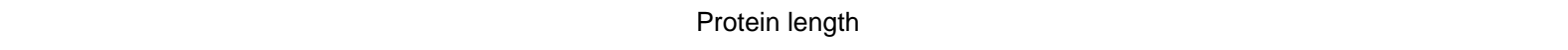
Molecular weight



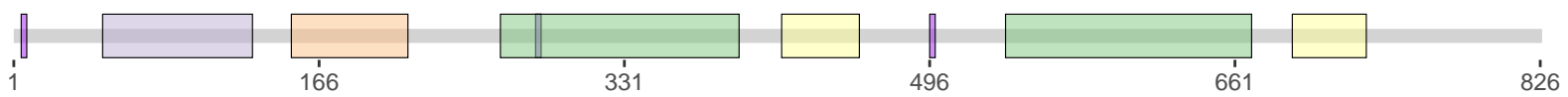
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00004 ATPase family associated with various cellular activities (AAA)
- PF02359 Cell division protein 48 (CDC48), N-terminal domain
- PF02933 Cell division protein 48 (CDC48), domain 2
- PF17862 AAA+ lid domain

Protein sequence:

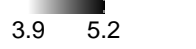
.EVLRIHTQNMKLAEDVDLERIGKQTHGYVGDAAALCTEAAAGGIREKMDVIDLEDESIDAEILNSMAVNTNEHFSTALGTSNPSALRETVEVFNWSDVDIGGLENNKRELGETVYGVFVEHPKFEKFGMSPKGVLFYVPPGCGKTLAKVAANEQGANFISVKGPELLTMVFGESSEANVREIFDKARQAPCVLFFDELDGIATORGSSSSGDDGGAADRVLNLQLLTEMDGMNAKTVFISGATNRPDIDRALLRPGRLDQLYIPLPDEDSRIHQIFKAEIKKSPLSKQIDLR

NbL15g24390.1 uncharacterized_LOC109229140 [MW = 23.47 kDa]

No. of times detected



log(intensity)



Values from



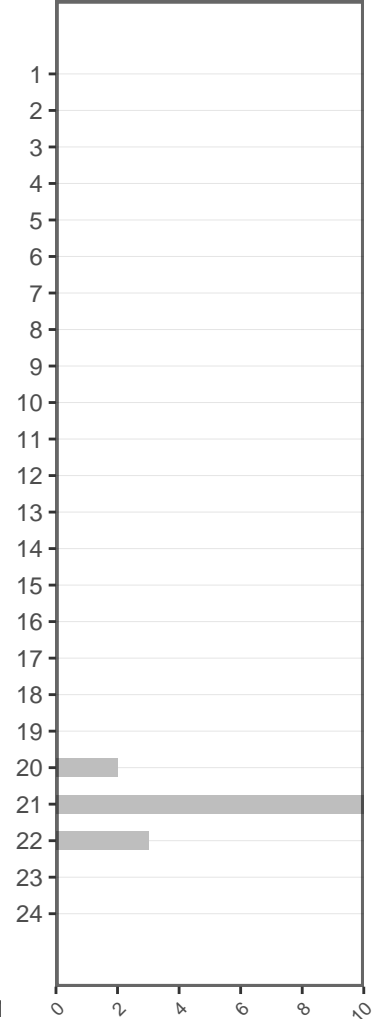
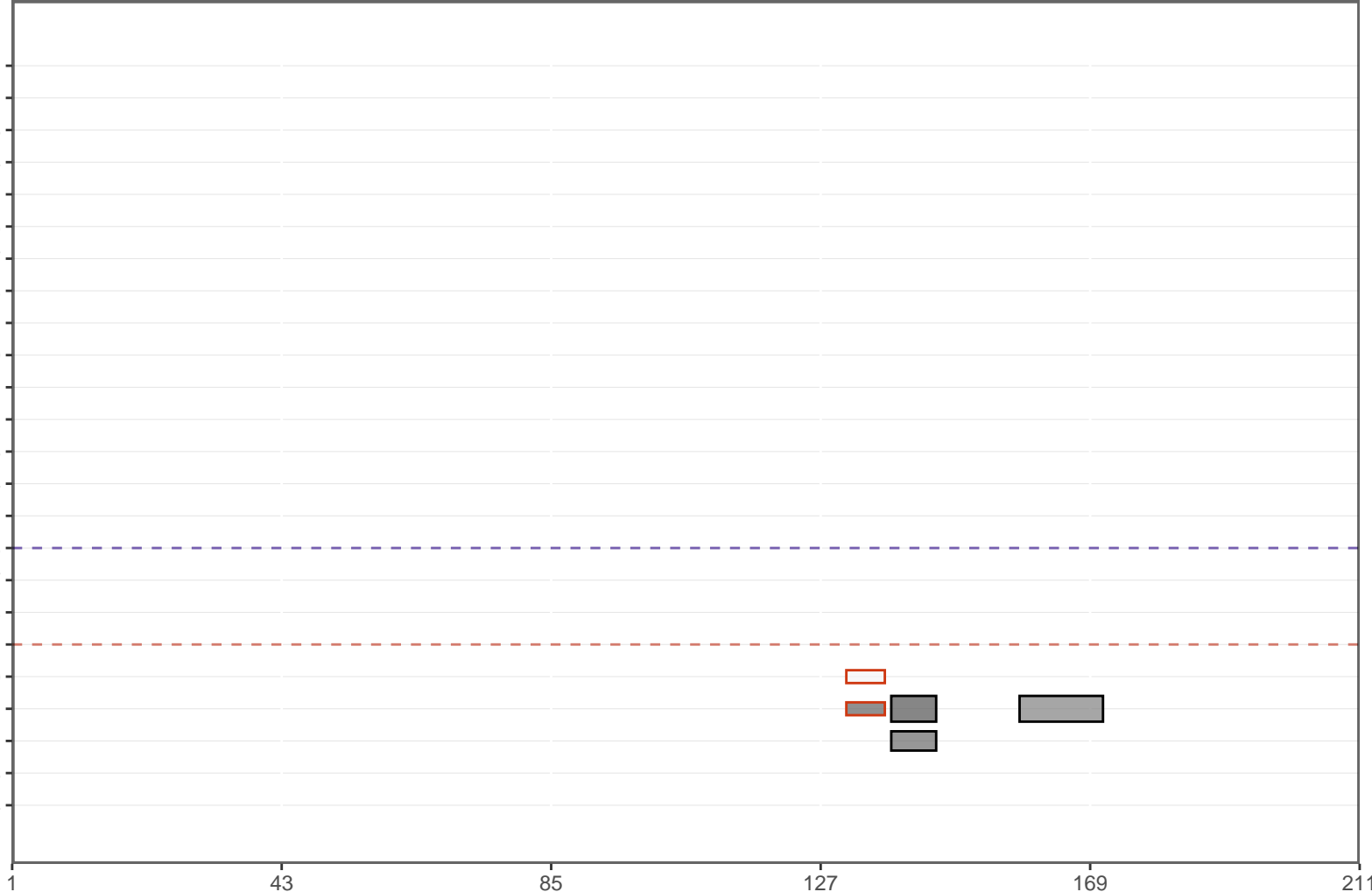
MW indication



Molecular weight



Gel Slice

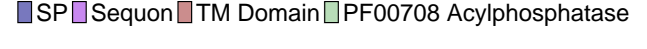


Protein length



Pfam domains

Pfam Description

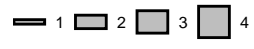


Protein sequence:

FRSPYFSSPMSSLTSDNNSMATPDQKTVRAVAVKGRVGVFEYRDWTVENAKELGKGVVRRNRDRDGEVEALFSGSPEKVDMEGRGRRGPPAAVITGLDVFDFDDDDPDTGFECKGGG

NbL15g24320.1 glutamate_formimidoyltransferase [MW = 35.83 kDa]

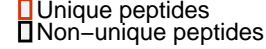
No. of times detected



log(intensity)



Values from



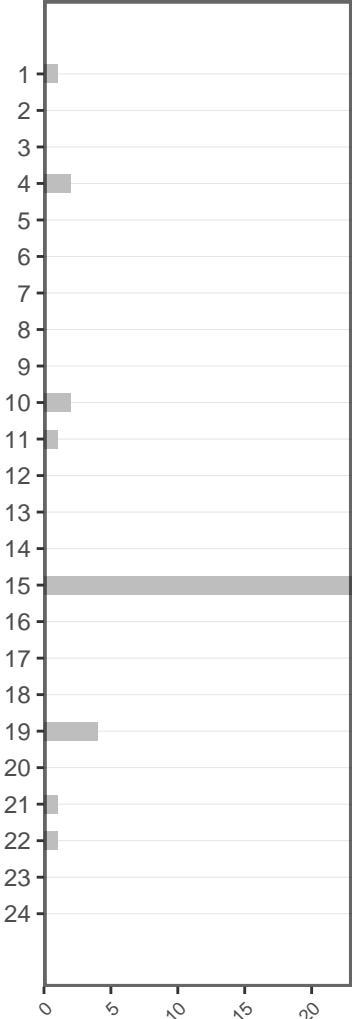
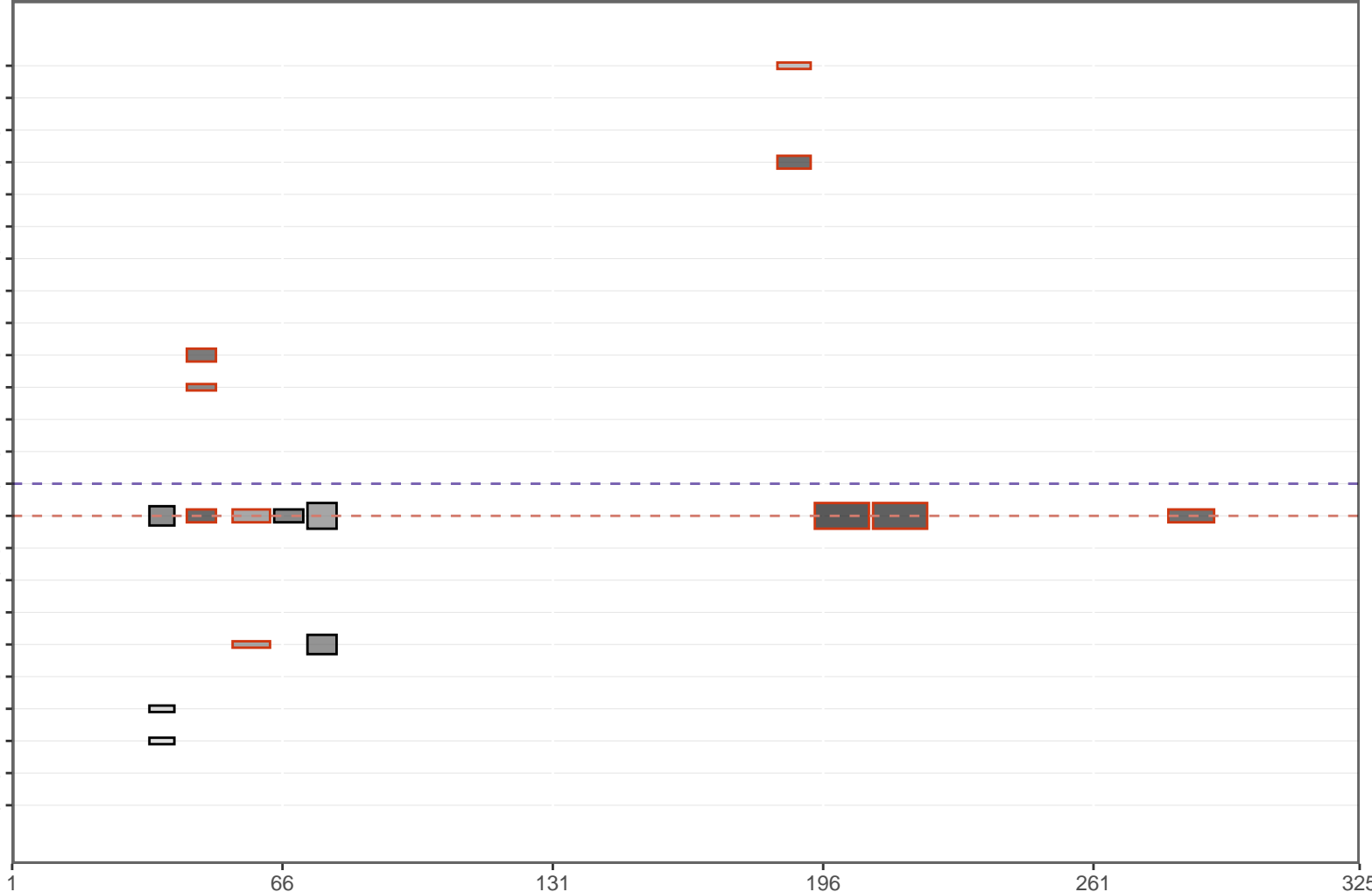
MW indication



Molecular weight

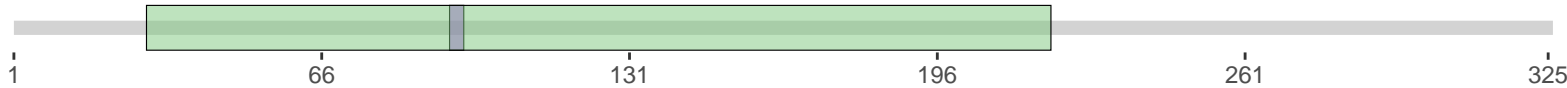


Gel Slice



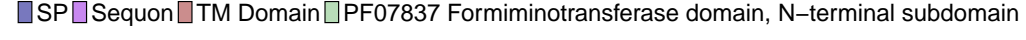
Protein length

Peptide counts over 4 repeats



Pfam domains

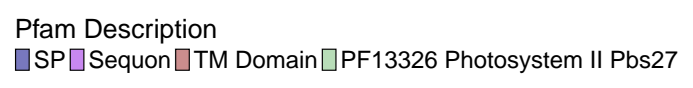
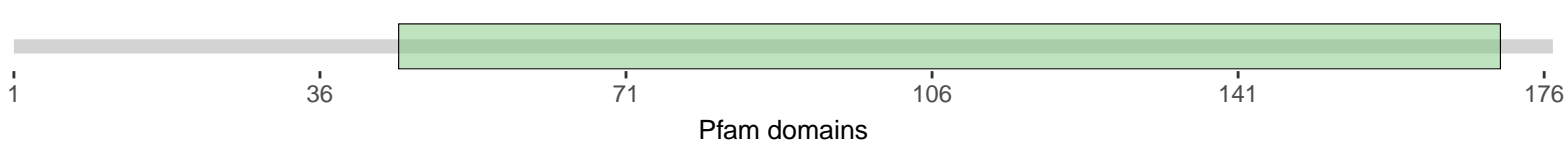
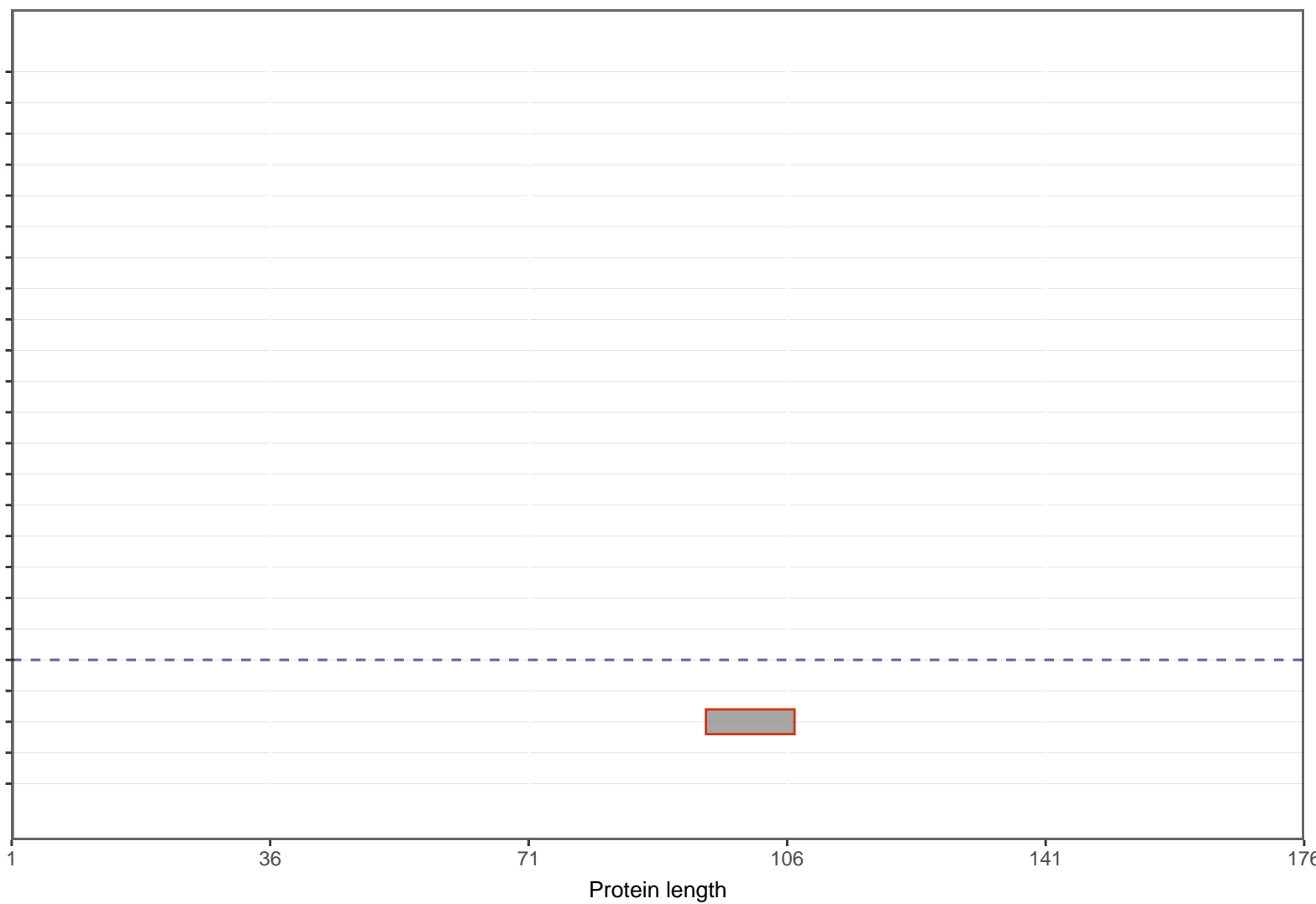
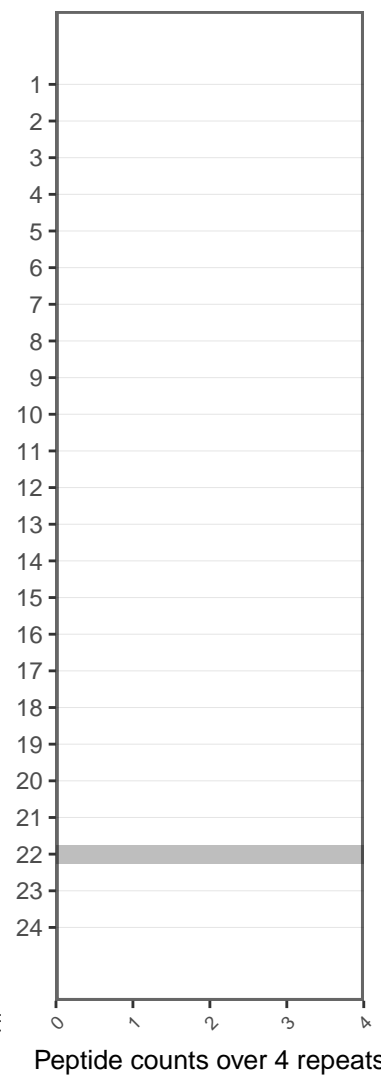
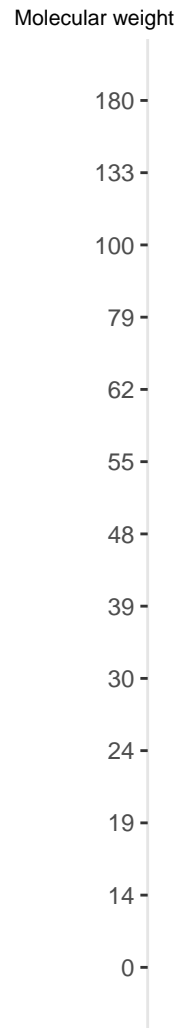
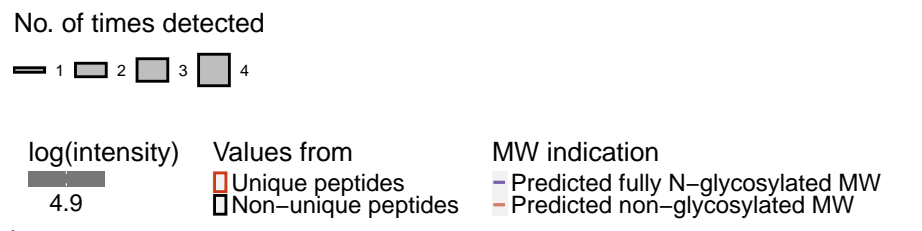
Pfam Description



Protein sequence:

NLQVPTLYGAAHGEGRSLDGRIRRELGVFRPDKENQWAGGPKWQTLGKLPDEGPRATQATGVITIGATRIWVQVYVNFVFTNDISVIRRIAKRVSGRGGGFPVQSMALHGGSTEVAQNLLEPARNGGDQVQLEVERLAREEGVAGKGVYTFDSEKIEYKLVGHSD

NbL15g24260.1 photosystem_II_repair_protein_PSB27-H1_chloroplastic-like [MW = 19 kDa]



Protein sequence:
 REASEVKKVRSSTLSMEKGDPADEVDLREABNYYWAKYRREKALLGRASFRDYSALNAVSGHYVDFGPTTFRPAWRKRIEEMDTAEKALGRGR

NbL15g24190.1 protochlorophyllide_reductase_chloroplastic-like [MW = 43.25 kDa]

No. of times detected



log(intensity)



Values from



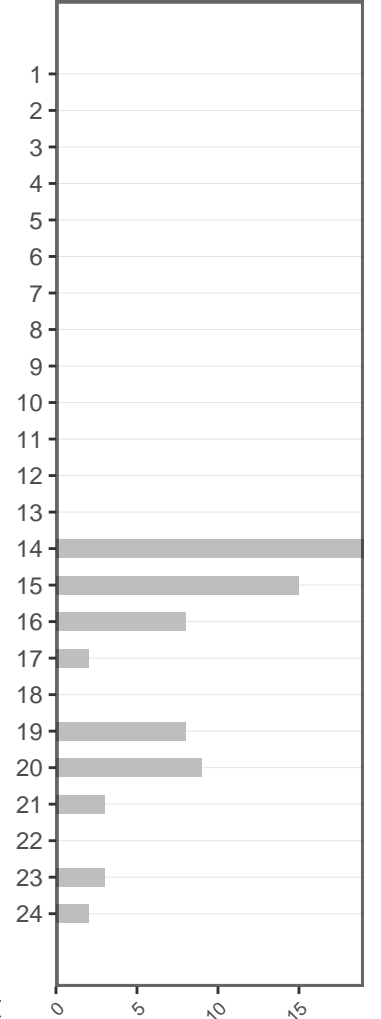
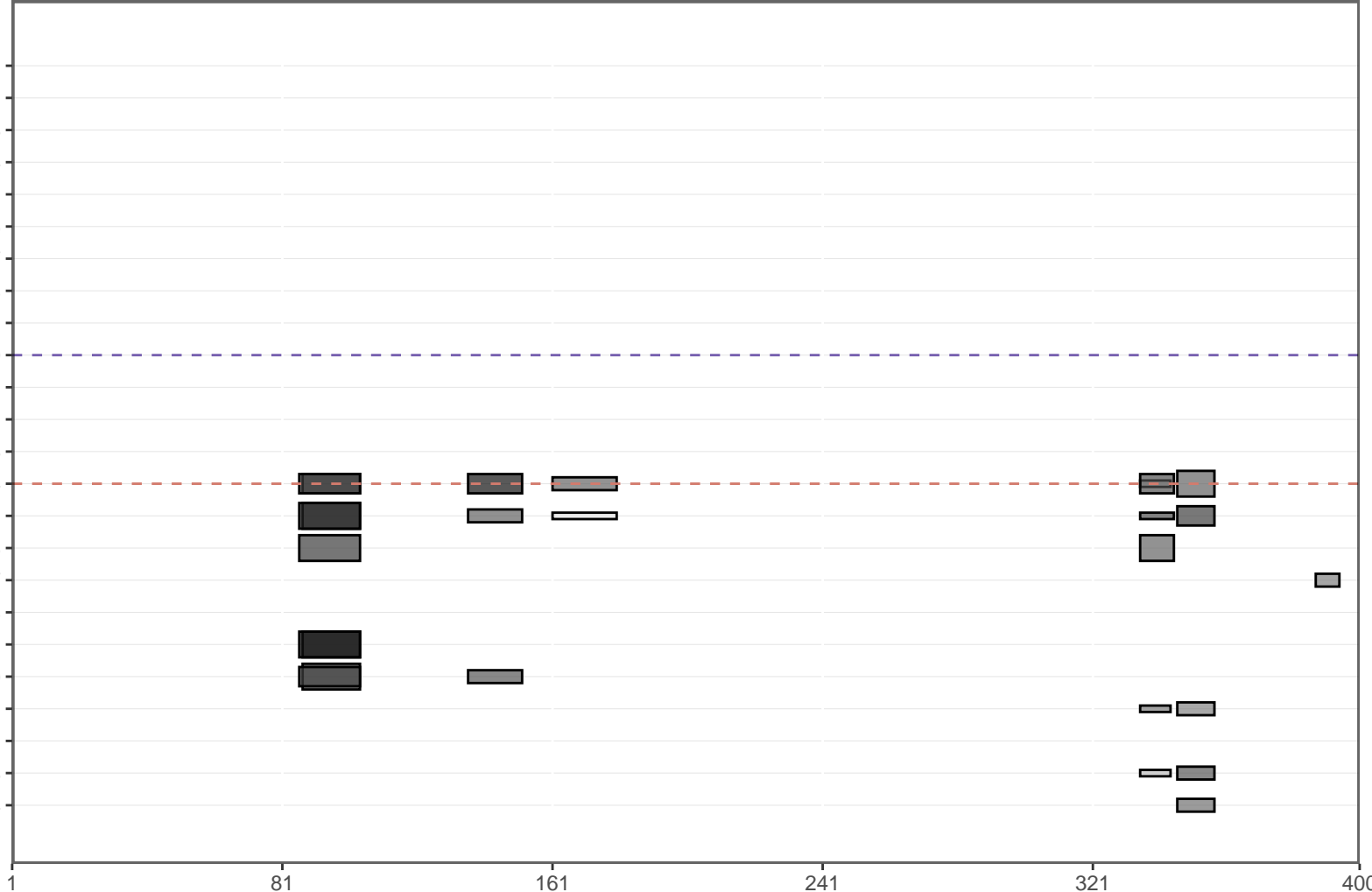
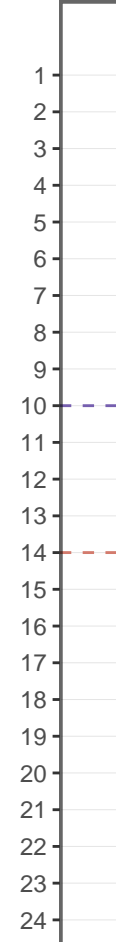
MW indication



Molecular weight

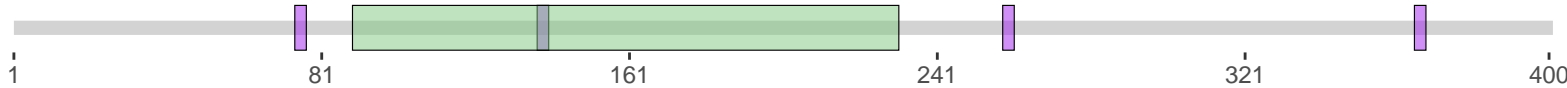


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

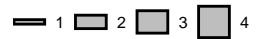


Protein sequence:

FELSVGTNHLGHFLSRLRLDGLKGGVDPKRIHIVGSITGNTNTLAGNVPPKANLGGRLGSGGLNLNCSFMDGGDFDGAKAYKDKVQCNMLTMGEFHRRHHEENGAFASLYPGCAETGLFRNHPLFRALFPFFQKYTKGVVSEAEAGKRLAQVVRDPLSLKSGVYVWVWNTSTSSSEFENQLSKEASDAEKARKLIVEVSEKLVGLA*

NbL15g24160.1 malate_dehydrogenase_glyoxysomal [MW = 19.31 kDa]

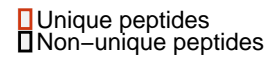
No. of times detected



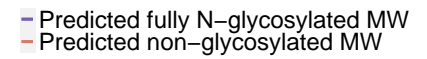
log(intensity)



Values from



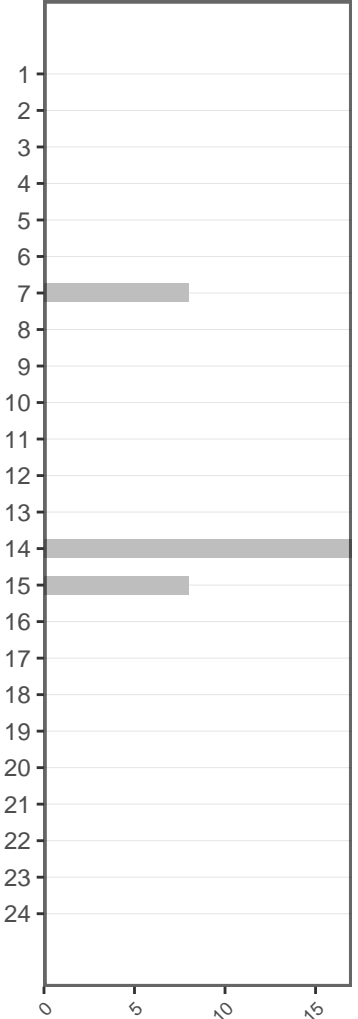
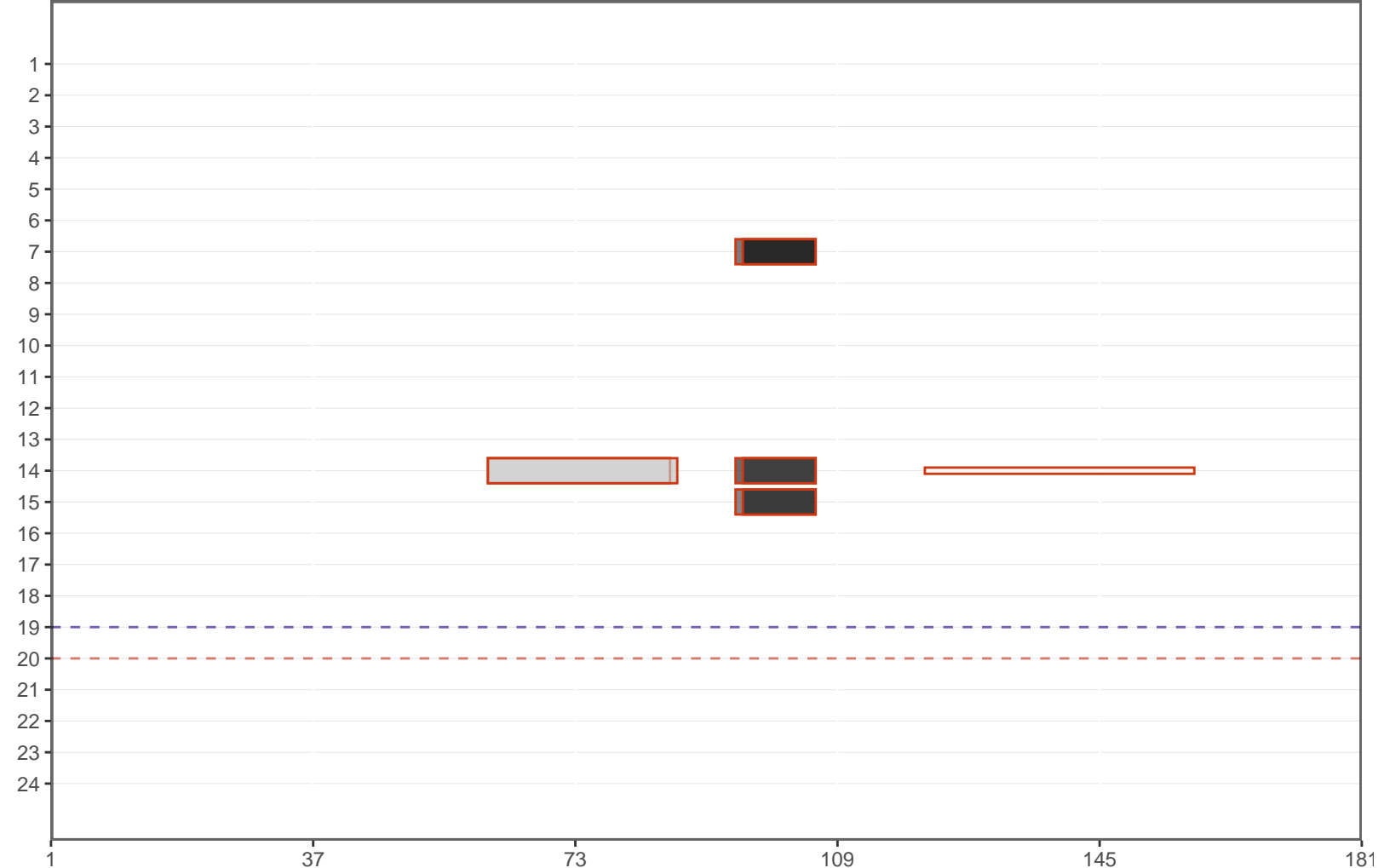
MW indication



Molecular weight

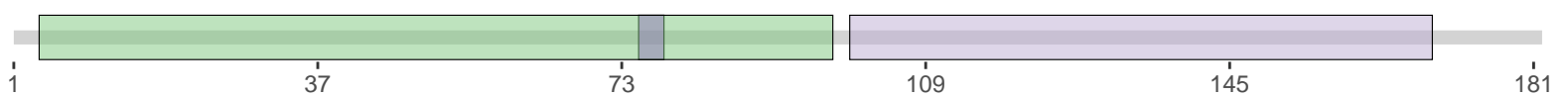


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF00056 lactate/malate dehydrogenase, NAD binding domain
- PF02866 lactate/malate dehydrogenase, alpha/beta C-terminal domain

Protein sequence:

VPIAAEYFKKAGTYDPKKLLGVTSLEWVRIITFVAEVLGLDPREVDFVAVGGHAGVTLPLLSQKPPCFSTQEEETELTKRIGDGGTEVVEVGVHLYGFSR

NbL15g24070.1 riboflavin_synthase-like [MW = 30.83 kDa]

No. of times detected



log(intensity)



Values from



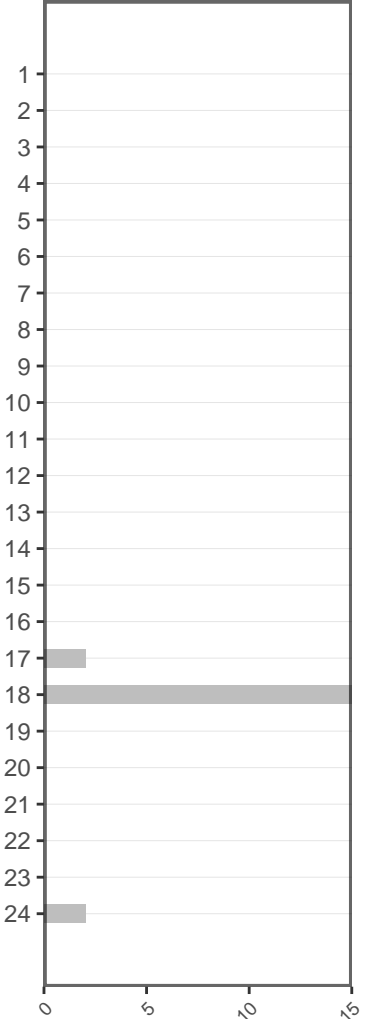
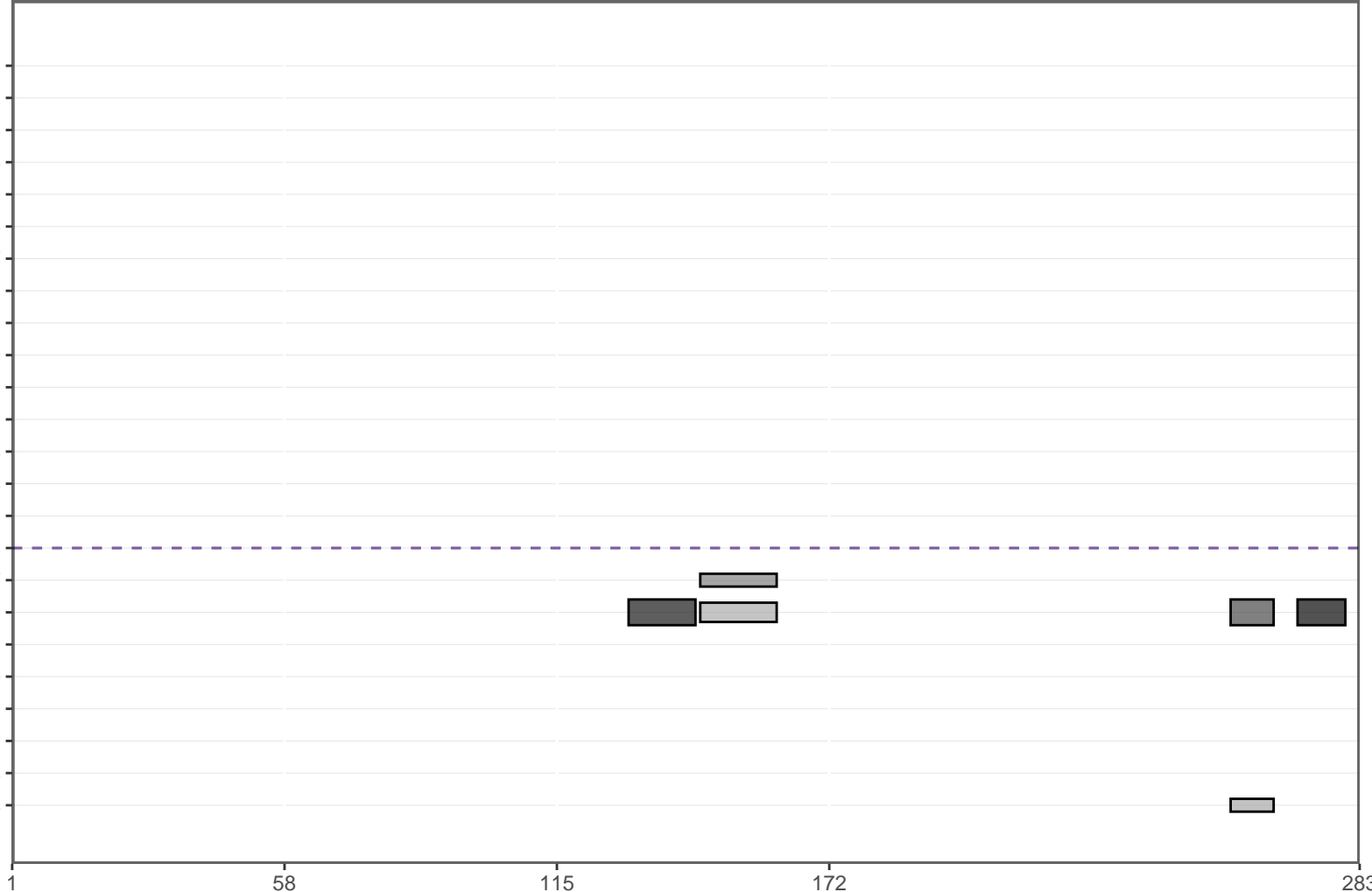
MW indication



Molecular weight

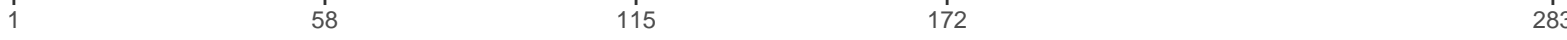


Gel Slice

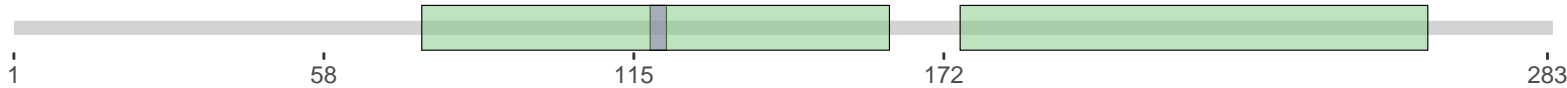


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

LSSEFSVGLAPETLRKTSLELEGGSIWLERALKPSTRMGHFVQGHVDGTGGIVELKPEGGSLWVYKSSKEILRYVPKGFIAVDGTSLETVVDVSEEDGCFNFMVAVTQGNVPIPKKVGQKYNLEVDLQKYYVERLLSSGFVAIKSS

NbL15g24000.1 tyrosine_aminotransferase-like [MW = 46.44 kDa]

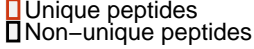
No. of times detected



log(intensity)



Values from



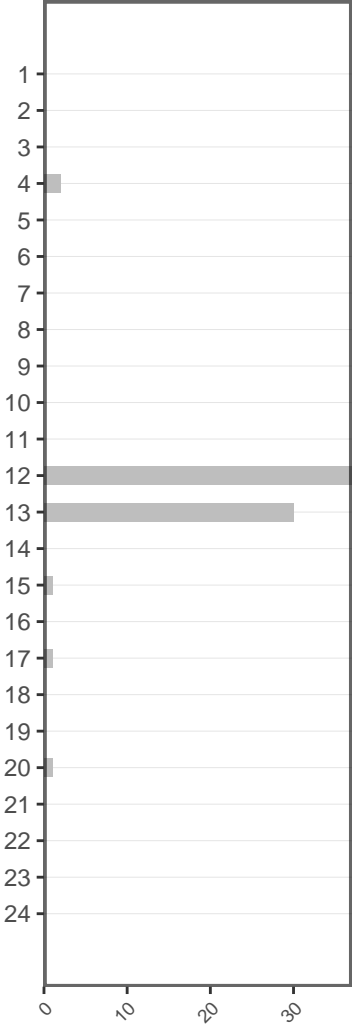
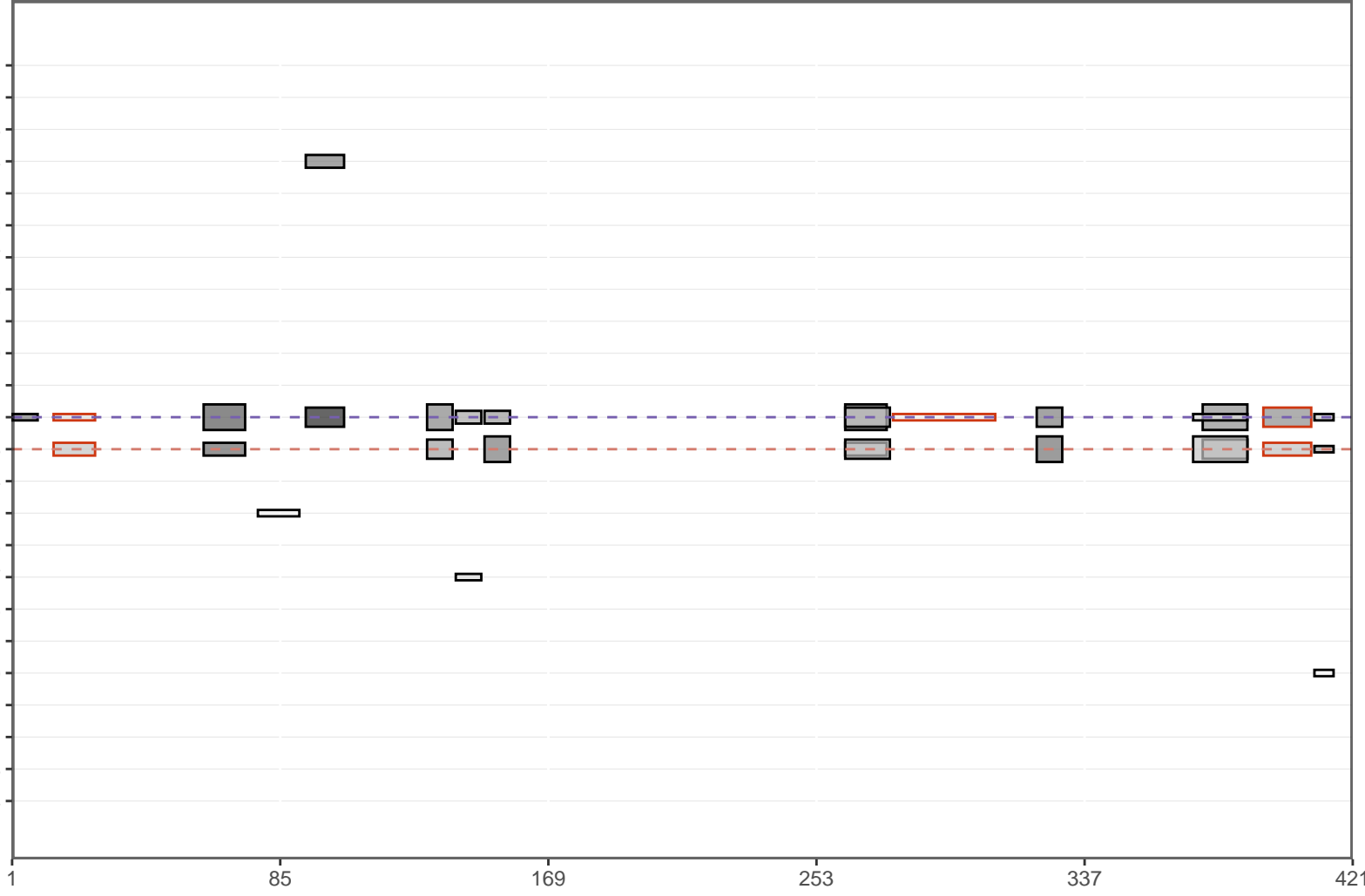
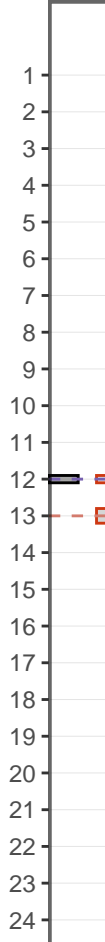
MW indication



Molecular weight

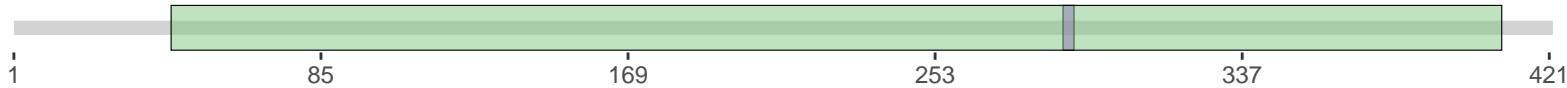


Gel Slice



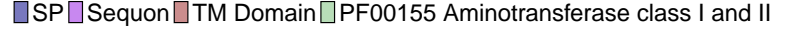
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

INVYTCOHLKEVEMARKLGLVIADEVYDHLTFQSGKPFVPMGIFGSIAPVTLGSGIKRWVPGWRIRLGLWVLTNDPDKLKHGVDSITGFLNISDPTFIFGAPIQHNTKDDFFKIVANMLRETADNGYDRIKDPCITGPKPKQSGMFMVWLRHLNLLADIEDDLDFGLKLAKESLHLPQVAVGLKNNWLRITFACEPSLEDDGLKRLNAFYQRHAKKQ*

NbL15g23810.1 uncharacterized_protein_At4g28440-like [MW = 16.17 kDa]

No. of times detected



log(intensity)



Values from



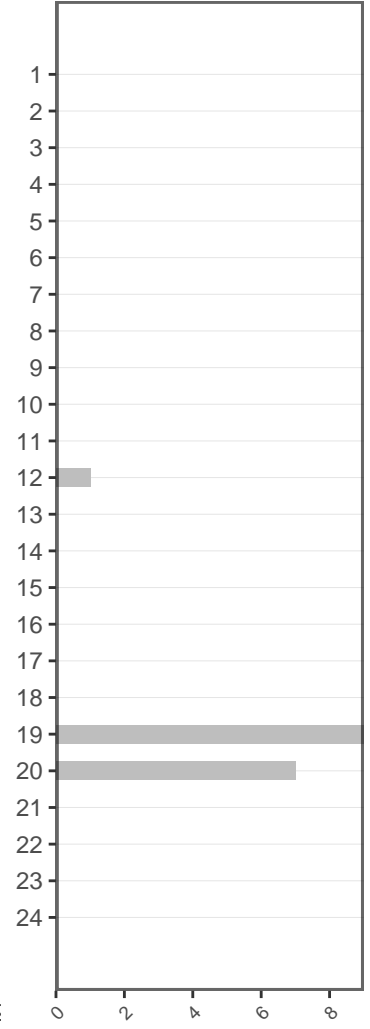
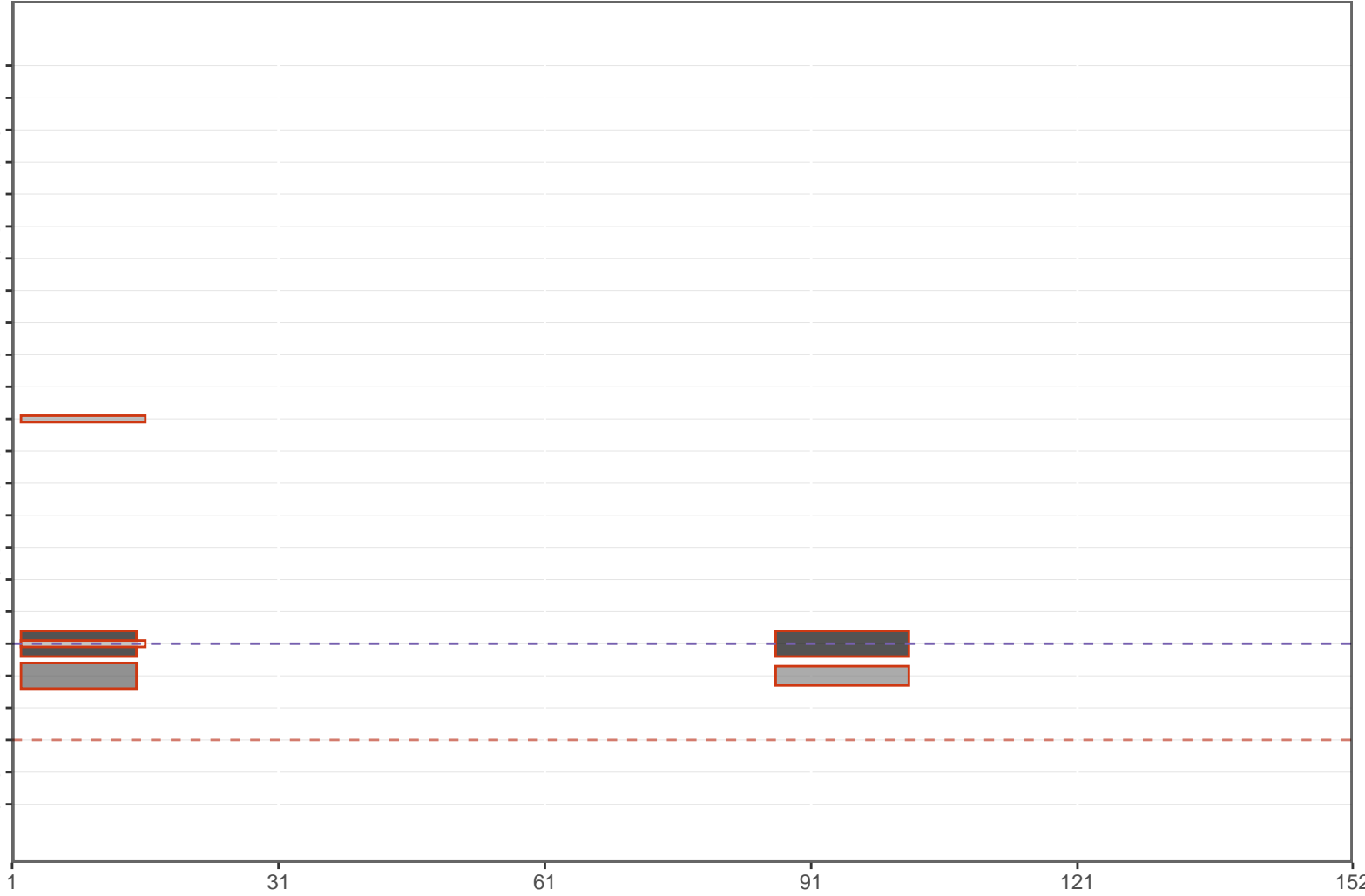
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

PRGPRRLAECLVGGDTGSILFTARNEGVDMMKPDATVILRNNAKIDMFKGSMRLAVDKWGRVEVTEPADFQVNEENNLSLVEVELNVEE*

NbL15g23780.1 26S_proteasome_non-ATPase_regulatory_subunit_2_homolog_A-like [MW = 78.02 kDa]

No. of times detected



log(intensity)



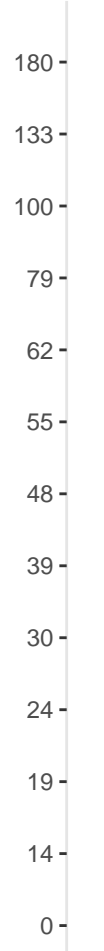
Values from



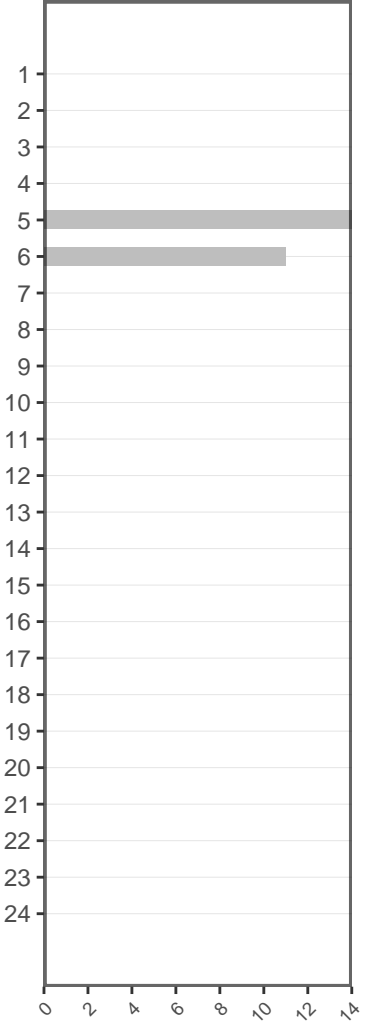
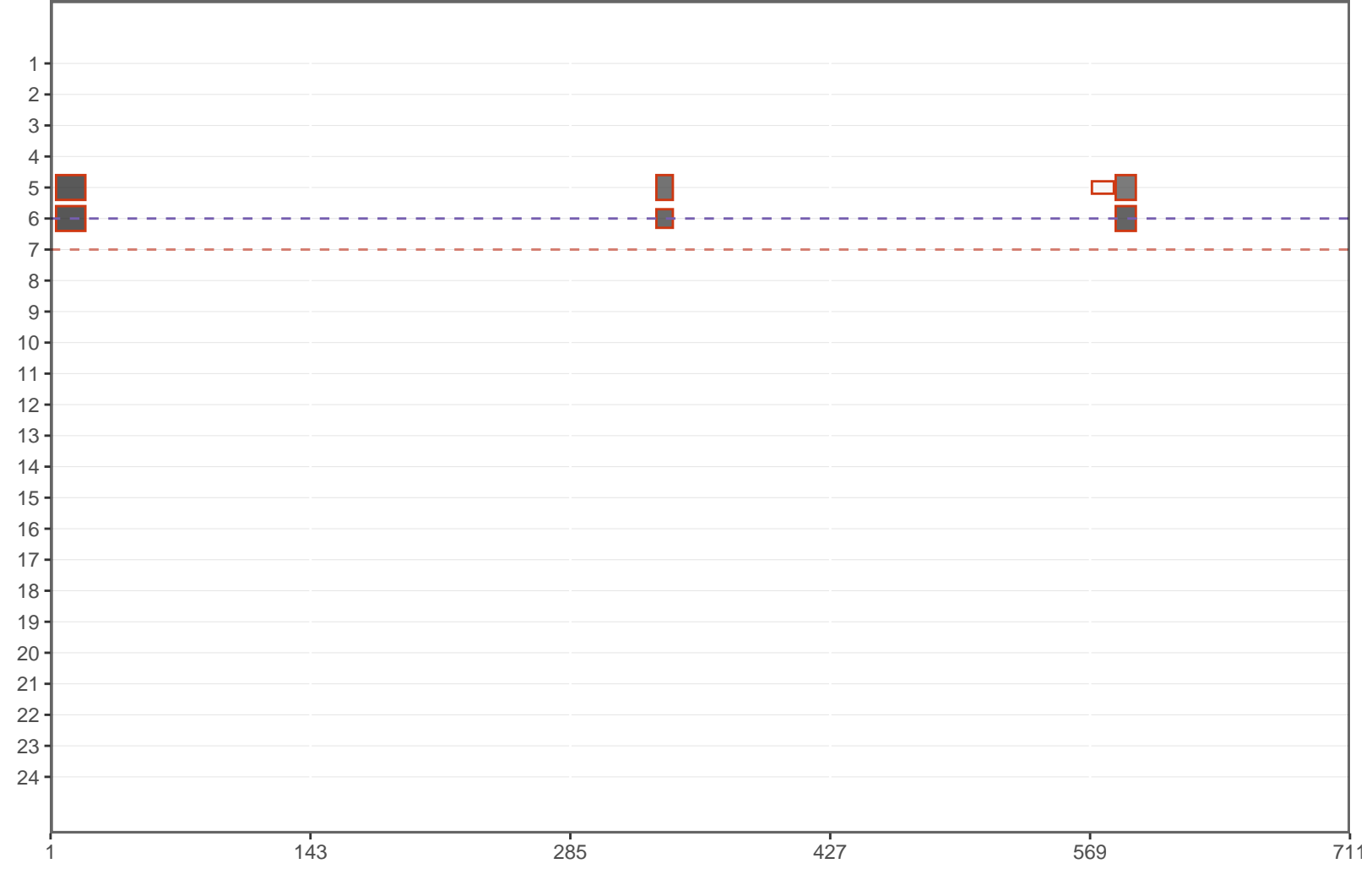
MW indication



Molecular weight

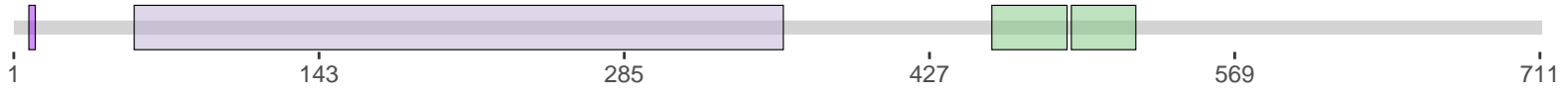


Gel Slice



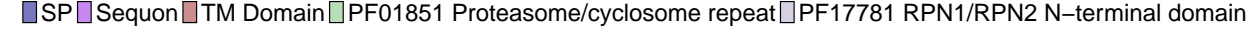
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RDIEVMEPKTPDQWPHLLDGRASAGASVDSARGNLAETFEVNAFVNAAGFGQDKLMTVPSEASGGGASTSWLFFKNEHGKASAAASLGMILLWVDGLAQIDKYFHSTDTHTVAAGALLGVGVNDCGRNNECDPALALLAEVTEKEDPSIRIGAIMGLGLAYAGSHNEGIRSKLTFPLGDSKASLDVLAFTAISLGLVYVGGNEEIAQAIFALMERSESELGEPFARMPLPLGLGLLYLKGQESAEATAEIVSKTFNEKIRKHCDMTLLSGAYAGTGNVLYVQHFLGQCAQHFEK

NbL15g23630.1 fasciclin-like_arabinogalactan_protein_9 [MW – SP = 23.98 kDa]

No. of times detected



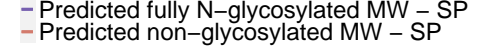
log(intensity)



Values from



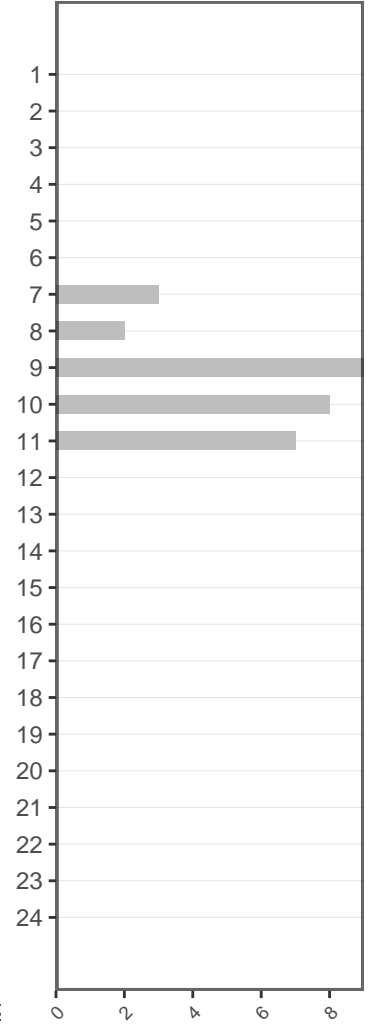
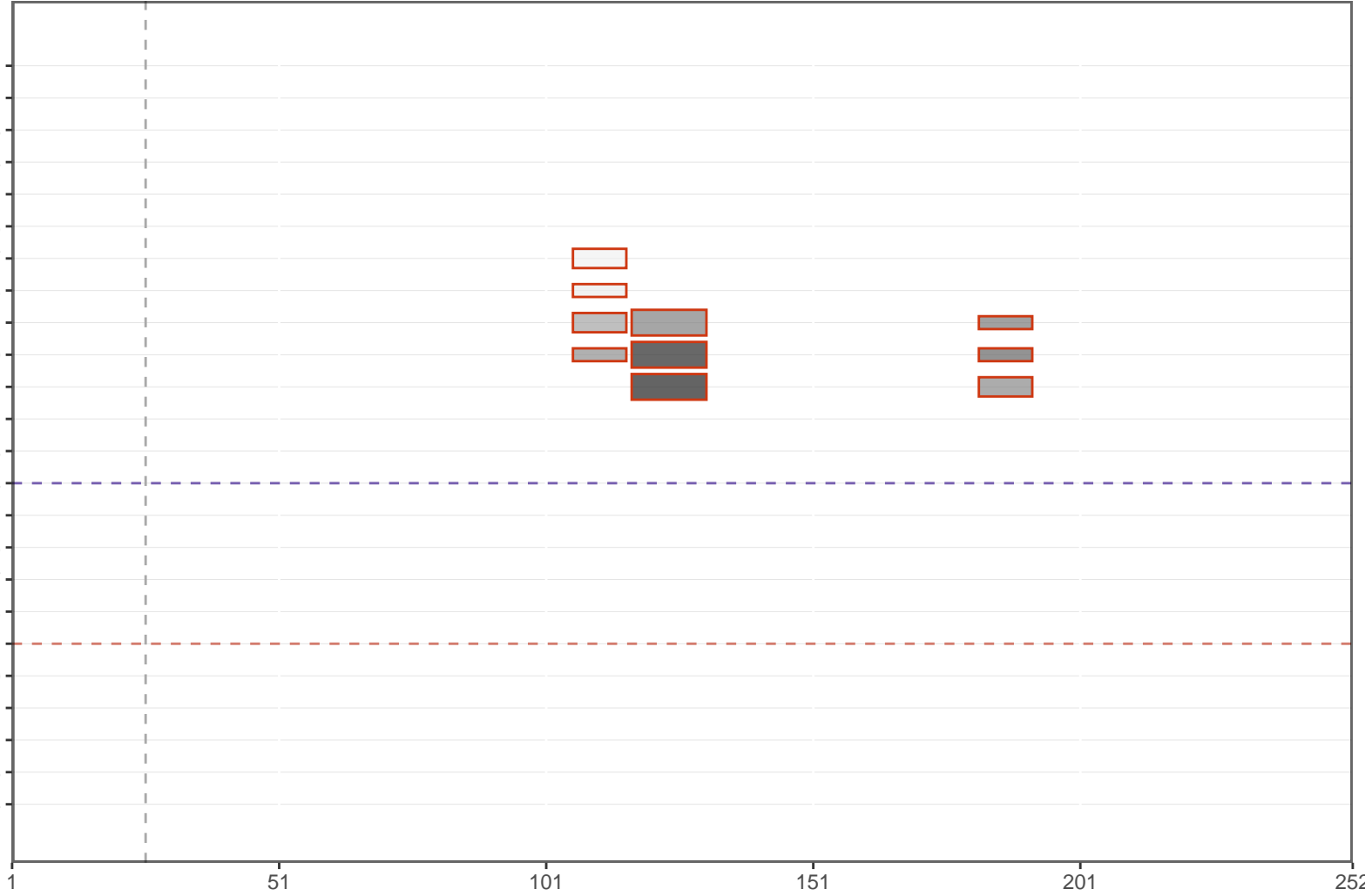
MW indication



Molecular weight

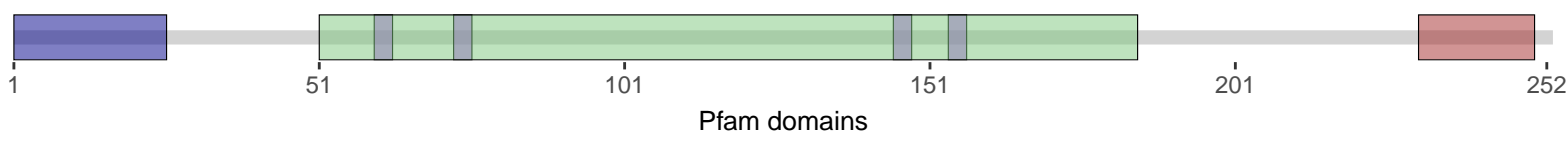


Gel Slice



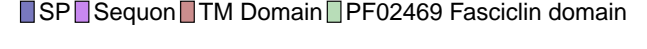
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PKFYSFDDLQTVSNPVRTGATGQKGEFFGLNFTGQNGQNVVSSGTVETNINMNRKDFPLAVYQLEKVLPLAFSDAKTPSSGDDAPPTDDSAKGGSTADKTKAGEPSPAPNGAKTRVGVFGLISGVFLFFMGALS

NbL15g23580.1 GTP-binding_protein_TypA/BipA_homolog [MW = 72.05 kDa]

No. of times detected



log(intensity)



Values from



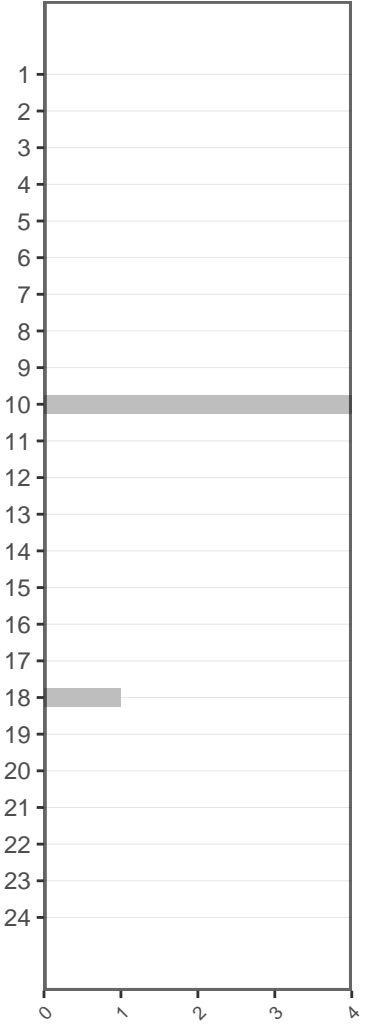
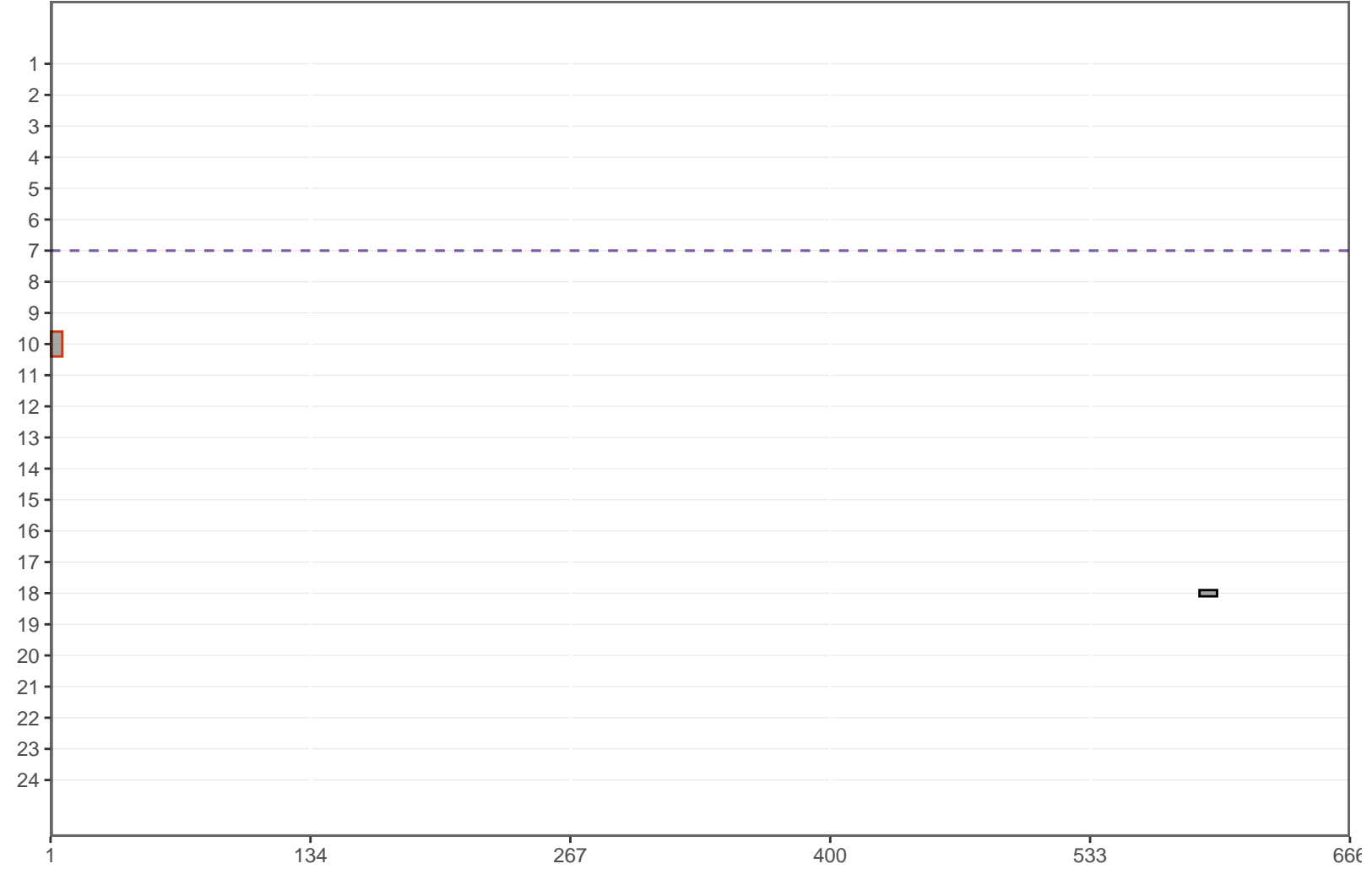
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AADPVDSAGAGDVISMAAGLSPTTGHVAVVEVMTALPTVLDPTTSMTFGVNDSPLAGSDGHLTGKGGDRLLAEAEINLAINLPTSESEYEVQGRGELGLGIENMRREGFELVSPPKVMYKVEKGVLEPIEEVETIEVDDHNGVLMSEALSHRRGEVTDMPGVPDNTGRTRMLTQPRRGLGVYRSVFSBQTRAGFMHRAFLYKRYKPLGNVYKGVLSMGRGLTAAHMLNLEARGILFVAPGMETVDMGMIHGEHRDTELDVNPVTKELTNVRAACKDE

NbL15g23440.1 uncharacterized_protein_At1g03900-like [MW = 32.47 kDa]

No. of times detected



log(intensity)



Values from



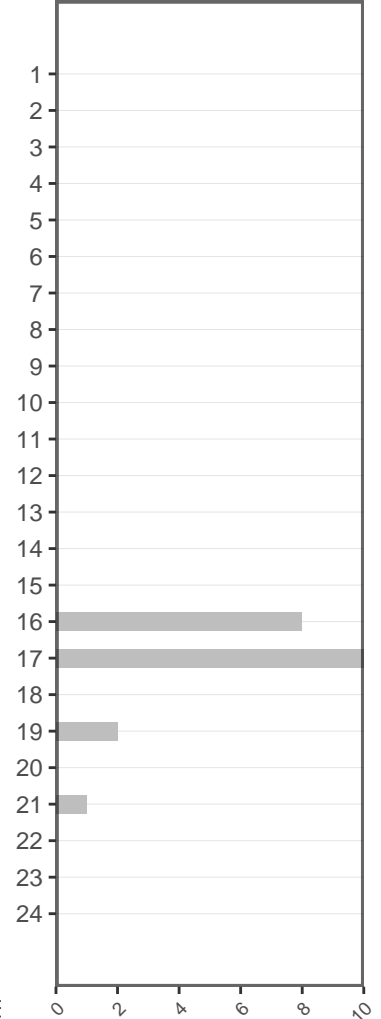
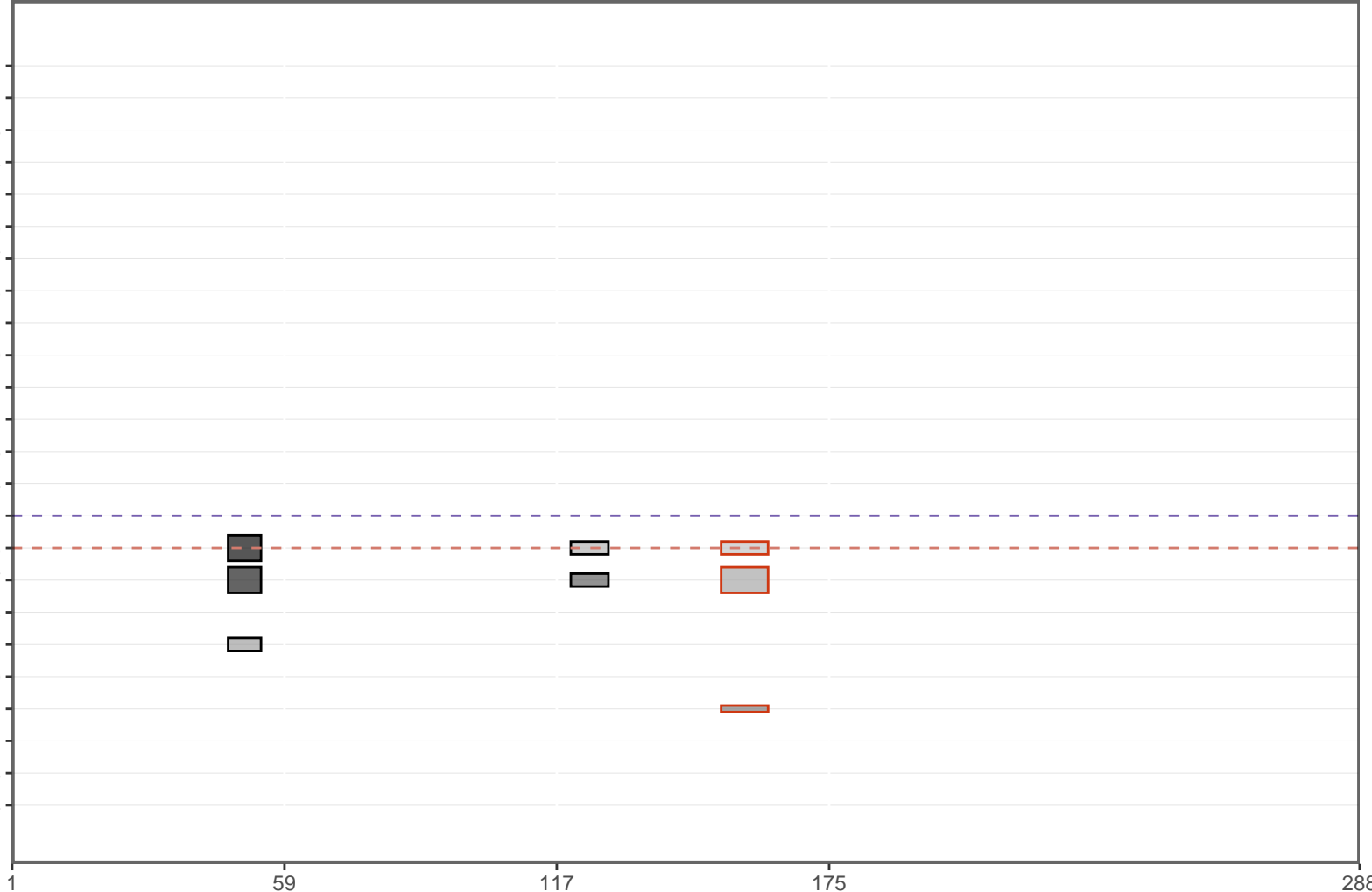
MW indication



Molecular weight

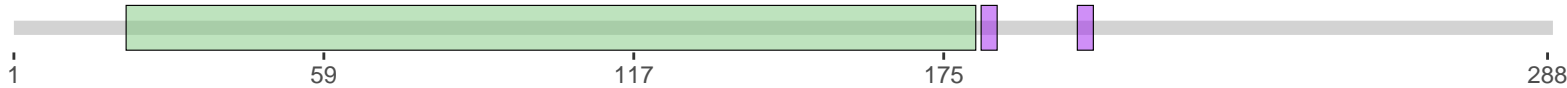


Gel Slice



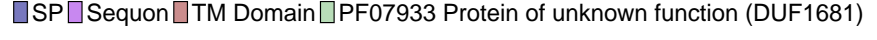
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

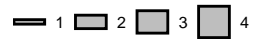


Protein sequence:

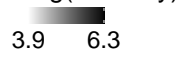
AYDFQALIHIDHMKLVNKKTAEEEMGGYQKSSVVDVSLKEGETLKGQKNTGSGSTRSKFFEGGLNLSLEEKANRKRKDTLKKPPPPAPLSPVDTAAMPVPSPKFSLGSAETKDSASAKEGTNTPESLKDDGGPGDVEDDDDFGFGAAG

NbL15g23370.1 ketol-acid_reductoisomerase_chloroplastic [MW = 63.33 kDa]

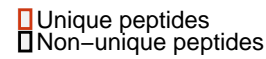
No. of times detected



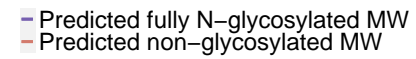
log(intensity)



Values from



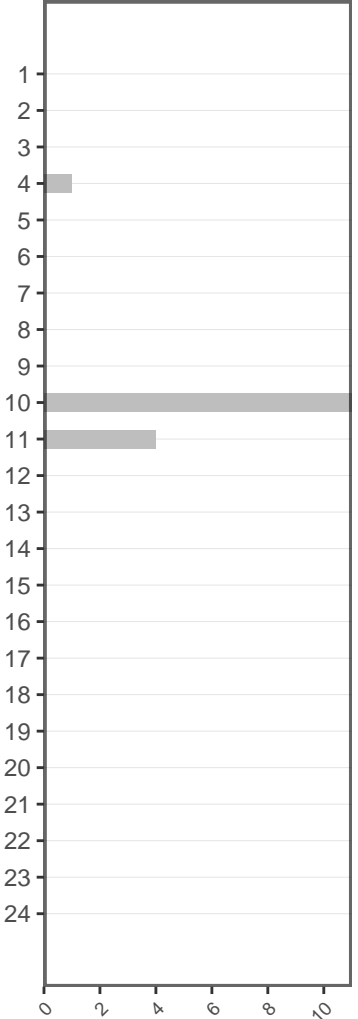
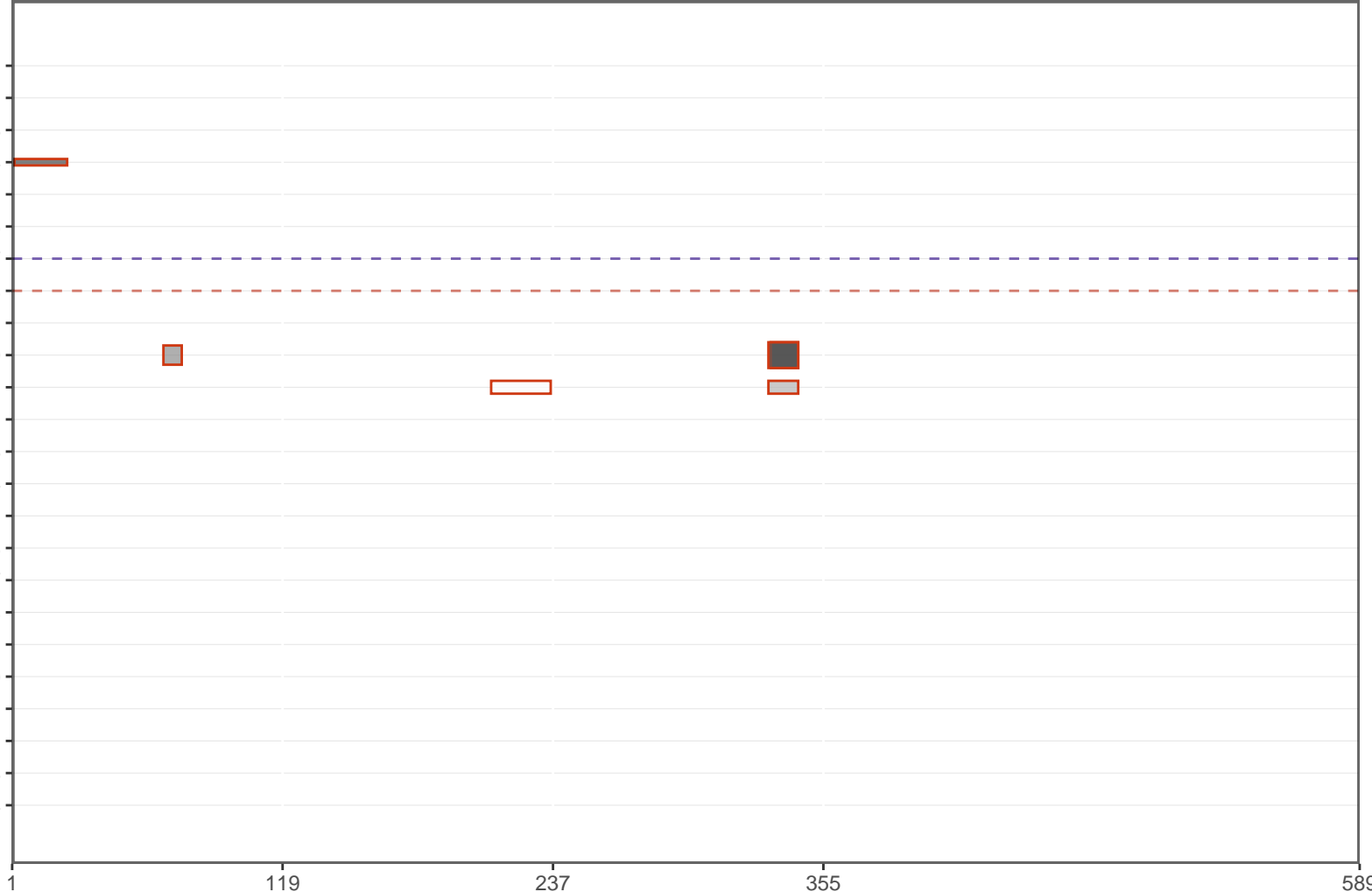
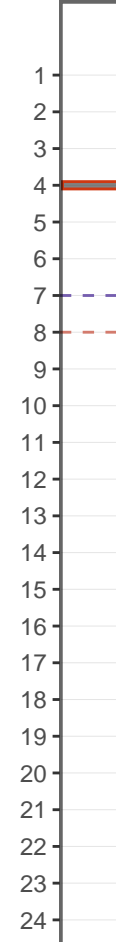
MW indication



Molecular weight



Gel Slice

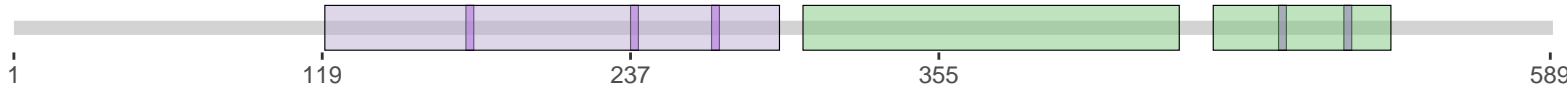


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ATDVALGIVSVALGSPFFATLLEGEYKSDIFGERGLLGAWHGVESLFRFRFTVNGMNDLKYKNTVEGDTGHSKTSKGLAVYNSLTFEEGKFEFAAYASGYPCMEILYEGYEDVATGSEIRDYVLAGRRFYEKEGLPFPFPGKIDQTRMVKVGERVRAKRPAGDLGPMYPTAGVYVALMMAQELRKKHSHSYSEHNEGIVEVDSLNPFMHARGVDFMVDNCSSTARLGSRWKAPRFDFYLTGQALVAVDNNAAINGDLISNPLSDPHGAEVGAQLRPTVDISYTDI

NbL15g23360.1 bifunctional_riboflavin_kinase/FMN_phosphatase-like [MW = 41.42 kDa]

No. of times detected



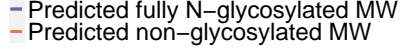
log(intensity)



Values from



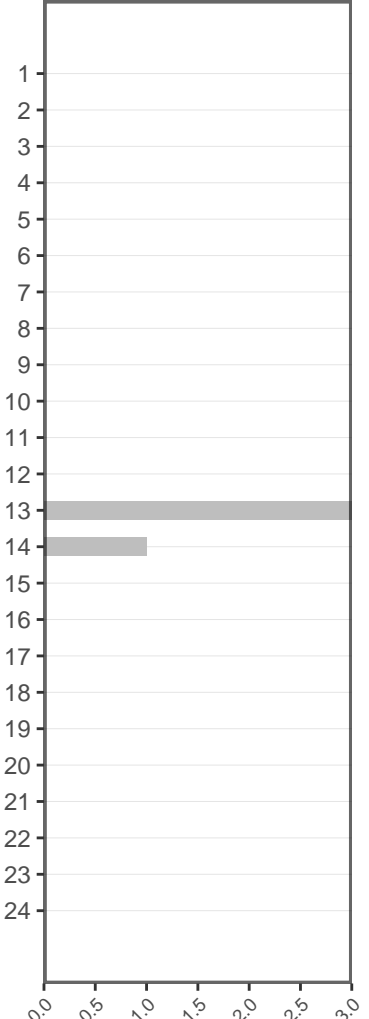
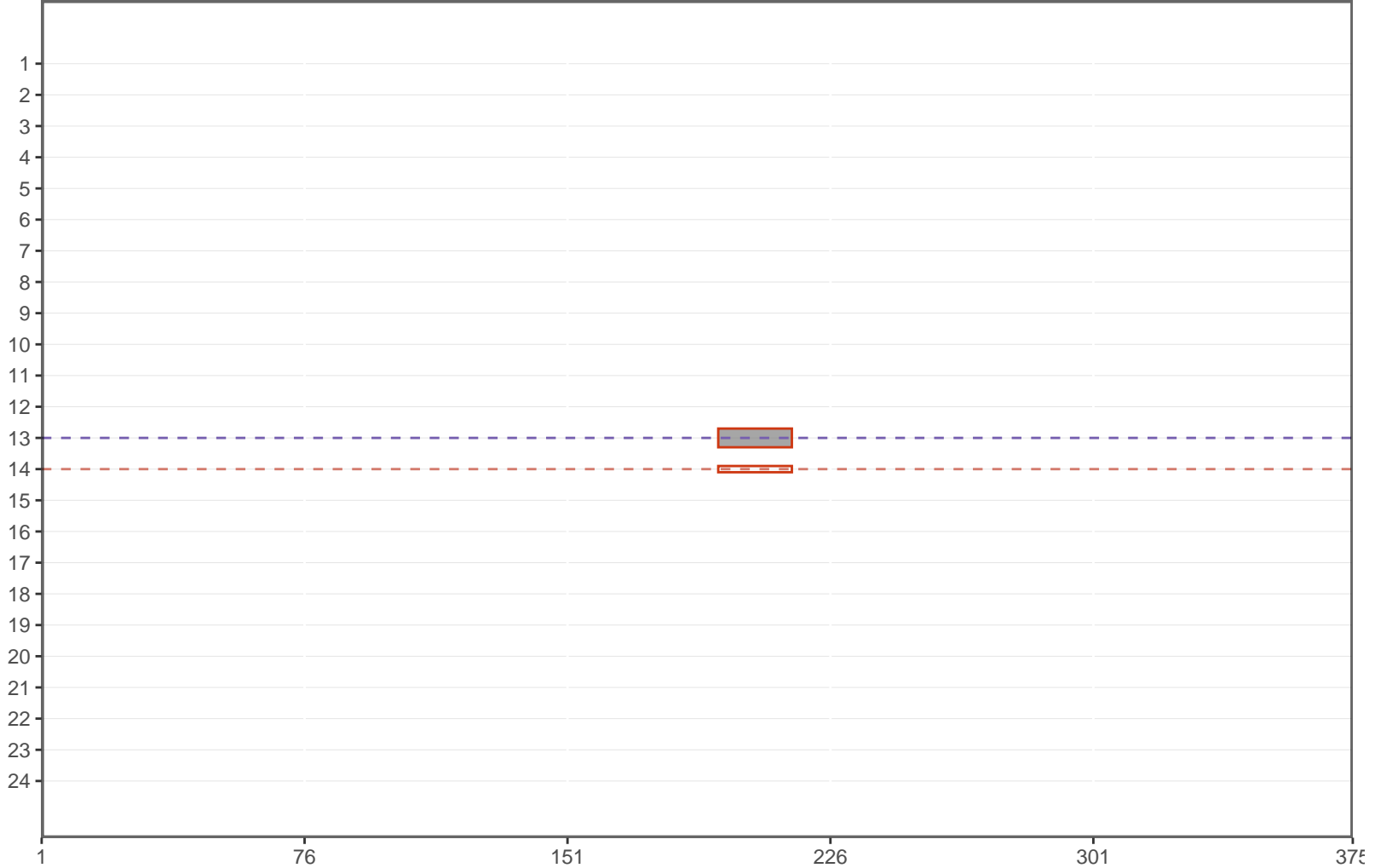
MW indication



Molecular weight

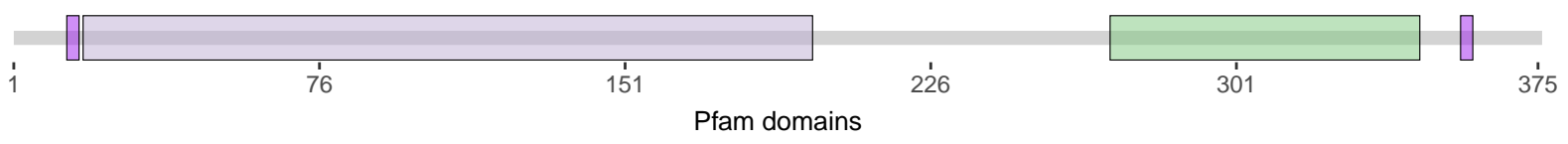


Gel Slice

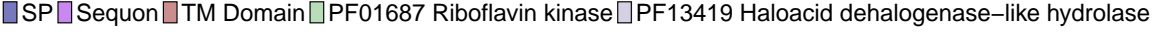


Protein length

Peptide counts over 4 repeats



Pfam Description



Protein sequence:

VIEDSYIGYKAGKAAARMVYVWPFHSEFDQYSHADSVLRSLLELKPVEWGLPPFDQWVGNALLVEPVSFRGLYRNGLLHDFDQDPSALPDQVYFGWGRLEAHKFKIVLGGDWHGCCSKRKMADAGIVDSSDEKQEKMEVYVYGRGSRDEGWKDKIELEEDKSIASALNRSESLGAFQSLFSEVAL*

NbL15g23350.1 14-3-3_protein_9 [MW = 29.54 kDa]

No. of times detected



log(intensity)



Values from



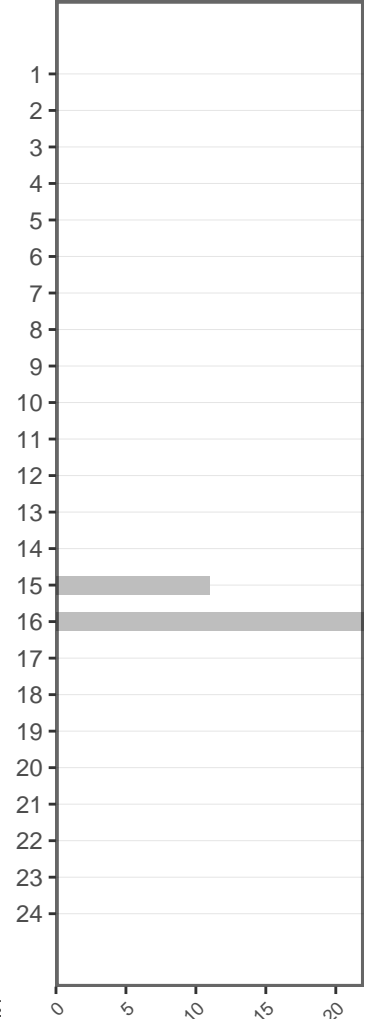
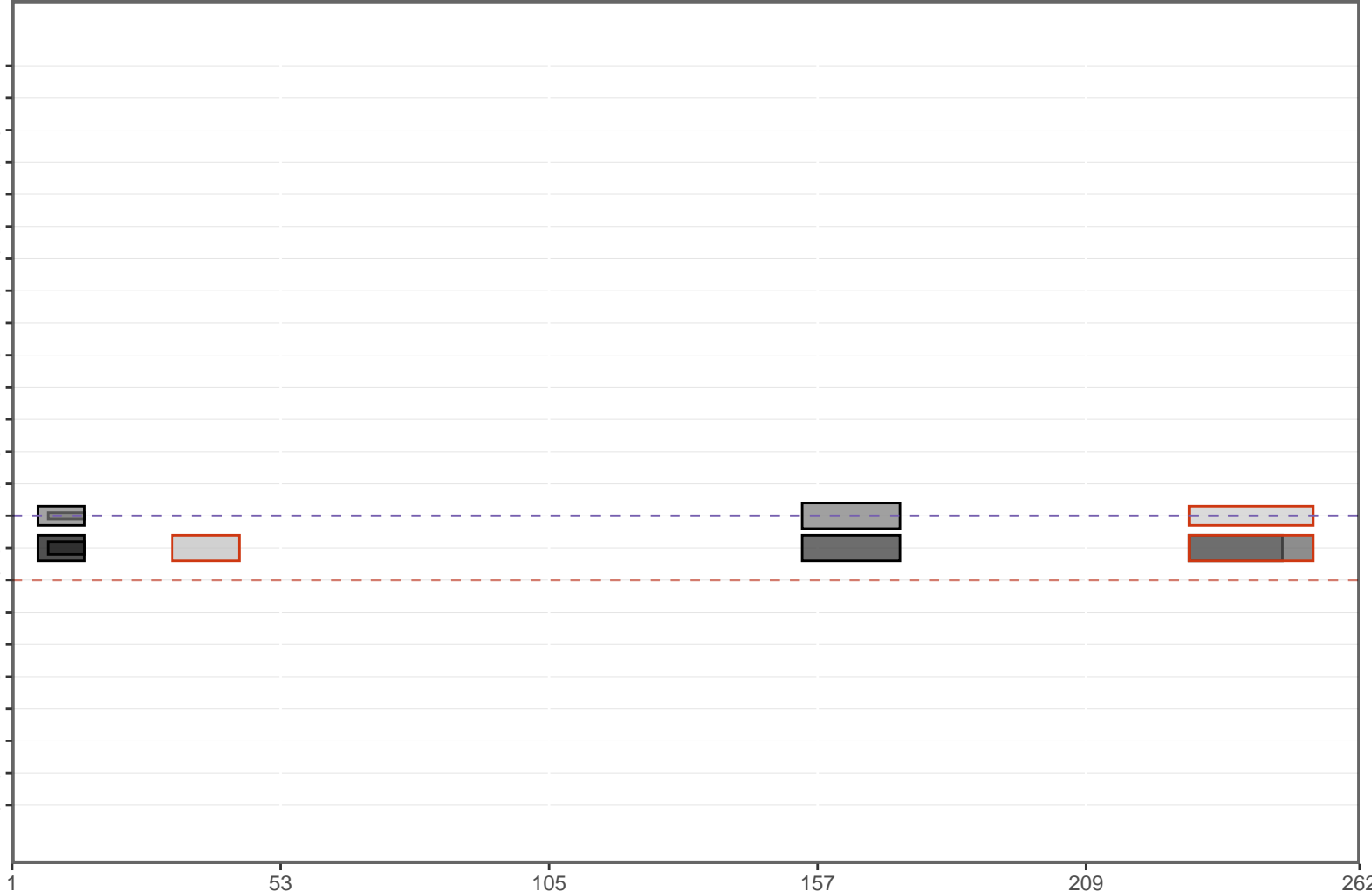
MW indication



Molecular weight

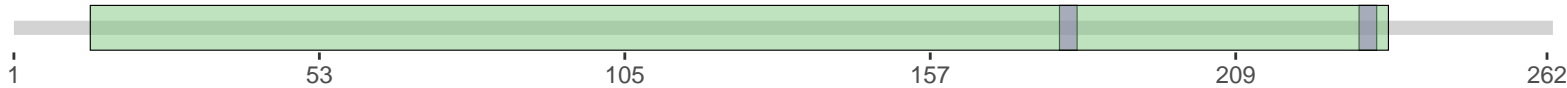


Gel Slice



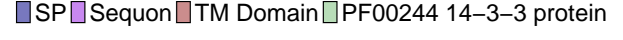
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SESTVYFHMKKGGDYRYLAERFKSGNDKKEVAELSLKAYGSAATAAEALPPTHPRRLGLALNFSVYFYEMNSPERACHLAKGAFDEAISELDSLNEDGKYKSTLIMOLLRDLNLTWTSQLPEDAEDAGKGDATNKASGGDEAE

NbL15g23300.1 phosphoenolpyruvate_carboxylase-like [MW = 110.04 kDa]

No. of times detected



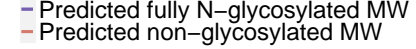
log(intensity)



Values from



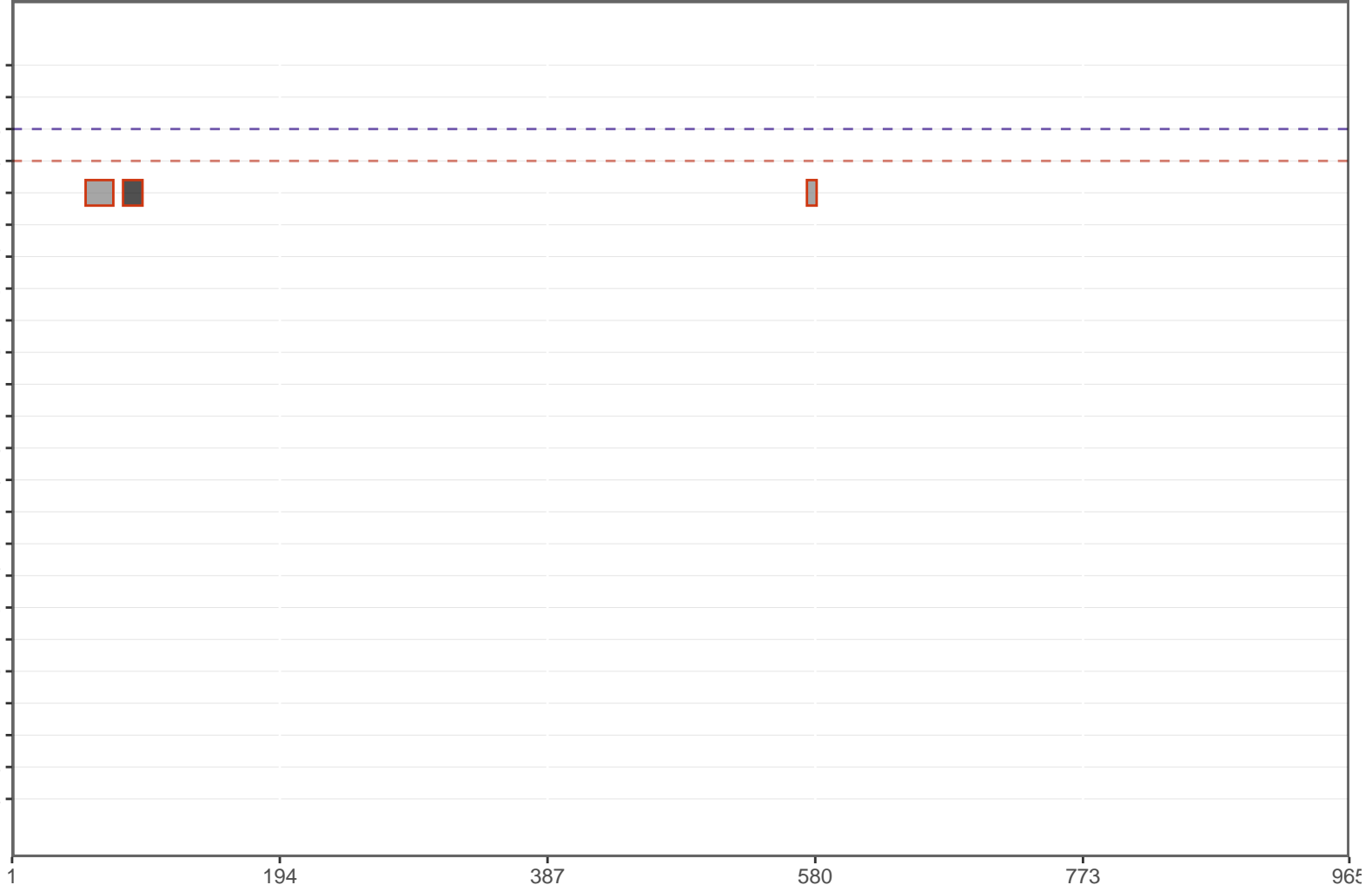
MW indication



Molecular weight

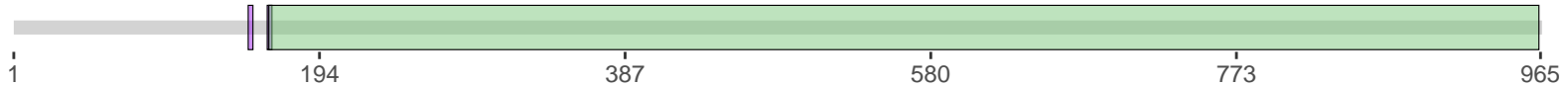


Gel Slice



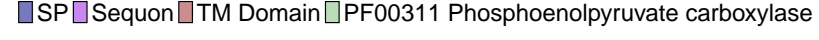
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SYKEVSEEDROEIVLLSELGSRKPLFGDLPKTDIADVLDFTFNIHELPAIDNFGAVIEMITPAISDVLAVELLEGREGHVKSPLRVVPLFEKLIADLESAPASVRLFSIOWYKRNIRKNGKQEVMDGVSDDSGKAGRLSAWQIKYKAGEELNVNAKEFGVKLTMFHGRGGTVGRGGPHTLALSGPPDTHGSLRVTVGQGEVIEQSFGEELGFRTLGRFTAATLEHGMNPPVAKPEWRALLDEMVAKEVRLVLFVQDPRFVEVFRLATPELEYGRMNGSRPAKRPKPSGGIE

NbL15g23290.1 protein_LIGHT-DEPENDENT_SHORT_HYPOCOTYLS_10-like [MW = 19.8 kDa]

No. of times detected



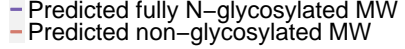
log(intensity)



Values from



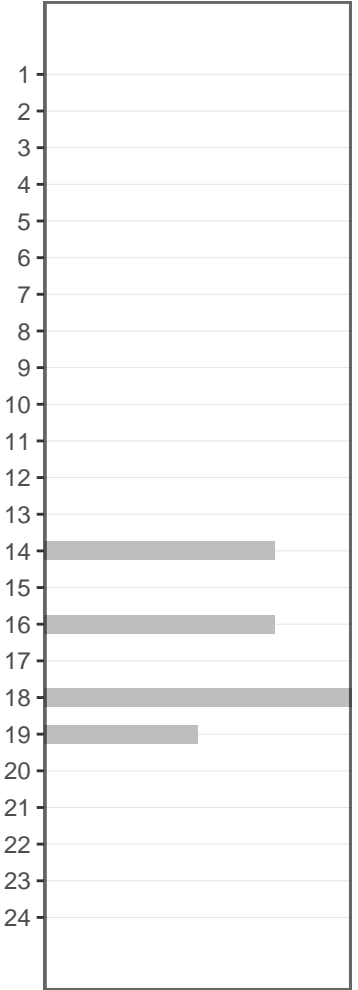
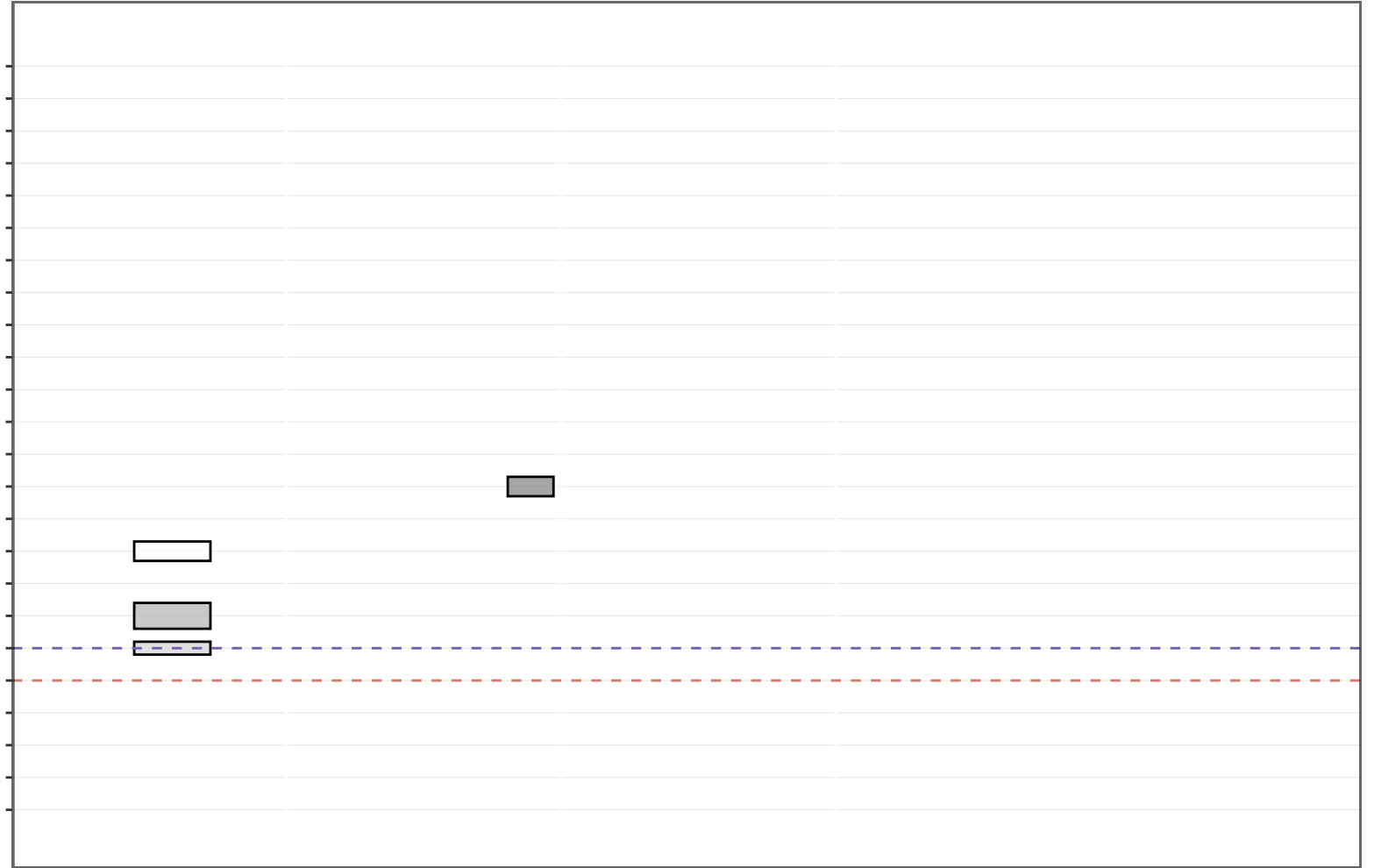
MW indication



Molecular weight



Gel Slice

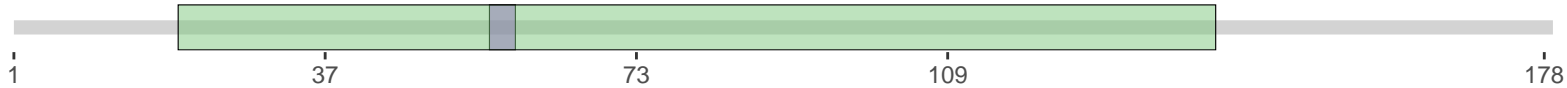


Protein length

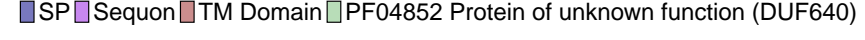


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

HLQGCIFYGQPEPPAPGCTGLRQAWGSLDLHGLRLRAAYEENGSGPETNPFASGAIIRVYLRVKEGSGKARGIPYKKKKKKIKGTSQKGGDDSDSHHPFS

NbL15g23210.1 peroxidase_P7-like [MW - SP = 31.54 kDa]

No. of times detected



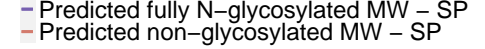
log(intensity)



Values from



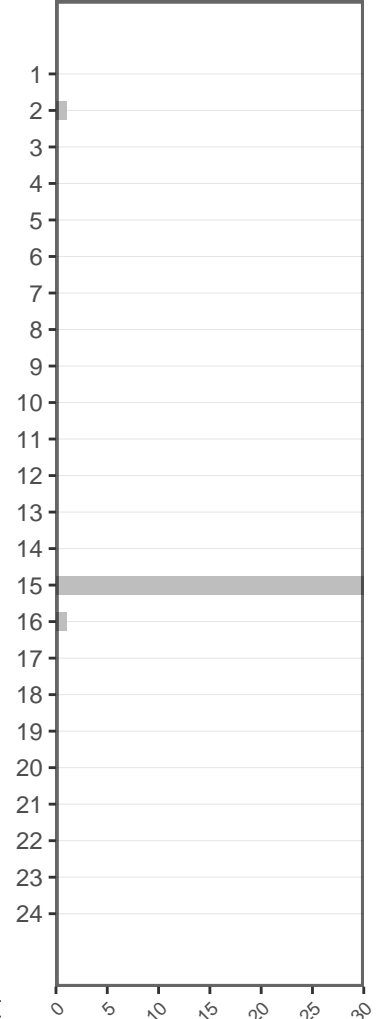
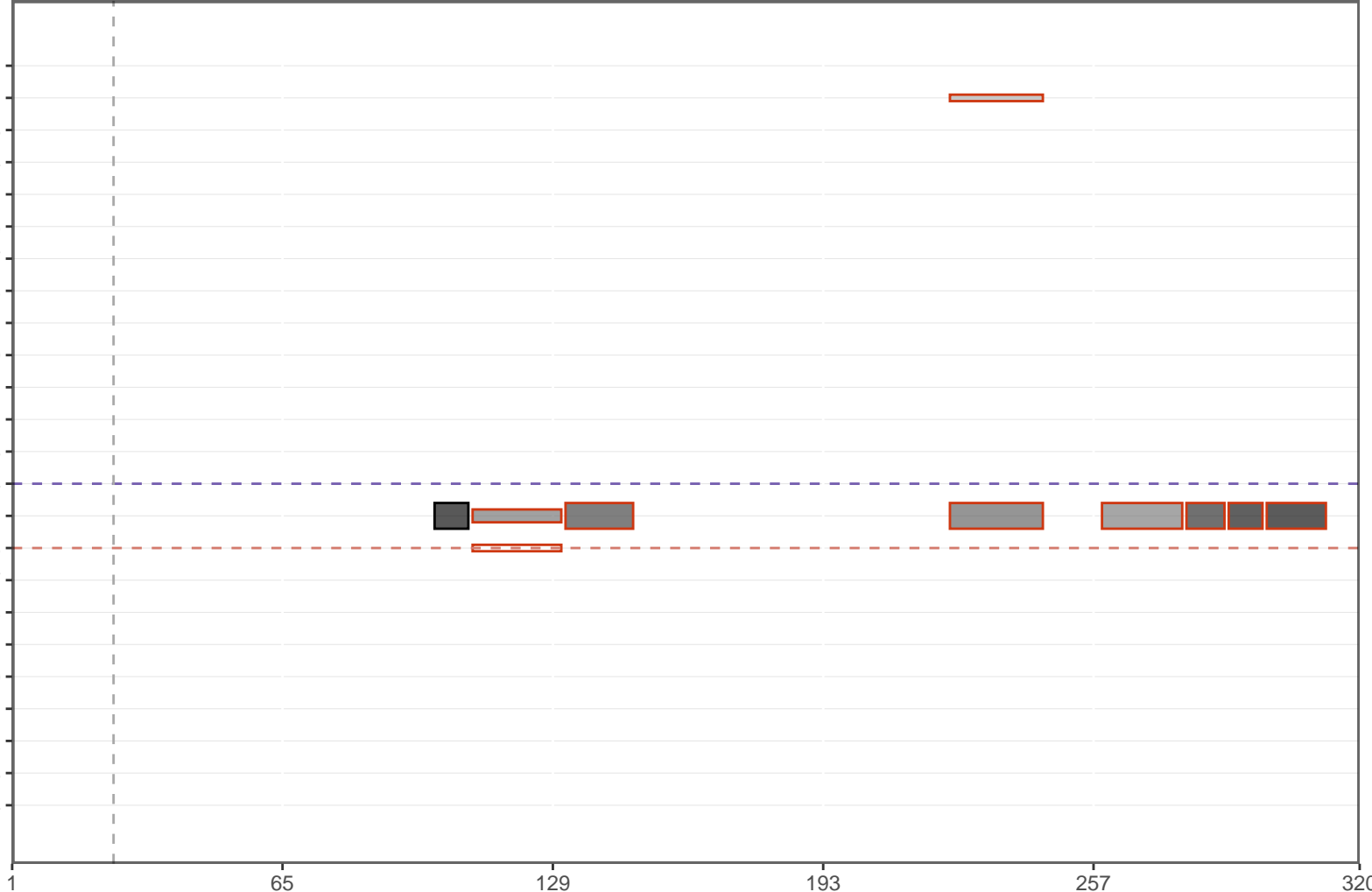
MW indication



Molecular weight



Gel Slice

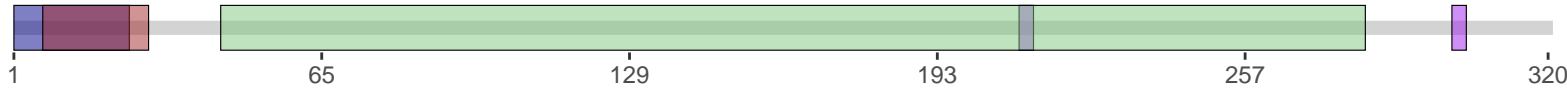


Protein length

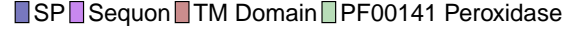


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

RRDARTASQSANFQIPAPTSLESLTLEMFSAKGLNARDMTALSGGHFTGGARCTFFTRIRHNDTNDMGFATKRKATGPSGGGANLAPLDIGTNRFDNDYQGNLVARRGLLHSDGELFNDGSDQALVREYGTNGAAFRDFDFAAAMVRMGNSPLTGNNGEIRNRGRAN

NbL15g23130.1 60S_ribosomal_protein_L11-1-like [MW = 20.76 kDa]

No. of times detected



log(intensity)



Values from



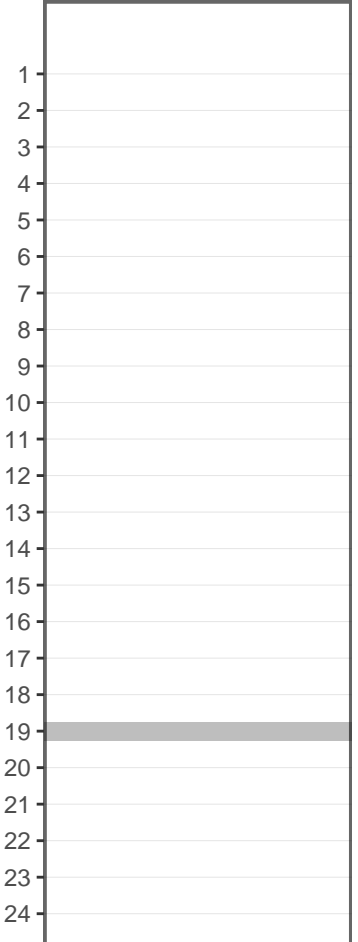
MW indication



Molecular weight



Gel Slice

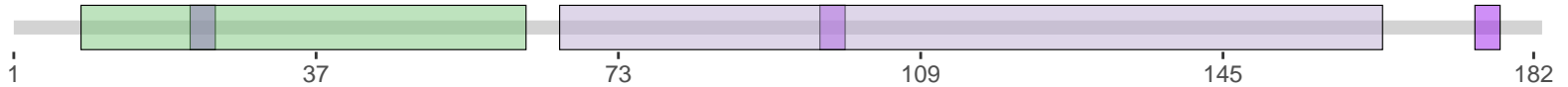


Peptide counts over 4 repeats

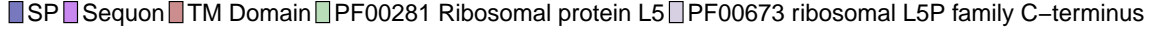
Protein length



Pfam domains



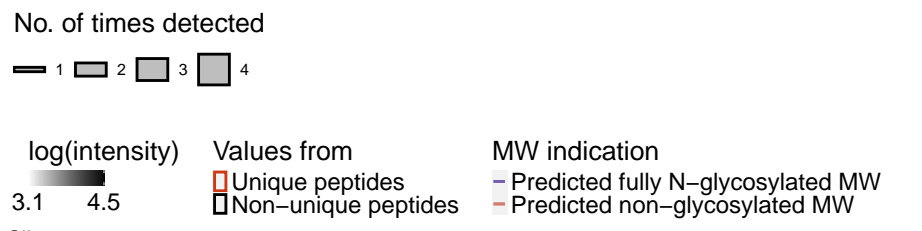
Pfam Description



Protein sequence:

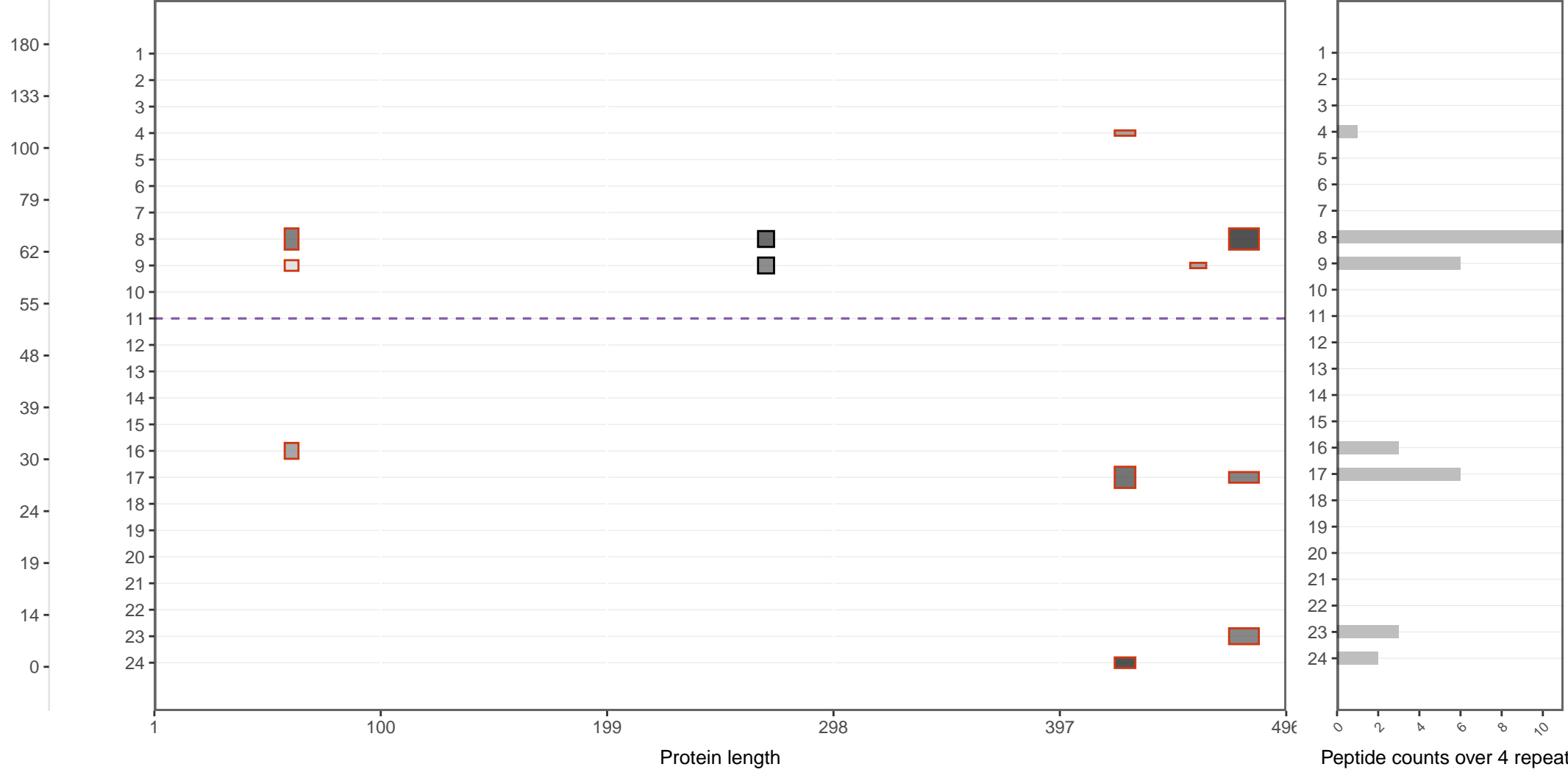
ITQLLESGLKVEYELLRRNFSETGCFGFGIDGHDIGIKYDPTGIGMDFVLLERPGYRVARRRCKGRVGIQHRVTKEDAMKWFQVYVEGVLNKSGNIQ

NbL15g23060.1 ATP-dependent_zinc_metalloprotease_FTSH_2_chloroplastic [MW = 52.72 kDa]



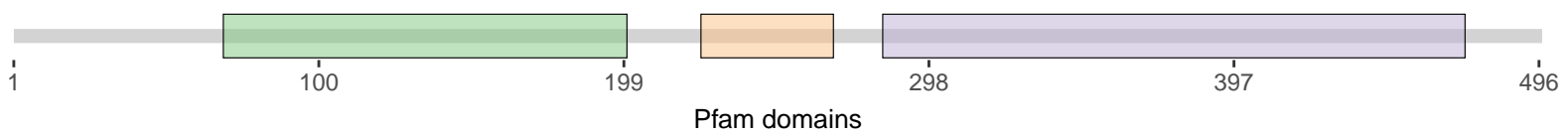
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- TM Domain
- PF01434 Peptidase family M41
- PF00004 ATPase family associated with various cellular activities (AAA)
- PF17862 AAA+ lid domain

Protein sequence:

RTPFPSGADLANLNEAAILAGRRGKTAFTSEKIDDSIDRTVAGMEGTVMTDGKSKSLWAYHEVGHHAIGTLFPGHDAVQKVLIPRGGAKGLTFIPADDDPLKSGQLFARIVGGLGSSAAEEVFGPEVETTTGAAGDLQHTGLAKGMVVTFGMSELGPWLSMDSAGSGDVTTRMMARNMSEKLAEDIDGAVKRLSDNVAEIALTHIRNNRRAIDKIVLELEKETMTGDEFRAILSEFVEIPENRVAIPVPTAAV

NbL15g22940.1 protein_STRICTOSIDINE_SYNTHASE-LIKE_10-like [MW – SP = 31.52 kDa]

No. of times detected



log(intensity)



Values from



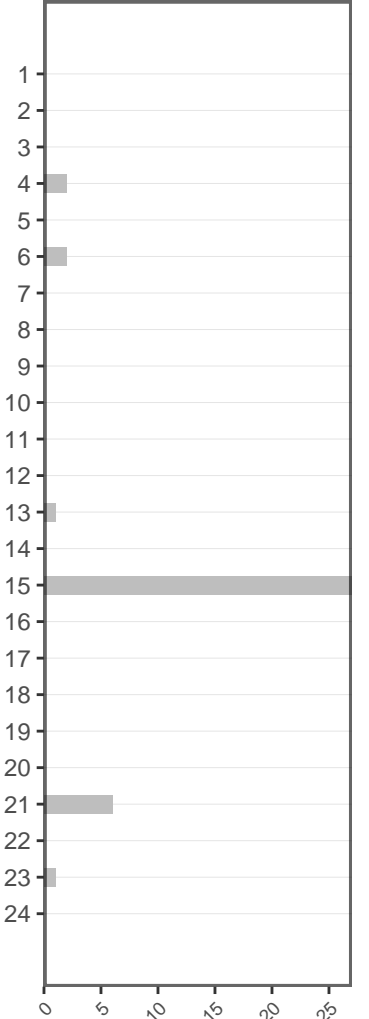
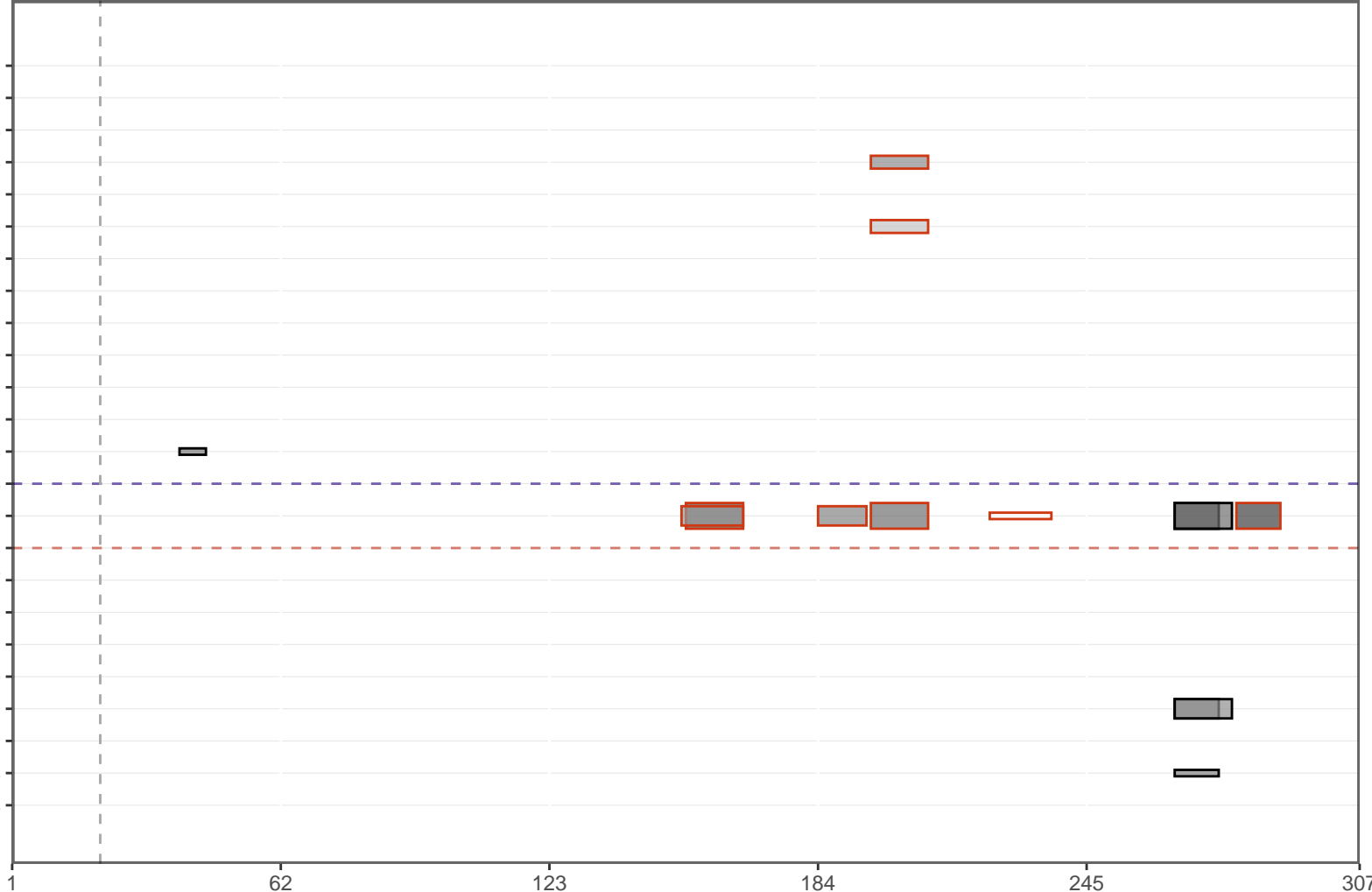
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IYFTDSSTKYORRRQFSAFVGGDTGRLMKYDKSTKWKVLLRGLALANGVALNKDGSFLVSETGNCRIIRYWKGPVGRHDFADVPGLPNIRINSRGEFVWLNAKTSATAKLSAEGRMLEVEDEEGKTLRVIHSEVEEGYKLVFGVMMPLGVYGLS

NbL15g22840.1 translation_initiation_factor_IF-2_chloroplastic-like [MW = 108.26 kDa]

No. of times detected



log(intensity)



Values from



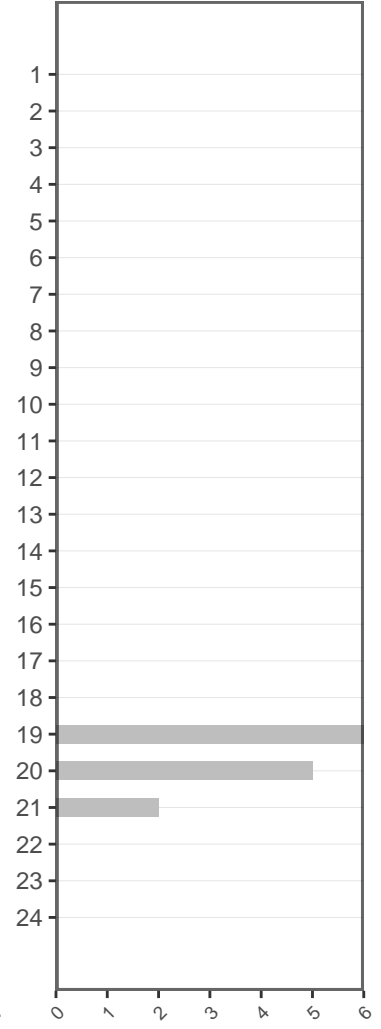
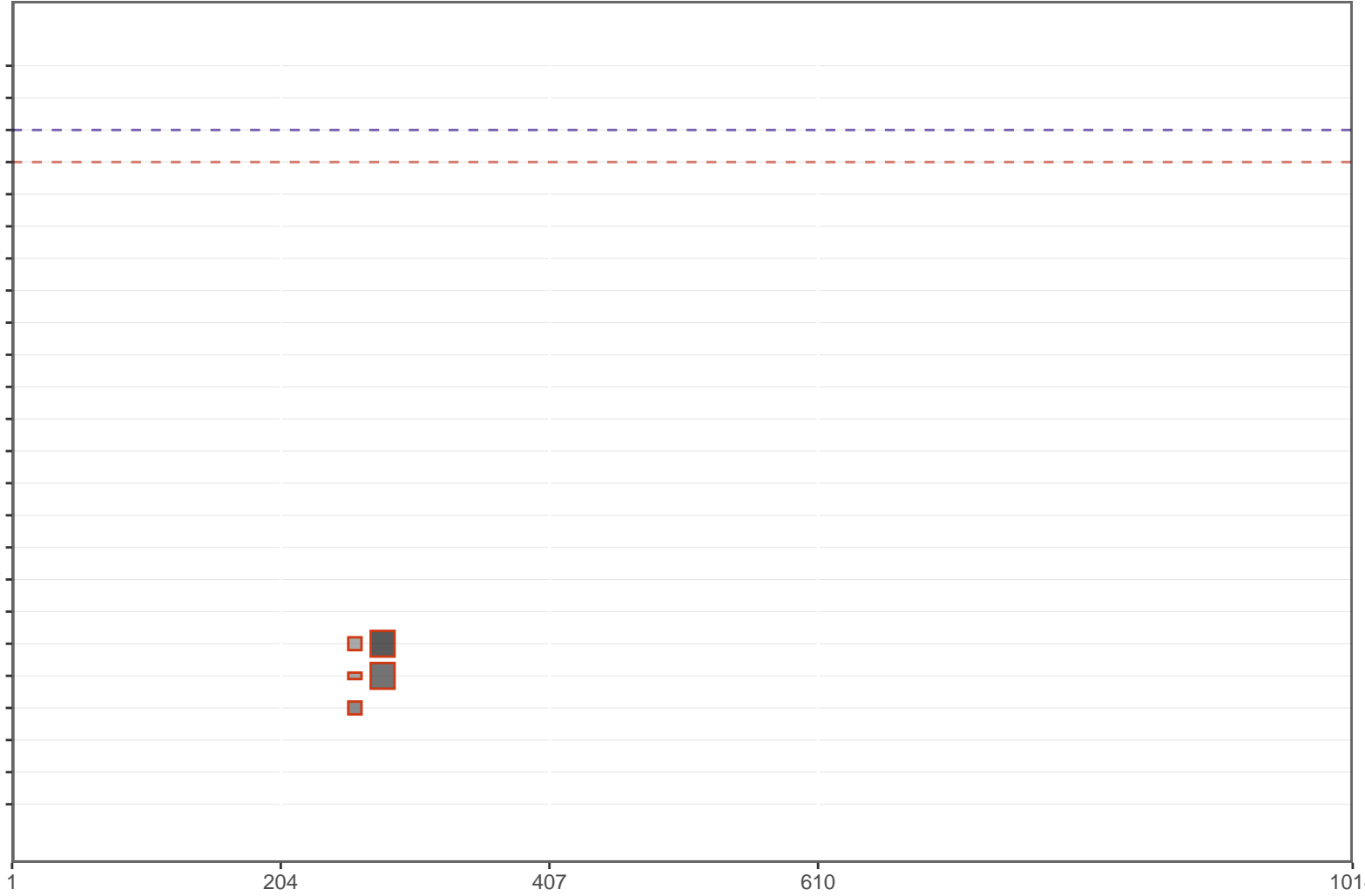
MW indication



Molecular weight



Gel Slice

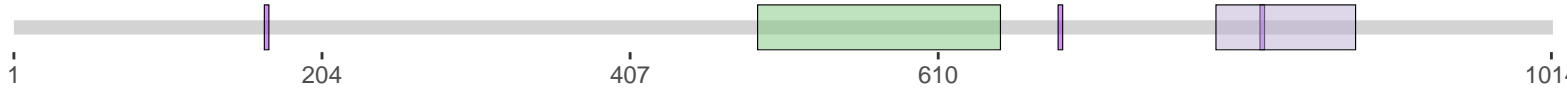


Protein length

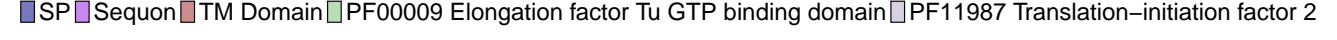


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

*PVITMGGHYDHIKFTLLDHRKTKVAASEAGGITGGIGAYKVGVPDTPKPGICVFLDTPGHKAFGAMRARGARVTDIAIVVAADGGIRPQTNEMAHAKAAGVPIVAINKIKKDCGANPERVMDGELSSIGLMPEDWGGGVPMQISALKGENIDDLLETVMLELQELKANKPQRNAGTVVEAGLQKSKGPAVTRIVQNGTLKGGDKVVGGEANGKVRALFDKQKRVDEAGSPVIVQVGLNVPVWAGDEFEVVGSLDVAEREKAEARGESLRTERLSAKAGDQKITLSSFASAI

NbL15g22830.1 uncharacterized_LOC104238148 [MW = 102.38 kDa]

No. of times detected



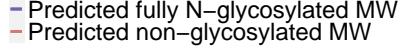
log(intensity)



Values from

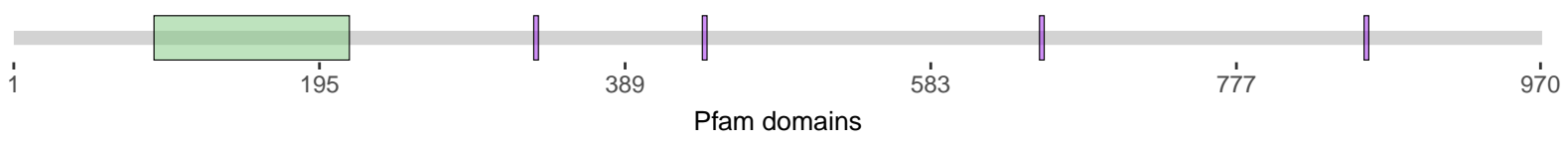
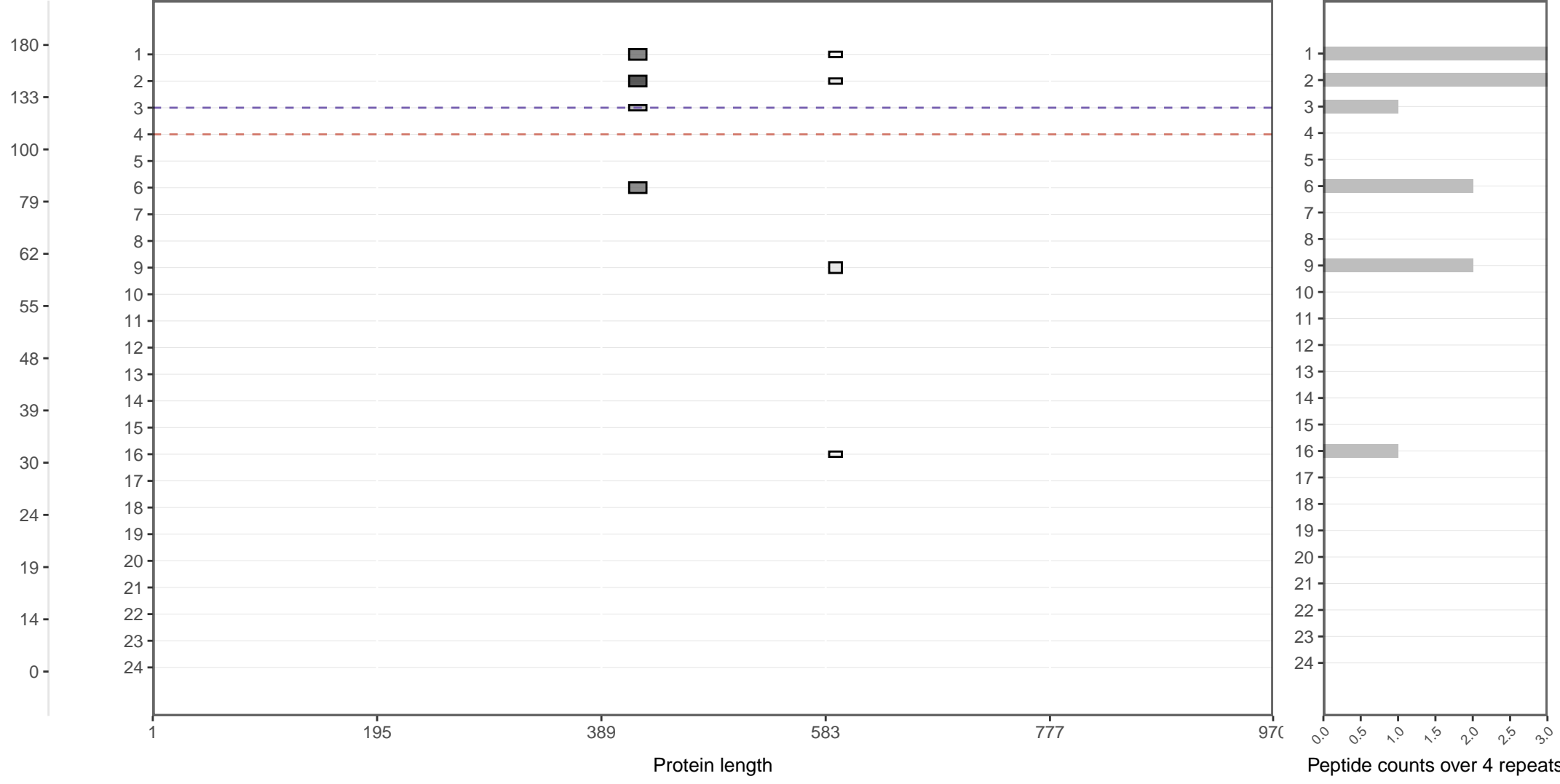


MW indication



Molecular weight

Gel Slice



Pfam Description
 ■ SP ■ Sequon ■ TM Domain ■ PF07967 C3HC zinc finger-like

Protein sequence:

EVGGHAASYESRGPSSRRKRLNEEGGTVDRPQLVQVADDEVEGTVDRDGDDEVNDGSGQYAGPKRAGGSDAFGDPOLTSYVKDSSGAGPLSLGFEKGRDARDDAFGRGQELTGMPTSRDSTHYVSSVAMDVTHSADDDSMESVENLPGDFDVFNPSTSVLRSDPVETSELNYSNQADGGSTPWVRRSAGEMGVSSFTNDEEVENNTDTATGNVDRDGFVDSGGSGMGASHEAEHGTDSVHRADSVAGDEVAWEITENGGQTGEFAPDPLGLMGDVPPE

NbL15g22750.1 glucose-1-phosphate_adenylyltransferase_small_subunit_chloroplastic/amyloplastic [MW = 58.89 kDa]

No. of times detected



log(intensity)



Values from



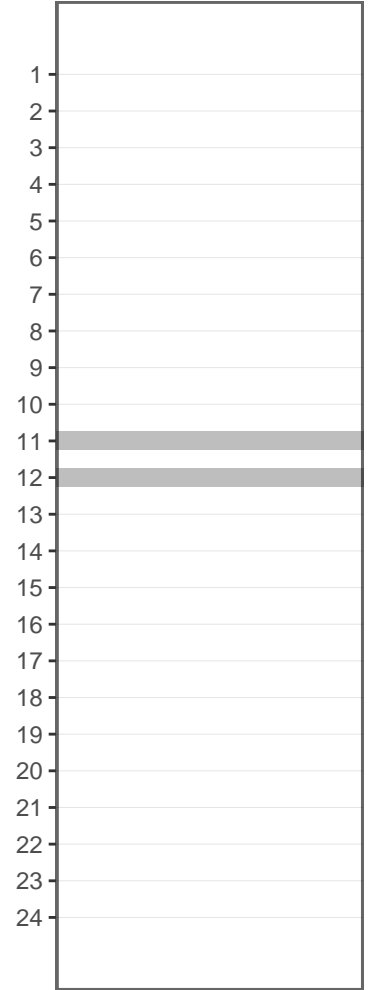
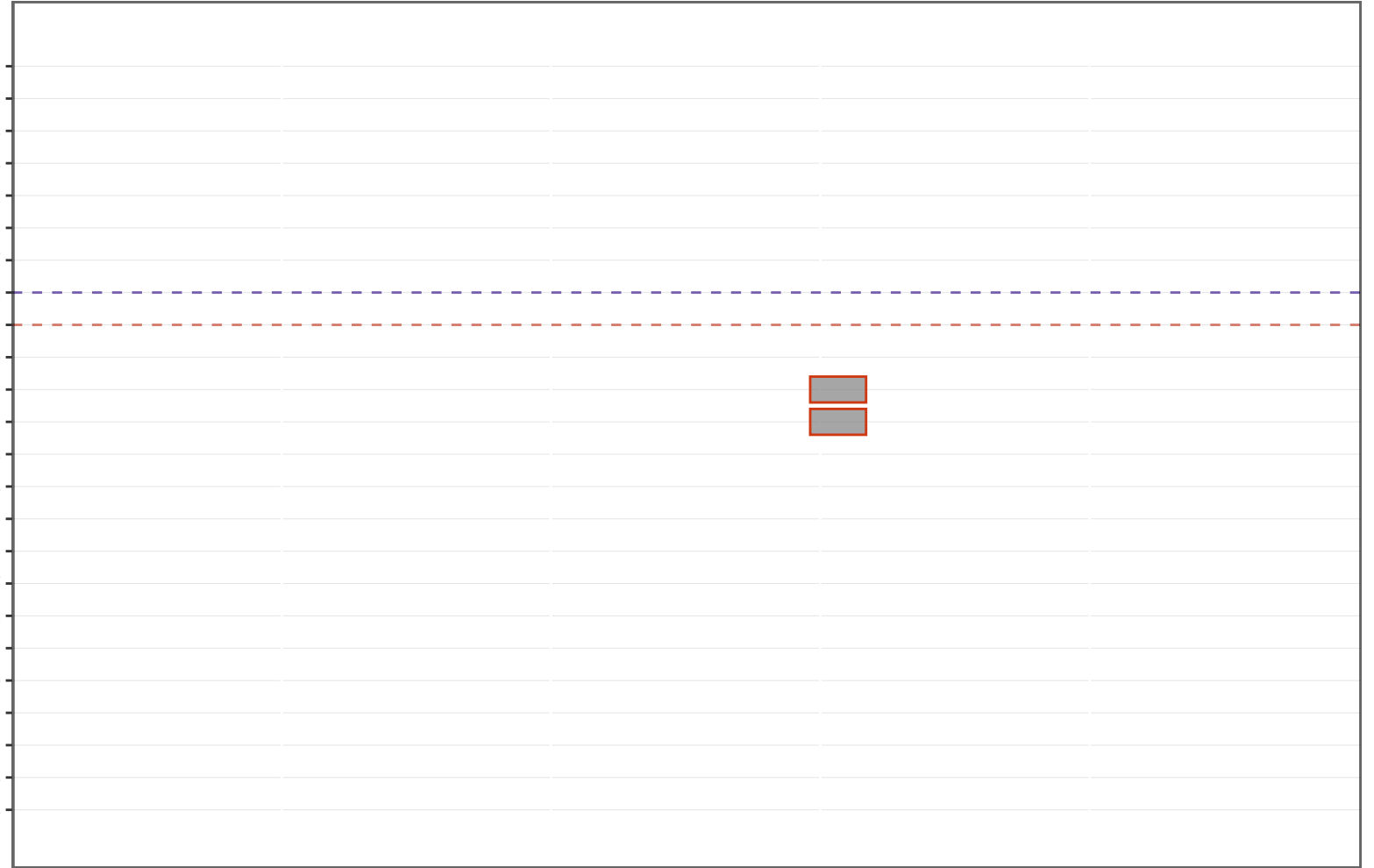
MW indication



Molecular weight



Gel Slice

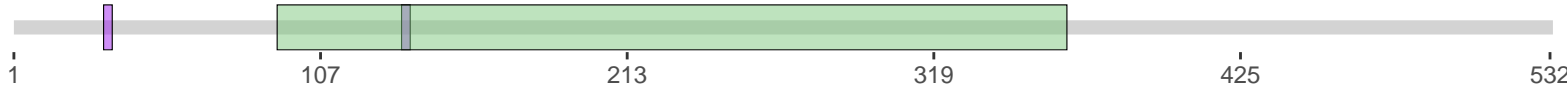


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

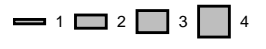


Protein sequence:

IGLMKDEEGRIIEFAEKPKGEGQLKAMKVDITLGLDDERAKEMPIASMGVYVSKDQVNLNRDKFPGANDFGSEVPGATLGMRVGAYLVDDGVEDDGTIEAFYANLGRTRKPKVPDFSEFYDRSAPVYTPRVLPPSKMLDADVYDSVIGEGGVKIKKHHHSVGLRSGISEGAMEDLLMGADYVETDADRRLAAGKSVPIGIGKNSHKRAHDKNRIGDNYKVKLFESCFSDLRFMSSFRHAKYLOPQVLDISGIVNLTLSRGGFFVSG*

NbL15g22710.1 subtilisin-like_protease_SBT5.3 [MW - SP = 80.06 kDa]

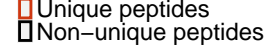
No. of times detected



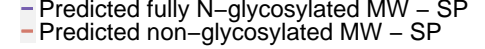
log(intensity)



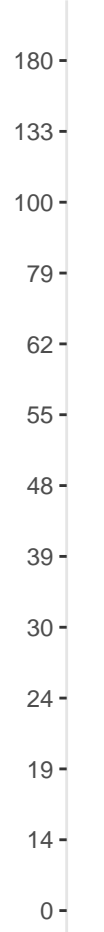
Values from



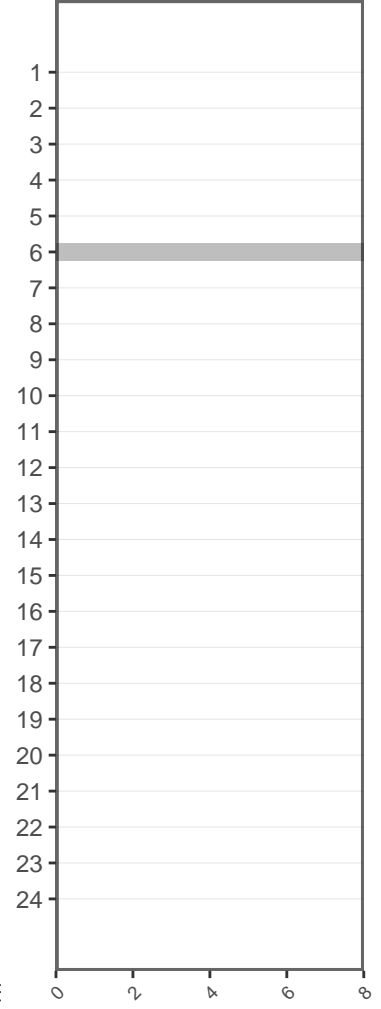
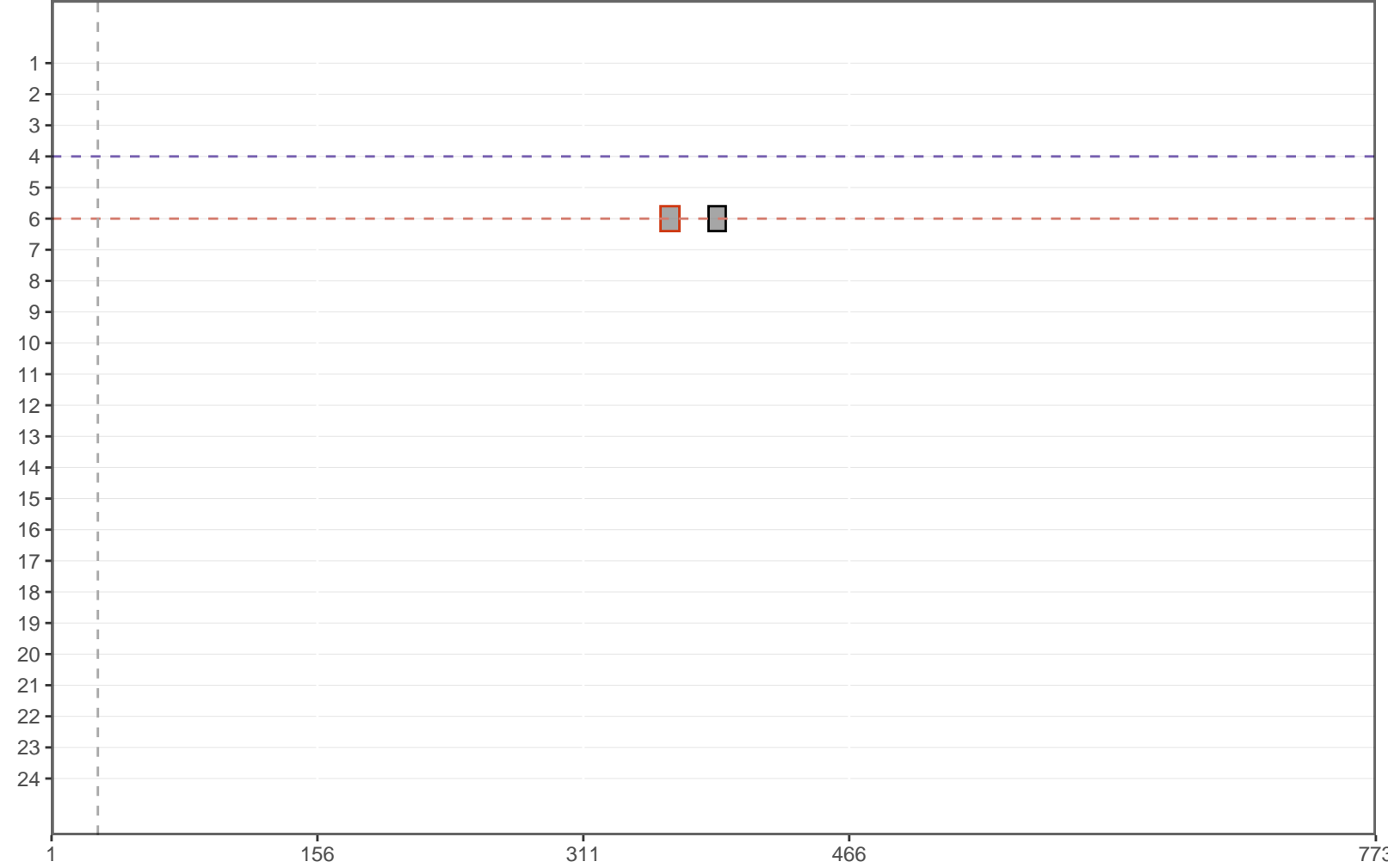
MW indication



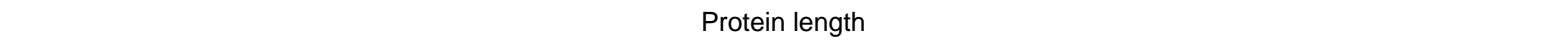
Molecular weight



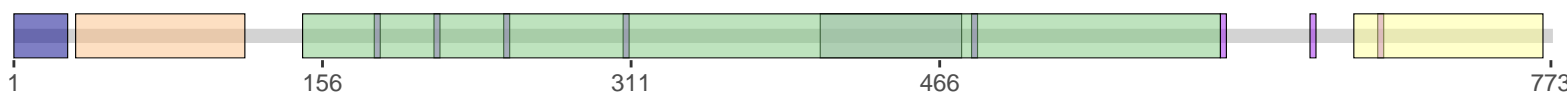
Gel Slice



Protein length

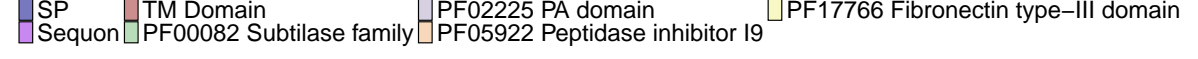


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YKGESLSVETLPKGGKFFPINAASAKAPHASTDDARLCKAGALDPKKVKGTLVGLRQGNARVQKGGQALAGAVGMVLANDVAGNEIADPHVLPATQISYTDGLLEFAYVNSTSTPTASITHPKTQLGTRKPKPVMMAAFSSIGNTVTFPEFLKPDITAPQVSHIAAVTGAEGPTNGDFDKRRVWFNEVSGTSMGSPHVSVDGVLKLTLYPTVWSPRAKSAIMTARTTRDIAIEPVLNASVYKTSFFAYGAGHVRFRNRAMDPLGLVVDLTIIDKLSFLYTGQVNETQIKTFTGPFYCA

NbL15g22480.1 peroxisomal_and_mitochondrial_division_factor_2-like [MW = 37.63 kDa]

No. of times detected



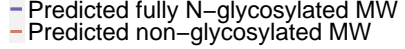
log(intensity)



Values from



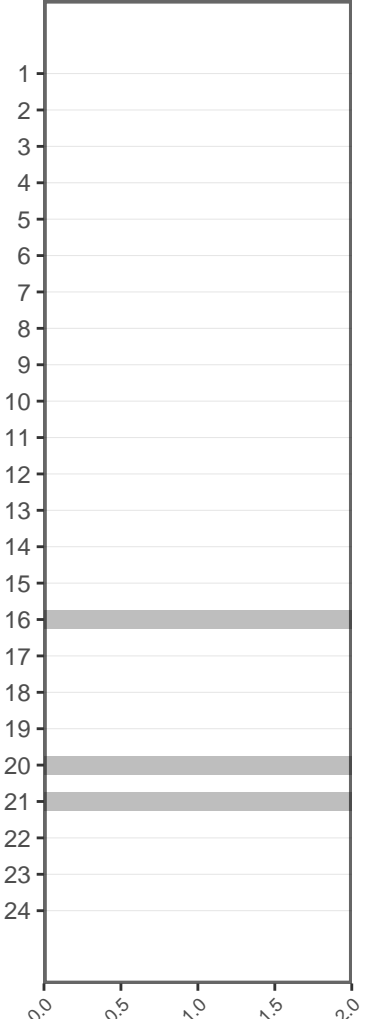
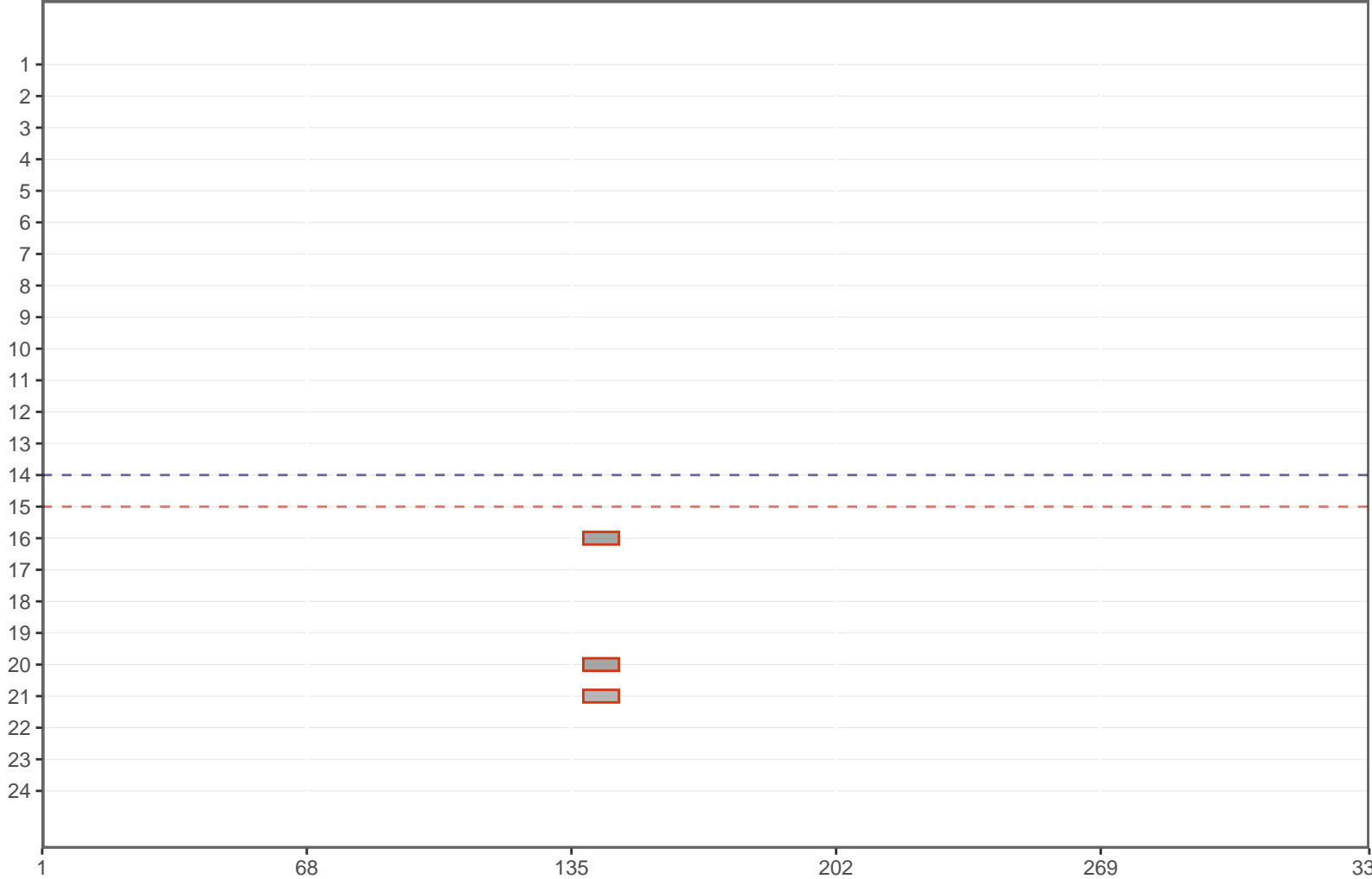
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

LDLHGSNSELGGVYKFTLEGLKSSSEKTKMLDAIEGRNLLLSKLEKLEASGNNGRGEVEVKEEERGLKXKHEELEGTVAANNEEWEKELKELHVMYKELEKRVKEMSRRAAELEKLEKLEKIVTERLWASNNIGIPVGFDFKVGYGFAEVLNPLVAASSVAVAVIGVYVLYKGRKA

NbL15g22260.1 probable_LRR_receptor-like_serine/threonine-protein_kinase_At1g07650 [MW - SP = 109.37 kDa]

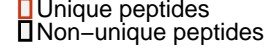
No. of times detected



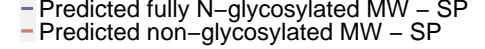
log(intensity)



Values from

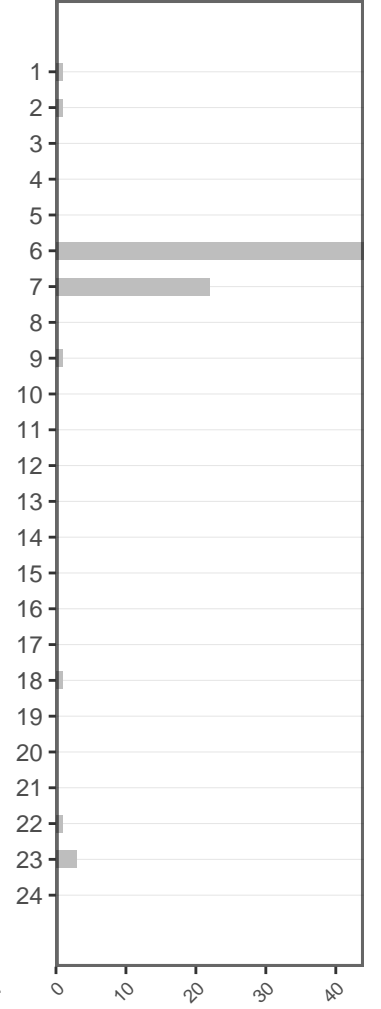
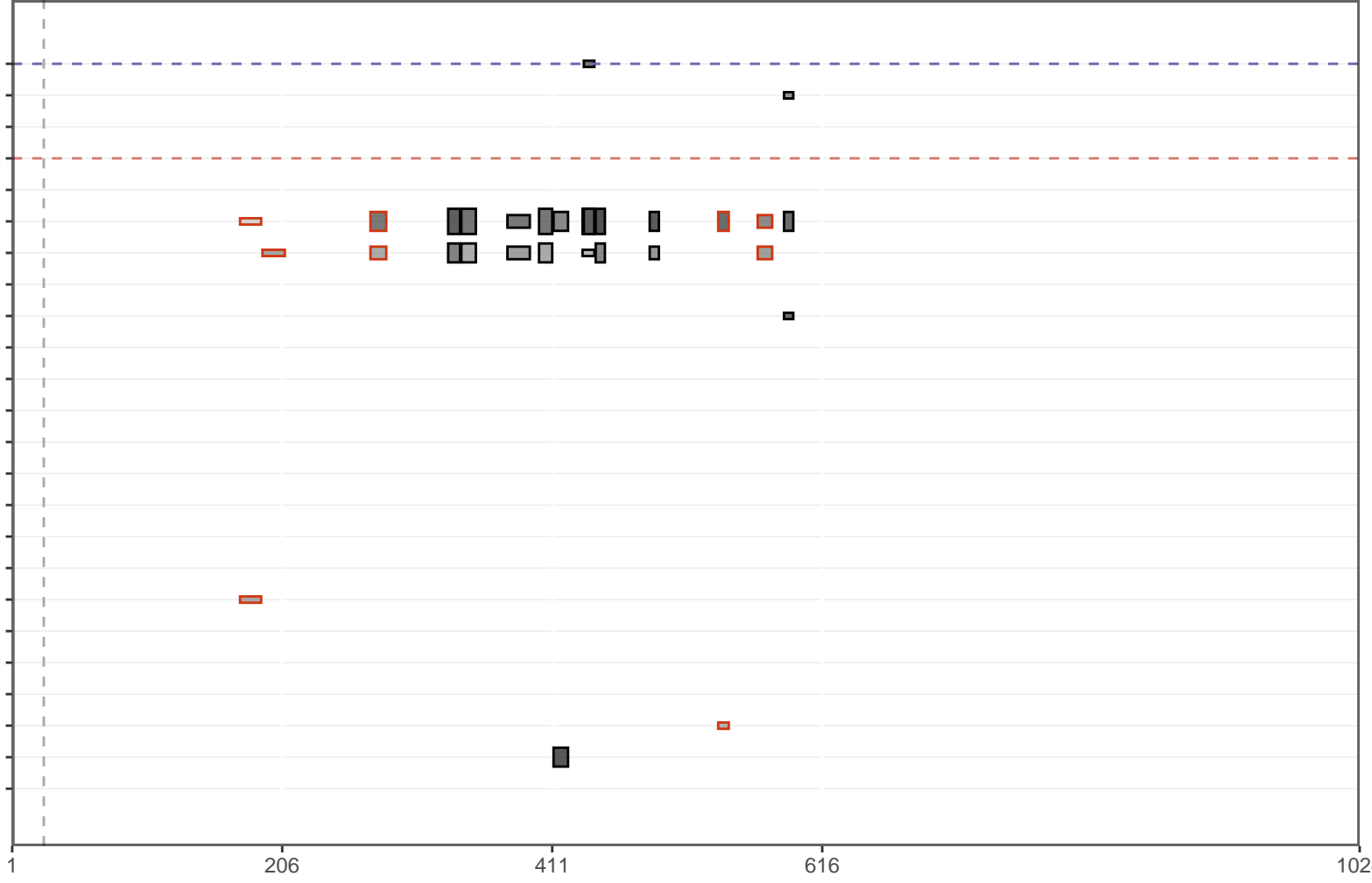
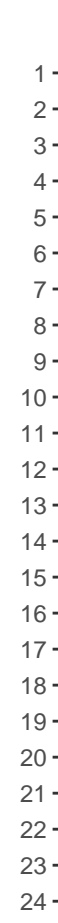
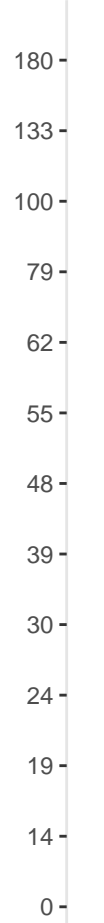


MW indication



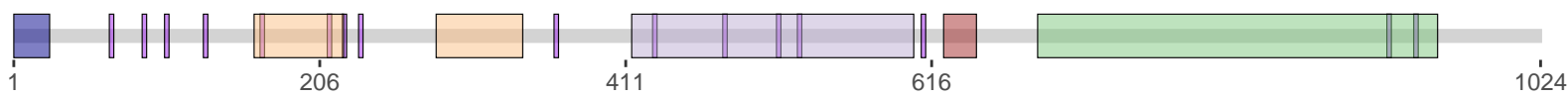
Molecular weight

Gel Slice



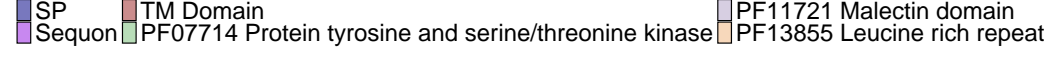
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LSLTYYGCLMNGNFTVKLHFAEIFFNDTSFNLSGERIFDVLGKLLKDFNIAEAGGPKPKVKTFSAAVTSHTLKHFFWAGKGTGIPVRGVYGPLSAISVDPNFTPLPATGRKIHVGLGAGAGSLFLILIGLKYTGCPGKVKSAKELGGDLGAGLFLRQKKAATKDFDPANKKGGEGGFSVYKGLLSDGTVAHWKGLSBSKSKQGTREFLNEVGMISAVQHPNGLVLYGGCGDGNLLVVEYVMENKCVSRALFGKGPVYKMLDWPTRKICLGIARGLAYLH

NbL15g22250.1 protein_STRICTOSIDINE_SYNTHASE-LIKE_10-like [MW – SP = 35.46 kDa]

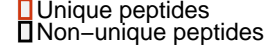
No. of times detected



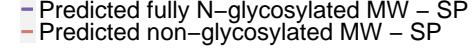
log(intensity)



Values from



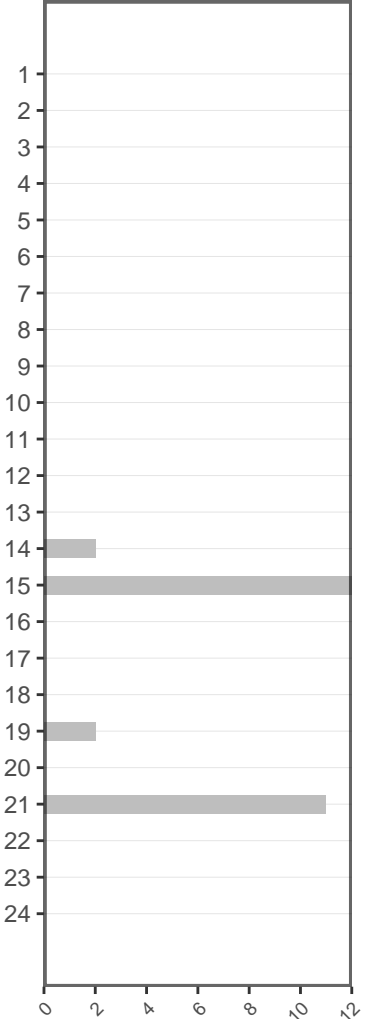
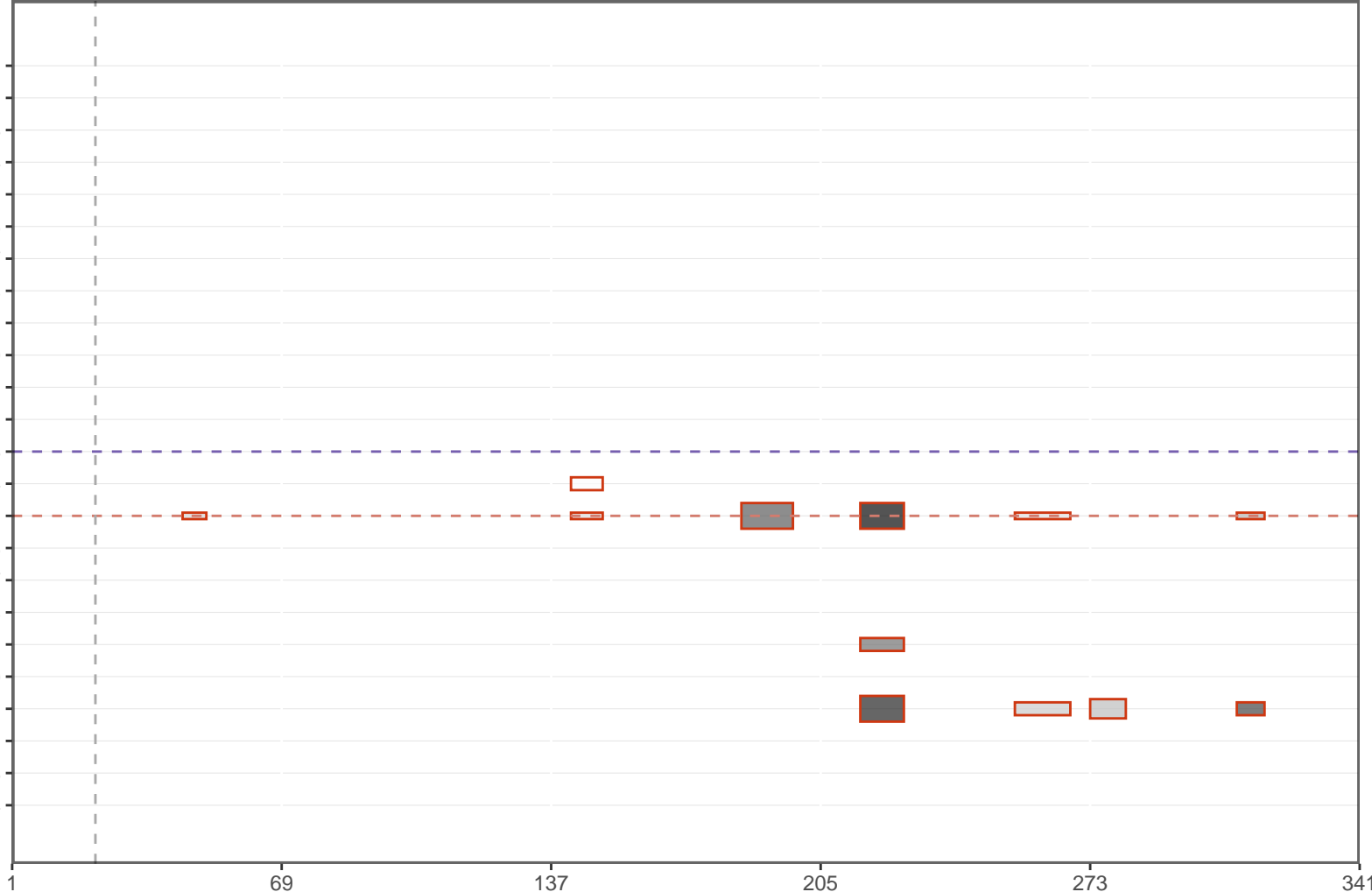
MW indication



Molecular weight

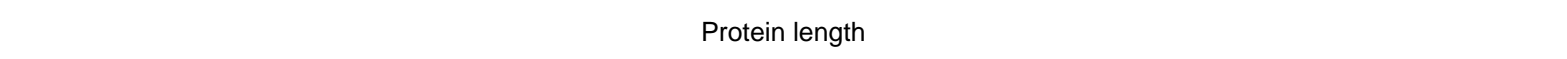


Gel Slice

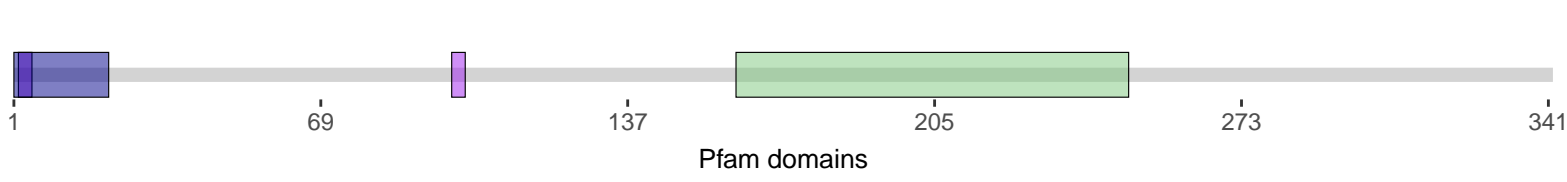


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

MTNDDIDNQNIVYFTDSSTKYGRREFFAFAFENGDTGRMLKMKDKSTKVTLLRGLAFANGVALNKDRSFLVSETNFRIRRWKGGVAGRHDIFADVPGFFDNRIRNSRGEFWALNKAATAKLETEGRMLEVLEDEEGKTLRDLRSGVVEKFKGLWFGVVTMPFLGVYGLFSSL*

NbL15g22220.1 probable_glutathione_S-transferase [MW = 25.6 kDa]

No. of times detected



log(intensity)



Values from



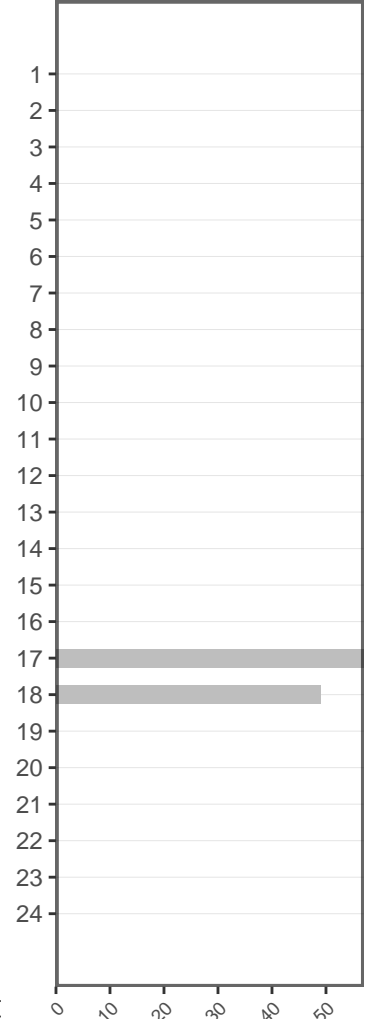
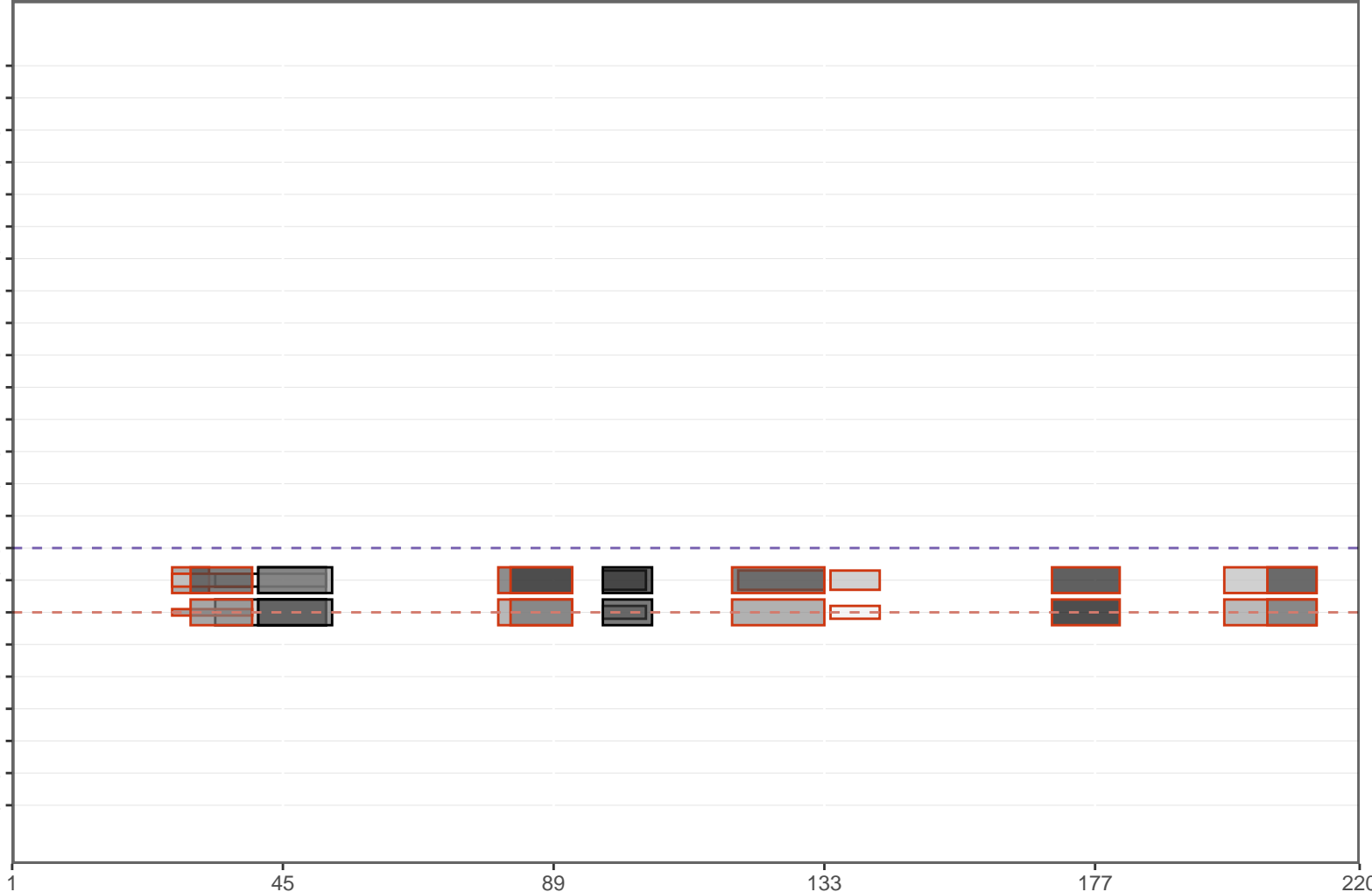
MW indication



Molecular weight



Gel Slice



Protein length

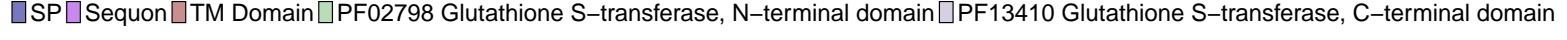


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VADYIDKKYDAGRKRWTTTKKEDQEAANKFEIKGKLELEGLGKPKYFGSGSGFVDMALIPYYGWFTYKFGNFSIEAEGPKRWAAKRCMQKEVSKSLADPKVYDFVYMLRGRFGIV

NbL15g22010.1 heme-binding_protein_2-like [MW = 28.61 kDa]

No. of times detected



log(intensity)



Values from



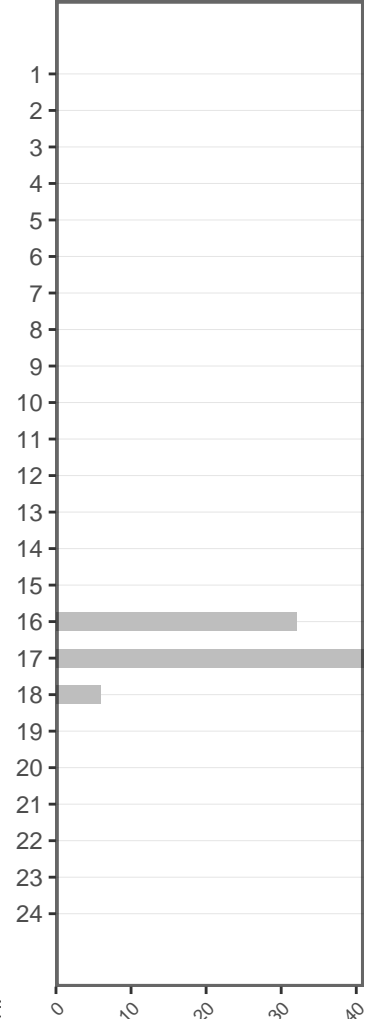
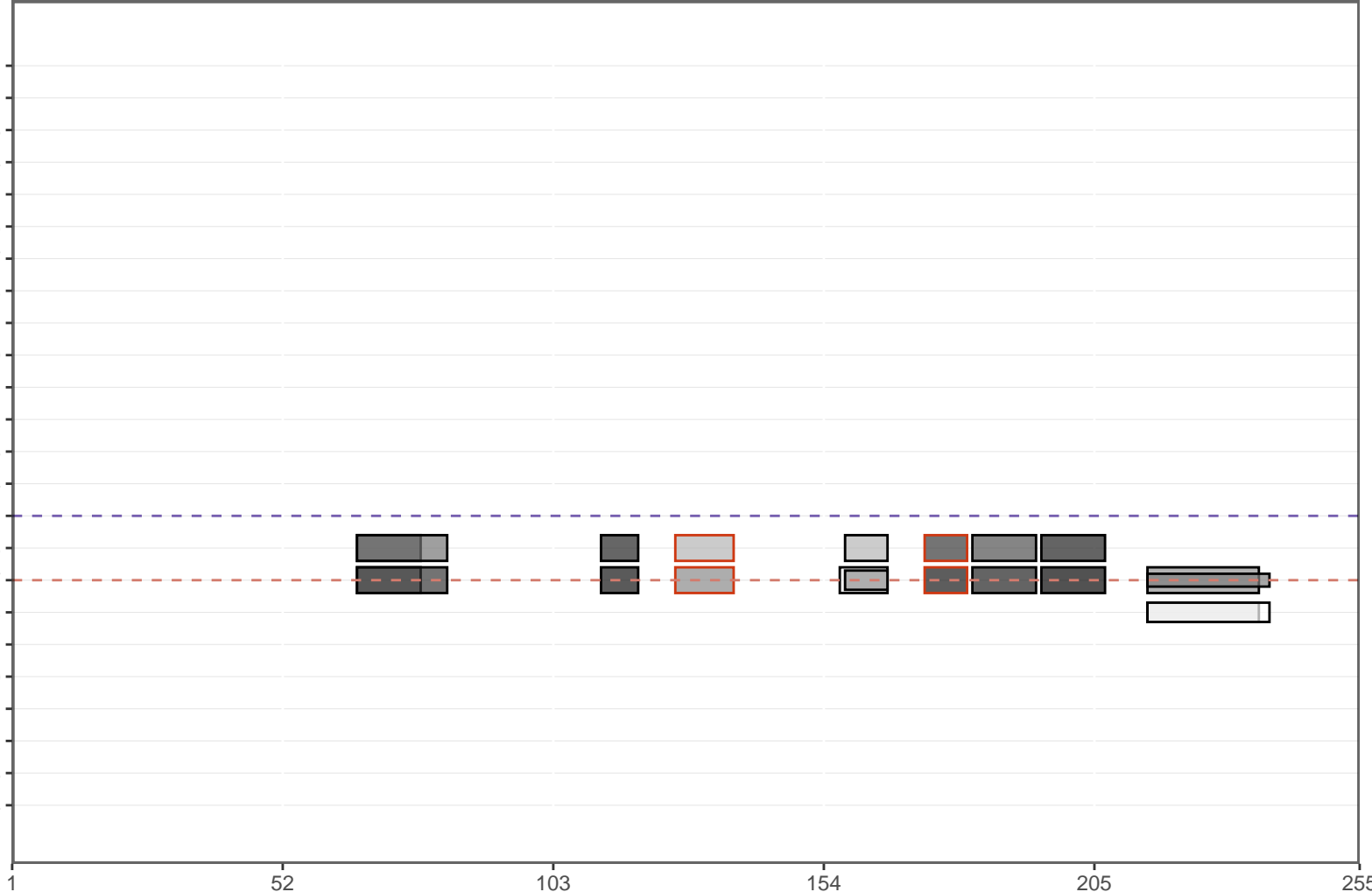
MW indication



Molecular weight



Gel Slice

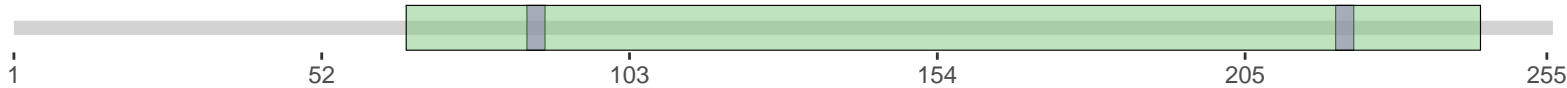


Protein length

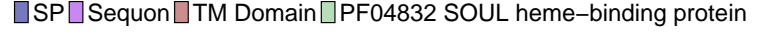


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

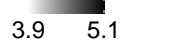
10GKNGYQEKEMTAPVTEVKPQDGFASSEVVFQYVPRKKNQPNPPAKGLHVGKWSNTYVAVRQGFGEVADVDVAKEAALSASADTKWAAVAEKSHAADNTMTVAGYNSPFPEKDRVNEWFTFLEKASAI

NbL15g21940.1 persulfide_dioxygenase_ETHE1_homolog_mitochondrial-like [MW = 32.36 kDa]

No. of times detected



log(intensity)



Values from



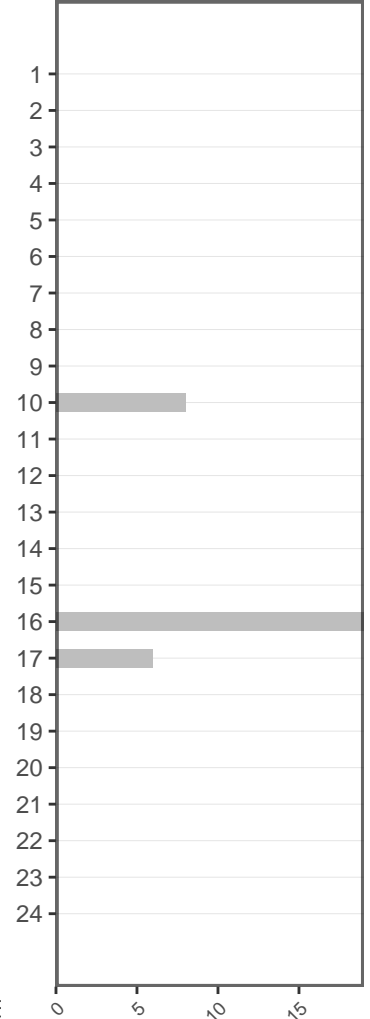
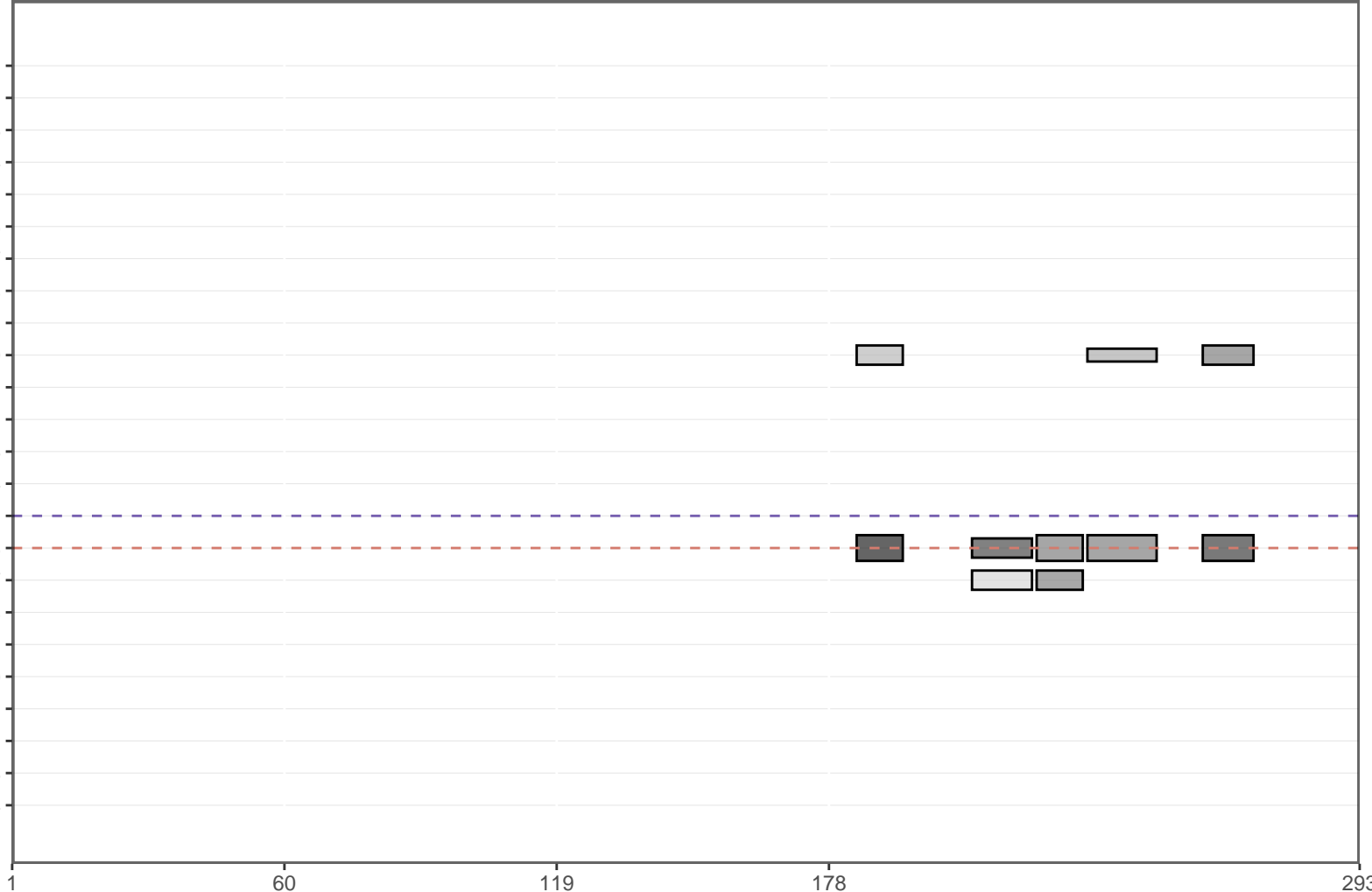
MW indication



Molecular weight

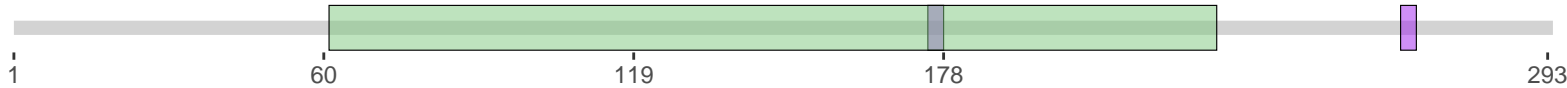


Gel Slice



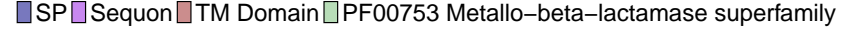
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IAKADLLVPEQDKIHFGDIFLEVRATPGHTLGGTLVYFGNGSNQHPHMAFTGDDALLIRGGRTDFGGGNSDKLYDSVHSGIFLPKDITLVYPAHDKHGFTVSTVGEEMQVNPRLKDKETKNNMQALNLSYFKMMMDVAVPAMVYGLGETKGEAG

NbL15g21900.1 solanesyl-diphosphate_synthase_3_chloroplastic [MW = 44.01 kDa]

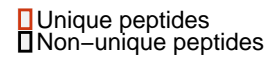
No. of times detected



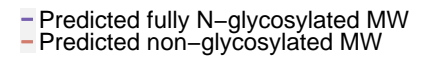
log(intensity)



Values from



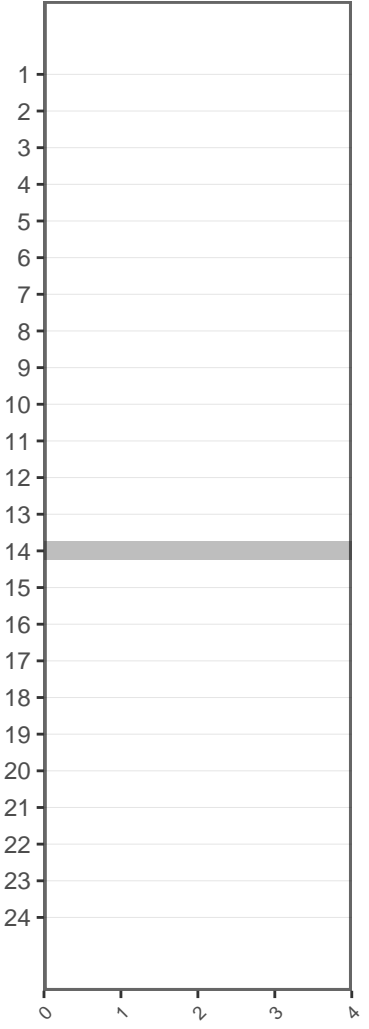
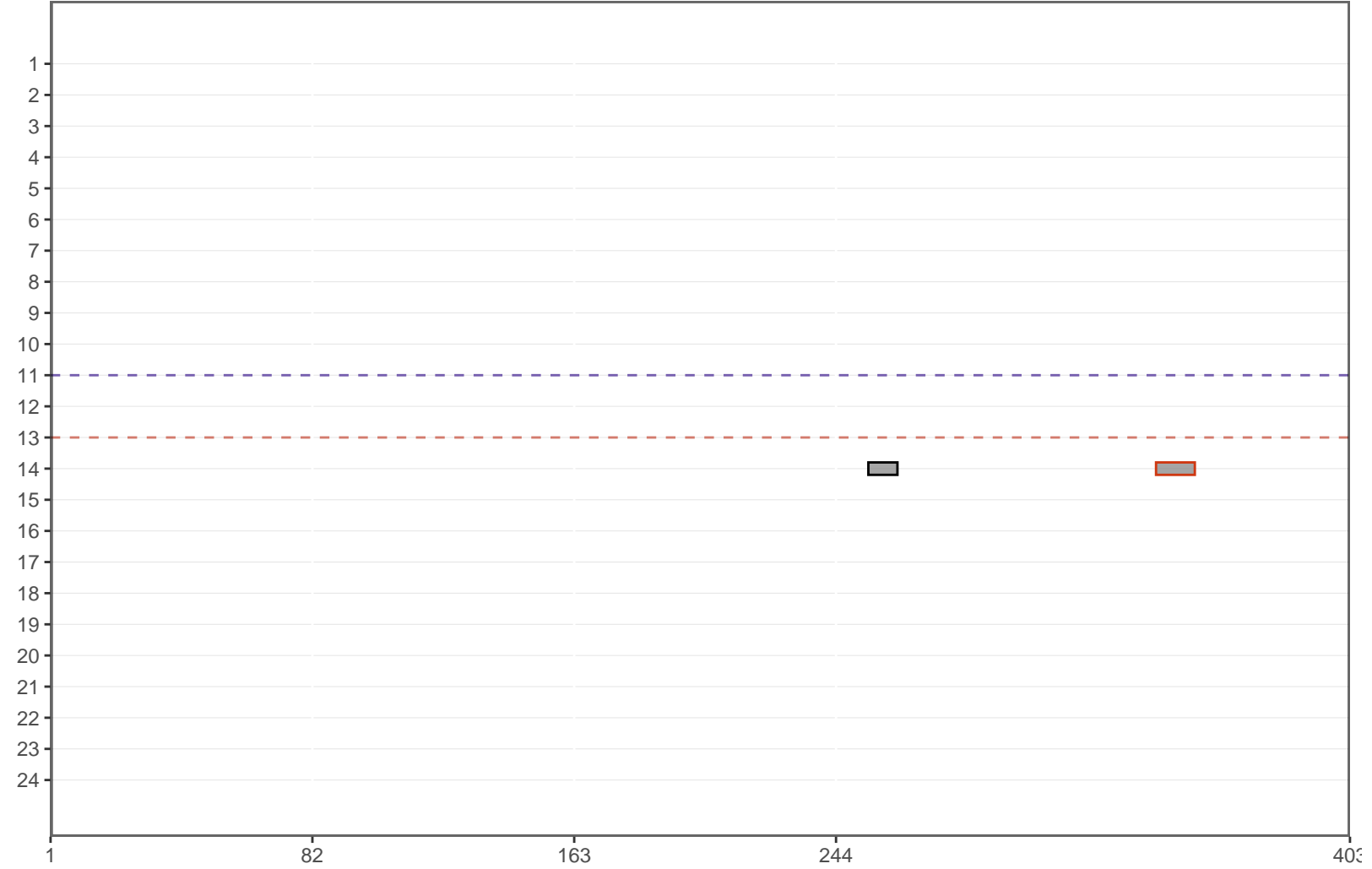
MW indication



Molecular weight

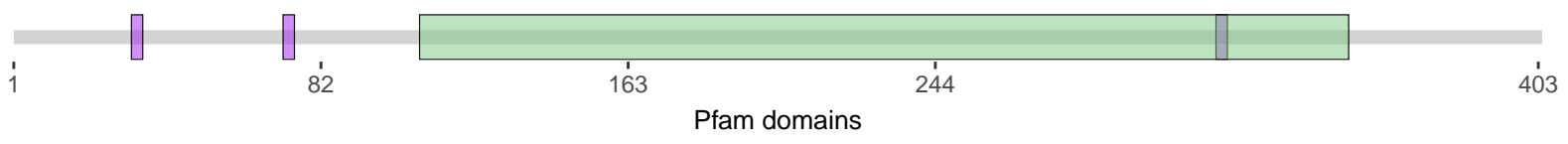


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ITRVAVLAGDFMFAQSSWYLANLENLEVKLGIVKDFASGEIKGASNLFDDGVELEEYLLKSYKTAISLAASTKGAIFSGVDRDISEQMPQYKNI-GLSFQVVDLIDFTGSAEQLGKPKAGSDLAKGNLTPVFALEKEPKLRNIESEFRDADLSEEAANLVKTTGGKRAADLAKEADLALGSLKLPSSPFRALAEVWYKLERIE

NbL15g21850.1 peptide_methionine_sulfoxide_reductase_B1_chloroplastic-like [MW = 25.75 kDa]

No. of times detected



log(intensity)



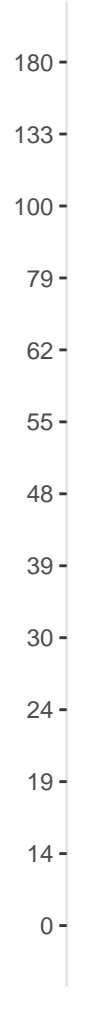
Values from



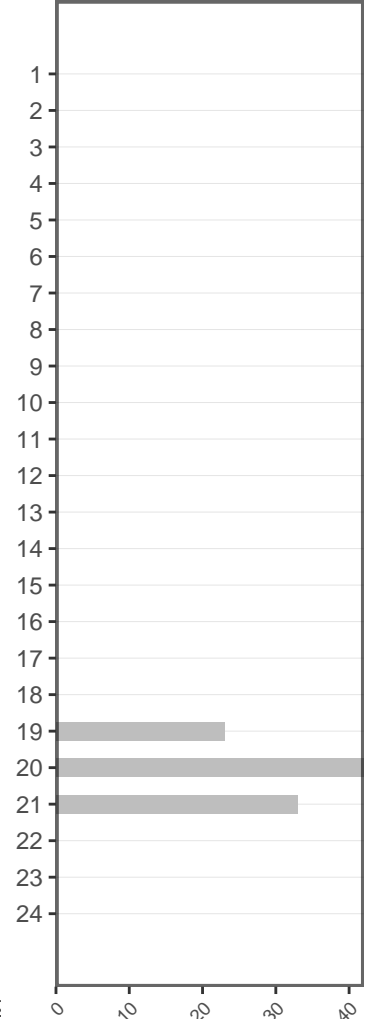
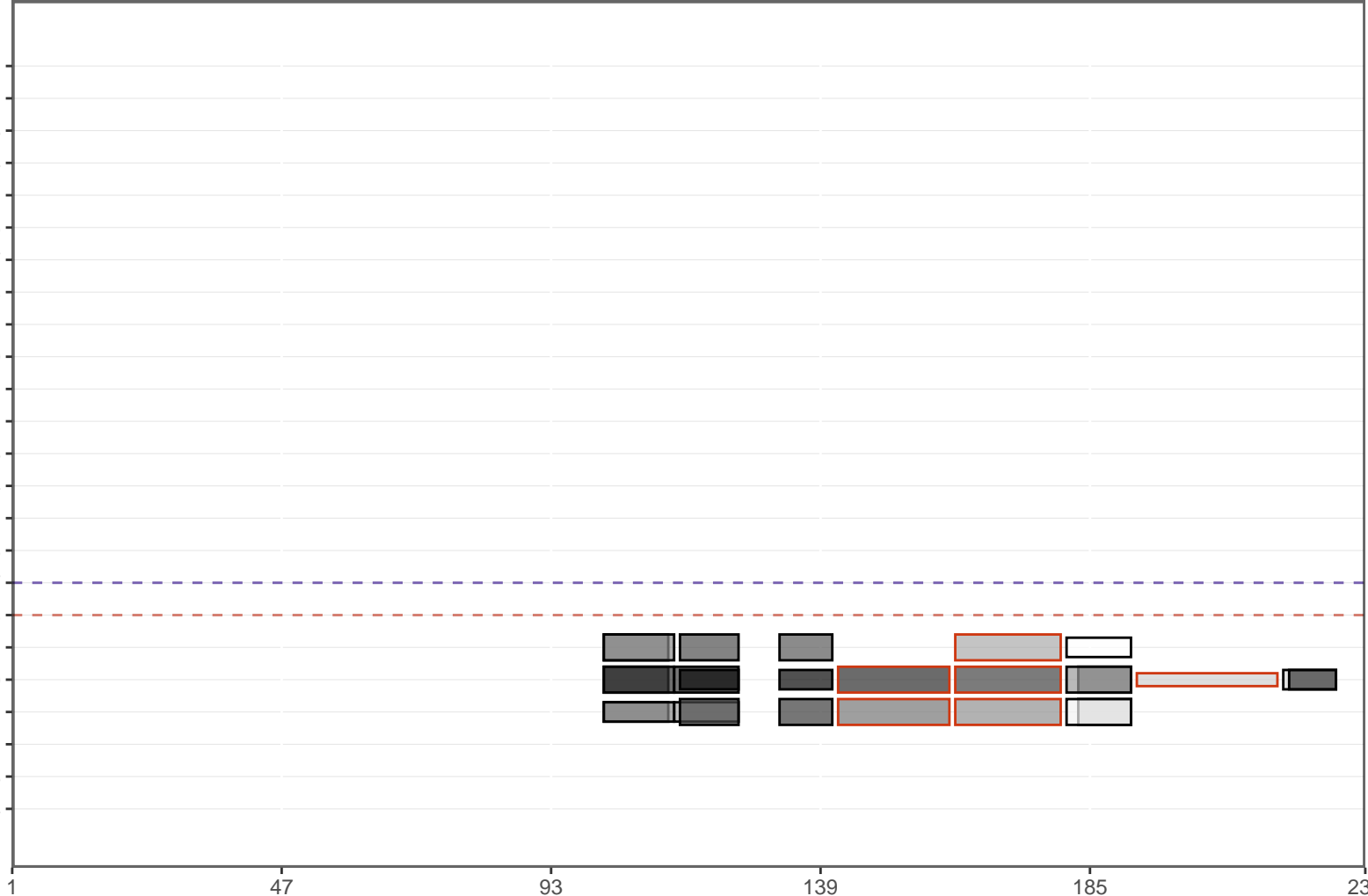
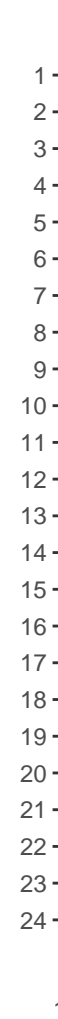
MW indication



Molecular weight

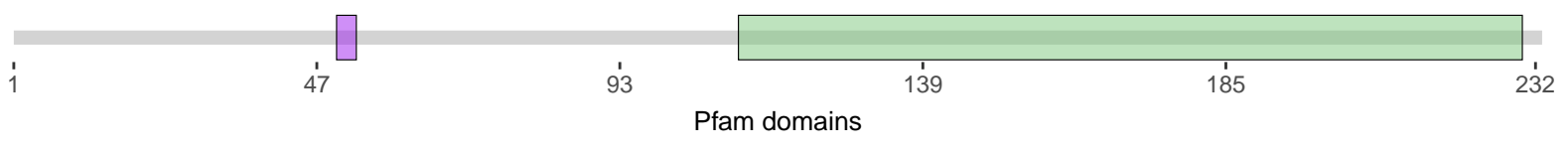


Gel Slice



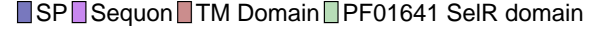
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SSVSDSEVWRKQLTNEGFVTRKGTGERAFTGEVWNTKTPGTYHGVCGDPLFESESTKFDGSGTWPEYVYQFVQNNVSKMKLSIFMPRGEVWCAVGDALHGHVFDGPPPTGKRYGINSAAALKKPKV

NbL15g21780.1 probable_rhamnose_biosynthetic_enzyme_1 [MW = 75.11 kDa]

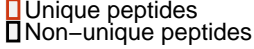
No. of times detected



log(intensity)



Values from

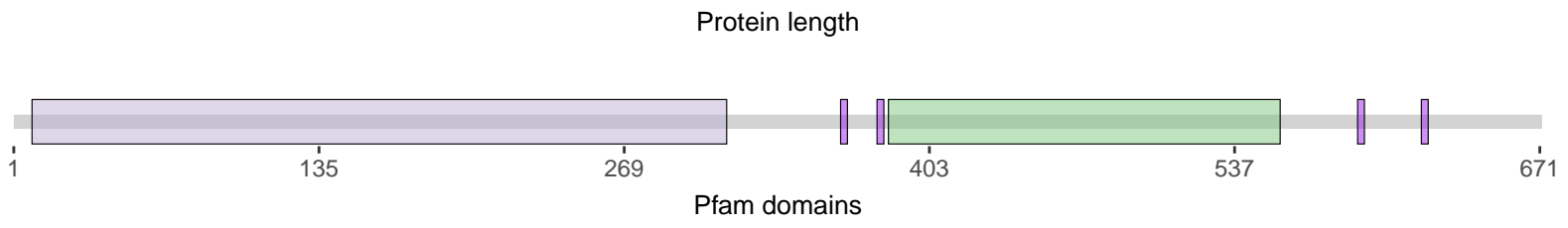
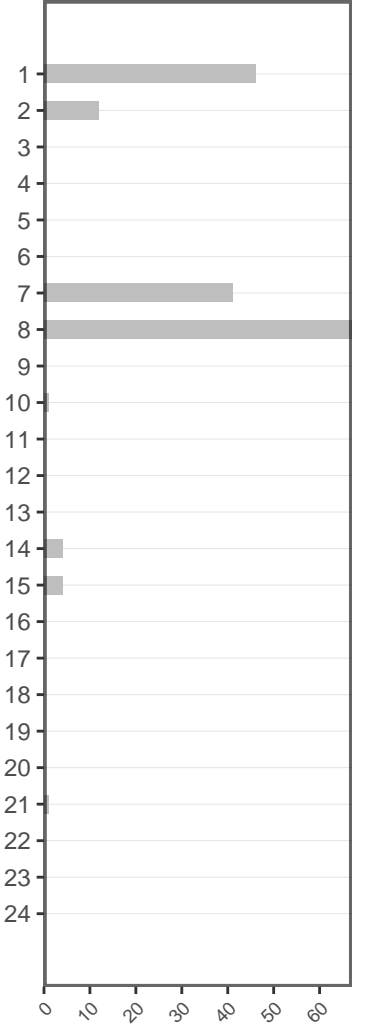
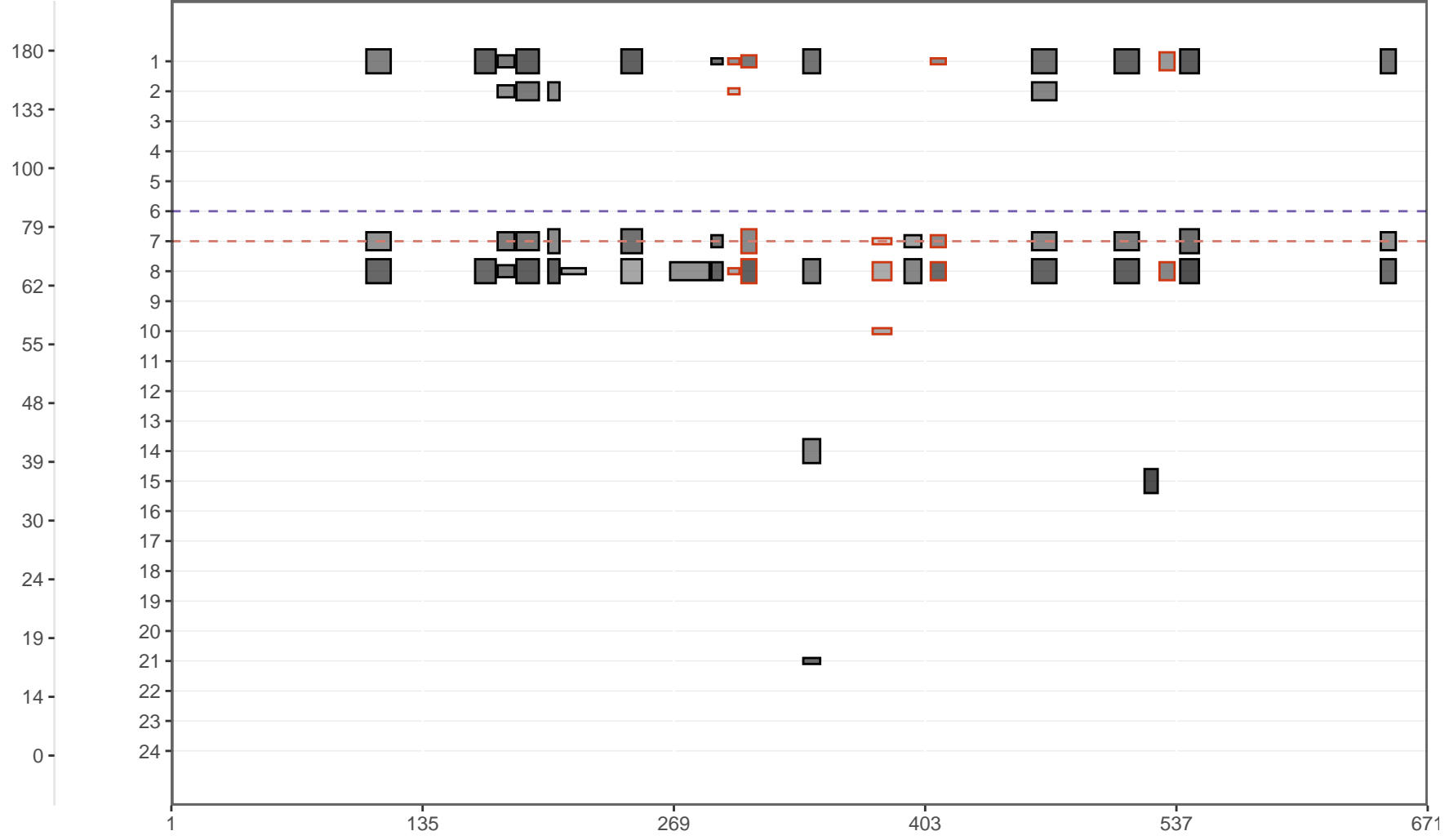


MW indication

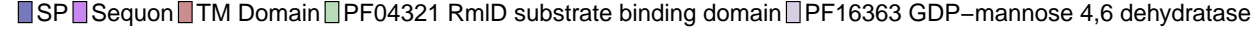


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

WWWGDSGALLPIPRMLMMPGGVGERGAEKDDSGSGEGSGNPNQTRMVAIPASKIGNPPKSPKFLYRGTGWSGLLGLKCEKGIPYDQGRGRIGDRSGLLADHAKKPTHFVNAAGVTRGRPNVDWGESHKETETRTNVAQTLNLDVCKEHLGMLLMNFATGCFEYDAHPEGSGSGFGKEEDTPNFAGSFGSKTKAMVEELLKEGENVCTLRVMPSSDLSNPRNFHTKISRNYKYVNFPMSTLDELLEPISIMAKRNLKGIWVFNTPGVSHNEILEMYKYYKPDF

NbL15g21490.1 secreted_glycoprotein_EP1-like [MW - SP = 31.36 kDa]

No. of times detected



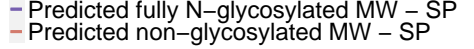
log(intensity)



Values from



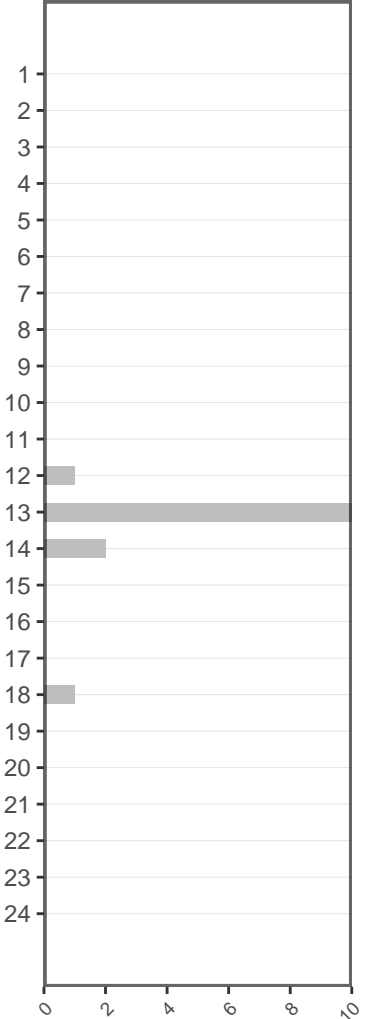
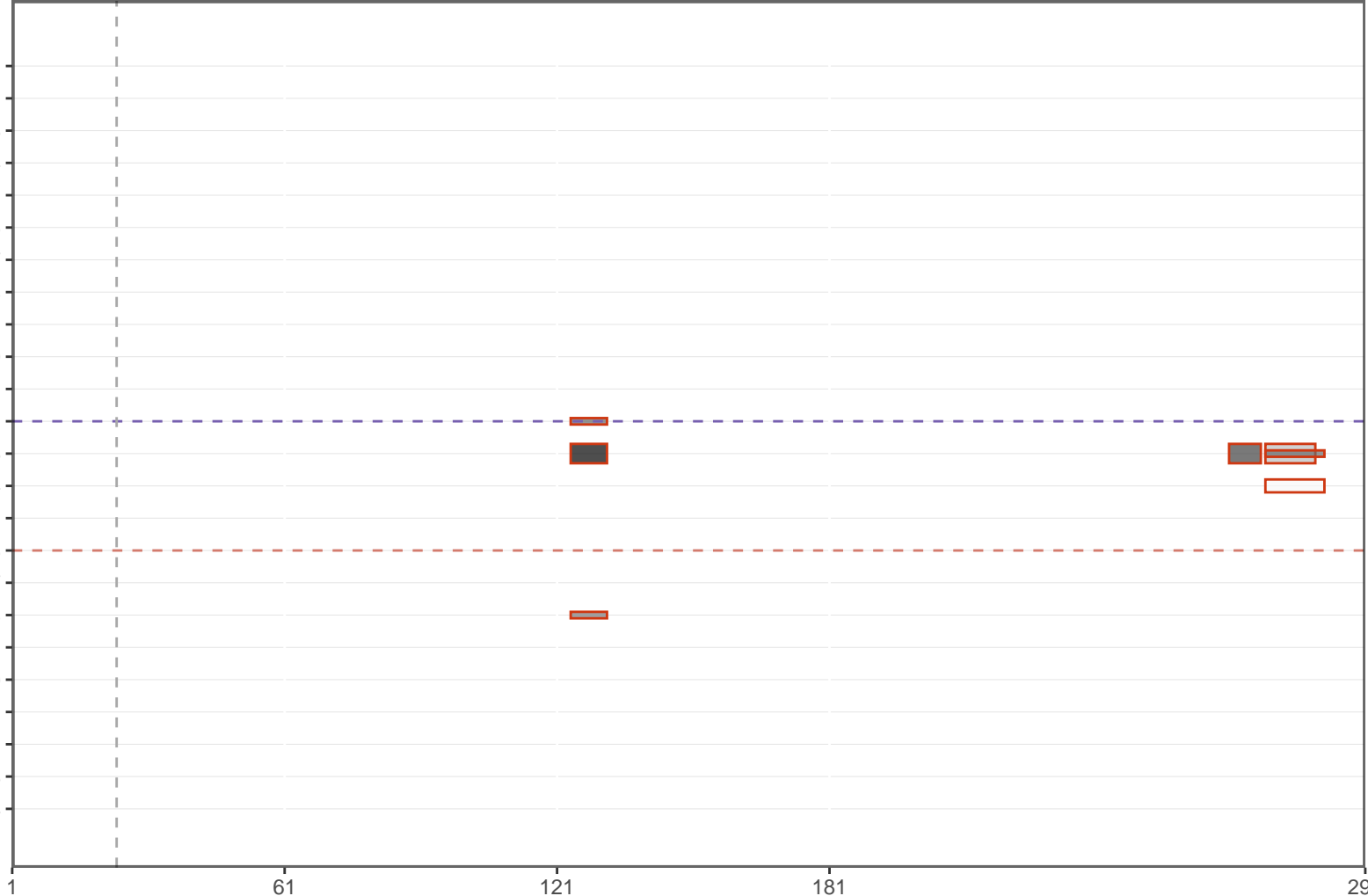
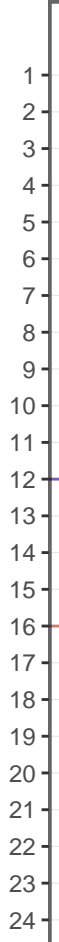
MW indication



Molecular weight



Gel Slice

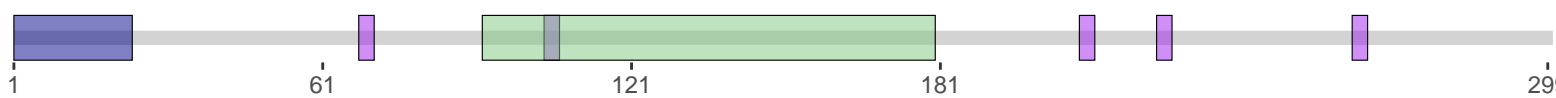


Protein length

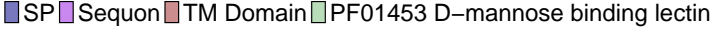


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

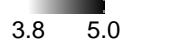
SGFKLLPQNGFYLDKSGKFWGSDHPDPTDLLVGGSLRISGPNKLVSRAGVKKNAANGPYSELVKPKFQGHYKTKLHVELAWFDKFNSTLESVKLNSGDRVKLQRLAKGSTRNSHVAFFEINTFTLYRLLEIDGNLRVYTFEEDKEEDRFRWRVYGMK

NbL15g21470.1 phosphoenolpyruvate_carboxylase-like [MW = 110.32 kDa]

No. of times detected



log(intensity)



Values from



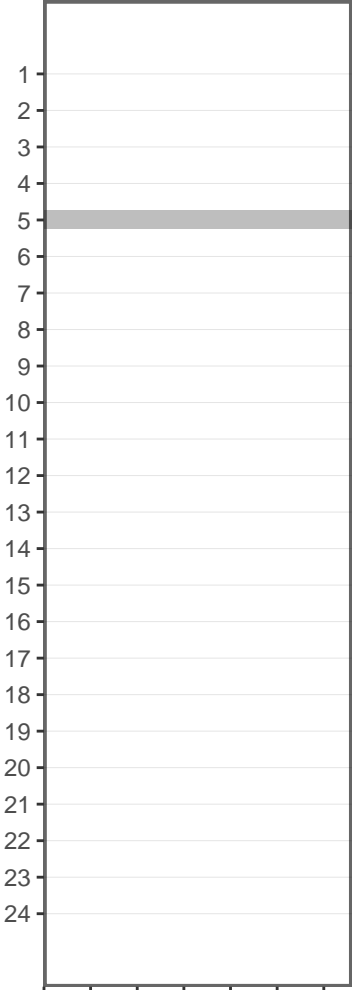
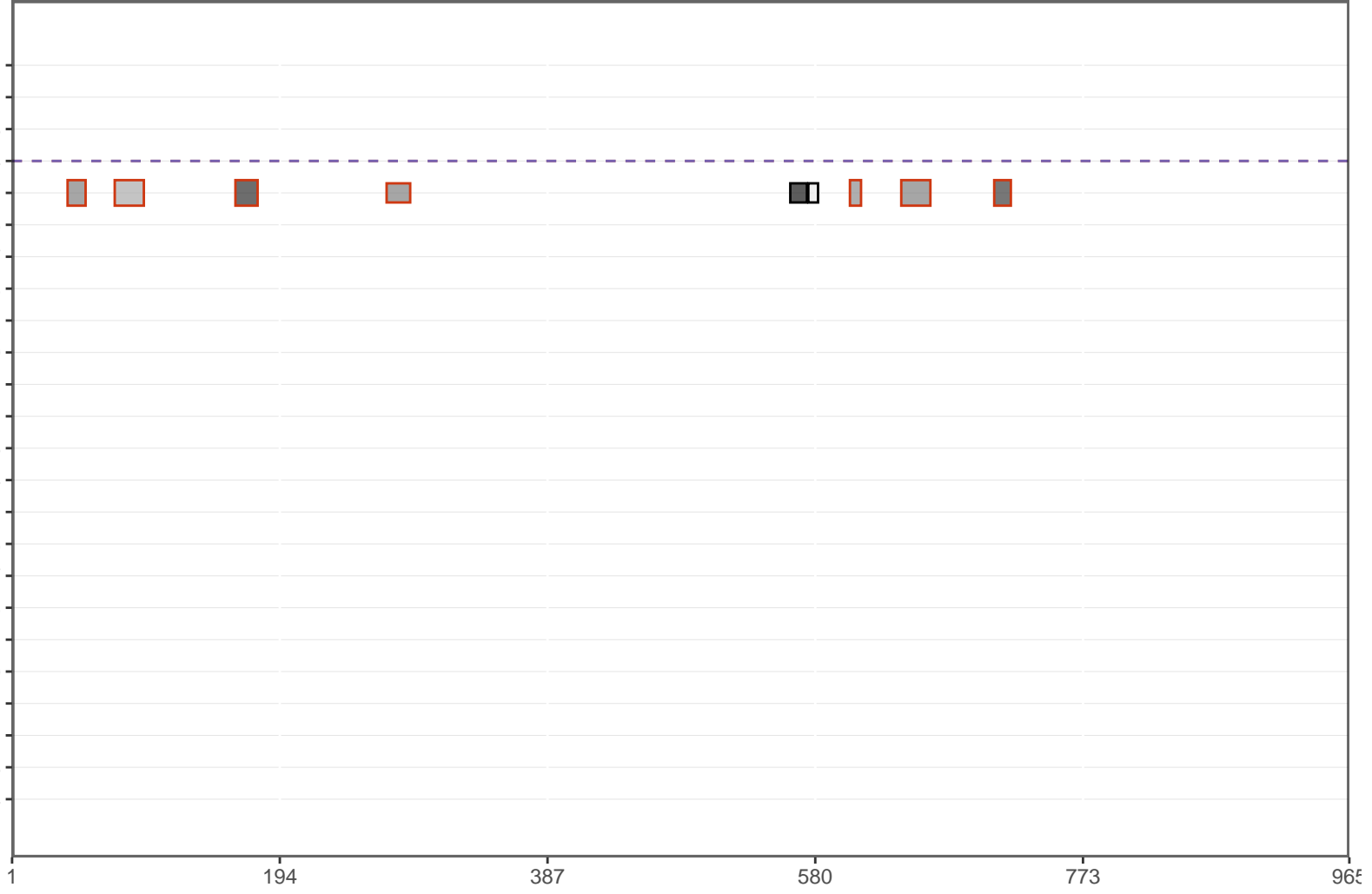
MW indication



Molecular weight

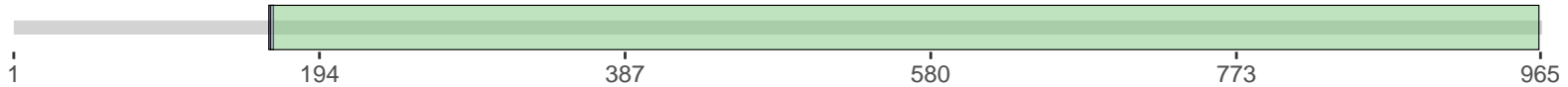


Gel Slice



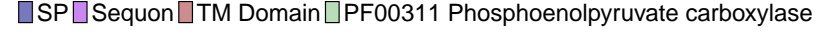
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ISYREWSEHRQEWLLSELSGKRPLFGDLPKTEIEAEVLDFHVVSELPDQCFGAVHISMATAPSDVLAVELLQRECHVKRPLRVVPLFEKLDLEAPAAVAWVLFSEIWKYKRNKQGEVIMGYSDGKQDAGRMEAAWQLYKAQEEELKWKYKGVLTMFHGRGGTVGRGGSPSHLALSGPDDTQGGELRVTVQGEVIEQGFGEELHGFRTLGRFTSATLEHGDMNPLSPKPEWRALLDEIAWATEKYRSIVFKPRPFVEYFRLATPELEVGRMNGSRPSKRKPSGGII

NbL15g21320.1 uncharacterized_exonuclease_domain-containing_protein_At3g15140-like [MW = 36.71 kDa]

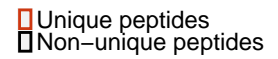
No. of times detected



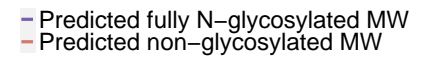
log(intensity)



Values from



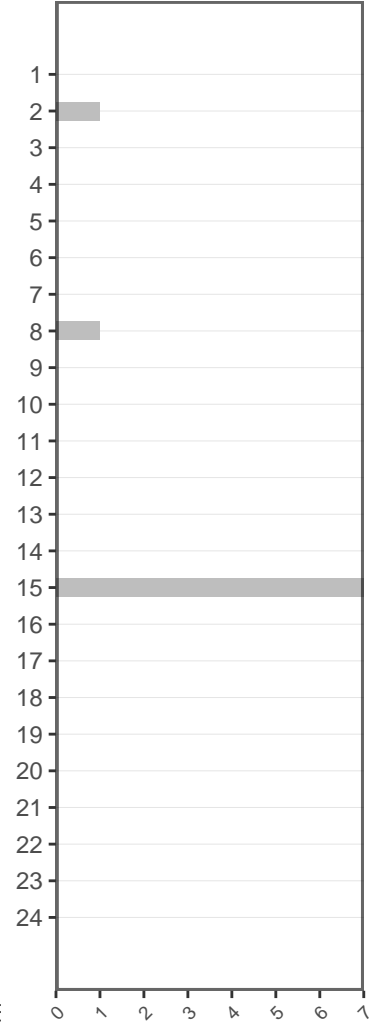
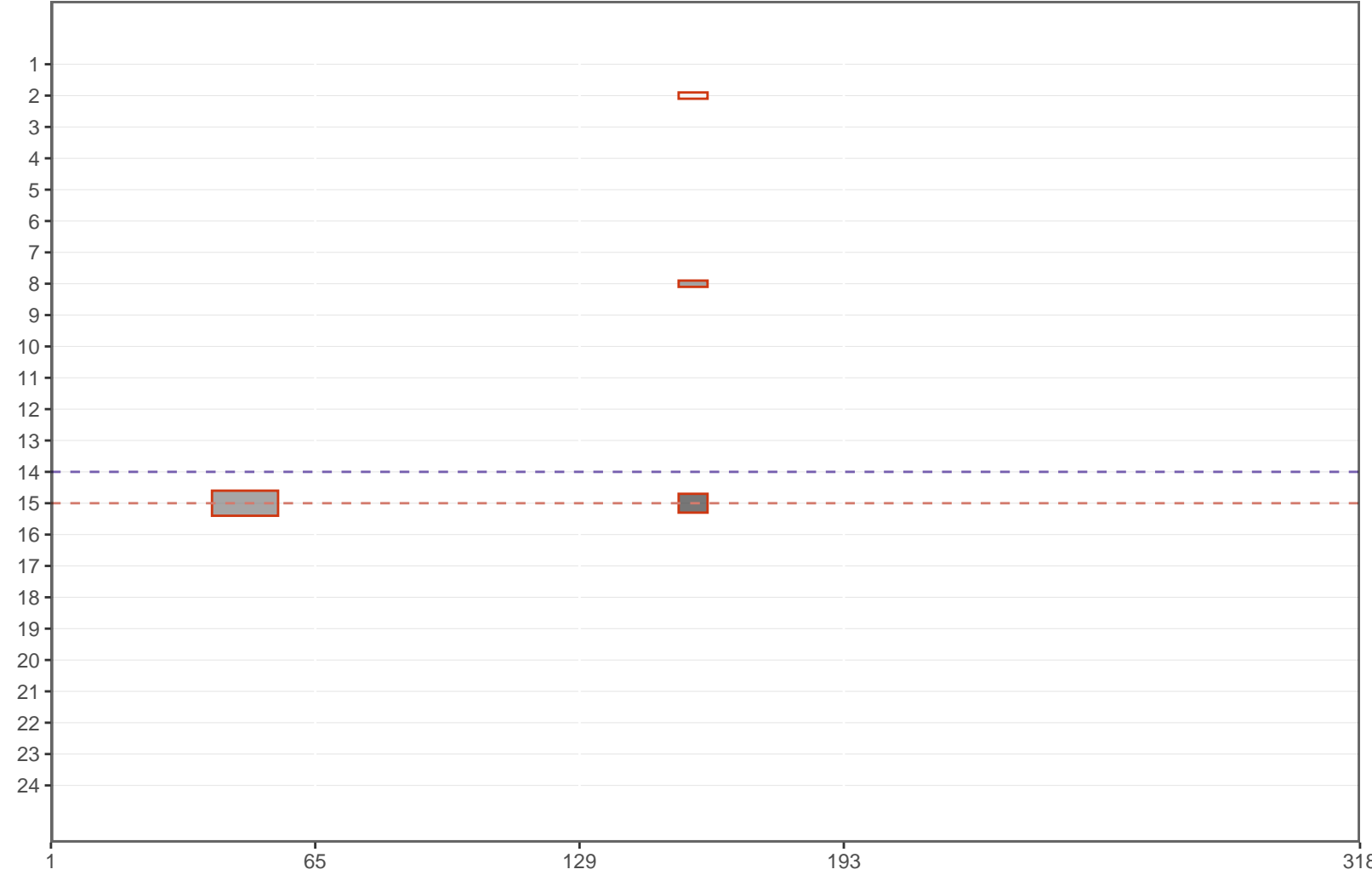
MW indication



Molecular weight

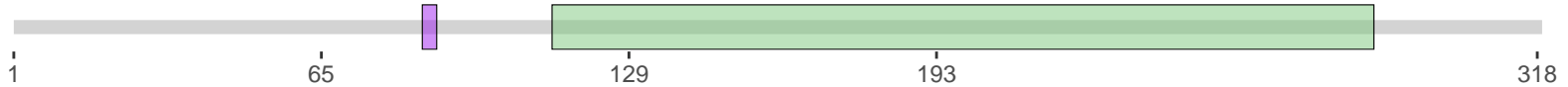


Gel Slice



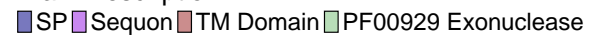
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MHEDRINIEYEGCKYKLGVDKRWVHDTAIPFGEVIEGFEVWLGSRQLWRNEPQGGLNKAAFVTOGNWDLKTKYVGGGKVGATLPPYMEWLNKDFLNFYKRRKAGMLSMRELGMPLLGSHHLGIDDANKIARVLGHMLSDGALVGITARRNPHSPKVEYLFEDRIVY

NbL15g21250.1 30S_ribosomal_protein_S20_chloroplastic-like [MW = 20.44 kDa]

No. of times detected



log(intensity)



Values from



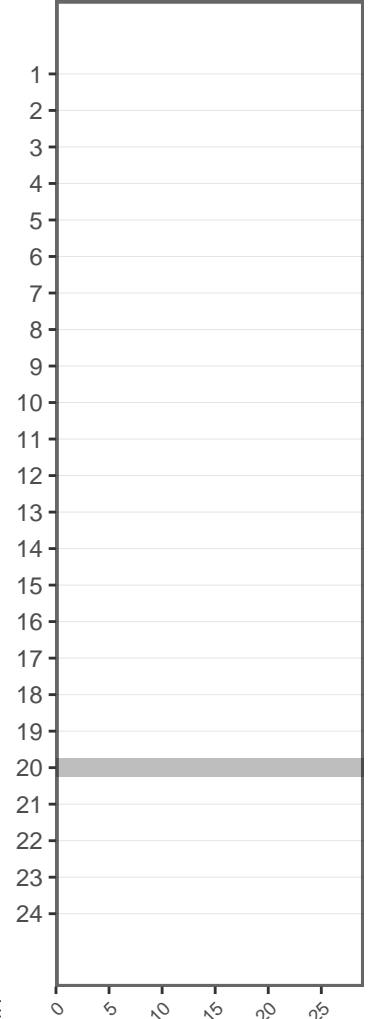
MW indication



Molecular weight



Gel Slice

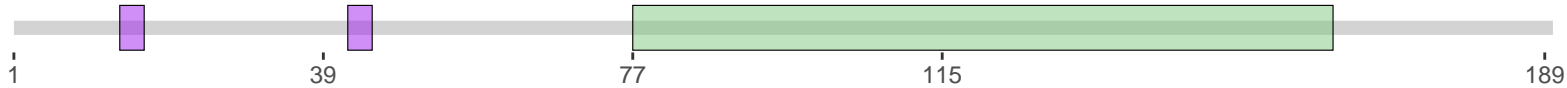


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

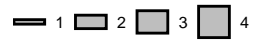


Protein sequence:

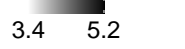
KRARRQAEKRRLYNNAKKSEVKTMRMKTVELEALDTLKKKTDAGSEEVSEVKLAEAYSAIDKAVKAGSLHRNTGARRKSRLLARRKKAVEHGHGWVYVMPVEEPLVATA*

NbL15g21170.1 probable_protein_phosphatase_2C_39 [MW = 31.01 kDa]

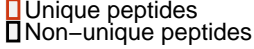
No. of times detected



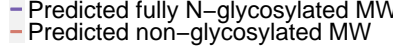
log(intensity)



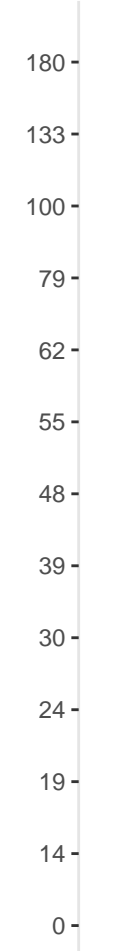
Values from



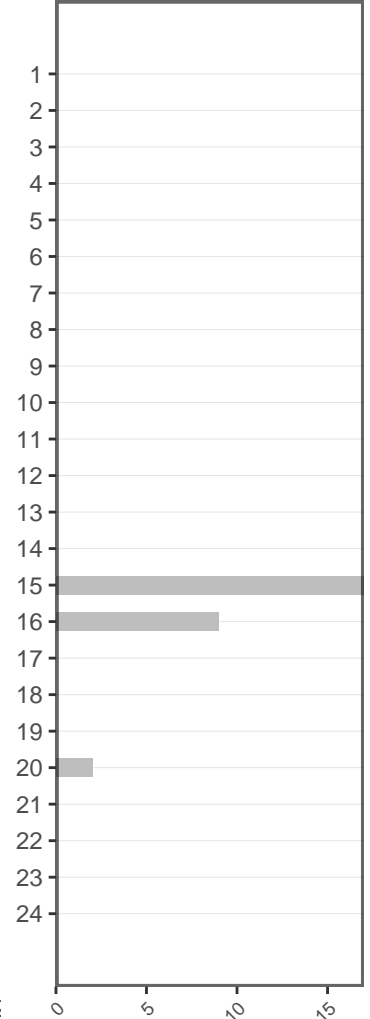
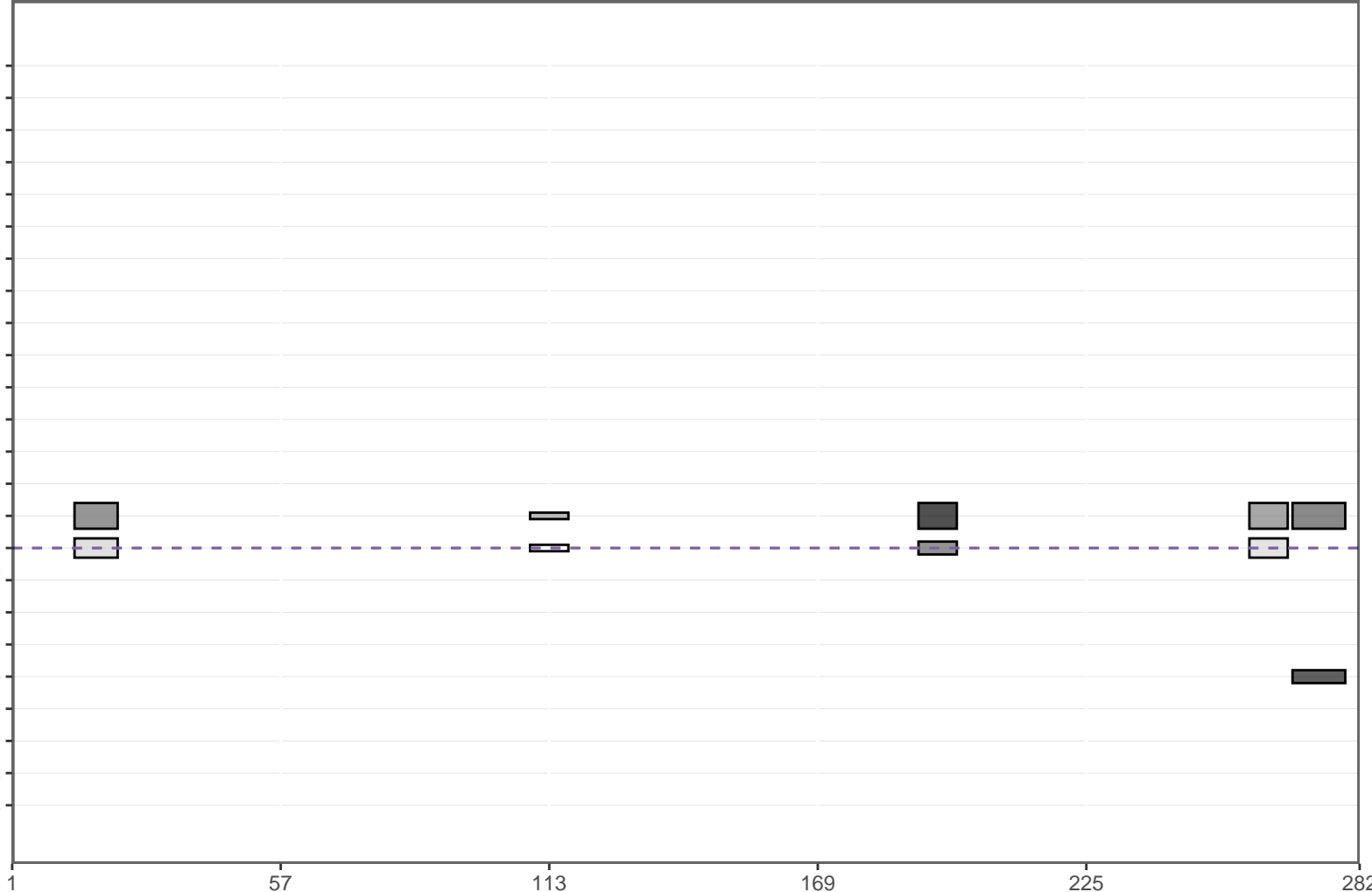
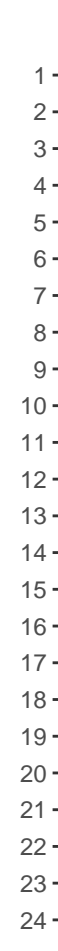
MW indication



Molecular weight

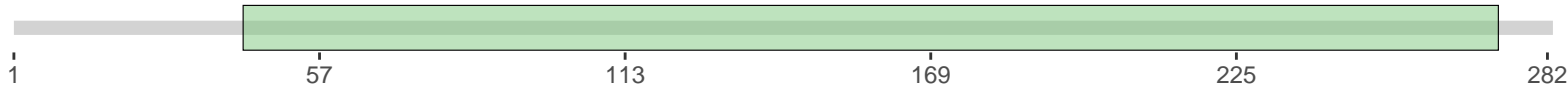


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

V/TALINGQKLVVAVNGDSRAVIGENGVAKQLSDIHEPGRERKIKIEDRGGFVFNFPFGDVPRIVDGQLAVARAFGDKLKMHLSEFPDVMVELIDENTEFILIASDGVVWVLSNQEAEADGKIKSINDARSAAKHLNEQALAGSTDDISGVVRFQ

NbL15g21150.1 3-hydroxybutyryl-CoA dehydrogenase [MW = 32.05 kDa]

No. of times detected



log(intensity)



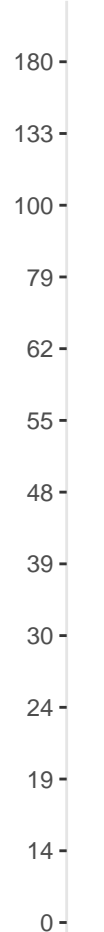
Values from



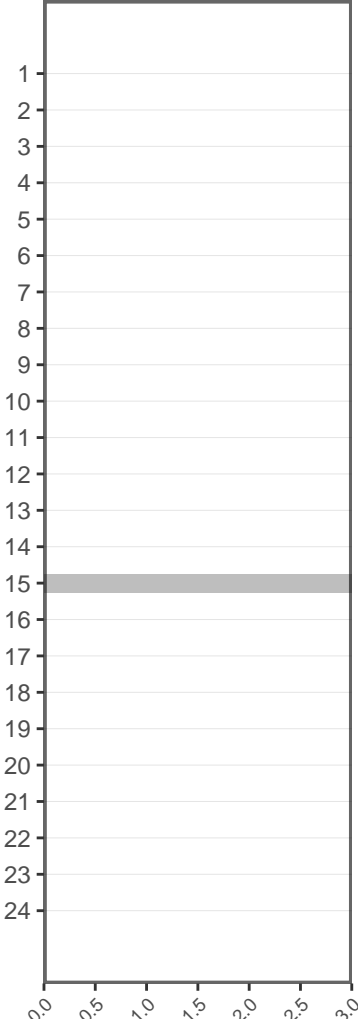
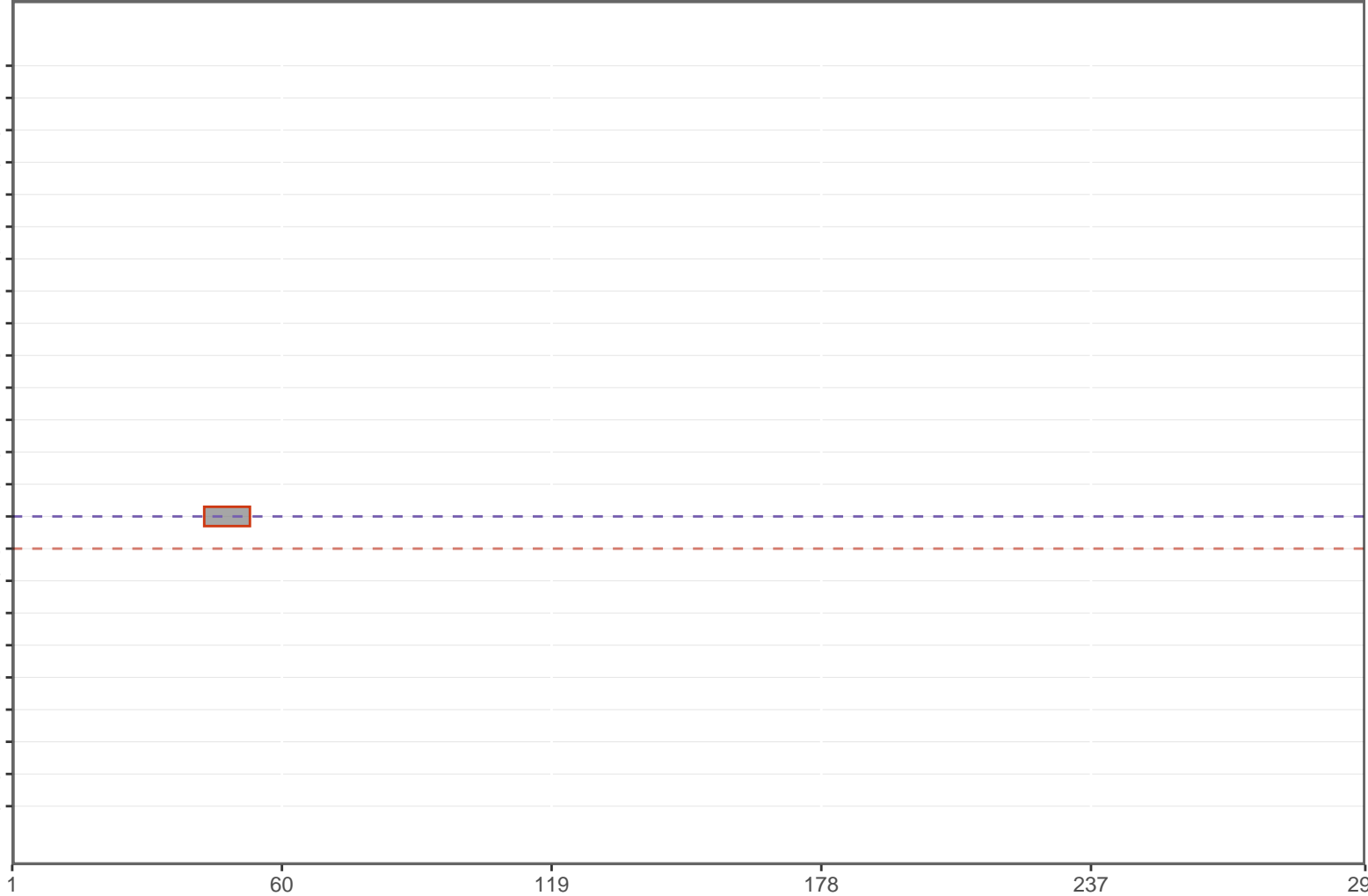
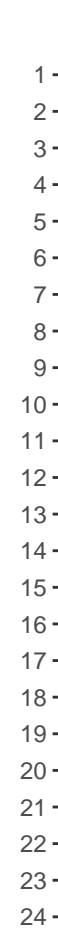
MW indication



Molecular weight

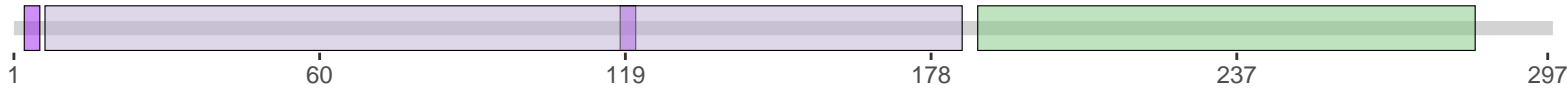


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

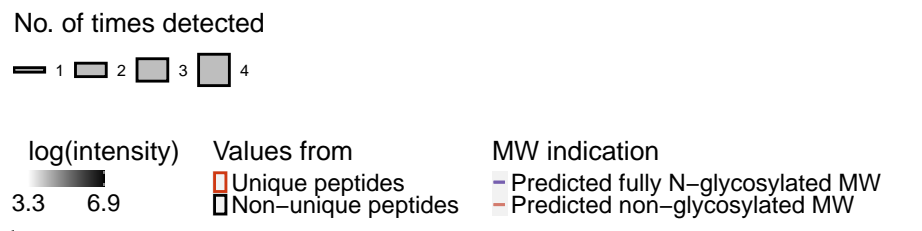
Pfam Description

- SP
- Sequon
- TM Domain
- PF00725 3-hydroxyacyl-CoA dehydrogenase, C-terminal domain
- PF02737 3-hydroxyacyl-CoA dehydrogenase, NAD binding domain

Protein sequence:

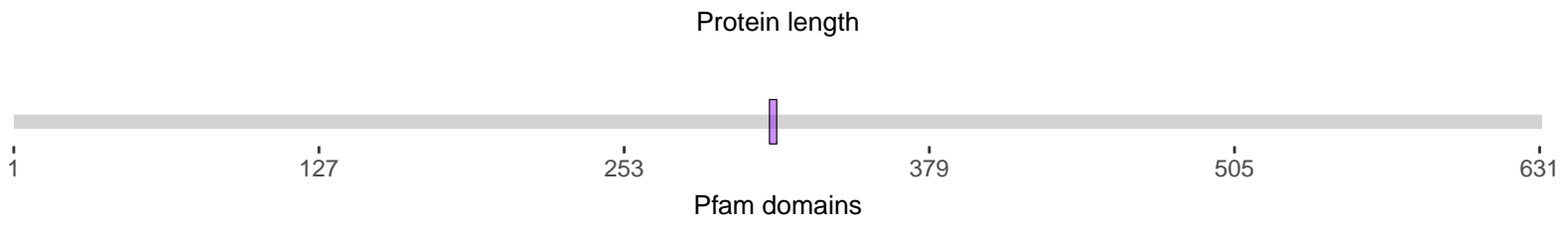
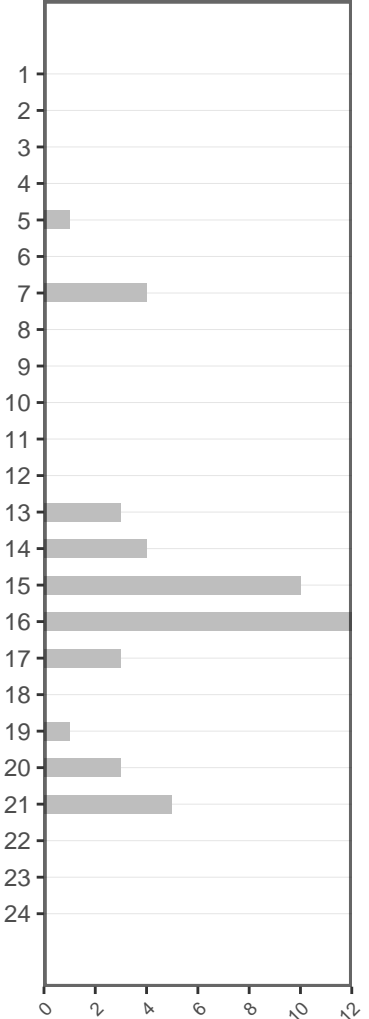
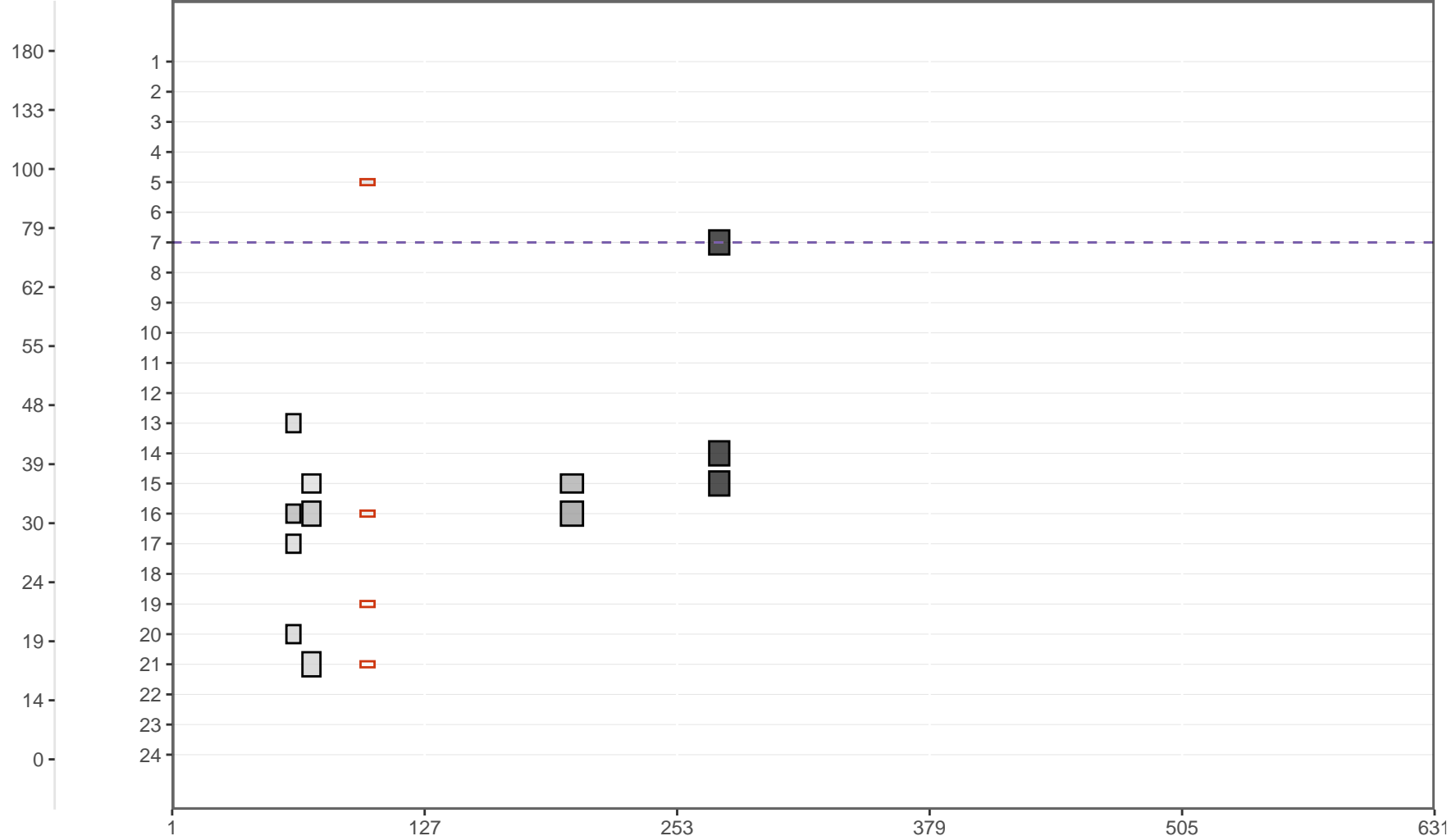
VIGMIFMNPPIIMKLVIEHIGADTSEDFYATKGLAERFGKTVICGDDYSGFVNRILMPMINEAFHLYTGVATKEDIDTGMILGTNHFPMGPLELADFIGLDVLSMKVLAHVLGDDKYPCLLVQYVDAGRLLGKRGVYDYSAAADTKGPRLL

NbL15g21060.1 proton_pump-interactor_1-like [MW = 71.95 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain

Protein sequence:

.RKQREDGNSSFYGNINVLHKVWGLADQKIVKELKELSVTEVDFKMSLWGGKPKFRDDYERRLLQSLDIRQLSRDGRMRNPKDEKPVLPPEVPTVSRTEVFRANAKLVKEDHASVDAAAPVQKQEKSSKQFNDAVYKNTKRAEKKDVVDEEEIYGLKIPKINLNSKNEVDEATLKEMKKEEIAKTRQAMERKKLAEKAKAKAKAKAGLEAKKLEKEREKRRKRGKGGSSVADDEPTEETFLAEVVEEKEAENVETTAAPKVKARKENTVRHRRATRARGSELP

NbL15g20960.1 thioredoxin-1-like [MW = 19.74 kDa]

No. of times detected



log(intensity)



Values from



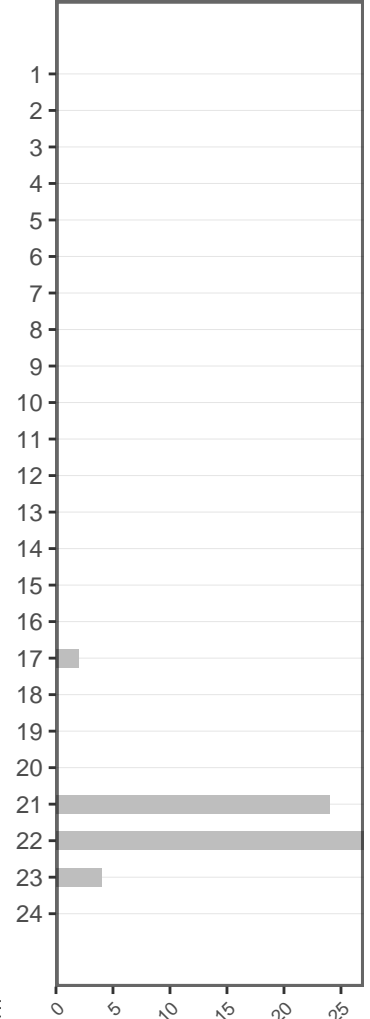
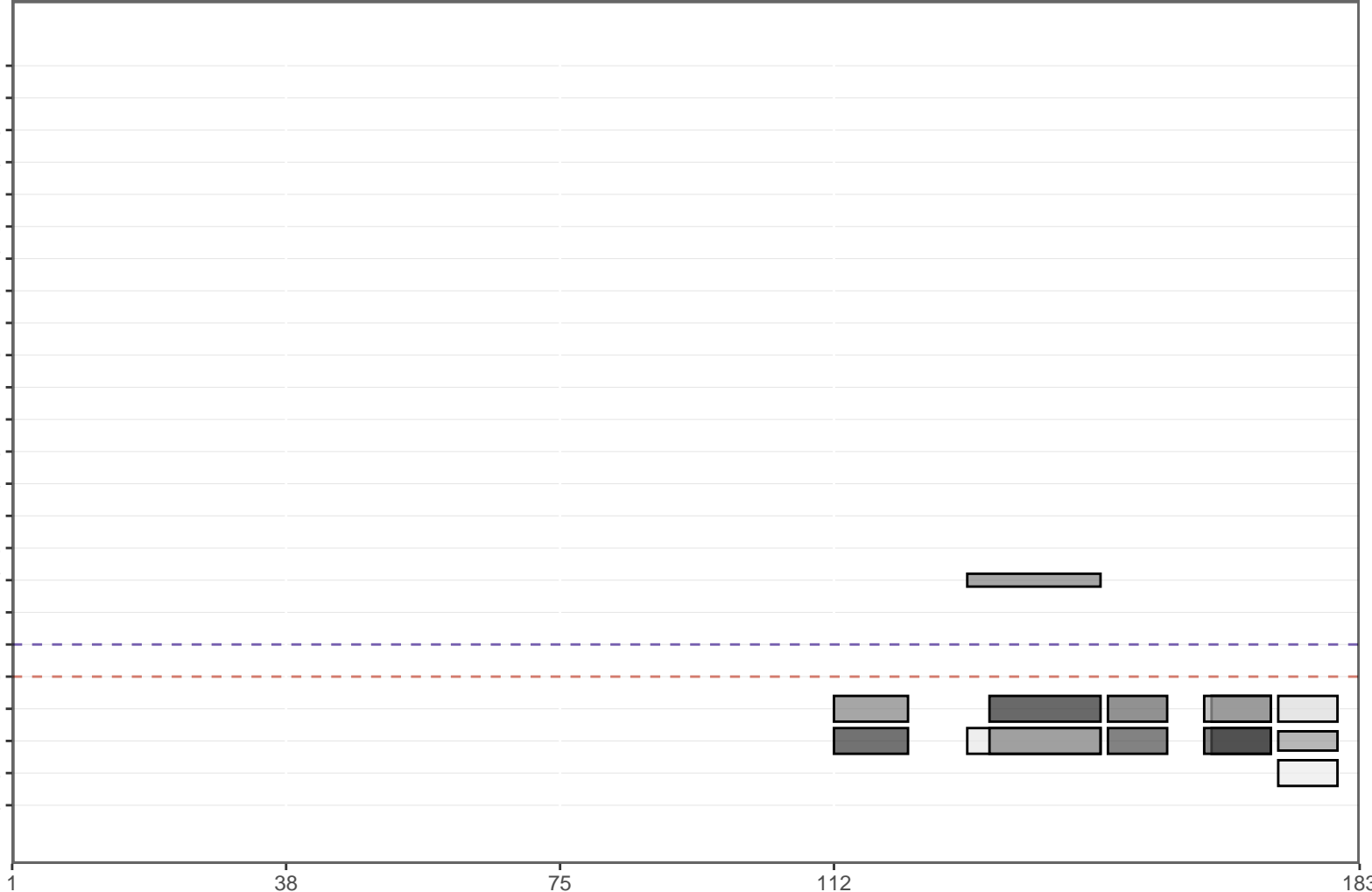
MW indication



Molecular weight



Gel Slice

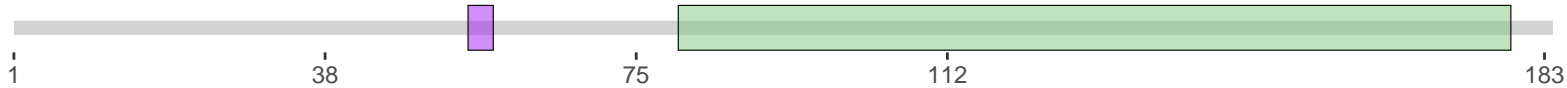


Peptide counts over 4 repeats

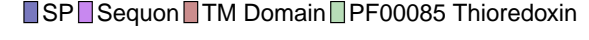
Protein length



Pfam domains



Pfam Description



Protein sequence:

.EVGAVNDKTYKSLVVESEDFLVEFWAPWGGPRMHPVIDELAKEYAGLKFELNLTDESPGATELGIRISPTVMFRNGEKKDAVGVKSTLFTGIEKFLV

NbL15g20620.1 uncharacterized_protein_YnbB-like [MW = 48.13 kDa]

No. of times detected



log(intensity)



Values from



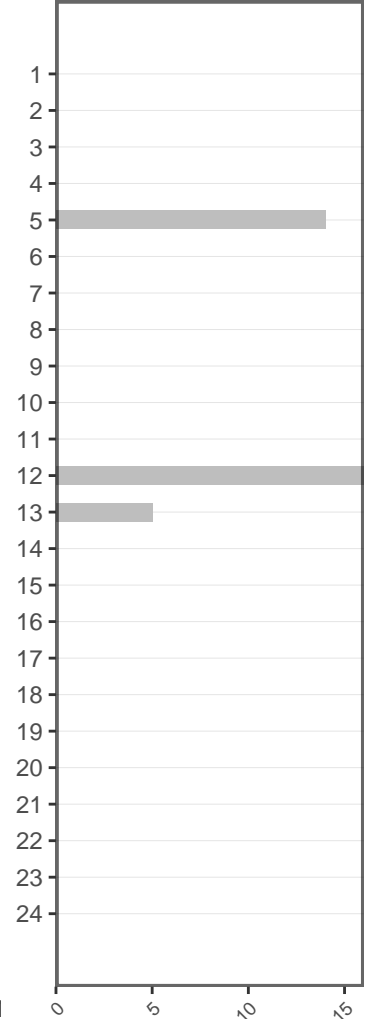
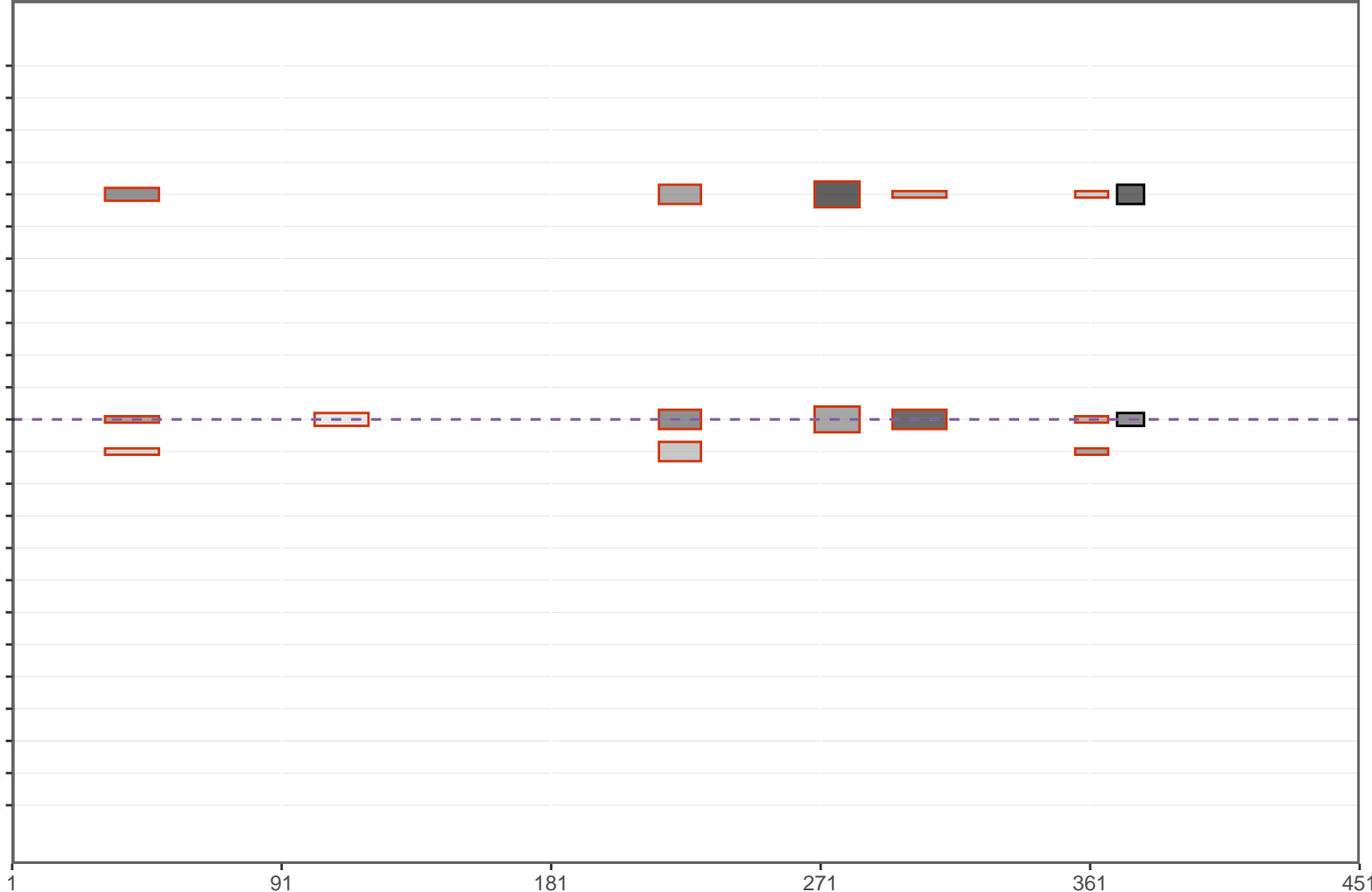
MW indication



Molecular weight

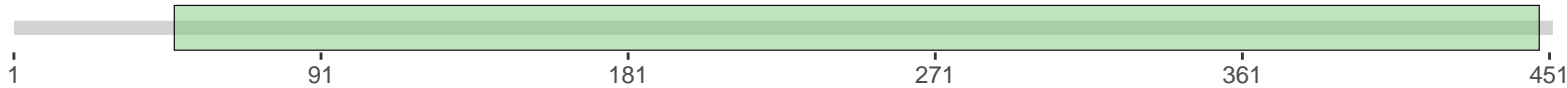


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SVRRSLVTEIGQASIRKMGKNSGLVMDNCGYGFVDDIEPPMVGADLIAGSLKINPGSTIAPGGYVAGRKRVYEAARLSAPGLVDGSGTDPDMRTFFDGLYLPQMVGSAKGFLEIVMAARGYKVGPLGRVKKRHDVQAVQLGSRERLLFCFVAGRSEPVSGFRIPVAGATGVASEVIFADGTFIDGSTSELSCDGPLREFPFVFCGGGTHWTQWGLVGEVLSKLA

NbL15g20500.1 vesicle-associated_protein_4-1-like [MW = 29.39 kDa]

No. of times detected



log(intensity)



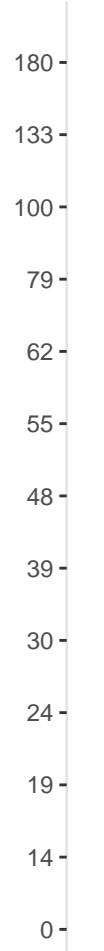
Values from



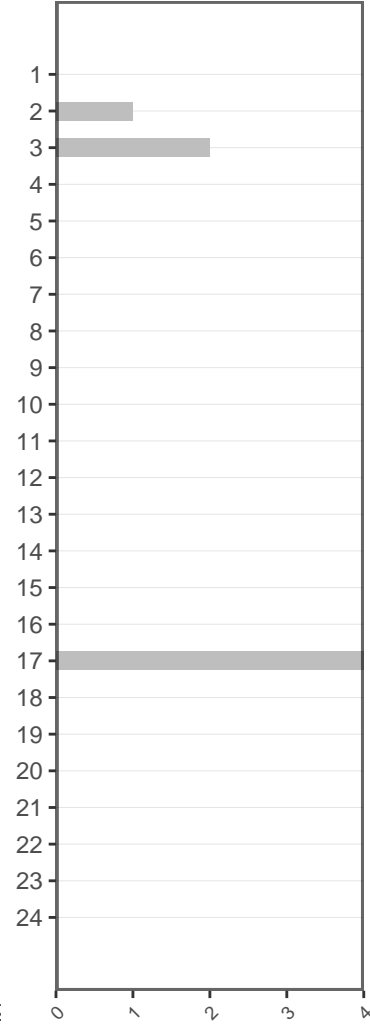
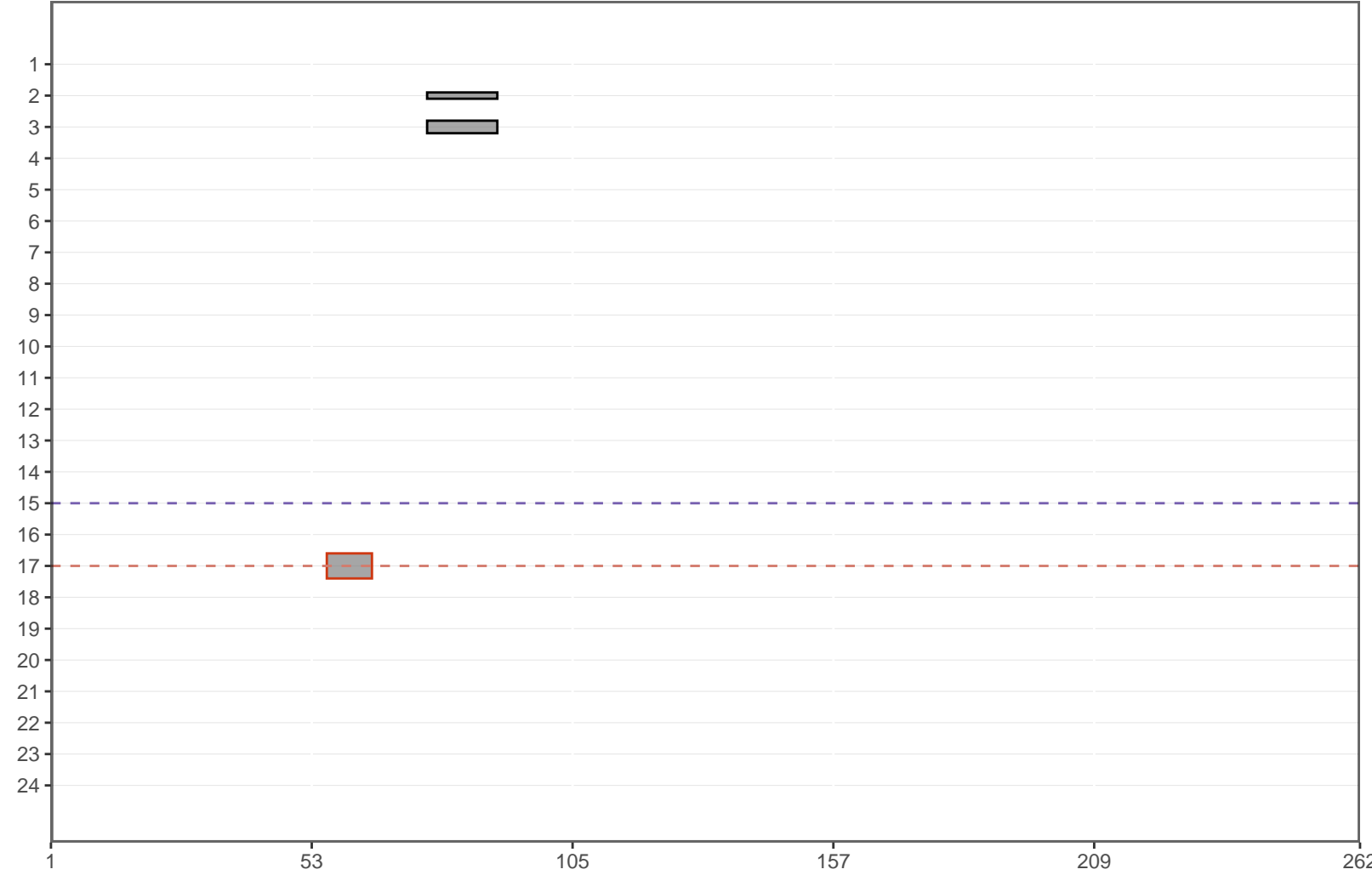
MW indication



Molecular weight



Gel Slice

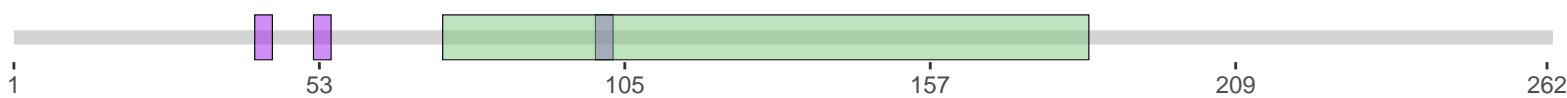


Protein length

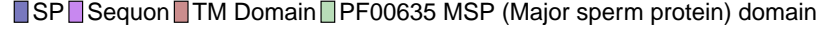


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SCYMRPPGGILEPGEVATVFKFVHEPNNKRVVDQKQKVKFKIMSLKVKEGTDVYPELFDKQDQVETIIVLRVVFLLDPERPSPALEKLRGLAEEAALESRIKPPVETGPKVYGGGLVDEWKEKREKYLARDQGVAEVDV

NbL15g20480.1 ubiquitin_carboxyl-terminal_hydrolase_14-like [MW = 88.94 kDa]

No. of times detected



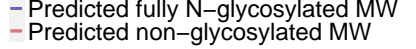
log(intensity)



Values from



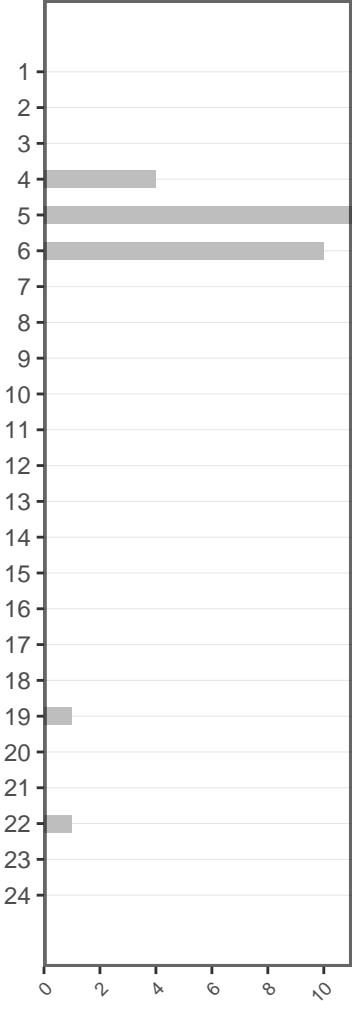
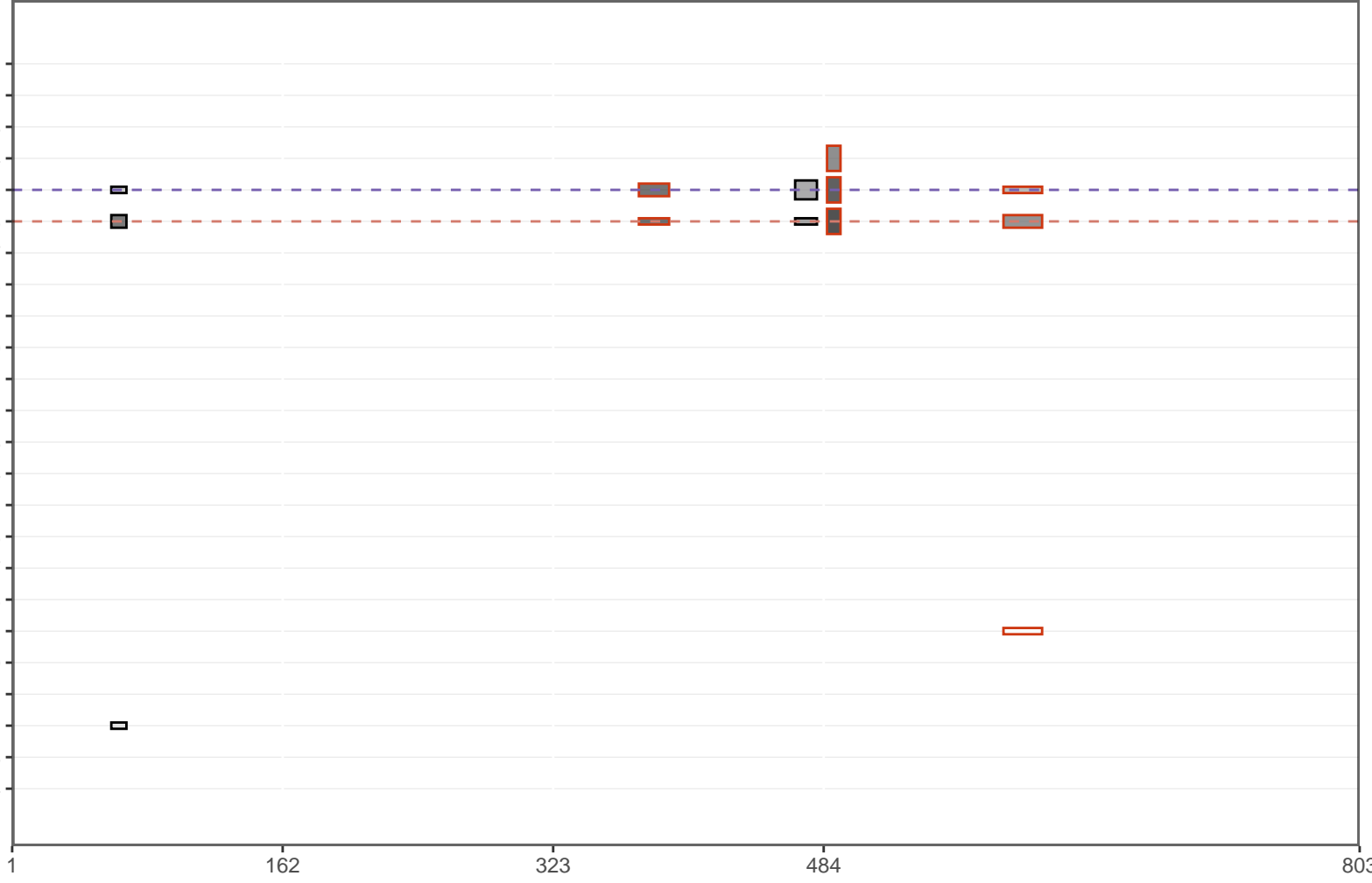
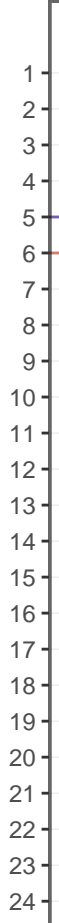
MW indication



Molecular weight

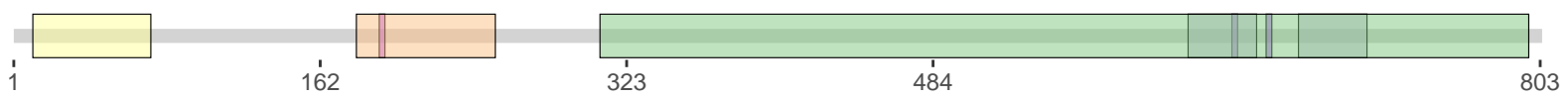


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

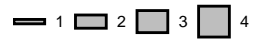
- SP
- TM Domain
- PF00627 UBA/TS-N domain
- PF17807 Variant UBP zinc finger
- Sequon
- PF00443 Ubiquitin carboxyl-terminal hydrolase
- PF02148 Zn-finger in ubiquitin-hydrolases and other protein

Protein sequence:

VASSPKQEGIRPRMFKGVAASHPEFETMRQGDLEFFLHRDQVVERMNSGKPKDFDPRSRKFGIEERLQCFSGKVAWNRNDVLSLNFLEKANKKELAEFQILSKTAAEGKELSADEIVRPRVLSKDKDLDFSAPEVHEFYSTALKARTTAIKTGLTSFFDYLVLHMRKFMVEEGWVPKKLDVYHDVPETDISGMRNSGHPGEEELPDSADAGDGEQSTKLLANEDGVAQLVSMGFNLHLDGKKAANTSNSGVVEAAMNWLLEHMNDSDIAPISGNVQNPQIDGSKDT

NbL15g20400.1 G-type_lectin_S-receptor-like_serine/threonine-protein_kinase_At4g27290 [MW - SP = 58.93 kDa]

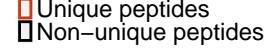
No. of times detected



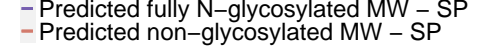
log(intensity)



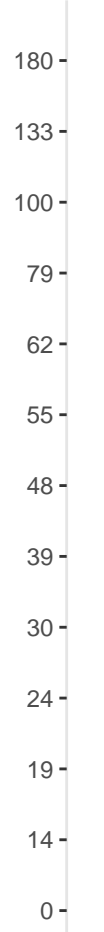
Values from



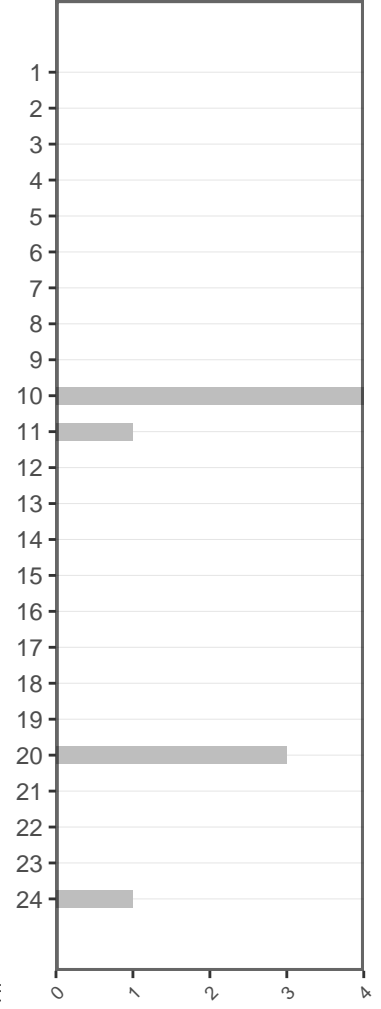
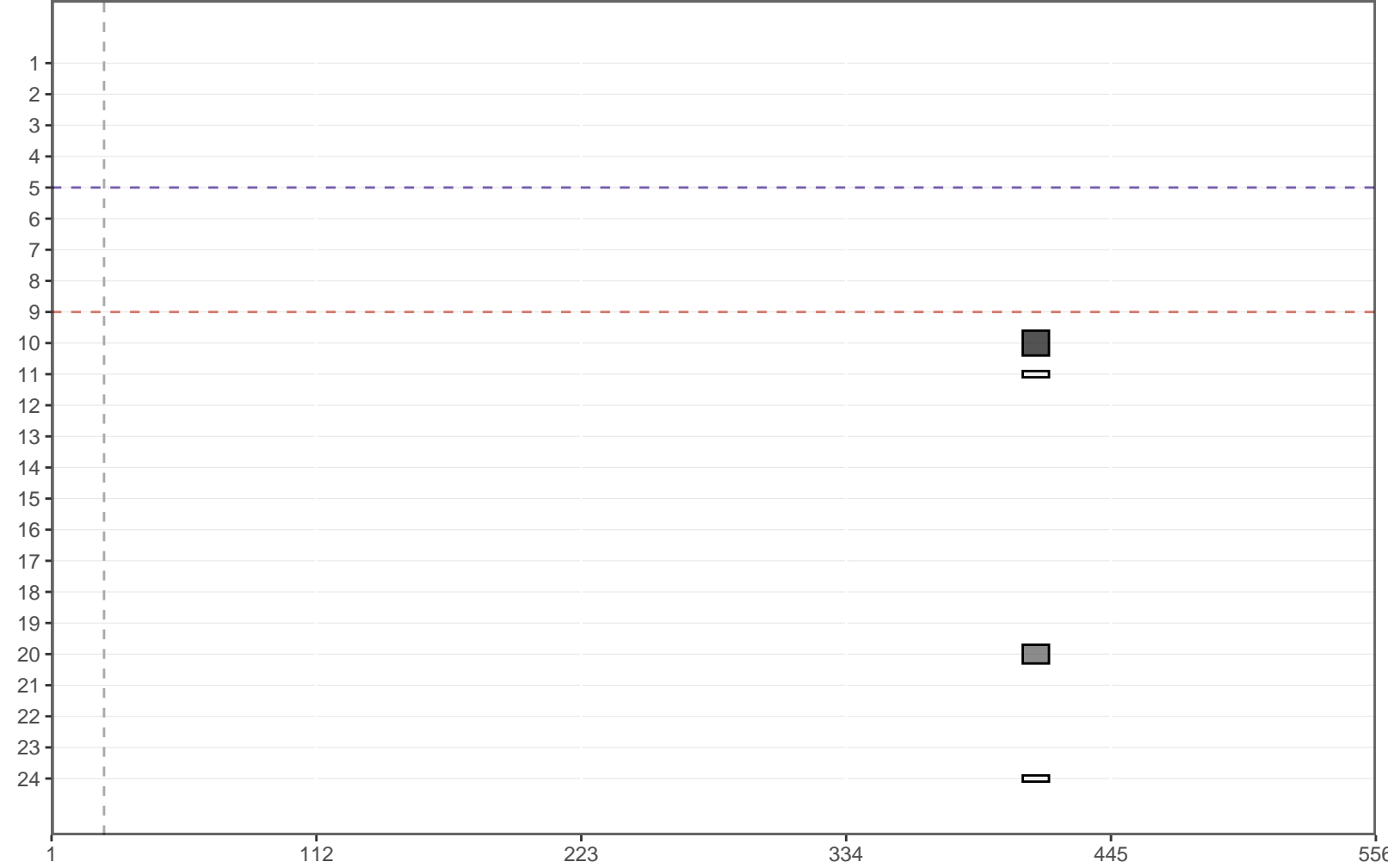
MW indication



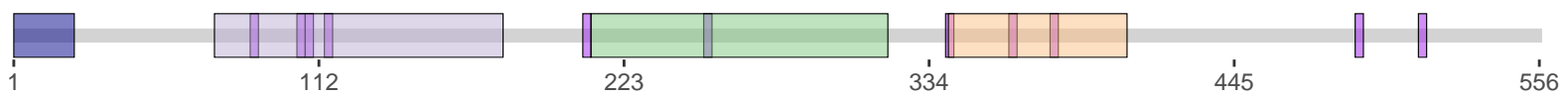
Molecular weight



Gel Slice

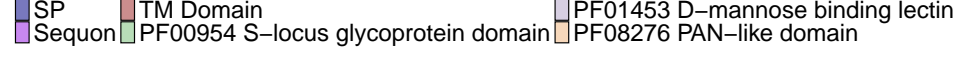


Protein length



Pfam domains

Pfam Description



Protein sequence:

GKTMCIKREKIQSWVNYHNSADADDGFTYALGGAYSTGNLSDPFGQGLDKFEPKHPDDWIRSDWSSGGVIRKRLNGTADGFLKYSGVHLPTFRFVWFNETMFLDEGRAVCLRLNSGDMGYTNLDIRNNGSGCLLWGEVLDIRLSDSGGGDVIIRMSASDDIVAGSAGSNGKAFILVALPLVAILLGLGVGLIKRRRREDPWITFKRGLRGLHSNKNINSNQSHSEDFELFLDFLTKATDNFENKIGEGGFGQVYKGLVLEGGGVAWRLEKIKRARTSRVQ*

NbL15g20240.1 probable_histone_H2A.1 [MW = 13.95 kDa]

No. of times detected



log(intensity)



Values from



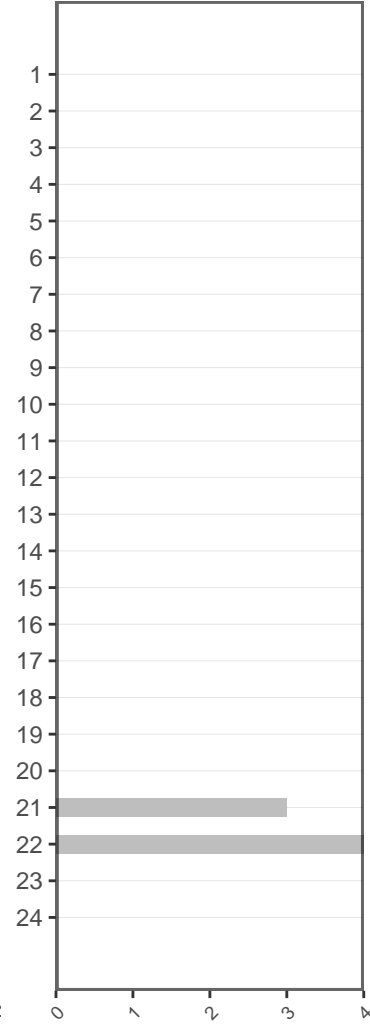
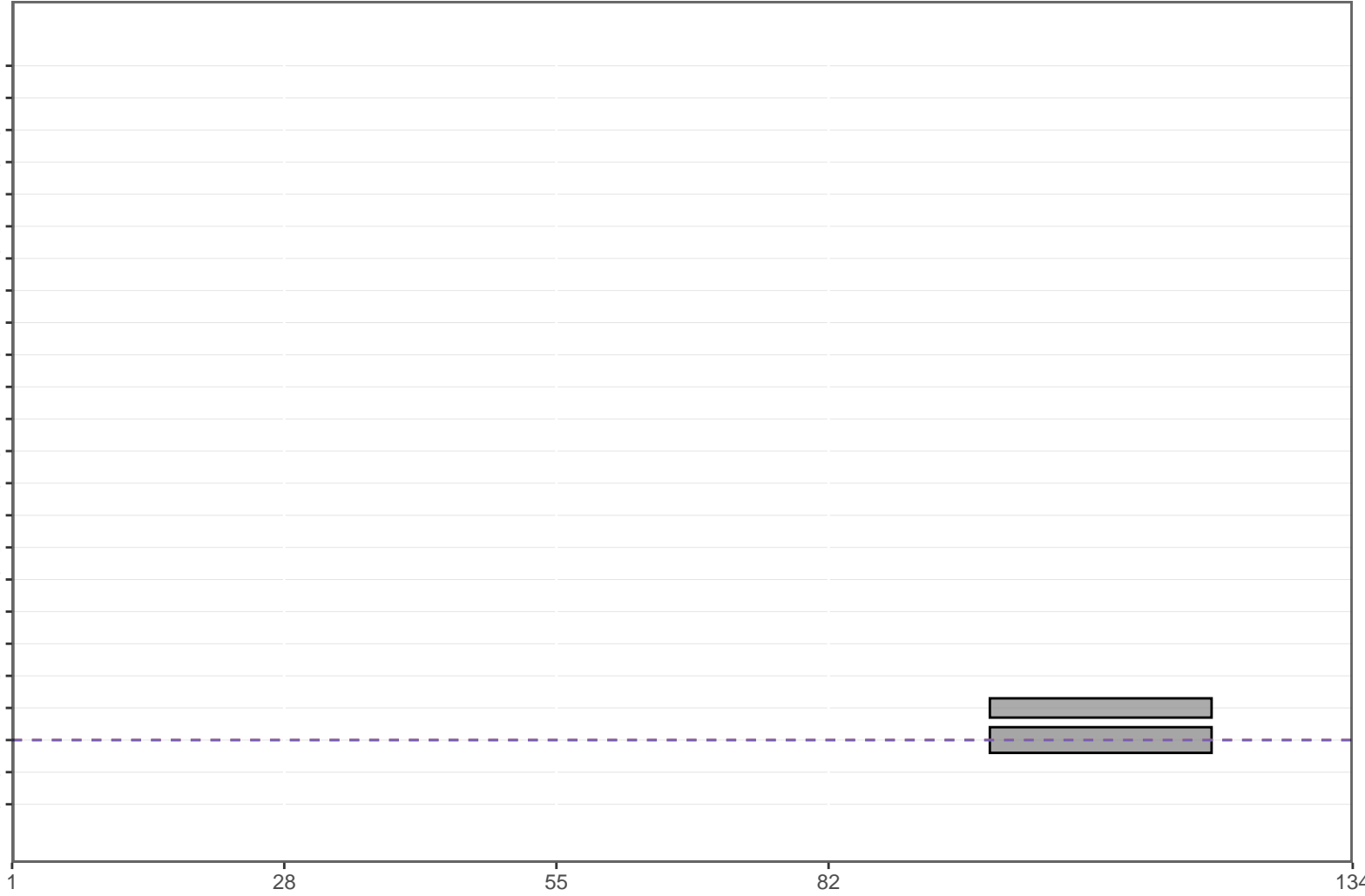
MW indication



Molecular weight



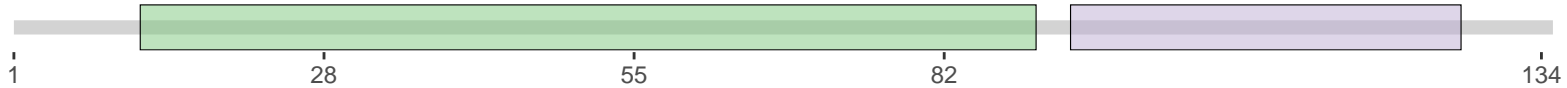
Gel Slice



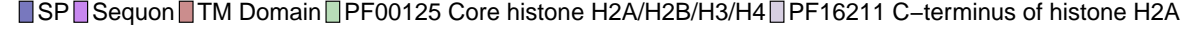
Protein length



Pfam domains



Pfam Description



Protein sequence:

AAWLEYLAEEVLELAGNAARDNKKTRIVPRHIGLAVRNDDEELSKLLGDVFIANGGVMPNHNLLLPKKTGGGSKPAAEDP

NbL15g20110.1 protein_translation_factor_SUI1_homolog [MW = 25.14 kDa]

No. of times detected



log(intensity)



Values from



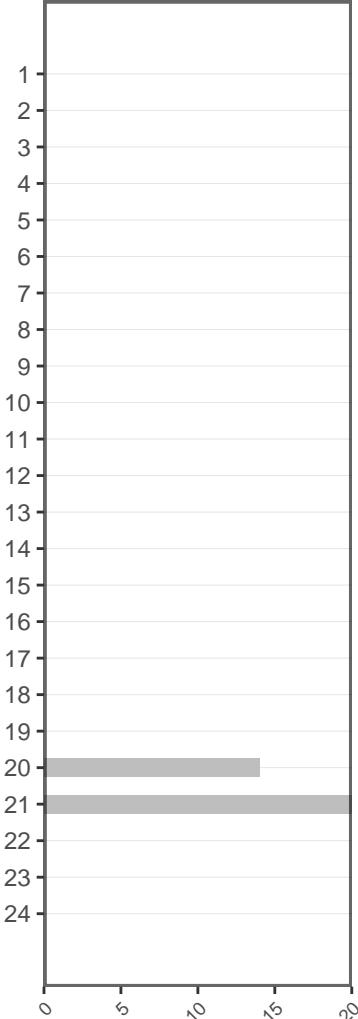
MW indication



Molecular weight



Gel Slice



Protein length

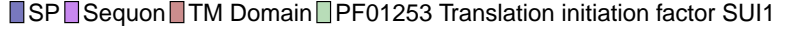


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LLLSSTTOPSFMSDLDAIGIPATFDPPFAEANADNSGAGSKVYVHIRHQGRNGRKSLLTVQGLKKEFSYKIKLKDLDKDFCGNGTVVQDFELGGVQLGGDRKHWSAFLVQAGVYKKEHKHGF

NbL15g20100.1 thiamine_thiazole_synthase_chloroplastic [MW = 41.76 kDa]

No. of times detected



log(intensity)



Values from



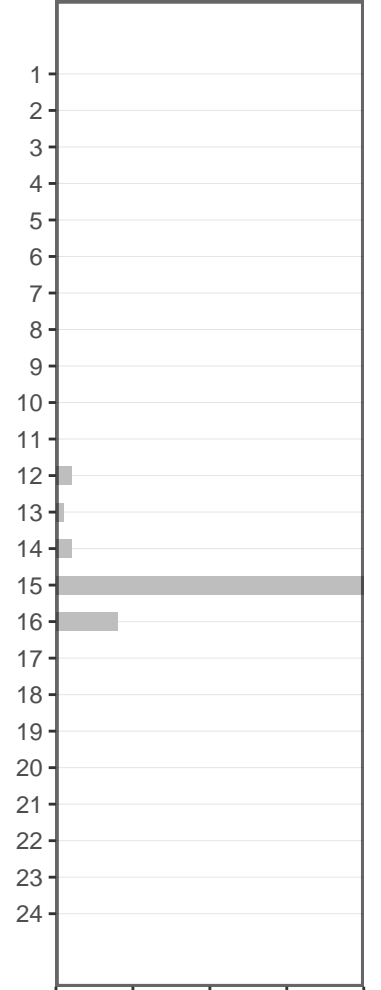
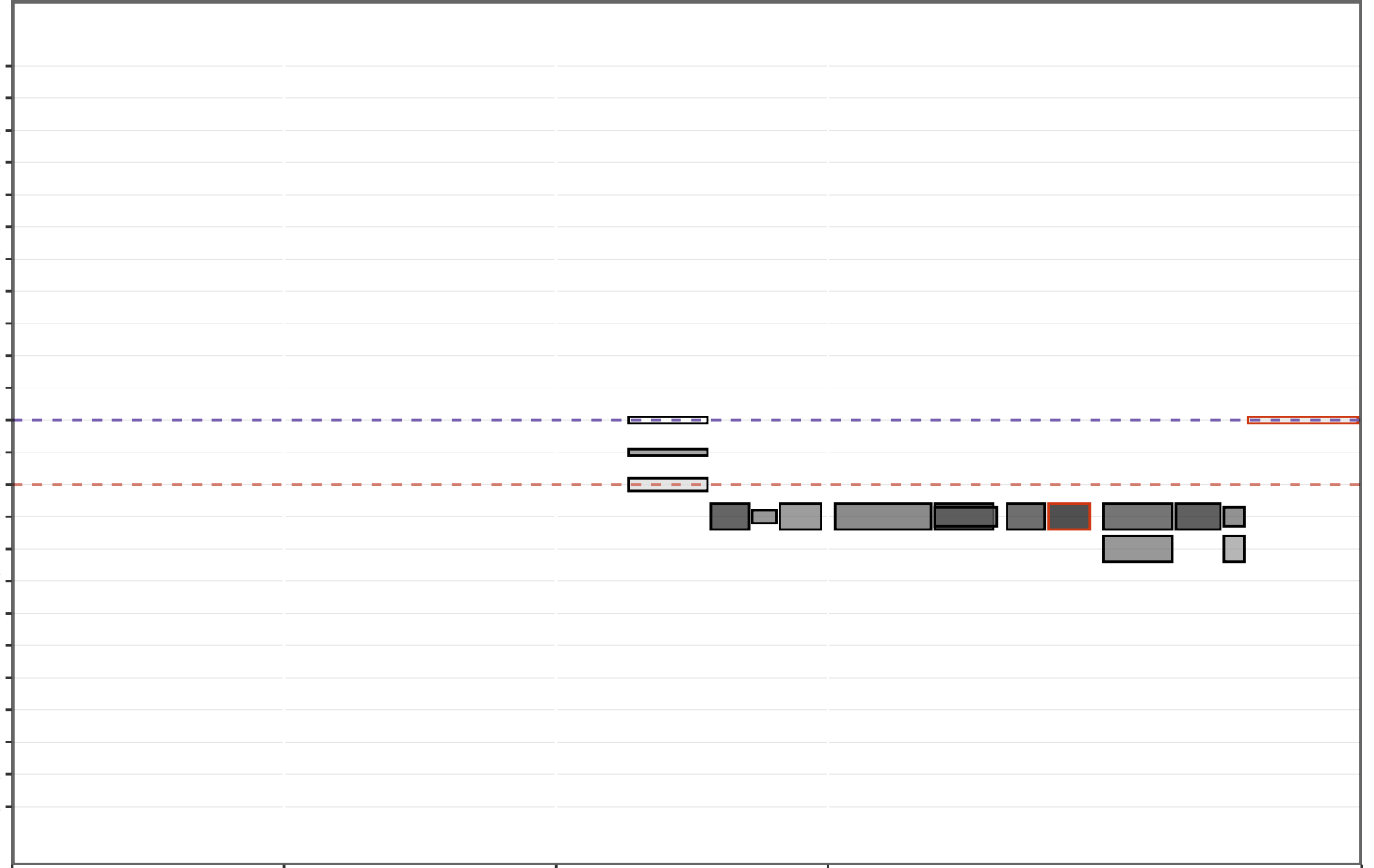
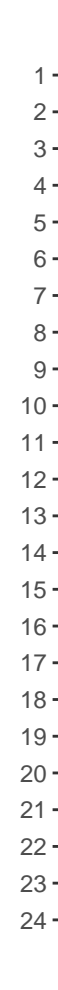
MW indication



Molecular weight



Gel Slice

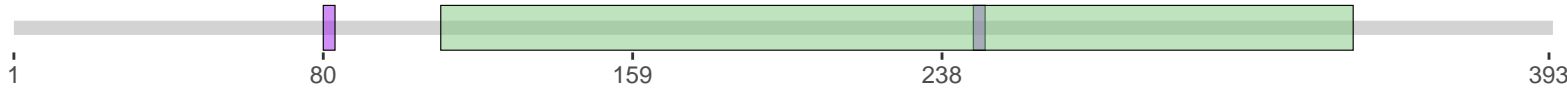


Peptide counts over 4 repeats

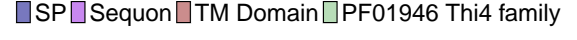
Protein length



Pfam domains



Pfam Description



Protein sequence:

LFLELGDYDECDNYVVKHAAFTFTSMKLLARPVVKLFNAVATEDLIVKNGRIVGGVVTNWEVSGNHDTGSGMDFNVAEAKIVVSSGCHDGRMSGATGVKRLKSGIMNHVFGMAKALDMNTAEDIIVRLTRVWPGMIVTGMVEAIEDGAPRMGPTFGAMMISGGKAAHLALRALGLPNAIDGTAESSHPPELLAAADDAETADAI

NbL15g20030.1 protein_translation_factor_SUI1_homolog [MW = 12.63 kDa]

No. of times detected



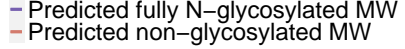
log(intensity)



Values from

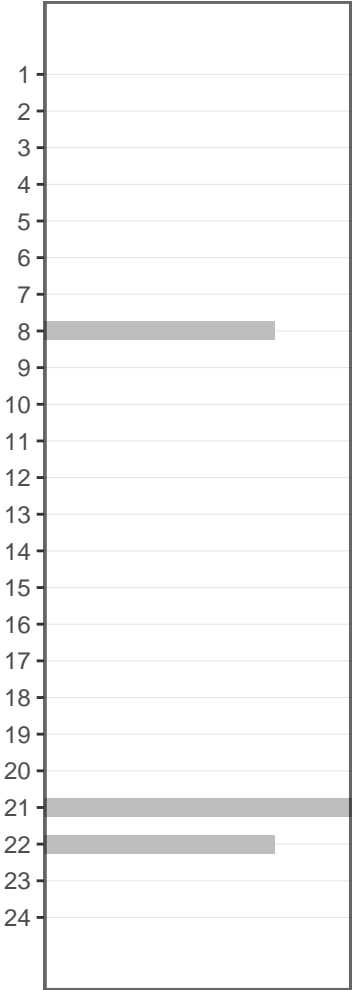
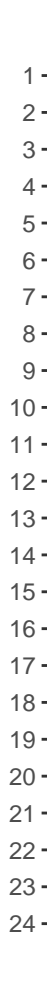


MW indication



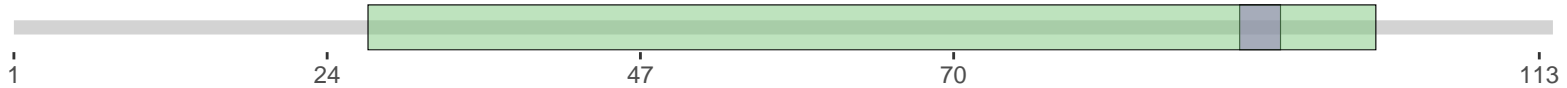
Molecular weight

Gel Slice



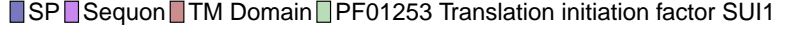
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TTVOGLRQFSYENIKDKKKEFGNGNIVGDKELGKWLQGGDRKNVSHFLVTDGIVVKKDQKHSF*

NbL15g19800.1 DNA_polymerase_I_B_chloroplastic/mitochondrial-like [MW = 128.57 kDa]

No. of times detected



log(intensity)



Values from

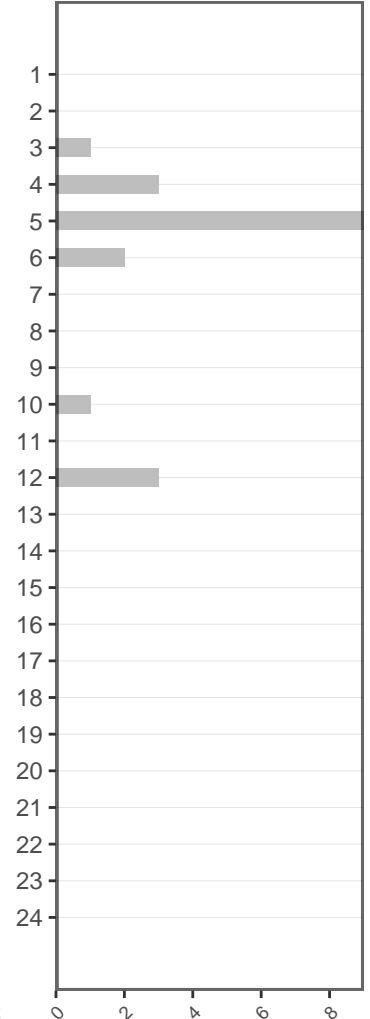
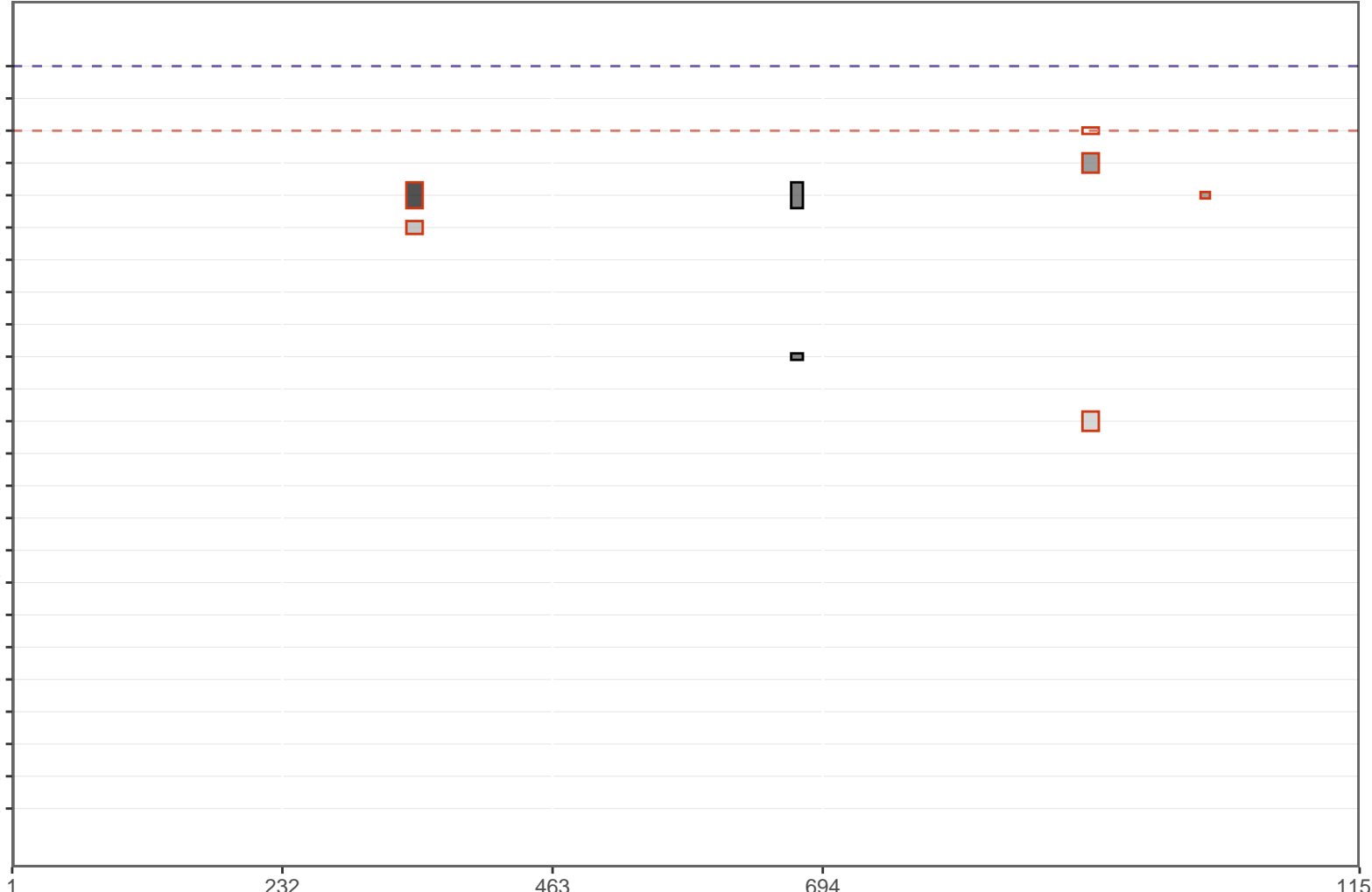
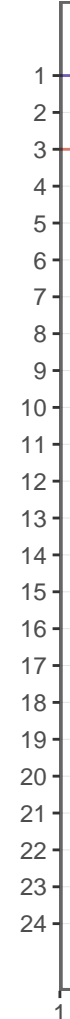


MW indication



Molecular weight

Gel Slice



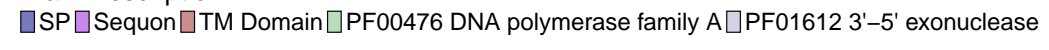
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DKTERELWICYSALDGIISLMLYELKKNLKRIRWTFDGVSKGMYEFYKRWRFPGELLYQMETEGVLRDREYLAIEKVAKAEGQVAANRFRNWAAYKDPDAKYMVMVGSDDTLRQLRFFGGQNRKNKDESLPVEKEFVFNKVKVIEEGKAPTKFRKIRLHRICDLIDTEMFTASGWPVSGDALKALSGKVSADFIDLEADDNAEEDPETSIDEALATNNEVPSGEPEFVYGSAYNAFGGGGKGEAGHAALGEMGSDLSLNFILPFGGGVSGENGRHCSLN

NbL15g19580.1 GDSL_esterase/lipase_At5g55050-like [MW - SP = 36.61 kDa]

No. of times detected



log(intensity)



Values from



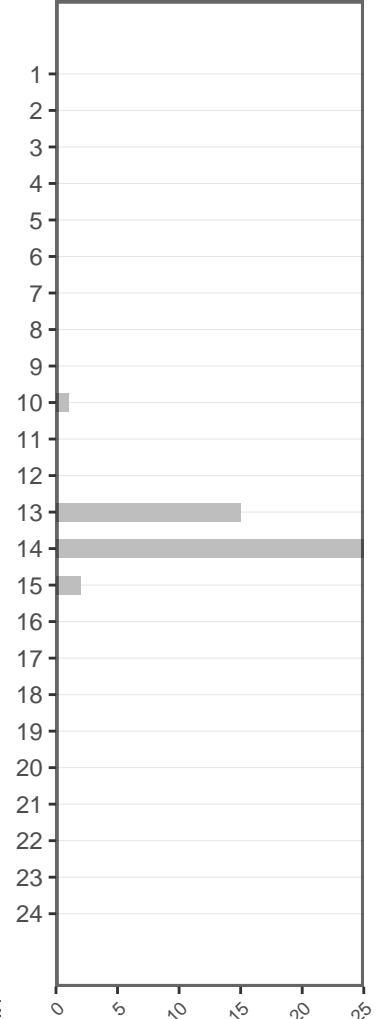
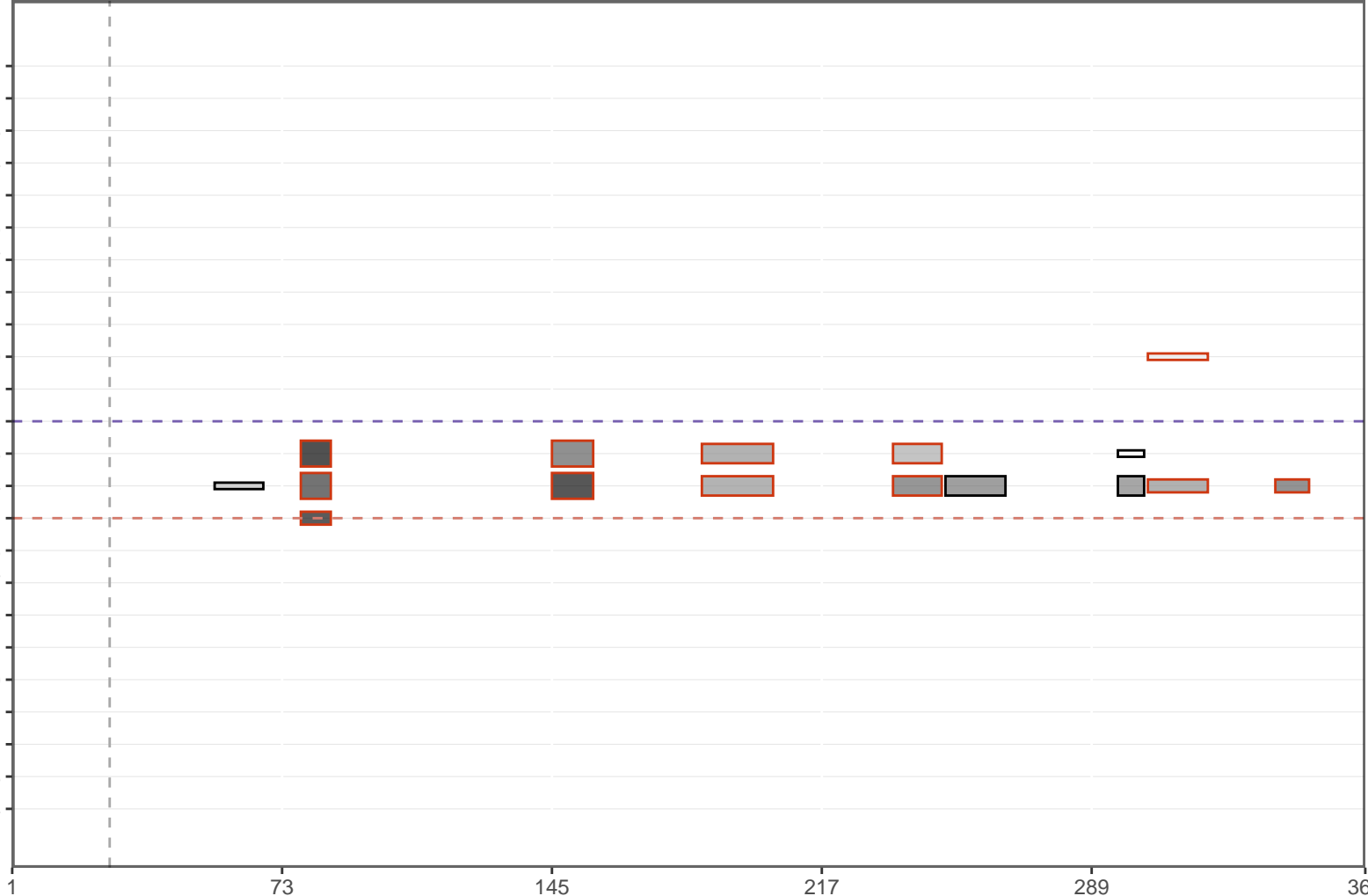
MW indication



Molecular weight

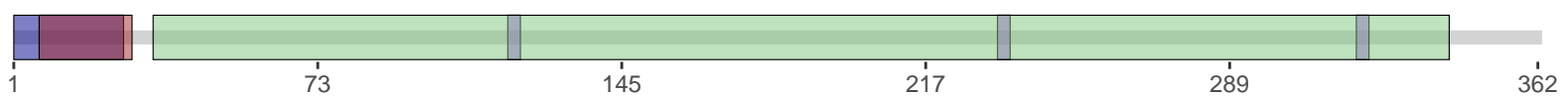


Gel Slice



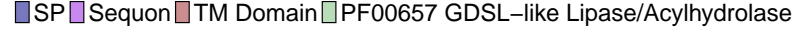
Protein length

Peptide counts over 4 repeats



Pfam domains

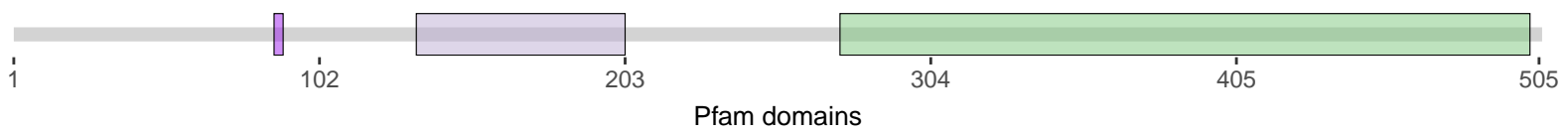
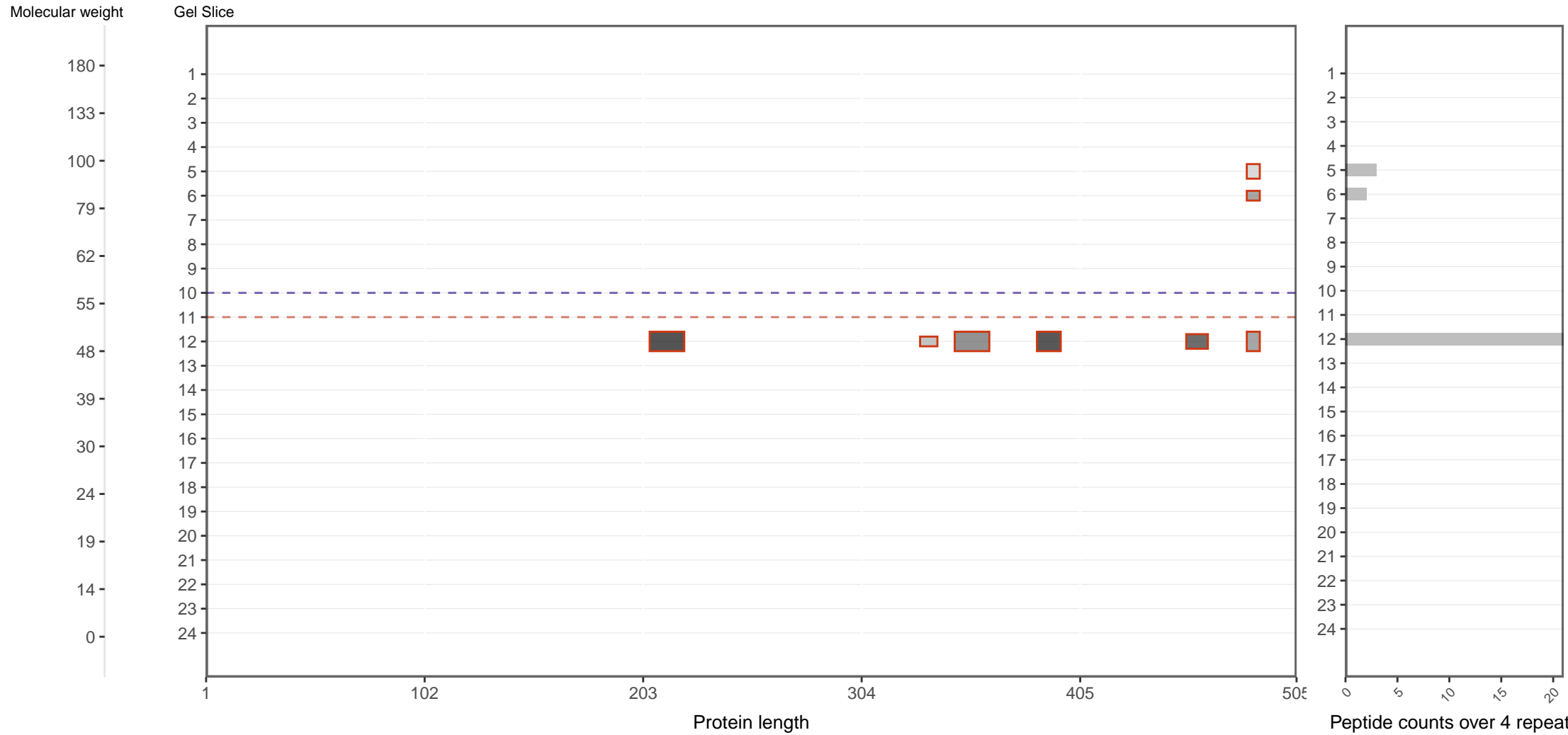
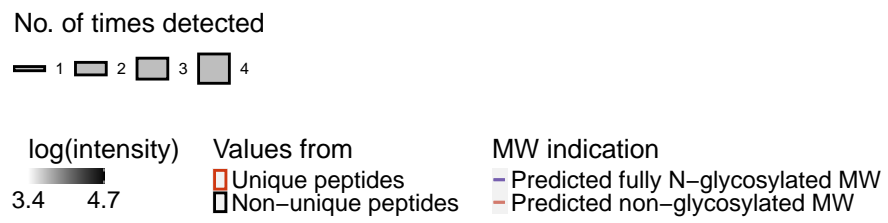
Pfam Description



Protein sequence:

SSNDINIFYKSDSKLPKTAPEQYVDGMVSLGGQLKQLGARKFVIVGSGVGGIPLLRYSANKSSEGESEGANYYWTKYKNGFGSIVLGGLSKELKDFSYVYFDTFNLLDVGQNPVYGFREYKAAACDGLGRLNANLPCPTPISTFCGRNRSHVFWDRYHPTTEANRIIDSAFDDGKGYVFLNWKGLTL*

NbL15g19490.1
dihydrolipoyllysine-residue_succinyltransferase_component_of_2-oxoglutarate_dehydrogenase_complex_2_mitochondrial [MW = 54.9 kDa]



Pfam Description

- SP
- Sequon
- TM Domain
- PF00198 2-oxoacid dehydrogenases acyltransferase (catalytic domain)
- PF00364 Biotin-requiring enzyme

Protein sequence:

DKAKSQVETTPVKEKPKESPPPPKRSPTLQLPRERETRVPMTRKRKRWTRLKDSONTFAMLTFFNEVDMTNLMKLRDVKDAFVEKHKYKLGFMISGPKAAVSAKSGPPVNAVVDGDDIYRVIDISAVGTPKGLVYVPLRRAEAGMFAEIKTINGLAKKANDGLSIDEMAGGSFTISNGGVYGLSLSTPHNPPOSAILGMHGVSRPMVYGGNYPRPMYALTYEYKRLDIDREAVFFLRRIKDVVEDPRRLLEDV

NbL15g19480.1 imidazole_glycerol_phosphate_synthase_hisHF_chloroplastic [MW = 65.01 kDa]

No. of times detected



log(intensity)



Values from



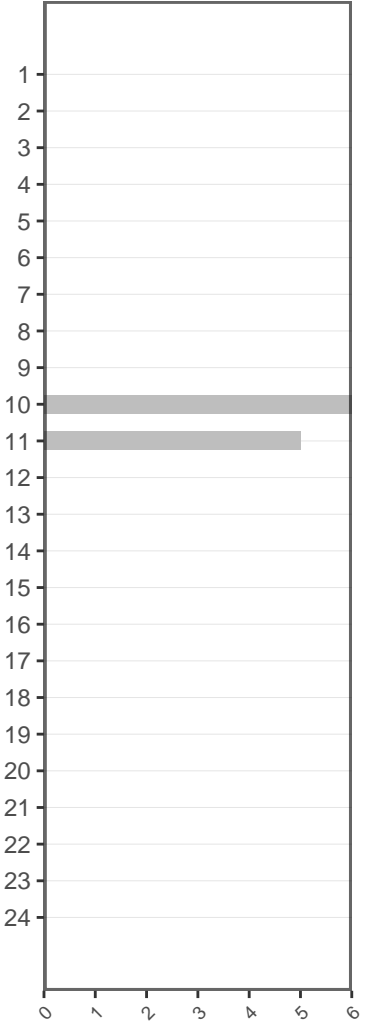
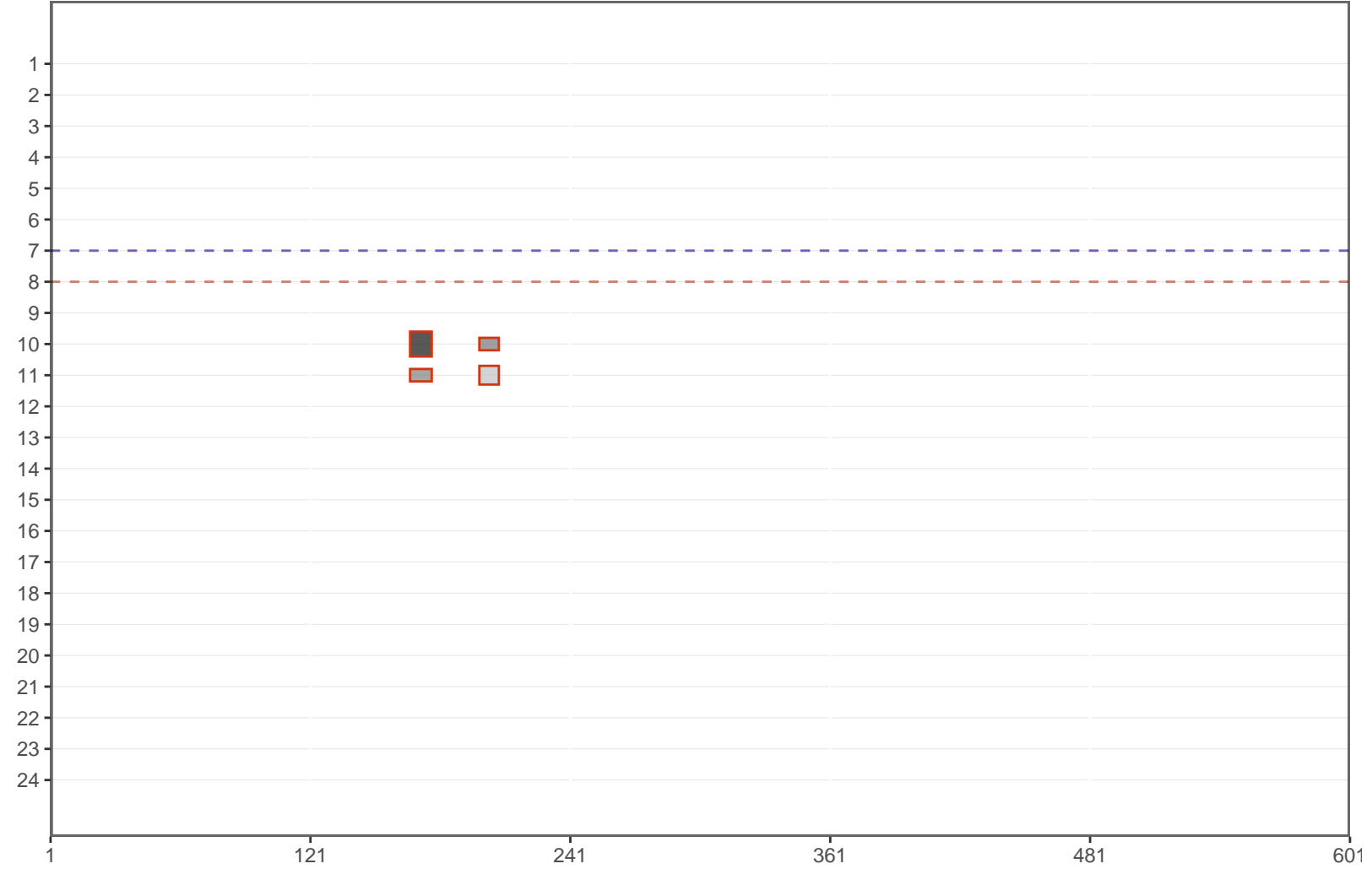
MW indication



Molecular weight



Gel Slice



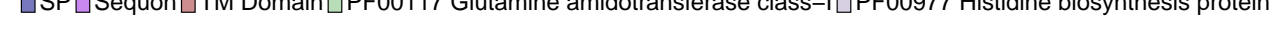
Protein length

Peptide counts over 4 repeats



Pfam domains

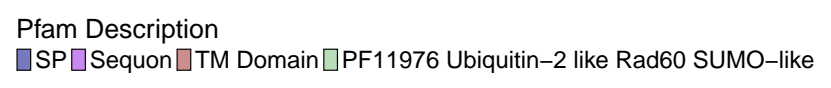
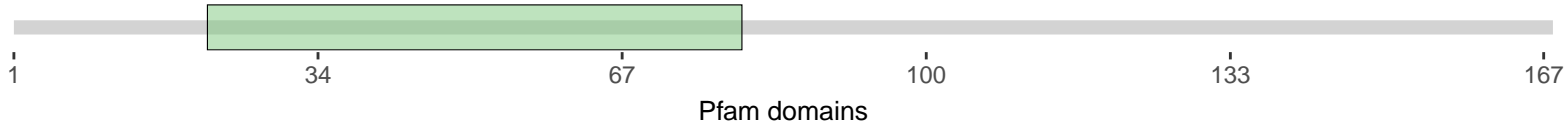
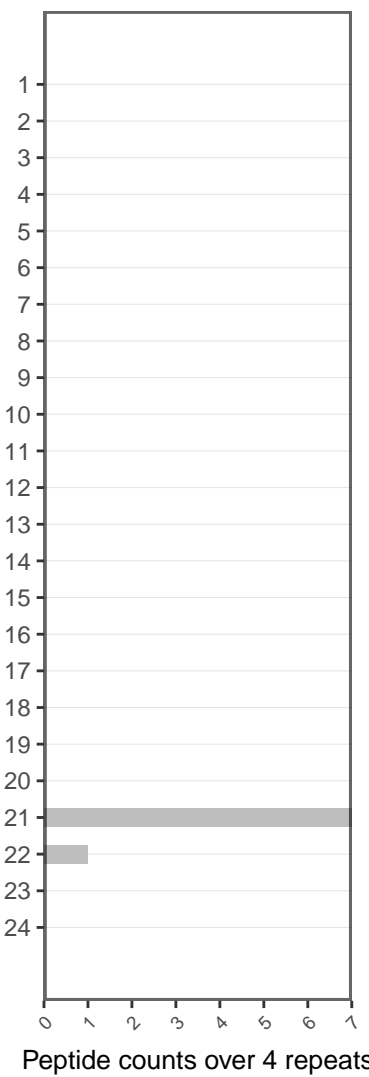
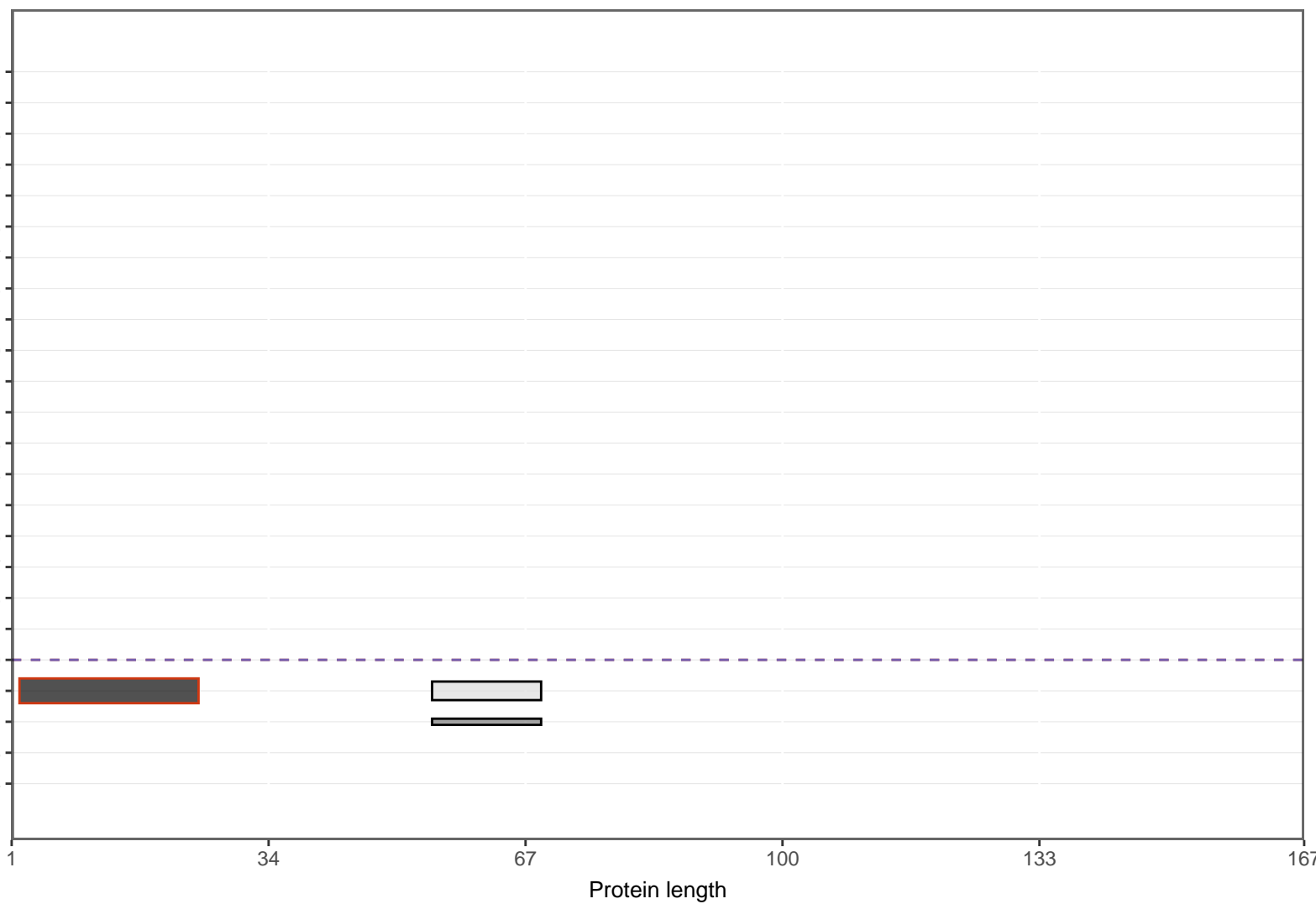
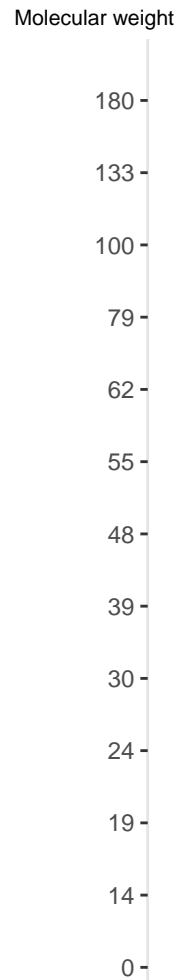
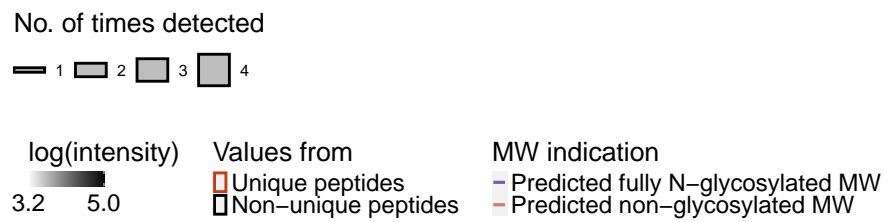
Pfam Description



Protein sequence:

LAKRYVACLIDYRTRNDKGGDLVYTKGGDGYDREHTKENEVRLNPKFVLDLAGQYYKDGADSEVFLNITAFRDFPLGDLPLMGLVRYASENVFVPLTGGGIRDFDGNCRYYSSLEVAASEVFRSGADKYSIGSDAVAAEEVLKSGVKTGKLSLEGISGRVYGNQAAVVSIDPRRYVWPKVAEERTVWVRSPPGNSGEVAVWVQCTVSGGREGRPGAVELAKAVEELGAGEILLNDICDGGDGGKGFDELKUISDAVSPVIASSGAGTVEHFSEVFTQTNASALAAGIFIRKI

NbL15g19410.1 small_ubiquitin-related_modifier_1-like [MW = 19.42 kDa]



Protein sequence:
 RRLRSEGTPEVSVSPFFFTNPHSHFNFPVFKDGRIGSVLSRYFFHILFGSLRWRMGKMLKCDRIIVDTWVRFSEDFGLNLYRVLAEELRV

NbL15g19340.1 GrpE-like [MW = 33.76 kDa]

No. of times detected



log(intensity)



Values from



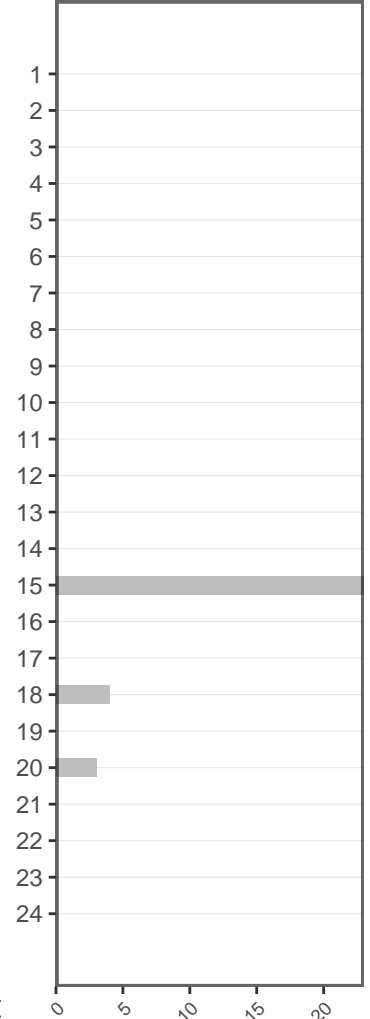
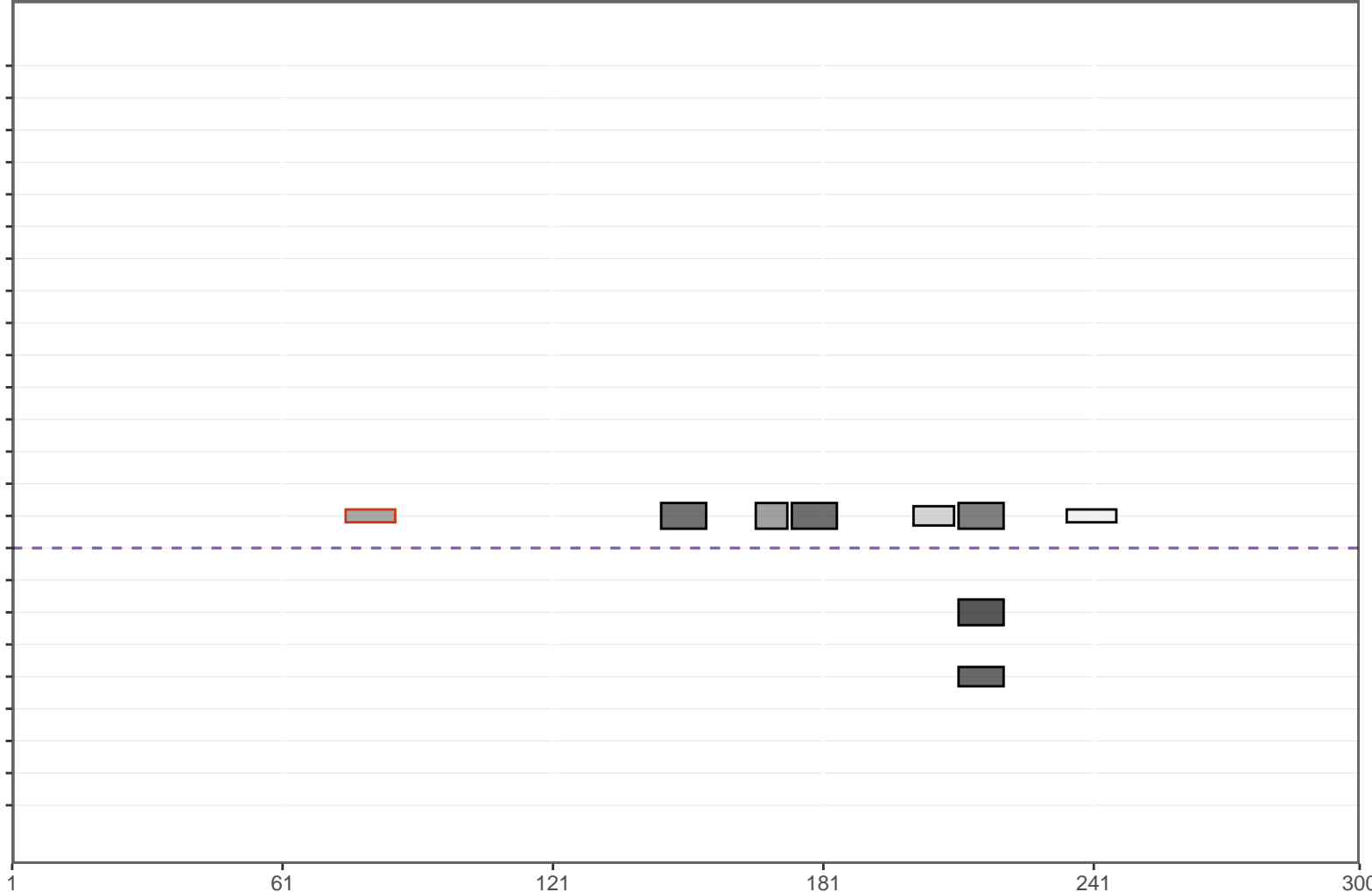
MW indication



Molecular weight



Gel Slice

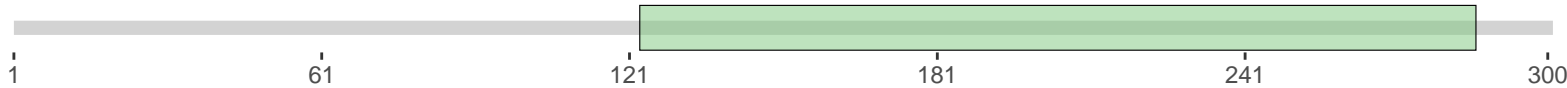


Peptide counts over 4 repeats

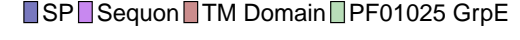
Protein length



Pfam domains



Pfam Description

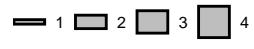


Protein sequence:

CLQDFLRSYAEIMENIMERTKREAEIKKFAIGNFKVALLVDPDLGRASSVVKESFQKIDASKDTVGMPLKLLLEGVEMTDKGLAEVFKFKGVEKYDPTNEGDFDNKHNVAWFQVDPPEKAPGVVAWLKPGYTLHDIRRPAEVSIVTVAWETEADQSTNS

NbL15g19330.1 trigger_factor-like_protein_TIG_Chloroplastic [MW = 60.48 kDa]

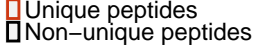
No. of times detected



log(intensity)



Values from



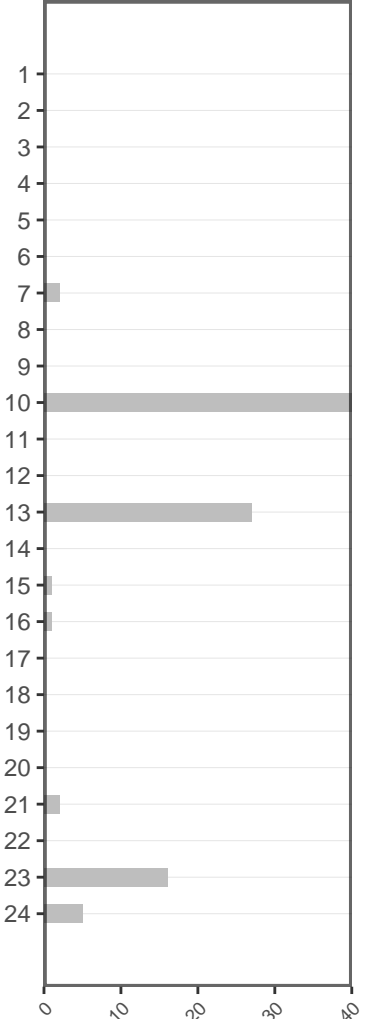
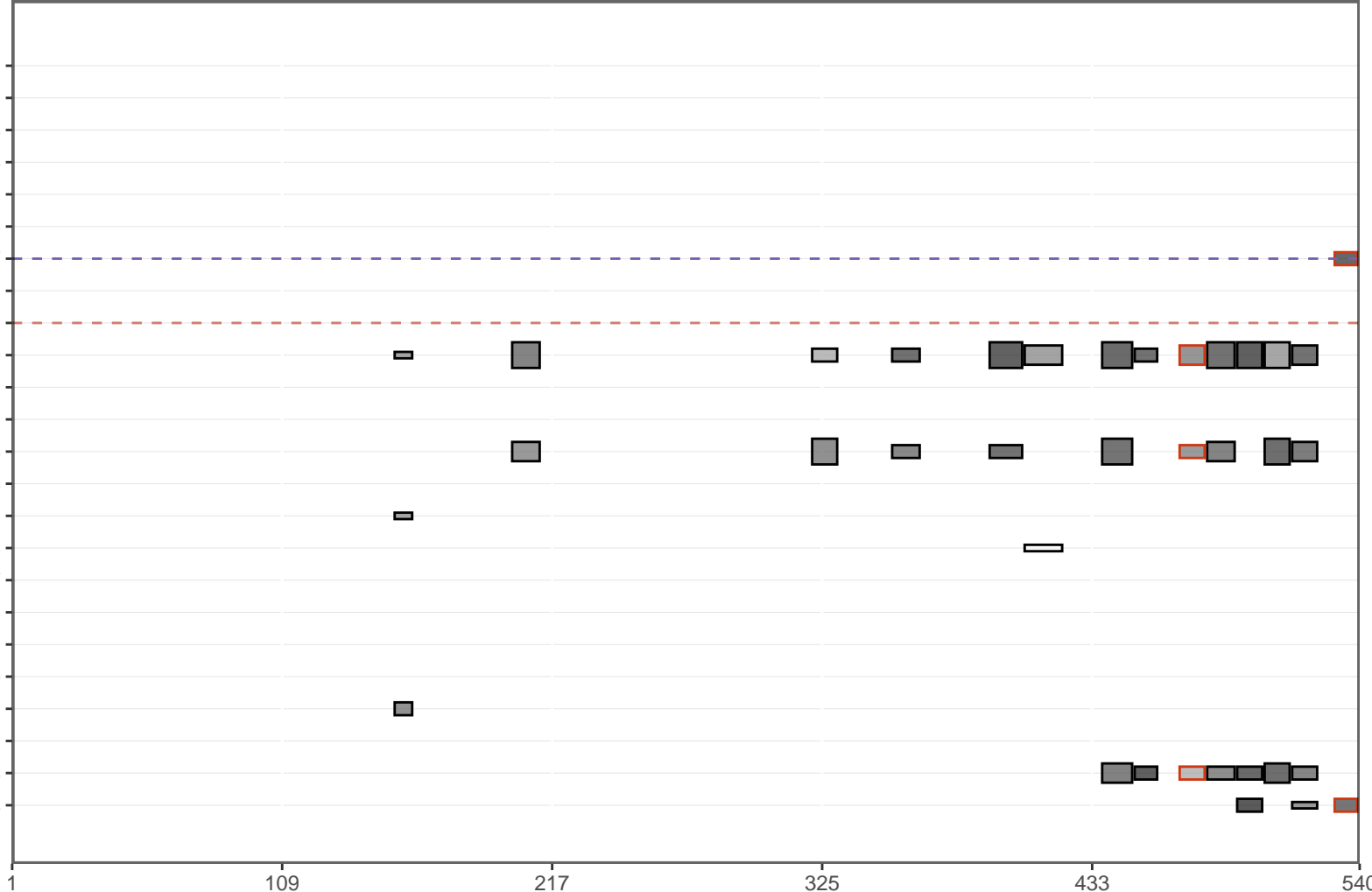
MW indication



Molecular weight



Gel Slice



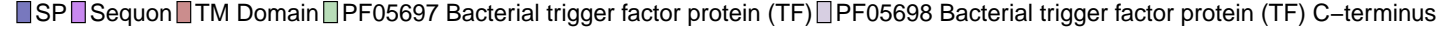
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

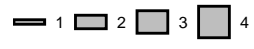


Protein sequence:

DRGLGVGDVAIDISATHEGDDGSDAKTPAEGKGFNFDTEDGDNLVLPGLDSDVGNKRGKTEKFFLVFDDSWKGDGLRGNVHAGFTVECKELFYRDLPEVNDGADKLPKGGSSIEEVKALLGRLEIEGAAKDGATDINALDQLYMMVEVDHPQSLFEEQGRGLYGAQLLQLQANMKLSEGQLALSSPRAVNEFLAAGKENTSIHKGNLAVGDITRENLFQSTEEILKVEVGNISIEEFKSGQGEYDEDNRVKGQVGEVLEGAKVLEWLRNADIQYTRP

NbL15g19320.1 65-kDa_microtubule-associated_protein_1-like [MW = 65.32 kDa]

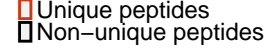
No. of times detected



log(intensity)



Values from



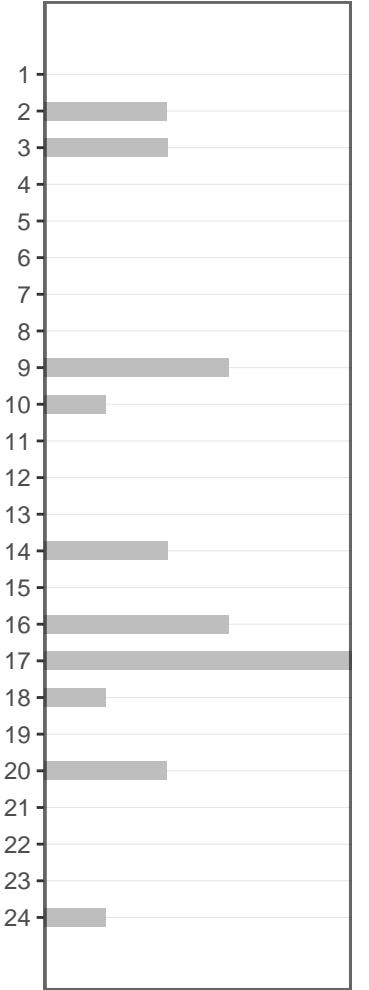
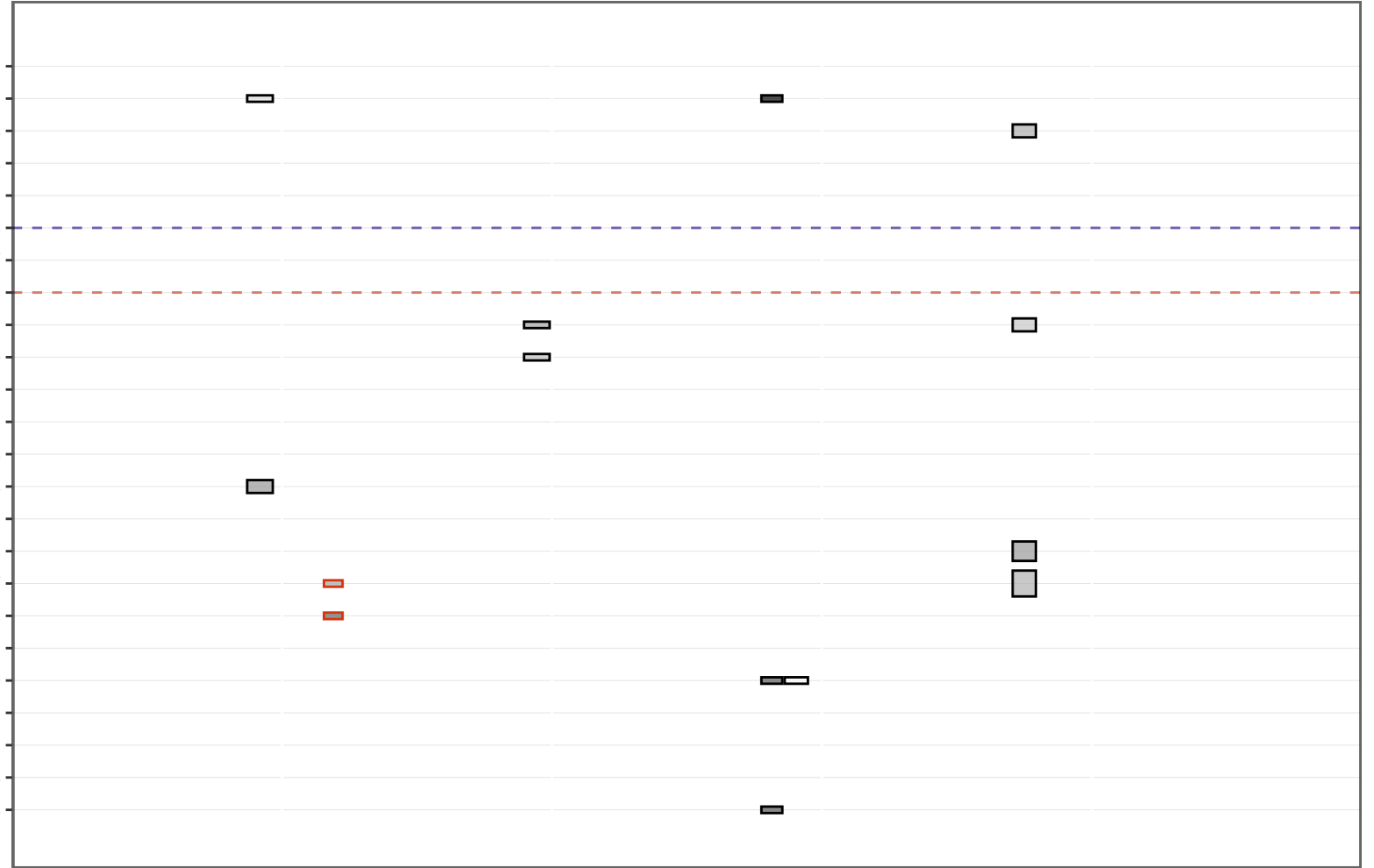
MW indication



Molecular weight

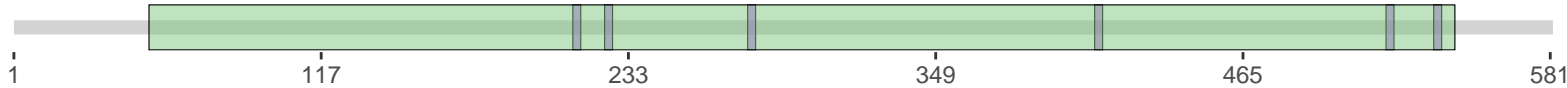


Gel Slice



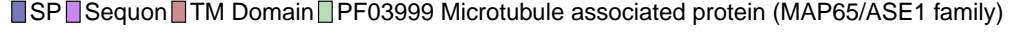
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL15g19270.1 serine/threonine-protein_phosphatase_PP-X_isozyme_2 [MW = 34.87 kDa]

No. of times detected



log(intensity)



Values from



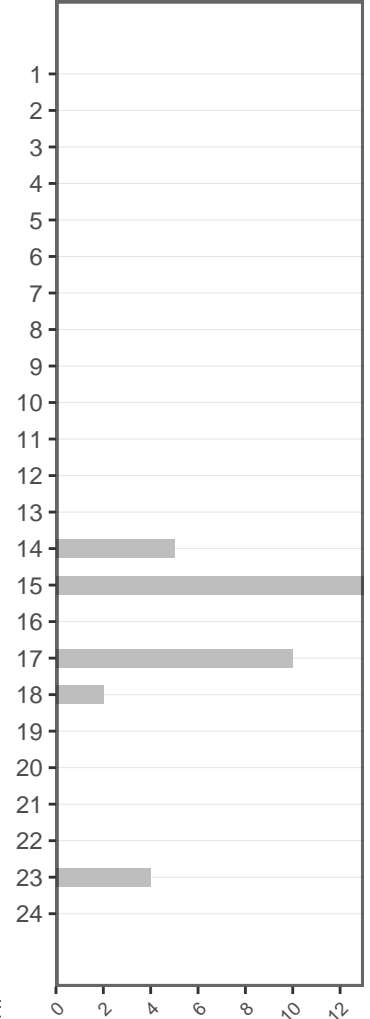
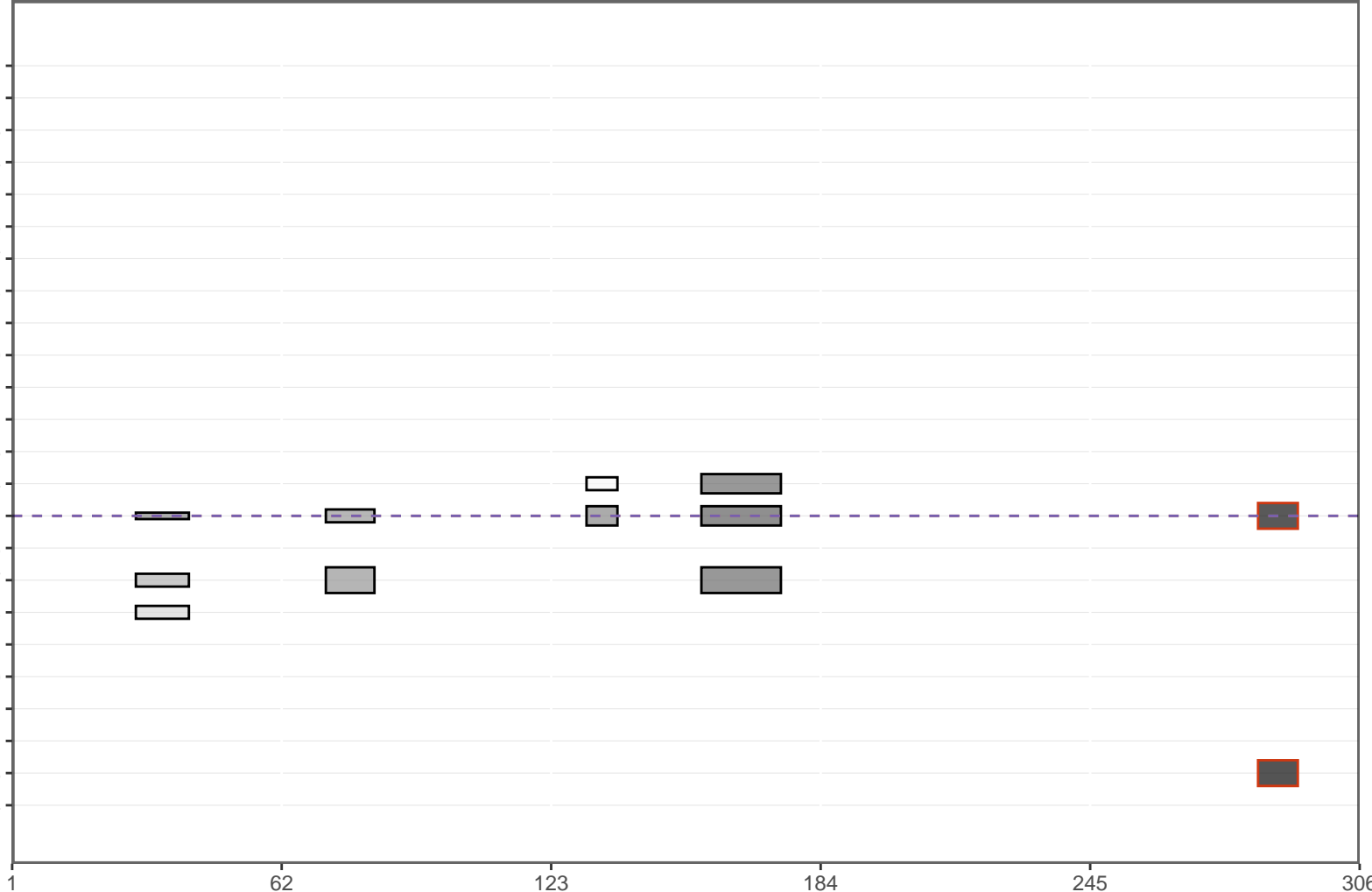
MW indication



Molecular weight

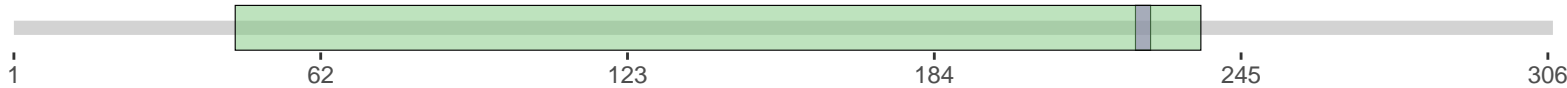


Gel Slice



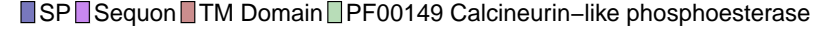
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

CTDIFDYLSSLSALINKEFVHGGLSPTFTLDDGRTDRKGEVPHLEGAMCDLILWSDPEDVDGWSLSPRGAGFLFGGVSVTSFNHTNNDYICRAHQGLMEGKVMFNNGIVTVVWSPAPNYCYRQGNVAALIELENDLNKQFRVDAAPQESRGAPKRPDPDFL

NbL15g19240.1 fimbrin-1-like [MW = 58.46 kDa]

No. of times detected



log(intensity)



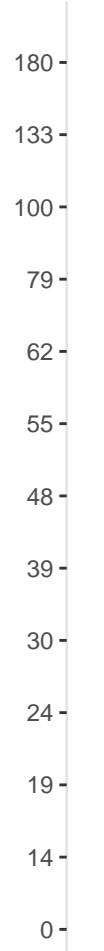
Values from



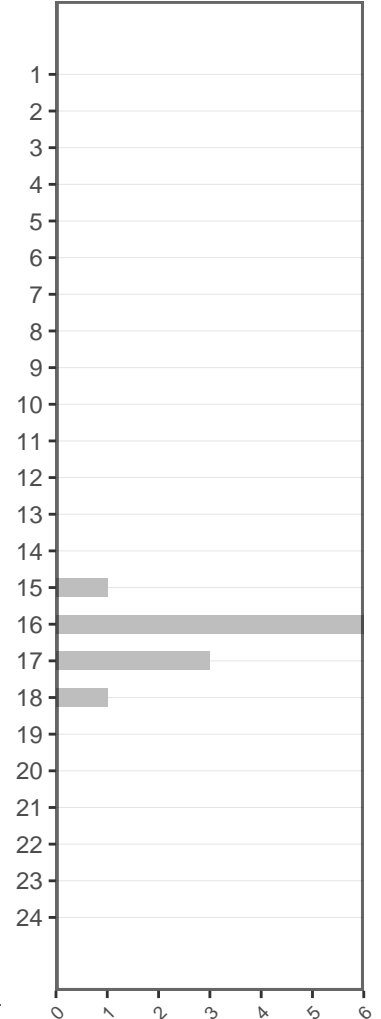
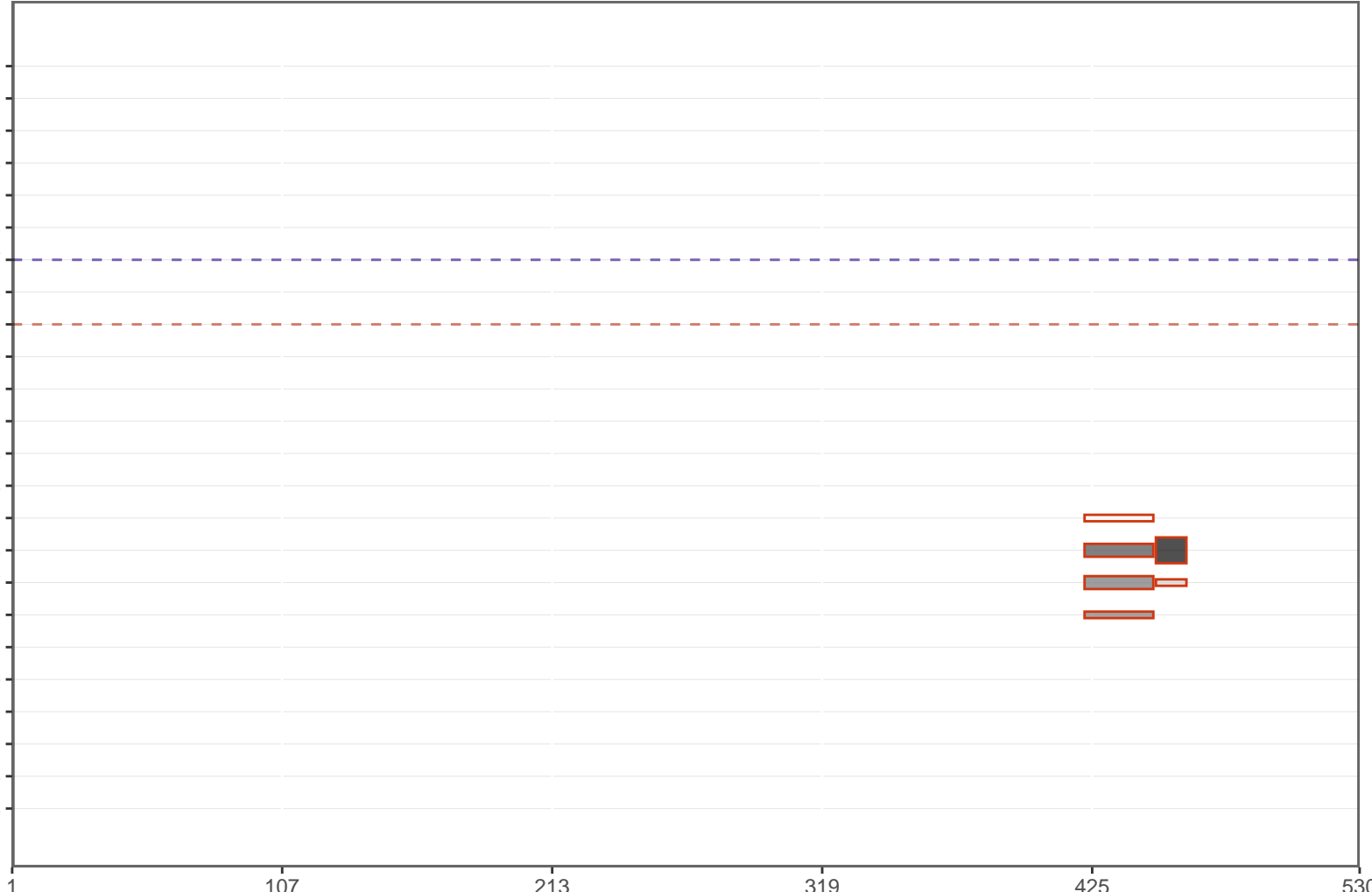
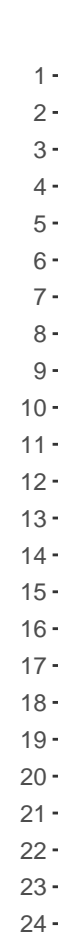
MW indication



Molecular weight

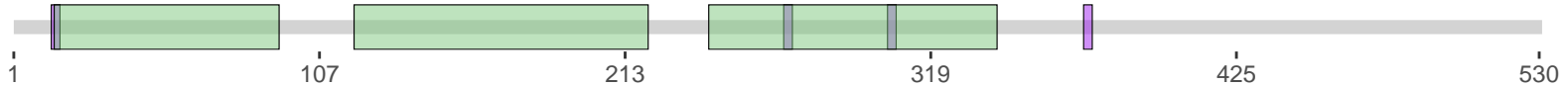


Gel Slice



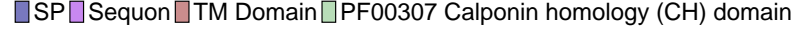
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KKVKTGTRTSKMEGFKDKNLSGGFLLELLSAVEPRVYVWVNLVTKGESDEAKLNATYBIAKRLGGGIFLLPEDIMEVNGKMLTASIMVWISLGGTAEEAESTSPSTTIDASVPRSTNGSMFLPLAASPDASPAVPSISGASSPVVDASPAVPSVNGDEEGLLAEVSKLADDDAASDDVLAASPEGAENVEIPSDVHRDAENAEIPSDVHRDAENAEIPTDVHRDDENAEIPTDVGTDADAEIPSDTPSPPOLEDTEGGGGLSHEVENEQTKPDEQ*

NbL15g19220.1 glycerophosphodiester_phosphodiesterase_GDPDL3-like [MW - SP = 79.45 kDa]

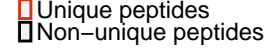
No. of times detected



log(intensity)



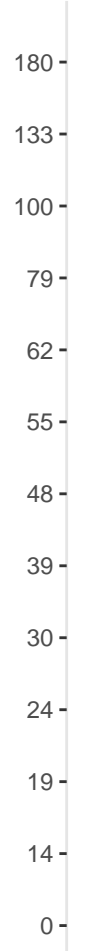
Values from



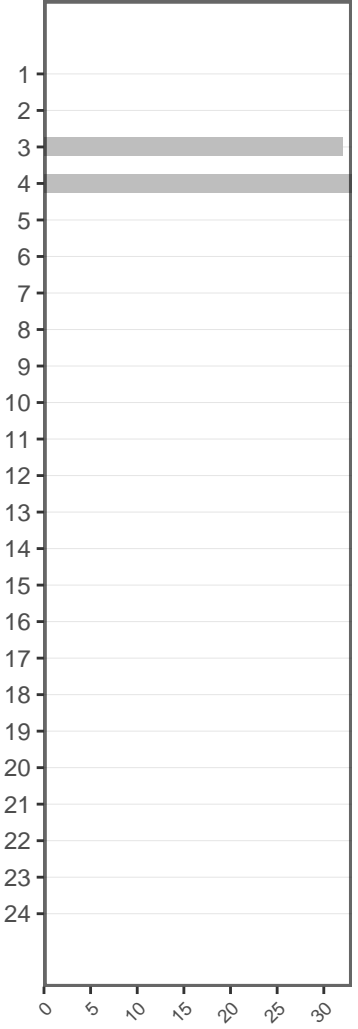
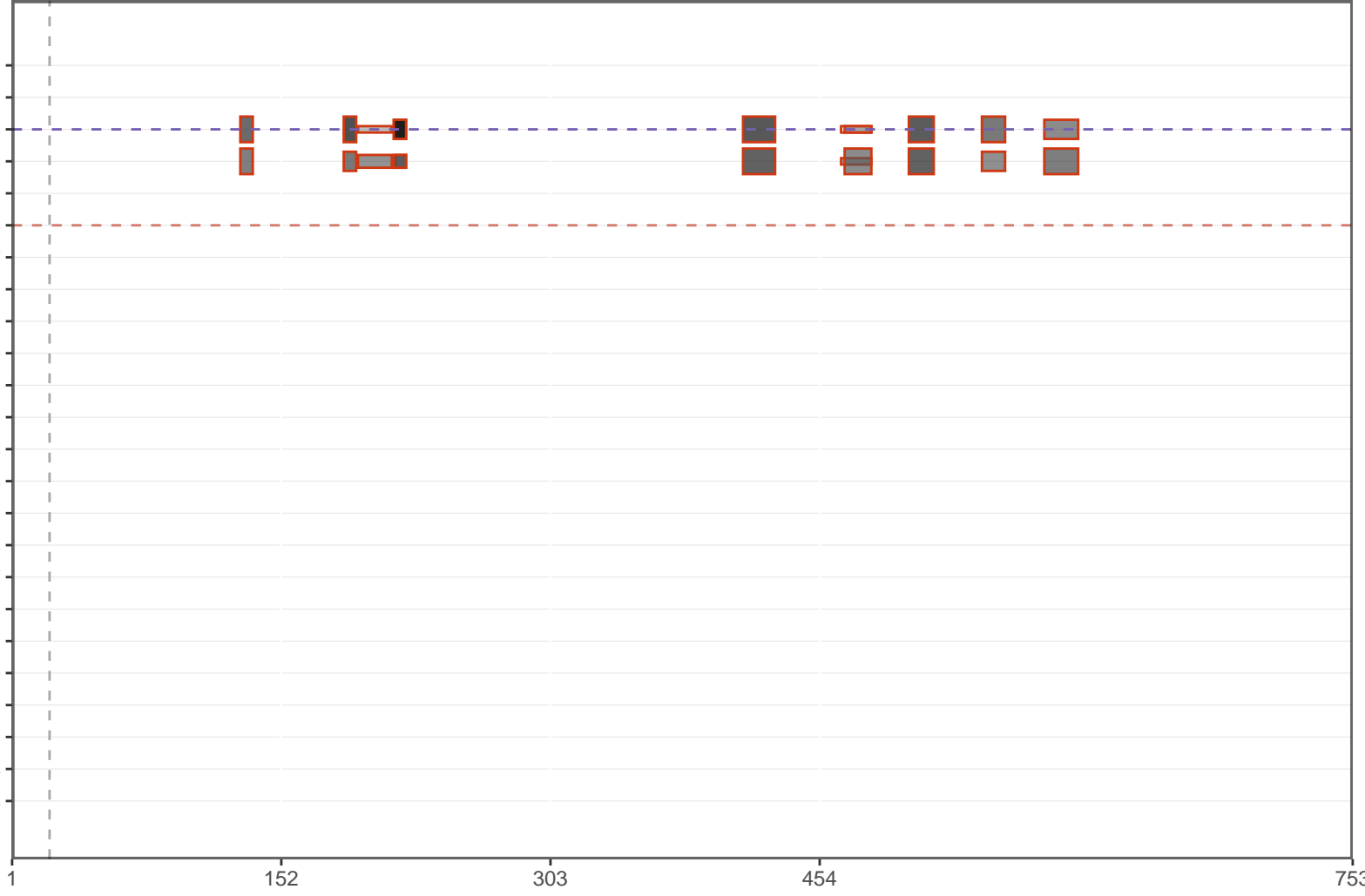
MW indication



Molecular weight

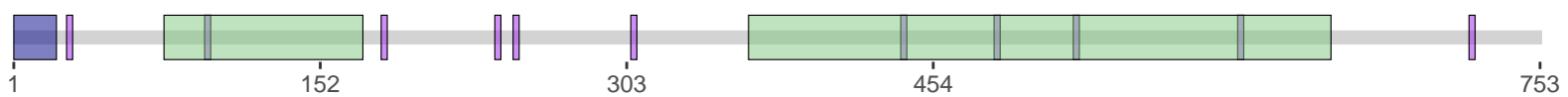


Gel Slice



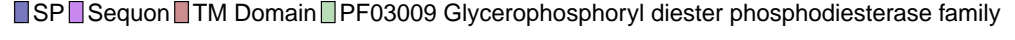
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ITSEGASGDYPCQTDLAVTKAASDGAADLQDPVQMTKDGIPFLGSLNIQKTTAAGSPFSNATTVPELKITNGLITNLVTEIHSGLKPAISNRWVDFRLFRNPKARNDGNFMSLADFLTFANNTTEVSGVMISENAAYLAKGDLGVTVGVALDGLSKGVNNGTAKKVLQSTDSVLEEFKKKSYELVYGVGDDRRDIESSTLEIKTFKAGVITKESVFPBEGAFIAGITNYYQKLGSSALTVYVQLFNNEFVSGAWDLFSDSLELNINWAVGAGHGKITEYPTAARYRNRCLL

NbL15g19070.1 uncharacterized_LOC109210041 [MW - SP = 46.5 kDa]

No. of times detected



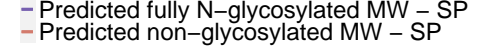
log(intensity)



Values from



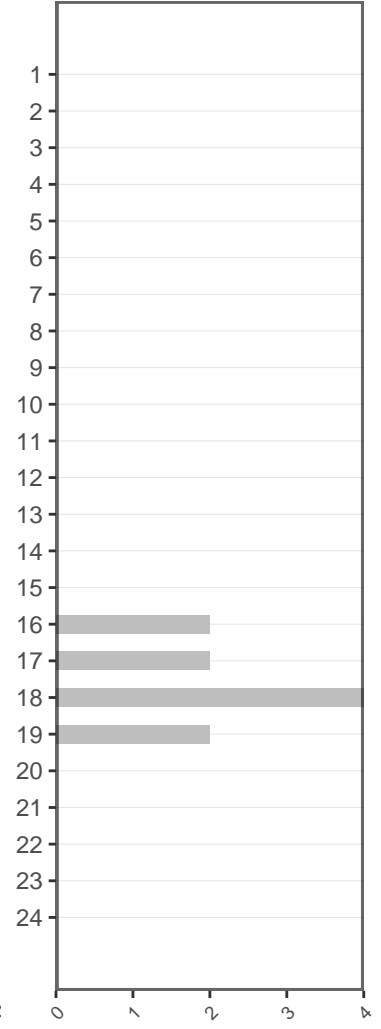
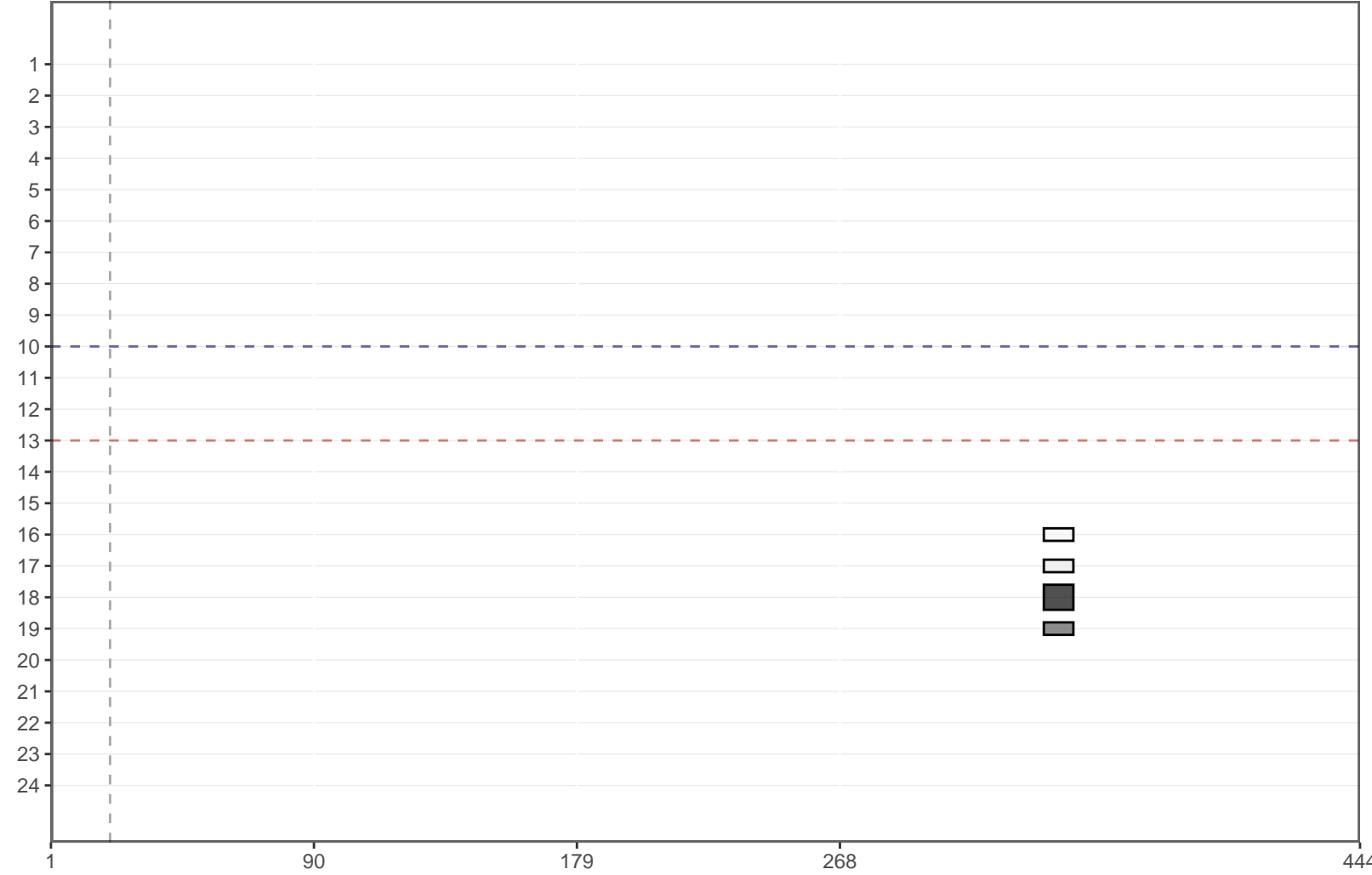
MW indication



Molecular weight



Gel Slice



Protein length

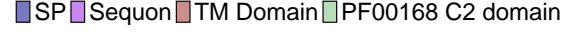


Peptide counts over 4 repeats

Pfam domains



Pfam Description

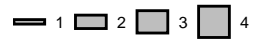


Protein sequence:

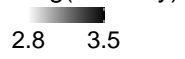
PVSVDTASRPPDSETPESLLKKEFDKIEFPDKILNENLNVSEYFNIPGTNLDDGSSDSFVSSDTENGLSSDQVHMEVFPDGVANFHRVYKREFRPTSVETIDSPSTLHPATSGSSDTGSAKSPGEEVAPAKSRDAERNSETKPSGAFPKPVAVVNIPEQKVVGQDQVDMVMKMSMDQFTESLAKMMLPLEMETRPTTSGNSSSDQGTGTPKSTGSRVYVGSRAFF

NbL15g18980.1 ABC_transporter_C_family_member_3 [MW = 174.35 kDa]

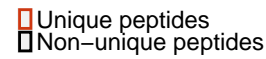
No. of times detected



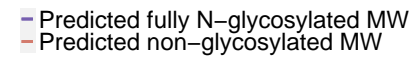
log(intensity)



Values from



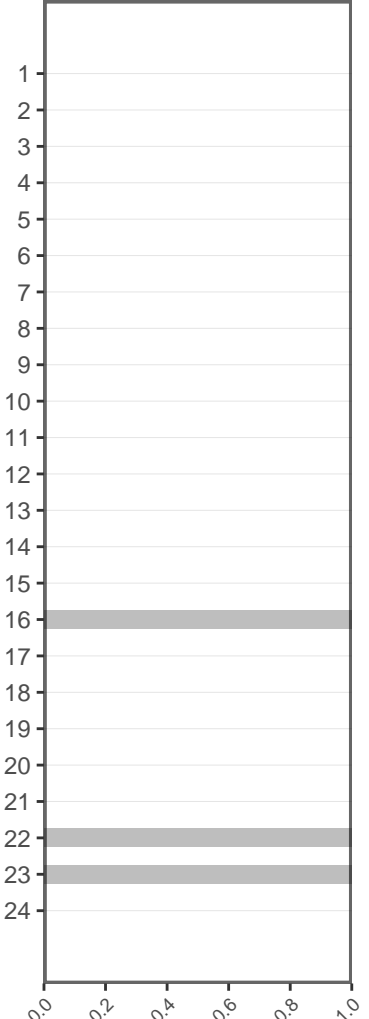
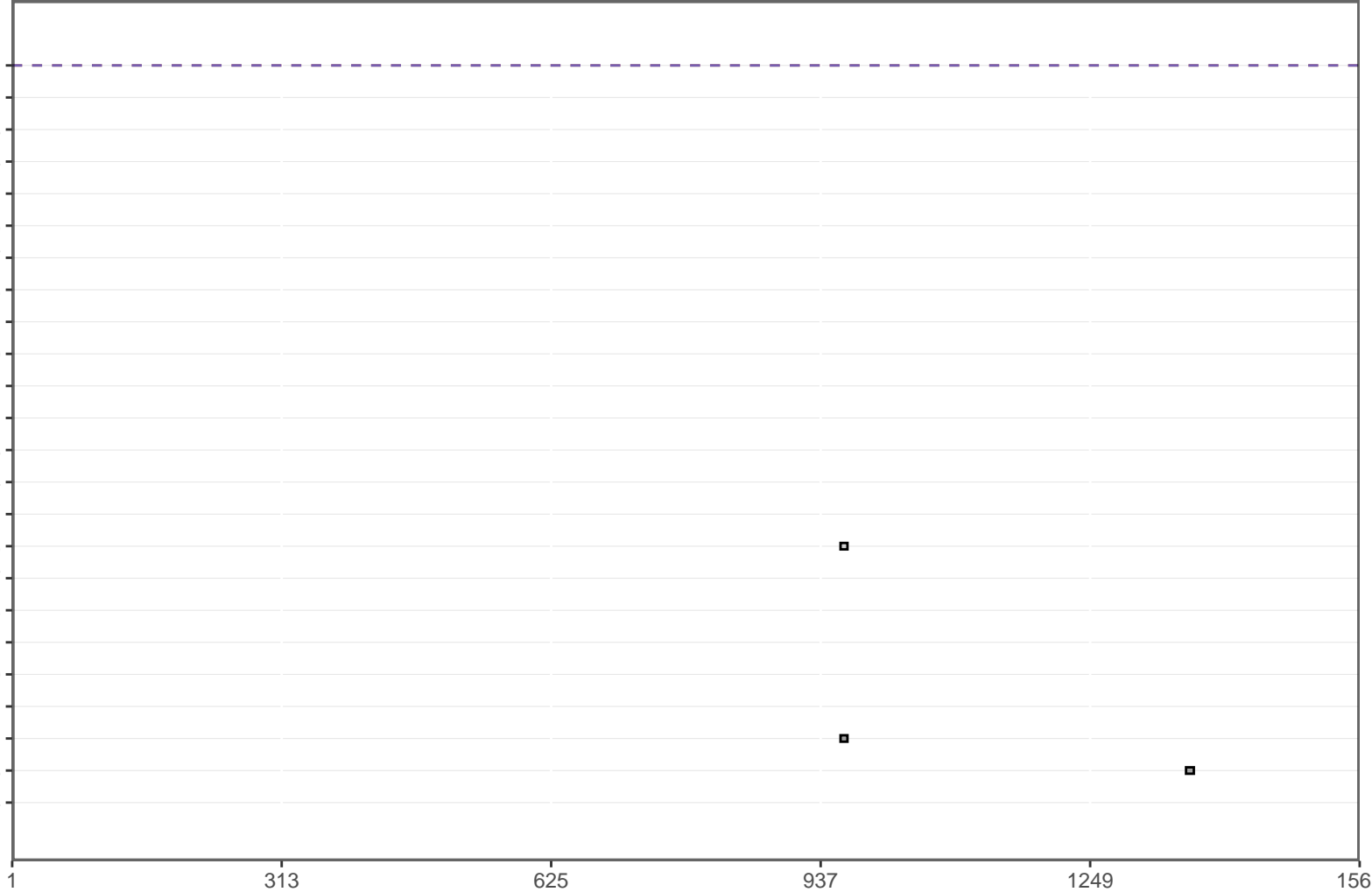
MW indication



Molecular weight



Gel Slice

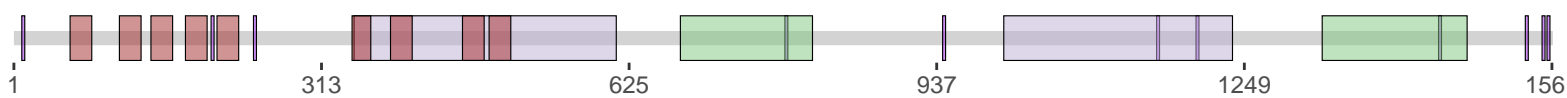


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

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NbL15g18830.1 DNA_ligase_1-like [MW = 73.68 kDa]

No. of times detected



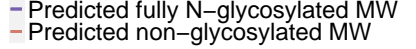
log(intensity)



Values from



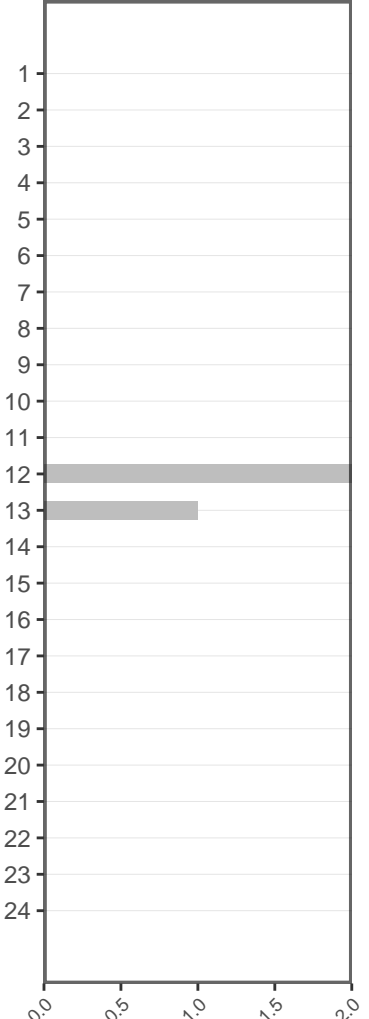
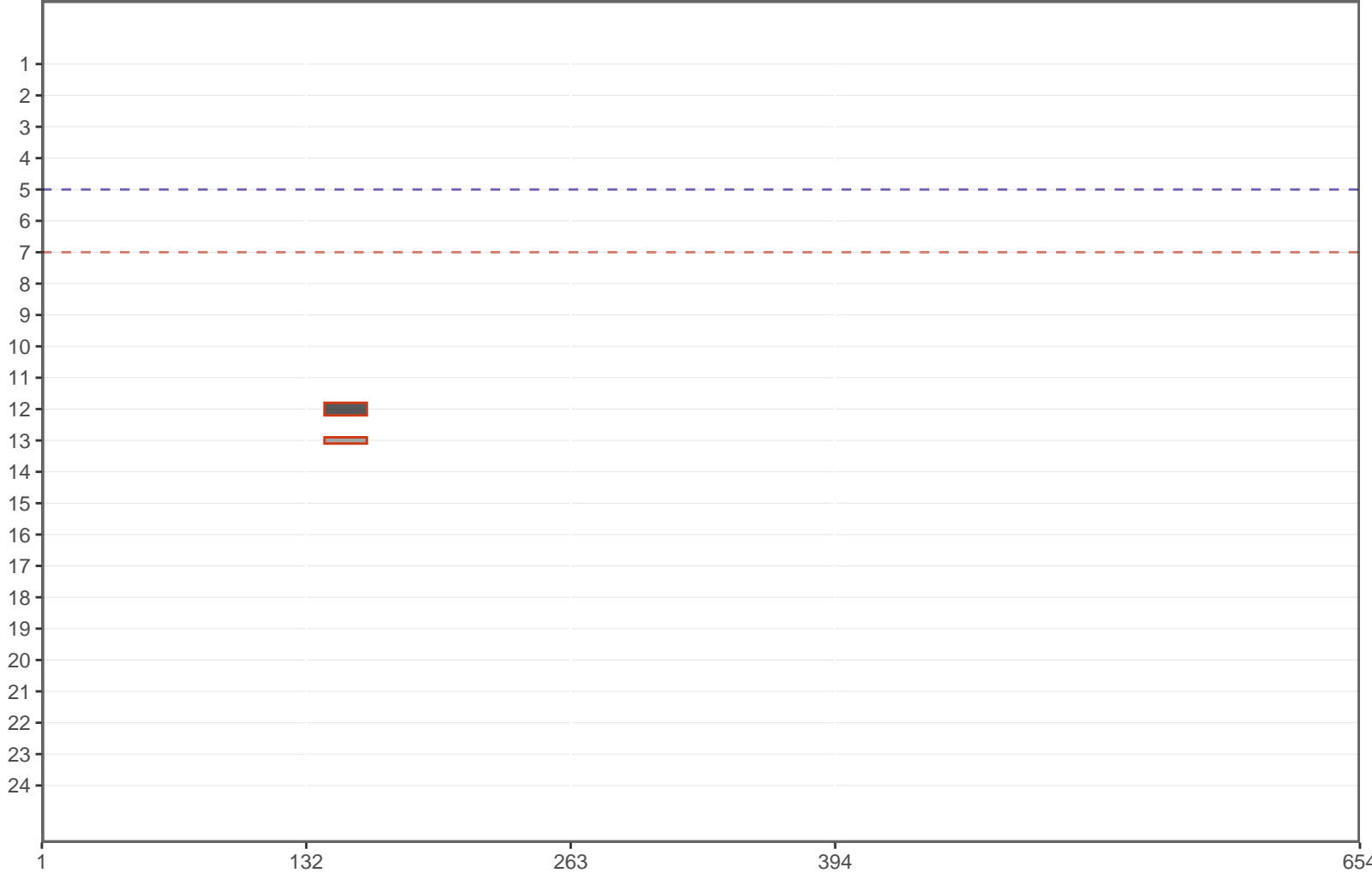
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

/KEKLDKYYKELLEFCQVLDIPVSKATSRKEDVTKLLDFLEAPHAMTSELLAENEKESGSGKRRKRRESKRPSSASVSEKGTSGKTKTETASQKAEKKTVHESEDESEGEDDHEEESSEKANGVPEKSDDEMSQAESEKESSENESESEEDRKKHKQGSNKSSTKKEPEKAAKTKPKWAKLPSAPAKKTKTPKSPKSKHNASTDAPPKVASAKKKKAEVVEKESSEPKGKSTKENTGKKNVKGKDKGKEDKLRPDDDELRNAIDELKEVDNFNTATTTDLKQLAKRFI

NbL15g18820.1 nudix_hydrolase_10-like [MW = 32.04 kDa]

No. of times detected



log(intensity)



Values from



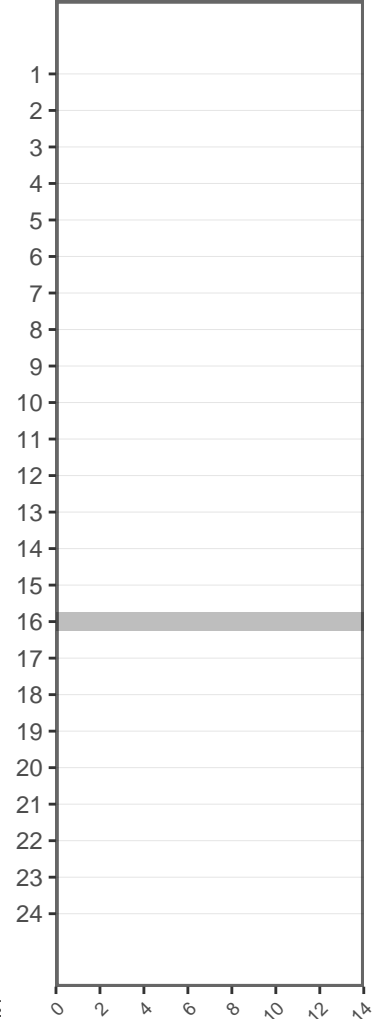
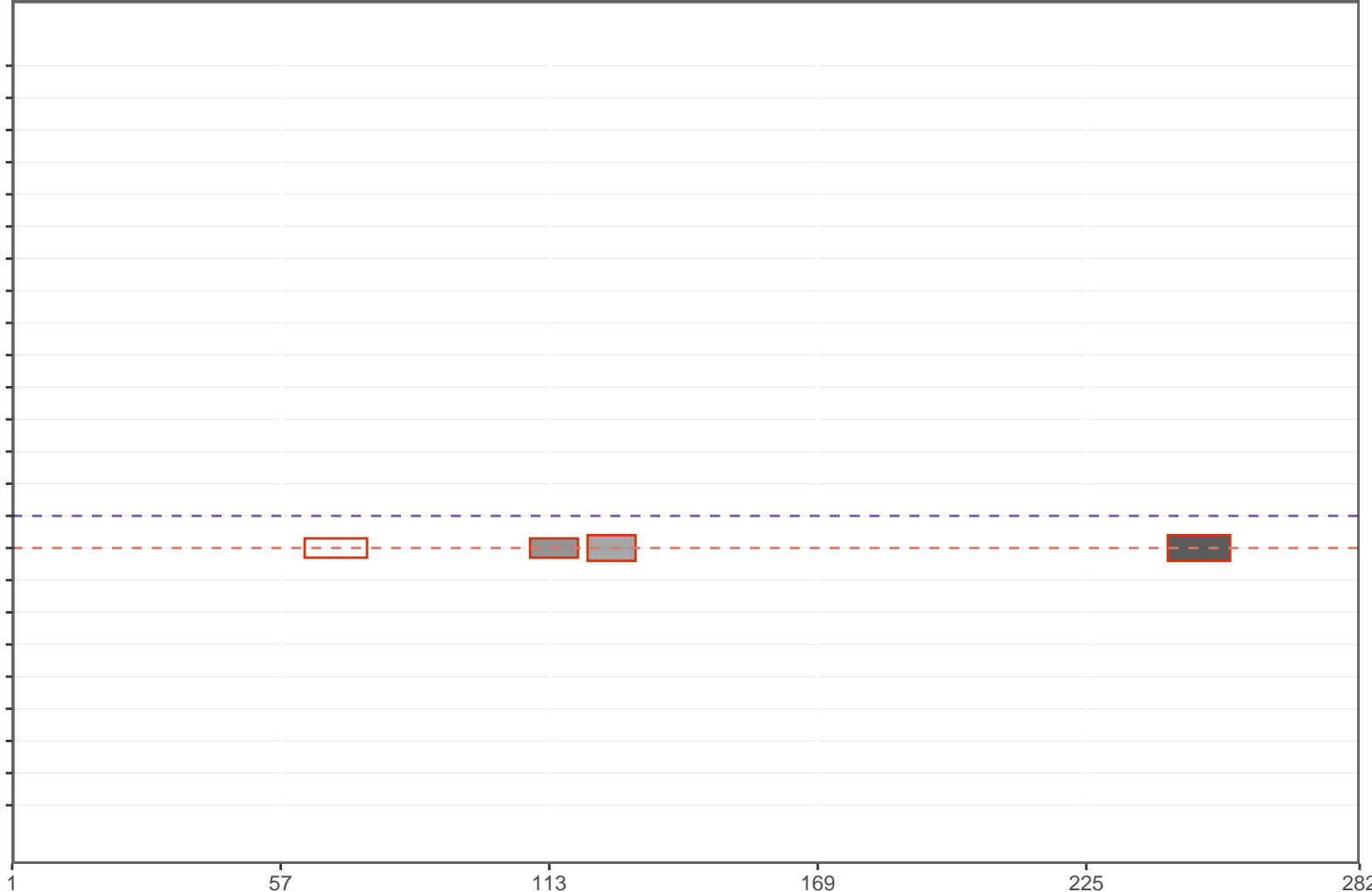
MW indication



Molecular weight

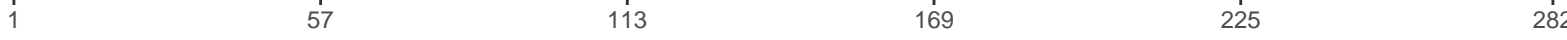


Gel Slice

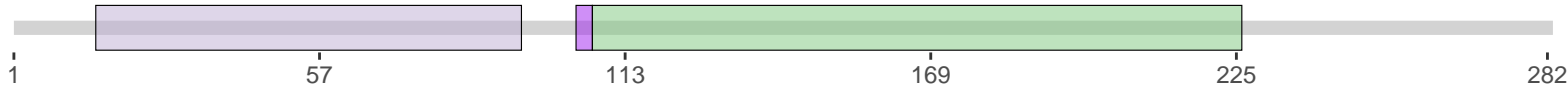


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

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NbL15g18490.1 putative_late_blight_resistance_protein_homolog_R1A-3 [MW = 106.61 kDa]

No. of times detected



log(intensity)



Values from



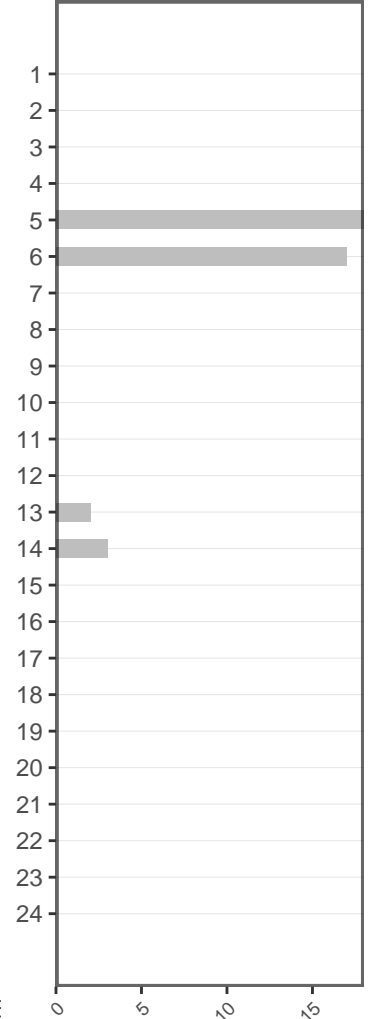
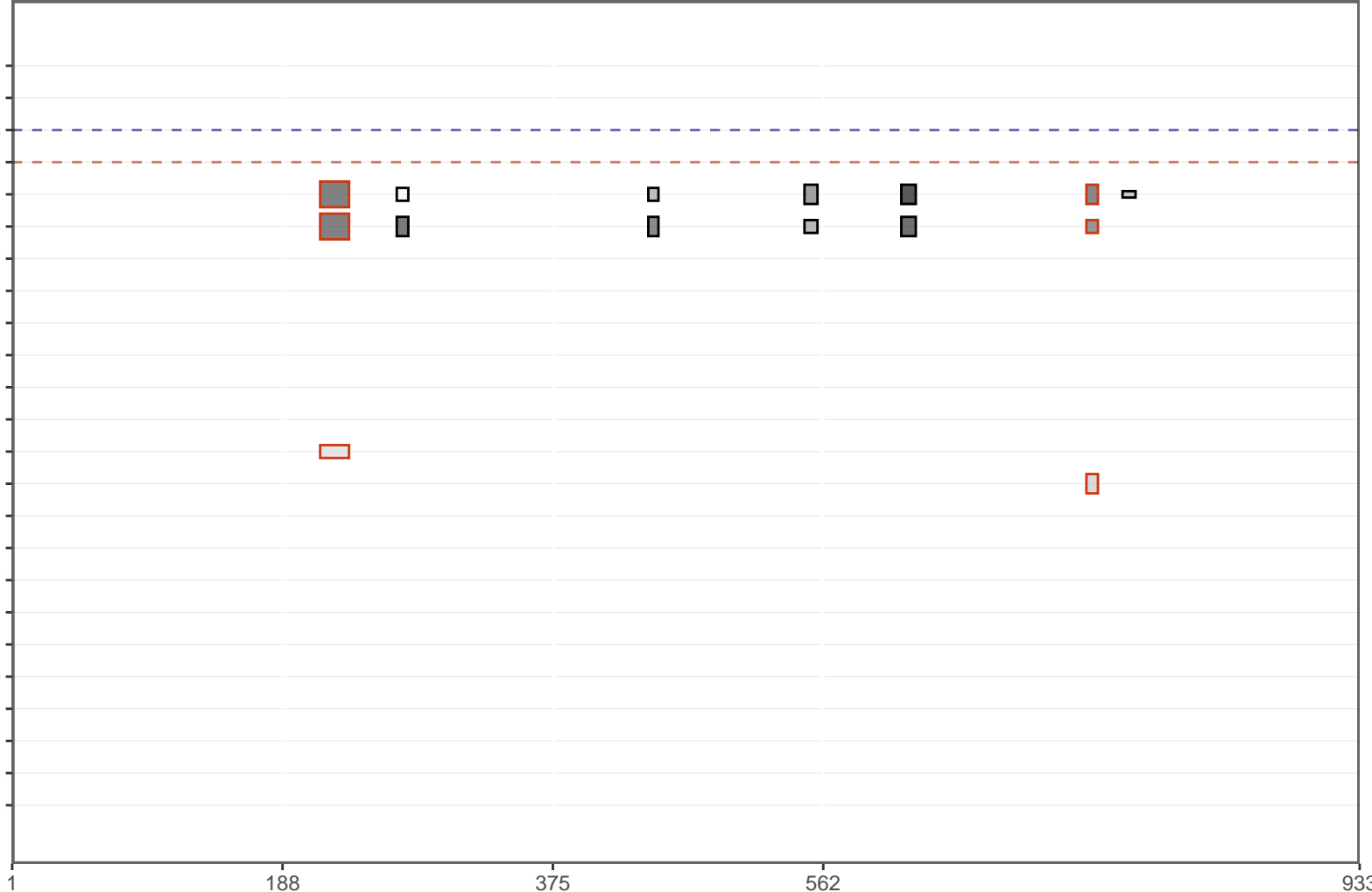
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

YDLKACFLYCGAFPGFEIPAWKLRILWAEFGHYKHLGLEKKAEDLNLDLNRNLVMMQRTSDGGKIKGRLDHMLHEFRGAEAMKEENLFGKILGAEQYFPGKRELATYRRLGHSSVLEFISTKPSGGEHVRSLFSGLKKEIPRSVDITPKGFLLRVFDVDSINFSRFSKEFFQLYLRYAFSSDTIKIPKHIGELVNIQTLINTQGRSLDGDANINWNERLRHLHTNSSAALPVPVTPRSGKVLVNGSLGLSTIAPESGTEEVFAKTPNKLGIKGIKLVLEPNK

NbL15g18400.1 heat_shock_cognate_protein_80 [MW = 80.19 kDa]

No. of times detected



log(intensity)



Values from



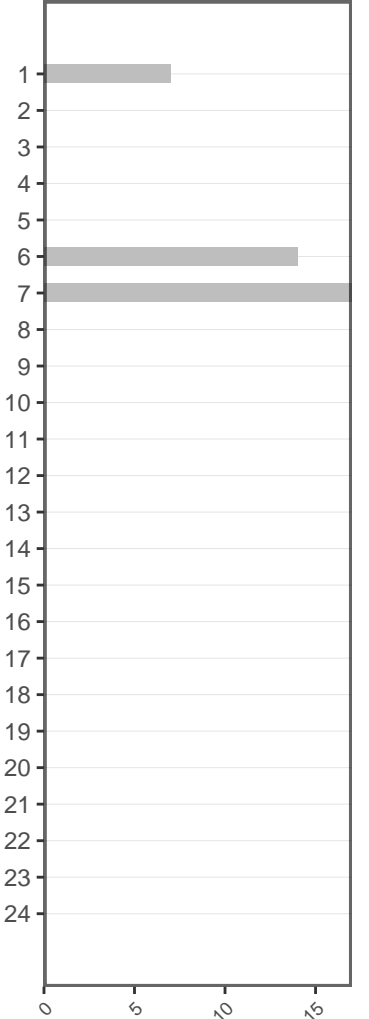
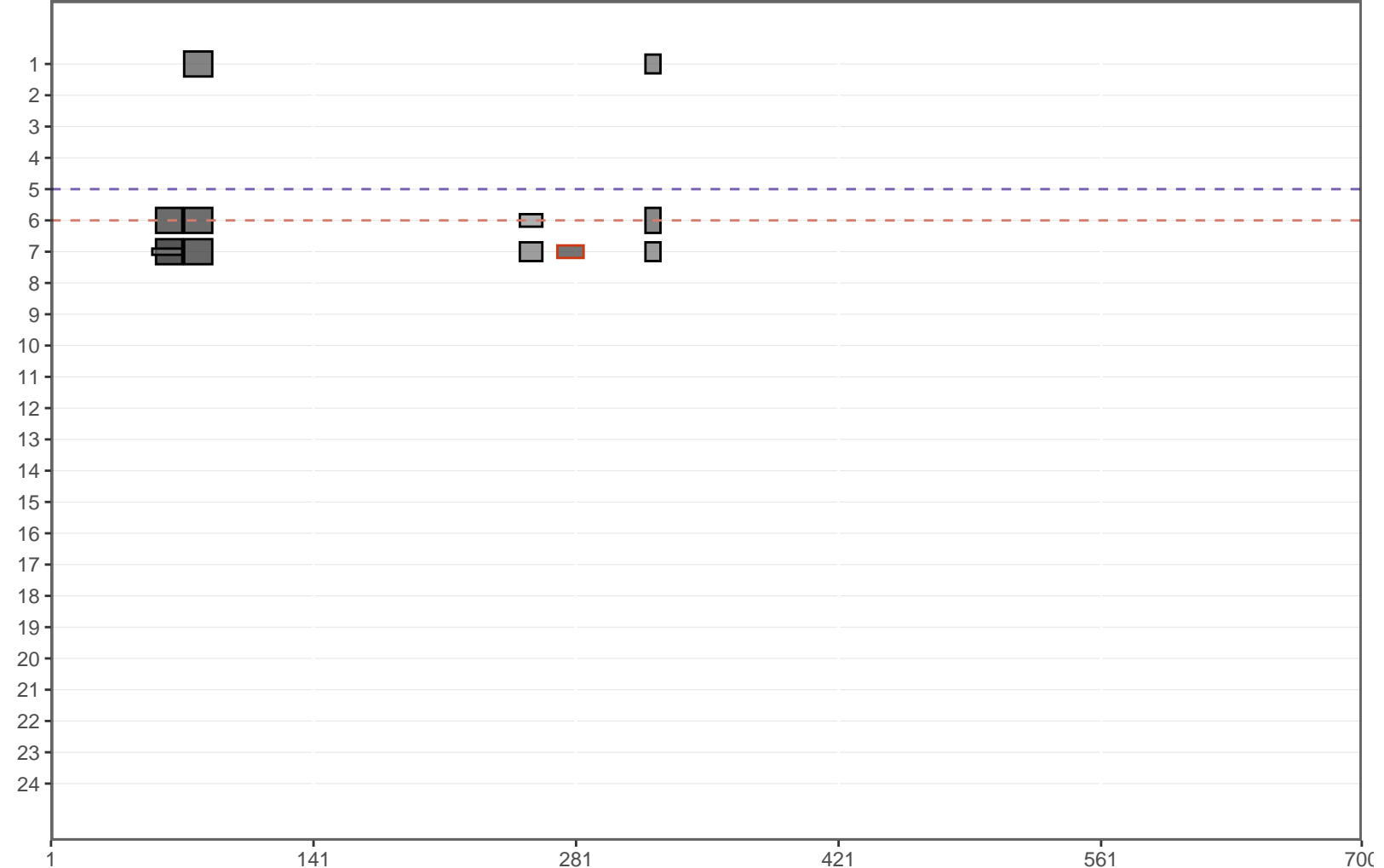
MW indication



Molecular weight

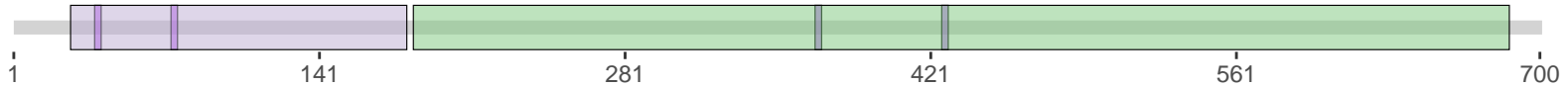


Gel Slice



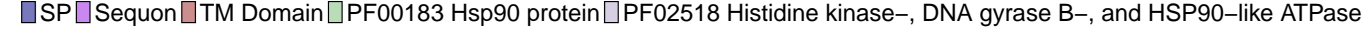
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

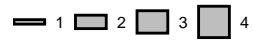


Protein sequence:

FIMDNC EELIPEYLSFVKGIVDSEDPLNISREMLGGNKIKVIRKLNKVKGVLFVFEIENKEDYKFKYFAFSKLNKLGHEDSGNNRSKFAELLRYHSTKSGDEMTSLKDYVTRMKEGGNDYYTGSSEKKAIVENSFFLEKTKKKGVYELVMVDAIDVYSIGGLKFEFGKIKVATKGEGLKLDSESEDEKKKQELKKEFEGLOKVKDVLGDKVKKVYVSDRVVDSFQGLVTGEVGVGTANKMERIMKAQALRDSGMDGVMSSKTKMEINPENNAIMEELRKRADAKKDKSVYDLSI

NbL15g17860.1 protein_RAE1 [MW = 38.28 kDa]

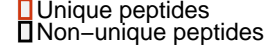
No. of times detected



log(intensity)



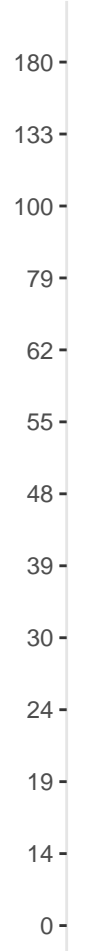
Values from



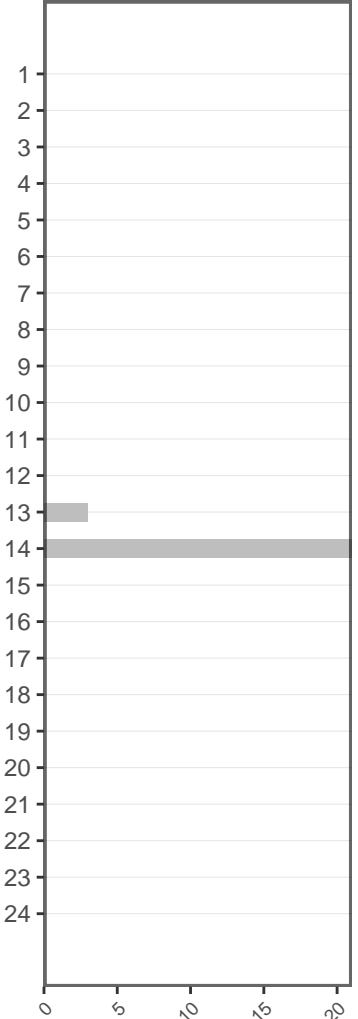
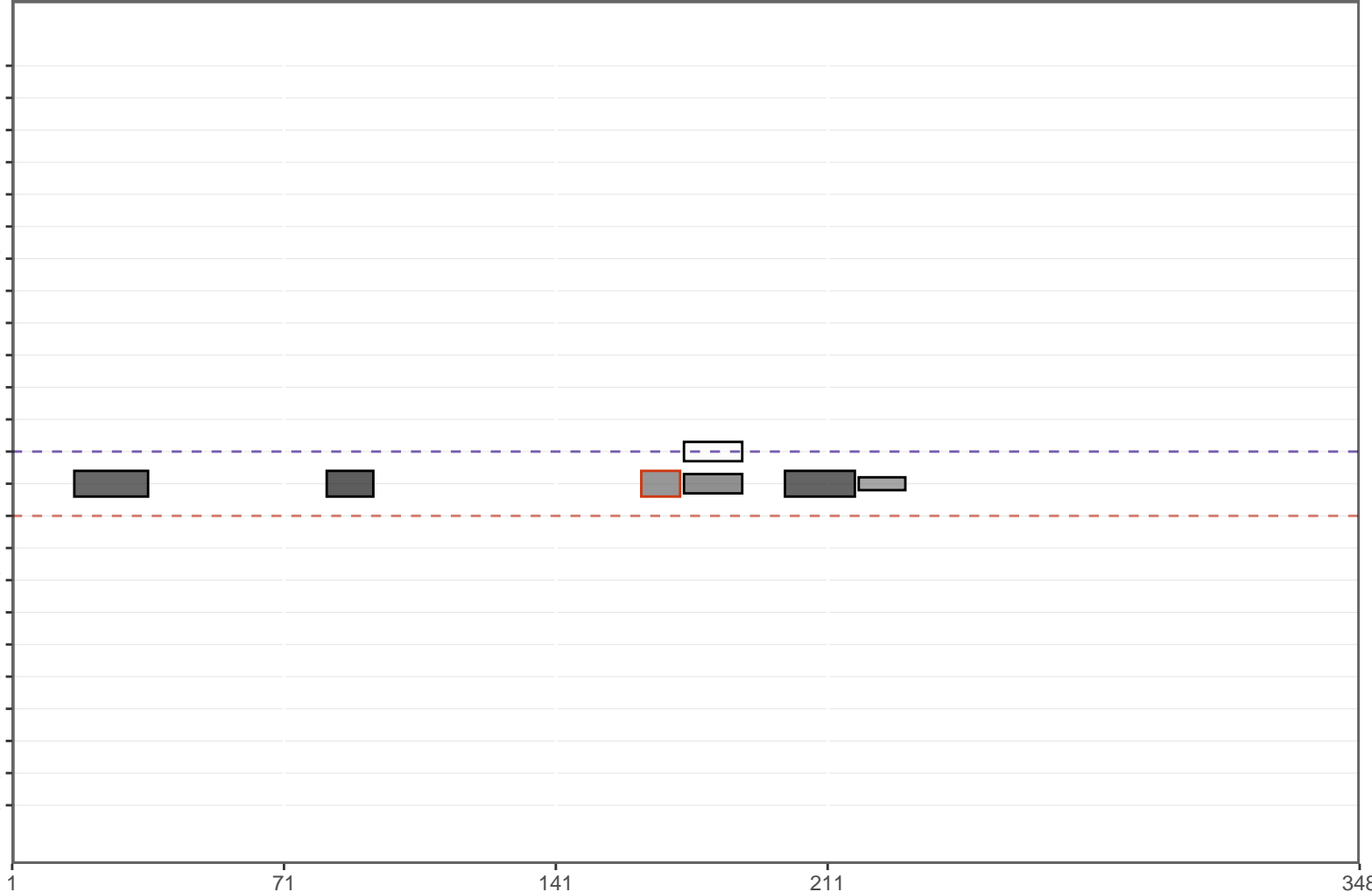
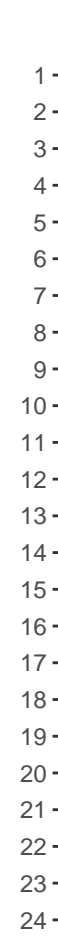
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

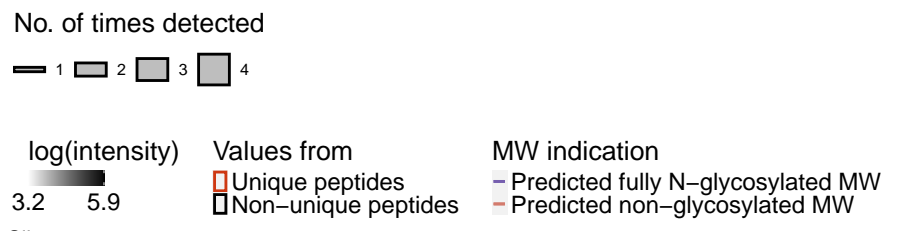
Pfam Description



Protein sequence:

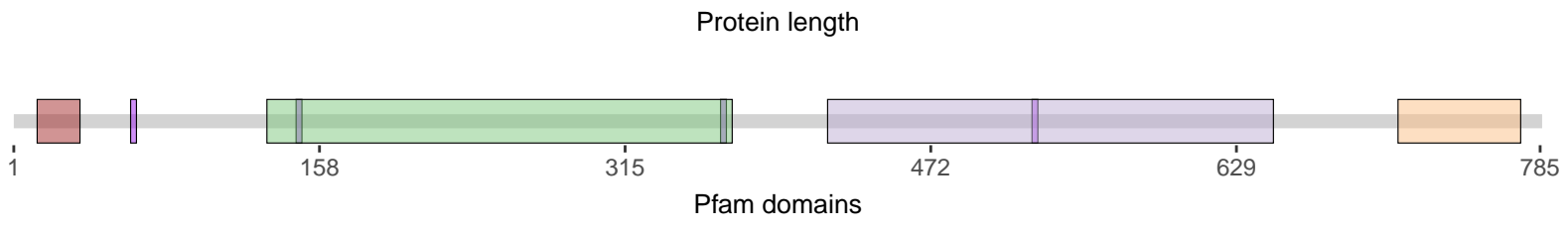
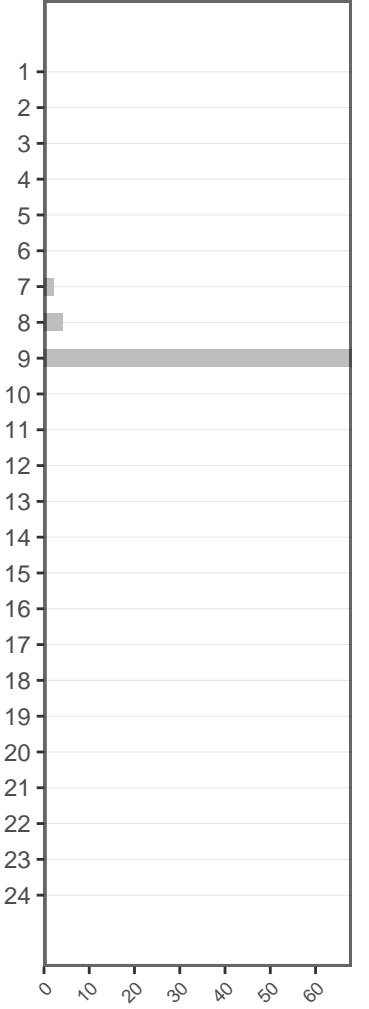
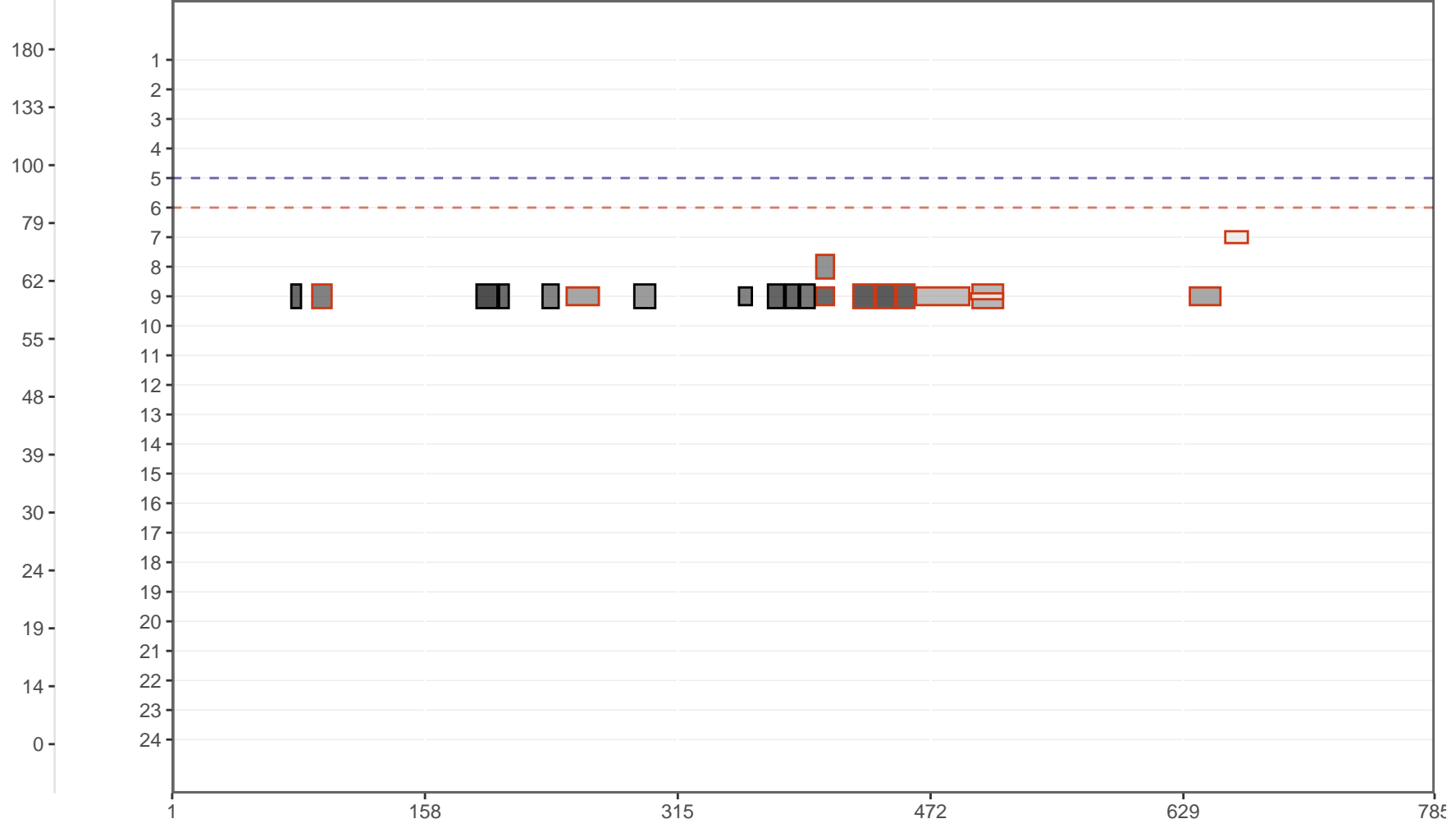
ITVKIPLMVAGTADRLNLFVNLGNPQTEFRNRITSLKPKYKTRGLAAPPDQGGFLVGSIEGRVGVHHLDDSSGSGKNTFKGCHREGNEIYSVNSLNFHPVHGTFATAGSDGAFNFWDKDGGKRLKAMSRGSGPQPSAFNHDGSIYAWAVCYDWSKGAENHPSTAKTYIYLIHFQDESEVKGKPRIGSSGRK

NbL15g17830.1 beta-xyloridase/alpha-L-arabinofuranosidase_2 [MW = 85.59 kDa]



Molecular weight

Gel Slice



Pfam Description

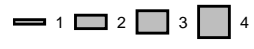
- SP
- Sequon
- TM Domain
- PF00933 Glycosyl hydrolase family 3 N terminal domain
- PF01915 Glycosyl hydrolase family 3 C-terminal domain
- PF14310 Fibronectin type III-like domain

Protein sequence:

TLMLRGLGFFDGNPRNHYKGLGPKDVGTFENDELAREAAARQGVLLKNAAGSLPLTPTAKLAWGPNADVTKTMTMGVYEGTDPKYYTFLDGLTASVAVYKPGGSDVSGNTAGLDDANKKASTADAVVMVMSDGSIERESLDRVNTFLPGQGVLAIEAVAKVAKGPKVILVMSGGGMDVGFVNDKPKTSILWVGFPGEGAGGAALADVFGYVNPSSGRPLMTVWYVQSYADVVPMTIMNMRPDKATNYPGRTRYREYTGPTVFTFGHGLS6YSGPKHRLDQAPTFYSPLKAKITC

NbL15g17790.1 dynamin-like_protein_ARC5 [MW = 86.95 kDa]

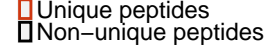
No. of times detected



log(intensity)



Values from



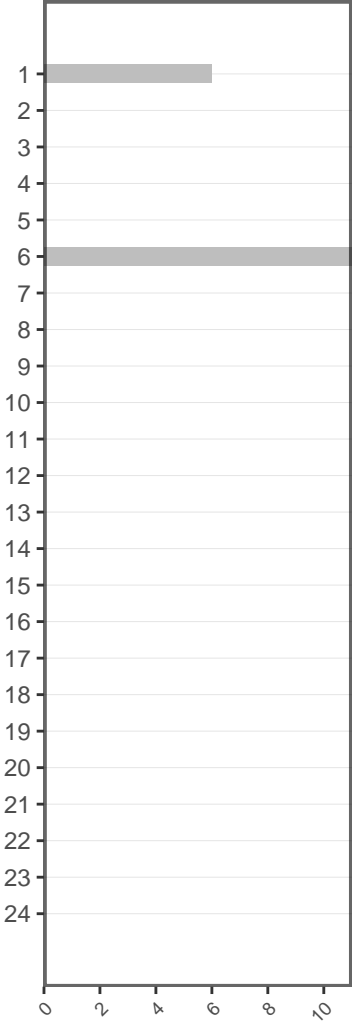
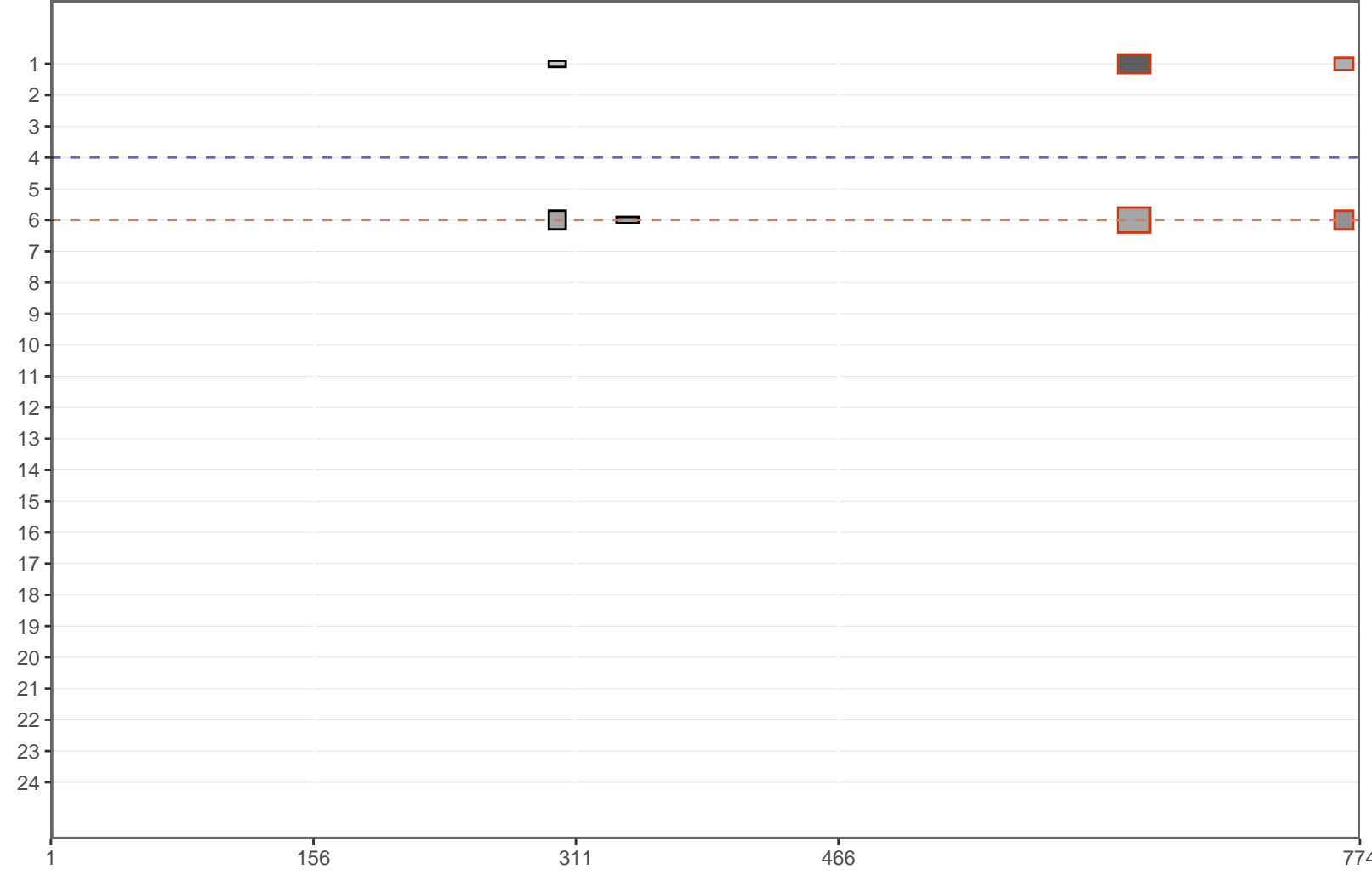
MW indication



Molecular weight



Gel Slice

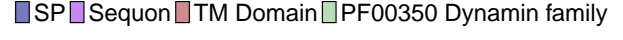


Protein length



Pfam domains

Pfam Description



Protein sequence:

KGRNFHDLFTLKLKLLKGTWAPPKFGFELQDERVNGGAFIGSDGLQFFPKLIPNAGMRLLYGGAGYHRAMAEFRFVVGKGPPTREEVNVAGGVEDIHDGNTYSRTAGVAAWKARDTFEPFLHQLGCRLLHLKRLLPVAYLLQKEGEVLSGHQVFLRRVADAFNFAESTEKSGREKCMEDLVSTTRYVTWBLHNKNRAGLRQFLDSFGGSEQSAKGNSTGLSGDLSTASVSDNKGDEVKPRTEVVKLSHLASGNDENSTSTGTTETRLADLLOSTLVNRRLPSS

NbL15g17720.1 GDSL_esterase/lipase_At1g28590-like [MW - SP = 38.02 kDa]

No. of times detected



log(intensity)



Values from



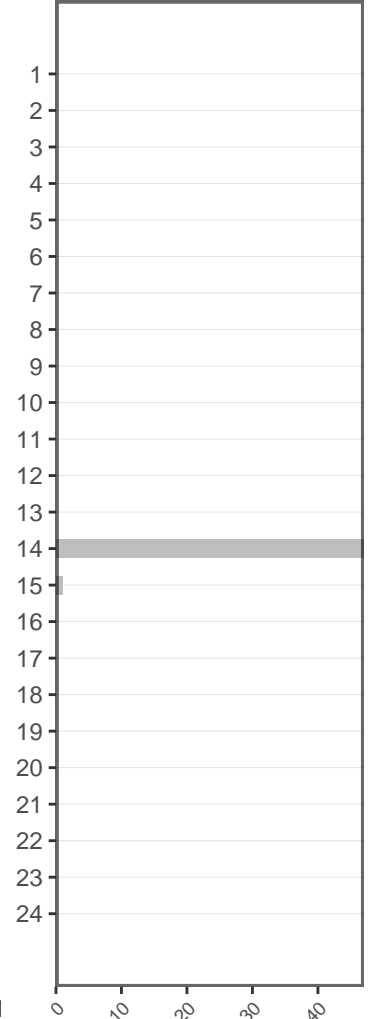
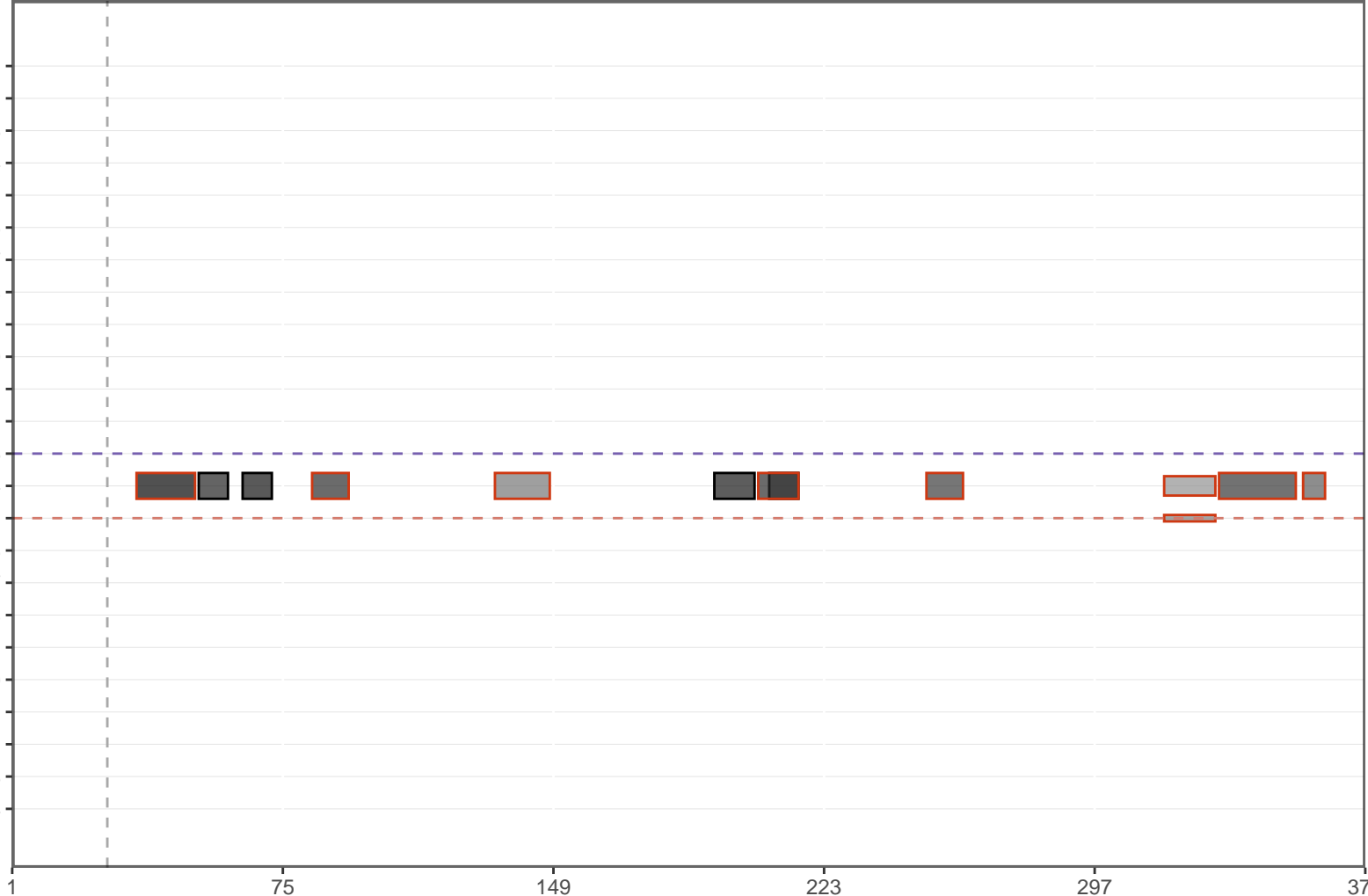
MW indication



Molecular weight



Gel Slice



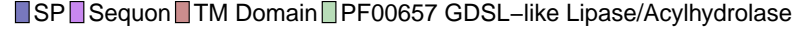
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

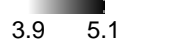
SGNDZYNNFQRKQLPEVRYVVFVAGIMRGKDWGLGATRLVPGFFPLGCLPLVLTFFPDNANAYDQLGLRNYNDFASVYHRYLNRGLDLRREFNVRVYGVNGAFLLTLOSASSFGFNQNTLLAACGGTGGRYNFFNSVCGSASVVRACSNPMQVYVHWGHLTDEAHRRTDINVKMLSRLLGGSVY

NbL15g17660.1 60S_ribosomal_protein_L3-like [MW = 48.51 kDa]

No. of times detected



log(intensity)



Values from



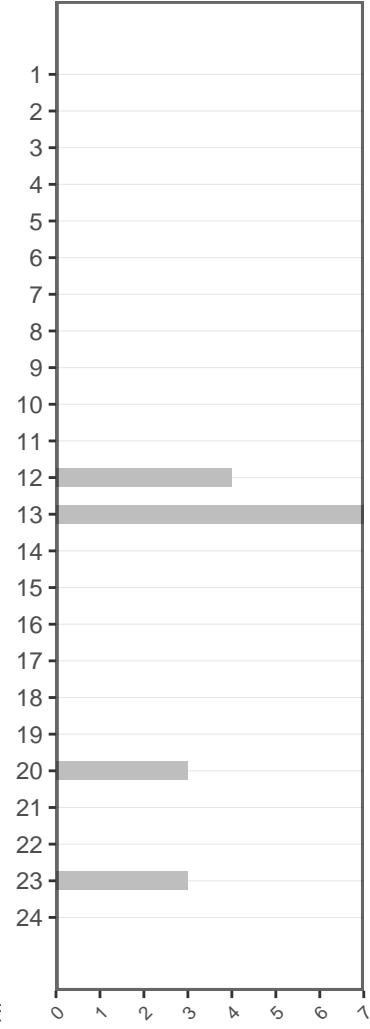
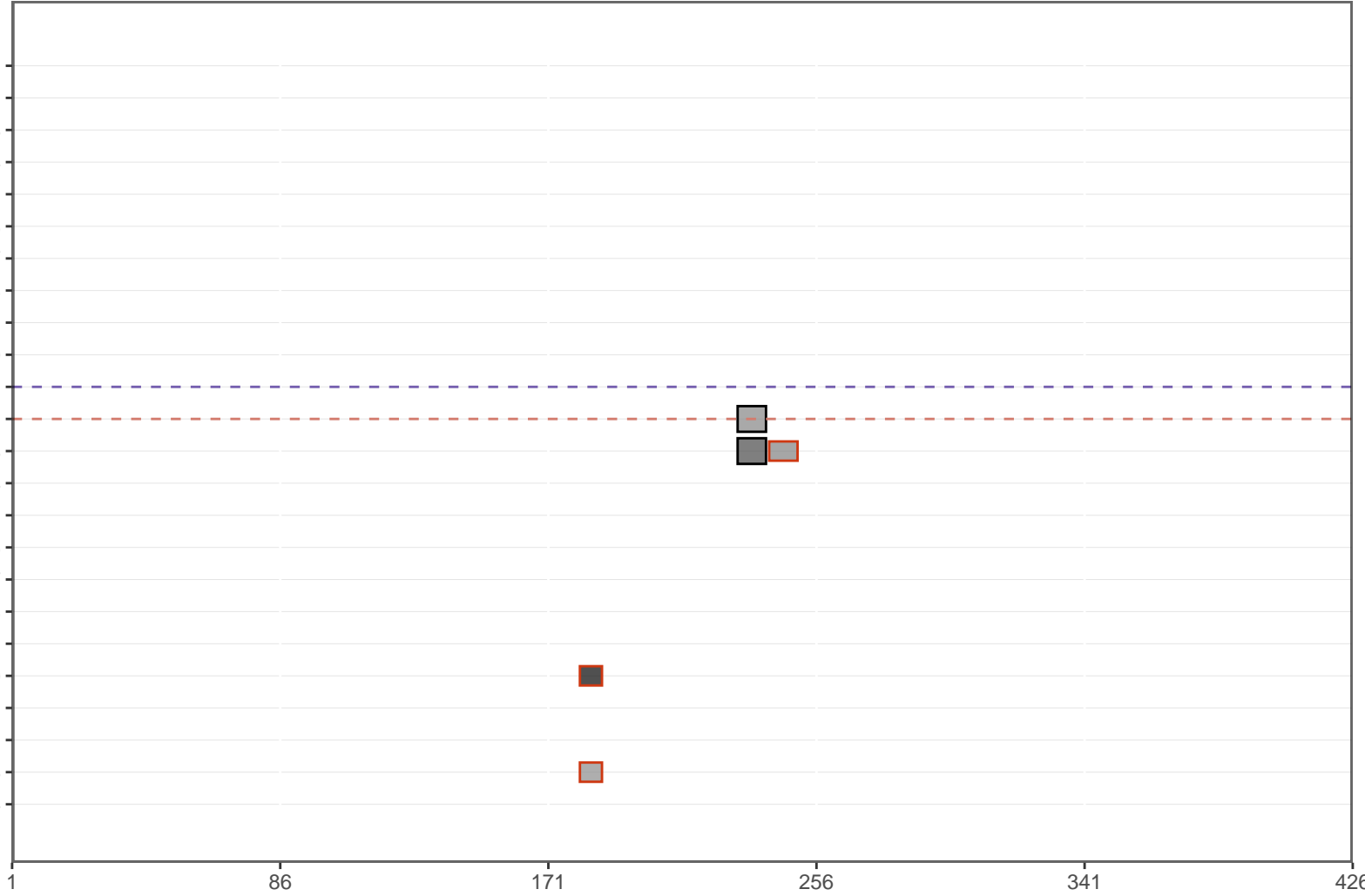
MW indication



Molecular weight

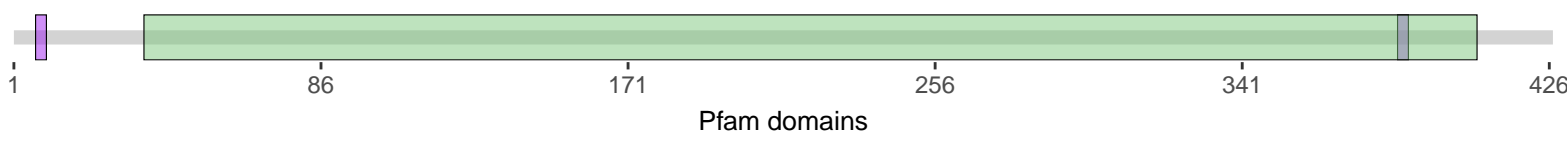


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam Description



Protein sequence:

MKGLKQKKAHLMKQVNGSTAGKVDWYGFYFEKQVVDVAFQKDEMDIGVTKGKVEGVYTRWGVTRLPKTRHRLRKAAGIGAWHFRVSYTVARAGNGYHHRTEMNKVYRLLGKAGGESHAAITDFRTEKDTIFMGDFPHYGVKEDYLLKGGCGVPRKRVVTLRGLLNGTGRVALEEIKLFRDTSKFGHGRFGTTGKQKFGYRLKA*

NbL15g17540.1 ankyrin_repeat_domain-containing_protein_2B-like [MW = 48.74 kDa]

No. of times detected



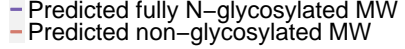
log(intensity)



Values from



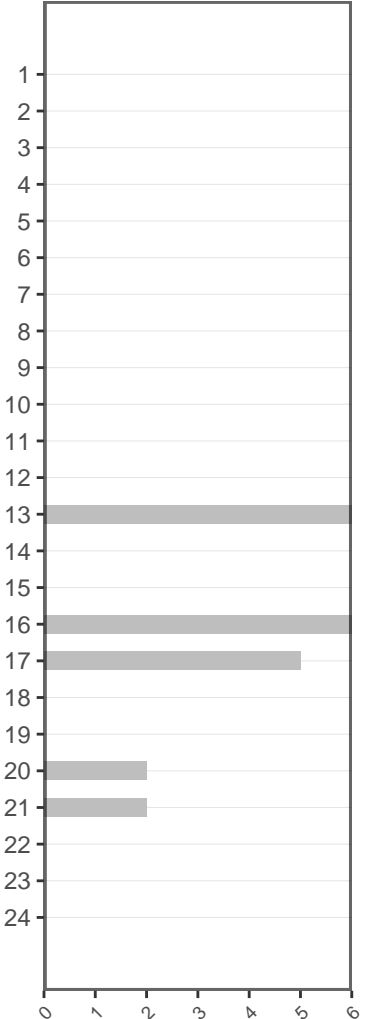
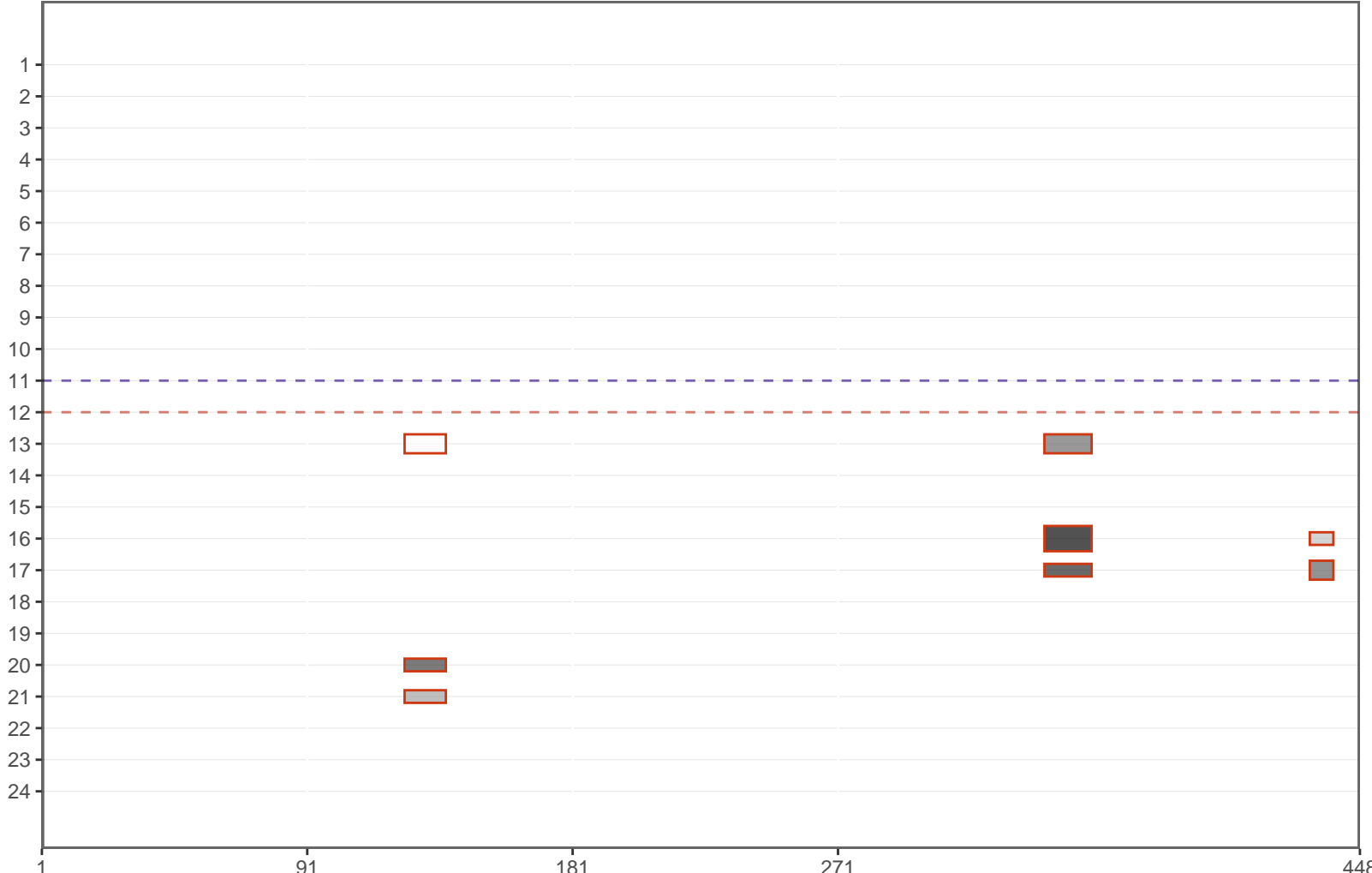
MW indication



Molecular weight



Gel Slice



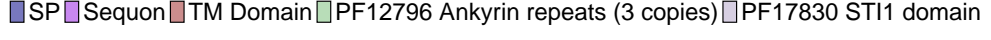
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL15g17440.1 60S_ribosomal_protein_L18-2-like [MW = 20.91 kDa]

No. of times detected



log(intensity)



Values from



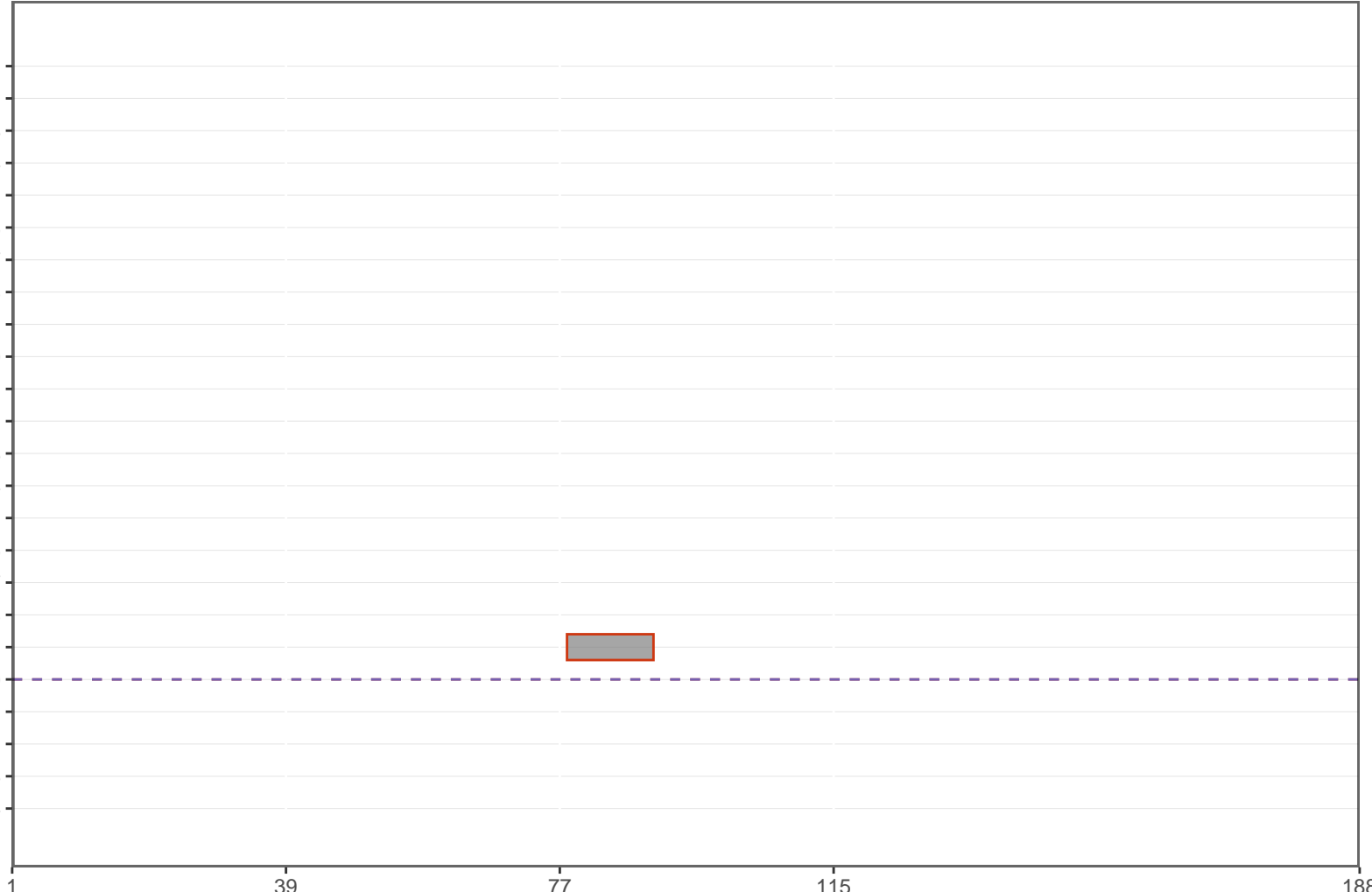
MW indication



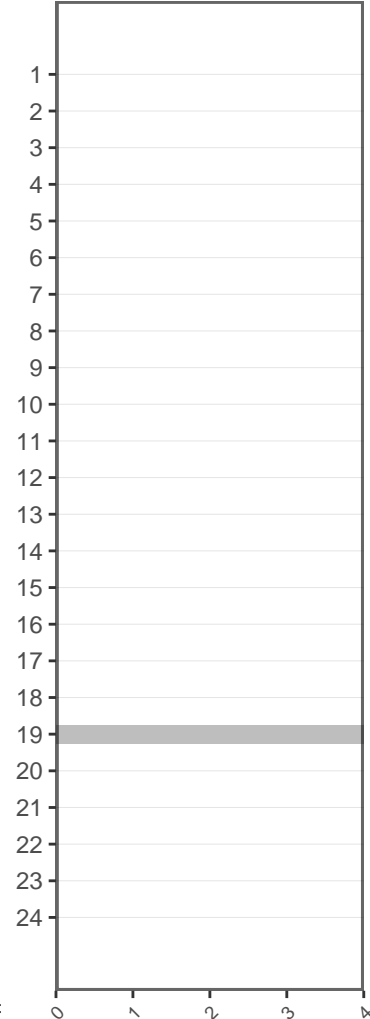
Molecular weight



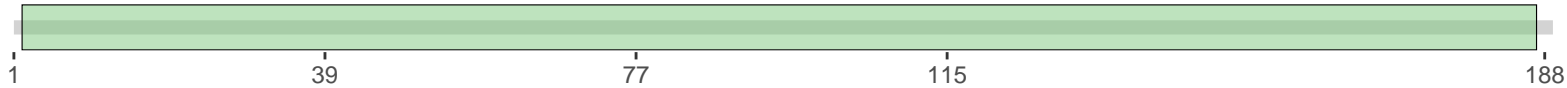
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

3TITDQVAYDVPITKIVGALRFETKARARIEKAGGEGELTFDGLALRAPLGGNTLLLRGPKNAREAVKQFGPAPGVPHSHTKPVVRSKGRKFERARGRRKSRGKYK

NbL15g17410.1 60S_ribosomal_protein_L22-3-like [MW = 14 kDa]

No. of times detected



log(intensity)



Values from



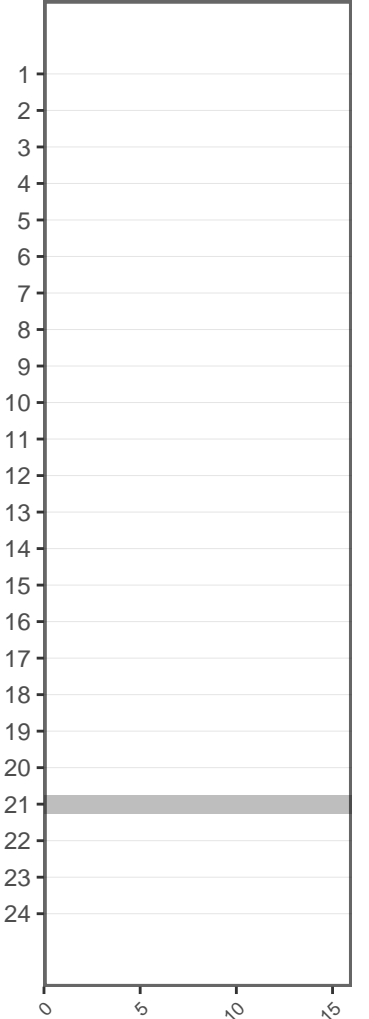
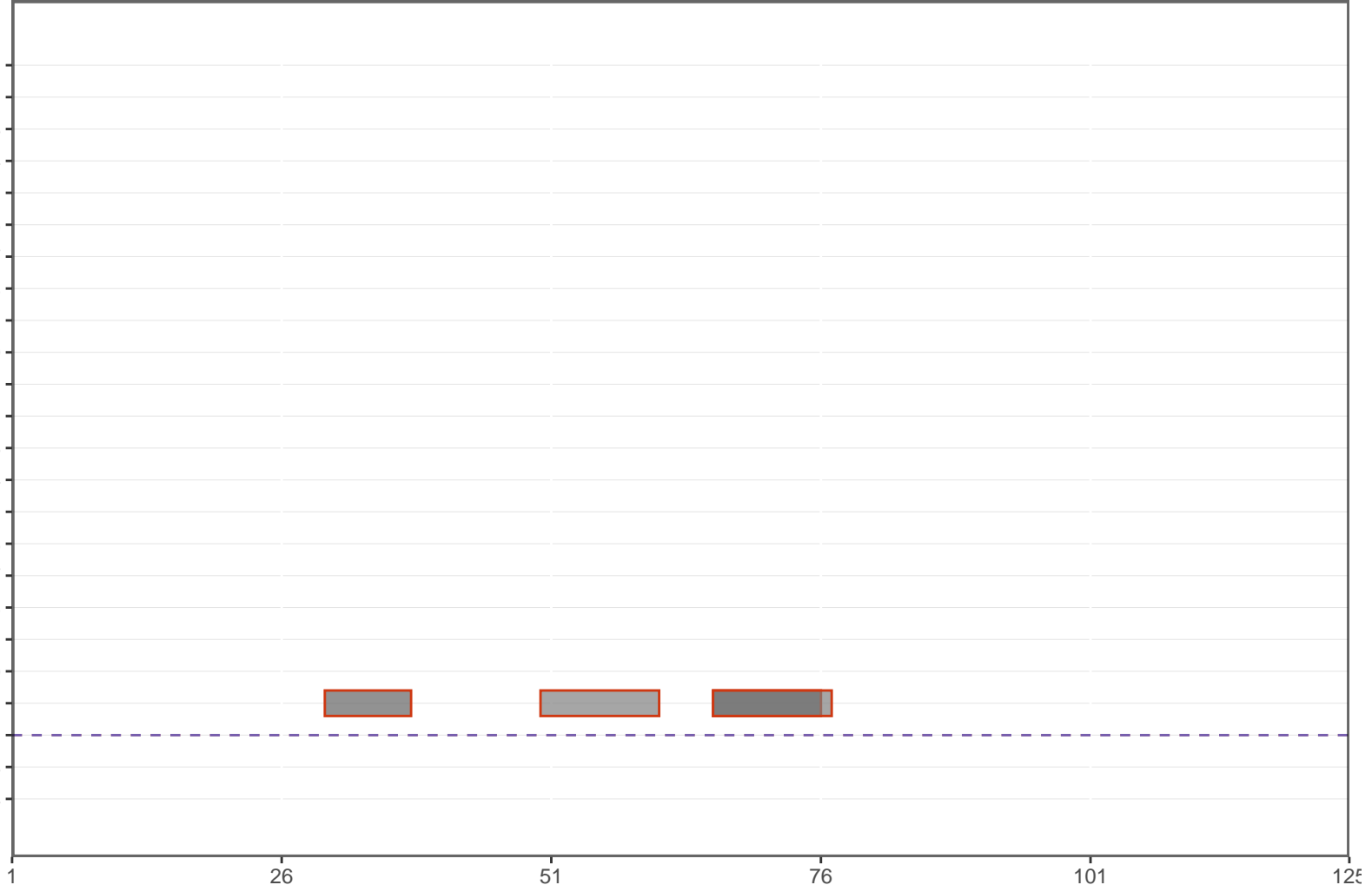
MW indication



Molecular weight



Gel Slice

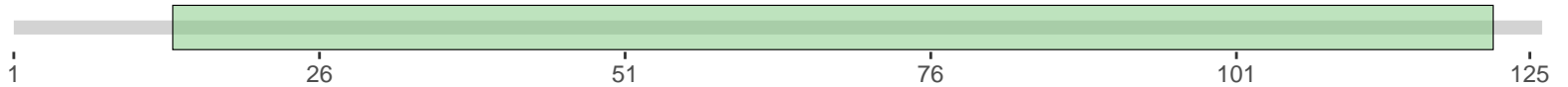


Protein length

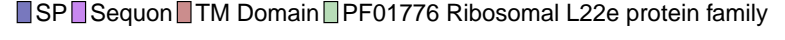


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

JAGALGDTVTVTRDKTKITVTSDSSTFSKRYLYKLTIKYLYKKNVNRDILRVISGNKDRNVVELRYFMAENEAEEDP

NbL15g17080.1 40S_ribosomal_protein_S5-like [MW = 23.37 kDa]

No. of times detected



log(intensity)



Values from



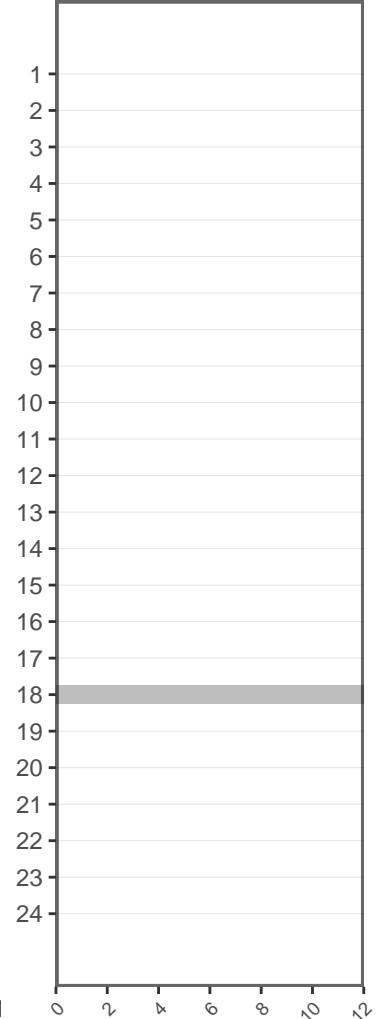
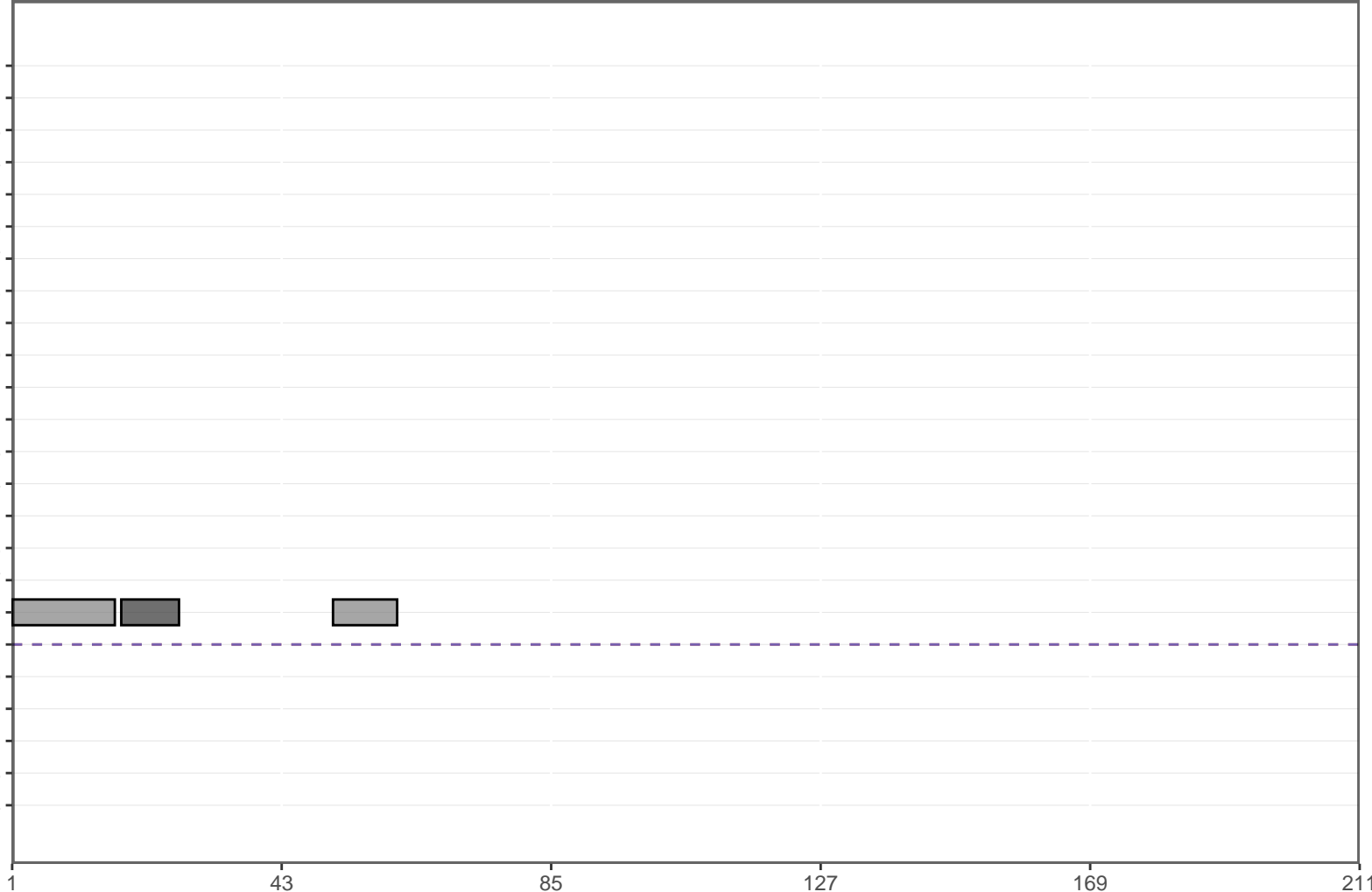
MW indication



Molecular weight



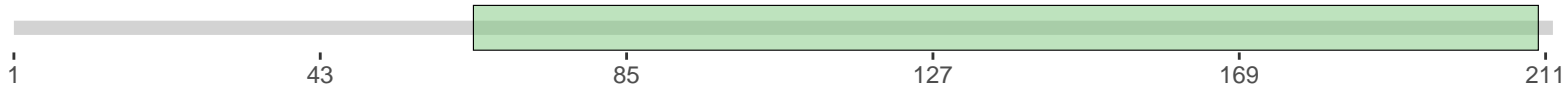
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

GKILMAVRIKIHMEIHLTDFQNFQVVDVINGSPREDATRIKSGAGVVRQAVDISPLRRVNDQAFLLTGGARESAFRNKITAEGLADELINAANKGSENSYAIKKKDEIERVAKNR

NbL15g17000.1 carbon_catabolite_repressor_protein_4_homolog_1-like [MW = 66.98 kDa]

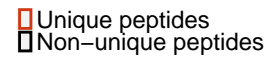
No. of times detected



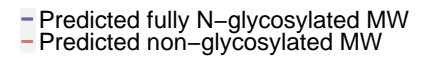
log(intensity)



Values from



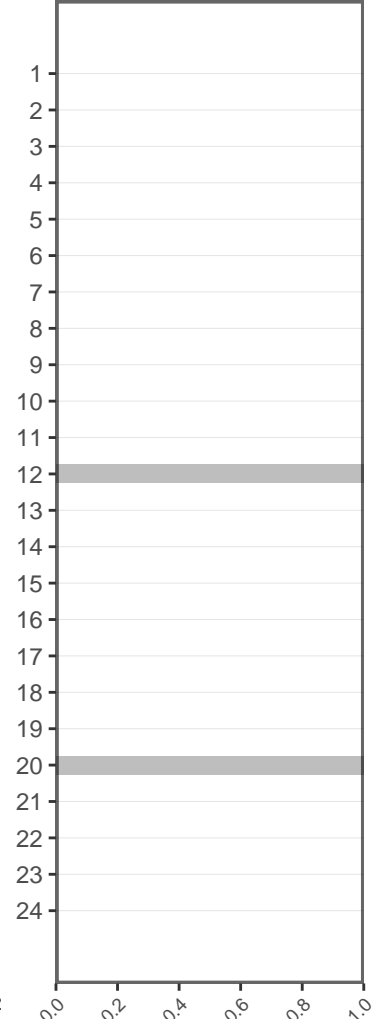
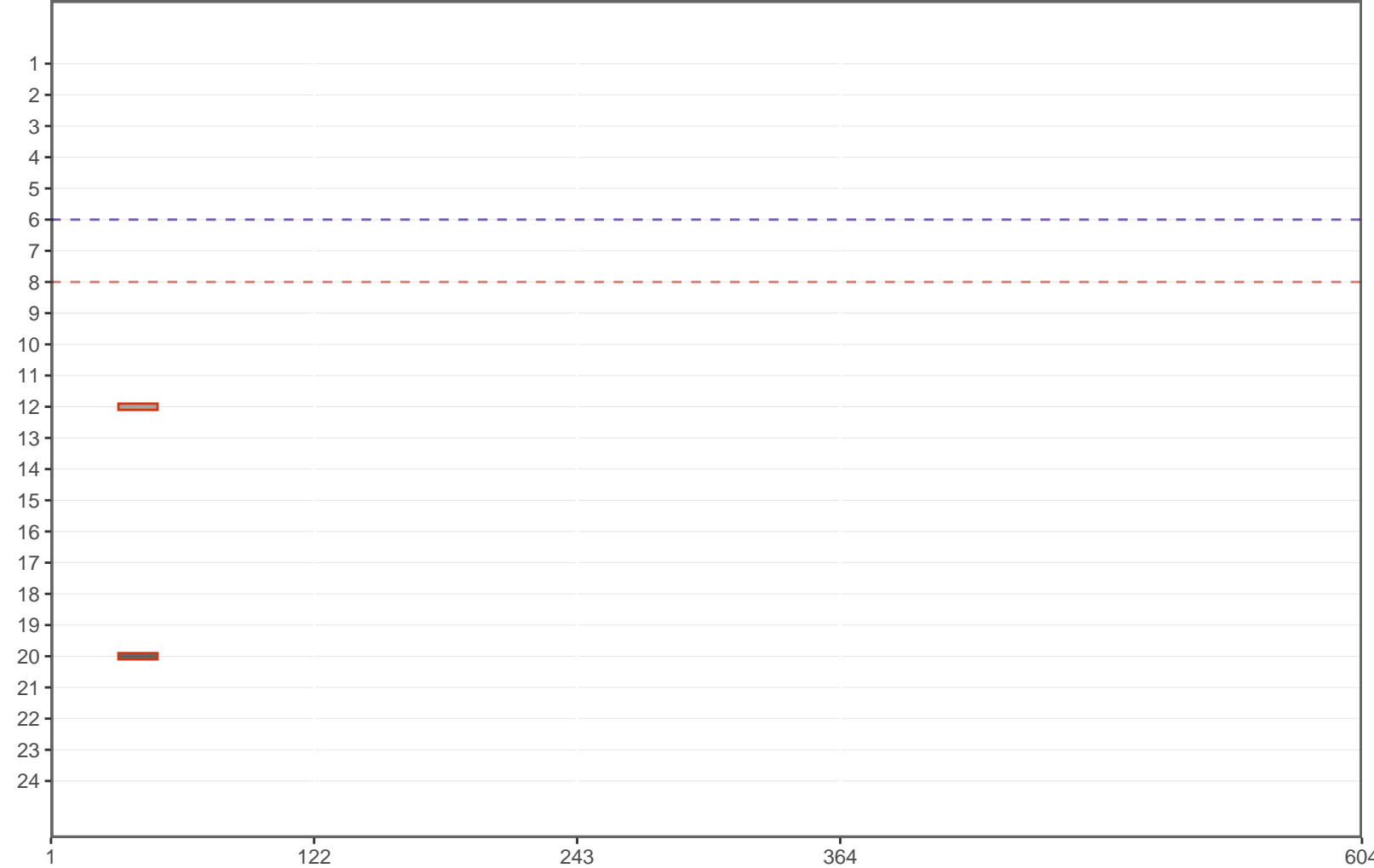
MW indication



Molecular weight

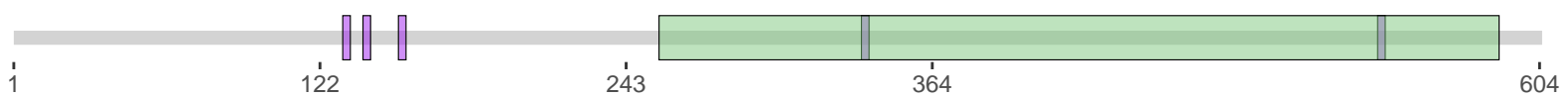


Gel Slice



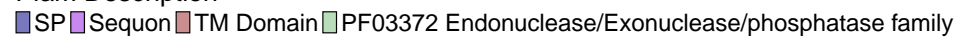
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

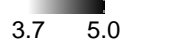
REIVGYRADIVCLQEVGSHFEEFFAPELDKHGVALFKRKTAEVFNQSNINIDGCAATFRDRFSGHKKYVEVFNKAAGSLTDVAIVPIAGKKTALNRLVAKDVALVLEAKFNSNOGVNPKRQLVGVANTHIVNQGELRDVKLVGVHTLTKGLEKIAASADIPMLVGGDFNSVPGSAPHTLLALGKVDPMHPDLAVDPLGILRPPTLTHQGLPLVSAVSEFARMGVGLGLEQGRRRMDPNTNEPLFTNGTRDFGTHDIYFVSDSLVTEGLLELLEDESLRKTALPSEV

NbL15g16830.1 enoyl-[acyl-carrier-protein]_reductase_[NADH]_2_chloroplastic-like [MW = 41.67 kDa]

No. of times detected



log(intensity)



Values from



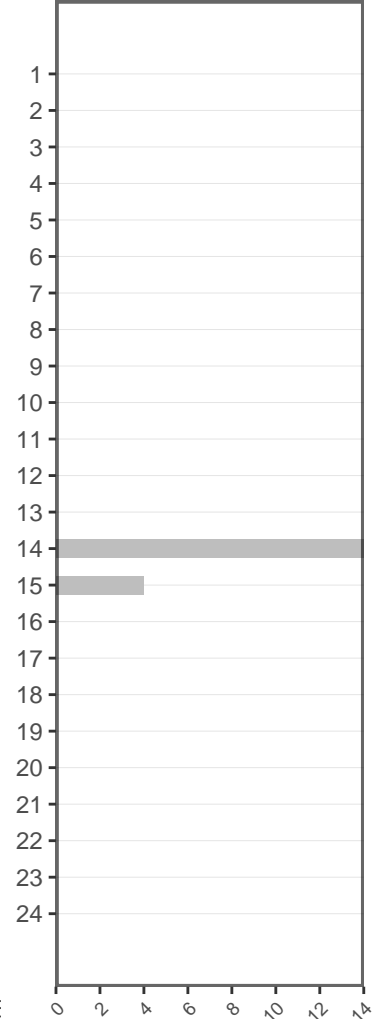
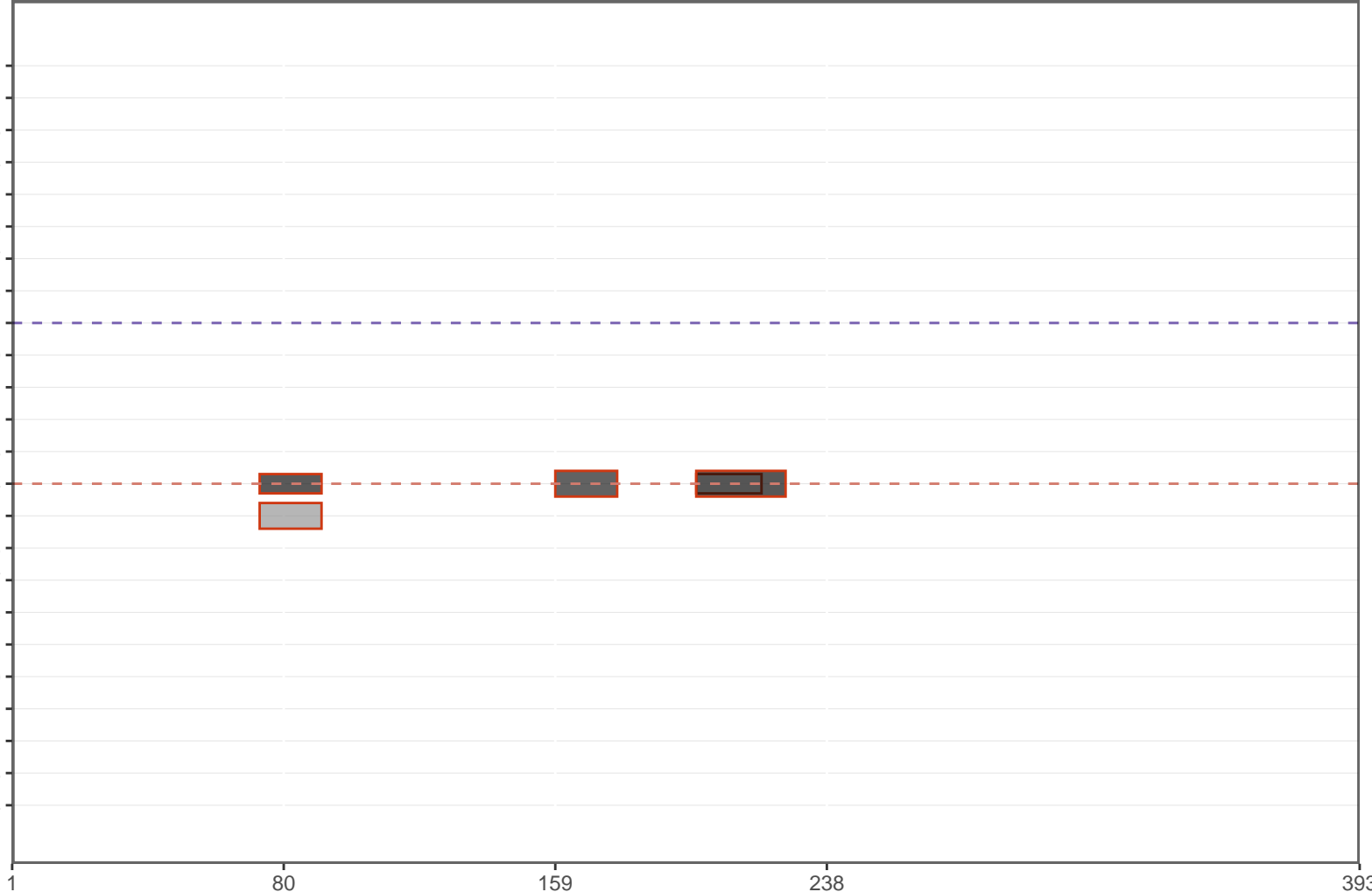
MW indication



Molecular weight



Gel Slice

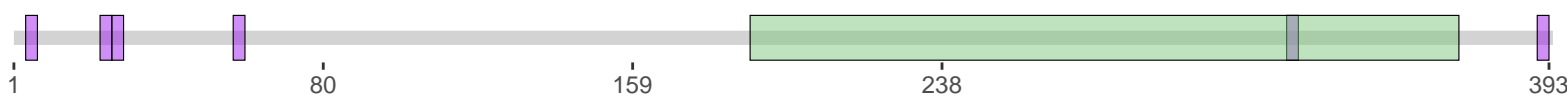


Protein length

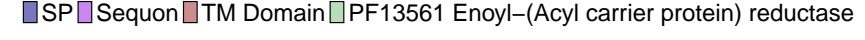


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SSSKWTVYKEVAECVKRDFGTDILVHSLANGPEVKPLGETSRKGYLAIVSASSYFRIILRHFLPILNPGGATISLTYASERIPGVGGMSSAKAALESDFRVLAFEAGRKHVVRVNTISAGPLGRAXKAKGFIDMMINYSLENAFLQKELVAEEVGNNTAFLASPLASAITGATVYVNDGLNMMGVGVDSPAFSGLDIPKDKNS

NbL15g16410.1 L-galactono-14-lactone_dehydrogenase_mitochondrial [MW = 71.75 kDa]

No. of times detected



log(intensity)



Values from



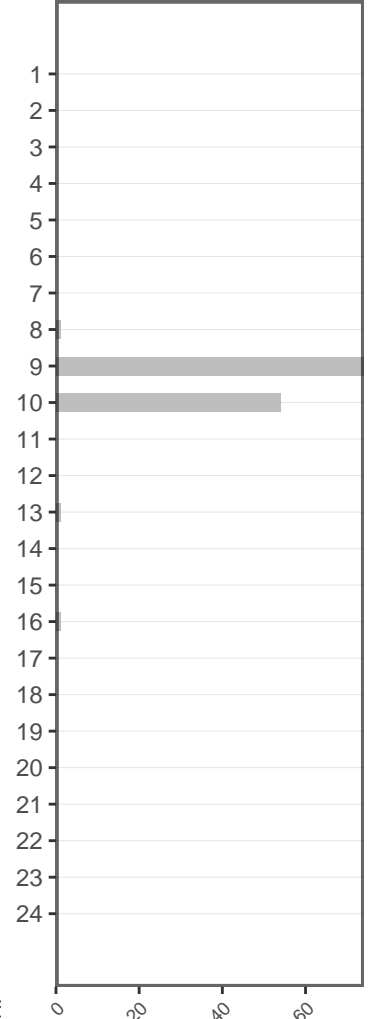
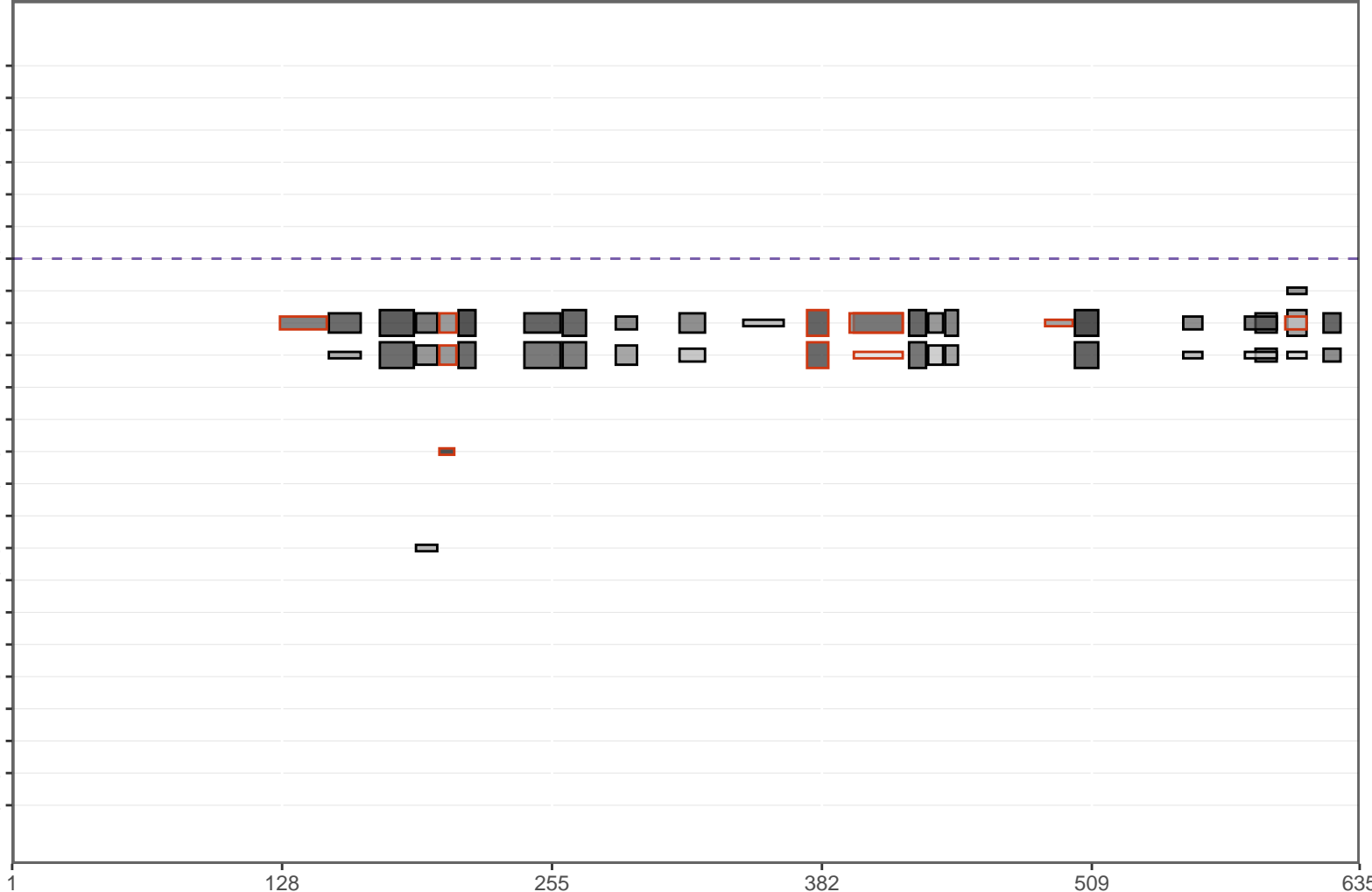
MW indication



Molecular weight

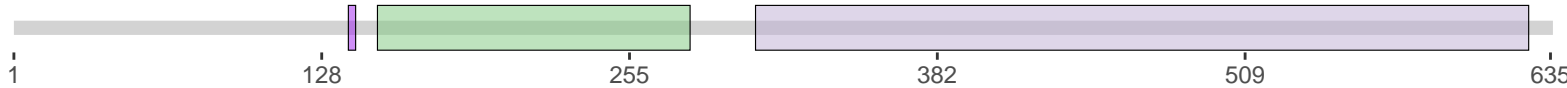


Gel Slice



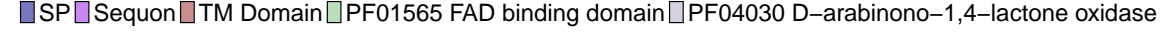
Peptide counts over 4 repeats

Protein length



Pfm domains

Pfam Description



Protein sequence:

TLQCYERQELVEHFFLSNMKDKKHKHFKFLSENKHVKYLIHPVTDAAVVVTGNPIKSRGPPKPKPKYTFEEALGHTRLVYREALKRYRGQVADSASPEAEIDELSFTELRDKLLADPLNKEHYEVNKAEAEFWRKSEGYPVGVSDDELGFDDGGHGWVSETGFPAGTLSKPSMKDLDDVEELMQLAKESVPAPIEGRWTAQSKGRMSPVWSADDDIFSWVGHIMVLPDMARGRRQITEEFFHYRHMFTQAGLWGHYSFAHEHMAKIEVPKDKEELAAALQARLKK

NbL15g16300.1 putative_glucose-6-phosphate_1-epimerase [MW = 34.76 kDa]

No. of times detected



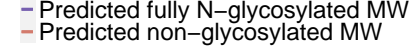
log(intensity)



Values from



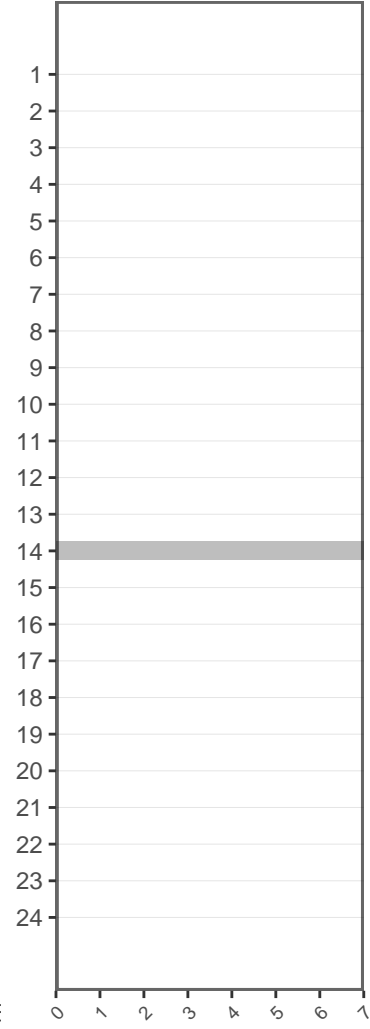
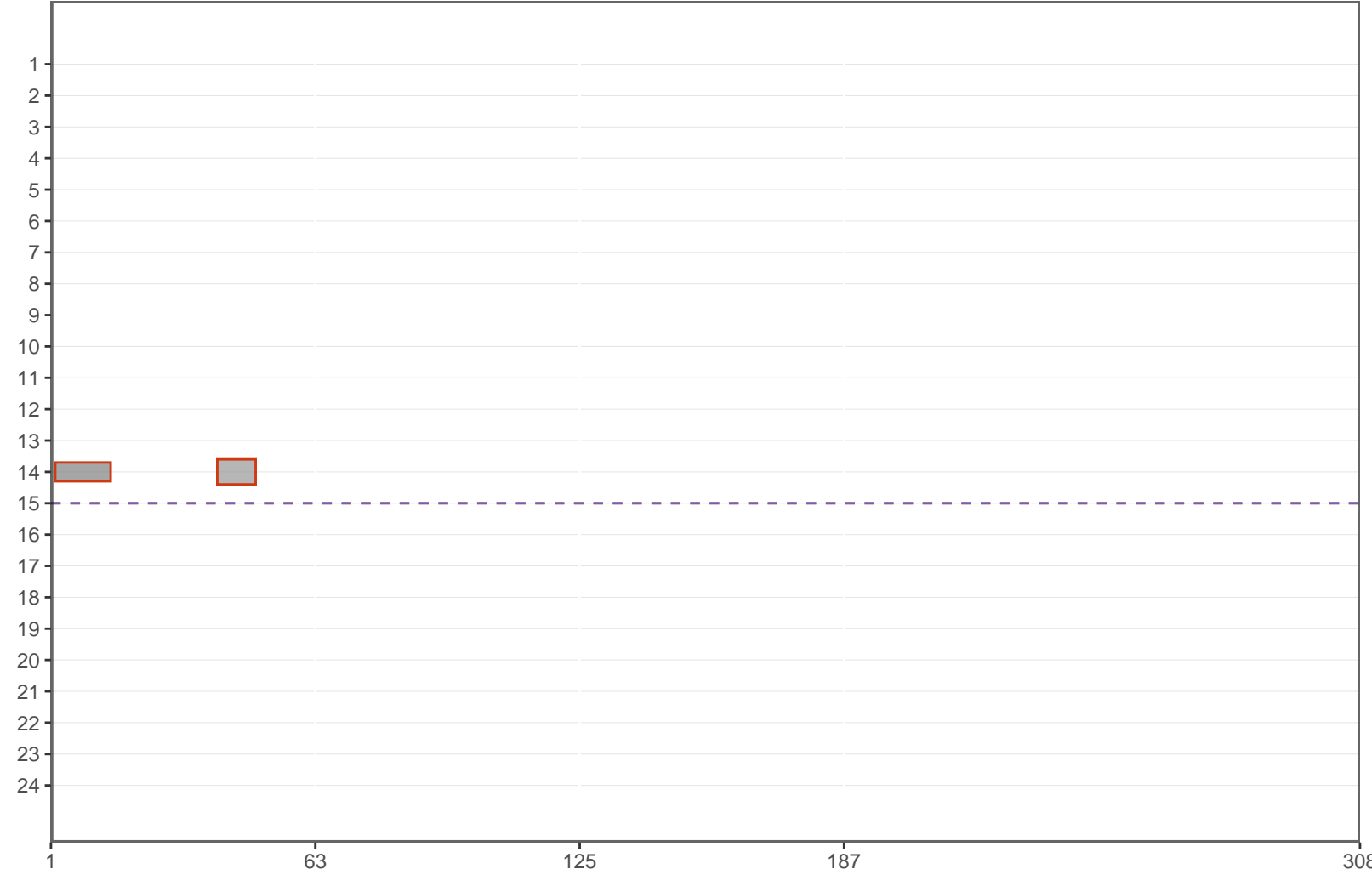
MW indication



Molecular weight



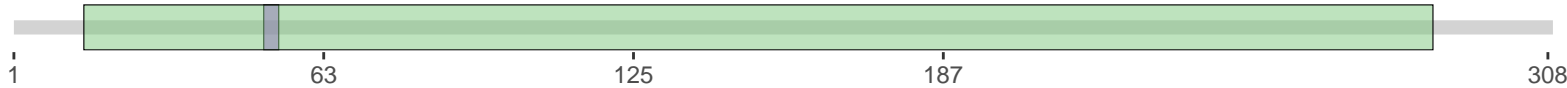
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

PRVRYNTDNKPFSSFISLRINLYLSDISEVRIEVEGLETLDFDFNLGQRERYTEGADAITFDSEIDRYLSTPKKIADHEKRYFYVQKEGMLDVAWNPWDKKAASLPDLGDEDKKMLCVDEAAVETPIVLPKSEEWKGRGELFTVSSBYGSGQLDPRKLYLGLA*

NbL15g16260.1 BAG_family_molecular_chaperone_regulator_4-like [MW = 26.07 kDa]

No. of times detected



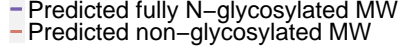
log(intensity)



Values from



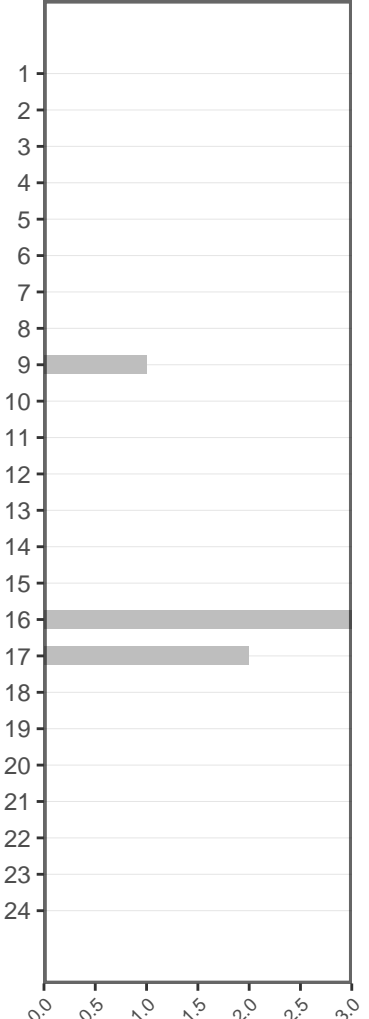
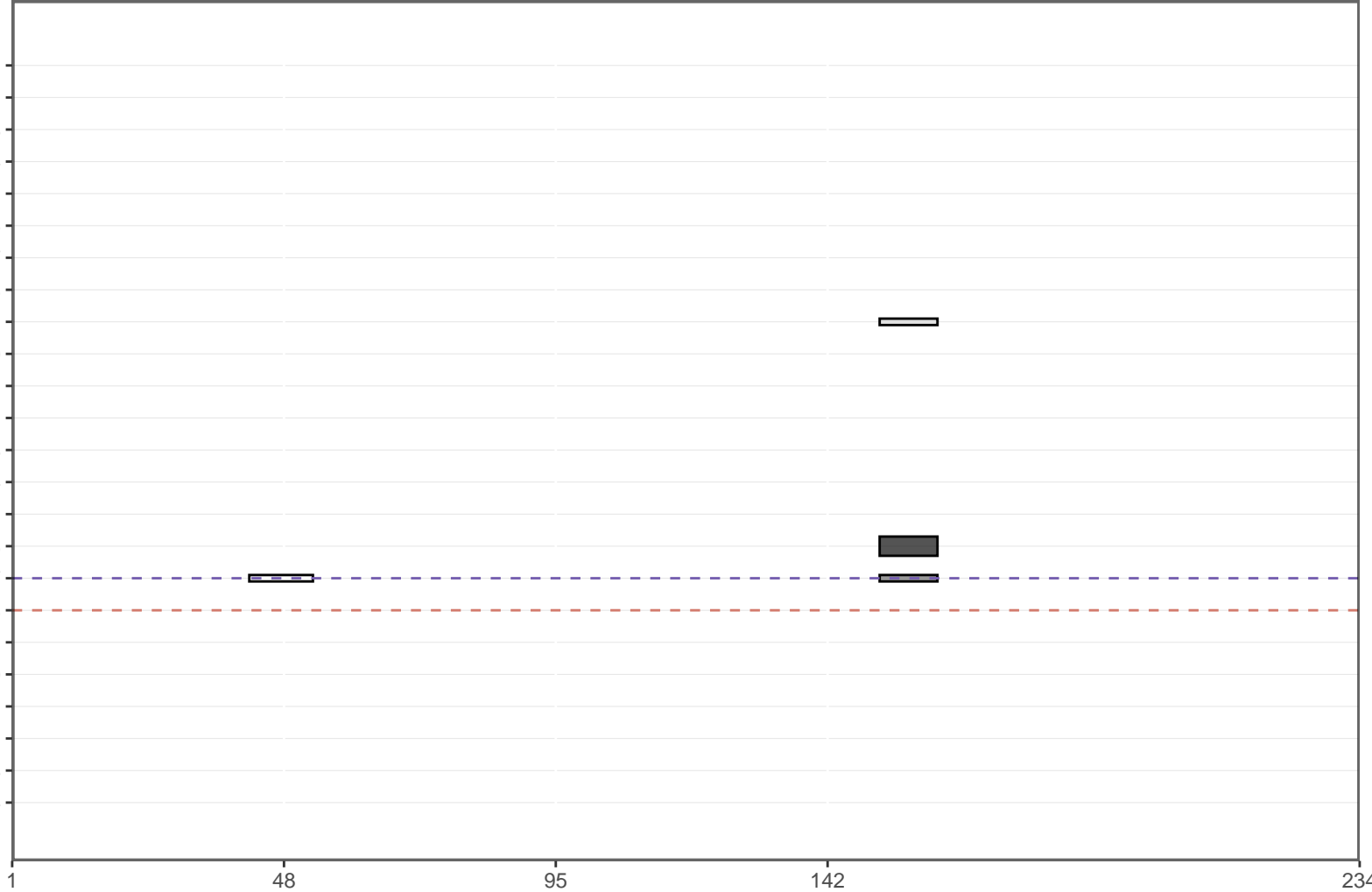
MW indication



Molecular weight



Gel Slice

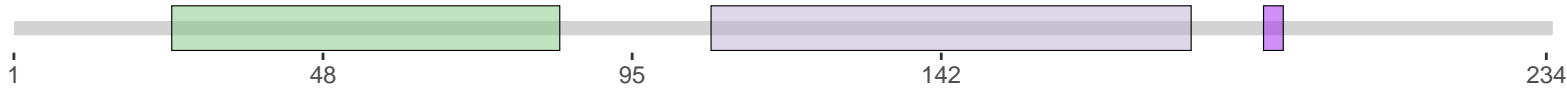


Protein length

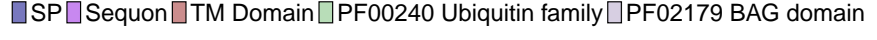


Peptide counts over 4 repeats

Pfam domains



Pfam Description

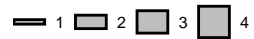


Protein sequence:

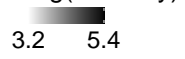
VAEYRTEVDKLSGQSAVQAVVFGGSGNVEEKDKICTEMLMRQLLKLDEIDAEGEQGRKRMVEYRRVGLVETMDAVKARNANPFNSNSAVSVTTQWETFESGSGVLSLNAPPPRPP66TVTEDEWEGFE

NbL15g15910.1 mitochondrial_amidoxime_reducing_component_2-like [MW = 34.14 kDa]

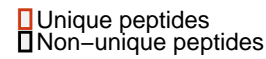
No. of times detected



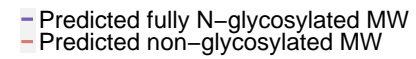
log(intensity)



Values from



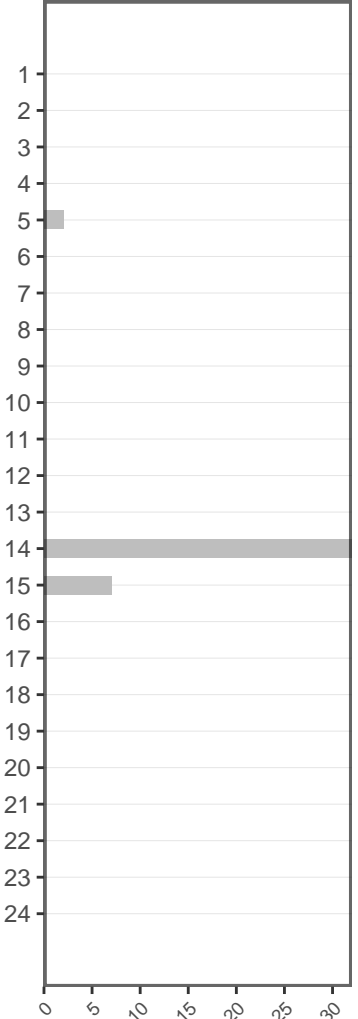
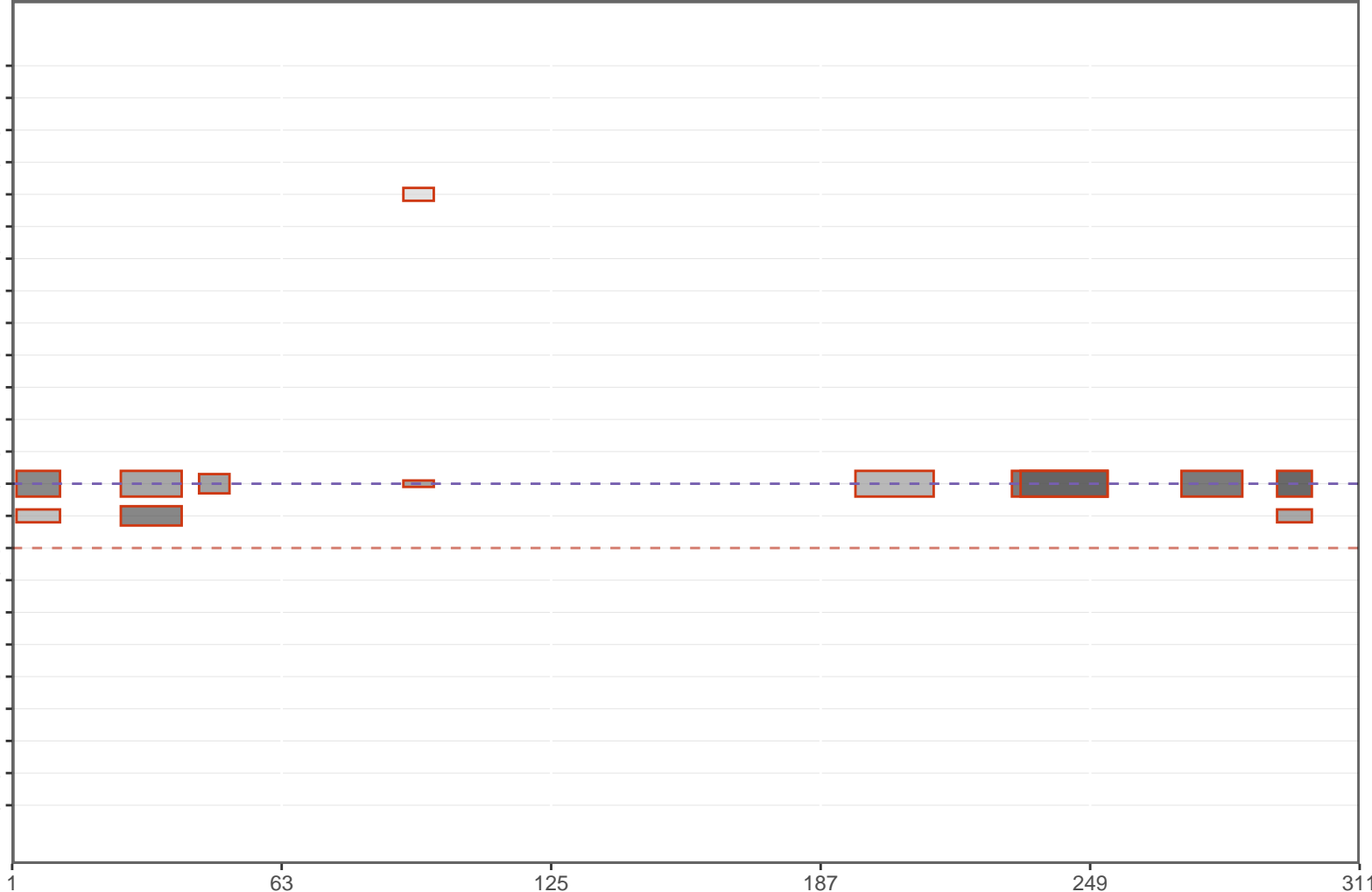
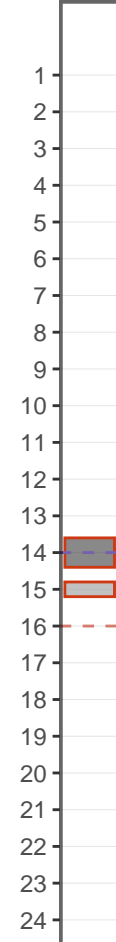
MW indication



Molecular weight

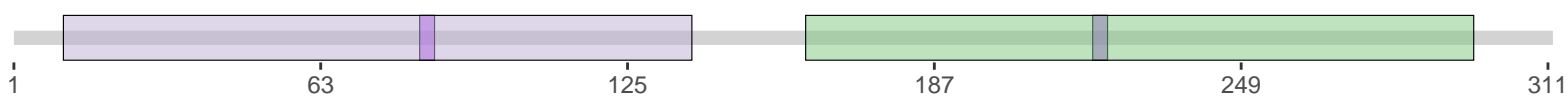


Gel Slice



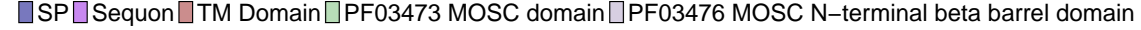
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

/RFSSEVKEMRVYDPIVAGGKVMFSDGYPYLVLSGGSLNALNSLKEPVPVNRFRFNVLVDGCEFFAEDLWKEIRINLTKFGVWLGSRGKVFPTINQETAAGSEPTETLTKFRSGKALPDKKGGKVVFGQNMVCGDALRGGKRIKVGDPVYLVKVPSSAEAPV

NbL15g15850.1 uncharacterized_LOC107826751 [MW = 20.62 kDa]

No. of times detected



log(intensity)



Values from



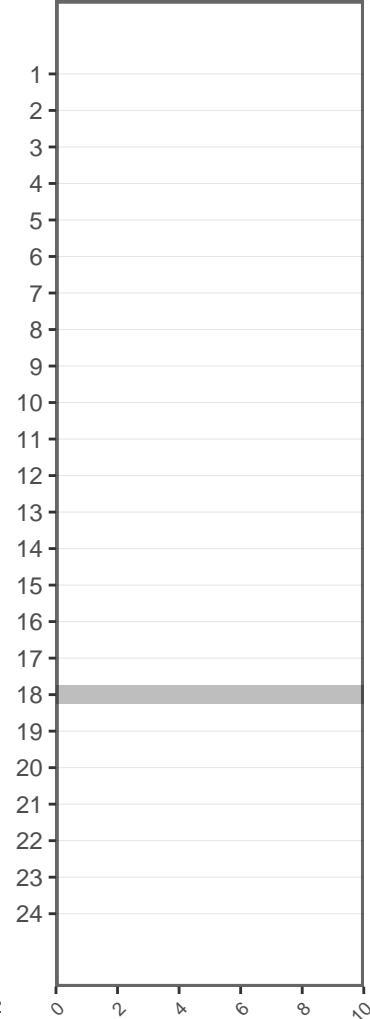
MW indication



Molecular weight

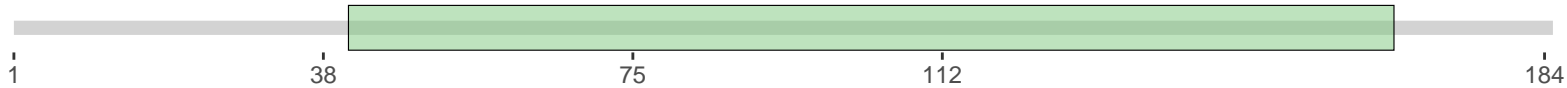


Gel Slice



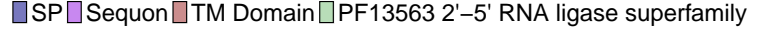
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SLPNDNLFLAPTPRLSLLGFHSOLFEMKKEGIEGEEHRPDTWYVCPVAEEVPKTRMGEAFTVLRDKLPLVAGYAMEALVEVPPREVFSVLGNTVER

NbL15g15800.1 40S_ribosomal_protein_S15-like [MW = 17.24 kDa]

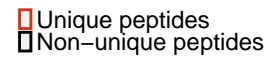
No. of times detected



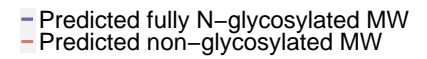
log(intensity)



Values from



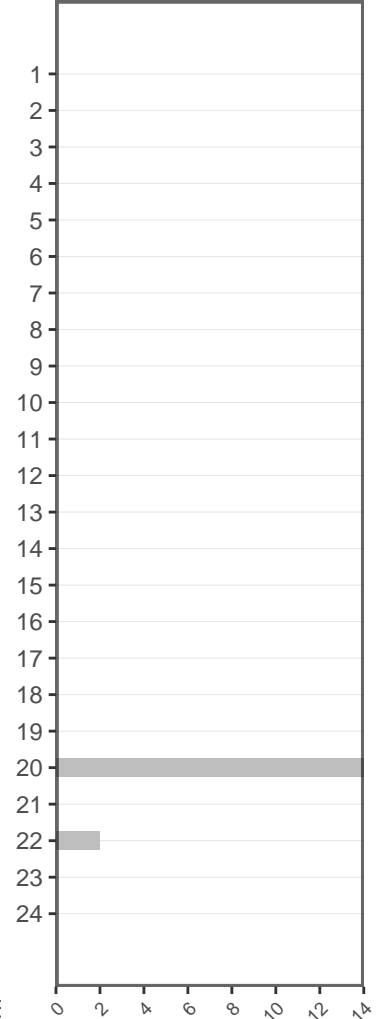
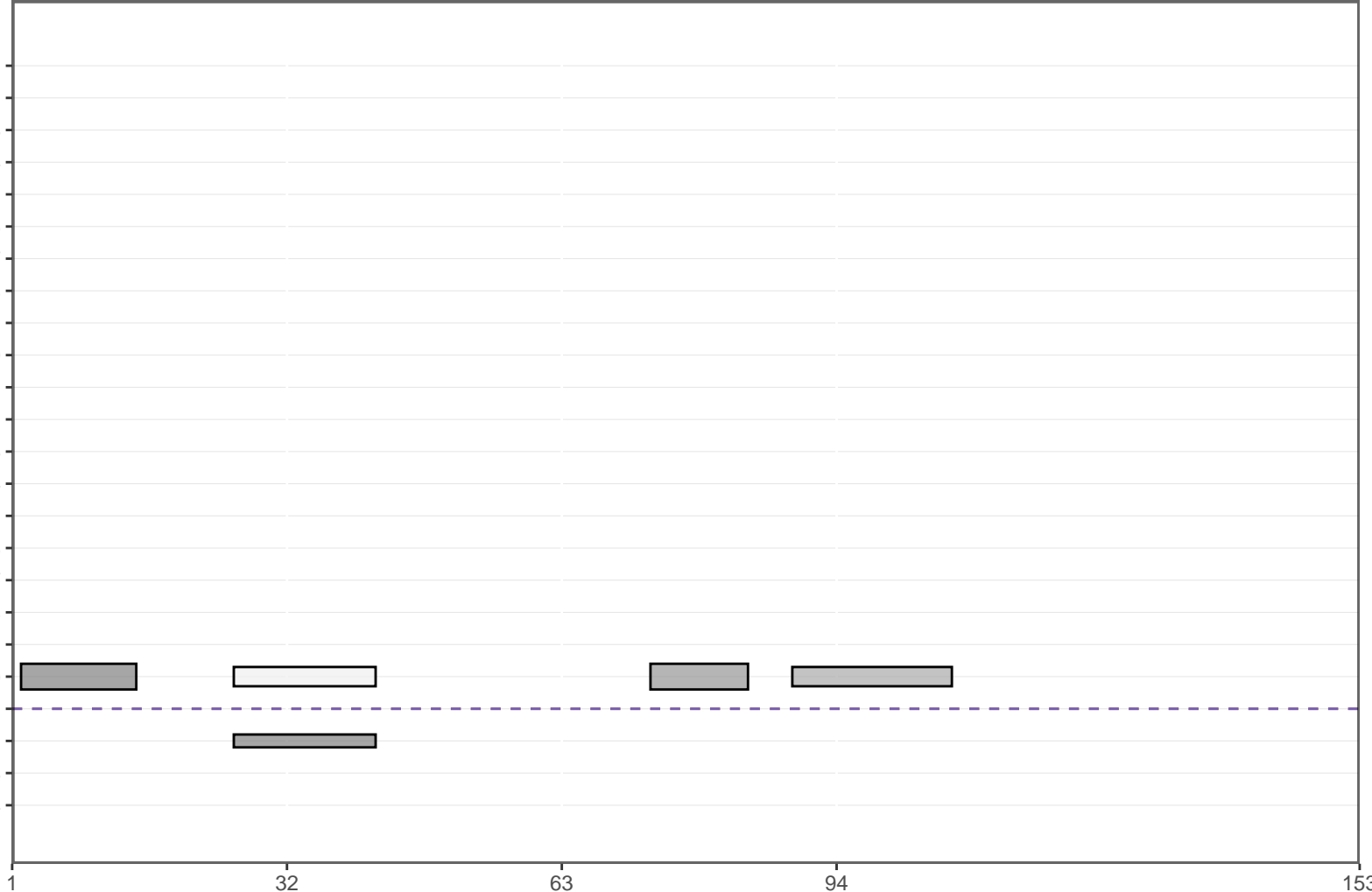
MW indication



Molecular weight

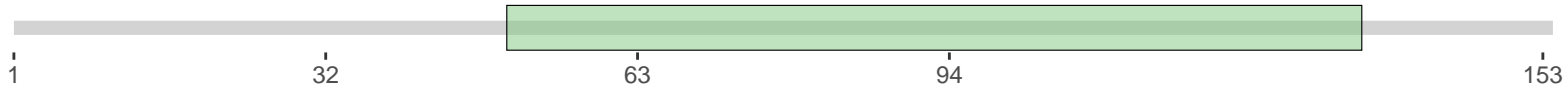


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ALLIKLRKAKREAPPGEKPEVVRTHLRNMIIVPEMIGSVIGYNGKTFNQIEVKPEMISHYLAEFSSGYPVHGRPGIGATHSRFIPLK

NbL15g15540.1 haloacid_dehalogenase-like_hydrolase_domain-containing_protein_3 [MW = 29.08 kDa]

No. of times detected



log(intensity)



Values from



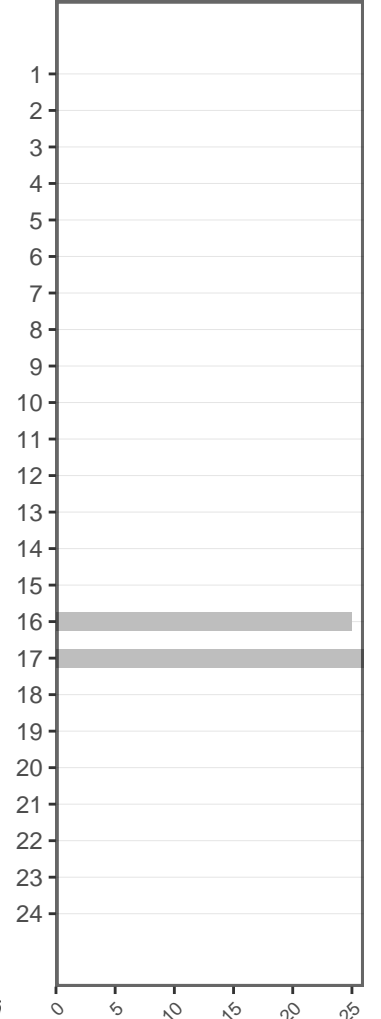
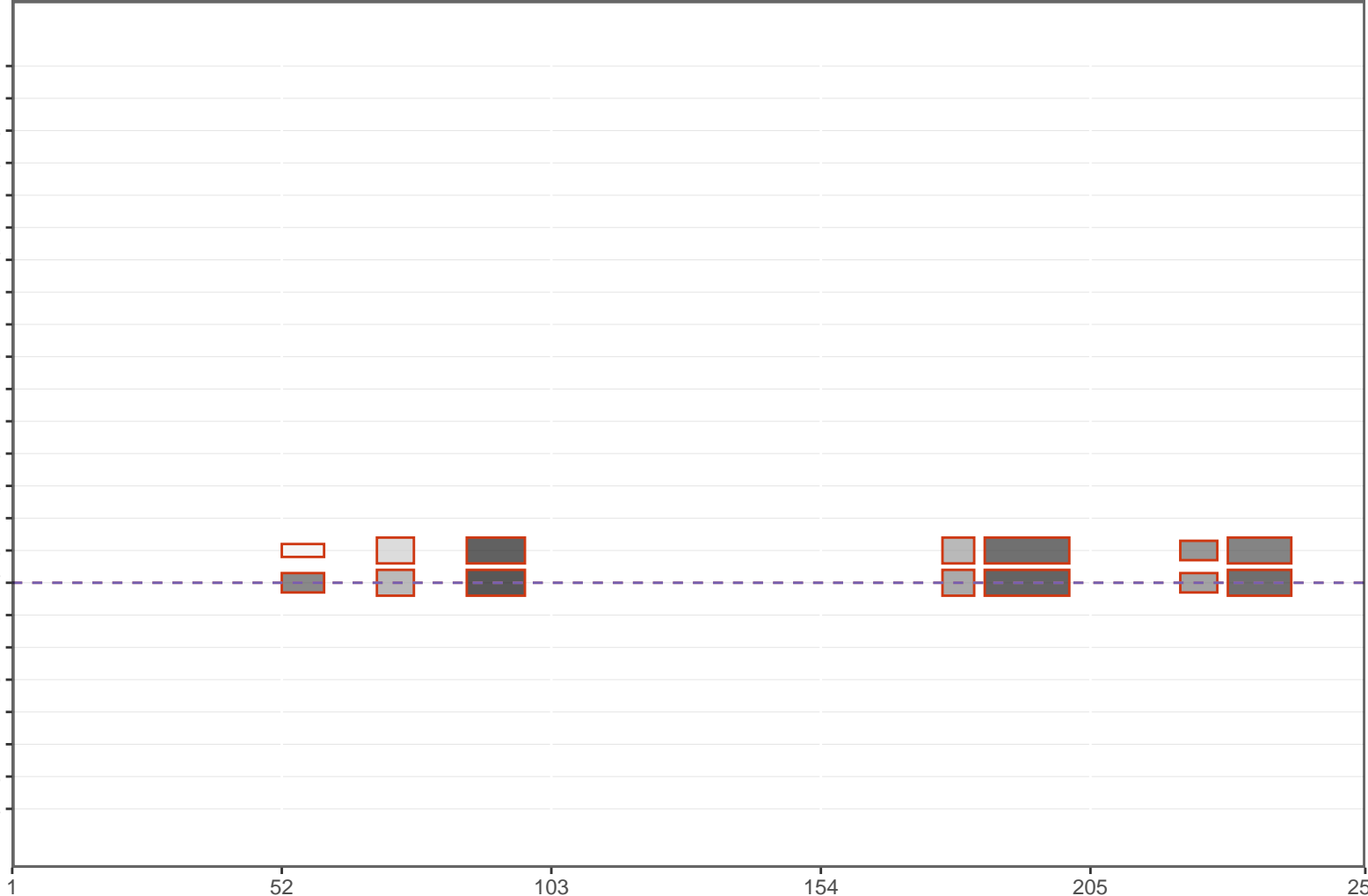
MW indication



Molecular weight

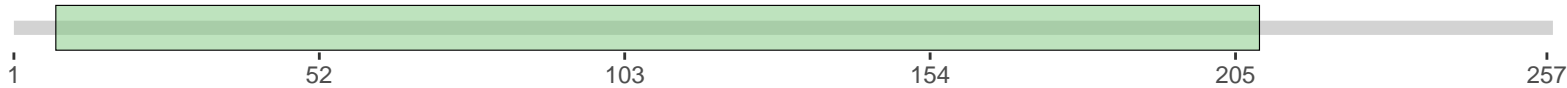


Gel Slice



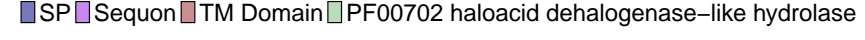
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

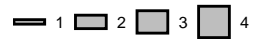


Protein sequence:

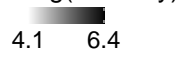
PDSSKPLRWLRLRGRFTVGLVSNAEYRYQGVILFPLGLHGGSEWDFGVFSGLEGVKNPDRFLFEALKRAGNVAPEEVLHIGDSMRKQVLPAREVGMHALLDRFKTADAVNWRKSGATVLPDLTATKQWLTCCELKGGDM

NbL15g15510.1 proteasome_subunit_alpha_type-4 [MW = 27.15 kDa]

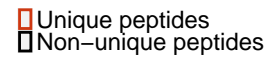
No. of times detected



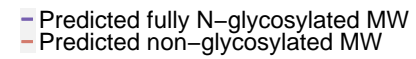
log(intensity)



Values from



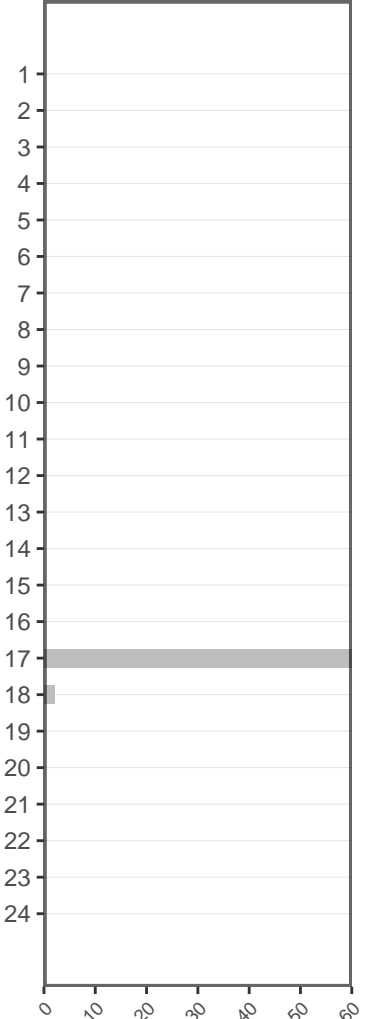
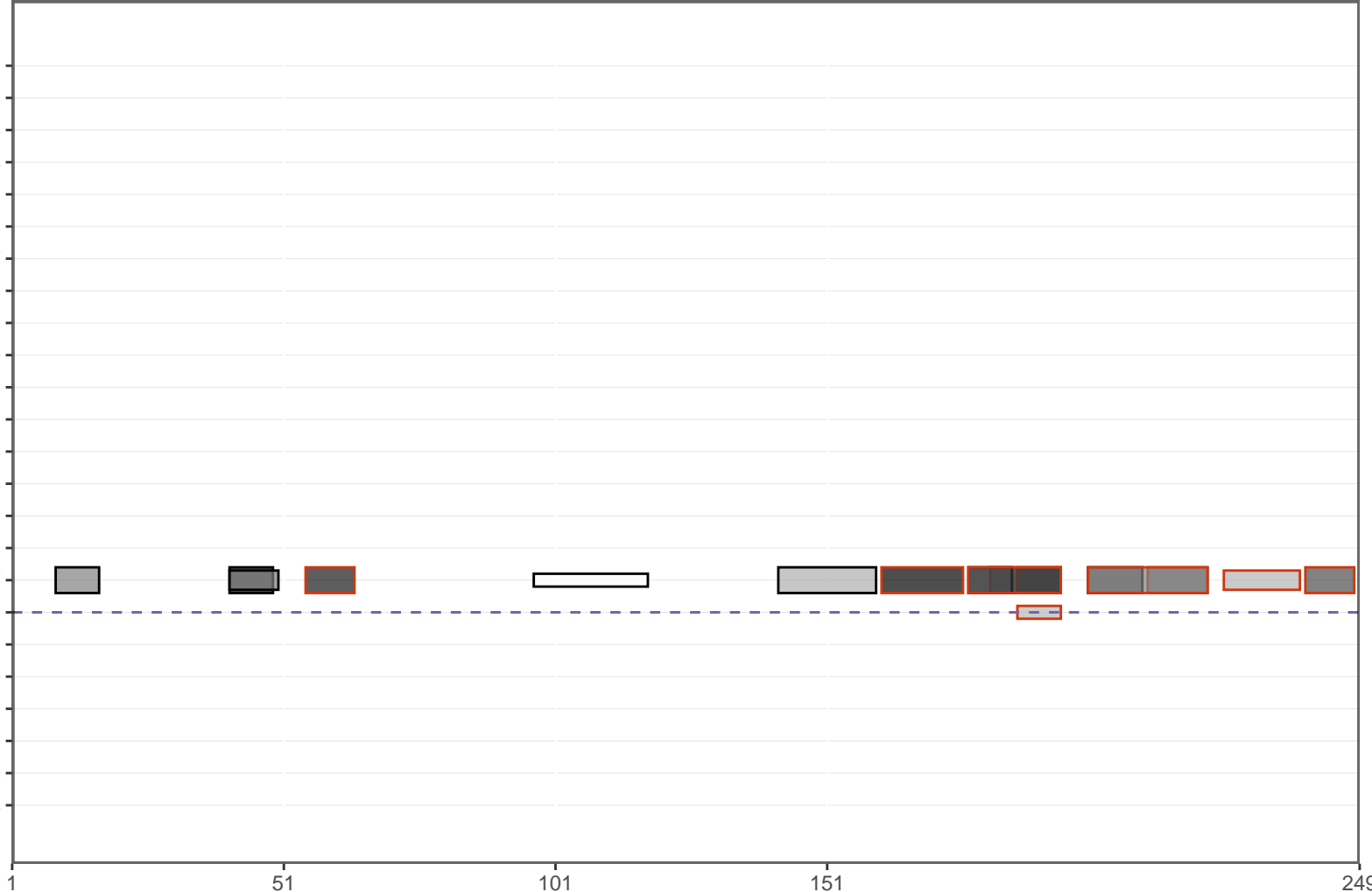
MW indication



Molecular weight

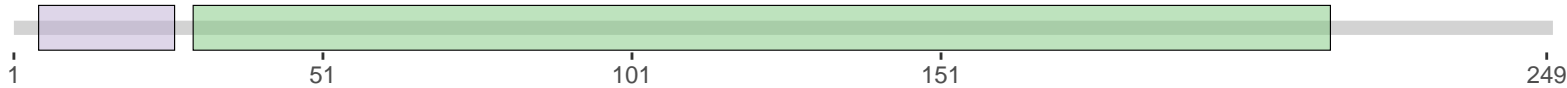


Gel Slice



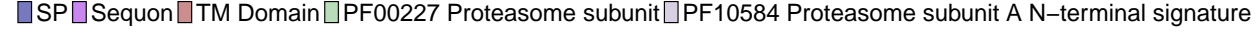
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

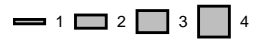


Protein sequence:

LCDTKGGYTFQGGLRPFQVSLFAGWKNVGFQIYMSDFSGNYGGWKAANGANNGAAGSILKGDYKDDITREEAVQLAKVLSKTMDSFTSLTSEKLELAIEVFLSNGKVKVYQAGSPELNAALVRSGLTQPAEE

NbL15g15100.1 L-ascorbate oxidase homolog [MW - SP = 57.57 kDa]

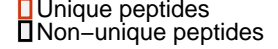
No. of times detected



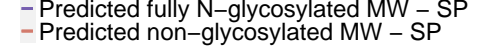
log(intensity)



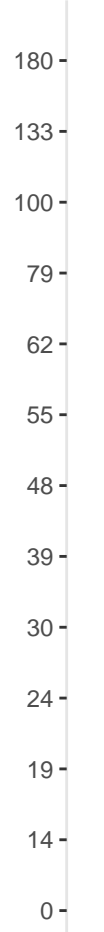
Values from



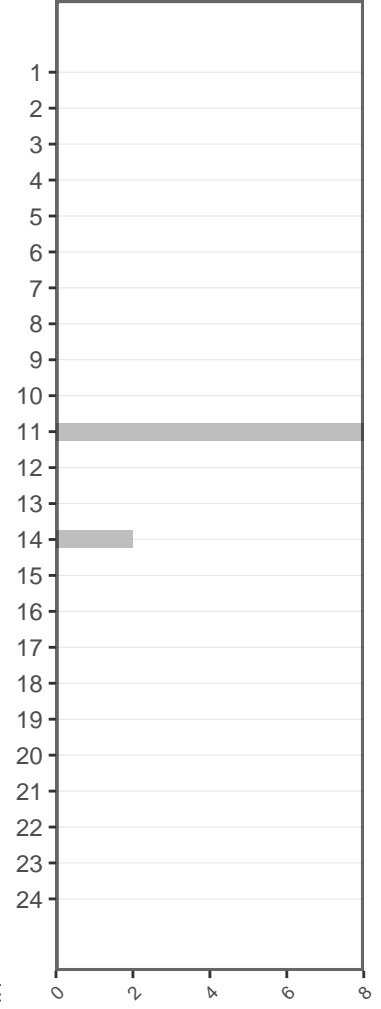
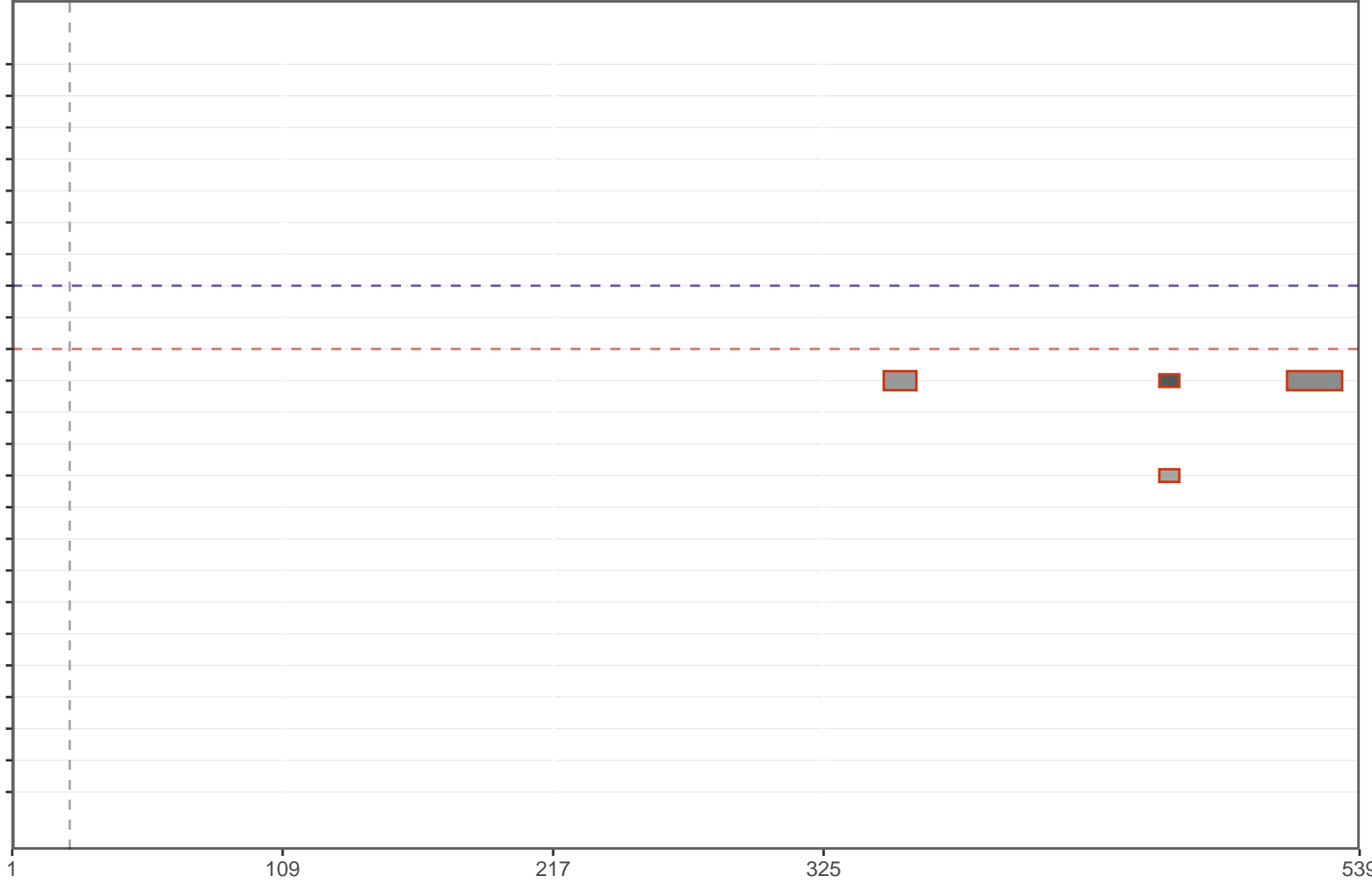
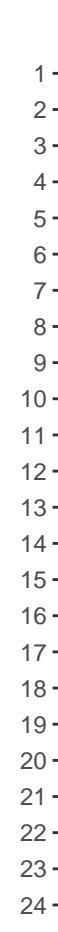
MW indication



Molecular weight

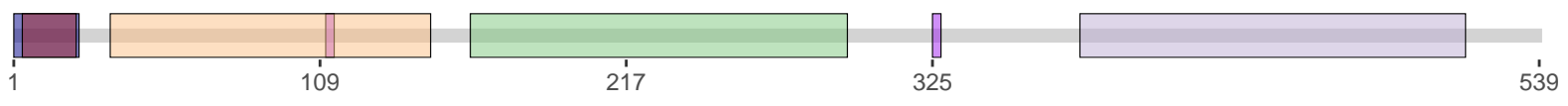


Gel Slice



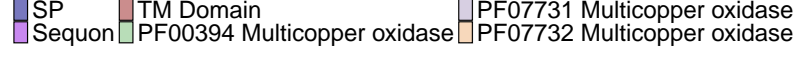
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

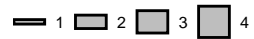


Protein sequence:

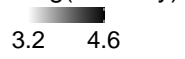
ASLVLTLDPPKDYVASTRFRITVLTATVHYS66GTSVSGPMPSPAGOMHWSMLGARTFRWNLTAARPNPQGRTHYQKTHRTFLVANSAPLNGKLRVWNRVSYVNPDTPLKLDHFNPCVFLNSIKGTFPSDGGSPYLATAVFFASHHDFIEIVFGNNEATMGSWHLGDYDFWVYVFGSGGTWTGASRNKRYLVDAFRTRHTAGVYFKGWTALVSLDNGMWNLRISAMWDRGVLGQGVYLRVYNPTQSLANEYIYPTNALLGGKAGRIP

NbL15g14860.1 ABC_transporter_F_family_member_5-like [MW = 78.54 kDa]

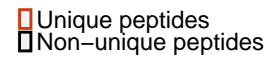
No. of times detected



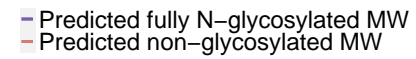
log(intensity)



Values from



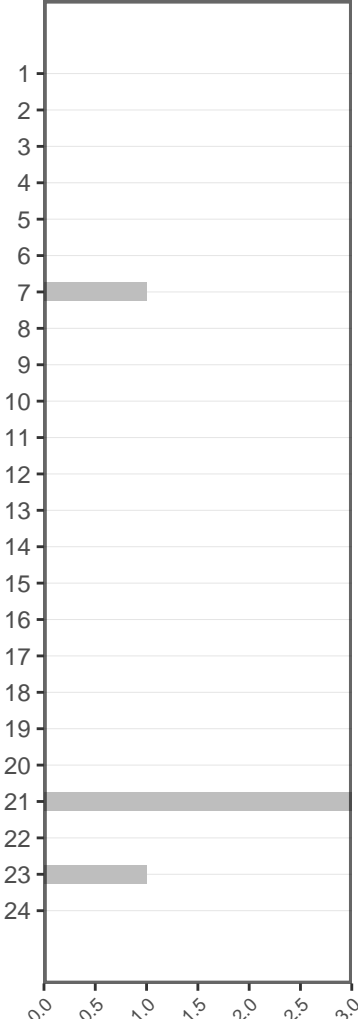
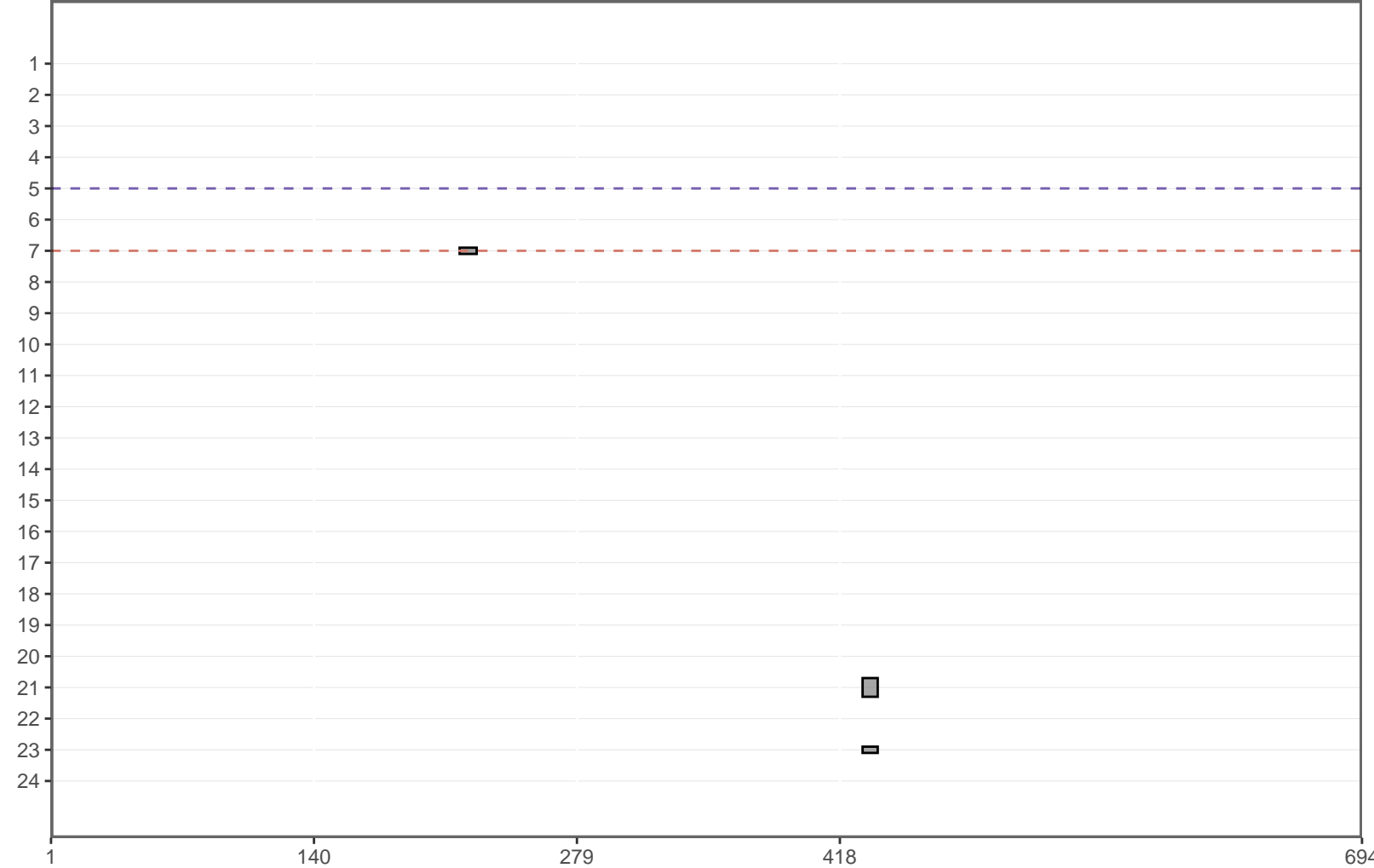
MW indication



Molecular weight



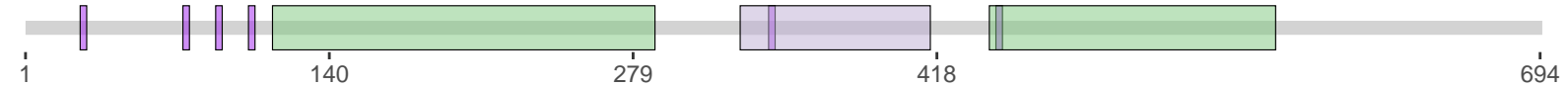
Gel Slice



Protein length



Pfam domains



Pfam Description

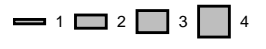


Protein sequence:

SRTYEGNYSDFIISRAEWEIETGNAAWEKGGQKEIGTRGURSRGAGANSGRASTAEKLEKLGDDGEGVDKPFIRKGMKIRFFPERERSGRTRVNVNKNLEFAYEDKLFKNANLITERGEEKAIKPNFGCKSTFLKLMGSLKPKTRGEVVLGEHNVLPNPFYEQNGAEALDLEKTVLETVAEAAEDWRLLDQIKLLGRGNFKADMLDRKRVFLSGGEEKARLAFGKFMVTPSTLLVLDPEPTNHLDRPTKEMLEEAFTEYKGTVTIVSHDRYFKIGWNRVALEVKDGLTHIDYEGDYDYLI

NbL15g14840.1 developmentally-regulated_G-protein_3 [MW = 41.25 kDa]

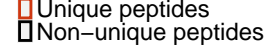
No. of times detected



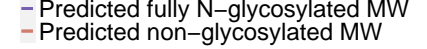
log(intensity)



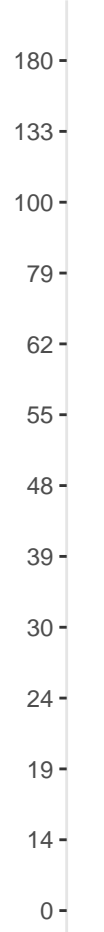
Values from



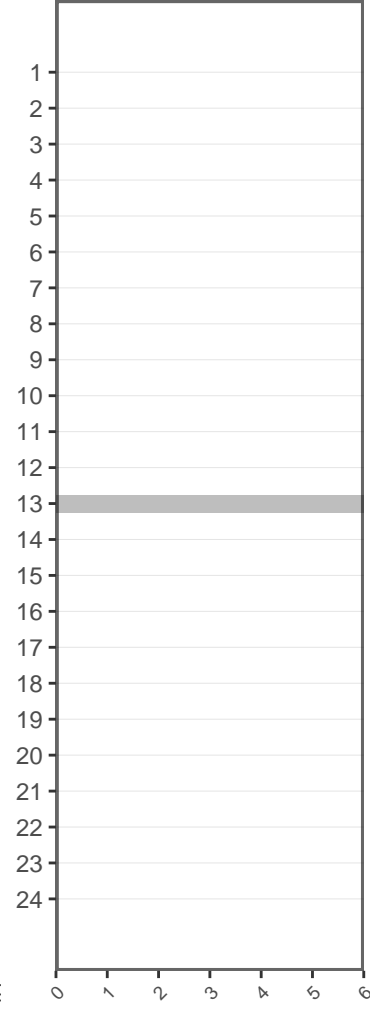
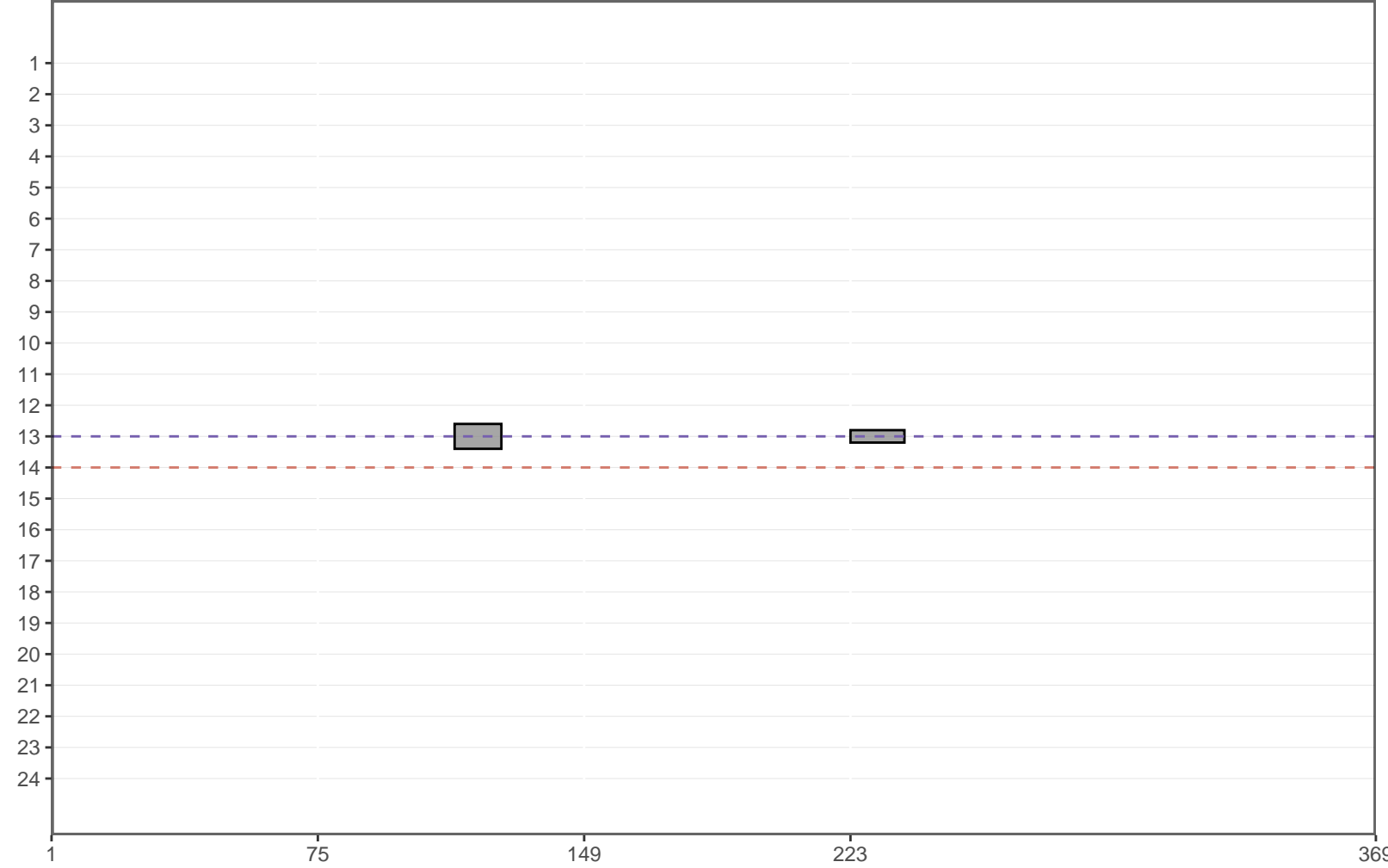
MW indication



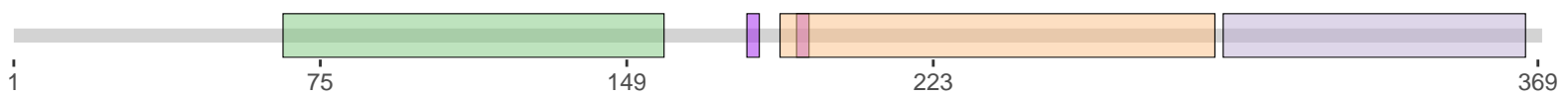
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

LNKEPPNLTFRKKKEKGGINLTSTVTNTHLDLDTFKAGSEVRHNAVHLRYDADADDIVIEGSRVYTPGVYVKNIGDITMEELELDKLPHYCPISALEWNLGGLLEKIWEYLSLTRYTKPKGMNFDVEDPVLSSKRRRTVEDFGDRHKDMWGFKVALVWSSSAKHKPGQRVGREHELEDEDVQIKRVV

NbL15g14820.1 shikimate_kinase_chloroplastic [MW = 33.22 kDa]

No. of times detected



log(intensity)



Values from



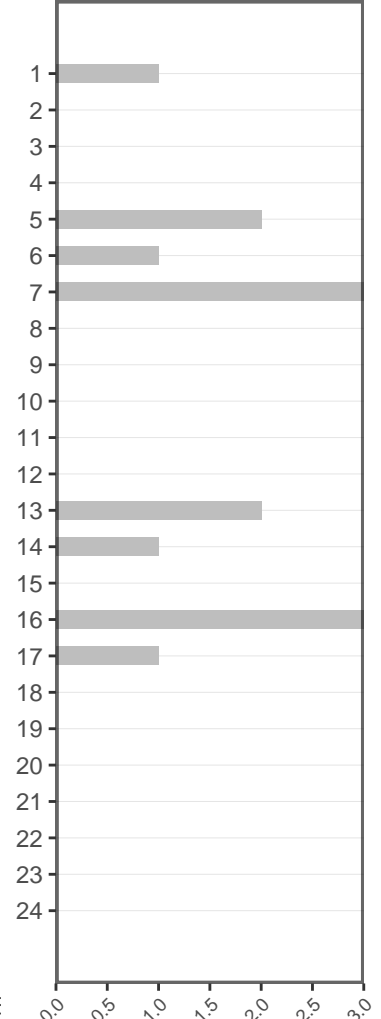
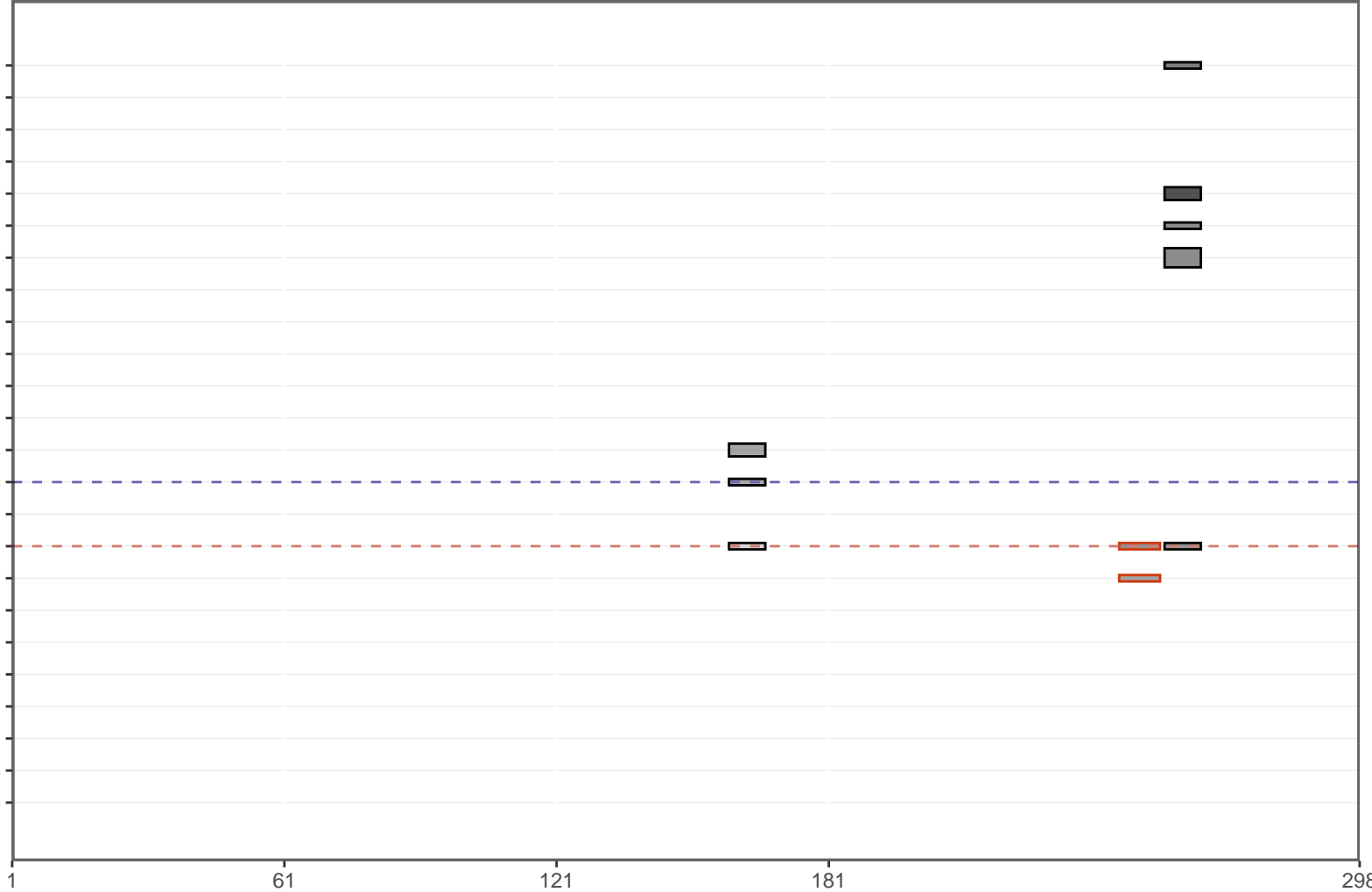
MW indication



Molecular weight



Gel Slice

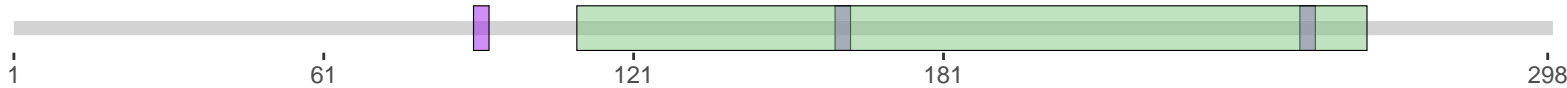


Protein length

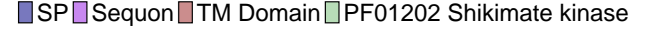


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

RLEQAVGGTTYAEIKFLRGESEFRDNETEVLHKLSSAMHRLVAVGTGGGAVVRPNWRHMHKGISVWLDVPLDALAKRVTAEGTKSRPLLHEESGGDYDKTKRLFTLLETGRGENYANASVRSLENIWVKRGGKDVCHITPTTEITLVLVIGIQLFKKGGESVVLV

NbL15g14720.1 4-alpha-glucanotransferase_chloroplastic/amyloplastic [MW = 65.37 kDa]

No. of times detected



log(intensity)



Values from



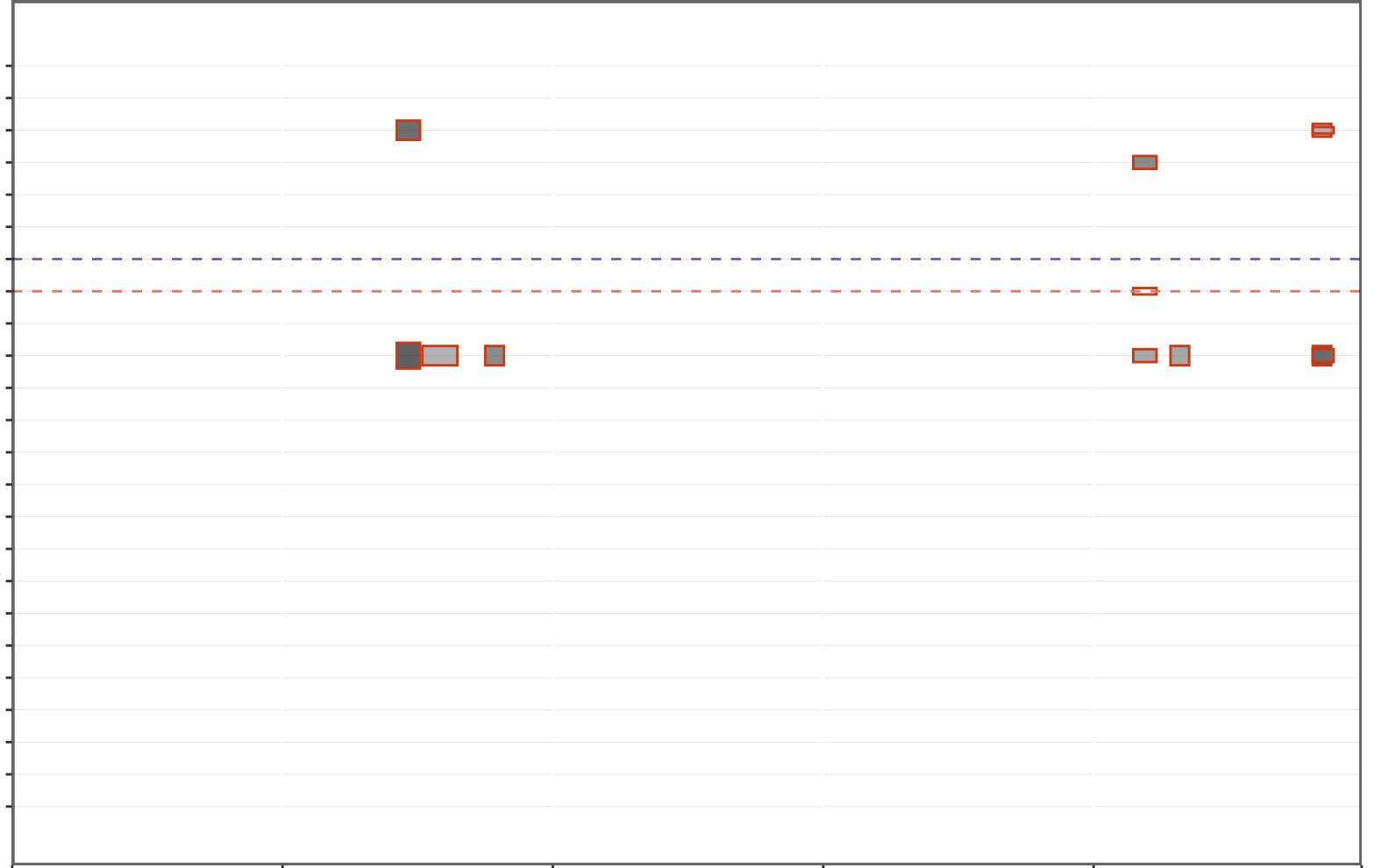
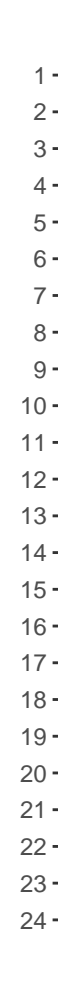
MW indication



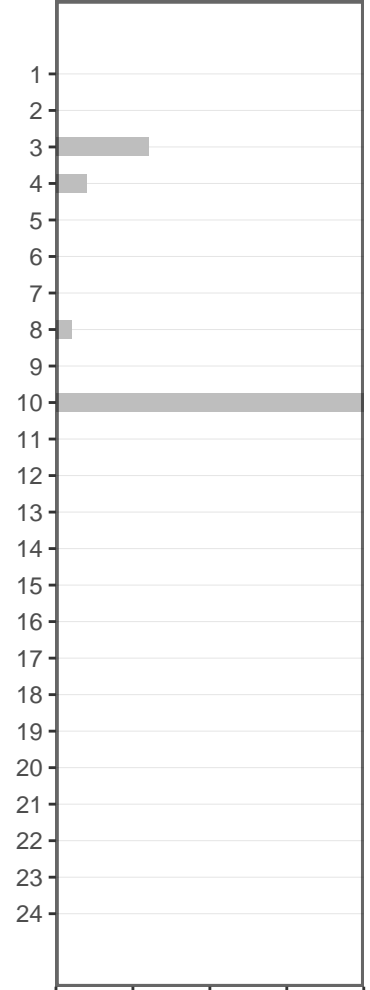
Molecular weight



Gel Slice



Protein length

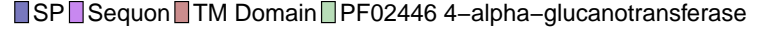


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

WVQKVDYARSKGSGMGMPIYVGHSAWVANKKHFLNRRKGFPLVSGVPPDAFSETGQLVGSPLVYDVKAMEKDFGFWWRIRRRATDLDFDFRHFHFGAGFVWVPEAKVWMLGRWVGPCKLFDLFDGAVGKINIAEDLGVTFEDVYQLRKGIEAPGMVALQFGFGSDAENPLPHNHGKQVYVYTGTHQNDTRRWVWDLPGEEKSNVLYKLENEEENISWGLEAASISVARIANVPMGDVLLGSGEGRMNIPATGFGNWSWRIPSTRFDSLDAEAKLR

NbL15g14640.1 2-hydroxyisoflavanone_dehydratase-like [MW = 35.73 kDa]

No. of times detected



log(intensity)



Values from



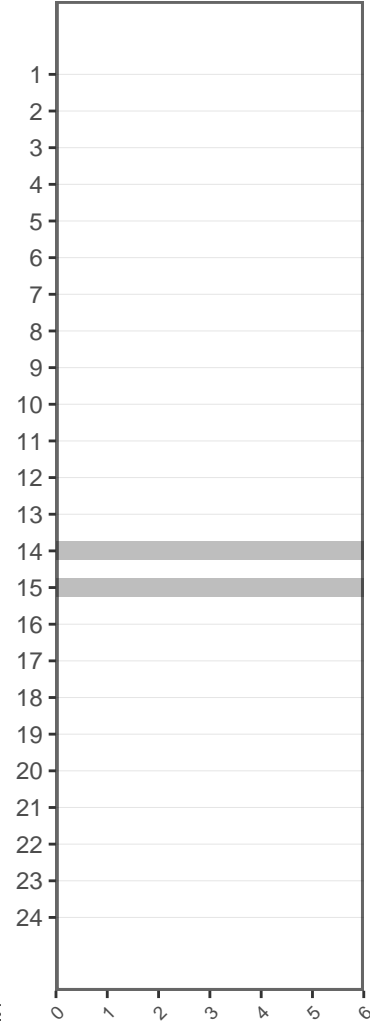
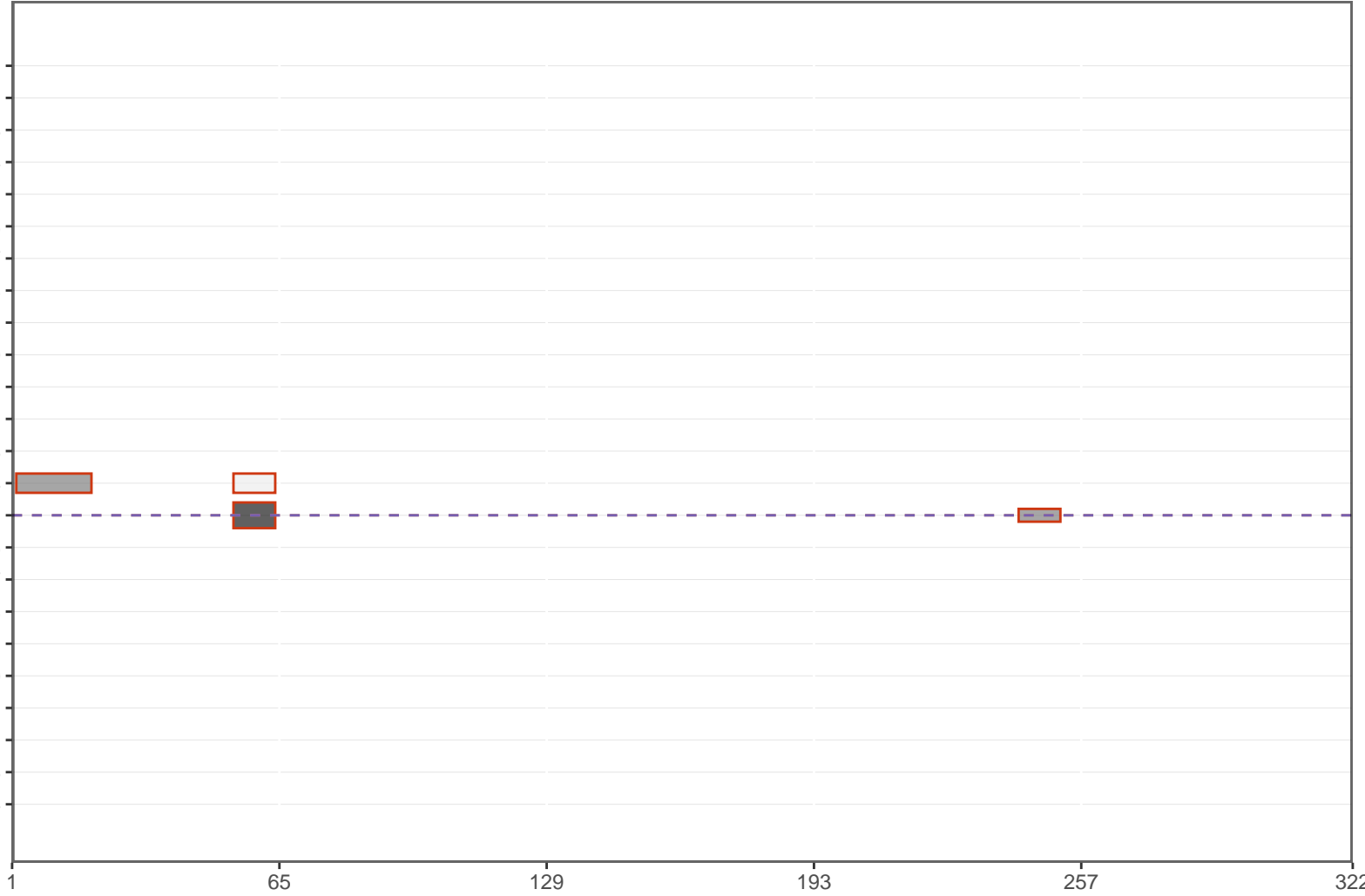
MW indication



Molecular weight

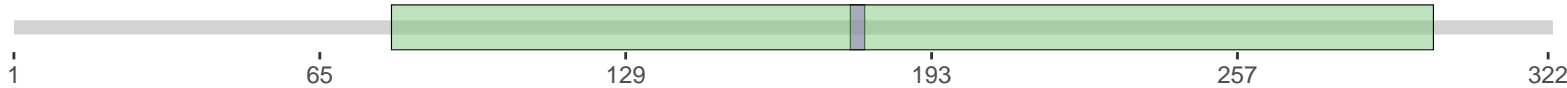


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DAEPWITNIGDFNRLFIAGDSAGGNVFNMTMRAGKESLIGGVKLVGAIFAFPELLIPVENIEGSLVYKLVNTICPPSEGGINSPIVNPVSEKGGQSLSELGCRIFLGAKEKDEHPVSEIVTRFAEAVNNGWKEVEFIEIEGVEHCFQAAVPEAEKSKLKRIMASFIQRK

NbL15g14540.1 uncharacterized_protein_At2g39795_mitochondrial [MW = 31.65 kDa]

No. of times detected



log(intensity)



Values from



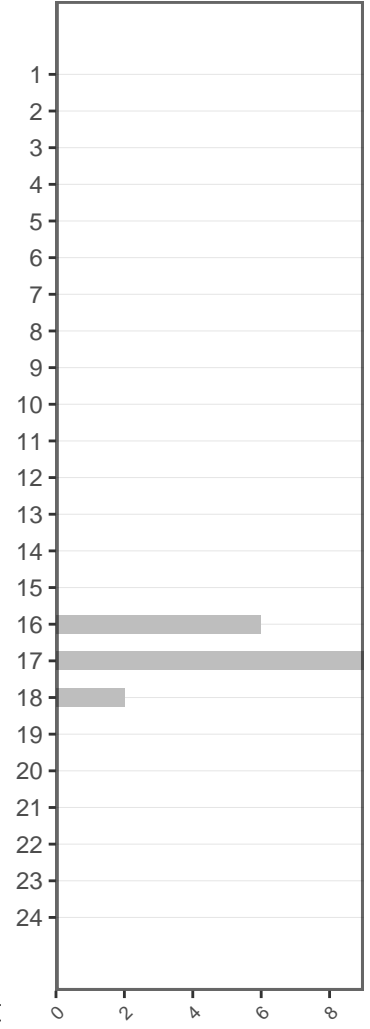
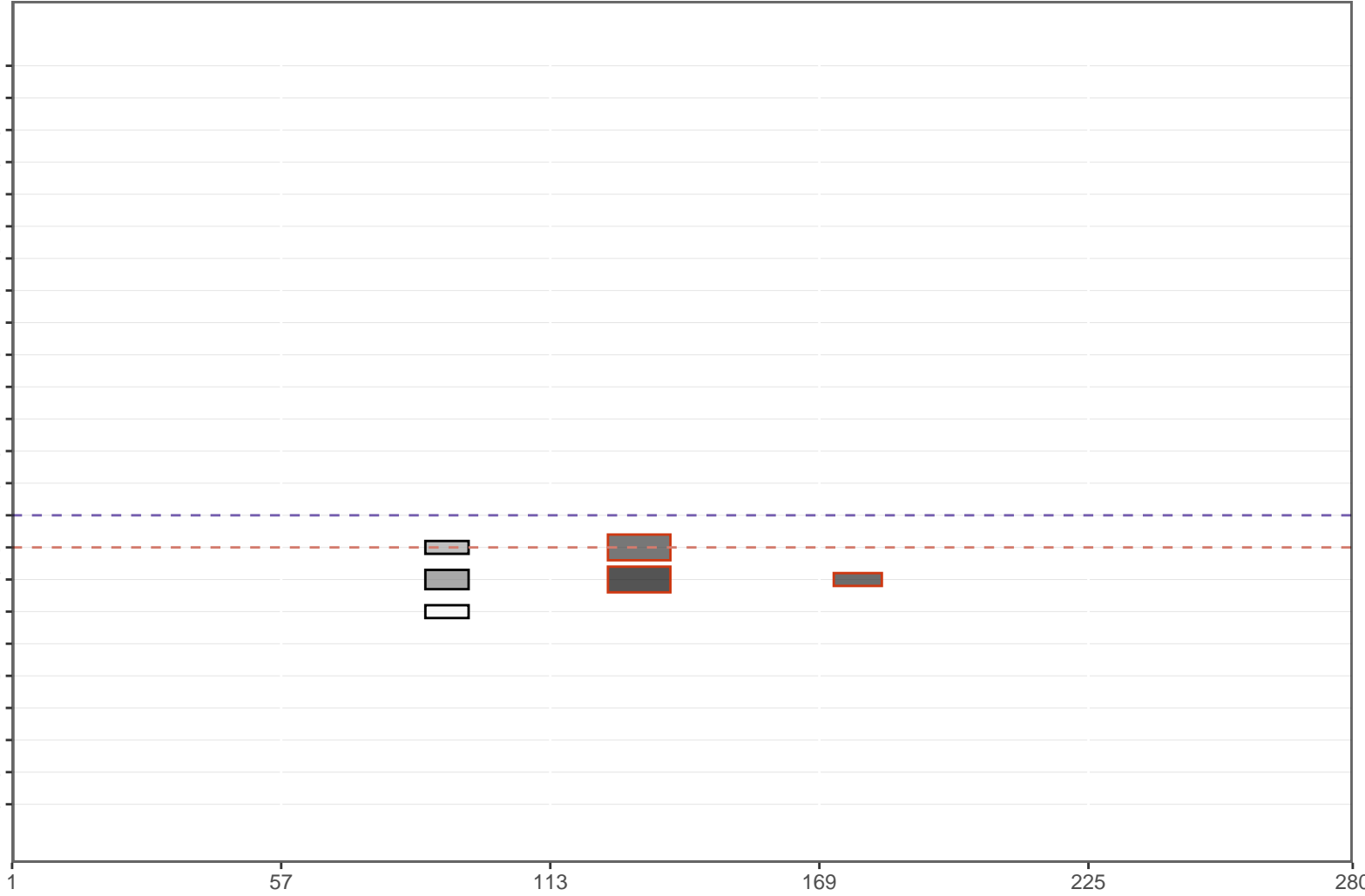
MW indication



Molecular weight

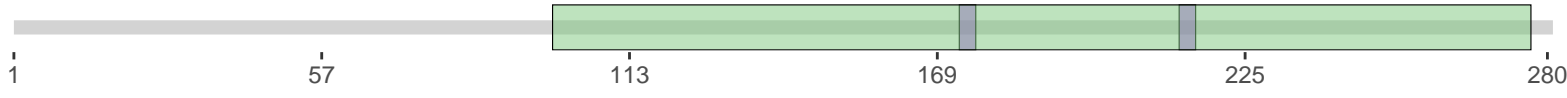


Gel Slice



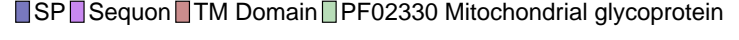
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

HPGQQTLYLREYGGESHVEVHMPDLVTGGDEEDNDNDNRERANGSGIPLVVVRVSKKNGSPLEFGGTAFADEIAIETLSIKDFNASEDQIAYEGPFDPSLDLENLQKAFHYKLEIRGKPSATNLFHEYMKDKGREYVWLVKLNKFKFIA*

NbL15g14460.1 7-deoxyloganetic_acid_glucosyltransferase-like [MW = 53.48 kDa]

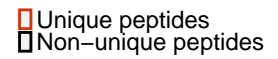
No. of times detected



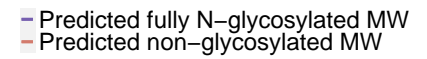
log(intensity)



Values from



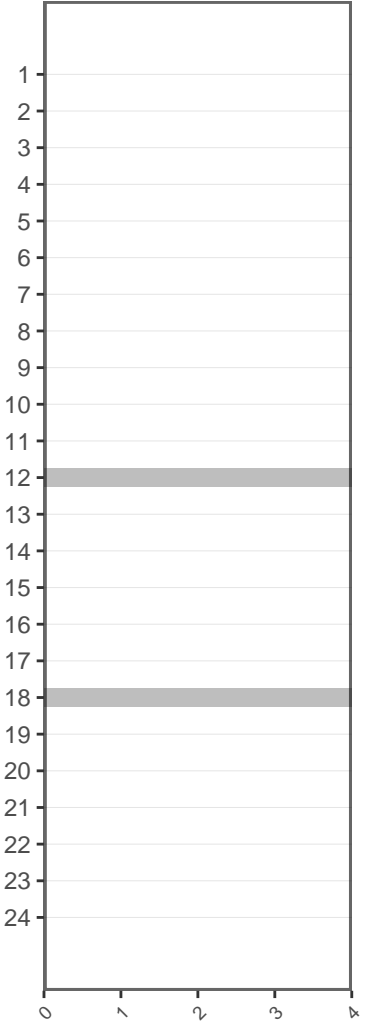
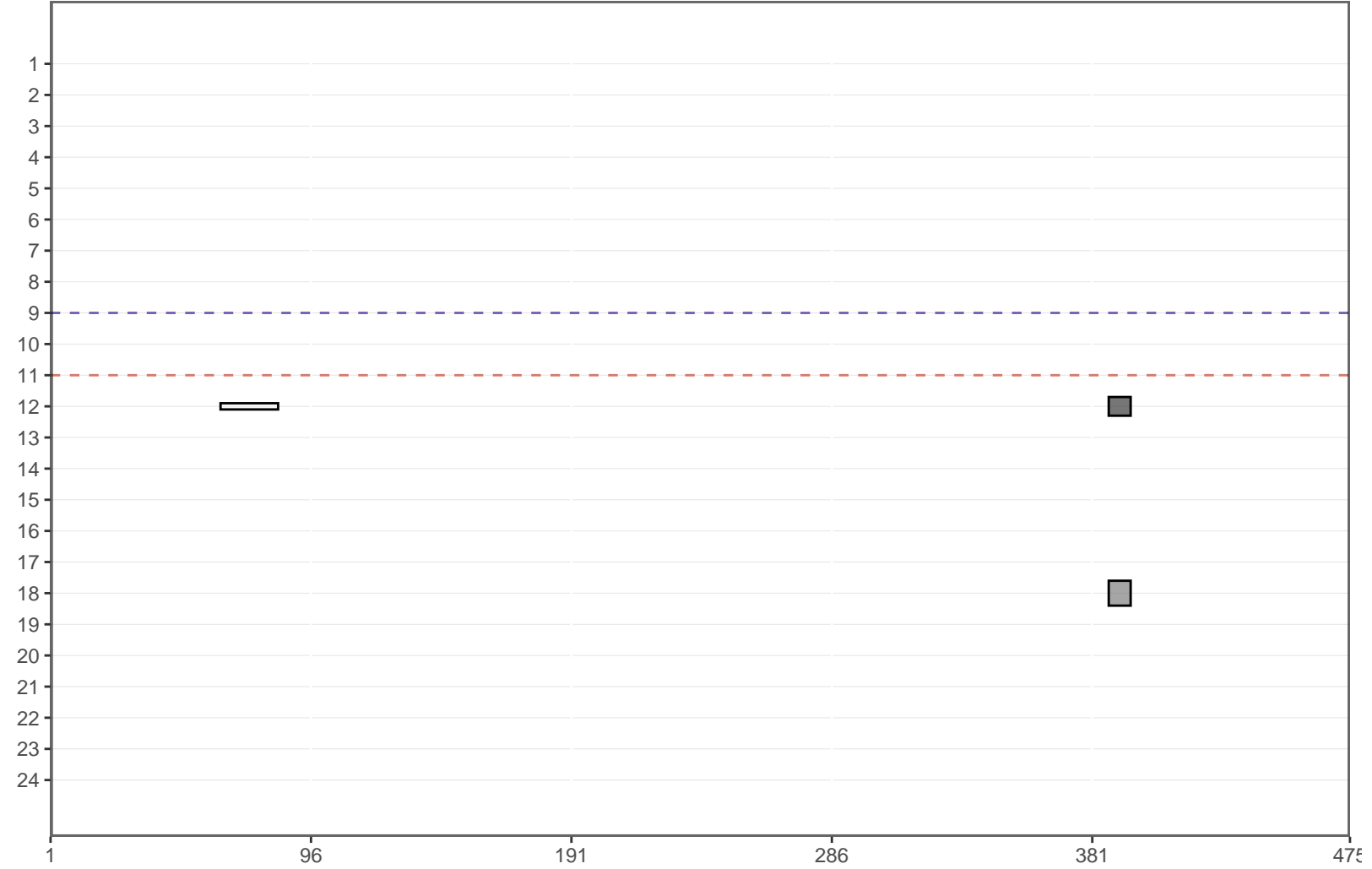
MW indication



Molecular weight

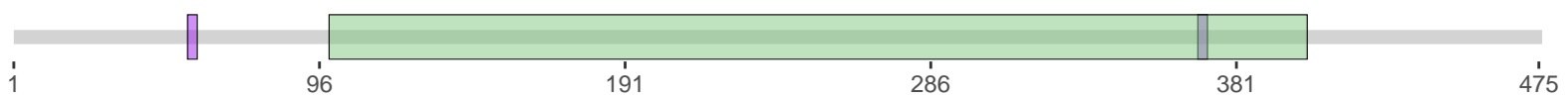


Gel Slice



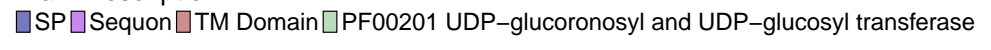
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

PILSQIRTVCPNYYTIGPVAHMLKTRLATKGTSSNSLWGEDENGINWLDTHPPKEVLYVFGSAGVTRREELLEFWYGLVNSDQNFLLWVRADLIGQGEKHEILEEGGTRKARGVMAWVYVPEKVLAAHTAIGGFLTHGQWNSLESIVGKVPICWPRFADQGVNSRFGEVWMMGLDNDTCDDRDIGKSGIKRDLMEKRRGEFLQTEGMSMARRTVNEGGSSYNLDRUQDRIQLMCLPLKQFS*

NbL15g14420.1 uncharacterized_LOC107802020 [MW = 32.76 kDa]

No. of times detected



log(intensity)



Values from



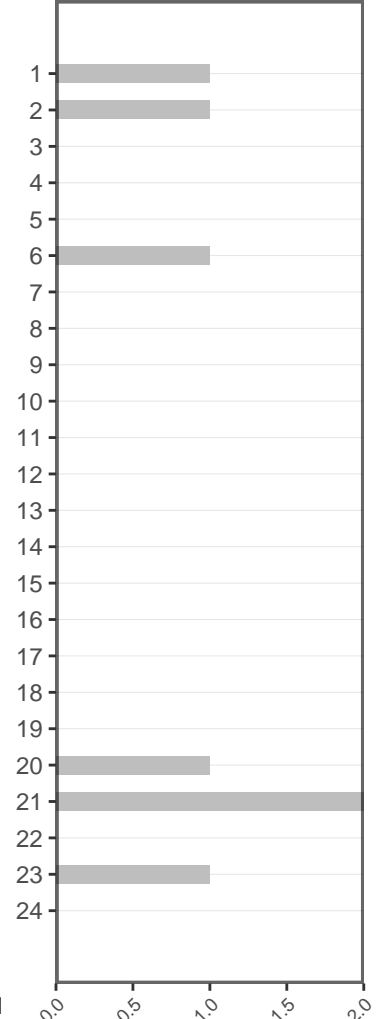
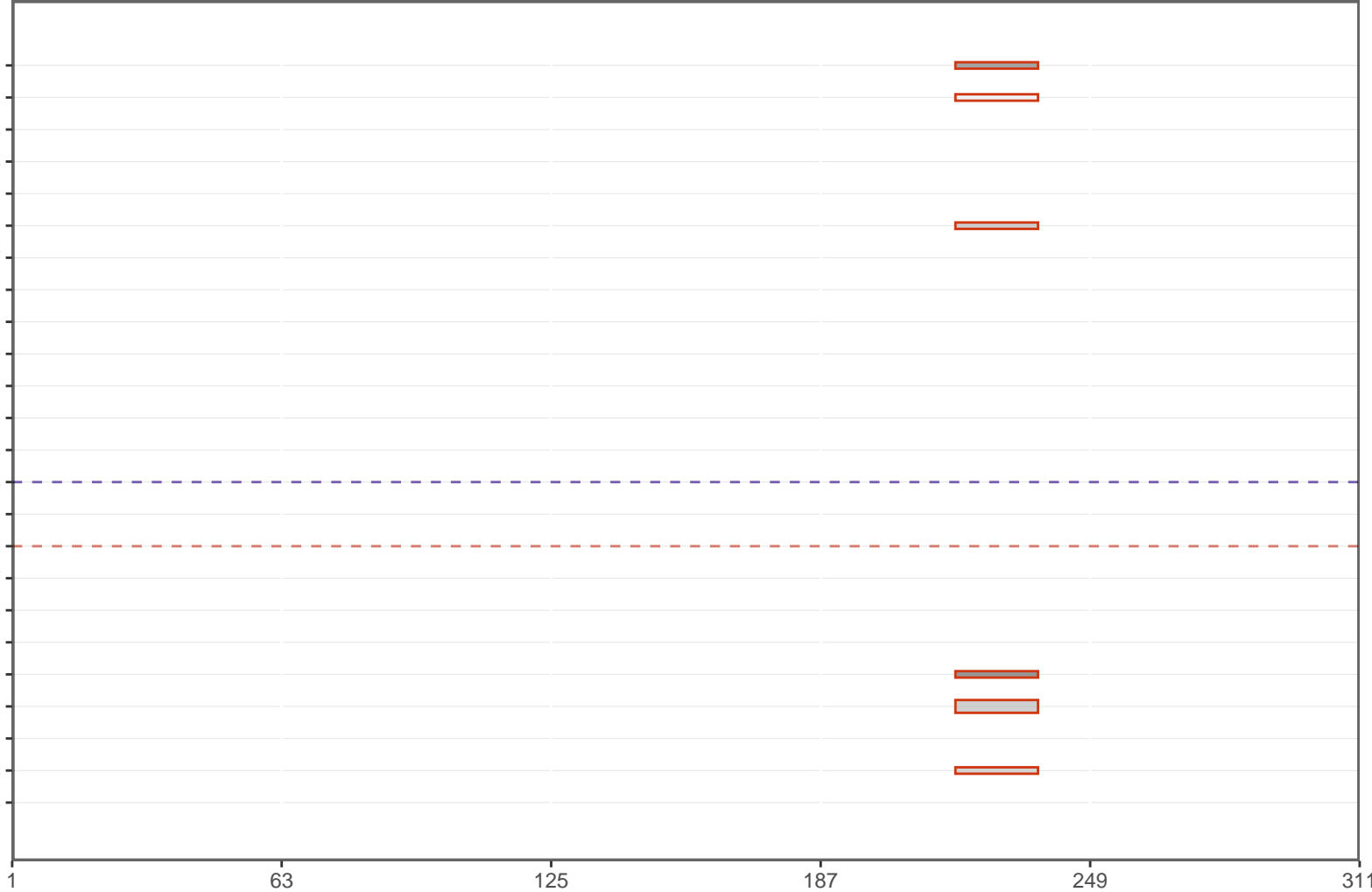
MW indication



Molecular weight



Gel Slice

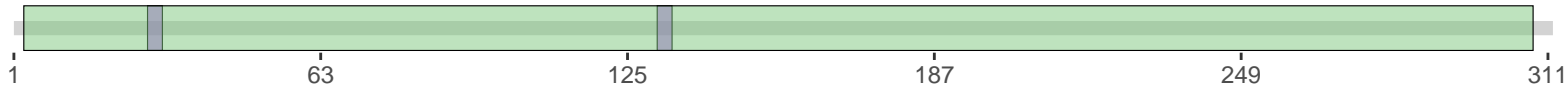


Protein length

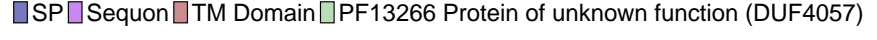


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VAKQRELSONLESESDSKKKHLSDANKTELKSGNDIFGPPPEVPTRLGAAARGLSEKESKDMGEPMPRTVTRVSVNPNAGGGSILFGDEPVGKTKKHKNQKFAELTGNDFIKGDFPPGADKPLGSANLKEMGGSDIFSDGKIEGRDHLGGVRRKPPGGESTISLV

NbL15g14380.1 tropinone_reductase_homolog_At5g06060-like [MW = 31.6 kDa]

No. of times detected



log(intensity)



Values from



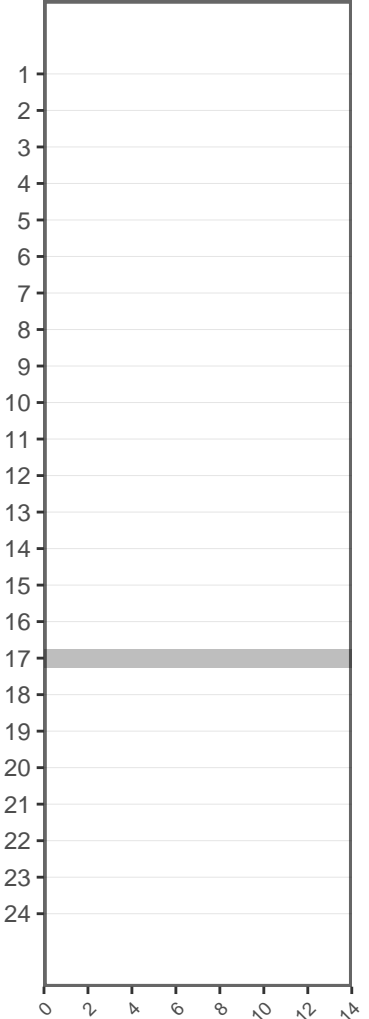
MW indication



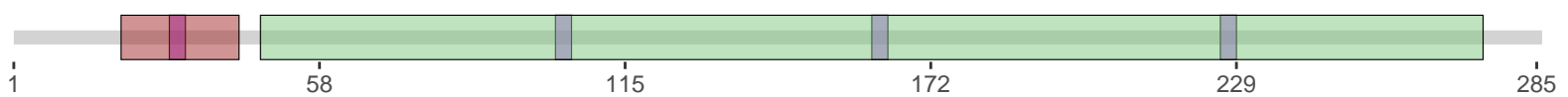
Molecular weight



Gel Slice

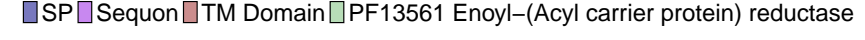


Protein length



Pfam domains

Pfam Description



Protein sequence:

TDYAAEEYARLLGLTALLESAYHIGQLAHLPLKASGNGSVYRFSVAGLVHISGGSYGATKGMNQLTRNLACEWAKDSIRVNGVAPVYRITSLVEHLENTKFLDGVWRTPLRPPGEGSEVSLWYLLQLPGASVYTGQIHAVDGGFTVNGFEMTSY*

NbL15g14330.1 actin-7 [MW = 41.76 kDa]

No. of times detected



log(intensity)



Values from



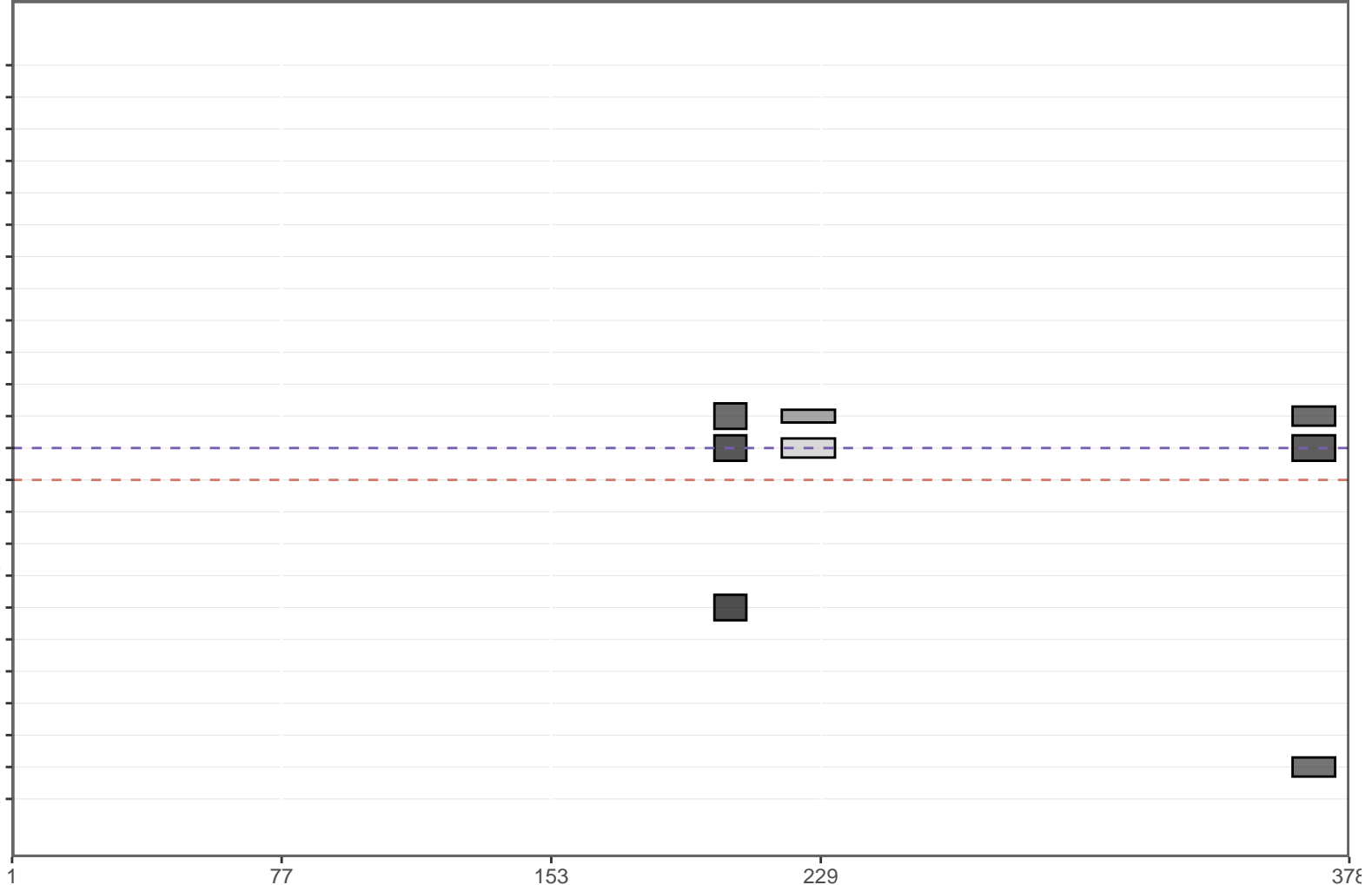
MW indication



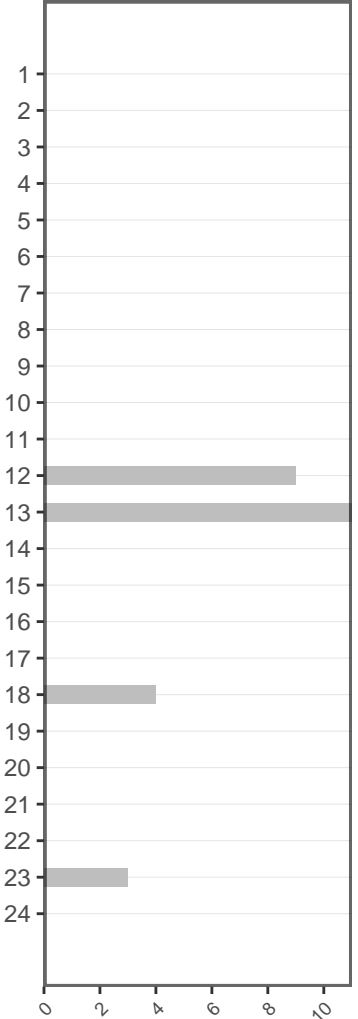
Molecular weight



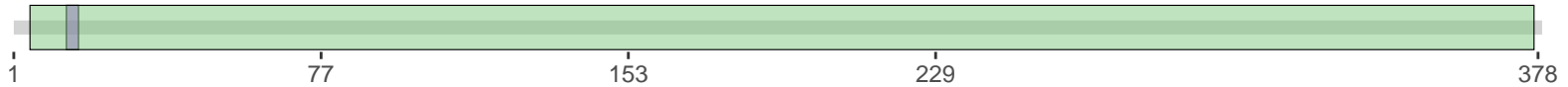
Gel Slice



Protein length

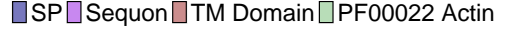


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

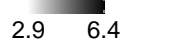
PHAILRLDLAQRDLTDELMLKLTFRGVMFTTAAERIVRDMKELAYVALDYEGELETARSSSSSEKNYELPDGGVITIGAEFRFCPEVLFPQSMIGMEAAHGETTYNSIMKCDVDRKDLGNVLSGGSTMFPGADRMKEETALAPSEMKIKVVAFFPERKYVYVWGGSLASLSTFQGMWMSKGEYDESGPSVHRKGF

NbL15g14290.1 40S_ribosomal_protein_S18-like [MW = 17.52 kDa]

No. of times detected



log(intensity)



Values from



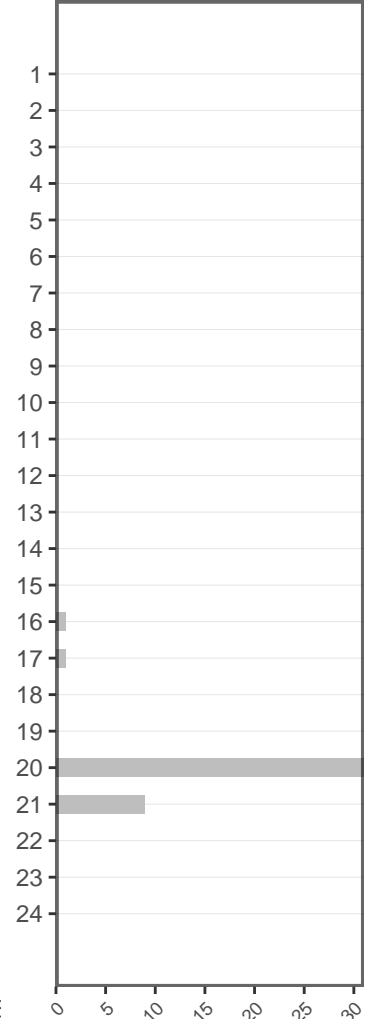
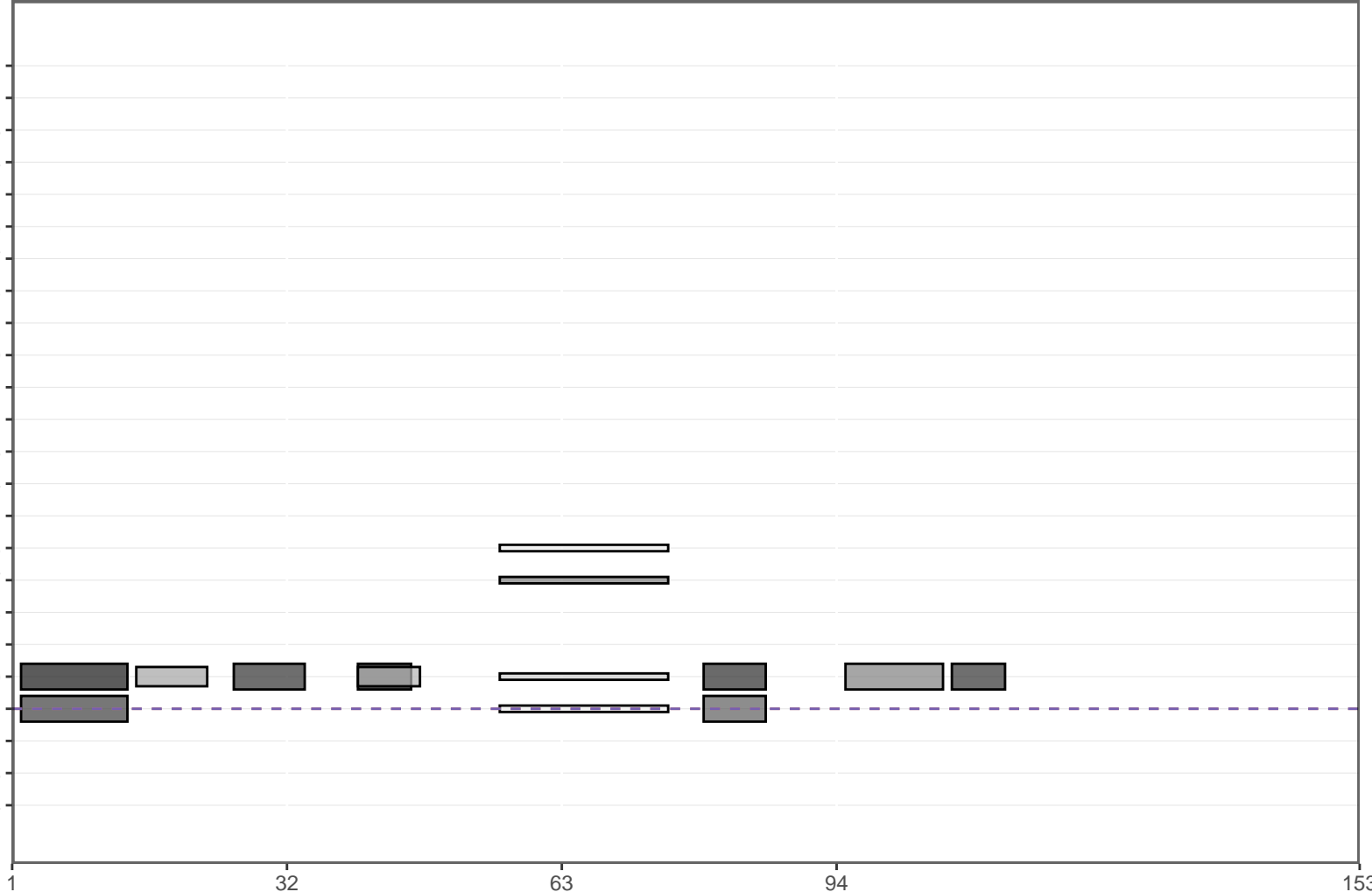
MW indication



Molecular weight

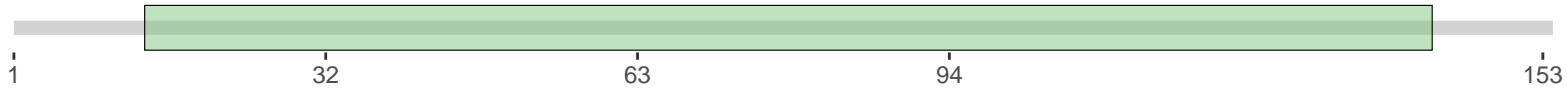


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SVMVVANPROFQKDFWFLNRGKDKDKGKFGVTSNALDMLRDLERLKKIRNIRGLRHYYWGLRVRGQHTKTTGRGKTVGVSKRR

NbL15g14280.1 uridylylate_kinase-like [MW = 35.72 kDa]

No. of times detected



log(intensity)



Values from



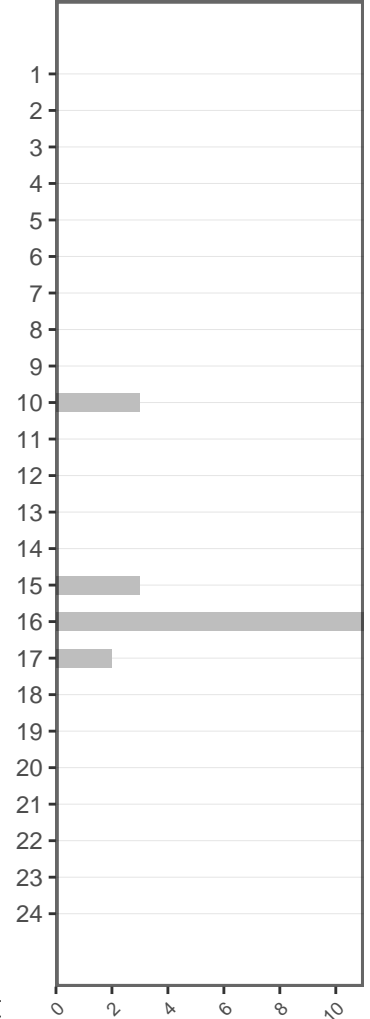
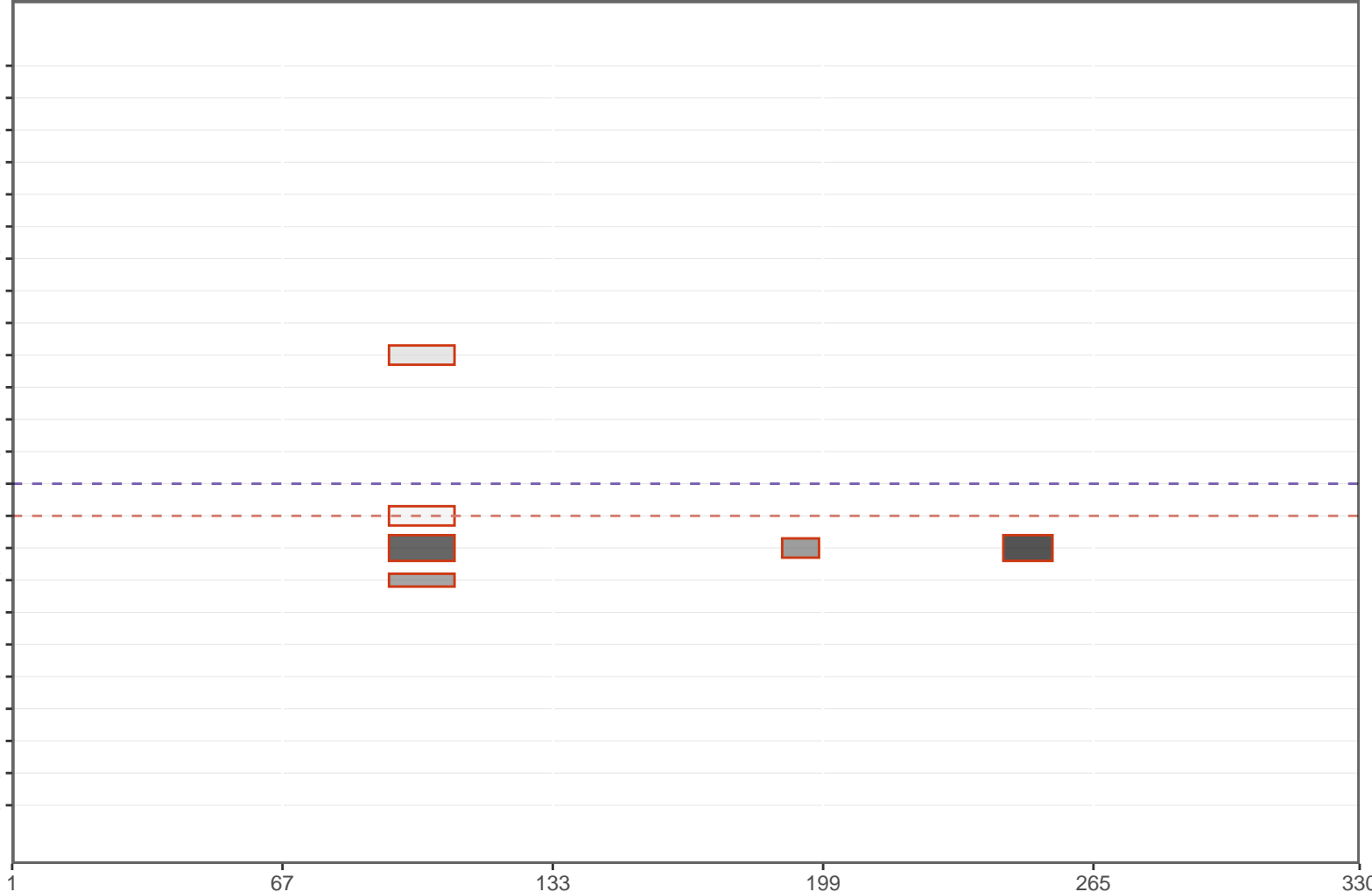
MW indication



Molecular weight



Gel Slice

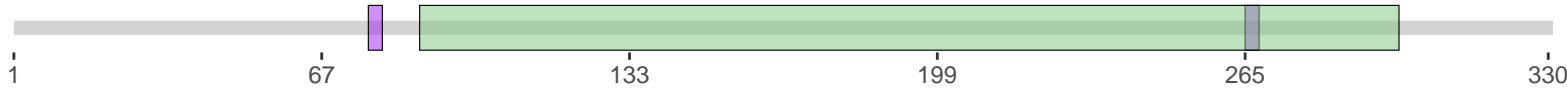


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

DRSSADYIGMLATVMNAIFLQATMESIGPTRVQTAFRMSEVAEPVRRRAVRRHLEKGRVVFVFAAGTGNPFPTDITAAALRCAEINAEVVKATNVGVDVDDNPRHNPDPARLGDNLTHYVSEKELSVMLTHTLLOGENIPVVFVFNLNKPNKAIKAKGERVGTGLDGTWNTAAVSI

NbL15g14200.1 thylakoid_luminal_15_kDa_protein_1_chloroplastic-like [MW = 23.31 kDa]

No. of times detected



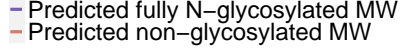
log(intensity)



Values from



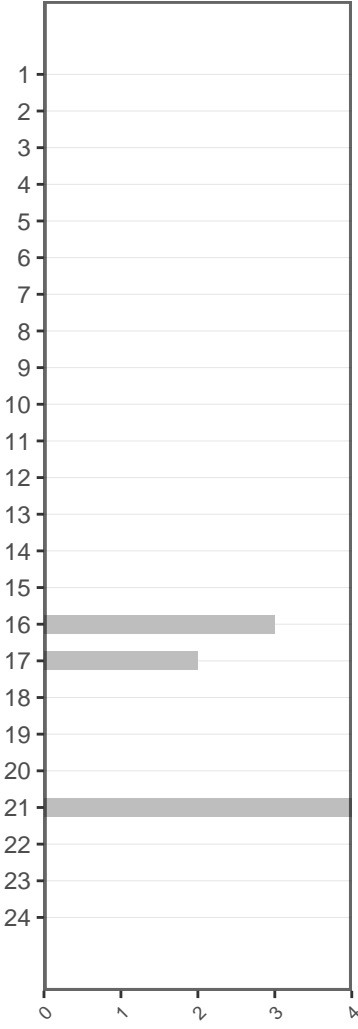
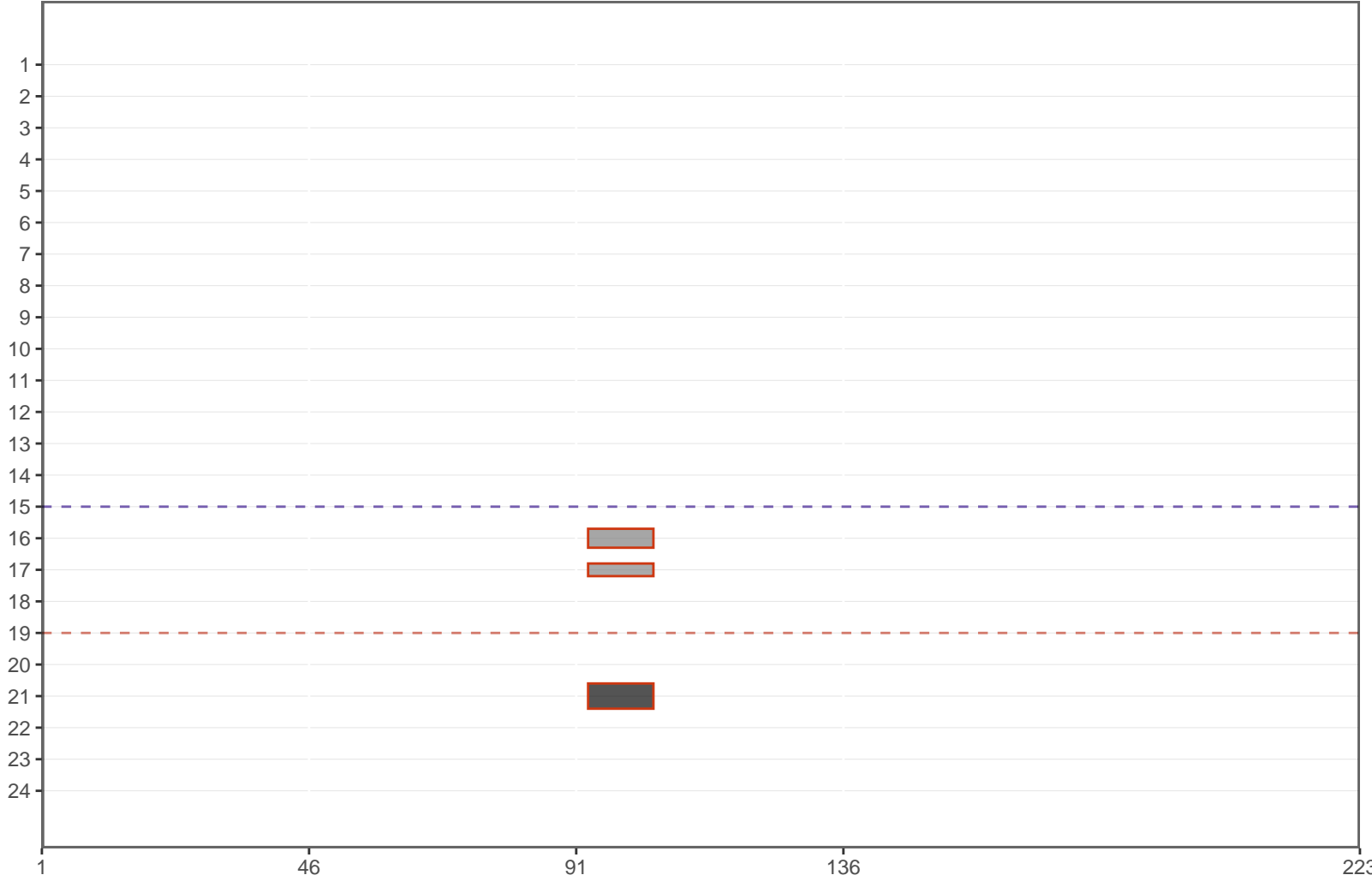
MW indication



Molecular weight

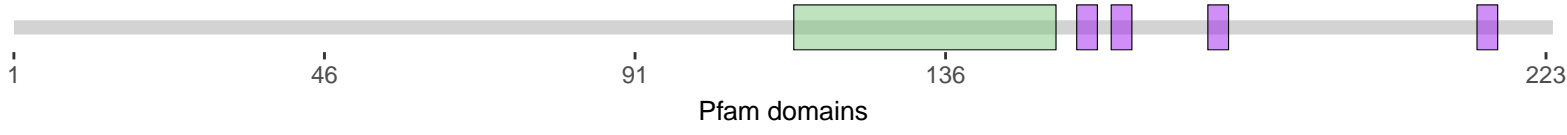


Gel Slice



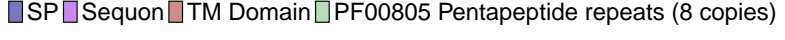
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SKDFSGKTLKGGDFKTSRLRQANFRGANLVGASFFDADLDTGADLSDALRGADEFSLANVTKVNLNSANLEGALTTGNTSFKGSGNEGADFTDPLRDDGQREYLYKADGYNPVTGNATRDLEFKV

NbL15g14020.1 3-hydroxyisobutyryl-CoA_hydrolase-like_protein_3_mitochondrial [MW = 46.8 kDa]

No. of times detected



log(intensity)



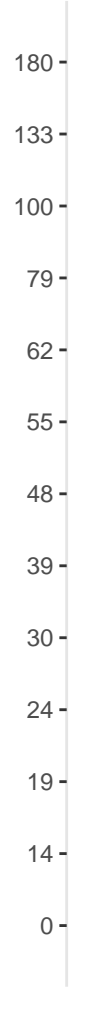
Values from



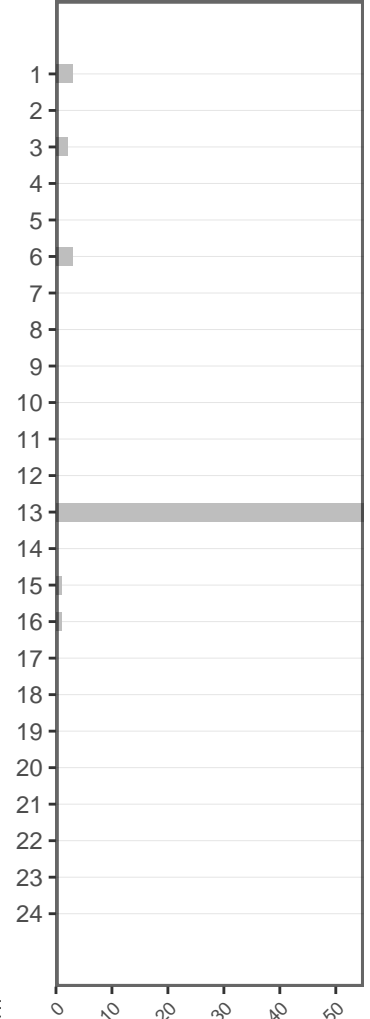
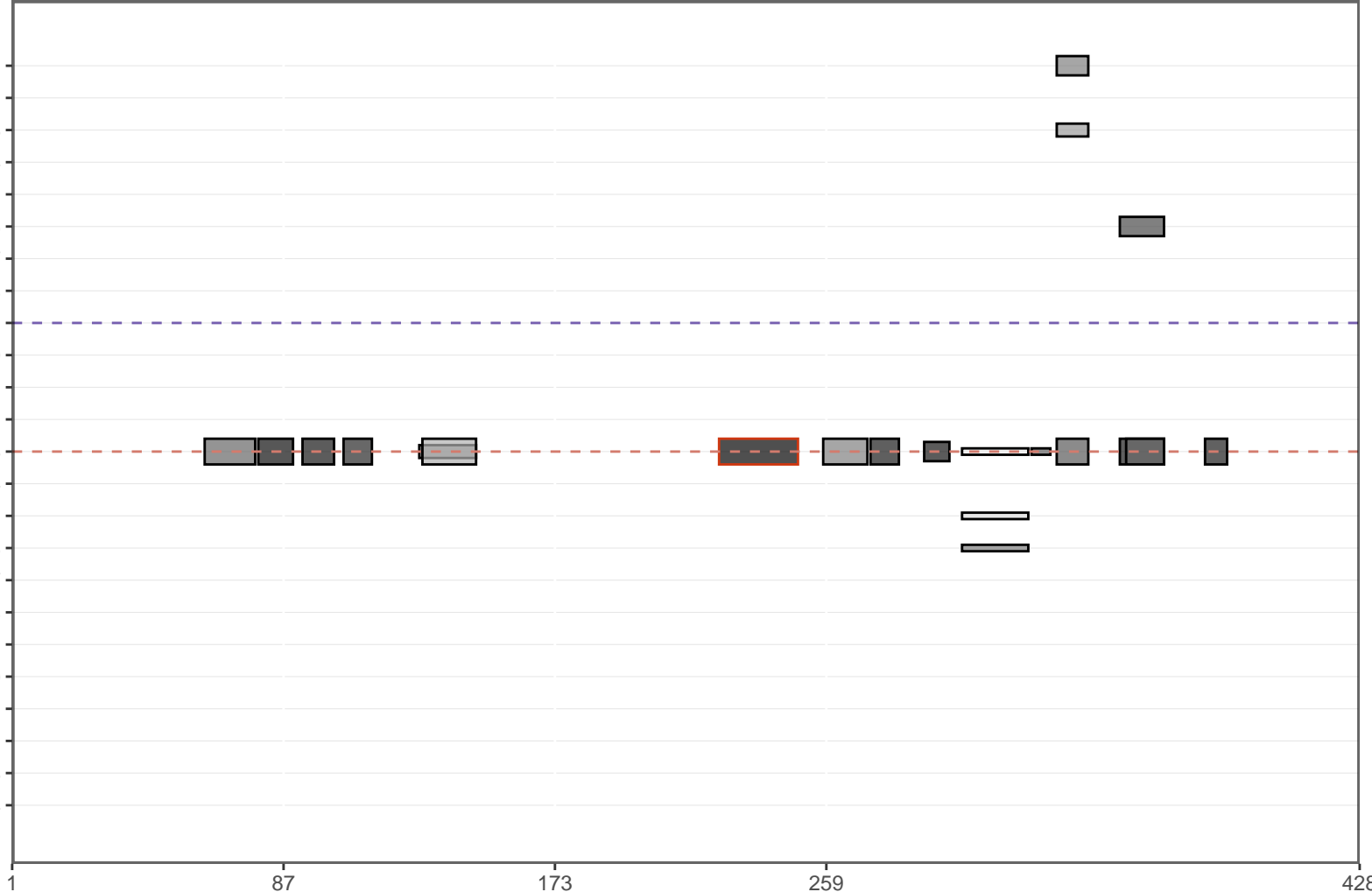
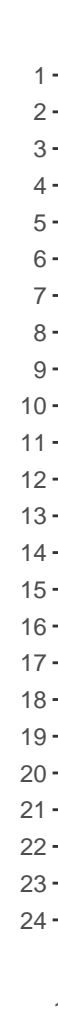
MW indication



Molecular weight

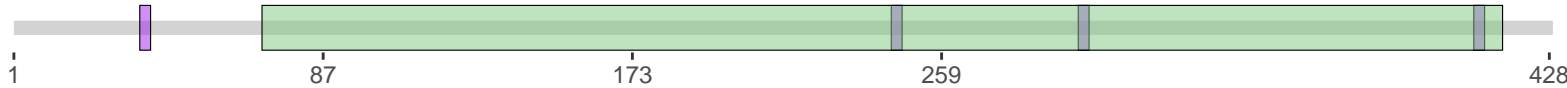


Gel Slice



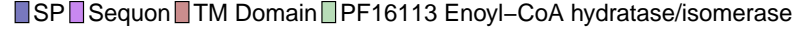
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

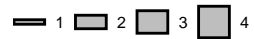


Protein sequence:

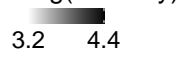
FSYIAIHGSPGCGTGVGVALTGNNRISTPDALYVGLGTHYVPSANLSTLKEALLATKFDSDPDEEKELLAAYSENPDSEPRKLSLLPRHSTFAGNKGRHEELENHGGGADTLVVEWAKDALGGLRKGAPFSLQTLTKLFRVVASARGKNENLSSLSNGVMRTEYRIARSLRSDFAEGVRAVLVEKDGSPKWNPDGLEVDNLSEVEALFELPDPVGLNLYV

NbL15g13940.1 serine-threonine_kinase_receptor-associated_protein-like [MW = 37.76 kDa]

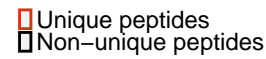
No. of times detected



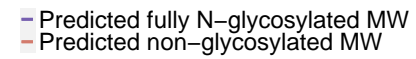
log(intensity)



Values from



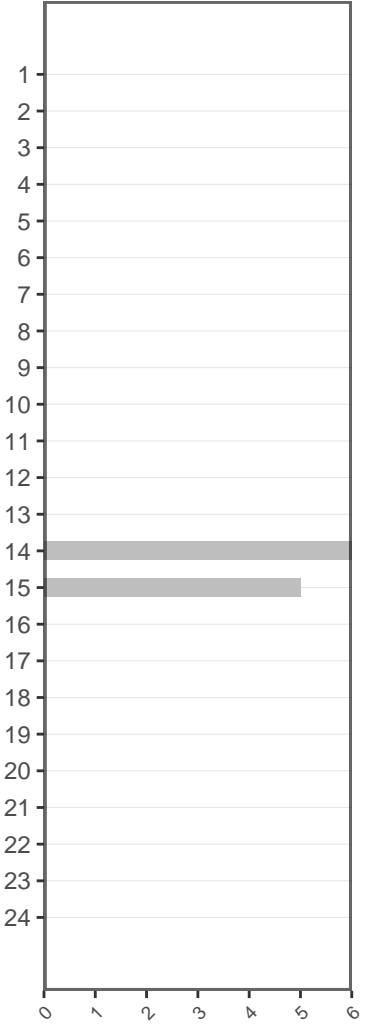
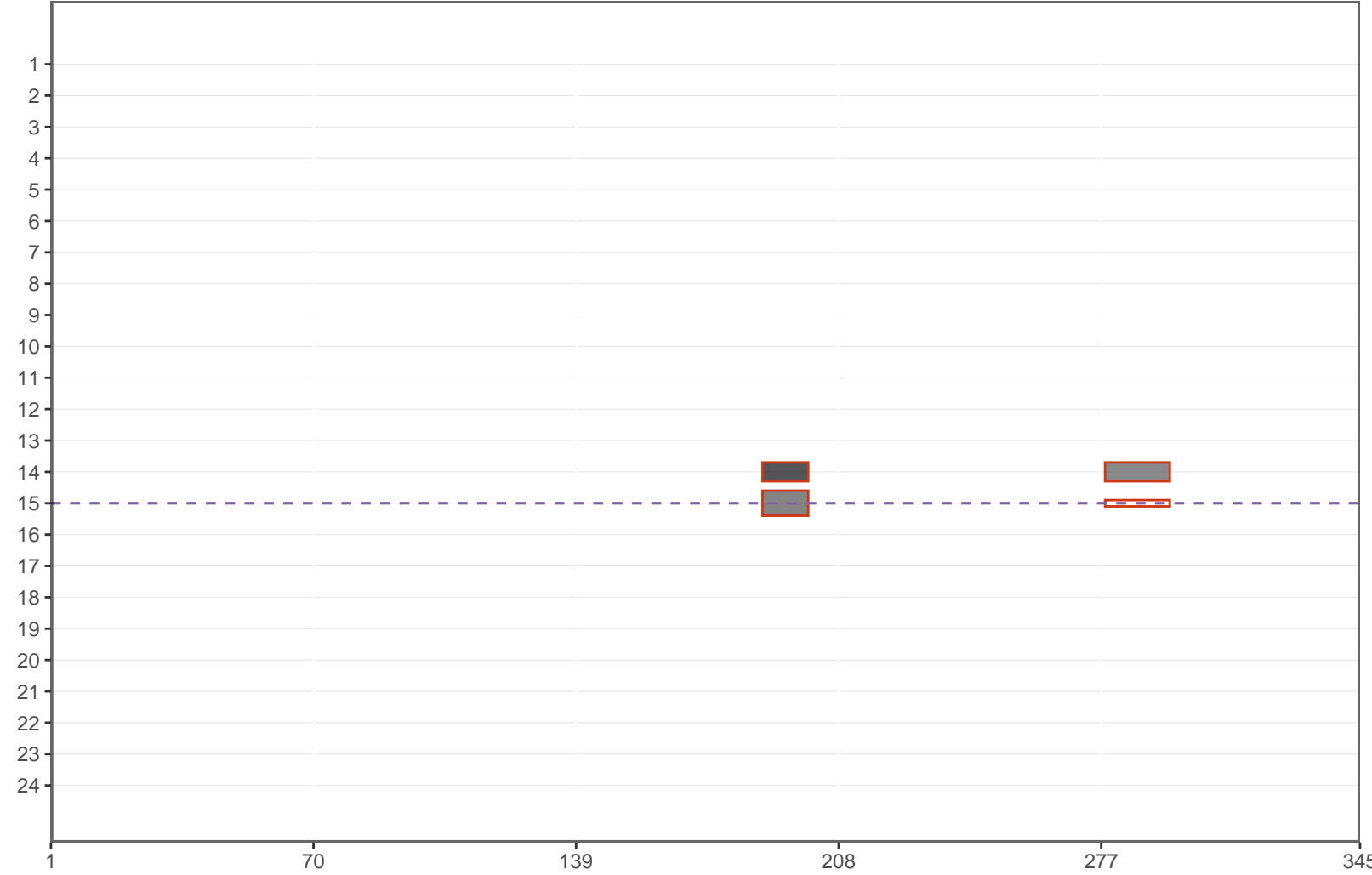
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TLSSCTDSGGVRLWDVIRTDGIVRILETKSPVTSAEVSGDGRVYFTDGFVKFVDANFGLVKYKINMPCTVESASLEPKYGLKPFVAGGEMWIRVFNKHTGEEELACNKGHHGSPVHVRFAPSGESVAGSGEDGTRIRWGTGLTNDVDVDMFTNGKVKVSAEEVSRNIEGFGDSERKIKKEEDLAD

NbL15g13870.1 protein_arginine_N-methyltransferase_PRMT10 [MW = 42 kDa]

No. of times detected



log(intensity)



Values from



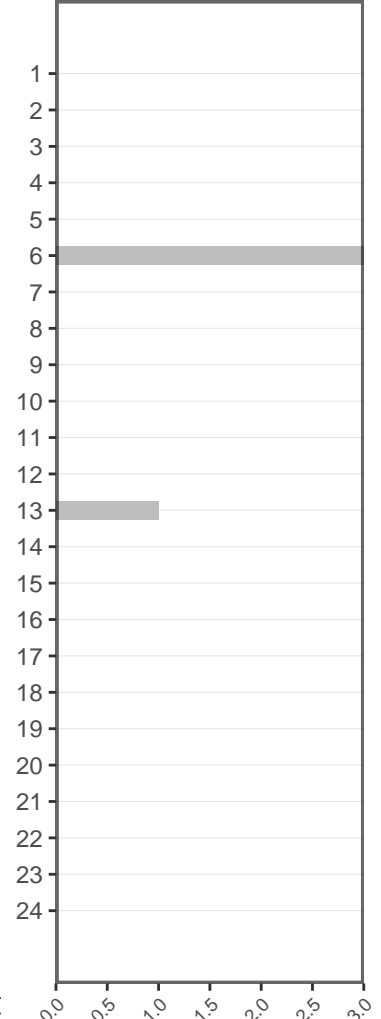
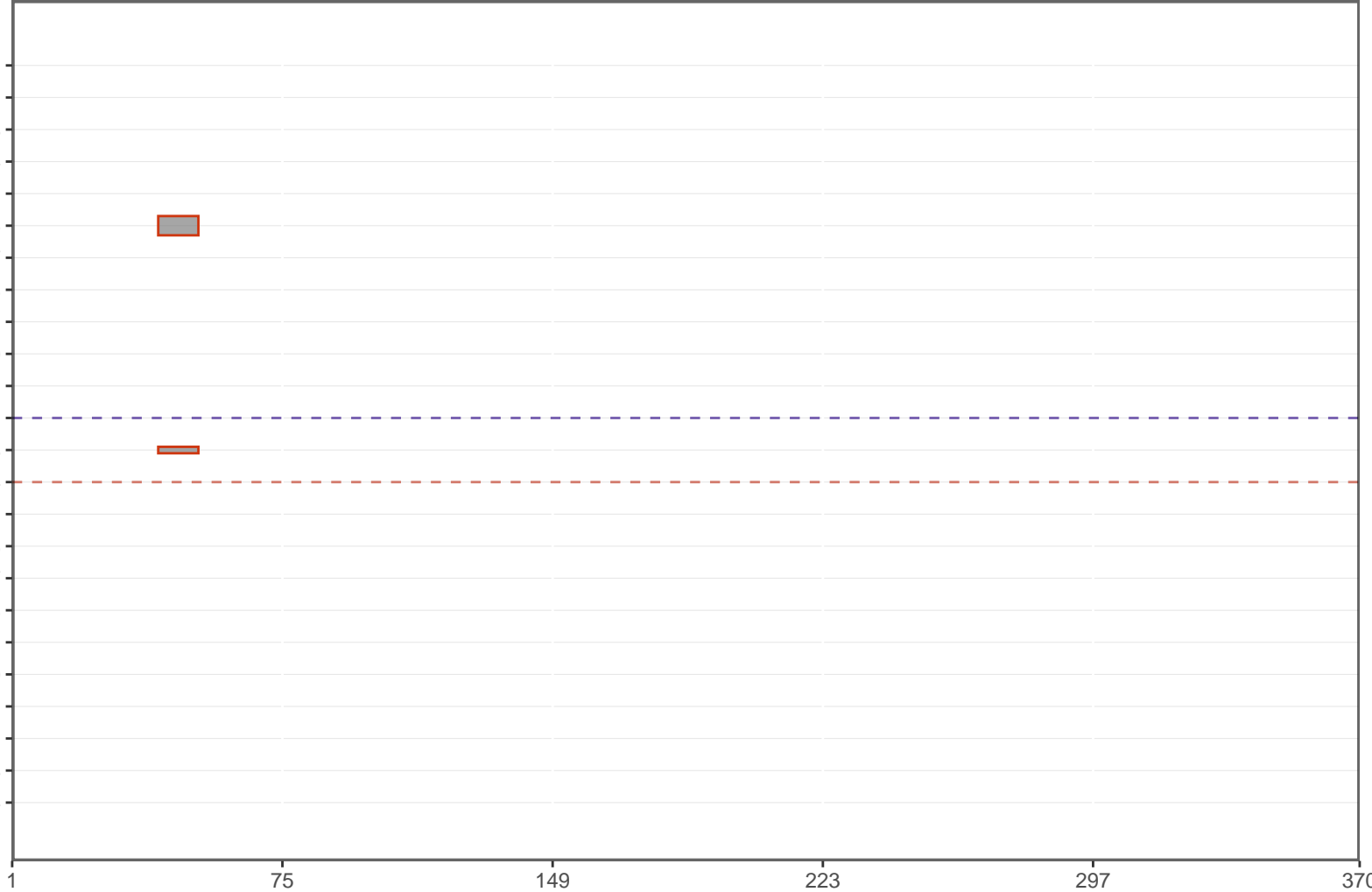
MW indication



Molecular weight



Gel Slice



Protein length

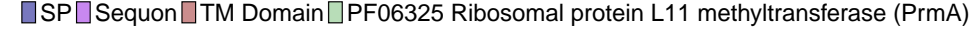


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SGLYDQKKIDYDRAMDWYHFVDETGTFFYGVDMISLSKPFTEGRKYLYLETSLVNNLHPNGVIGKRWIMEDCLTSSVNDILSQAHISSITAENSLRGGFGWFDVHFRGRKESFKKHEIETAPSEDLGTWHVGGQVFLHHPBIRVSGGDEMTNFMGMVRKRNHLLVEFQCELRSSSGKSLPSFKKFKHE

NbL15g13740.1 protein_phosphatase_1_regulatory_subunit_pprA [MW = 35.98 kDa]

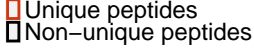
No. of times detected



log(intensity)



Values from



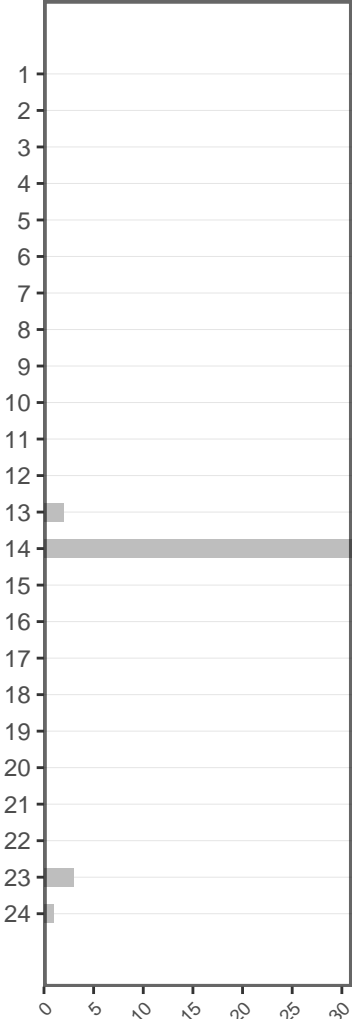
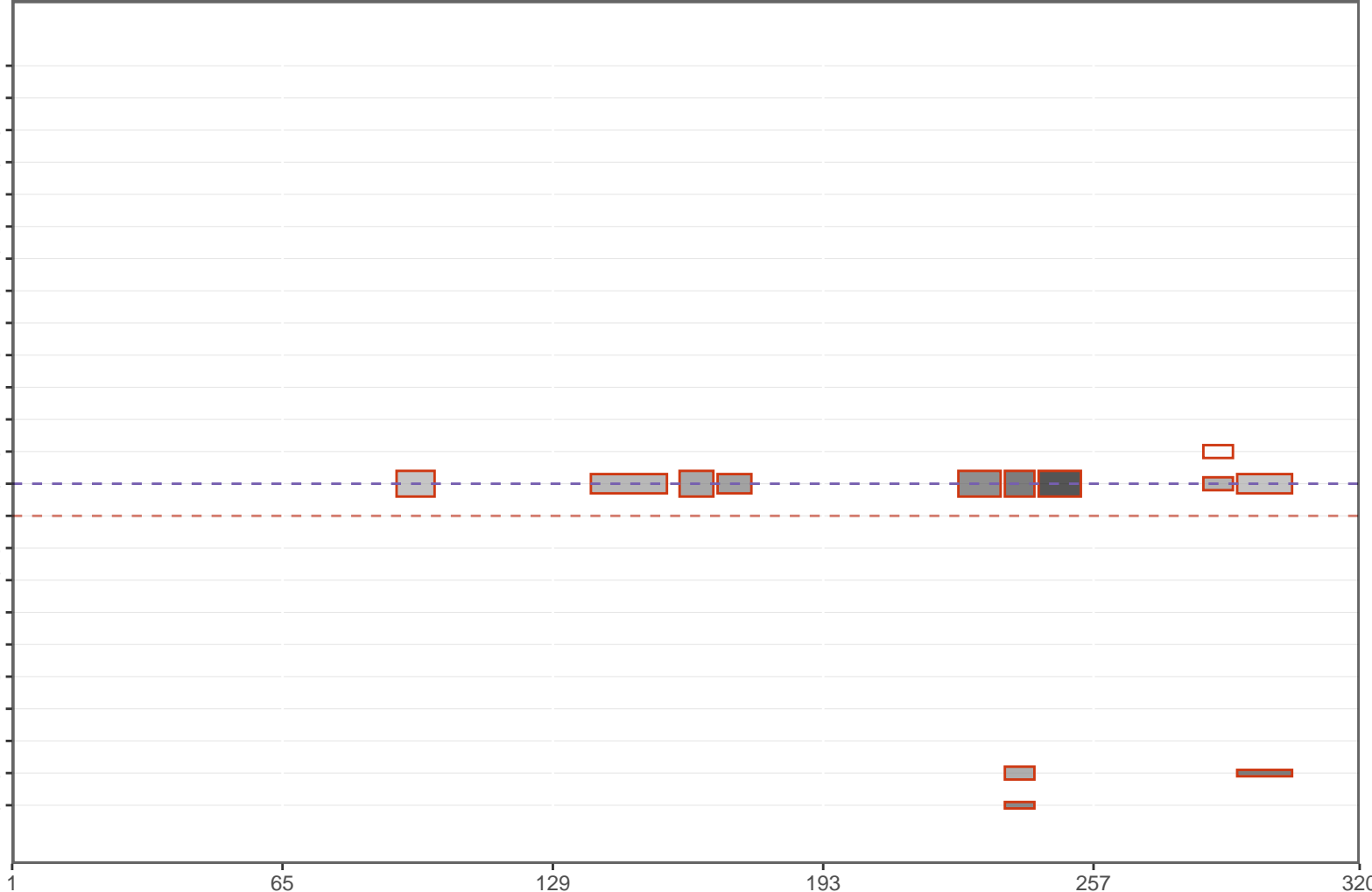
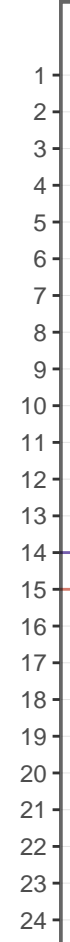
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LDLLELGSNRLRVMLLELNKNGELWGRNRIRTVNLGGLKIKKISLQSNRLTSMIGFDQCVALEEVLKSHNGIAKMEGLSTVNLRVLDVSAANKLTENDIENLRKLEDLWLNDDNNAISGLVLAFAWAGAKEKLTITVLERKPGAGSPNYTSLRGIFFNIEGIDSEVVA

NbL15g13600.1 vacuolar_protein_sorting-associated_protein_32_homolog_2-like [MW = 24.32 kDa]

No. of times detected



log(intensity)



Values from



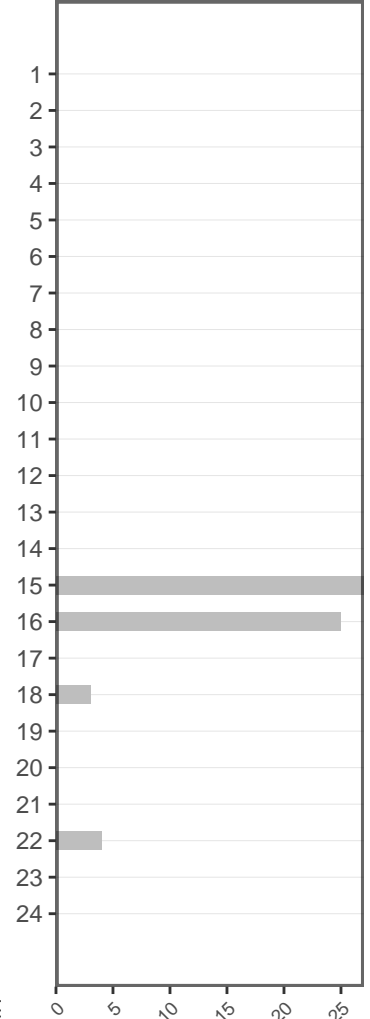
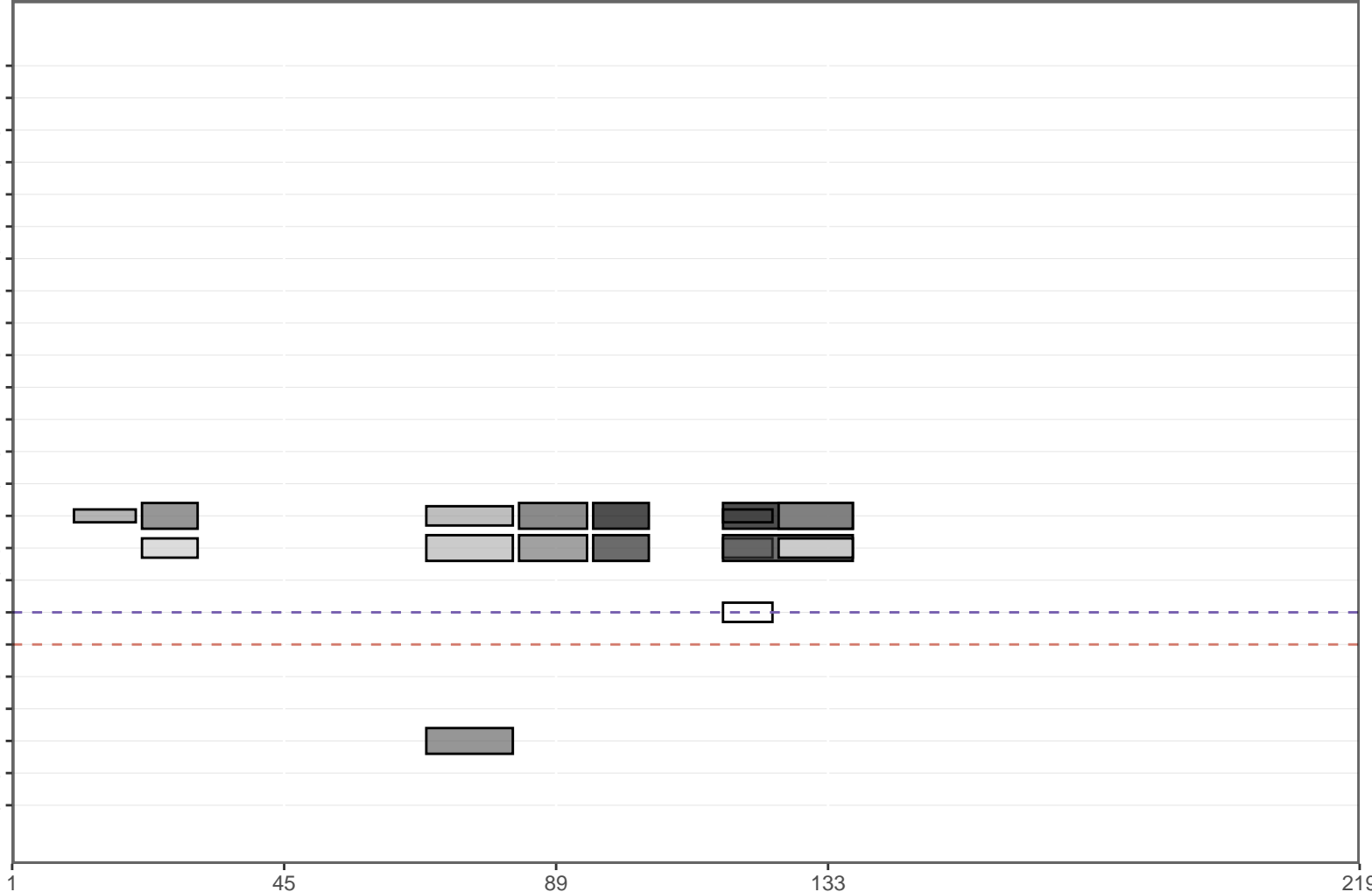
MW indication



Molecular weight



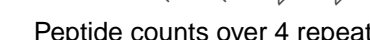
Gel Slice



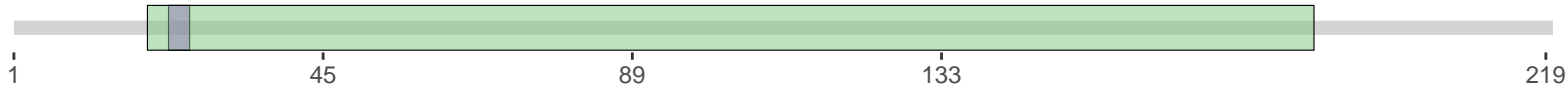
Protein length



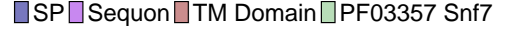
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

TETVDAALRTGASAMKAMKATNDDVDVKTMDENIEQFENMKQIGALATPGAAADFDEDELEAELEEEGAELEEQLLQRTTAPAPVHVPAGRQPARPIQRRTAEDELAAQAEAL*

NbL15g13580.1 mitochondrial-processing_peptidase_subunit_alpha-like [MW = 54.62 kDa]

No. of times detected



log(intensity)



Values from



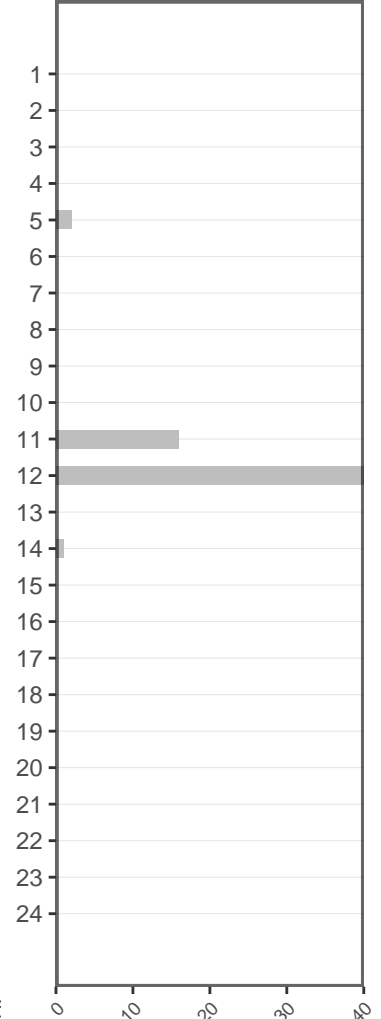
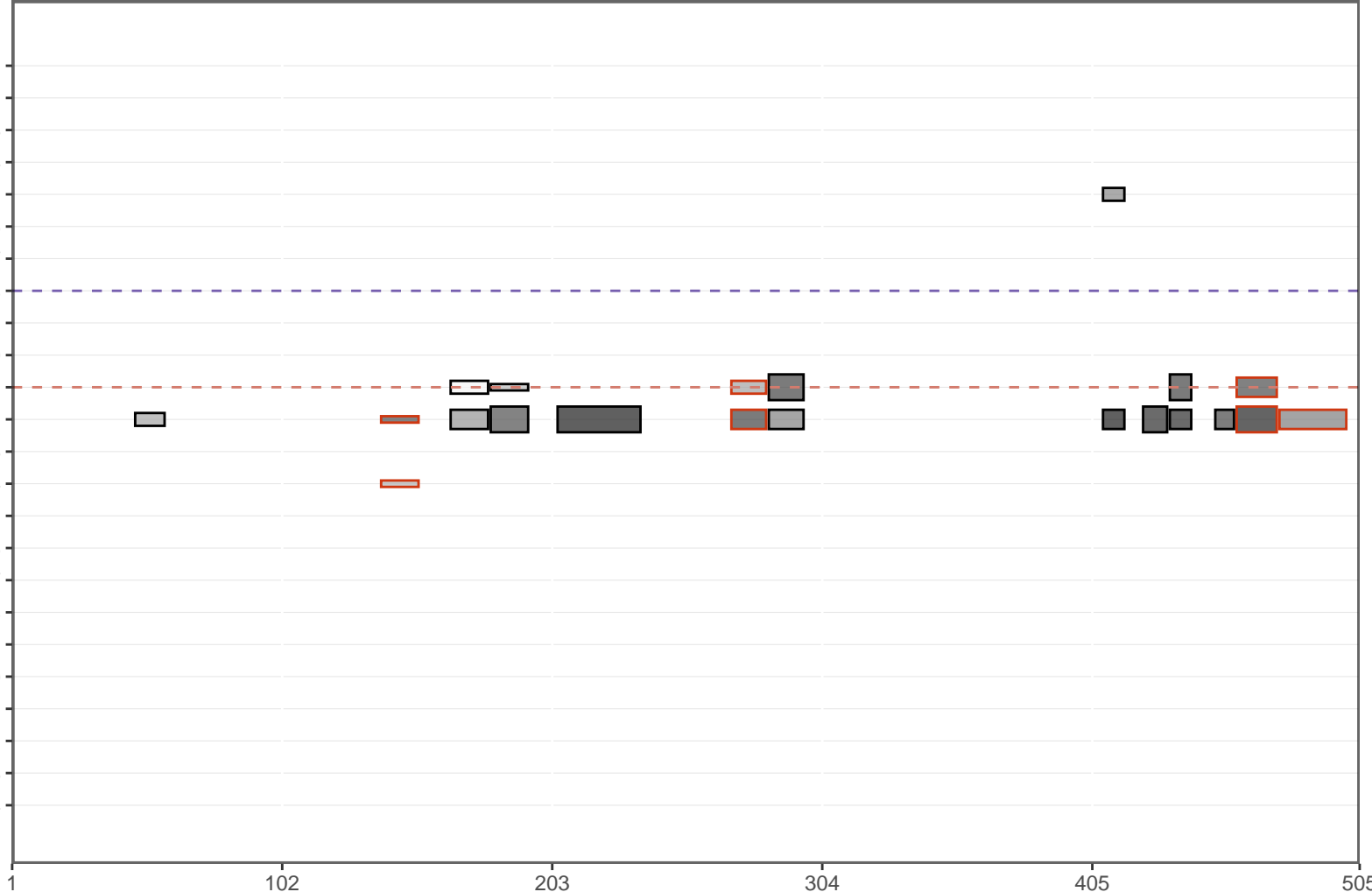
MW indication



Molecular weight

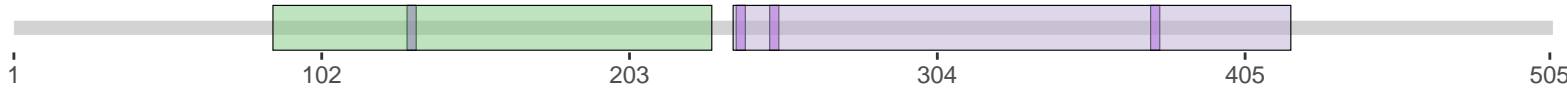


Gel Slice



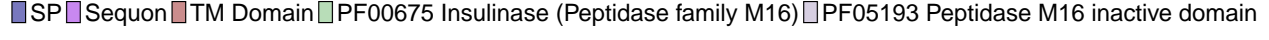
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ITYLEEFVAENYTAPRIVLAASGVHEHELLKVAEPLLSDLPTVPRAEETPTVYVGGDHRRGADSGMTHFALAFEVGGVWKEKDMFTLVLOMLMGGGGSGFAGGPGKGMYSRLVLRVLAIVPQHFASAFSSHYNTGLFGQGAATTSDFAPRAIEVAKELTAVANPKVEVDGVLDRAKGSKKALMLNLSRMVASEDGRQLTYGERKPVHFLKADATANDASVAEKLISSPLTMAASYGDVLSLPTYNVSSRFHK

NbL15g13530.1 probable_methionine--tRNA_ligase [MW = 90.64 kDa]

No. of times detected



log(intensity)



Values from



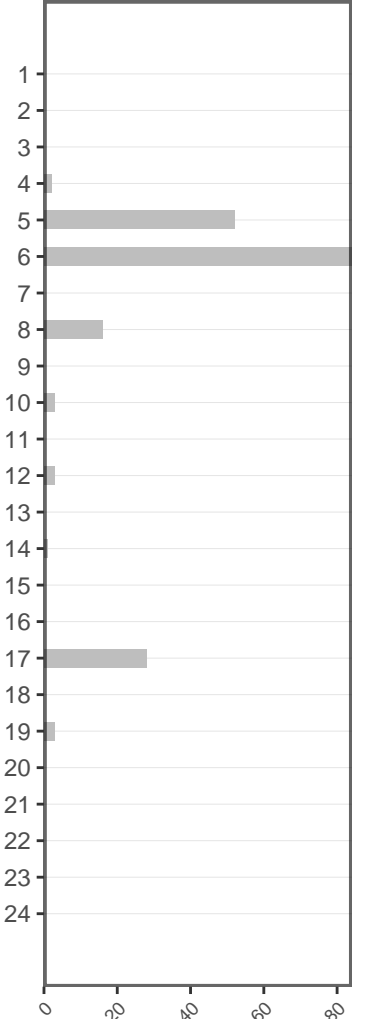
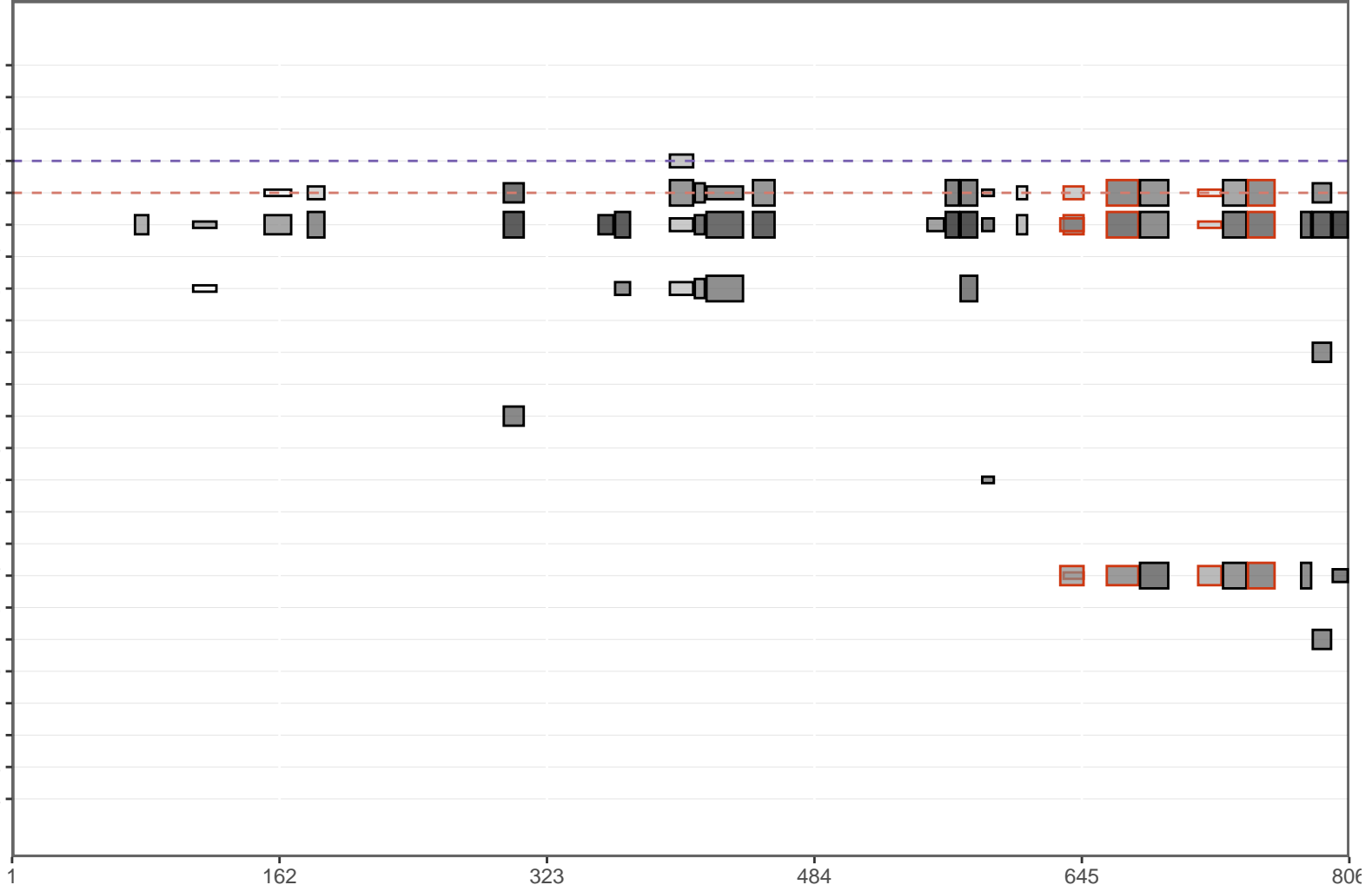
MW indication



Molecular weight

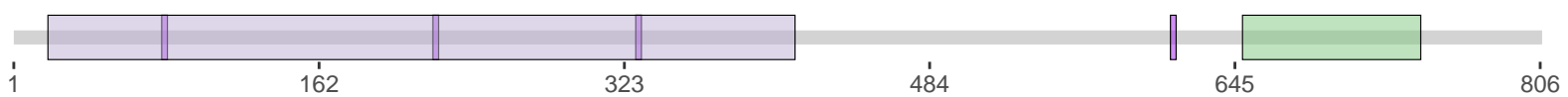


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01588 Putative tRNA binding domain
- PF09334 tRNA synthetases class I (M)

Protein sequence:

FTYADLQAKLNSELLNMLGNFVNRVLFIAKDEASGVGSIIPDVEGAESHPLTKALGEKVENVVEQIEAMEKVKLKGGLKVMMSISGEGNGVYQESGDFKWKYKEDRRSGSIVMRTAGSLVLLAGLLEPFMPSFGRVLEKGLNLPPEMQLSLADEKGDVANSKRFVNIIPAGKIKGTAPLFLKELKDEEVEFYREKFTAGSADRADRAKAEADAKKMAEQLNKRISDGNKERRAKKISSEKSKAPATVEGEISISALDRVGLLTKAQKHPNADSLVVEEDVGEAMPRTVV

NbL15g13490.1 chalcone_synthase_2 [MW = 42.64 kDa]

No. of times detected



log(intensity)



Values from

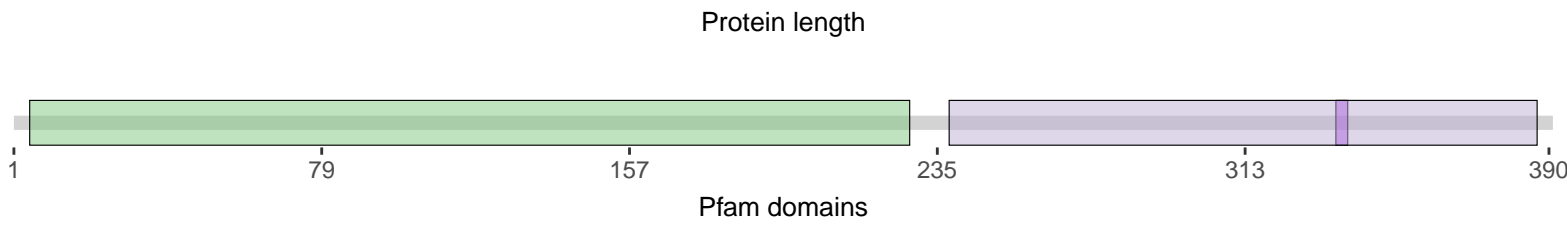
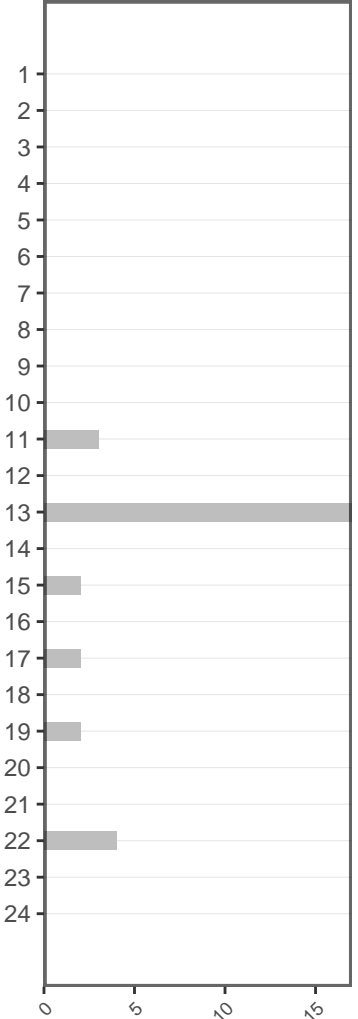
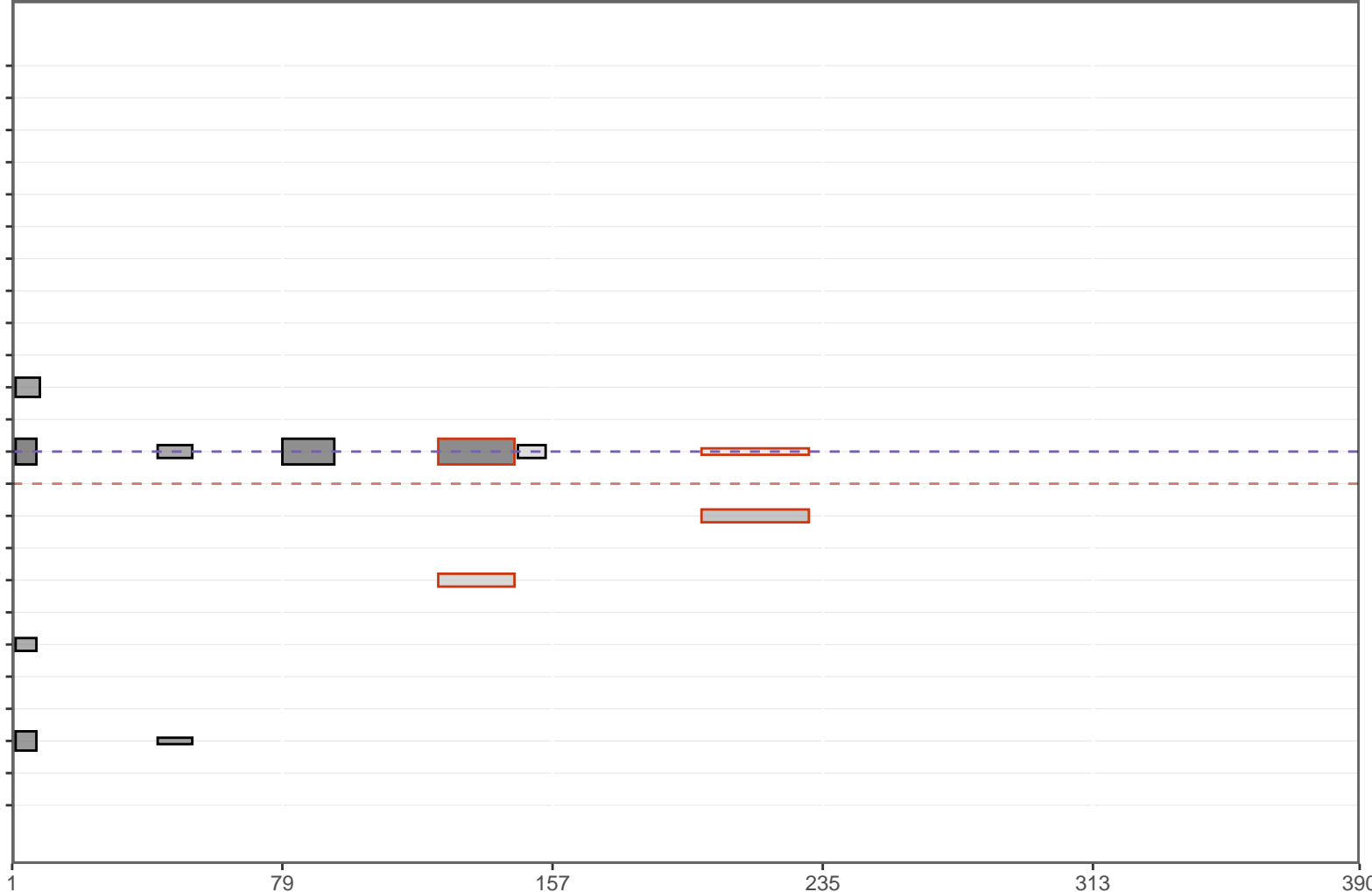
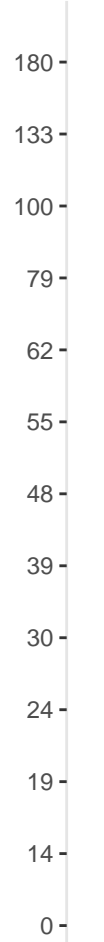


MW indication



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00195 Chalcone and stilbene synthases, N-terminal domain
- PF02797 Chalcone and stilbene synthases, C-terminal domain

Protein sequence:

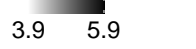
IKGARVLYVCEITAVFRGPDTHLDSMVGQALFGDGAANHGSDPVRPRVRFELFVSTQTLFDFSEGADGHLREVGLTHLLKDDVPLGSLNIEKLEMEAFQPLGLSDWNSIFWVHFGDPAIDGVLEKLGKPEKLRATRQVLSDFYGNMSSACVLFILDEMRRKASAKEGLTGTGEGLDWGVLFQFGPGLVETVVLHGVSPT

NbL15g13470.1 dihydroxy-acid_dehydratase_chloroplastic-like [MW = 72.72 kDa]

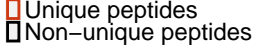
No. of times detected



log(intensity)



Values from



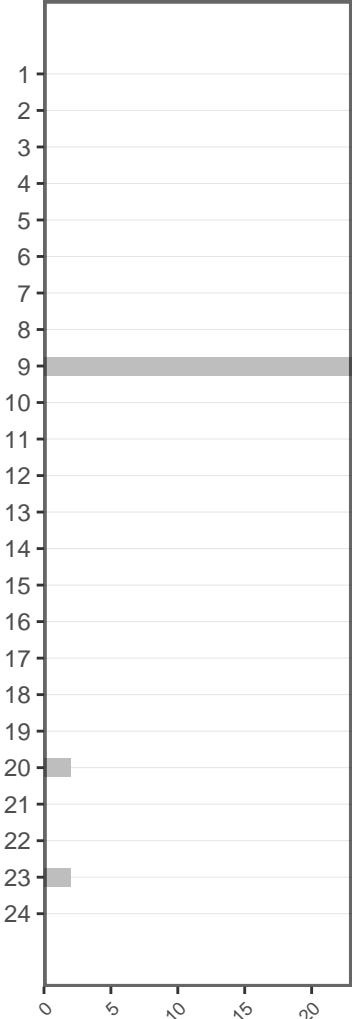
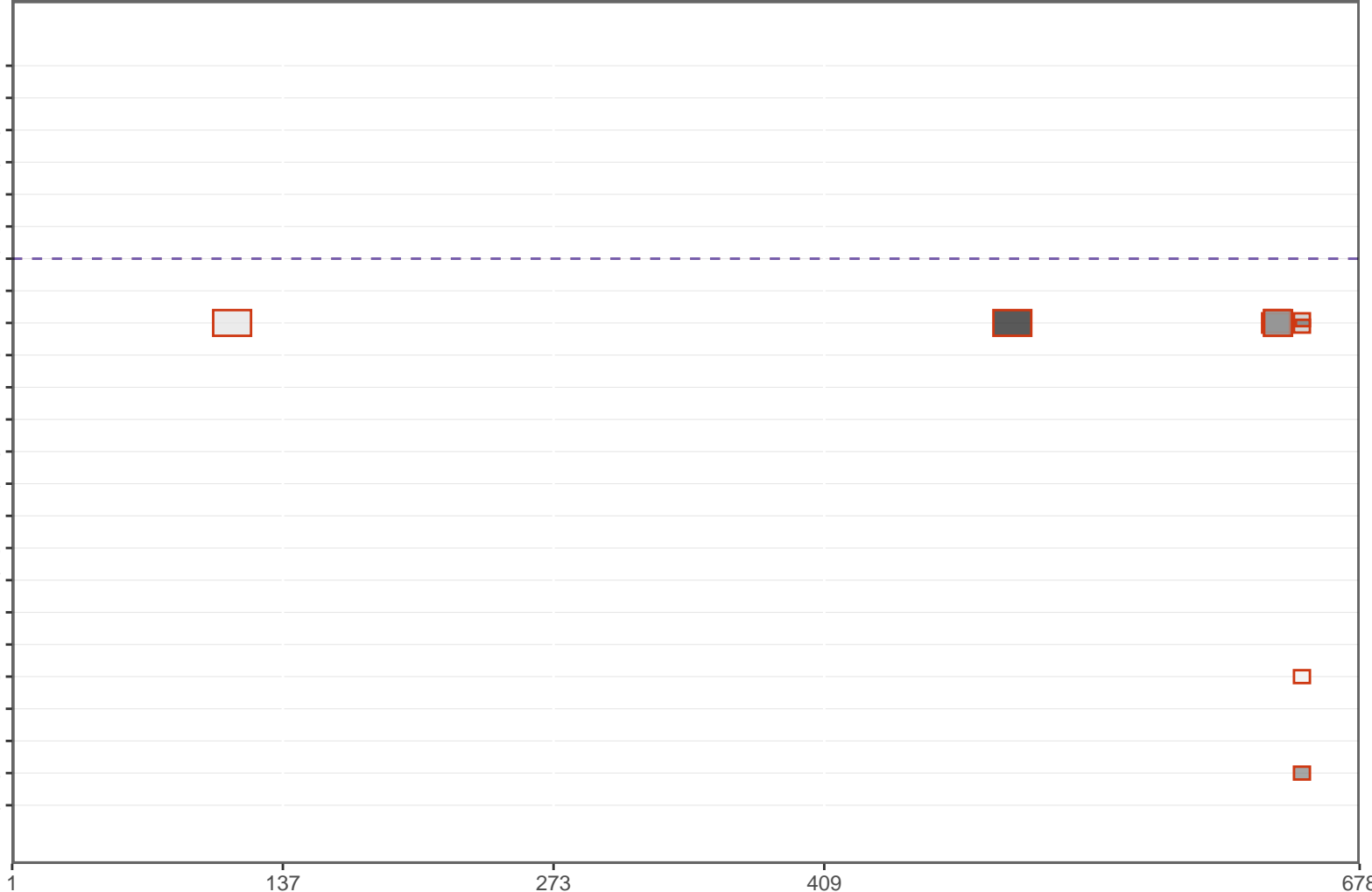
MW indication



Molecular weight

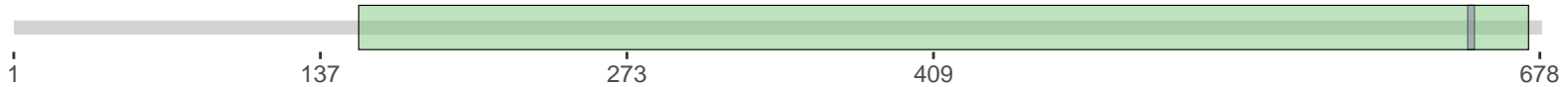


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

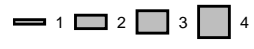


Protein sequence:

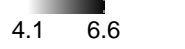
SAIEVLGMSLPYSSSTPAEDPKLDEGRLAGKYLELLKMDLKRDRDITKSLRINAMVMVVALGGSTNAVLHLMIAIRVGLLEFLDDFKVSDAVPFLADLKPGRKYMEDVHKIGGTRVIRHLEELGVLDDGDCMTVYTGKTLAENAKLFLSLAEGGQIRPLSNPKETGHIGLYGNLAFDQGEVANITGKEGMVYFSGFALVFEGETEAMAAIAEDPLRFKGVKVVIRGEGPKGGPGMPPEMLTPTSAIMSAGLGGKDALTDGRFSGGGHGYVYGHGPEAEEGGPIGLVDDDI

NbL15g13400.1 chaperonin_CPN60-2_mitochondrial-like [MW = 61.09 kDa]

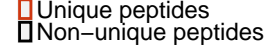
No. of times detected



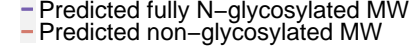
log(intensity)



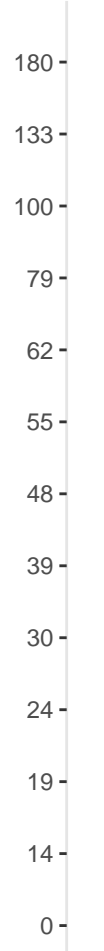
Values from



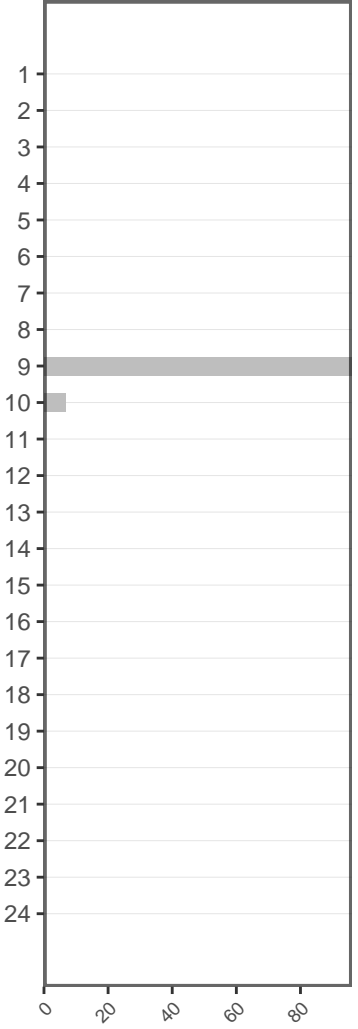
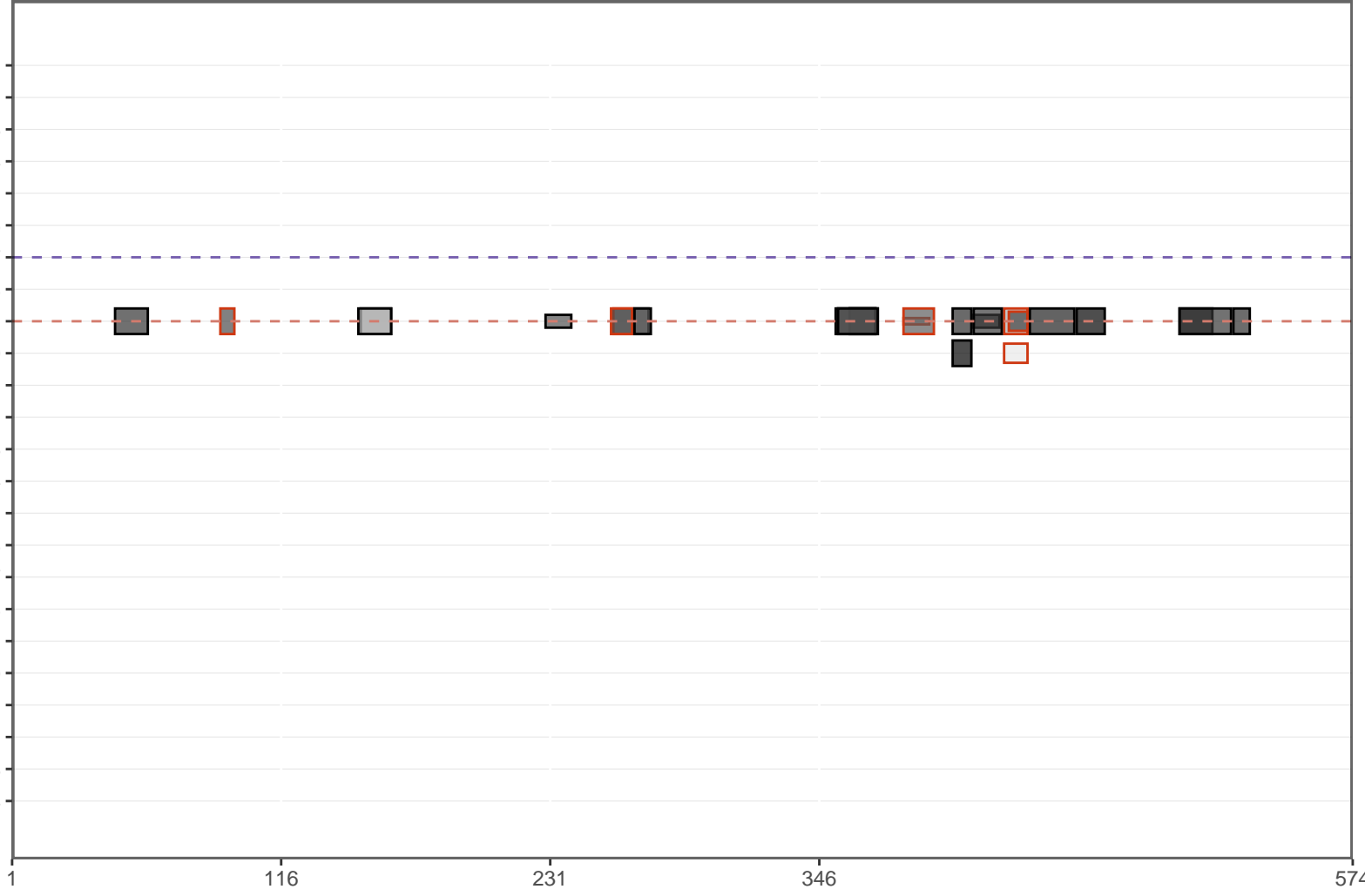
MW indication



Molecular weight

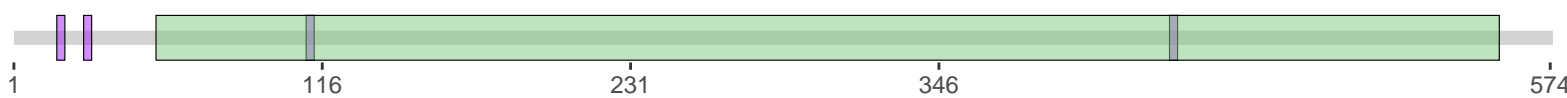


Gel Slice



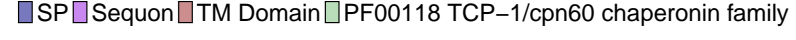
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KRDRPLLVSEDEVGEGLATLHLNKLKAGKVAKAPFGFENRKNLGDAAALTGDDVTEELGLNLENVELDMLGKDKVVTISKDDTVLDDAGEKKAIIEERGEQIRSAELSTSDYDKKLERLAKLGGGVAWLVKVGASELVESEKDRFTDALNATKAAVEEGVPGGGVALLVASKELDNLPANFDQKIGVQIGNAKTPVHTASNAQVEGAVVWVKLLEGGDDPLGYDAAKGEVDMVWVSGHDPLKVRTALVDAAVSGLLTFTEAVVVELPKETTPSPMPGGV

NbL15g13280.1 pto-interacting_protein_1-like [MW = 39.03 kDa]

No. of times detected



log(intensity)



Values from



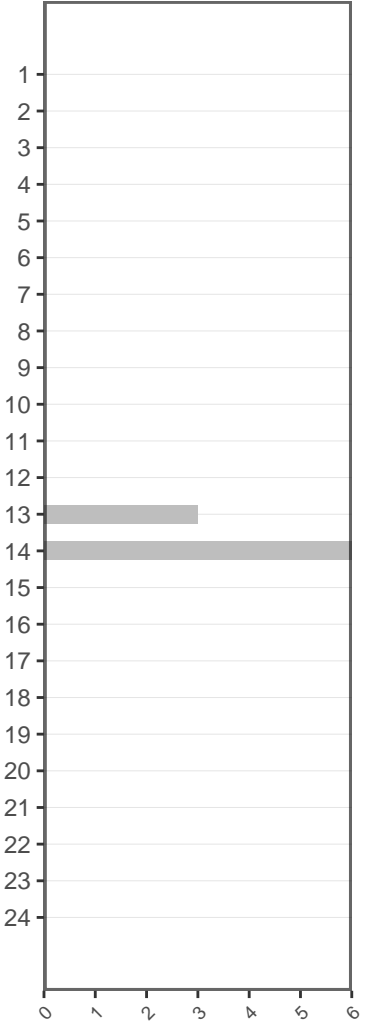
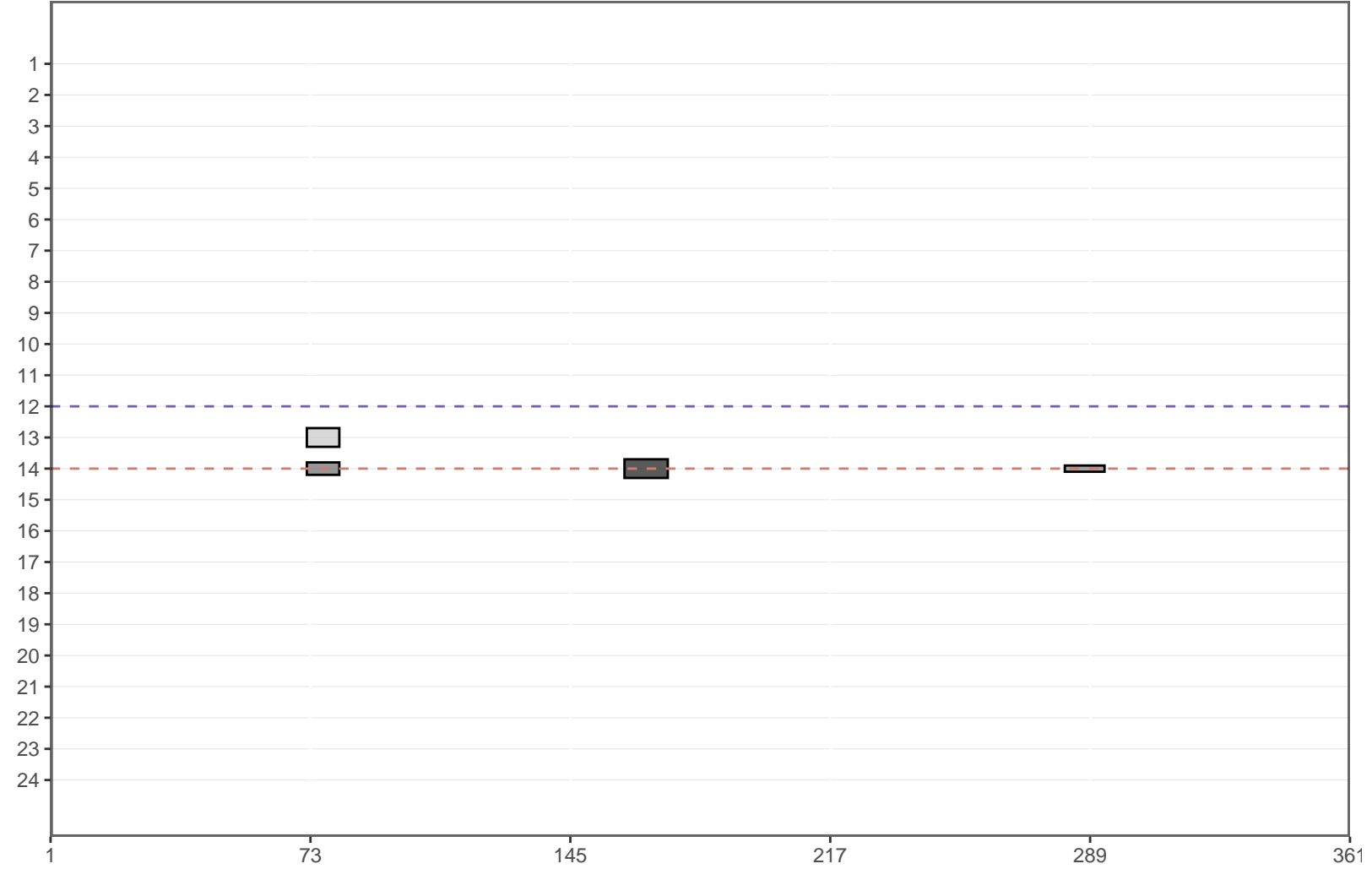
MW indication



Molecular weight

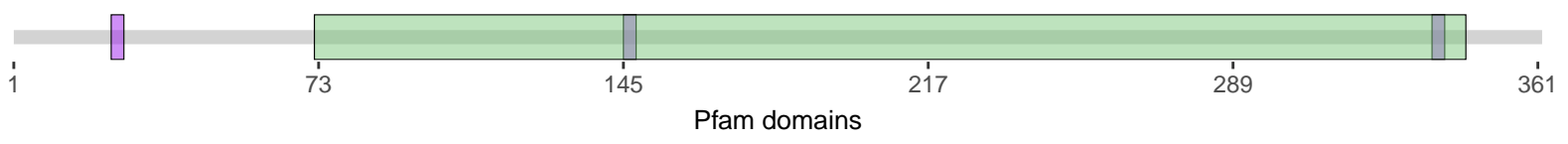


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LSLVAQRKAVGAAKGLKLELHEKAGPHIHRDKSSNLLFDQDVKIADFDLSNGAFDPMARLHSTRVLGTFDGHAPVAMTQQLSEKSDVYSGVLLLELLTGRKPKVDHLPRLGGQSLVYTWATPRLSEDKVKGQVDARLGTETVPPKAAKMAVAALGVQYEAADFRPNMSEIVKALGPLLHARSAPTETSNM

NbL15g13180.1 dihydrolipoyl_dehydrogenase_mitochondrial [MW = 53.53 kDa]

No. of times detected



log(intensity)



Values from



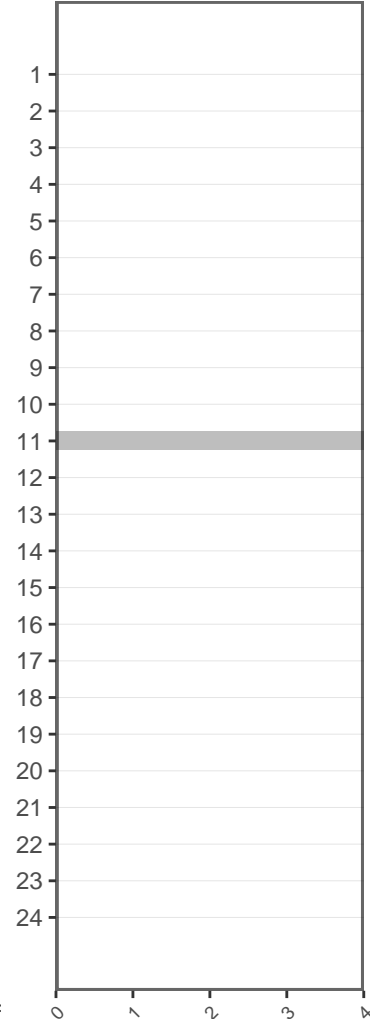
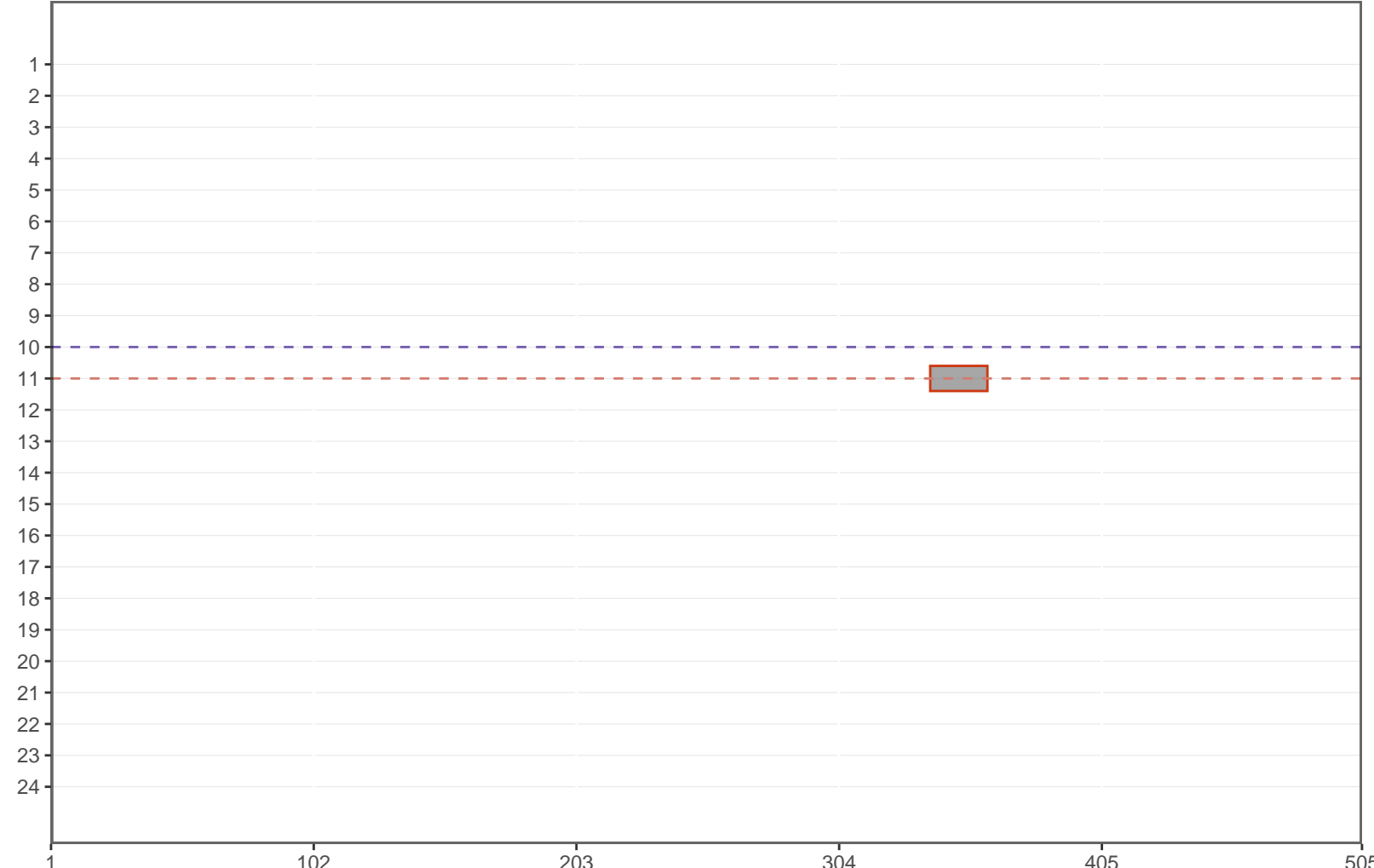
MW indication



Molecular weight

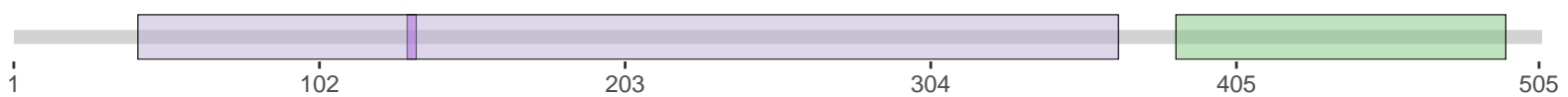


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF02852 Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain
- PF07992 Pyridine nucleotide-disulphide oxidoreductase

Protein sequence:

VEFGPDVPSMDGEVRKQFQRSLKQMKFLKTRVSVETVGDGVKLTLEPMAGDGGDTTLEADVLLVAGRIFFTSGLGDKKGVETDKAGRIILNERNFVTVNPGVHAGSDVPGMLAHKAEEDGVAGVERIAGKEGHVDVLDVPGVYTHPEVASVGTKEEGVARGVDYRVGKFFPLANSRKAIDDAEGVYVLAEKETDKLGVHMSFNAGELIHEVLAHLHYGASSEDARTCHAHPTMSEALKEAAMATYQKPHI

NbL15g13110.1 cell_wall/_vacuolar_inhibitor_of_fructosidase_1-like [MW – SP = 15.67 kDa]

No. of times detected



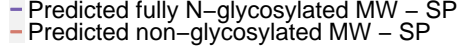
log(intensity)



Values from



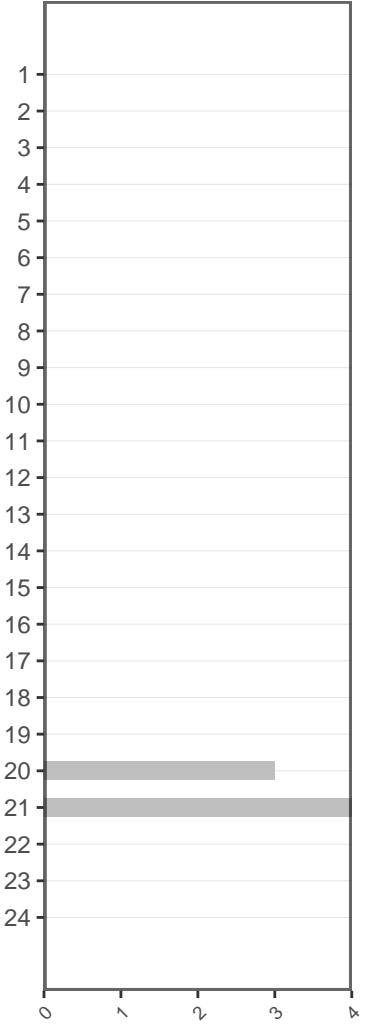
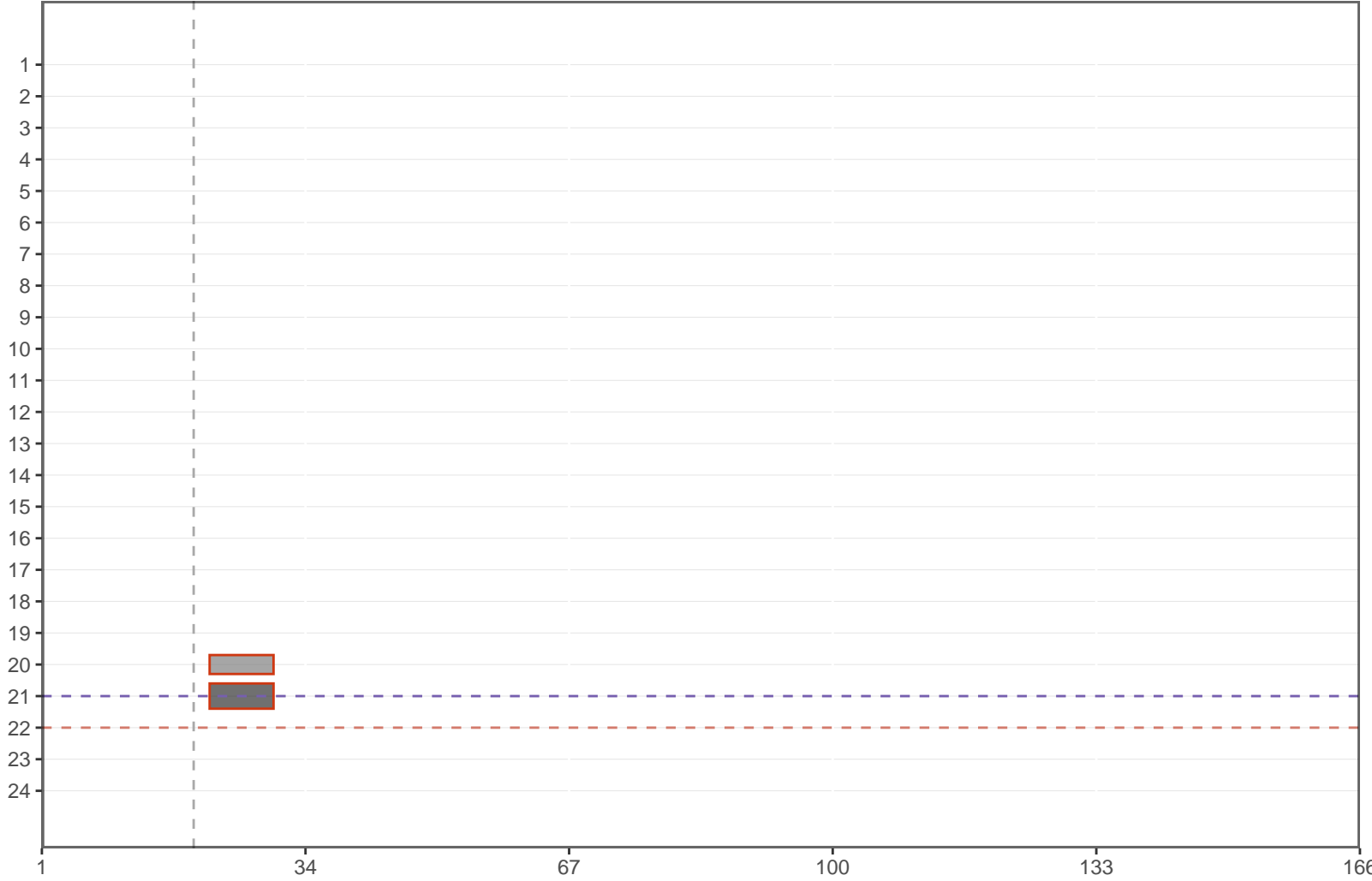
MW indication



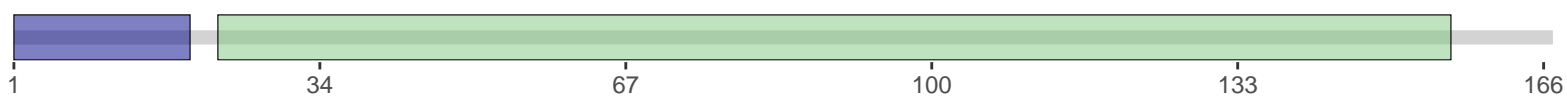
Molecular weight



Gel Slice

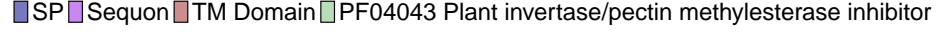


Protein length



Pfam domains

Pfam Description

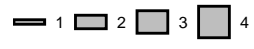


Protein sequence:

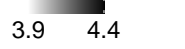
IIISKLRQSNPPAIVWVPLKKGDFYKYLTVLPLPEAEALTGKPKPAEDGMVGGFDGDDGDEENFKSGFSPLTGLNTAVLELSVWGRAIRNLL

NbL15g13040.1 DNA-directed_RNA_polymerases_II_IV_and_V_subunit_9A [MW = 13.11 kDa]

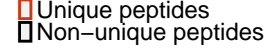
No. of times detected



log(intensity)



Values from



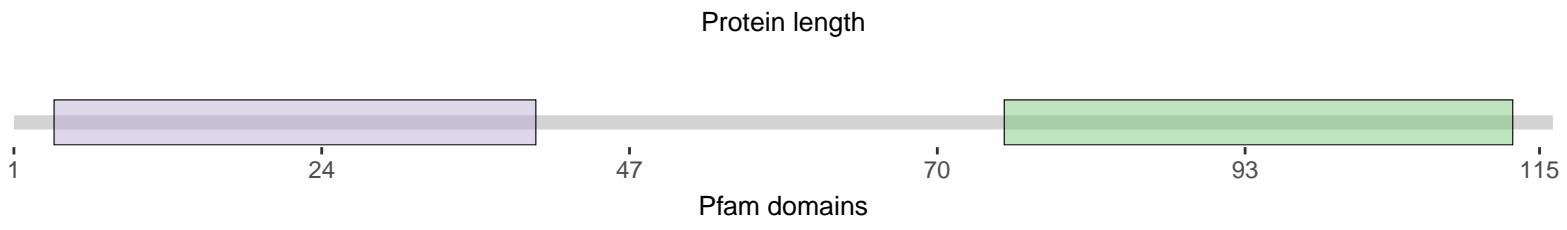
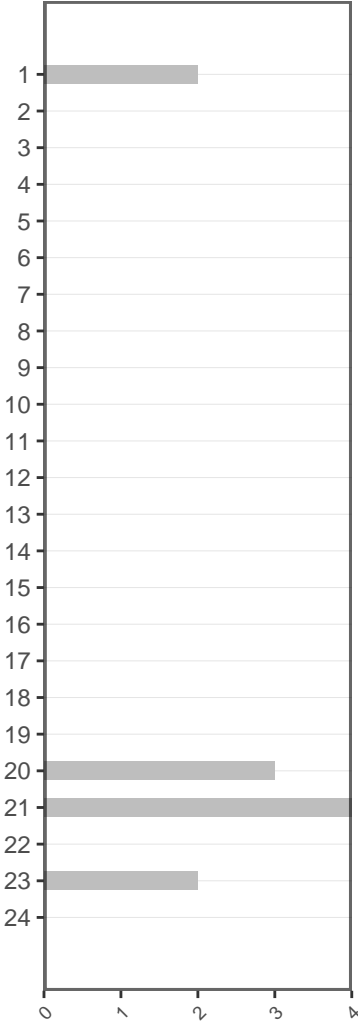
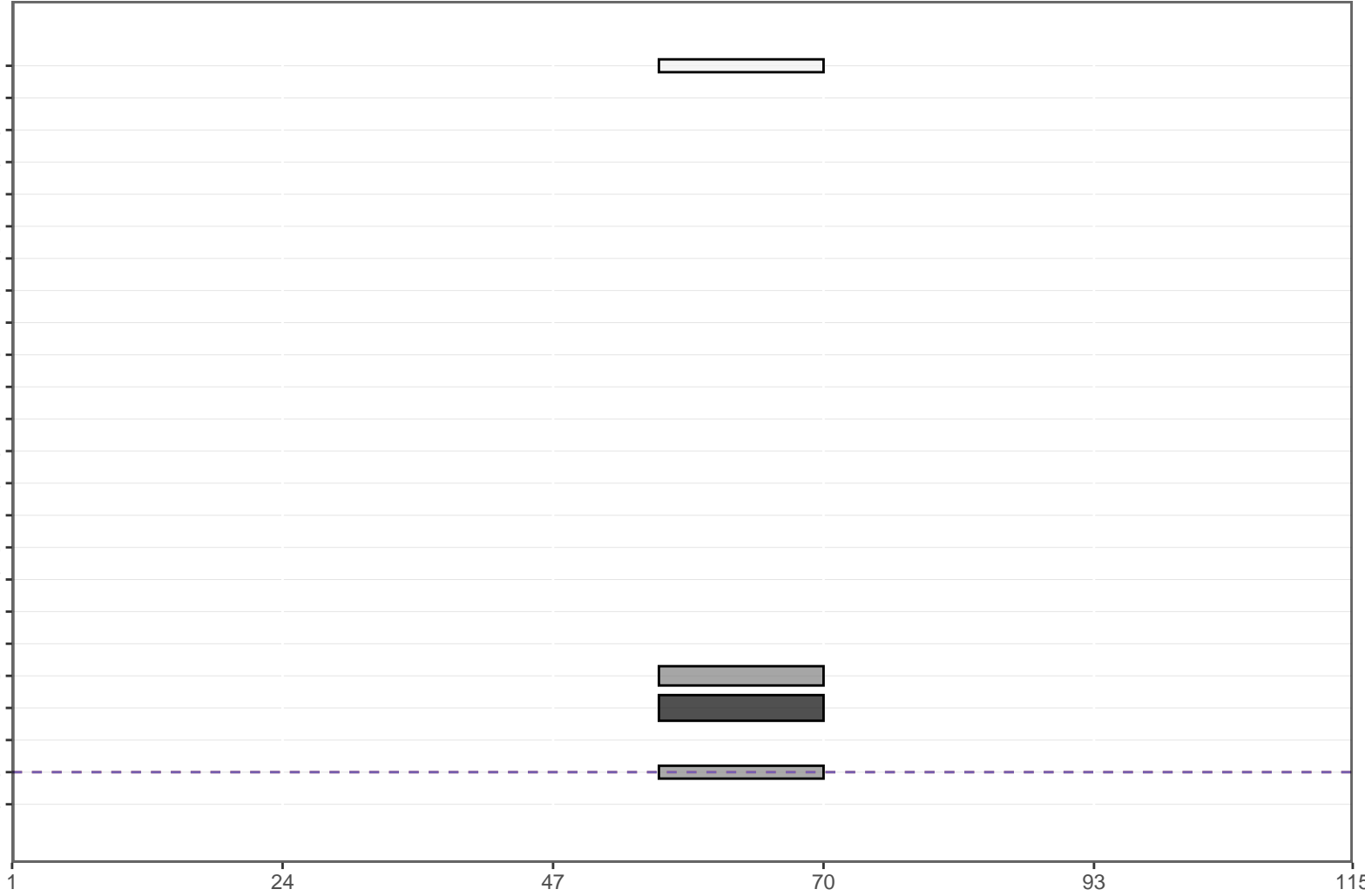
MW indication



Molecular weight



Gel Slice



Pfam Description



Protein sequence:

NEIHSAAERTQVLDNVAADPLPRKSVRSGGGHHGEAVFFQATARGEEGMFLFFVDCNPNQGHRRWD*

NbL15g12970.1 L-type_lectin-domain_containing_receptor_kinase_S.4-like [MW - SP = 74.31 kDa]

No. of times detected



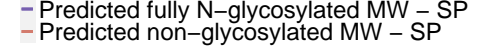
log(intensity)



Values from



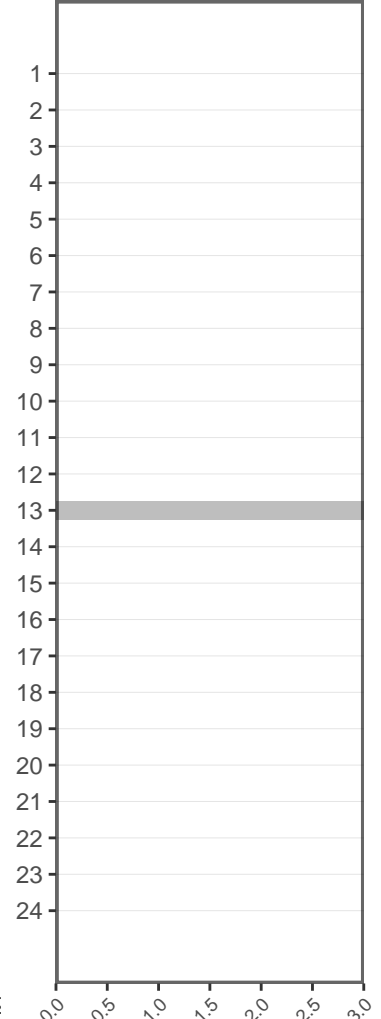
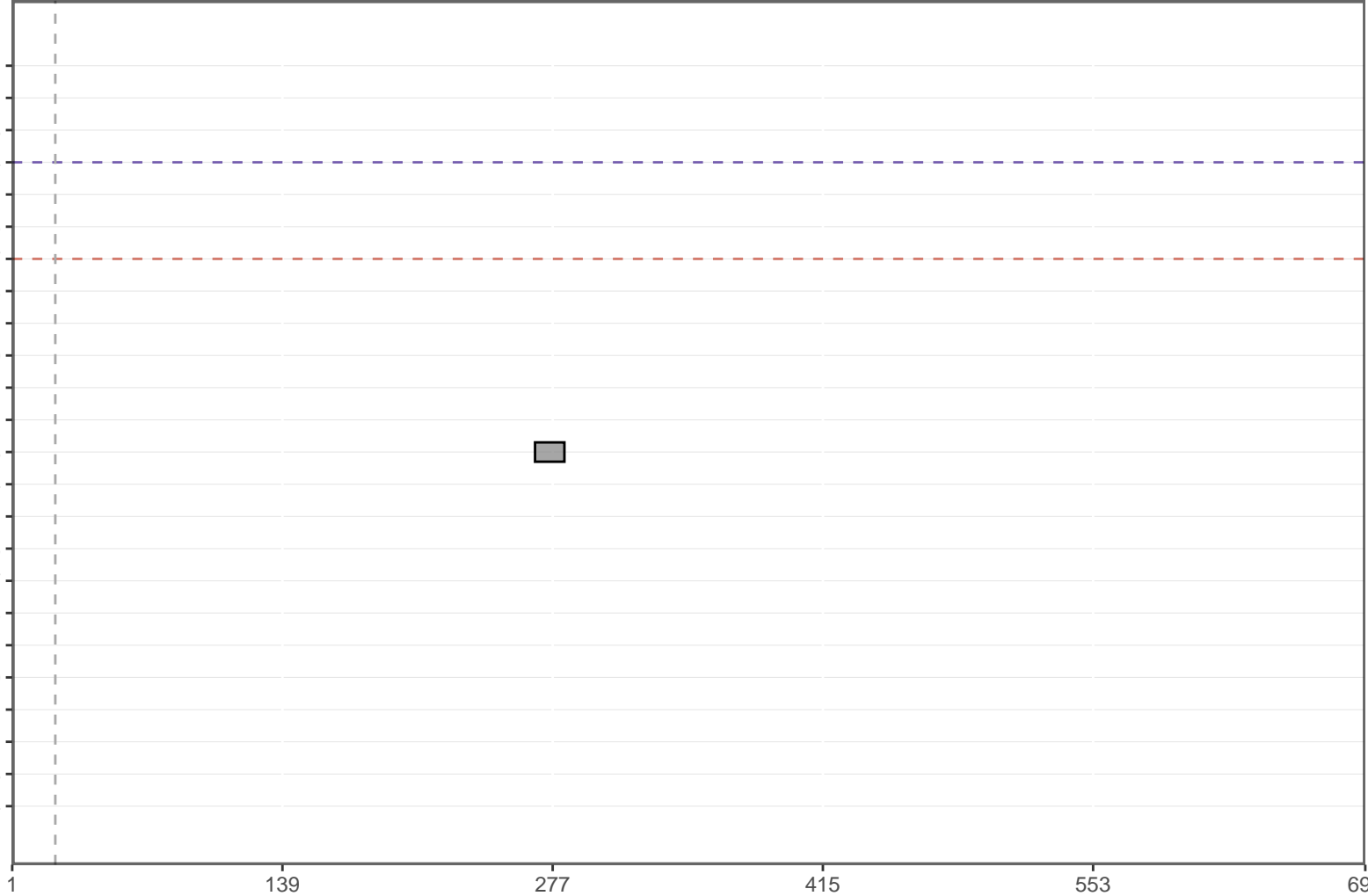
MW indication



Molecular weight

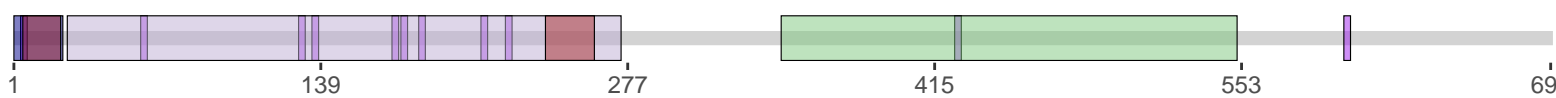


Gel Slice



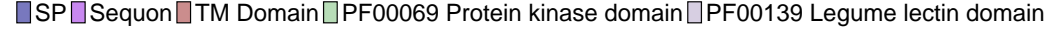
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ELKKATDFDFKELKELGGFGFRVYKGLPKTKSTEAAVKRINHDKAGGLGEPVSEIATGRRLRHRLVQLGHWGRRRKGDLLLVDFMPNGSLDKVYDFEPRILTWDRFRHKKGVASGLLYHEEVEQTVIHRDKAGNVLDAEMNGRLGDFGLANLYEHGANPSTRVYGLGLAPELTKTKGPTTSSDVFYAFGALLLEVAGRRPIEAKALPEELILVDVWWDKWKEGALEVVDPRLNKDYDEMEAAVVKLGLGMSNNTPKRPSMRLVRYRLEGEVLPPEMLAAPDEY

NbL15g12940.1 probable_methyltransferase_PMT11 [MW = 76.2 kDa]

No. of times detected



log(intensity)



Values from



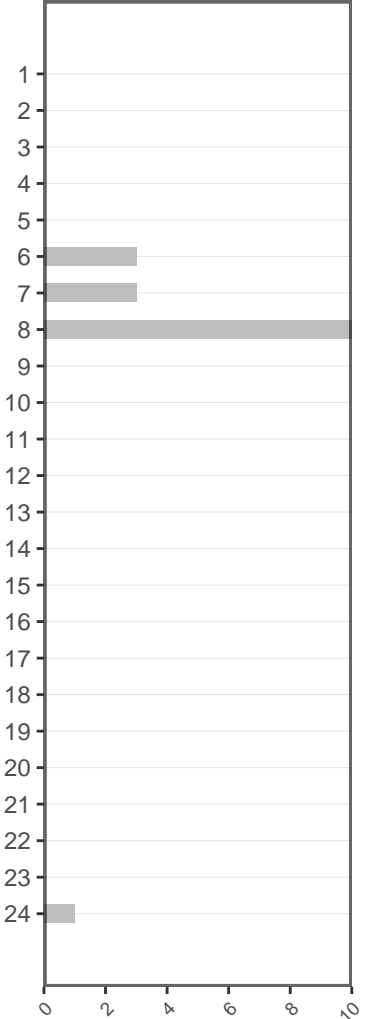
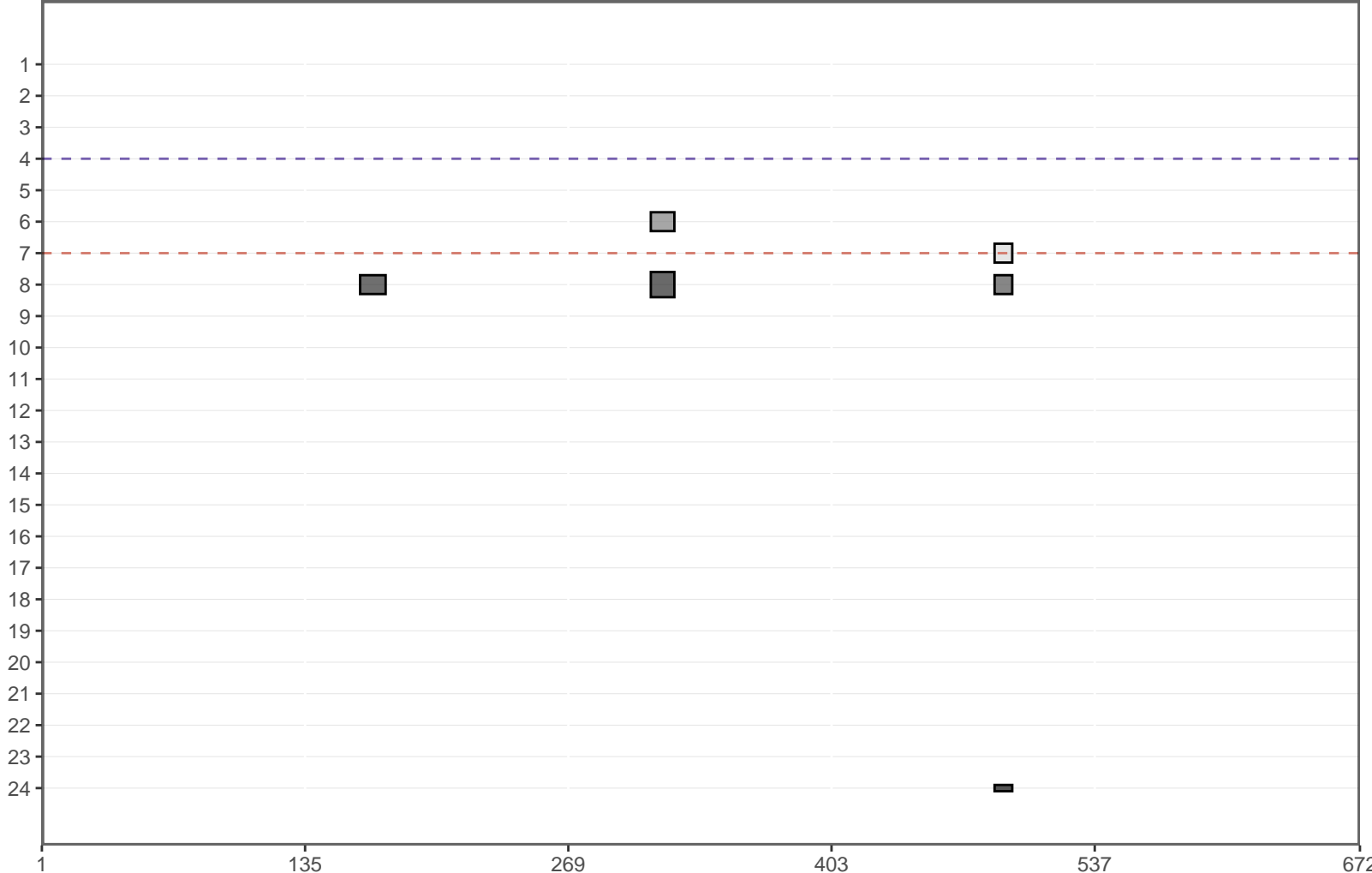
MW indication



Molecular weight

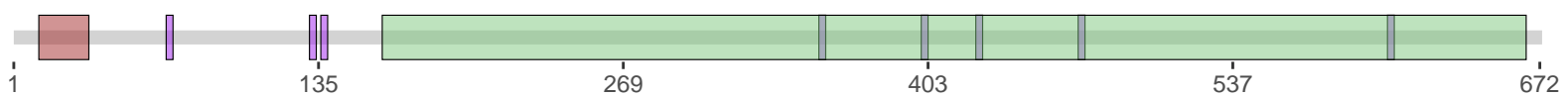


Gel Slice



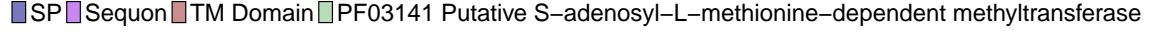
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

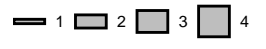


Protein sequence:

PMVAUATHRLLYPQDAFELHDSGRINWTRDDGILLLEVNRLLRADGFFIWAAGFVYKHEAVLEGGVWEEMNLTFLGWNLVKKEGYIAWQKFLNNGCYLSREEGTQPLDGDHDDPNWVYDLKAGIARLP EEGYGANITFTWPSRLGYPPDRLKSIGVDSFVSRKELFVAESKFWKEESYVRAWHWKKFKLRINWMDMRAGYGGFAAATENQLDCWVNLVYVPSGGNTLPIVFDRLGLLVMDHWGCEPDFYPRTYDLHLHANSLSFIEGKRCNMSTMLEMDF

NbL15g12860.1 protease_regulatory_subunit_8_homolog_A-like [MW = 47.18 kDa]

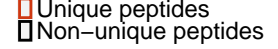
No. of times detected



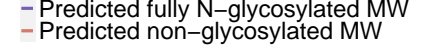
log(intensity)



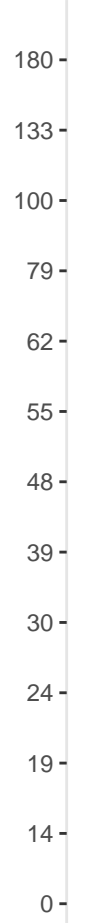
Values from



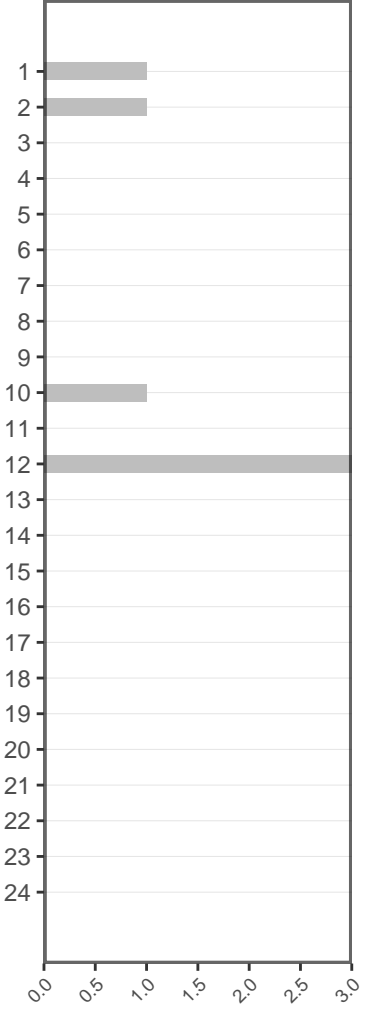
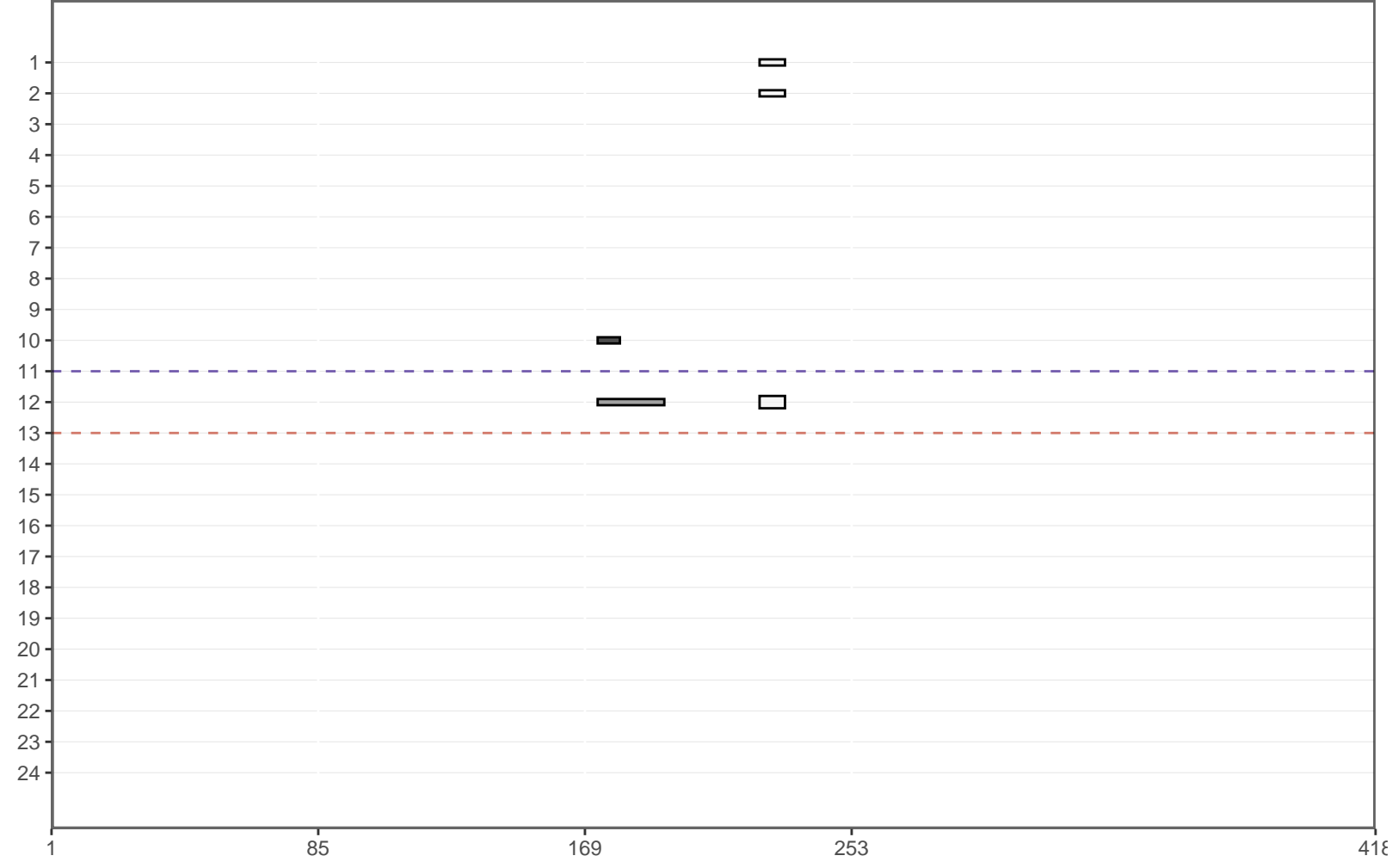
MW indication



Molecular weight



Gel Slice

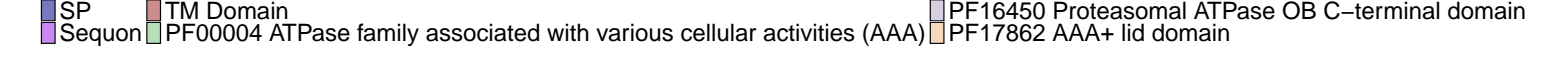


Protein length



Pfam domains

Pfam Description



Protein sequence:

LLYGPPTGKTLARAWHHTDCTFRVSGSELVQKYIGEGSRMRELPMAREHAPISFIMDEIDIGSGARMEGGGNGDSEVQRTMLELLNQLDGFASNKIKVIMATNRIDLDQALLRPGRIDRKYKFFNFEESRLDLKIHERRKMNLMRGIIDLKHAEMKMGASGAEUKAVGCTEAGMFLRERRVHYTQEDFEMAVAKVMKTEKNMMLRKLWK*

NbL15g12790.1 ras-related_protein_RABD2a [MW = 30.95 kDa]

No. of times detected



log(intensity)



Values from



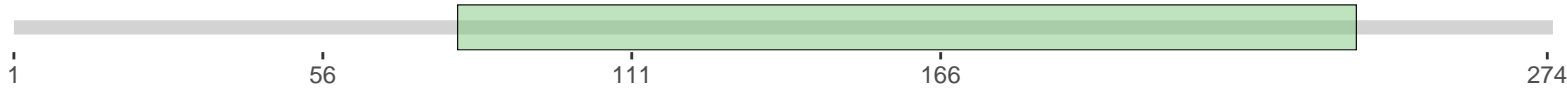
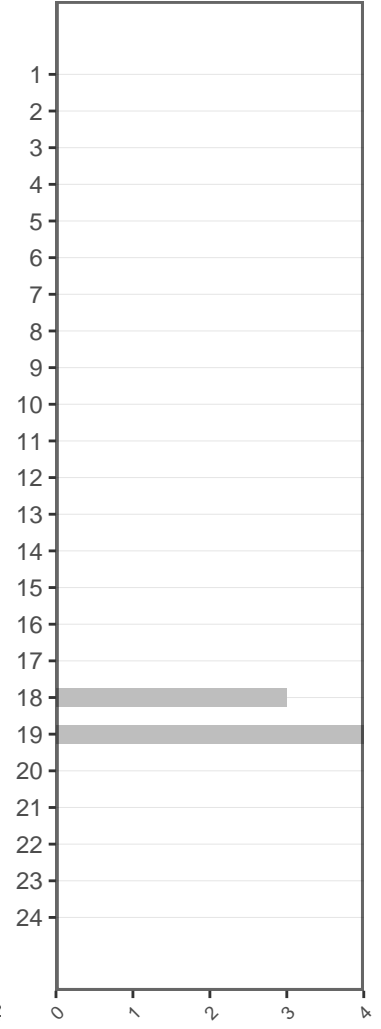
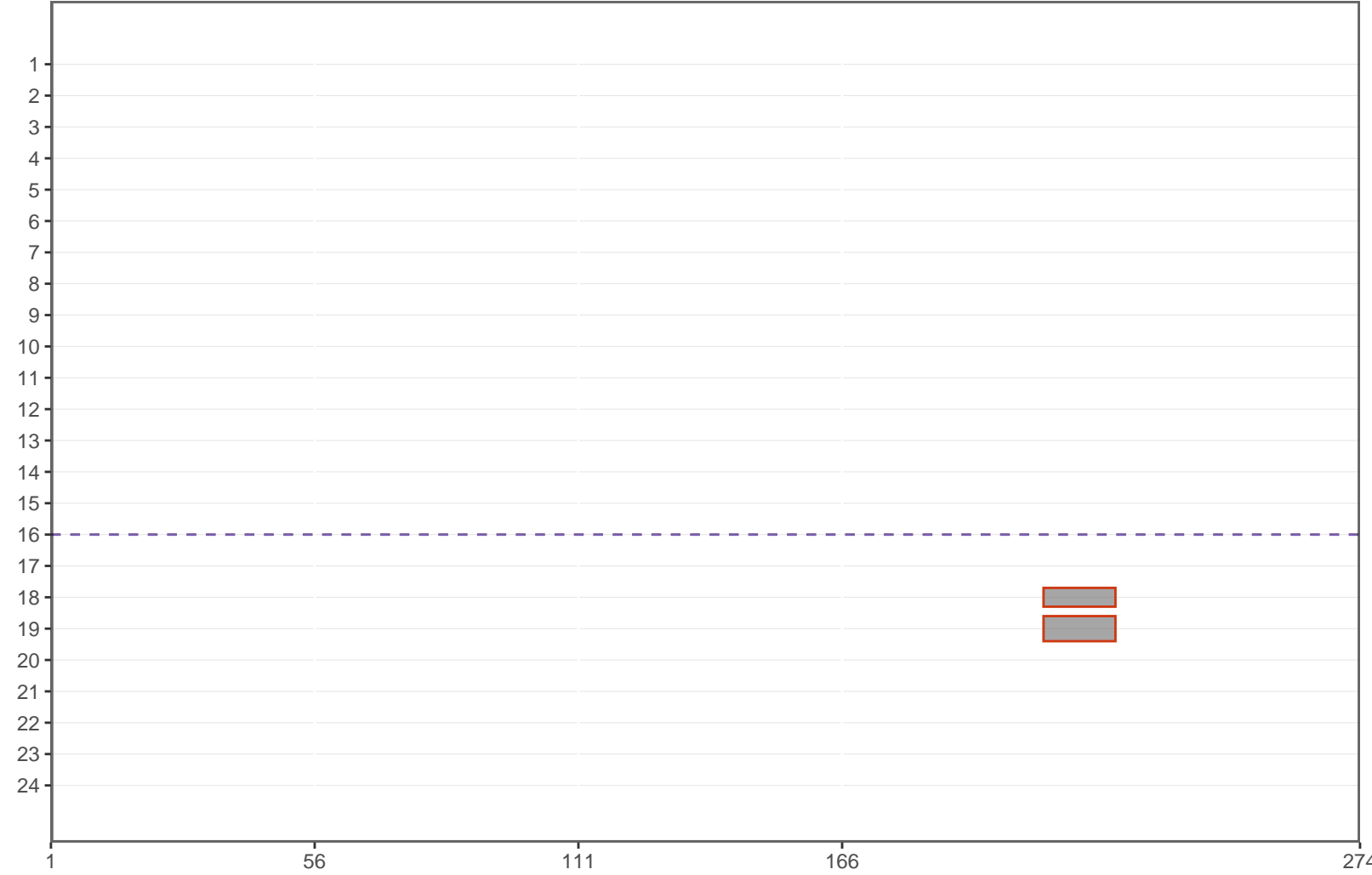
MW indication



Molecular weight

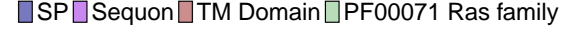


Gel Slice



Pfam domains

Pfam Description



Protein sequence:

IKLQIWDTAGGERFRITTSSEYVRGAHGHIITVDYFDGEGFNWVQWVLSRIDRYASENANKLLVGNKCDLTDNRVAVEYDITAKAFADGIGPFMETSAKSATNVEGAFMAMAAEIKNRMASGPTSNMRRPTVQIRGGPNNQKSGCCST

NbL15g12760.1 glutamate_dehydrogenase_A-like [MW = 44.7 kDa]

No. of times detected



log(intensity)



Values from



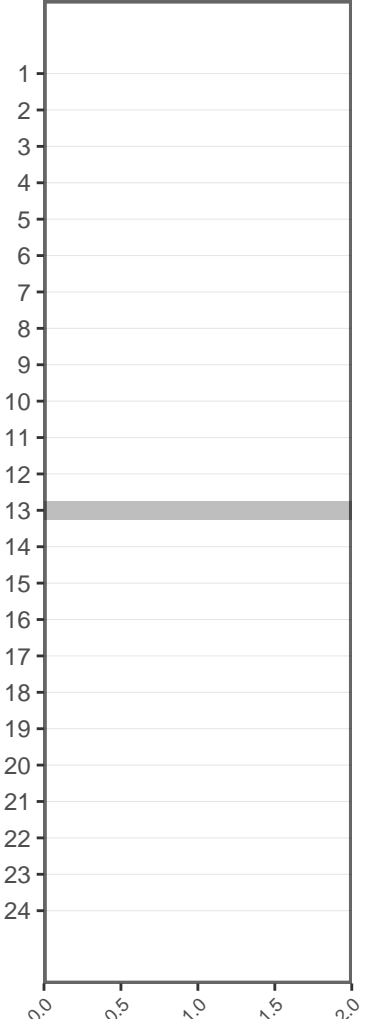
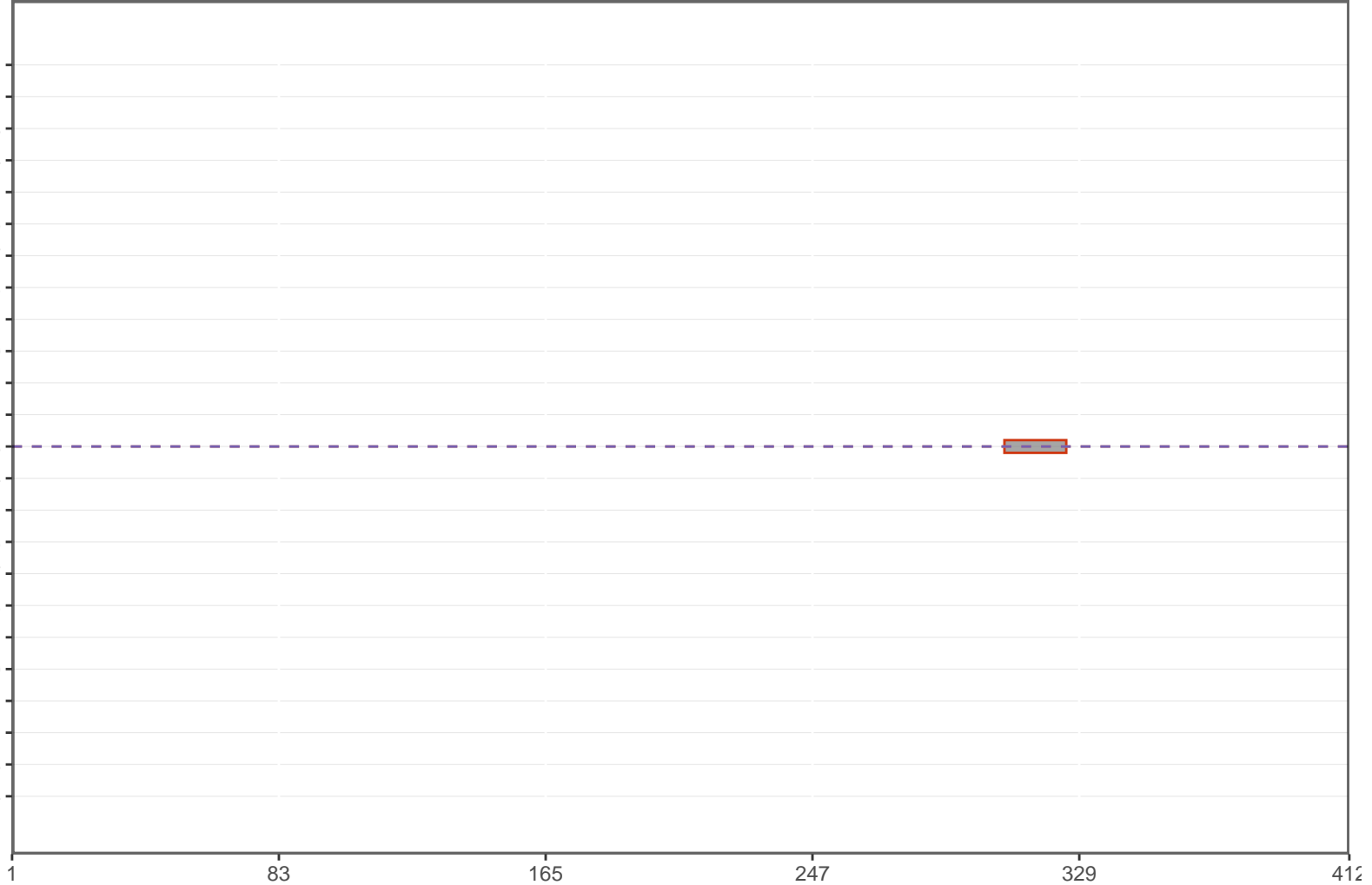
MW indication



Molecular weight

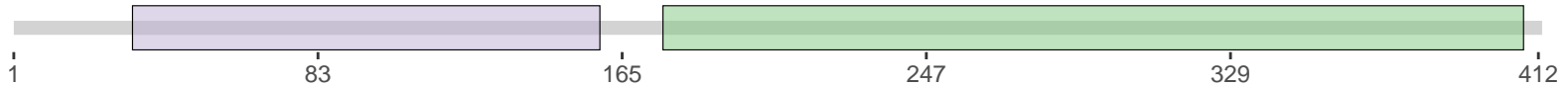


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00208 Glutamate/Leucine/Phenylalanine/Valine dehydrogenase
- PF02812 Glu/Leu/Phe/Val dehydrogenase, dimerisation domain

Protein sequence:

ALLAEHGKIKDMFFAIGFGNVAWAARIHERGGKVAVSDITGAVKPNPGLDIPALLNKEATGTLAIGFSGSDAMSSDELTHDGDVLPICALGVLRNRENADKVAKYVEAANHTPDPADELKKGKVVLPDYANAGGVTVSYFEWVGNIGFMWDEEHVIRELKKYMTRAFPHLNKNMCKSHNGLRMGAFTLGVNRVWATQLRGWEA

NbL15g12740.1 ATP_synthase_subunit_delta'_mitochondrial [MW = 27.92 kDa]

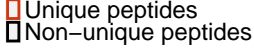
No. of times detected



log(intensity)



Values from



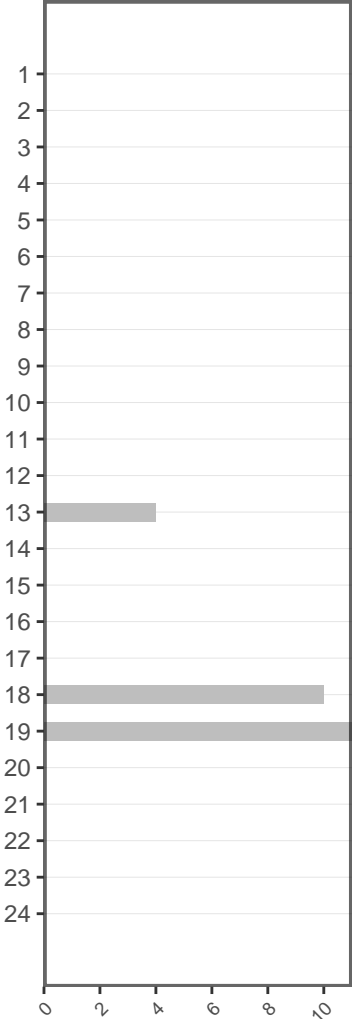
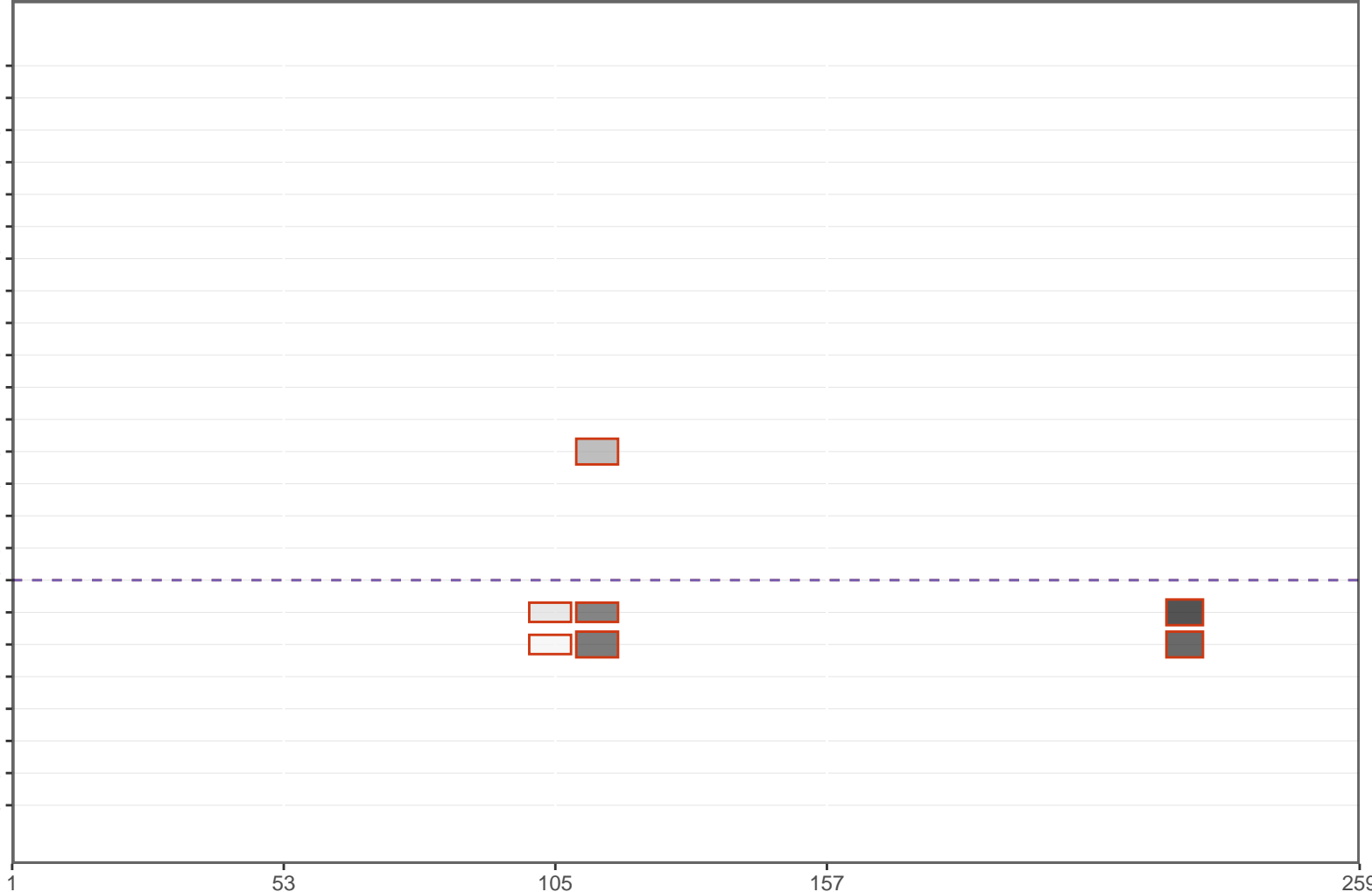
MW indication



Molecular weight



Gel Slice

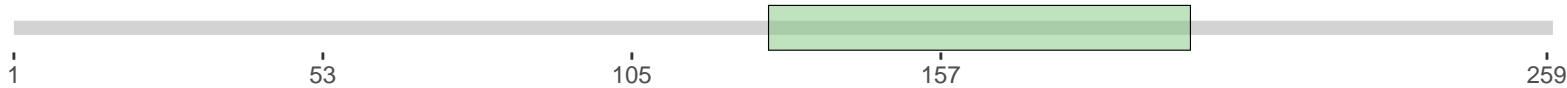


Protein length

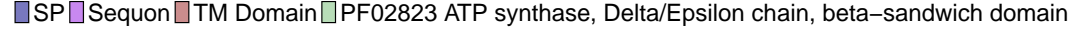


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

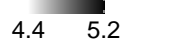
ARRPITPSSIPSKLTYANFVLPYBSELGKGEVDMVIRPATTGGMGVLPGHWATIAELKPGVLSVHEGNDYKYFVSGGFAFVHANSFADIAHVEAVPLDRIDPNIIVKGLDFTQKLISTASTDVEKEAQIGVDVHSAALALGT

NbL15g12660.1 macro_domain-containing_protein_VPA0103-like [MW = 30.74 kDa]

No. of times detected



log(intensity)



Values from



MW indication



Molecular weight



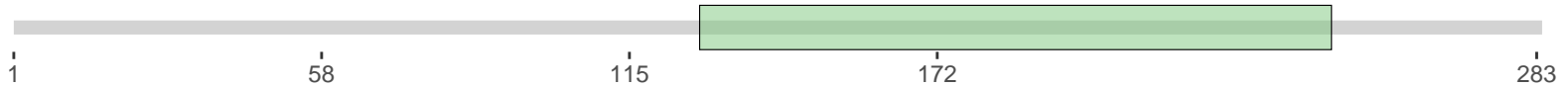
Gel Slice



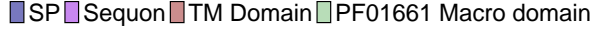
Peptide counts over 4 repeats

Protein length

Pfam domains



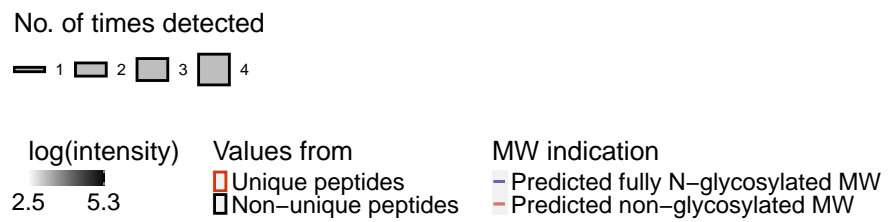
Pfam Description



Protein sequence:

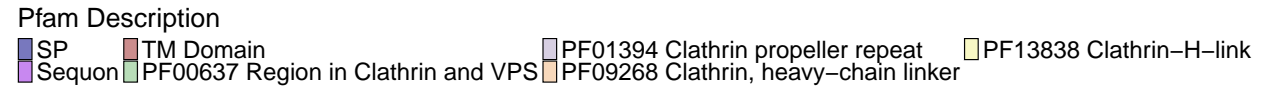
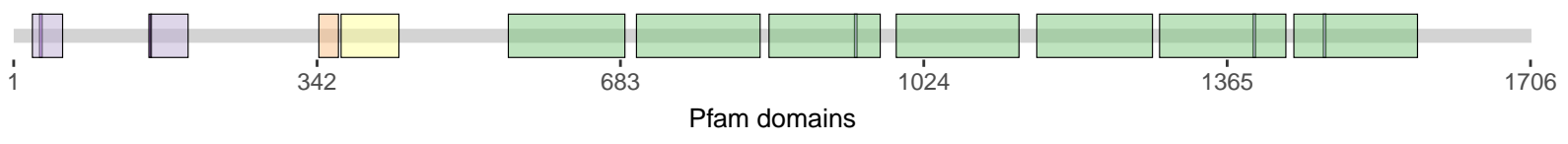
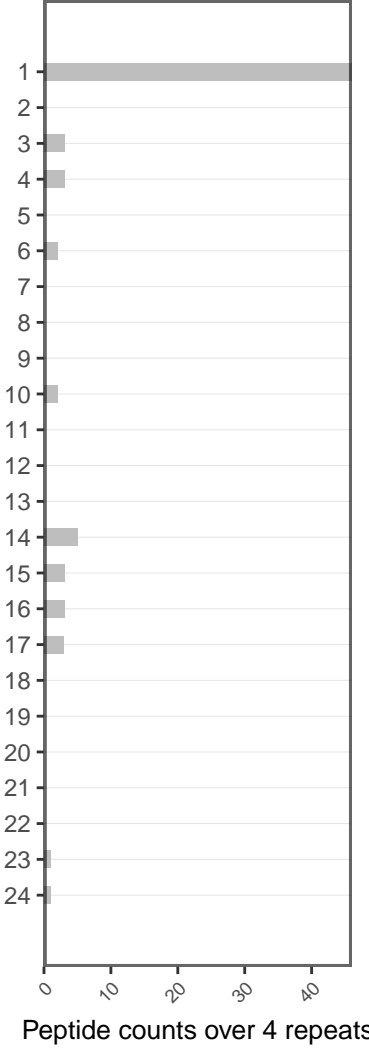
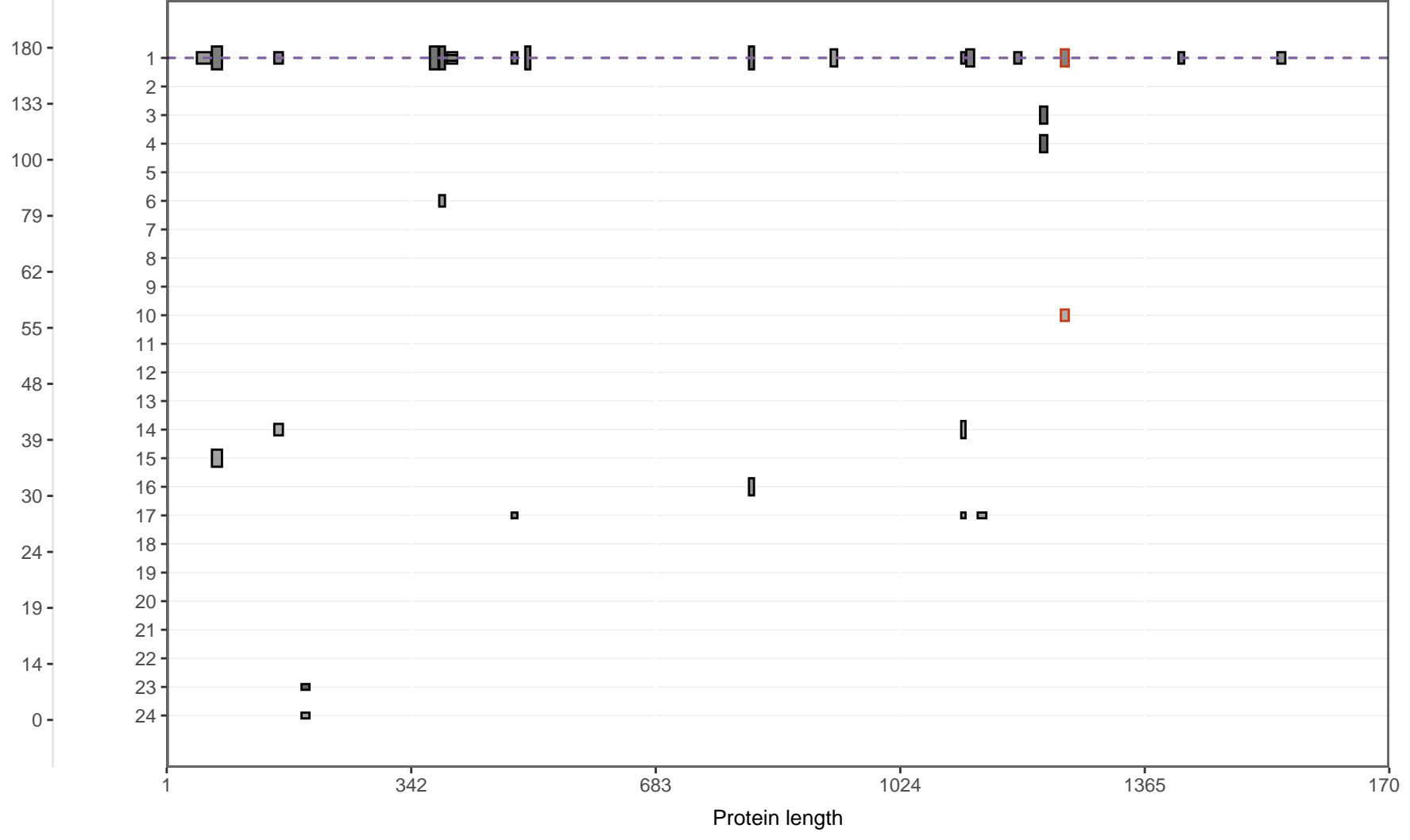
NPANERIALGGGGADGAHRAAGPELRDAGYKVEVRPGVIRGPTGEARITLGFRLPFSHWIHTVGPYDAVFNPKAVLTNSYRNSLRWAKENNGYIAPFMSGGVFGYPFDEAATVAISTVKEFGSDLUKEVHFVLSDEYDAWLKAKNELLGN

NbL15g12410.1 clathrin_heavy_chain_1-like [MW = 192.69 kDa]



Molecular weight

Gel Slice



Protein sequence:

IFKGLLSVRSLLPVEPLVAEGEKRRRLRLTGFLEHLVSEGSDVHVHNNALGKIHDSNNPEHFLTNPYYDSRVVGGYGEKRPDLAVWVRRGGDDEELNVTNKNLFGARYVVERMDGDLWEKVLTPENEFRRRLQHDGVSTALPEKSPGEGVSAWAFMTADLPHELELLEKVLGNLAFSGNFNLGNLILITAKADPSRVMYVNRLLNDFDGRWGEVVEAQLYEEAFKFKFNLVGAVNVLNDINPDRVAFRVEEDAWWSQVAKLREGLVSDAEI

NbL15g12340.1 dual_specificity_protein_phosphatase_12-like [MW = 40.24 kDa]

No. of times detected



log(intensity)



Values from



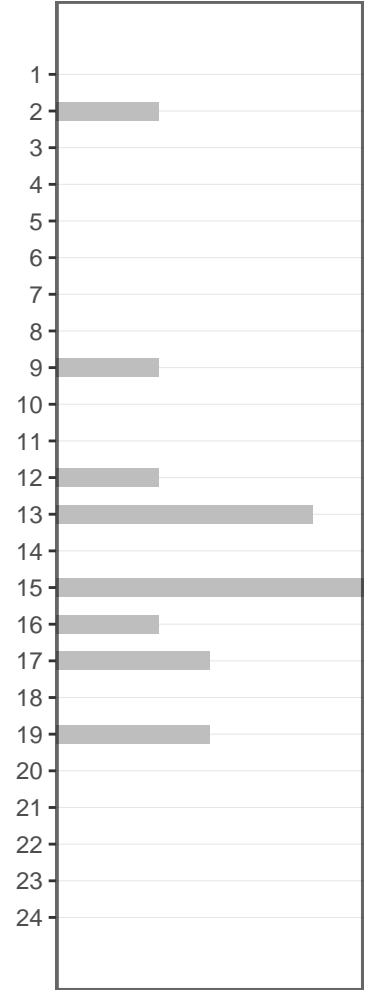
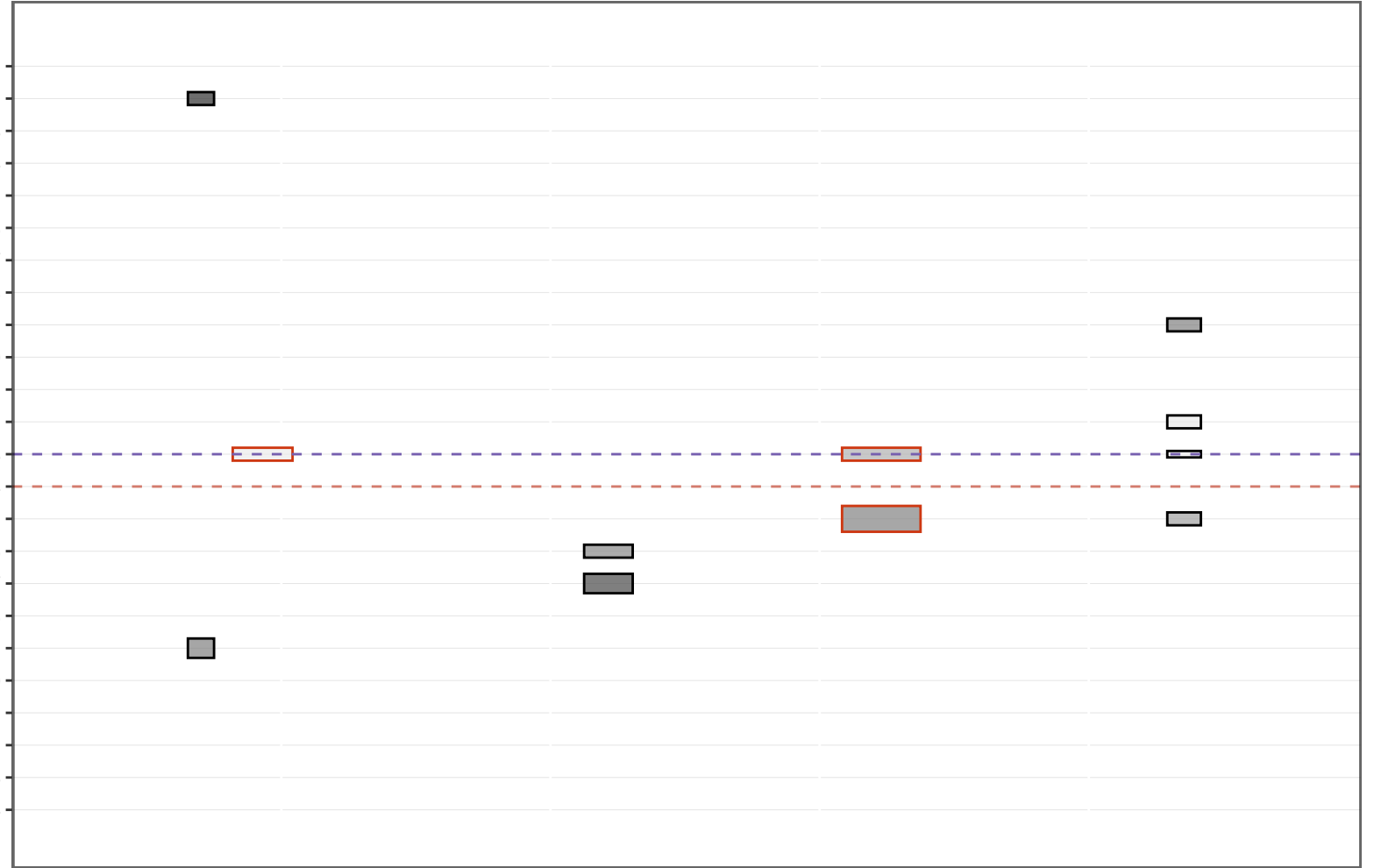
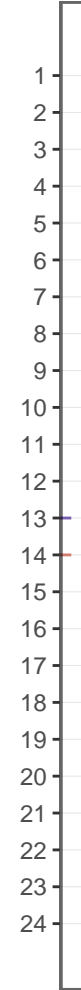
MW indication



Molecular weight

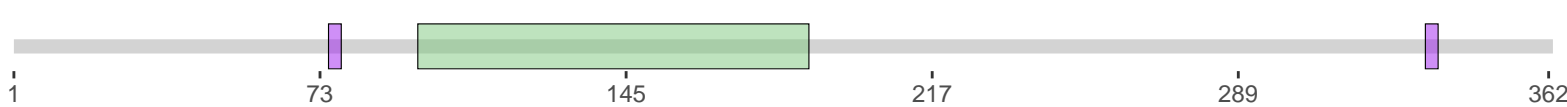


Gel Slice



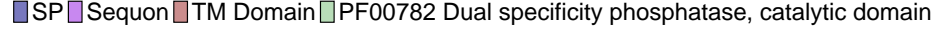
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TVCPNDGFLVQLKMFEEEMFRVYDKSSPIYKRFHLKVLGDYVNRGERIDTSKFGADPGSAEISPEQMDVSLTKETTPAVYVYKDKGRVYVALQGNVDHVPDGEGETAFQWIKRRSGNPFNKPDDGEGSSVYFVEPLKVMRTVEEGALEGKLLGAGCEARLGYFNWSGHCGCGGQGWTFMQLHKSRVDISM

NbL15g12310.1 sedoheptulose-17-bisphosphatase_chloroplastic-like [MW = 42.55 kDa]

No. of times detected



log(intensity)



Values from



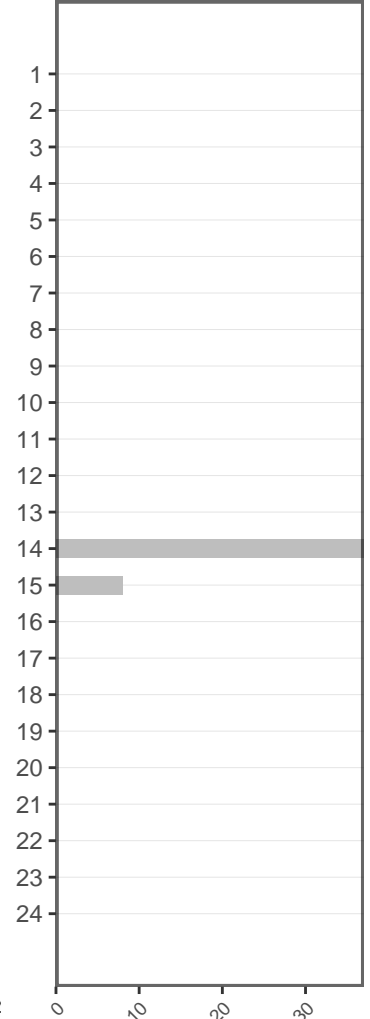
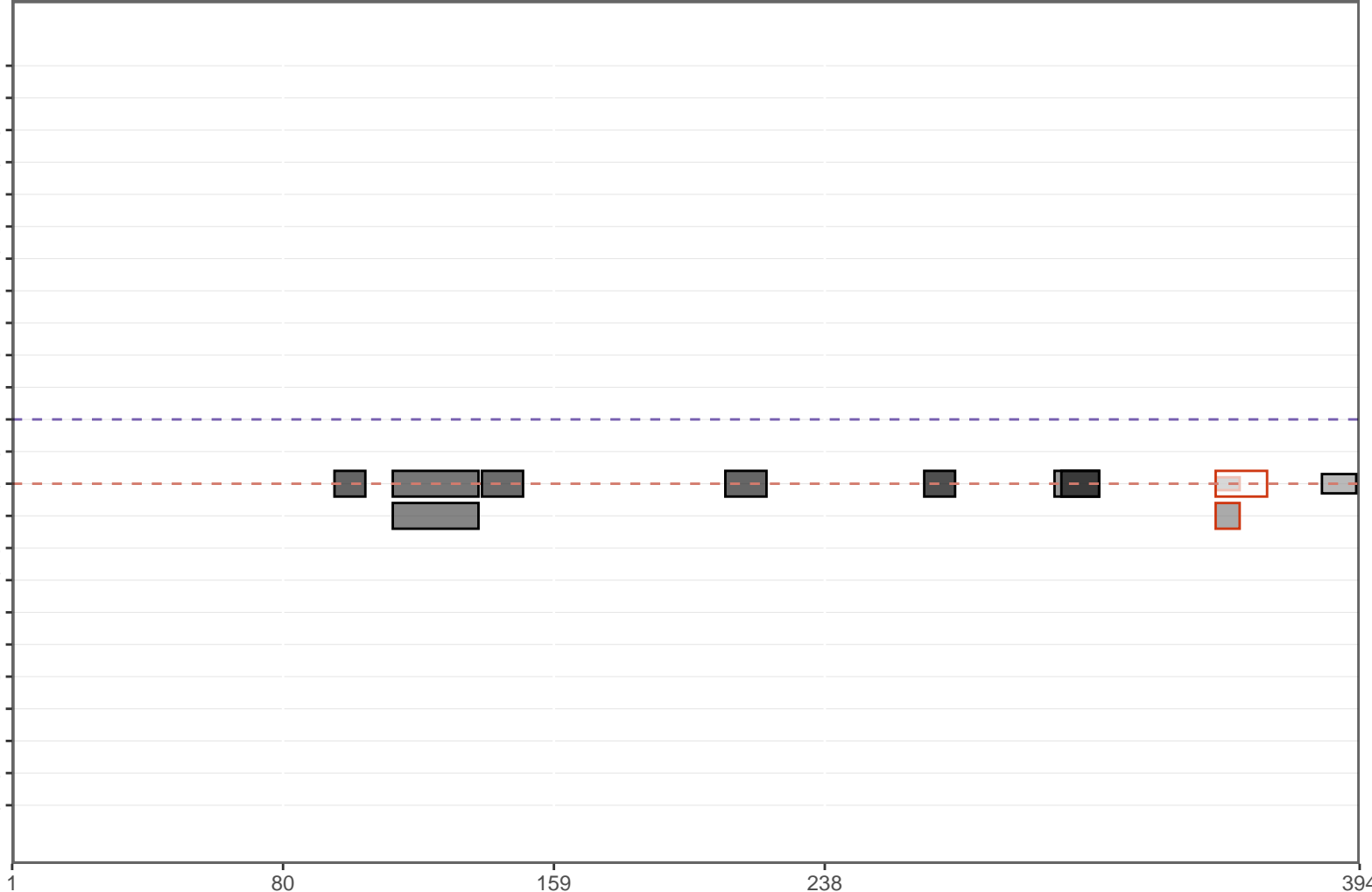
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00316 Fructose-1-6-bisphosphatase, N-terminal domain
- PF18913 Fructose-1-6-bisphosphatase, C-terminal domain

Protein sequence:

I/DNFTVGTFGVWPGDKLGTGTRDQVAAAMGIVGPRFTYVLAALKDVPQTHFLLDEQKWHVWDTTEKGGKMFSPGNLRATFDNPDVAKLIDYVYKELYLRVYTGSMVDPVNIQVVEKGIFTNVSPTTKAKLRLLFEVAPLGFUEKAGGYSDGKQGVLDRIWVWLLDRDRTQWVWGKNEIRFEETLYGSSRLKGAEEVGAAM

NbL15g12220.1 30S_ribosomal_protein_S31_chloroplastic-like [MW = 11.06 kDa]

No. of times detected



log(intensity)



Values from



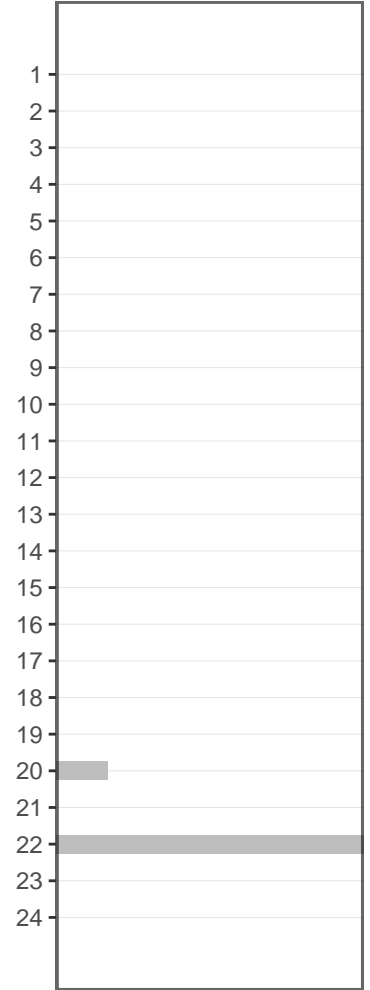
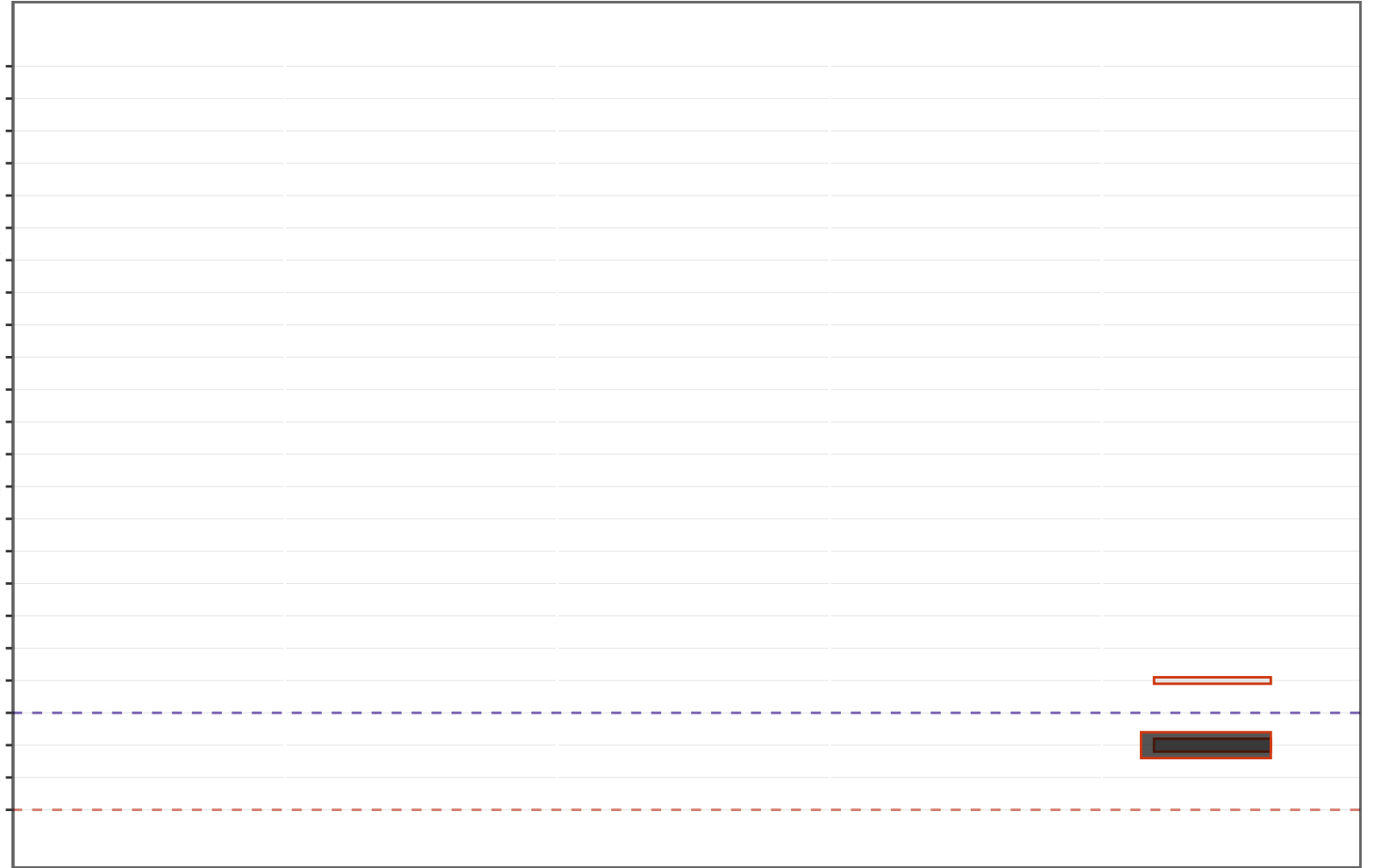
MW indication



Molecular weight



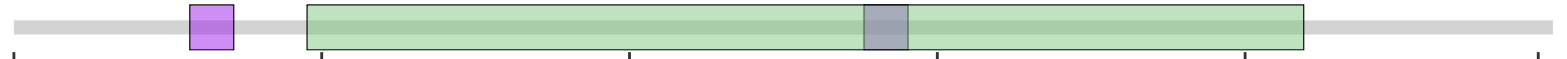
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

PLYCGRGDKKTANGKRFNHSFGNARRRNKKKGRGPRVAVAPPAKRRPFDDGGVWIEVES

NbL15g12210.1 pleckstrin_homology_domain-containing_protein_1-like [MW = 16.88 kDa]

No. of times detected



log(intensity)



Values from



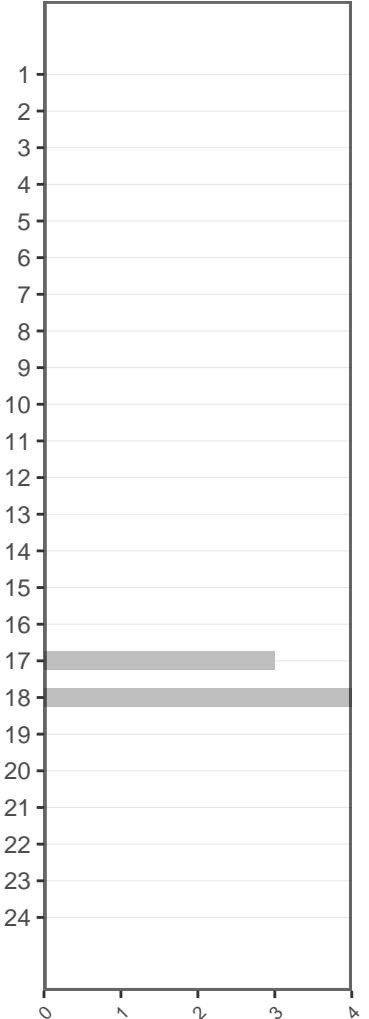
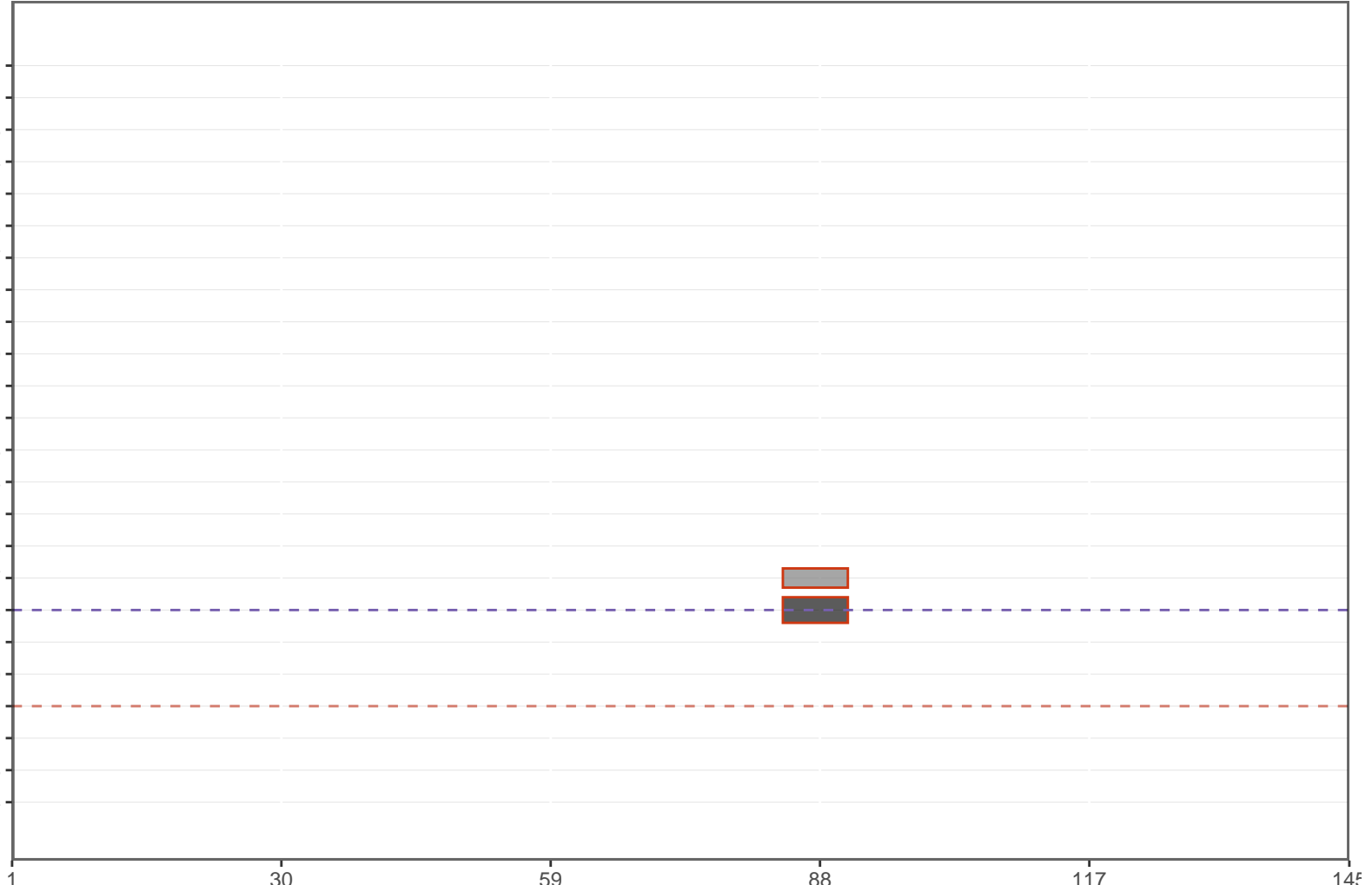
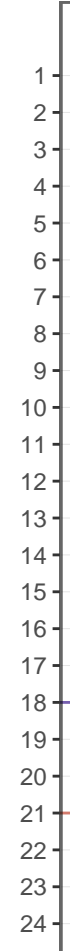
MW indication



Molecular weight

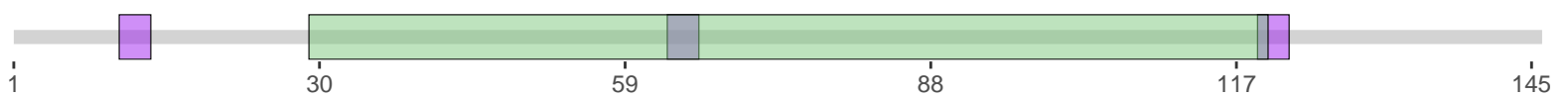


Gel Slice



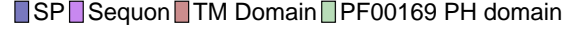
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

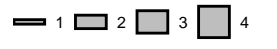


Protein sequence:

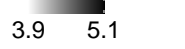
WPKKANITRSGSKPRGVHPVADGLTVKGAEDLNKGFAFELSTRADTMVFIADSEKEKEDWINTSGRGVGHHSRIVTHDELQVDSRK*

NbL15g12090.1 7-deoxyloganetic_acid_glucosyltransferase-like [MW = 60.48 kDa]

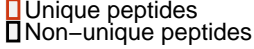
No. of times detected



log(intensity)



Values from



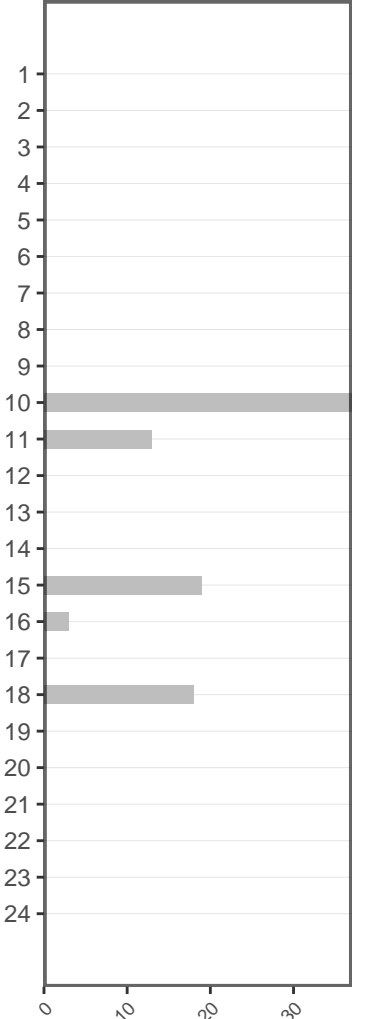
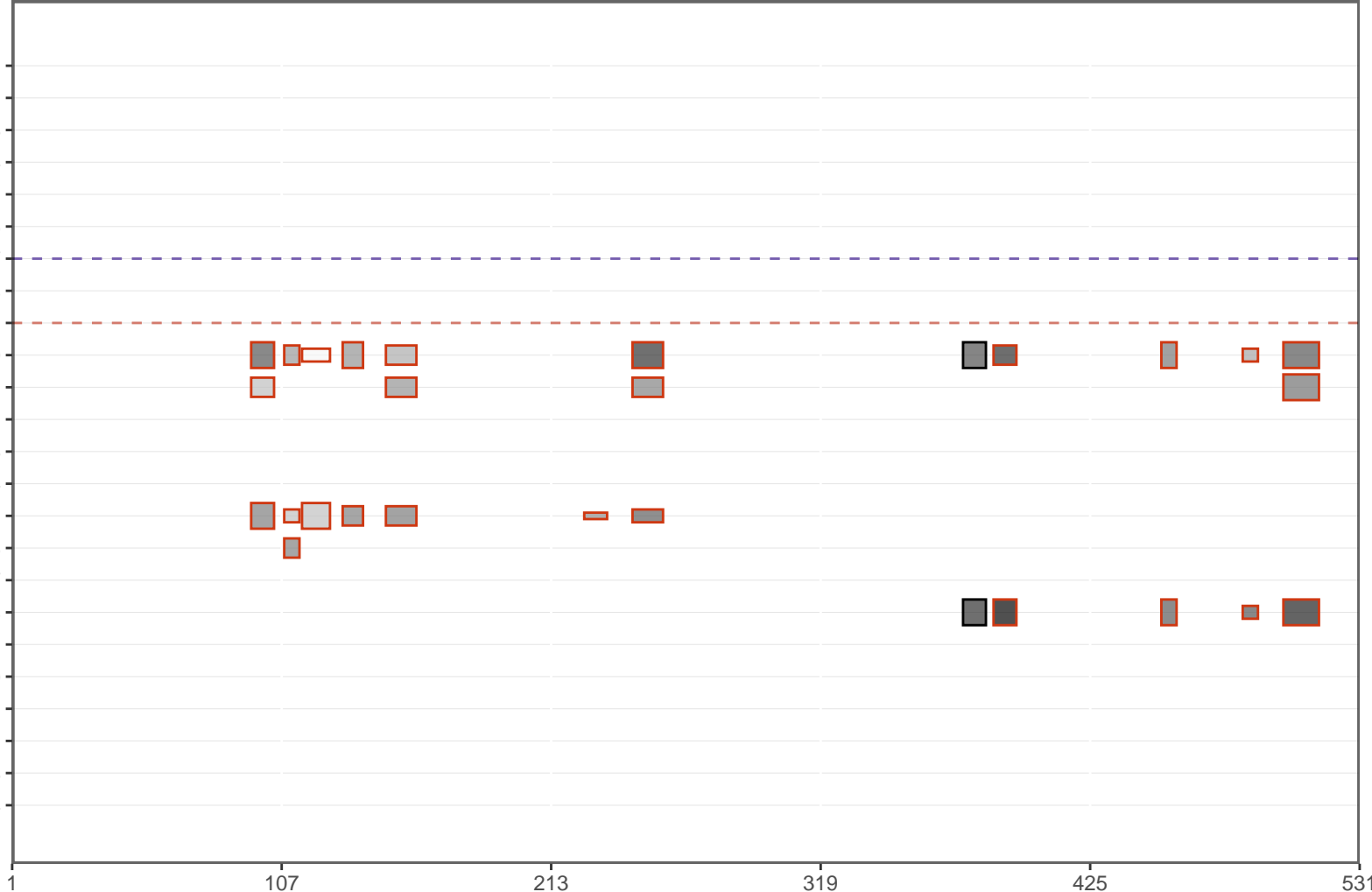
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGQENSRAYGLINFFFEELDGHLLSGMRNNGVNPYFQPLHAHLKHLKLNSEENSLPDSNFSFEEDKSCNWLNLNPPNBYVYVDFSGSIATMTKEQLMEFVYGLVNSKGRFLWVIRLDEWAGDDNKKKSEVLAEGTKERGVYGVWAPQEVLAHPSVSGFWTHCGVNSLETVYEGKPMGWPYFMDDQGVNRFVEAAWKLGLMDKTDGREIVEKMKKDLVAVRKDFELERANGMSKFAKECLVEGGSSYSNFERLNDIKLSKVRHY

NbL15g12020.1 ribose-phosphate_pyrophosphokinase_1-like [MW = 45.67 kDa]

No. of times detected



log(intensity)



Values from



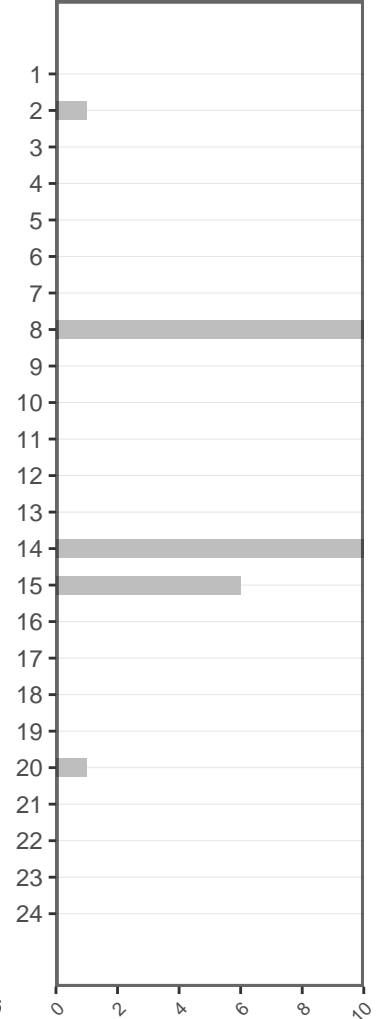
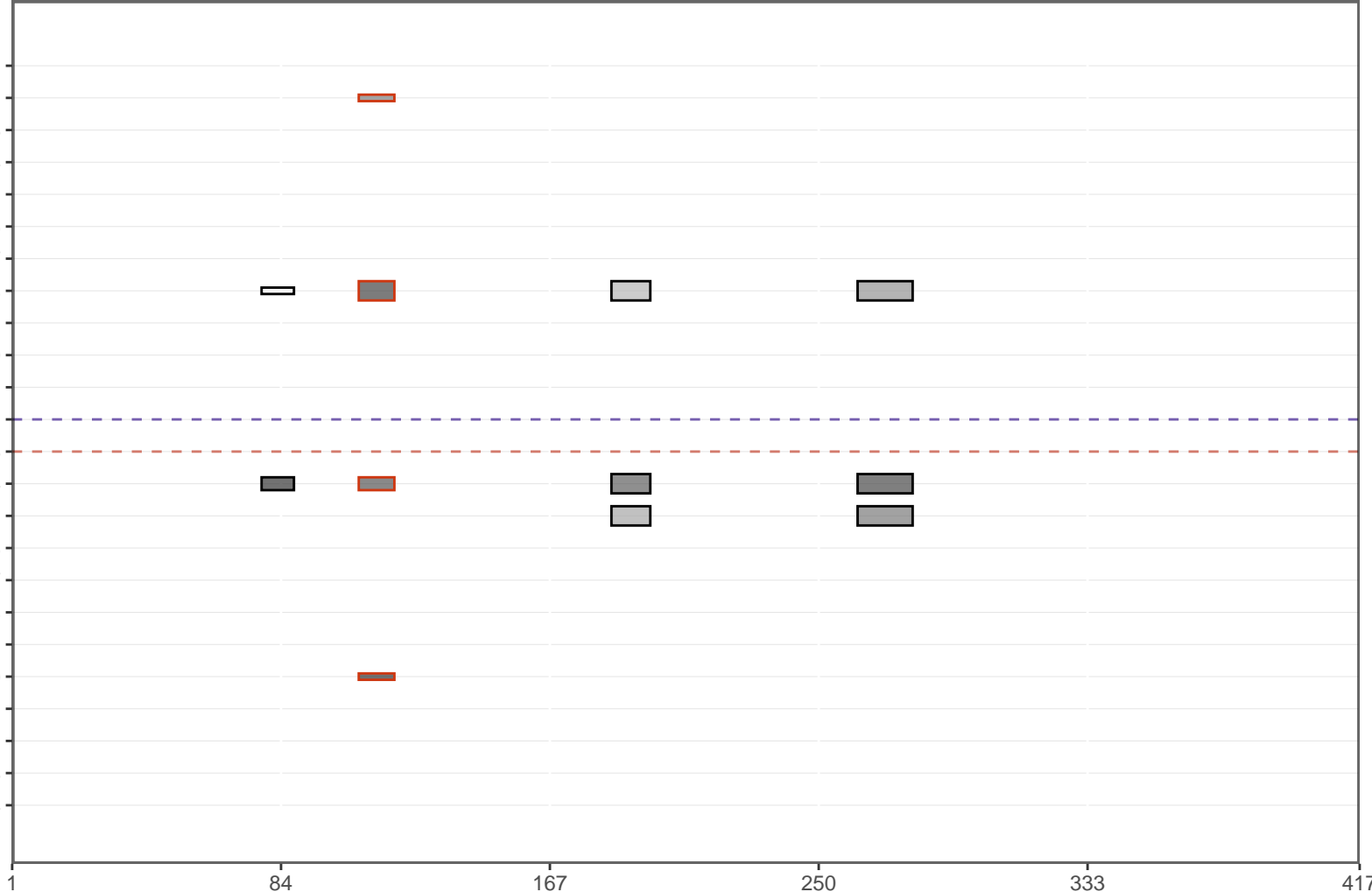
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF13793 N-terminal domain of ribose phosphate pyrophosphokinase
- PF14572 Phosphoribosyl synthetase-associated domain

Protein sequence:

YARADKTKGREGSIAKLVANLFEAGADRVLAGDLHSGGSMGYFDIPVHVYGGPVVLDVFLASKKISNDLVVSPDVGVARARAFAKLSDAPLAVDKRRGGHNVKMEVNIJSDVKGKAWMVDDMDTAGTAKGAALLHGEGAREVYAGCTHAVFRFRPNIERLISGLFGEVVSNTIPVMEKNYFPQLTFLSVANLLGETIWRVHDDGVSISIFQ

NbL15g12010.1 pyruvate_kinase_isozyme_G_chloroplastic [MW = 68.12 kDa]

No. of times detected



log(intensity)



Values from



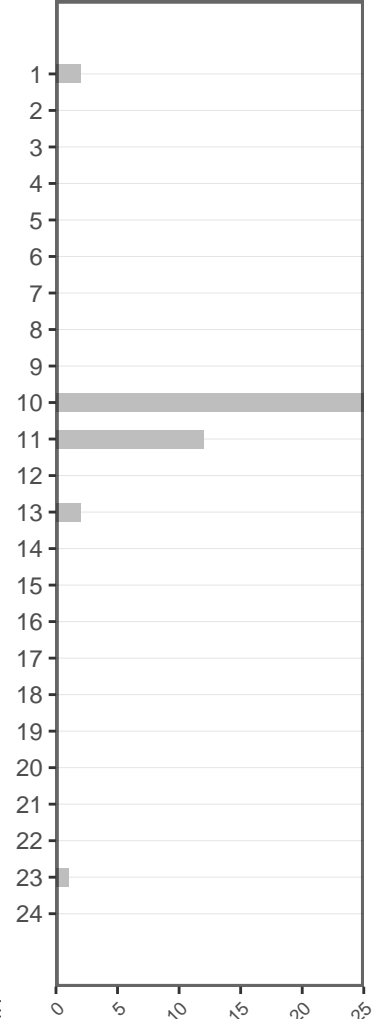
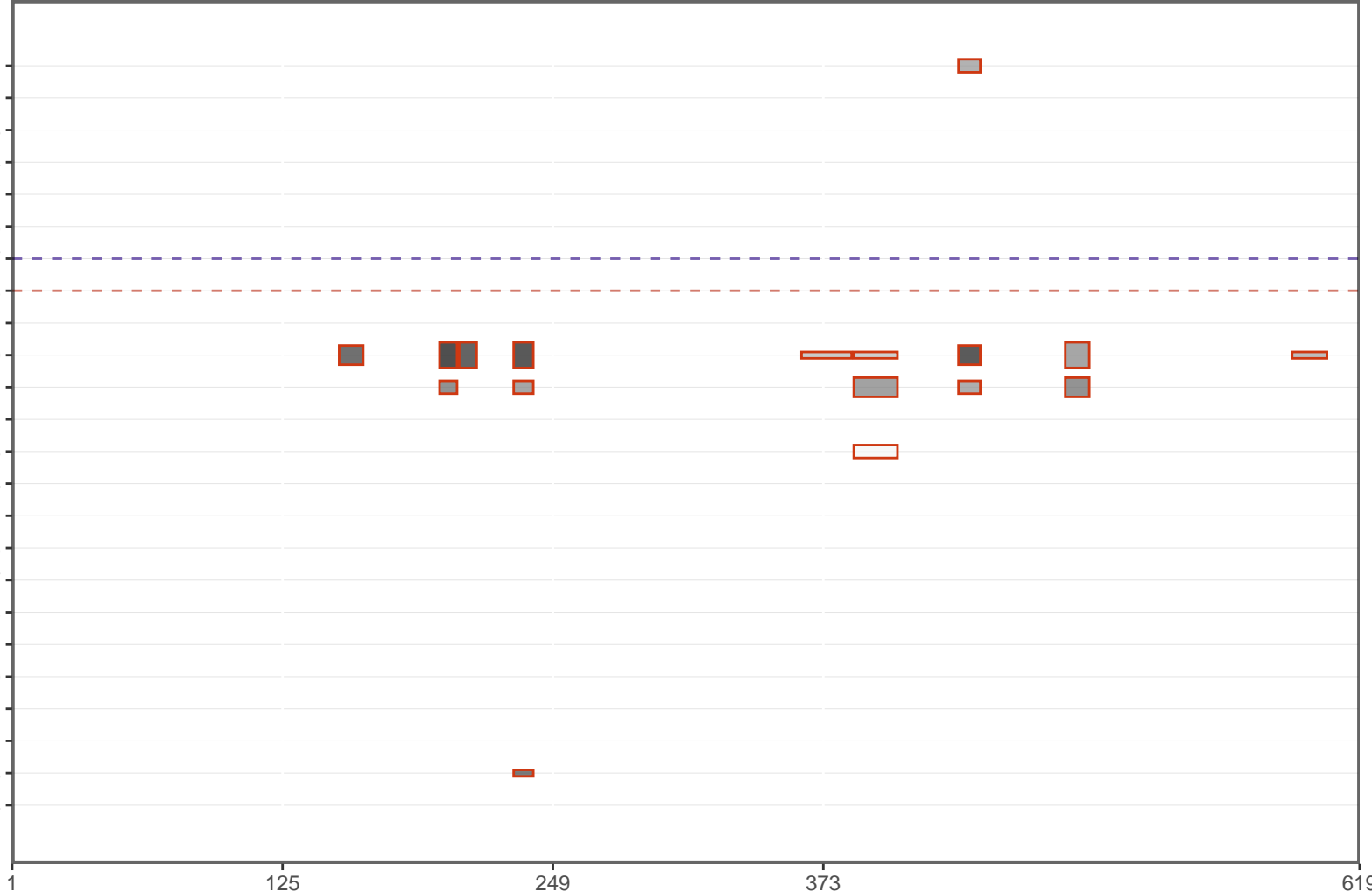
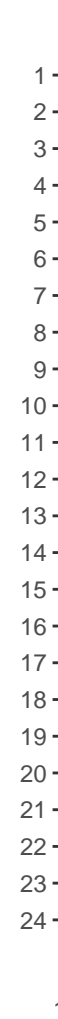
MW indication



Molecular weight

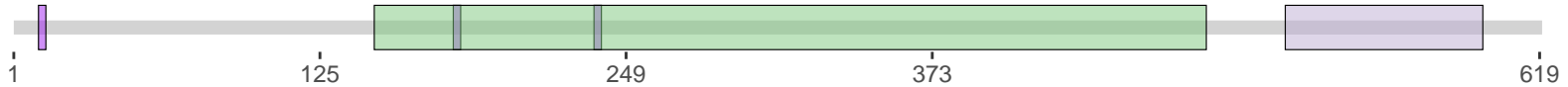


Gel Slice



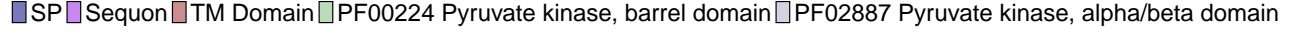
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LKSRRLNVRGKSKATLPSITEKDWDDKFGVDNVDYFVAVSEVKDKAVVHELKQVLEKGNADHIVYKIEASDIPNLHGISASDGMVARGDLCAELPIEVEVPLLGEDHRRGSGMOKPVIWATNMLESMIDHPTPTTRAEVSDISIAVREGADAVMLSGETAHGKYPKAVVMMHVALRTESSLGKSTGSSPSGSAAYKSHMGEMFAFHSSGMANTLSTPIVFTRTGSMAILSHNRPDSSTVFAFTNERVKGRLAIHGVGVPRVMEFSSDAEETFRAKLLLSKSLVKGQGYLT

NbL15g11960.1 syntaxin-22-like [MW = 30.04 kDa]

No. of times detected



log(intensity)



Values from



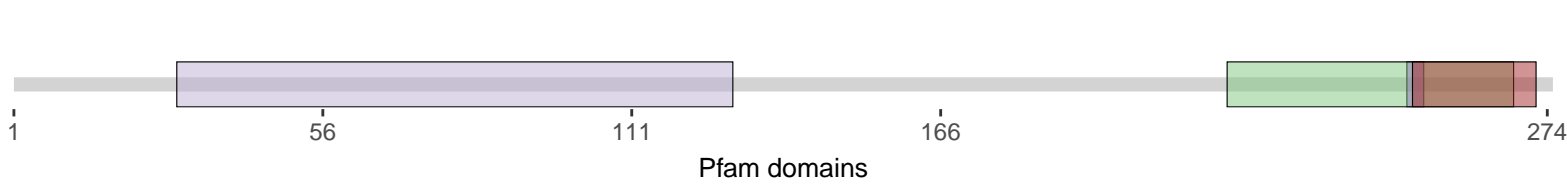
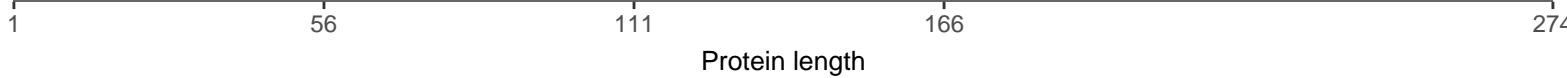
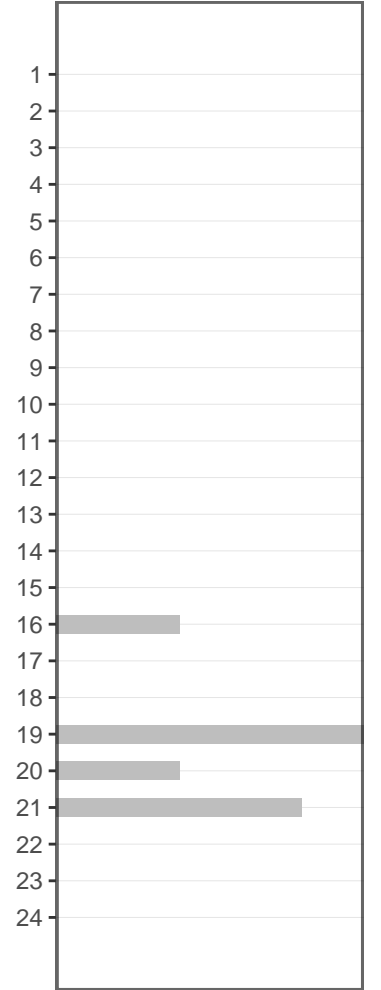
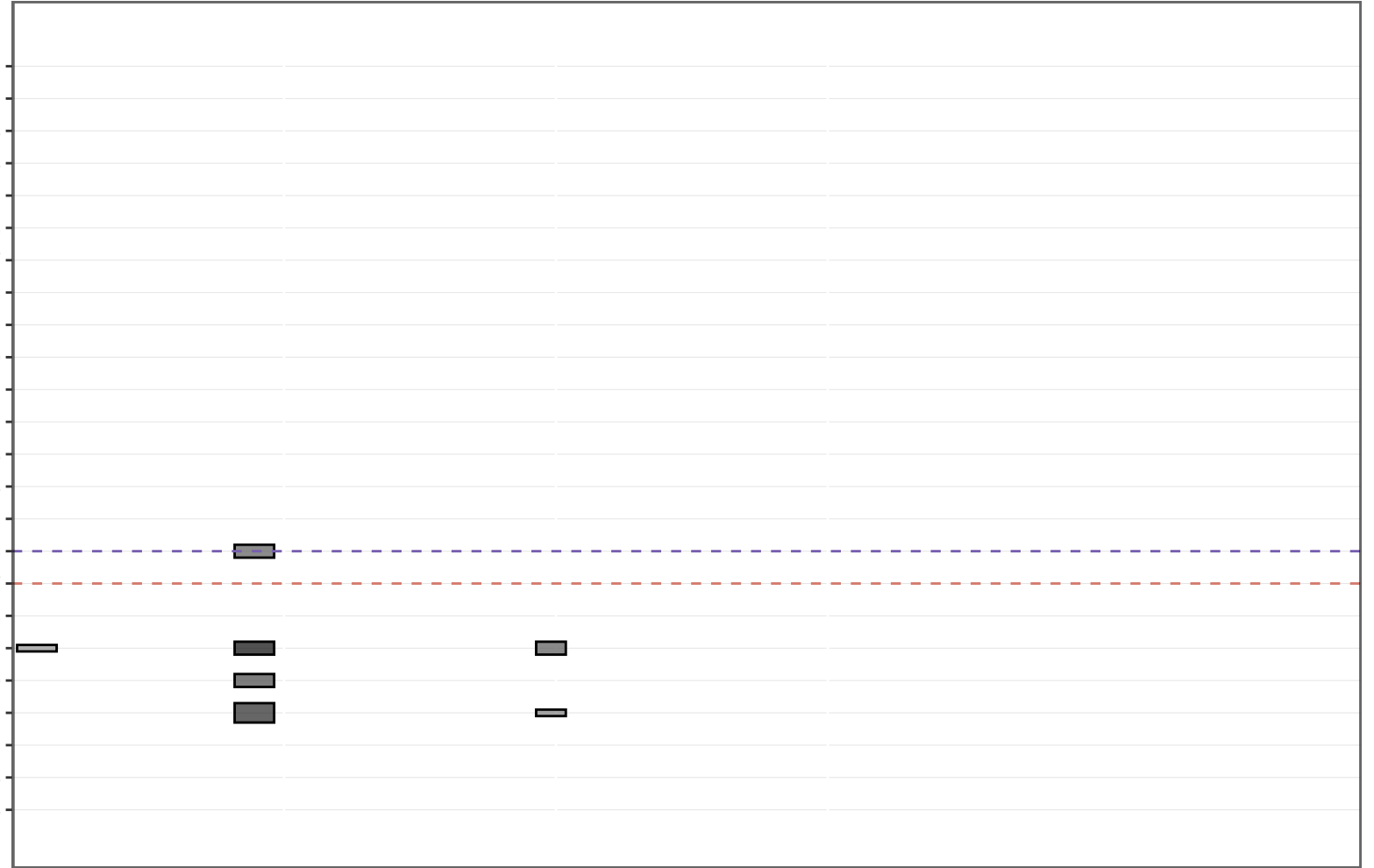
MW indication



Molecular weight



Gel Slice



Pfam Description



Protein sequence:

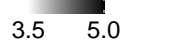
LLAAERETAYTPFVPGAVLPSGYSYTAISEIVSTKSPQGRALLVSRRQGVLLDSEIAFNEAIEEREQGGQGGQGGVNEIFKDLAVLVHEQGMIDDIQGNVENAHATAGGRSLAKAAKTRQNSLSLTOLLVIFGIVLLVIVLAA*

NbL15g11810.1 uncharacterized_protein_At1g32220_chloroplastic [MW = 32.74 kDa]

No. of times detected



log(intensity)



Values from



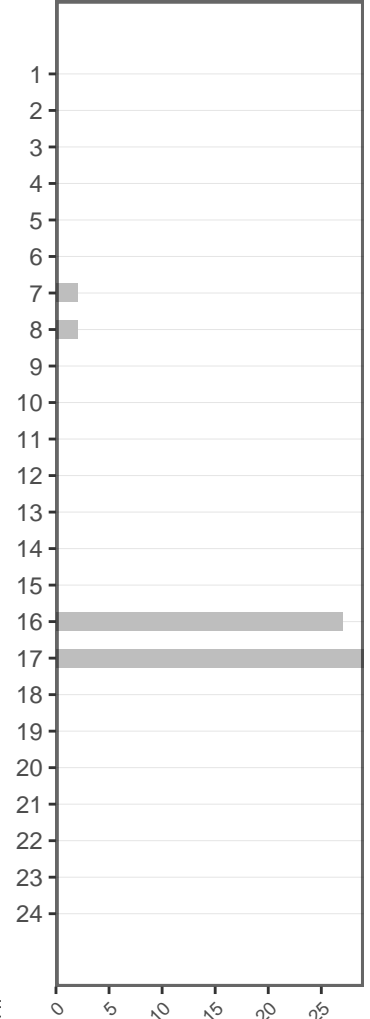
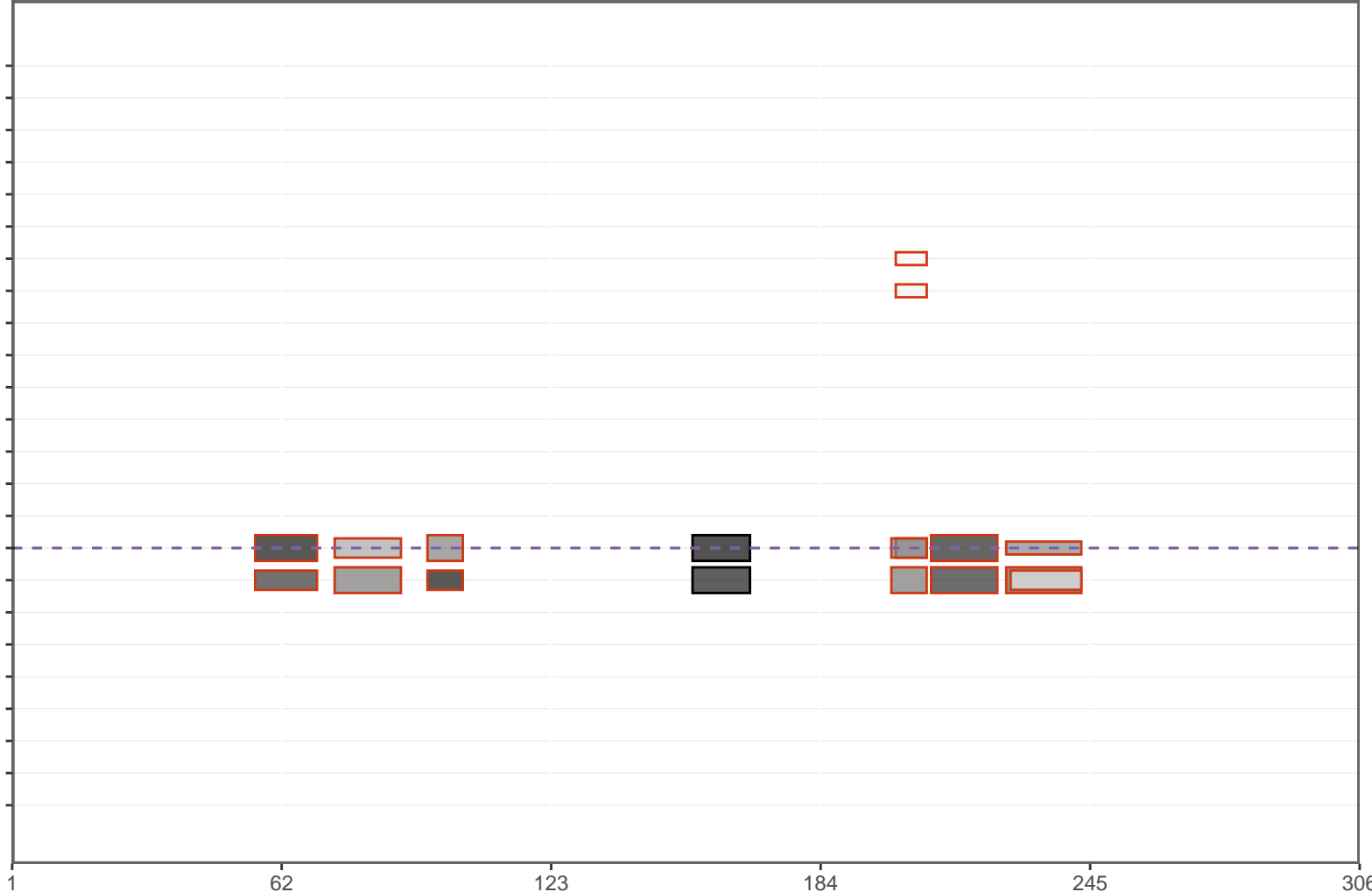
MW indication



Molecular weight

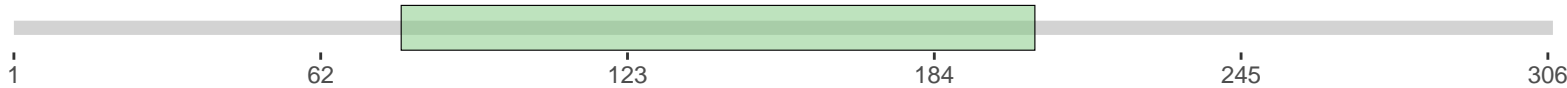


Gel Slice



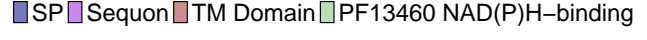
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IAVISTLGGFGSDEGMGRINGEANVAVNAAKDYGIFKFLIIVSHVDYALPSFLLOGGYFTGKRKAESSEVLSKYPNSGVVLRPFVYGRKRVDFEIPLDLIGELPKLRATESFTKPLSLSFASDLLLAPPVSVDDVAWAVINAVKDDDFGFIETGGIKEAAAGWVY

NbL15g11780.1 glycerol-3-phosphate_acyltransferase_chloroplastic [MW = 51.37 kDa]

No. of times detected



log(intensity)



Values from



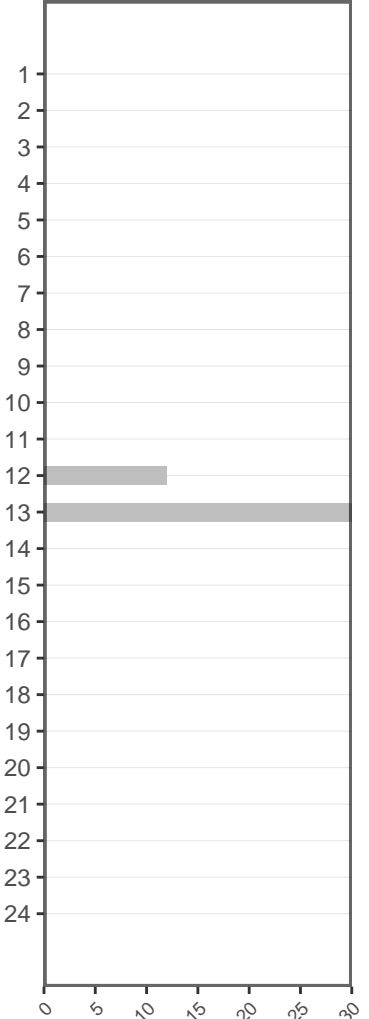
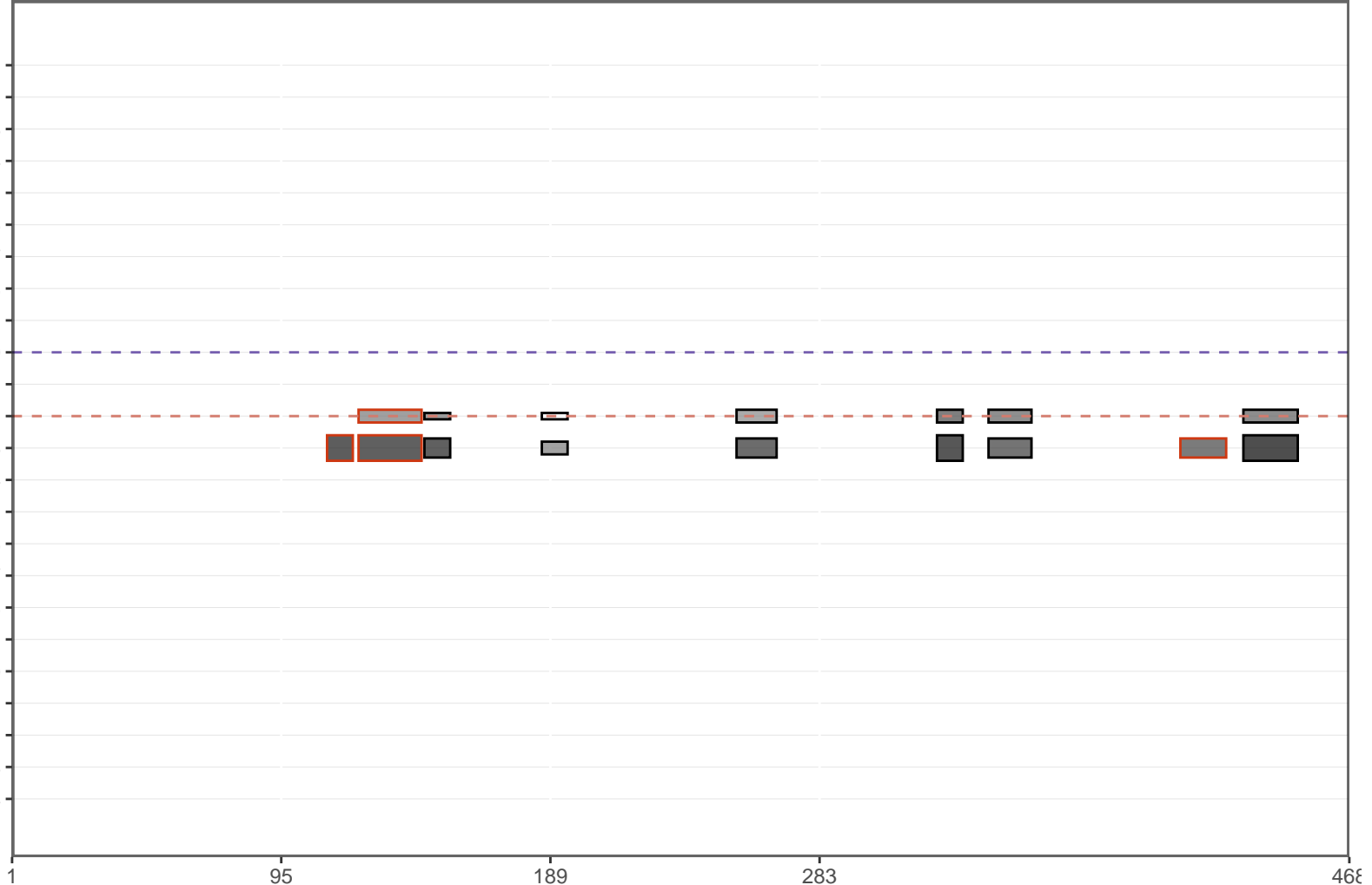
MW indication



Molecular weight

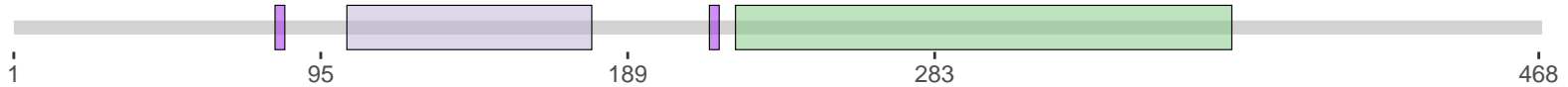


Gel Slice



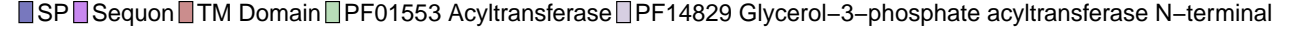
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KLKGGVNVLMNHQSEADPWVALLLESRPVIAENIYVAGDRVTDPLGKPFMGRNLLGVSKKHMGDDPKLVEKRRANTRLSKEMAVLLRGGSKLIWAPGGGRDRPNVTKEVYAFDFASSTDNMRRLVEHAGVPGHIYFLALCYDIMPFPQVEKNGEKRIISFHGAGIGVSPKIDFHEVAGALEDPPEAKMAYTKALYDVSVNGQYVNLNSAIHSGKGGQGEASTREVSLSGPWQ

NbL15g11460.1 3-isopropylmalate_dehydrogenase_2_chloroplastic-like [MW = 48.03 kDa]

No. of times detected



log(intensity)



Values from



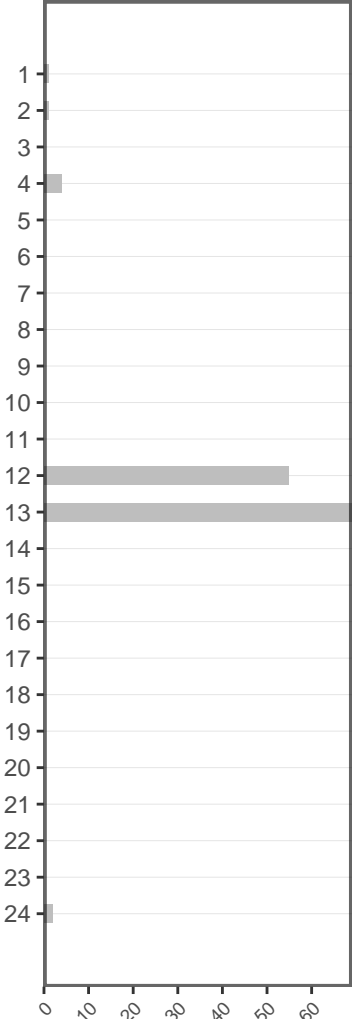
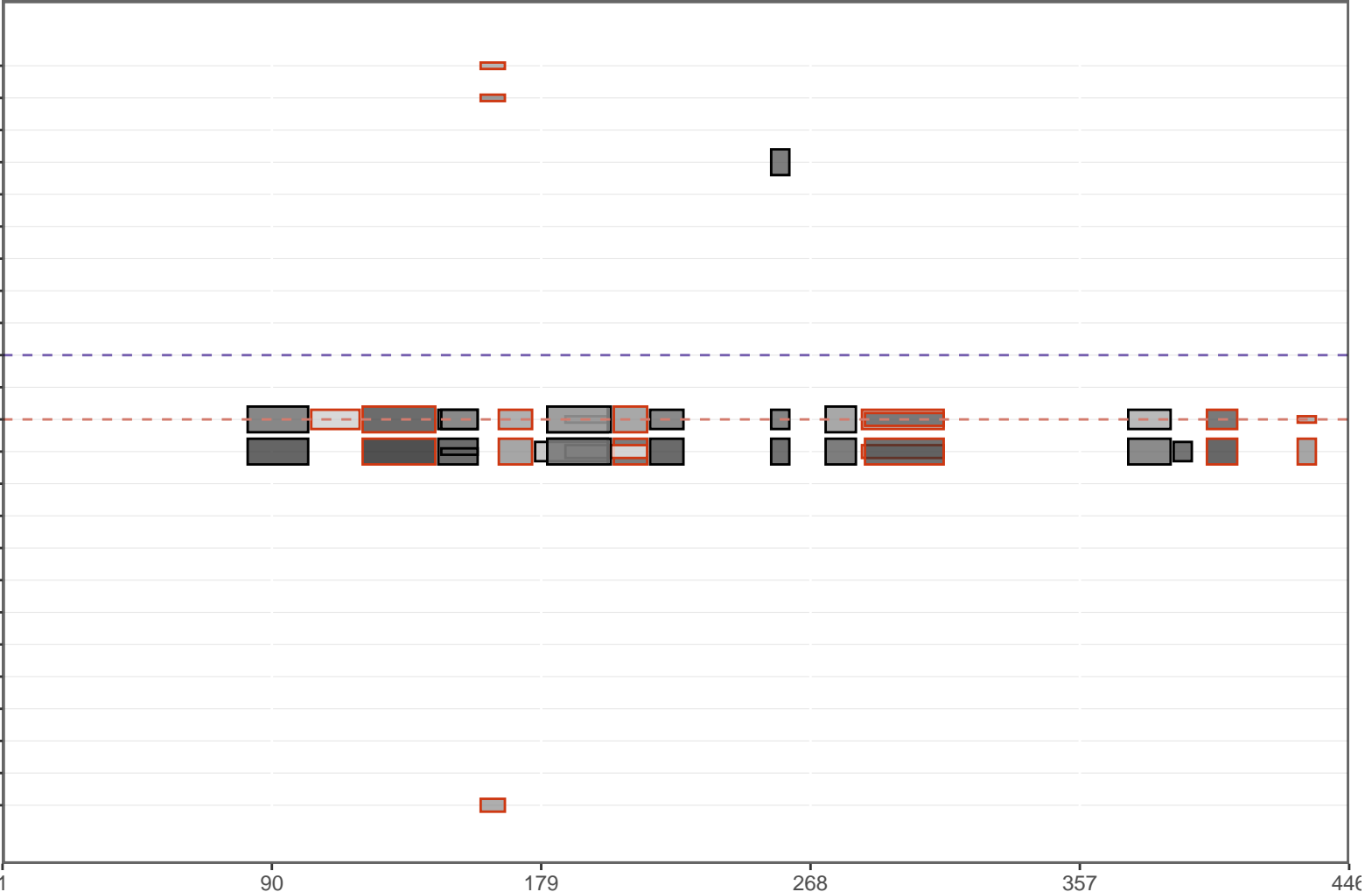
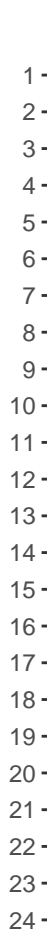
MW indication



Molecular weight



Gel Slice



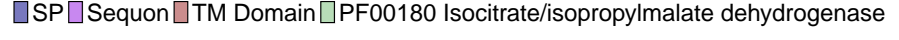
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LMVYRELTGQYIGEPKQNTSENGEIGFTEVYVAEIERIARIAFETARKRRKGLSDVKANVLEASMLWRKVKVTLASEYFDVELSHMYVDNAAMQLVNRPKGFDLTFNFDGLSDSEASMTGSGMLPSASLGETGPGLEFPHIGSAPDIAGDDKANPLATVLSAAMLKYGLGEEKAADRIEAAVLDLNLGRFRGDIHSHGHLKVGCKKMGEEVLKSIDKTRAV

NbL15g11380.1 O-methyltransferase_MdmC-like [MW = 32.12 kDa]

No. of times detected



log(intensity)



Values from



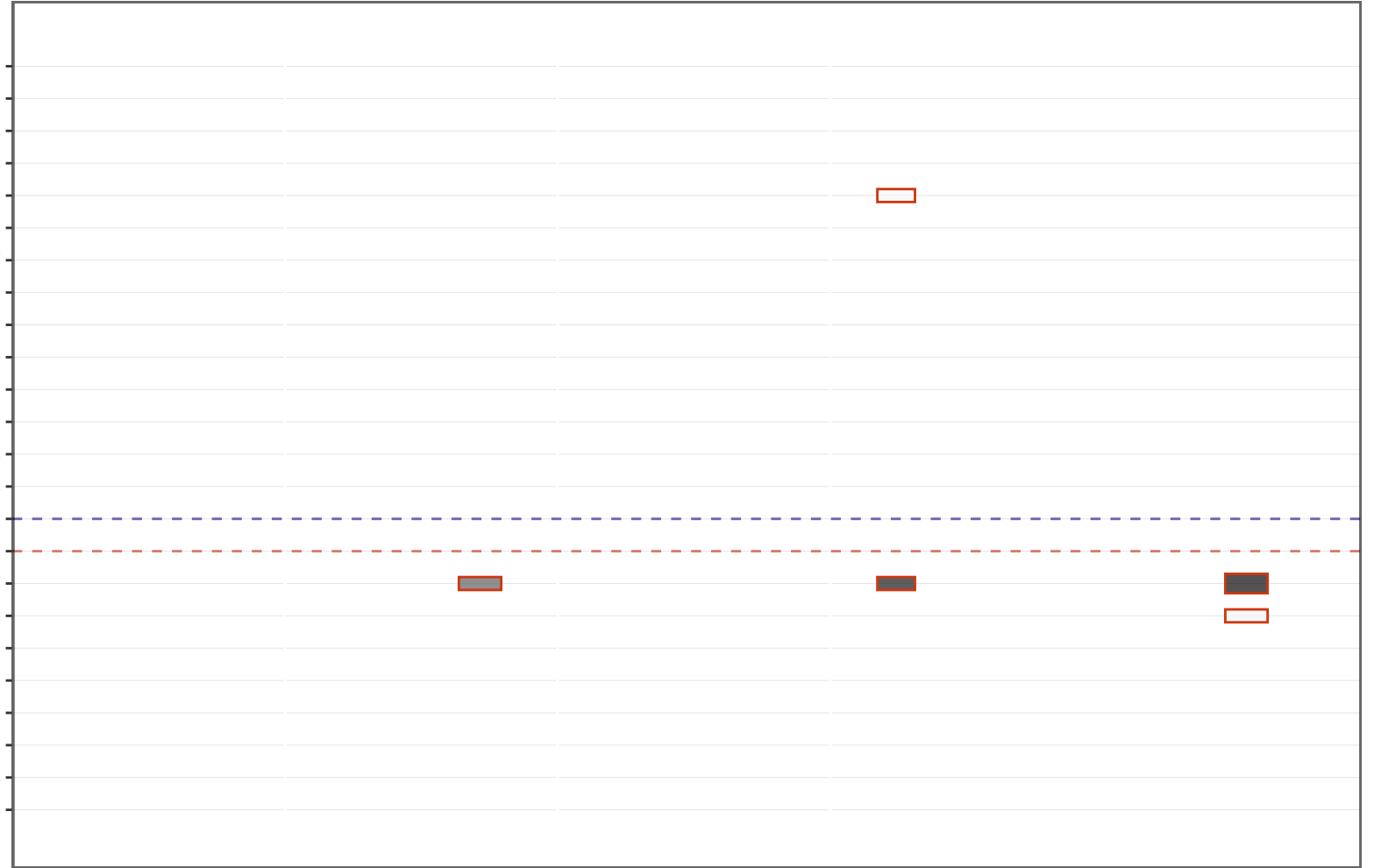
MW indication



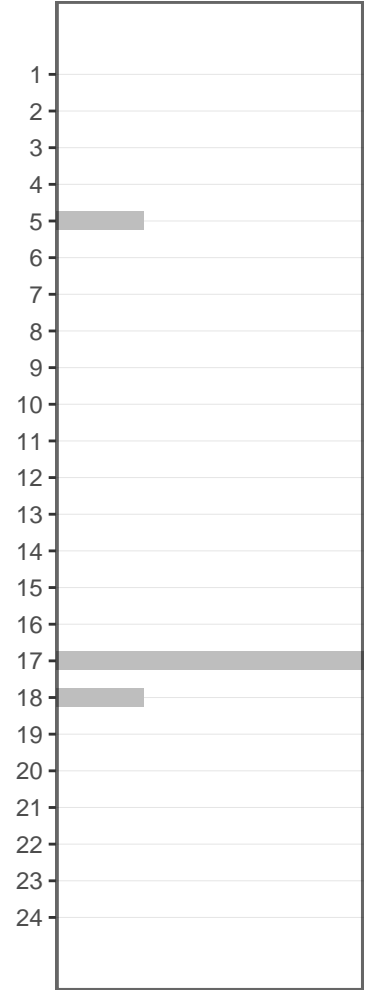
Molecular weight



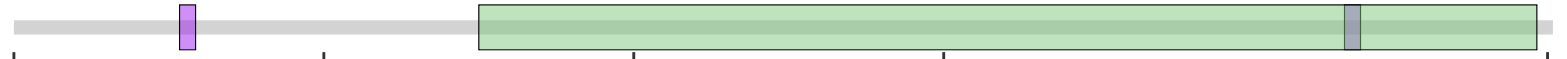
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

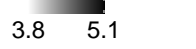
EVGTYTGYSSLAVALVPEEGGLVACERDGGKSEVAKRYVDGAVLHKVDVHRHGLAADTLKSLIQNGESGRYDFAFVDAEKRMVYDYFELLGLRVGGLVVDNVLVHGRVTDPLVNDSKTLGRNFNGNLMEKRDVDSIMVPIGGDMTIGIKR

NbL15g11350.1 early_nodulin-like_protein_1 [MW - SP = 16.64 kDa]

No. of times detected



log(intensity)



Values from



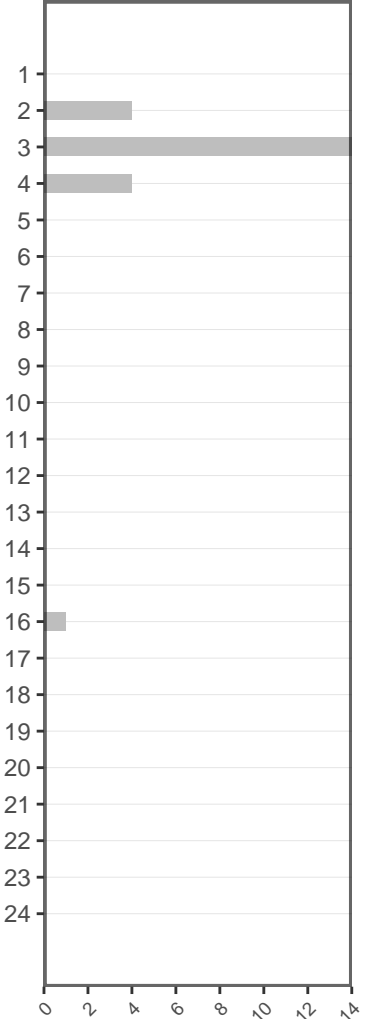
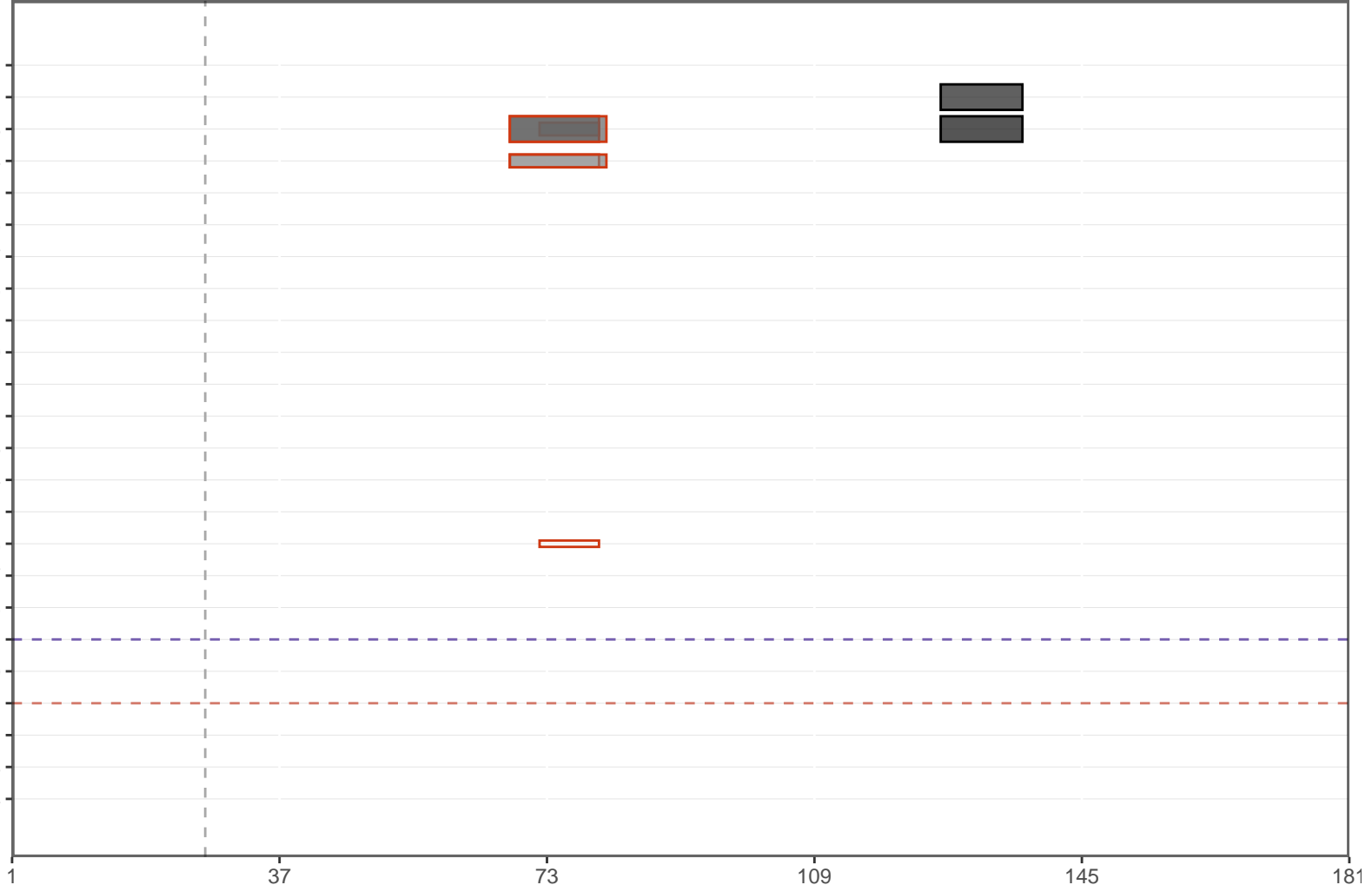
MW indication



Molecular weight



Gel Slice

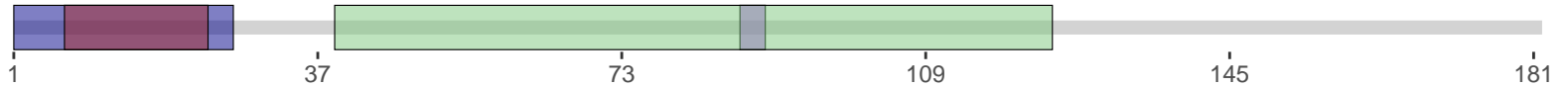


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VSKRDVYTCNSSSPVAHNDGNTKIELHGGAYFISGAKGHGEGGKLVTLSENMRFRMAAPSPAEFDGPMAPTSSASLKPFLMFGVLGFLP

NbL15g11290.1 probable_phospholipid_hydroperoxide_glutathione_peroxidase [MW = 25.74 kDa]

No. of times detected



log(intensity)



Values from



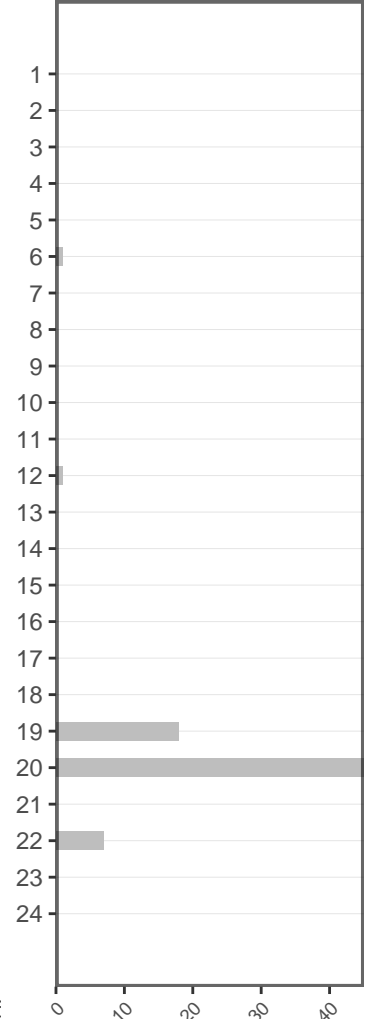
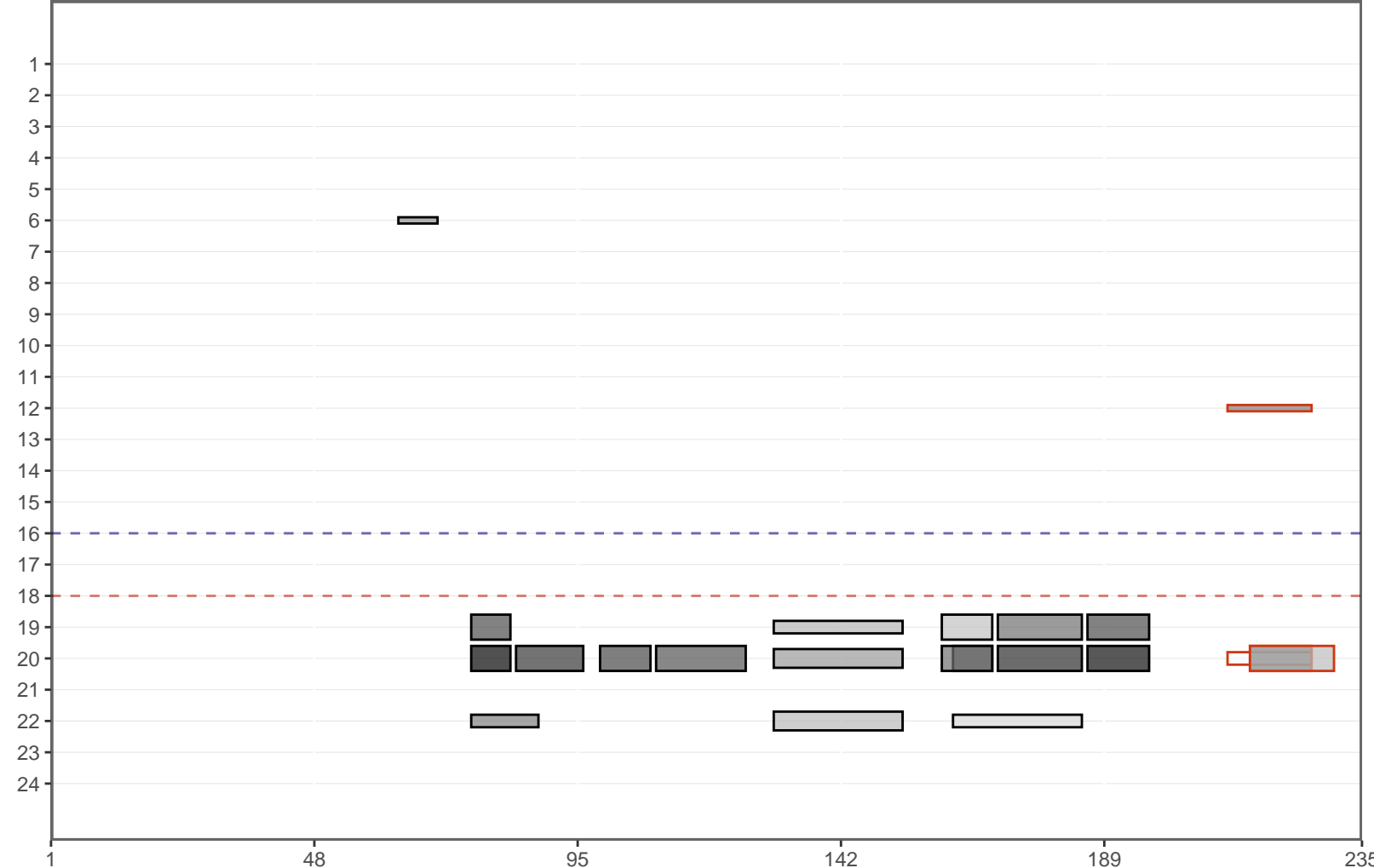
MW indication



Molecular weight

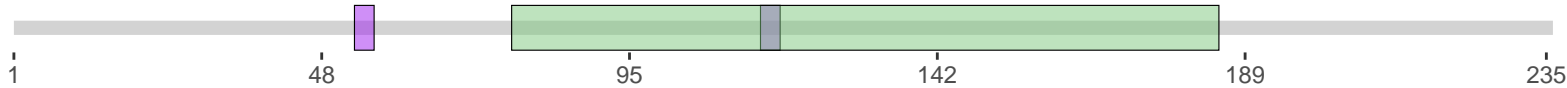


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ASRCGLTSTNYTELSGIVYKYEKTKGLLELAFPGNGFGAAGEPGSNPEIKDFACFRFAEFPFDKVDVNGPNTAPVYGLKSKSAGGFLGDLNKNWFELFLVDKNGKIVERYPPPTFSPVQIEKDKLLAA*

NbL15g11220.1 luminal-binding_protein_4-like [MW - SP = 70.34 kDa]

No. of times detected



log(intensity)



Values from



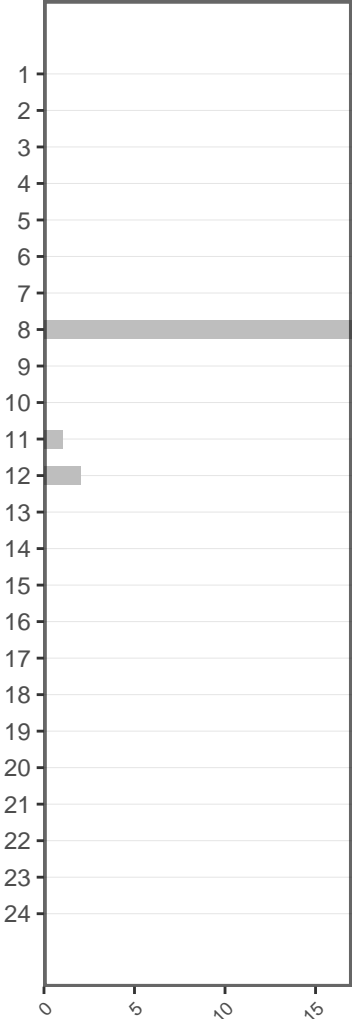
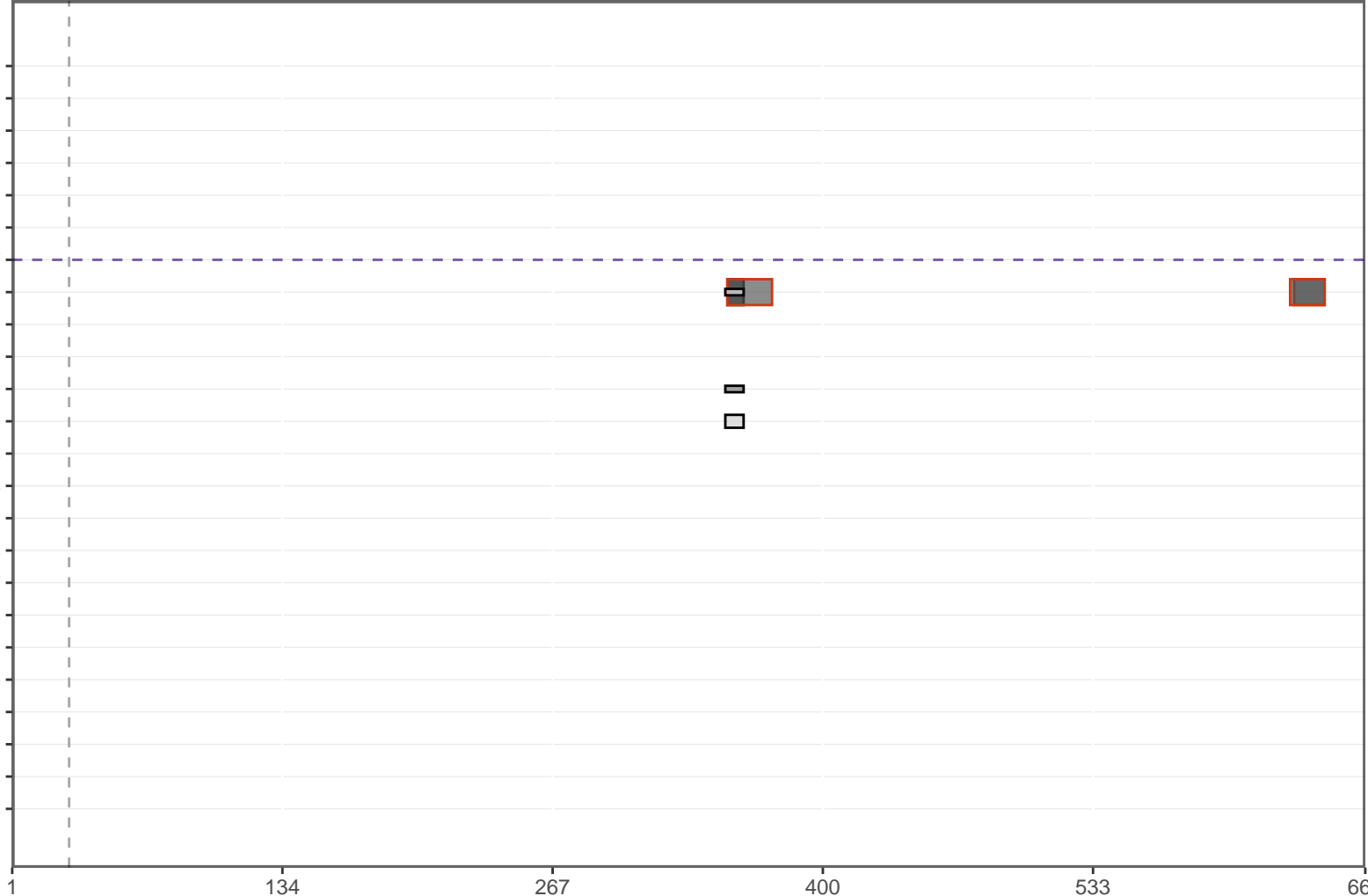
MW indication



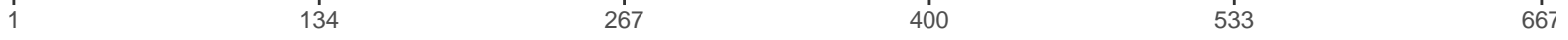
Molecular weight



Gel Slice



Protein length

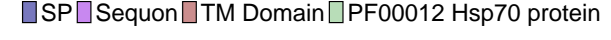


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGTDFSEPLTRARFEEINNDLFRKTMGPKVKKAMDDAGLEKNQIDEVVLVGGSTRIPKVDGLLKDVFEGKEPNKGVNPDAAWVGAAVQGGILSGEGGDDTDKLLLDVAPLTLGIETVGGVMTKLIIPRNTVPTPKKSGVFTTYDQGGQTTVTSIVYVEGERBLTKDCRLLGNFDLGGPPAPRGTPOEIVTFEVDANGLNVAEDKGTGKSEKITITNDKGRLSQEEIERMVRSAEEFAEEDKKVYKDRIDARNGLETVVYMNKNGINDKDKLADKLESDENEKIDTAVYKEALEVLDON

NbL15g11190.1 nuclear_pore_complex_protein_NUP50A-like [MW = 47.78 kDa]

No. of times detected



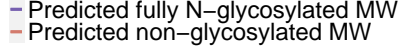
log(intensity)



Values from



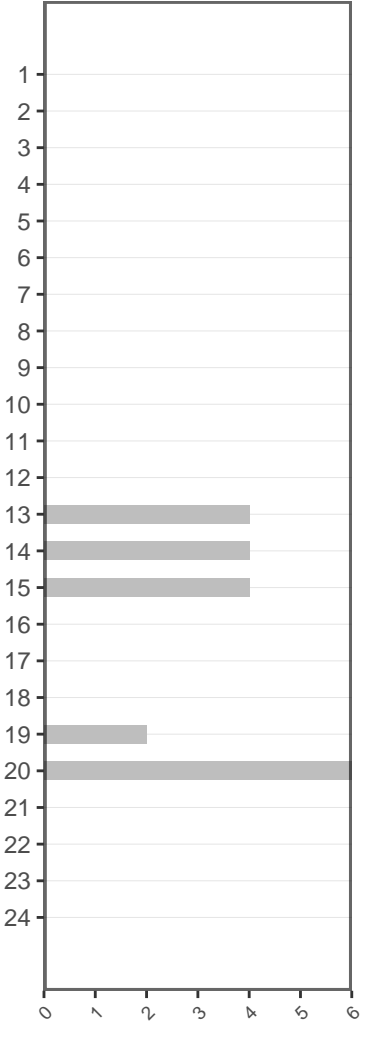
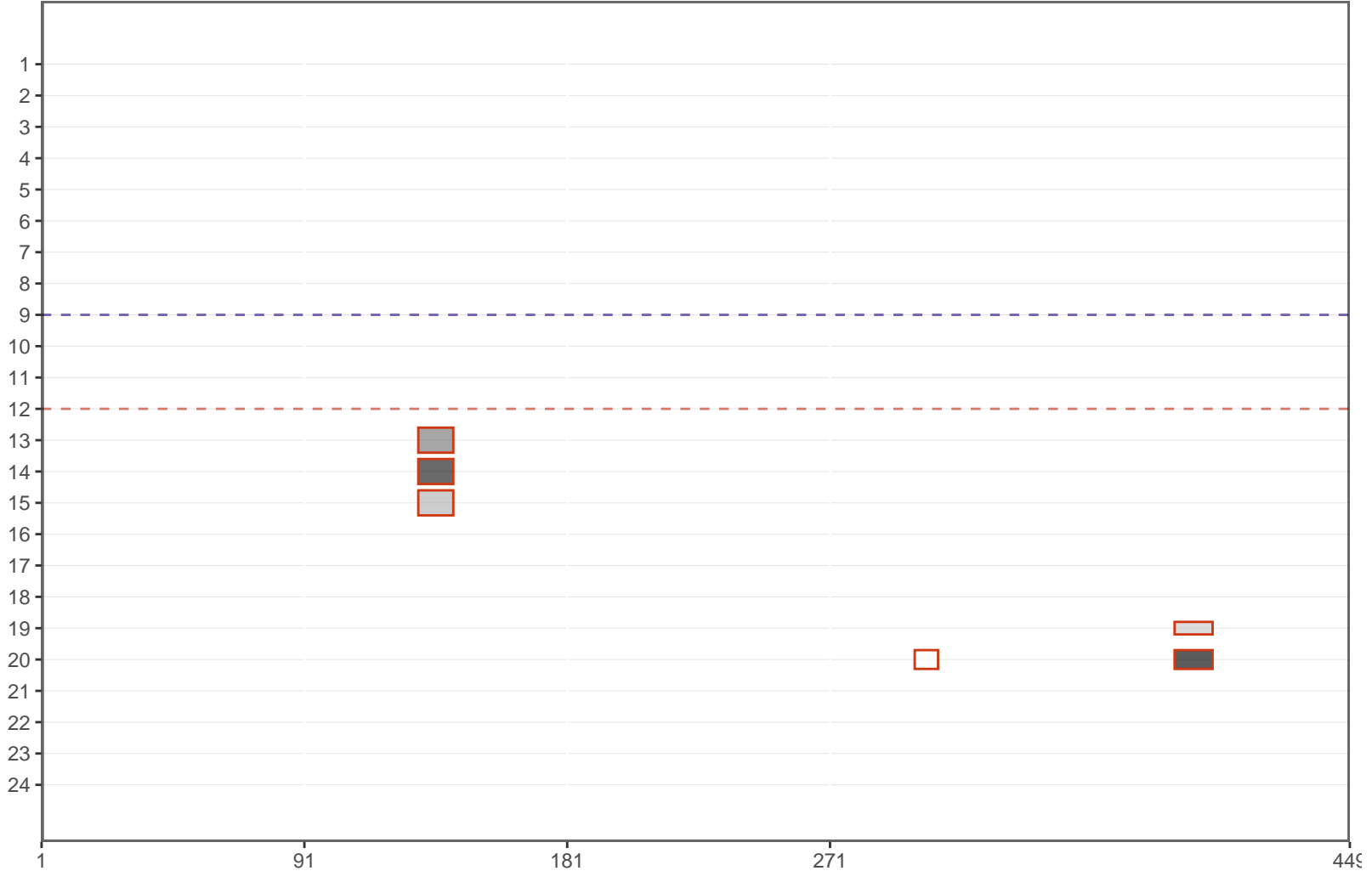
MW indication



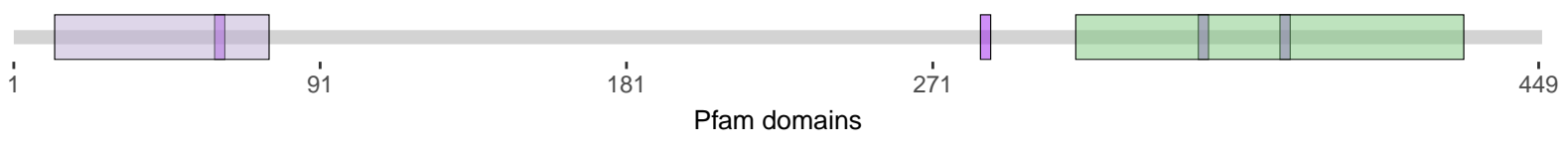
Molecular weight



Gel Slice

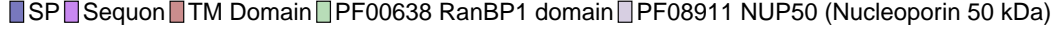


Protein length



Pfam domains

Pfam Description



Protein sequence:

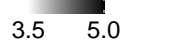
ITASFSFQQLSSSQNAFTGAGTGFRTTFDFGAIKKGSPALFGGSEGGAVGGELFGAKSDQPFGLTLPTNGNMLFGNKGSSIVNKGEGTGFPPKKEVSVETGEEENKPVFTADGVLFELFDGGWKRKGGELKVNVTAREGKARLVMRTKGNVRLINASLYPEMNLTMMDKRGVLFACLNAGDQKKEGLSTALKFKDKASIVEEFAAAVAKHKGTSTGSLKTPENSPKASDDY

NbL15g11140.1 MAR-binding_filament-like_protein_1-1 [MW = 81.9 kDa]

No. of times detected



log(intensity)



Values from



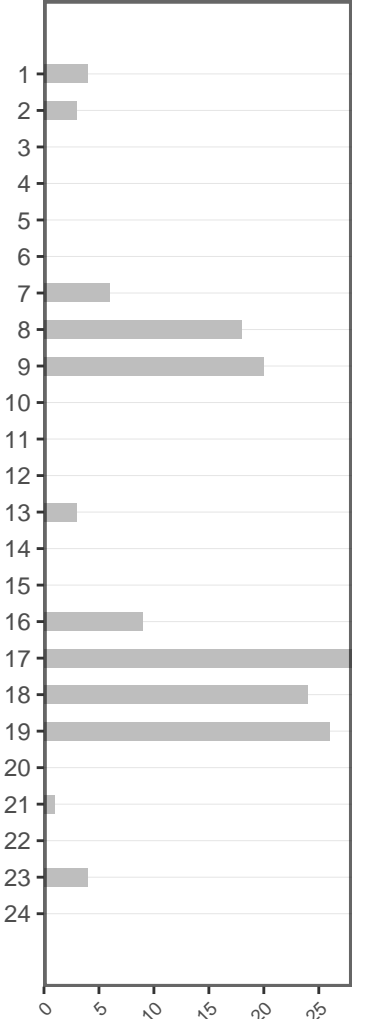
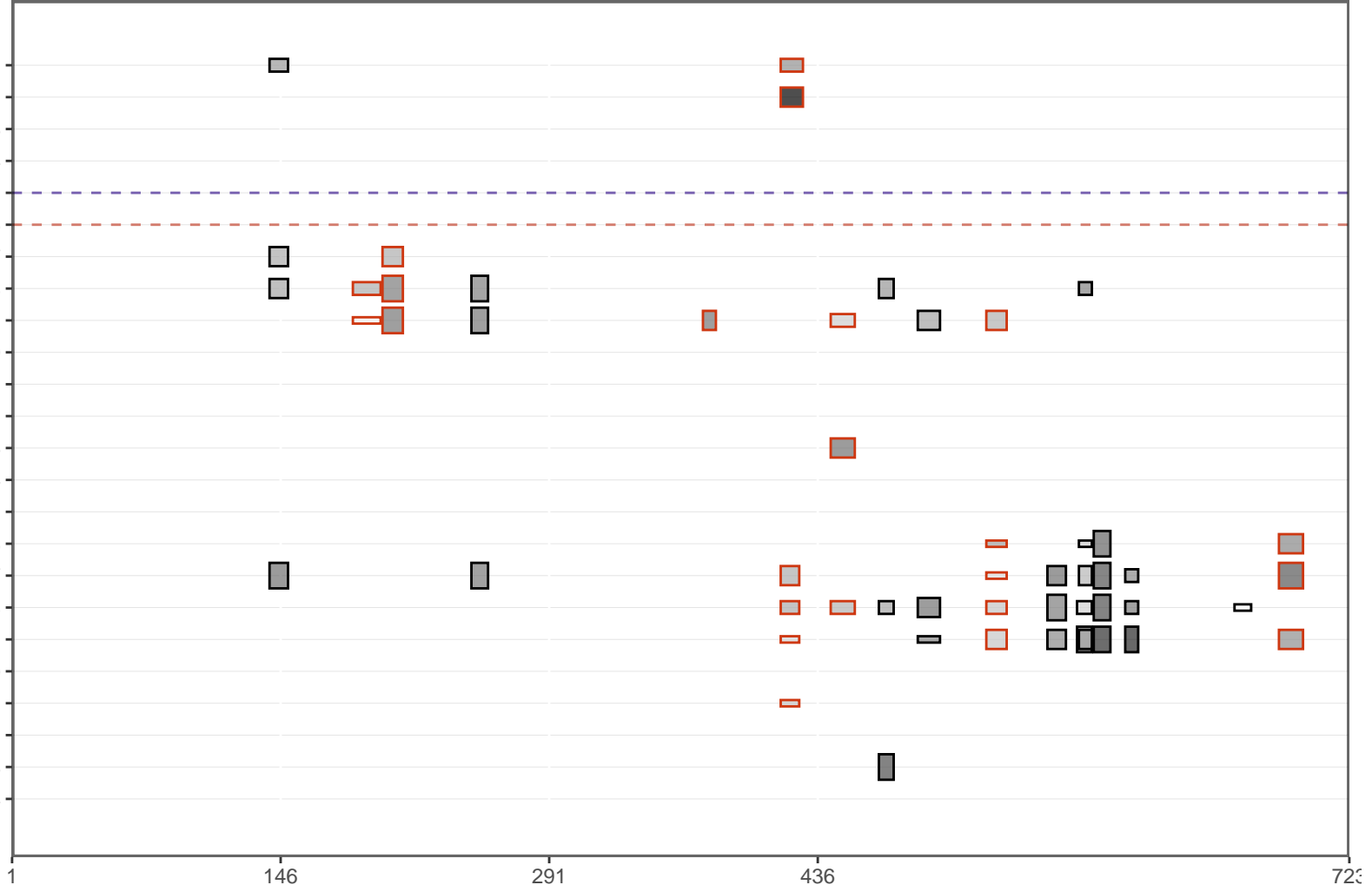
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KELDIOKEYSEFYSISEKIVASDAKLLGEGENRHLHOLEEQGLGAASAEVCKNKVLIADLTGKEKNGRMLDIAELENKSLKLEVDQTELEKSRSEASDAEGLGGSRHLCSKLEAEVSRLOMEEETRTSLGRKIDETKRGAEALLAELFTTRDLKTKTKEMHTMSELAAVVTENRDLGTELDVYKKAERAADELKGGKRVHVTJKKELTFLEAGITREKSRKNLEEELEERATESLDEMNRNALALAKELKELANSRISRLGDREVLKGVSEKGLSDQARENLEDAH!

NbL15g11020.1 uncharacterized_LOC107817663 [MW = 45.8 kDa]

No. of times detected



log(intensity)



Values from



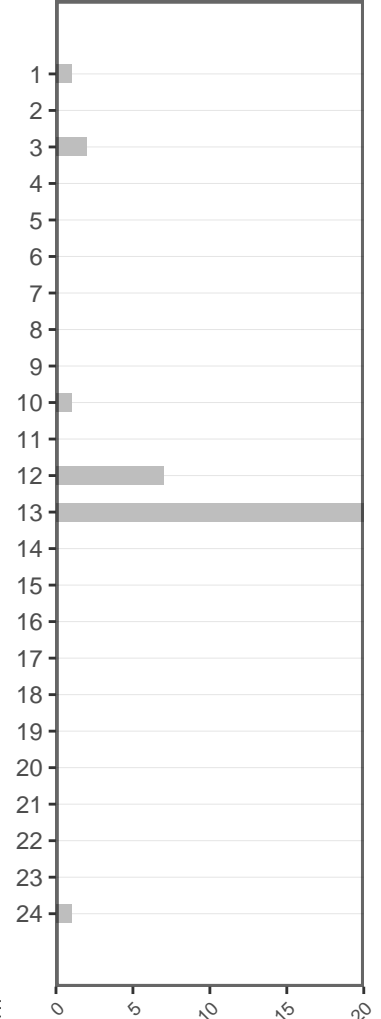
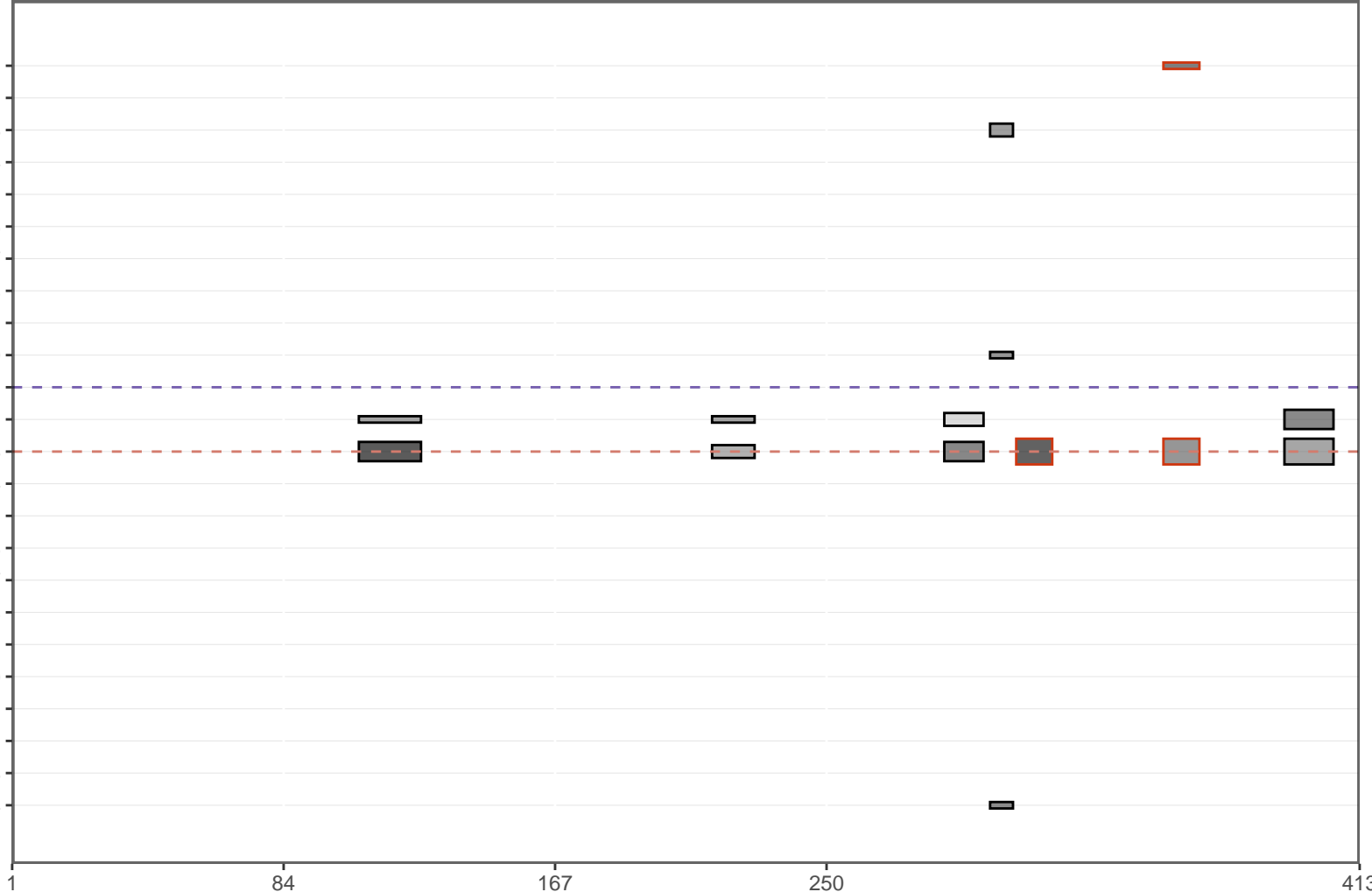
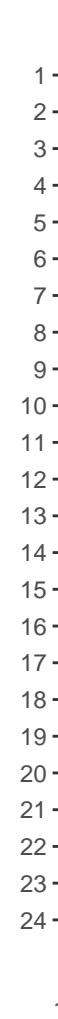
MW indication



Molecular weight

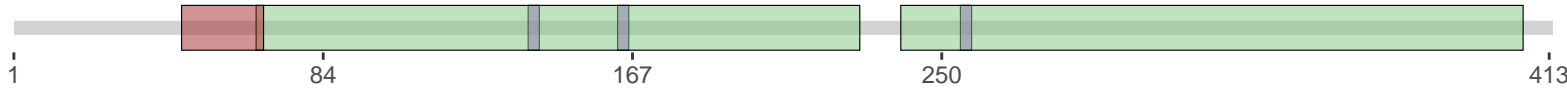


Gel Slice



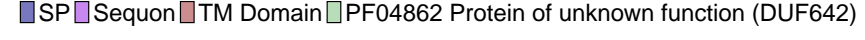
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

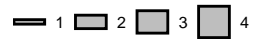


Protein sequence:

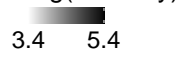
[SWGLAGANEIDMLNPNAEKDPADGGLDFIALKALKNPHRPGKGNMLKNGNFEEGGYIFRNTFVWGLVLPNNEEDHSPLPGWMEISLKAVKYDAAHFTVPEGRKRIELVAGREAAIGDVTTRGKYVDLMFVYGDASNSGGEMLEAFAGQIFLRVPEYESTGNGGFRKRAKLRPKAVSERTRVRFLESTYYHMKSDHSGLGPPVDDVRLVGRVPP

NbL15g11010.1 serine-threonine_kinase_receptor-associated_protein-like [MW = 38.45 kDa]

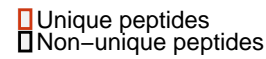
No. of times detected



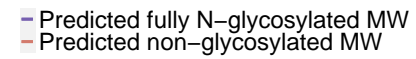
log(intensity)



Values from



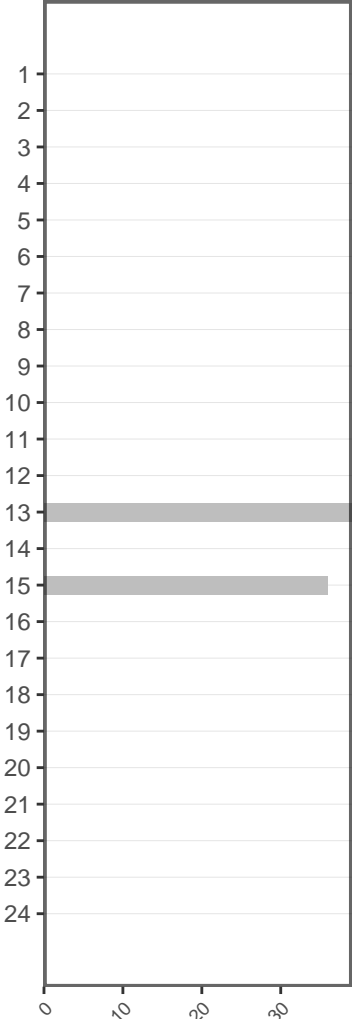
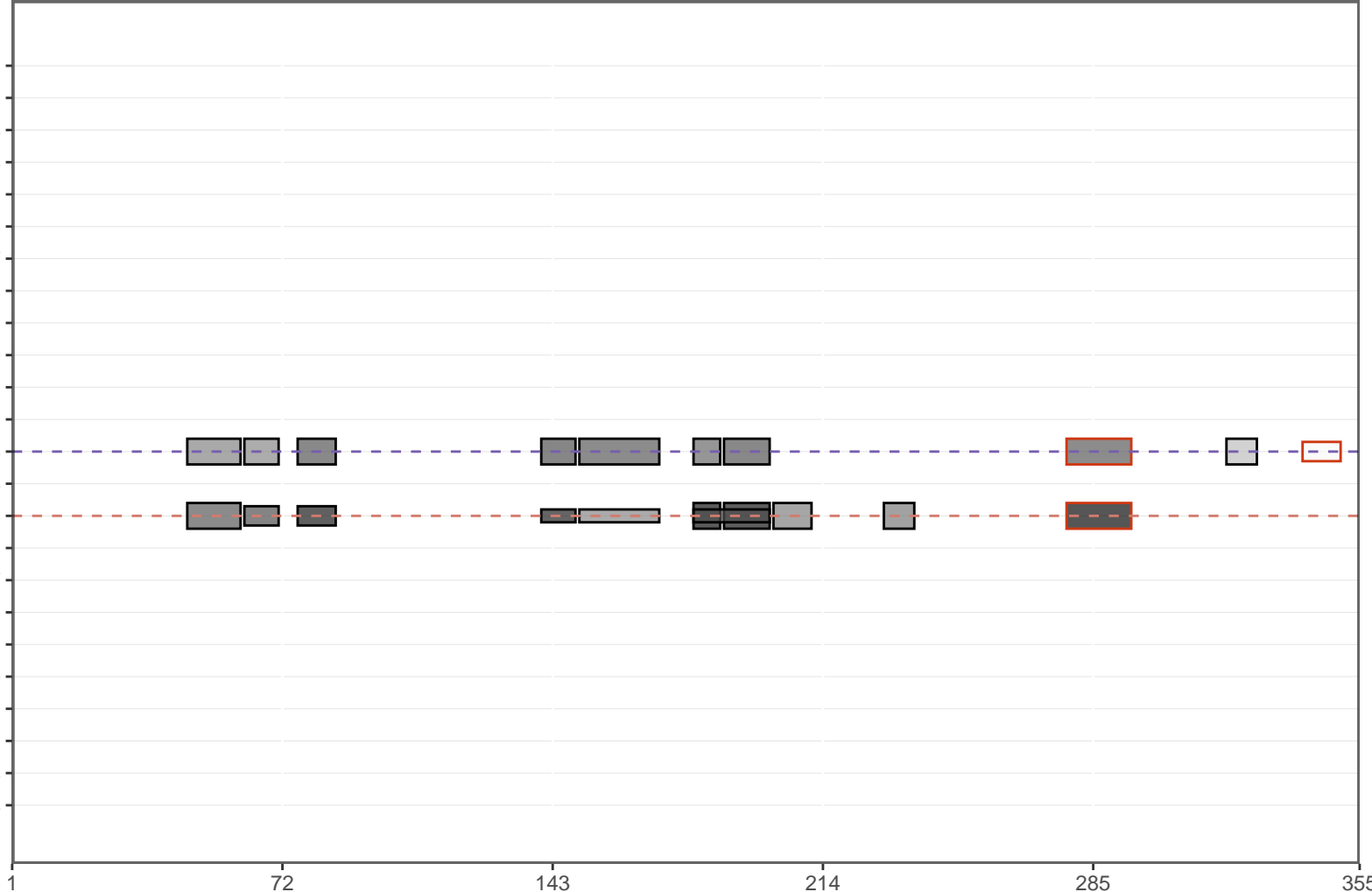
MW indication



Molecular weight

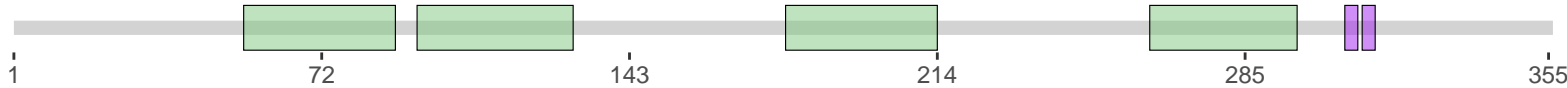


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

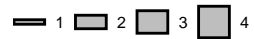


Protein sequence:

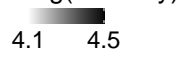
AGGLRLWDVRSQKHWQLETRKFPVTEAEVSGDGRVYTTADGSGVDFWDAHFGLVYKSHDLPOKVEASBLEPKFGNRFAGGEDMWWVDFDHTGEEIGKNGKHGHGFPVHQLRFSFVGDYASGSEEDGTVRIWQLGPLGQNEGNATANGSIANKKDDMGEVTVQKIEELVSEANKTEETQMDGAVKVVADA

NbL15g10750.1 ATP-dependent_Clp_protease_adapter_protein_CLPS1_chloroplastic-like [MW = 17.49 kDa]

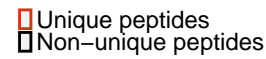
No. of times detected



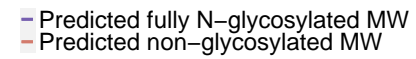
log(intensity)



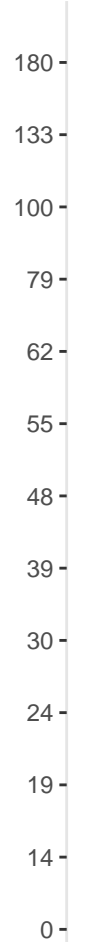
Values from



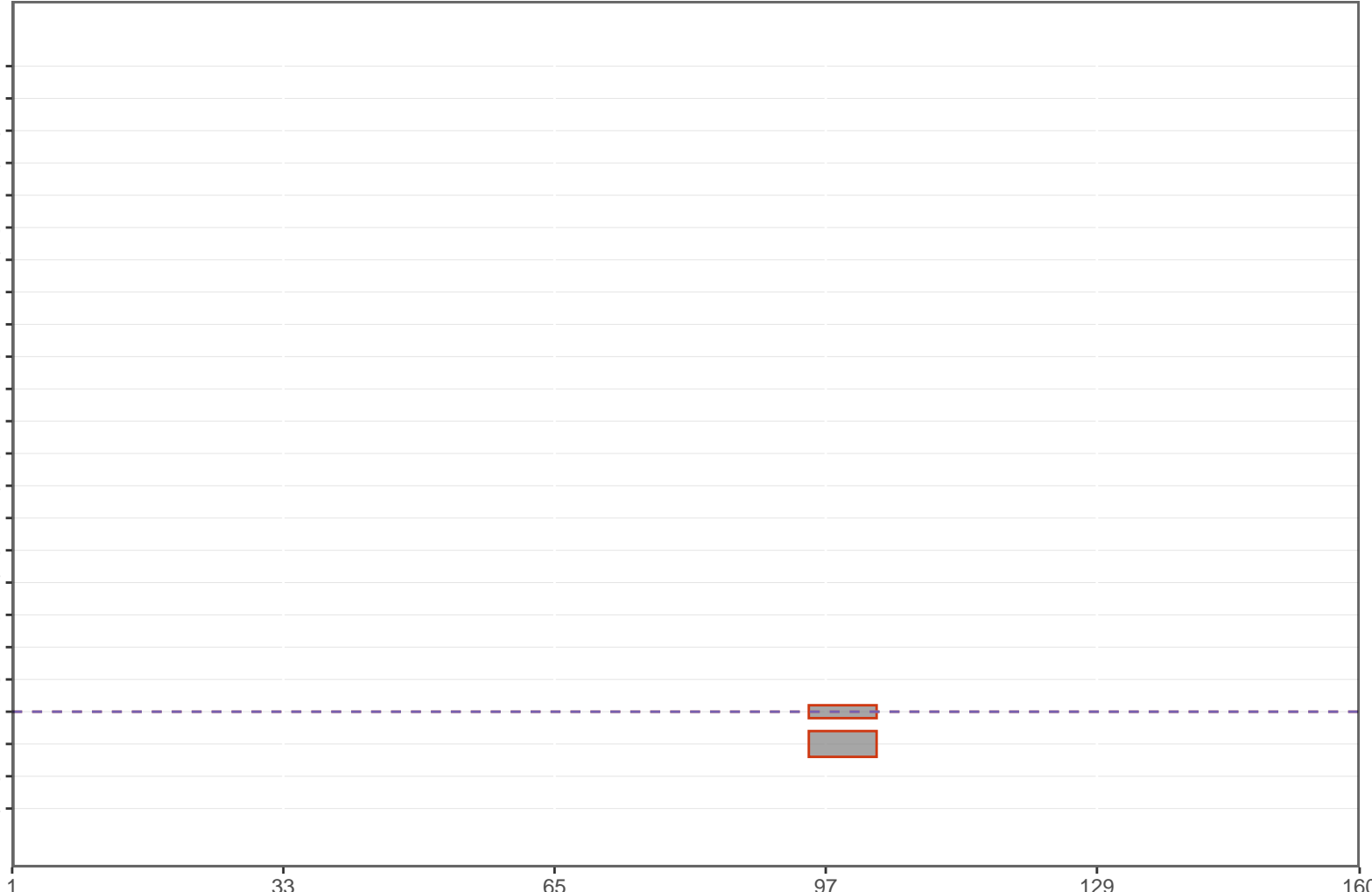
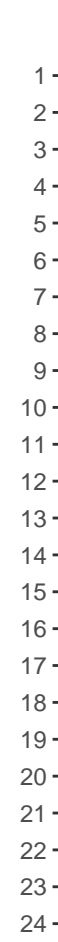
MW indication



Molecular weight



Gel Slice

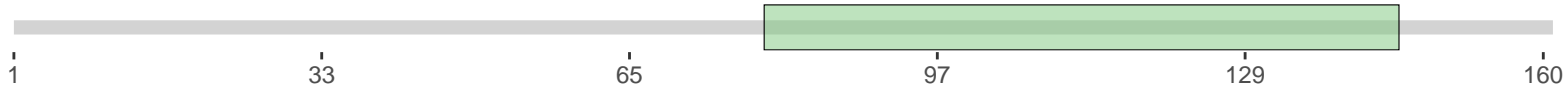


Protein length

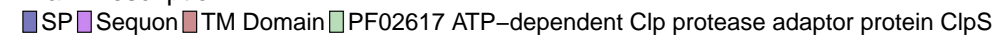


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ISEFDLRKSRXKMSPPYRVMLHNDNNYKREYVQVLMKVIPIGMVFNANVMGEAHYNGLAVVIGADAAEEHGTQLRGNGLLSIEPAGGGC

NbL15g10740.1 protein_ASPARTIC_PROTEASE_IN_GUARD_CELL_1 [MW – SP = 49.22 kDa]

No. of times detected



log(intensity)



Values from



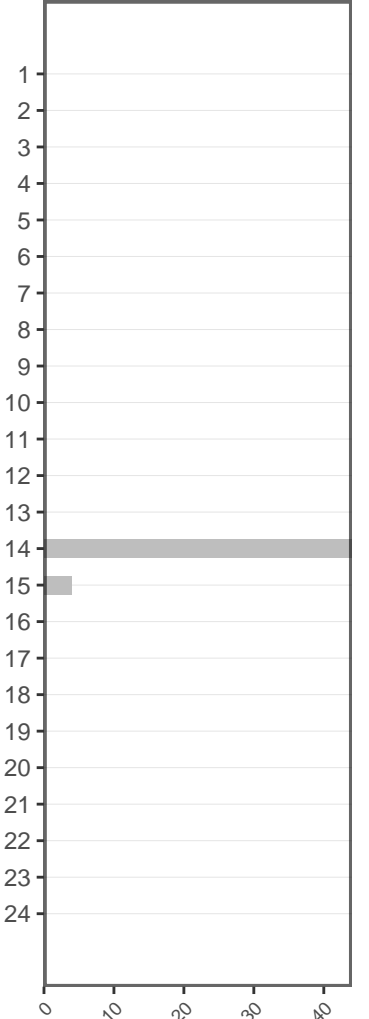
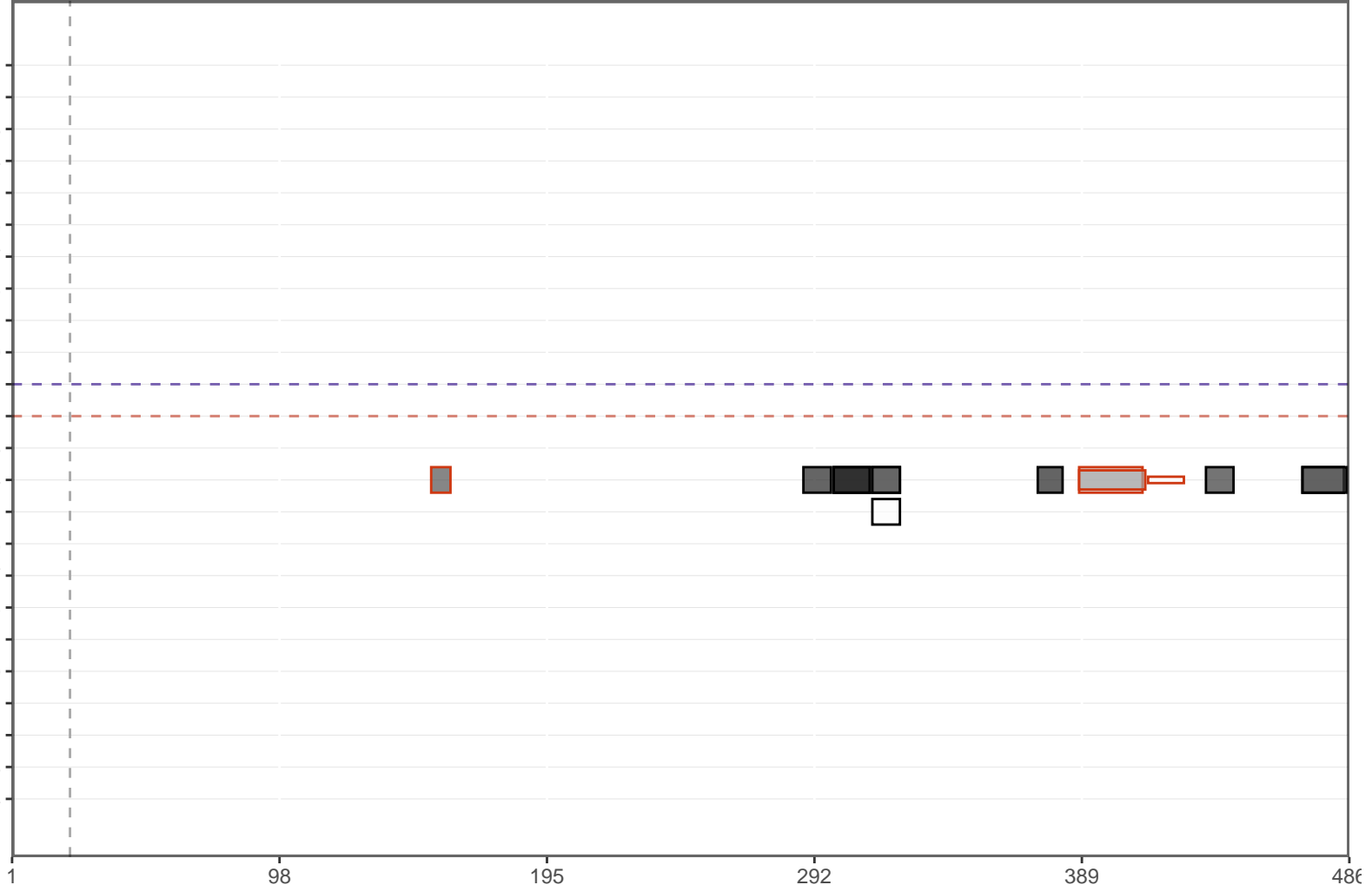
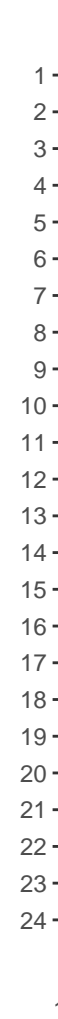
MW indication



Molecular weight

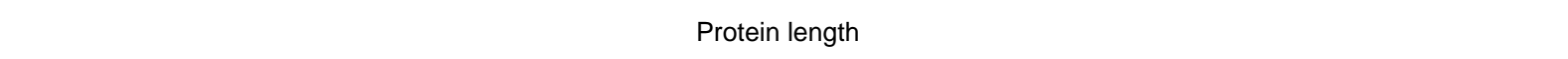


Gel Slice

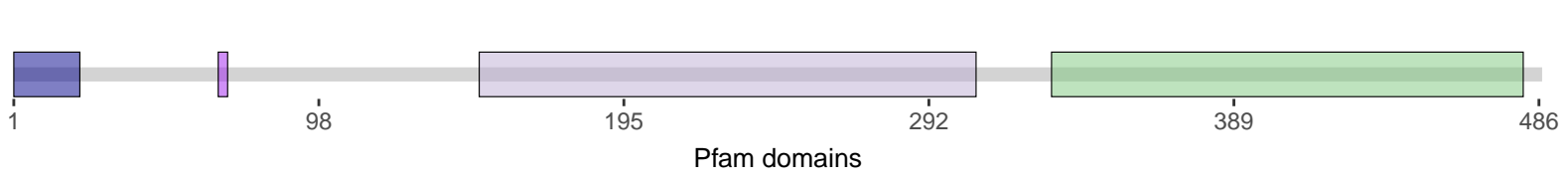


Peptide counts over 4 repeats

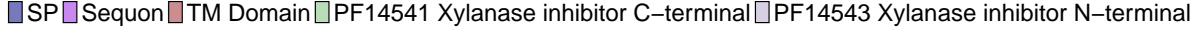
Protein length



Pfam domains



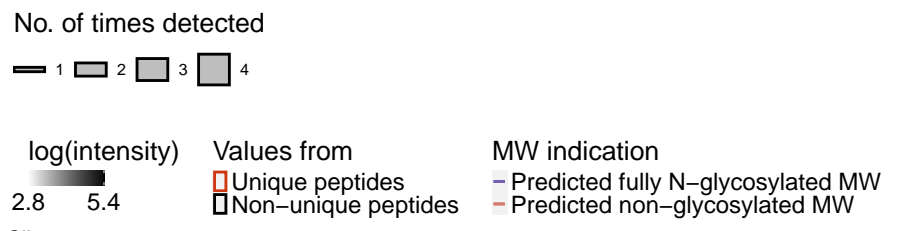
Pfam Description



Protein sequence:

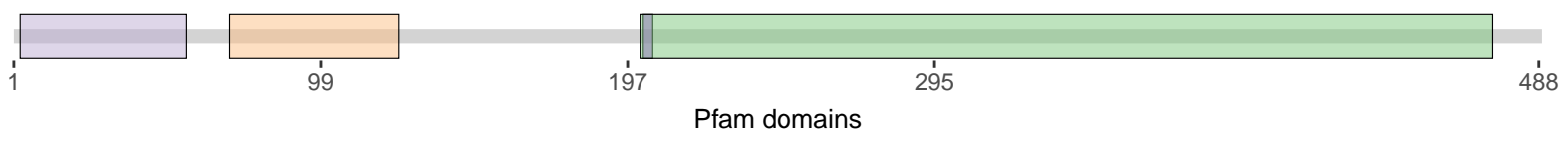
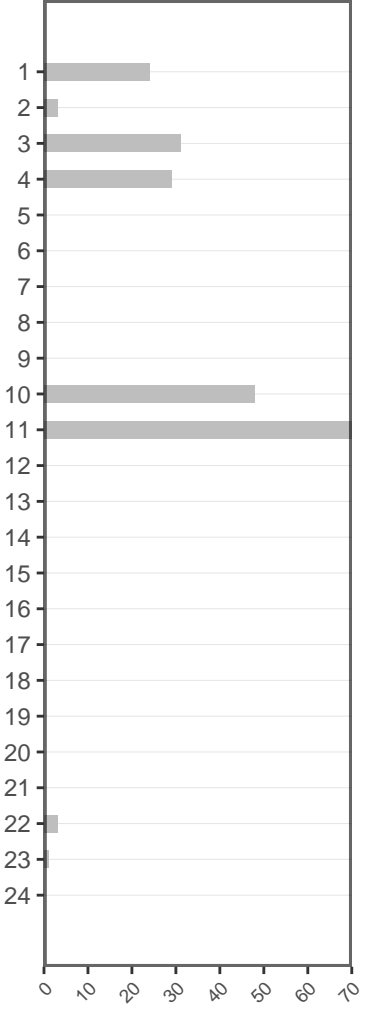
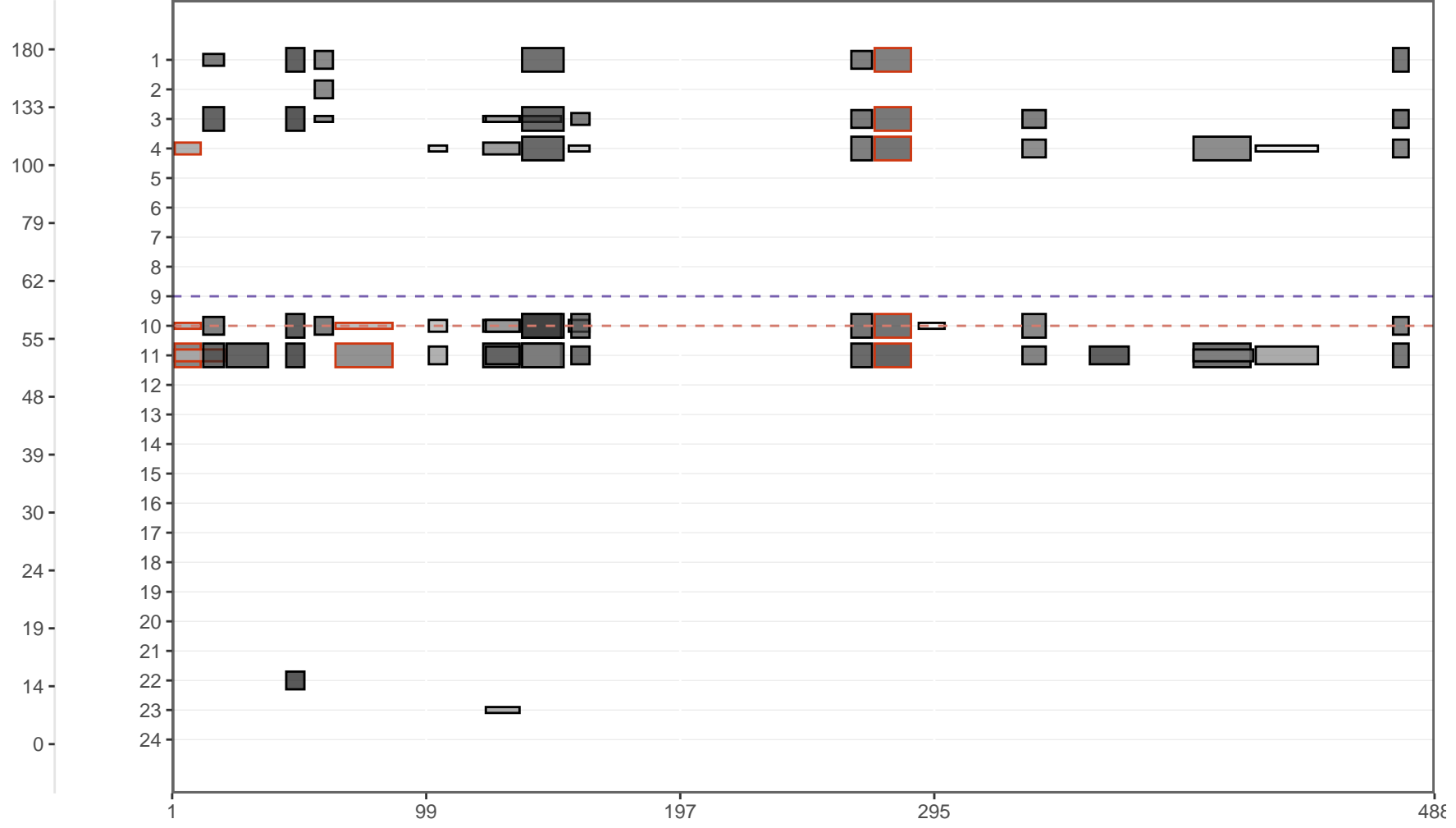
DDGSFTVGEFATETVDFGNSGAFKVAIGGGHDEGLFVAAGLALGGGTLRLPQKASSFSYCFVDRDSASSSTLDFNSARPDGDSVIAPLRNSRRSTFFVGLTGIVSGGMLSPASVFDVDSGNGGIVDSGTAVTRLGTTAVNALRDSFVKFTQNLPSGGGFALFDTCYDLSEMKVSVPTVALHFHNGDKTSLHPKHYLIPVDSGGKFLAFAPTEGSLSHGNQGGQTRVSYDLANNLVGFSPDKC

NbL15g10620.1 phenylalanine--tRNA_ligase_alpha_subunit_cytoplasmic-like [MW = 56.3 kDa]



Molecular weight

Gel Slice

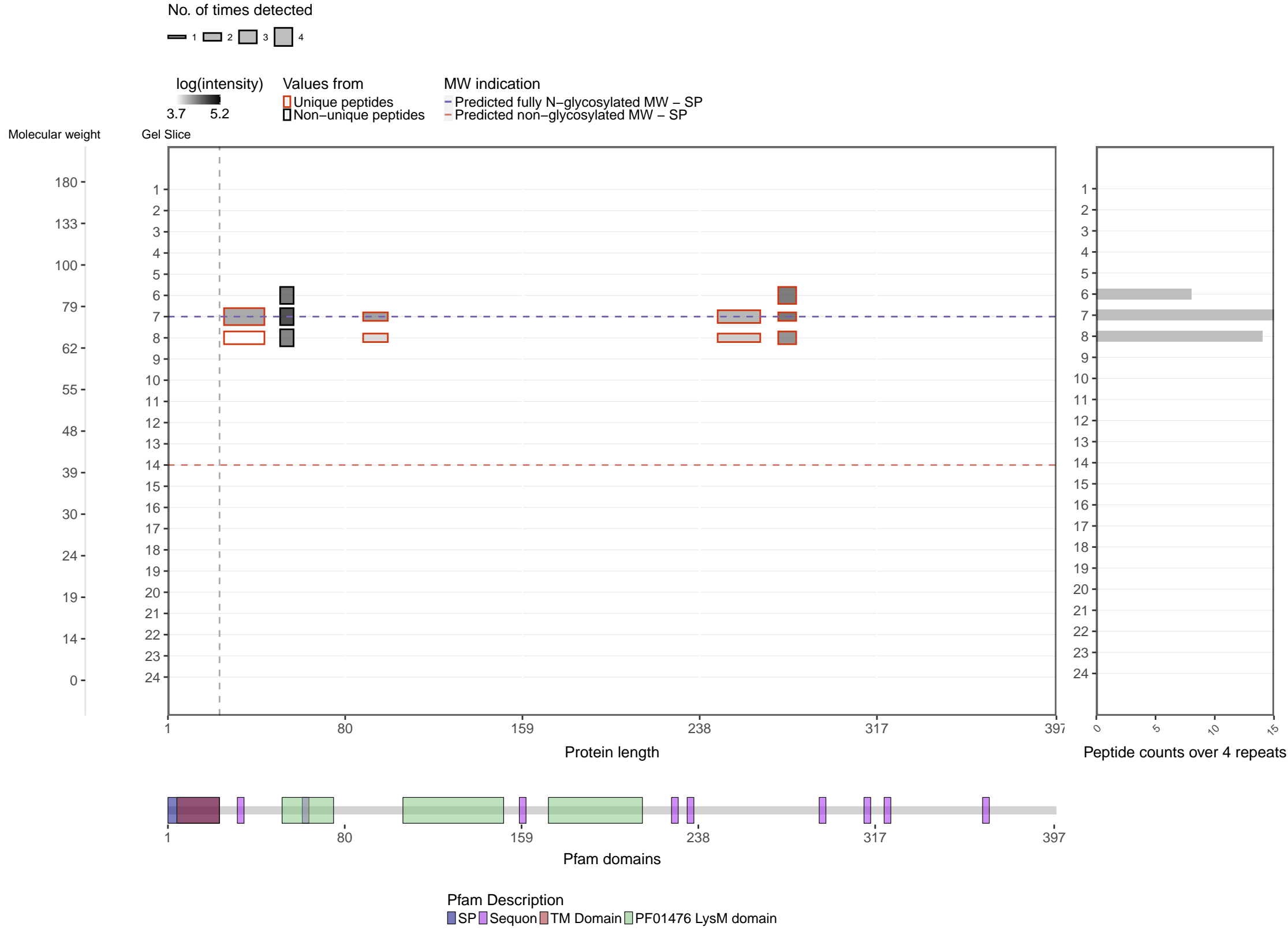


Pfam Description

- SP
- Sequon
- TM Domain
- PF01409 tRNA synthetases class II core domain (F)
- PF18552 PheRS DNA binding domain 1
- PF18553 PheRS DNA binding domain 3

Protein sequence:

IMGFEEPTNYYVSEFFWDFALFQPGQHPRDGHDTFFLKYVPTTNMLPEEYVERVKKQVHESGGYGRGQYDVKREANKNLLRTHHTAVSRMLRALGKFPAPKYYSDIVFRNEAVDRTHAEFHQIEGLHCDRLTLDLIGLVHDFARLGMKLRKPKWVNYPTESMEIFSVEGLKWKVEVNGSMGRPREMLPMGLPEDIIVRIAWGLSLERPTMILYGDNRDLFGPKVDIGLKRNPICRLGI



Protein sequence:

SVTQNLGIINGLGGPQVDPGDLAIPLAGSSANLNWYNESLIVPNSGVALTANNIKGGGRPTDLGLEGEASGIVKQDKHLQCKDSNLFIGERREKHTAFGNGNNTAGVYRGLHGGKTRFLSLVNSDVAKGLNGSGHTGLSMASPAADLALEKPSKPSKPSYFVSHSKNHTSELMNYSFPHRHSKKSLSLALHFNLMLLELLEIFL

NbL15g10490.1 40S_ribosomal_protein_S7 [MW = 25.17 kDa]

No. of times detected



log(intensity)



Values from



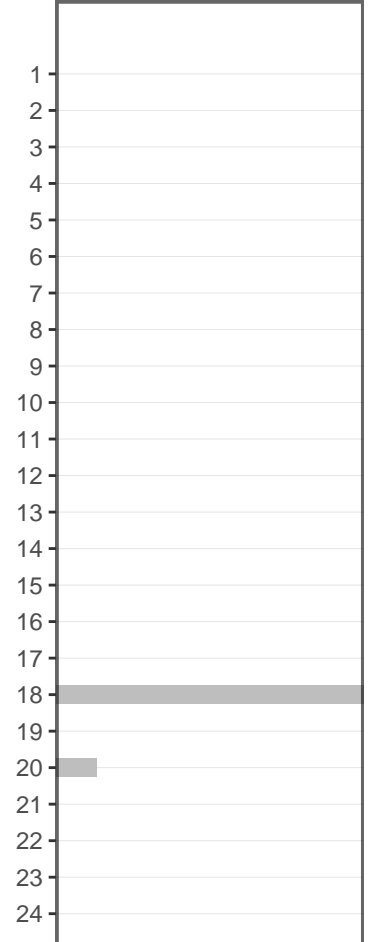
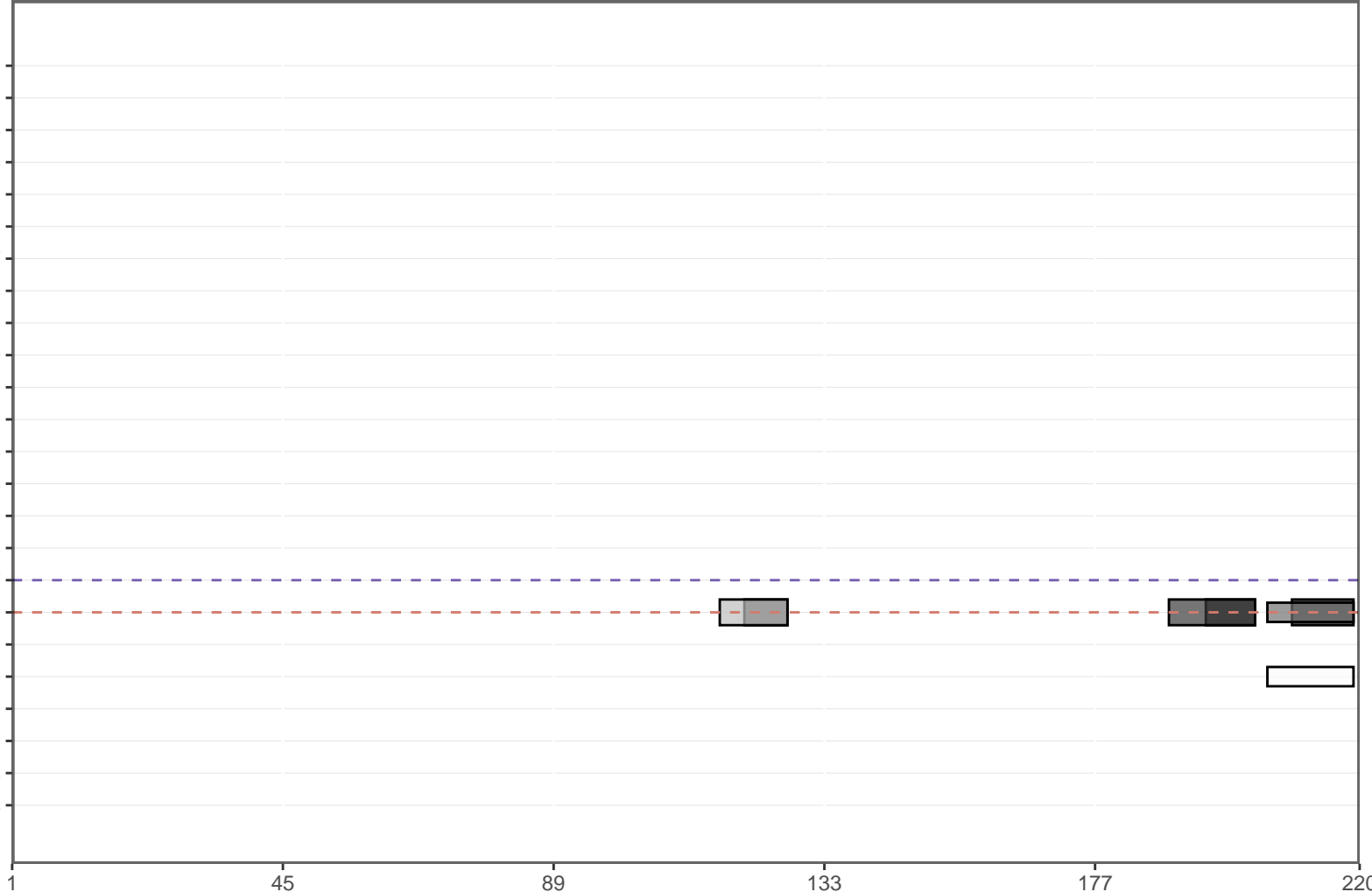
MW indication



Molecular weight

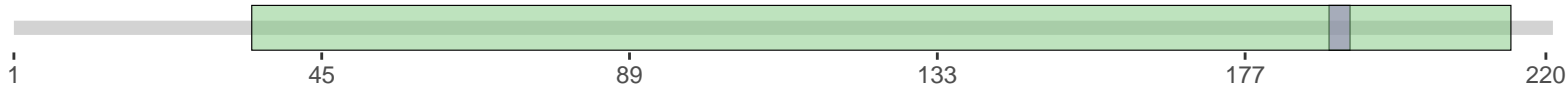


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

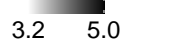
LRKAFKRVHYRLVRELEKFFSGKDVFIATRRIVRPPKRGSAQRPRSRITLTVHDAILEDLVVPAEIVGKRTFRYRIDGSKIMKVFDPKERNTEYKLETFSAVYRKLGGKDVVEFYPTFA

NbL15g10410.1 histidine--tRNA_ligase_chloroplastic/mitochondrial [MW = 56.7 kDa]

No. of times detected



log(intensity)



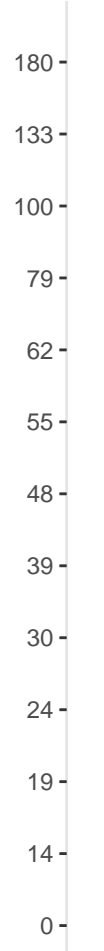
Values from



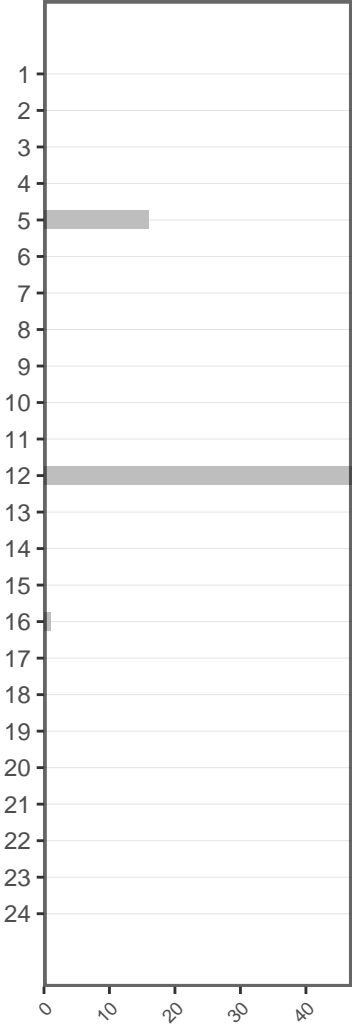
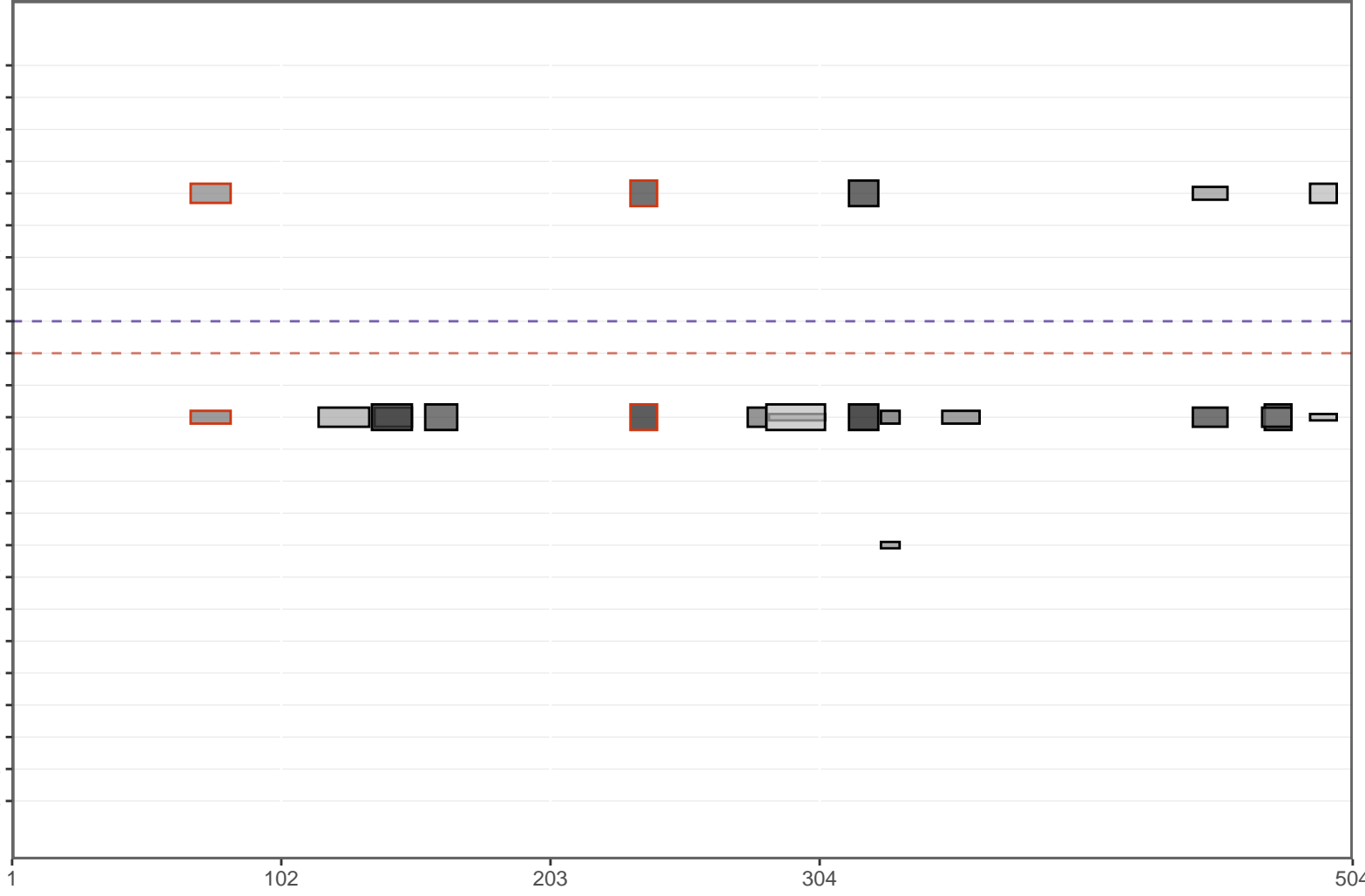
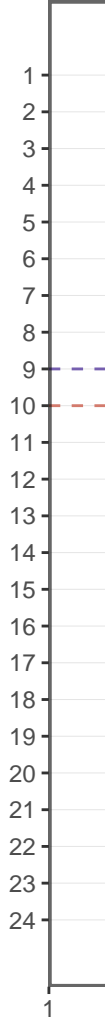
MW indication



Molecular weight

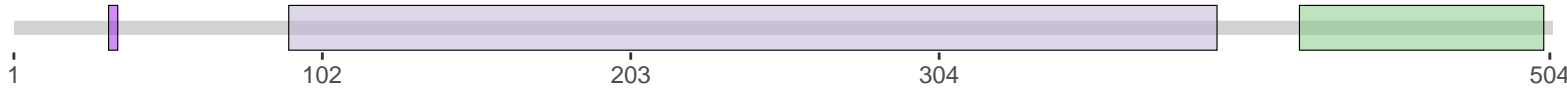


Gel Slice



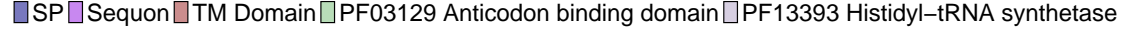
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DVGFKISSRXYLQEVLRGVYVPENFMRVGVCHIDKIKGIPMDIRKDLQGDADMSEVAIEELQVLKSLAKLEEKLGASGEALSDKGLFSLAEKYGYSEWLFQFASIVRGLAYTGVFEGFDRKRLRAKGGRRYDRLLSTFGDDLPAGFGFDVAIVVLLKERRGLLPELNLGVENVCSLQDELQGAASAWATLREKGGSDVLALENKPLKVVFKRAARINARRLIIVGNAEWQKGMNIVKTLSTGEGVEIKDELE*

NbL15g10300.1 palmitoyl-protein_thioesterase_1-like [MW - SP = 36 kDa]

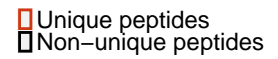
No. of times detected



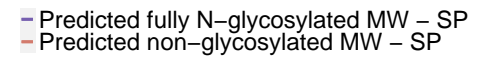
log(intensity)



Values from



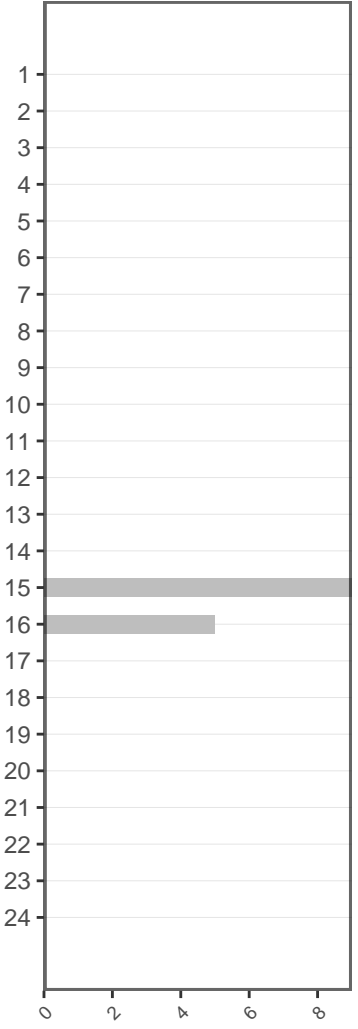
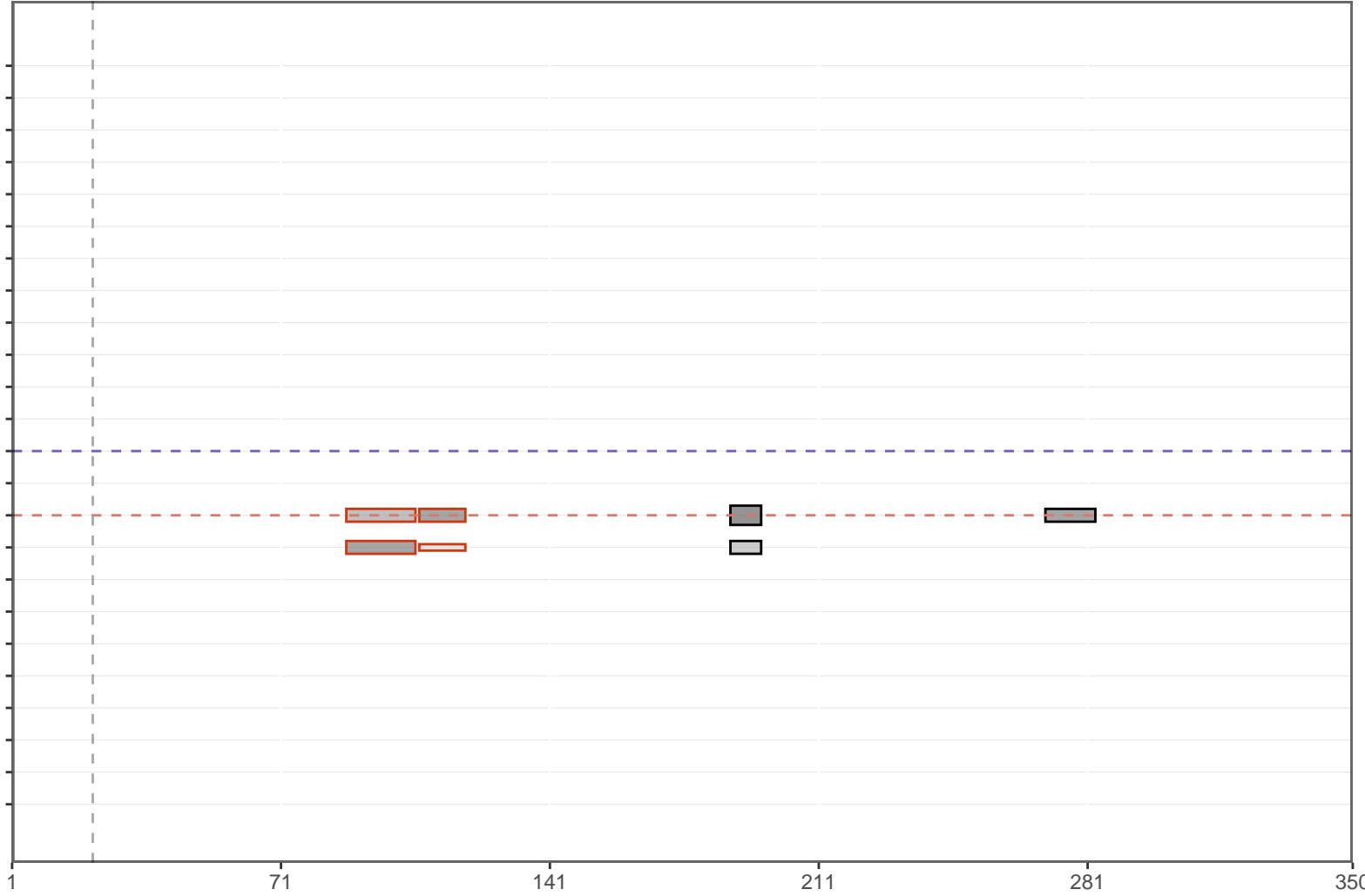
MW indication



Molecular weight

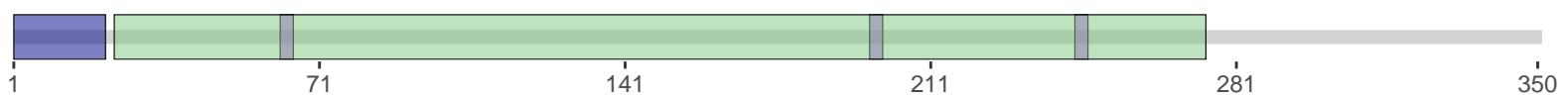


Gel Slice



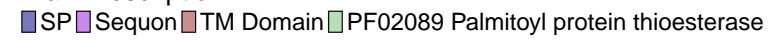
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILAPSGYLKLPNIAQYMKAGHFLPKLNNEIPSHRNSTYKKRFSSLENLVMFEHDTLIPRETSWFGYYPDGAFDPLPNNKTELYTEWGLKLTLDGSGKQVYKVAQNHQISGSSDMRKHVVPYLAENAADGSSVDVESMMHGLQDESSTIFFEGSSSYNAPAPKSFADLLGLTDEGVS

NbL15g10190.1 peroxisomal_acyl-coenzyme_A_oxidase_1 [MW = 74.28 kDa]

No. of times detected



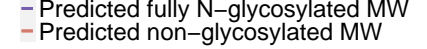
log(intensity)



Values from



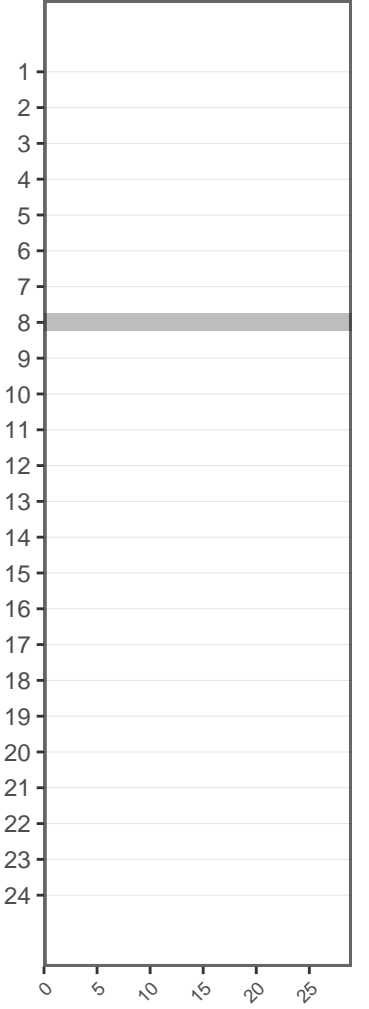
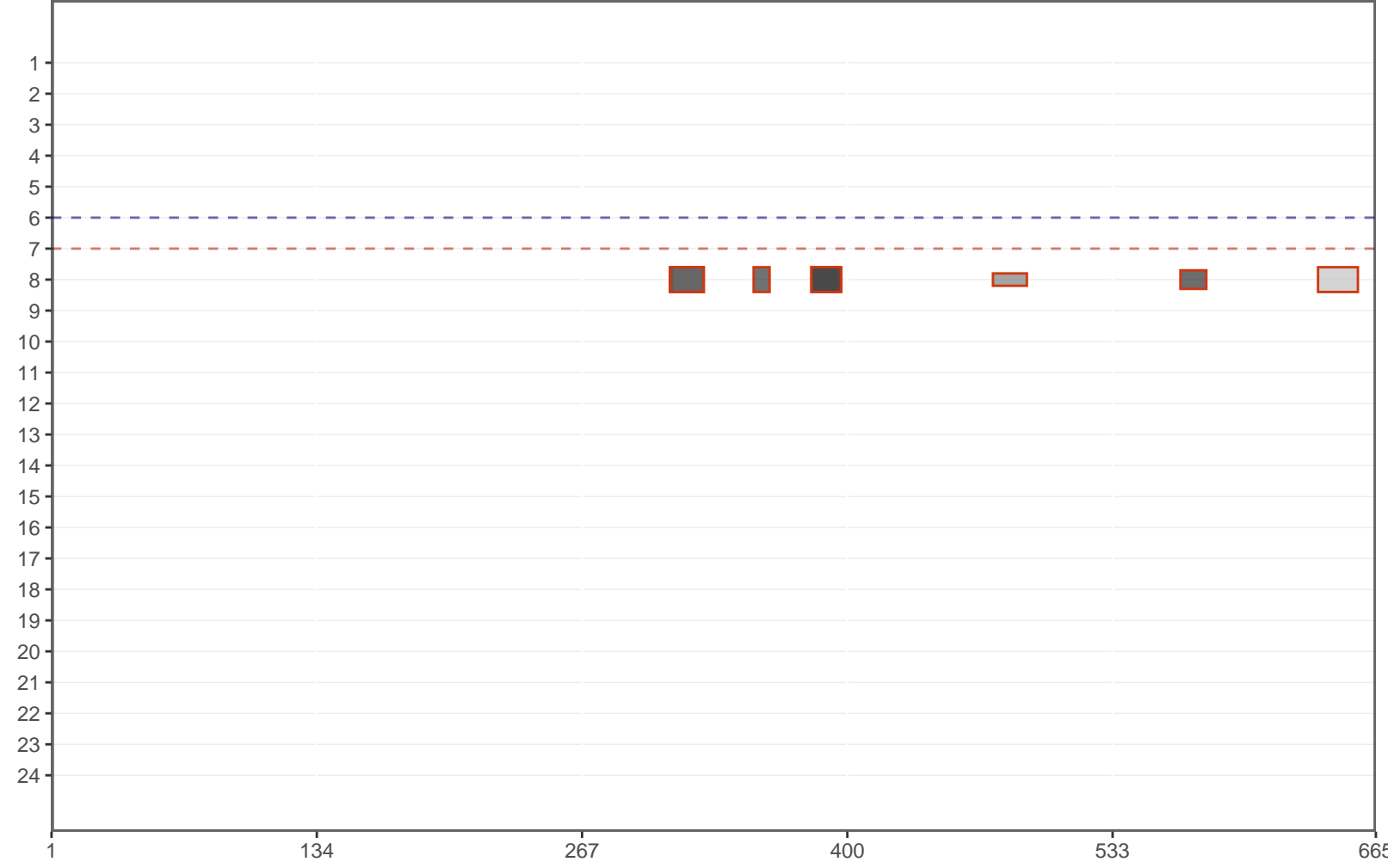
MW indication



Molecular weight

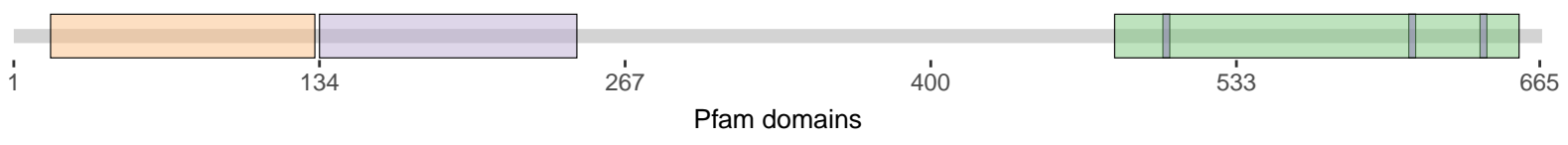


Gel Slice



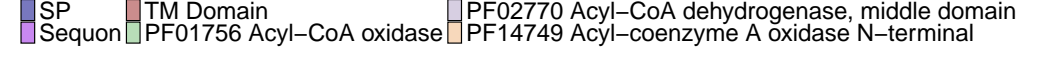
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SGQEIQVIGYKTOGSRLEFLLASAWFRFVGDWIKWLHTDVTORLQANDFSTLPEAHAGTGLKSLTTFTDAGIEECRKLGGHGVLGSSGLPELFAVYVPACTYEGDNTVLLQVAFLEMTKTVSGLGSGKKPKVGTISYMGKIEHLMGCRSDVKGADWIKPVSVALEAFEARAARMSEVAGAGNLKSKFDNPEEGFAELAADLAEAAVAHCGQLVWVKFKLGGDIPGKGVGQLEVLGGYSFLHKKHQADFLGTGVTTSKQASLANDQLRALYKLRPNASLVDAFNYYD

NbL15g10070.1 uncharacterized_LOC109231245 [MW = 231.86 kDa]

No. of times detected



log(intensity)



Values from



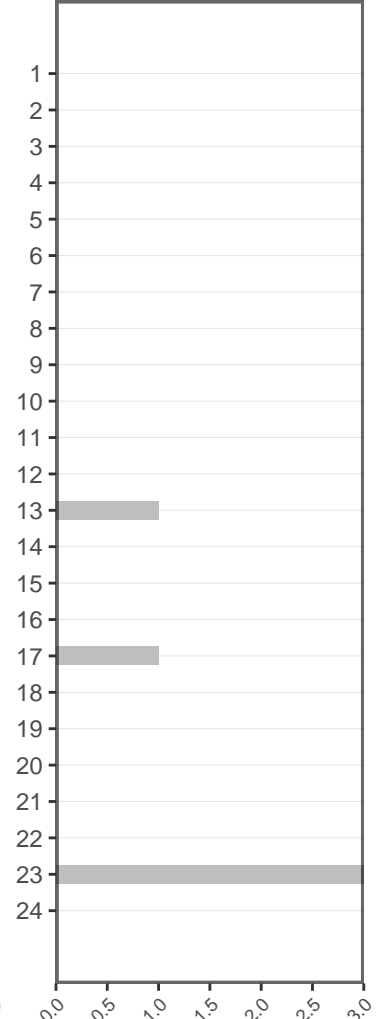
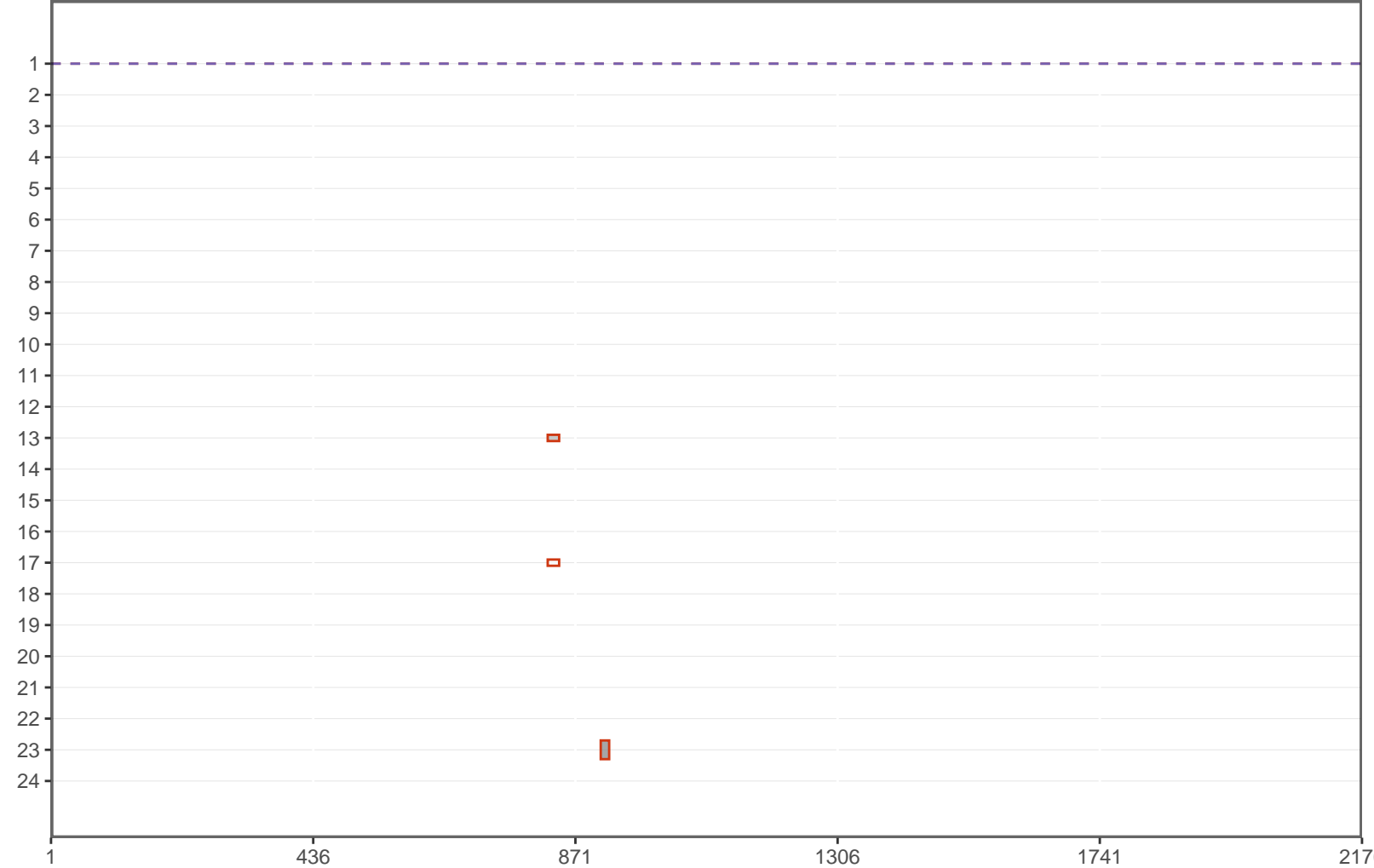
MW indication



Molecular weight



Gel Slice

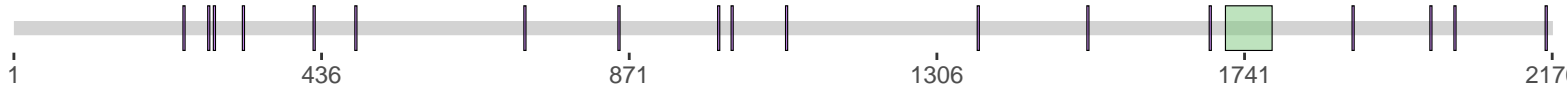


Protein length

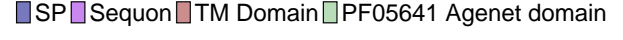


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

DRIRGQRSHITGNNETPSHPRSGPRTPDQANKVMHQKNTTPAAGRAAGKANSRAVSPHFLSSPLWNIPTFGDGLPSGGMARGAVIDKALSFMHHPQTPTRNFVGHSTAGWLPQAPFFSGVWASFPQISAFPLPVTPEVWLTFTPKESLSISAGAKHATPVGVVAHAGEGSLAGASPRDEKAKLLSADGKSRKRKKAAGTDRHAKSLRGTSSSEVPAWVQTLGSSKAPASDNFGGSSVAVAFPLWAGSGTGPAWAAPLGHFSTEVVAIPLSSAPINNSDPISTP

NbL15g09790.1 autophagy-related_protein_8f-like [MW = 14 kDa]

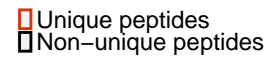
No. of times detected



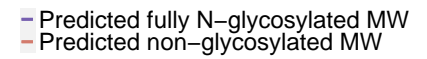
log(intensity)



Values from



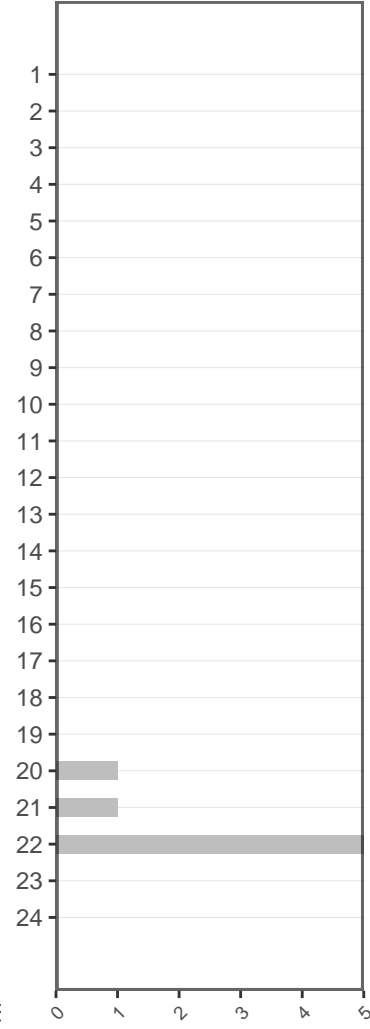
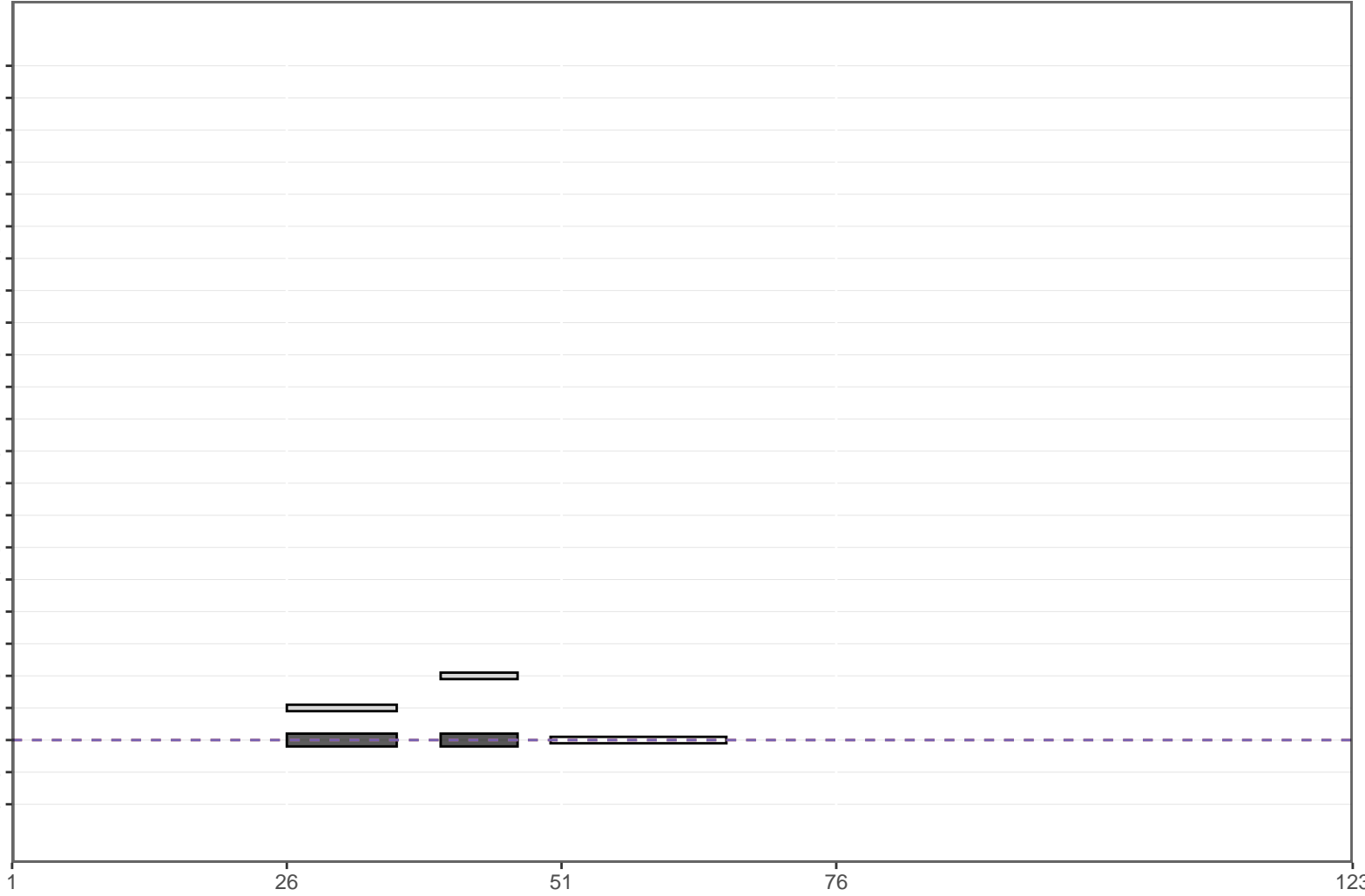
MW indication



Molecular weight

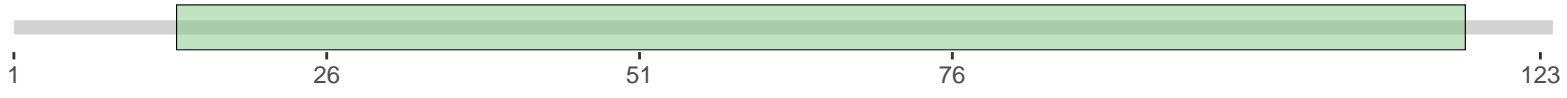


Gel Slice



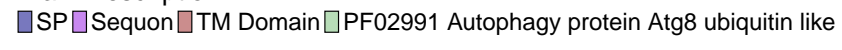
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

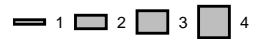


Protein sequence:

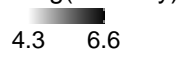
00KLYLPDLTVGDFVYWRKRKLSAEKAFIFIDNALPPTGAI8A8YDEKDKEDGFLVYTYSGENTFGDRLNLS

NbL15g09670.1 adenine_phosphoribosyltransferase_3-like [MW = 20.03 kDa]

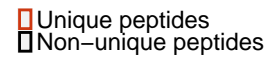
No. of times detected



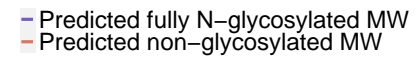
log(intensity)



Values from



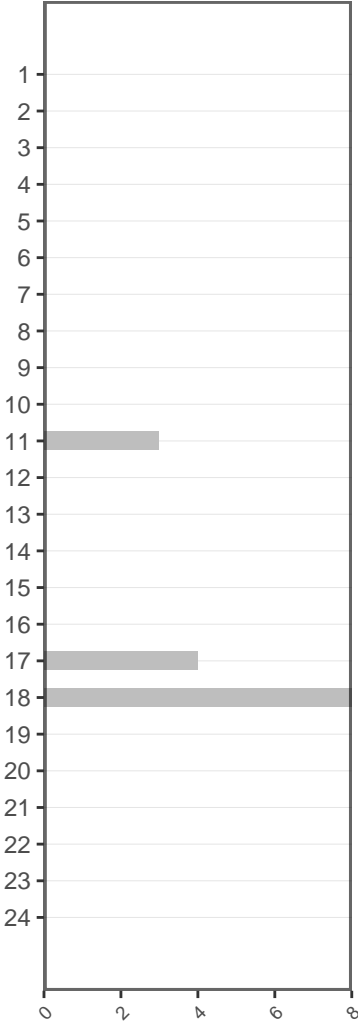
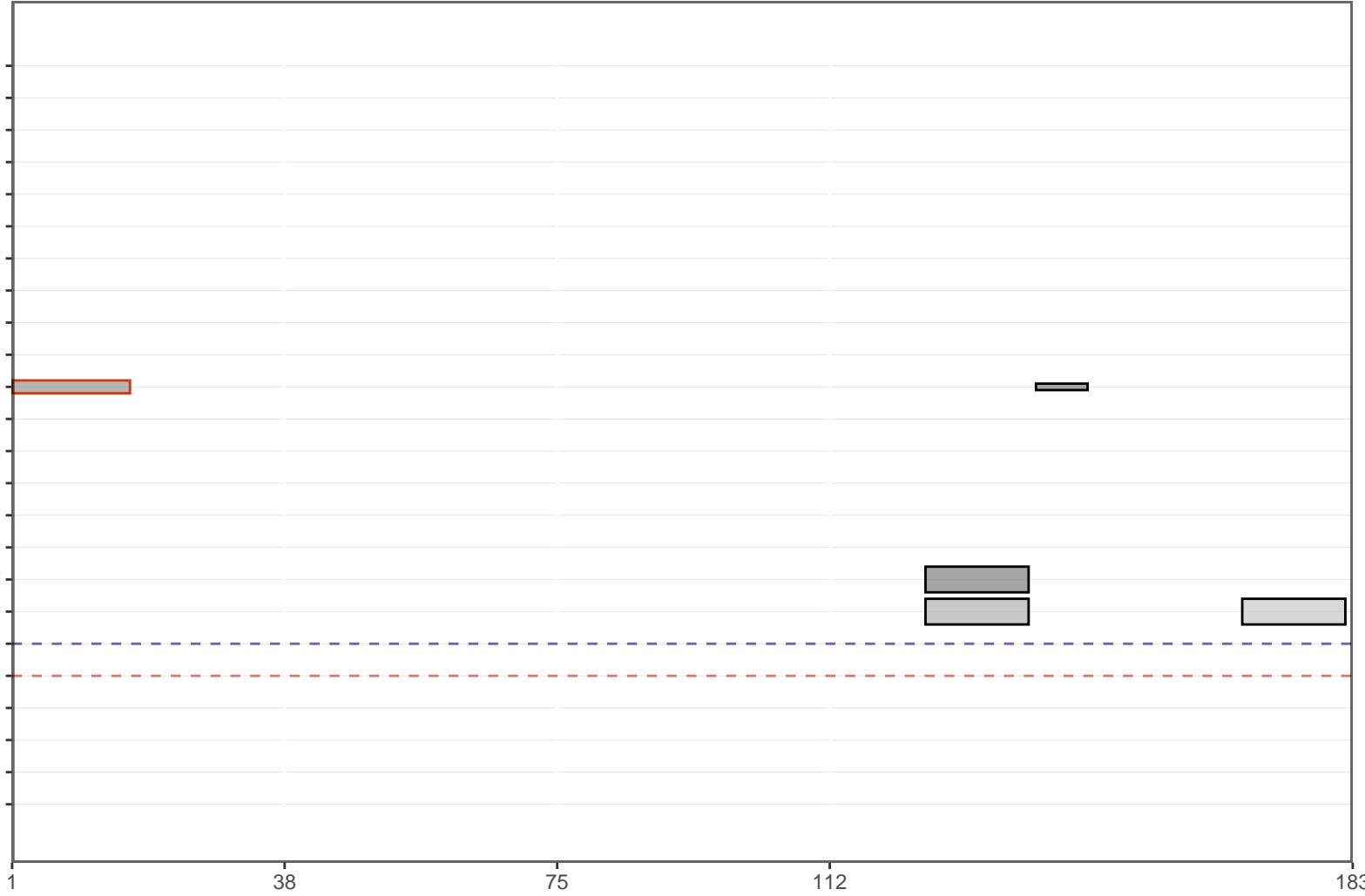
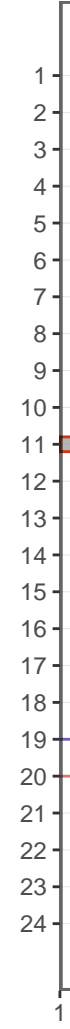
MW indication



Molecular weight

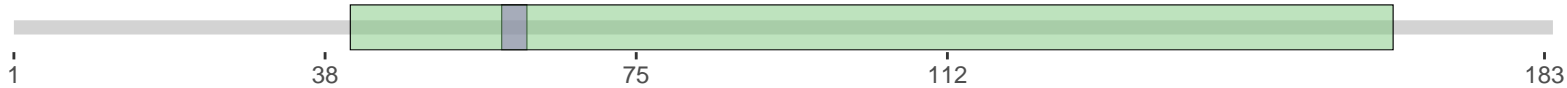


Gel Slice



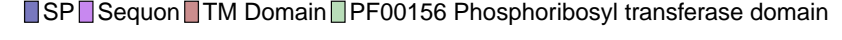
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MGAKYVPLRFPNKLPGKVFHGEYDLEVGSDGLEMHGAVEAGERALVVDLIATGGTLRAMNLLERADAEVVEGAGVIEIPDLKKGEGLNKPLVLYVEGQ

NbL15g09610.1 transaldolase [MW = 48.02 kDa]

No. of times detected



log(intensity)



Values from



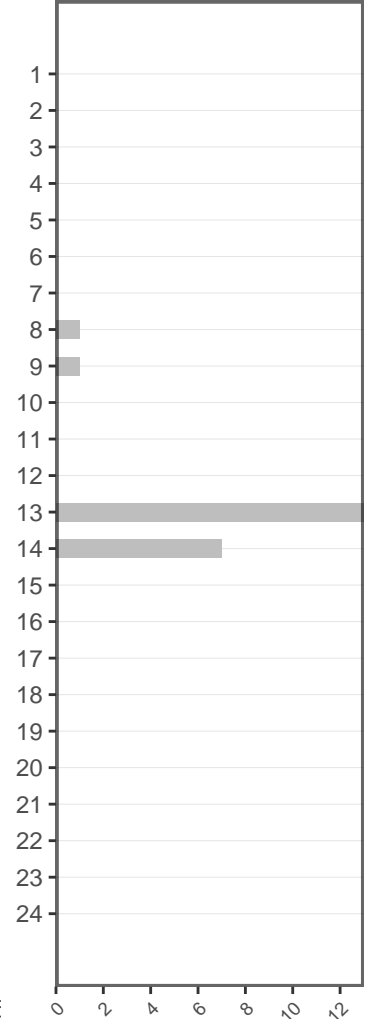
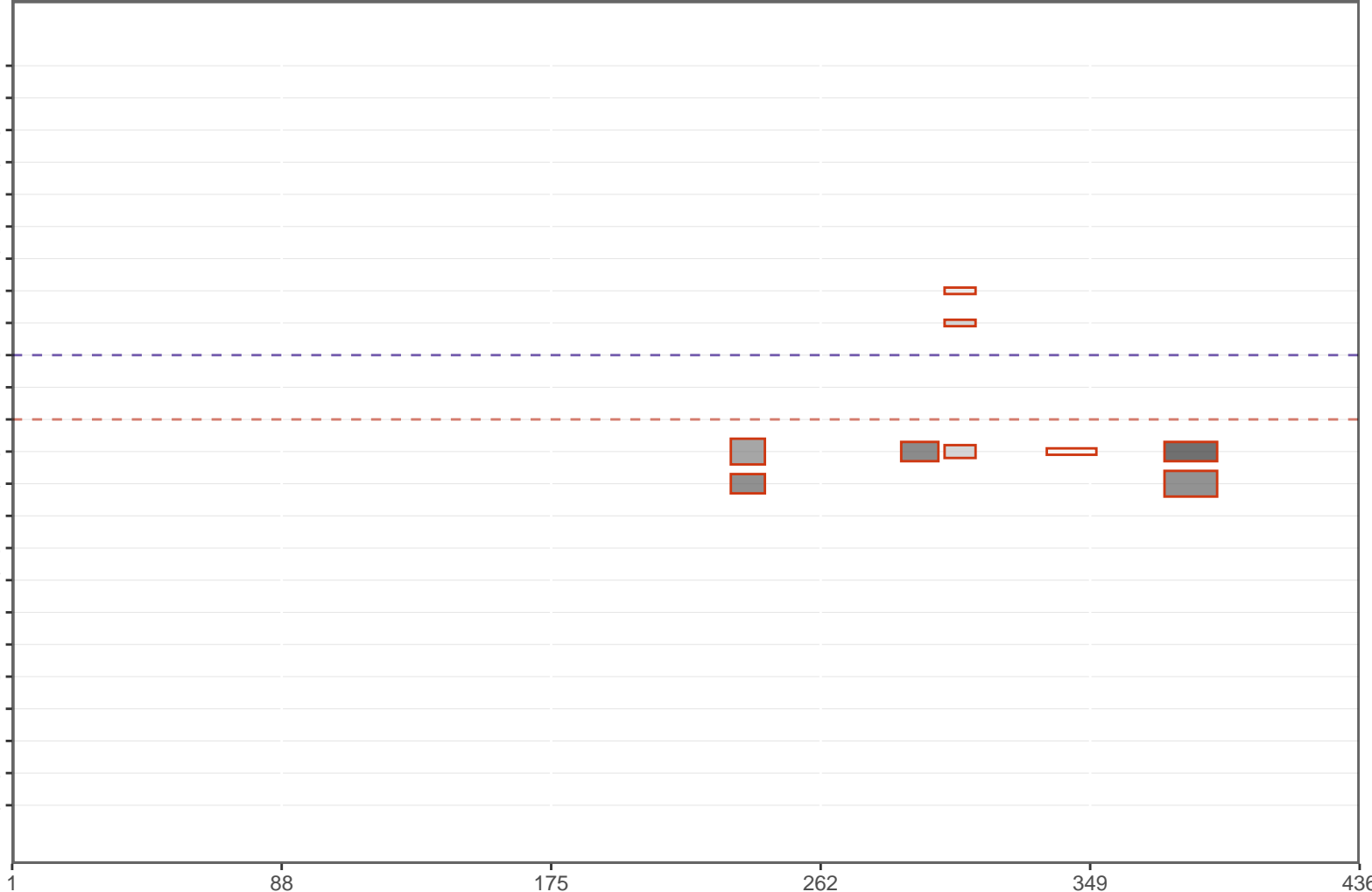
MW indication



Molecular weight



Gel Slice

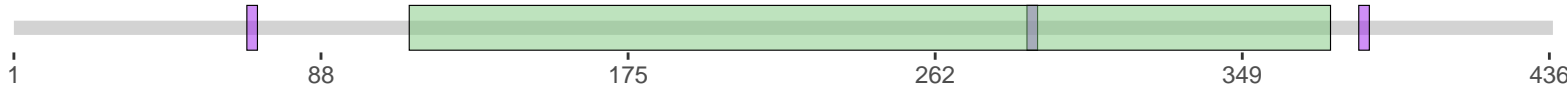


Peptide counts over 4 repeats

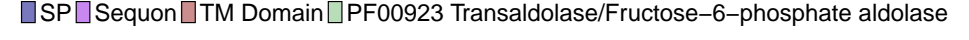
Protein length



Pfam domains



Pfam Description

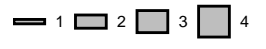


Protein sequence:

HGIVRKVHDLKAYNEIEVPERLLKIPATWGGIEASRVLEAEGIGTHLTFVYFSGDAAAAGAGASVQIFVGRLRDWSRNHTGDSEIESALKRGEEDPLGALYTKAWYHKYHKSKLMAAAVRRNKGDVFNLLGVGVHTPLKVLQSLKEVTPDDEKYSFIRRLSPGSAAAFNFDTDELGKWDQVYFSSSAMGPAALVELLTIGMDGYTNGAKRVEEFFGKRWPPFNV

NbL15g09590.1 monocopper_oxidase-like_protein_SKU5 [MW – SP = 63.74 kDa]

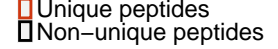
No. of times detected



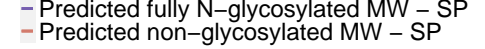
log(intensity)



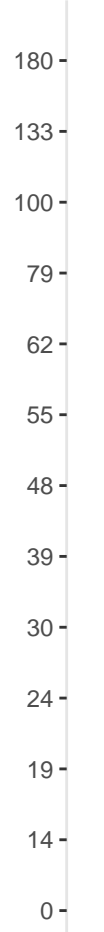
Values from



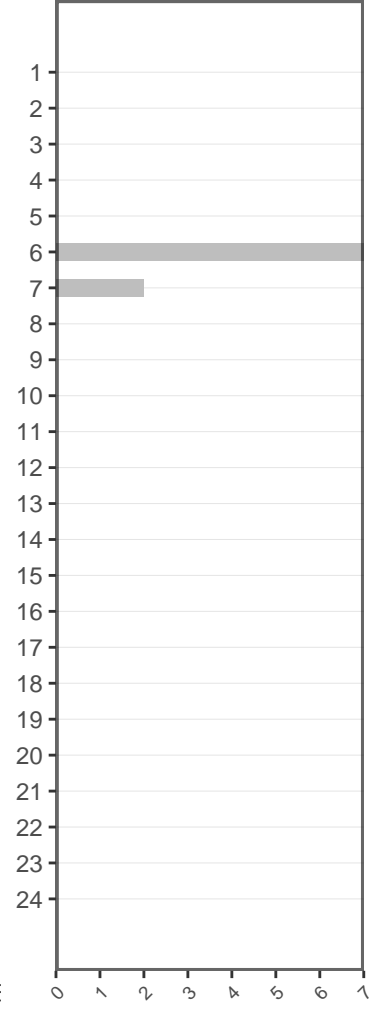
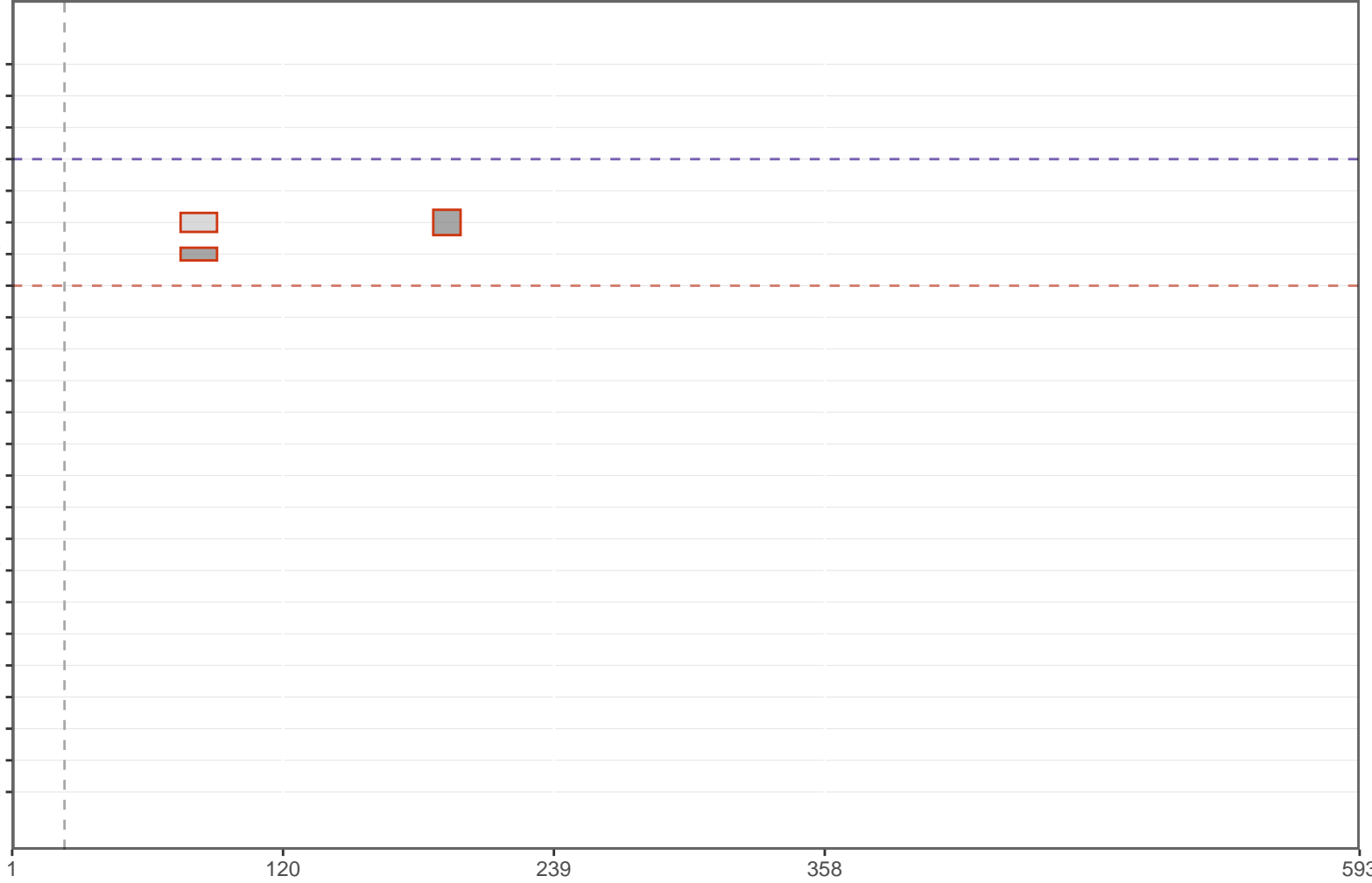
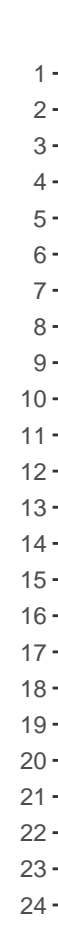
MW indication



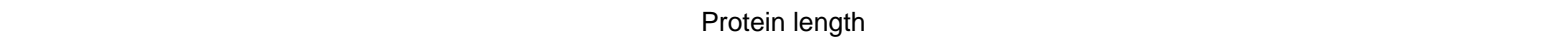
Molecular weight



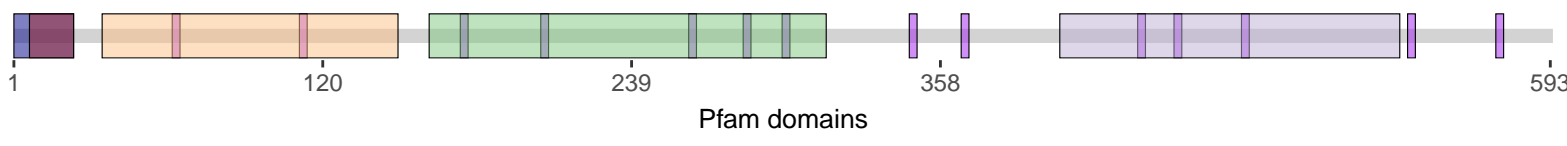
Gel Slice



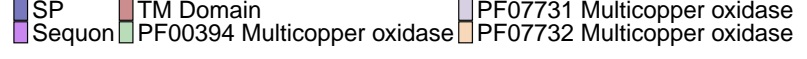
Protein length



Pfam domains



Pfam Description



Protein sequence:

ISDYIYASARFYNGSGWGRVETGVGLKYTNKGGKAHGLPEPPQDEFDKTYSMNGARSRIRWVYASGARPNPQGSFRYGSNVTEIYVGNKPPMTMDGKRRFTLNGISFYNPKTRLRADKYKLVGKLVKDFPTAPLTPGPKMETSVINGTYRFGMEHLQNNDRKHVHTYHMSGYAFFVVGMDYGVWNSNSRGTYNKWDGIARTTQVFPFGAWTALVLELDNNGVWNLRTENLDGWFVLSGOETVIRVYVNFPEPNKTEMPMPDNLFGGGLKLGKPDQSSATSIRGNQSP

NbL15g09570.1 thylakoid_luminal_protein_At1g12250_chloroplastic [MW = 28.5 kDa]

No. of times detected



log(intensity)



Values from



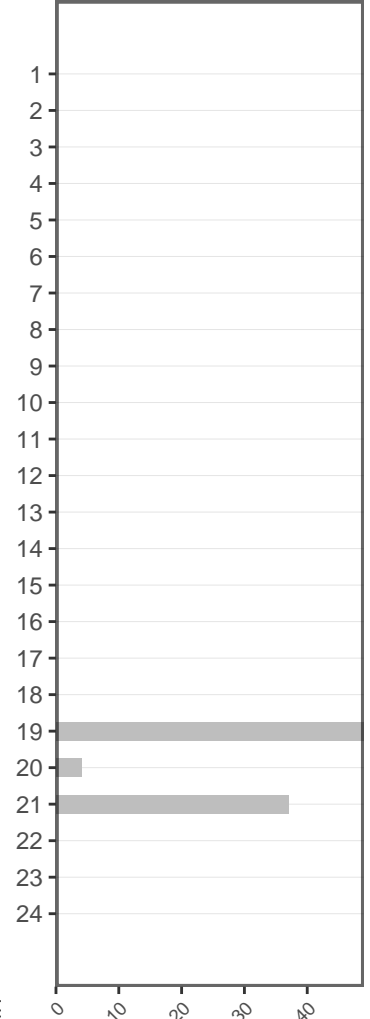
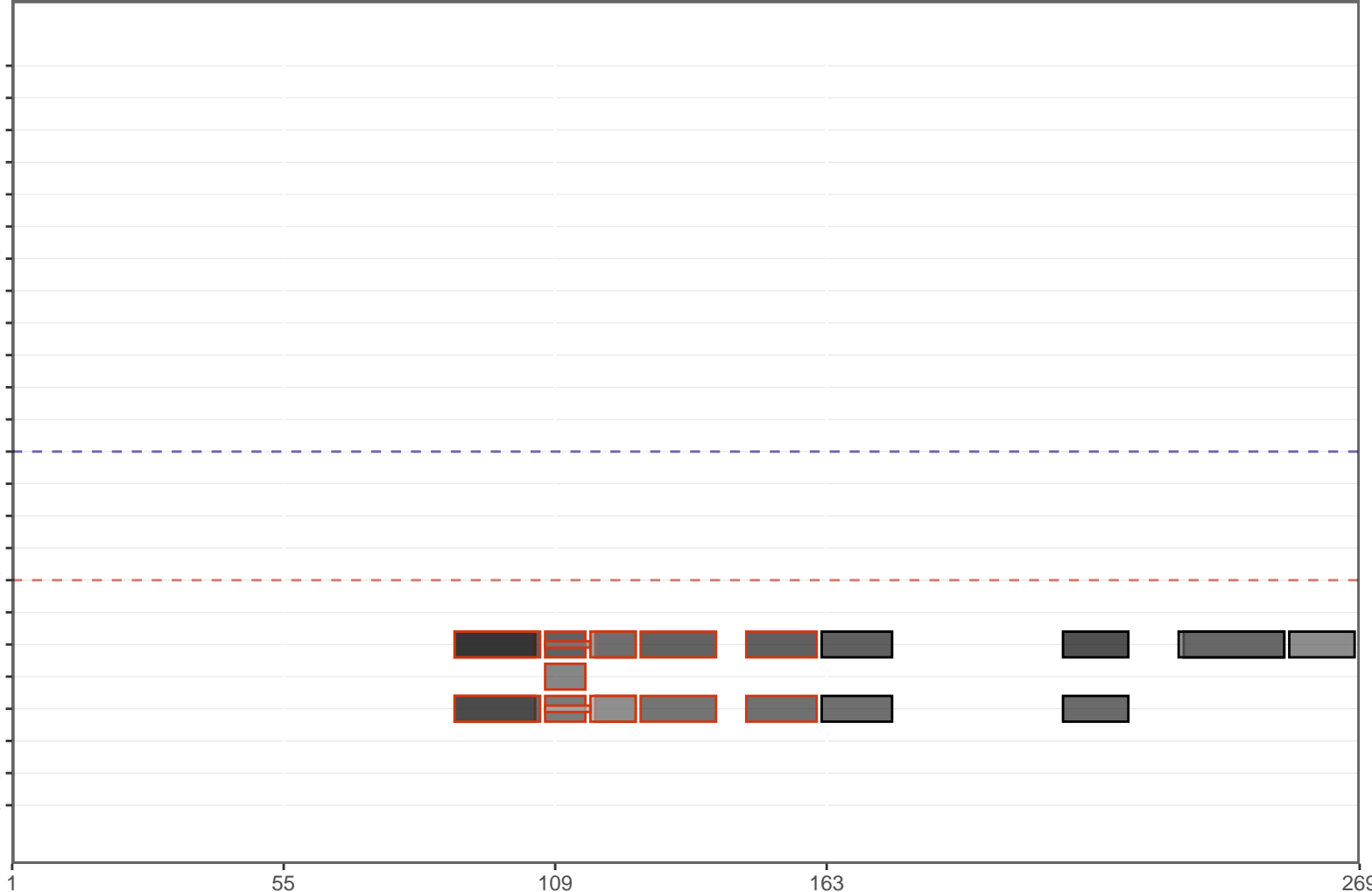
MW indication



Molecular weight

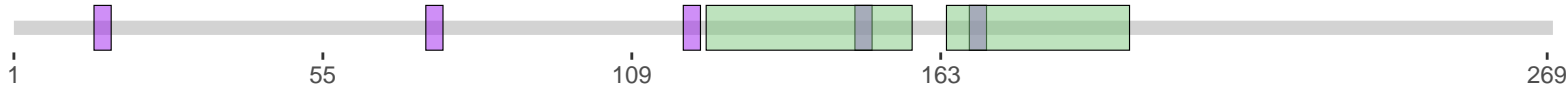


Gel Slice



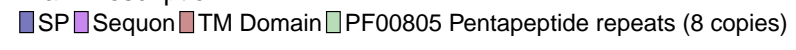
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

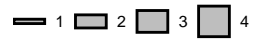


Protein sequence:

DMRESDFSGSTFNQAYLEKAWKANKFSGADLSDTLMDRMLNEANLITNAVLRVSLTRDLOGAMEGADFSDAVIDLLGKQALCKYAGTNPVTGVSTRKSLGGCNRNRNAVSPSPPLLSAPPQQLLRDGFCDPTGLGDAS

NbL15g09520.1 hsp70-Hsp90_organizing_protein_2 [MW = 67.64 kDa]

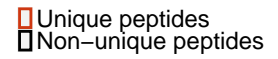
No. of times detected



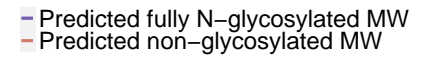
log(intensity)



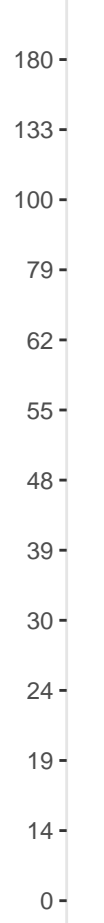
Values from



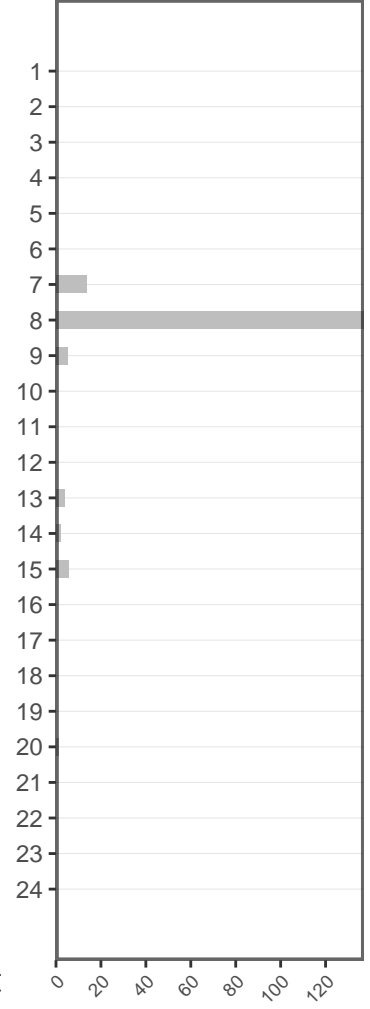
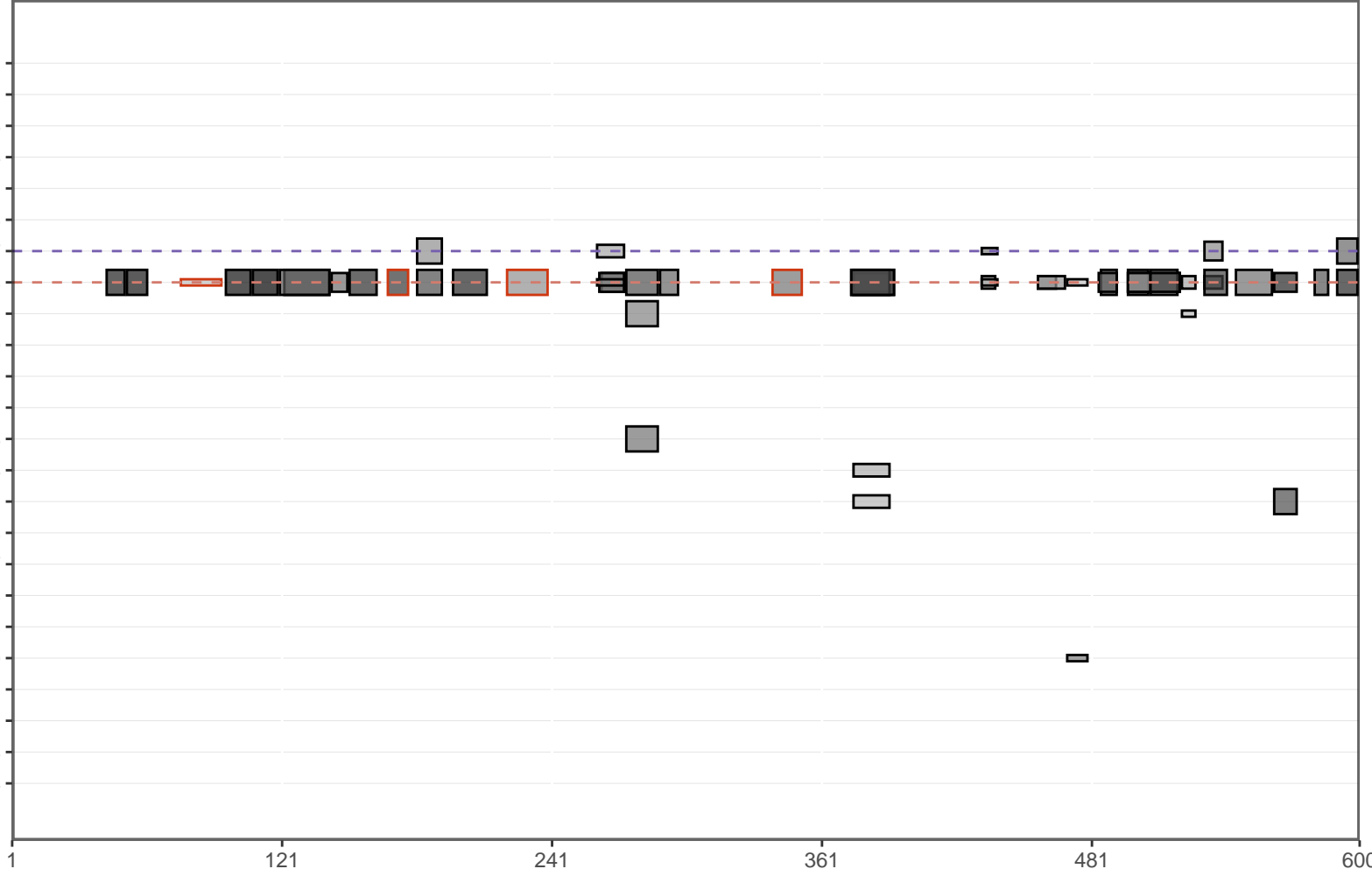
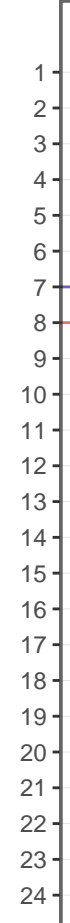
MW indication



Molecular weight

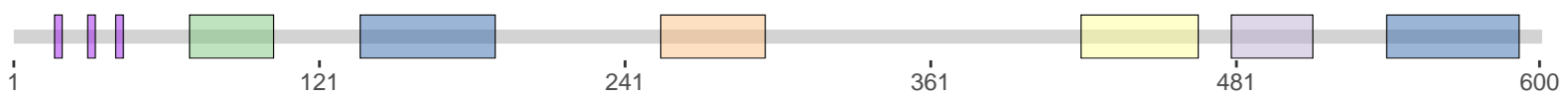


Gel Slice



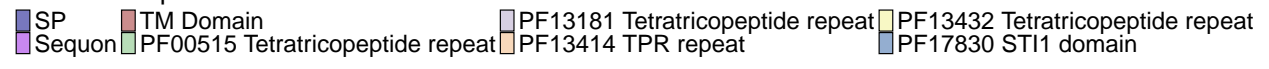
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IRAAVYLEMGKYEDGKIDGQAVRGRGLRSDFKMARALTRKGTALAKMANNKDFEVAIEAFQKALTEHRNPDTLKLNDAEKARKELEGGVEYFNQIDAEEREKGFLLMLSELYSYVGNFLHYVAGNGFFKEMKYPFAVNHHTESIKRINPKDPRVSNRAADYTKLALPEGLKDAEKGEIDPTFVKGYTRKGAVQFFMKEYEKAMETVYQEGLKHDPNGELLDGWRKGVQINRGSFGDLPPEELKERGAQKMGDPFEKINLTDPAVRGVLTDQENPKAAQDP

NbL15g09510.1 elongation_factor_G-2_chloroplastic [MW = 86.04 kDa]

No. of times detected



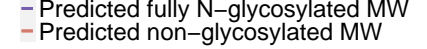
log(intensity)



Values from



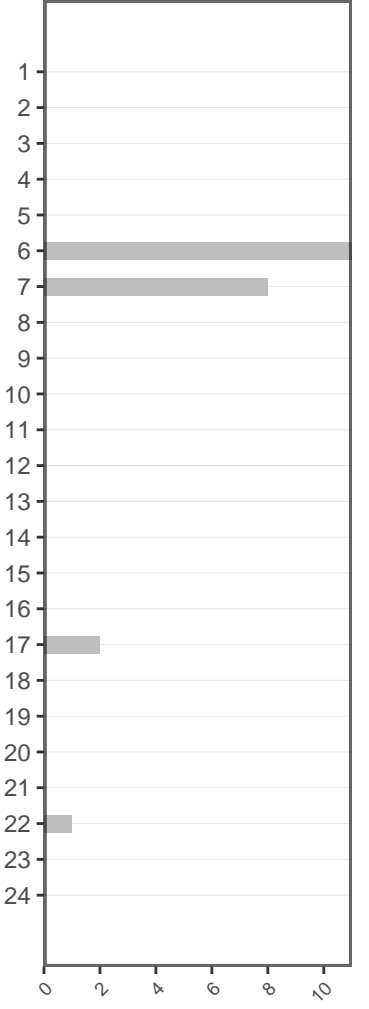
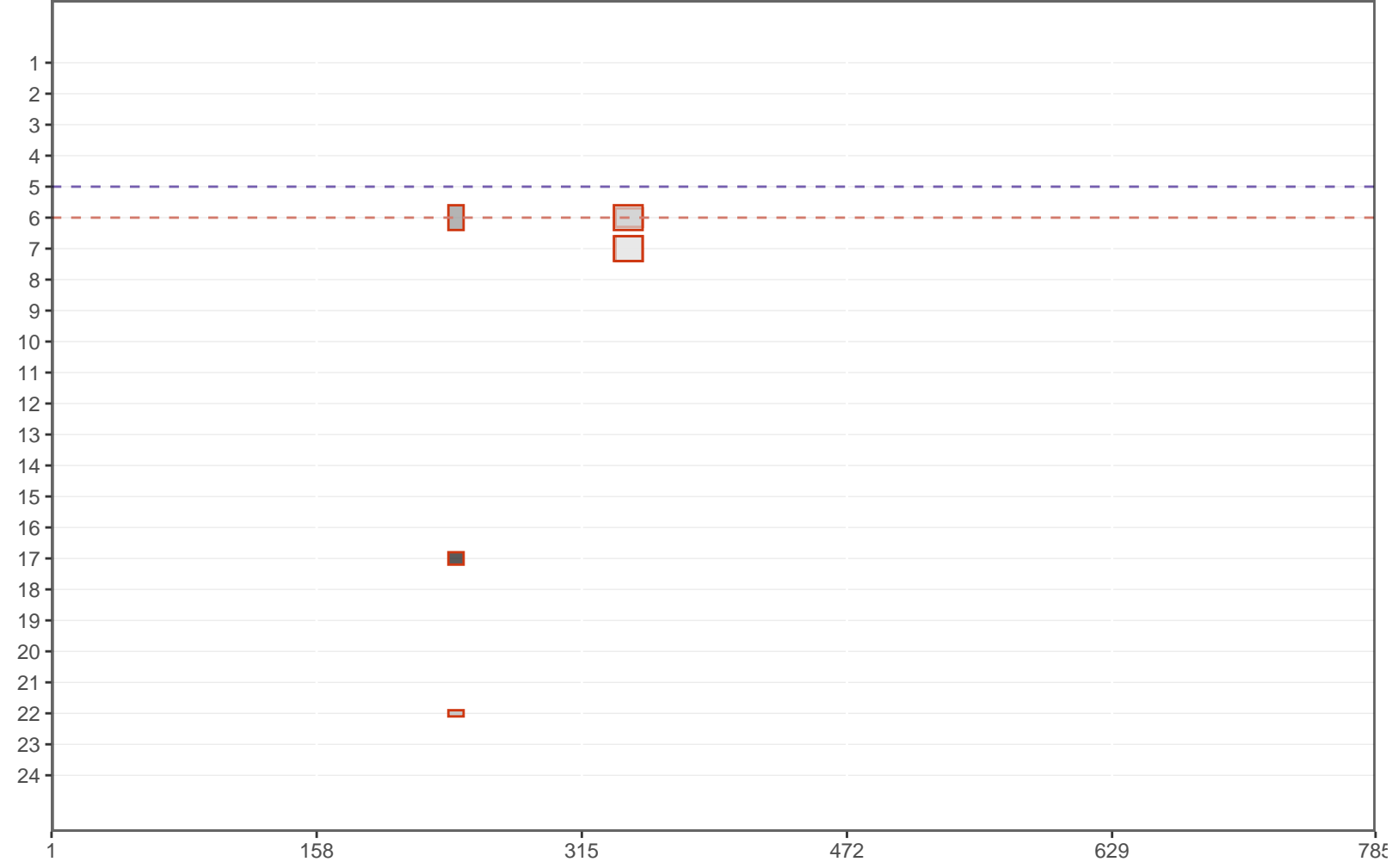
MW indication



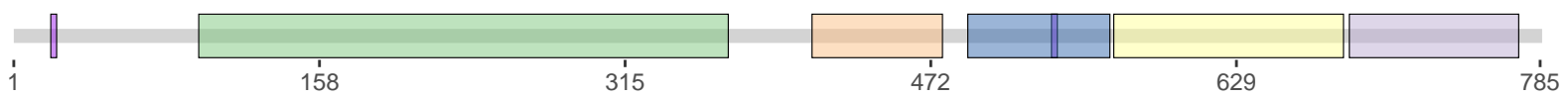
Molecular weight



Gel Slice

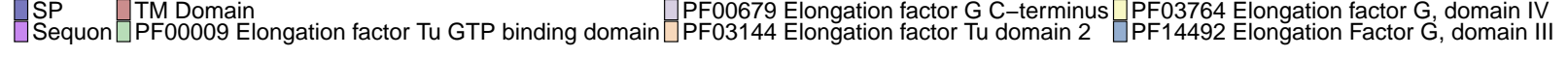


Protein length



Pfam domains

Pfam Description

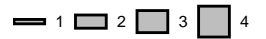


Protein sequence:

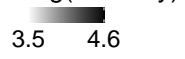
PDNPEVTIERAASDDEPFAGLAKIMNDPFVGLTFRVRYSGKLSAGSYVYVANKGRKERIGRLLEMHANSREDIKTALTGDVALAGLKDITTGELTADPKPQVLERMDFDPVYKAEPTKADIDKMATGLIKLAGEQPSRHFBRDEEINQTVIEGMEGLHLEIVDRLRKRFKVEANVAGPQVYVRESIKISEVYVYHKKQSGSGGQFADITVRFPEMETGGGYEFKSEIKGGAVPKVEYIPGVYMKGLEEGMSNGVLAGFPVAVDVRALVDSGSHQVDSSVLAFLQLAARG

NbL15g09260.1 purple_acid_phosphatase_2-like [MW - SP = 51.36 kDa]

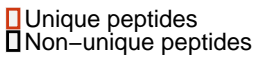
No. of times detected



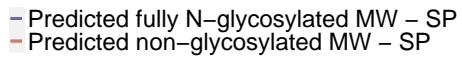
log(intensity)



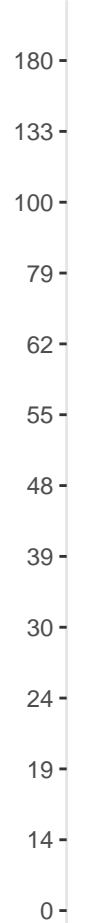
Values from



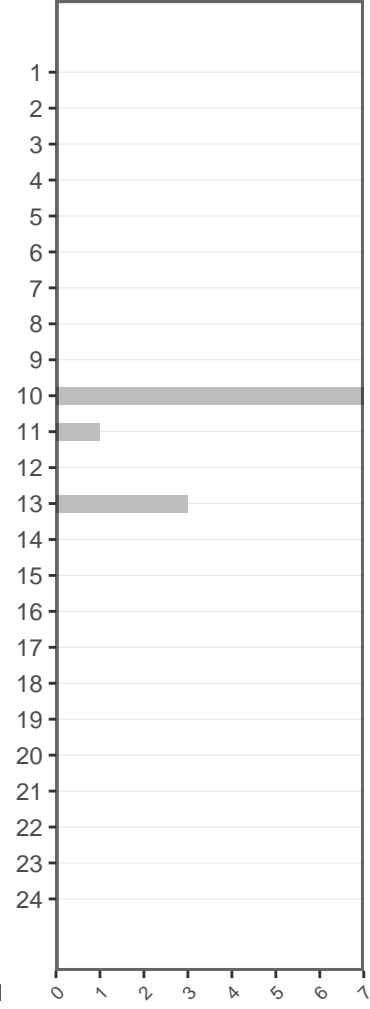
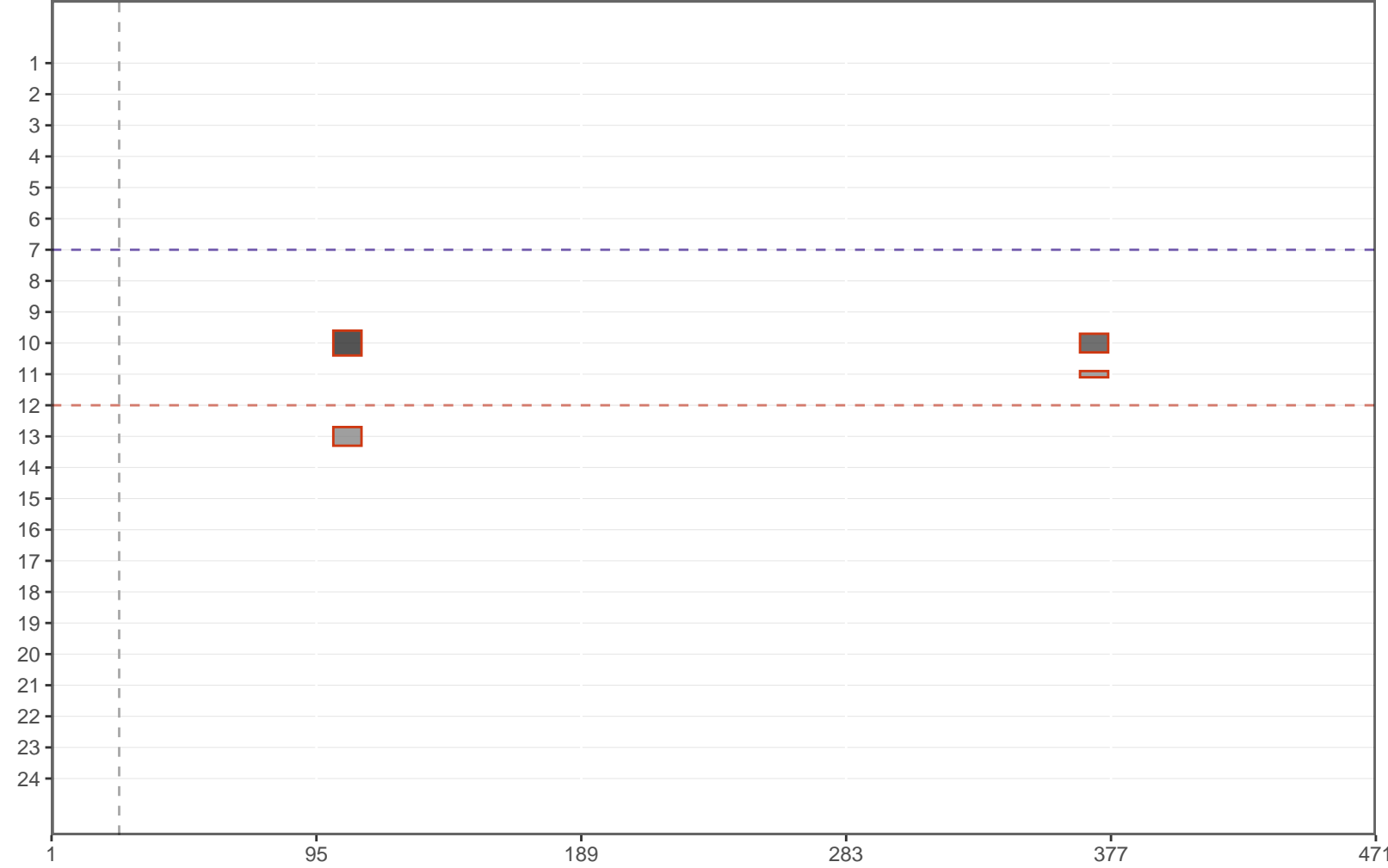
MW indication



Molecular weight



Gel Slice



Protein length



Pfam Description



Protein sequence:

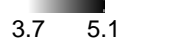
AAYQPWVWYTAGNHELDFVPEIGESIFPVYKHFSTPYRVSDSTPLWVYKIRASAYHIMSSYSAFGTYTPQWVKLTELKPKVNRSETPWLVLVHGMPSYVHHYMEGETMRVMYEPFVNYKVDVVFAGHYHAYERBERVNTVAYNIIRKGPVXDESAPVYTVYDGGNGEGLATEMTQPRYSAYRASFHGHGILDKNRTHAYFGVHRINDDGYAEADSLVFNRYWKLDEPSASHGMR

NbL15g09210.1 zingipain-2-like [MW - SP = 45.33 kDa]

No. of times detected



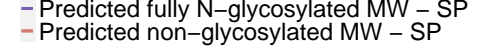
log(intensity)



Values from



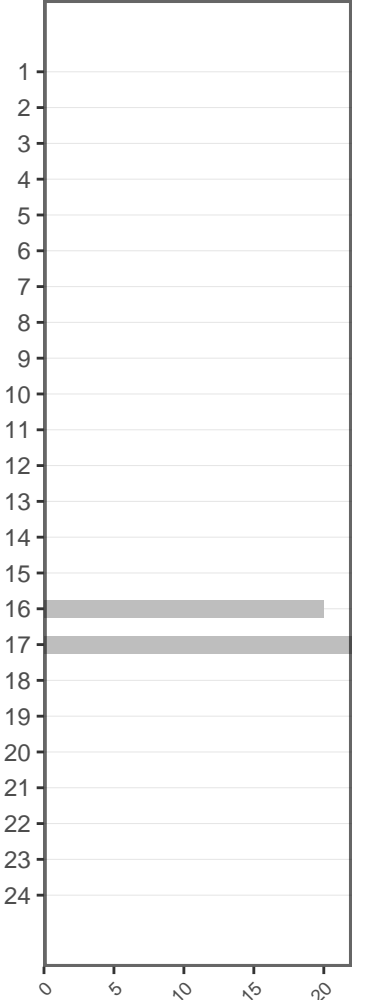
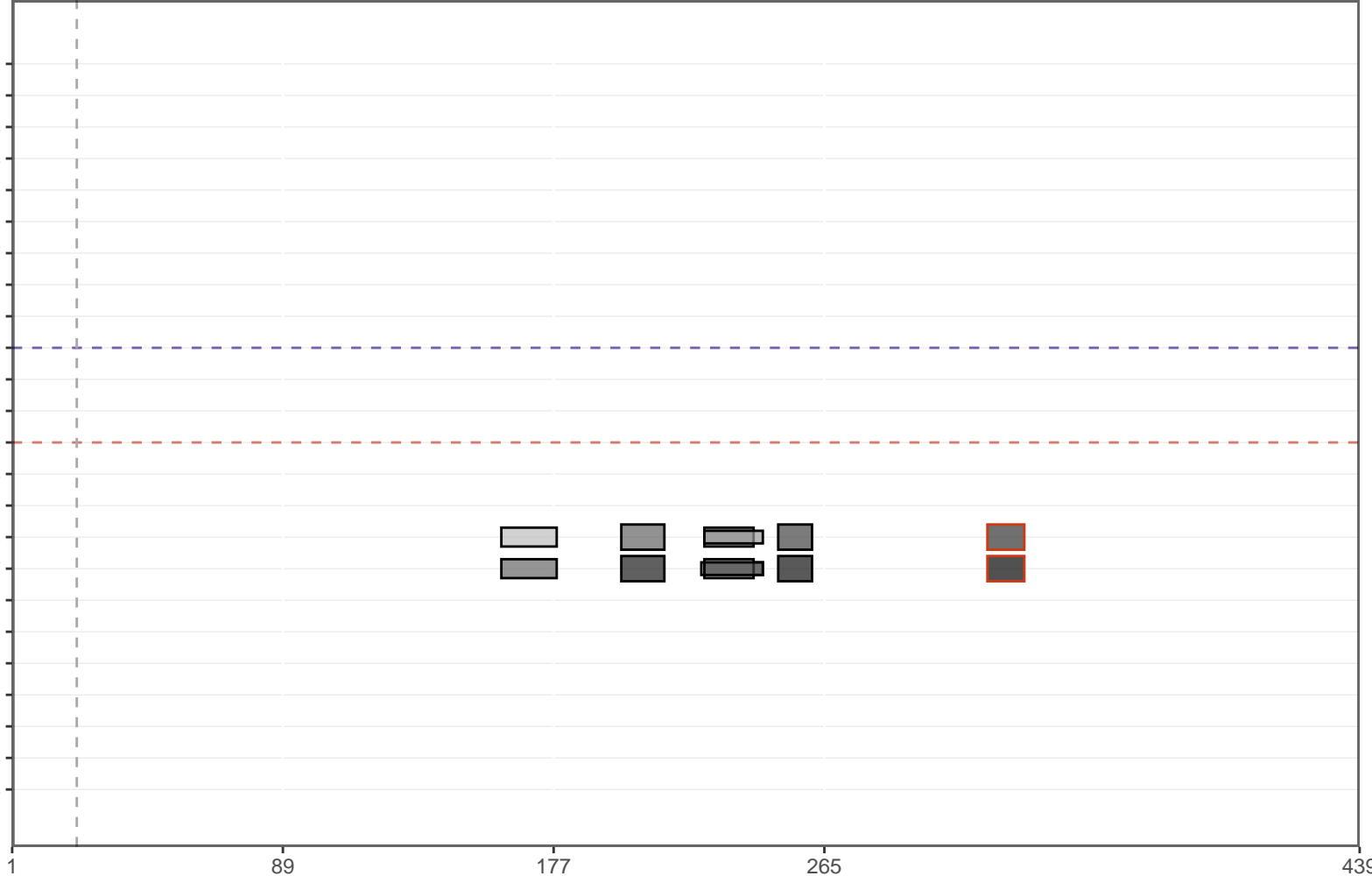
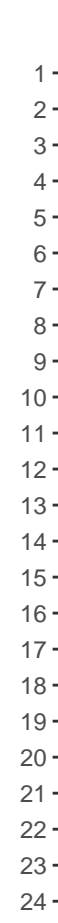
MW indication



Molecular weight



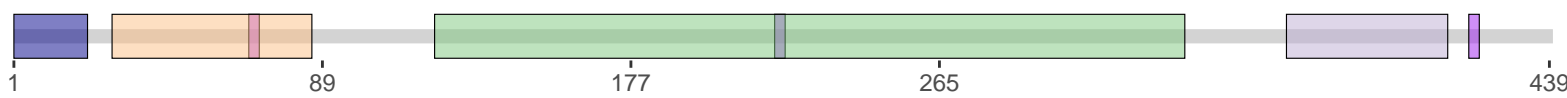
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FNREGCTCKLQRRVVTIDGYTDVFNQDEKLLKAWAKQPVVGVGGGERAFQDYENKGIPTGPGSTALDHALVLVGVGGENGVYWIKNISWGTGHWISGIVYMHQRNSGTGEGGGINKLABYPTKSNPNPFPFPGPGVGGGSMFTSGGGGETGCGGWRFGLGVCLSWKDGGLDLSAVVCKDGGHCCPHDYPICDTSRNLLGLKGMASNATVGGQPKAFSGKFLVFP

NbL15g09200.1 Ion_protease_2-like [MW = 32.55 kDa]

No. of times detected



log(intensity)



Values from



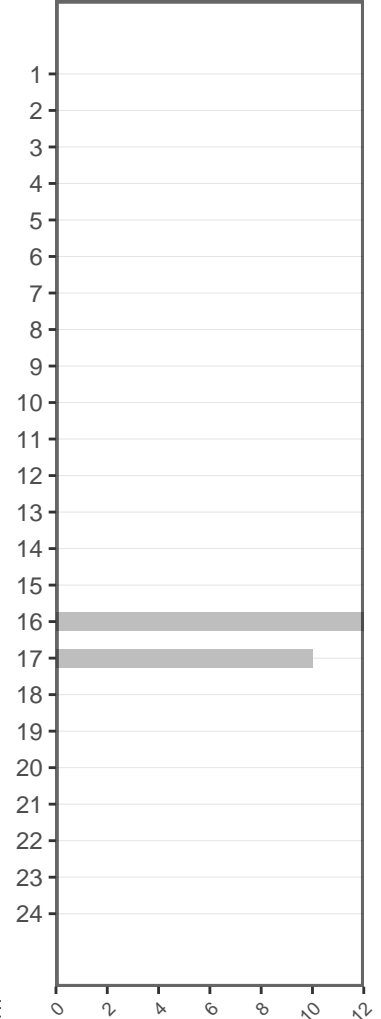
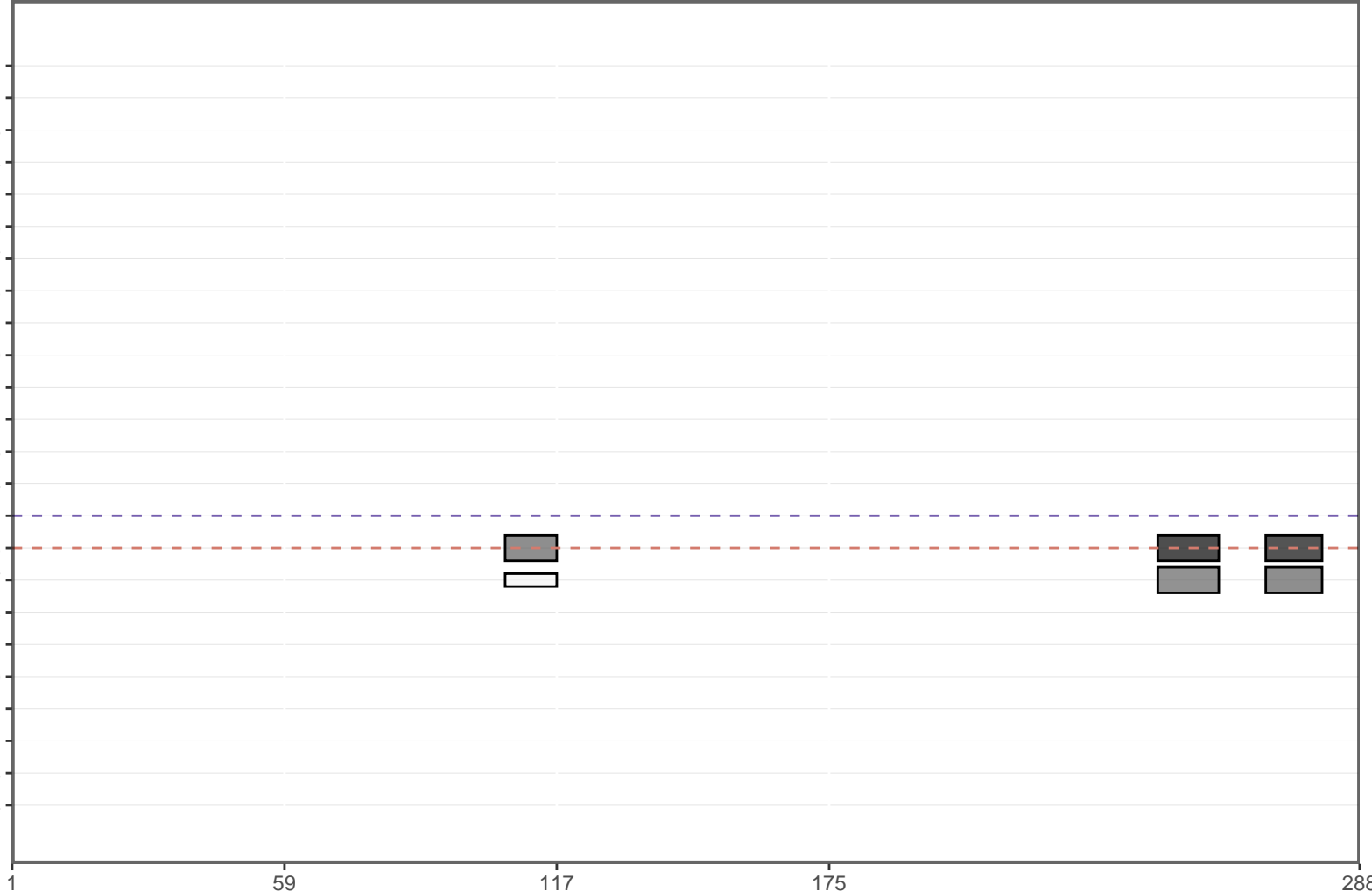
MW indication



Molecular weight

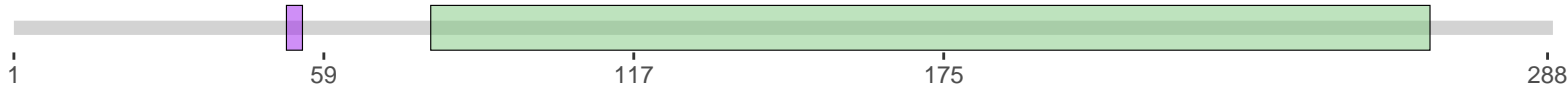


Gel Slice



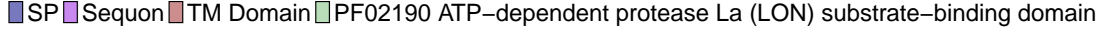
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGCYGEVYKHERLVDRFFLQKGGDERFRVSKVIREKPKYLVAEVTWLEDRPSANGEDDVEGLANEVENYMKQDVRLSNRLNGKAKEATDLRRNLFFTFDFSFVGGTFEGAPREGQALLEDTAVRLKREKELRNLFLNHLTAASAVKDVPPSSG

NbL15g09000.1 50S_ribosomal_protein_L31_chloroplastic [MW = 14.55 kDa]

No. of times detected



log(intensity)



Values from



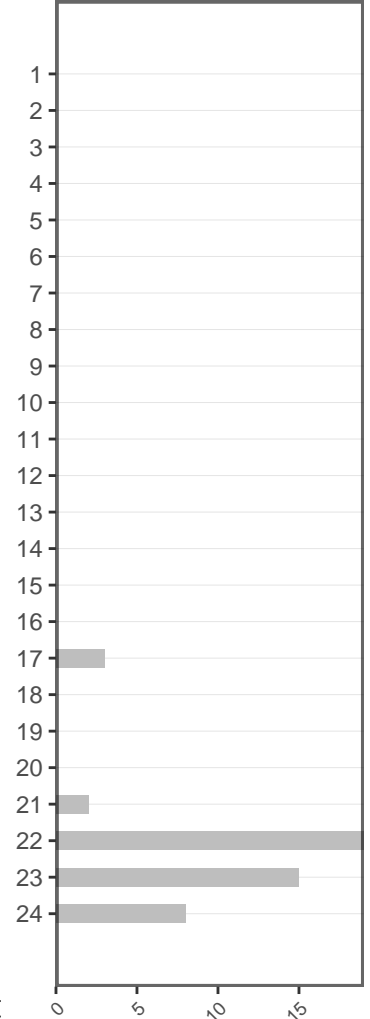
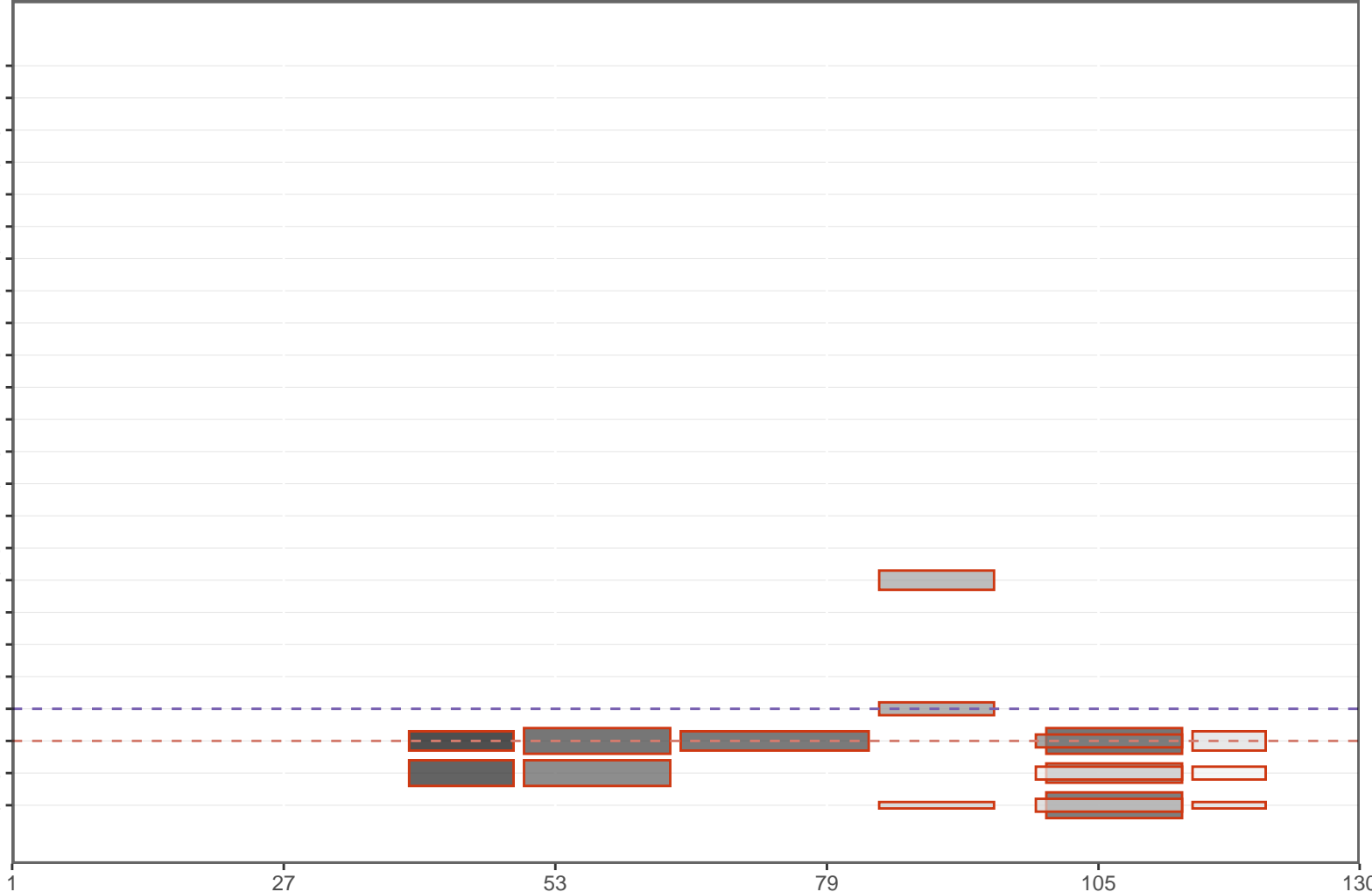
MW indication



Molecular weight



Gel Slice

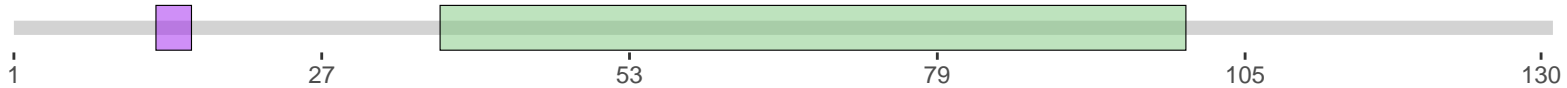


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

`2NNGEOMTTGGTKNEYTVQVWWSGNHPFVYLGSRSAVVADQGVKFRNFKFSLGQIMQIFLKGENLPPKQKQKATKKK`

NbL15g08950.1 proteasome_subunit_alpha_type-1-B-like [MW = 29.86 kDa]

No. of times detected



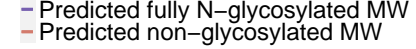
log(intensity)



Values from



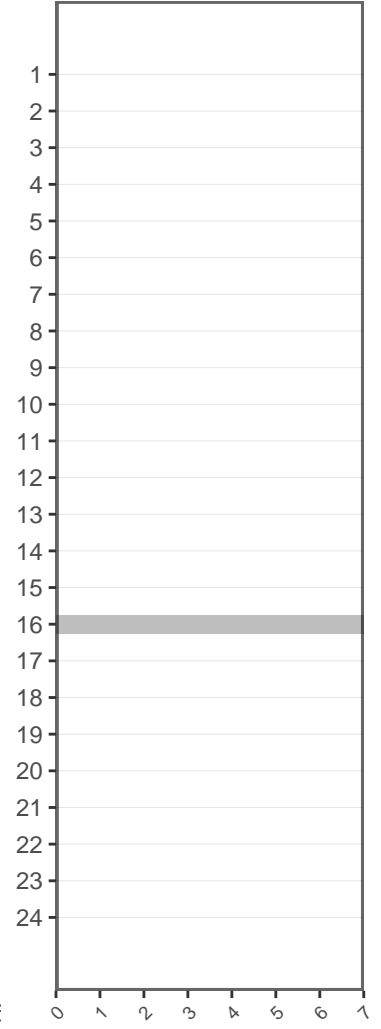
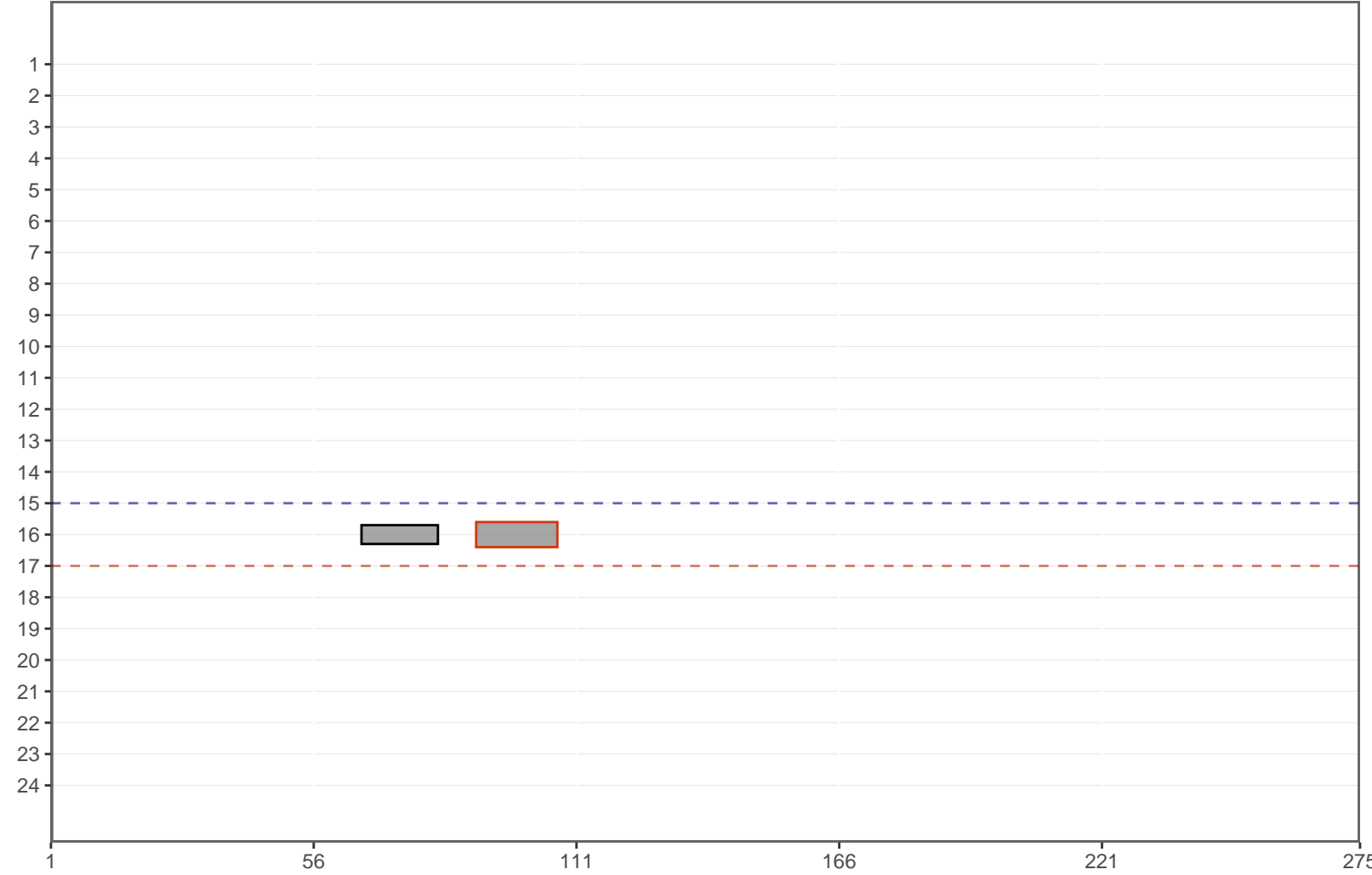
MW indication



Molecular weight



Gel Slice

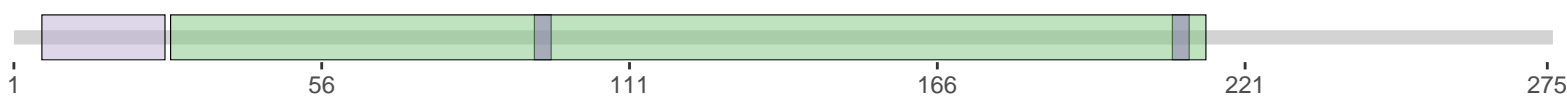


Protein length

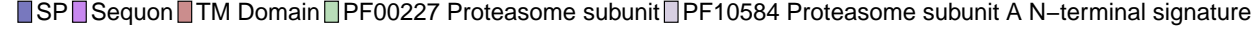


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

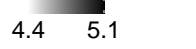
IKRPYGVGLLVGGLDESGAHLVYKRPNGNYFEYGAFAIGSRGAANKTYLERRFETFMDSREGLKDALFALRETLGGEKLTSTNCTVAVGVGEAFHMLDKETIGALNEFEVAGEEAPAAPDEAGSDPEAAPEEGAPADQGAAPMDI

NbL15g08920.1 isoflavone_reductase-like_protein [MW = 37.79 kDa]

No. of times detected



log(intensity)



Values from



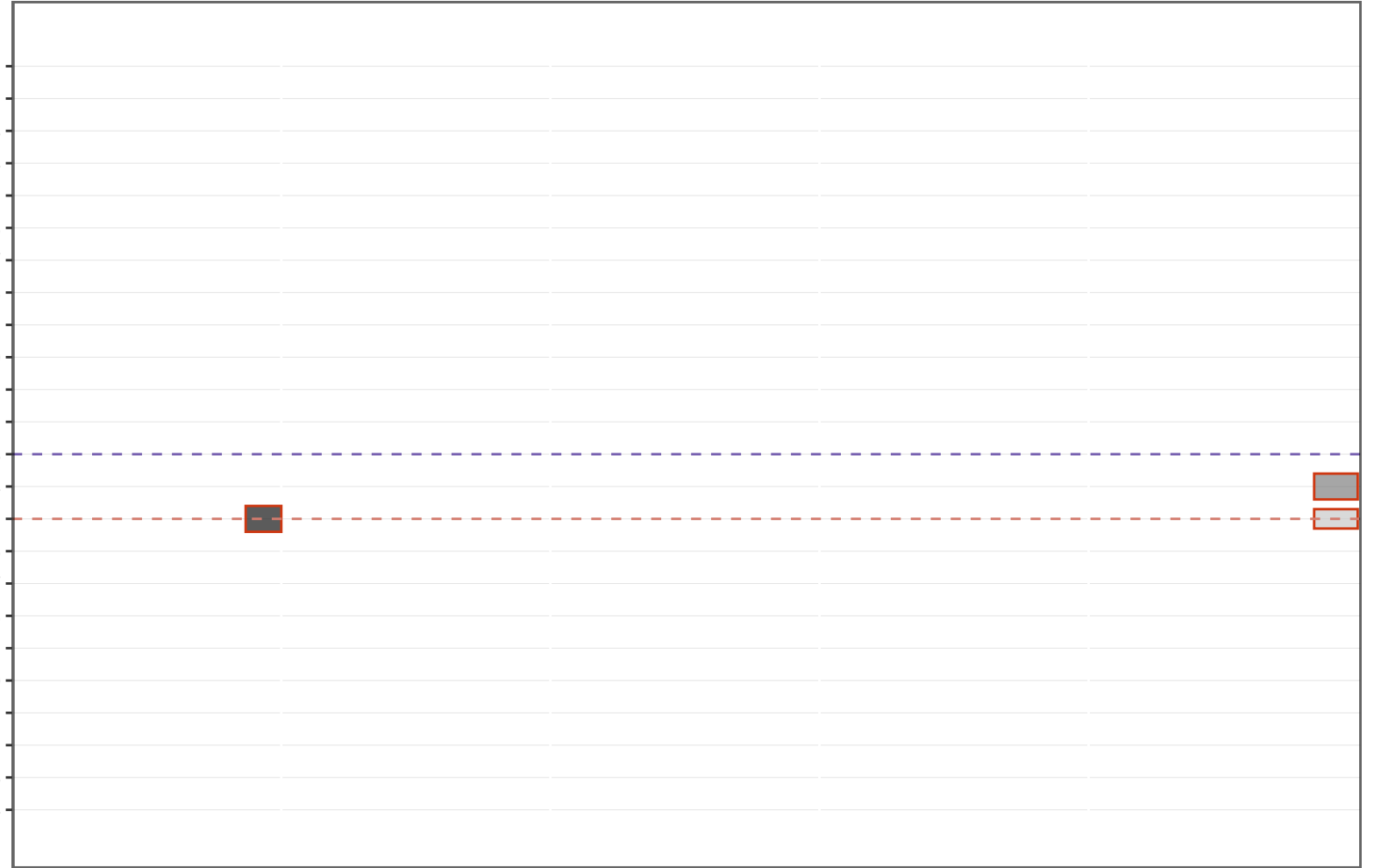
MW indication



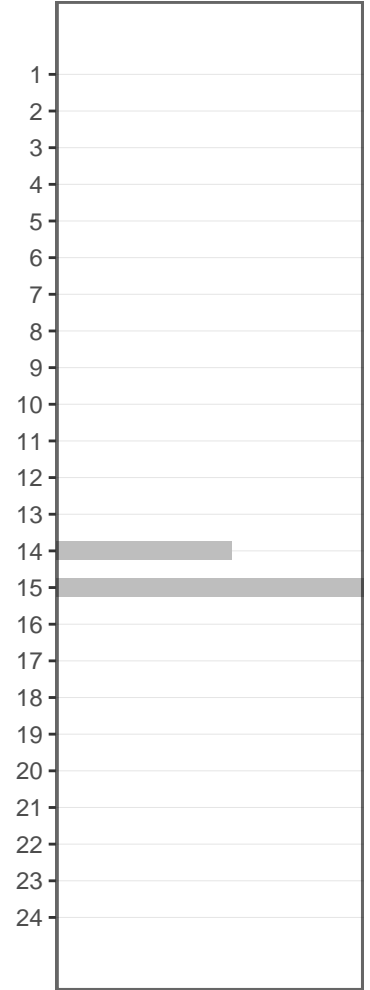
Molecular weight



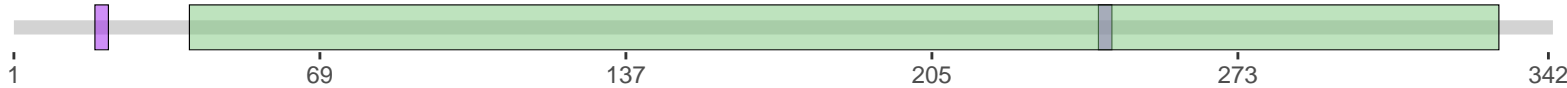
Gel Slice



Protein length

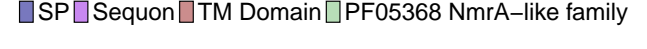


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EPAKSAFAVYVQIRRAIEAEGIPYTVYVGNDFAGYFLPTMVGPGATAPPRDKVIFPGDGNKAVFNEEHDIGTITKVVDDPRTLKTLVKKPKNTLSFNEELVAVWKKMGKTLKTYPEEQLKDIETSPMFLPVLAINATFVNGDQTNFKIEPFGVEASELYPDWYTTVEEVLGHFY

NbL15g08860.1 flocculation_protein_FLO11 [MW = 83.19 kDa]

No. of times detected



log(intensity)



Values from



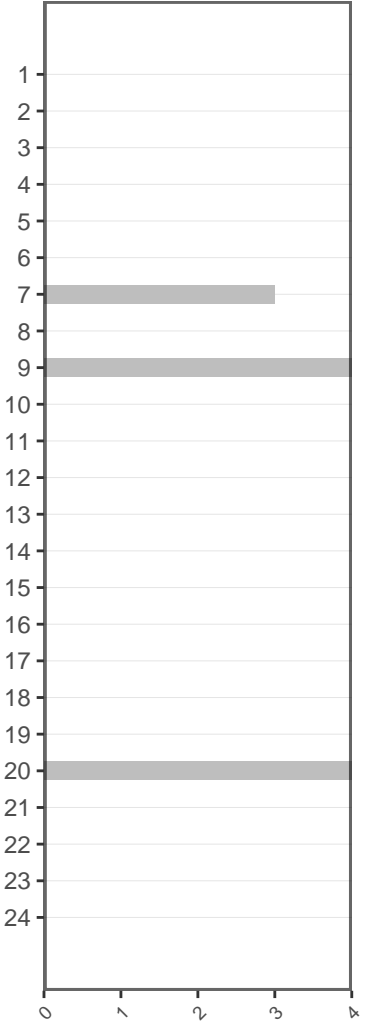
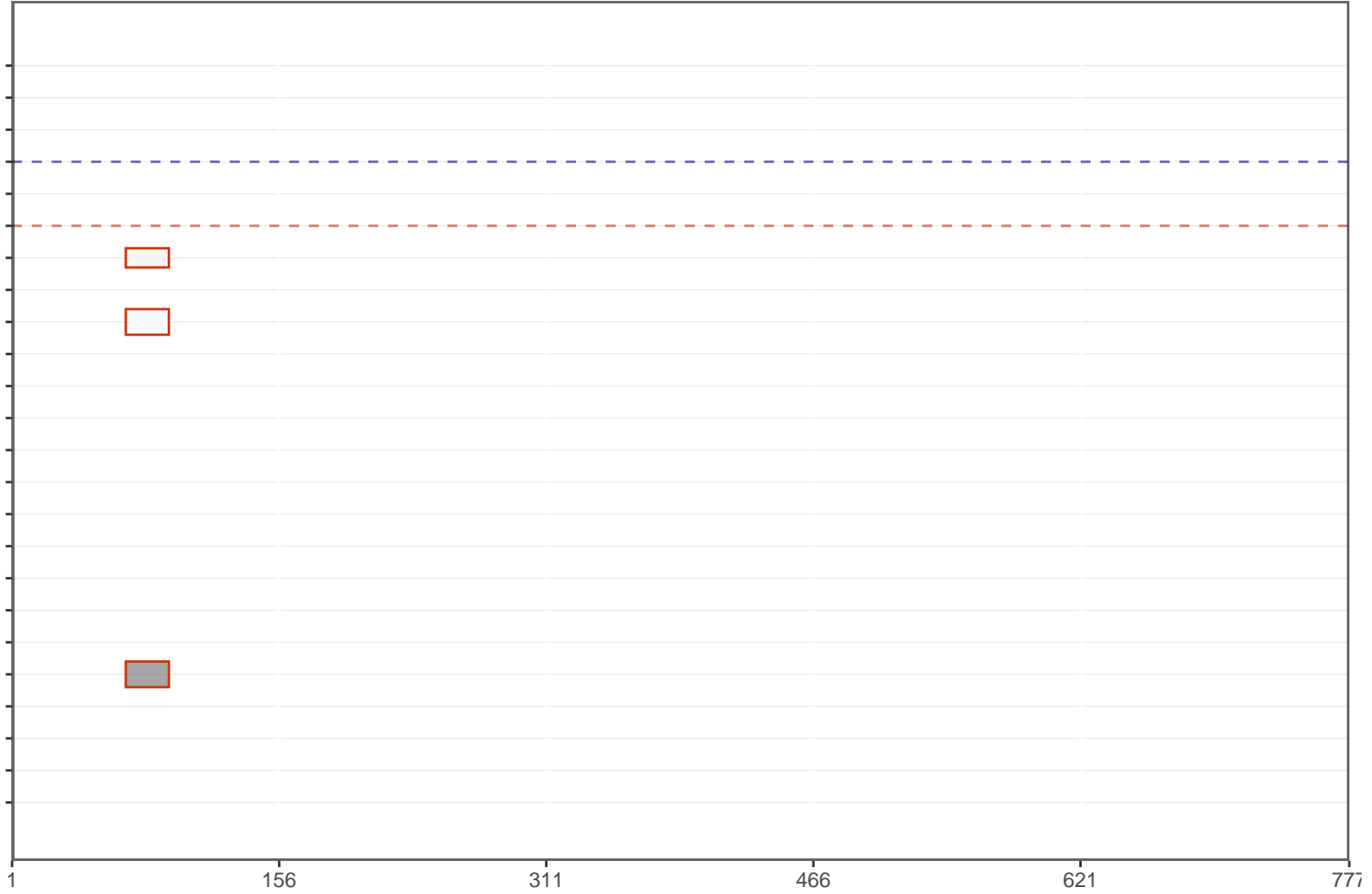
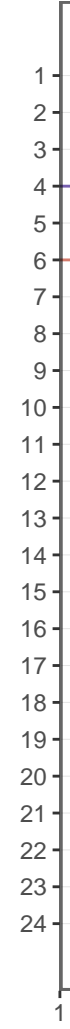
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

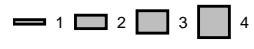


Protein sequence:

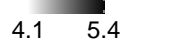
ISKSTEATSSISGKEPKFTAIRPQSGMELLKKETISDTVAEANKKPEKVMKPSLSEKSTRGTGQEPGQISDSSGIDEPKMVRQGETNIGETREKVEKVMRNNKNGTGEKIVGLLSTKQPGTAFQSKKAVTEKQSDNSDNDQIRVNLVSNGNHTKTVSSGPKNKTIIVNSSEKTAGFAEIDMPLNKEVKDKNSKFIHRMAVGDGKGNLEEGFPVSMITLAGDNRGASMLQSGSDSRKEGAHRRRGVKNMNPDESADATDDEGYSSEGRGPKBARTMEDOEIAYLNCNV

NbL15g08780.1 maf-like_protein_DDB_G0281937 [MW = 26.92 kDa]

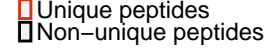
No. of times detected



log(intensity)



Values from



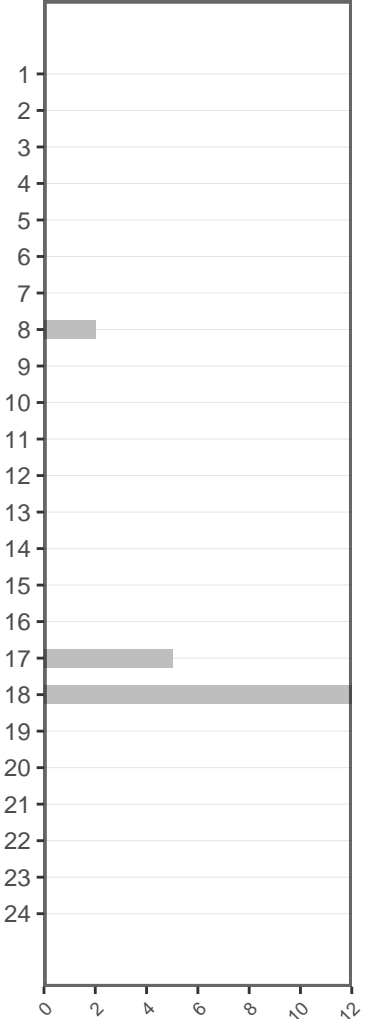
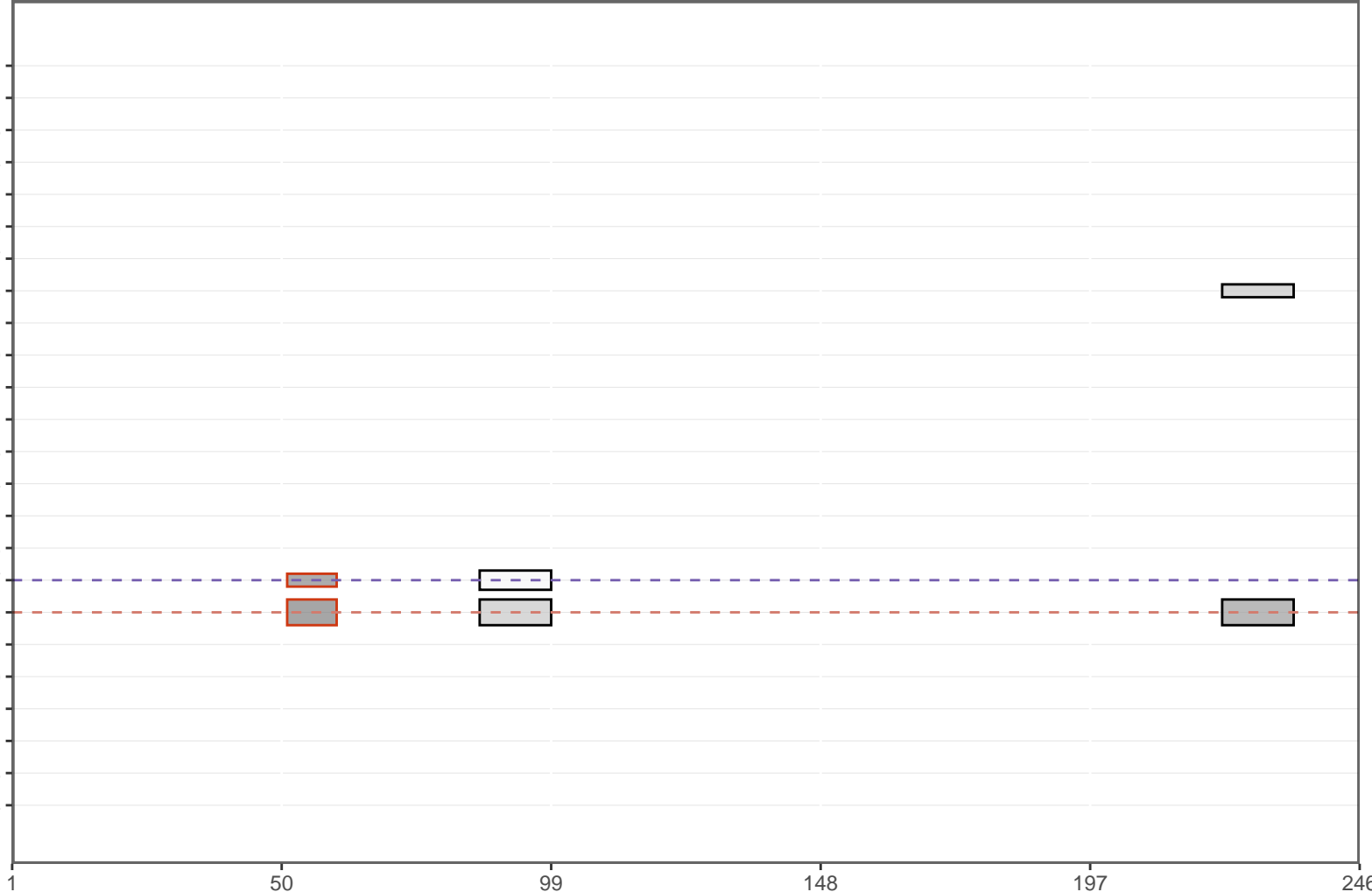
MW indication



Molecular weight

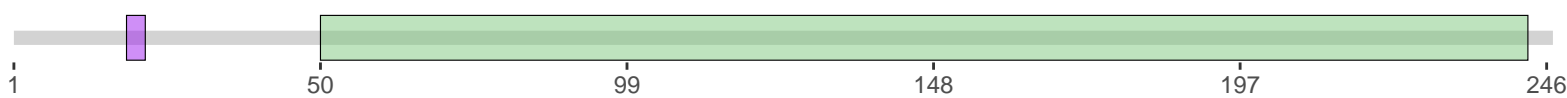


Gel Slice



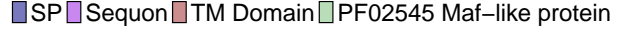
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ISENLKHSNPITLLVAADFTVVVVEGVREKPSSEAEARGFMKDYANGHAATISSEVLTNLTGRRGGEWQVEVYFHDIPRVDIKLIEERIMLYAAGLIEHPLLPCIKVEVVGSTDSVMGLPKALTERLKEVLR*

NbL15g08590.1 glucan_endo-13-beta-glucosidase_7 [MW - SP = 46.83 kDa]

No. of times detected



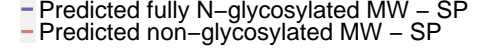
log(intensity)



Values from



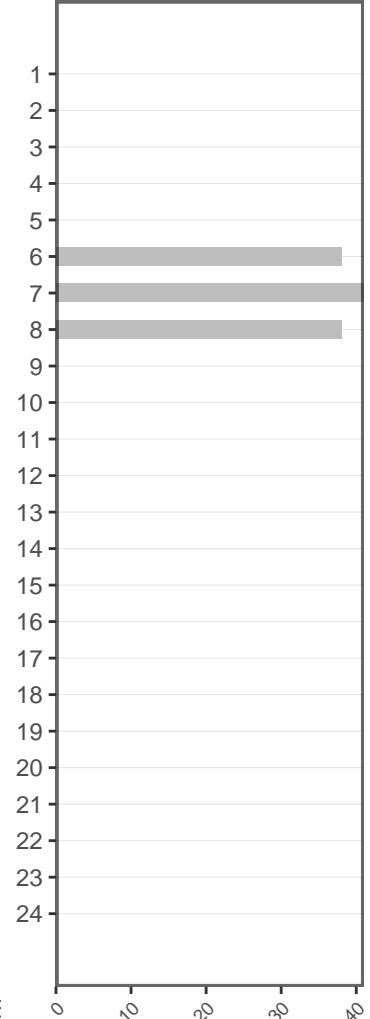
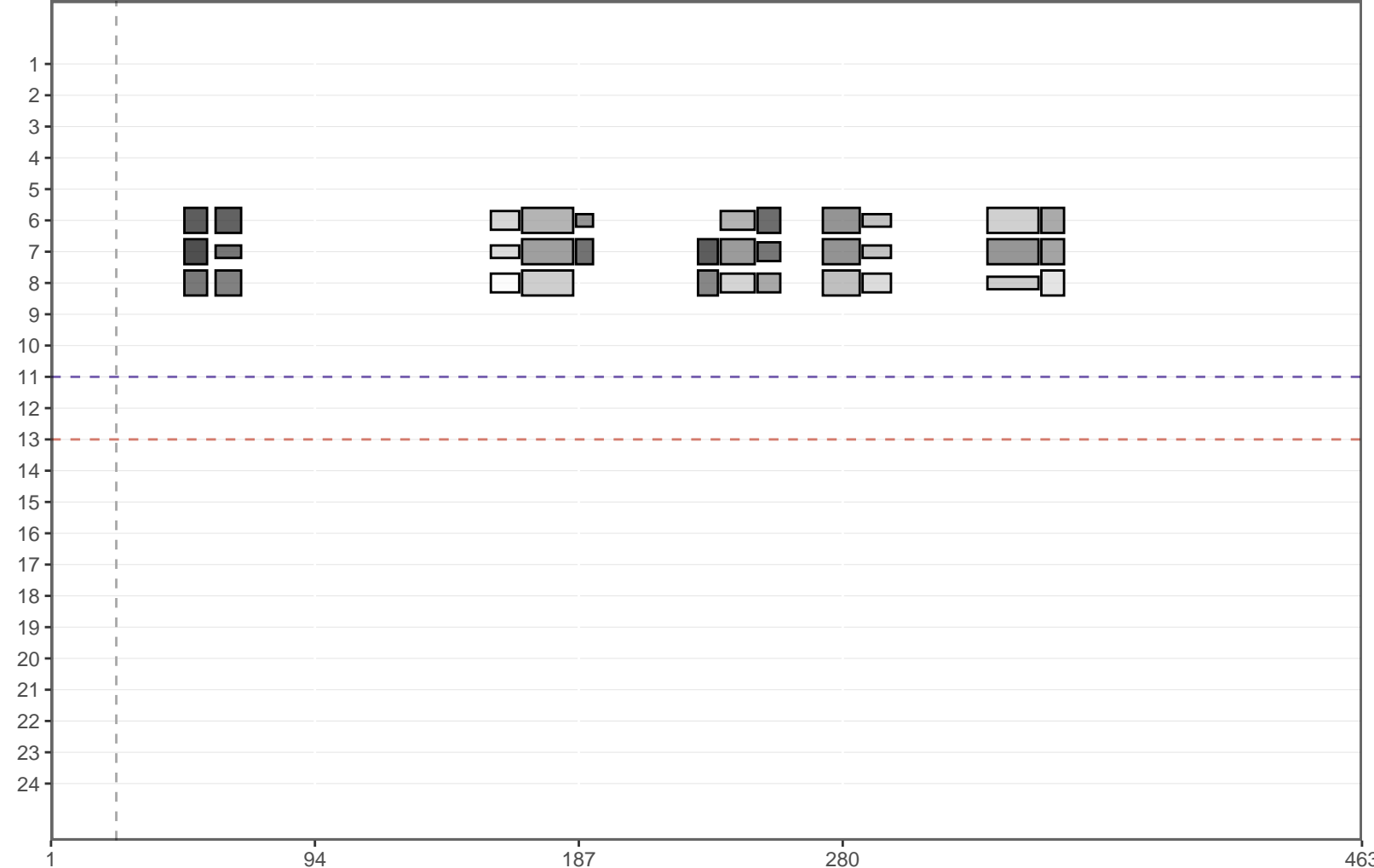
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FDPNNGRFDAGTNTKYSMEFDAGVDVAREALNALGPKVEVIAETGWPYKGDSENEVGPSEIAKAVNGNLISHLRSMVGTPLMPGIVDTYLFALVDENLKPQPTSERSEFGLFKPDLTMTYVDAGLSEKANGDQPMPKTLVTPSNTSMPPSPKPTGTSSSPETPIVTPSLPKTSMPPSPETRTATSSLPKPPVLSSSPKTKSVKTKVDSDARLQANNVYVAGFNLGVLVLSQLWHPMLHVL*

NbL15g08560.1 uncharacterized_LOC107783365 [MW = 200.02 kDa]

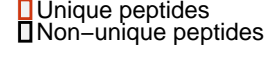
No. of times detected



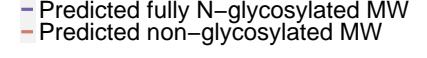
log(intensity)



Values from



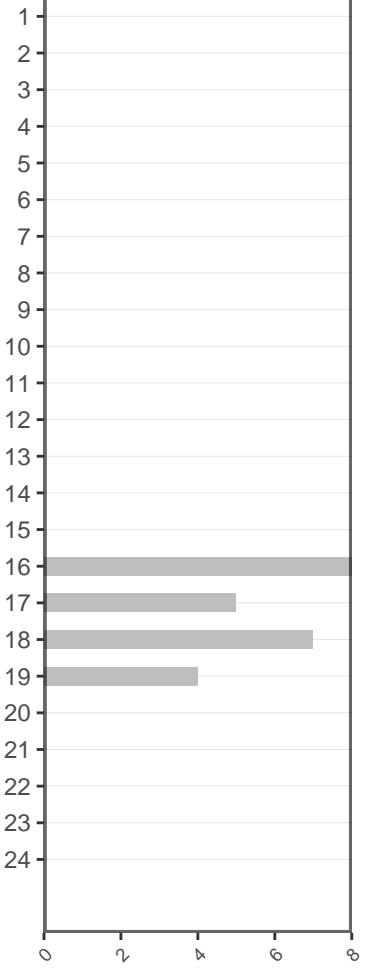
MW indication



Molecular weight



Gel Slice



Protein length

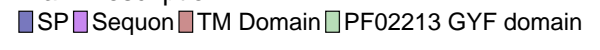


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

POLLNLLCOOYLMDLGGGAALGGPQGLSLLDKFLMKKGGGGGGGGGGGGGGGGGGGGGEEHQMLLGGGGLLGGVLSDFPHQRFGEGPYGKLPFGISAGNATVDPTRFGPSPNLSMNTGVQHPVMEESAHAENFVLPSSGGVYQKGSFETSSLHLPHQMFKDASSGRSWSGFAEQDQKGVPRMATAMVDPSSHTFIAKHPLPLECTENNEPLAVTTFEIAHFPLVEGVKSVLLPPLAVDNDLHQNKLESPPAASSEPPQVERDPHNGLEVTXELKSVYEPREV

NbL15g08470.1 uncharacterized_LOC104247649 [MW = 72.82 kDa]

No. of times detected



log(intensity)



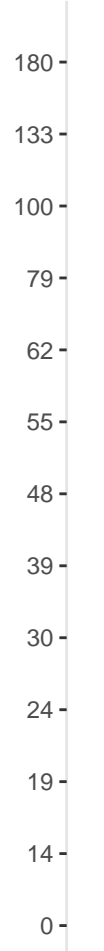
Values from



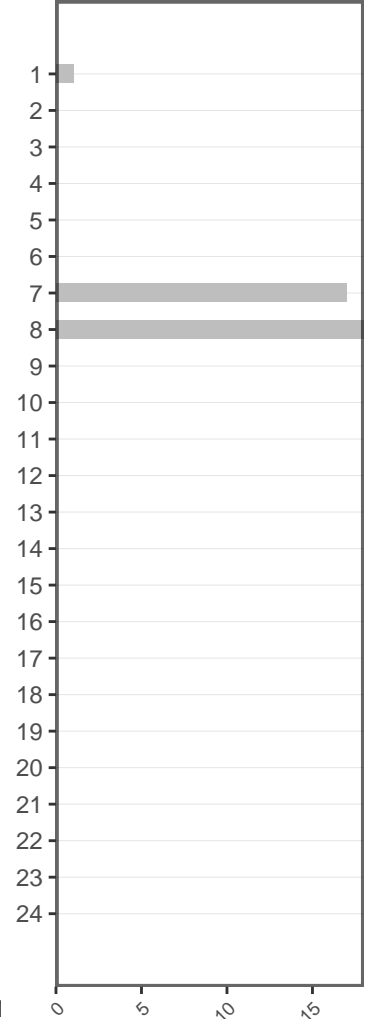
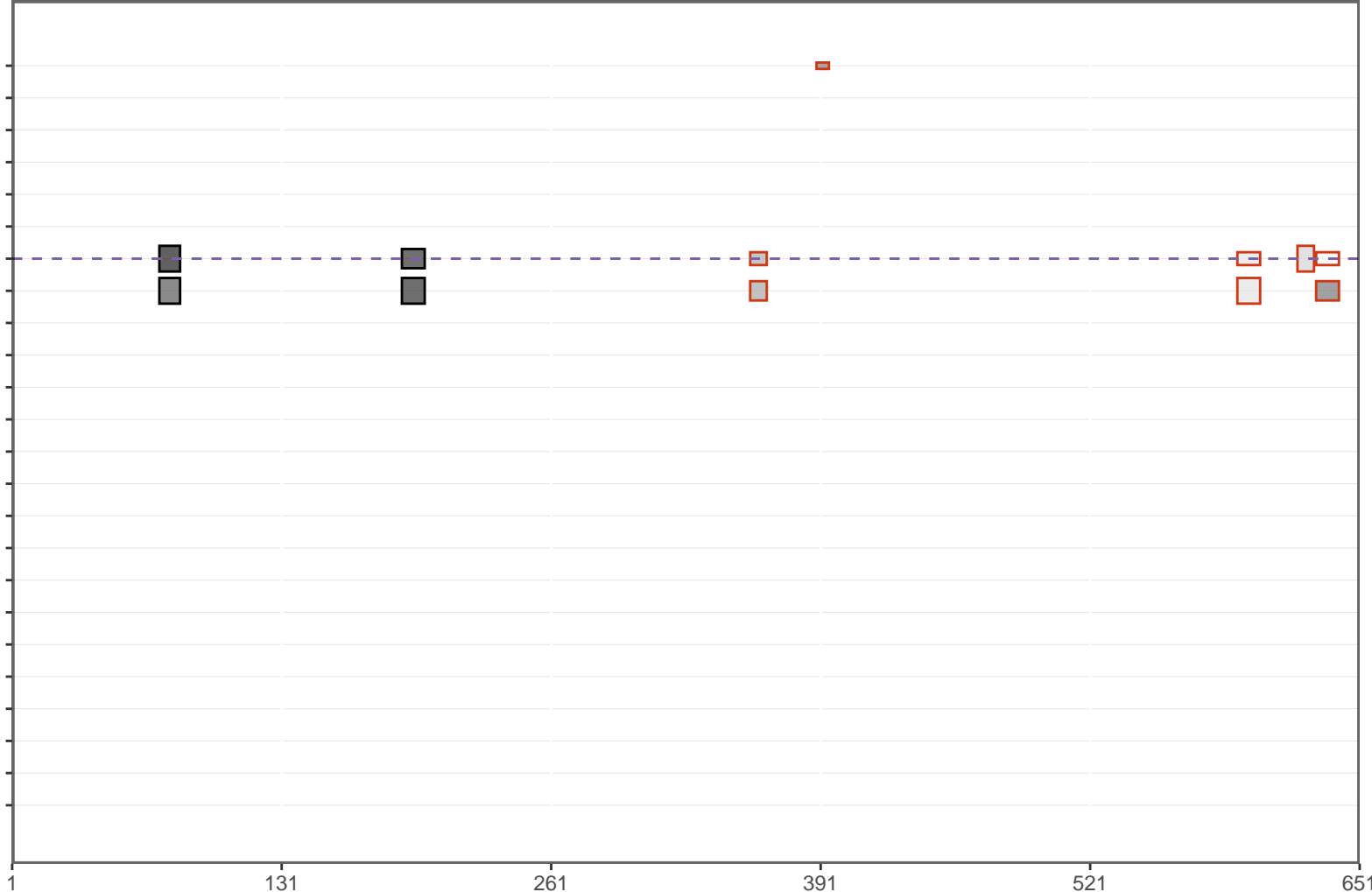
MW indication



Molecular weight



Gel Slice



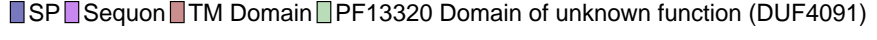
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

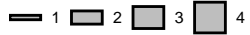


Protein sequence:

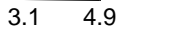
QLLDHFVWLLQYRISPFYGRWNGMRLVYTSRWPADHPKSDVYLSRDLAAVAVPYGLVPCDGTAKDYLRRREVILRTKNHWKAYFYLVWDEPLVVEGYDAIRSMASEHAWAFDARVLTYYGGSDAPLASNFEEFLKVPFLRPHYQVCTSEWVGNREDLAKDVAEIGTENGEWWTYVGLGPGDHPNWHLGMRGTHRAVAMWRVWKEGGTGLYWGANGYEKATVPSAEIRFRRLGPPGGDLVFPYGGVFS660GPIASLRLEILLGLODIEYLI

NbL15g08380.1 histidine--tRNA_ligase_cytoplasmic [MW = 94.21 kDa]

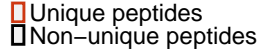
No. of times detected



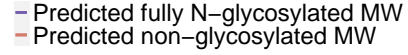
log(intensity)



Values from

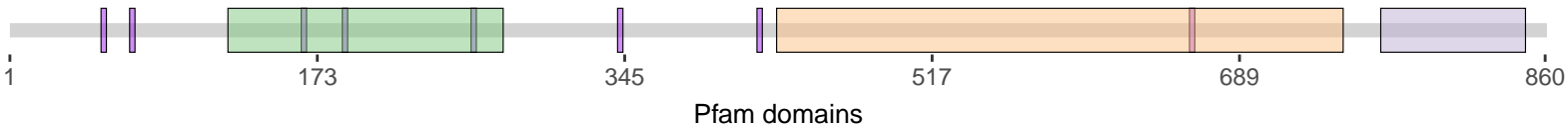
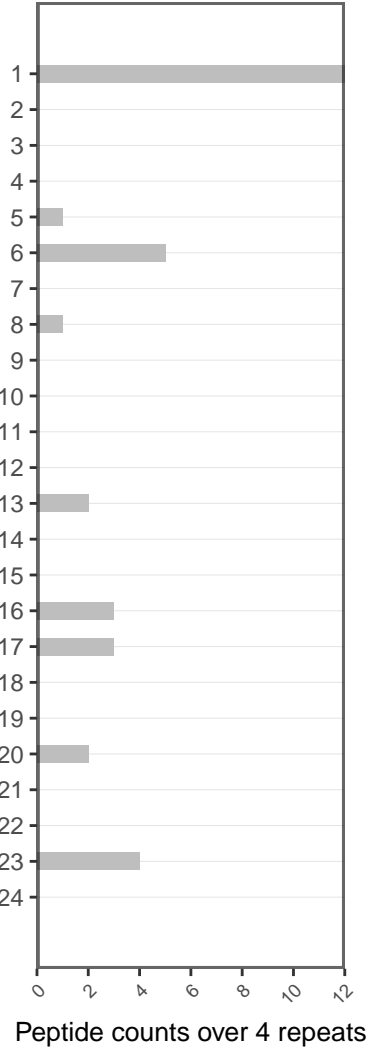
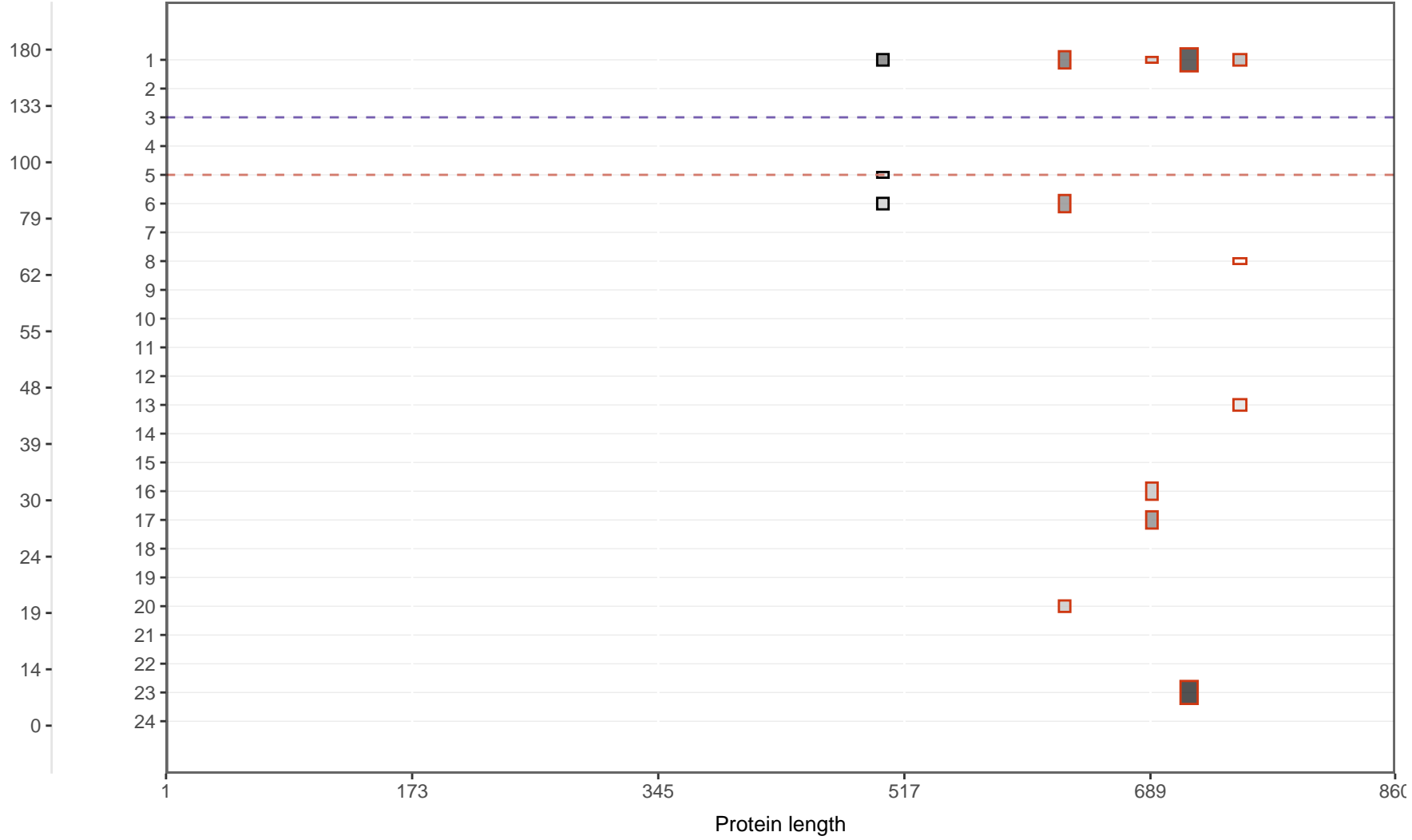


MW indication

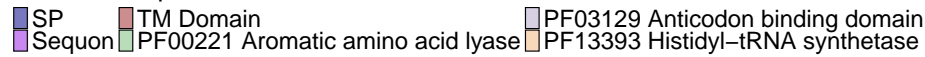


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

IESRRLPKLPGKTRDFANEQMAIREKAFSIVEVFKRHGASALDTFAFEMRETLMGKYGEDSKLFDLADGGELGSLRYDITVDFARVYAMNGLTSFKRYQIAKYYRRDNPKGRVREFYGGDFDIAGGFENMMDFEVIKLTTELLDELDIGEYEVKLNHRKLLDGLMLAGCVQDEKFRITGSSIDKLDKGSFEGQIKEMVDEKGLSDEISDRIGTFVKKWRGPPVELLKLNGERSFLENNESSLALDELDMFKALERBGIDRIVFDLGLARGLDYVTFGVFEAVYKGTATVC

NbL15g08340.1 hydroquinone_glycosyltransferase-like [MW = 55.78 kDa]

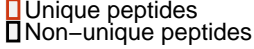
No. of times detected



log(intensity)



Values from



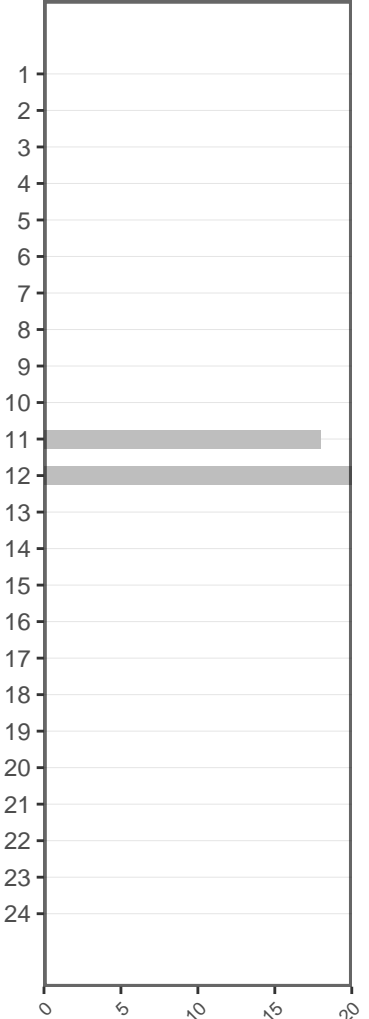
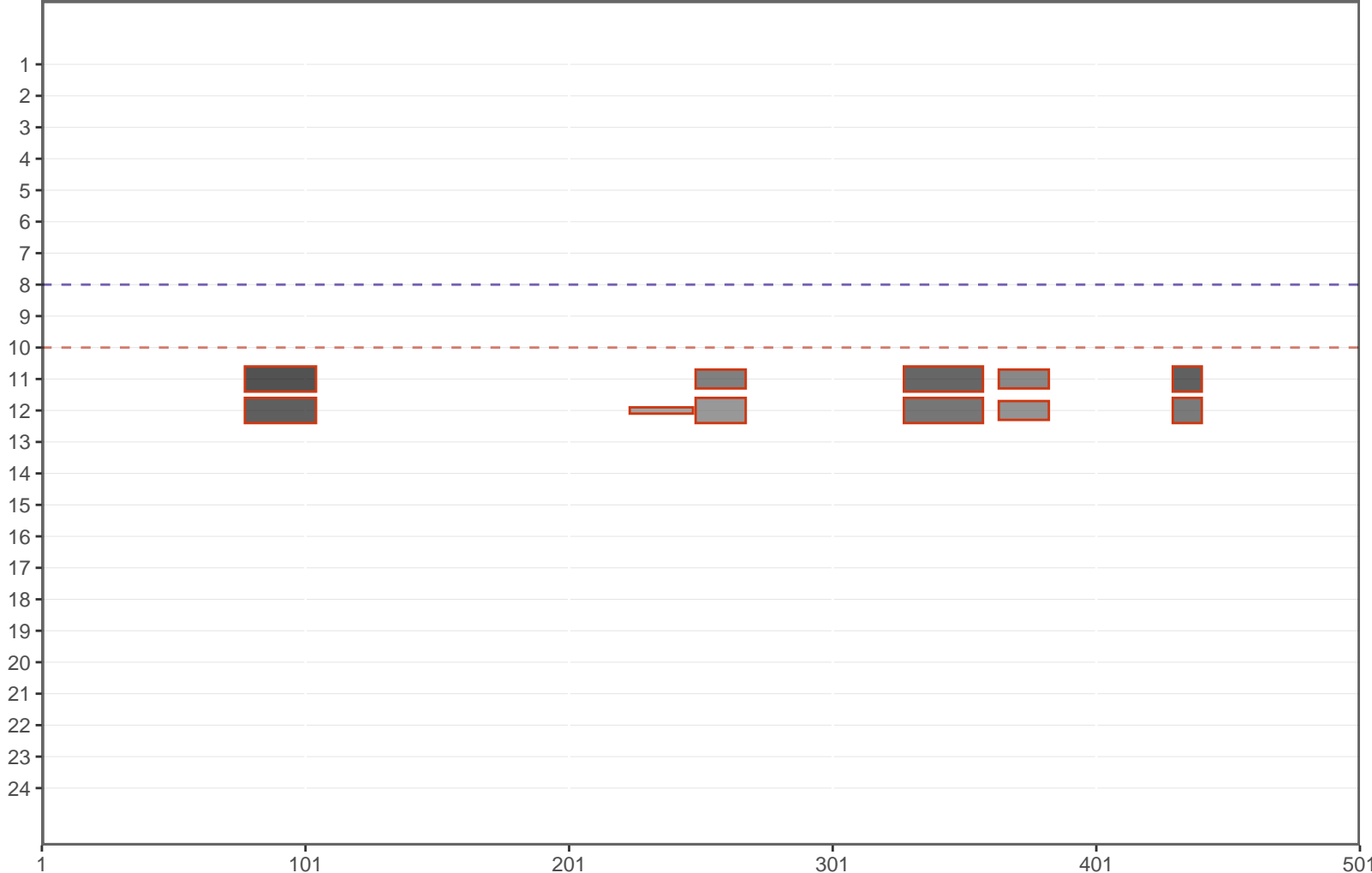
MW indication



Molecular weight



Gel Slice



Protein length

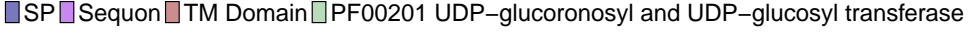


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

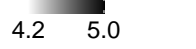
LEALKRNSFFONIPPPVHTIGPLKGDVEVTEKDAQILTWLDNPPDPSVLFVFGSGGTLTSEQLTELAWGLEMSHQRFILWARKPSDASASAAFFNVGSDENDPLMLPEGFANKTEGRGLVPSWASQVALNHPSTRAFFSHGCVNSTLESVYHGVPMIAPLVAEQRMNATFLAEVGVTKMFLVPGELSRKEIKMVRVMEGEKGMAMRRRAEELKESAKIALNGSSDDSLGRVQFVWSDQLGQ

NbL15g08300.1 NEDD8-conjugating_enzyme_Ubc12 [MW = 20.98 kDa]

No. of times detected



log(intensity)



Values from



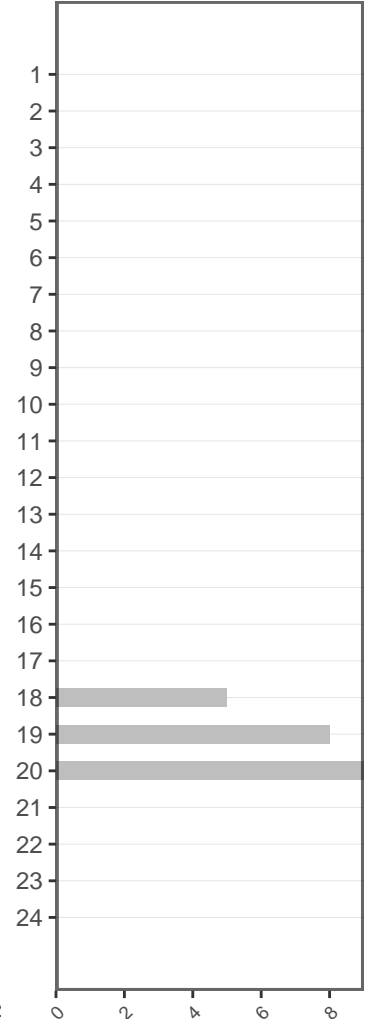
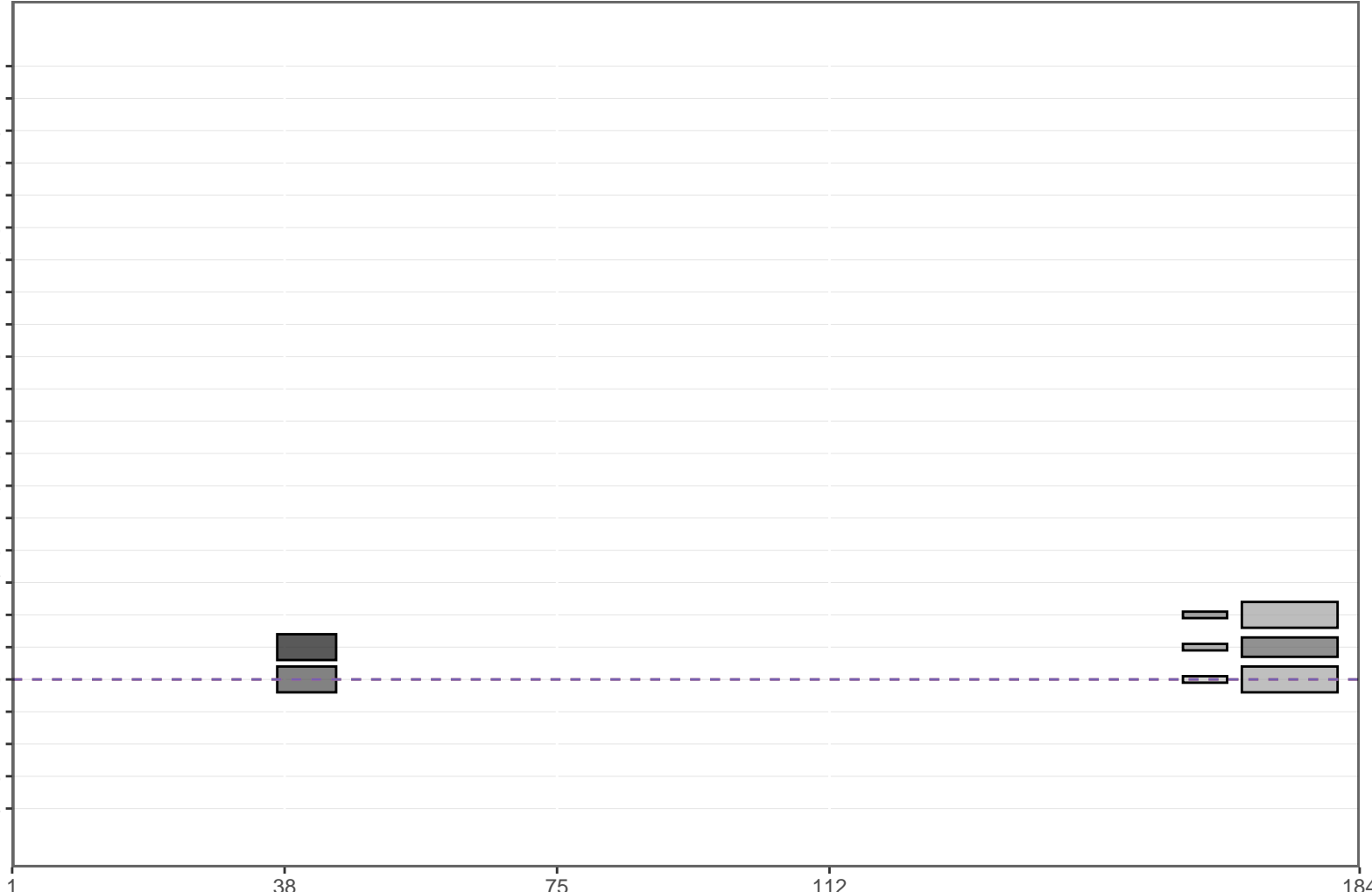
MW indication



Molecular weight

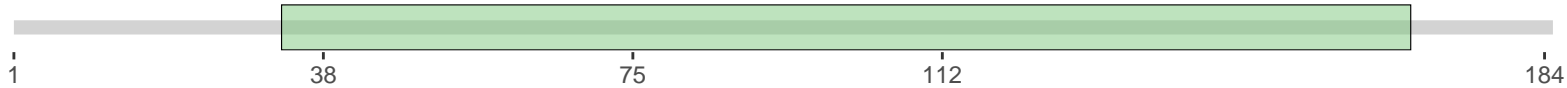


Gel Slice



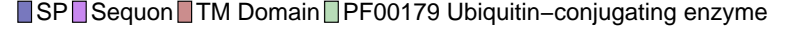
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

FSFSISPLMYPIHEAPKVKDKTRVYHFNIDLEGVGLNLRREDWKPVLNINTRIVGLYHVFTEPNHEDPLNIDAAVLRDNPFLFESNVRBRAMHGGYVGGTFPPRCM

NbL15g08290.1 geranylgeranyl_pyrophosphate_synthase_chloroplastic-like [MW = 39.56 kDa]

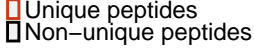
No. of times detected



log(intensity)



Values from



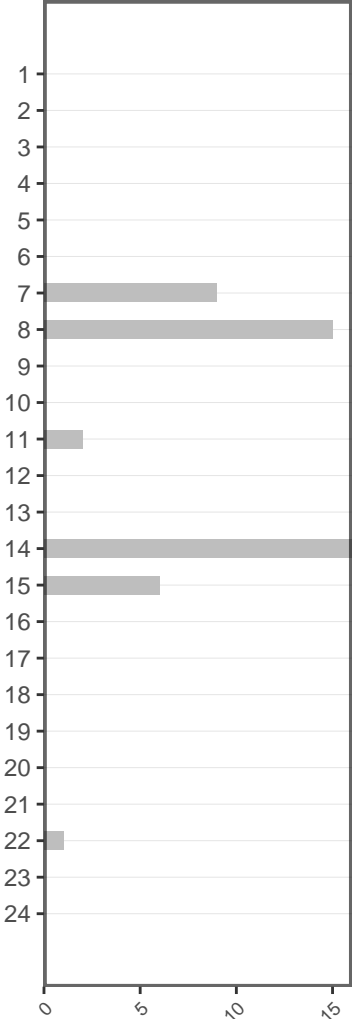
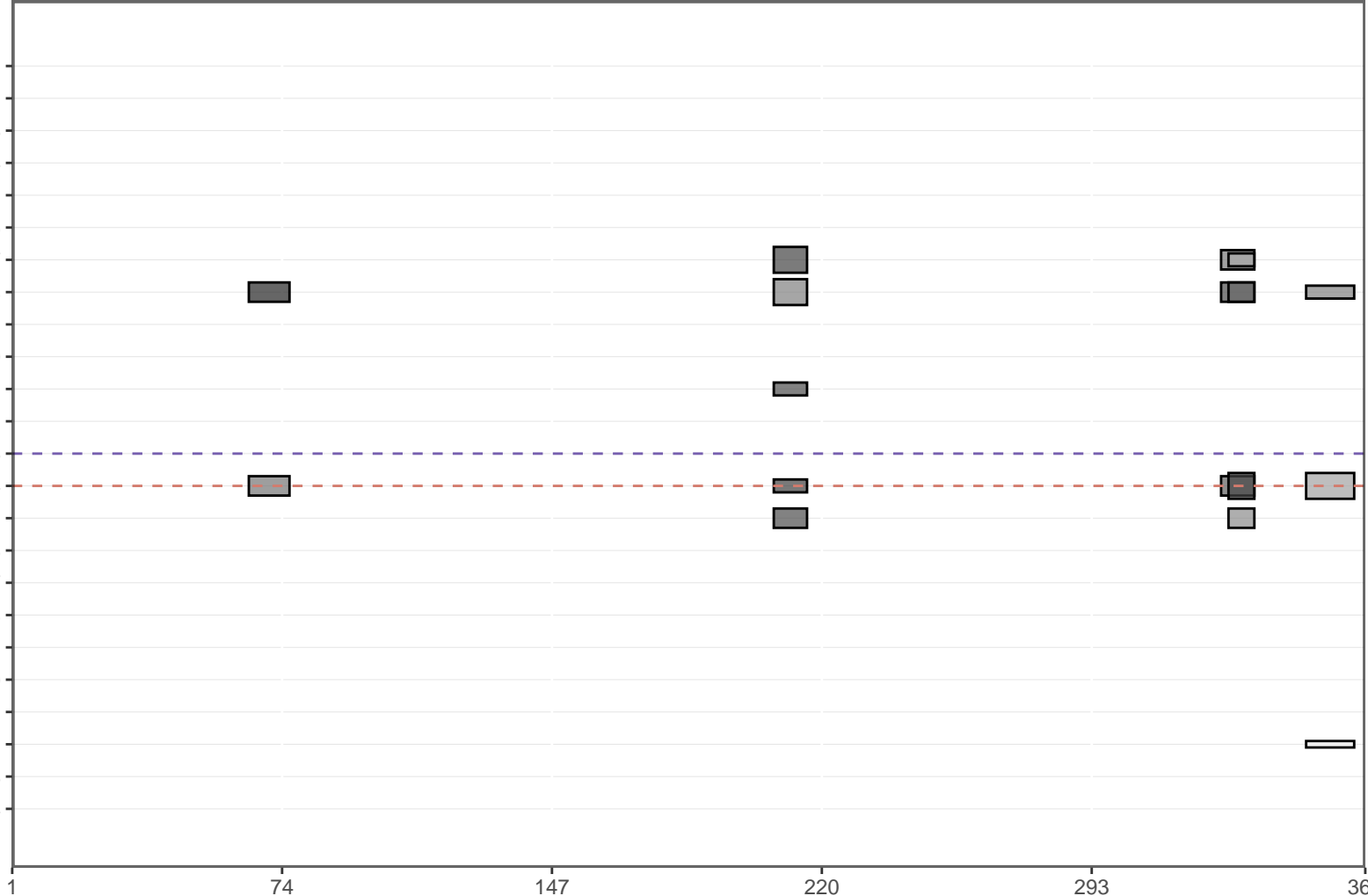
MW indication



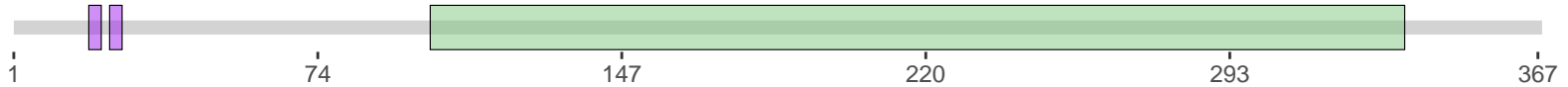
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

SKPTNHYKYGEDAVLAGDSLLAFAYVATATAGVSPSRILAMGELAKSIGTEGLVAGGVADIAGTGNPNVGLDTELEFHHKTAALLEASVVLGAILGGGTDEEVEKLRFRFARGIGLLFGVVDRLDVTNKSSEELGKTAKDLVVKTTYFKLLGLEKAKEFAEELNRDAKQGLADFDPHKAAPLALADHYVREN

NbL15g08100.1 photosystem_II_CP47_reaction_center_protein-like [MW = 56.02 kDa]

No. of times detected



log(intensity)



Values from



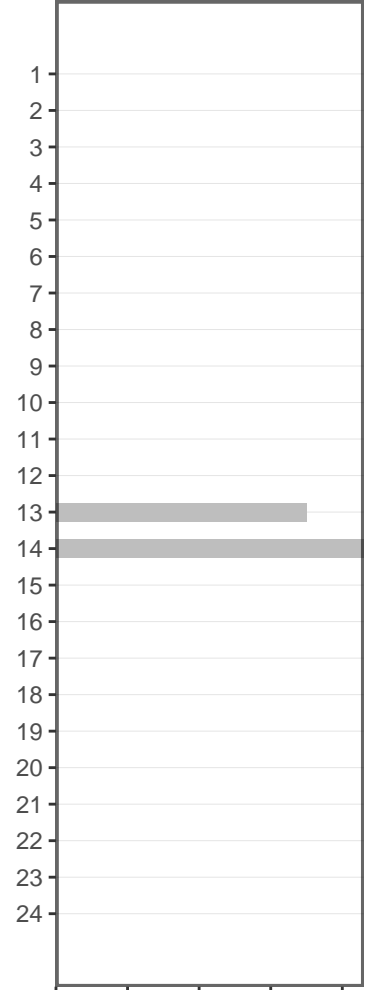
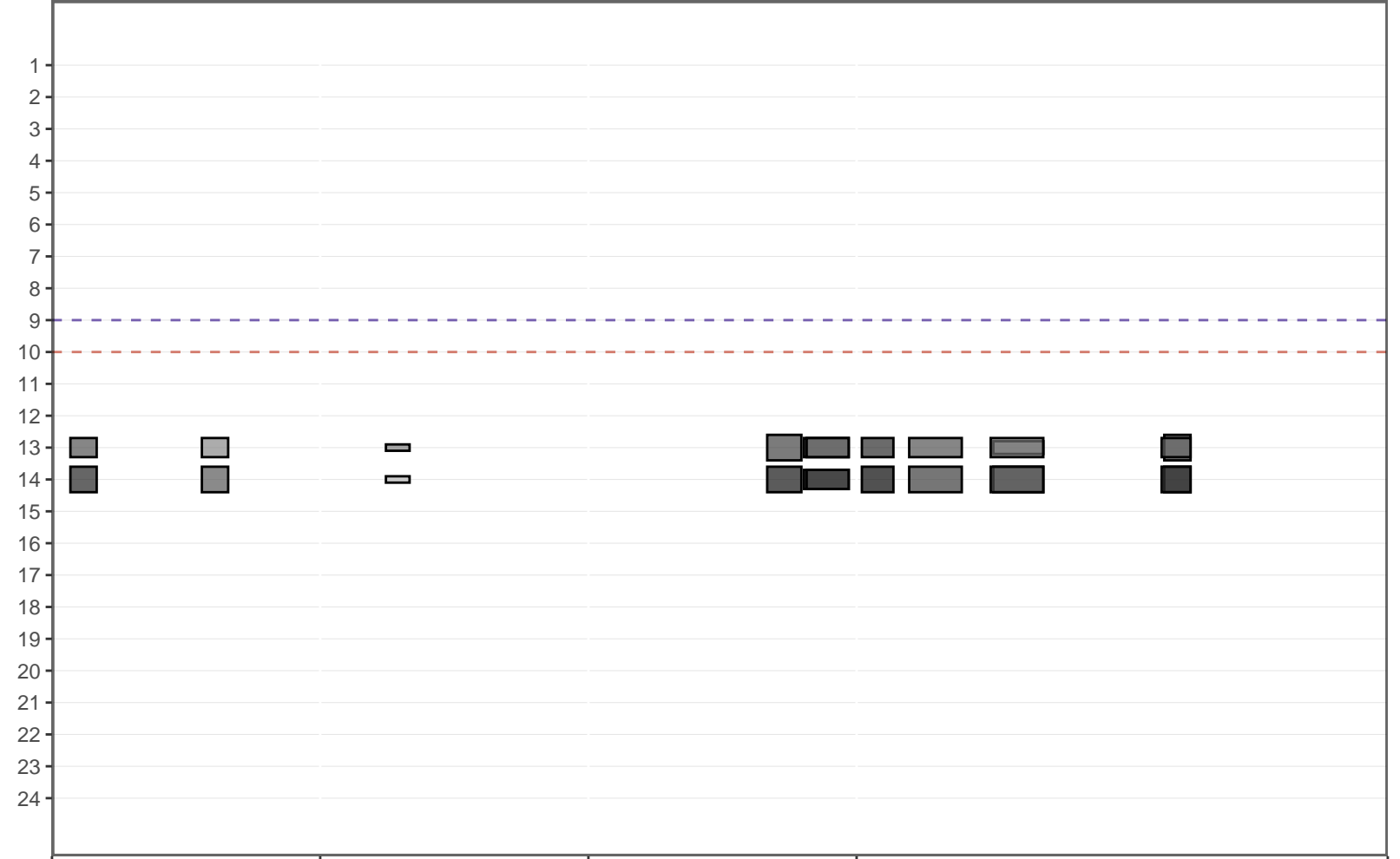
MW indication



Molecular weight

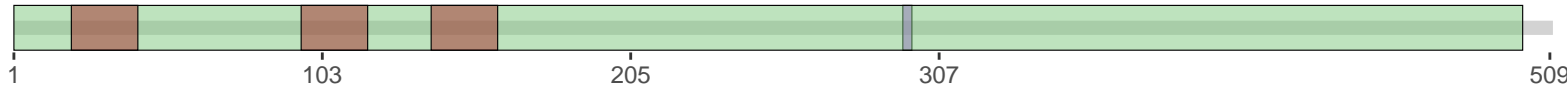


Gel Slice



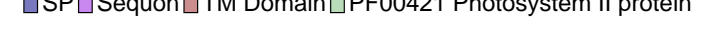
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IAVFFAAYVAGTMMWYGSATPIELFGPTRYQWDGDFYFQGEYRRVSGLAENGLSEAWSKPEKLPFYDYGNNPAKGGFRAGEMDNGDIAGVWLGHPFIRDKEGRELFVRRMPTFFETFFVLLVDGSGVIRADVPRFRAESKYSVEQGVTVVEFYGGELNGVSYSDPTVKYARRAQLGEIFELDRATLKSDDGFRSGPRGWFTHGHASFFLFFGHWHGARTLFRDVFAGIDPDLDAQVEFGAFKLGDPPTKRGAAI

NbL15g08090.1 ATP-dependent_Clp_protease_proteolytic_subunit-like [MW = 16.4 kDa]

No. of times detected



log(intensity)



Values from



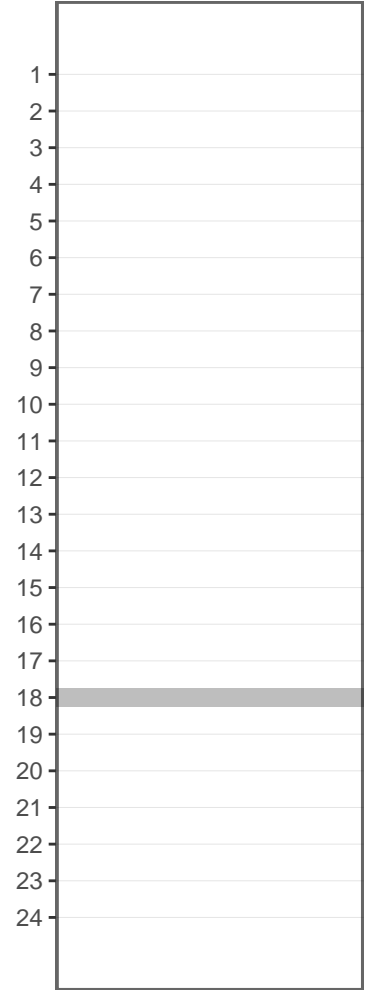
MW indication



Molecular weight



Gel Slice



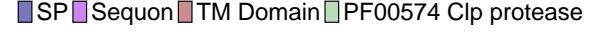
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EITKRLAFPHAWWIMHQRASSFYEAGTGEFVLEAEELKLRKTRFRVYVORTGKPLWVYSEDMERDFVMSATEAGAGVLDLWVE

NbL15g07870.1 probable_phenylalanine--tRNA_ligase_beta_subunit [MW = 66.8 kDa]

No. of times detected



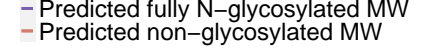
log(intensity)



Values from



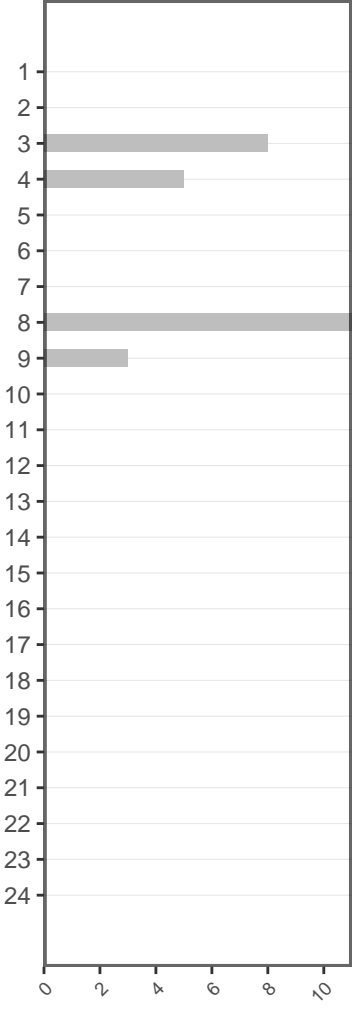
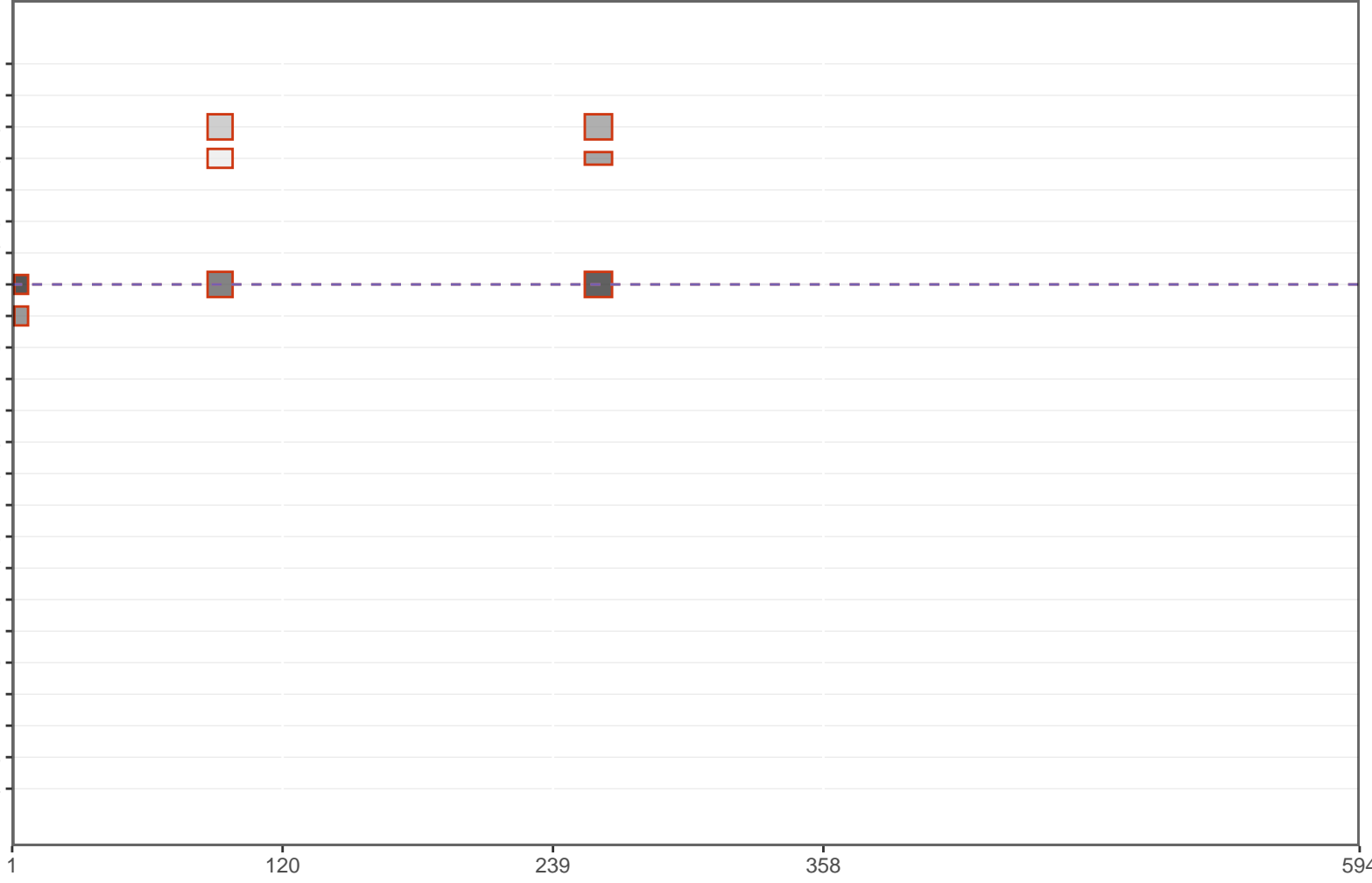
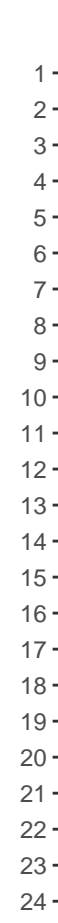
MW indication



Molecular weight

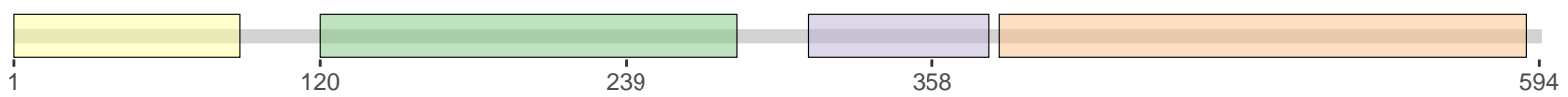


Gel Slice



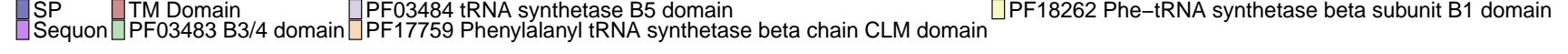
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

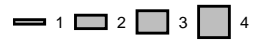


Protein sequence:

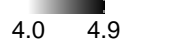
FEVEPKVAYFDGKSFVYFDLSEYNNMPLSEVHTGIGVLPENEVAGLLHKMQLRAVEISENAEYKVFVSVPPTRRSDVLPKDAEDVAIYGVYNEIKRPPASLKLPLSGFSDLRSEIAMAGYTEVLTWILGSKKEISMLNGEEDKSAVIAIDRRTSEFEVFRVNLMPQLLRVGHNDKHPKPKMKEVGDVLLDGTGDVAVNRRLAALYGGANGSGFELHGLVDRIMEATGTSFVSPDGDGEGYIERSEEPFLGRRGAKVYKRNIGTFRGIVHPKVLKEFDPPDCI

NbL15g07320.1 protein_TIC_22_chloroplastic [MW = 33.21 kDa]

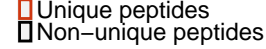
No. of times detected



log(intensity)



Values from



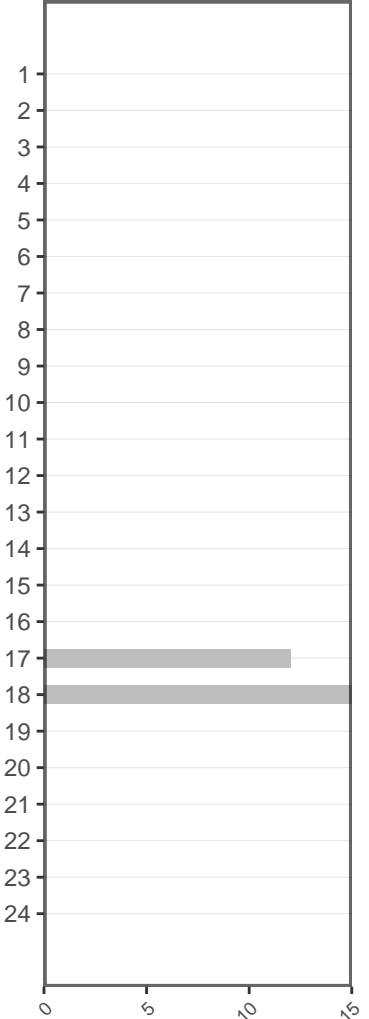
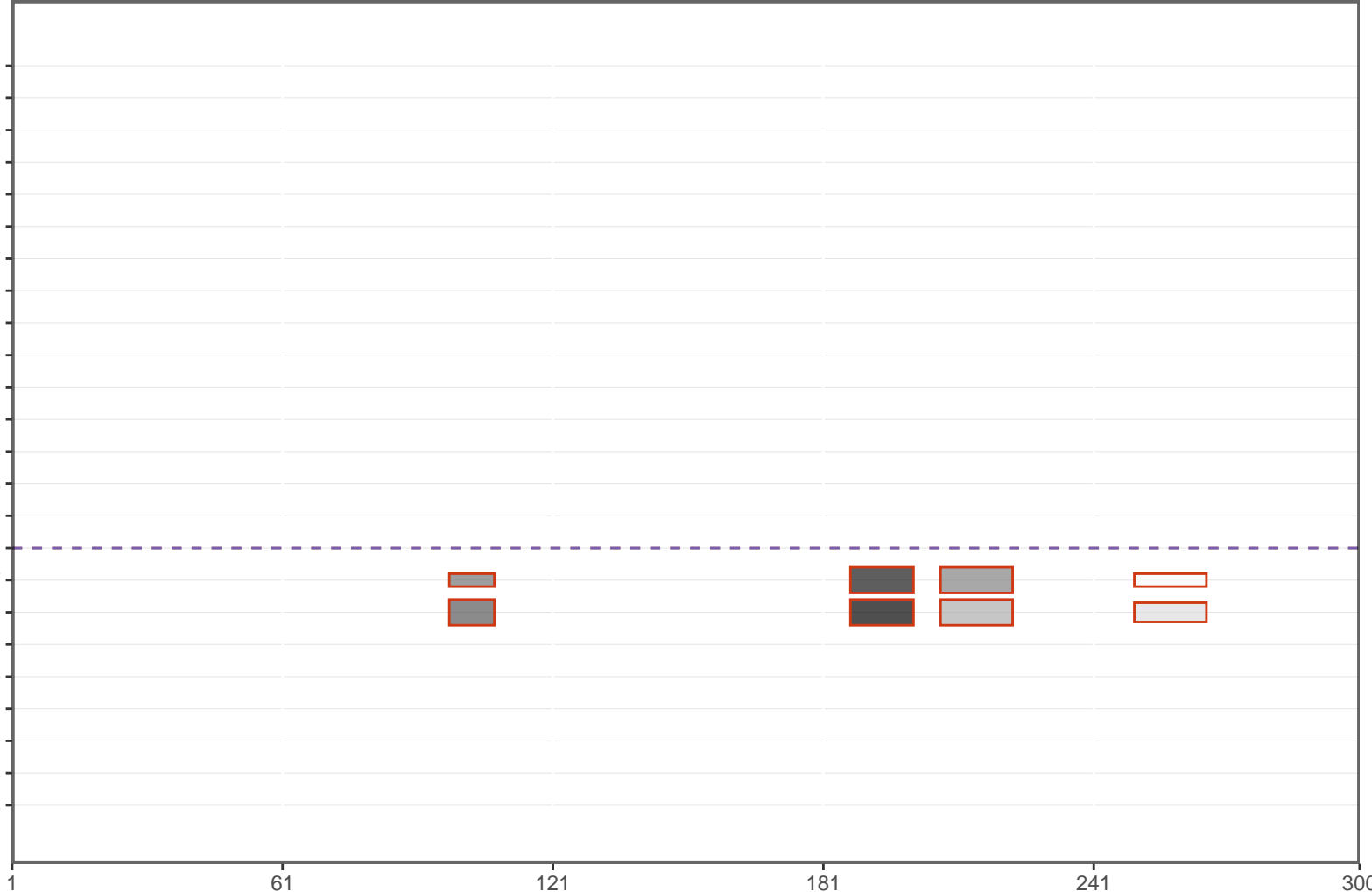
MW indication



Molecular weight

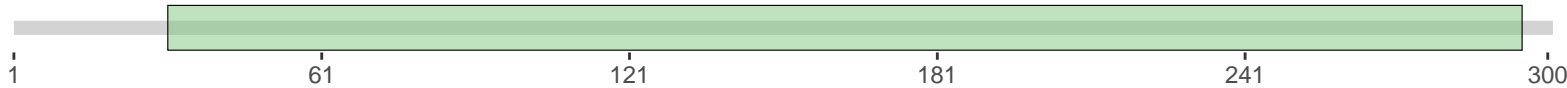


Gel Slice



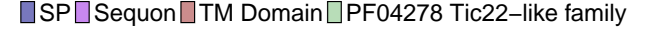
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SLLCFRQEDAEAFIAQVRLRKRKGEVRRGGAKVVPFLFDGVMMLKVEGIAFRFLPDPVGVQNAIESKLSGVNKTFFNGVVPVFDGDLVWKKRNRPRVPIYFRKEDIKELSSRASRAGVSGNHIMVGSLEDVLRKMEISGRHSGWEDLFRPPGKSHSGHQIDVTKA*

NbL15g07200.1 non-specific_lipid-transfer_protein-like [MW = 13.79 kDa]

No. of times detected



log(intensity)



Values from



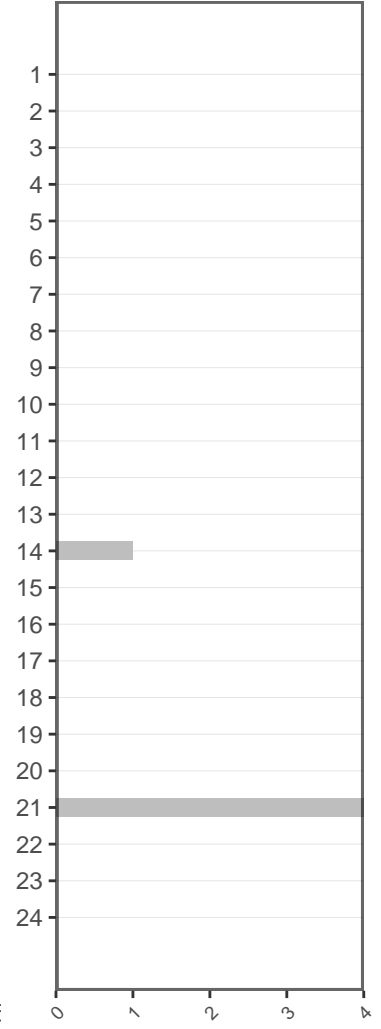
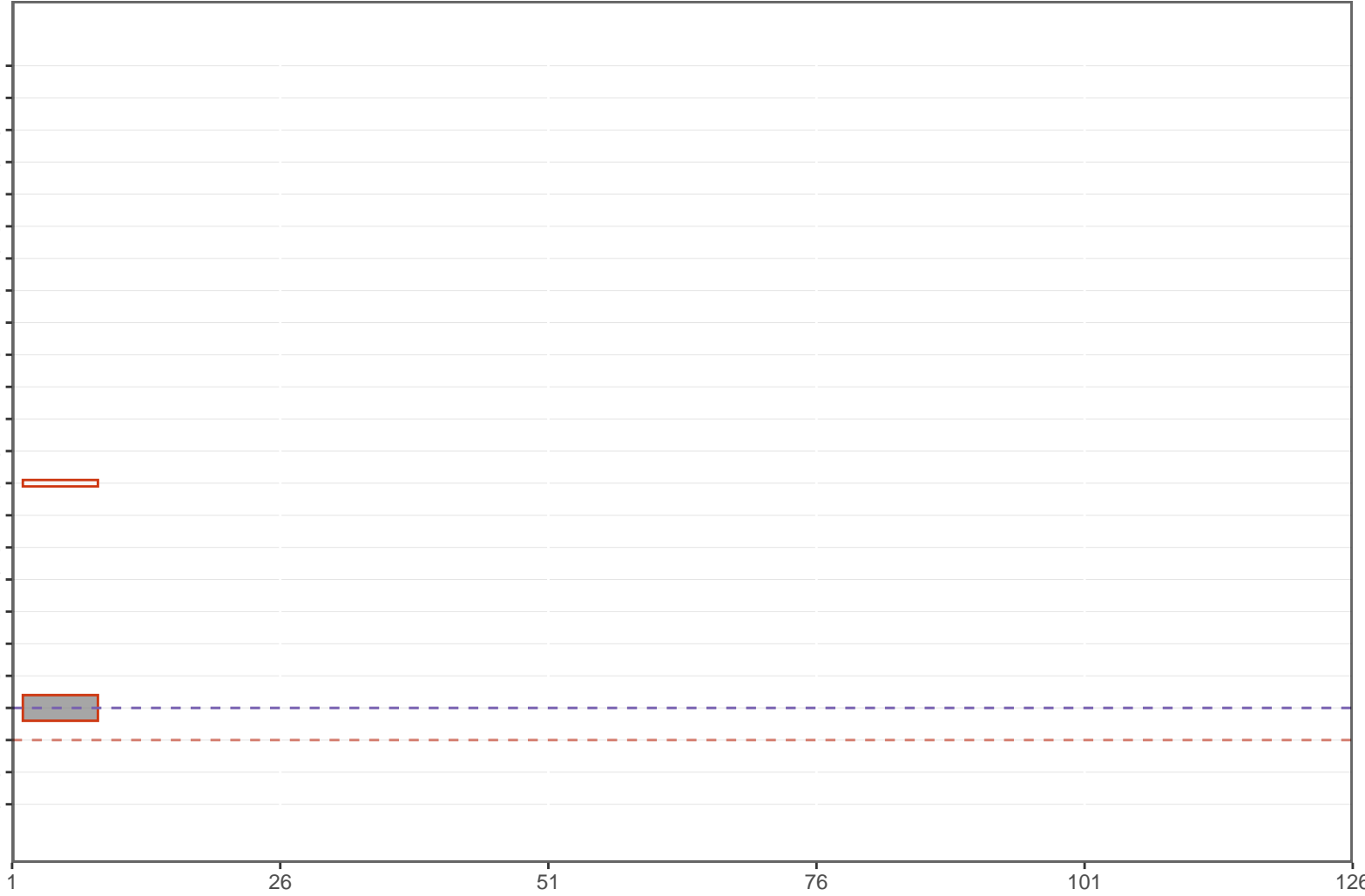
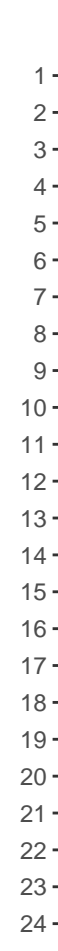
MW indication



Molecular weight



Gel Slice

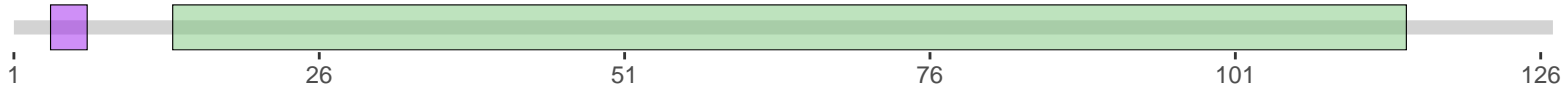


Protein length

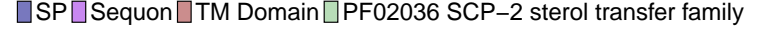


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VVYVLDLKKGETKEGPEYEGGKPDATFSFKDDDFVKATGKMPQIAFMRGAMKKKGSISAQKFTPDFPKPKM

NbL15g07080.1 annexin_D5 [MW = 35.56 kDa]

No. of times detected



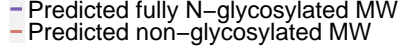
log(intensity)



Values from



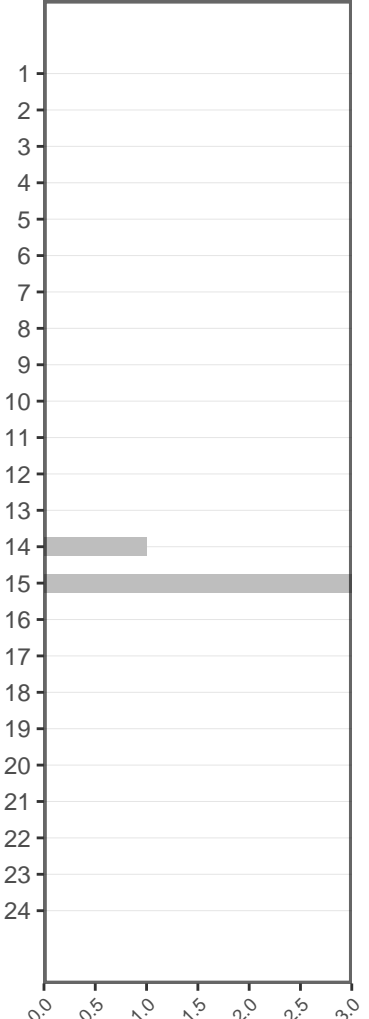
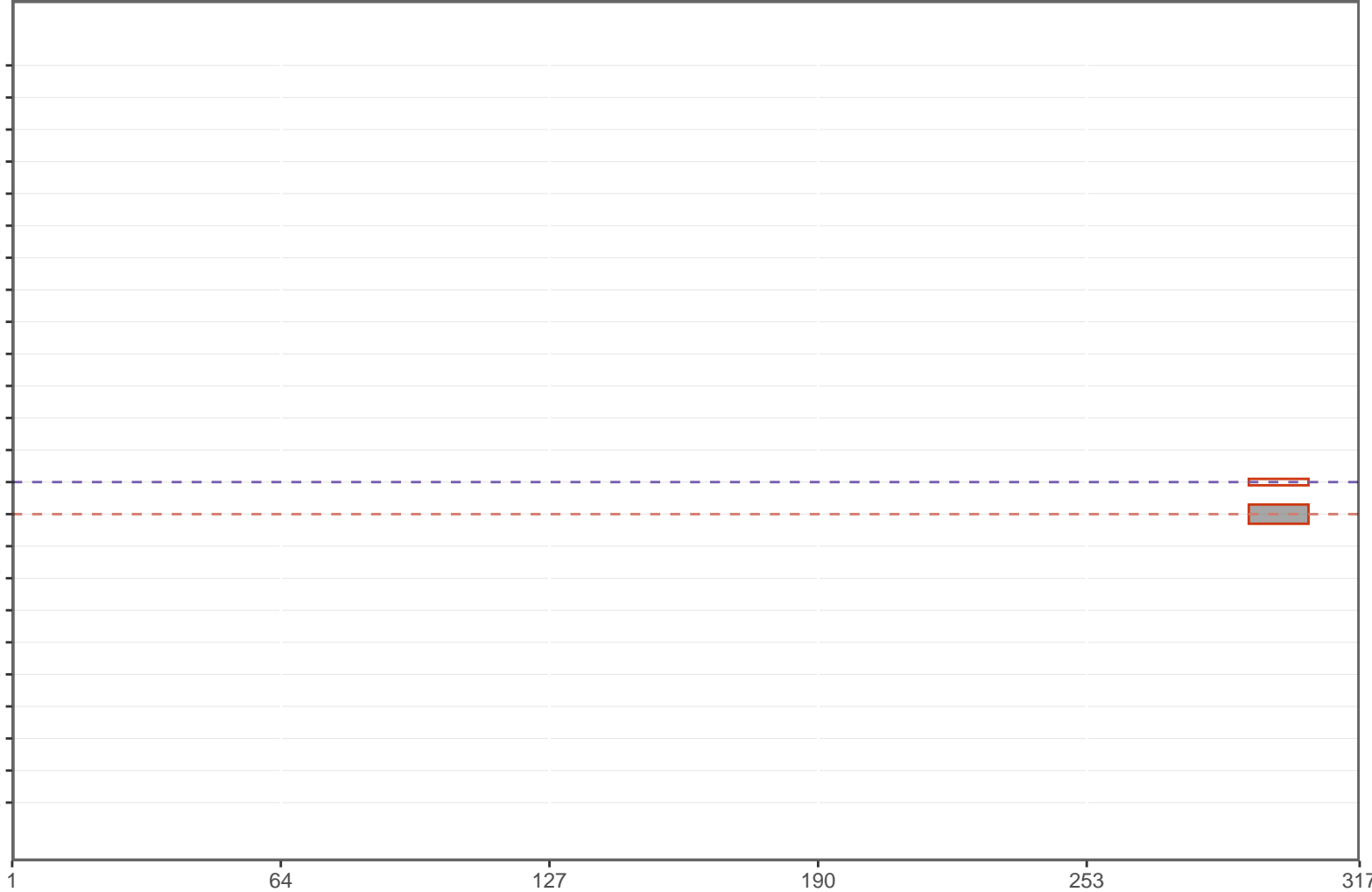
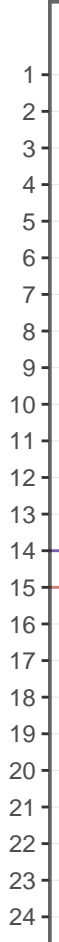
MW indication



Molecular weight



Gel Slice



Protein length

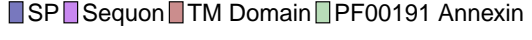


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KKLLLAFLVSTMRVYEGPEVDRAIVDQDAKALFKAGEKLGTDKTKRIRFSEBRRAHLAAVBAAYHSMYGRELKKAVNETSGHFEGLLTLILLCAENPKYFKALHKAMKGLGTDNDTLIRIVVTRTEIDMQYKAEYQKHKKSLNDAVHSETSGDYRFLLSLGGPH*

NbL15g07050.1 MFP1_attachment_factor_1-like [MW = 23.63 kDa]

No. of times detected



log(intensity)



Values from



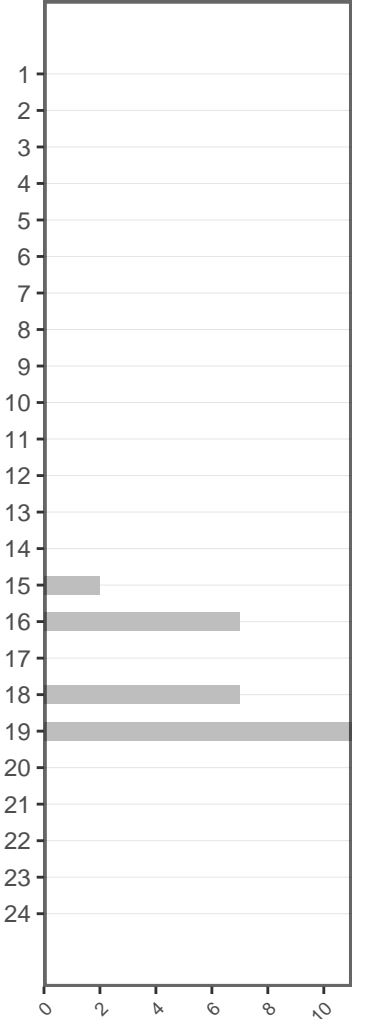
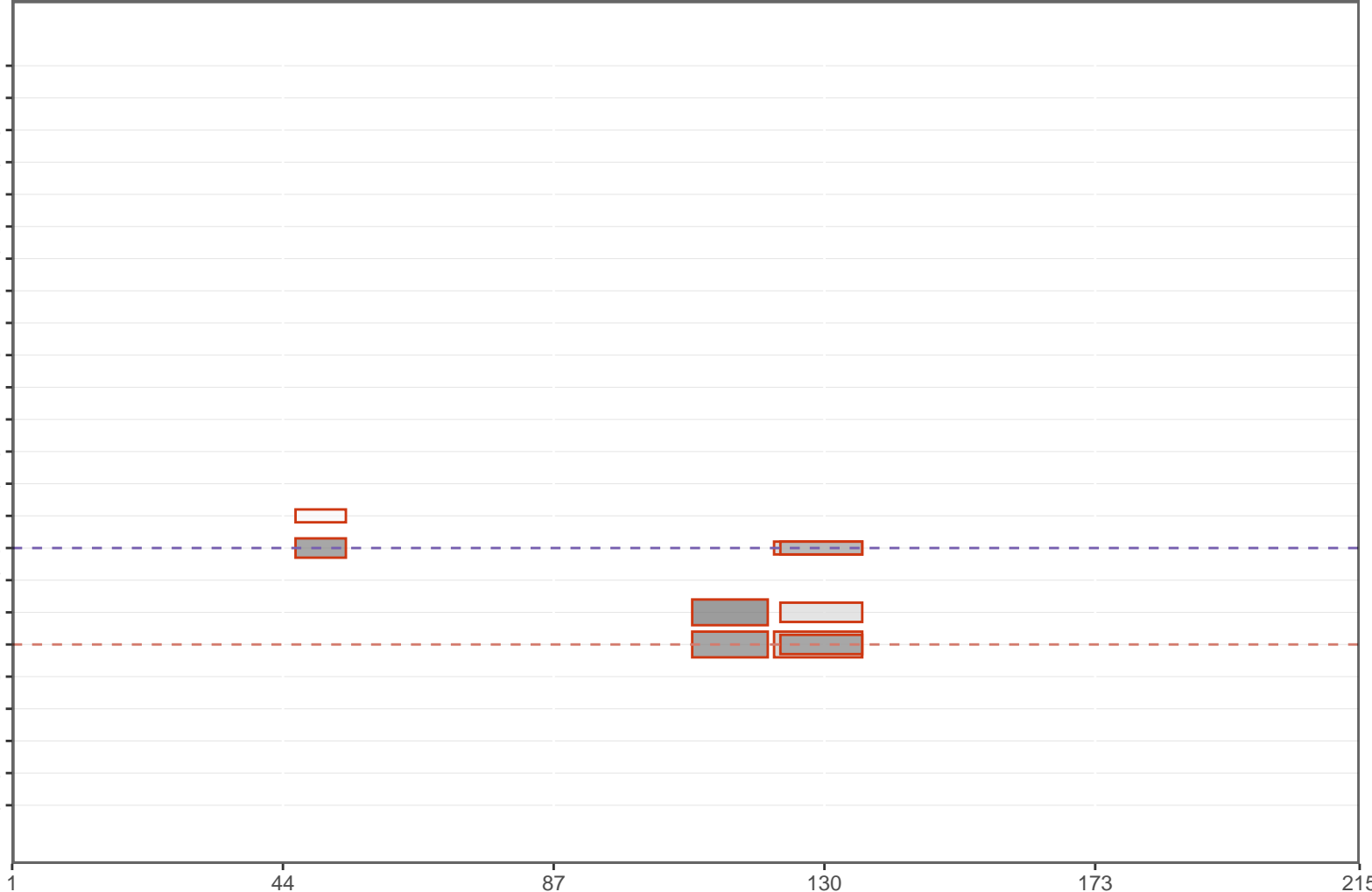
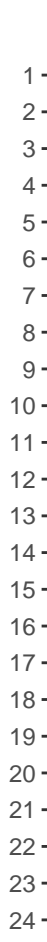
MW indication



Molecular weight

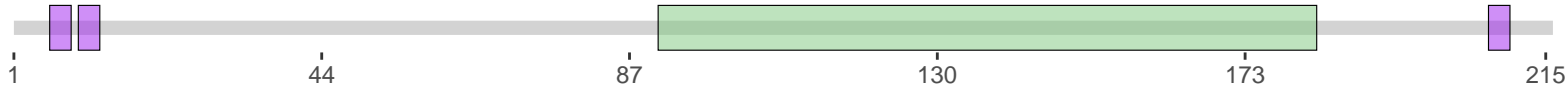


Gel Slice



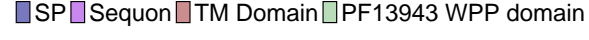
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FSIVPPTORTRDVWGRUEGLSTPBLEKRYGTPIHDEASDIANKLIEEFAFTAGTAGDDDDIEIQVYKESIKRMLDAVGRSTPSADDSAAITDTETREPIGDSAVTGENSSVYKFP

NbL15g06830.1 low-temperature-induced_cysteine_proteinase-like [MW - SP = 49.15 kDa]

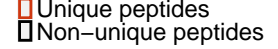
No. of times detected



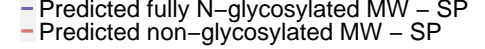
log(intensity)



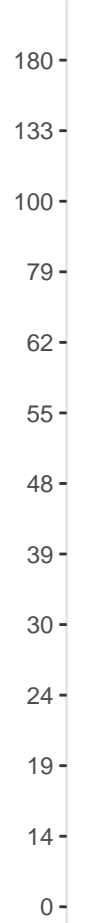
Values from



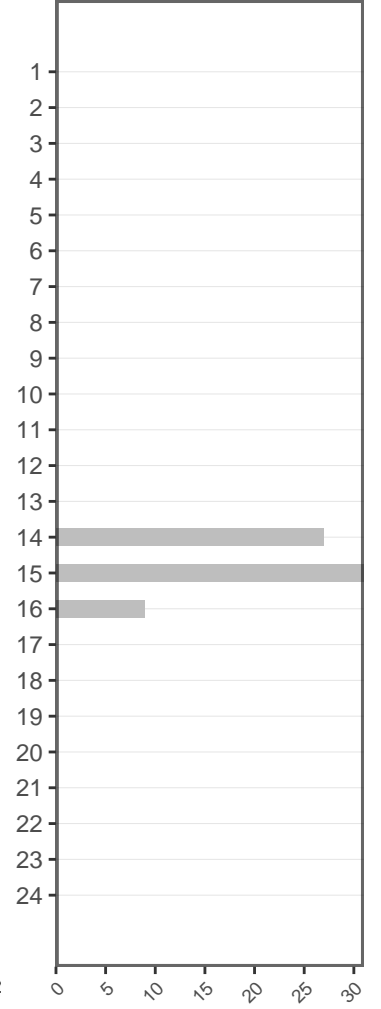
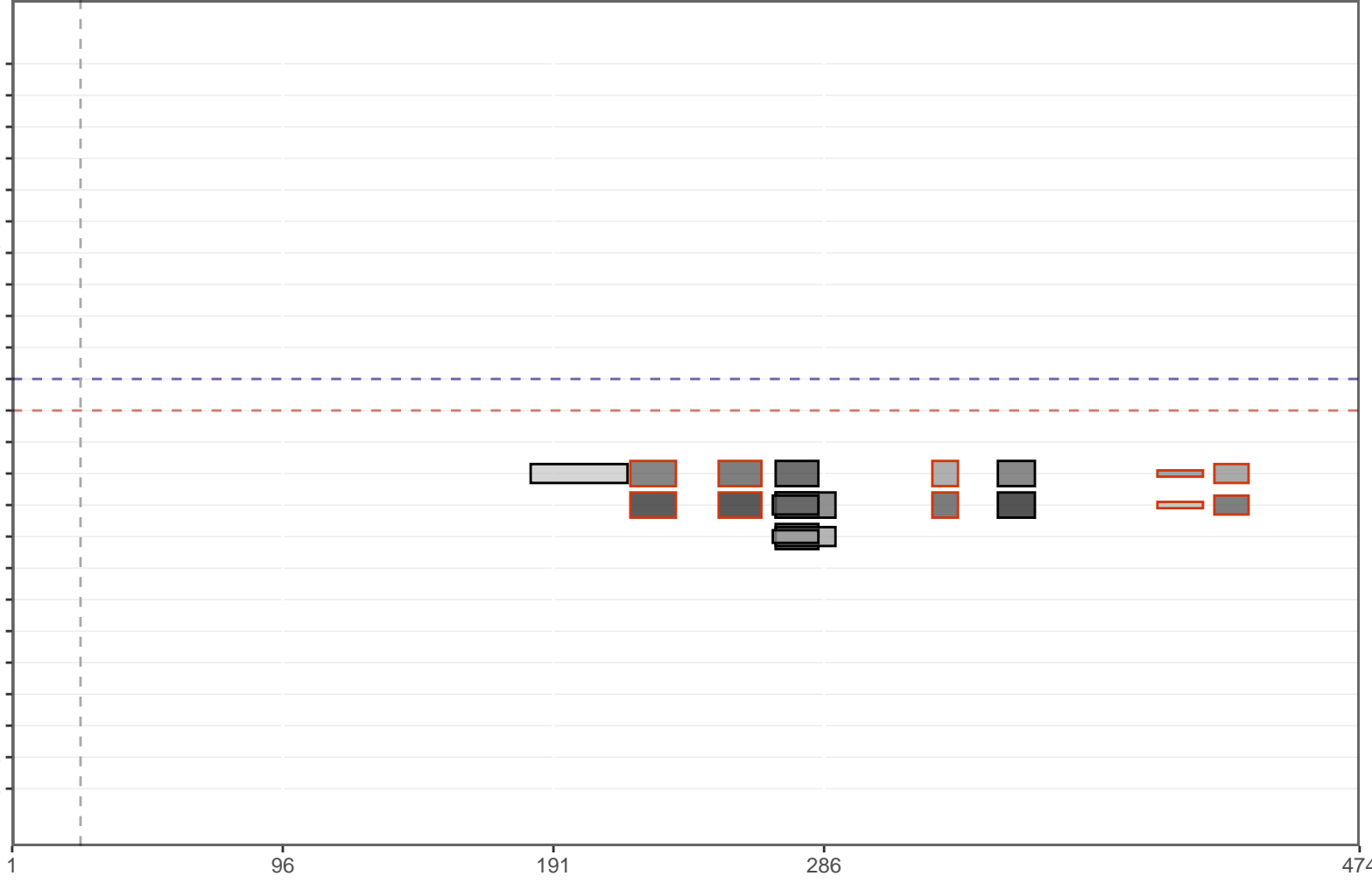
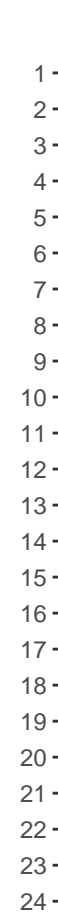
MW indication



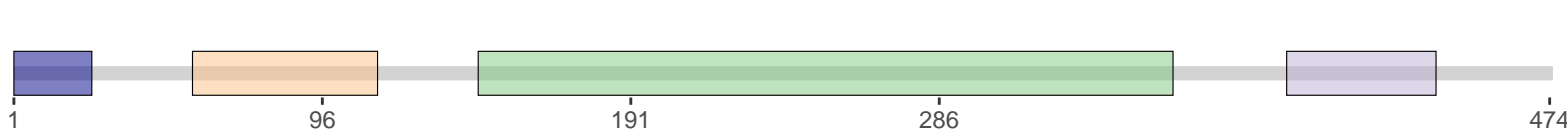
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

IEDDYFYKAKDQKGDGARKNARVITFDVYEVDPNDEKALKKAWAGGPVSVAIIEAGGKDFHYSKGFTEGEGAAVDHGVVAVGYGSENGMDVWWRNRNWSGASWGEKYLRMQRNINGNPKGLGGIATISYPLVKTGQNPKPAPSPSPSPKPTGCDDENECFPTGTCDDVYEHYKGFVWGGPMEGATCGDKHKBGGPHDVPVGNVYKAGTCSISKNNPLGVKAMQHLAKPSGTFANEKGRPS

NbL15g06780.1 uncharacterized_LOC104223854 [MW = 58.49 kDa]

No. of times detected



log(intensity)



Values from



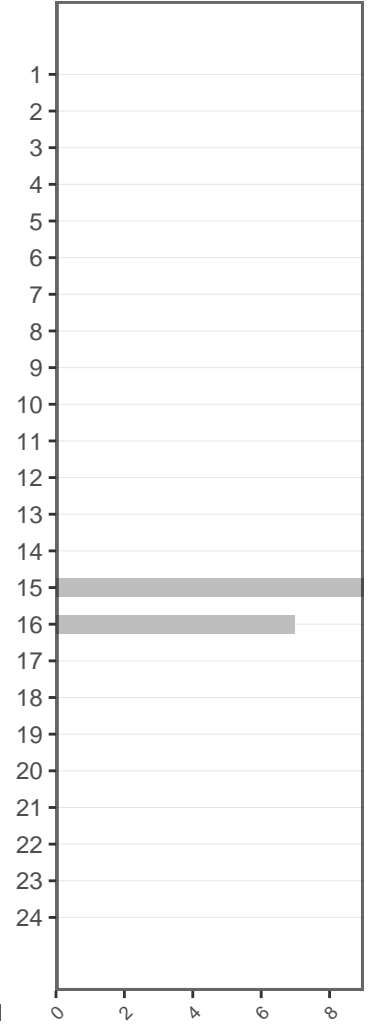
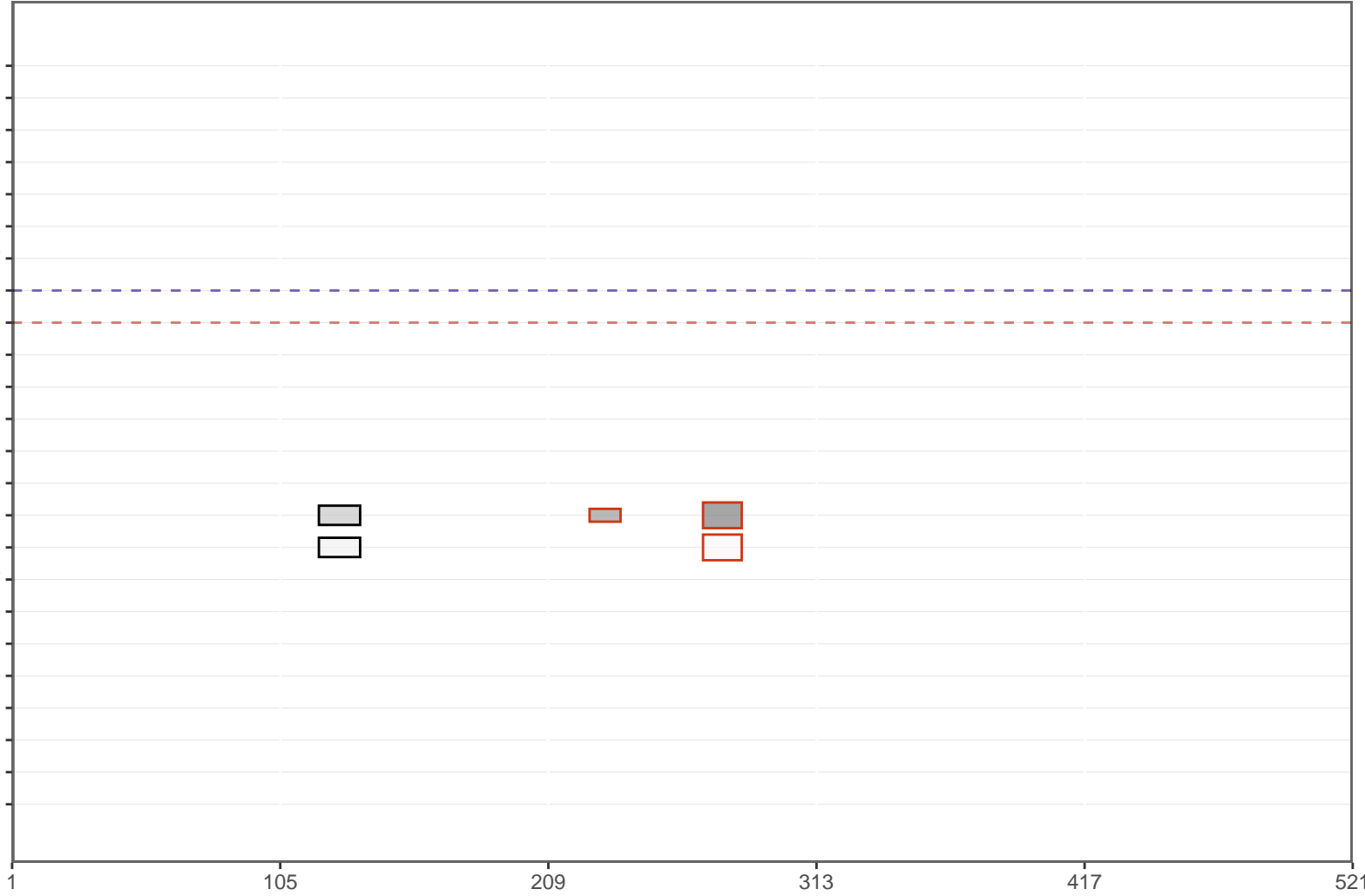
MW indication



Molecular weight

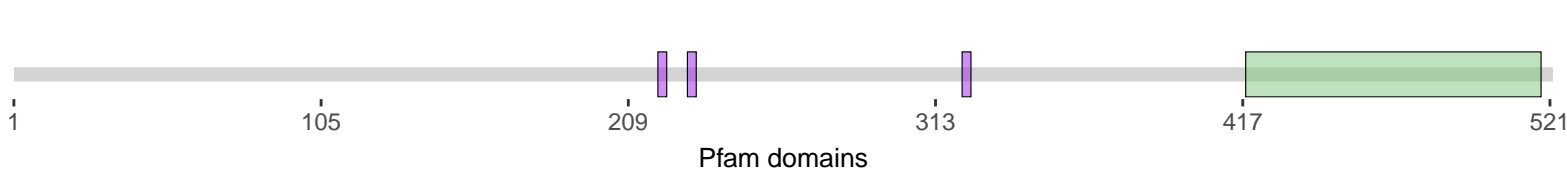


Gel Slice



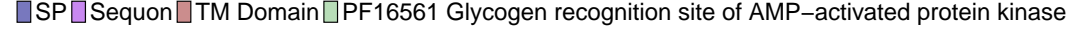
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

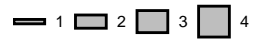


Protein sequence:

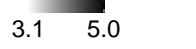
IQNGELSDVVEDSGFQIFNERGSEGVGVGQNVYKTESTTPNGNSAEIFNGNSMPRSPQHVHEPCDGLSFDIRNNSLSTELTMAEGRNSADVEPQKVENQAEINRKFMLHKGKELETLQKGGEEERLLSLGKQKAREISEAQKLISEKDAELNAEDSLGKLEVEVQLADGESVEVAGSFGVWHHKKMKDLESSESTIDPDQELSSGDVDVDTGTRKPRLWKTMLWLYPGMVEKFKVVDGHVTTDPQMESEVIRGAVHNNLRLVDR

NbL15g06760.1 S-adenosylmethionine_synthase_3-like [MW = 43.66 kDa]

No. of times detected



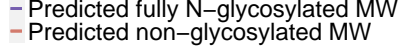
log(intensity)



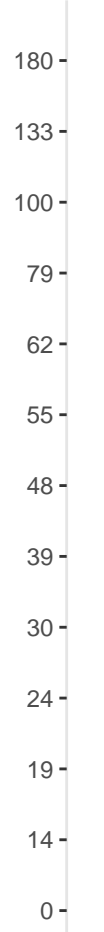
Values from



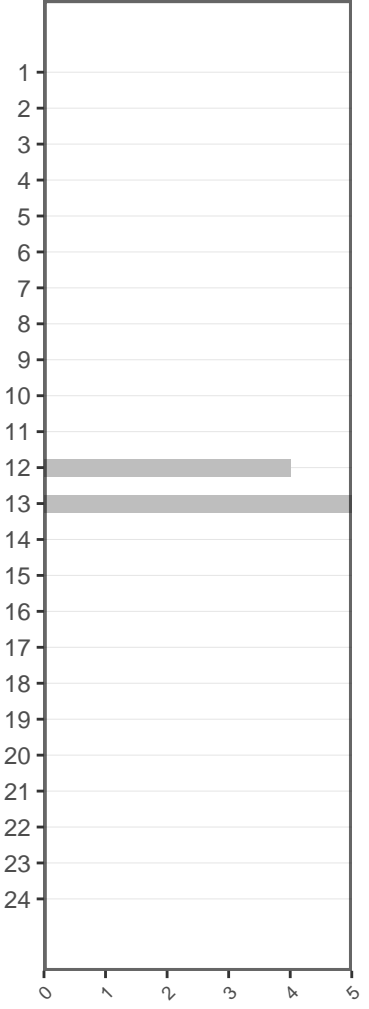
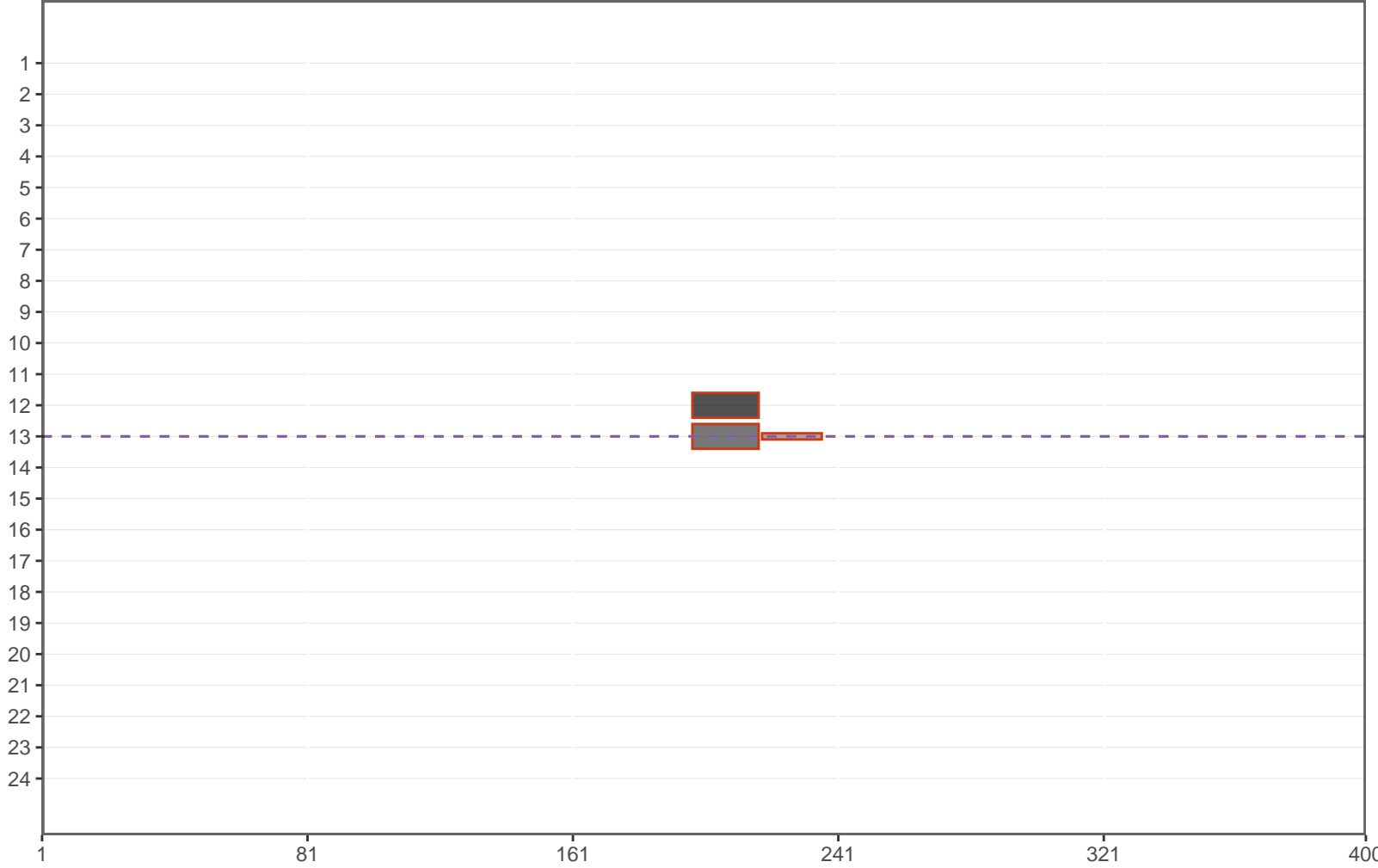
MW indication



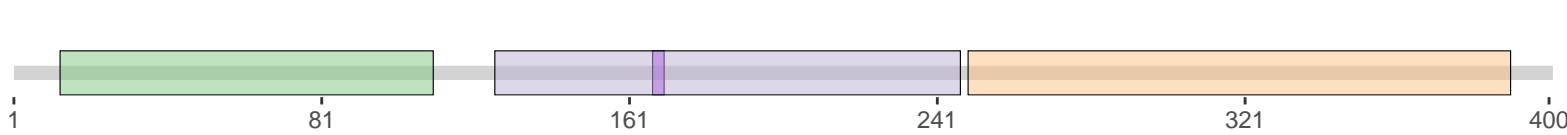
Molecular weight



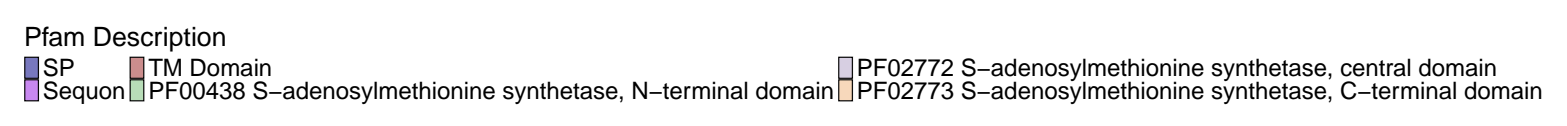
Gel Slice



Protein length



Pfam domains

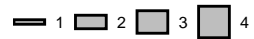


Protein sequence:

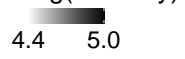
<small>NDNGAMVPRVYITVALJSTGHDETVTNDGIADLKEHVKRVPAGYLDEKTFHLPNSGRFRVGGPHGDAGLTGRNIDTYGGWGAHGGGAFSGKDPFKVDKRSQAVVIRGAASKVAAGLARRCIVGVSEVAGVAEPLSVFVDTYKTKGTIPKDKLALKEKDFDRPGMMSINLDLRRGNFRYQKTAAYGHFGRDDPDDFTWETVKKLKPKA</small>

NbL15g06610.1 E3_ubiquitin-protein_ligase_MIEL1-like [MW = 34.18 kDa]

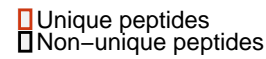
No. of times detected



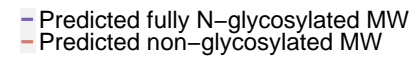
log(intensity)



Values from



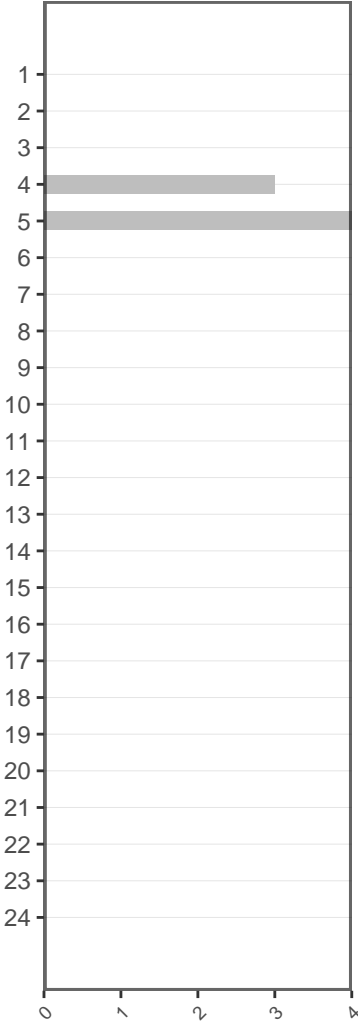
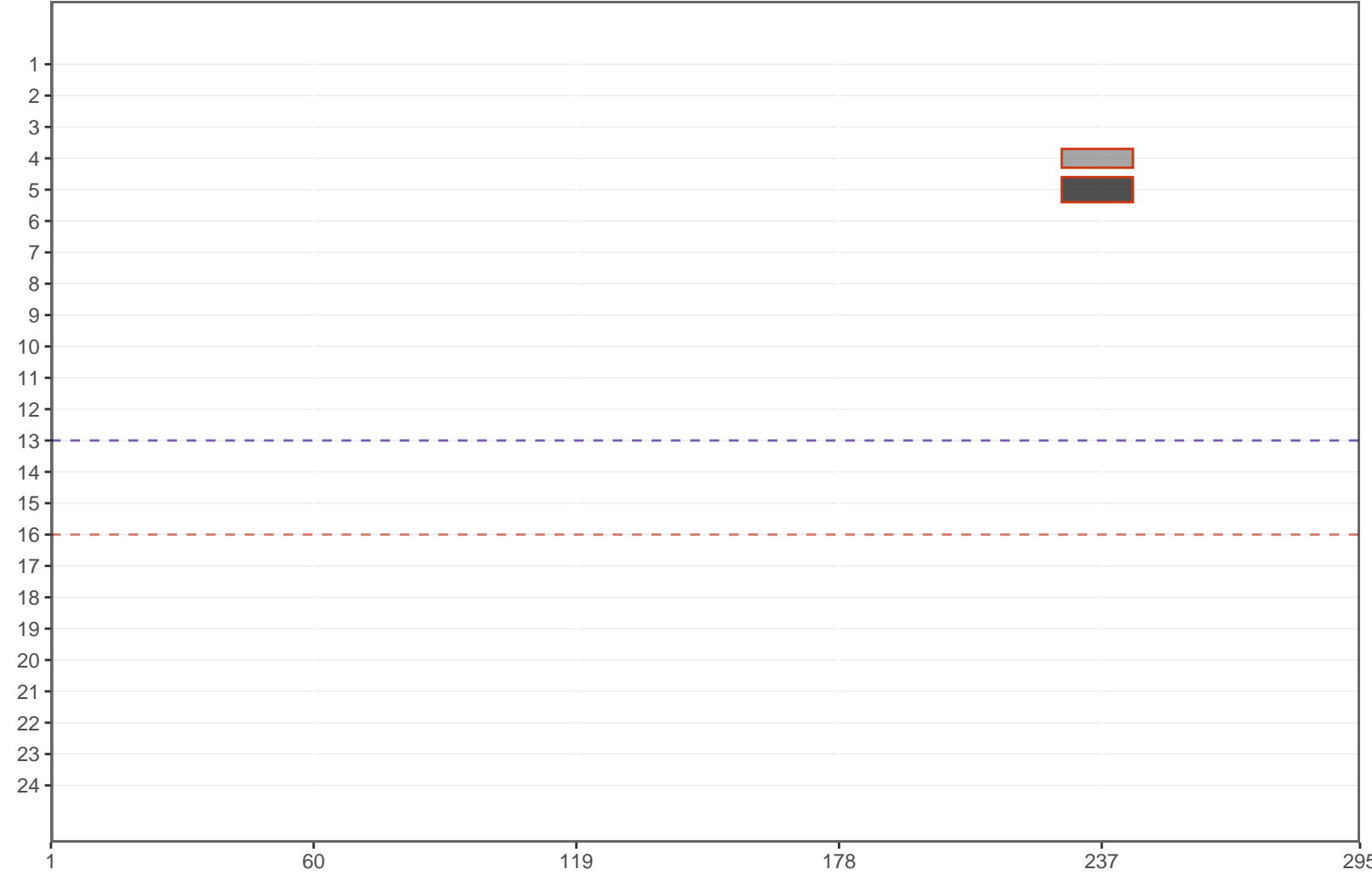
MW indication



Molecular weight



Gel Slice



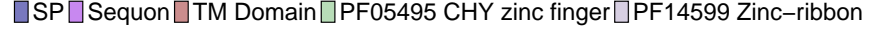
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL15g06460.1 UDP-glycosyltransferase_73C3-like [MW = 55.83 kDa]

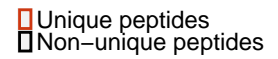
No. of times detected



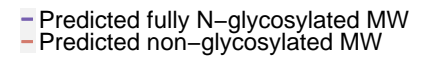
log(intensity)



Values from



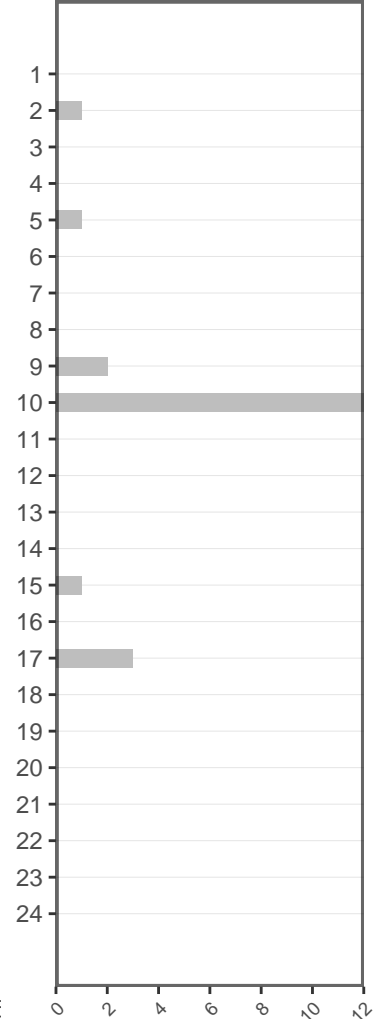
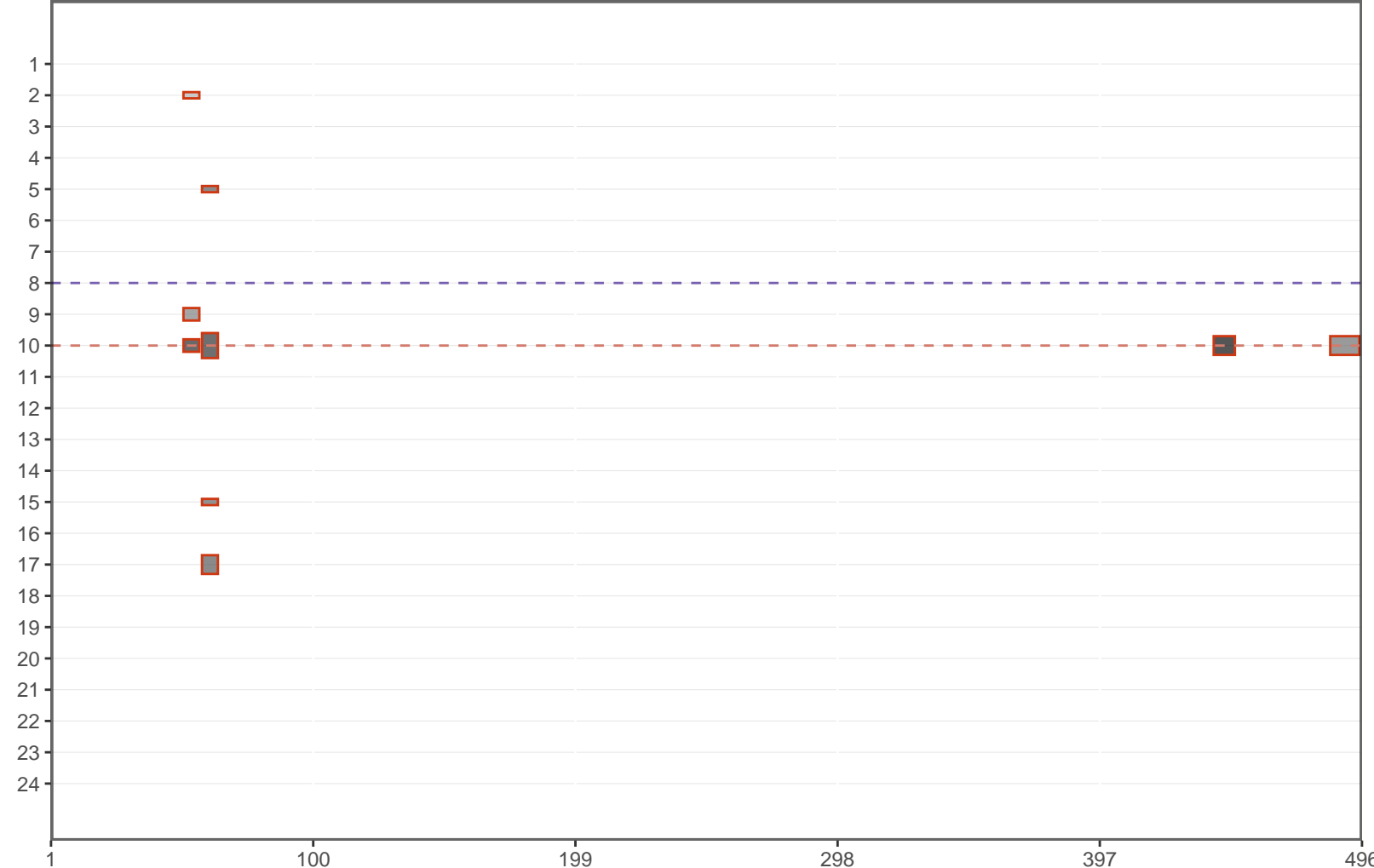
MW indication



Molecular weight



Gel Slice



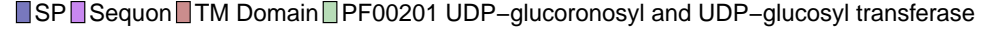
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LKKAKGKQWITGIPVSLCKNEKQDKAERGSKASIDEHHCLKWLNSKEPDSVLFVGLSLRFPASQMIELGLALESSKRFPIVVRHSDELKKVLSNEENFEERIKEGQILHGWAPQVLLSHASVGGFVTHGGWNSISIEGISTGVPMITWPLFAEGFQNERLFTNVLKGTGKSGVENFVVFLEEEKVDTGVNKKDDNKMKIEKLMGEEEAARRRERANKLGEIARKAVEEGSSHLNLTLDGDKVKEGANFLENGFDV

NbL15g06380.1 threonine_dehydratase_biosynthetic-like [MW = 60.67 kDa]

No. of times detected



log(intensity)



Values from



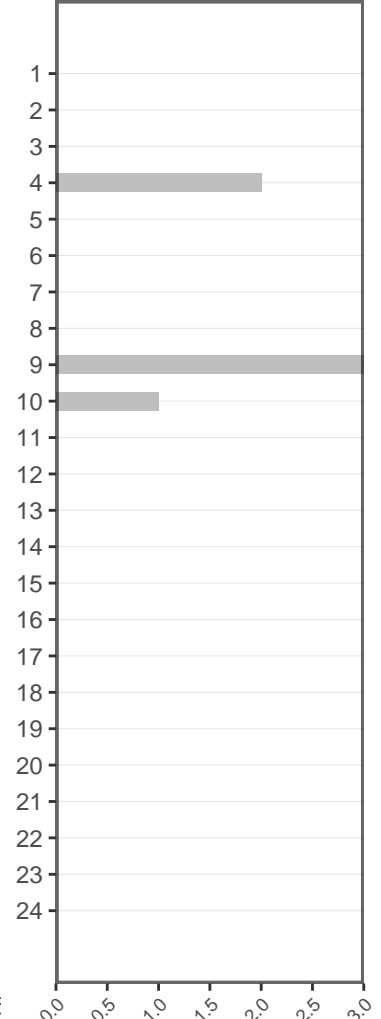
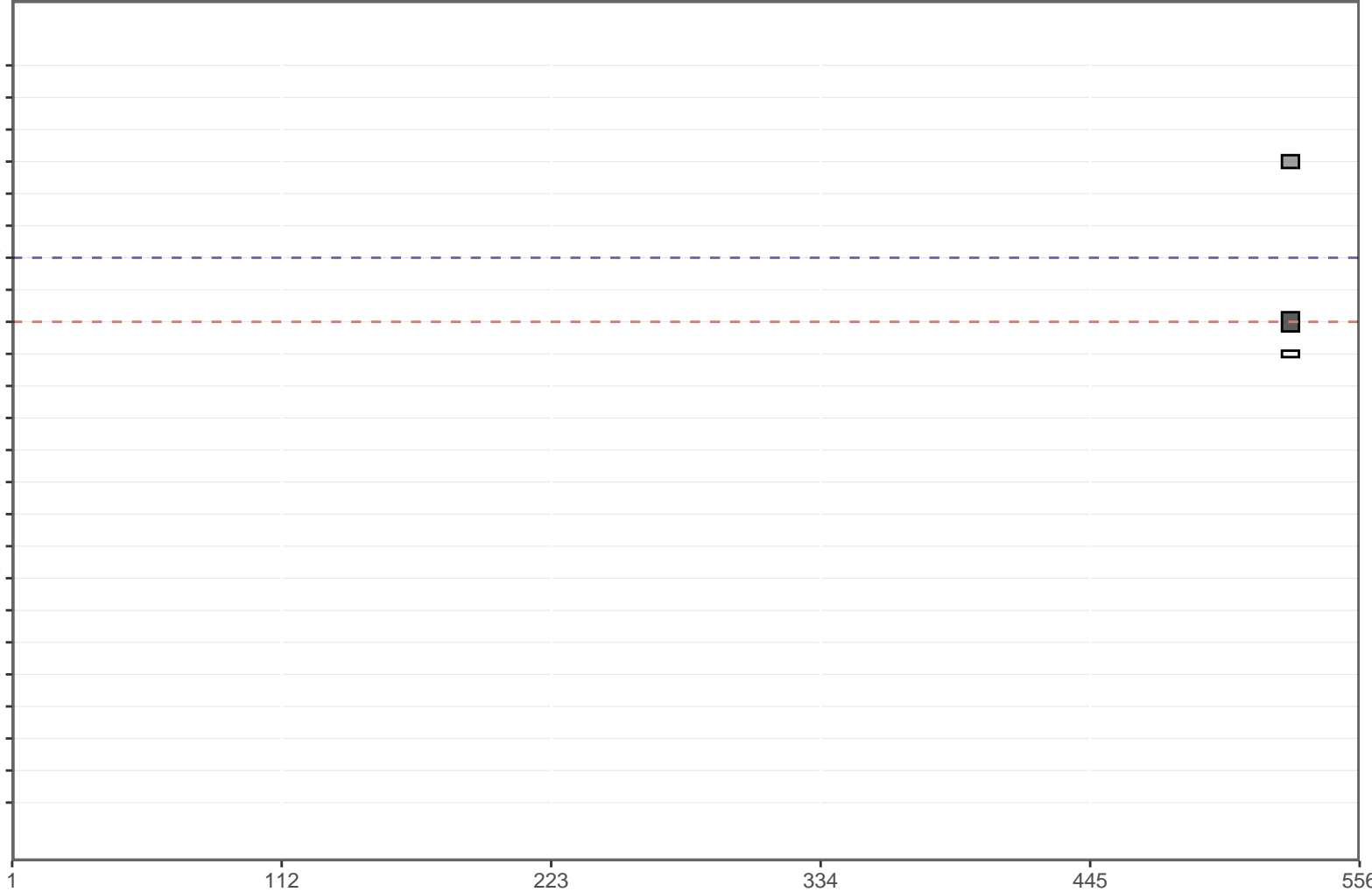
MW indication



Molecular weight

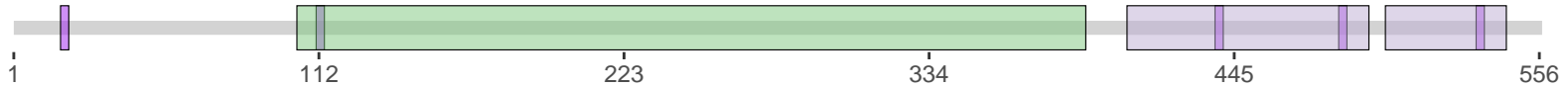


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00291 Pyridoxal-phosphate dependent enzyme
- PF00585 C-terminal regulatory domain of Threonine dehydratase

Protein sequence:

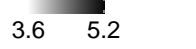
LIAGVATYFKRVAHPHTKIGVEPFGASSMTQSLYRGERVLEIGVDNFADGWAVAVLVGEETFRLLGKDLIDGMLVSNDAISAANKDYYDEGRNLETSGALAIAGAEAYCKYYDKGSEVVAVASGANMDFSKLKLVDLADIGGQREALLATFMPEEPGSKKFDGLAGLNMTEFKYRYSRGRKDALVLYGVVTTKSDLESMLERMKSSGLNTVYNTNINLVKHEHRLMCGGRSEPSNEIFQGFPEKPGALRKLDFASPRWNSLFFHYREGGELGVWIPSSKR*

NbL15g06370.1 peptidyl-prolyl_cis-trans_isomerase_FKBP16-4_chloroplastic [MW = 25.06 kDa]

No. of times detected



log(intensity)



Values from



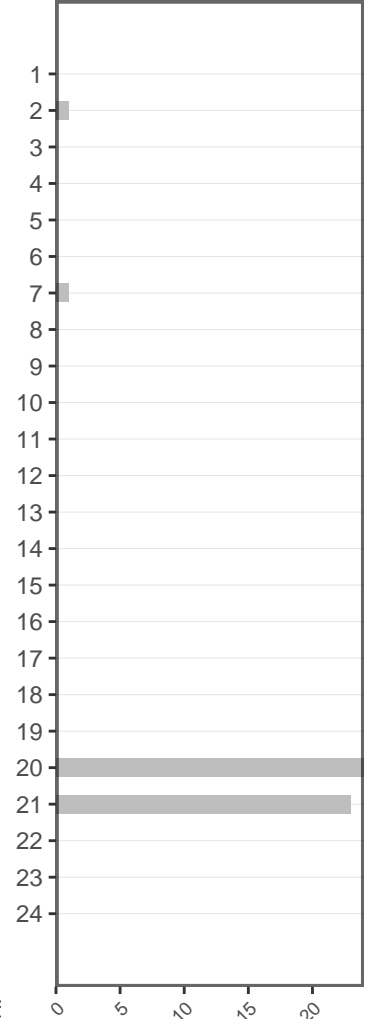
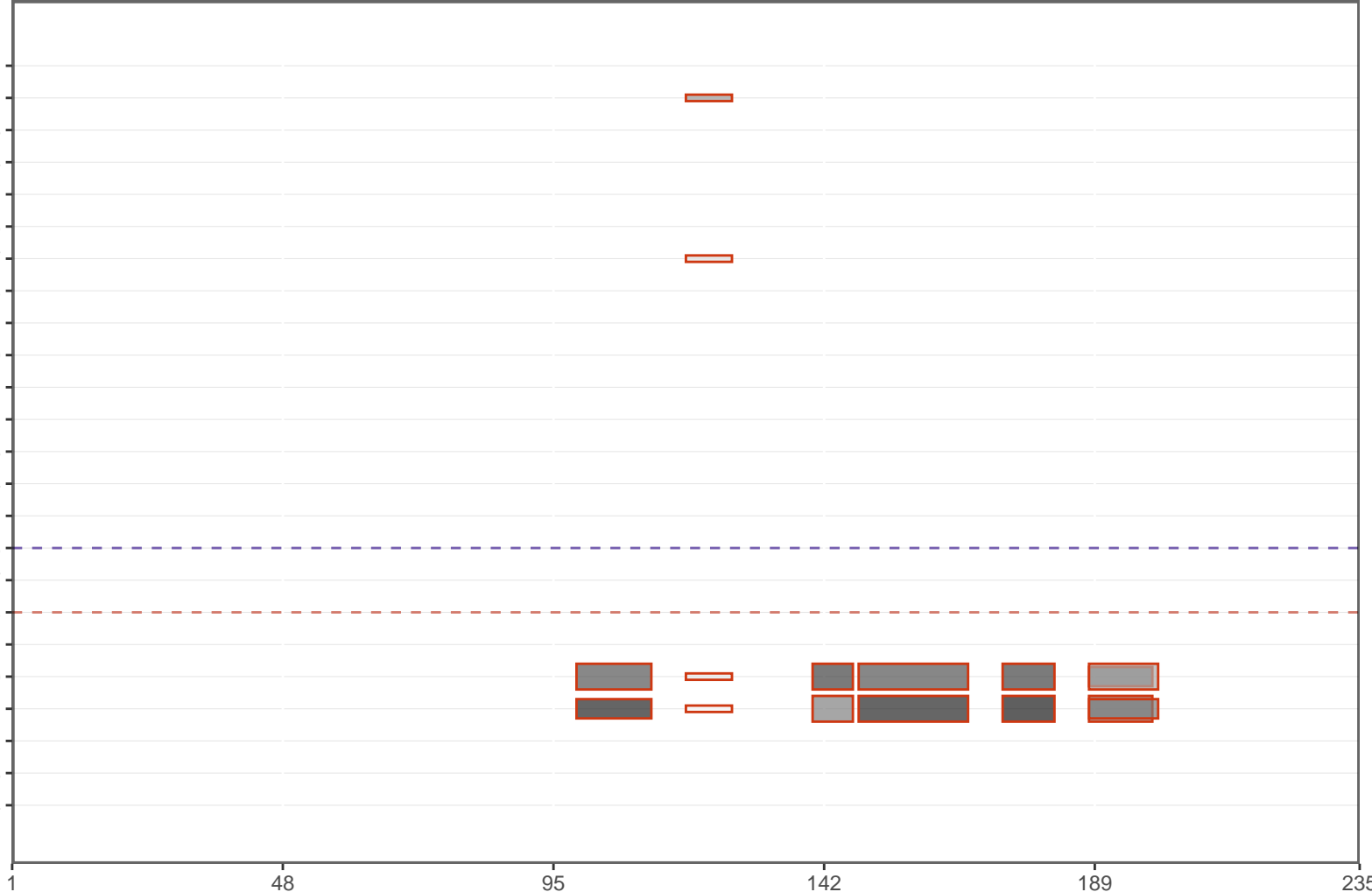
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

TLPNGUKYDLYKVGNGAEAVKGRWRWHYVAKWRNFTMTSRGGMGVGGGTFYGFDFVGGSERGTVLKGLDLGVGGMRVGGORLLVPPELAYGKKGVDGIPPNTAIEIDELLSIKGSPFGTAVKVVVEG

NbL15g06150.1 geranylgeranyl_pyrophosphate_synthase_small_subunit_chloroplast-like [MW = 36.05 kDa]

No. of times detected



log(intensity)



Values from



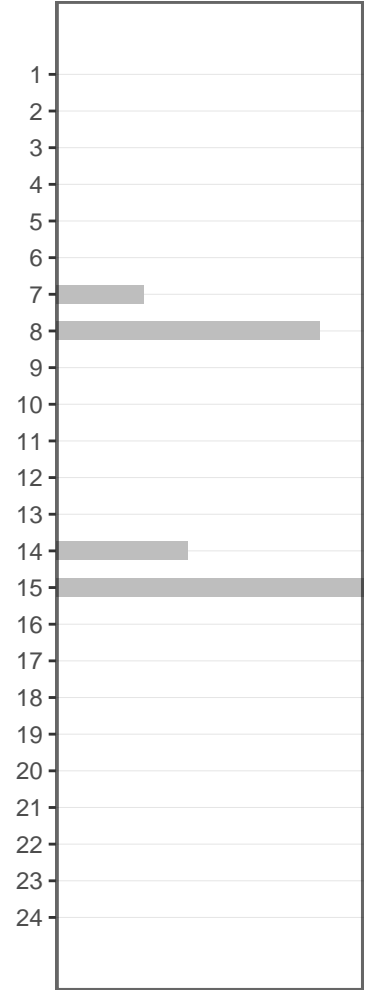
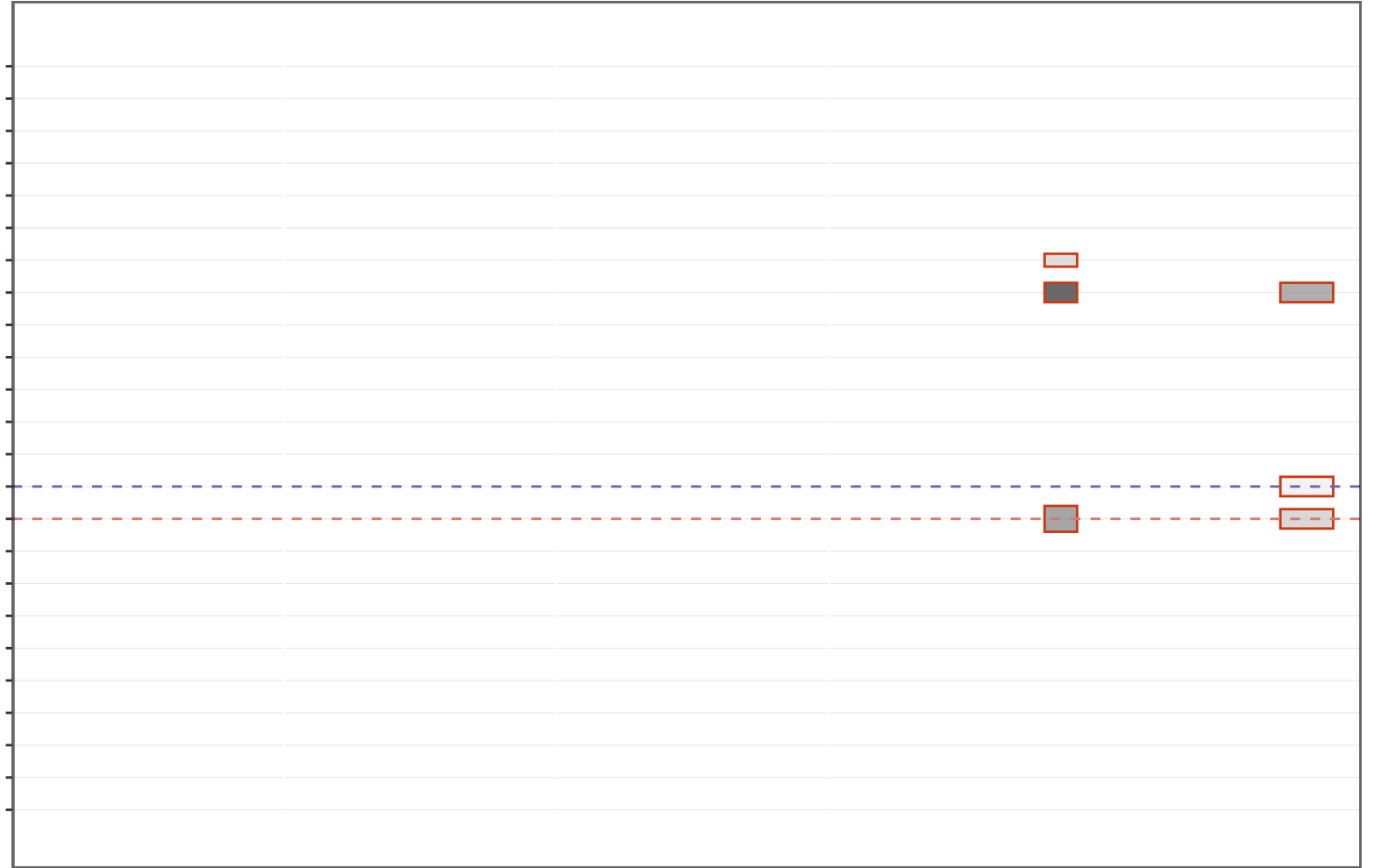
MW indication



Molecular weight

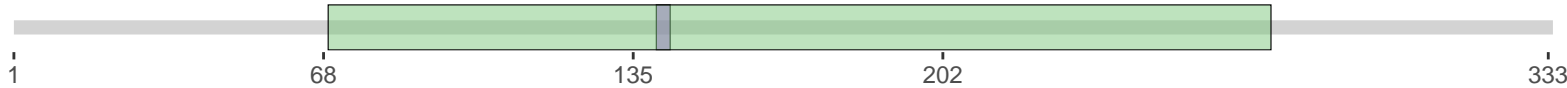


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DALFPLGQYSHFSPDNLVPEDRVLRKVTETARAVGSGTGMAGGFLGLEGGPNAVDVGEKKYKYMGECSAVCGGLLAGASDEEIQHLRRYGRVGVLYRVVEDLLEAKETGDKSEGGKXKXGKSYVSLYGIKAKKVAEDLRAGAKRELDGLGKYGDKNVPLVYFVDVAADRGFSLDN

NbL15g06100.1 peroxiredoxin-2E-2_chloroplastic [MW = 32.8 kDa]

No. of times detected



log(intensity)



Values from



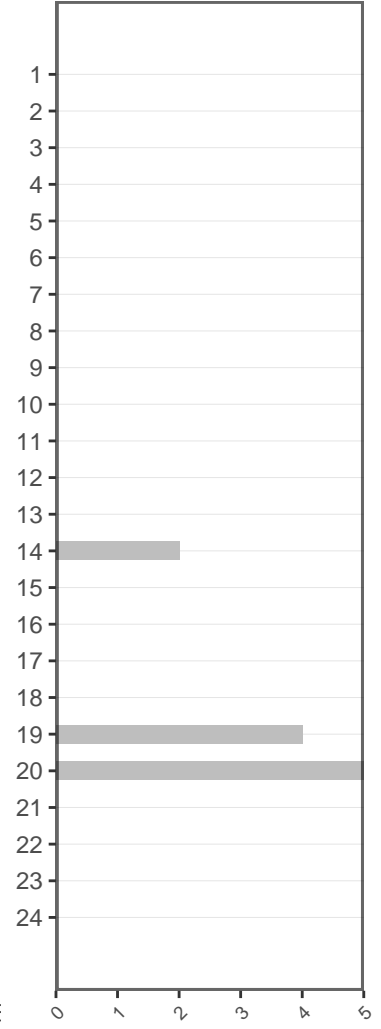
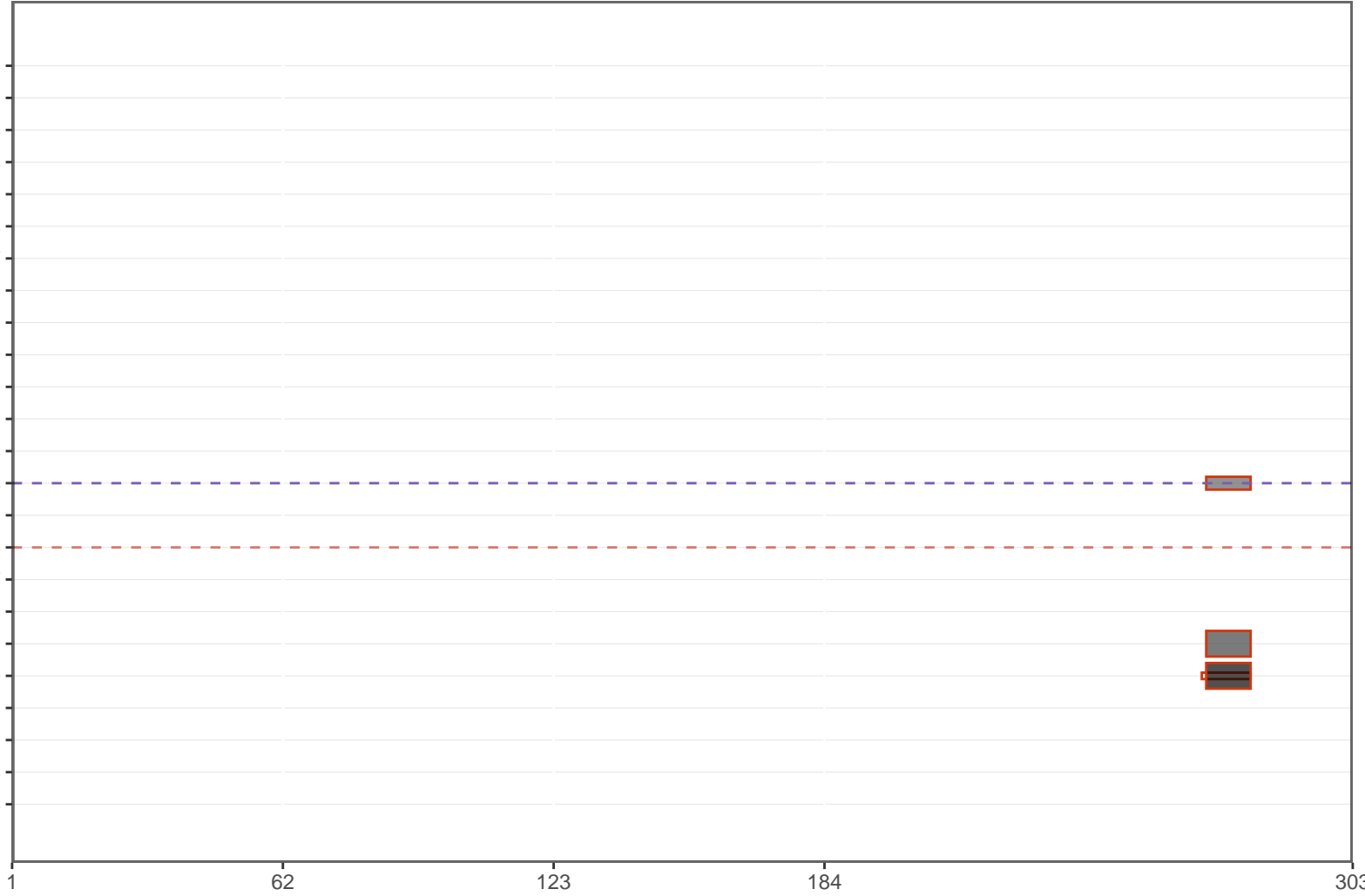
MW indication



Molecular weight



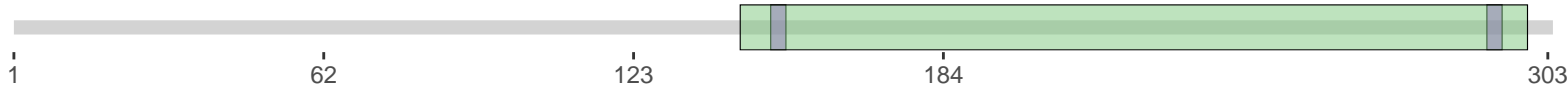
Gel Slice



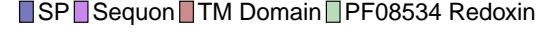
Protein length



Pfam domains



Pfam Description

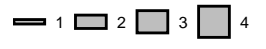


Protein sequence:

MTISVGDKLPNCTLSYFDSDDELKTLHSDLTNGKKVLLAVPGAFTRPTGSGKHLPGFVKEKELKSKGVDTIACISVNDAFVMKYWKENLGINDEVMMLEDGKLEFTRKAGCELDLSDKPKVGLGIRSRARYEMLVDDGVVWLNLEGGGAFNVSSEDLKAL

NbL15g06080.1 NA [MW = 47.87 kDa]

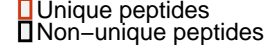
No. of times detected



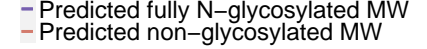
log(intensity)



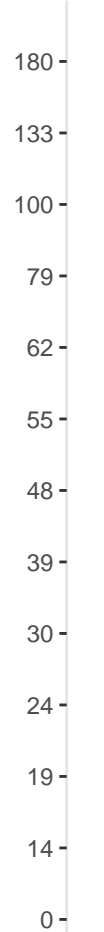
Values from



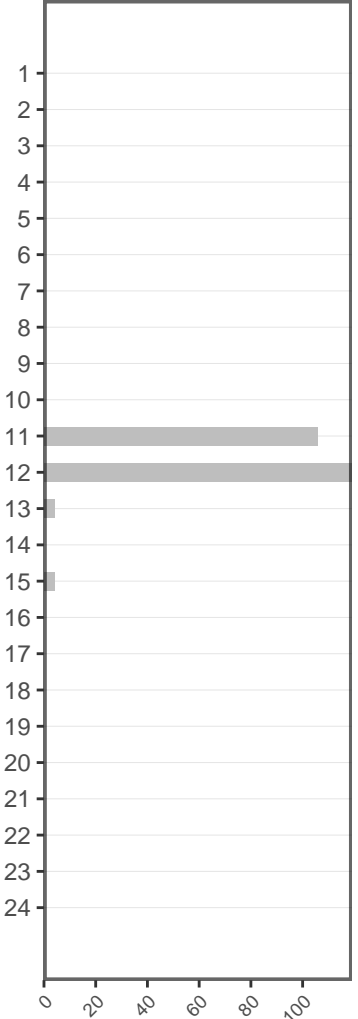
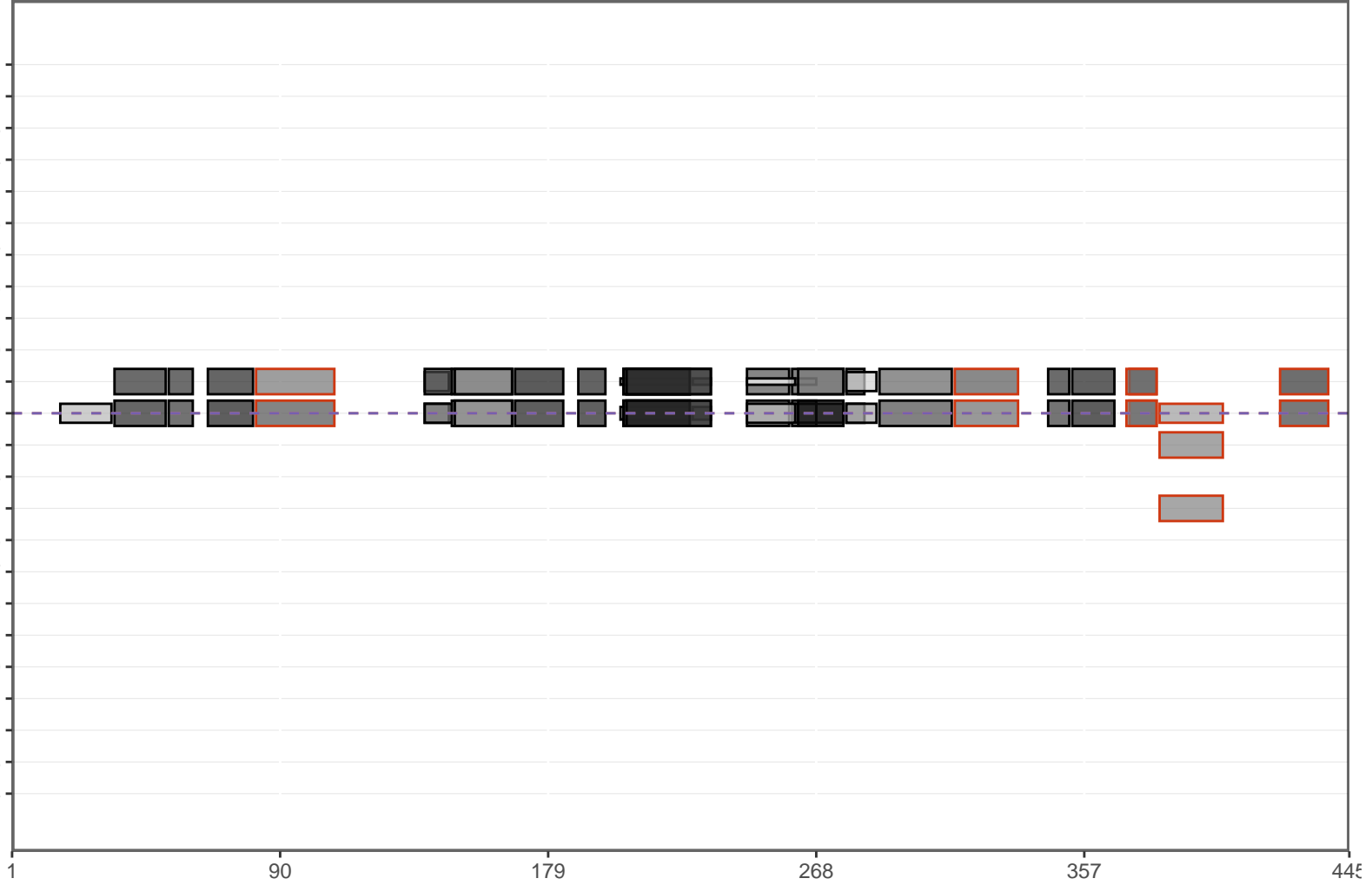
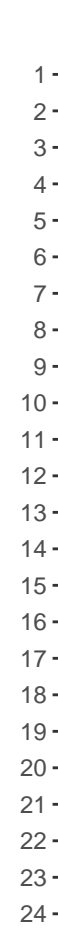
MW indication



Molecular weight

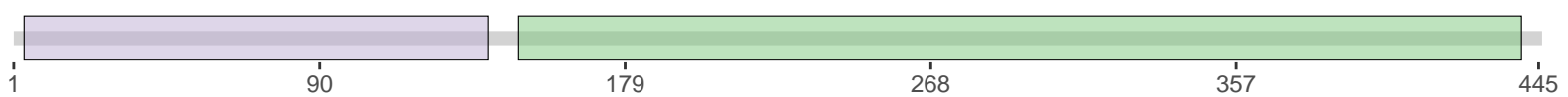


Gel Slice



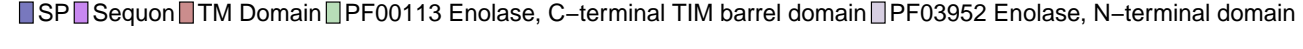
Protein length

Peptide counts over 4 repeats



Pfm domains

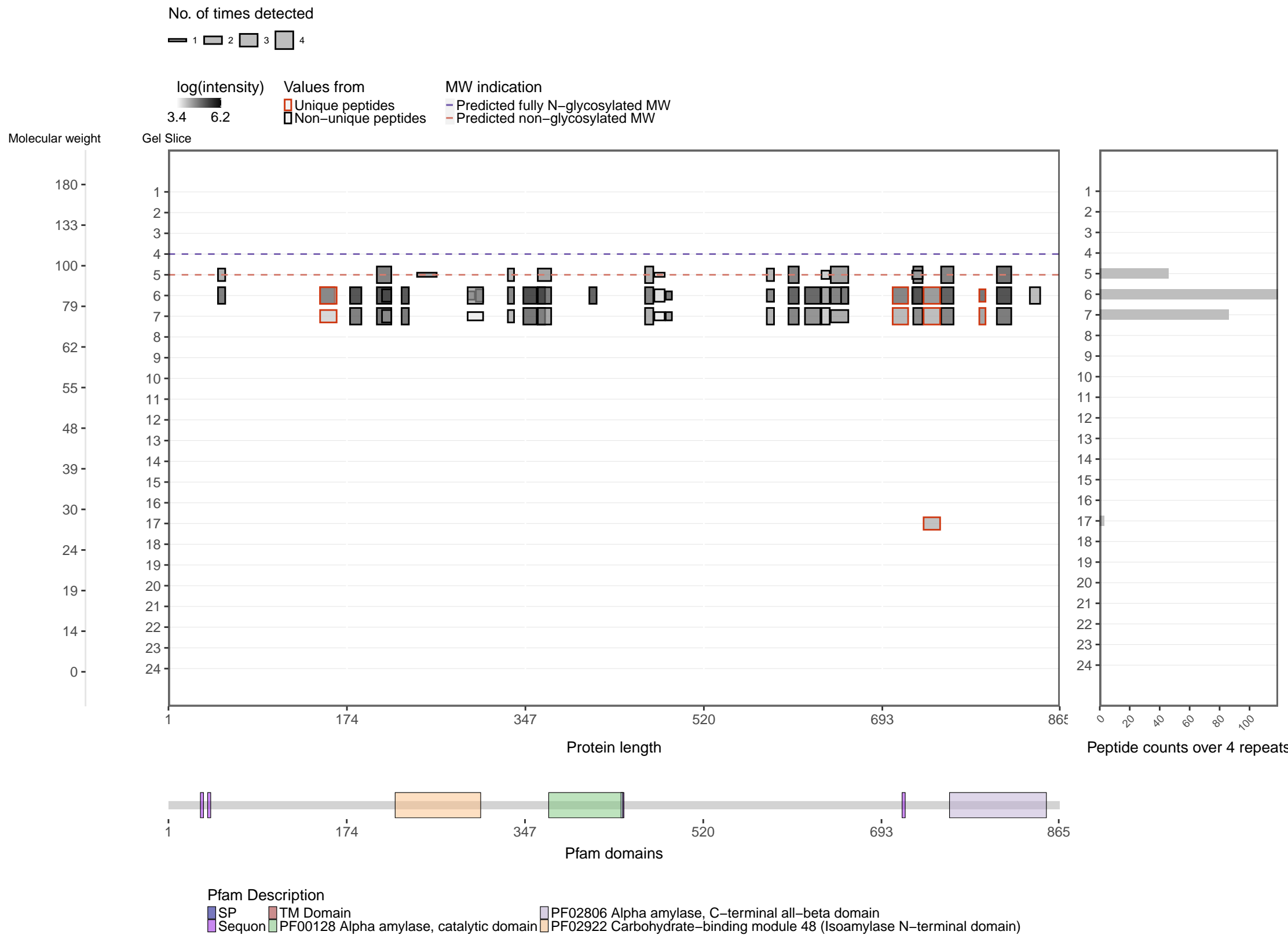
Pfam Description



Protein sequence:

MTNVDDEGGFAPNNGENKEGLELLKTAEKAGYTGIVVIGMDVAASEFLLKDKSYDLNFKENENDGGQNGISGDLKDKYKTFVSEVPVISEDFFDGGDWTYAKLITTEMSEGVGIVGDDLLVITNPKRVAKAAEKTGNALLKVNIGISVYTESIEAVKMKRAGWGVMTSHRSGEETFADLAVGLSTGGKGTGAPRSERLAKYNGLLRIEELGSDAVYAGASFRKPVDPY

NbL15g05910.1 14-alpha-glucan-branching_enzyme_1_chloroplastic/amyloplastic-like [MW = 98.76 kDa]



Protein sequence:

IELGIIVLMDVYHSHANNITLQGLNMFQDGTDSGYFHSGRGRGHHMMWDRRLFNYSGHWEVLRVLLSNAARWLLDEFKDFGRFDGVTSMVYTHHGLSVAFTGQNYEYFGFATDVAIVVLMVLDLHGLFQATIGEDVSGMPTFFQIPVQGGVGFDFRLHMAIADKWIPELLKKRDEEDWRVGDVHTLNRWSEKGVSYAESHDQALVGDKTIKFWLMDKMDMYDFMADRPESTPLDRGIALHKMLRLTGMAGGEGYLNFMGNEFGHPEWDFPRAEQRLPQGGVIPG

NbL15g05890.1 probable_DNA_double-strand_break_repair_Rad50_ATPase [MW = 19.8 kDa]

No. of times detected



log(intensity)



Values from



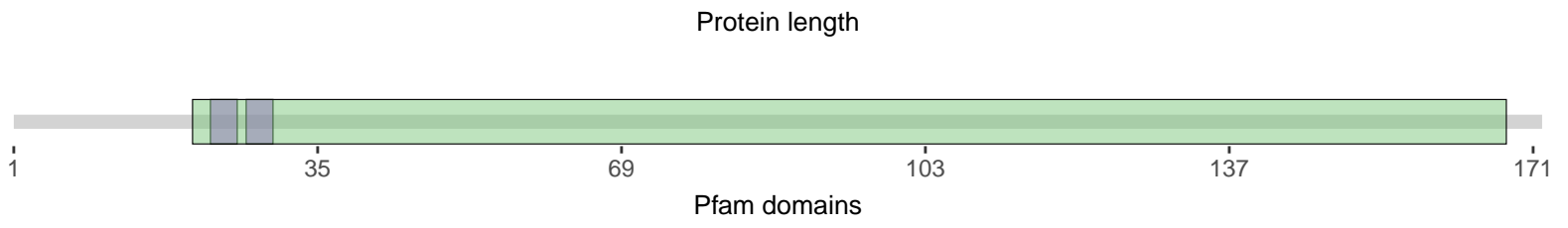
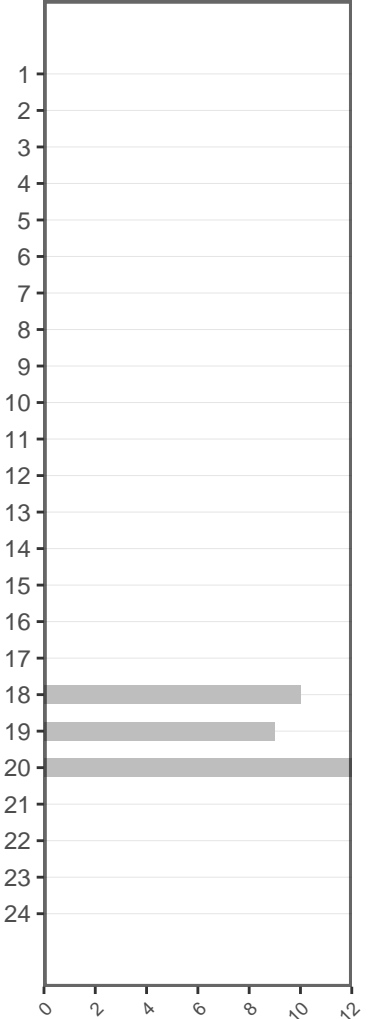
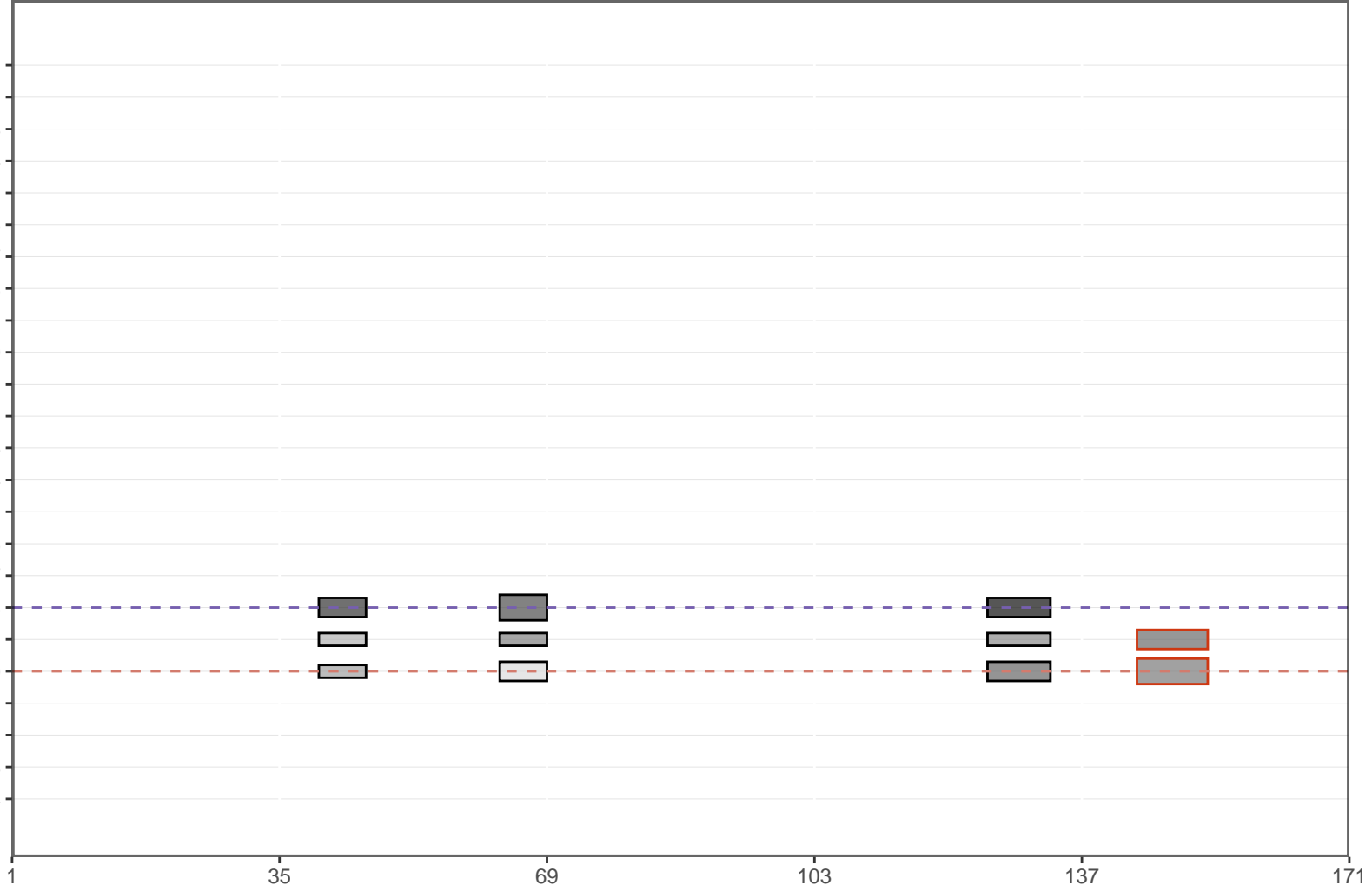
MW indication



Molecular weight



Gel Slice



Pfam Description



Protein sequence:

IEETRLAIRRELEALADPMKKEVSTVTKRIDAVNKEKPLGDTGQKKEREYKEALEAFNEKHKEKVLISRLMELVGESEKMRMKKLEELSKBIETQ*

NbL15g05850.1 fructose-bisphosphate_aldolase_cytoplasmic_isozyme [MW = 38.55 kDa]

No. of times detected



log(intensity)



Values from

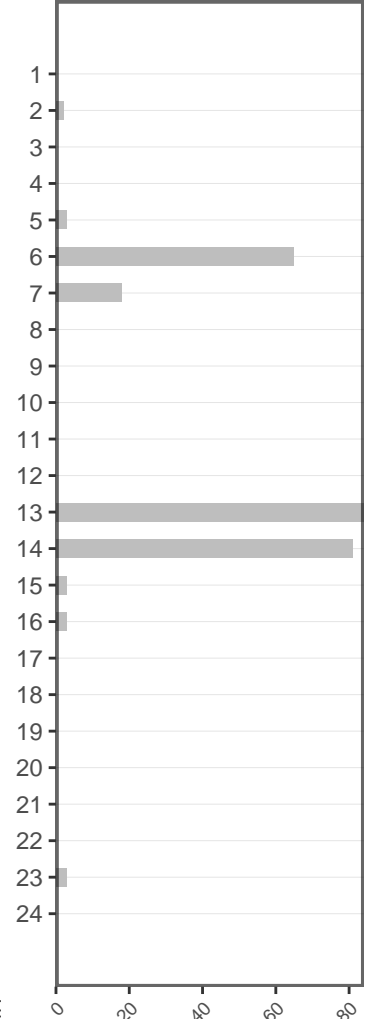
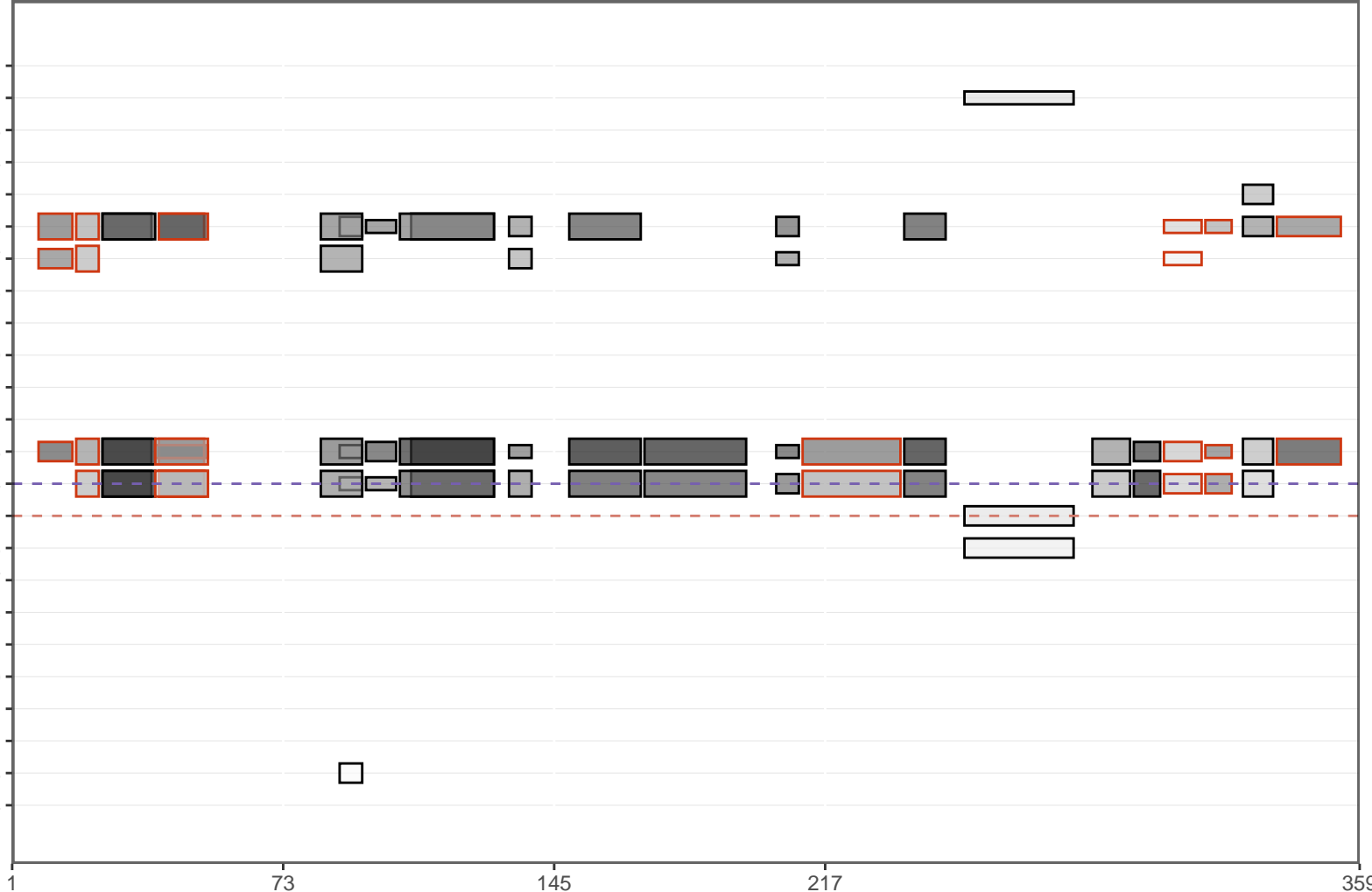
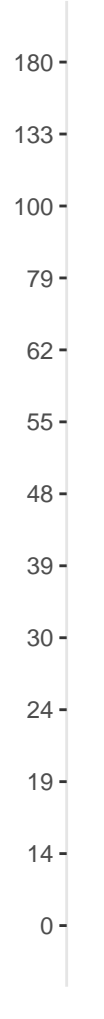


MW indication



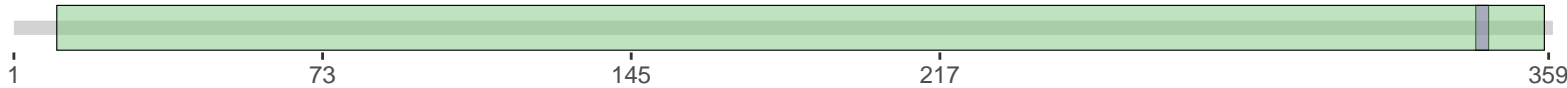
Molecular weight

Gel Slice



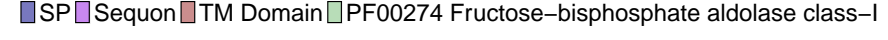
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ARYAICQNGLVFWEPELVDGSHDKGADYTERVLAADYKALNDHHLLEGTLLKPNMVTQSGEAAKVAPEVIAEYTRALGRTPKAVPWVFLSGGGGSEEAATVNLNAMNKLGTQKFWLSFSGFRALQGGTLKAWAGKEENVQKAGAAFLTRKANSSEATLGRYAGATNLEDGASELHWKQKY*

NbL15g05680.1 ADP-ribosylation_factor [MW = 22.9 kDa]

No. of times detected



log(intensity)



Values from



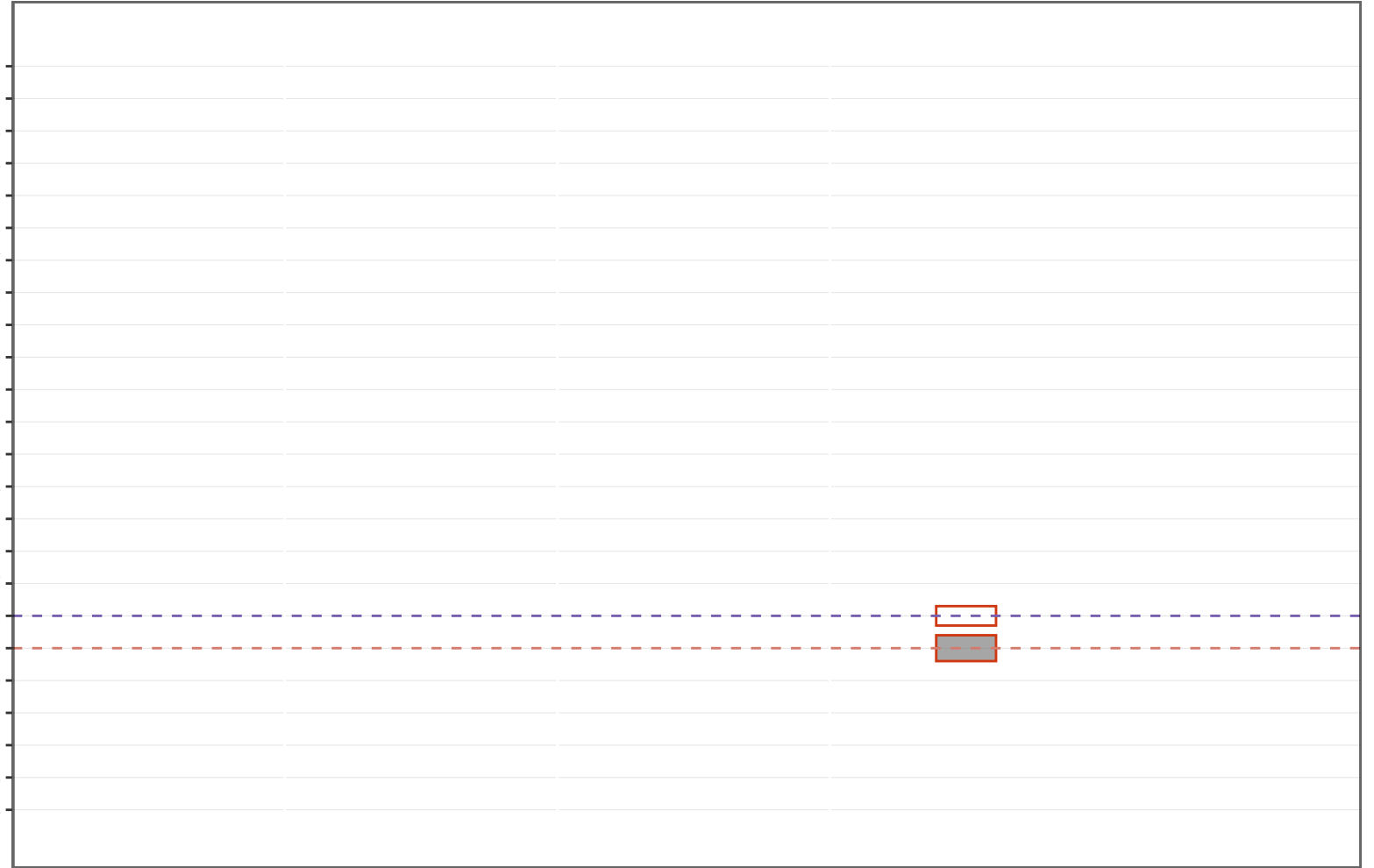
MW indication



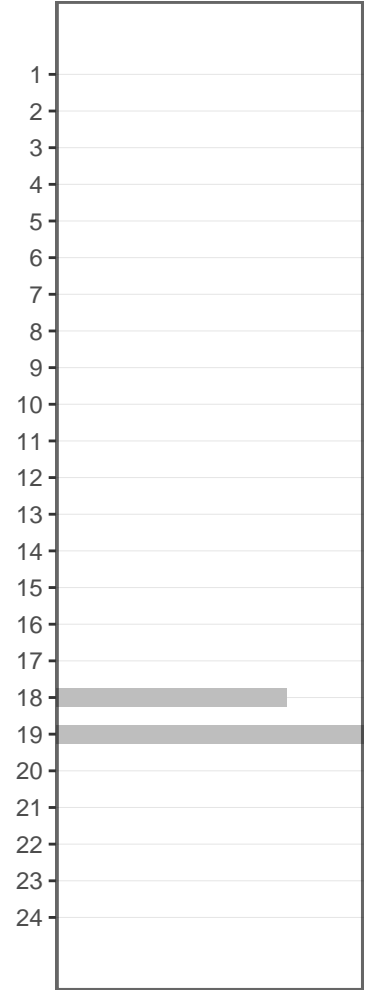
Molecular weight



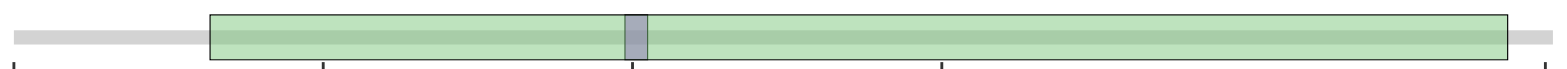
Gel Slice



Protein length

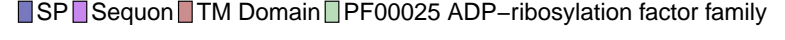


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGQDKRPLVRIHYFQNTQGLIFVDSNDRDRWEARDELHRMLNEDELRDVLLLFANKQDLPNMMNAAEFDKGLGSLRQRHWYIGSTCATSGEGLYEGLDWLNNIASKA*

NbL15g05480.1 probable_pectate_lyase_5 [MW – SP = 41.95 kDa]

No. of times detected



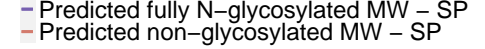
log(intensity)



Values from



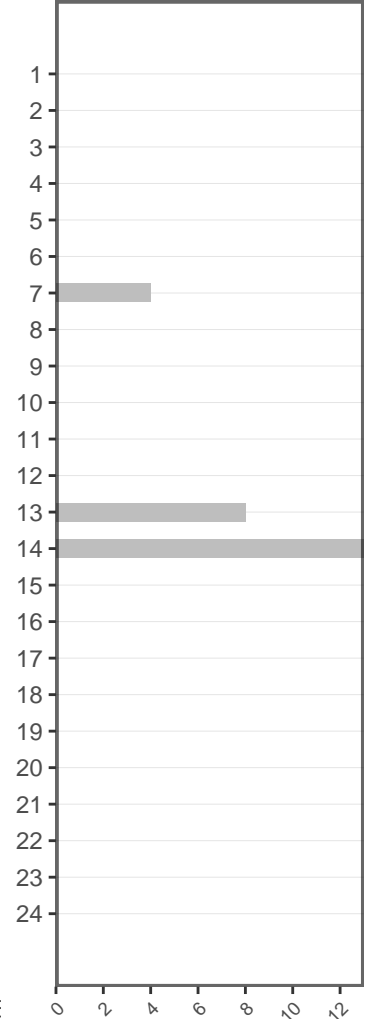
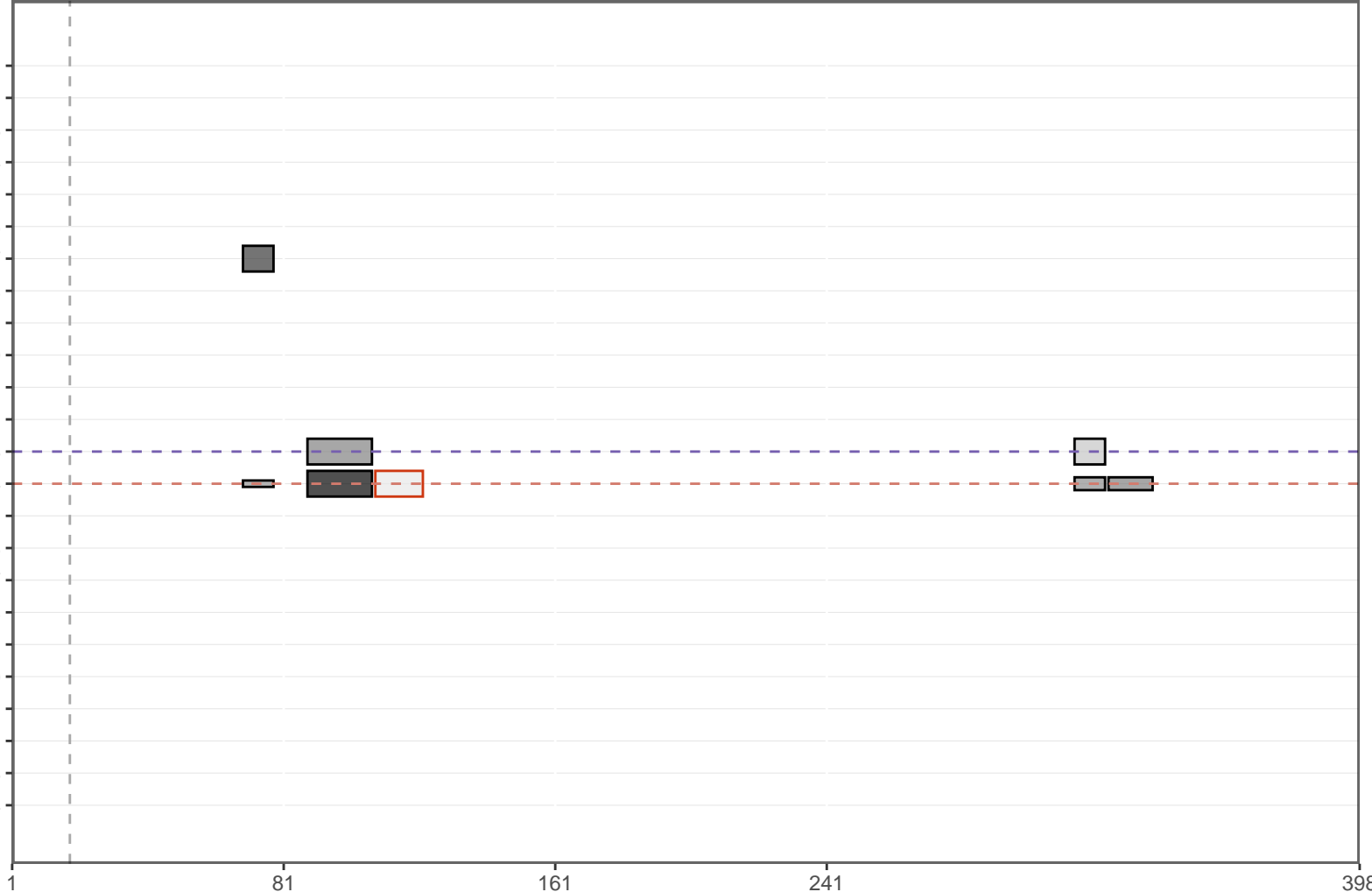
MW indication



Molecular weight

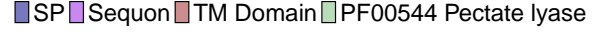


Gel Slice



Pfam domains

Pfam Description



Protein sequence:

IRTLSDGGGVSYFGGSHVWVHDLGSLNCRDGLDARIGSTATTISNNYMTHTNKVMLLGHSDSFRDKNMGVITAFNHFGEGLVGRMPRGIRHGIVYVWVNDYTHWEMVAVGGASPTINSQGNRFLAFNDIFNKVTHHEDAASEWKKVWNRSEGDMLMGAFTRISGAGASKEVAKASLSARPSTLVSSFLNAGALGCKKARQ

NbL15g05280.1 glyceraldehyde-3-phosphate_dehydrogenase_cytosolic [MW = 37.02 kDa]

No. of times detected



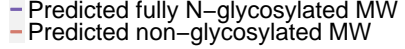
log(intensity)



Values from

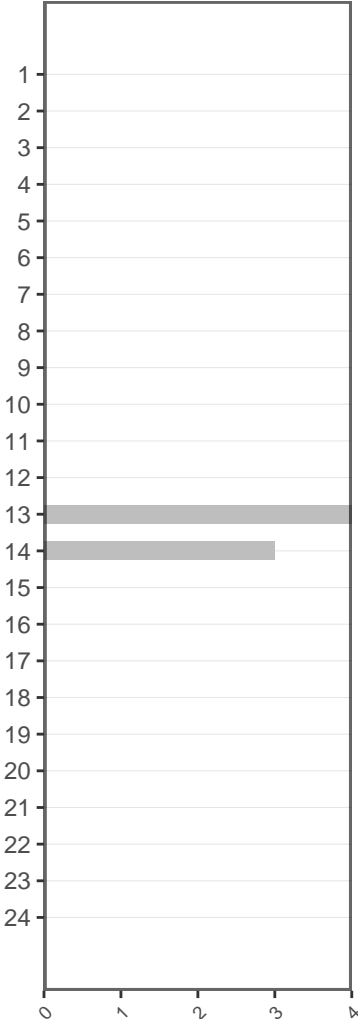
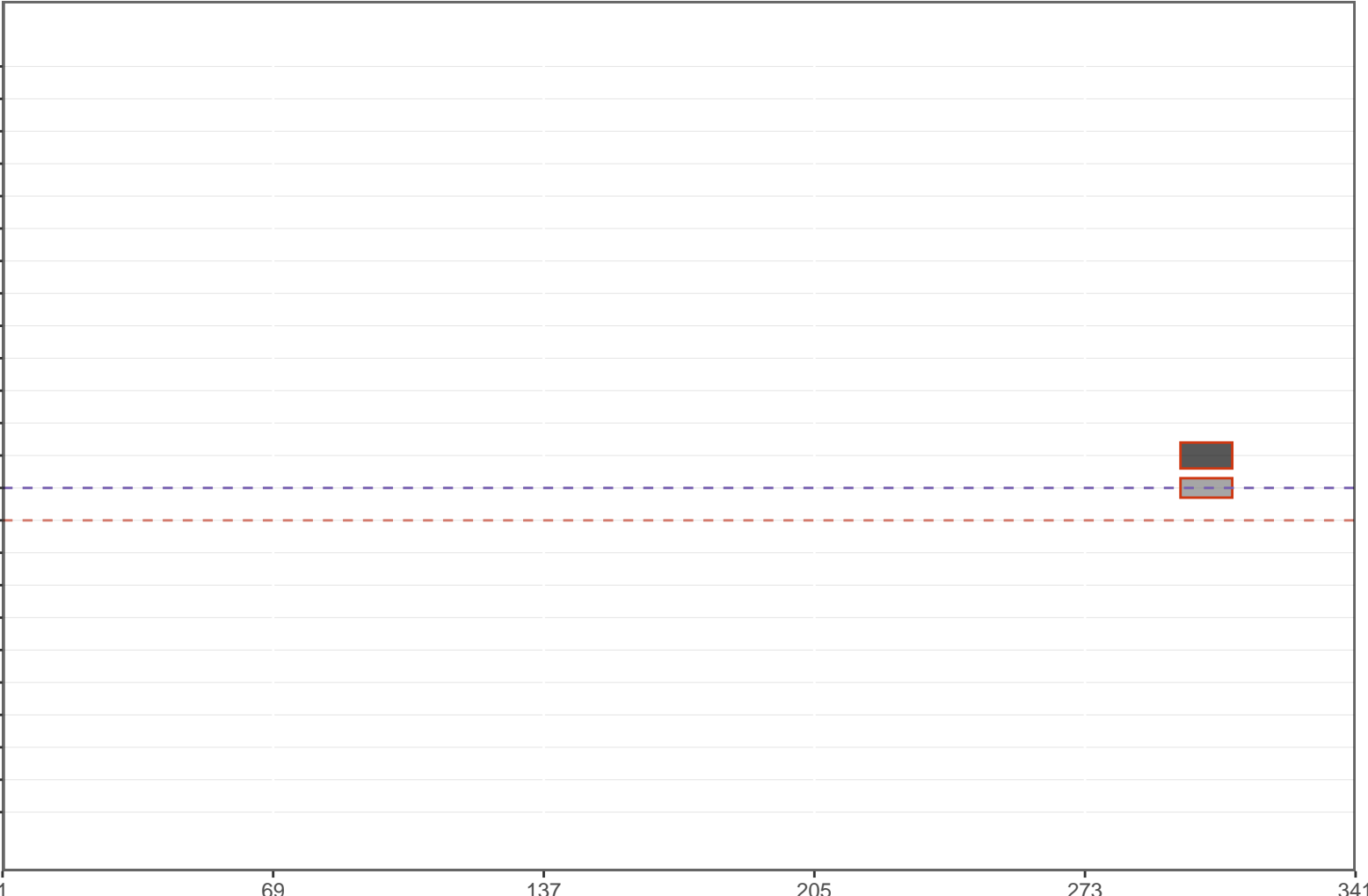
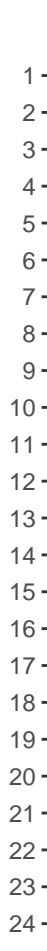
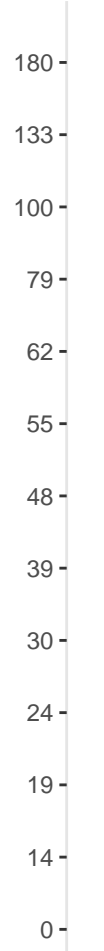


MW indication



Molecular weight

Gel Slice

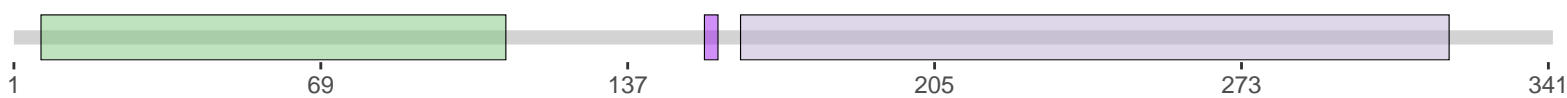


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF00044 Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain
- PF02800 Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain

Protein sequence:

CTTNCFLAPLAKVINDRFGEGLMTFTVHSLSLTKATQKTVDPGPMKDWIRGGRASFNIPSTGAAKAVGKVLPAINGKLTGMAFRVPTVDVSVDLTVRLEKEASVDEKAAKKEESEGLKGLGFTFEDDVAVSTDFVGDGRSRIFDAGAGIALSKNFYKLVWYDNEWGVYSRVIDLICHMASVA

NbL15g05130.1 urease [MW = 89.74 kDa]

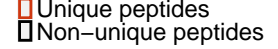
No. of times detected



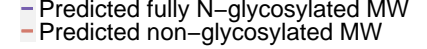
log(intensity)



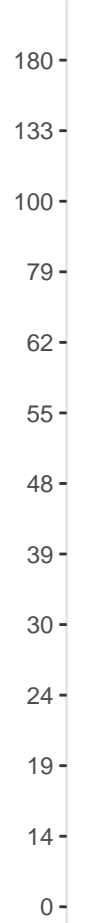
Values from



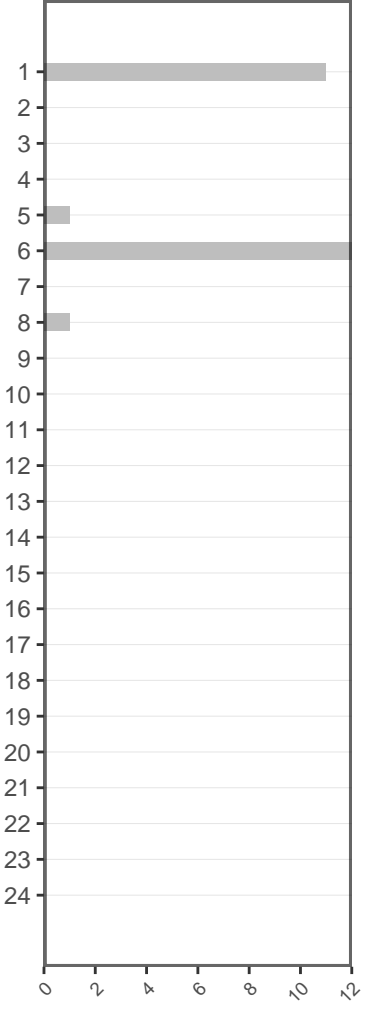
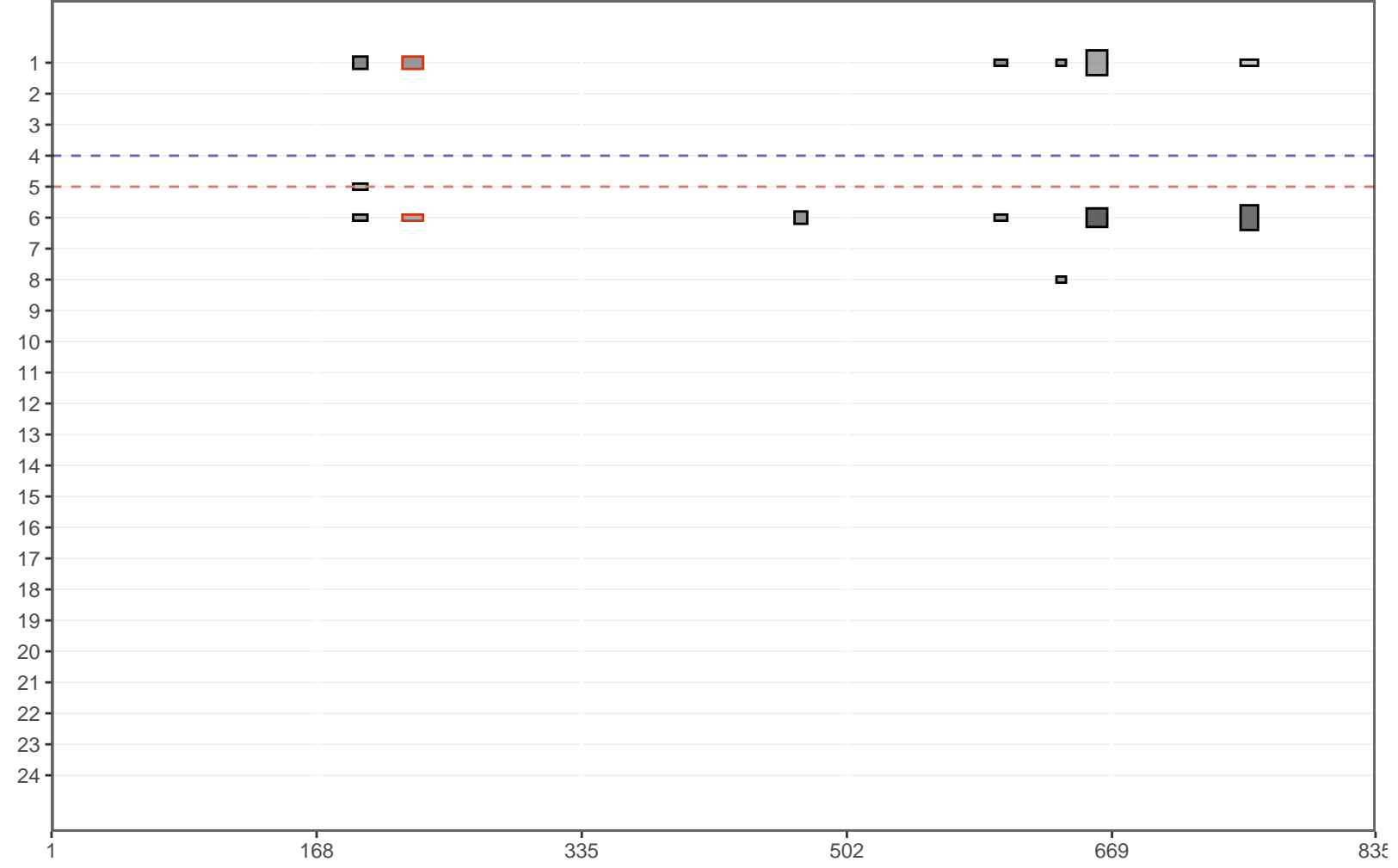
MW indication



Molecular weight

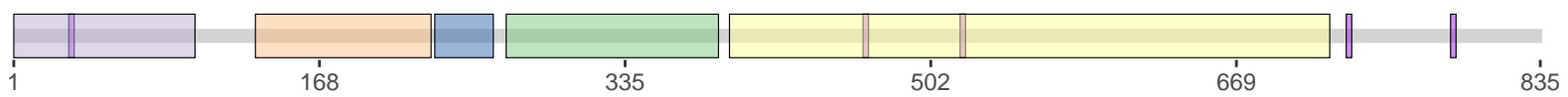


Gel Slice



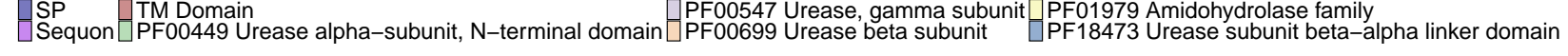
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

1CPQLAYEAISSGIFTMVGGGGTGPVHGTRATFGTGPVHMEMLMGSTDELPLNFGFTGKGNSSKAEGLHEIKAGAMGLKLIHEQWGTTPAIDMLCLAVADGVQKVNHTDNLNESGFVEHTIAAFKGRTHIYHSEGAAGGGHAFDKIKVGVKNVPSSTNPTFRPFLNLTVEHLMLMVGHHLNKDIREDVAFASGRIRAEETIAAEDILHDMGABISISDSQAMGRIGEVHRTWGTAKMKKFRGLDIDGPDNDINFRKRYWAKYTNFMANGISGHWGSEVYGLKLDLVV1

NbL15g05110.1 adenylate_kinase_4 [MW = 26.51 kDa]

No. of times detected



log(intensity)



Values from



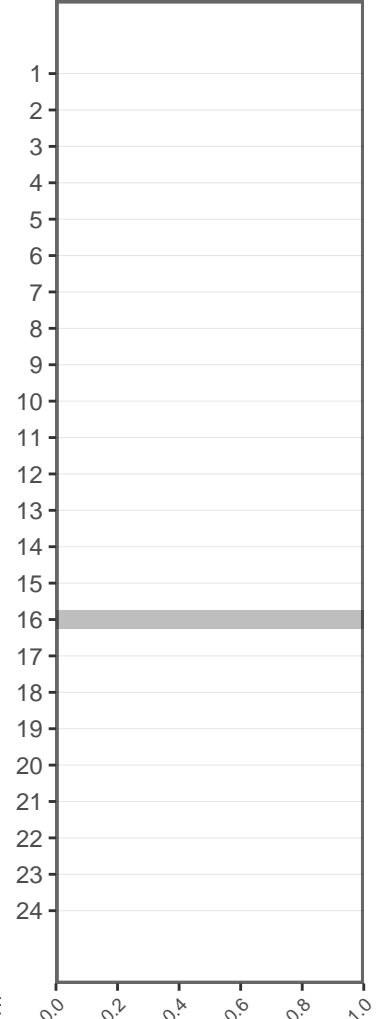
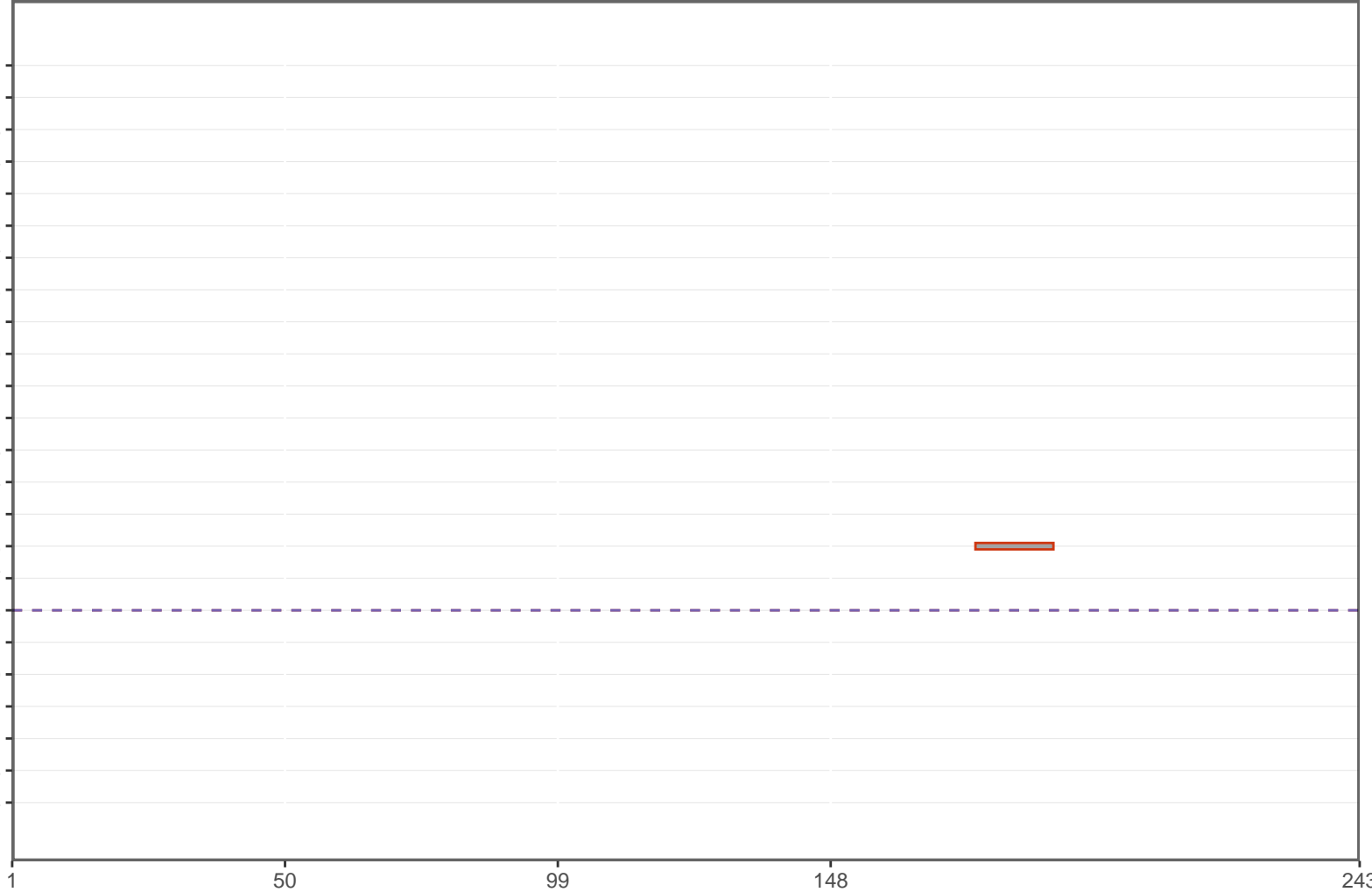
MW indication



Molecular weight

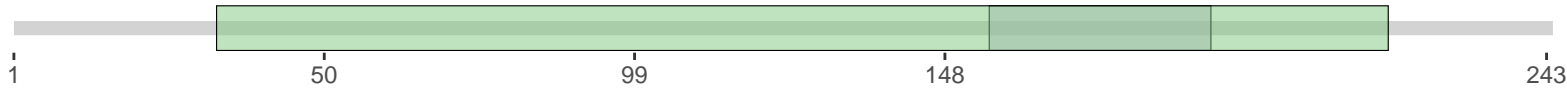


Gel Slice



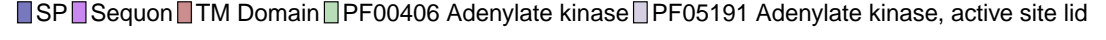
Protein length

Peptide counts over 4 repeats



Pfam domains

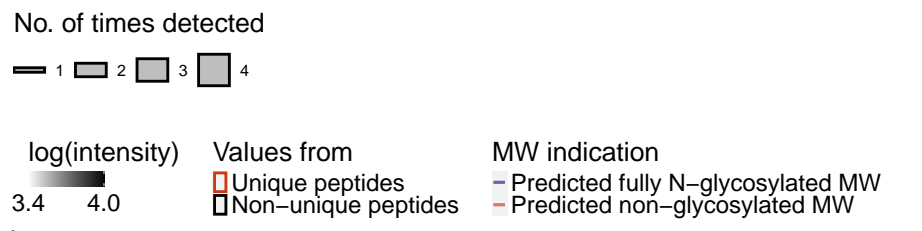
Pfam Description



Protein sequence:

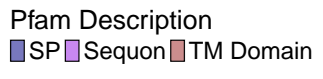
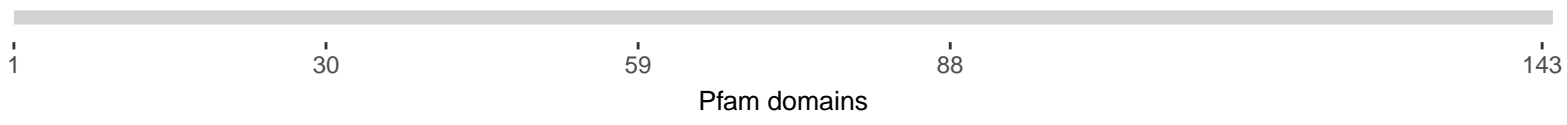
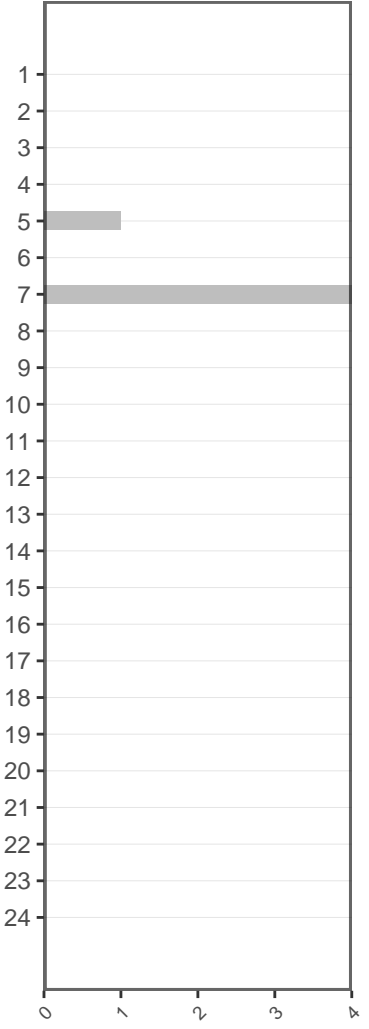
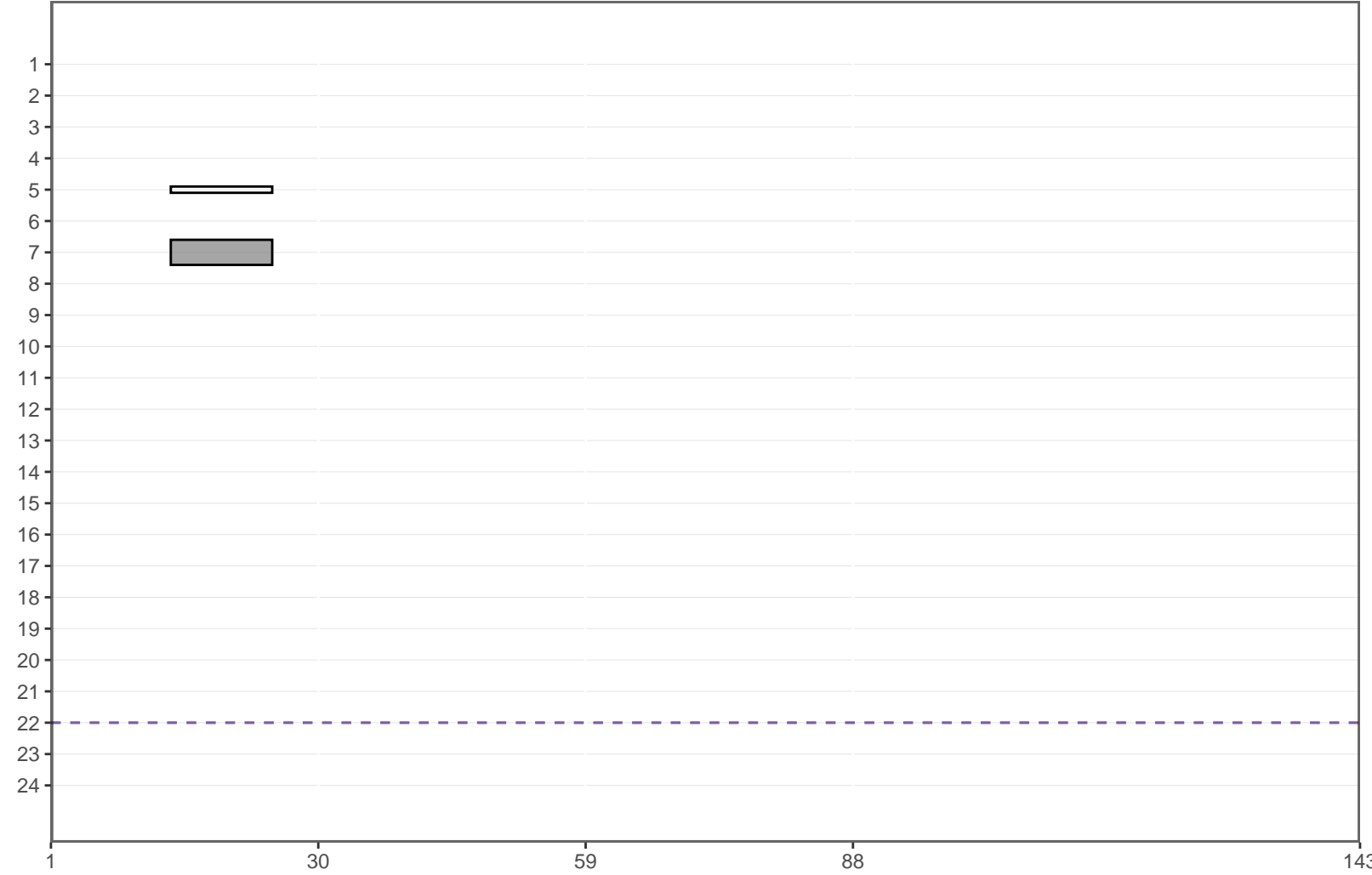
IFILDGFRPTVAQAKLDEMLKGGTNDKVLNFAIDDAILEERITGRWHIPSSGSRVHTKFPKPKVPGVDDTGEPLIGRDKDTAEVLRRLDAFRHGTETPVINYYSKKGVVASHLAEKPKQKQVTEWNVLSF

NbL15g05100.1 probable_pre-mRNA-splicing_factor_ATP-dependent_RNA_helicase_DEAH4 [MW = 16.11 kDa]



Molecular weight

Gel Slice



Protein sequence:
 EASLKTADIHVREPEGDILFLTGGVRFVSPFPNDRRFTVSTNIAETSLTVGGVWRFLFNCKPFGKERVAFPNVNPGRGKK

NbL15g05080.1 NADH_dehydrogenase_[ubiquinone]_flavoprotein_1_mitochondrial-like [MW = 55.46 kDa]

No. of times detected



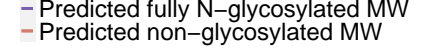
log(intensity)



Values from



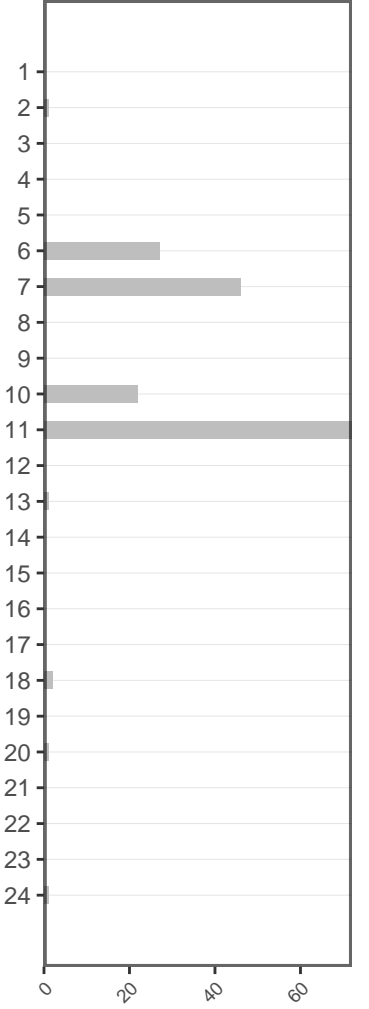
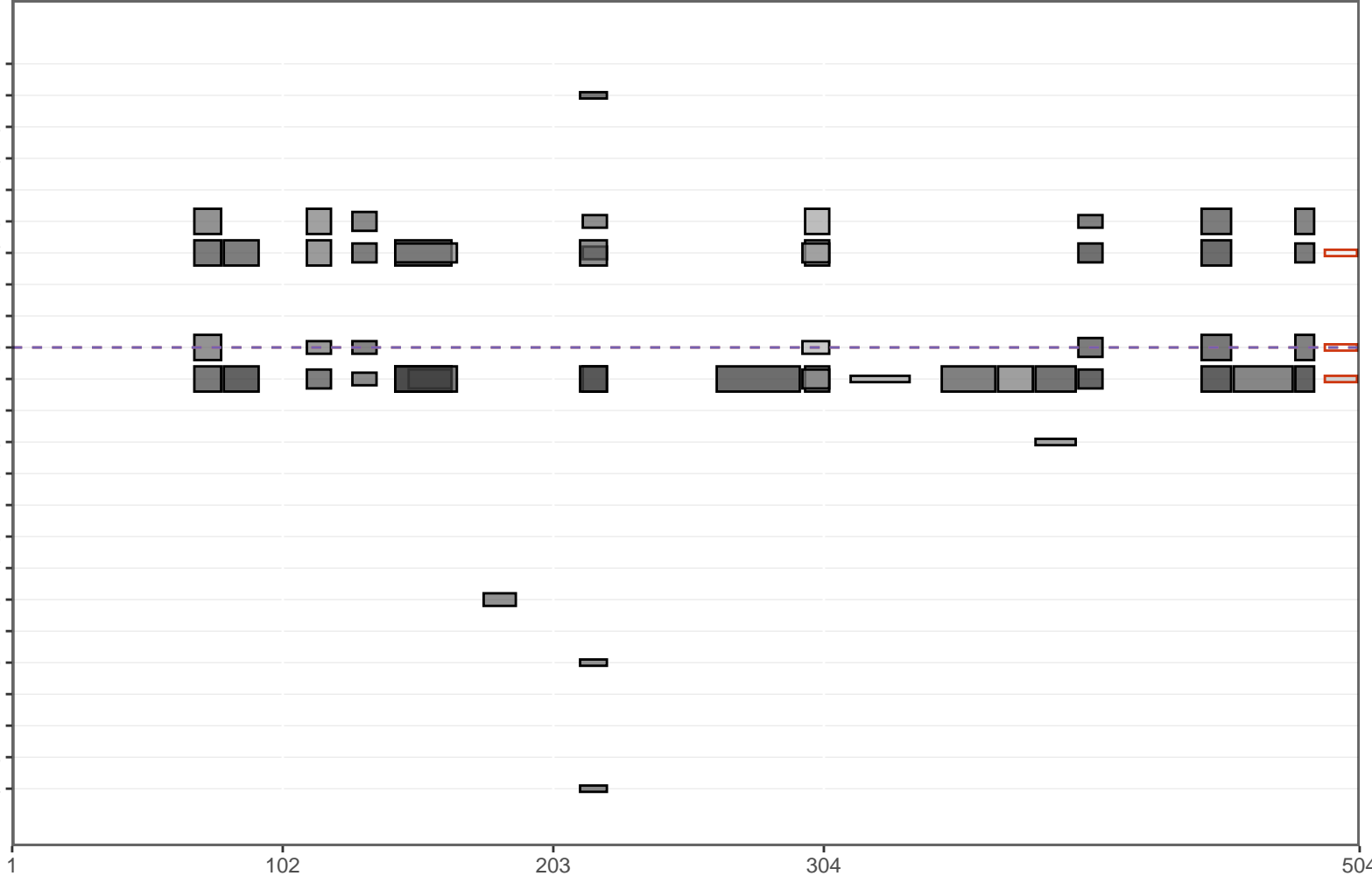
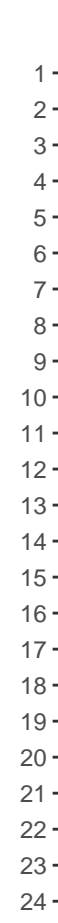
MW indication



Molecular weight

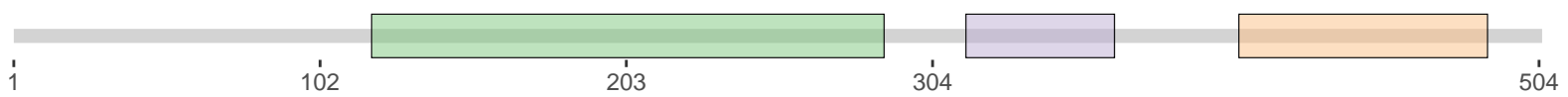


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01512 Respiratory-chain NADH dehydrogenase 51 Kd subunit
- PF10531 SLBB domain
- PF10589 NADH-ubiquinone oxidoreductase-F iron-sulfur binding region

Protein sequence:

GAGAYCGEETALLELEGKGRKRLKPFANAGLYGGPTTIVNVEVAVSPTLRRGPEWFAFSGRIKNNAGTKLFGISGHVNNKPTVEEEMSIPLKELIHRHGGVGRGWDNLLAVIPGGSEVPLIPKNCEDVLMDFDALKAVGSGLGTAAVVMKSTFDVDAIARLGFYKHESGGGGCTPREGCTGVLWMMERMKVGNANLEEDIMQEVTKQIEGHTICALGDAAWPFVQGLRHFRPELERRIRRHADRELGGAAAV

NbL15g04880.1 non-specific_lipid_transfer_protein_GPI-anchored_1 [MW - SP = 18.17 kDa]

No. of times detected



log(intensity)



Values from



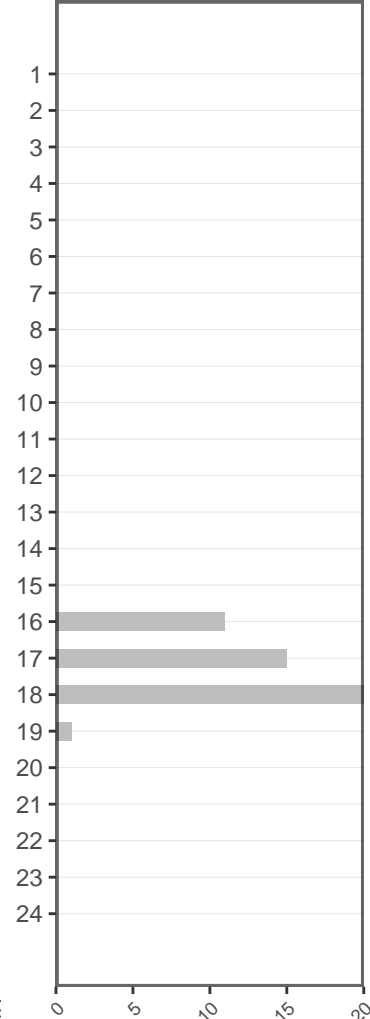
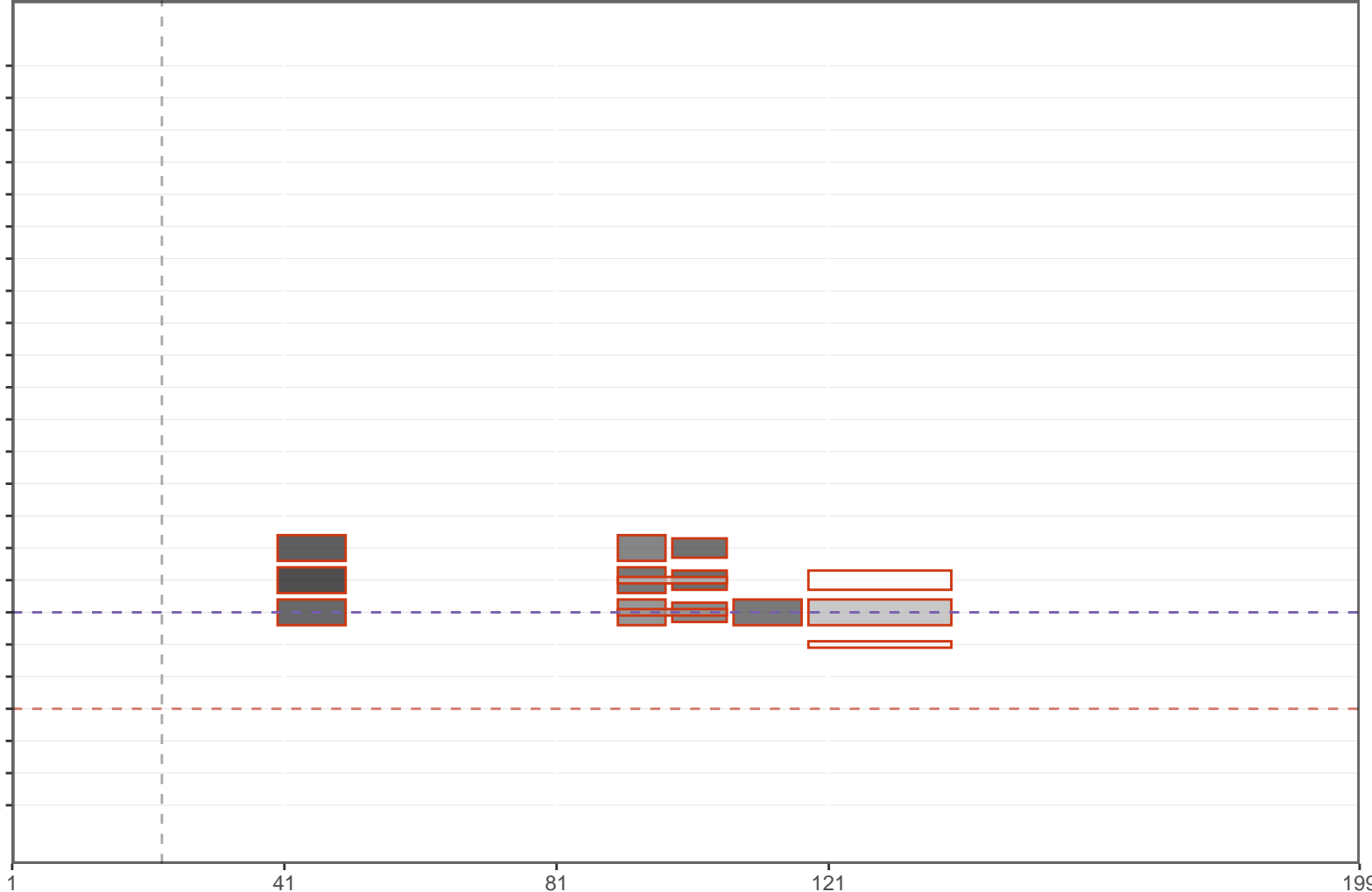
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IPELKSMGIQEDKLLQLPFAAGKLTNAISNGPKLLINIPETFPDVAIFITNAGTASKTVAATPFGASGSSSSPDITTKDSDSNGFNKGPQLSIFGTVAAAWVDSGVIPIRRTTSVLM*

NbL15g04800.1 2-Cys_peroxiredoxin_BAS1_chloroplastic [MW = 29.9 kDa]

No. of times detected



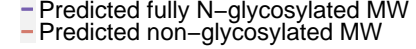
log(intensity)



Values from



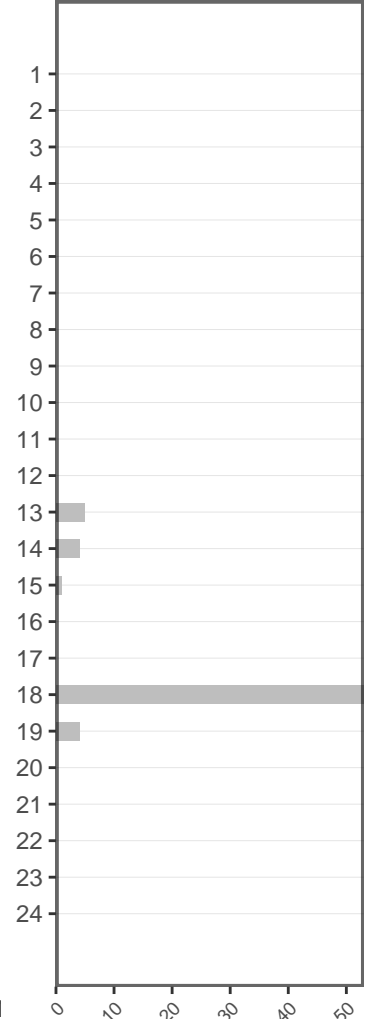
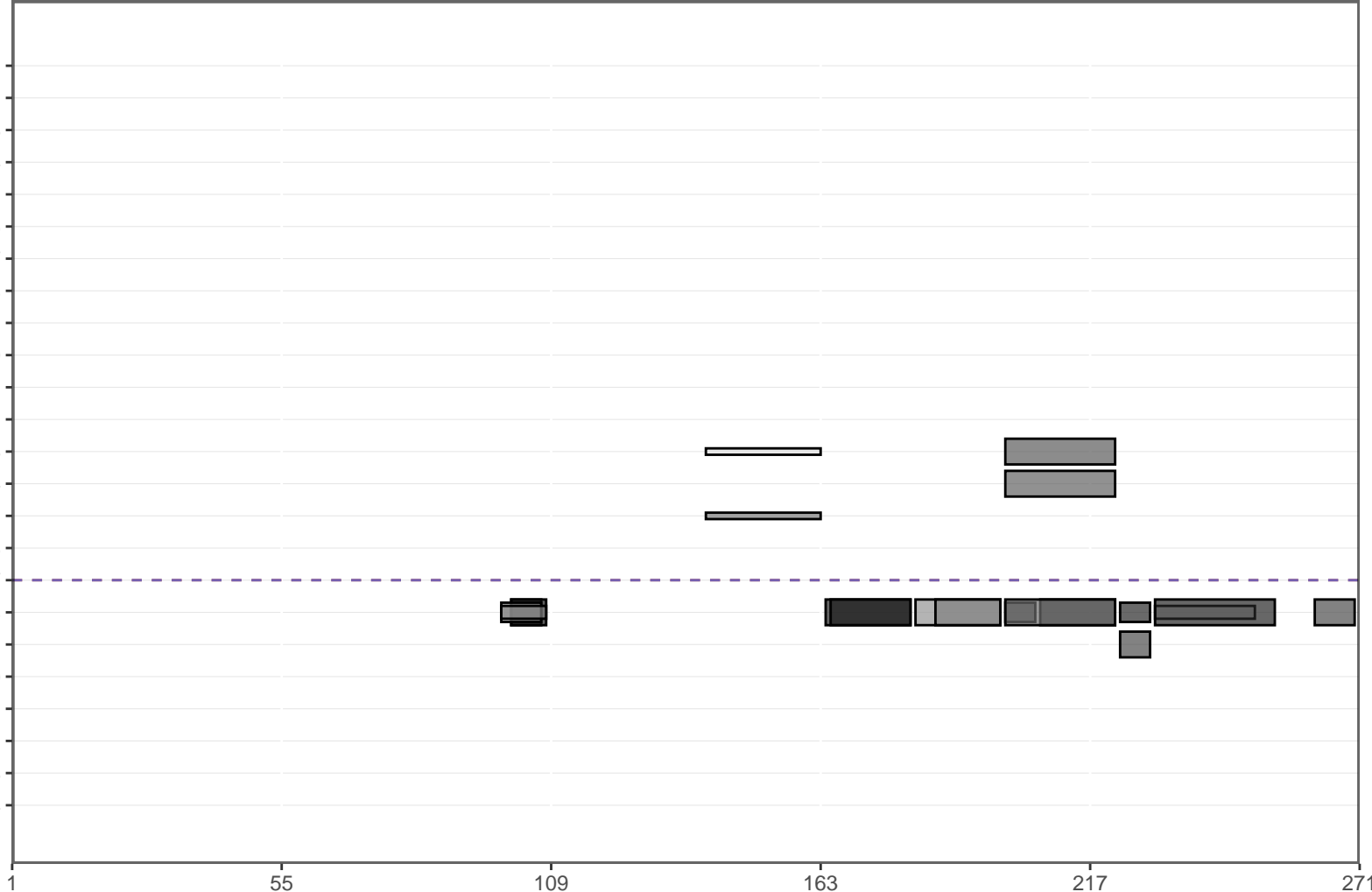
MW indication



Molecular weight

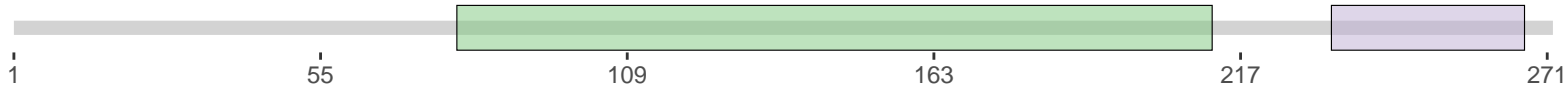


Gel Slice



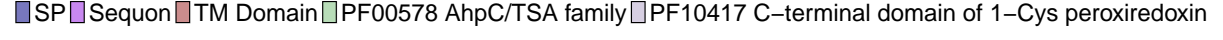
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

/CPTETAFSDRYEEFEKLNTEILGVVDVGFHSLHAWVGTERRKSGGLGDLNYPHSDVTKSGIKSYNNLIPDGGIALRGLFIDKEGVQHSHTNNLIGIGRVDDELRTLQALQVYVDNPFDEVCVPGKGVKPKGKEMKPKDPKGGKEYFASD

No. of times detected



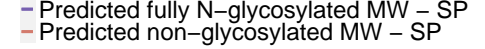
log(intensity)



Values from



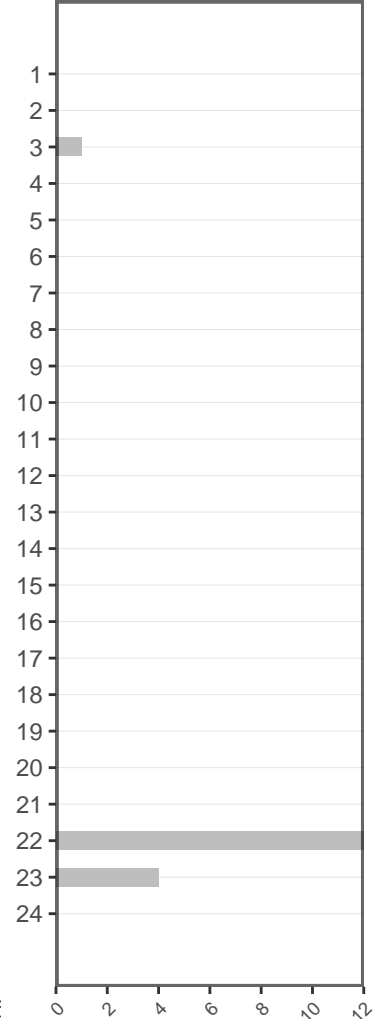
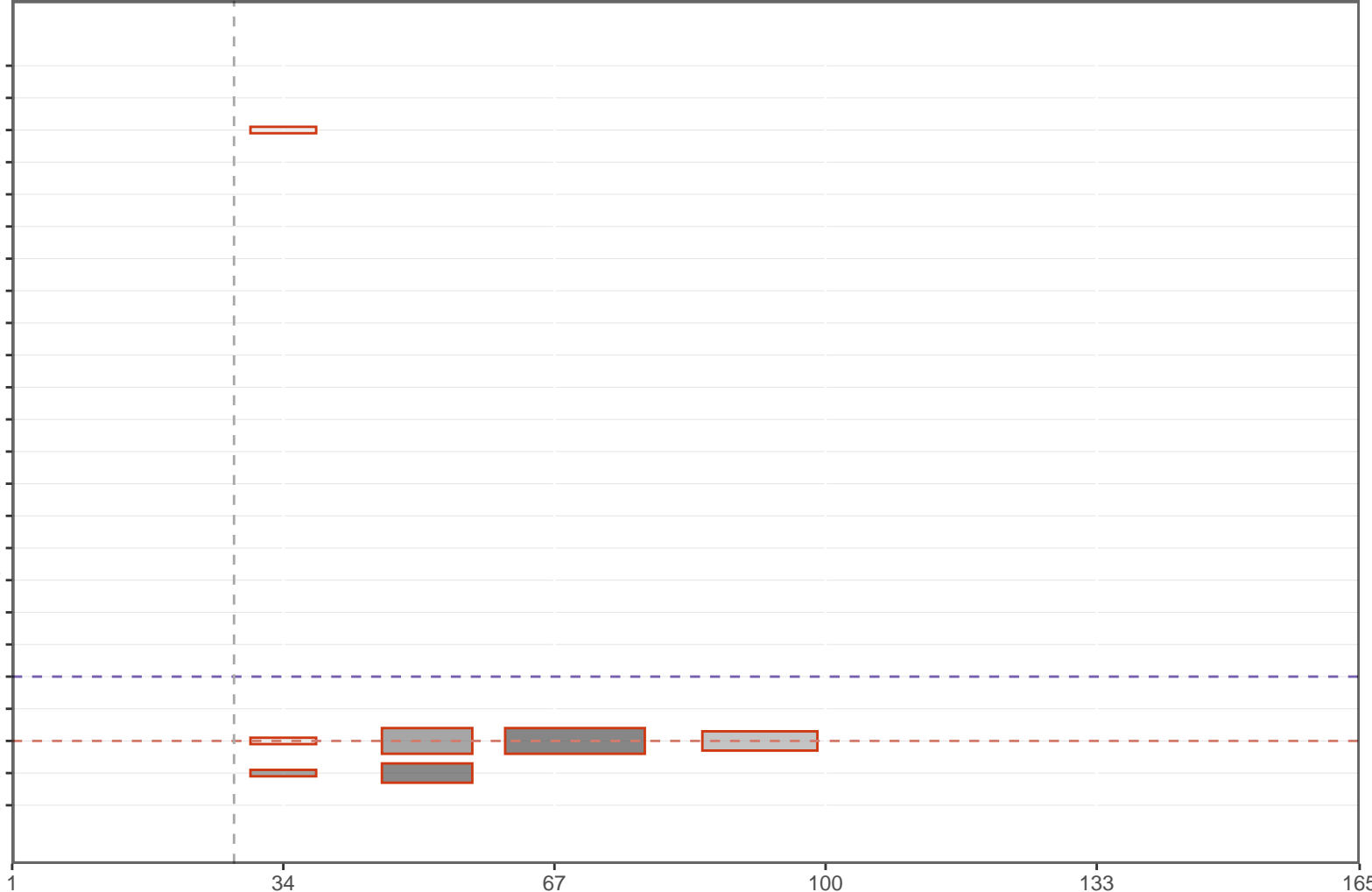
MW indication



Molecular weight



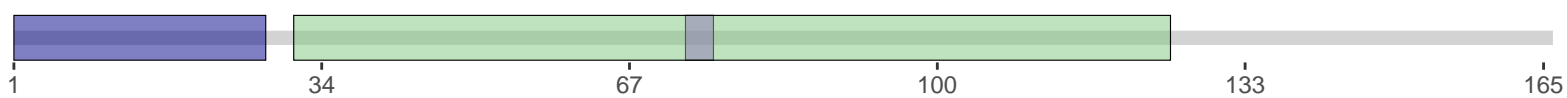
Gel Slice



Protein length

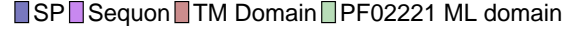


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TDENISGKLVIVKYLFLHWGESHDKKETSQPVSGDFVLHSHQALPGTFPPVSHLSSLSGKLVFVMSFSGPLFCIAFKRGSASFLDFSDS*

NbL15g04420.1 sucrose-phosphatase_2-like [MW = 47.96 kDa]

No. of times detected



log(intensity)



Values from



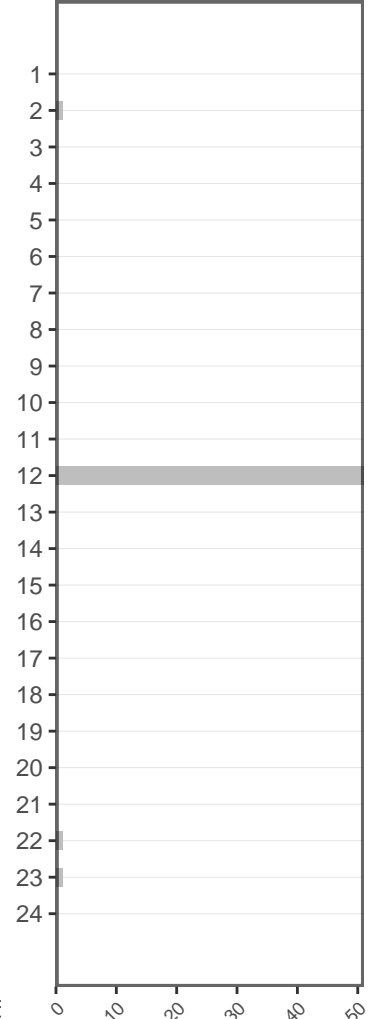
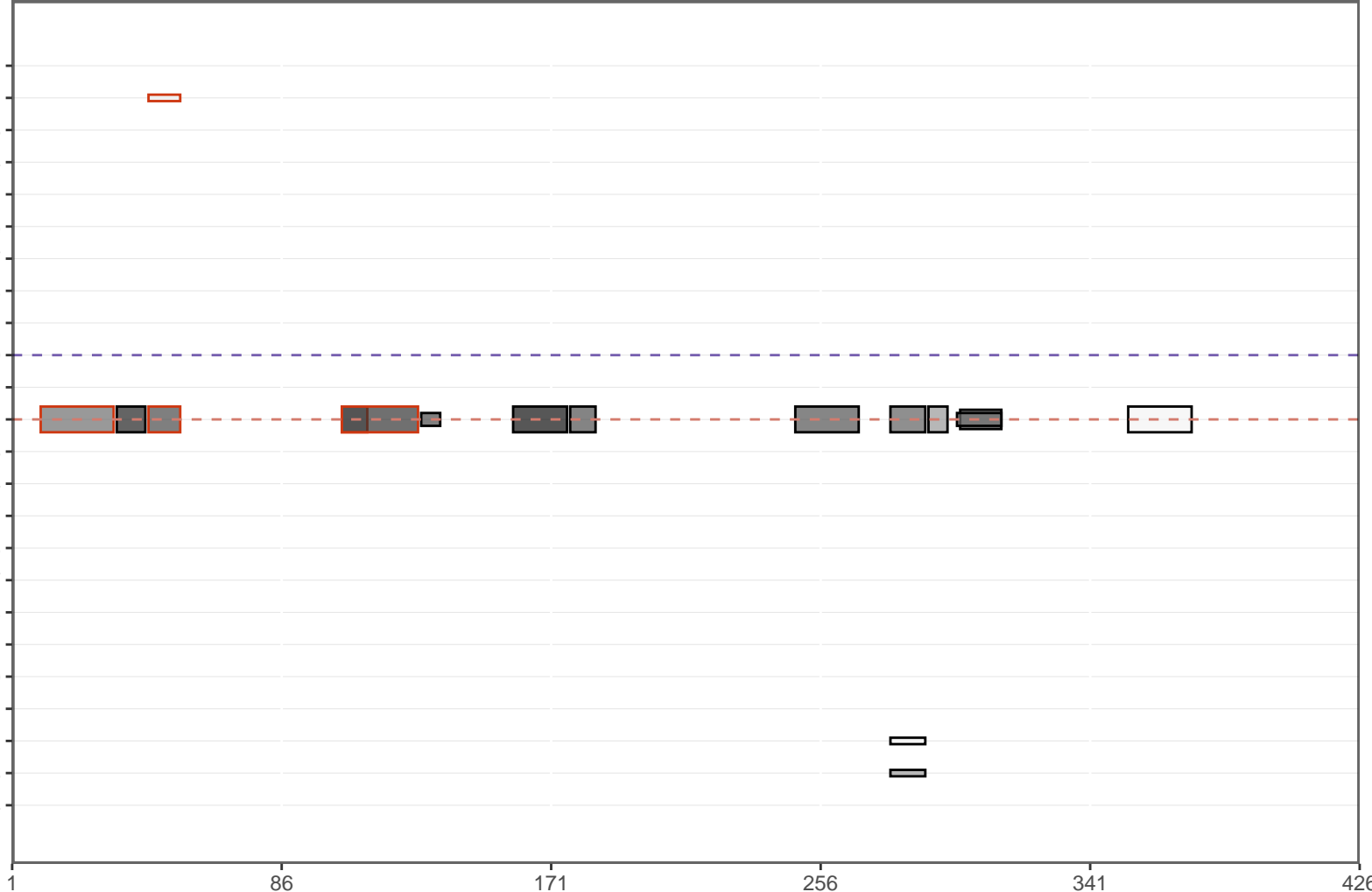
MW indication



Molecular weight

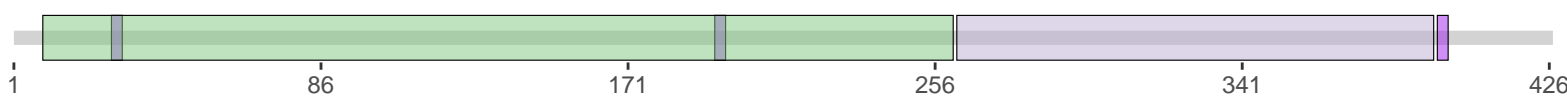


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

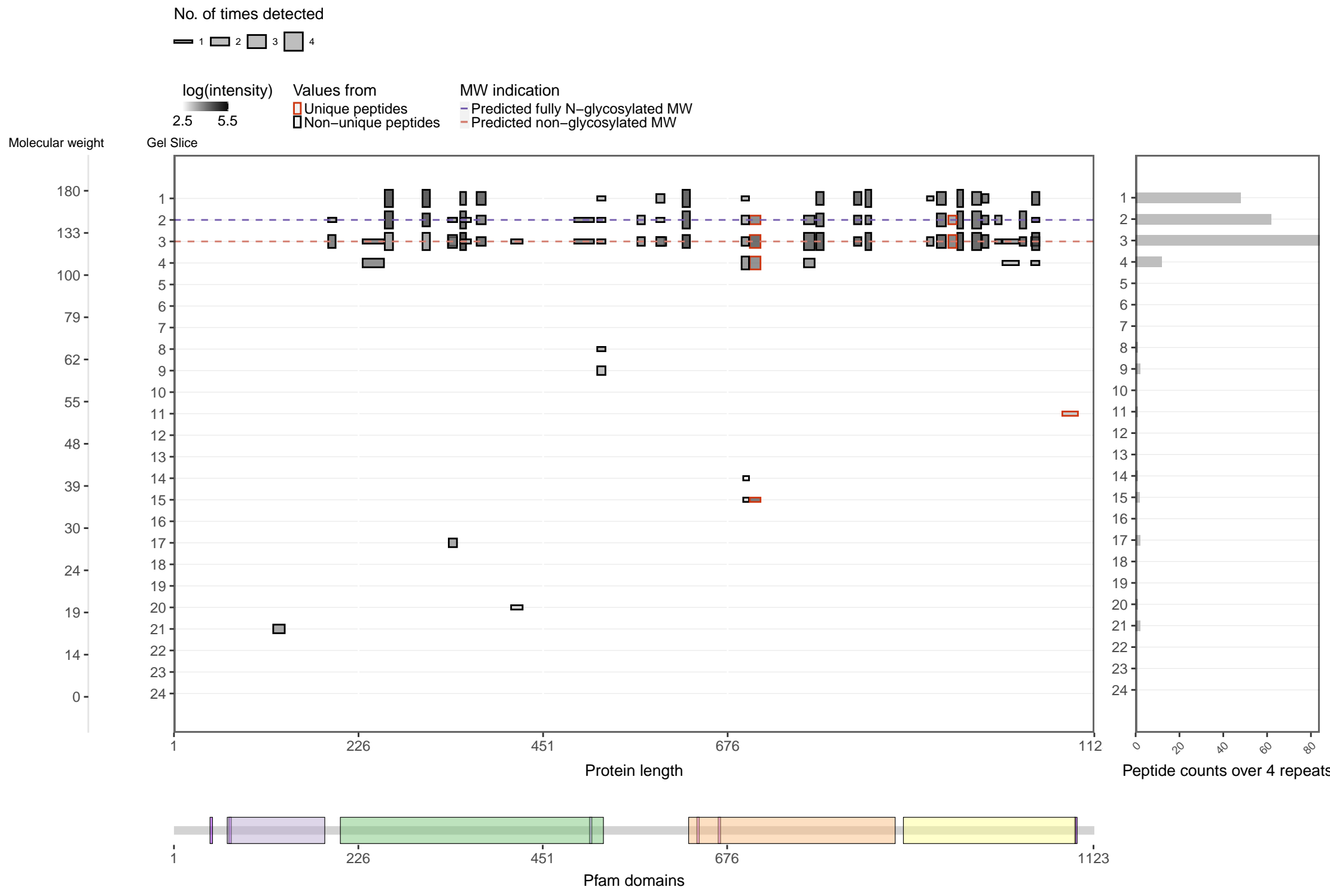
Pfam Description

- SP
- Sequon
- TM Domain
- PF05116 Sucrose-6F-phosphate phosphohydrolase
- PF08472 Sucrose-6-phosphate phosphohydrolase C-terminal

Protein sequence:

3SGNDAELFSPDVGVMVANAQELLQWHAANAKNFKVHATERGAAGHGAHGFNLGPSTSPRDVMDSSDCKMENFVPEVEVKFYLFKWRREIEHSEHLENLKA/CRP6SGSFVHPSGVEKSLGECVTLFTMCHGDGKGGKQFRWWDQVLPVQVSGSD6WLVSPKXWELSGEDRRGGITTVLLSGKNKTVADGLTWTWHVHGTVLNGAAASDSTWFF

NbL15g04370.1 ubiquitin_carboxyl-terminal_hydrolase_12 [MW = 131.51kDa]



Pfam Description

- SP
- Sequon
- PF00443 Ubiquitin carboxyl-terminal hydrolase
- TM Domain
- PF00917 MATH domain
- PF12436 ICP0-binding domain of Ubiquitin-specific protease 7
- PF14533 Ubiquitin-specific protease C-terminal

Protein sequence:

QDAHLRLKKEGEEKEDKRRYKAGAHLYTRKVARDEDLREGIGKEYFDLVHDHDKVRSFRIGKQMPFNLFKEEVAKELGIPVQGRFVWAKRQNHLYRPNLRPTQEELEQTVGQREVSNKTNNAELKLFLEVDLGGDLVSPPPDKDKDILLFFKLYDPEKEELGVYGRLFVYKSTQPIELPKLNELAGFAPDQEIQLFEEIKFEPSPVMDERLDDKASFRFRSQIEDGDIQFQKASPEVEEGVRFPPNPSVLEYVKNRQVHFRALQPKKEDDFGLELAKSDTYDDVVE

NbL15g04300.1 5-methyltetrahydropteroyltriglutamate--homocysteine_methyltransferase-like [MW = 84.52 kDa]

No. of times detected



log(intensity)



Values from



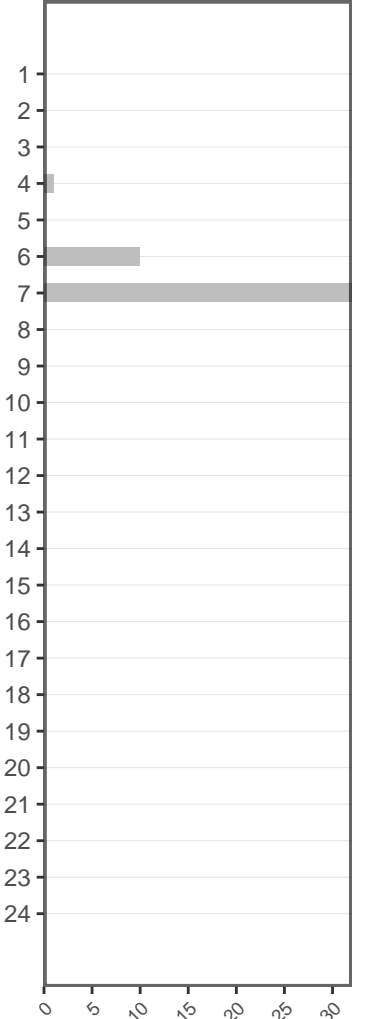
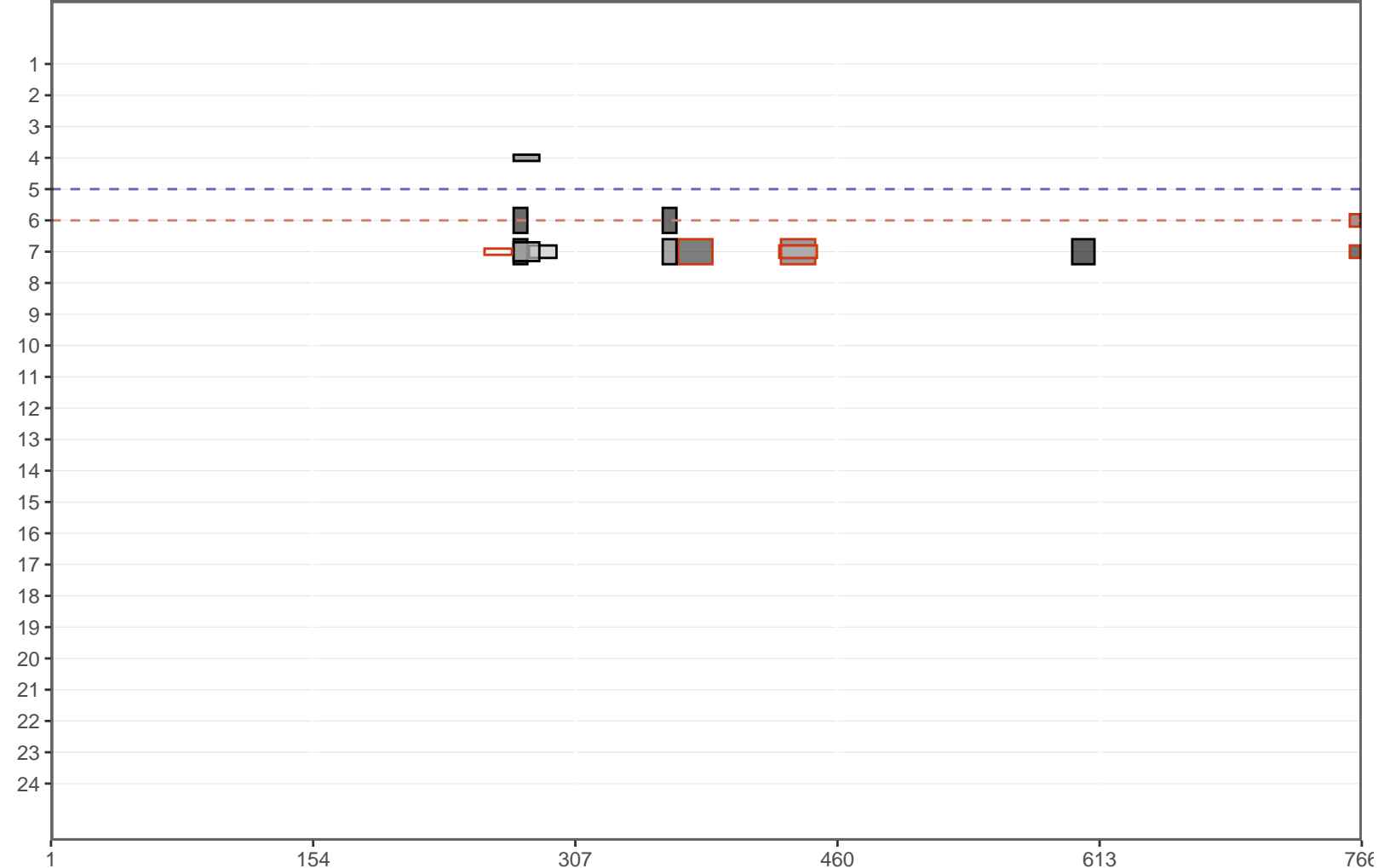
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01717 Cobalamin-independent synthase, Catalytic domain
- PF08267 Cobalamin-independent synthase, N-terminal domain

Protein sequence:

GAKDEAFFSANAAMQASRKSPRVTEAVQKASALQGGSDHRRATNVSARLDAGQKLNLPILPFTTGGSPQTVELRRVRRREYKAKKISEEYVKAKEEIKKVVLDGEEILDVYVHGFERNDMVEYFGEQLGFFATANGWVQVYGRCKVCPPIVGVGVSRPKPMTVFWVSAAGSMTRKRPKMGMLTGPVTLNWSFVLRNDQPRFETQYQALAKDEVEDLEKAGITVQIDEALREGLPLRKEHAFYLNWVWHSFRITNVIQDQTFQHTHMDY'SN'NDIISIDMD

NbL15g04170.1 probable_small_nuclear_ribonucleoprotein_F [MW = 12.01 kDa]

No. of times detected



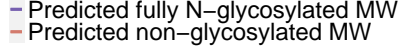
log(intensity)



Values from



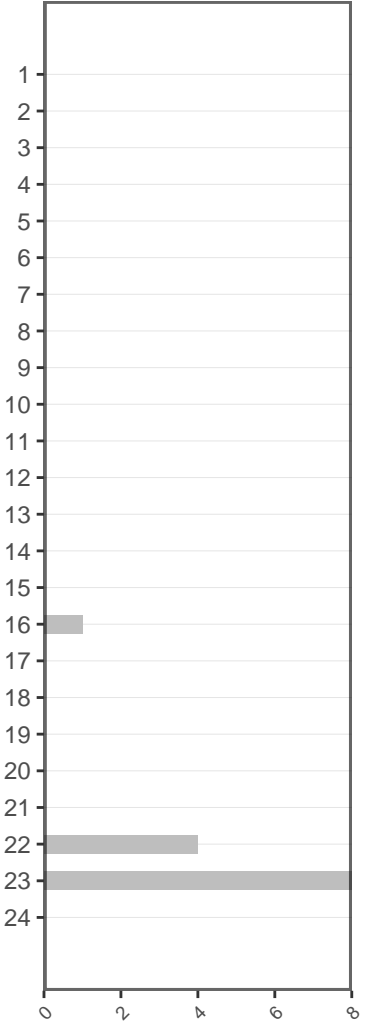
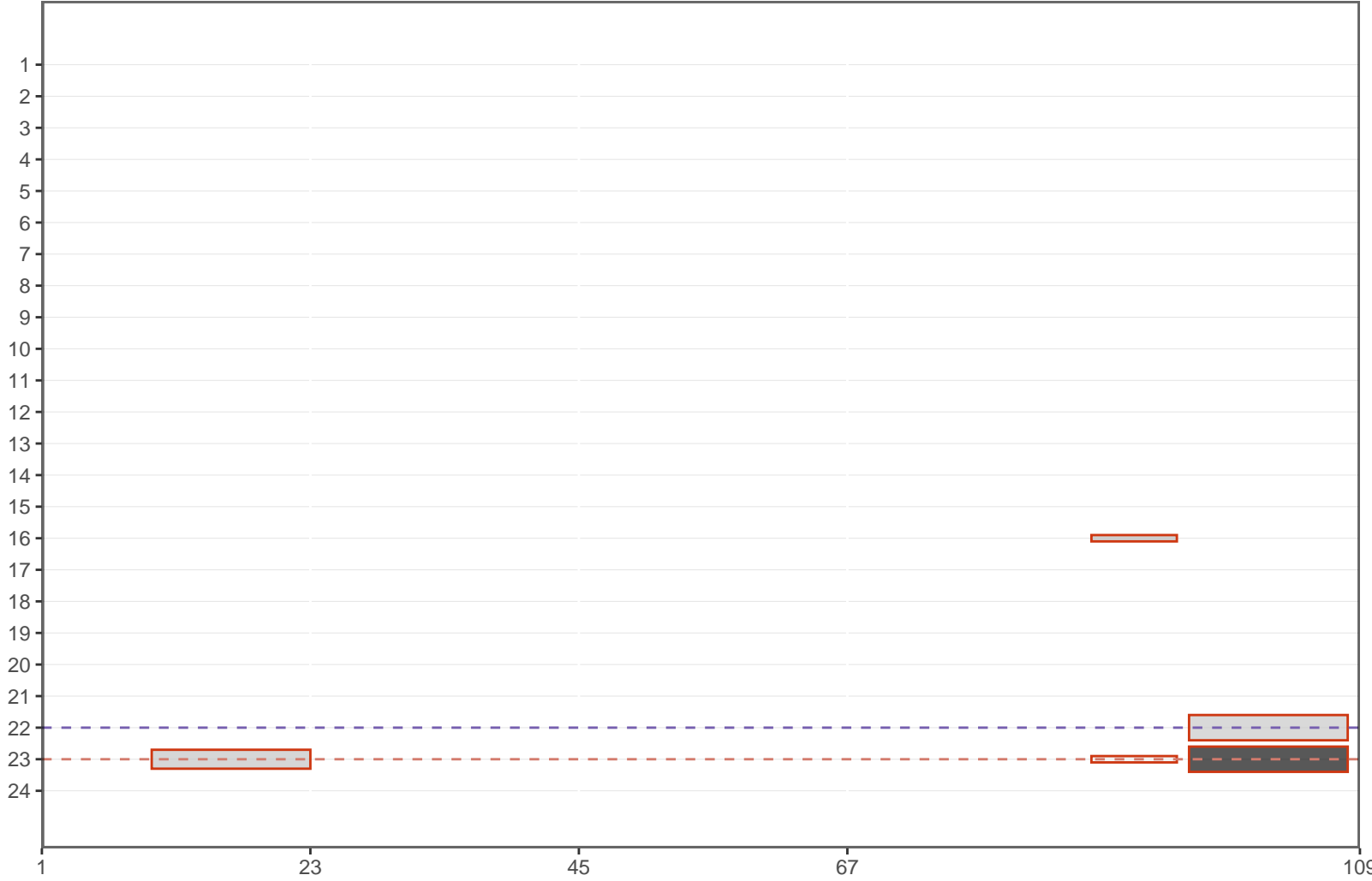
MW indication



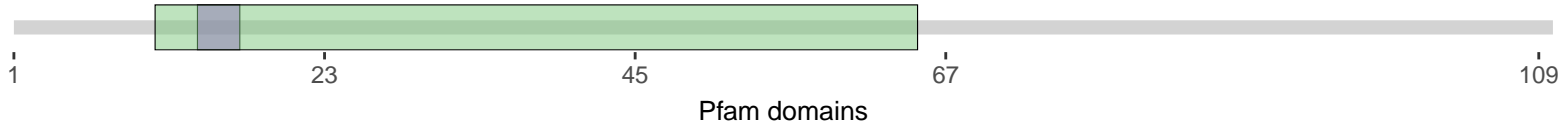
Molecular weight



Gel Slice

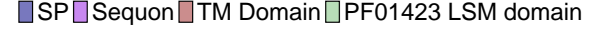


Protein length



Pfam domains

Pfam Description



Protein sequence:

MANLQLANAEYIDGGTGSLSGEIUSKATRFIFLRLAPFSACIRDNVLYLRGVPEDEELDDARDP

NbL15g03880.1 40S_ribosomal_protein_S16-like [MW = 16.75 kDa]

No. of times detected



log(intensity)



Values from



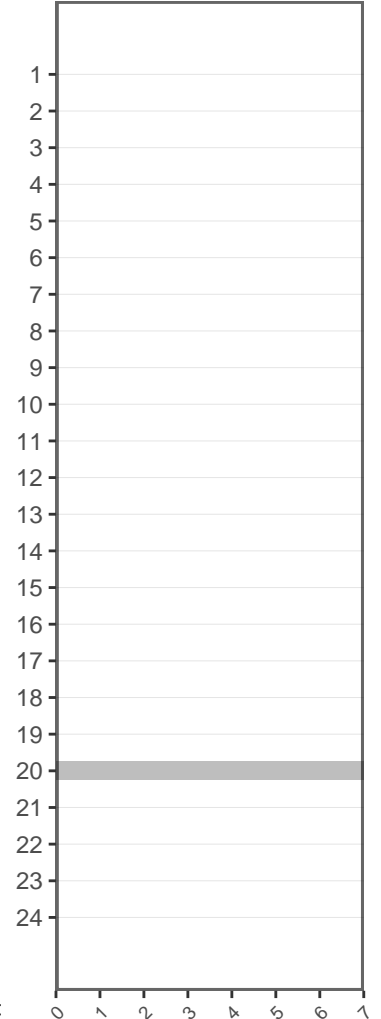
MW indication



Molecular weight

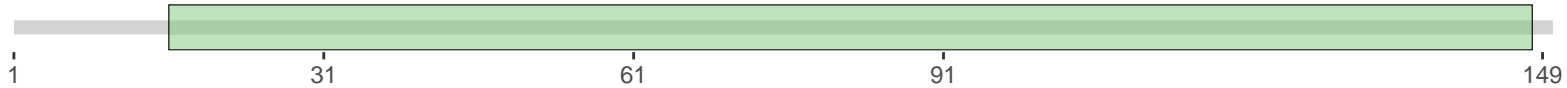


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IHRFAGVDMRIRVINGGHTSQIWRGSIKALVAFYQKIVDEGSKKIDILRYDRTLLWDRPRCEPKQFGGRGARARFQKSYR

NbL15g03860.1 40S_ribosomal_protein_S10-1-like [MW = 20.01 kDa]

No. of times detected



log(intensity)



Values from



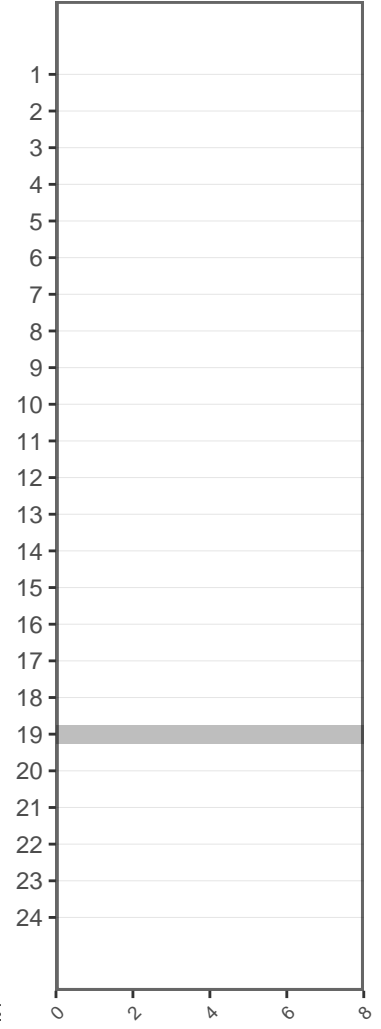
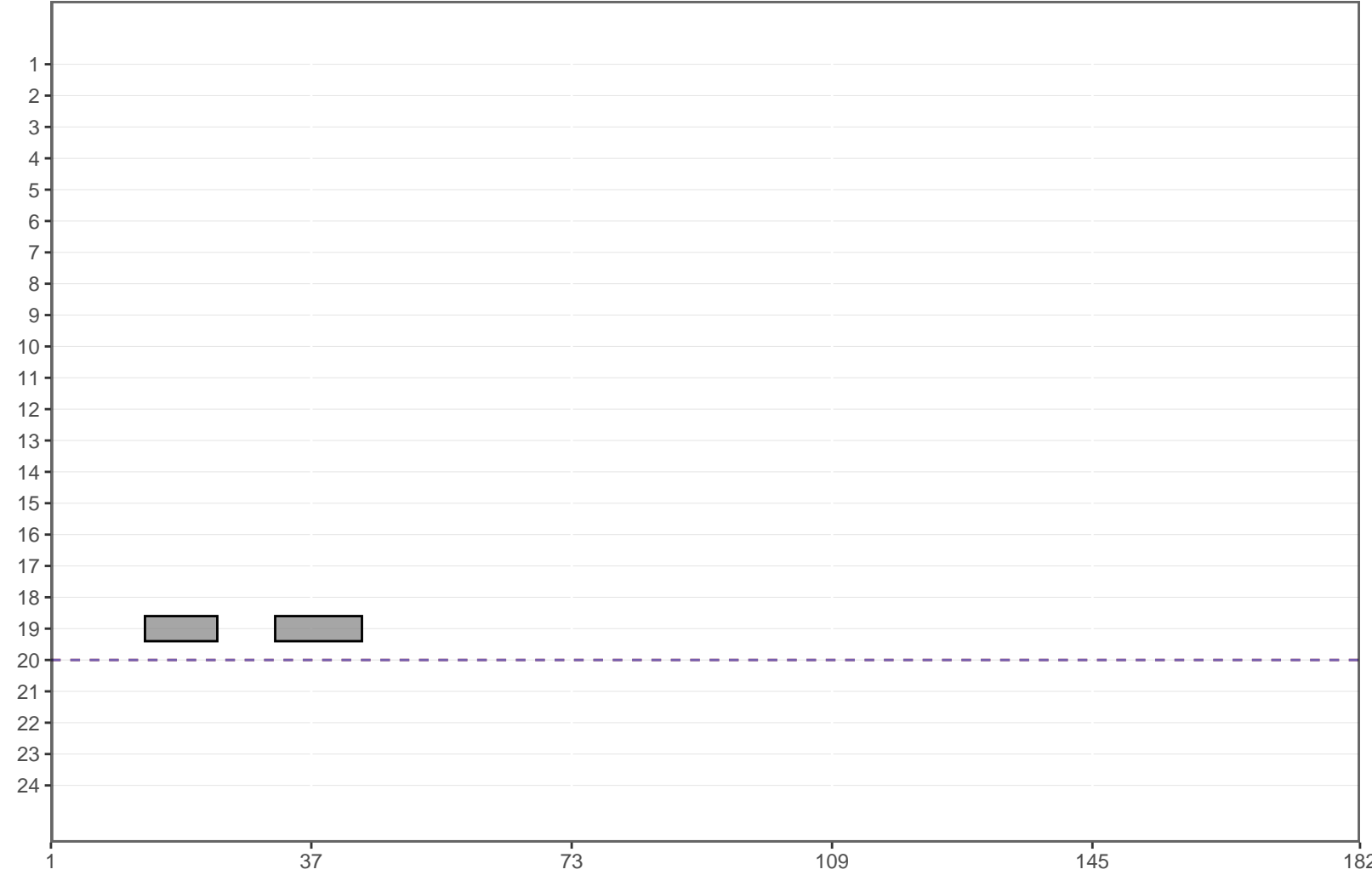
MW indication



Molecular weight

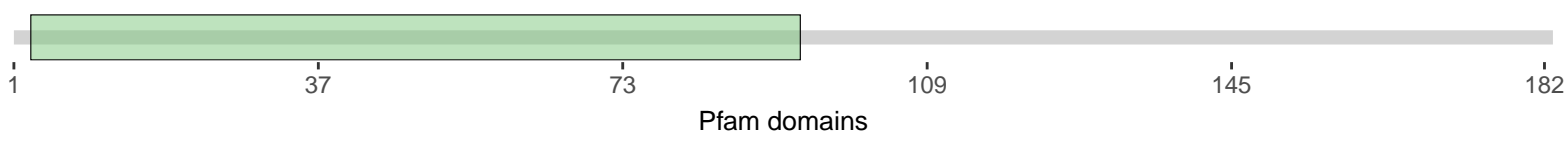


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

⋮PSEIVPATLKKSAKPLGRFMGGPPGDRPRGRPRRFEGDRPRFEGDRREGYRAGPRGPPGFGEENGAPADVDQVFRGGGGRPGFGRGAGGFGGAPPSSSFS⋮

NbL15g03820.1 uncharacterized_LOC107811196 [MW = 28.71 kDa]

No. of times detected



log(intensity)



Values from



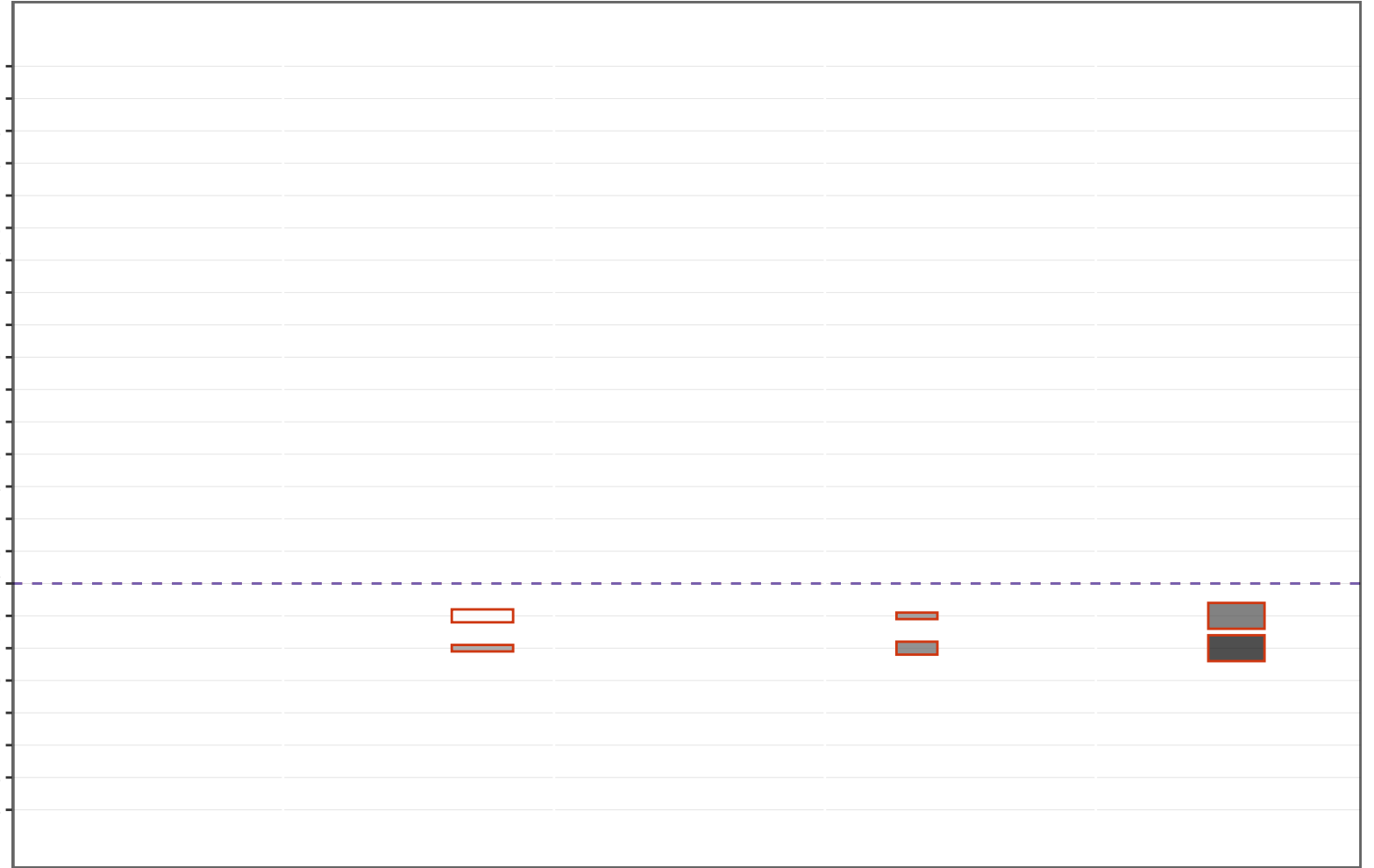
MW indication



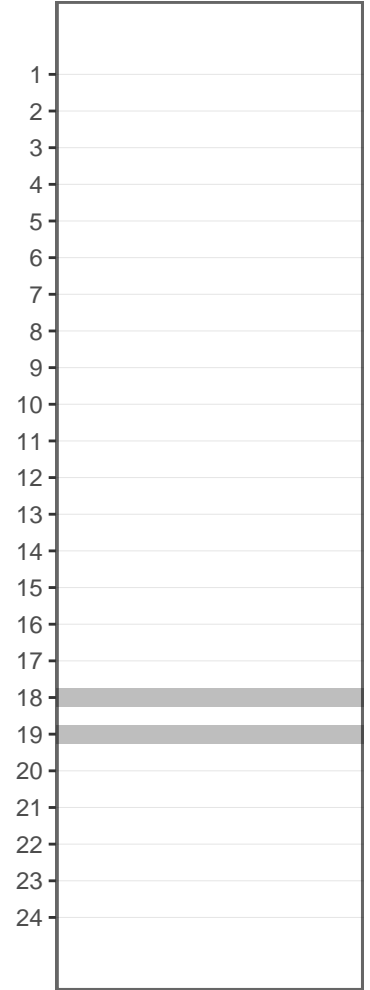
Molecular weight



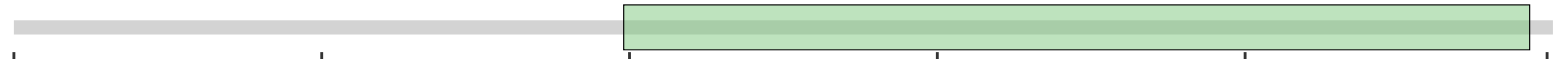
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LTEPEDYNAGLSLSDGKAKPKKFAAFASDRBEVLVSVIRPSNGLKIFFLEAKDVTDLGSLKEAAKIFVAGATLVGGREKIKEDGFRRTYVYEFARDEQHWLVAAVNSGHAYAGATAPESKWNDDGLKLRSAVSLMVLV

NbL15g03800.1 uncharacterized_protein_At2g34160-like [MW = 11.34 kDa]

No. of times detected



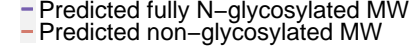
log(intensity)



Values from



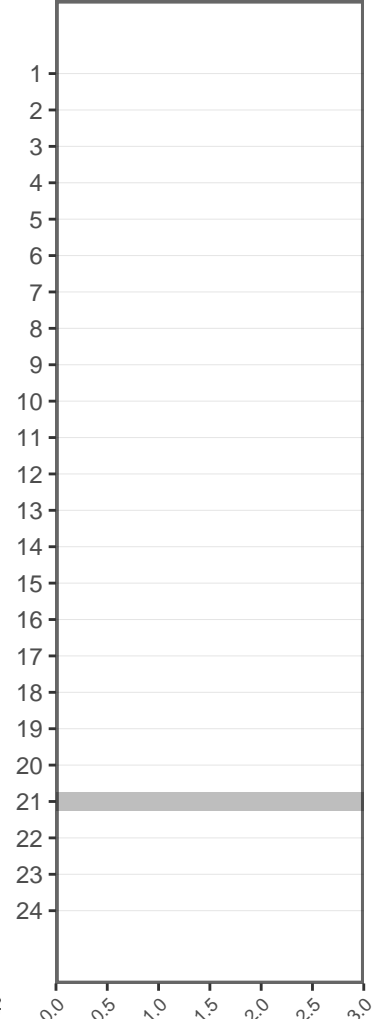
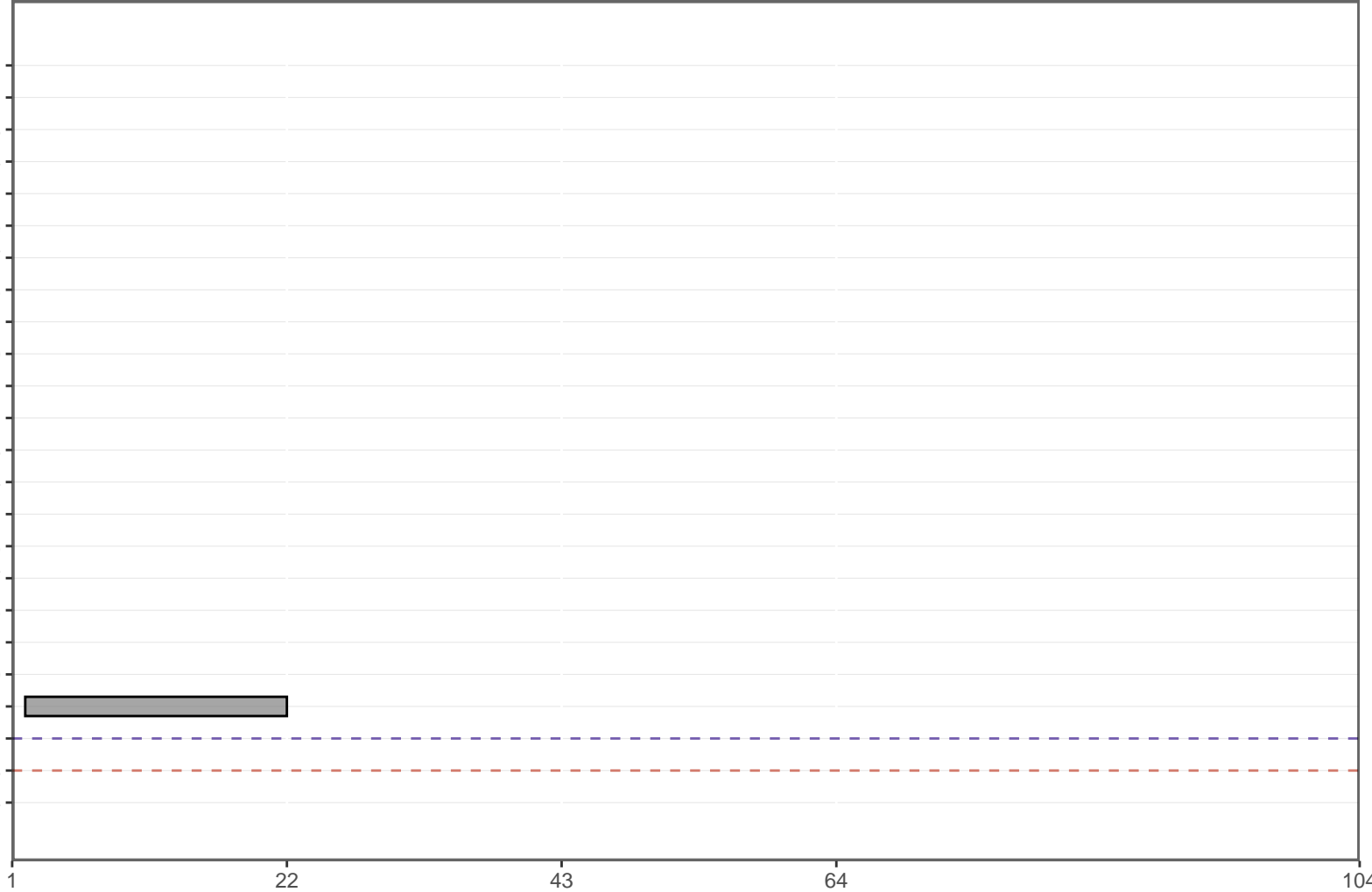
MW indication



Molecular weight

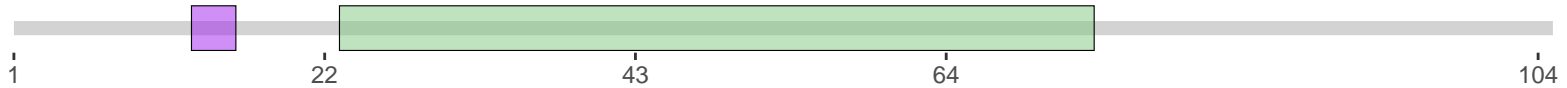


Gel Slice



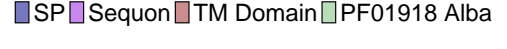
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

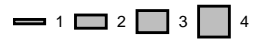


Protein sequence:

/NLAKRYMOOYNDVELGALGMAATVVAIEILKSGNGFAVEKKIMTSTVDVKKDGRGRPVSKAKLA*

NbL15g03770.1 26S_protease_regulatory_subunit_6A_homolog [MW = 47.47 kDa]

No. of times detected



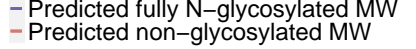
log(intensity)



Values from



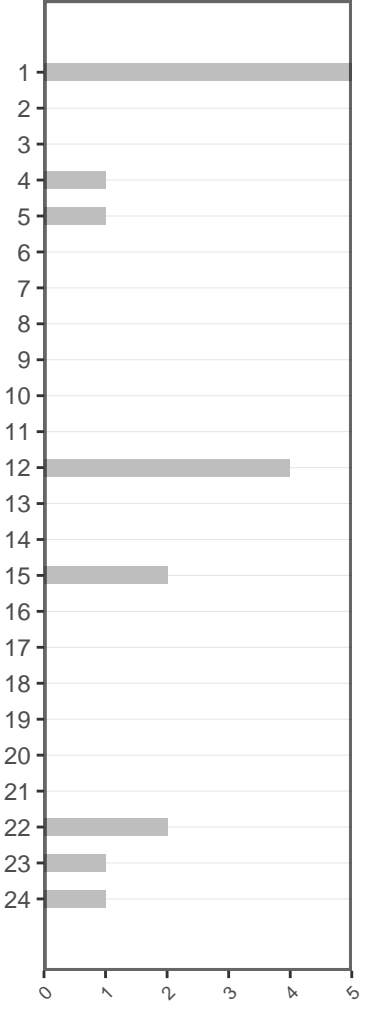
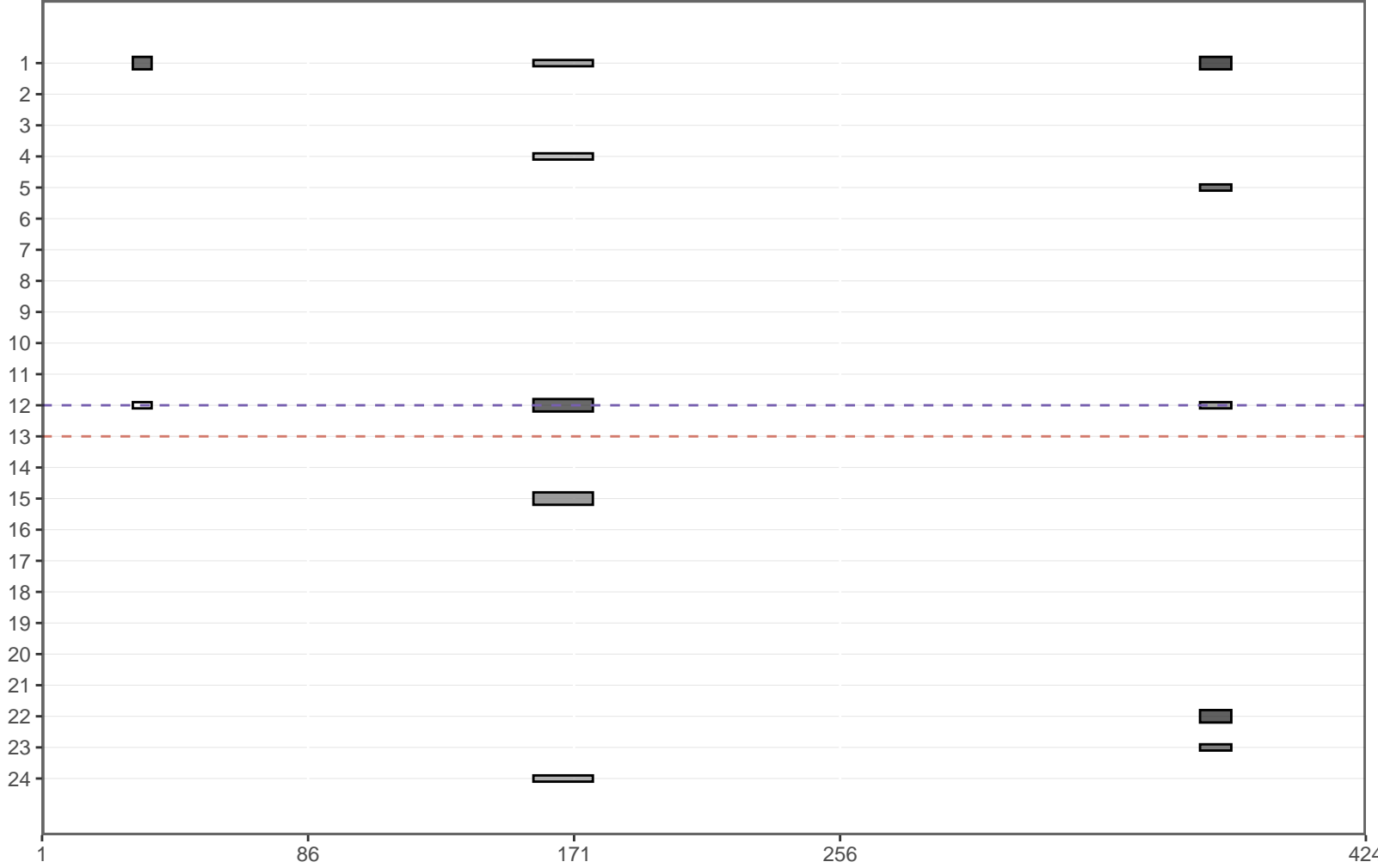
MW indication



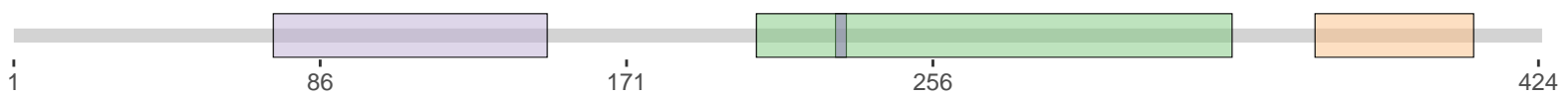
Molecular weight



Gel Slice

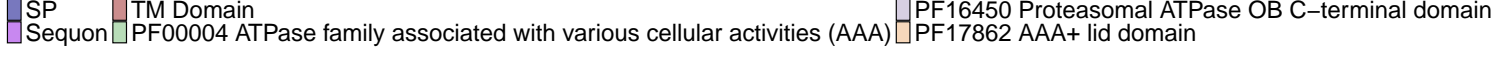


Protein length



Pfam domains

Pfam Description



Protein sequence:

GVRPPKGVLLYGPPTGKTLMARAGAAQTATFLKLAGPQLVQMFIGDGAALVRDAFLAKEKSPGIFDEDAIGTKRFDSEVSGDREVQRTMLELLNLQDGFSSDDRIKVAATNRADILDPALMRGRLLDRKIEFPHPTFEARARLQHSRKMNVHPDVFEEELARSTDDDFNGADLKAVCVEASMLLRDATEVTHEDFNEGIVGAKKKALNYVA

NbL15g03560.1 ferredoxin-dependent glutamate synthase chloroplastic [MW = 177.03 kDa]

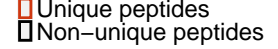
No. of times detected



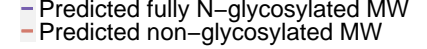
log(intensity)



Values from

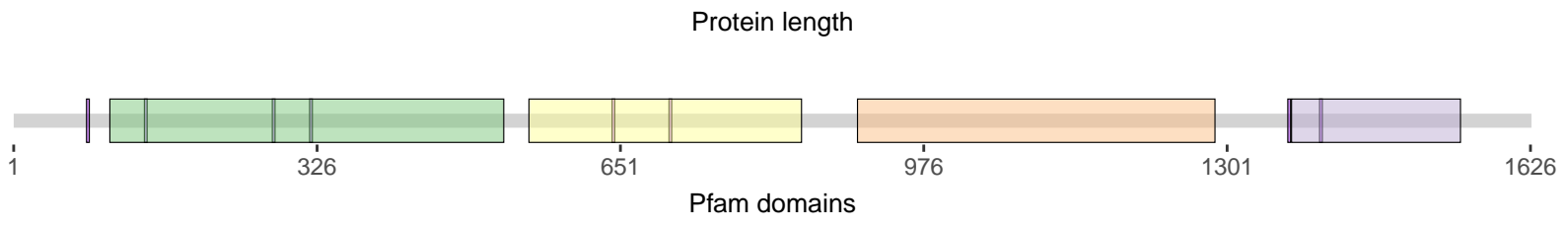
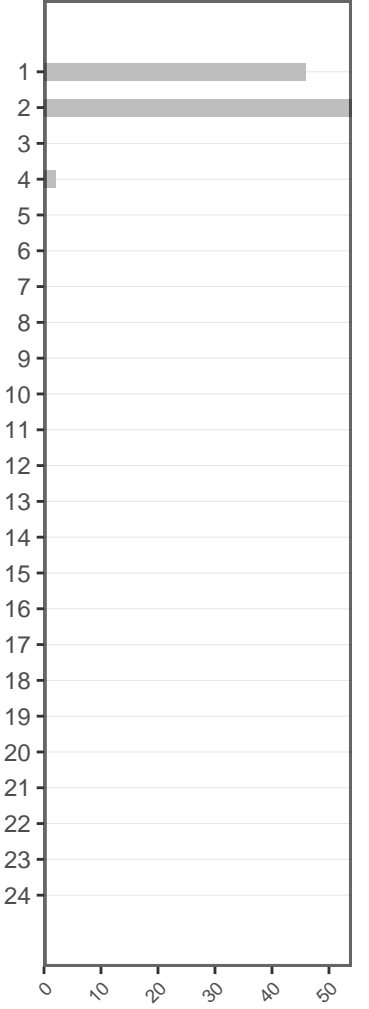
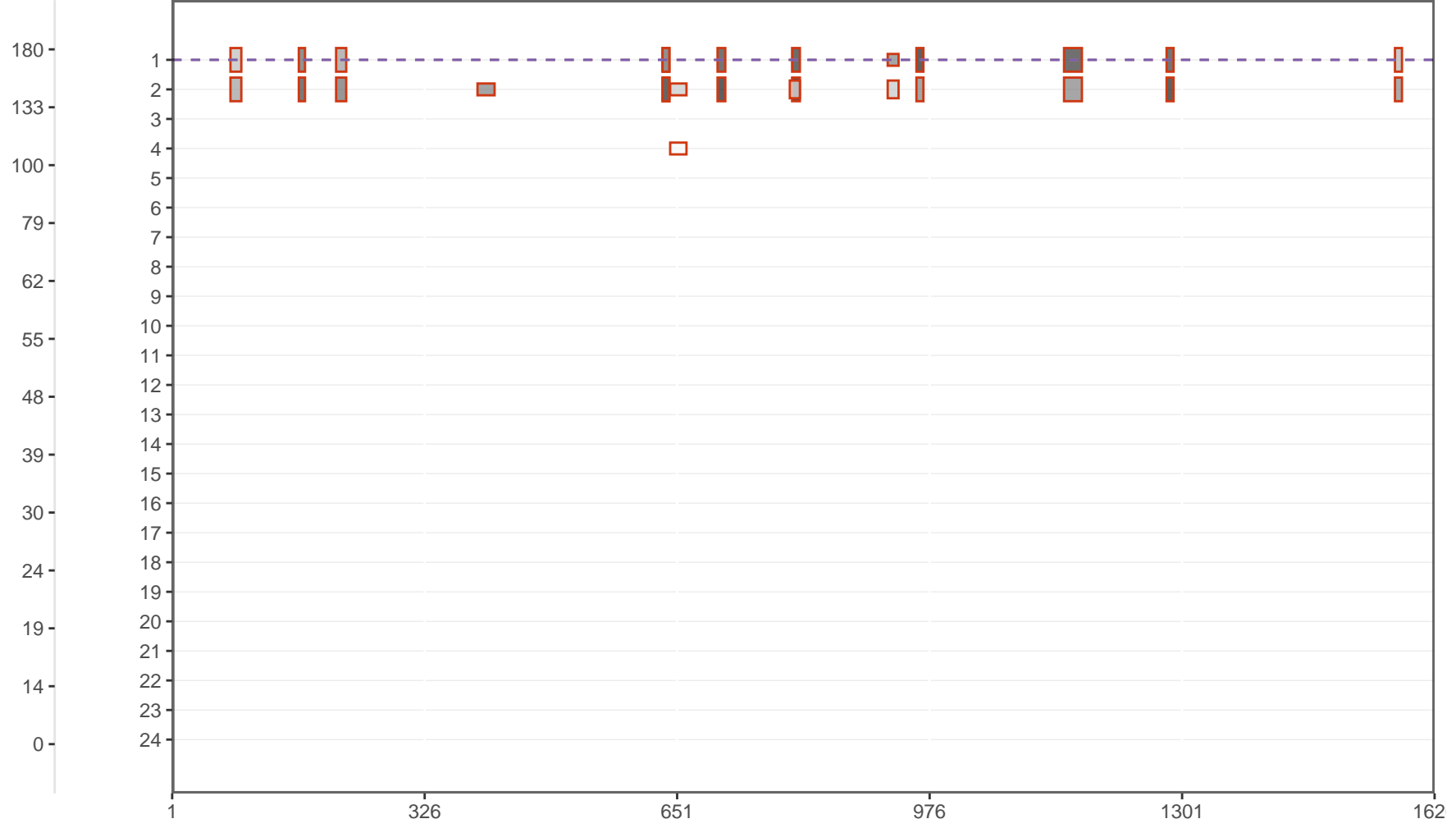


MW indication

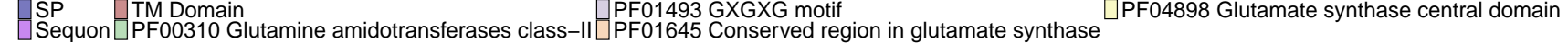


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

MPTVTVEQACKNFGKAVKSGLLMLSKMGISLLSVDGQAFIYVGLGKEVDDVAFQGGKSSIGGLTLDLARELRFWVAFSEDTAKRLNLYGFIQFRGGGEYHGNPEMKSLLHKAVRQKGGSAVSYVQGHLANRPVNVLRDLEFKEDRPIVQGRVPEASAVVORFDTGGMSLGAISRETHEAAMANNRLLGGKSNSEGGEGEDPIRWKPLTDVVDGVSPTLPHLKLGLNGDGTATSARKQWASGRFGVTPPTFLANADGLEIKWQAKPREGGGGLPGRXXYSAYIARLRN

NbL15g03310.1 glucose-6-phosphate_1-dehydrogenase_chloroplastic [MW = 70.75 kDa]

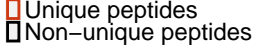
No. of times detected



log(intensity)



Values from



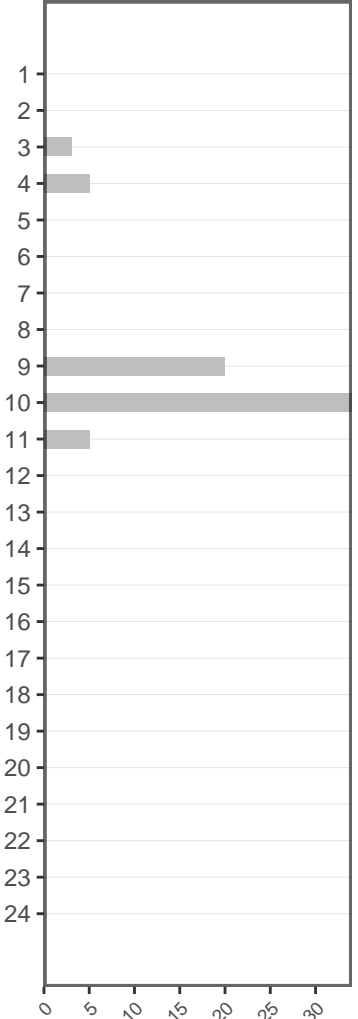
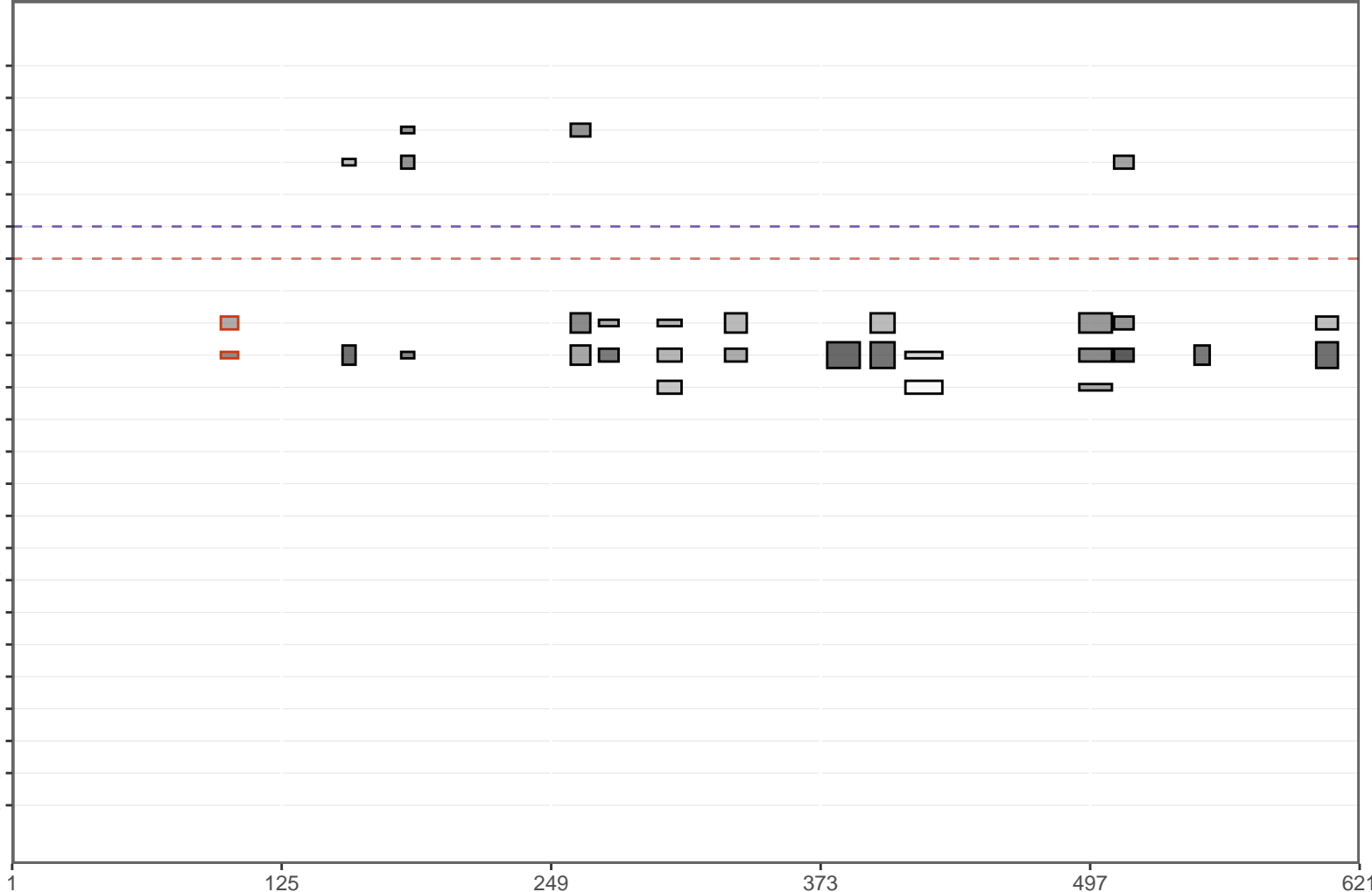
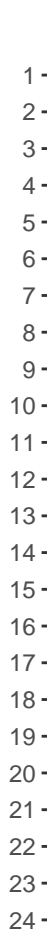
MW indication



Molecular weight

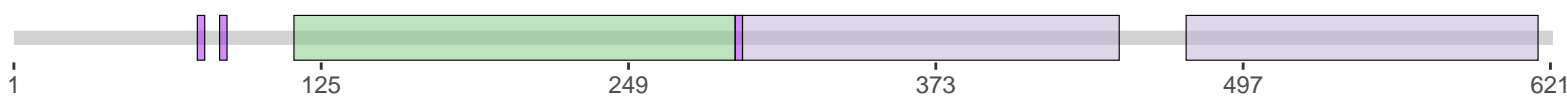


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00479 Glucose-6-phosphate dehydrogenase, NAD binding domain
- PF02781 Glucose-6-phosphate dehydrogenase, C-terminal domain

Protein sequence:

.RFSNLIFEPLVSRGHIRNQGIFSEDFGTEGRGGVFDHYGHIRDMQNHLLQLALFAMETPVSLDAEDIRNEKVKVLRMRPLGLDDVIGQYKDKFKSGDFTYPGYTDKKTVPKDSLTPPTFAAALFQNRARWDGVPFLMKAGKALHTRRLVKNPTAFLLHFHFTYHFFPFQFSASAEIRVQGRHVPGNLNNKFKGSDLDGATNELVIRVQGNPNEAYLKNKVPGLGMRLLDGSNLSLVSARYSKEPDAVERLLLDIEGERLFRFSDLDAAWLSFTFVNLLELDDKXVPEYF

NbL15g03120.1 ubiquitin-conjugating_enzyme_E2_variant_1D [MW = 16.59 kDa]

No. of times detected



log(intensity)



Values from



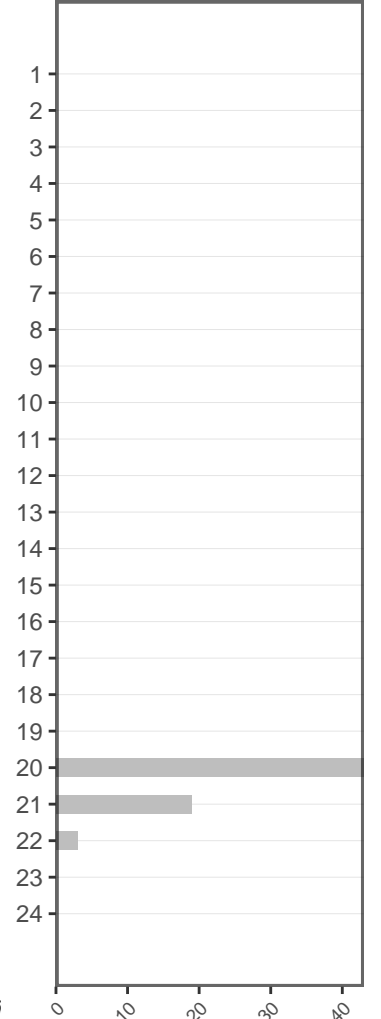
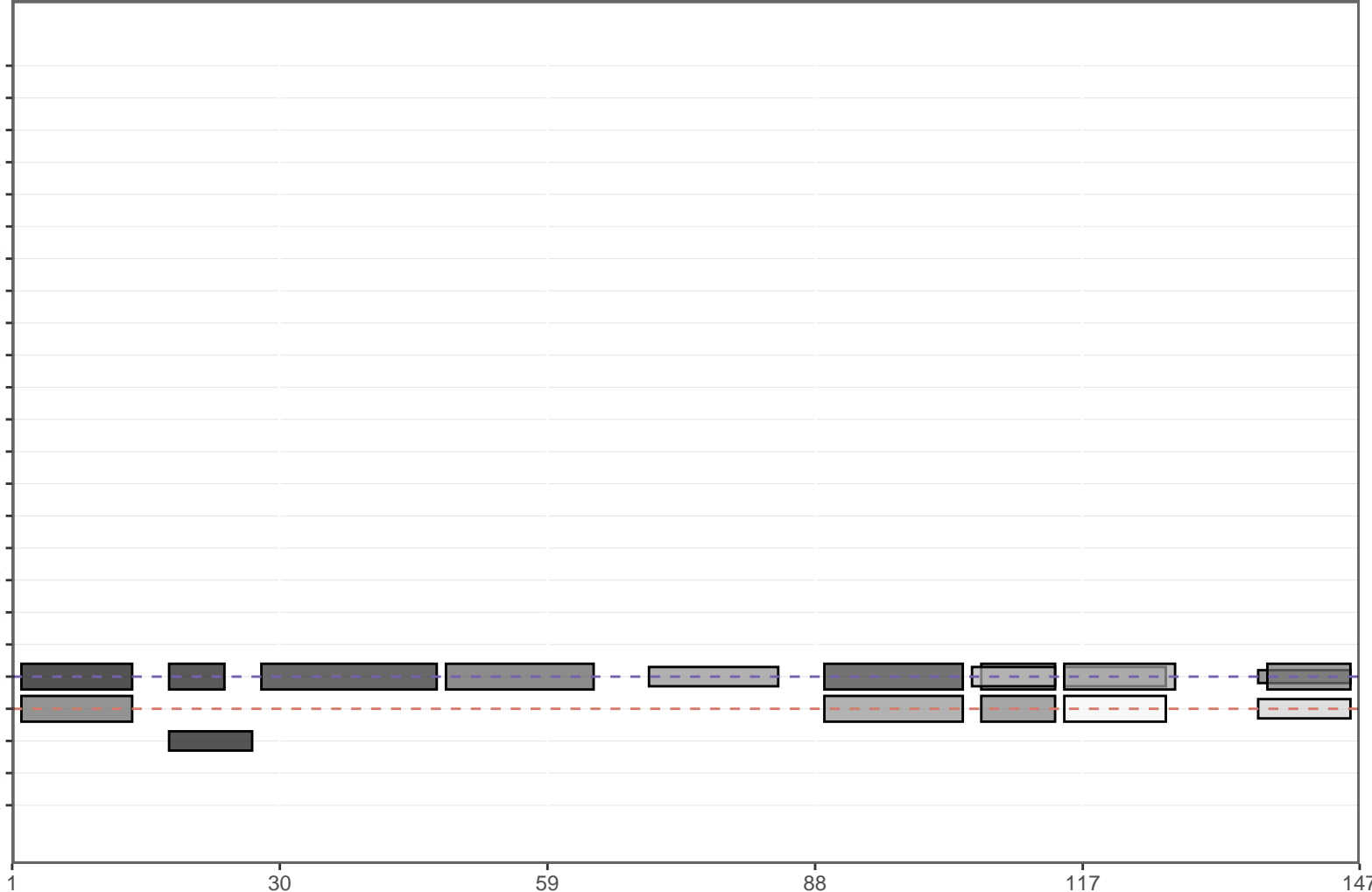
MW indication



Molecular weight



Gel Slice

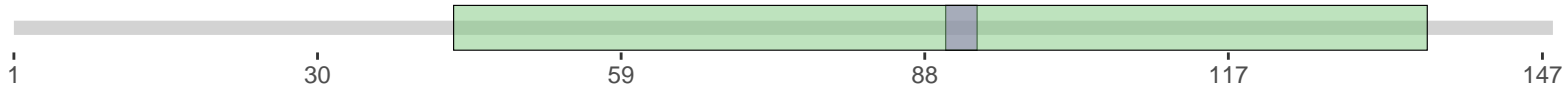


Protein length

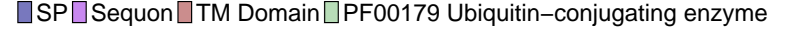


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

1EGRIVQLKLFCDKDKYPEKPPSVRFHSRNVNMTGVNHTGVAVERPKFALLANVQREYTMEDLVQKKEMAAPHNKRLVQPPGTYE*

NbL15g03090.1 TLD_domain-containing_protein_1 [MW = 46.98 kDa]

No. of times detected



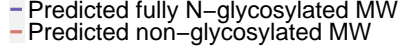
log(intensity)



Values from



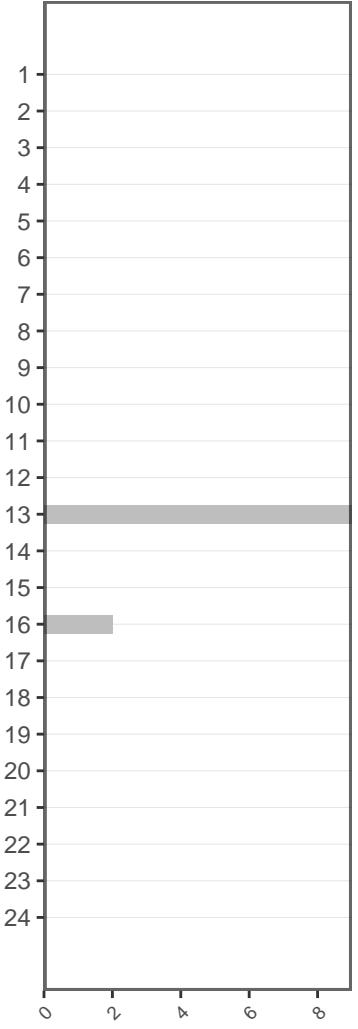
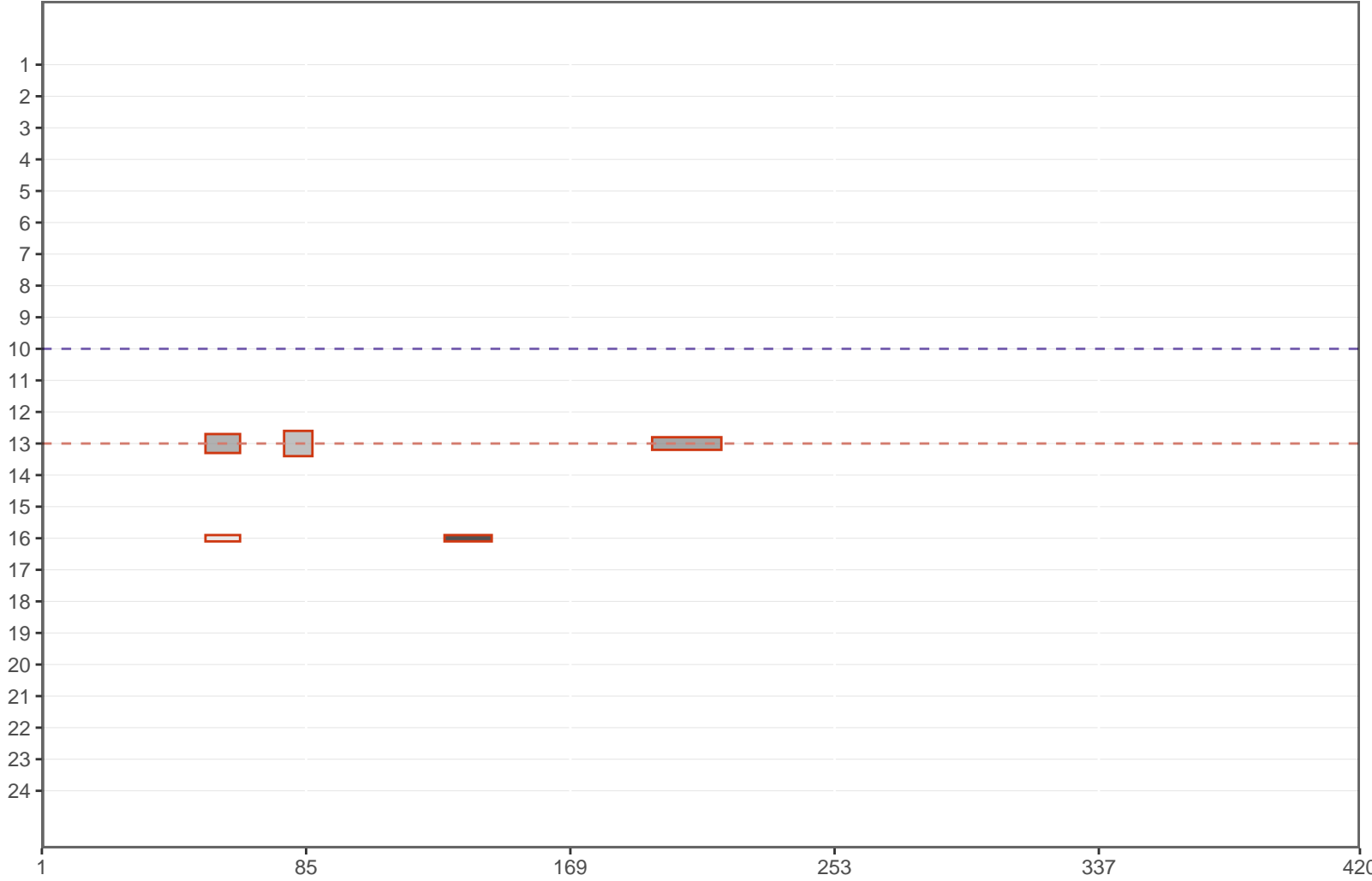
MW indication



Molecular weight



Gel Slice



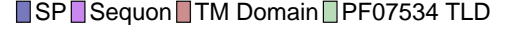
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SSEVPIILYIPENDFWALLLRKEVAWHGGALPQDELHEWRLLVHSTVHGLSFNTFLGTSDDKGPFLIKKDKKGGVGGYASQVPEKHADFYGDMMKFLFQLYPKASVYRPTGANTNLQWGAINFSSSESPNGIGFGRRVHIFGLFISANFDQGHHTFTCTFFGSPLEKTPQIFPEVEQWGWATKRVGDDNHDRKGLKGYLDRFKEDRHMILNMVGLANSSG

NbL15g03070.1 secoisolariciresinol_dehydrogenase-like [MW = 29.48 kDa]

No. of times detected



log(intensity)



Values from



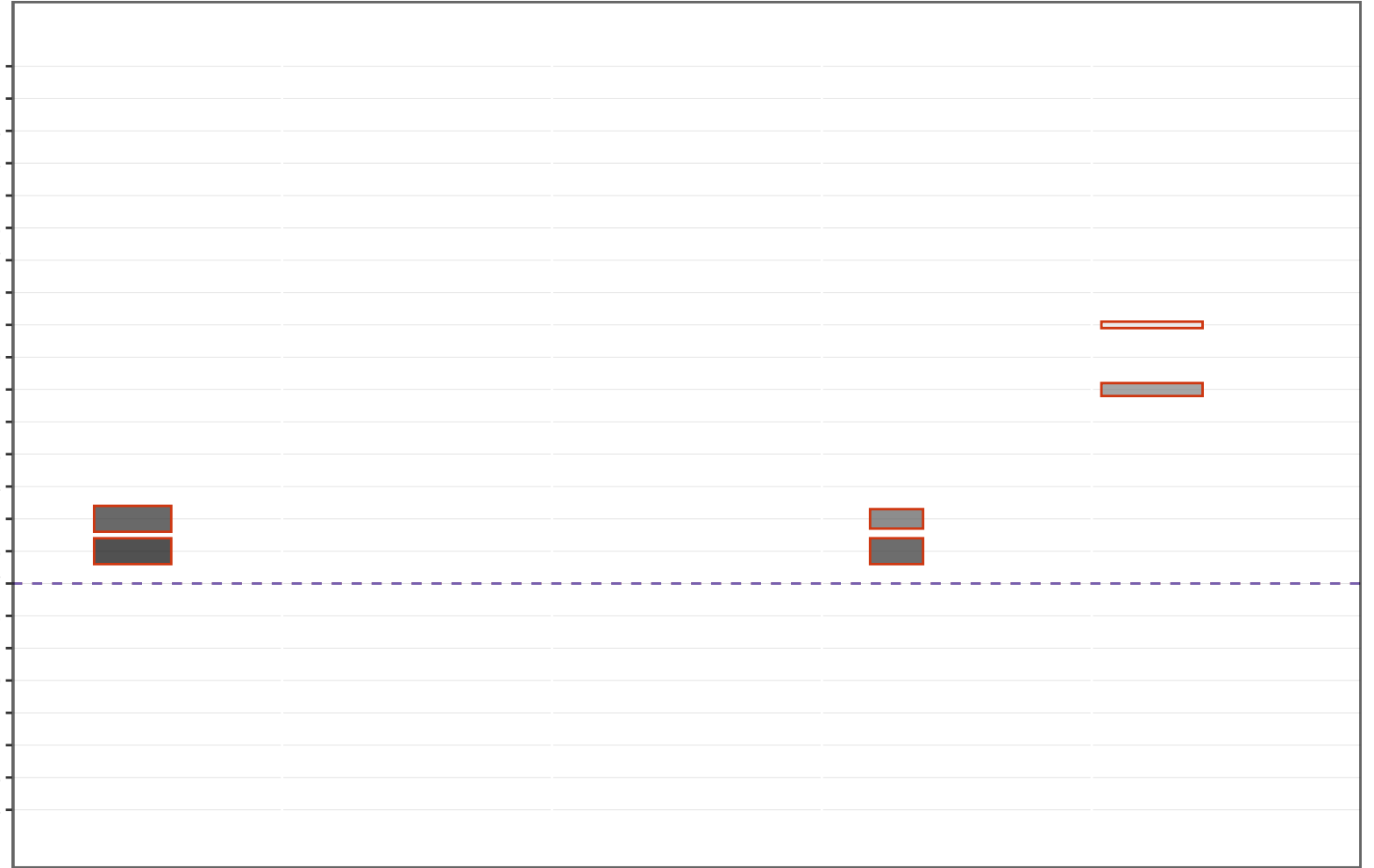
MW indication



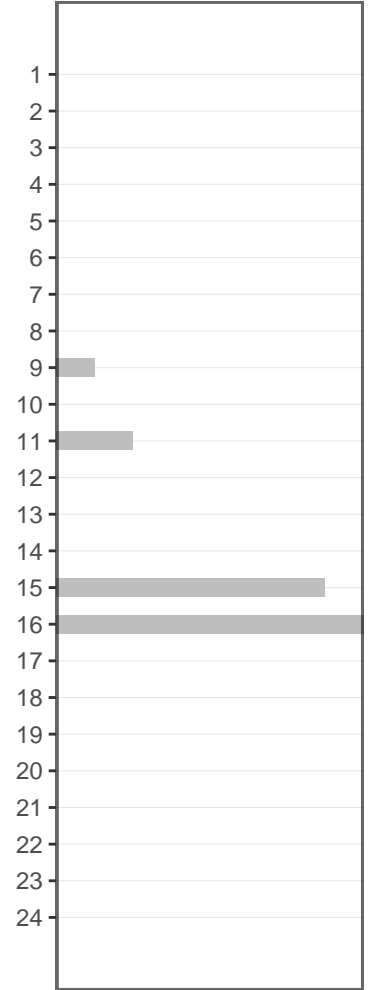
Molecular weight



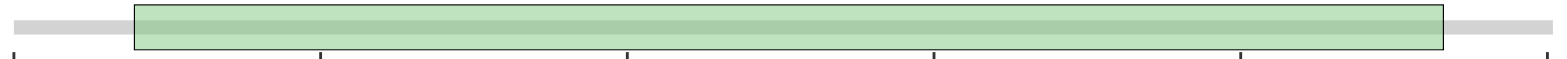
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YGSFLGAKYARVMPKMKGVLFSSVAANAGESPHSYTVKHHAVVGLTKNLGAELGGYGRVNGVSPCAWTRLLVKKAMGAEKSVVDGIGSSANLKGVVPTAEDAEAAHLASDESKFVSGLNLVDDGGYSTTNGAVMKTGQVLFSTV

NbL15g03000.1 glycine-rich_RNA-binding_protein_4_mitochondrial-like [MW = 14 kDa]

No. of times detected



log(intensity)



Values from



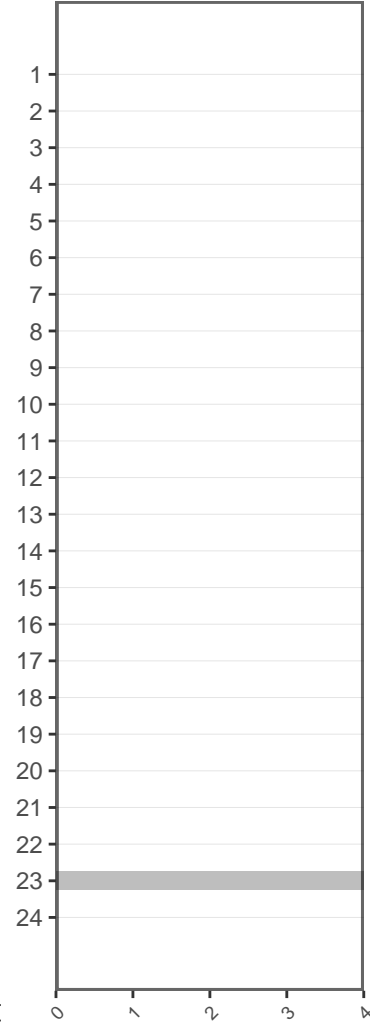
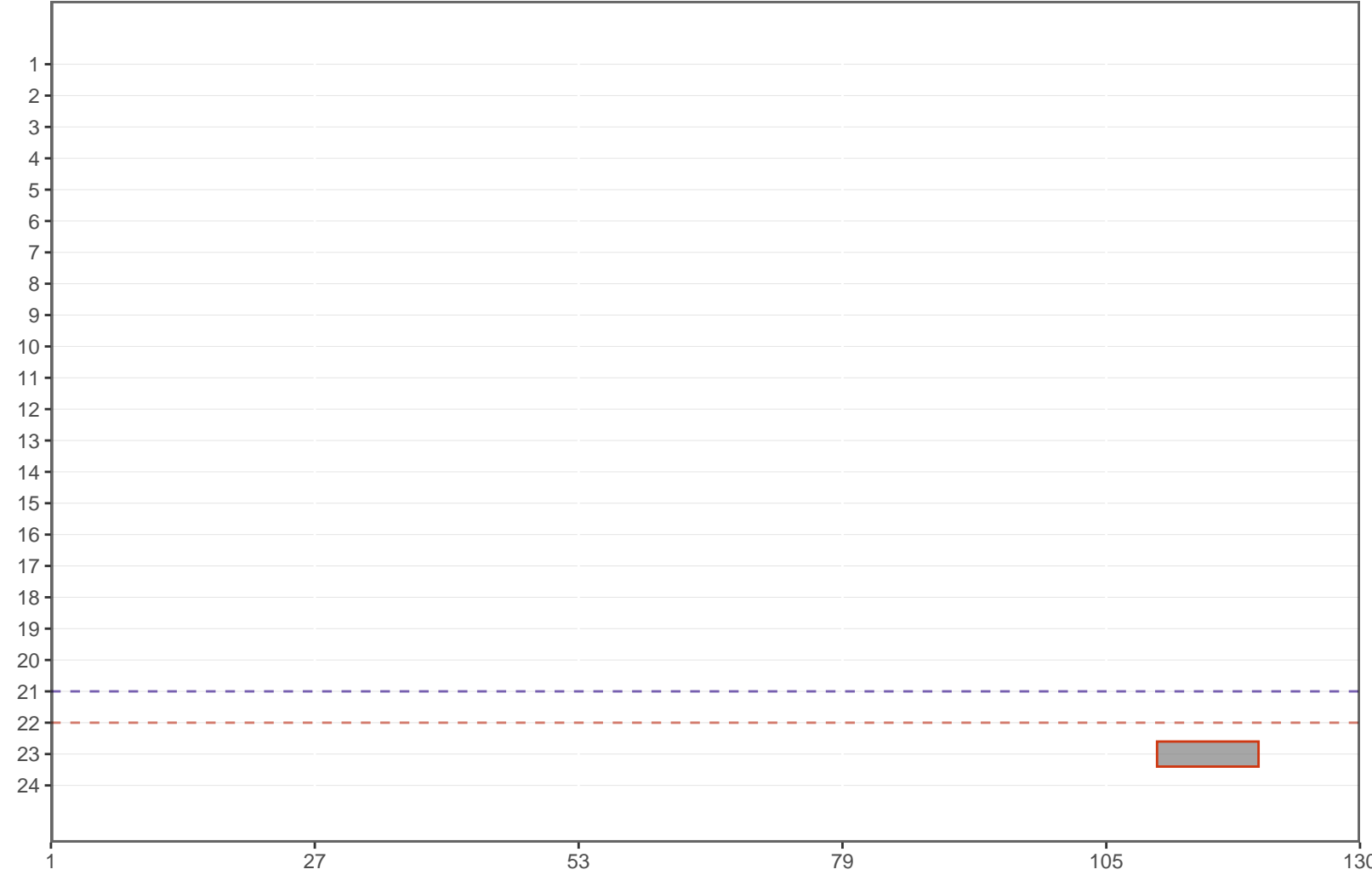
MW indication



Molecular weight



Gel Slice

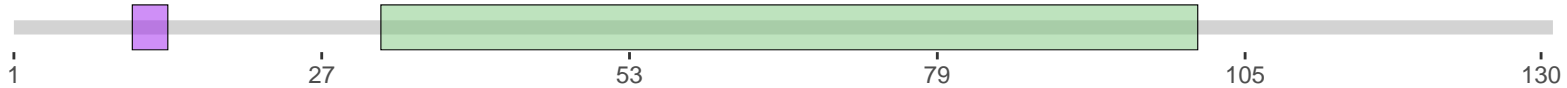


Protein length

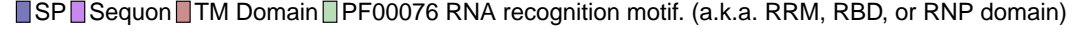


Peptide counts over 4 repeats

Pfam domains



Pfam Description

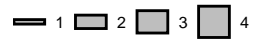


Protein sequence:

IGQVIEAKVMDRVEDKSKGFGFVYASDDAKKALGEMNGKPLNGRIVFDVAKPKADFGGAMPARGPPEPTEQ*

NbL15g02960.1 protein_ABHD11-like [MW = 36.84 kDa]

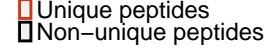
No. of times detected



log(intensity)



Values from



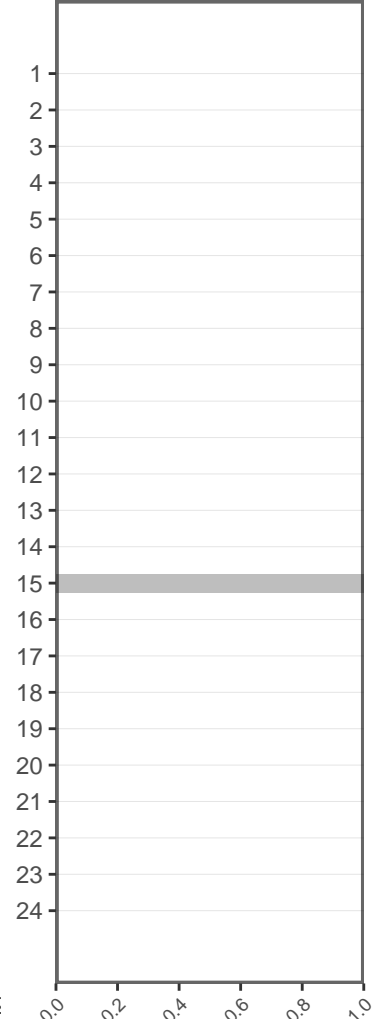
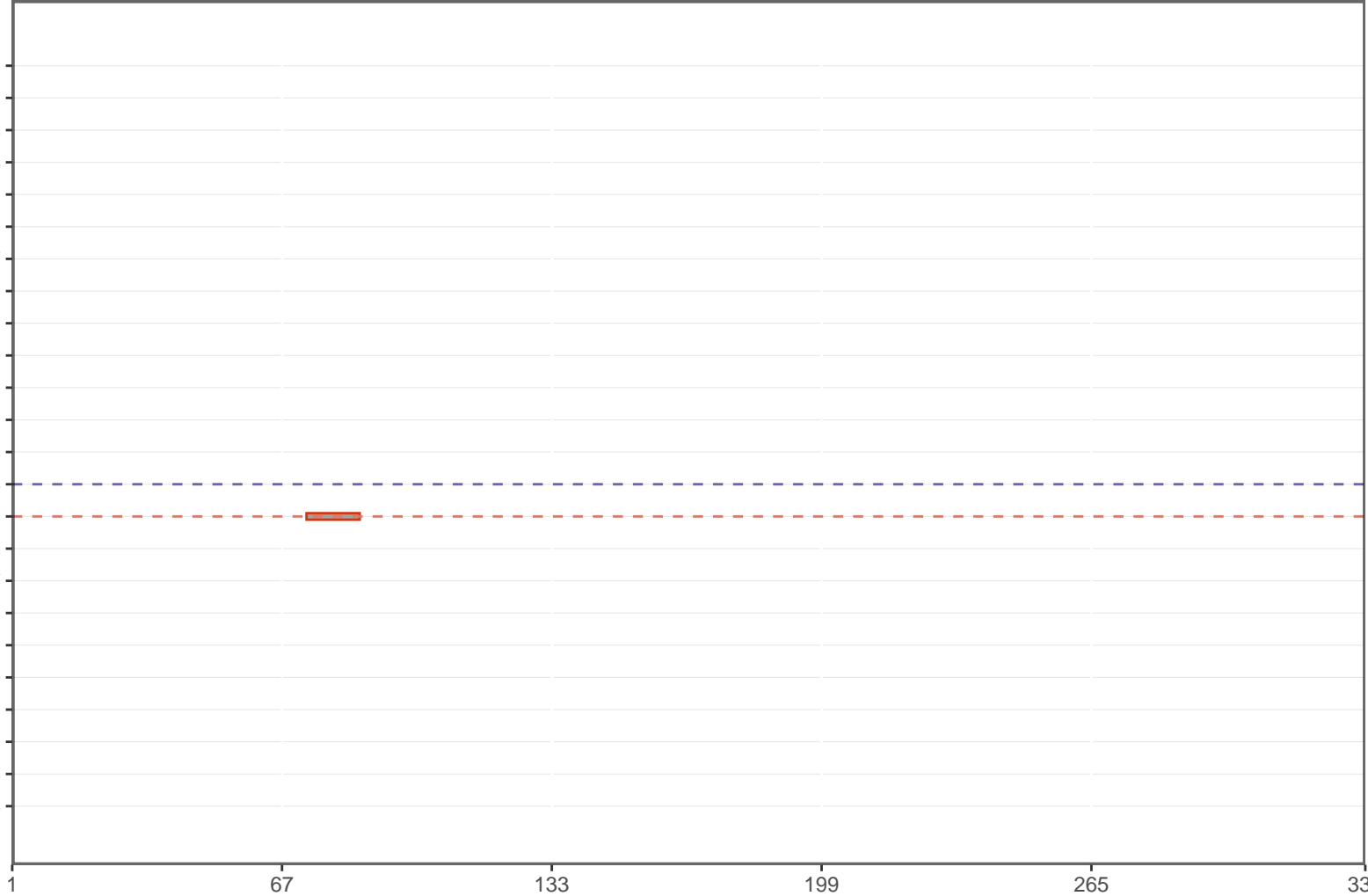
MW indication



Molecular weight

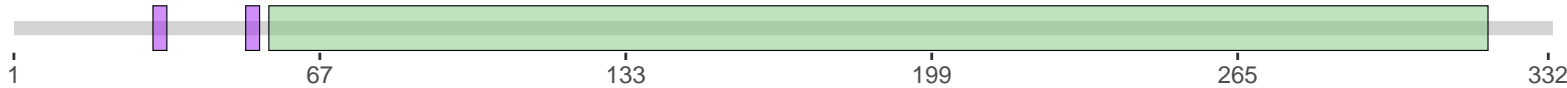


Gel Slice



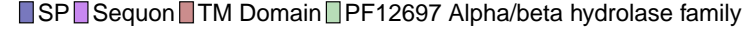
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YGG SARLPKQLVLDGVPKGVDPEDGSRVEKVMQTLQSLPSBPSRKWLDHMLKGFSAKLEWLGSLQKSGDMMWTFNIEAAMDMSVREKDYCPLEHPKGTETAVRAERSDRWDPEYVQKLSFASNGGSEGECHMSYHLPLNSGHWHVVENPRGLLEITPKLASLV

NbL15g02940.1 beta-fructofuranosidase_insoluble_isoenzyme_1 [MW - SP = 62.37 kDa]

No. of times detected



log(intensity)



Values from



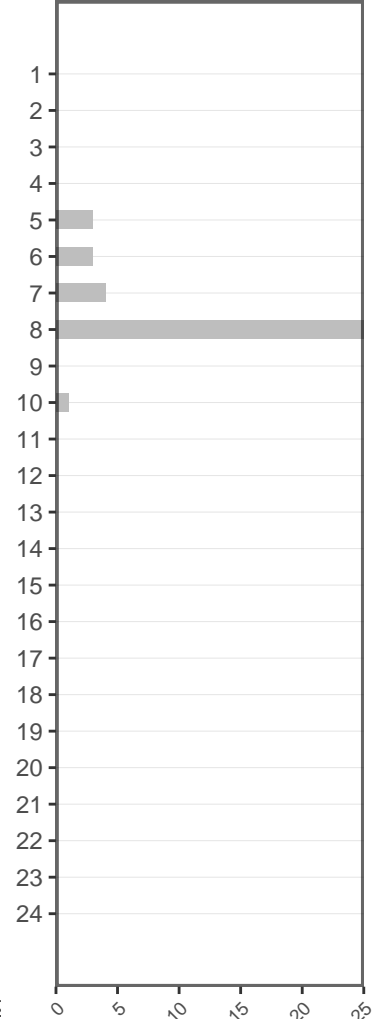
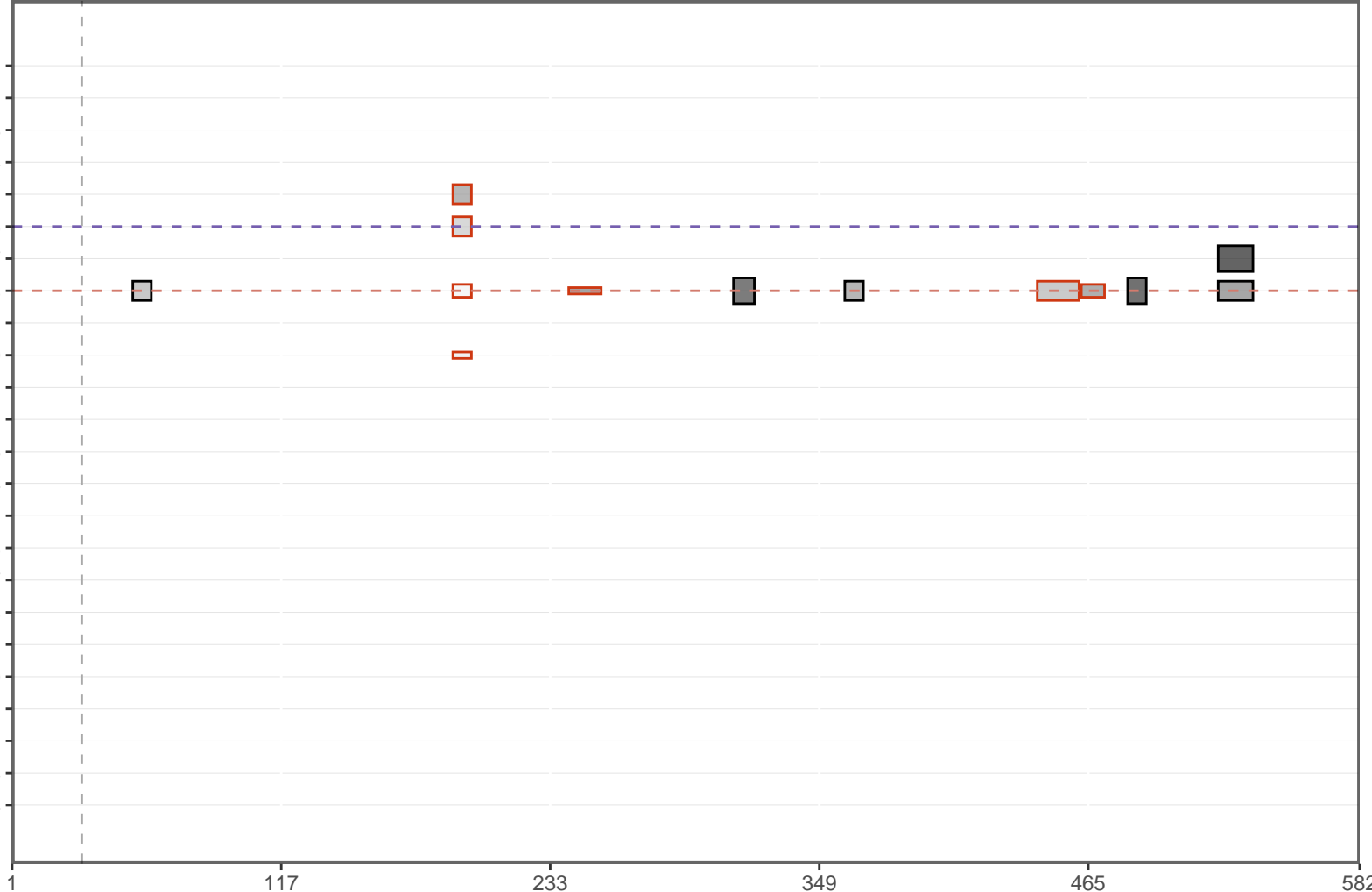
MW indication



Molecular weight

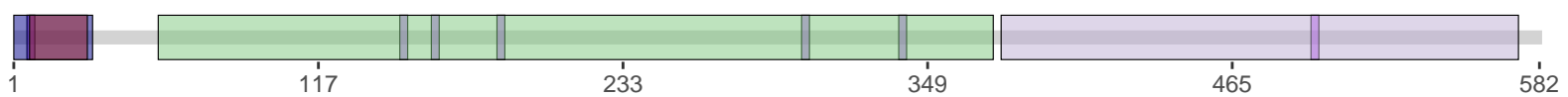


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00251 Glycosyl hydrolases family 32 N-terminal domain
- PF08244 Glycosyl hydrolases family 32 C terminal

Protein sequence:

I.LD.VTRFEYTYTGTDTHKDRVDPNTEVDGKGLRLDLGNYAASKSEYDPSKRRIMLGWANESDVTDDDKVKGWAGVHPTPRKLVLDPSGKGLVGPVEELETURKEKVLQNSHRYKGEKIEKIGTAAQADVEVHFSFASLDKAEFFDPGAWADLVADVCAKGSTVGGGLGPFGLRLAKNLEEYTPFFRFRVKAQDKYKLVMSDASRSTLNKNETMYKPSFAGYVDVLDLADKLSLRSLDQNSVVEGFGAGKTKGTSRIVYPTLAFDKAHLFAFNNGKEATIKTL

NbL15g02790.1 pyruvate_decarboxylase_1-like [MW = 65.25 kDa]

No. of times detected



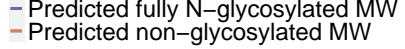
log(intensity)



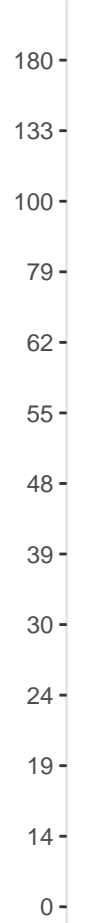
Values from



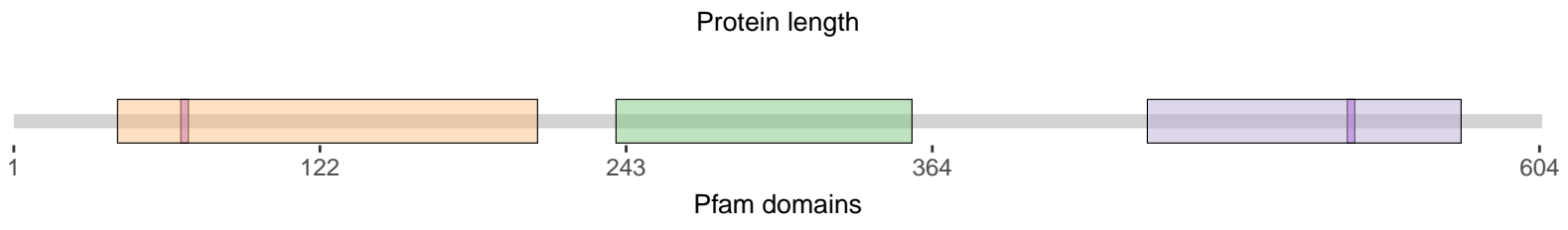
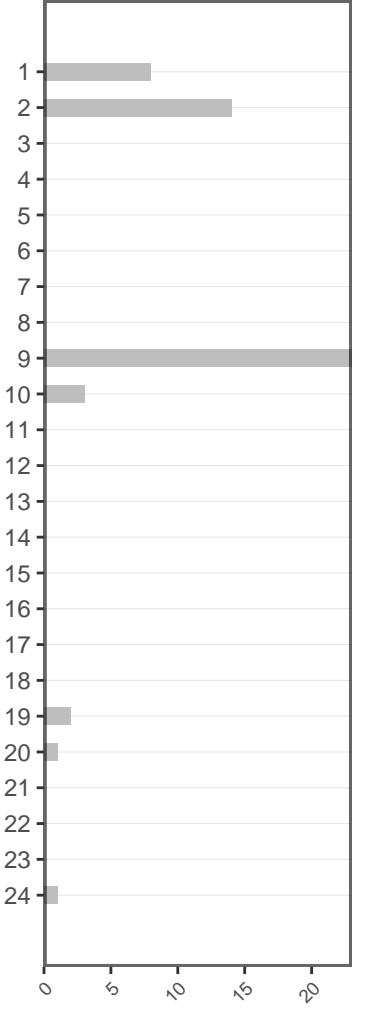
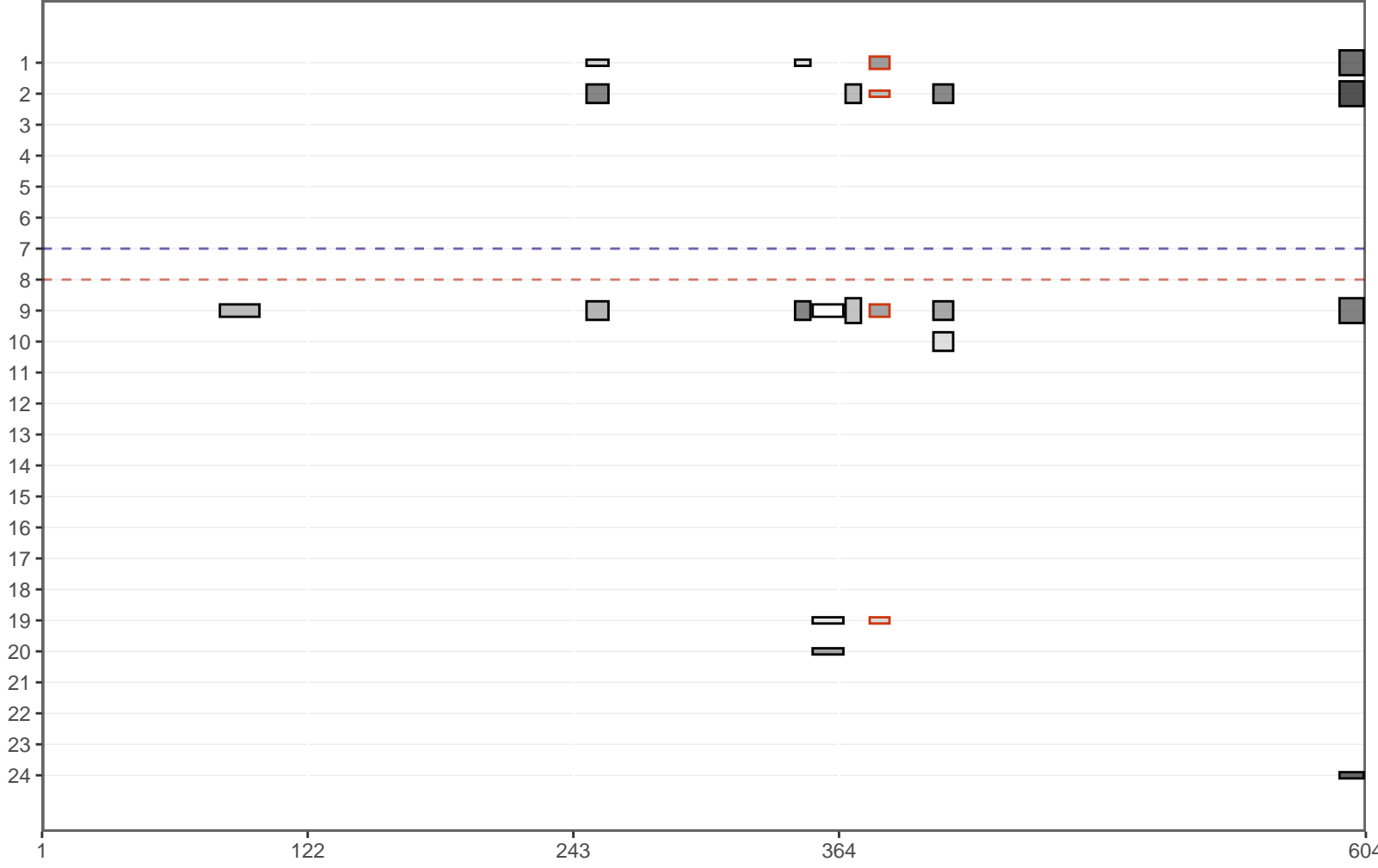
MW indication



Molecular weight



Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00205 Thiamine pyrophosphate enzyme, central domain
- PF02776 Thiamine pyrophosphate enzyme, N-terminal TPP binding domain
- PF02775 Thiamine pyrophosphate enzyme, C-terminal TPP binding domain

Protein sequence:

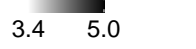
I/VPEHHPHFQGTYYGAVSTAFGAIEVESADAYLFGAPFINDYSSVSYSLKLLKKEKAIIVQDRVTIANGPFGVLMKDFLAALAKRLKYNPTAVDNYRRIYVEGHPLKCEPQEAIRVNLFEHGRLMSGDTVAIETGDSWVFNCGKLLKPEGGYEFQMGVYSSIGVSWGATLGYAGAAAREKRVVAFDGDGDFQVTAQDQITMLRGGQRTIFLNLNGGYTIEVHSDGPIVNIKWVNYTGLVDAIHNGEGKGVWTRKVCCEELVEAETATEAKKDGDFREVIWIKDQTSKELU

NbL15g02760.1 acyl-coenzyme_A_oxidase_4_peroxisomal [MW = 48.4 kDa]

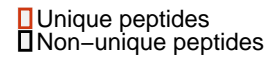
No. of times detected



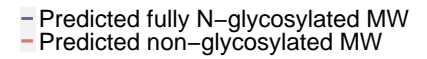
log(intensity)



Values from



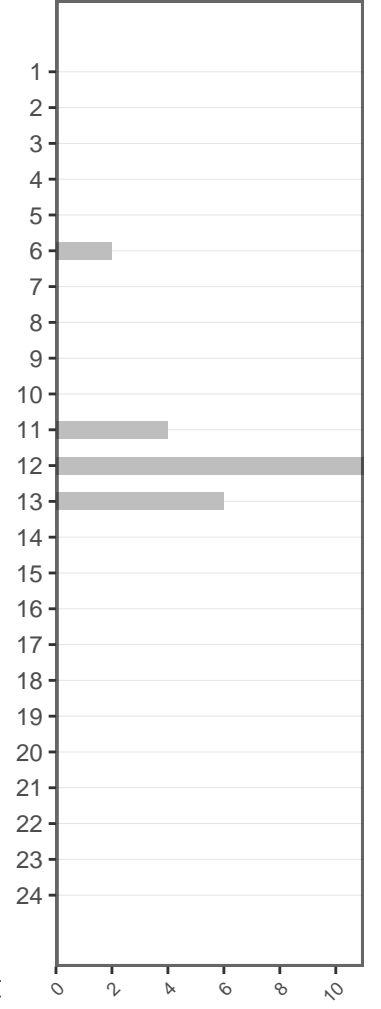
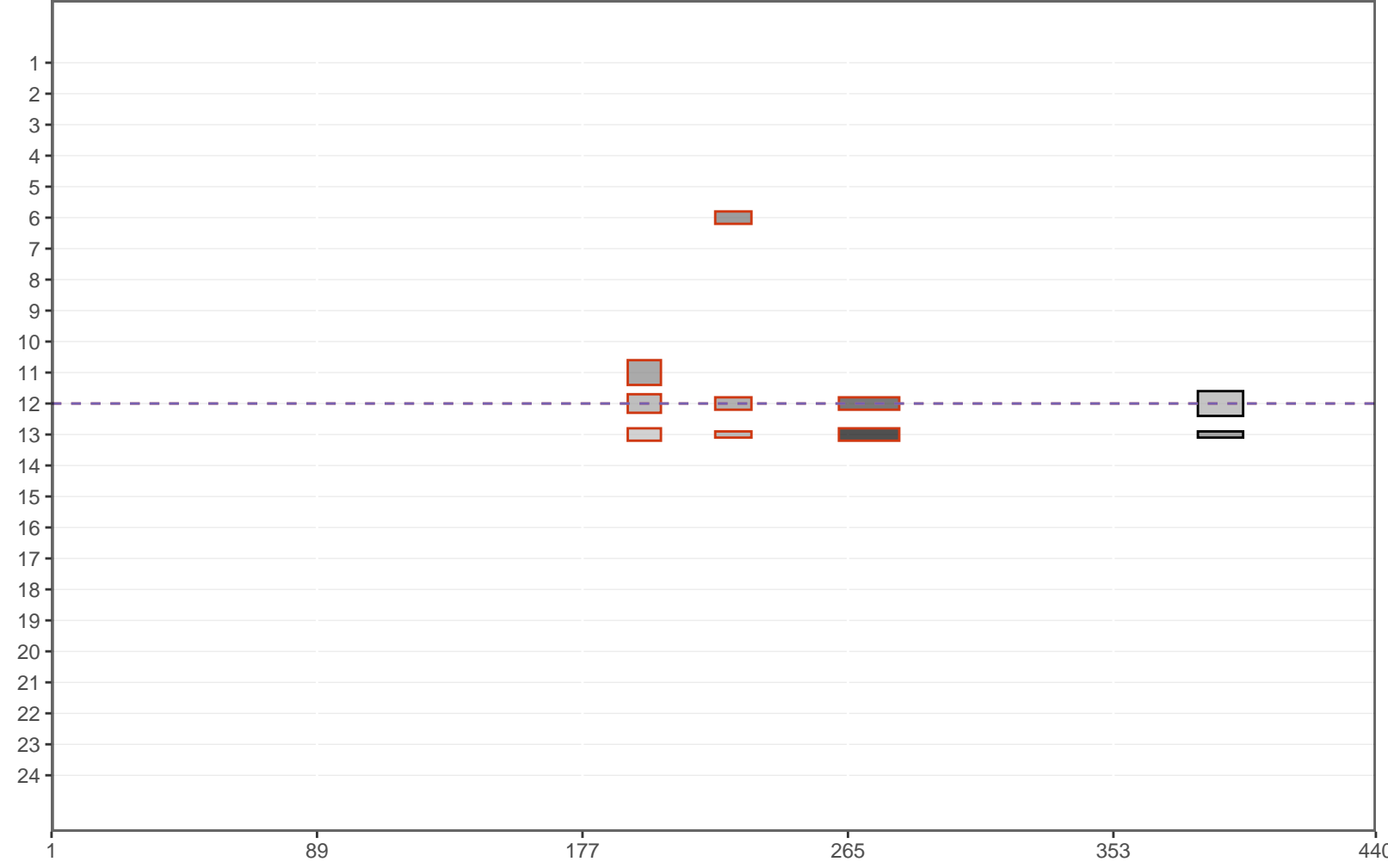
MW indication



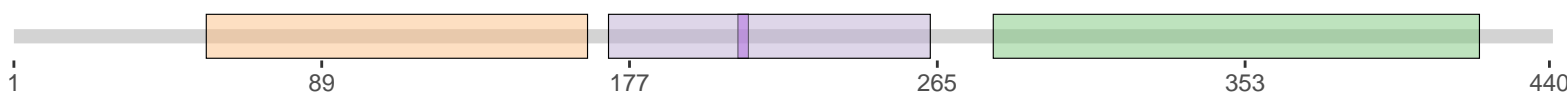
Molecular weight



Gel Slice

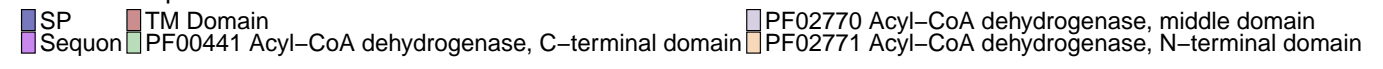


Protein length



Pfam domains

Pfam Description



Protein sequence:

SNSTFADLVVFARNTATNGINGFVIRKDPGLGATKENKIGLRMVMVNGDILLKNVFPDEDRLPGVNSFGDTEKVLAVGRVMVSWDPGIGAMGVYDMCHRYLKERKGFAPLAAFQINGDKLVQMLGNQAMLLVGVRLGKLYESGKMMPPGASLGGKSWISLRARETVSLGRELGGNGLADFLWAKAFQDLERIVTYEGTYDINSLVYGREITGLPSFKPWLRPKSRLL

NbL15g02730.1 rhodanese-like_domain-containing_protein_10 [MW = 24.28 kDa]

No. of times detected



log(intensity)



Values from



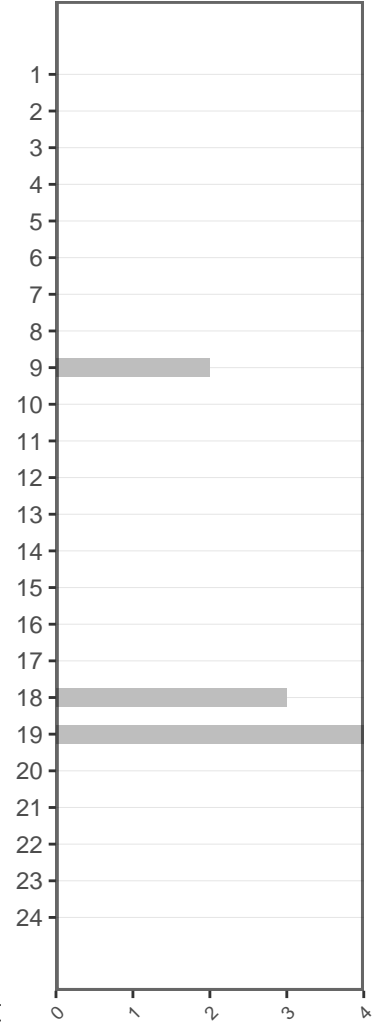
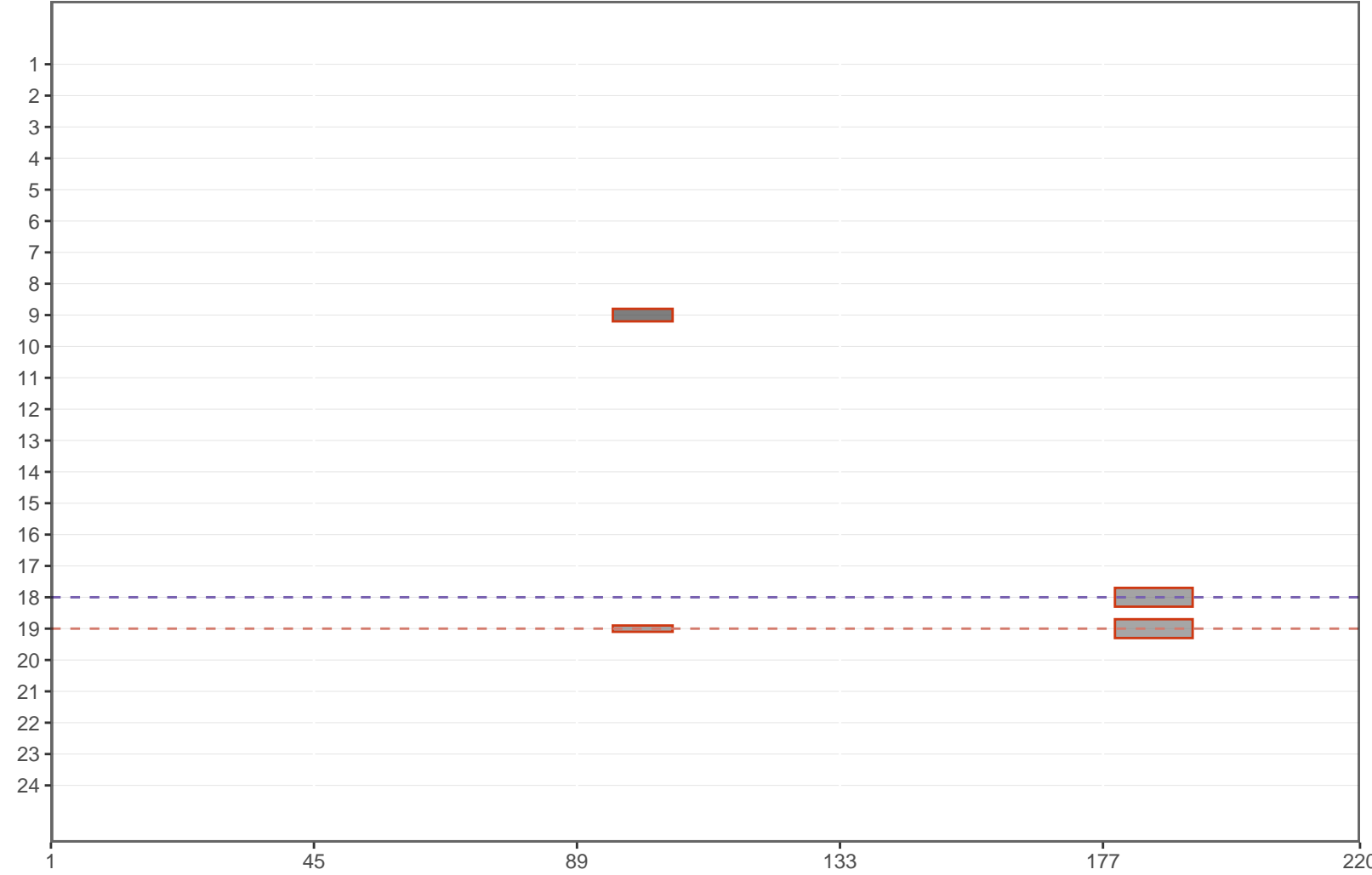
MW indication



Molecular weight

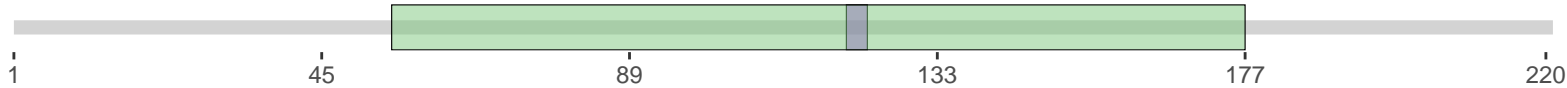


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISPTLLKXVYHFGVIGAWTGFMTMINDFVKGVGGQIPDKNNAKVAVGGEGRLMAISKLHKGEYKNLAWLVGGFTRASDSDFRWVEGPEKLGQATIGGVSYVLLQLLVLKLVGKES*

NbL15g02610.1 fructose-16-bisphosphatase_chloroplastic-like [MW = 45.75 kDa]

No. of times detected



log(intensity)



Values from



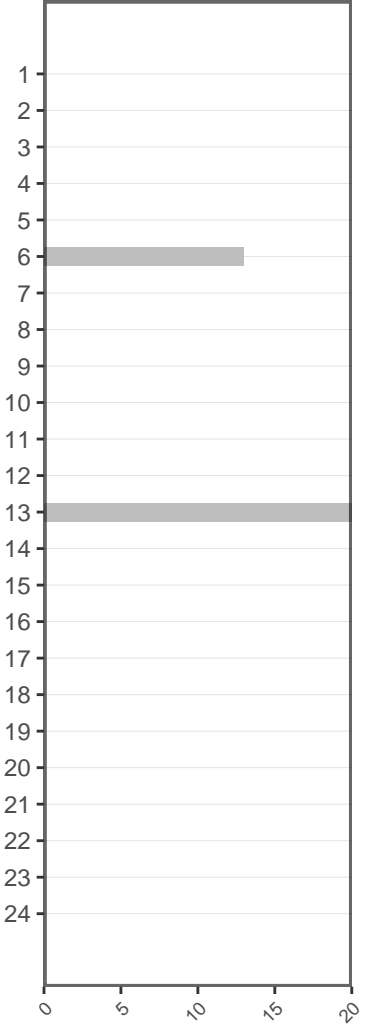
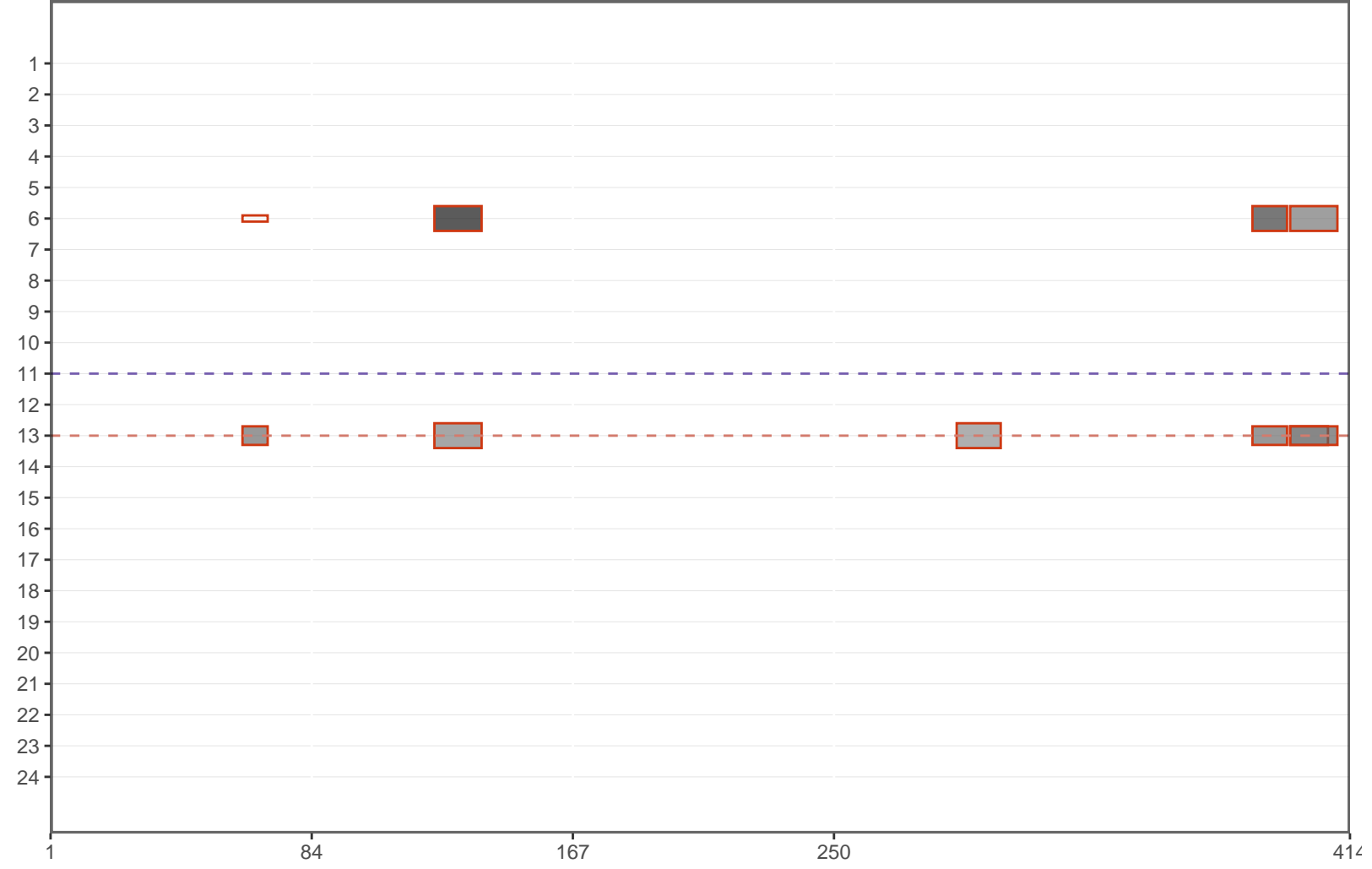
MW indication



Molecular weight

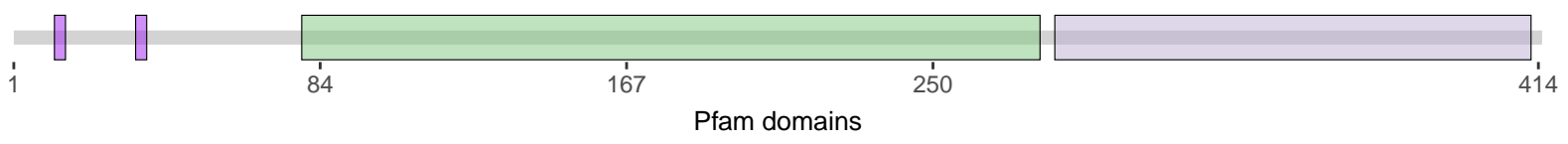


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00316 Fructose-1-6-bisphosphatase, N-terminal domain
- PF18913 Fructose-1-6-bisphosphatase, C-terminal domain

Protein sequence:

DAVSTGSGFYSPNDGDLVLEDFTLMDNVEGRGIVNVGDPGNLLAAGVGMYSB6VFLVTLGKGVFSTLDFMFGFELTYENIQPKTGKIVAFNEGVNQLWDRLLKNYIDHLKEPFGNPKYEARVYIGSLVGDHRTLLVGGVGYPRDKKRNKLLRLLVEGAPMFFVEGAGKGGSDGGRILDKQPEIHRVPLFIGSTEEVEKLEKYLSP

NbL15g02590.1 protein_PLASTID_MOVEMENT_IMPAIRED_1 [MW = 105.09 kDa]

No. of times detected



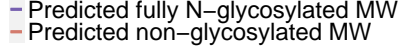
log(intensity)



Values from



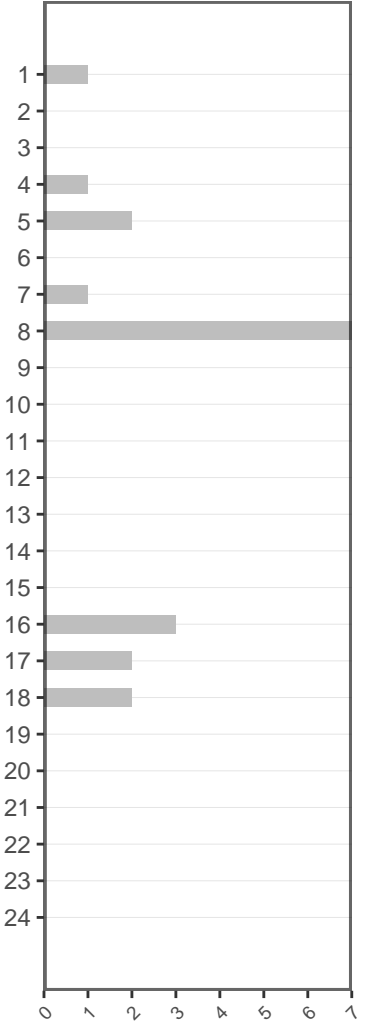
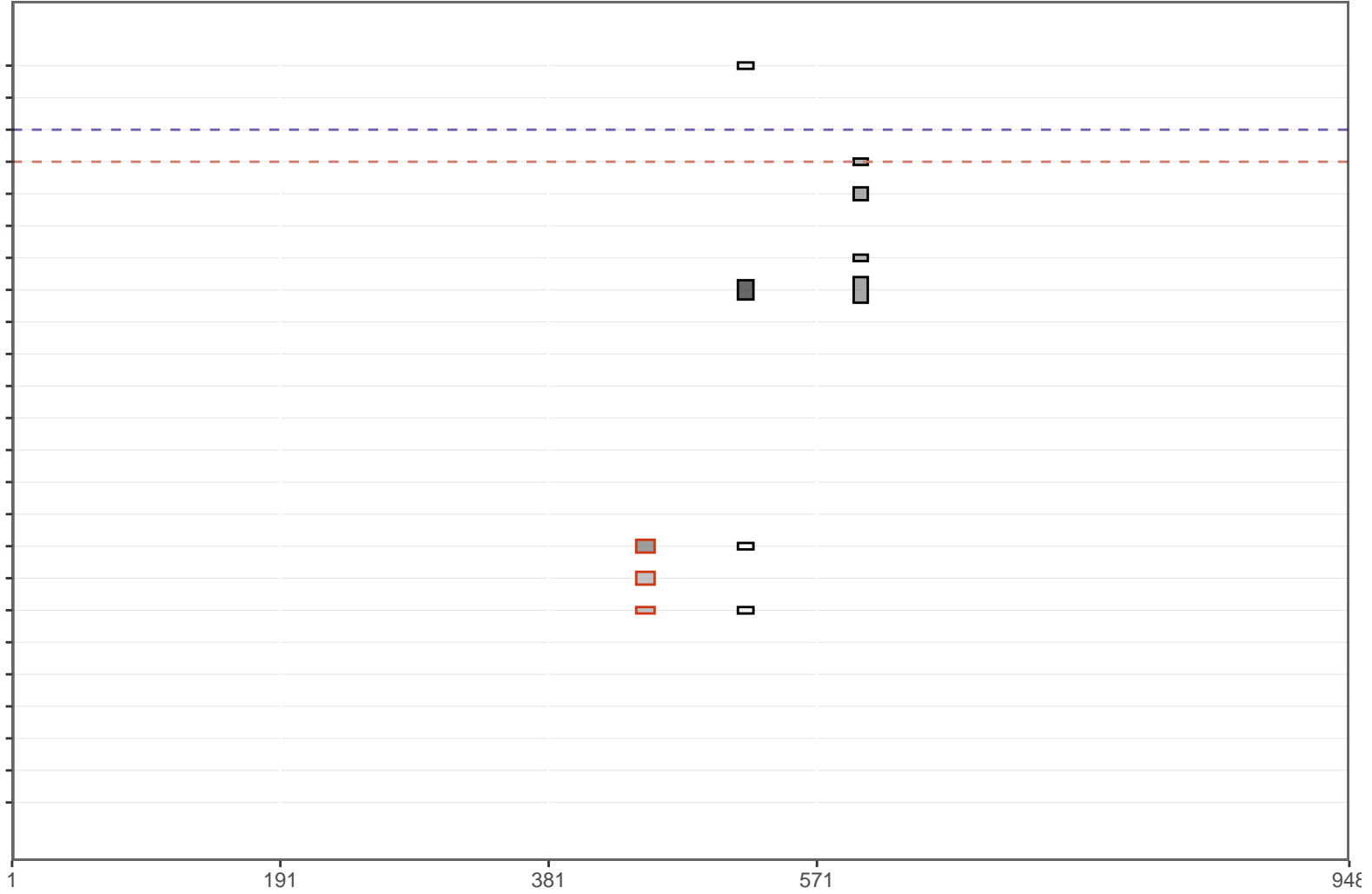
MW indication



Molecular weight



Gel Slice



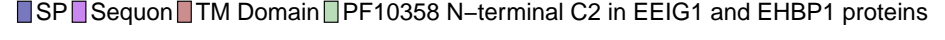
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

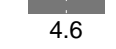
DEYKKEVEVKEEEEEAEEEEEEGSEGNSDKRVSSEHEVKEIVHQDHHLRLSELDSIADGQKALESMFKDENGVKTEDDDSEGRILDADENVTRFLQMLEDDGGVNGFKTDGQETPTFLKGGGDESDKKRESVIFIPDLQKLGQVQTRNGFLAAMPNLTNVVSRKDTPLAMQISKPFVFPFLSMMNGFEIFGRMAAIGMEEFSTKLSMMPMEELVGTAEQIAFEGIASAIKGRNKEVGSASTAARTVAWKMATAMNTRNERISTGIWNICDEPLTVDI

NbL15g02550.1 NHP2-like_protein_1 [MW = 13.89 kDa]

No. of times detected



log(intensity)



Values from



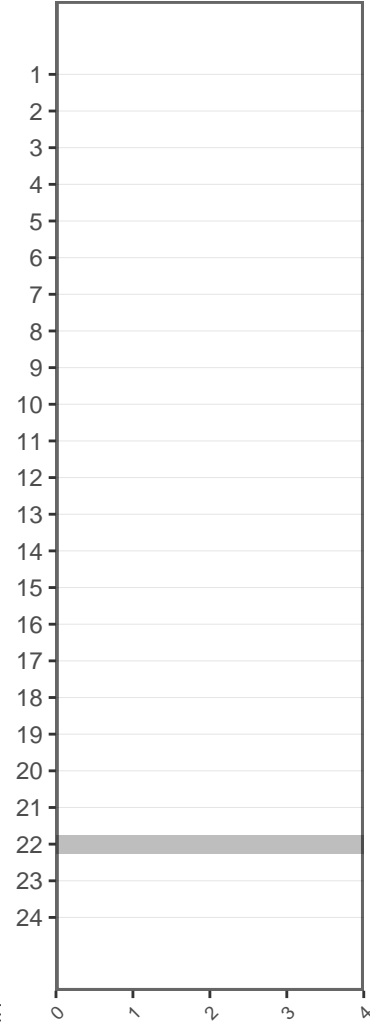
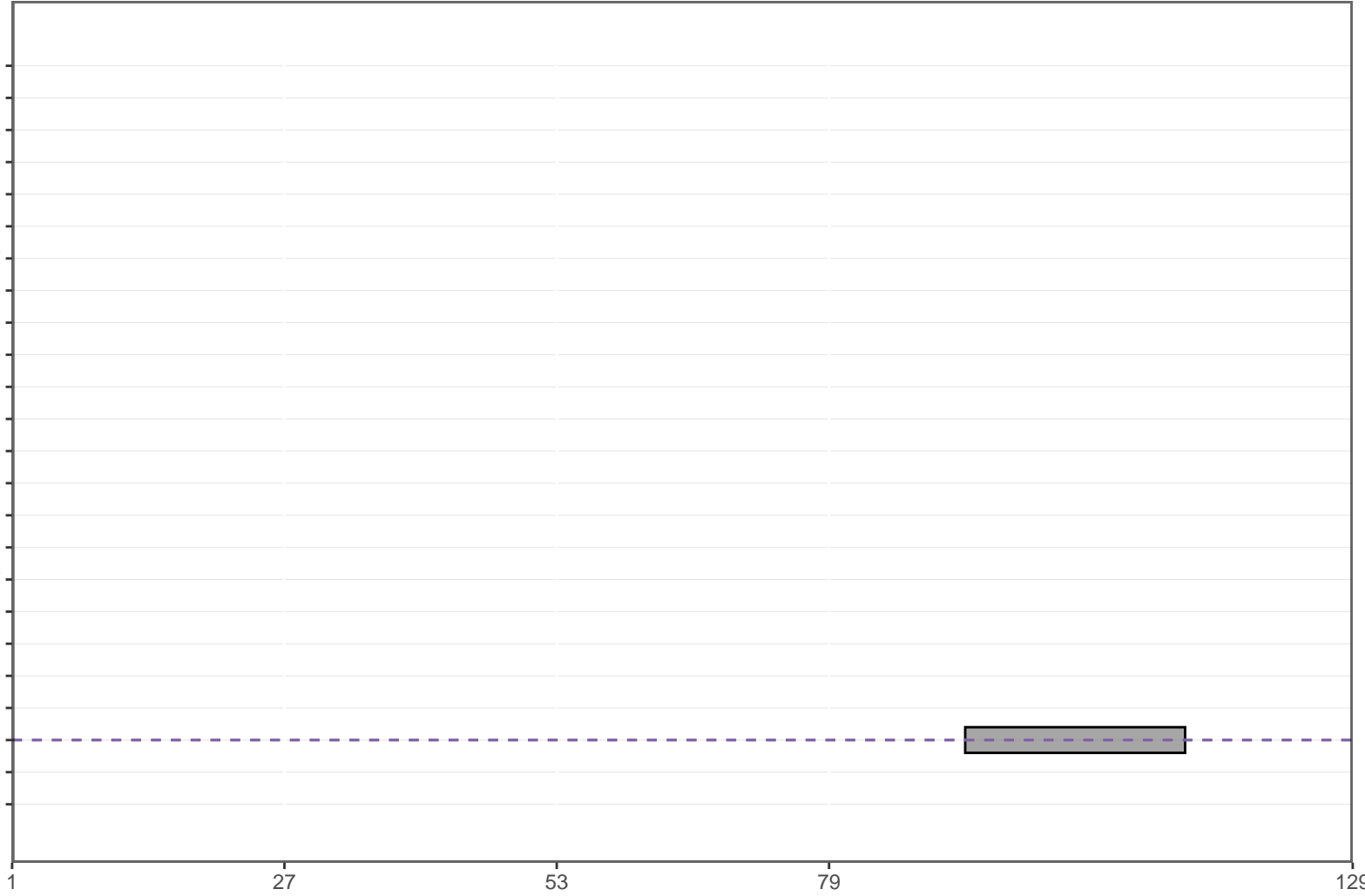
MW indication



Molecular weight

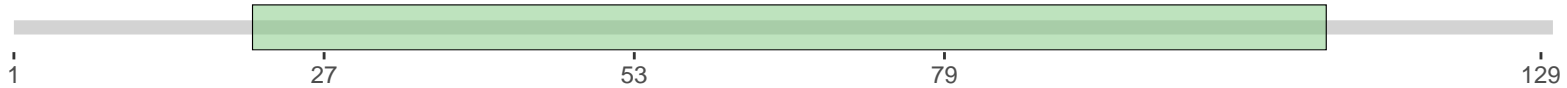


Gel Slice



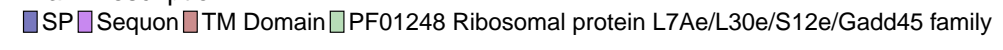
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AETIVMAADTEPLELHLPLLAEDKKNVYVFPKQALGRAGGVTRPVAABVTSNEGSQLKSGIQQLKDAEKLIP

NbL15g02500.1 ribulose_bisphosphate_carboxylase/oxygenase_activase_2_chloroplastic [MW = 48.33 kDa]

No. of times detected



log(intensity)



Values from



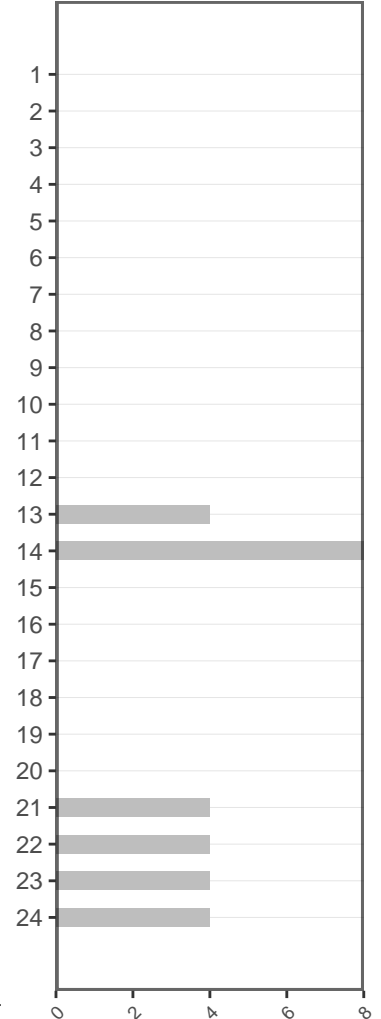
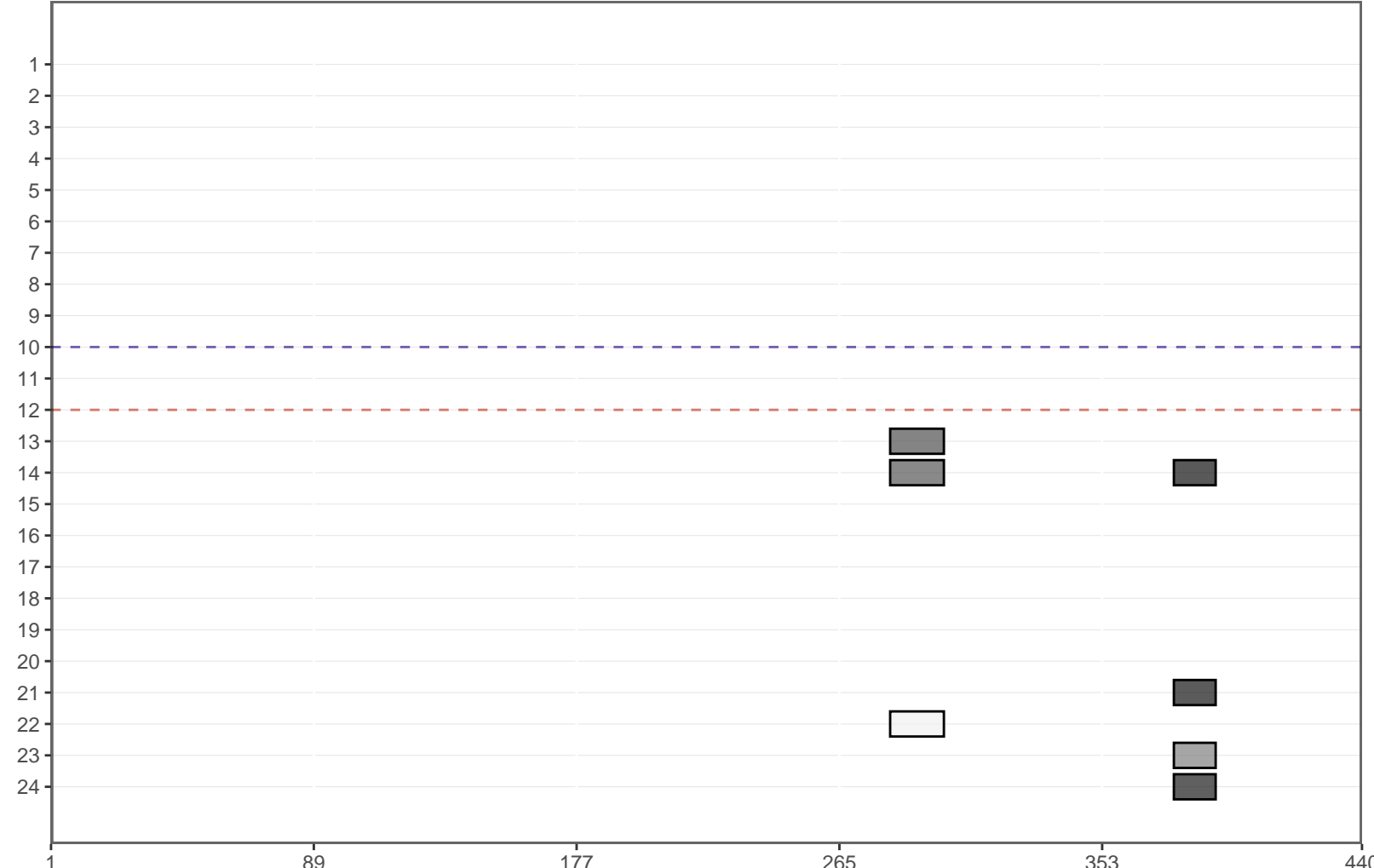
MW indication



Molecular weight

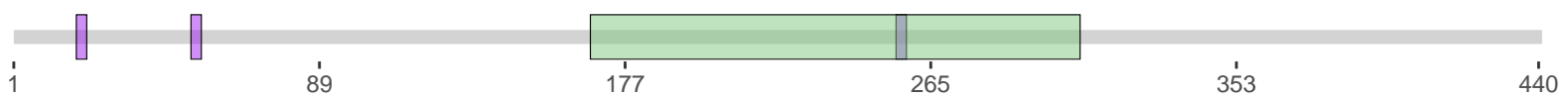


Gel Slice



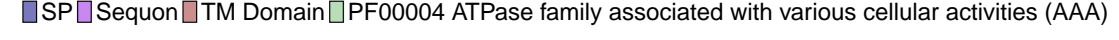
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PAKLRDORYREAAEHRKGMGGLFINDLDAGAGRMGGTTGQYTVNNGMVAATLMMNADNFTNVLDFPMYKNGENARVPIVDTGDFSTLYALPLRDRMEKFFYWAPTRDRKGVCKGIFRTDNVPEEAVIKVDTFFPGSGIDFFGALRARVYDDEVKRWVSGTGIEAGDKLNLNFDGPPTFEOPKMTVEKLELVGNMLVQEGENKRWVLAETYLEKAAALGDANDANTGNF

NbL15g02490.1 uncharacterized_LOC104104784 [MW = 16.88 kDa]

No. of times detected



log(intensity)



Values from



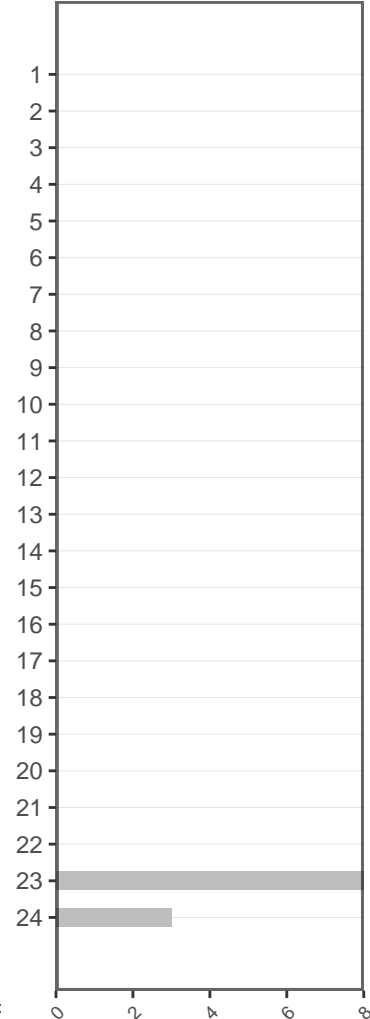
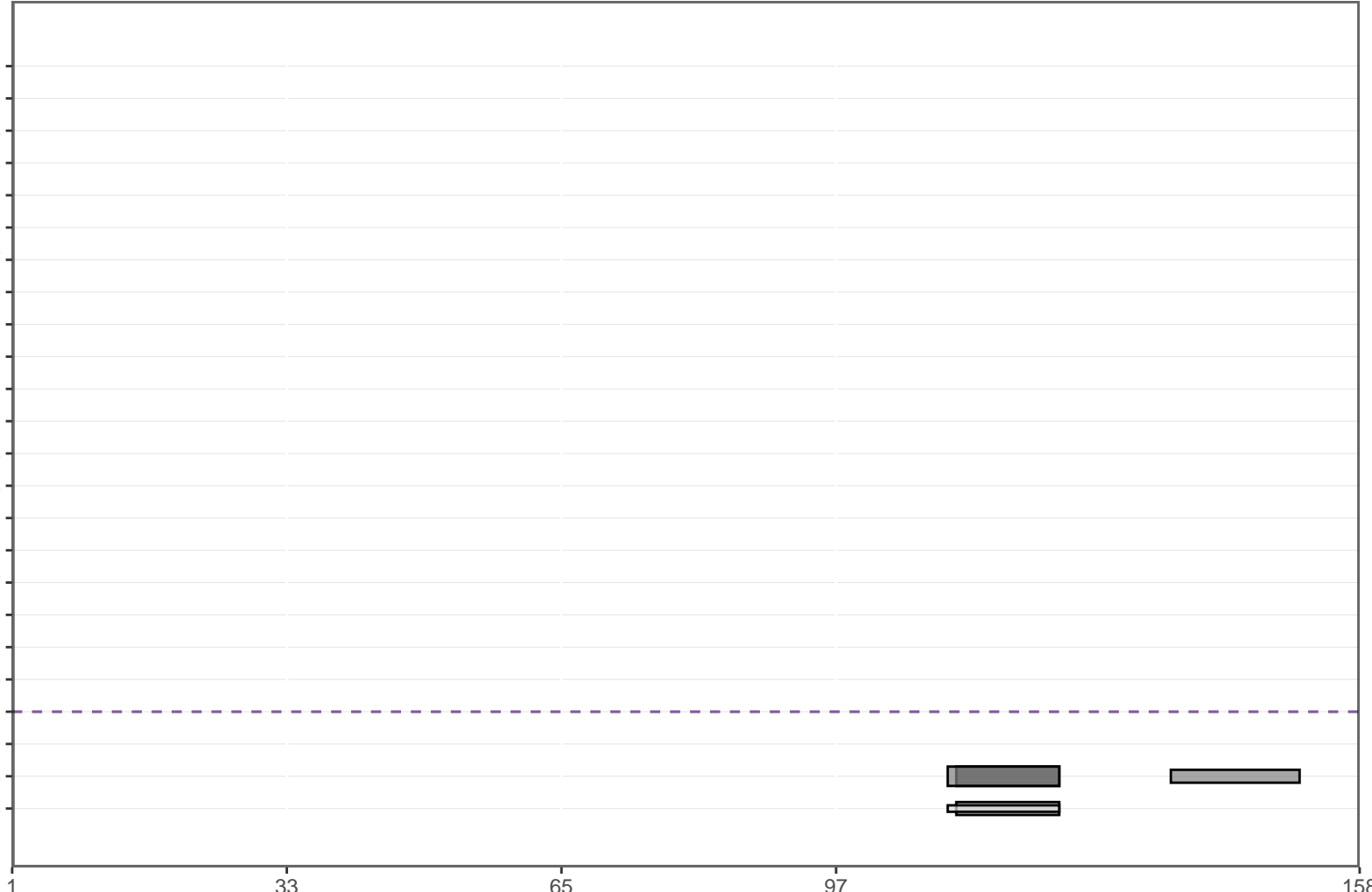
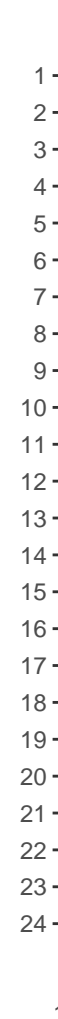
MW indication



Molecular weight

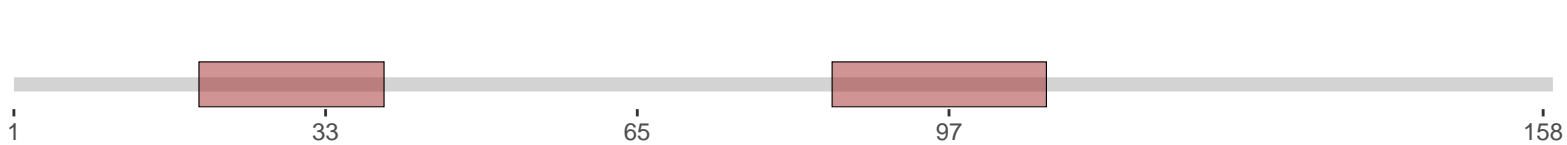


Gel Slice



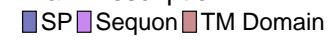
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

KHRSLSKYYVAAGDVSSGGTTLAAGAAVALLGTAFILFSRKDTGPEGDGAGFVRKGGATLRANAARKDGVGVGANGNGLGKLGVDK

NbL15g02430.1 mitochondrial_import_inner_membrane_translocase_subunit_Tim9 [MW = 13.93 kDa]

No. of times detected



log(intensity)



Values from



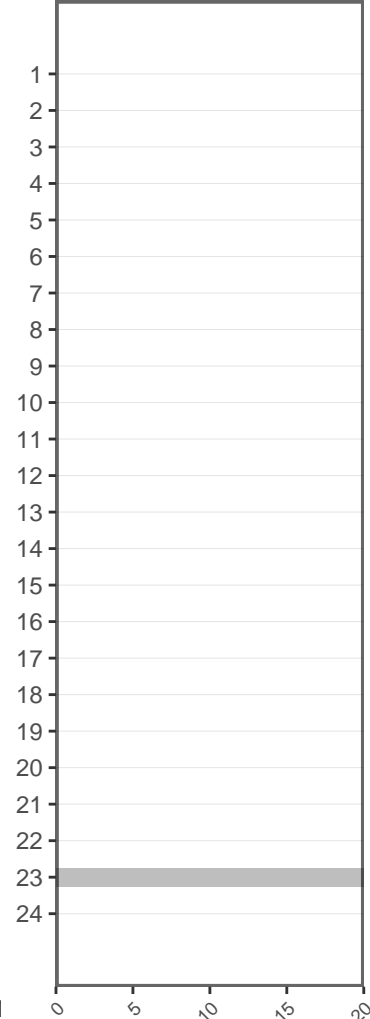
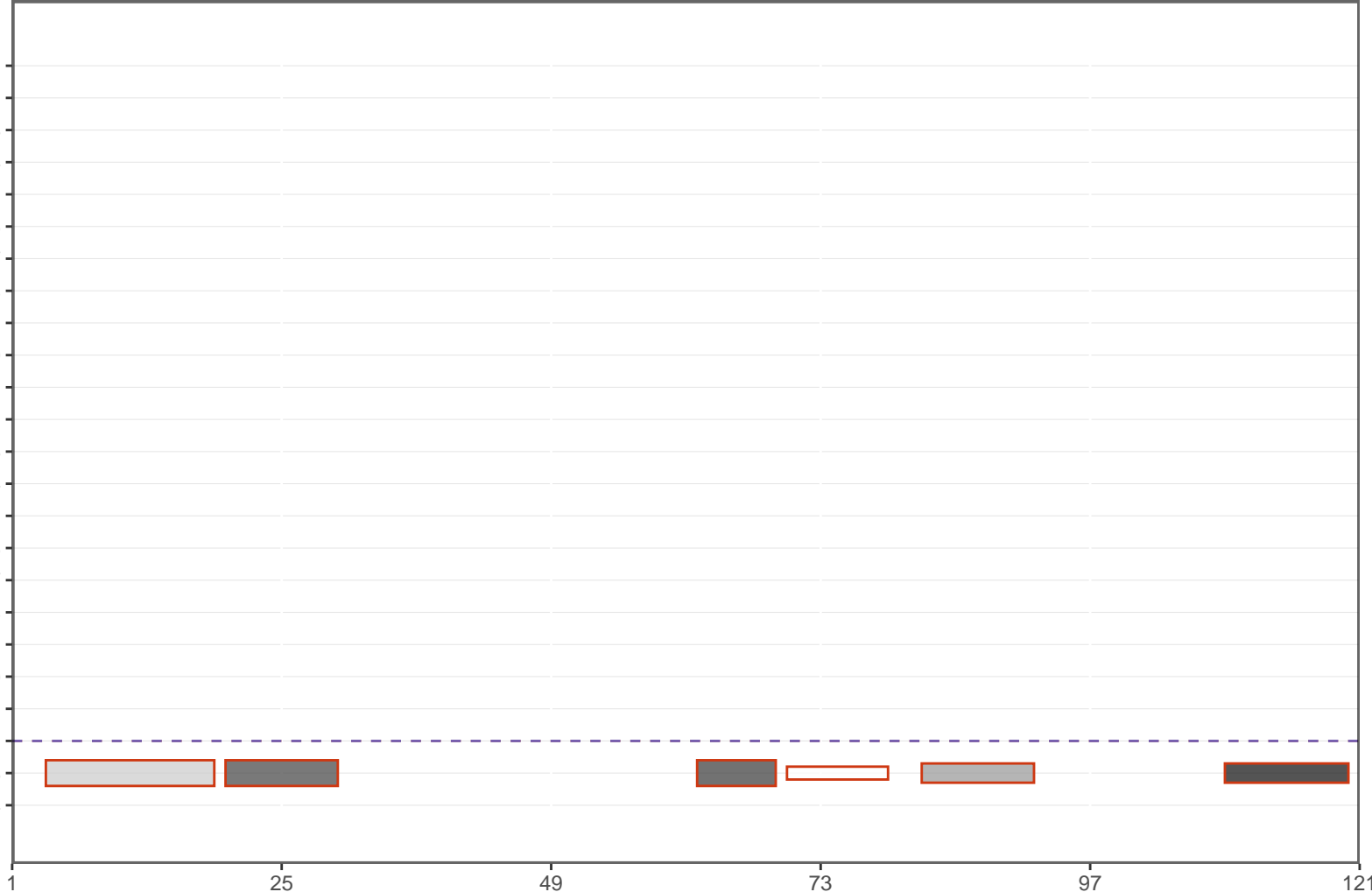
MW indication



Molecular weight



Gel Slice

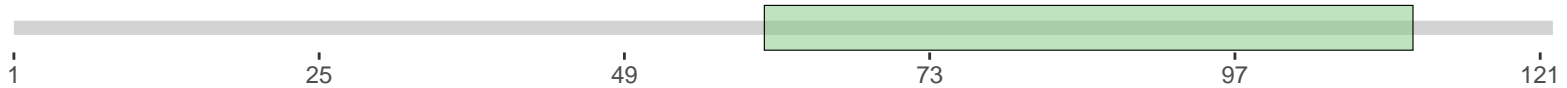


Protein length

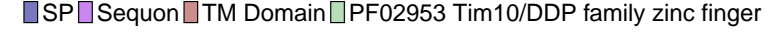


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

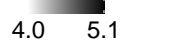
ISDITDYGKGHSLRMYNLSLVERGFTDGVDFKRRKTLKQKEETGVRRGAEKFLKHSMRVGMRFALNQGAPTPD

NbL15g02390.1 uncharacterized_LOC109223268 [MW = 20.95 kDa]

No. of times detected



log(intensity)



Values from



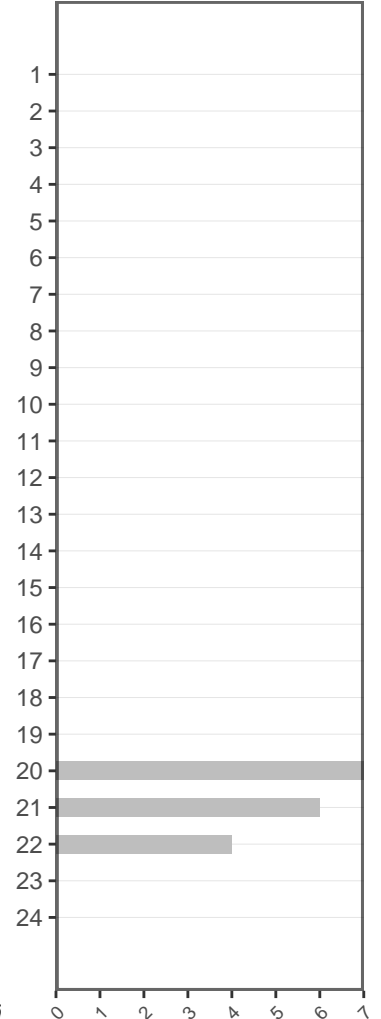
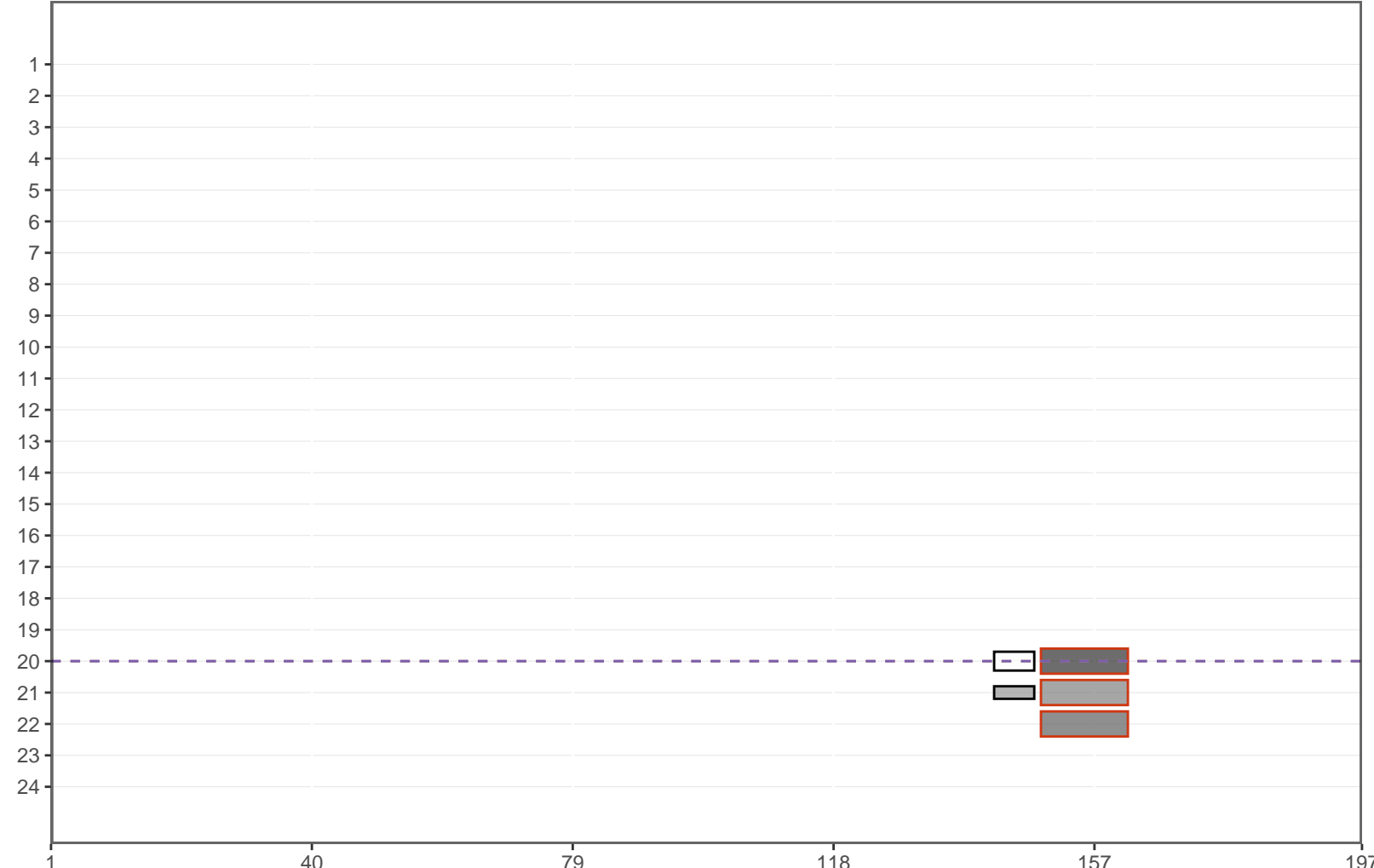
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

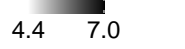
GAEAAEQLTQGEINGETFSNVPQTLSGEGVEGKDKKAKIQRPKSRQAETGTVKGVNTGIRGGLGSPGEGPLNVRRLPLVFKGGFRSRGQVLVEGSDKICILIRDGEDGP

NbL15g02340.1 heat_shock_cognate_70_kDa_protein_2-like [MW = 71 kDa]

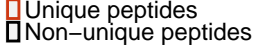
No. of times detected



log(intensity)



Values from



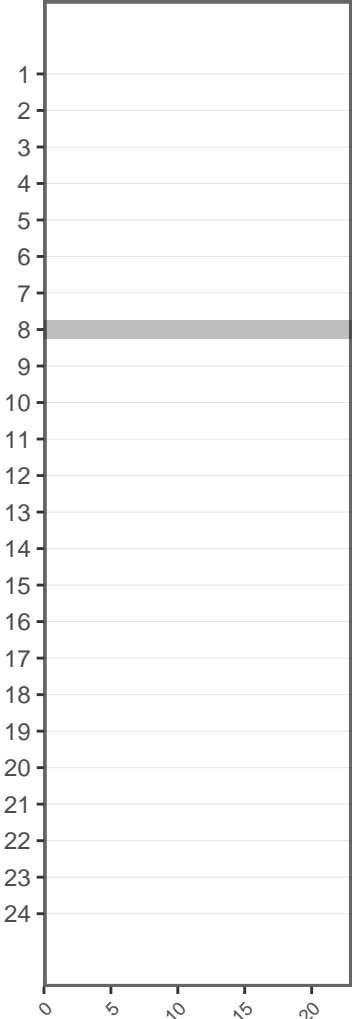
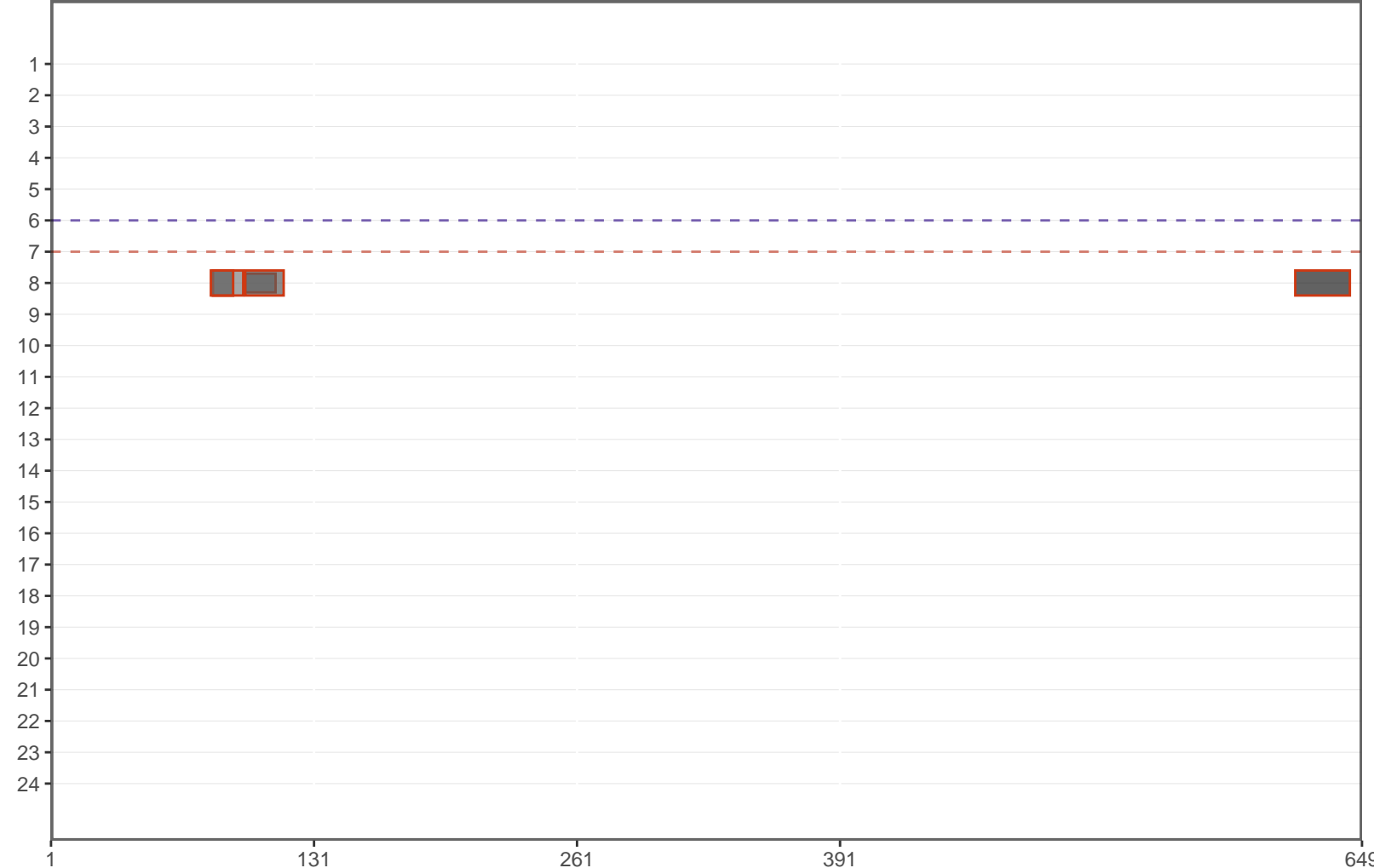
MW indication



Molecular weight

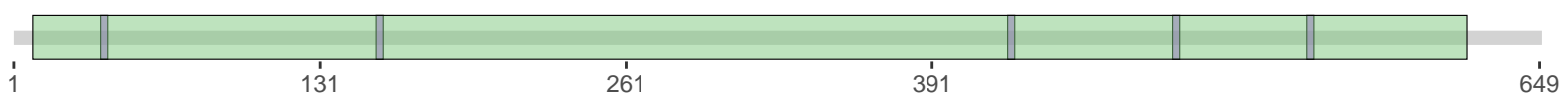


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL15g02330.1 THO_complex_subunit_4A-like [MW = 27.08 kDa]

No. of times detected



log(intensity)



Values from



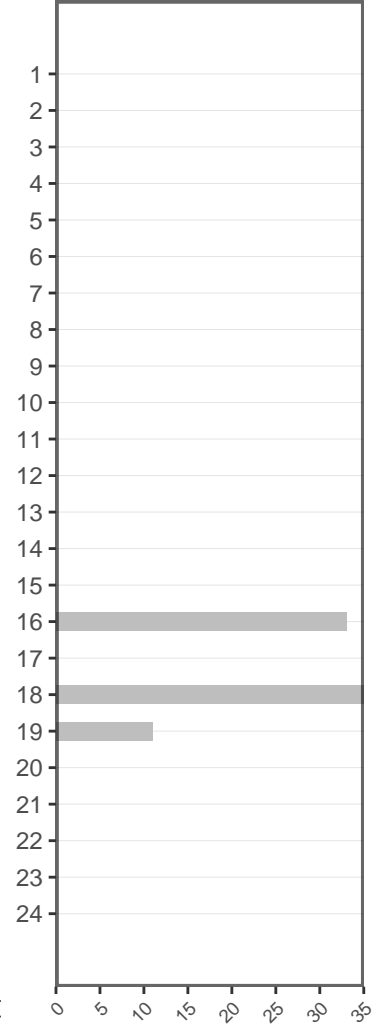
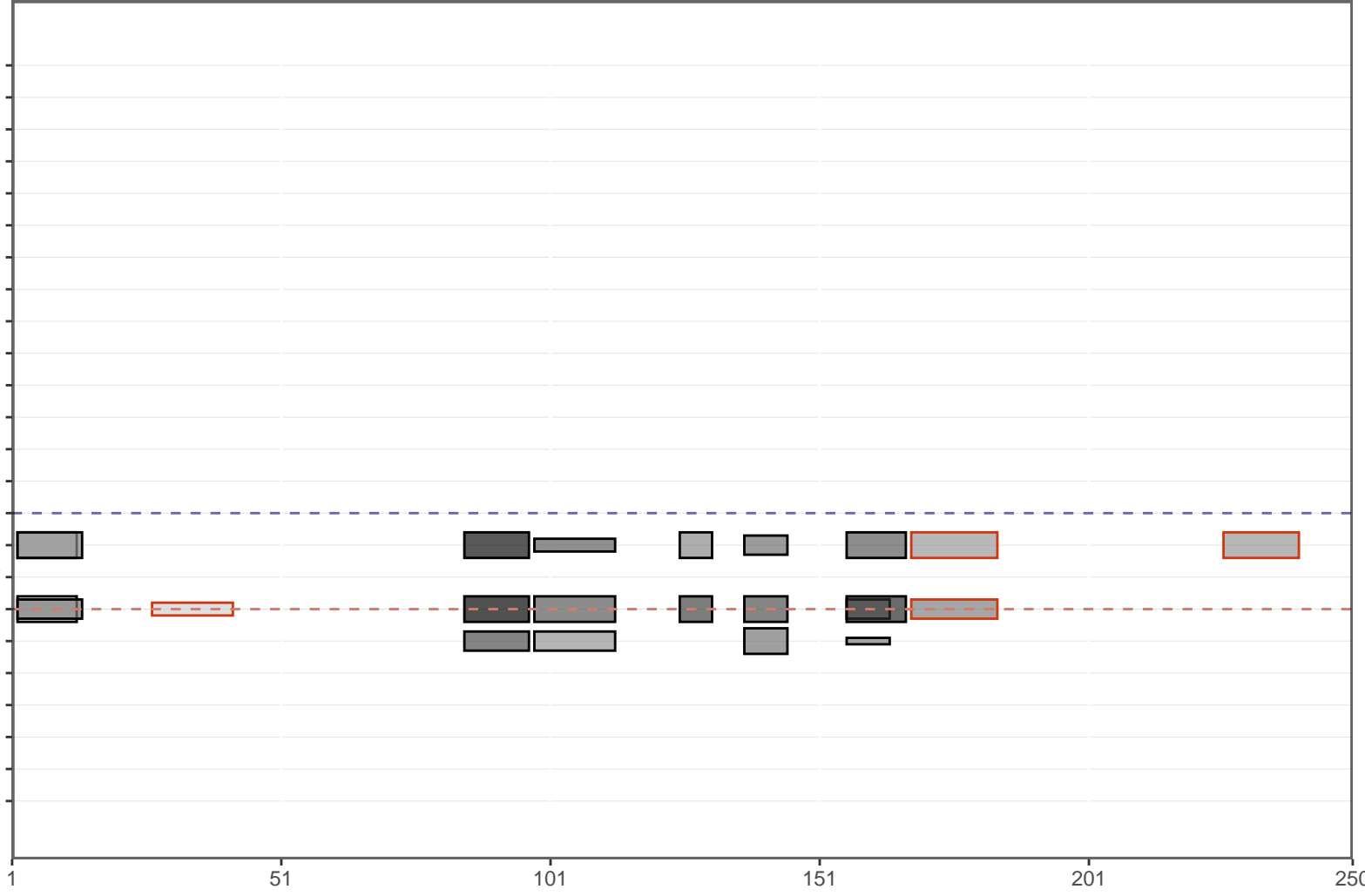
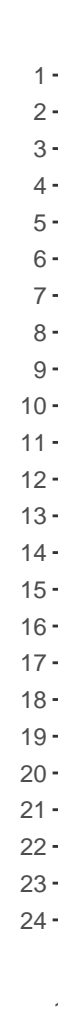
MW indication



Molecular weight

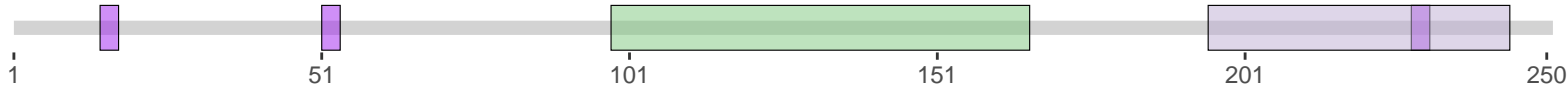


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- PF13865 C-terminal duplication domain of Friend of PRMT1

Protein sequence:

IKELFSEAGDIKRYSHYDKBGRSKGTAEVFSRRRDAEAAIKYNNVQLDQKPKMIEFAGPNIGAPTLPLLNRLYRNPAPRSGQGGGFRPRRGGMRKKEGGRRGRVENITAEIDLDALEKHYHSEAMETN

NbL15g02200.1 translin [MW = 34.53 kDa]

No. of times detected



log(intensity)



Values from



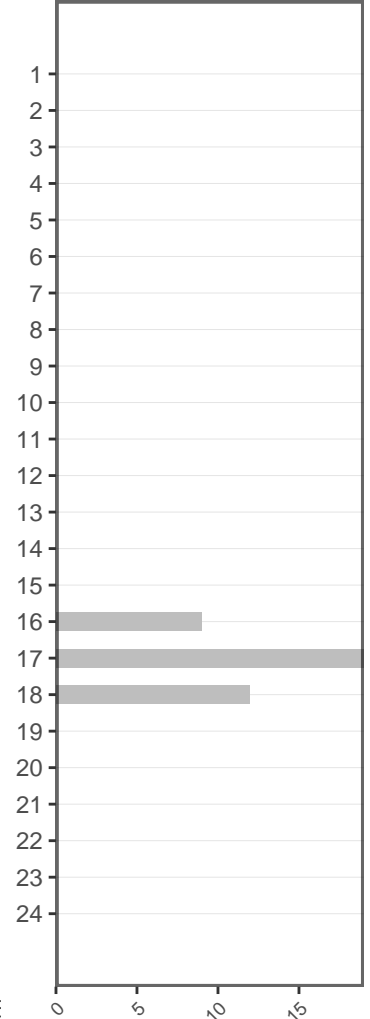
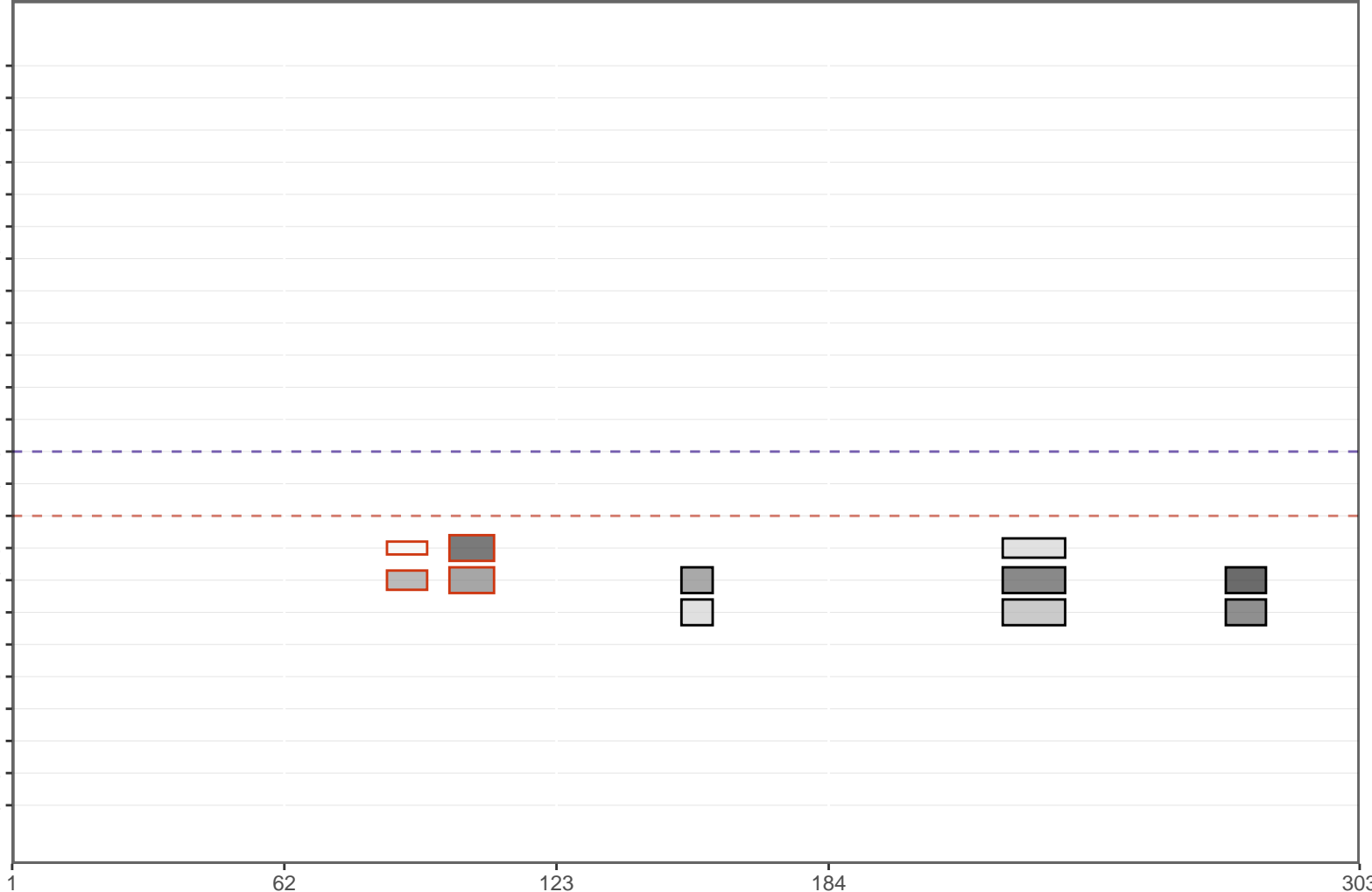
MW indication



Molecular weight

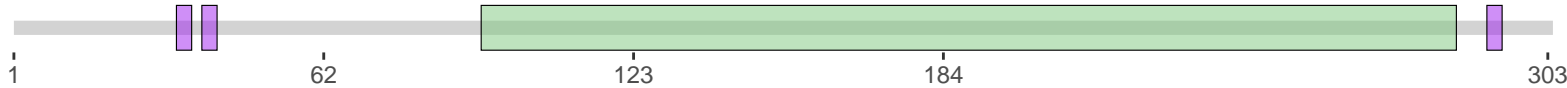


Gel Slice



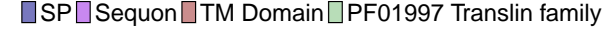
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LYSRLSEIVREPCGGVFRHYHGDWIKSETQVLSLLAFMHWLETGDLVHNEVEEKLGLTPEFGLEDVEDVLGIGFMSNELPRVYVNGVTAGDQCRKVKLFLTDJHAAFRMLNLRNDFLRKFKFDGMKYDLRKVEEVFYDVKIRGLAANGNBSGEGKVGGGG

NbL15g02180.1 adenosine_kinase_2 [MW = 37.51 kDa]

No. of times detected



log(intensity)



Values from



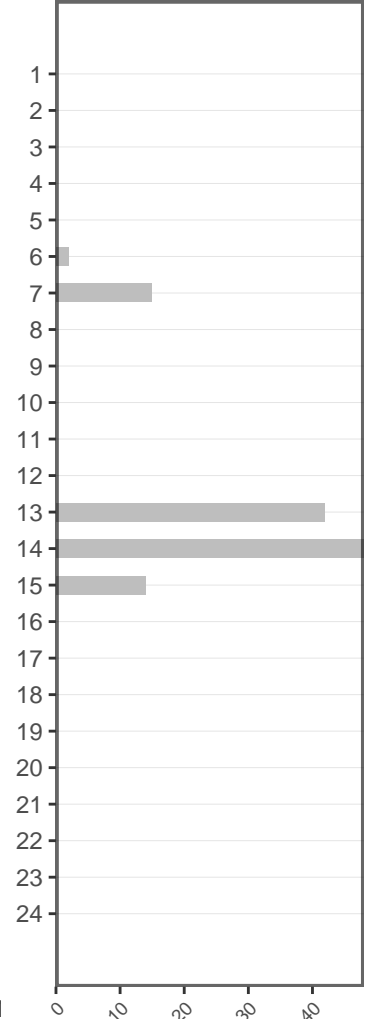
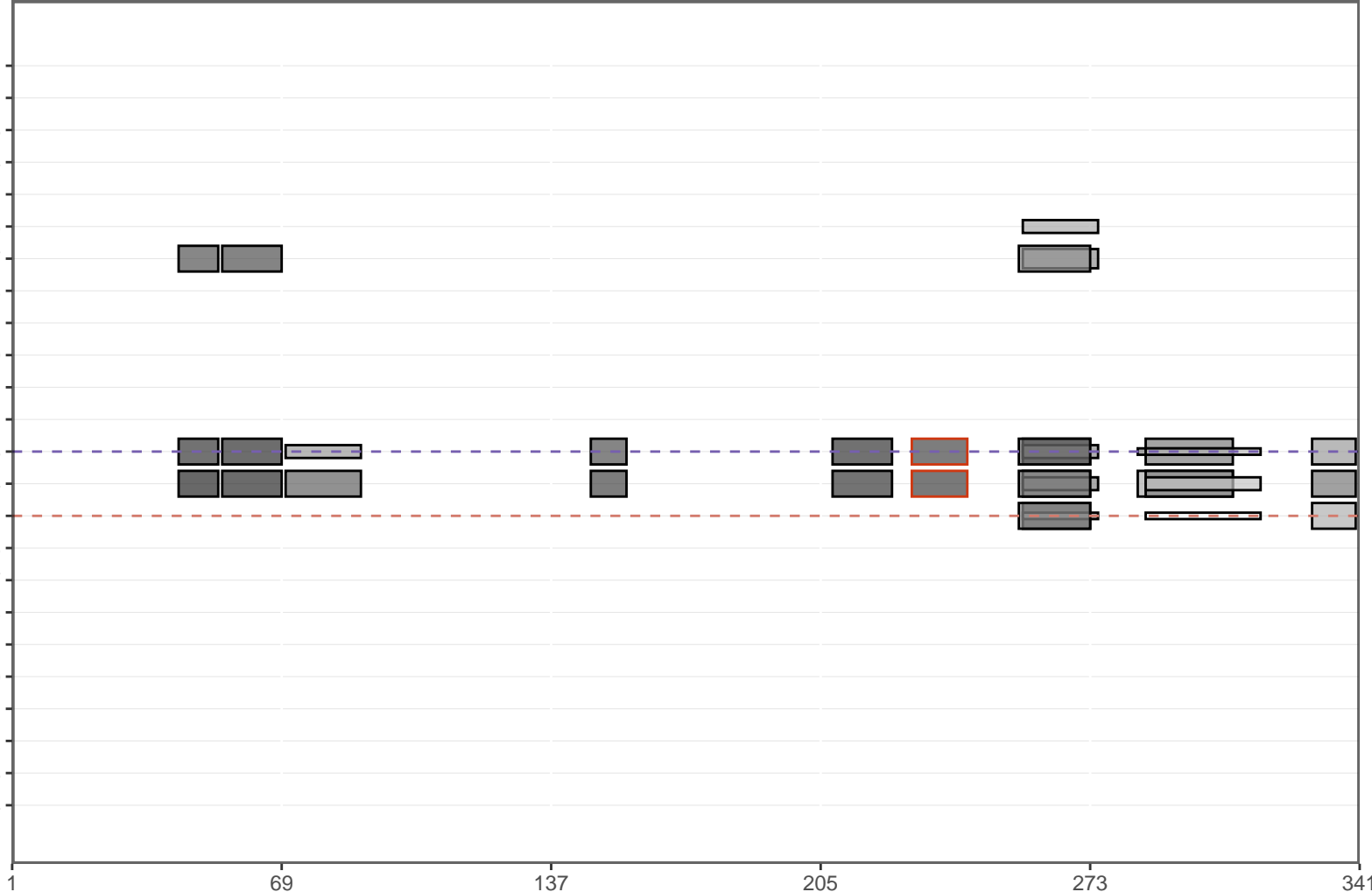
MW indication



Molecular weight

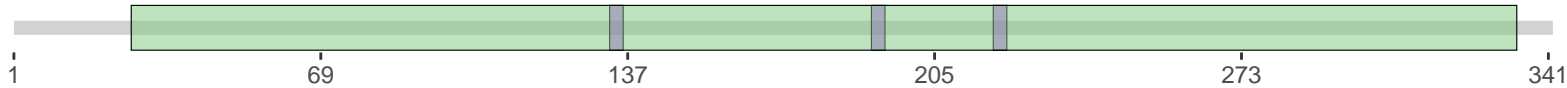


Gel Slice



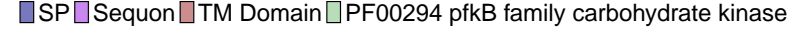
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

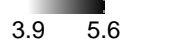
AKYYIAGFLTYSPESIQVAEHAANNKVFSMNLBAPFICFFKDGQEKVLPYMDVFCNETAARTFSRVHWETDNVEEIALRISQWPKASGTHKRITVITDGGADPVAVEDGKVKLFPVFLPKKLVDTNSAGDAFVGGFLAGLVGGKPIADGKAGDYSANVHQIRSGGCTYPEKPDFE

NbL15g02170.1 phenylalanine_ammonia-lyase [MW = 77.44 kDa]

No. of times detected



log(intensity)



Values from



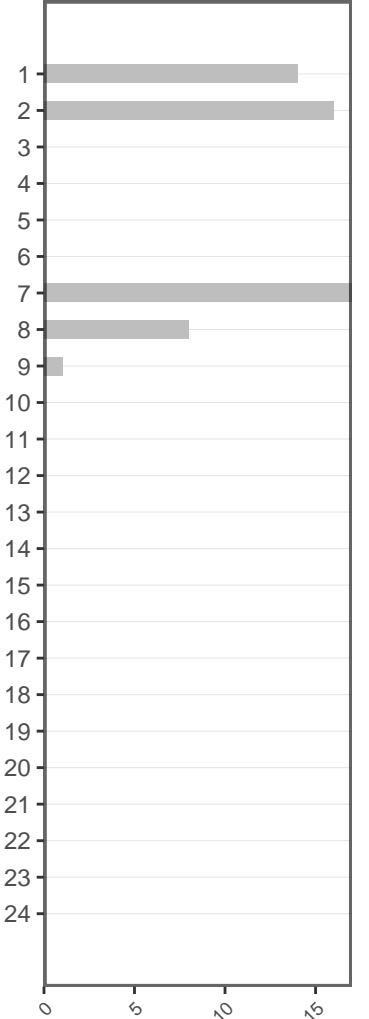
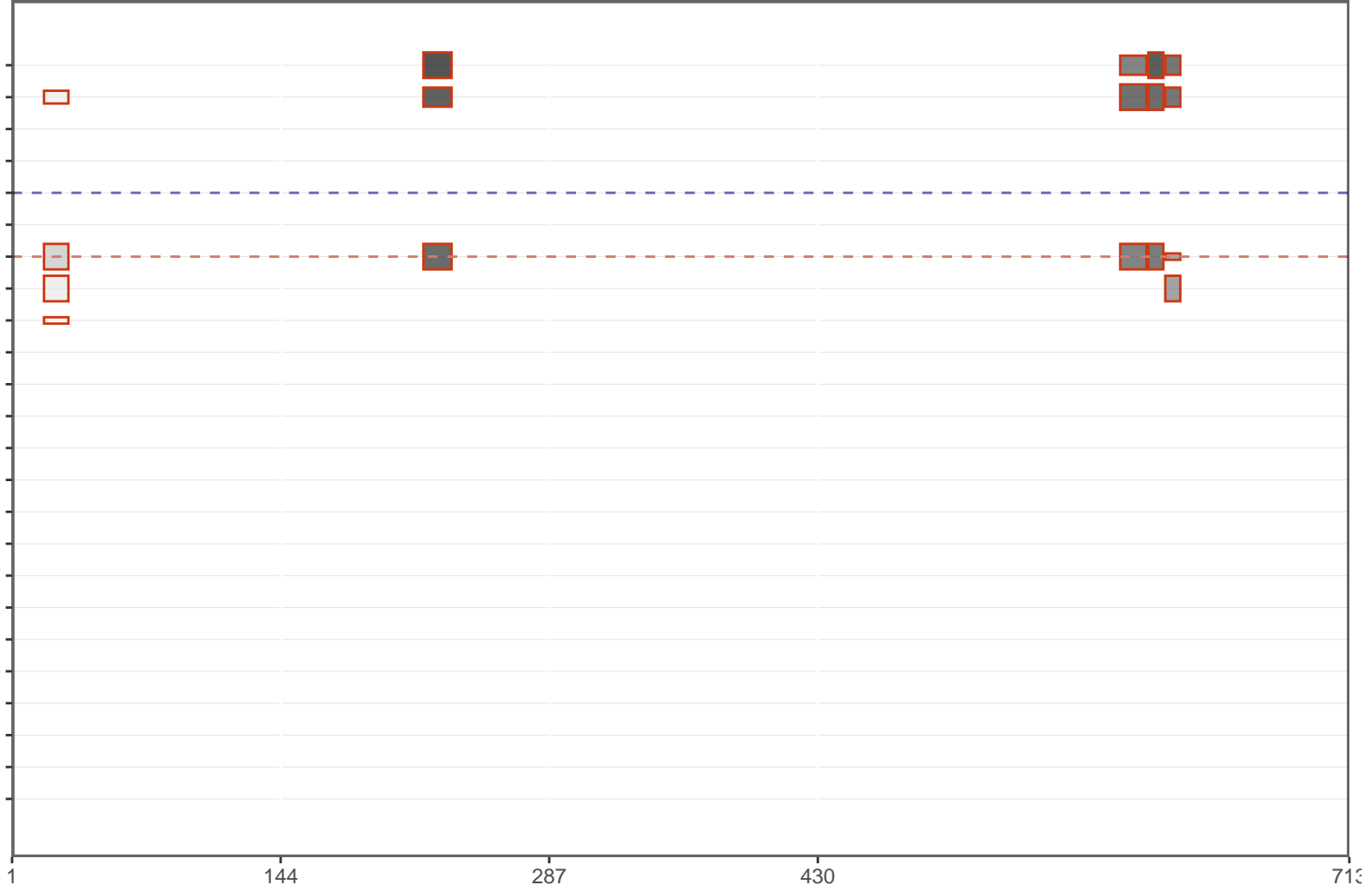
MW indication



Molecular weight

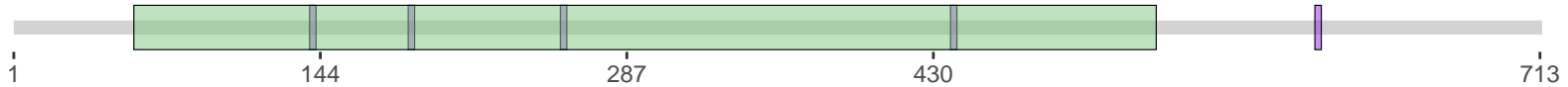


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PKQDRYALRTSPQWLGPQIEVIREATKMIEREINSEVNDNPLIDVSRNKALHGGNFQGTPIGVSMNARLALASIGKLMFAGFSELVNDYNNGLPSNLTAGRNPLSDYGFKGSSEIAMASVGEELQFLANPFTNHVQSEAGHNDVNSLGLSARKTAEEAVDILKLMSTYLVALGDADRHLHEENLRNVAKNTVGGWAKRTLMTGANGELHPBPFCEKDLFRVVDREYVFAVADGAGSANYPLMQLKRGVLDVHALGNGENEKNTNSIFQKILFEEELKAMLPKEVESARIA

NbL15g02160.1 29_kDa_ribonucleoprotein_B_chloroplastic [MW = 31.36 kDa]

No. of times detected



log(intensity)



Values from



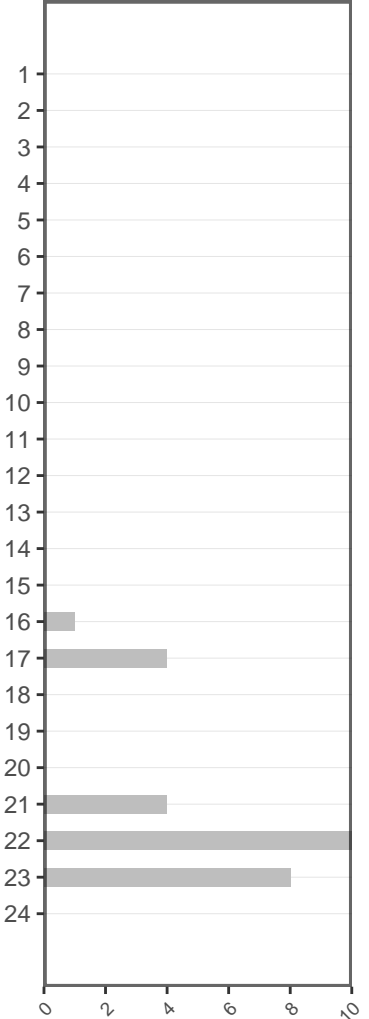
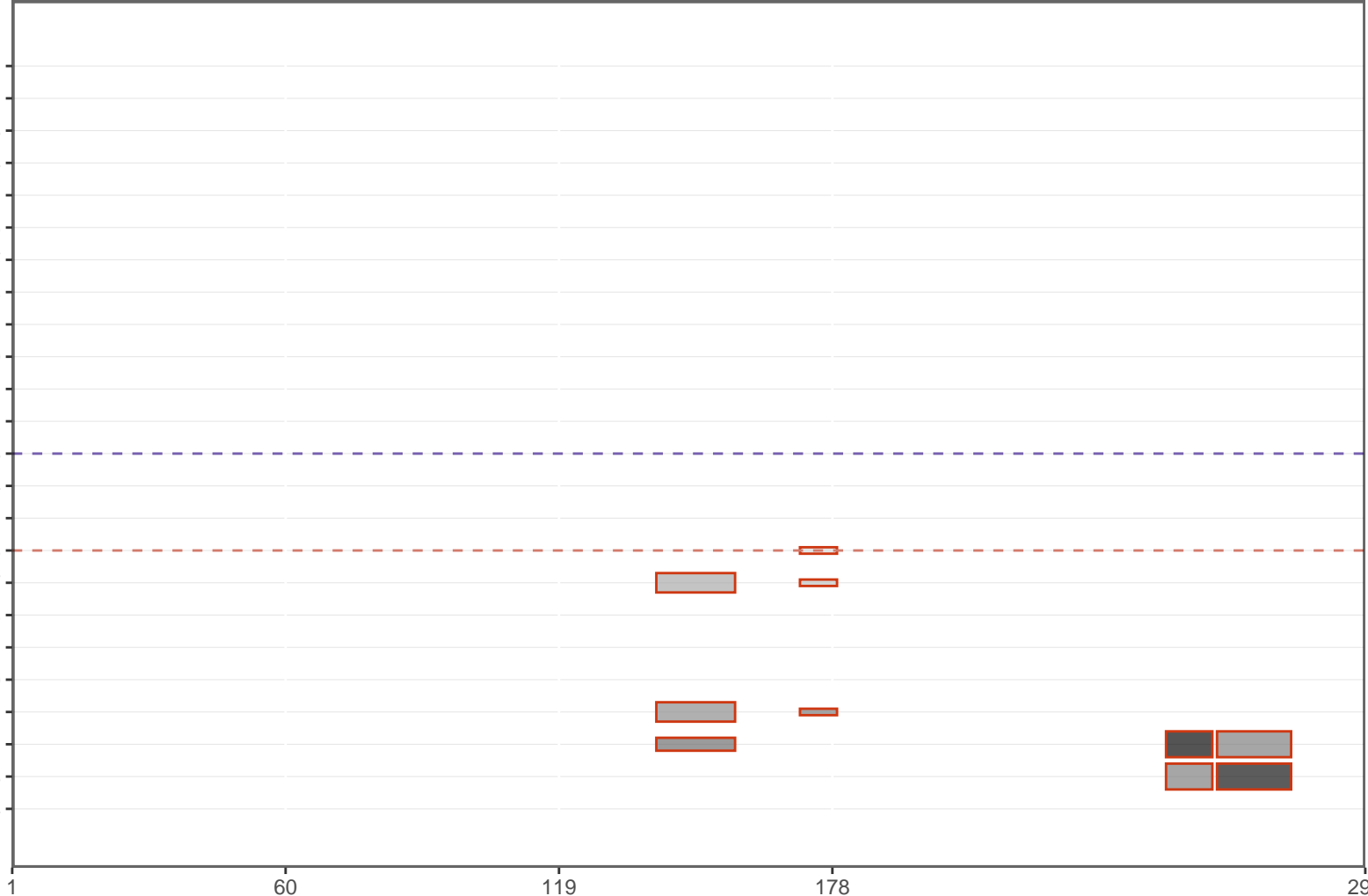
MW indication



Molecular weight



Gel Slice



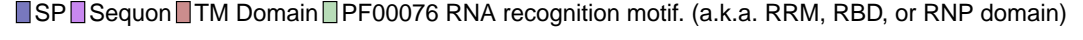
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

STKEEVDAAEQCFNGYEIDGRAIRVNVAGAPAKRENLSFGGGRGNSBYGGGRDRNSFSGGARGGRVDSNRYVGNLSEWGDLDLAKELFSEQQNVVDAKVVYDRDGGRRGFGFVYFSTKEVNDLIDSLNGVDLDGRSRVSAAEERPRRF

NbL15g02100.1 WD_repeat-containing_protein_20-like [MW = 59.42 kDa]

No. of times detected



log(intensity)



Values from



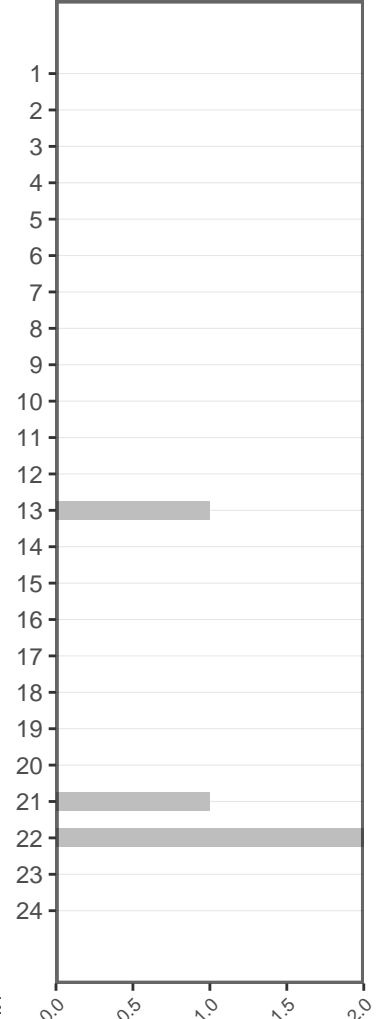
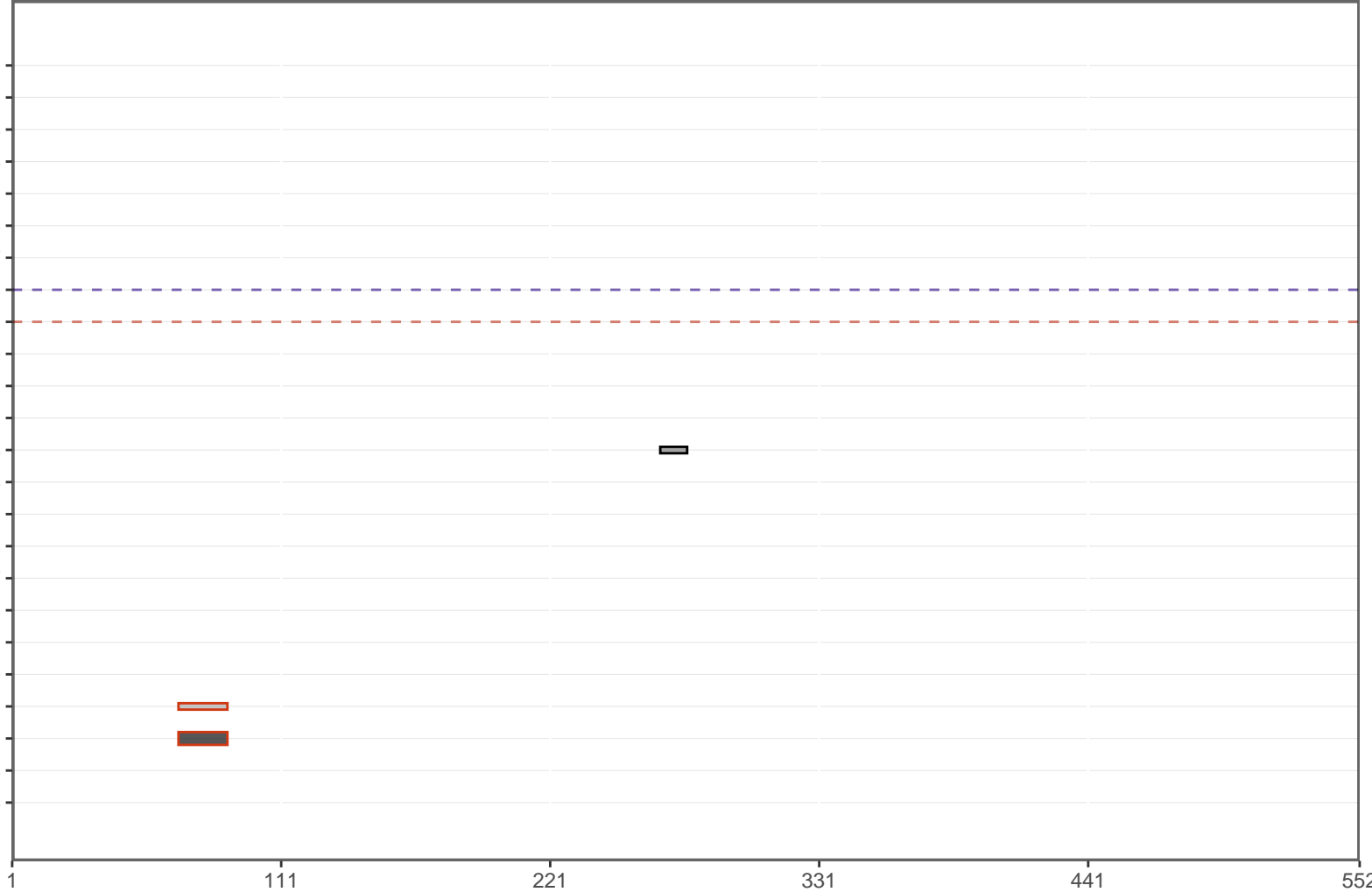
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KSKDGSADPFFPKDGTQFVWAHARYSKNPVNRWHHGGGNSVAFSTDGAHATVGRDGYLRFDYKNEGLDGGKYYGALLCGAWSDMGKYLAGEGDDLVQVWVWMDERKVVAVWGECHSSVWGVAFDGHVWAPNSDGTDENFVRFSGVGGDTQLLLWLEMDDEVVPMRRPHGSGPFTFTSGGSGSHVDRAFVGLQAPAPMRDIPKLSPLVTRVHTEPLGLFTGQEVLTGREGHKHVVRRPFGGETGTNSLSL6TSLKDKPKSGKVVSSKLOAMT

NbL15g02020.1 60S_ribosomal_protein_L4-like [MW = 44.7 kDa]

No. of times detected



log(intensity)



Values from



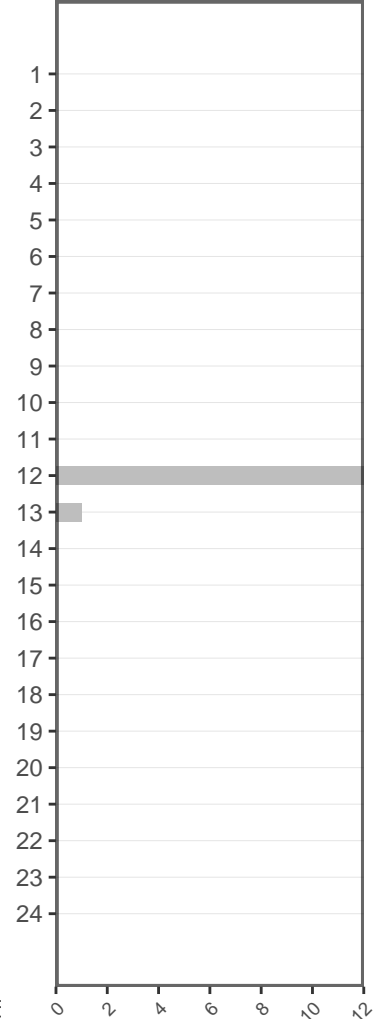
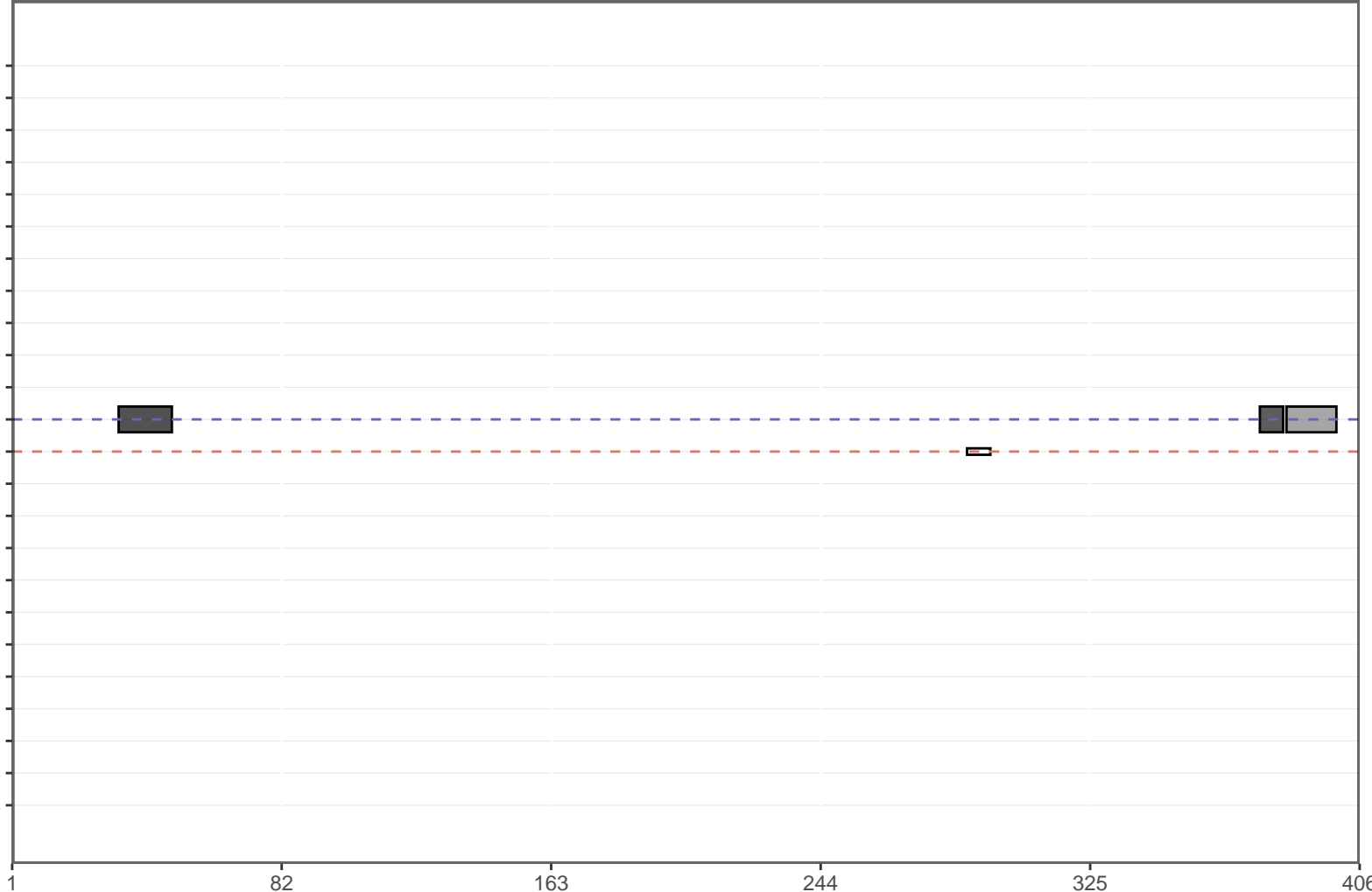
MW indication



Molecular weight



Gel Slice

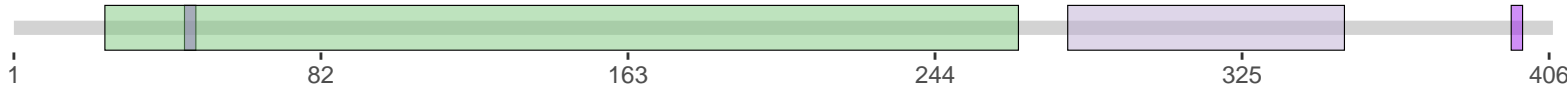


Peptide counts over 4 repeats

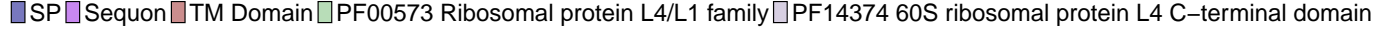
Protein length



Pfam domains



Pfam Description



Protein sequence:

IHAIRPGKGMRRNRVYERKGLPLVYGTGAKLVKAFRNIPGVGHVDRLLNLLKLPAGSHLGRFVWTKSAEKLDEYVGFDFKASEKKKGVYLRPRKMNADLARINDEYVGSVVRPKKQVNRKATLKKRFLKLNLLKLNLPVAKTARRMGLLAEGRIVKAKKEKDKKRHQVTKKEEASAIRAAGTSWFKTMSDSDYTEFENFTKWLGVGTQ

NbL15g01970.1 protein_MODIFIER_OF_SNC1_11-like [MW = 30.03 kDa]

No. of times detected



log(intensity)



Values from



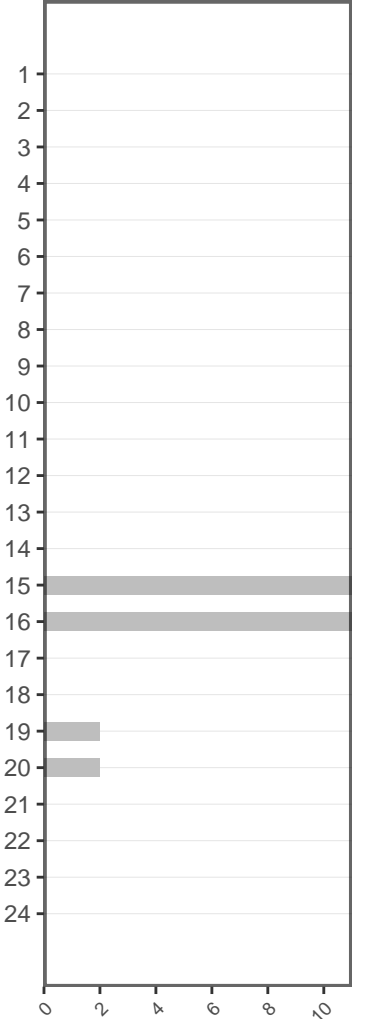
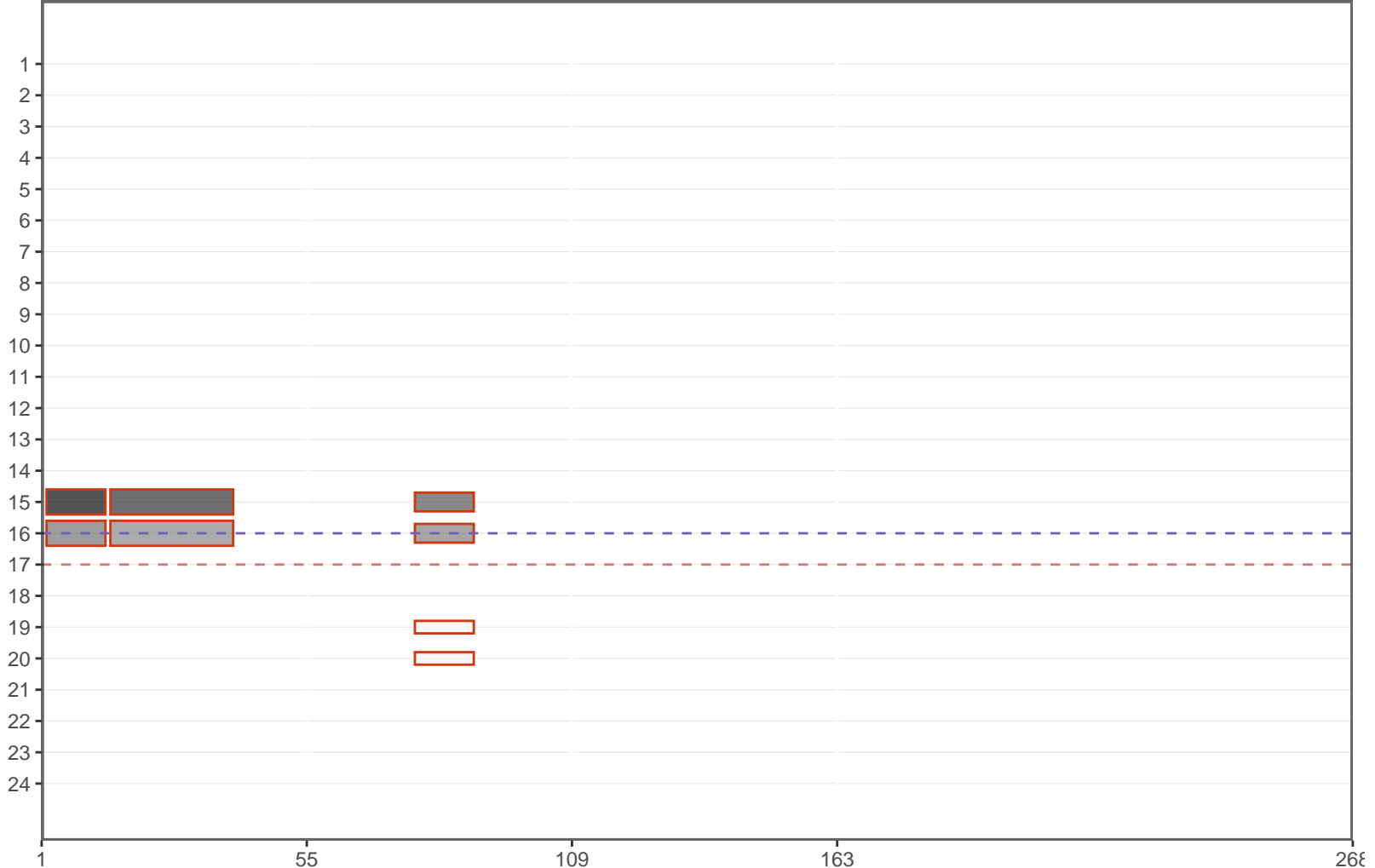
MW indication



Molecular weight



Gel Slice



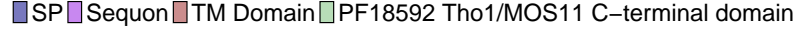
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AERFGLYKSDTTEEEAKKKALTRFAPPVKTDFVEEDKRRKARALSFHSPSLLNHNKQMARLETLSRMMLLWAKLERLNDSYLTWLKSRWARILMFLSSPVDRIQTFRKFTAKTFSLLMHHAVFGSNTRIIDNHLGGVKLPEMTGGDY

NbL15g01900.1 UDP-glycosyltransferase_73C5-like [MW = 55.45 kDa]

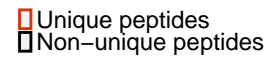
No. of times detected



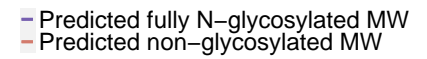
log(intensity)



Values from



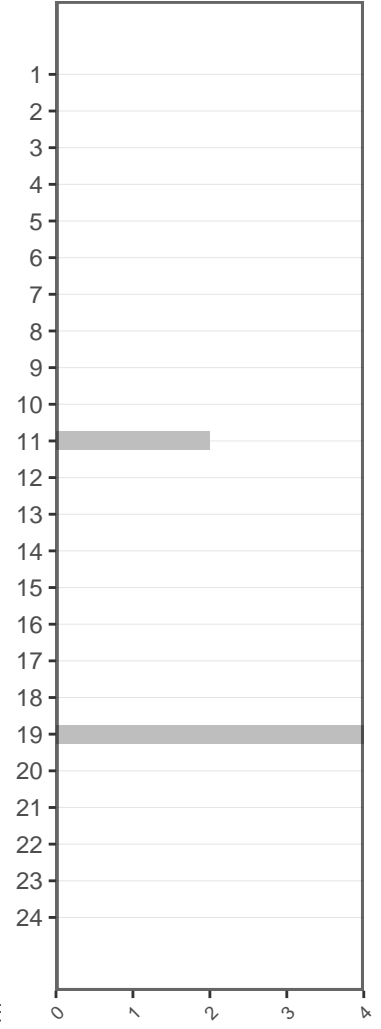
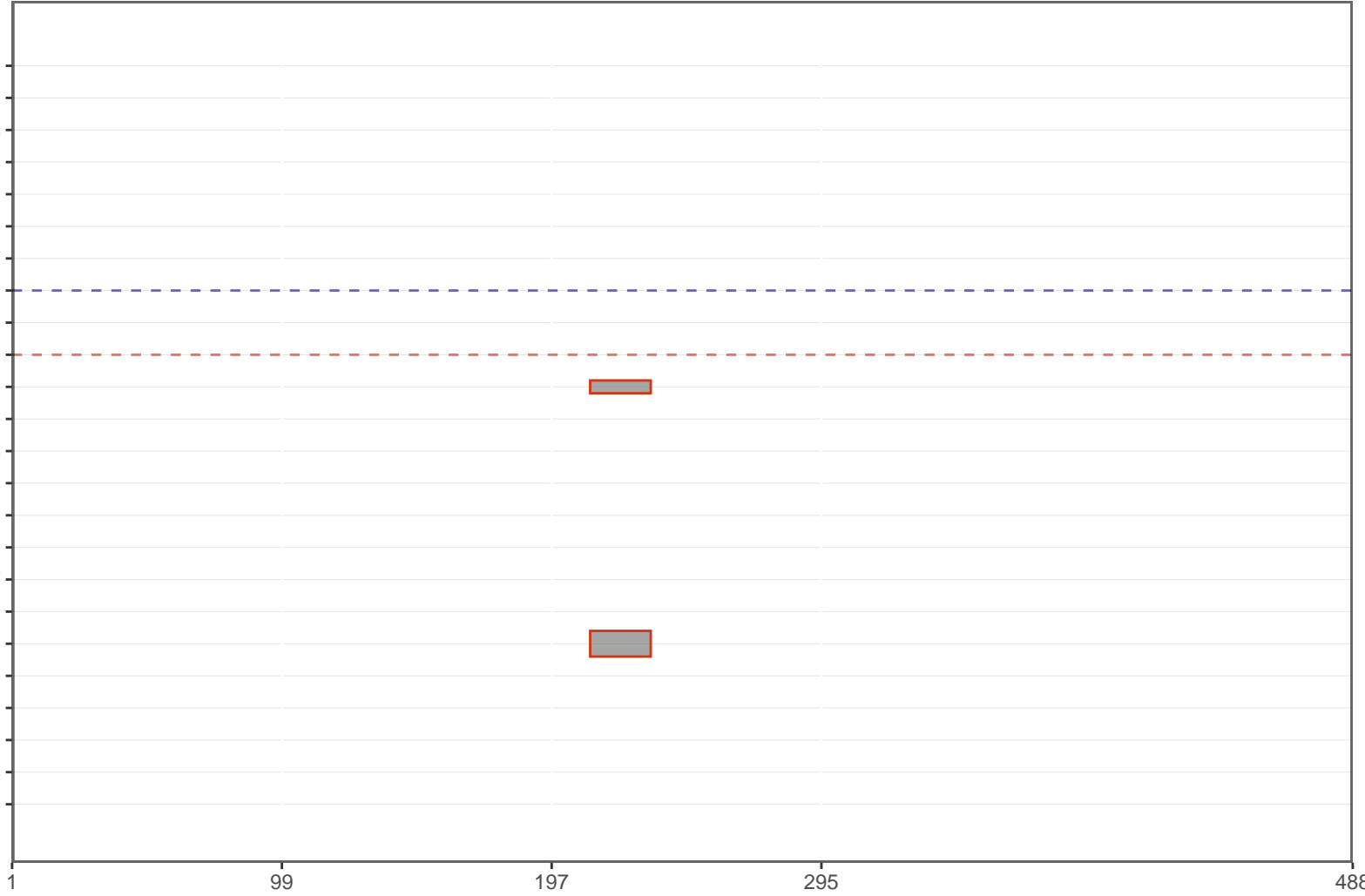
MW indication



Molecular weight



Gel Slice



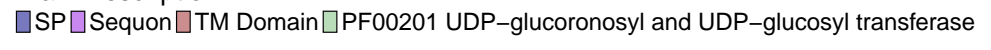
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KGLLKAHDKWITGPIVSLGNEKDKAERGNKASVDEHGKWLDDWEENSFLVGLGSLRSLPTDGMELGIGLESSKRPFIWVRHKSDEFQKVAEENFEERWKGGLIHGWAPQVLIHSHTSVGGFLTHGQWNSLSEGTADGVPMTIWPMPFAEFGQNERLIWVLLKTVGRACIENPVMFDEEEKVGAQVSKDDKVKVEEVFGEEVEADVRRKRKAKELGEMAKRAVEEGSSSYFALTKLQDVTGAKF

NbL15g01610.1 protein_LURP-one-related_10-like [MW = 23.83 kDa]

No. of times detected



log(intensity)



Values from



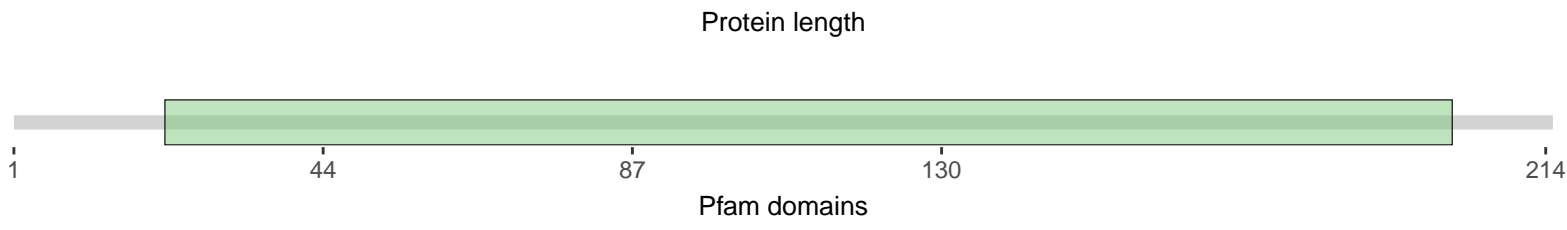
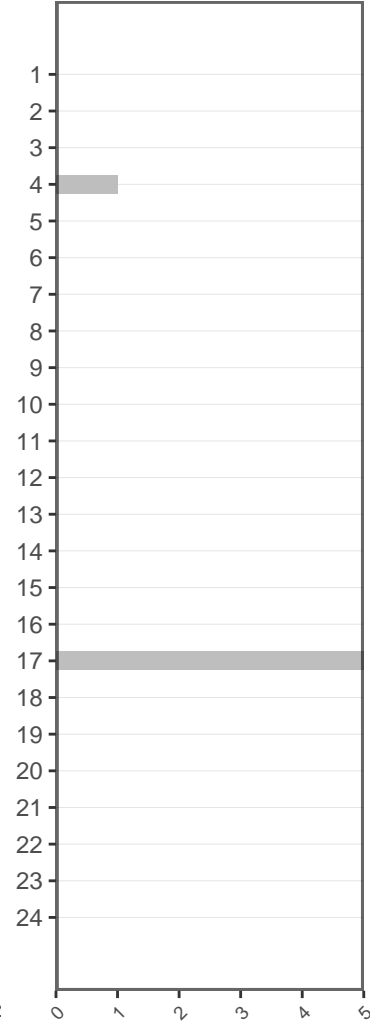
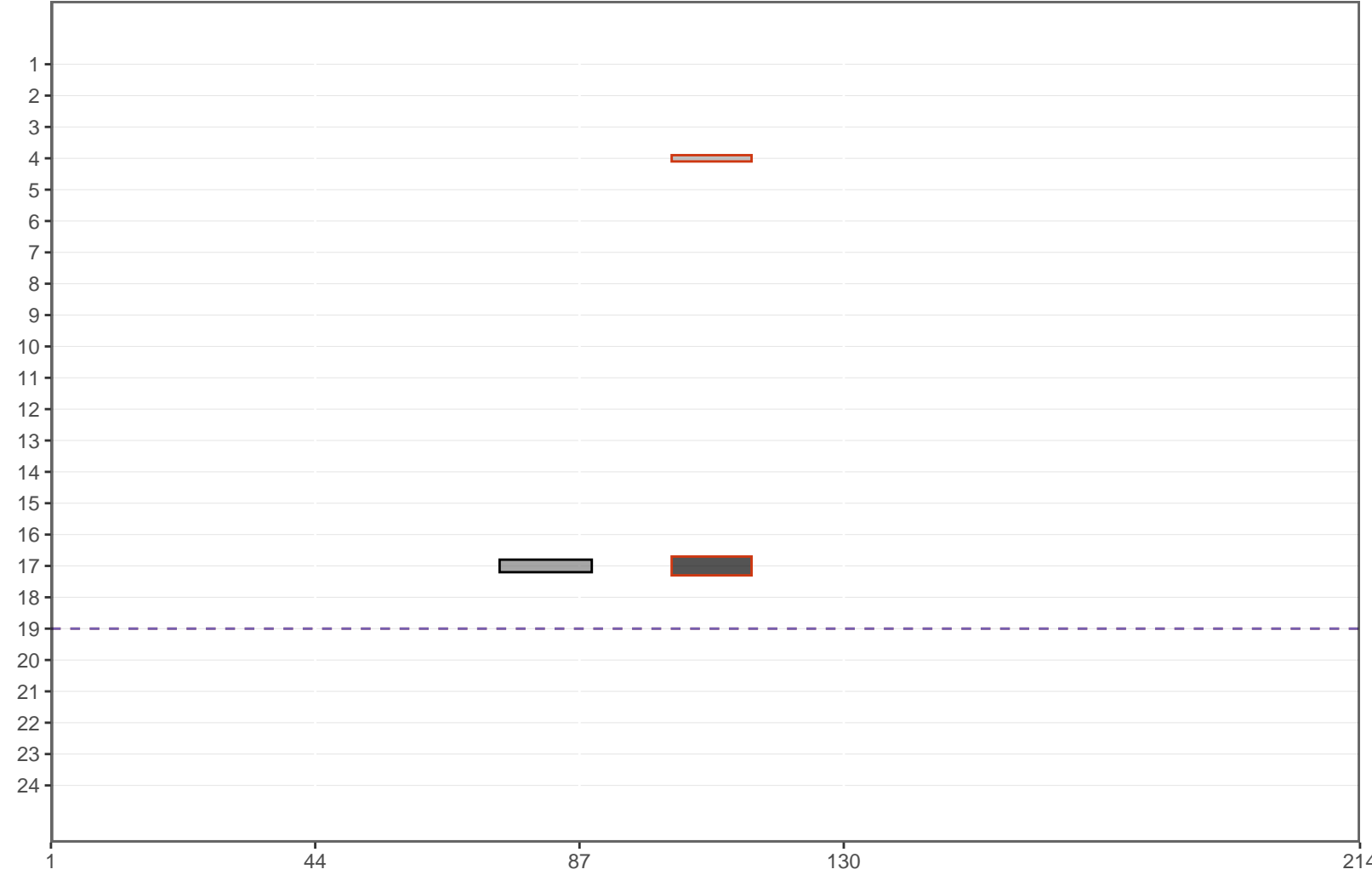
MW indication



Molecular weight



Gel Slice



Pfam Description

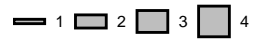


Protein sequence:

HRRWQVYRGESTDNENFLFVWKSLSVGFKTLDFLAHNTKEIVCDFRIEGSIFERFCGVVAGNTNTIAGMHRKHDTAGILLGKDNFGVTVYVNPVDVAFVWLVILEEINEDRSGAD*

NbL15g01430.1 laccase-17-like [MW = 67.29 kDa]

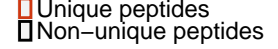
No. of times detected



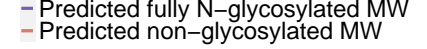
log(intensity)



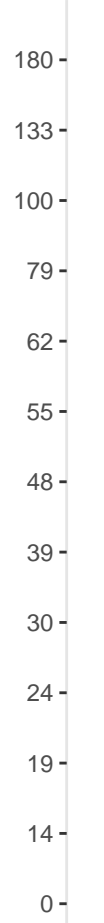
Values from



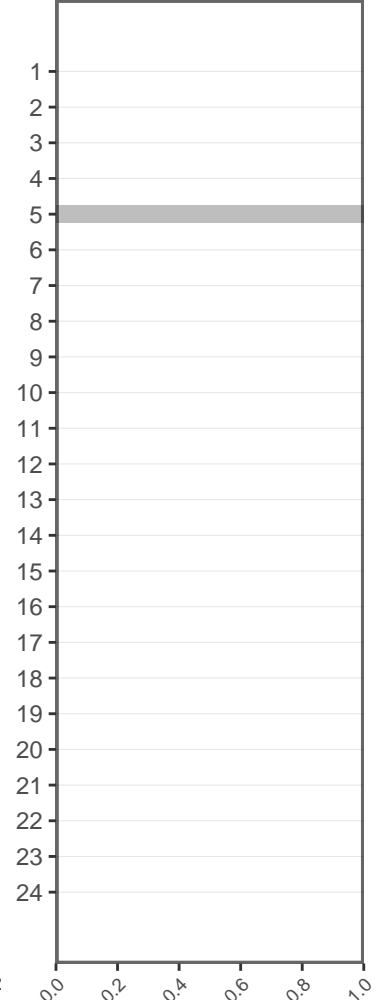
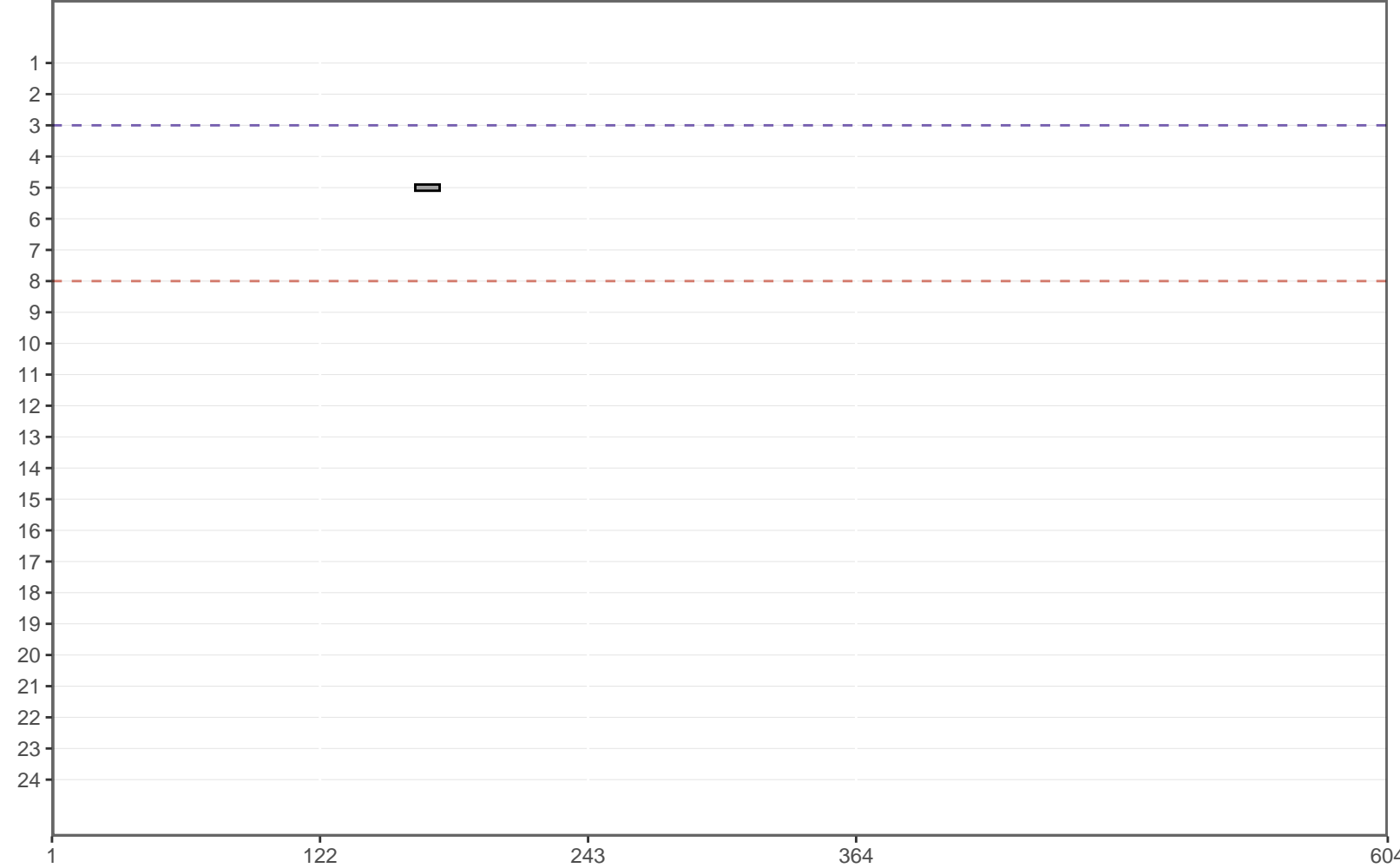
MW indication



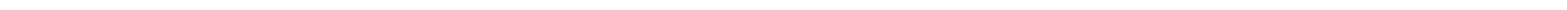
Molecular weight



Gel Slice



Protein length

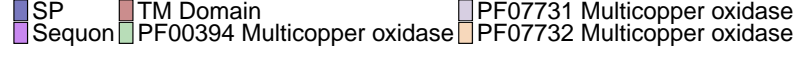


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TPGQTTNLLKTKSEVPSATFLMTRPKVVTGGGTFDNDSTVAGILEVESPIPHSTKSKIKLPLKPTLFPPLNDTSFATNFSKILRSLANSQFPAKVPQNVKHLFETVGLGTPCDKNGTGGPTNTTKFAASINNSFVQPTTALLGSHFTGGSDGYSYFPRFPLNLENWENTGNPPNNTMANNQTKVLLFPNTSVELIMQDTSILGAESHPLHLHGPNFFVVGSGFGNFDNFKDKPAKFLIDPVERINTVGVPSAGWVAIRFLADNPGWVFRMHCHLEVHTSVGLKMAWLVLDK

NbL15g01250.1 serine_hydroxymethyltransferase_mitochondrial-like [MW = 59.75 kDa]

No. of times detected



log(intensity)



Values from



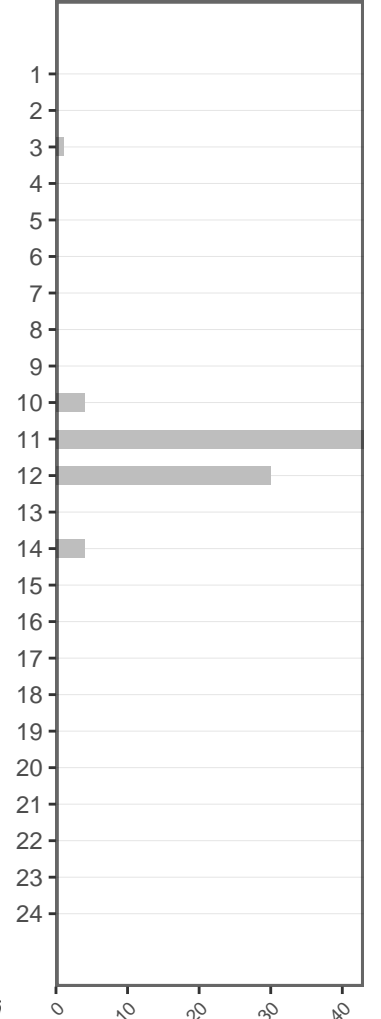
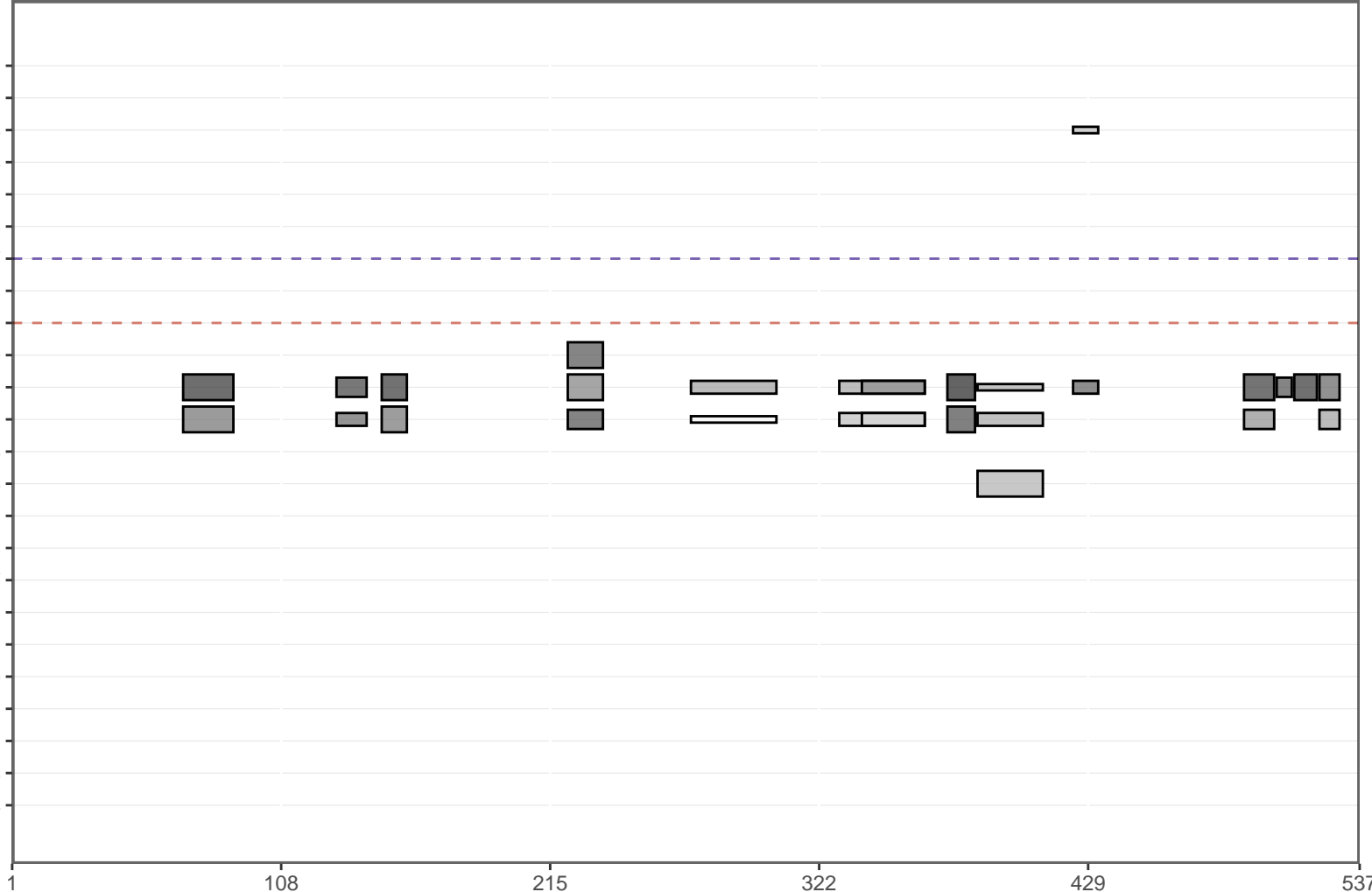
MW indication



Molecular weight

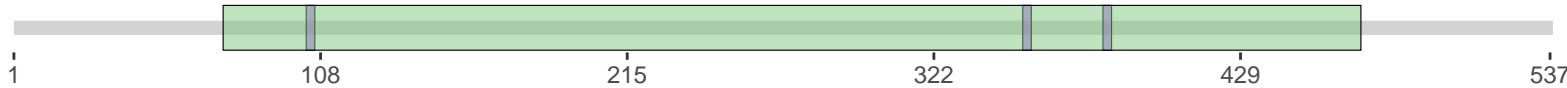


Gel Slice



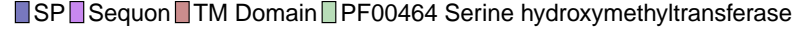
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LYDARIRKVCCKQKAVLLADMAHISGLVAAGVIRPFEEHADVTTTTTHKSLRGRPGAMIFFRKGLKEMNKGGKVEVMKYDEKINQAVFPGLGGSPHNHTISLQALVKLQVMTPEKAYGEQVLENSGSKFAEELLANGYDLVSGGTENHLVNLNRKKGIDGSRVEKYLEVHAAANKNTVPGDVSAMVPGGIRMGTPALTSRQFIEDPVKVAEFFDAVRLALVKVAETQGTGLKDFVETLSSDSKIQSEIARLRGDQVEDVAKQKFTVGFKEKEMKYKD*

NbL15g01150.1 tubulin_beta-2_chain [MW = 50.18 kDa]

No. of times detected



log(intensity)



Values from



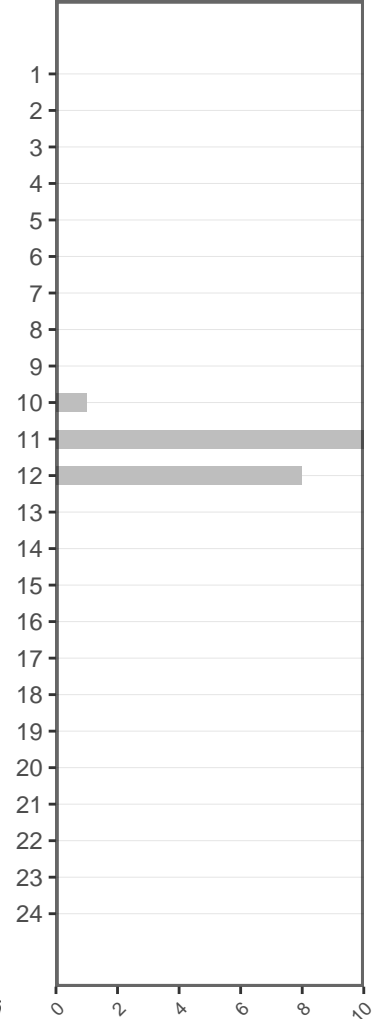
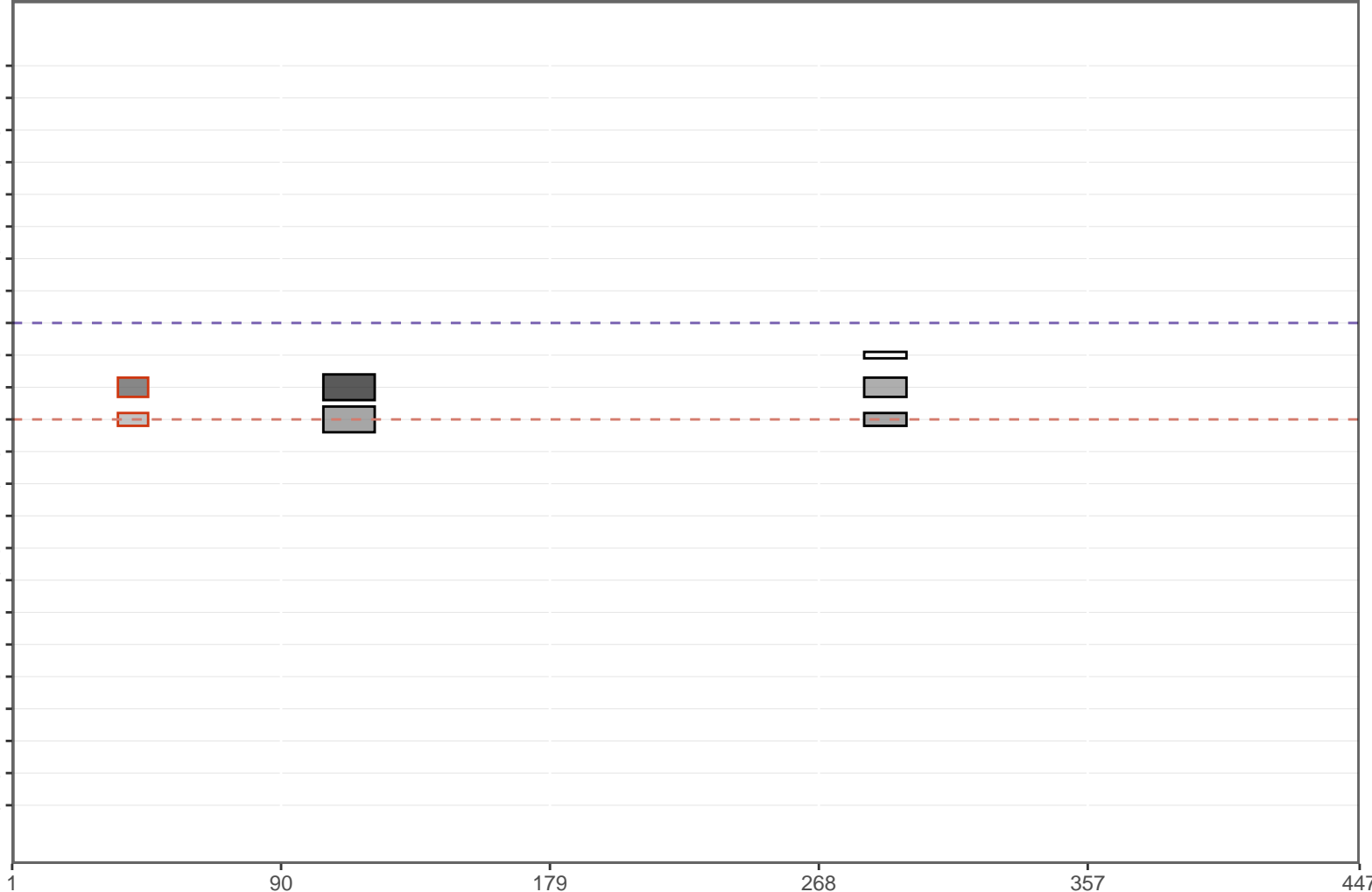
MW indication



Molecular weight



Gel Slice



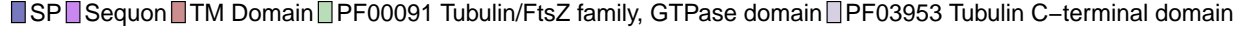
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MFRTLKLITPSPGDLNHLISATMSGVTOGLRFPQGLNSDLRKLAVNIPFPRLLHFFMVGFAPLTSRGGQYRALTVPFLTQGMWDSKNMIMCAADPRHGRVLTASAMFRGKMTKSTVEQGLNVDGNNSVYFVEWIPNPKSTVGDIPPTGLKMASTFRIGNSISGEMFRFRVSEQFTAMFRKAFLHWYTGEGMDMEFTAEAGNNDLVSEYGGYQDATADEEGDYVEDEEEAAGEQ

NbL15g01090.1 GDSL_esterase/lipase_At2g38180-like [MW = 27.78 kDa]

No. of times detected



log(intensity)



Values from



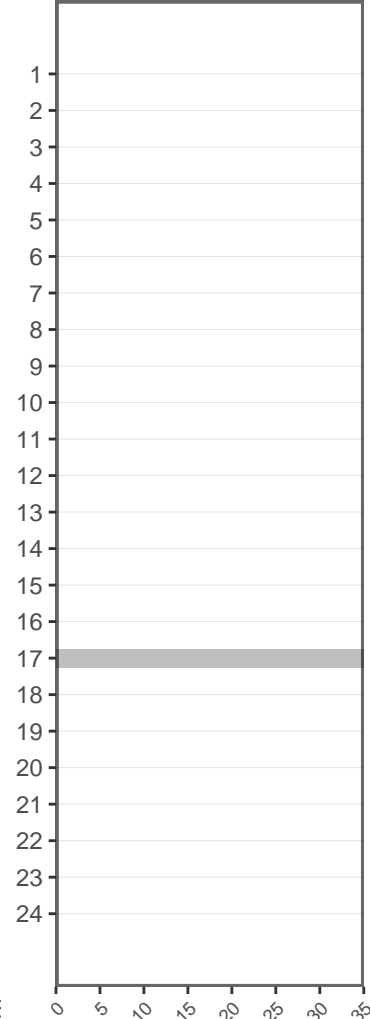
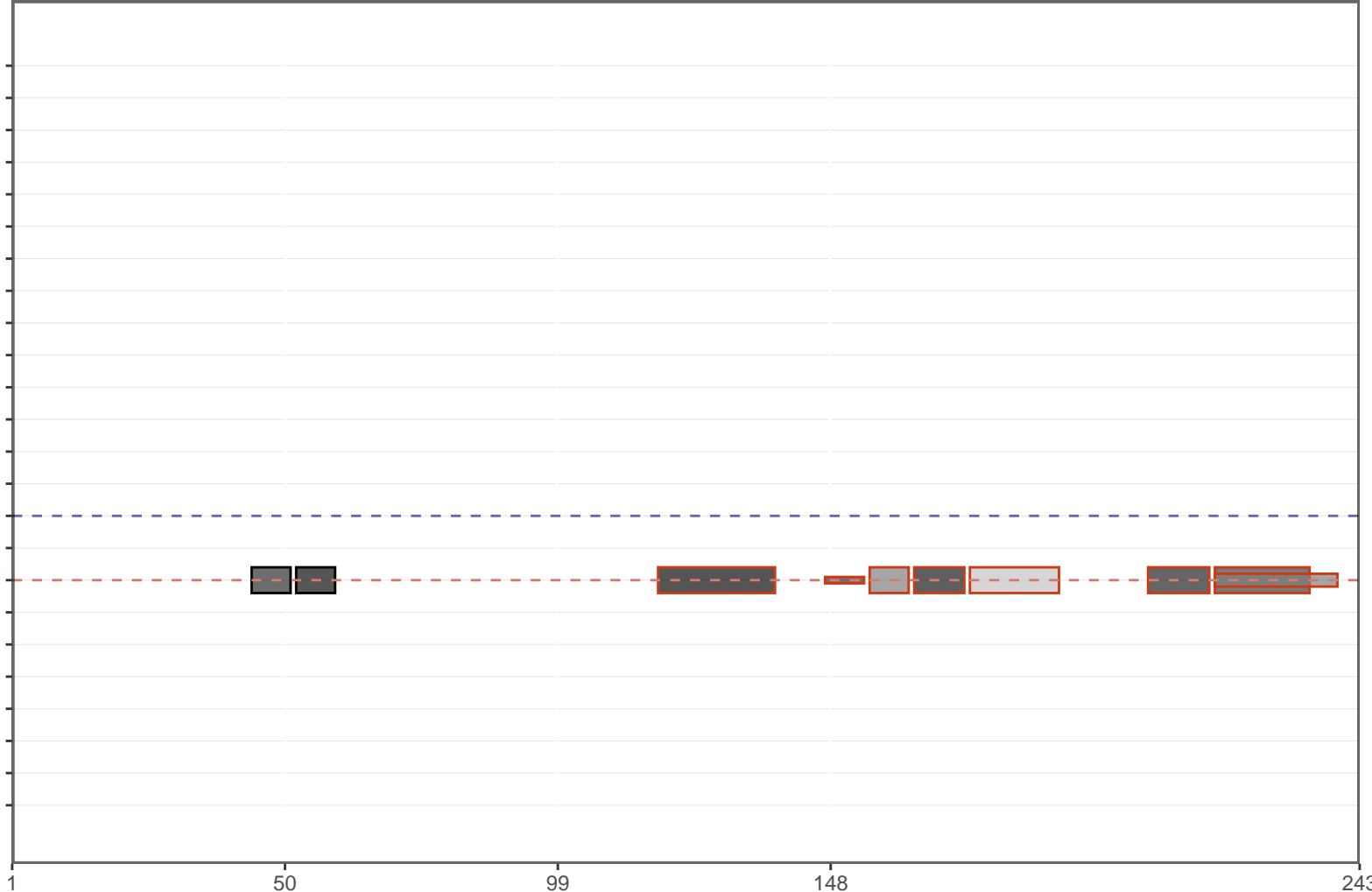
MW indication



Molecular weight

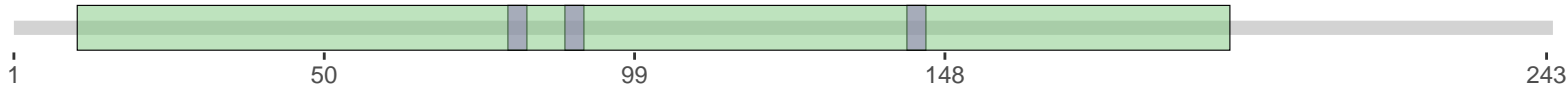


Gel Slice



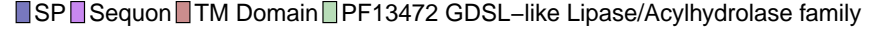
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KSLSEKTRLLMLSSAPPVNEEGHQHYEDNRGRDNETGRVYSEAGIKLAGELGVKVIDFWSALGKSPDWLTTVFVWDGMHLKKEGSDILVEKILEVKEADWEPSPVYWEKMPDEFSDGPPVMMNLLDKDSGKGRV

NbL15g01020.1 fructose-bisphosphate_aldolase_1_chloroplastic [MW = 42.95 kDa]

No. of times detected



log(intensity)



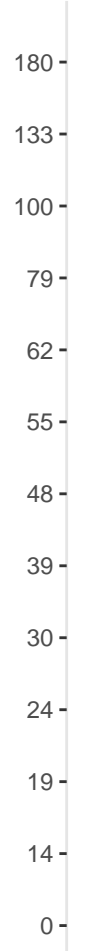
Values from



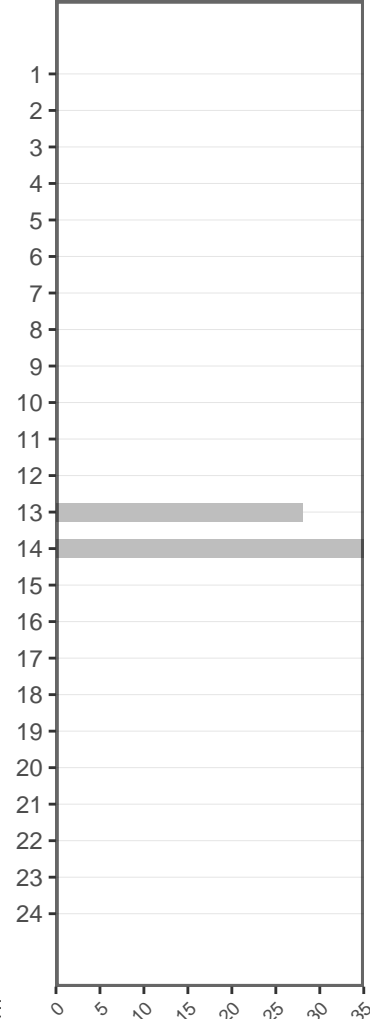
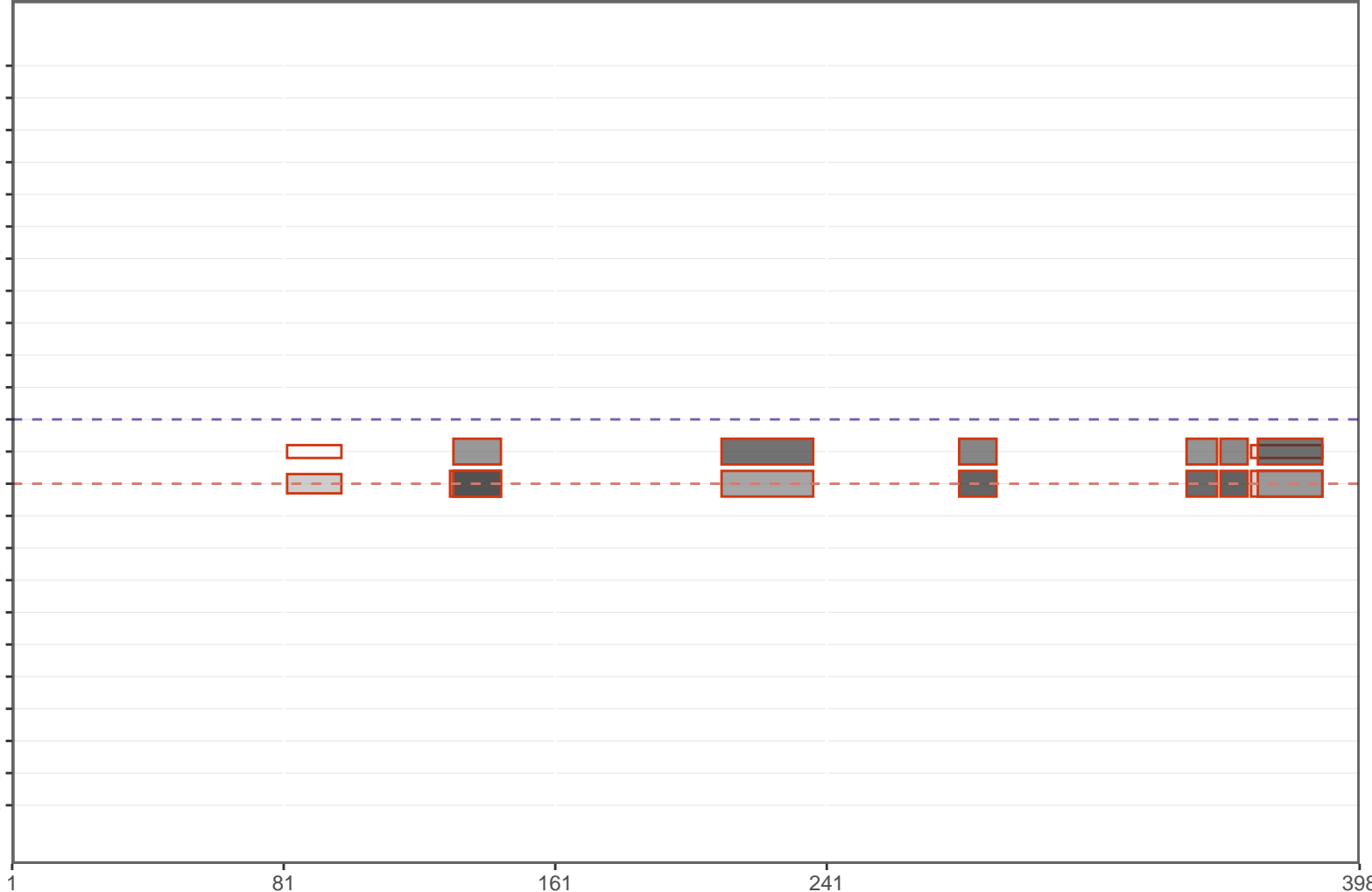
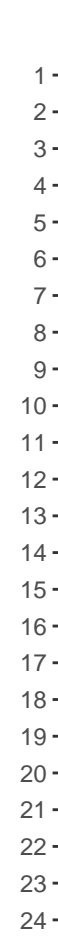
MW indication



Molecular weight

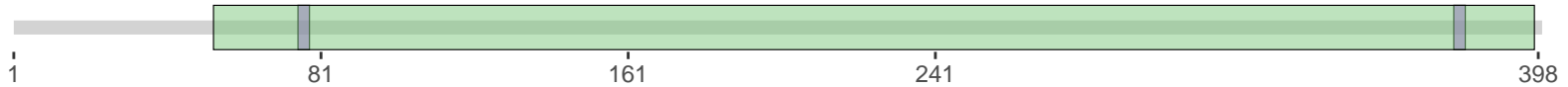


Gel Slice



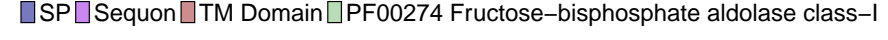
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VVSPINPSPSALAVKEAAWGLARVAAMQDGLPVEPEILLDGEHGIDRFEVAQGVAAEVEFFYLAENNVFEGLLKPSMTPCAECKDRATPEQVADYTLKLYRRIPAAVPGIMFLSGGGSEVEATYNLNAINDAPNPWHVYFSYARALQNTGLKTKWGLPENKAAQDALLVRKANSLAQLGNVYTGEGTDEAKGGMFKGVVYV

NbL15g00990.1 arginine_decarboxylase-like [MW = 79.12 kDa]

No. of times detected



log(intensity)



Values from



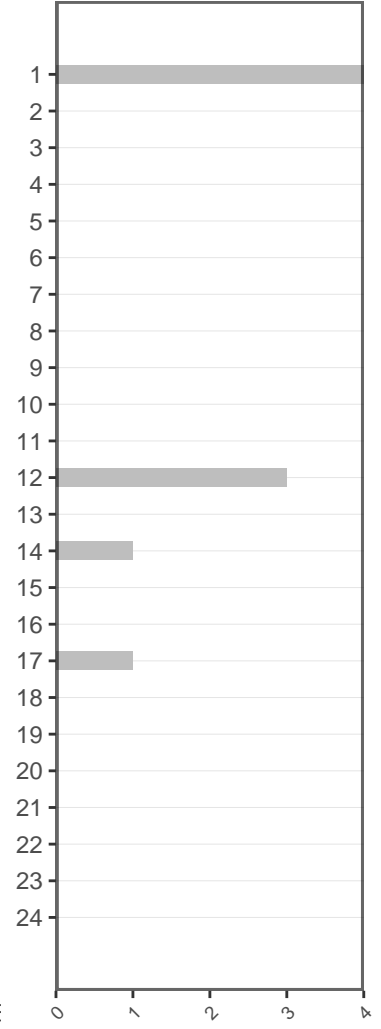
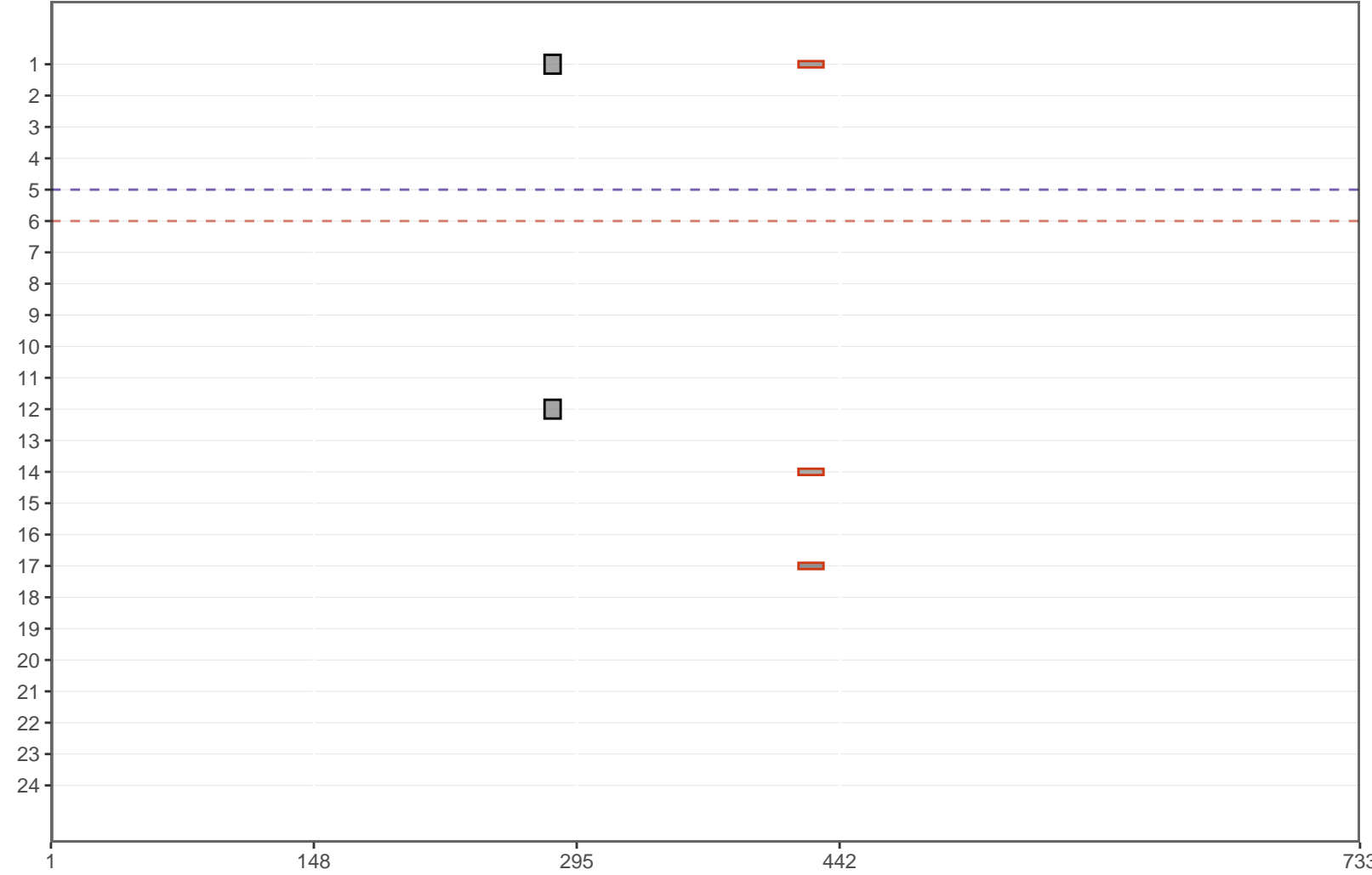
MW indication



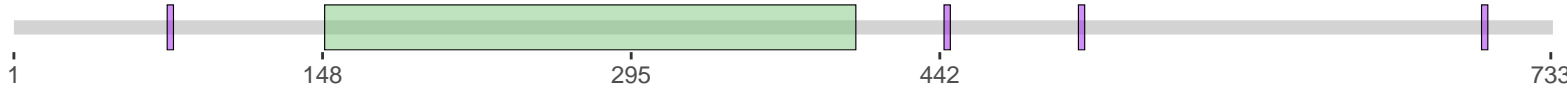
Molecular weight



Gel Slice

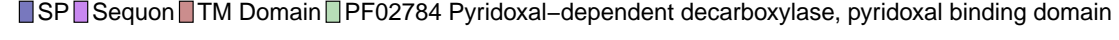


Protein length



Pfam domains

Pfam Description



Protein sequence:

KSCDSDCSVGYGLGQEVASTYKAVQFVGDRIKWKHPVQSESGRAVSHHSVLFEAVSSTTRISQELSSVDLQGFVEKLNDDGRADYRNLSAAAIRGEVDYVAVDQLKGRVGEFGKDGDLNIEQLAAVDDGIDFVSKAAGSDPVRTYHVALSIFTSIPDFVAIDQLFVPHKLDERPEVIRGLSDLTGDSGDNDKDFVGGESLPLUHELGSNGGGSDGGKYYLGMFLGGAYEEALGGLHNLFGGPEVLRVSGNSPHSFVAVTSPGPEADNLRAMQHEPELMFE

NbL15g00930.1 eukaryotic_translation_initiation_factor_3_subunit_A-like [MW = 111.44 kDa]

No. of times detected



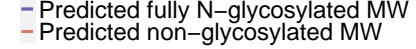
log(intensity)



Values from



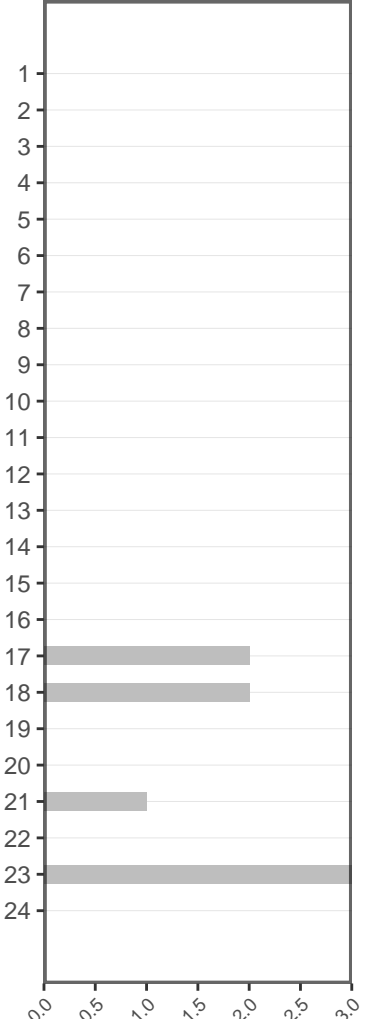
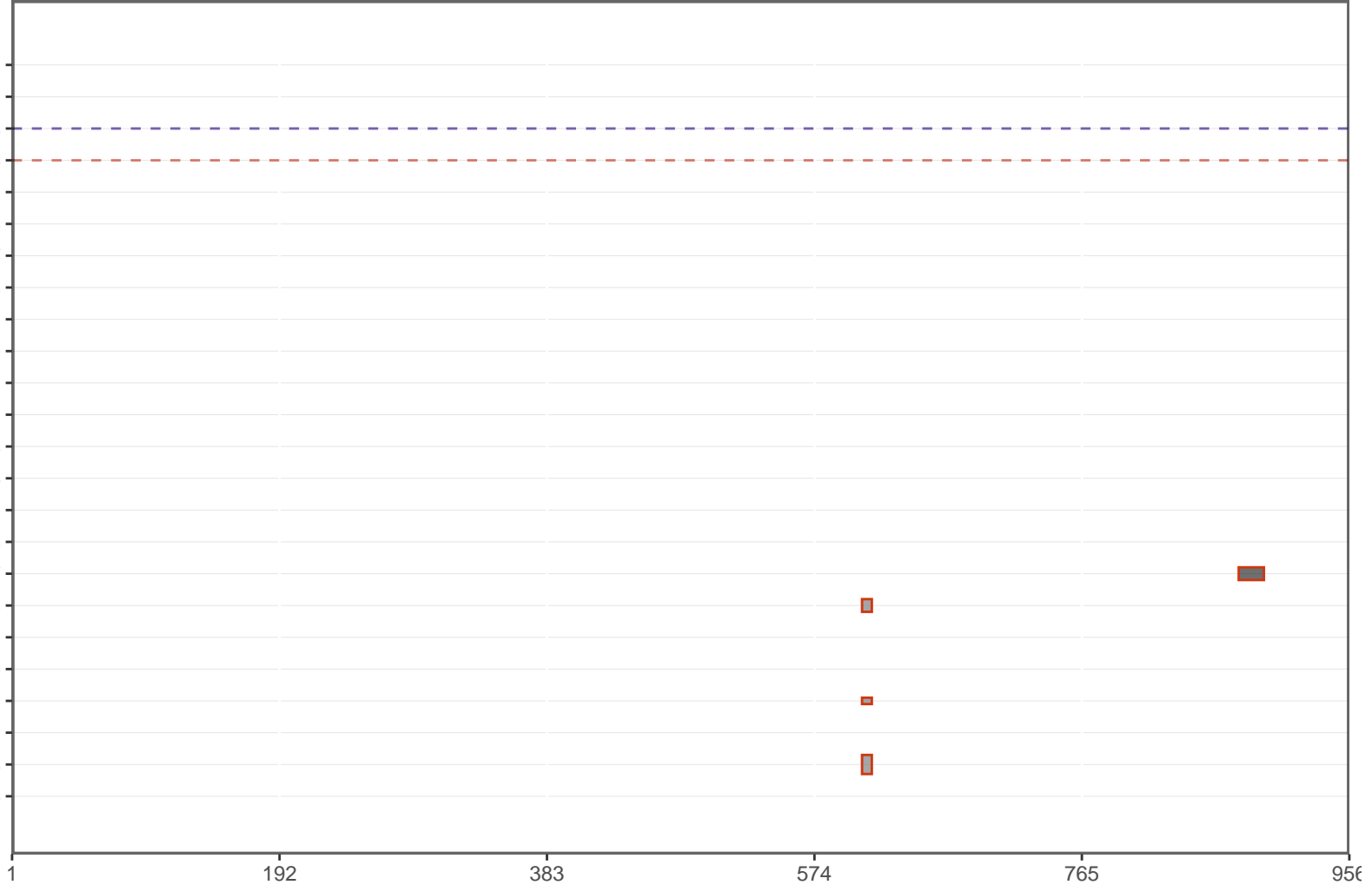
MW indication



Molecular weight

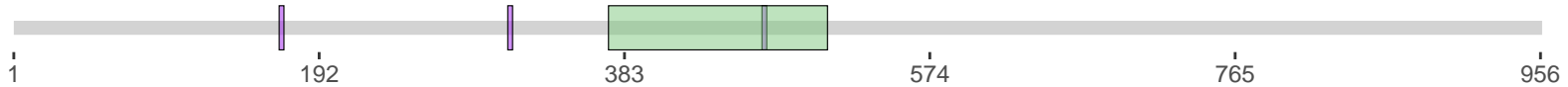


Gel Slice



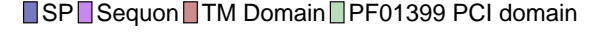
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

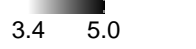
SNLSKMSIFDFDAAEKIAVDVIRHNFVAKVDHMKHVAFFGKQSEAEGLRDHLSLFAESELKARLMYFPWAKAAALGDALSNLAEVKEKHKRLARKBIKREKKEGDEGLLEMERVEETNRREMOKITEEAEGKRMMAELEGRRTQRILKIEEERELEEAGALLGEAEKRSKRKKKPLVDGKNTKQVIMELALNEQLRERQEMEKLLKFKAKTMDYMERARRREEAAPLESFQRRLAEAAALHEREGOOLELSGRQRHAGDLEKRRKLRGMFENKRIFQERAVSSREA

NbL15g00860.1 oxysterol-binding_protein-related_protein_3A [MW = 52.19 kDa]

No. of times detected



log(intensity)



Values from



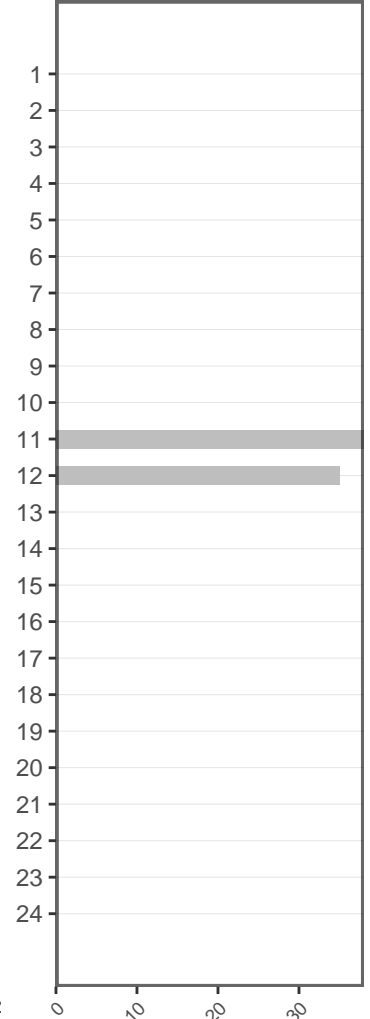
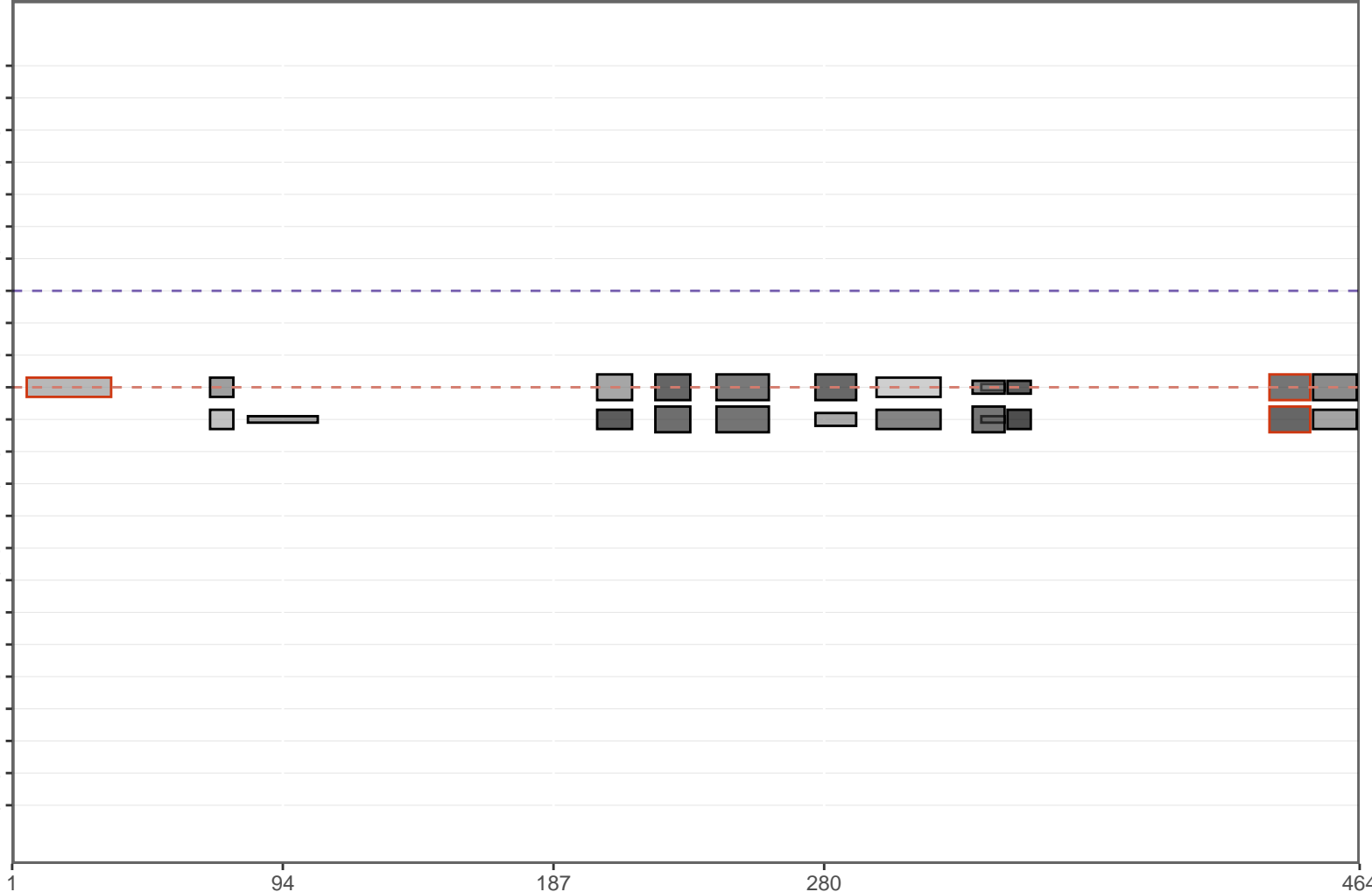
MW indication



Molecular weight

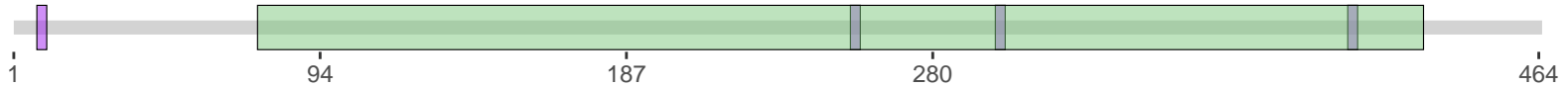


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

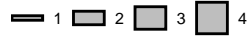


Protein sequence:

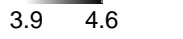
KGSGVLDLVPPPTKVNHLFGRTWIDSPGEMILNTTGDKLVLYFQPGWFGAGRVEVDGYYNSEEPEKMLTGKWNESLSYQPDLEGEPLPGSTKKEVWRAADAPNNDKFGYTFYFAHKINSEFDTAPKHLASDSRLRPDRVALEKGDLEKASSEKSRLEERQADRRTREANGDEFKPKWFLNLSNEVCPPTPWGDLEVEYVNGKYHEHRAIDSDSDKVEEADKKTTEFNPNWQYEDSVSAI

NbL15g00710.1 glycine-rich_RNA-binding_protein-like [MW = 16.89 kDa]

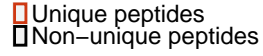
No. of times detected



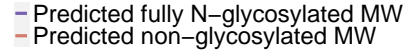
log(intensity)



Values from



MW indication

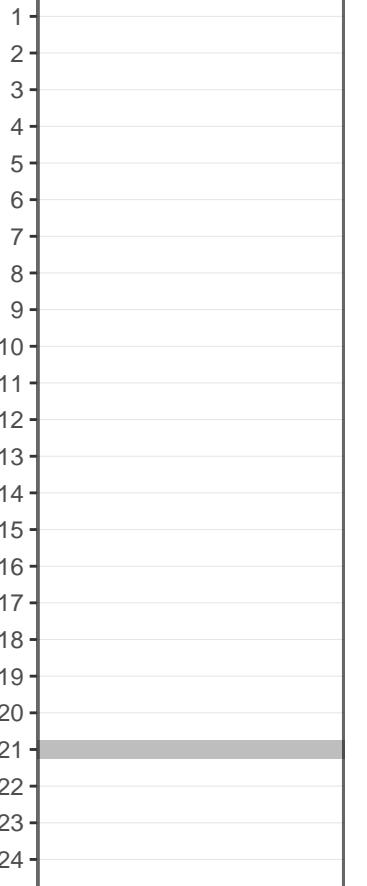
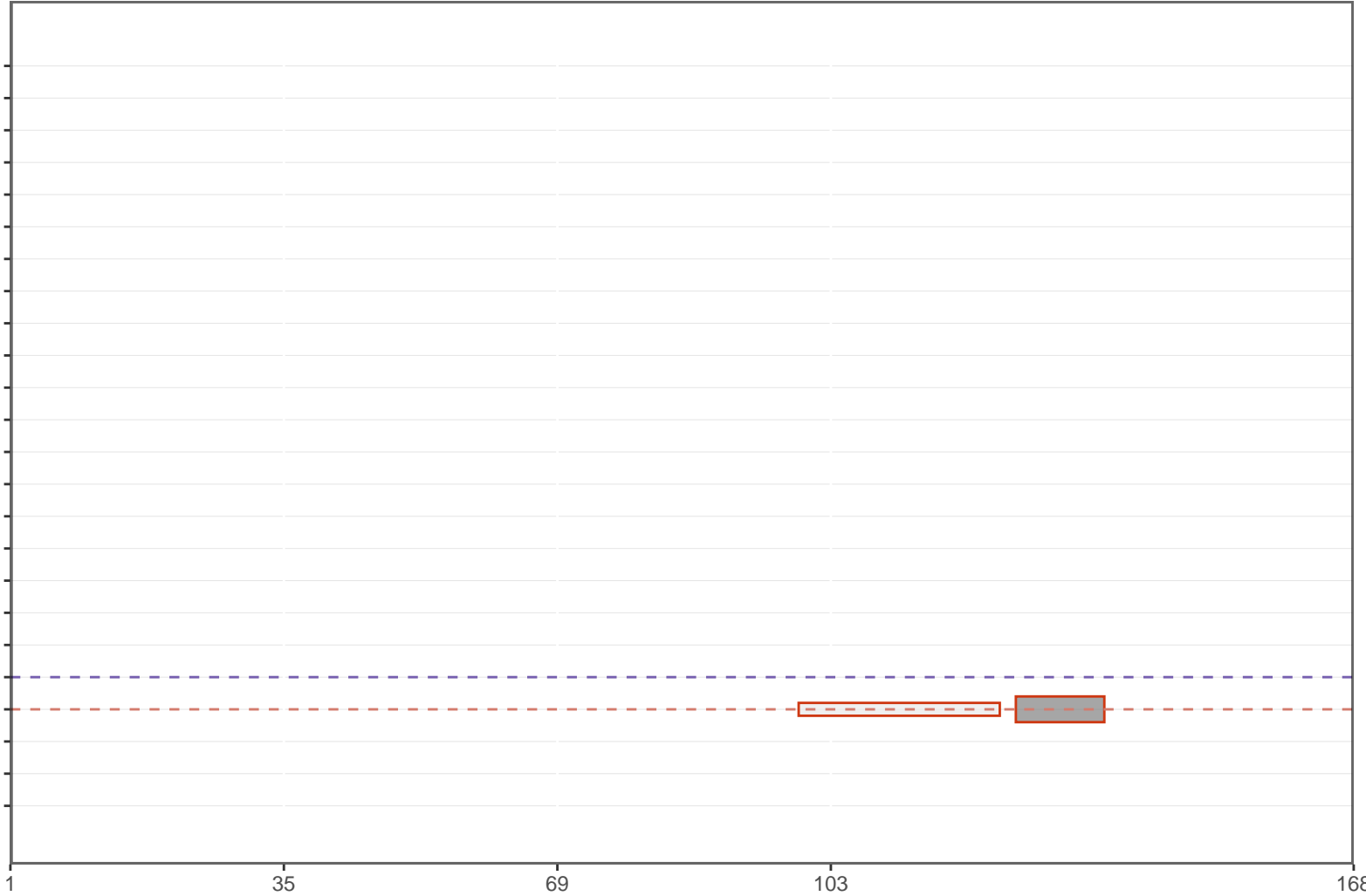


Molecular weight

180
133
100
79
62
55
48
39
30
24
19
14
0

Gel Slice

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24



Protein length

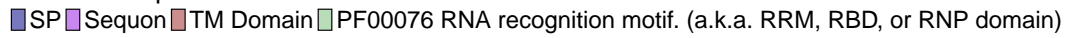
1 35 69 103 168

Peptide counts over 4 repeats

Pfam domains



Pfam Description

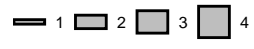


Protein sequence:

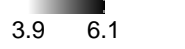
IRNITVNEAQSRRGGGGGFGRRREGGYSGGGYSGGGYSGGGYGGGRREGGYSGGYGGGRDRGYSGGYGGGDSRRYSRGGGASEGSGWRN

NbL15g00670.1 ATP-dependent_Clp_protease_proteolytic_subunit_6_chloroplastic [MW = 30.88 kDa]

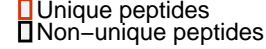
No. of times detected



log(intensity)



Values from



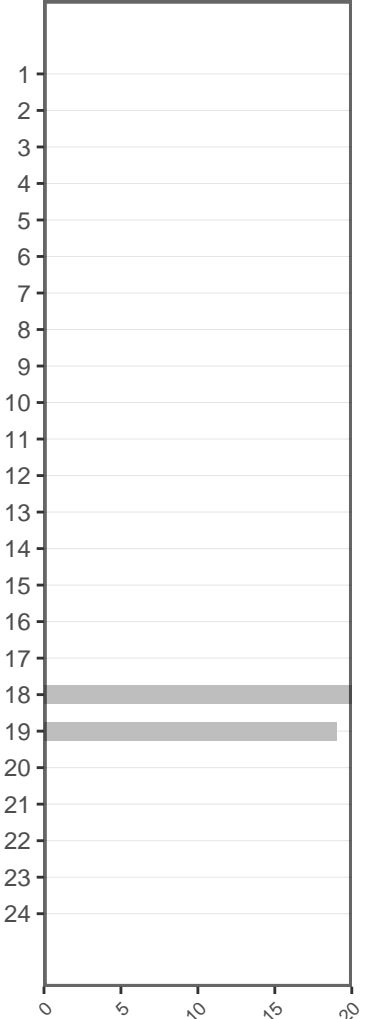
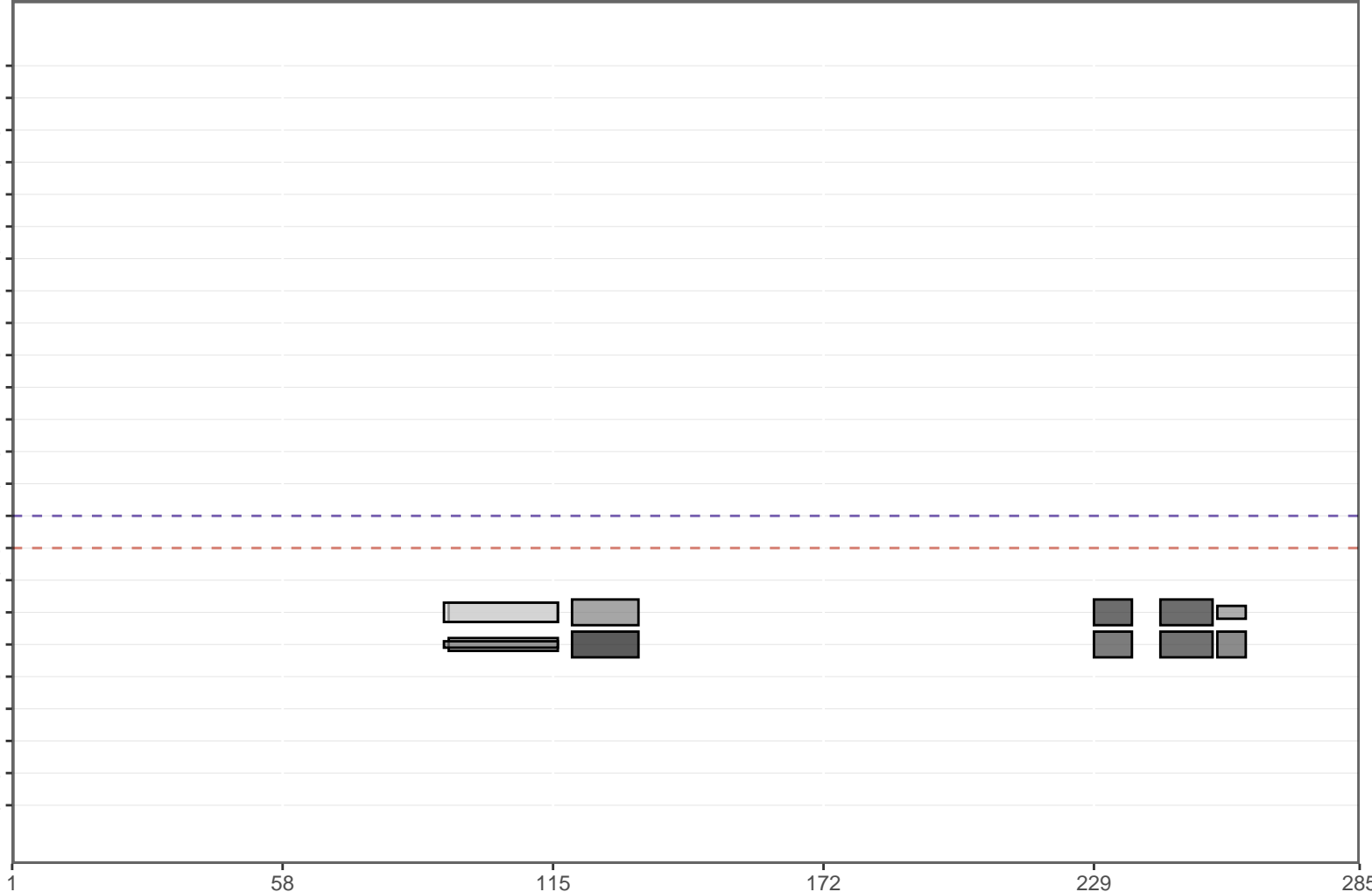
MW indication



Molecular weight

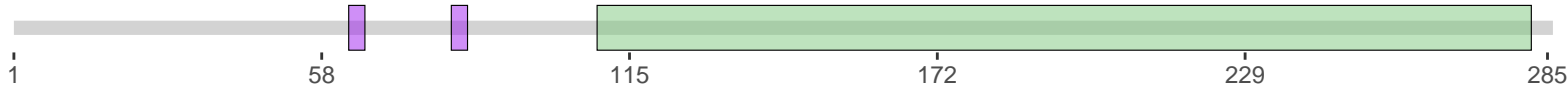


Gel Slice



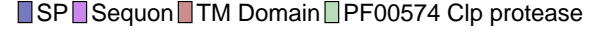
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

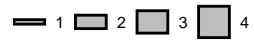


Protein sequence:

IQRVTSQVLTLATIDENADLRLNFGPGSTYVLAIKDMSBWKPKVGTVFCGVAASGGALLAGGKGRMRYAMPNARIMIHQPGSGGGHVEDVRRQVNEAVGSRHNDKMYVAFTGGSEIKVQGYTERDRFLSVSEAMEFGLDGVLETEY*

NbL15g00650.1 protein_TIC_62_chloroplastic [MW = 68.55 kDa]

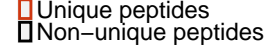
No. of times detected



log(intensity)



Values from

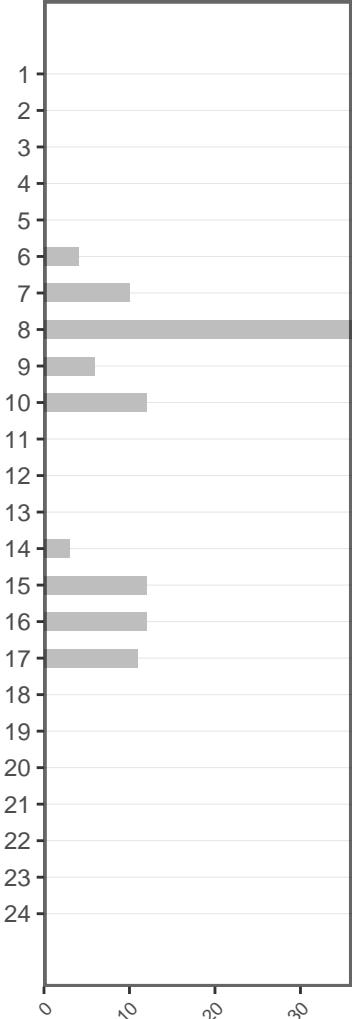
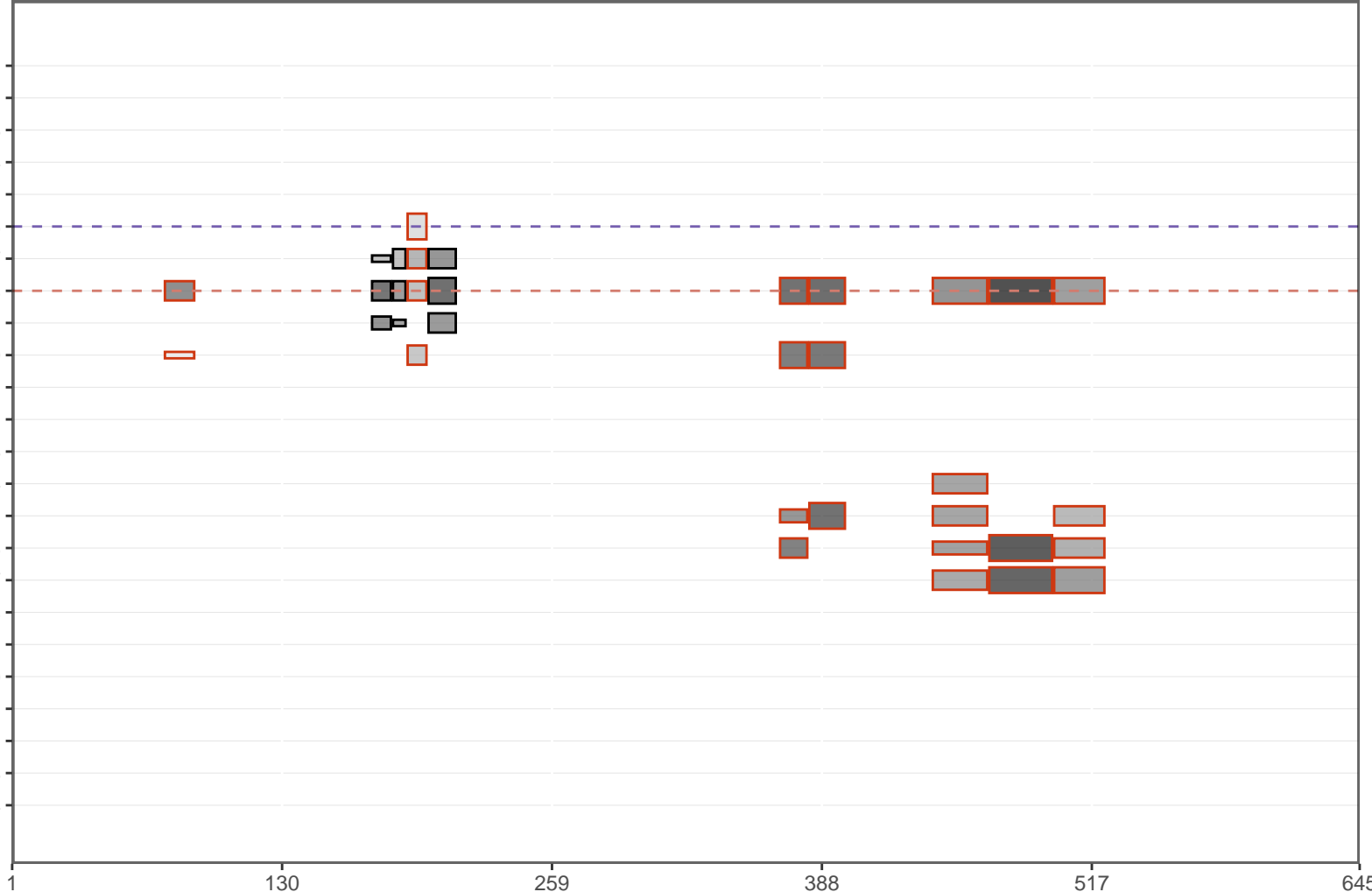


MW indication



Molecular weight

Gel Slice



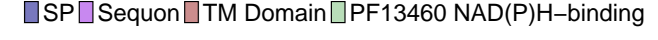
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

APLTPMEDLLANIPGDRVEVSPAMEGDLQKPKASBSITSEIPSTGSEKEAETKLAASALSPVAIVEDRNPPTSPPTTPGIGTGLTKESKAVSPVVAANDSPSSSEINFSESSIPETDSTTQGTDKKXKTPSPSPVTFYEDLKKPPTSPPTNPNPQGRLASAGTDEGDPDTVASVDGTSQKAEELLARPLSPVTVVEDLKKPPTSPPTTPGPKASIAETISQLAGNAISPFITITTEKDPSTVAFCHSPVYFVEDLKKPPTSPPTTPGPKASIPVVEISPLGQNDVVISATNS

NbL15g00590.1 ferredoxin--nitrite_reductase_chloroplastic-like [MW = 65.6 kDa]

No. of times detected



log(intensity)



Values from



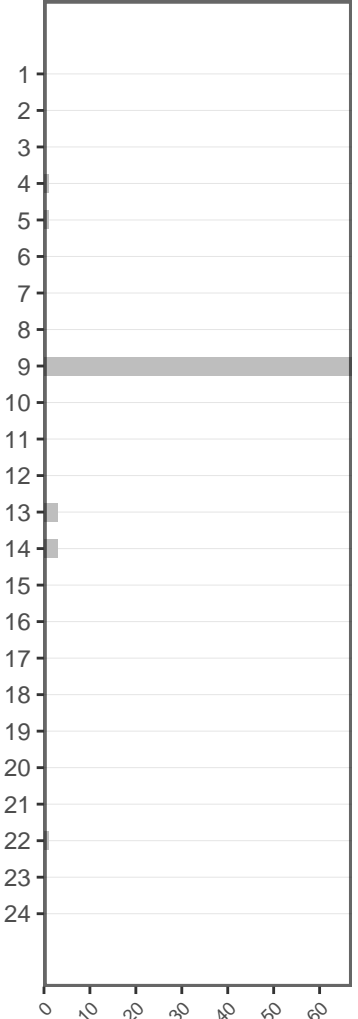
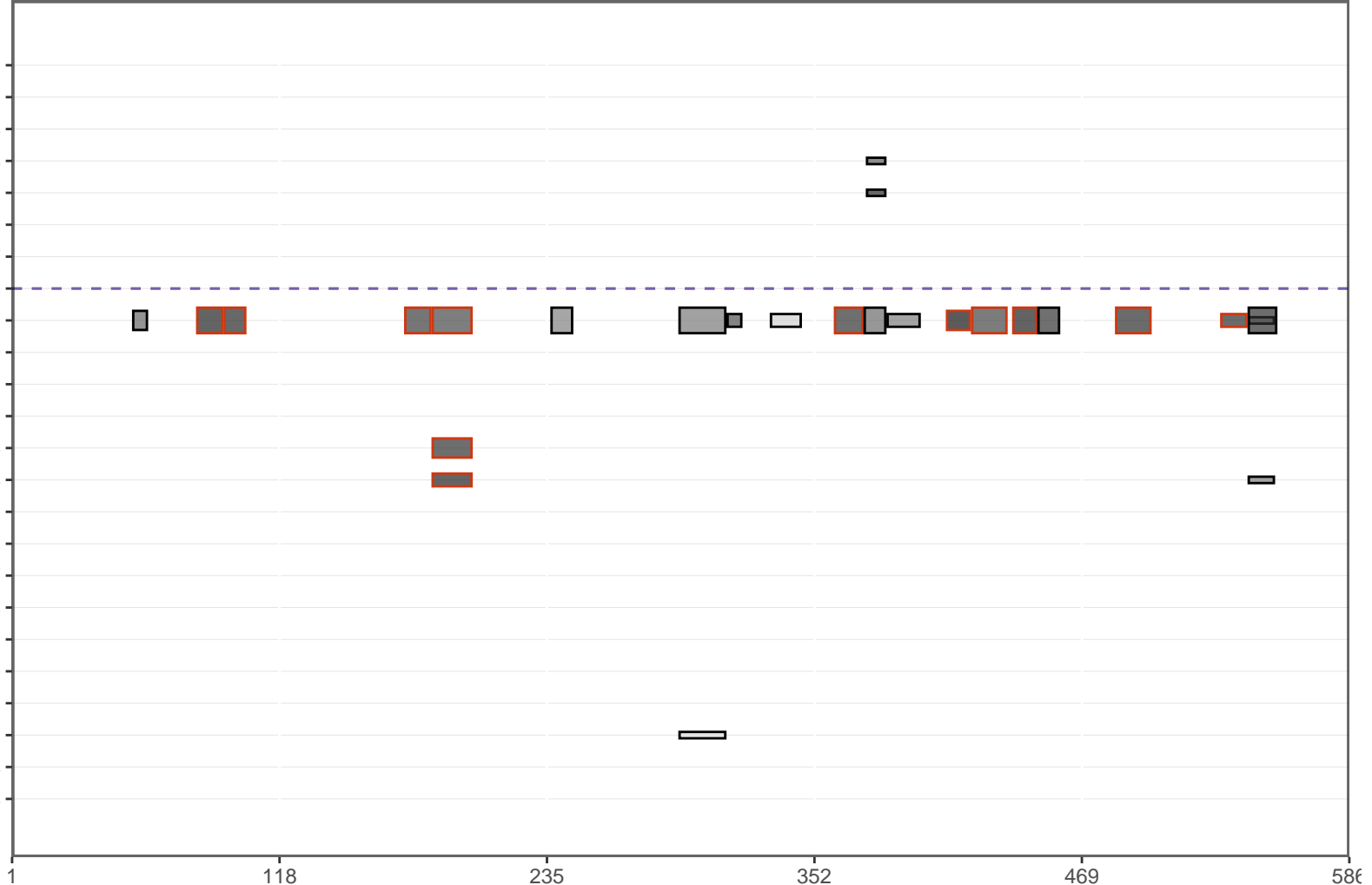
MW indication



Molecular weight

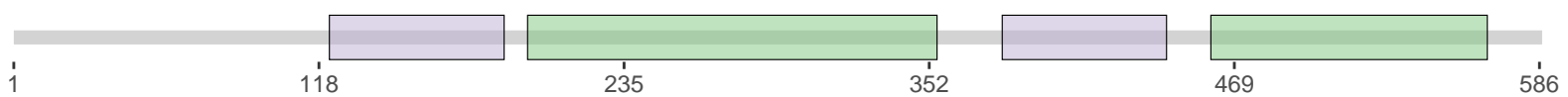


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01077 Nitrite and sulphite reductase 4Fe-4S domain
- PF03460 Nitrite/Sulfite reductase ferredoxin-like half domain

Protein sequence:

ILLVGGFFSPKRCAEAVFLDAWVFDADVAVPVCKALEAVRDLGTRGRKTRMMWLVDELGVGFRSEVAKRMPKQLDRSTEDLVGNQWERREYLVHPKQKQEGYFVGLHVPVGRVQADDMDLRLADDVGGSELRLVTEGNIHPNIENSKIKALLNEPLLNIRFSTDPILMKTLVACTGNVFGGDAIETKARSMKITEEVQQLVSVTKPVRIMHWITGGPNSGGVQVADIGFMGLTRKEKTVEGADVYLGGRIGSDSHLGDVYKRVKVPCELDVPIVDLLVNNI

NbL15g00470.1 uncharacterized_protein_At5g01610-like [MW = 19.27 kDa]

No. of times detected



log(intensity)



Values from



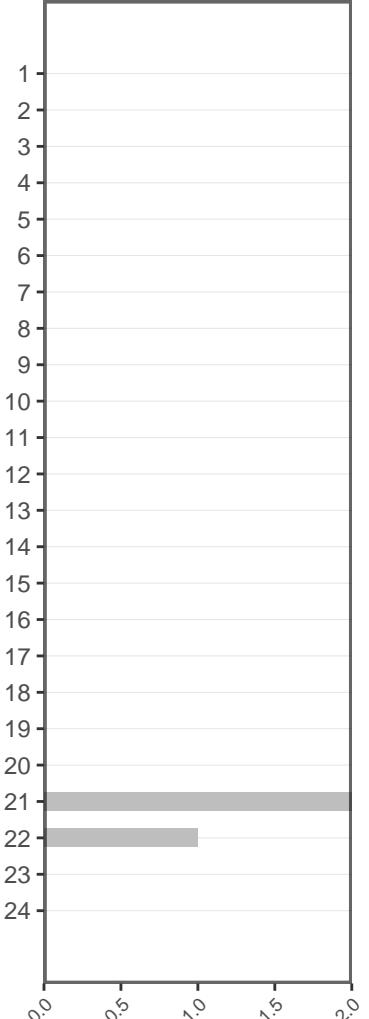
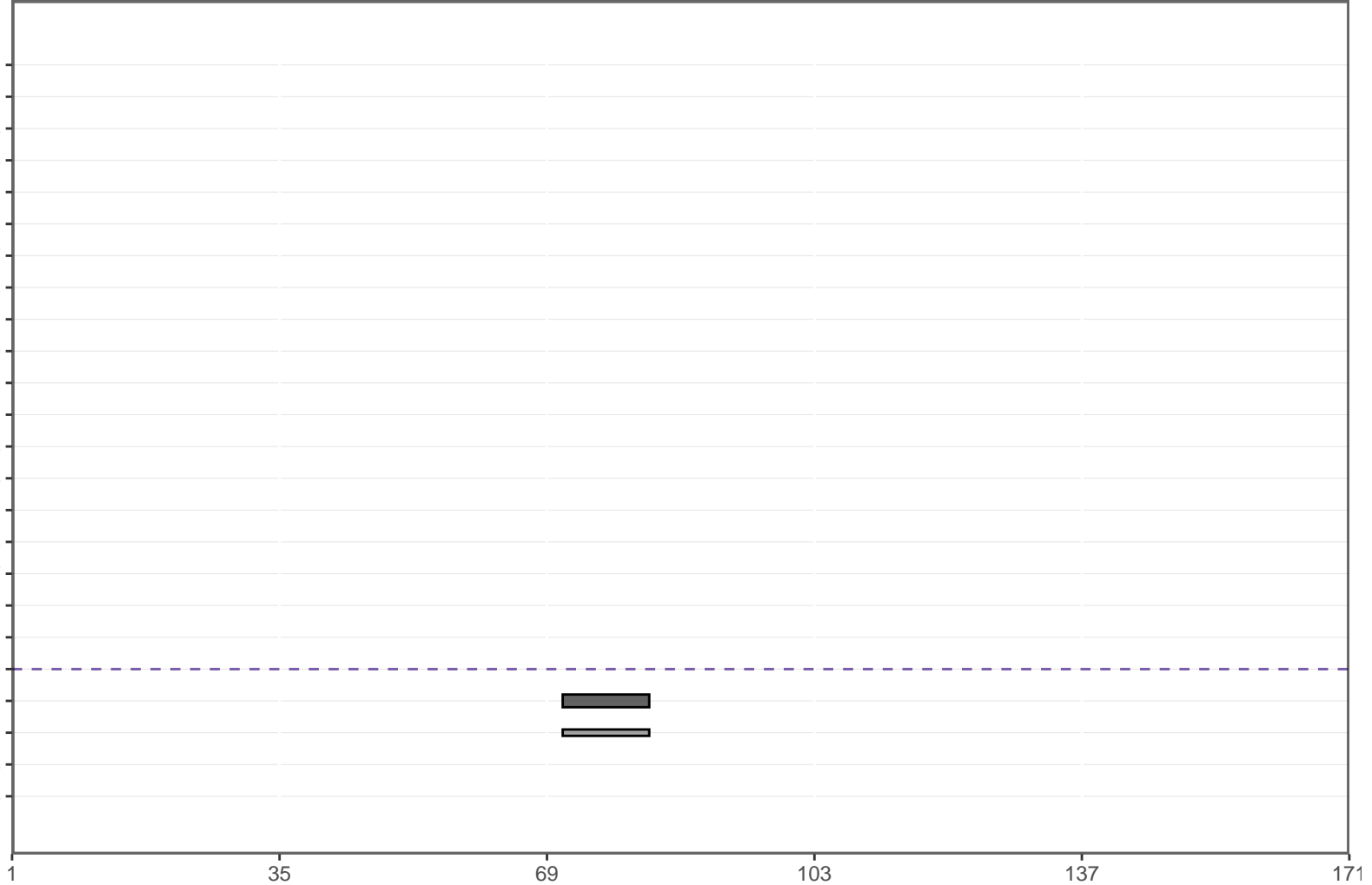
MW indication



Molecular weight



Gel Slice

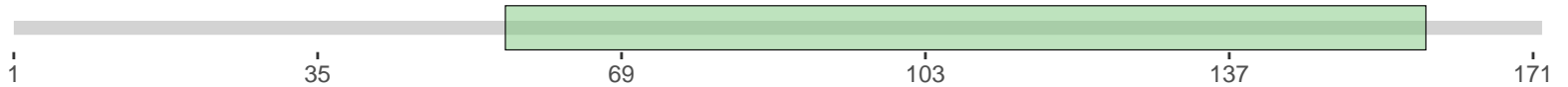


Peptide counts over 4 repeats

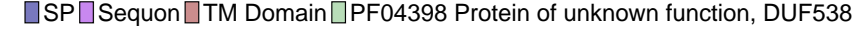
Protein length



Pfam domains



Pfam Description



Protein sequence:

MTNYEFNEETRKLTVIPDVEGVGKDSVLRFSSTAVTGYLEKGLKLVDEGMKTRVMMWVTSISSEKSKHFTAGLKKTRREAEVLRDGVAMEKPF

NbL15g00360.1 fructose-bisphosphate_aldolase_6_cytosolic-like [MW = 44.5 kDa]

No. of times detected



log(intensity)



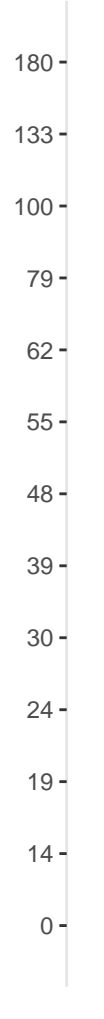
Values from



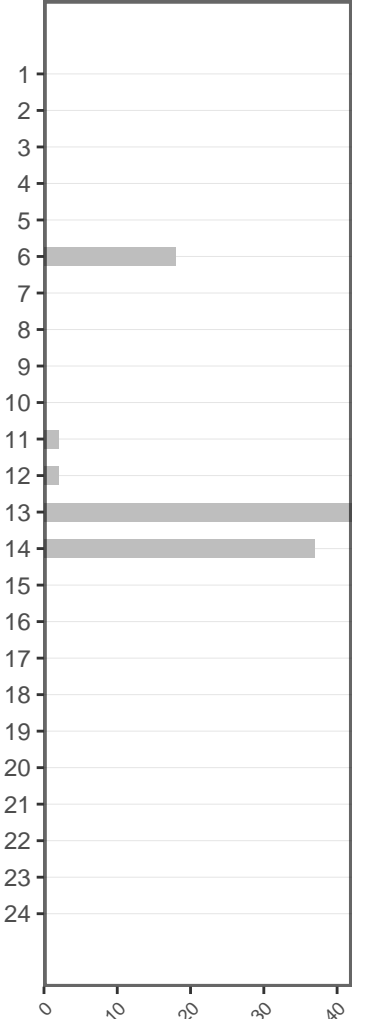
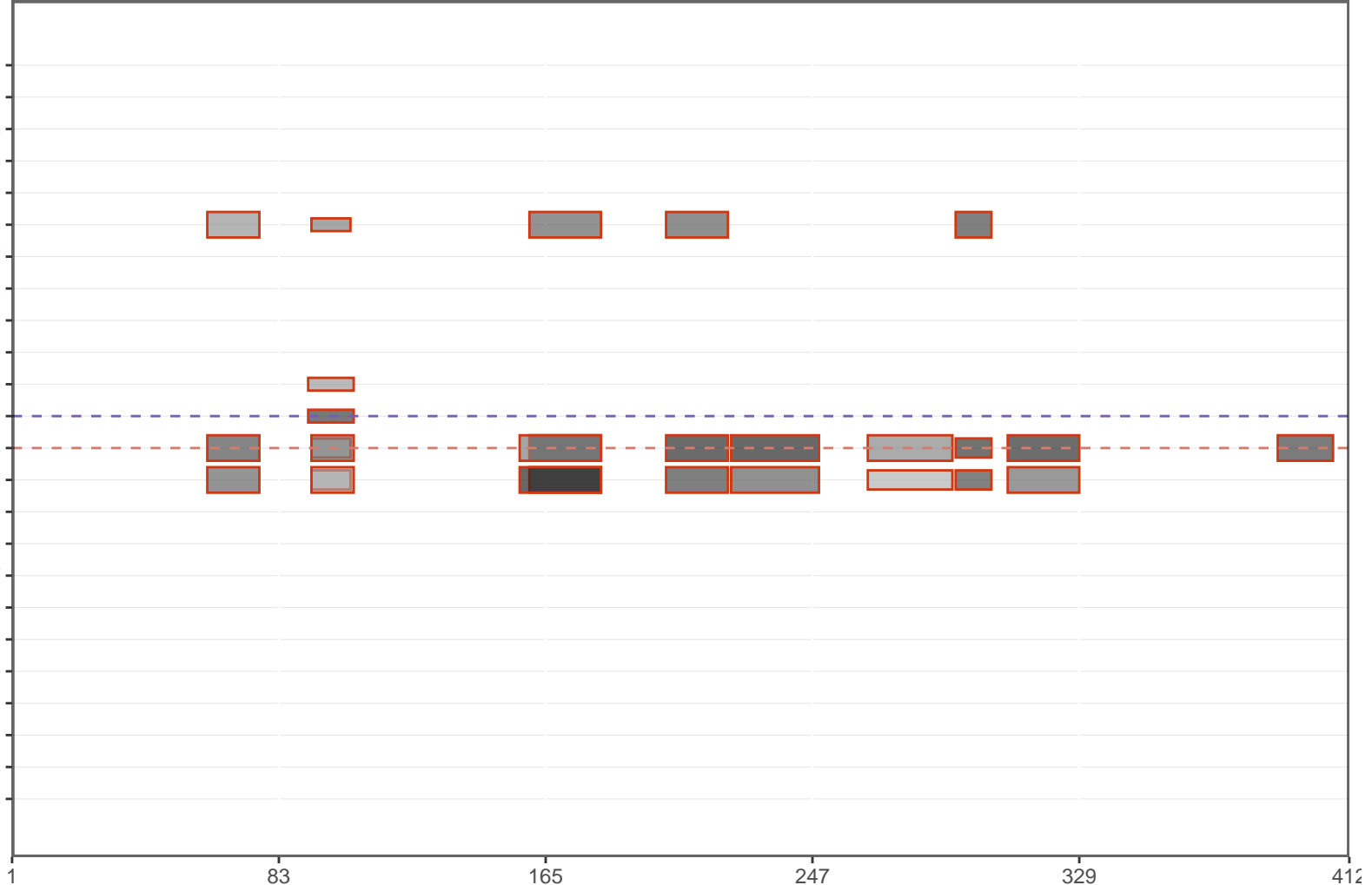
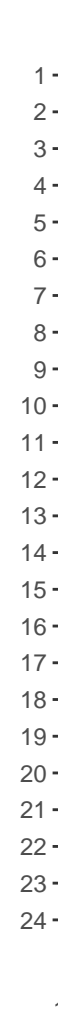
MW indication



Molecular weight

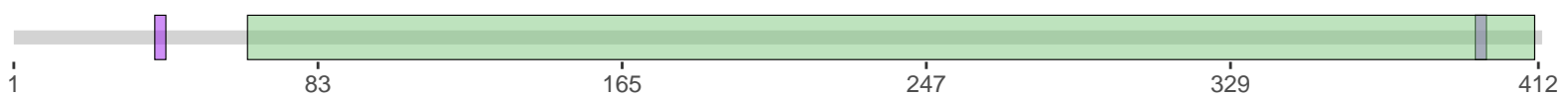


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

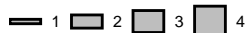


Protein sequence:

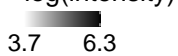
VRALVKGANEPFSQLANDNANGLARVAIGGGNGLPIVPELIVDGGHDNKGADVTERVLAAGYKALNDHVALEGTLLKPNMVTGSGESPKVAPEVIAEYTRVLRGRTMPAVWVFLSGGSGSEEAIRNLNAMNKLGGKRPVTLBFSFCRALGGSTLKAHWGGKVENVEKARAALFTRCKANSEATLGGYLGSSNLSEGASELHKKDKY

NbL15g00210.1 uncharacterized_LOC104247352 [MW = 26.34 kDa]

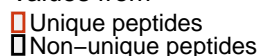
No. of times detected



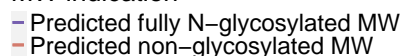
log(intensity)



Values from



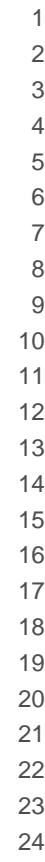
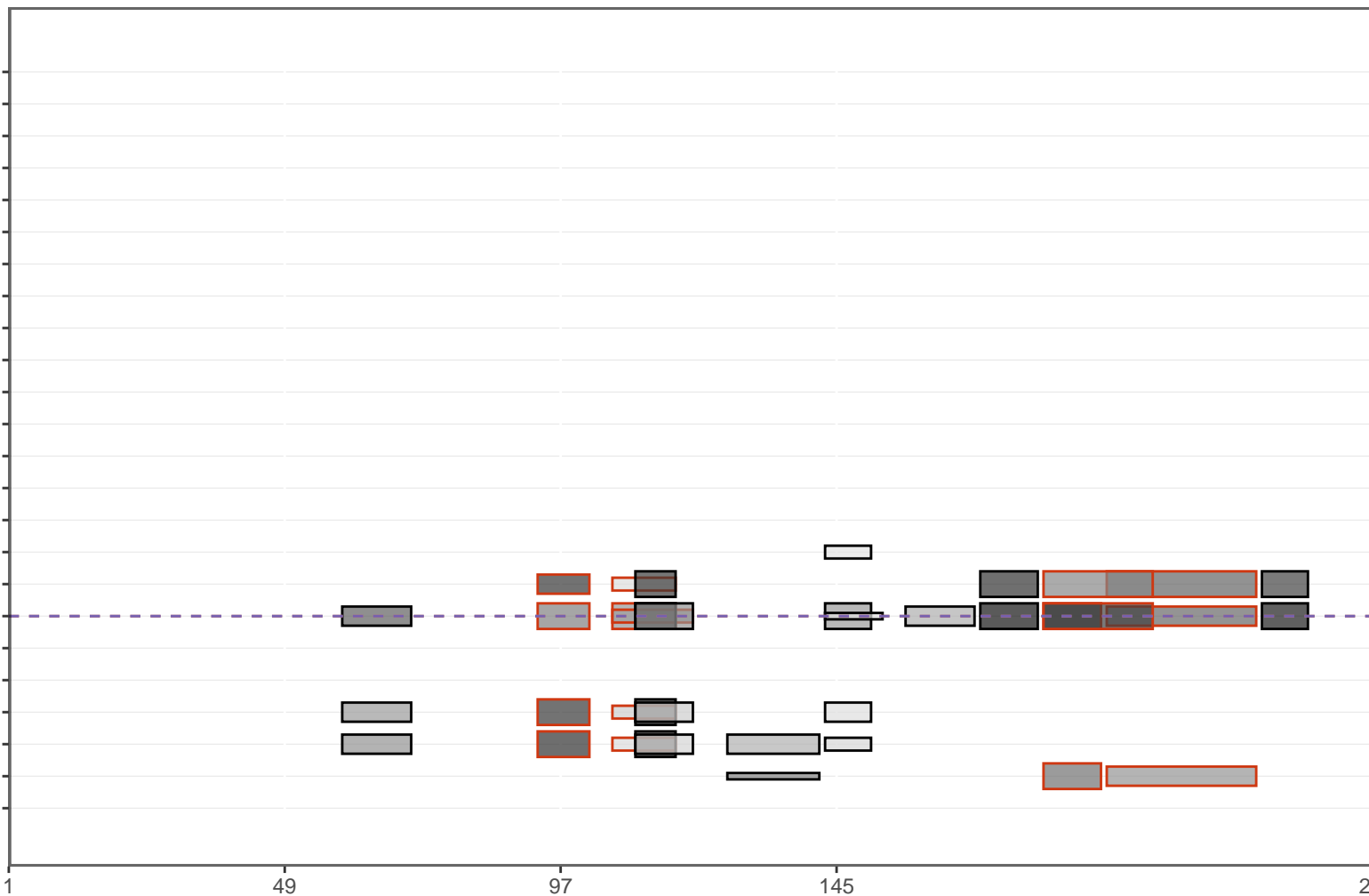
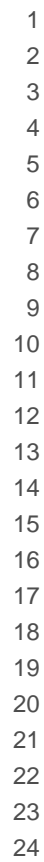
MW indication



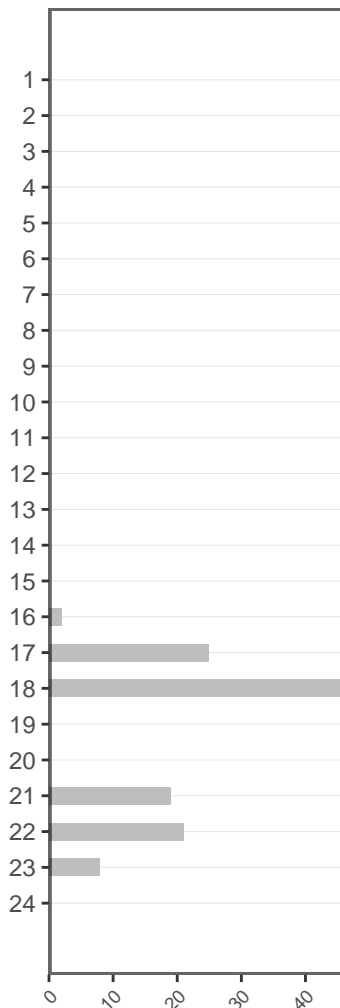
Molecular weight



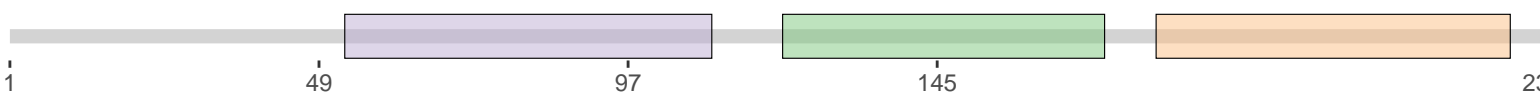
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

ISKIEEANTYKTKQFTYKDGAGFVMDLTSVEEYRLNEKIVGDKAKFLKEGMDGSLFWNGKVIDFELPITVWLTVDVDRPLKGDTAGGGSKPATVDTGAVINFLFIGRGEELVDTRNGGVMRAKEA*

NbL15g00200.1 apyrase_1-like [MW = 51.8 kDa]

No. of times detected



log(intensity)



Values from



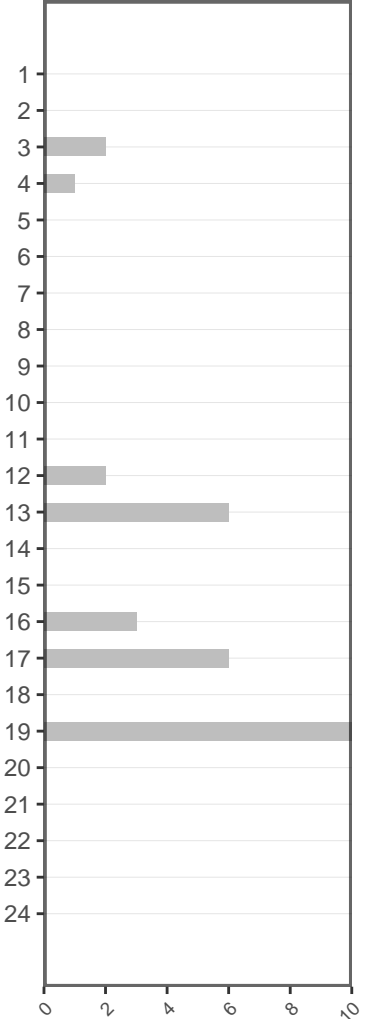
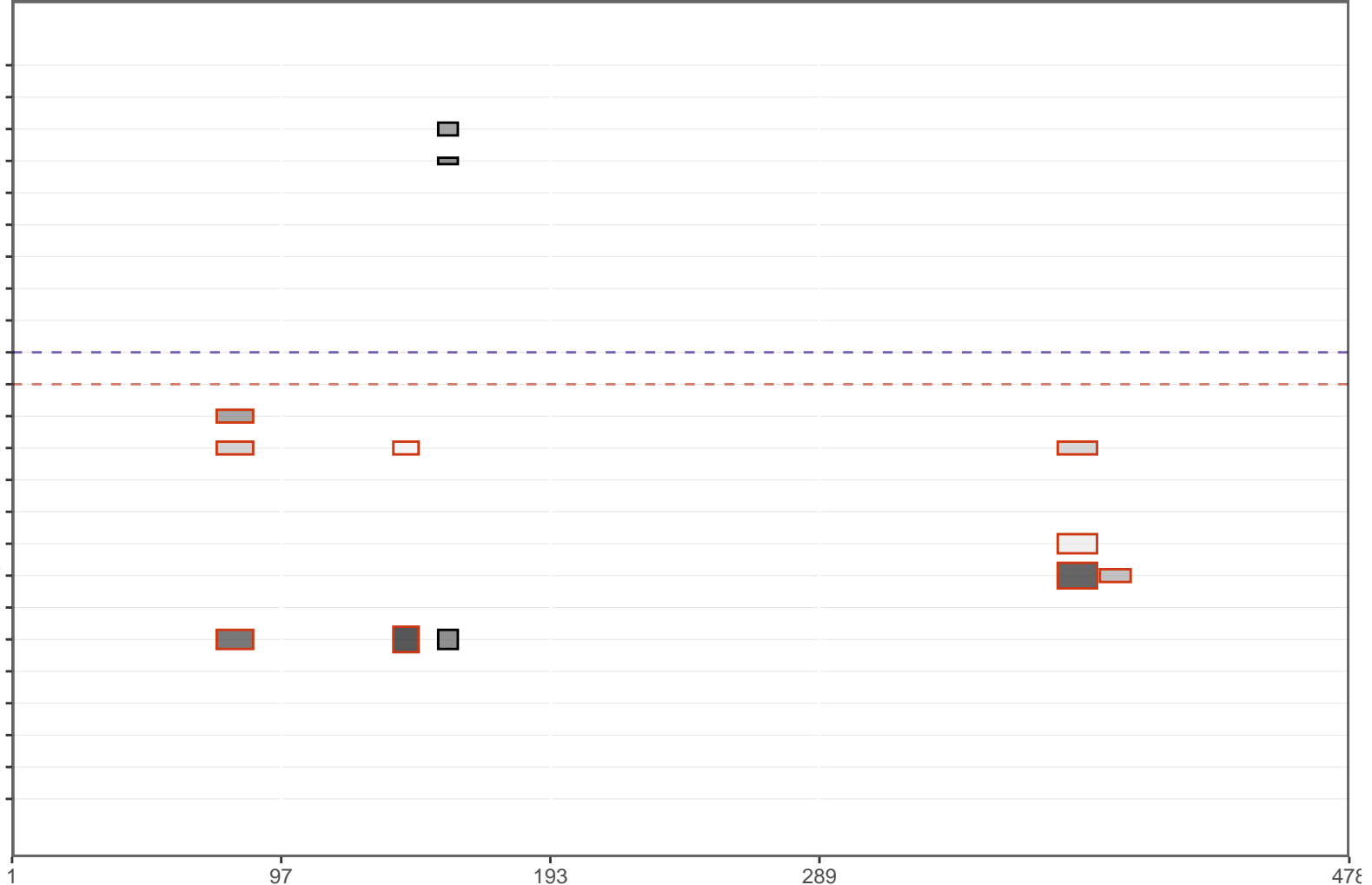
MW indication



Molecular weight

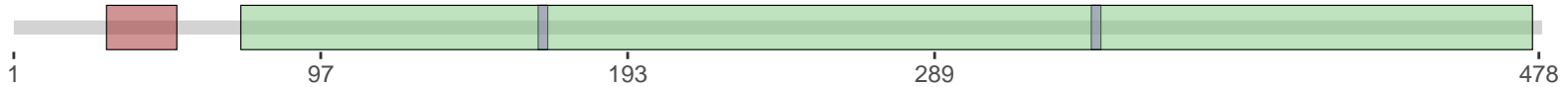


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GGGSVQMAVAISEADAEKAPRLGGEDTYVDEMFLKGAQYLVHSHVLYGGLLAARAERLKVTKESGGSPDLTGHGSGYKYGKTYTASAMSGSGLTNRMLVAKLKVNESACTHMKCTFGGVWNGGGGGGKMFVAFSFFDRAVEVGFVDPNAVAWVRRPDPFESAAGRACDTRIDDAKATFFRVDPNLFLQMDLVYQYTLVDGFLDARGEMTLVKKVYKNSLVEAAWPLGSAIEVASSMN

NbL15g00180.1 uncharacterized_LOC104223818 [MW = 66.21 kDa]

No. of times detected



log(intensity)



Values from



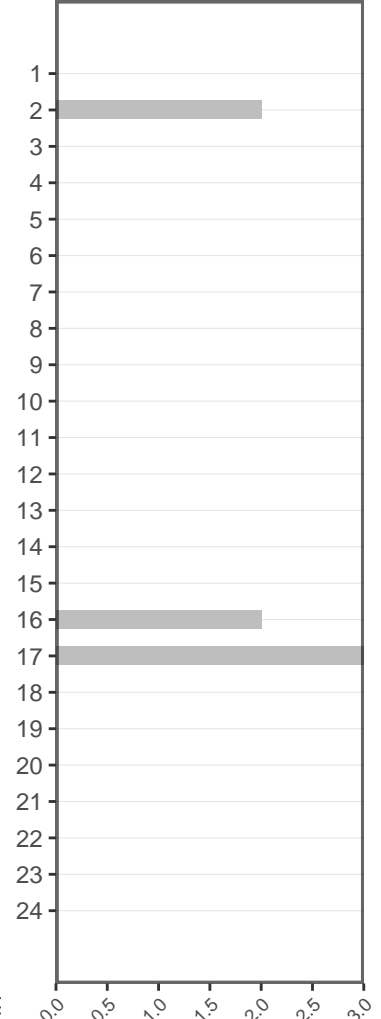
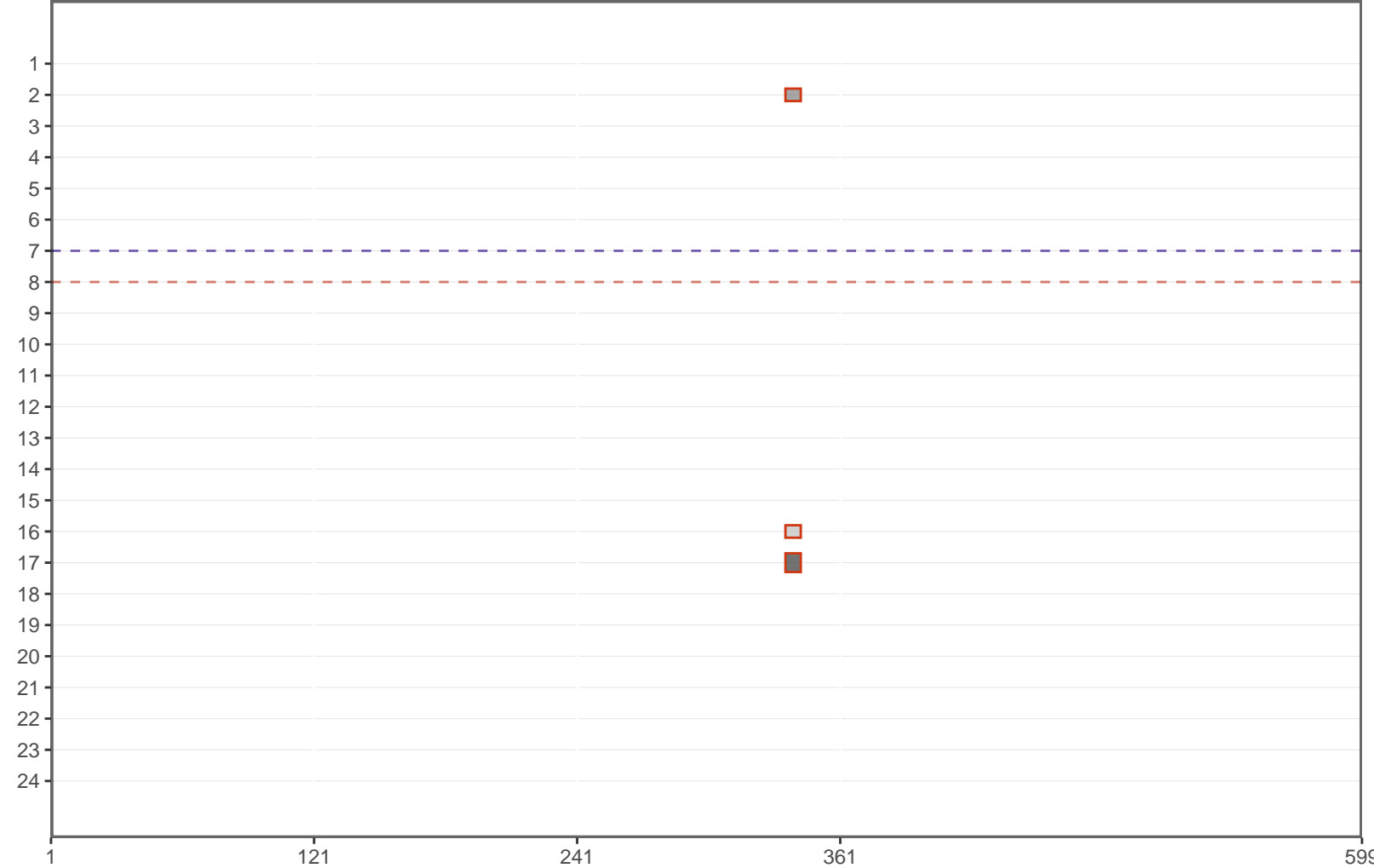
MW indication



Molecular weight



Gel Slice



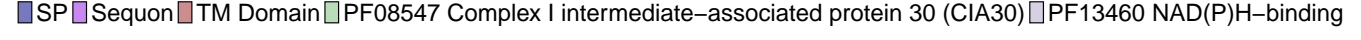
Protein length



Pfam domains



Pfam Description



Protein sequence:

SEDSLNGVEVROGTYFDQVASKYDGGMDATFEFFTERGEAFSGVYFRGGVVELTRKLSPLGLYFLDRYEGLVFVDDGNREYVILEAGPSADTTGSKLYFARISTKAGFCRVRVYFSSFRPVPDPPPLDFLVLHFLTRFPRRGRPDGSPGVNDLRFQFQLEMEYKALPTGGQTFVIVSGTGGIEPTTRREGVLRKAKRAGEDSLRRRGLGVTYRPGPLMEEPGGQRALFDGGRNRISGGISGADVADKVKALHDSTARKKFDVNGYEVVAEPQKELYEVLAHLPI

NbL15g00090.1 26S_proteasome_non-ATPase_regulatory_subunit_12_homolog_A-like [MW = 39.02 kDa]

No. of times detected



log(intensity)



Values from



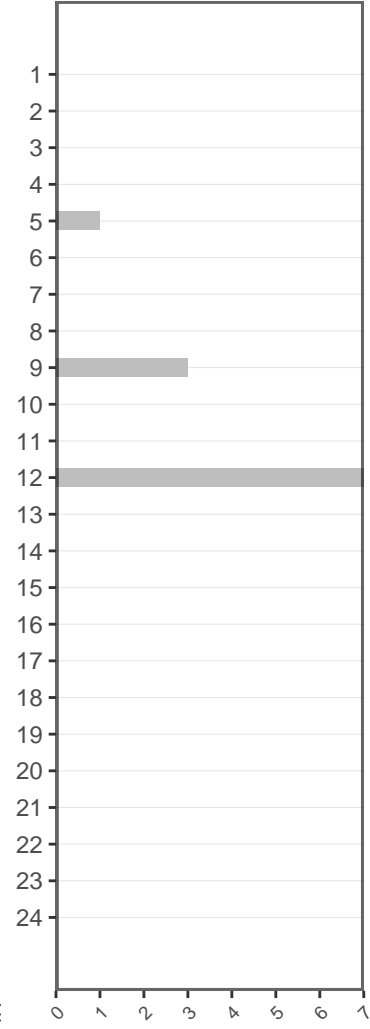
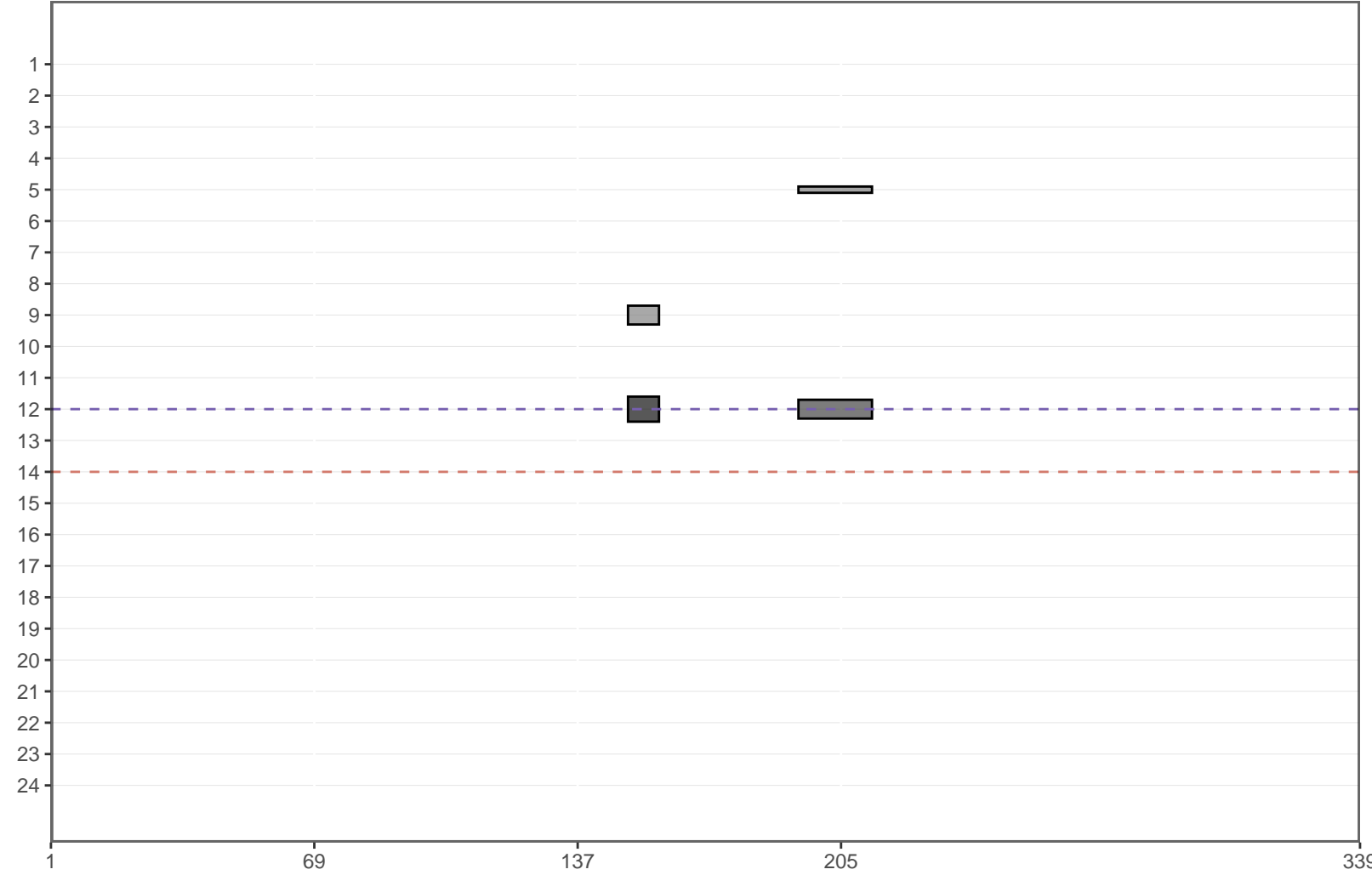
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



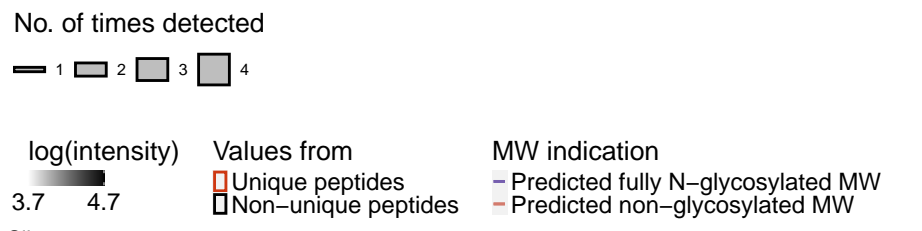
Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

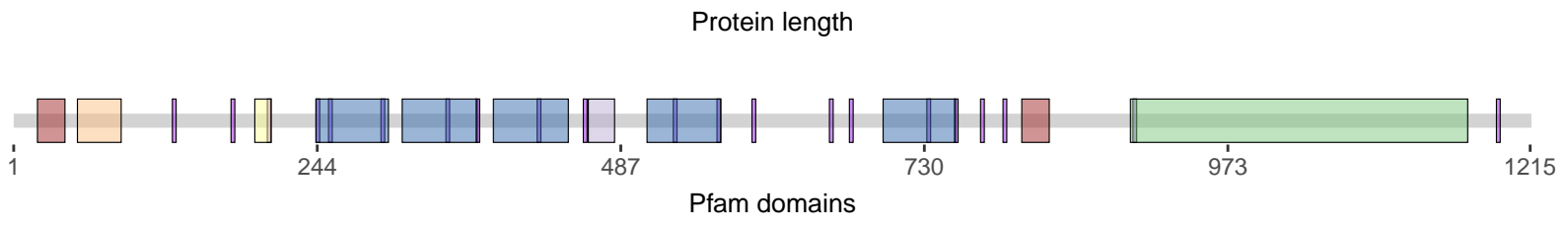
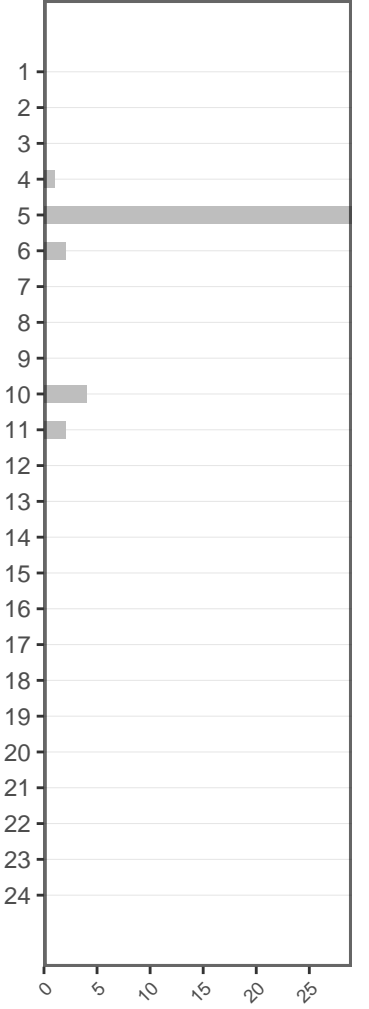
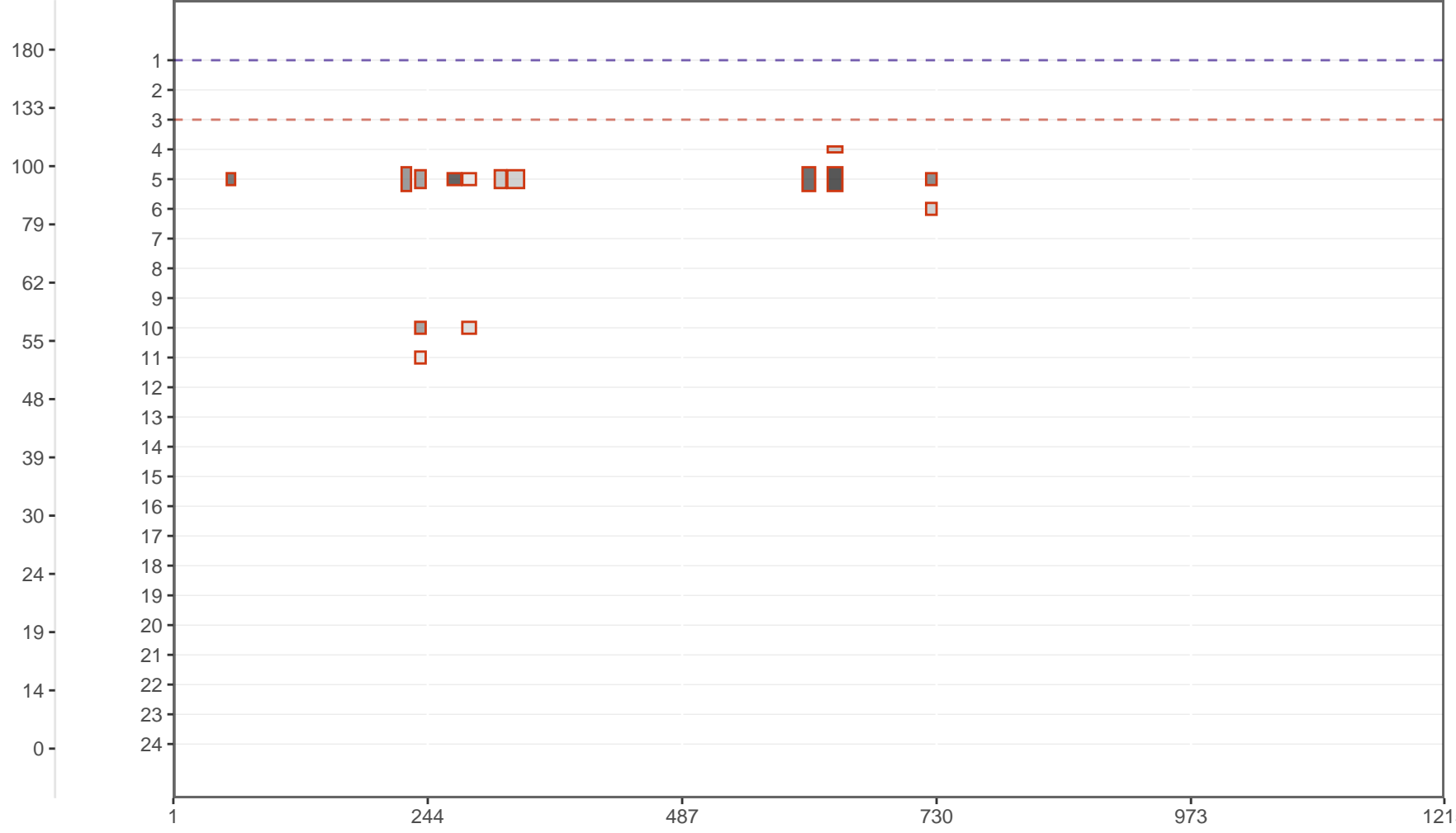
CVRLCLRDQYVRAQLSRKINPRVFEAVPSKEKKPKKEGENVVEEPAADIPSELLKQYVQLMIRYVSHNDVLEICRCYKAYEIPSVKEDPAQWVPLRKGWYVLSPHDFMGGSLHNSTLEDKQLSEPHFRLLKQLTMEVQWNTALWNTFKMISLKKRIGLWVTRLPKISD

NbL15g00030.1 systemin_receptor_SR160 [MW = 132.88 kDa]



Molecular weight

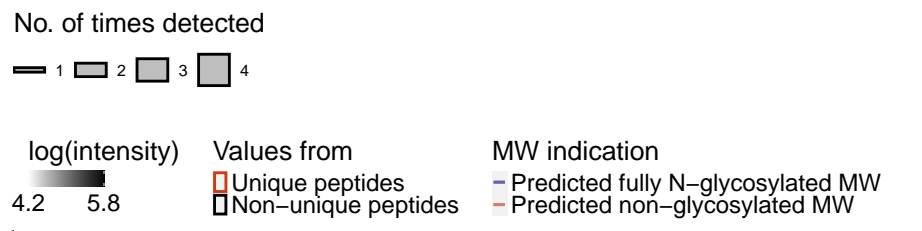
Gel Slice



- Pfam Description**
- SP
 - TM Domain
 - Sequon
 - PF00069 Protein kinase domain
 - PF00560 Leucine Rich Repeat
 - PF08263 Leucine rich repeat N-terminal domain
 - PF13516 Leucine Rich repeat
 - PF13855 Leucine rich repeat

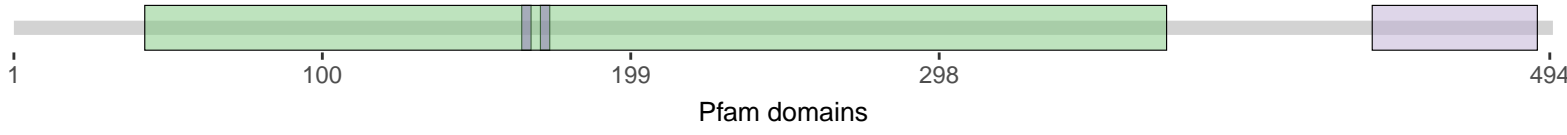
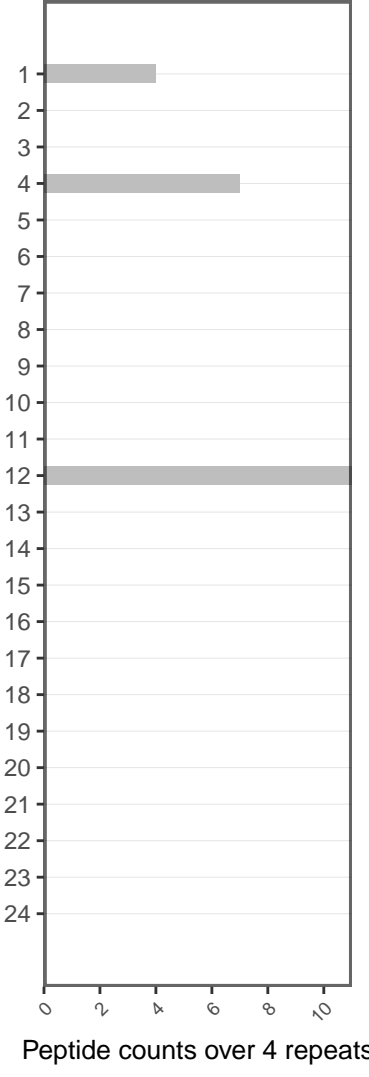
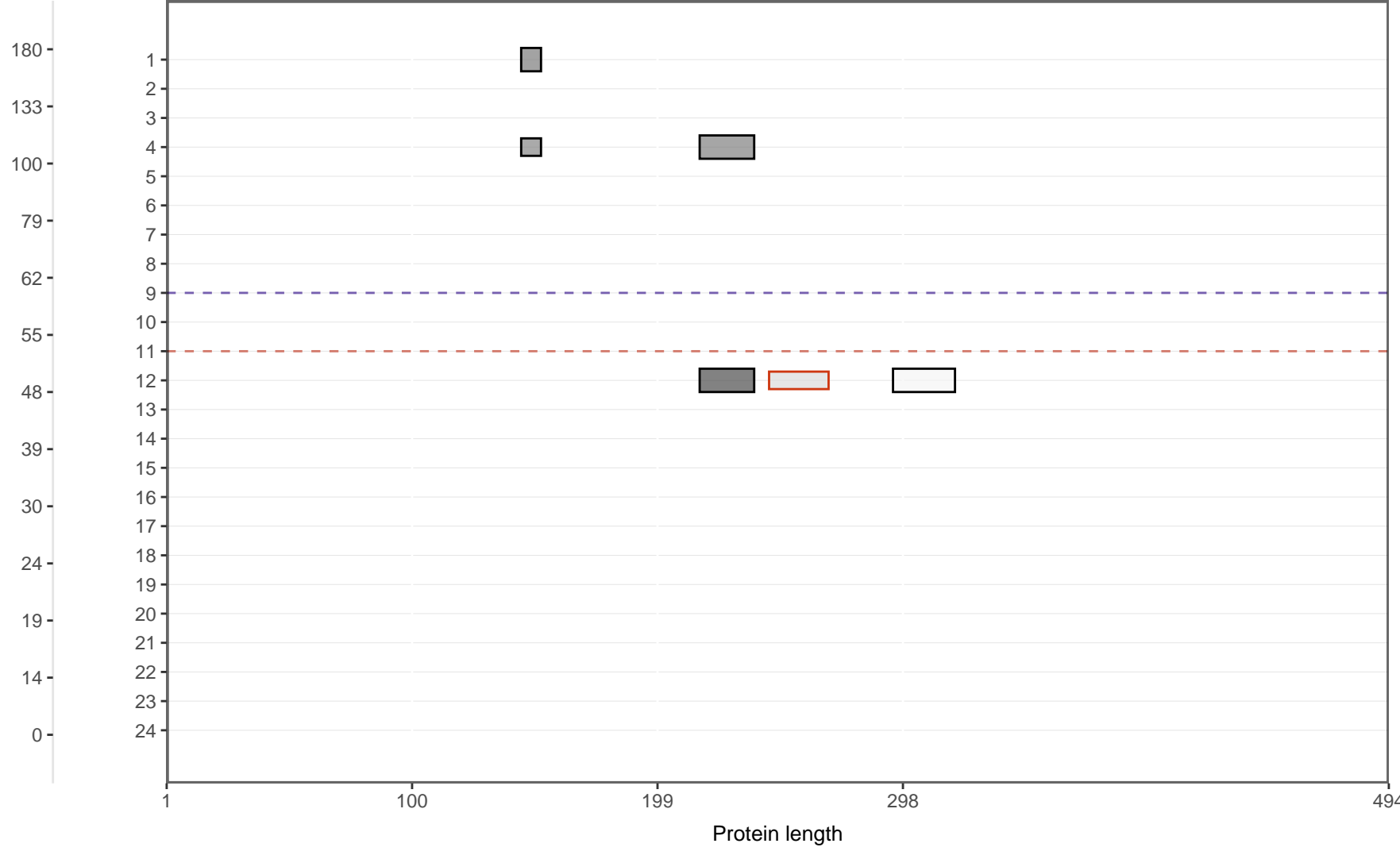
Protein sequence:
 GPLFKQSGNAVALLTGKRVYKNDGSKKECHGAGNLEFGGIRGEQLDRISTRHPCNFRVYRGGFQPTFNINGEMFLDLVYNKLEGGSPKELGSMYYLBIKLNIGHNDFGQVDPQELGGLKNAWLDLGVNRLNGSIPNSLFTLLGELDELNNLITGPIRESAPDFTFDFQRFANTSLGQYPLGPGGVSNSNSGQHKSHRKGASLAGSVAMGLLFLSFGIFGLIWAETKRRKKKEALEAYMDGHSNATANSAAWFTSAREALBINLAAFEKPLRKLITFADLEATNGI

NbL14g22030.1 fumarate_hydratase_1_mitochondrial-like [MW = 53.3 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00206 Lyase
- PF10415 Fumarase C C-terminus

Protein sequence:

YATQVYKIDRVLGALPHMYGLAGGGTAVGTGLNFKGDFDKIAAAVAEETNLPFVTAENKFEALAAHDAFVETSGAINVAASLMKVGNDIRFLGSGPRGLGELLPENEPGSSMPGKVNPTDCEALTMVGAQVMGNAHWVTGGSGNGHFELNFKPKMANALLHSVRLGDSASAFENKQVVRGIGANTERIAKLLHESLMVTLGNPKIGYDNAAAQKAKHKEGTSLSKDALNLGVLKSEEFDDLVVPEKMGPTD

NbL14g21940.1 methionine_aminopeptidase_1B_chloroplastic [MW = 39.53 kDa]

No. of times detected



log(intensity)



Values from



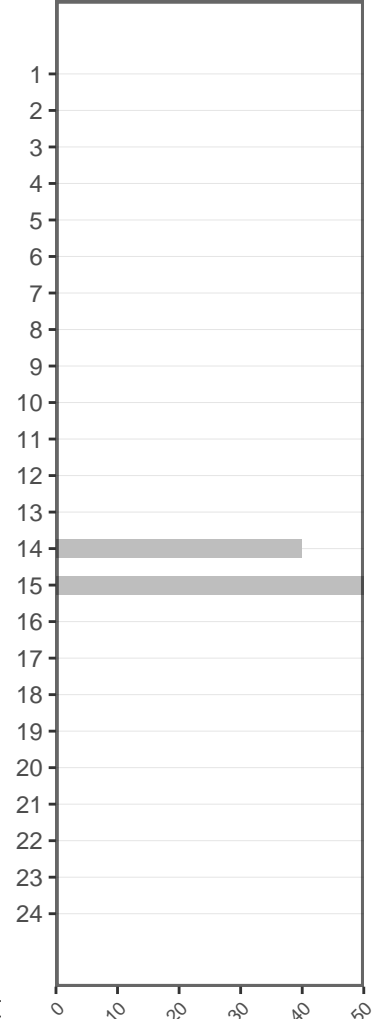
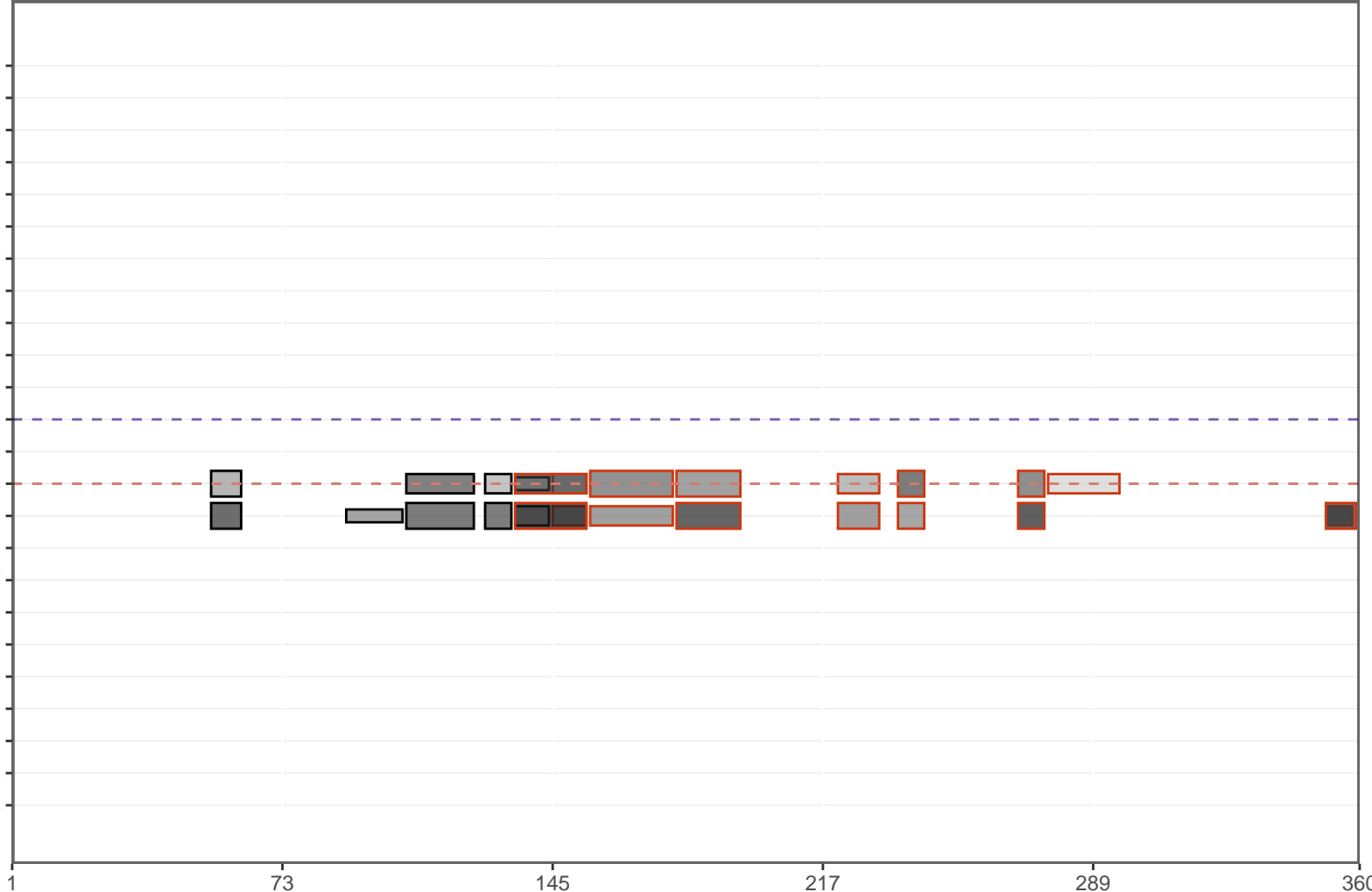
MW indication



Molecular weight

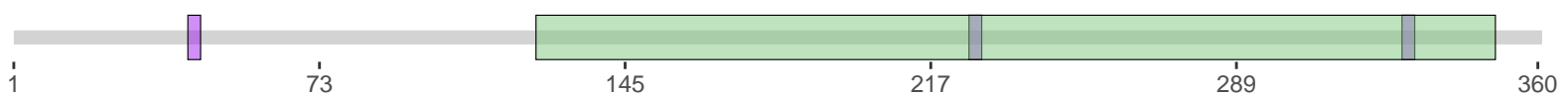


Gel Slice



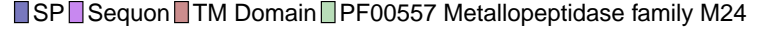
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

'SPLGYGGFPKSYGTSVNEGMCHGIPDSRLGDGDHINDVTVYLVNGYHGDTSKTFFGQNVSESKRLVAVTEECLEGRGAVCKDGLFRKIKRRISEHAKEFGYGVVDRFVGHGIGTVFHSSEPLVHHRNDKSGSMVEGGTFTIEPLILGSGTEGVTVEDNWTFLADGTPAAGFEHLTKTGAEILKY'

NbL14g21860.1 HD_domain-containing_protein_2 [MW = 37.33 kDa]

No. of times detected



log(intensity)



Values from



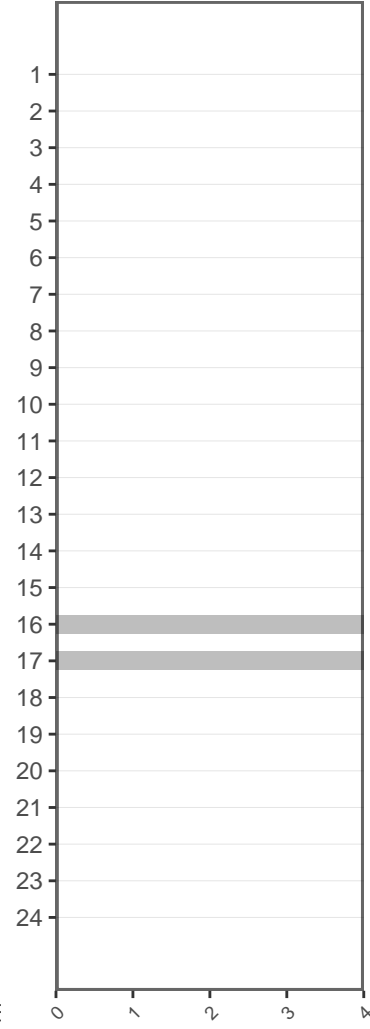
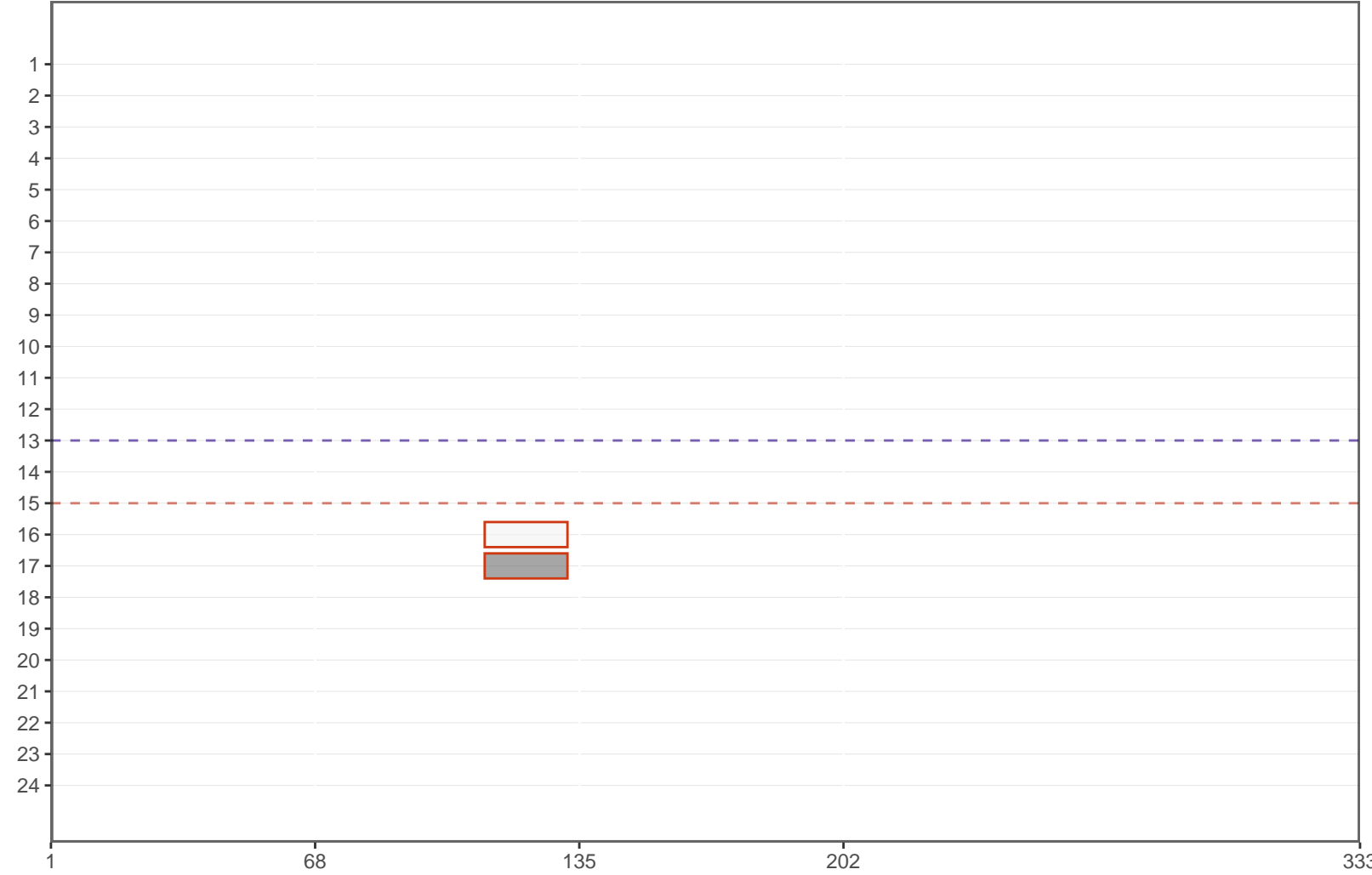
MW indication



Molecular weight



Gel Slice

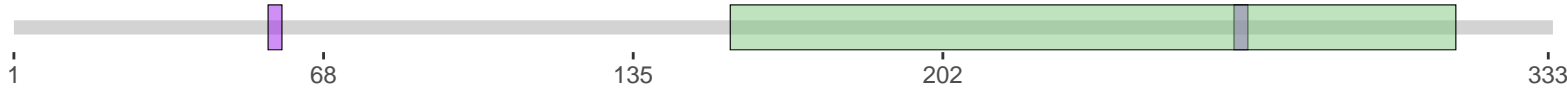


Peptide counts over 4 repeats

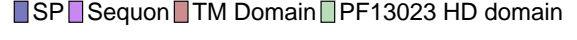
Protein length



Pfam domains



Pfam Description



Protein sequence:

.CHSLKTKRKGWVNHGKGPESGIADHMYLMSVMAIAGLPLDVRNRERGHMAVHDIAEAIVGDTFSDGVPKAKSRREGAALNEMCEIIGGGMRARAEIKELWGDYENNALEANLYKDFDKVEMILQAFEYSEHGKVLDEFLLSTAGKFGTEIGKSWAAEHSRRNRLENRVN

NbL14g21720.1 protein_decapping_5 [MW = 63.98 kDa]

No. of times detected



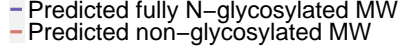
log(intensity)



Values from



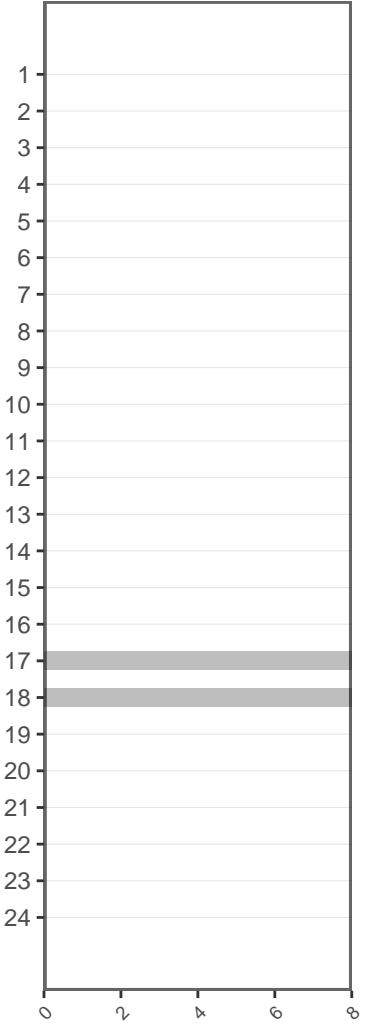
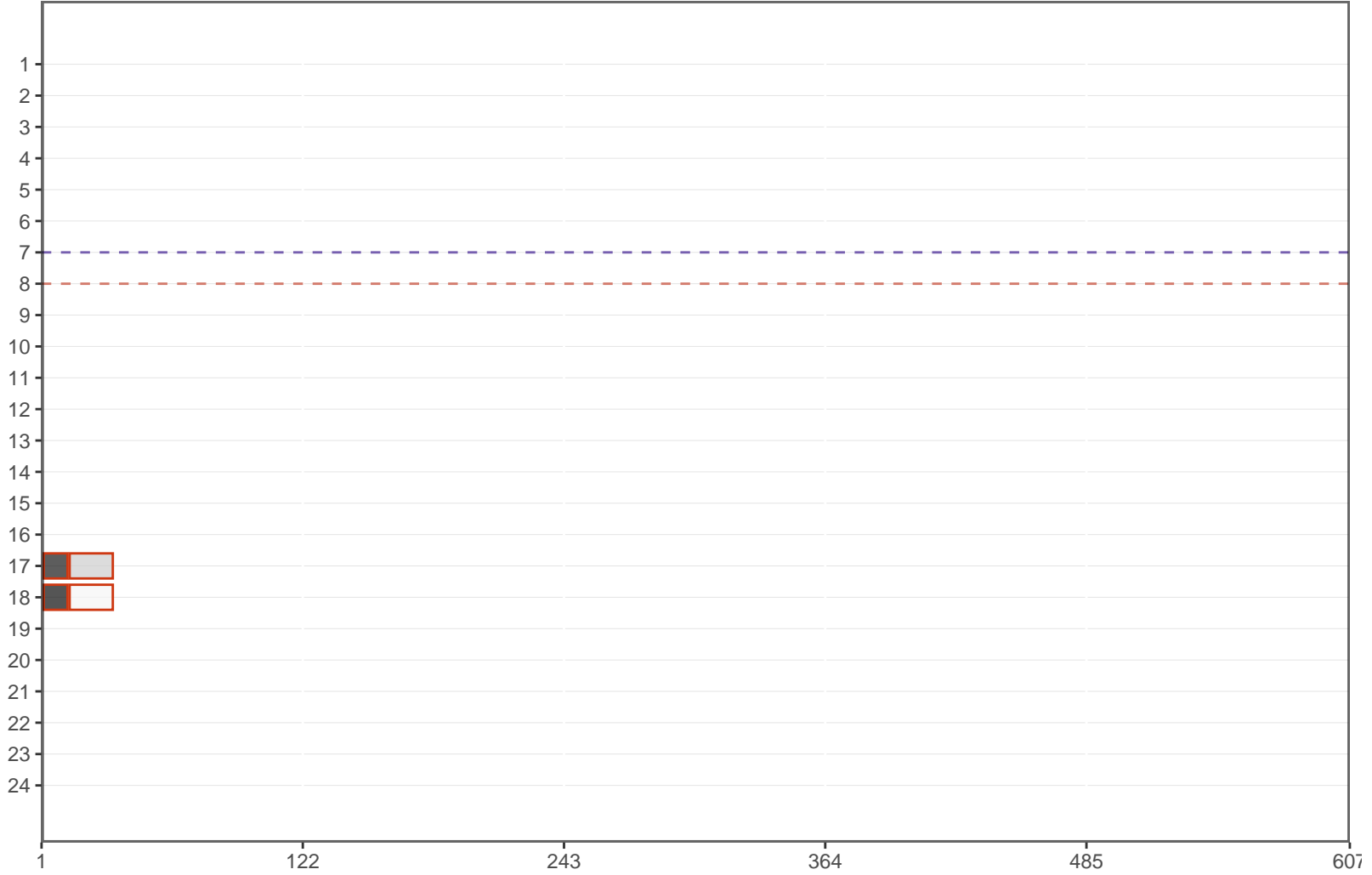
MW indication



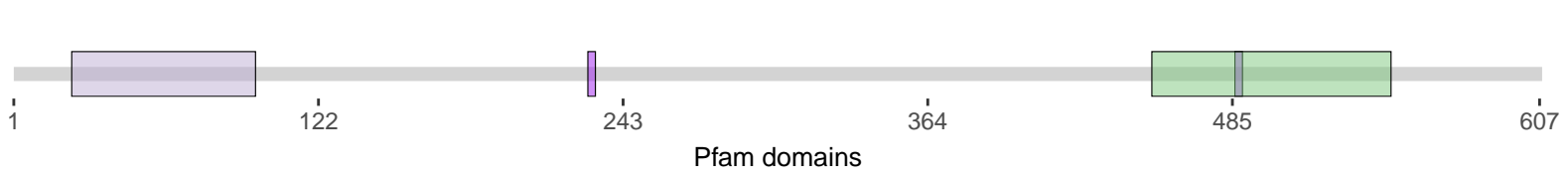
Molecular weight



Gel Slice



Protein length



Pfam Description



Protein sequence:

VSSIAPSLSASLFLPLLTETFDNPNVDPKPKNFVPSGALGSGVSTMGPSGSLVETPTPLSLVTPGQLLGFDPIDVPTSGTGTAKDKVEVQVFPAPSBETAFLVYKTEAGPPLPLFPQTRVQKTNENAPYQARVNNYRGRGRGMGVSRVPTKFEEDFDMMANKEFKKDEWVWGLGKSNREGDGNSSDEISFNKYDDDLPKIDKPPVYKDKDFDLSLSNALDNDPEHGRTRFSEGRKIDVETFGDFSRVYRGRGRGPRGPRGRGSGYYGRGGYGGY

NbL14g21620.1 uncharacterized_protein_At1g26090_chloroplastic-like [MW = 12.16 kDa]

No. of times detected



log(intensity)



Values from



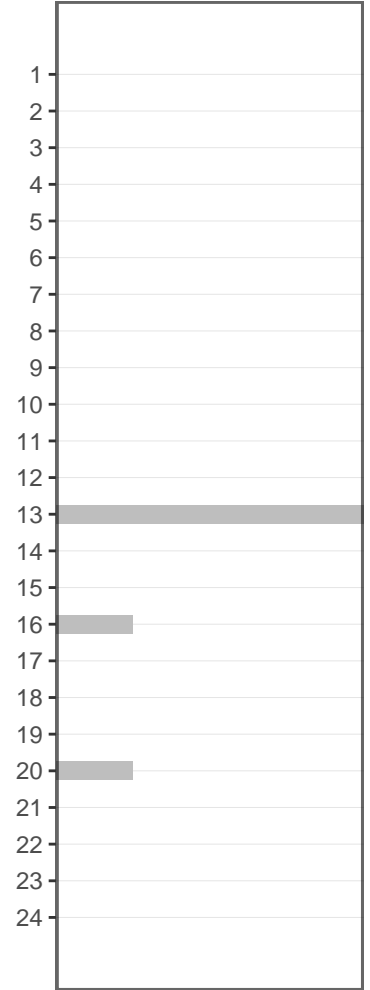
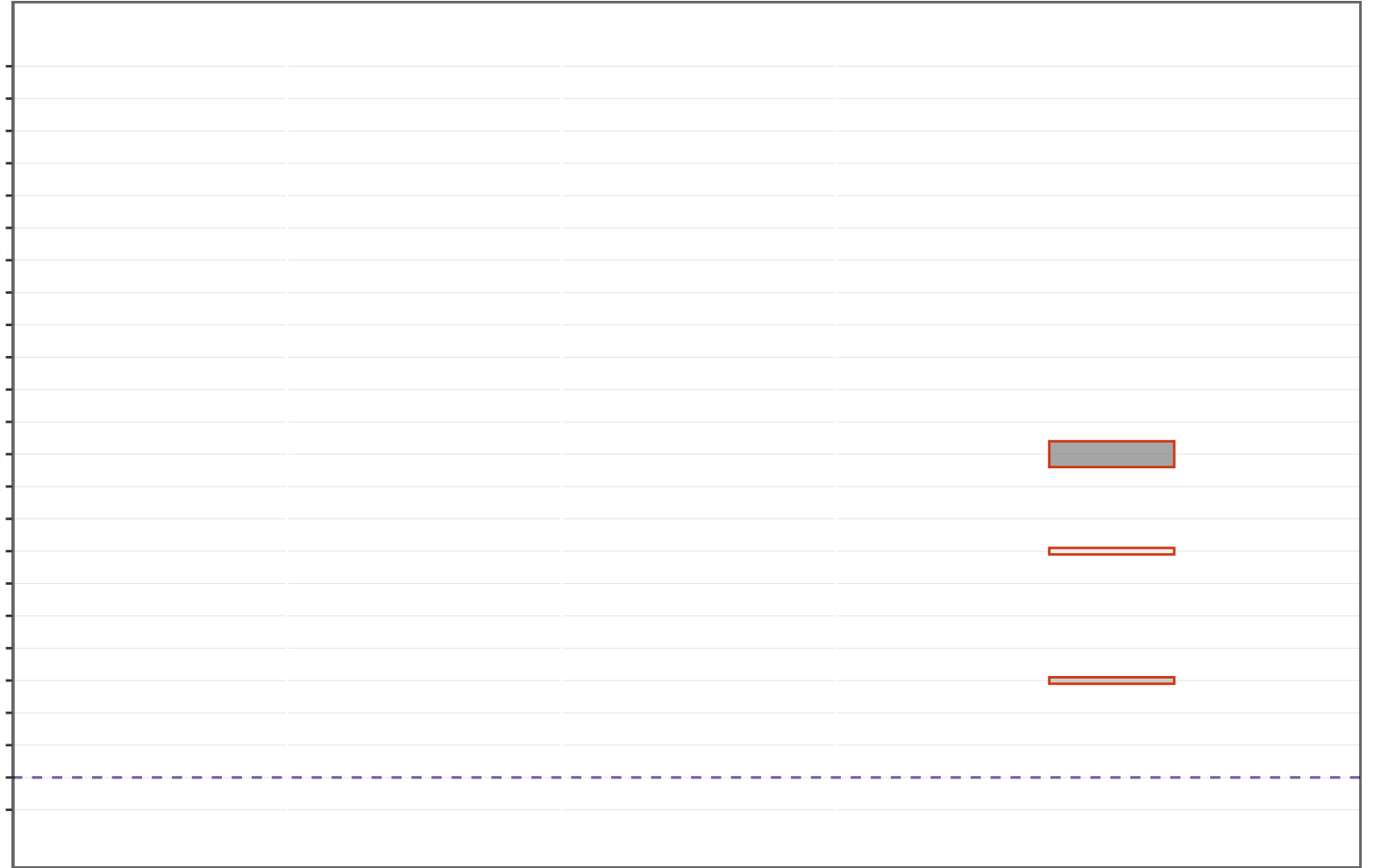
MW indication



Molecular weight



Gel Slice



Protein length

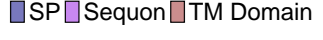


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SISTEEMIRMGASKARVLYKYLNRVAEKTDLGRLAGPRLRLRVDEAMFLSGRRKLNINQKTSSEIWDV

NbL14g21380.1 MFP1_attachment_factor_1-like [MW = 16.36 kDa]

No. of times detected



log(intensity)



Values from



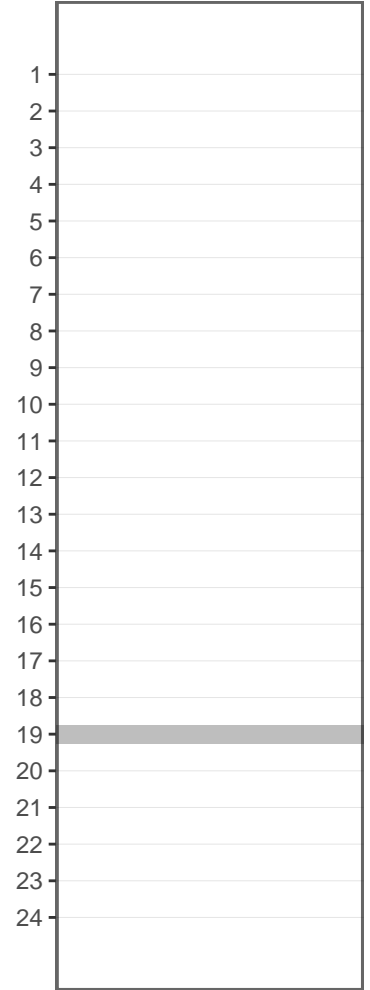
MW indication



Molecular weight

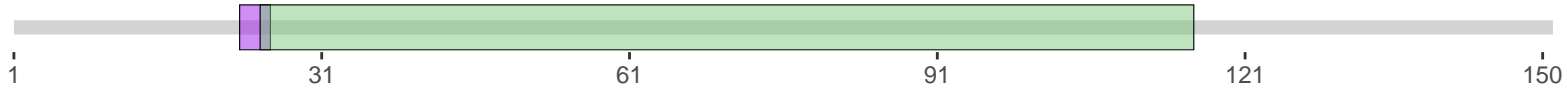


Gel Slice



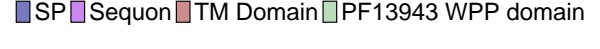
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

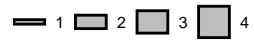


Protein sequence:

INEEASDIARSIIEEAFTFAGSVPDDGHEIQVYTKKIKRMLDAVKRBAATTSPEAGTKPSEGLVDASESAHTGDHSIESEP

NbL14g21330.1 polyadenylate-binding_protein_2-like [MW = 72.04 kDa]

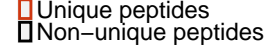
No. of times detected



log(intensity)



Values from



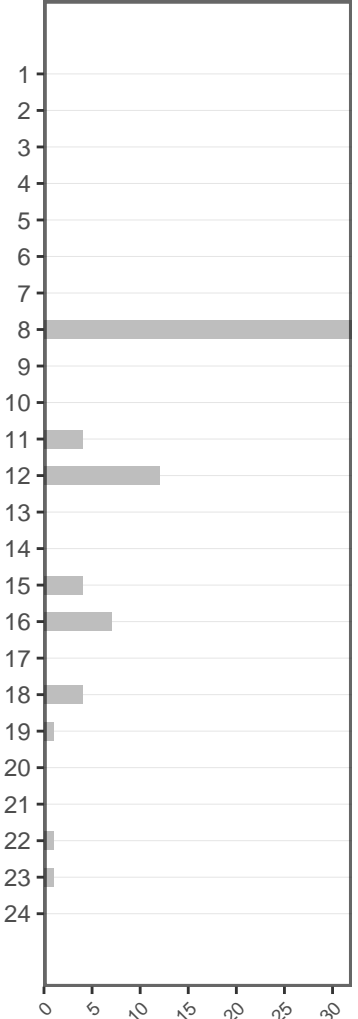
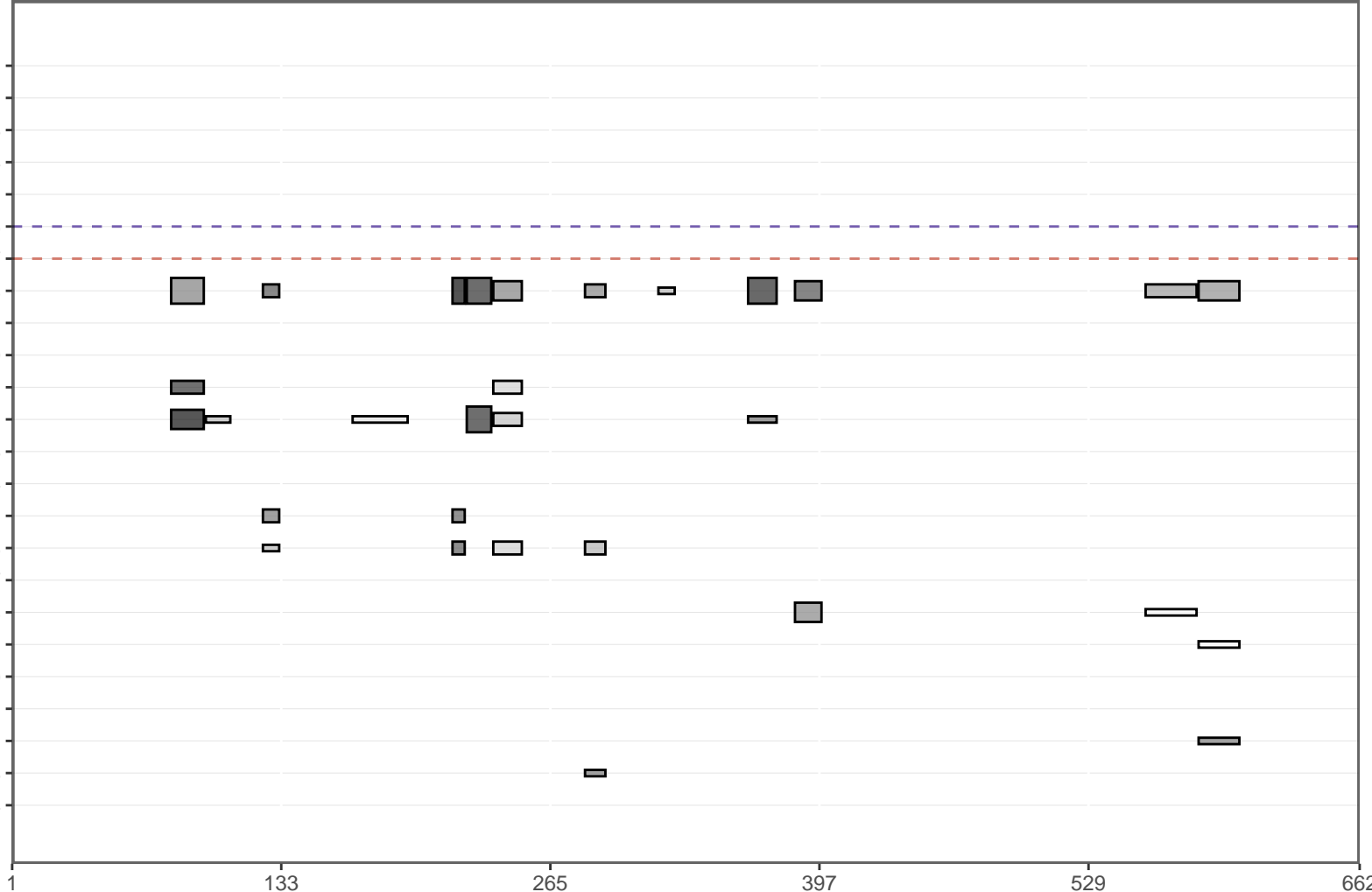
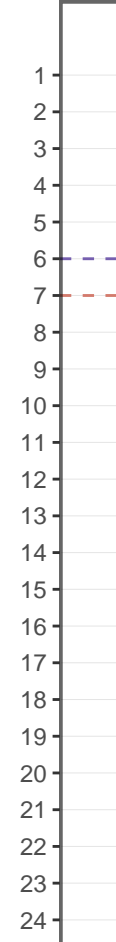
MW indication



Molecular weight

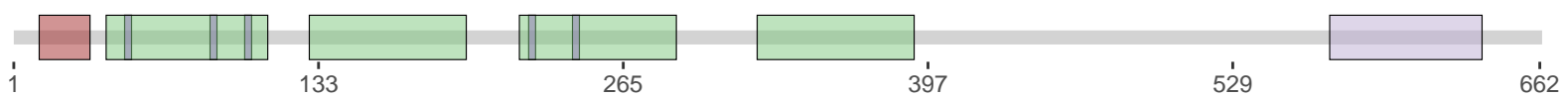


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- PF00658 Poly-adenylate binding protein, unique domain

Protein sequence:

LNLVYKXLDLTDIDKELKELFSEFGDMITSGKVMRDPGSGVSRGGGVAFTSTEEASRALSEMNKGMVSKPLVYALGRKEERRAKLGLVQAGFSQLRPVAMPPLSRPMVYPPGVPDGGQGLFYGGSPMIPDQAGFGVGGGLVPGIRPGGAPMNFVPLVGGGGGGRRGRRGAGFVGGTQGPLMPLMGQMLPRGRMRYRPPGRNGPEGMPGVPDGMMLVPPVDMGGMLPRDSAMGSPMPTISLALANAPPEQQRITLGEISVPLVQLEIHAAX

NbL14g21320.1 50S_ribosomal_protein_L4_chloroplastic [MW = 34.4 kDa]

No. of times detected



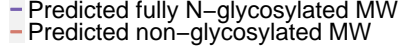
log(intensity)



Values from



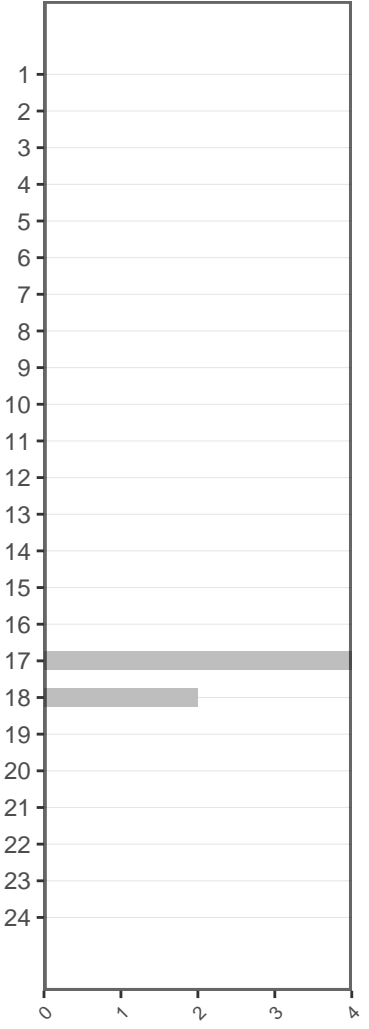
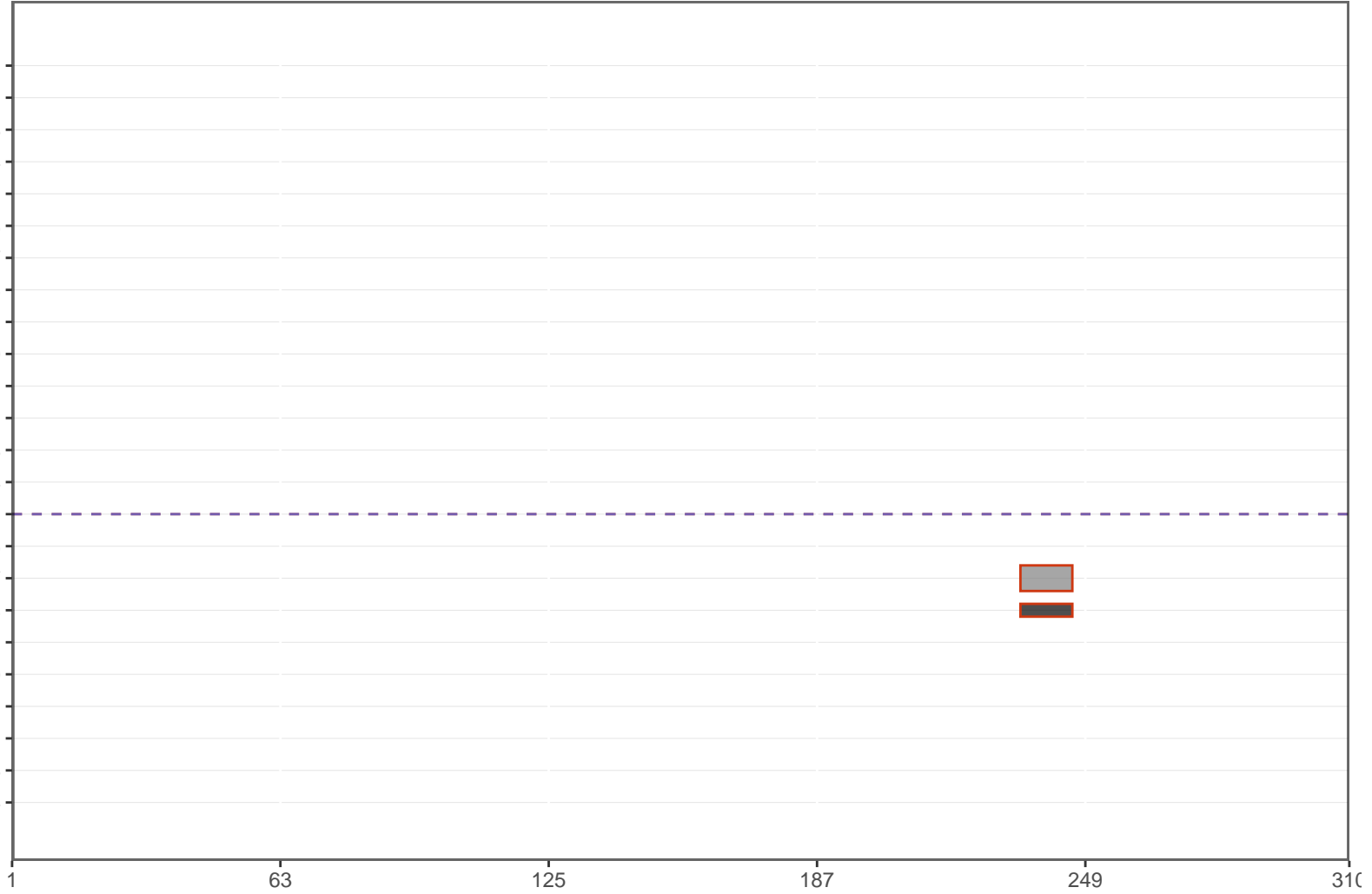
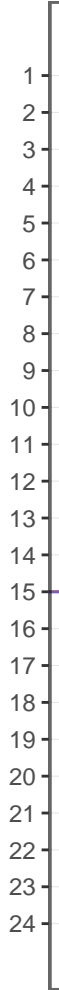
MW indication



Molecular weight

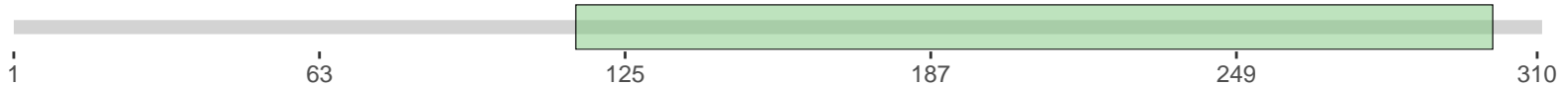


Gel Slice



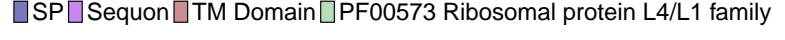
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

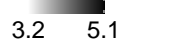
GTHSTKTSIEVSGTGRKPKWRKQGTGRARHGTLRGAQFRGGAAAHGPKPRSHAKLNKKVRRLLGKIALSARAEGLMVFEDLELSHKTKNVYVFNQLENTKLLLVDDGGPSEKIKLATQNVHYVNLPSGLNVAIBLLHDTLVMRDVAWRRVEMHTPINR

NbL14g21060.1 protein_EXORDIUM-like [MW - SP = 31.13 kDa]

No. of times detected



log(intensity)



Values from



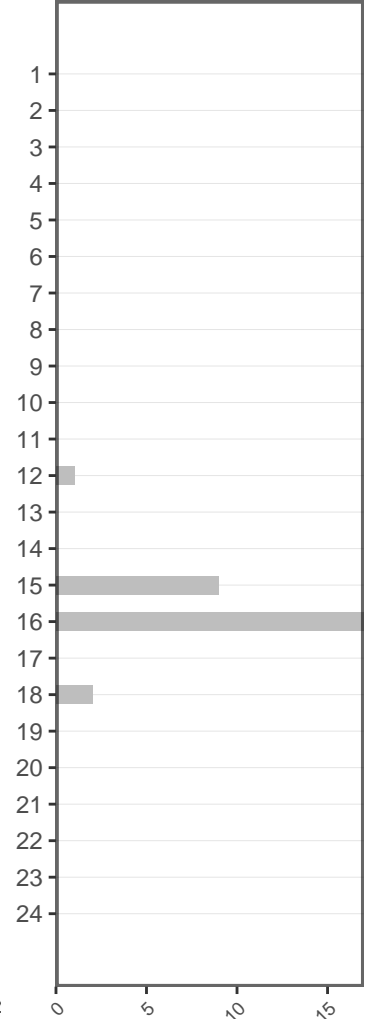
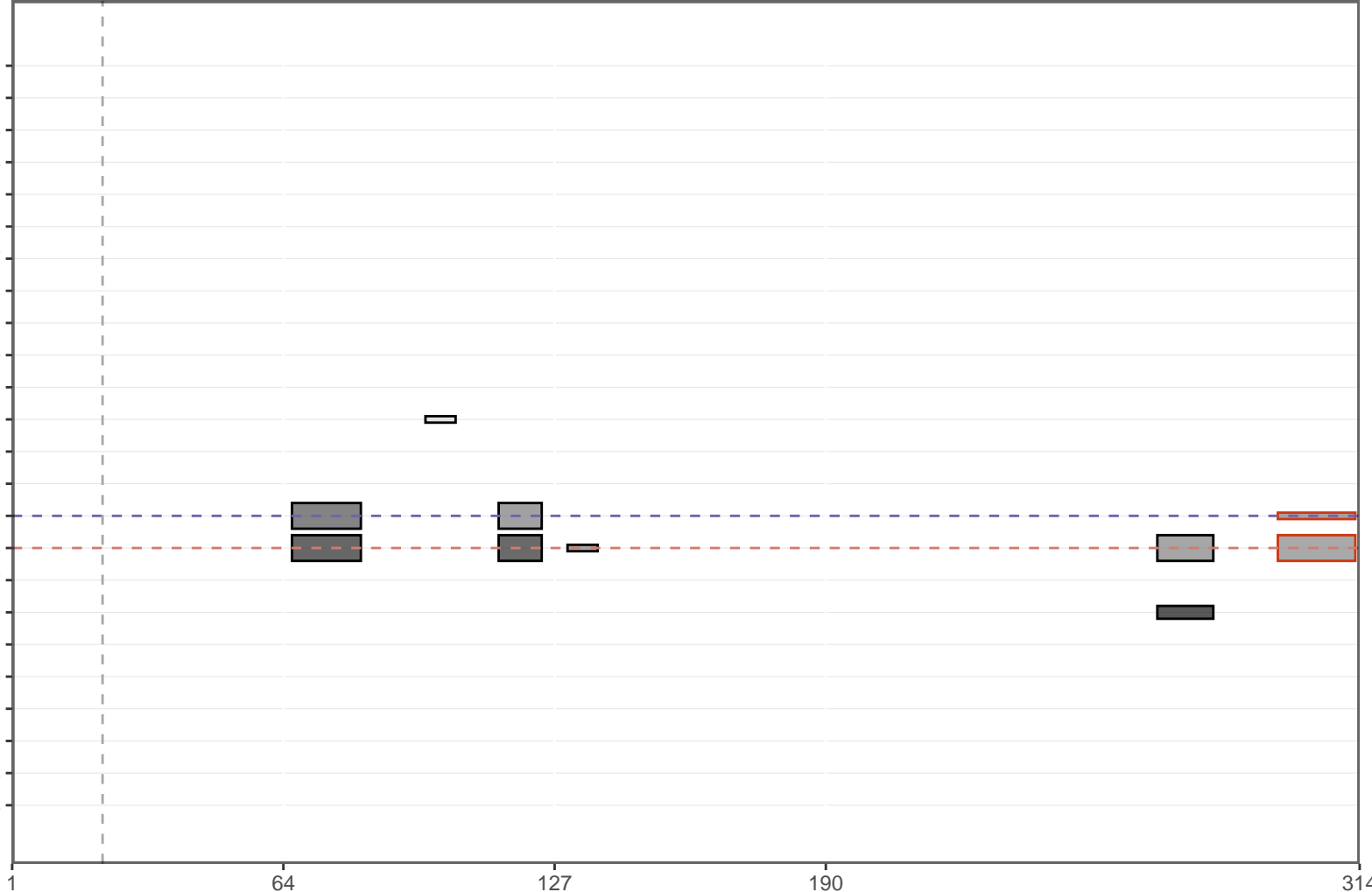
MW indication



Molecular weight



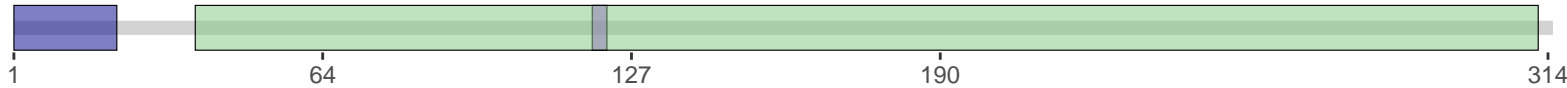
Gel Slice



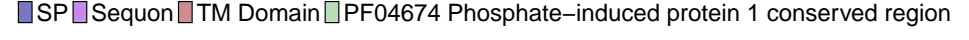
Protein length



Pfam domains



Pfam Description



Protein sequence:

VLTASDAVVDGFCVNRDGHGSSKGAIRGKTKYKFAWVWQNSSETGCGAGYCAWPHHPIYGPQSPPLVAFNNDVGVDDGMVNLASLLAGTATNPFNGNGYVGGADAPLEAASAGPQVYAKGAYPGVAGDLLVDKTTGASVNAHGANGRKIVLPLALYDPTSTGSLV

NbL14g20920.1 cryptochrome-1-like [MW = 77.06 kDa]

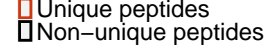
No. of times detected



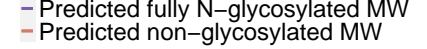
log(intensity)



Values from



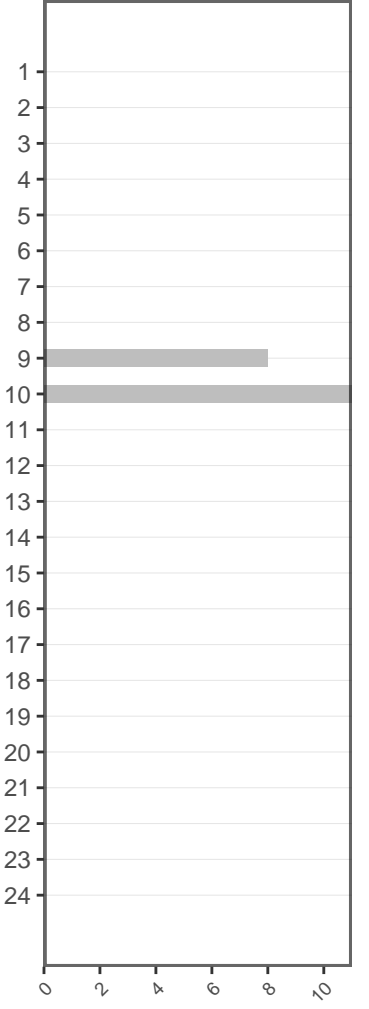
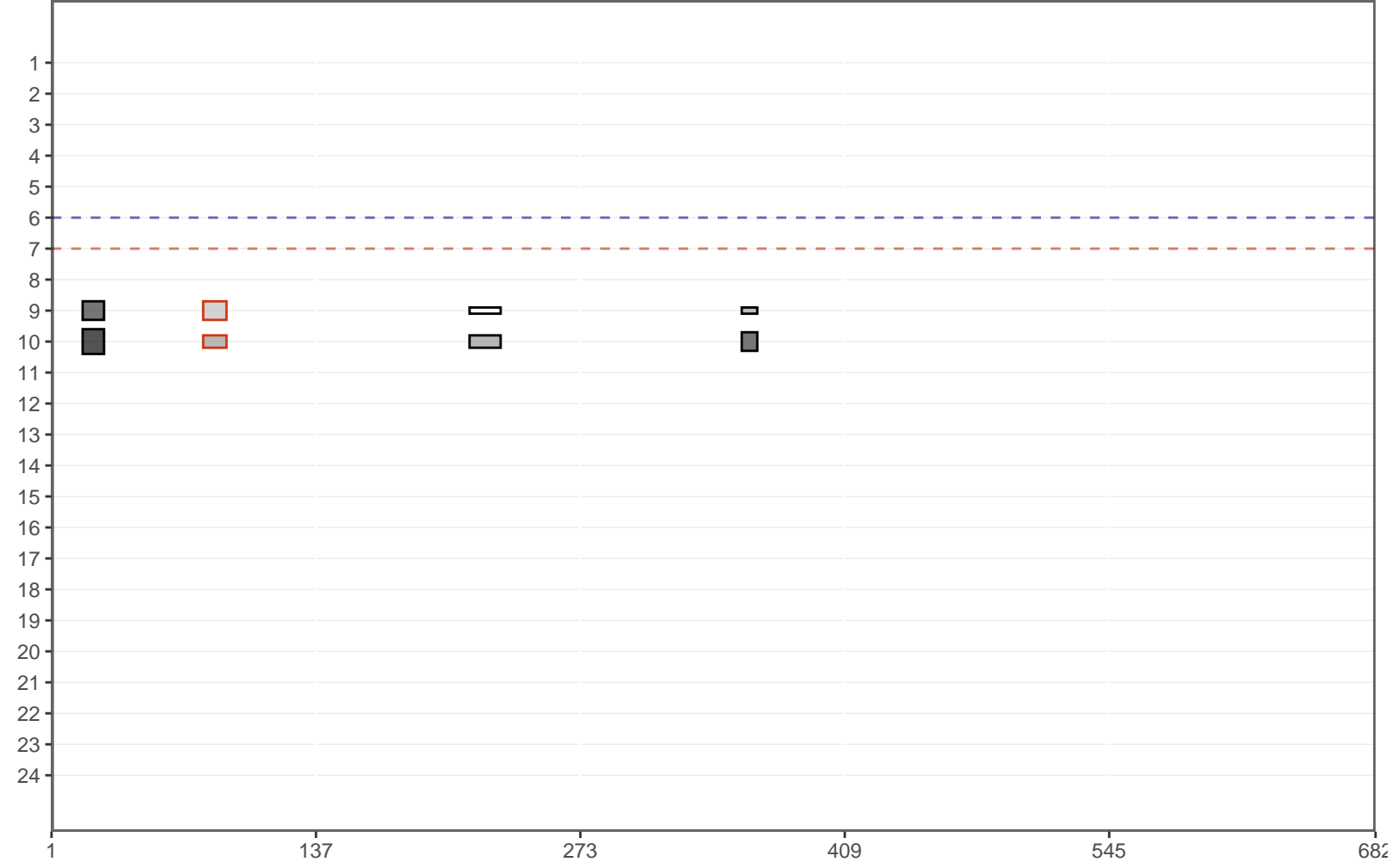
MW indication



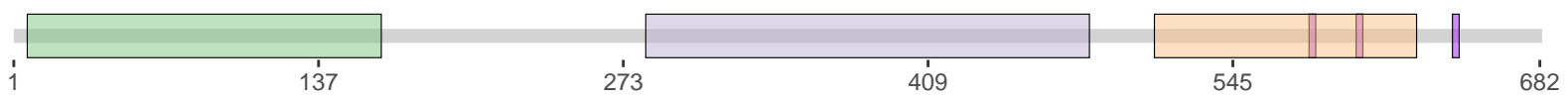
Molecular weight



Gel Slice

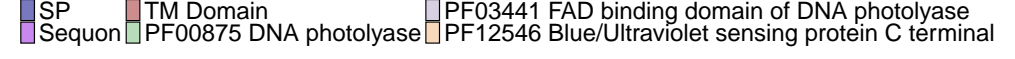


Protein length



Pfam domains

Pfam Description



Protein sequence:

GYPLVDAGMRELWATGWLHDIRIRVAVSFFVAVLGLPLPWRWGMKYFWDTLLEADLESDALGWYHSGTLFDGREFDRIDNPQFVYKGDPEHGYRWRVLFELGRLPTEWHHPWAPAEVLEAAGIELGSNYFLPIVEIDAAKVRLEGALEGMWQHEAASRAAENGMEEHGDGSDSPFAFPQAMHMEMDHEPVRNNPNVITVIRRYEDQMVPMSMTSLFRVDDDEETSVNIRNSVYDTRAEVPMQVNVTEGPRRDLDGAVTGRARTNATPPQNFVVGRRNSDE

NbL14g20810.1 pumilio_homolog_9-like [MW = 74.75 kDa]

No. of times detected



log(intensity)



Values from



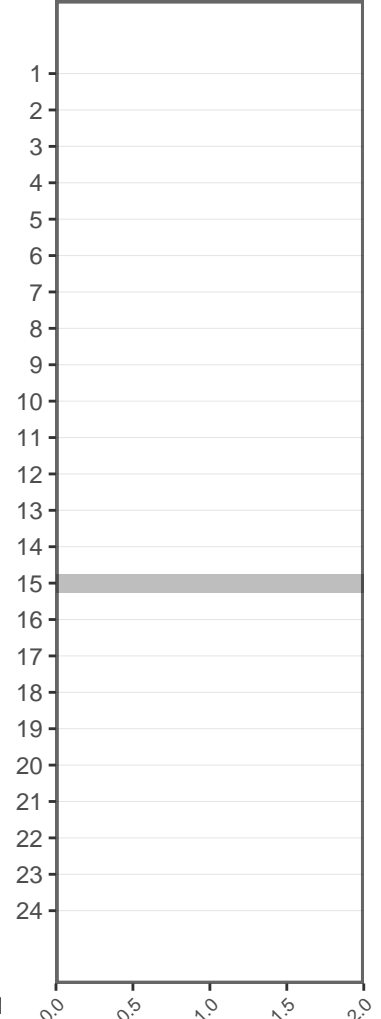
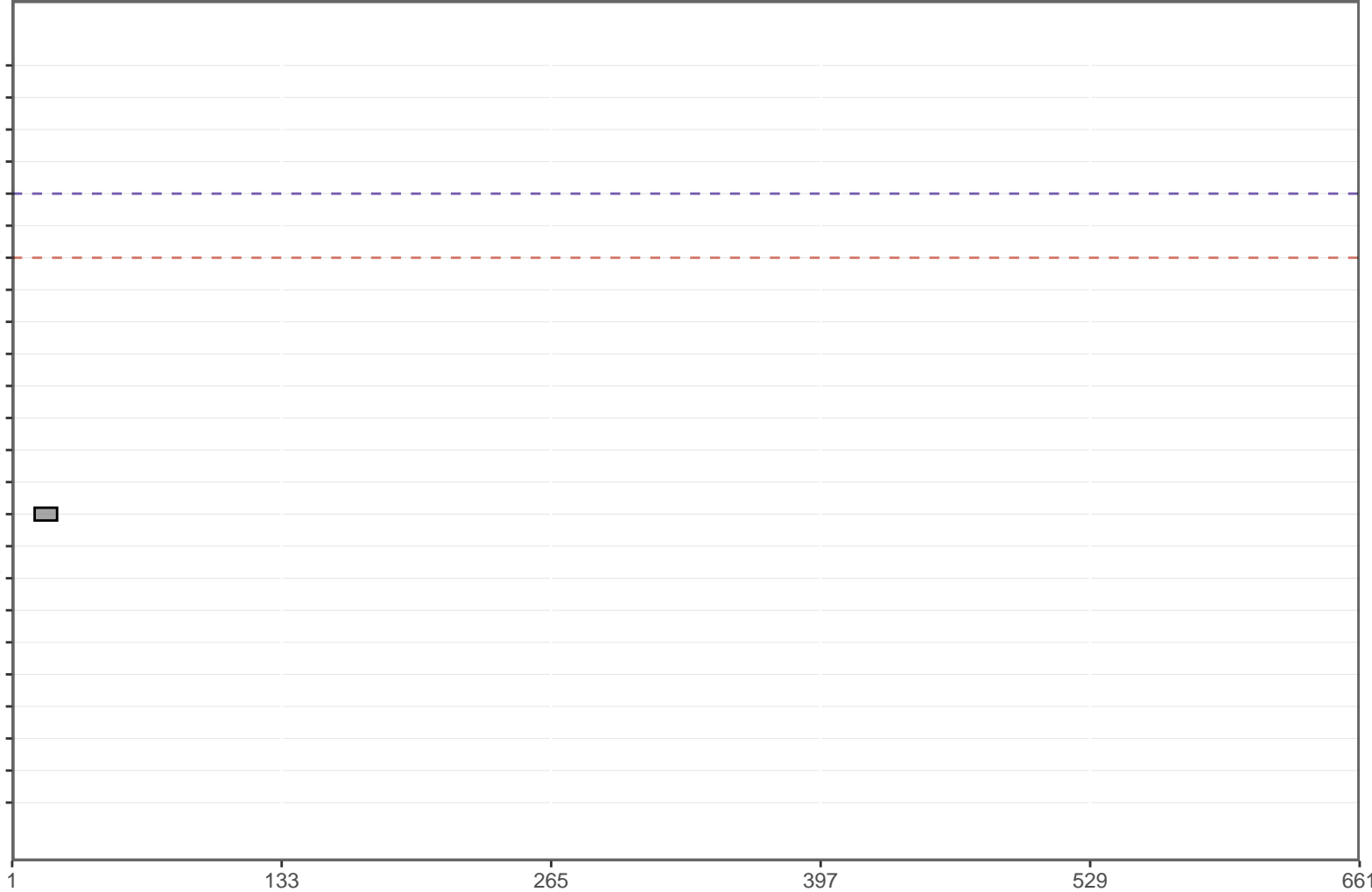
MW indication



Molecular weight



Gel Slice



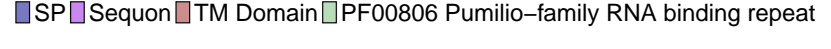
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

INGLDTEFDVIRGVKNGKLSARDVAALTRSEFNNVYLAADQLGGRYLGRIFDEGTSDEVDQIFNGHNFELMKDFFGNVVGKLLTVGSDQRMQFVLMVTDNPGELMKTSTKTHGTRVYVQKLIETLKRLEISLIVRALGPGILVMMDDVHGNHVVQRGLHGLNKHDKLIFDVAASKHGDIATHRYGGCVLNGKITYSTGKQREKLLVGGISNGLKLAGDPPFNYYVQRIELKIASAAAMLLSGFDGHYVYLRGKFGSHVVEKFLKGVVEEGRRIINELVSETHFDLLOLC

NbL14g20800.1 uncharacterized_LOC104112265 [MW = 30.44 kDa]

No. of times detected



log(intensity)



Values from



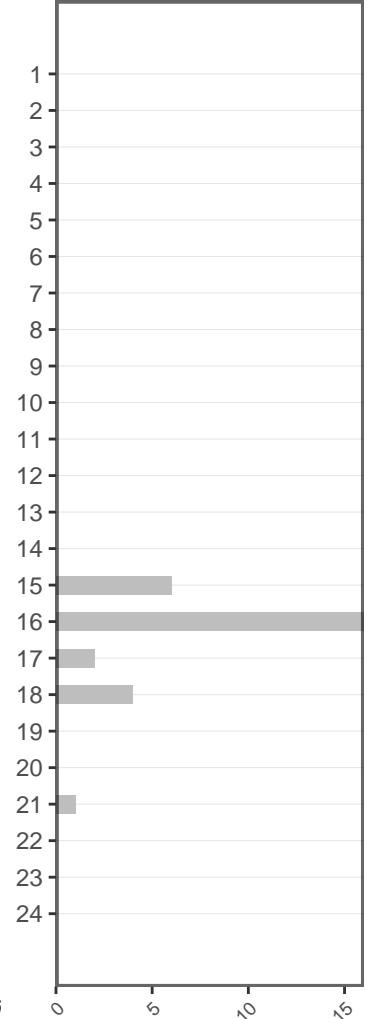
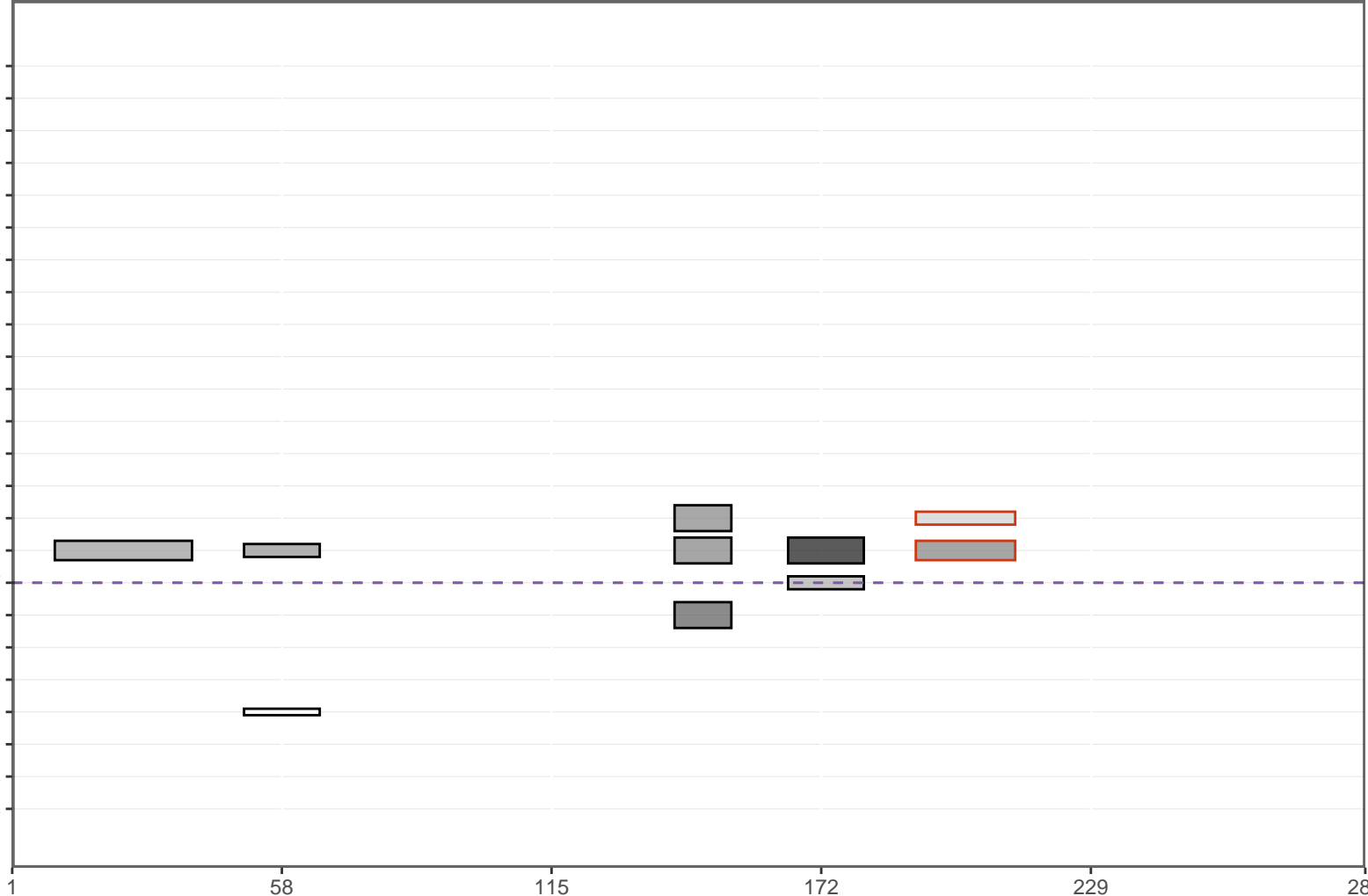
MW indication



Molecular weight

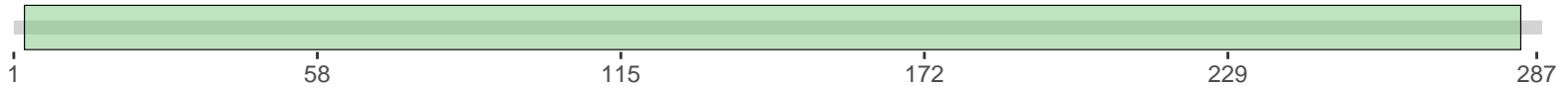


Gel Slice



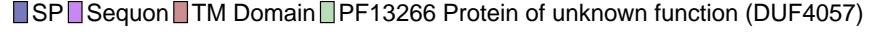
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KPVTPEVAKQRELGGTLESEAEMKLNKGLSDAKTKELVGHDFAPPEIGRPLAARALALRESIANGEPANNDVSGDEQAVKTKAHPENKLAELTGNDFIKGDTTPPAEAKHLSAALREMSGSENFADQKVESRDFYGGVRRKPPGEGESIALV

NbL14g20650.1 probable_beta-D-xylosidase_7 [MW - SP = 82.7 kDa]

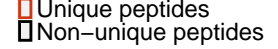
No. of times detected



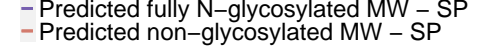
log(intensity)



Values from



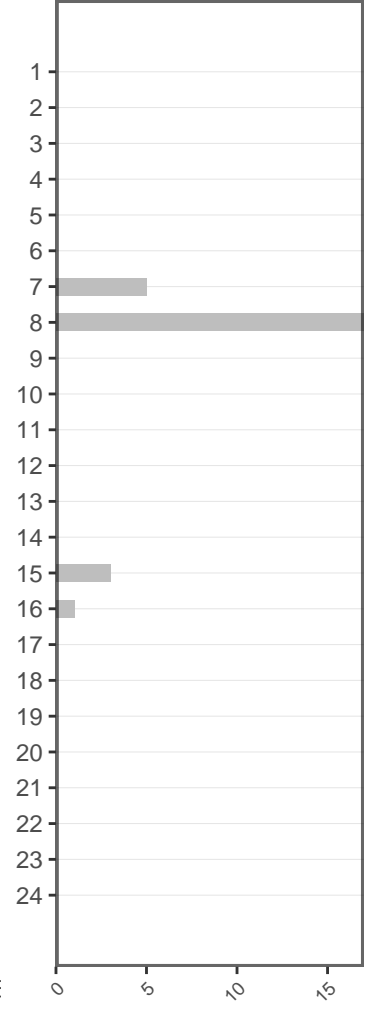
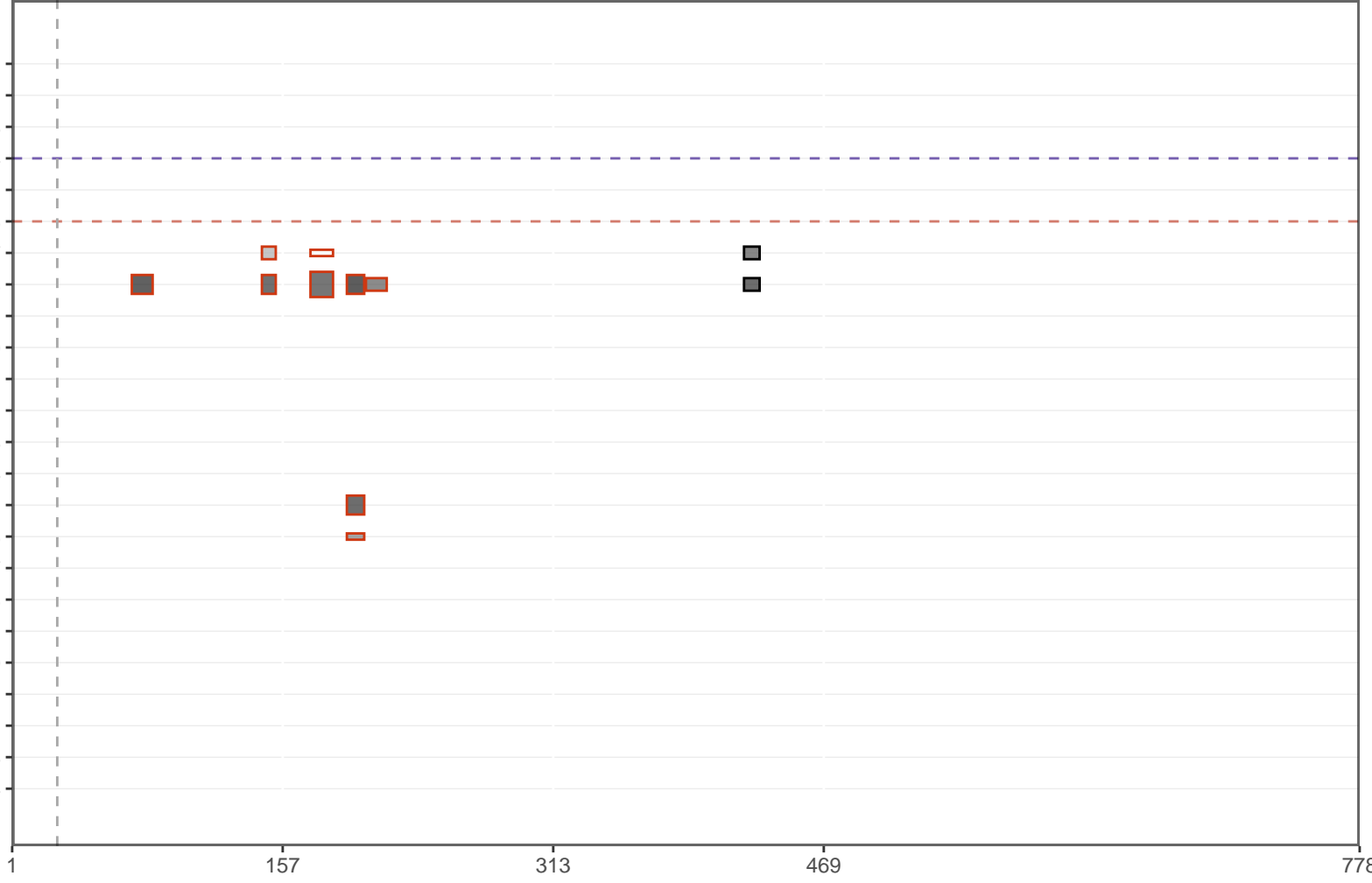
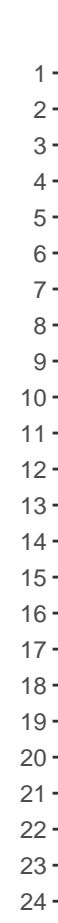
MW indication



Molecular weight

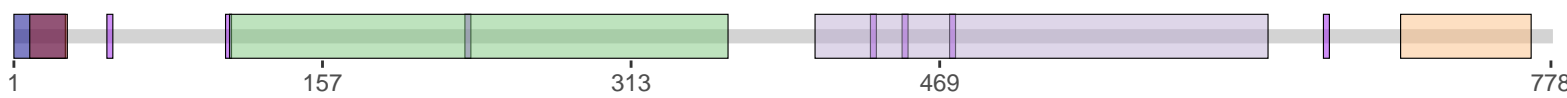


Gel Slice



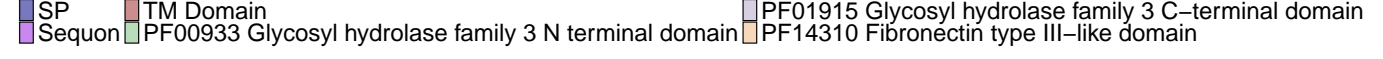
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DPKRLKLEYGDISSAEVCSGQHRALALEAARNGVLLKNSAKLPLAKIKTTSBLAVIGPKANDESEVLLGNVEGYPDKNFTLGGIGQEVYKNNMHPGNNYVNGTSAAGEAVDIAKKADCVVLLMGLDGTLEREKLRTELGLPGMDSELTETIAQAAKPVLLVMGGGFPVDVSAFADKNGNGALVWVYVPGEGGATALAEILFGEHNPGGRLPVTWVYPKFNKISMTDMRMRPLSGTGYPGRTYRFYNGPKVFEFGVGLS6YTAWSYAVASVNGDKLHEKNPKVYKATENGSLN

NbL14g20610.1 23-bisphosphoglycerate-dependent_phosphoglycerate_mutase [MW = 38.18 kDa]

No. of times detected



log(intensity)



Values from



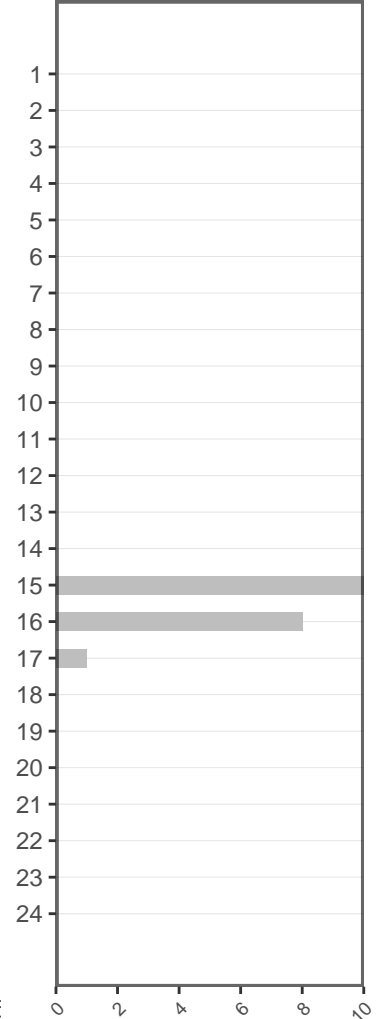
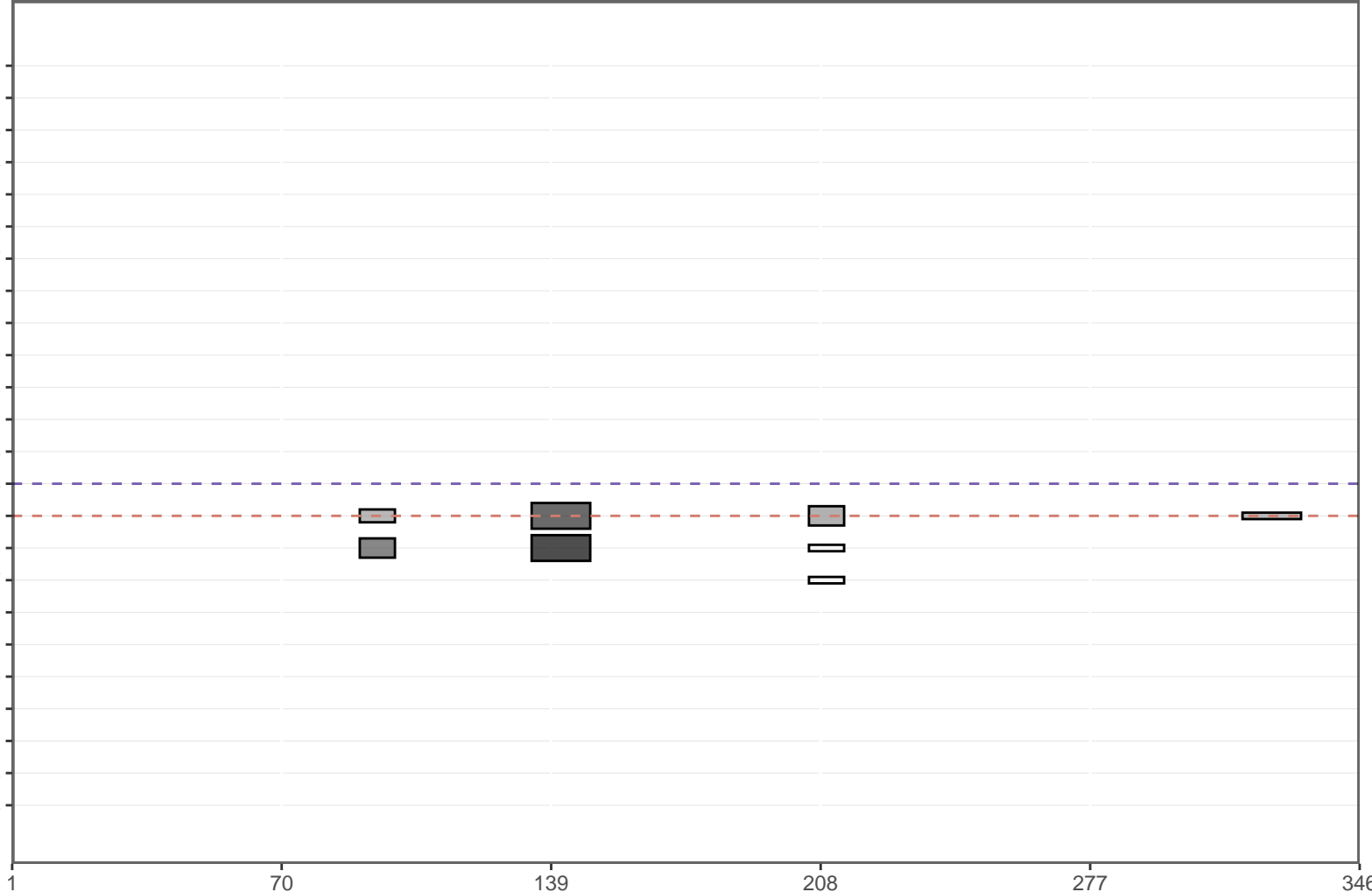
MW indication



Molecular weight

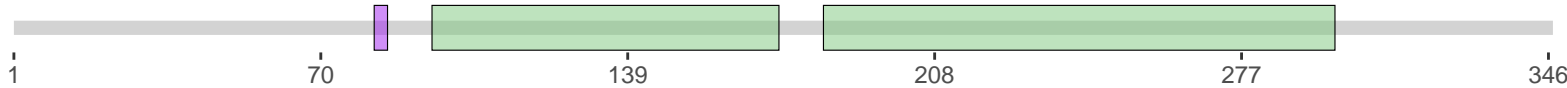


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IQHRRKKVPTIHEESEGAGAWGIFSEETKGGIPVYFAVQLNERNMVGELQGLNKQETADRYKQEGVHEWRREVDIPPPNGESLEMCARAWAVYKHEHPQLAGKNMIAAHGNSLRISIMVLDKLTSGDEVISLELSTGIPMLYFKKQKFRIRGSPAAPTEAGVYVYTKTLADYRQKLNMMVQV

NbL14g20010.1 uncharacterized_oxidoreductase_At4g09670-like [MW = 39.81 kDa]

No. of times detected



log(intensity)



Values from



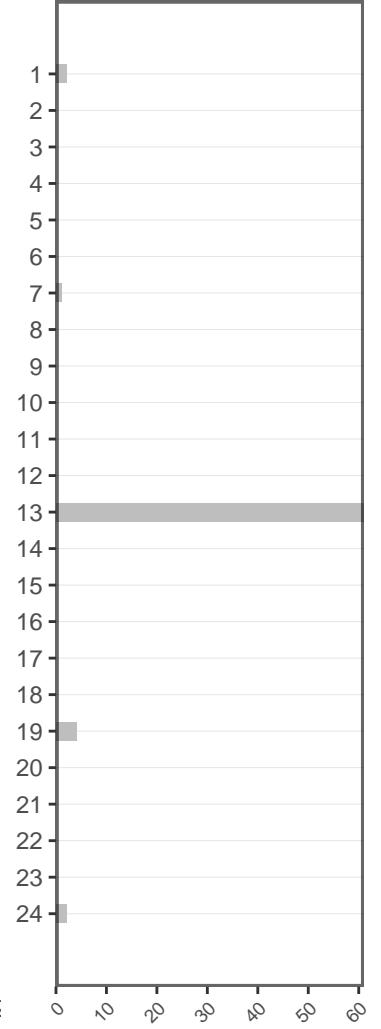
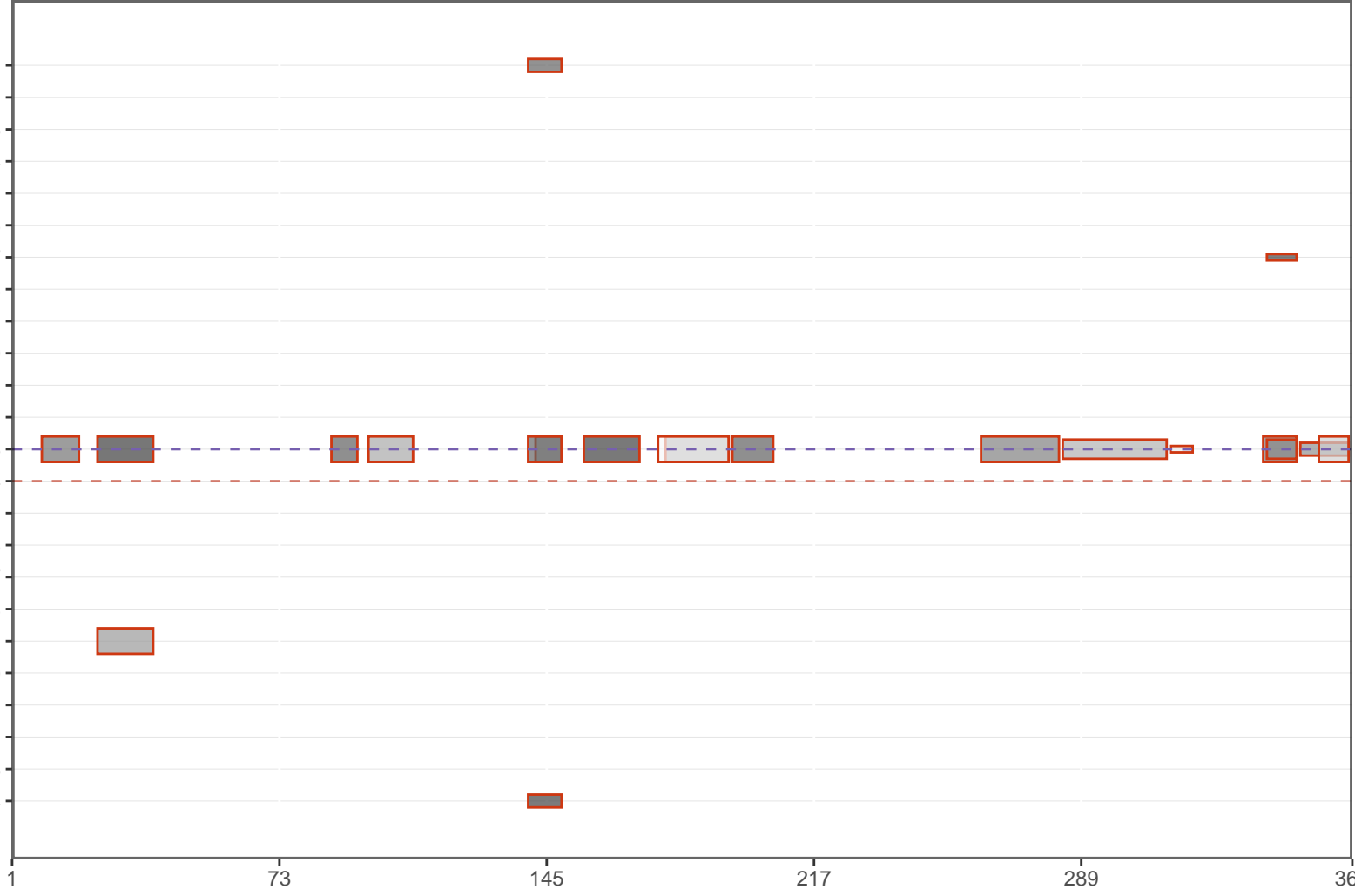
MW indication



Molecular weight



Gel Slice



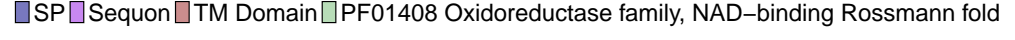
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FLKNDIRVKAADLDNAGALGDAGWYSRILWTTDVELPKTVTALPQPELNEAGVLSGGASLSWWDGRVWTFYKQFLANLMDIAANGSKGNLRVHDFVFPFGDGNWAFYTVVSSRFGLSISHPAPNEGVSTLDPGEALMVKFEFNLVRSIKGGGCKPEKRWPTISRKTQLVDAVKASIDKGFPEVWVY

NbL14g19890.1 ras-related_protein_Rab7 [MW = 22.91 kDa]

No. of times detected



log(intensity)



Values from



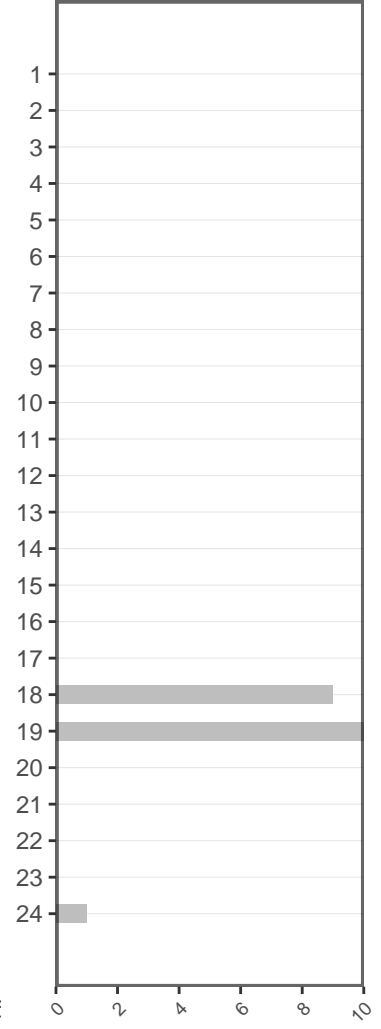
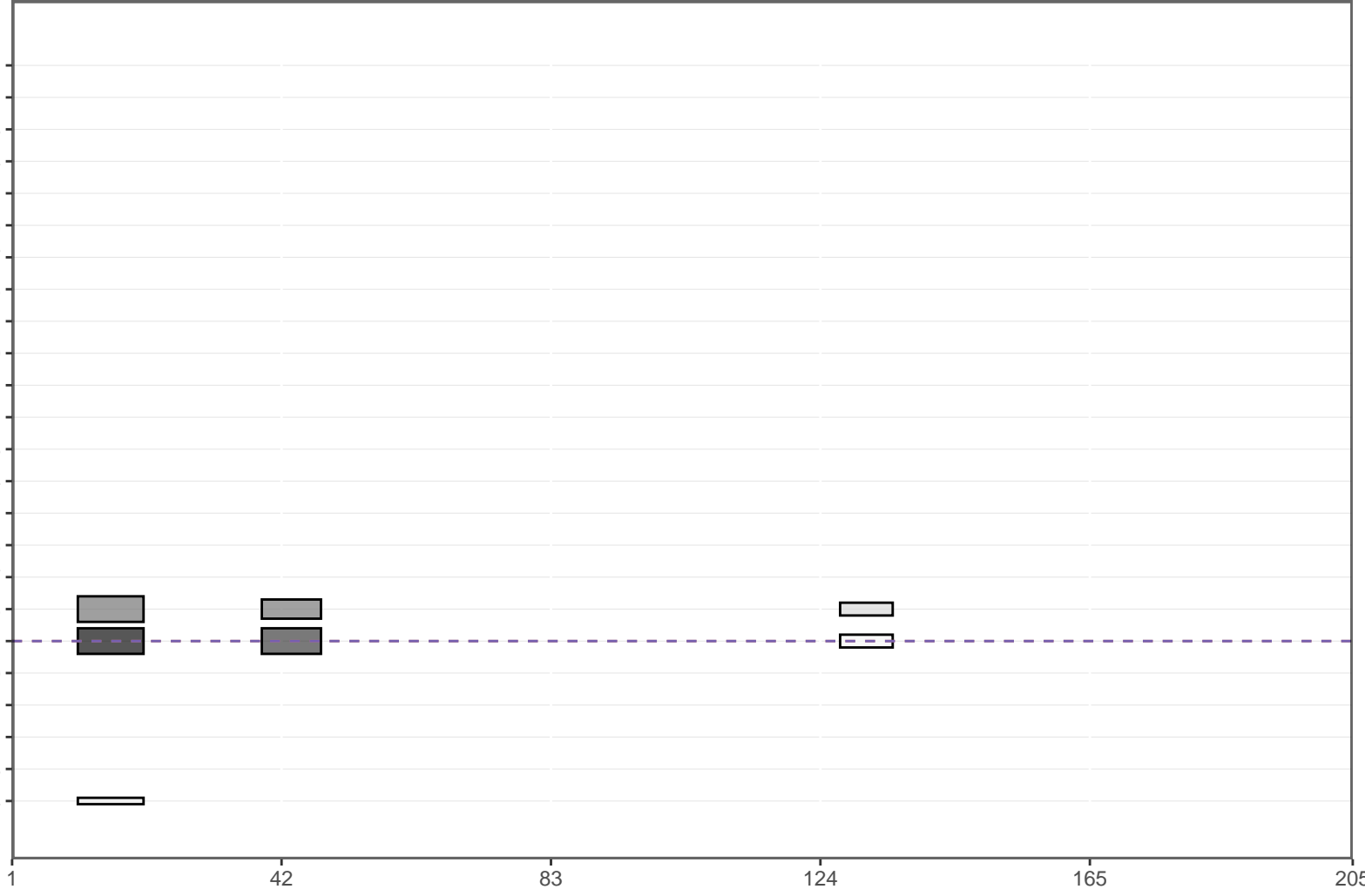
MW indication



Molecular weight

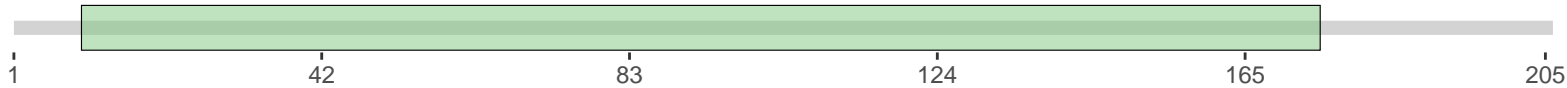


Gel Slice



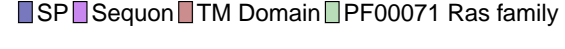
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YVWVNRVSDNLDNWHHEEFLKAGANPPDKTFPFILLGNKIDIDGGNRRVSEKKAKEWGAASKGIPYFETSAKEDINVDAAFLSIKTKALANEHEGDDYFQGGPEAVSETEGRGGAC

NbL14g19870.1 probable_ATP_synthase_24_kDa_subunit_mitochondrial [MW = 27.58 kDa]

No. of times detected



log(intensity)



Values from



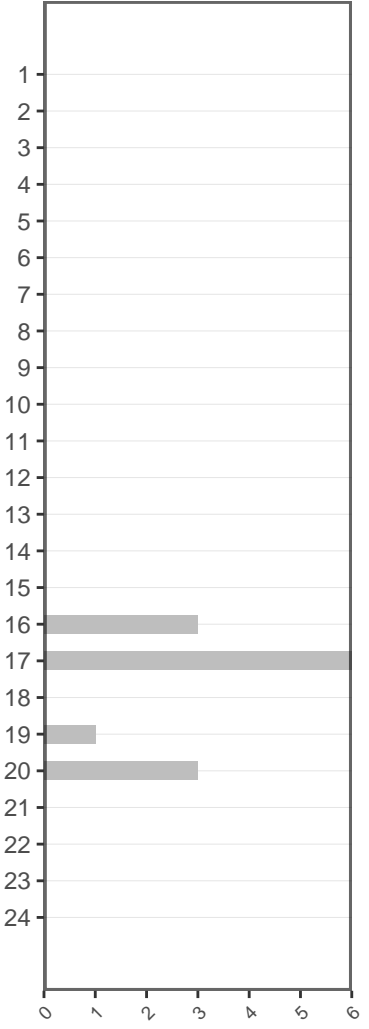
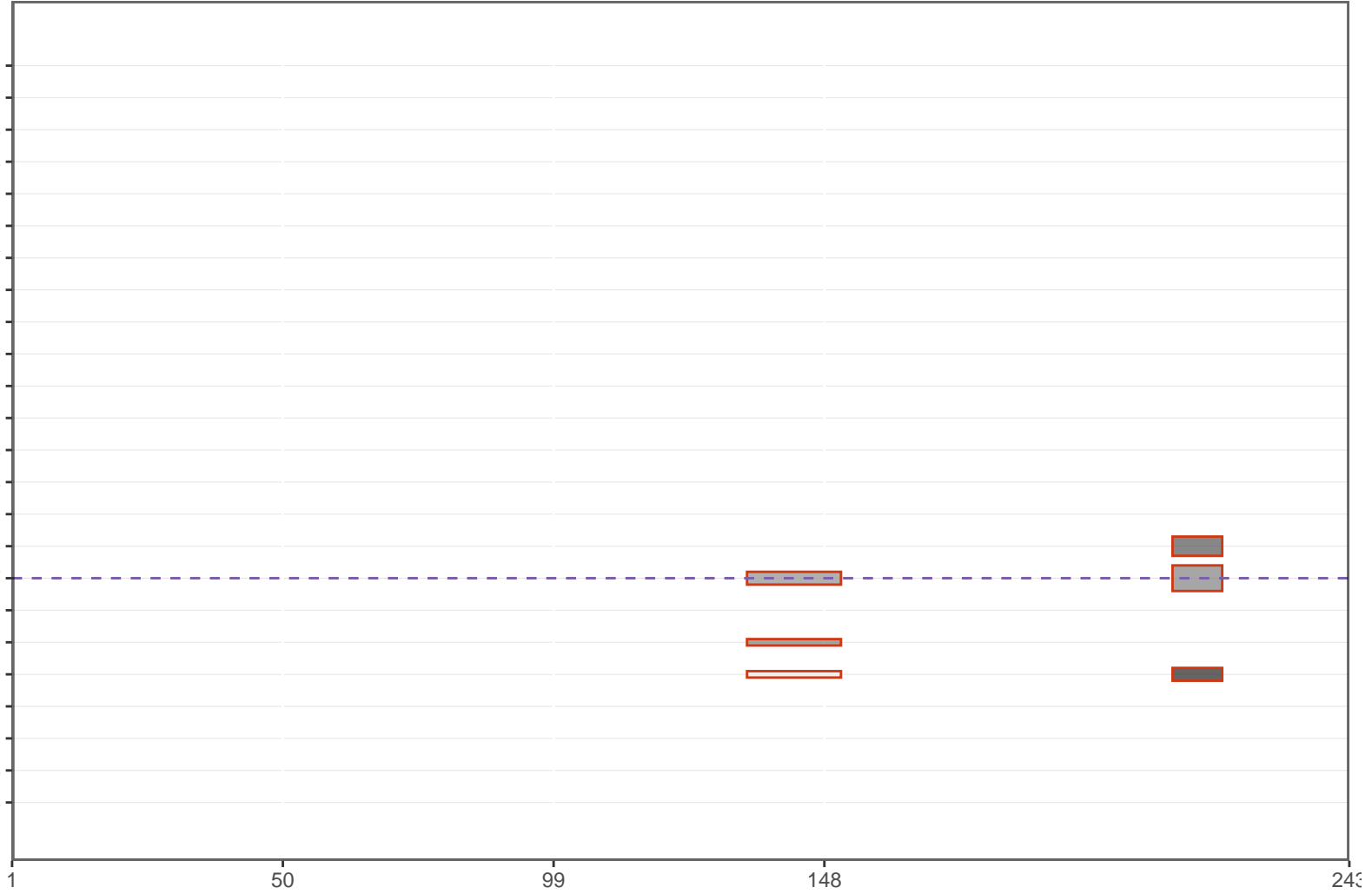
MW indication



Molecular weight

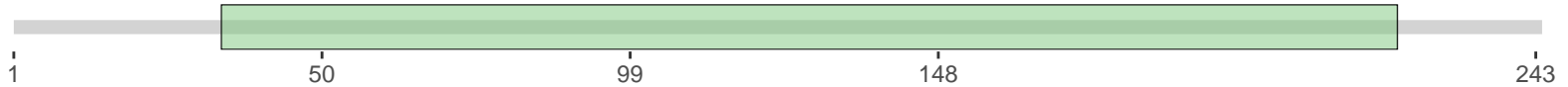


Gel Slice

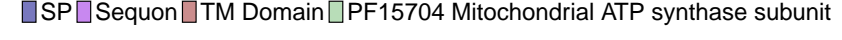


Protein length

Pfam domains



Pfam Description



Protein sequence:

NIEVETHIIPDARTYLLKLUKEMRVRKGLIDEGIEDLQMAALDKVEKEIKKPLMRNDKKGALLTAEFDKINQKLGIRKEDLPKYEQLELKIAGLEELKDKDALEAMETQKRRKFEKDEEMPVSKLDIRNFY

NbL14g19730.1 30S_ribosomal_protein_S1-like [MW = 59.43 kDa]

No. of times detected



log(intensity)



Values from



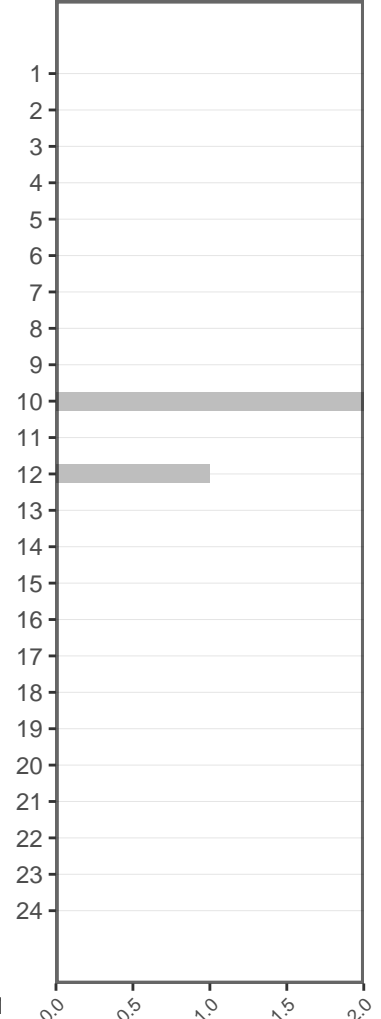
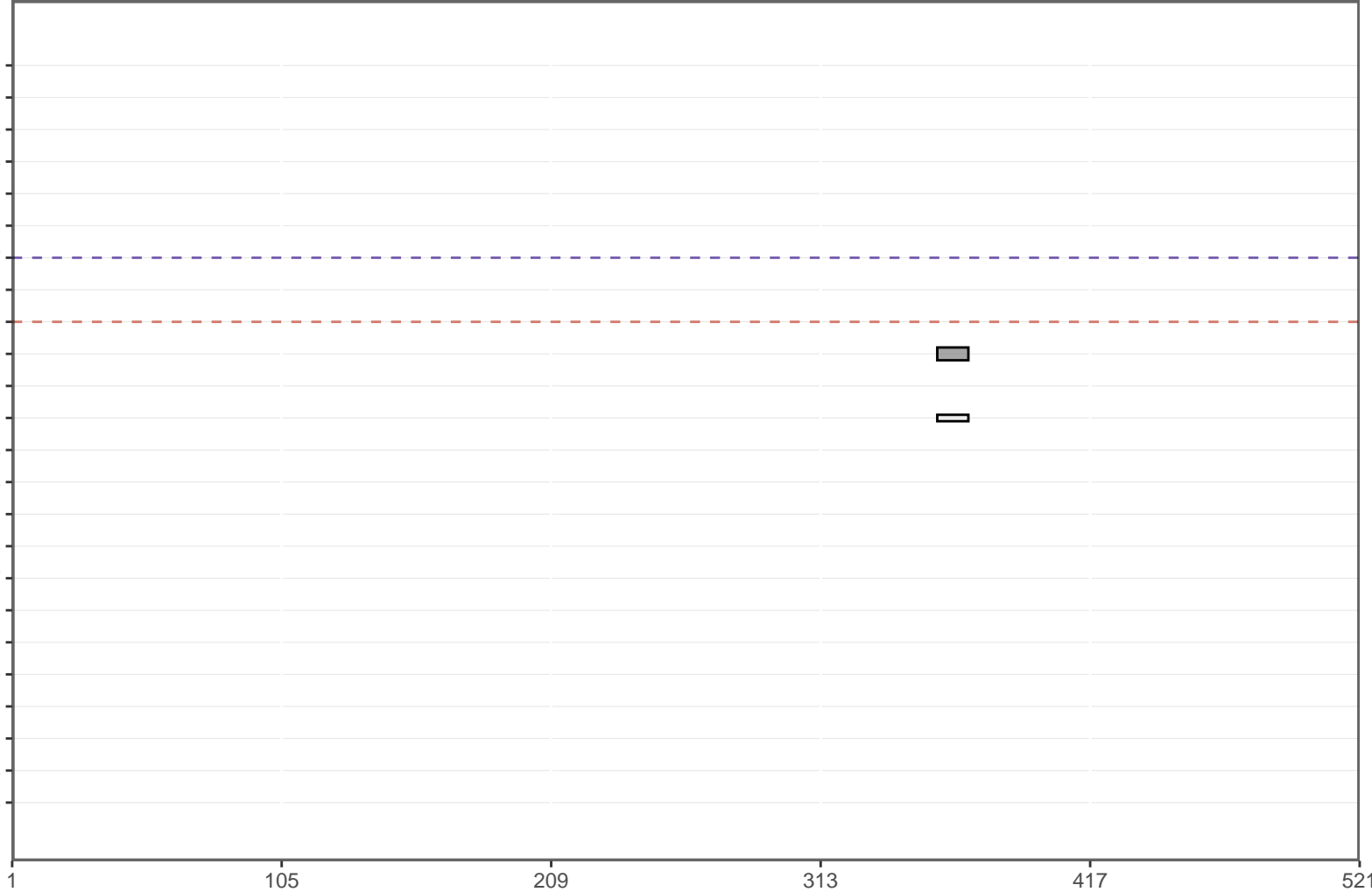
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VESEPMPOGKPVVEPGTVLFAEVLGRTLSGRPLLSSTRLLFRRIAWHRVRIQIKQLNEPIEWTEWNTGGLLTRVEGLRAFLPKADLMNRVNSYTELKENVGRINVLTRINEETNDLISEKEAWQMLNLEQVLEGTVYKHLFFPGAQIRIGETNRSGLLHNSVTRGKTSINNLAVDEKVMVMVKSMPDNLISIAELESEPGFLDKDEKVFSEAKEMAKKYRGNLRVGSATRKPEPLPTDRLPFDEESGLYANWKKVFERDEV

NbL14g19580.1 xanthoxin_dehydrogenase-like [MW = 29.42 kDa]

No. of times detected



log(intensity)



Values from



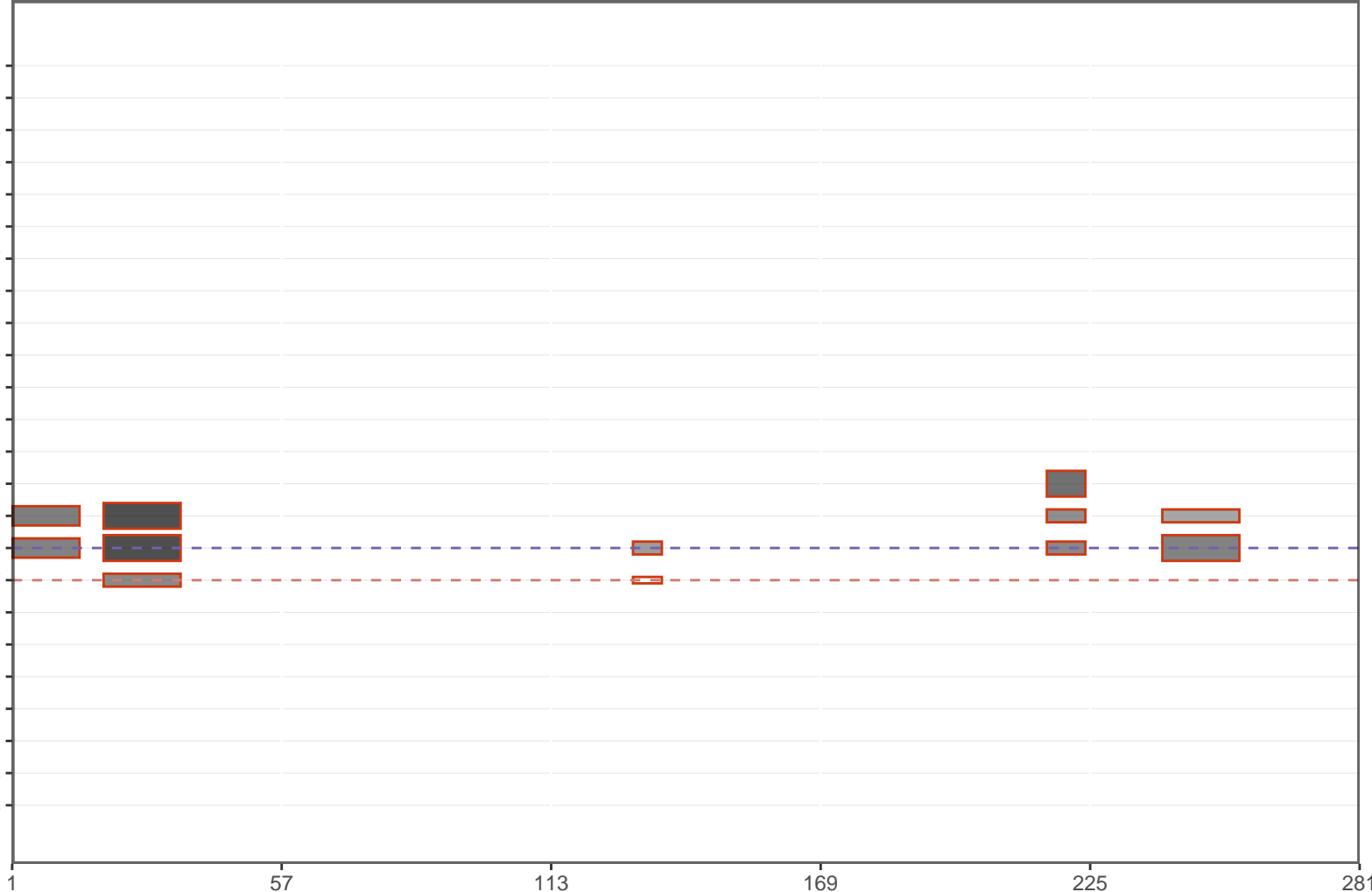
MW indication



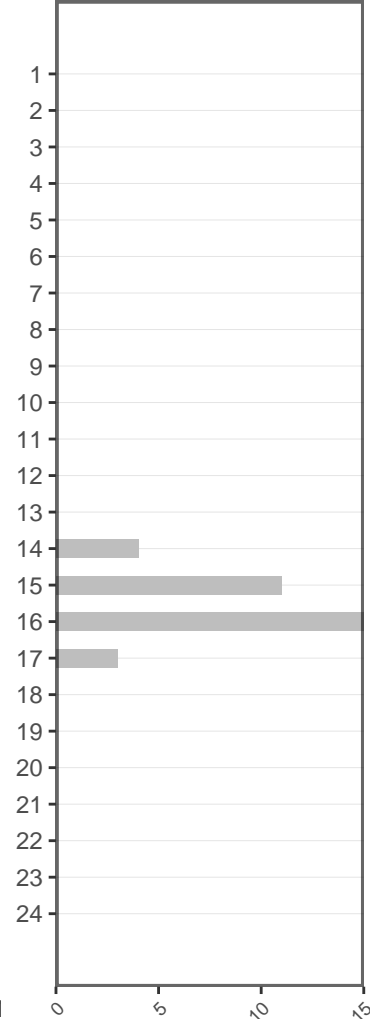
Molecular weight



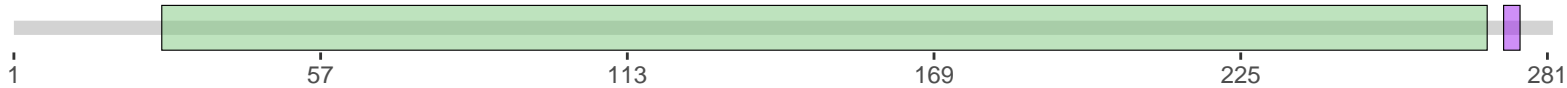
Gel Slice



Protein length

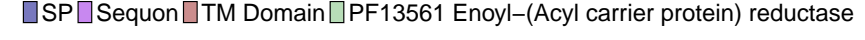


Peptide counts over 4 repeats



Pfam domains

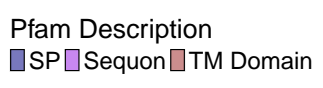
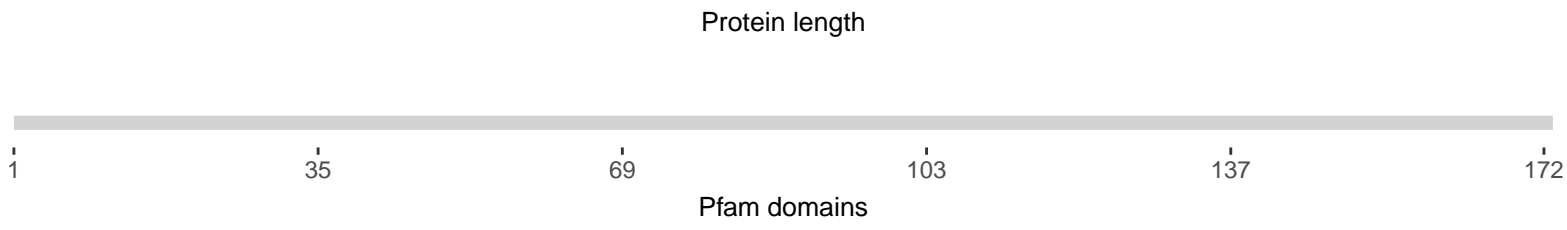
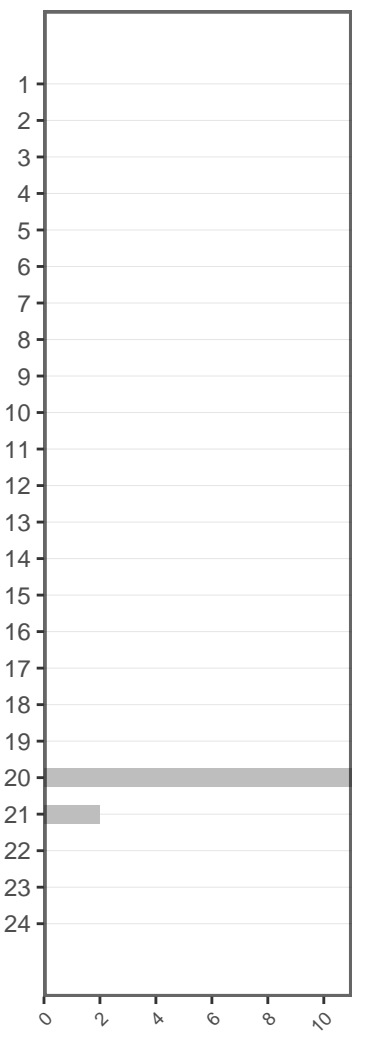
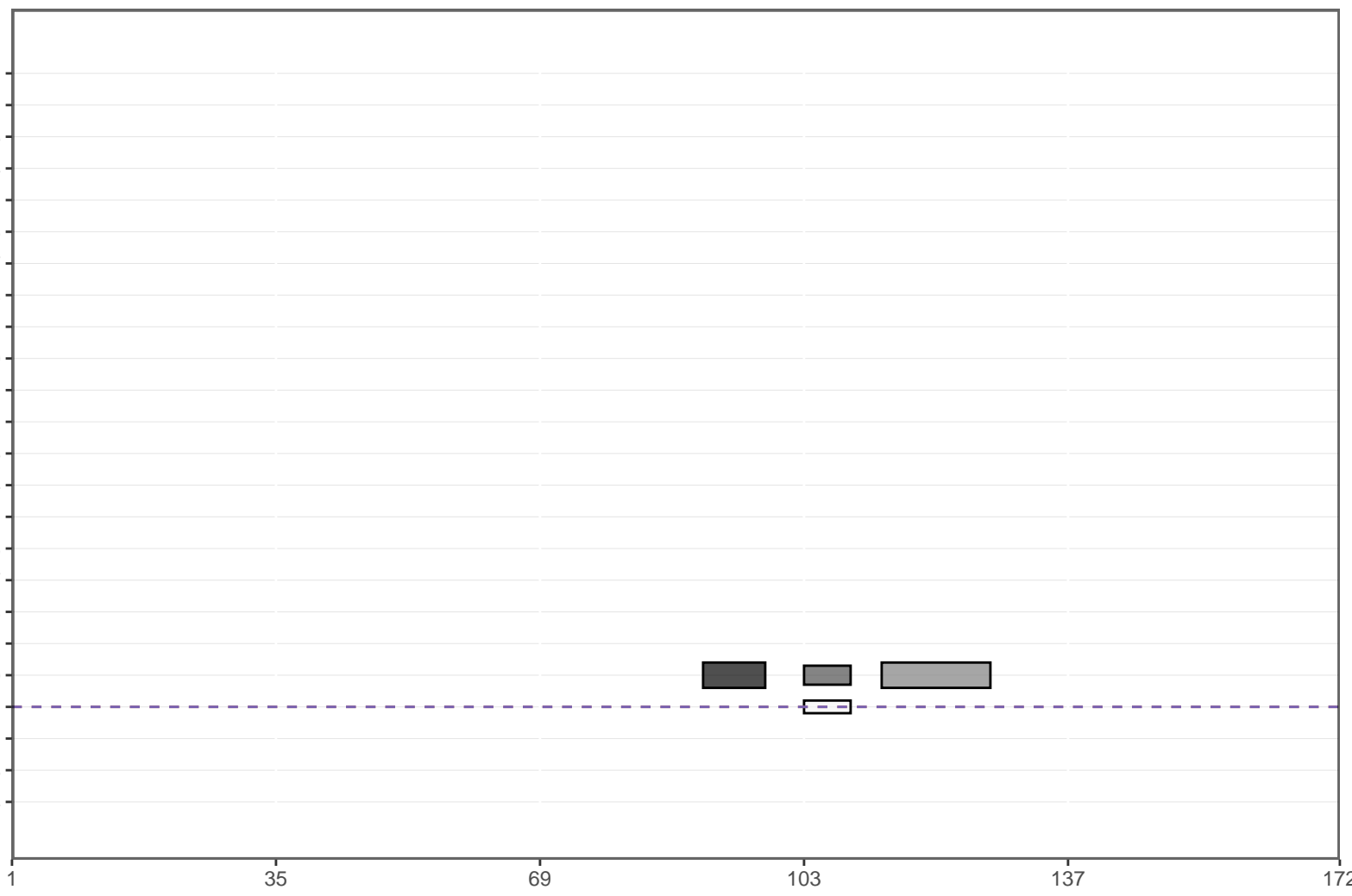
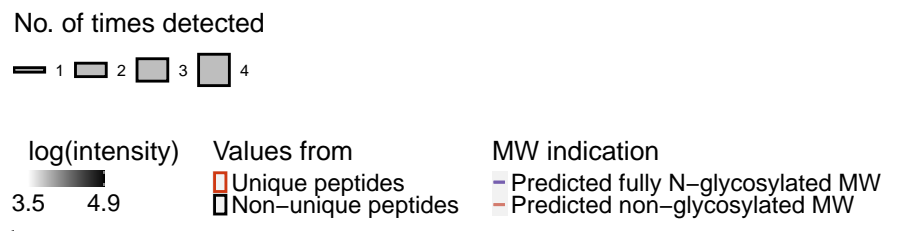
Pfam Description



Protein sequence:

ILKGTTLGKHIAARMIPGKKGIVLGGVGEAIVGIGPHAYIAKHAHLGLTGNVAEMKKGIVRVNCSVPAWATGLALAHLPEDERTNDALAGFRAFTGKNANLGGVELKTDGVAWAVFLASDEARIVSGHNLMDGGFSDVNHSLRIFR

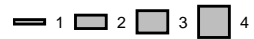
NbL14g19570.1 uncharacterized_protein_DDB_G0284459-like [MW = 18.42 kDa]



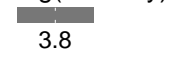
Protein sequence:
 PSAPPKQVTVVAALDGGKVVITMFEFRGKAKELQEVYKGGKLEAANGGPFPGFKNEISGRWAMFGFVAGLATEVATGSDVFDGDKILLNFGIVDLE

NbL14g19390.1 aminoacylase-1 [MW - SP = 47.7 kDa]

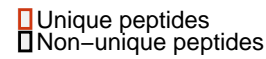
No. of times detected



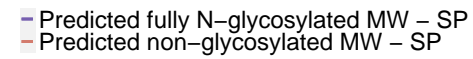
log(intensity)



Values from



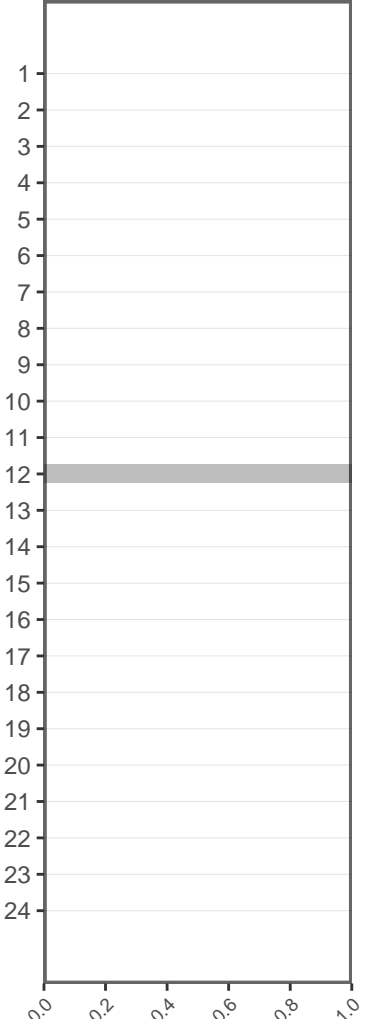
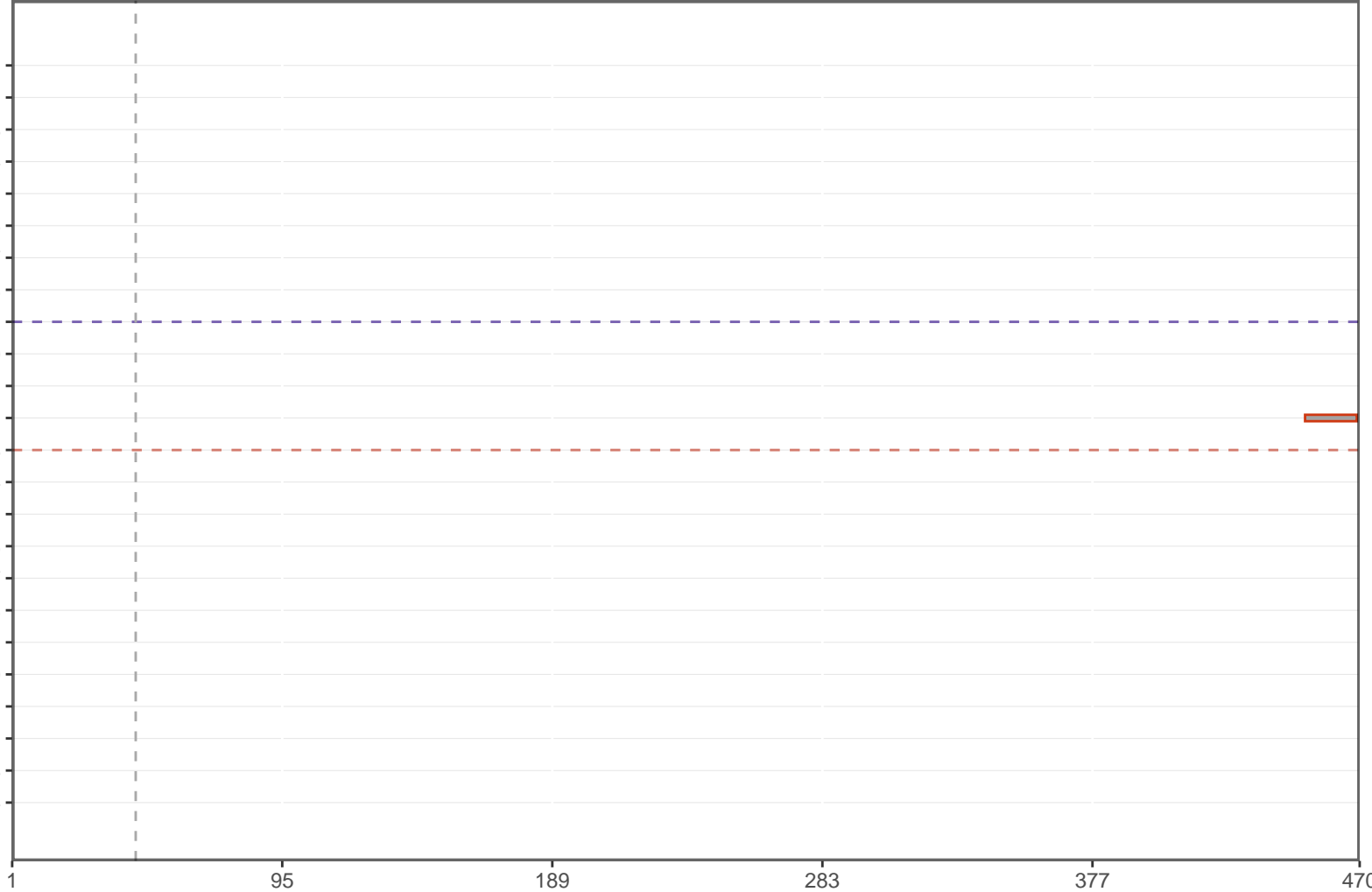
MW indication



Molecular weight

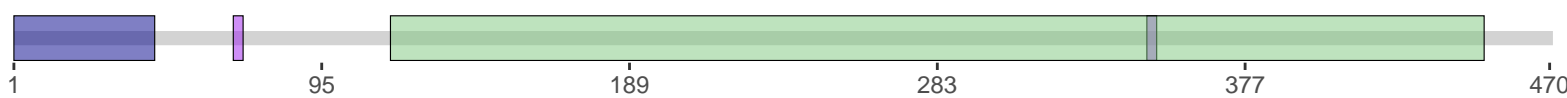


Gel Slice



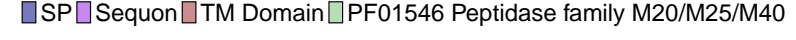
Peptide counts over 4 repeats

Protein length



Pfam domains

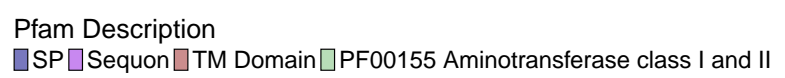
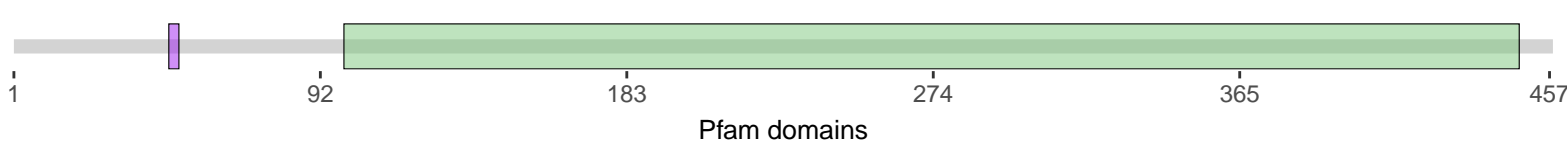
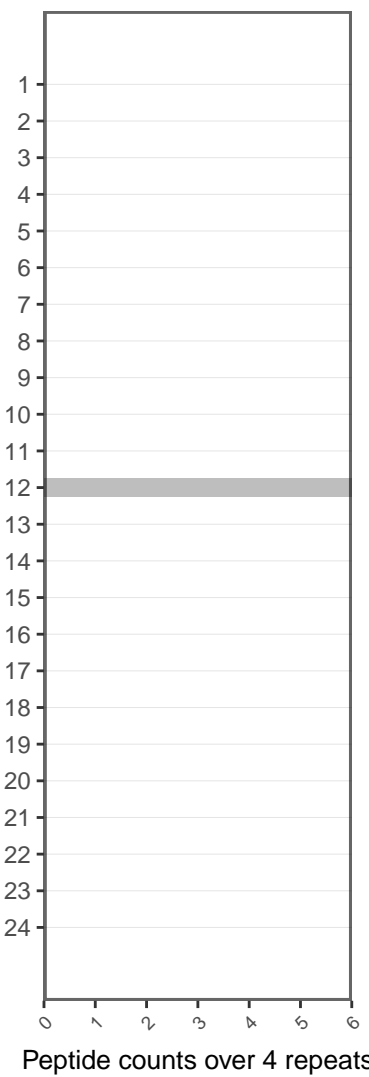
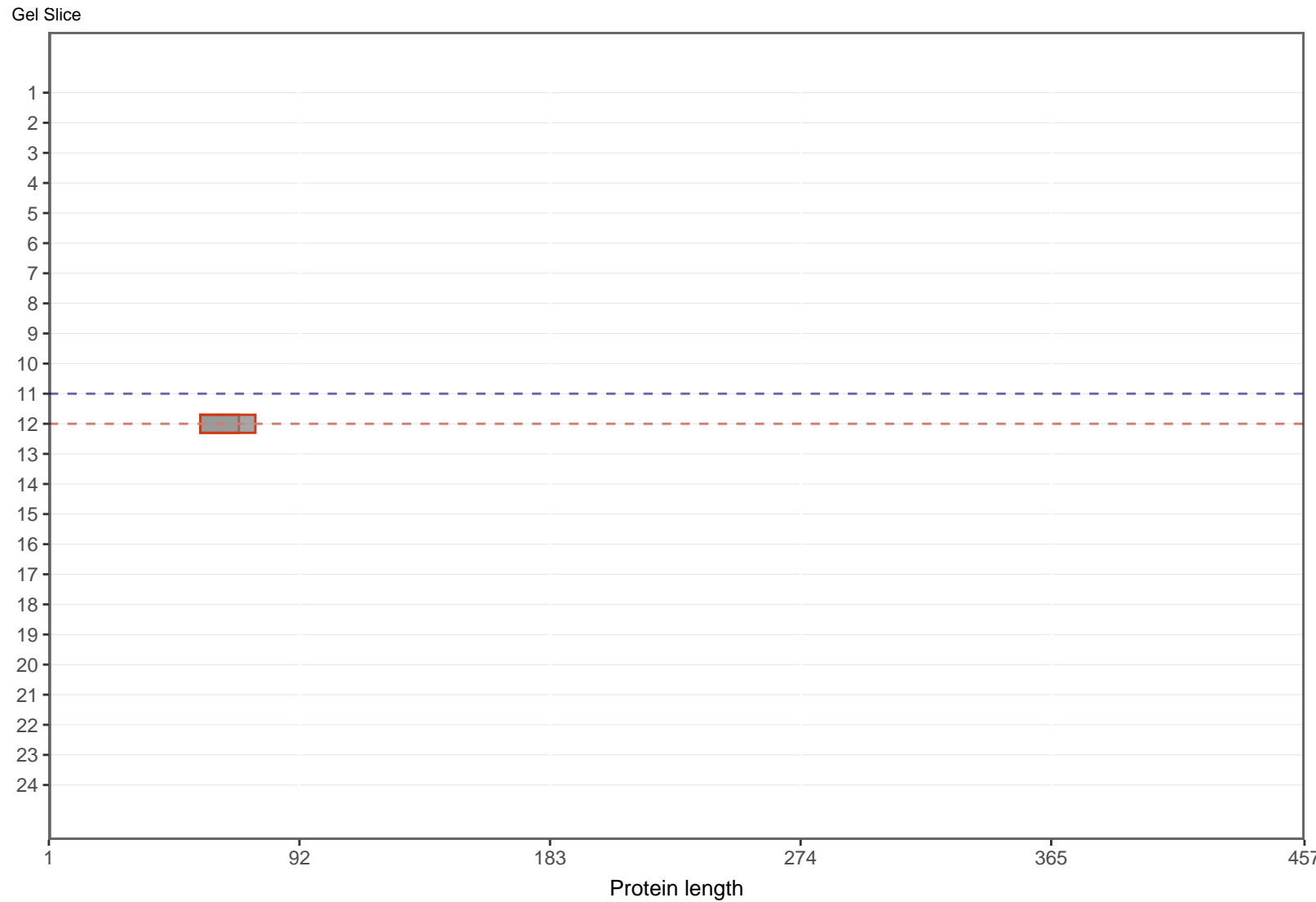
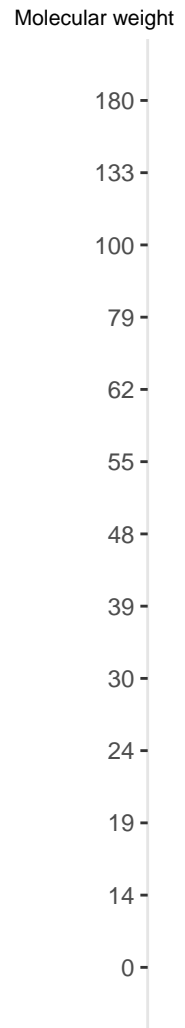
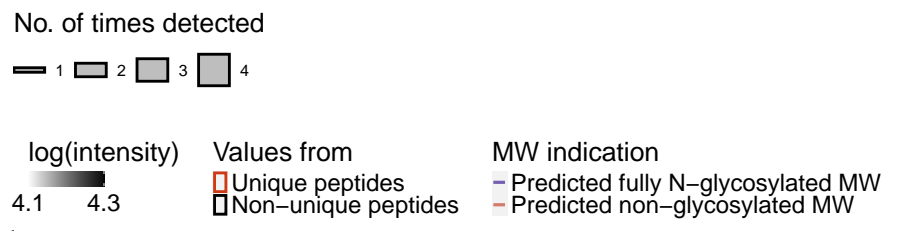
Pfam Description



Protein sequence:

MEFRVYADRTPTVHMVKAVGTPGHGSRVNDNTAMENLMKSEIVTKFKRESKFDVVKAGLAANSEVSEVNPVFLKAGIPSPGTFVMMQPSSEAEGLDIRMPPTADLPQLMRKHIEEQWAPWRRNMTYEITEKGLRDNMGPLMLTSDSNFVWVFNFAVTRAGGLSKPELASTTDARFMRLGPTFGFSPMNTPLLDHNEFLKDTVYLEGKVVYESIKLSGFEQSYEHQGNVSDQ*

NbL14g19280.1 probable_N-succinyldiaminopimelate_aminotransferase_DapC [MW = 50.92 kDa]



Protein sequence:
 SLPIDELKSVVSKNFRALLNTPHNPFGKMFNREELNVAISLGIENDILVFADEVYDKLAFEMEHISIASLPGMYERTVTMNSLGGKTFSLTGWIKGVAIAPPHLTVGVRGAHSEVLTFTSTFMQVYAATALRAPDSVYEELKRDVSSKKAIVLVEGLKAAAGFTVVPSSGTYFVVVDHTPFGLNDIAFGEHLKEVGVVWIPRTSVFVLPNPEEGKILVRFTECKDDDTLKNVAVGRMVKQLSKK

NbL14g19240.1 biotin--protein_ligase_2 [MW = 41 kDa]

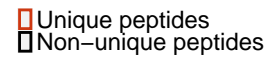
No. of times detected



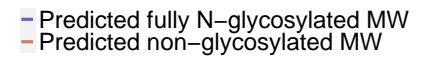
log(intensity)



Values from



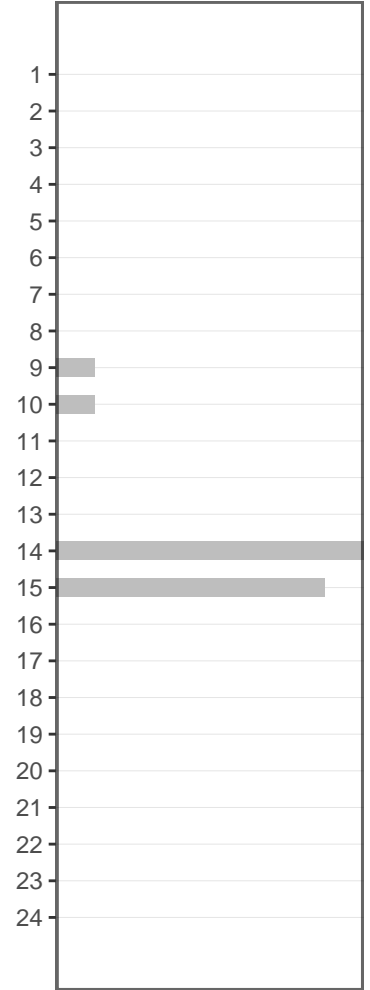
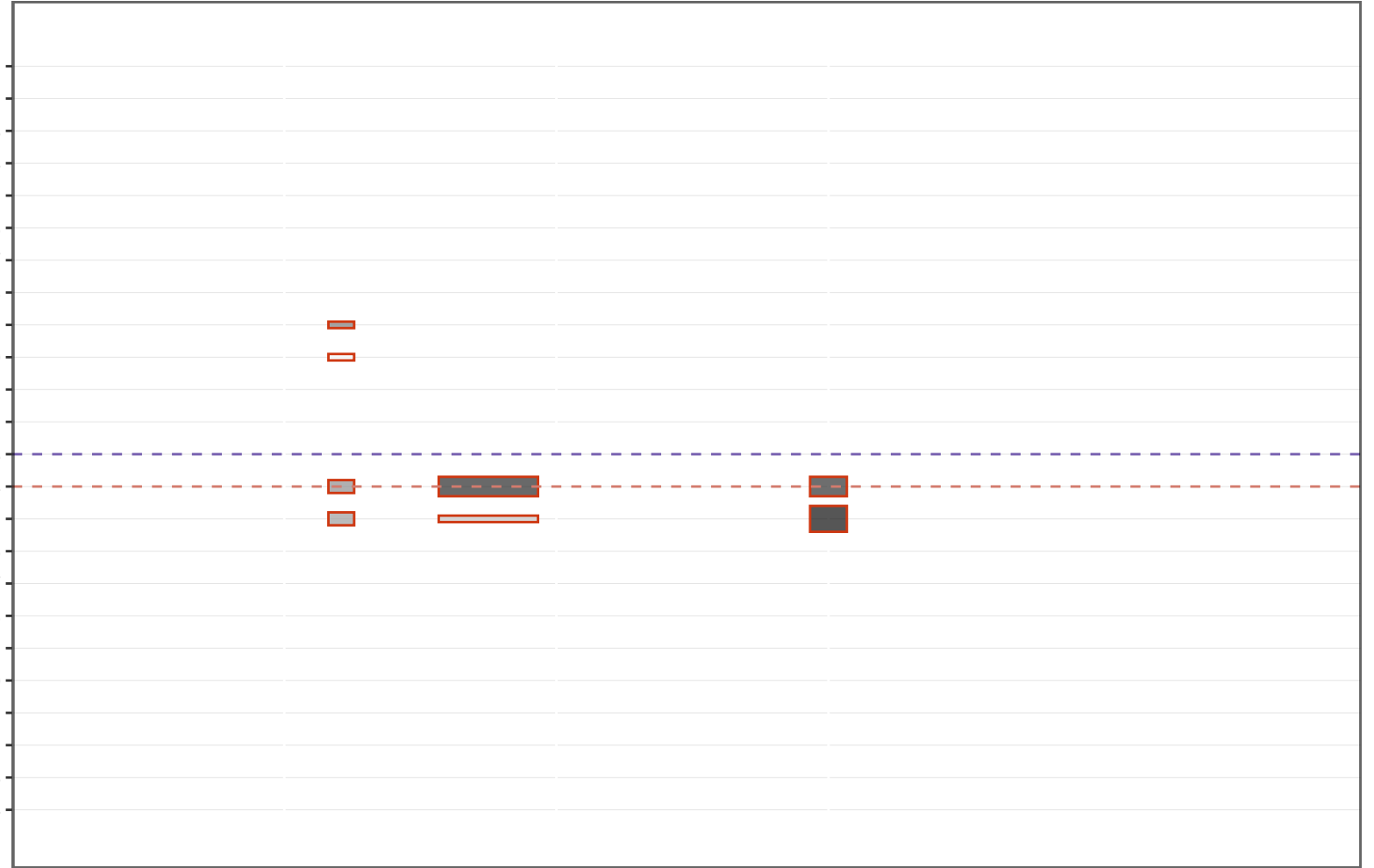
MW indication



Molecular weight



Gel Slice

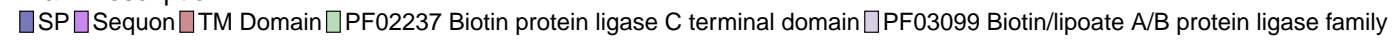


Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

IRVVPHIQYVYVCLAMTEAKAVGLEKTPLELDVRKWPNDLYLGGVKGGLSTSVRSKPFVYAGVGLVGVGNEKPTTGLNVLKKNPLRLKREDVIAAFNKFENLYDFSEGGFGALEGLYKRWLHSGDRVIVGERGGDDYFFETVVTIQGLTSSGVLGTFITDDGGMCELHPDGNFDFDFKGLKRRMS

NbL14g19030.1 probable_eukaryotic_translation_initiation_factor_5-1 [MW = 50.84 kDa]

No. of times detected



log(intensity)



Values from



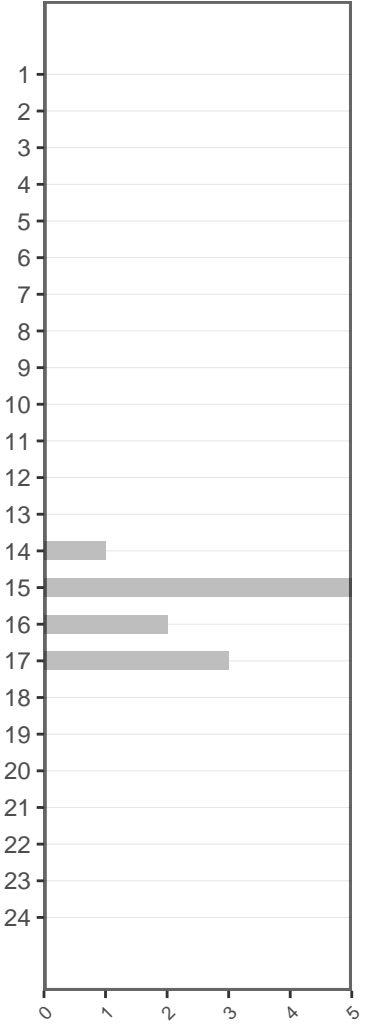
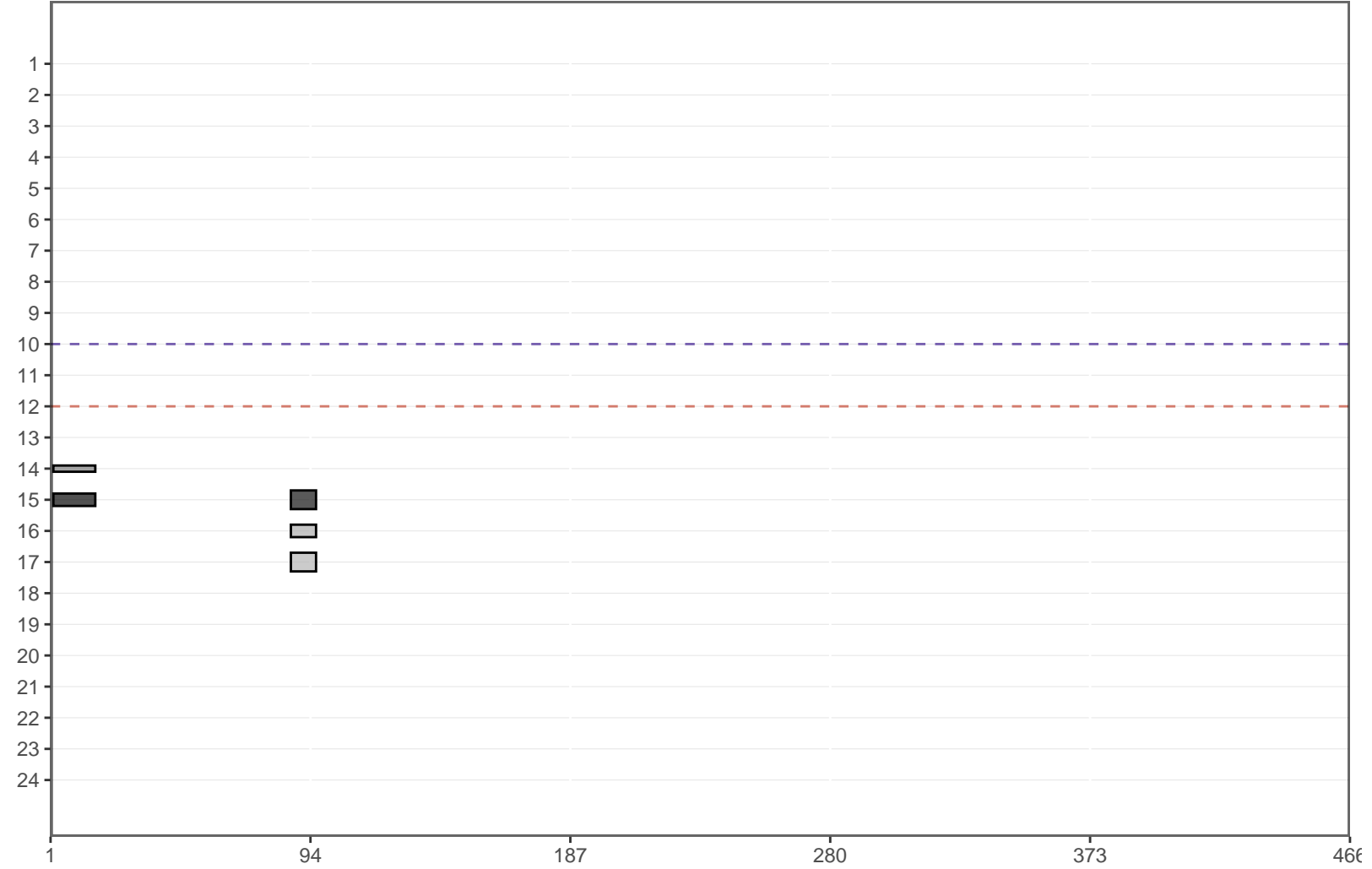
MW indication



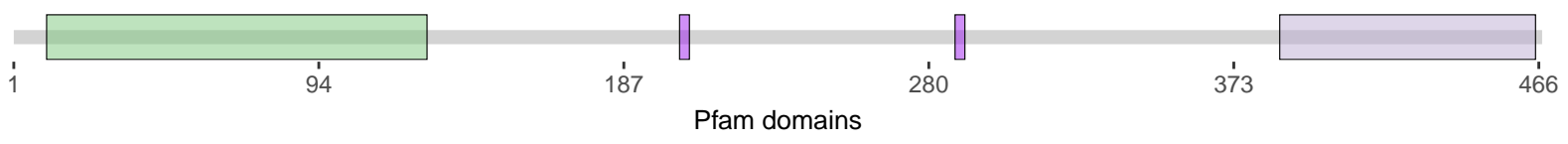
Molecular weight



Gel Slice

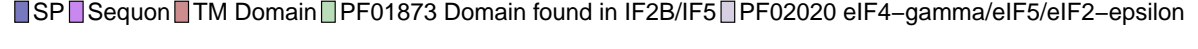


Protein length



Pfam domains

Pfam Description

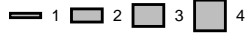


Protein sequence:

EAPPADSDDDVEVGTDTSMMAAAGRIGEGLNVTASMMLSATEEKGSGKSPAREKPKANGGCTGVNGENFKESLIAGTNGVVERSNKDKLVDAKERLADEKEHLNKGSSVAGLKSFLGSSGTHEDIVDALFEALFGGVGKGFKEVTKKKNYLAALVLDGDSGLALLHAESFGKSSSEAVKEVALVLAALVDMVEEFVVEYKGGKGNLSPWKNKPFVVELGSAESETED

NbL14g18940.1 nitrate_reductase_[NADH]_2 [MW = 101.96 kDa]

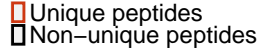
No. of times detected



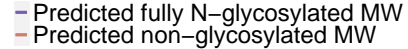
log(intensity)



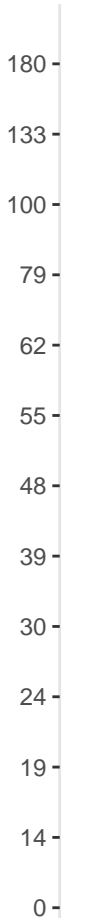
Values from



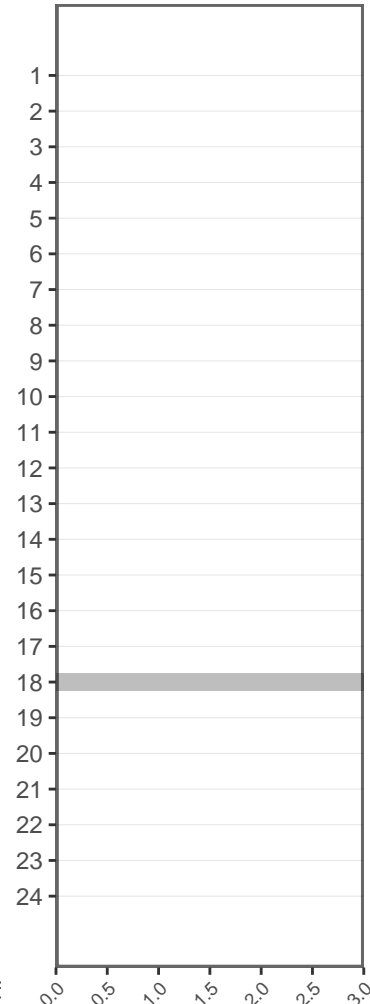
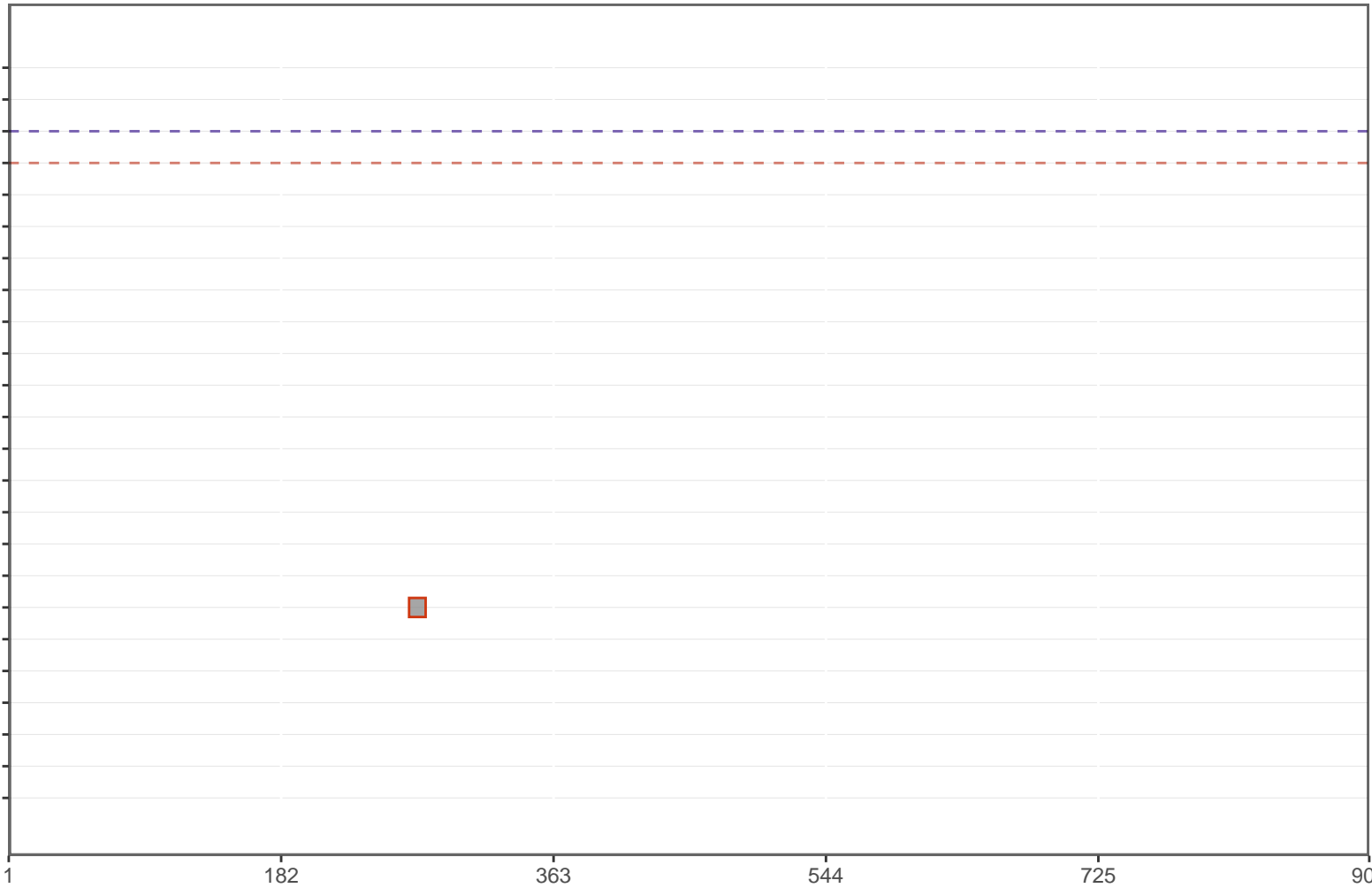
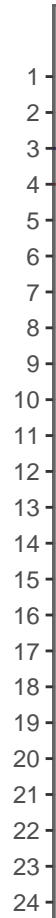
MW indication



Molecular weight



Gel Slice

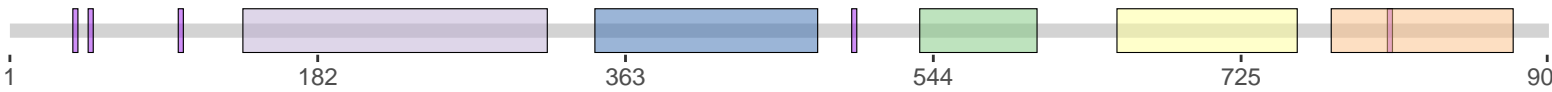


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

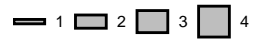
- SP
- Sequon
- TM Domain
- PF00173 Cytochrome b5-like Heme/Steroid binding domain
- PF00174 Oxidoreductase molybdopterin binding domain
- PF00175 Oxidoreductase NAD-binding domain
- PF00970 Oxidoreductase FAD-binding domain
- PF03404 Mo-co oxidoreductase dimerisation domain

Protein sequence:

DLLSAKEIAVRAVDEFLNTQPEKLIWVWMMGMNNGWFRVMNVKPKKGEIGVFEHPTLPGNQSGGVMMAKERHLEISAEAPPTLKKSGISTPMTAKMYSMSEVRRKHSASDAWIWHGHYDATRFLLKDHFGGTDGSLNAGTDCGTEEFDAIHSKAKKLEDFRIGELITTGYSDFQNSVHSGSSFSFLAPIKELVPAQRWVALIPREKPKLIDKQSHSDVRRFRFRFALPSEDQVVLGLPVGKHIFLGAVIDDKLGMRAYTPTSTDEVDGYFELWVYTKYKGIHPKFPNG

NbL14g18880.1 G-type_lectin_S-receptor-like_serine/threonine-protein_kinase_At1g34300 [MW - SP = 89.96 kDa]

No. of times detected



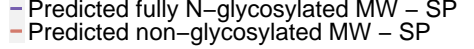
log(intensity)



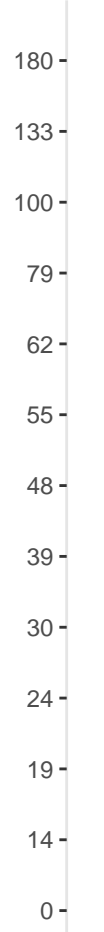
Values from



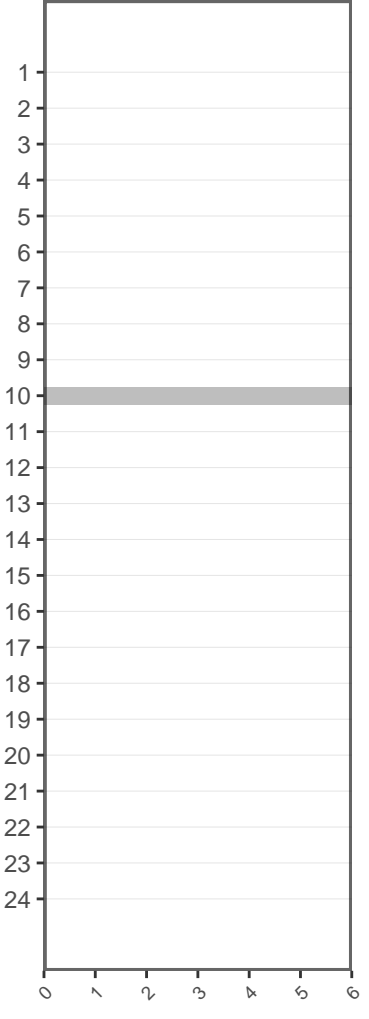
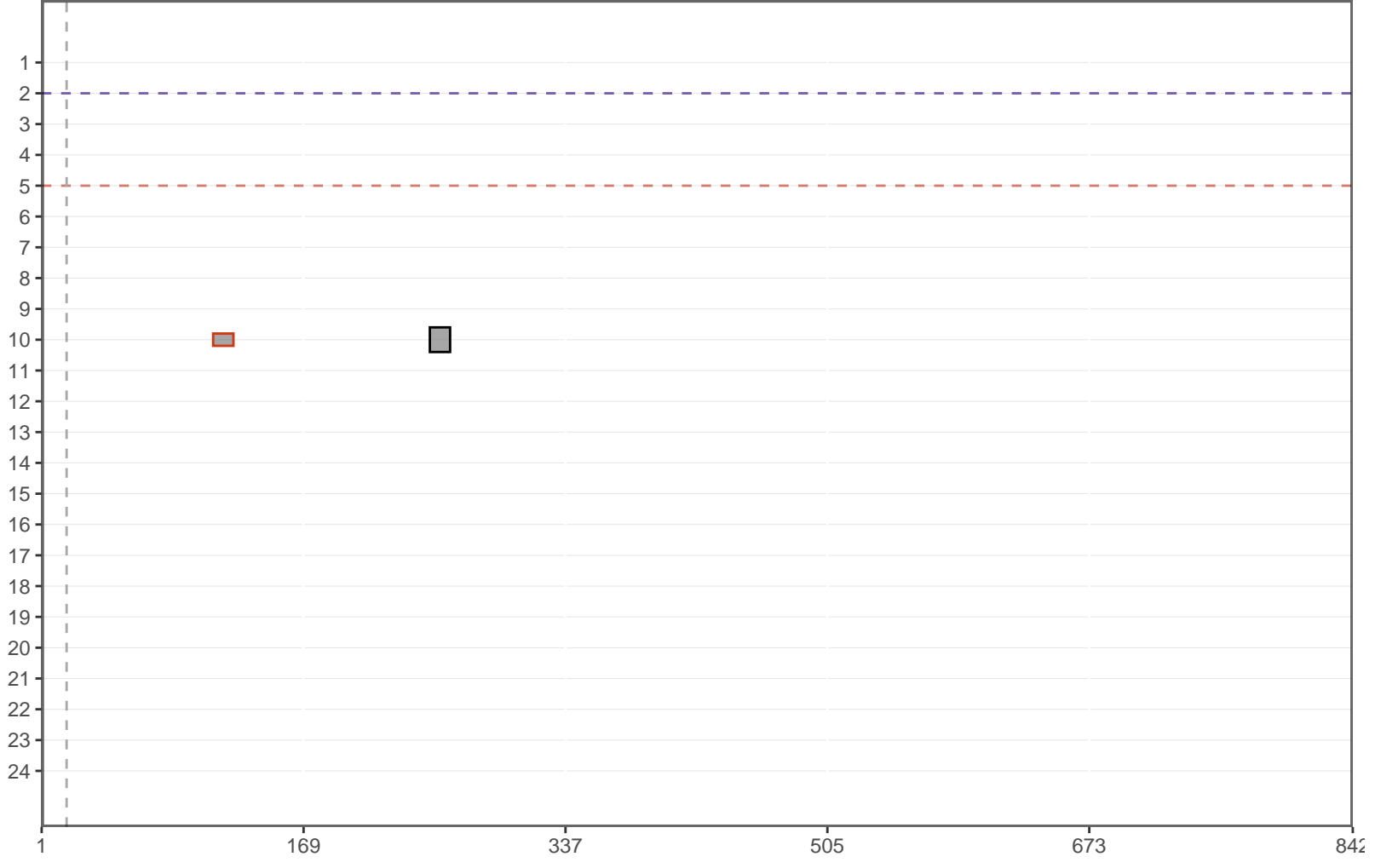
MW indication



Molecular weight



Gel Slice

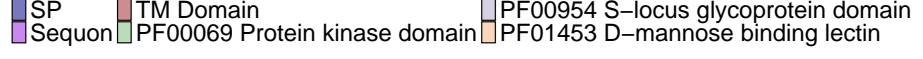


Protein length



Pfam domains

Pfam Description



Protein sequence:

IIVSETVQKXNRGRVPSGVVAIVAVASLLGLLLEGGWVWVGRFRNSKFAFLSSQYALLEYASGAPVDFTYKELGRRTTKGFKKELGAGGFGAVVRAVLANKTVAAVKLEGGEGGKGRFMEVATISSTHLLNLVRLKGFQSEGRHRLLVYEFMKNGLDKFLFAEDYLSGKLLNWEHRVYVALGTARGITYLHEEGRDGVVHDKIPENILLDENYAKVSDFGGLAKLNPDKHRRHRTLTSYVRRTRGYLAPEWLANLPITKSDVYSGVMALLEVSGKRFVSEETSRYK

NbL14g18810.1 RNA-binding_protein_8A-like [MW = 24.79 kDa]

No. of times detected



log(intensity)



Values from



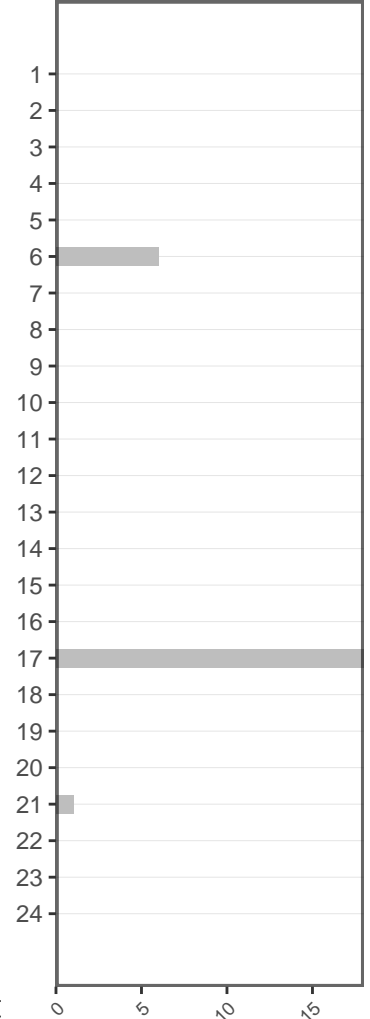
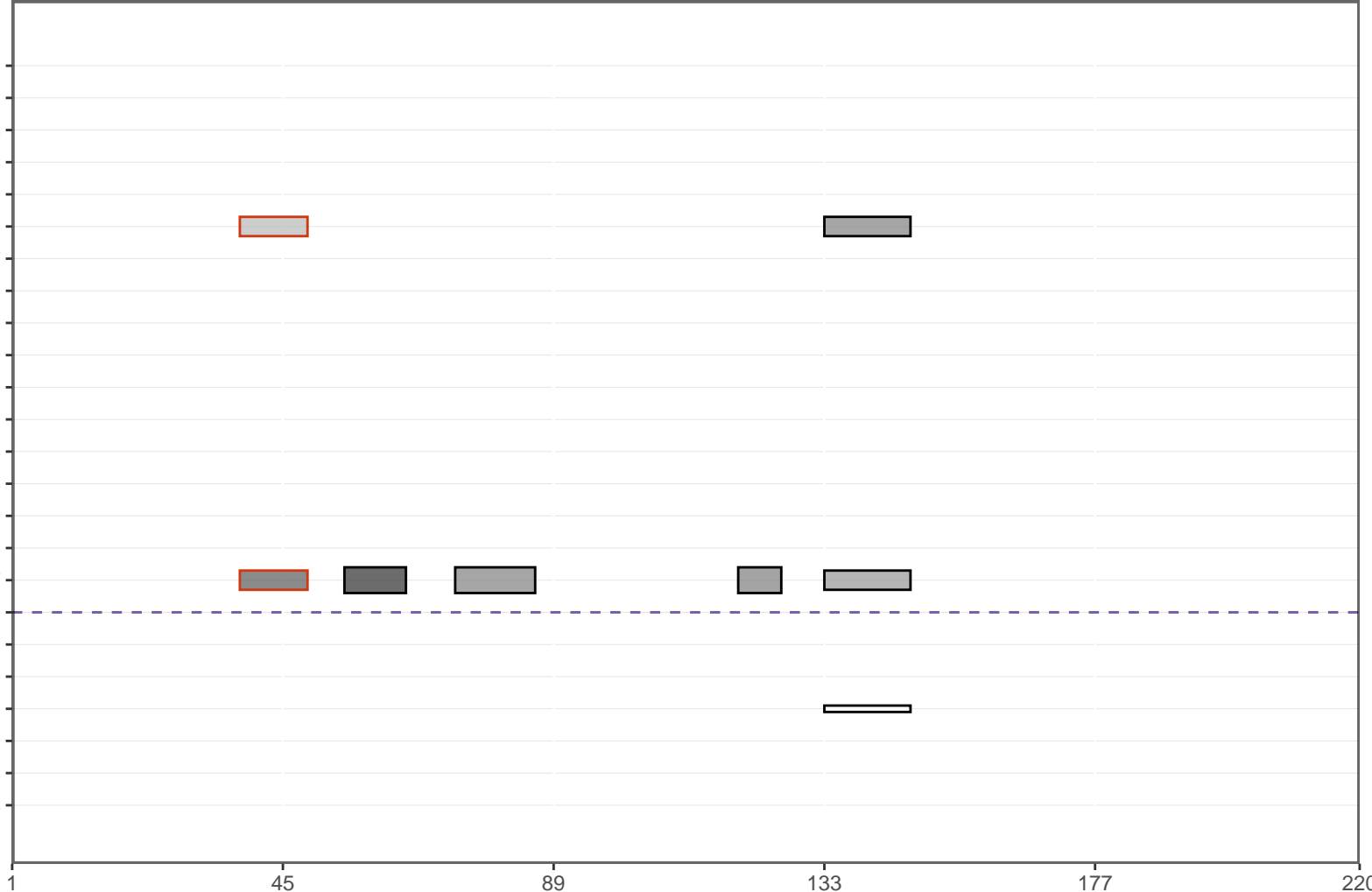
MW indication



Molecular weight

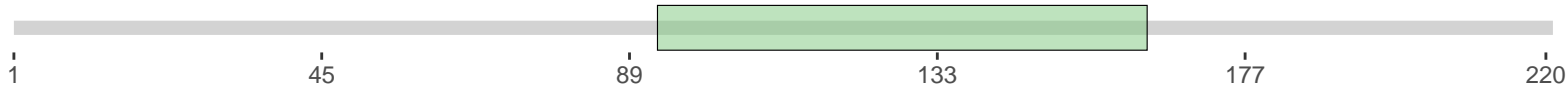


Gel Slice



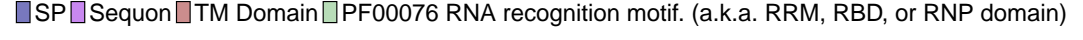
Protein length

Peptide counts over 4 repeats



Pfam domains

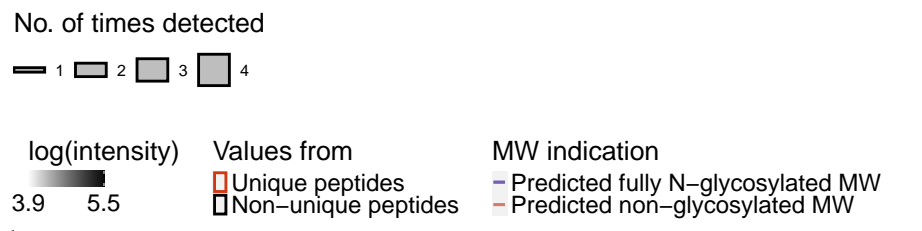
Pfam Description



Protein sequence:

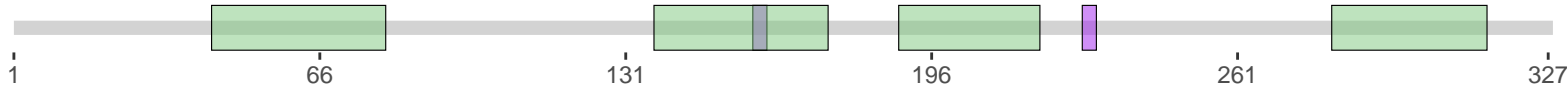
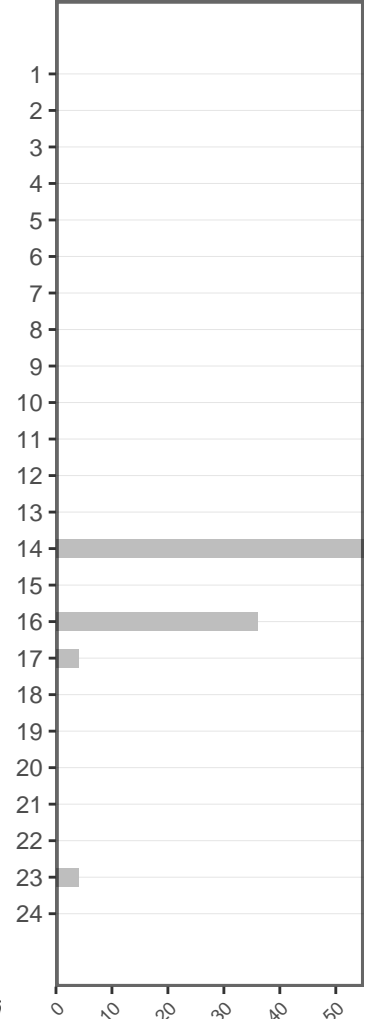
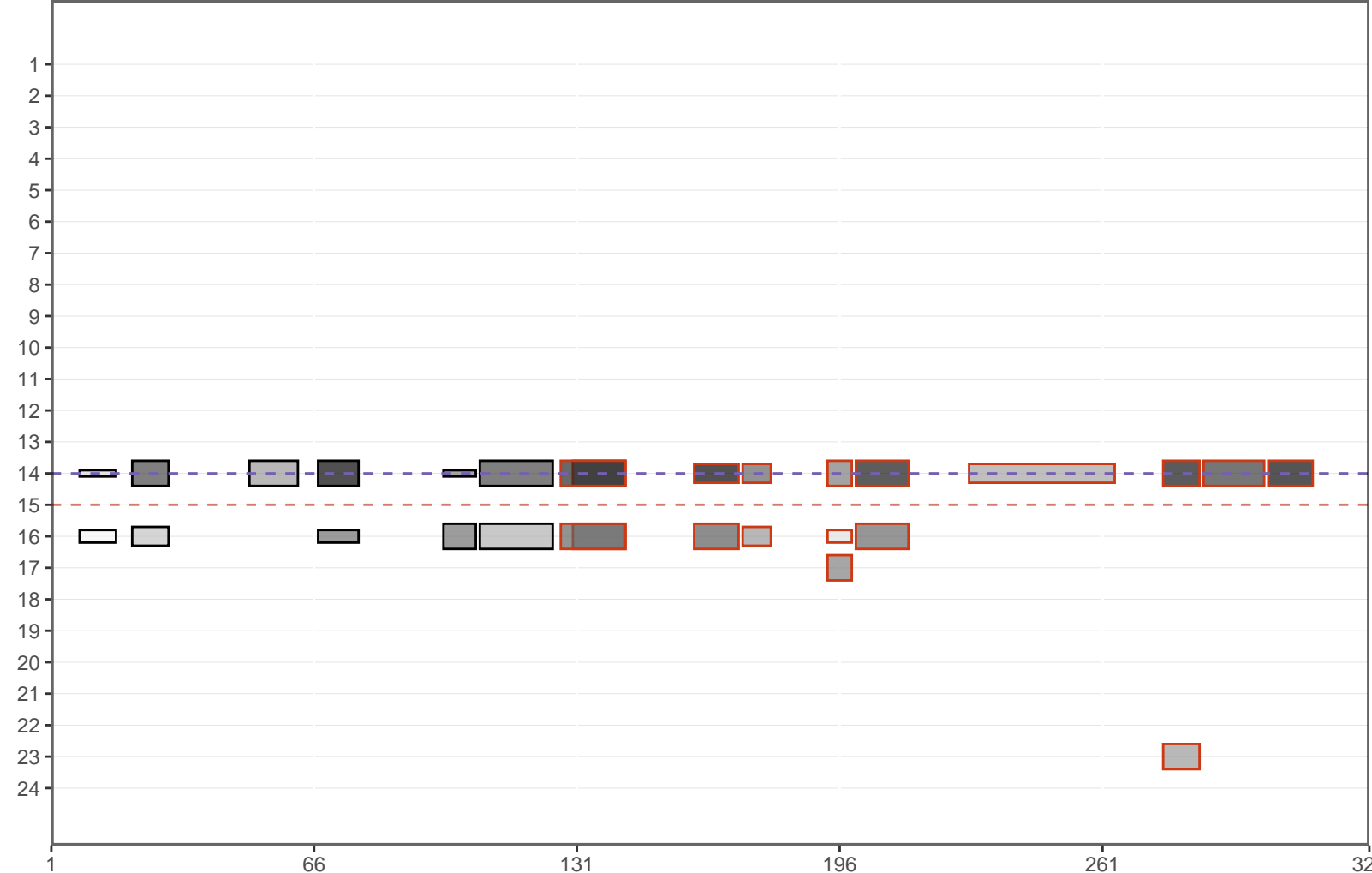
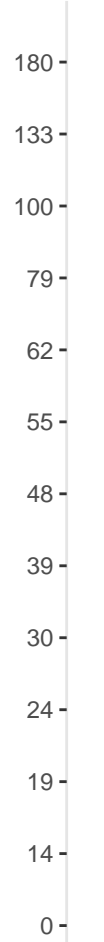
YVNEETQEDDLINIEFGEGEKNVHLLDRRTGFVKGVALIEYENFEEAGRAINEKDKGAELTQTHVDVAFSGRGPKRNRARRVYHSLMLLLYHMRFMENEAEESSEEMMPAHVWHDHFSFL*

NbL14g18760.1 eukaryotic_translation_initiation_factor_3_subunit_I-like [MW = 35.91 kDa]



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain PF00400 WD domain, G-beta repeat

Protein sequence:

INRAVWGPLNRTSAGEDAVIRVNDVETGKILMESDKEVGHKKGITSLGKIVDGHFFITGSLDKSAWLWDRTFLKKNYTERPVAIVAVTMSPLLNHVLGGGDABAVTTTDRHAGKFEAFYDKILQDEIGGVGKHFGPINALAFNPDGKFSFGGEGDGVVRLHFDHDFNKI

NbL14g18660.1 uncharacterized_protein_ycf37 [MW = 34.46 kDa]

No. of times detected



log(intensity)



Values from



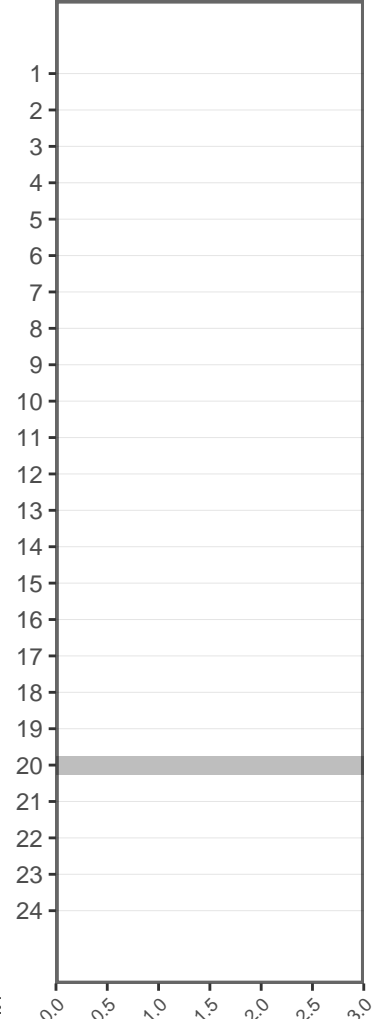
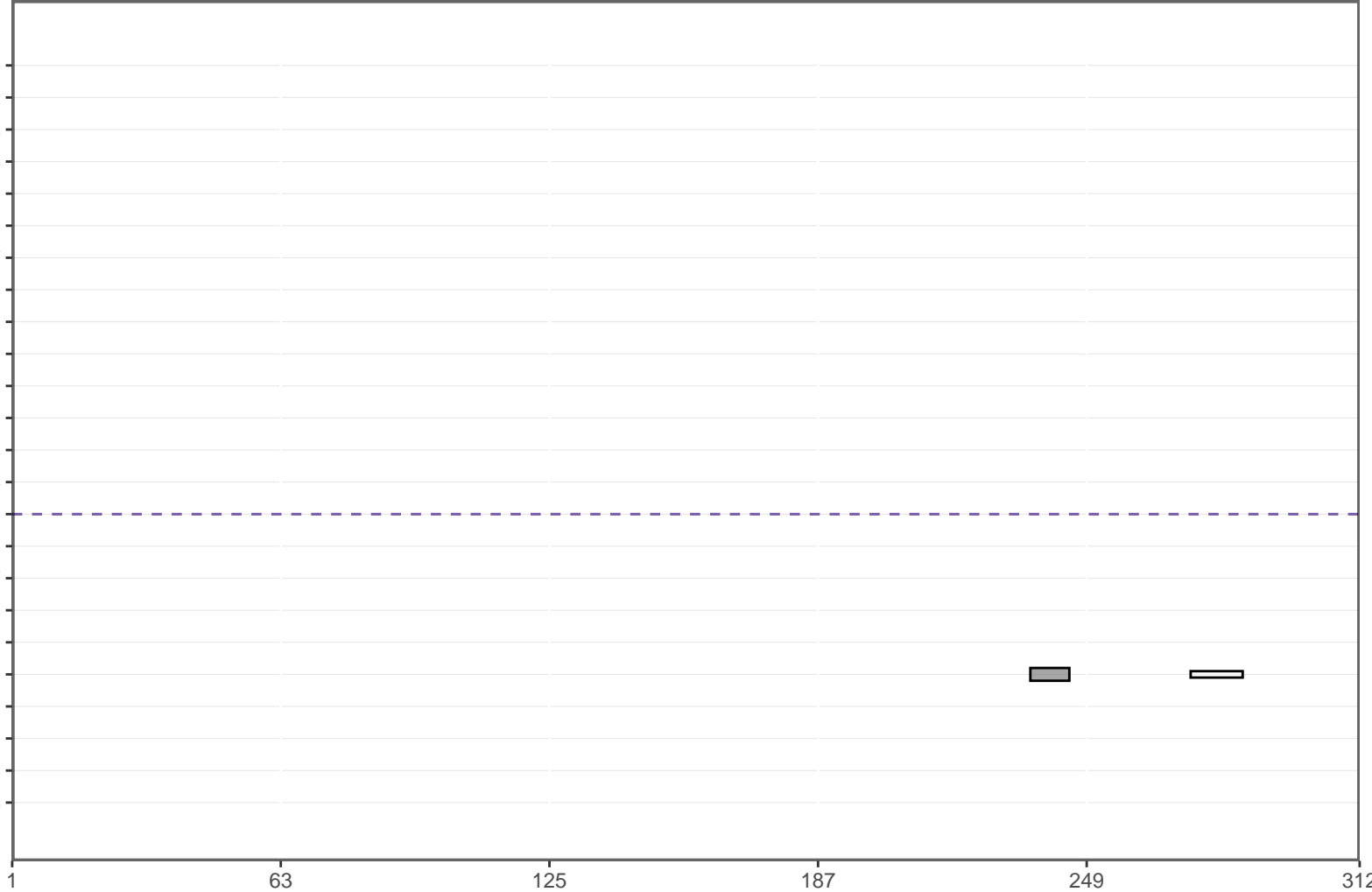
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

AGSFFVIRQVLYRRELDLSAKELGEGVRSDDASATELFEFGAVMLRRKFPYATKYLGAAGKWDGDDDLADVYNALGVVYLDEKIDKGIAGFENAWLGPYVVTAWNLGDVYEKTDLTSALKAFEEVLLFDPNKKIARRPRRDALKEKVGMYKGVPPVKEKKE

NbL14g18650.1 chorismate_mutase_2 [MW = 29.38 kDa]

No. of times detected



log(intensity)



Values from



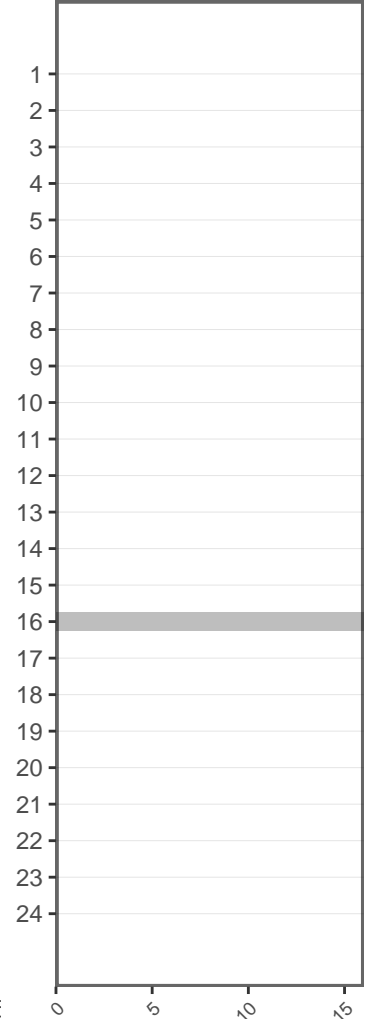
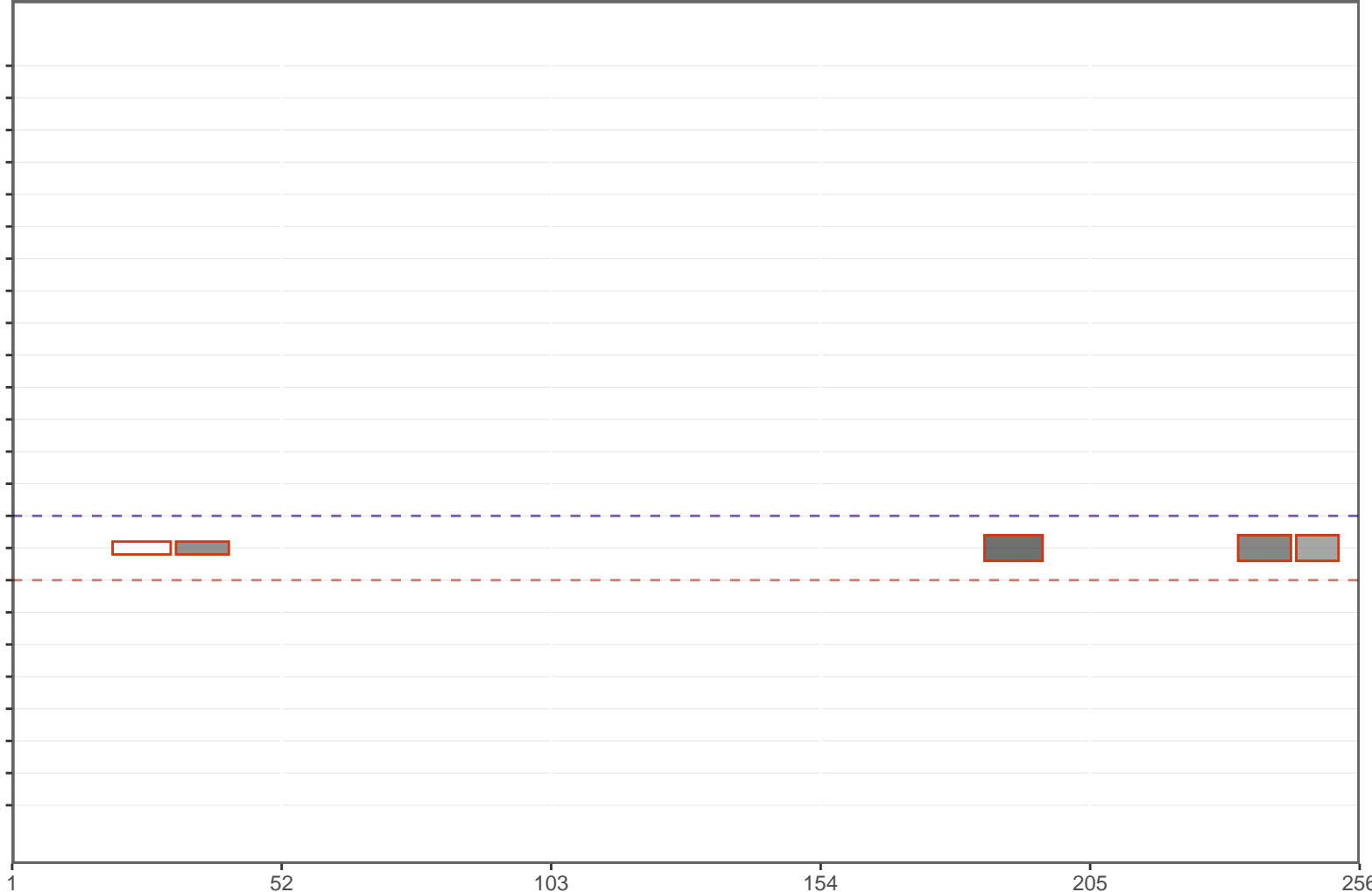
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

IKQLLPLFCTQADDEANFATASGDHLLGLSRRHHYKGFVKEVKFRDCTDGYKPFILANDRDALMKLLTFEAVEEMVKRIVANKALTFGGQVTLNDDSTKEVKCKVDPSSLVSRLYDEWIMPLTKLVEVEKLLRRLD*

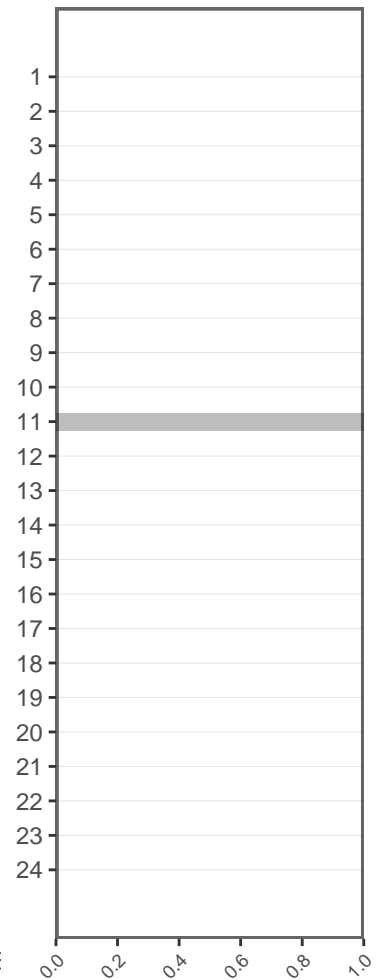
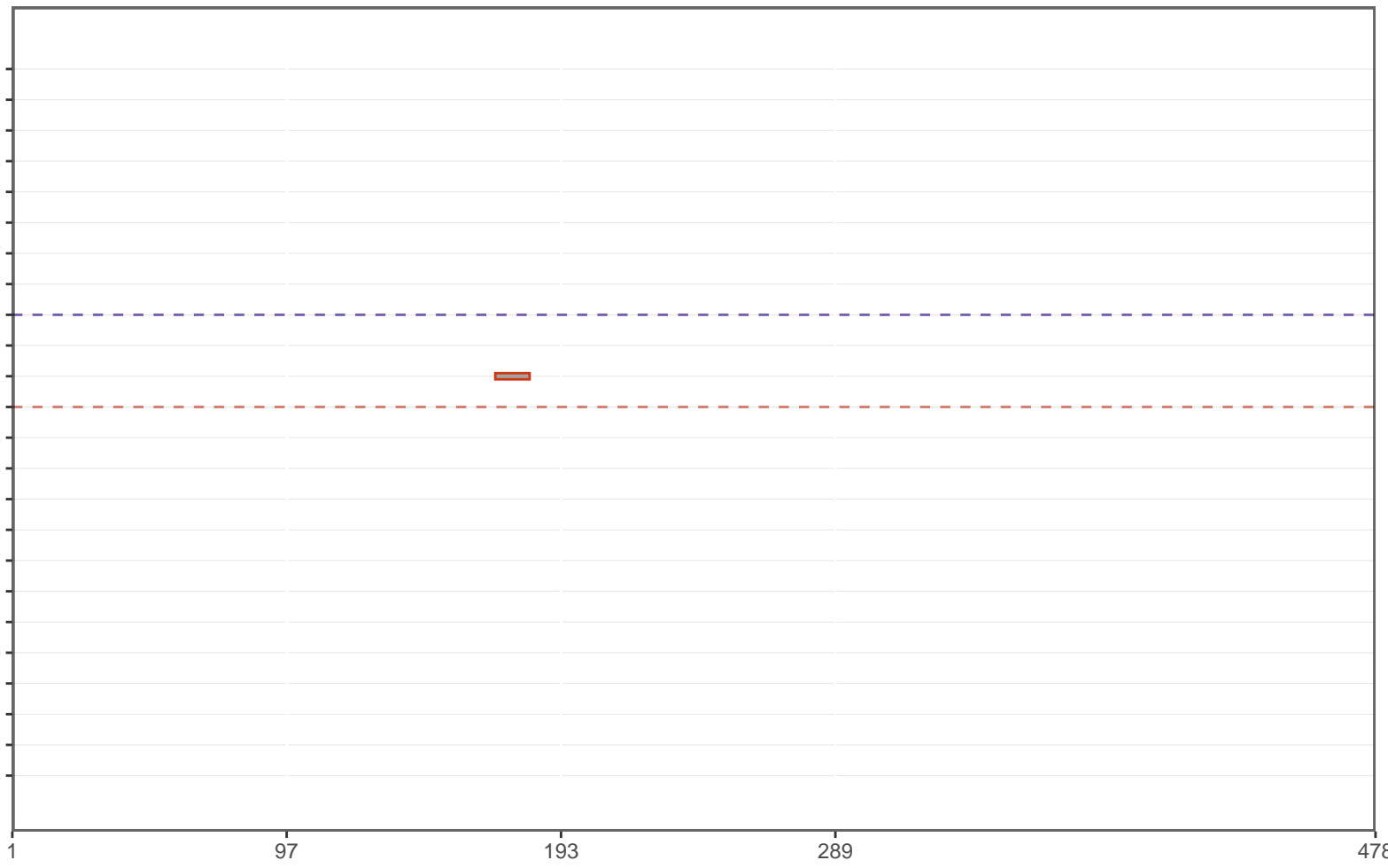
NbL14g18640.1 dihydrolipoyllysine-residue_acetyltransferase_component_5_of_pyruvate_dehydrogenase_complex_chloroplastic [MW = 49.6 kDa]

No. of times detected
 1 2 3 4

log(intensity) 2.9
 Values from Unique peptides Non-unique peptides
 MW indication Predicted fully N-glycosylated MW Predicted non-glycosylated MW

Molecular weight
 180
 133
 100
 79
 62
 55
 48
 39
 30
 24
 19
 14
 0

Gel Slice
 1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24



Pfam Description
 SP TM Domain PF00364 Biotin-requiring enzyme
 Sequon PF00198 2-oxoacid dehydrogenases acyltransferase (catalytic domain) PF02817 e3 binding domain

Protein sequence:
 ISTRAPVGSVVGTTAQPSSGAPVAPVVELGFTYVPTTMDNAYSRNIVSELAVPTFRVGYHTTNALEDALYKKKSKGVTMTALLAKATALALAKHPVYNSCRDGGKFFYNSINAWAVIDGGELTPVLODDKVDYLSLRKWKELVAKARAKGLOPHEVYTTGFTLSNLMGFVDRFDALPPGTGAMVAGASHPLVGTGDRIGLKNMGQVNYTADHRVYTGADLASFLDTLGGIEDPKDITL

NbL14g18480.1 beta-galactosidase_16-like [MW - SP = 77.88 kDa]

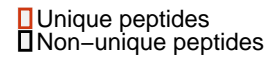
No. of times detected



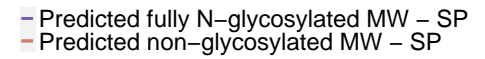
log(intensity)



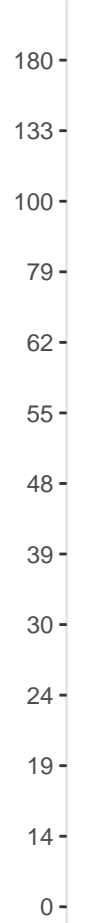
Values from



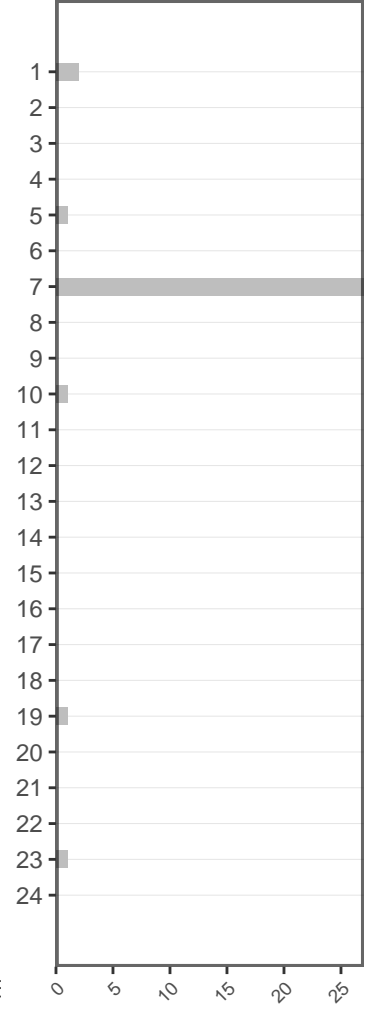
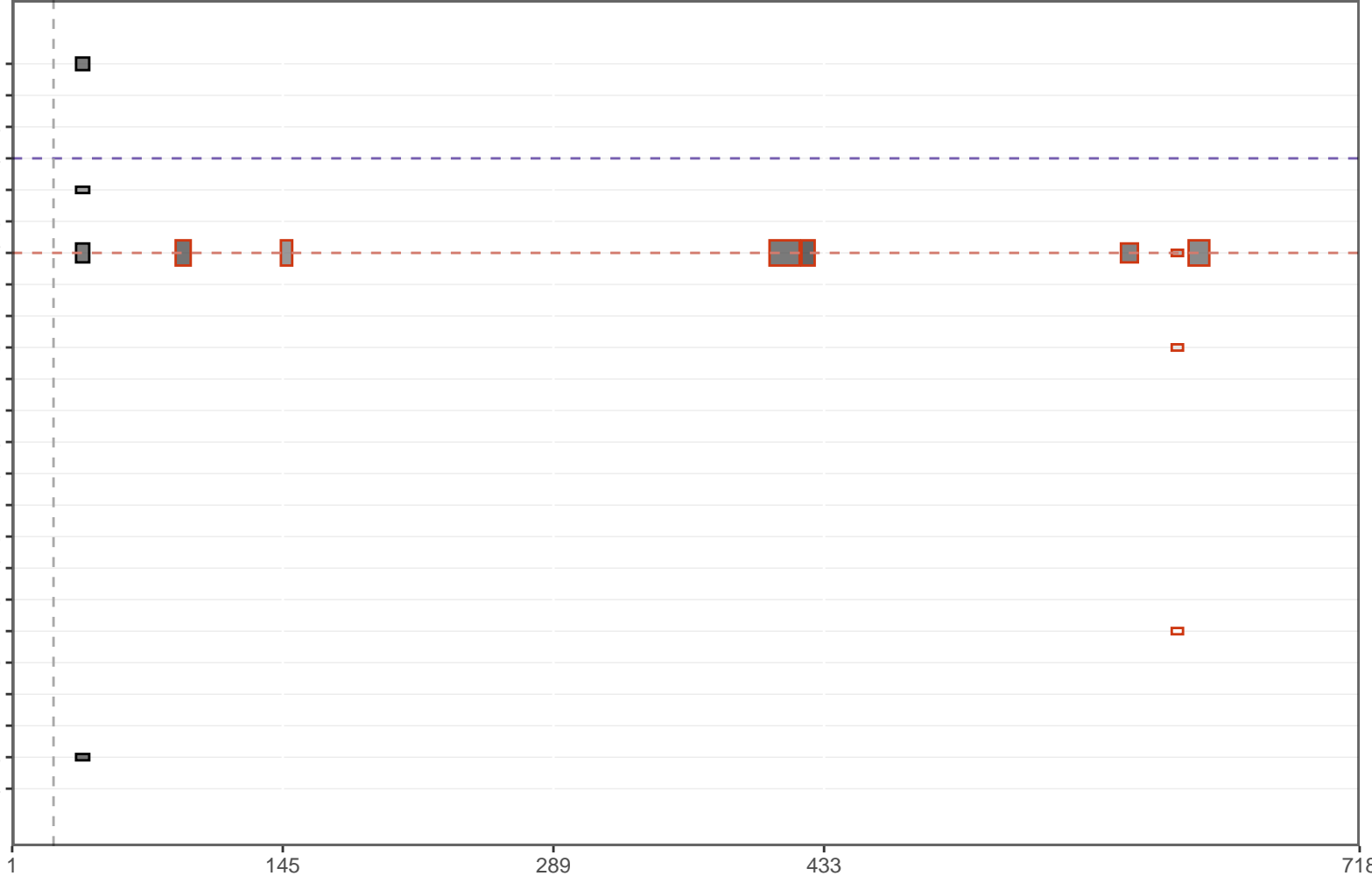
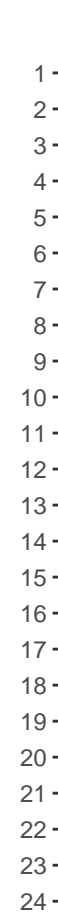
MW indication



Molecular weight

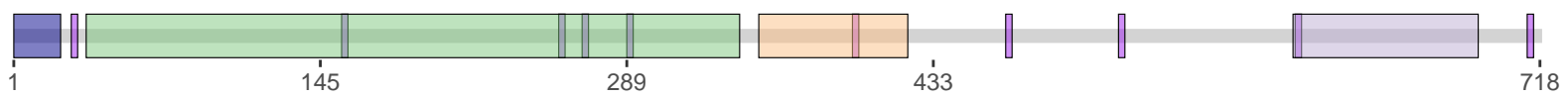


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

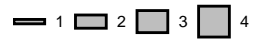


Protein sequence:

CSEALLSFPPTMOSLGGGEGAVYFSGDGGAGAAFLVNTDRRSATVRFQNLTYQLPKKSSILPDCNVAFTAKVNTGFNTRTSRPAIKFDGAEKWEQFQEVPOQDATTLLRSGTLLEGTNTRKDSGLHWYASFEQDGGDEPQARLGVKGLGHVLAHFVNGALVGSAGHQDFRNTSFTLEETVGLNKGQTNQISLSATVQLPDSGAFLERRRLGVRSVHKNSRGVKVFTVFPWGGYGVLLGEKLGKTHEGSKNANWSYGS6GQLTWYKTFSAKKGKGFIALNLGSMGP

NbL14g18470.1 beta-galactosidase_16-like [MW - SP = 76.47 kDa]

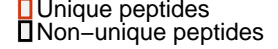
No. of times detected



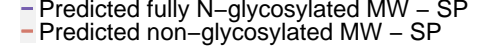
log(intensity)



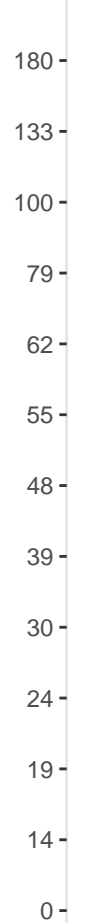
Values from



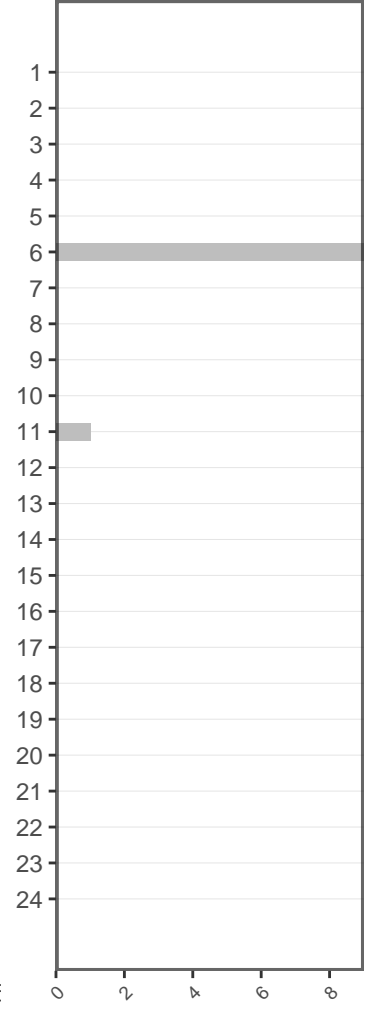
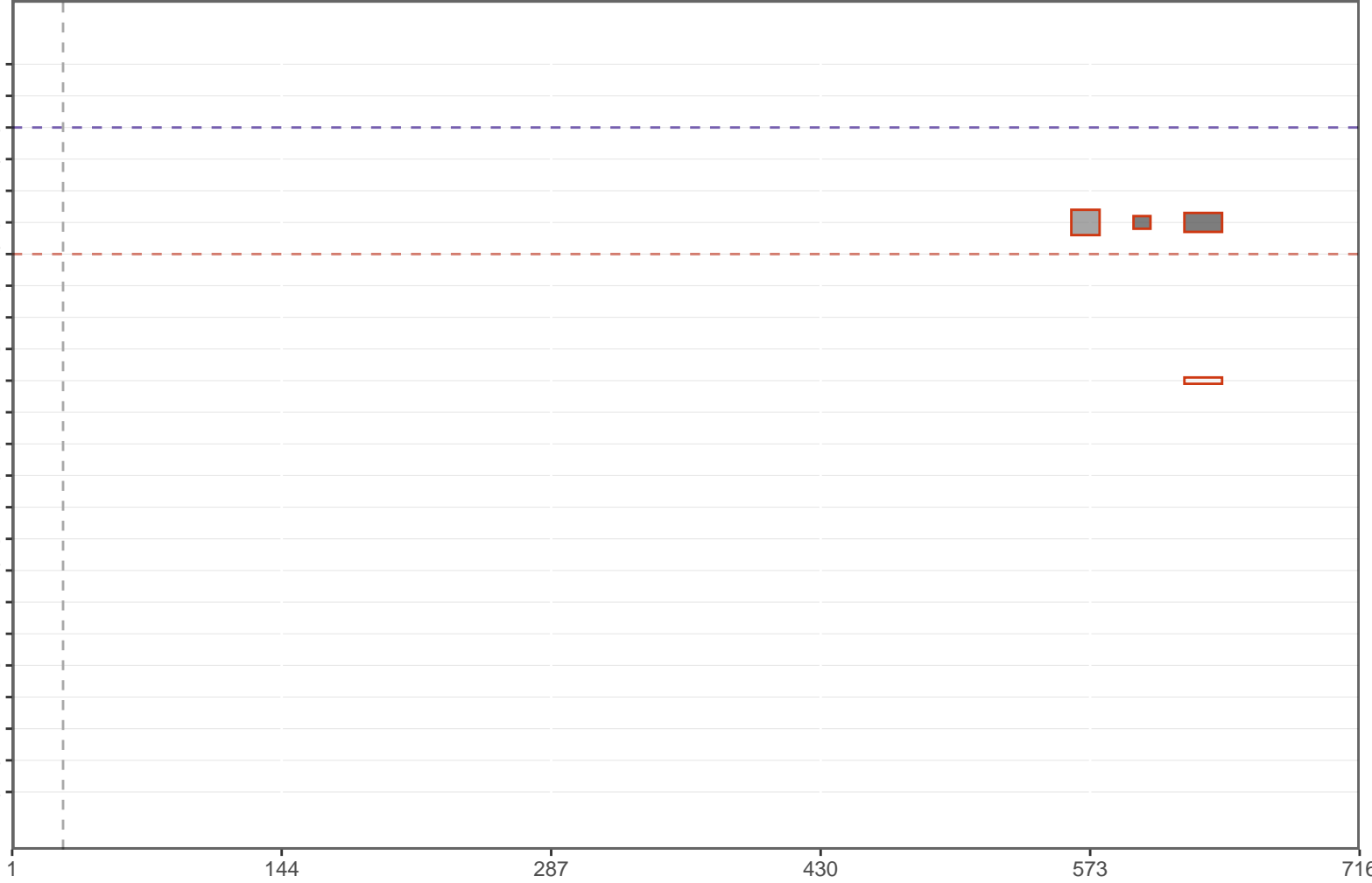
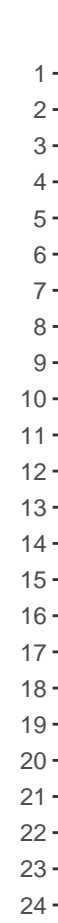
MW indication



Molecular weight

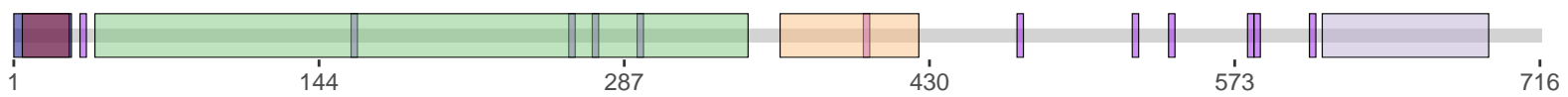


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- Pf01301 Glycosyl hydrolases family 35
- Pf17834 Beta-sandwich domain in beta galactosidase
- Pf13364 Beta-galactosidase jelly roll domain

Protein sequence:

JHAYVLCSETLSVFPFMSGLGEGGEAYVFGSDSGAGAAFLVNDNRKVVVQFLNSYELPRGSIPLDQKTVSFNTAKVSTGQFNTRIALPAWKFDAAEKWDFGFEVPLQDLSLRSGLLEHMMNTTKDVSQKLVWYTFSSIQGDSPDQKLVTLGVKGLGHVLAHYVNGAHAGYGHGQFRNTSFTLESTLKNKGTNNISLLSATVGLPDGSGFLEHRAALGVGSIQGDNEAKNNTYVSWGVQVGLLGEKLGYSSEGSKANWSSLSSGQPLTWKBAFDAPEGDQDPIALN

NbL14g18290.1 uncharacterized_LOC104240053 [MW = 38.14 kDa]

No. of times detected



log(intensity)



Values from



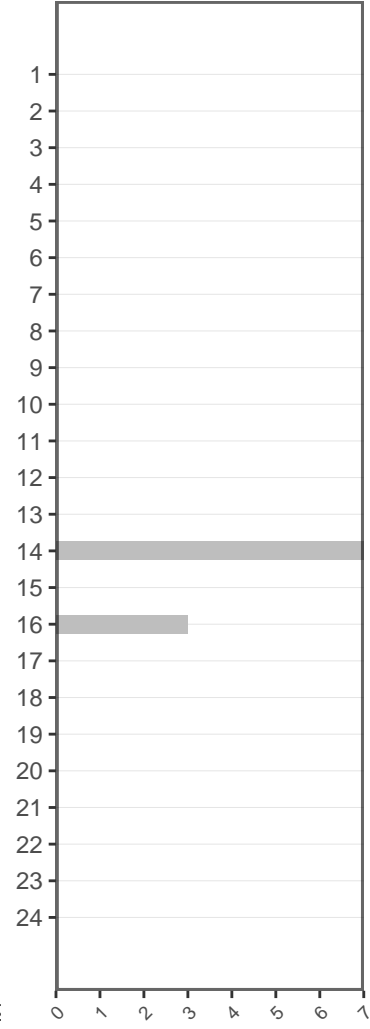
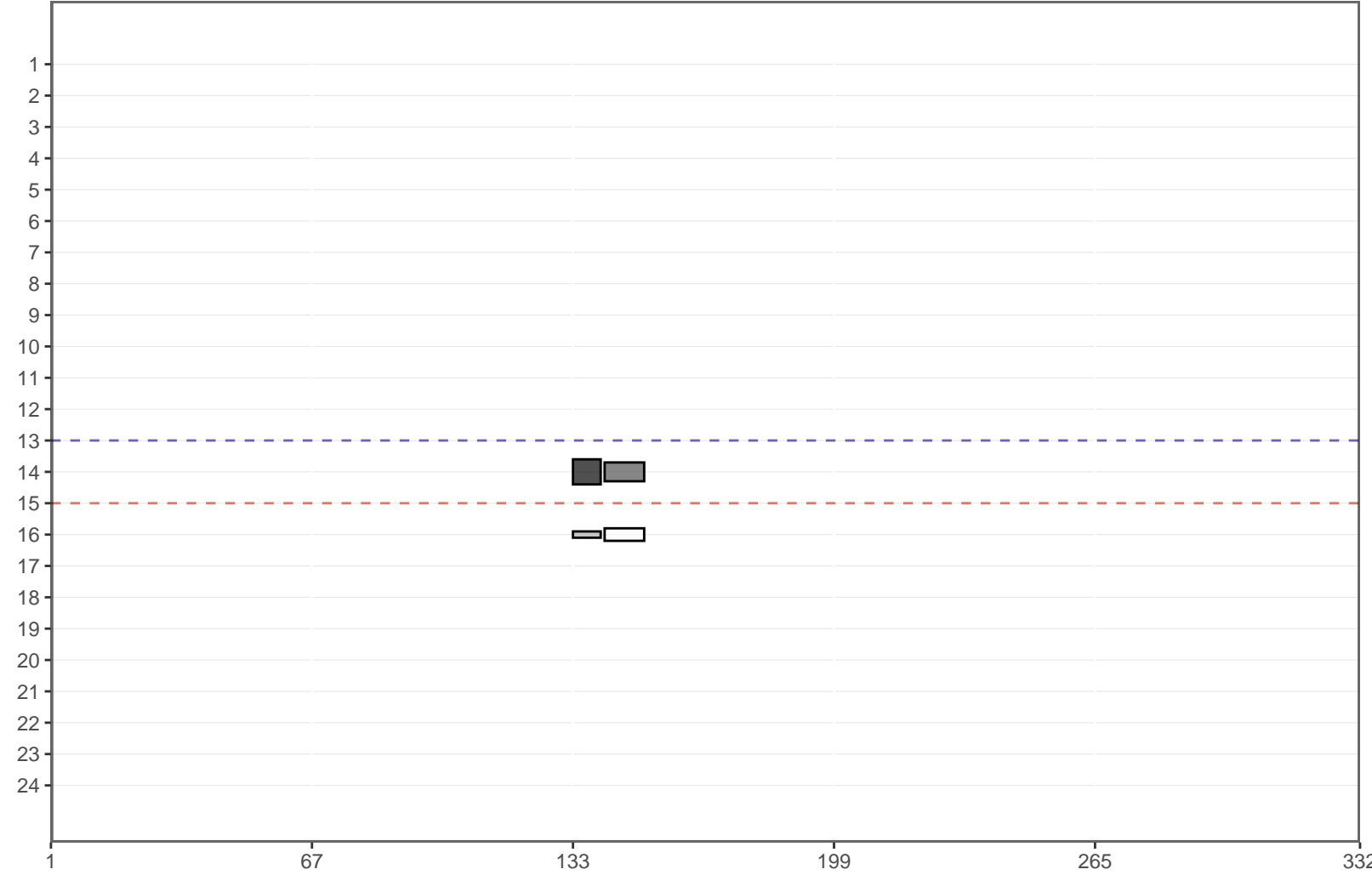
MW indication



Molecular weight



Gel Slice



Protein length

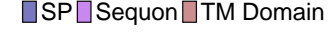


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

PDPDNDYDFREMKVTPDQTDHAIIRVLAPMPQKIVRCAMSDYGCYVVFEPDAPRDPMKYKSEREVKVFLENHYRNRVVGDFEALDFEEVYDSDKTKGTRVKKVVTVPGRNRDRKNDLLVIRQNGNSFNIPSEERDDFTTVEKEEWWKGRGDMERHLRKLRFDFEVSNIWF

NbL14g18210.1 40S_ribosomal_protein_S15a-1 [MW = 14.78 kDa]

No. of times detected



log(intensity)



Values from



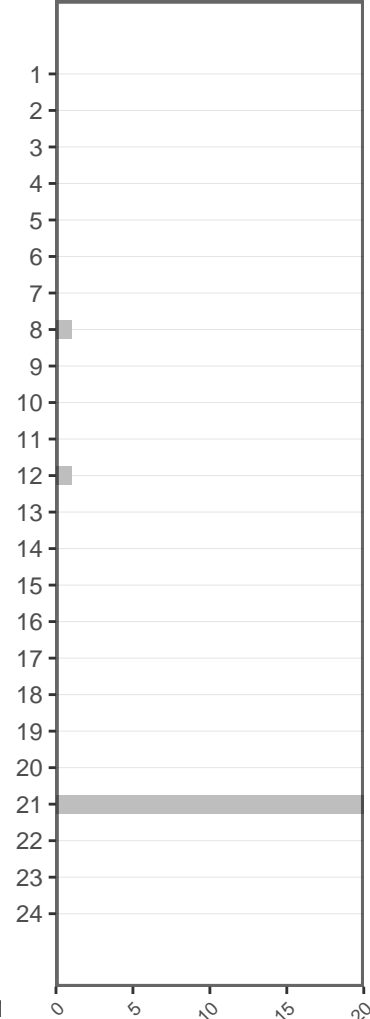
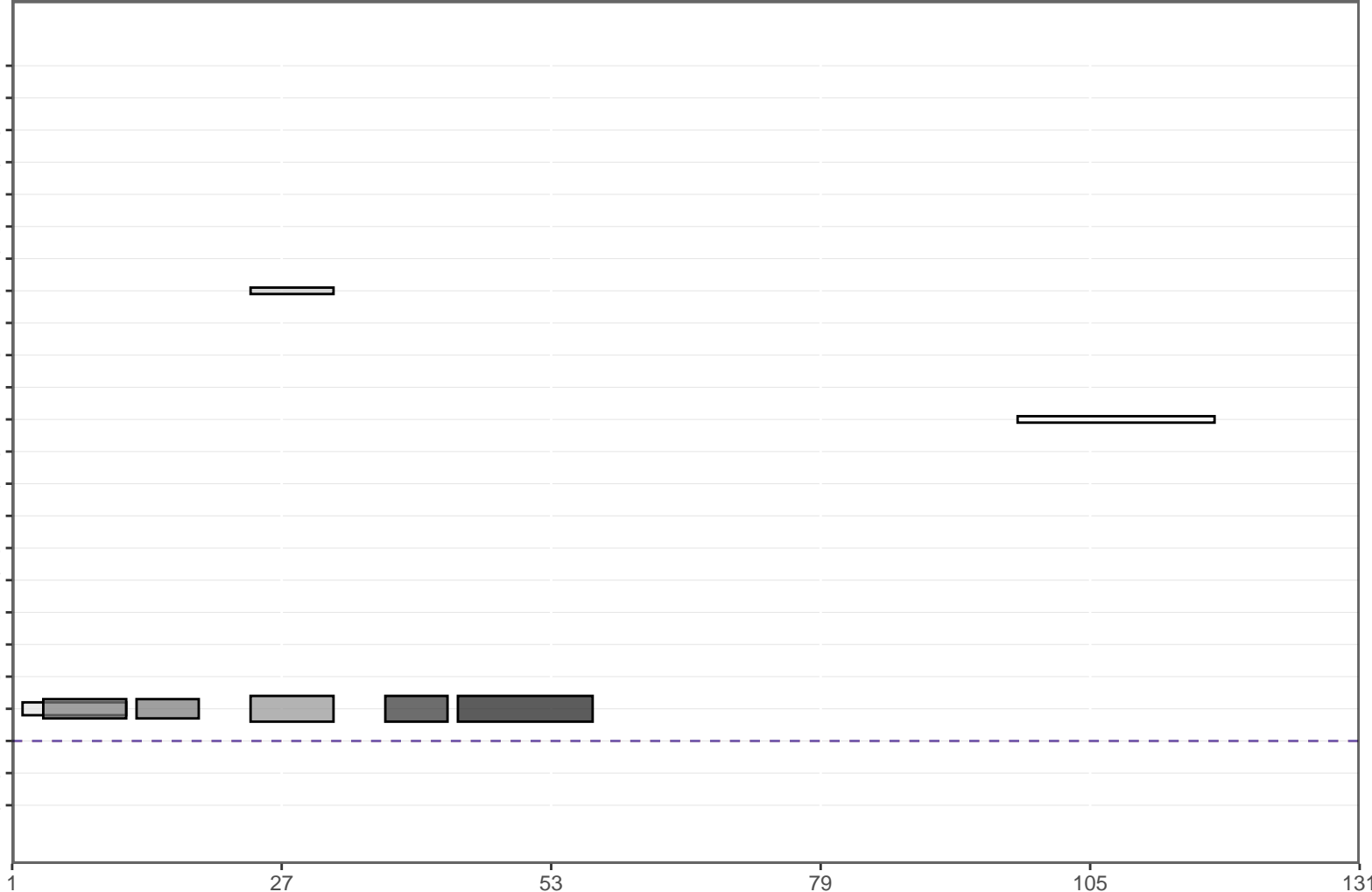
MW indication



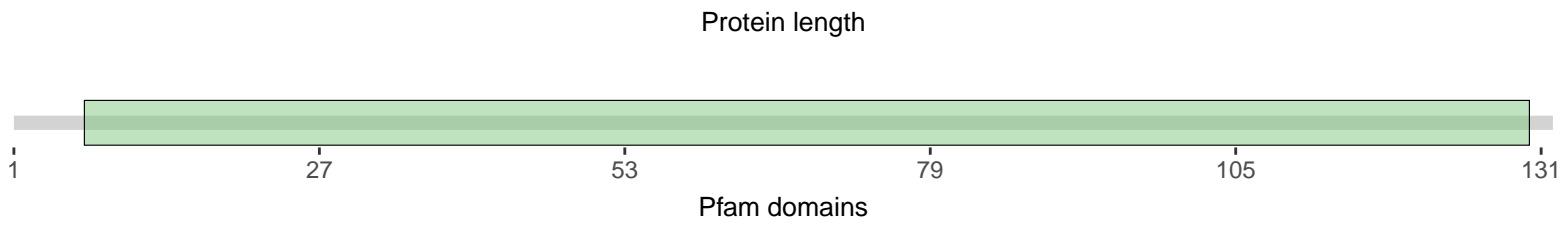
Molecular weight



Gel Slice



Peptide counts over 4 repeats



Pfam Description



Protein sequence:

VDDHRSKIVVELNGLRNKGGVSPRFDMGVEIEGWTARLLPSRQFGYVLTTSAGIMDHEEARKNVGGKVLGFFY

NbL14g18160.1 UDP-sugar_pyrophosphorylase-like [MW = 68.76 kDa]

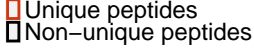
No. of times detected



log(intensity)



Values from



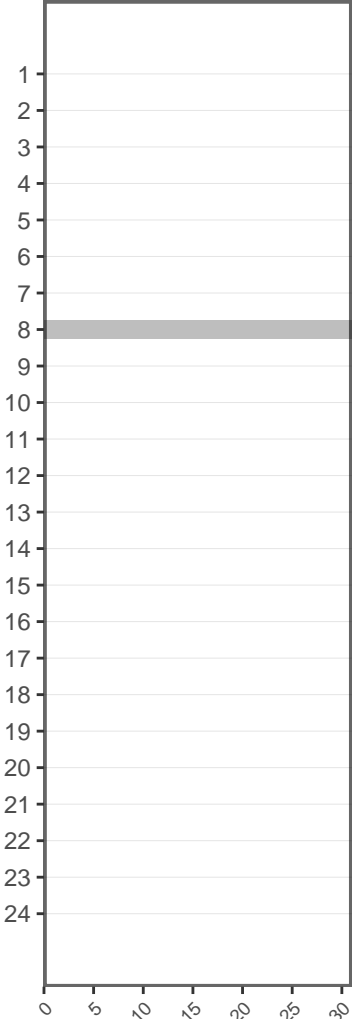
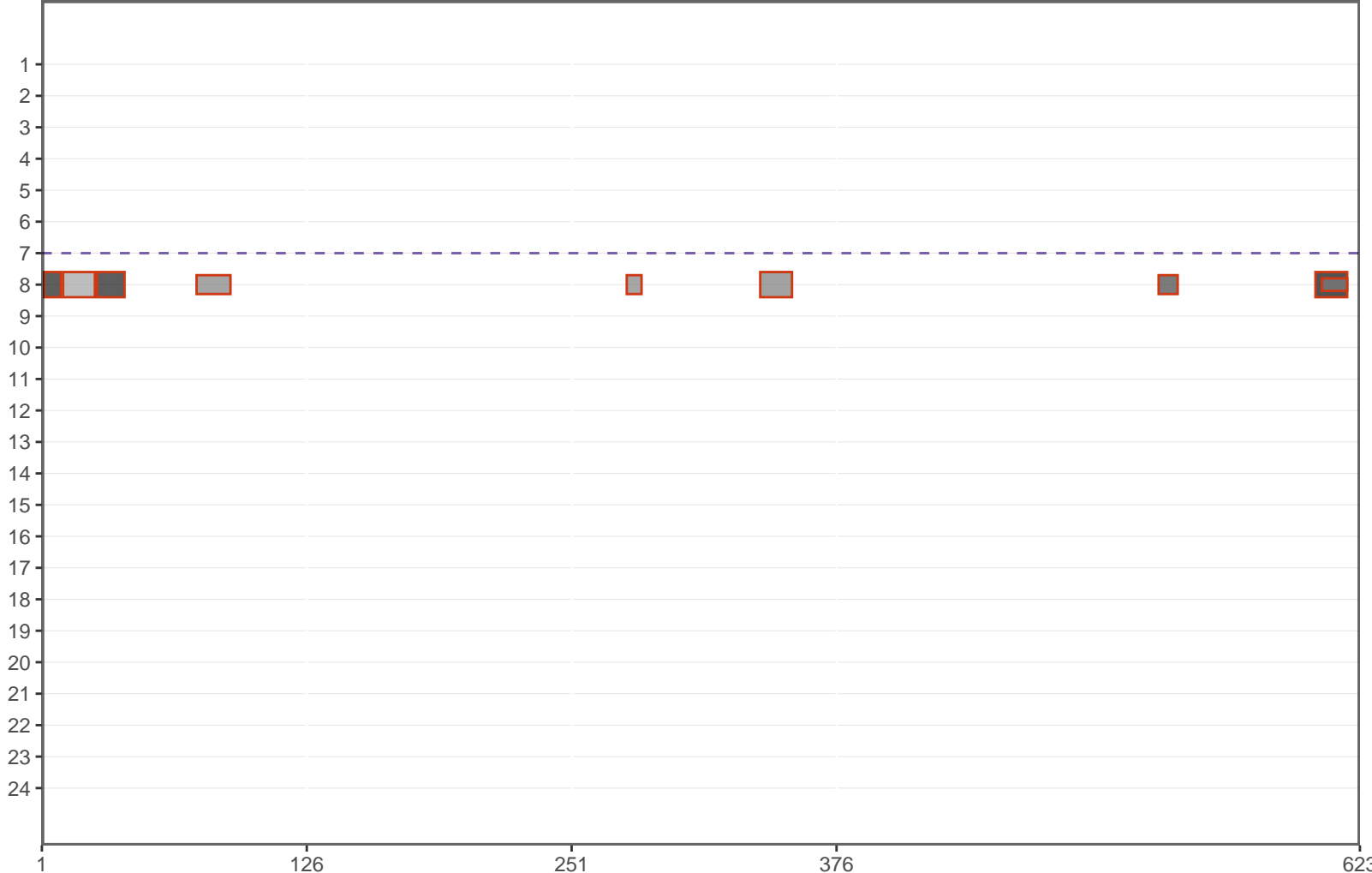
MW indication



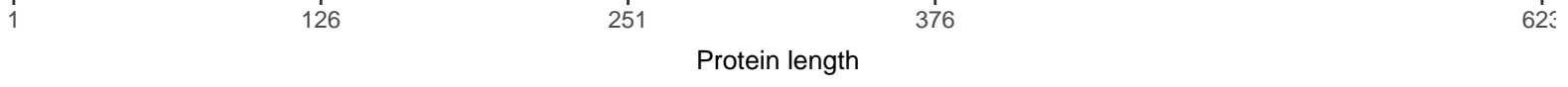
Molecular weight



Gel Slice



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LFKAIPALGVSAIKQHYHNSLAWPKKAKKAIGGDKLTHKDRAMVINVEYNGLDLPLRAAGYPDGDEVNSETGYEFPFGNNGLIFEIGPYEELTKGDKAEFVNPKYKDATKTFKSGSTRLEGMMDGDPKTLRPSARVQFTMDAWLAVPAAVKNNPEDAANKVPGKPNPHSATSGEMAIYRSHSLLRKAGVKGDGDPVIGVFNQGEVEVWSRVVWKRKVALTFSEVKKRVKSGNDSIGRSTMAKGRDALEDLSLGDALFEAVDGAEVKVGSGVQKGVWTEINDYEDTSI

NbL14g18030.1 TOM1-like_protein_2 [MW = 56.92 kDa]

No. of times detected



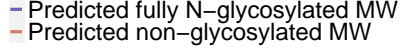
log(intensity)



Values from



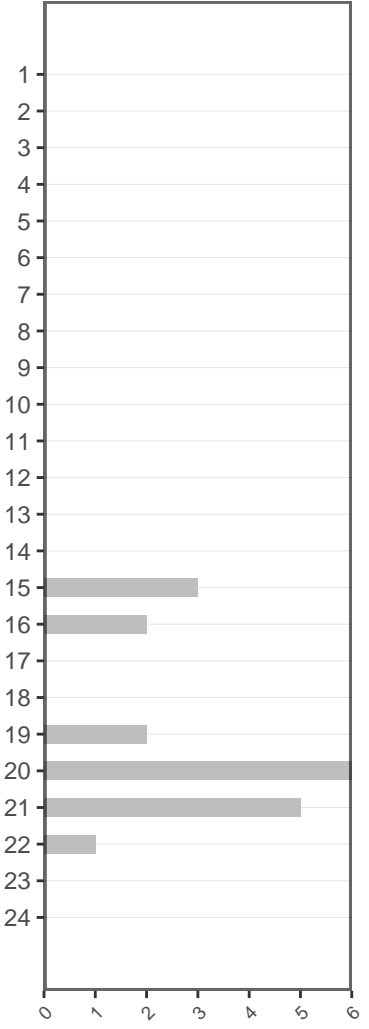
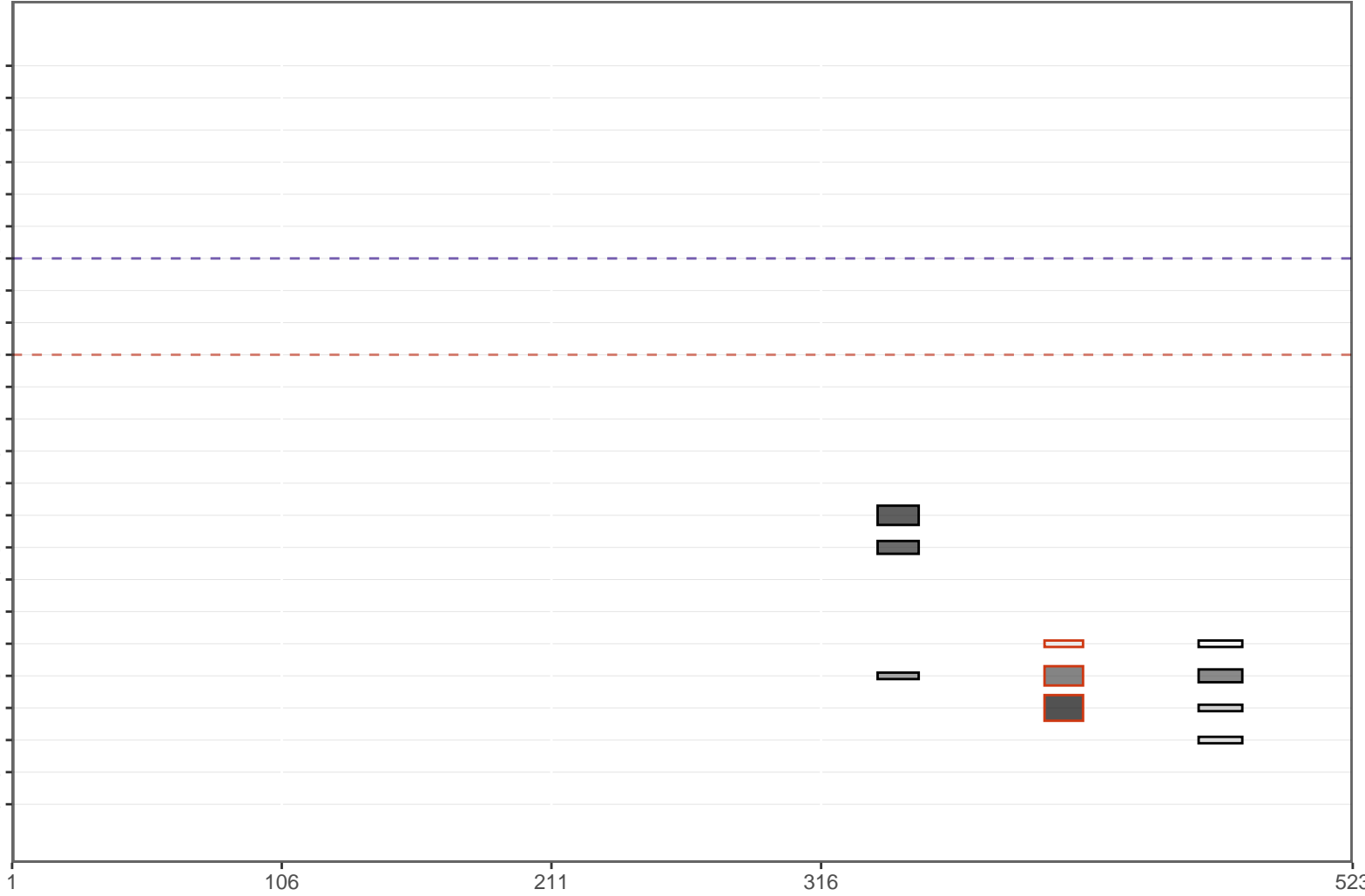
MW indication



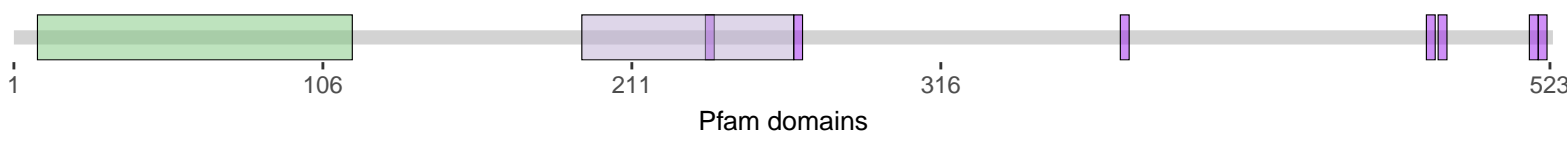
Molecular weight



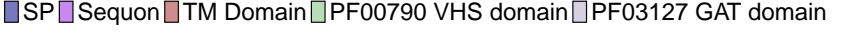
Gel Slice



Protein length



Pfam Description



Protein sequence:

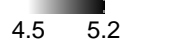
SLQRLRRHDDIAANGTSATVQPRETPVAFMLMNVNHEDESEDDFSLHARRSSKDPGDAQGRKTVGVKSEFMRITPLAPPSSRRPVSTDMGVVYLSGERFESERFGTAGSSPIAVGTNNNNVSSIPRSPKPPSSAPPDOLLNPRADDQDFVNFPTAGLFTGKSNNGEEDTKARSAHLPPAPVWADAPPTTLFPPPARVYNGRQGYFENVFGGGSSSYDSVVGQTKNLGINS66SPKQEKPEDALFKDLVDFAKAKSS66SN66SRSP

NbL14g17990.1 40S_ribosomal_protein_S2-3-like [MW = 30.24 kDa]

No. of times detected



log(intensity)



Values from



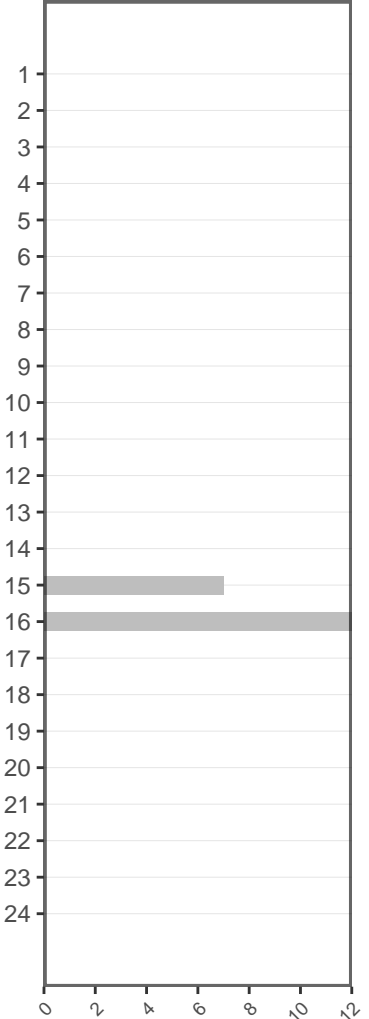
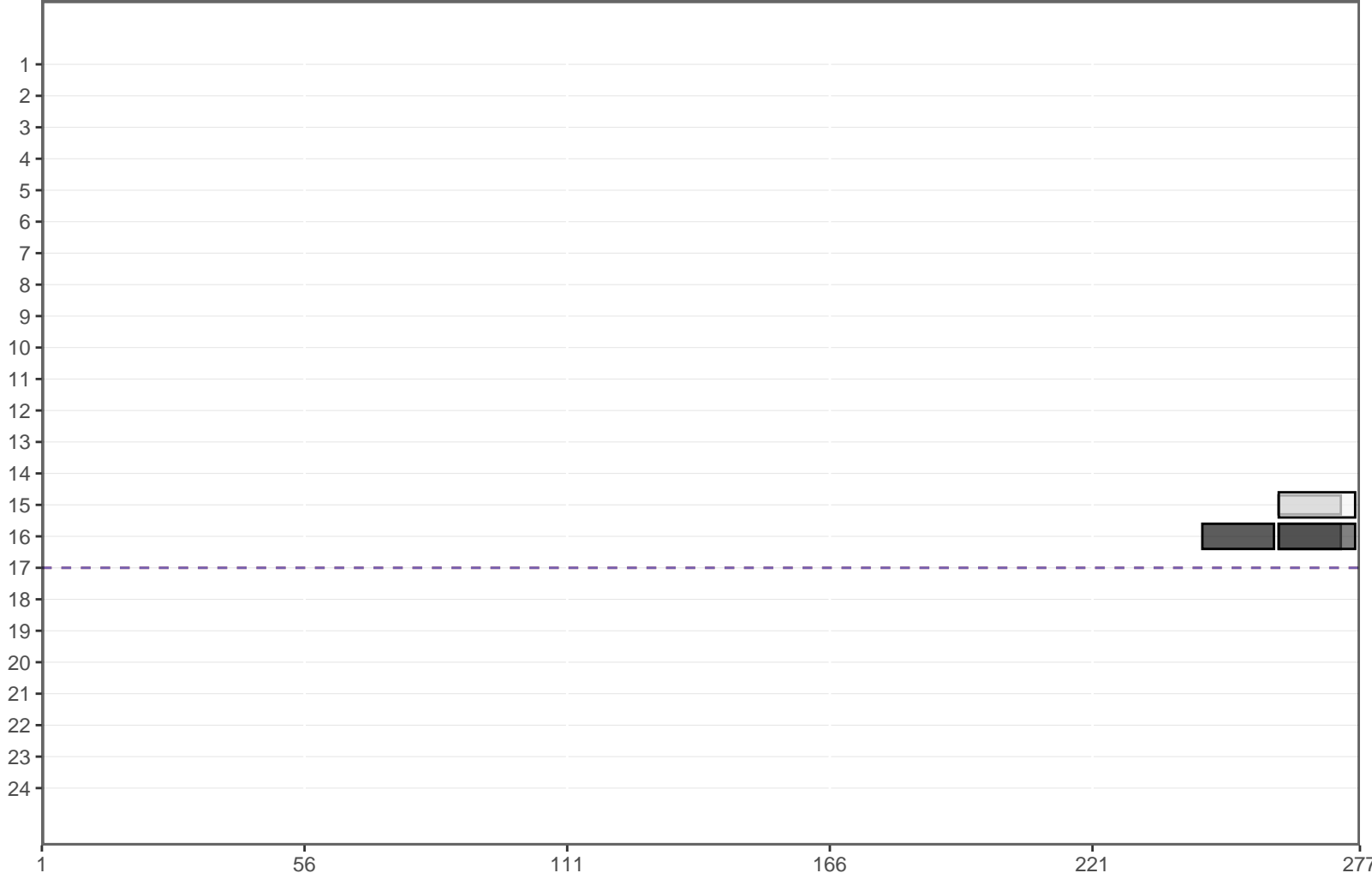
MW indication



Molecular weight



Gel Slice

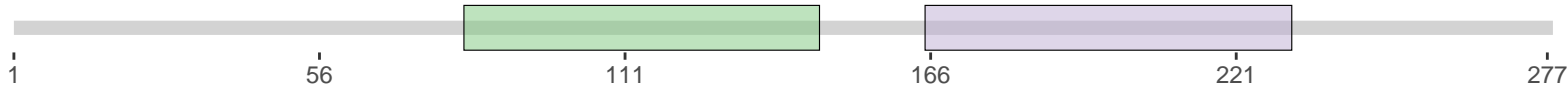


Protein length

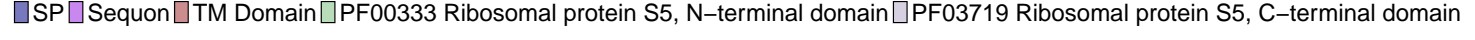


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

CSKEVATARGAILAKLGVPRRRGHWGNNGKPKHFPVQKVTGKGGVTVRIMVAPRAGAGAAARVKKVLFAGIEDVFTSSRGSTKTLGNFYKATFDLKMITYGLFLPDFWIKETRFKSPFGEVADLSKPKANKVIVYSTEETAAPPERVEA

NbL14g17950.1 2-oxoisovalerate_dehydrogenase_subunit_alpha_1_mitochondrial-like [MW = 13.77 kDa]

No. of times detected



log(intensity)



Values from



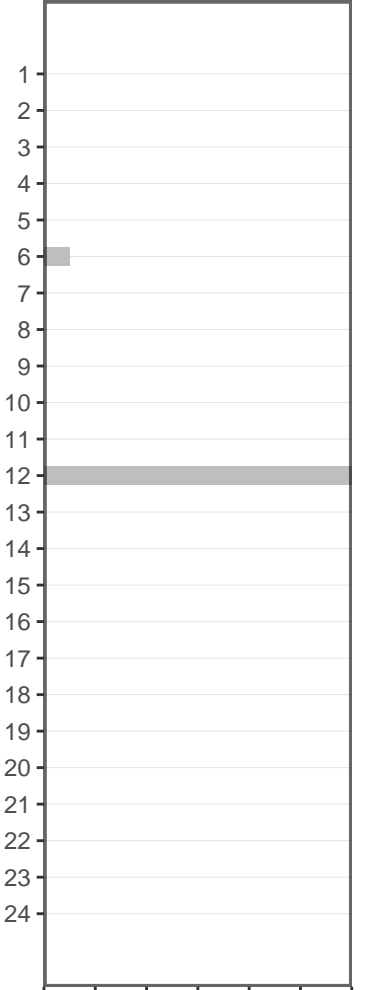
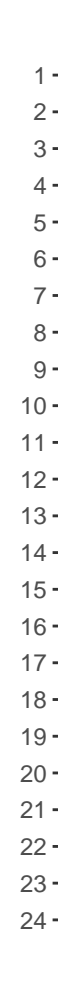
MW indication



Molecular weight



Gel Slice

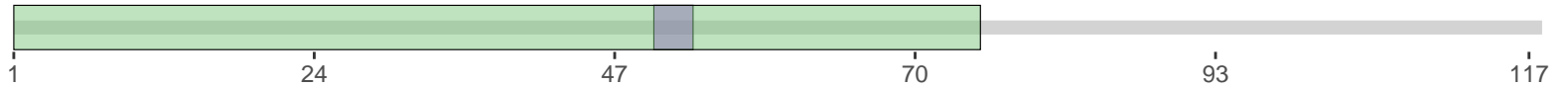


Protein length

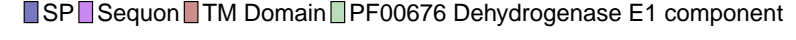


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

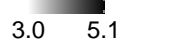
WVDNESELKRGDTRNKVLGAMGAEKVEKPKPLDLDFTVYVYKVKPLNLGEGHKFIRDVAWRSPKEYPSDVPV

NbL14g17870.1 probable_protein_phosphatase_2C_11 [MW = 46.48 kDa]

No. of times detected



log(intensity)



Values from



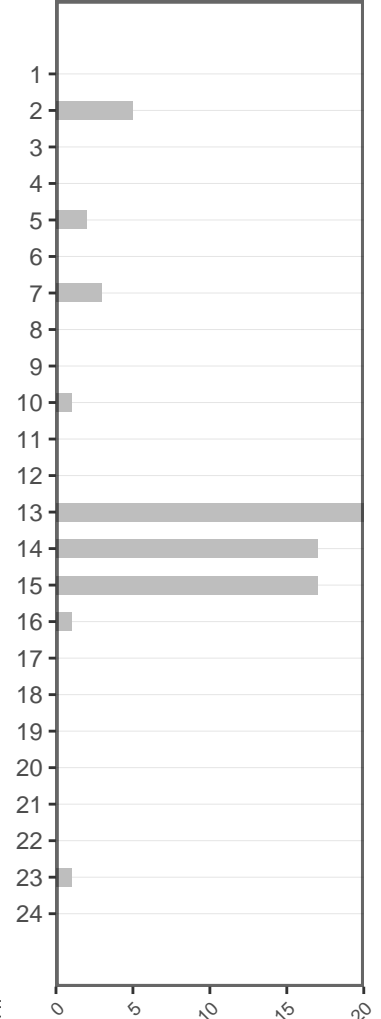
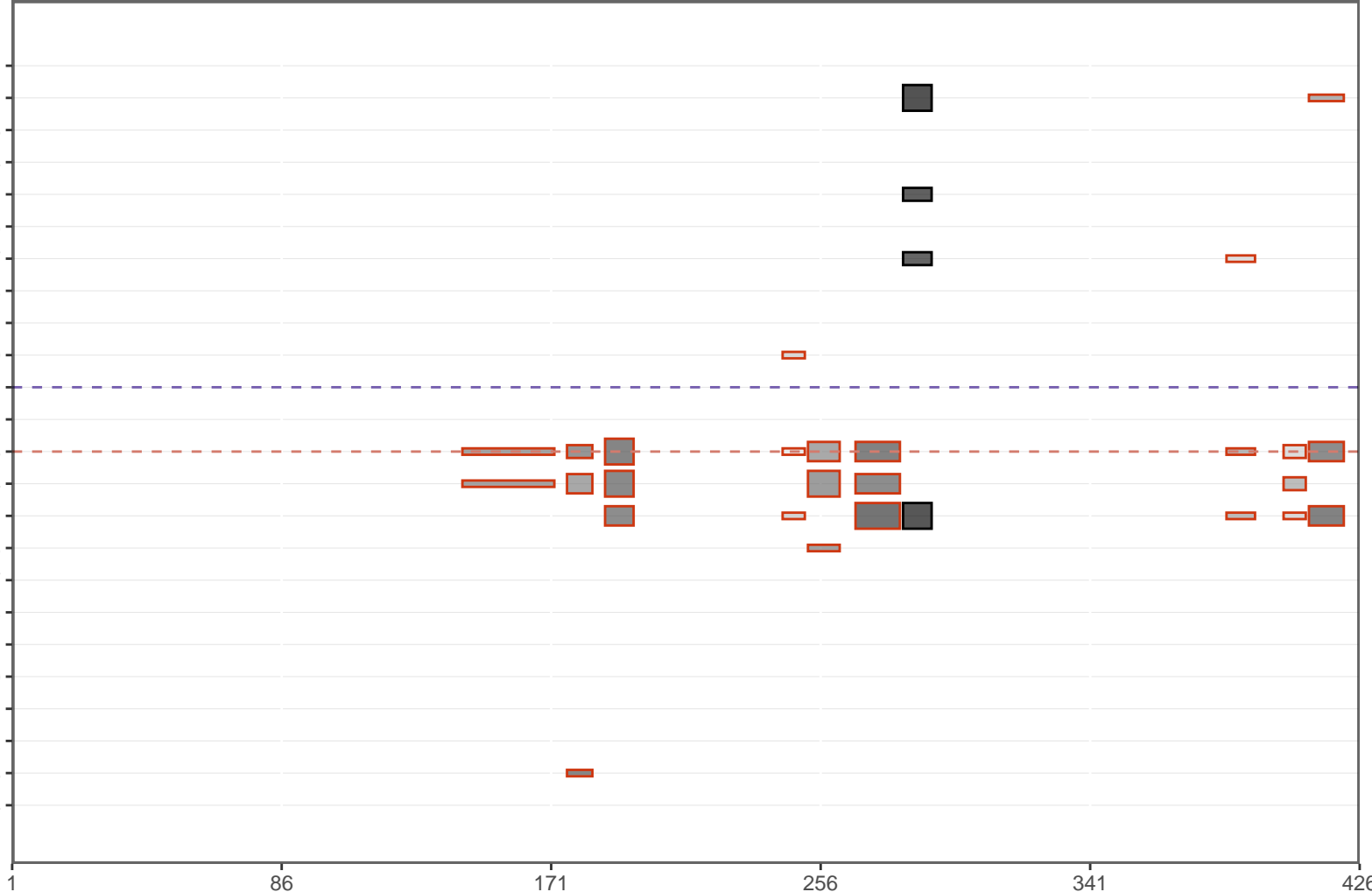
MW indication



Molecular weight

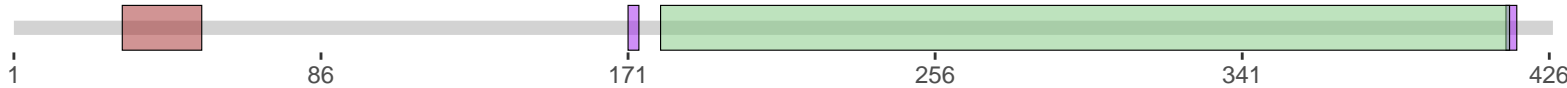


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEVDDQMVAFVFGVFDHGSGRTAEYLNKLNFLNGLGHPDFRDKTSAAVEAFKGTDAADLNEEKGGQKDGASTAVLLGDRLLVAVNGDSDRVAAGRDGSAIPLSDIHPKDRSDERERIEQAGDFRWAGTWRVGGVLAIVSRAFGDKLLKFPVVAADFEIQEEEDGVDFHASDGLWVLSNKKDAWAVQAKDAEAAASRLIEEAVSRGSDSDNTGVAVRFESA

NbL14g17630.1 serine_carboxypeptidase-like_42 [MW - SP = 50.43 kDa]

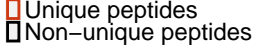
No. of times detected



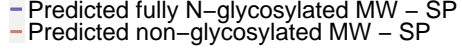
log(intensity)



Values from



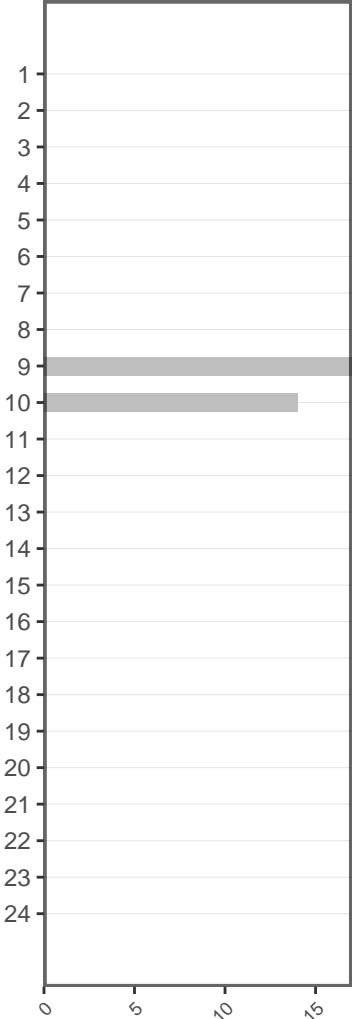
MW indication



Molecular weight

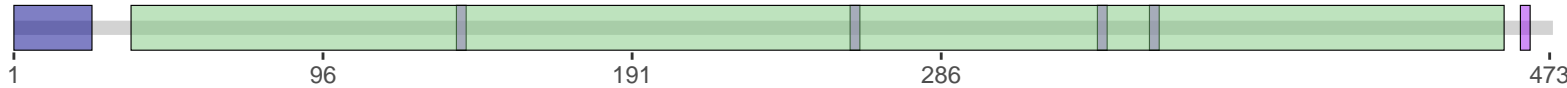


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PATYEYFVSHGMSDEVLGAMINGCDFEDYTFGSPHNVSHGECNAISEANDIKGEVYNNYDVLDDVYPSVIGELRLRNMATKMSVGVDDVCMSEYRRFFYFLNPEVQKALHANRTNLAYSWSMSSSILYSDVDGNINLPLFKRIQNHPPVWFSGDDSDVPLLGSRTLVRELAHDMGKFTVPYGVWFFHKGQVGGWQTEYGNLTFATVRSAAHMPVYAGPDRALHFFSSFRGRRLPNNTFRSIED

NbL14g17590.1 uncharacterized_protein_At2g24330-like [MW = 44.61 kDa]

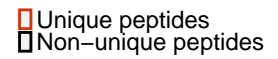
No. of times detected



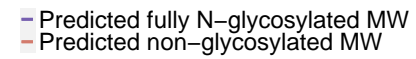
log(intensity)



Values from



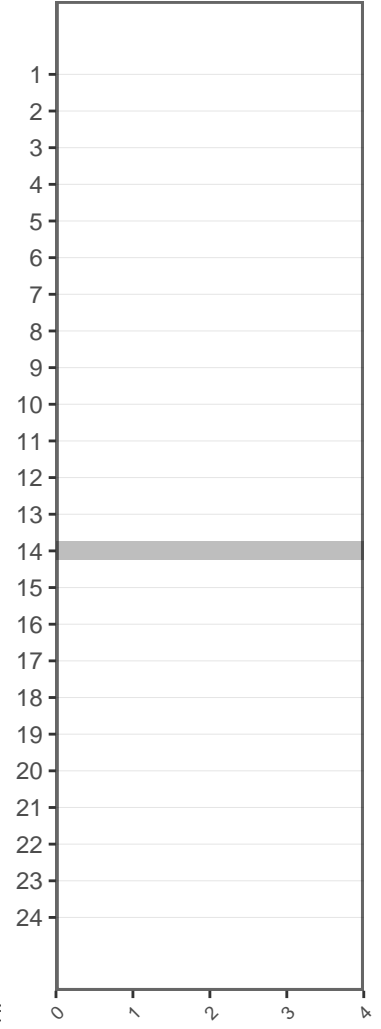
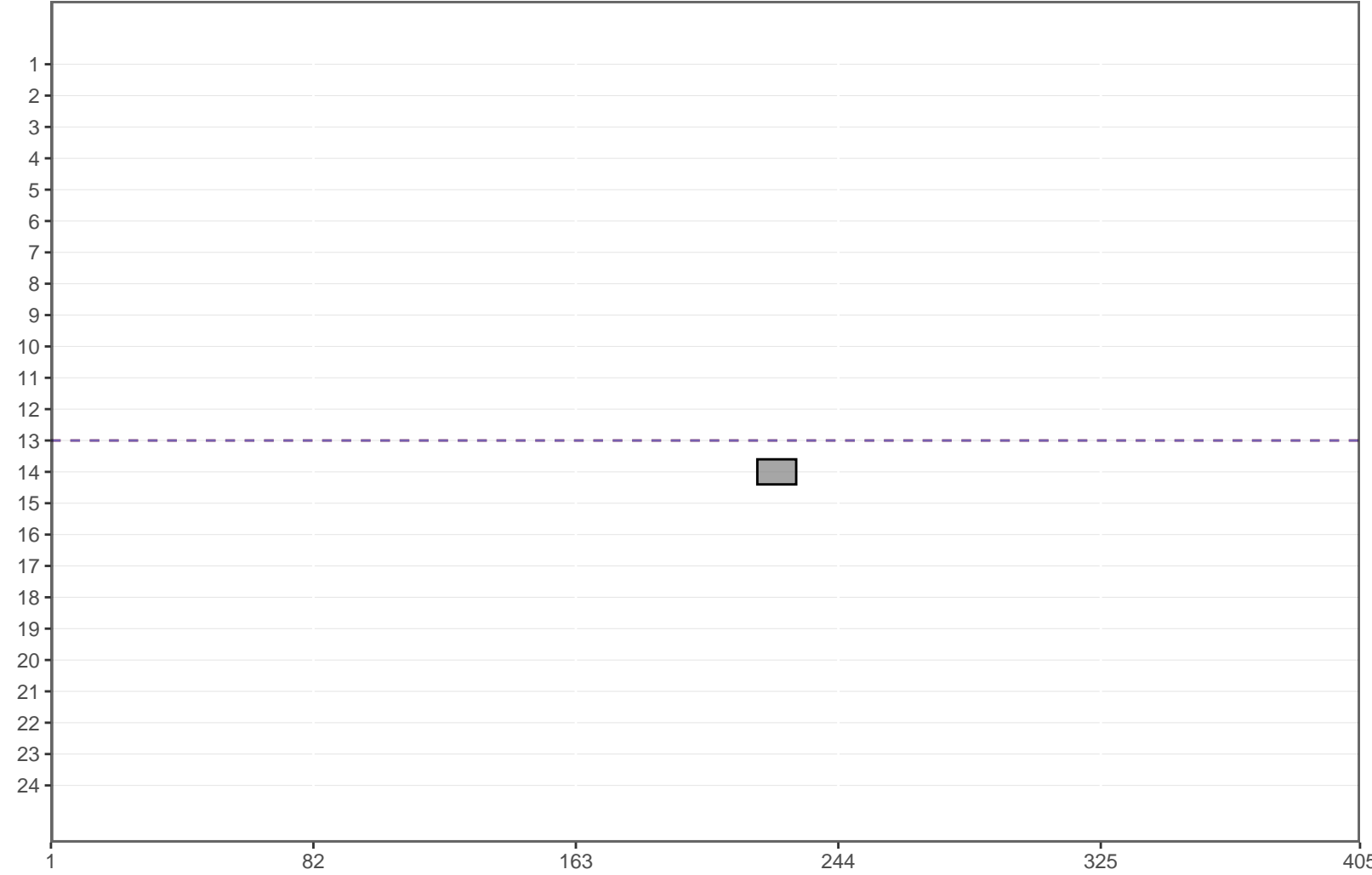
MW indication



Molecular weight



Gel Slice



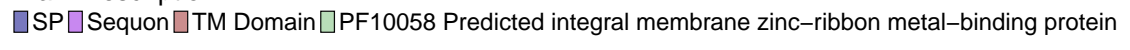
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ASLKGADTGLKPIYGGDDTLNINVPTGKNDVVEVQSTGLRNRKGGRE6SFESAVLDHIEAEMLGGQLEGG6TMDHQQTVEHYNPTG6STQGGWLSKIAALLVGE6PTG6VALICG6NCHMIE6NGLARKEDFPYFTY6PHG6HALNKG6KVD6R6GG6T6T6N6L6G6T6TV6AD6L6V6D6GG6S6P6K6IS6AS6G6SP6A6P6P6W6TE6GEN6IV6ST6N6P6

NbL14g17580.1 vacuolar_protein_sorting-associated_protein_45_homolog [MW = 65.21 kDa]

No. of times detected



log(intensity)



Values from



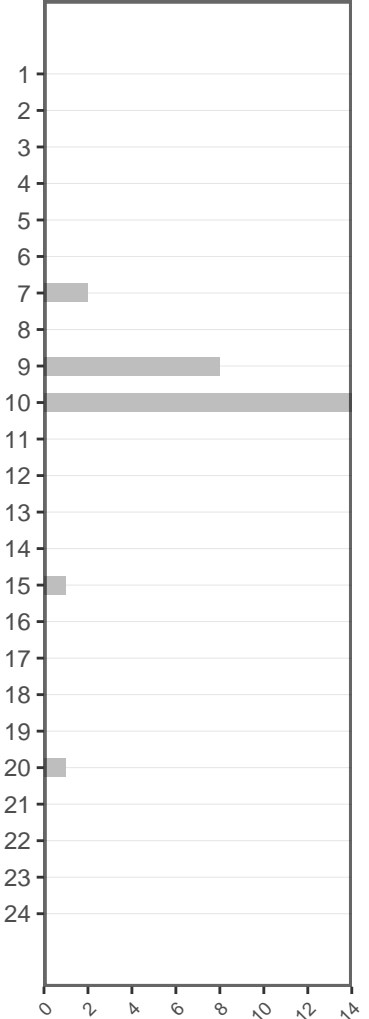
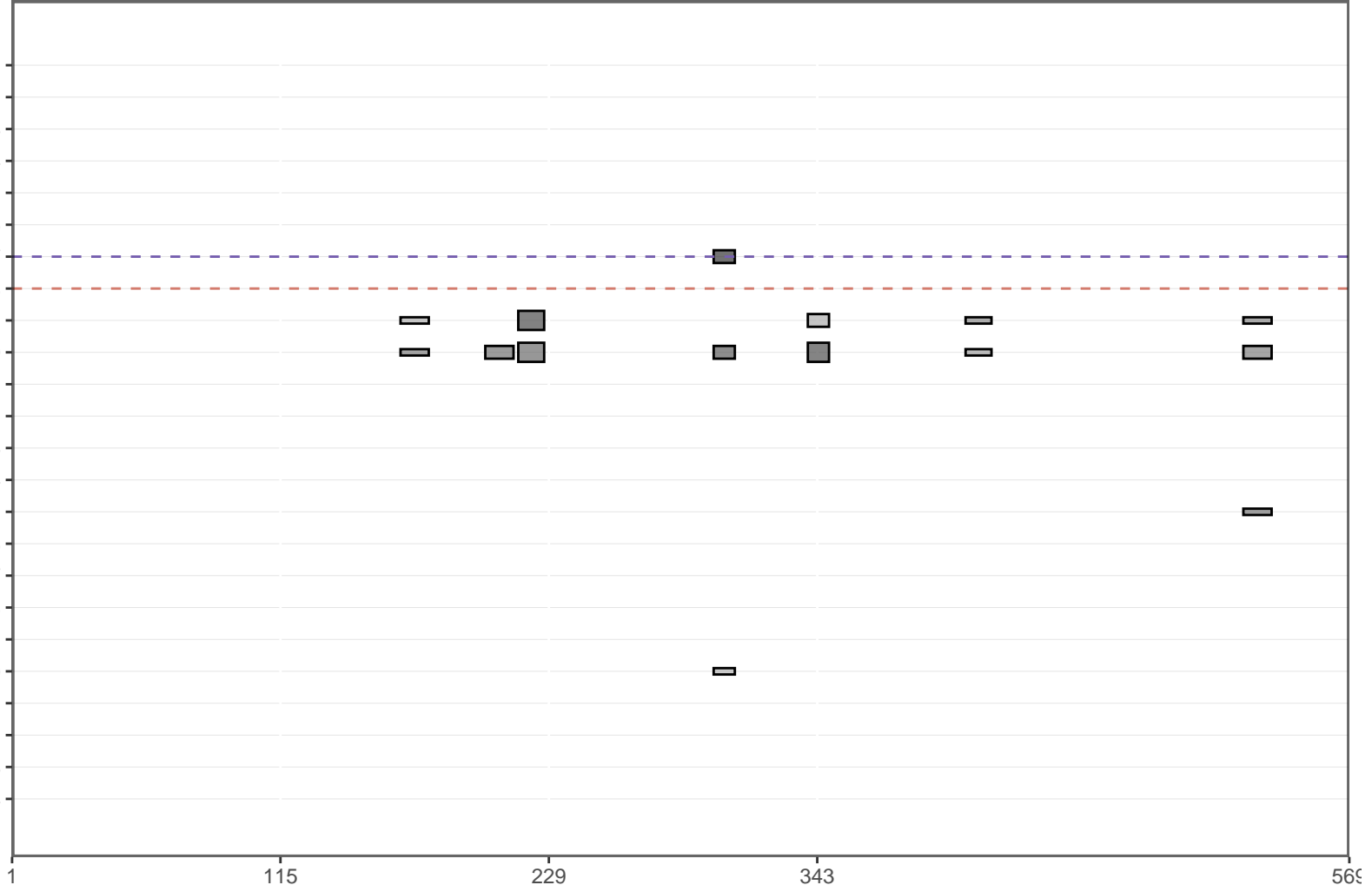
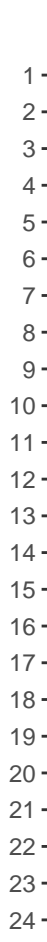
MW indication



Molecular weight

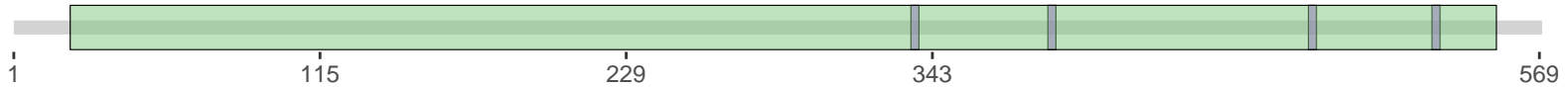


Gel Slice



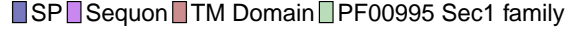
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISEQDAFFKTNMYDNFGDGMNKKMVDVDFGVAKSNNGTIEDMAKFFVQNYPEYRKMGGVNSKHVTLVTEMSKIVEERKMLMVSQTGELAGNGGGAFAFEAVTLLNNDNSMDRRLRLMLVALRYEKESFVQLMQLFNKLASRSPYKPGLVDFLLKAGVDRKRTDGLVGNRDLNIAARNMARGLKGVENVYDQHPQLLFTQMENTRGLRLRDVDPVYGNHFQGARQGEVWIFTVGGTTYEESRSVALGNSTNSGIRFILGSSALLNKRRLRDLLEAQRARTS

NbL14g17520.1 uncharacterized_LOC107768657 [MW = 29.09 kDa]

No. of times detected



log(intensity)



Values from



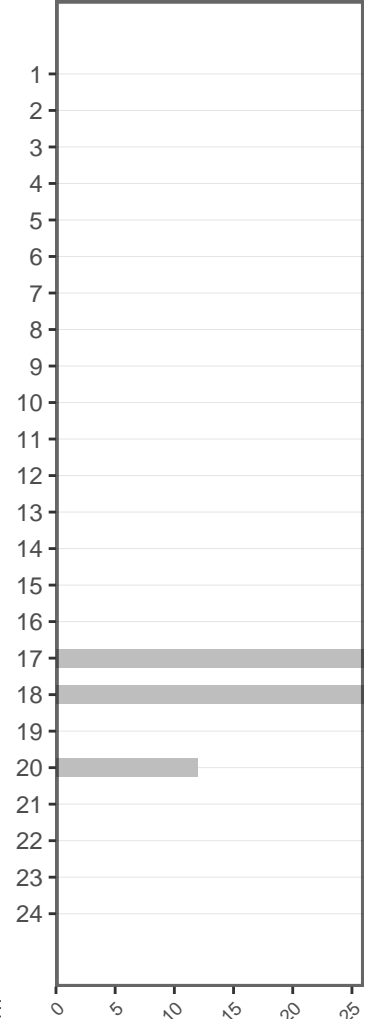
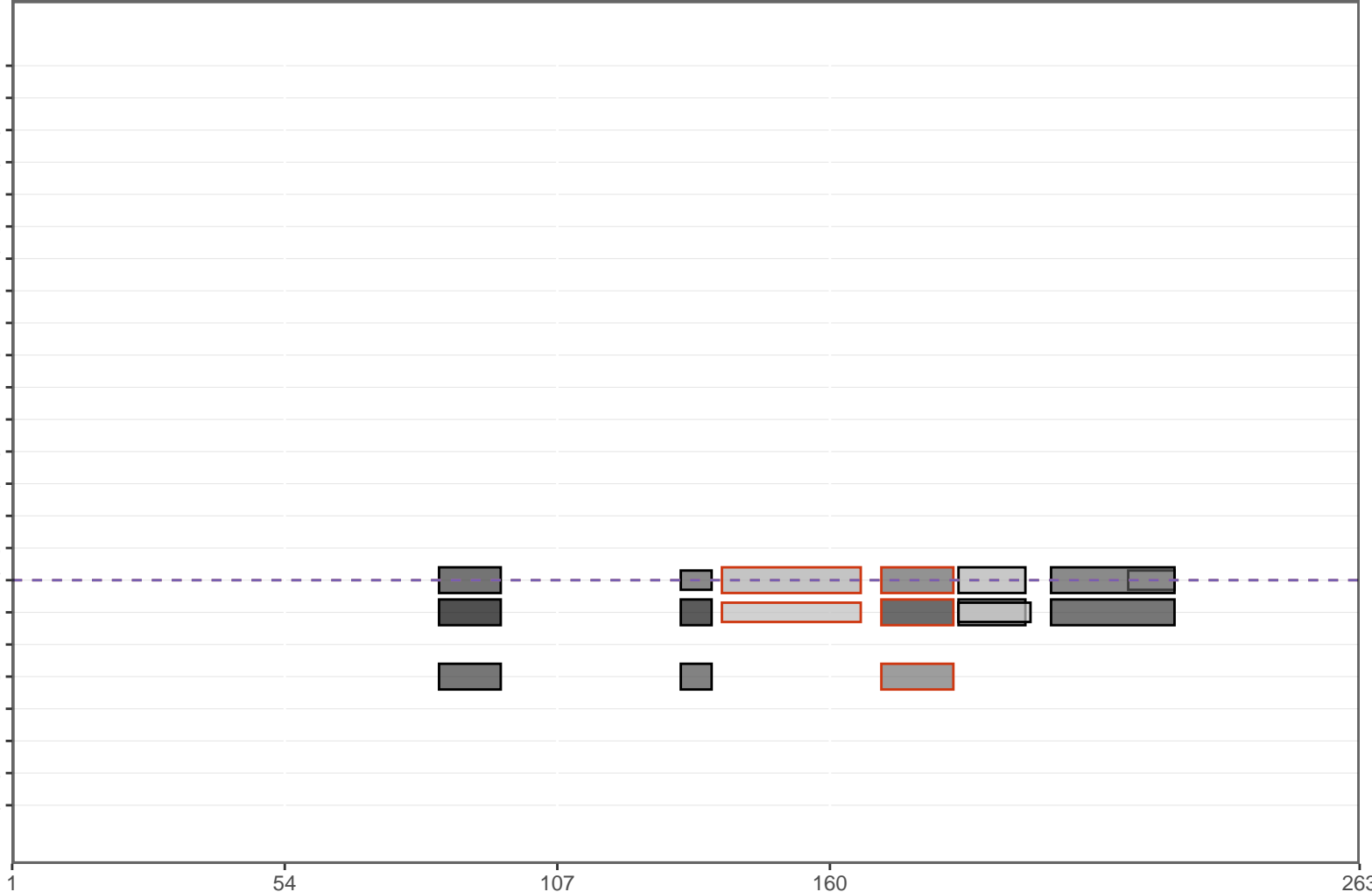
MW indication



Molecular weight

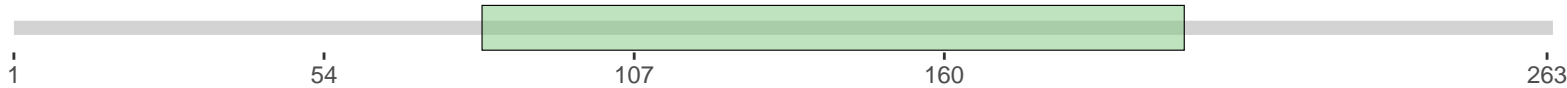


Gel Slice



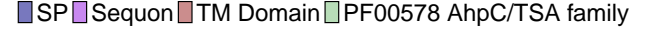
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VHLLKDDVLSNFYMKKGLAVVNSNSVATHPDGDFPEFMAEDAKLFRKYPFPVLYDESGEVAKDFGAVCTPEFFLFRKDGRRPFELVYHGGDFDSDRSPNAPVTGRDLGLAIDVLSGGPVSSEKQKPSGGCEKWHFPGAKQ

NbL14g17390.1 RNA-binding_protein_2-like [MW = 33.27 kDa]

No. of times detected



log(intensity)



Values from



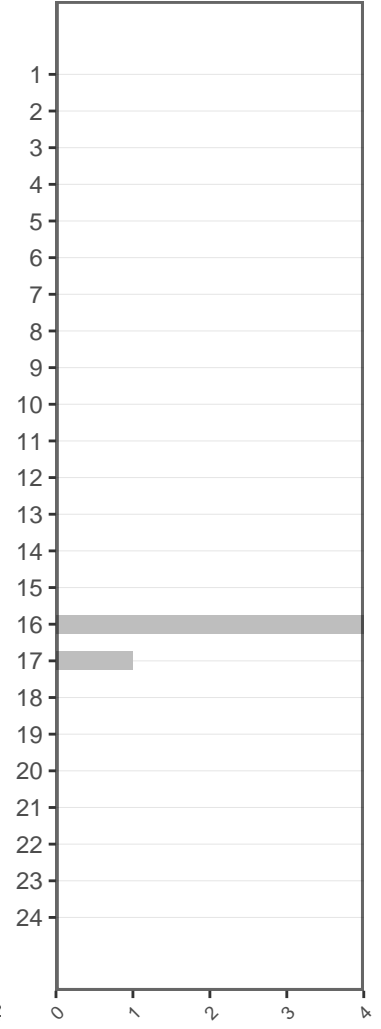
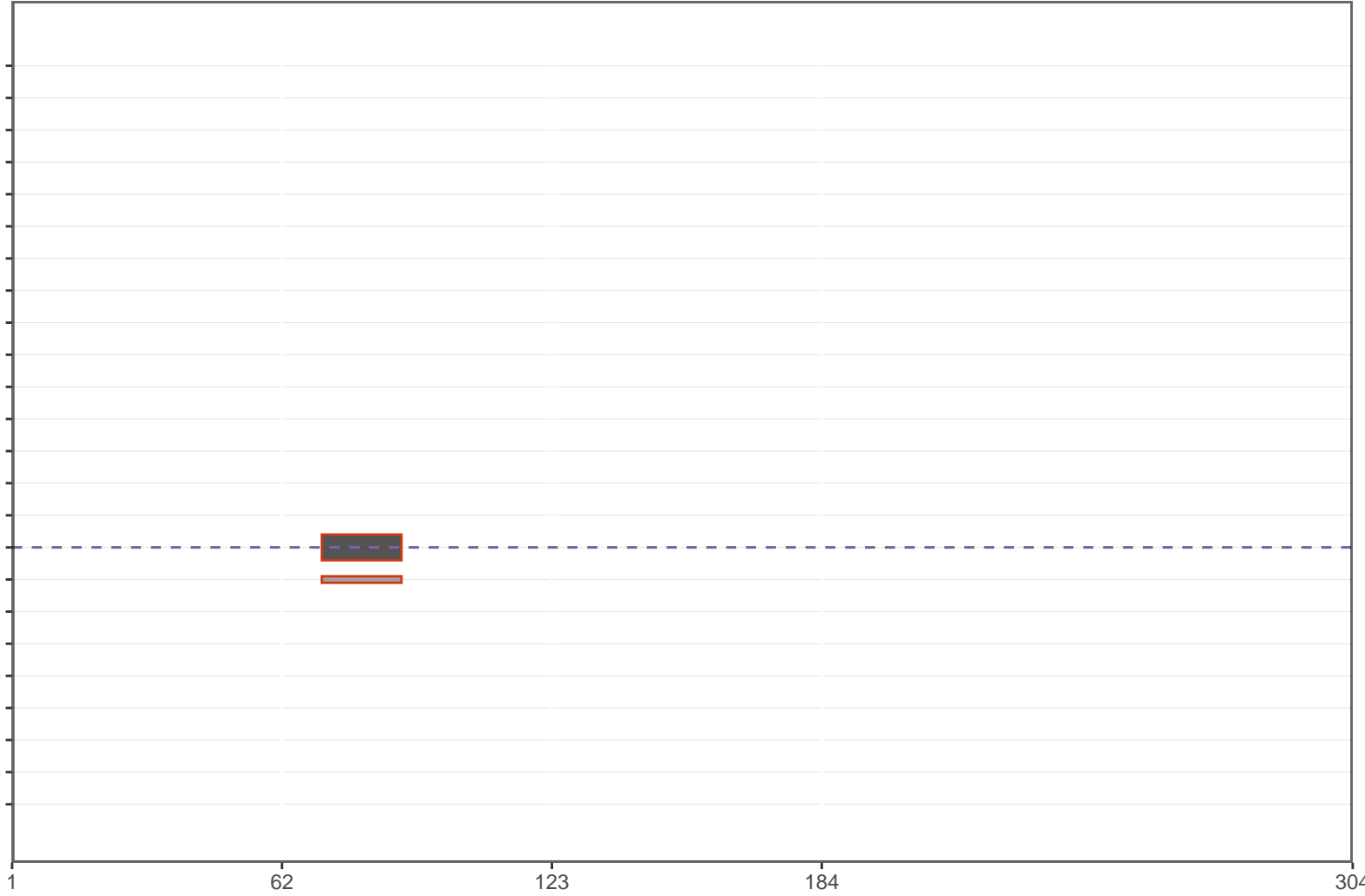
MW indication



Molecular weight



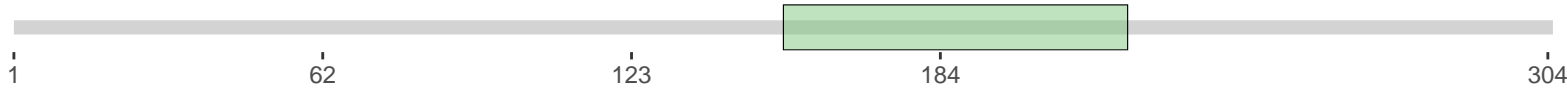
Gel Slice



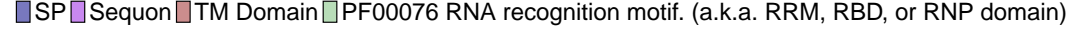
Protein length



Pfam domains



Pfam Description



Protein sequence:

SLPRPRETLPLPPDAISNTLYEGLPDSGRREVAHIFRPFVGVYKEVLRKESKRRGGDPLKCFVDFVDPDCAATASALQVLEVRSEVWVLGEGSEWAEINSHQLFYFYFLLLRNRLLLGTVTGICNDGLAGRAVSKVTVLGLTLVFEVGGFSLGGPLKPKVLESG

NbL14g17090.1 protein_FAM188A-like [MW = 68.19 kDa]

No. of times detected



log(intensity)



Values from



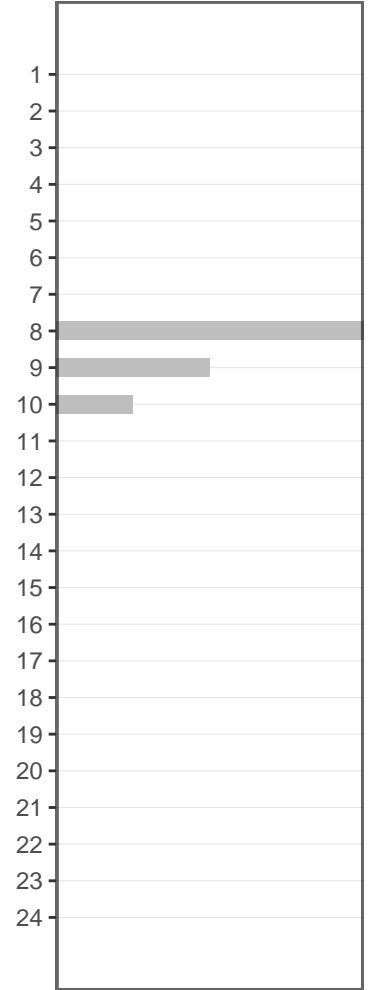
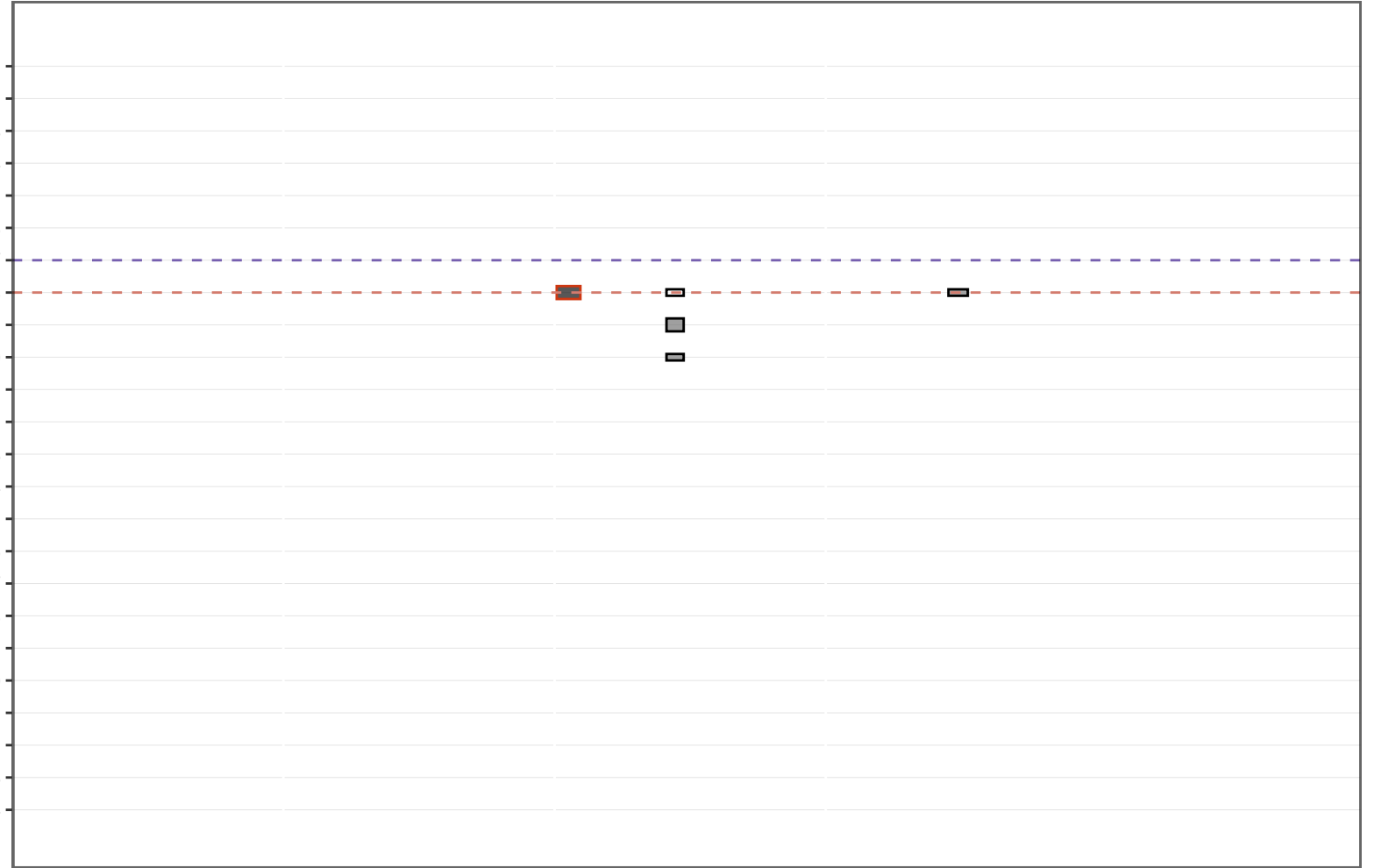
MW indication



Molecular weight



Gel Slice

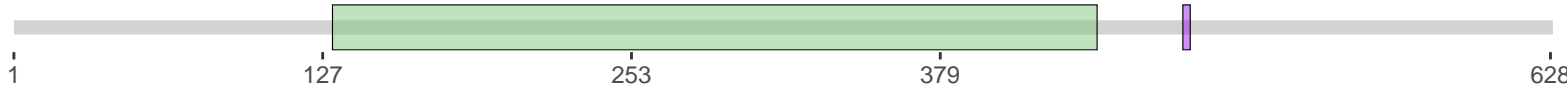


Protein length

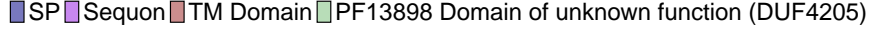


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SRLEALLPVRSRSMGAMLFHLSALLSRGMDVQADRRDDPSGLVTPAFGHASGEIVNLLSGEAWANFDGRMDLGGGMFVKGISTTVEHGLTLESLNFCRQVGLHLKCPKWPWVYVGSSEHYTVLFDLTKVDEENELEGRETKIRRAFDAQDGGGGGFVEGFHQLVRETNVSLPAKLNQLGSSGVIWSEFVGLVLLDNLKDKMGKLPDPSGLMGKRVFDLVHFNGLAKGVMNMGNOVSEVNDFFVQRRLTKLRVSVPRWTPPEEFM66SGPSTGAKDSVT

NbL14g17080.1 fructose-16-bisphosphatase_cytosolic [MW = 37.22 kDa]

No. of times detected



log(intensity)



Values from



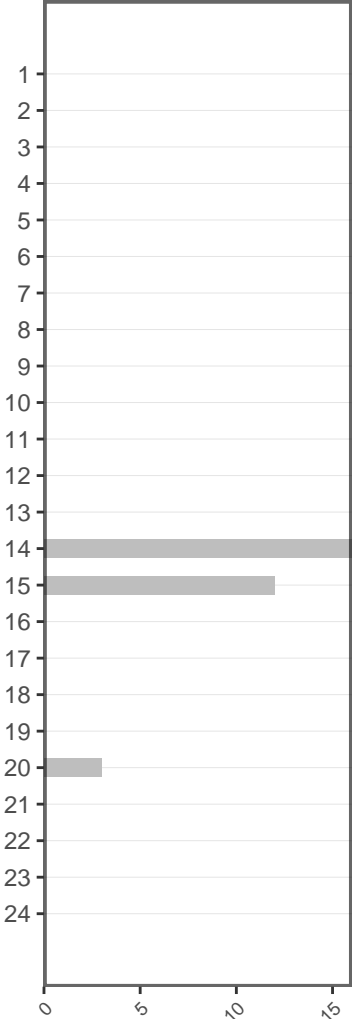
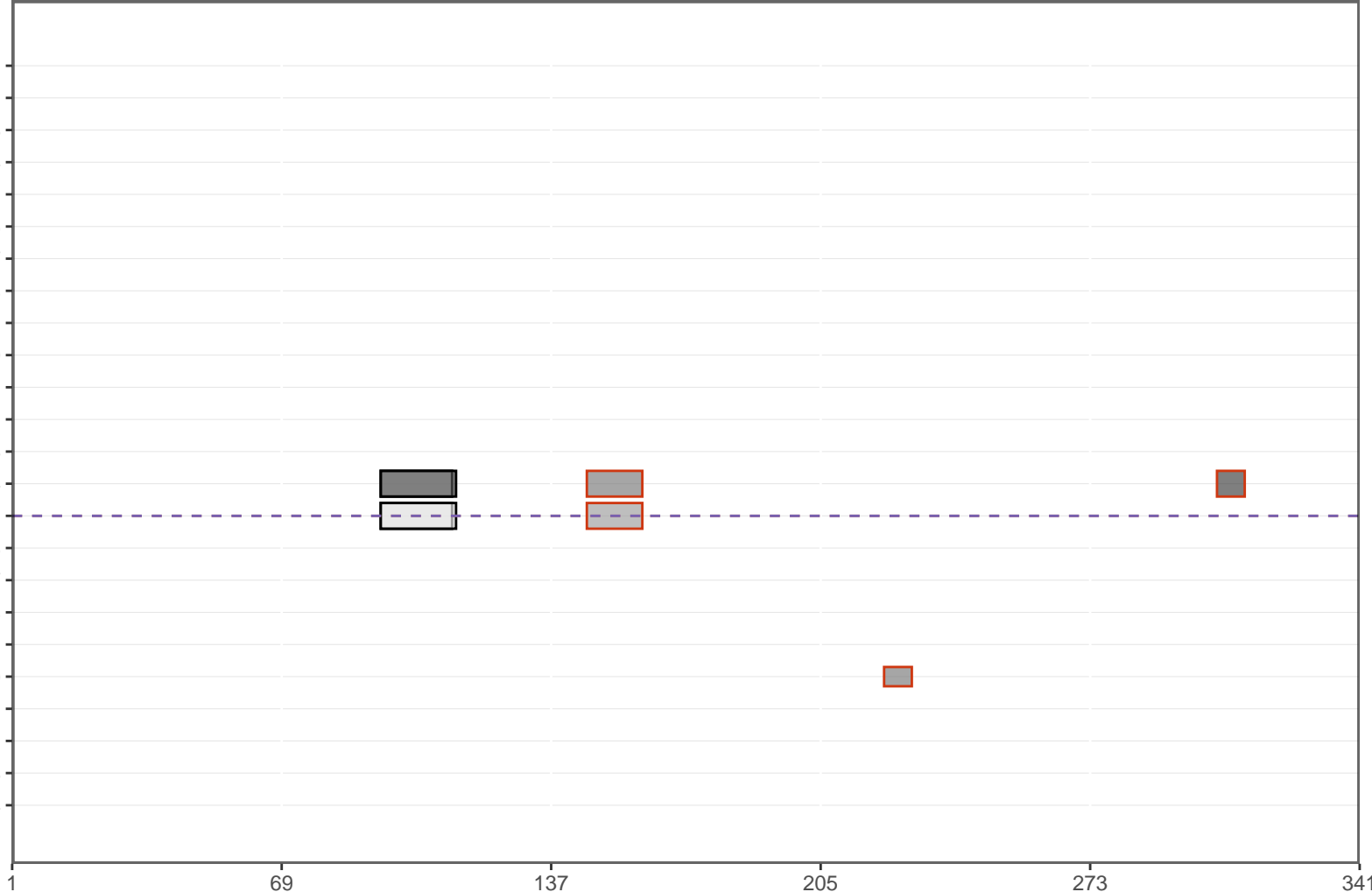
MW indication



Molecular weight

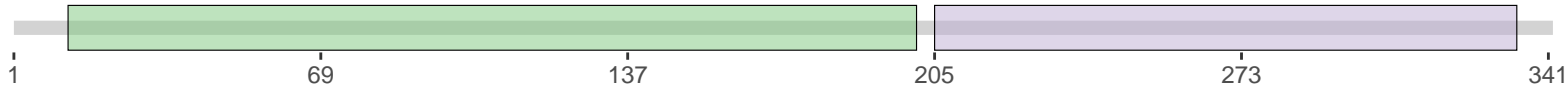


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfm domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00316 Fructose-1-6-bisphosphatase, N-terminal domain
- PF18913 Fructose-1-6-bisphosphatase, C-terminal domain

Protein sequence:

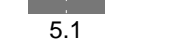
QKNNLAAGYCMYGS66GTLVSTGSGVNGFTLDPISLGEFILTHPDIKPKGKIKYVNEGNKKNWDAPTEKYYQNGKYPTDGS6PKSLRYGSMVADVHRTLTYGGIFLYPADKKSNGKLRVLYEVFPM5FLMEQAGG6FTKQGRALDLVPEKHERAFPLGGYDVEEIKKLYAAEEQN

NbL14g16880.1 thioredoxin_Y1_chloroplastic-like [MW = 19.08 kDa]

No. of times detected



log(intensity)



Values from



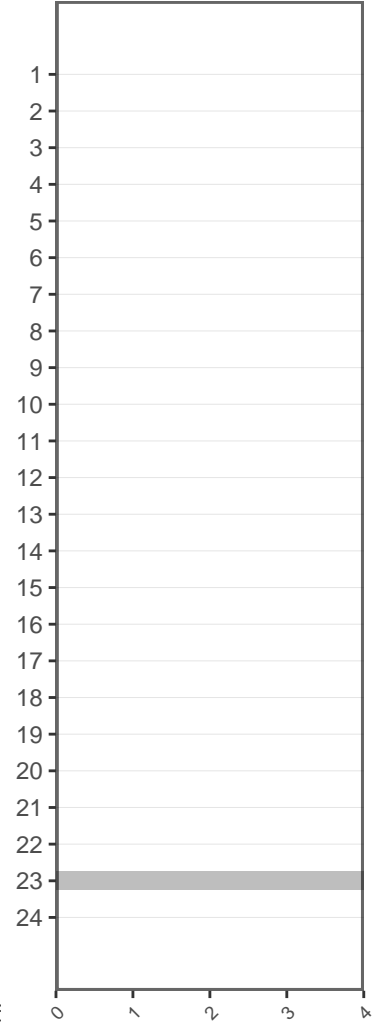
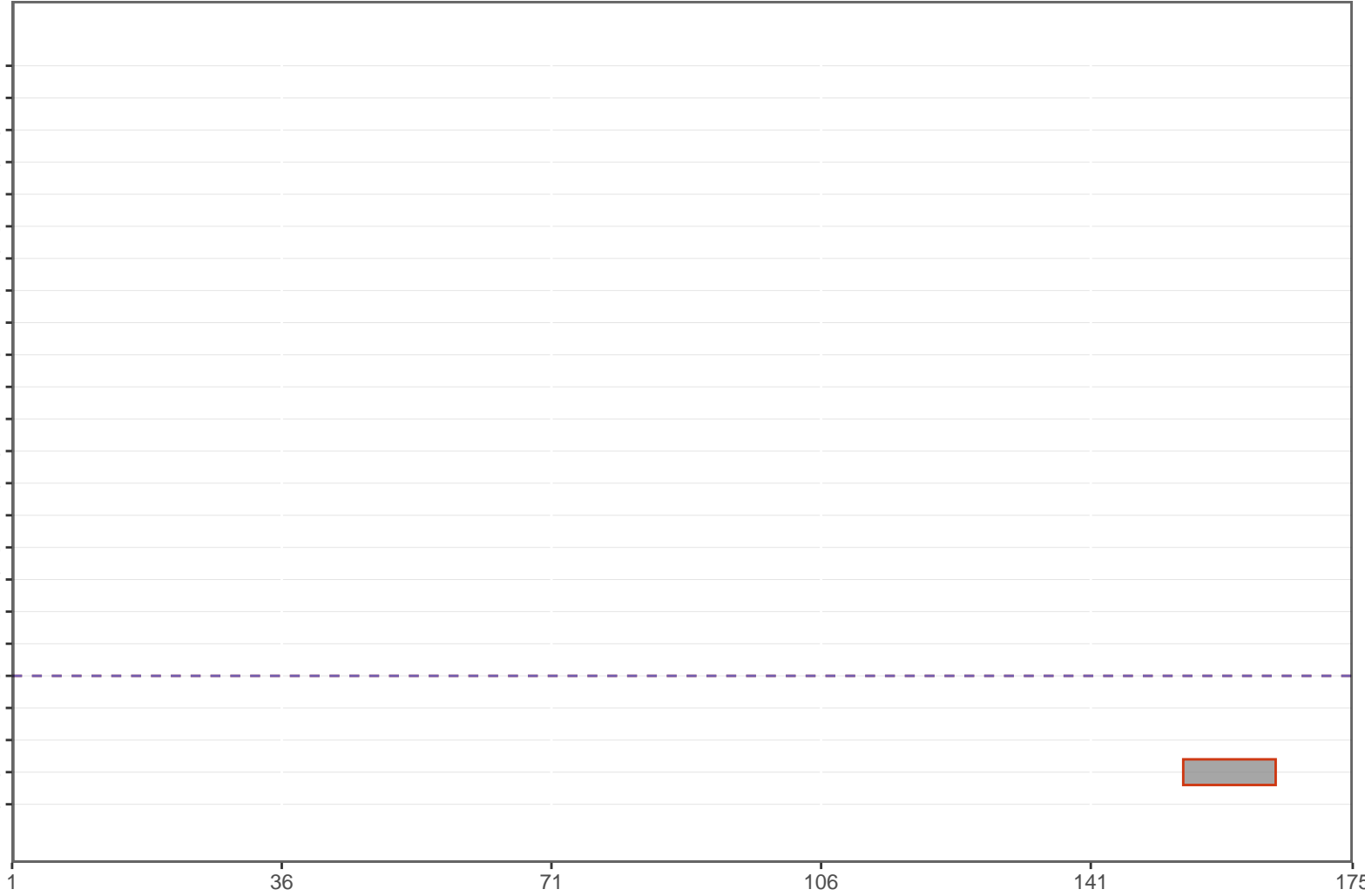
MW indication



Molecular weight



Gel Slice

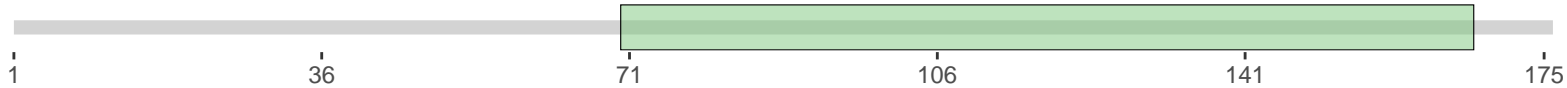


Protein length

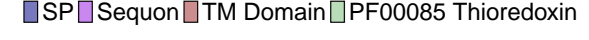


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SFEELLEKSEKPLVDFVATWGGPGQFMPIILNEVGESEMKDKIGVVKIDSEKYPALADKYKIGALPTFLFKDGEVDRFEGALNAPSLIGRIESALEVKG

NbL14g16810.1 stress_protein_DDR48-like [MW = 28.51 kDa]

No. of times detected



log(intensity)



Values from



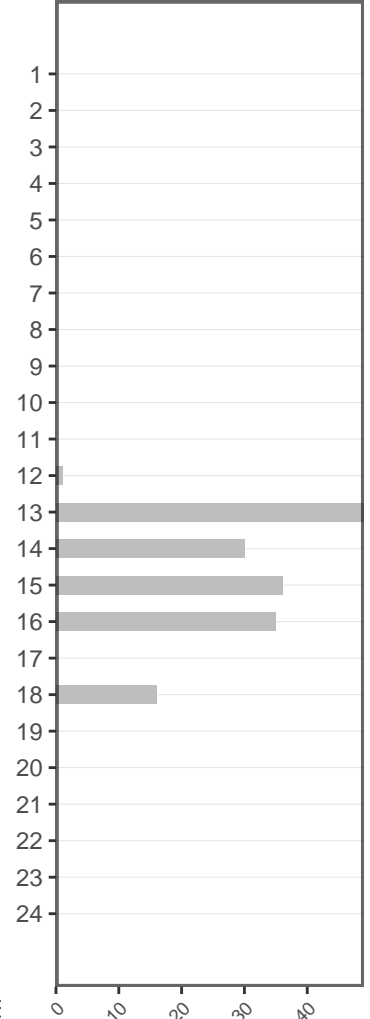
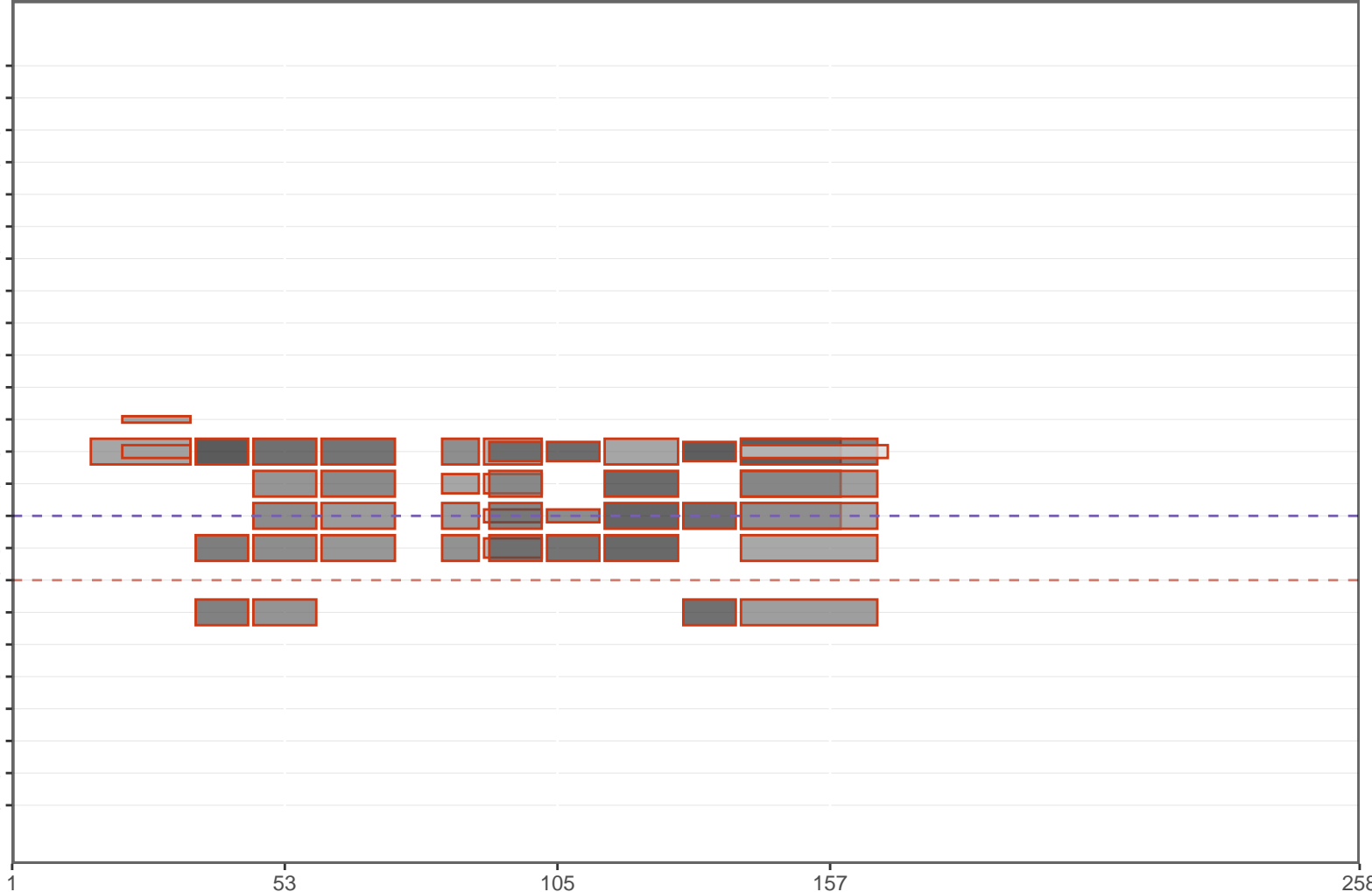
MW indication



Molecular weight



Gel Slice



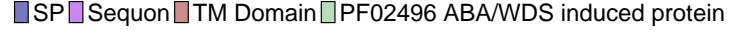
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GYGDPSSETTYGKNTNYGEGDITYGKAAAHSSSETTFNFEENTDDGKTDGEDYKEKRHHKHLHVVGLGAAAAGAFALILAWKFGHEKHKAENKDPHAAHKHRIIEEIAAAAAVAGGDFAFHEHHEKKAEEEEEAEGKXKHIFP

NbL14g16790.1 uncharacterized_LOC107797753 [MW = 15.74 kDa]

No. of times detected



log(intensity)



Values from



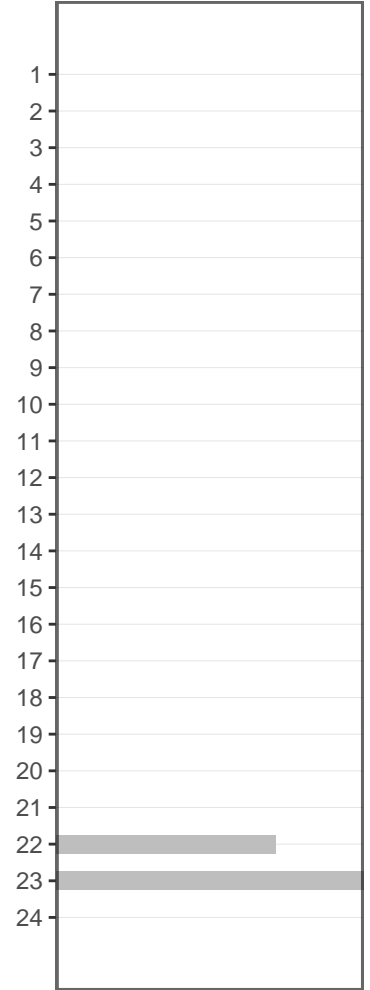
MW indication



Molecular weight



Gel Slice

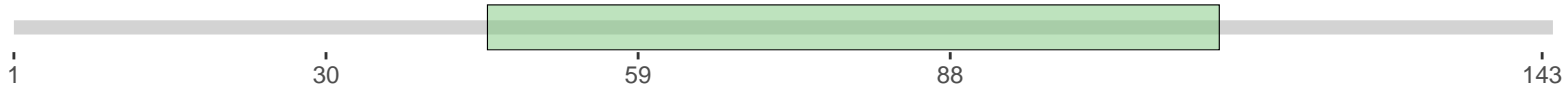


Protein length

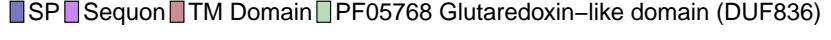


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SLKEKLNAAFSLSTPHSLHDVQLGVRDITSNPEWEKAYQVEIPVLARVRPDGTEWSRLAVYSKARYGKGRLENEAARPLVIV

NbL14g16730.1 gamma-glutamylcyclotransferase_2-3 [MW = 21.1 kDa]

No. of times detected



log(intensity)



Values from



MW indication



Molecular weight

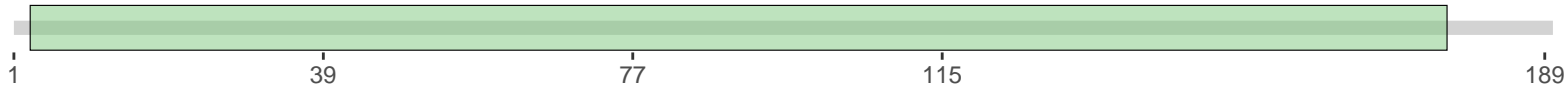


Gel Slice



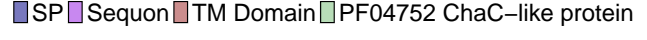
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

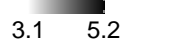
YLEVREKQYDXXAVVDLFTFPAASERWISGVLVYIGSSDKKNGNVLGPAISVEEIASQIVRAKGPSGPNRDHLYFQLEKRLGLLGGEDKHVSDIAKEARRLISEEVTS

NbL14g16700.1 uncharacterized_LOC104218264 [MW = 47.65 kDa]

No. of times detected



log(intensity)



Values from



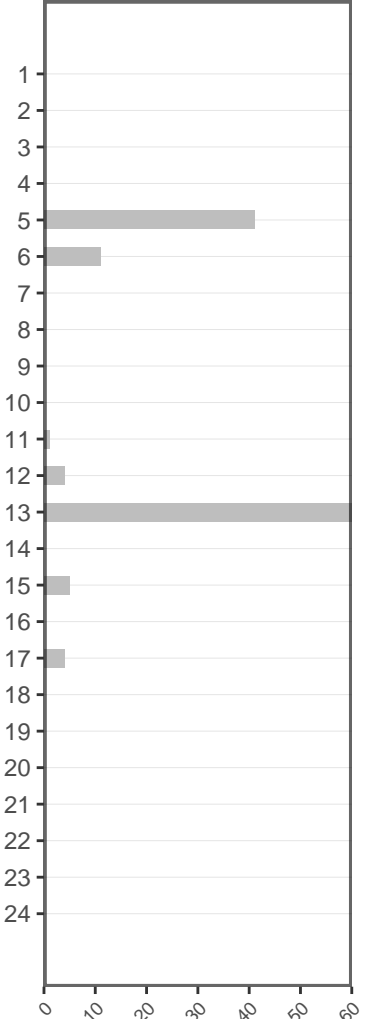
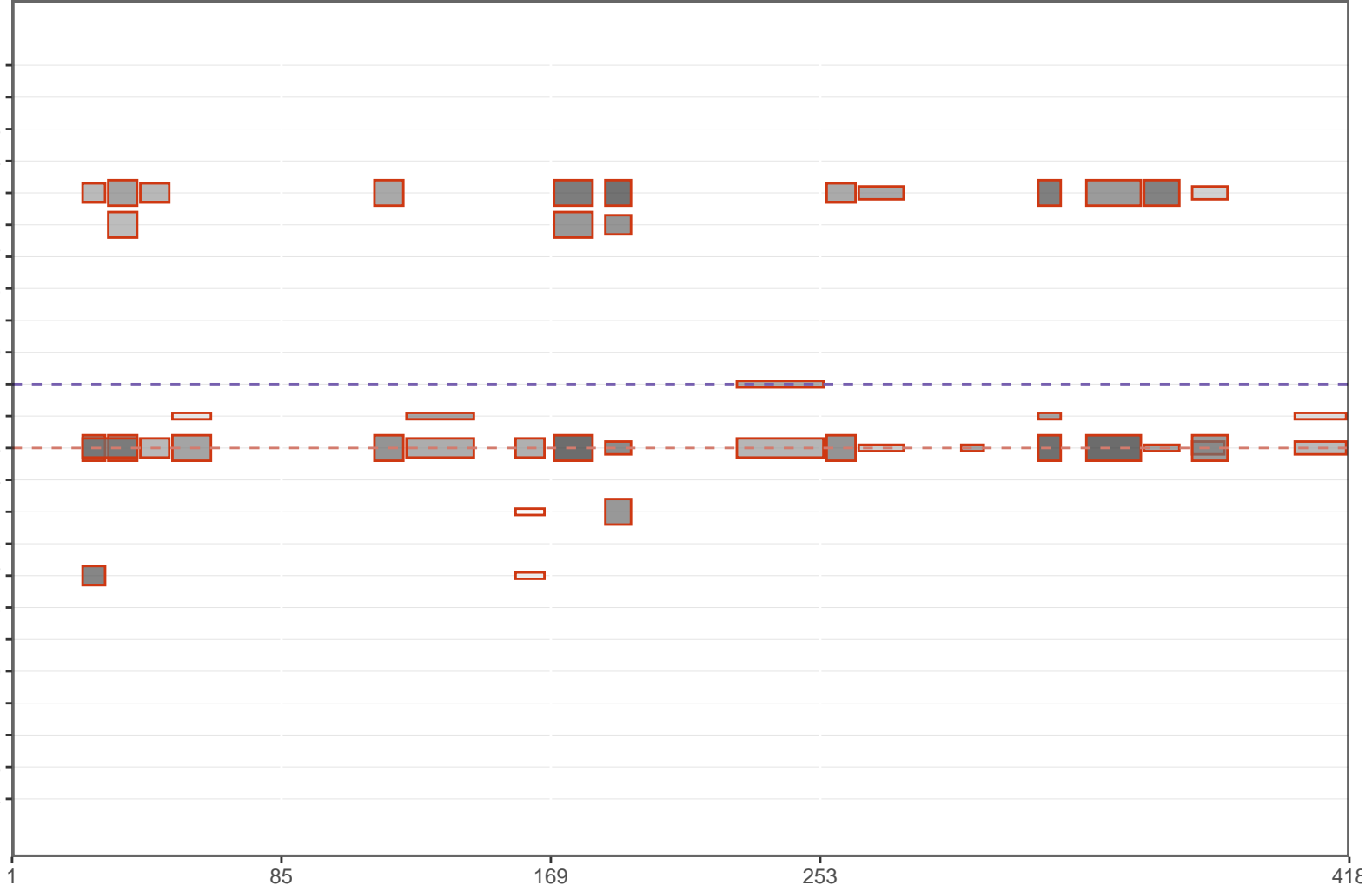
MW indication



Molecular weight



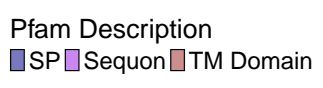
Gel Slice



Protein length



Pfam domains



Protein sequence:

/FLLLMTMADFSDQLFNFDLFDNSGRLFEFGNNNDQILWPGDQKPLGWMNSIRMSALYSLVREEDIFEGNGHVGGRDEEELWPPVFDTORRVLDELQKEARELVWEGVCEASKRGLDWAEEERLLTGVENPFVGEPHVVLGGVYLSKGVYEEAEKEKGLRILEWGSPPWDKRMSVEGWVWVTRVLLMKAKEKWPQHSWGLNLGLVTK*

NbL14g16690.1 lysM_domain-containing_GPI-anchored_protein_1-like [MW - SP = 40.75 kDa]

No. of times detected



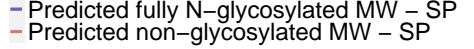
log(intensity)



Values from



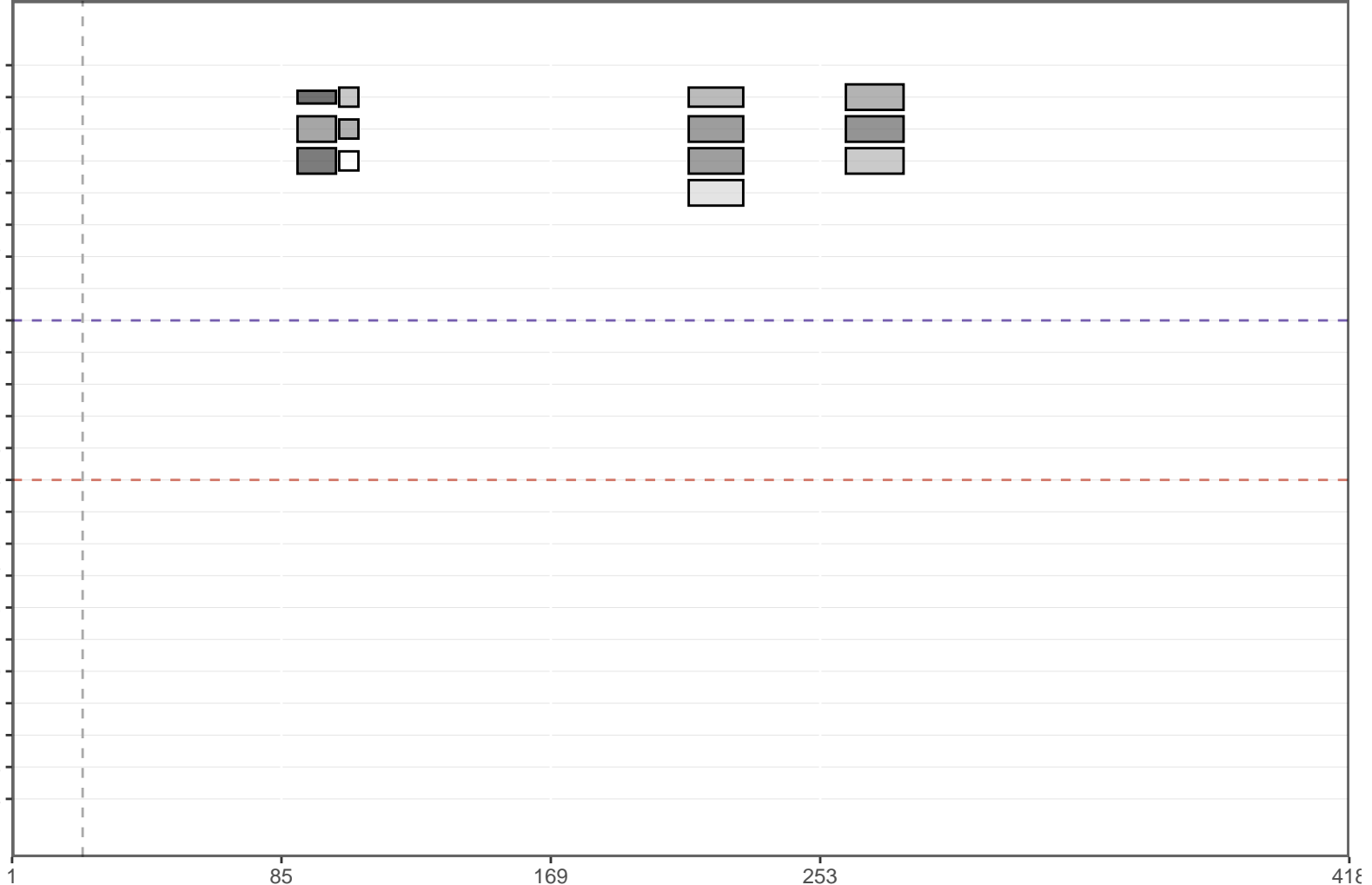
MW indication



Molecular weight

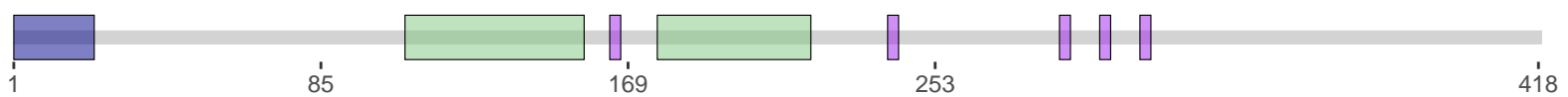


Gel Slice



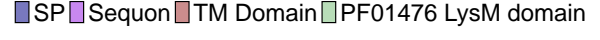
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MVNLGSPAKEGDILAIPLGACASSFRFAADVALSVANGSVATASHVQGGSGPGRSNLYGMFASLAVSGSSMDGKNSNLMIGNTVGGTGGGCVNTSGNYGGFVNGTFTLSSSLQPRCPGQGFPLVPPTSVGPDMFAPAPRSEGGAPMDGPHSSVVPAGGVIAFPFSGGPGGSASSAWSLNPLVFFRIALLLVGVKVVISLPL

NbL14g16510.1 uncharacterized_LOC109217160 [MW = 47.31 kDa]

No. of times detected



log(intensity)



Values from



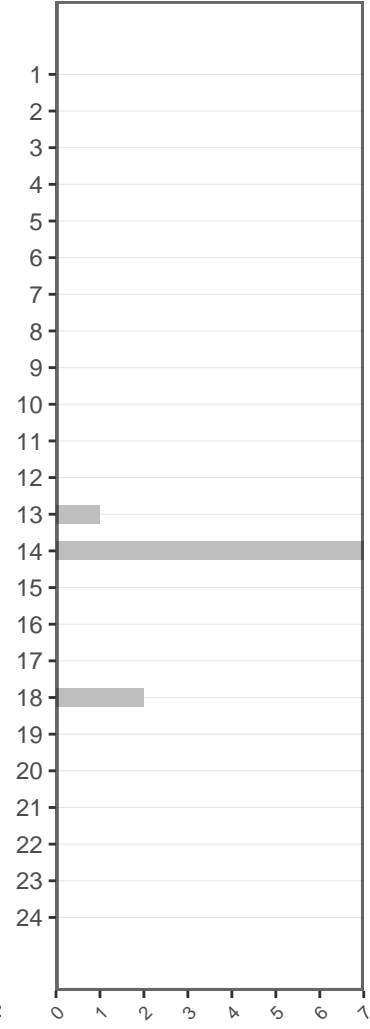
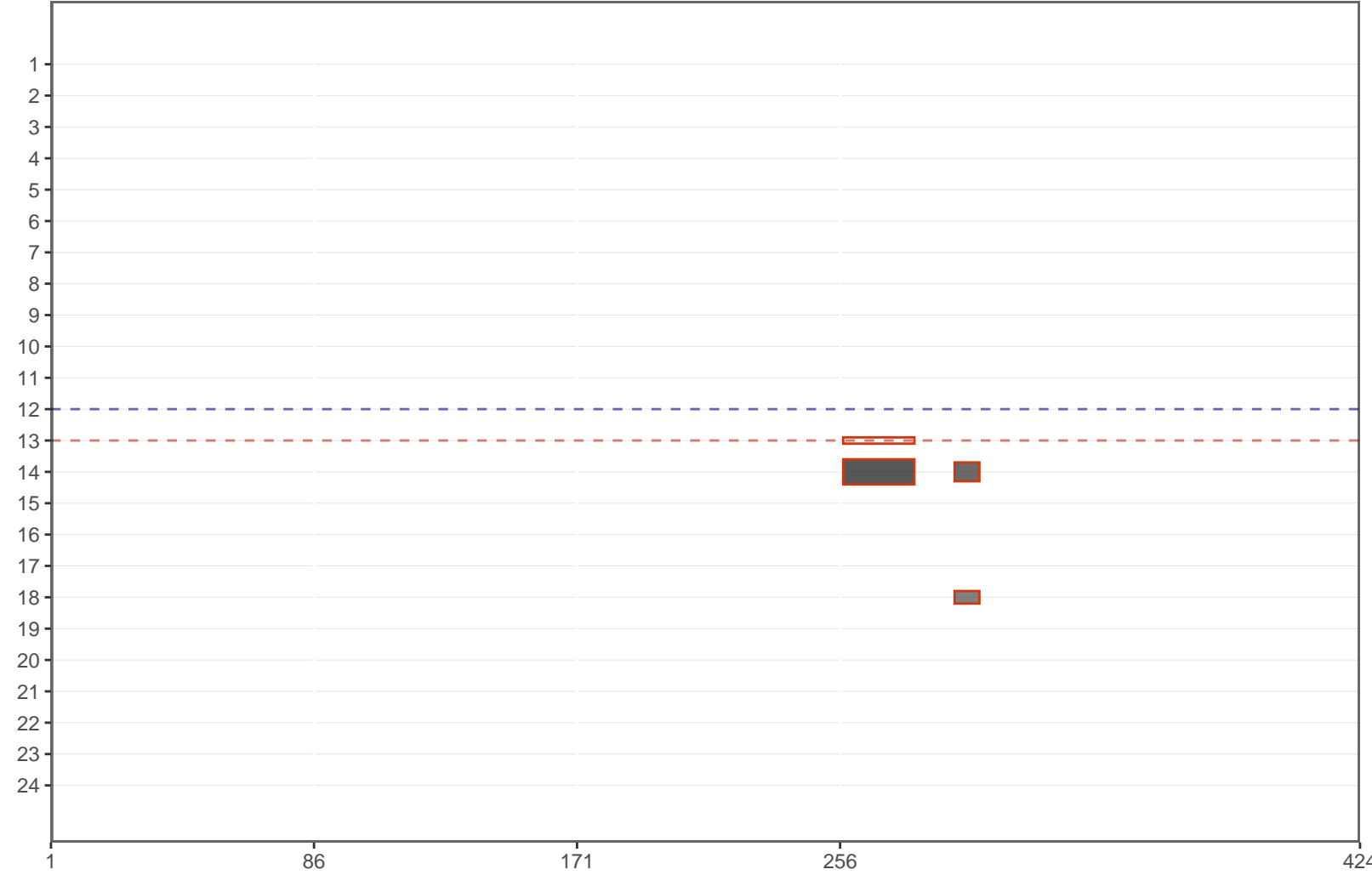
MW indication



Molecular weight

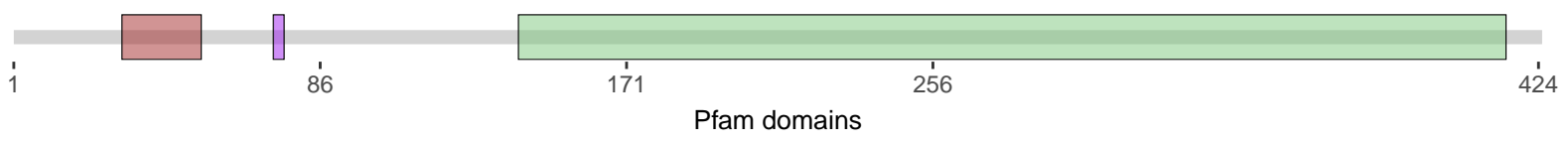


Gel Slice



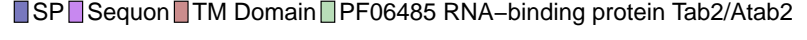
Protein length

Peptide counts over 4 repeats



Pfam domains

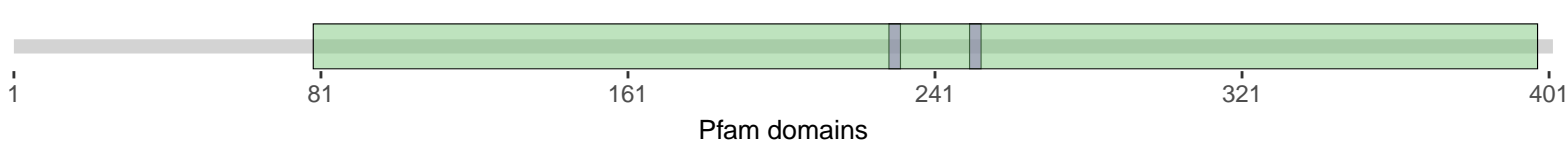
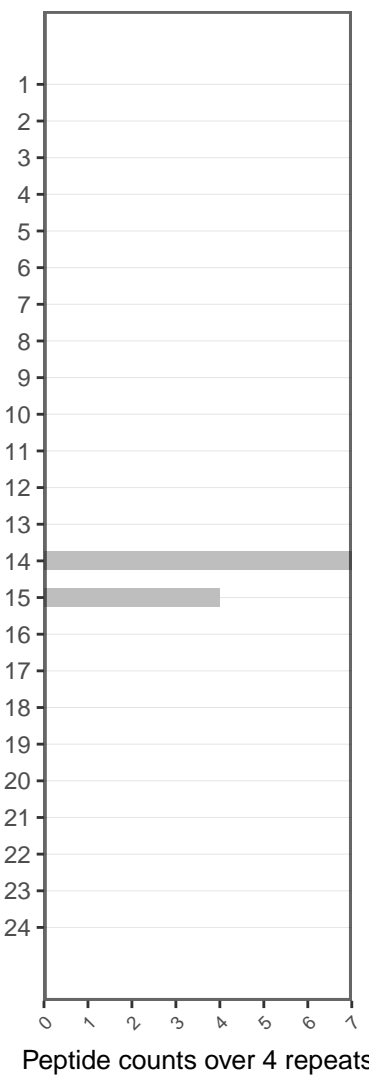
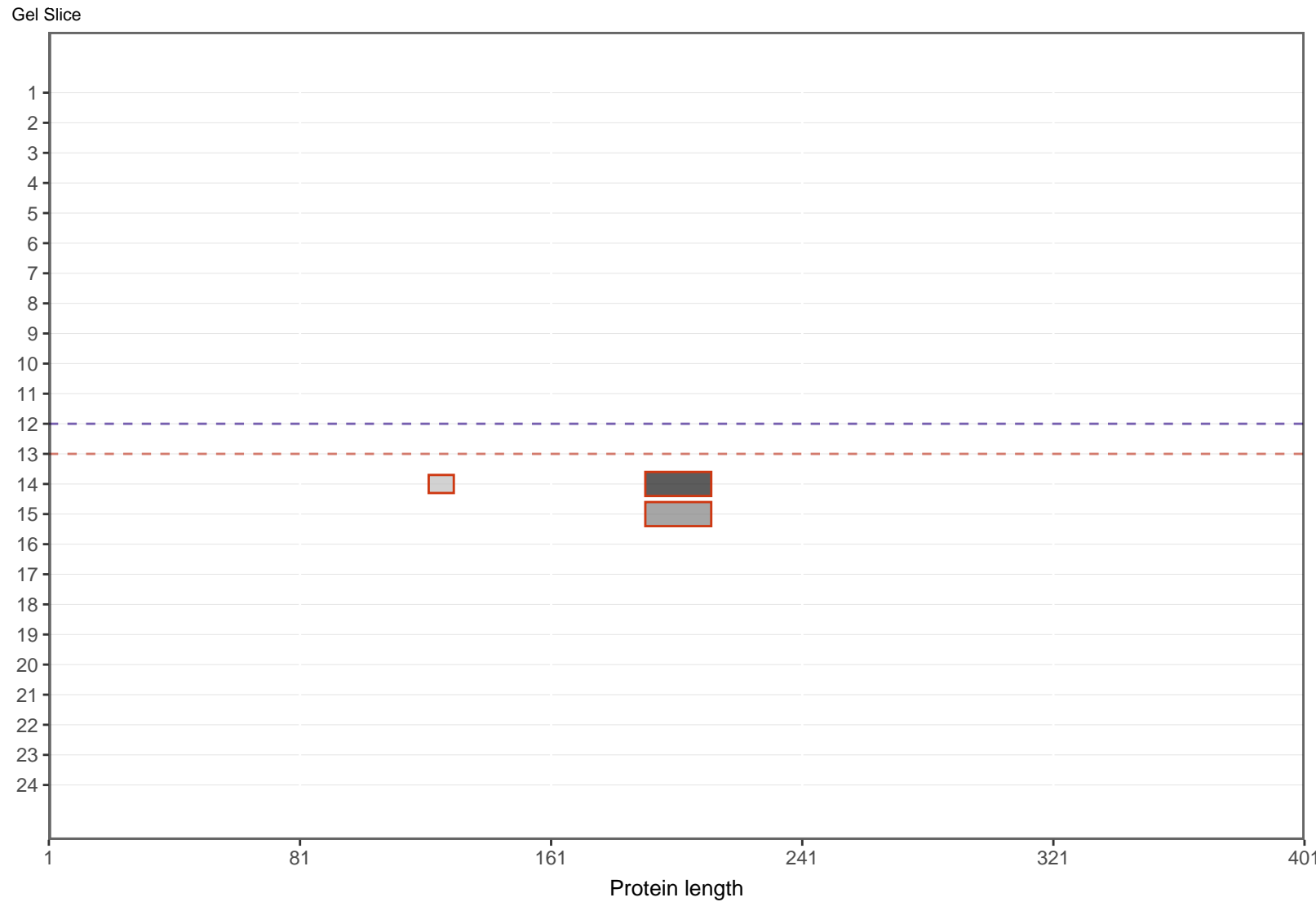
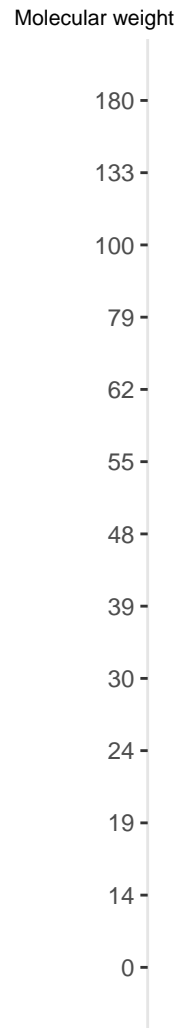
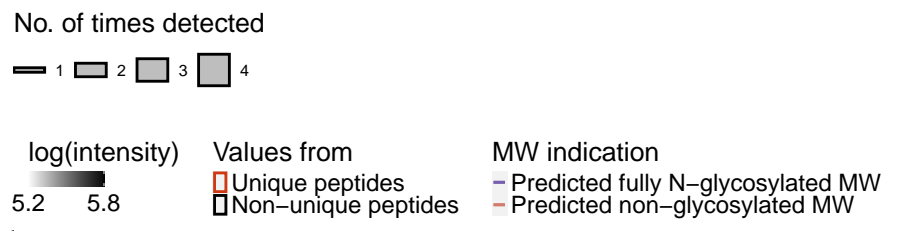
Pfam Description



Protein sequence:

PKIKRFRFSQMTIHRACNELGKPKVSKRGLSLVLIWLEDRYETVYTRHPGFKGTRPLLALNPFMELPENLYGKNAFVQLPFSAVRREEVSNLETRLVFGASLDLDDLGIEIEKTLRPLGLAVATGRAXPLAAWMMNGLEVSGEADVARASLSEVGISTRYIWFYKKNPVTSEAEAEAAKKAKGGHLFLAIGNDLN6DDCVGFWLLGLPPPPV

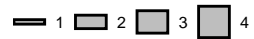
NbL14g16250.1 photosystem_II_stability/assembly_factor_HCF136_chloroplastic [MW = 43.48 kDa]



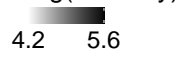
Protein sequence:
 TGEESAEMVTDGAGYVTSNKGYNWKAHQETVSATLNRTVSGSGHAGSYTYGTFTSTVNRSPDGRVYVWSSRGNFVLTWEPGGAYWDPHNRVARRIGNMGRADGGLLVLRGGGLYLSKGTGLSEDFEEVSVDSRGGFGLDVGVRSGDEAWAAGGGGLLKTNGGKTVWRDKAADNIAANLYSVKFNINDGGFVLDGNDGVLVLYG

NbL14g16220.1 ATP-dependent_Clp_protease_proteolytic_subunit_2_mitochondrial-like [MW = 26.41 kDa]

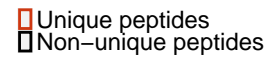
No. of times detected



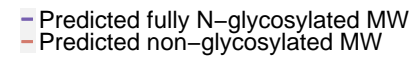
log(intensity)



Values from



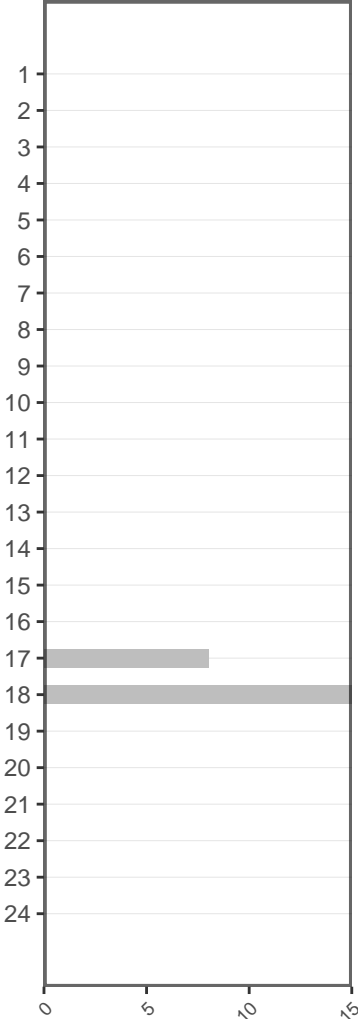
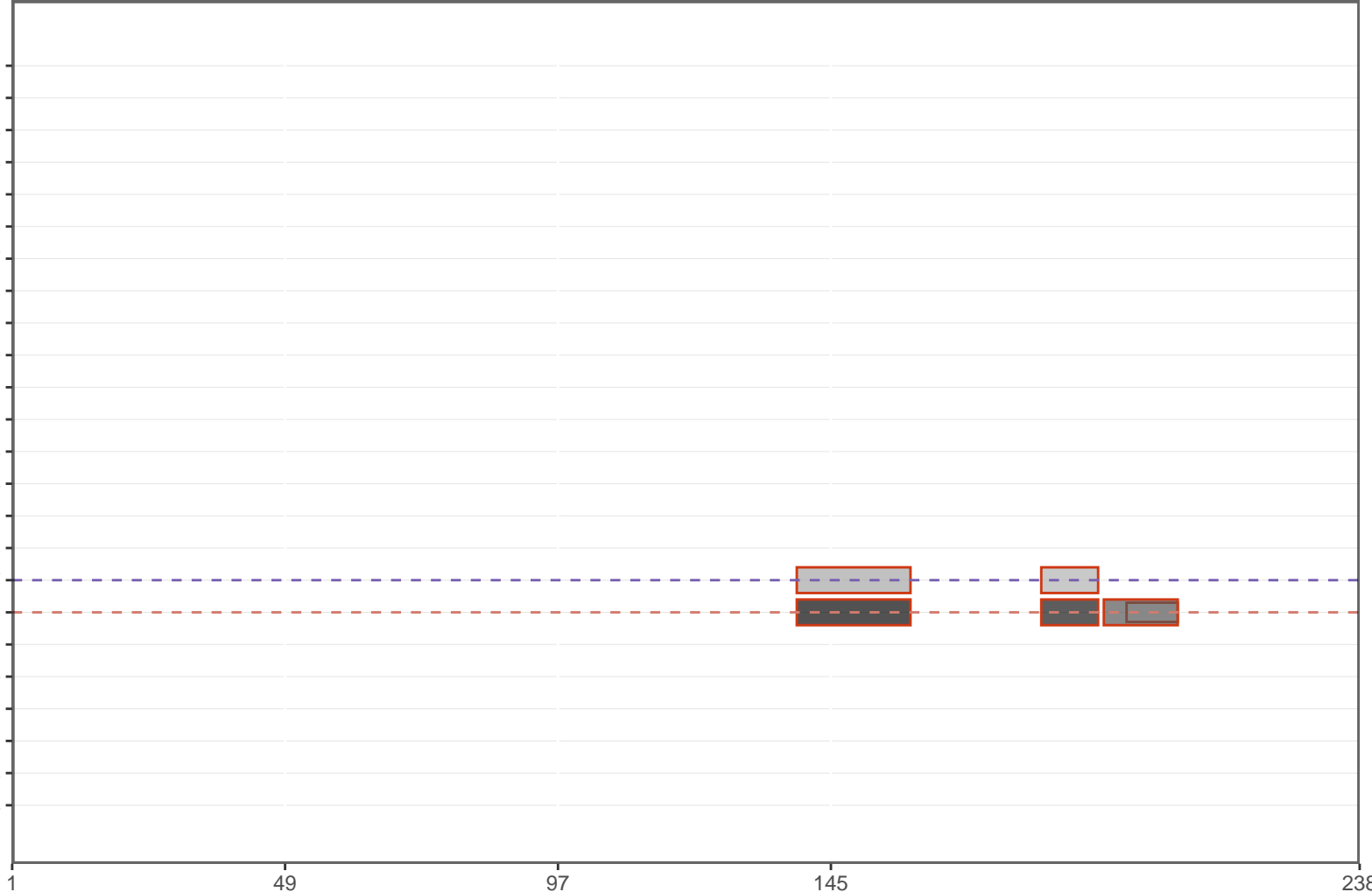
MW indication



Molecular weight

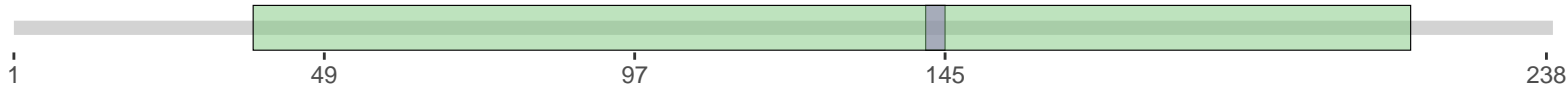


Gel Slice



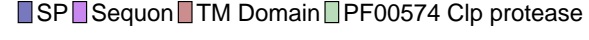
Protein length

Peptide counts over 4 repeats



Pfam domains

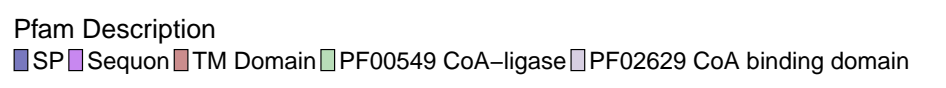
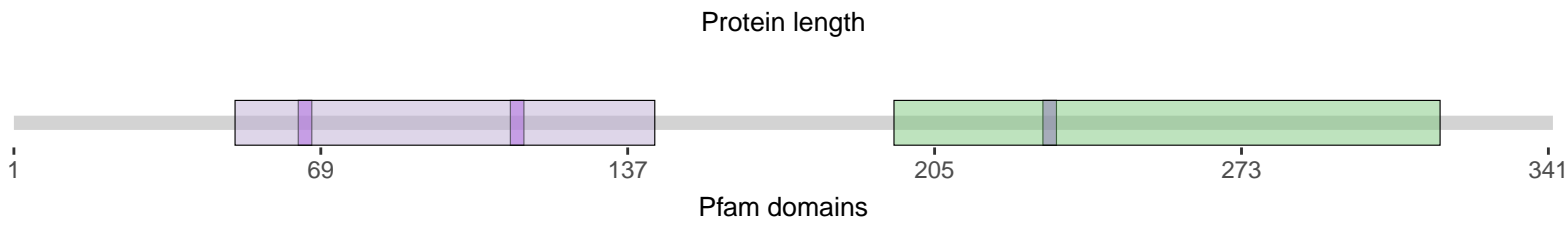
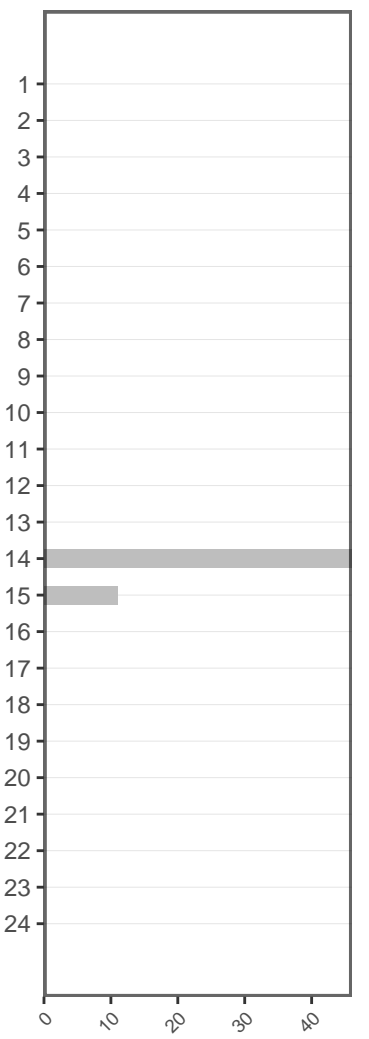
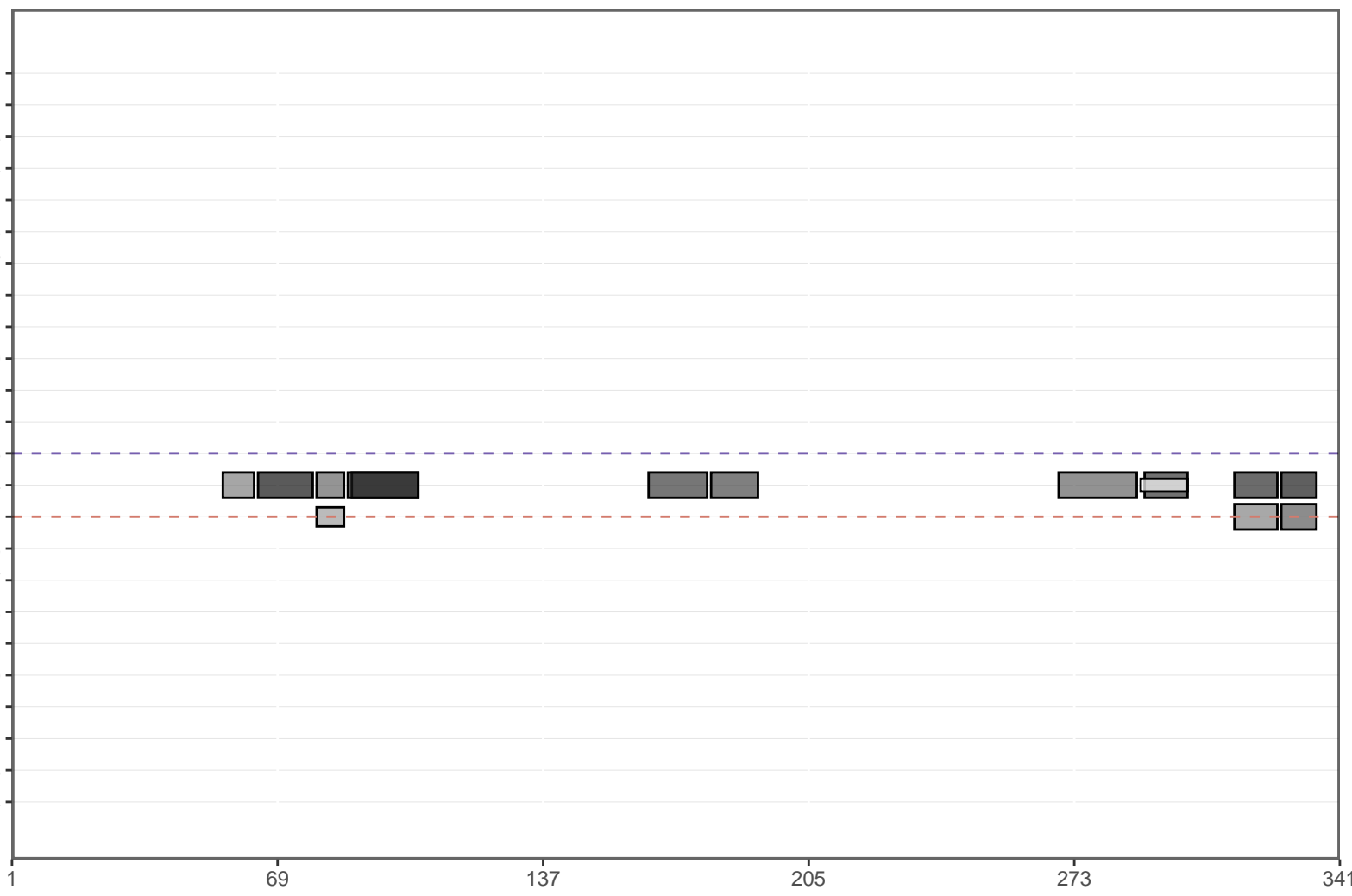
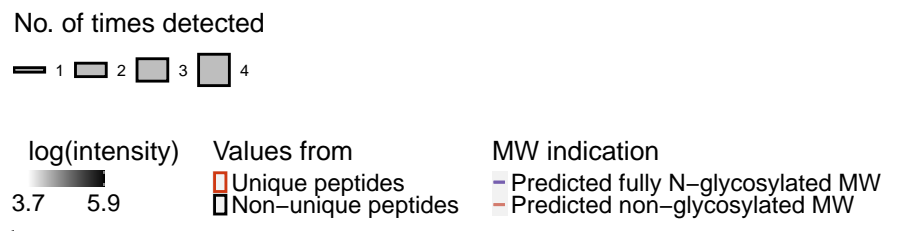
Pfam Description



Protein sequence:

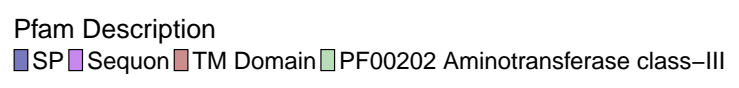
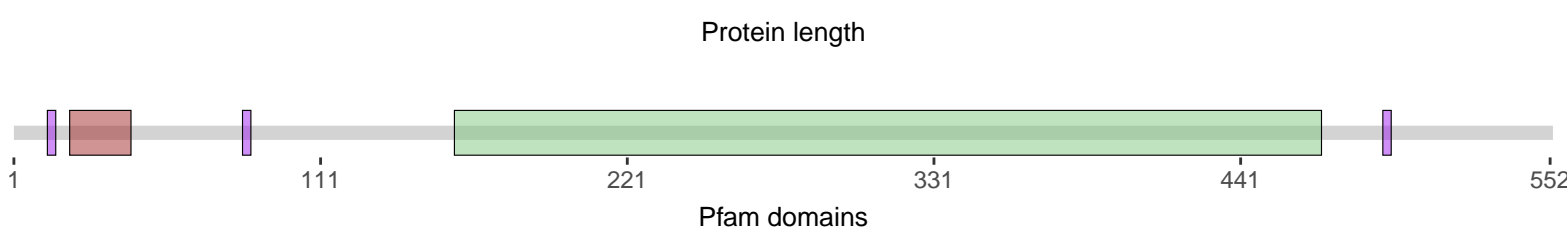
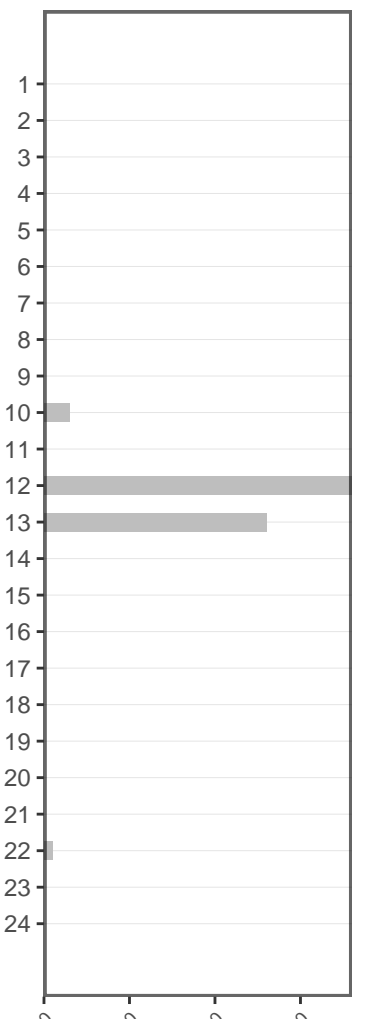
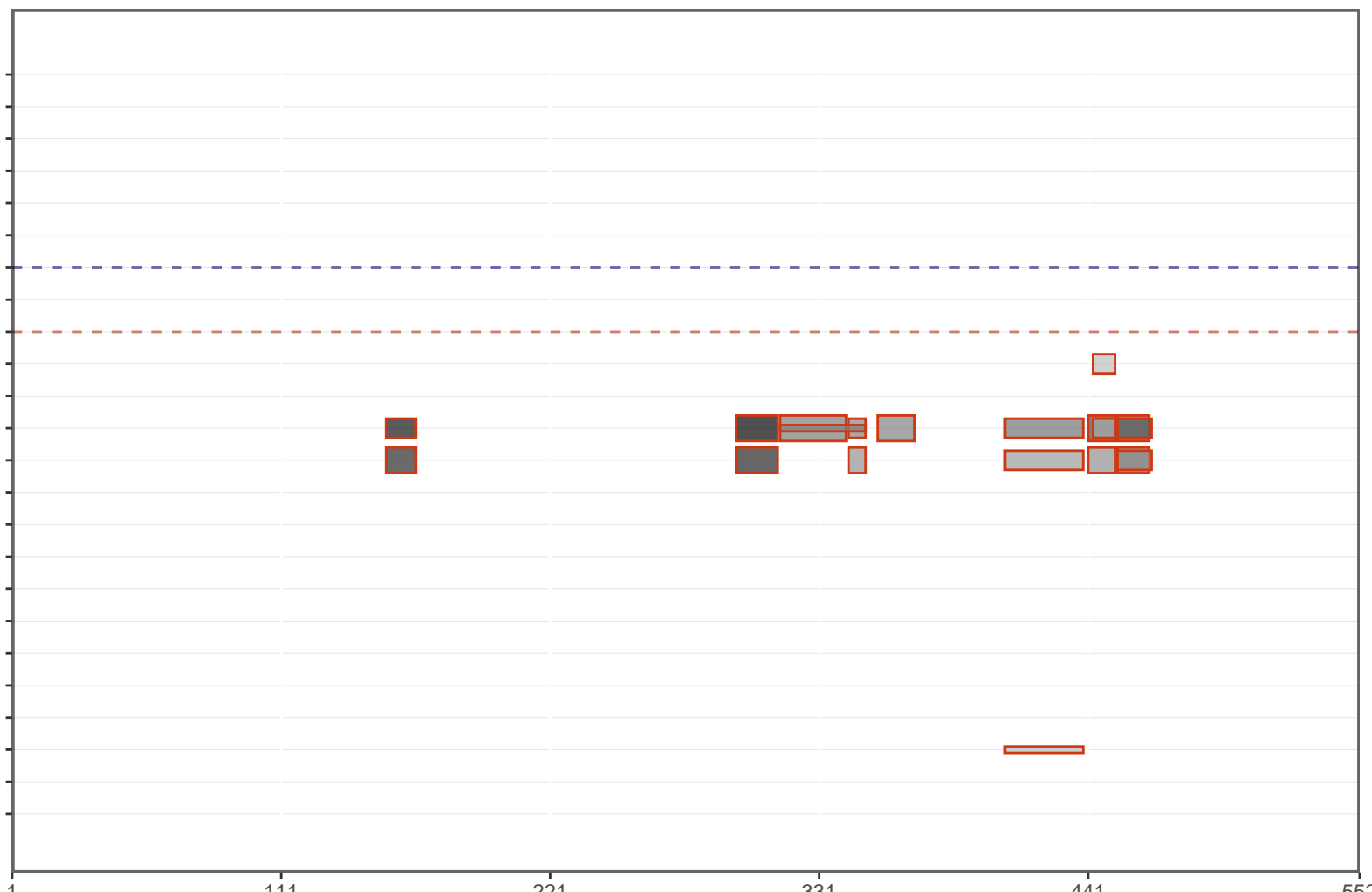
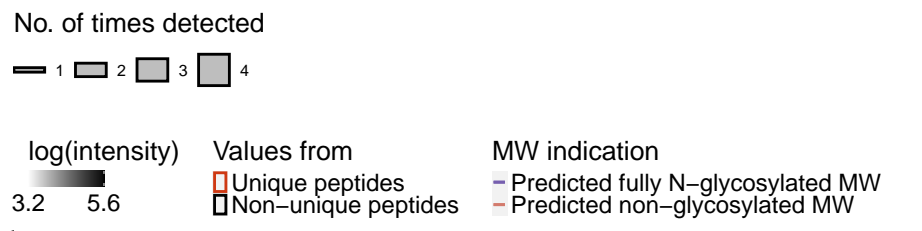
IQYIRSPNTICLGGAAASMAELLAAAGKERRRLPNATIMIHQPSGGYVSGGAKDMTHTKQIVRWWDALNGLYSKHTGDPVEIQKNMDRDVFMATAEEAKFQIIDEVIDQRPMALVTDAAIANKKSSS

NbL14g16170.1 succinate--CoA_ligase_[ADP-forming]_subunit_alpha-2_mitochondrial [MW = 35.58 kDa]



Protein sequence:
 LKKGDKTRLGPNPSPGKPKGECNIGMPQYHKPKRIGVGRSGTLYEAVFQTTAVGLGGSTCVGGDDPFNFTNFVDCLEKFIADPQTEGVLIGEKGTAEEEDAALKEGGTKPVAVFIAGLTAAPPGRRMGHAGAVVSGGKGTAGDKKIKLKEAGVTVGEFPAKIGVTMLDVFQKRGIA*

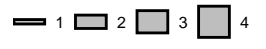
NbL14g16110.1 glutamate-1-semialdehyde_21-aminomutase_chloroplastic-like [MW = 59.69 kDa]



Protein sequence:
 MKKFECCYHGADDFLWAGSGWTLGLPDSGVPKATGDTLTPYNDISAISLFDONKGEIAAILLEPVVGNISGFIPKLEFLDVRDITKENGALLIFDEVMTGFRFLVGGAEVYGFITPDLTLGKGGGLPVGAYGRRDGMVAPAGPMVQAGTLSGNPLAMTAGINTLKRLLKPGPAYEHLDKITGELIGGLDAGKRTGHHAMCGGYSGMFGFFFTGSPVHNFSDAKKSDAAKFAKFKYRGMLEEGVYLPASGFEAGFTSLAHTVEDDGGTAAAEKYLROL

NbL14g16020.1 protease_2 [MW = 86.34 kDa]

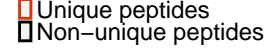
No. of times detected



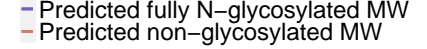
log(intensity)



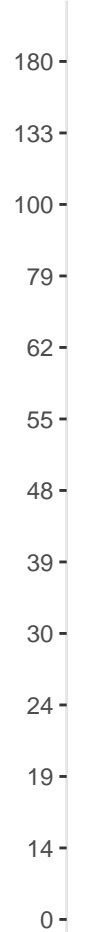
Values from



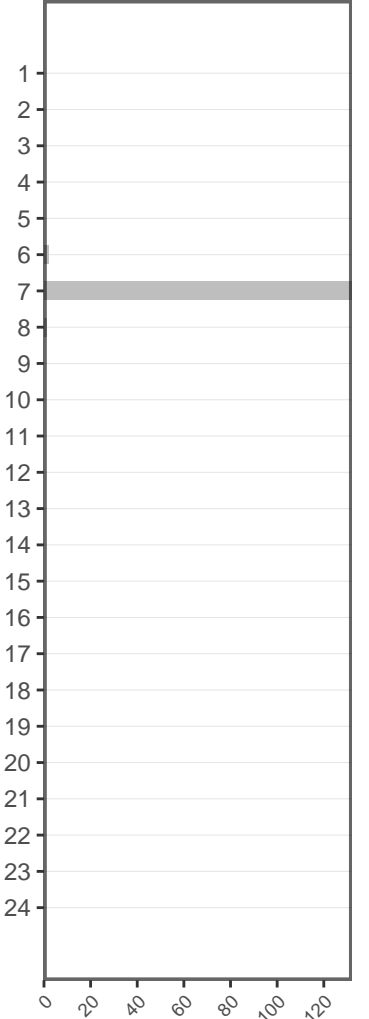
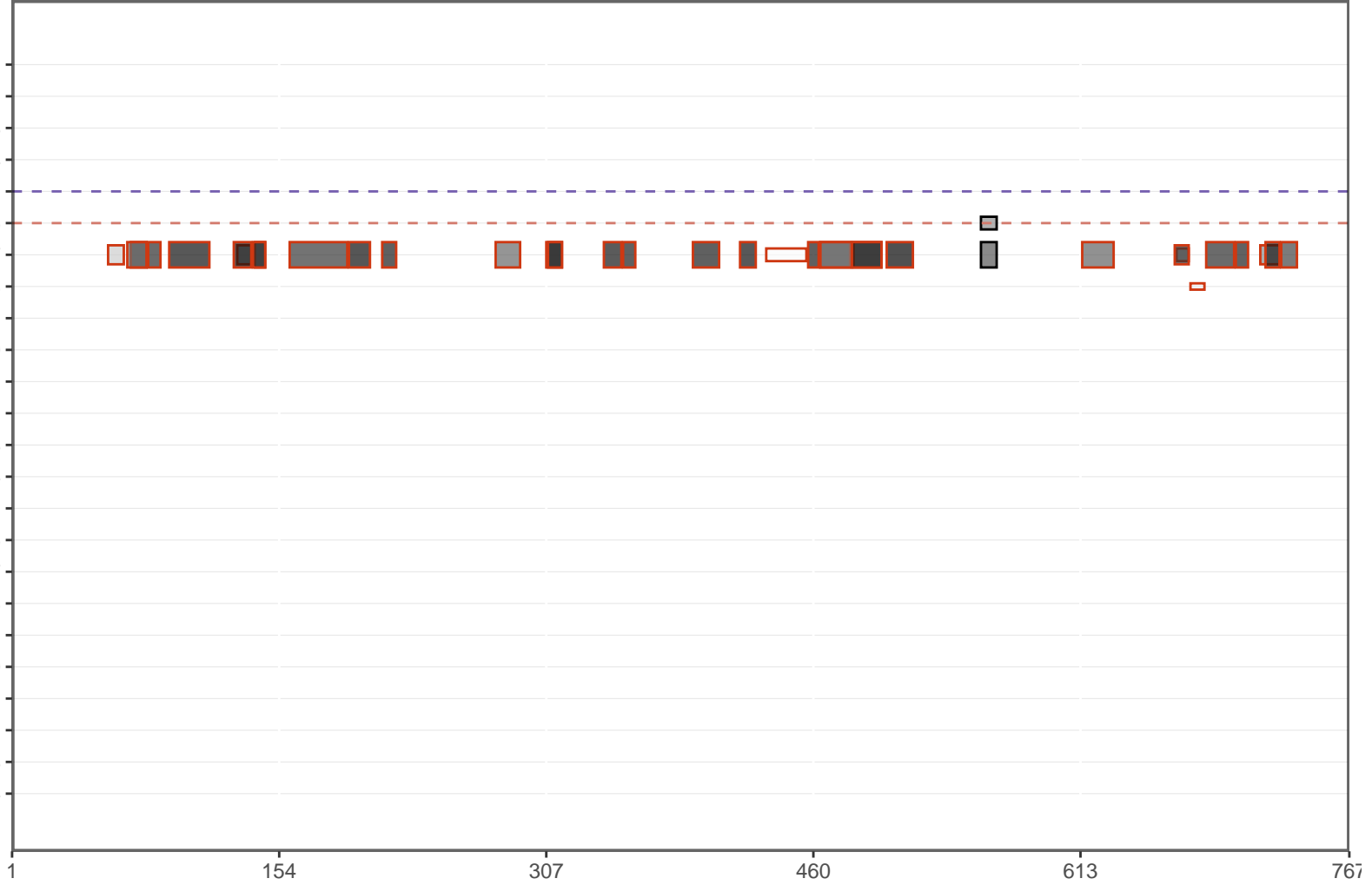
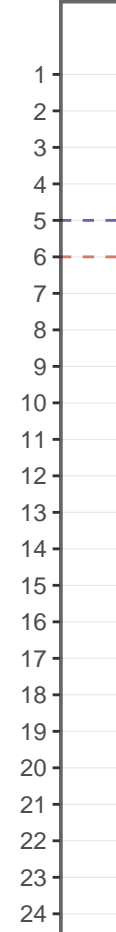
MW indication



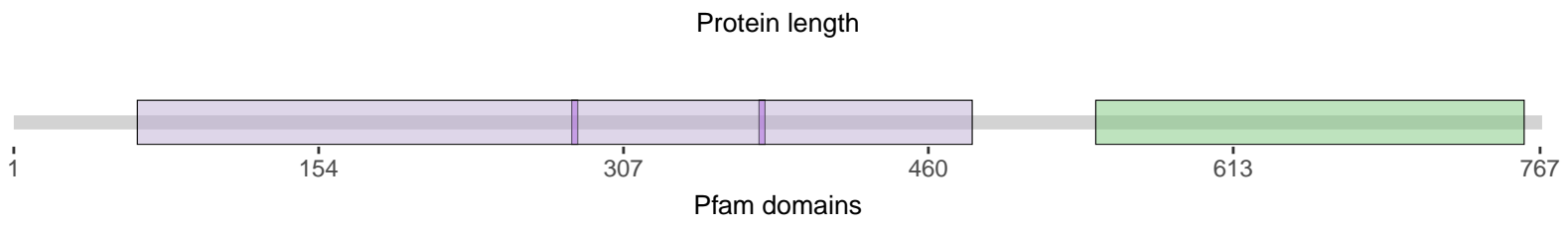
Molecular weight



Gel Slice



Peptide counts over 4 repeats



Pfam Description



Protein sequence:

CPVENISATSVILPHRPSVKLGGDLFTDHLAVHERENGLPRITVYVLPVWGEPLERLGGRAVDFVDPVYSADPLESEFESGLRFYSYSSMRPLSVYDYMDDTGVSVLKKIETVYGGFDANVYTERQRATASDGVQIPISIVRKNLWLDGADPLLLYGYGVEIGDPTFKASRLSLLDRGFYAAIAHRGGGEMGRGWYENGLKKKNTFTDFIADAEYLDKKYGSKEKLGINGRSAGLLIGAVANNMRPDLKAAVAGVFPVQVVTMLDPTPLTTSSEWEEWGPDKI

NbL14g15810.1 proteasome_subunit_beta_type-7-A-like [MW = 35.43 kDa]

No. of times detected



log(intensity)



Values from



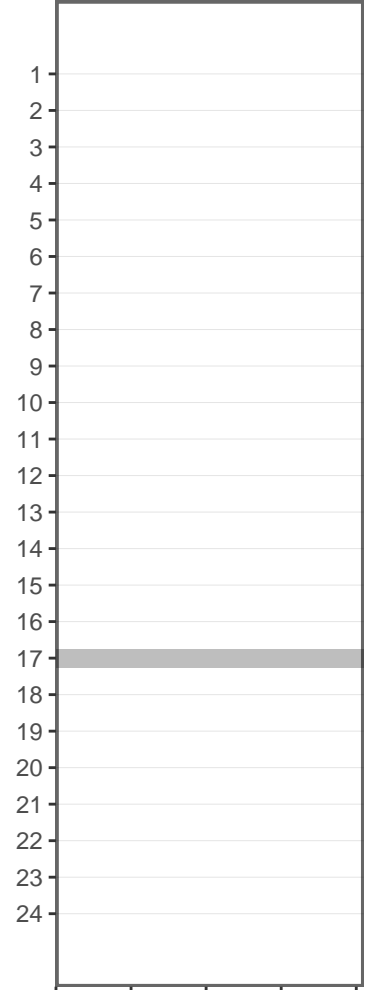
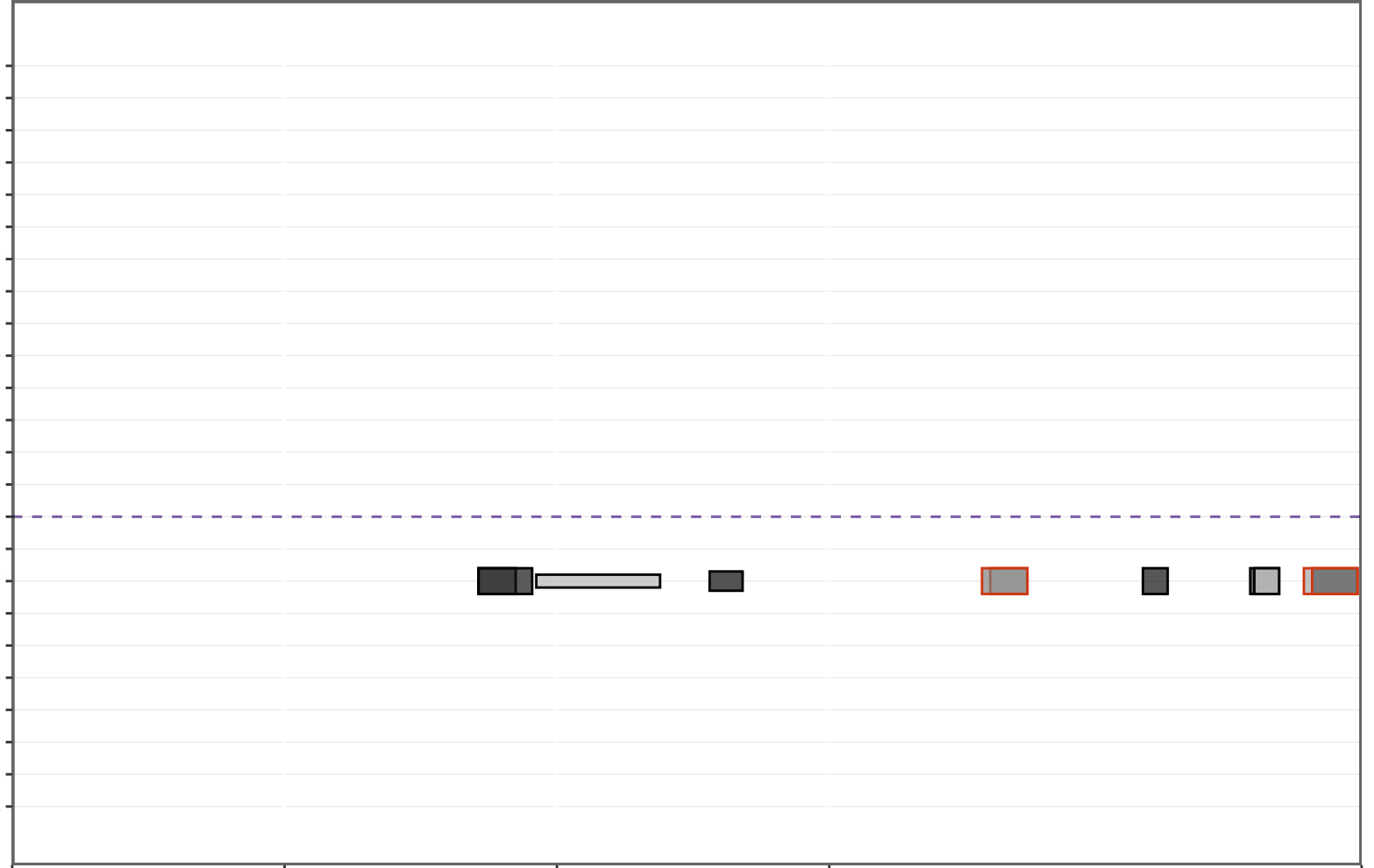
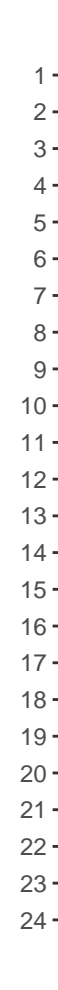
MW indication



Molecular weight



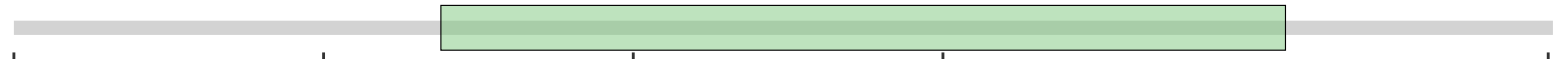
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

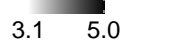
MYSSQLKJRYHTGREERVATLTLKHLFVYQGYVSAALVGGVDYFGPKLHTYVPHGSDTLPVATMGGSLAAMFEEKYREGLSKDEGKIVAEALGGVFNDLGGGNDIGITKQTEVLRNHLNMLPNRTYPOKGVDFPKRTEVLFNITPLRERVEIEGGDAMEE*

NbL14g15730.1 ribose-phosphate_pyrophosphokinase_4-like [MW = 44.73 kDa]

No. of times detected



log(intensity)



Values from



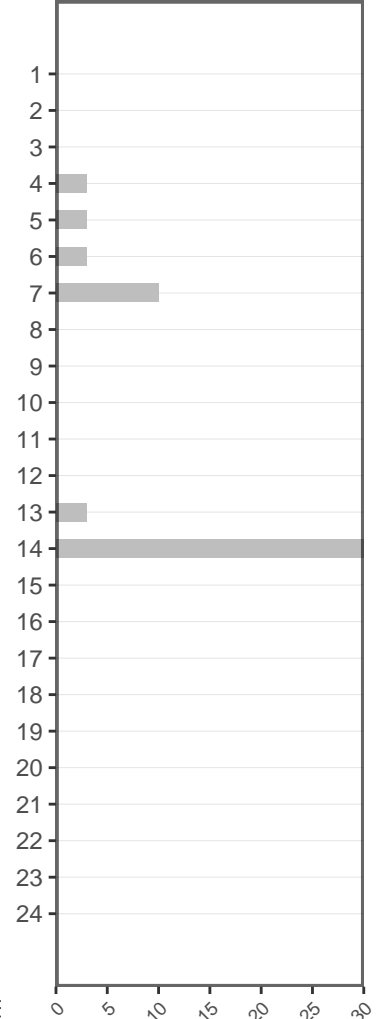
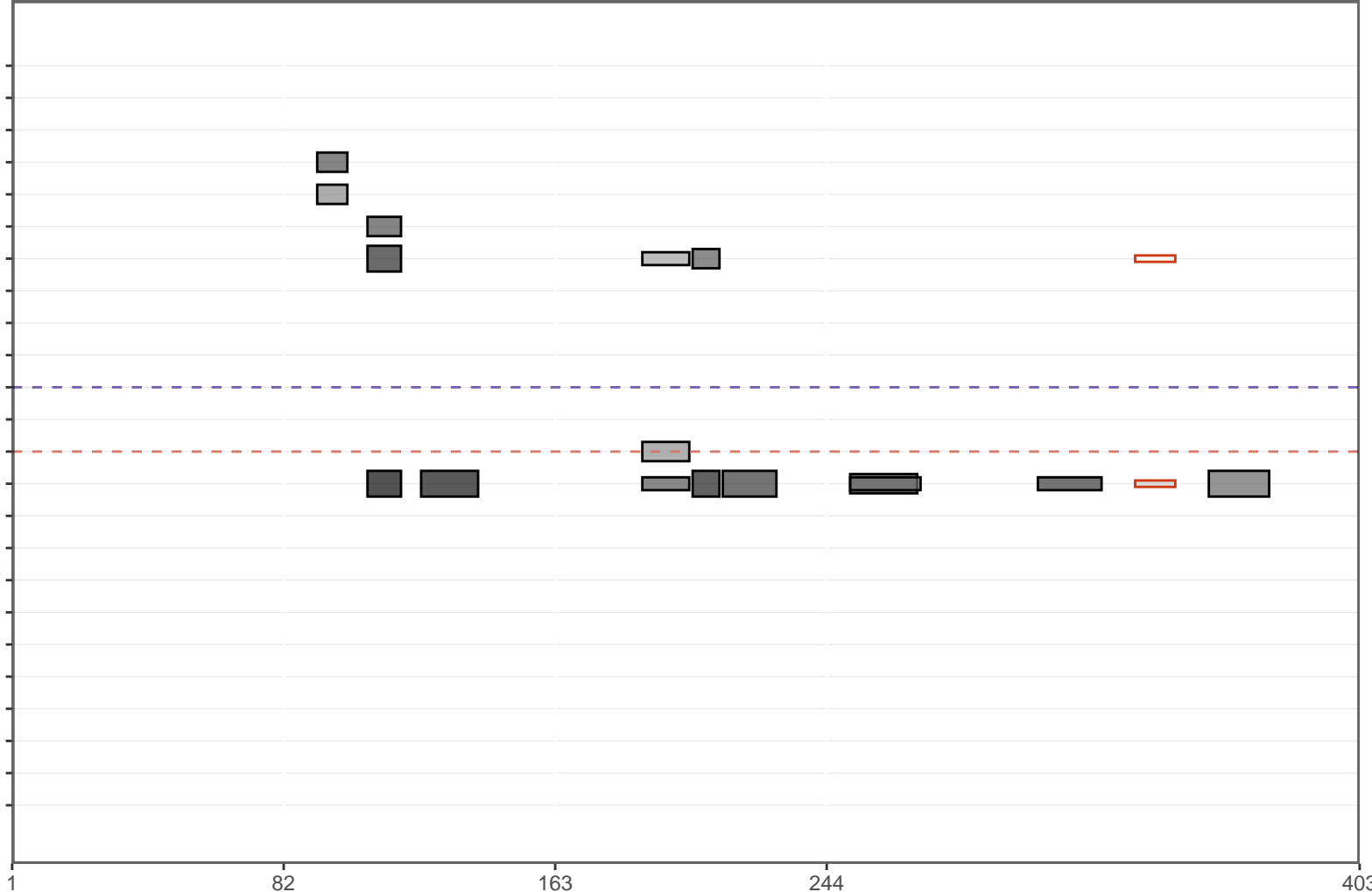
MW indication



Molecular weight



Gel Slice

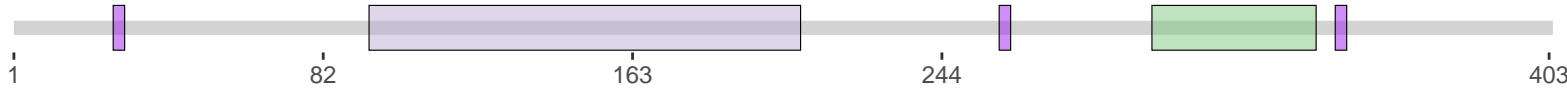


Protein length



Peptide counts over 4 repeats

Pfam domains



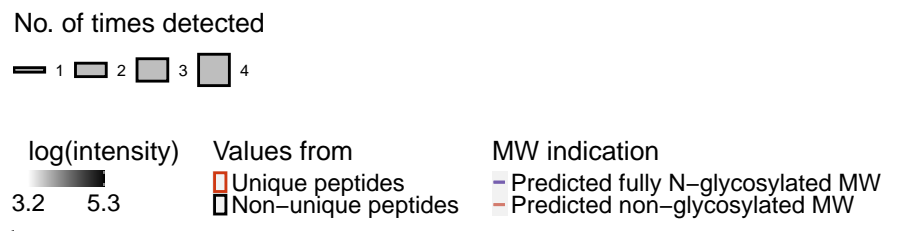
Pfam Description

- SP Sequon
- TM Domain
- PF00156 Phosphoribosyl transferase domain
- PF13793 N-terminal domain of ribose phosphate pyrophosphokinase

Protein sequence:

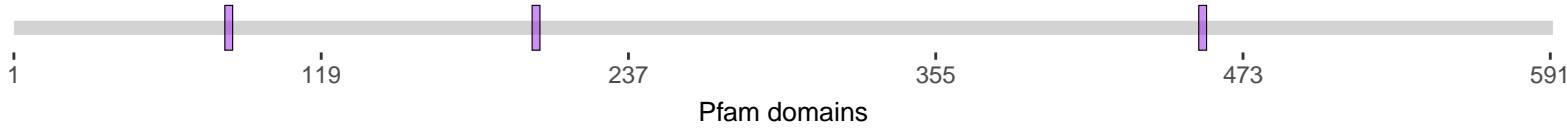
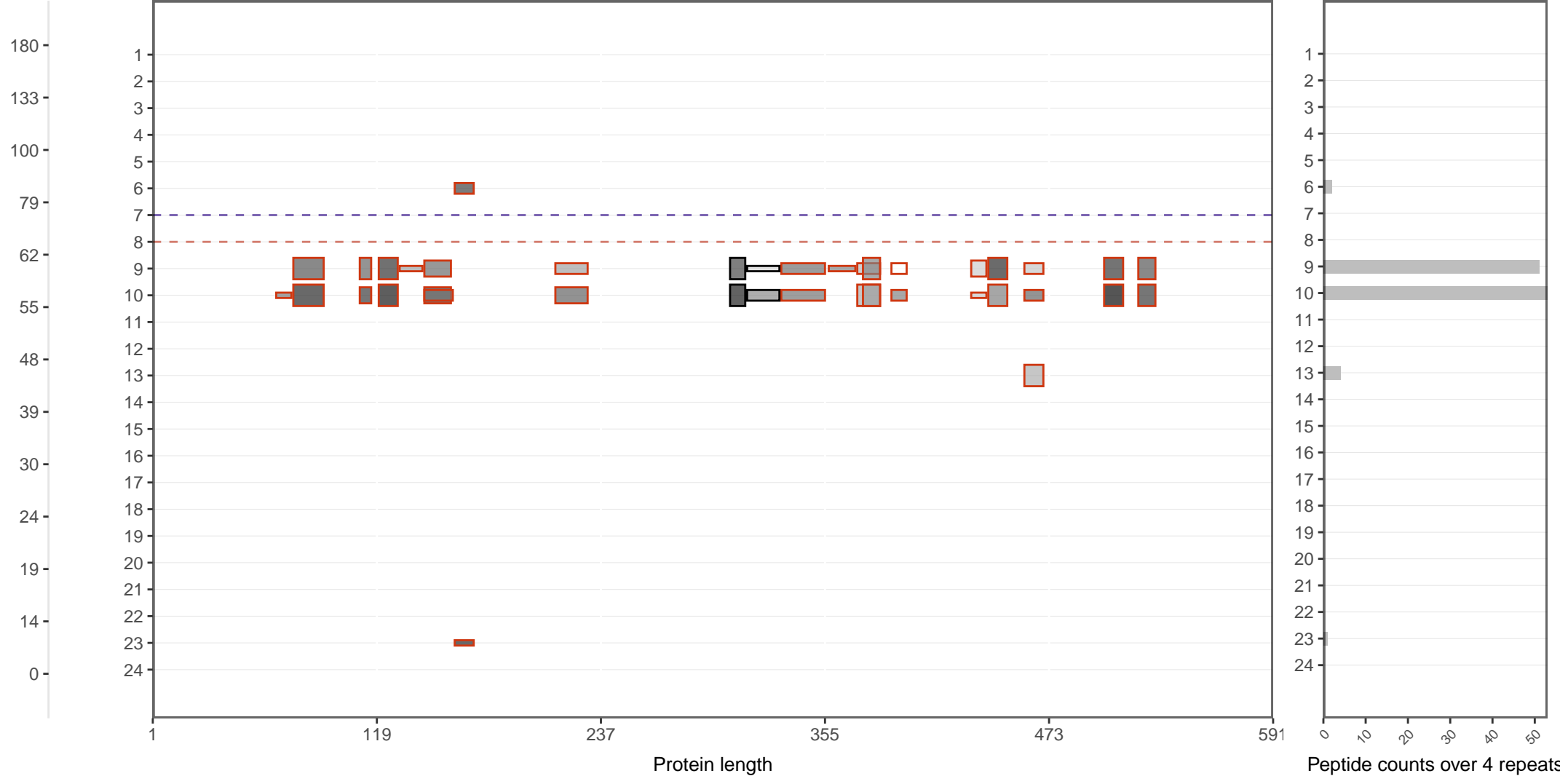
EDEGGVATFTLARIISNPVFRGGTSLVTFDHALGERFYFDNLPGFESGIPRLLLNRLQGLPDSNLSLAFDDGAWRFHKQLGHFPMVCAKVRGGDRIKRIKEDPAGRHVAVVDLVS6GDTLTCQKVLARHGAKKISAVTHGIFNRIWQRFNHDKGGPE6GMYFWTDSGPRTVKEVKDKRPFELSLAIPAALGPI

NbL14g15720.1 uncharacterized_LOC104221143 [MW = 64.93 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain

Protein sequence:
 VADVNSLTHYGEPYDGNTRYFRSTLFLVAWRSGYSGESGLLHGVDVMPKPKGGTTEQMLFMFGANTHLPDQARLLEDDVEVGFYHSGREARPSLVLGSLRHHKRPPLATAEKVQGVNRRARKEAIVAGFYHGGVEEPLMLMRRRGVHAGLVKGGEGALSMTRLRRTANASKGFPVNYGSGFRSMNLAPAGAVDGTGLPYGVRESFNEVNAKDKYGFAPDTPRTDRSVAKNIELGLAALRGEKGPWDRIVLNAQMIDHLLGSDGAGDISAFAFDRAAREADSGKA

NbL14g15690.1 ATP-citrate_synthase_alpha_chain_protein_2 [MW = 46.61 kDa]

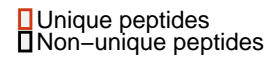
No. of times detected



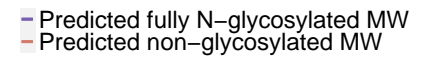
log(intensity)



Values from



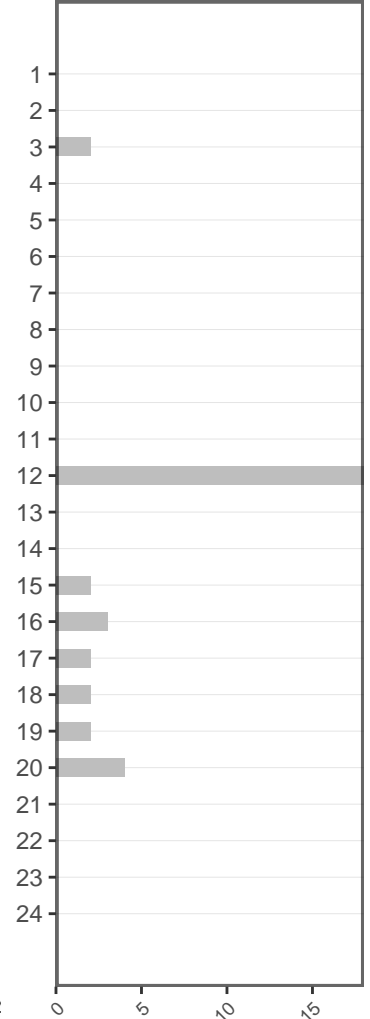
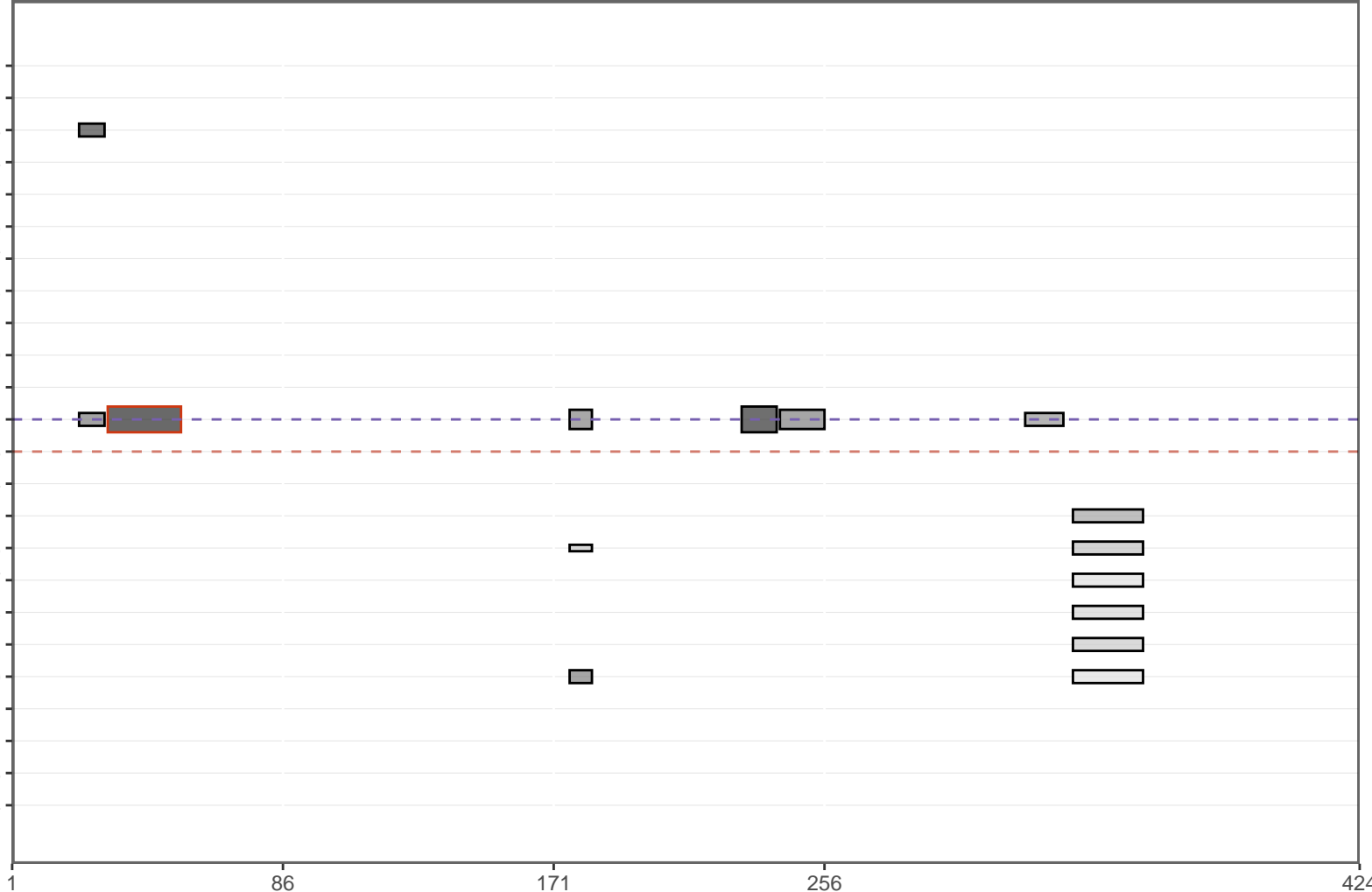
MW indication



Molecular weight



Gel Slice



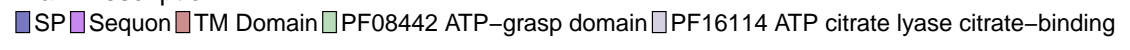
Protein length

Peptide counts over 4 repeats



Pfm domains

Pfam Description



Protein sequence:

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NbL14g15560.1 probable_splicing_factor_3A_subunit_1 [MW = 89.33 kDa]

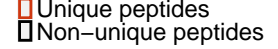
No. of times detected



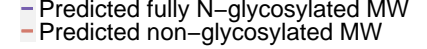
log(intensity)



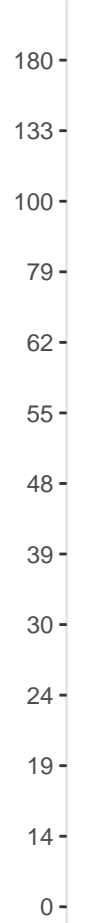
Values from



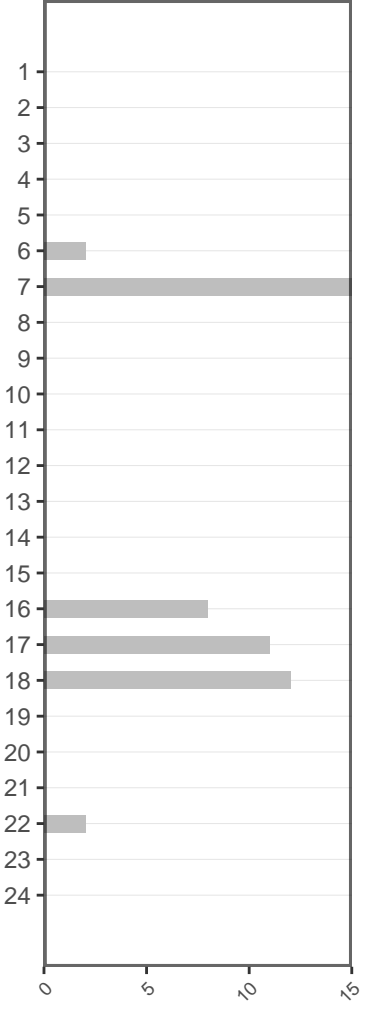
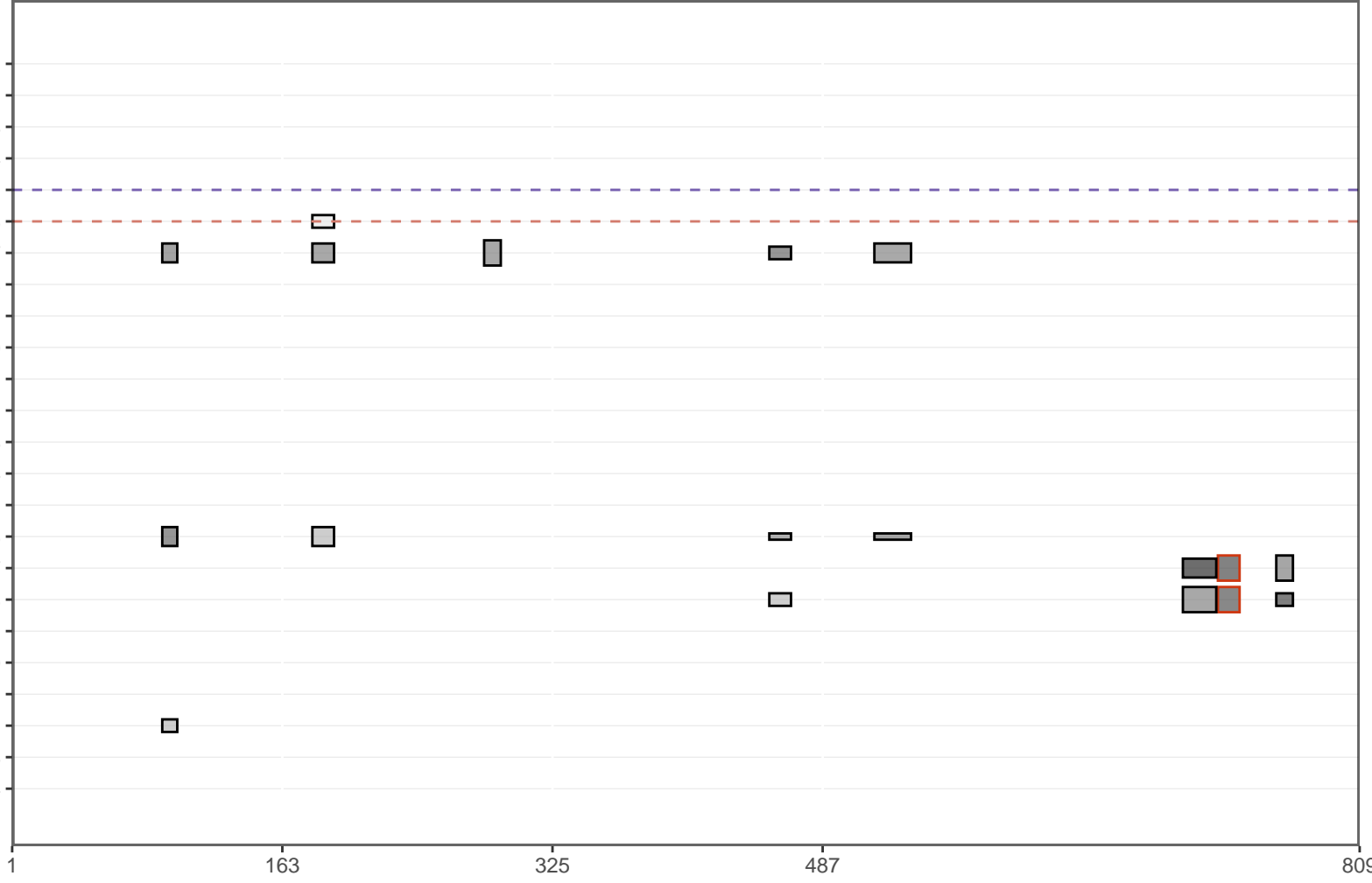
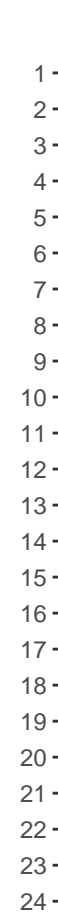
MW indication



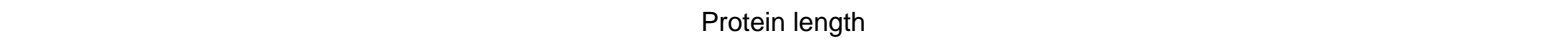
Molecular weight



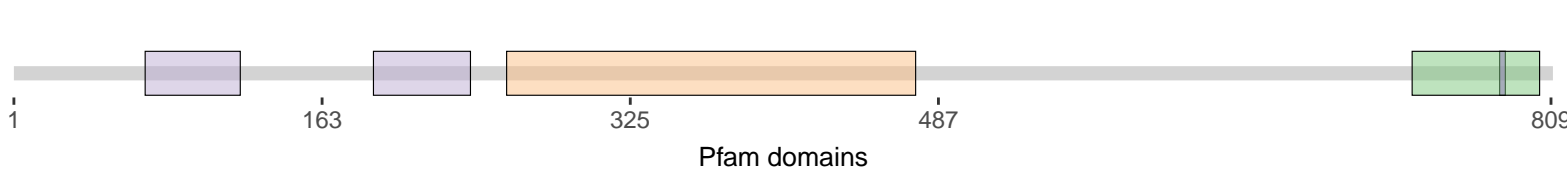
Gel Slice



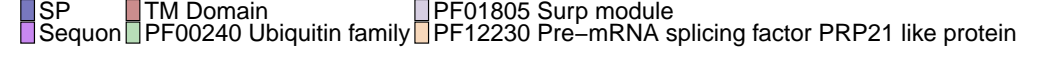
Protein length



Pfam domains



Pfam Description



Protein sequence:

PPMRIVNXYKSPKEERIPTESDPTKYVSRITGELIPNEMSEHMRISLIDPKYKEGKDRMFAKIKETFLAGDDEISRNVGLARTRPDIQFTTEEEVSNVAKAEIKKKEEPKQVIWDGHTGSGIRTAGSAMSGNTNADDQNDANDERNLPGDQAPPPRRPGFVSVRFLFPPDGLALNRPPTVQYVSTGAGVAALPSRPPRMVNMIPQVRRPPPPMPQMLGGONLIMVNRPPMPSPMAMNSHGHPPIPPPGGQFTPLGAPRAFVPLPMGQPMMSVPPPPPLGMP

NbL14g15350.1 protein_GAST1 [MW = 13.45 kDa]

No. of times detected



log(intensity)



Values from



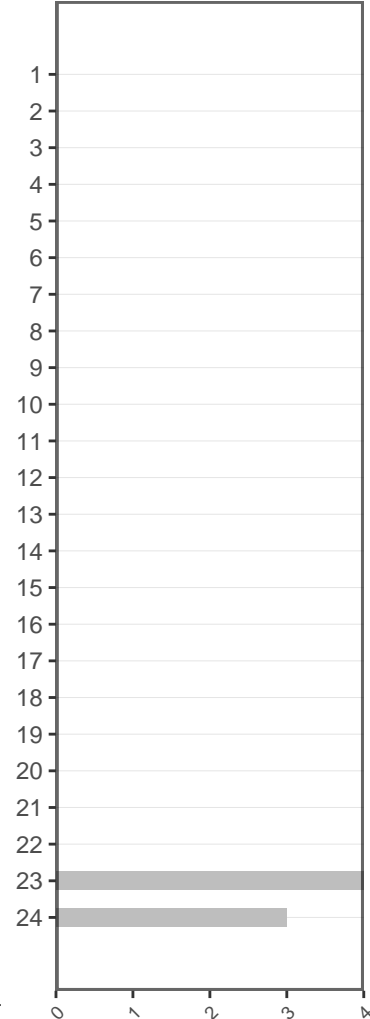
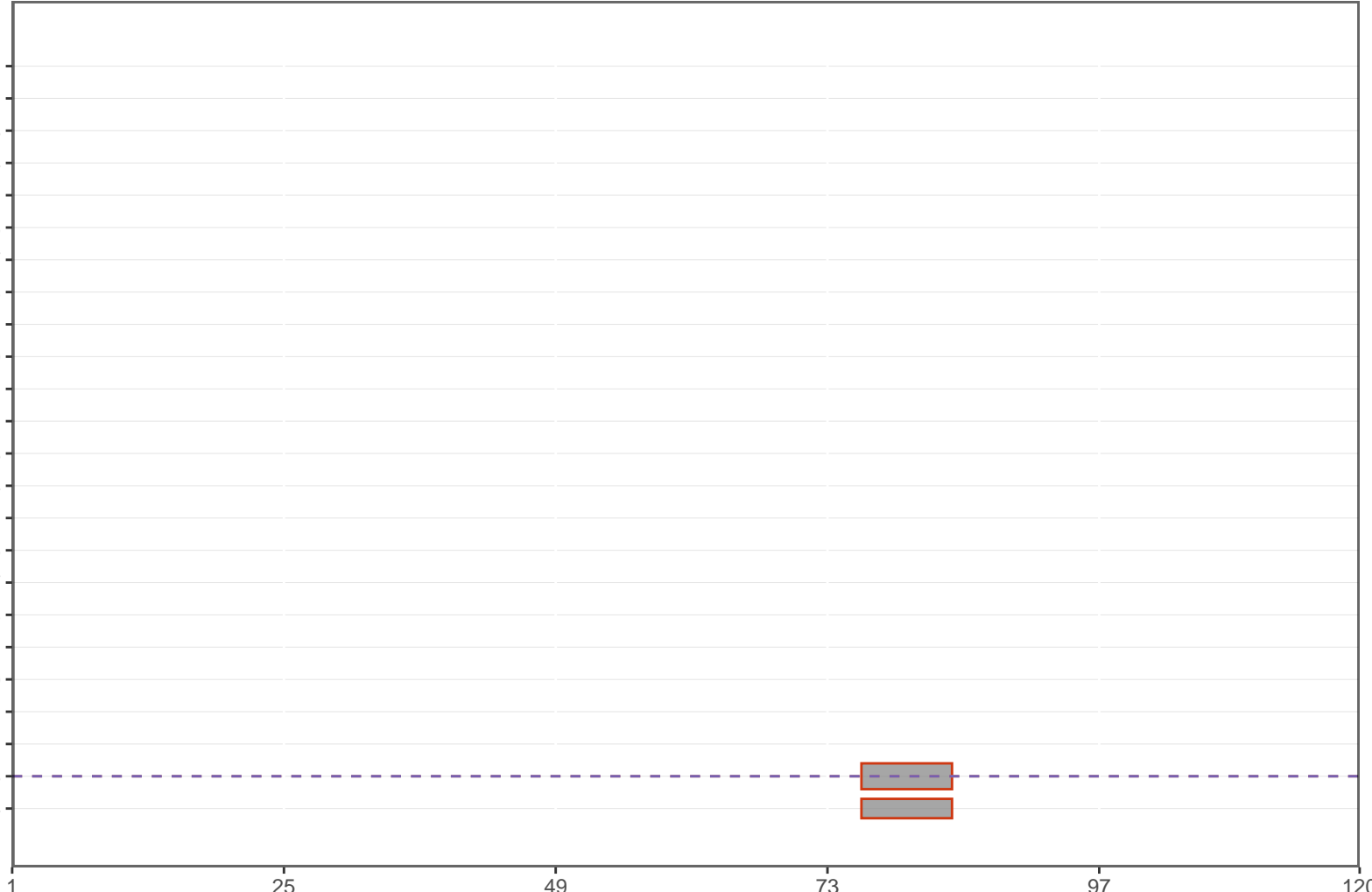
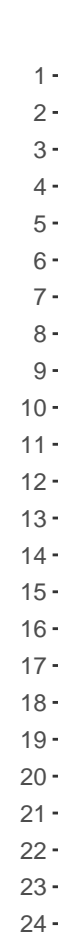
MW indication



Molecular weight



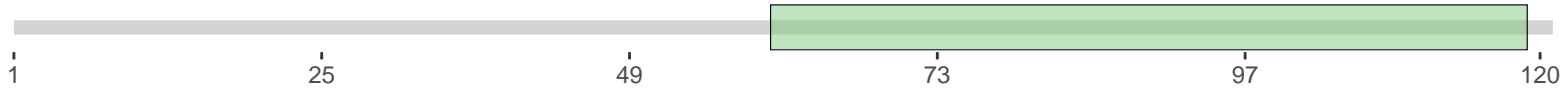
Gel Slice



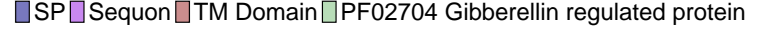
Protein length



Pfam domains



Pfam Description



Protein sequence:

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NbL14g15310.1 40S_ribosomal_protein_S19-3-like [MW = 17.99 kDa]

No. of times detected



log(intensity)



Values from



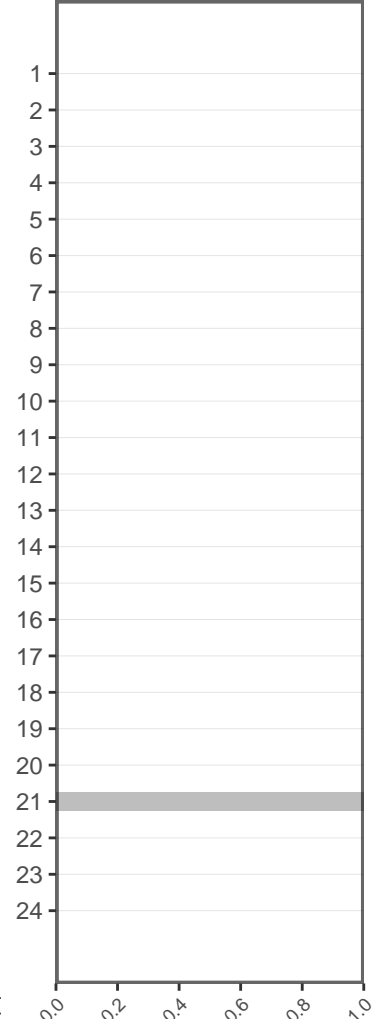
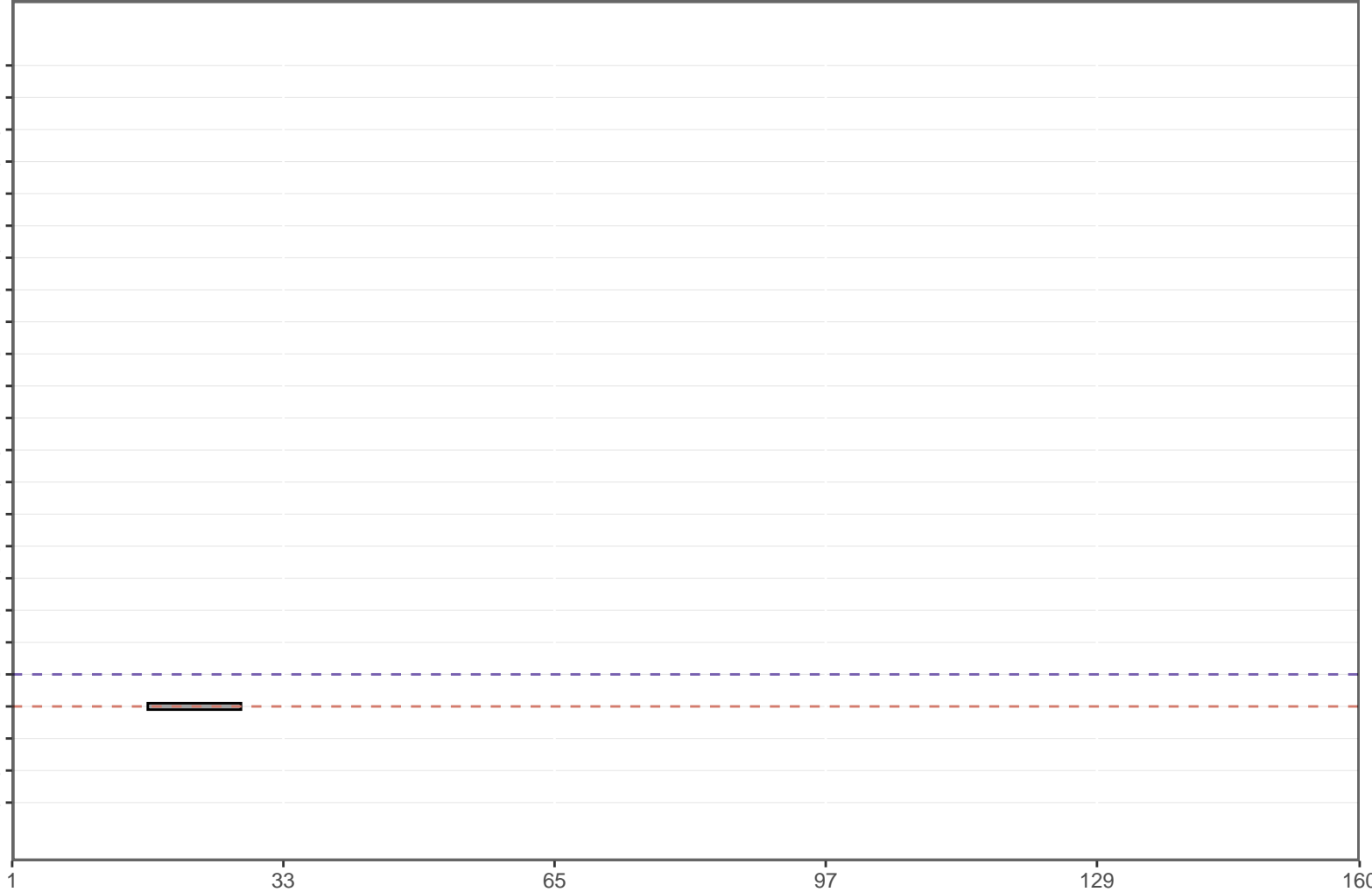
MW indication



Molecular weight

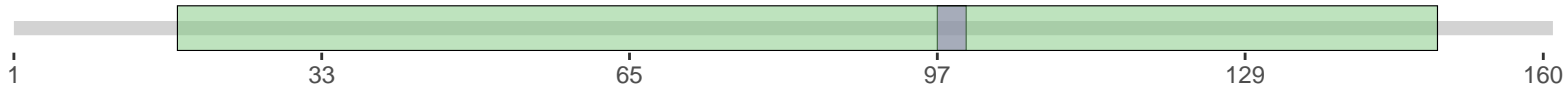


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RAASMARKIYLRGSLGVGFRRIRYGGNGRNGRNGRPRHFCKKSGGVARNLQQLGMNIDFDPKGGRRITSENGRDLDHGIRGGDRRLNLP

NbL14g15290.1 S-formylglutathione_hydrolase [MW = 31.9 kDa]

No. of times detected



log(intensity)



Values from



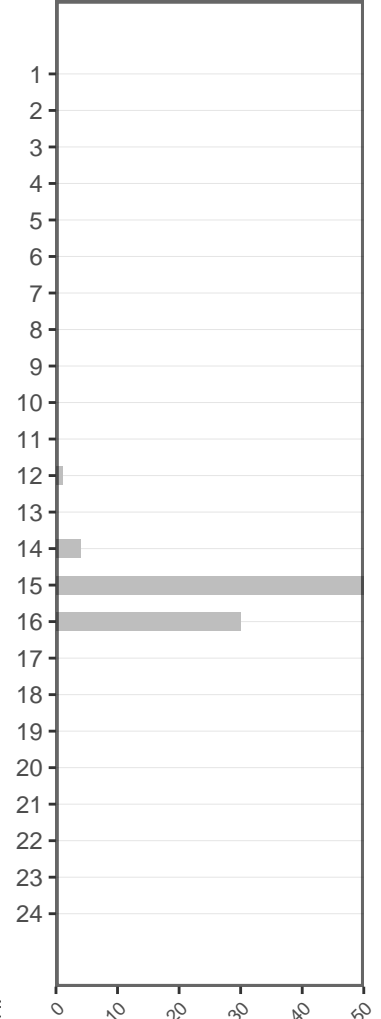
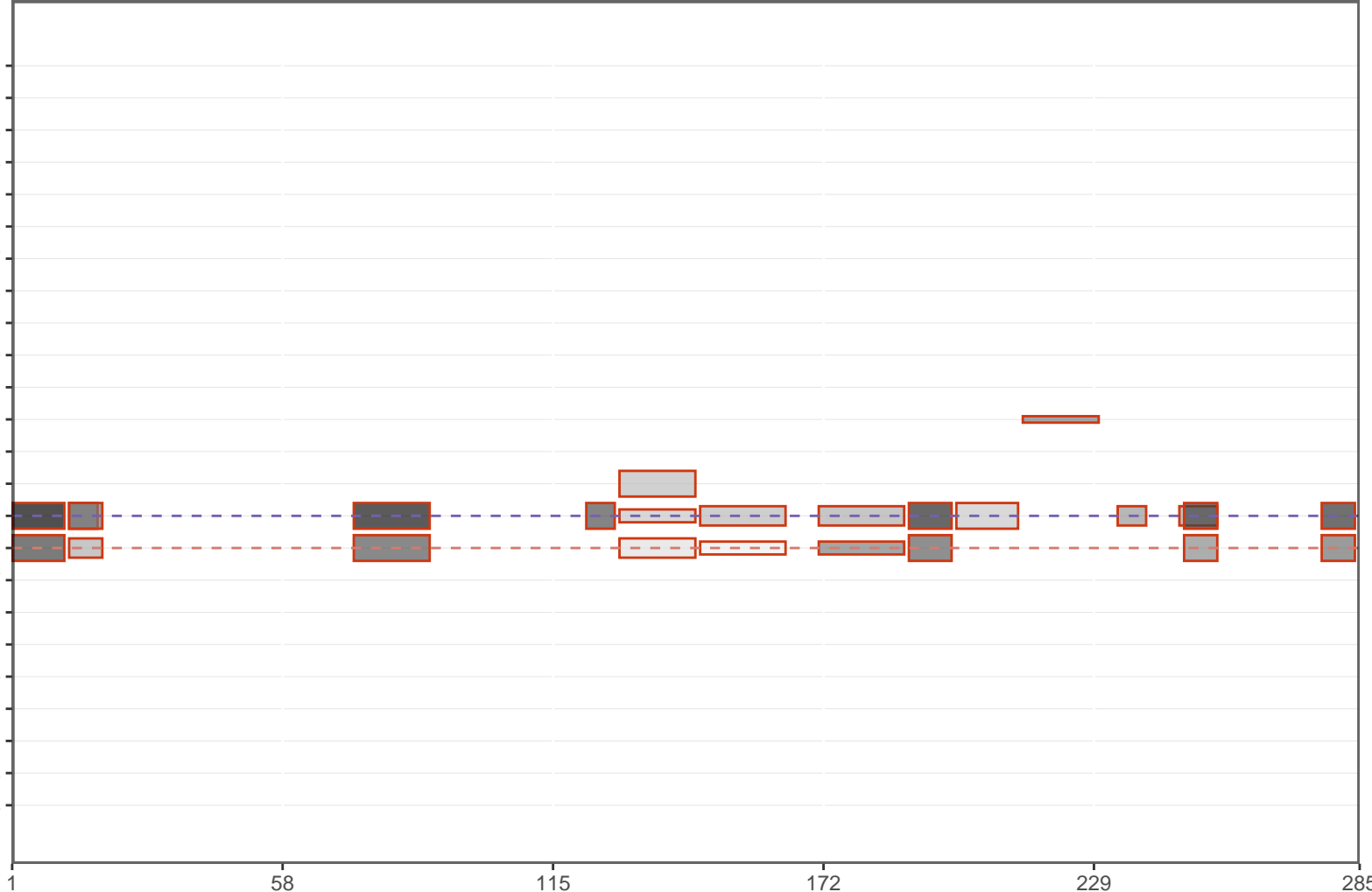
MW indication



Molecular weight

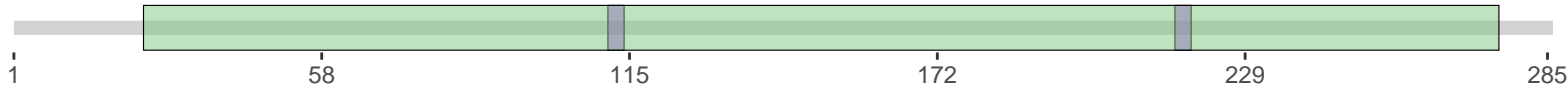


Gel Slice



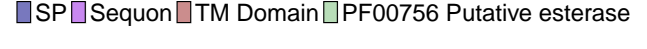
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KELPSLLENFPELOFSRBSIFGHSMGHGALTYLKNLDRYKVSFAFAPANPNPGWGLKAFNTYLGKNAKADWEEYDQTLVSRFNNVSRATLIDGGEDDKFLKDKLLPHKFEKACKKVGYPVLLVRLQPGYDHSYFYIATFDHHRHHAGALNL

NbL14g15180.1 U4/U6_small_nuclear_ribonucleoprotein_PRP4-like_protein [MW = 70.1 kDa]

No. of times detected



log(intensity)



Values from



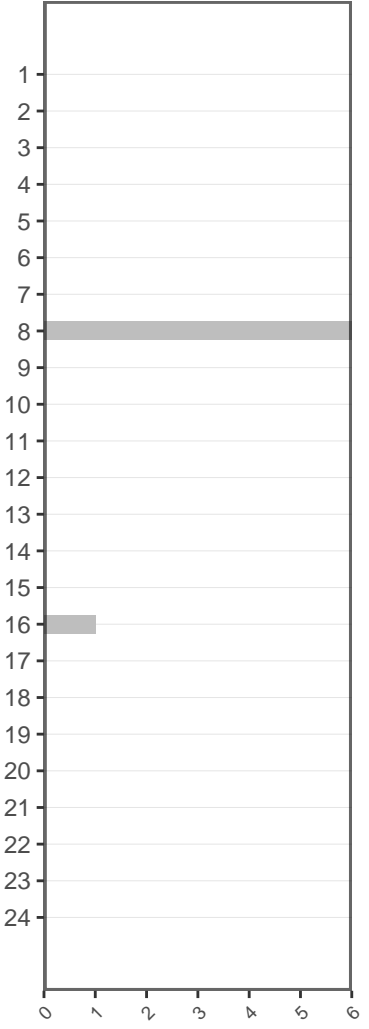
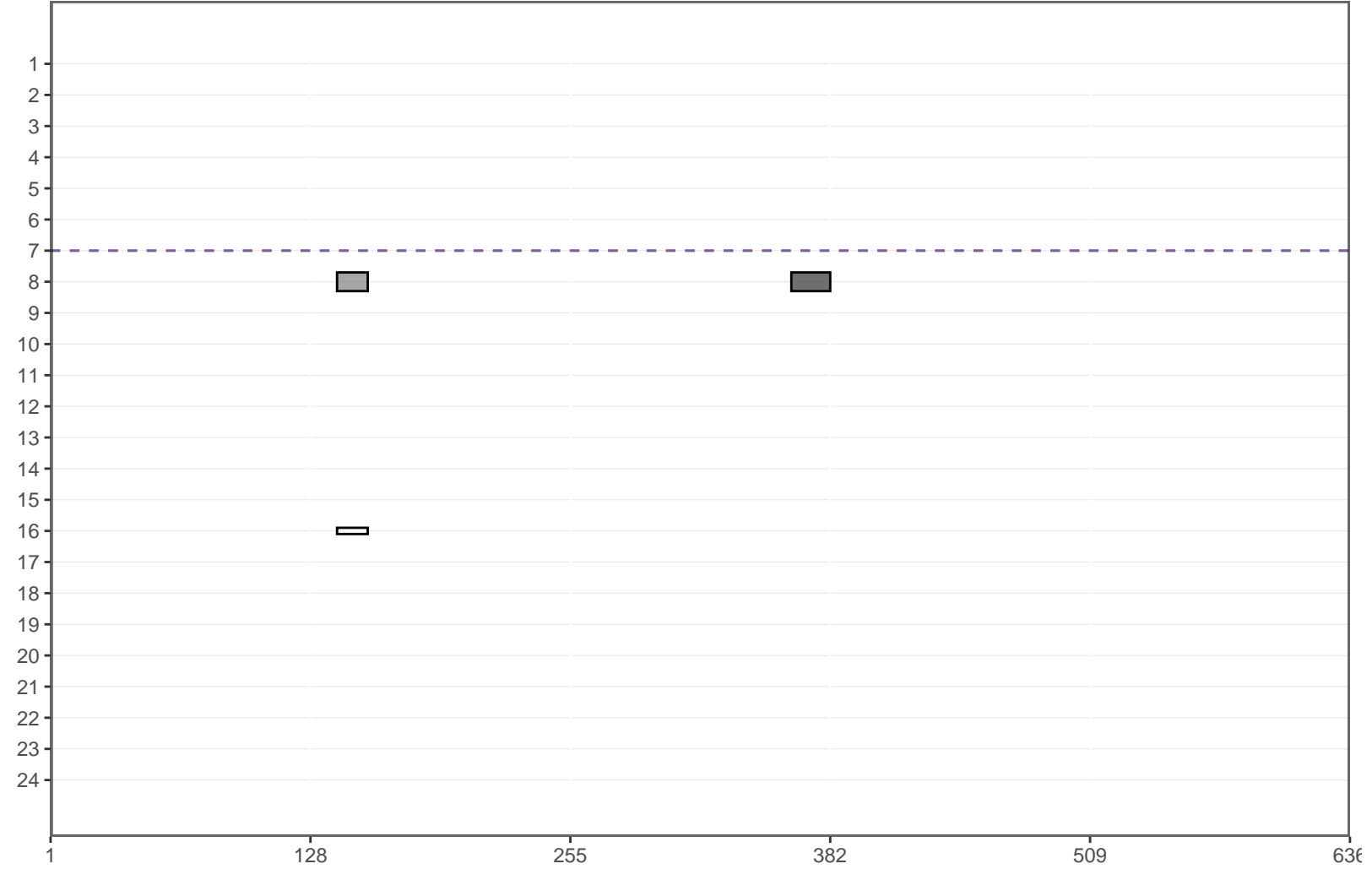
MW indication



Molecular weight



Gel Slice



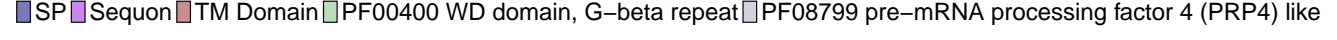
Protein length



Pfam domains



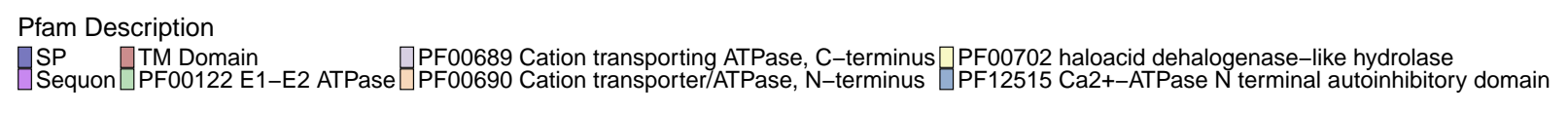
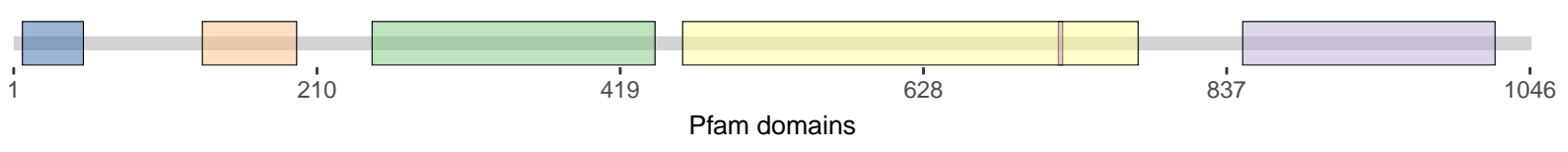
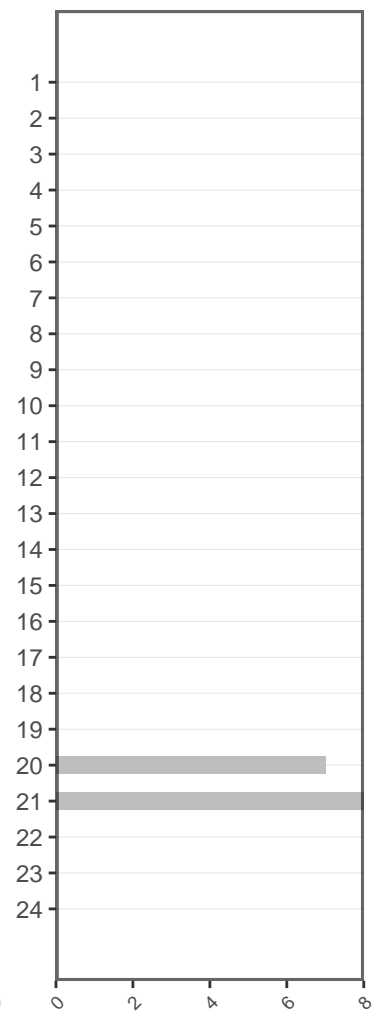
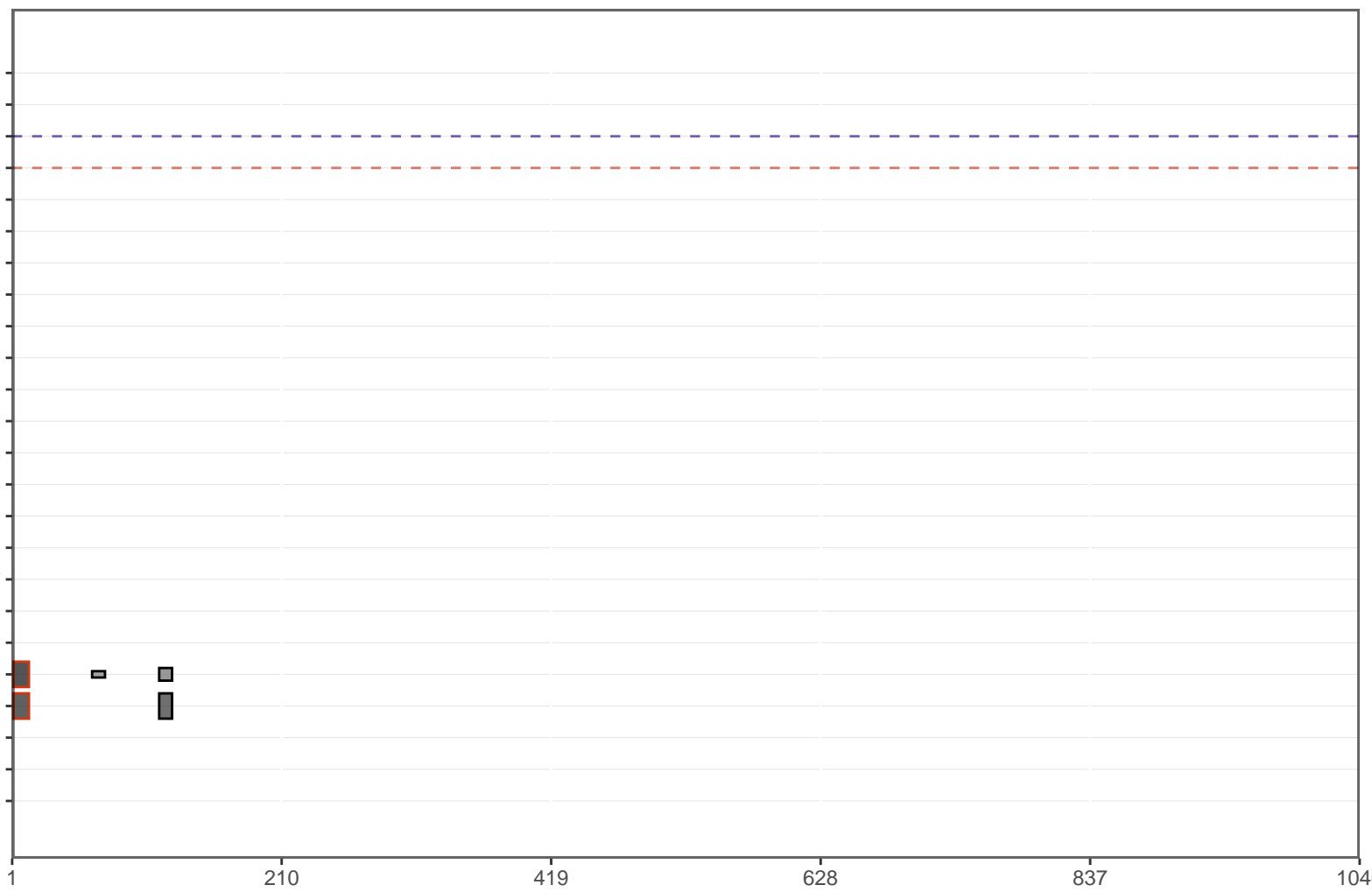
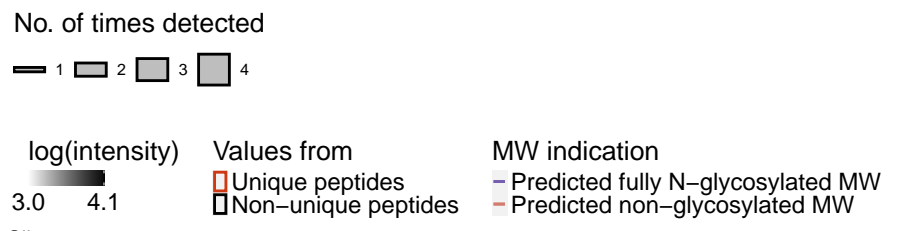
Pfam Description



Protein sequence:

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NbL14g15110.1 putative_calcium-transporting_ATPase_11_plasma_membrane-type [MW = 114.28 kDa]



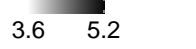
Protein sequence:
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NbL14g14920.1 villin-3-like [MW = 104.22 kDa]

No. of times detected



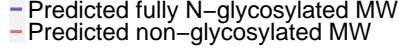
log(intensity)



Values from

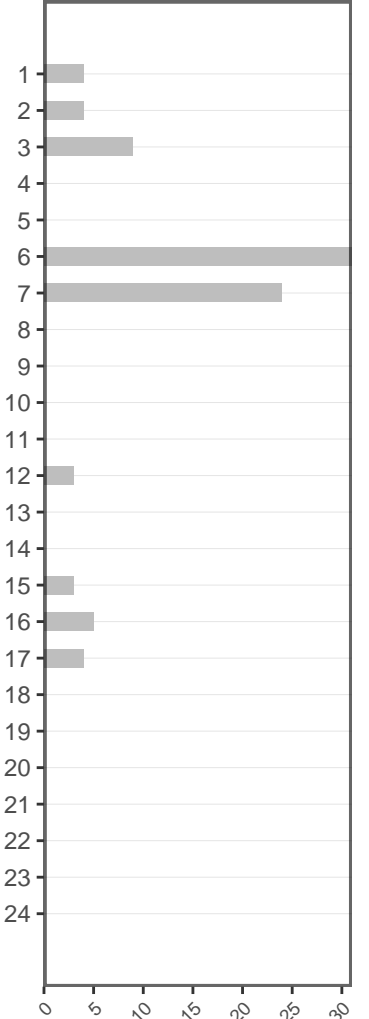
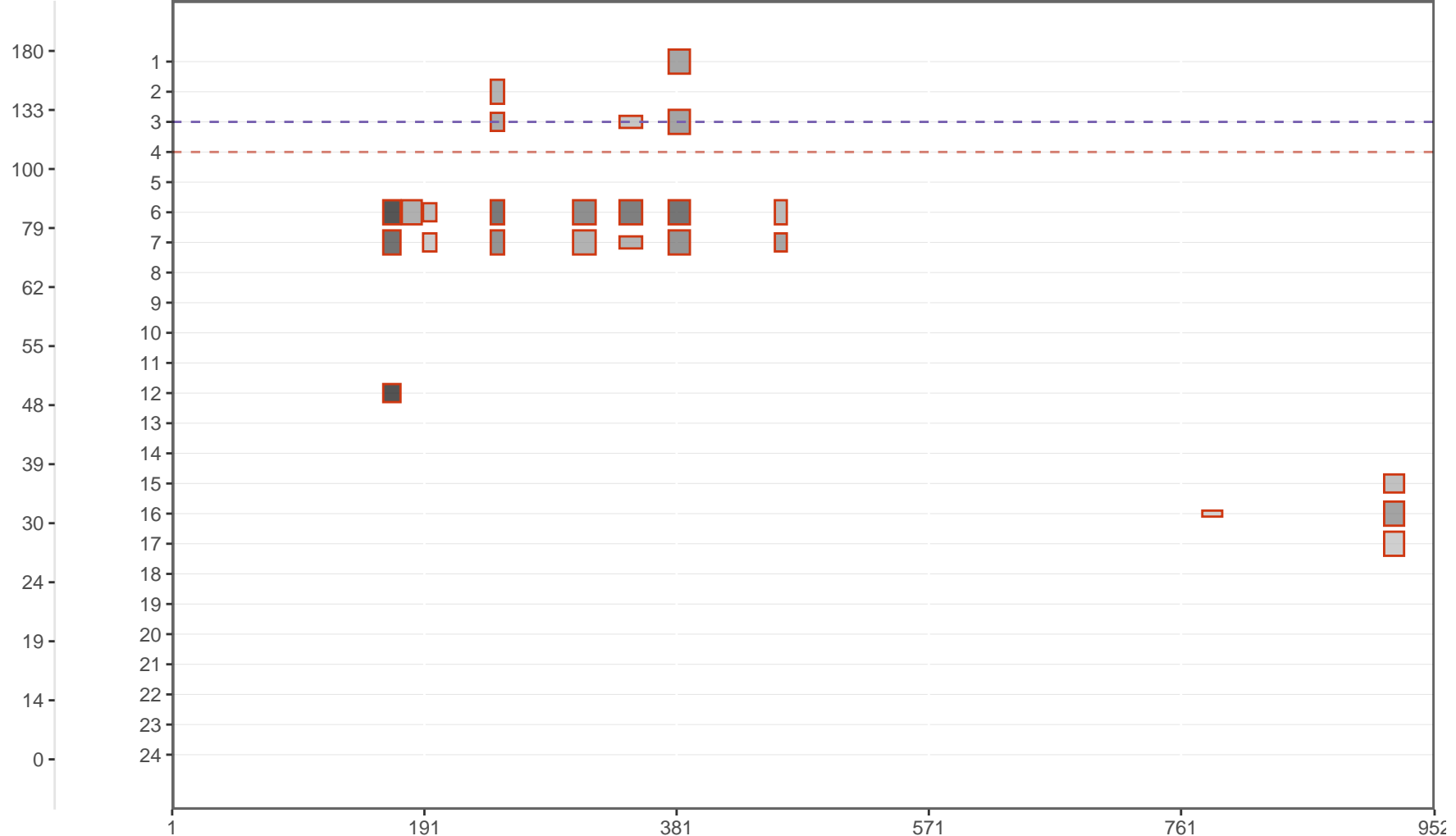


MW indication



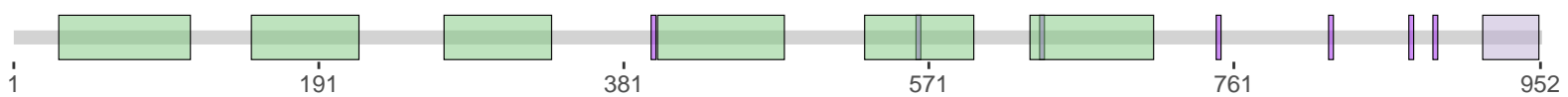
Molecular weight

Gel Slice



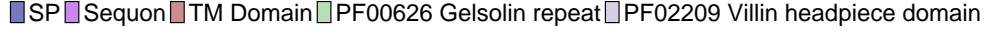
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

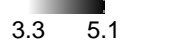
SPVLRVYFGKPEPQFVAIFGFMVLRKGLGSLGGKKNHIAKGLNDETYAASVVALRILGSTRVHNKAVQVDVAPSLNNECFLLGSGSGLFSWHKNGSTFYEGGQLAKVAEFLKPGATVYKTKEGTESSAFVWALGGKQSTSRKVAPEVSRDPHLFAYSFNKGKFEVEEYVNFSDQDLLETEDVLLDTHAEVYVWIGGSADSKKQSAFDKGGKHYVEMAAALEGLSPNVPVLYKYTEGNEPQFFTTFFSWDPKASAHNSFGKQKMLLFGVGHAEINQQRNSNGSGGI

NbL14g14900.1 magnesium-chelatase_subunit_ChIH_chloroplastic-like [MW = 153.8 kDa]

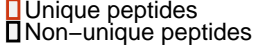
No. of times detected



log(intensity)



Values from

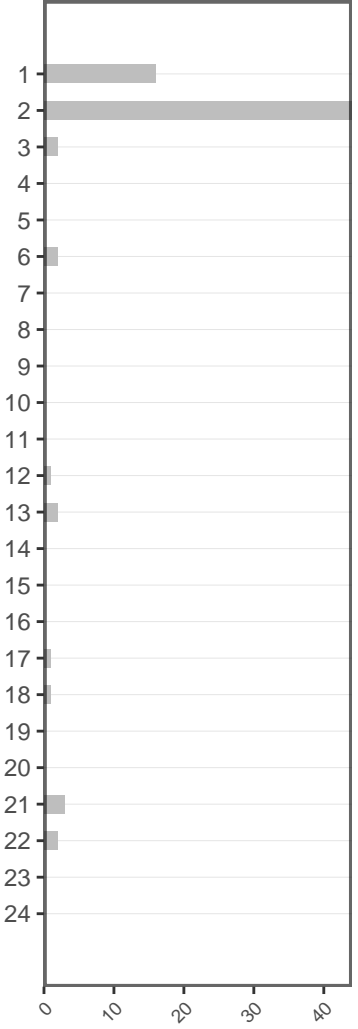
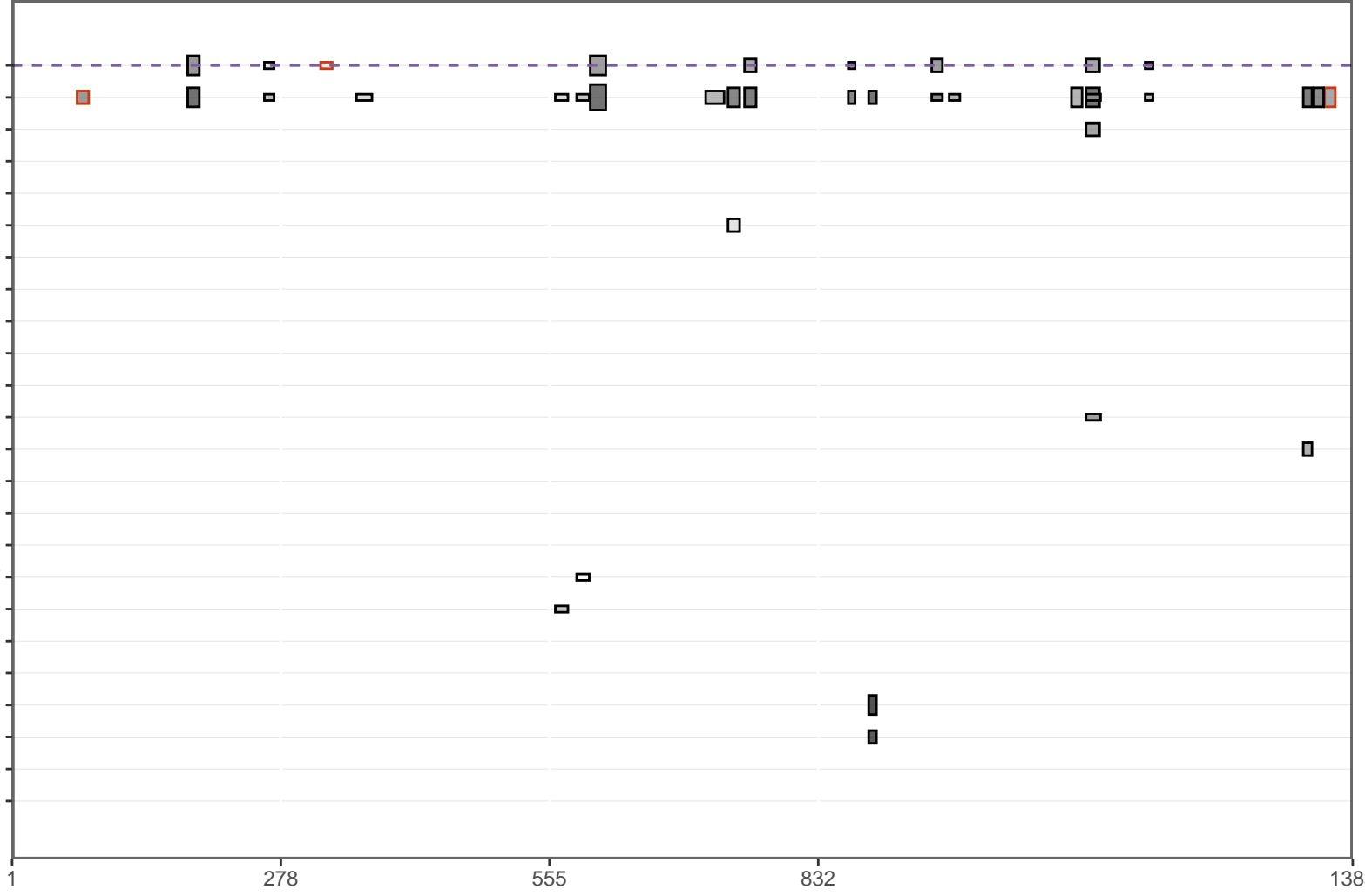
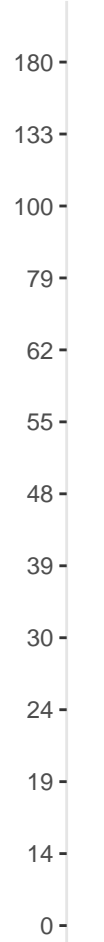


MW indication



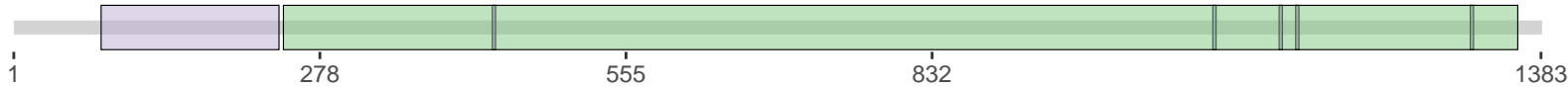
Molecular weight

Gel Slice



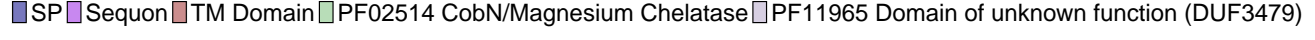
Protein length

Peptide counts over 4 repeats



Pfam domains

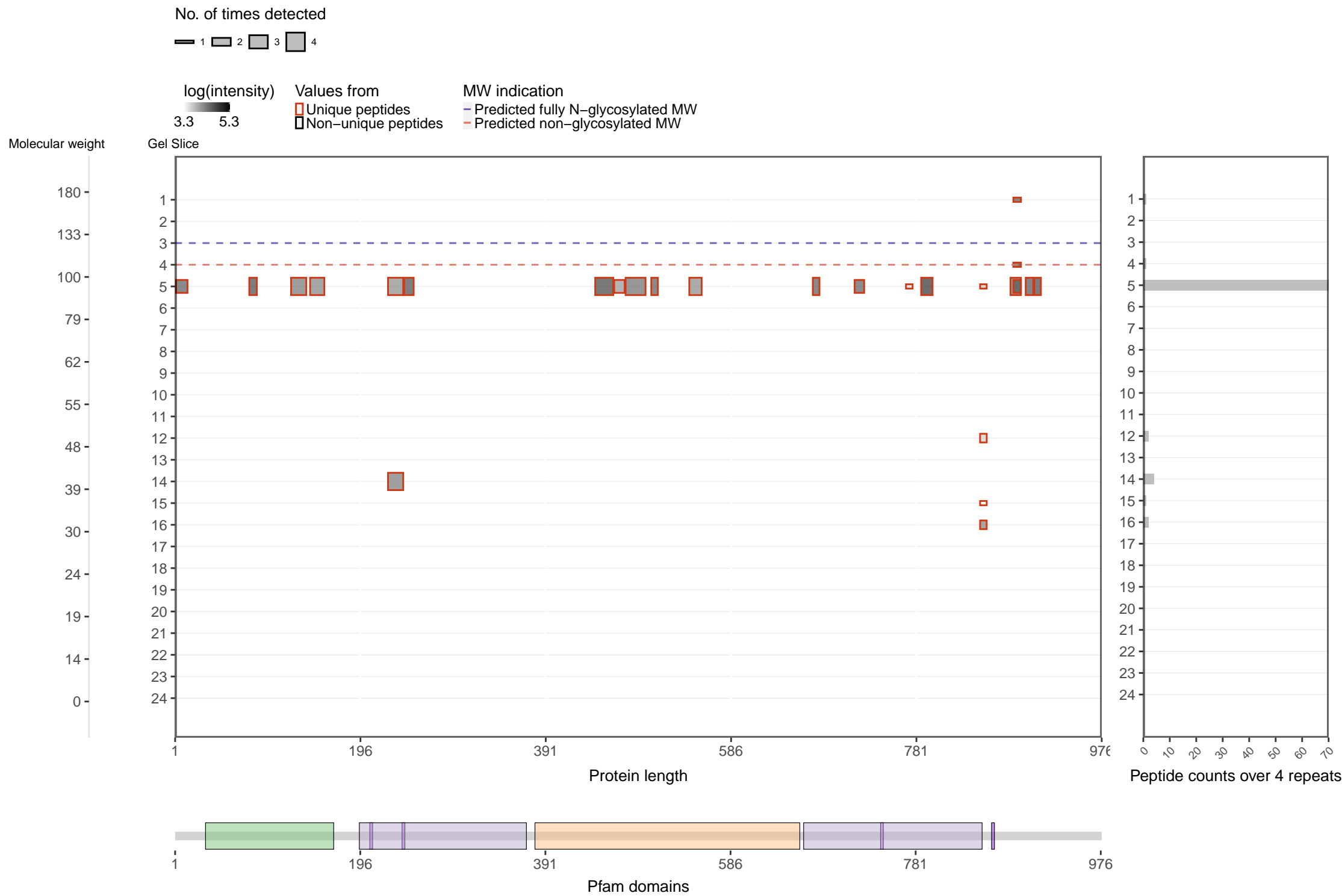
Pfam Description



Protein sequence:

DVGMSDACFPDLSLGNFNYVYVYANNPSEATAKRRRWYNTSIVLTPPEANAGLYGLKQLSELSESYQSLKDEGRGGGVNSHSTARGCNLKHQVLPPEEGEISAKERDLVGVKVIKMIIEGRLLPCGLHIGEPPTAMEAWATLVNIALDRPEEGISALPSLATVGRSIEEYVRRNDGGILRDLVLLRQDTEARSGAISAFTVTRTNNGGVVWVNDKLTSLGLGNEFPWQLSNTQFYRADREKLRVLFQFLGEGQLKLVANNEVGLKQALEGKVV/EPGGDPIRNP

NbL14g14870.1 zinc-metallopeptidase_peroxisomal-like [MW = 112.34 kDa]



Pfam Description

- SP
- TM Domain
- PF05193 Peptidase M16 inactive domain
- Sequon
- PF00675 Insulinase (Peptidase family M16)
- PF16187 Middle or third domain of peptidase_M16

Protein sequence:

IWEKAPDGNLILPVPIMFVPTDLGKIKTVSNKMNFFVLLRKSPPVSRLLWYKPDFLFSMPKGYIIDFSGPQGRSSPEGSVLSFIRLLMDYLNEVAVYAEIAGLQYWSISHWYGFQVTVTQYNNKMRVLLKVKIKDKTFKVEPRDFVKELEFTKGYGKQFKFGQPYEGAAIYGSLLREHAWGWSWVWDELEVLNLEVDLWKPYLLLRFLLEQYVAGNDSKEAVSMQIHEDAFYKGAQPLSRALFASEHPGSRHKLEESTNYFYAAEGLNTSDENSAIHWYHTHPDEYIKYVRCG

NbL14g14850.1 insulin-degrading_enzyme-like_1_peroxisomal [MW = 92.47 kDa]

No. of times detected



log(intensity)



Values from



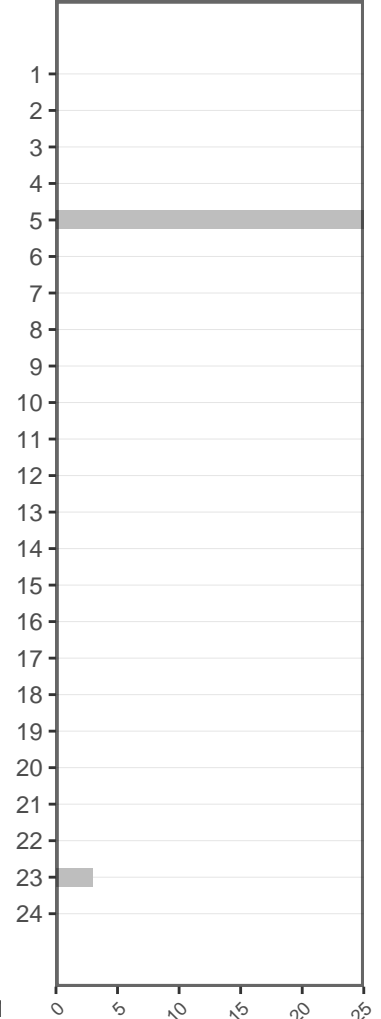
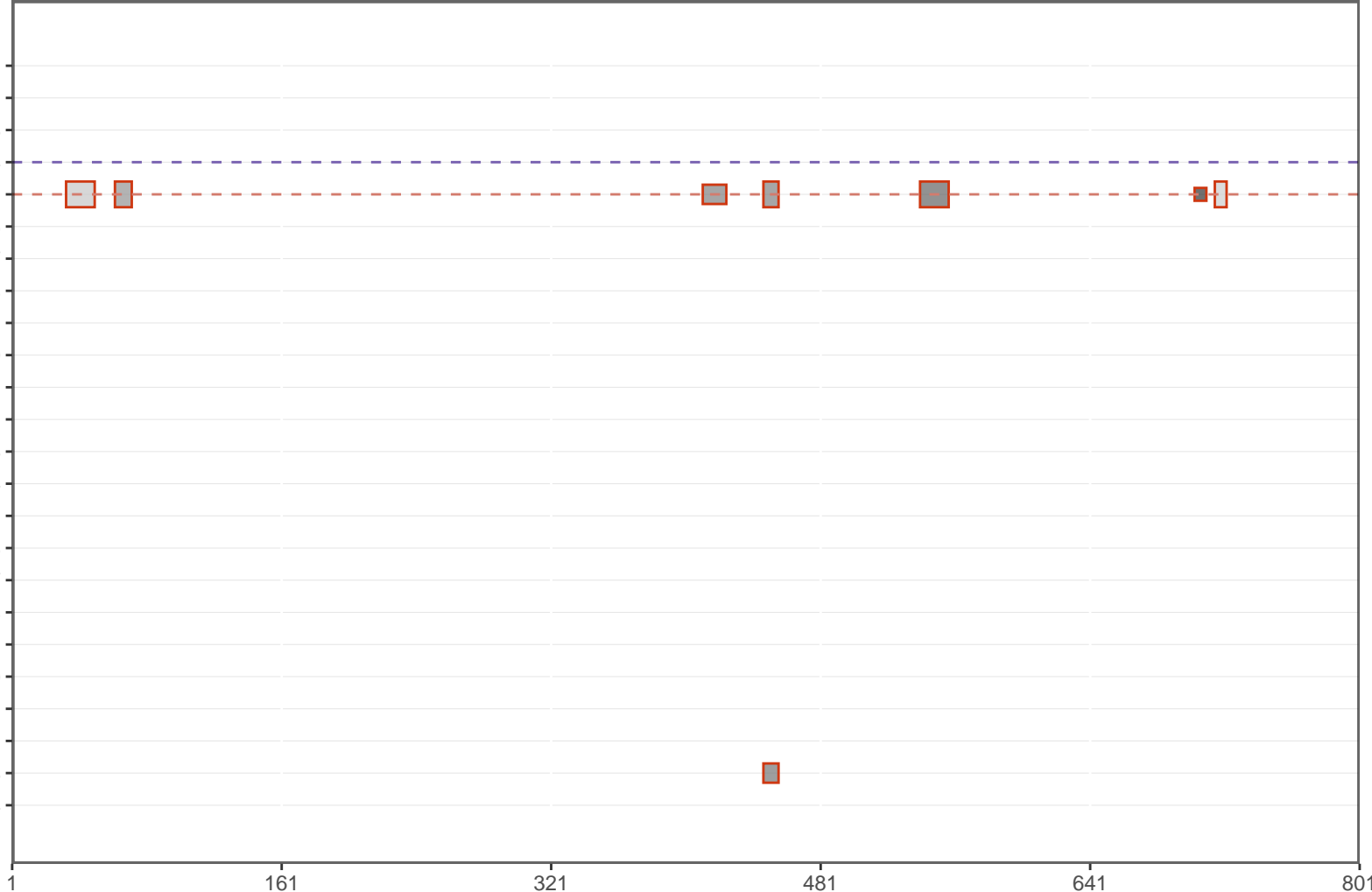
MW indication



Molecular weight

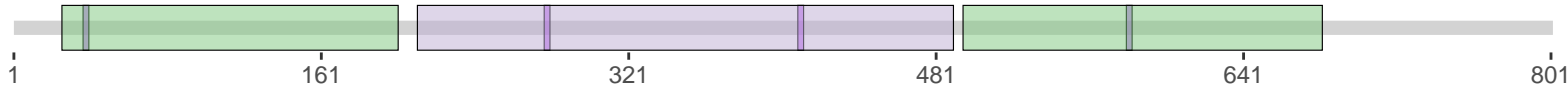


Gel Slice



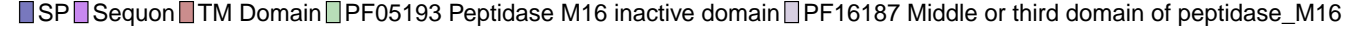
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

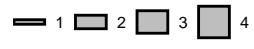


Protein sequence:

MDYLNAYIAQVAGLHYGINKTNGDGLFLFGYNDKLRVLLLEAVVEKIAKFEVKKPDRFSEVIGELVTKQGFQNYKFGQPYDQAMCYGILLGENTWPTDELEVLPHLKADGLVKFYLLARSLFEGYVAGNEGAEAESMTGLIEDVFFKGPQPIKPLFASGHLNTRVNLERGVNYFYAAEGLNPDENSGLLHYGVHQDQDFLNKLGQLFALLAKRPFHQLRSEVEQLGYITVLMGRSDSGVHGVQFQIGSTAKDPKGDGRVLEFLKMFESKLEMTSDEFKSNVNALIC

NbL14g14740.1 beta-glucosidase_BoGH3B-like [MW - SP = 66.15 kDa]

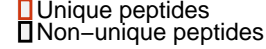
No. of times detected



log(intensity)



Values from



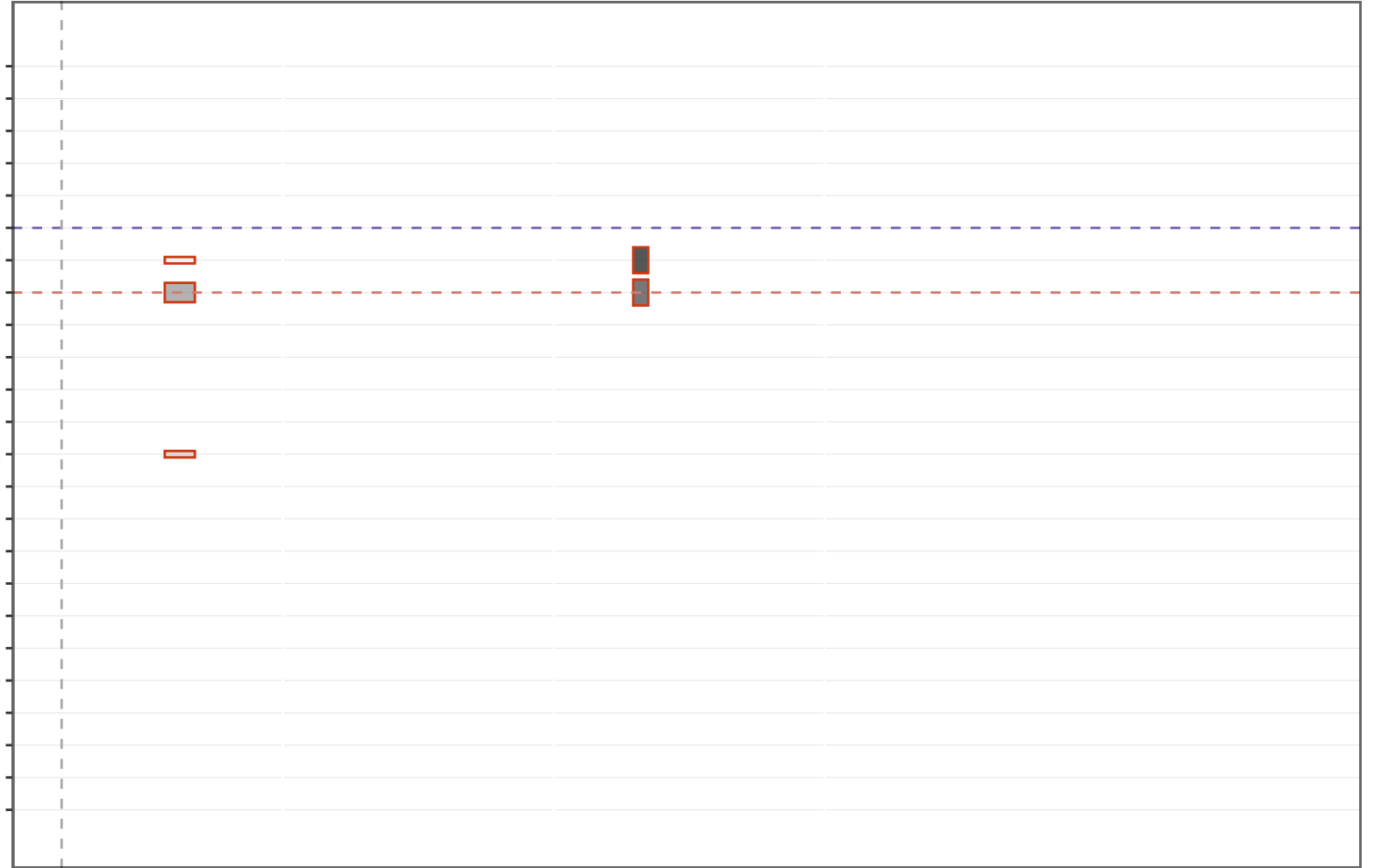
MW indication



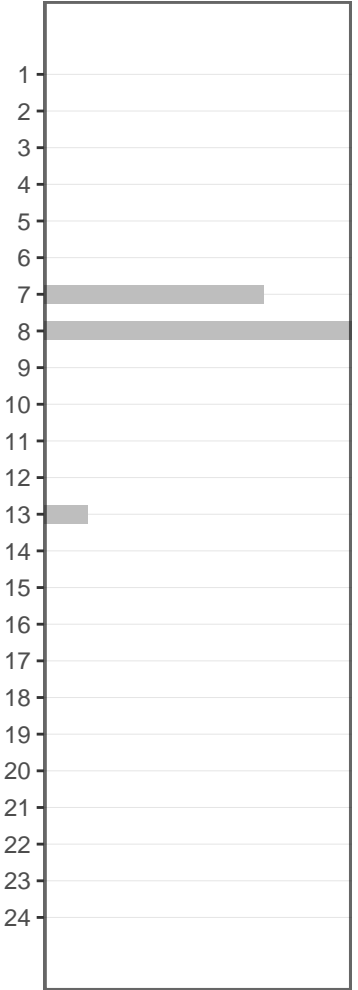
Molecular weight



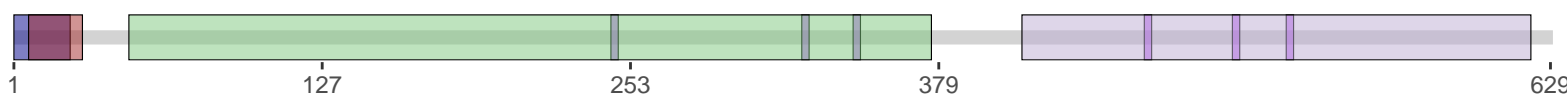
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

SP Sequon TM Domain PF00933 Glycosyl hydrolase family 3 N terminal domain PF01915 Glycosyl hydrolase family 3 C-terminal domain

Protein sequence:

.RFKGFVLSDDWAGIDKLETPWHANNTYSILEGVNAGIDMMLPNNTTEFDIGLTYLKNFVMSRISDIAWKRLRKFQDMSLFESPLADSMVKYLGSAEHRLEAREAVRRSLVLLKNGANADEPLPLPKKTSGLVAGHANMVGQCGGWTTWQGLSNTTGTTLTSAIENTVDPETKVVFKENPQSEFIKSNFSAVAVVGETPVAE66GDTLNLTRFPGPDTMTTVGASVKGWVWLLTGRPVVHQPYLADIDALVAWLPQTEGHGWADYLFSDV/GFTGKLRARTFK

NbL14g14640.1 magnesium-chelatase_subunit_ChID_chloroplastic [MW = 83.19 kDa]

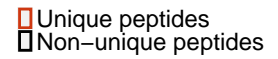
No. of times detected



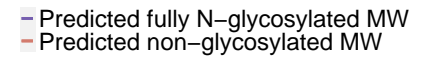
log(intensity)



Values from



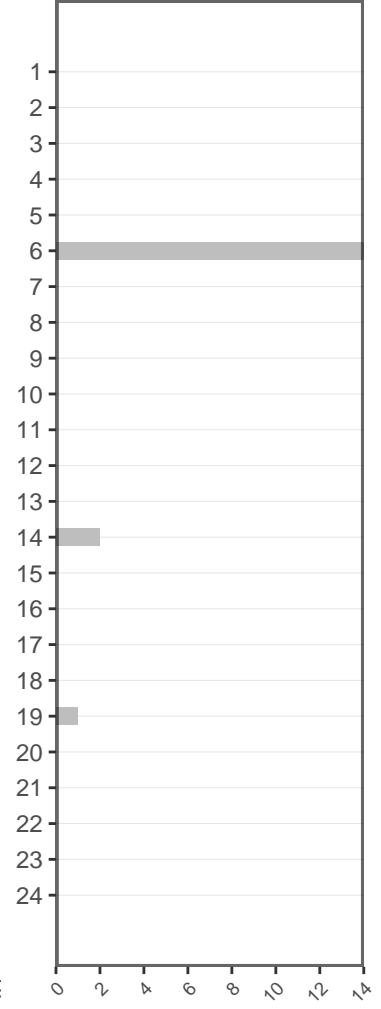
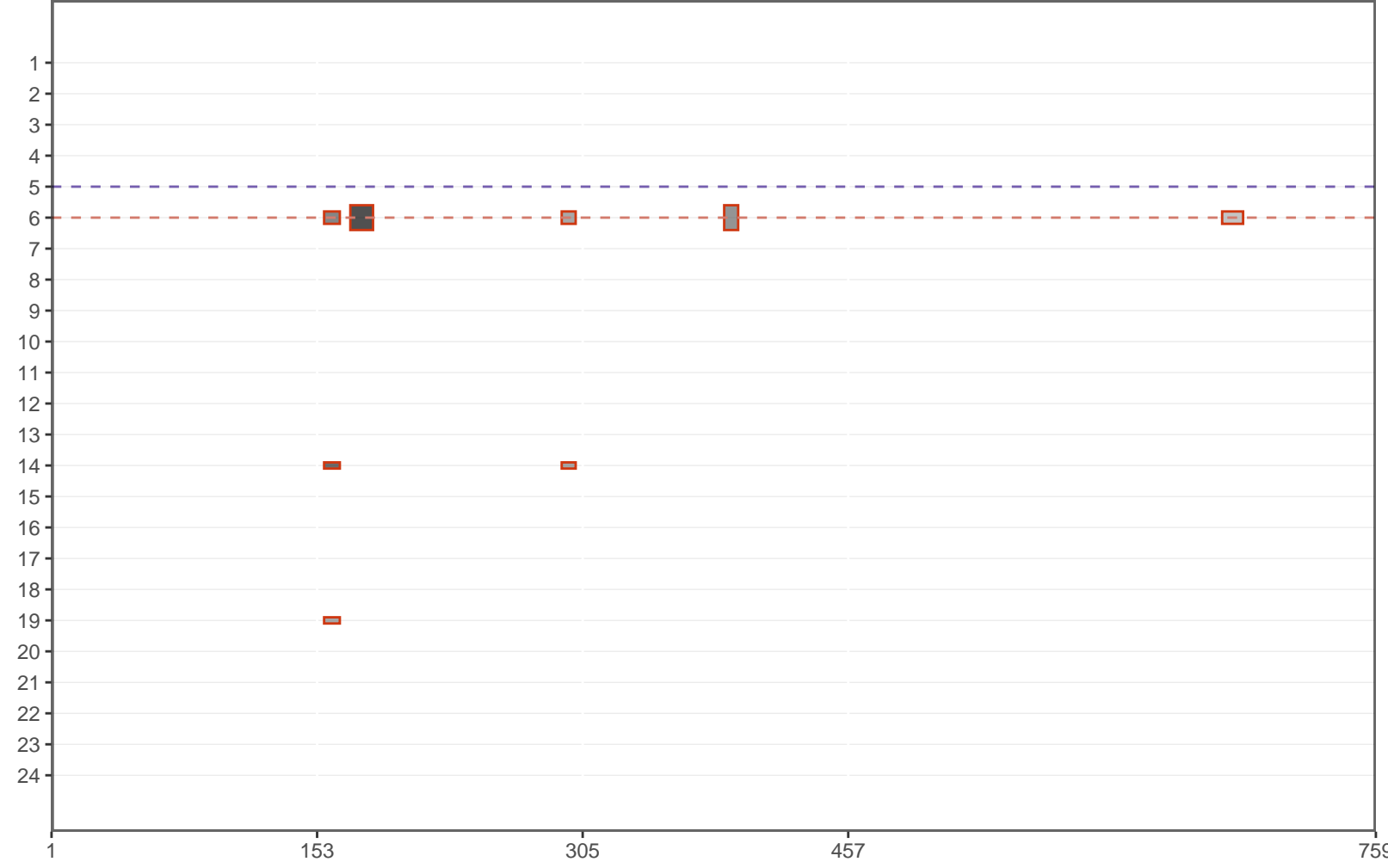
MW indication



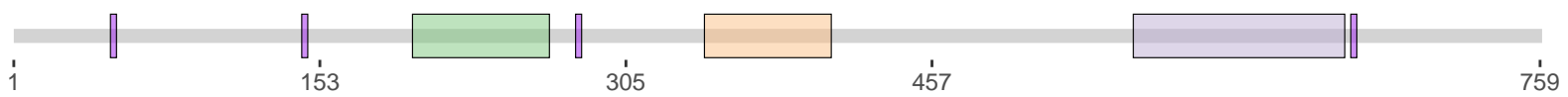
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

AJDRGEKVGVDLKKAVELVLPSTVENPPDQNGKGFPPPPPPQNGDSSEGNKEEEDKDEKDEENEGQGPVDFDFDAEGGLVDEKLLFFAGQAGRRKKGAKRANKNFSEDRGRYKPKALPKGPKVRLVDTLRAAAPYVKLRRAKDKQKTRKVVVEKTMRAKRMARKAGALVFWVDAQSGSMALNRMGNKAGALKLAEYSYTSRDGVCIFFRGDAAEVLLPFRSISIMARNLRLRPLCGGGGFLAHGLTTAVRVRGMNAEKSGDVGRRMVAIT

NbL14g14490.1 serine_carboxypeptidase-like_27 [MW - SP = 49.56 kDa]

No. of times detected



log(intensity)



Values from



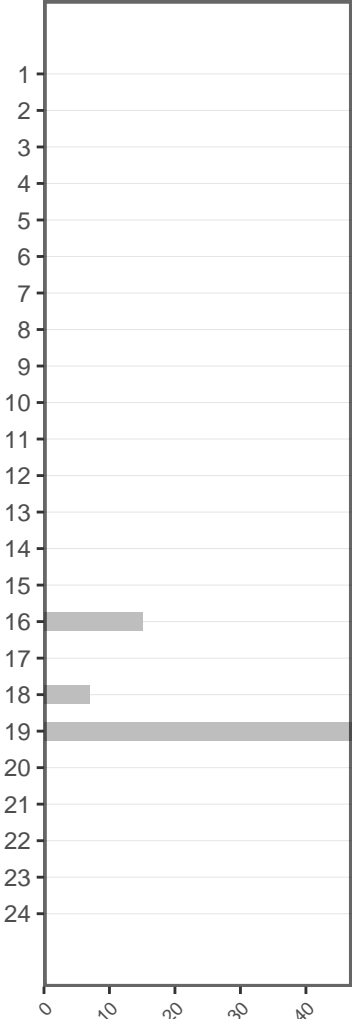
MW indication



Molecular weight

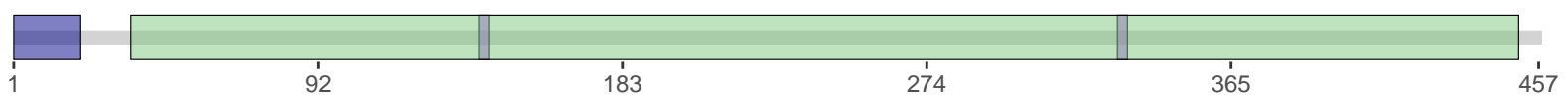


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

AVTDQYIDYIGTFEYWWTHGLSDSTYKLLGFGDGKGSSEHPSTDCIKALLAEDEEGNDPYSRTKPCASTSSLRRLRHYPWMSRAVDPCRTARYGEVFNLPVQKAFHANNTKWVWPKTCSQDIVGNWADSPLSMLPIVQELIAAGLRWVFGSDTDSVVPVATATRYSDALKLPTITKWPVWYGNKRVGGWSQVYKGLLTVTVGAGHEVPLHRRRQAFILRFLEKNKMPSP

NbL14g14480.1 uncharacterized_LOC109211791 [MW = 28.85 kDa]

No. of times detected



log(intensity)



Values from



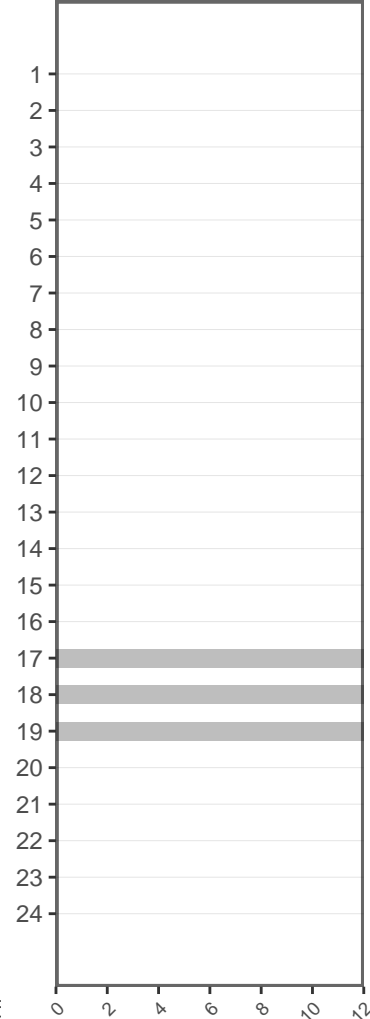
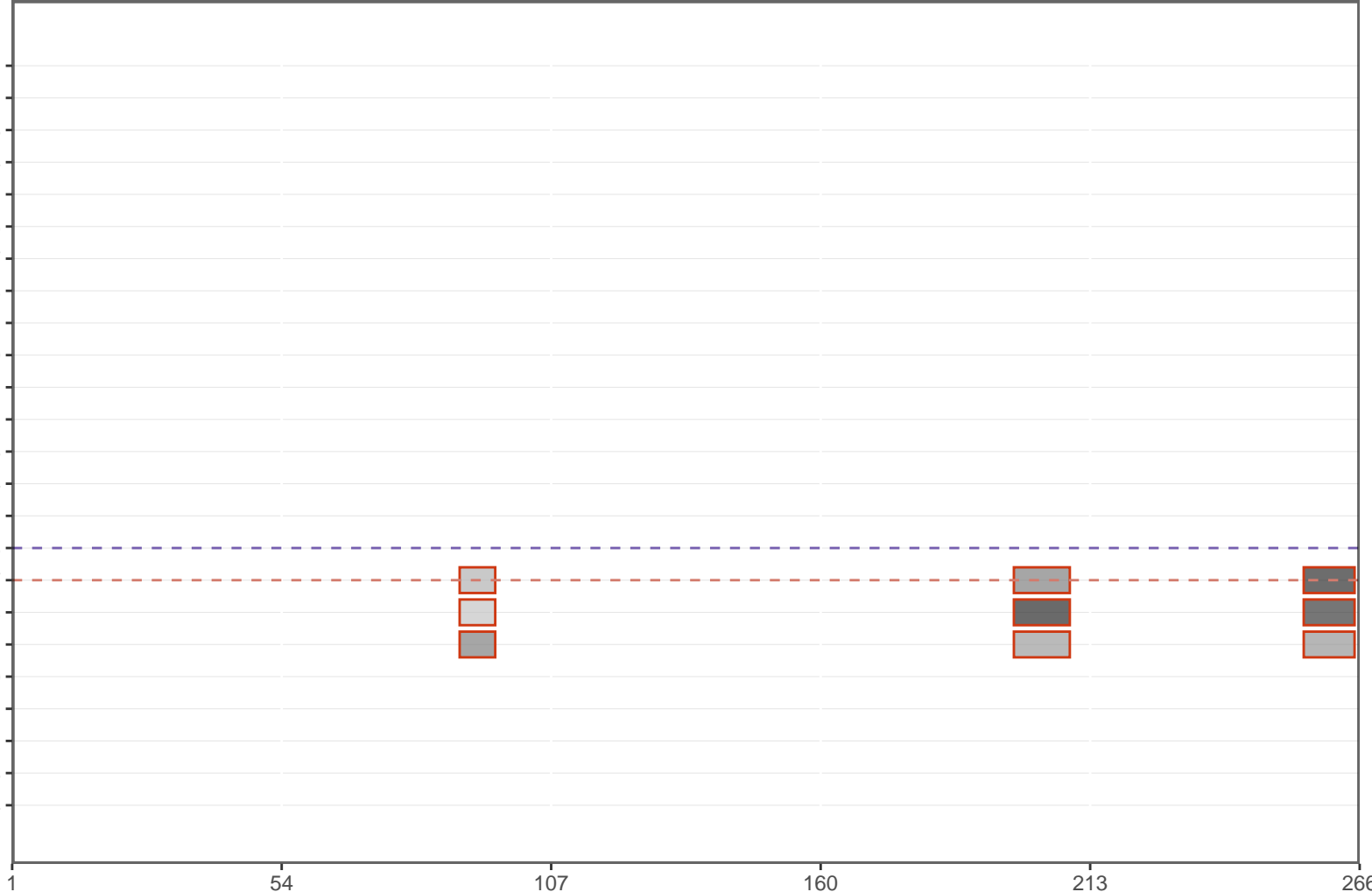
MW indication



Molecular weight

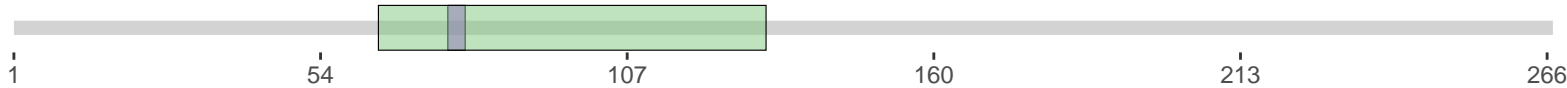


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

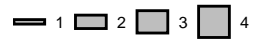


Protein sequence:

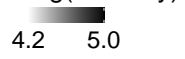
RETLTMDEQVQAFBEAEHFRISFYVWAMDDGQTAELHKAQKYSRDEILTMCMGMHNRGWEEAASMLGGVVELKTSNAALLEATQKQWEEIAPASFSTGICISDKAKKLESRGPKKAFSLAGPGGWIQGLKPKDTSV

NbL14g14370.1 nuclear_inhibitor_of_protein_phosphatase_1 [MW = 45.96 kDa]

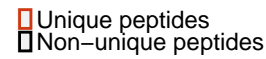
No. of times detected



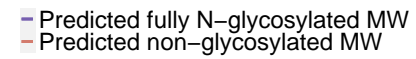
log(intensity)



Values from



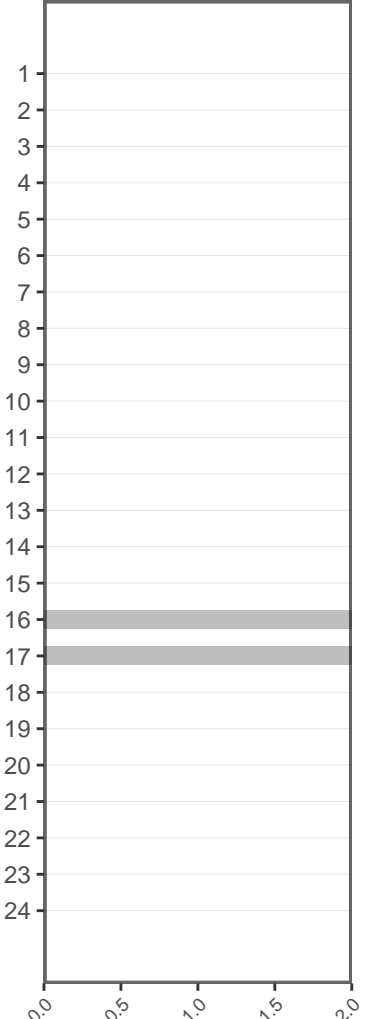
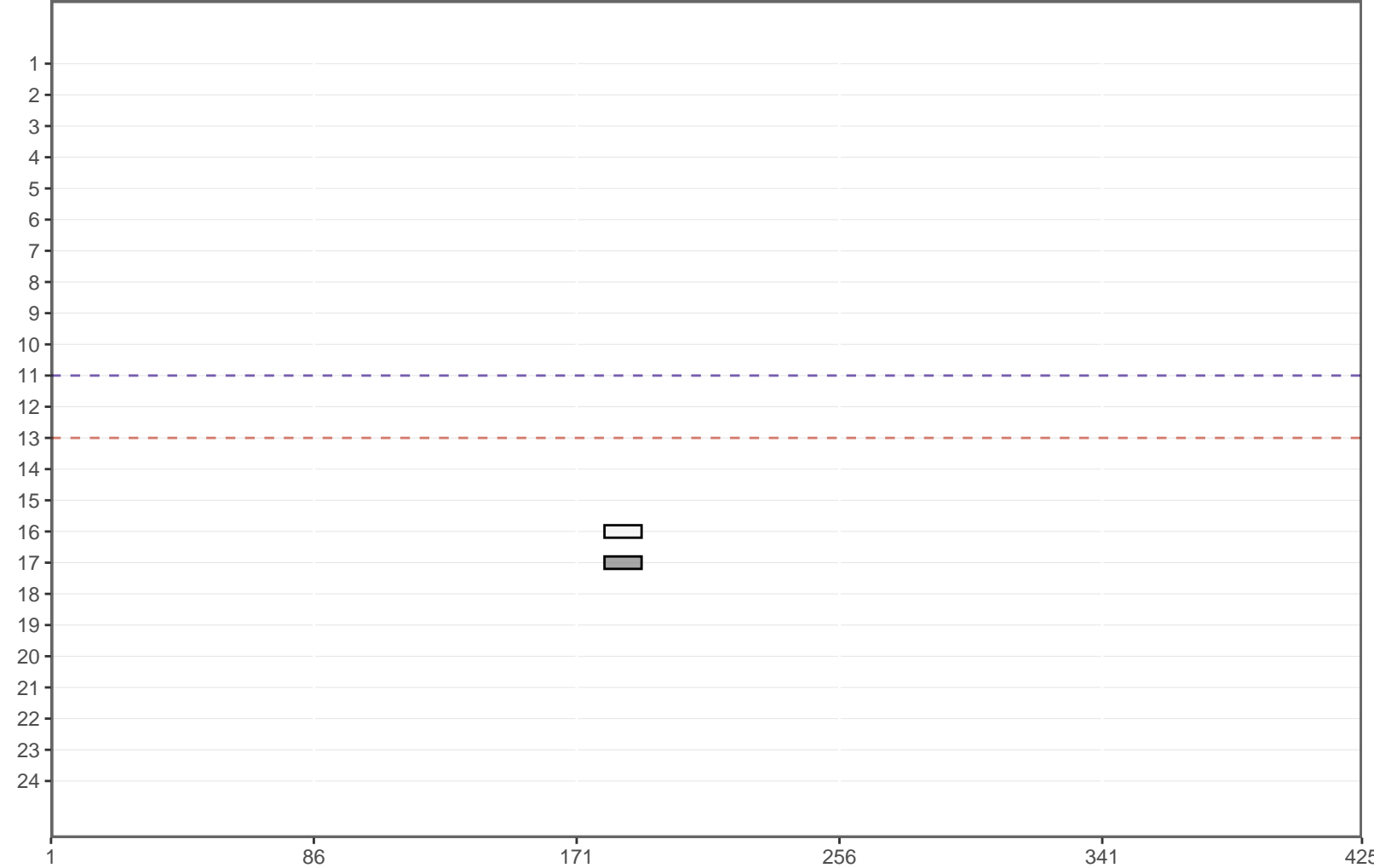
MW indication



Molecular weight



Gel Slice



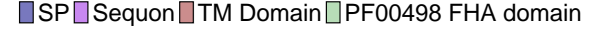
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TYLRLKNGALFPPRQMEIDLPPPPDPSDEEAVLWNTFLNRYGLMRPDELKSKTLETSGEDVNHLSERRAKRIRRTVSVFKDQVGGELVEVVGIDGADVETEPKLVGKKEGLVGVKYESLIETTVPKQKEQSGVKDQATVQTGVTQKIKQLVNLKVKKPKKGGYDDLVGESAPKVGSWAYSD66QTASTNDAKRDPGSLGRISGNISNVDGDDTDLDFG

NbL14g14310.1 trafficking_protein_particle_complex_subunit_5 [MW = 21.75 kDa]

No. of times detected



log(intensity)



Values from



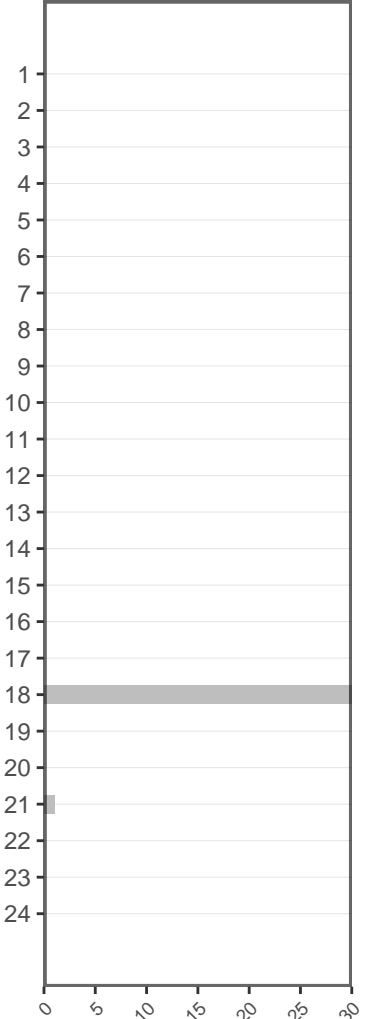
MW indication



Molecular weight



Gel Slice

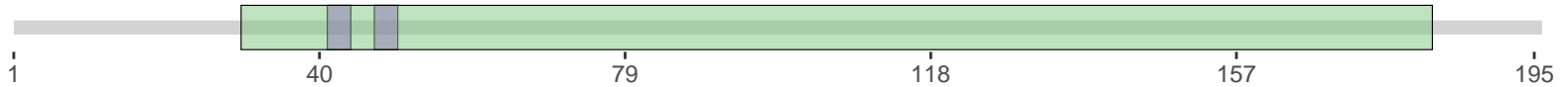


Protein length

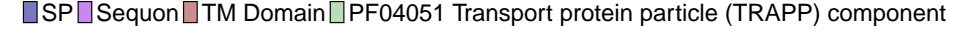


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

.LGLSFVHSTVWKVLFQKADSELEKGTETHEDEYMSSEKELLNRFISPKDMGAFNGSFFVAGVIRGVLENAQGFPAWVTHHFVPEVGGQORPRITLIKFAEVLRRERLQ*

NbL14g14300.1 peptidyl-prolyl_cis-trans_isomerase_FKBP16-3_chloroplastic [MW = 27.25 kDa]

No. of times detected



log(intensity)



Values from



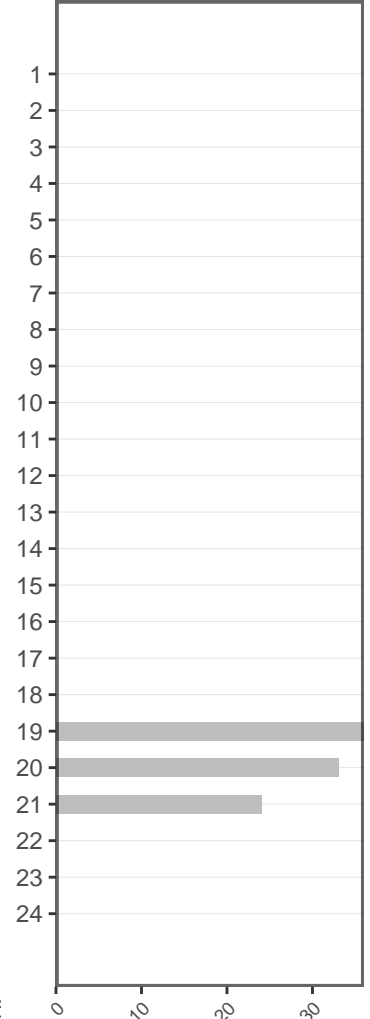
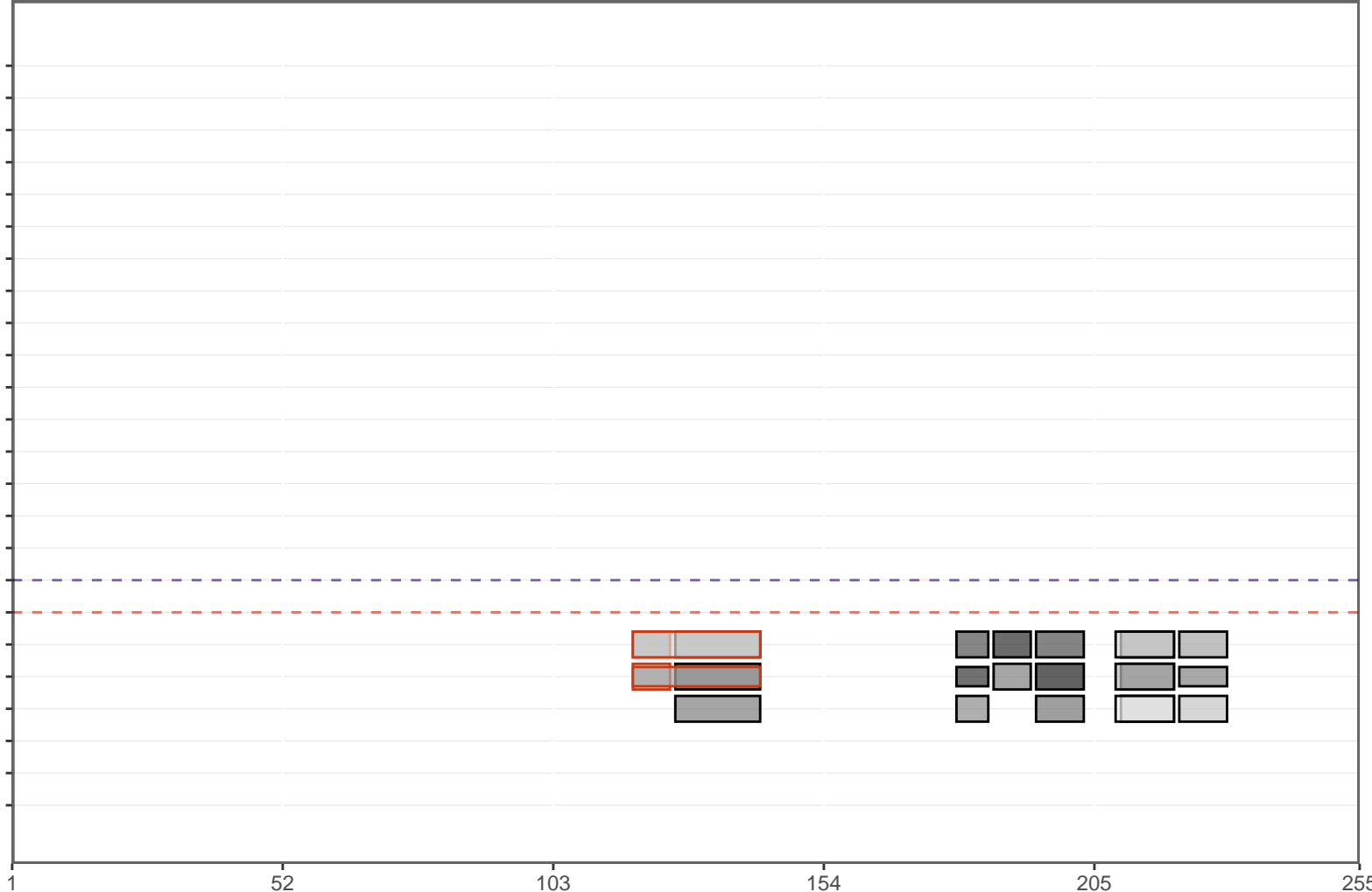
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

KPKLGDATCEKELNVPMTFTESGLQYDKIKVGGGSPVGFQVAVNGVAVVPSGGQFDSSLEKGLYFRVAGAGVHKGLDEGLSMKVGKRRRLVIPGLAFPKGLTAPGRFRVAPNSPVIQVLEVIPLGLEYDEE

NbL14g14100.1 tropinone_reductase-like_3 [MW = 27.07 kDa]

No. of times detected



log(intensity)



Values from



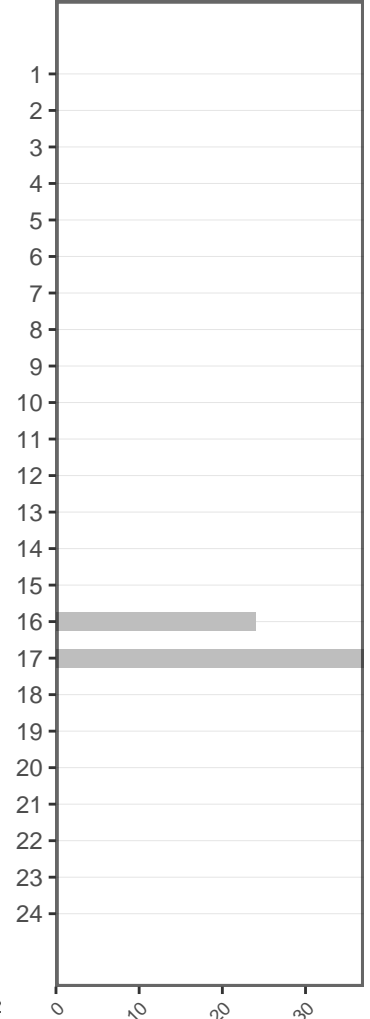
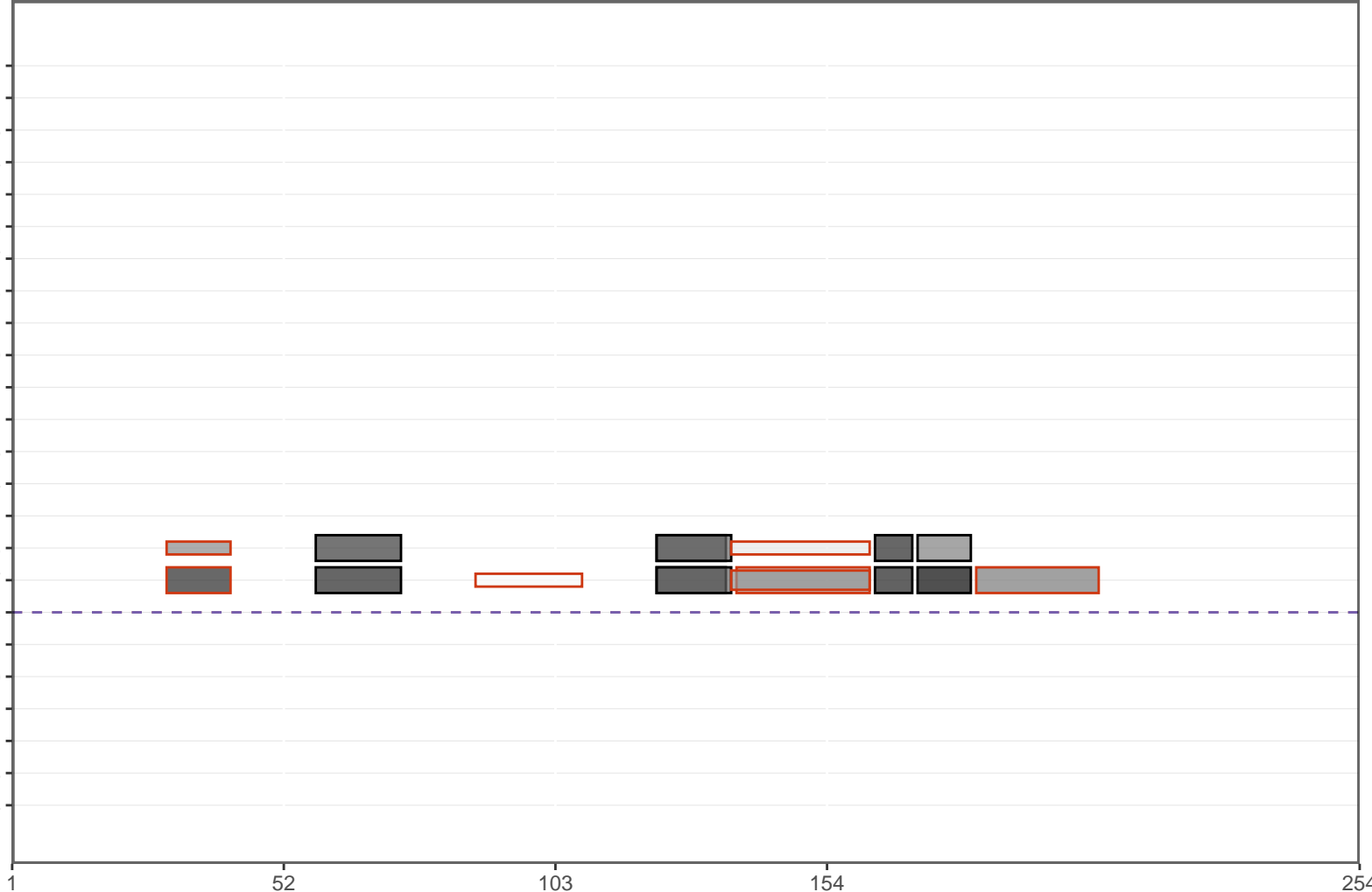
MW indication



Molecular weight

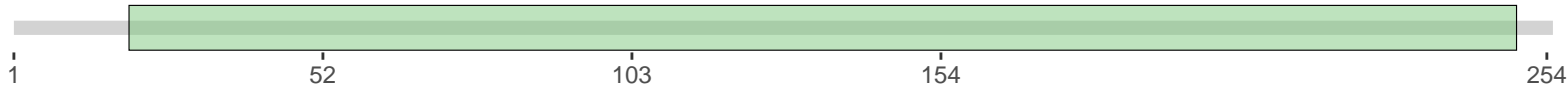


Gel Slice



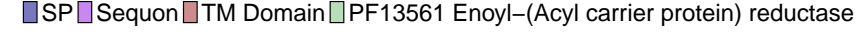
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LWIDINVKASILLQGAAPYLKKGSSVLIISISIGYSPRPSMSMGVYTKTALLGLTKALASEMSPDTRRNQVAPGFVPTHFADRTQNEHVRREIEGKTLNRLGTFQDMAAAWVLAASDDAAVVTGETLVVAGMPSRL

NbL14g13980.1 THO_complex_subunit_4D-like [MW = 29.2 kDa]

No. of times detected



log(intensity)



Values from

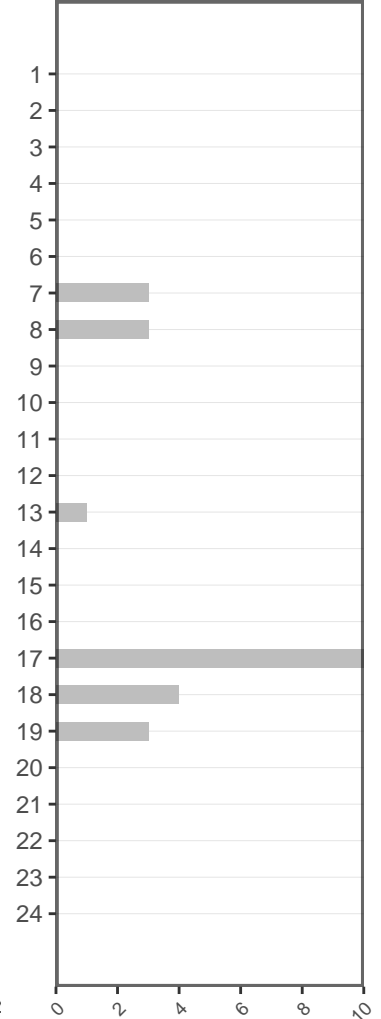
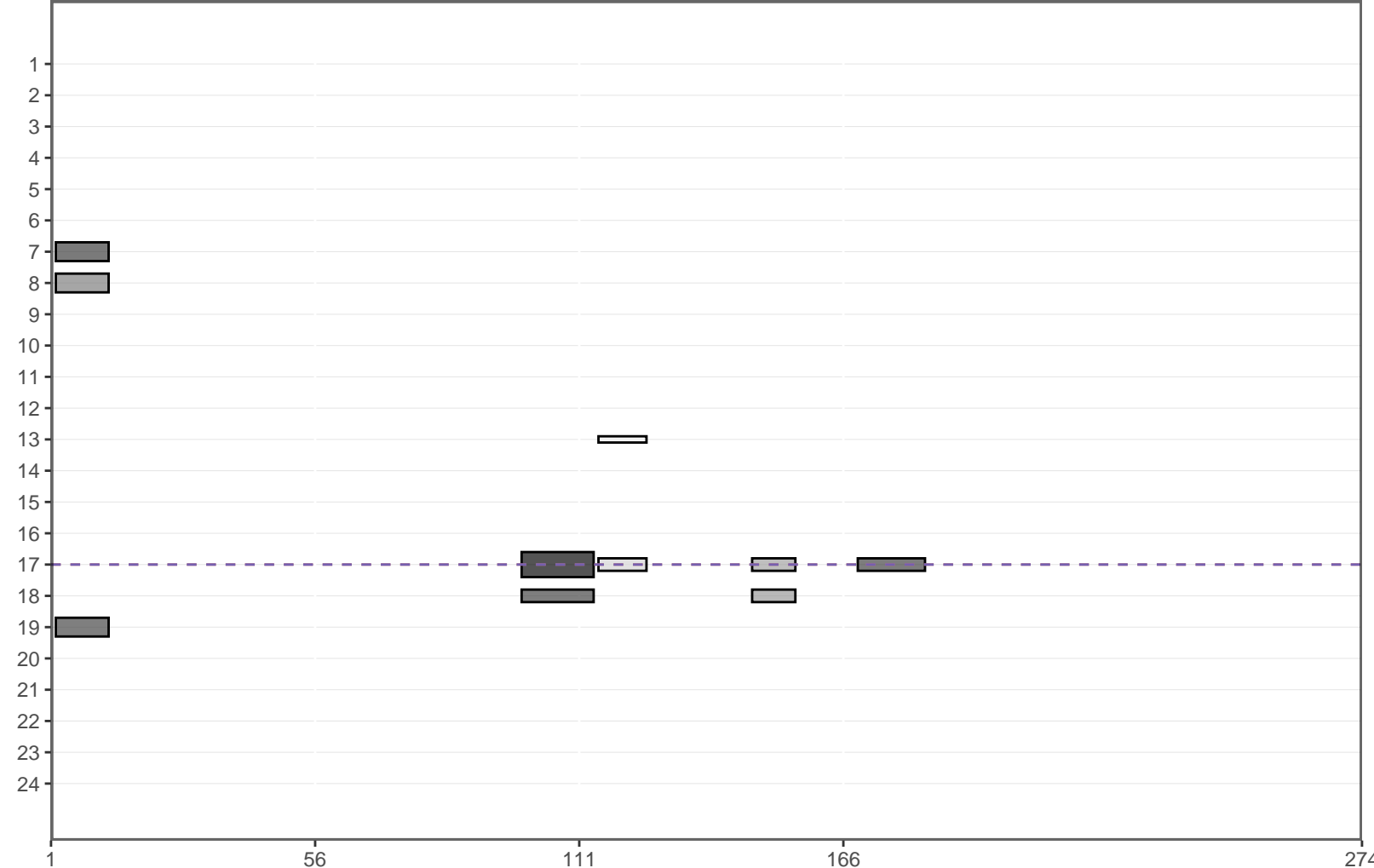
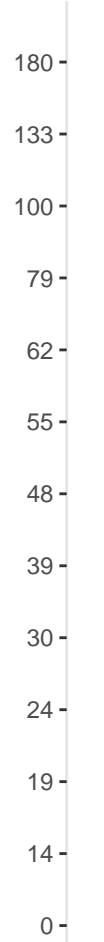


MW indication



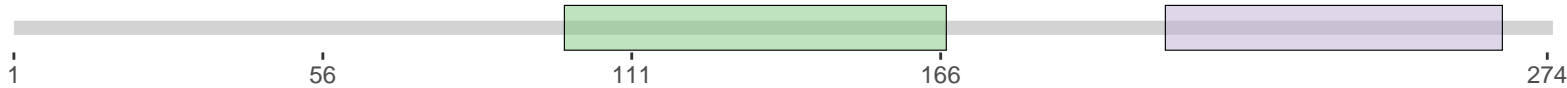
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- PF13865 C-terminal duplication domain of Friend of PRMT1

Protein sequence:

/AIHYDKNGRPSGAEVWFARRSDAYGALKRYYNVLQDQPKMKIEVVAAPTDMPLSARVDVGRGSSRRFTVMTPQSAIRGRGAAPMANRGS6SGRGGFGTASGRGRSAGHSGRGRGRGRKNGVENSAAEELKELENYHATADAMQT

NbL14g13820.1 ATP-dependent_6-phosphofructokinase_5_chloroplastic-like [MW = 59.1 kDa]

No. of times detected



log(intensity)



Values from



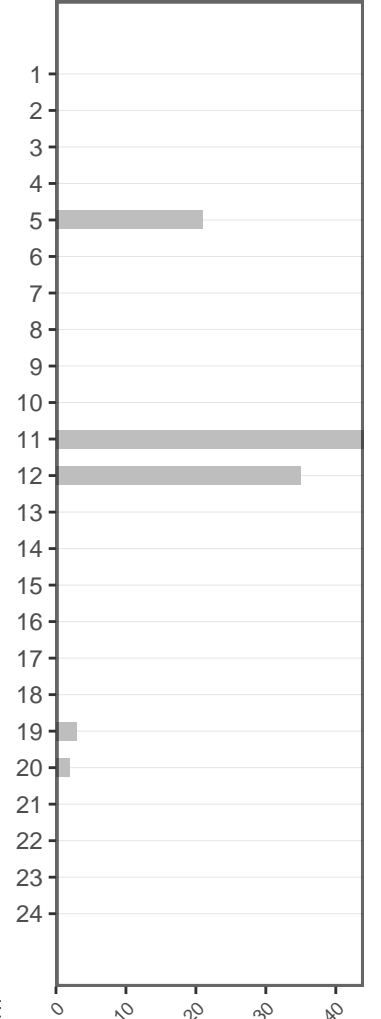
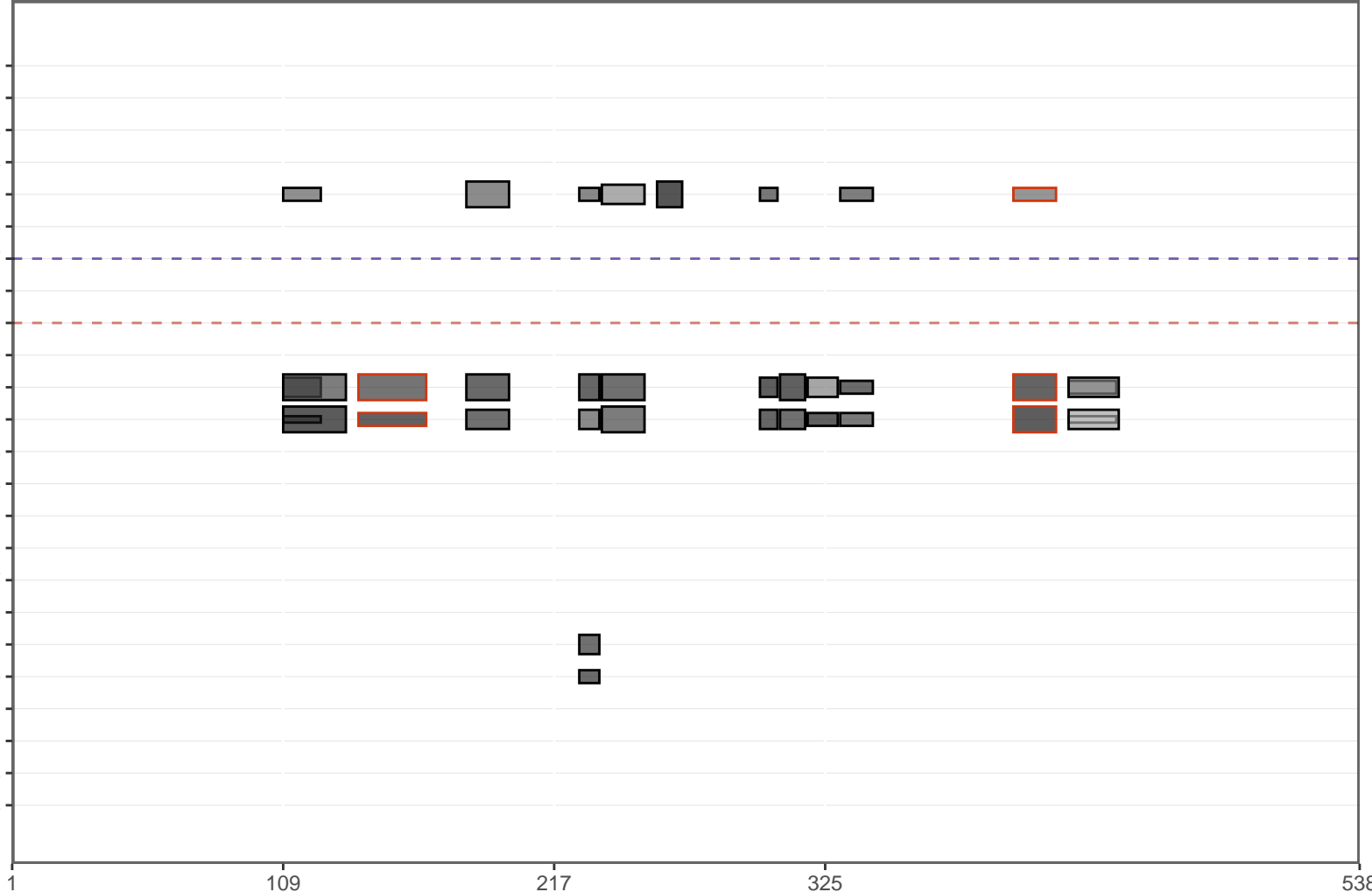
MW indication



Molecular weight

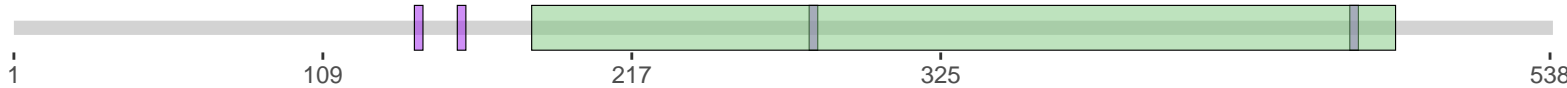


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

PKVSDIVDSIERGINMLFVLGGNGTHGANAHDEGRKRMRKVAVGVGPKTFENDIMLMDKTFGFDTAVEEAGRAINSAYIEAHSAYRGGVGLMGRSSGFIAMQASLASGGIDGLIPEVFNLHGHVGLRHLKYLKLLATKGSVAVGAEEGAGDDFLEKTNADASGNVLDGGVYLGQEKIKYFKEMGETSDVYKIDPTFYMIRACRANASDGLCTLVGGNVAHGAFAGYGGFTVGDENTHYVYFFPIPEVIGKPRVWDPNSRMVHRGLTSTGGPDRF

NbL14g13670.1 14-3-3-like_protein_A [MW = 28.77 kDa]

No. of times detected



log(intensity)



Values from



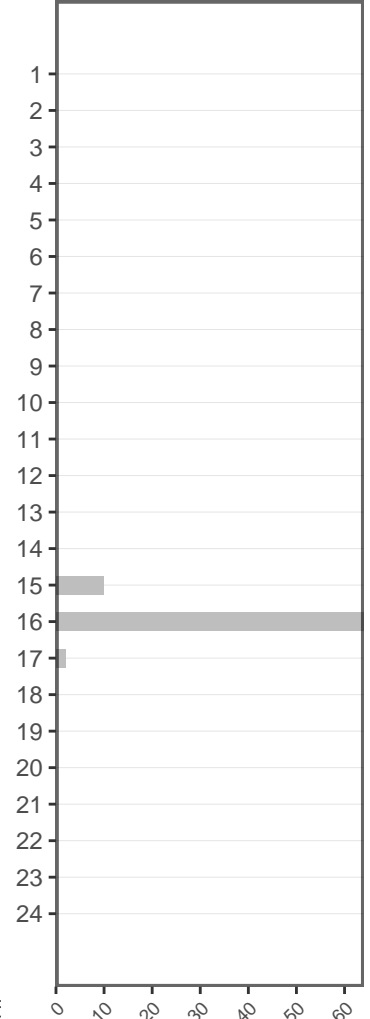
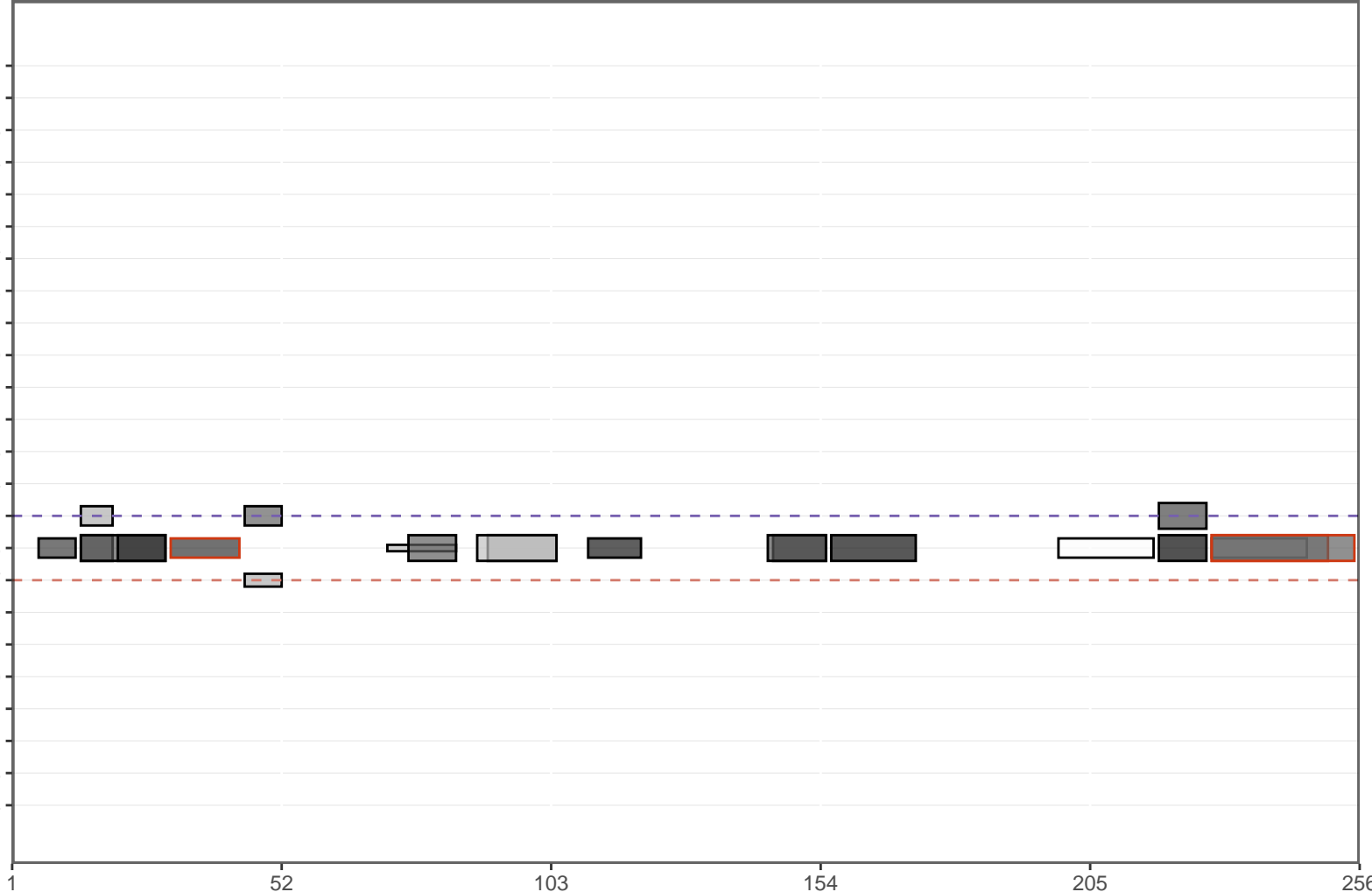
MW indication



Molecular weight

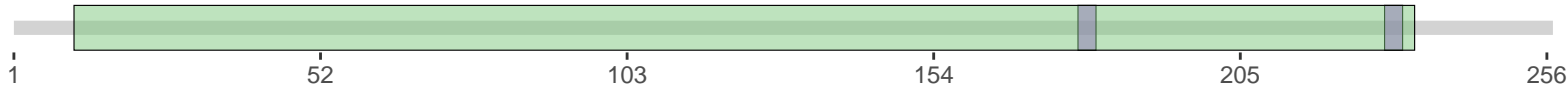


Gel Slice



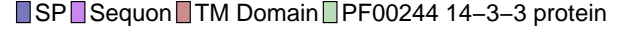
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IGDSKVFYLYMKGDVYRFLAEFKTGAERKEAENTLSAYKSAQDQANVELAPTHPIRLGLALNFSVFYVEILNSPDRAGNLAKGAFDEAAELDTLGEESYKDTLIMQLLRDNLFLWTSMDQDDGDTDEIKEPSKAEEGQV

NbL14g13380.1 peptidyl-prolyl_cis-trans_isomerase_FKBP20-1 [MW = 19.98 kDa]

No. of times detected



log(intensity)



Values from



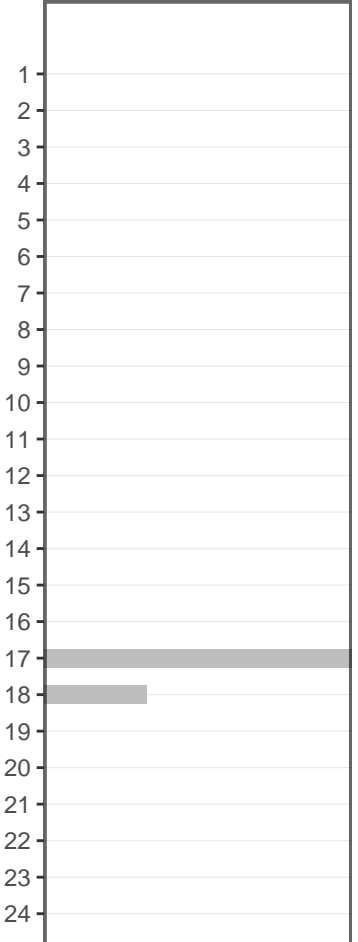
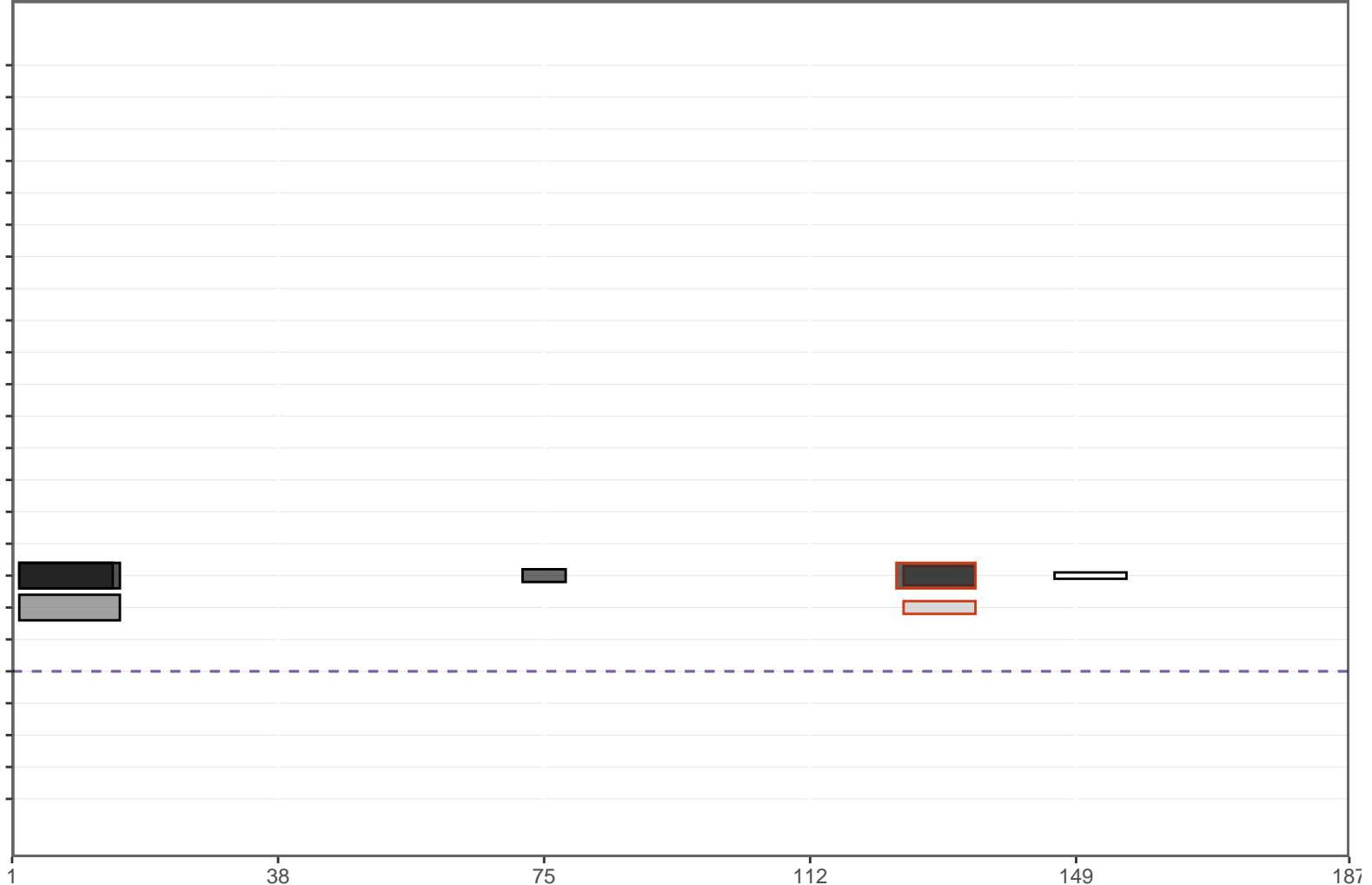
MW indication



Molecular weight



Gel Slice

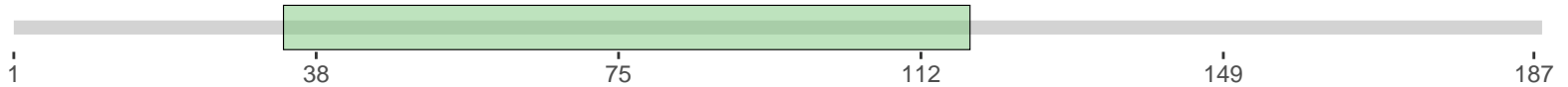


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

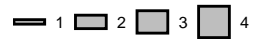


Protein sequence:

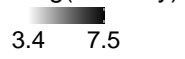
KVGEVALTCKFEYAYSGAGSPDPDPTLVFEVELVACRRPKKGGSSISVSDERARLEELKKGREMAAAAKKEEKKREEAKAAAAARIQAKLEAKKGGKGGKAAK

NbL14g13300.1 triosephosphate_isomerase_cytosolic [MW = 27.15 kDa]

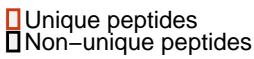
No. of times detected



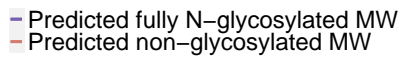
log(intensity)



Values from



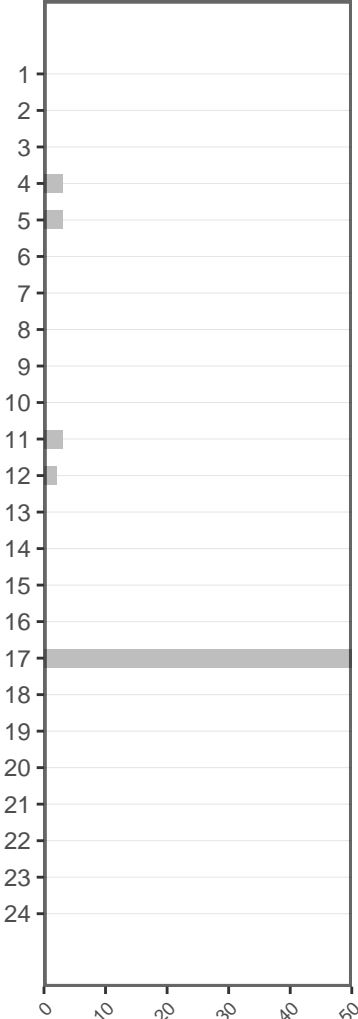
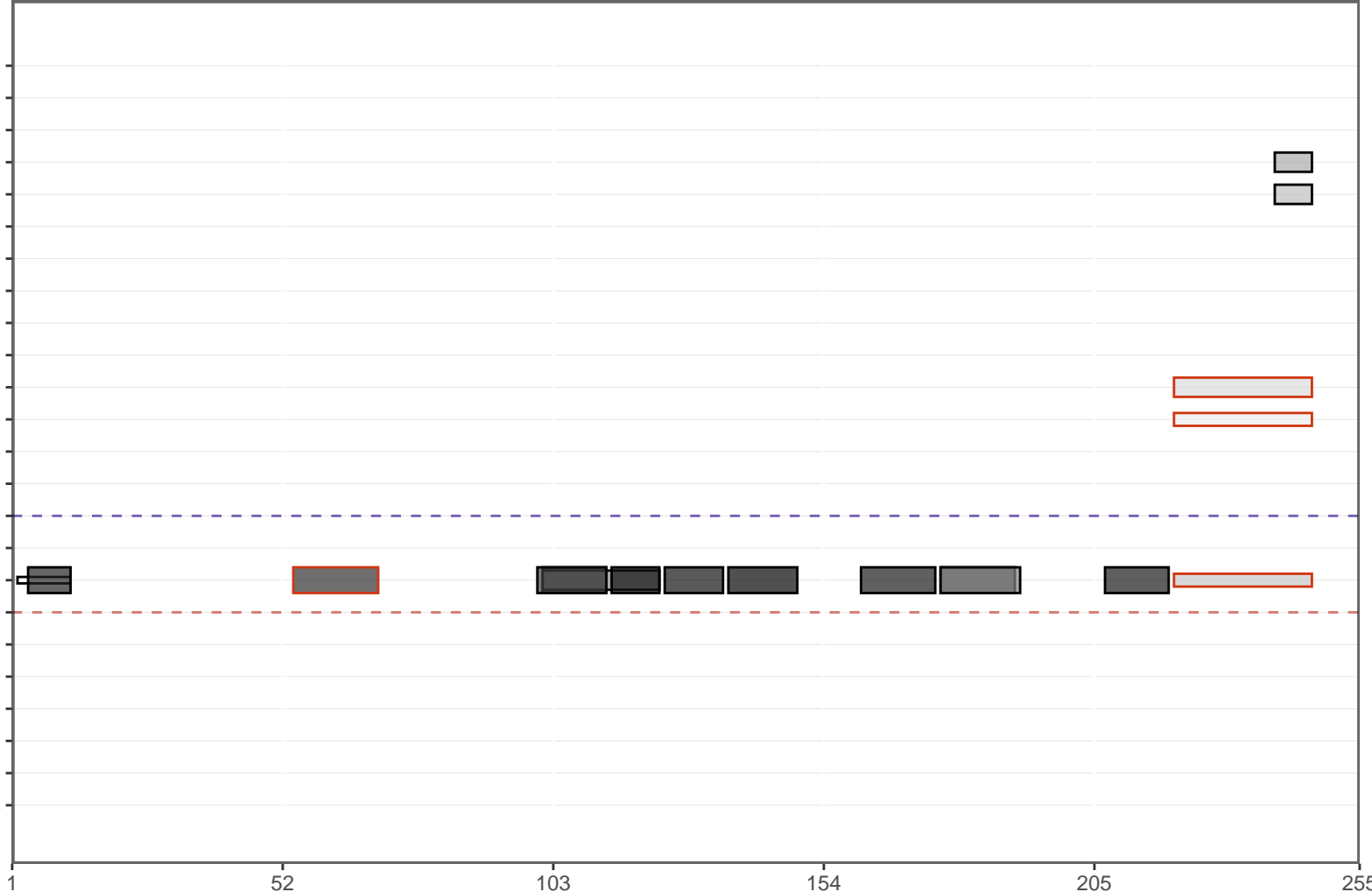
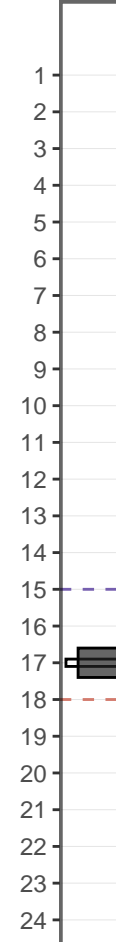
MW indication



Molecular weight

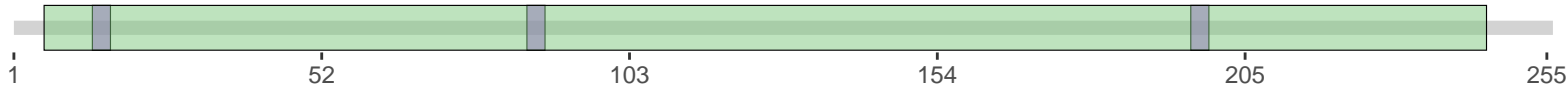


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

KXVAYISQGLKVIAGVGETLEGRREGSTRDVAAGTKAIADRVKDWTKVVAIEPVAWGTEKVASRQAGEVHAELEKRWLGNVNSADVAASTRIIVGGSEVNGANGKELAGGPDIDGFLVGGSLKPEFIDIKSAEIKKNA

NbL14g13290.1 actin-97 [MW = 41.7 kDa]

No. of times detected



log(intensity)



Values from



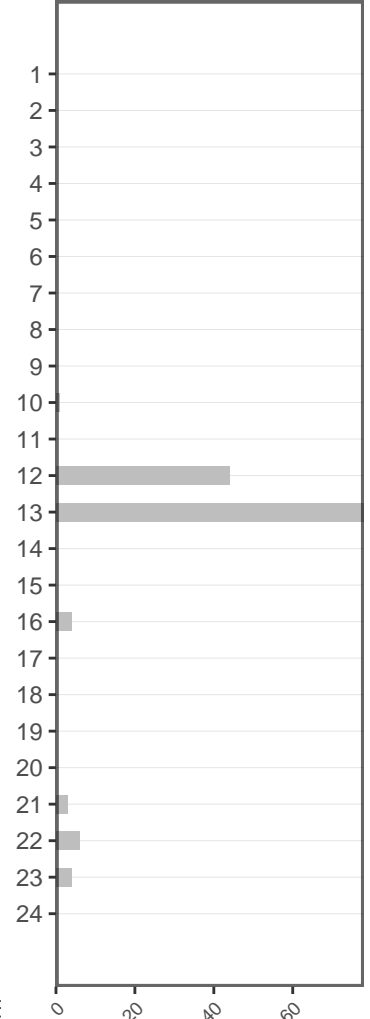
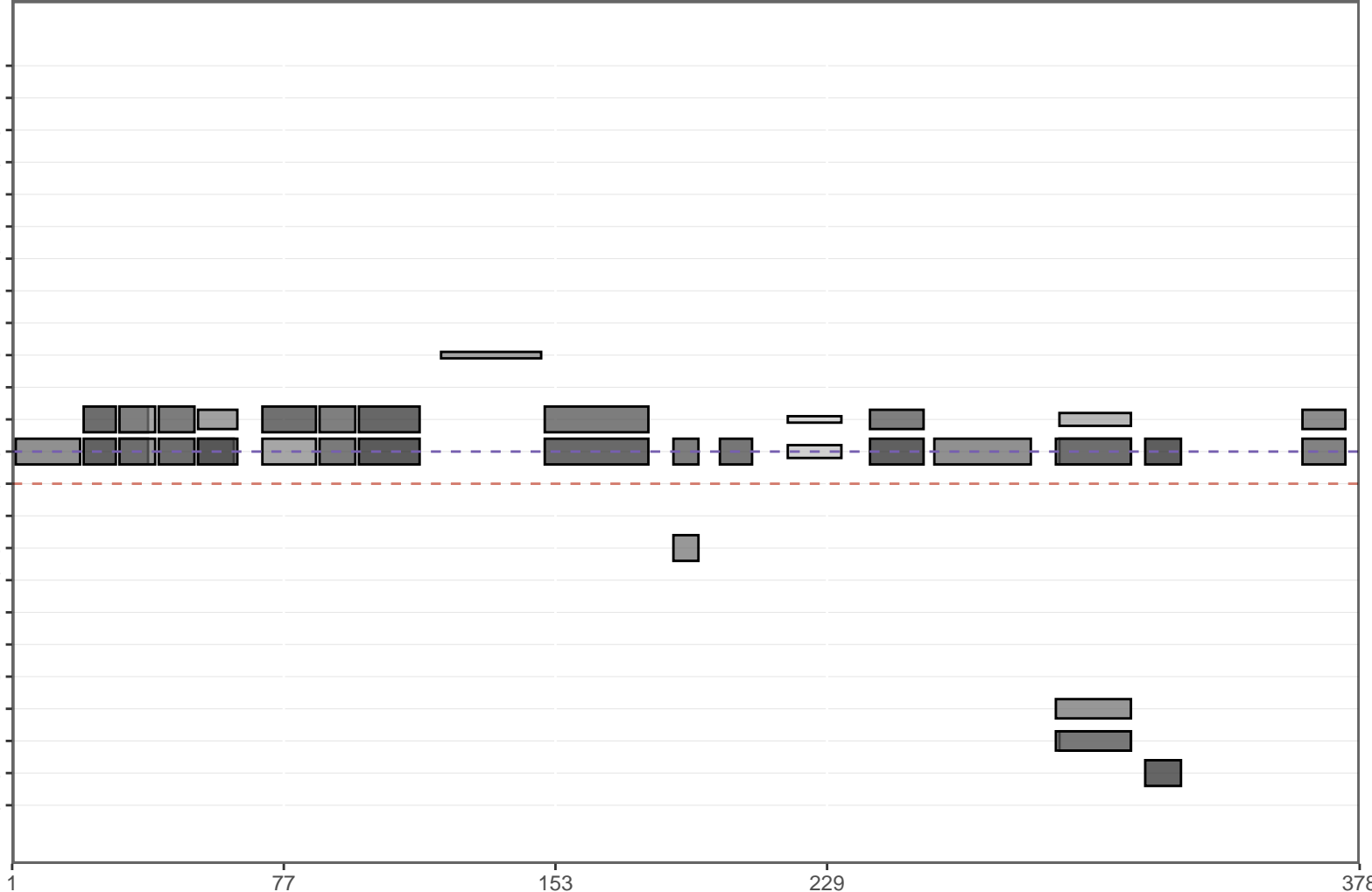
MW indication



Molecular weight

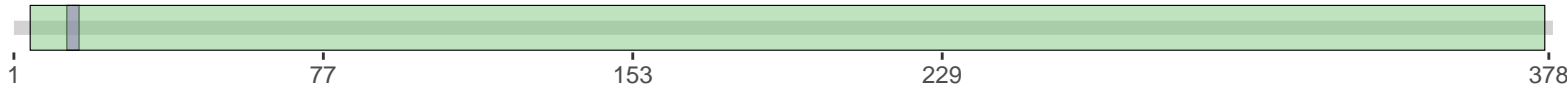


Gel Slice



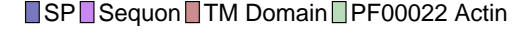
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

PHAILRLDLAQRDLTDFSLMKLTERGVYMTTSAERREIVRDVKEKLAWALDYEQELETAKTSSSEVKNYELPDGQVITGAEFRFCPEVLFQPSMIGMEAAAGHETTYNSIMKGDVDRKDLVGNVLSGGSTMFPGIADRMKEITALAPSEMKIKVWPPERKYVYVWGGSLASLSTFQGMWAKAEYDESGPSAHRKGF

NbL14g13180.1 UDP-glucuronic_acid_decarboxylase_5-like [MW = 38.65 kDa]

No. of times detected



log(intensity)



Values from



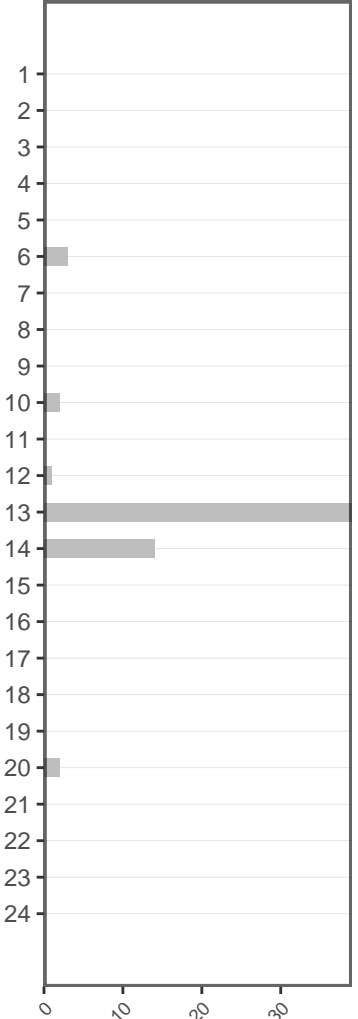
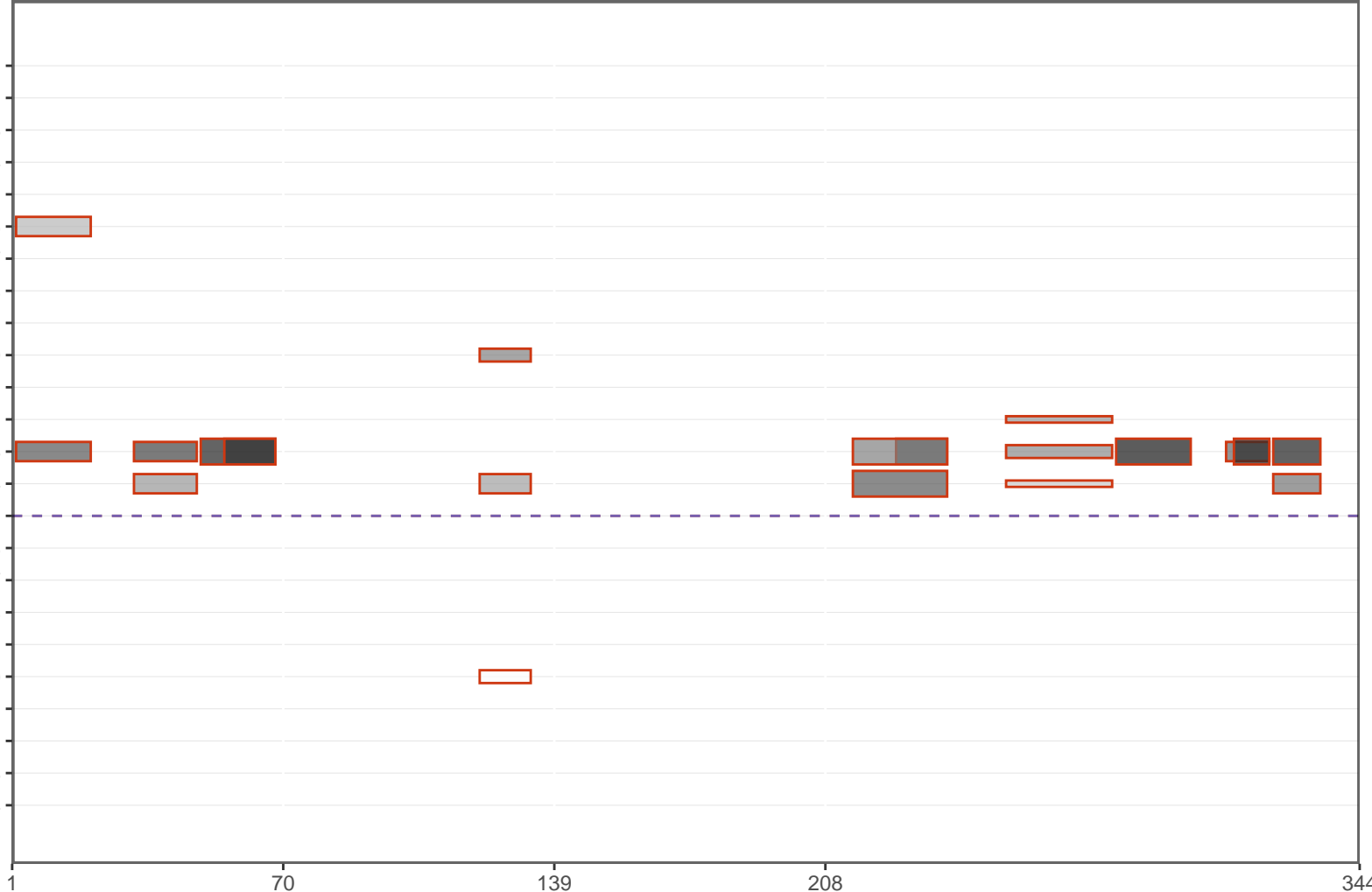
MW indication



Molecular weight

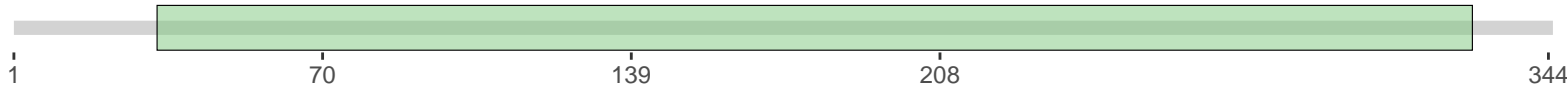


Gel Slice



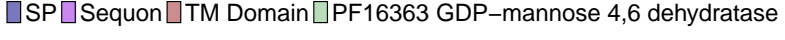
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SYWGNVNPQYRSCVDEGRKRAETLMFDYHRQHGIEIRIARINFTYGRMNDGGRVSNFIADARDEPLTVQVLPSTGRFCYVSDMVDGLRLMEGNTGPIINGNPGEFTMLELAETVKEILNPEVQITVENTPDDPRGRKPDFTKAKELLGWEPTRKLRDGIPLMEDDFRGLGIERKI

NbL14g13150.1 actin-depolymerizing_factor_2 [MW = 18.16 kDa]

No. of times detected



log(intensity)



Values from



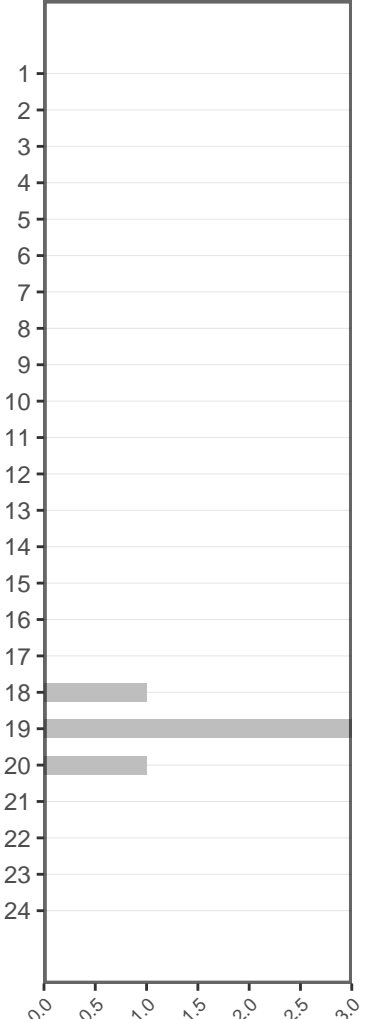
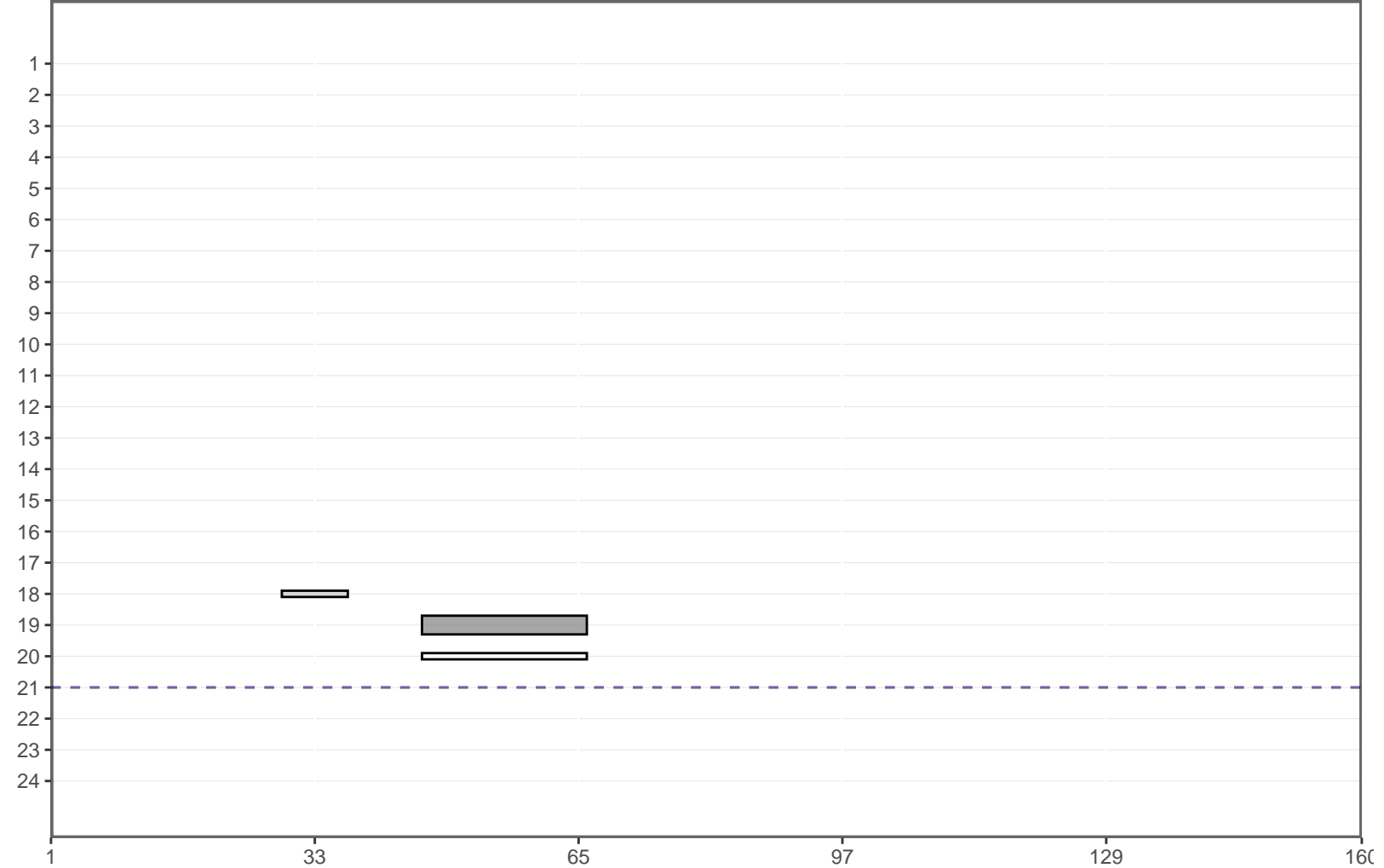
MW indication



Molecular weight

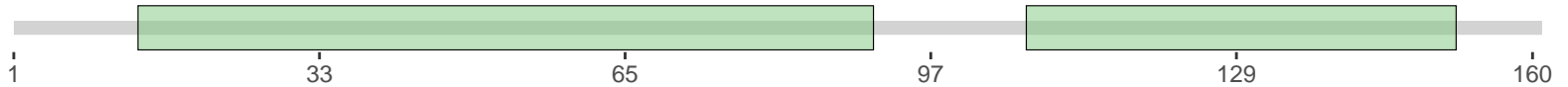


Gel Slice



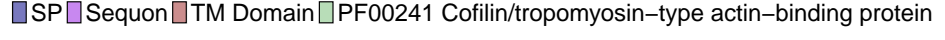
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

/AVYDFDFTTEENLVQKSRFFIAWKRVRPVEIATAGCKNAGSPDARVRBKMVYAGSKDRFKRELDGFOVELGATDPTFEMGLVFRIRVGGIEC

NbL14g13140.1 ras-related_protein_RABE1c-like [MW = 23.96 kDa]

No. of times detected



log(intensity)



Values from



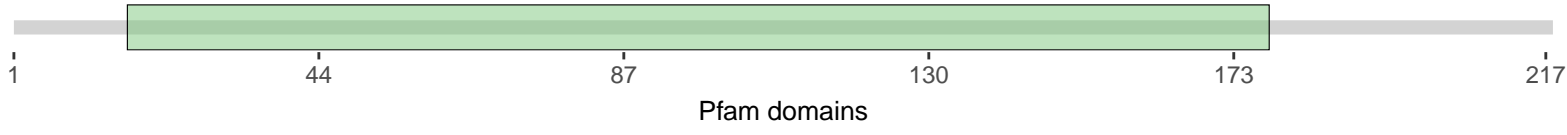
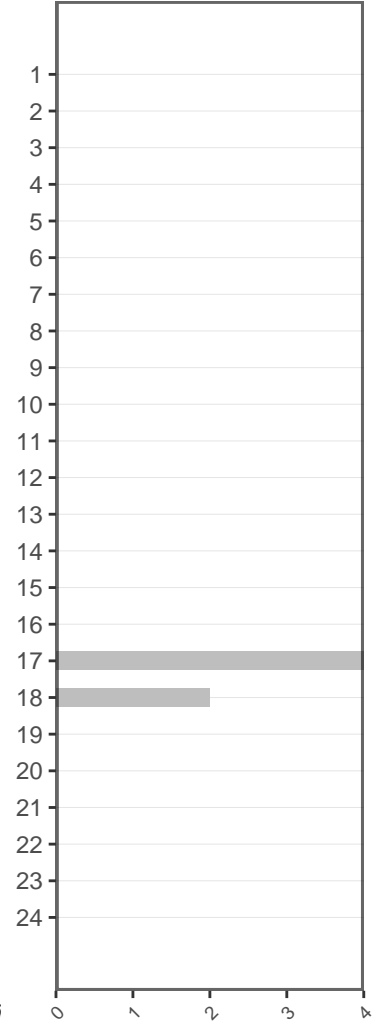
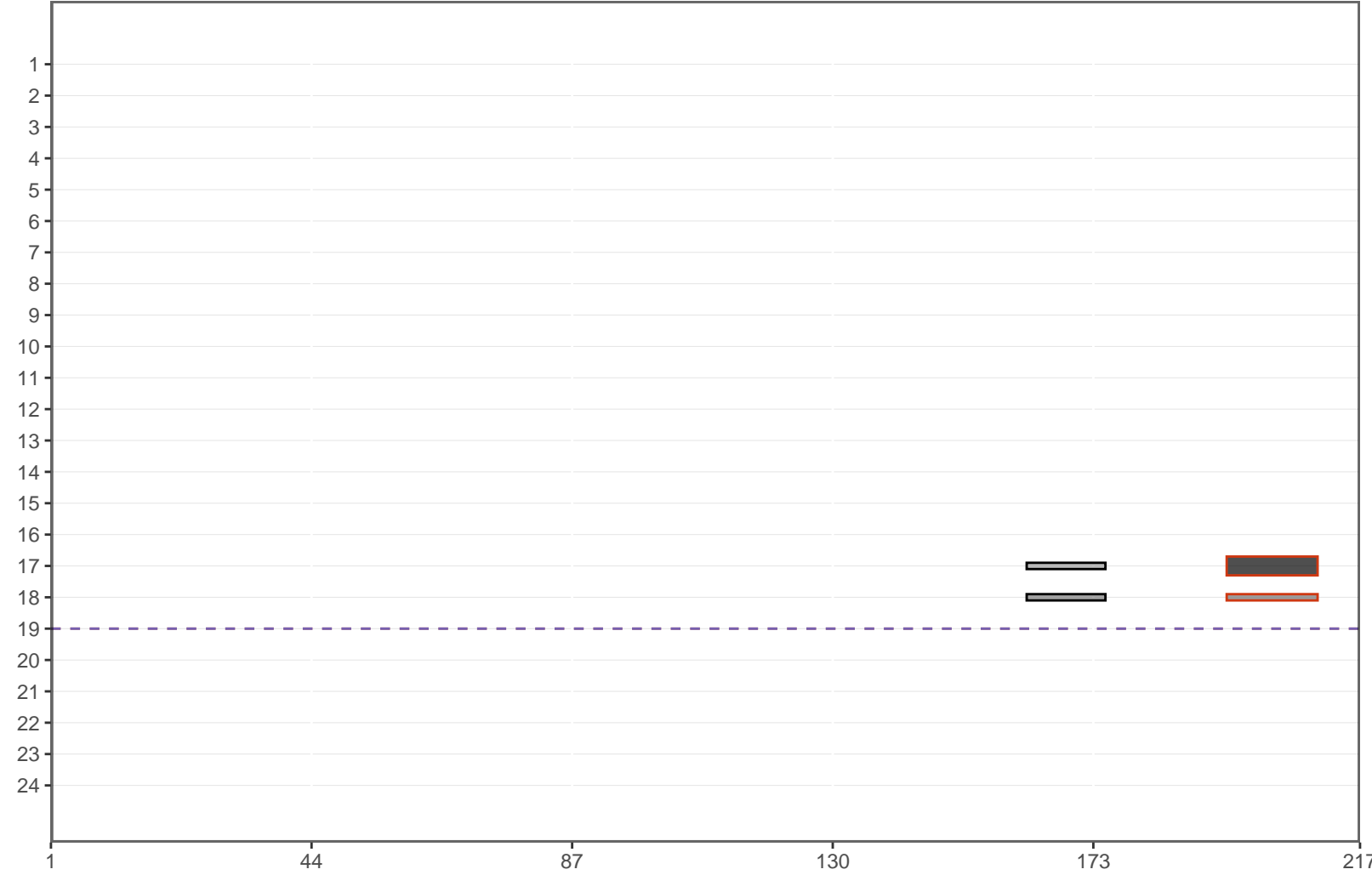
MW indication



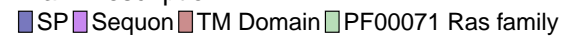
Molecular weight



Gel Slice



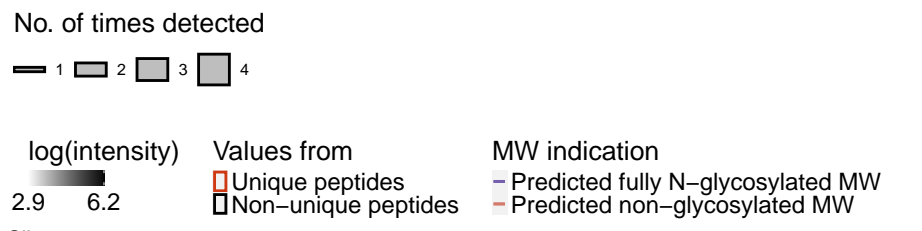
Pfam Description



Protein sequence:

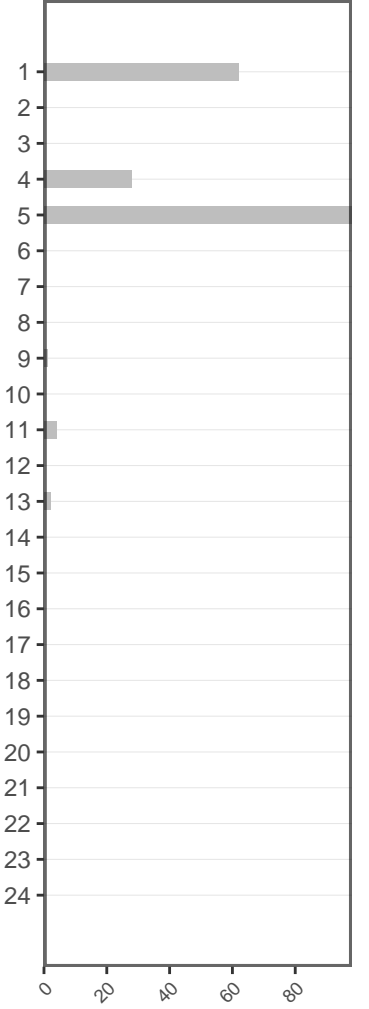
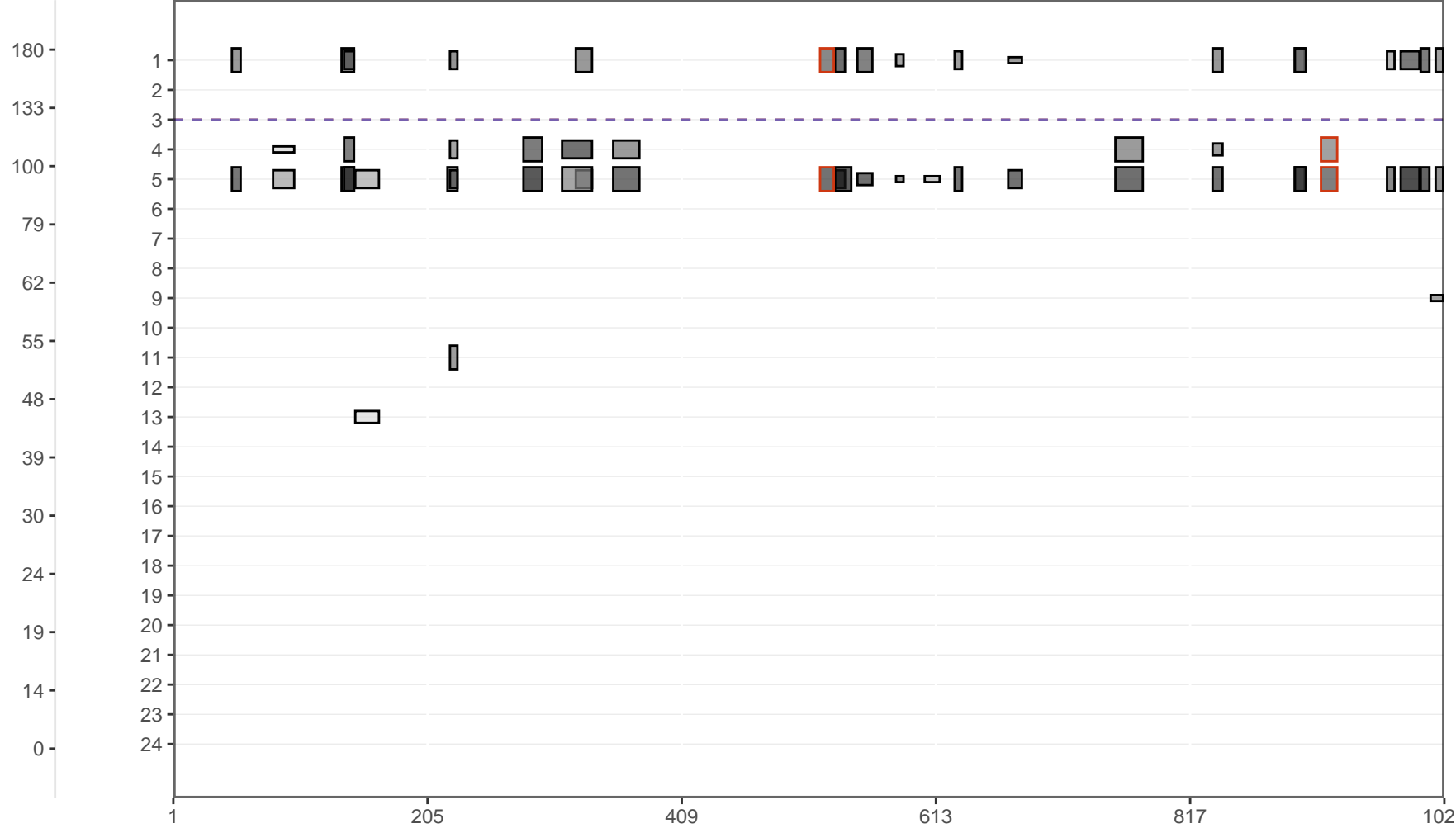
DESSFNIRNWRIRNEGHASDINVKILVGNKADMDSEKRAVPTSKGGALAEVGIKFFETSAKTNMNVVEVFFSIARDIKRLSESDSKTEPQAIRINGADGAGTGGAAEKSSGGGG

NbL14g13130.1 2-oxoglutarate_dehydrogenase_mitochondrial-like [MW = 115.58 kDa]

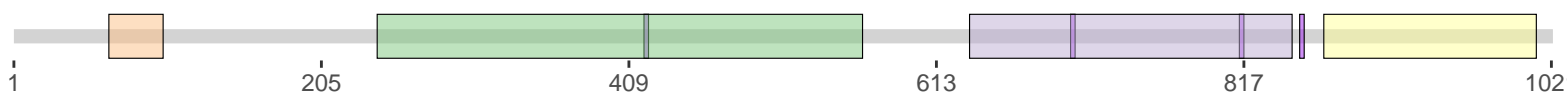


Molecular weight

Gel Slice



Protein length



Pfam domains

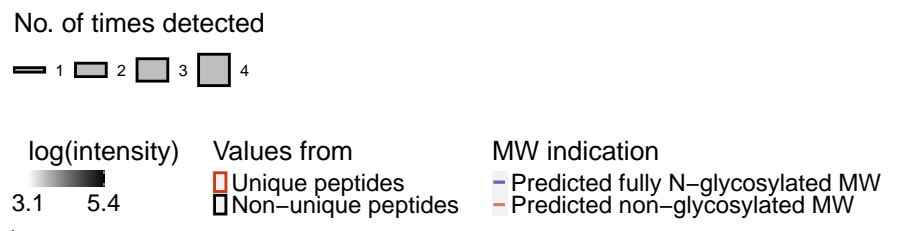
Pfam Description

- SP
- Sequon
- TM Domain
- PF00676 Dehydrogenase E1 component
- PF16078 2-oxoglutarate dehydrogenase N-terminus
- PF02779 Transketolase, pyrimidine binding domain
- PF16870 2-oxoglutarate dehydrogenase C-terminal

Protein sequence:

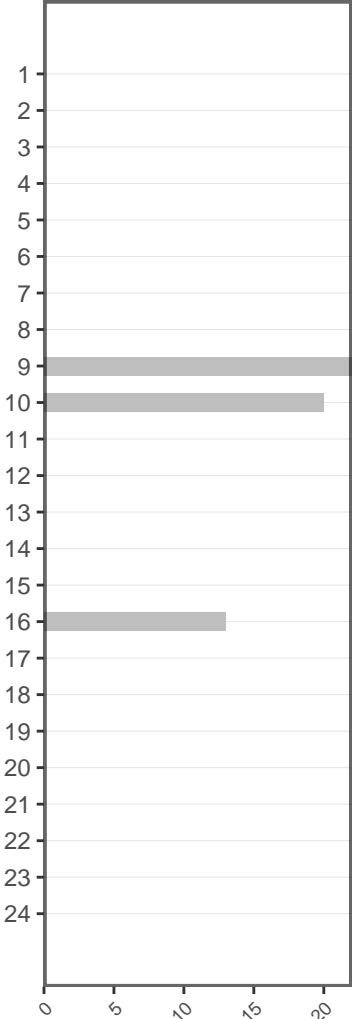
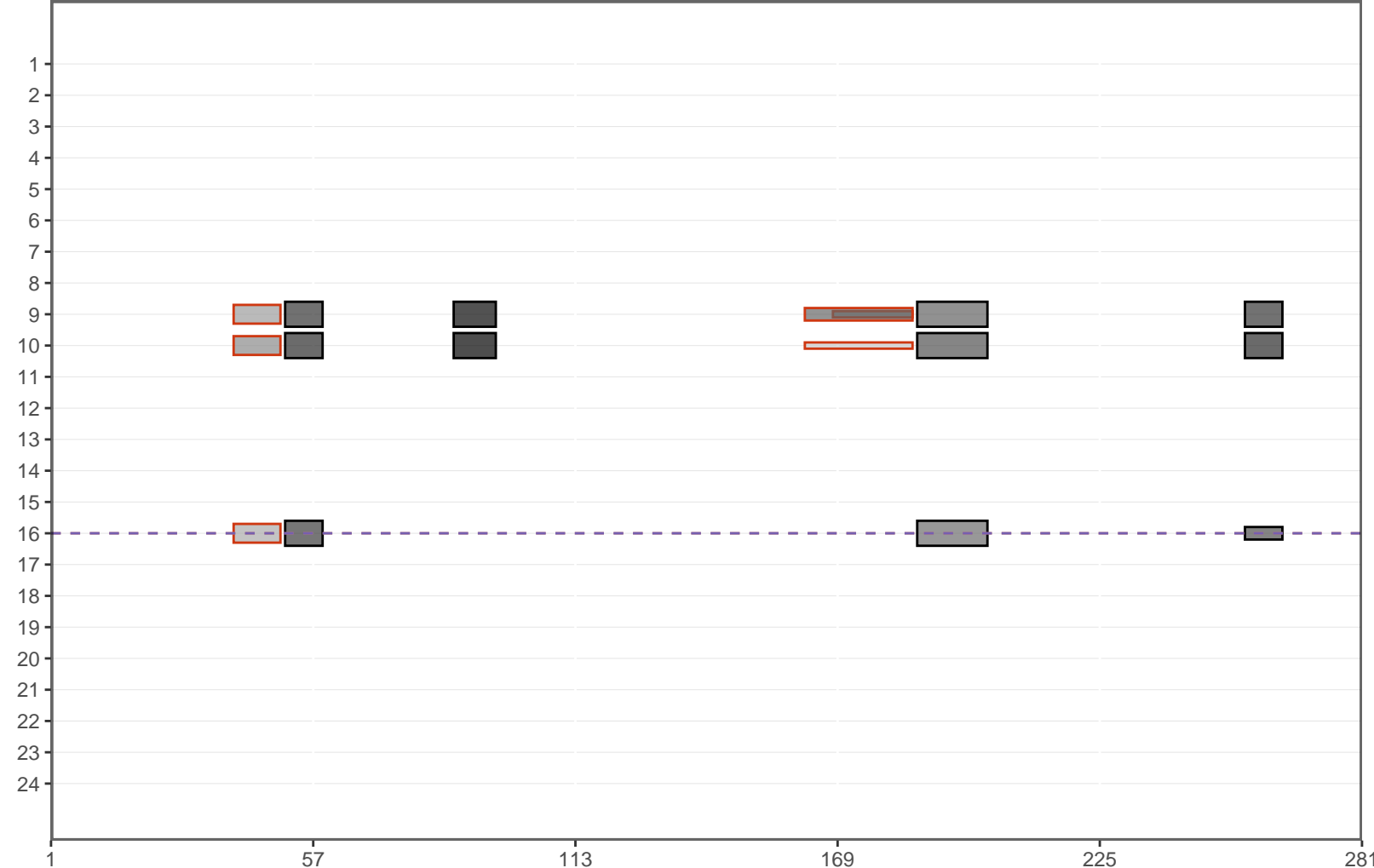
IRFGHNEIDPSFTGPKMKYKVRIRHPALEHFNKLLQSGGVTKDDVEKIHKNKINLNEEFVASKDYPQKRDWLGAFVSGFKSPAGLRVRYNTGVKPELKDVGKAITLPEDFKPRAIKKVVYDERKKMETGERVDWALGEALAFATLVEGNHVRISGGDVERGTTFSHRHVSLHDOETGAKYPLDHWMMNQNEEMFTVSNSSLSEFGVLGPELGYEMENPNLWVWAGDFGDFSNAGVDFDQFLSSGEAKWLRDTGLVLLPHGYDGGGPEHSSARLERFLQMS

NbL14g13000.1 histidine_biosynthesis_bifunctional_protein_hisIE_chloroplastic-like [MW = 31.54 kDa]



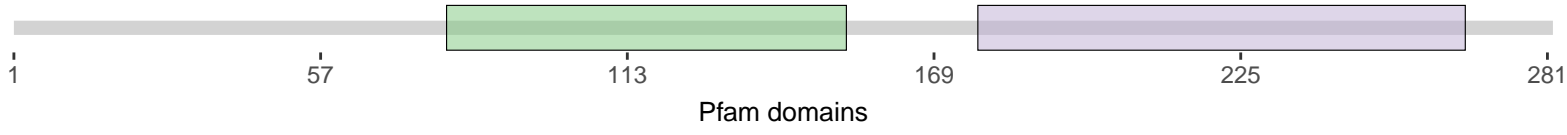
Molecular weight

Gel Slice

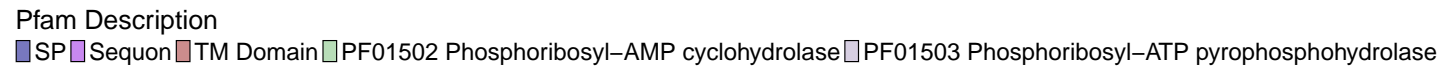


Protein length

Peptide counts over 4 repeats

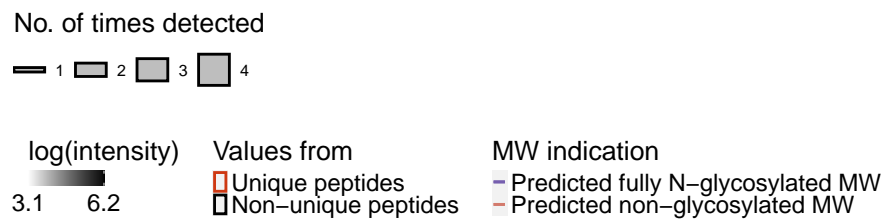


Pfam domains



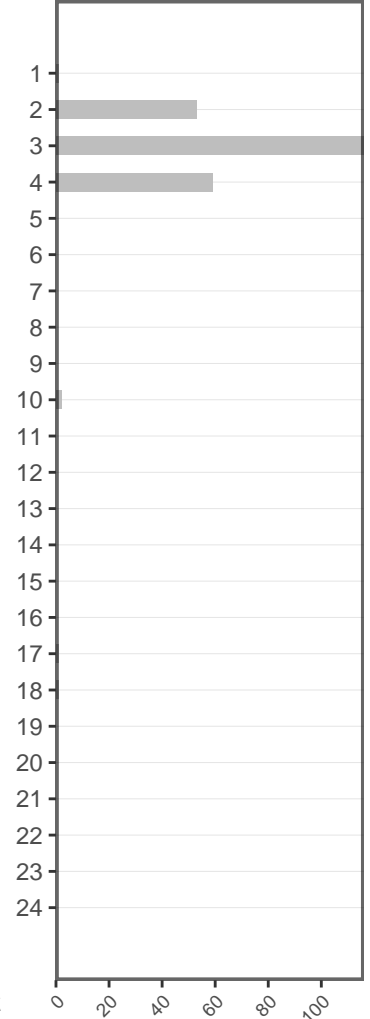
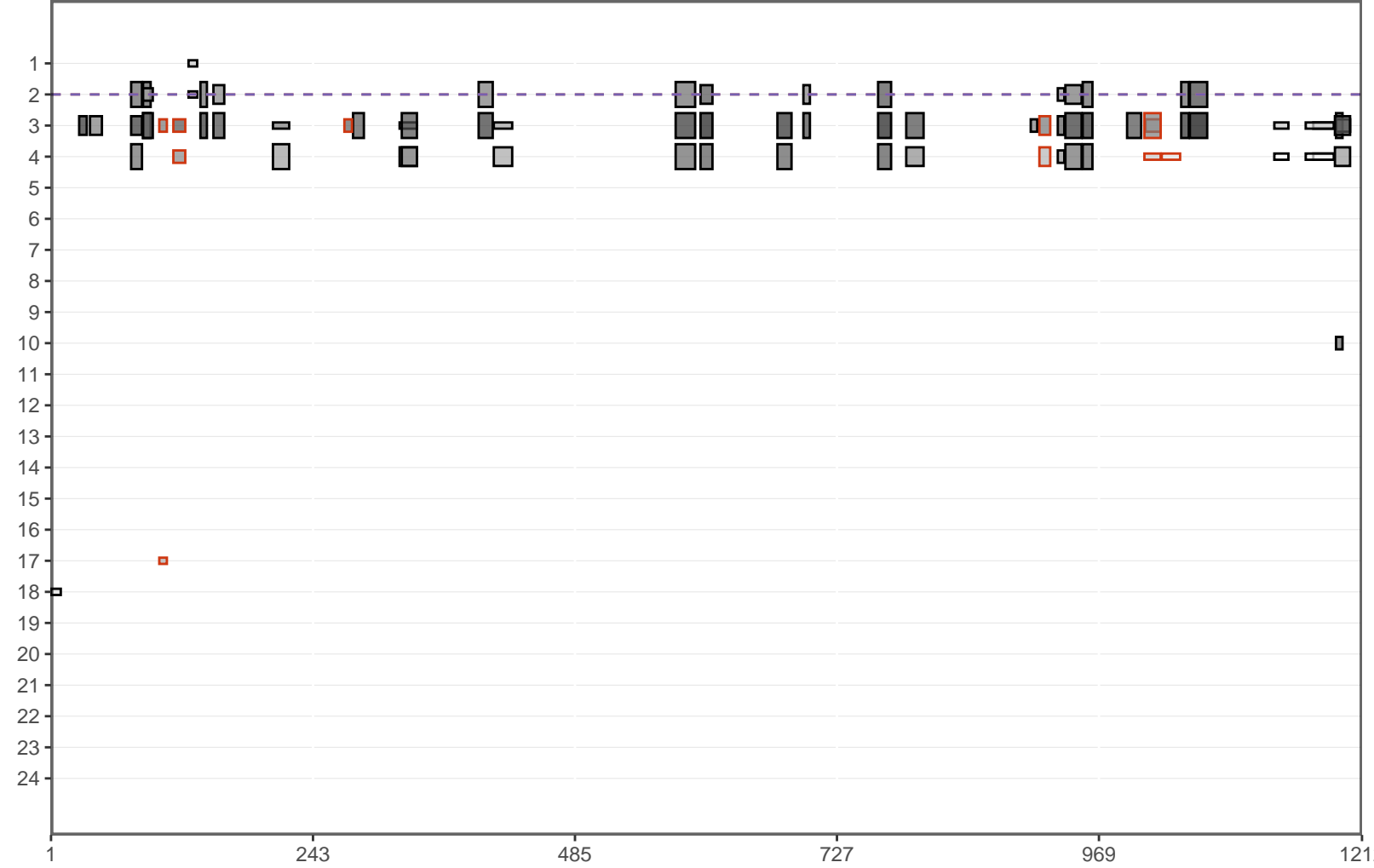
Protein sequence:
 CDCRDSIYLKPGDPTGHTGSETGYVYTSVDGLKNPEVEKNEKELAMFTFLVALESTINERKAETS655566KPPWTKRLLLDKLLCGKIREAEDELGRLEENEDKGRITASEMADLVHAMVLLSLRQGVWIEEVLGVLQRQRFKSGIEEKNRKE

NbL14g12980.1 splicing_factor_3B_subunit_3-like [MW = 134.52 kDa]



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon TM Domain PF03178 CPSF A subunit region PF10433 Mono-functional DNA-alkylating methyl methanesulfonate N-term

Protein sequence:

DSRSFLVGSYDNTIRILSLDPDDGMVLLGLGVSPPPELFLFVQVQSGGEGDGDHPSLFLNAGLGNGLVFRFTVDMITGQLSDARSFLGLRPAKLFISVVRGRRAMLGLSRPFLGVYHGHFLTLPLEYETLEFAASFSDDGQAEQVVAAGDALRVFTIERLGETNETAIPLRVYTPRRFLQPKRMVIMESDQGYTAEREAAAKKECFETAGNGENGAEQVENGEDDNDPLSDEQVGYPKESGRWVSGIRVLDPRSTGTQELLEQDNEAAFSICTVN

NbL14g12870.1 diphthine--ammonia_ligase-like [MW = 82.4 kDa]

No. of times detected



log(intensity)



Values from



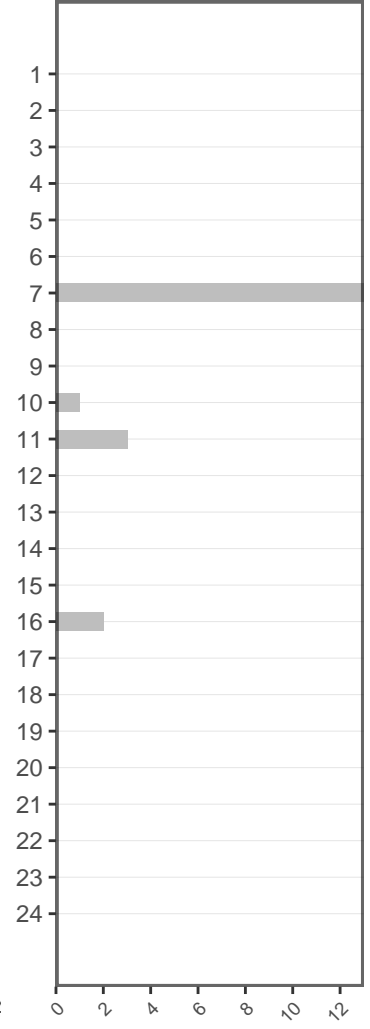
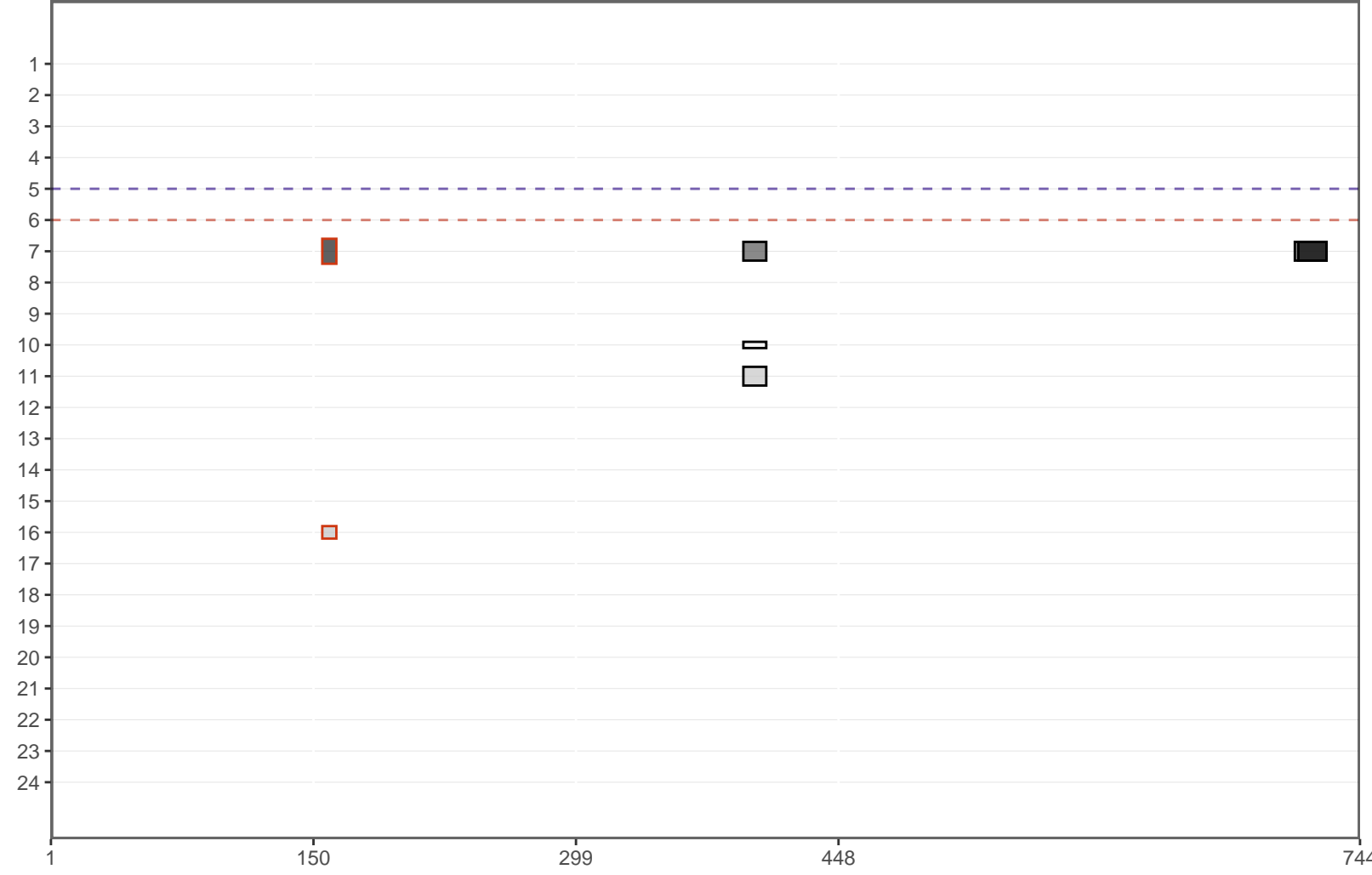
MW indication



Molecular weight

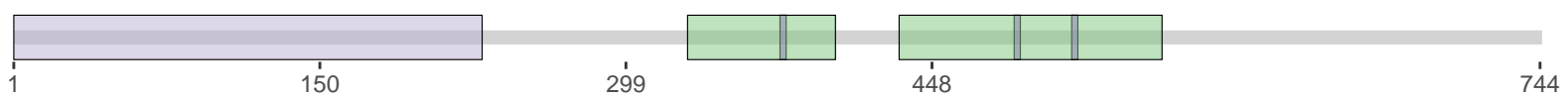


Gel Slice



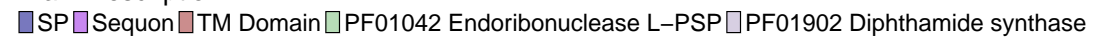
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LYIHLIADMDIEFAWNETVYRRTDGEKRFQVPSRETIELPLLLGLGRAYIEVLVNDPTKQVLLHVSISGVAWPSGIPVSGATLHNDLHMAGQLGDPMTMLCEGGFVAEEGLEENSEAWAGSFGNSIGTSAVFFVYGSABLETSERVLVQNKTEALLNQMKSLSHAEGTKKSRVLDPIFLYLVLDLKRALVEVKPMLYTGEMSAPESDHAMQHGSTGGYWGFEYETWHDGLQKQVWYGVKVTALSLVTEELAAKIGSPANNVAGHSVKSQVPEKEHVMARFCYR

NbL14g12820.1 RNA-binding_protein_42-like [MW = 27.09 kDa]

No. of times detected



log(intensity)



Values from



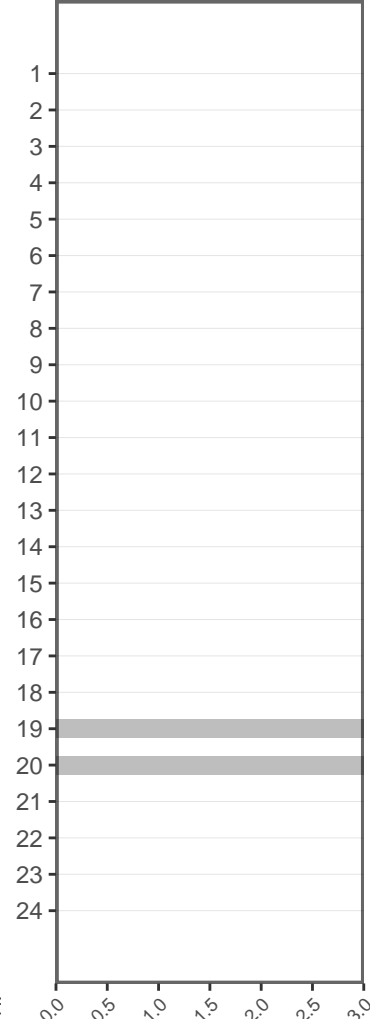
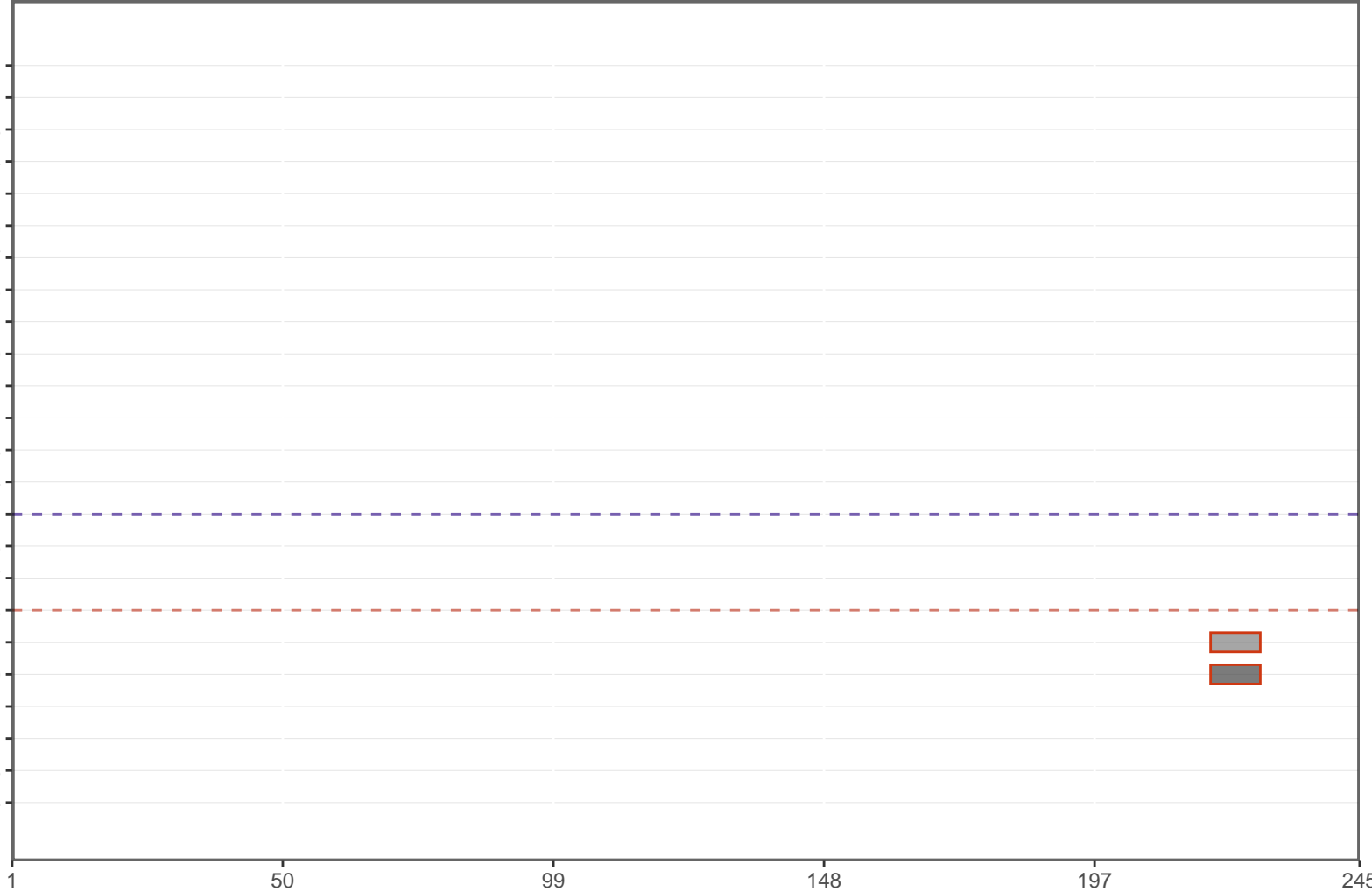
MW indication



Molecular weight



Gel Slice



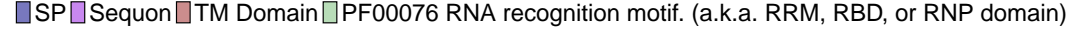
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

KKAVPRKAUGLSWEDPTLAEWFPENDYRLFQGDGNGEVNDVLSKAFSRFPFTFMMAKVVDRKRTGKTGYGFVFSNLLDAAALKEMNGKYGVNRPKLRKSKWGERDYEALESKNRSHKKPKLTKKSLHK

NbL14g12780.1 probable_low-specificity_L-threonine_aldolase_1 [MW = 38.76 kDa]

No. of times detected



log(intensity)



Values from

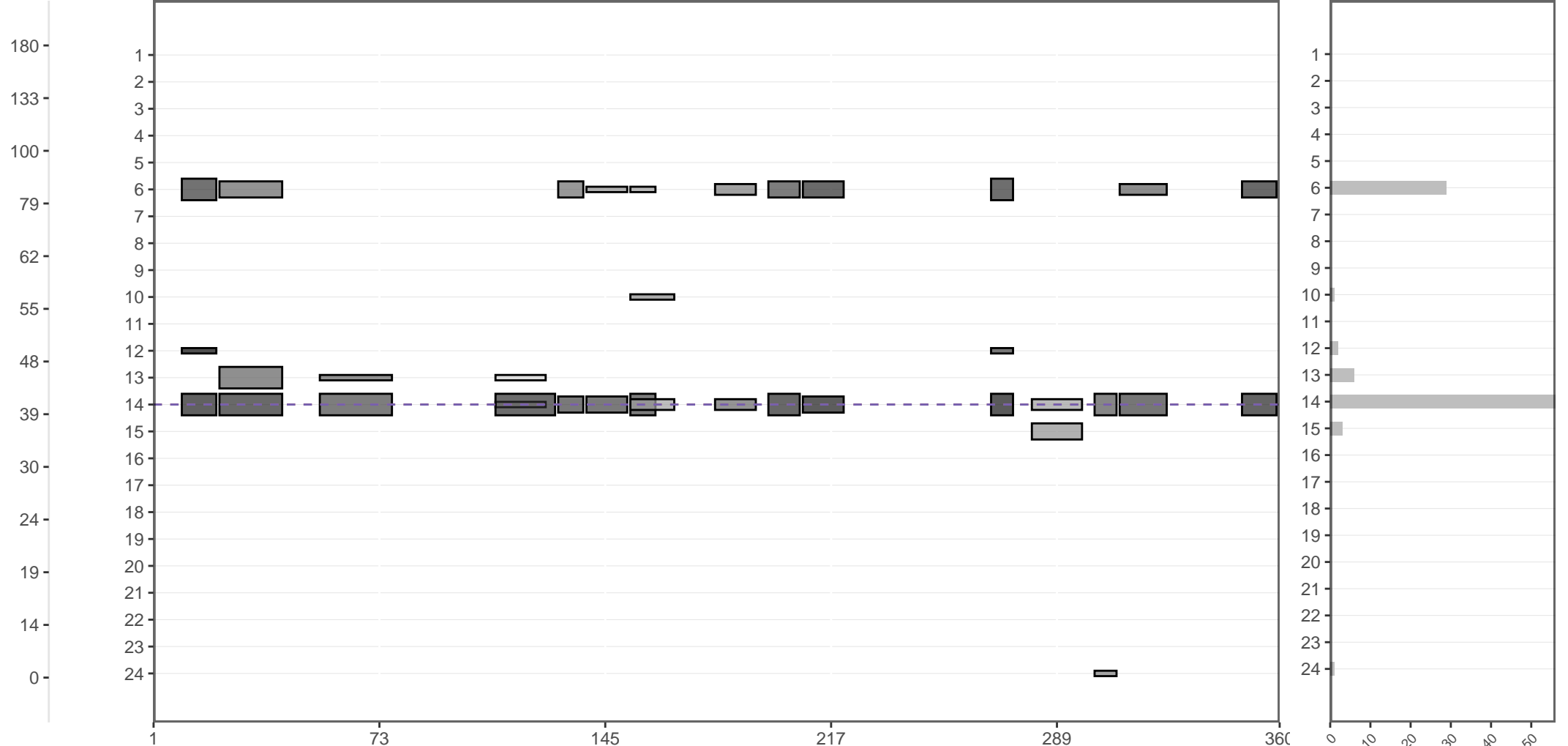


MW indication



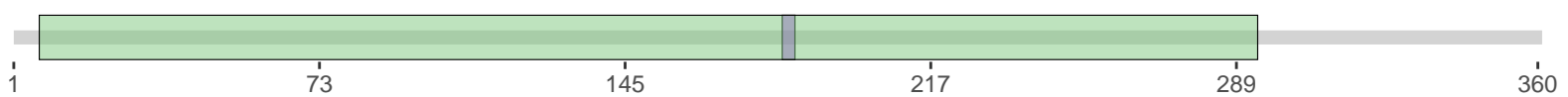
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VKYGKGLKHIDGARFNASVALGVPVHRLVRAADSVSVGLKGLGAPVGVVGVGSKSFIAMAKLRKTLGGSMRQVGVLGAAAFIAGFQENLVKLEGDHKNKAKLAELNKKIKGLKVDAAVETNIVYQDLKGGKISSETEMCKTLEQHGLLLPVGGPQRIRFVHHQISENDVHYAALGVQRALSGVAEENGSK

NbL14g12710.1 1-aminocyclopropane-1-carboxylate_oxidase_homolog_1-like [MW = 46.41 kDa]

No. of times detected



log(intensity)



Values from



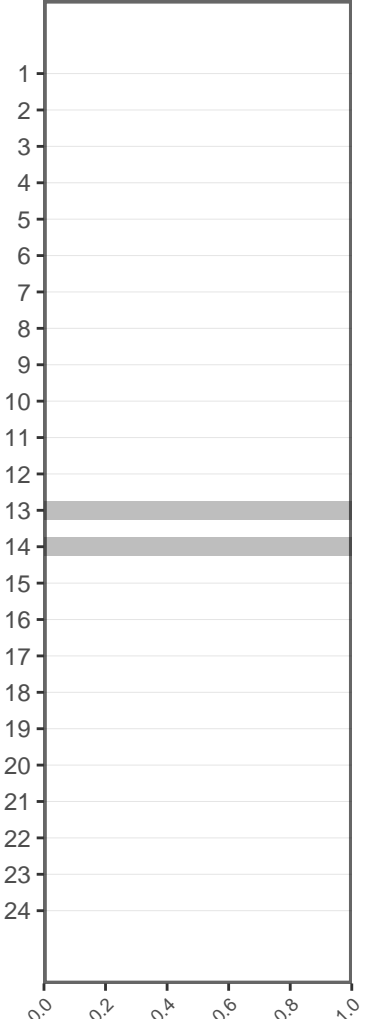
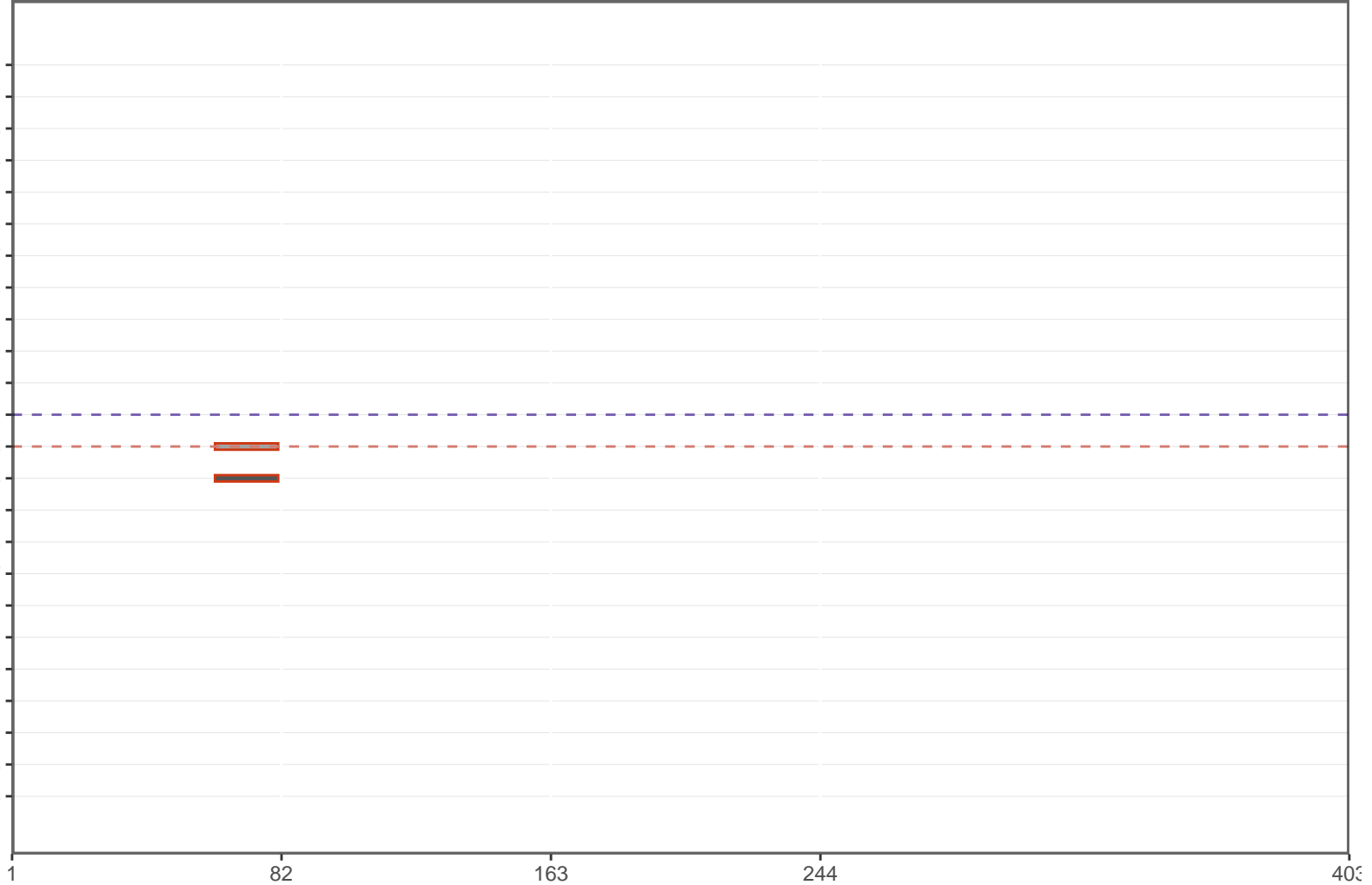
MW indication



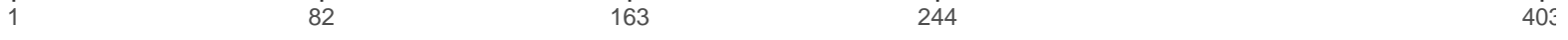
Molecular weight



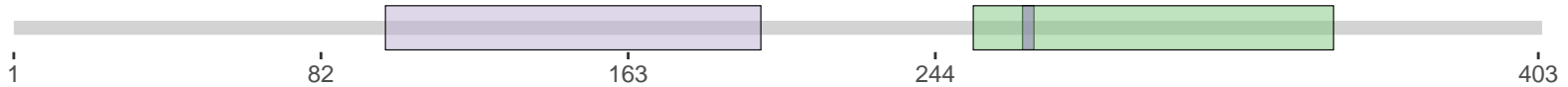
Gel Slice



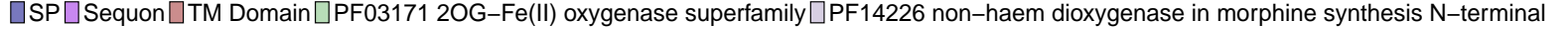
Protein length



Pfam domains



Pfam Description



Protein sequence:

NRDYLGCIMAFNFRSDLELPETGRKELLEYSQHVRLKIGITFELLAALGLNPNHLEMECAKGFILSHYPPCFEPNKTGRTKHTDPPDFLLGDHIGLQYHQNQWIDHPTVGTALVNLGDLLOLLSNDKFKSAEHRVLSKQIGRISVAGFFTTQGFQFDRLYGPKEKLLSDENLPMYKETTFRDQVSYNSKGLGARPSLLHLRL*

NbL14g12700.1 C-Myc-binding_protein_homolog [MW = 14.44 kDa]

No. of times detected



log(intensity)



Values from



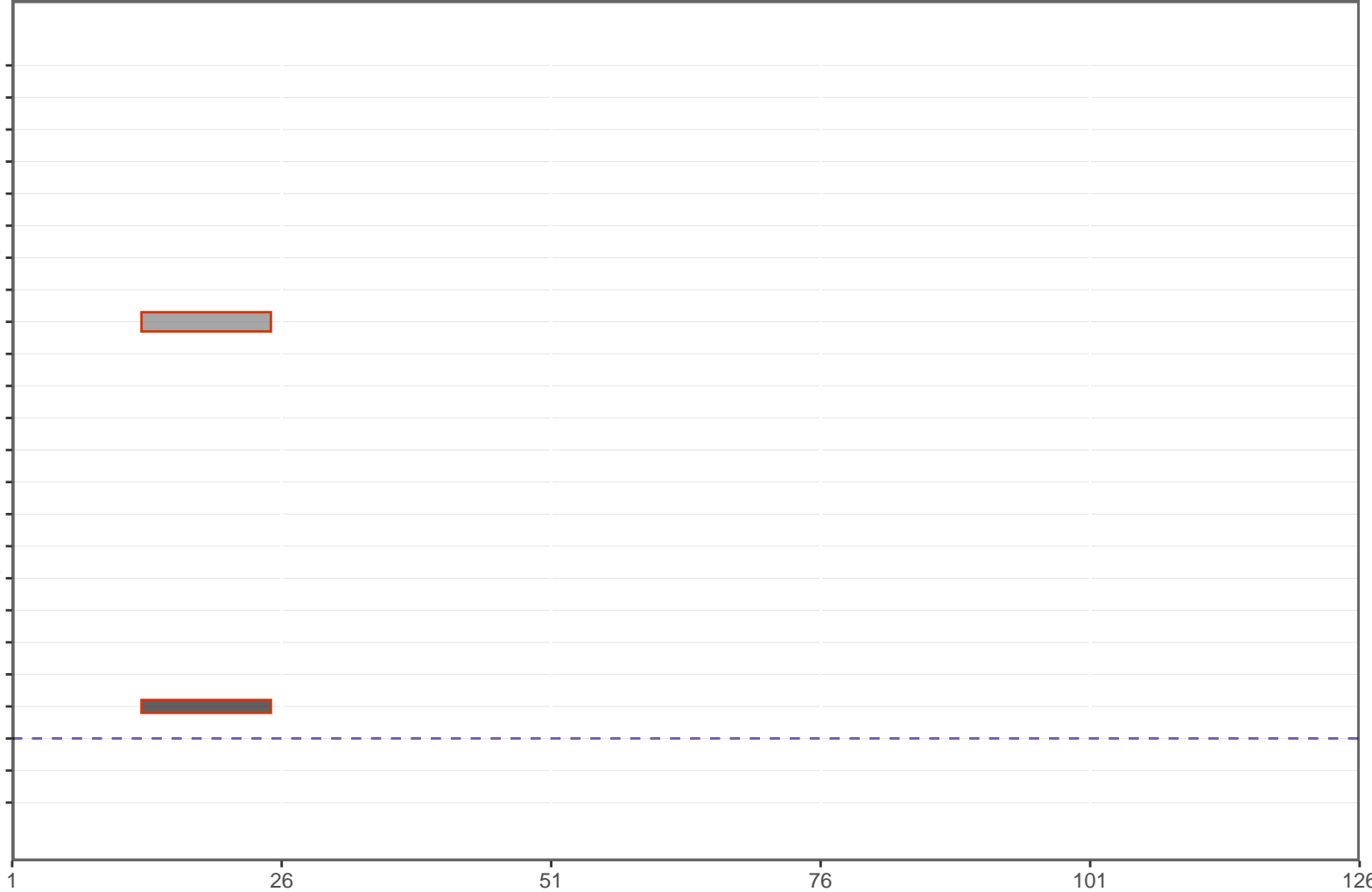
MW indication



Molecular weight



Gel Slice

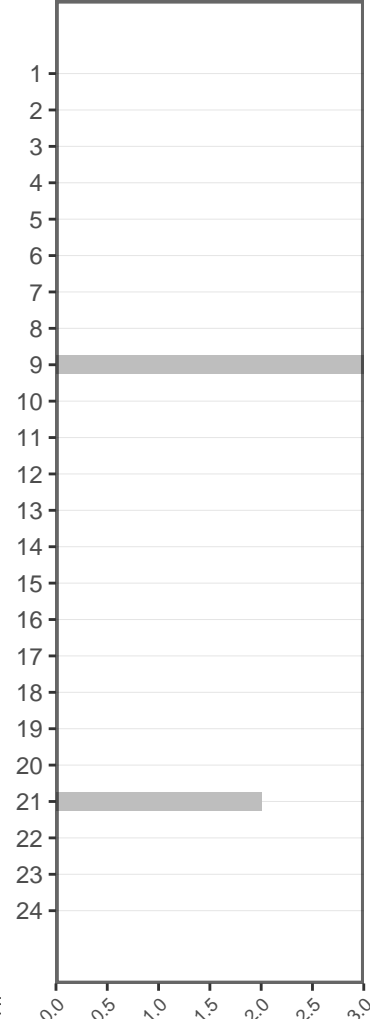
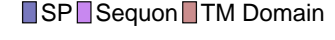


Protein length



Pfam domains

Pfam Description



Peptide counts over 4 repeats

Protein sequence:

IPITYSEYKLAELSDLQRYDELLKEHGEKRELEELKHTQVEASTKEPNNVNAHEEELKSTVEGSKPEKNAQFF

NbL14g12630.1 alpha-glucosidase-like [MW - SP = 98.15 kDa]

No. of times detected



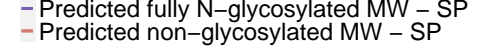
log(intensity)



Values from

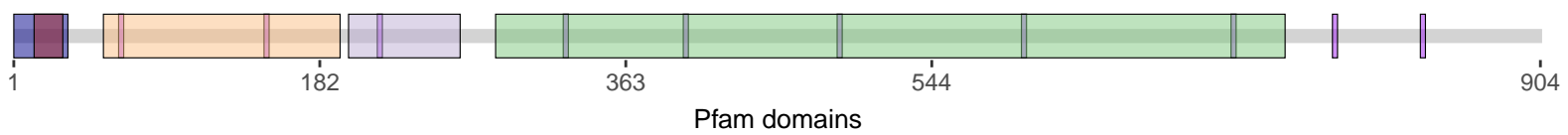
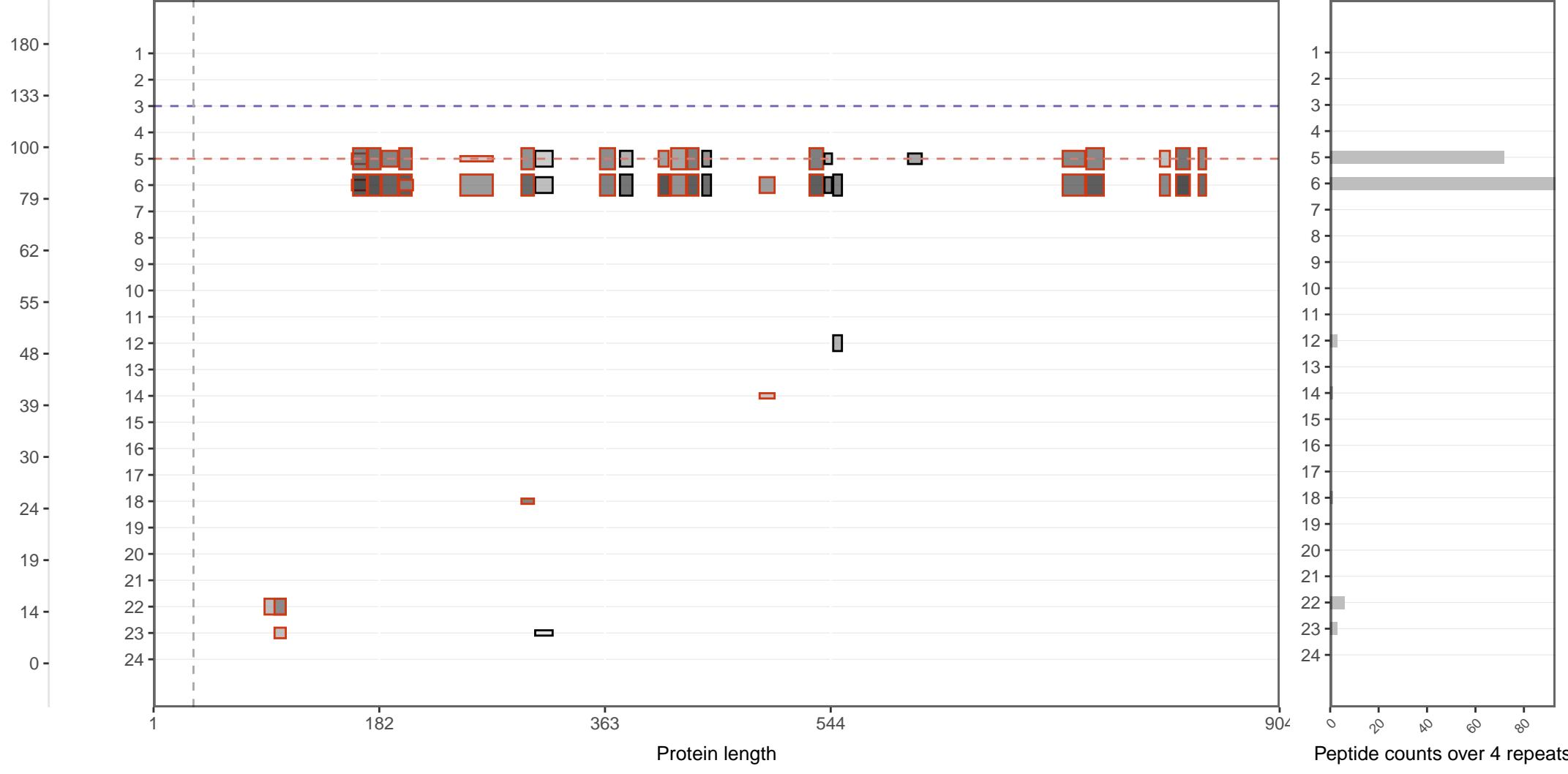


MW indication



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF01055 Glycosyl hydrolases family 31
- PF16863 N-terminal barrel of NtMGAM and CtMGAM, maltase-glucoamylase
- PF13802 Galactose mutarotase-like

Protein sequence:

ARVFWYSEIKFHKRLPVDGLVMDMNELSNFISPPSPSTLNDPPYKINNGSTLLPNKTKTQVTEVHYGNTLEYNHNLVGFLEAKMTNALVDITKRPPIELRSTFVAGAGKYTAHWYGDAAATWDDLAVSIPSLNSGLFGIPMVGADICGFGKNTTEELGRRWGLGAFYPSRSDHDKFTHQELVLDVDSVATAKKVLGLRYRLLPFYHTLMEAHSRGVVPIARPLFFSFPEDNTFYEDSGFLGKGLIHPVLTSFGAVSNVAFPPGQTFWDFLNFYENHNNMKSQNYNL

NbL14g12470.1 50S_ribosomal_protein_L10_chloroplastic [MW = 30.62 kDa]

No. of times detected



log(intensity)



Values from



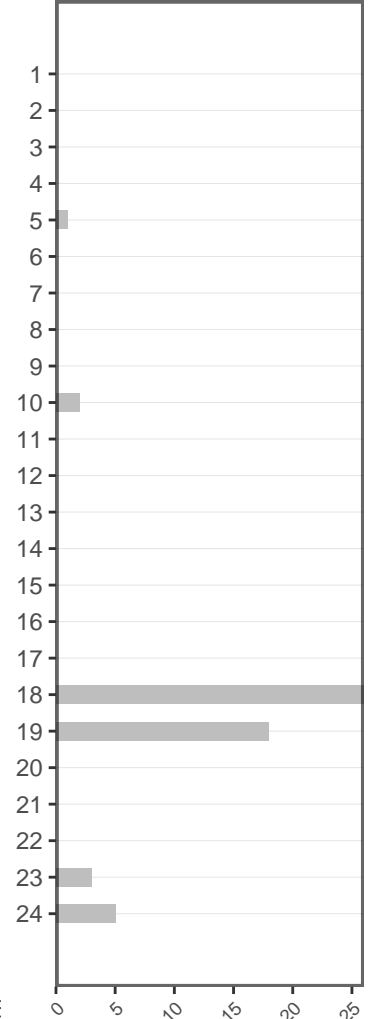
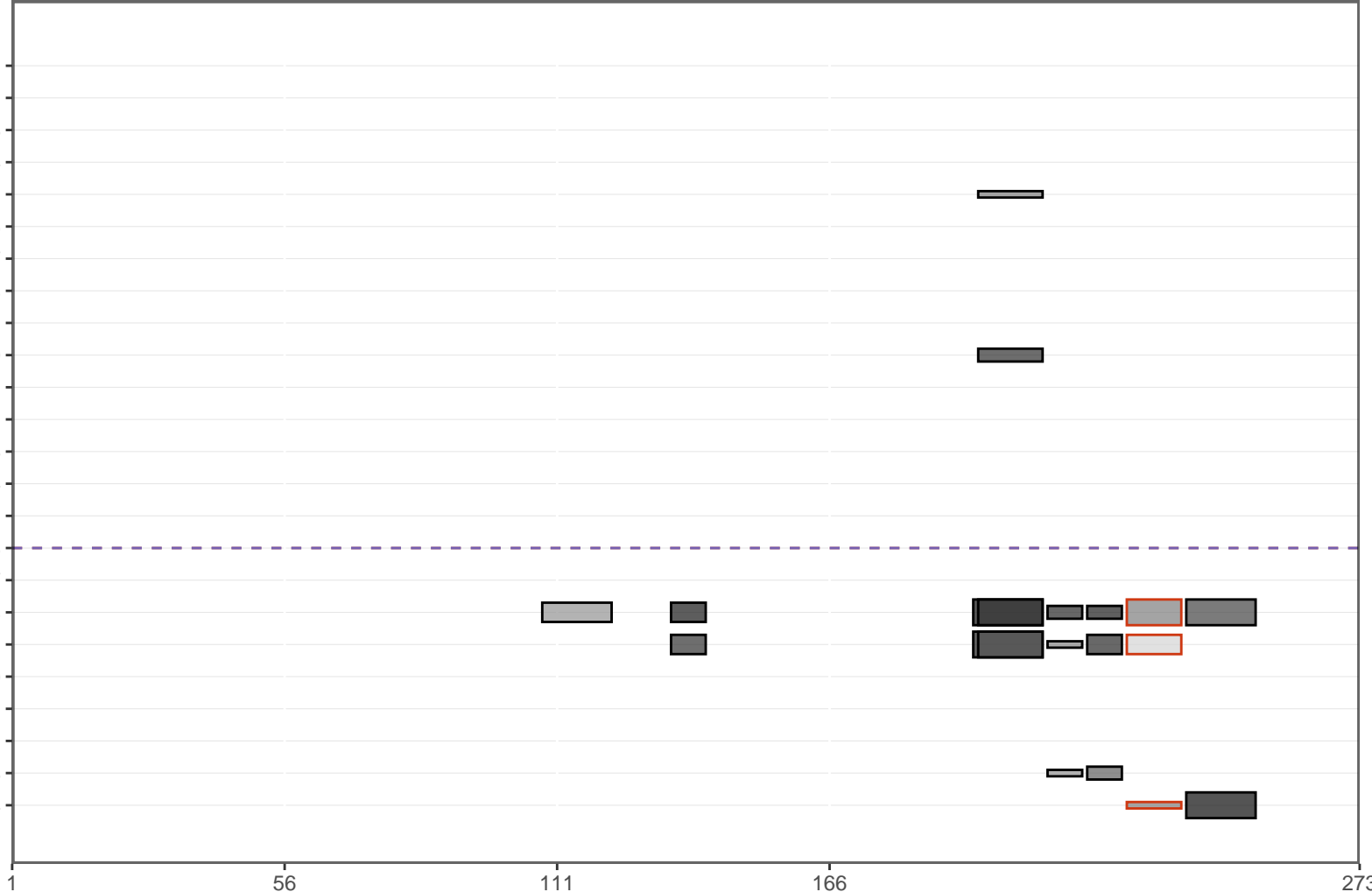
MW indication



Molecular weight



Gel Slice

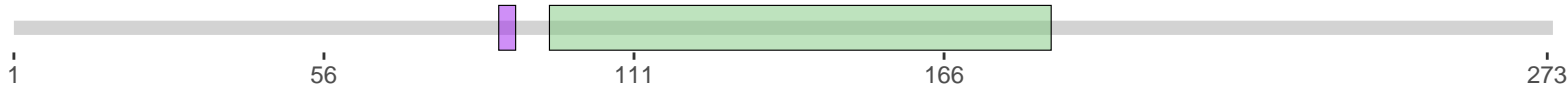


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

/KQFQELRSQLPDTRKLLVANNLTKVKEGTRWEALKPKGMKMNWALFVHSEEPALKPYRTFQKEKLEQNDFTGAVFEQKFGYGFPEEFKALELTPTRAIEYSGLLGLKGPASAVVGTIQAPRNLMVAKVWVKKLEEGGSGQ

NbL14g12380.1 psbP_domain-containing_protein_2_chloroplastic [MW = 28.01 kDa]

No. of times detected



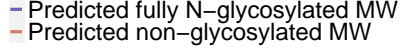
log(intensity)



Values from



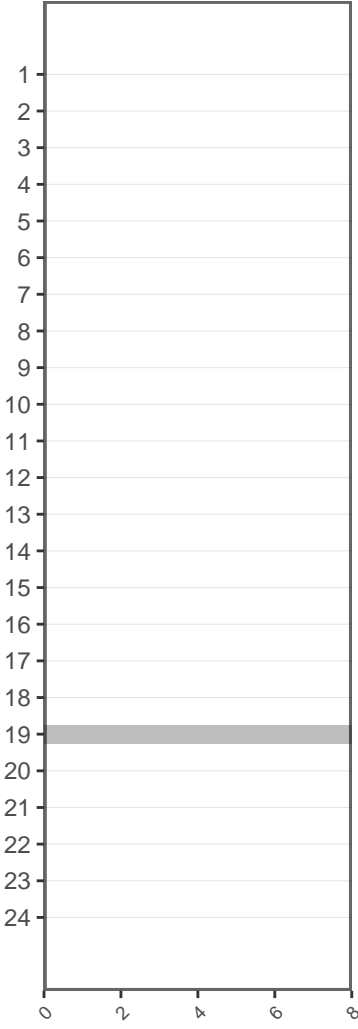
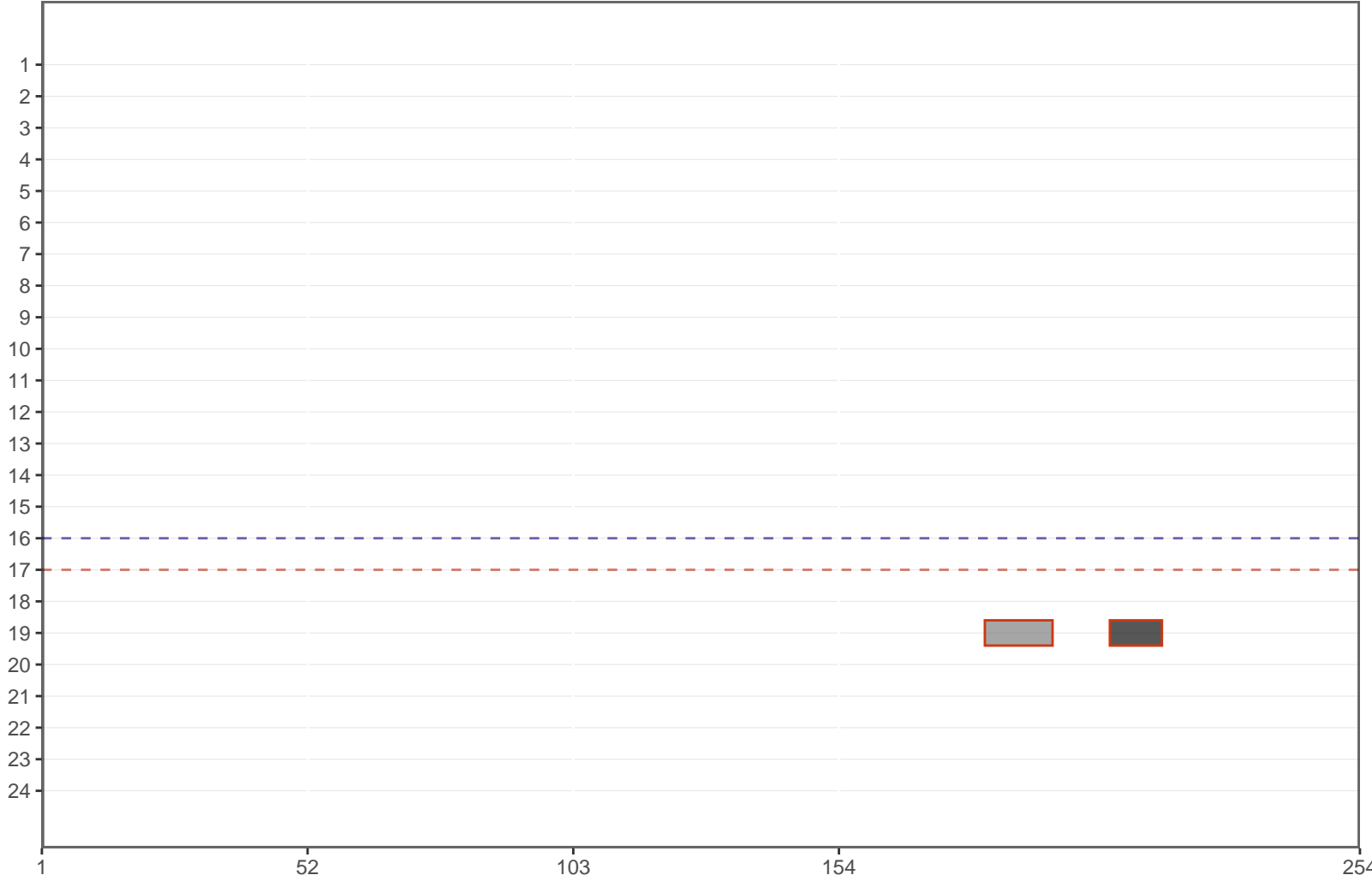
MW indication



Molecular weight

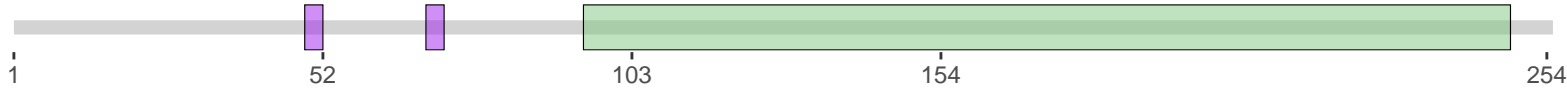


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KYDKAGATVLFQDANKGNNVGVVVPKVTLLSGFGTGFQFADKLLAEKRKESTKEAEVWVWERTGEGGLQVYEFYKIDSTRGGMKRVLEAFAFVAGSKVLLNIAHSDGLESPIDPVRIRNTLEQLHGFDTAPST

NbL14g12360.1 cytochrome_b-c1_complex_subunit_Rieske-3_mitochondrial [MW = 29.2 kDa]

No. of times detected



log(intensity)



Values from



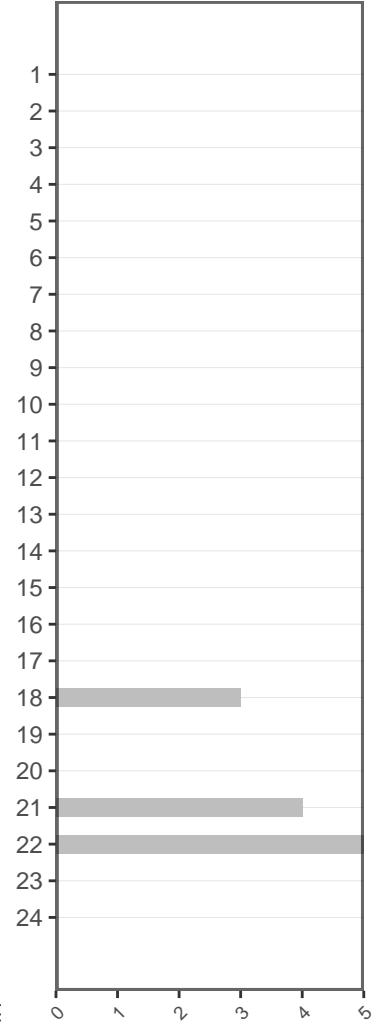
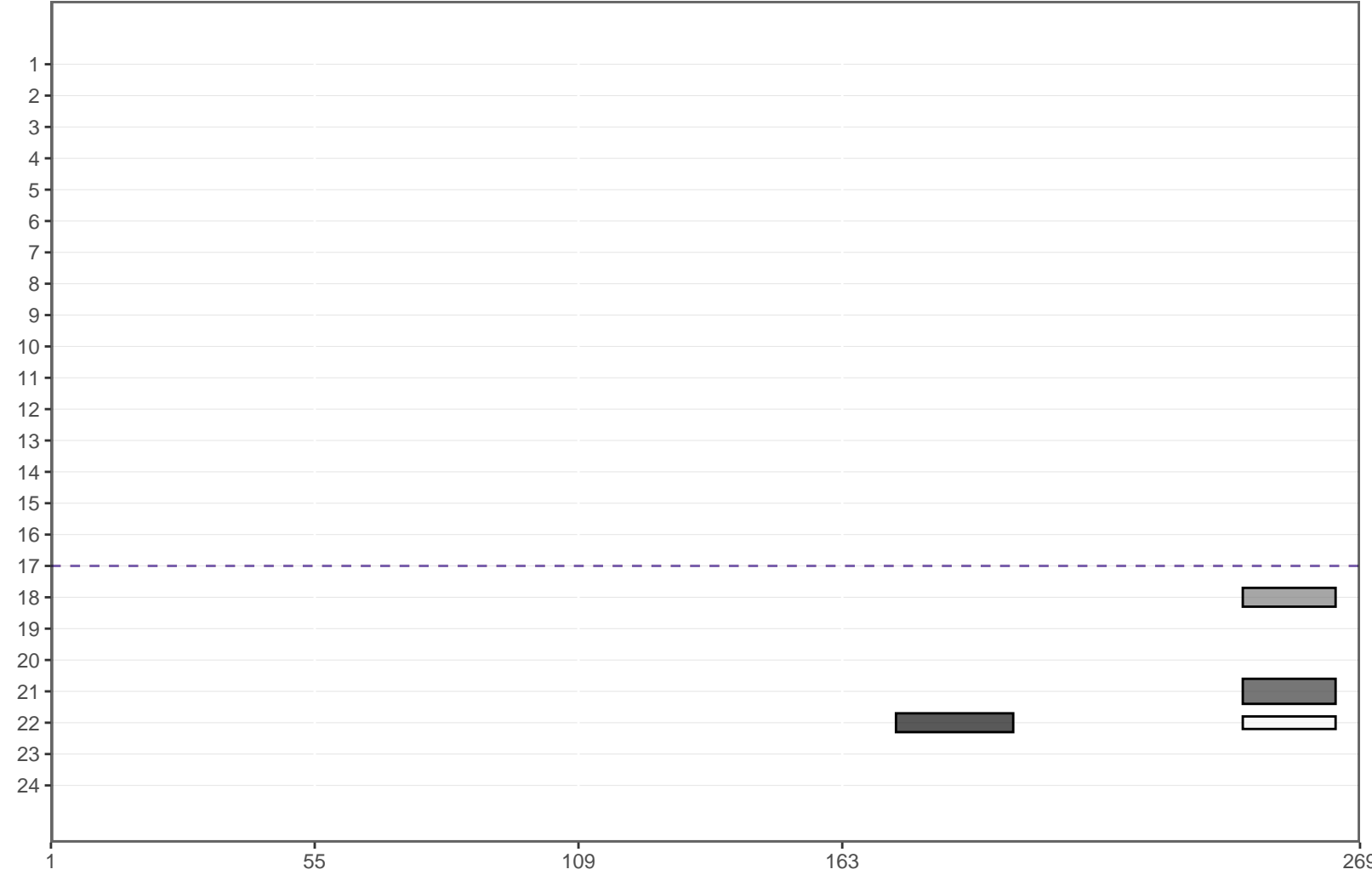
MW indication



Molecular weight

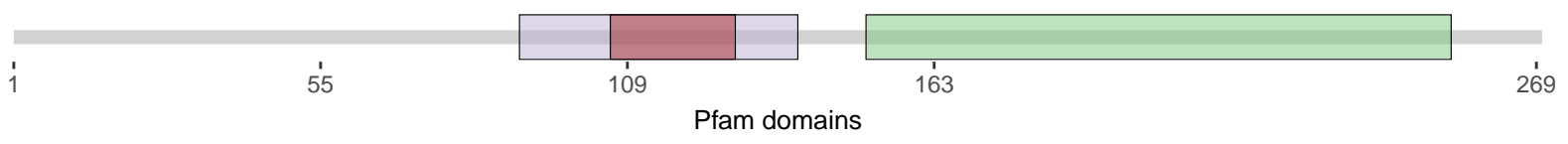


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILVRLILKLYLSMSASKDVALALASLEVDLSSIEPGTFTVWWRGKPVFRRRTDEDINLANEVDLGSRLDPQGDAAERVKVPEWLVVIGVCTHLGQIPLNAGDFGGWFCPCGSHYDISGRIRKGPAPYINLEVPTYSFMEENKLLIG*

NbL14g12350.1 glycine--tRNA_ligase_mitochondrial_1-like [MW = 81.63 kDa]

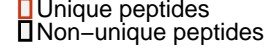
No. of times detected



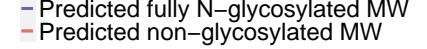
log(intensity)



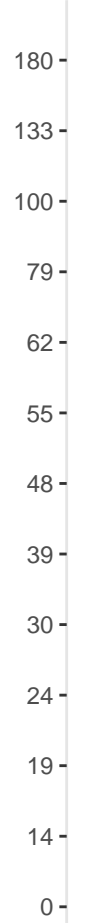
Values from



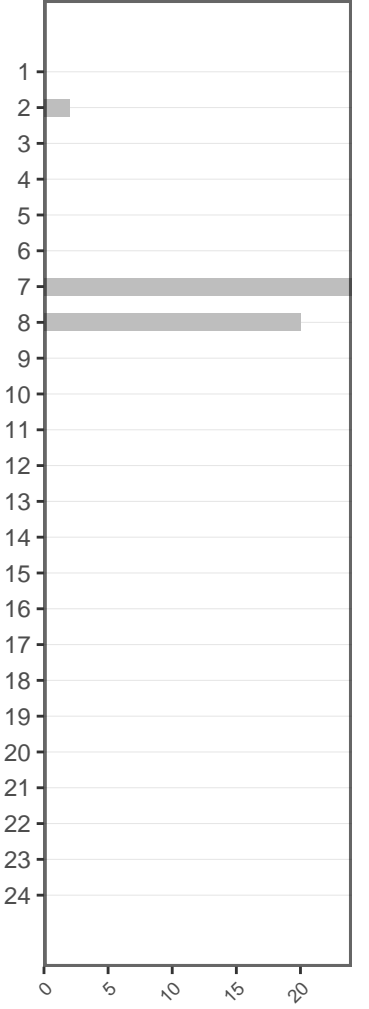
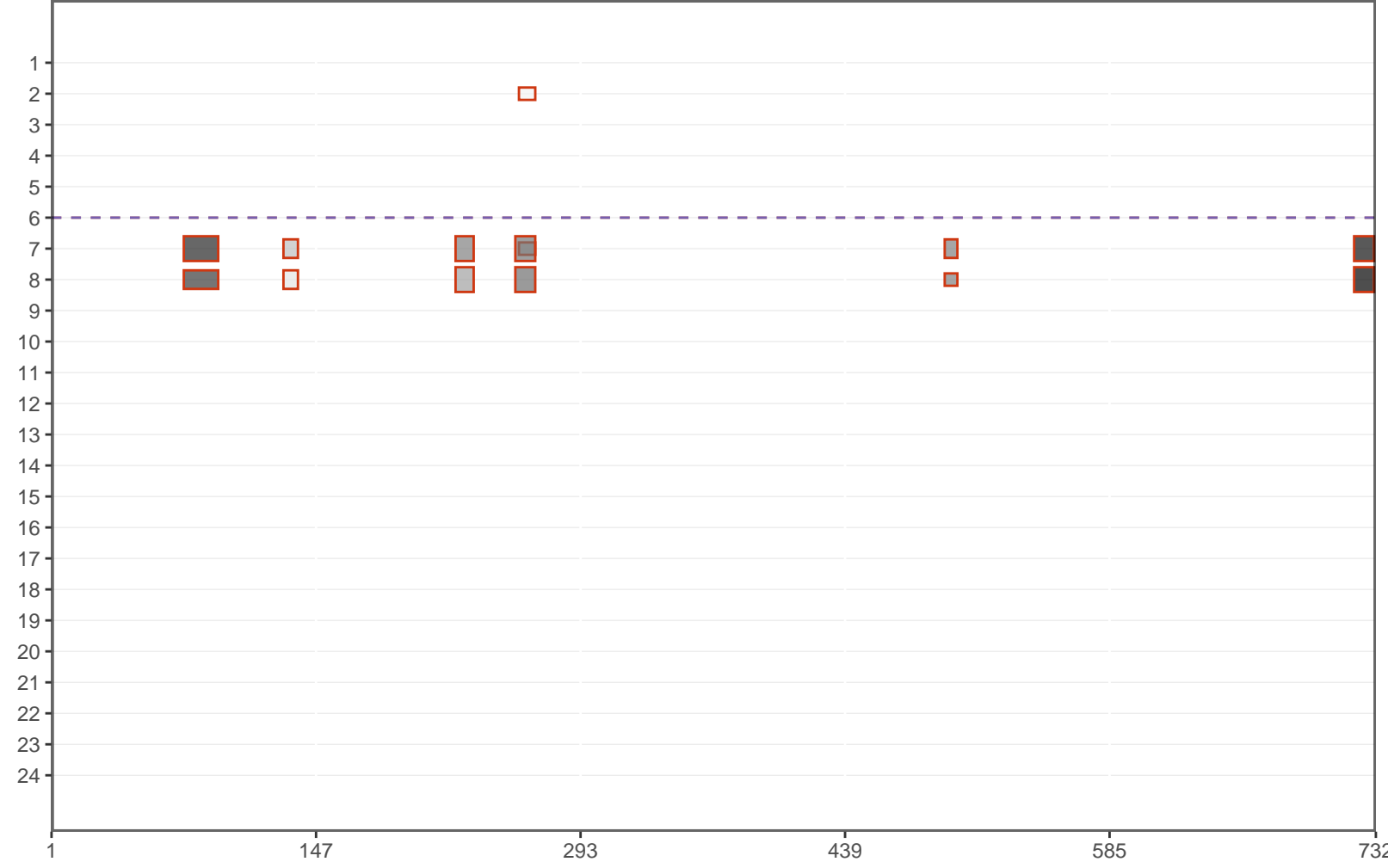
MW indication



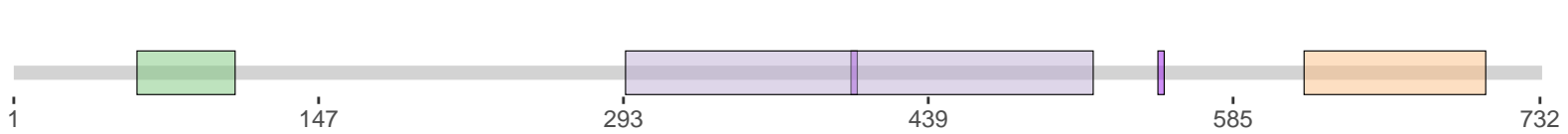
Molecular weight



Gel Slice

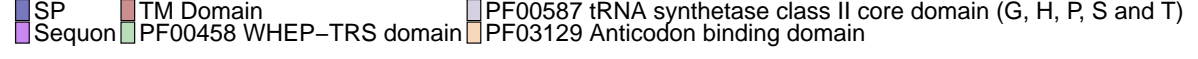


Protein length



Pfam domains

Pfam Description



Protein sequence:

HFVDPQDKSHPKFSDWANLEFLMFRDEQVSGGAKRLQLGSEAVSSGINNETLGYFGRVYLLFLRLGDKERLFRQHLANEMAHYAADQWDAIESSYGWIECGIADRSAVLRHASEKSESVAVLVAQEKFAPEVEKLVITPKIKELGLAFGRGNQKMVTEALEAMEEKVAMEMKADLESKGEVEFHVCTLGKNTIKKGMVBSIKKKKHQRVFTPSVIEPSFGGRINGLYEHHSFYTRPSKGGDEGLNVRFRPPLVAPIKGTVFFPLVQNGQYEEVAVLISKSLTAGIS

NbL14g12330.1 transaldolase [MW = 49.64 kDa]

No. of times detected



log(intensity)



Values from



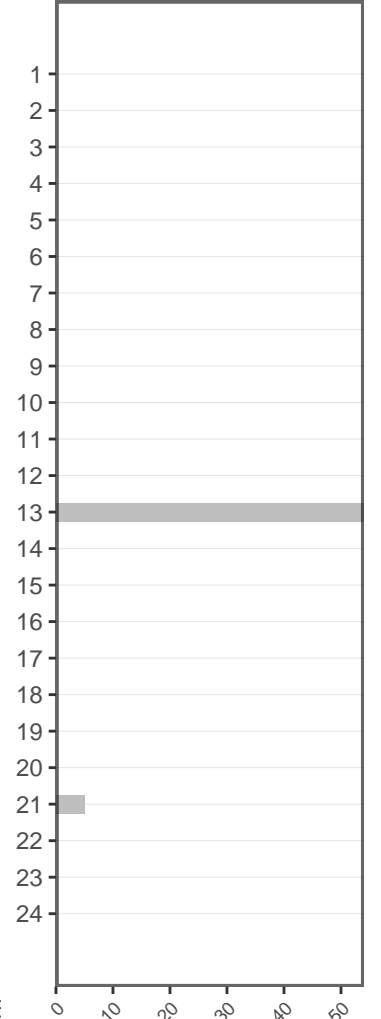
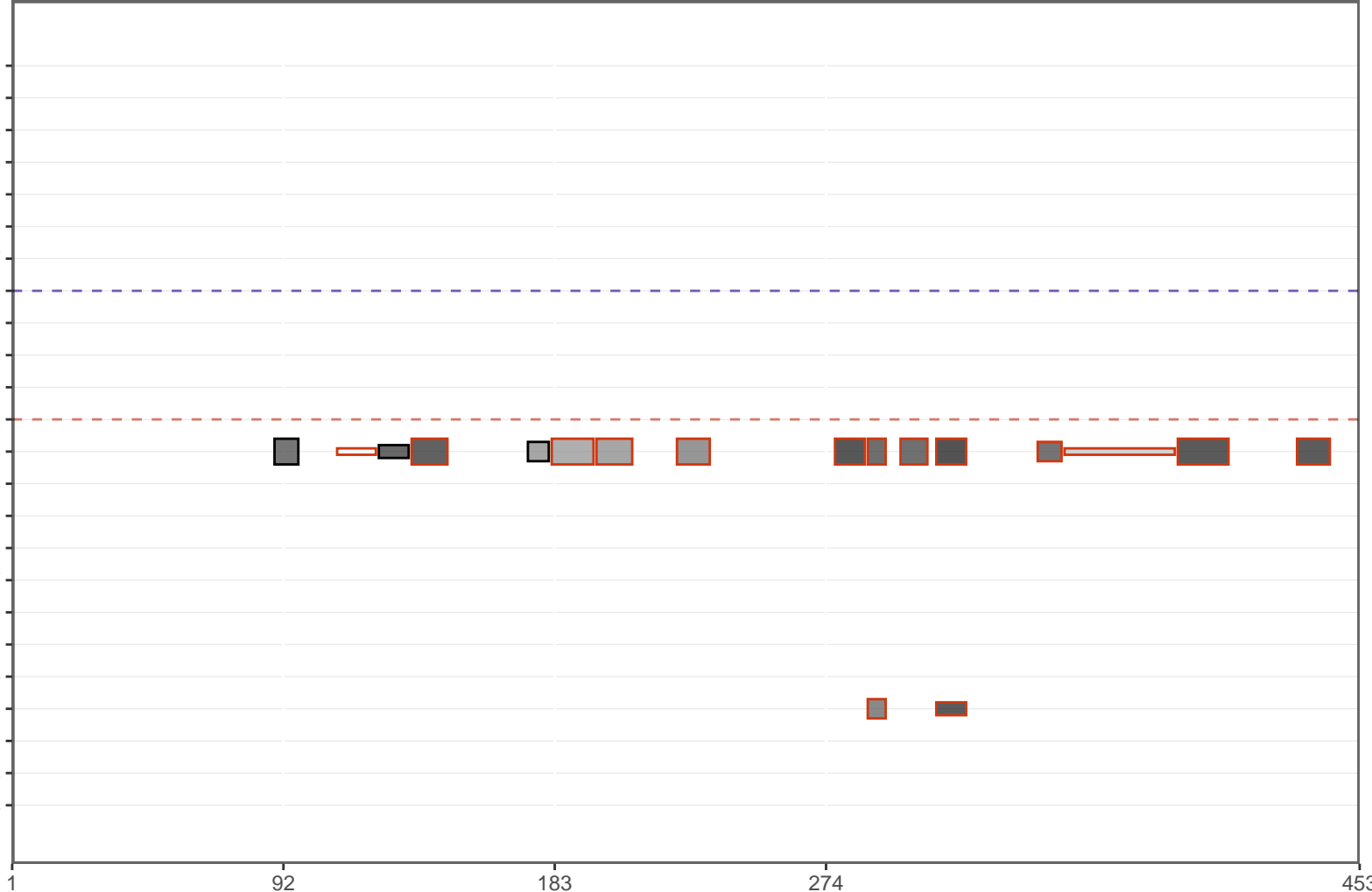
MW indication



Molecular weight



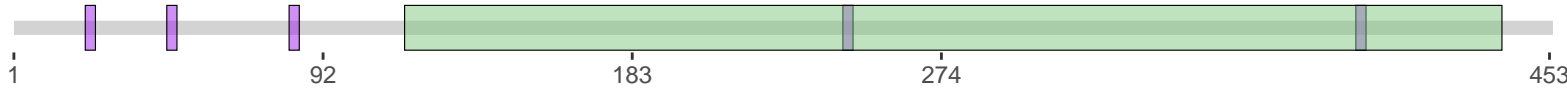
Gel Slice



Protein length

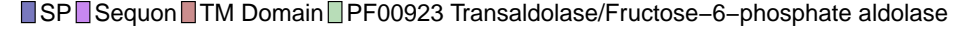


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LHKYVERSNYYIKPWATPQIPRSKEVLSGISVNTLFLSLARYEAVIQVLDGLEASGLSDLSRVTVSAFFVSRVDTLVDKMLEKIGTPEALDLRGAANAGAAALAYKLVQKFKSGPRWEALVKKGGAKKGRLLWASTEVKKNPVPDVLVVDPLHGPDVTSTMPDQALGAFIDHGSVARTIDENESEAEIGVSALEKLGIDWISFVSGQLLELEGVDGFKKSFDFLSDLSGKANTLKLVL

NbL14g12320.1 peptidyl-prolyl_cis-trans_isomerase_FKBP19_chloroplastic-like [MW = 27.82 kDa]

No. of times detected



log(intensity)



Values from



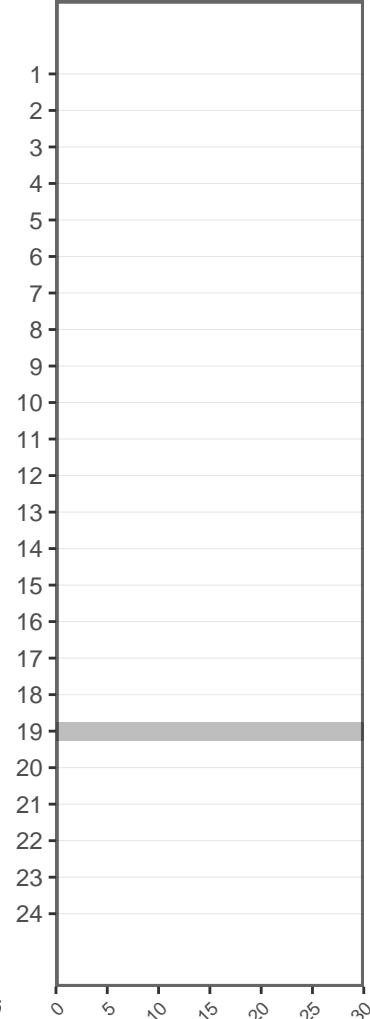
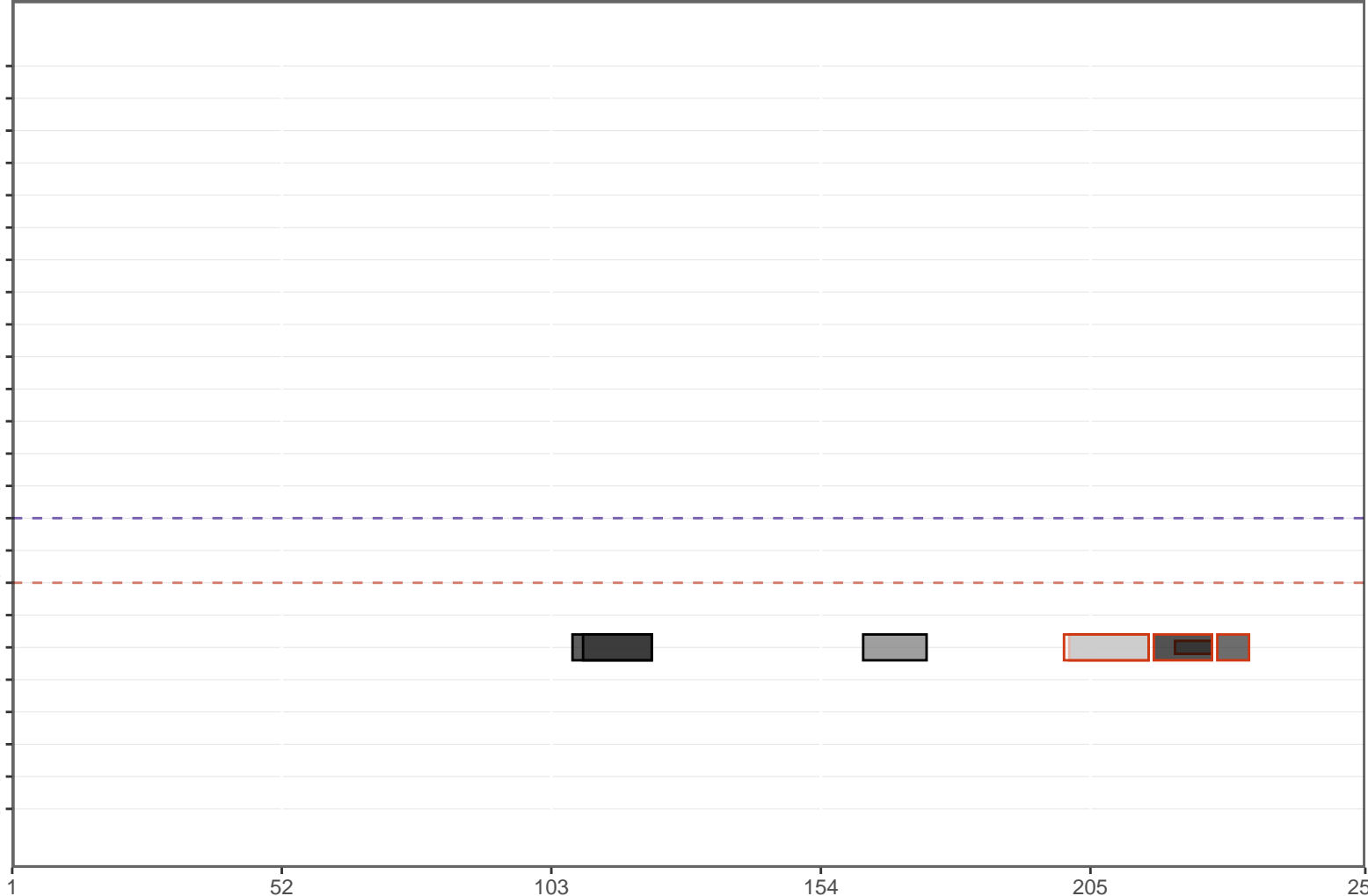
MW indication



Molecular weight



Gel Slice

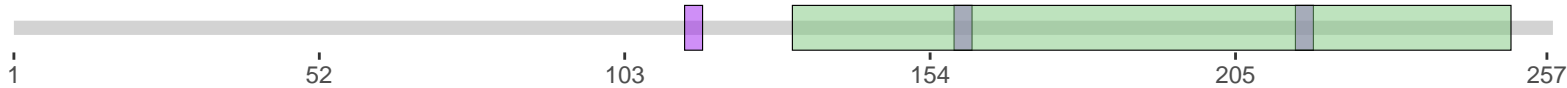


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

TQSGLOYKDLRYGSGPTKGETVWVDWDGYTYGYGRIFARNKTKGSGFEGDDKDFKFRVGSQGVIPFEEATGMAIGRRIVPELGYPNQYKTSRPRPTTFSGQRALDFLRNGSLQDKTLFLDIELKIVPK

NbL14g12130.1 pseudouridine-5'-phosphate_glycosidase-like [MW = 36.11 kDa]

No. of times detected



log(intensity)



Values from



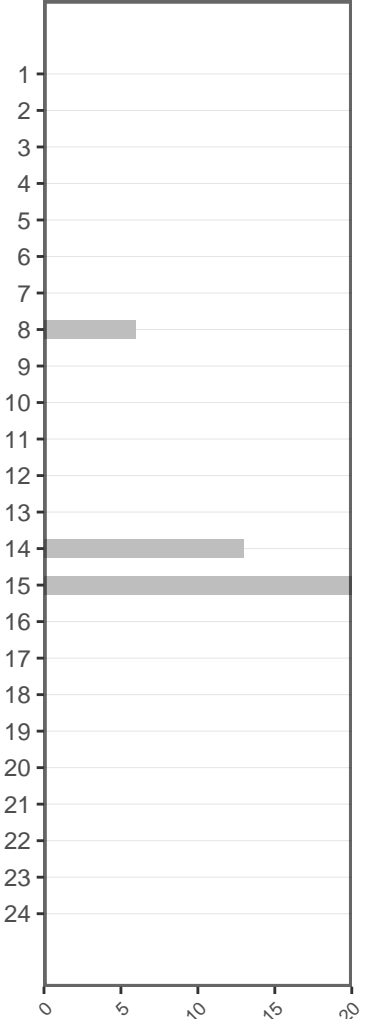
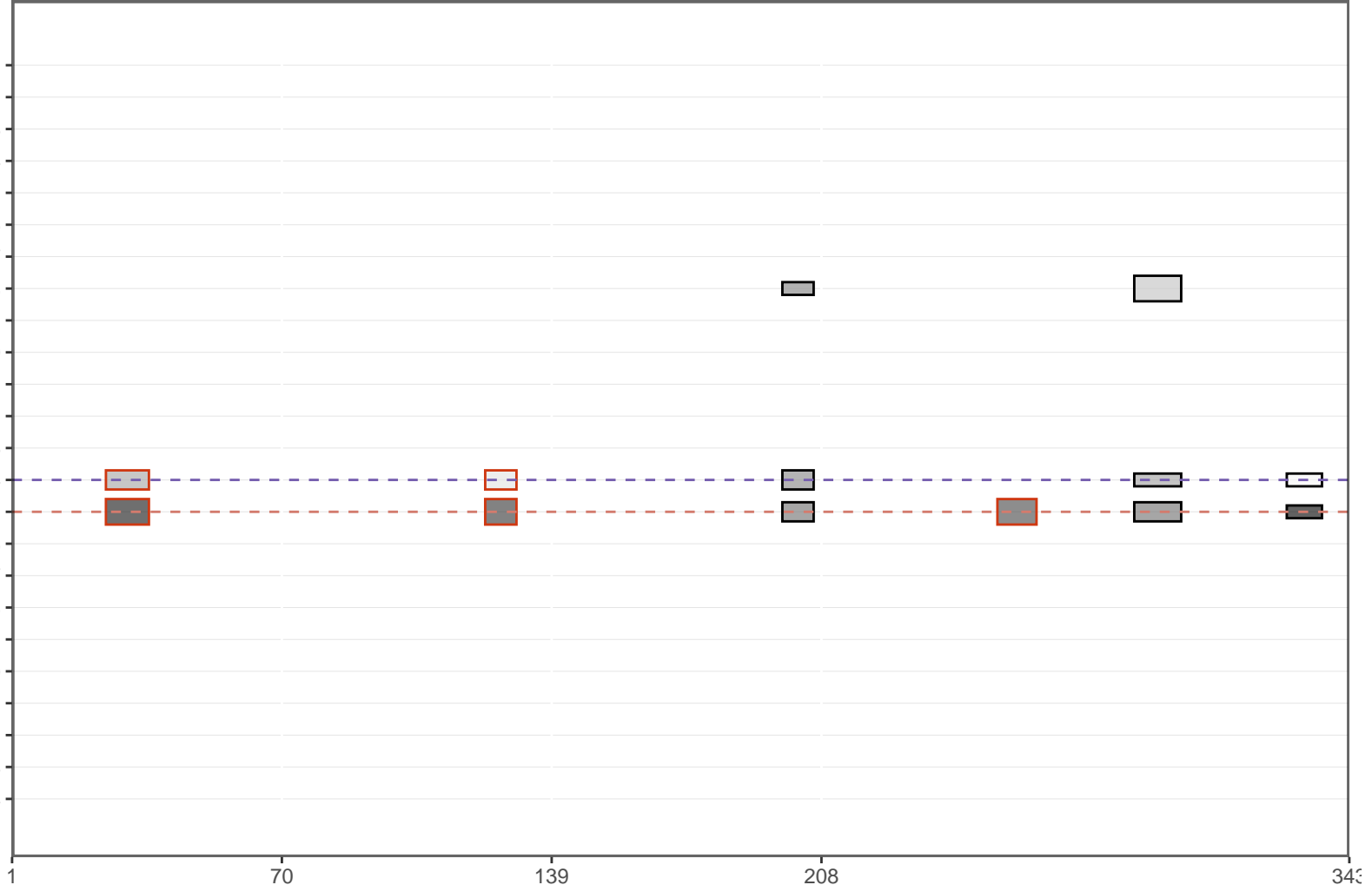
MW indication



Molecular weight

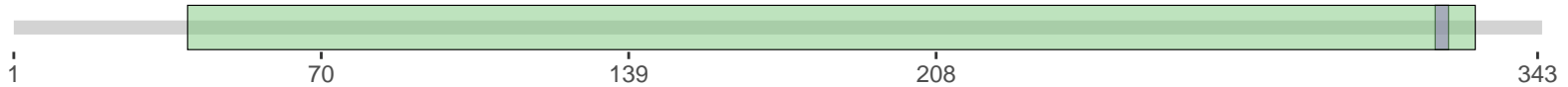


Gel Slice



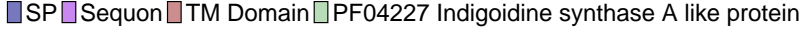
Protein length

Peptide counts over 4 repeats



Pfam domains

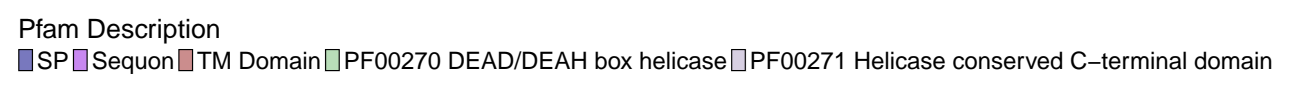
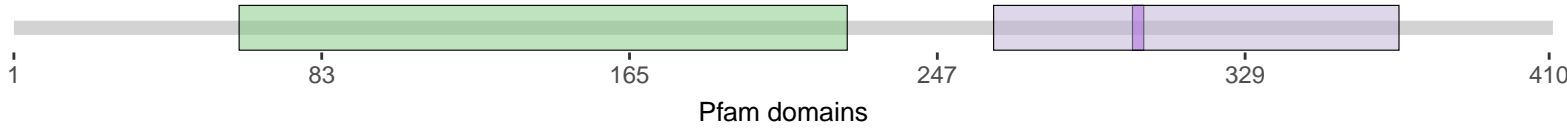
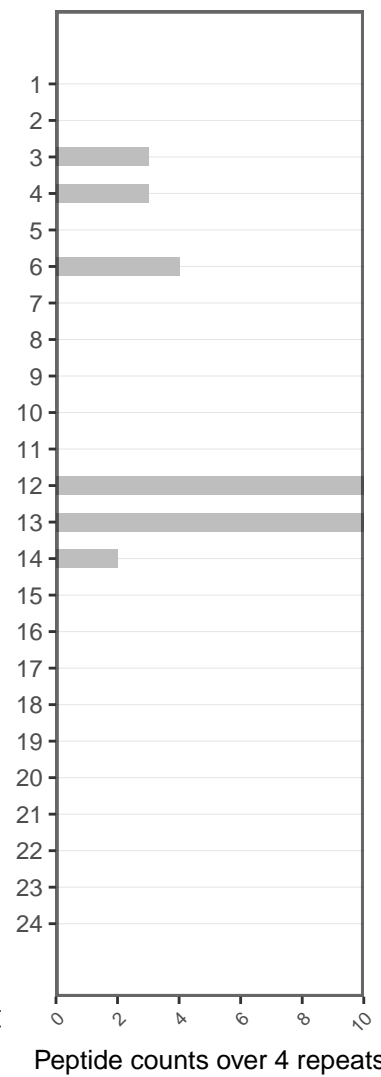
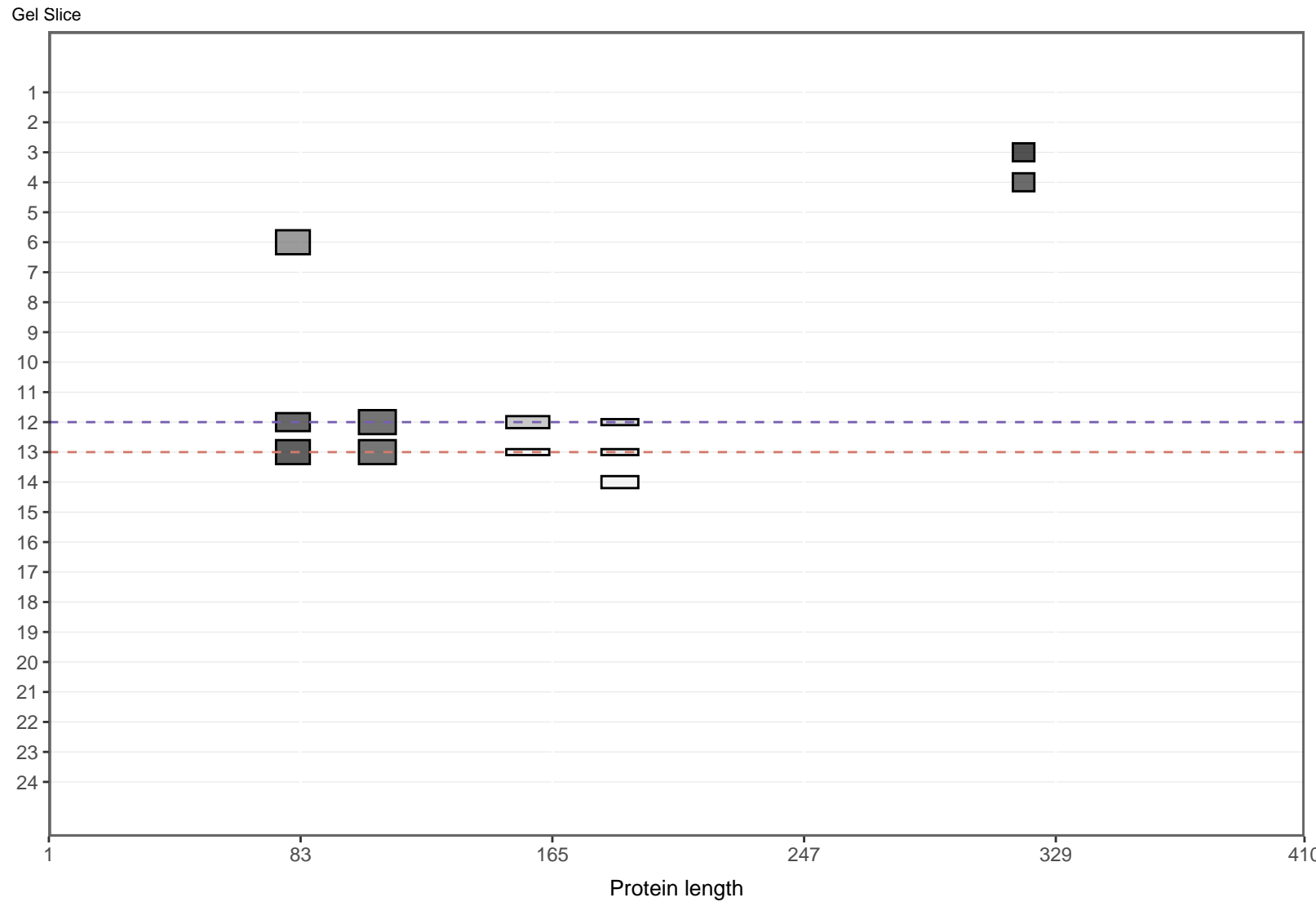
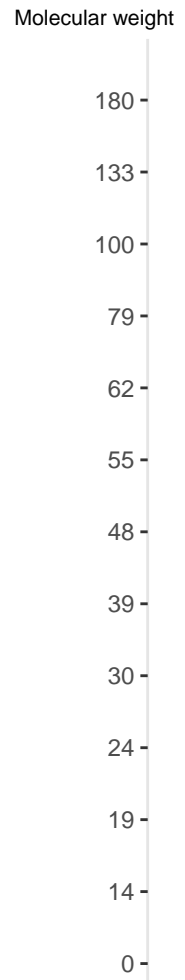
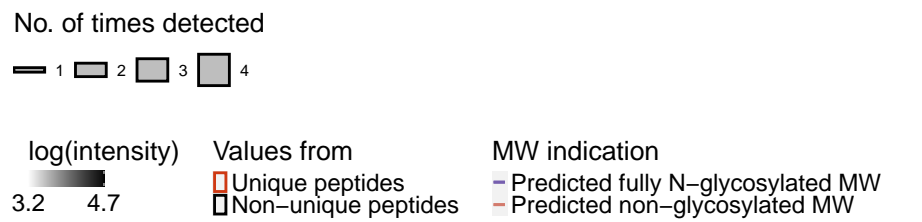
Pfam Description



Protein sequence:

IVHRHIGENTLDSISDTELGGTPVAIVSAGVSKBILDFRTELELQRTVVAAYGTDFPFFFTQTSGGKAPRVESPEHGCARVMDANRLEKRSGLIAVPIPREHSAGSHLIESAIGQALGEAREKIKSGNAETPFLLARVNELTGGASLASHVKNNAASVGGAKIIVSLAQLEKHSGRF

NbL14g12100.1 eukaryotic_initiation_factor_4A-3-like [MW = 46.04 kDa]



Protein sequence:
 .SRGFKDQIDYDYRRLPPELGVVLSATLPNEILEITSKFMFDPRVRLVKRDELTEGKGFVVAWEKEEWFDFLGDYDILTTQAVFQNTKRKVDVLTSKMRENNFTVSSMHDGMPQKERDAIAAEFRGGTRVLTITDVAWARGLDVGGVSLVINYDLNPNRELYHRIGRSGRFRKGVANFVKSDDKLRDEEGYVSTQIDEMPMNVADU

NbL14g12070.1 uncharacterized_LOC107823533 [MW = 25.31 kDa]

No. of times detected



log(intensity)



Values from



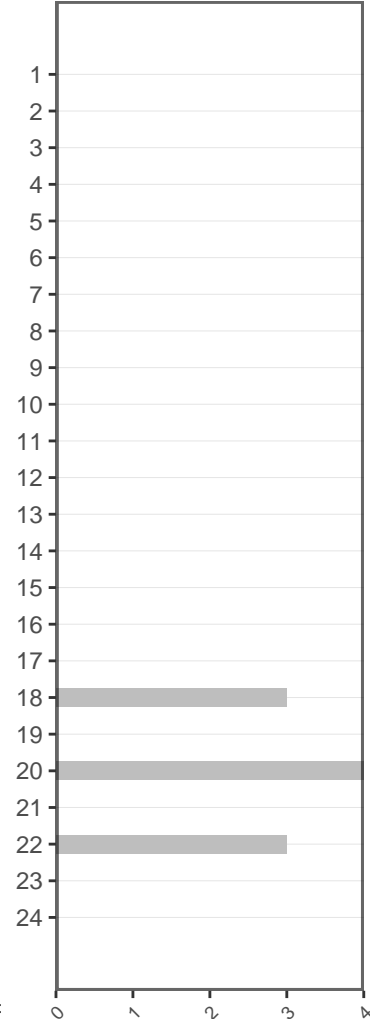
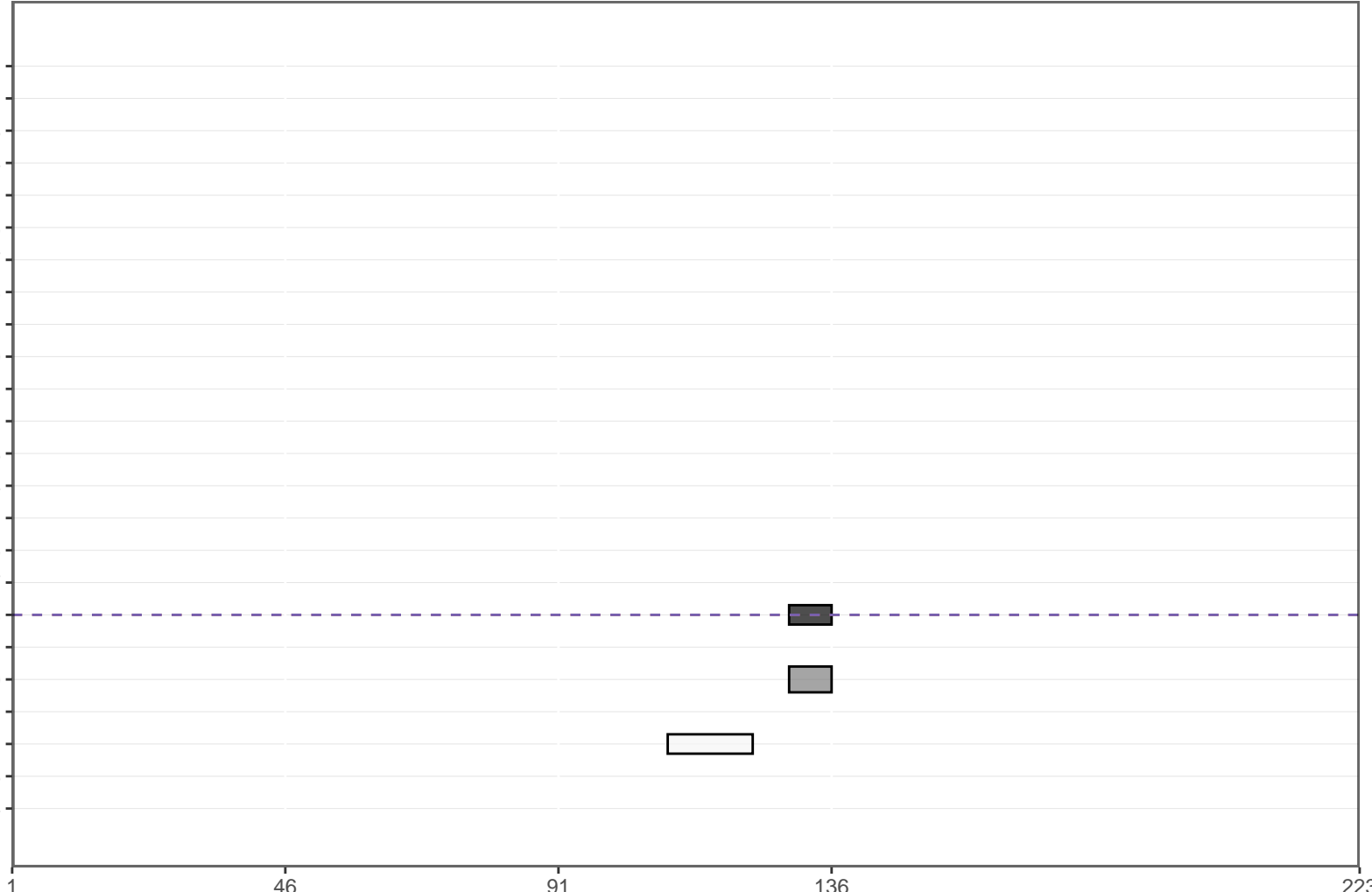
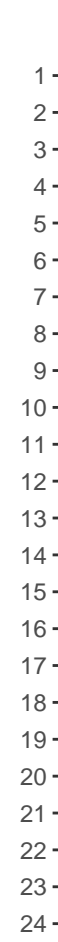
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

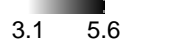
RRNLERIVGRDSSAFSGIDLAALIRNKYGRBYDVLKKEFMGNLALNVMWKYRGRSPLTEEEYLLRLDDVANTLKGWGAVSHVRNLSLEKVKRPRIGKAVSIFDMDESGGRANEWYK

NbL14g12050.1 histidinol-phosphate_aminotransferase_chloroplastic [MW = 46.28 kDa]

No. of times detected



log(intensity)



Values from



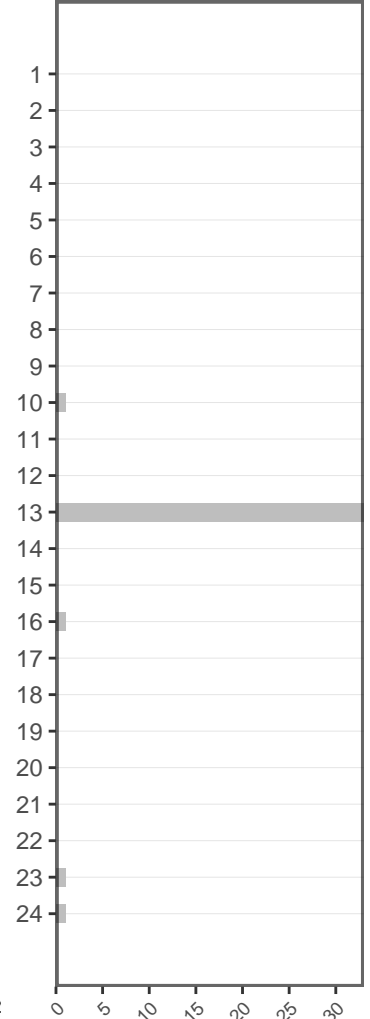
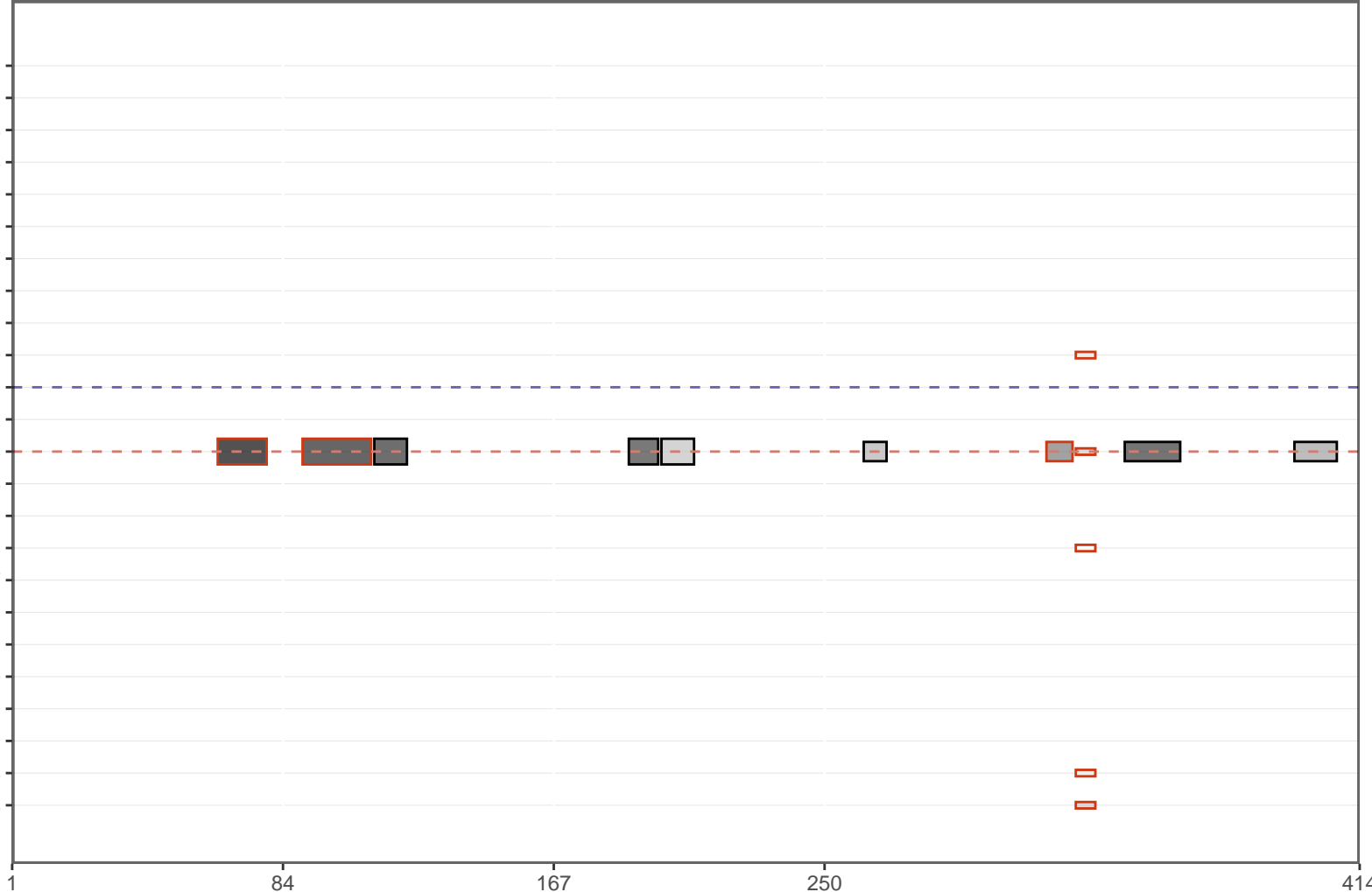
MW indication



Molecular weight



Gel Slice



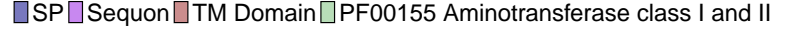
Peptide counts over 4 repeats

Protein length



Pfam domains

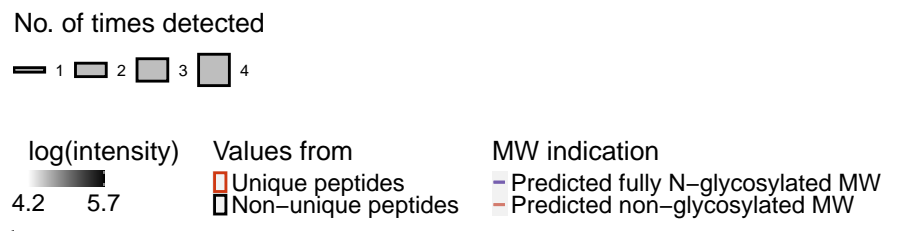
Pfam Description



Protein sequence:

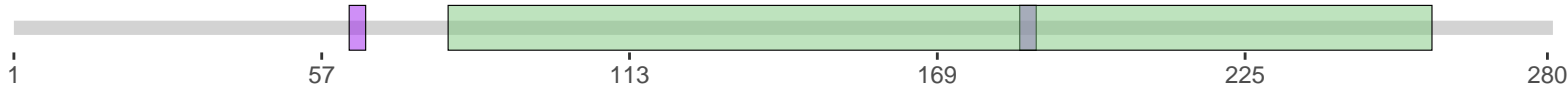
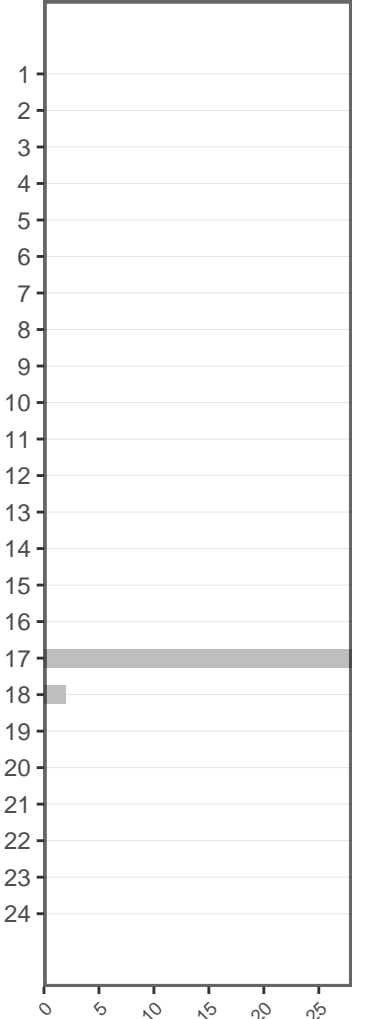
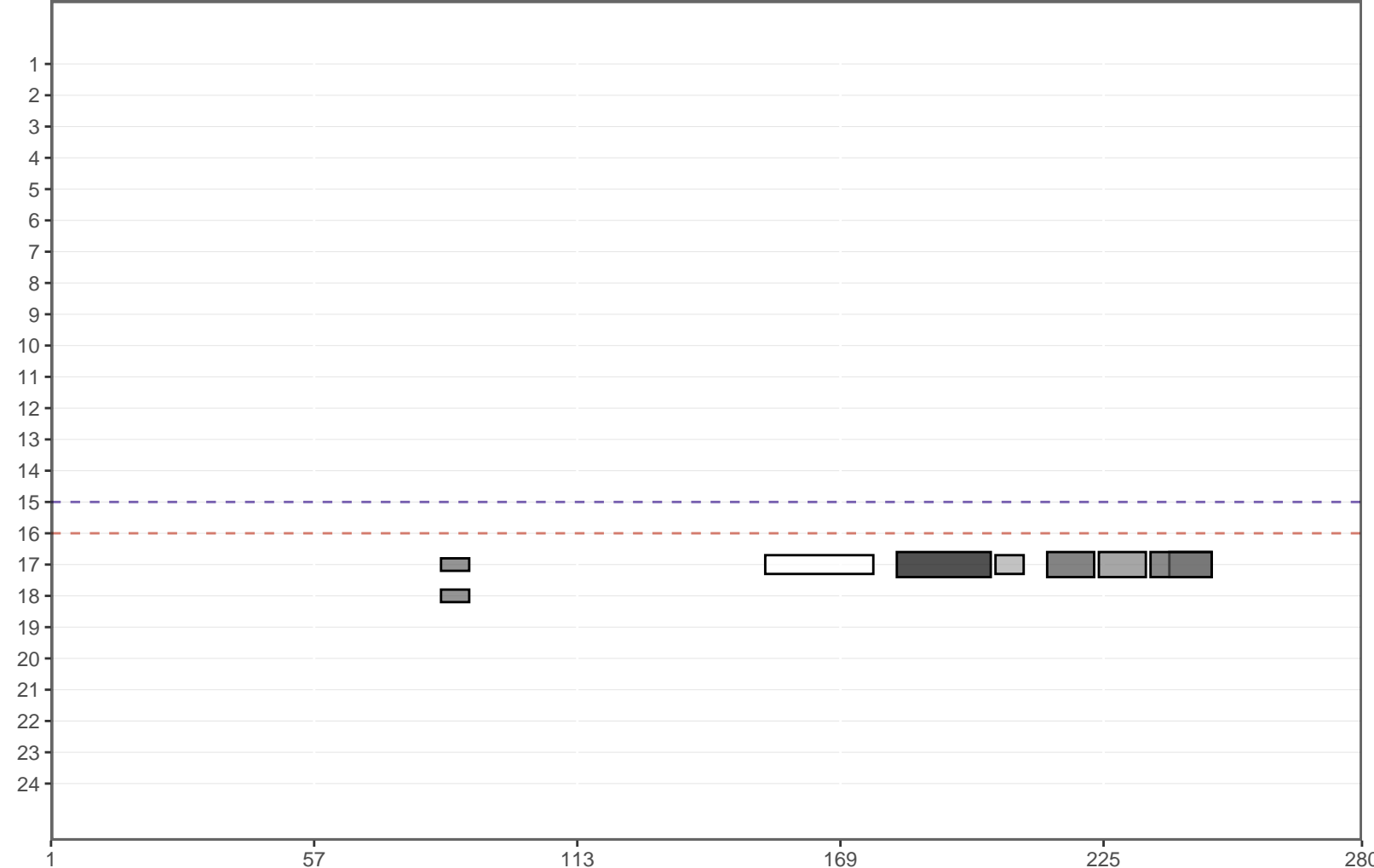
SLDVERIAEVVEHEKPKGIFLTFRNIPDGGSHDDFTLEILDPLILVLDVAVVDFSGMSEKMMVWKKHLENLIVLRTFSKRAGLAGLRVYGAFFPMSEIEFLWRKQDPYNSVAEVAACAALKNPVLENVMMALVGERERLFLNLLKEVFLDPYPSYNSFLGKVTSGMDANKLKEADLTMGVMRHYNSEIKELGYVRRVRSVQKPEHTEALMKGLKHFV

NbL14g12010.1 ATP-dependent_Clp_protease_proteolytic_subunit_2_mitochondrial-like [MW = 30.99 kDa]

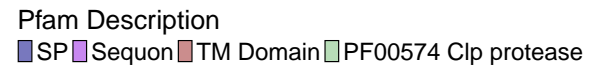


Molecular weight

Gel Slice



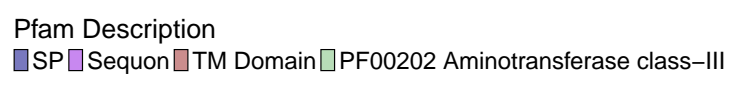
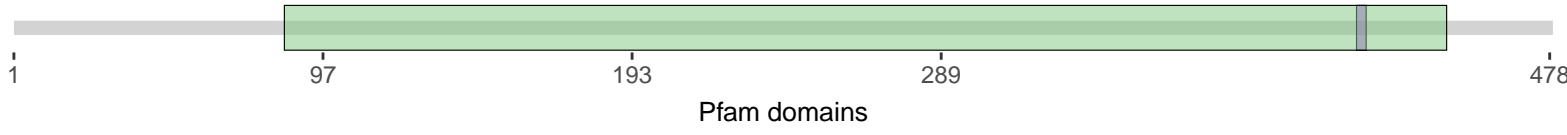
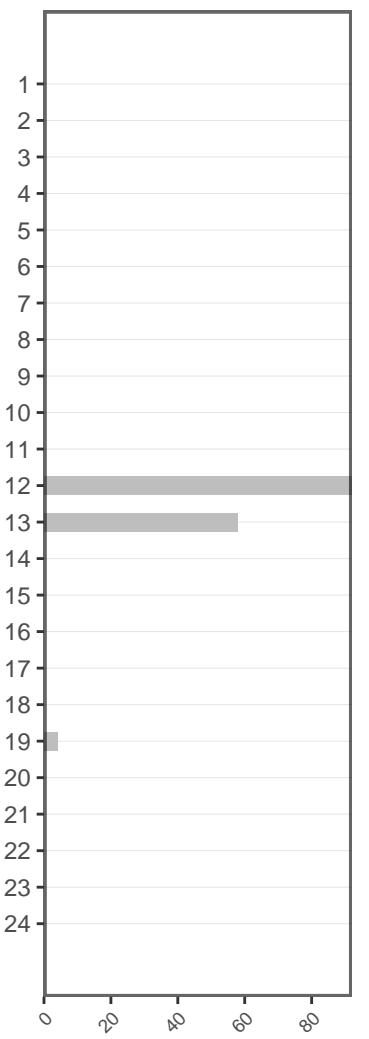
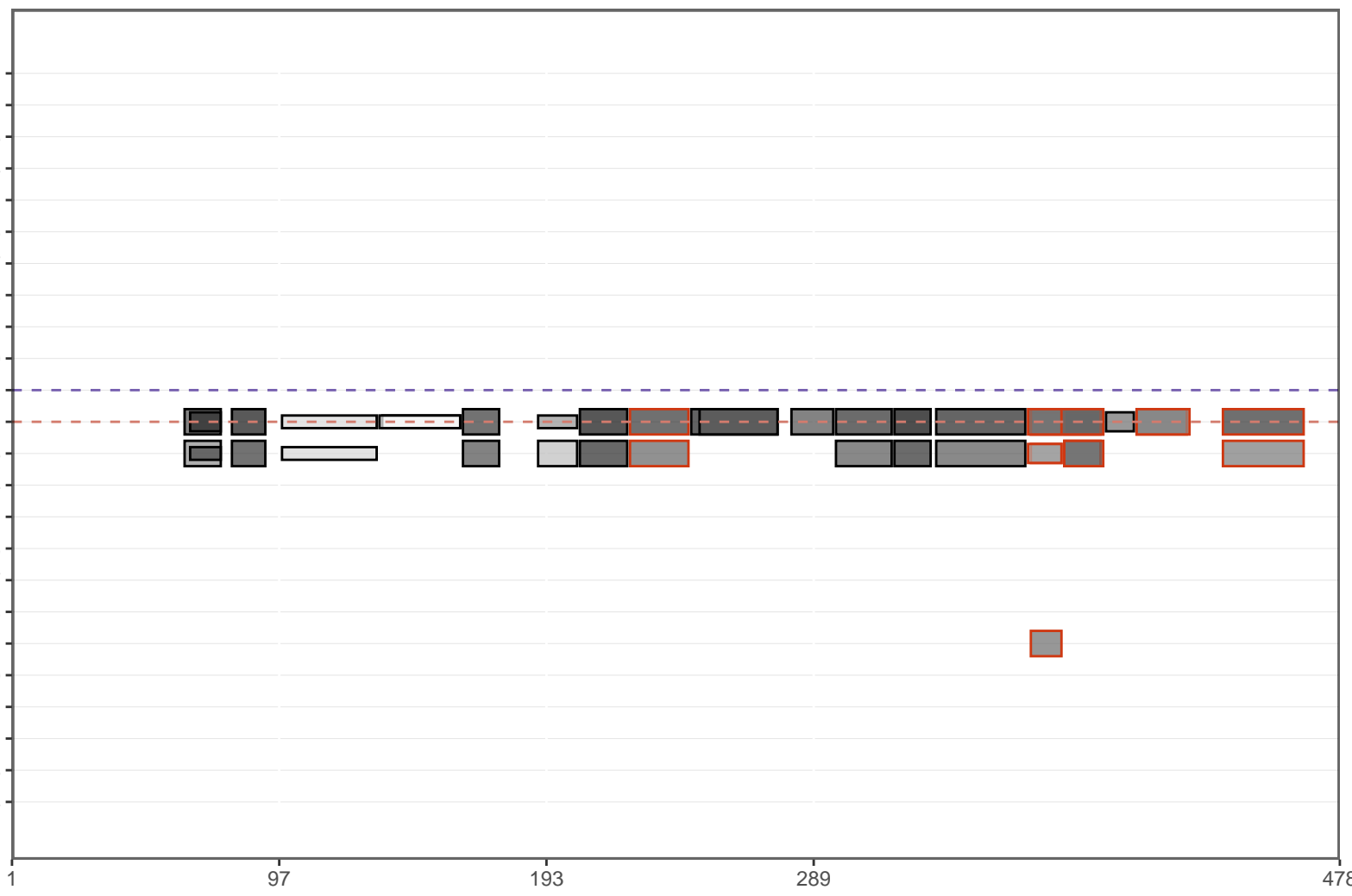
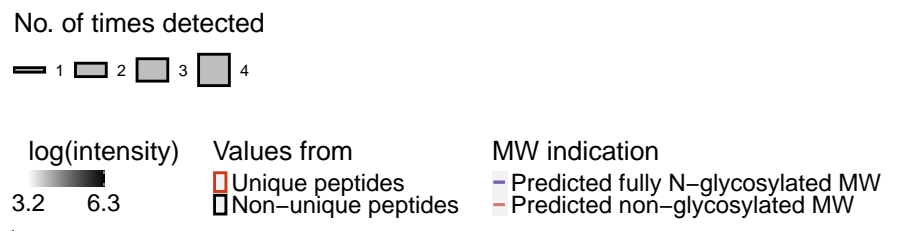
Pfam domains



Protein sequence:

IMVLSNPGGAVTVGLANDTMDQHRSPHTICLGGAAAMGSLLLAAGAKGERRSLPNASVMHQPSGGYSGGAKDLTHTKGVRVWDTLNDLWYKHTGGQIEIKKIMDRDYFMTPEEAKKEFGIDEVIDERPMALVTDAAWANEAKKEKGGP

NbL14g11940.1 glutamate-1-semialdehyde_21-aminomutase_chloroplastic [MW = 50.98 kDa]

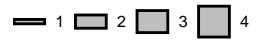


Protein sequence:

ITDITLTPYNDISAWESLFRKHKGEVAHLEPVPVGNAGFRQPNPDLAARWIKENDALLFDEVMTGRFLAYGGAGEYFGTDLTLTKIKGGGLPVGAYGRRDIMEVAPKGPVAGTLGSGNPLAMTAGHITLKRLOGPQTVYDYLKIKITGELTQGLGAGKTKGHAMCGGYRGMFGFFFAEGFPVNFSDAKKSDTEKFGFRVVRGMLEEGVYFAPSQFSEAGTSLAHTSEEDKQRTVATAEKVKKP

NbL14g11700.1 probable_leucine-rich_repeat_receptor-like_protein_kinase_At1g35710 [MW - SP = 62.93 kDa]

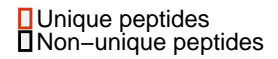
No. of times detected



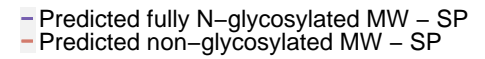
log(intensity)



Values from



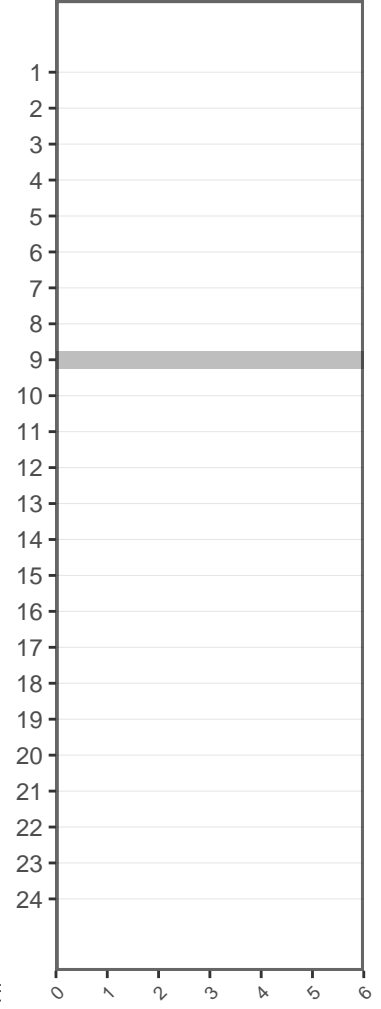
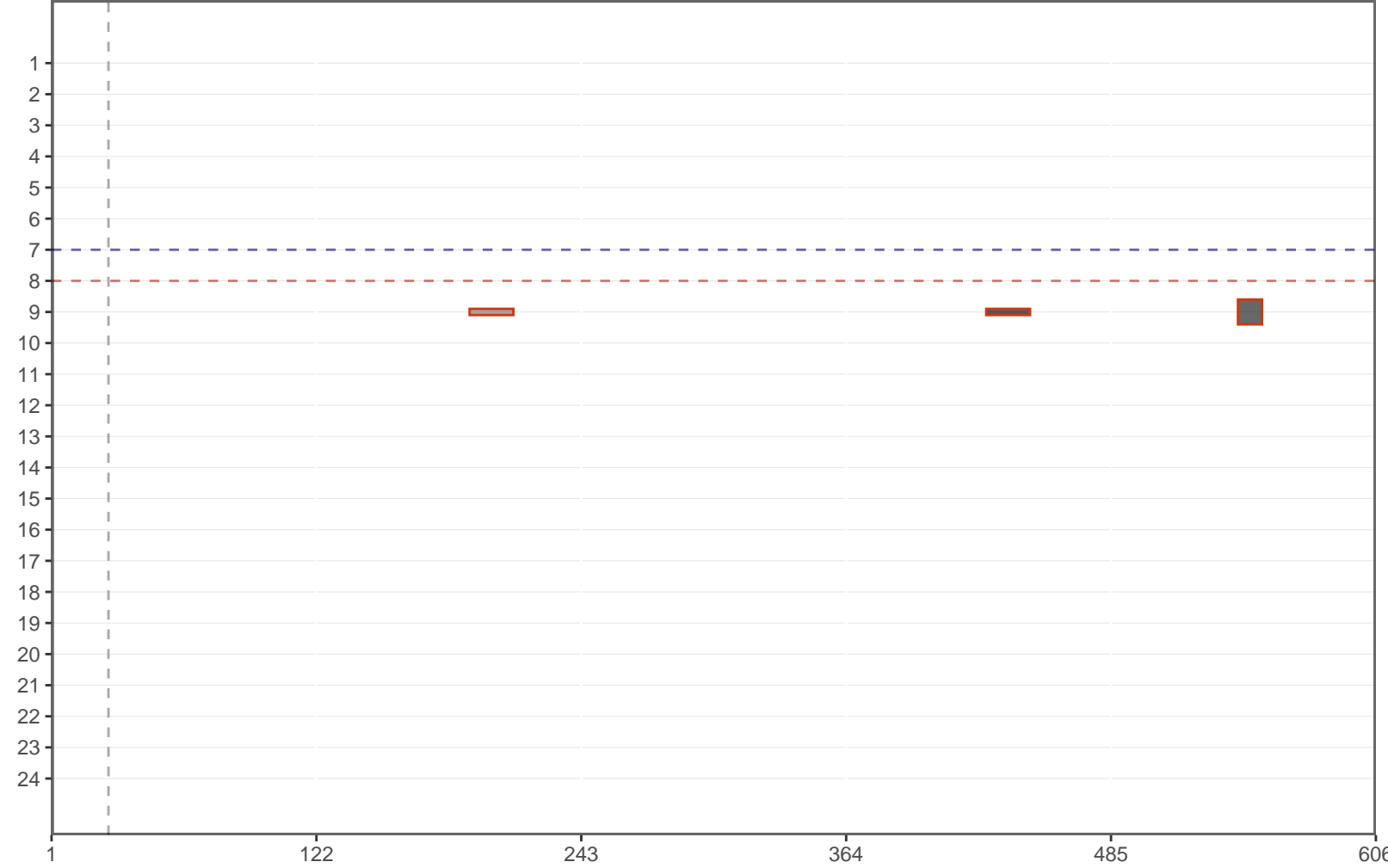
MW indication



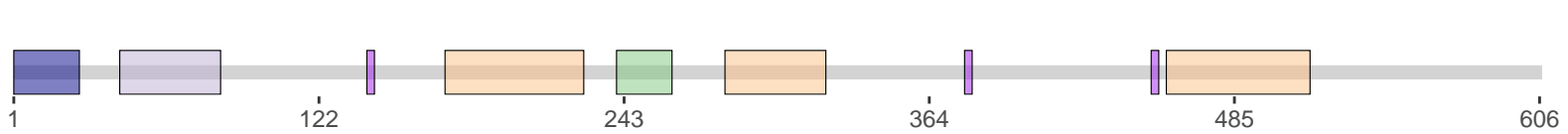
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

LTSLSLSFNKLTCQPEESAGLPHNLWSELGRNLSLDPPLPAFSGNLPALLSIDLGVNFFNLGTVFDWIRNRELSDVNLAGGKLRGALPNFTRPDGLNSIDLSNFFDTGDSNFFARMSSLSGAKASINQKSDVALKLPDGSLSLHSHNGLFGLSKMLSNKTSKFLVEDVSNNGLSGNPEFSSGLNKKVNLNLSNRIRAGDPTSDISNLDKLERLDPRNMGITPIGLGSLKLEWLDLSNKGSKPEGLLGEELRHNFRANRLGGEIPDGRPYNFFMAAYAHNLCLCGKPI

NbL14g11690.1 40S_ribosomal_protein_S26-3-like [MW = 14.36 kDa]

No. of times detected



log(intensity)



Values from



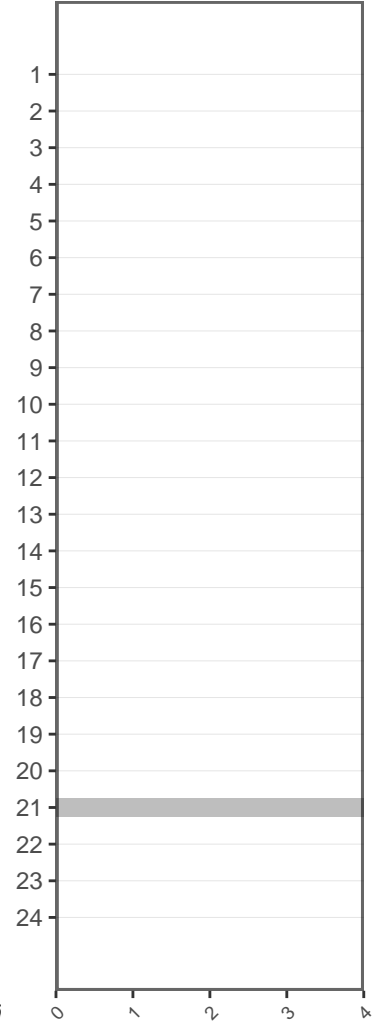
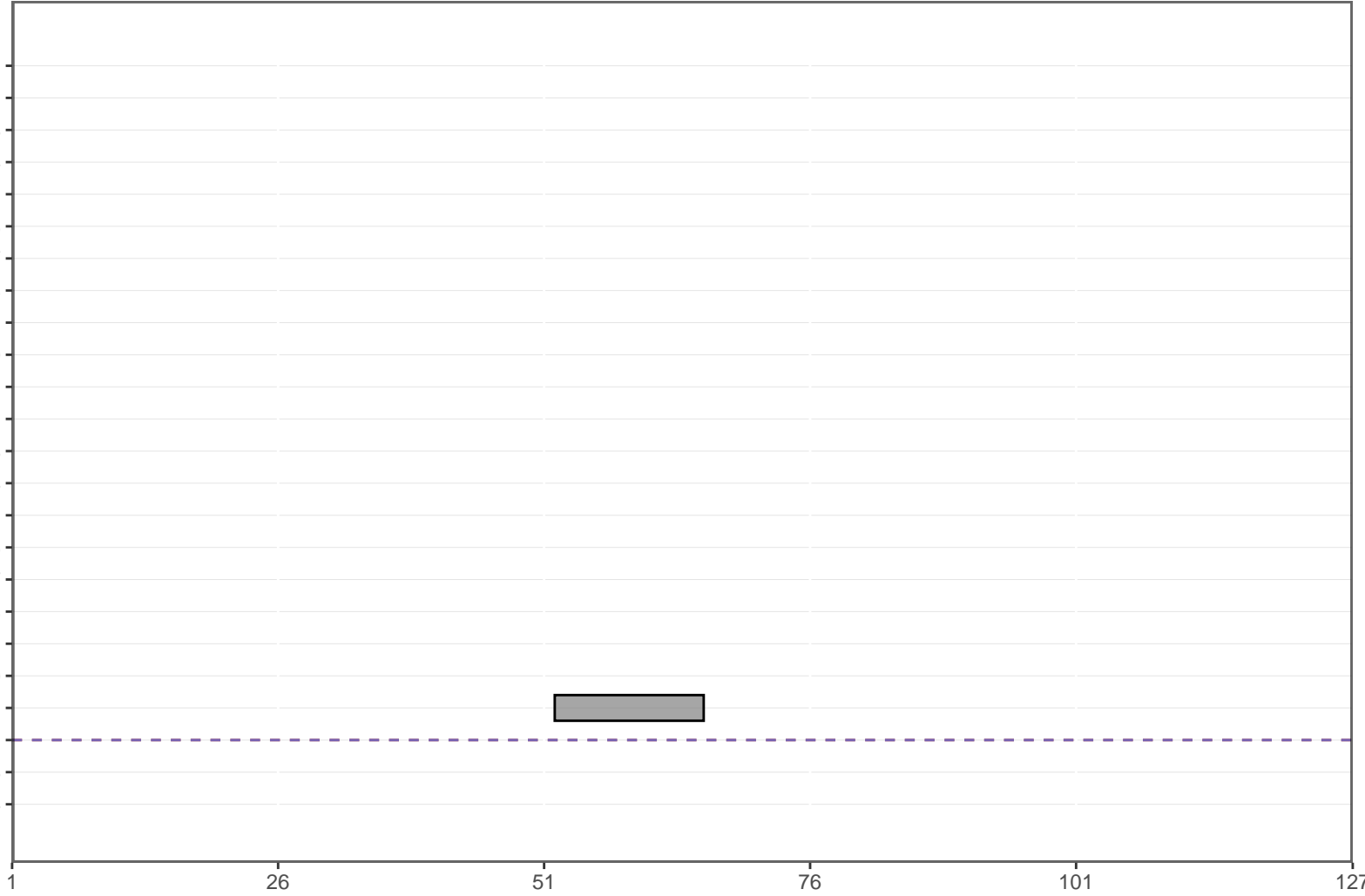
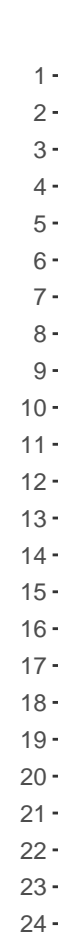
MW indication



Molecular weight



Gel Slice

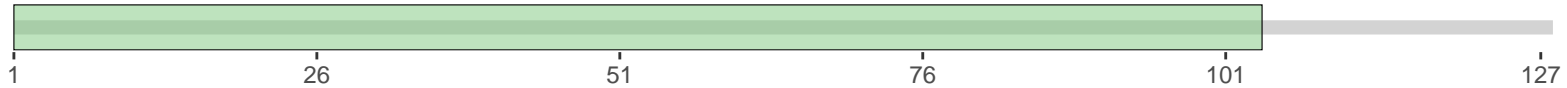


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

RDVQECACAFELYLTPKLYLKMGMQVCSGAHSHKVRVRSVTDHRRVREPPQRFRRPRDDAPKPGQAFRRMGAFARAT*

NbL14g11680.1 uncharacterized_LOC107810722 [MW = 21.15 kDa]

No. of times detected



log(intensity)



Values from



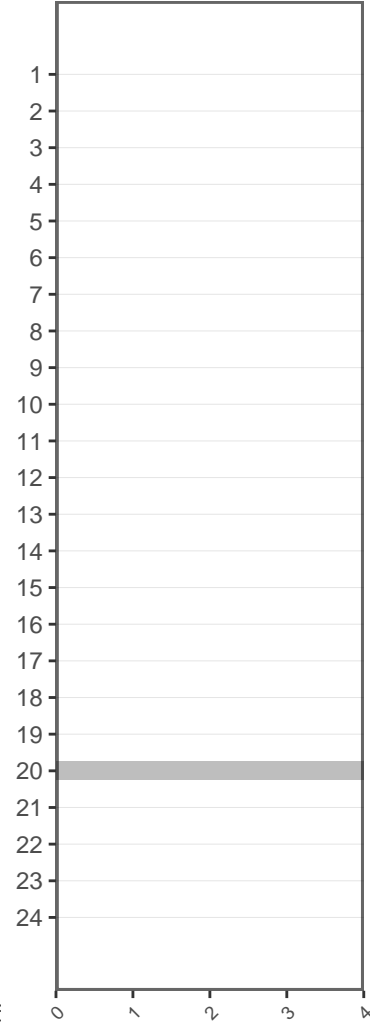
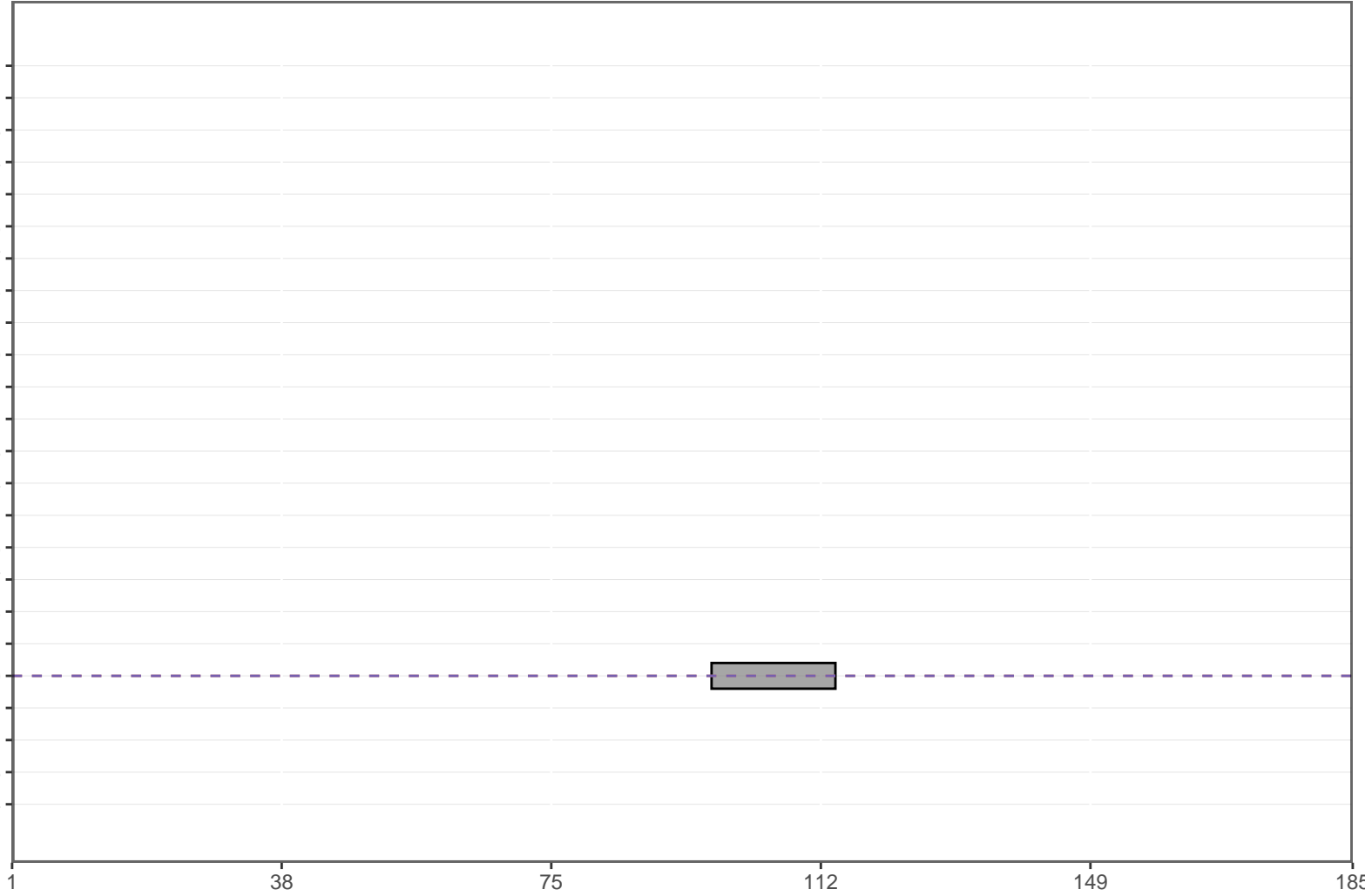
MW indication



Molecular weight



Gel Slice



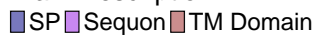
Protein length

Peptide counts over 4 repeats



Pfam domains

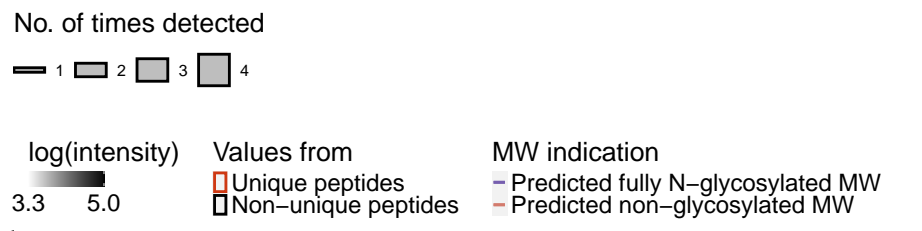
Pfam Description



Protein sequence:

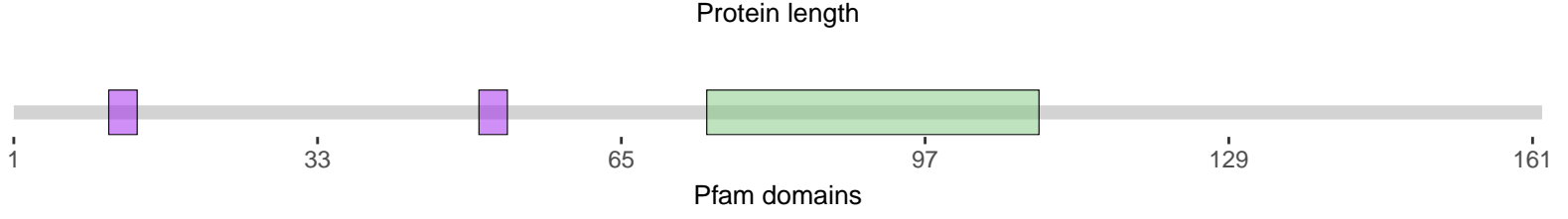
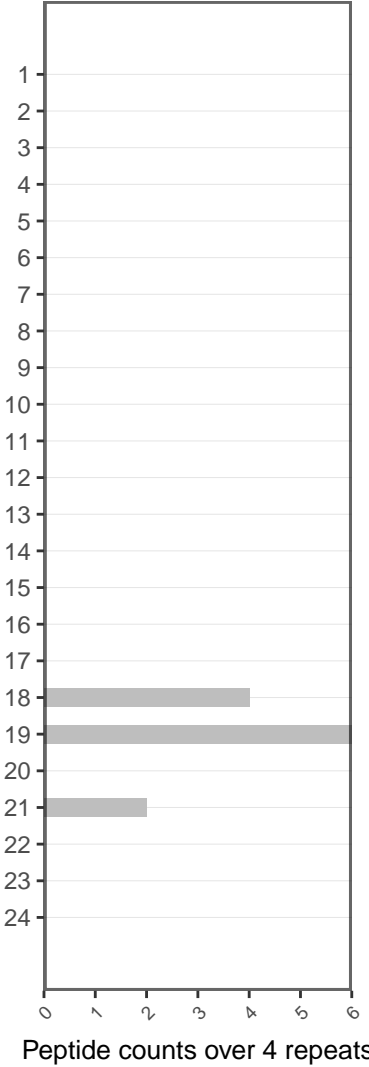
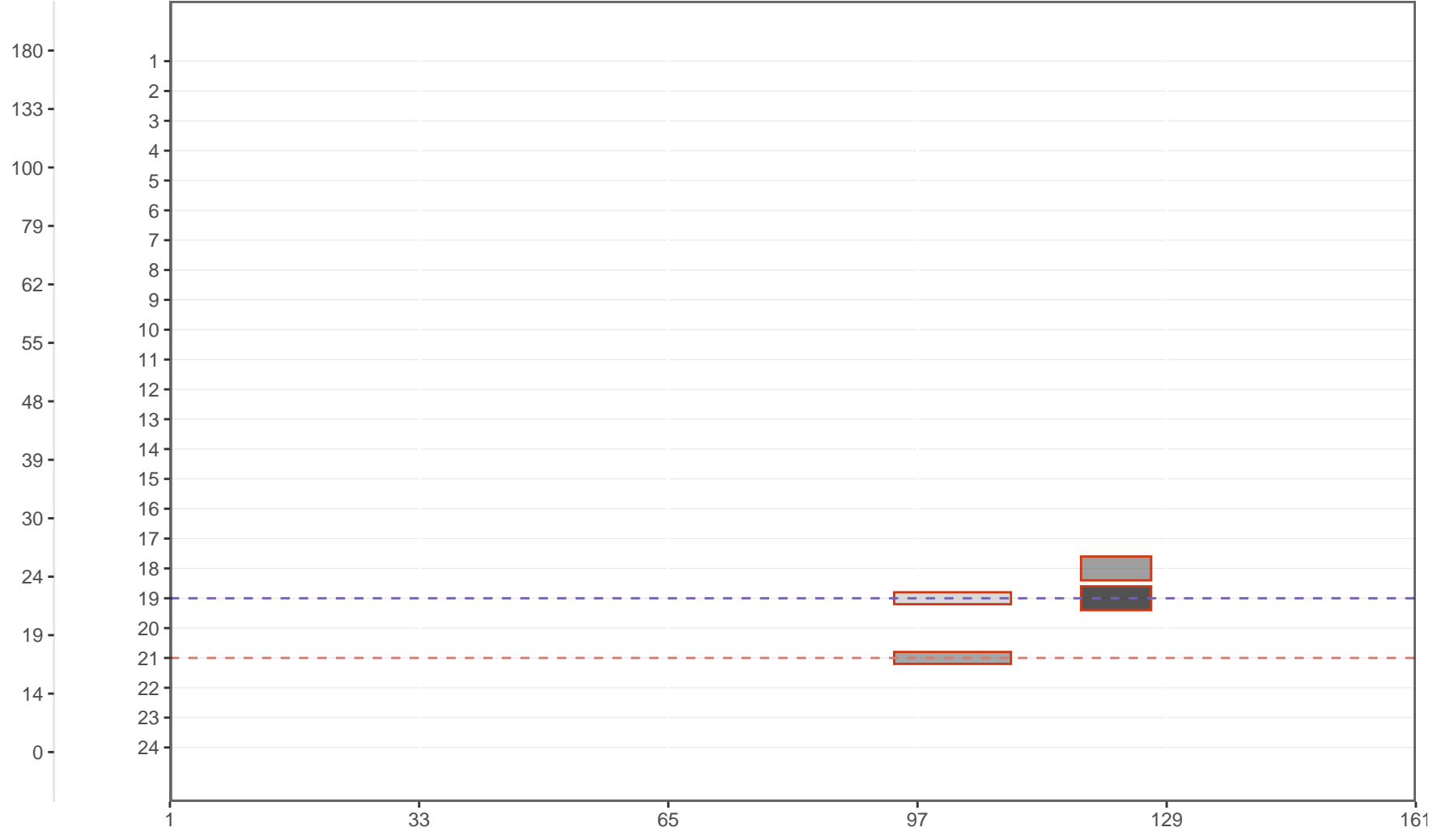
GRASLKPFGPYWVWVYVPEIPSPNPNNEGGVRRNRKRKRIGGGKAFILAEKKRKKAGLQEAHRKQKMKRVRERKMAAVARDRAWTERLAEKLEEKKAAMA

NbL14g11660.1 mitochondrial_intermembrane_space_import_and_assembly_protein_40-like [MW = 17.52 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF06747 CHCH domain

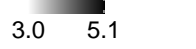
Protein sequence:
 HLRSGPCGNGQFSDAFLGFLKSTADEKGGSDCVNPFVAGSGCHKVNPNAFSGKLEDDNTRKQDEVKKEETPKGEYRIPPIWSEVSGKGRKKA

NbL14g11630.1 alpha-galactosidase_1-like [MW - SP = 44.49 kDa]

No. of times detected



log(intensity)



Values from



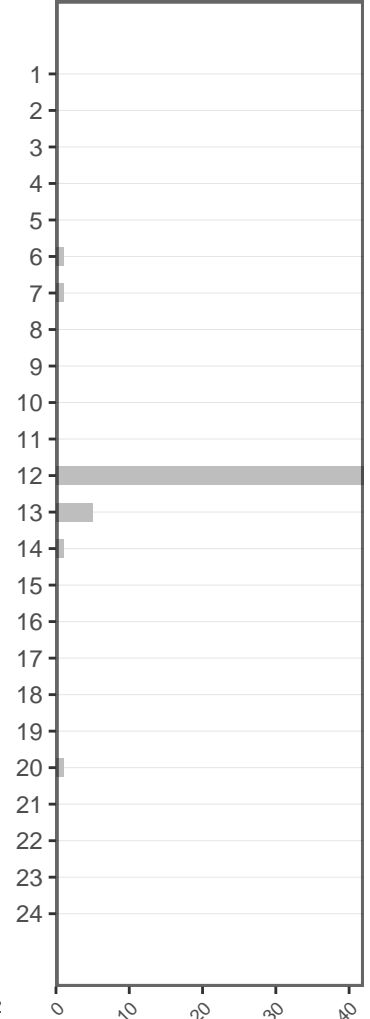
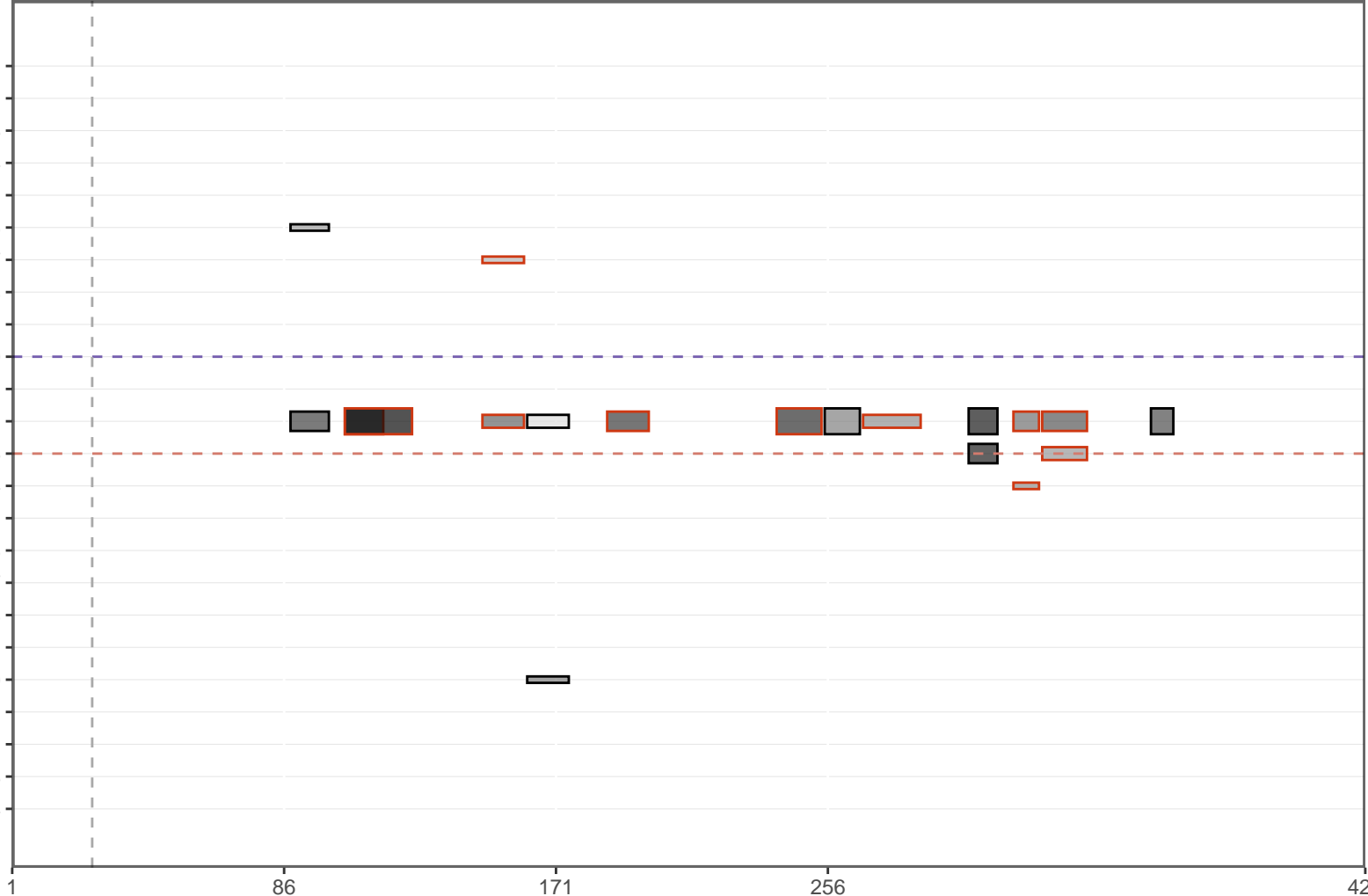
MW indication



Molecular weight

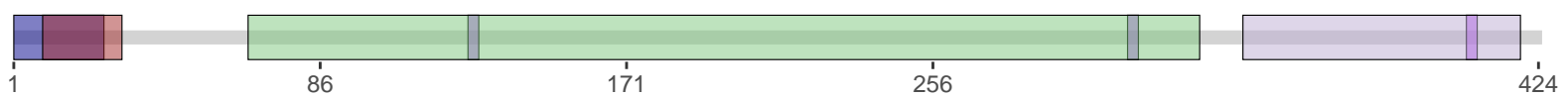


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF16499 Alpha galactosidase A
- PF17801 Alpha galactosidase C-terminal beta sandwich domain

Protein sequence:

VRYPVTRALMLNAGRPFSSLCEWGDLPALWGGKGVNSWRNTDITDITWESMISRADQNEVYADLRLRGGVNDPDMLEVNGGMSKDEVIHFSLWAKPLHGCDVRNITKDTMDLANKVEIVAVNGDEKGVGKVRMEGGDIEVWAGPLGGYRVALLLNRGPKYETFAHWDDTGIPPNVYVEARDLWEHKTFRFGKGLTATVNSHAGKMYVLPFAV

NbL14g11610.1 lateral_signaling_target_protein_2_homolog [MW = 18.77 kDa]

No. of times detected



log(intensity)



Values from



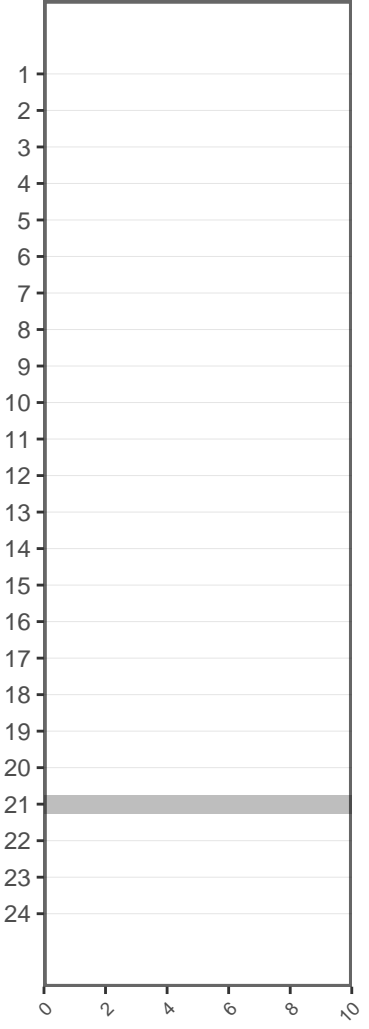
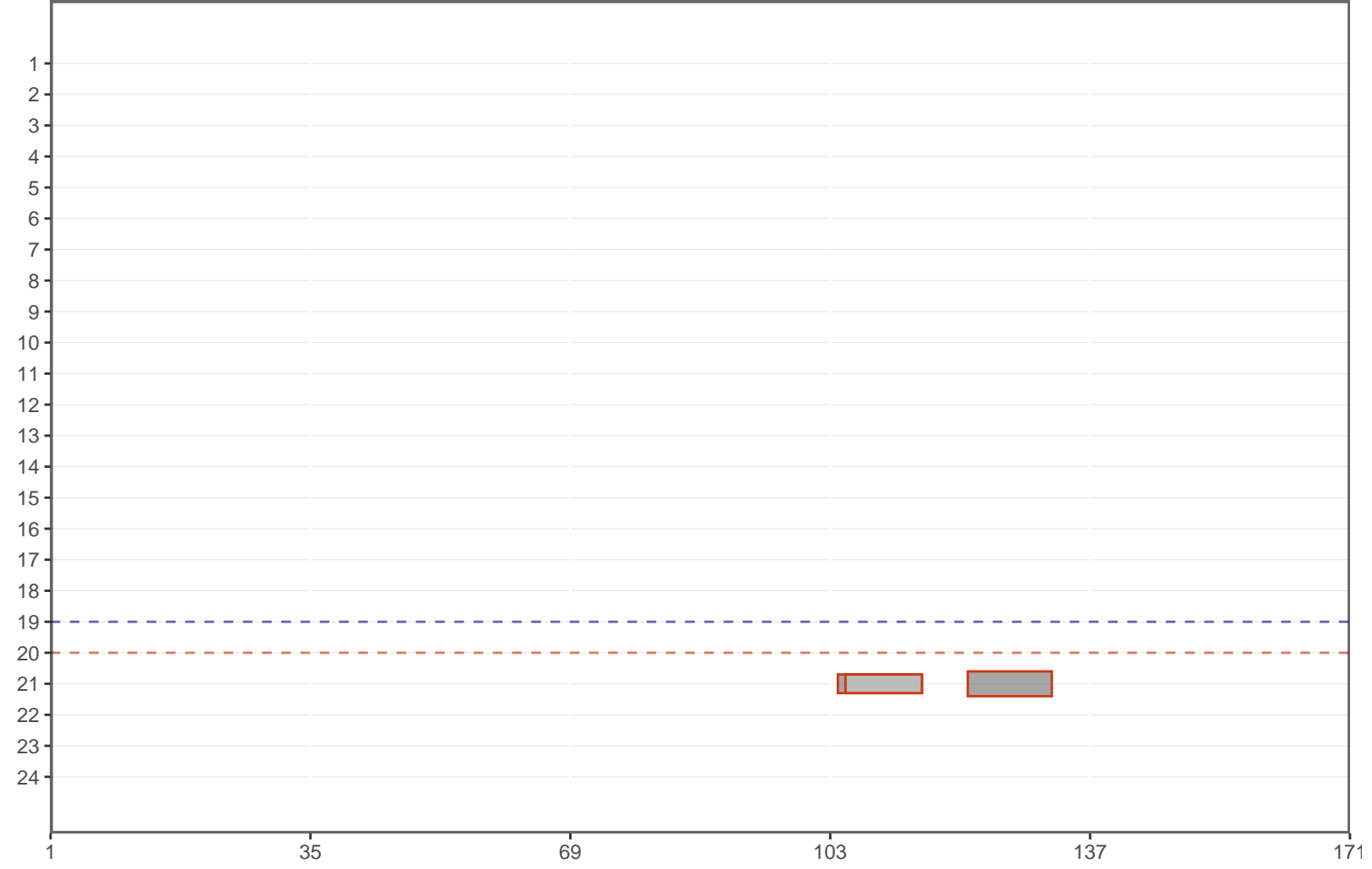
MW indication



Molecular weight



Gel Slice



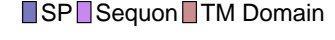
Protein length



Pfam domains



Pfam Description

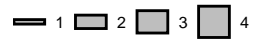


Protein sequence:

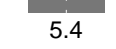
MPSVSRWTSLSSSSRAS6SQVIRMAPEEEKMTRRGLDFPIEWERPKPGRRPDIFFQFSPMKTLPPLPLADPPPEDEEEENKEEEEDPEKEDPKPKDEI

NbL14g11580.1 vegetative_cell_wall_protein_gp1-like [MW - SP = 8.63 kDa]

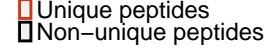
No. of times detected



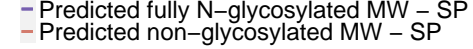
log(intensity)



Values from



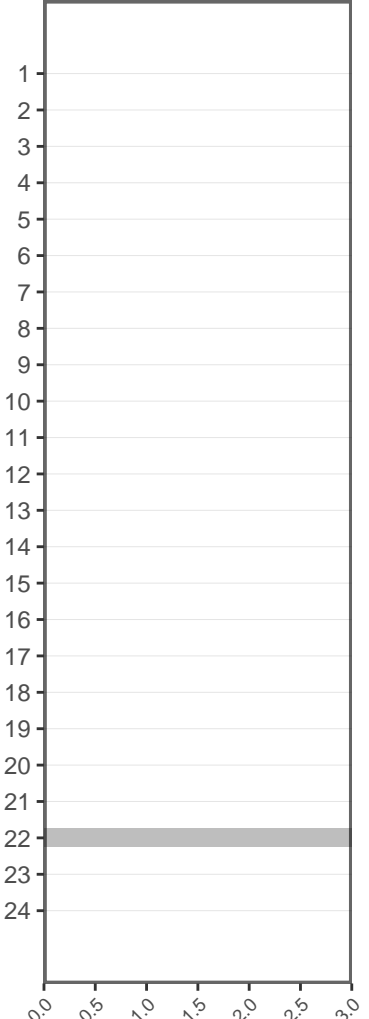
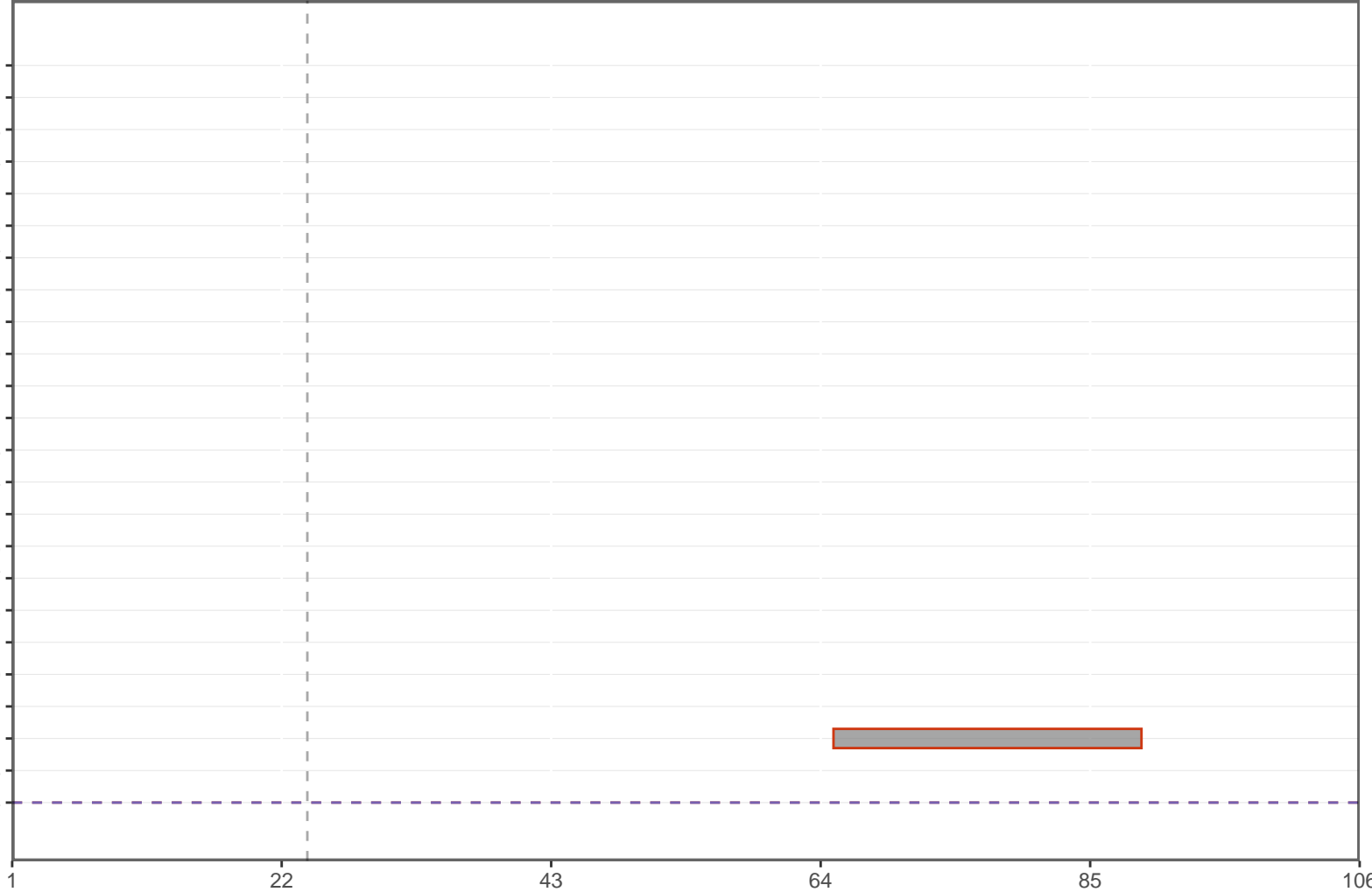
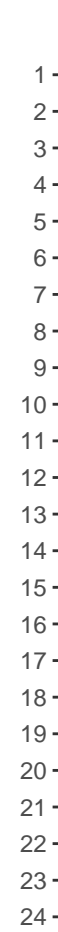
MW indication



Molecular weight



Gel Slice

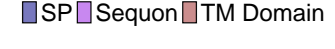


Protein length



Pfam domains

Pfam Description



Protein sequence:

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NbL14g11400.1 NADH_dehydrogenase_[ubiquinone]_1_beta_subcomplex_subunit_7-like [MW = 12.2 kDa]

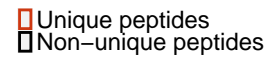
No. of times detected



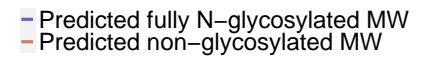
log(intensity)



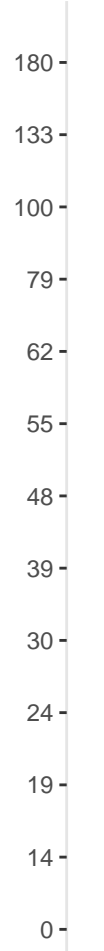
Values from



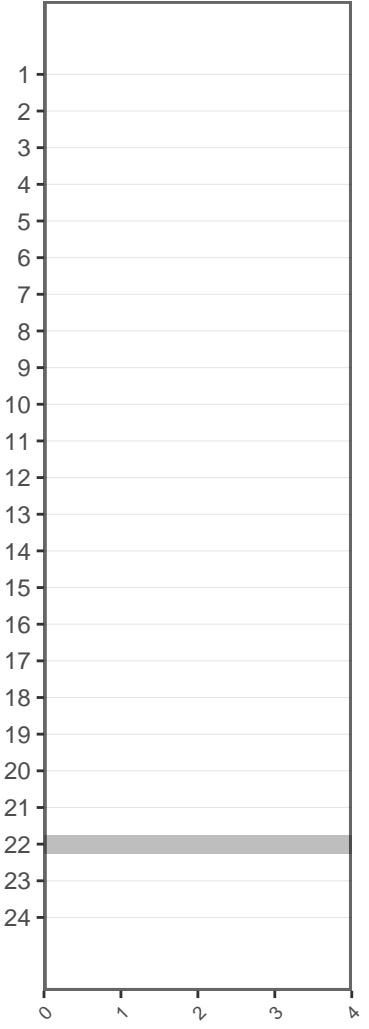
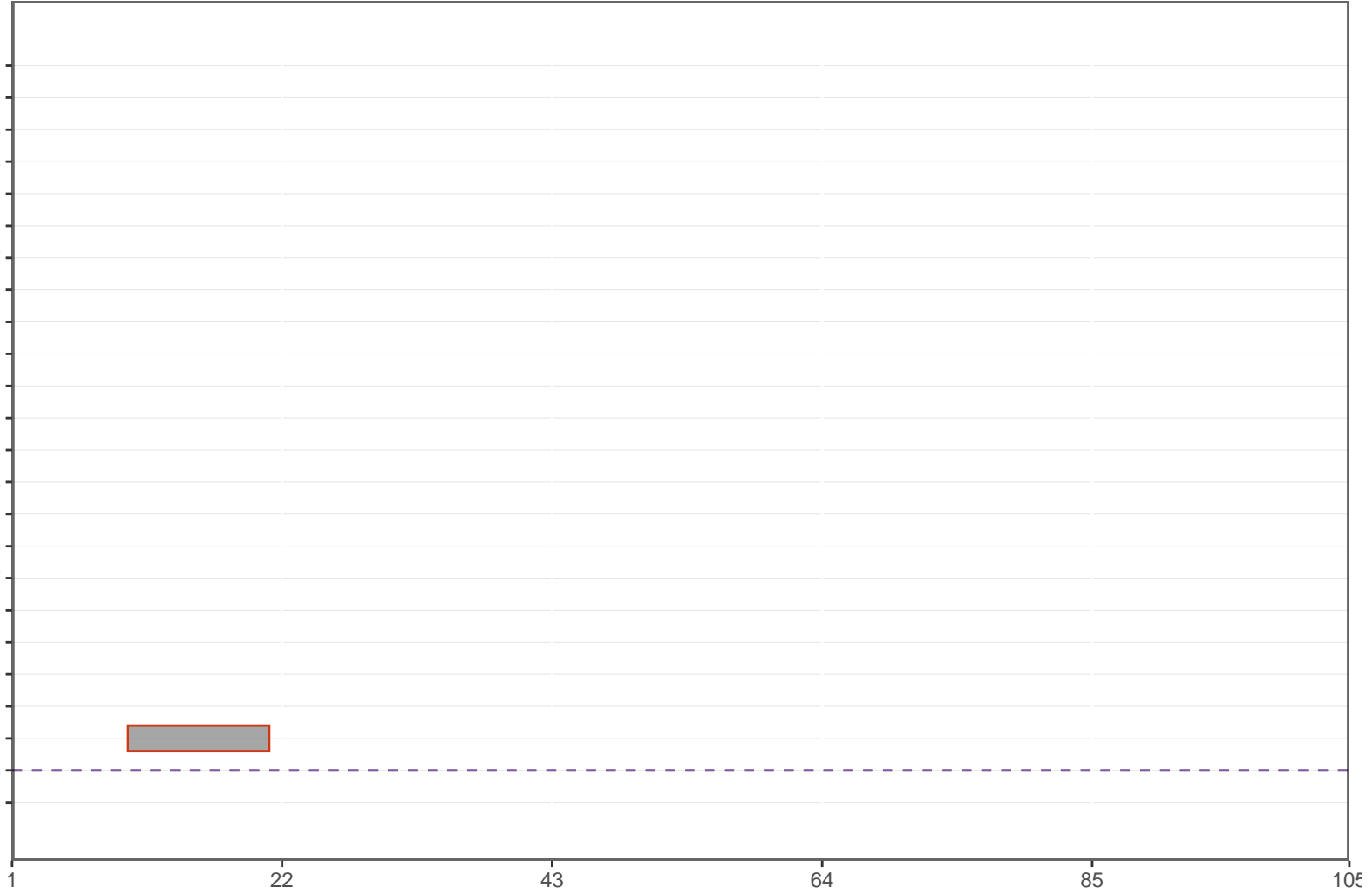
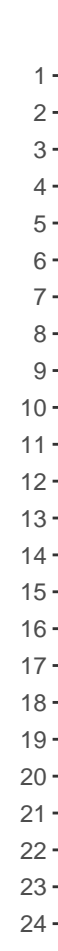
MW indication



Molecular weight

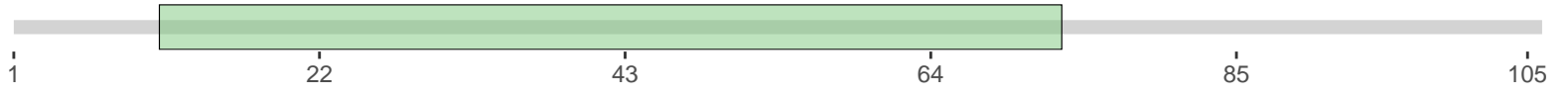


Gel Slice



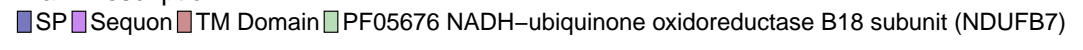
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CRQSEFYLPLVWKCEDERHSYKGEYELVMERMILGMQKIKREEEARLKGKGGADGGTILPIPKTAA*

NbL14g11260.1 putative_4-hydroxy-4-methyl-2-oxoglutarate_aldolase_2 [MW = 17.76 kDa]

No. of times detected



log(intensity)



Values from



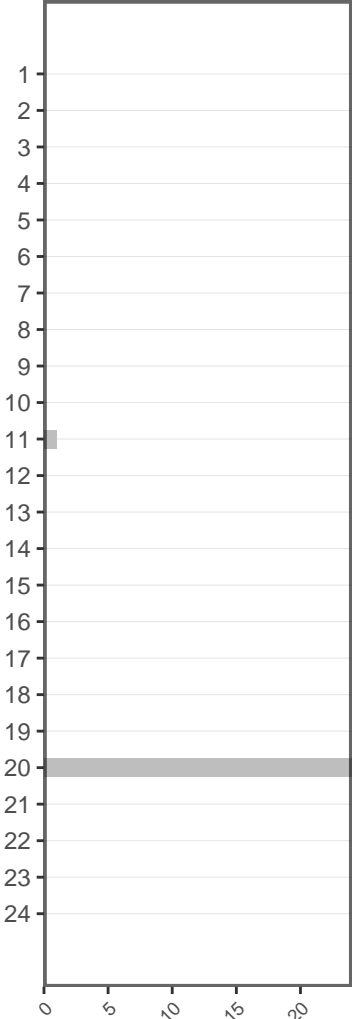
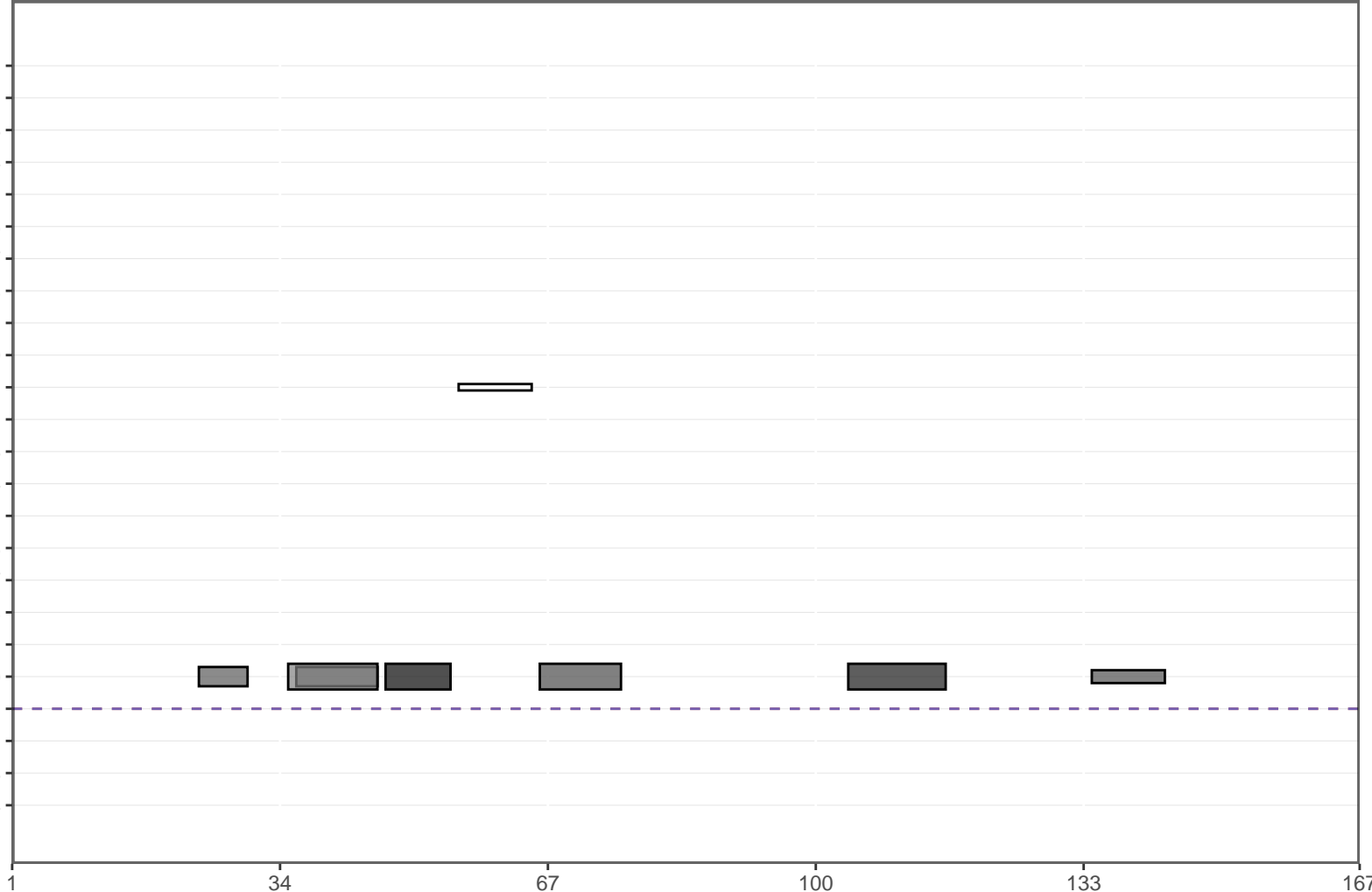
MW indication



Molecular weight



Gel Slice

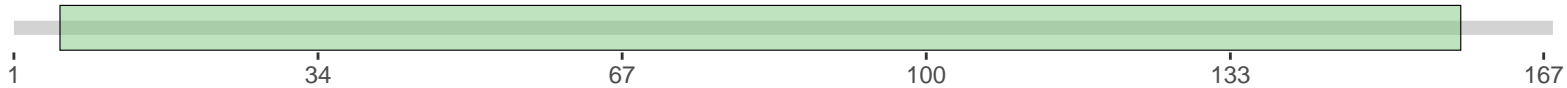


Peptide counts over 4 repeats

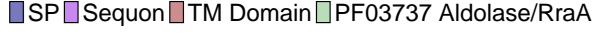
Protein length



Pfam domains



Pfam Description



Protein sequence:

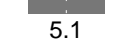
GGGSLRCALGGNFVVGAGNNGWAGHVVNGGVRDVEINGGDKGVRALASHPMKANKKGGIKKHVPTIAGTRIGDGEWLVADTDGLISKMELEV

NbL14g10930.1 HMG-Y-related_protein_B-like [MW = 21.03 kDa]

No. of times detected



log(intensity)



Values from



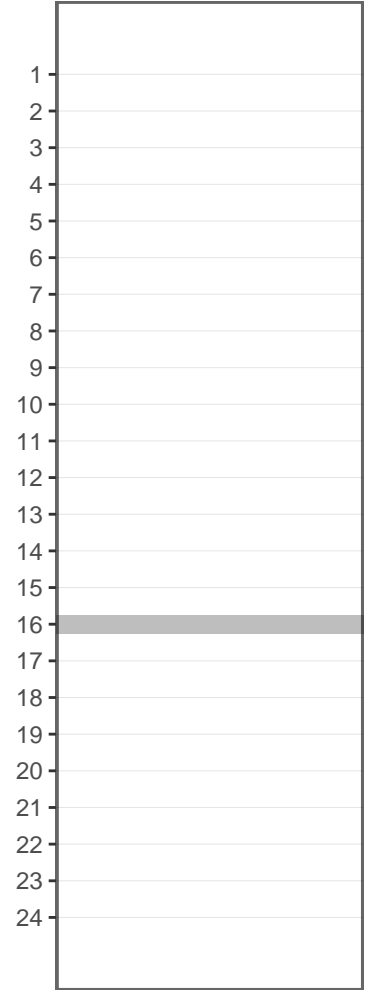
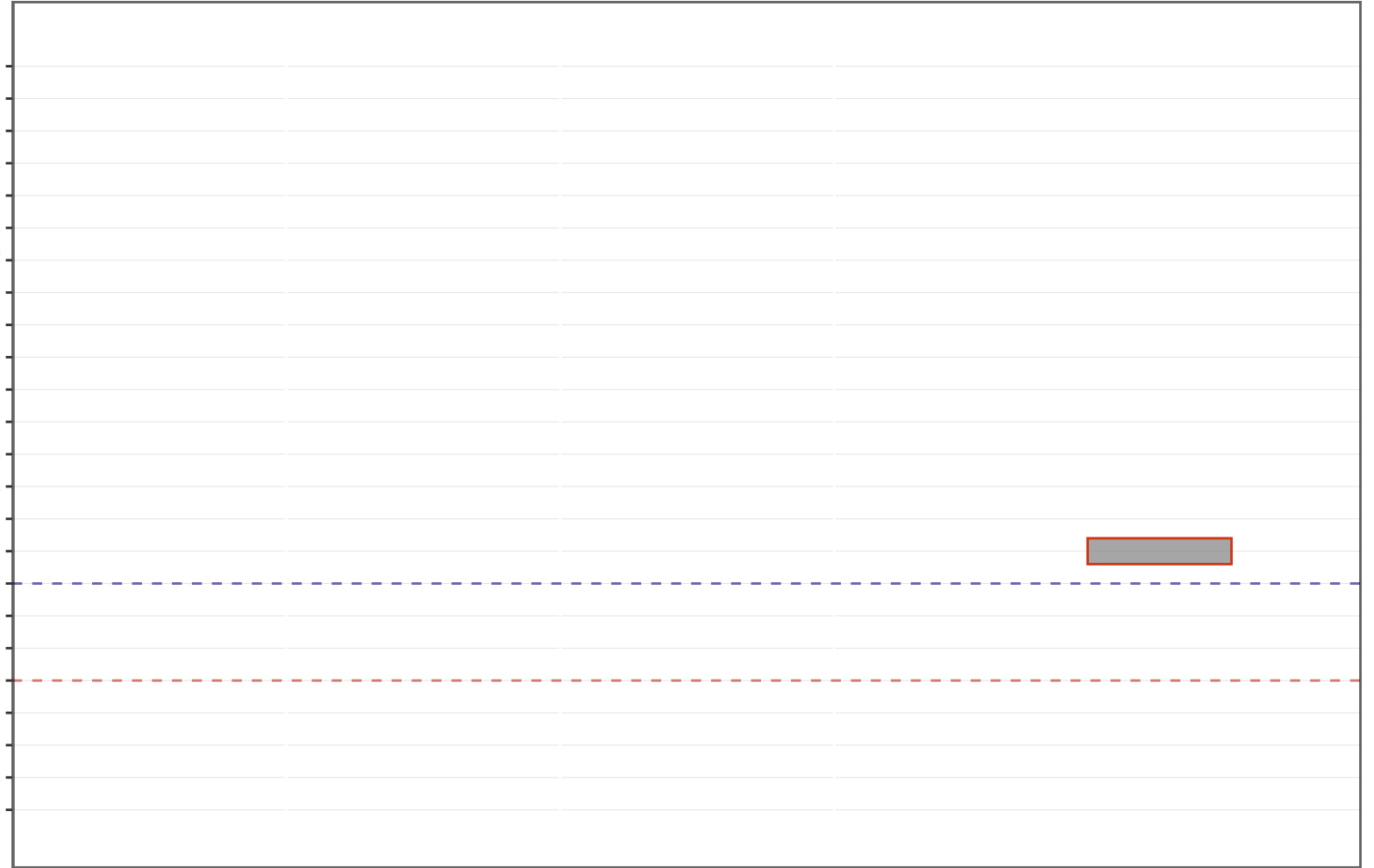
MW indication



Molecular weight



Gel Slice



Protein length

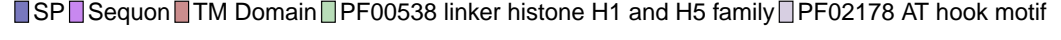


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IKPDNAPRRGRGRPKKAPLPEGVVPPPPRRGRPKKERDHPAPISVFMKVTSPSSGGTGKIKRGRPKYFNDTSSPSAVFPPPGGTRGRPKKVRNIPVAEVA*

NbL14g10730.1 kirola-like [MW = 19.69 kDa]

No. of times detected



log(intensity)



Values from



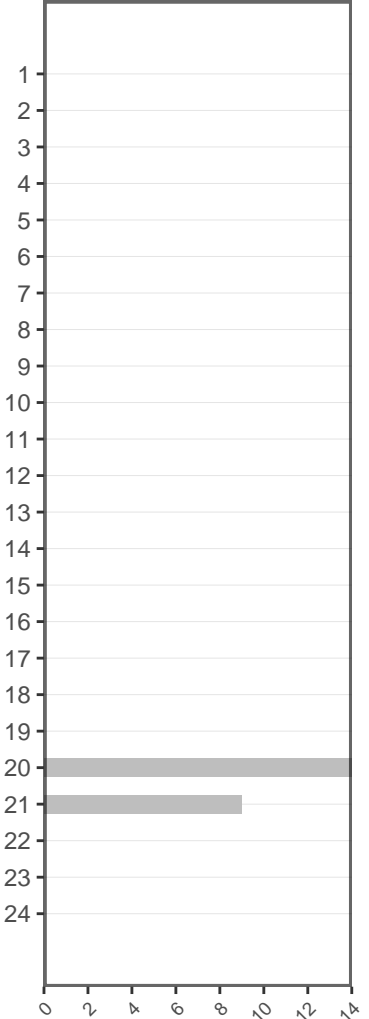
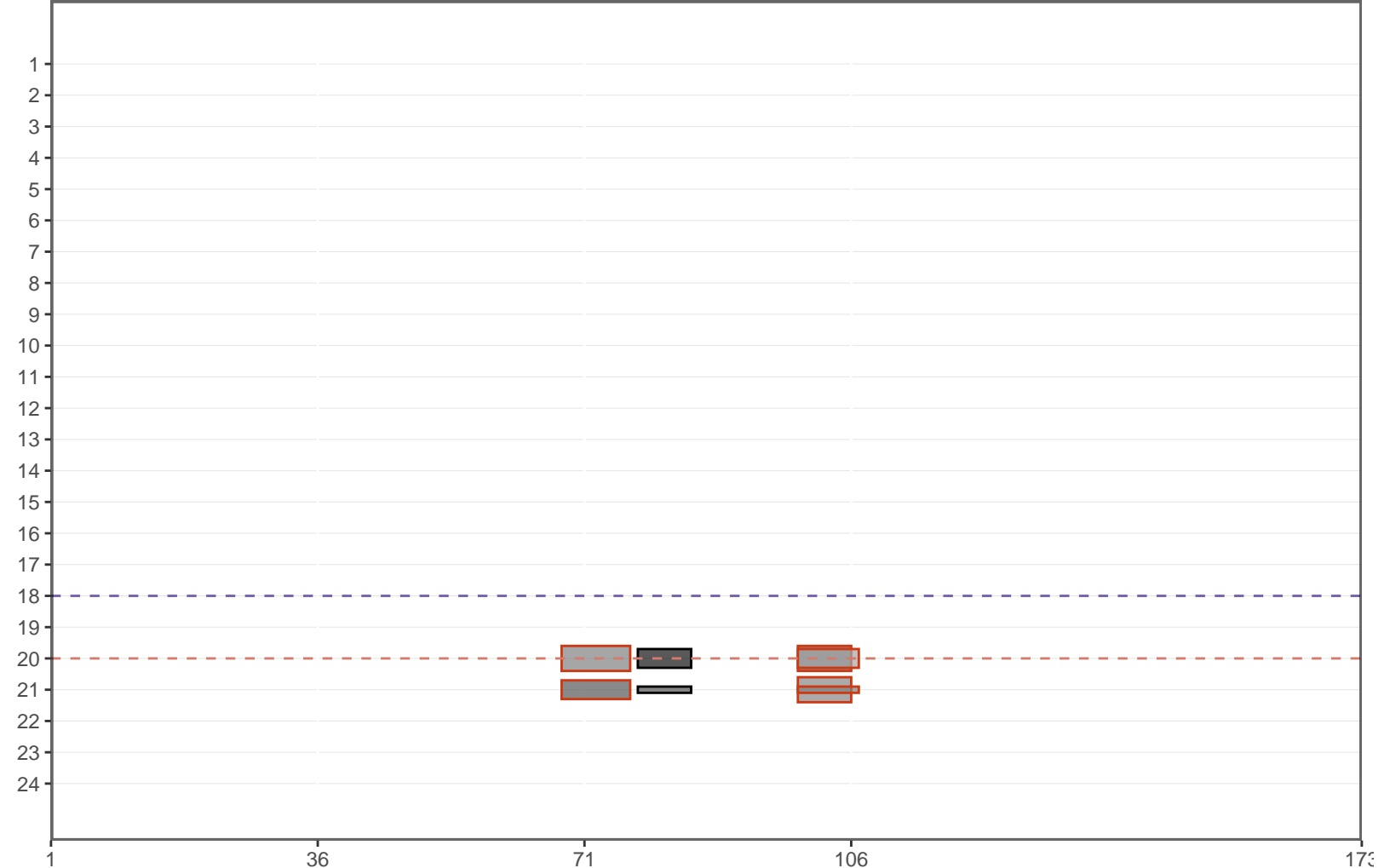
MW indication



Molecular weight

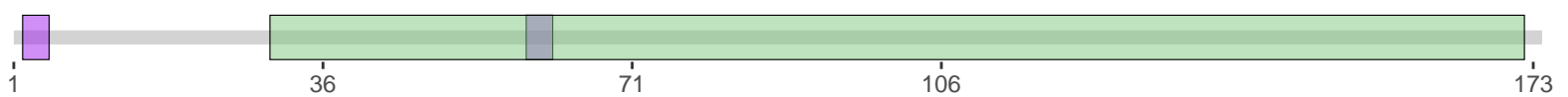


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TVKYGSVVWVWYNDGGKDKKDKKQKIEVDHVKKSTWVWVGGDLLELYNSFTTTSDDHQWTFVVEKKTEDTPEPLVLLGFVHVKDIEGHLK

NbL14g10560.1 probable_ribose-5-phosphate_isomerase_2 [MW = 28.85 kDa]

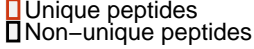
No. of times detected



log(intensity)



Values from



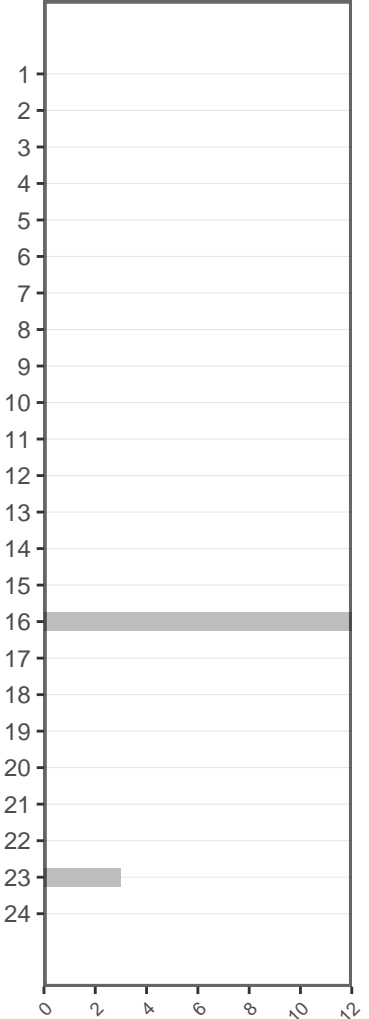
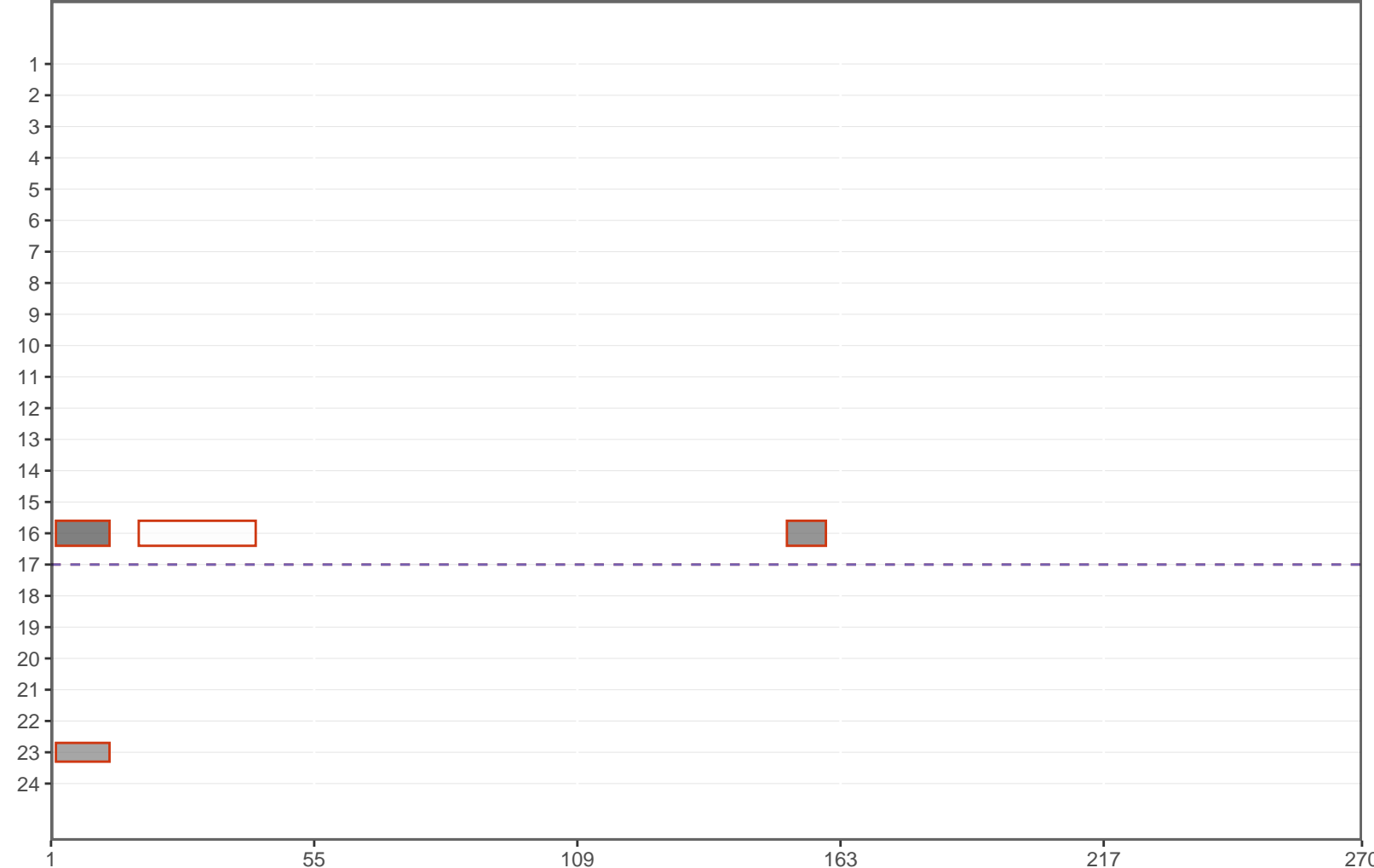
MW indication



Molecular weight

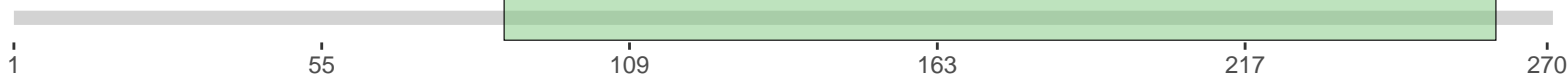


Gel Slice



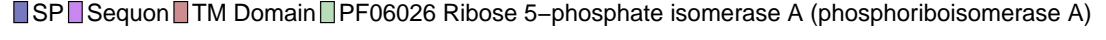
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EVDRRLNLYKGRGGSLLENMVEAAKPKFVIVDEKLVSHLGGGSLAMPVENPFFQWETLKRLEMLFIEAGGVGKLRRTVGGEPVYTDNGNHIDLYFKSDMDLKAASDAILRLAGVVEHGMFLDMATTVVAQKLGVEVTK*

NbL14g10460.1 peptidyl-prolyl_cis-trans_isomerase_FKBP13_chloroplastic [MW = 23.7 kDa]

No. of times detected



log(intensity)



Values from



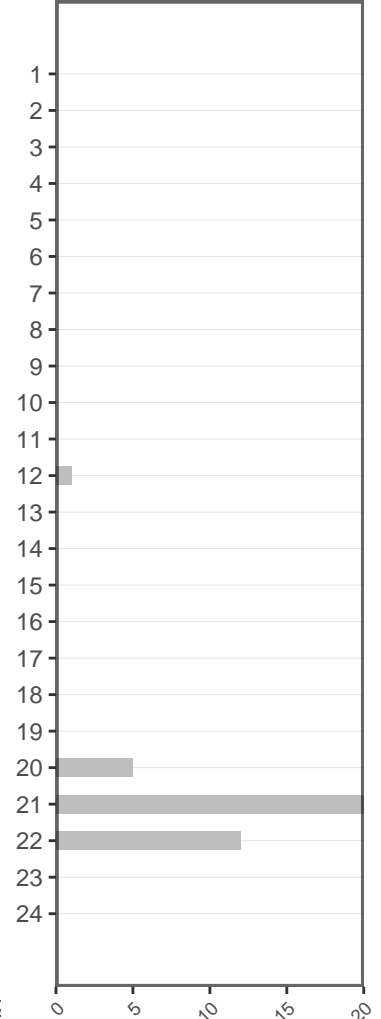
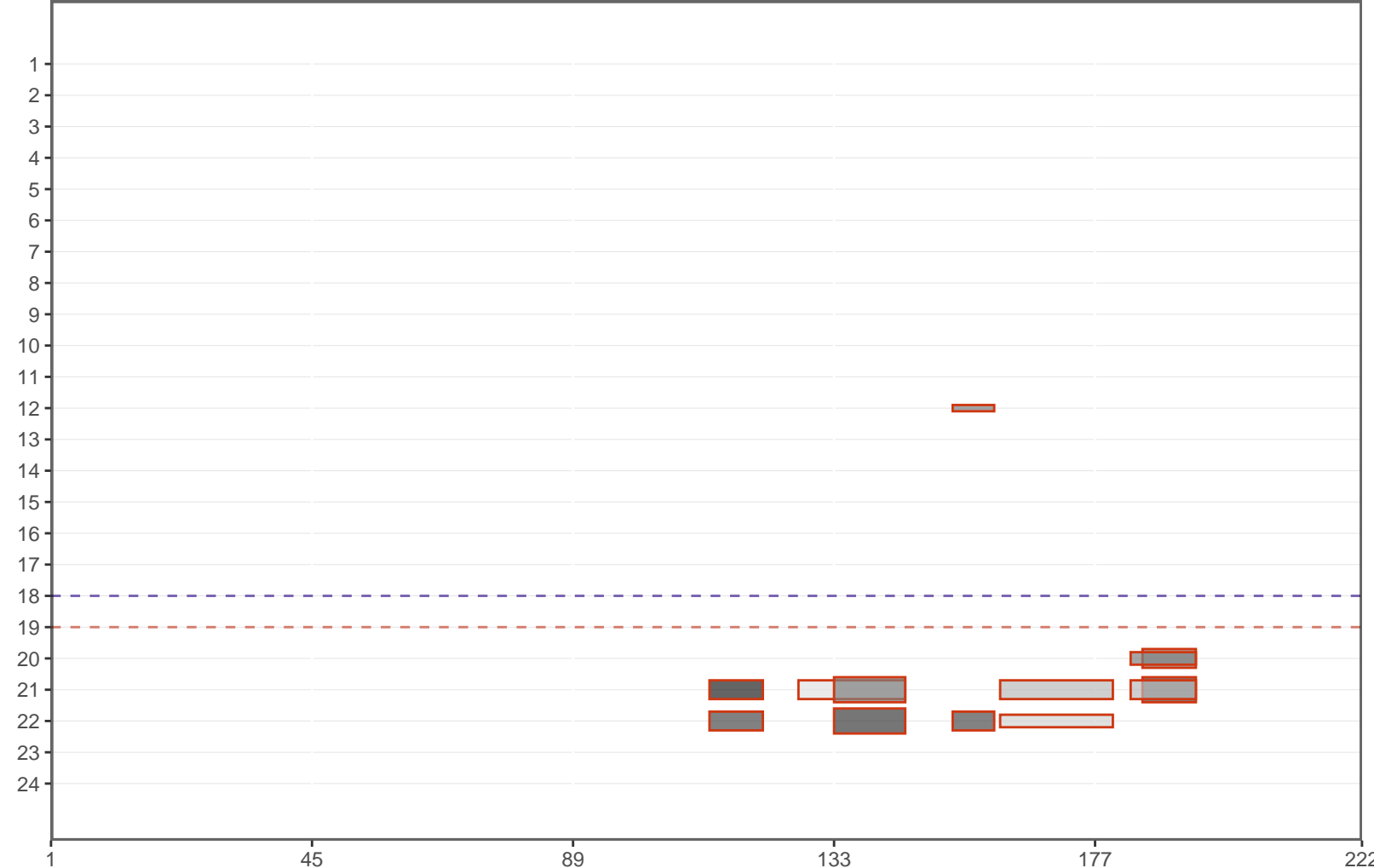
MW indication



Molecular weight

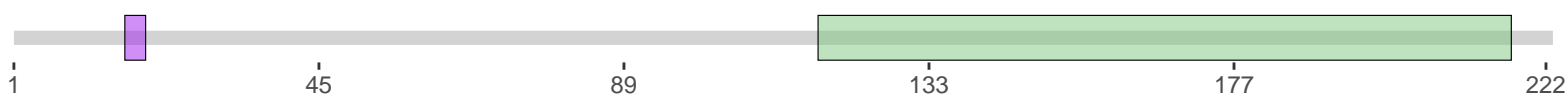


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

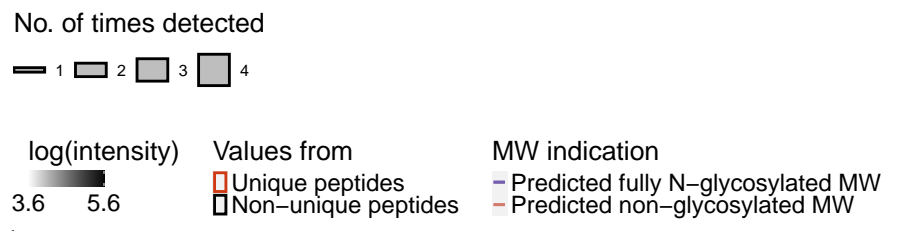
Pfam Description



Protein sequence:

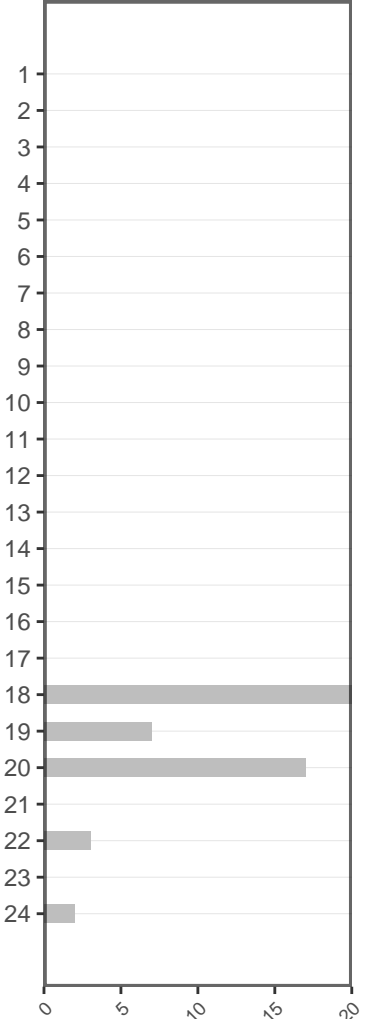
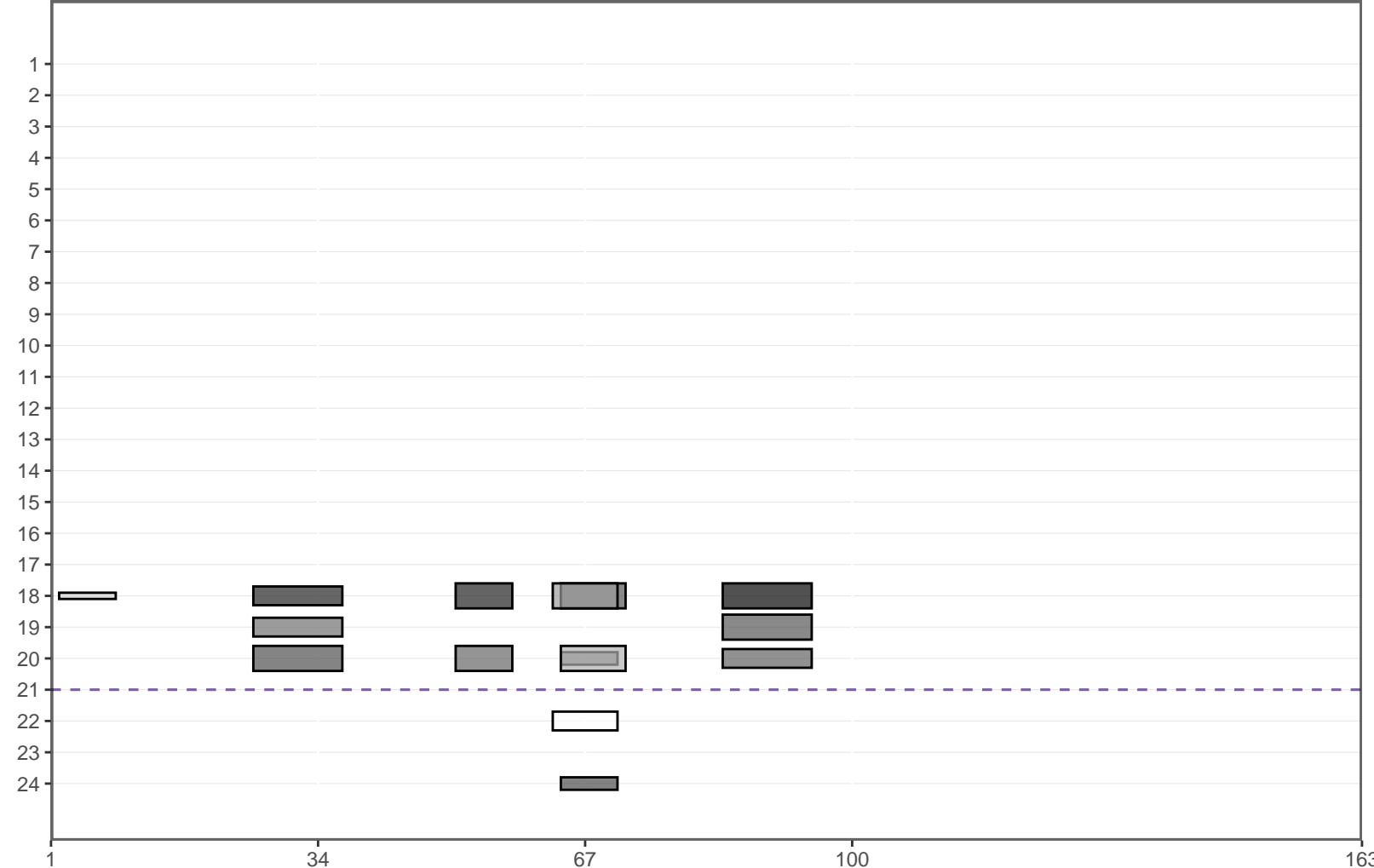
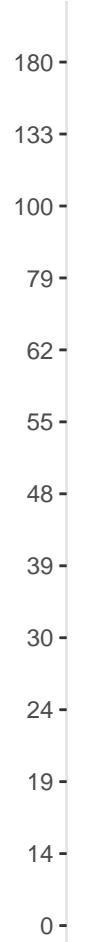
/TPSLGLCYCDKIVSYGFEAWKGLKHAHYVVKLENGVDFDBSYNRGKPLTFRVGVGEVKGWDDGLGGDFPPMLTGGKRLKIPPELGYGMRGAGRGSGIIPPNSVLLFDVFEVGVKA*

NbL14g10350.1 60S_ribosomal_protein_L24-like [MW = 18.44 kDa]



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01246 Ribosomal protein L24e

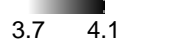
Protein sequence:
 AAKRRRATQXPYSRSGVATLEVWQKRTREPEVRDAAREAAALREIKERIKTKDDEKAKKAEVTAHQKAGGKGNLPKSGKPKLGGSGKGR

NbL14g10270.1 DEAD-box_ATP-dependent_RNA_helicase_38 [MW = 55.2 kDa]

No. of times detected



log(intensity)



Values from



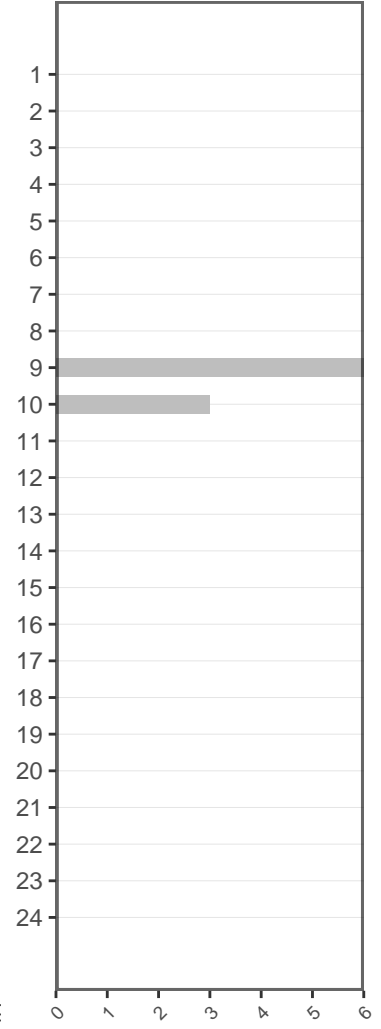
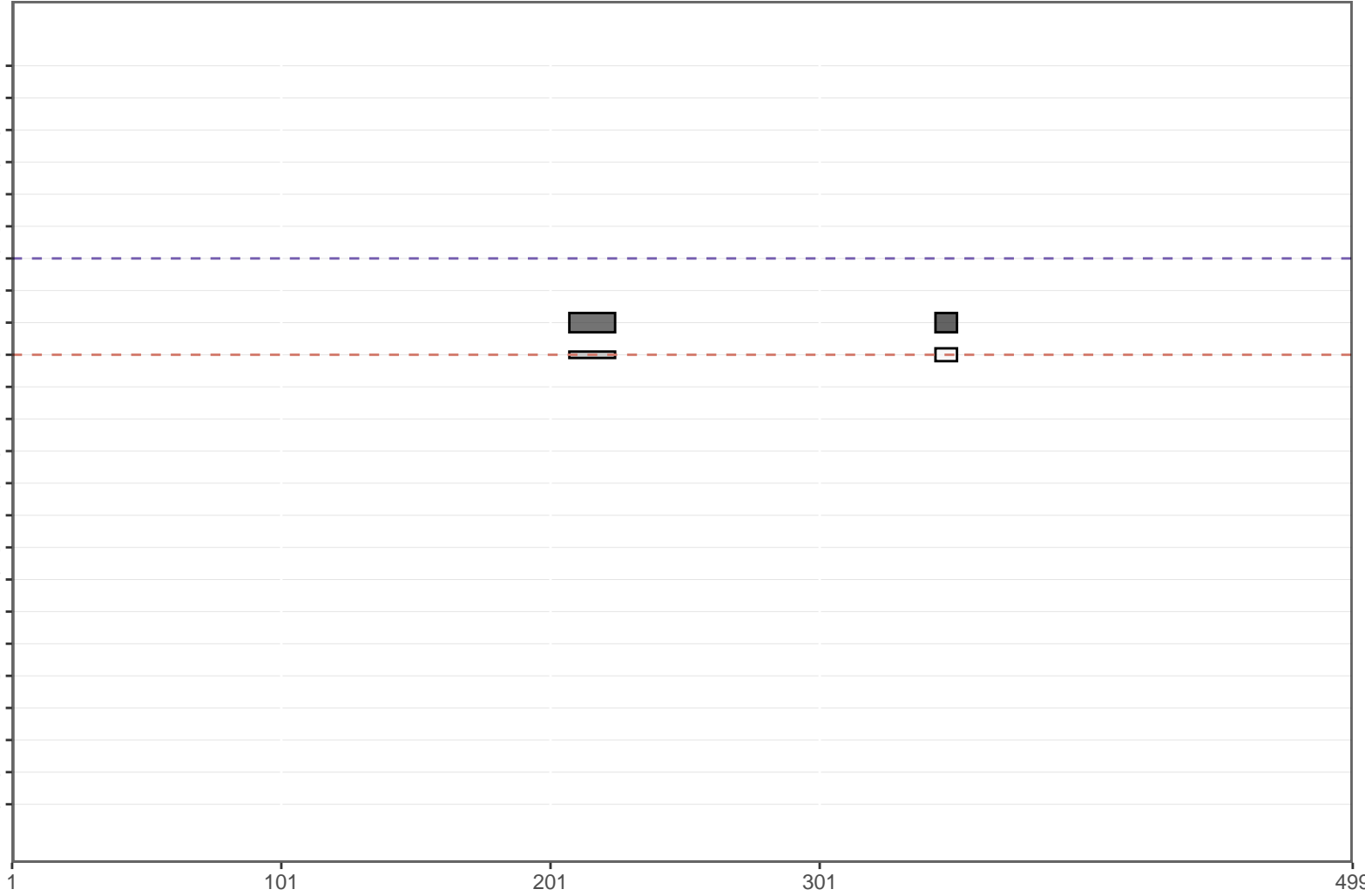
MW indication



Molecular weight

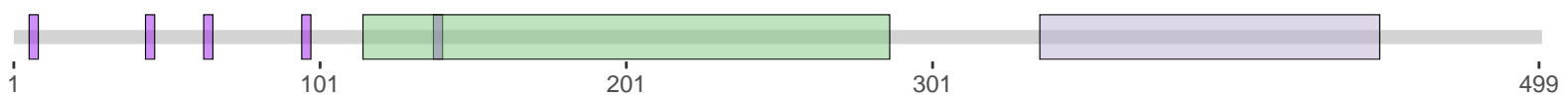


Gel Slice



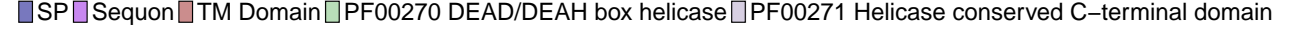
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

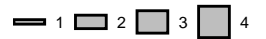


Protein sequence:

IKLVFDEADHMLAETGFGDDSRIMKAVKASADSGVLLFSATTFGENVAFVTKVIRDLFVNDHGMFVKEELSLDSVWQYKVGCPDELISKVMWIKDKILELGGKVGDTIFVIRTKNGASMLHKGLVDYGVGVETTTGGALKGEDRDKIKFKRGLTQVLISTDLLARGFDGSGVNLVWYDLPVRIHESFSEPHKEVYLHRIKGRAGRFGRKGAIFNLGNDRDGMMLMSKIEGHFNQGVTEIASWKSDEDFENALKKAGLL

NbL14g10190.1 protein_MODIFIER_OF_SNC1_11-like [MW = 21.18 kDa]

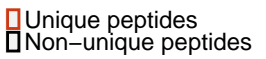
No. of times detected



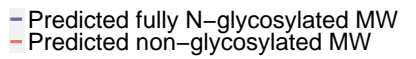
log(intensity)



Values from



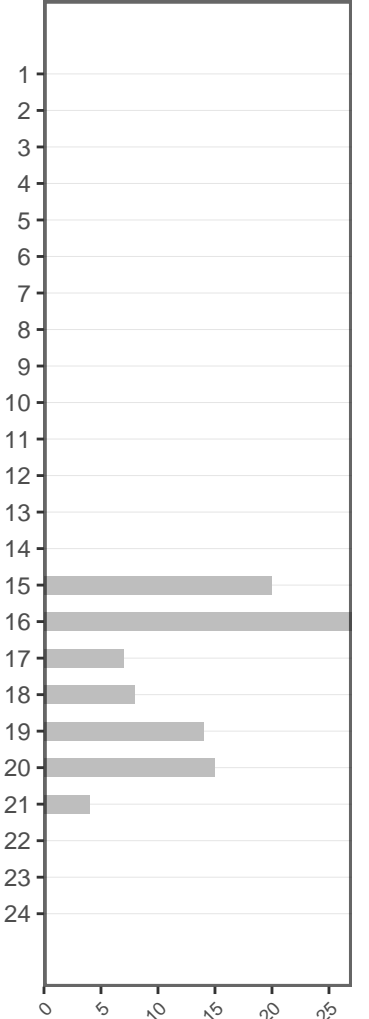
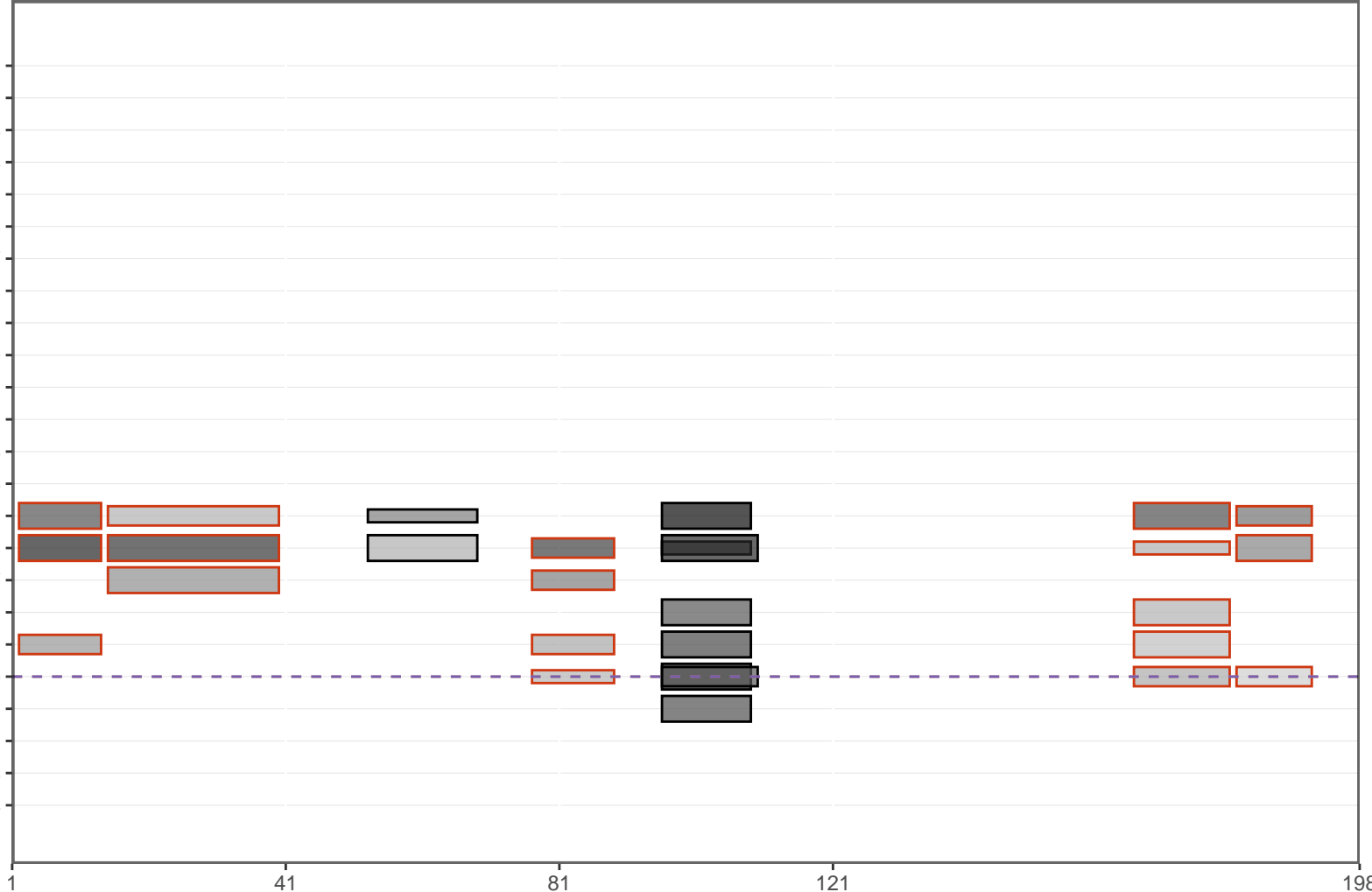
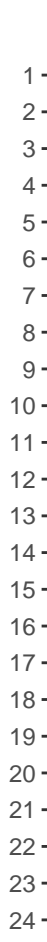
MW indication



Molecular weight

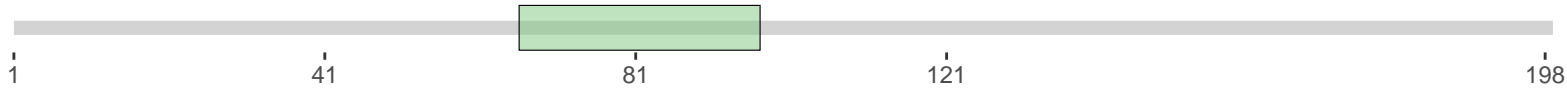


Gel Slice



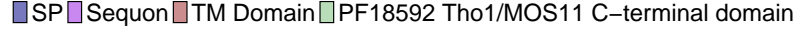
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

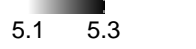
IKRNSRAERFGTGSSEVGGSDALKKAEHRQRARERFGLVKSDDTTEEEANKKALTRFAPPVKTDPVVEEDKRRKARALRFSGPQASGASQANGKNGIEGDDVAVDKAGAEPEI

NbL14g10180.1 translin [MW = 34.56 kDa]

No. of times detected



log(intensity)



Values from



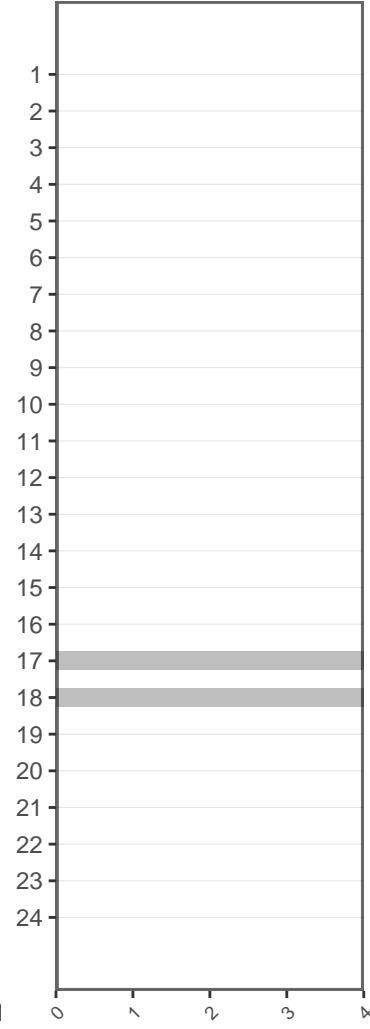
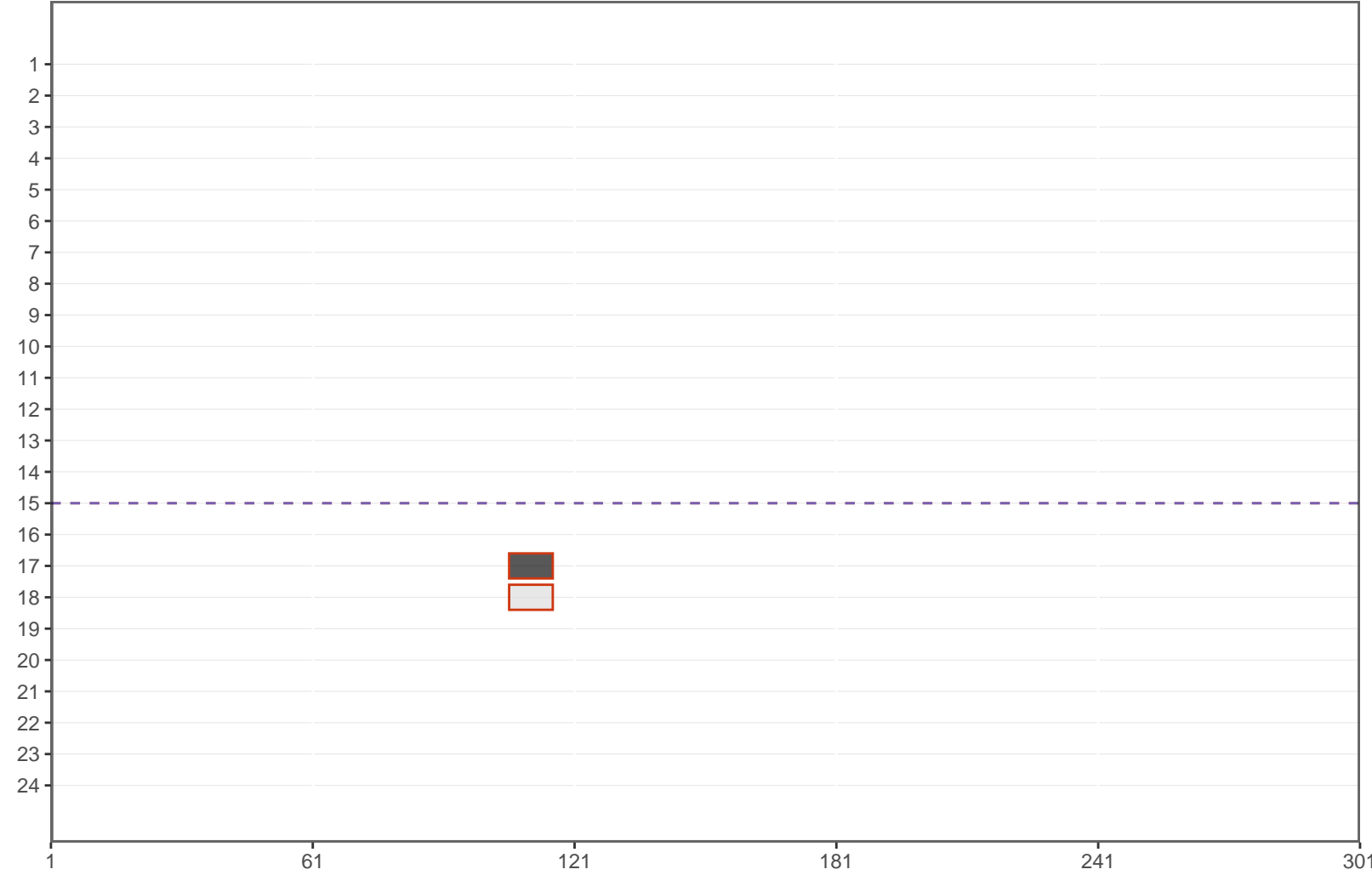
MW indication



Molecular weight

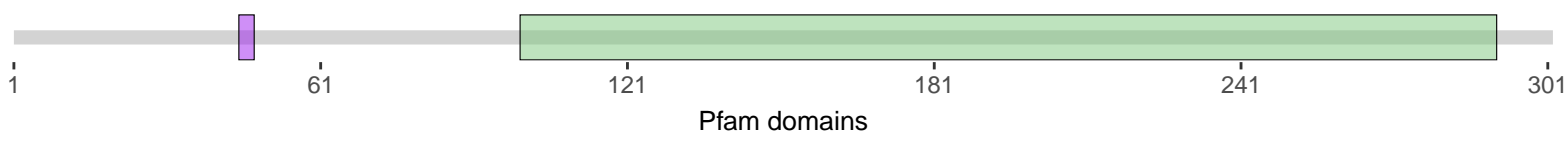


Gel Slice



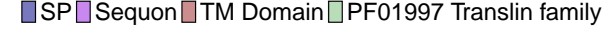
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

QAQIGELKELYSRLLSEVRECPGGYFRHYHGDKWIKSETGTVYVLLAFMHWLEFGTLVHNEVEEKGLGTPTEFGLEDKLGIGCFMSNELPRVYVNGVITAGDYDGPRIKLFKLTDLHAAFRMLNLRNDLRRKFKFDGMKYDLRKEVEFQVKIRRLAANGESA

NbL14g10170.1 adenosine_kinase_2 [MW = 37.46 kDa]

No. of times detected



log(intensity)



Values from



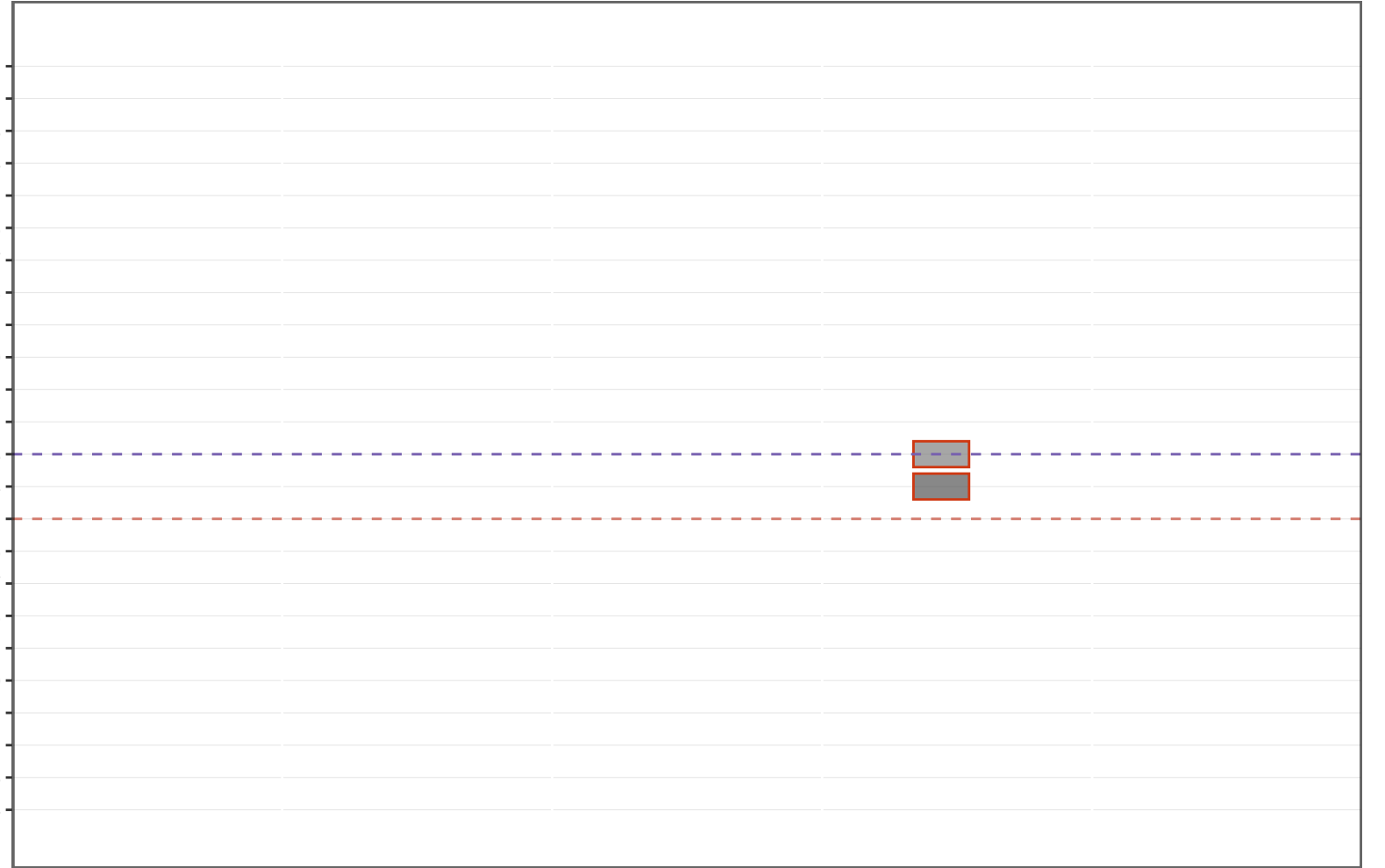
MW indication



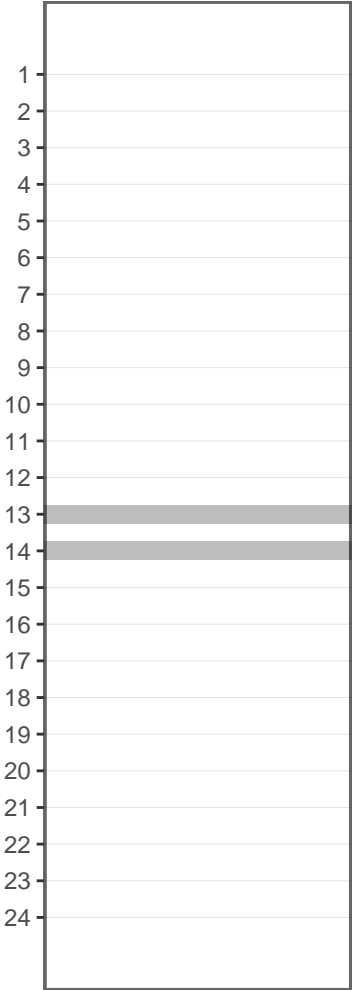
Molecular weight



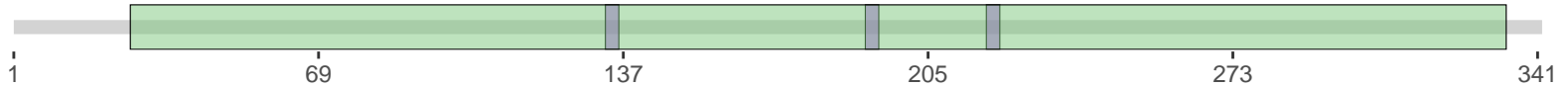
Gel Slice



Protein length

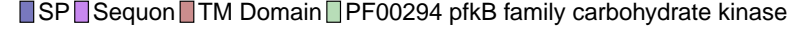


Peptide counts over 4 repeats



Pfam domains

Pfam Description

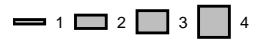


Protein sequence:

IAKYYIAGFFLTVSPEISQLWAHAAAKIKVFSMNLBAPFCIEFFKGGKVLPLYMDPFCNETAARTFSRHHWETDNVEEIALKISQWAKASGTHKRITVITGADPVAVAEDGKVKLFPVPLPKKELVDITNGAGDAFVGGFLAGLVGGKPIADCVKAGGFSANVHQRSQCTYPEKPDFE

NbL14g10160.1 phenylalanine_ammonia-lyase [MW = 77.45 kDa]

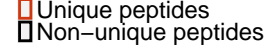
No. of times detected



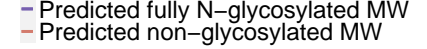
log(intensity)



Values from

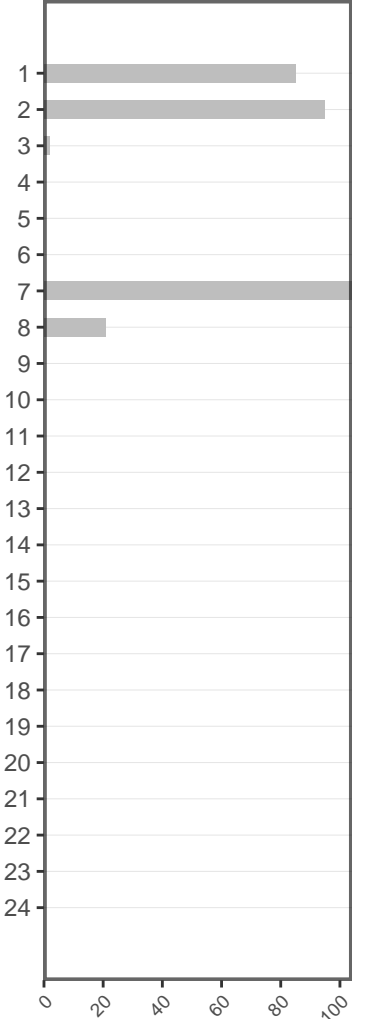
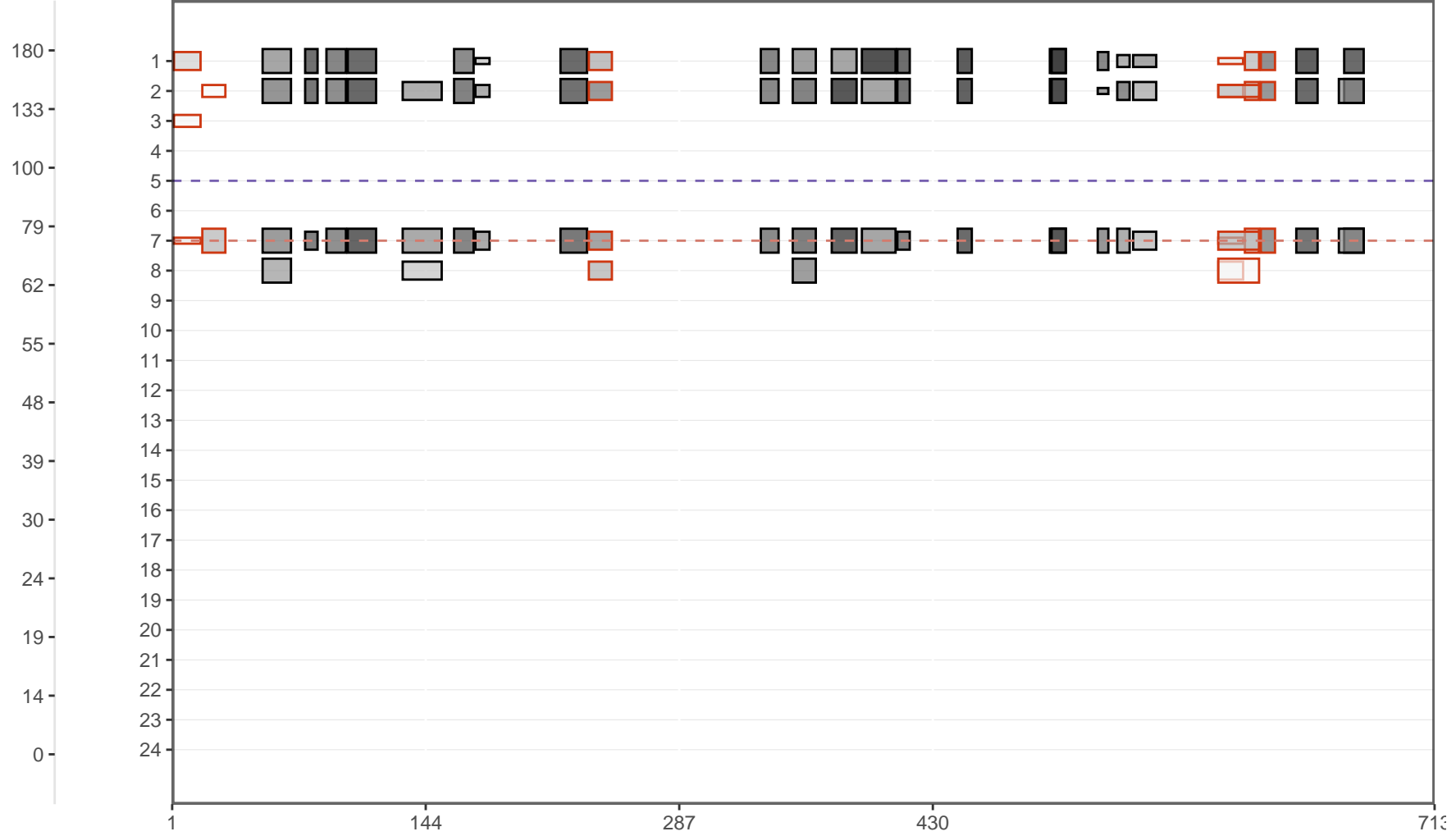


MW indication



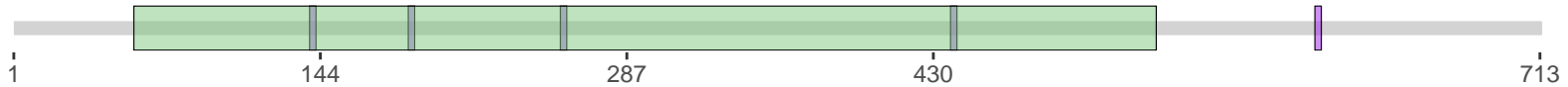
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

*KDDRYLRSTSPWLVGQIEVIRSATKMERIENBNDNPLIDVSRNKALHGGNFQGTPIGVSMNARLALASIGKLMFAQFSELVNDYNNGLPNTAGRNPLDYGFKGSEIIMASYSSELGFLANPVTNHVGSAGHNGDYNLSLGLSARKTAEAVDILKLMSTYLVALQGAIDLRLHEENLRNANKVNTVSGVAKRRLTMTGANGELHPSRFGEKDLRVDREYHVFVADDAAGSANYPLMQLRGLVLDVHALENGENEKDANSIFQKILAFEGELKAVLPKEVESARIAL

NbL14g10150.1 29_kDa_ribonucleoprotein_B_chloroplastic [MW = 34.81 kDa]

No. of times detected



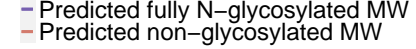
log(intensity)



Values from



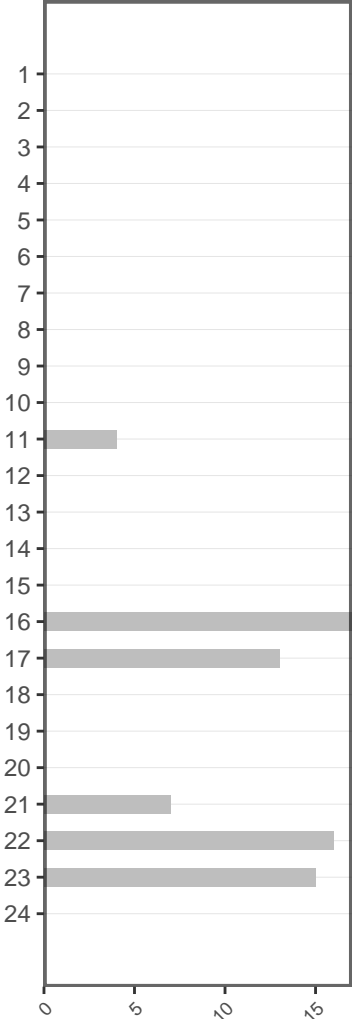
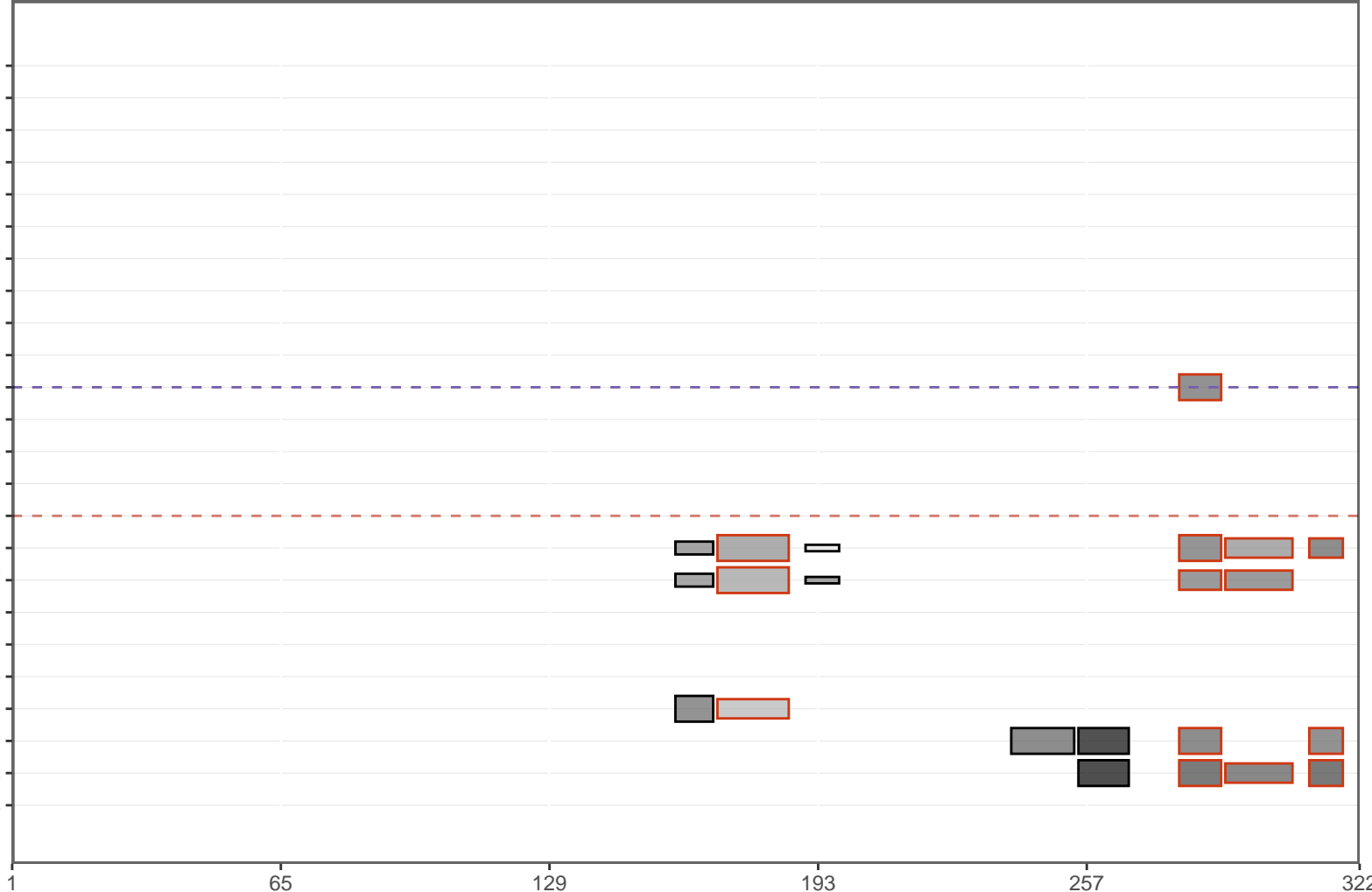
MW indication



Molecular weight

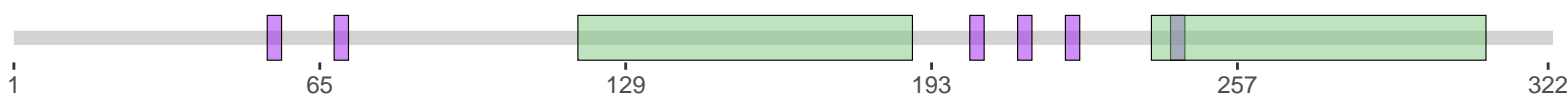


Gel Slice



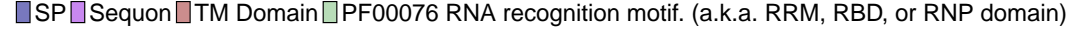
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

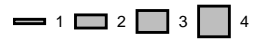


Protein sequence:

LTGRSRGFGFVTMTKKEVEAAEQGFNGYEDGRRAIRWAGPAPAKRENSSFGGGGRGNSYGGGRDRNSFGGARGGREVDRENRVYVGNLGSVDDLAIKELFSEGGNVVDMKVVYDRDGRGRGFGFVYSSKKEVNNADSLNGVLDGRSIRVSAEEQPRRF

NbL14g09940.1 S-adenosylmethionine_synthase_2-like [MW = 42.61 kDa]

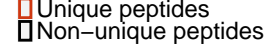
No. of times detected



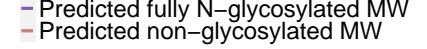
log(intensity)



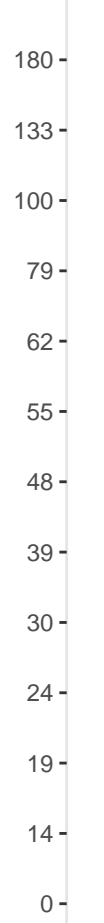
Values from



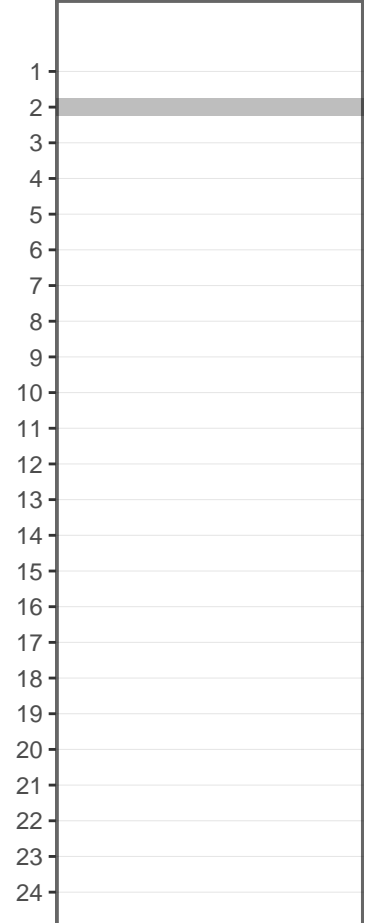
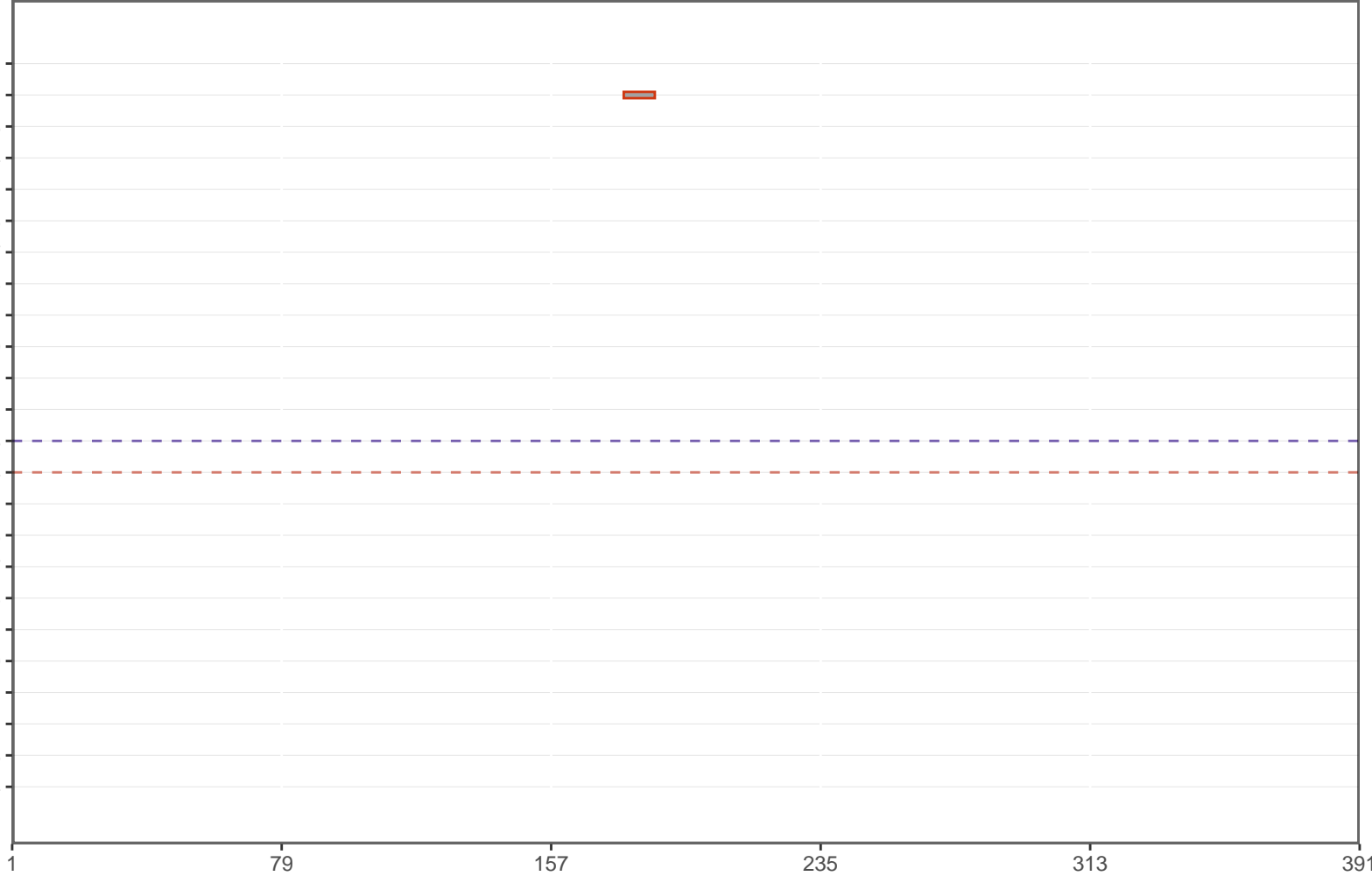
MW indication



Molecular weight



Gel Slice



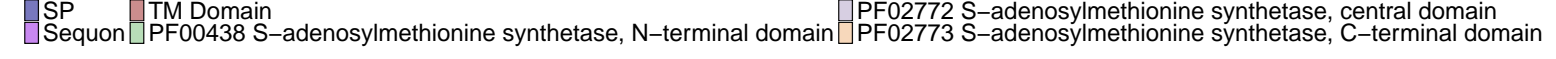
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IGAMVPIRIVYITLISFGHDEFTVNEGIAGDLKEHVKIPVPAKYLDKTFHLPNGSRRFVGGPHGDAGLTGRKIIDTYGGWGAHGGGAFSGKDPKVDREGAVYVRAAKSVAAAGLARRGVQVSYAGVWAEPLVDFVDTYKGTIPDKDLTLIKENFDFRPMIANDLKRGGNFRYQKTAAGHFGRRDDPDTWETVKALNPKV

NbL14g09860.1 60S_ribosomal_protein_L23a-like [MW = 17.48 kDa]

No. of times detected



log(intensity)



Values from



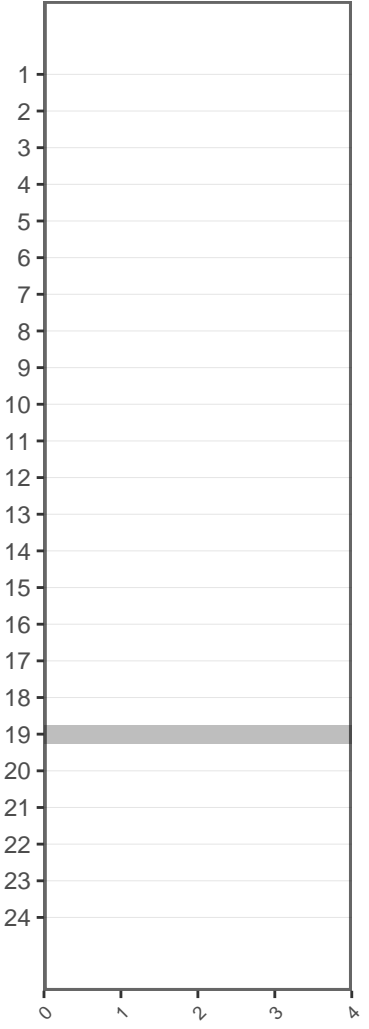
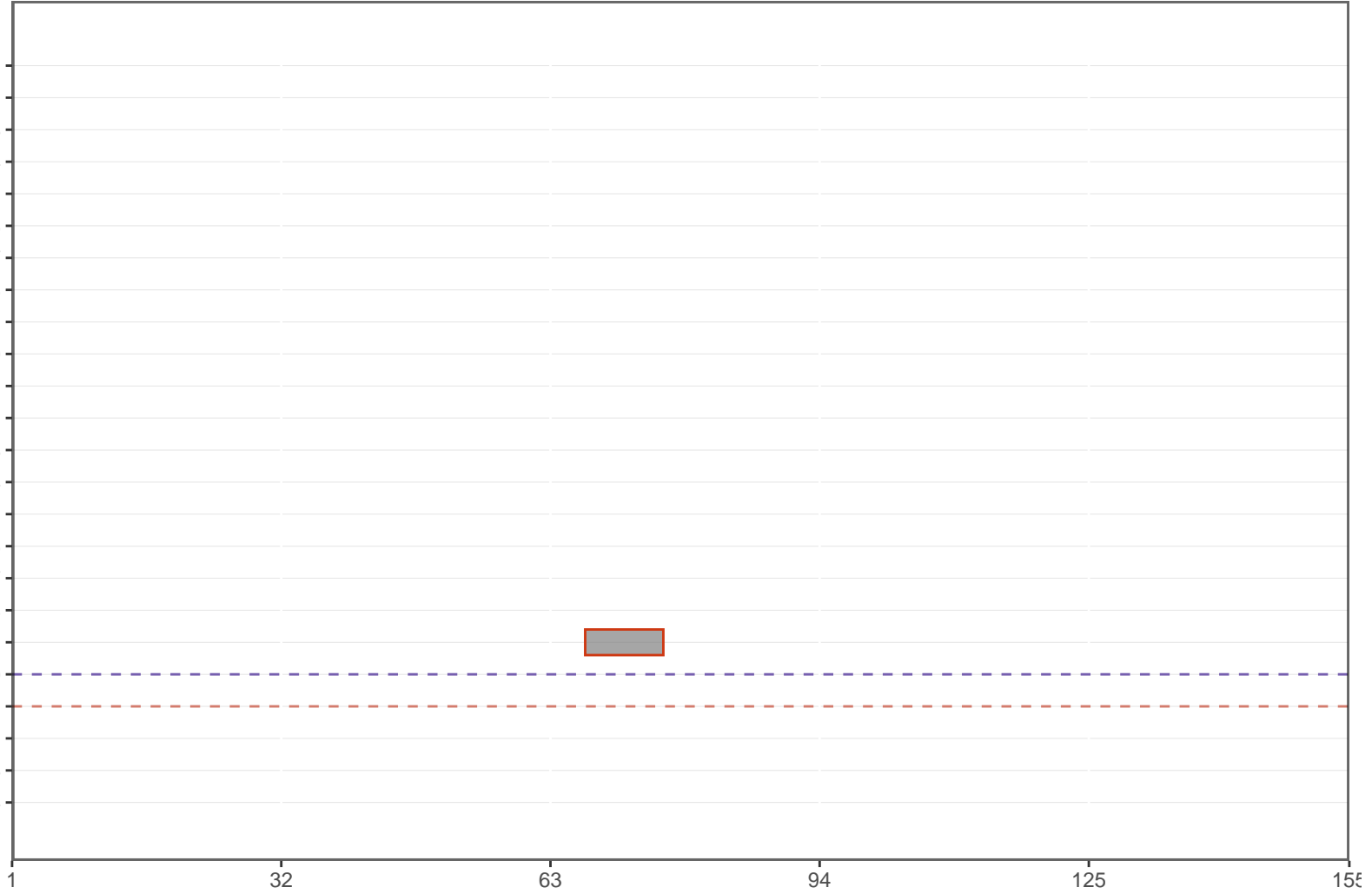
MW indication



Molecular weight

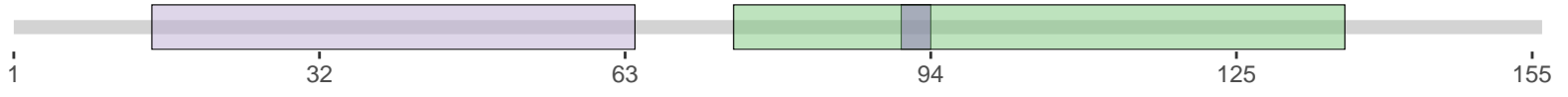


Gel Slice



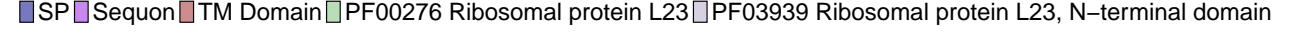
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IAPGRNKLDOYEILKYPLTTEESAMKKIEDNNTLFFVFDKADKKKKDVAKKMMYDGTGKVNFLIRPDGTRKKAVVRLTFDVALGVANKGII

NbL14g09790.1 THO_complex_subunit_4A-like [MW = 26.71 kDa]

No. of times detected



log(intensity)



Values from



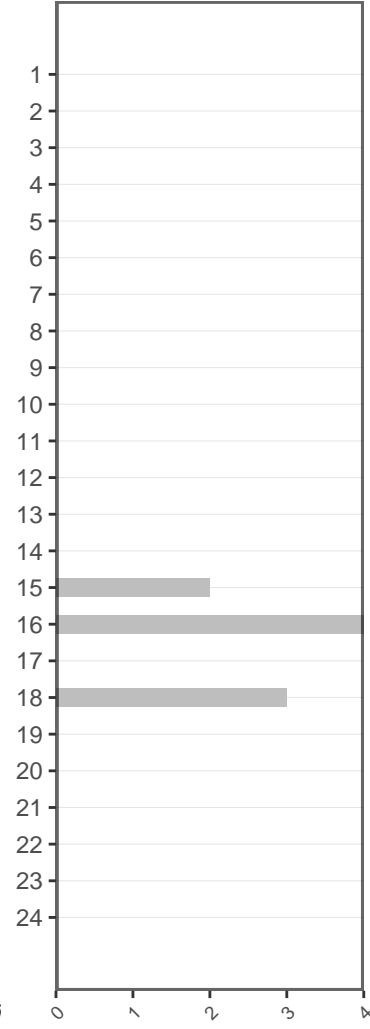
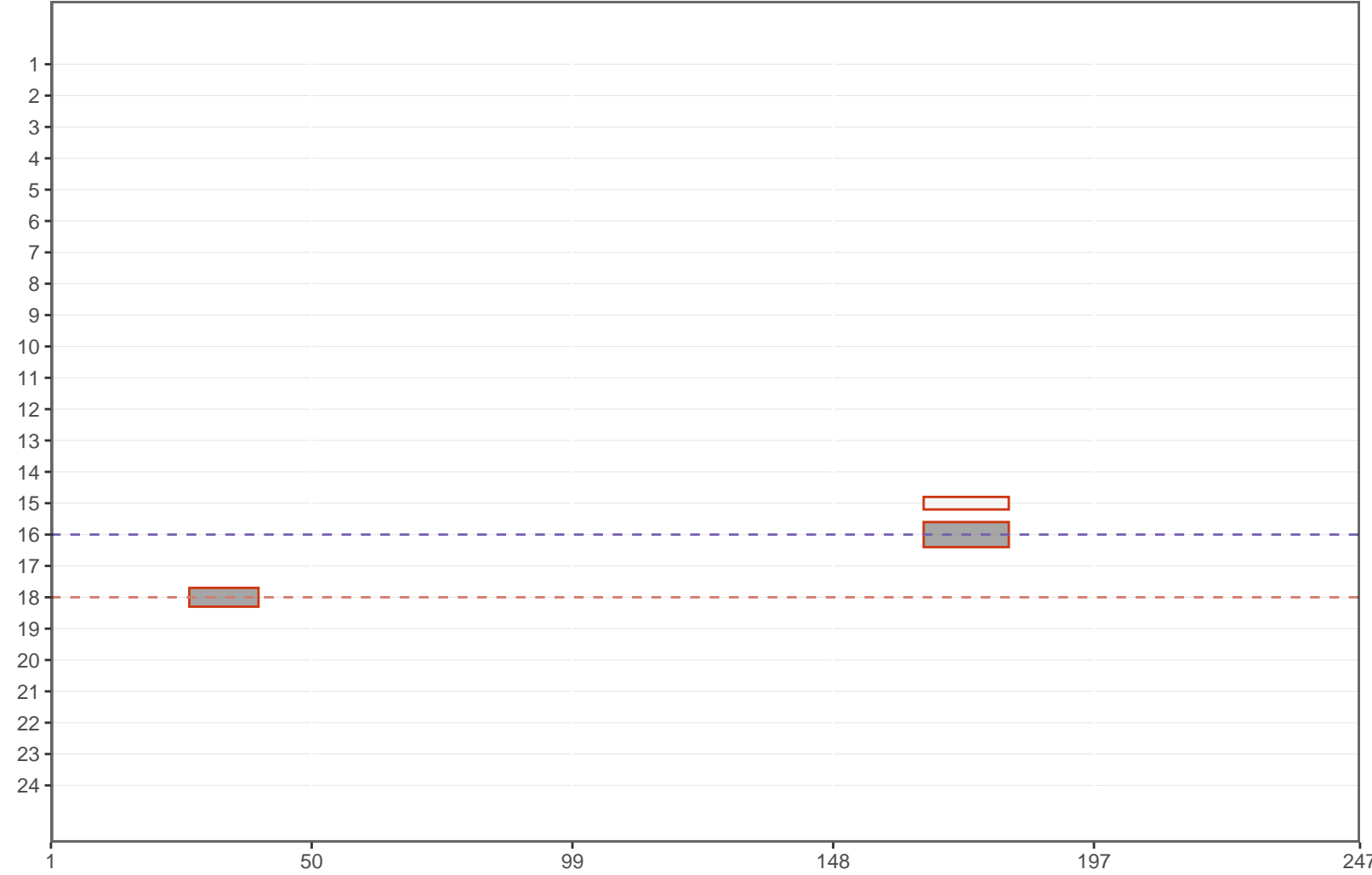
MW indication



Molecular weight



Gel Slice



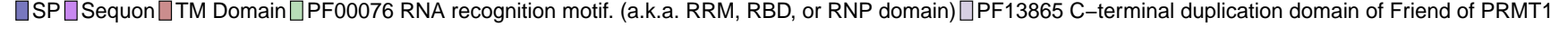
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ELFSEAGDIKRYSHYDKSGRSGKGTAEVFGRRRDAEAAKKYNNVLDGKPKMEFAGPNIGAPLPPRRNRLYRNPAPRSGQGGFRPPRRGGGRGMRKEGGRRGRGENEAELELDADLEKHYSEAMETN

NbL14g09780.1 heat_shock_cognate_70_kDa_protein_2 [MW = 70.9 kDa]

No. of times detected



log(intensity)



Values from



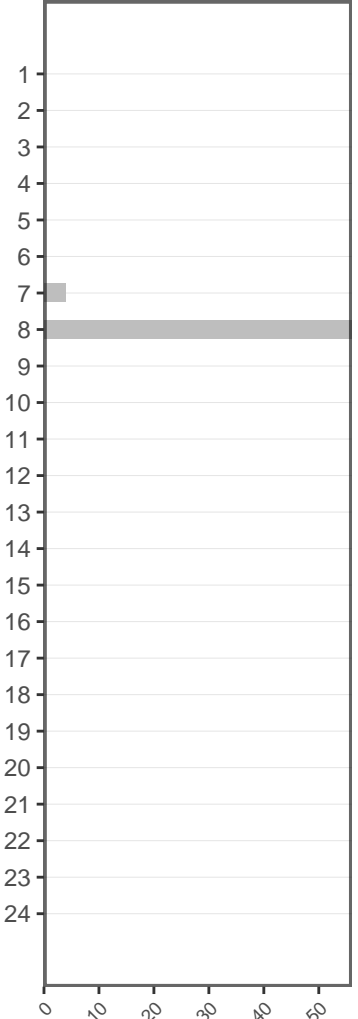
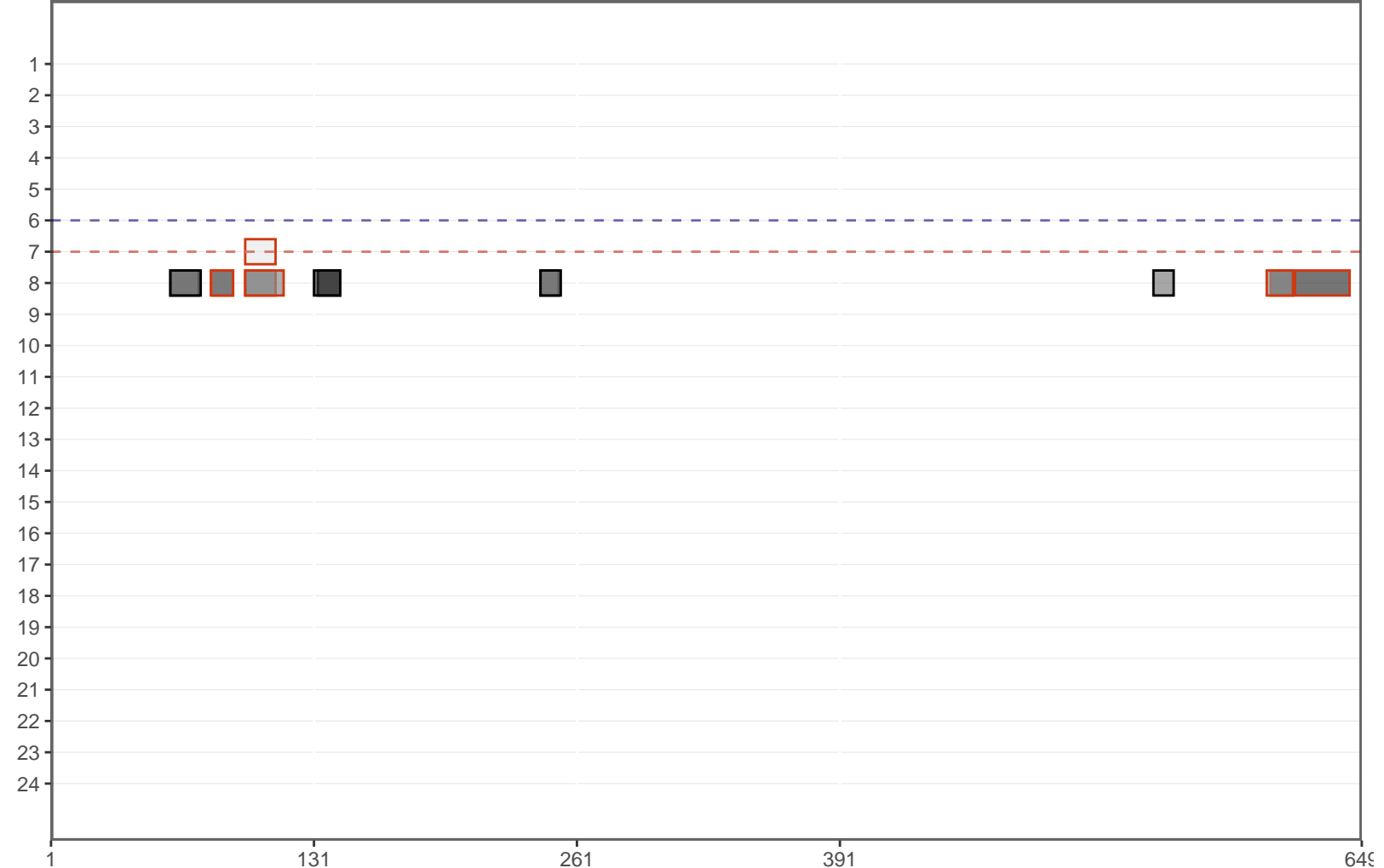
MW indication



Molecular weight

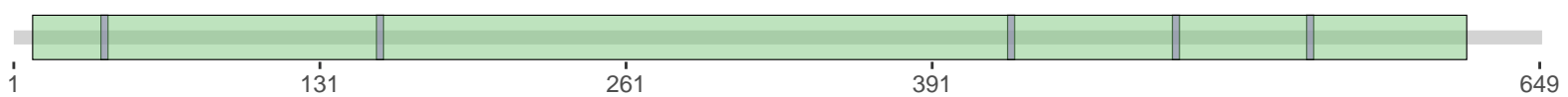


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILFRKCMIEPVEXCLRDAMDKSTVHDAVLVGGSTRIPKVDQLLGDFFNKGELCKSNPDEAWAYGAAGAAISGEGNEKVDLLLDVTFPLSLGLGTAGGVMTRVLRNTRTPTTKGEQVFTSYSDNGPGVLIQVVEGERTFRDNLKLGKFLSGIPAPRQVPOITVCFDIDANGILNVAEDKTTGGKNITITNDKGRLSKEEIEKMMVGEAEKYKSEDEEHKKVVEAKNALENVSYNMRNNTVKDEKIASKLSAEDKKKIEDAEAEAGWLDGNGLAEADEFEDKMKLEGLC

NbL14g09600.1 ribulose_bisphosphate_carboxylase/oxygenase_activase_2_chloroplastic [MW = 48.51 kDa]

No. of times detected



log(intensity)



Values from

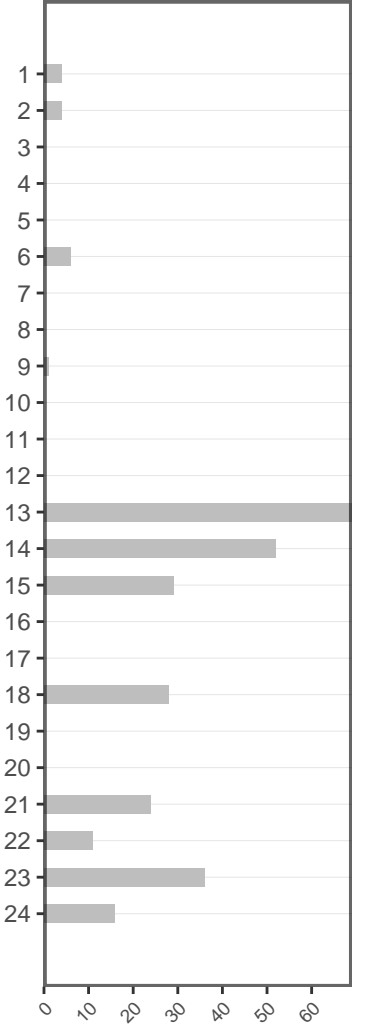
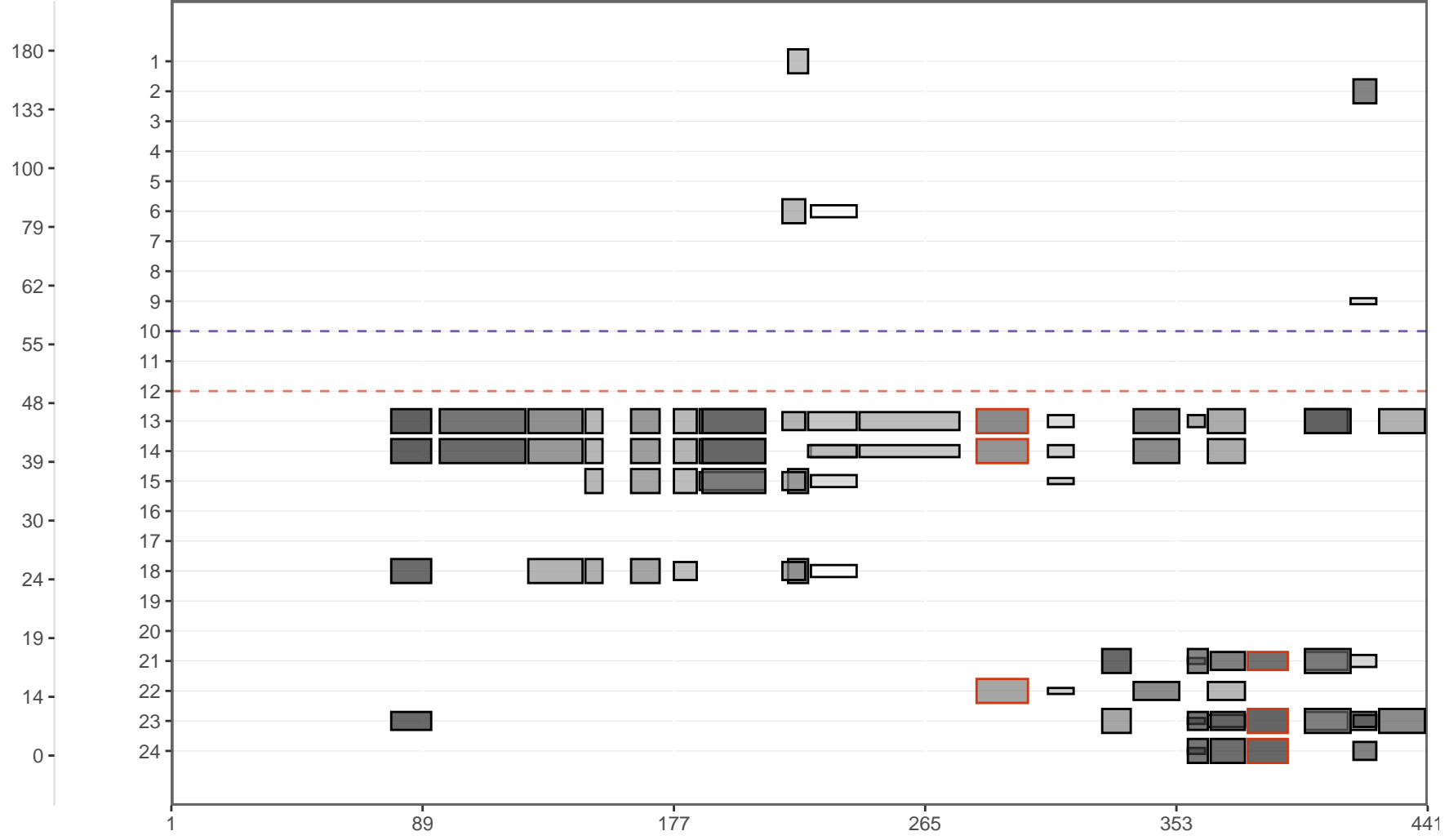


MW indication

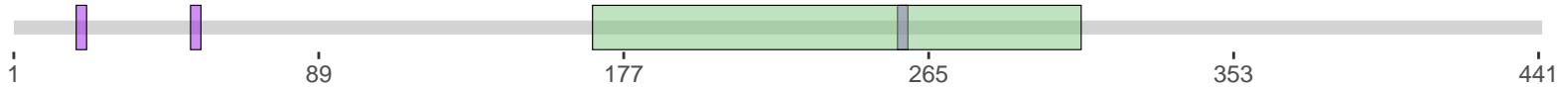


Molecular weight

Gel Slice

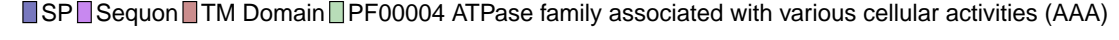


Protein length



Pfam domains

Pfam Description

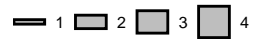


Protein sequence:

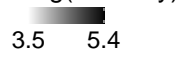
PAKLRQRYREAAEIRKGMGCLFINDLDGAGRMGGTFTQYVNNQGMVATLMLNADNPTNVQLPQGMVYKQENARVPIVVTGNDPSTLWPLURDKRMEKFFWAPTREDRIGVKGKGFRTDNPPEAAVWIKVDTFFPQSGIDFFGALRARVYDDEVRKVVSGTGEIAGDKLLNTFDGPPTFEGPQWMTVEKLLQYGNMLVGEQENKRVQLAETYLKEAALGDANADNTGNF

NbL14g09340.1 proteasome_subunit_alpha_type-4-like [MW = 30.38 kDa]

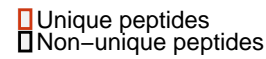
No. of times detected



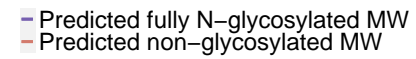
log(intensity)



Values from



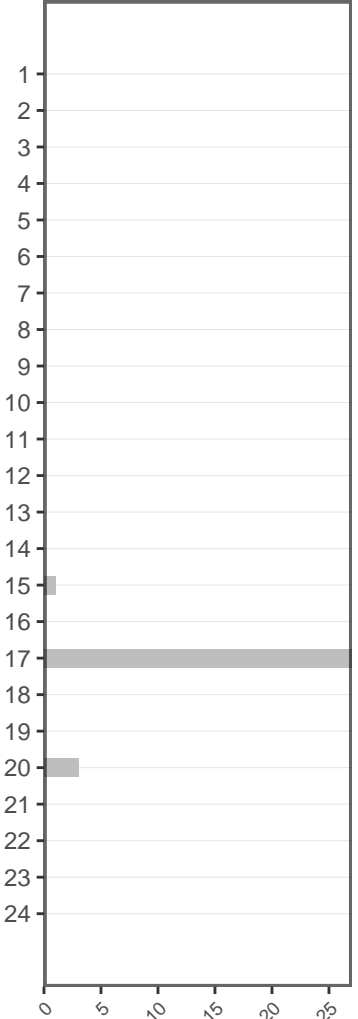
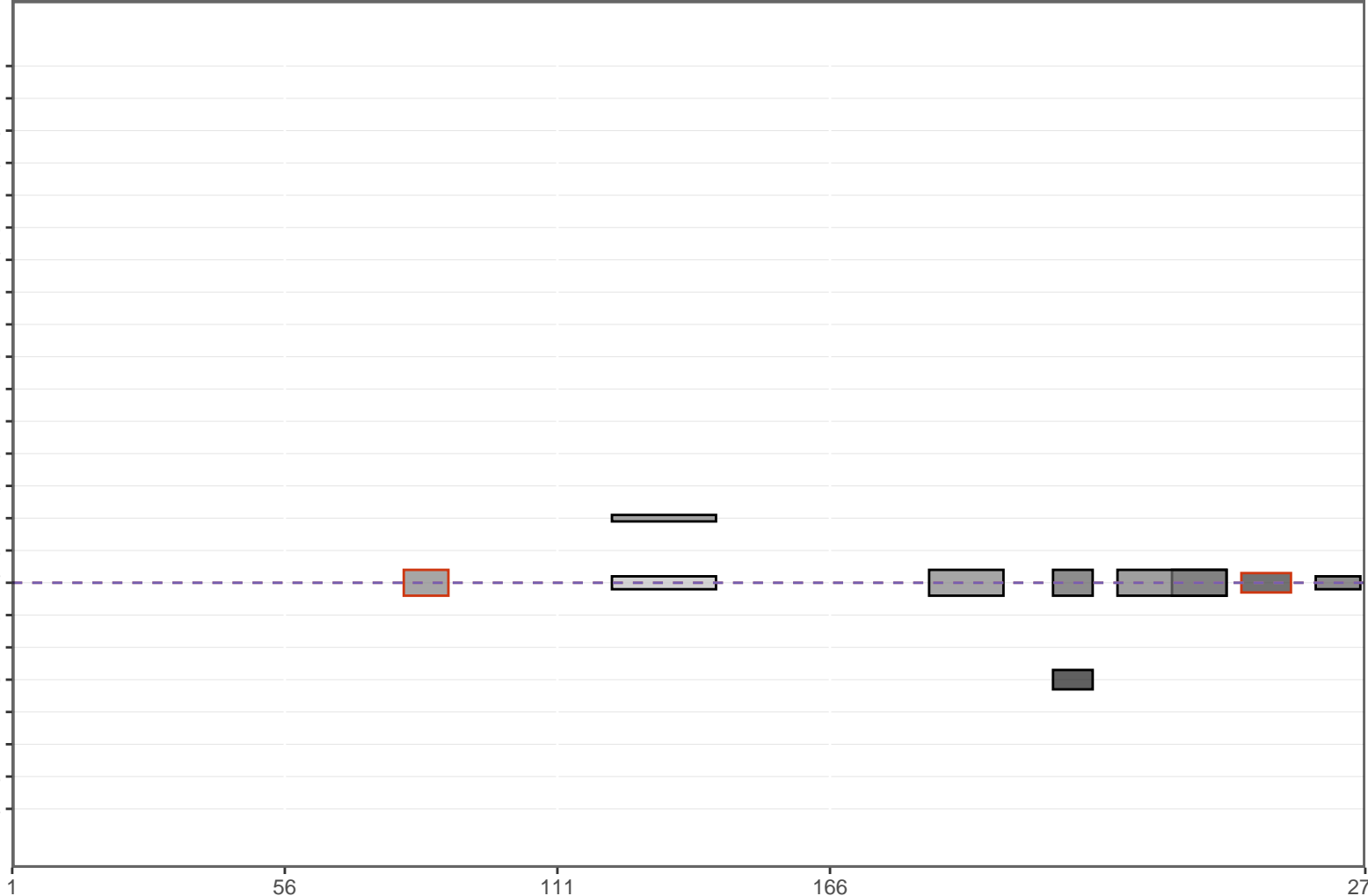
MW indication



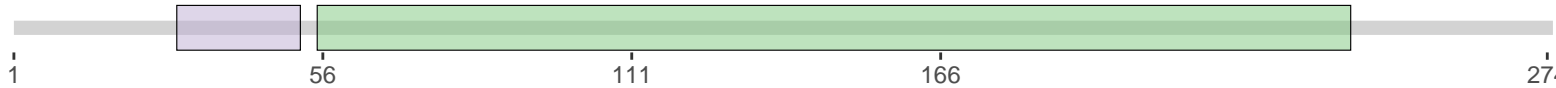
Molecular weight



Gel Slice

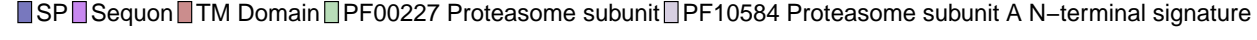


Protein length



Pfam domains

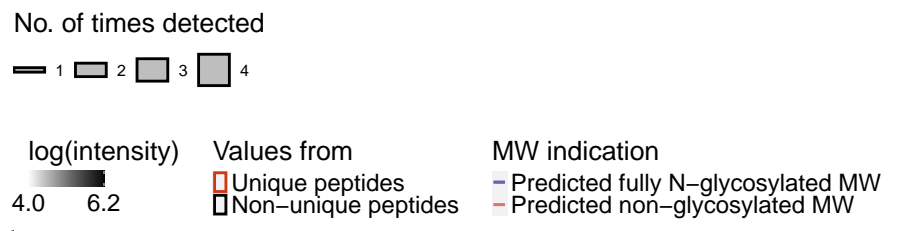
Pfam Description



Protein sequence:

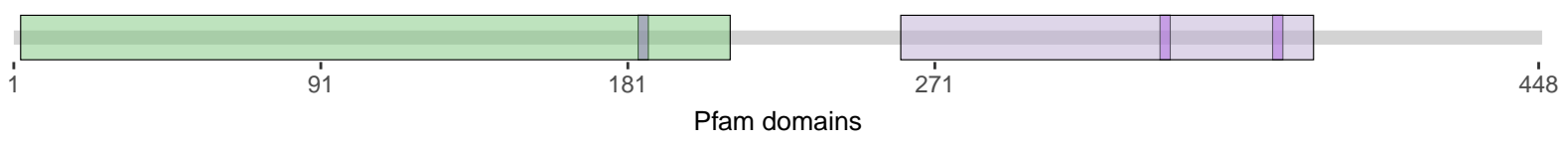
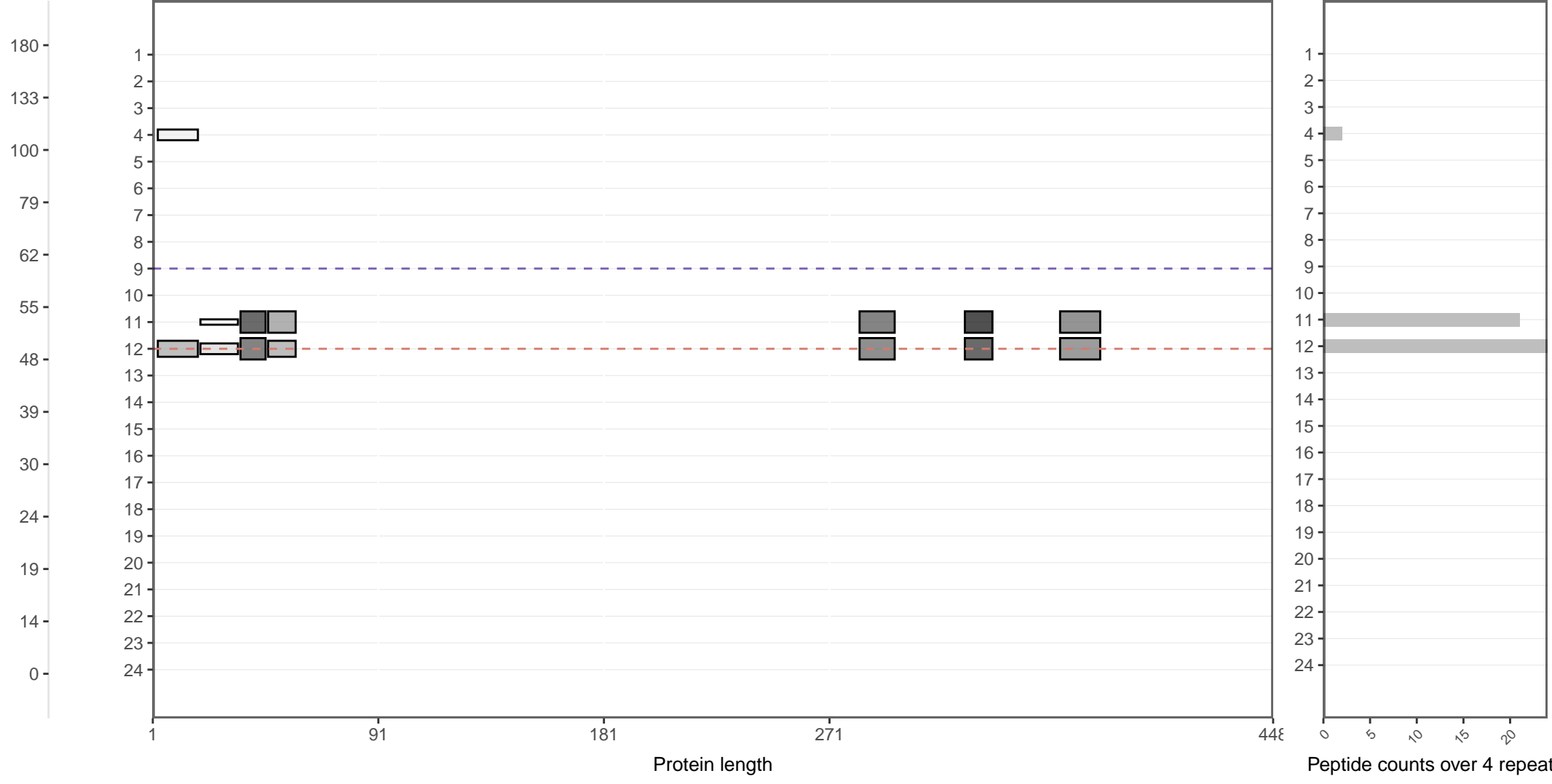
DEPMFVEQLVQSLGSDTKGQYTFQFGLRPFQVSLFAGWKNYGFQIYMSDPGNGYGGWKAASGANNGFAGEMLKGDYKDDITREEAVGLKLVKSKTMDSTLSTSEKLELAEVFQTNKRWKHHVHSEPELNRIKLLKYLGTQAPEN

NbL14g09320.1 tubulin_beta-2_chain-like [MW = 50.28 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF00091 Tubulin/FtsZ family, GTPase domain PF03953 Tubulin C-terminal domain

Protein sequence:
 FRTLLKLTTPSGDNLNLSATMBSGVTGGLRFPQGLNSDLRKLAVLIPFRLHFFMVGFAPLTGRGSGQYRALTVELTQGMWDKNNMGAADPRHGRYLTASAMFRGKMKSTKEVDEGMNLVGNKNSYFVEVWIPNNVKSFLVGDIPPTGLKMASTFRGNSTSGEMFRFRVSEQFTAMFRKALHVVYTGEGMDMEFTFEESNNDLVSEYQYQDQATDEEGDYVEEEEEQLIEA

NbL14g09270.1 probable_glutathione_S-transferase [MW = 26.54 kDa]

No. of times detected



log(intensity)



Values from



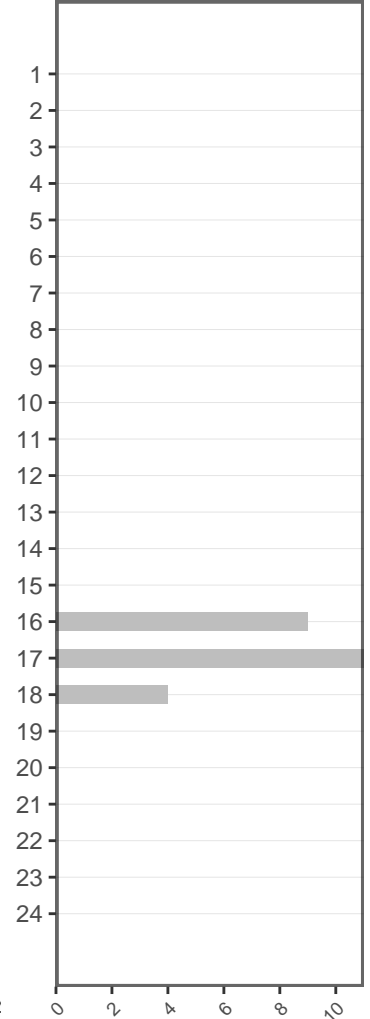
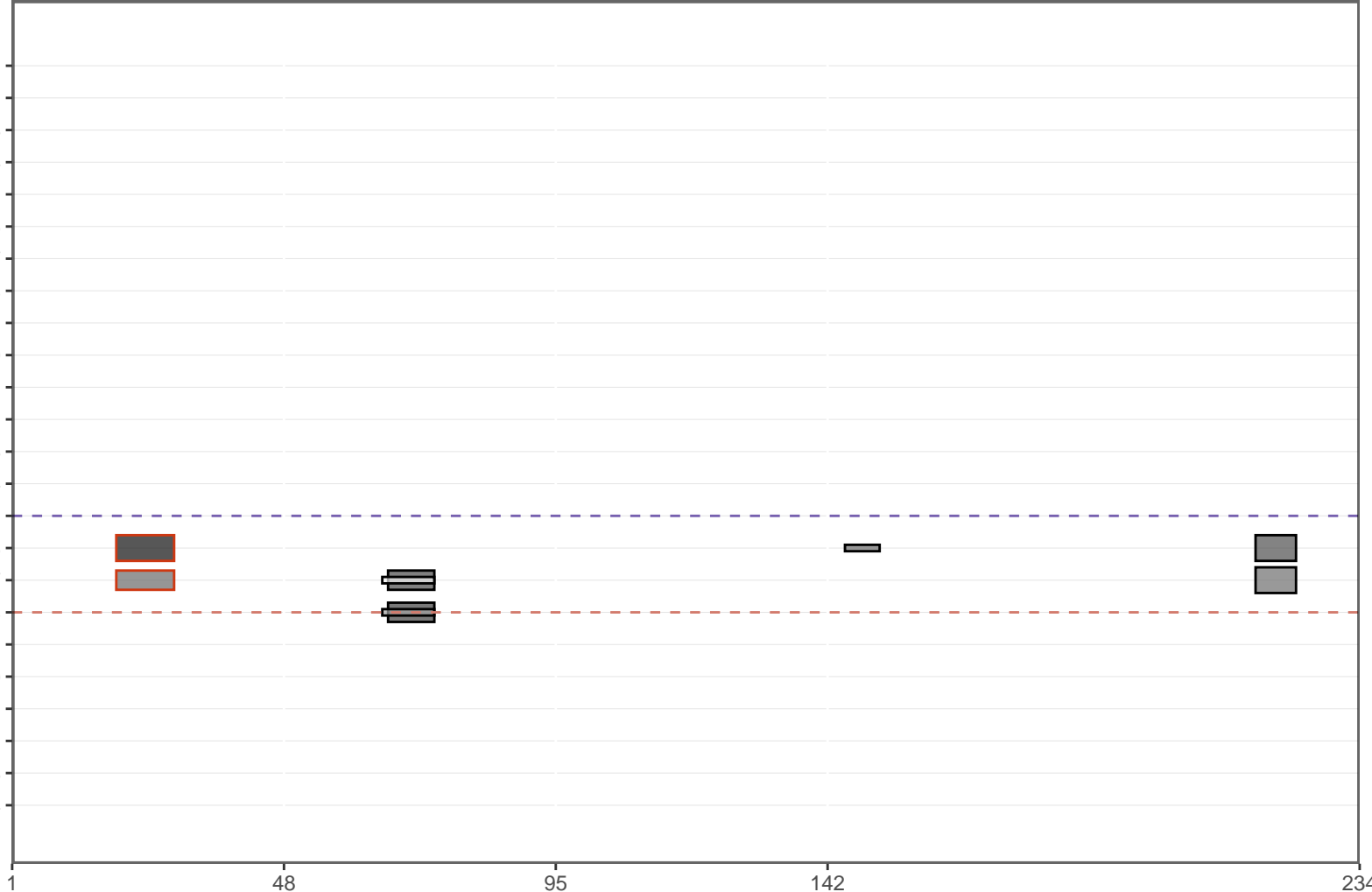
MW indication



Molecular weight



Gel Slice



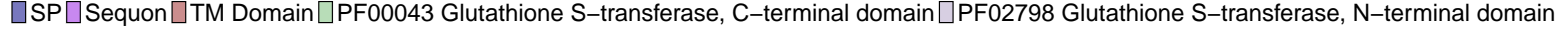
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IRFLVYKFLDEKCLPAWAKWALWKGEGGDKKEEAYEVKLVLDNEVVDKDKYFGGKIGIVDAAANFVGFVWGVVEATGVLLVTSKPFPHFGTWRREYVINGSGVKEKMPNREMLLGYFKGRVRAATPK

NbL14g09180.1 ribulose_bisphosphate_carboxylase/oxygenase_activase_1_chloroplastic-like [MW = 48.61 kDa]

No. of times detected



log(intensity)



Values from



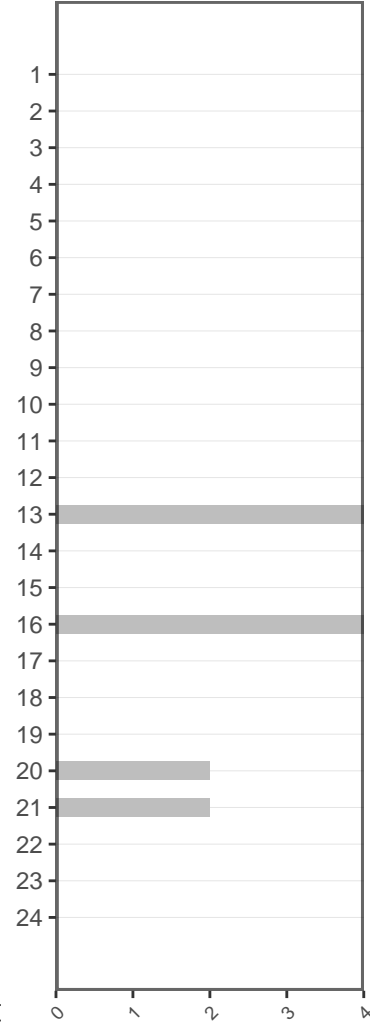
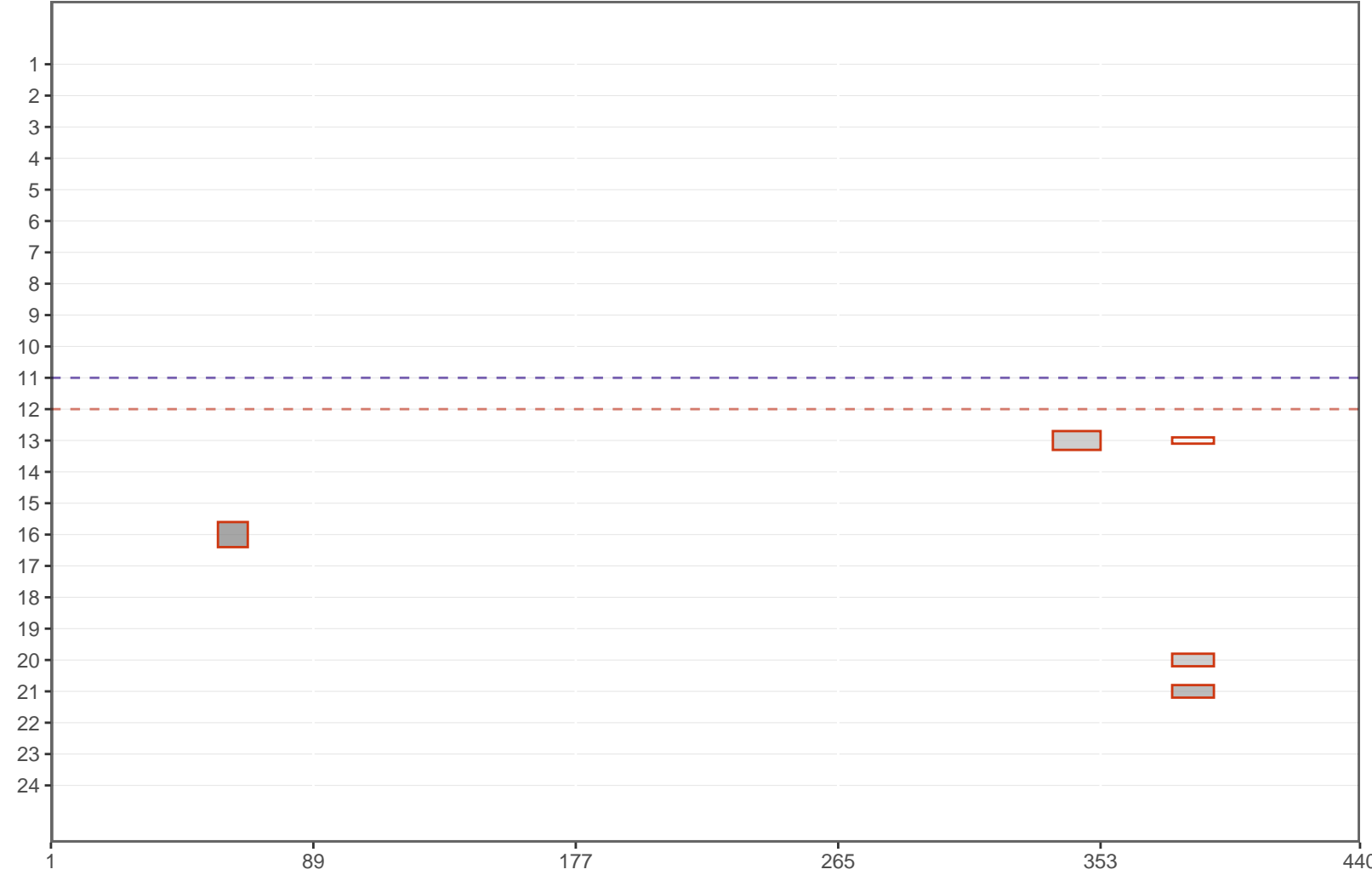
MW indication



Molecular weight

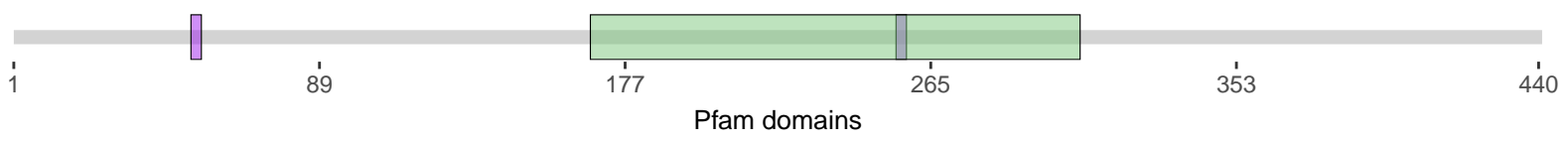


Gel Slice

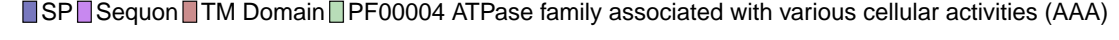


Protein length

Peptide counts over 4 repeats



Pfam Description



Protein sequence:

WKLIRQRYREAAEIRKGNMGVLFINDLBDAGAGRMGGTTQYTVNNGM/NATLMAADNPTNVLQPGMYNKGENARVPIVGTGNDFTSLVAPLRDGMENKFWWPTREDRIGVCKGFRITDDEVFDEHVVRLVDAFFGSDIFFGALRARVYDDEVKRWIESTGIEQVGEKLNLSIDGPTTFEQPKMTIDKLLKLEYNGLLVDEGENKRVQLADKYLKEALGDANADMTGTF

NbL14g09160.1 glucose-induced_degradation_protein_4_homolog [MW = 23.77 kDa]

No. of times detected



log(intensity)



Values from



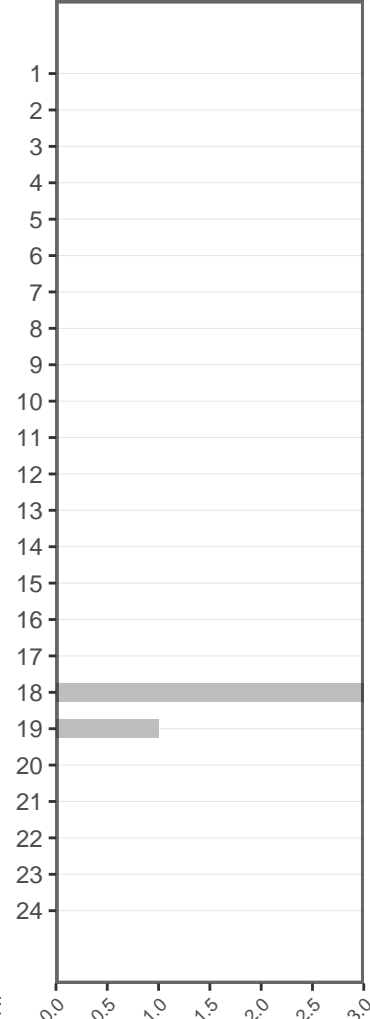
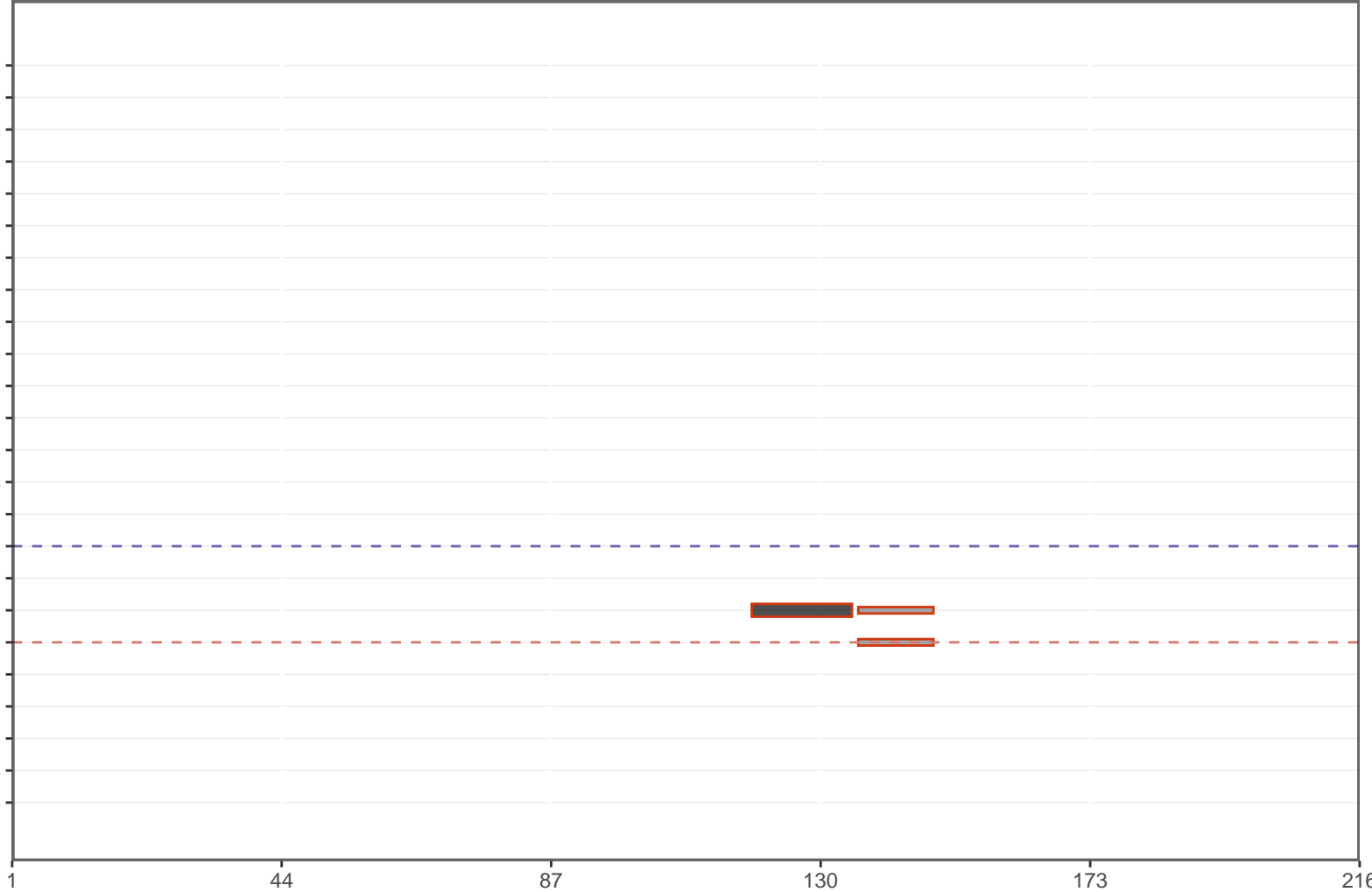
MW indication



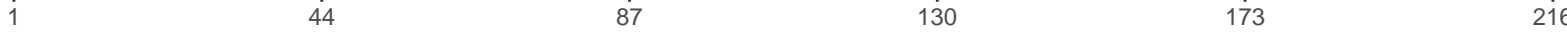
Molecular weight



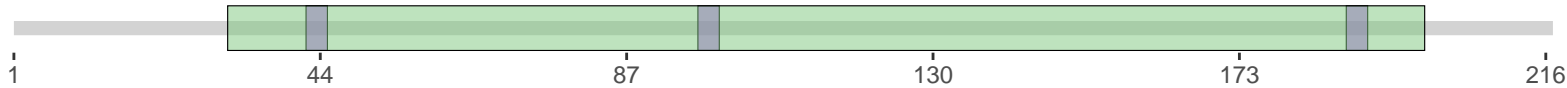
Gel Slice



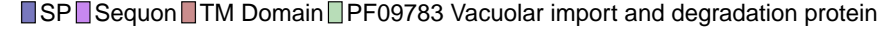
Protein length



Pfam domains



Pfam Description



Protein sequence:

ITKNTYFTFGKVGATSEDDKHGHTKFPFSPLLSGVEVDGKSLDLSNYPVFMRWKEQYFVAVGTDGGLTAGFYVYVFCGSDGSGNFYVDPNSFPQKLELKSTNEGRGSGFSSVEYLG*

NbL14g09090.1 acyl-coenzyme_A_oxidase_4_peroxisomal-like [MW = 47.02 kDa]

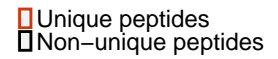
No. of times detected



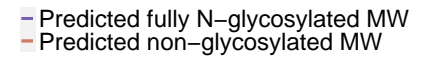
log(intensity)



Values from



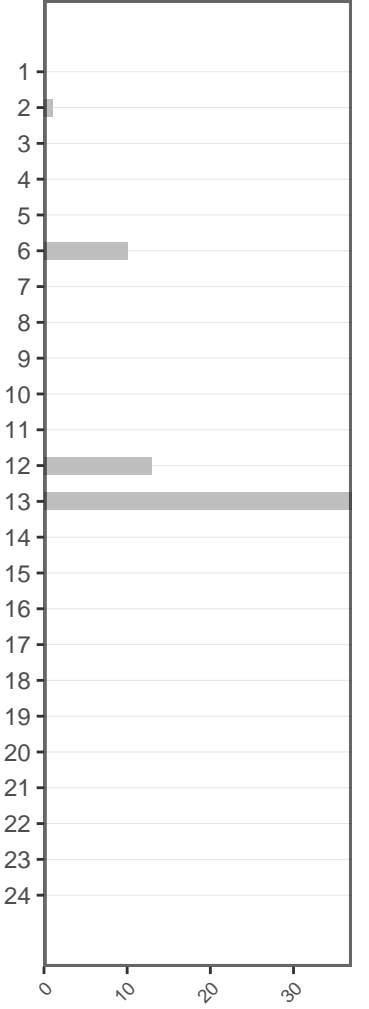
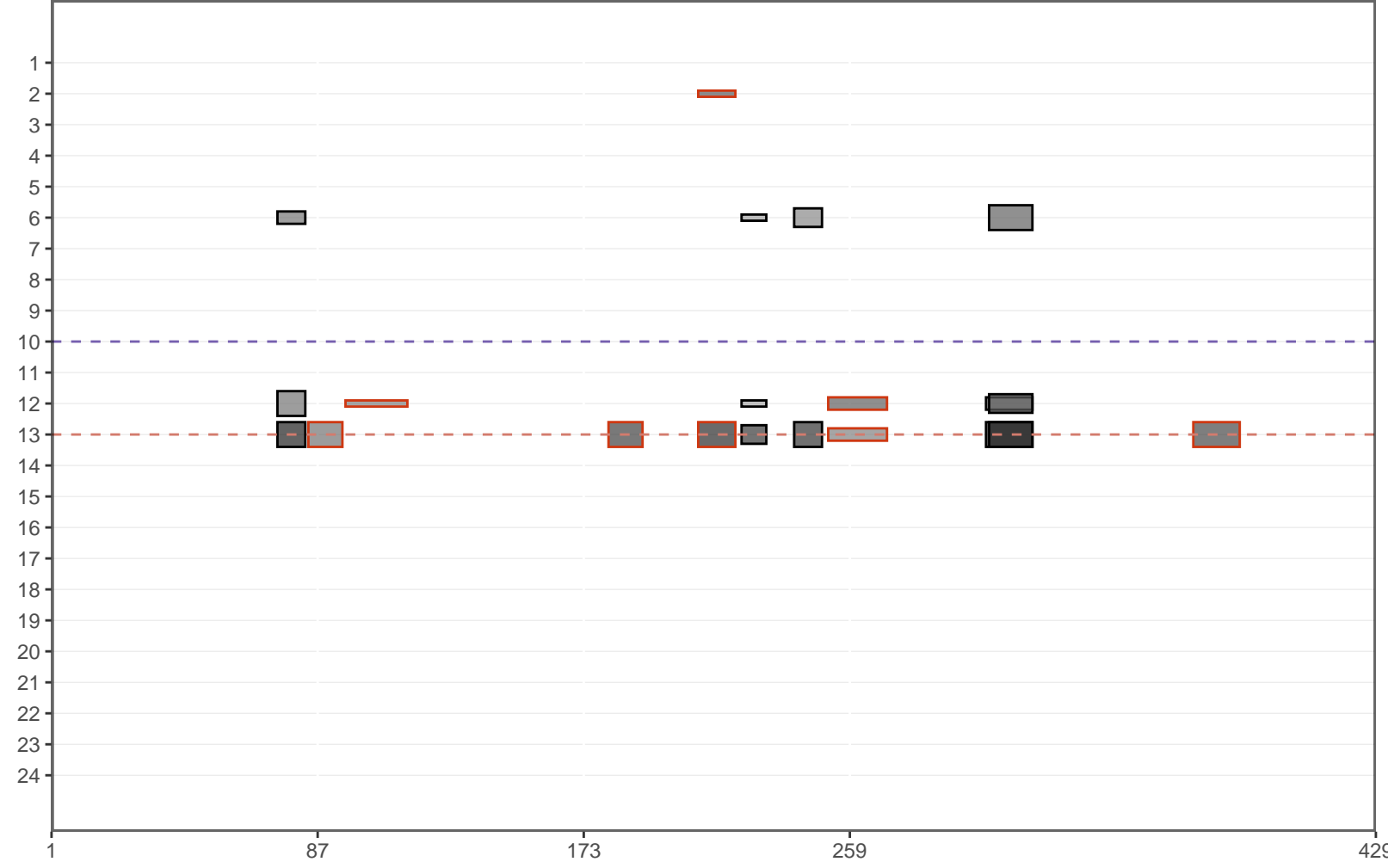
MW indication



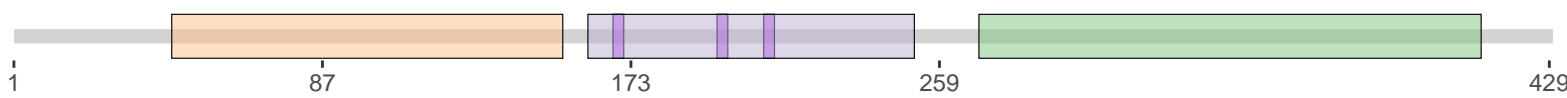
Molecular weight



Gel Slice

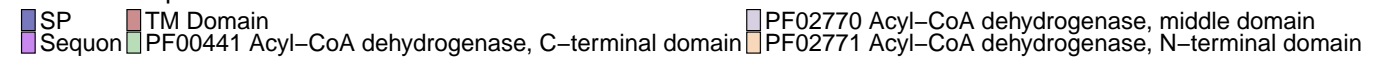


Protein length



Pfam domains

Pfam Description



Protein sequence:

FADLVFARNTSTNGNGFVKKDAPGLQATKIKIQLRMVQNSDILKKVFPDIEDLPGVNSFGDITNKVLAVSRVMAVWQPIGIMGVYDMCHRYLKERIKGFGAPLAFAFGINQKLVGMLGNQAMLVGWRLKGWLVESGKMTFPGHABLGKSWIFLRARETVSLGRELGGNGLADLVAKAFCDLEPRVTVYEGTFDINTLVTGREIFGLASFKPPLRQKSRV

NbL14g09010.1 uncharacterized_protein_At5g01610-like [MW = 19.21 kDa]

No. of times detected



log(intensity)



Values from



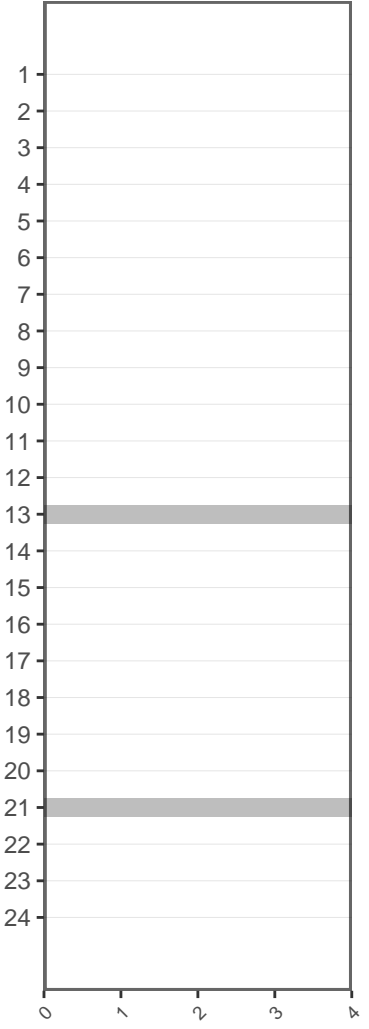
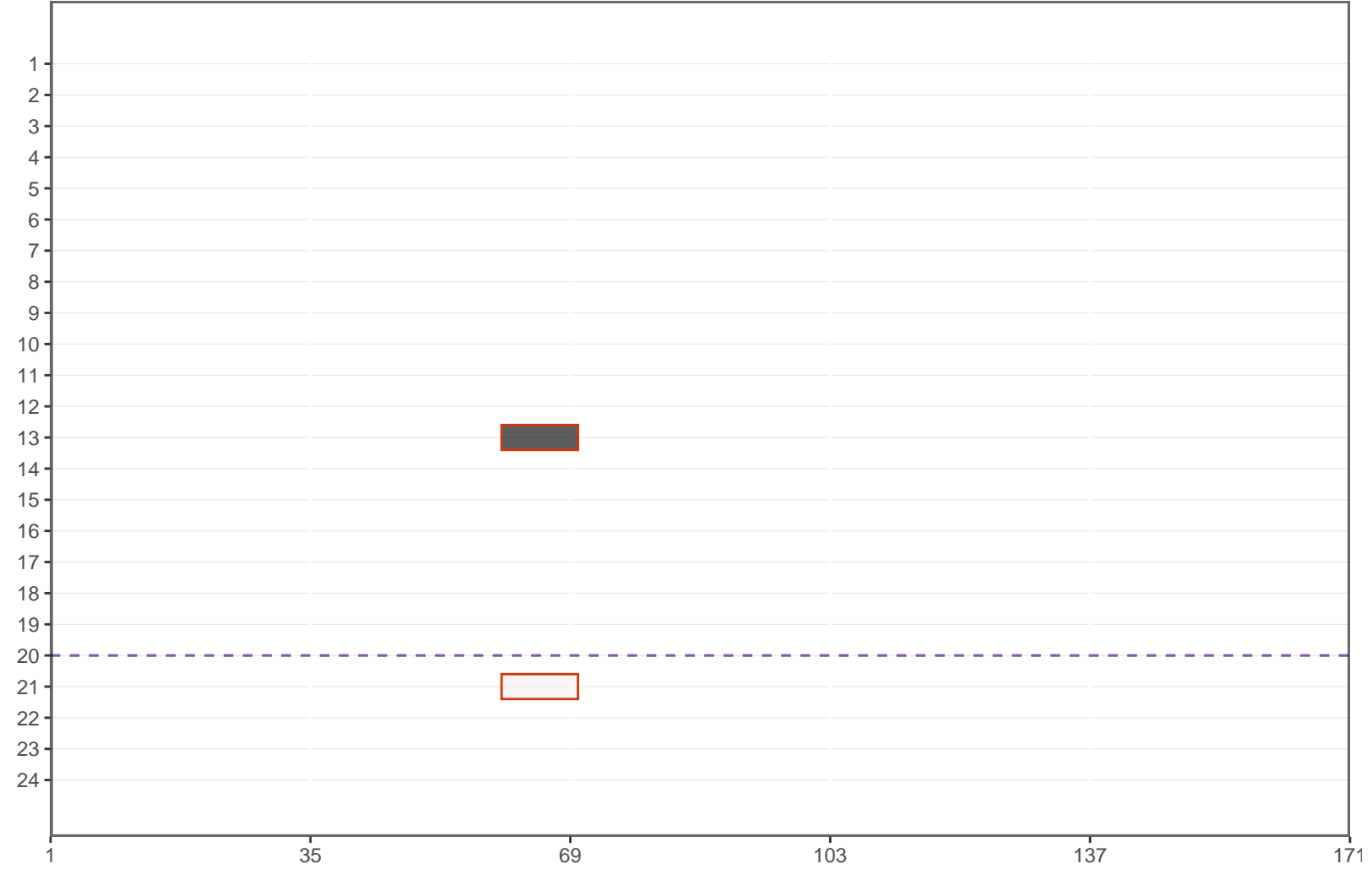
MW indication



Molecular weight



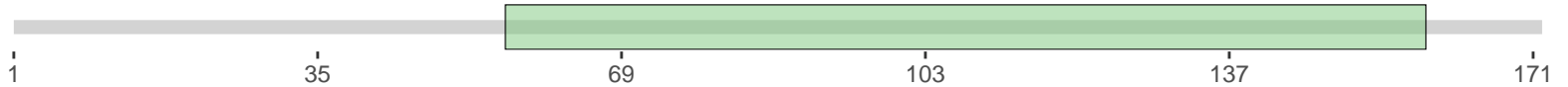
Gel Slice



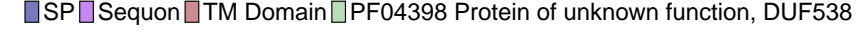
Protein length



Pfam domains



Pfam Description



Protein sequence:

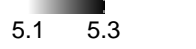
ATNYEYFNEETKTKFTYIPVGVCEVGYMDSSVLRFSYAVTGVLEKGLADIEGRKTKVMMWVVTASSEKSLHFTVGLKKTGRSEAYEVLRDGVAVDKF

NbL14g08960.1 macrophage_migration_inhibitory_factor_homolog [MW = 12.07 kDa]

No. of times detected



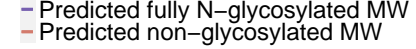
log(intensity)



Values from



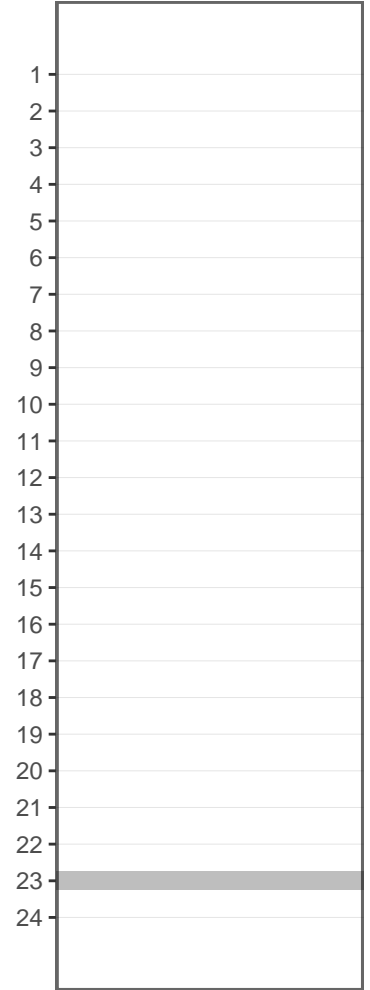
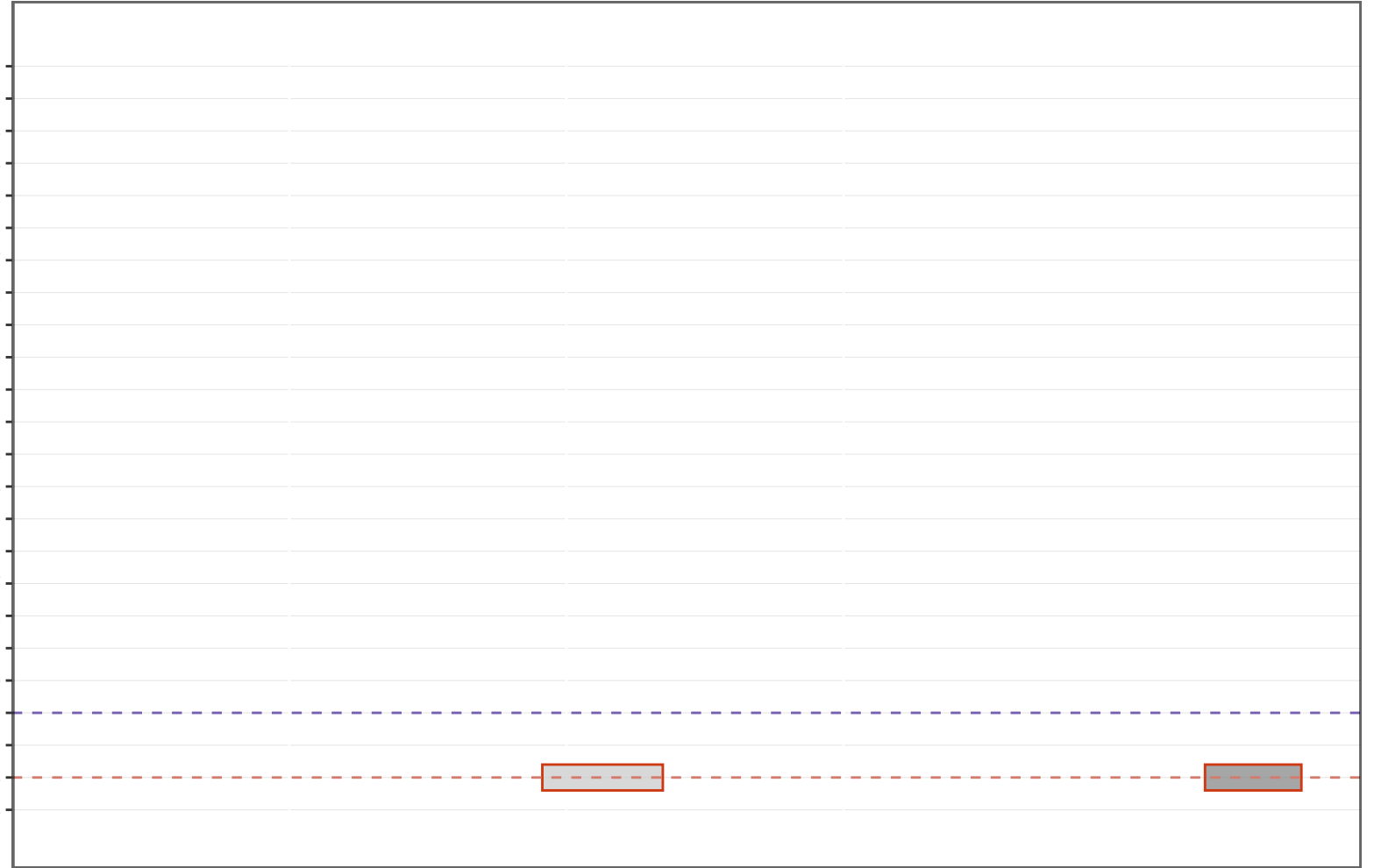
MW indication



Molecular weight

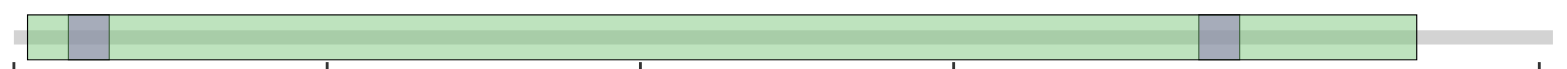
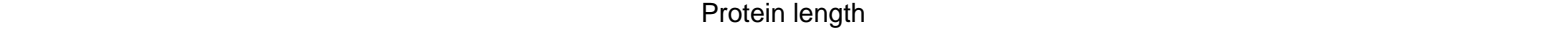


Gel Slice



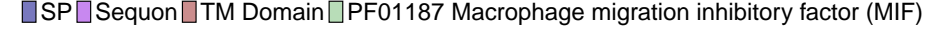
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LKGSVDISFGNKEAAFAEIVSMGGINSQKRNLIWLGTLHNNFSIPRTRFFLKYVDITMATKFSKL

NbL14g08740.1 non-specific_lipid-transfer_protein_2-like [MW - SP = 11 kDa]

No. of times detected



log(intensity)



Values from



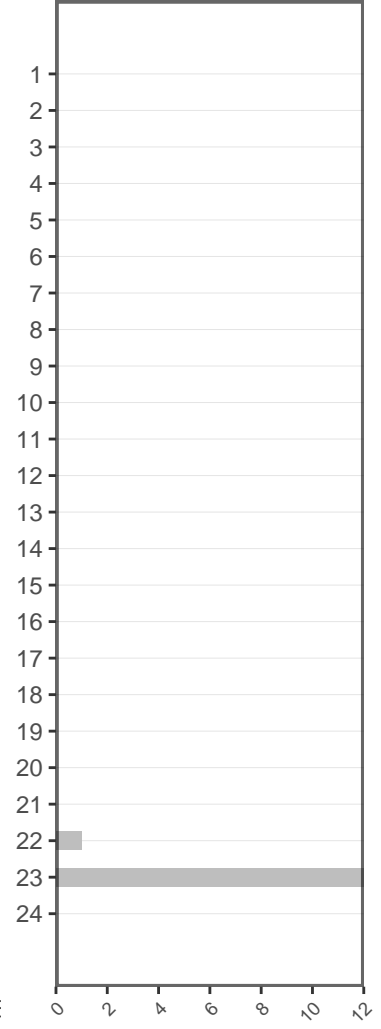
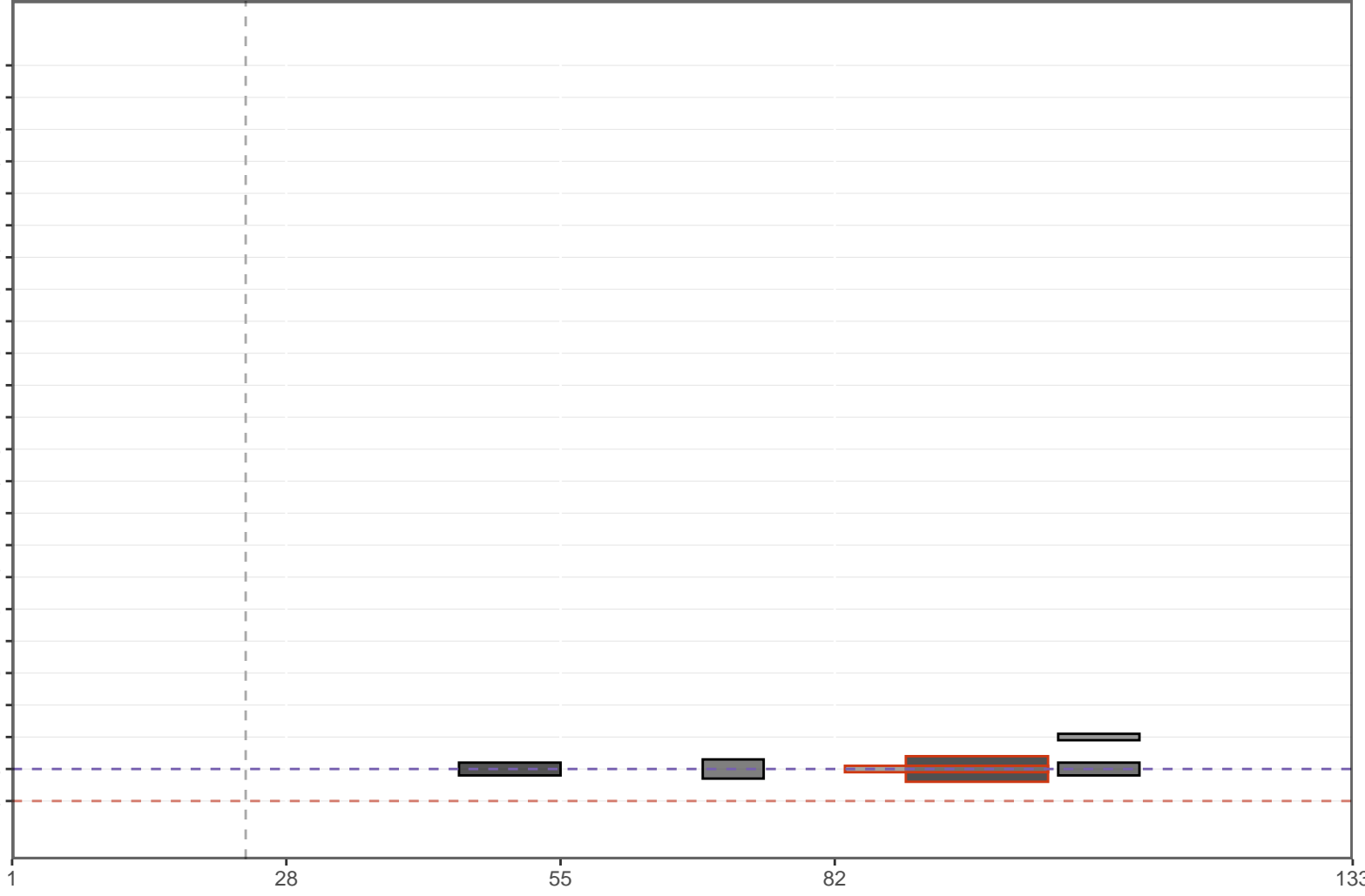
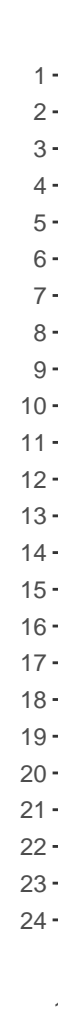
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

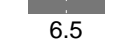
GGVKGLLGAALKSPADRKTACTGLKSAANAIGIDMGKAALFPAAGGVNIPWISPTDGSKYVSPFLSYVAFMLSSFEYV

NbL14g08730.1 non-specific_lipid_transfer_protein_2-like [MW - SP = 10.17 kDa]

No. of times detected



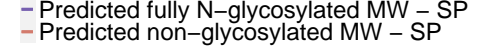
log(intensity)



Values from



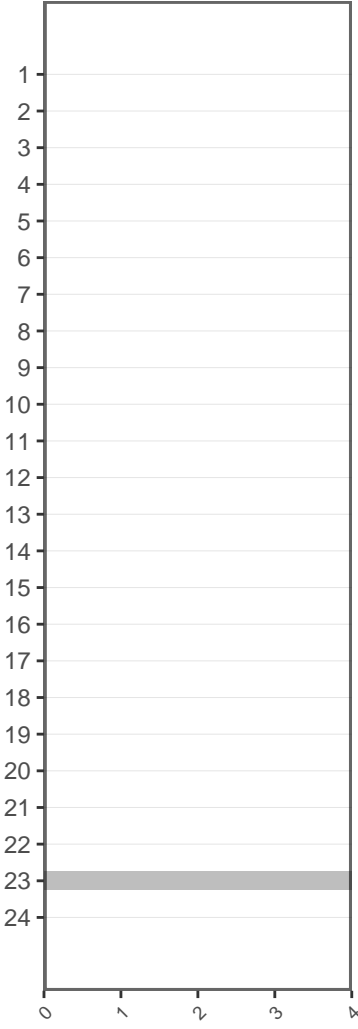
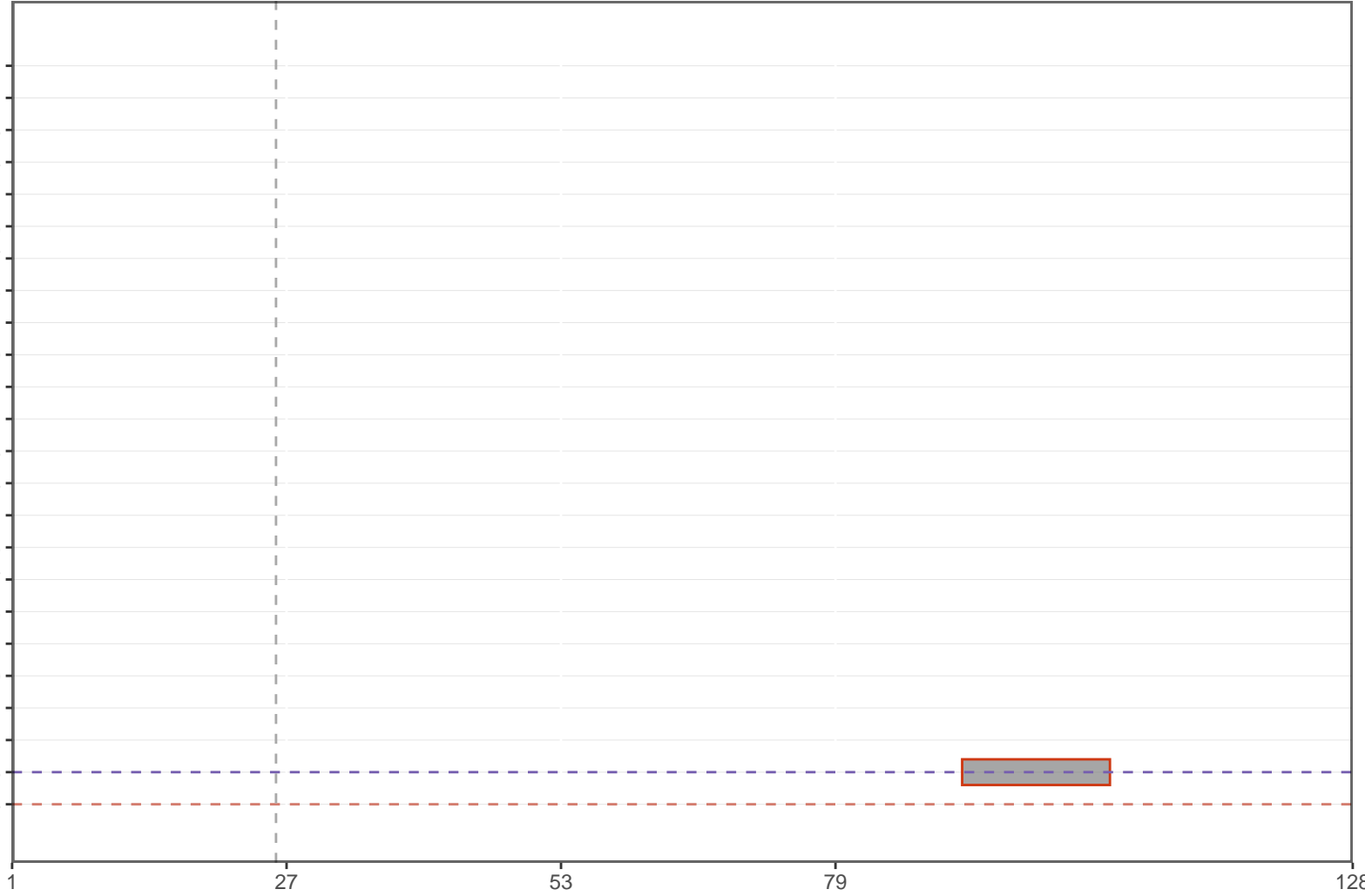
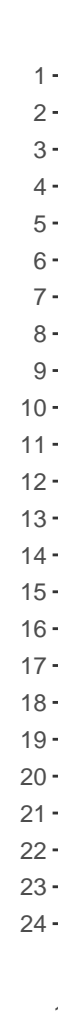
MW indication



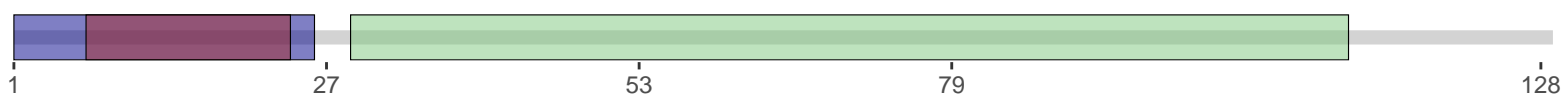
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

IGCCGGYKLLGAAKSGTDRKTAAGLTKGSAANAKGIDMGKAAAGLPGAGVNPYKRPSTGCEKYVQQLLFLTEL*

NbL14g08710.1 non-specific_lipid-transfer_protein_2-like [MW - SP = 8.56 kDa]

No. of times detected



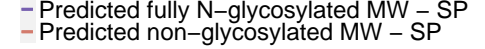
log(intensity)



Values from



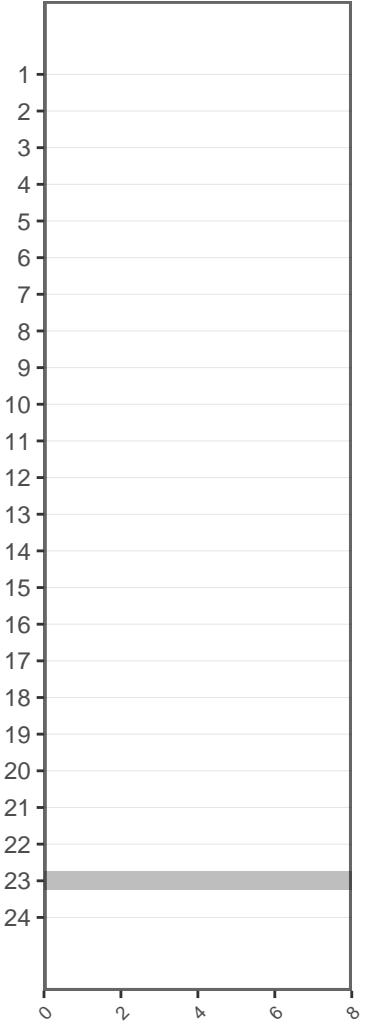
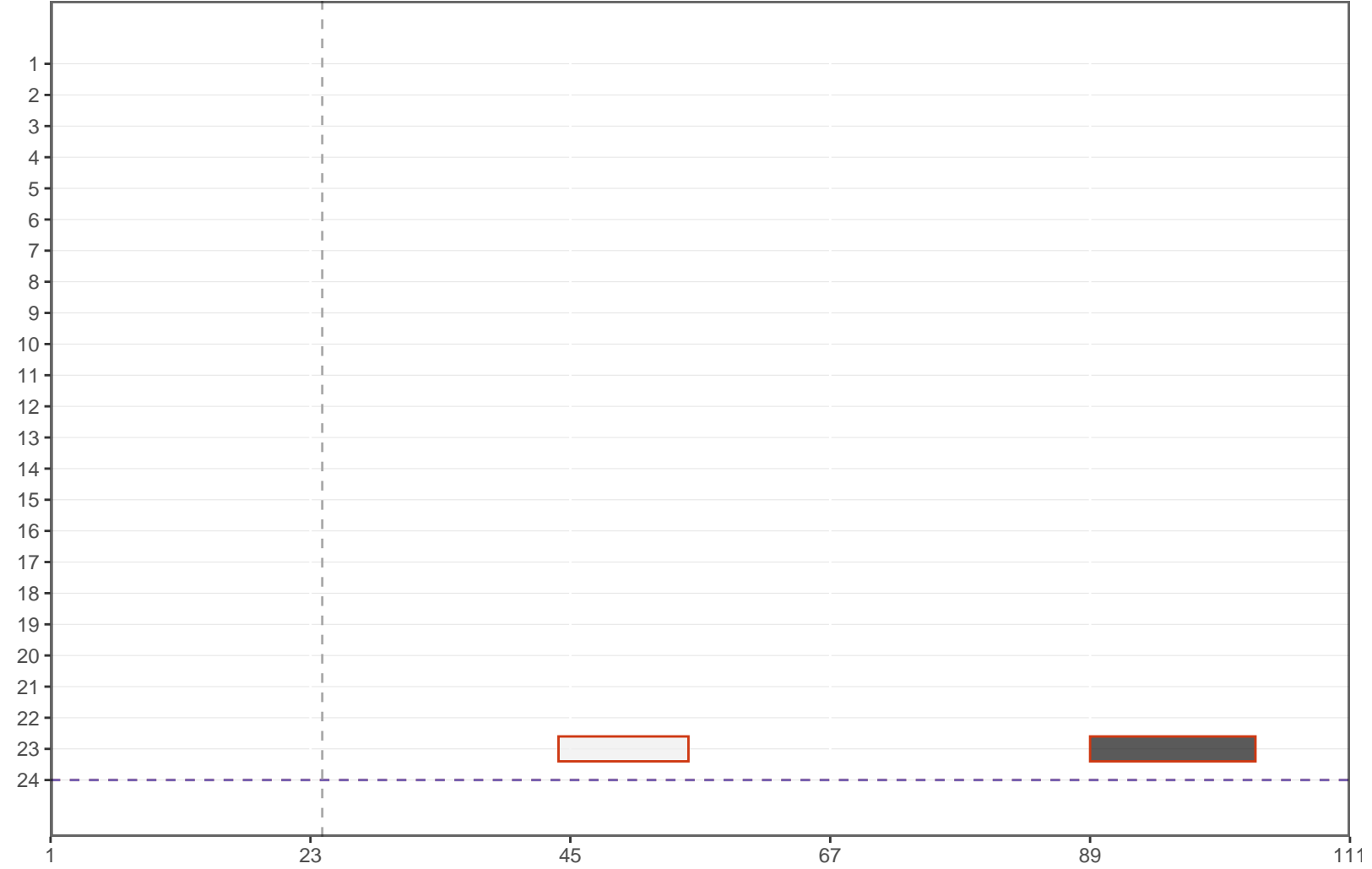
MW indication



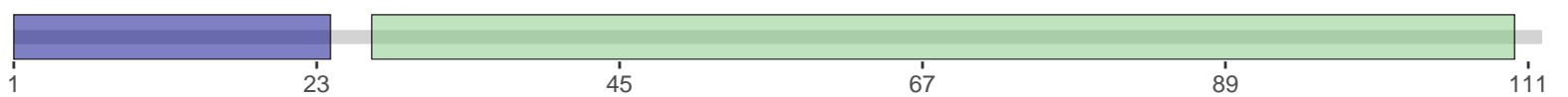
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

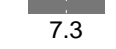
RRGLGGCCGGYKLLGAANKSPDRKTAGSGLKSAANKIGIDMKKAAGLPVGGVNIPIYKIPSTDCG

NbL14g08700.1 non-specific_lipid-transfer_protein_2-like [MW - SP = 9.28 kDa]

No. of times detected



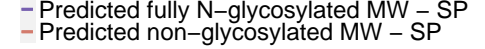
log(intensity)



Values from



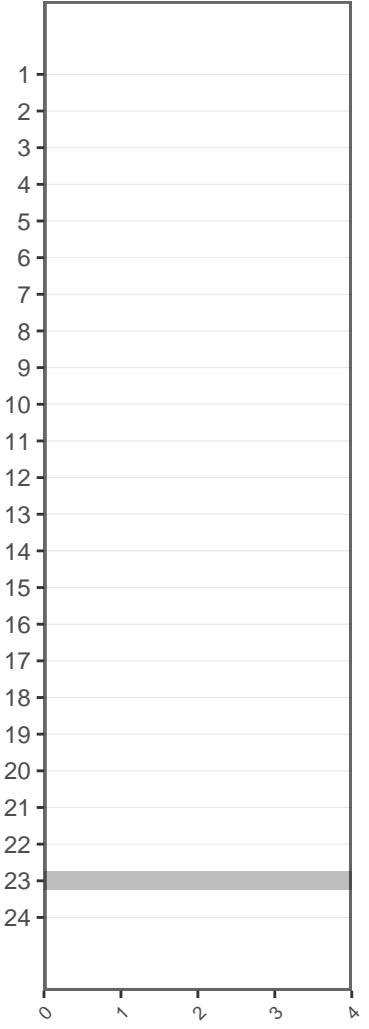
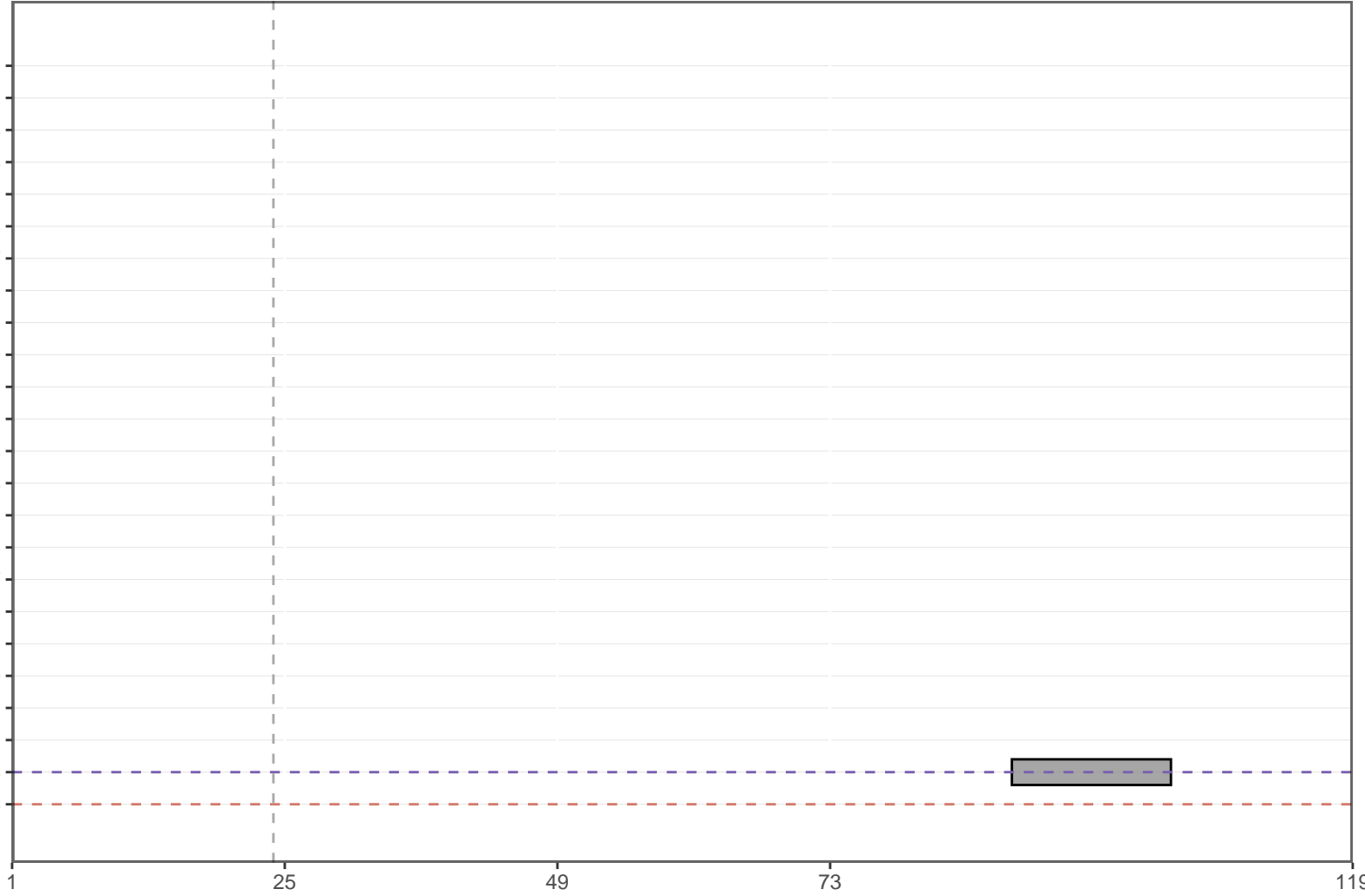
MW indication



Molecular weight

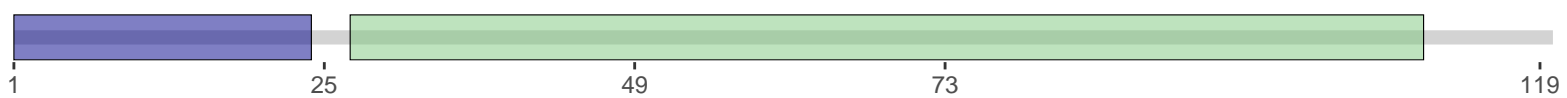


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

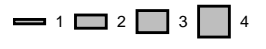


Protein sequence:

PLGGCCGGVKQLLGAANKSPDRKTAICTLKLKSAANAIGIDMGKAAGLPBADGVNIPYKISPSTDCSKYVFSSE

NbL14g08660.1 elongation_factor_P-like [MW = 25.79 kDa]

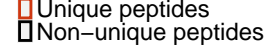
No. of times detected



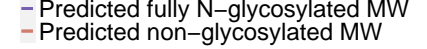
log(intensity)



Values from



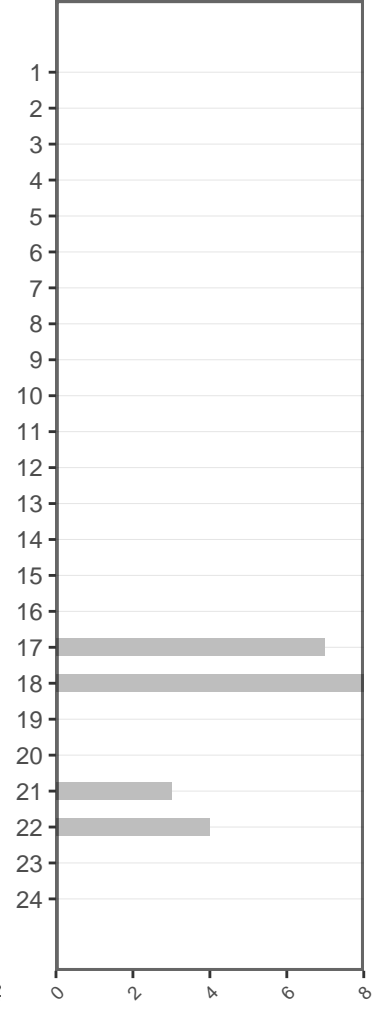
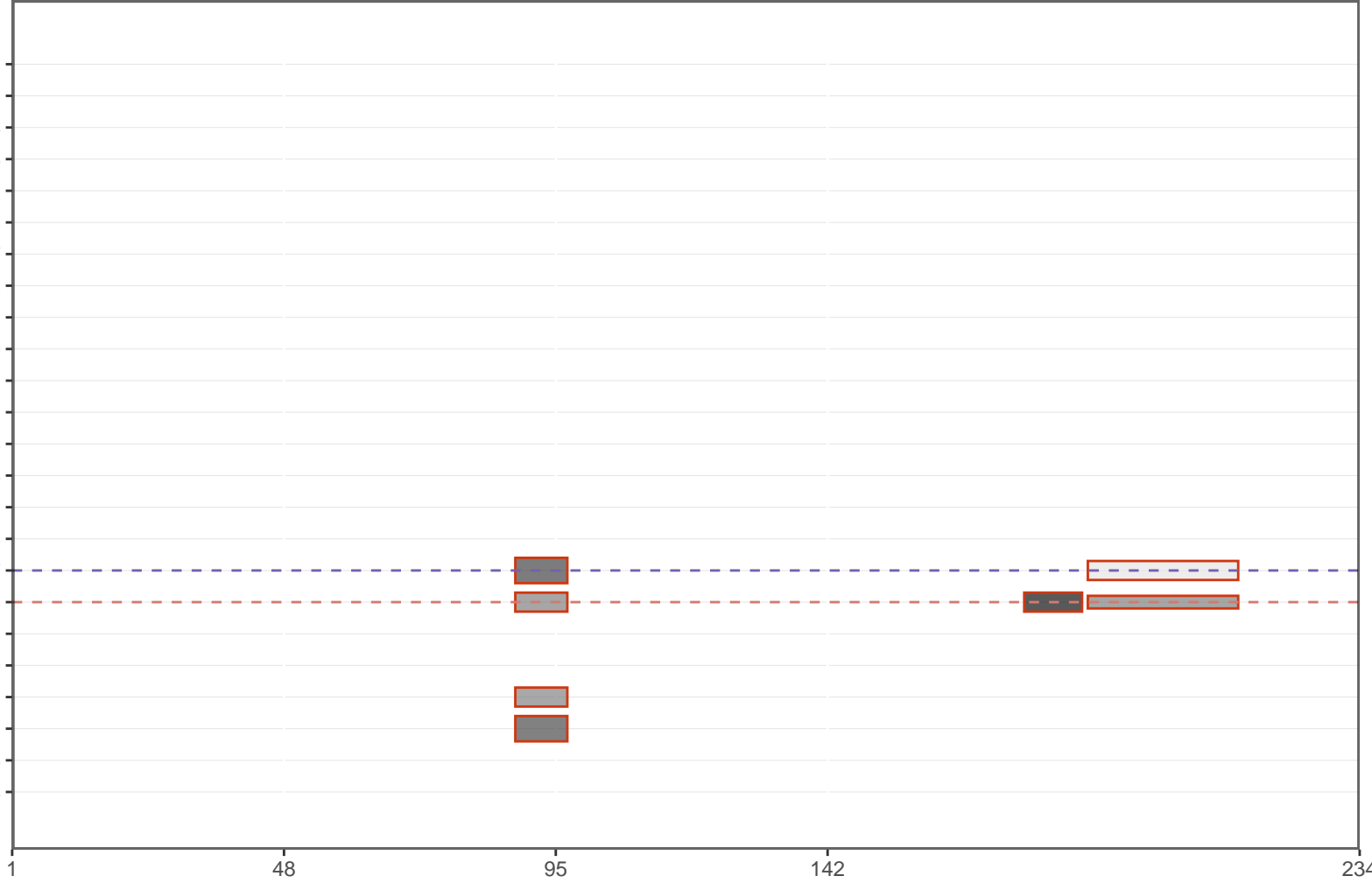
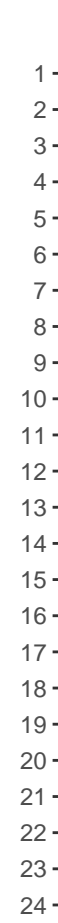
MW indication



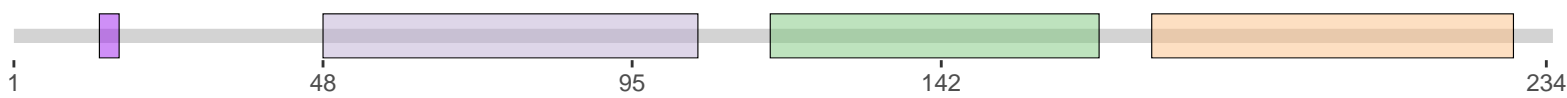
Molecular weight



Gel Slice

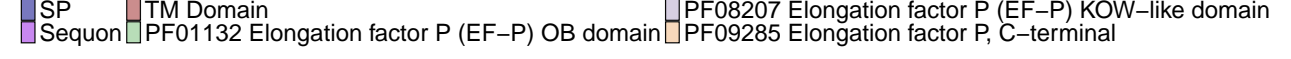


Protein length



Pfam domains

Pfam Description



Protein sequence:

IEEANYKETKQFTYKDGAGFVMDLTSVEEYRLNEKDVGDKAKFLKEGMDGSLFLWNGKVIDFELPITVLTVDVDPQVKGDTAGGSGKPAITDGVAVNPLFGRGEEIIVDTRNGDVMRAKEA*

NbL14g08640.1 vacuolar-sorting_receptor_1-like [MW - SP = 67.44 kDa]

No. of times detected



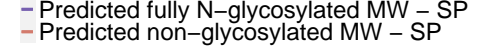
log(intensity)



Values from



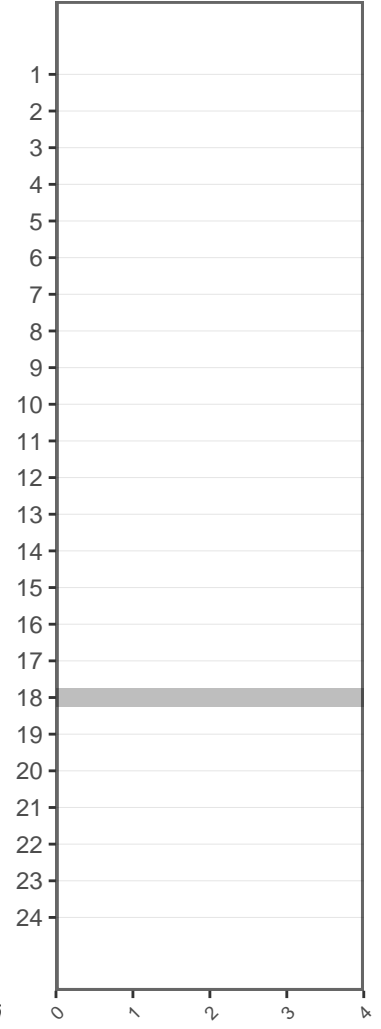
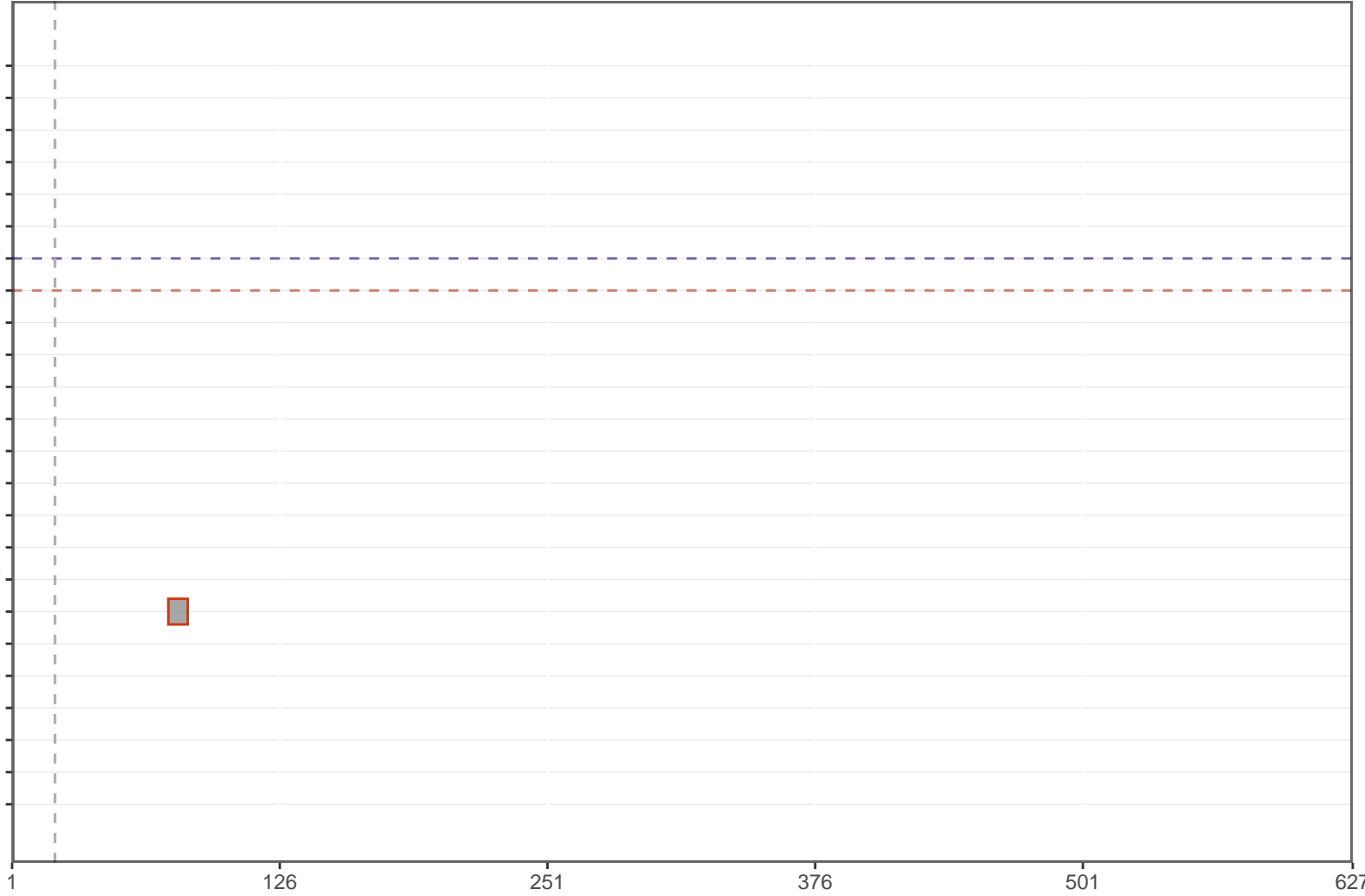
MW indication



Molecular weight



Gel Slice



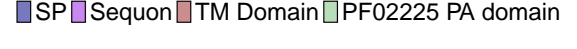
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IYVTDFAIRCPMAKEKRYTRKEGADGVVSLGFDVKGIDKGVSDPEADIDNPVLAKEGEADGKDFRGGVFTLPLVNNRIGVRGKLDKGA/LKAGSGFEETEPNGLTDDQDTNCELESNGSGWQDKAANTAGRDTRFRGKVGCECPMVGQVWFVSDGYTLCEASGALRGGINNSGQWGTNDGRFRSAGIDDDHTKGGKCPDFGKGGVNSGDEDDECKERLADGCPCEKDKNTWGGVDSGNGNLLYMHHEHDTGINAGKDKKTEFSWGFVWVWILGLTAGVGA/VYK

NbL14g08590.1 histone_acetyltransferase_TAP1 [MW = 28.54 kDa]

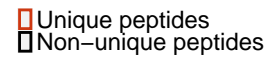
No. of times detected



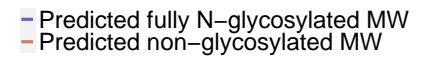
log(intensity)



Values from



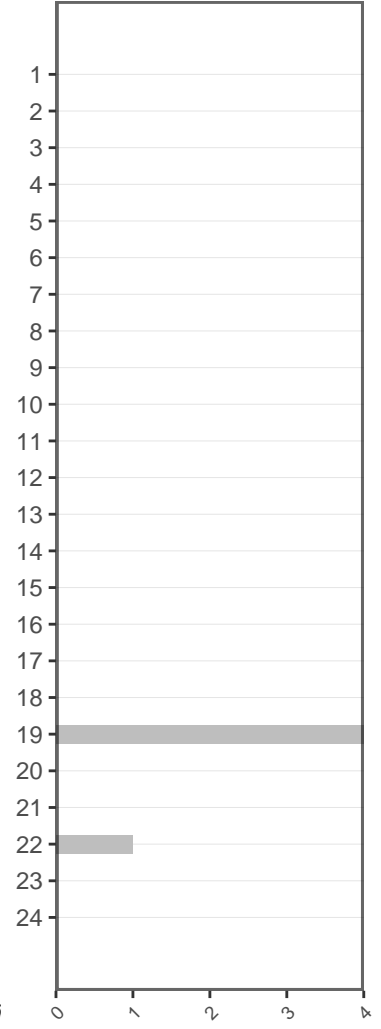
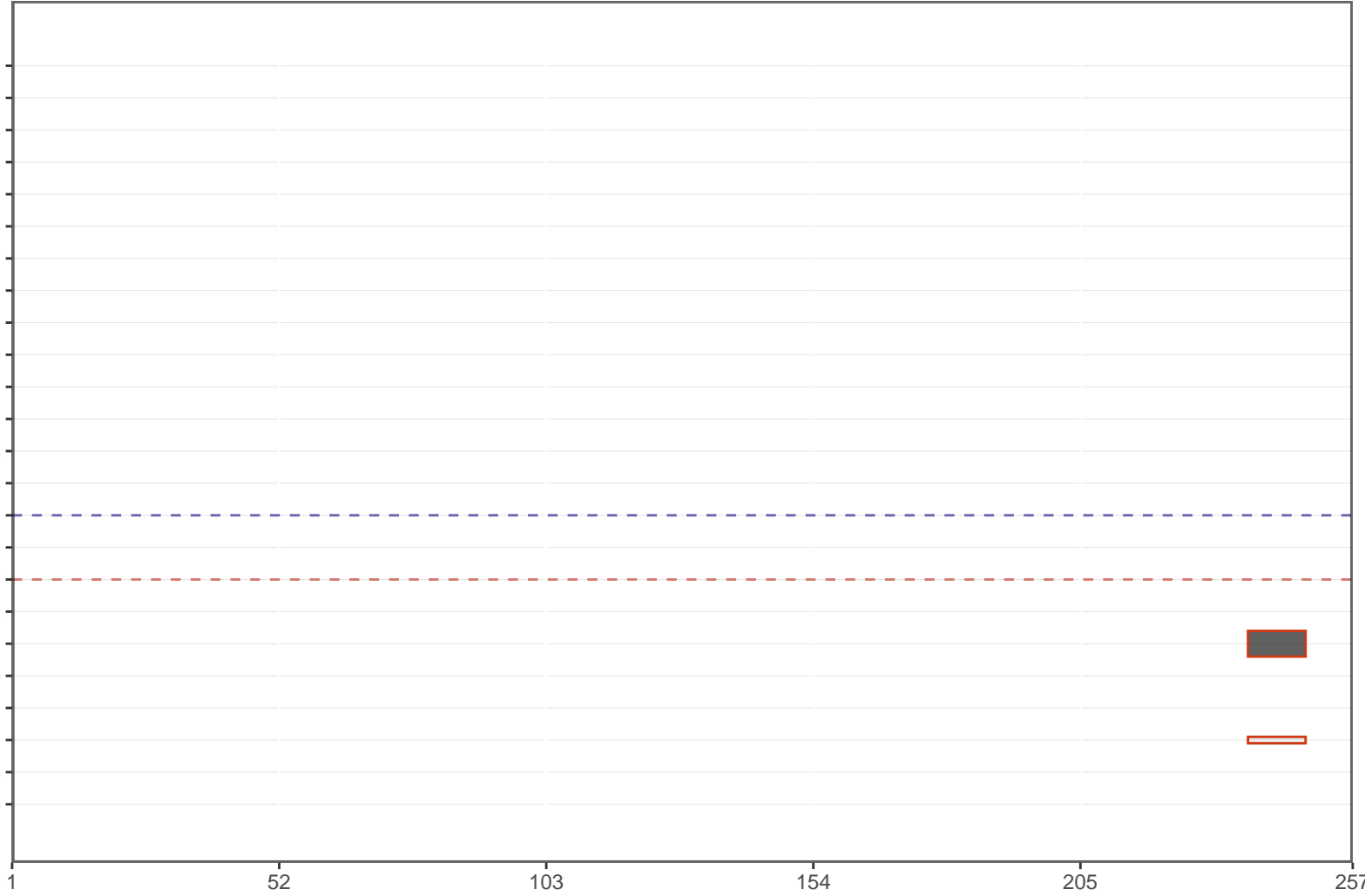
MW indication



Molecular weight



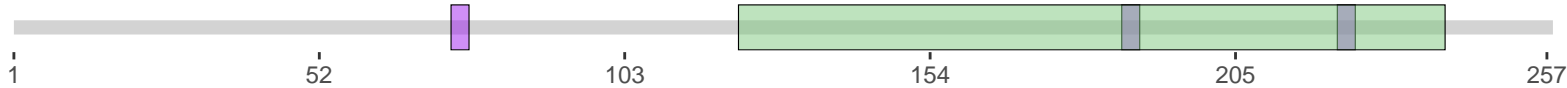
Gel Slice



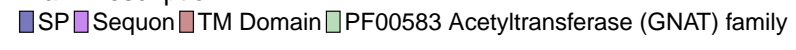
Protein length



Pfam domains



Pfam Description



Protein sequence:

SSGGDVDYDLOALGDKVGVWRRRPLKLAALKNVIVATLHRRKFSGGEGENKELKGMARATSDHAFNATWVWLVDFPVGGGLGKALIEKLRITLGRDIGNISLFDSDGVVEFYKNLGFADPEGIKGMFWVPMY

NbL14g08490.1 calcium-binding_protein_CAST-like [MW = 22.71 kDa]

No. of times detected



log(intensity)



Values from



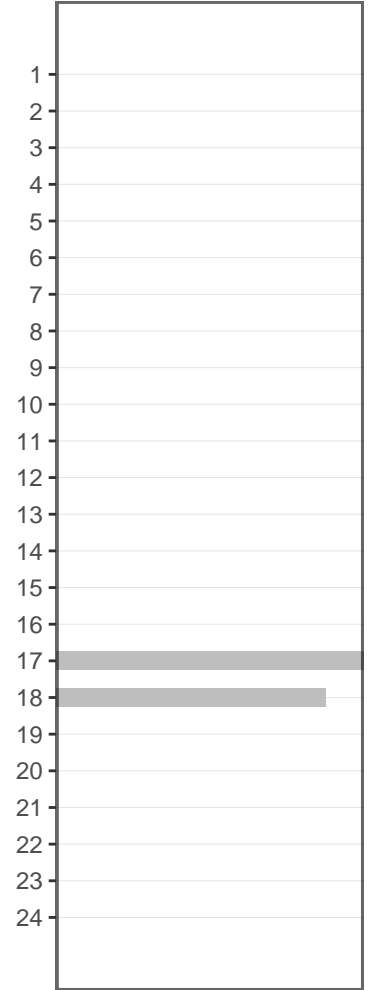
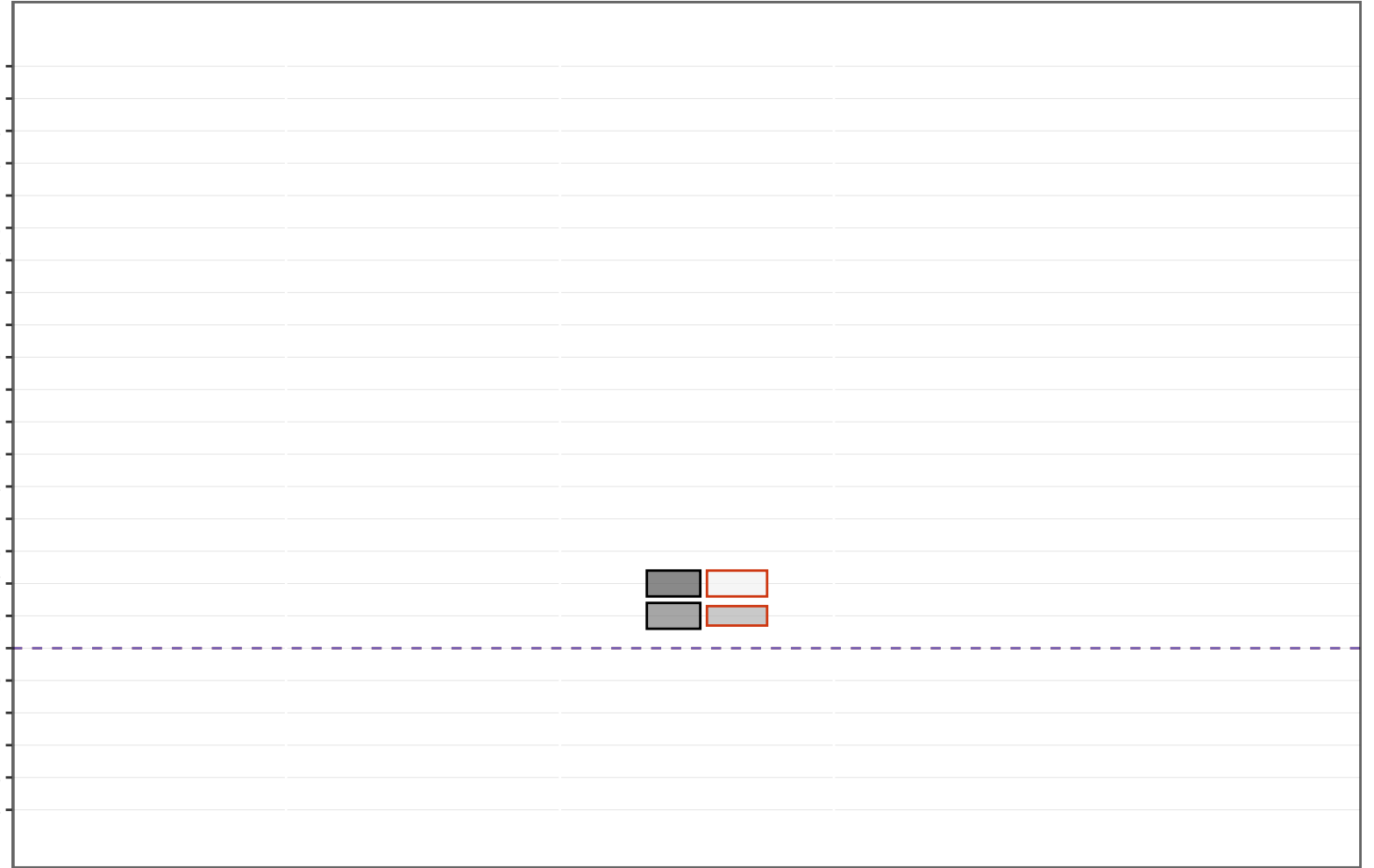
MW indication



Molecular weight



Gel Slice



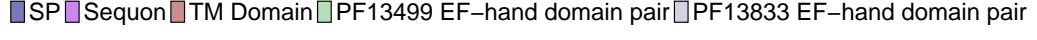
Protein length



Pfam domains



Pfam Description



Protein sequence:

GNVGLRFEDFALHRSLDDVFFGSKYEDKIGLDGDDPDDDEVDLKDQFNVFDENSDGFRSAKELQAVLEKGLPEGNEIDRVEMMISVDGDDHGGVDVFEFKDMRRTVNPSS

NbL14g08390.1 protein_transport_protein_SEC31_homolog_B [MW = 122.31 kDa]

No. of times detected



log(intensity)



Values from



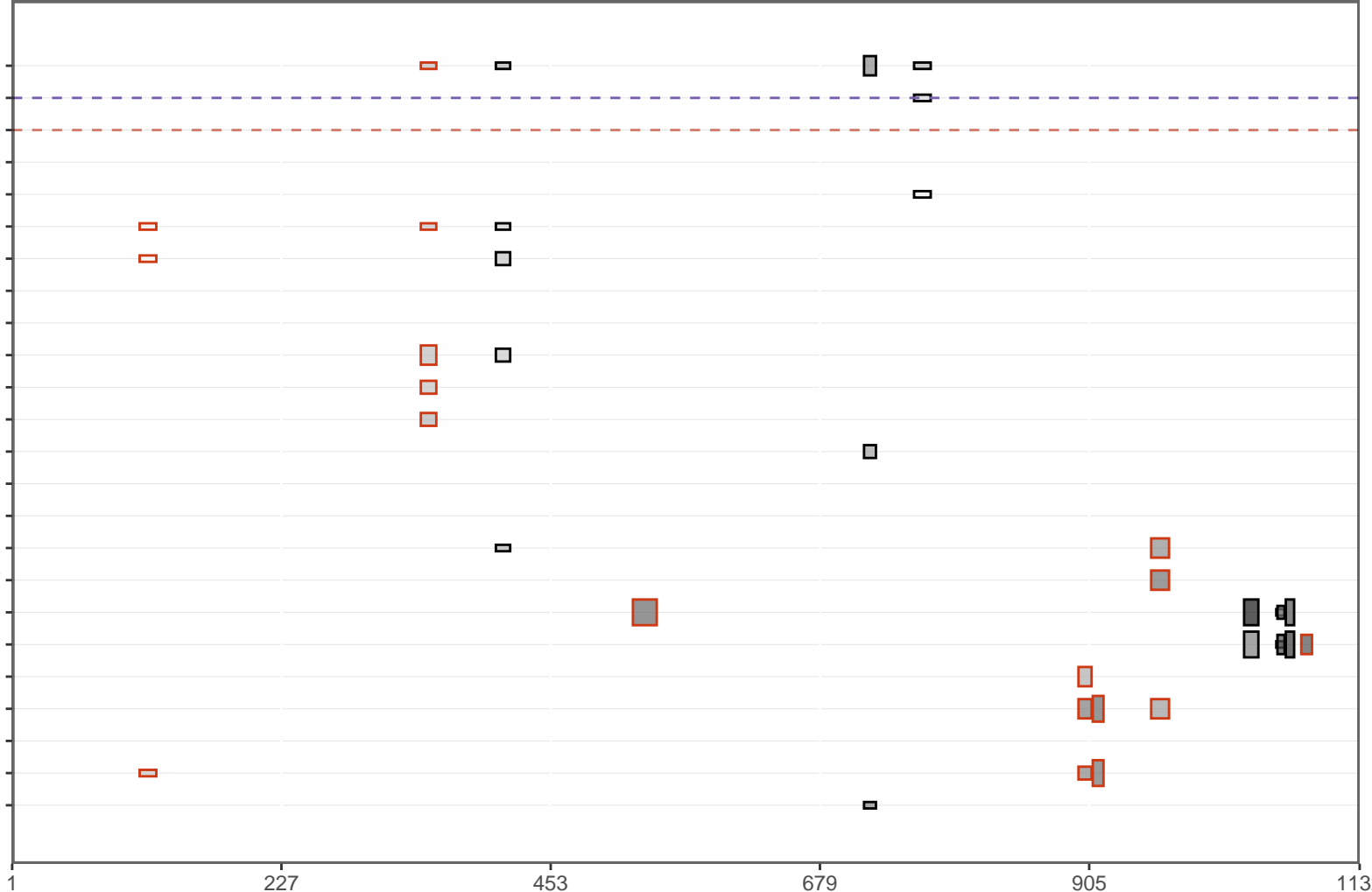
MW indication



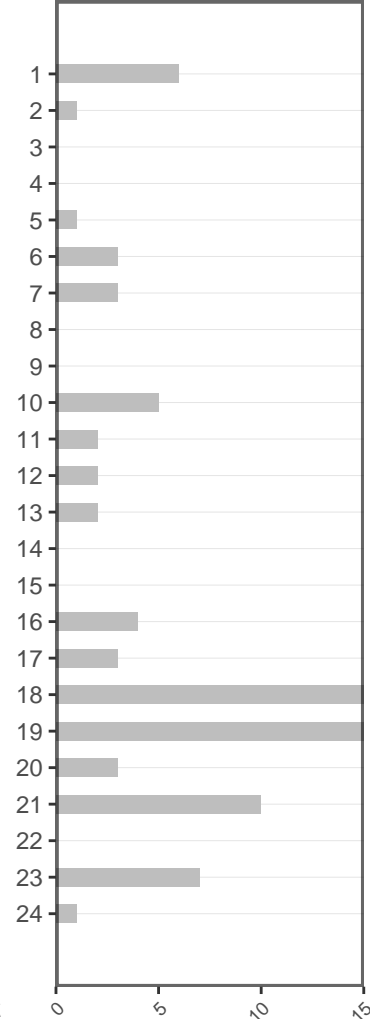
Molecular weight



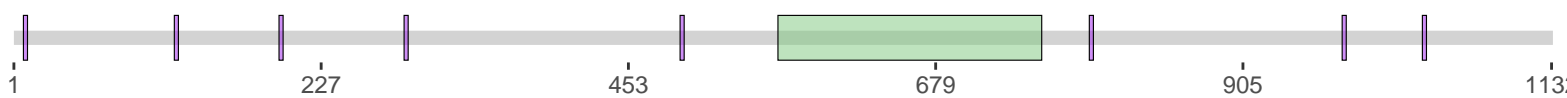
Gel Slice



Protein length

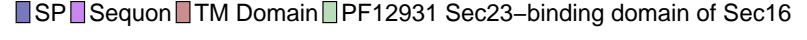


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

QCESADTSFDEIVGSAIVGGKGVAGGGSANRMADALVAHVGSASLWEHTRDQYKTSQSSYLRYVAAAMVNDLMSLVNTRPLKRWKTELALLGTFAPQDEWTSLSGLDLSRLLAAGETLPATLQYICAGNDIKTIEIWSRLLAGKRDGKIVDLDLDMKETAFFALATGGRFSAFLGKLEKAEILASGGLLTAMEYKLMGSEELSPELTLRDRIALSTPAKIDASKVAFNELLHAGSGYVADQSGYGMVDPGQHYYPEGSKPKQPSISNPAENYOQPFGS

NbL14g08290.1 50S_ribosomal_protein_L1_chloroplastic [MW = 37.05 kDa]

No. of times detected



log(intensity)



Values from



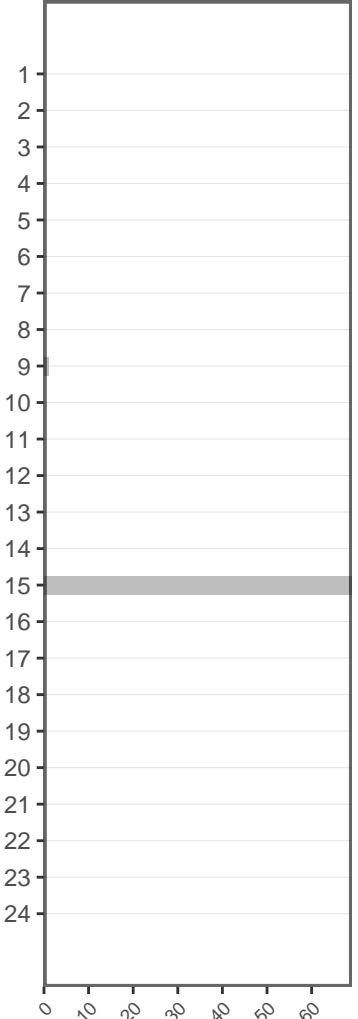
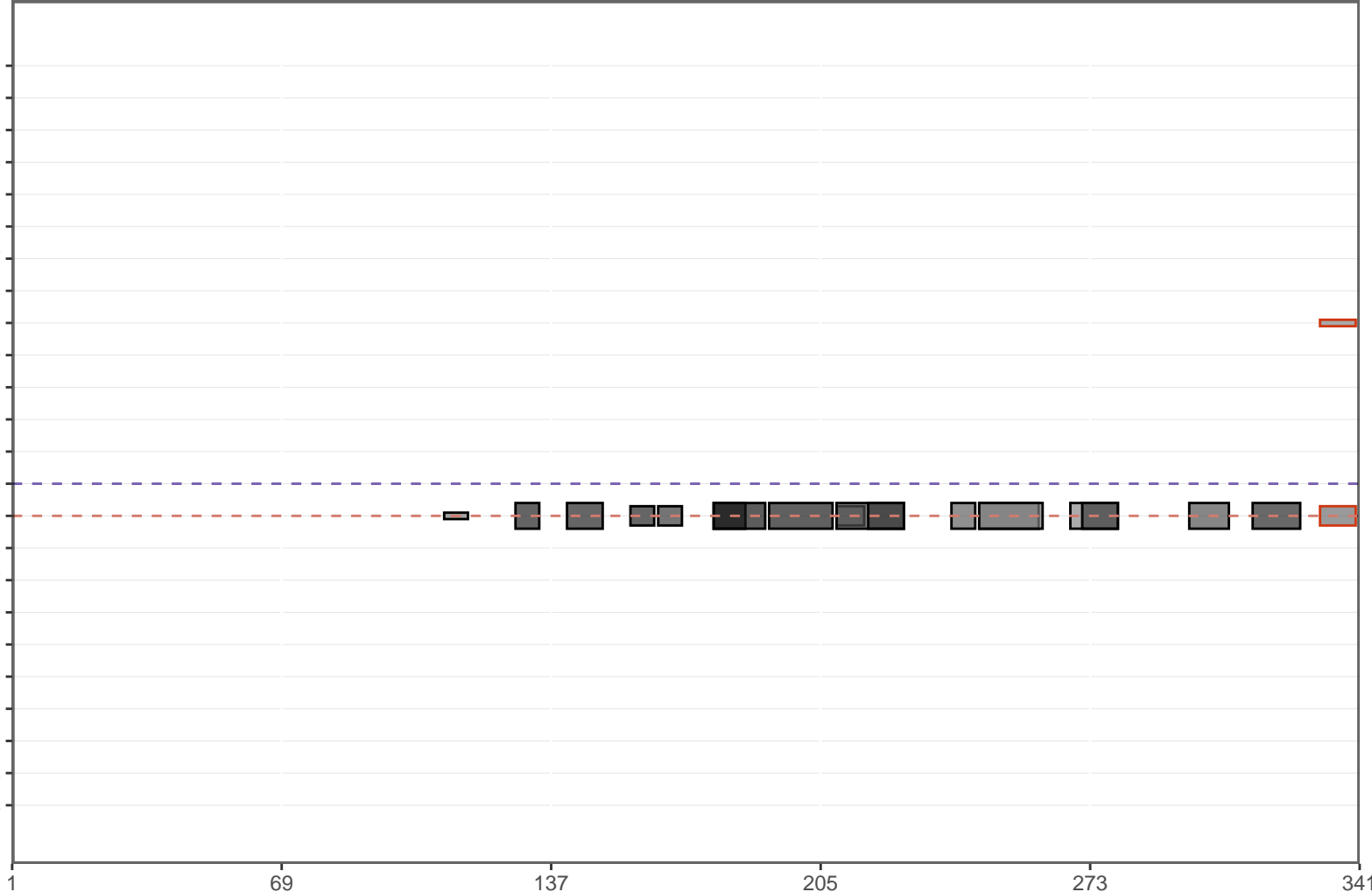
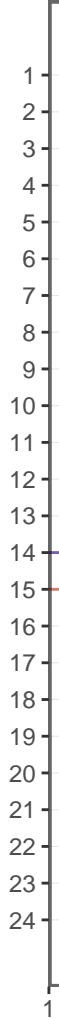
MW indication



Molecular weight



Gel Slice

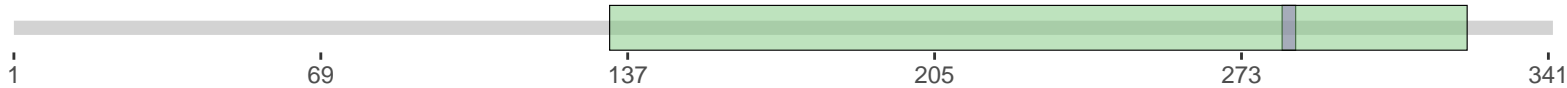


Peptide counts over 4 repeats

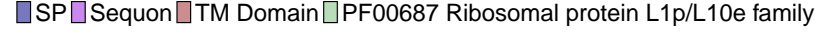
Protein length



Pfam domains



Pfam Description



Protein sequence:

IQQLRATYNLPKGTGGTVKWWLFTGGEKFEAANNAGADLVGGEDNIEGKGGFMDFDKLATPDMMPKVAWLSGRILGPRGLMPNPKAGTVFTNIPQAEFRKQKVEYRAKDTGVHLPFGKANFSEEDLINFIAWKSIEANKPGGAKGVVWKSAAHVCGSSMPSRILNVRREMLEYKLPNA

NbL14g08210.1 alpha-N-acetylglucosaminidase [MW - SP = 89.81 kDa]

No. of times detected



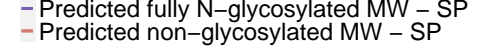
log(intensity)



Values from

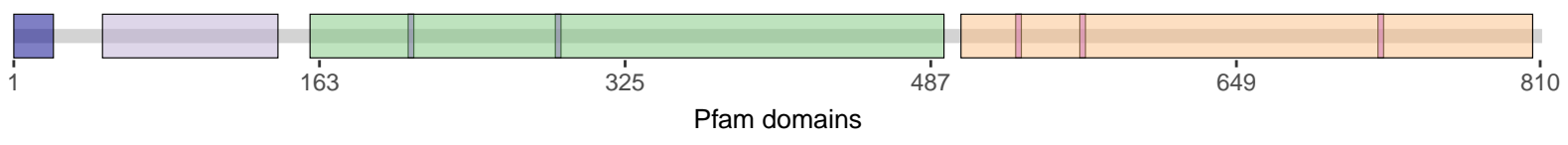
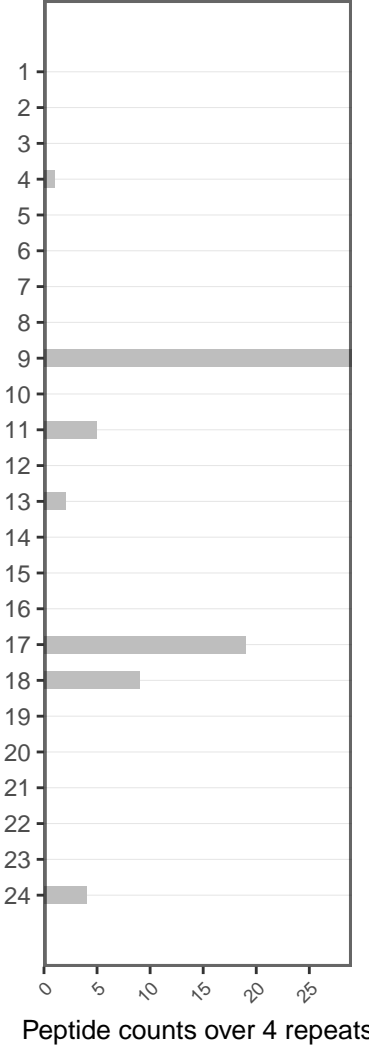
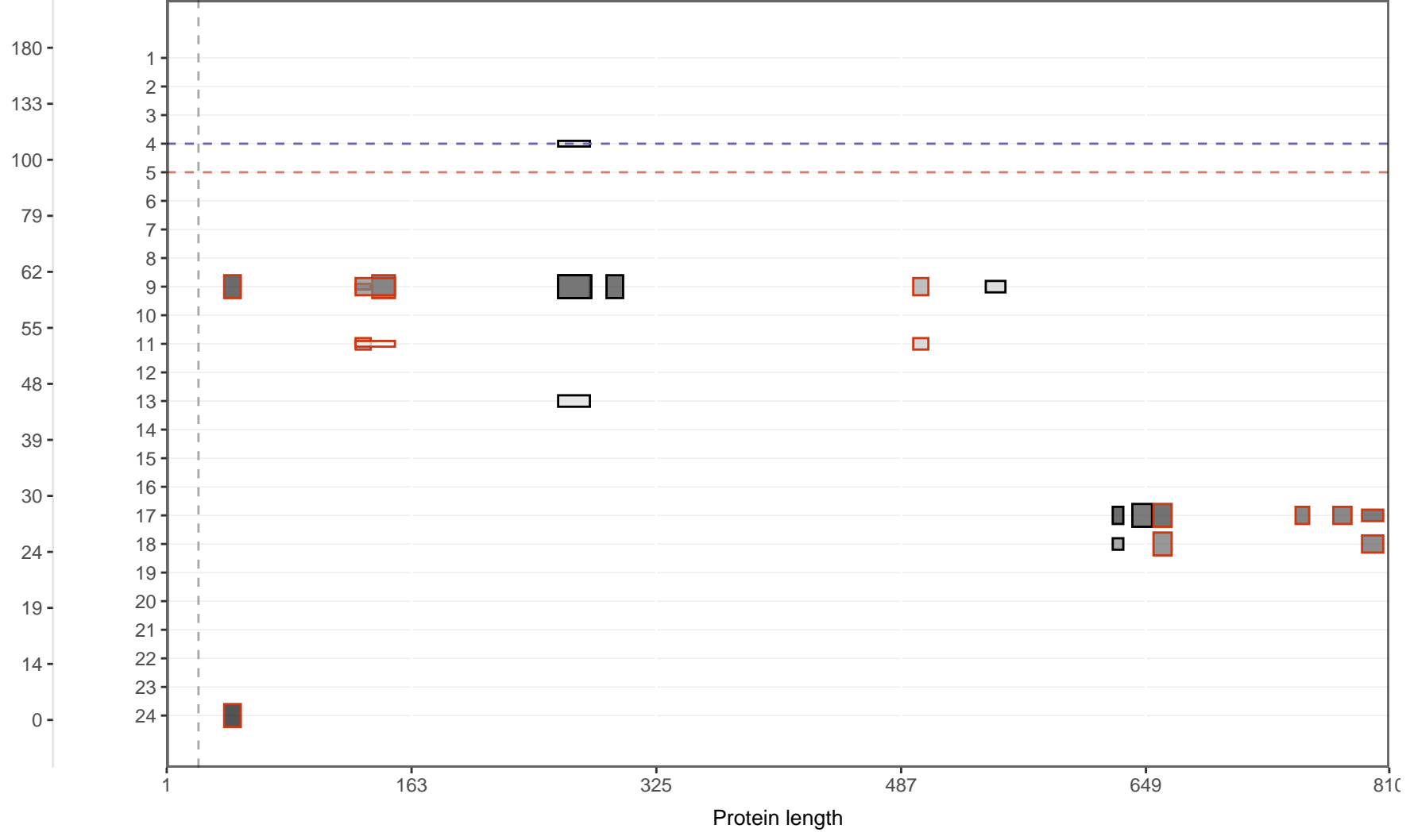


MW indication



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF05089 Alpha-N-acetylglucosaminidase (NAGLU) tim-barrel domain
- PF12971 Alpha-N-acetylglucosaminidase (NAGLU) N-terminal domain
- PF12972 Alpha-N-acetylglucosaminidase (NAGLU) C-terminal domain

Protein sequence:

PPQMEALLISVPRGMVLDLFDADKPKWKSSEGFYGTPIWMLNFGDNIEMVGVLDVAVSGPDAISENSAMVGVGMCMEGIEHNPVYELMSEMAFRGDGDFLGGWLVKYSRRYGVKVNDDQEAADWLVHTVYNGTDGDIADHKKDYVEFPDWDPSGKTGTDSGTDNSSQGMQKLAGFQWNRRLFFFKSSSLPKPHLVYSTEIVKALKLFDAGTSLGGSLTYRYDLDLSRQSLSKLANGVYLDASAFRRDEAEALSHSGKFLGLKIDIRLLAADNFI

NbL14g08120.1 ferredoxin-thioredoxin_reductase_variable_chain-like [MW = 19.24 kDa]

No. of times detected



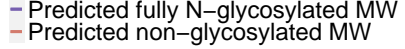
log(intensity)



Values from



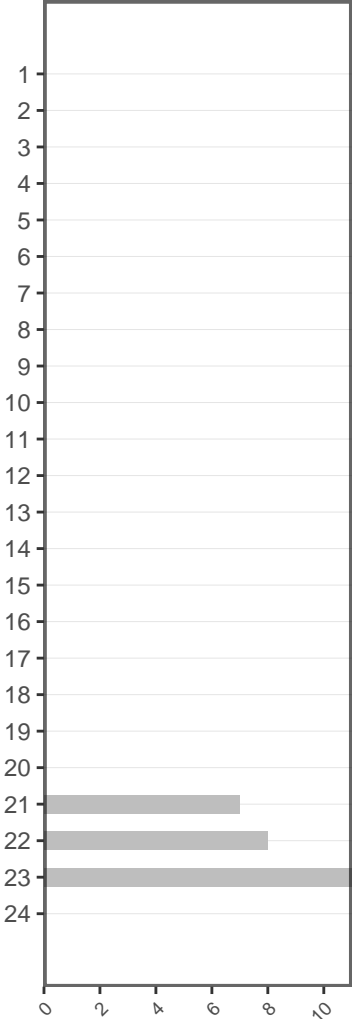
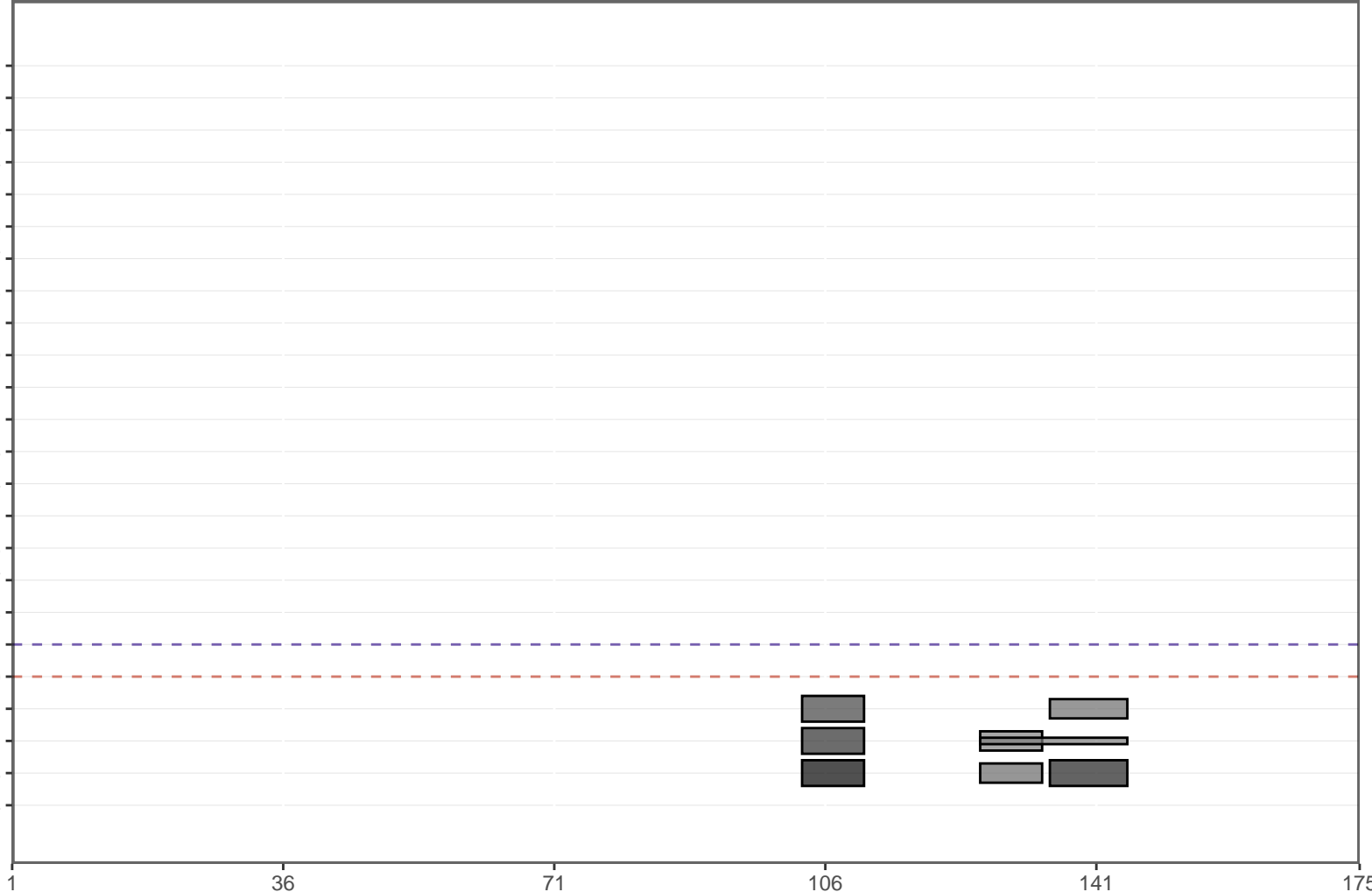
MW indication



Molecular weight

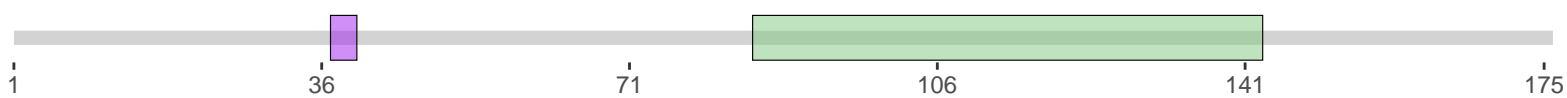


Gel Slice



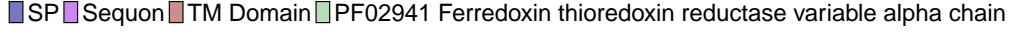
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EKTAEAIGKVGSR:RVFTVPLKVVYHPKVFELDINRIGTLKGYVGFHKGGISANLPYKVEFVVDNLEGRDGGKWKFMELLLCGVDHGLINRGMKN

NbL14g08060.1 tRNA-dihydrouridine(20/20a)_synthase-like [MW = 47.93 kDa]

No. of times detected



log(intensity)



Values from



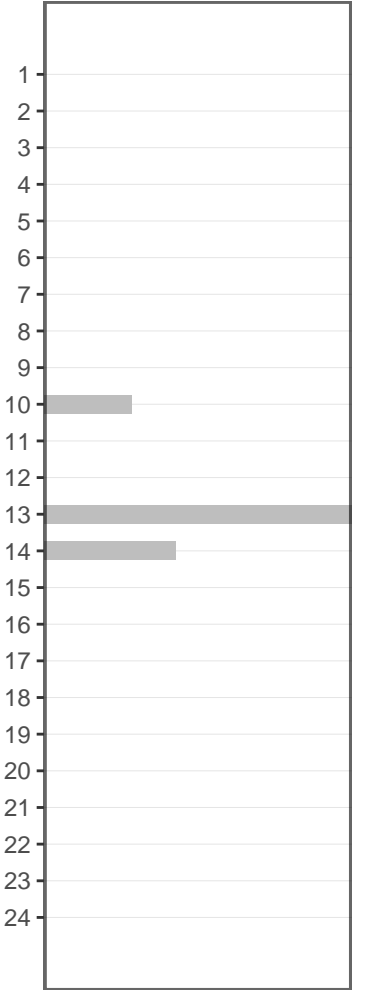
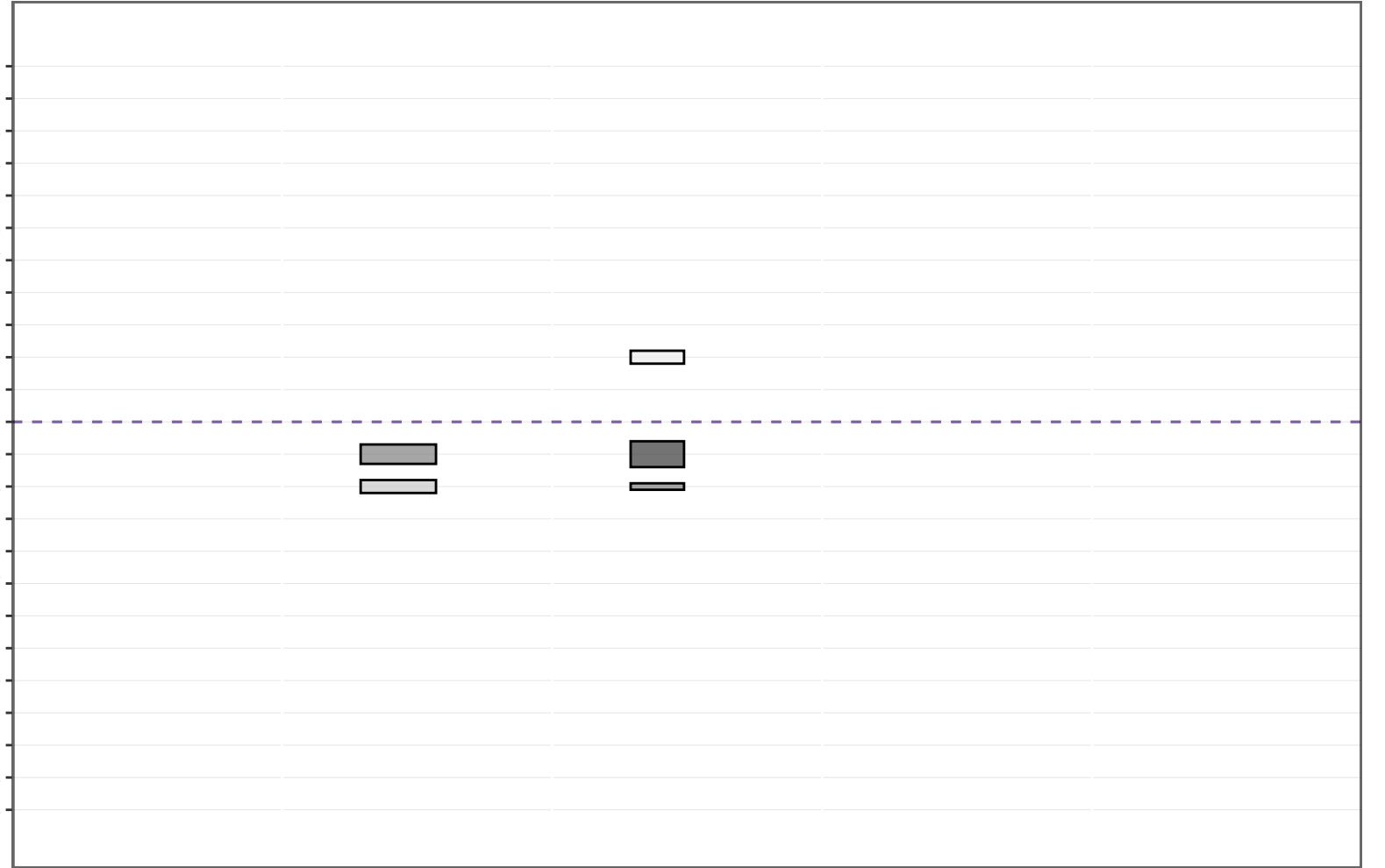
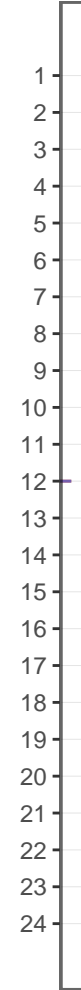
MW indication



Molecular weight

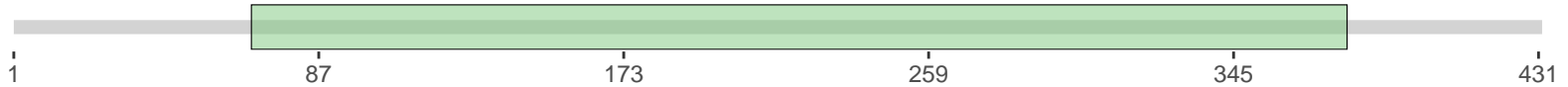


Gel Slice



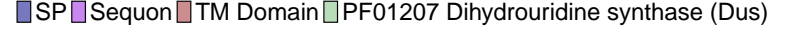
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MDHSTNELCDFYIKVSSGQSTRFHIERKALLNGISPDNRKIPPKYEVYKALLRDFDLPDQFTINGGINSIEEVNEARTEGAHGVMGRAAVSNPWQVGLVDSAVYGLPLRFRFRQVLEQYGVYGVDSVYGMVYGLKPKSMRDVVKPLRLGLFHPANFGNGAWKRKVDAAFKHYTKIKSFEETLVAIPQWVLDSPVTEVPGGCTDKFSKAKLLPPPYTVNEEELVA*

NbL14g08040.1 carotenoid_910(9'10')-cleavage_dioxygenase_1-like [MW = 61.92 kDa]

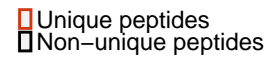
No. of times detected



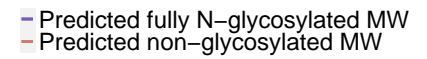
log(intensity)



Values from



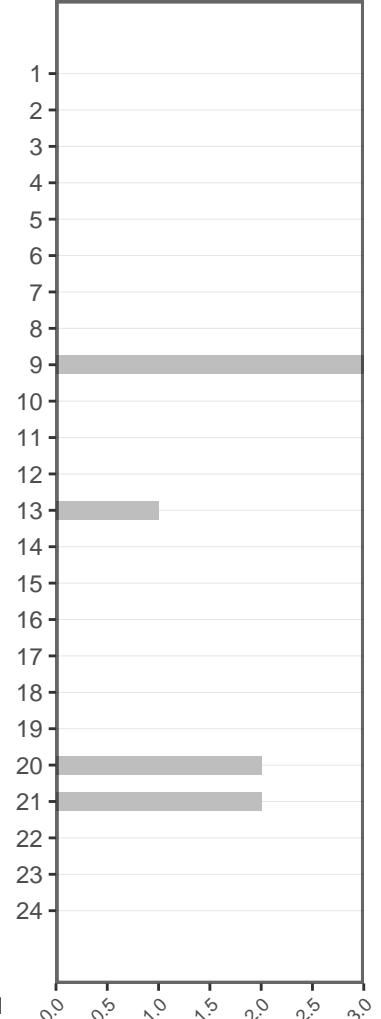
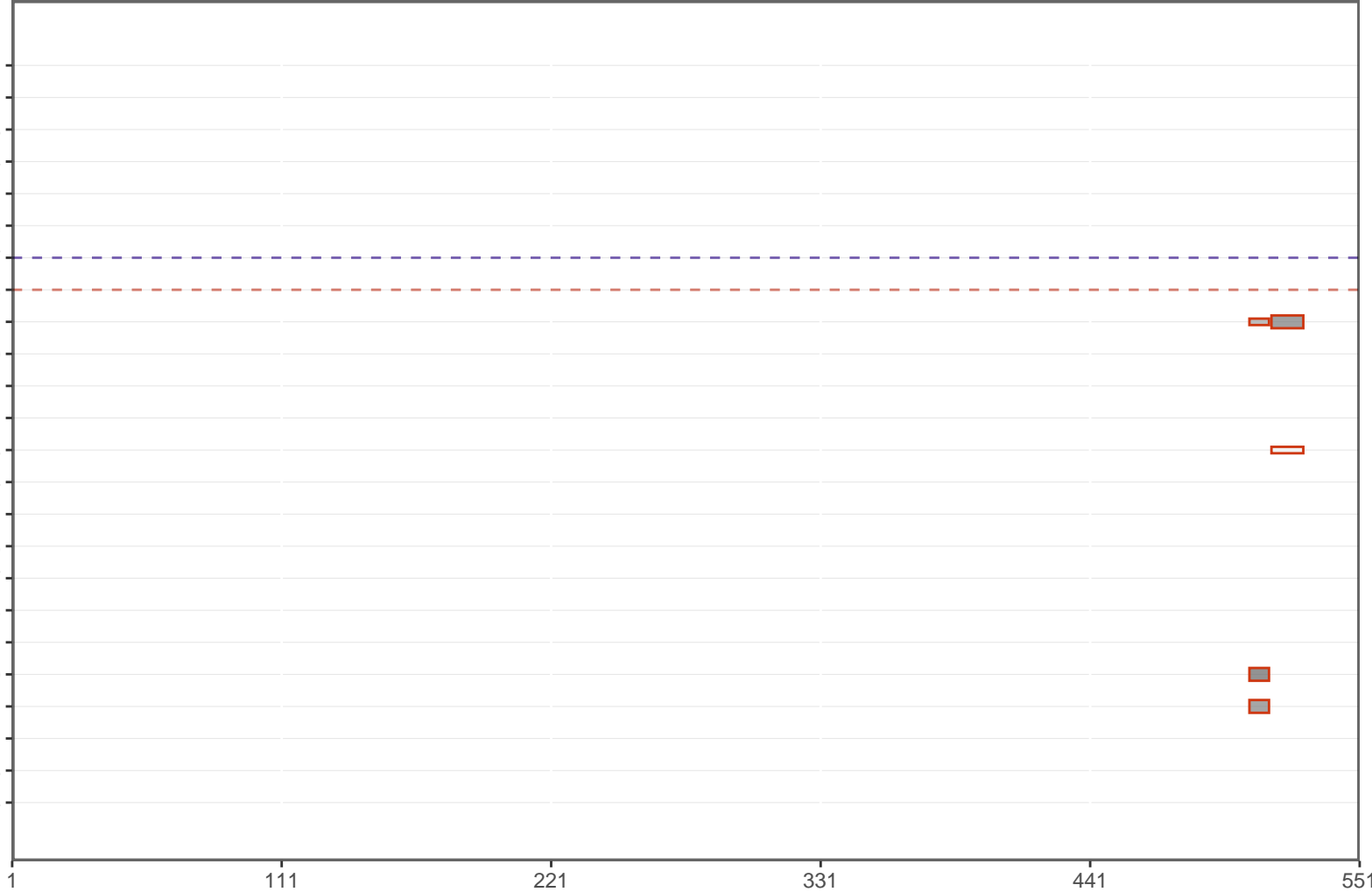
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

IGVMDPVPITPISVMHDFATENYBIMMDLFLVFKPKEMWKNKLLAYSFDPTRKARFGLPRVAKNEGLKWFELPNCFFHNAANAVEGGDDVALITCRIGNPDLDANGTEKEQGRDGFTELNEVMRFNMKTGLASQKLLSESAVDFPRVNEHYTRKQRVYYGTILNMAKITGVYKFDLHAEPDGTGKTRLEVGNVLGIFDLGPRGRGSEAFVPCDPTGEGDEDDGYLILFVHDENTGKBSVNVDAKTMSEPVVAWVLEPKRVPVYGFHAFVFEQIQEQAAL*

NbL14g07980.1 uncharacterized_LOC107829775 [MW = 25.35 kDa]

No. of times detected



log(intensity)



Values from



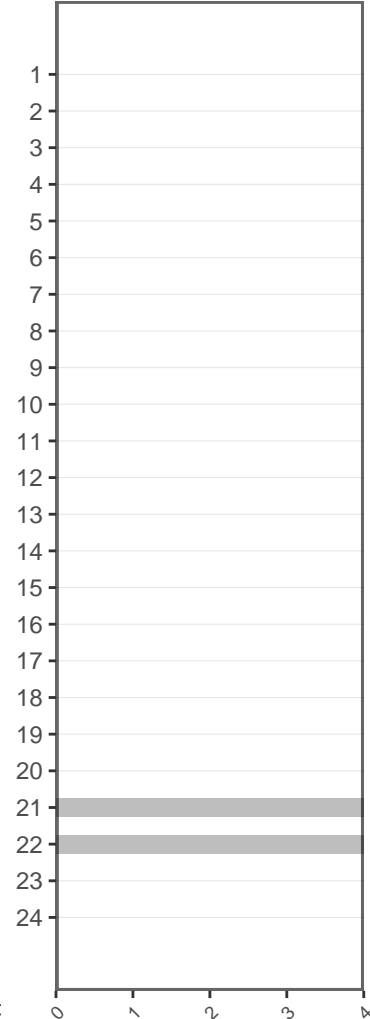
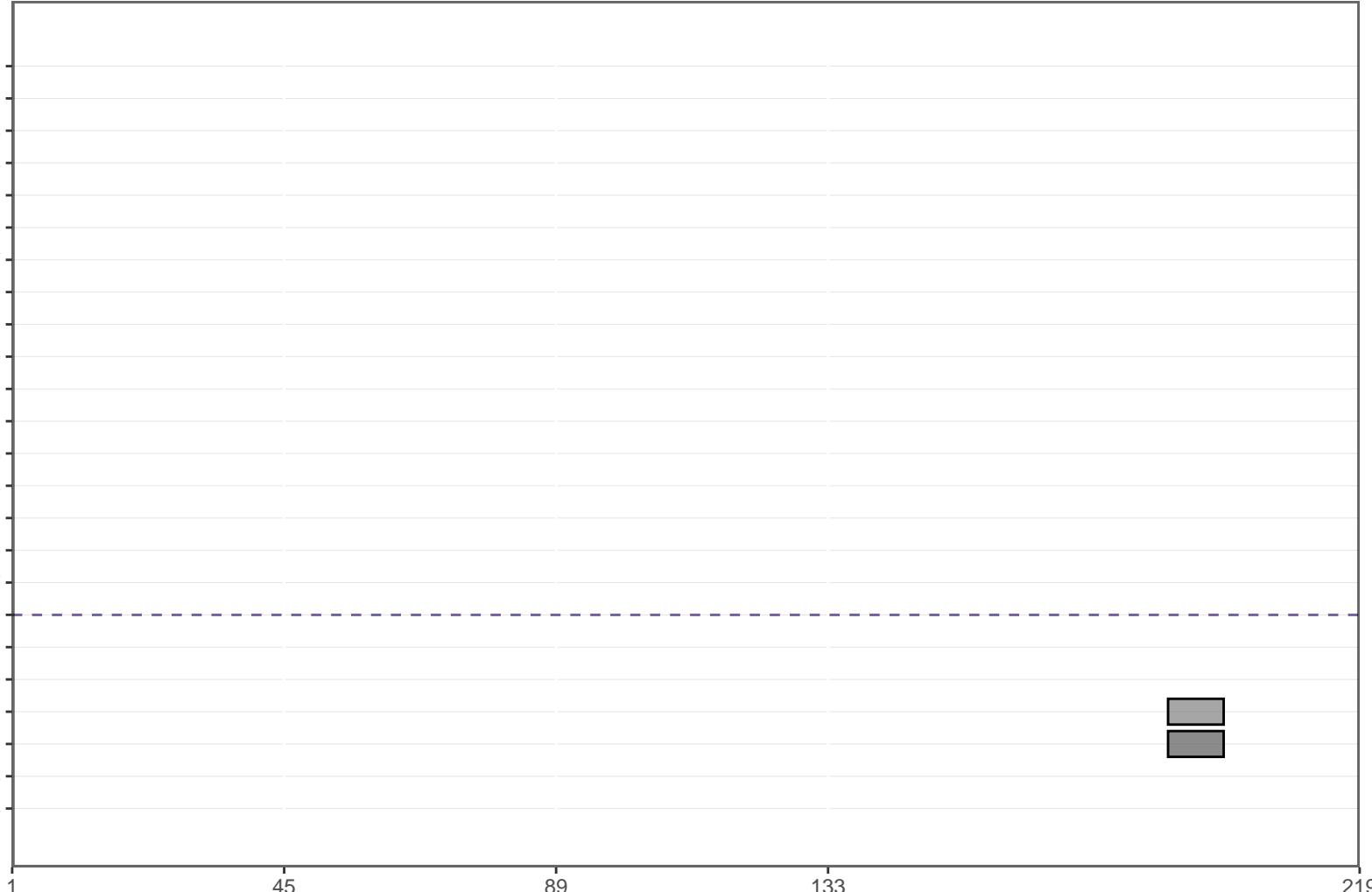
MW indication



Molecular weight



Gel Slice

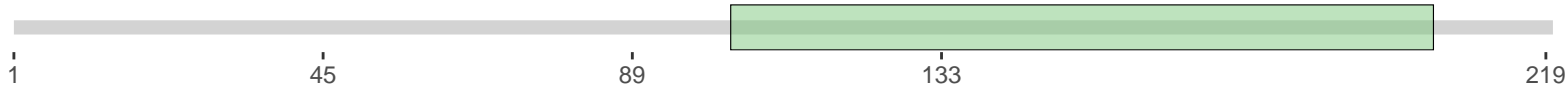


Peptide counts over 4 repeats

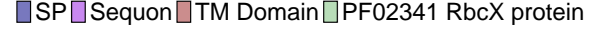
Protein length



Pfam domains



Pfam Description



Protein sequence:

DDDSGEDYKNEINWTFKAVRTVLAQGLVEMNPPGYTFYFNFVNHVPTNGKDFLGGFLFKERKRELAERVMTIRLNLYSWMGKGDHAEVLYNRISDQNVLMRERLAGTIVWLSEDEEIAAGSLD*

NbL14g07950.1 uncharacterized_LOC107772121 [MW = 34.86 kDa]

No. of times detected



log(intensity)



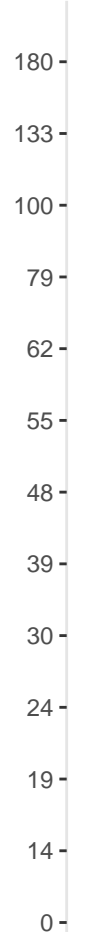
Values from



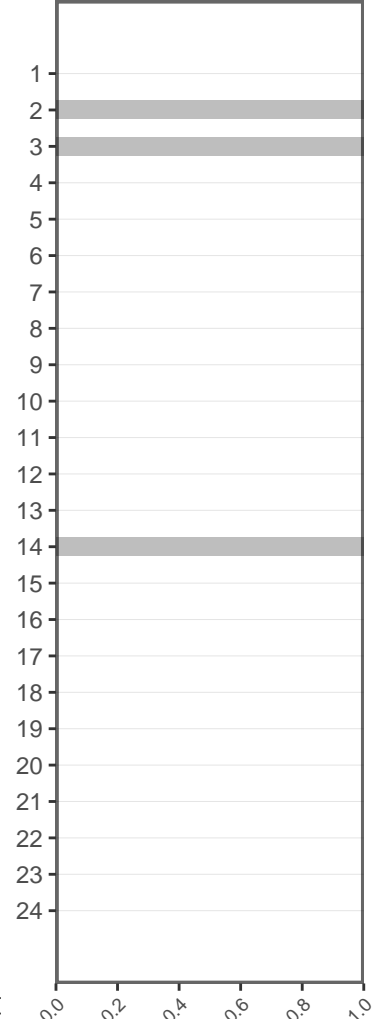
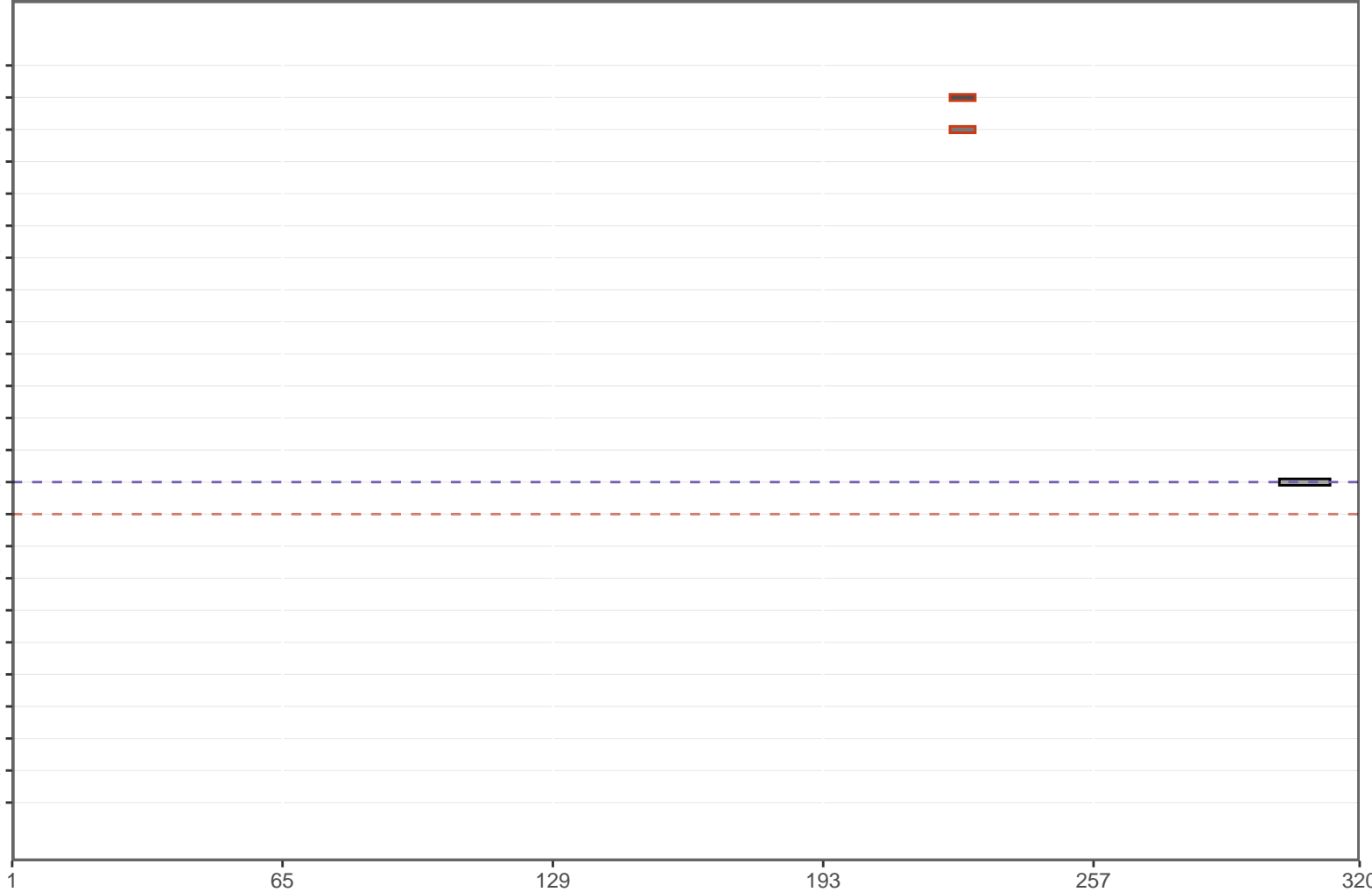
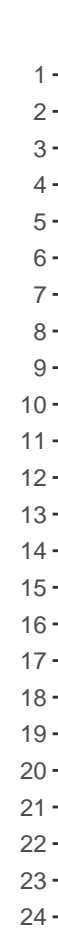
MW indication



Molecular weight



Gel Slice



Protein length

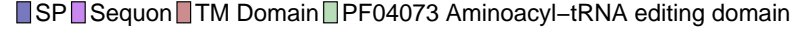


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

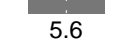
LDLKLSSIGKPKFYVDLEANPFVKGKPPDLATFVPSDTIVLPGHYKEAPLGVSDTNHAPVSNKATGVSAKAWPEADVLKEKLSNGVSPNSFADPEKFFLEKTSLSVLSSELTEENWQDDEKLGSAISNKIRNKLATEFKSMATMFKNTAVSEGFQAGIRHQAKRP

NbL14g07870.1 photosystem_II_22_kDa_protein_chloroplastic [MW = 29 kDa]

No. of times detected



log(intensity)



Values from



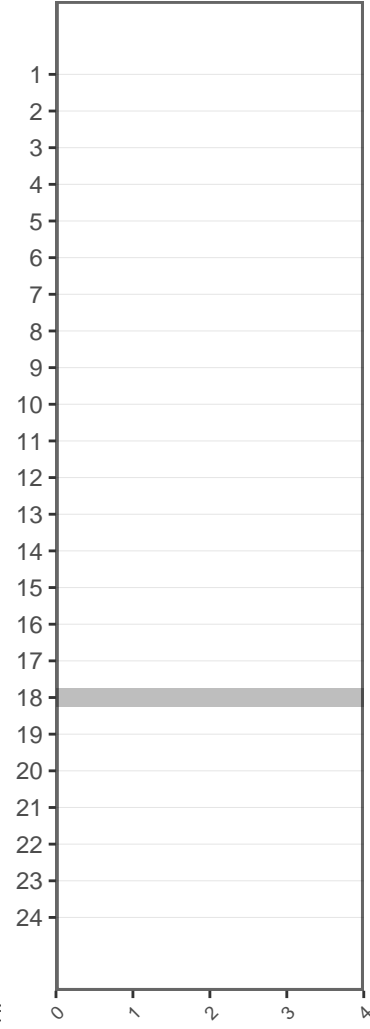
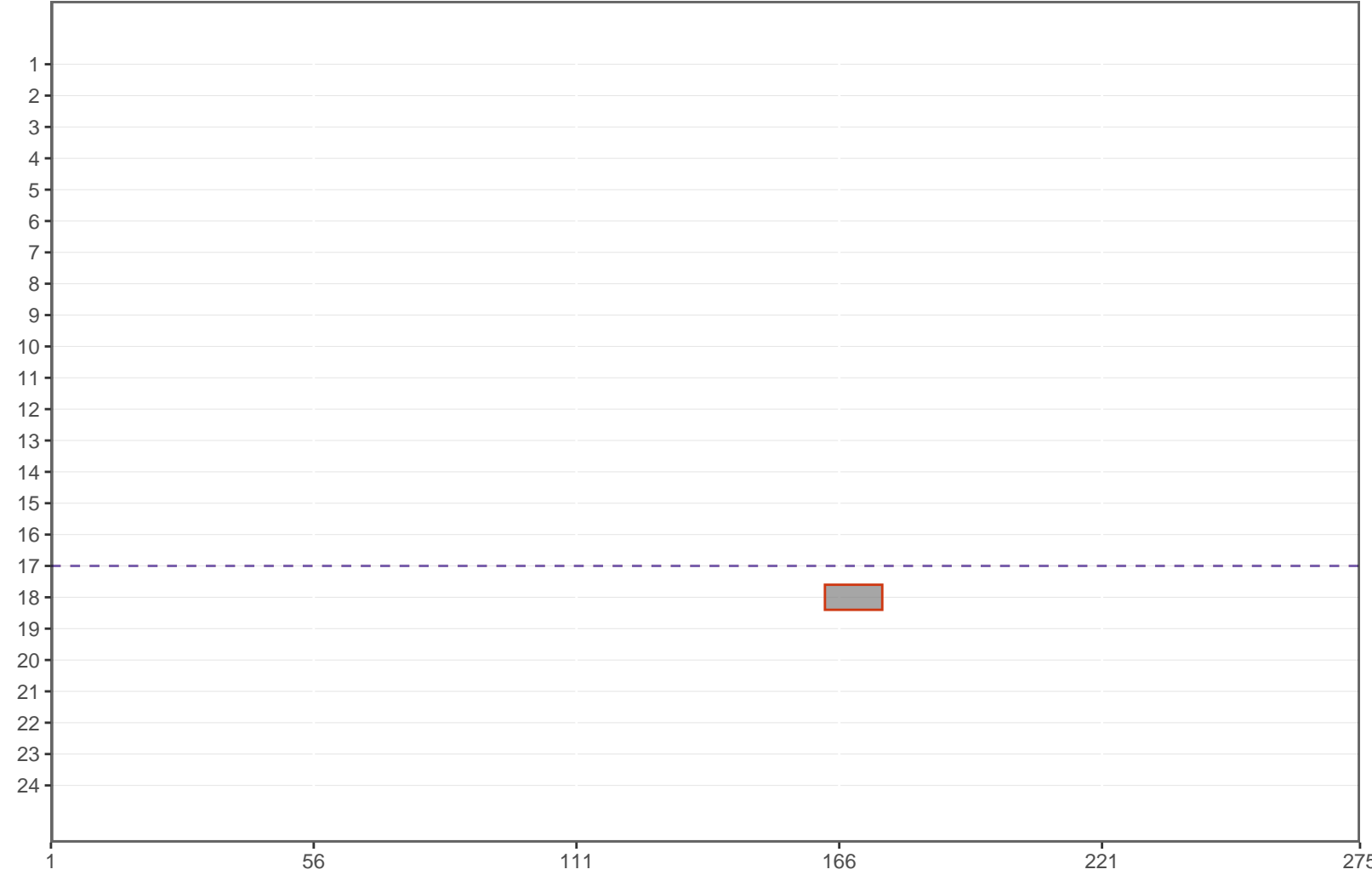
MW indication



Molecular weight



Gel Slice

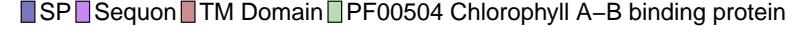


Protein length

Peptide counts over 4 repeats

Pfam domains

Pfam Description



Protein sequence:

IGLAQLNLETGPIPYEAEPLLLFFILNLLGAGALGDRGKFDIDPVPATGLDNKAVPPGKGFNSALGLSEGGPLFGFTKANELFVGRLAQLGAFSGISGHTGKALAGLNFFETGVPNIEIPELLFNIVFFVVAANPGTKGKFTDEEEEI

NbL14g07840.1 SWI/SNF_complex_subunit_SWI3C [MW = 86.13 kDa]

No. of times detected



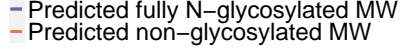
log(intensity)



Values from



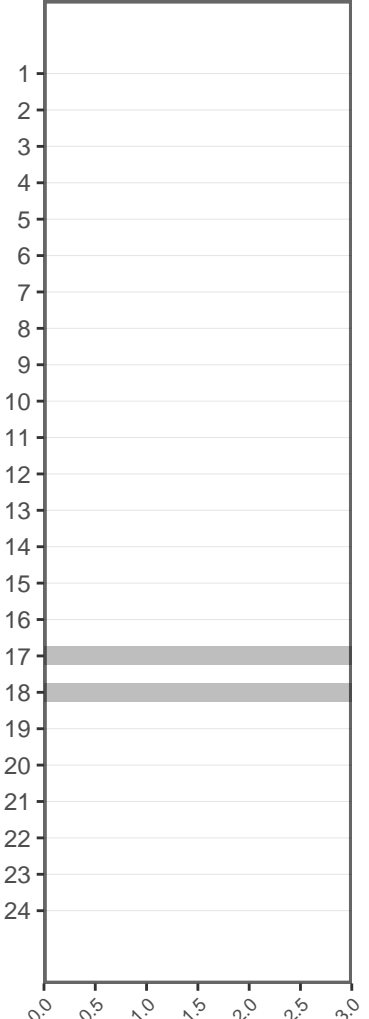
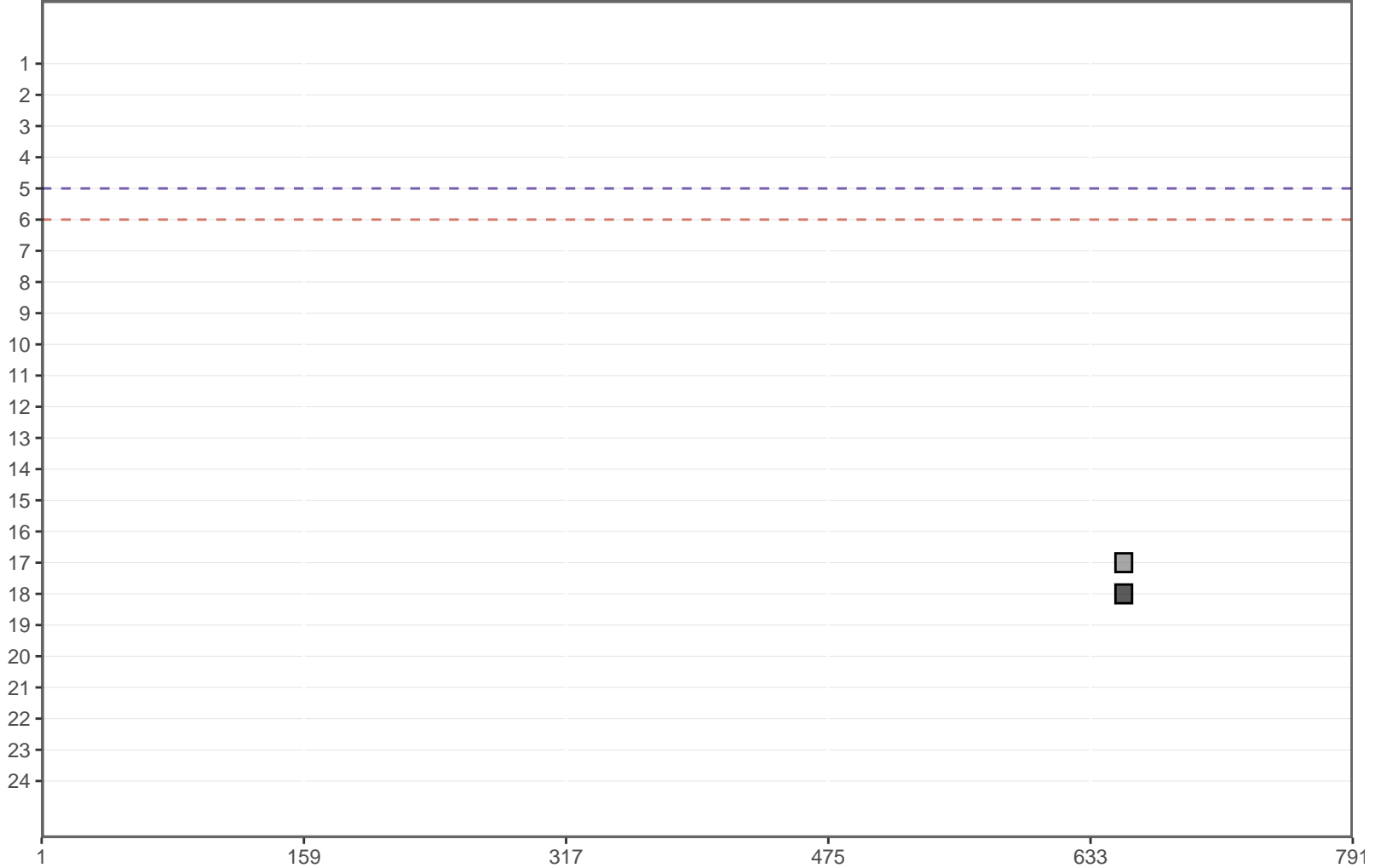
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains



Pfam Description

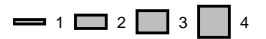


Protein sequence:

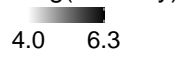
LVSSMKDYGDLDGDTWTDQETLLLEEGMLNENWNGIAEHVGTKSKAQGLHFVRLPVDGAPLENELPGASGSPSSFAGEDRSKGSGSLNGLNLAGPSTENLDSDGSKFFFNENGNPCMSLVIAFLASVGRVRAAAGAHAFALALSKDDSLTRNMTQIDGSTANNIGSIGKHGKDGSPHGDVGNVQLKDEKPGGGGPPWGGHDAGGAPVSTERVRAAAVGLAAAAKAKLFAADHEEREIGRLSANVNHQKLRLELKLKGFVEETLLMKEGEGQLRTRRFAAERA

NbL14g07700.1 protein_disulfide-isomerase-like [MW - SP = 54.91 kDa]

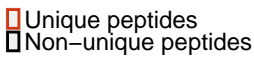
No. of times detected



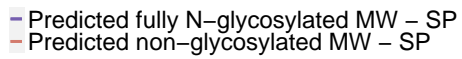
log(intensity)



Values from

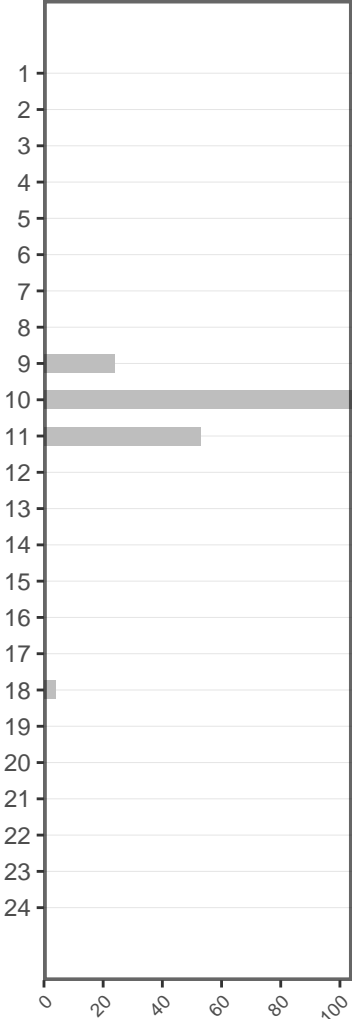
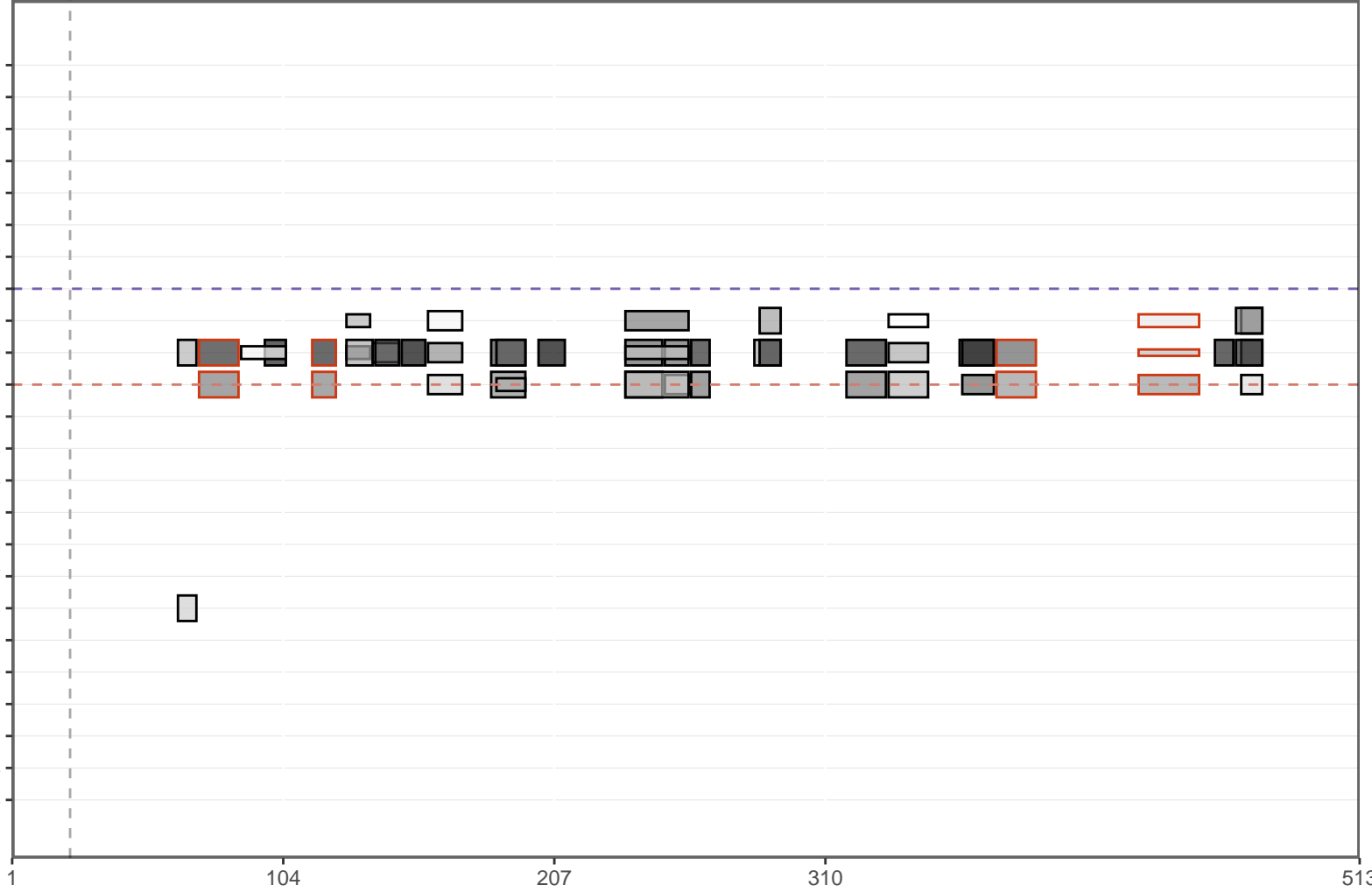
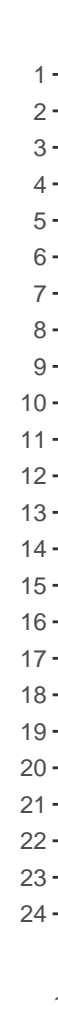


MW indication



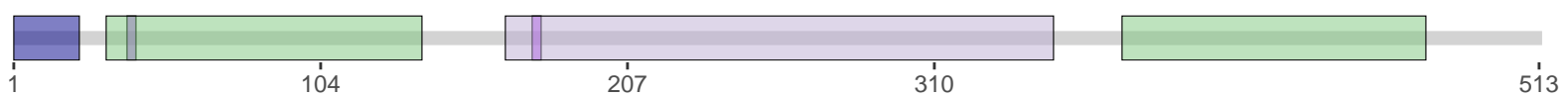
Molecular weight

Gel Slice



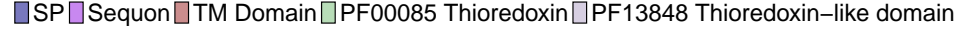
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

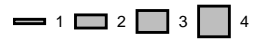


Protein sequence:

LFNKDPNNSIPFYKFFNSPNAKAMLFVFNESDLIDTFKSKYHEVAGYKGNIDISFLGDEVEASGQAFQYFLGKEDGVPLIQGTNDGKYLKPNVEPDHABWVKDFKDKVYKPFKIKSEPIPEVNSPEPKVYVADTLQEMVFNFAKYNLLEFYAPWGGHCKQLAPILDEVAWVFESGADMMIAKIDTANDIPGGTFNVDGYPTLVFKTASGKISQYEGDRTKEDIIDFIHNRKKAADGGRIATRGDFKFGGHWYVGLGTFYGVQV

NbL14g07440.1 ISWI_chromatin-remodeling_complex_ATPase_CHR11 [MW = 101.01 kDa]

No. of times detected



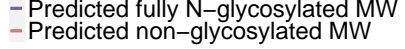
log(intensity)



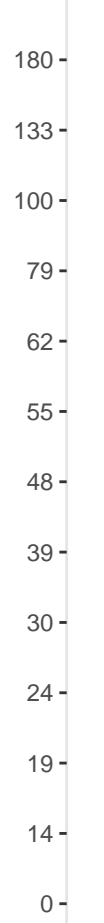
Values from



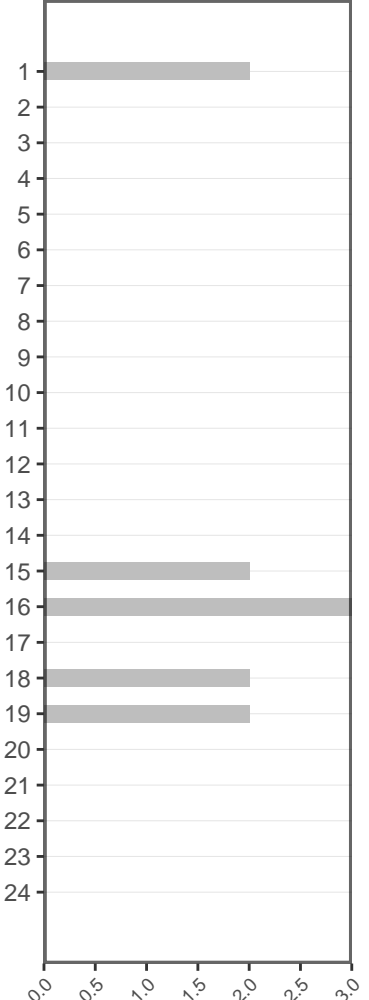
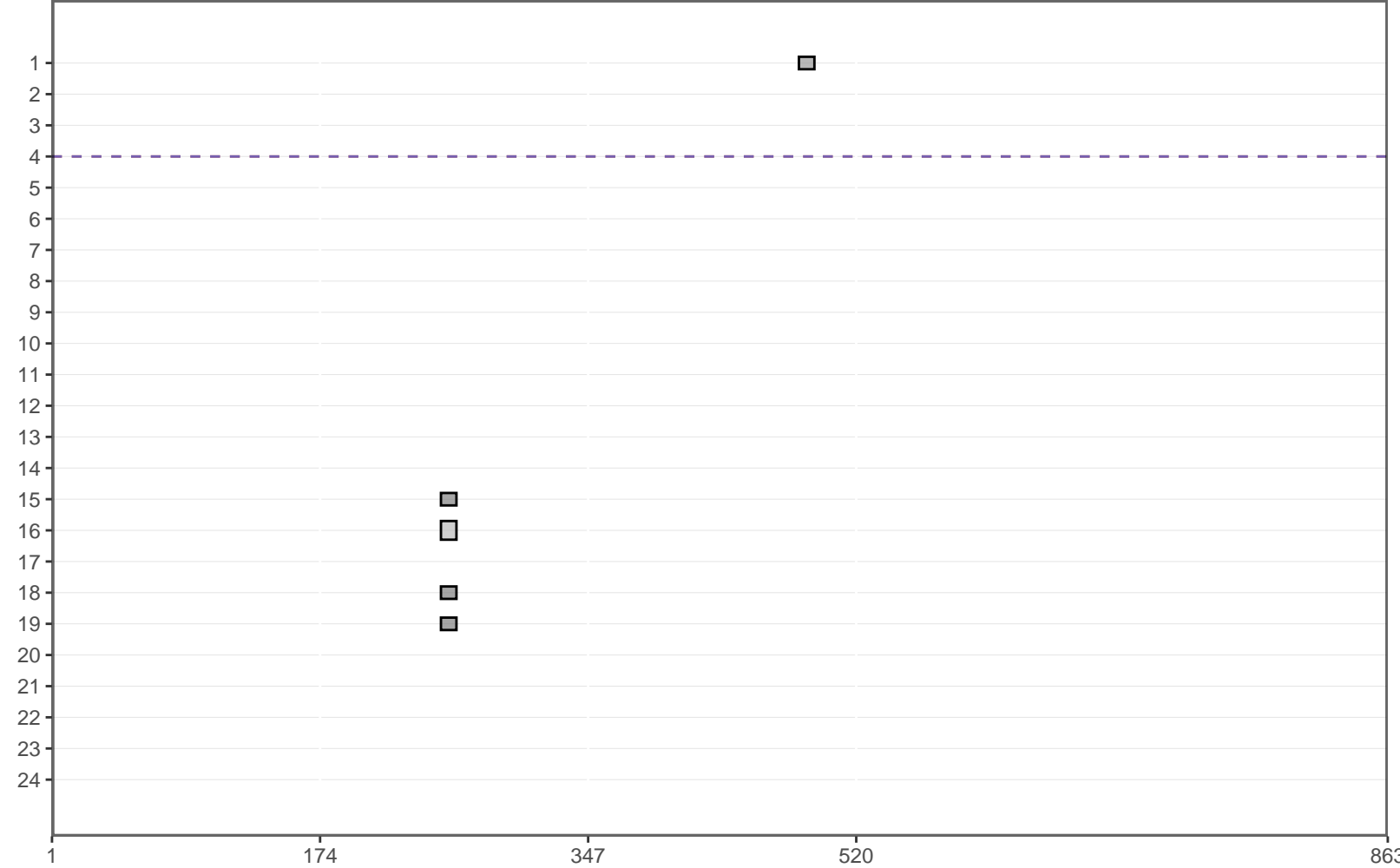
MW indication



Molecular weight

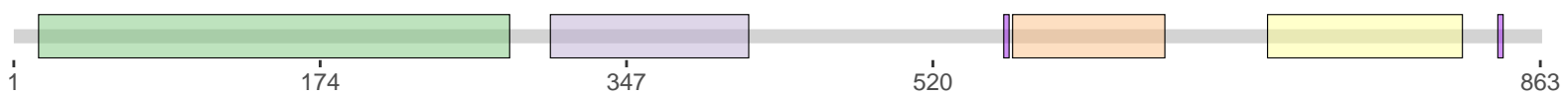


Gel Slice



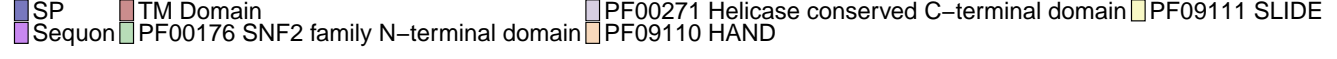
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VGVFRFCTEYIEEKVIERAYKKLALDALVGGGRLAEGKAVNKKDELLGMVRFQAEVVFSSKDSITDEDRIIAKGEAAKAEALDAKMKKFTDAKFKMDDTADLYDFGDEEDKNNVDFPKKISDNNVVEPKRKRKRNVSESEYFKGTMRGSAFAPKPKPRIPRMPQLHDFGFFNTGRLLSELVEKVEVYLMGTHGRNGVYKDIEMEEDPAGEDPLTAVEGEEKRLLLEEGFSTWERRDFNTFRAGEKYGRNLRKSAAMEGKTEEEVERVAKVFKERYKELNDYDRIKN

NbL14g07400.1 uncharacterized_LOC107810922 [MW = 37.42 kDa]

No. of times detected



log(intensity)



Values from



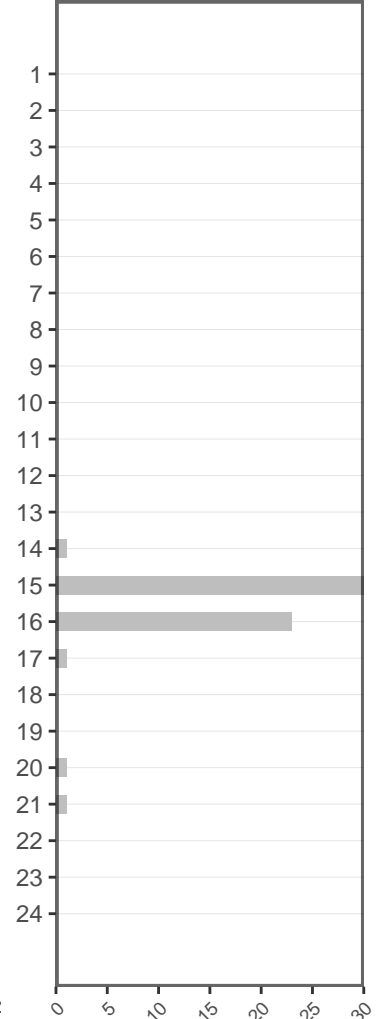
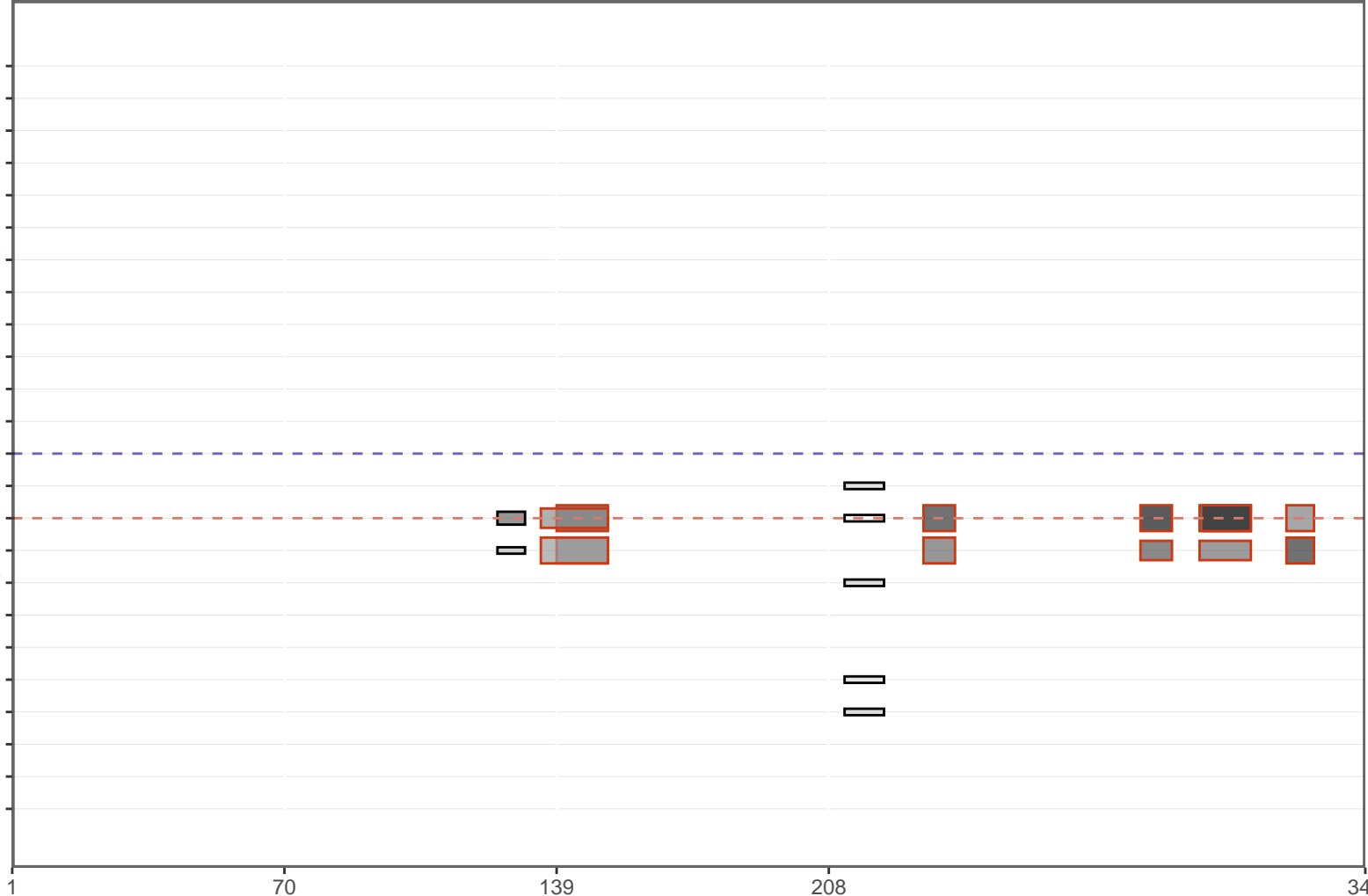
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

AALSINWGEISFLFTSSAPYDFGNNGINEDGPIVPIGRSFRDVLKKAENVALDFDGGVRLAGLYKADRGAHYVWQKGGCDIRPDHNLHYYEDAASLSVTLKRLRGGQIFLGGDNHPLSRGEVMDLVKSGTDFDKFEGFTGSDPLGKLNNSKTRAEGLGWEPKYPFSAQFLGVSE-

NbL14g07390.1 probable_prolyl_4-hydroxylase_4 [MW - SP = 29.94 kDa]

No. of times detected



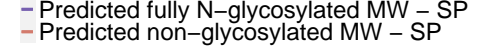
log(intensity)



Values from



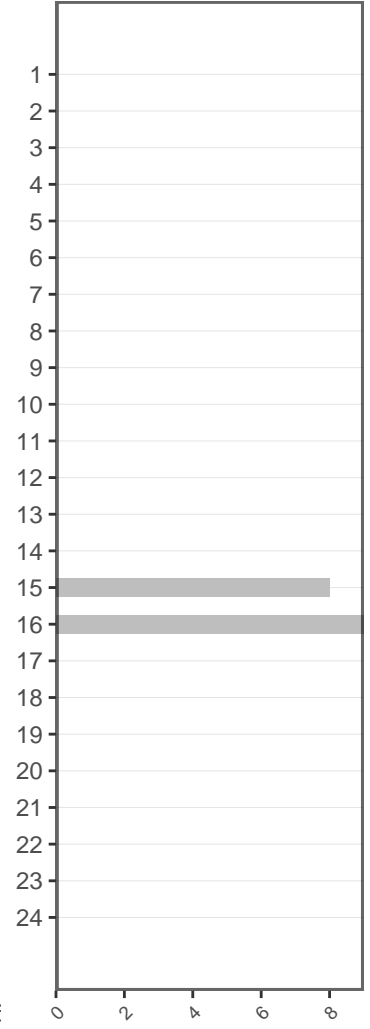
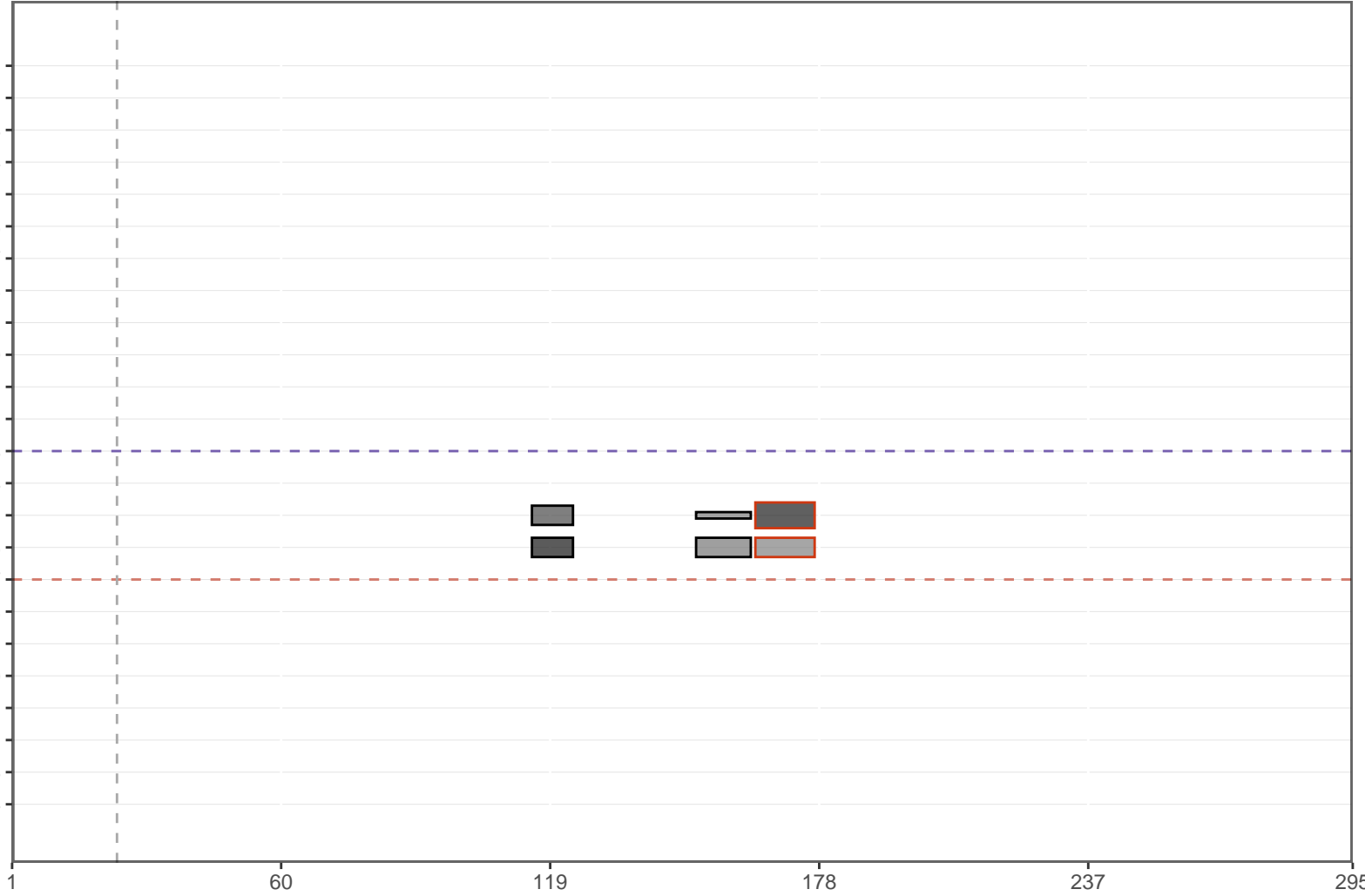
MW indication



Molecular weight

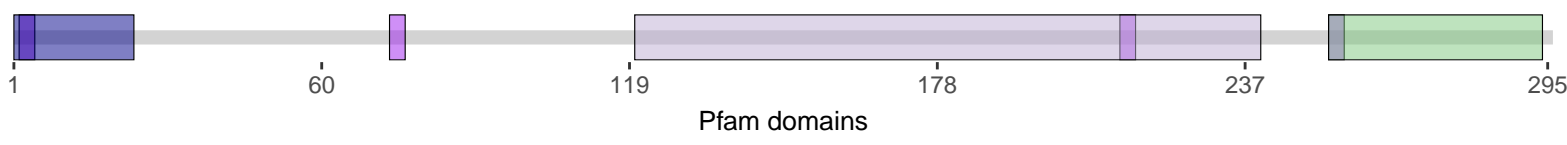


Gel Slice



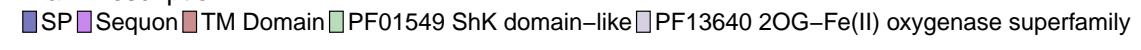
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

YDVEINARGGHRLATVLMKLTDEKGGDETFFNAEEFRRRSMTADDBLSEGAKKGIPVKPRKGDALLFVSLHPNATPDRLSLHGCGPVIGGEKWSATKWHVDSFVKTVETVYNGSGDRDENECERVAALGECTNRPYMLGGAGLPGYGRKSGKAD

NbL14g07260.1 photosystem_I_reaction_center_subunit_II_chloroplastic [MW = 22.63 kDa]

No. of times detected



log(intensity)



Values from



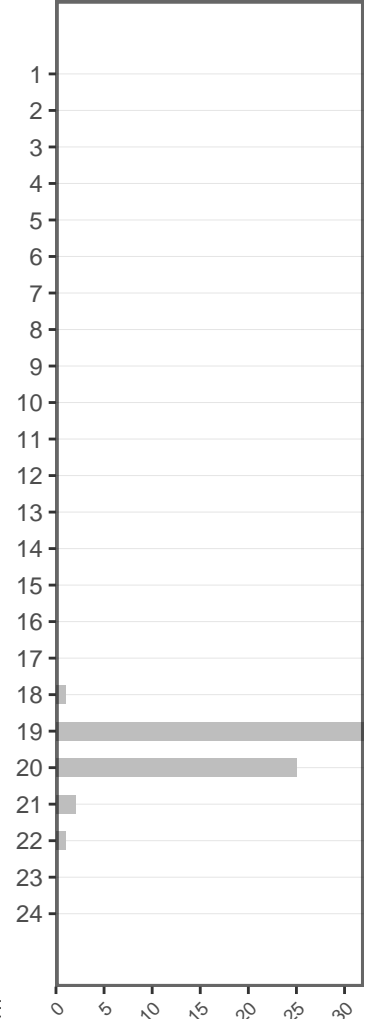
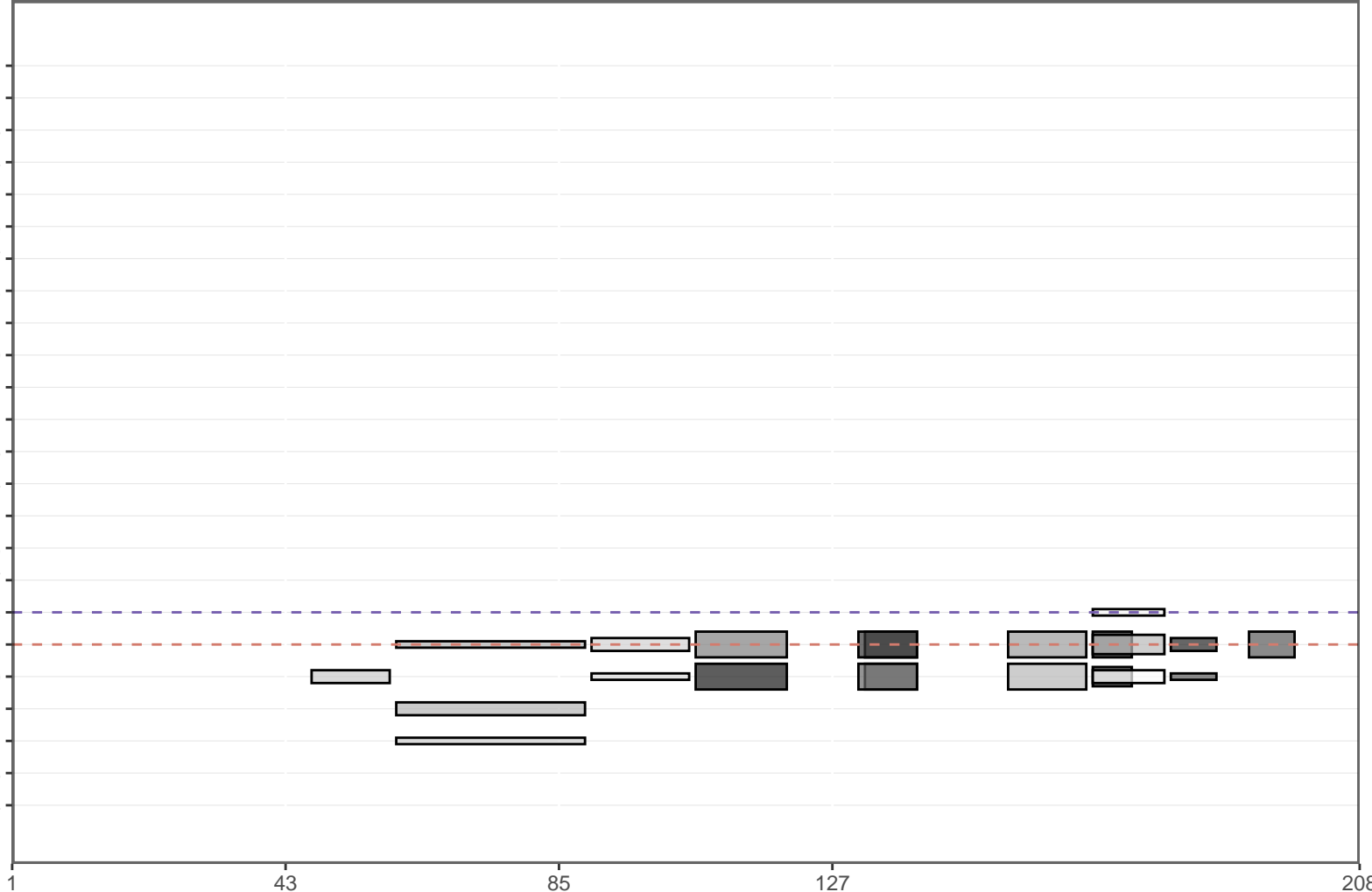
MW indication



Molecular weight

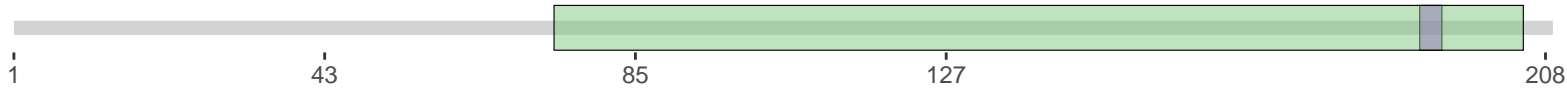


Gel Slice



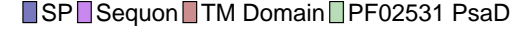
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

QVEEFYITVESPKEDFEMPTGGAIMREGANLLKLARKEGCLALGTRLRKRYKINRYFRVRFVFNQEVQYLIHPKDGVPYPEKWNAGREGVGGNFRBGRGNKSPYKFTGKQVYDL

NbL14g06980.1 60S_ribosomal_export_protein_NMD3_pseudogene [MW = 58.56 kDa]

No. of times detected



log(intensity)



Values from



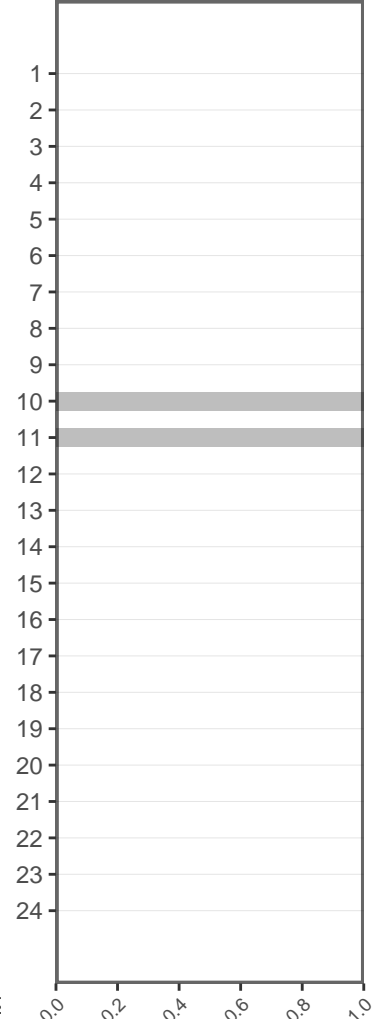
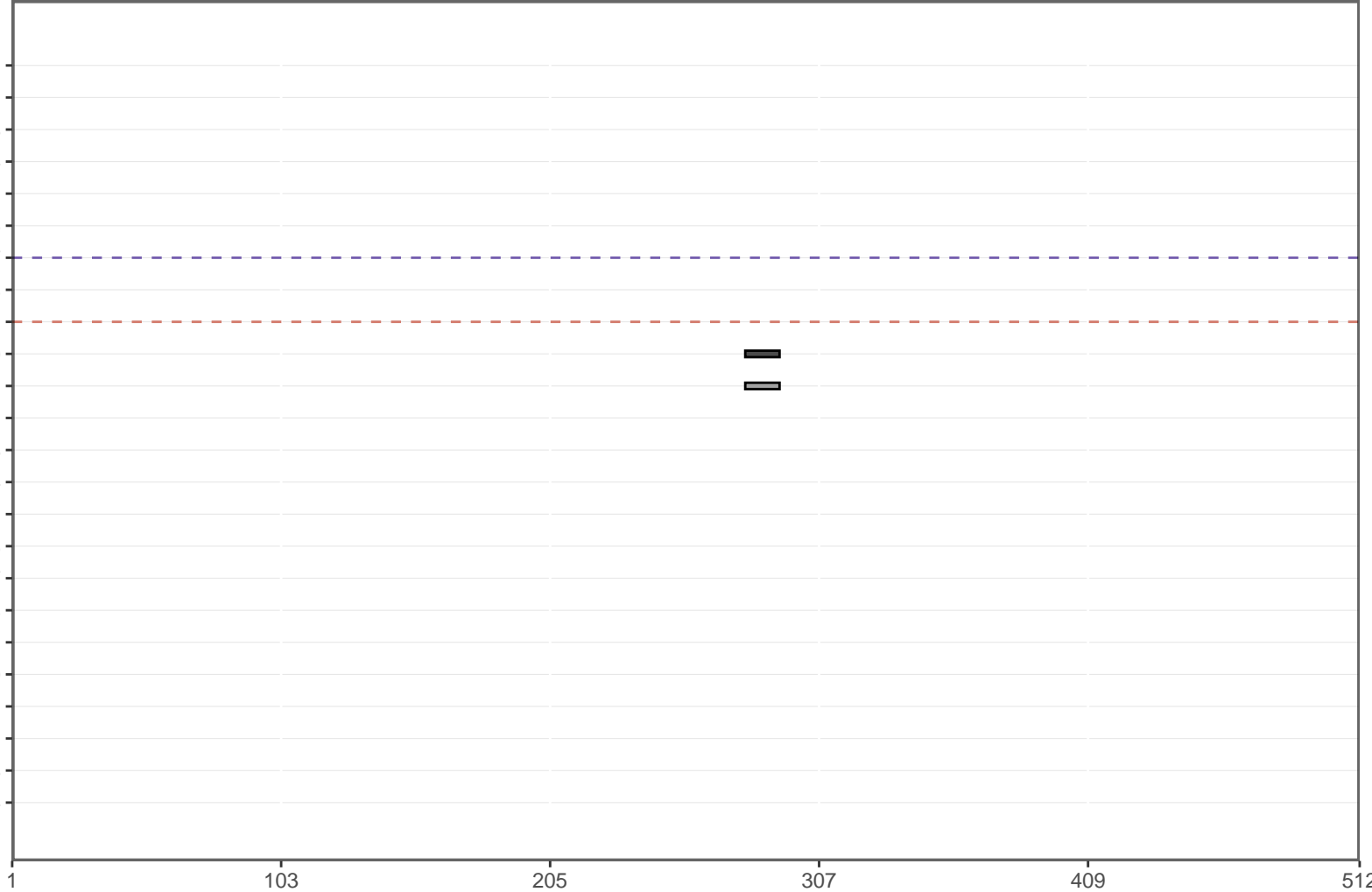
MW indication



Molecular weight



Gel Slice

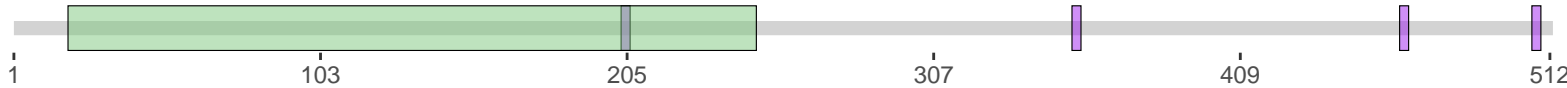


Peptide counts over 4 repeats

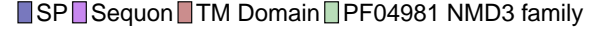
Protein length



Pfam domains



Pfam Description



Protein sequence:

IFSVEICPCYCRELDLGLFPKWIDGLGNLGLVIGTKVSNHALLDPFTLRNGLDAEGYWRASFKLLSSRQLVEYVLENEVSVSEVNIHGSGKVALADAGVAVRSDFGKNDITFNVRTHLGHLLNPGDVALGVDLVAANSNDNELDKYKGFVLPDVLVWKKYEEKWQKKRGRPRVWKLKSLNMEIDDNVKGKRDHEKMSSEYEGFLRDLLENPDLRFNLSYRNRVYQPEMASVTDGDDAPTVALEELLADLDLSEEEADNDMSRE-----

NbL14g06950.1 beta-glucosidase_BoGH3B-like [MW - SP = 65.7 kDa]

No. of times detected



log(intensity)



Values from

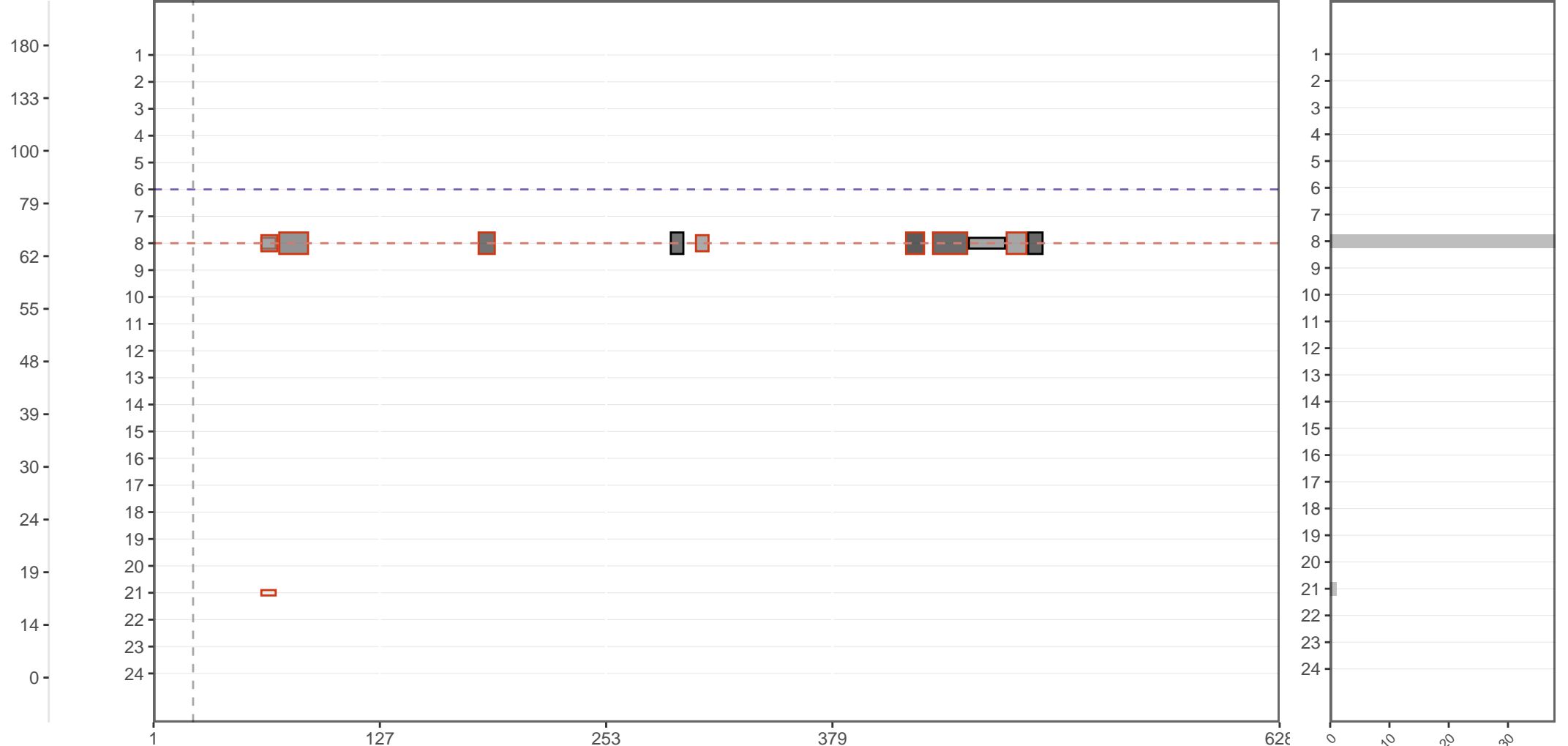


MW indication



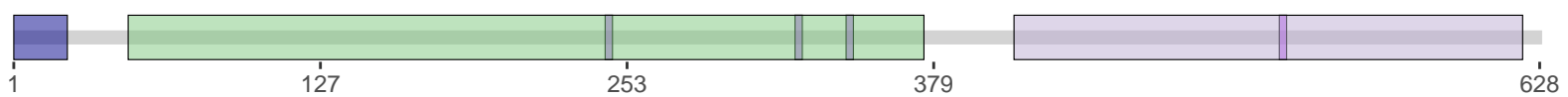
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

SP Sequon TM Domain PF00933 Glycosyl hydrolase family 3 N terminal domain PF01915 Glycosyl hydrolase family 3 C-terminal domain

Protein sequence:

GFVISDVKGDKITDPPHANYVYSGAGVLGIMMGPEINTEFLDDLAFGVGNINIPMSRIDDAVKRILRVKFKVAGLGFENPLADLSLANGLGSGEHRERLAEAVRKSILVLRKGVVSDLLPLPKKAKILVAGSHADNLGYCGGGWTRSWGGIGGNDLITGTTLITAVRNTVHPSTQVYYRNDPDAVFKSNHFSVAIVVGETPVAETFGDGANLTIPEPSPETITNCGVVKGVVWISGRPVVVEPYLANIDALVAWLPGSEGGGWADLVFGDHFQTKLARTWFKSV

NbL14g06940.1 lysosomal_beta_glucosidase-like [MW = 72.43 kDa]

No. of times detected



log(intensity)



Values from



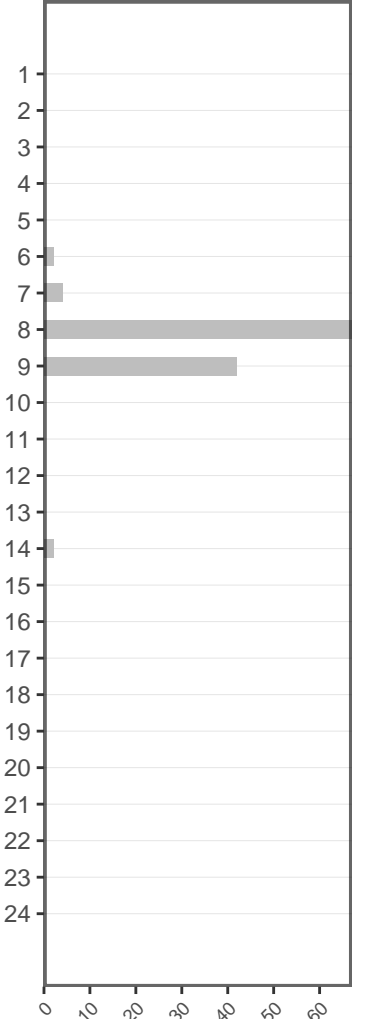
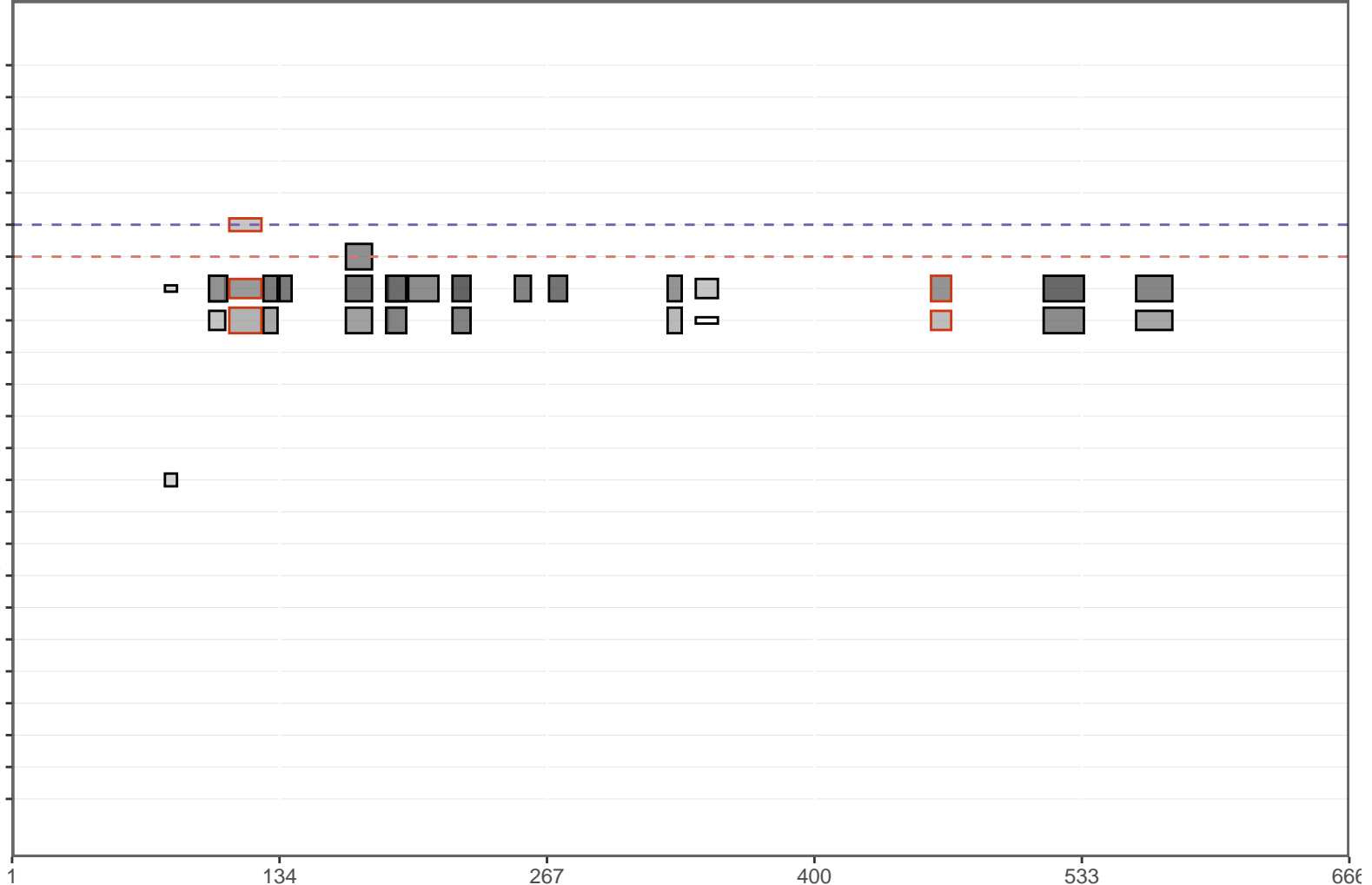
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

SP Sequon TM Domain PF00933 Glycosyl hydrolase family 3 N terminal domain PF01915 Glycosyl hydrolase family 3 C-terminal domain

Protein sequence:

MMHMANRGLTGFKIGKLFKRFVISEDWEIKITDPPRANYSYSGAGVLGIDIMMGDENLFEFLDGLAFQVRRNINFTSRIDDVAERLRVKFKVGLFEKPLADLGLANLGGSEHRELAREAVRKSLVLLKNGKIVSGPLLPKPKVWKLIVAGSHADNLGYGCGGWTGWDGGNDLTTGTLISAVKNTVHPSTGVVYQGNFDFNVKSNHFSYALVYVGEVYAEVEMFGDSAKLTAEKPGPTITNVGGVVKGVVWVMSGRPVVIEPVLNIDLVAWVLPSEGGQVVA

NbL14g06720.1 2-methylacyl-CoA_dehydrogenase_mitochondrial [MW = 44.93 kDa]

No. of times detected



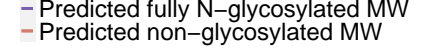
log(intensity)



Values from



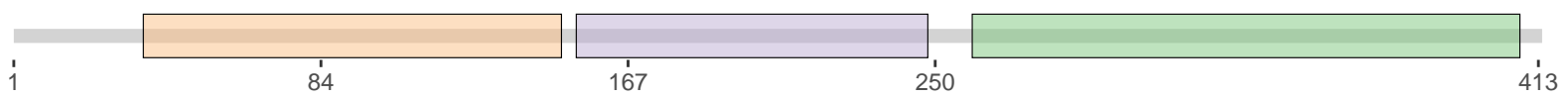
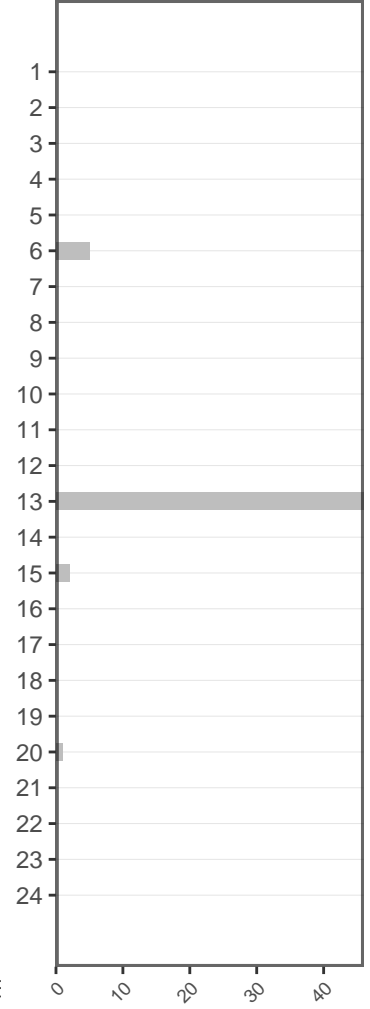
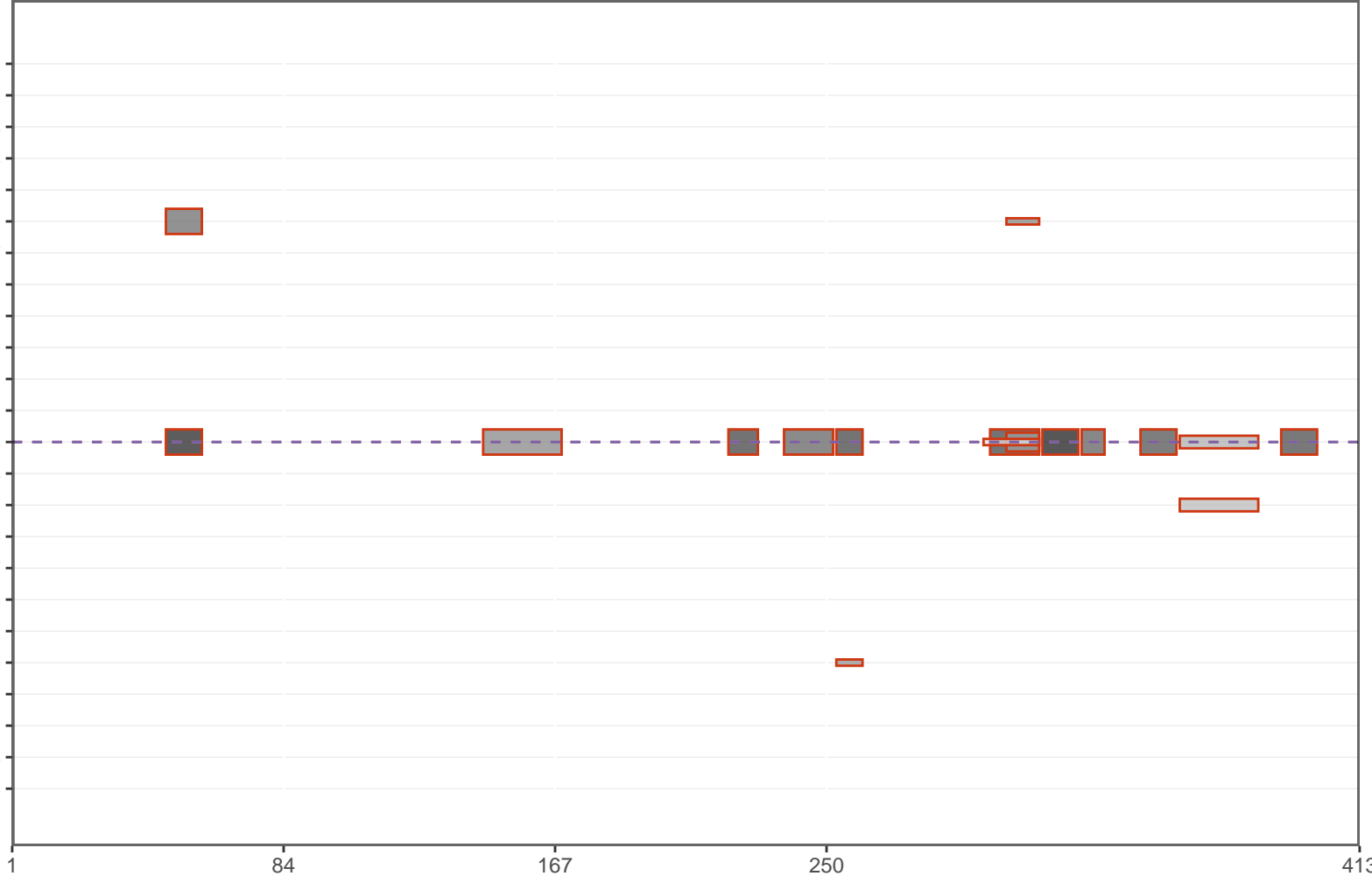
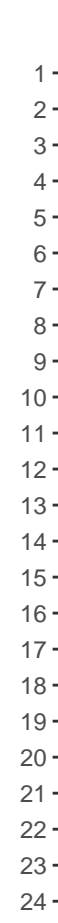
MW indication



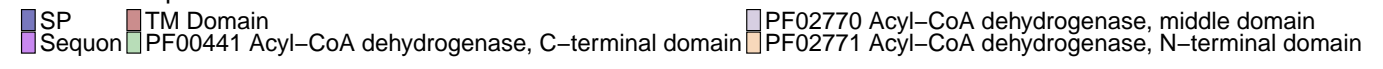
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

PVANTLIVIAKTDITAGSGKGTAFIEKMGSGFSTAQKLDKLMRGSBDTDELVFENCFVPEKENVLGGEGKGVYVLMGDLERVLAAGPVGIMGAGMDVLPVVRDREGFGKPGVEYLOGKIDMTALQSGSRVYVAWAKDQDNGKIDPKDQSGVILVAERATQVALQAGDGLGGNGYNEYPTGRLLRDAKMVEIAAGTSEIRRHIGRELFKHQ

NbL14g06640.1 probable_glutathione_peroxidase_2 [MW – SP = 22.45 kDa]

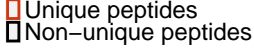
No. of times detected



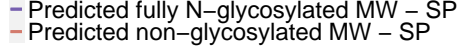
log(intensity)



Values from



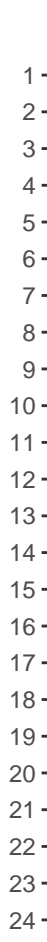
MW indication



Molecular weight

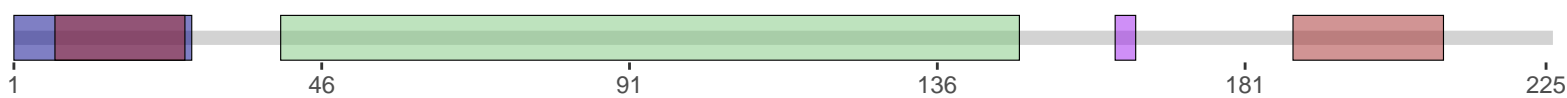


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CNQFLVCEPQGTNSEEIGDETGTTRKAEFFVFEKVDVNGDAAFLKFLKSEKGGFLGNAKAWNFTKFLVAKGKVERVAPRTPPLQFEVTLNGYFFGDFHYLQGPVLVWKGSGNKRKTLSEYLR

NbL14g06100.1 heterogeneous_nuclear_ribonucleoprotein_R-like [MW = 88.15 kDa]

No. of times detected



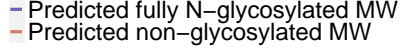
log(intensity)



Values from



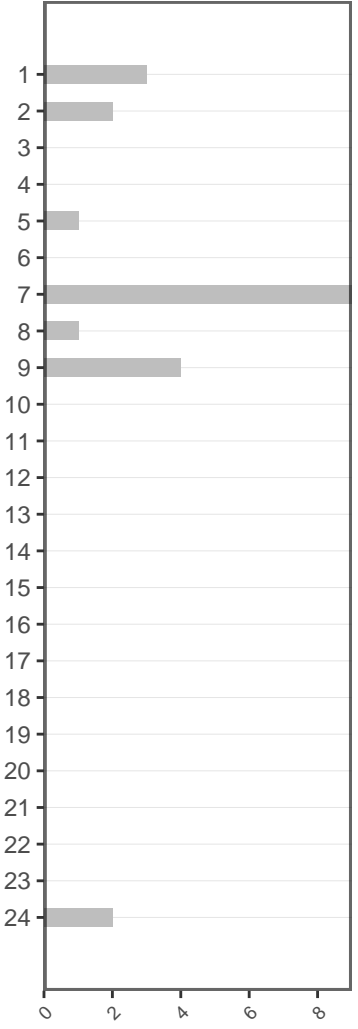
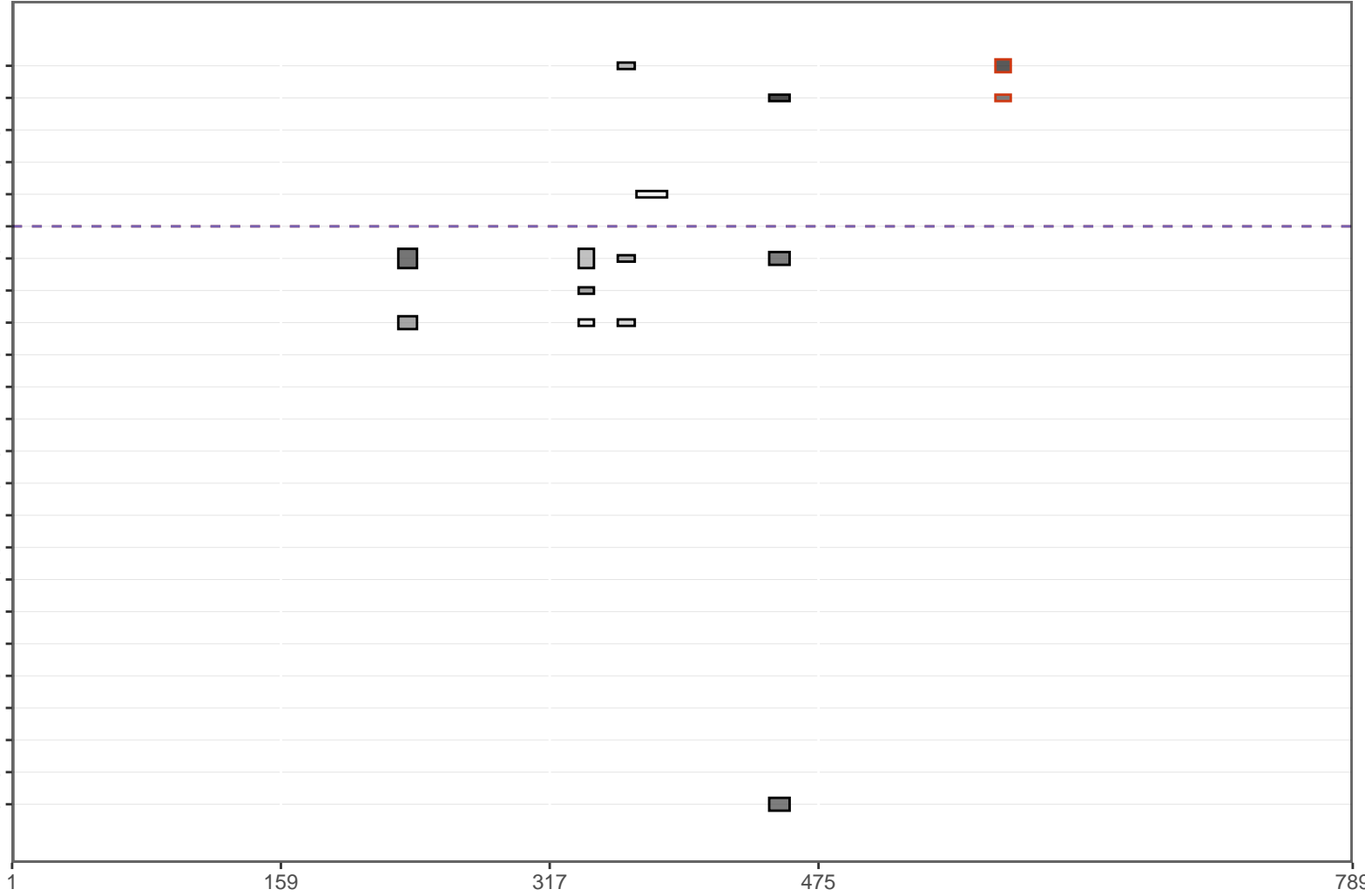
MW indication



Molecular weight

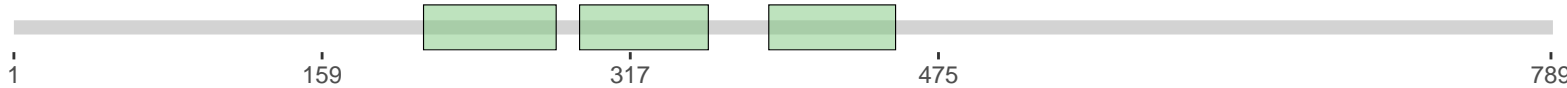


Gel Slice



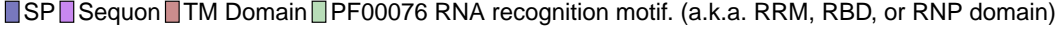
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KTVFDGLSASVDEEDRVRDLKKEYGNEKELARNMPSAKRNDKGFVFDTHAEAVGAKSINNEELGEGDKKVKVRAFLSRPLVGRGRGRVARDLRPLGLMRGPRAPWGRPVHRLPLVGRGSRVSTRVPLGDRGFRKPAAMRDRRPVMVAAPRGRVPAPLSRSGYGRPPVHGVYKSKREYARHEIIPPRSAAVDYPGRFSDRRSGYRDDYSSRSGYRDFPRGHARTSTRRAYVDGFEERYERPPPTFYREGRGREYDSVSGEKREYSLSLDEVPPRYAE

NbL14g06040.1 dnaJ_homolog_subfamily_C_member_17-like [MW = 33.34 kDa]

No. of times detected



log(intensity)



Values from



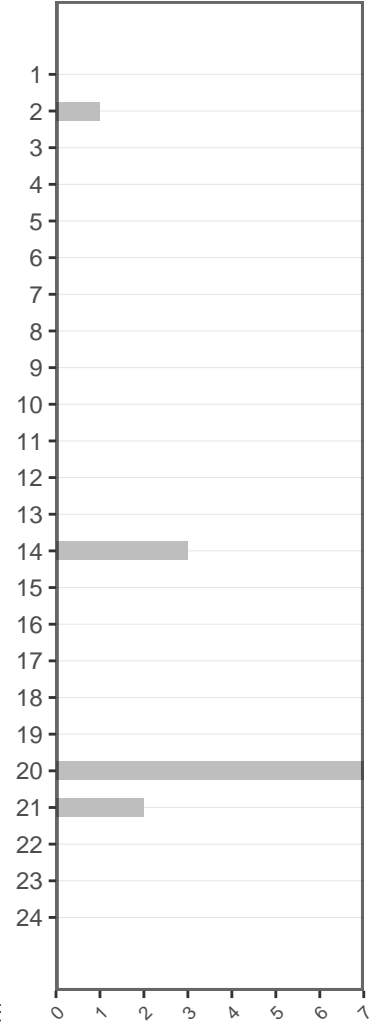
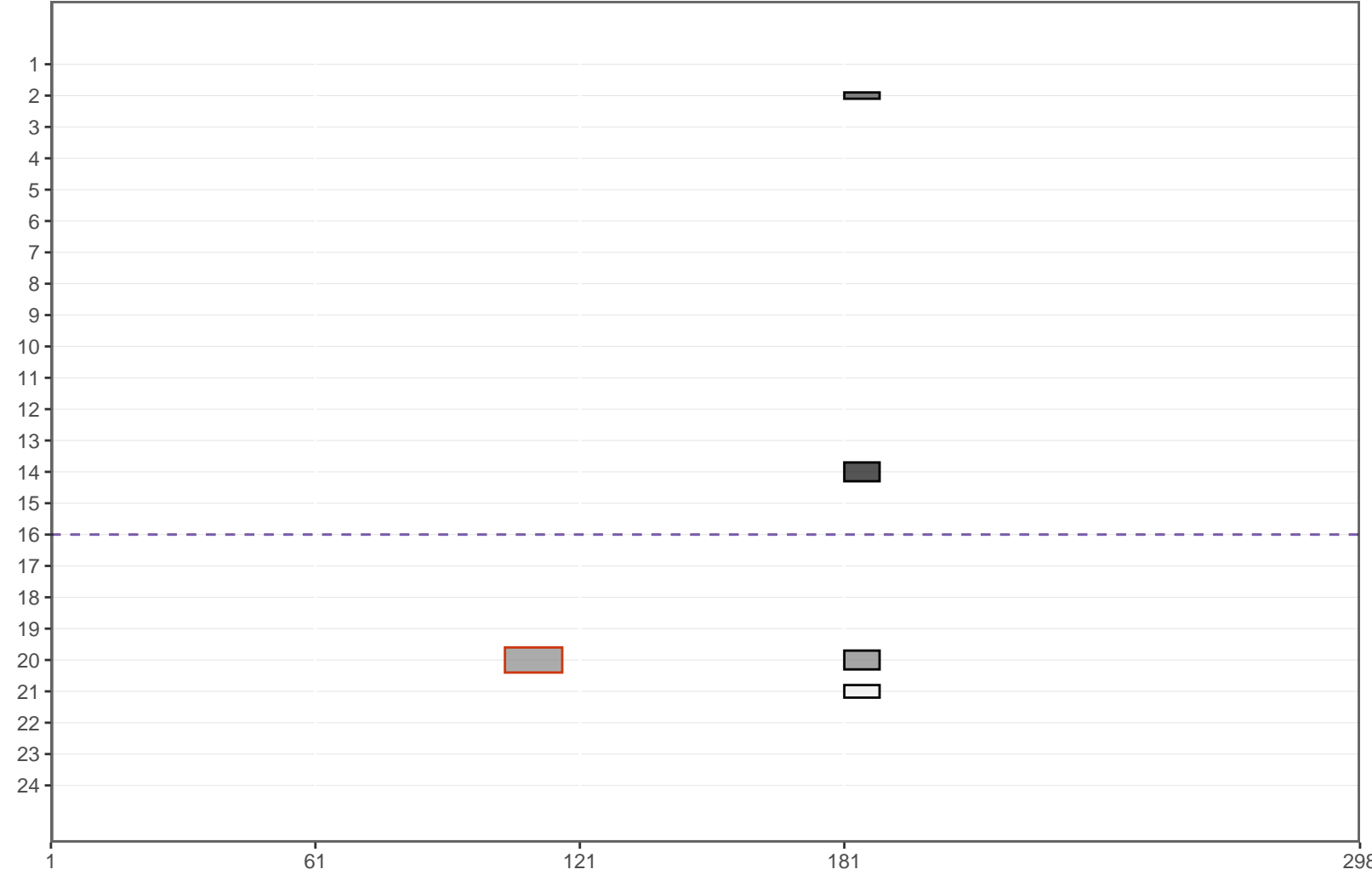
MW indication



Molecular weight



Gel Slice



Protein length

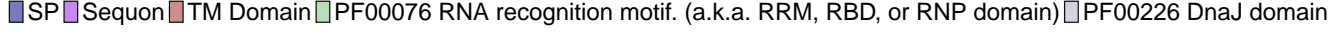


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IHSNKVPTATDPSQKETHAKAKASTEGKSSVDEKELVAVSWERIGEDYTAQRLRELFSFEFGEVEDVVKSSAKKGSALVMSKDAKAVCGNVLGDLNPLLVPLQPTVQPTMPAFFNAEKDREPEFGPLSLNLVAGYQKFDGVLKMRKAQRKK

NbL14g06000.1 eukaryotic_translation_initiation_factor_4G [MW = 194.39 kDa]

No. of times detected



log(intensity)



Values from



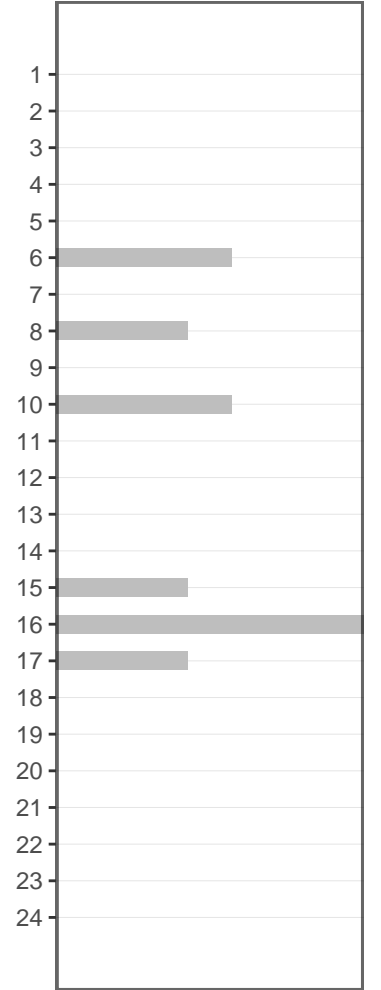
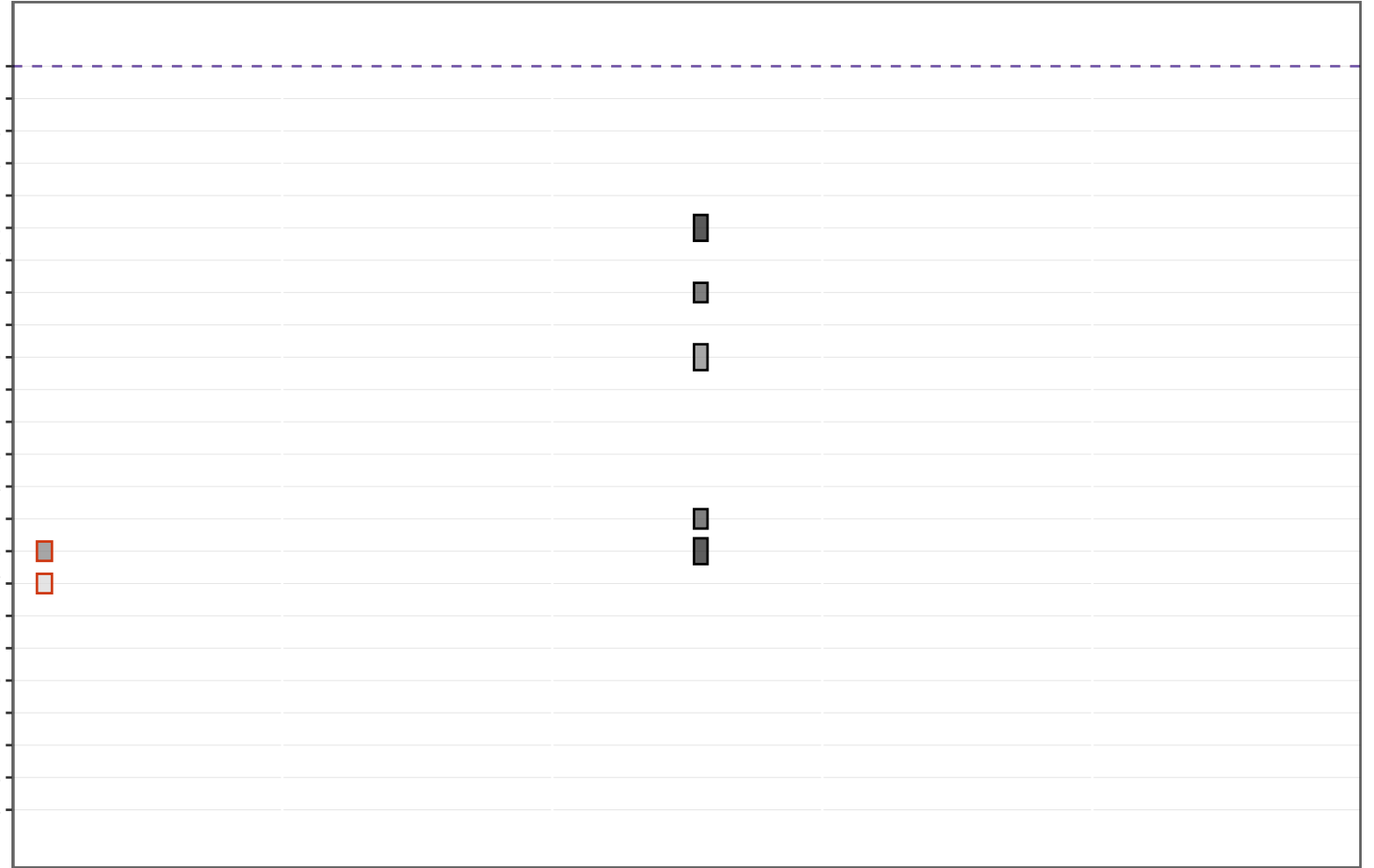
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

DLYMAYGPEKDELAPSEVPEGETSKNNKPLSDDPQEDLSTKVKSEVKAEPDDWEDAADISPKLEAAPEHKKGVDDGDDGDMTTKVKSRDFLLKVFVGGIDIPQGFVPSDADLNNANNEVREPCPSGRALDRPSSGHRERRGGGGDGDVSKVPCPLMPGRDQDFLVYGGVNMGRFRPQGGVGLRHPRAPTFQVWAGLISGPMQSMGPHGVGRNGVQADRWGRGTAFGKGLMPSPQTPAQIMHKAERKVEVQKTFDEEGAKORQLKALNKL

NbL14g05930.1 10_kDa_chaperonin_1_chloroplastic [MW = 14.84 kDa]

No. of times detected



log(intensity)



Values from



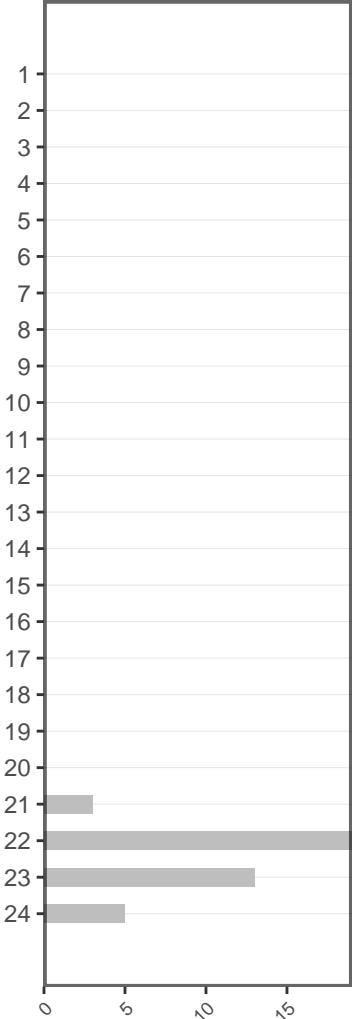
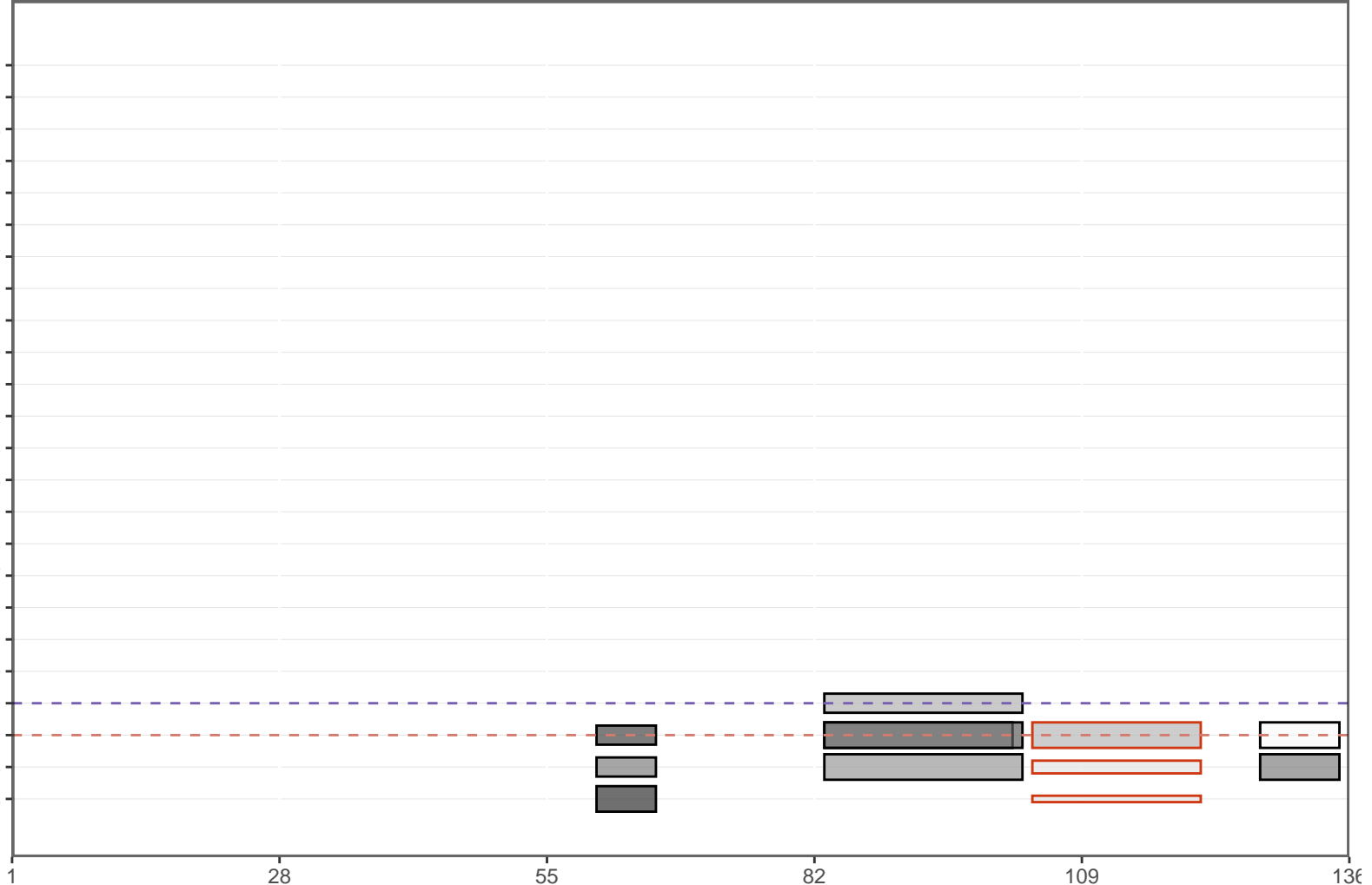
MW indication



Molecular weight

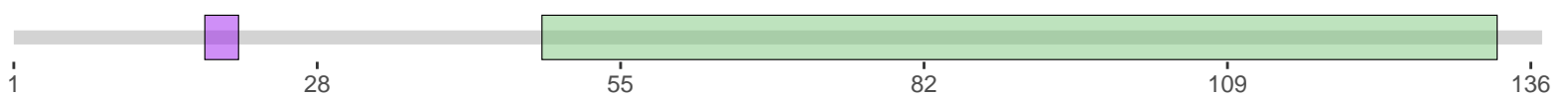


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

VLLRLEELSEKSGGVLLPKBAVWFERVLMGEVLVSGSEVAQVEAGKVLVFDNVAVEVDLGTDRHCFCKESELLAVE

NbL14g05880.1 ras-related_protein_RABH1b-like [MW = 23.12 kDa]

No. of times detected



log(intensity)



Values from



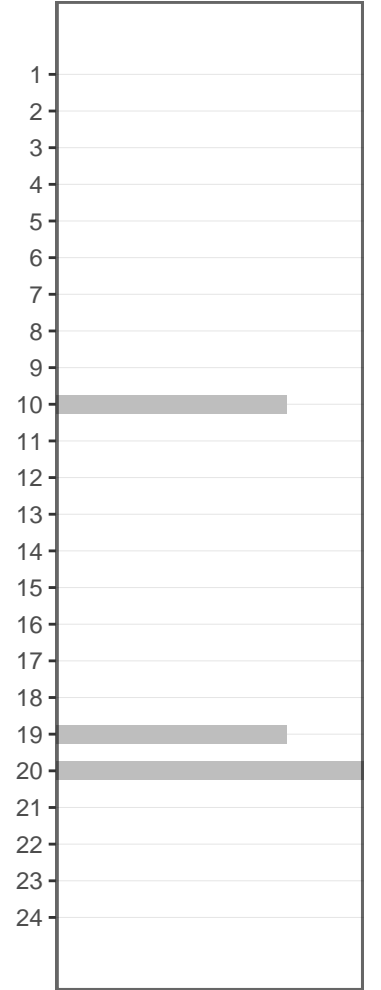
MW indication



Molecular weight



Gel Slice

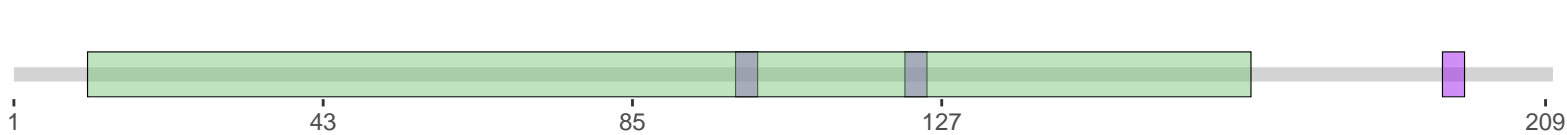


Protein length

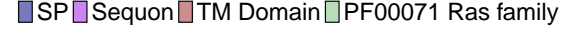


Peptide counts over 4 repeats

Pfam domains



Pfam Description

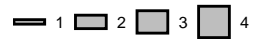


Protein sequence:

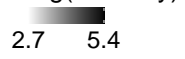
SRQSLNTSKWIEEVRTERRGSDVHVLGNKTDLVKDRQVBIIEEGEAKARELNVAFRIETSAKAGFNKPLFRKAAALPCMETLSSAKGEDMVDVNLKSNPNAGSGPQSGGAC

NbL14g05790.1 eukaryotic_translation_initiation_factor_3_subunit_B-like [MW = 82.58 kDa]

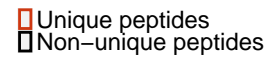
No. of times detected



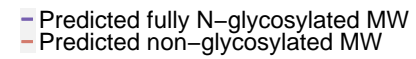
log(intensity)



Values from



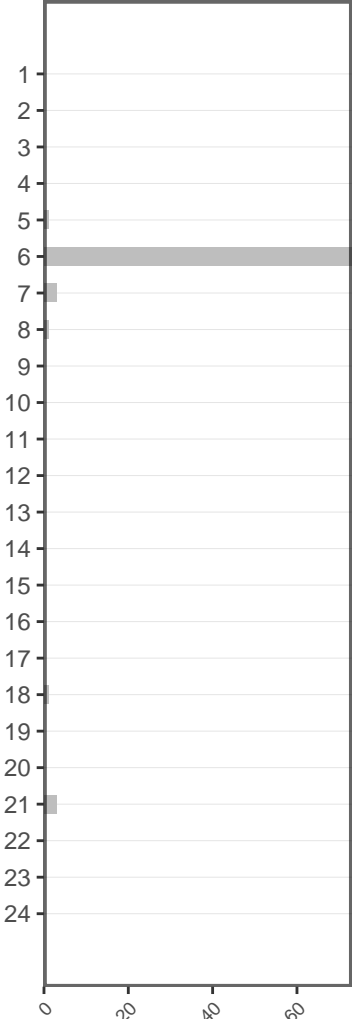
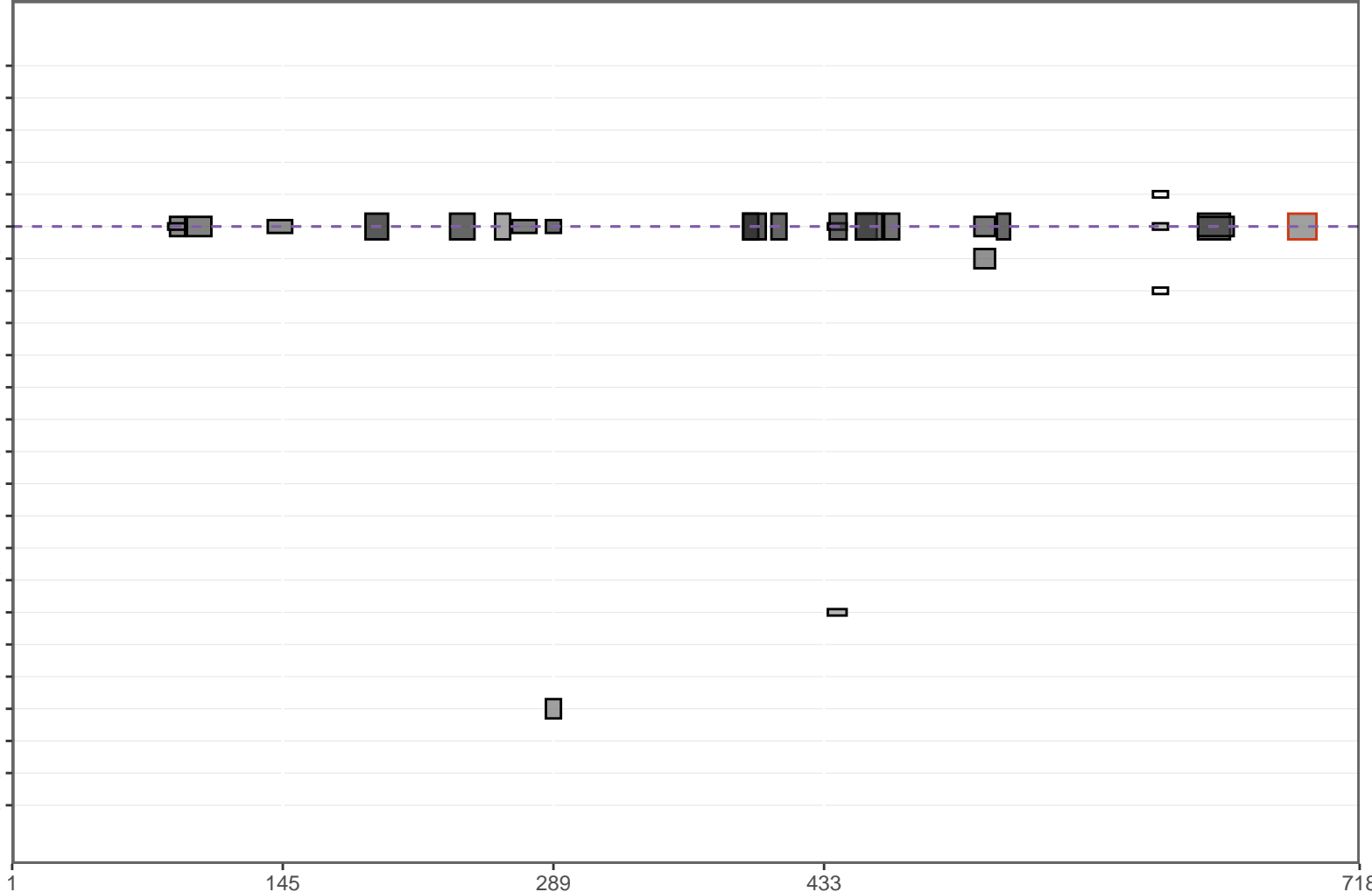
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

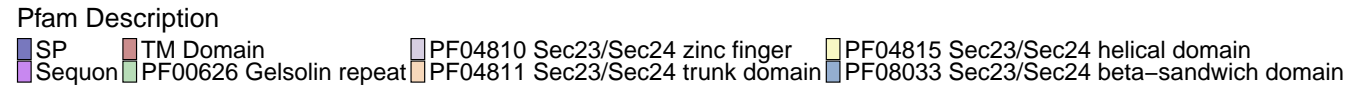
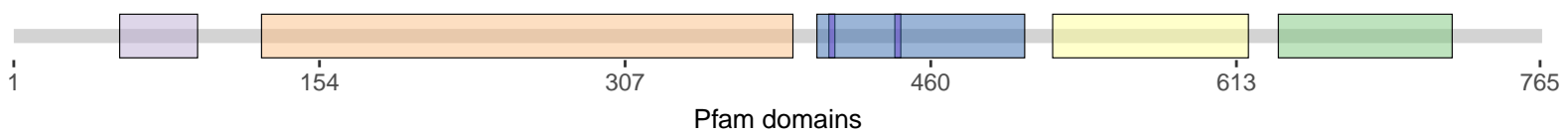
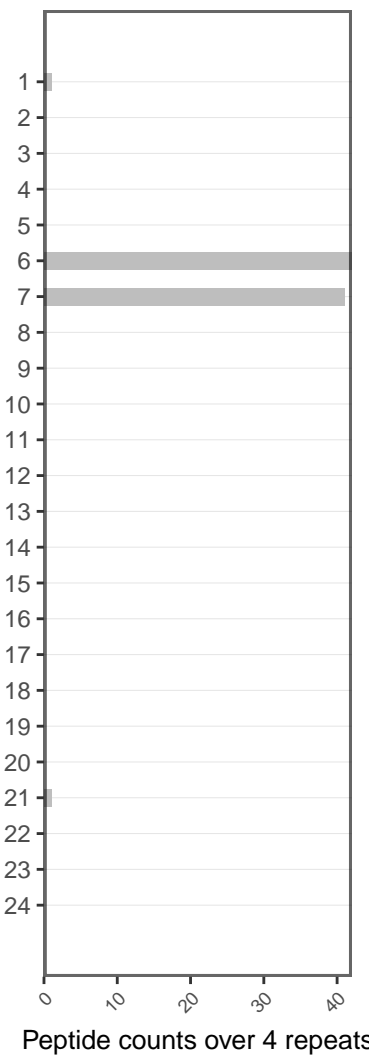
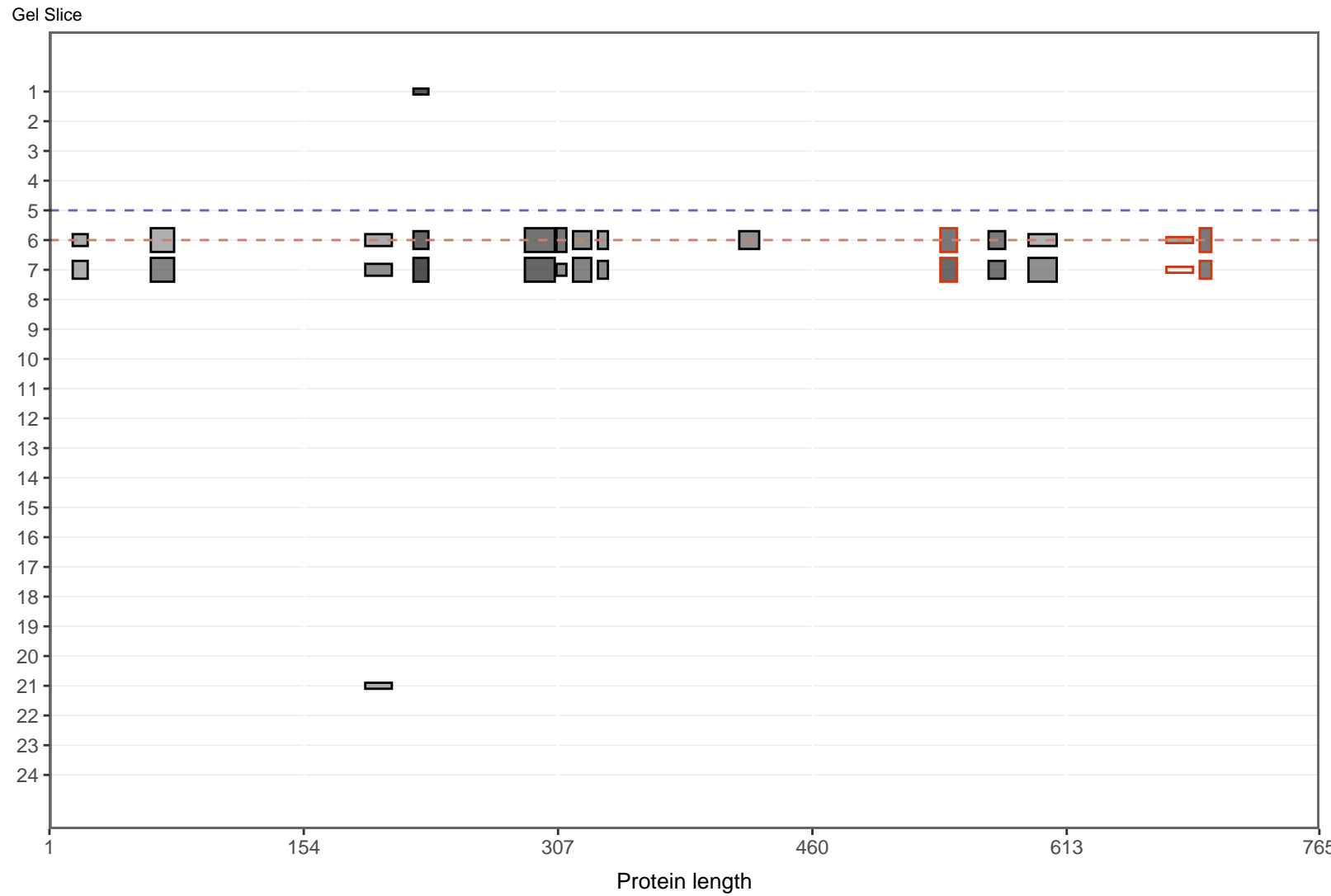
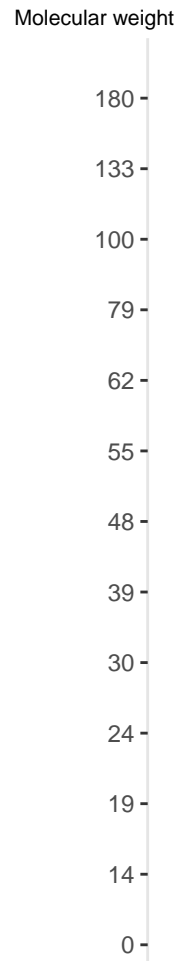
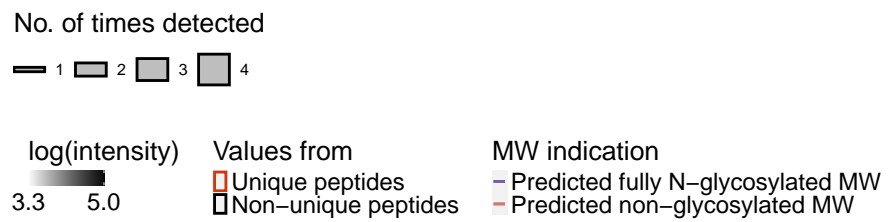
Pfam Description

- SP
- Sequon
- TM Domain
- PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- PF08662 Eukaryotic translation initiation factor eIF2A

Protein sequence:

VYETETSLIDKXSKIVENIMDFSWFADPILALFVPEGCGNPARVSLVQPSKEELRGNLFSVSDKMMWOSNGDYLAWKVDRYTKTKGKSTYTGFEFRKERDPIEVLKLNKNDKIAFAWEPKGRFVAIWHGNDPRPDSFYVRSKGTNTRVRSKLTLLKGGKANNALYVSPGGRFLLAGLKGFGLEFFDVELETMASAEHFMATDVEWDFTRGVATSVTSVHEMENGFNWVSNFKGLYRILKDHFFQYLWRPRRPPFLSKKEEEIAKLNKRYSKYEAEDCC

NbL14g05640.1 protein_transport_protein_SEC23-like [MW = 84.69 kDa]



Protein sequence:
 LVVLAESFGHSVYKDSLKQVFGSGNDLGLSSNGIFEVNSGKDKVYGGVIGPCASLEKKGLPCEVAVVGGGNTTAWMCGLDKTTSLGLIEFAKKNPEAAGANPQFYQFLTYQHPSGGMRLRVFTLGRRWAGVPGVQDLIAGFDGEEAAAVVMSRQVSGFKMETETDFDPRVWLDKSLHIGSRFGDYGKDKSPSFTLSRPSFISFQFMHLRRSGFVQVFGNSPGETATVFRMLNRENVANSVAMVIGPSLHYVFGSGPEPVLLDVAIAADRILLDSFTTIVFHK

NbL14g05550.1 phosphoribosylaminoimidazole–succinocarboxamide_synthase_chloroplastic [MW = 38.64 kDa]

No. of times detected



log(intensity)



Values from



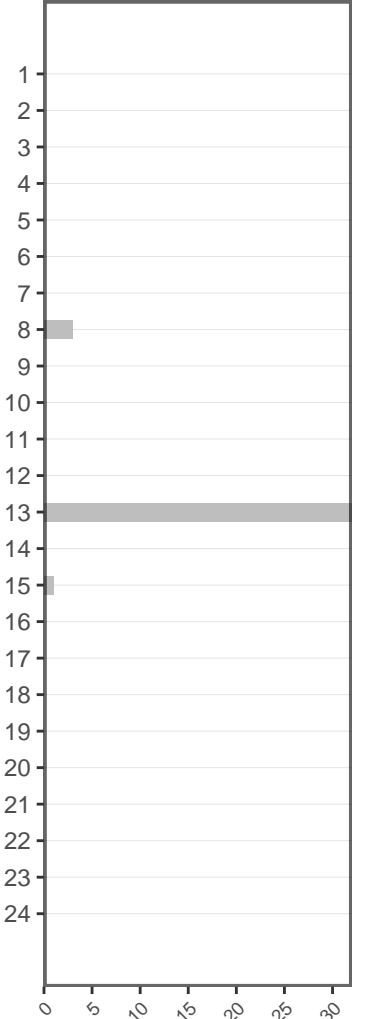
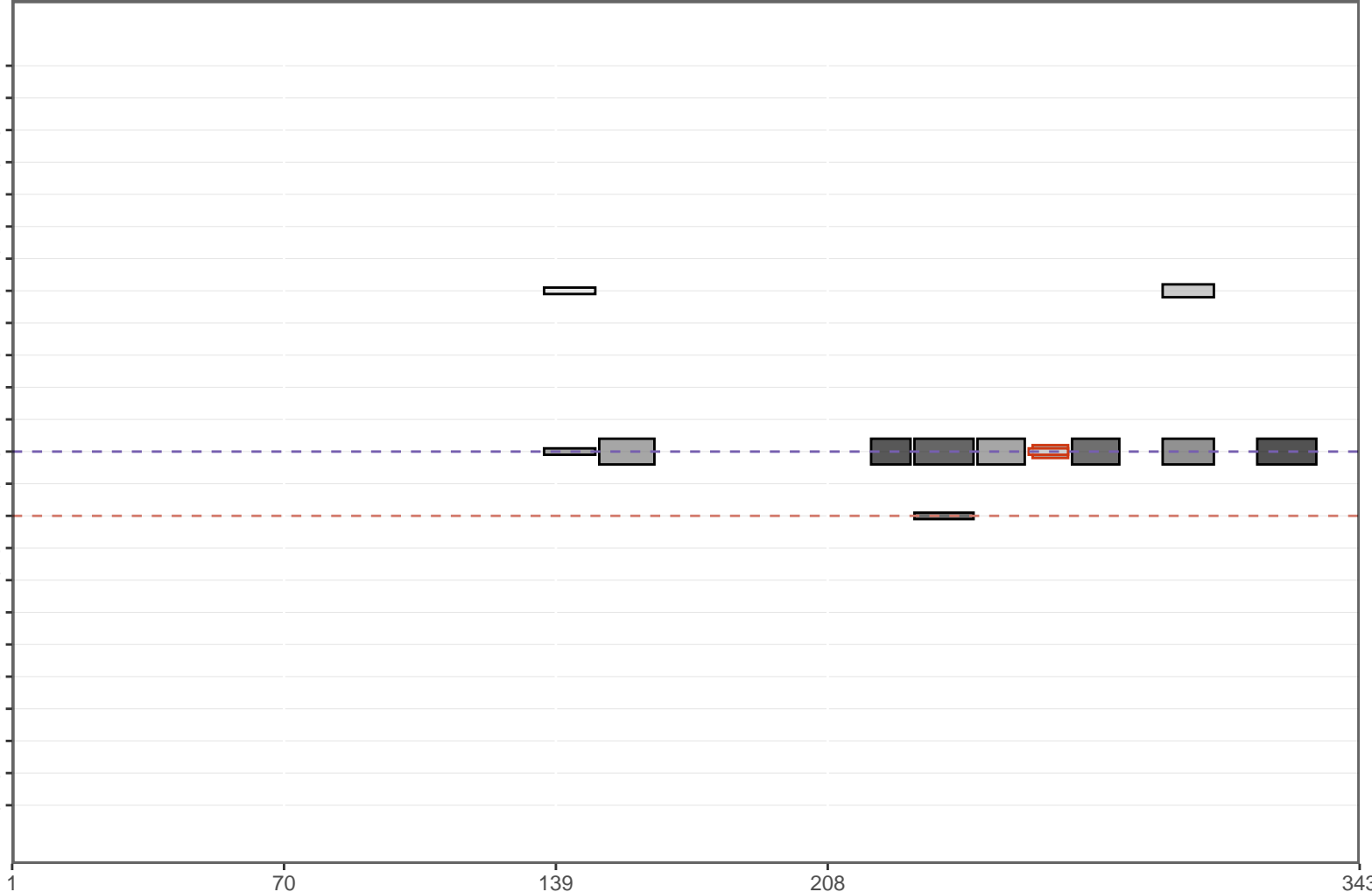
MW indication



Molecular weight



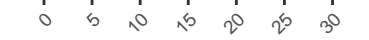
Gel Slice



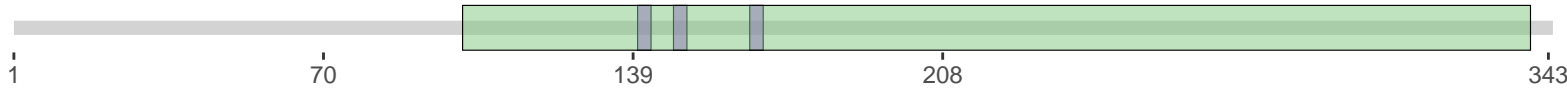
Protein length



Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

VFDNRNVTIARKCCSVTFEYFVRGYYTGGSTDTSLWTFVYKNGVYRNVYGGNLLPDGLVYKNGKLGKNGENLPTFTKAAADHDVYPTDPEIVQRGLMTGADYDEVSRKATSLFEFGQRVALDHSLGLVDTKYEFYFGKADGKIKYLDEIVHTPDSSRYWVAHSGYGERFQSGLEPNIDKEFLRLWFRNHHKPY

NbL14g05380.1 uncharacterized_LOC107827413 [MW = 35.43 kDa]

No. of times detected



log(intensity)



Values from



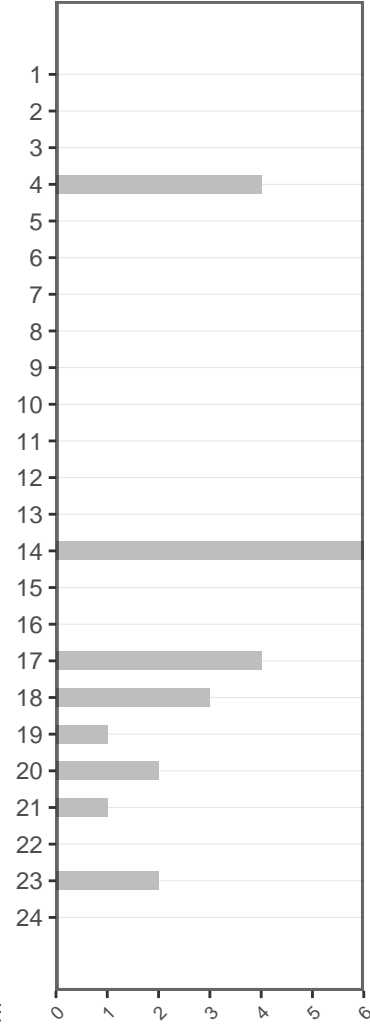
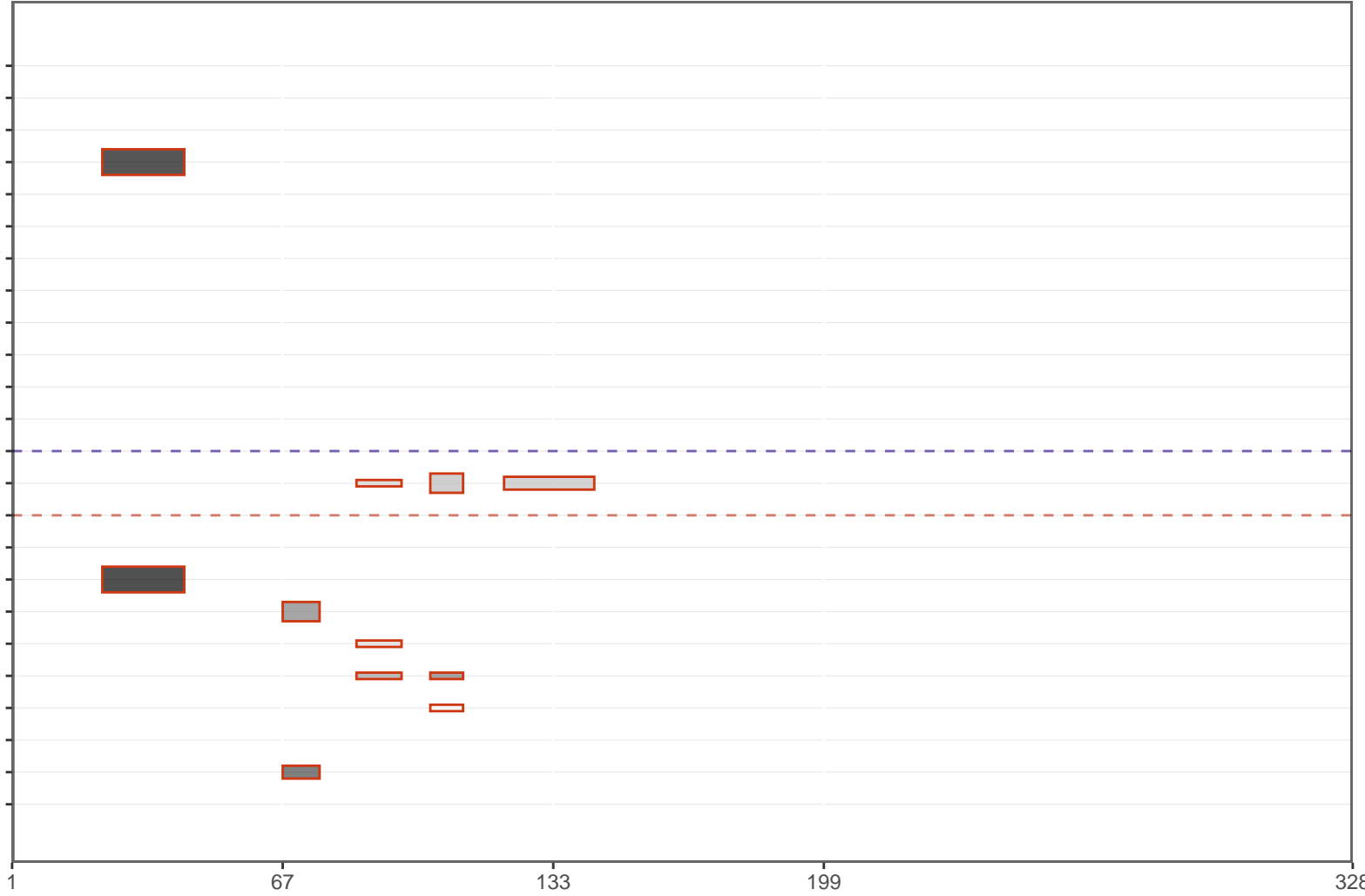
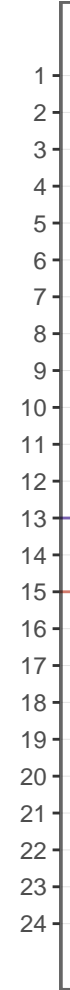
MW indication



Molecular weight

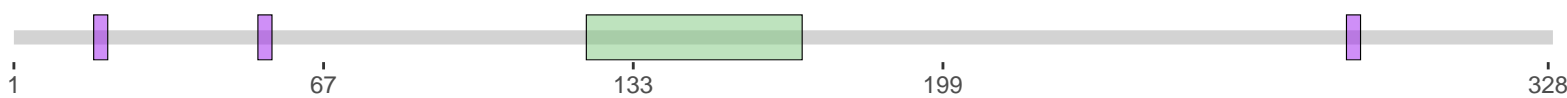


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LDVSLLLTGTPLPPKGLPGVIDQTRGLLYVVEHGAKAVYSPQLRVYCIAGRYIGGSRFLGSSSTVSSLELAGVDPTSEVAAVSNINSETASTFRARFRVGGYKGVGGADWVGGDGVPEVSAHLKGANLFDGVVHSPVGSDDATRPWQRKIENFREMILRVCLVGLGL*

NbL14g05270.1 serine/threonine-protein_phosphatase_PP2A-5_catalytic_subunit [MW = 35.77 kDa]

No. of times detected



log(intensity)



Values from



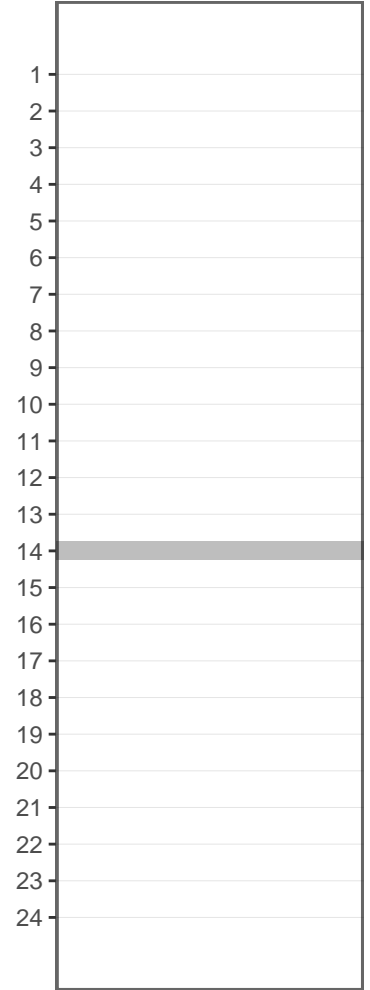
MW indication



Molecular weight



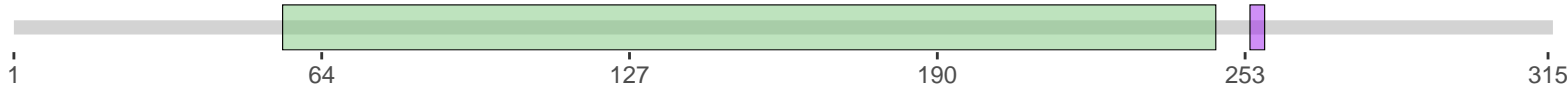
Gel Slice



Peptide counts over 4 repeats

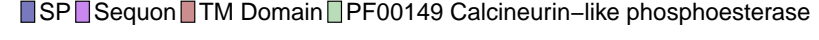


Protein length



Pfam domains

Pfam Description

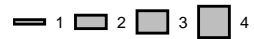


Protein sequence:

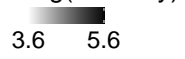
NIWKTTDLFDYFPTALVSESEIFLHGSLPSIETLDNVRGFRVQVEVPHGAMCDLLWSDPDDRCGWGMSFRGAGYTFGGDISEGFHQTNNKLIARAHQLMEGVNWSHEGKQVTFISAPNVCYRCGNMMSLEVDGDRGHFTFGFDMPRRRGEPEVTRRTFDVFL

NbL14g05230.1 V-type_proton_ATPase_subunit_D-like [MW = 29.18 kDa]

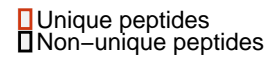
No. of times detected



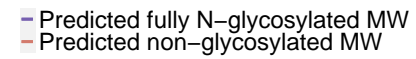
log(intensity)



Values from



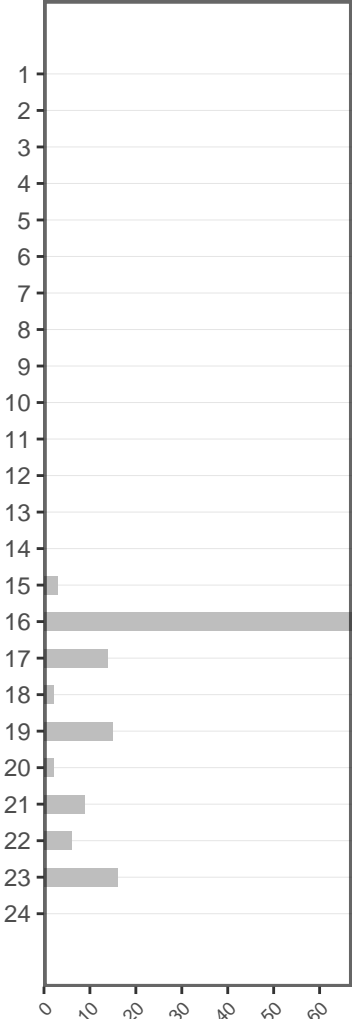
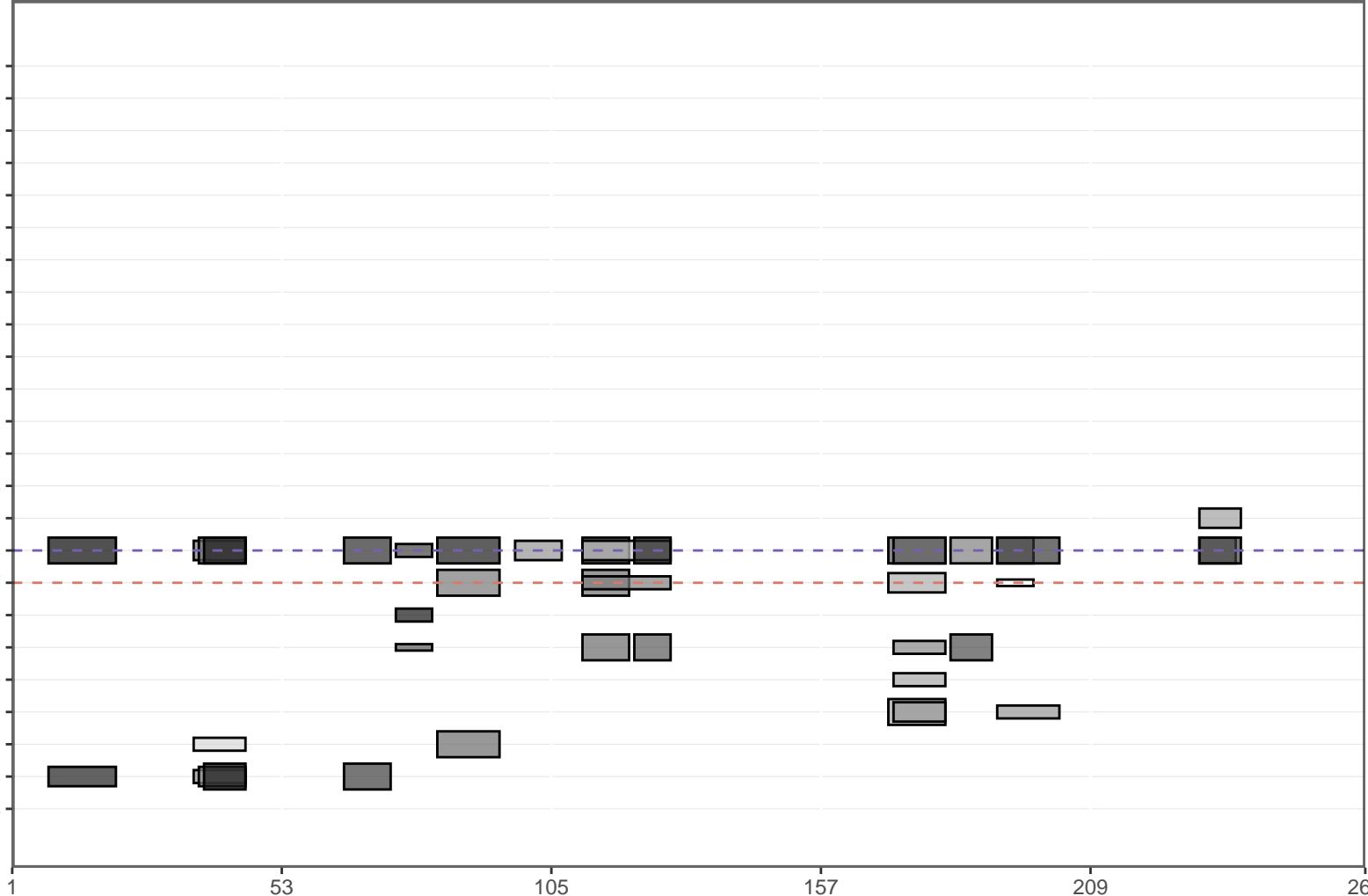
MW indication



Molecular weight

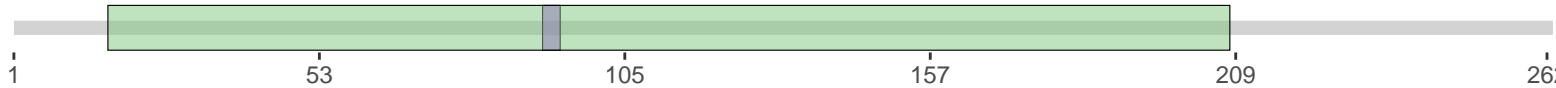


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

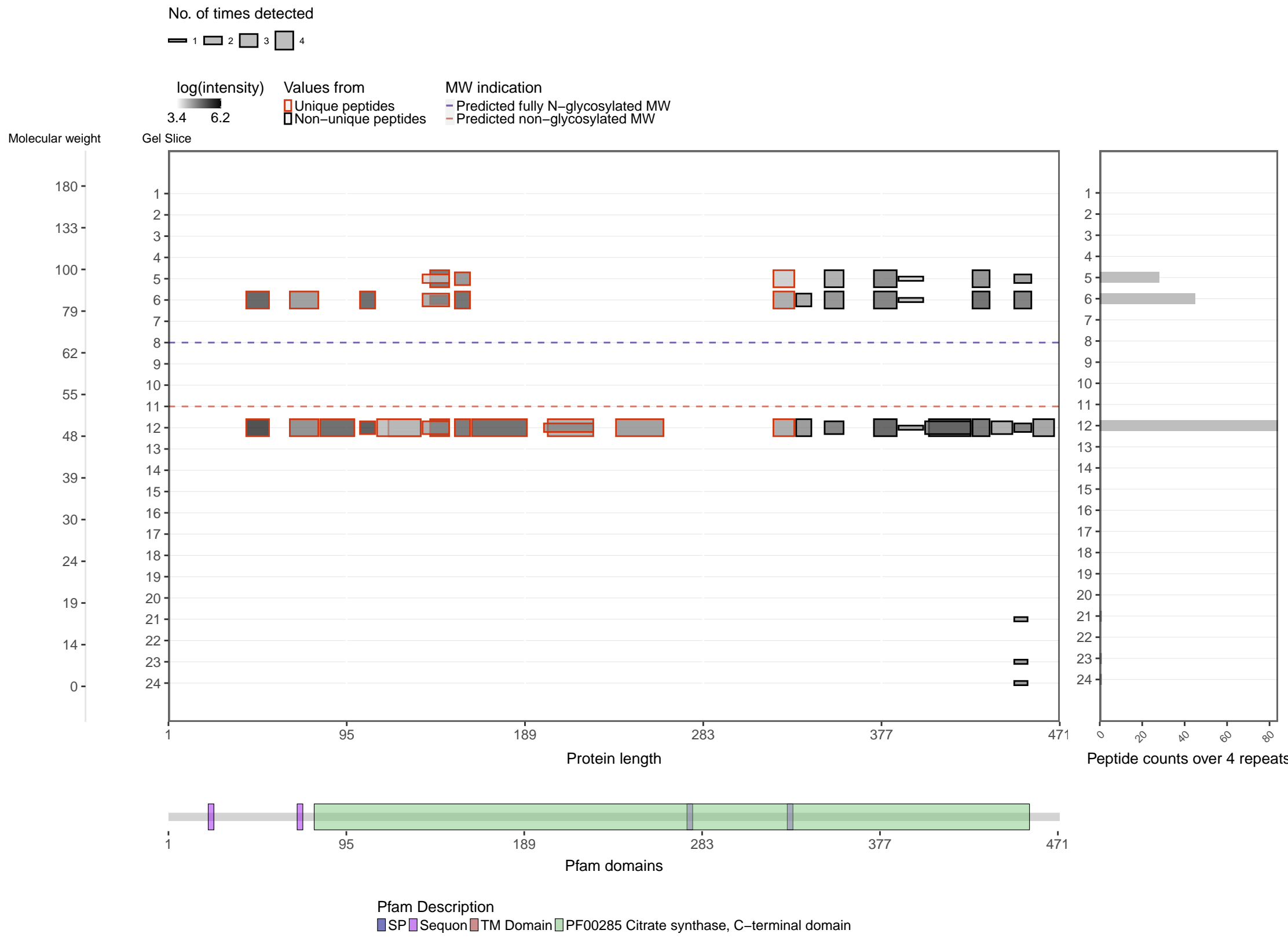
Pfam Description



Protein sequence:

GETKNDLTGLARGGGGVGAGRAAVVSIIELVELASLQTSFRLTDEAIKTNRRVNALENVVKPRLNTLVYKIGELDELEREDFFRLKKIQGYKRIERQMASARQVAEERAEEELSLKKGITLGSAHNLSHASQKDDDF

NbL14g05180.1 citrate_synthase_mitochondrial [MW = 52.43 kDa]

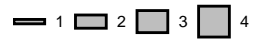


Protein sequence:

YYRMYKNGNTIPKDDLDYGFANFAHMLGFSSDDMHELMRLVYTHSDHEGGNVAHTGHLVASALSDPPLSFAAALNGLAGPLHGLANDGVLLWIKVVEEGGENTSEKQLKDYVWTKLKSQKVPVPGFGHGLVKRKTDPRTYTGREFGLKHLPEDFLQVAKLYEVVPLTELKGVKNPWPVNDVHSGVLLNYGLTEARYTYVLFQVSRALGIGSQIWDRALGLFLERPKSVTMEWLENHCKKA

NbL14g04980.1 clustered_mitochondria_protein [MW = 153.86 kDa]

No. of times detected



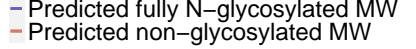
log(intensity)



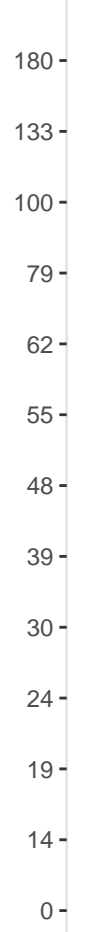
Values from



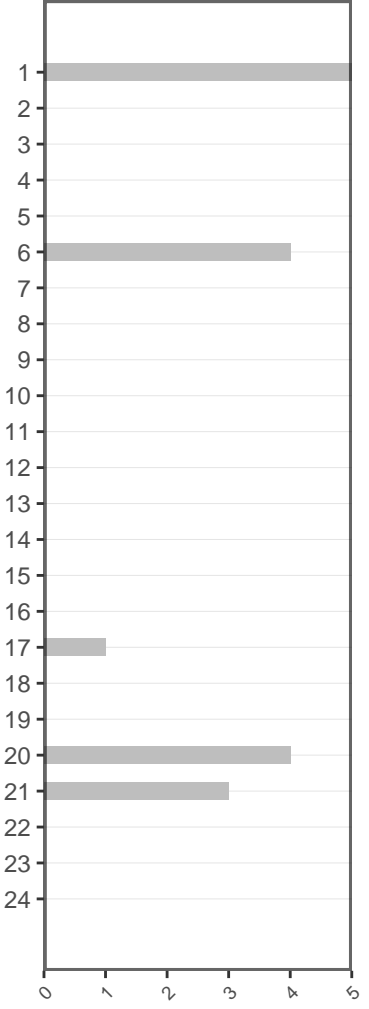
MW indication



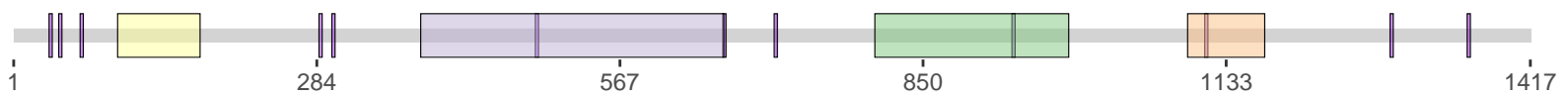
Molecular weight



Gel Slice

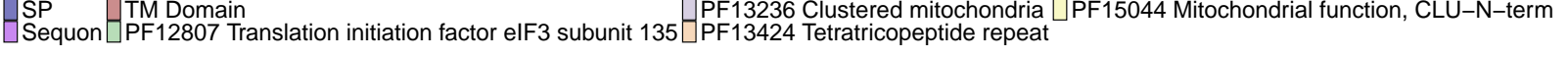


Protein length



Pfam domains

Pfam Description

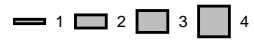


Protein sequence:

IGEVPIVSDSSSTVNNTEELQTTDGVVPMVEVDNNTGKGVKDGAGNNGGSHGRADTEDILFNPVFTDFPLAGSEEEIVADQVLYKVKVSLYKDTVLPKFKDGLTLEVSPMDGRTLTLEALHAHGNLRVLYGKVAECTRLNPLHWDLGSENEVVRGAKHLKQVLRDAEDHDLANTVSHFCNGLFNGTIVSNKGGANSALSKNGKDKHENGQKSGKGRKRVGPKAKKLSVYLNFTSDGLWSDHQEFALKYGFELPEDAKMLIKIPVWRNLGGKGVTVVARKYDLVSA

NbL14g04950.1 DNA-directed_RNA_polymerase_I_subunit_2 [MW = 133.46 kDa]

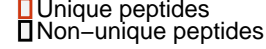
No. of times detected



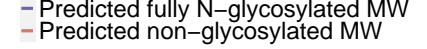
log(intensity)



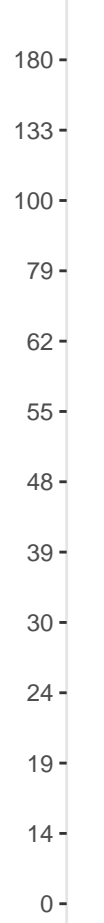
Values from



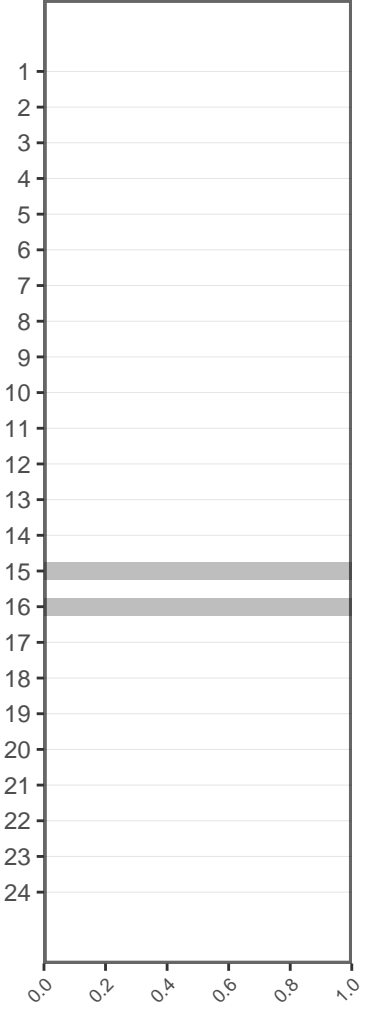
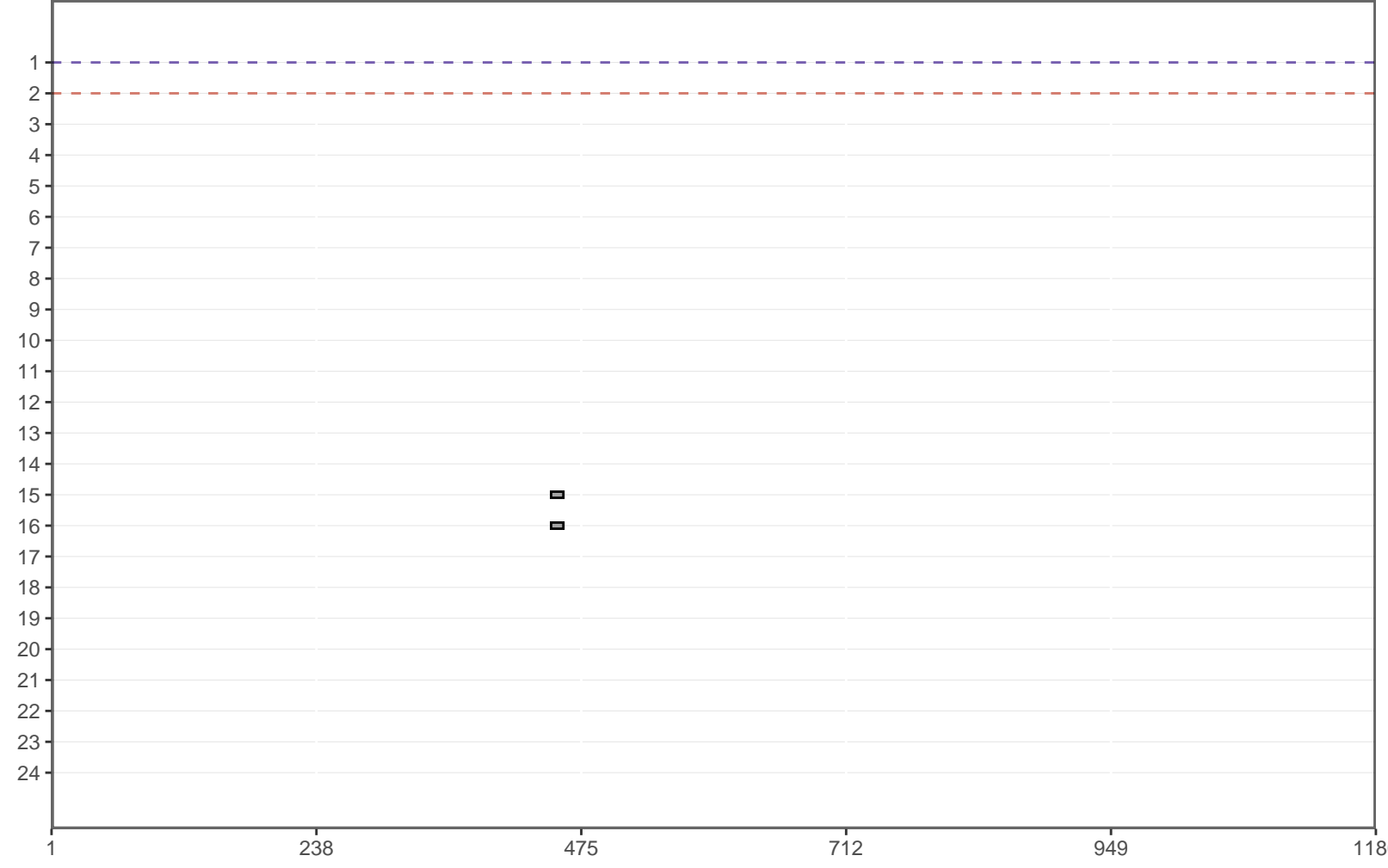
MW indication



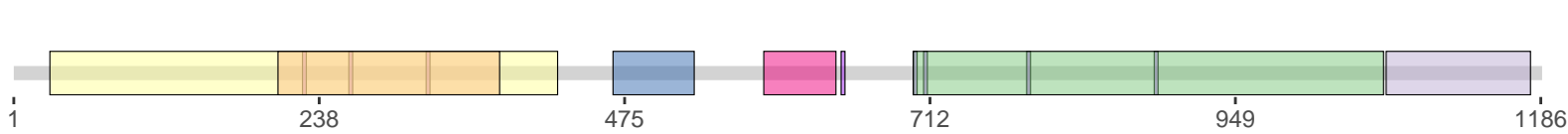
Molecular weight



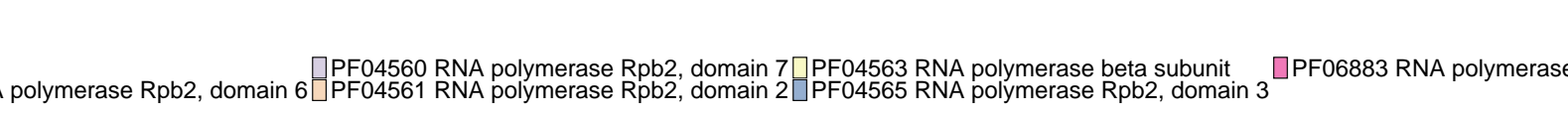
Gel Slice



Protein length



Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF00562 RNA polymerase Rpb2, domain 6
- PF04561 RNA polymerase Rpb2, domain 2
- PF04560 RNA polymerase Rpb2, domain 7
- PF04565 RNA polymerase Rpb2, domain 3
- PF04563 RNA polymerase beta subunit
- PF06883 RNA polymerase I, Rpa2 specific domain

Protein sequence:

IGSMRSKDEEA/TYLRRKVAASIPVDELVGHPLEMSGAYPLVYLFTRFRFRVPRVNRINSAFAEEGNDLEHGPFEGVYMEISGPDGDDGGRKNVFPATHREHPTNLSVGNLTPWSDHNGEPRNMYGGQMGKTMGFSGQALSCRADGKLYHLGTPGTPVTRTKAYEKYGVDDVPLGTNAWVLAWSGVDMEDAMVLNKSVDRGLGHGHYGTETIDLTFGSAKSGRAGRFRREVLKSKSHQLIDSDGLPVVGRINPHEPYCTVNEIFGQTTNMLKXGSEPVV

NbL14g04880.1 putative_tRNA_(cytidine(34)-2'-O)-methyltransferase [MW = 31.36 kDa]

No. of times detected



log(intensity)



Values from



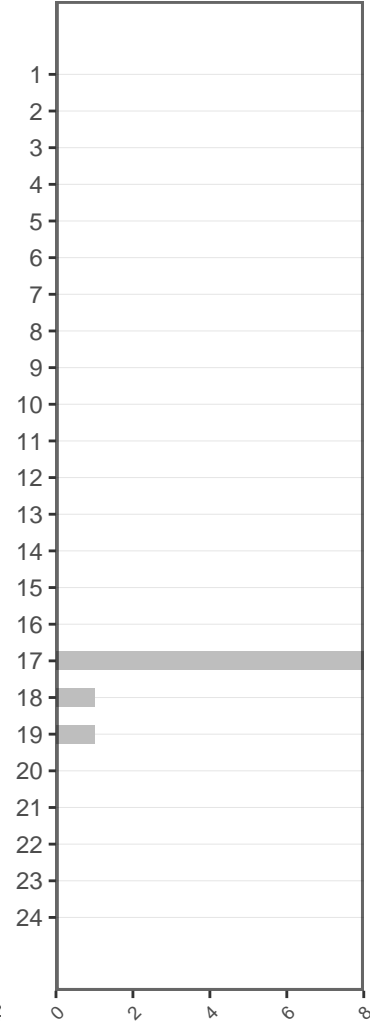
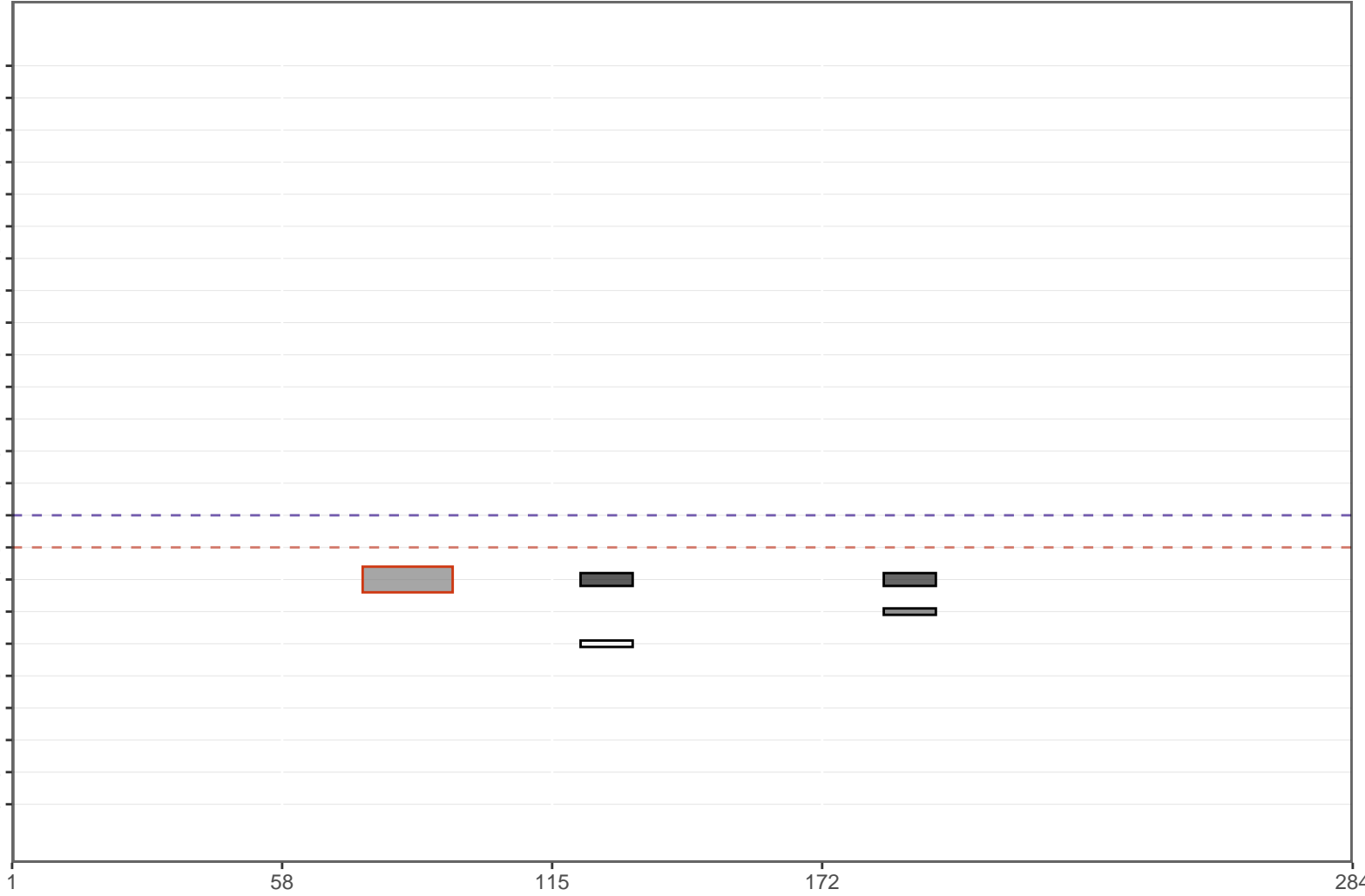
MW indication



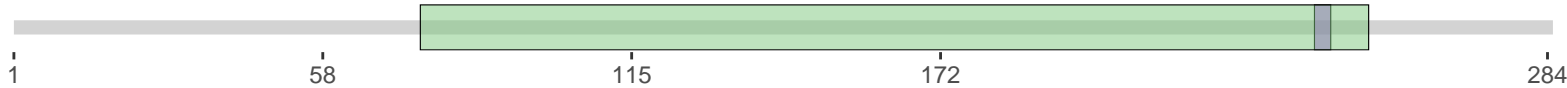
Molecular weight



Gel Slice

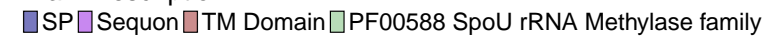


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

...KVIHRSDVDFREYFRGGVFLPHSBSFKTRFRVTKIILFPLQAGENRLLAFTKRGTTTHSDFSYKGGDWLFGSETKGLPPEALLDCNSESILGGTGLRIPMVEYVRCGLNLSVSVGIWVYEASRQNYEQLGCPPTDMDIETSFVTEDIWA...

NbL14g04870.1 DNA-damage-repair/toleration_protein_DRT100-like [MW – SP = 36.68 kDa]

No. of times detected



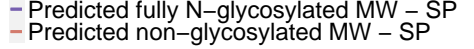
log(intensity)



Values from



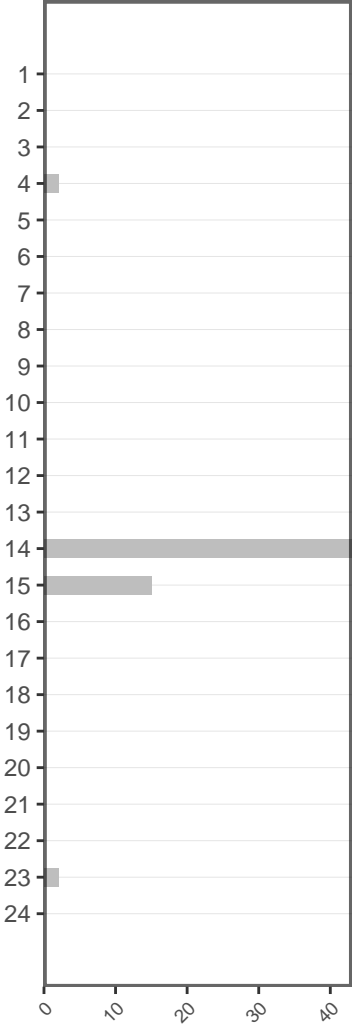
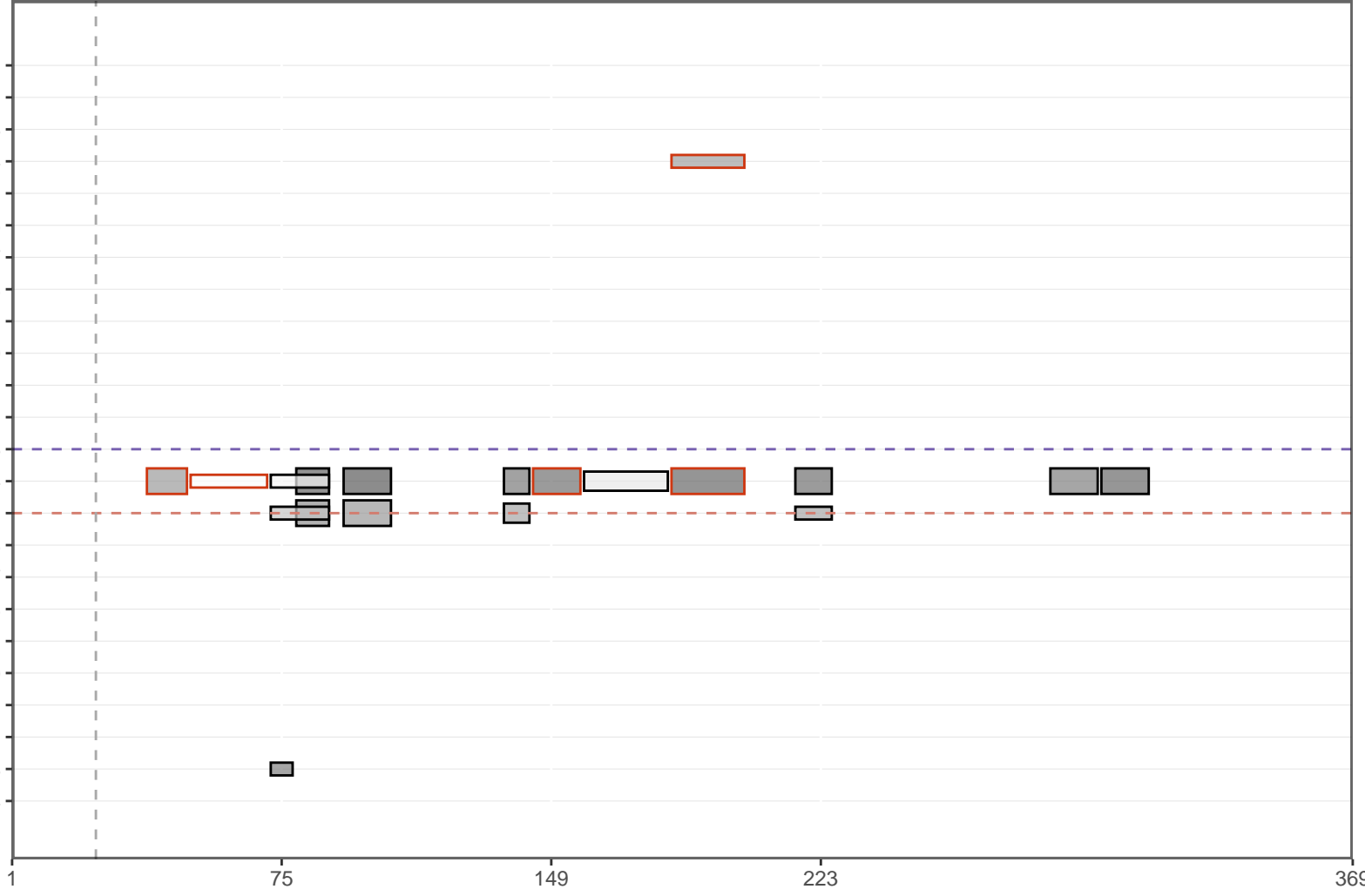
MW indication



Molecular weight

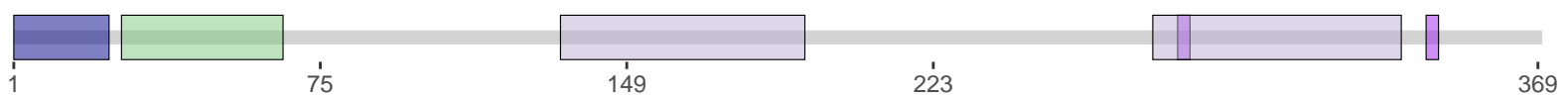


Gel Slice



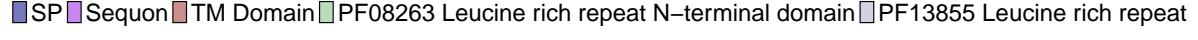
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

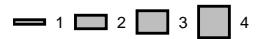


Protein sequence:

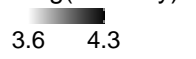
IPGSIYNLGKLMHLELSENNQLSGEIPADGKLEMSRALLNKKIKTGSIPNSIKLYRLADLILAMNQTGSPINQLGMPVLETLNLDGSLGSGIPINLLSCPOLNINLERNLEGLLPDVFSGKTYFTHLDLSEYNNLRGSPKLSASAKYVGHLDLSEYNHLEGGPIPCGFFDHELEASSFNNDLGGSLRITC

NbL14g04820.1 pre-mRNA-splicing_factor_SYF1-like [MW = 106.71 kDa]

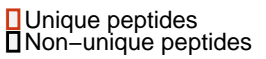
No. of times detected



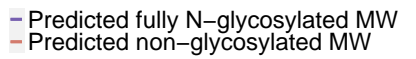
log(intensity)



Values from



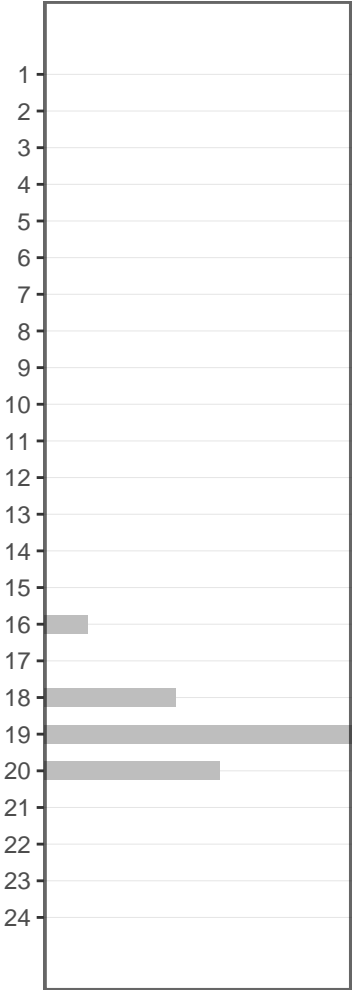
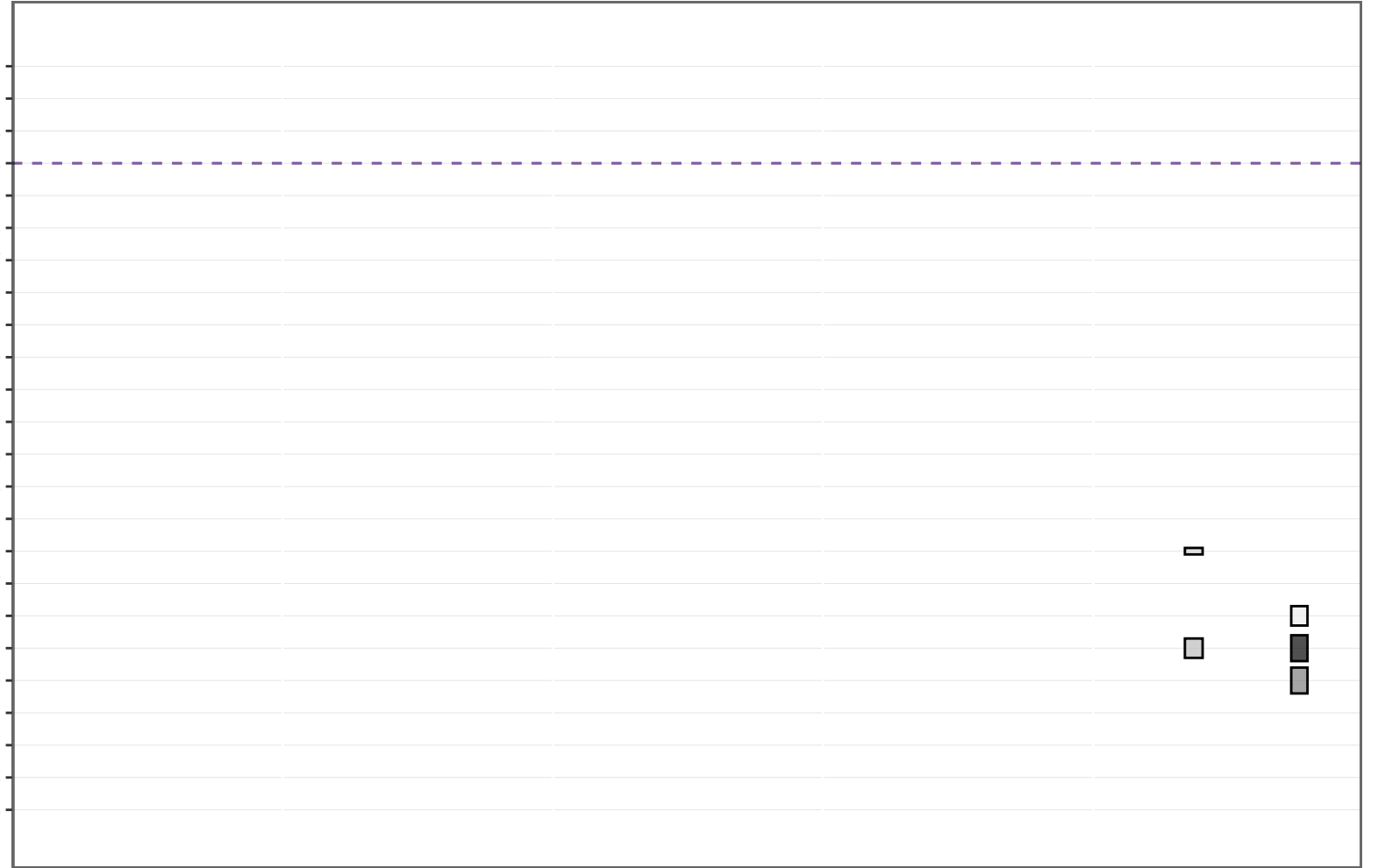
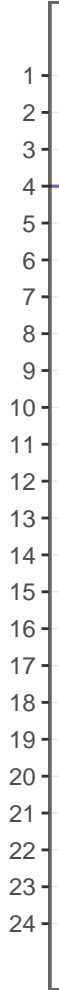
MW indication



Molecular weight



Gel Slice



Protein length

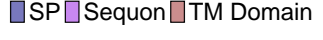


Peptide counts over 4 repeats

Pfam domains



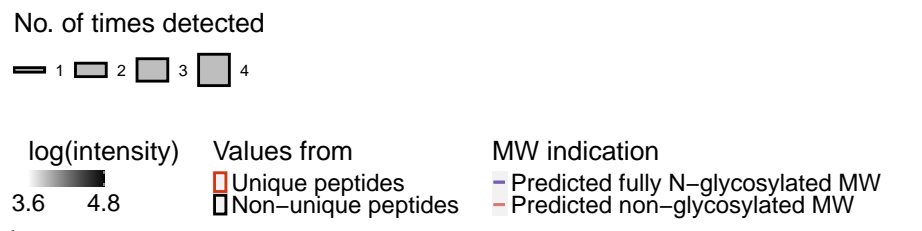
Pfam Description



Protein sequence:

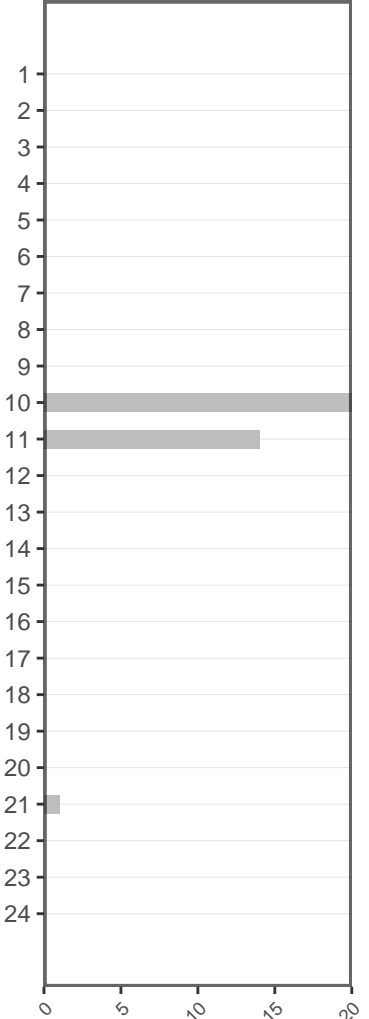
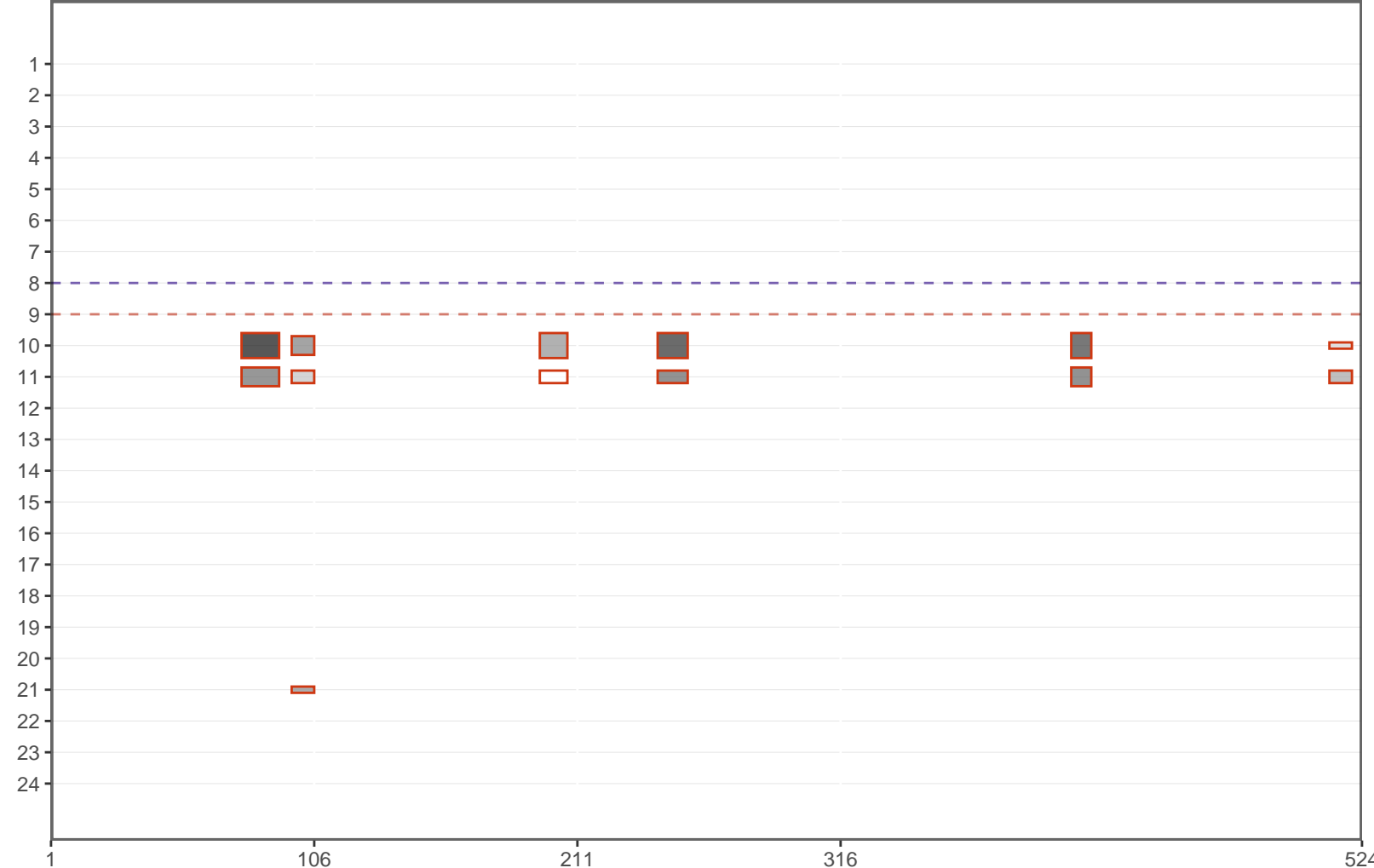
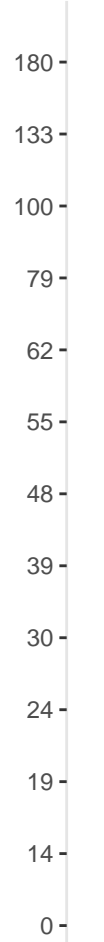
KSVQVNYKTVDFHLASVWGEWAEMELRHRNFKGALELMRRATAEPTVEVNRVVAADGNPFVQMKLHKSLRLWLLVDFLEESLGLTLESTRVYERILDLKIATPQHNVALEDDHYFEDAFKVERGVKFKYKPHKDKWVTLYSKFKVRYGKSLERARELFEHVAEETPADAVKPLVQWAKLEEDYGLAKRAMRVYDQATKAVPNEKLMYEVYVRAAEIFGVPRTRREHQAIEGSLPKDKVYKMLKVAELEKSLGEIDRARALYKHSDGFADPRSDPQVYKWHFEI

NbL14g04620.1 flavin-containing_monoxygenase_FMO_GS-OX-like_4 [MW = 59.48 kDa]



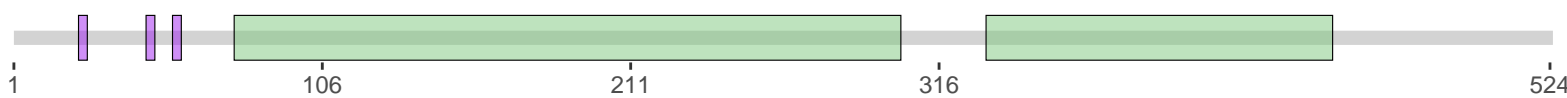
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

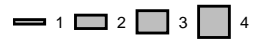
Pfam Description
 SP Sequon TM Domain PF00743 Flavin-binding monooxygenase-like

Protein sequence:

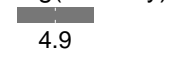
IEVVPQKHSHNWRVDFDFRNGVYVLGSAABATDISREIAEVAKEVHISRSATSGVPLKPGYDNIWQHSMIEAVGSDSGVNFRRDGSKVAADMLHCTGYKHYHFFLETNGVITVDONRVYGLKXHFPPAFAPLSLGFVGLFVWVPPPLGELQKWAAGVLSGRISLPEKEDMADIEALYSMEASGPKRYTHNMDDGDFYDDWLAEEGGSPPEEWRKGMFYFSRKNKKTQFETVYRDQWDDDDLIQAHEGDFVYVPELAQAQKLPK

NbL14g04590.1 14_kDa_proline-rich_protein_DC2.15-like [MW - SP = 11.5 kDa]

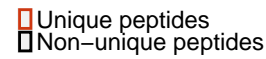
No. of times detected



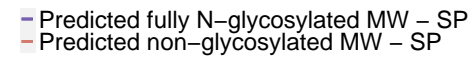
log(intensity)



Values from



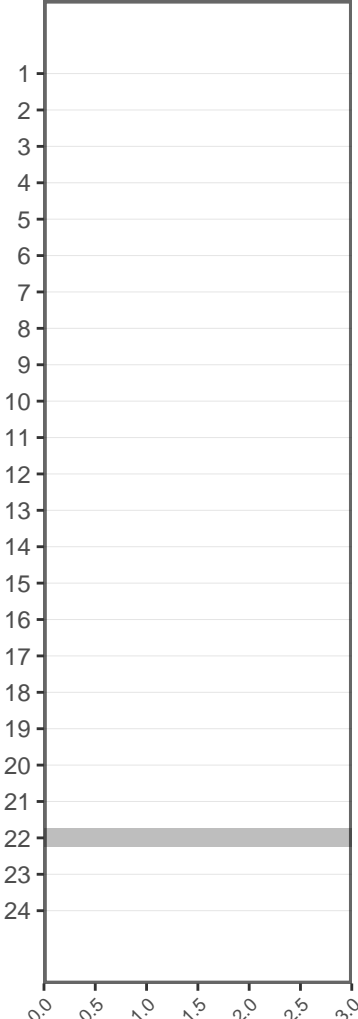
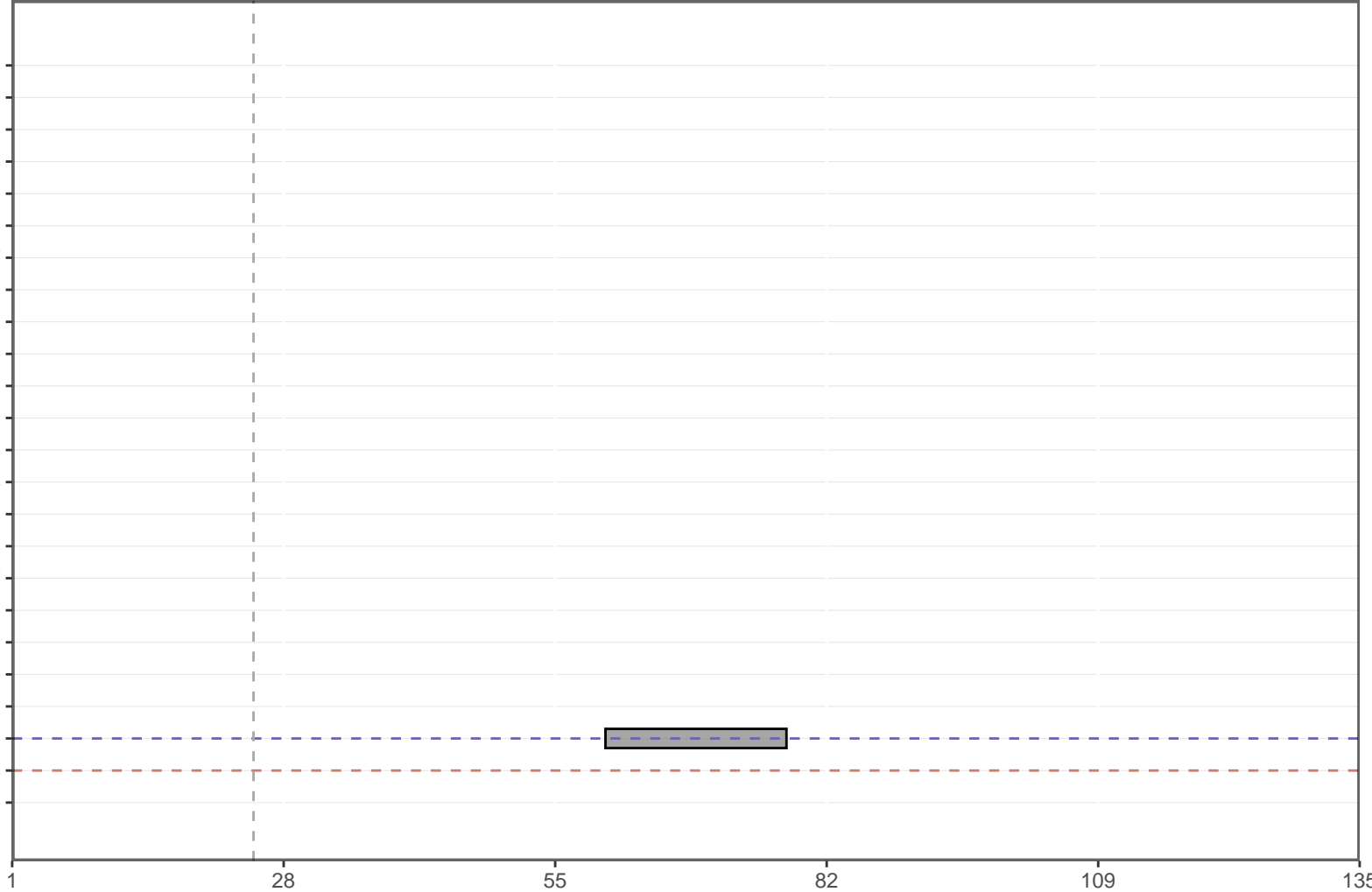
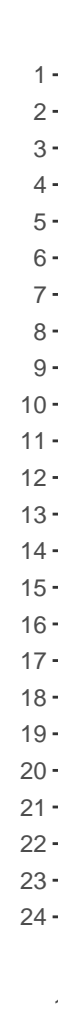
MW indication



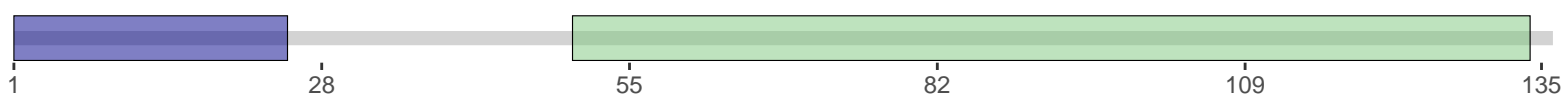
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

ITLKLKVCANLLNDLWVHVGSSKSSGGSLEHLEADVDVAAGLGTAKAKLLGTNLDLALSLLELLNNGKTVPKDFGCA

NbL14g04560.1 peroxisome_biogenesis_protein_19-1-like [MW = 36.9 kDa]

No. of times detected



log(intensity)



Values from



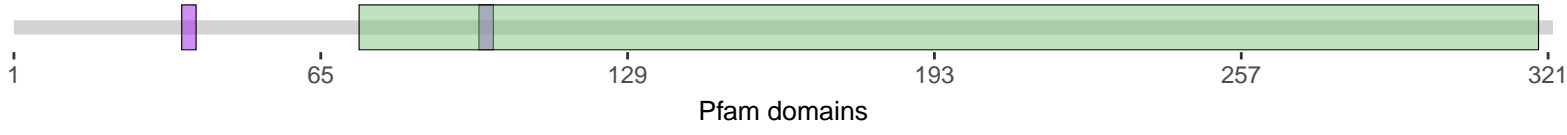
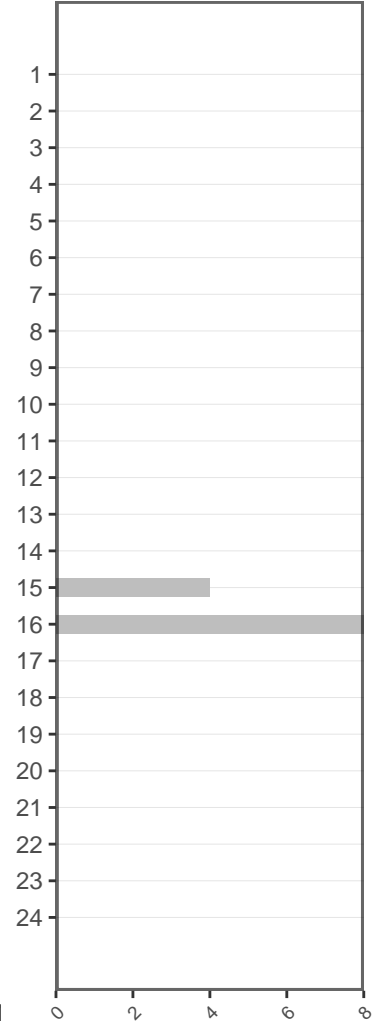
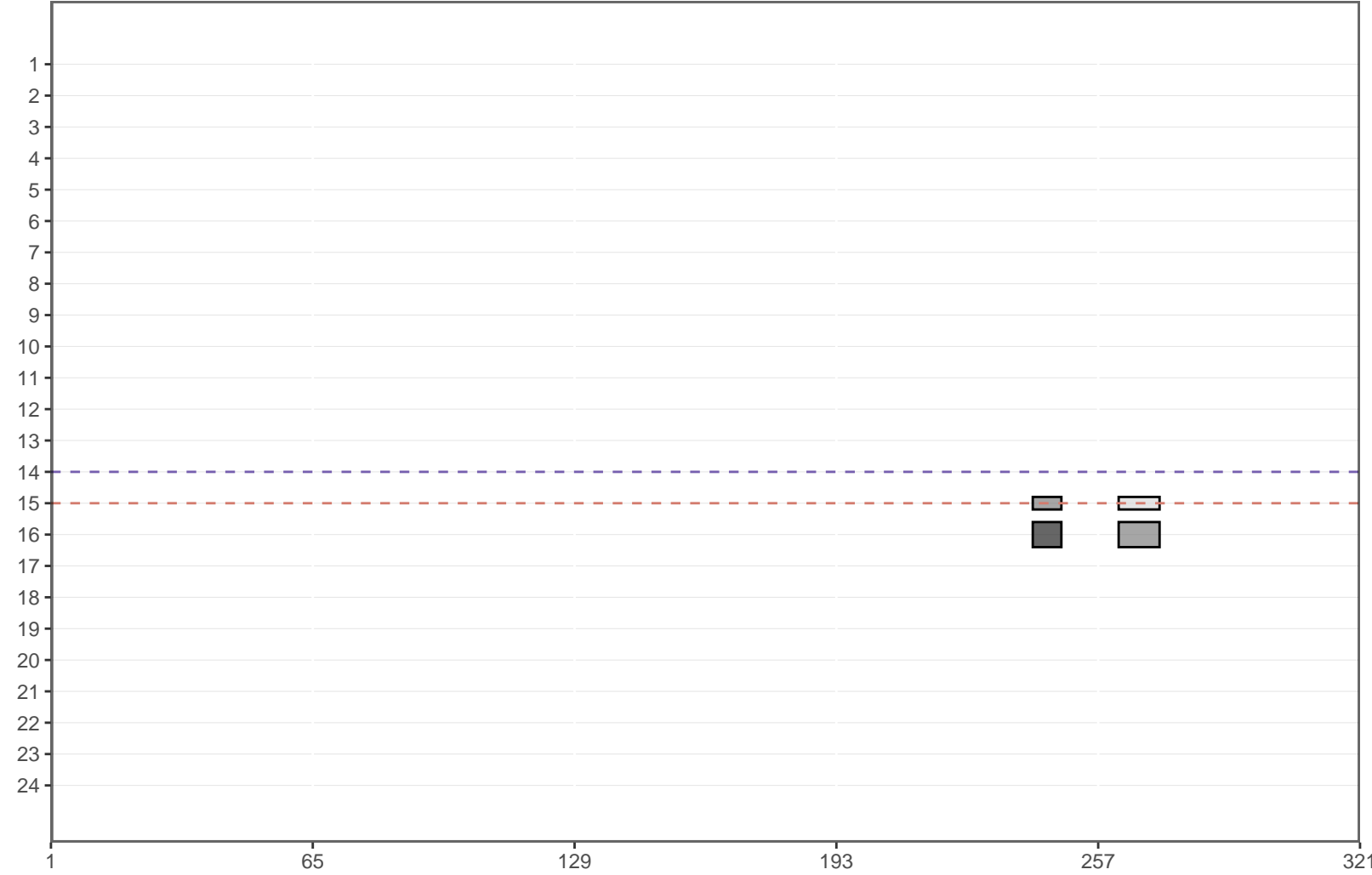
MW indication



Molecular weight



Gel Slice



Pfam Description



Protein sequence:

VSEALDKLREQTRKALKGLSEWVPRPGLSEFGSDPMMEIWAQKQFELAGSGDMESIVETMMQQLLSKEILYEFMREIGERYPKWLEDNKAALSBEDYERYHQVELIRDLNKKVYETEPNFKNKVELMQKMQDEGGPPNDVHELAPDFDITLGGLSPEMLSEGGQNGCIM

NbL14g04470.1 2-oxoglutarate-Fe(II)_type_oxidoreductase_hxnY [MW = 23.65 kDa]

No. of times detected



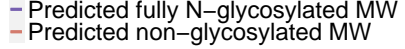
log(intensity)



Values from



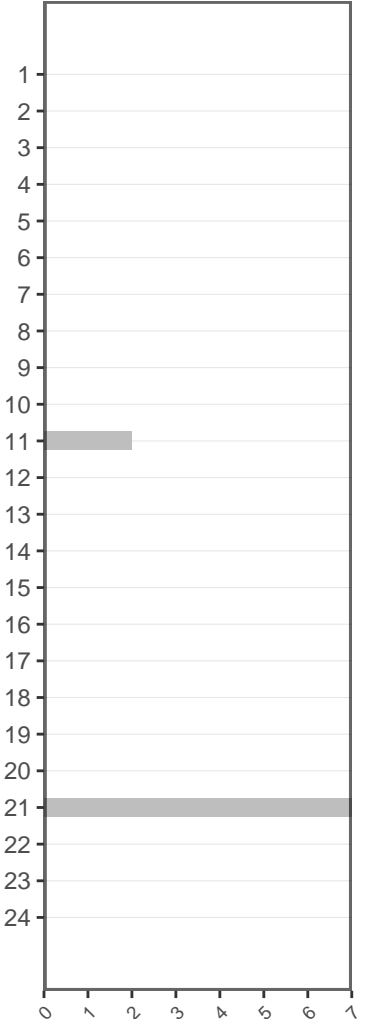
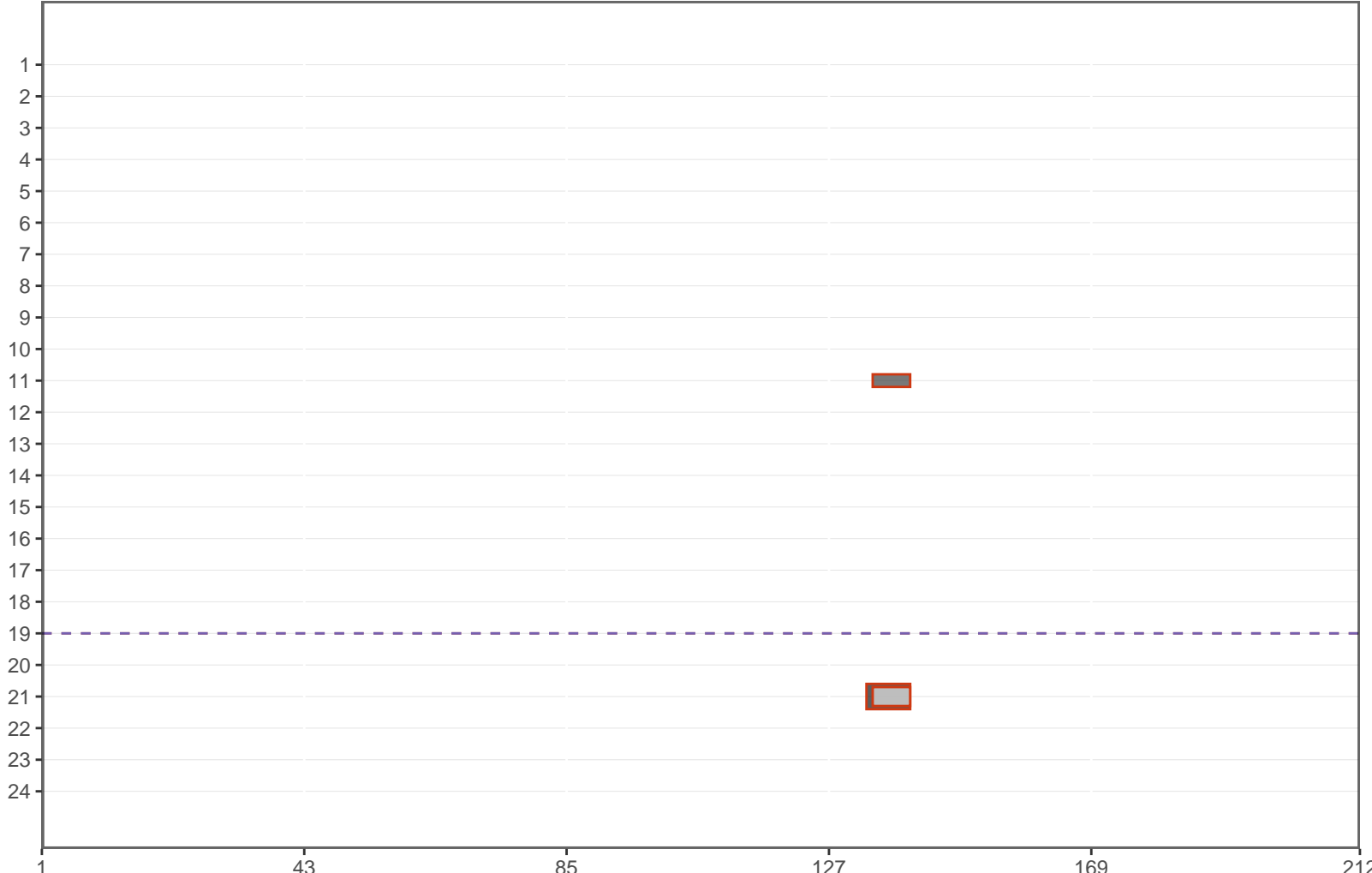
MW indication



Molecular weight

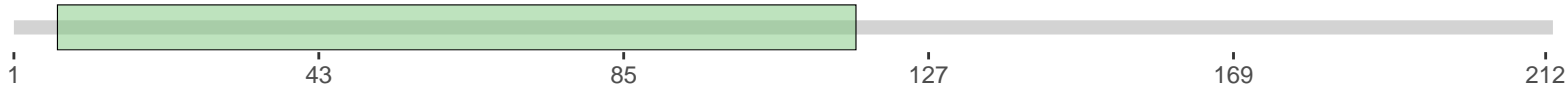


Gel Slice



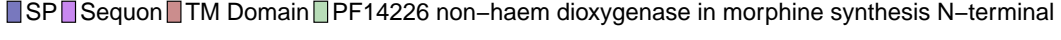
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KESFYIGPLEDKRQWNLNQWPAEELPCWRSTMEDYKRVLDAGIRLTSIALALELDEDFHKGAGCDSFNALRLVHYPGELRLSEGVYGSASHSYGMILFLTLDGVGGLGHVY

NbL14g04360.1 plasminogen_activator_inhibitor_1_RNA-binding_protein-like [MW = 39.37 kDa]

No. of times detected



log(intensity)



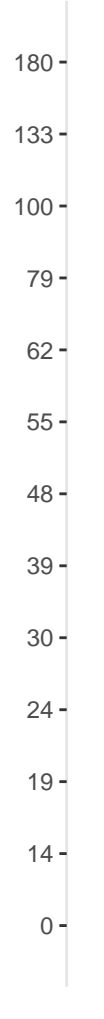
Values from



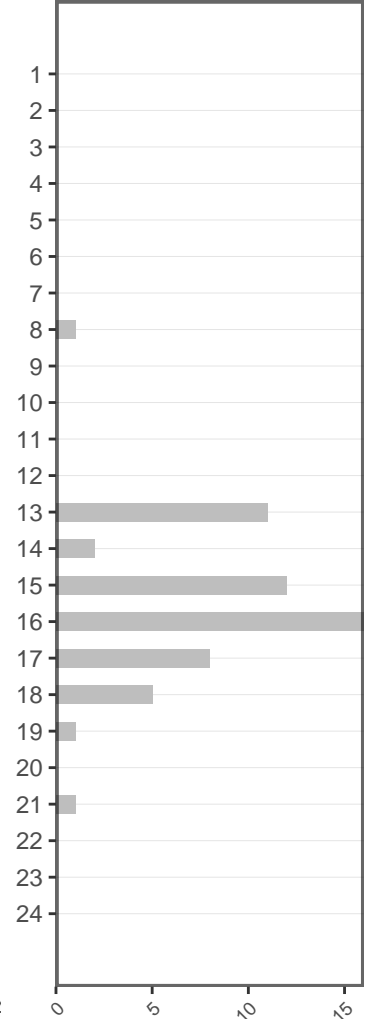
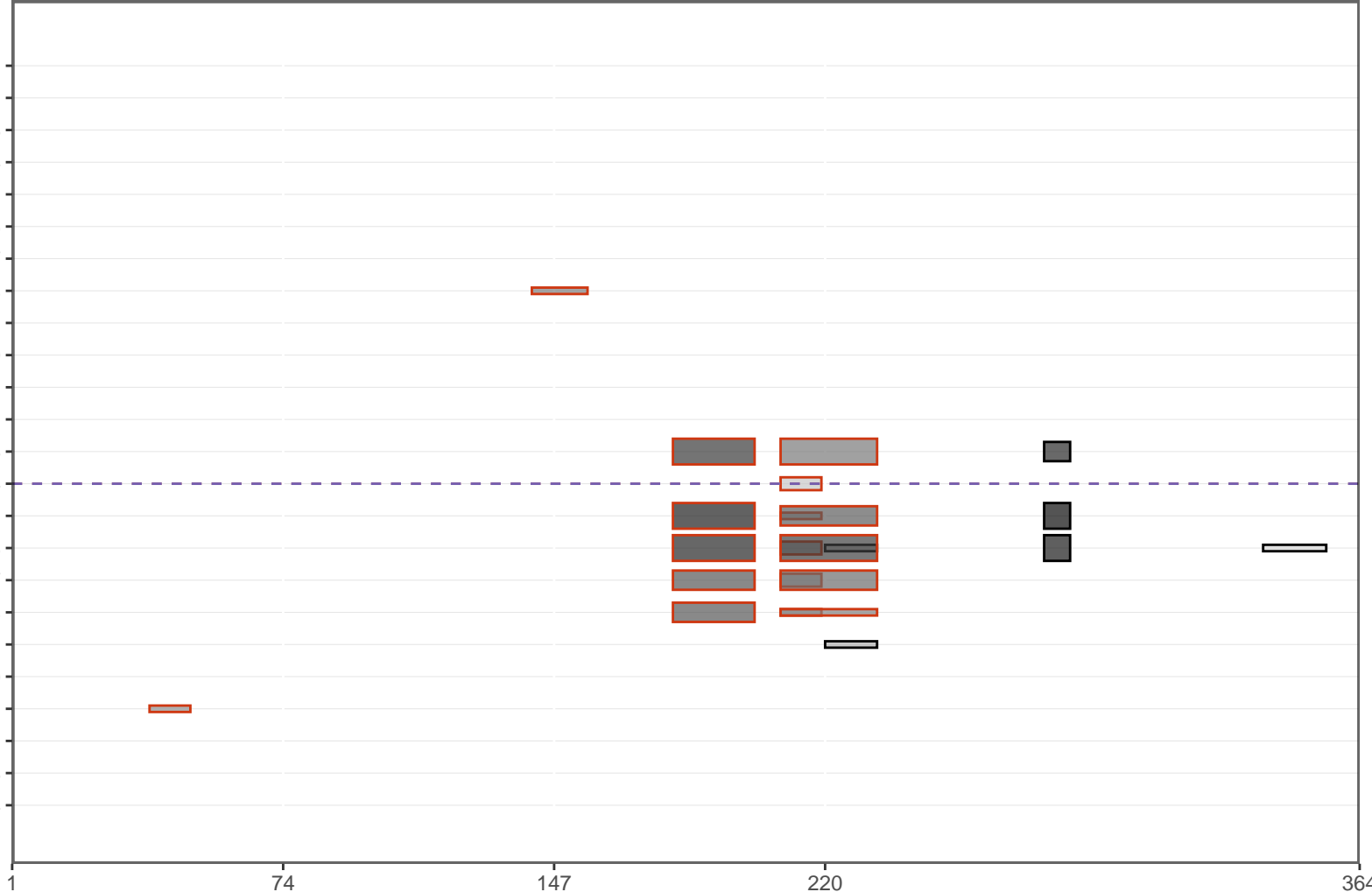
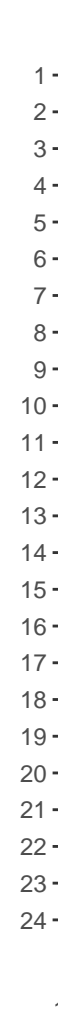
MW indication



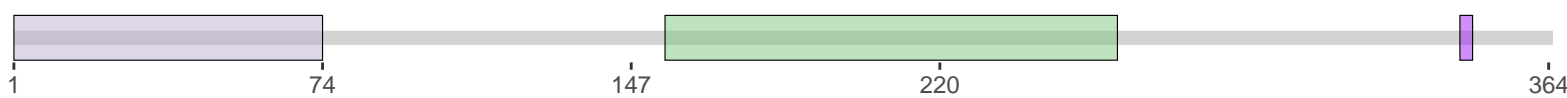
Molecular weight



Gel Slice

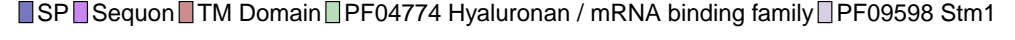


Protein length



Pfam domains

Pfam Description



Protein sequence:

IGNEFKREGAGRGWGTFADELAPKEKEEPEEVEKQAVQADAEQTSKDSRAEAFQEKPEEEMTLEEVKLEEKRKALLAKPEERVNLKDELEGMOLLNKRSDDEVFKLGGSEKDKRKETVEKVKTKSINEFLKPADGESVYVGGGRGRGRGRDRGRDGFVGNNSVAPSIEDVRFQFSLGAK

NbL14g04330.1 FAD-dependent_urate_hydroxylase-like [MW = 25.55 kDa]

No. of times detected



log(intensity)



Values from



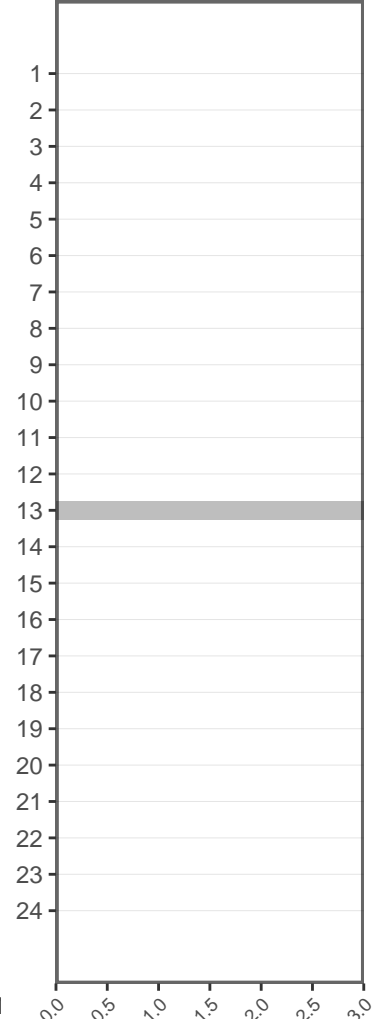
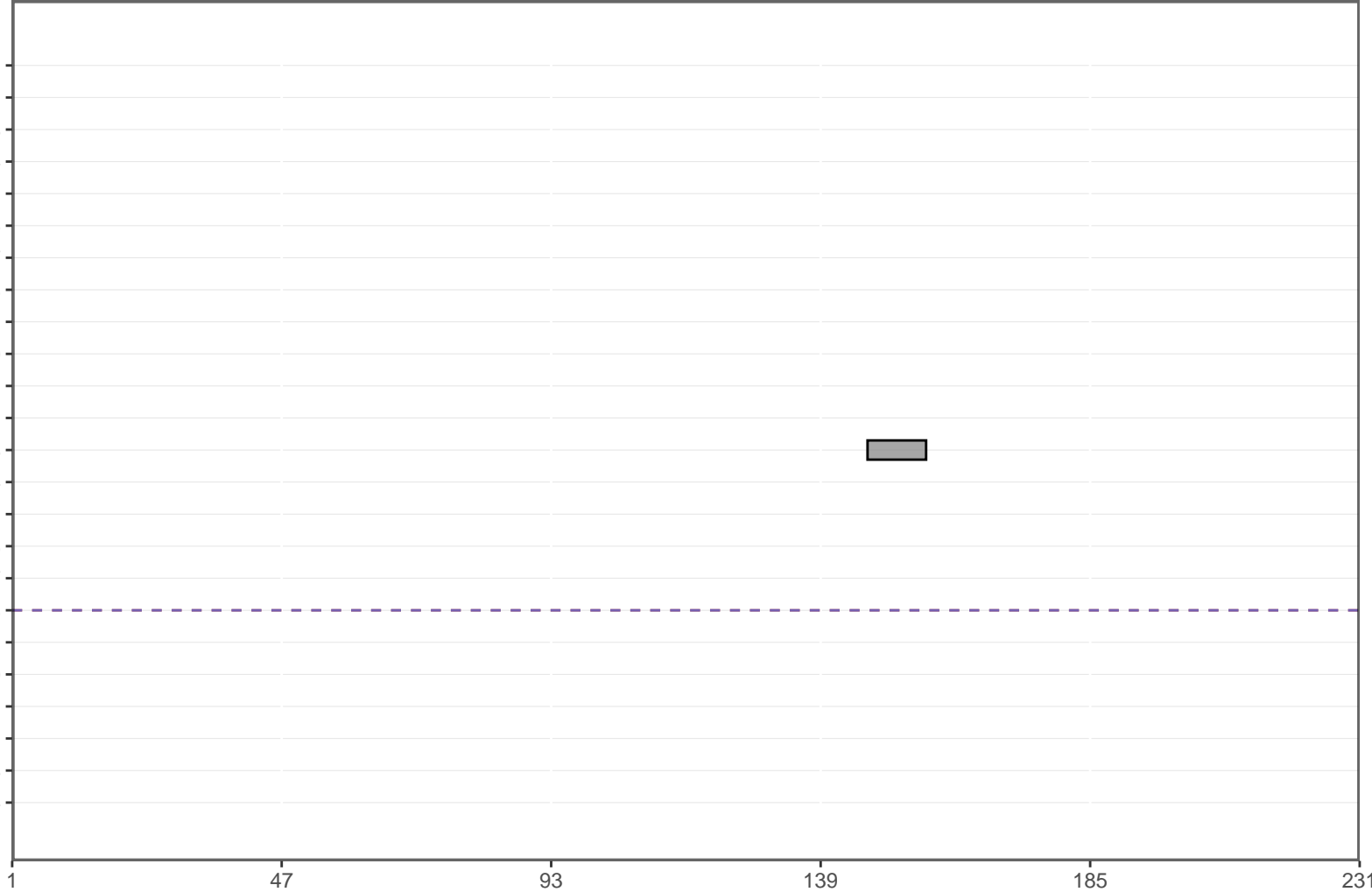
MW indication



Molecular weight

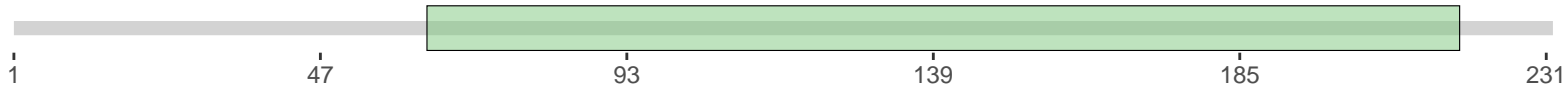


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

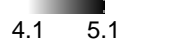
.LSKNGWKALDAIGVINDLRTDFLEIGDMVVKSGEDGRELRFRRFKDDEDESGEVRVERRVLLLETLAENLPDVAISFSKLANVERSENGETMLEEDGHSAKLIACDGRSPWPGWDFGSLTM*

NbL14g04140.1 uncharacterized_LOC107766858 [MW = 25.5 kDa]

No. of times detected



log(intensity)



Values from



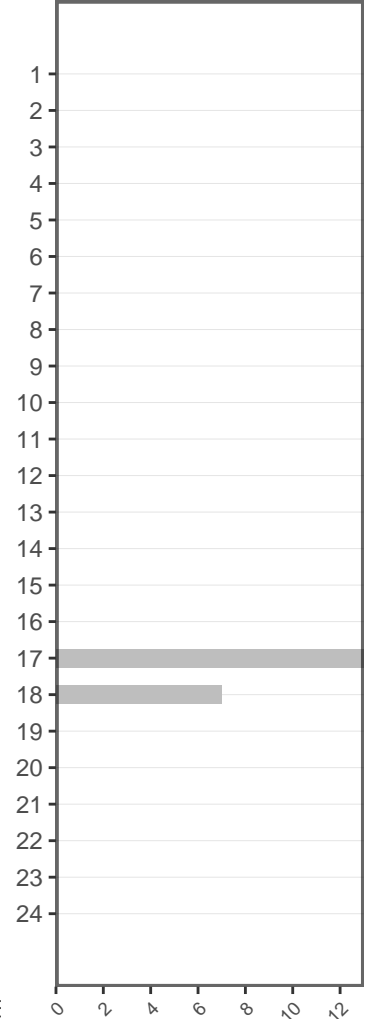
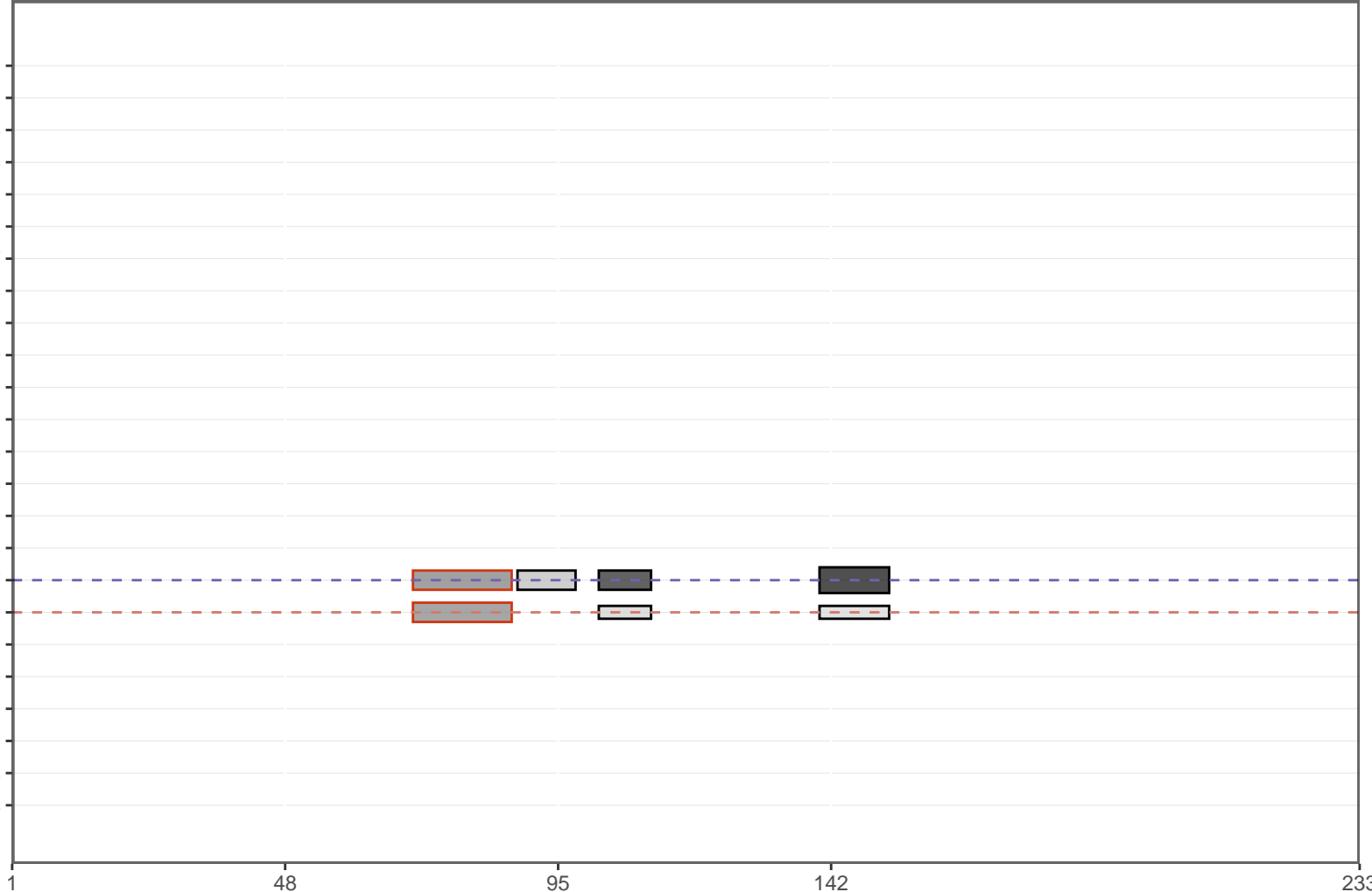
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats

Pfam domains

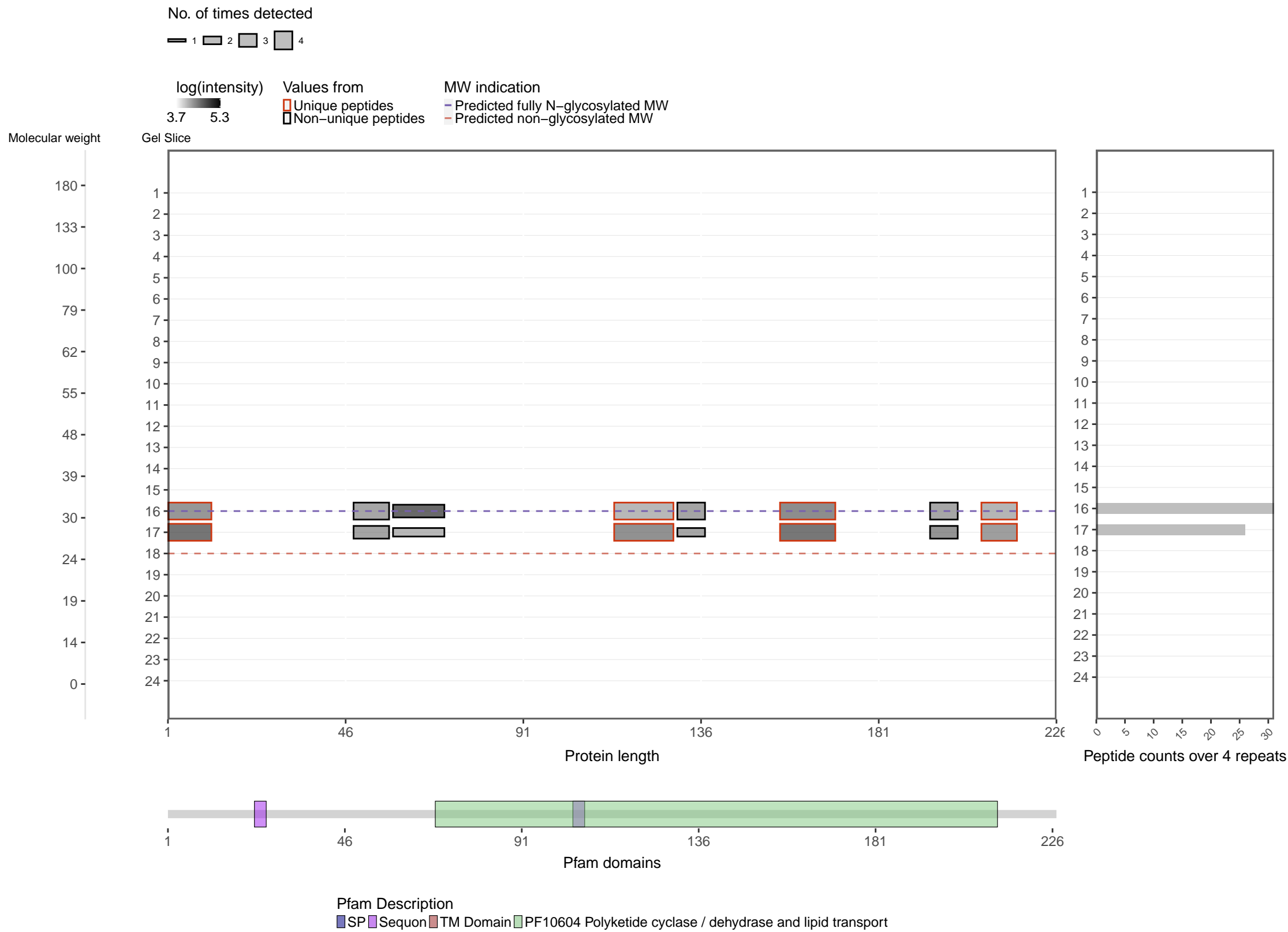
Pfam Description



Protein sequence:

MFNPEGYRSTDDYDFFDAFLFYWAEDGGRIPLKVGSGGAALFDVWARGGPDFGADGLLGFPLAPVMGGFAGPDTNSGGDLRQAKSLGLG6WKRPDGKESLFGDESKAELDEVLVFGSPQASLY*

NbL14g04040.1 abscisic_acid_receptor_PYR1-like [MW = 24.98 kDa]



Protein sequence:

SVGENFSIVGATRIYVWISGLPADTSTFRELIDLDEKVTGFSIGSGEHLRLNRYRSTVTYVHGFQGLDGGKISTVAMESEYVDDPDGNTEEDTRLFDATVAKLNLGKLGSAEAIARGNGVSEEN

NbL14g03890.1 phosphomevalonate_kinase-like [MW = 55.05 kDa]

No. of times detected



log(intensity)



Values from



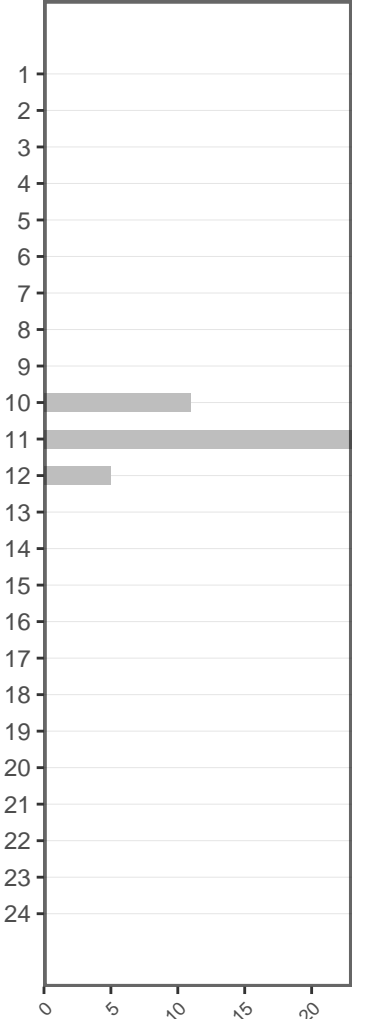
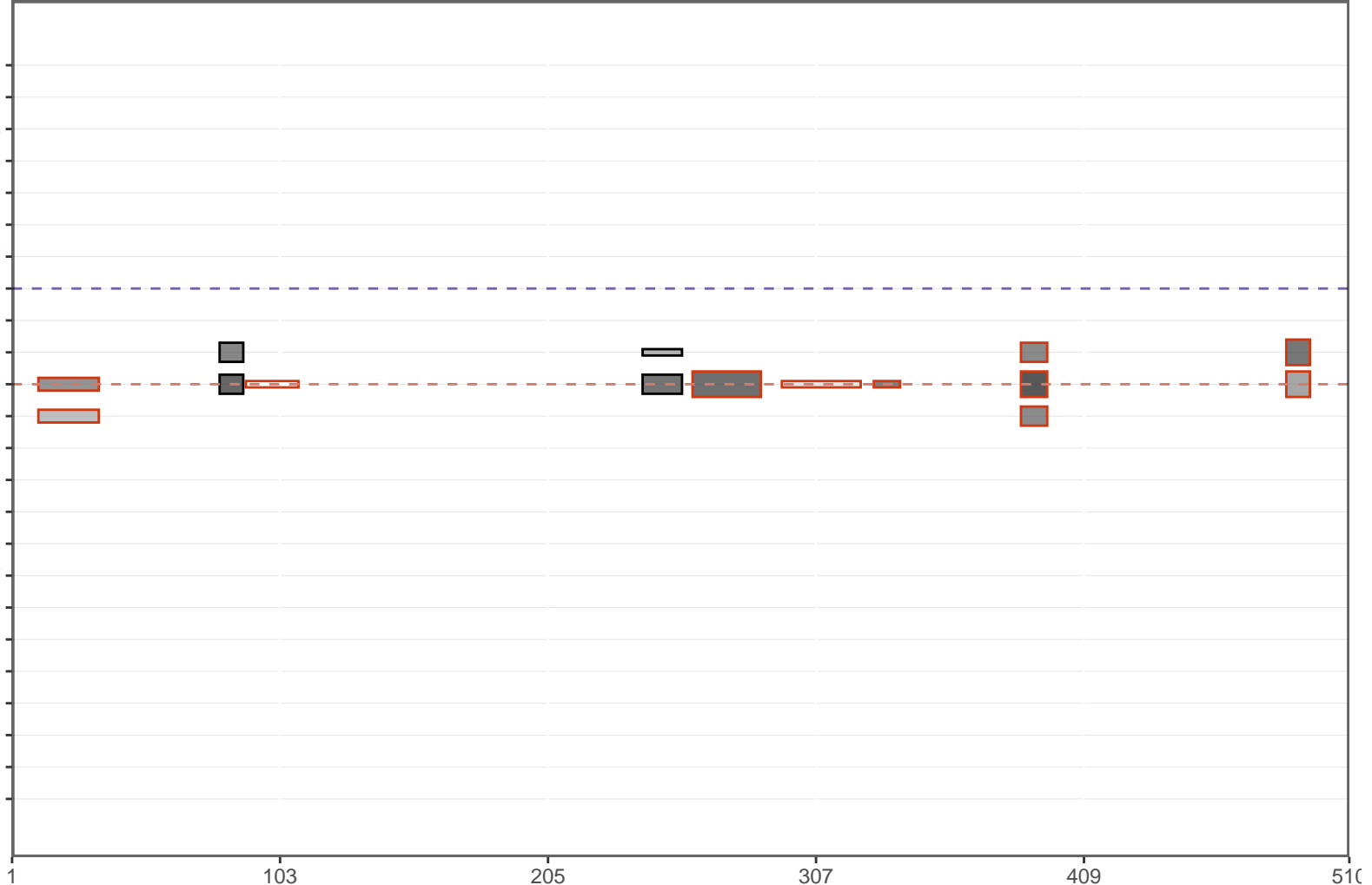
MW indication



Molecular weight

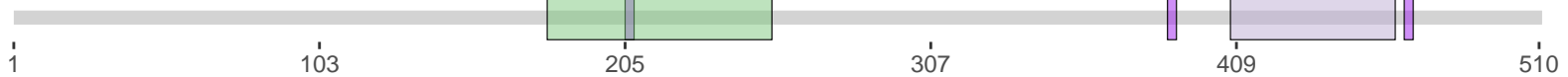


Gel Slice



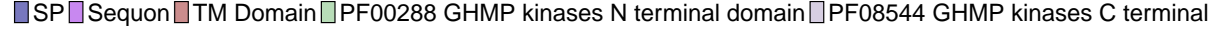
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DVSSAVYGSORYVRFSEVLESSAGNMGATPLTEVDDLVKAKWDHERTKFSLPLMLTLLGEPDGGGGSTPBMVGAWRWQKSDPQSSLETWRKLSGNGALEMHLNFKLKAERNVNYVEGVNAGSLTAEKWBERANESGSAENKELLGAREAMLGIRYMRKMGAEAGPIEPESSQTHLDDTTMSMEGVLLAGVPGAGGFDAVFAVTLGASSKNVTKAWSLNVLVAMLVTEPRGVSLLEDNDPRANETAVSSHLQ

NbL14g03770.1 uncharacterized_protein_At2g34160-like [MW = 14.32 kDa]

No. of times detected



log(intensity)



Values from



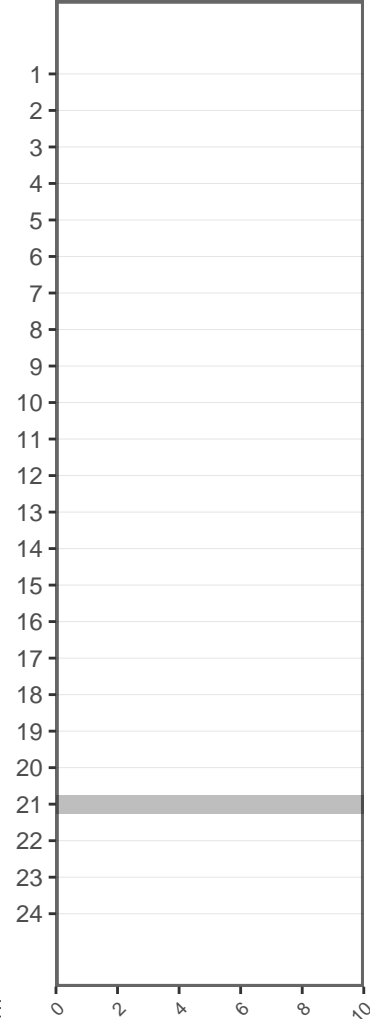
MW indication



Molecular weight

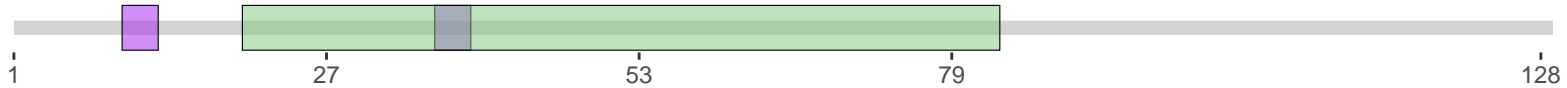


Gel Slice



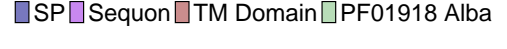
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LSALGMAISTVYTWAEIKKNGFAVEKIKRFLTIDMRDEPDGARPIPKAKIEVLGKTEKFDLMAAAEAGNGDNEGN

NbL14g03450.1 uncharacterized_LOC107795122 [MW = 32.75 kDa]

No. of times detected



log(intensity)



Values from



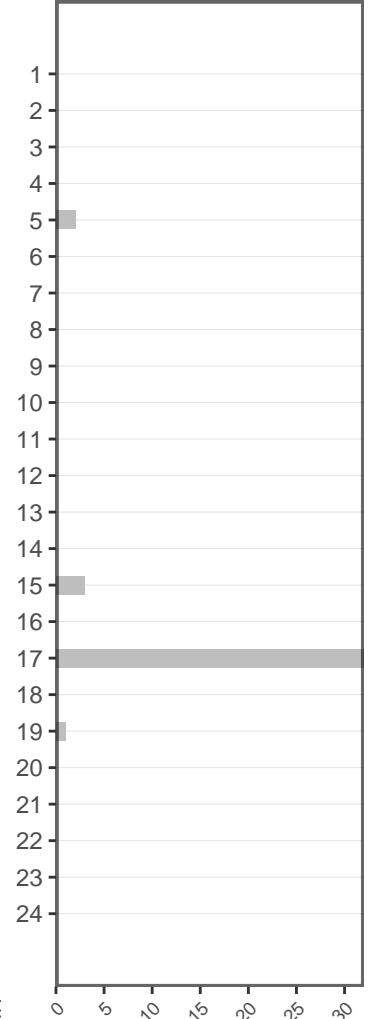
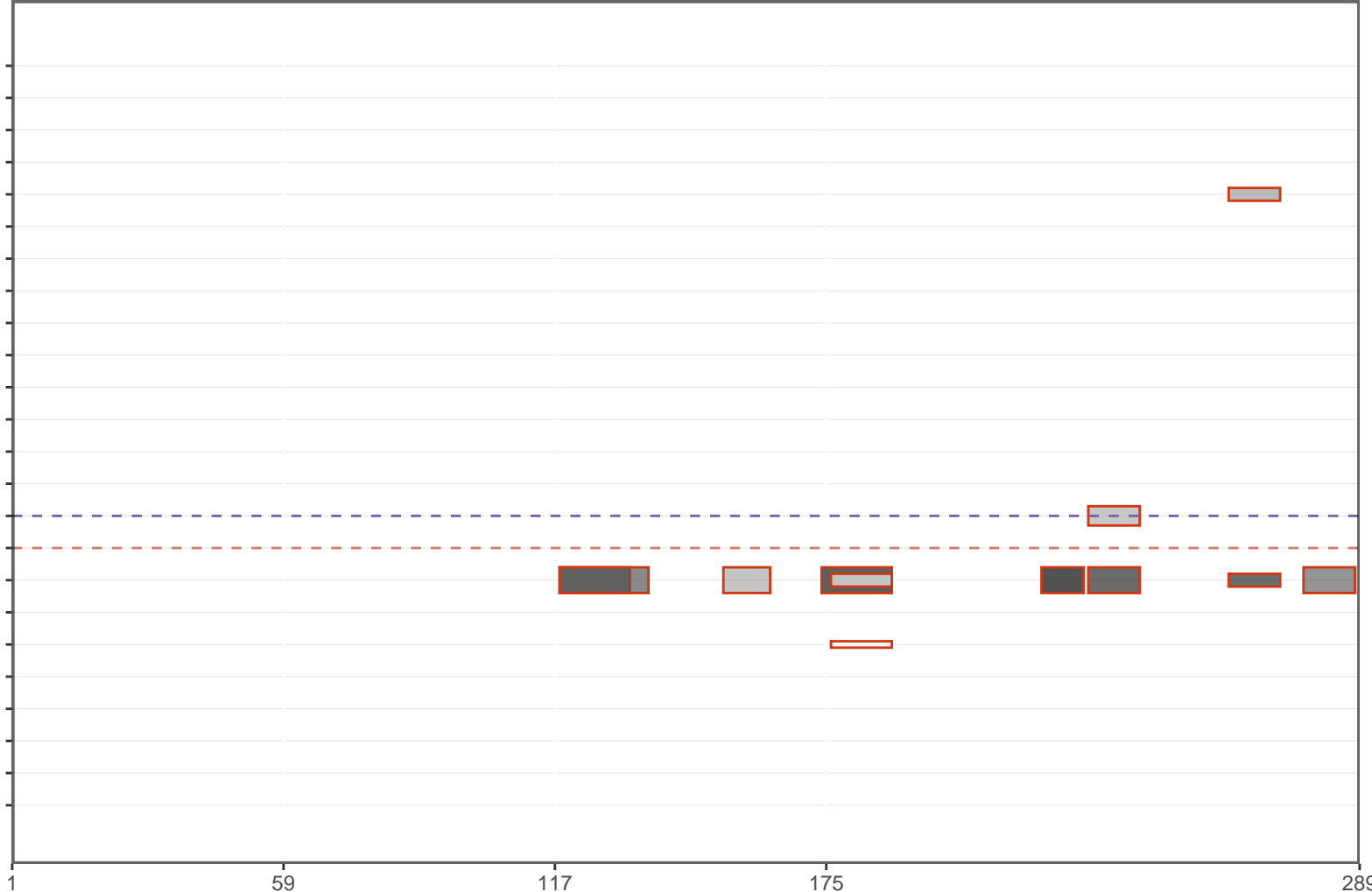
MW indication



Molecular weight

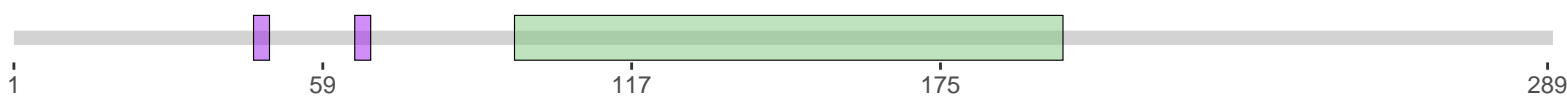


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DTKSEIKLNEUINRYKDRKPKGFVILGFLVDKKKEGKSGYGRGKQEIINTAEFFLFDKVLNKEKHEHWYGDENKRDDELYFLKKEKGGDTEEPVKILVDWGTGVPNGRYDFFPLHDETKXKSEIAKSGEDPOTTVGLRDDPREVLENAATLVR

NbL14g03440.1 probable_phospholipid_hydroperoxide_glutathione_peroxidase [MW = 25.75 kDa]

No. of times detected



log(intensity)



Values from



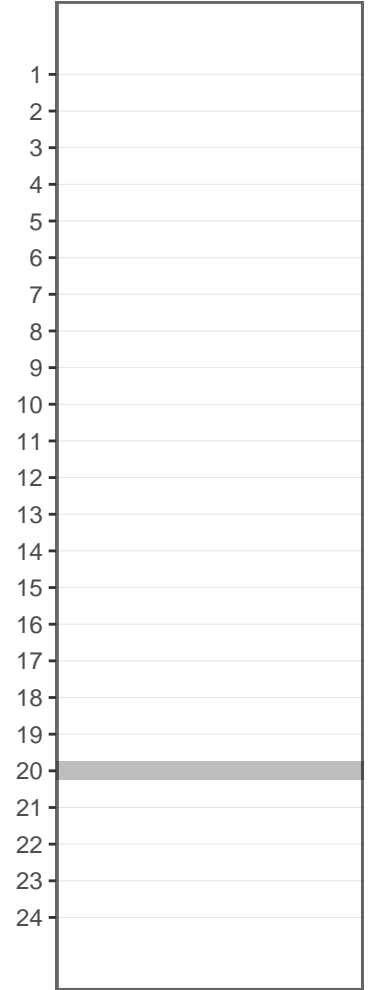
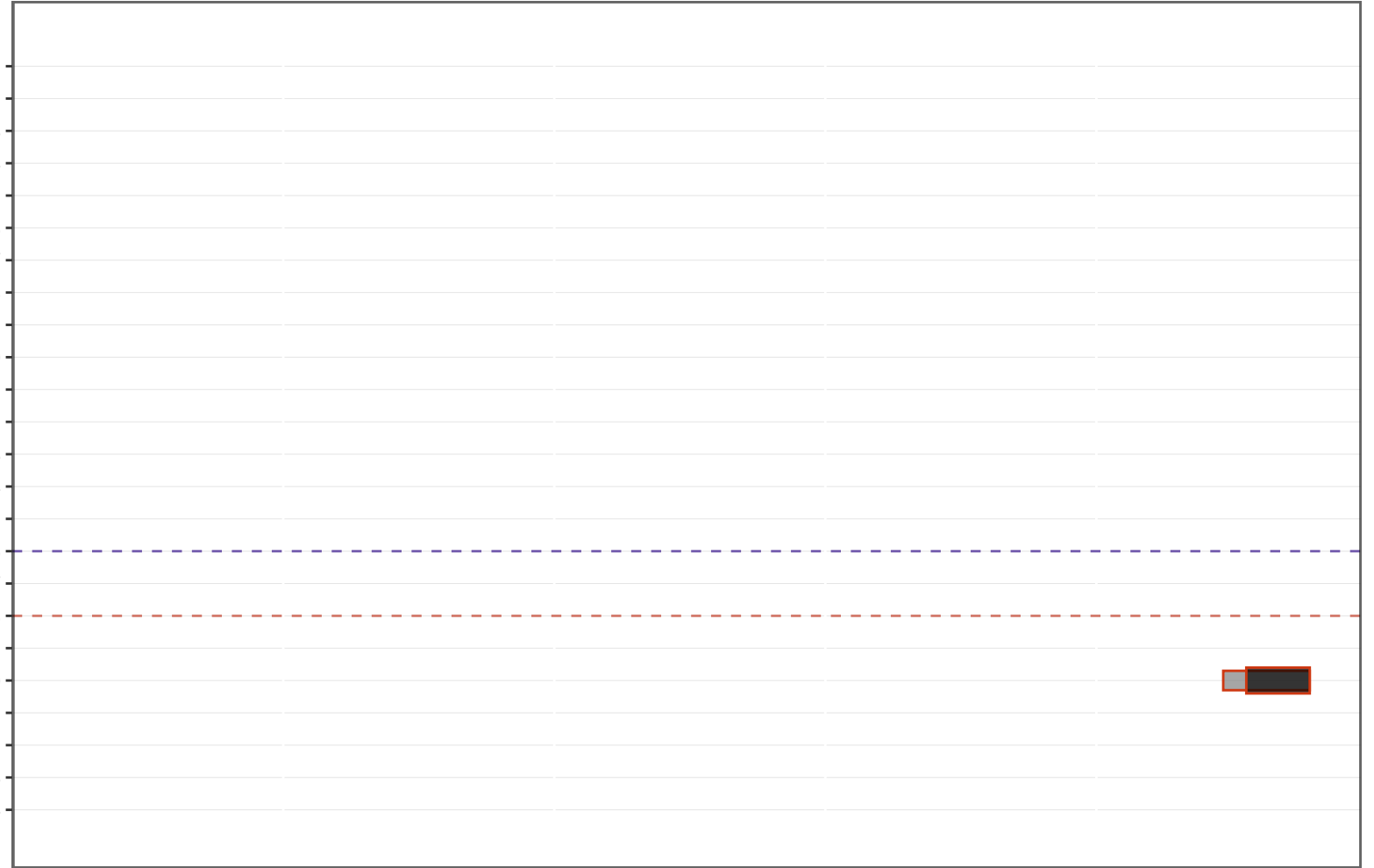
MW indication



Molecular weight



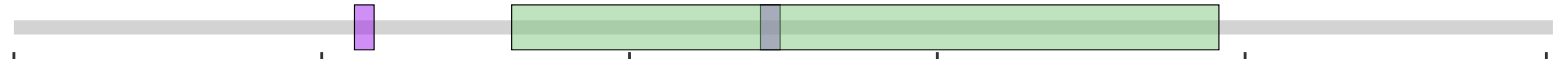
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

ASRRCGLTTSNYTELSGVYKRYKTKGLELAFPGNGFGAGEPSSNPEIKHGFACFRKAEFFFDKVDVNGPNTAPVYGLKSEAGGLGDVWVNFKFLVDRNGKYVERYPPTSPIGIEKDGKLLAA*

NbL14g03340.1 uncharacterized_LOC107797087 [MW = 30.98 kDa]

No. of times detected



log(intensity)



Values from



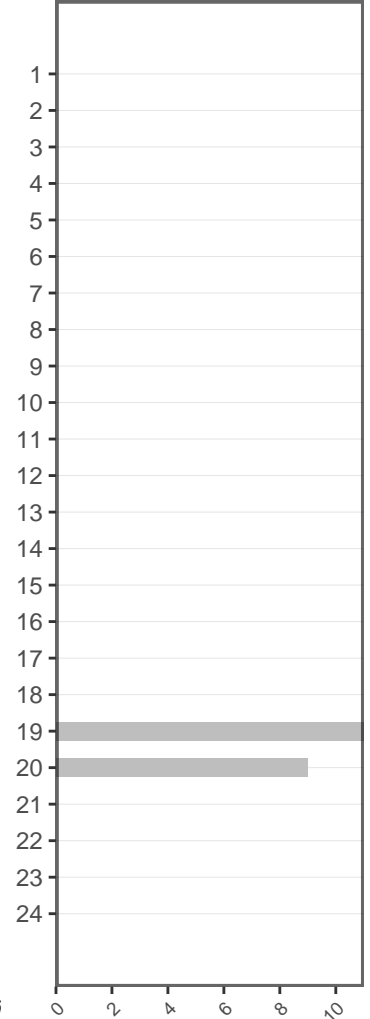
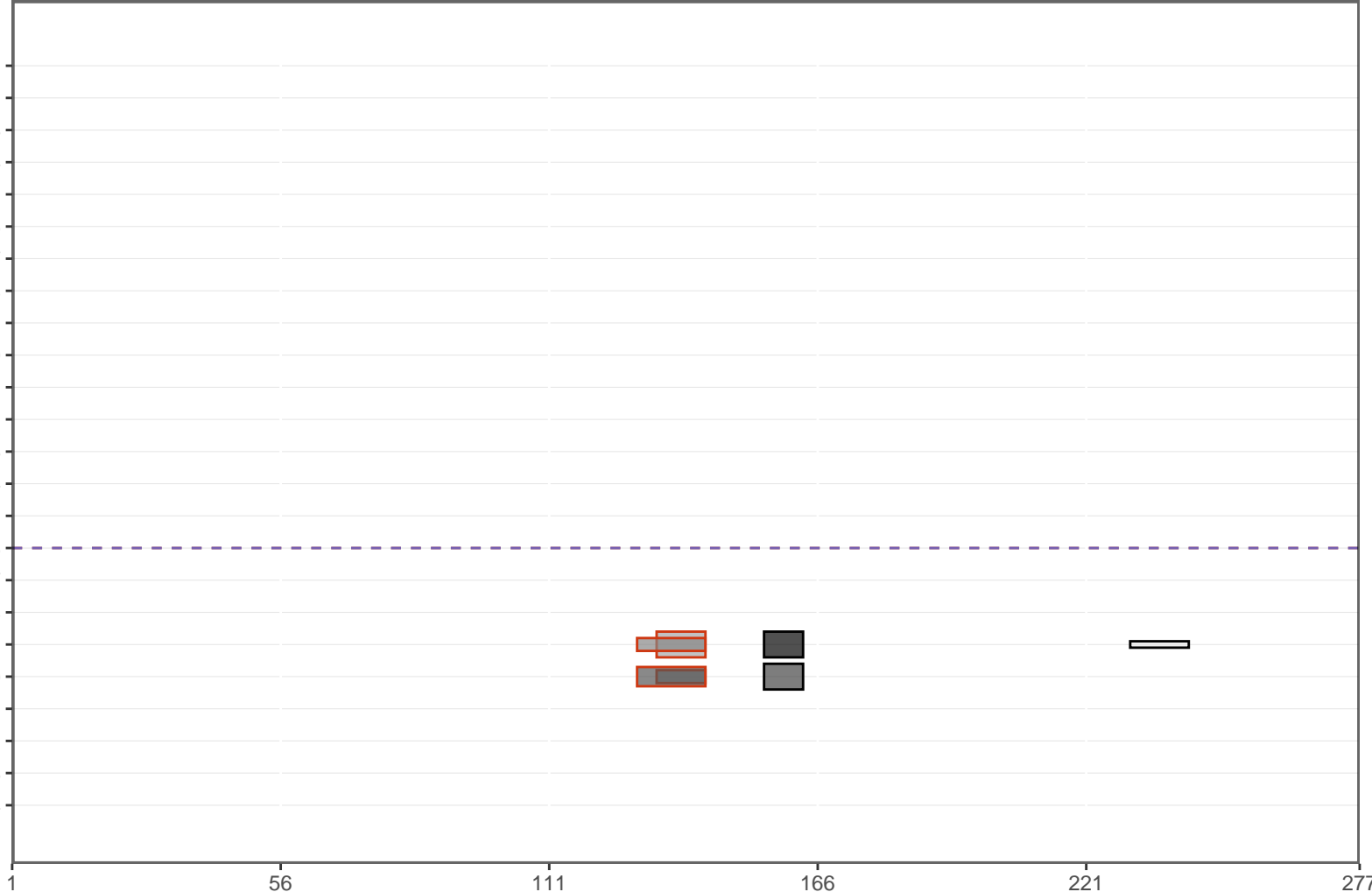
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

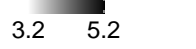
LKNAKEENYAQAATIRDLRLLEDGSKASVLAANARFYNSFKHGDLAAMGTLSKGENGVVHPGVSGITGVDLVMSGSEFVWAEVDFPLDIERDVGVHYRGGDGYVTGEMVVRTKGSWGGKFATNFEKNGGWFMDIHHASVIDL

NbL14g03290.1 pectin_acetyltransferase_8-like [MW - SP = 41.81 kDa]

No. of times detected



log(intensity)



Values from



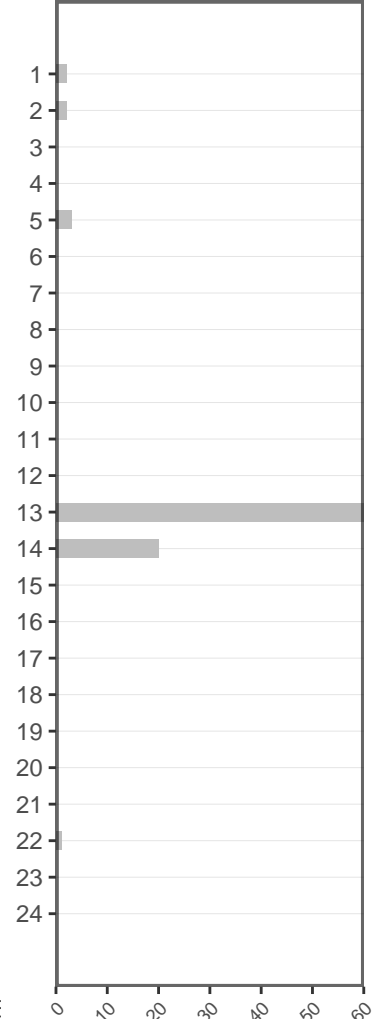
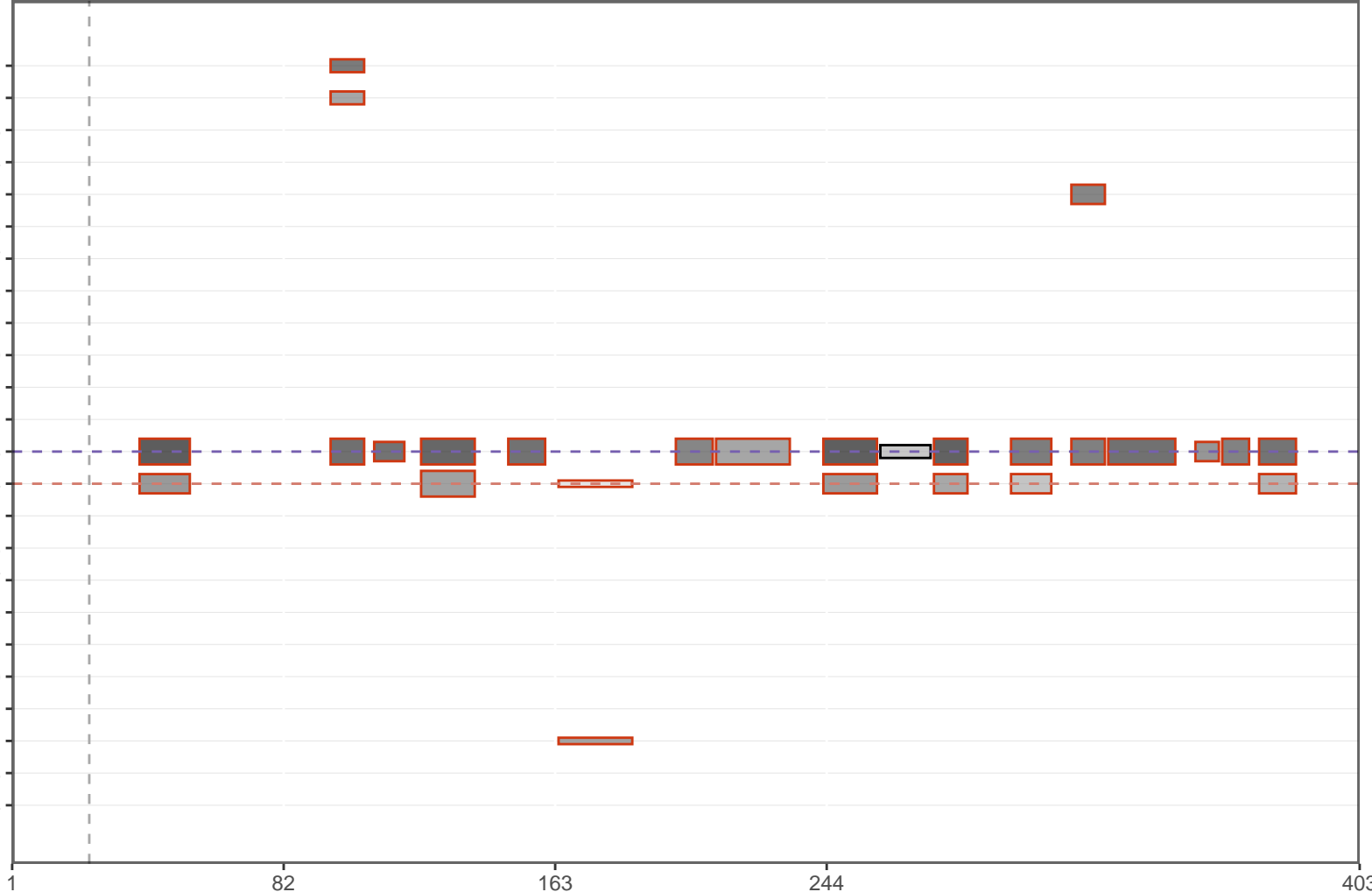
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SLLPQAKYKCLSDAGFFNAKTRIGASHIEGFYSDVNIHSHGAKNLPQSGCTSRKPKLGFPPQVAQGRITPLFLVNAAYDSWQKNIAPGVAAPRGTWRNKKLILKQSSAQLETMDGYRNEFLKALNGLGPSSTRGYNNSCYAHGDTGTGETWLRDQSPRLASTTIKAAWGDWYFDRNRFQEDICPYPCDKTKGNRFESGVDQPIQMDL

NbL14g03150.1 protein_arginine_N-methyltransferase_1.5 [MW = 73.56 kDa]

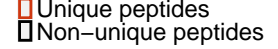
No. of times detected



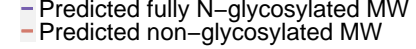
log(intensity)



Values from



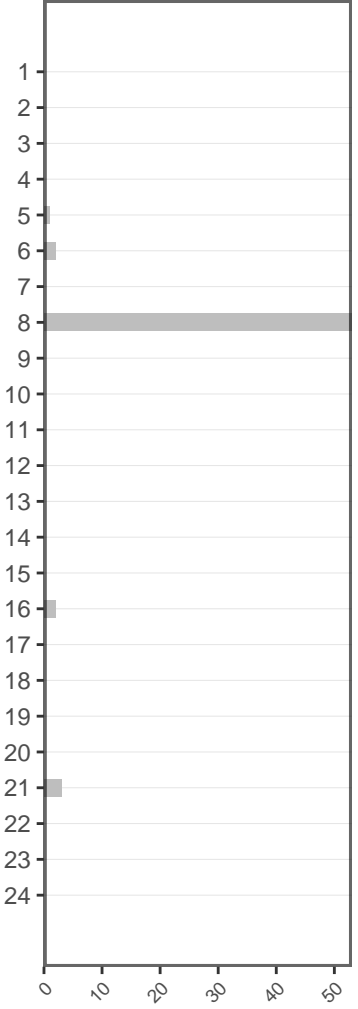
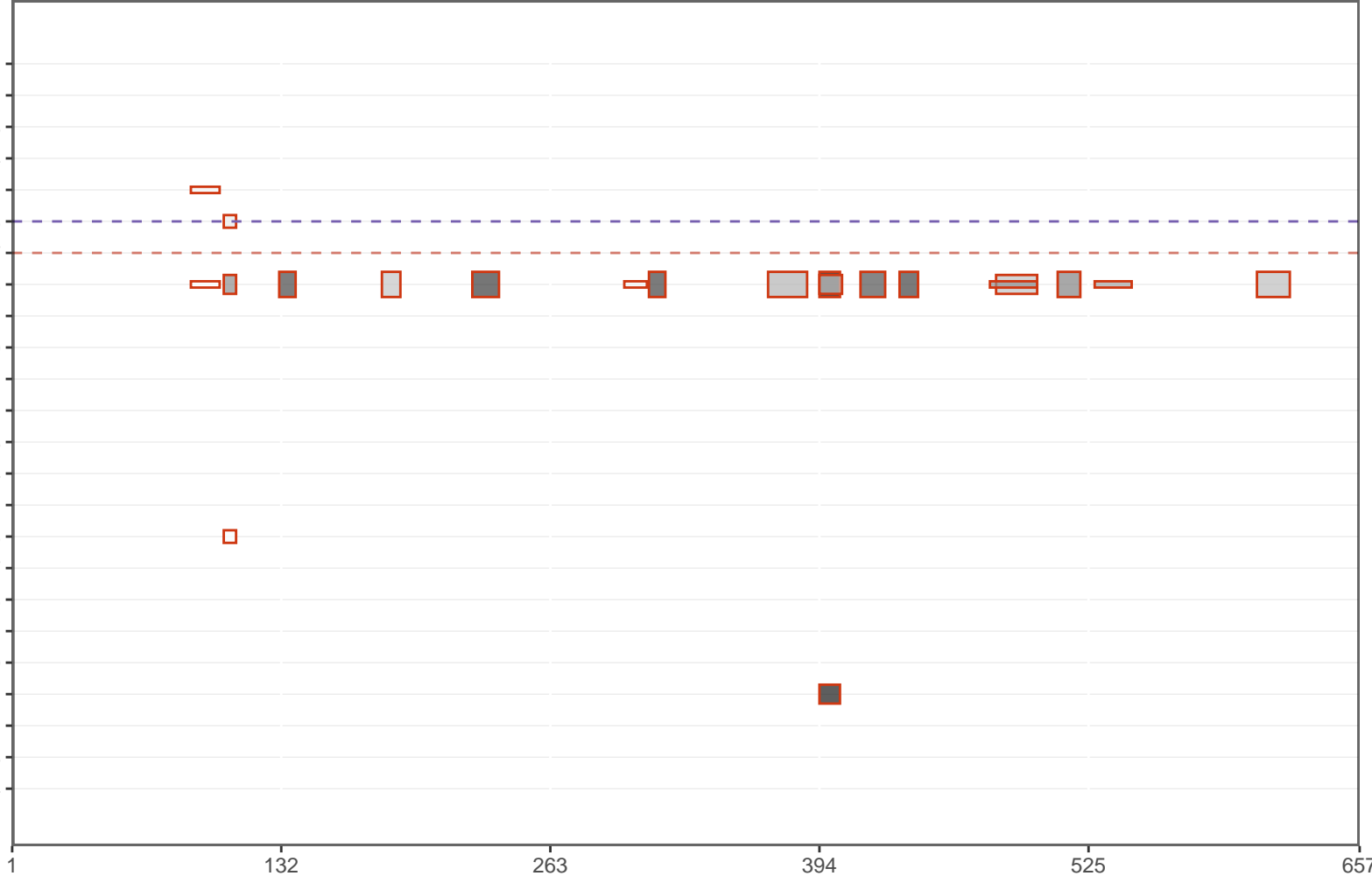
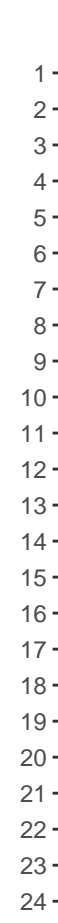
MW indication



Molecular weight

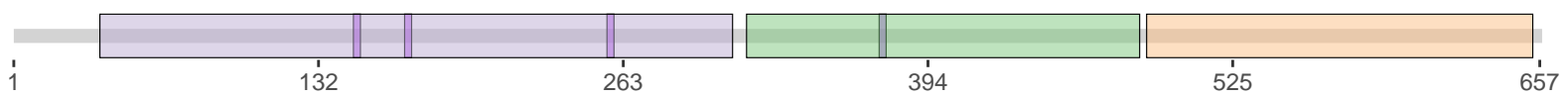


Gel Slice



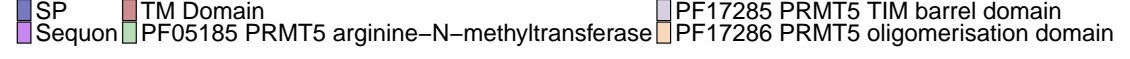
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MDPLPEOERFELGVRDYLGEPLGFLMNDLEAGTYETFEKDKIKYQYGRAWAKALVDRVFDENASTITTTVMVYGAGRPLVRSLSGAAEETGRKLRVYVAKNPVAVTLHLLKIEGWENKIVTVSSDMRQWDAPFAKADLVSELLGFGDNLSPKELDGAQRFLKEDGSPSSVYTFQFPVTSKLYNDKIKHKDLVHFETAVVYKLRHRIARLTSPQPVFTFNHPEHSTTKSNRHYKRLRFEIPTDTGSAIIVHGFAGYFDALYKDVHLGIEPSTATNMFSWFFPFLRTPV

NbL14g03090.1 AIG2-like_protein_D [MW = 19.85 kDa]

No. of times detected



log(intensity)



Values from



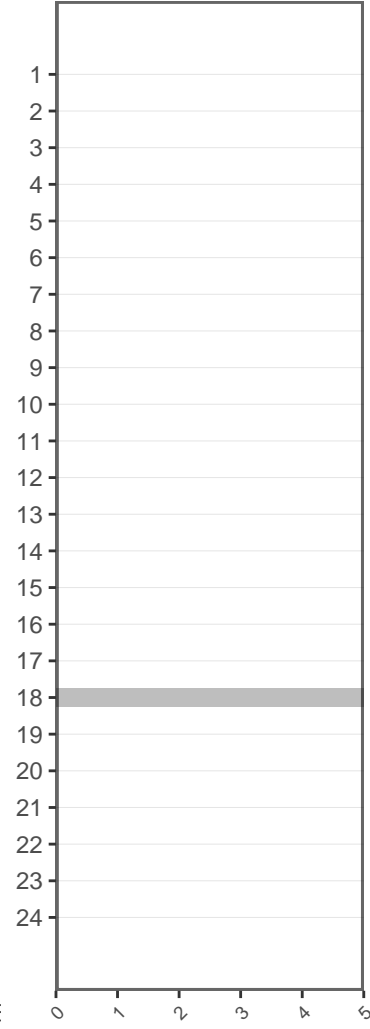
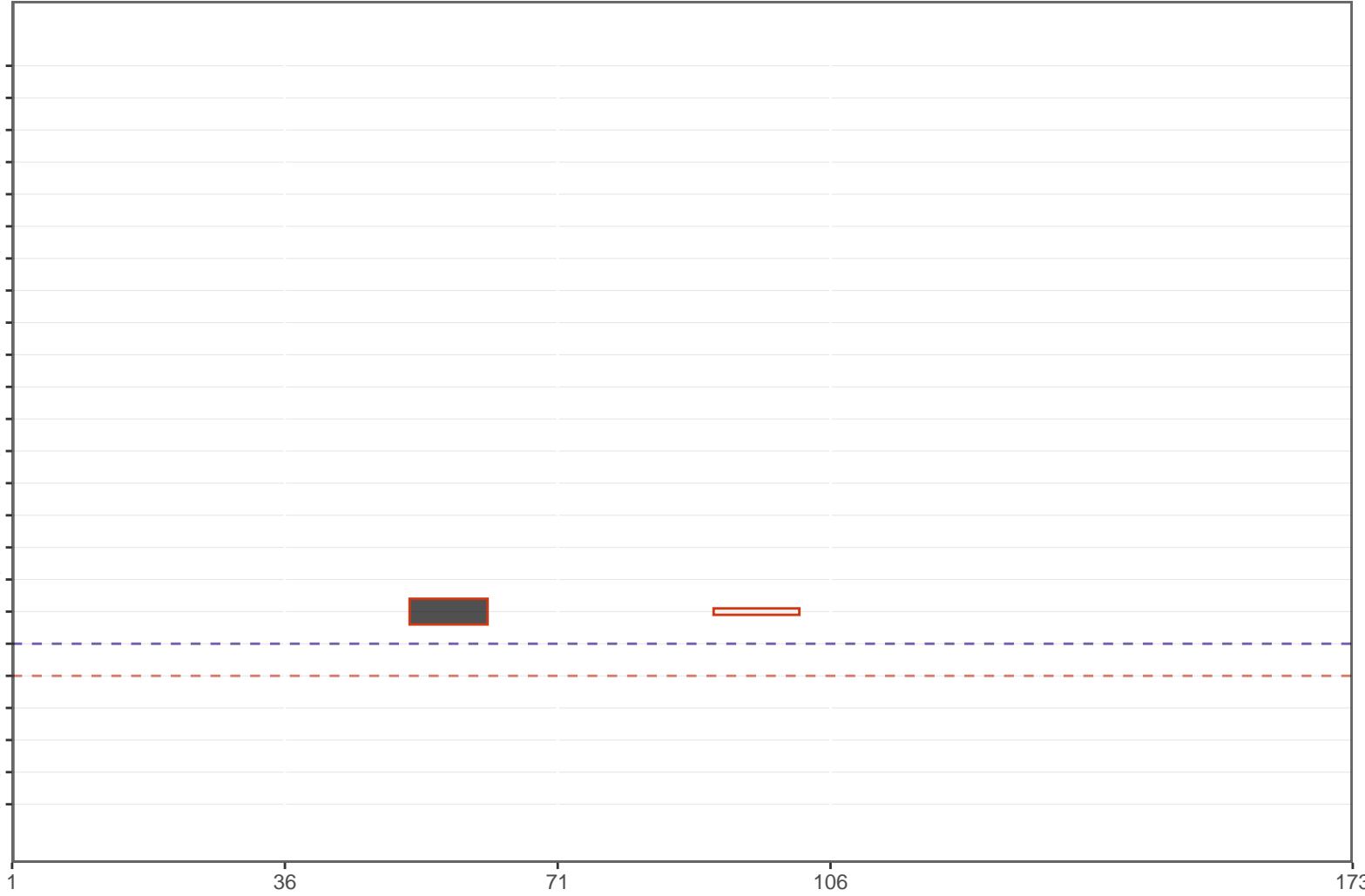
MW indication



Molecular weight

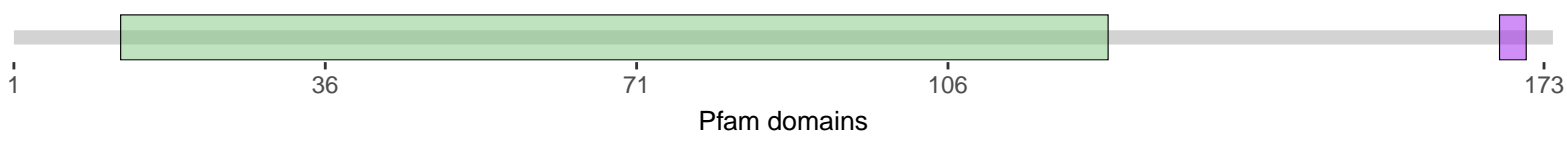


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ELNLDIFEDVEYERTFTVDVSLMDSKTLAETFYVWVKRDPNLYGEWDFEEVWQLHKGDFLKMTMGFSKELKELPEKTRIVATYESGFVAGEDNKSKP

NbL14g03060.1 peptidyl-prolyl_cis-trans_isomerase_CYP18-1 [MW = 17.47 kDa]

No. of times detected



log(intensity)



Values from



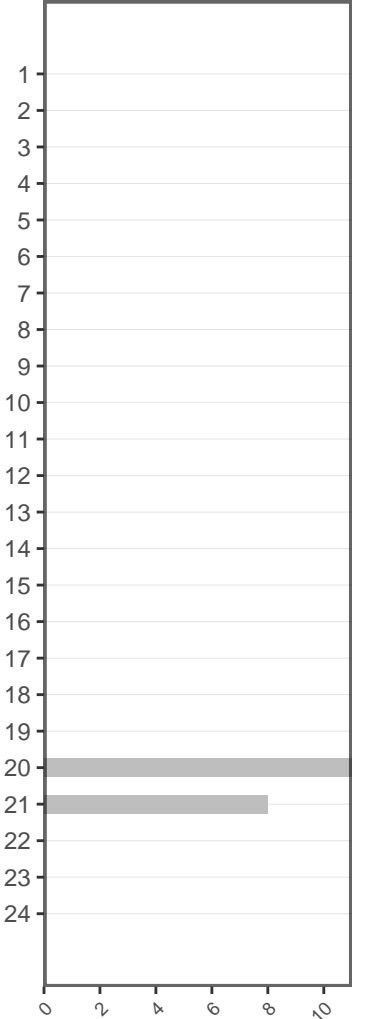
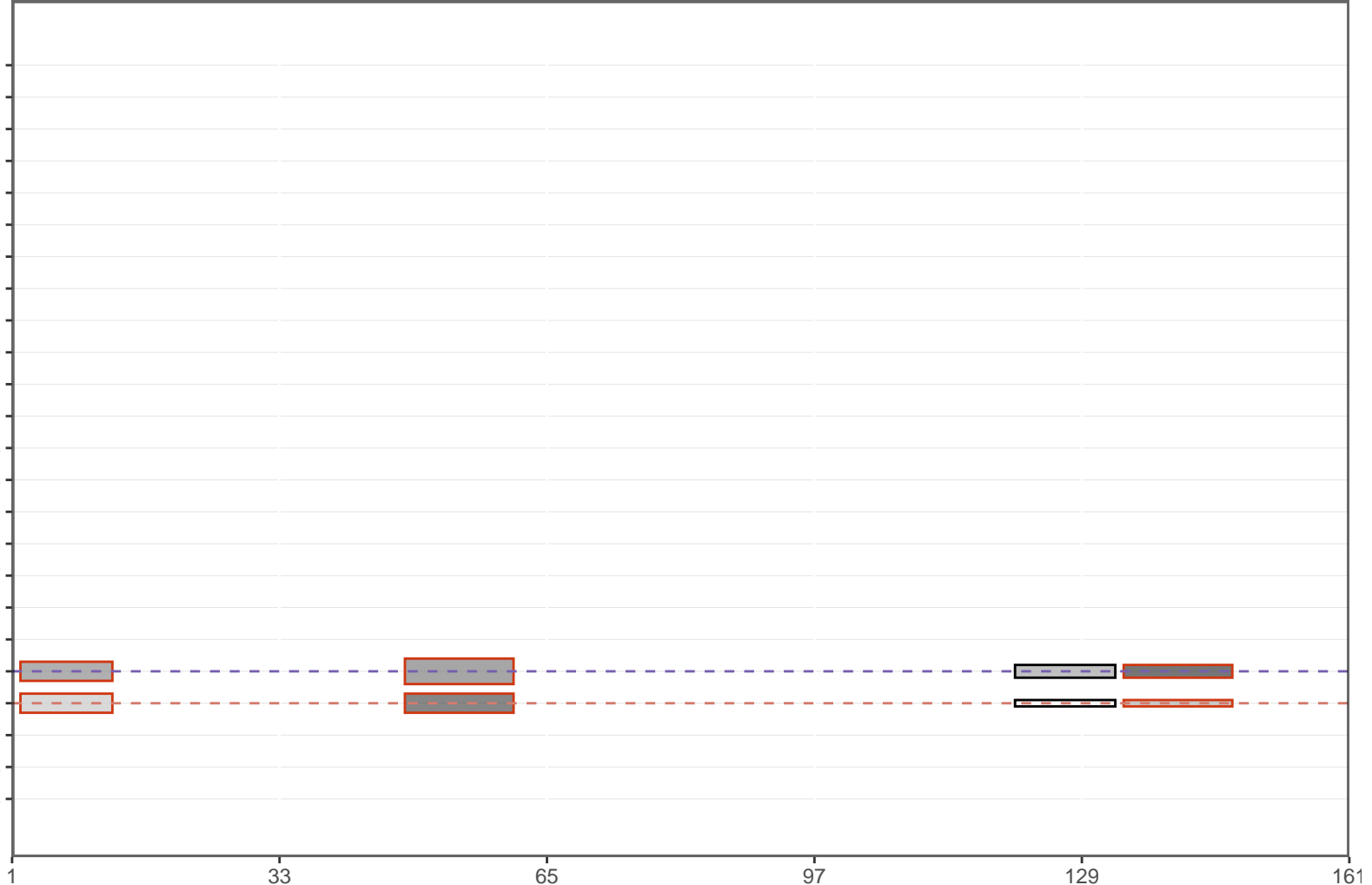
MW indication



Molecular weight

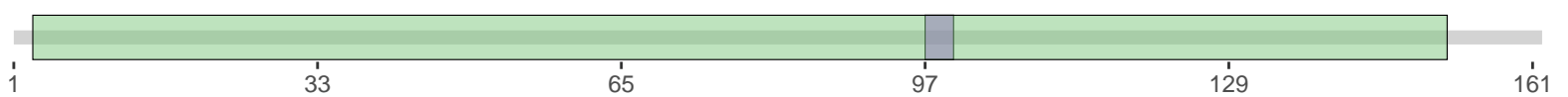


Gel Slice



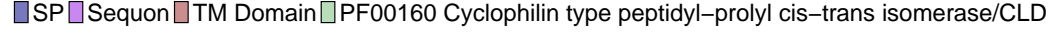
Protein length

Peptide counts over 4 repeats



Pfam domains

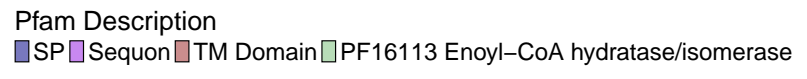
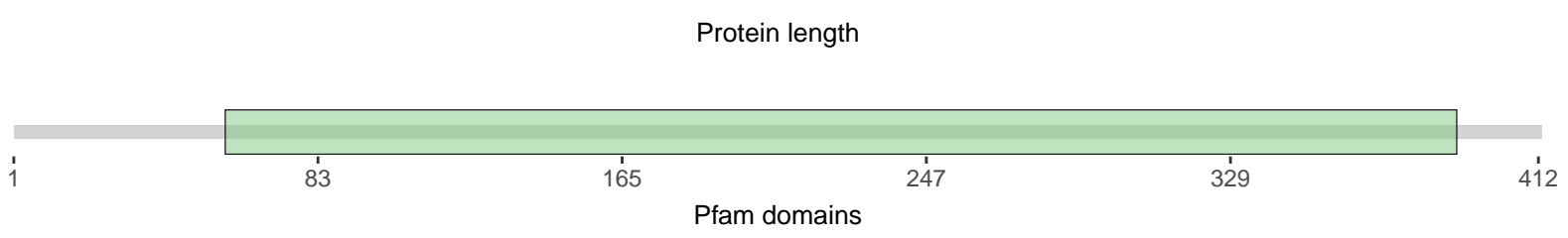
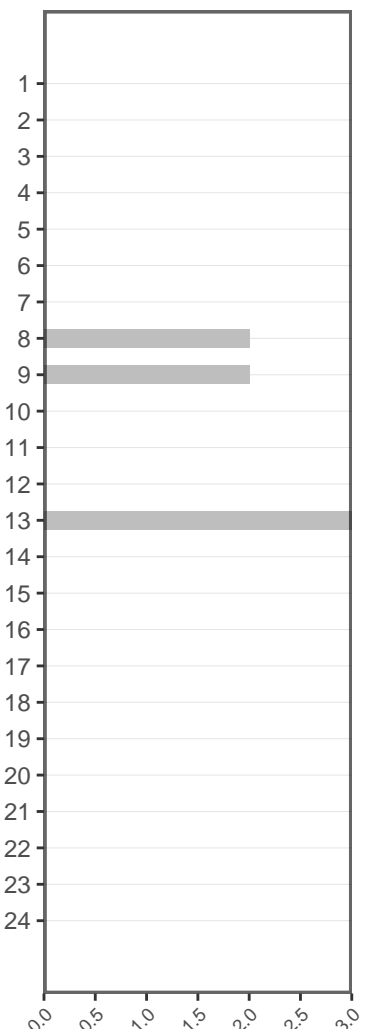
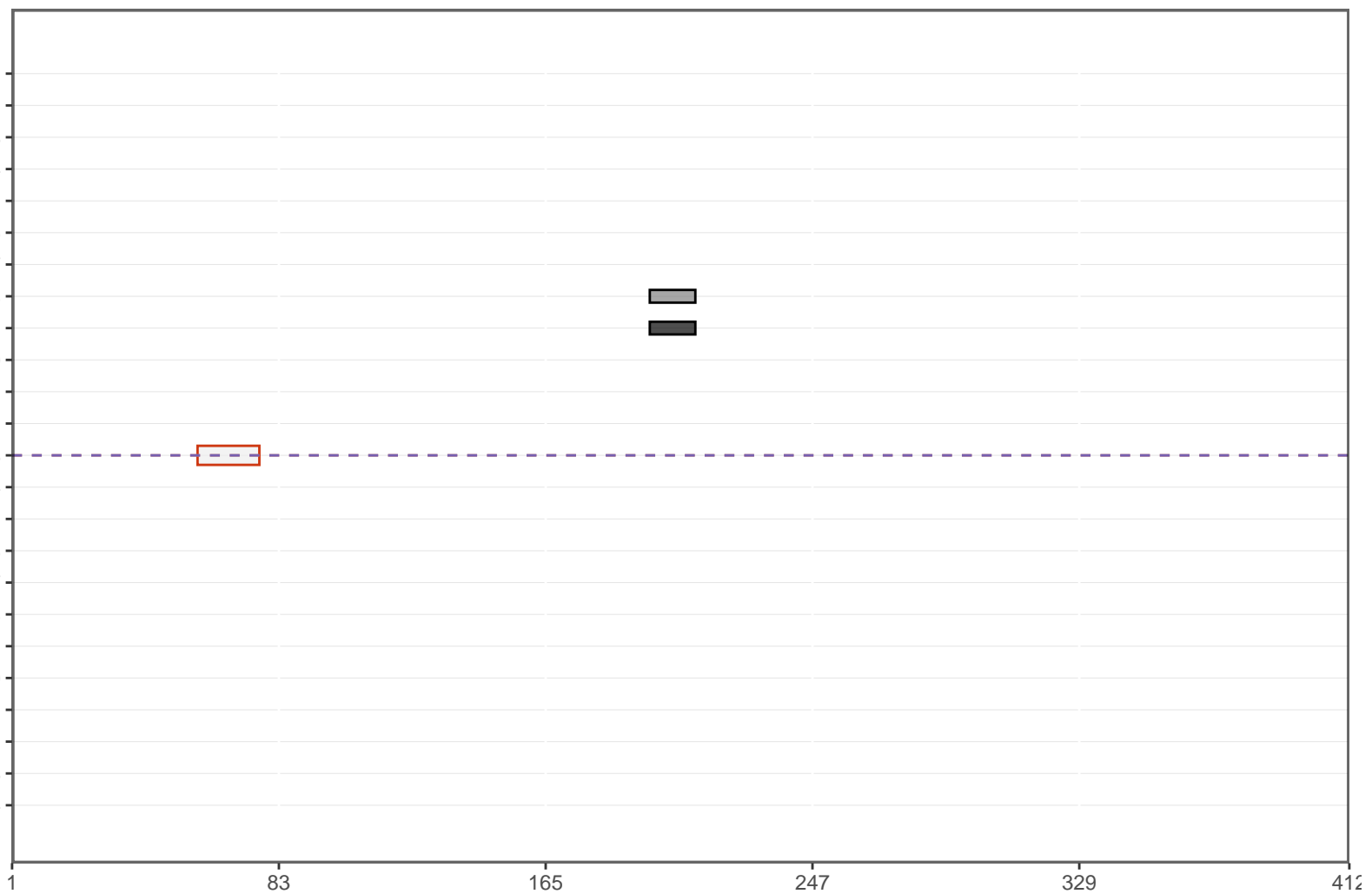
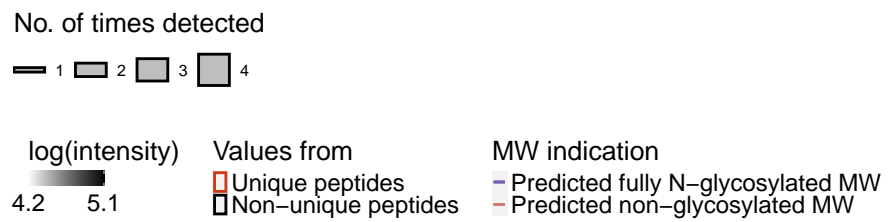
Pfam Description



Protein sequence:

ISKKFNDREIRSLQHNARGILEMANGSPNTNGSGDFMFAKQPHLNGLYTFIGKVIHGFVLDIMKPTTGPGDPLAEIRLNRIHTHANPLAGI

NbL14g02490.1 3-hydroxyisobutyryl-CoA_hydrolase-like_protein_2_mitochondrial [MW = 46.56 kDa]



Protein sequence:
 YYLSRLPGYLGEYLAITGKGLNGVEMADGLATHYSLKERLPWMEERLKGKLTDDRLLVIENSIAEYGDLYVPDSKVLHKFEKIDKFFDQEHIEHLEVERAAEYHDEWDAALNNKIVASFLGLKLVKLSIREGRFQFLDQGLVREYHSDVNVKSRMSGDFGEGVRAARLVKDKFAPKIKWGPTRLEEVTTMVAWCFSPRLGELPELNLAATALREFPM

NbL14g02320.1 macrophage_migration_inhibitory_factor_homolog [MW = 12.22 kDa]

No. of times detected



log(intensity)



Values from



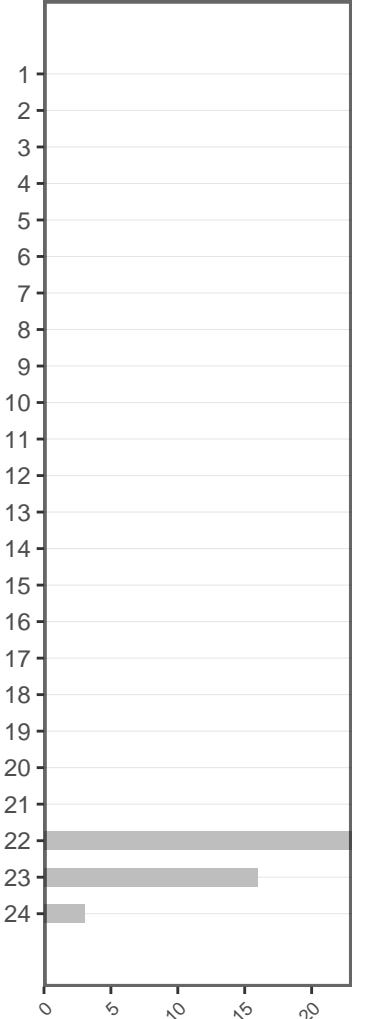
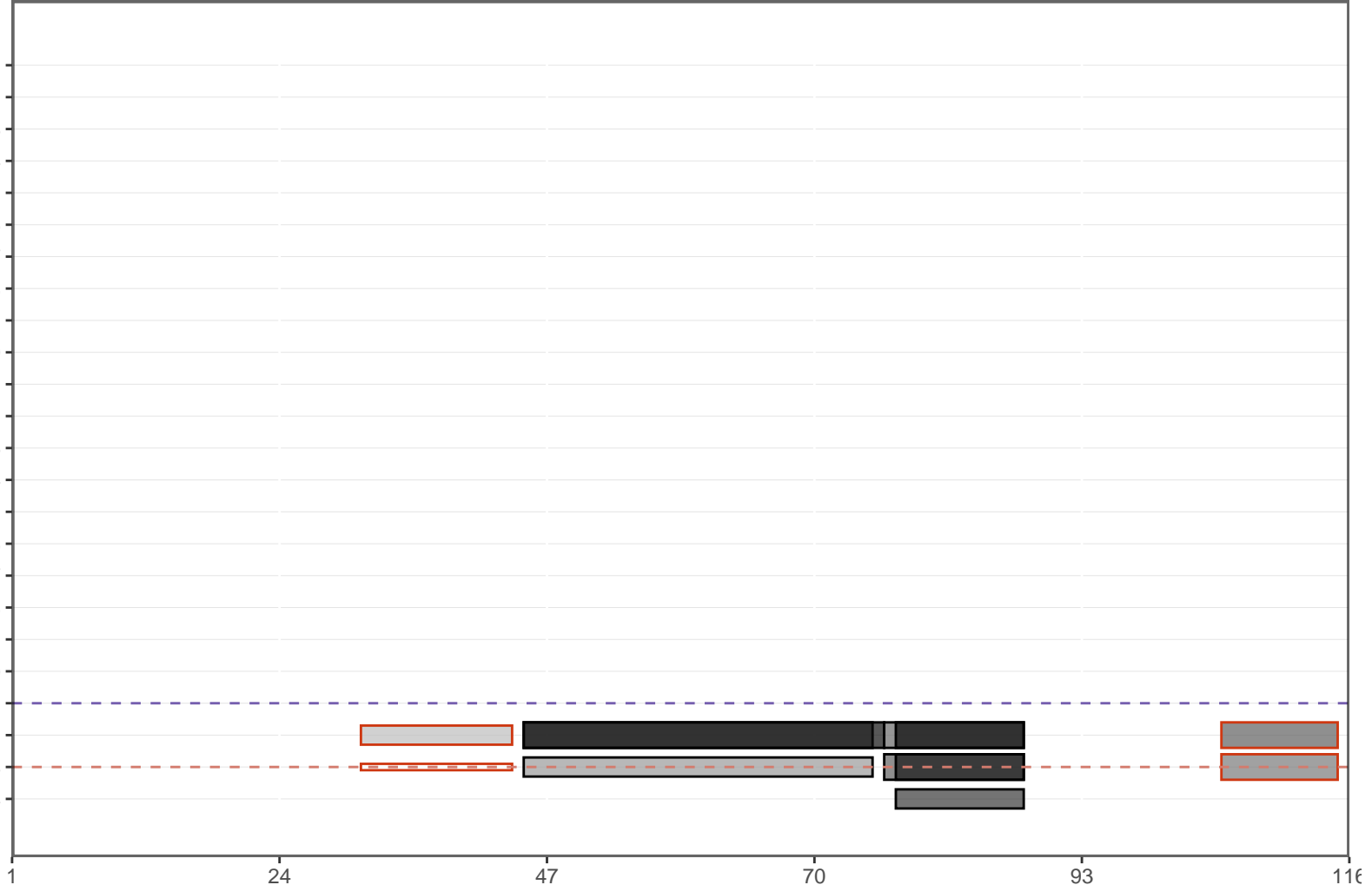
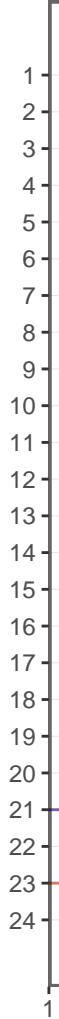
MW indication



Molecular weight



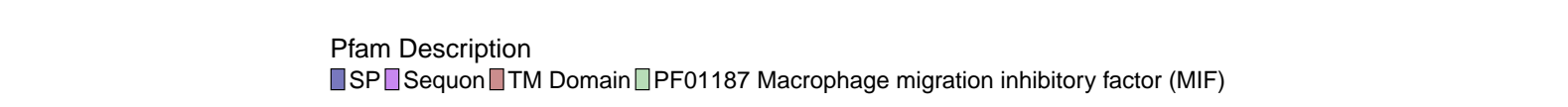
Gel Slice



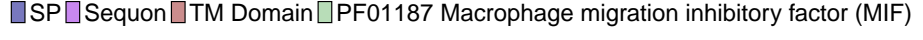
Protein length



Pfam domains



Pfam Description



Protein sequence:

ISVPMISFGTCEQPMANGELVSRIGLNADVNNKLSAAMGILETKLSIPKSRFFLKFYDTKSGFFGWNSTP

NbL14g02040.1 upstream_activation_factor_subunit_UAF30-like [MW = 16.82 kDa]

No. of times detected



log(intensity)



Values from



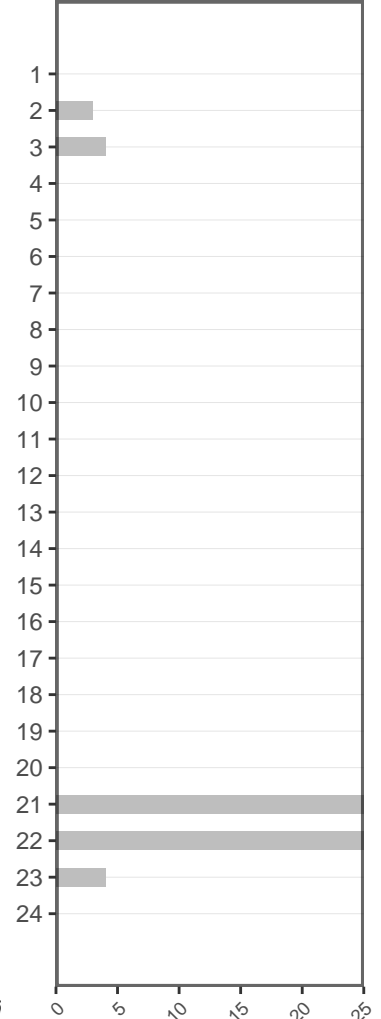
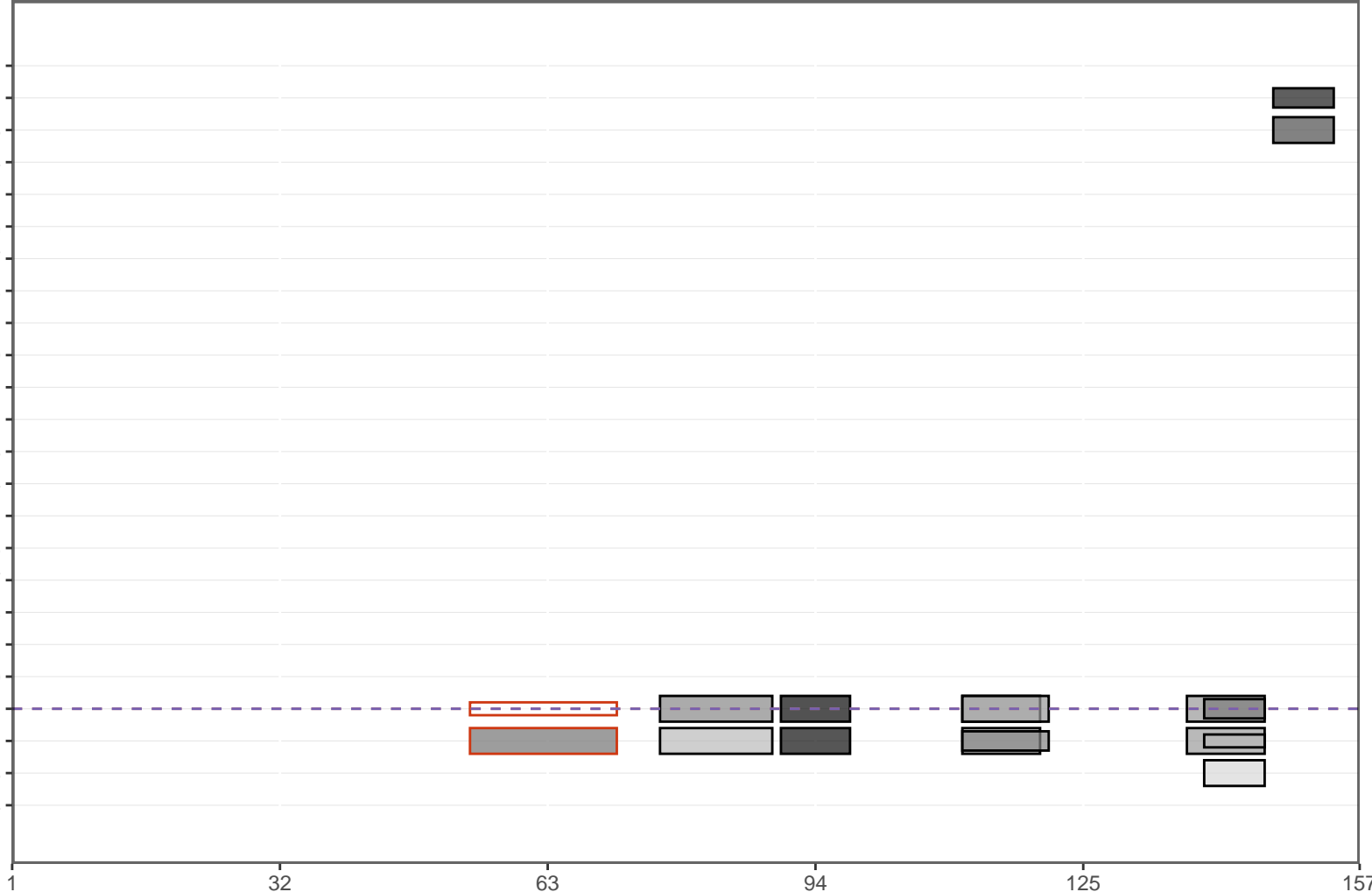
MW indication



Molecular weight



Gel Slice

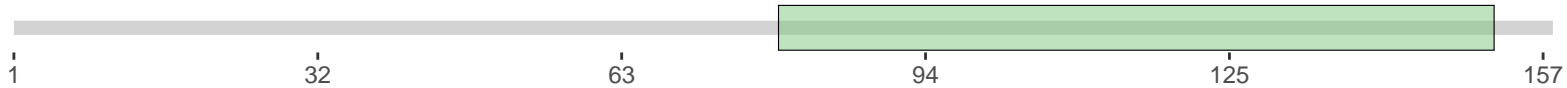


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

AAASATGKGRIRKGIKPLPVPSPALGKFKVGSSEISRTDAVKKVVWDYIKTNLGNPANKKEINGDENLKTIFAANKDKVGFLEAKLLESHFQKAS

NbL14g01960.1 tankyrase-like [MW = 31.96 kDa]

No. of times detected



log(intensity)



Values from



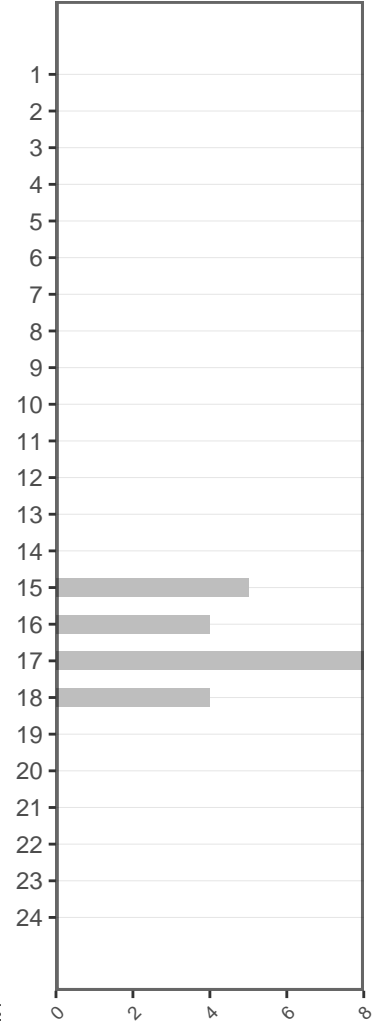
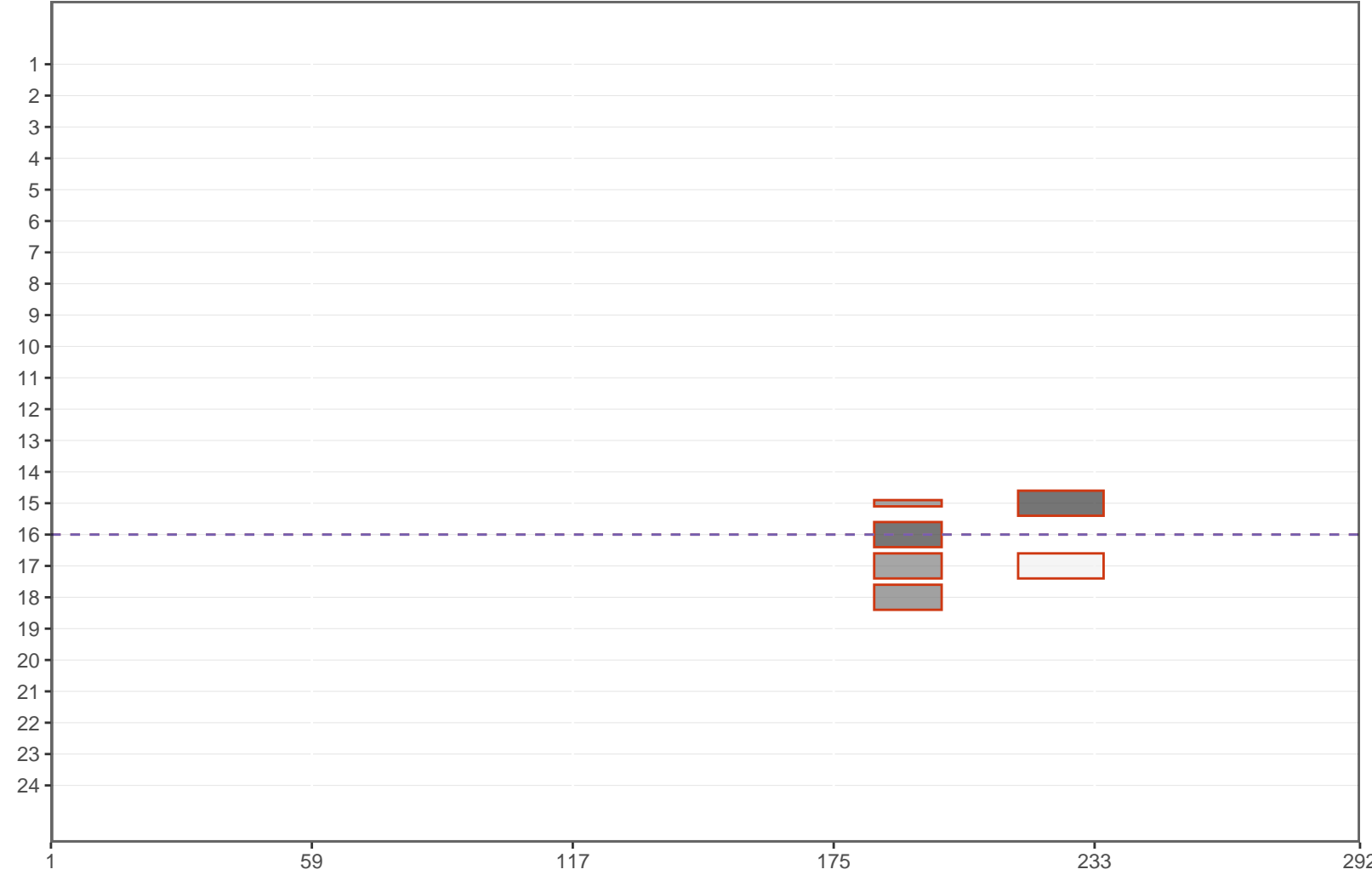
MW indication



Molecular weight

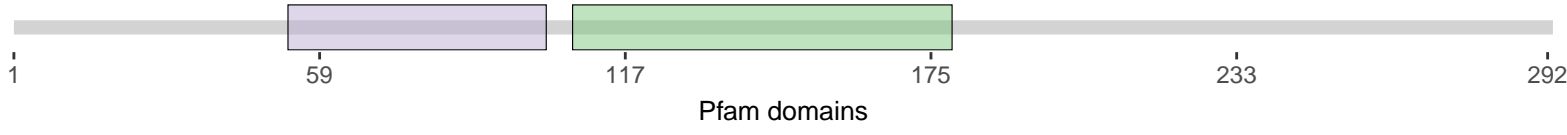


Gel Slice



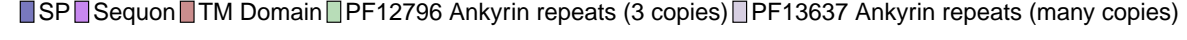
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RLLVSSGVSIKSCNRKGMTPLHYAAGDSHLELVKYLKKGANVNTKKNAGKTPDLASNEEVSSILRQPVTAPEKAVNREEKRGPEESGSSGSDGKGVATEEGEAEKDESLNPKKDDHETSEKSKETKAKVGLNHLAADDNGEEDENL

NbL14g01640.1 plastid_lipid-associated_protein_3_chloroplastic-like [MW = 46.24 kDa]

No. of times detected



log(intensity)



Values from



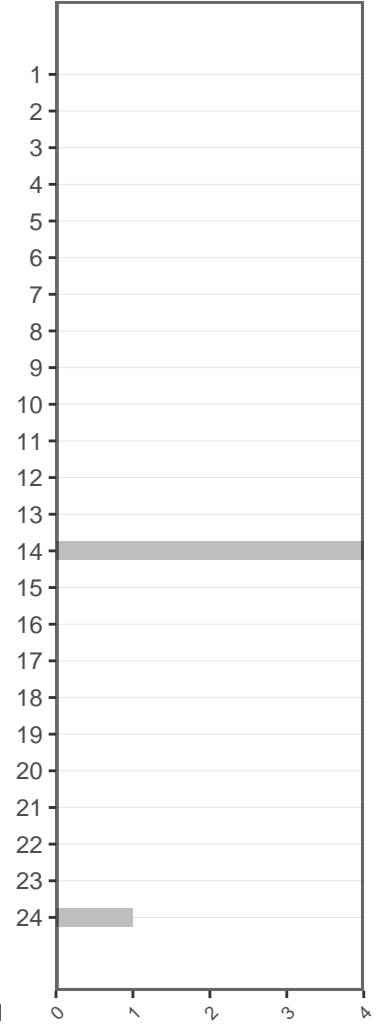
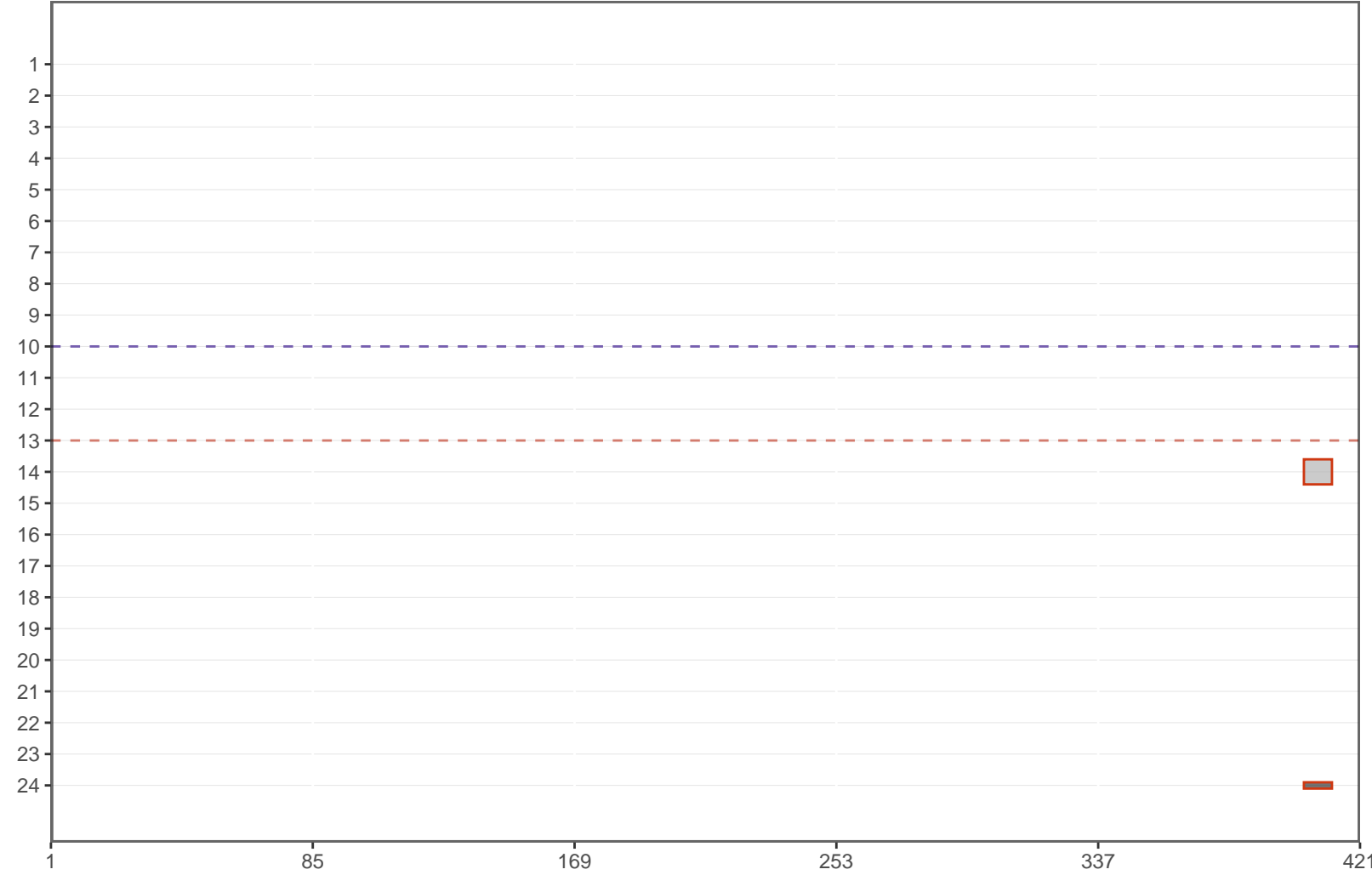
MW indication



Molecular weight

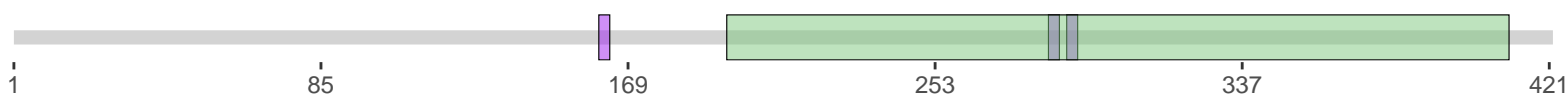


Gel Slice



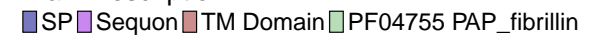
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RVAELKRCCLMDTYVGTNFGLRASSGQRAEALVLSGLEAANFTSPVSEPELLDGNWLVTFATFSELLPLLVGTIPRLKVKESGDTIGTGNLSIENSTFLSSPFAFSSFSANAAFEVRSRPSRIQVEFKEGTVNPPPEVSKNIDLPENVGFQGTISLSPQSGLGPVENVAGIARAISGLPSLKVITPQERTKSWLFTTYLKDRLRISRGDGLFVLVKESSLDQ

NbL14g01490.1 probable_ADP-ribosylation_factor_GTPase-activating_protein_AGD8 [MW = 43.47 kDa]

No. of times detected



log(intensity)



Values from



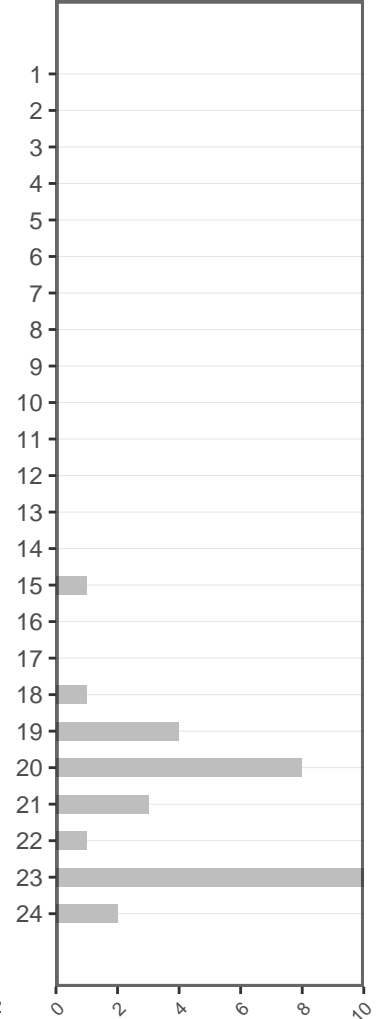
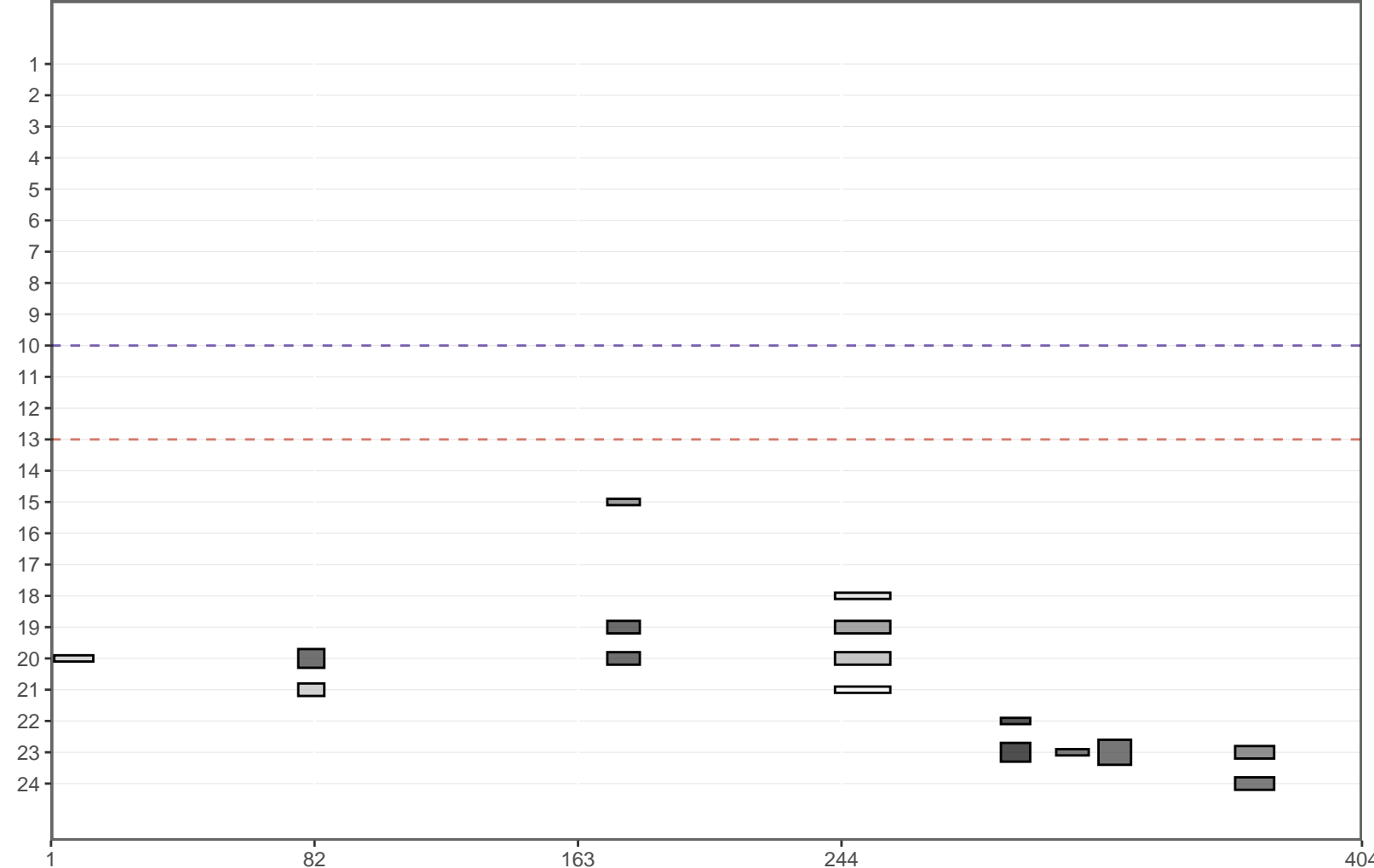
MW indication



Molecular weight



Gel Slice

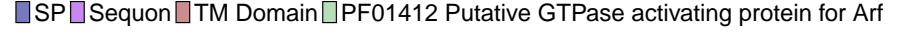


Protein length



Pfam domains

Pfam Description



Protein sequence:

XFQKPGGGLGARLTKLSESLYDQKPEEPVQVSSNFTGNAFTVGSFASRFYTDNVQPKEMSSGGPRVLRNHYVAFPMSSFFSDYQMDGSGFTKTSSEKSKVQIETDEARKKFSNANAISEAGDFGDKSKAEMEABVSLQKFGSGSSAISADLFGNDRADLDLDTAGDLNRLSFGAGQDSSLKNAGETGKHLGSLAATFMSDFQDRIL*

NbL14g01230.1 regulator_of_nonsense_transcripts_1_homolog [MW = 139.26 kDa]

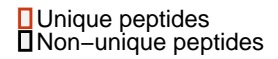
No. of times detected



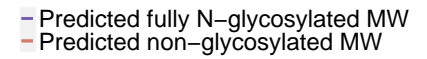
log(intensity)



Values from



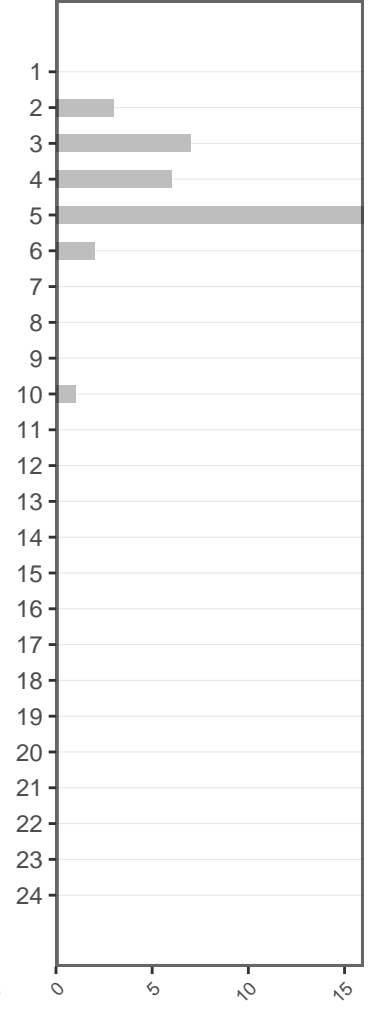
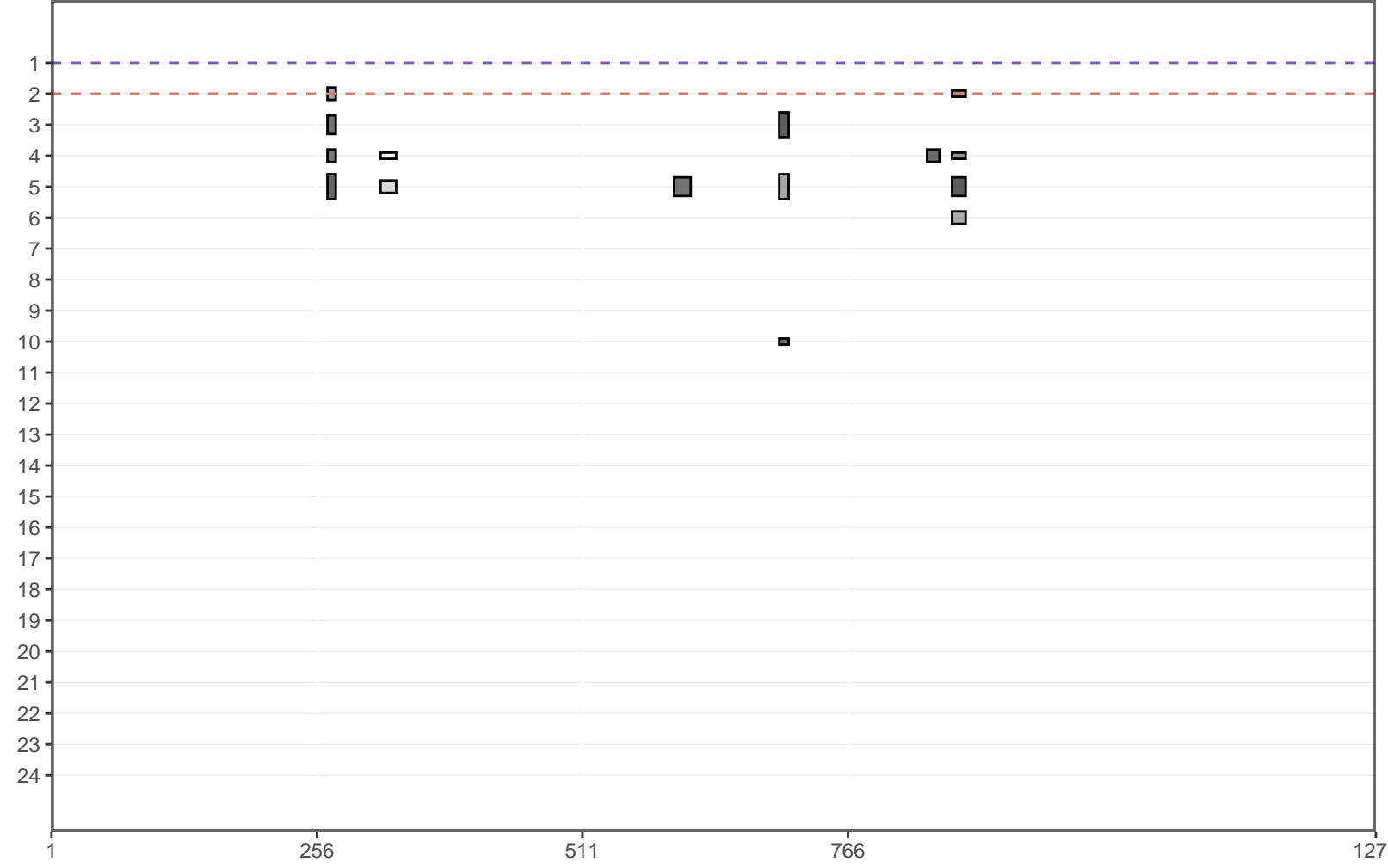
MW indication



Molecular weight

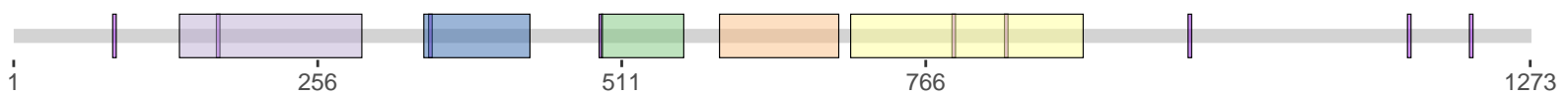


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- TM Domain
- PF09416 RNA helicase (UPF2 interacting domain)
- PF13087 AAA domain
- Sequon
- PF04851 Type III restriction enzyme, res subunit
- PF13086 AAA domain
- PF18141 Domain of unknown function (DUF5599)

Protein sequence:

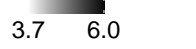
SEIAQSDVCCCTCGAGDPRLANFRFRGVLEIDESTQATEPEGLRPLVLGAKGAVLGDHDLGSPVIMCKKAAARAGLAGSLFERLIVLGVKPRRLQVQYRMRPALSEPPSNSEFYEGTLLGNGVTINERQSTGDFPVPVNRPMFFVYVQMGDEEISAGTSLNLRTEAANKKVTTFKSGVYVPSQKGVTPYEGQRVAVNVMARNSLSRQGLYKEIEVASVDVDFQGRKQVRLSDVRSNEHQGGFLNDRPRLNVAITRARYGIVLGNPKVLSKGPLWNGLLTHYKHECLV

NbL14g01190.1 60S_ribosomal_protein_L37a [MW = 7.11 kDa]

No. of times detected



log(intensity)



Values from



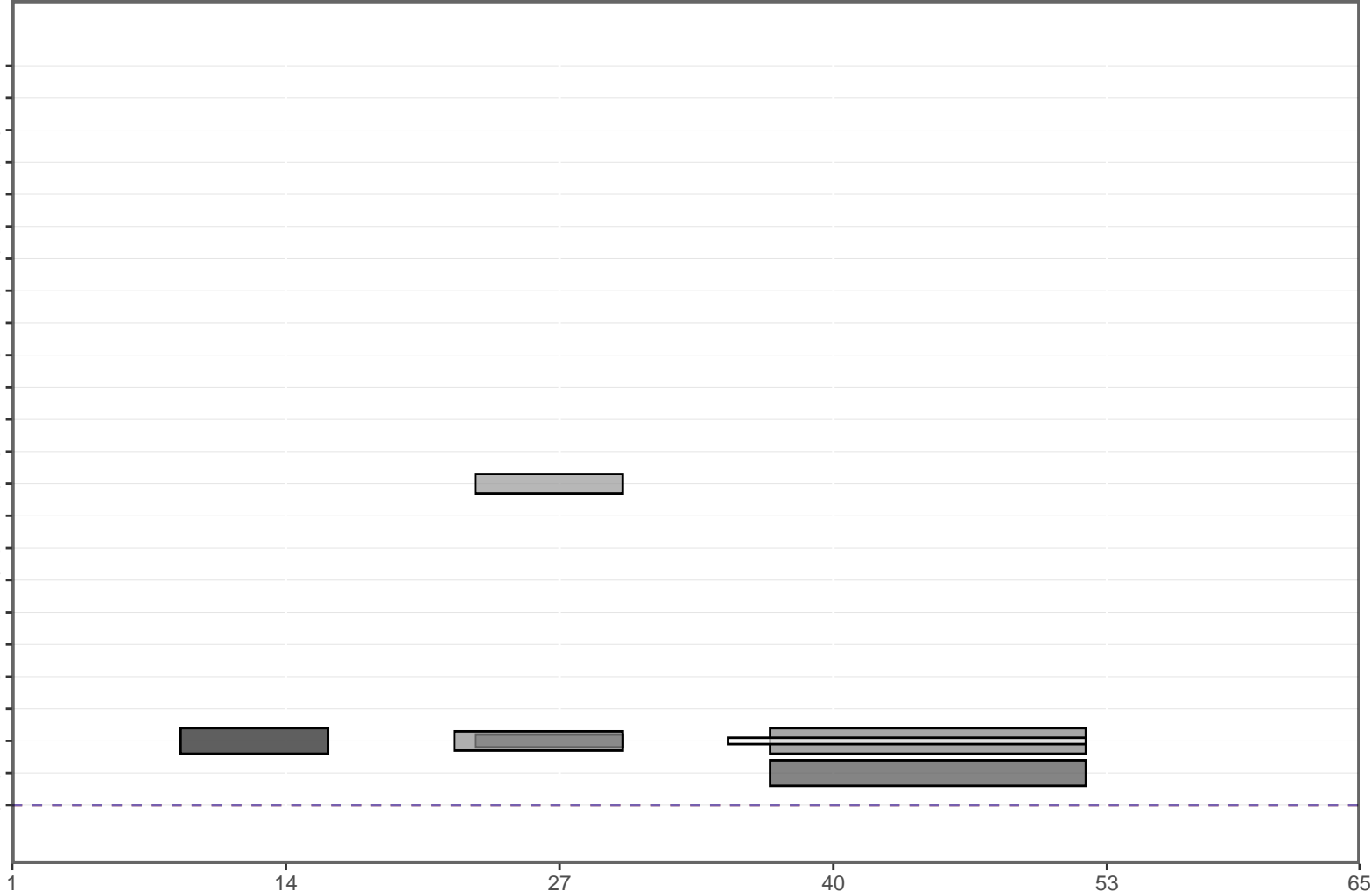
MW indication



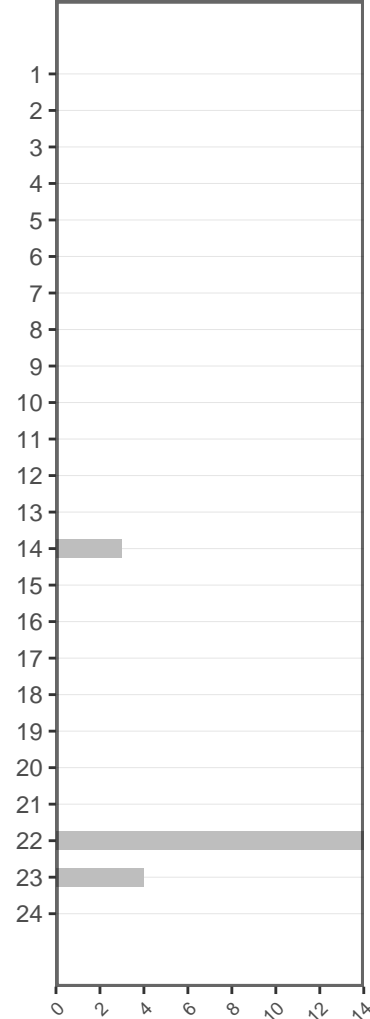
Molecular weight



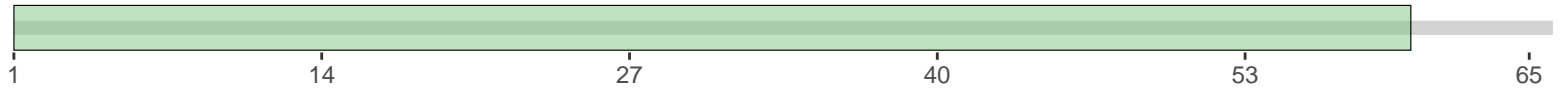
Gel Slice



Protein length

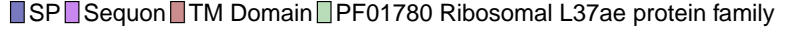


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

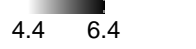
IKRKAIVGIWGCKDGGKWKAGGAYTLNTASAVTVRSTIRRLRQGTES

NbL14g01150.1 LL-diaminopimelate_aminotransferase_chloroplastic-like [MW = 50.09 kDa]

No. of times detected



log(intensity)



Values from



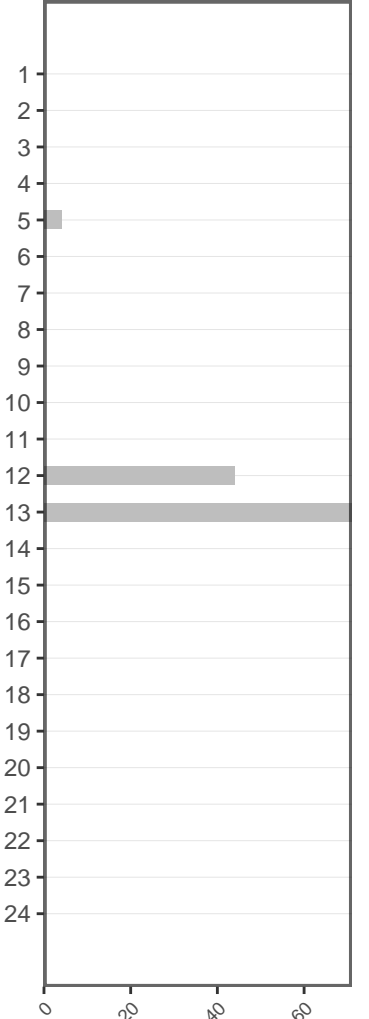
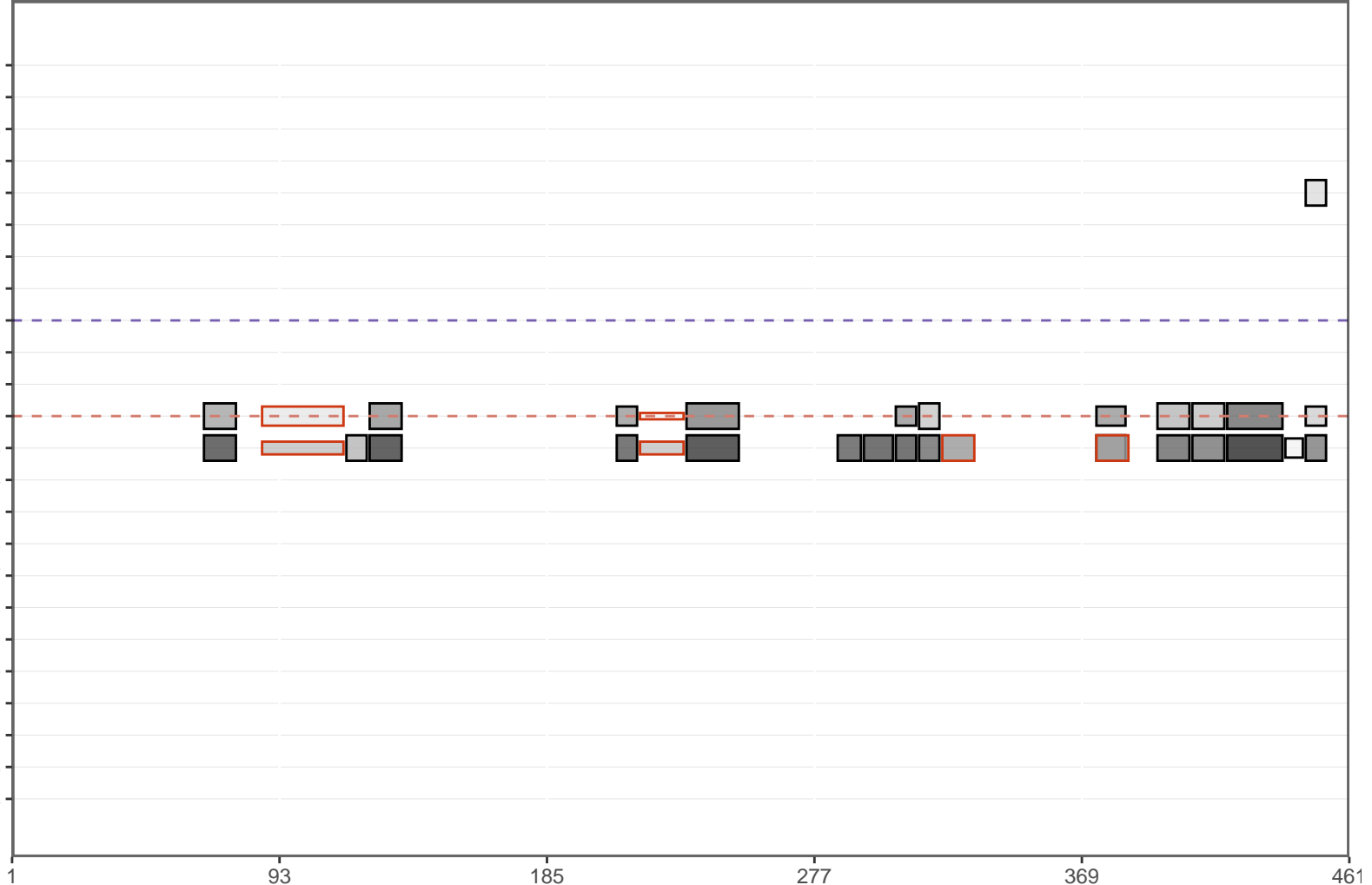
MW indication



Molecular weight

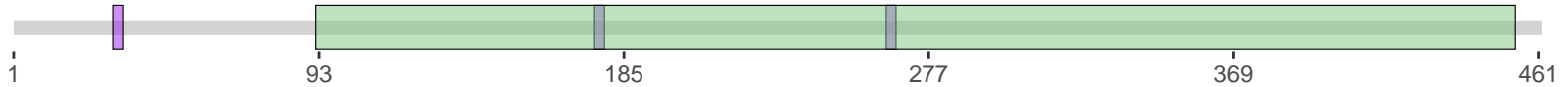


Gel Slice



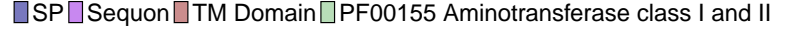
Protein length

Peptide counts over 4 repeats



Pfam domains

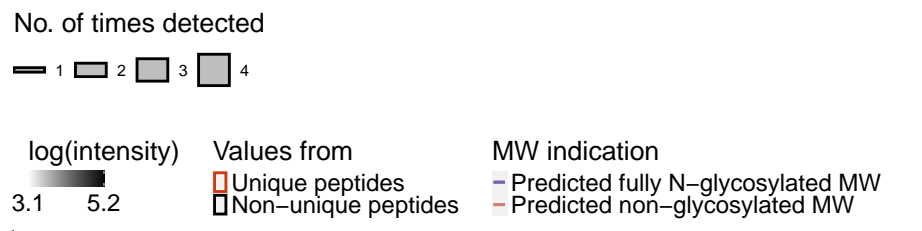
Pfam Description



Protein sequence:

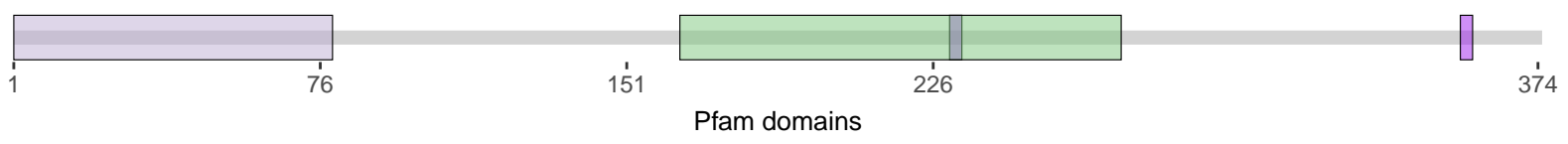
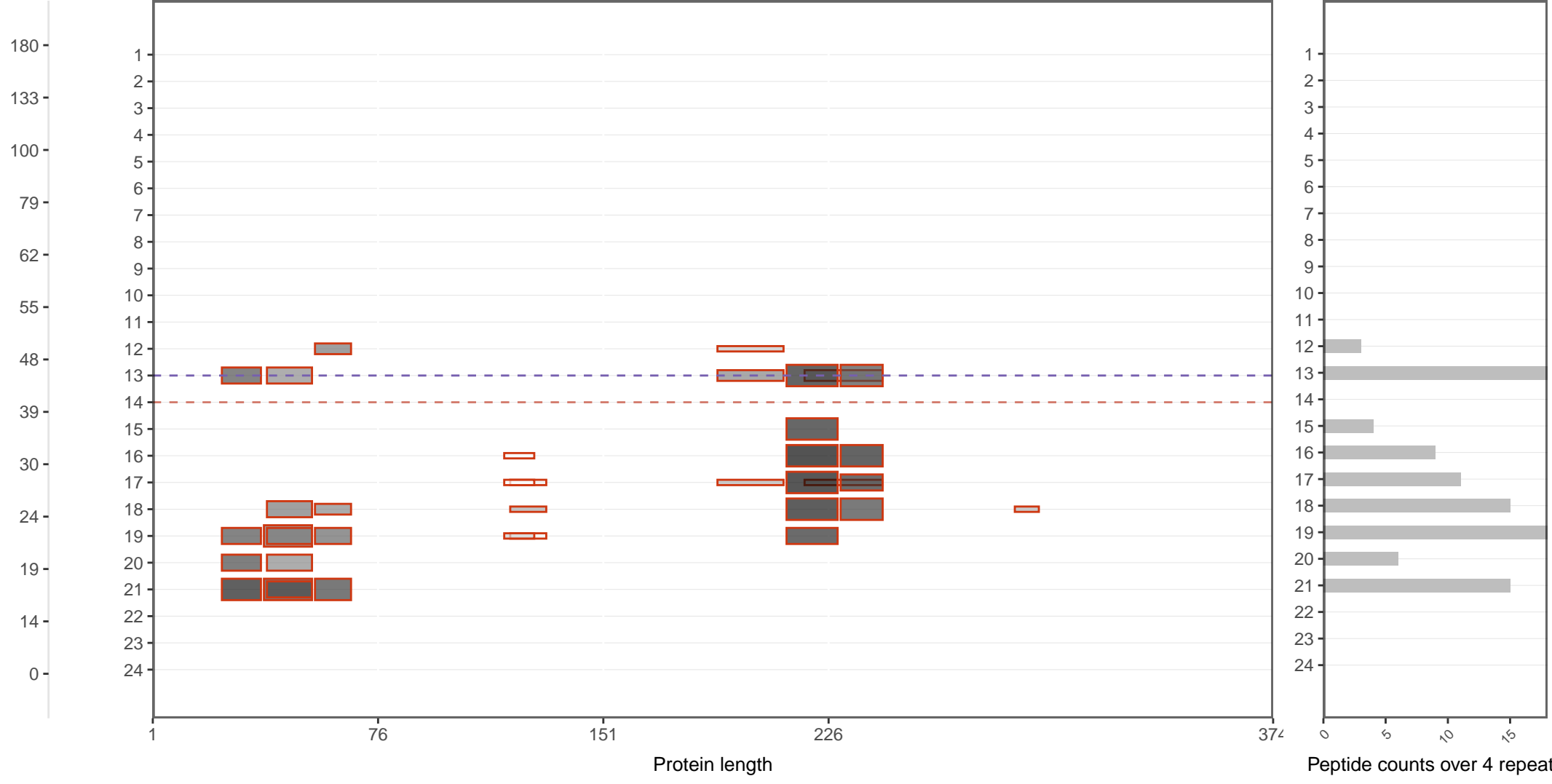
TPENGFFDLSSVSRDTHFFGSPNPTGAAASREGQLTKLVHFAKNGSLLVDSAVAMHGDDEPKBFIEIPGAKVEVSEFSKRYAGFTGVRLLGWTPAKPALLFSDFPVAKDFNRVICTSFNGASNAQAGGLAAGLADGFKAMKNVSYFKKENTETIMETFKRLGKVVYGGKNAPVYWHFPGRSSEWEVSEILEKTHVITTPGGGFGPGGEGFVYVSAFGHRDNYVEAGRFRKELV*

NbL14g01130.1 plasminogen_activator_inhibitor_1_RNA-binding_protein-like [MW = 40.24 kDa]



Molecular weight

Gel Slice



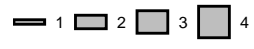
Pfam Description
 SP Sequon TM Domain PF04774 Hyaluronan / mRNA binding family PF09598 Stm1

Protein sequence:

ISQTRGRNEYKREGGSGRGNWGTADDAQETEVAVVNDGKHEVETEKAGGDEAEDTNKKNSTAAEPEEKPEEKEMTLEEVKLMEEKRKALMALKPEERVKNLQKELGSMQLLENKKNDDDFVHLRSEKKEKRAVEKARKTQGSNEFLKPAEGESNHYRRGGRRGGRRGAGGGGGVGGKNNYKAPBEDAGGFSLVAK

NbL14g01120.1 protein_ECERIFERUM_1-like [MW = 42.08 kDa]

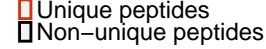
No. of times detected



log(intensity)



Values from



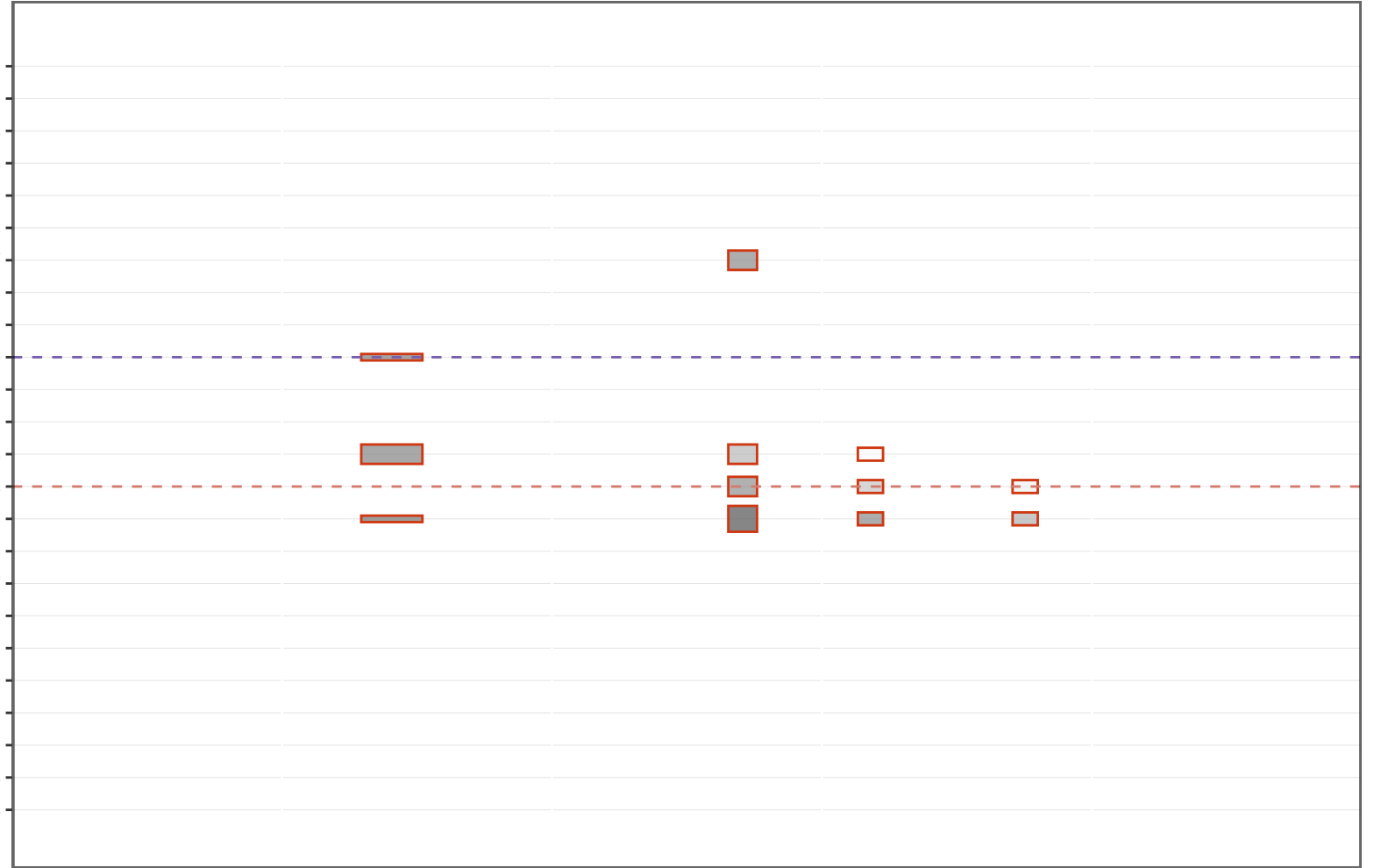
MW indication



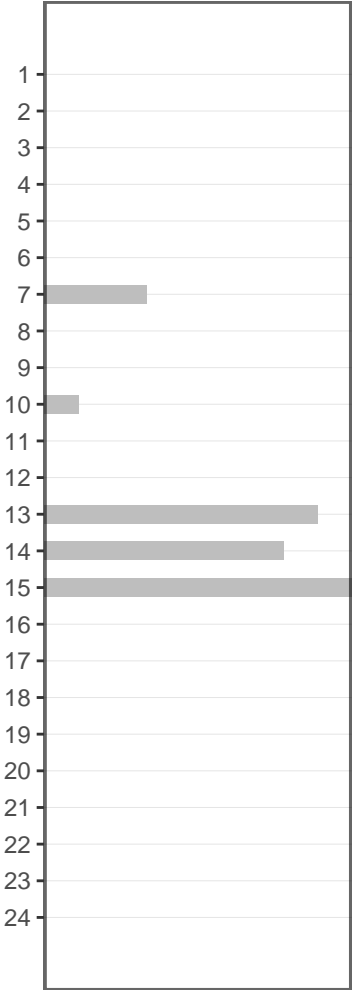
Molecular weight



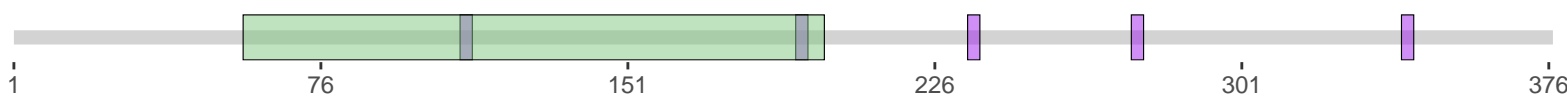
Gel Slice



Protein length

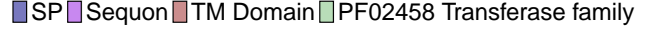


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YISIGSCLFLADPFVMTNFKWWSKHKLGISGDAPKIPFPYTPNLRKIGLLPTISLSTNKKTTQTILFKIPKQPLNLLNNFLKLNLSKSGIEIEEKIGTNSKFSLPFYTERANSENIVKVEIQEIKKIDEGGLIYKNGGLISVSWDGLGGDKVIFNEGNKAINISQWNAENQDLAMITPSTDESSQLNIFTVFN

NbL14g00930.1 L-lactate_dehydrogenase_B-like [MW = 37.93 kDa]

No. of times detected



log(intensity)



Values from



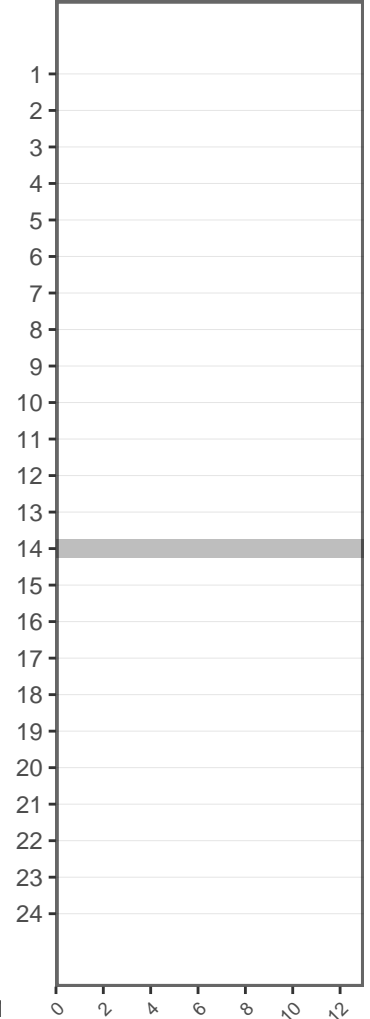
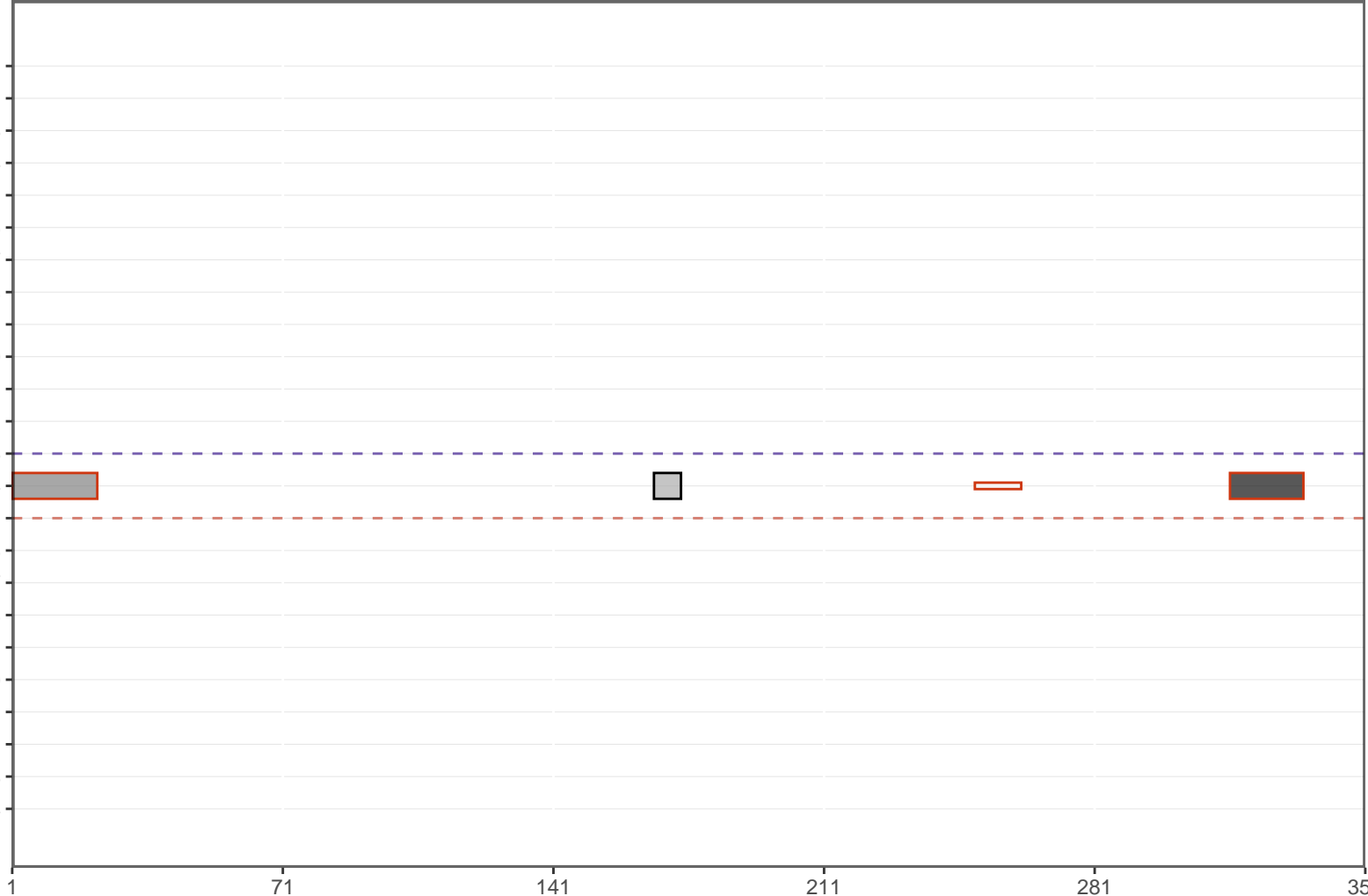
MW indication



Molecular weight

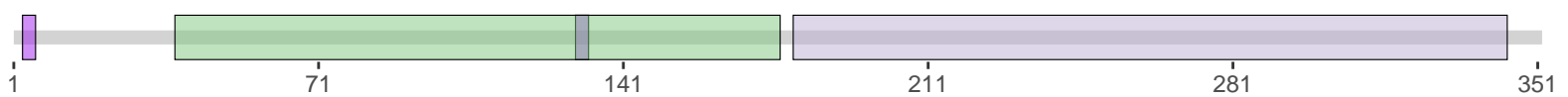


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00056 lactate/malate dehydrogenase, NAD binding domain
- PF02866 lactate/malate dehydrogenase, alpha/beta C-terminal domain

Protein sequence:

VAVKLSGFPNIRVVGSGTNDSSRFRFLADHLELVNAGDQGVAYVGEHGDSSVALWSSISVGGVPLSFLERQDAFEKETLEKHKGVVESAYEIVBLKGYTSAWAGYEVANLARSIRDQRRIHPVSVLAKGFYGDSDGVFLSLFVQLGRGSLGVTVNHLTDEEIQGLRNSAKTILDVQNLGPF

NbL14g00890.1 hsp70-Hsp90_organizing_protein_3-like [MW = 66.5 kDa]

No. of times detected



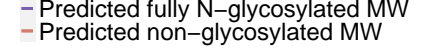
log(intensity)



Values from



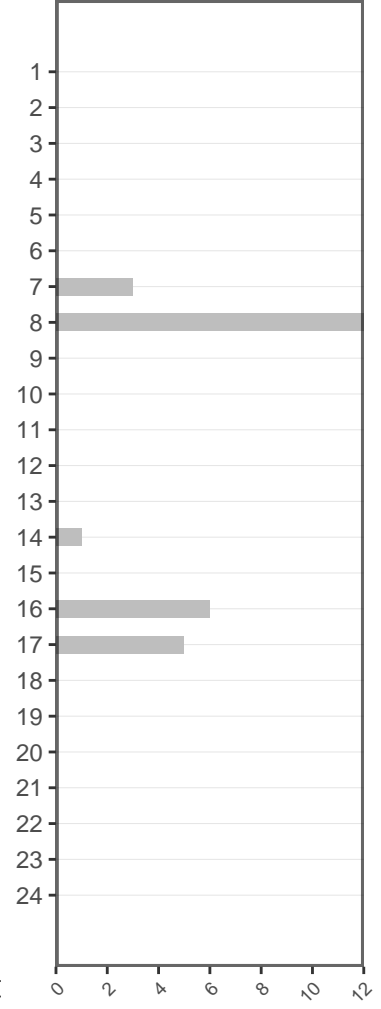
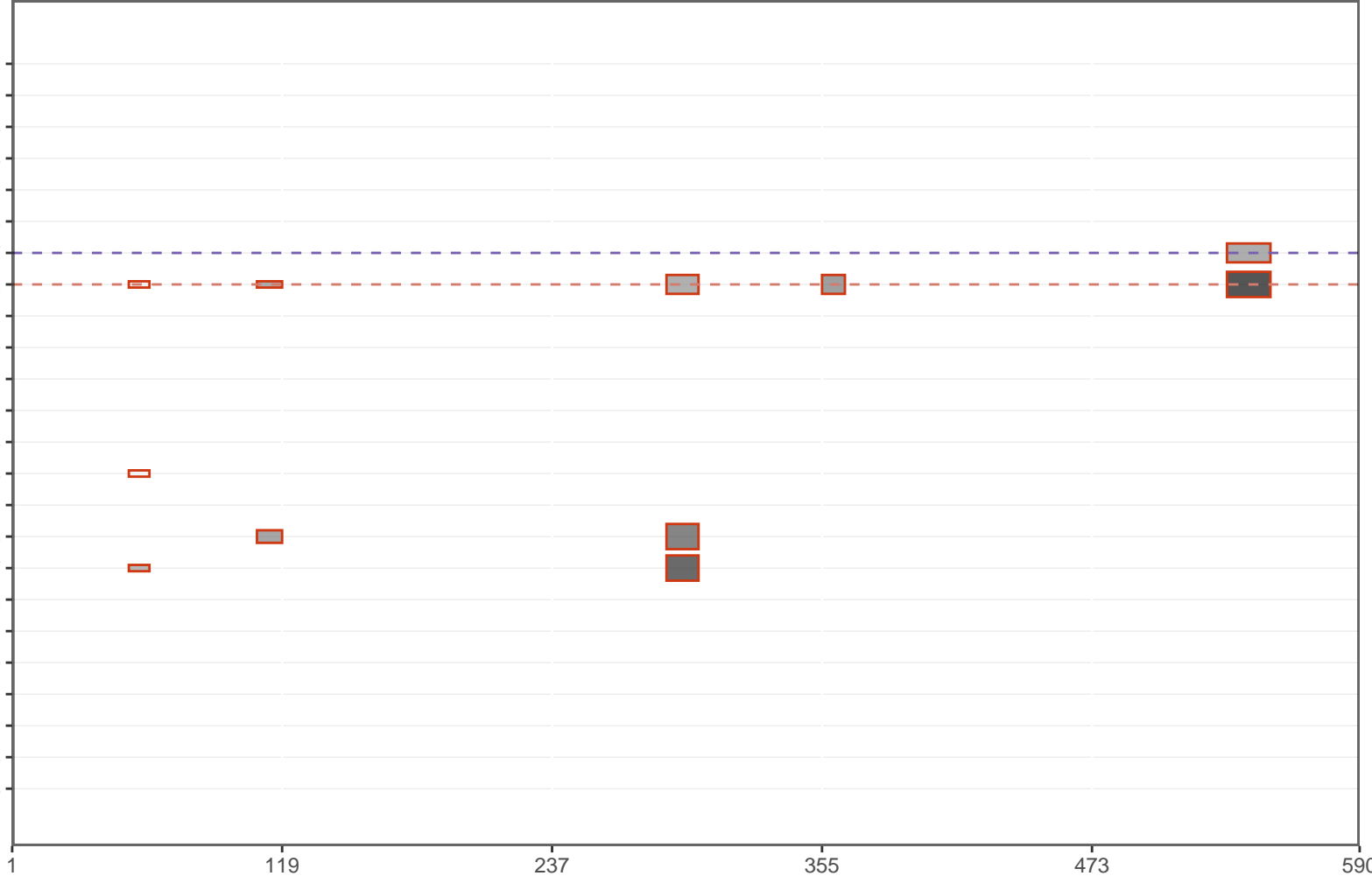
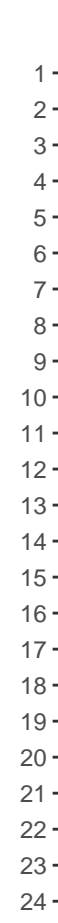
MW indication



Molecular weight

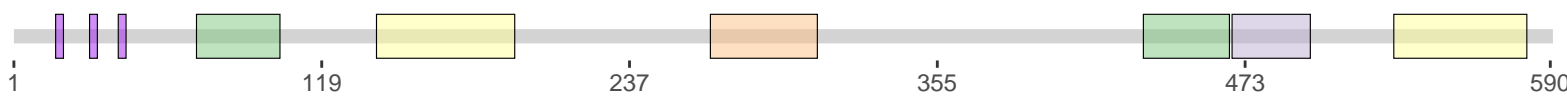


Gel Slice



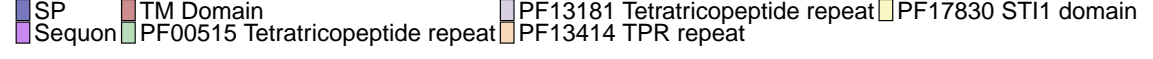
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TAIQHYSKALDLDDEDSIFENRAAVYLEMGKYGEDGKDGKVAVERGRRELSDPHMIARLTKGTLALVMAKTKDFERNMETTFQKALTEHRNPDTLKLNDAEAKKAKKELEGGYFDPPQADEEREKNGVYFKKQYDVAVKHYTELSLRNPKDPRVSNRAADYTKLGALEGLKDAEKIQLDPTFAKGYTRKGAIGFFMKVEYKALETYQEGKHKDAGNGELLDGVRKVEQINKASRGDLTPEELKERGAAMQDPEIGNLIDPVMRQKLVDFGQENPKAADEHMKNF

NbL14g00880.1 lipid_transfer-like_protein_VAS [MW - SP = 10.23 kDa]

No. of times detected



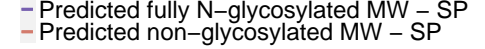
log(intensity)



Values from



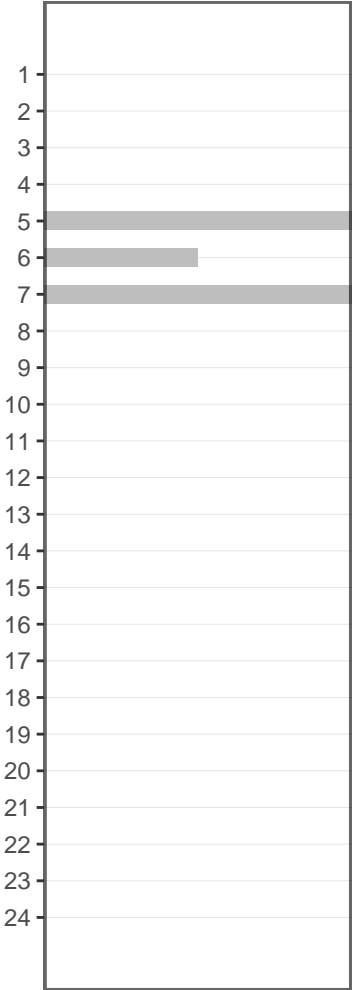
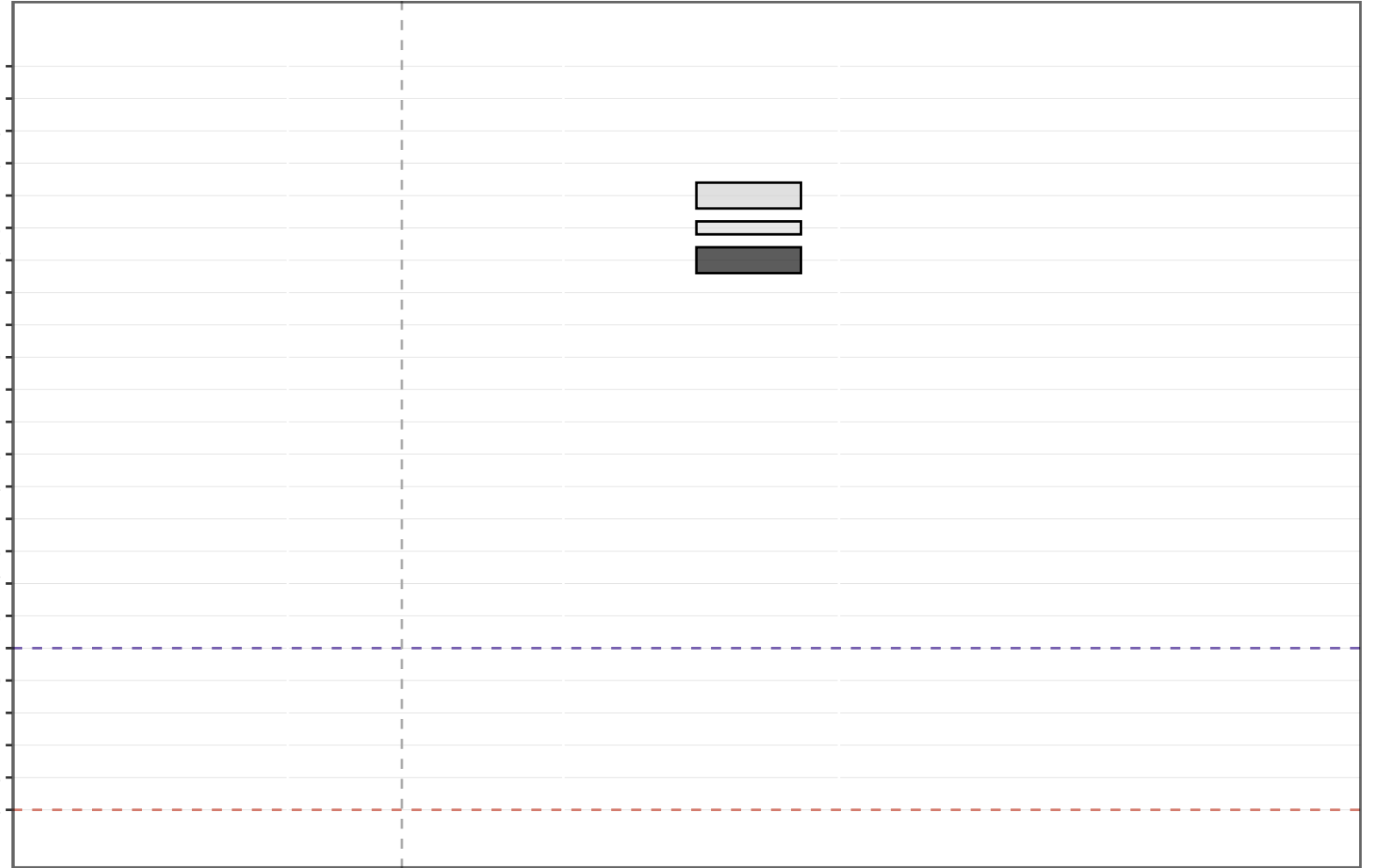
MW indication



Molecular weight



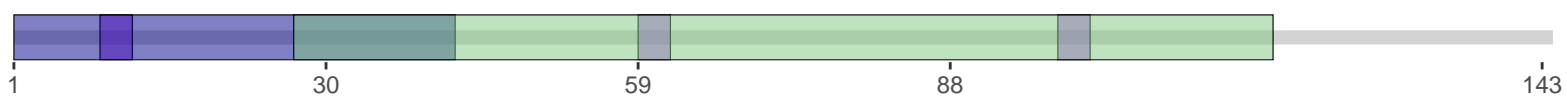
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

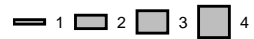


Protein sequence:

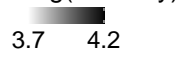
.NSTKTPAECCDPLKEATFNEIDGLGKLVENFTLLPFGNITGALALPKAGNPGDLSSGNGKAPGPGSETLPPPGPEAAFGS

NbL14g00720.1 serine_racemase-like [MW = 35.59 kDa]

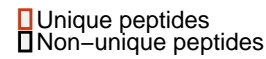
No. of times detected



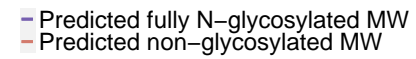
log(intensity)



Values from



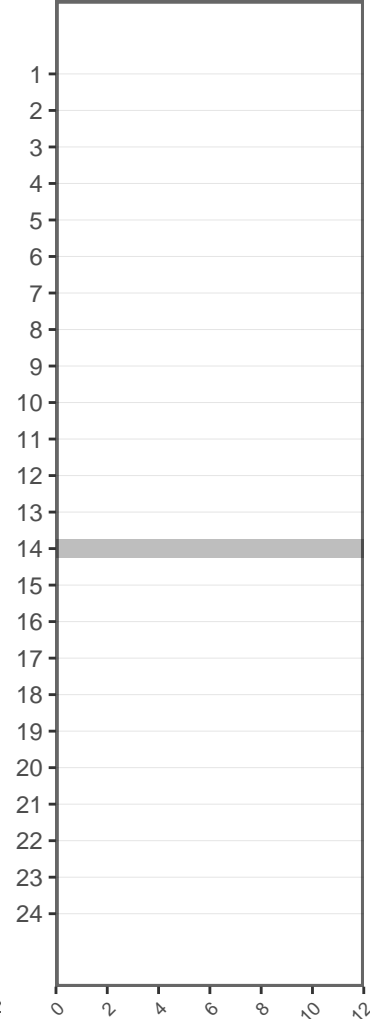
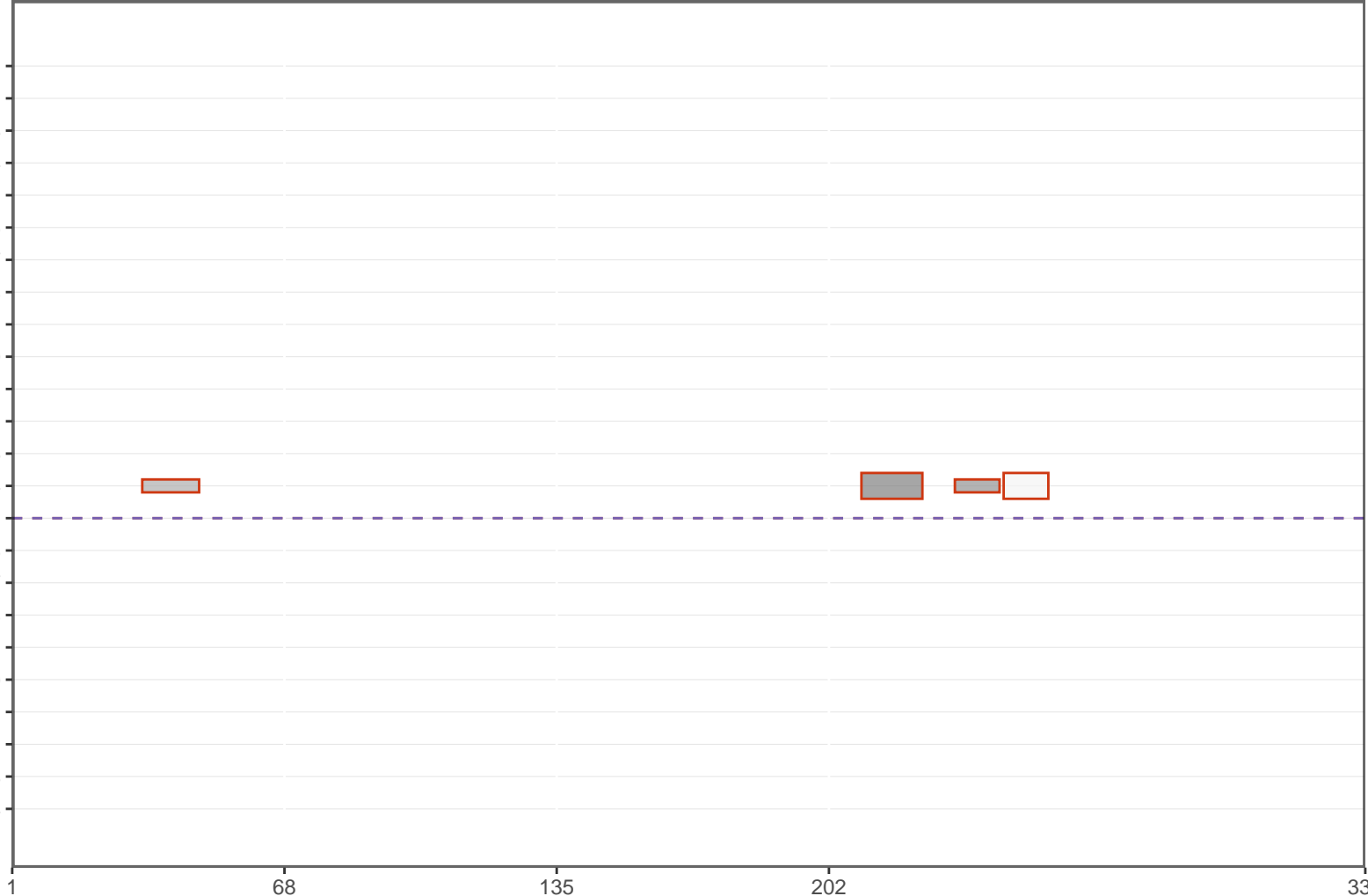
MW indication



Molecular weight



Gel Slice

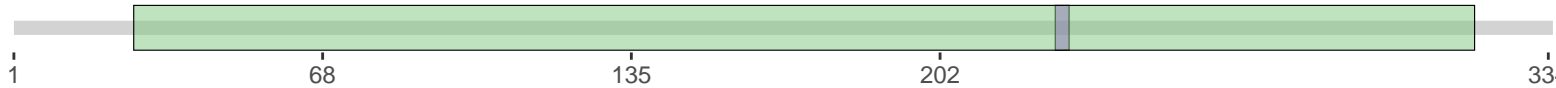


Protein length

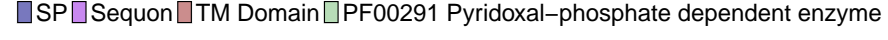


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

TGAVLHPYNDGRISGGGTELEFLEGAIEGTIVPISGGGLISGVALAAKANPARIILAAEPMGADDAFGKNGSITKLSSEVNTIADGLRAFLGDLTWPVIRDLVDVIVVDDKEIQAMKLYEIKIAVEPESGAIGLAILEDAFQKNPVPVSECHHGIVISGGNVDLGLLWNSLEK

NbL14g00600.1 hydroxymethylglutaryl-CoA_synthase-like [MW = 51.04 kDa]

No. of times detected



log(intensity)



Values from

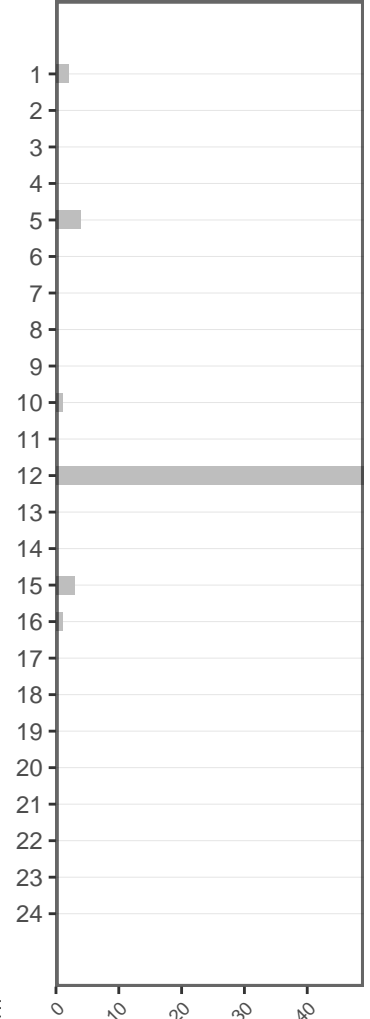
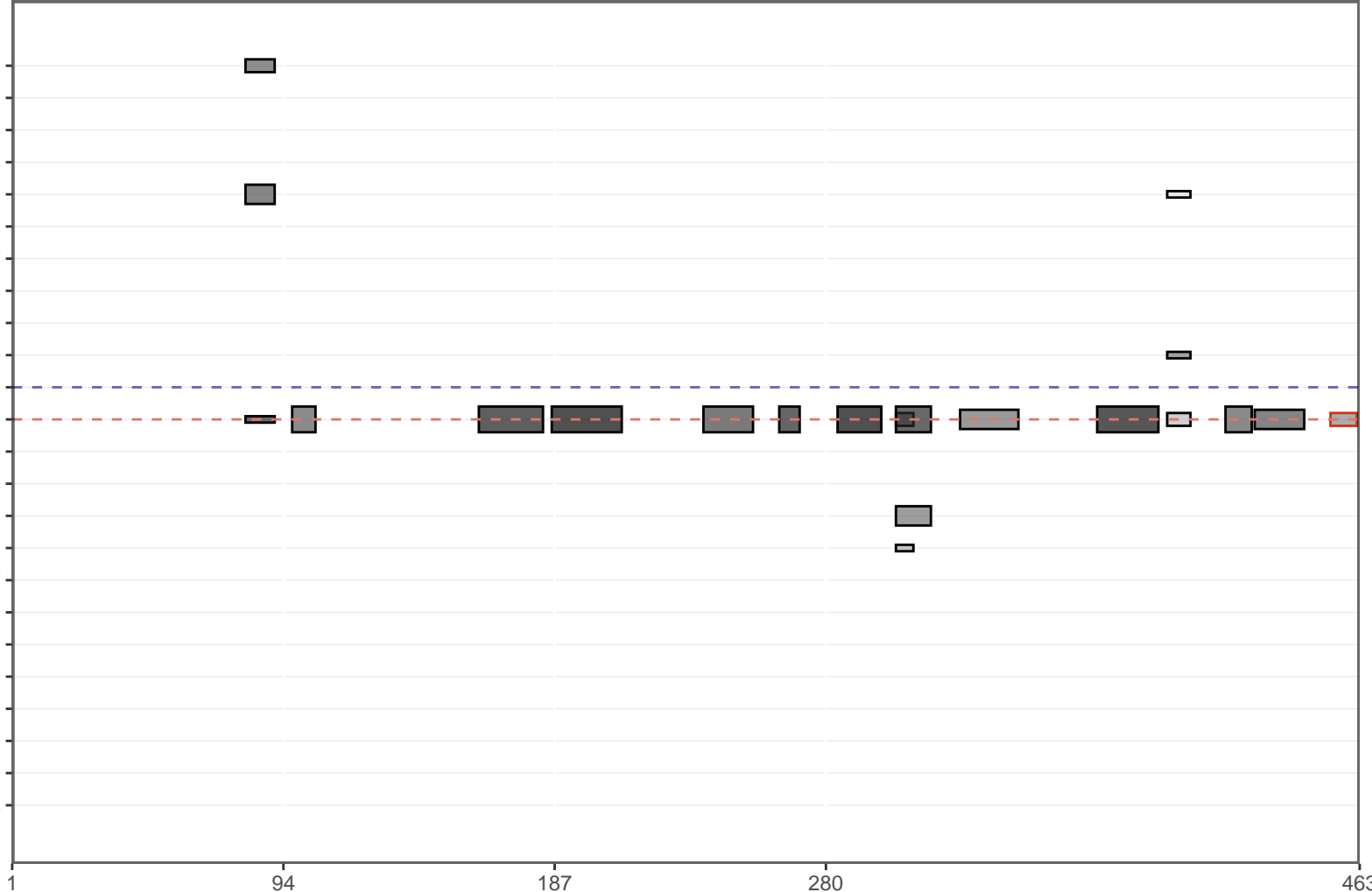
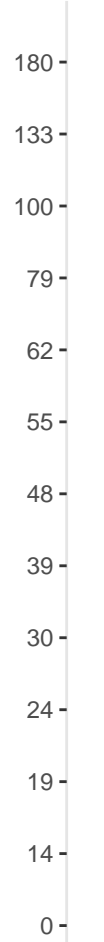


MW indication



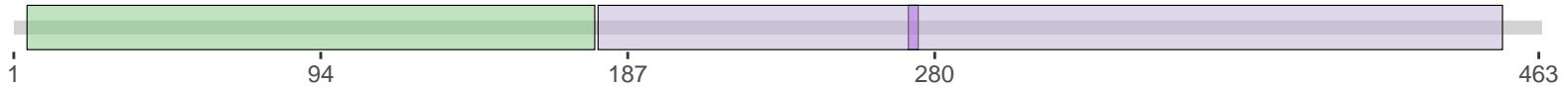
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01154 Hydroxymethylglutaryl-coenzyme A synthase N terminal
- PF08540 Hydroxymethylglutaryl-coenzyme A synthase C terminal

Protein sequence:

ALDSCYKSLCKGKYENLEGRGFSDDAAVFNVHSPYKLVKQSTARLQMFDFIRNASSIDESAKEKLAPFSLSLTGDESYGSRDLKRVSWQVAKPEYDEKWKATLIPKQVGMVYASLVAFAFLNKHSSLAGQRVILFVYGGSLTATMFSLRLENGQHPFLSNAAVMVDEKLRKRHEFTPEKPVETMIMHEHRYGGKDFVTTKDGSLAPGTYLLEVDKSKYRFYAKFAENGLANGP

NbL14g00590.1 PGR5-like_protein_1B_chloroplastic [MW = 42.73 kDa]

No. of times detected



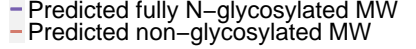
log(intensity)



Values from



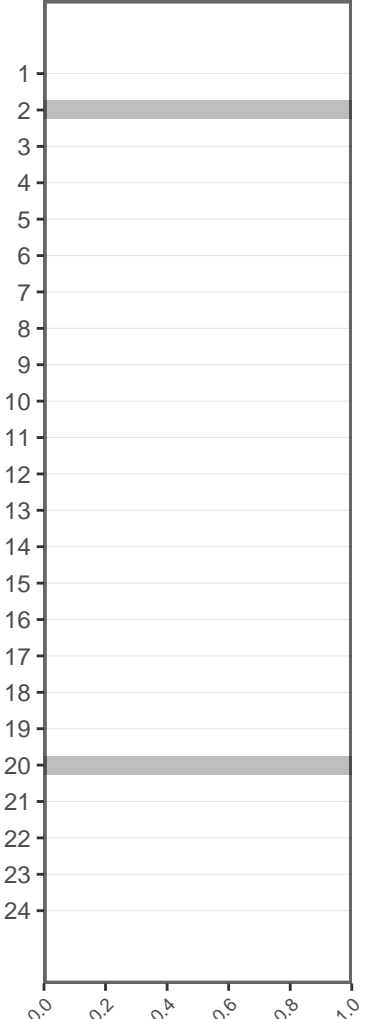
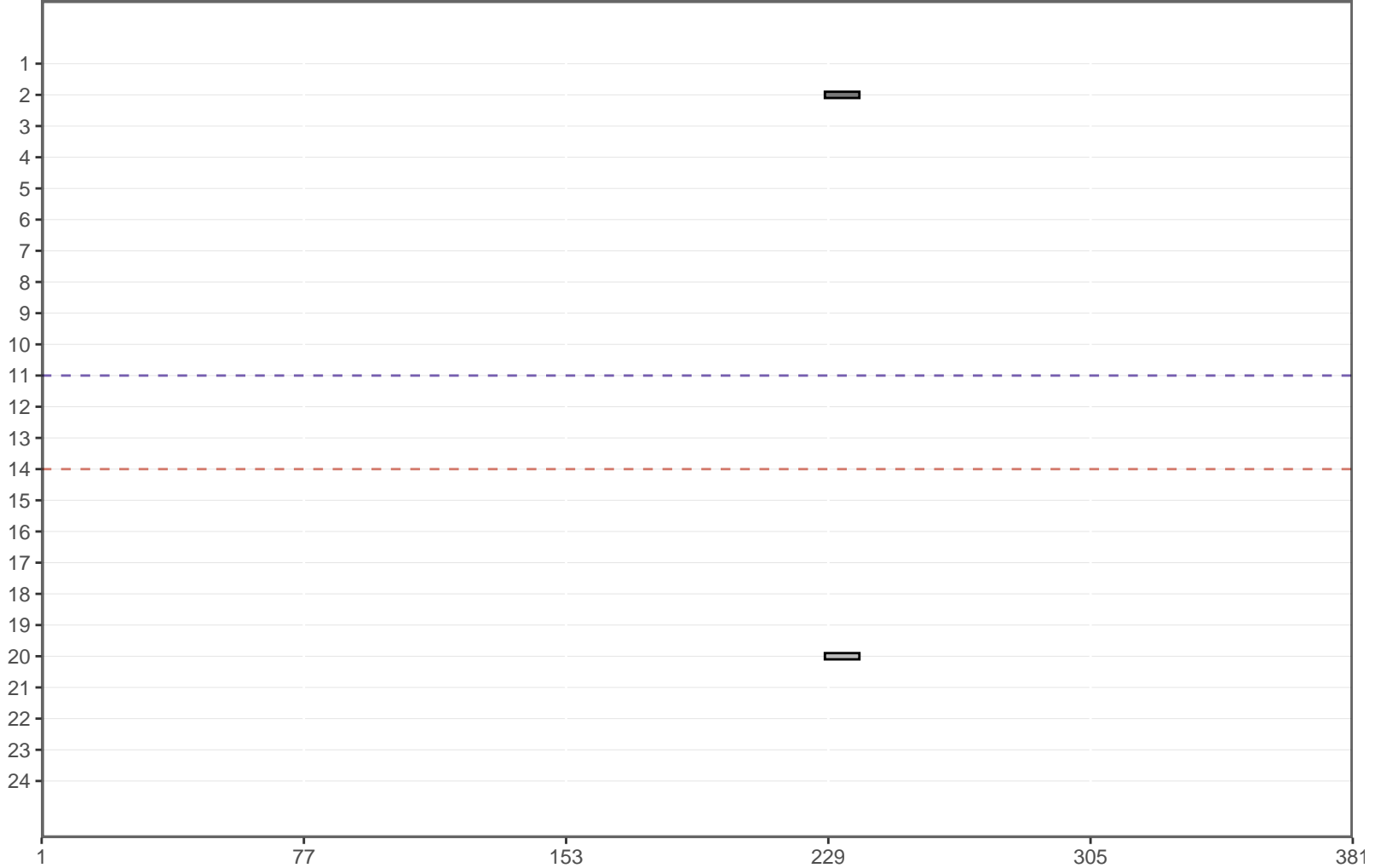
MW indication



Molecular weight



Gel Slice



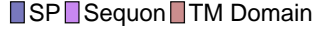
Protein length



Pfam domains



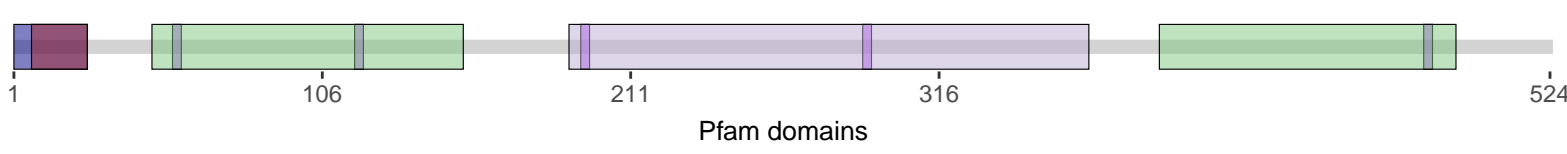
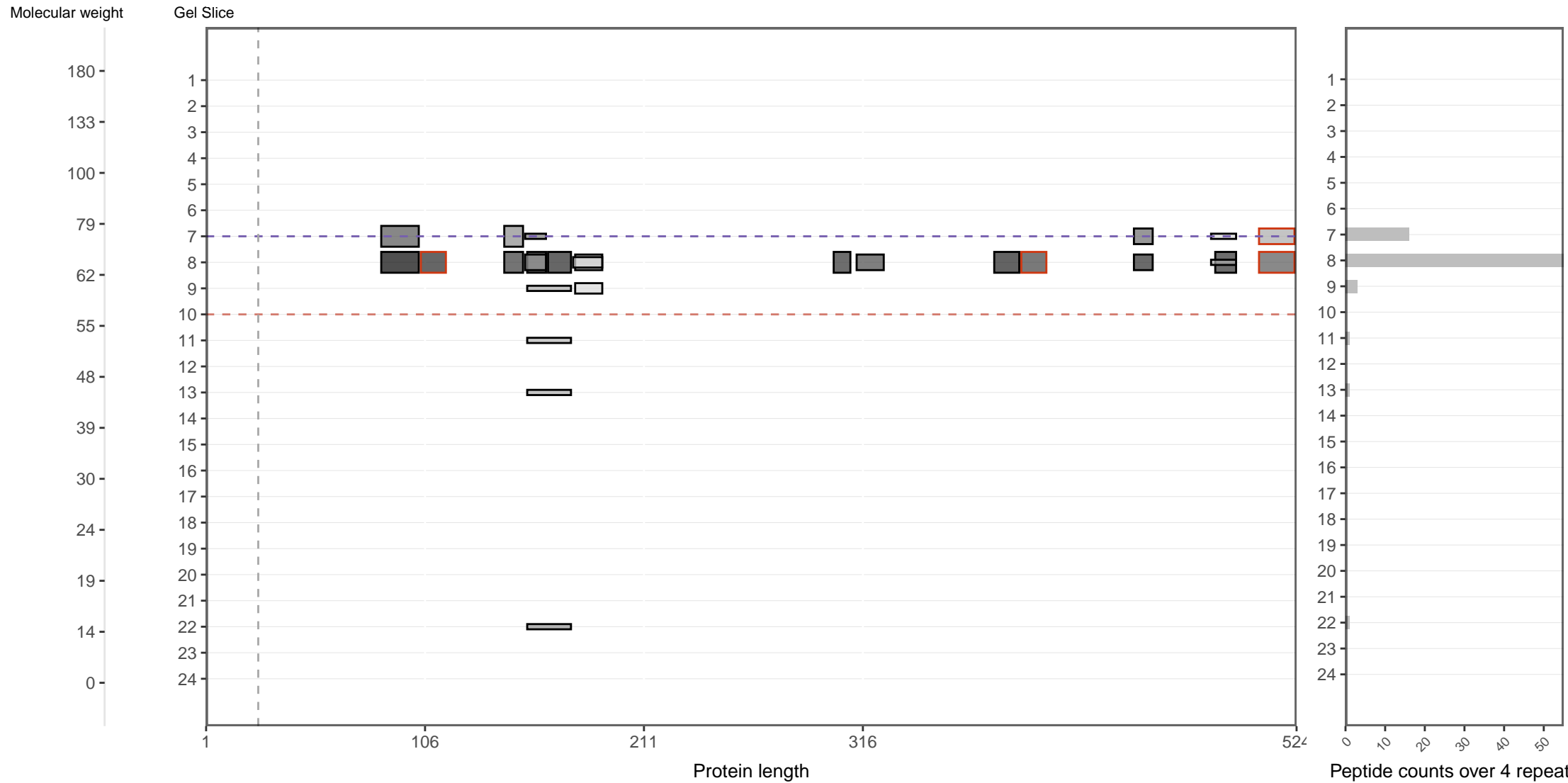
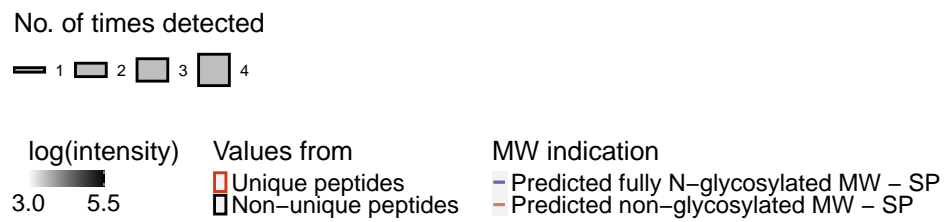
Pfam Description



Protein sequence:

NLKEELMVEGSSVWMLSTDEGKFLKASMAVYVGNPIMTQKEYDKLHKMLKRDGSDVVEGPRCGLRSRKVYSDLSVDYKMLFLNVPWVVALGLFFLDYITGFETIYLELPEPFSFIFTWFAALPULVLSFTTNVVKDFLILKGPDPDGGTENASFGTILSISGGSTNKKIKDGGGDTLVYDSDTRLITPEGSSA

NbL14g00420.1 protein_disulfide-isomerase-like [MW - SP = 56.03 kDa]



Pfam Description

- SP
- Sequon
- TM Domain
- PF00085 Thioredoxin
- PF13848 Thioredoxin-like domain

Protein sequence:

INFIETSPIMALDDKPENGAFVSHFHSPPGDKVFLFLNFTMDLDFKSKYYDLAASVYKGEANFLFGDAETGKRALEYFGLNTDGVPLFVLMADGTYVQRHVGPDLAAWVKDFNDGKLPKPKSQPIPEVNNPEPKVMVAETLEDMVFKSGKDLLEFVRLGGKYCEEFPALDEIALGFENDADVLAIKIDGTENDIPRERFEVGGFPTLMISTAGLSLRFDPGNRTKEAVIEFRGTNRTPAPSDFAKSLTASEHAGTDSMKDEL

NbL14g00410.1 calcium-dependent_protein_kinase_1-like [MW = 57.73 kDa]

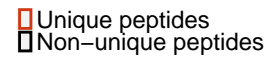
No. of times detected



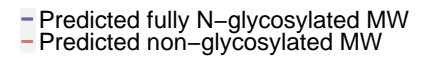
log(intensity)



Values from



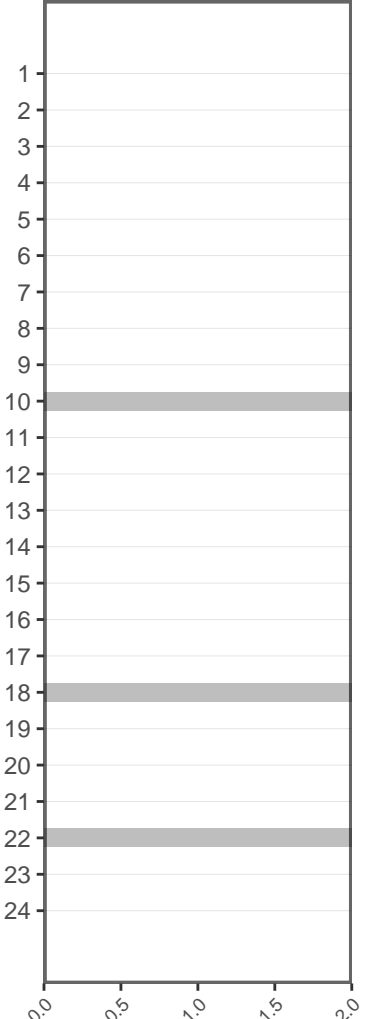
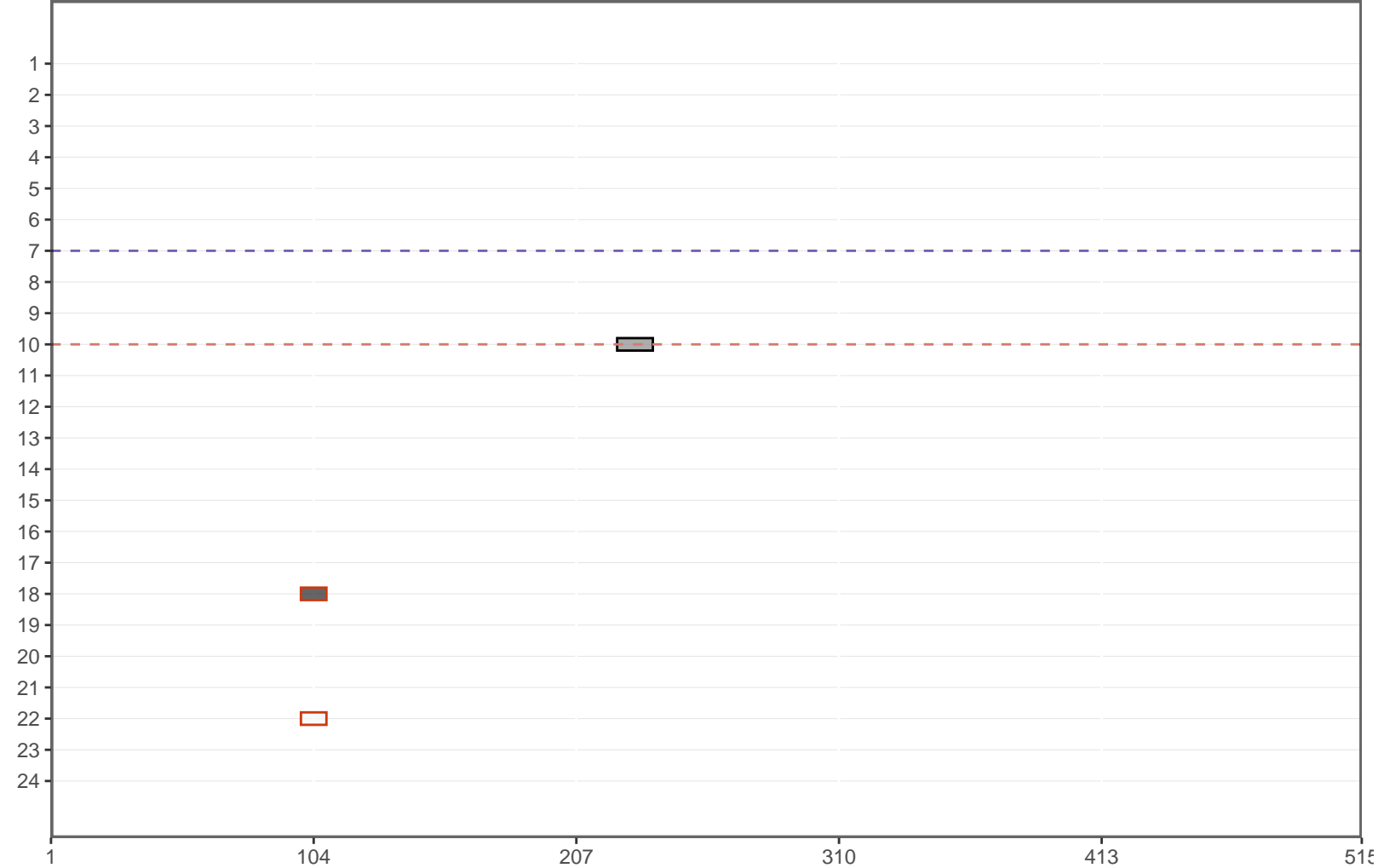
MW indication



Molecular weight



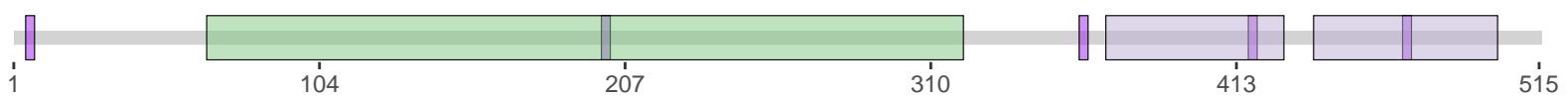
Gel Slice



Protein length

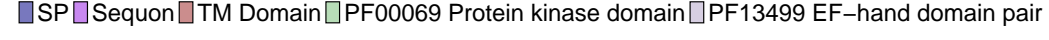


Peptide counts over 4 repeats



Pfam domains

Pfam Description

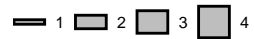


Protein sequence:

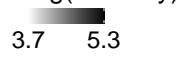
ADIVSAGVLYLLSGVPPFYGENDGGIFDVALRQHGDFSDPWPVPSVSSAKDLVKKMLRQDPRERLSAAEVLNHPVMREDDGASDKPLDIAVLRMKGFAMNKLKVALKVAENLSEEEIQLKEMFKSISDTDSGGTTFYEELKAGLTKMGTSLSESEVRQLMEADVDGNGTDHLEFDTATMHNMREREDHLYKAFEFYDKKSGVYTMDELEHALKKYNSDEKTKIEIAEVDTDNDGRINYNDEFAAMMRKGNPDPVNNRRRRI

NbL14g00380.1 V-type_proton_ATPase_subunit_E-like [MW = 27.67 kDa]

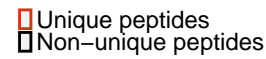
No. of times detected



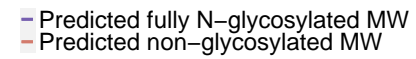
log(intensity)



Values from



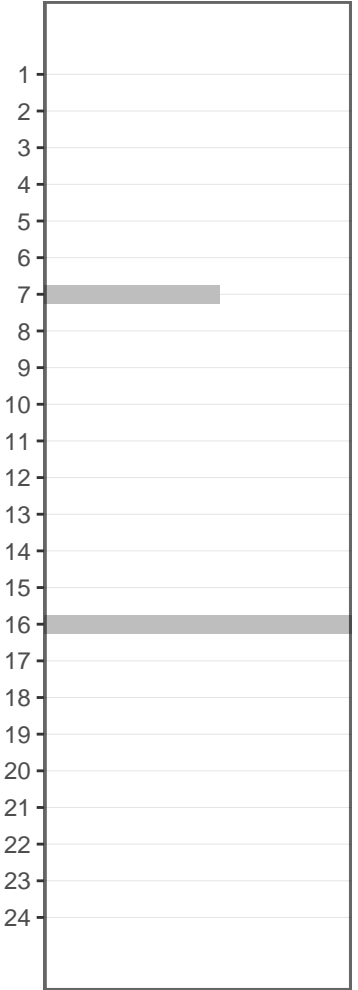
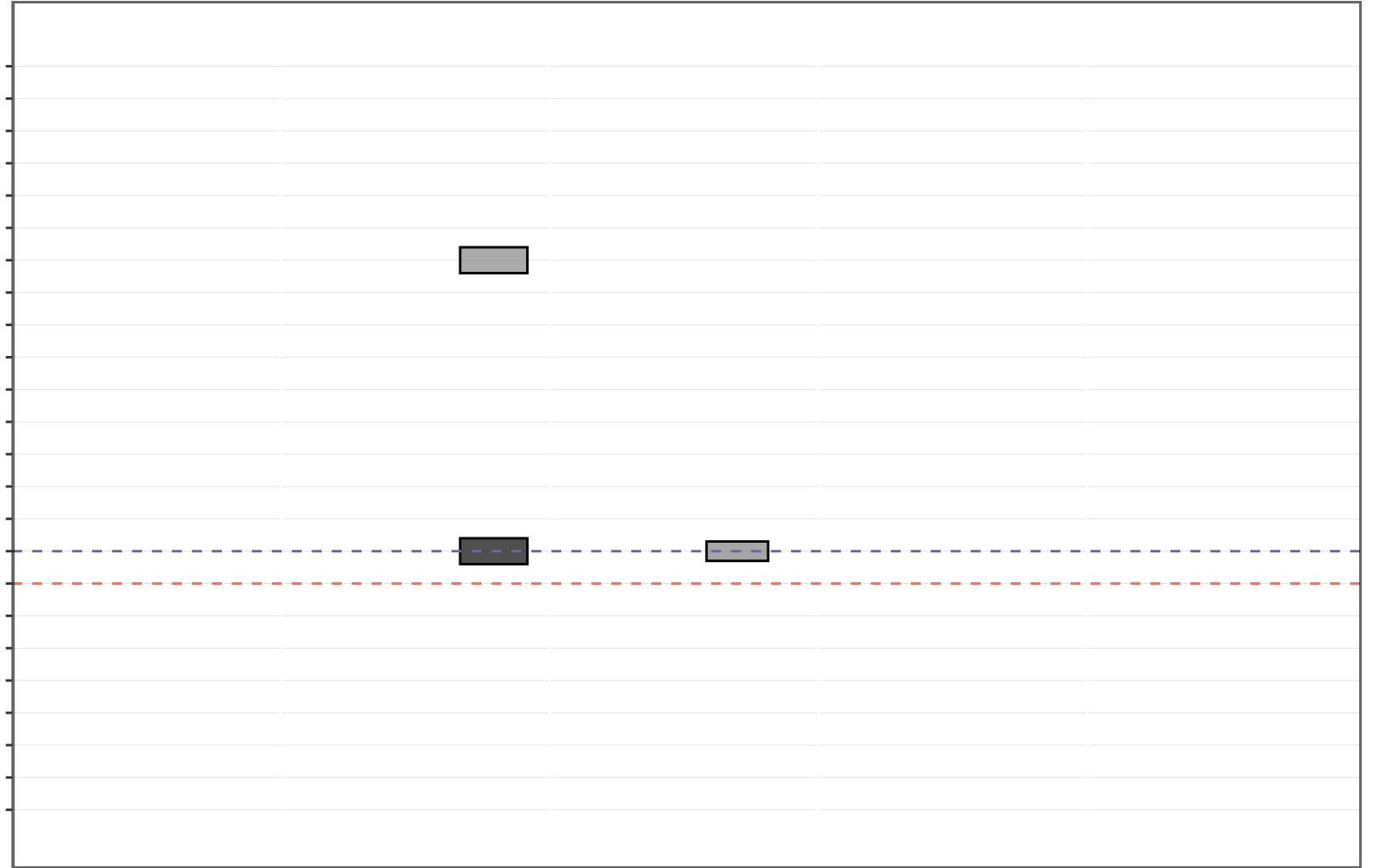
MW indication



Molecular weight



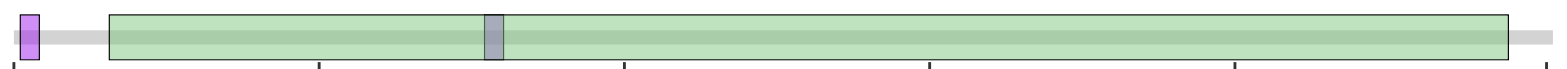
Gel Slice



Peptide counts over 4 repeats

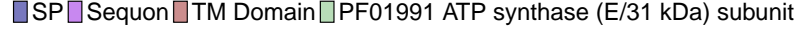
1 49 97 145 193 242

Protein length



Pfam domains

Pfam Description



Protein sequence:

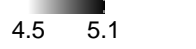
INELVLEVLPIHODSYKKLHNLVDSLLRLKEPVLRLGRKHVHLVEHVLDAAKEEVAEKANVHAPENVDHILPAPSHNNMHPGSSGGVWLABRDGKIVGENTLDARLEVYFRKLFPERKGLFGGVTA

NbL14g00280.1 uncharacterized_LOC109214535 [MW = 25.8 kDa]

No. of times detected



log(intensity)



Values from



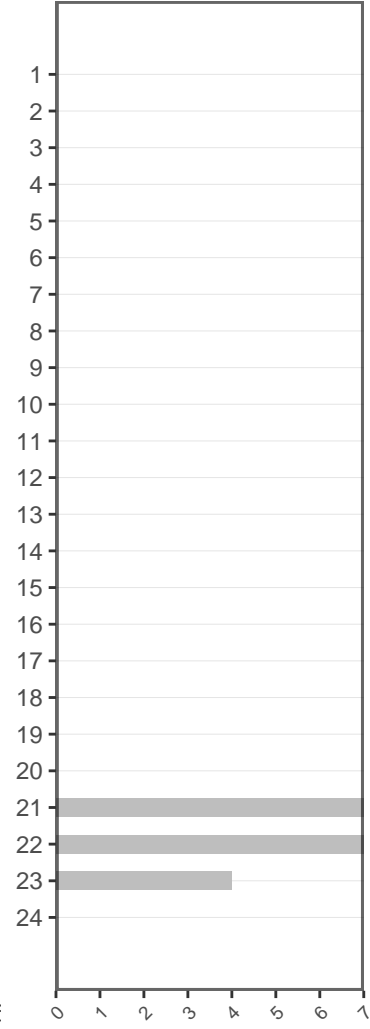
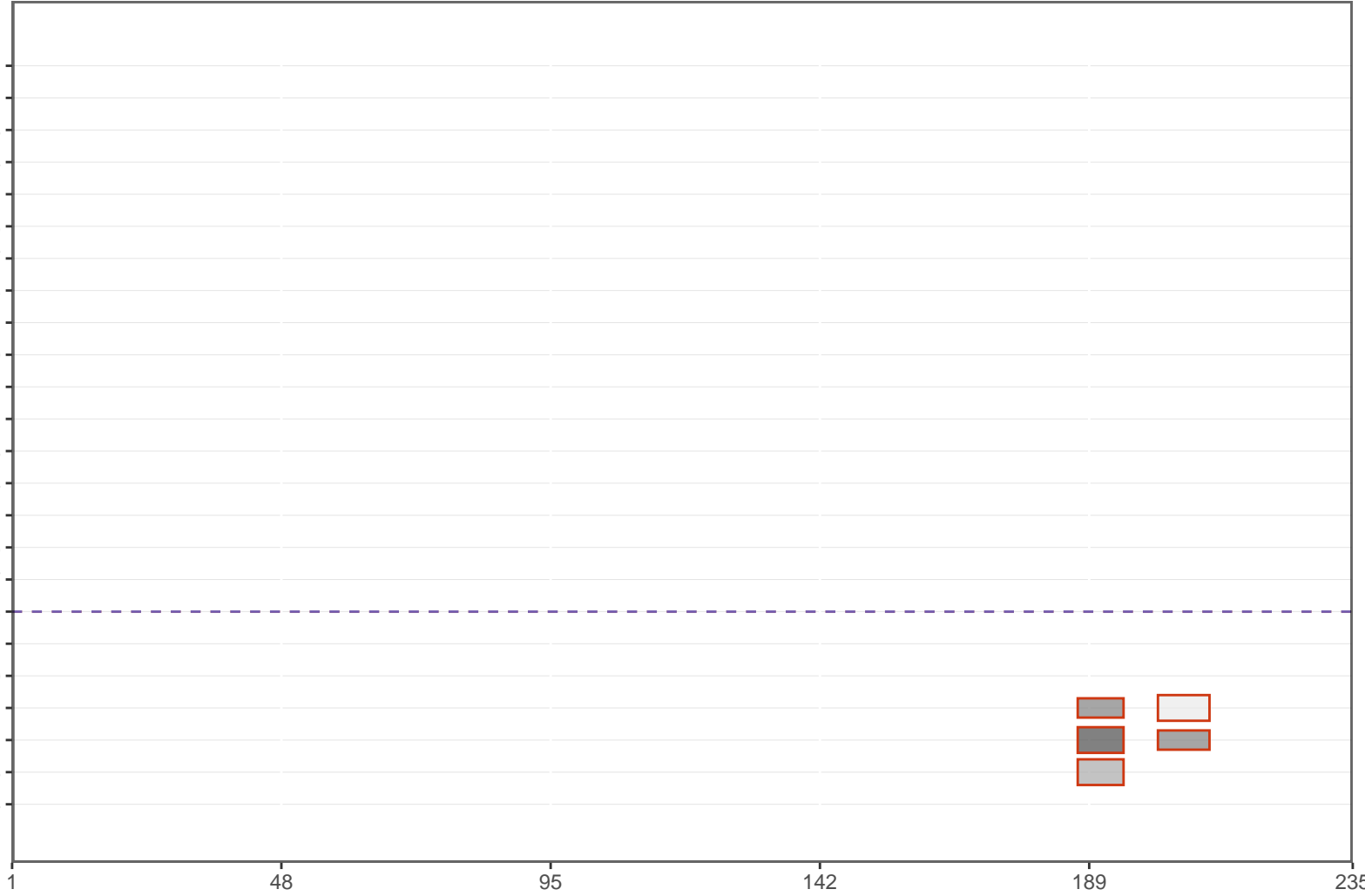
MW indication



Molecular weight



Gel Slice



Protein length

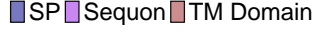


Peptide counts over 4 repeats

Pfam domains



Pfam Description

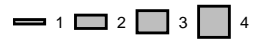


Protein sequence:

IGRGCSDCKQATPTSNREIVS6SLPKK6S6WREGGREGSIWKQPLYPYRVGVAAIFAL6LLVWYFLANRPS6T6GNS6HQK6TAA6EAPRTFF6SR6P6M6VAK6AD6PK6RTP6V6GEE6ID6ILL6GG6I

NbL14g00210.1 luminal-binding_protein_4-like [MW - SP = 70.4 kDa]

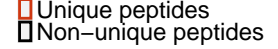
No. of times detected



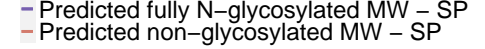
log(intensity)



Values from

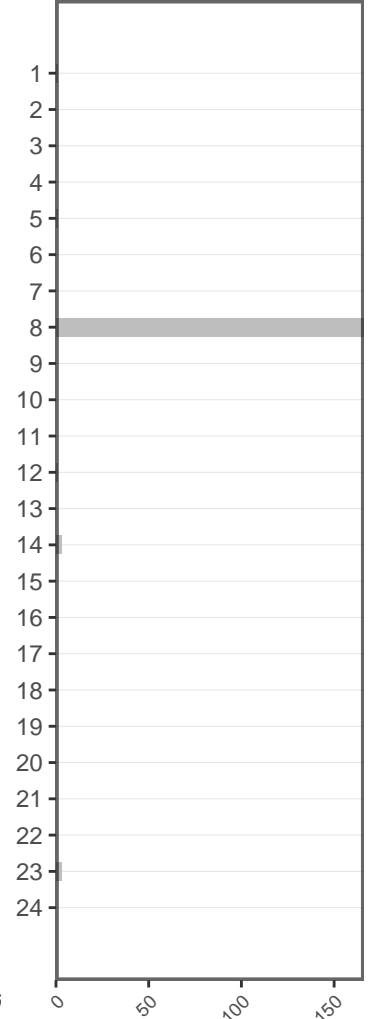
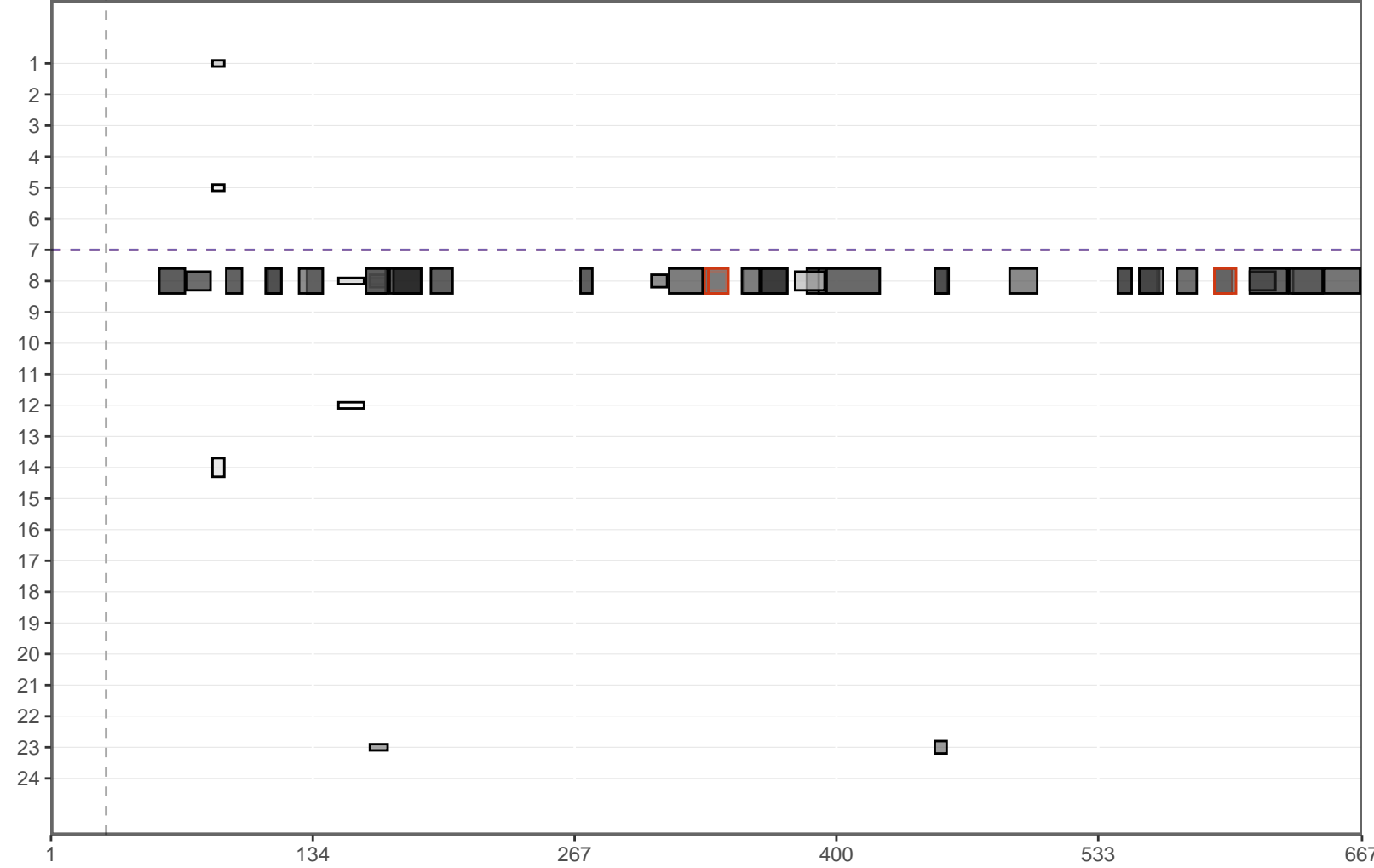
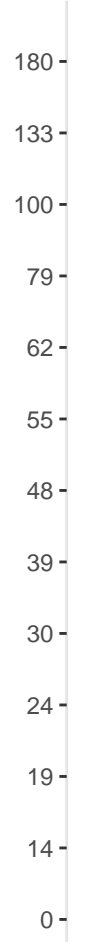


MW indication



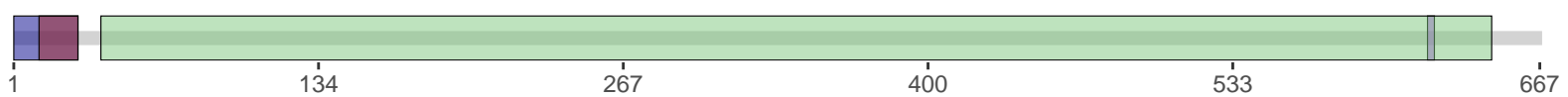
Molecular weight

Gel Slice



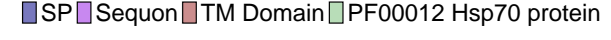
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GTDSEPLTRARFEELNDFKKTGMPKVKKAMEDAGLEKNQDEIVLVGGSTRIPKVDGLLKYDFEGKEPKGVNPDVAWYGAUVDGGLSGEGGDETKDLLLVAFLPLTGLIETVGGVMTKLIPRINTVIFPTKKSQVFTFYDQDQTTVTSVYEGERLTKDGRLLGNFDLTPPPAPRGTPEQVTFEVDANGILNKAEDKGTGKSEKITTNDKGRLSQEEIERMVRAEAEFAEEDKKVKERIDARNGLETYYNKKNGINDKDLADKLEVDKEKIEIYKAEALVLDNC

NbL14g00110.1 beta-carotene_isomerase_D27_chloroplastic [MW = 32.98 kDa]

No. of times detected



log(intensity)



Values from



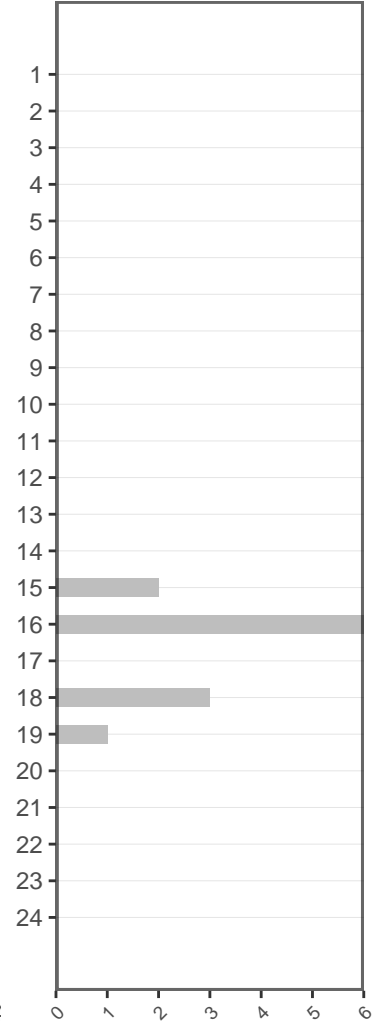
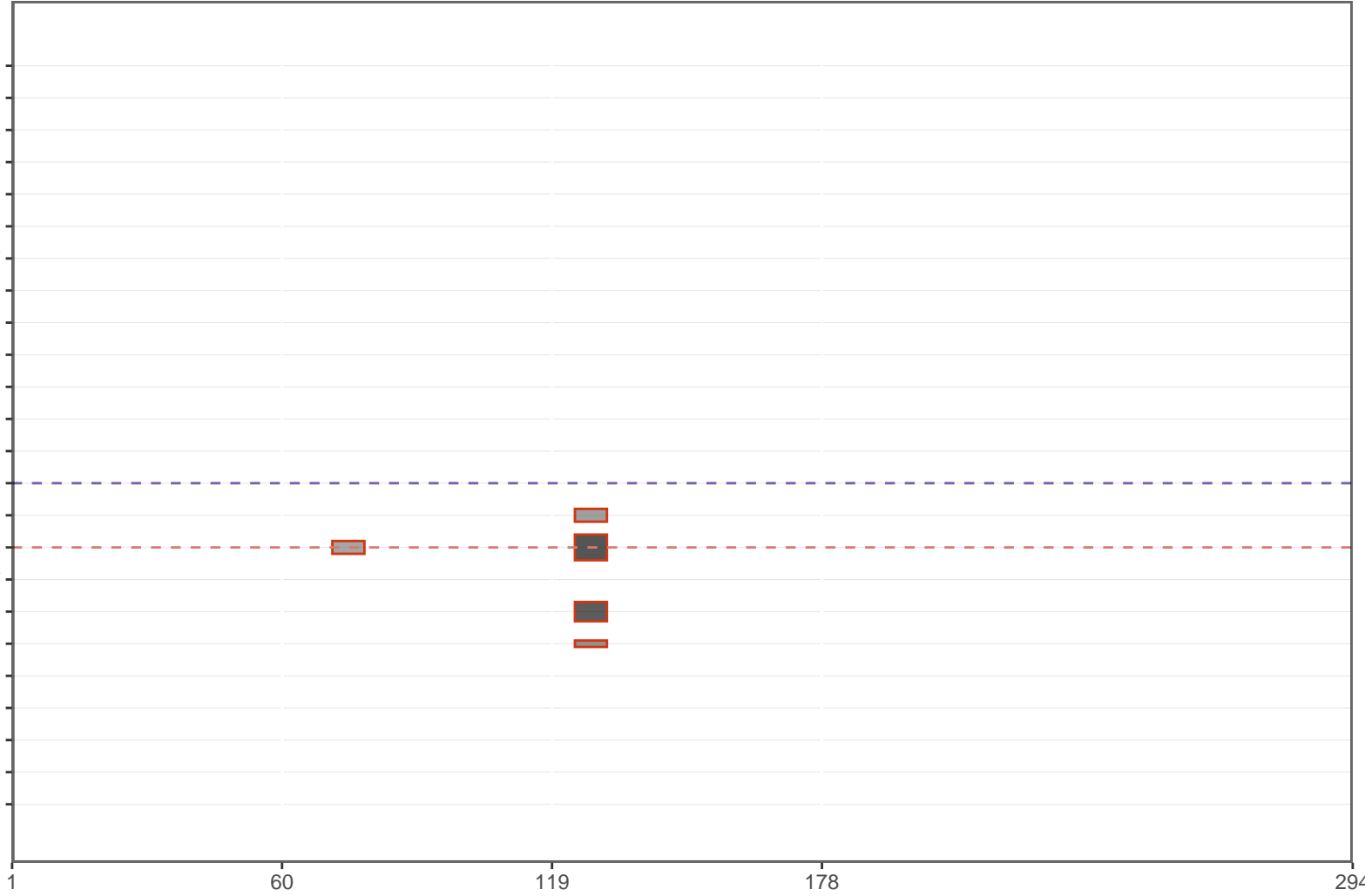
MW indication



Molecular weight



Gel Slice



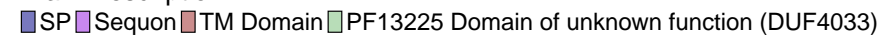
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILMSLLPPGAPAGQLLETAFLPFRVFERKLFPPRTKWAAEFNAITVFFFVLIQFSEVVEVGGVWQKSGVHKKGRYLENSGGVGMGVNMGKIPFGDFFTFEGLPLTMNPNFEDMSGEMVYGGVPPPFEEQPAVAKQPLADICTIANPSSSFGPKLQA*

NbL14g00070.1 photosystem_I_reaction_center_subunit_N_chloroplastic [MW = 18.06 kDa]

No. of times detected



log(intensity)



Values from



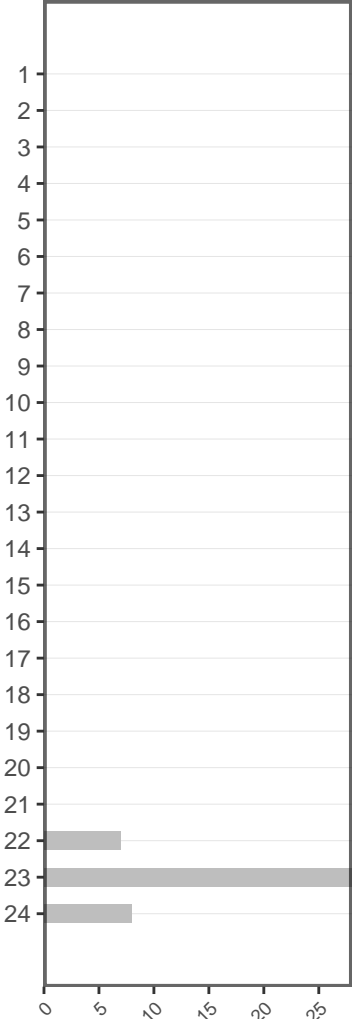
MW indication



Molecular weight



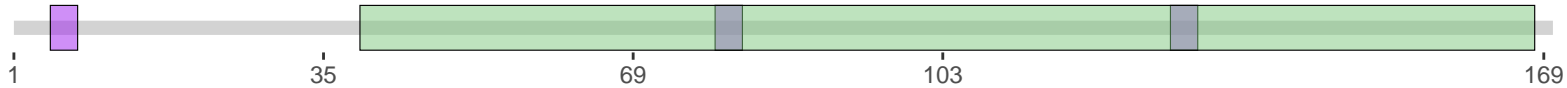
Gel Slice



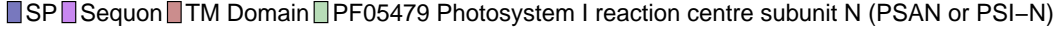
Protein length



Pfam domains



Pfam Description



Protein sequence:

FTAASSNSANAGVDDHLEKSKANKELNDKRLATSGANFARAYTVQFGTCKFPENFTGGDGLAKGKVPFRISDOLALECEGGKDKYKGGSNVFWWV

NbL13g27700.1 40S_ribosomal_protein_S9-2 [MW = 23.05 kDa]

No. of times detected



log(intensity)



Values from



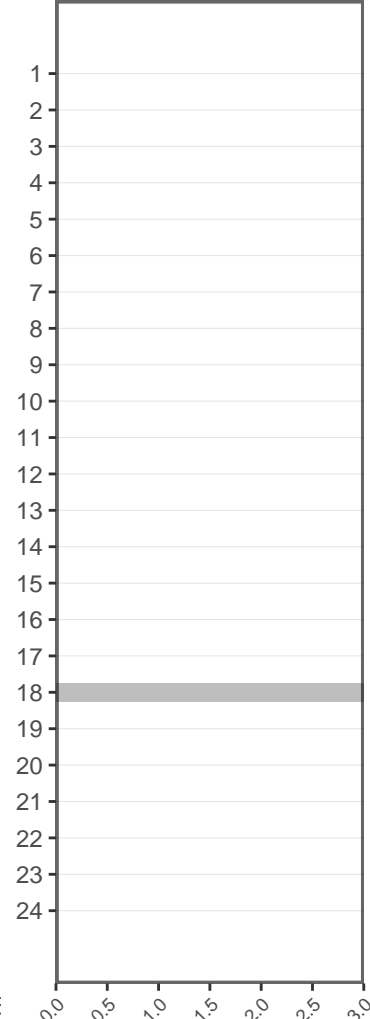
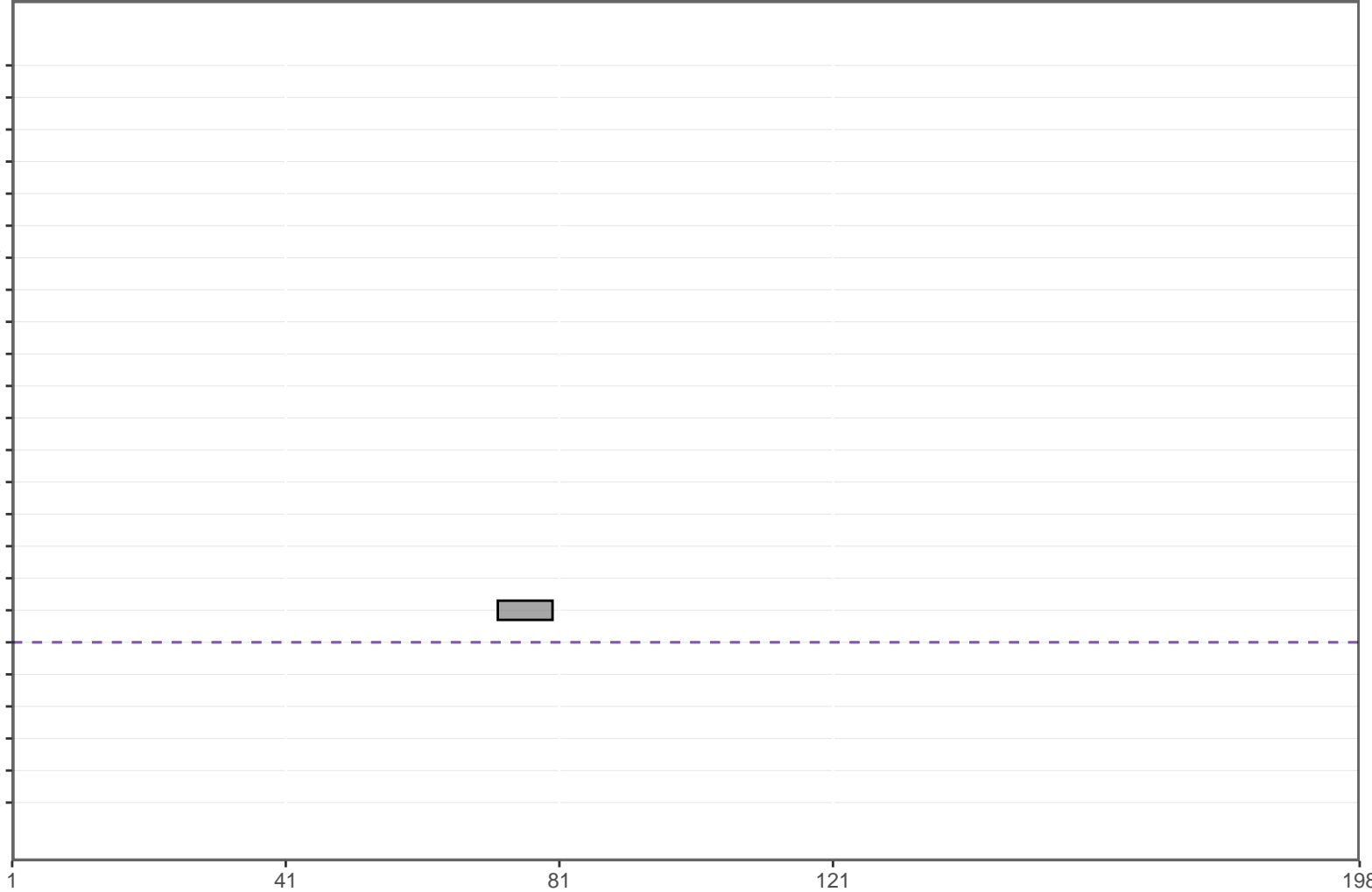
MW indication



Molecular weight



Gel Slice



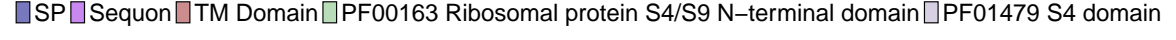
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SLLDESQKLDYVLSLTVENFLERRLGTLVFKTGMAKSHHARVLRQRHVRGRQVWVPSFMVRLDSQKHDFSLTSPFGGGRPRGRVRRKRNQKAAKAKASGGDGDDEE*

NbL13g27530.1 isoleucine--tRNA_ligase_cytoplasmic [MW = 135.17 kDa]

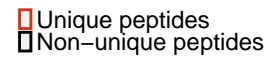
No. of times detected



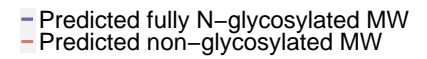
log(intensity)



Values from



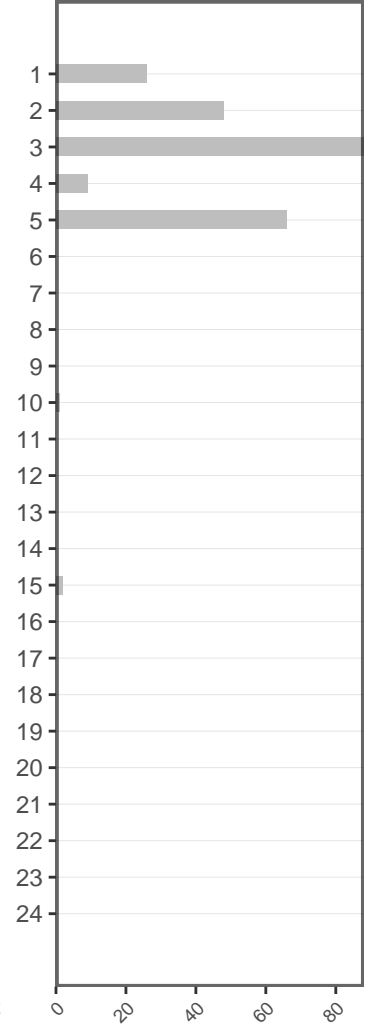
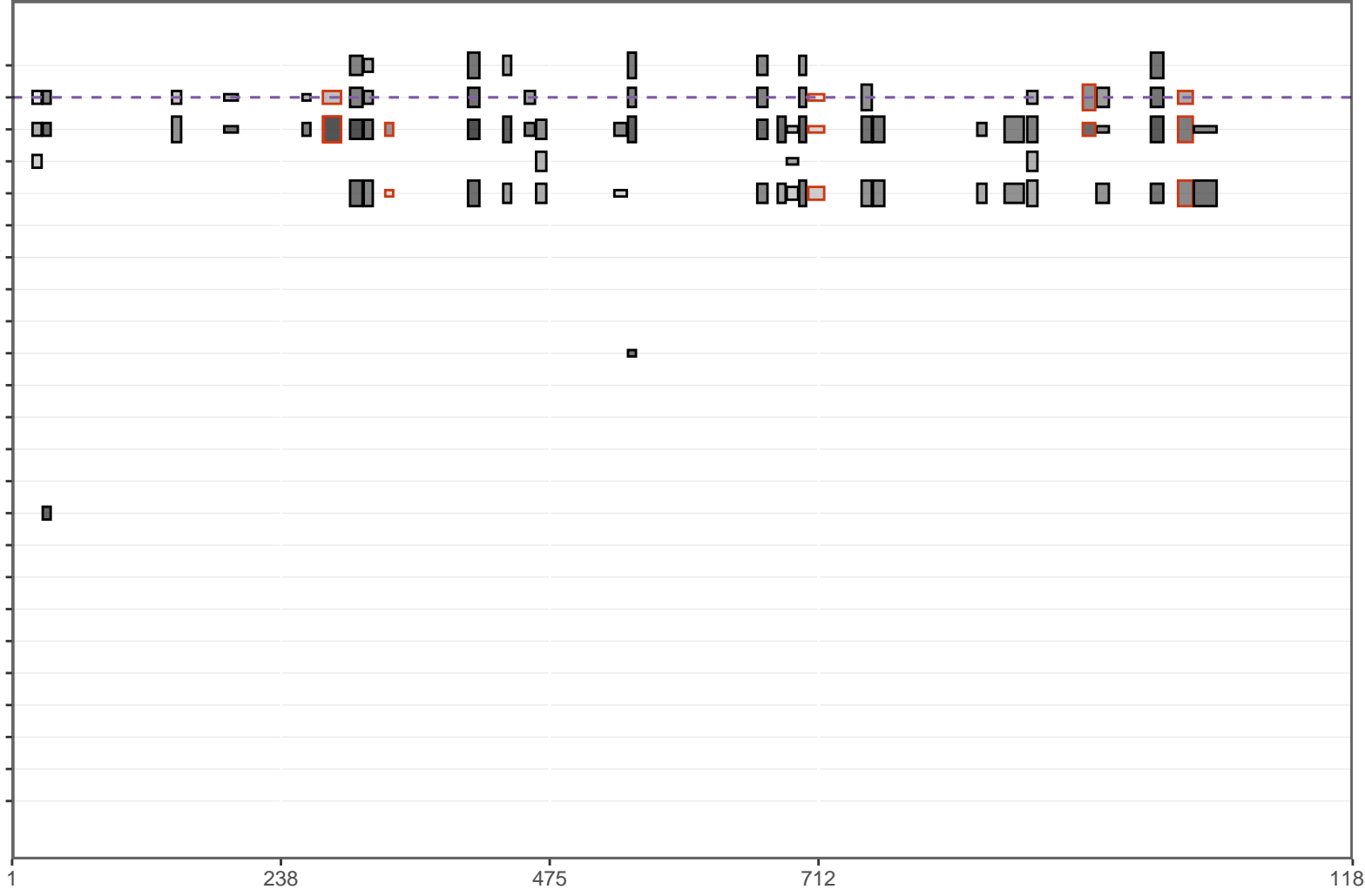
MW indication



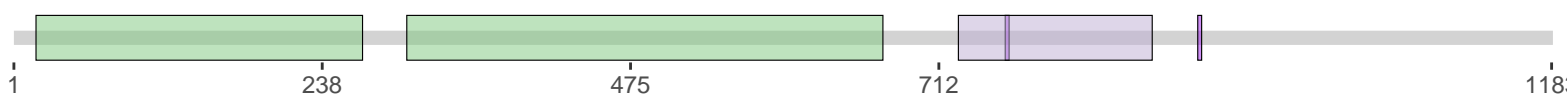
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

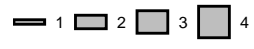
- SP Sequon
- TM Domain
- PF00133 tRNA synthetases class I (I, L, M and V)
- PF08264 Anticodon-binding domain of tRNA ligase

Protein sequence:

PFENVLFFENFPGHFVAEGLDGTGRFYMVLTMLGSLTALFGKPAFRNLINQGLVAEDGKMMKRLKNNYQDQSEVINDYGDALRLVYLNISPVVRAEPLRFKPKGQVFAVYKDFLPWYVYVFLVQNAKRLIEDGKPIPTDQKTLGSSNVAEDGWNATGSLVHFVQEMDARLNTVYVPLKLFQNLNINVRFNRKRLKGRTEGDCRITALSTLYVYVLTSGKAMAFITPFFTEVLYQNLKRVWEGSESHYQSGVPEVEGKRWERIEQSNVNRMMITDCLARNRERHNK

NbL13g27510.1 transcription_initiation_factor_IIF_subunit_alpha [MW = 59.25 kDa]

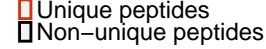
No. of times detected



log(intensity)



Values from



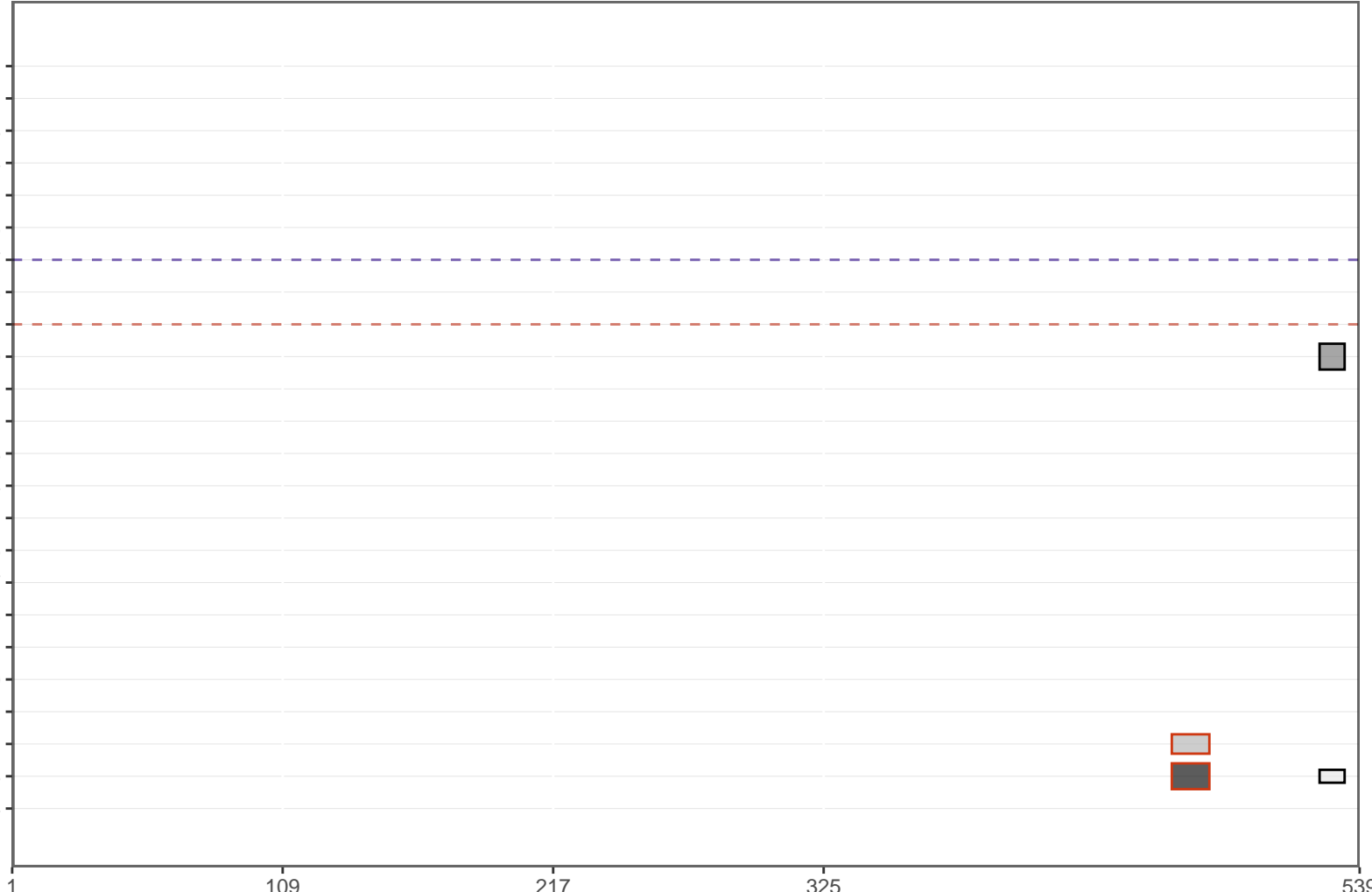
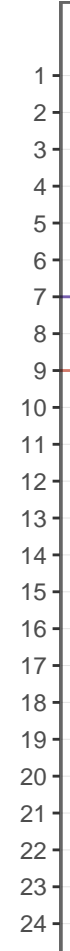
MW indication



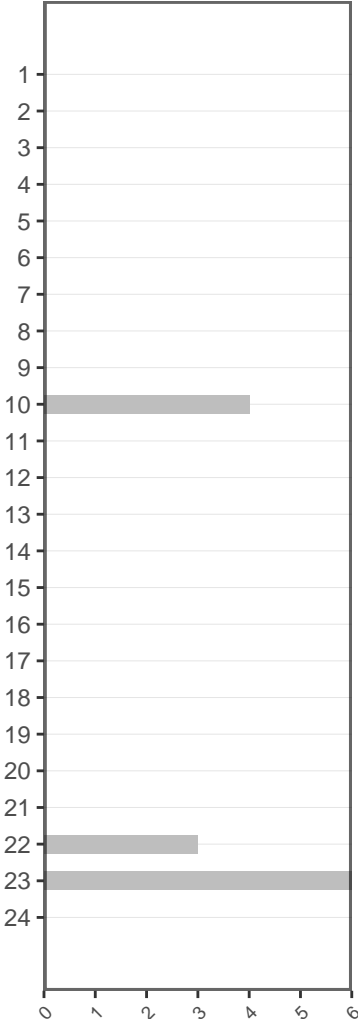
Molecular weight



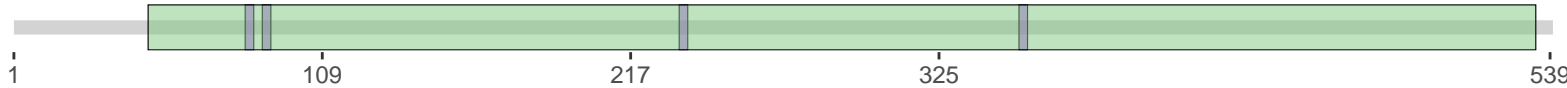
Gel Slice



Protein length

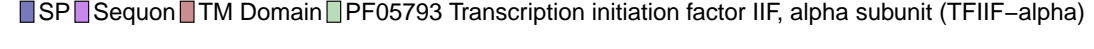


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GLNKRGAADDEEGPRGGDLDDDDKEKDDWHEHEIFTDDEAVGNDPEEREDLAFPIRPPPEIKGDDDEDEGGEGGLKSGKELKLLGKANGLNEGDAEDDDDDDDTEEDSEPLAPKPKPEAKPEEFDTS6SPKPSASGPTRTGTPPTSASAKTKRKAADDGKPTNGAPLKKVKTETDAKPKGKDETPSTAKNSVLPKGSPPSKTAPSPATGPIVTEEEIRAVLLGRKPVTTGDLVSGFSGRLKCKEKEDKAAFDVLRKISKIKGTGTGTGKVVLRERTNQ

NbL13g27500.1 fumarylacetoacetase [MW = 49.23 kDa]

No. of times detected



log(intensity)



Values from



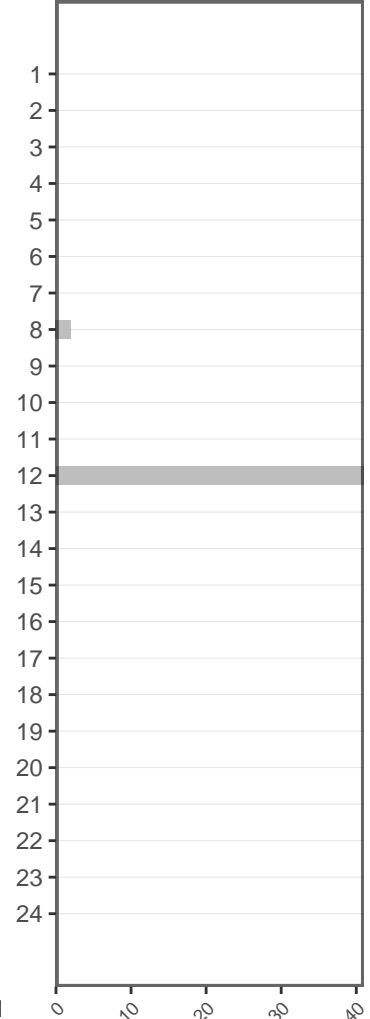
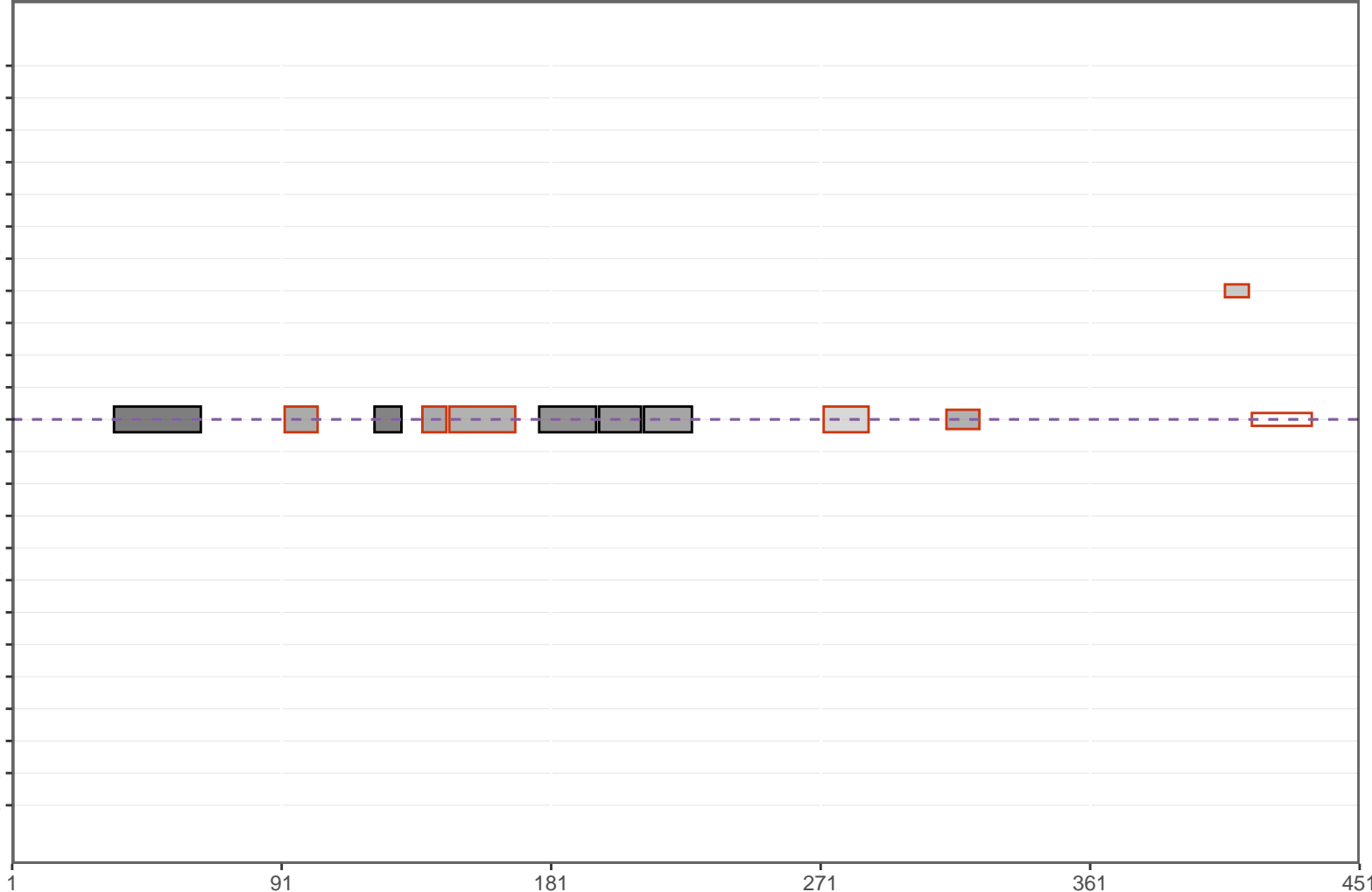
MW indication



Molecular weight

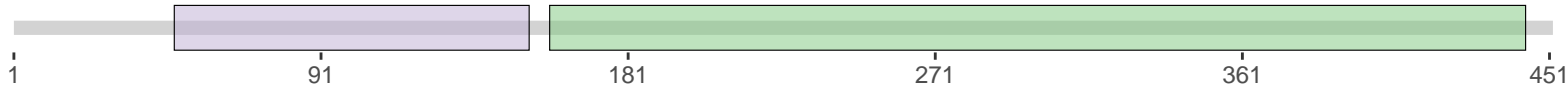


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MPTGNLSAPYFGPERKLDFELEMAAVVGFQNELGTTVDVNEAADIHFGLVLMNDWBSARDIGAWVEYVPLGPFGLGKSGFTTSPWVLTDALEFPAGEAPKQNFPSPLTLEKTSRNYDLSLELVKPSGGAADSCVTRSNFNHLWTTTQGLAHTINGGQNLKRPDGLFOTGTRSGPEPEYGGLELWNGKPLKFGGTRTRTFLEDDGDEVFFFGYGGNGKVKVGFGRCSGKIVMPQ

NbL13g27390.1 cysteine_proteinase_inhibitor_1-like [MW - SP = 9.84 kDa]

No. of times detected



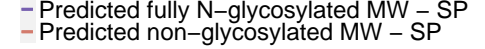
log(intensity)



Values from



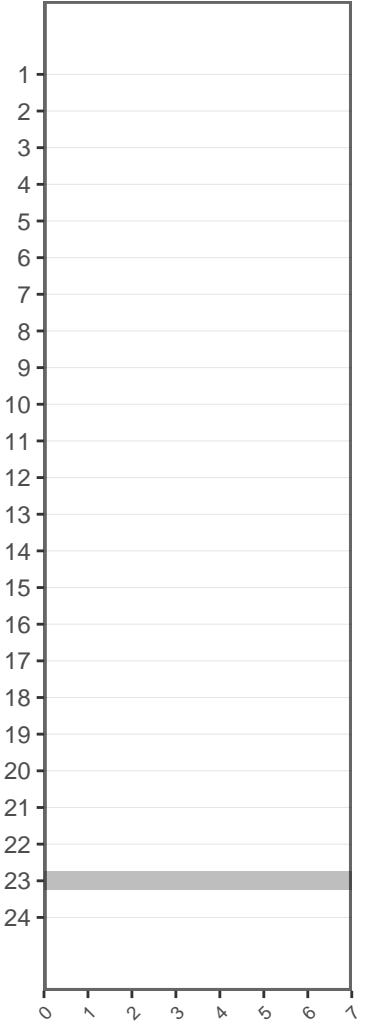
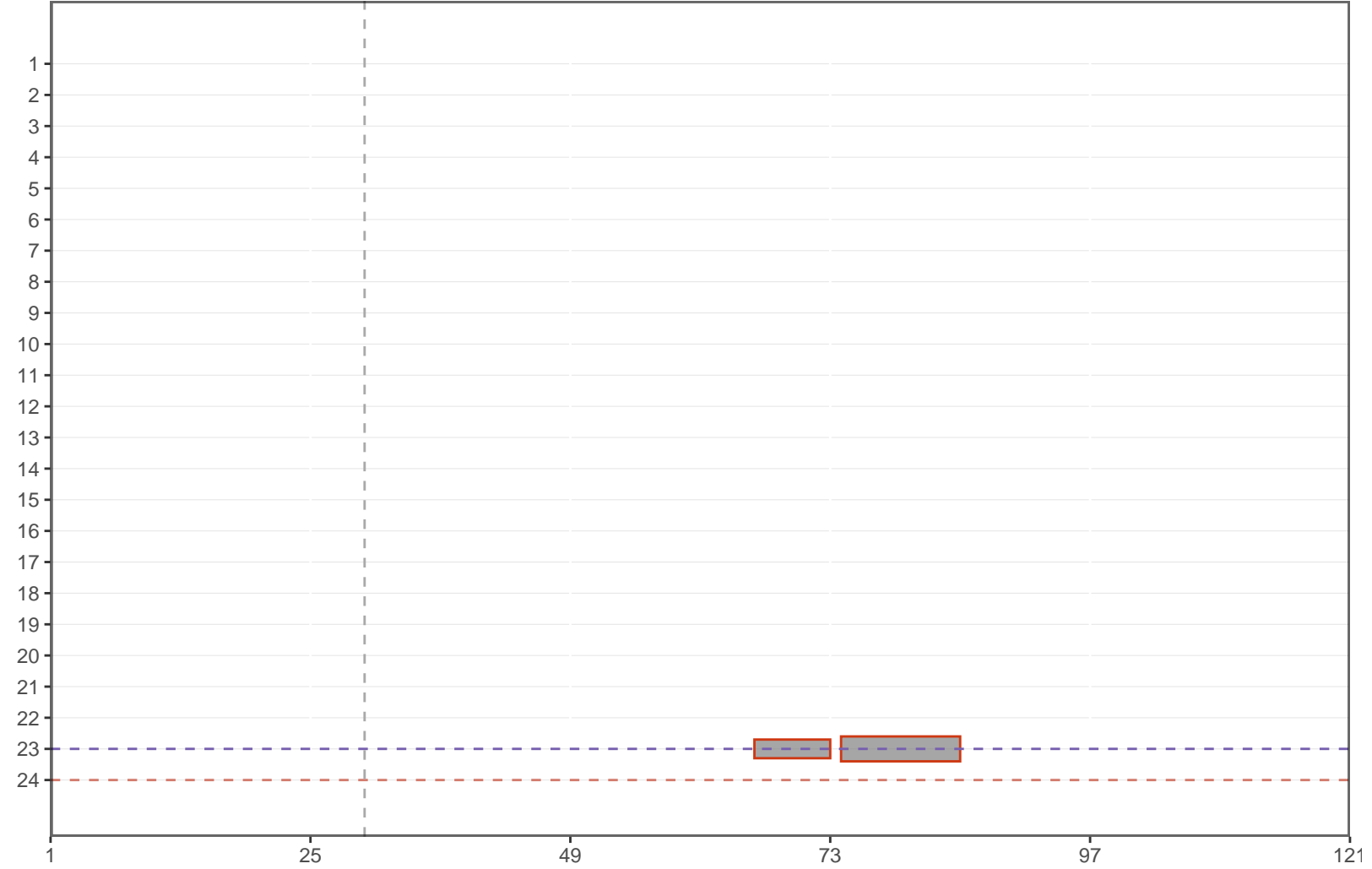
MW indication



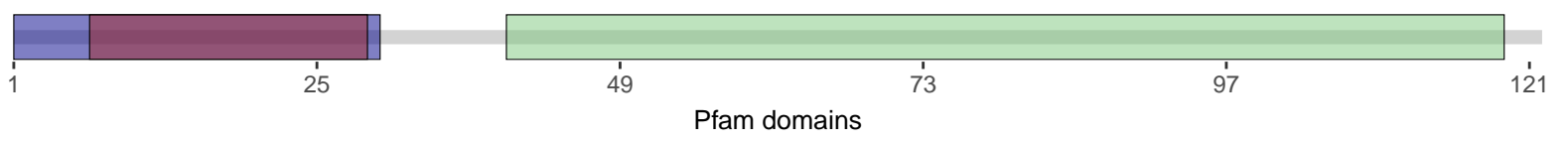
Molecular weight



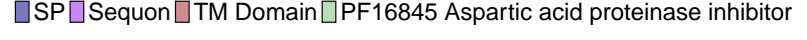
Gel Slice



Protein length



Pfam Description



Protein sequence:

AIGQFVNEHNKAEGTKLEFGNIKGETQVIAGTNYRLVINAEDGGVHKYLAVAWDPKPEKWKLTFRKMP

NbL13g27370.1 inositol_monophosphatase_3-like [MW = 29.49 kDa]

No. of times detected



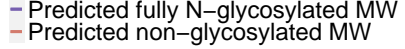
log(intensity)



Values from



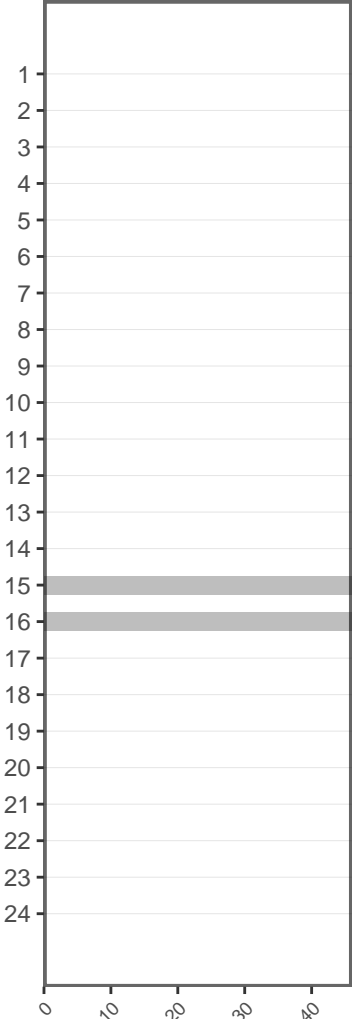
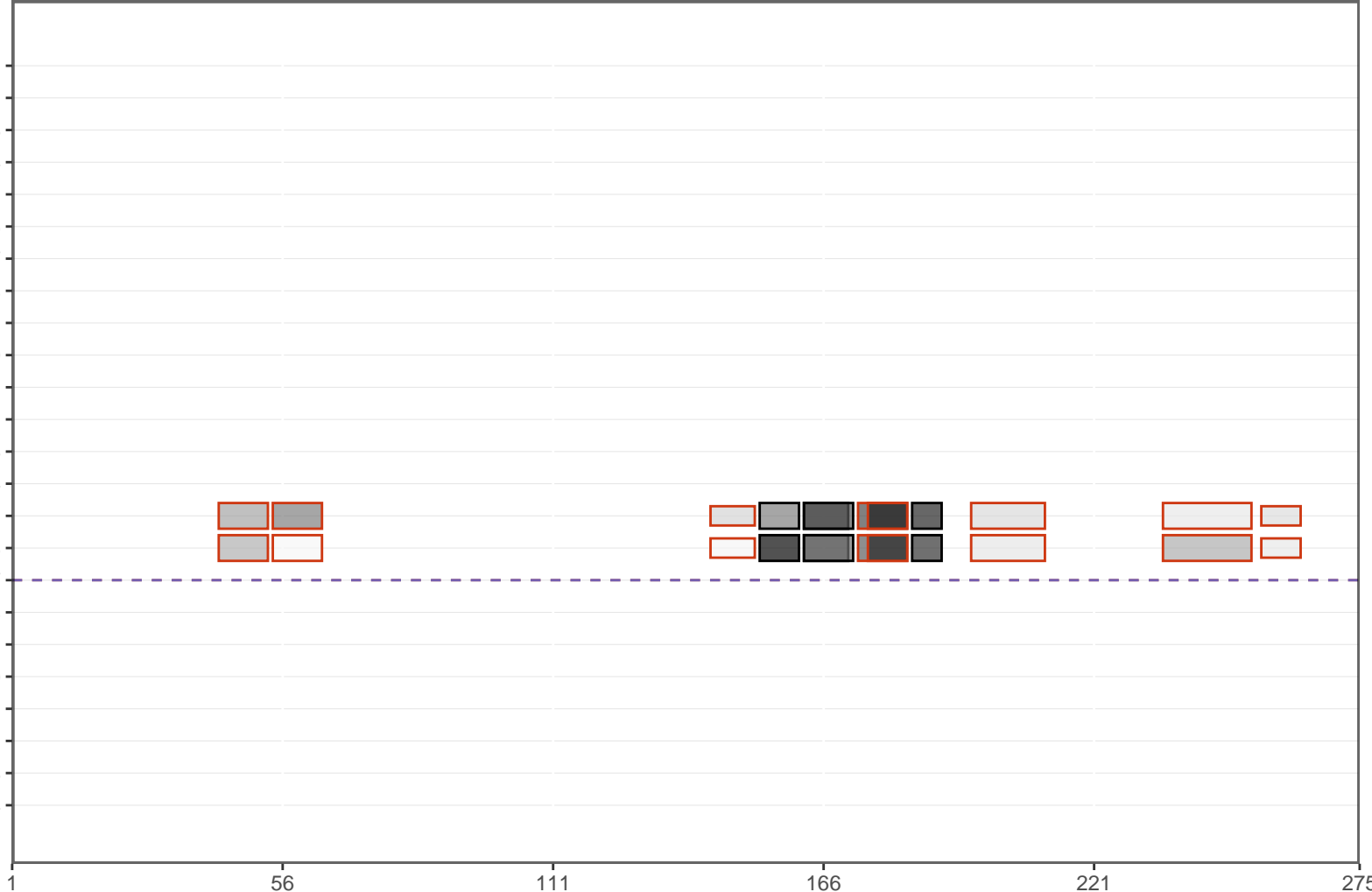
MW indication



Molecular weight



Gel Slice

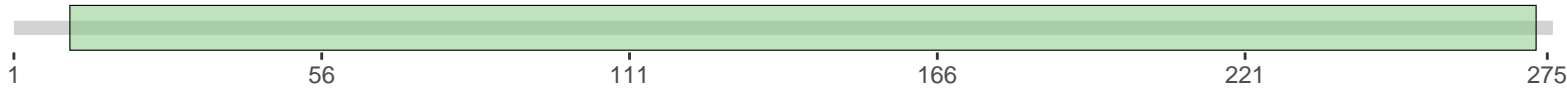


Peptide counts over 4 repeats

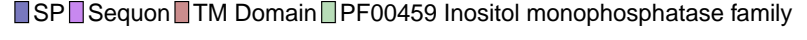
Protein length



Pfam domains



Pfam Description



Protein sequence:

/GVVYYPIDELFTANGKGAFLNGKPKVSSQSELVKAALATEAGTRDKLFLDATTGRINSLFKVRLRMGGSCALNLGGVAGGRLLDFVLELEFGPPWQVAGAVIKVKEAGGFVDFPSGSEFDLAARRVATNAHLKDAFKALKESEI

NbL13g27320.1 60S_ribosomal_protein_L6-like [MW = 25.31 kDa]

No. of times detected



log(intensity)



Values from



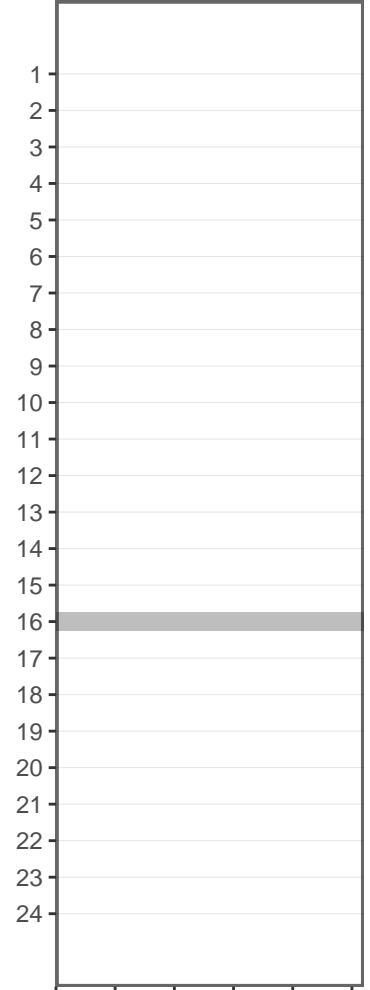
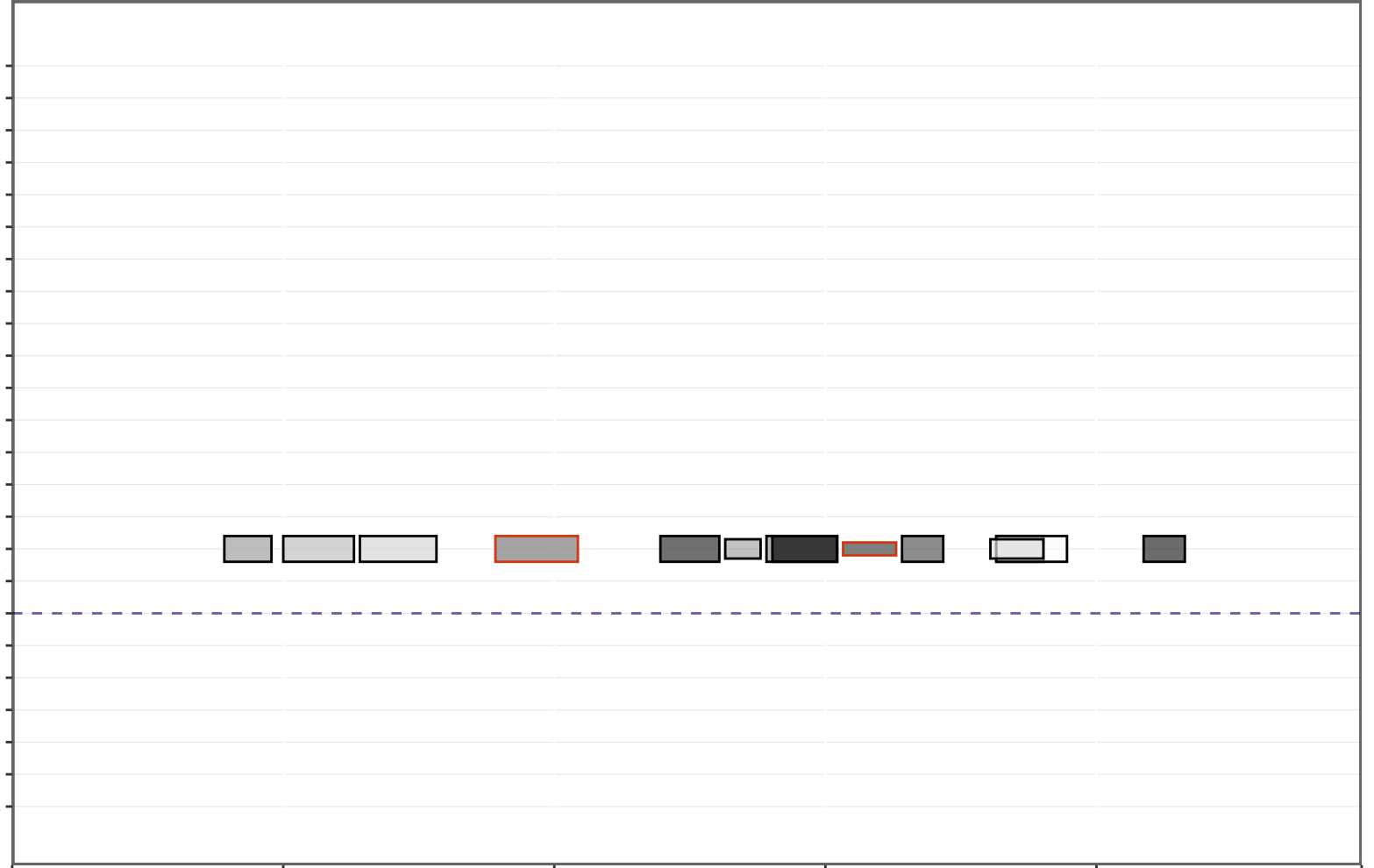
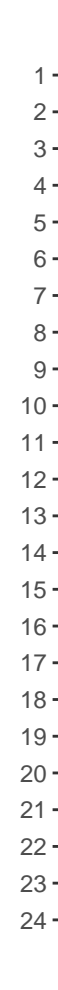
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

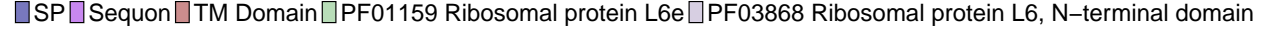
Protein length



Pfam domains



Pfam Description



Protein sequence:

VVFLKQLKSGLLLVSGFFKLVNGVPLRRVNGQAVYGTSTKVDVSGVSVKFDKDYFAKQVKEKGGKGGEGEFFEDKKEENNVPDQKKDDQKAVDEALIKAVEGVPELKAVLSARSLKSGMKAHPELVF

NbL13g27310.1 phosphoribosylglycinamide_formyltransferase_chloroplastic [MW = 33.19 kDa]

No. of times detected



log(intensity)



Values from



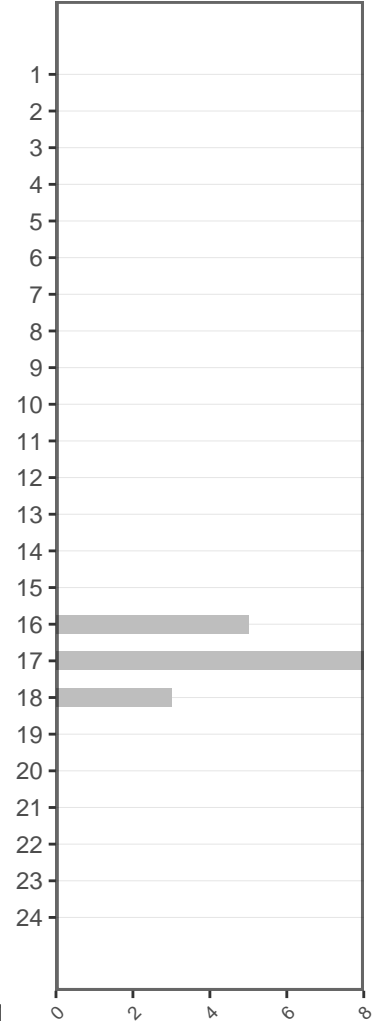
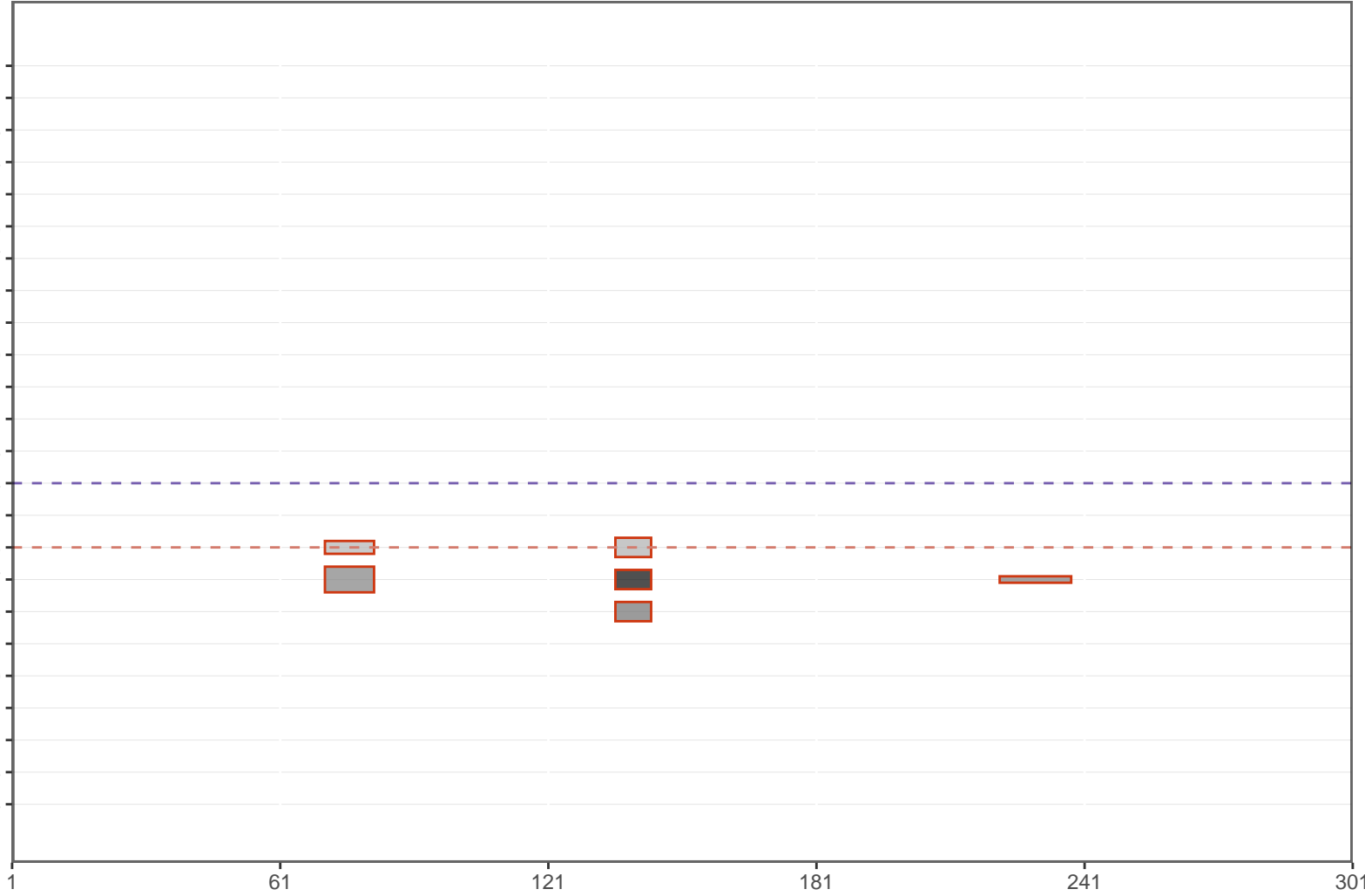
MW indication



Molecular weight

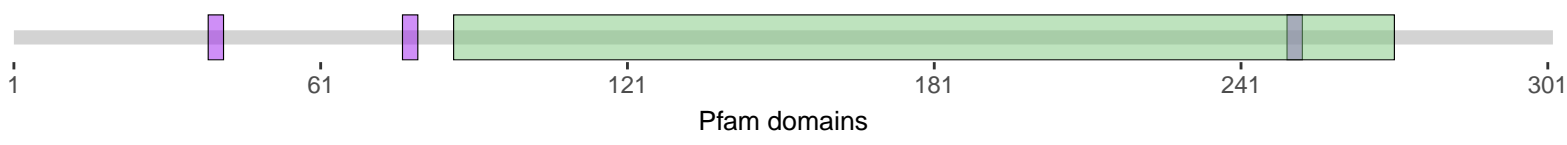


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam Description



Protein sequence:

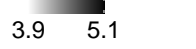
IPVILFPKAKDTFEGLSIEDLWHLRRTYNDIFLLAGYLUKIPTELWGAFFRSFENHPSELLPFGGKGYGKMKVKKAVASGARYSGPTHFVDEHYDTGRILAGRVVPLANDTADTLAARVLQEEHKLVVEVAALCEERWVREDDGVLIGSKEQPDHYK

NbL13g27280.1 acyl-protein_thioesterase_1-like [MW = 27.98 kDa]

No. of times detected



log(intensity)



Values from



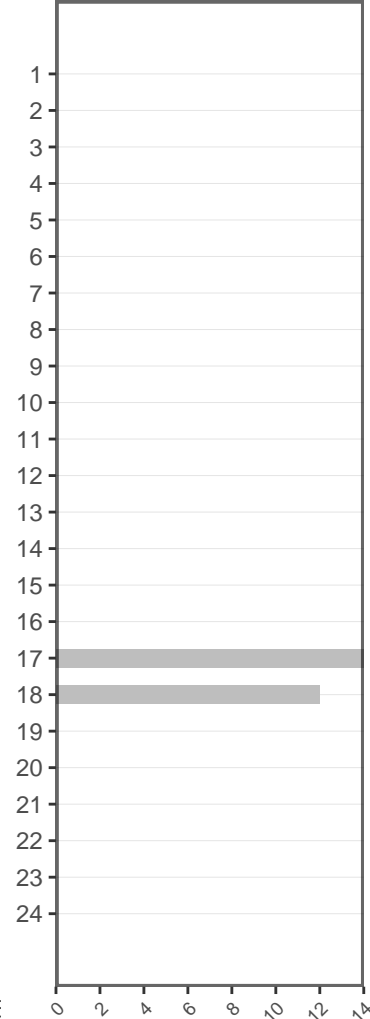
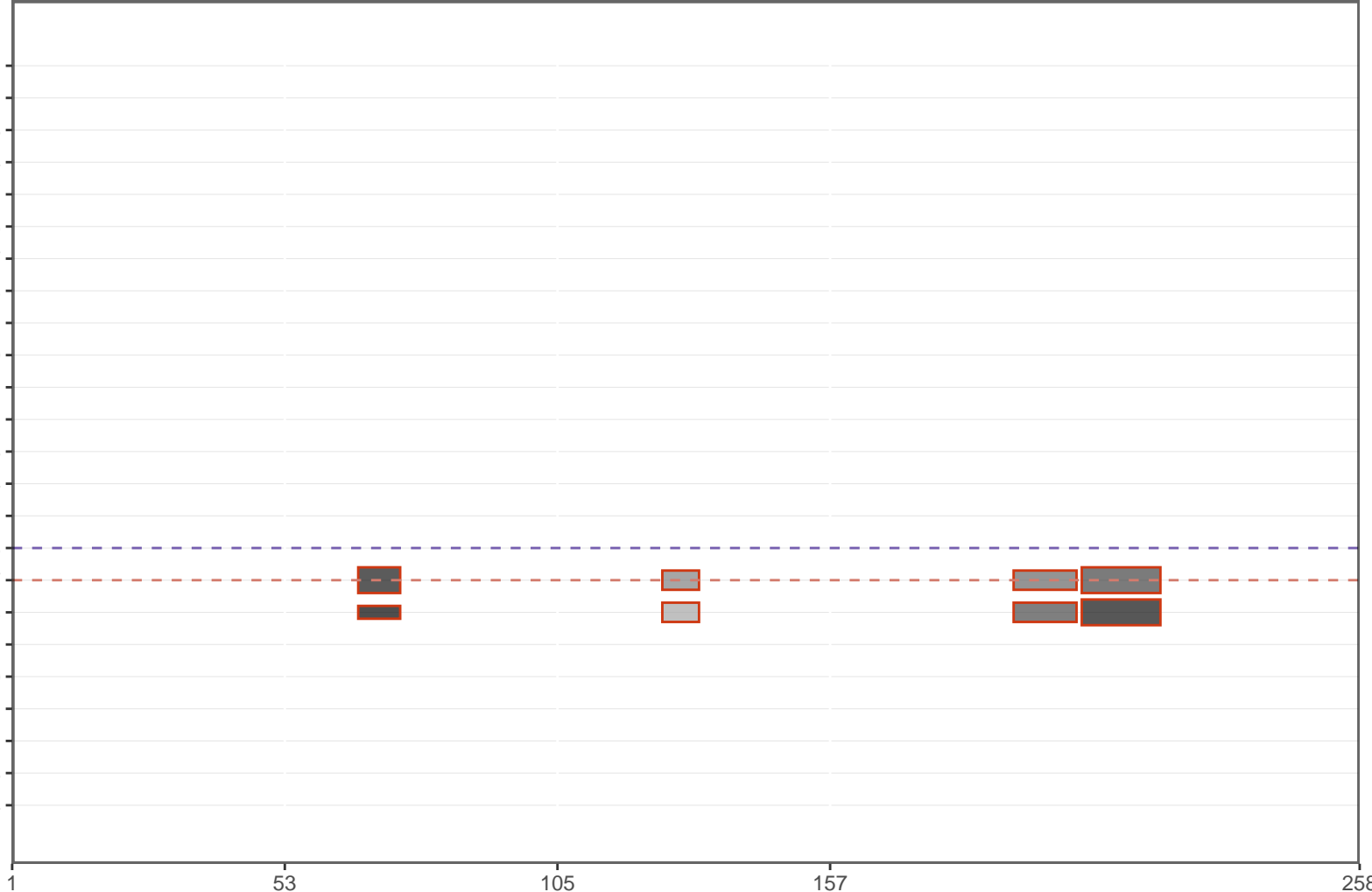
MW indication



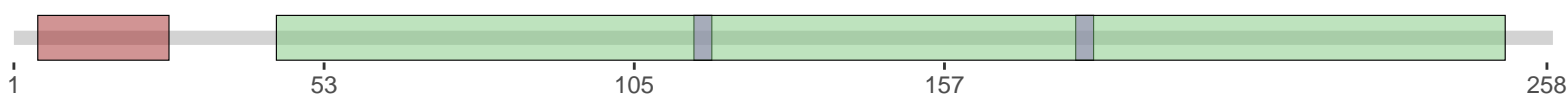
Molecular weight



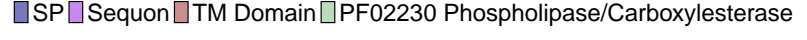
Gel Slice



Protein length



Pfam Description

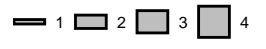


Protein sequence:

SGLLKVXNVIHMDKEIDAGTNPNNVFIGGFSGGALTLASVLLVPKTLGGGAIFSGVWVFNNSILEKGTPEAKKTPILWHSIGADKTVLFEAGGEGEPFLERAGMTDFEKAVPLAHNSINNEELKNLESGWIKTRLQNSK

NbL13g27150.1 UTP--glucose-1-phosphate_urydyltransferase [MW = 57.21 kDa]

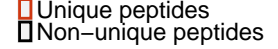
No. of times detected



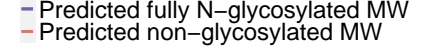
log(intensity)



Values from



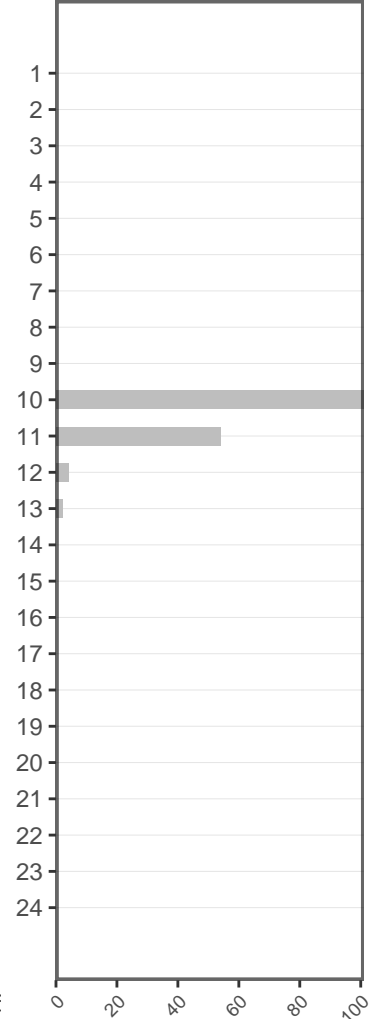
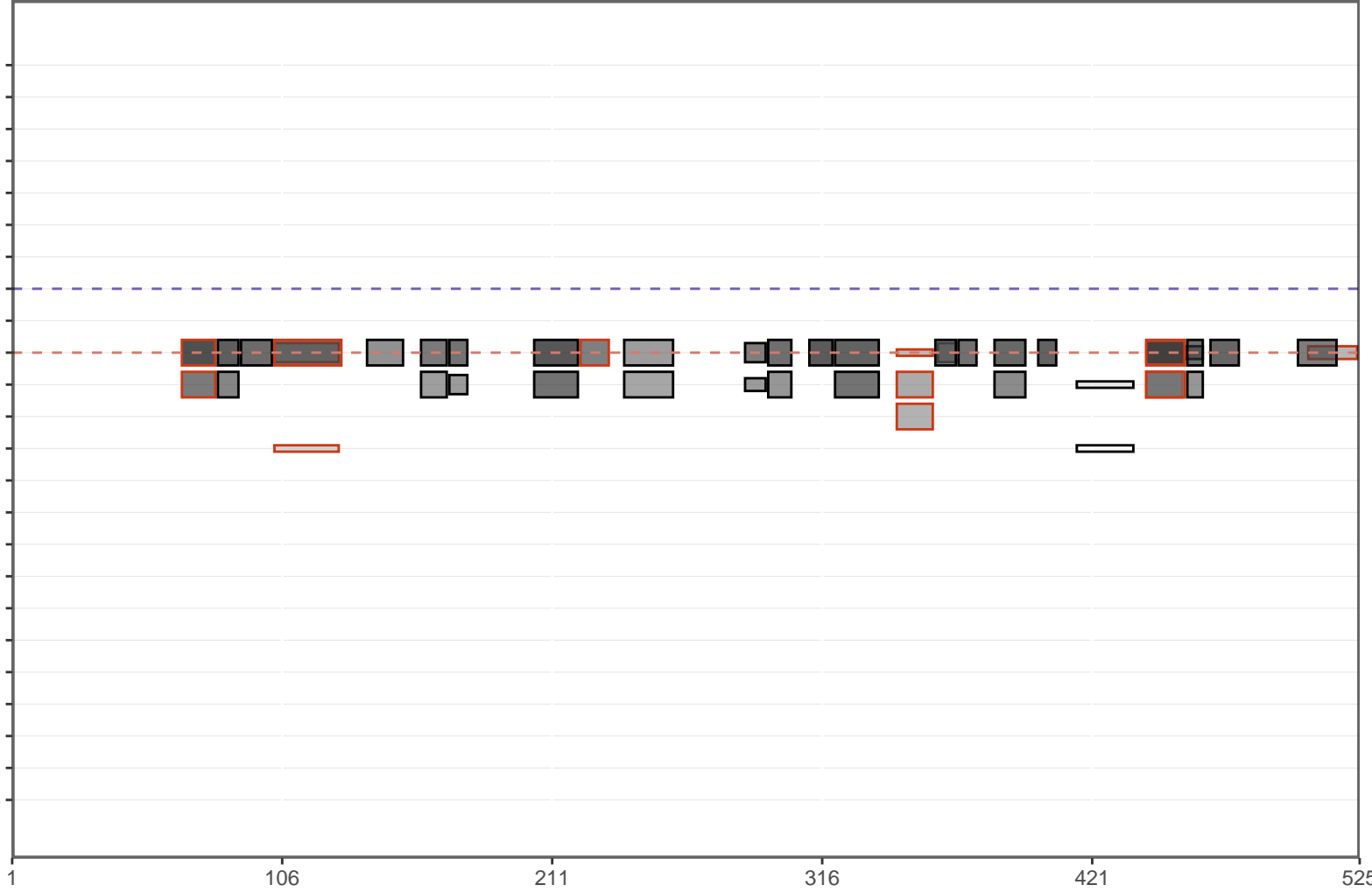
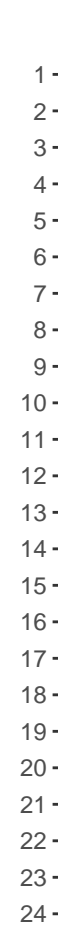
MW indication



Molecular weight

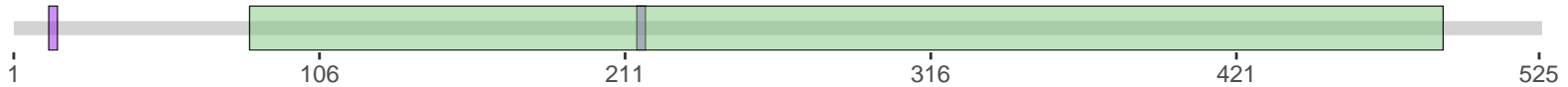


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LDVFPALNSGKLDALANGKEVYFVANSNGLGAVDKLNLHGNKNEYMEVTPKTLADYKGGTUSYEGKVVLLLEIAGVDFEHWNEFKSIEKRFKFTNLLWNLNARLRLEADALKMEIPNPKVEYDGVKVKLQLETAAGAAIKFFDRAIGVWFRSRFLPKVATSDLLLVQSDLYLTDEGVYRNLARSNPNPAIELGPEFKKAVNLFGRFKSPISFIELDLKVTDGVWFGSGVTLKGVTVAAKSGVKLEIPDGAIVANKDINGPEDI

NbL13g27100.1 isocitrate_dehydrogenase_[NADP]-like [MW = 55.17 kDa]

No. of times detected



log(intensity)



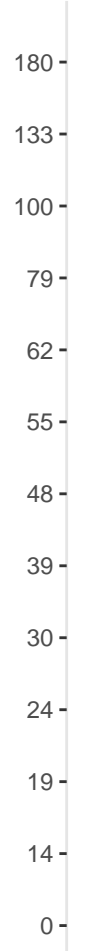
Values from



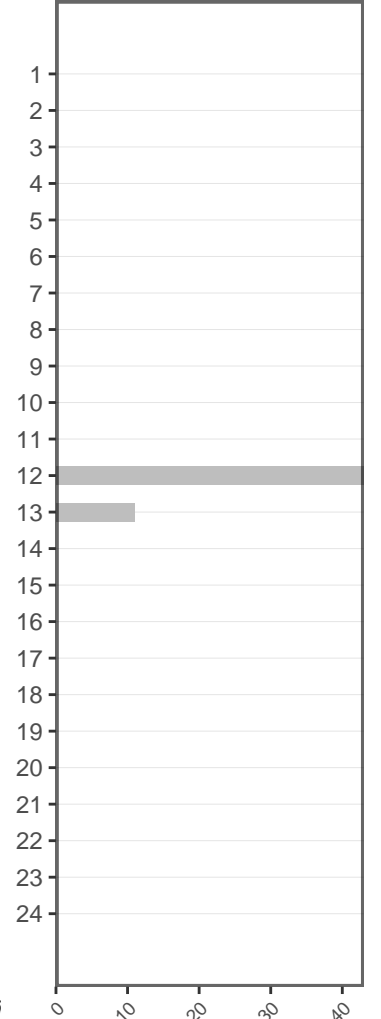
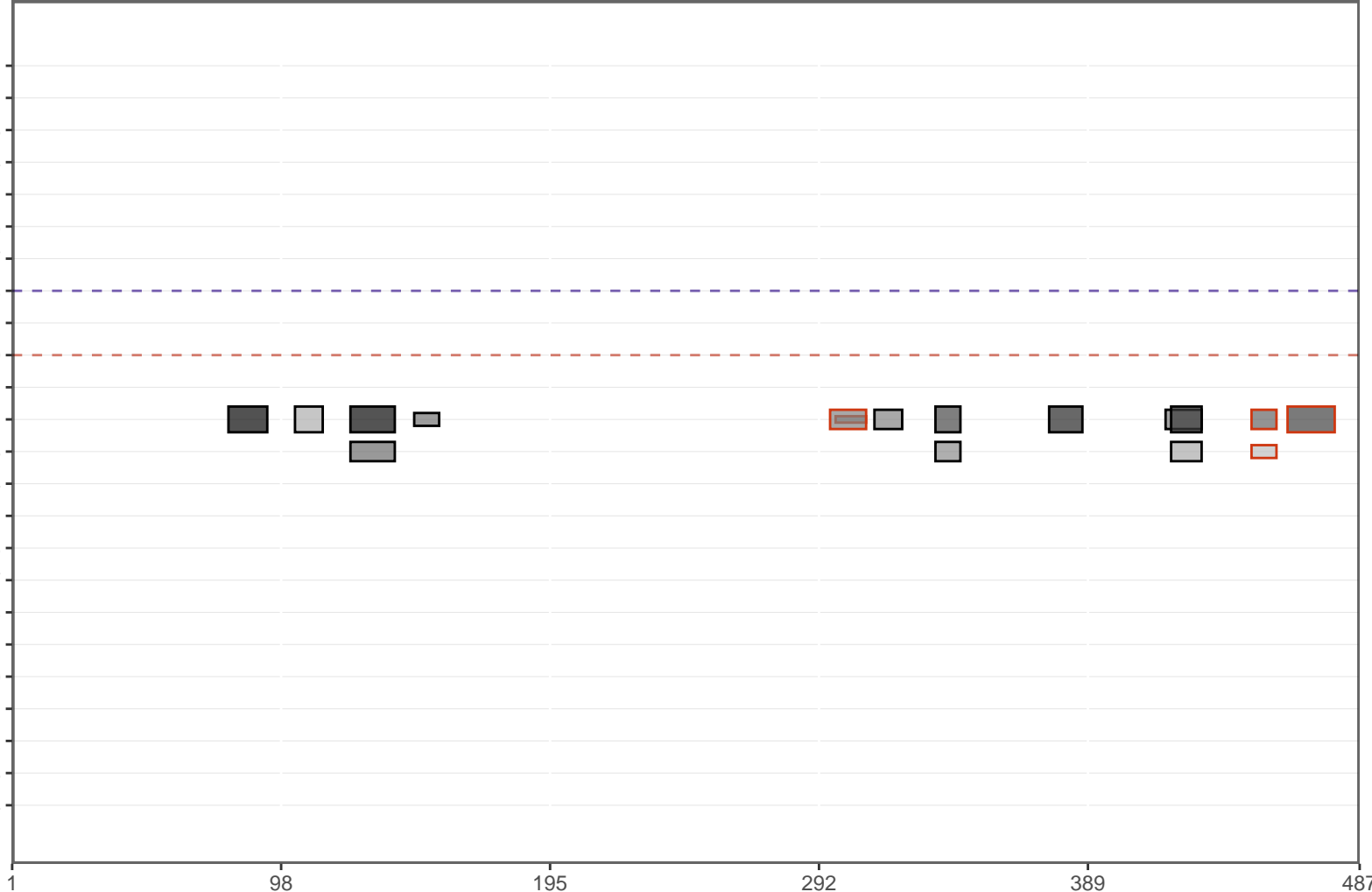
MW indication



Molecular weight

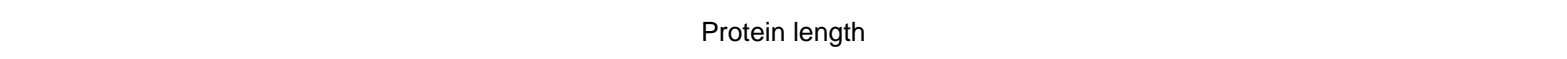


Gel Slice

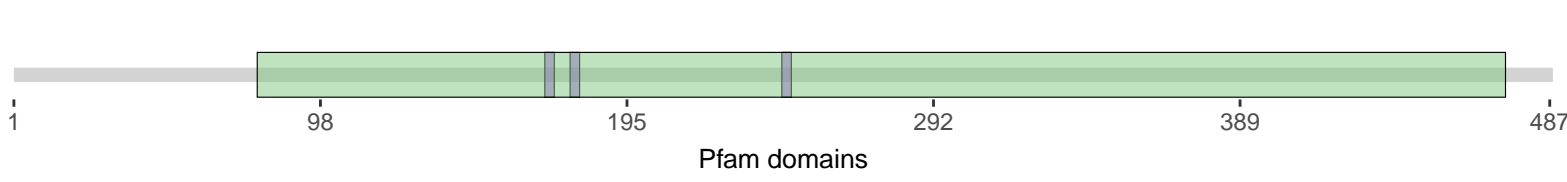


Peptide counts over 4 repeats

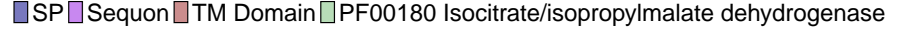
Protein length



Pfam domains



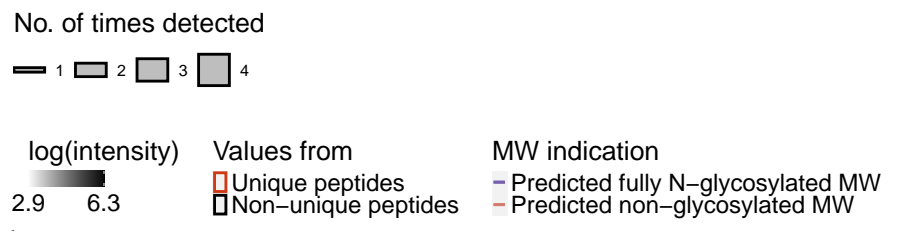
Pfam Description



Protein sequence:

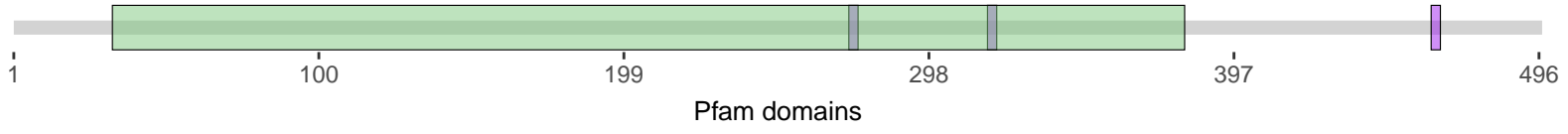
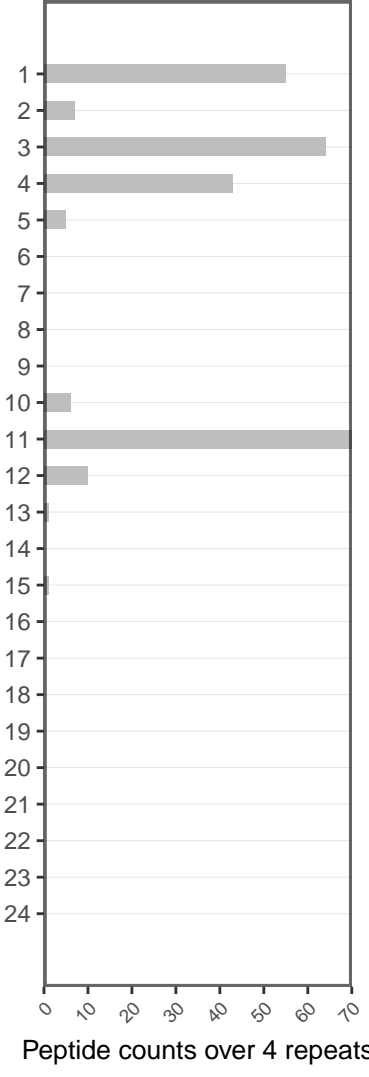
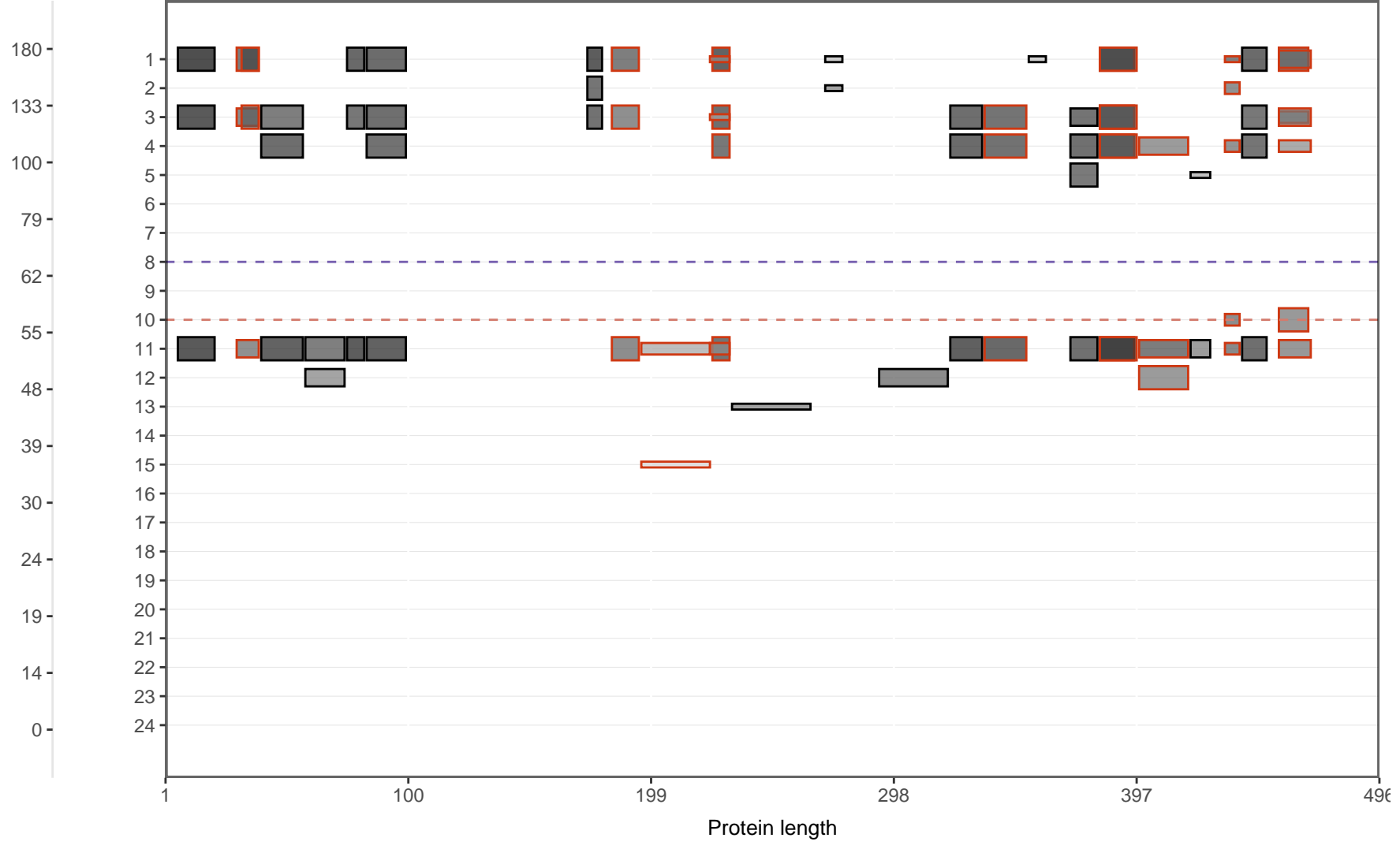
GKIDKIEFEVYNTFGAGGVLSMNYTDESIRSFSAEASMMAYQKQKWPVLYLSTKNTLTKKYDGRFKDFQGEVYSNWKLFEEAGIWEYHRLIDDMWYALKDGGGYYWACKNYDGDVGSDFLAGFGSGLGLMTSLICPDGKTISEAAHGTVTRHYRVHQKGGSETSNISAFWTRGLAHRKAKLDNNAALDFTKKLEGACIGAVENGKMTKDLALAHGSRVARHGVYNTTEEFIDWADLKARLLKAKI

NbL13g27090.1 glutamate_decarboxylase [MW = 55.77 kDa]



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain PF00282 Pyridoxal-dependent decarboxylase conserved domain

Protein sequence:

IKETGWDTPHIVDASGGGFAPFLYPELEWDFRLPLPKSINVSQHKYGLVYAGIGWAWRNKEDLPDELFTHINYLGADGPTFTLNFSGKSSQVYAGYQLRLGFEQYQINMENCNGENARVLRLEKIGKRFNISKKEGVPLWAFSLKDNQSHNEFEIGENLRRFGWVPAWTPMPNAGHVTVLRVVIREDFRSTLAERLVDEKVLHELDTLPRVNRANKLVAEVNSGSHKKTDRVQLEVTAAWKKLVADRKKTGVC

NbL13g27040.1 cysteine-rich_receptor-like_protein_kinase_2 [MW - SP = 67.81 kDa]

No. of times detected



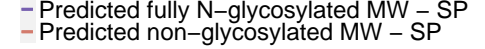
log(intensity)



Values from



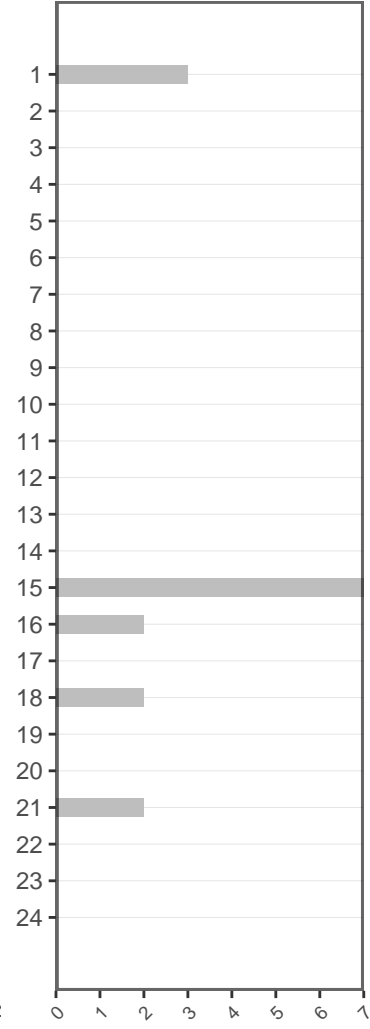
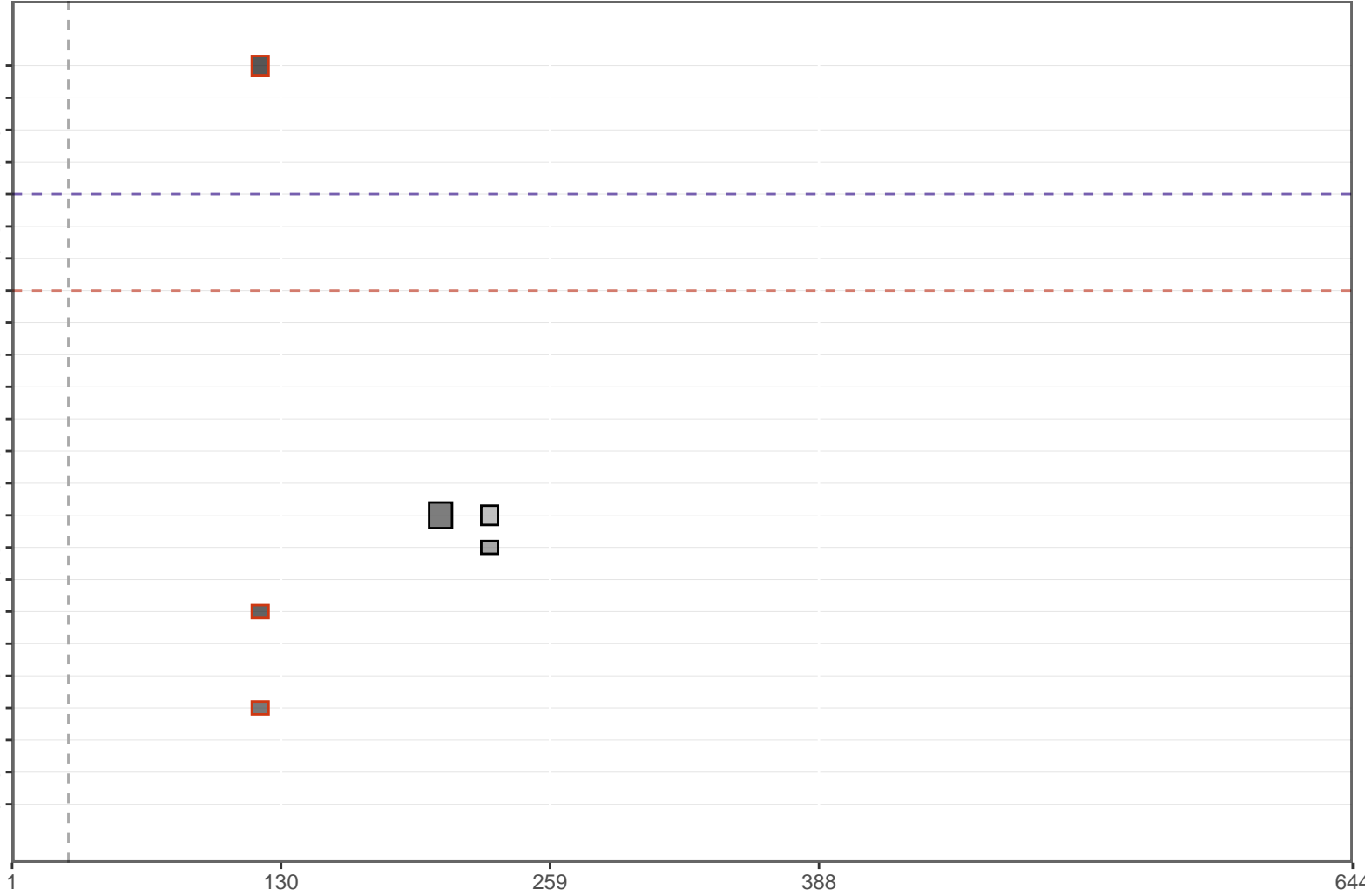
MW indication



Molecular weight

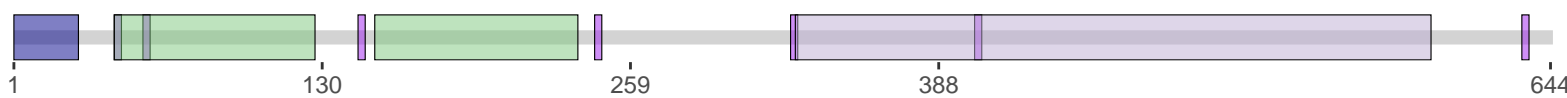


Gel Slice



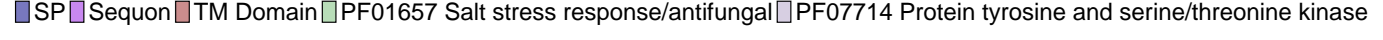
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

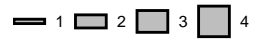


Protein sequence:

LRGPIYSYRFDLKGATGDFNEENKLGEGGFGDVAKGTLNGHVAWVKLAFMSRRAKAEFETEVRLSNVHRNLRLLGGENKGADELLVVEYMANGLERLVYGDKRGMLNWKGRFDIFGTARGLAVLHEGFHYGIIHRDKSNLLDGGFQPKIADFGVLRLLPEDQSHYSTKFAGLGYTAPEVAHGHLETKVDVYDFGVVLEHISGRGRNDMQIEPVTYELLEKAWKLIHETGMPEKLVDELDPNEYDEGEAKKRIEALMCTGSRNLRPTMSEVYVMLLSRSTDI

NbL13g26740.1 NADH_dehydrogenase_[ubiquinone]_iron-sulfur_protein_1_mitochondrial [MW = 80.19 kDa]

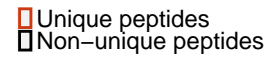
No. of times detected



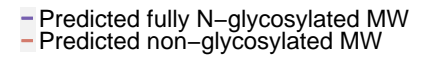
log(intensity)



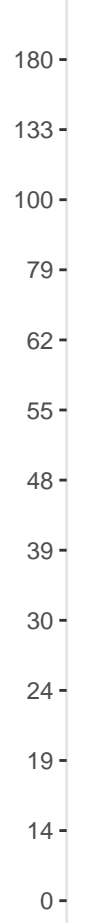
Values from



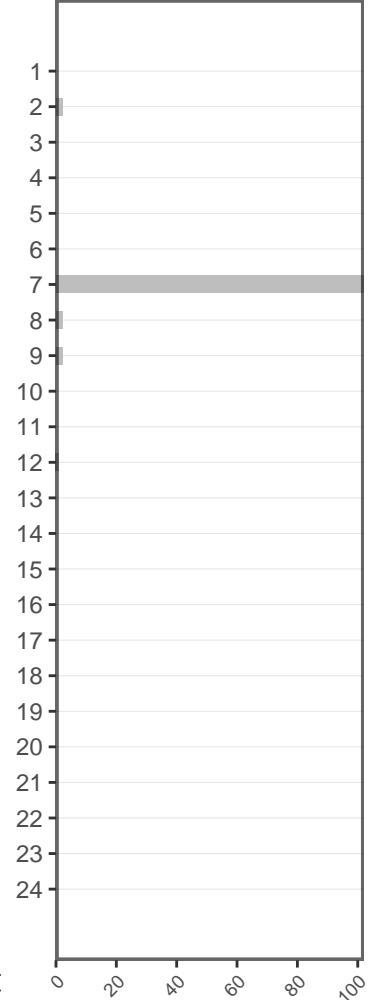
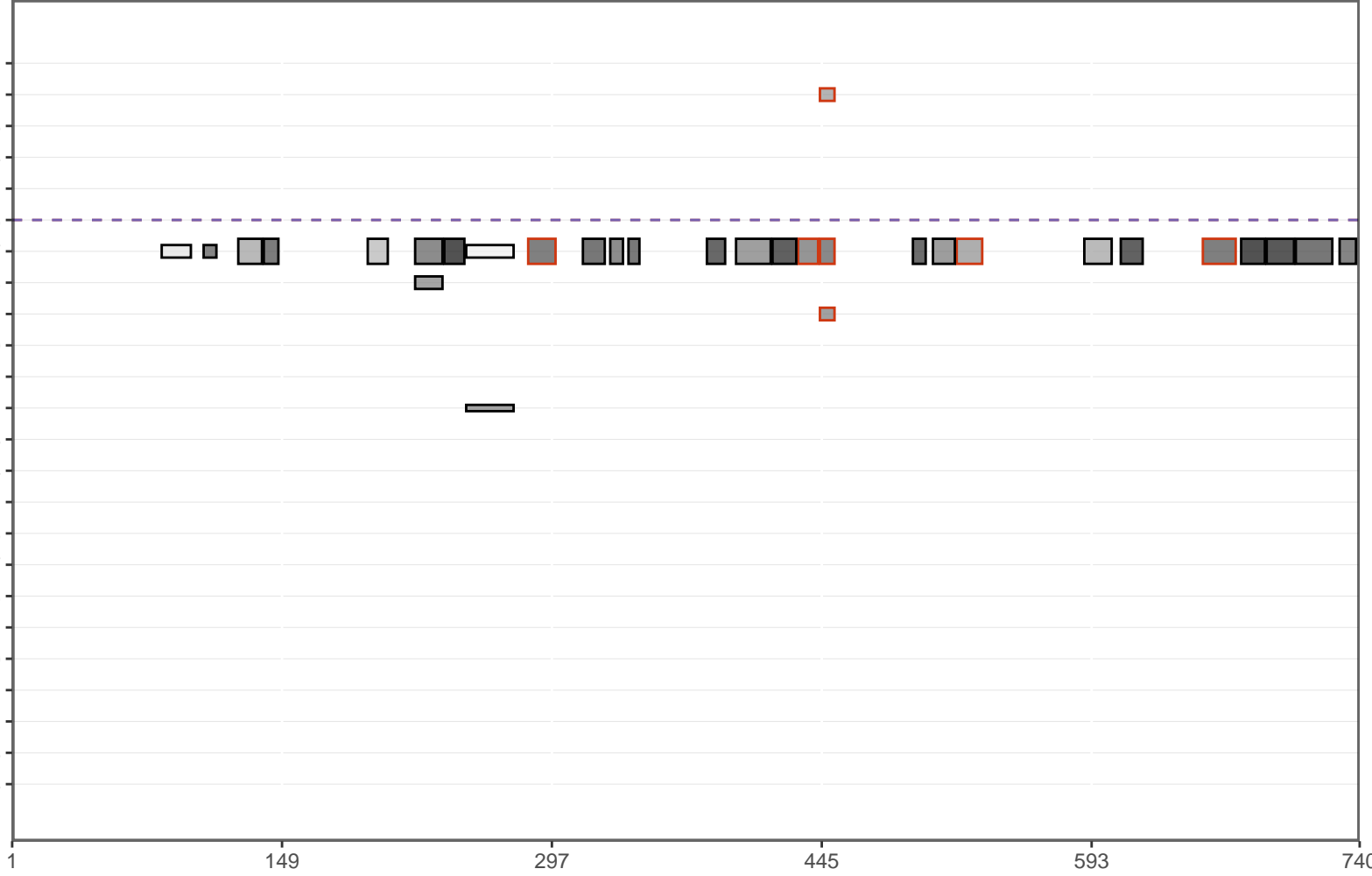
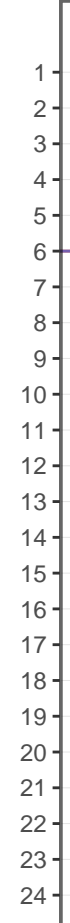
MW indication



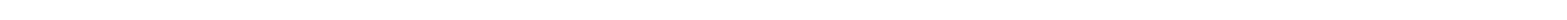
Molecular weight



Gel Slice

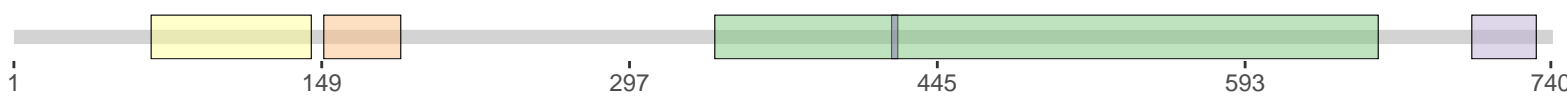


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

- SP
- TM Domain
- PF09326 NADH-ubiquinone oxidoreductase subunit G, C-terminal
- PF13510 2Fe-2S iron-sulfur cluster binding domain
- Sequon
- PF00384 Molybdopterin oxidoreductase
- PF10588 NADH-ubiquinone oxidoreductase-G iron-sulfur binding region

Protein sequence:

WRDALVAEVMHQKPEELHGVAGKLSDAESMMALKKLLNKMGSNFCFEGNGMGPADLRSGYIMNTSISGLEKADVFLVGTQPRAEAAVMNARRIKTVRANNAKVGIVGAWADFNVDKQHLGTDPTQTLVEIEGRHPFSSALKNAKNPVIVGAGVFDREKDAVFAVDVTKNNNVVRSQWNSLWLLNNAQAALDLGLVPESEKCIDSAKFLVLMGADDVSLKLPDDAFVYQSHHGDRGVYRANVILPASAFTEKHEGENTEGGAGTLPVPTVGDSSDD

NbL13g26690.1 NADH-cytochrome_b5_reductase-like_protein [MW = 36.28 kDa]

No. of times detected



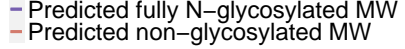
log(intensity)



Values from

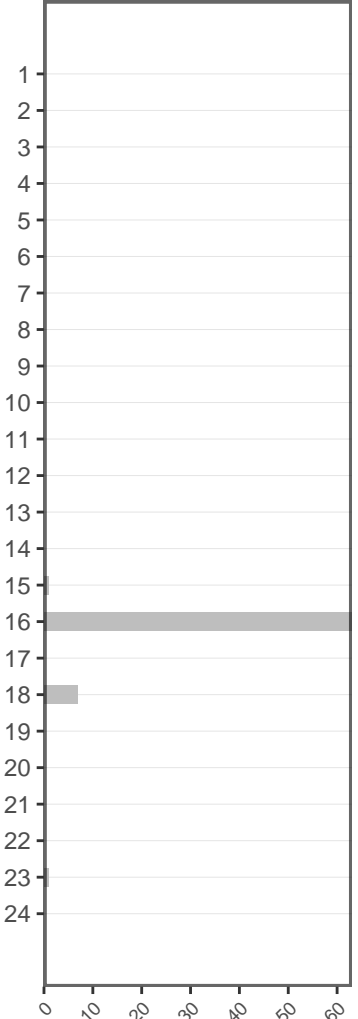
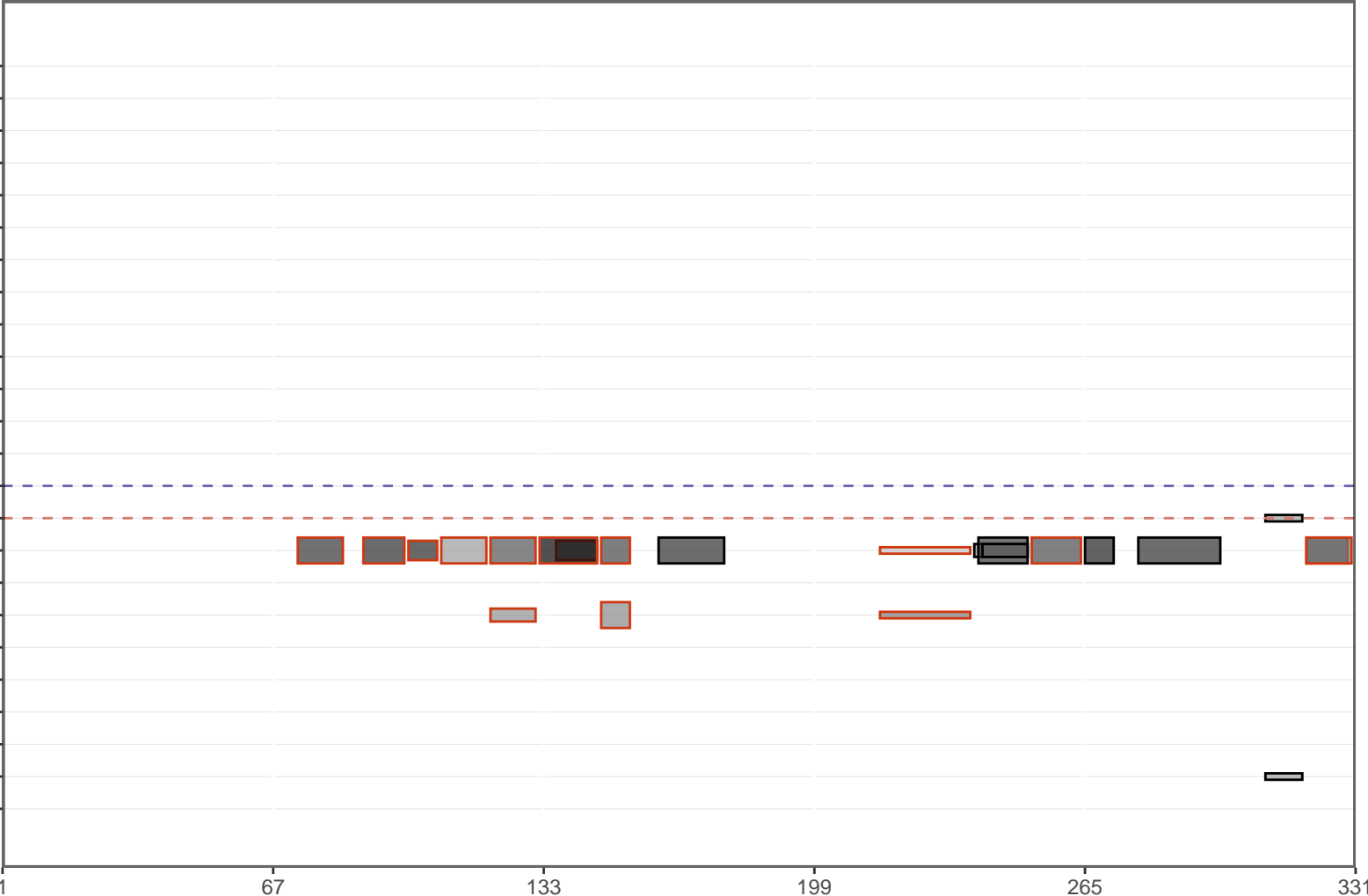
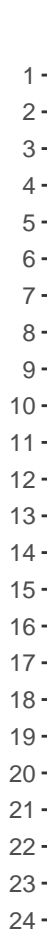


MW indication



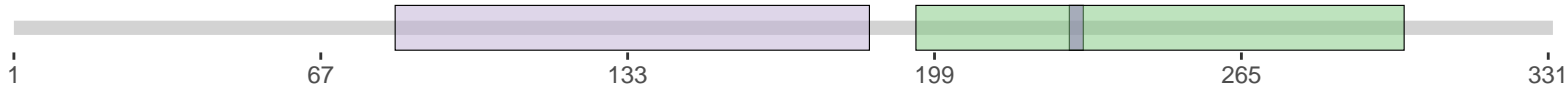
Molecular weight

Gel Slice



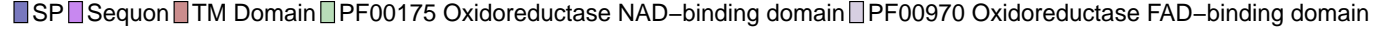
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL13g26620.1 glutamine_synthetase [MW = 38.84 kDa]

No. of times detected



log(intensity)



Values from



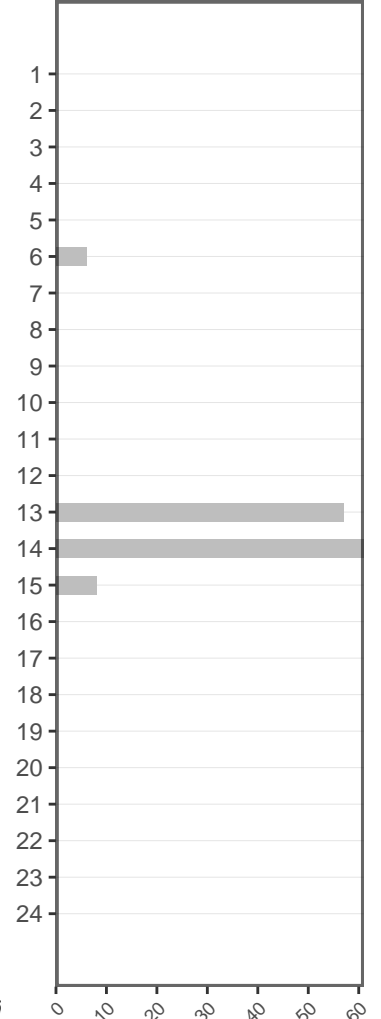
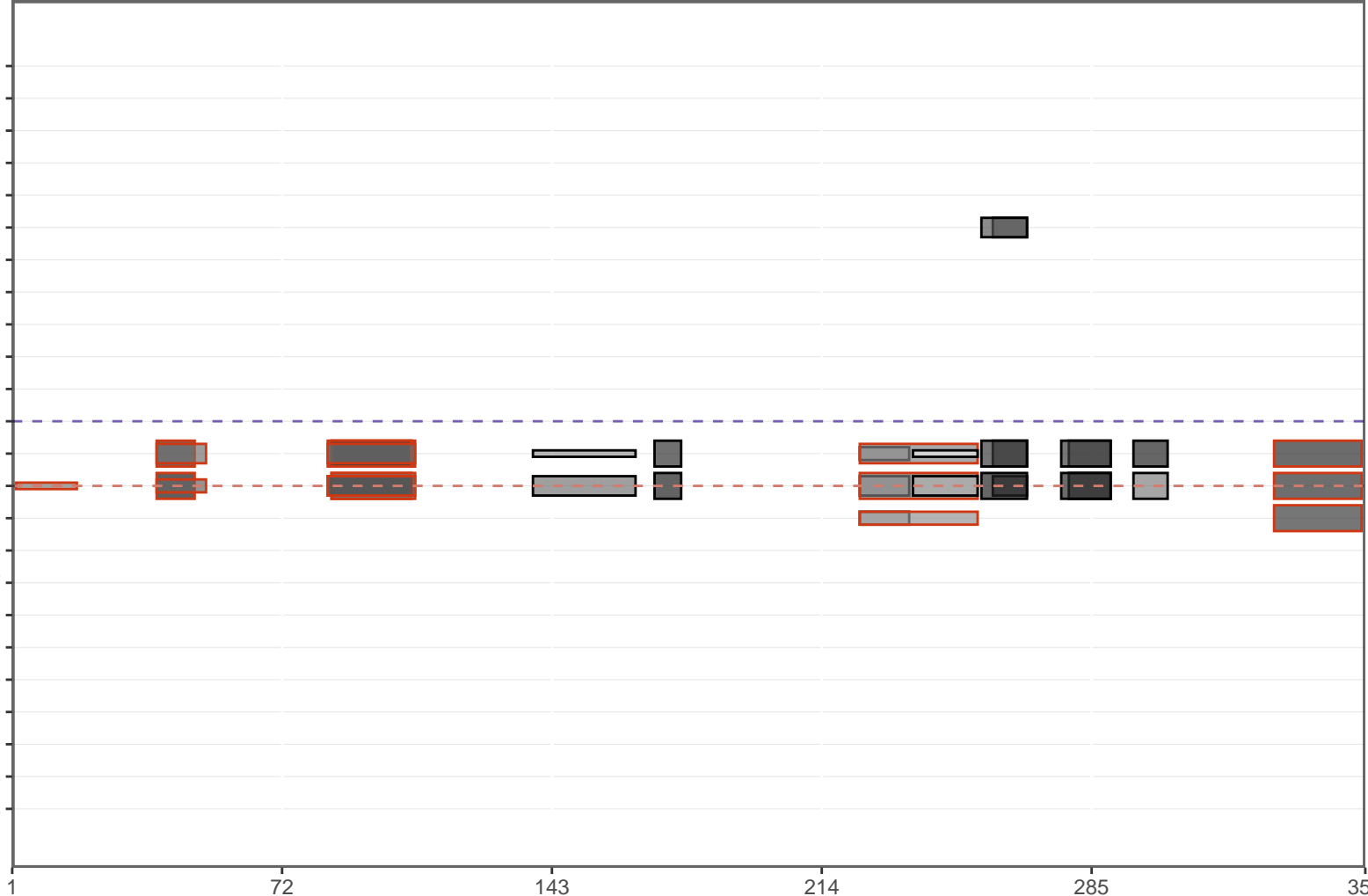
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

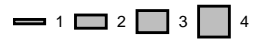


Protein sequence:

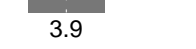
AFGRDIDSHYKAGLYAGINSINGEIVMPGGWFEFGVPSVGSISAGDEWVWARYLERIAEIAAGVVVDFDKPFGDWNAGAHFTNYSTKGMREDGGYEVILKAEIKLGLKHKHEHAAVGEENRRLTKGHETANISTFKWGVNRRGAEVRVGRDTEKAGKGYFEDRRFASNMDDPVVVTAMADTTIKKPI

NbL13g26560.1 probable_inactive_receptor_kinase_RLK902 [MW – SP = 67.19 kDa]

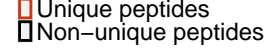
No. of times detected



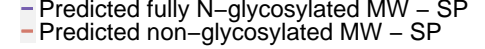
log(intensity)



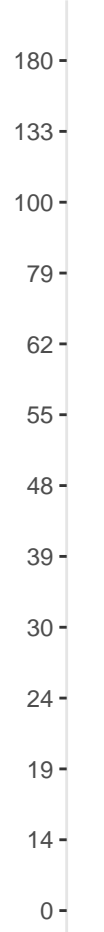
Values from



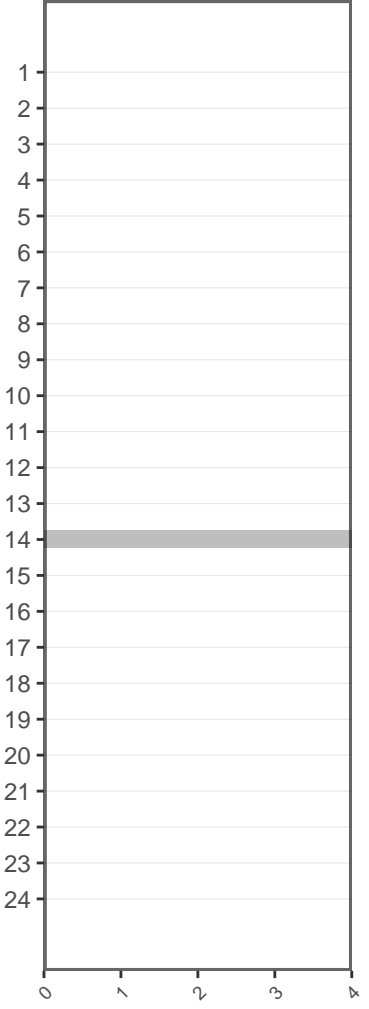
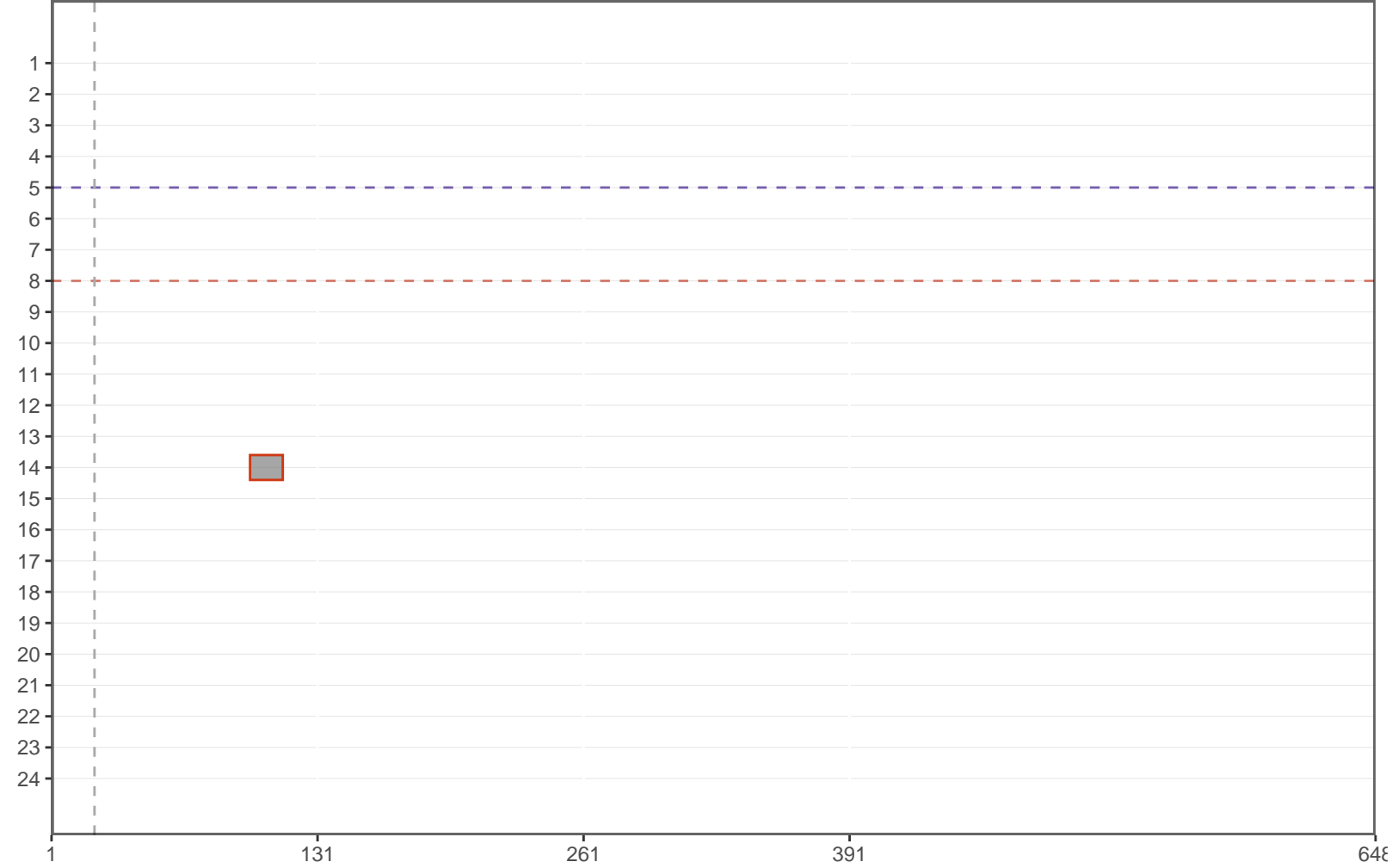
MW indication



Molecular weight

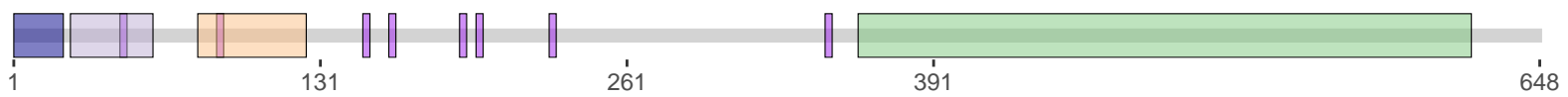


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGVGGNKKDKKAEAVNGKSLVFFGKMKKGFDDLLKASAEVLGKGTFTGTAWKALESGITLVYWRLRDVTVPEKEFREKIEEVGKLDHENLPLRAYVYSGDKLIVYDHSMGSLALLHGNKAGARTPLNWTETRAGIALGAARGIYVHAGGSPVSHGNKSNVLTKEVYRVSDFGLAQLVGFSSTPNRIVAGVRAPEVTDPRKVSQKADVYSFGVLLLELLTGKAPTHSLMNEEGVQLPRVYVQSVWREEWTAIEVDFLELLRYGNVEEDMVLQLQLAVDCTAQY

NbL13g26550.1 protein_TIFY_10B-like [MW = 26.13 kDa]

No. of times detected



log(intensity)



Values from



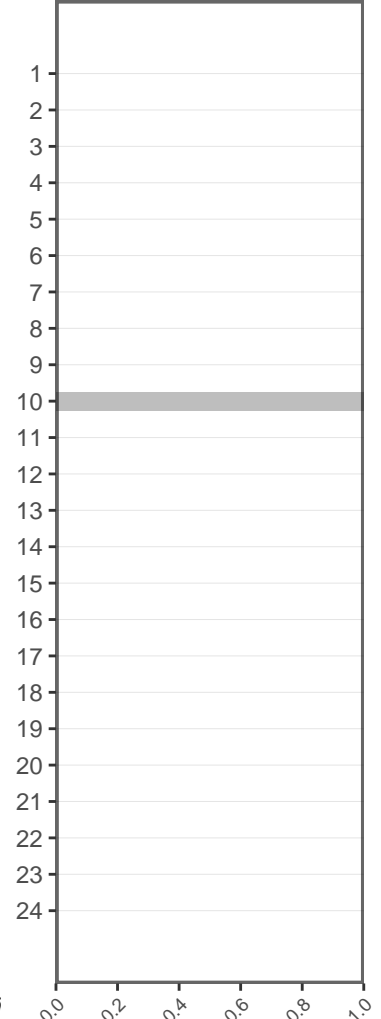
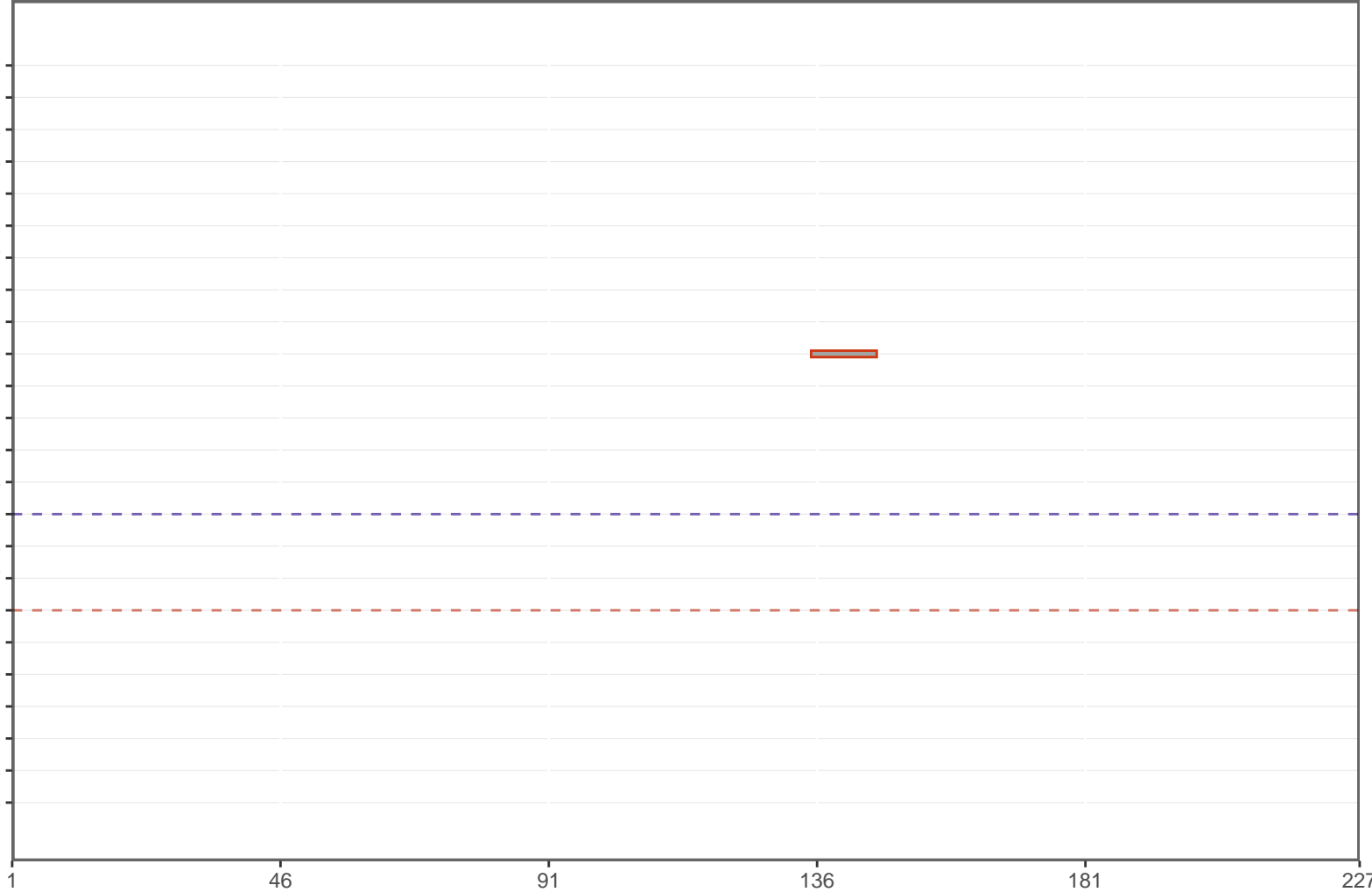
MW indication



Molecular weight



Gel Slice

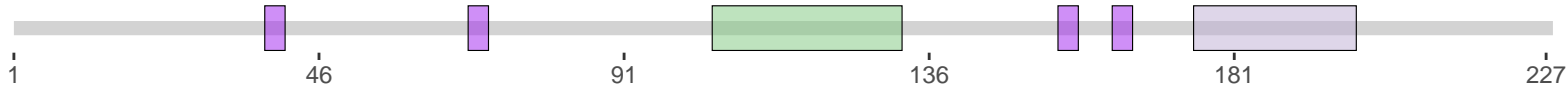


Peptide counts over 4 repeats

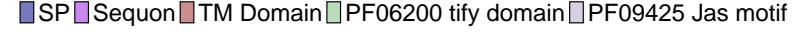
Protein length



Pfam domains



Pfam Description



Protein sequence:

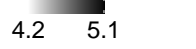
KPESLTLILYMGVEVHFQDITPEKAEIVMDLAKSTNLHMTLEKGNKEKSEANKSEFPSTNASTNYKAGALAMARRATLARFLKRRKRRLUTARPYGVGKTKPKFFPFEMHQEEETASSGFHWEE

NbL13g26480.1 glucan_endo-13-beta-glucosidase_2-like [MW - SP = 51.79 kDa]

No. of times detected



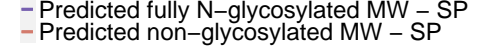
log(intensity)



Values from



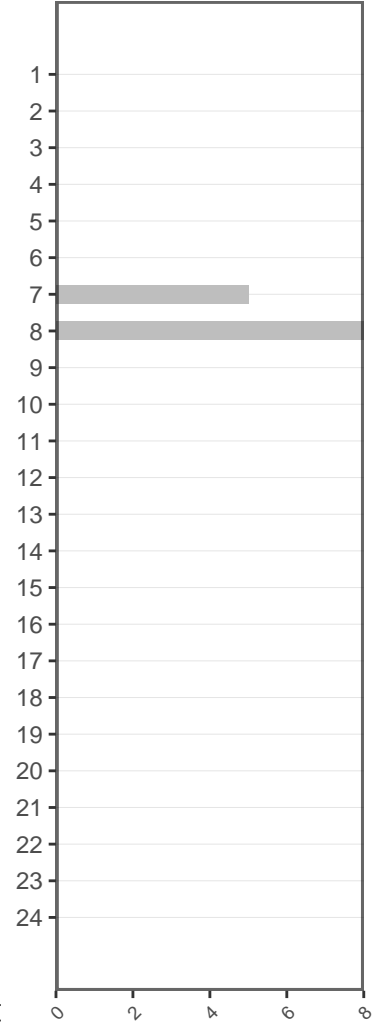
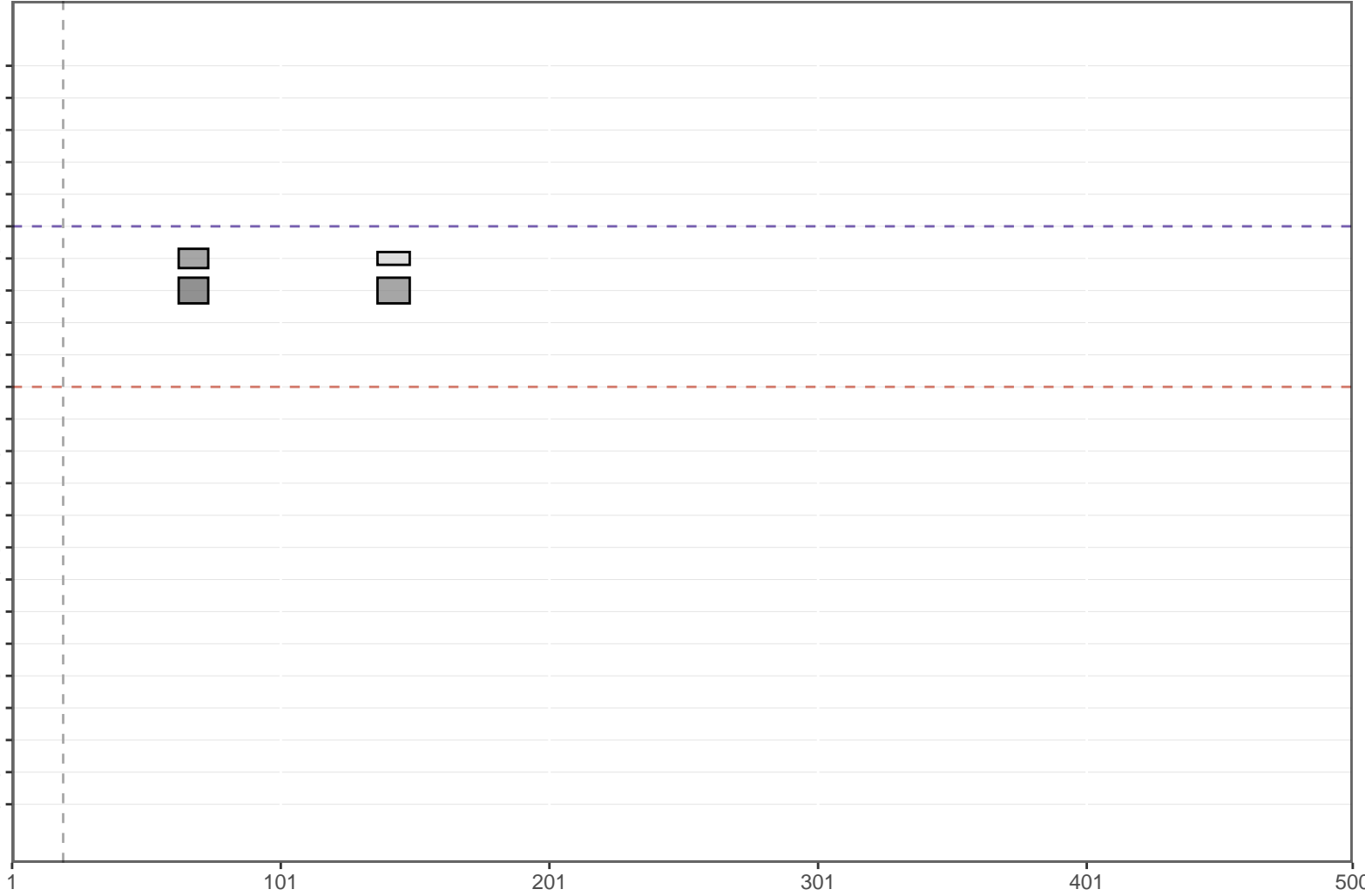
MW indication



Molecular weight

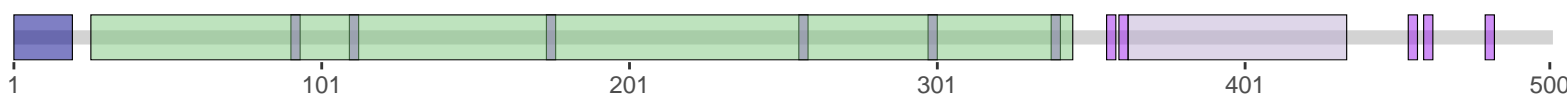


Gel Slice



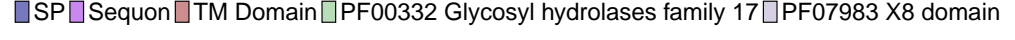
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

TDAMVDAAYFAMLDLNFNIPVAVETESGWPSGGDDEPDAFLDNANTYNSNLRKHYLNKGTGPKHPGAVSTYHYELYNEDNPKPHLSEKNHWLGNFNGTPVYILRLTESGSMFANDTNGTYCAAKDGADSKMLQAALDWACGPKVDSALLGGEPYEPDVAHAATYAFDQYHMMGRAPGTCDFNGVATITITNPKHGSGCVFSGSLGRNGTFLNGTAPAMDSTTS66SPRWLNNTY6TFLMLGLVW6KILL

NbL13g26420.1 HMG-Y-related_protein_A-like [MW = 18.37 kDa]

No. of times detected



log(intensity)



Values from



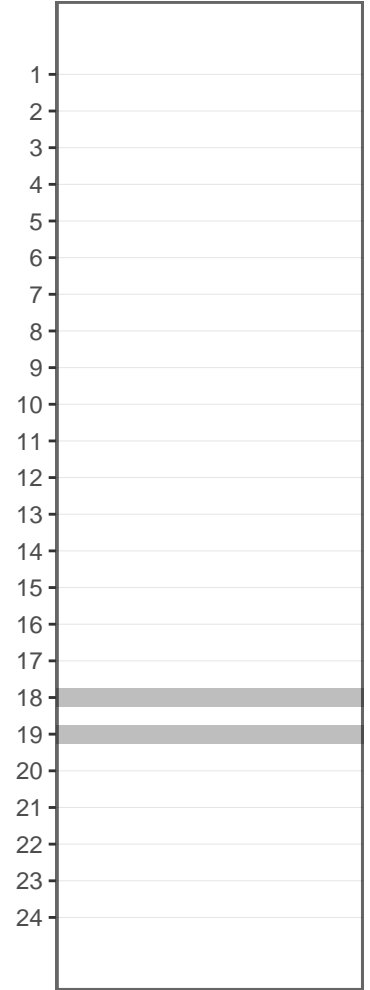
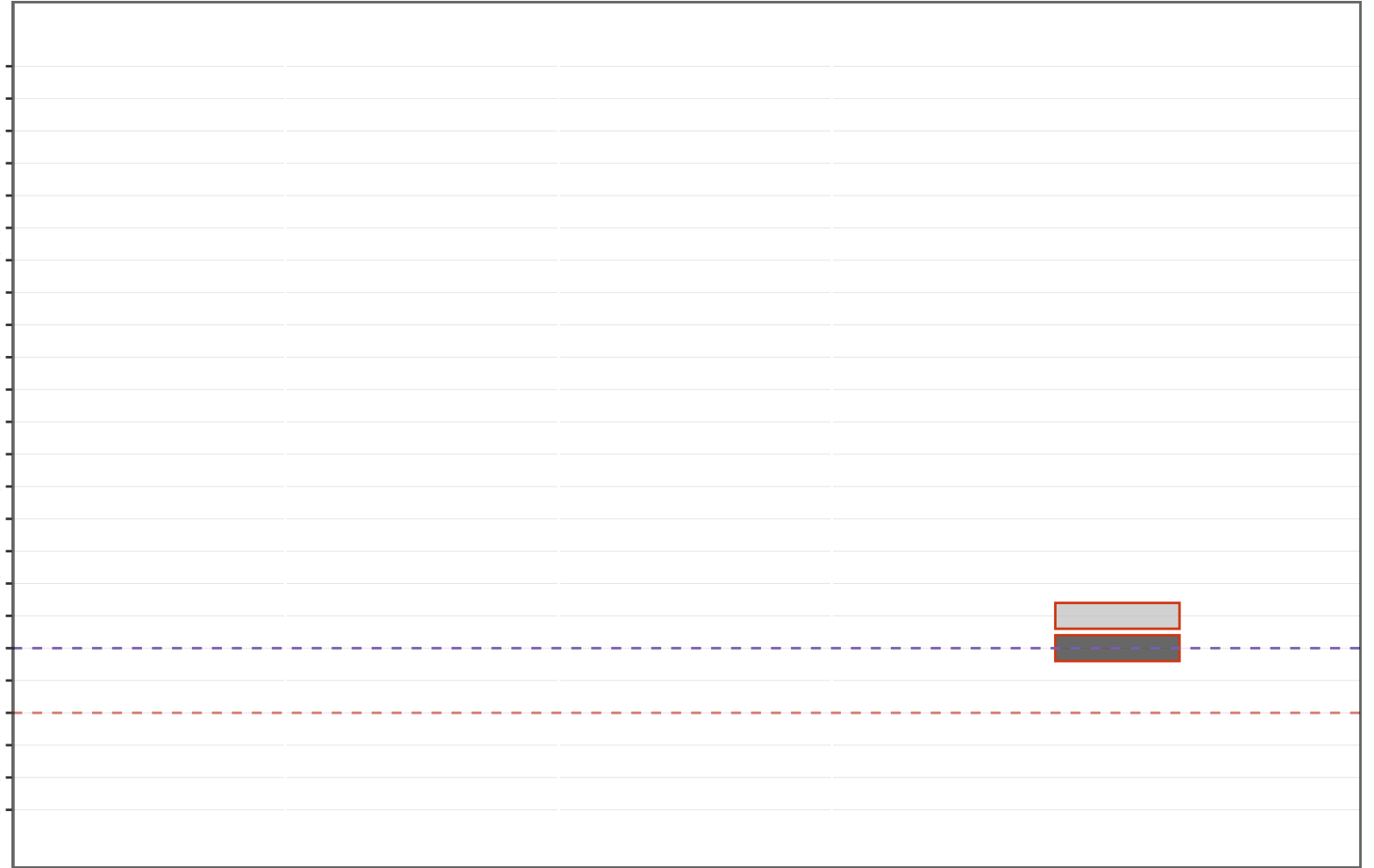
MW indication



Molecular weight



Gel Slice

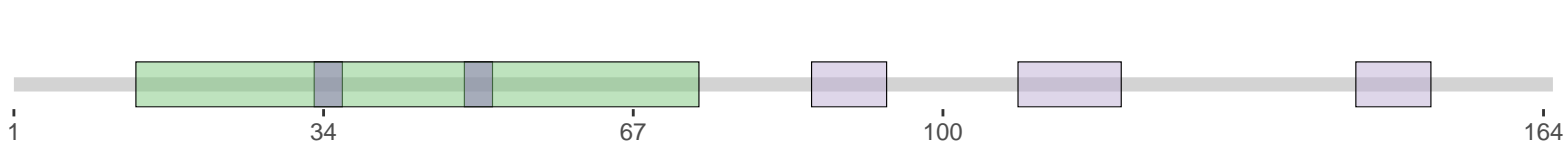


Protein length

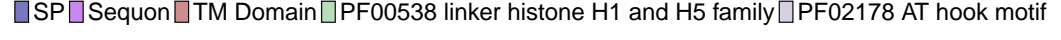


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IFLNKNNYIKRQFNVFPKRGGRGRPKPKFTLLPQDTEIVAPKPRGRPKKDFNPAPPTPKLKFPTVPIINLIANFVKTGRPRGRPKVMPQSGAGNVE

NbL13g26320.1 glutathione_S-transferase_DHAR3_chloroplastic [MW = 28.39 kDa]

No. of times detected



log(intensity)



Values from



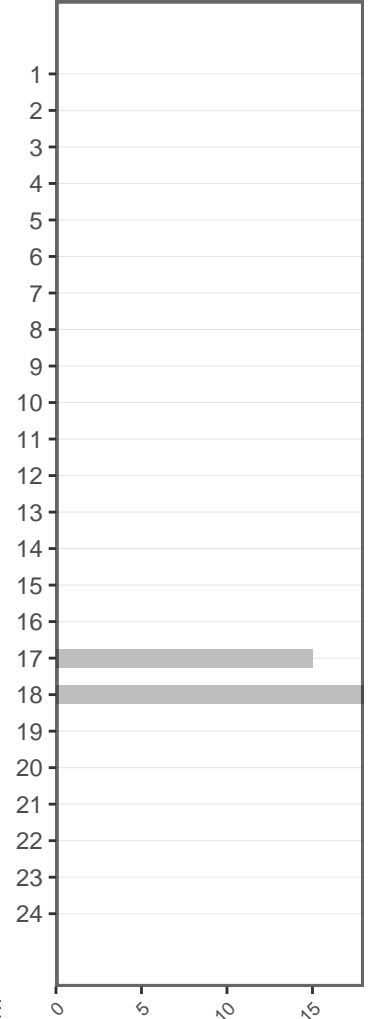
MW indication



Molecular weight

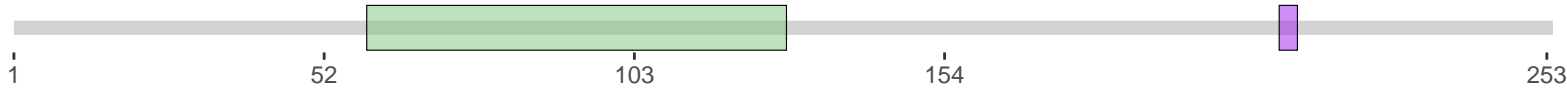


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

M/I/T/Q/L/E/E/K/F/P/Q/P/L/T/T/P/P/E/K/A/S/V/G/S/K/I/F/K/F/W/F/L/K/K/D/L/S/D/A/E/G/E/L/D/E/L/T/A/F/N/D/L/K/E/N/R/P/F/N/G/E/V/S/A/D/L/S/L/G/P/K/L/H/L/E/I/A/L/G/H/Y/K/N/W/S/P/D/S/V/P/Y/Y/K/S/Y/M/K/S/F/S/R/G/S/F/N/T/R/A/K/E/D/V/E/G/W/R/P/K/M/G

NbL13g26210.1 8-hydroxygeraniol_dehydrogenase-like [MW = 39.37 kDa]

No. of times detected



log(intensity)



Values from



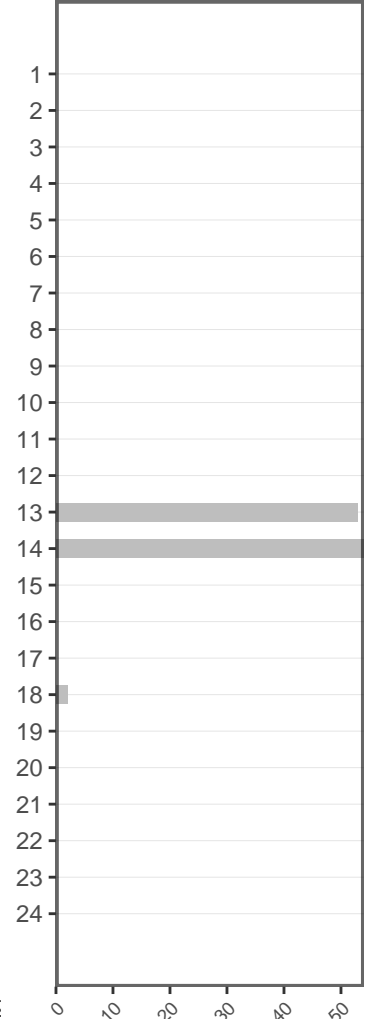
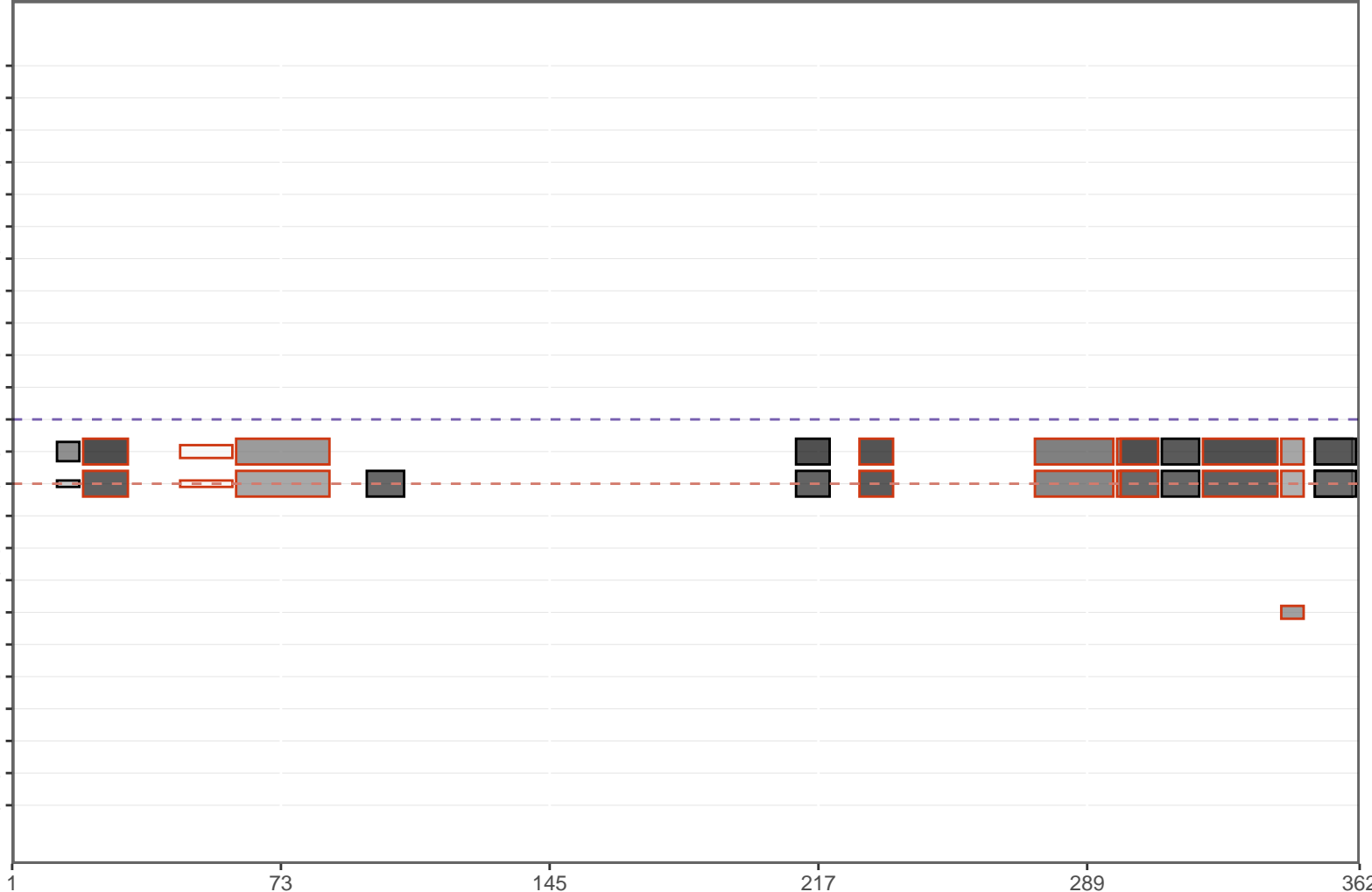
MW indication



Molecular weight



Gel Slice



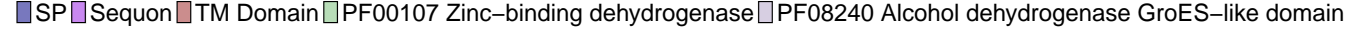
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LLNAGITTYSPLYKFGLEKPGMHGIVGLGGVGHMVKFAKAFGKTVVISTSAKKQGEIERLGAESFLLESRDPDQMGAAATDSLGDHDTVAHPLLPINLLKTHKGVIVGAPDKFLELPVLPDLLGRKLVAGSAGGMKQETGEMVDFAAKHNIPTDVEVVPMDVNTAMERLAESDVKYRFVLDGNTLANKS

NbL13g26200.1 8-hydroxygeraniol_dehydrogenase-like [MW = 39.25 kDa]

No. of times detected



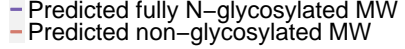
log(intensity)



Values from



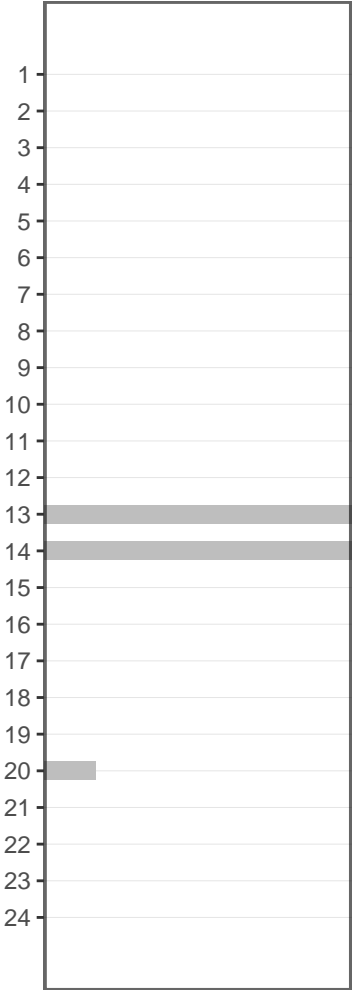
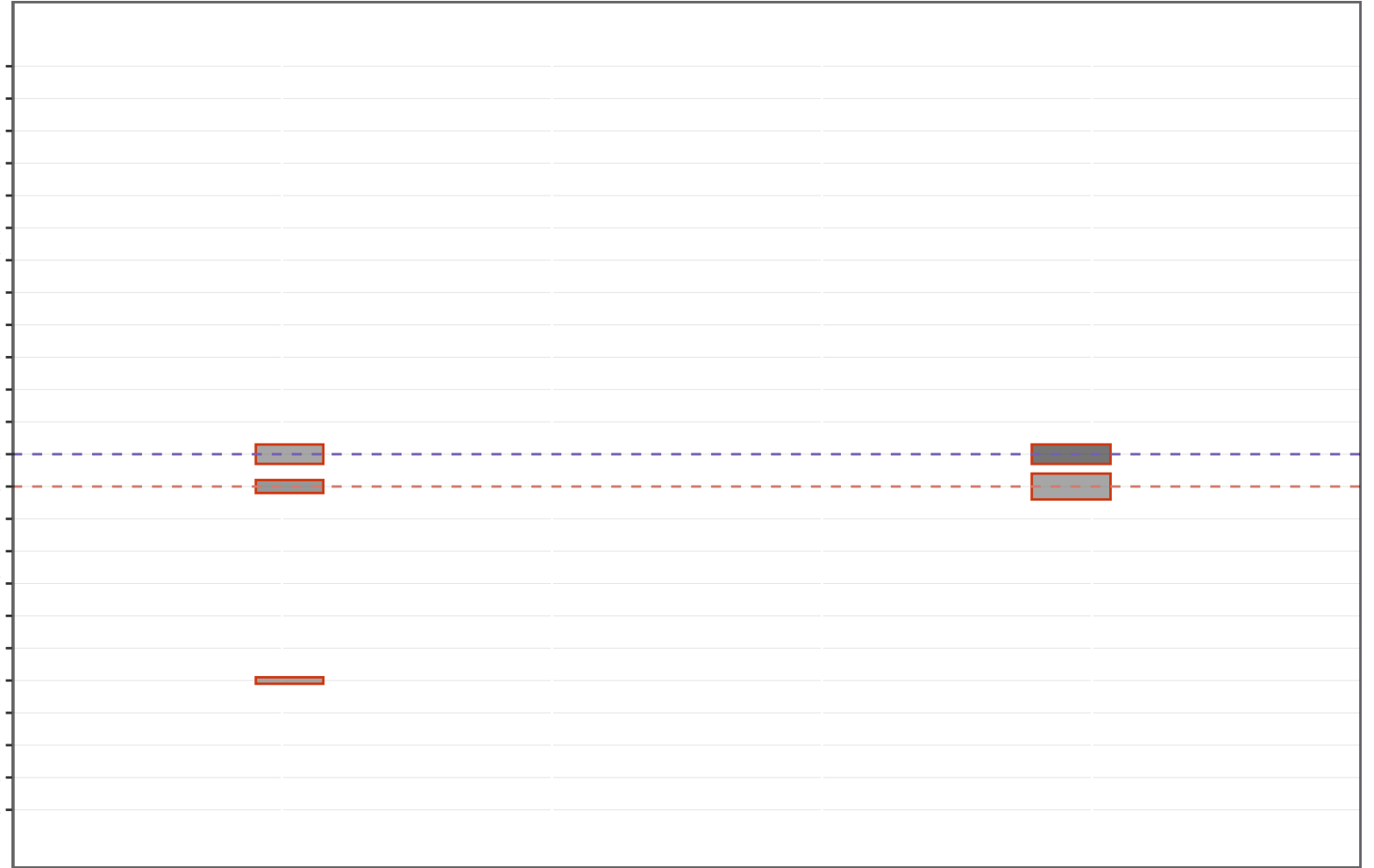
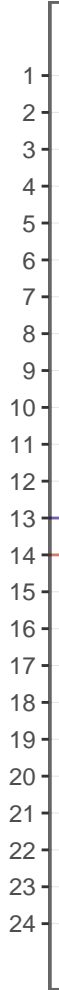
MW indication



Molecular weight



Gel Slice



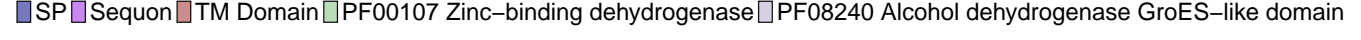
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LCAGITTSPLKYFGLKPKGMHGVVGLGGLGHMAVFAKAFQTKVTVISTASAKGAEIERLIGADAFUERDPEGMQDAMSTLGDHDTVSAVHPILPLLLKLSHGKLMVGAPEKPELFPVFFLLLRKLVAGSGGGMKQETGEMVDFAAKHNTPDIEVWPMEEVYNTALDRLLKSDVWYREFLDGNTLKAAN

NbL13g26170.1 probable_mannitol_dehydrogenase [MW = 38.7 kDa]

No. of times detected



log(intensity)



Values from



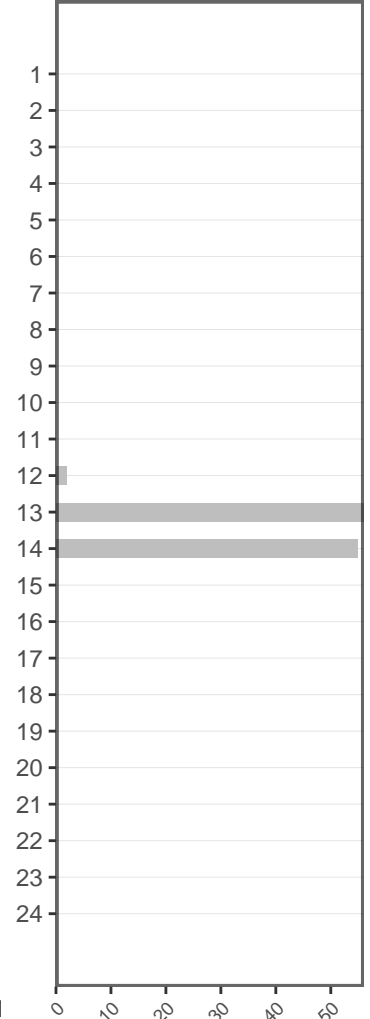
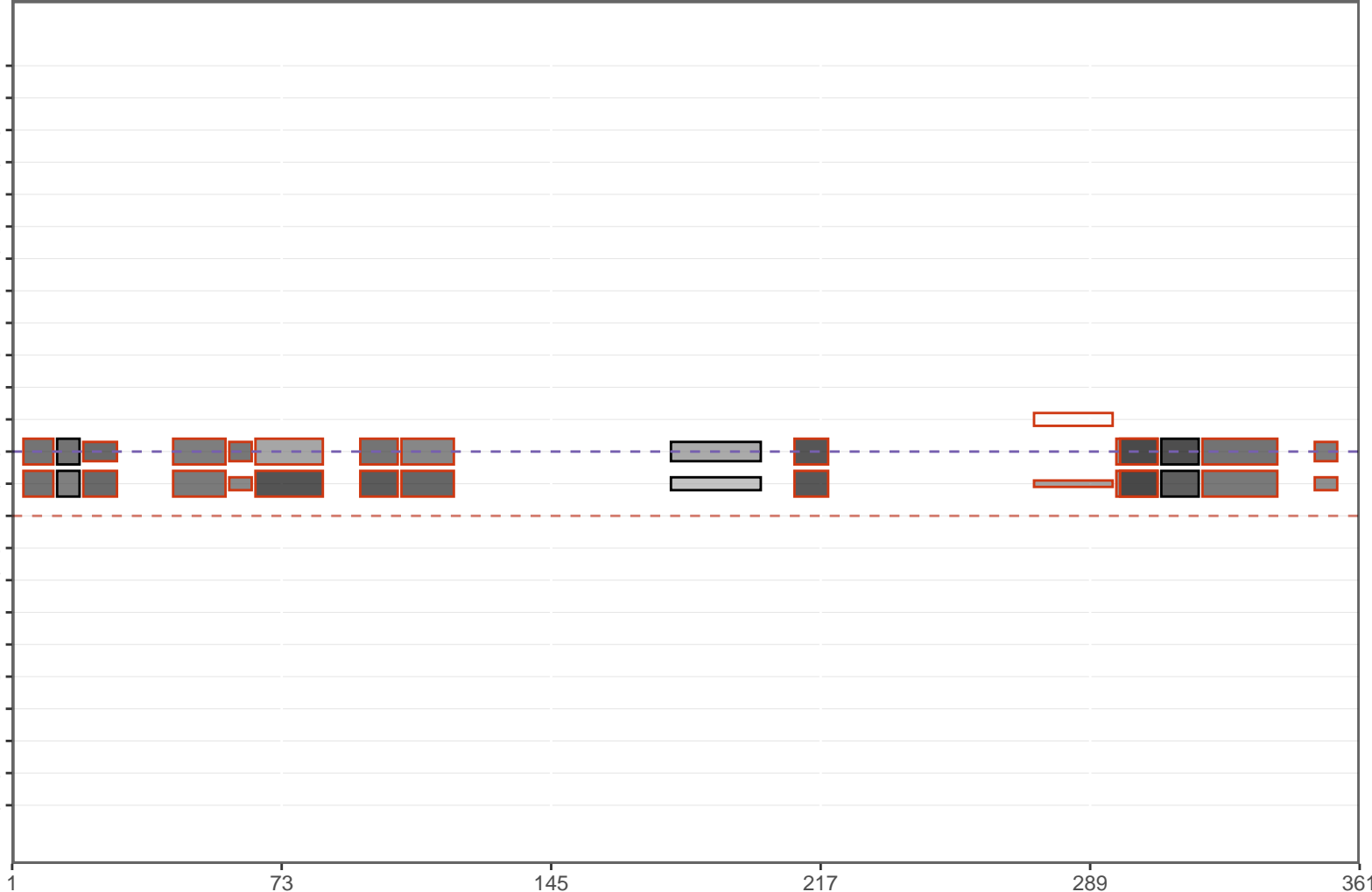
MW indication



Molecular weight



Gel Slice



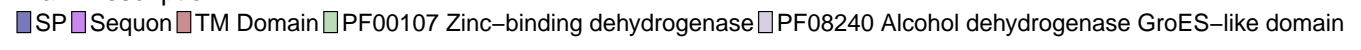
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LLCAGITTSPLRYFGLDKPGLHGVVGLGGLGHVGVKFAKALGLKVTVISTGSGKAEHLGADSFLLSTDPDLGAAMGTMDGHLDTVAATHPLVPLVGLLKTNGKILLGALKLEPLFVFFLLMGRKLVAGSGGGMKGTGEMLDFAAKHNITADIEVPMQVINTAMERLAKADVKYRFVDVAKTKAE

NbL13g25970.1 germin-like_protein_subfamily_3_member_2 [MW - SP = 20.88 kDa]

No. of times detected



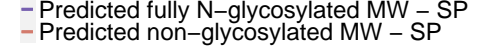
log(intensity)



Values from



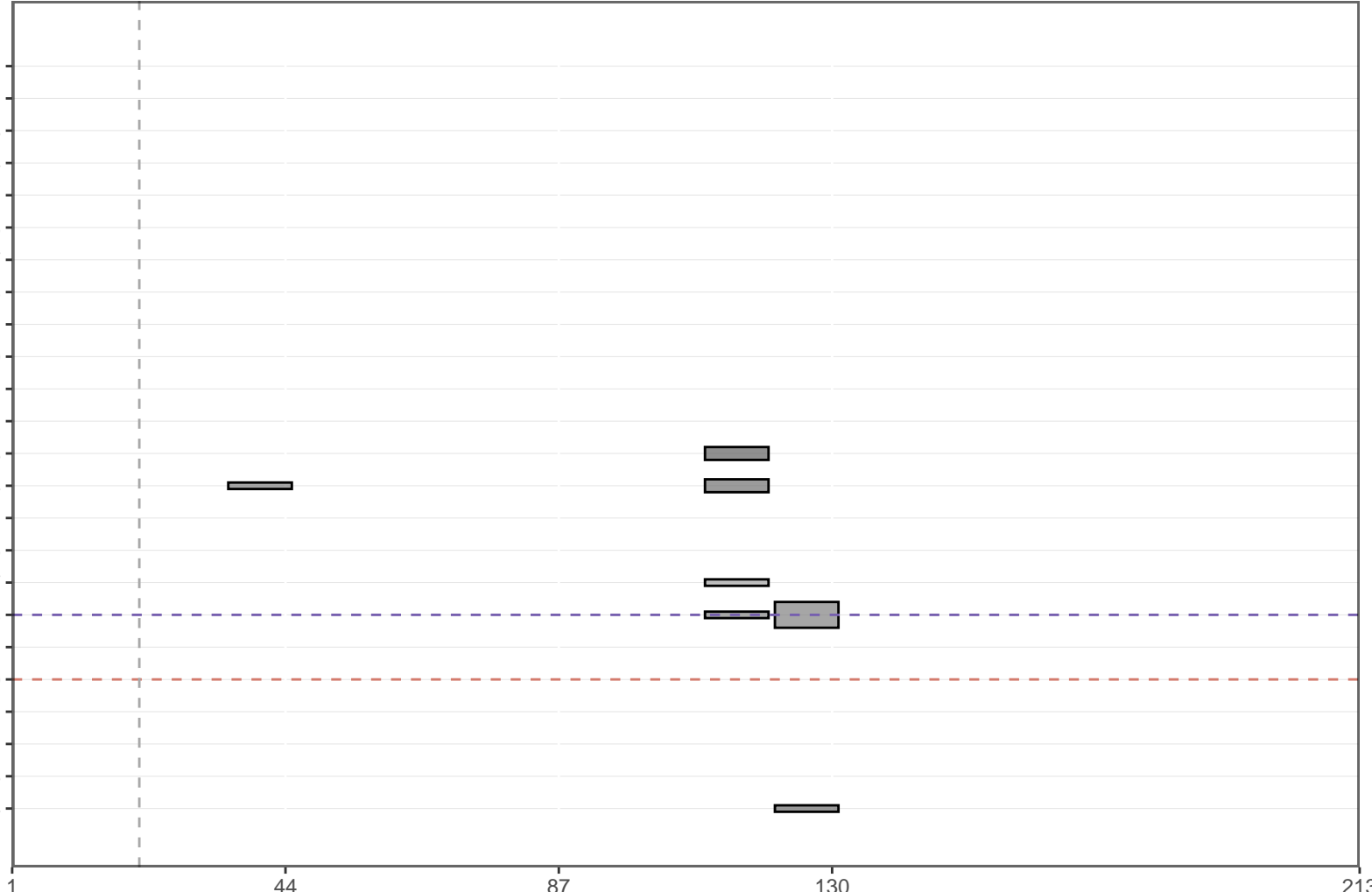
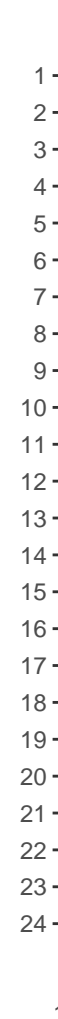
MW indication



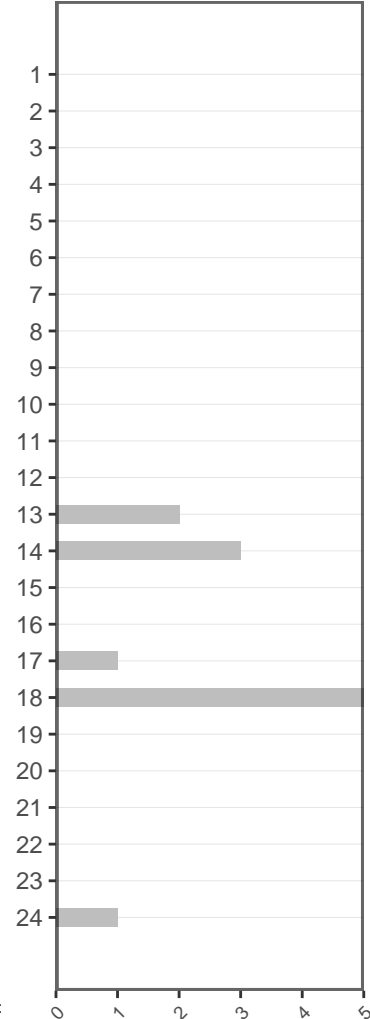
Molecular weight



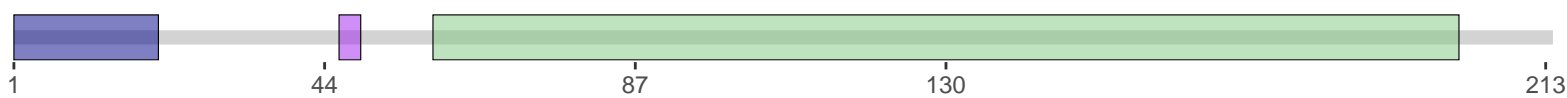
Gel Slice



Protein length

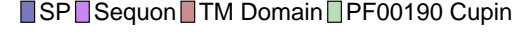


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LDFTDLDGIVNPHIFIPRAETETAPVLEGGYSGFVDSGNRIRFAKYLEKGEVMMVFPKGLVHFQMNVDGSDPATLGSFNQNPGLVKIPSAIFGTGIEEELMKAFGLNKEIAKLRKRFIPQ

NbL13g25940.1 ACT_domain-containing_protein_ACR12-like [MW = 36.99 kDa]

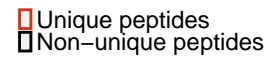
No. of times detected



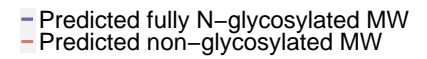
log(intensity)



Values from



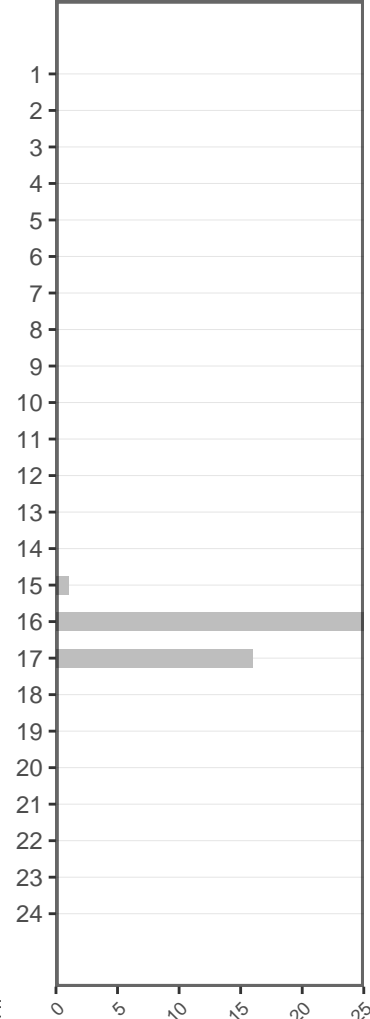
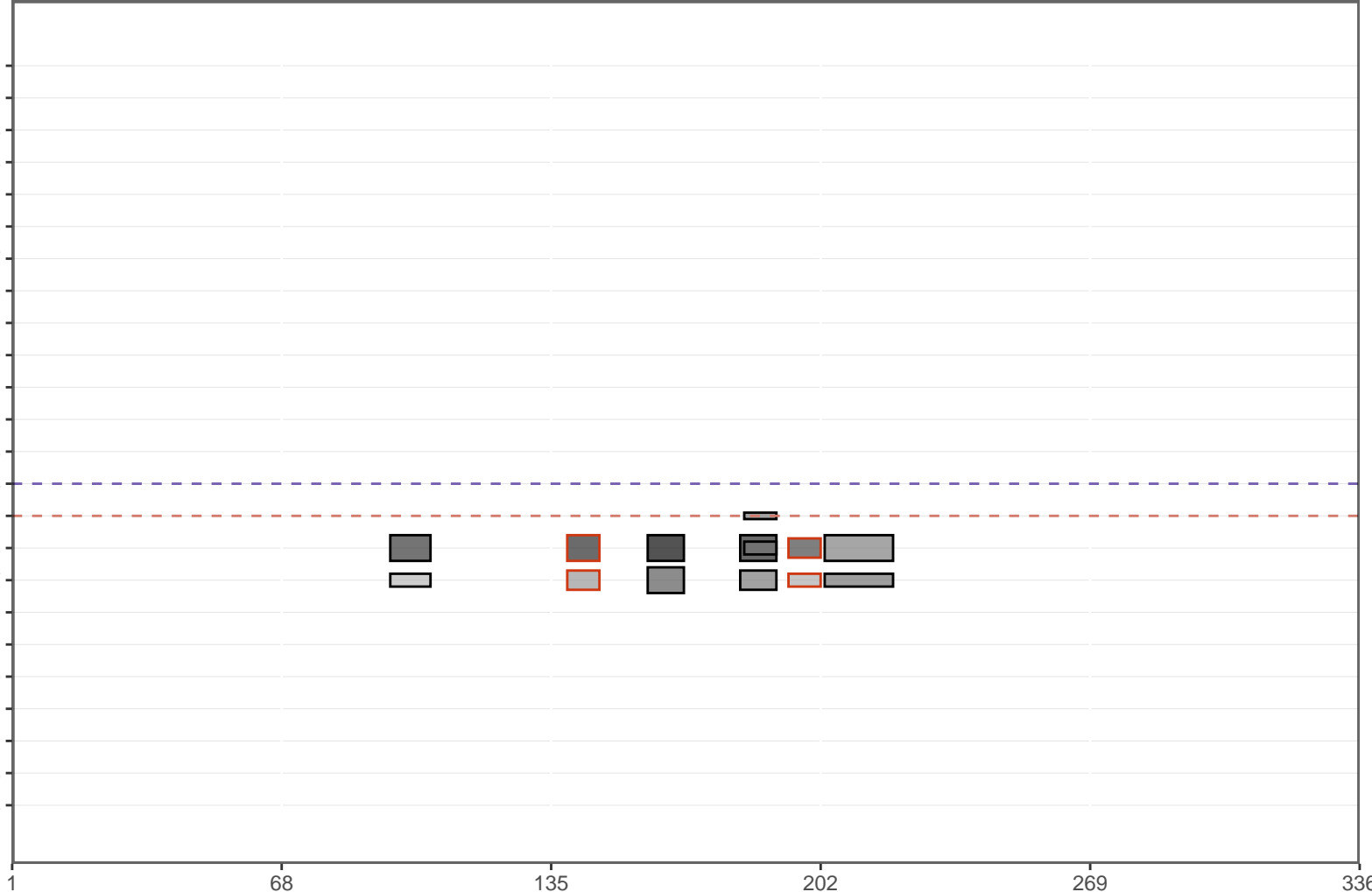
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

DVYKGIIVTTEGSVYKTKFRLFDTRKAVKEDPDLLEIRIRLTINLKYVHPESSEQLMGEAFGKAFKPKPDVDTATHHKDDGPKRSLIHVETADRSGLLVEVYKIMADINDESAEIDTEGLVAKDKFYVSYRGAALTSLSLGGVYQIGFSSGGNHSHVSRLLRYLFMVSANRFVY

NbL13g25890.1 probable_small_nuclear_ribonucleoprotein_G [MW = 4.54 kDa]

No. of times detected



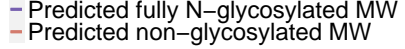
log(intensity)



Values from



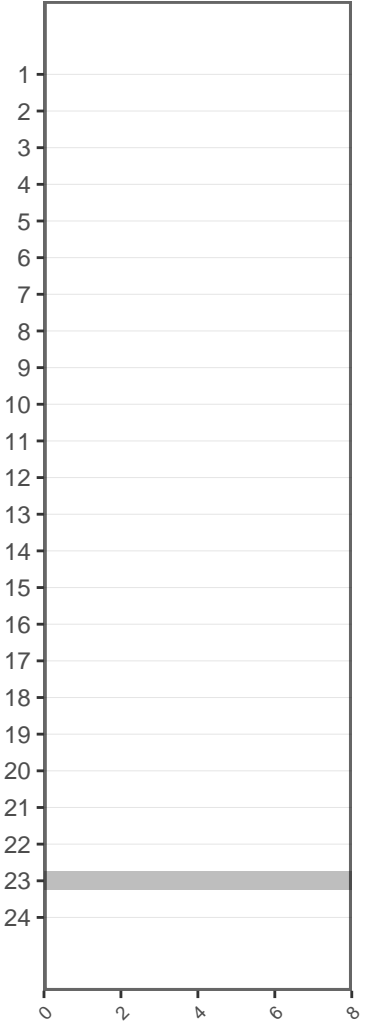
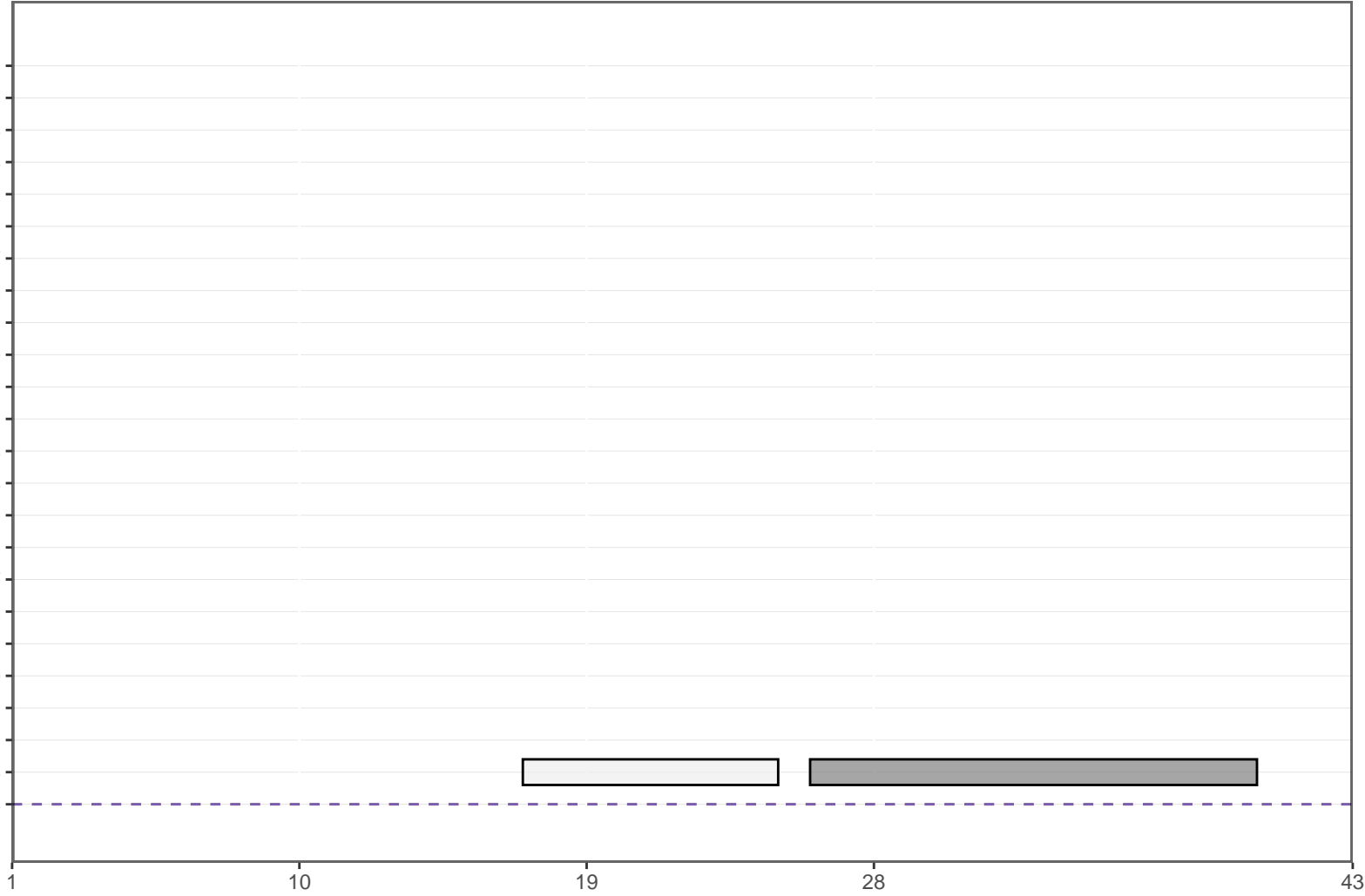
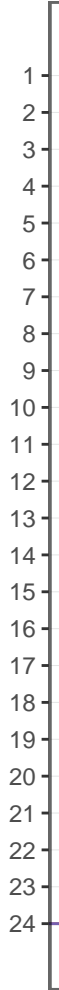
MW indication



Molecular weight

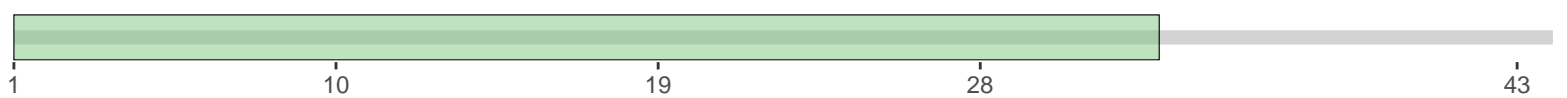


Gel Slice



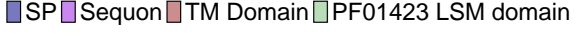
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

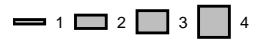


Protein sequence:

VEVNGNEKNEIGMIVIRGNSVITIEALEPVARAD

NbL13g25520.1 phosphoglycolate_phosphatase_1A_chloroplastic-like [MW = 39.79 kDa]

No. of times detected



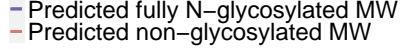
log(intensity)



Values from

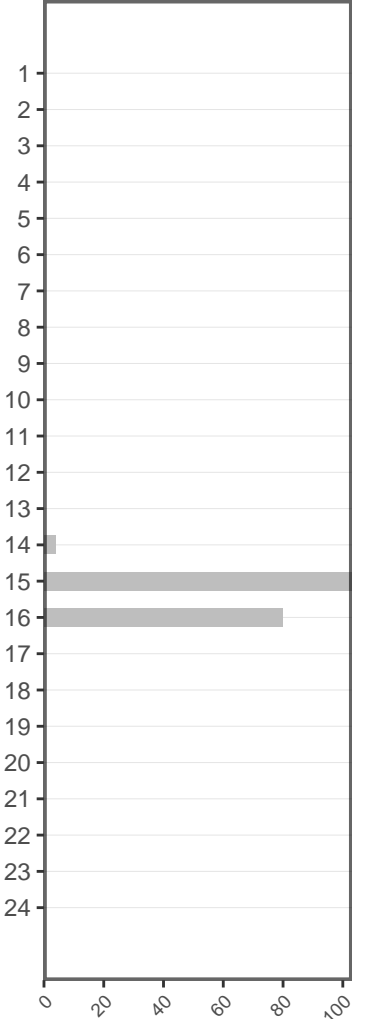
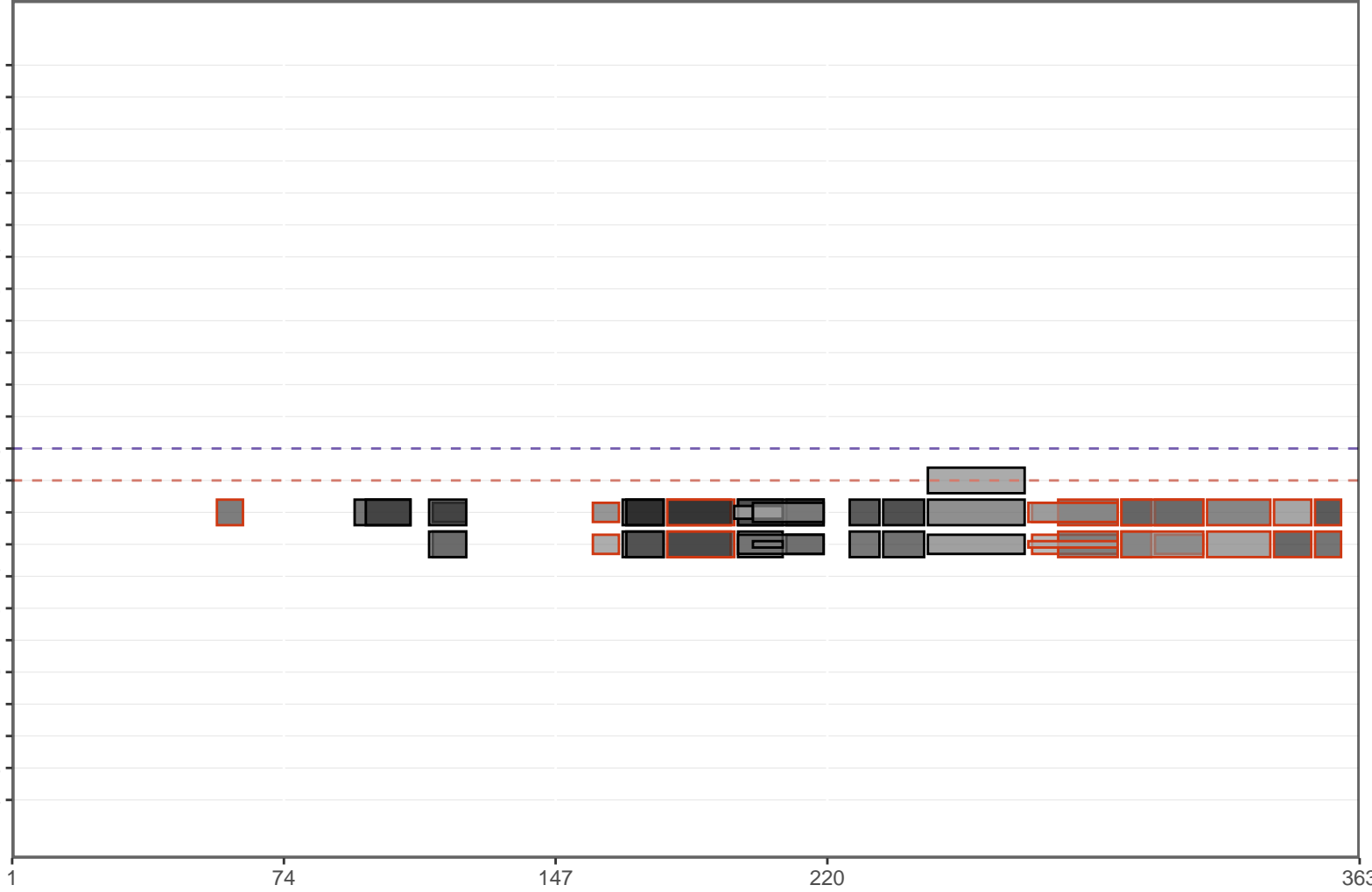
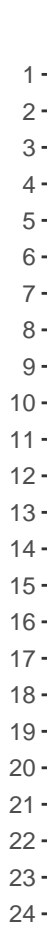


MW indication



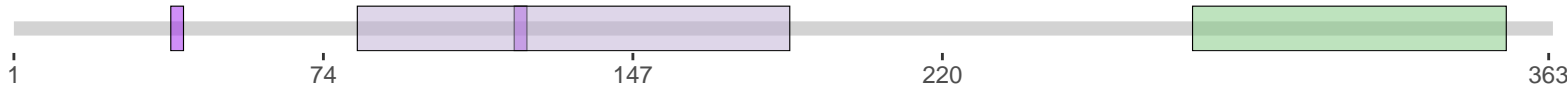
Molecular weight

Gel Slice



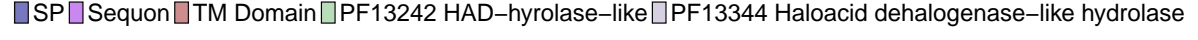
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

/GEEGLKLELAGKHGGDDGDKLEKPKYMMEGDKDGVAVVGFDRYFNHQQWALGIRENPGOLFATNRDAVHTLTDAGEWAGGGEMVGAIGLSTKREPLVVGKPTFMMDHLANEFNKGSKQICMVGDRDLDLFGQNGGKTLVLSGVTSLEMLQDPKNSQPDFYANKSDFLSKATAV

NbL13g25510.1 omega-hydroxypalmitate_O-feruloyl_transferase-like [MW = 51.21 kDa]

No. of times detected



log(intensity)



Values from



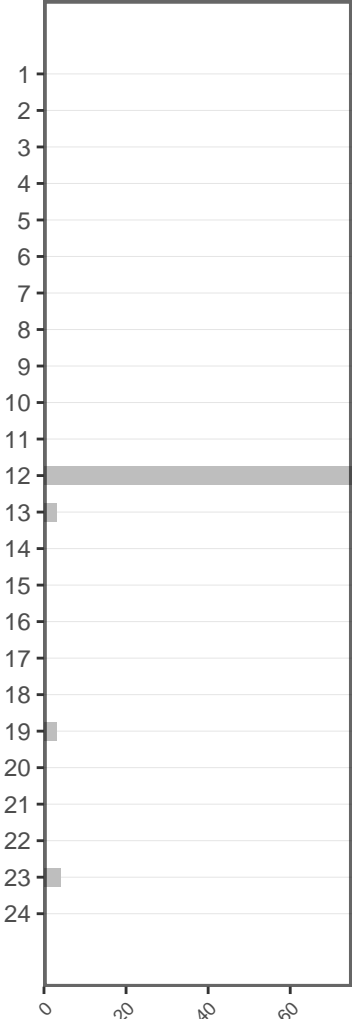
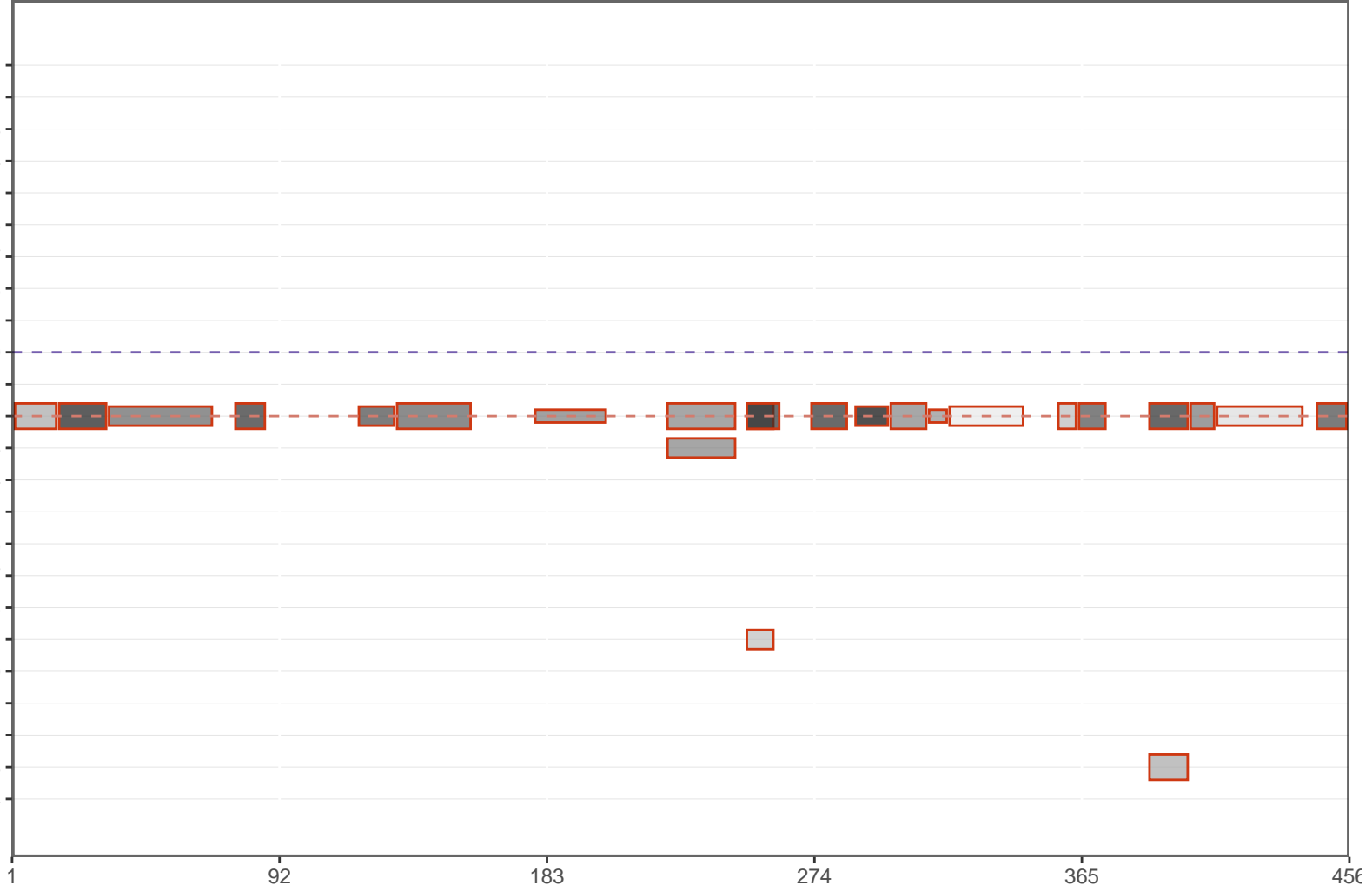
MW indication



Molecular weight

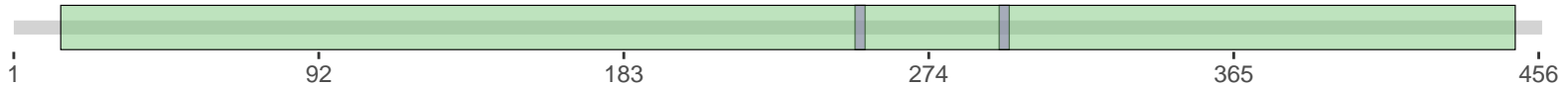


Gel Slice



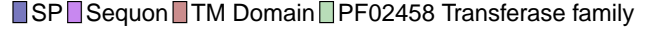
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PHPELLKLEVPYIGEEINPTVFQALQEEELVFKIFLNSDSSLSLKKKAKDENAPAAKVTGFNVTAHVWYKGLSDFDVENNSERISTVLFVDIRPRLNPLPKYVIGMVALSSVYASAAHLEEEVFFYKIDMVSKGAMRMTDEYARSHVDWGEFYKGFNDFEFLISSWRLGFSEVEYYPWQPKYSGPLVSHRDKDLFFPNDGDISSNNDGVNIVALPAKQMEKFEYFHQFLLA*

NbL13g25460.1 uncharacterized_LOC107801208 [MW = 21.1 kDa]

No. of times detected



log(intensity)



Values from



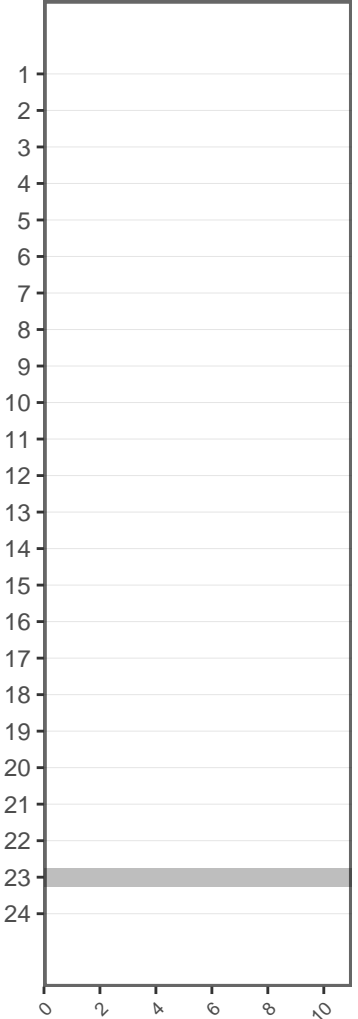
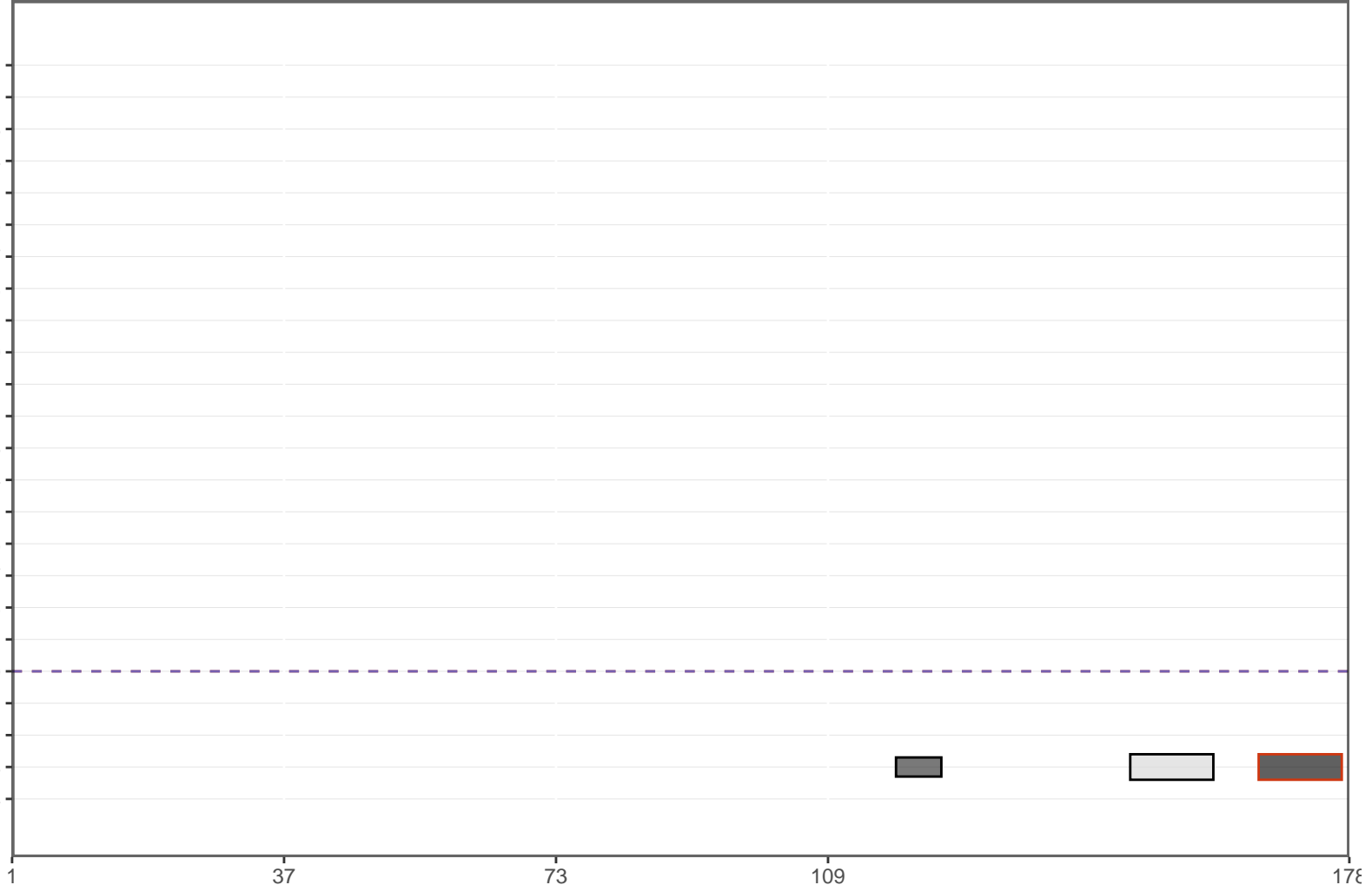
MW indication



Molecular weight



Gel Slice



Protein length

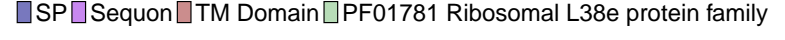


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

GHVRRRSPDAQDDMTFMQVSEDFLDRKVVRSRIKPKGHEKDFLLTARRKDAEKKKKKNDMKFKVRSKYLTLGVSDFEKADLKGSLPPGLSEVDL

NbL13g25270.1 protein_transport_protein_Sec24-like_At4g32640 [MW = 117.14 kDa]

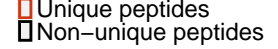
No. of times detected



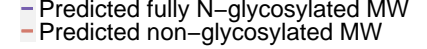
log(intensity)



Values from



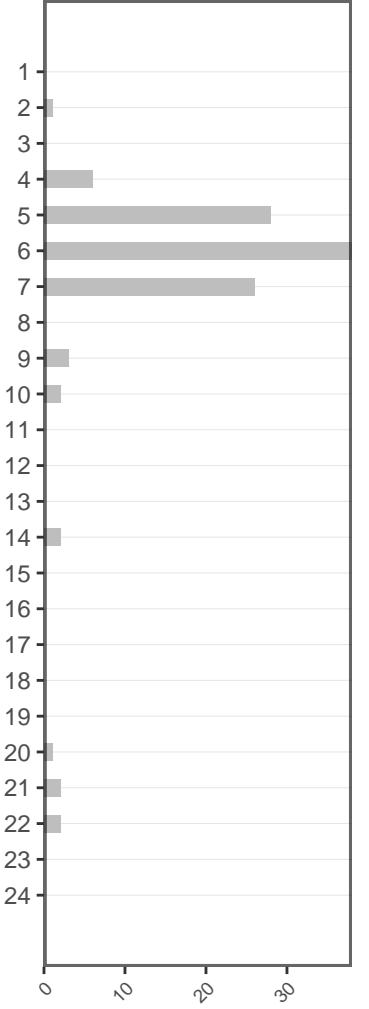
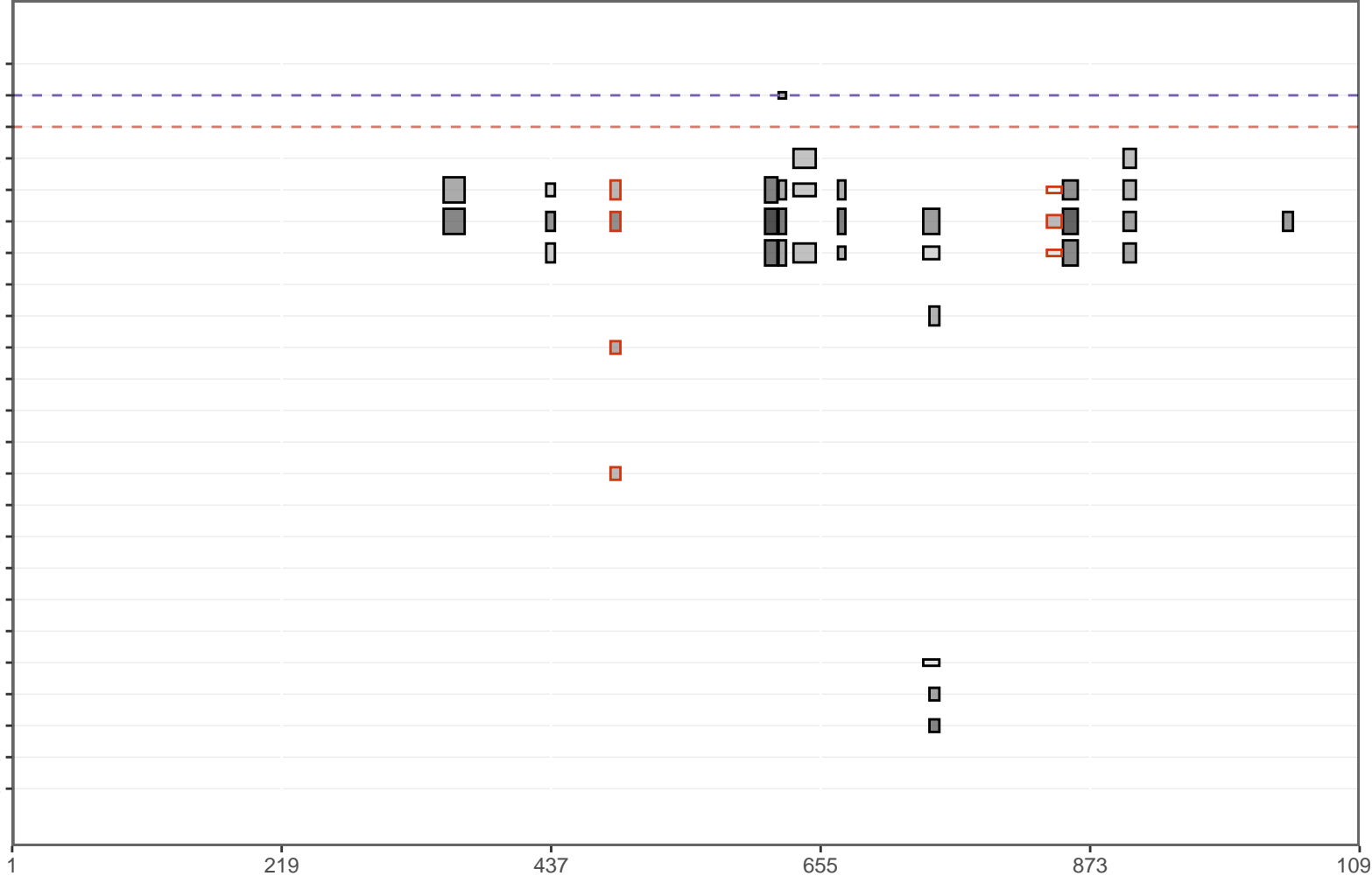
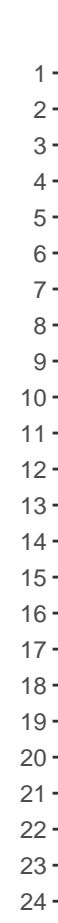
MW indication



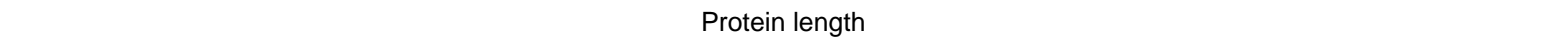
Molecular weight



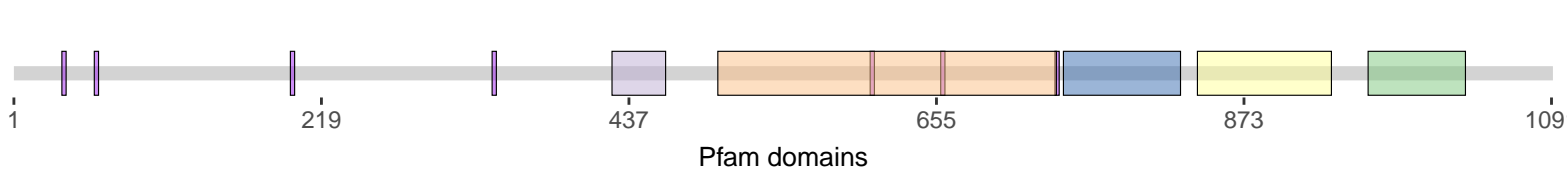
Gel Slice



Protein length



Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF00626 Gelsolin repeat
- PF04810 Sec23/Sec24 zinc finger
- PF04811 Sec23/Sec24 trunk domain
- PF04815 Sec23/Sec24 helical domain
- PF08033 Sec23/Sec24 beta-sandwich domain

Protein sequence:

SATAAACSAISQVITLPEGPRTLVGVATFDSTHFVNLKRALGGPLMLVFDVGDVYTPLGTDVIVQLSEGRGHLLELLLESTPMFGNRRITADSAFGAAWKAFLAMKSTGGKLLVFDGVLPTDGLSAREAEGRITVNSAAEKEAKHLGPAKDKLKTMAEFAEYGVGVDFVLTGSHVDHNSISWPKTGGGVYVYFFPSALADGAKLYNDRWNTFRPQGFVAMVRVRCGGGKGVGEVSGNYSKRNPTDVLPAIDCDKRTMVSLSKHDDKLGDDGSEGGFQSAVLYTTIDGQI

NbL13g25260.1 uncharacterized_LOC109239406 [MW = 57.94 kDa]

No. of times detected



log(intensity)



Values from



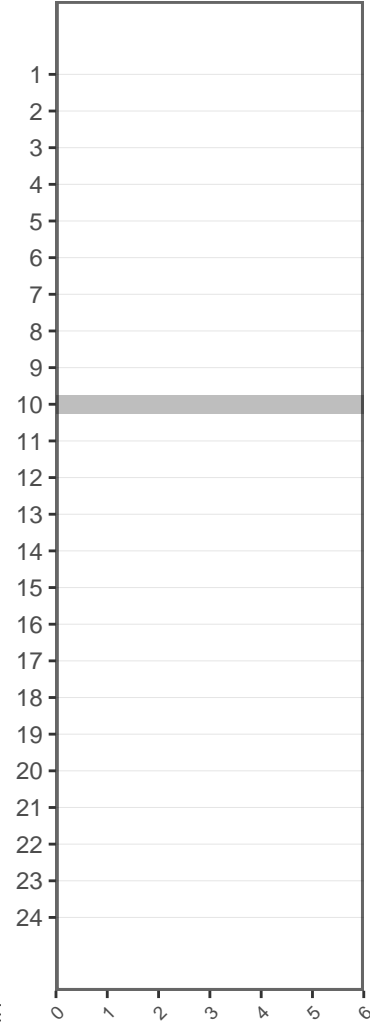
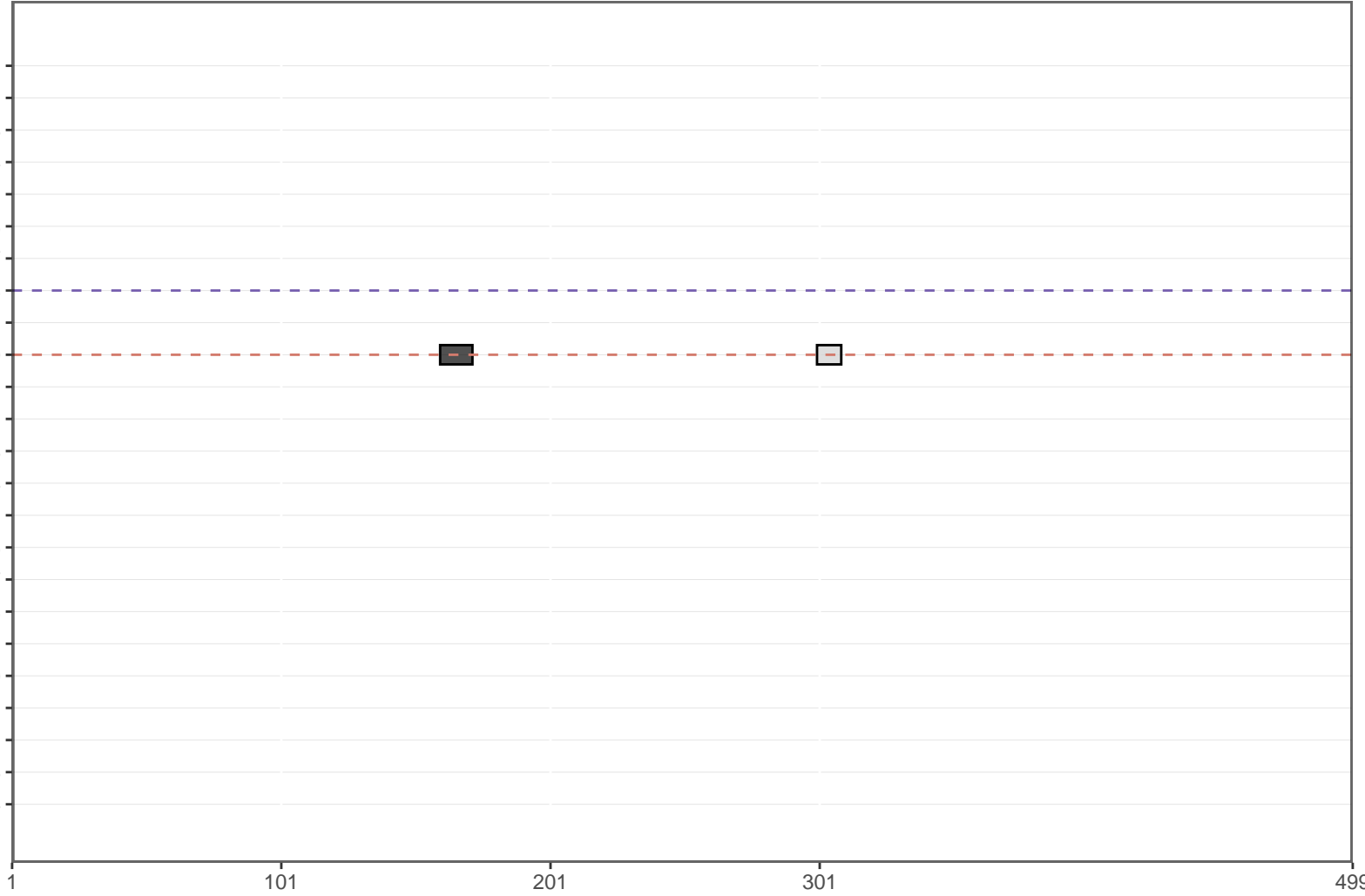
MW indication



Molecular weight



Gel Slice



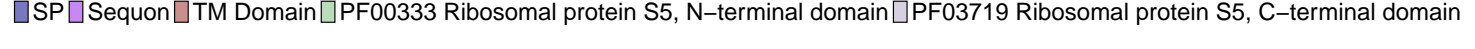
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

2ENYGIQHEDVGFNVDLLEHAGFEKEKEMIGGGDDDDDDIEFDDMKKDDILLEKLNADRKLEEKLAELDHTFGKRGKLLLEEIRDLAERNSLTEKRRPLRYKGFDFWLVLDVNRTRCKVTKGGQVWYWTALLADGNHGVVGFPAKAKGPAIPALQKAVEKFGQLHYVERHEHTSHAVGTNHYKTRVYVWFPPTGTGMKAGRTVGTILHAGFRNWKVWVGSANFNHTKALFKALNSIEPKDVEEKFGRTVVEGYLL

NbL13g25160.1 beta-hexosaminidase_3 [MW - SP = 57.13 kDa]

No. of times detected



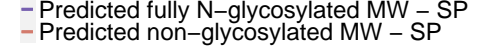
log(intensity)



Values from



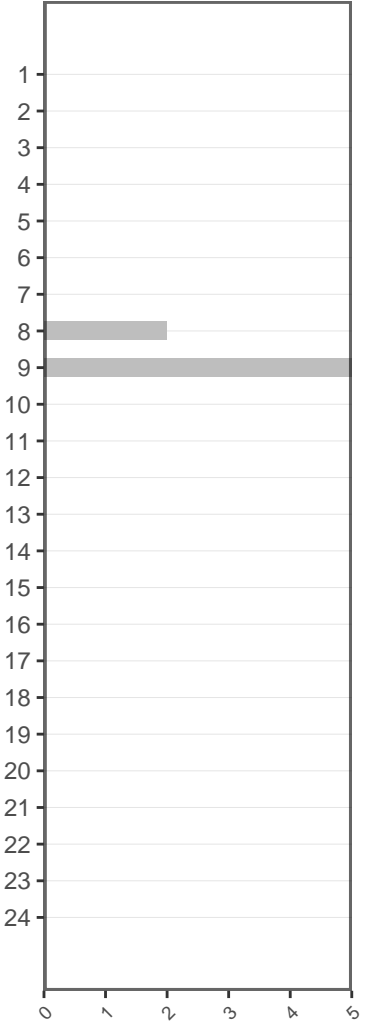
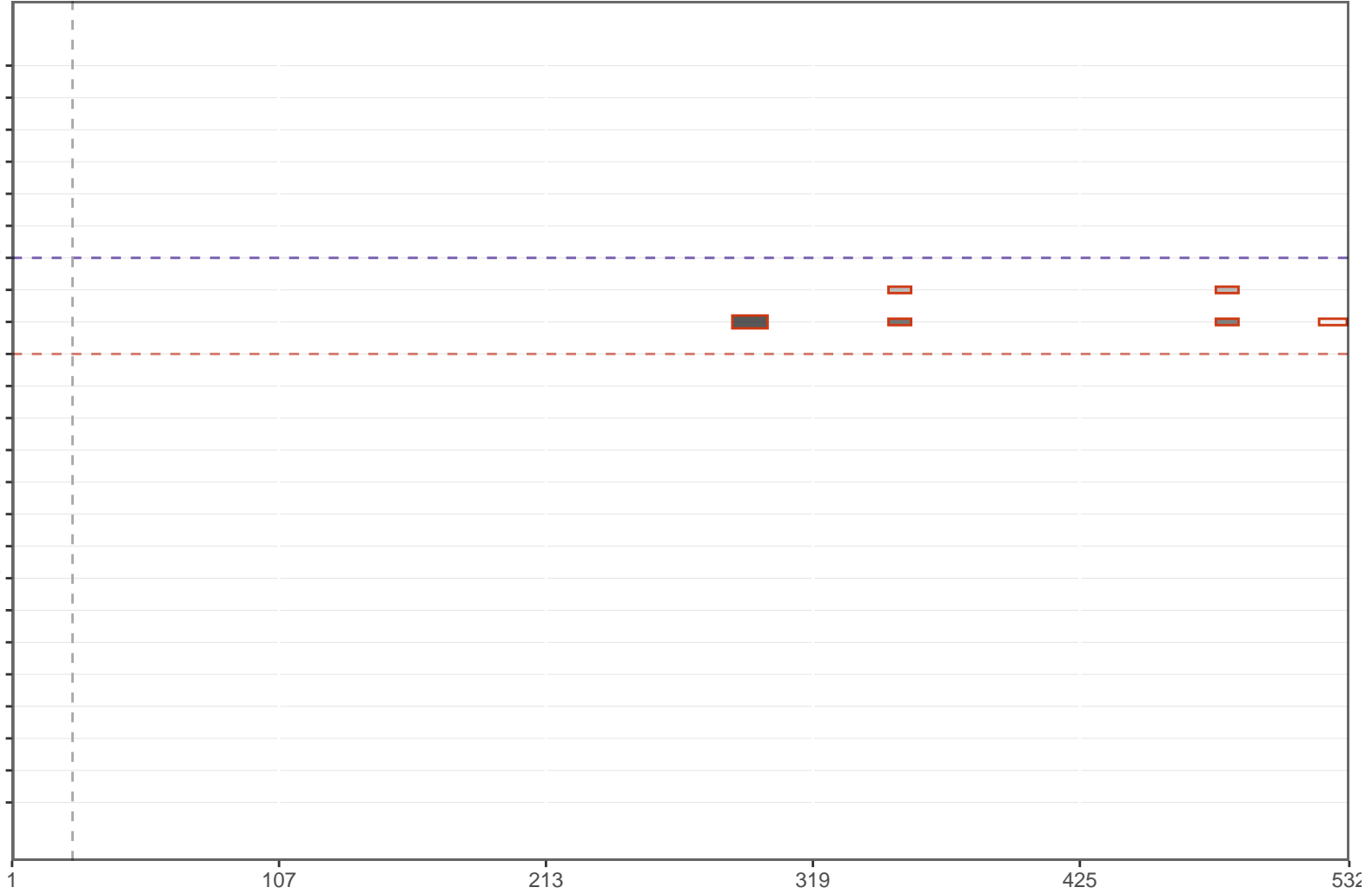
MW indication



Molecular weight



Gel Slice

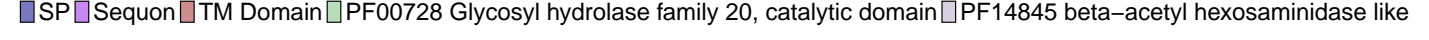


Protein length



Pfam domains

Pfam Description

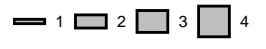


Protein sequence:

SRRGIVLAELDVPQAGSWSGTGVPBLWPKKDGQGPLDISNDFTFKLIDGILSDFSKFYRFVHLGGDEVDTSGWTLTPRIRKWLKQKLNRTTAYEVFLRAGKIALSHGYEIRNWEETFNFNFGKILPNTVHWLGGVAGQVTAAGLRGIVSNGQKWLKLDHDTTWGDFYSNEPLTNRNFKQRLVIGGEVGMWGEHIDGSENIETTWPRAAAAAERLWTAYDLAKNPSGVTRRLAHFRLLNDRGVASVFLTGGRAAPEDPQSGYQQ--

NbL13g25120.1 protease_Do-like_10_mitochondrial [MW = 65.9 kDa]

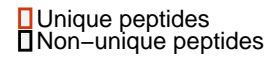
No. of times detected



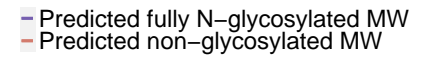
log(intensity)



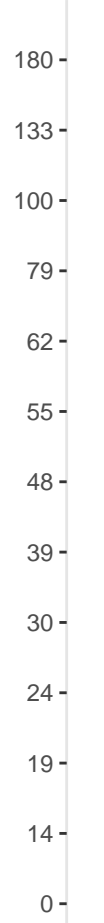
Values from



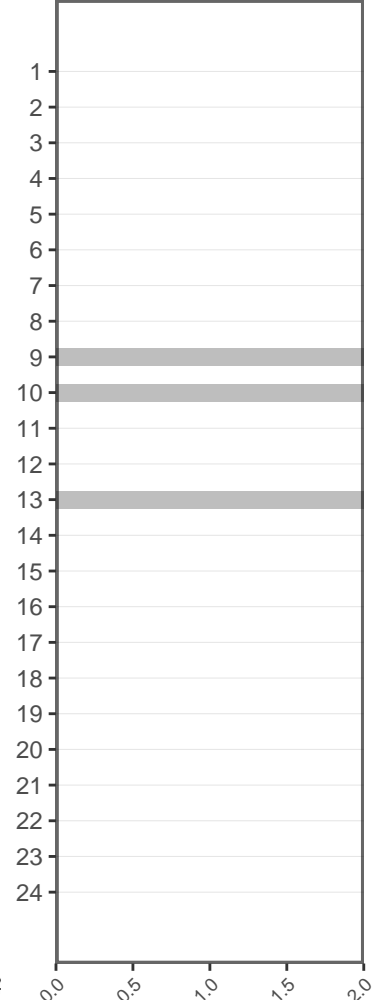
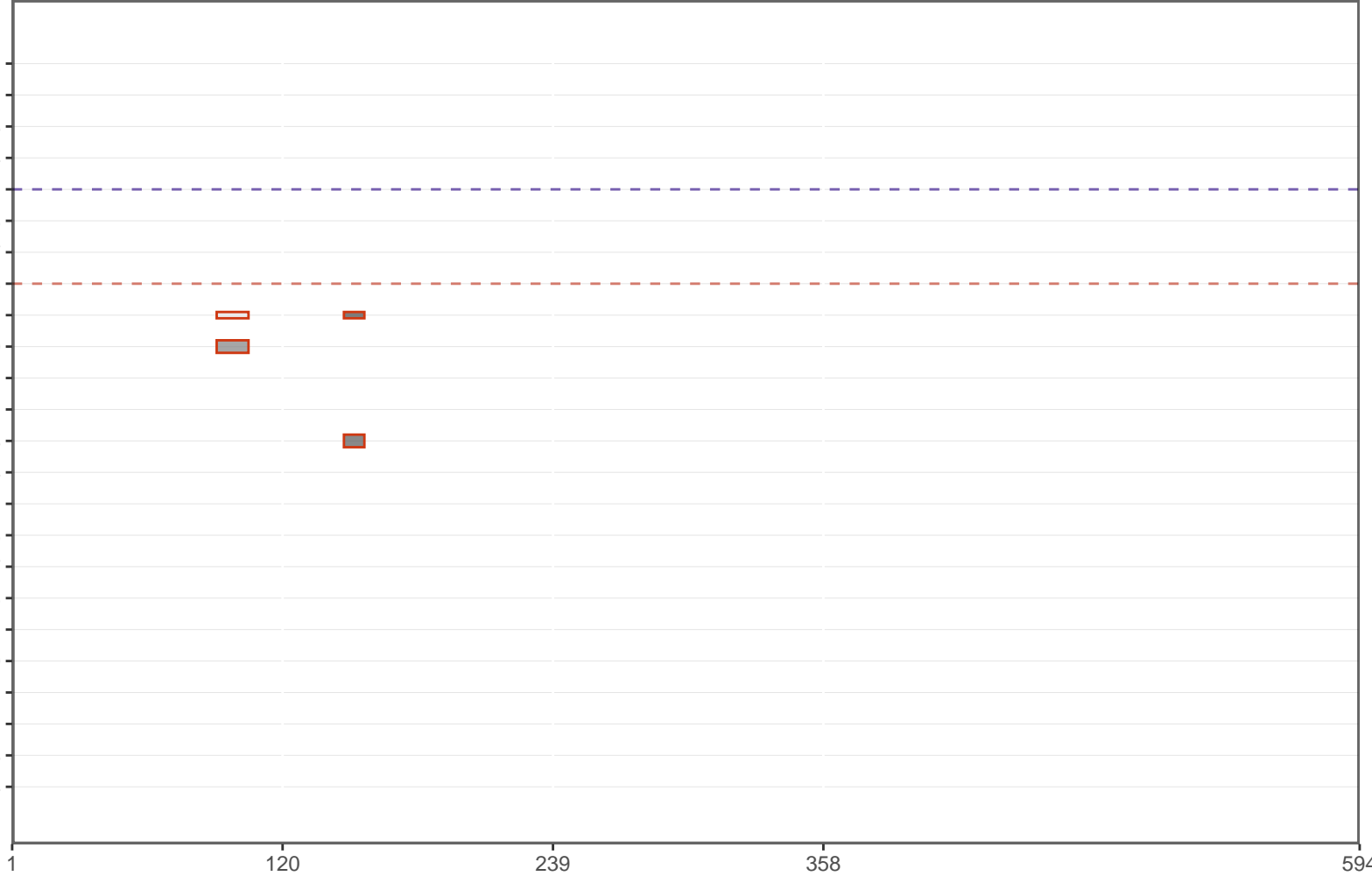
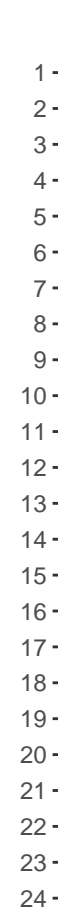
MW indication



Molecular weight



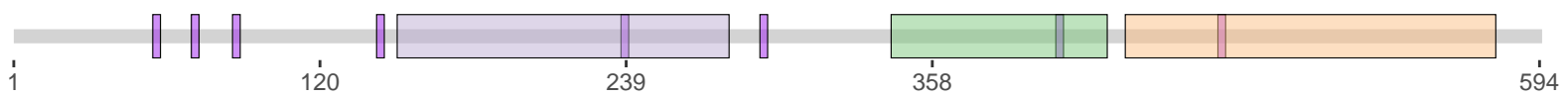
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

KVAGVAFQNLSCAENIGYHPVPIKHFAGVEERGEYVGFGLGLGSCOPTENAGIREYFMQDGLTGVLVSRINPLSDMRVLLKDDVLSFDGVPVANDGTVDFRNRIRITFDHLSVMKKPNETAELKVLKNGEVHDFKGTLLPLGLVPHVHGFQDLPSYFFAGLVFPLTQPLFHEYGEDVYNASPRRLGERALRELPKPKGEGFHLGVLMDNDNAGYERLAELGVKVKVNGIEVLLKHLRQLGVLEDGNGKRVFDDLDDERVVLLNVEIARIATSRILKRRHPIIAMISTDLTDGI

NbL13g25080.1 reductase_2-like [MW = 67.54 kDa]

No. of times detected



log(intensity)



Values from



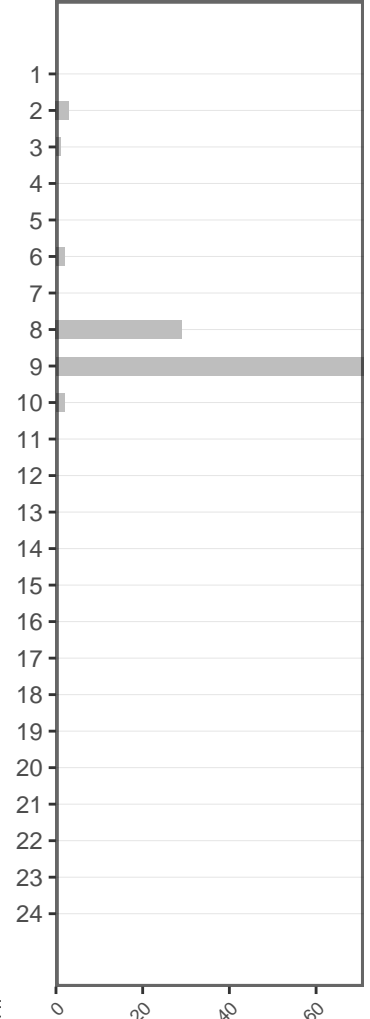
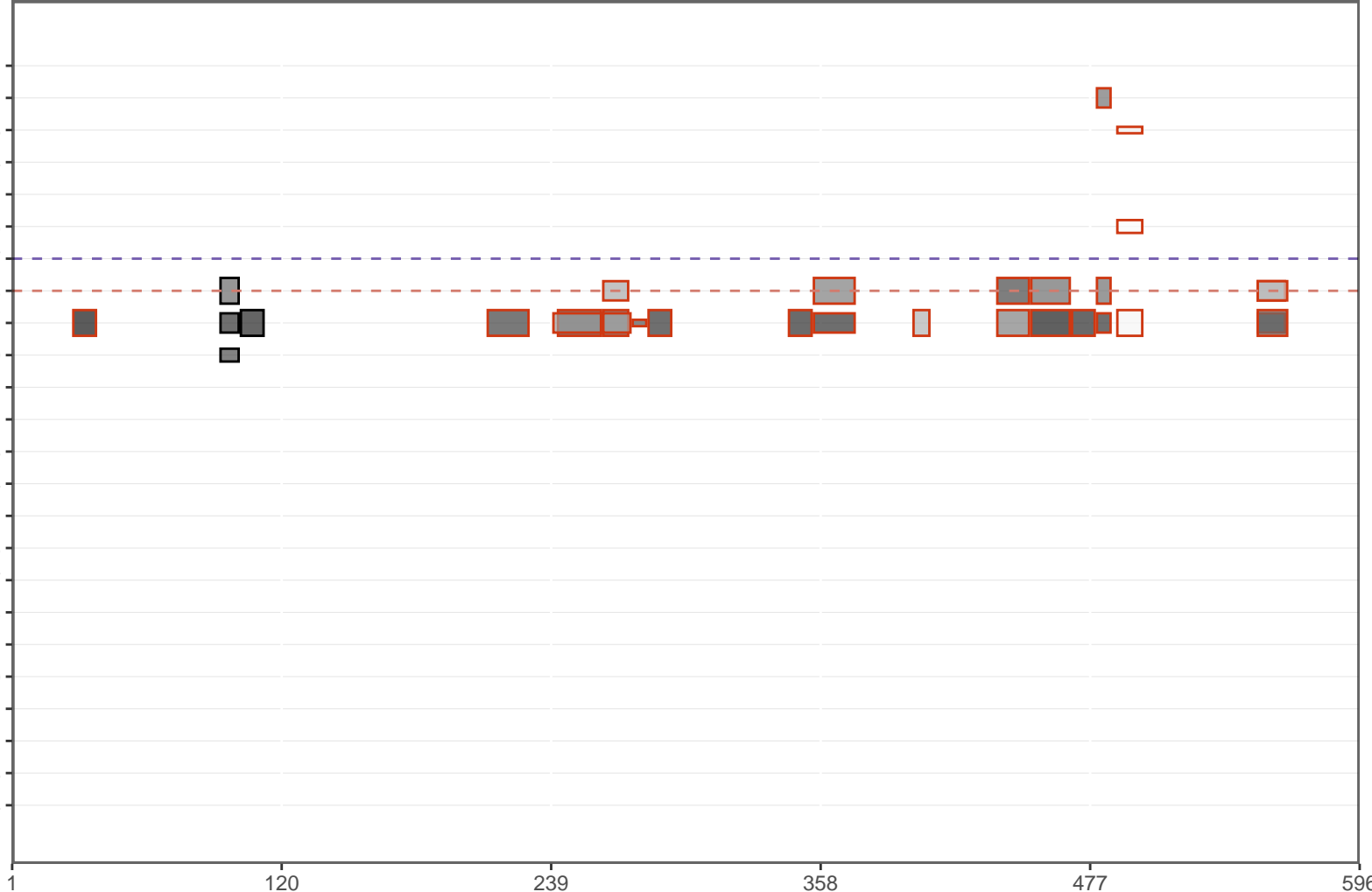
MW indication



Molecular weight

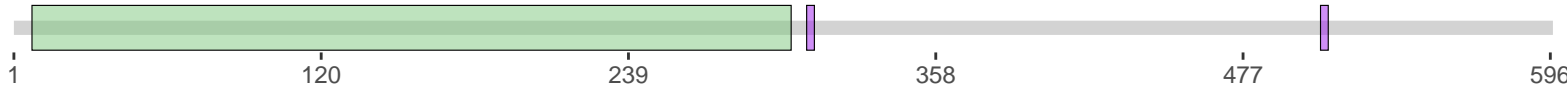


Gel Slice



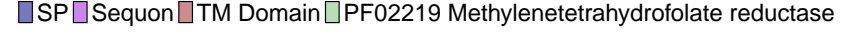
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

VDKSLAALLMNLGLEESNISRPLFWRRPTNIFVRVKEDVRRIFWANRPKSYHSRTLGDWEYVPHGRVGNAGINPQYGALEDHGFLLRARSRDKKLGQEEVVAALNVEEDLYEKFDPYGLGLRCPWSELDGLQPTKINEKLGHWYTKGLFTINSQPAWNAEKSDSPKGVGGHGGVYQKALEFFQSGSEKLTFLVEKOKAFYLYTMAVANKEGMWNISGTDNAVATWGVFPAKEVQPTVVDPAQFMMWKADEFENWSRGWALQYPETDPRKLEQVQNCYYLVLV

NbL13g24990.1 membrane-associated_protein_VIPP1_chloroplastic [MW = 26.93 kDa]

No. of times detected



log(intensity)



Values from



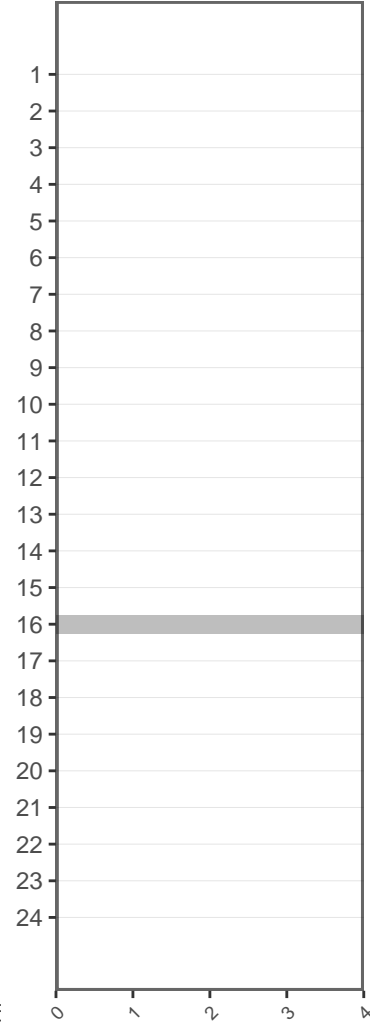
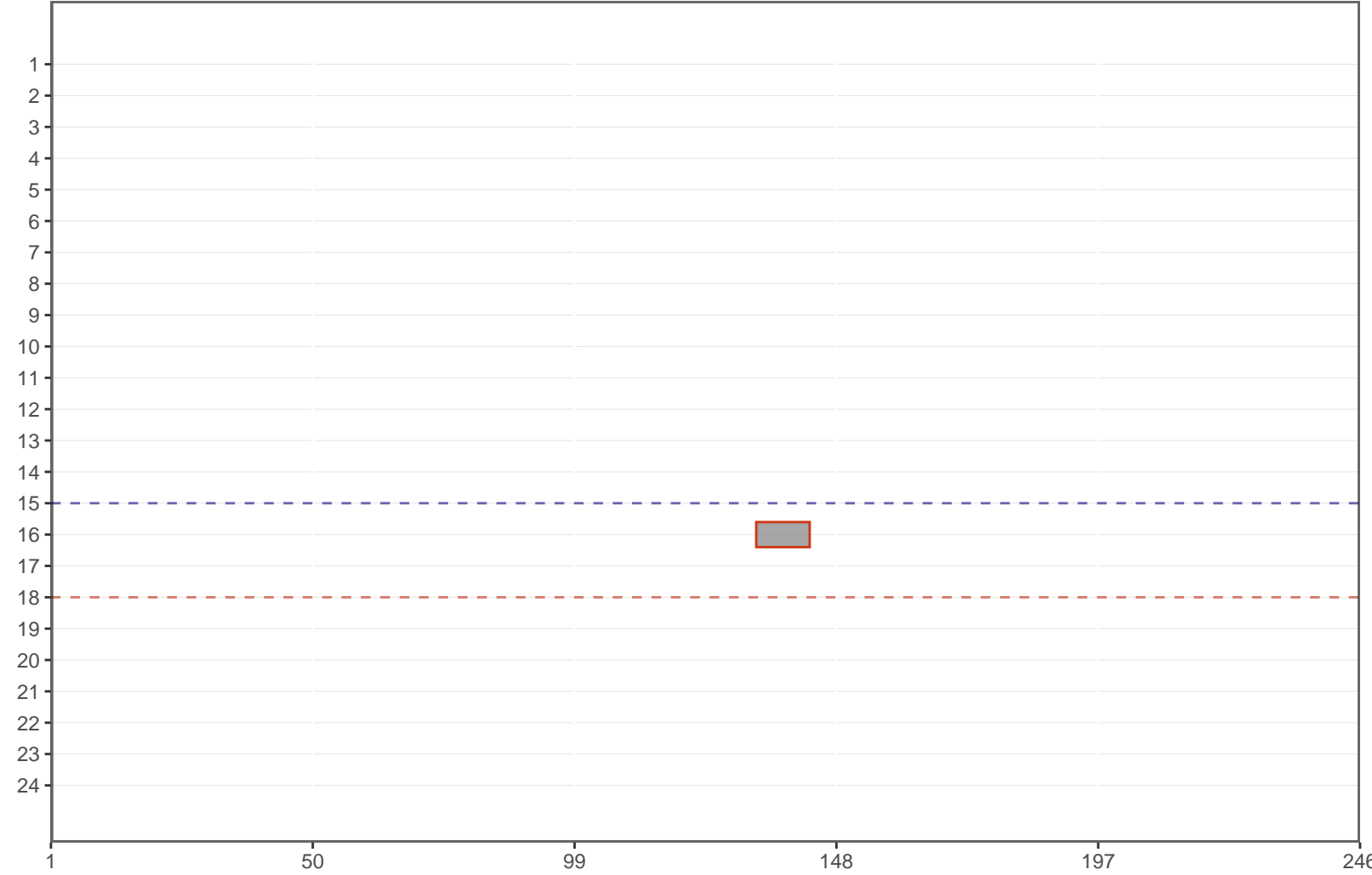
MW indication



Molecular weight

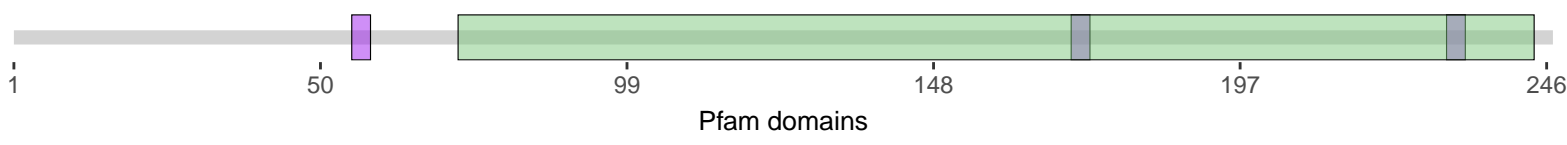


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KMIRDATAGVLAASKGLENKYYKAAQGAASEWYRRADLALGKGDDEDLAREALKRRKAWADNASALKAGLDGQKGVVENLVNTRLLLEKIGEAQSKKDTLAKARAGSAKTATKIVSEMIGNVNTSELSAFEEWKKP

NbL13g24760.1 14-3-3-like_protein_16R [MW = 29.1 kDa]

No. of times detected



log(intensity)



Values from



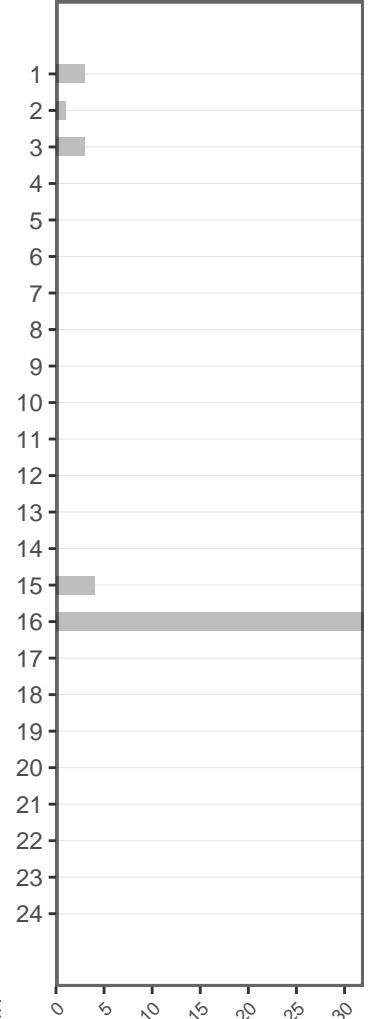
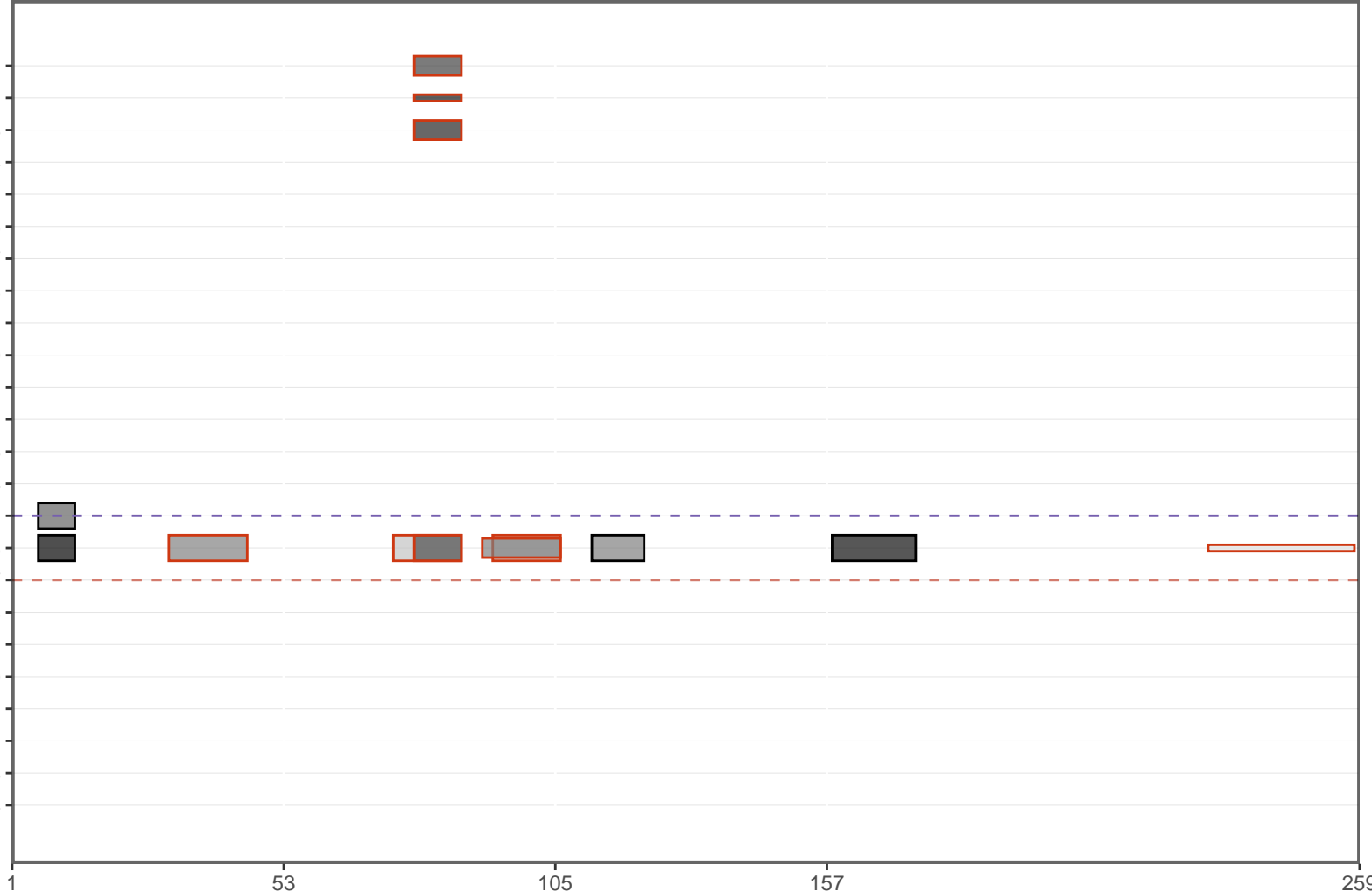
MW indication



Molecular weight

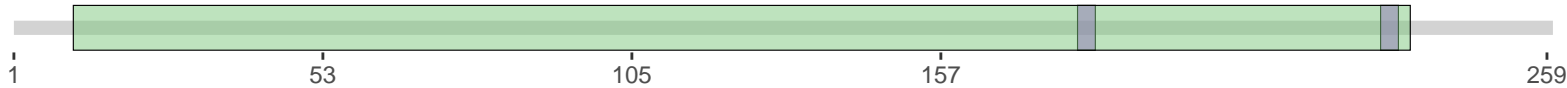


Gel Slice



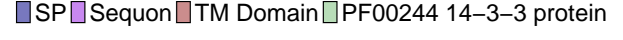
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ITGDSKVFYLMKGDVHRVLAEFKTAERKEAENTLSAYKSGAGDIANTELAPHTPIRLGLALNFVVFYFYEILNSPDRACNLAKGAFDEIAIQLDTLGEESYKDGSTLMLQLLRNILTLVTSMDMDDGDTDEKEAAKPNQEGQ

NbL13g24690.1 bifunctional_riboflavin_biosynthesis_protein_RIBA_1_chloroplastic-like [MW = 59.27 kDa]

No. of times detected



log(intensity)



Values from



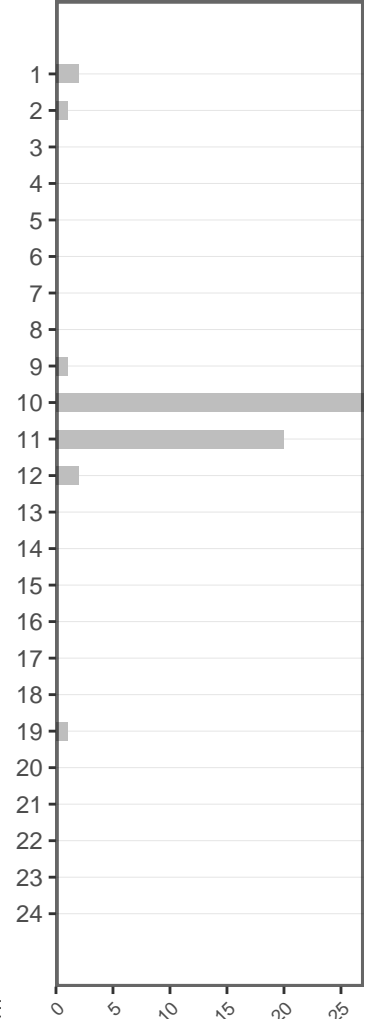
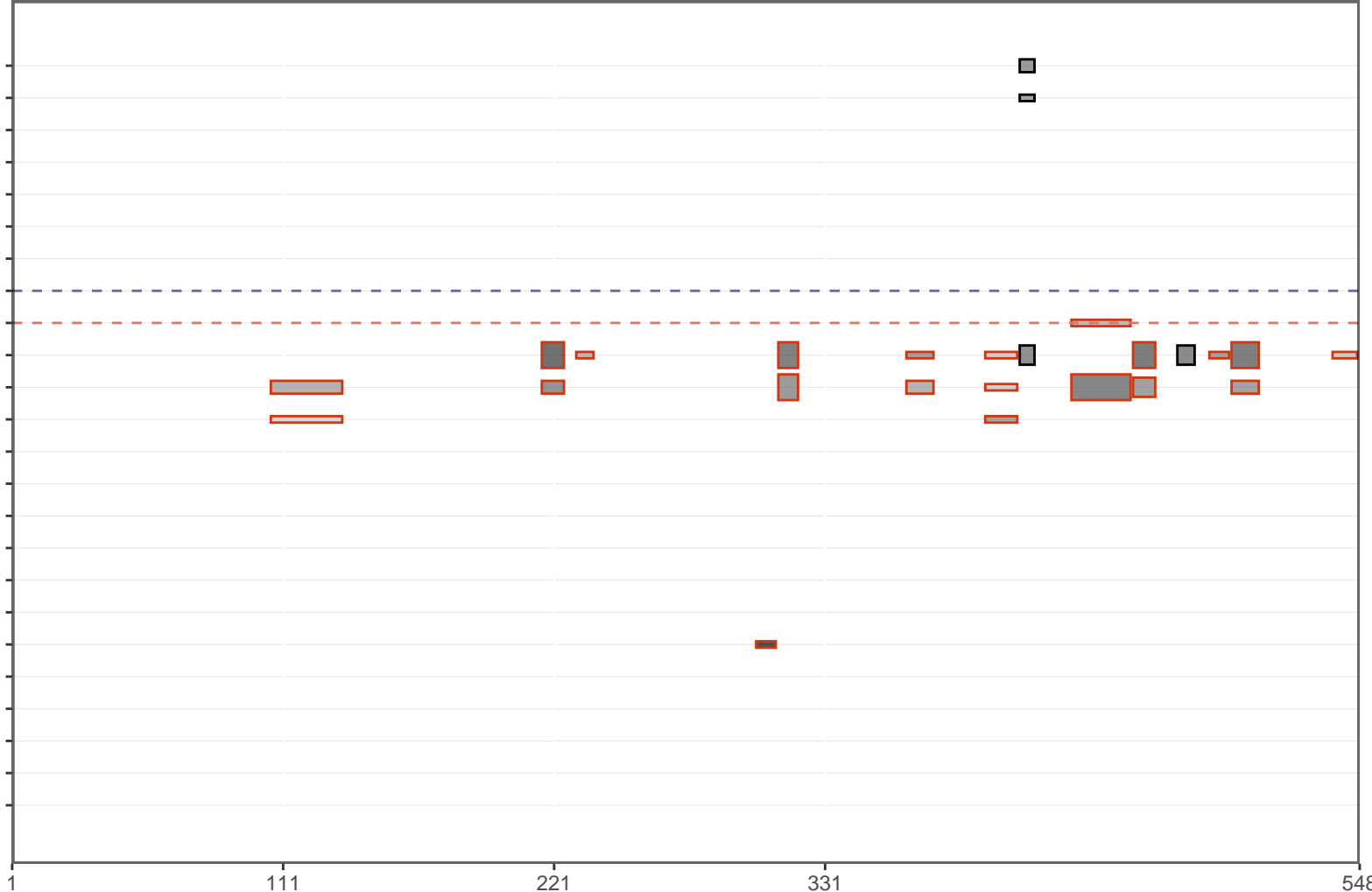
MW indication



Molecular weight

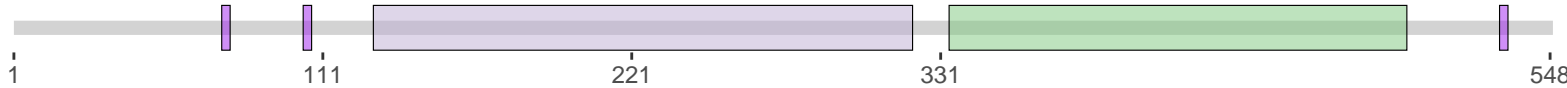


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LKRAGHTEASVLDLAVLAGLDPVAVLGEVDDGDSMARLPRLRQFAEAEENLKHISADLRVRRKREKVELAAAPFTMVGPFKAVCFKSVLDGIEHIAWVKSGDGDGKDLVLRVHSECLTGDVFGSARCDGKQLALAMEGIEQAGRGVLLVLRGHEGRGIGLGHKLRAYNLQDDGHDVTEANEELGLPVDREYGGIGAGLRDLGVRTMGLMTNPKWYVGLKGYGLAAGRVPPLAPITFENRRVLETKHVKLGHVYSDANGHNGSEVGRASSDELSDNAA

NbL13g24590.1 esterase_AGAP003155-like [MW = 24.84 kDa]

No. of times detected



log(intensity)



Values from



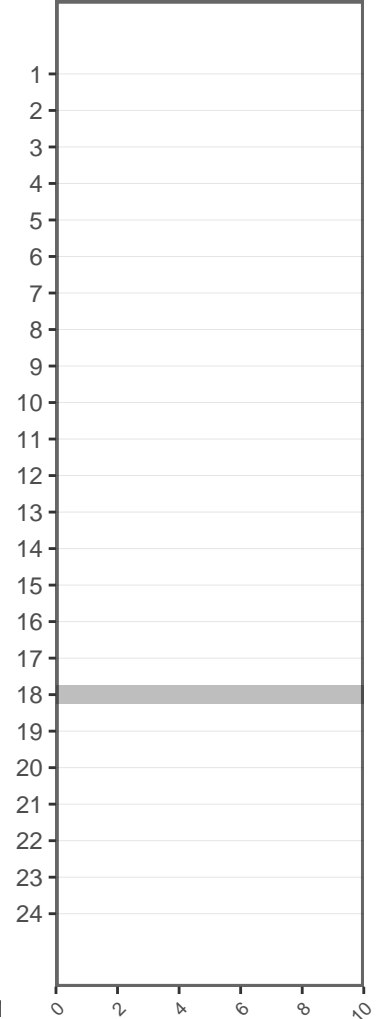
MW indication



Molecular weight

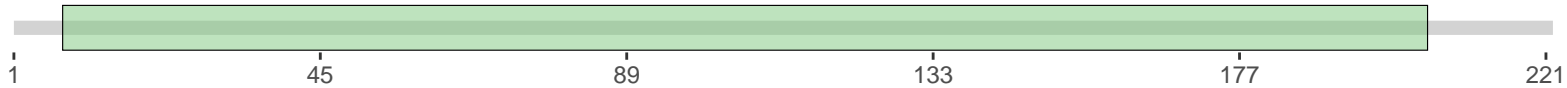


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SFFDGLGFSDQAVLAGAGIPGMQRERVLTKVDEIKFVHISGAKFGSPFVPLAANVFSSPINDPLHLFLGKDFQKDKGELLGSLFVDPQVHHHPKGHFTVPLKDDSSLEIMLEFIEIKDKL*

NbL13g24560.1 14-3-3-like_protein_D [MW = 28.26 kDa]

No. of times detected



log(intensity)



Values from



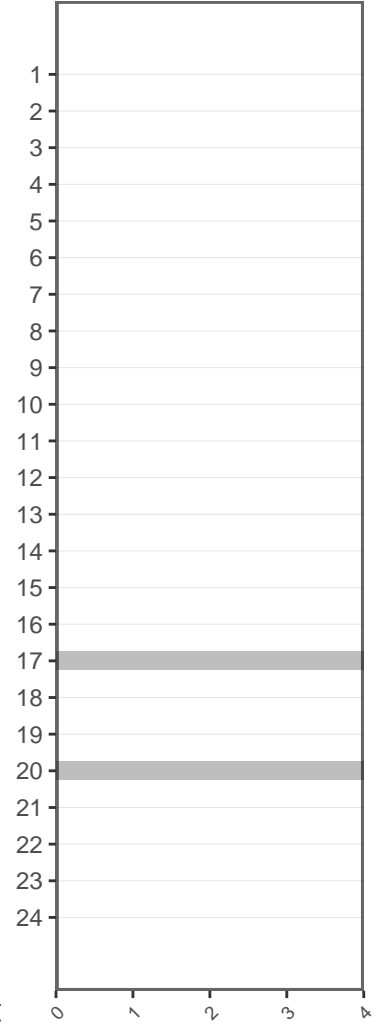
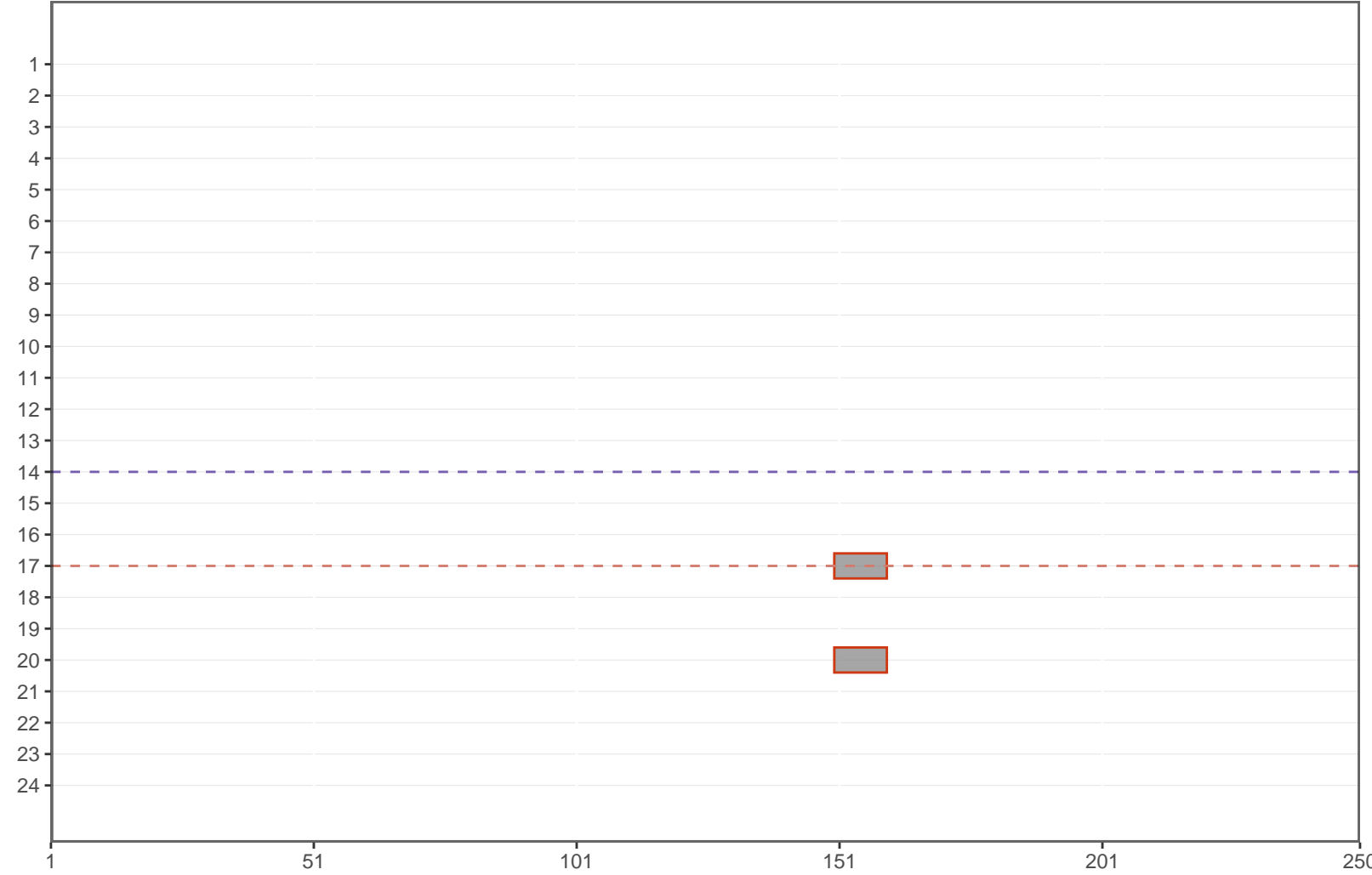
MW indication



Molecular weight

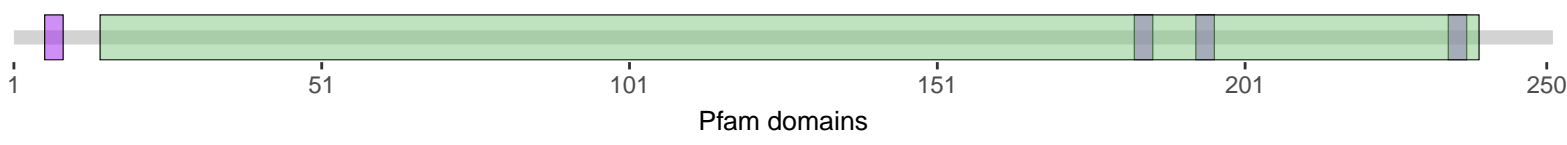


Gel Slice



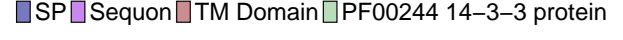
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IQYLIPASAGESKVFYLMKGDYRVRVAEPRKVGNERKEAAEDTMLAVRAAGDIALAEALPHRIRLGLALNYGVFYIEILNASEKAGIMKQAFEEAAIETLIGEESEYKDSLIMQLLRNLTFLWTSQMDEQMDIAI

NbL13g24550.1 protein_CURVATURE_THYLAKOID_1B_chloroplastic-like [MW = 25.65 kDa]

No. of times detected



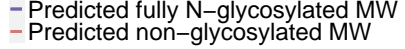
log(intensity)



Values from



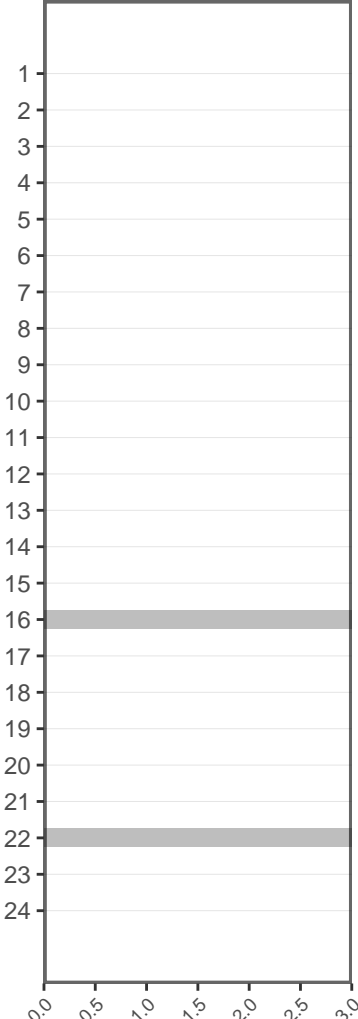
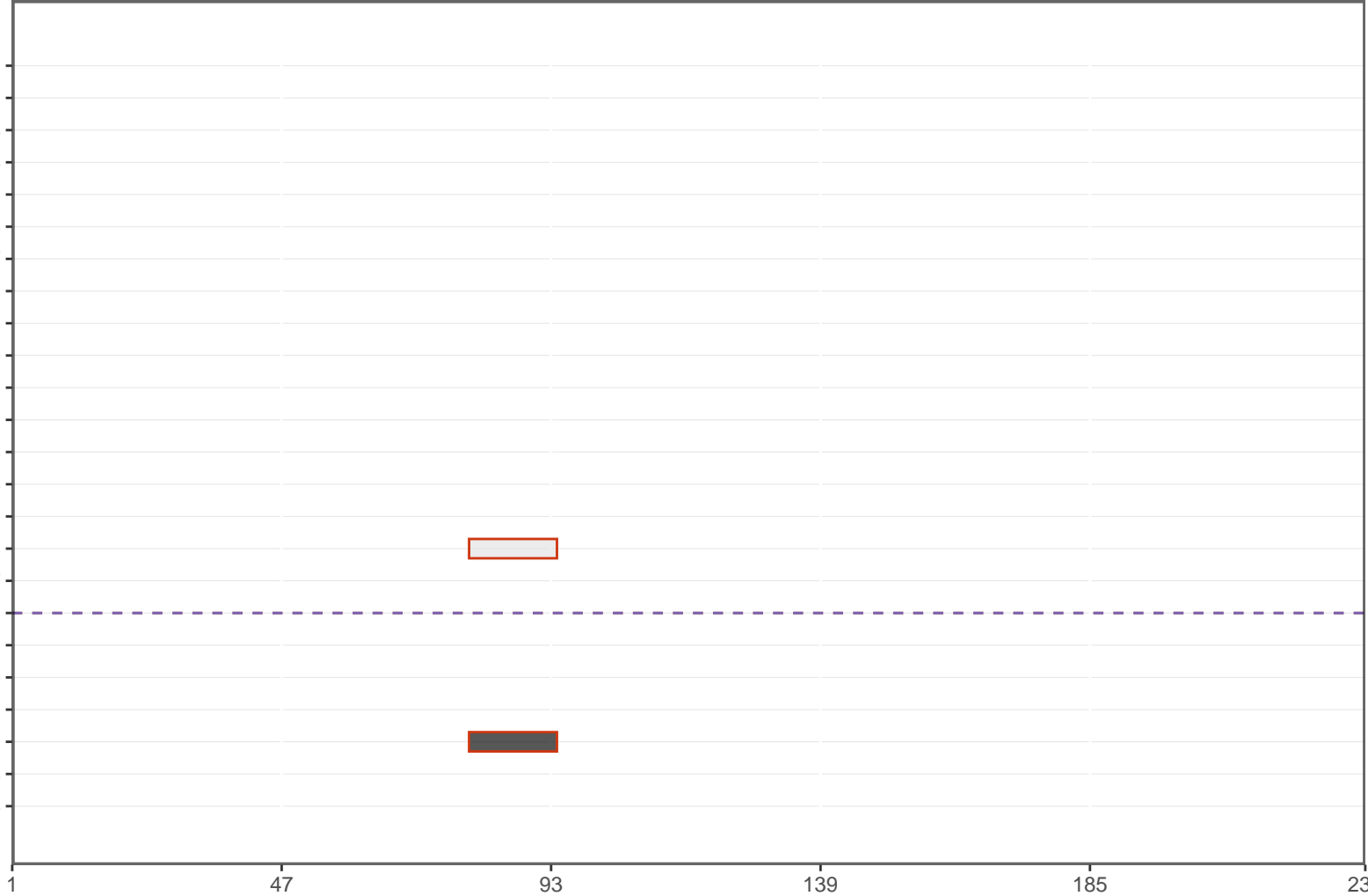
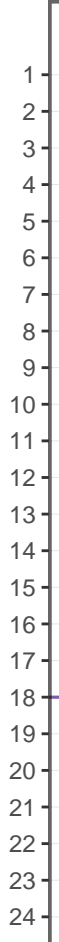
MW indication



Molecular weight



Gel Slice



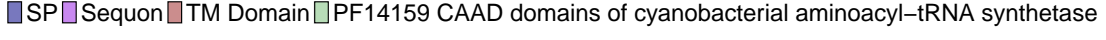
Protein length



Pfam domains



Pfam Description



Protein sequence:

'GSLVYEPKYLEEVEEKGGVYQAEETEDSPLDFDGLPKLFDKLNKFDLEDSSSILFGGAATLWLTAVVGAIDGIPFPLKLELVGLGYTWFSTRLLPKKRDLELANKEELKKEVLGGNYG'

NbL13g24320.1 diphosphomevalonate_decarboxylase_MVD2-like [MW = 22.34 kDa]

No. of times detected



log(intensity)



Values from



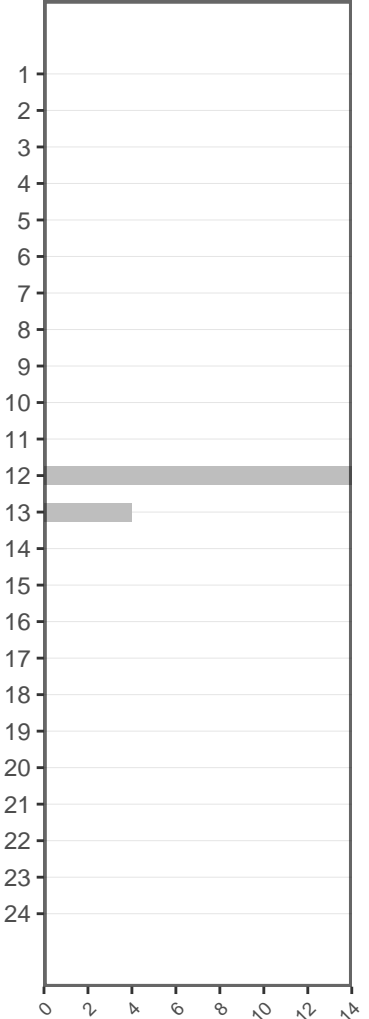
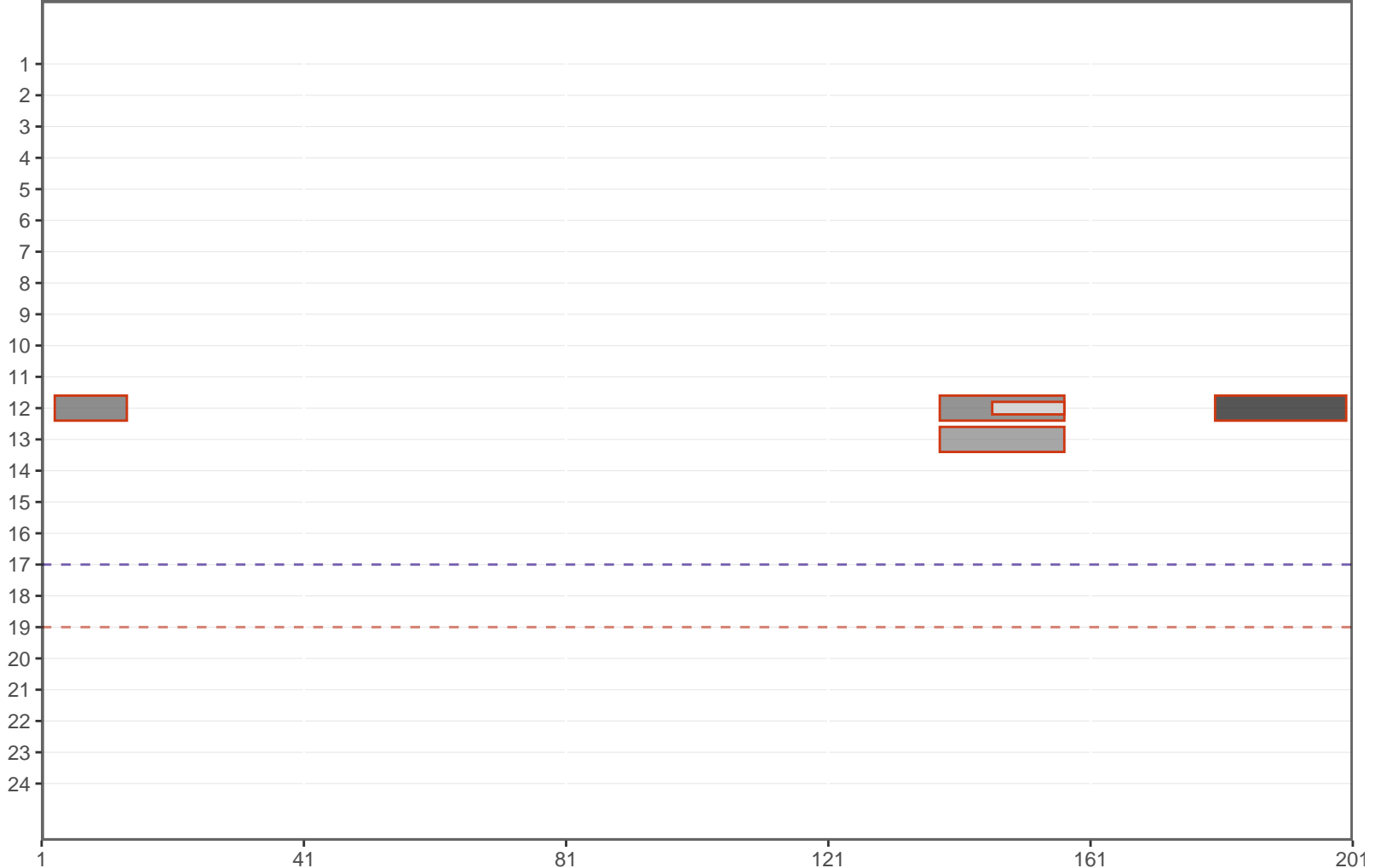
MW indication



Molecular weight



Gel Slice

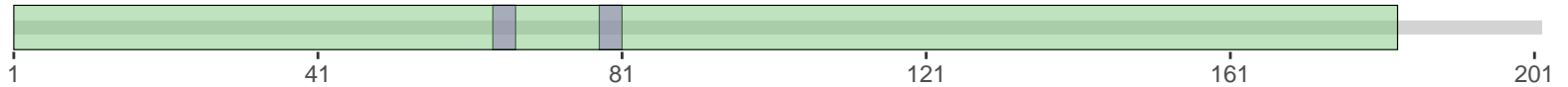


Protein length

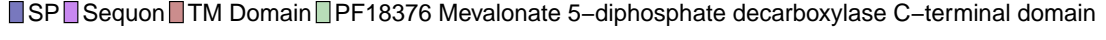


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VAYTFDAGPNAVLARNRKAATMLGRLLFFHPNSDITLNSYVIGIKSLKDGAGIDKIDVEALPPPEIKDKVPAQKYKGEISYFICTHPGRGPVLLTDDSHALLNPETGLPKV

NbL13g24290.1 probable_aspartyl_aminopeptidase [MW = 59.88 kDa]

No. of times detected



log(intensity)



Values from



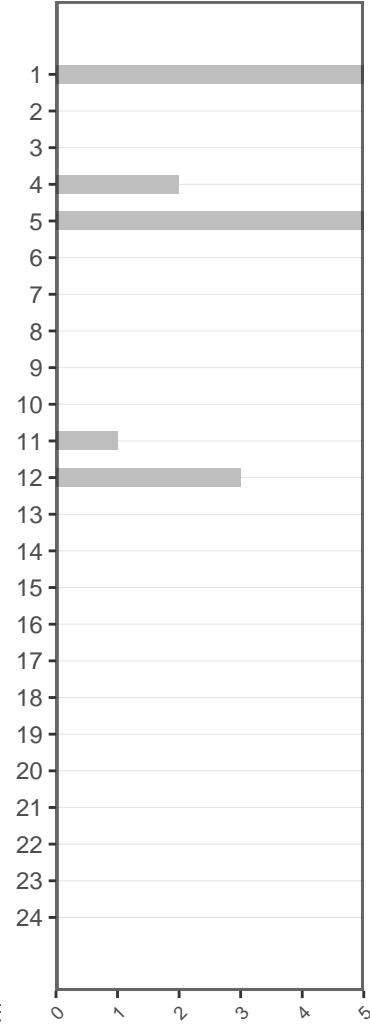
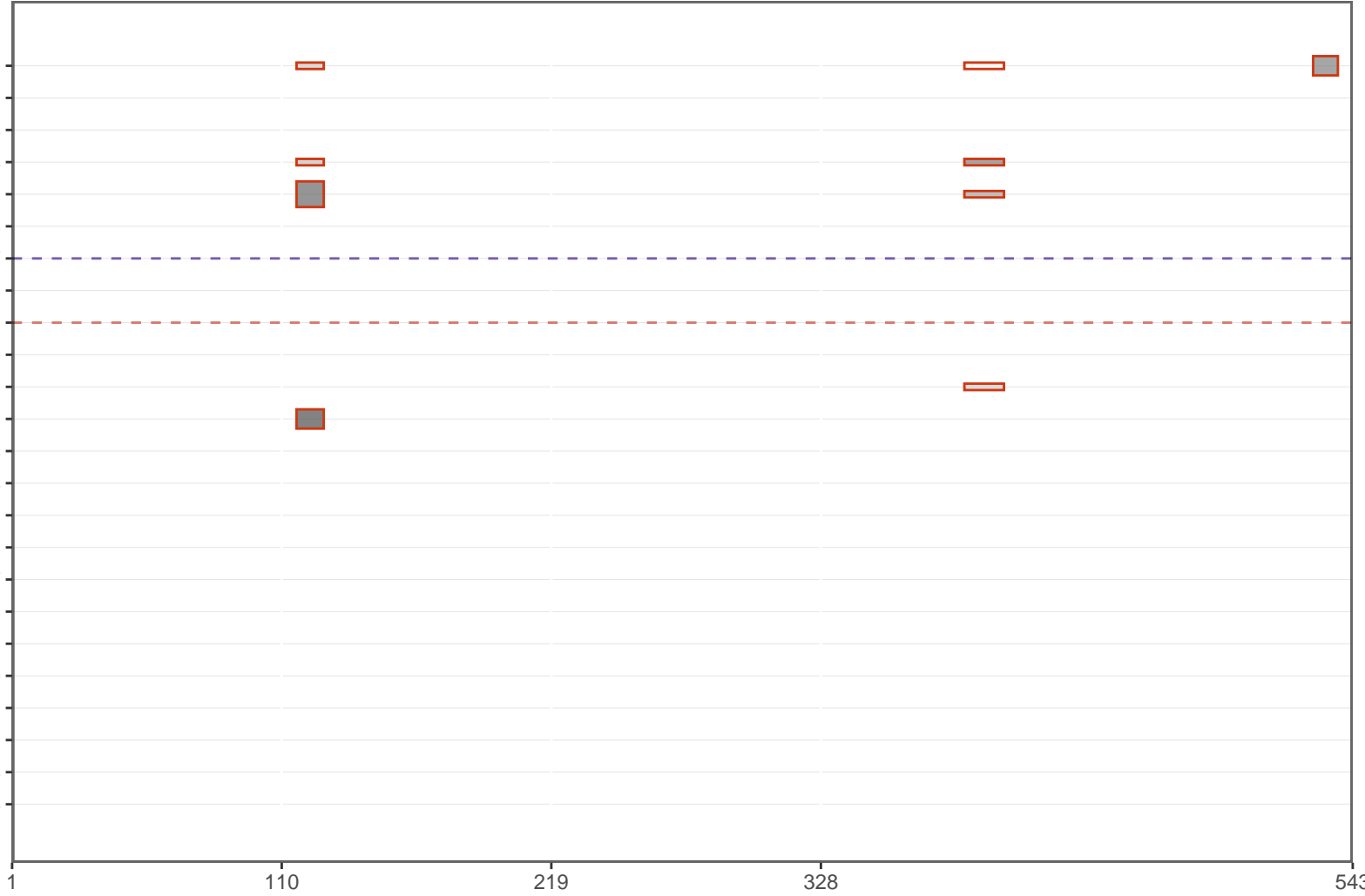
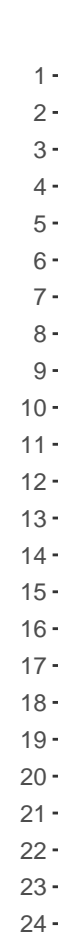
MW indication



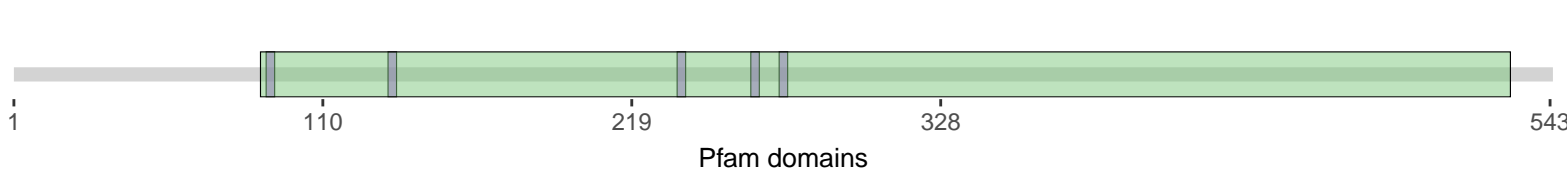
Molecular weight



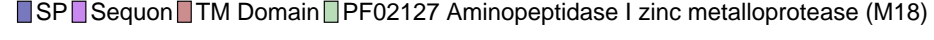
Gel Slice



Protein length



Pfam Description



Protein sequence:

ITENATADSTKSNVSSKDKHHQLLQLSDELSGKDDIVSVELNLGDTQPSCLGAGANFEFFSGRLDNLASSFGDLRALVDSGCTTFREDLNEHAFIRMALFDNEEVGSDVQAGAPTMFEAMRRITDCLSHQSGAGESDFARAICHYLYLSADMAHGVPNFDKHEEHHPELQKGLVKKHANNQRWTSQVTFSLFKEVARLHSLPTGDFVWRNDMCGSGTICPLASGVGRITVQGGIAGLMSHVAIEGCKEDIDYAKHFKAFYQTFSSIDRKLIVD

NbL13g24250.1 nifU-like_protein_4_mitochondrial [MW = 32.9 kDa]

No. of times detected



log(intensity)



Values from



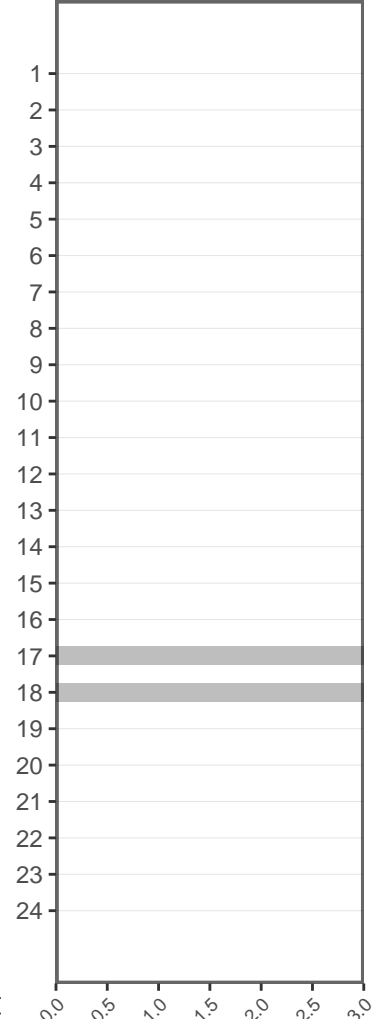
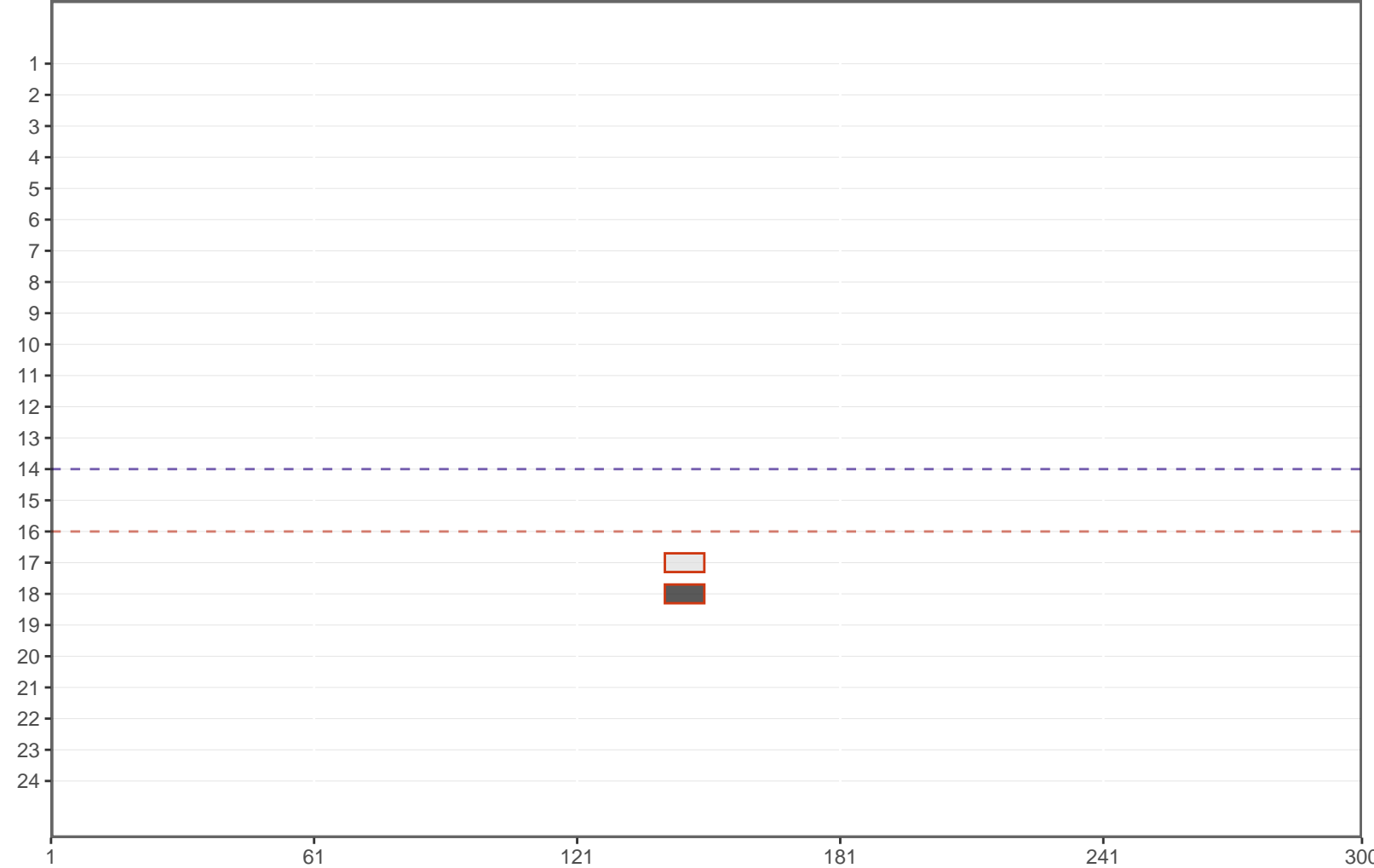
MW indication



Molecular weight

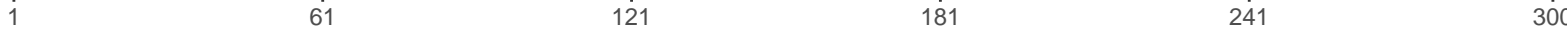


Gel Slice

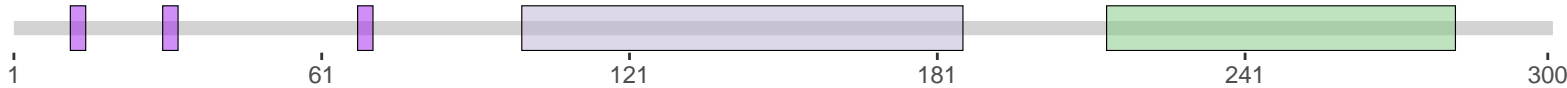


Peptide counts over 4 repeats

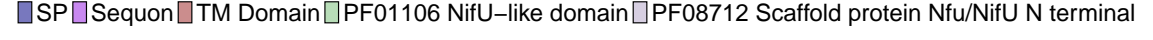
Protein length



Pfam domains



Pfam Description

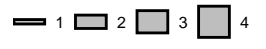


Protein sequence:

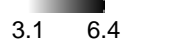
PLAKALFGIDGITRVFFGSDFTVTVKSEDAWDFLKPFEFAAAMDYVSGKPLFLDSSTAAGMDTAIHEDDSETVAMIKELLETRIRPWVDDGGDVIYVRGFLDTGIGWIKLMQAGAGCGPSSSVTLKSGIENMLMHHVPEVKGVEGEMDEDEEPGLTGAPVE-

NbL13g24160.1 protein_disulfide-isomerase-like [MW = 57.13 kDa]

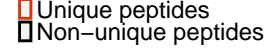
No. of times detected



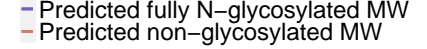
log(intensity)



Values from

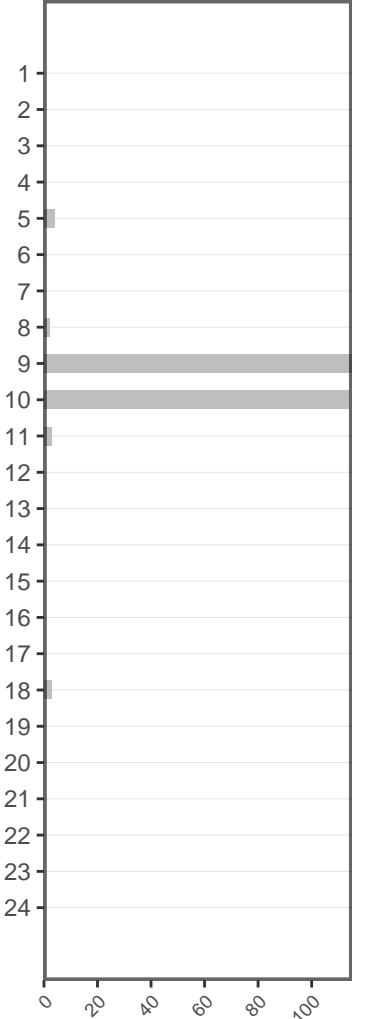
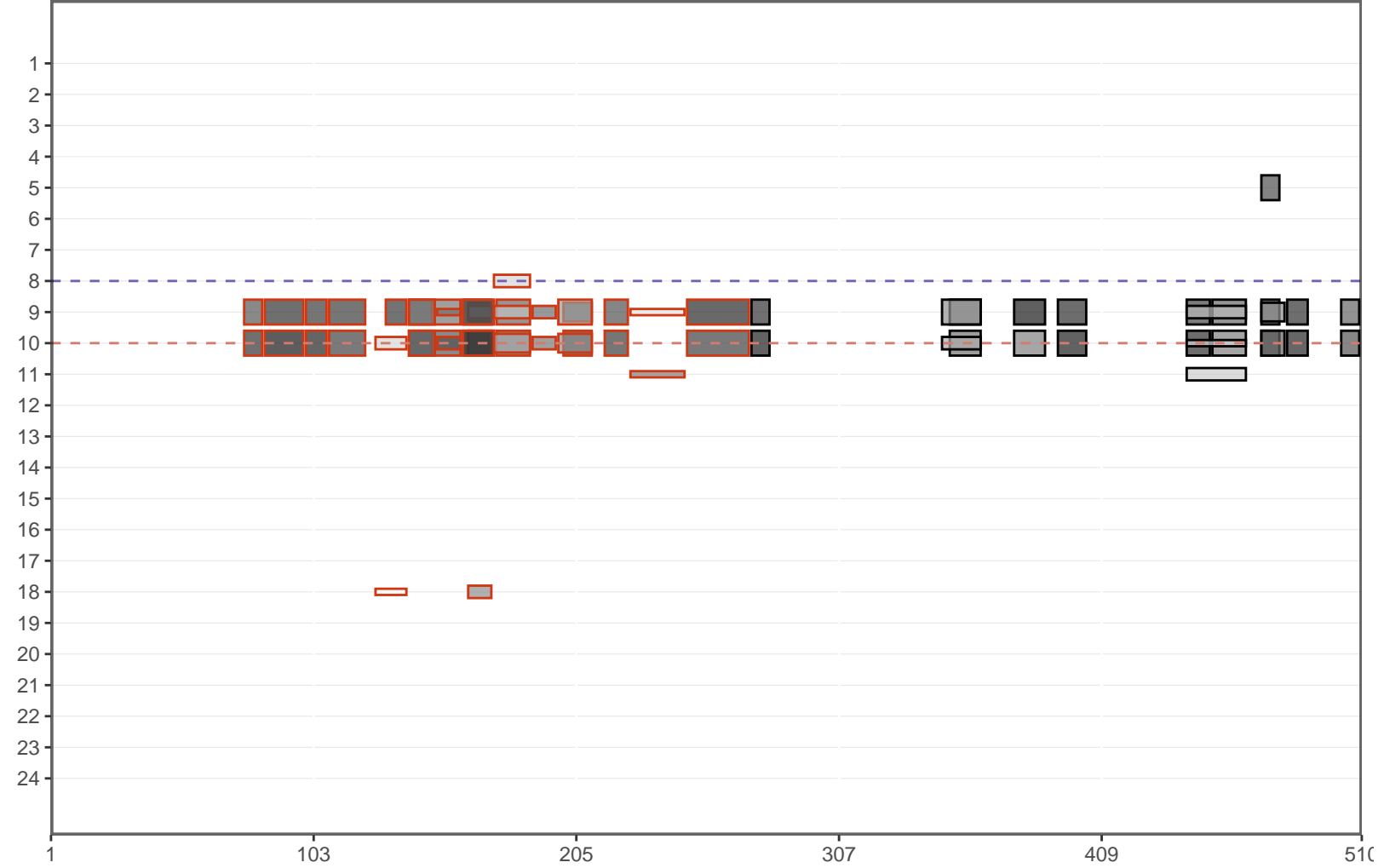
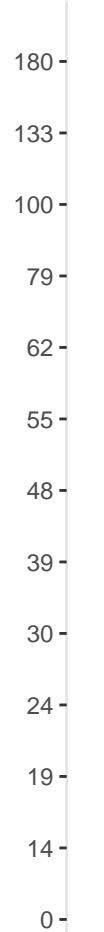


MW indication



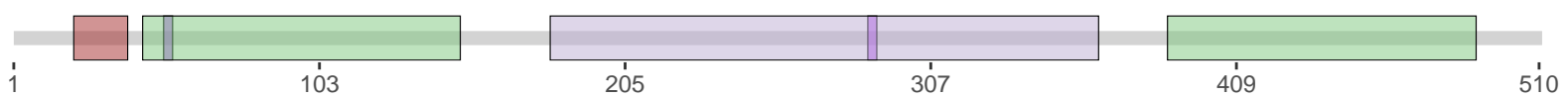
Molecular weight

Gel Slice



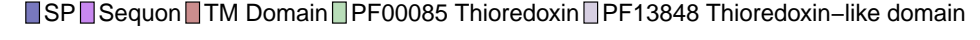
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

MLEKFIADISIPVTVFDNDNNHEVYKFFDGTNSKALLFVNFSTLEAFKSKYNDAKLYKGGCVSFLLLGGVEAGEGFEVFLKPEQALVIMGDTNGKYLKHKHVEPDAVAWLKDKDKLKPVYKSGPIPETNDPEKVVVVRDLDGDMVFNKGNKYLLEFYAPWGGHCKKLAFLKDEVAVSDSDSDVLIANKLDTLNDLPKDQDFVGGFPTMYFRSASGKLSQYDGDRTKEAMIEFKNRDKPVGSDSARTDSAKDEL

NbL13g24070.1 copper_transport_protein_ATX1-like [MW = 12.45 kDa]

No. of times detected



log(intensity)



Values from



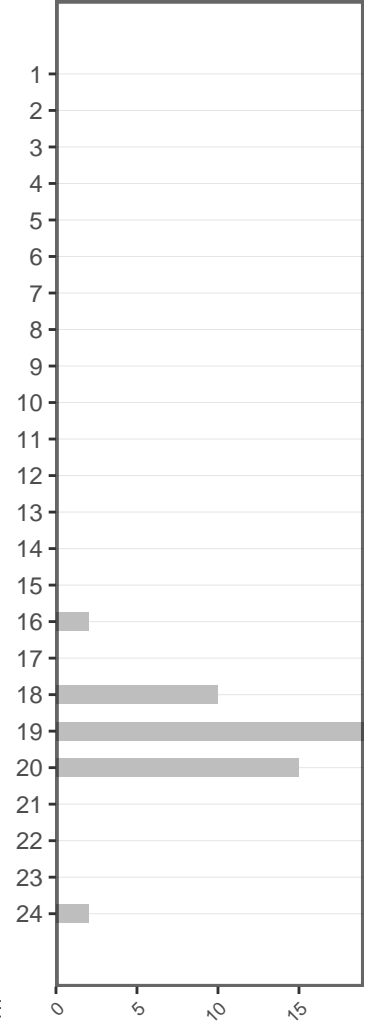
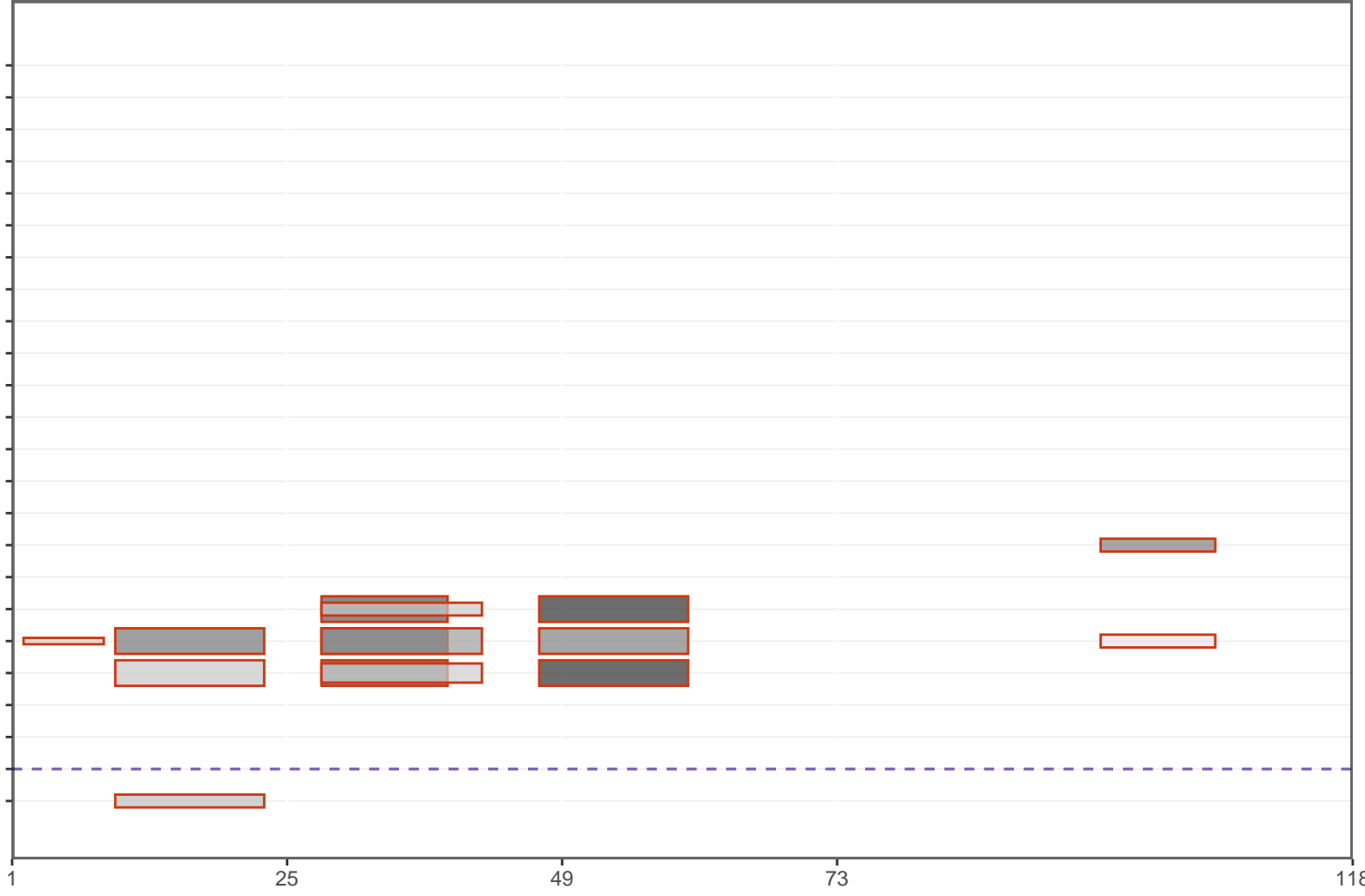
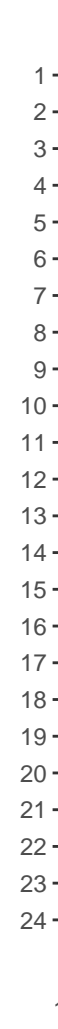
MW indication



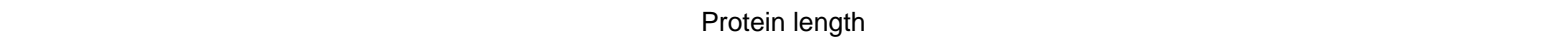
Molecular weight



Gel Slice

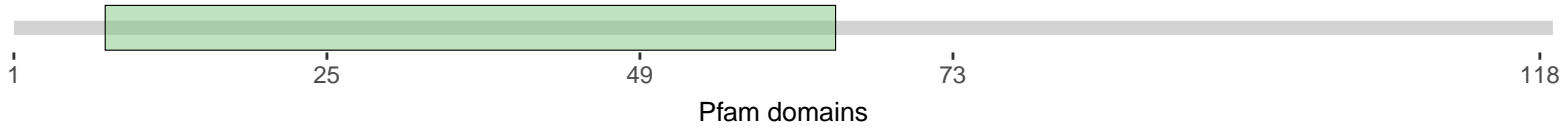


Protein length

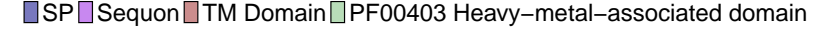


Peptide counts over 4 repeats

Pfam domains



Pfam Description

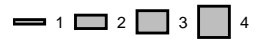


Protein sequence:

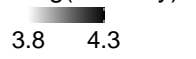
IKGNVEPEAVFQTVKTKGKTSFWEAETRAPAPAPTEPETKRFVEVKPTEENPADTPAEPAKADENPAEAAV

NbL13g23910.1 probable_bifunctional_TENA-E_protein [MW = 26.33 kDa]

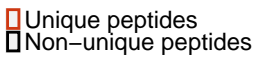
No. of times detected



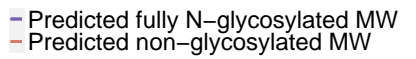
log(intensity)



Values from



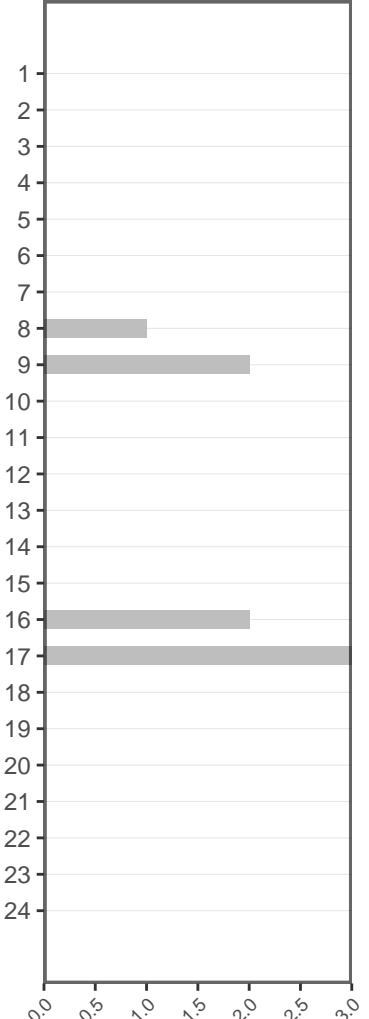
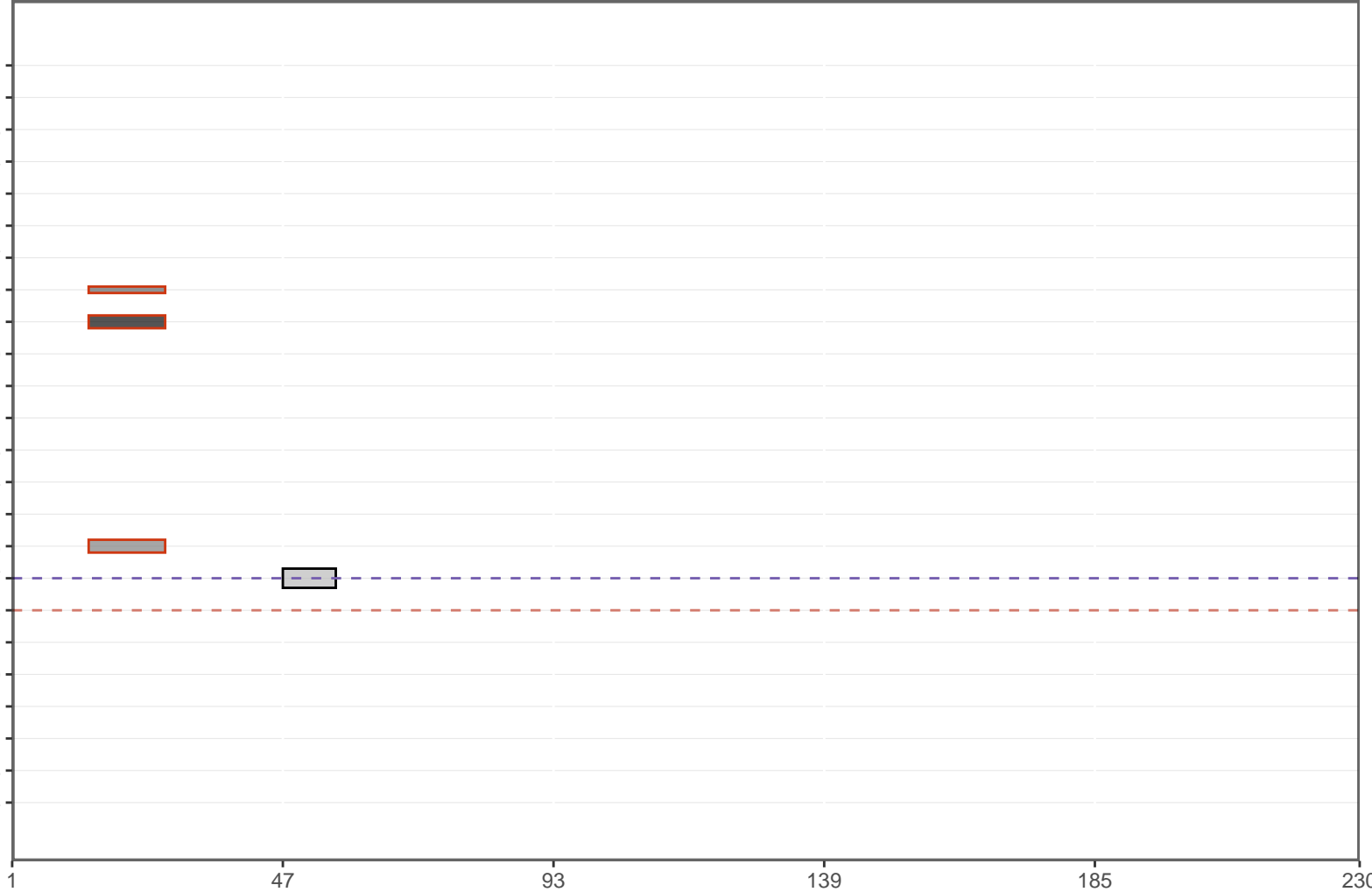
MW indication



Molecular weight

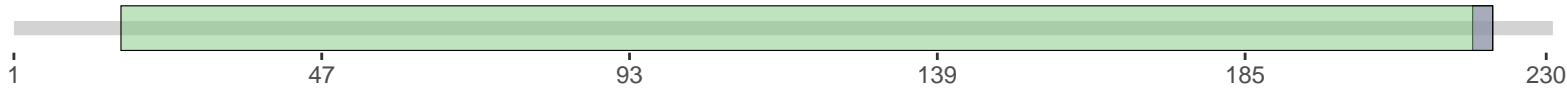


Gel Slice



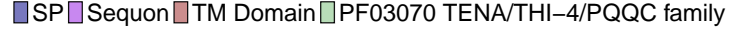
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

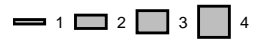


Protein sequence:

YWSYSLPSIVPOKANLEYGRFLLEGLMSPEVEYTVATPFWAIEVWYQESYAHQLADGSKTLDELKETFQGRVWGNDFGGVYRSLGDIANRRLEKSPEDIHSAKAEAMVRVLYKEVEFWNMRGGKLSAP

NbL13g23800.1 pyruvate_kinase_1_cytosolic-like [MW = 57.64 kDa]

No. of times detected



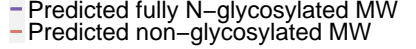
log(intensity)



Values from

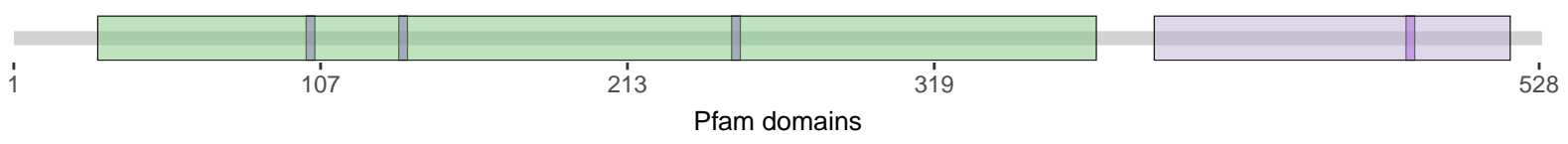
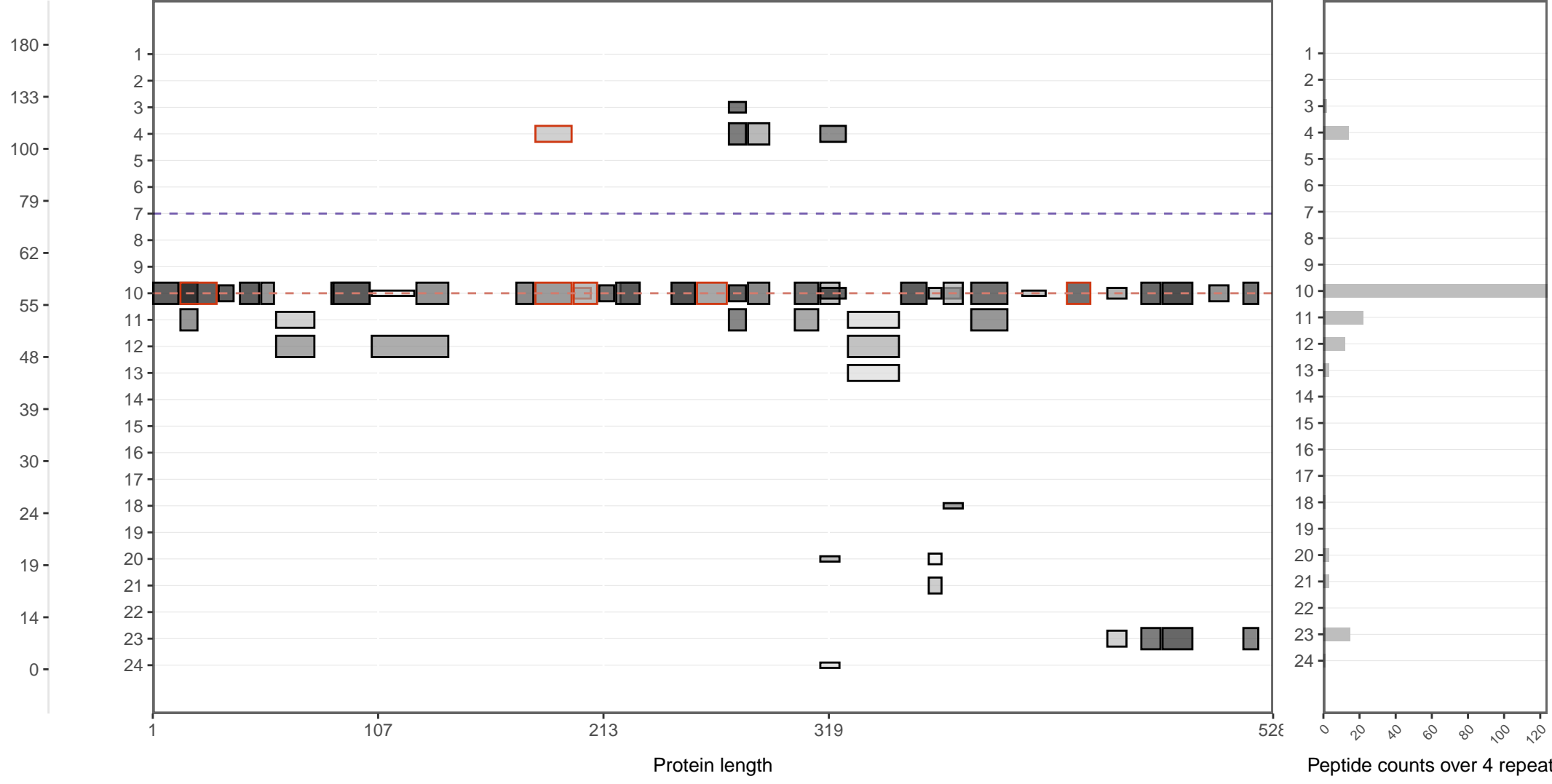


MW indication

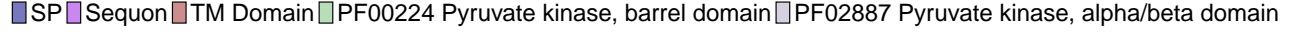


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

ITQIFAKIENVEGMAMFDELRLREADGILSRGNLGDLPPEKVFLLFQKAAVHKGNMAGKPPVTRVVDGMDTDLRPRRAEATDVAWAVLDGSDAILLGAETLRLGLYVETISVIGKICAEAEKYYNGDVFYKRAKYYVGEPMTHLESIASAVRAAKVWASVIGFTS6GRAARLIAYKREPMPVLSVYVPRLKTNDLRTWTFSGAFQARQGLVIRGLFPLIADPRHFAESTNATDESVLKVALDHGKTAGVVKPHDRVVVFQKVGDS6SVKHELEN

NbL13g23780.1 uncharacterized_LOC104235088 [MW = 33.47 kDa]

No. of times detected



log(intensity)



Values from



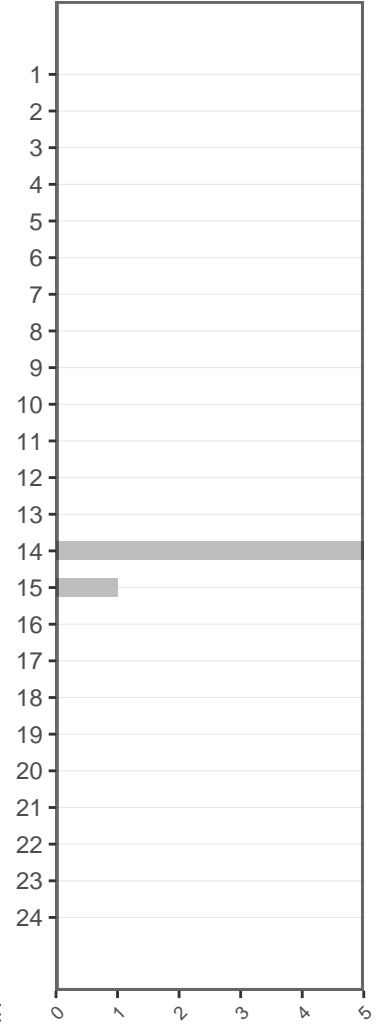
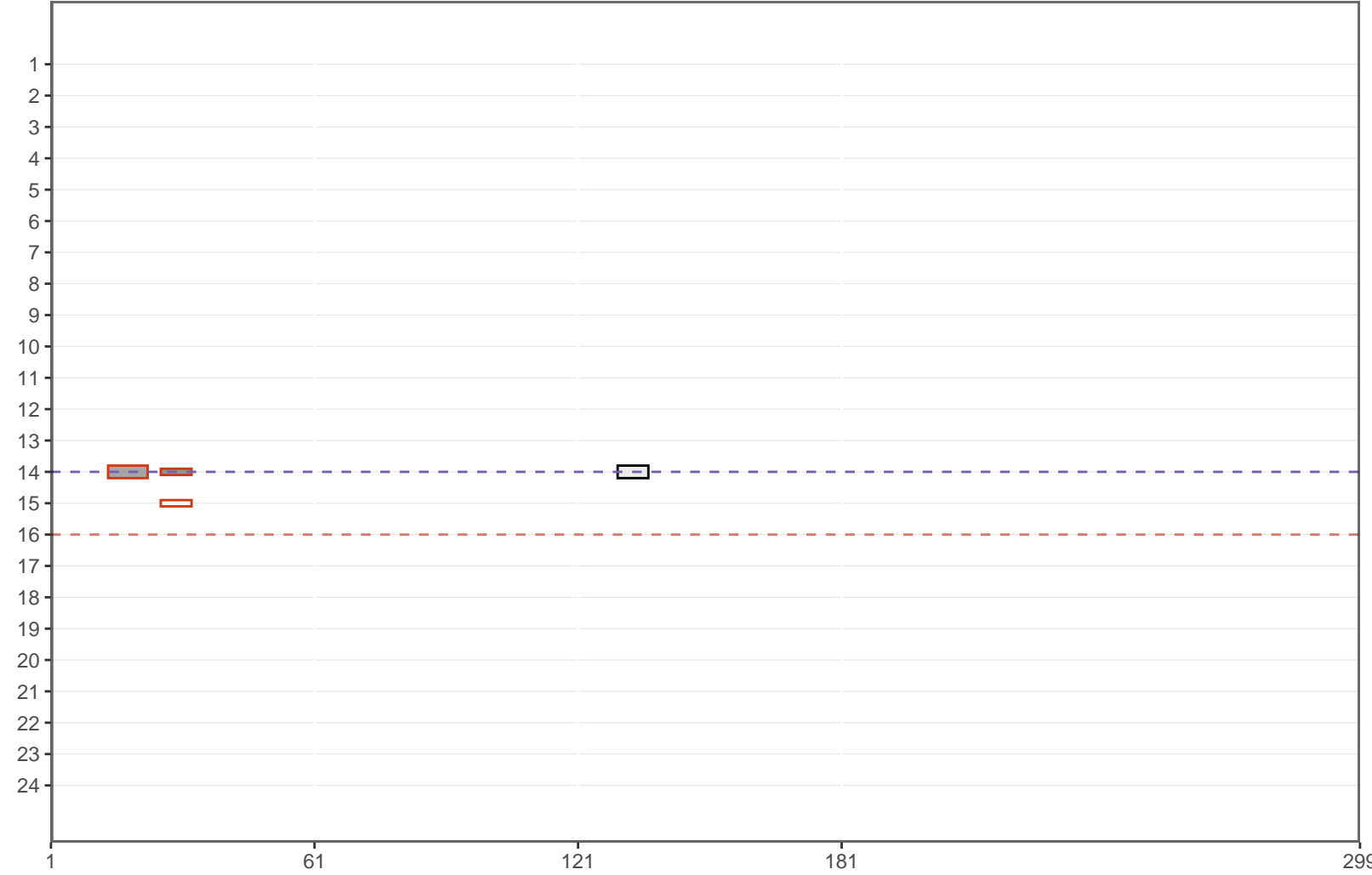
MW indication



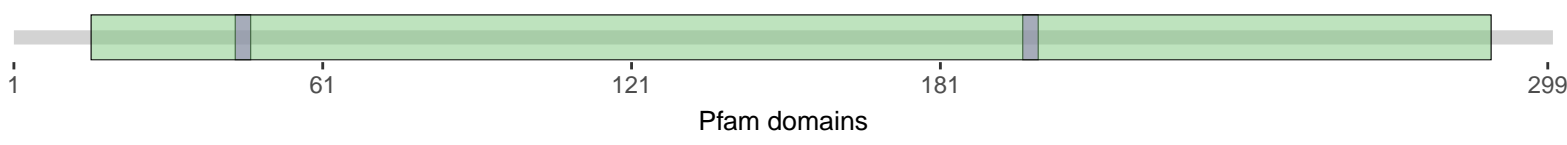
Molecular weight



Gel Slice

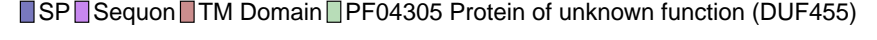


Protein length



Pfam domains

Pfam Description



Protein sequence:

LKELGSPYGLPNDGLWDSGATSKDLARLAIEHQVHEARGLDVPTTISRFRNGGNDGTAELLENVYPEETHCAAGVWFKYLGLRBNPNPGDLPSGENSEDTMVDNEVQRHSTVRRHFRGLKPPFNEQAREAAAGFQWVEPLAVKDYME

NbL13g23750.1 ribosome-recycling_factor-like [MW = 32.81 kDa]

No. of times detected



log(intensity)



Values from



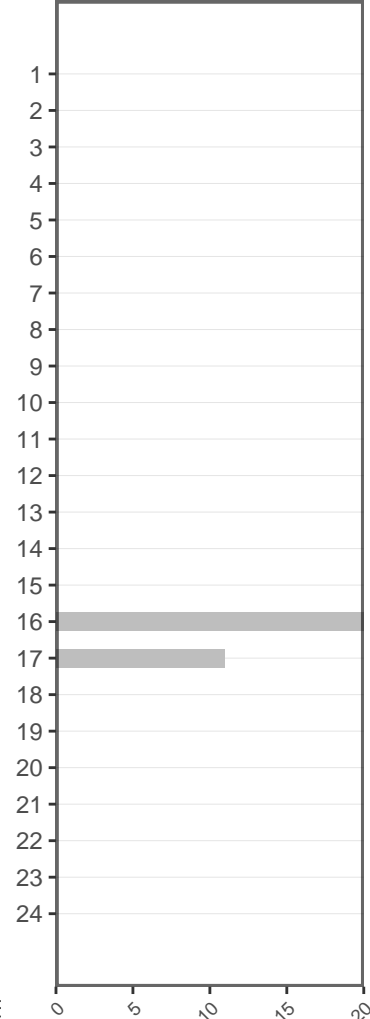
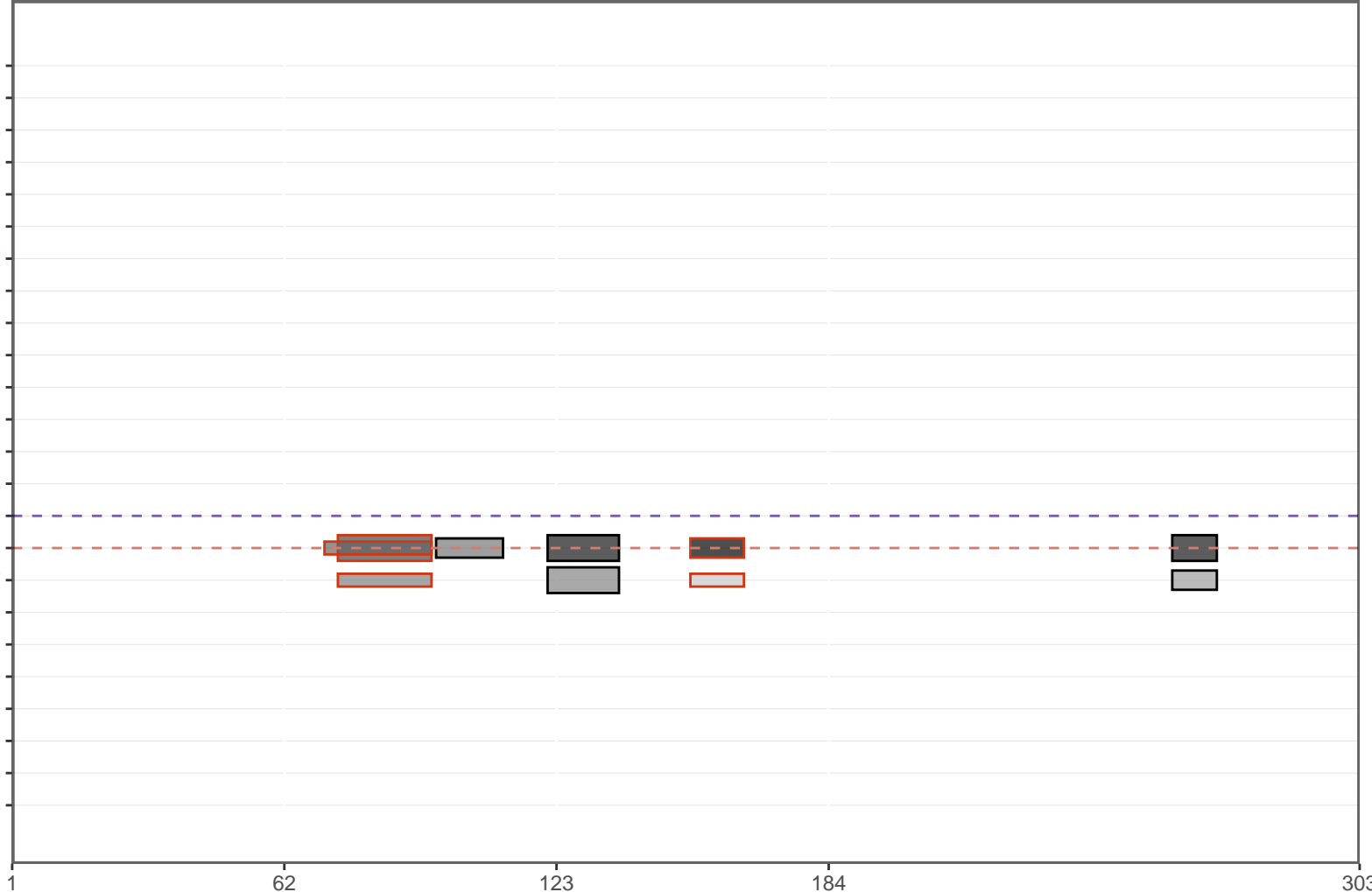
MW indication



Molecular weight



Gel Slice



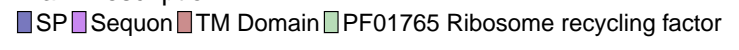
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

TPLCRMVIVSLDFKTLGVTPYDPTVKELDKAVVBSPLGILNPOVDNGRLVPIPPFPMDFDSAFLLFLAIRATSRLLTKEHYGVAVCKVAVKSSVDKGVGVRRRARQKALDTRKSLPRKKDNDKAAAFSEDDAKRLEKEIDDLTKFKFVSAEDMCKSKKEIKETS

NbL13g23650.1 5-epi-aristolochene_synthase-like [MW = 63.13 kDa]

No. of times detected



log(intensity)



Values from



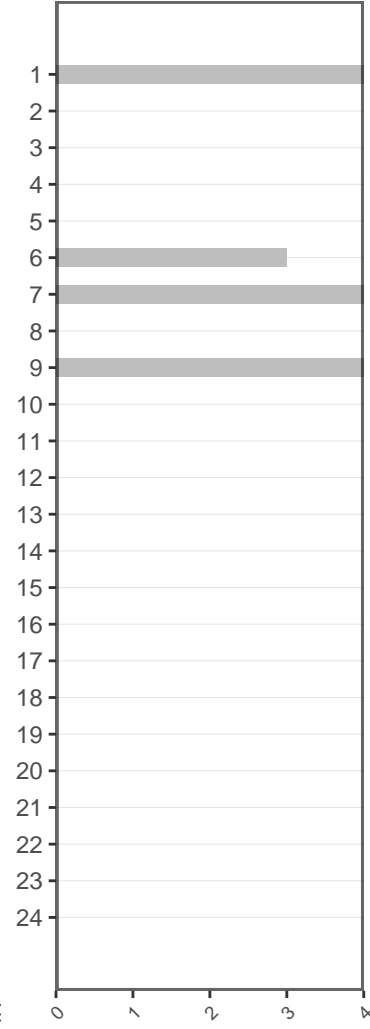
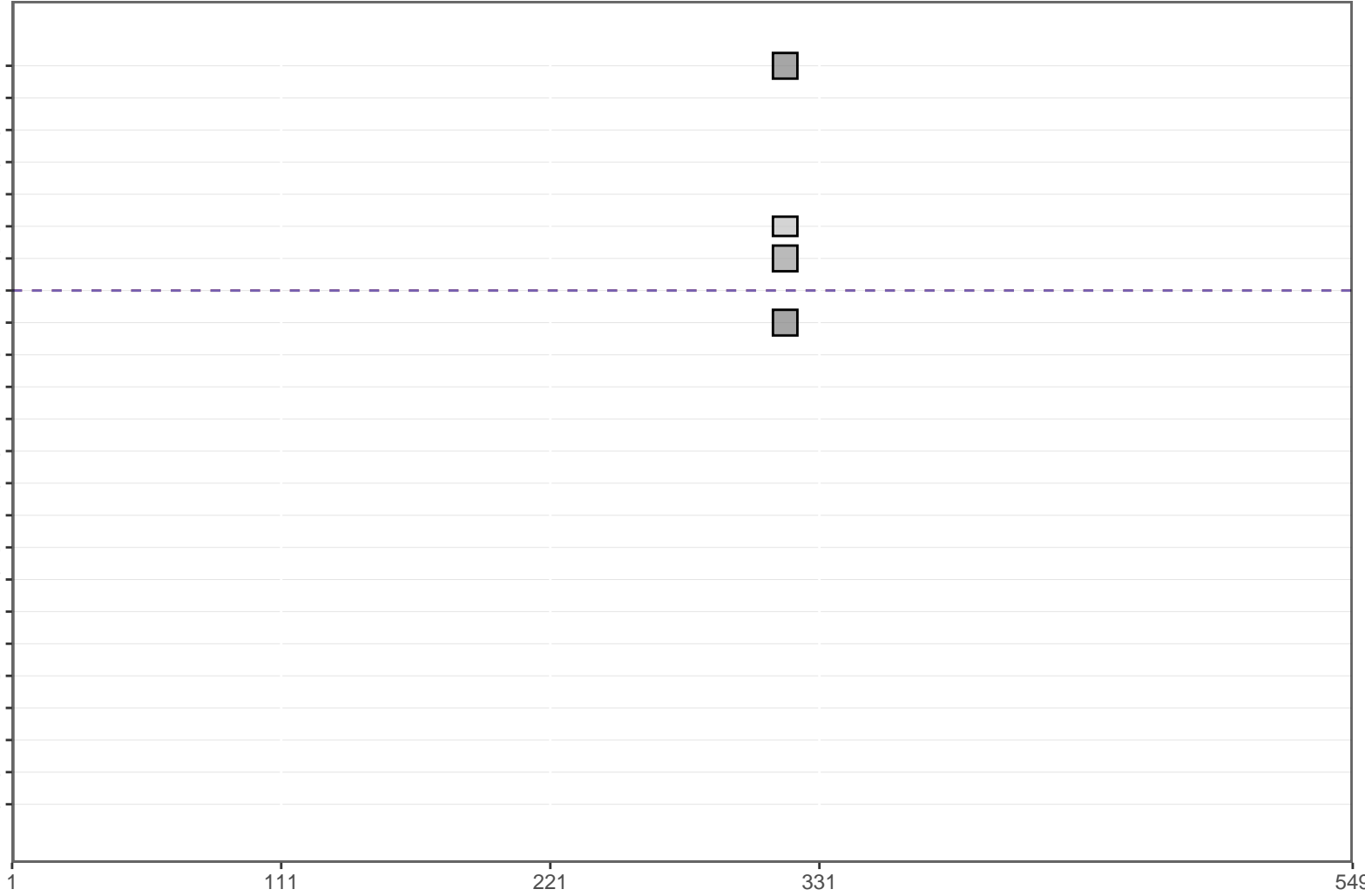
MW indication



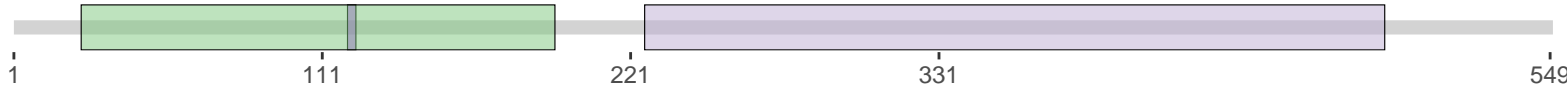
Molecular weight



Gel Slice

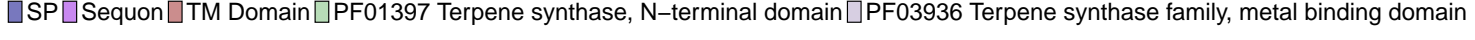


Protein length



Pfam domains

Pfam Description



Protein sequence:

LPYARDRVECYFWALGVVFEFGVSGARVMLKTKTSMISIVDDTFDVGTVKLEAVTDAQRWHKEIDRLPDMKMSYKALDLVNDYKELSSAGRSHVSHAGRMKEVVRNINVESTWFEGKPPVSEYLSNALATFTYYLATTSGVGMKGVTEQDFEIVLSKPKLEASVGRVDDTATYEVEKSRGGIATGEGCMRDVGLSTREAMDKFQKMAETAWKDLNEGLRPTFPVSAEFLNPLNLARIVETVYHNLDGVTHPERKLVKPHWALLVDSIQI

NbL13g23640.1 5-epi-aristolochene_synthase-like [MW = 63.09 kDa]

No. of times detected



log(intensity)



Values from



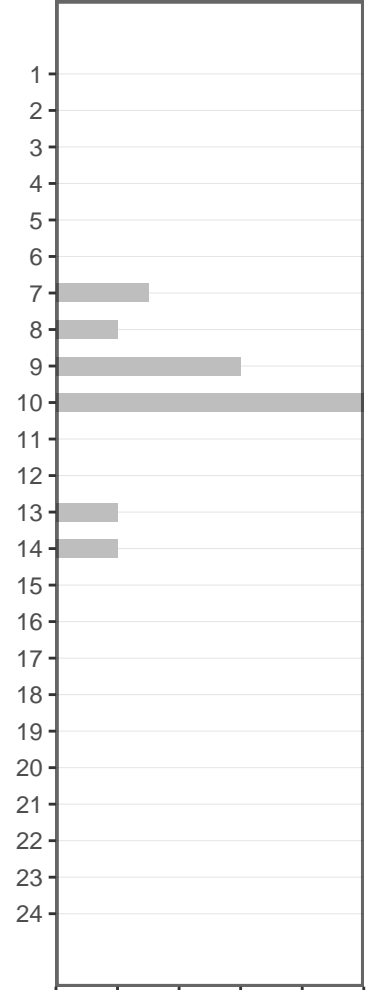
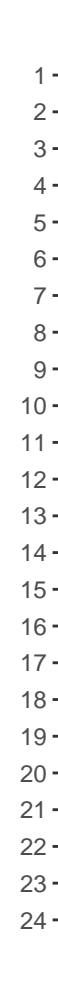
MW indication



Molecular weight

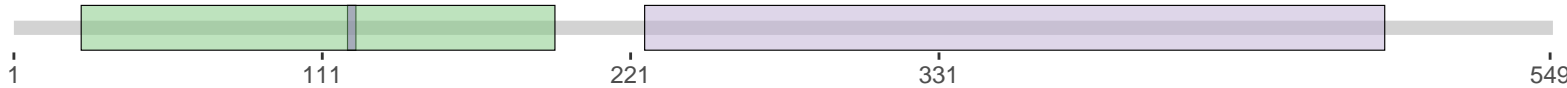


Gel Slice



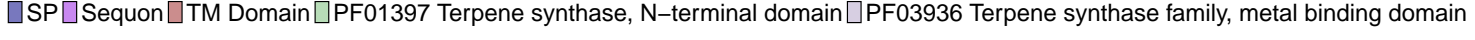
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LSYARDRVVCEYFALGVYFEPQYSGARVLMVKTSMBSBVDFTFDAYGTVKELEAYTNAQRWHKEIDRLPDYMKISYKAILDLVNDYKELSSAGRSHVSHAQRMKVEVVRNYYNESTWFIEGYPKPYSEYLSNALATTTYYLATTSEYLGKISVTEQDFEWLKSNPKILEASVIVDDTATYEVEKSRGQATGIECGMRDYGLESTKEAMDKFQKMAETAWKDLNEGLLRPTFVSAEFLNPLNLRARIVEVTYHNLGDGYTHPEKVLKPHVALLVDSIQI

NbL13g23610.1 phosphoglucan_phosphatase_DSP4_amyloplastic [MW = 46.85 kDa]

No. of times detected



log(intensity)



Values from



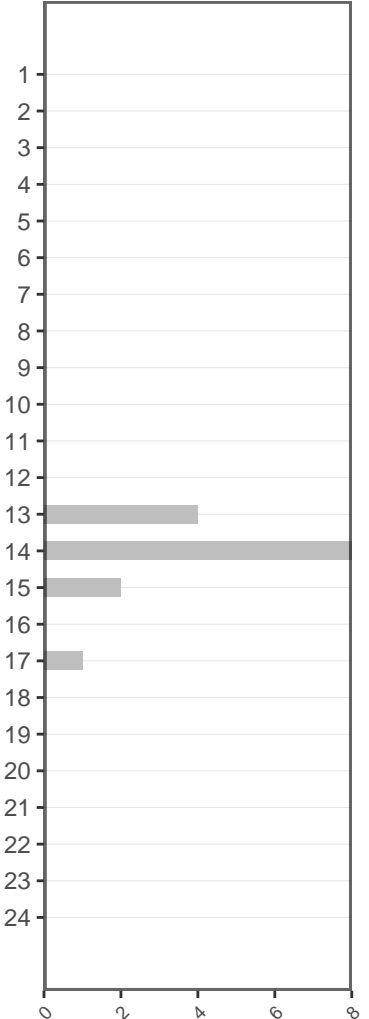
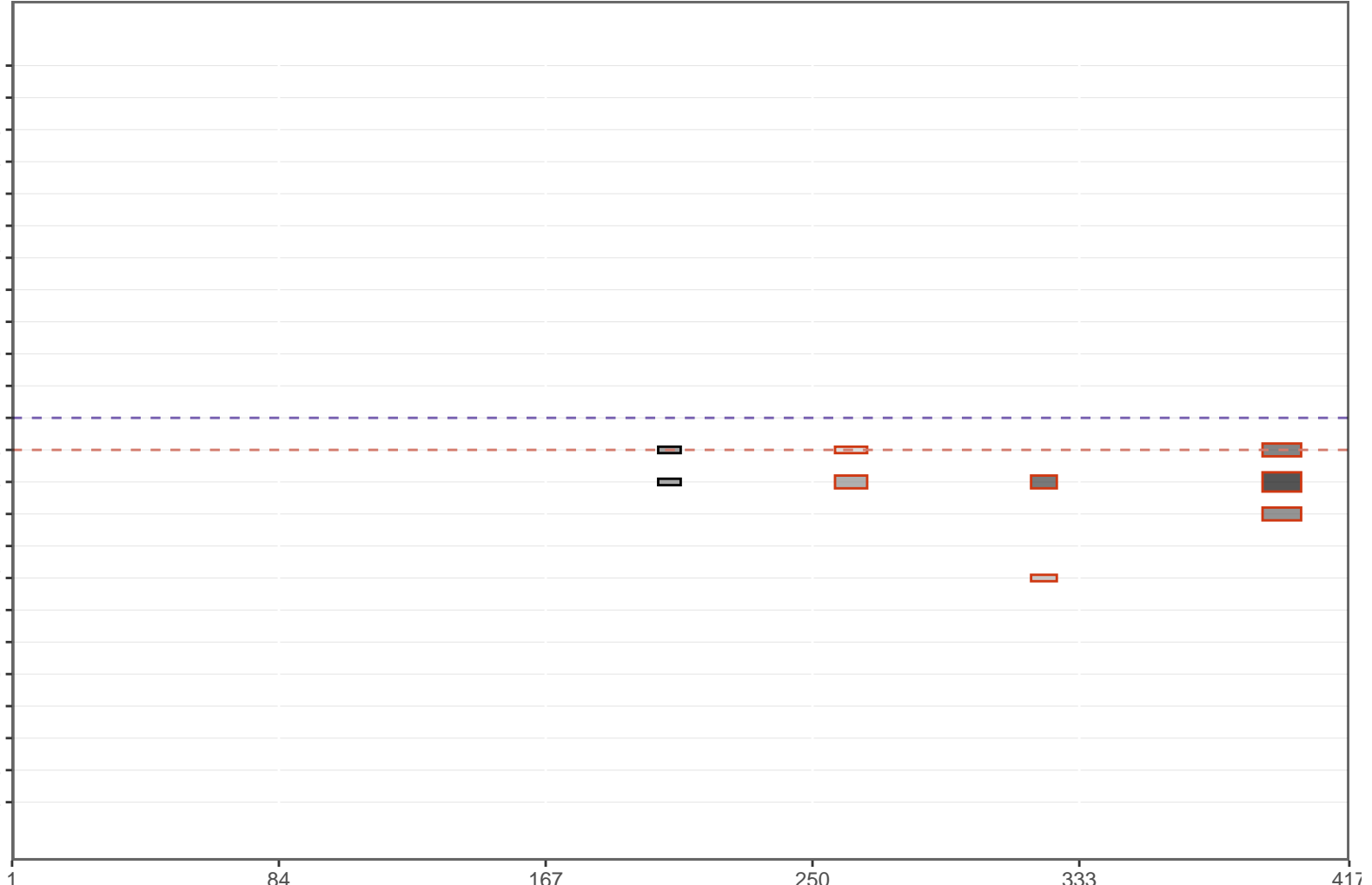
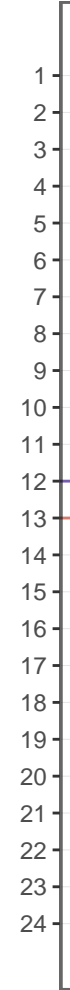
MW indication



Molecular weight

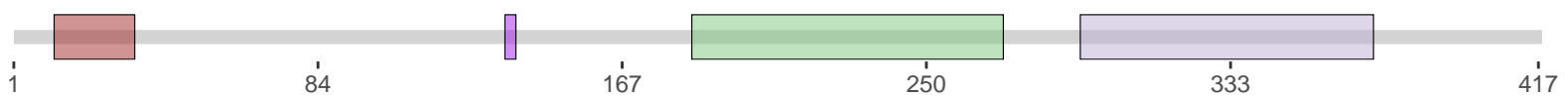


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00782 Dual specificity phosphatase, catalytic domain
- PF16561 Glycogen recognition site of AMP-activated protein kinase

Protein sequence:

...RAEIRDFAFDLRLRLRFAVVEKLSKAVNRNGGVTVYHCTGLGRAPWALTYMFWVGGYKLEAFNLMKRGCFPKLDAKNSATDLTGLKRRKATLTWGGDCGTVVEISGLDVGWQRPLFDEERGLWTLGRDLPEGHYEVYKVDGVTGTCNEFEPTSPNKDGHVNNYKGVLDNPDGISAARNRRLTSDGDDPLTSDERLIREFLEAYDDEE...

NbL13g23340.1 malate_dehydrogenase_[NADP]_chloroplastic-like [MW = 48.31 kDa]

No. of times detected



log(intensity)



Values from



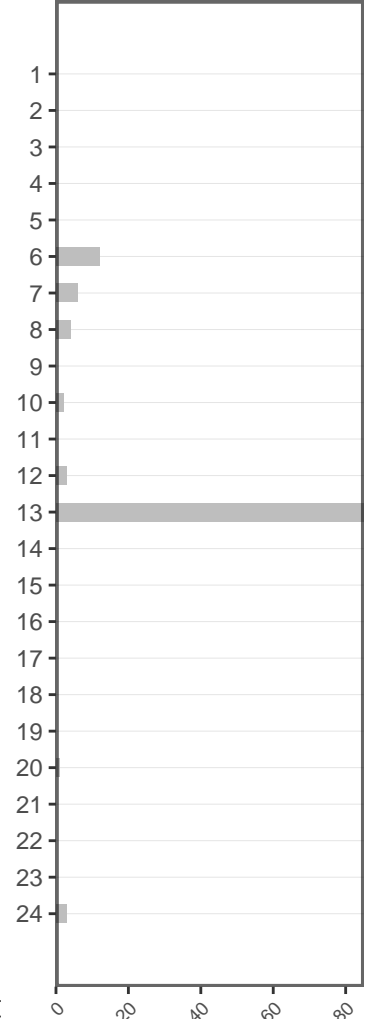
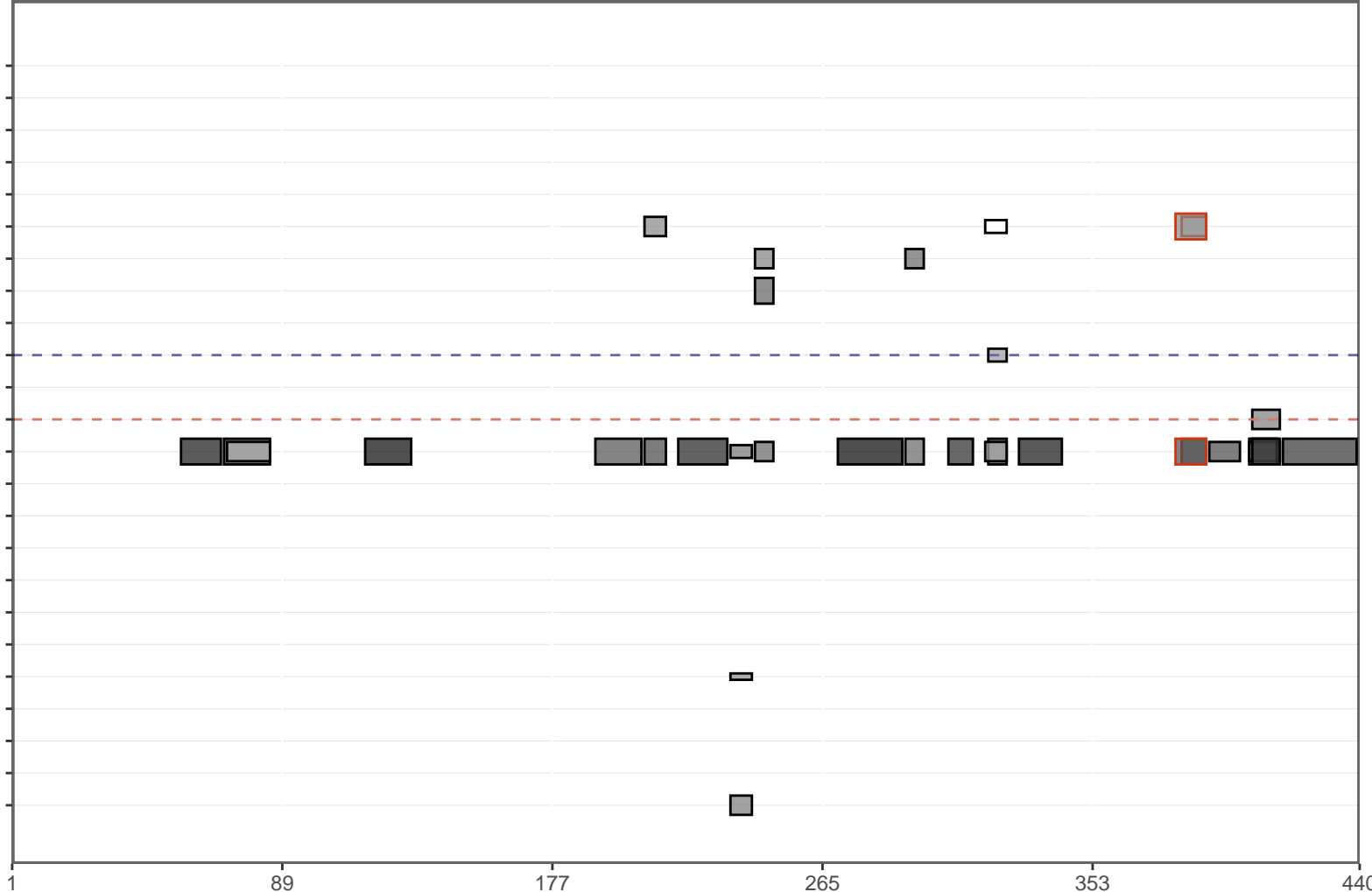
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00056 lactate/malate dehydrogenase, NAD binding domain
- PF02866 lactate/malate dehydrogenase, alpha/beta C-terminal domain

Protein sequence:

ALNVAASRNKKVAVGNPENTNALKGNAPINPKNFHIALTRLDENRAKGLALKAGVFDKQVSNVITWGNHSTGVPDFLNAAKINGLPVKEVKGIDRMLLEEFEKVKQRGVDLQKWRGRSSAASTAVSIVDAIRSLVTRTFEGDWVSTGQVYTSGNPYGIAEDIVFSPMPQREKGGDGYELVKEVFDQYLSRRIKKEDELLAEKRGVAHLTGEQIVGDLPGDTMLPGEM

NbL13g23330.1 5-epi-aristolochene_synthase [MW = 64.08 kDa]

No. of times detected



log(intensity)



Values from



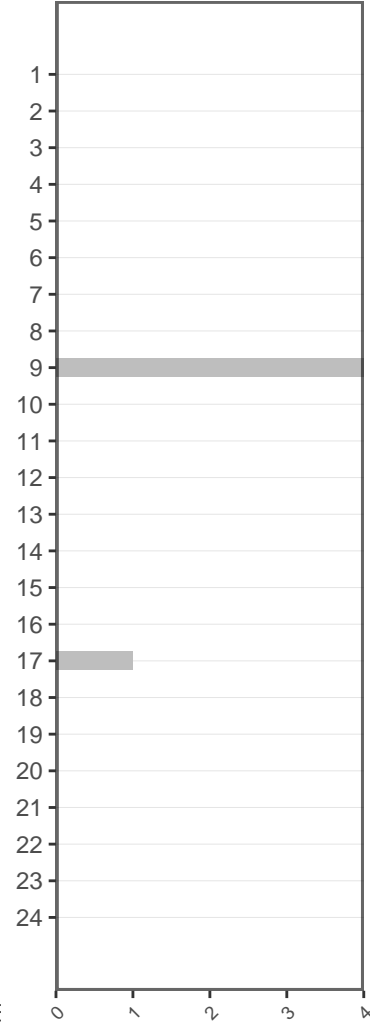
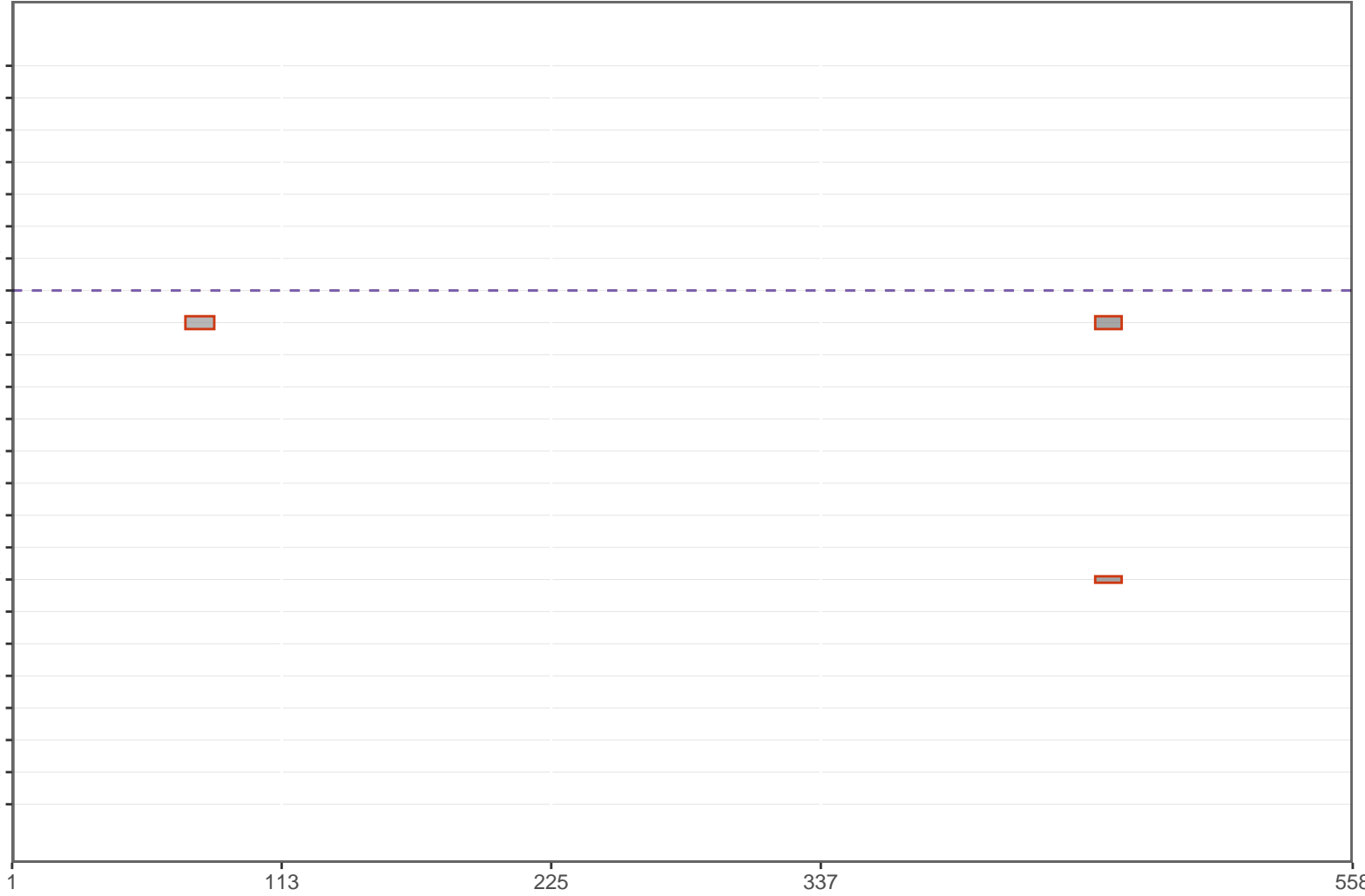
MW indication



Molecular weight

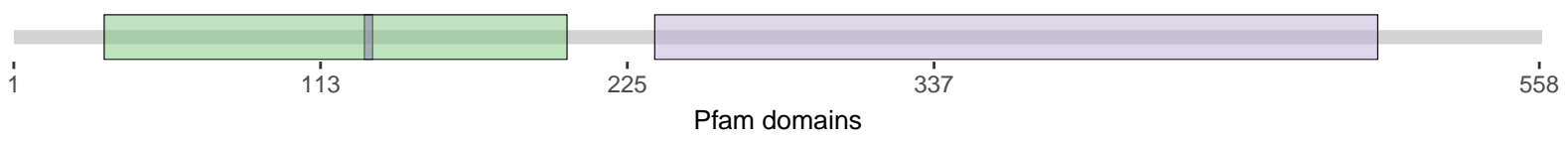


Gel Slice



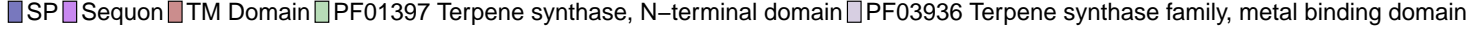
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FVITLPIARDIVVSDYFWALGVVYFEPQYSGARVMLKTKIMSGIVDDTFDAYGTVKELEYNTNQRWIDSEIDMLPDHMKISVKAILDLVQDYKELSGVGRSHVGHAIERKKEVIRNNVSTFWIEGYPKPPVSEYLSNLAATTTYYLATSRYLGMKSVTEHDFEVLGKPKILEASVVICRAIDDATYEVVEKRGSGIATGIEGCMRDYGVISTEAMTKFDQEMEAAWKDLNEGLLRPTPVSTEFLSRIINLARIVETVYHNLDDGYTHPEKVLKPHNALVVDISIEI*

NbL13g23310.1 protein_BTR1-like [MW = 39.37 kDa]

No. of times detected



log(intensity)



Values from



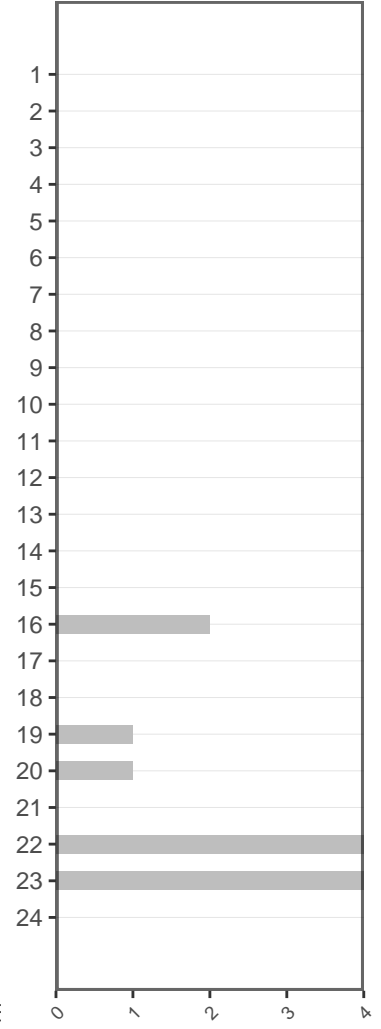
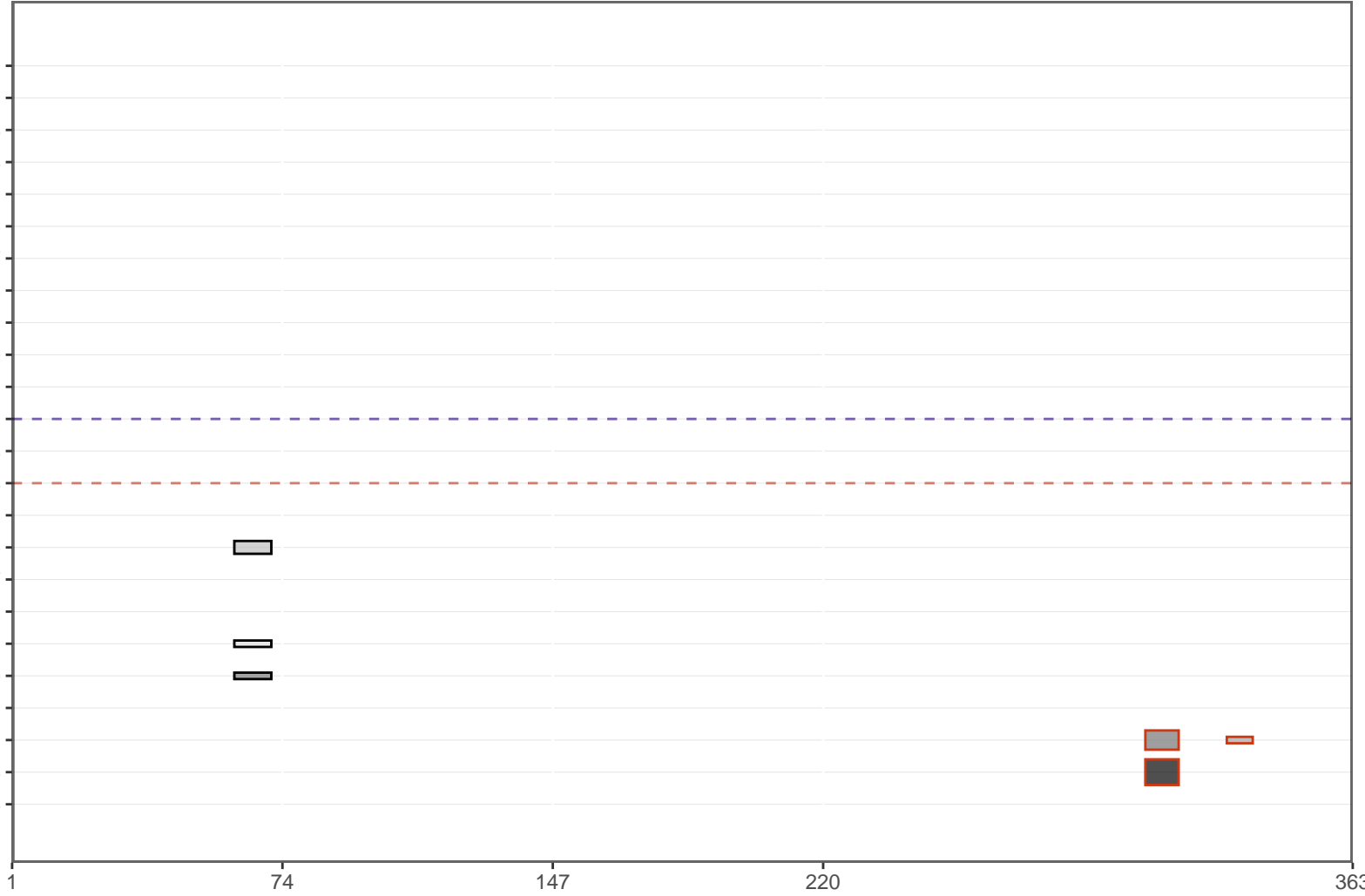
MW indication



Molecular weight



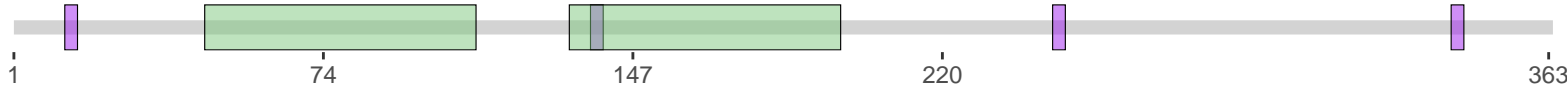
Gel Slice



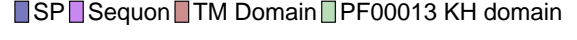
Protein length



Pfam domains



Pfam Description

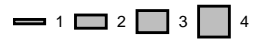


Protein sequence:

NNFPGIHDRVTVTGTGLEDGMRRAIEILKLAEDPHYMDSMNAPFQVAWVGMNYPGPNVGVGRYFNNRHHQNKEDRNNTVTGVADEHVLGLVGRNRRSIMEISGVCKLFLGLVGHYAKLLSLQLSGARIKESDRGDFLGGTSDRKVITVSGRAIRTAEGMSRRIANVSRSTVGEDLPFEELGINTVH

NbL13g23290.1 acyl-CoA-binding_domain-containing_protein_4 [MW = 56.75 kDa]

No. of times detected



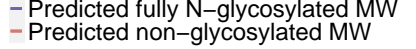
log(intensity)



Values from



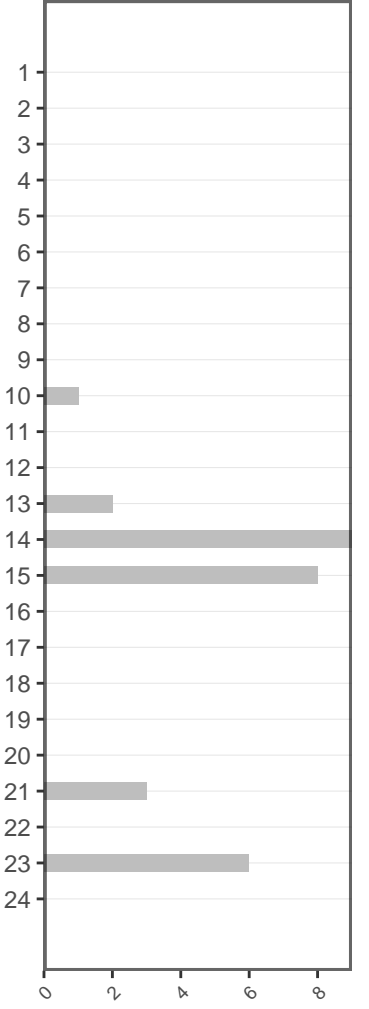
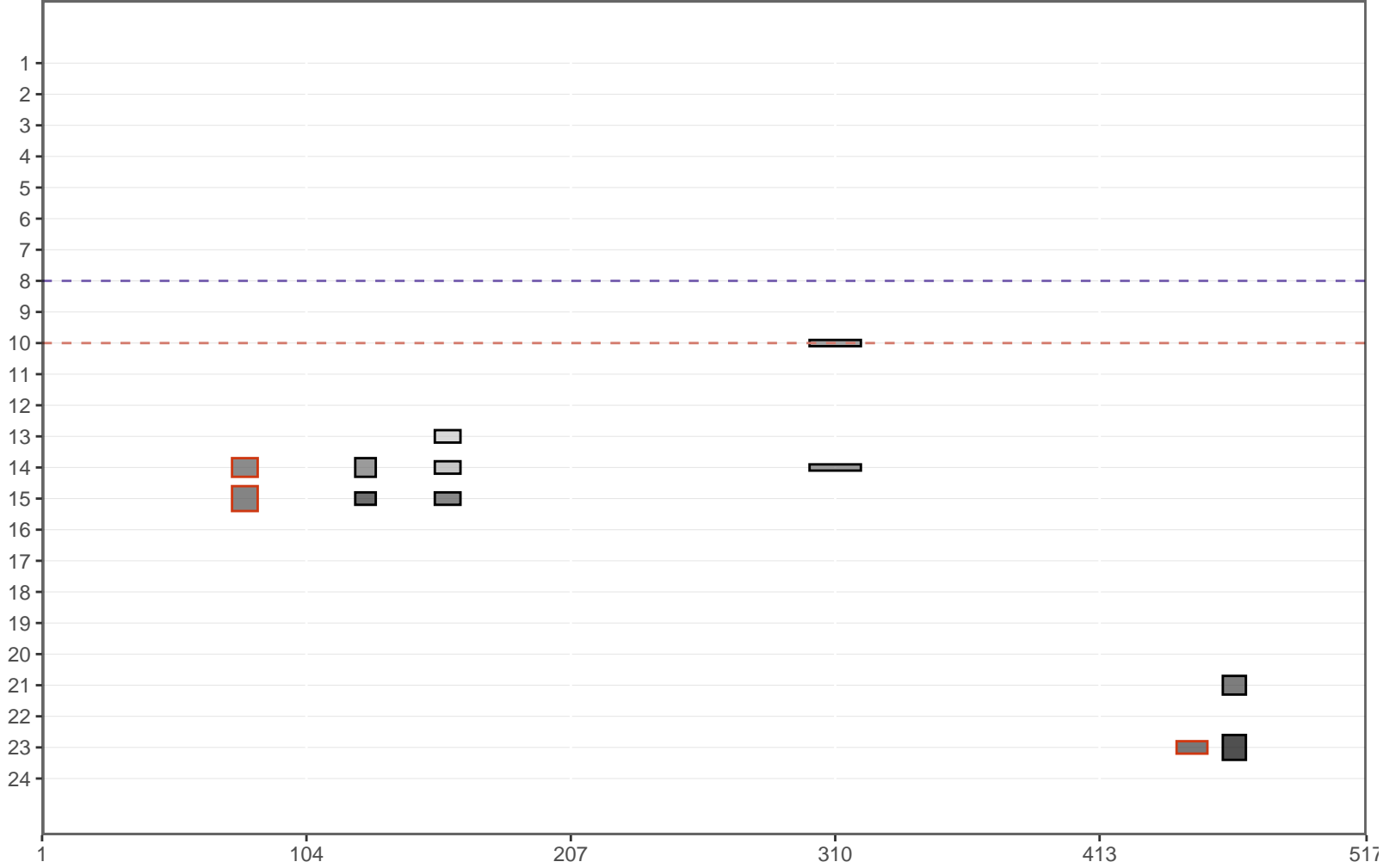
MW indication



Molecular weight

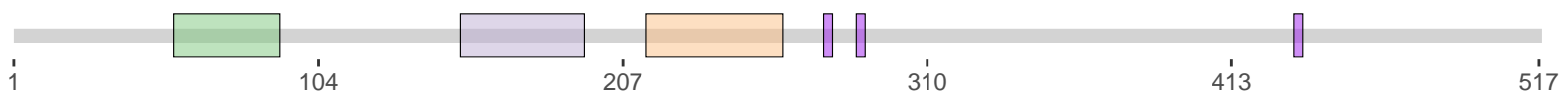


Gel Slice



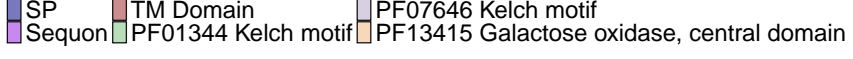
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GDLVSPRAGHAGVFLGDNWYVGGGDRNGVPEFLVLSNMSKLVSVLAVTKGRDPLASEGLSVSSALLDGEKFLVAFGGYNGKYNEVYVMRPKPRDLVHPKMLGSPRAEAAAASVRAVAALTKPEKLDLSERENSNFKEVHYDNTQDKLSAEISAHGLKQKALESSLADVGAENANLAKAKIEEVNHTHTDLSKELGSGVGGQLSERSTGAKLEAGIQLKMLGSMGQSEEEVQALRKEKSELERDMERAVSVQKGGGGAWKWTG

NbL13g23170.1 uricase-2_isozyme_1 [MW = 34.72 kDa]

No. of times detected



log(intensity)



Values from



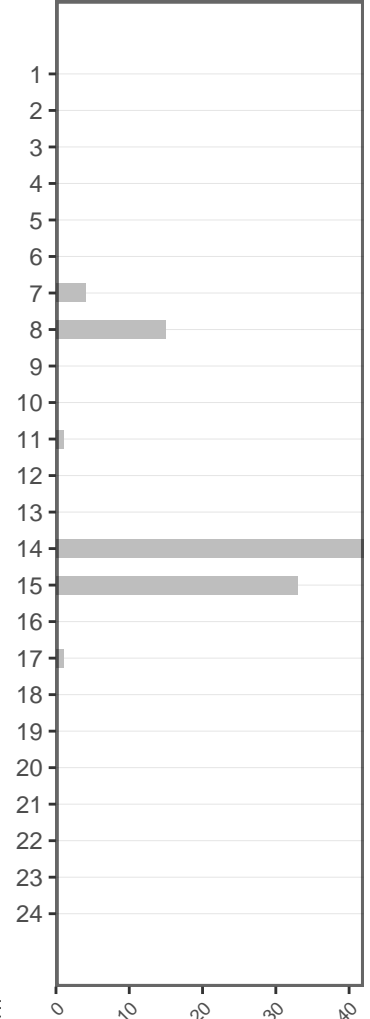
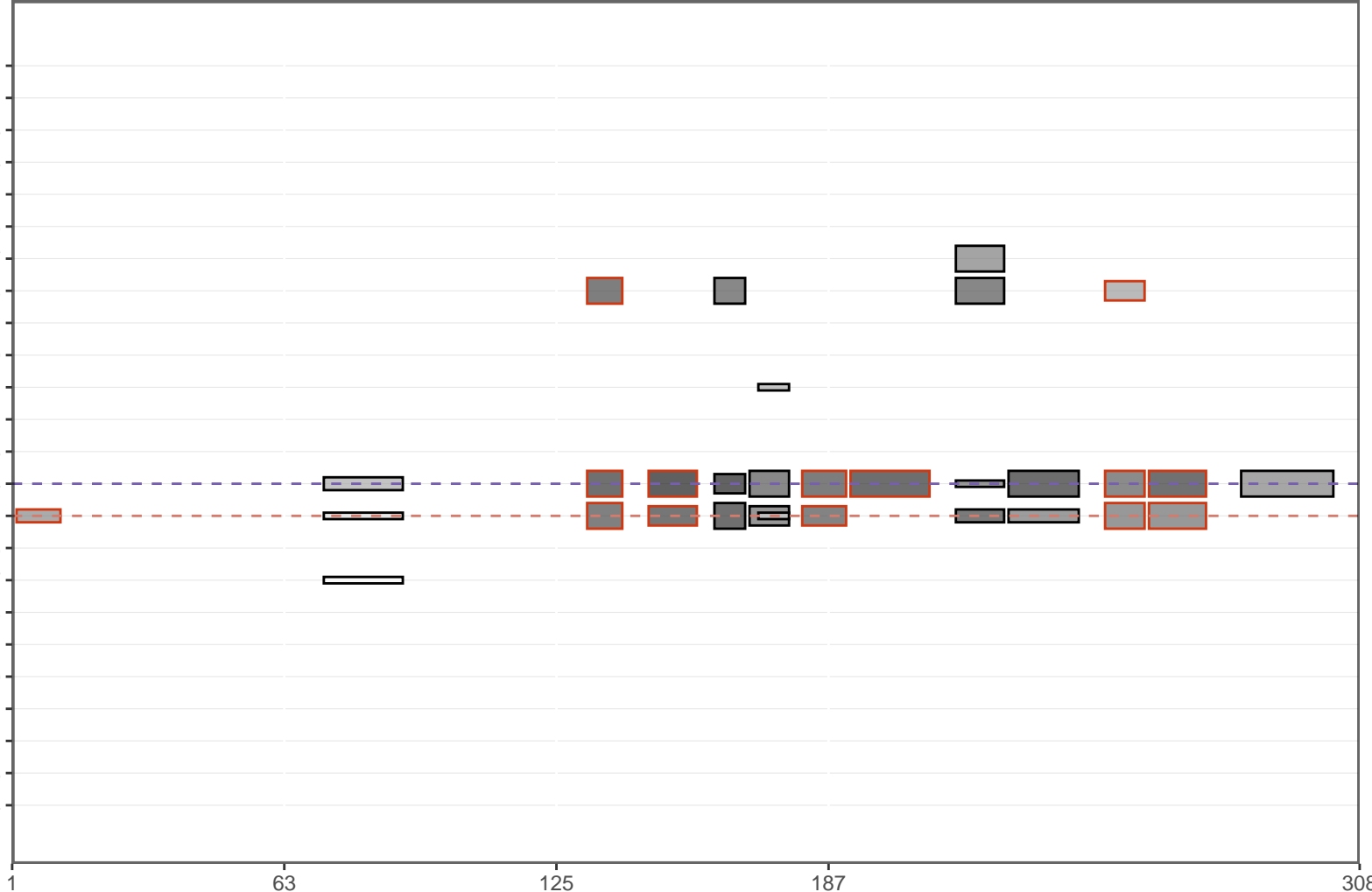
MW indication



Molecular weight

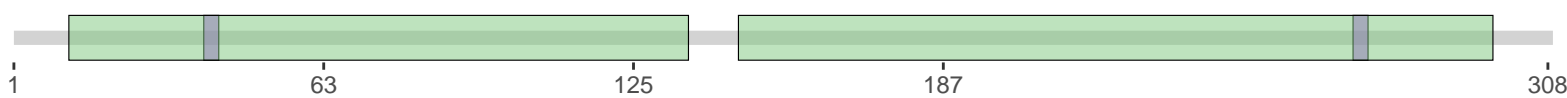


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ISGTLRMTSGVGLGVLKTTKSGFEGFGRDKYKTYMLPETRRERMATEVTSWRYLFEGLSSLLPLKPLFYTFERYMDKVEVLLNTFFGPKGKGVYSPVQATLYEMAKALGRFPDVGFIELKMPNLHFLPVLNLTSKDNPIWVVFQNDVYLPFDPEHGTHQATLNRIRSKM

NbL13g23030.1 phosphoribosylaminoimidazole_carboxylase_chloroplastic [MW = 68.47 kDa]

No. of times detected



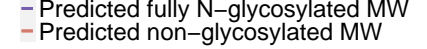
log(intensity)



Values from



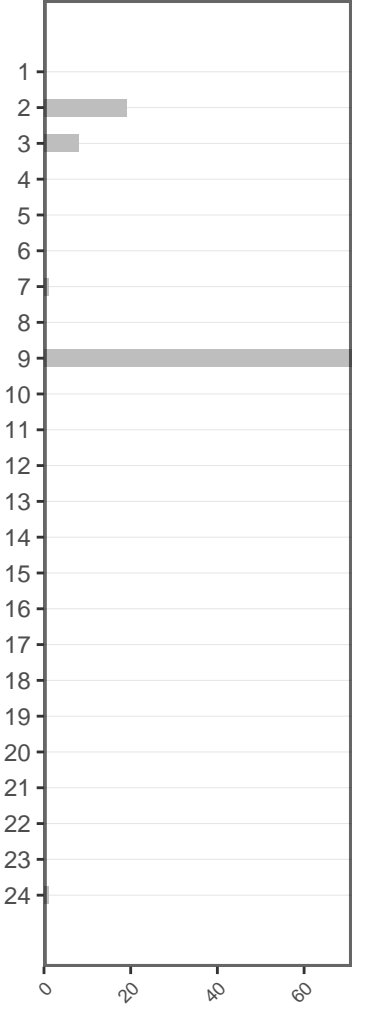
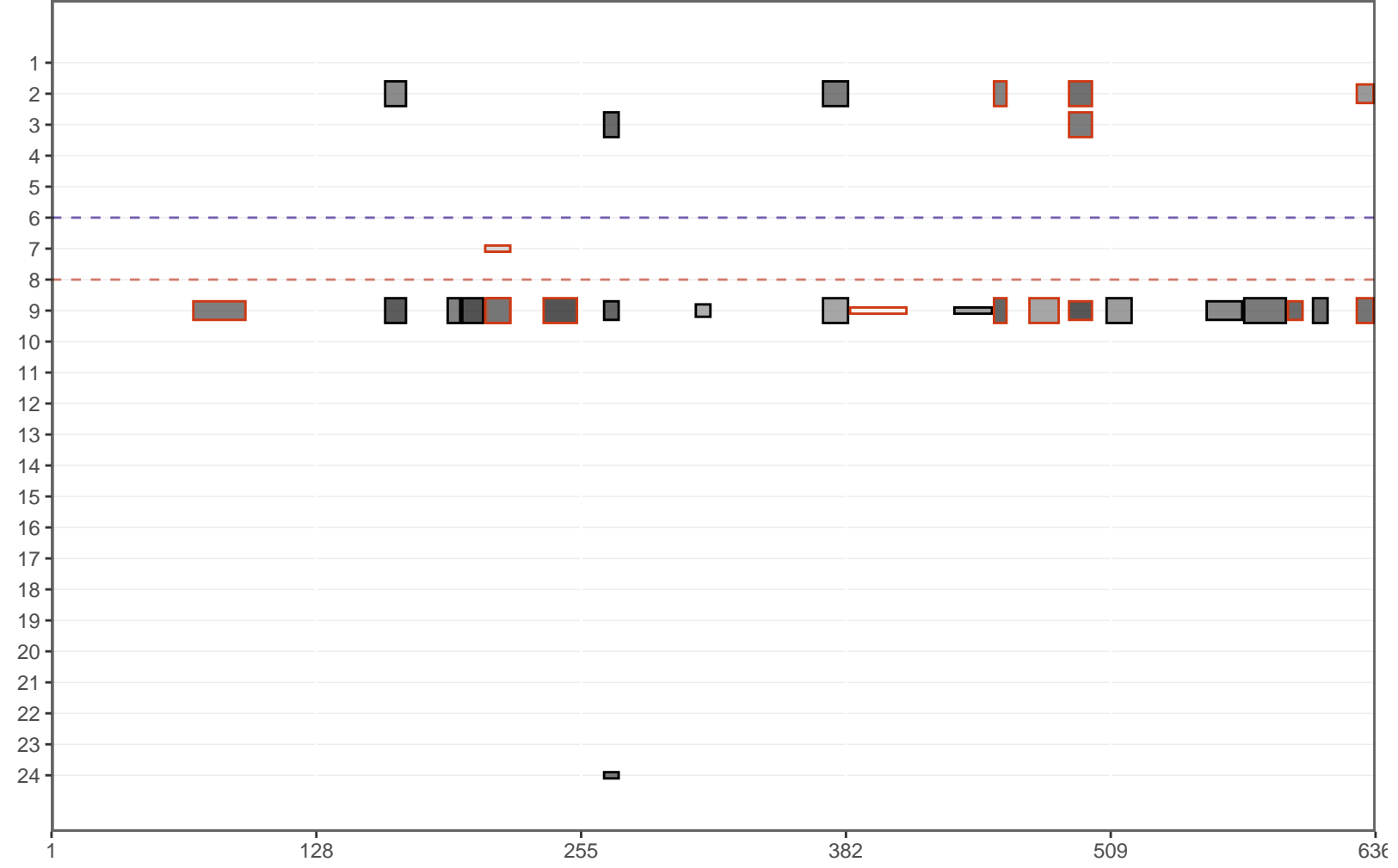
MW indication



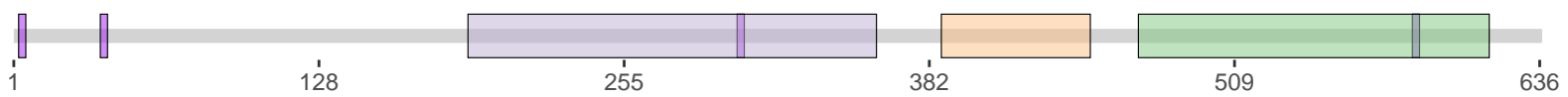
Molecular weight



Gel Slice

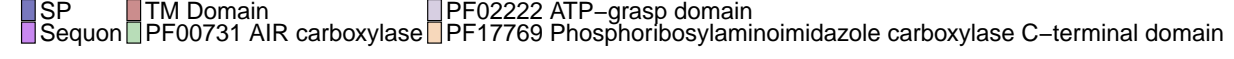


Protein length



Pfam domains

Pfam Description

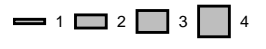


Protein sequence:

IWKSMKLTADVAIRAVSSELEGAGVFAVEFLFTEEDGGILLNEVAPRPHNGHHTIEACFTSGFQGHLEKRAVVDLPLGDPMSKTRAVMVMYKLGEDDGEQRLNANLQGLRALGIPASVHHVYDKPERKQRKMGSHITIVGPMGIVEAQLRVILNEGRVNGHPWASRVDGIMGSDSDLPVAKDAKILNEFDVFAEVKIVSAHRTPEMMFYSALSARERGGIVAGAGAAHLPGMVAALTPLVGIVPVRASTLDGLDLSLLSIVGMIPRGVPTVATVAINNATNAGLLAVRLLGISDKL

NbL13g23020.1 ubiquitin_carboxyl-terminal_hydrolase_12-like [MW = 136.83 kDa]

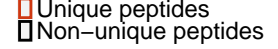
No. of times detected



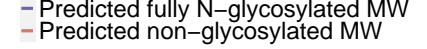
log(intensity)



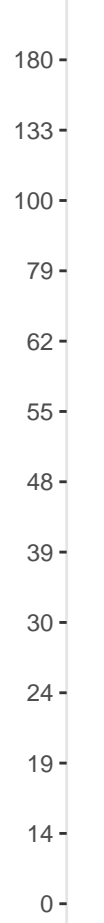
Values from



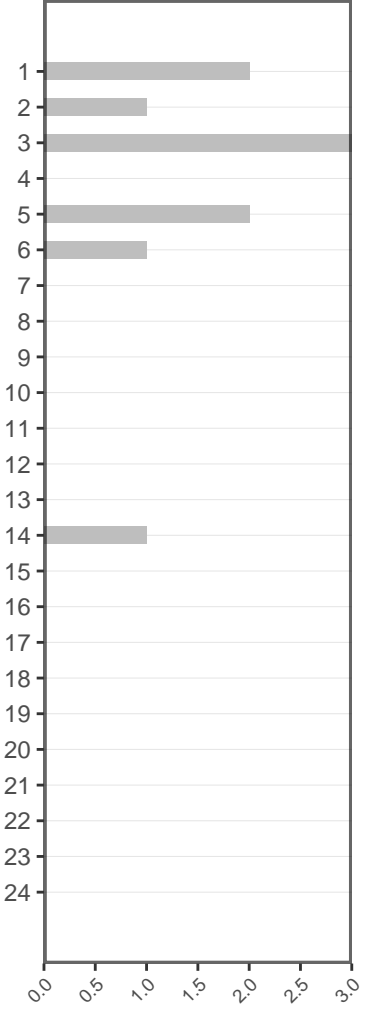
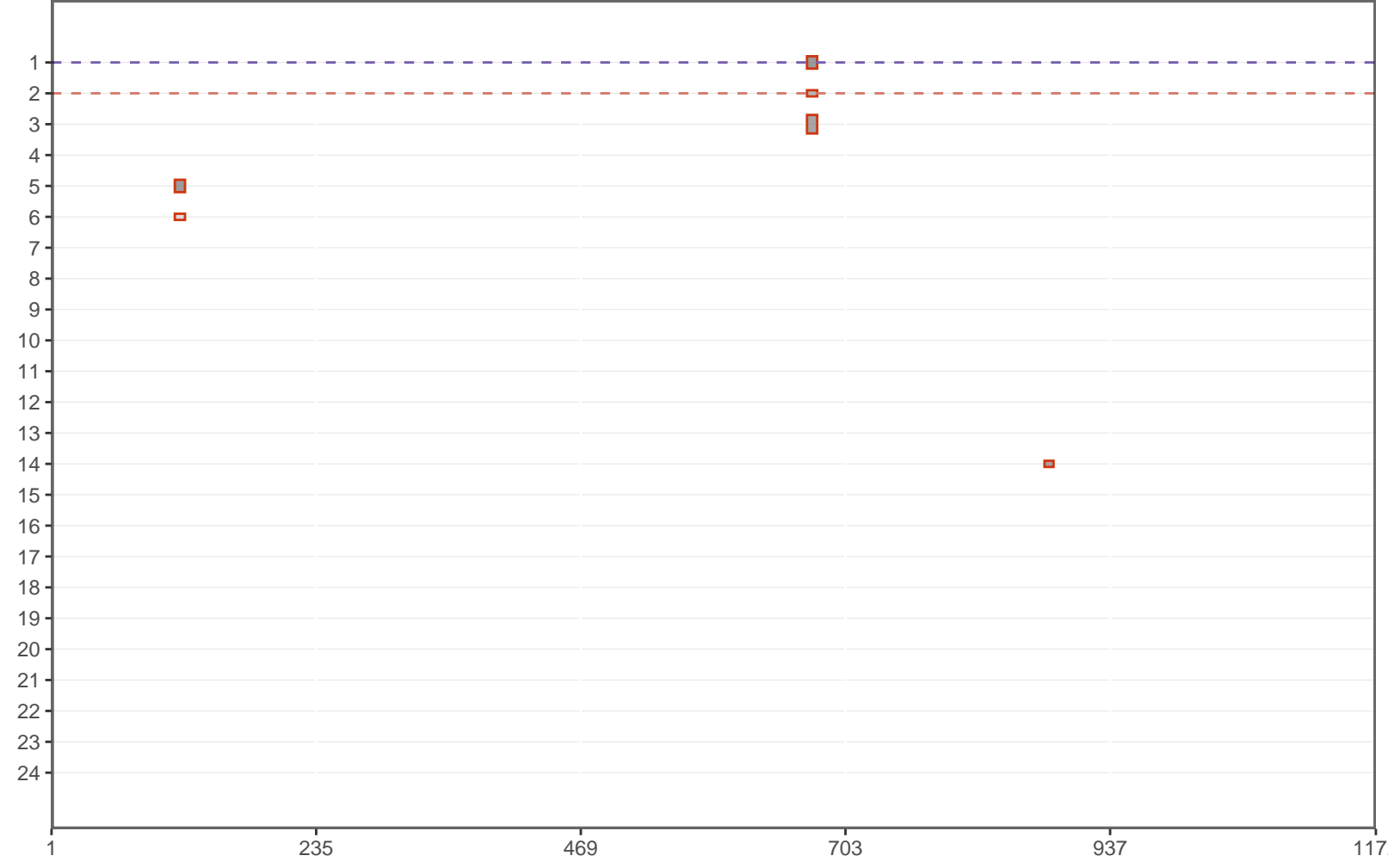
MW indication



Molecular weight

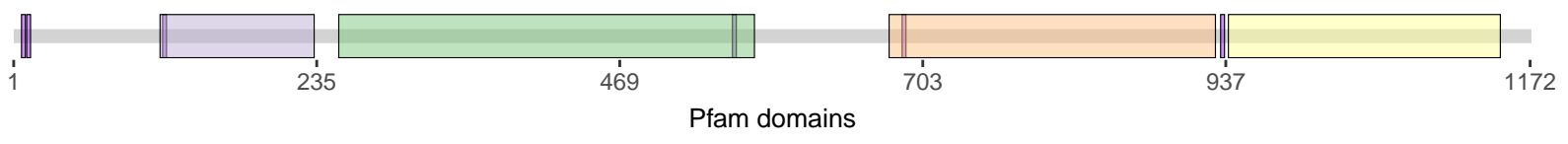


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00443 Ubiquitin carboxyl-terminal hydrolase
- PF00917 MATH domain
- PF12436 ICP0-binding domain of Ubiquitin-specific protease 7
- PF14533 Ubiquitin-specific protease C-terminal

Protein sequence:

AYMLYIRESDKEKHGNVDEKDHAEHLRVRLLKKEGDEKQRKEAEAHLYTIKVARDEDLGEGIKKHFQDLVDHDKVHSFRIGKGMFTQFKEEVAKLGFVQIGRHWLWAKRQNHITRPNRPLTQEEAAGSVGLREVSNNANNAELKLFLEVEFDLNRPPDPPEKTKEDLFFKLYDLKEMRYIGLFLVKGSGKPLLEILPKLNELAGFSPODEELFEEIKFDNVMCEPIDWALTRFGSQLEDDGHDGFKPLRSQTSQGRFPDVPVPSFLEVYVHNRQIVRFRSLK

NbL13g22990.1 GDSL_esterase/lipase_At5g33370-like [MW = 41.49 kDa]

No. of times detected



log(intensity)



Values from



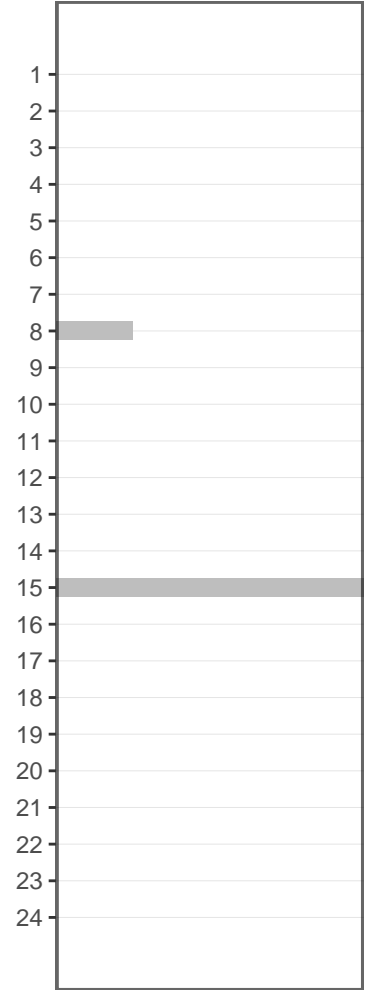
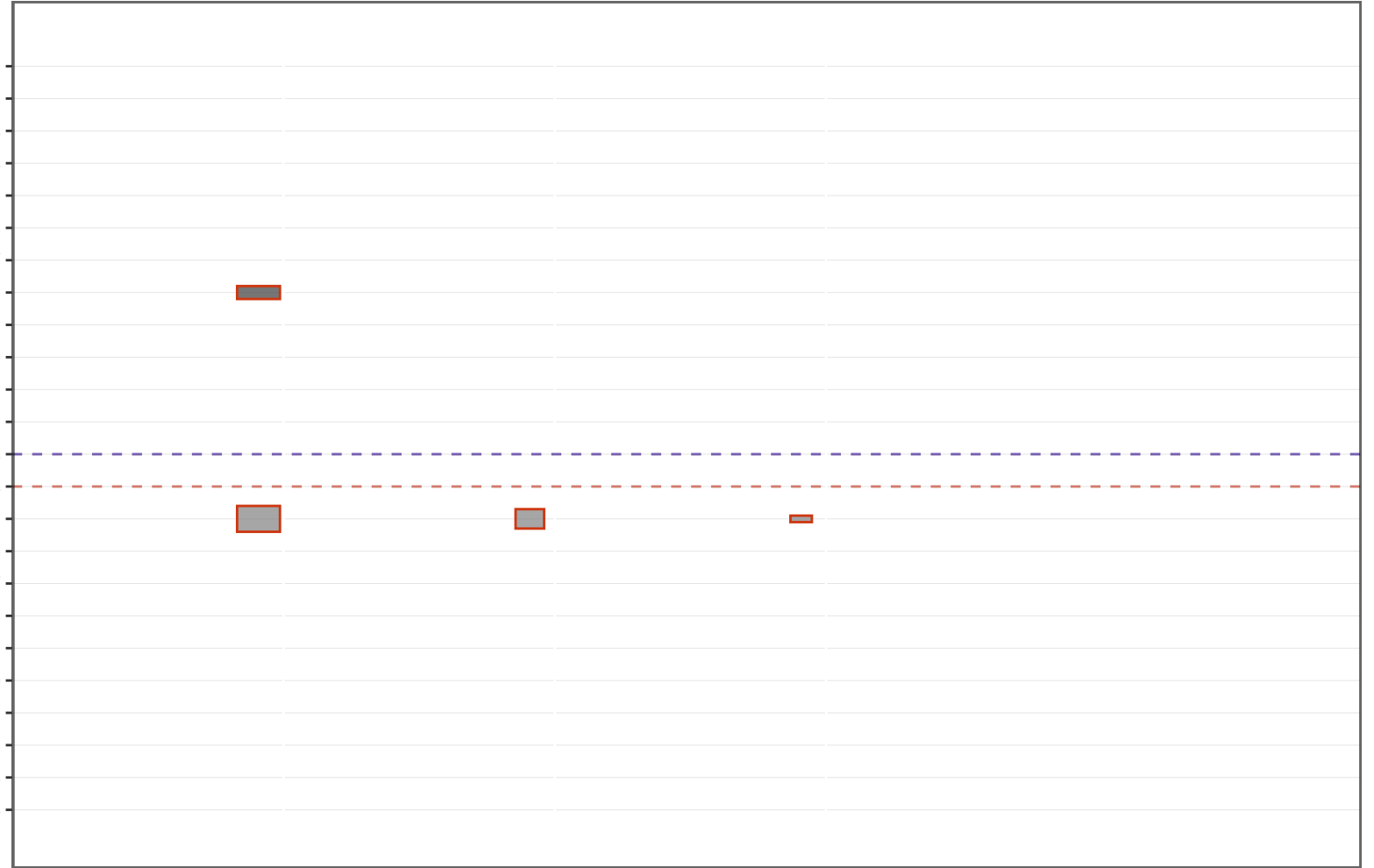
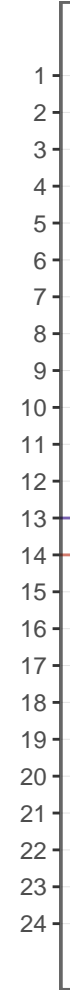
MW indication



Molecular weight

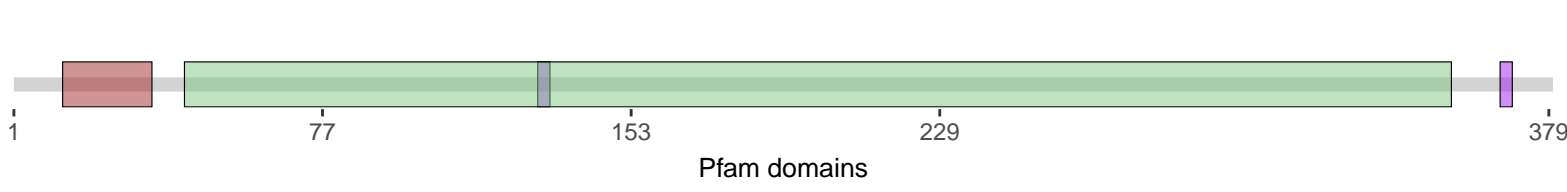


Gel Slice

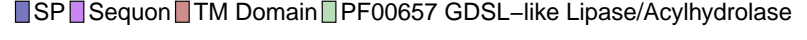


Peptide counts over 4 repeats

Protein length (1, 77, 153, 229, 379)



Pfam Description



Protein sequence:

SNDFVNYLYLPSNSARSRGVALPQVPLFLSEYRKLIRVYNIIGARRVLTGTGPLGCVPAELAQRRIRNGEGAVELGGAAALFNPLQITQMLGDLNSELGSLFAANTQGMHDFINPQAYGFVTSKACGGGGPNGLGLGTALNGLNLRDVFVAFWDFPHPSERANKIVGGMTGSSEYINPAINLSTILAMDSMA*

NbL13g22920.1 small_nuclear_ribonucleoprotein_Sm_D2-like [MW = 12.06 kDa]

No. of times detected



log(intensity)



Values from



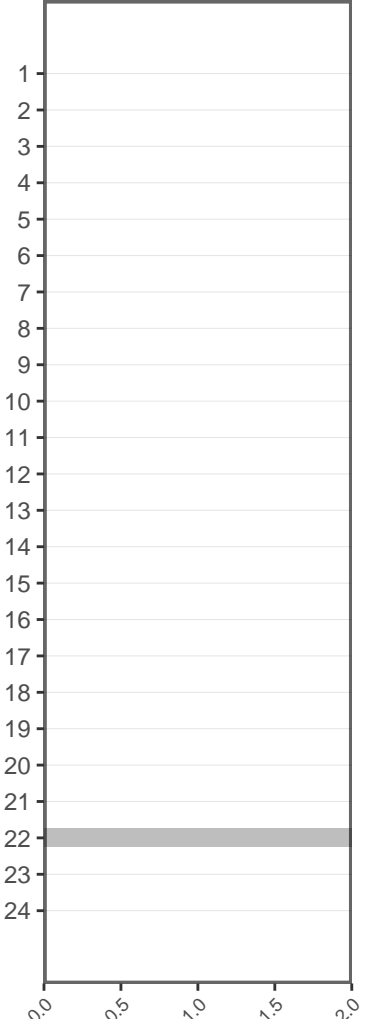
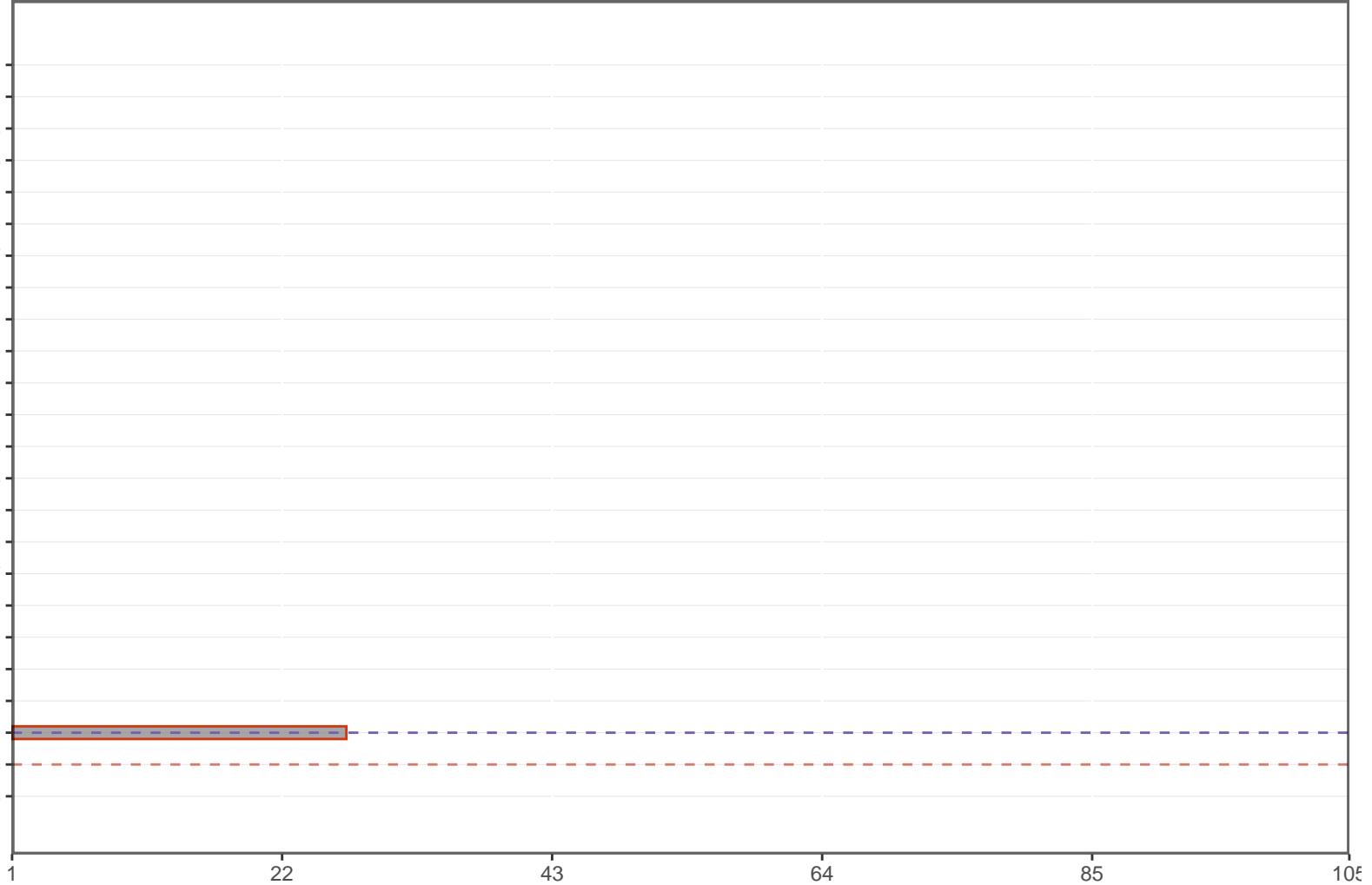
MW indication



Molecular weight



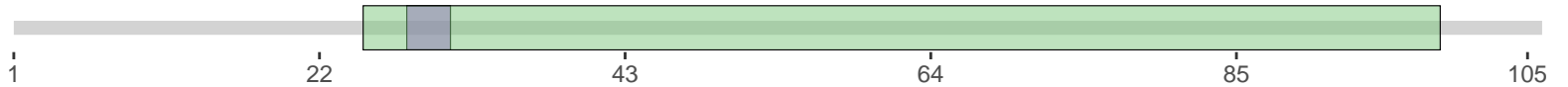
Gel Slice



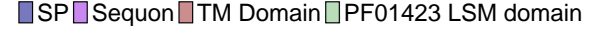
Protein length



Pfam domains



Pfam Description



Protein sequence:

RKLLGRVRAFDRIHGMVLENVREMVFEPKTKGKGGKGGKAGPNNDRFISKMFLRGDSVIVLRFK*

NbL13g22910.1 NAD(P)H-quinone_oxidoreductase_subunit_O_chloroplastic [MW = 16.72 kDa]

No. of times detected



log(intensity)



Values from



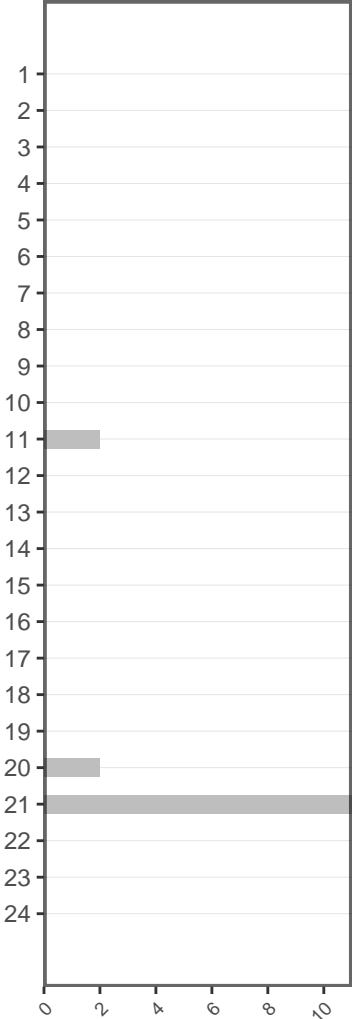
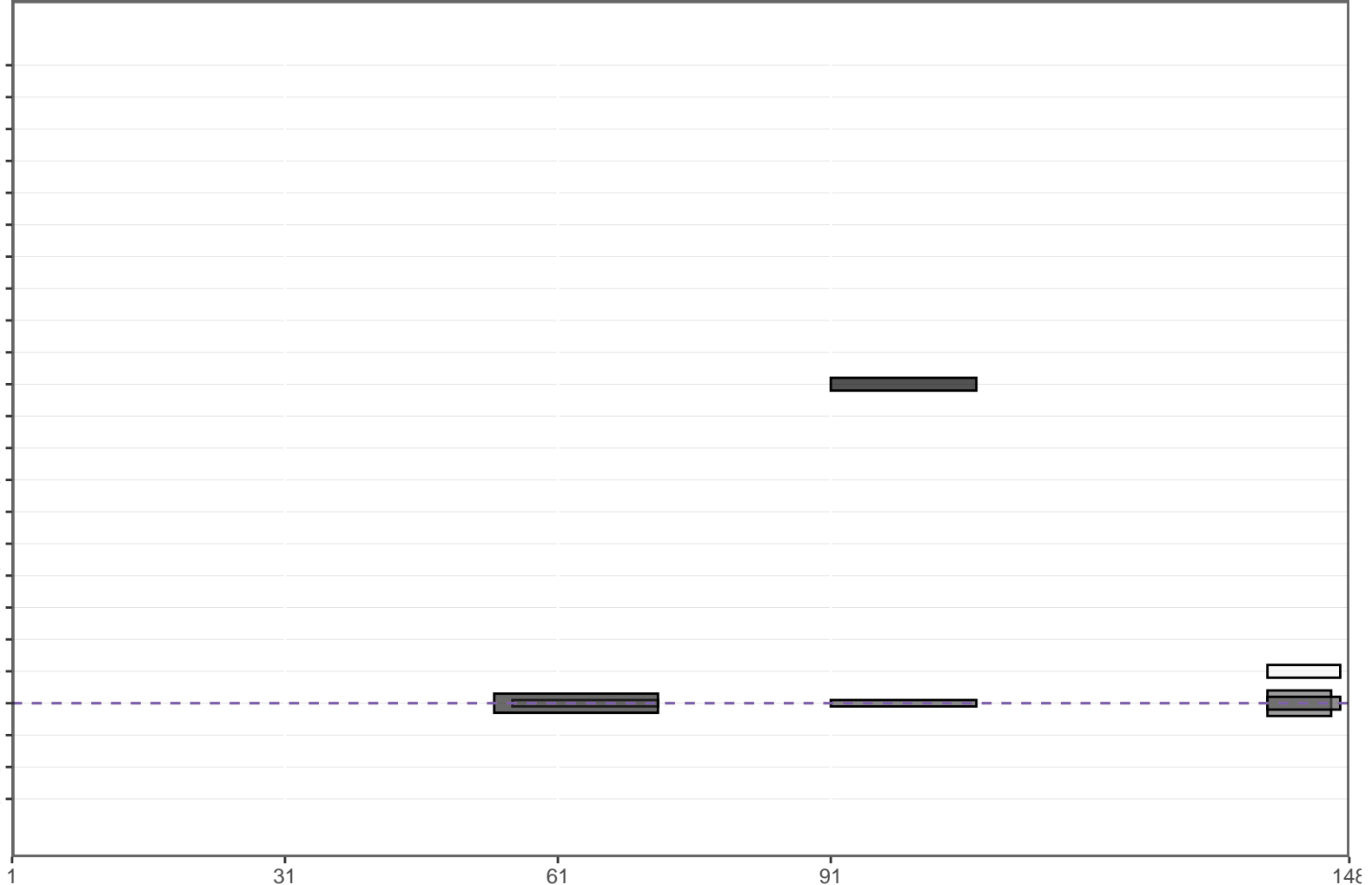
MW indication



Molecular weight

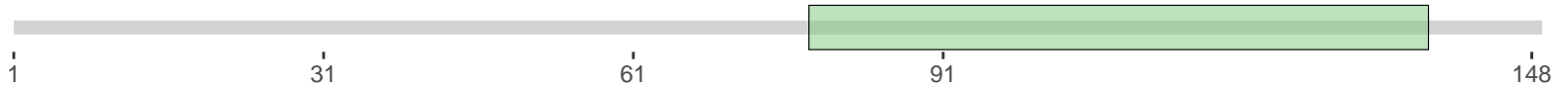


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

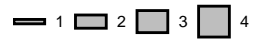


Protein sequence:

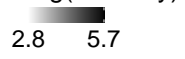
MTSSTATATKPKPKFYVSMKKGGVRRVDEKRYLNSINYLSDVHPPYKGLDHYEDRGEIGWIGPTAFWLPTEMLKSDKLDVERI

NbL13g22890.1 receptor_protein_kinase_TMK1-like [MW - SP = 100.84 kDa]

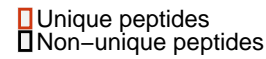
No. of times detected



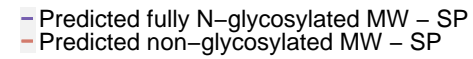
log(intensity)



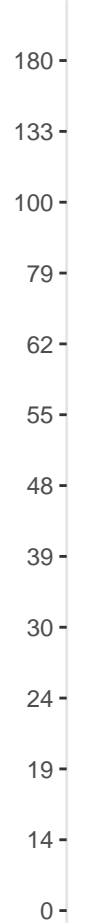
Values from



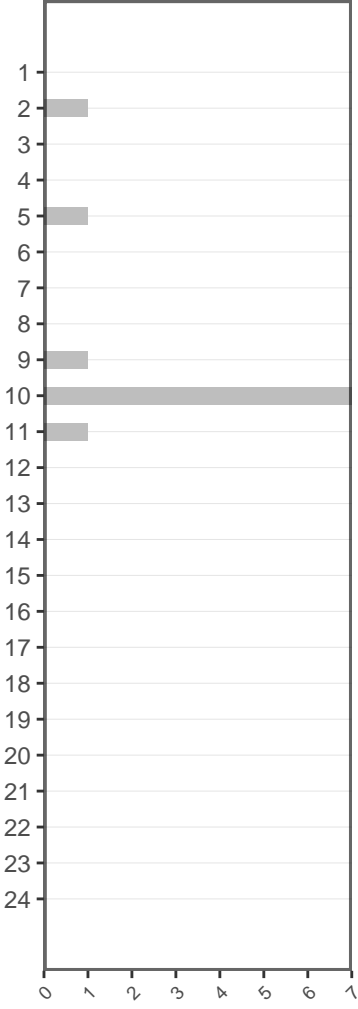
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PVSGPSGSDGDDGASRKKSNRWIGVLFVSVGGVFLVGFIGTAFLVLRKQKRFSGVGSFNTVVMGPRNSGSDNDVKTVAAGSIVVGVAVGEVHTVSTSETGDGDMVEAGNVMISQVILNVTNFSSENLGGGFGFTVYKGEIHDGTKIARMEGGFIAGKGLTEFKSEIATVTRVRRHILVGLLGVLDGKEKLLVYEMPGQTLSSHLENWREEAKPLEWTKRLTALDVARGVYELHSLAHGSHFHRDLKPSNILLGDDMRKAVDFGLVRLAPEGKGSIT

NbL13g22830.1 peptidyl-prolyl_cis-trans_isomerase_CYP19-3-like [MW = 19.03 kDa]

No. of times detected



log(intensity)



Values from



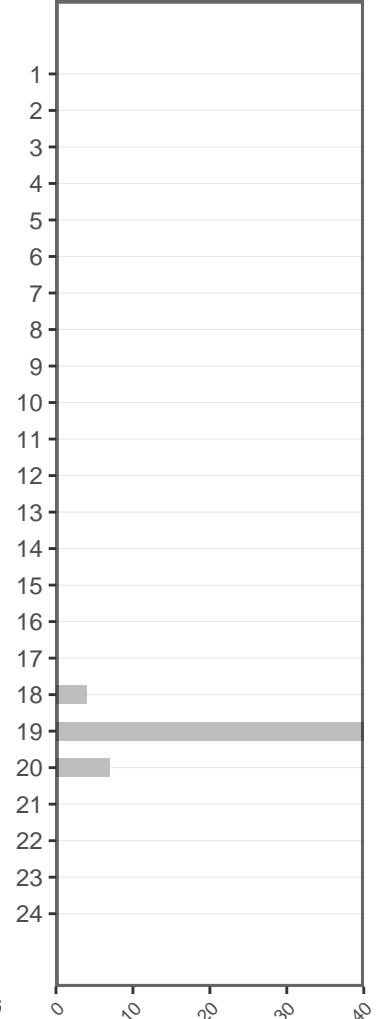
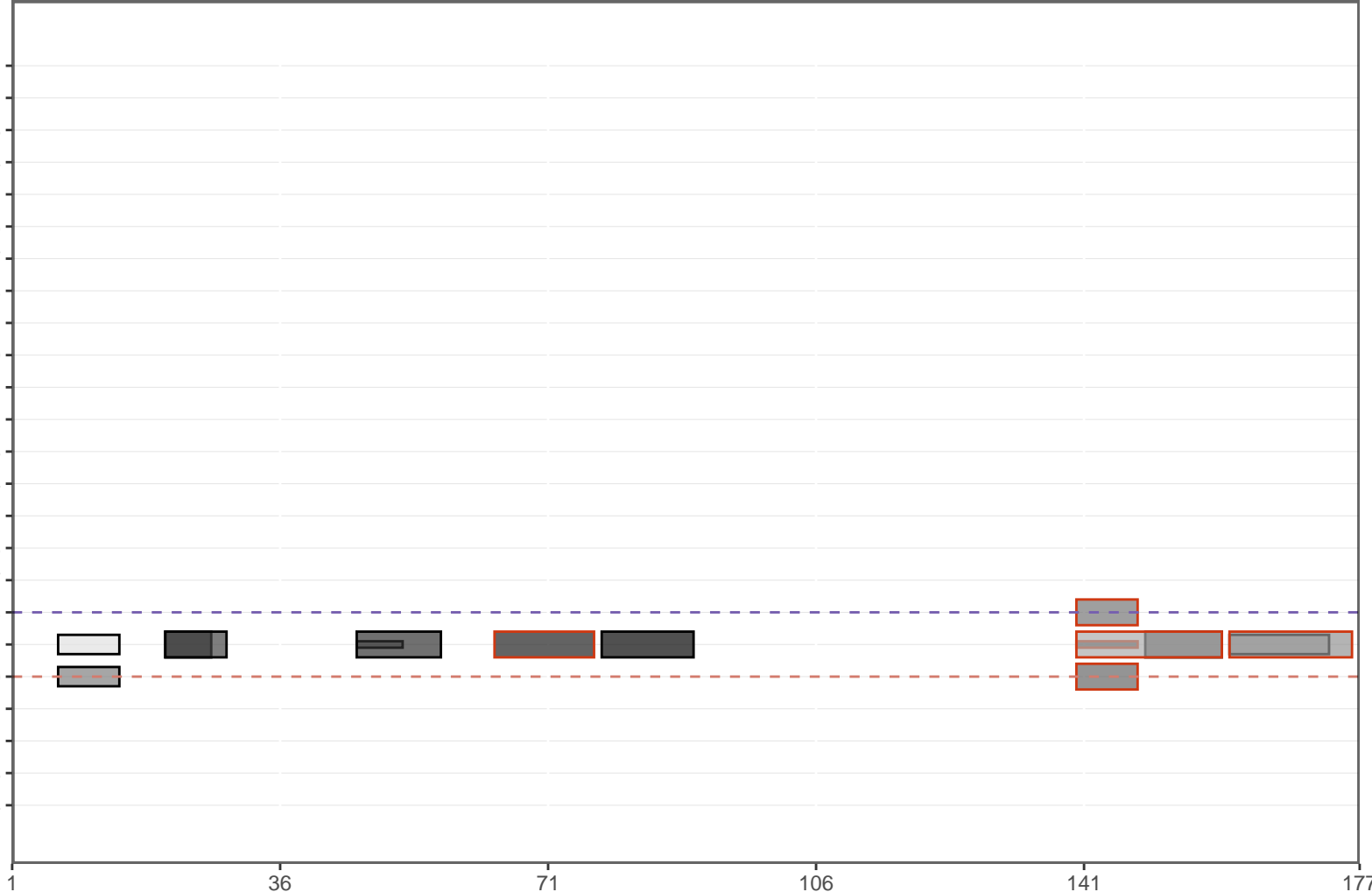
MW indication



Molecular weight

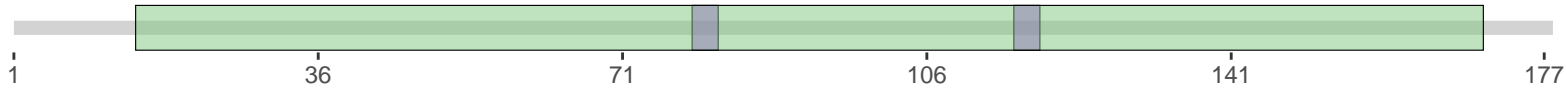


Gel Slice



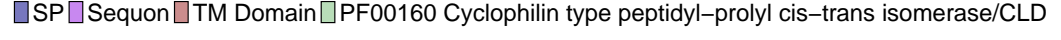
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGNGTGGESISYGANFSDSEDFVMMHTPGLLSEMANAGPNTNGSOFRTTPTPWLDGKHVFGKVDGYNVVKEMENVGSDSGKTSCTVSEIDCGGELKETK

NbL13g22760.1 AT-hook_motif_nuclear-localized_protein_14-like [MW = 33.96 kDa]

No. of times detected



log(intensity)



Values from



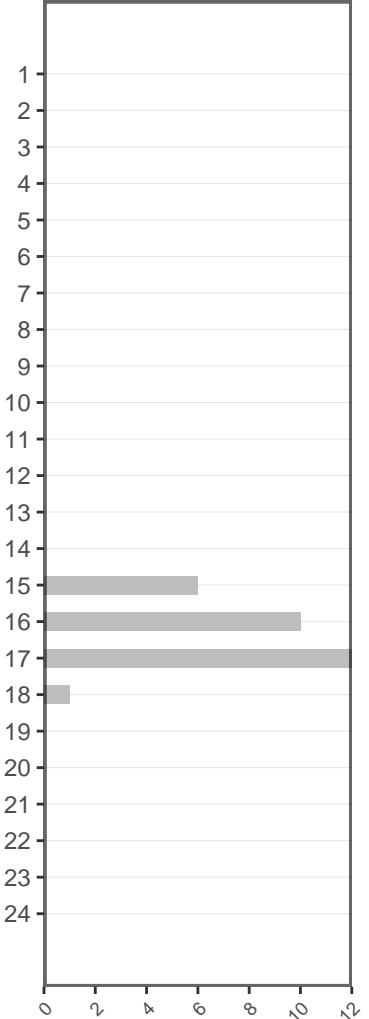
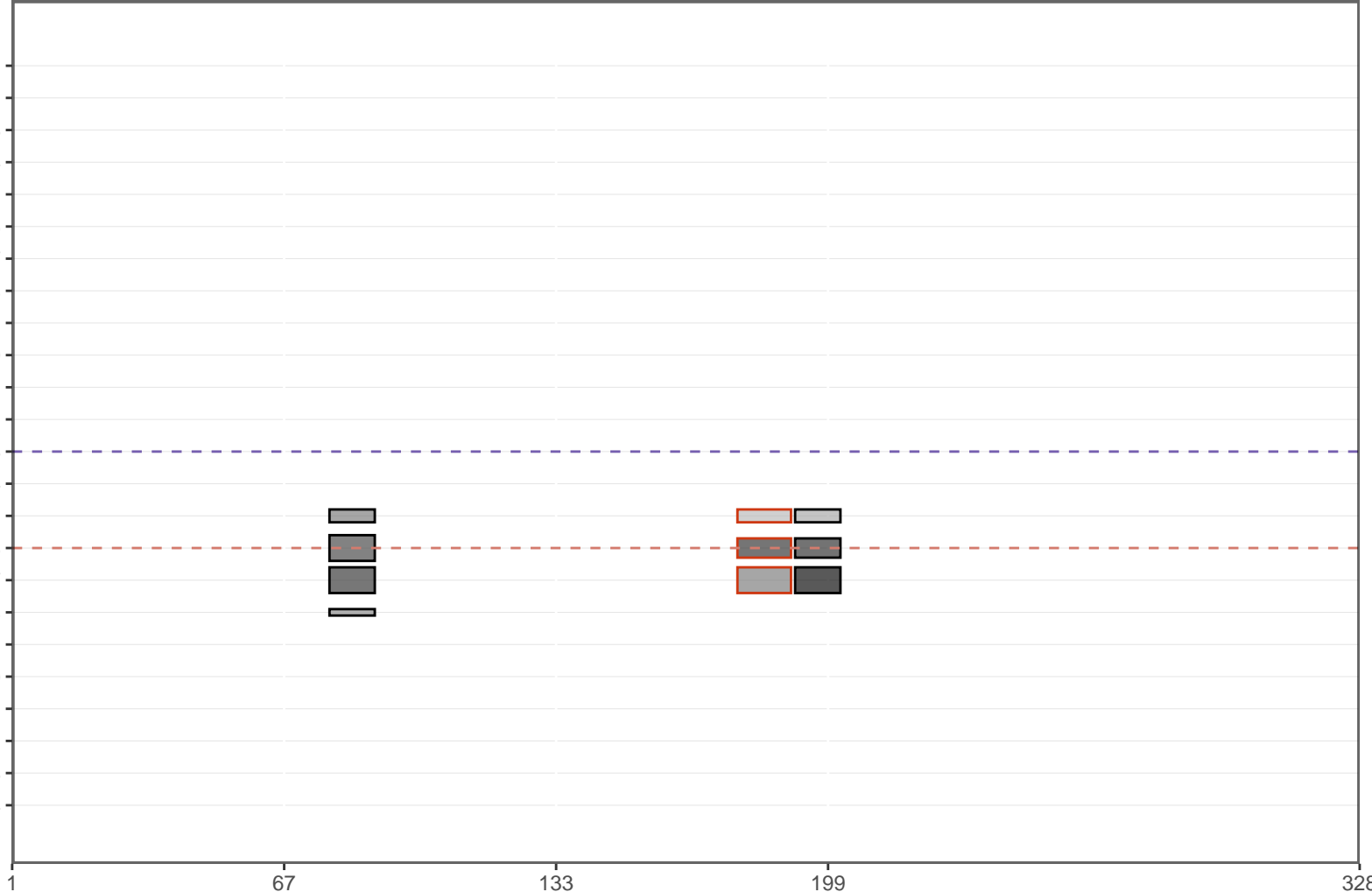
MW indication



Molecular weight



Gel Slice

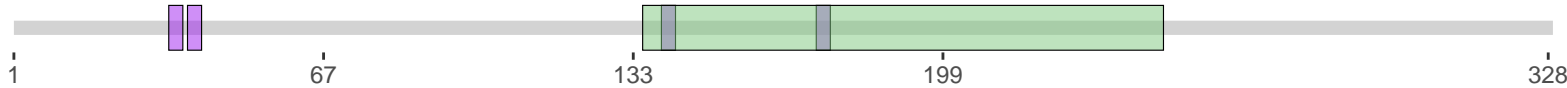


Protein length

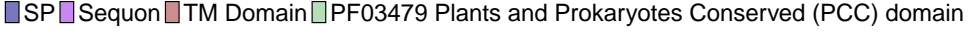


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

/MFMQSKYELCLVLSASGGSHNABLRQPTSGGGSTVEGRFDLTLGGSVRTEHGRTGGLEVLGLASTDGGHGGGVGGPLIAGGPIGVVSGFVSDKAGGVNNDISHQISGSPMSVGFREVVDSSHQNMGGGDFMIGSRGMQPAHLHQTETWRVSTGGGMHQSPENGVDHLGE*

NbL13g22740.1 uncharacterized_LOC109225749 [MW = 24.42 kDa]

No. of times detected



log(intensity)



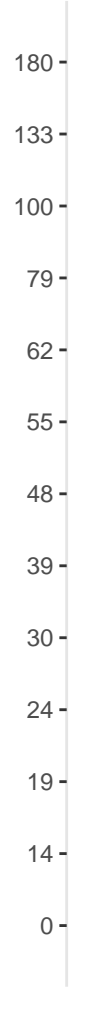
Values from



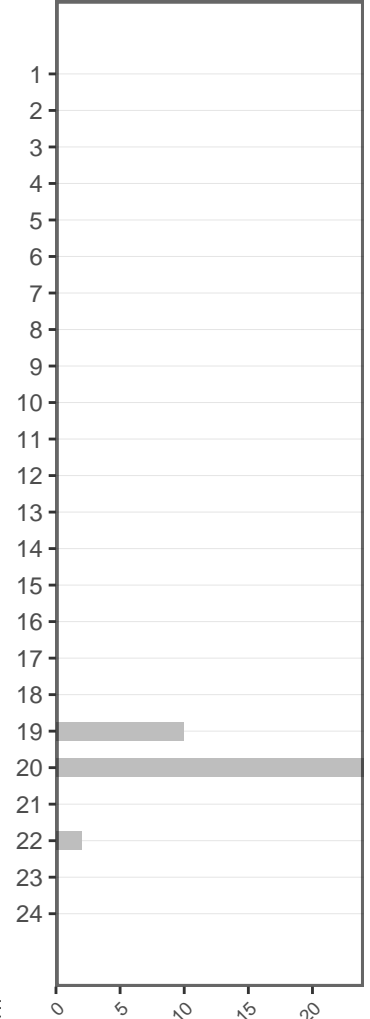
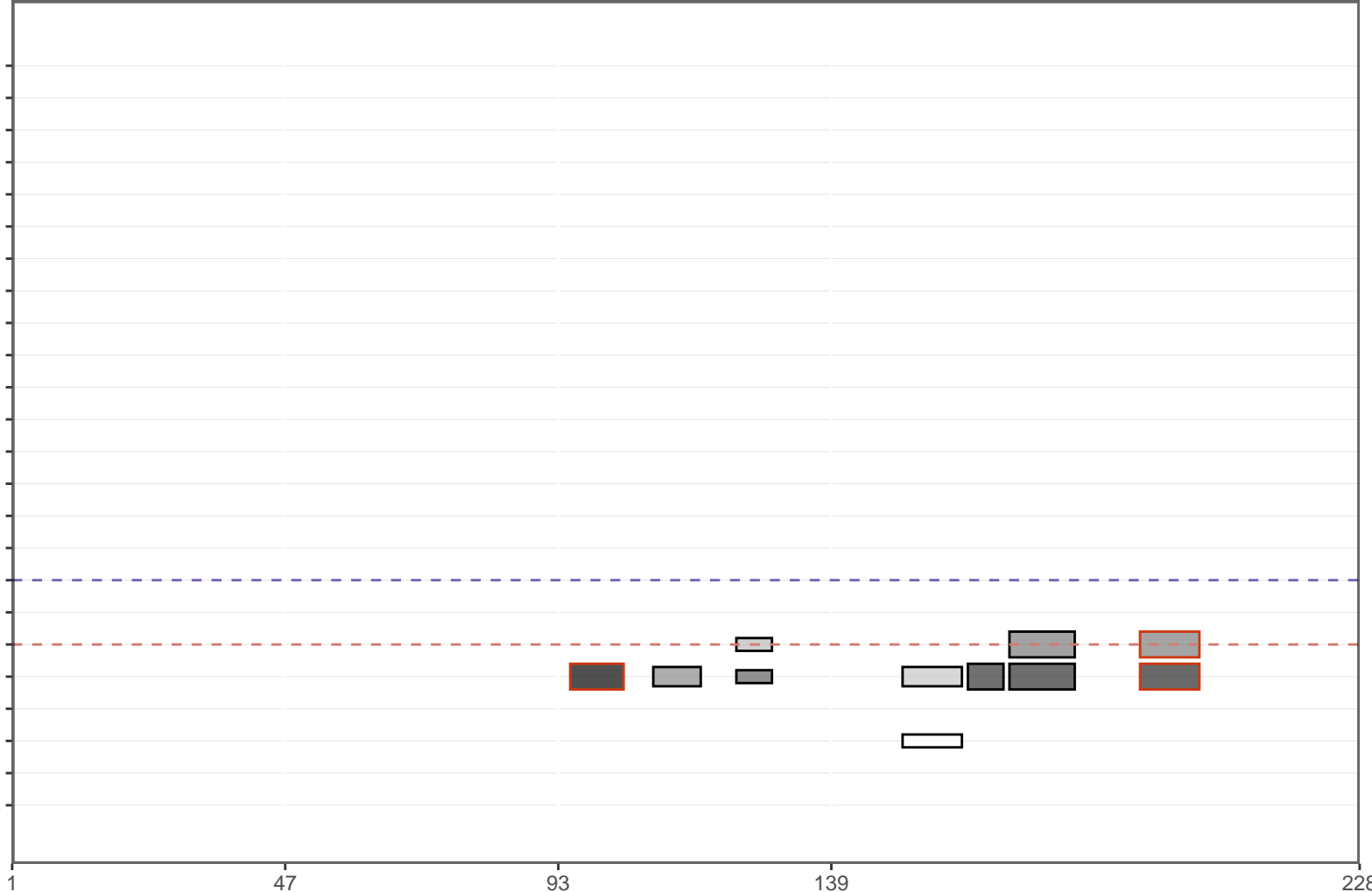
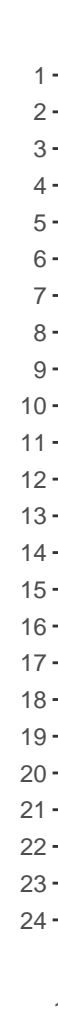
MW indication



Molecular weight

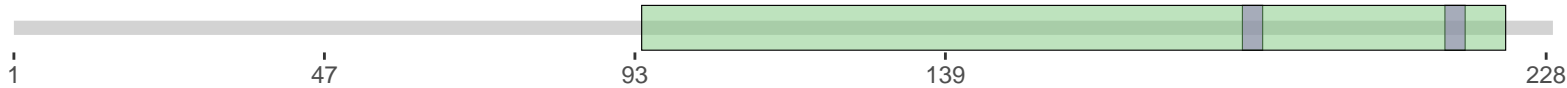


Gel Slice



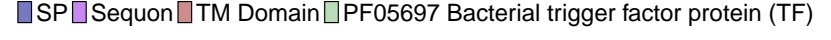
Protein length

Peptide counts over 4 repeats



Pfam domains

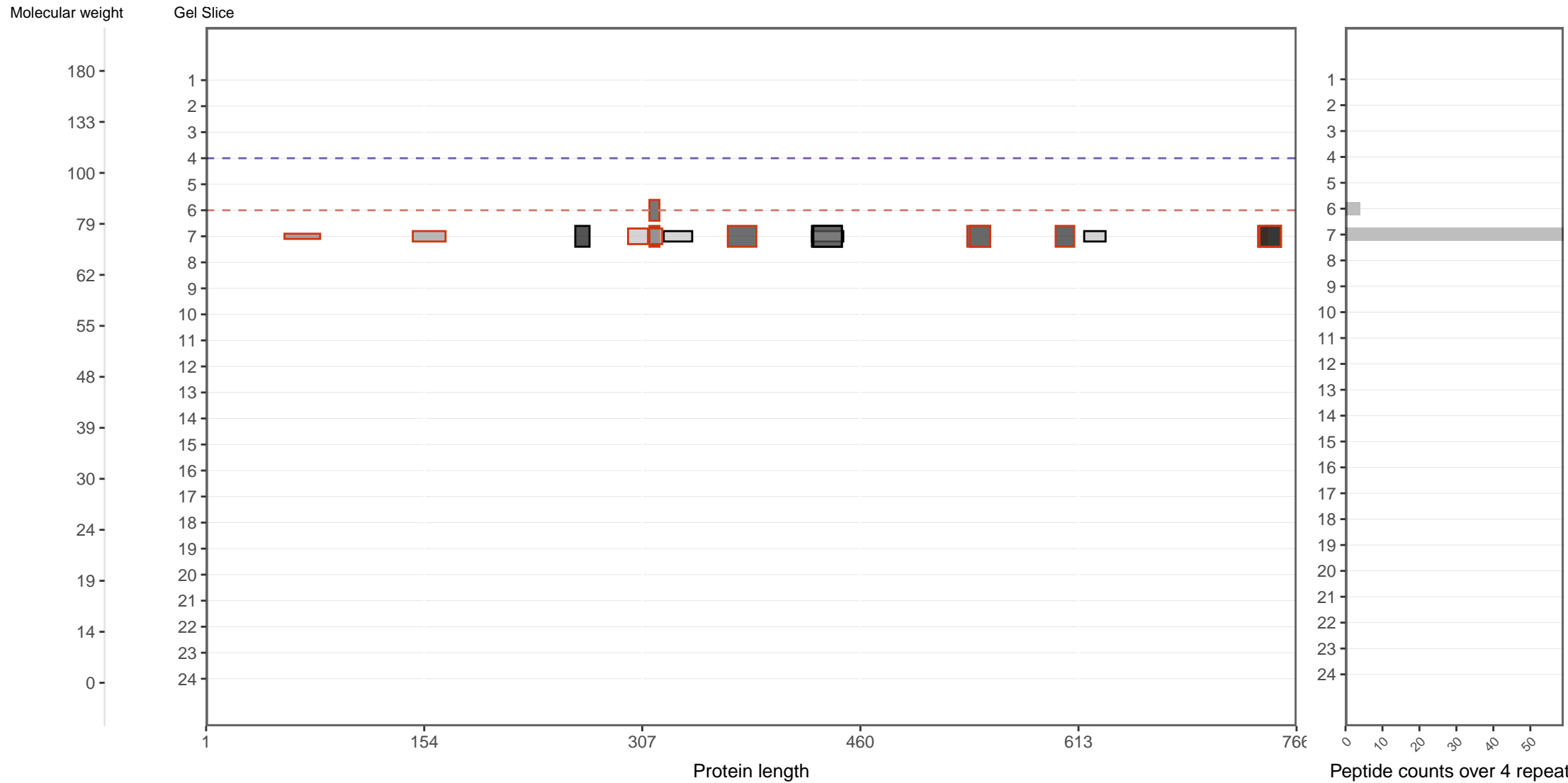
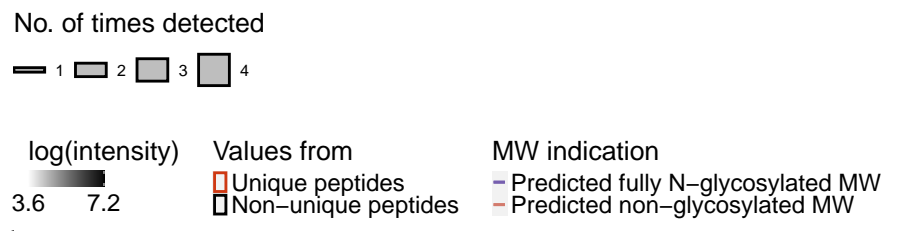
Pfam Description



Protein sequence:

JAEKHIVRVD/DKEDTRIVFEKVLNLANLARGAPPVPGRRREKGGKTSKVPDRDFLLQQLGEDRVTNFIKREIVTSTLADVKKENLGVKDKNKISTFTQTAHELKS68FTIGAEFGFNATLELEDAKTEATF

NbL13g22560.1 5-methyltetrahydropteroyltriglutamate--homocysteine_methyltransferase-like [MW = 84.52 kDa]



Pfam Description

SP Sequon TM Domain PF01717 Cobalamin-independent synthase, Catalytic domain PF08267 Cobalamin-independent synthase, N-terminal domain

Protein sequence:

IKDKDAFFSASAAAGASRKTSPRVNTEAVGKAAALRGSDHRRATNVSARLDDAGKKNLPLVPTFTTGGSPQTVELRRVRRREYKANKISEEYVKAKEIKKVVVLGGEELDIDVLVHGFPERNDMVEYFGEQLGGFAFANGVWVGGYSGRCVKPPVIGDVSRRPKMTVFWSSAGDMTRKPKMGMLTGPVTLNWFSEVRNDQPRFETGYQALAKDEVELEKAGISVIGDEALREGLPLRKAHAFPLNVAHVSFRITNVDIQDFTQIHTMDCVSNFNDSIISIDMA

NbL13g22460.1 calmodulin [MW = 16.83 kDa]

No. of times detected



log(intensity)



Values from



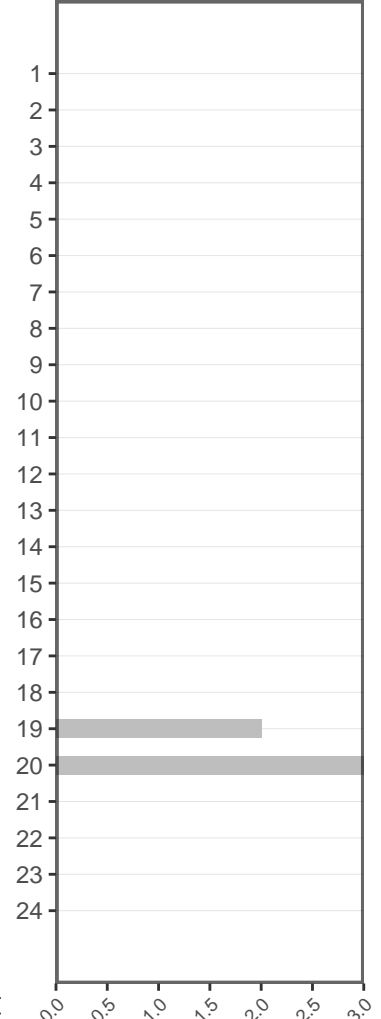
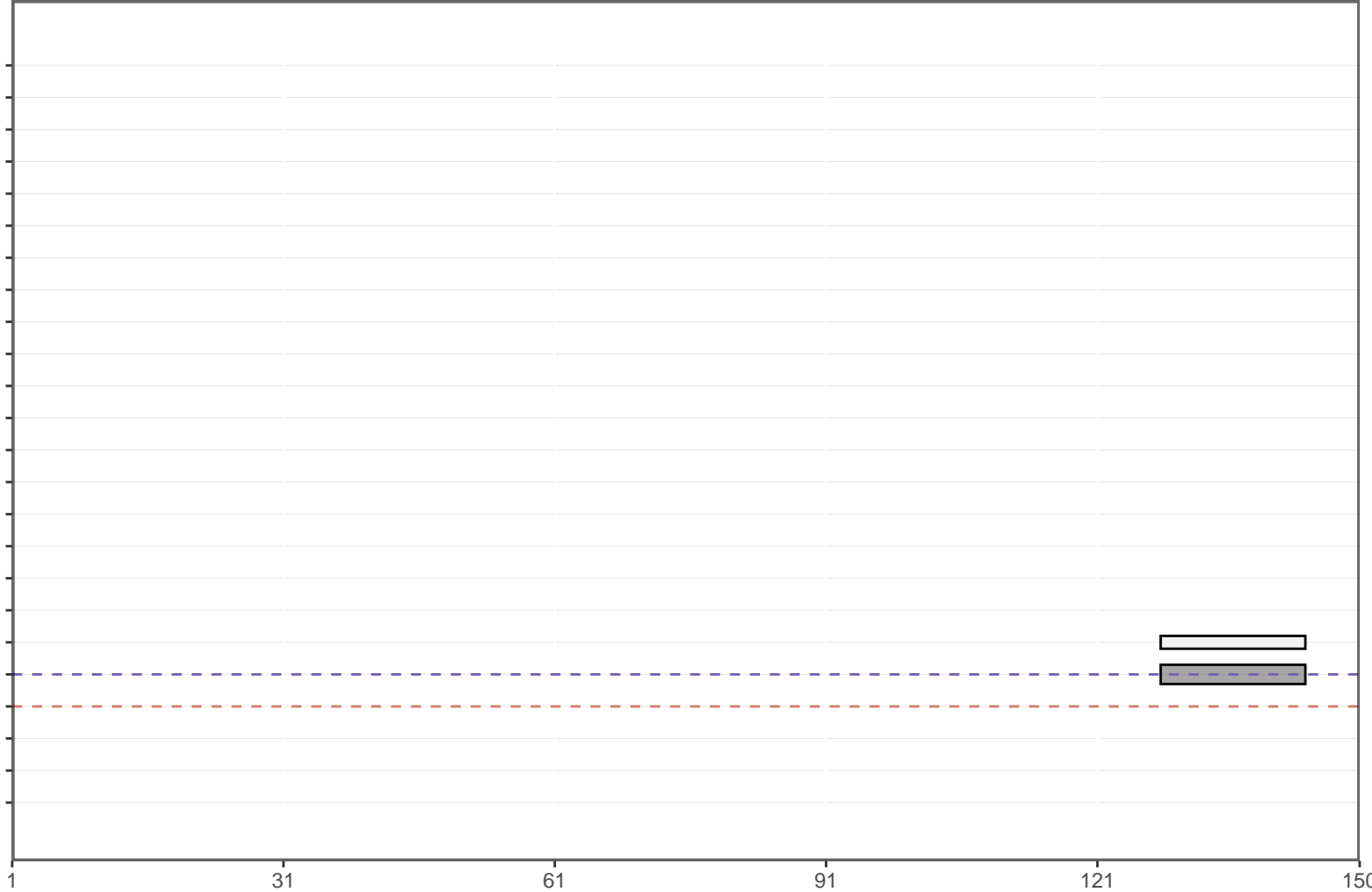
MW indication



Molecular weight

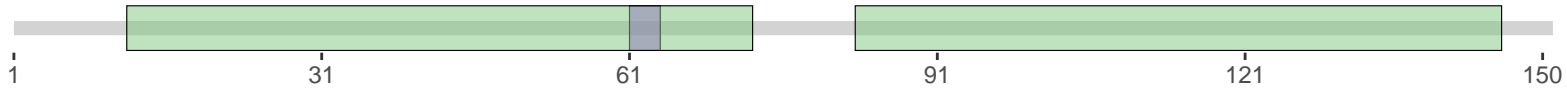


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

STIDPFPEFLNLMARKMKDTSDEEELKEAFRFVFDKDNQGFISAAELRHMTNLGKLTDEEVDEMIREADVDDGGQNYDEFVKVMMAKI

NbL13g22450.1 uncharacterized_LOC109236586 [MW = 77.89 kDa]

No. of times detected



log(intensity)



Values from



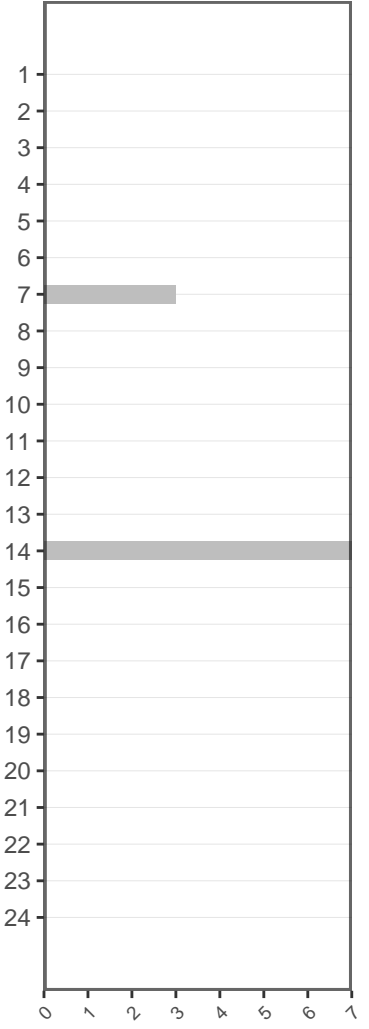
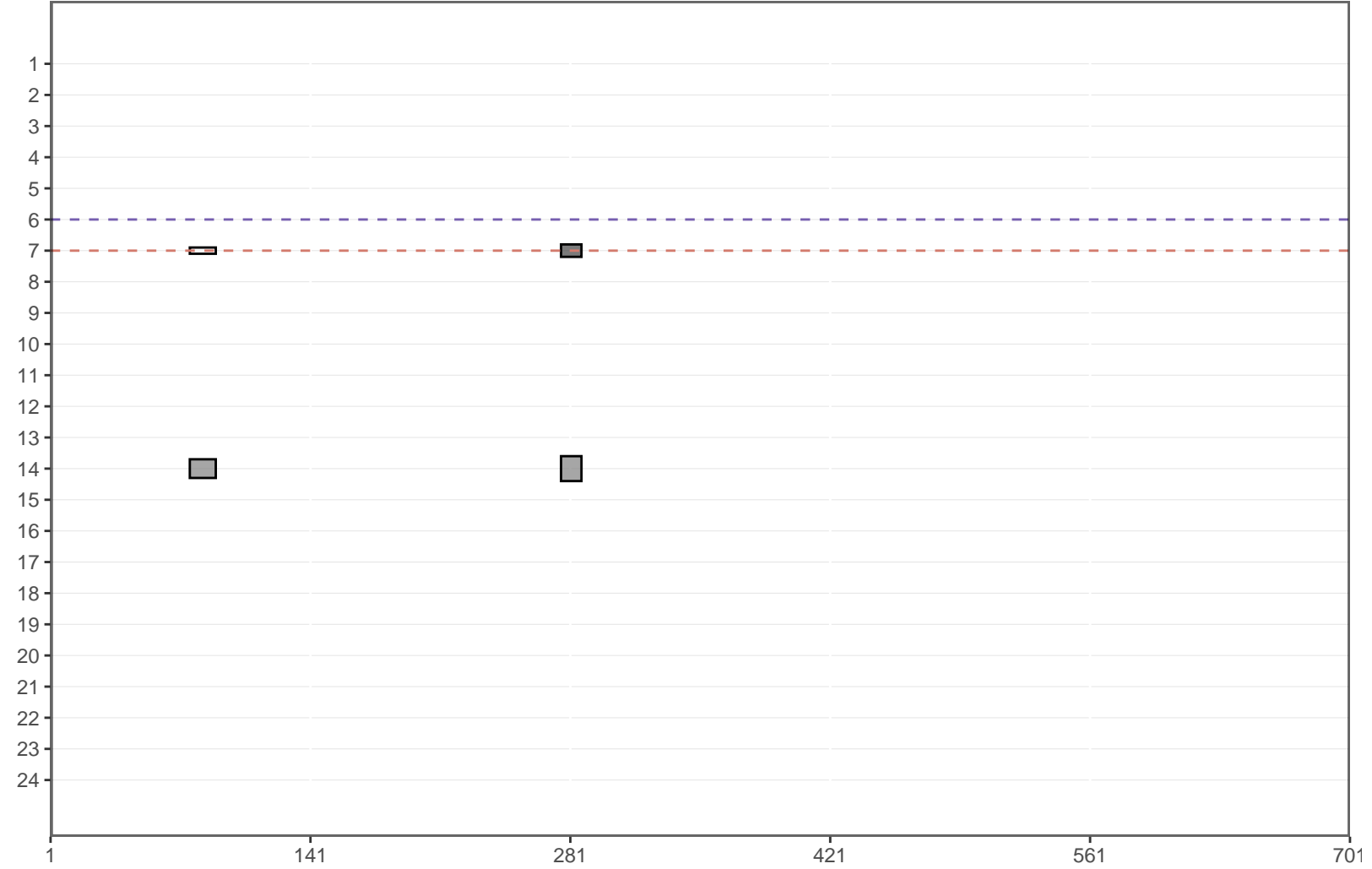
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

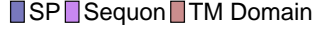
1 141 281 421 561 701

Protein length



Pfam domains

Pfam Description

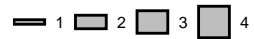


Protein sequence:

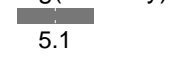
IQLGDSKANGNLFRFGQREASPEIVEHEEESFGLPEPKSMKLEVGSIVLIEDSNWQKGVQINEVLTHDEEPYHASSVEDPQTTFLFLVYSHPSQLERAWEDMKLWYVQGRGTVKLVGMKGRGLWSKYLPLQKASGRNHPGGGRRPSGGGSDLPWGGTFLVLTSPVGRIVADMVRLGGFGTDEAKGDHDCLSALSAASSAGIRHGDIRPENWYVNSGVRGPFVFLIGWGHAALEERDRPAMNLHFSBTYALQEGKLGASBSAEGLVMLVFCGGQMPNLDV

NbL13g22420.1 proteasome_subunit_alpha_type-3-like [MW = 27.2 kDa]

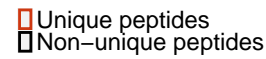
No. of times detected



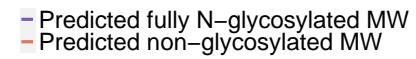
log(intensity)



Values from



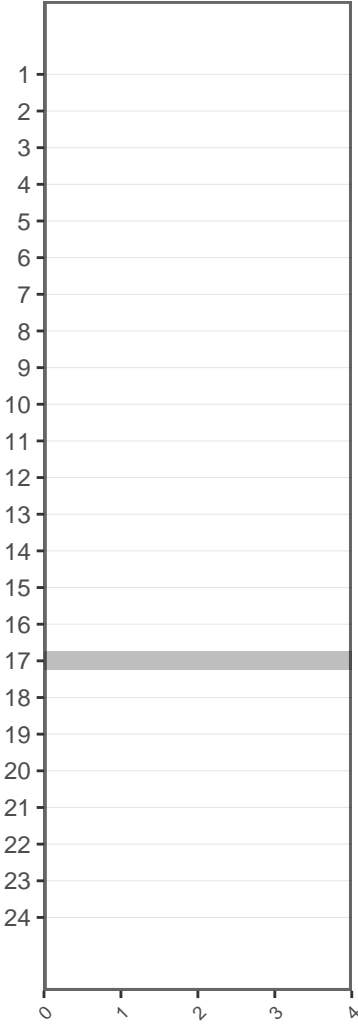
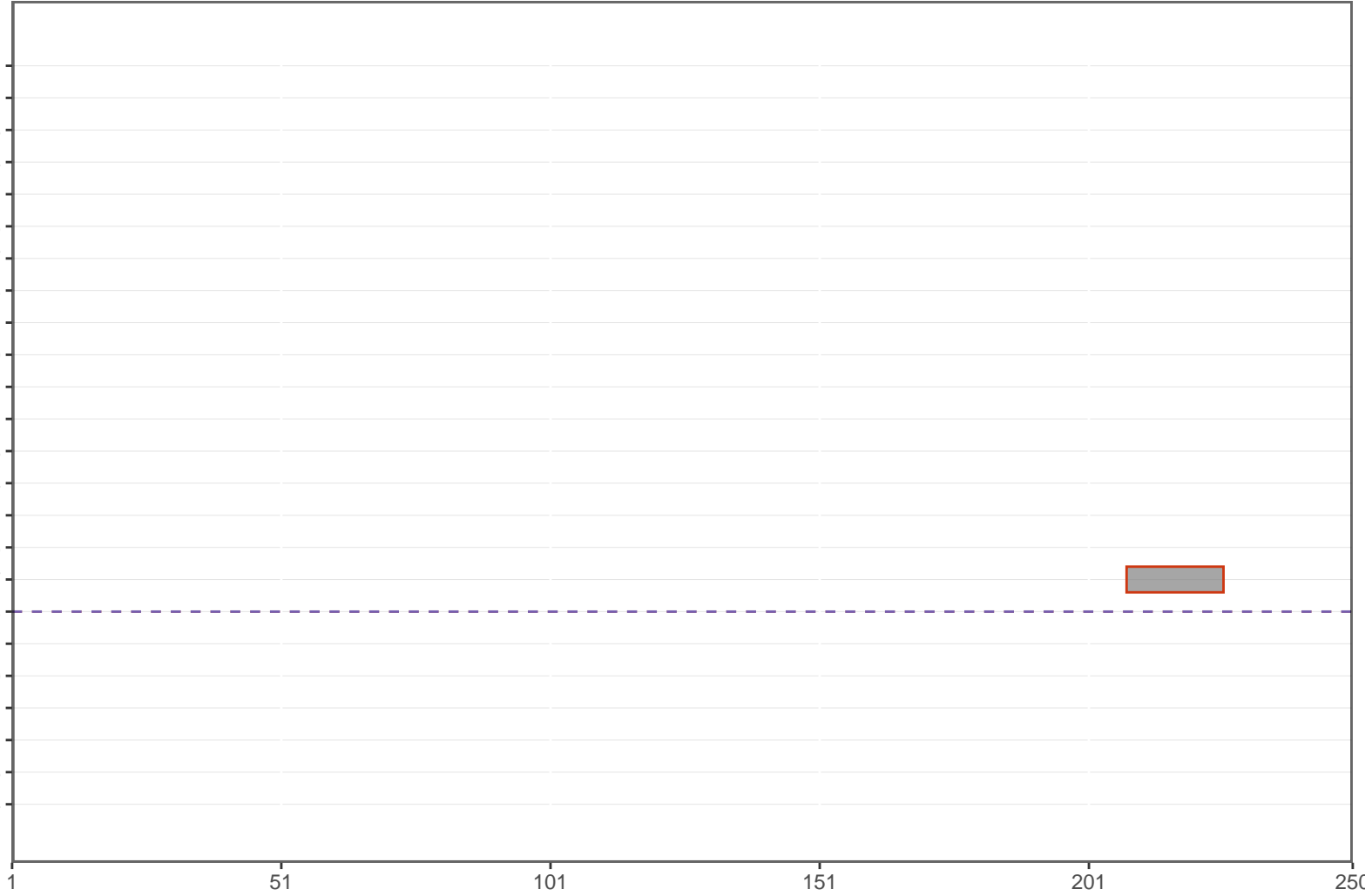
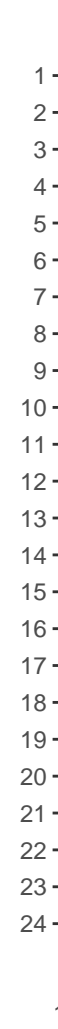
MW indication



Molecular weight



Gel Slice



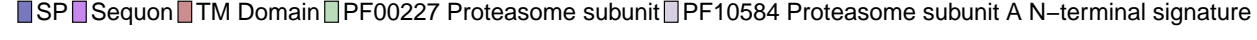
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

AERVASYVHLCCTLYWALRPFQGGVILGGYDRDGPQLYLVFPGVGYRFRFGAAGKGRGAAKTEIEKLLKLSMTGRGGVIEVAKIHYGVHDEAKDKAFELMSWDCDESNHQHGHKVPDQILEAKTAKAAALEEMADP

NbL13g22380.1 histone-lysine_N-methyltransferase_H3_lysine-9_specific_SUVH1-like [MW = 78.32 kDa]

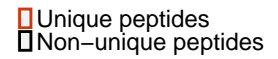
No. of times detected



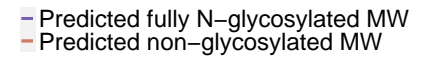
log(intensity)



Values from



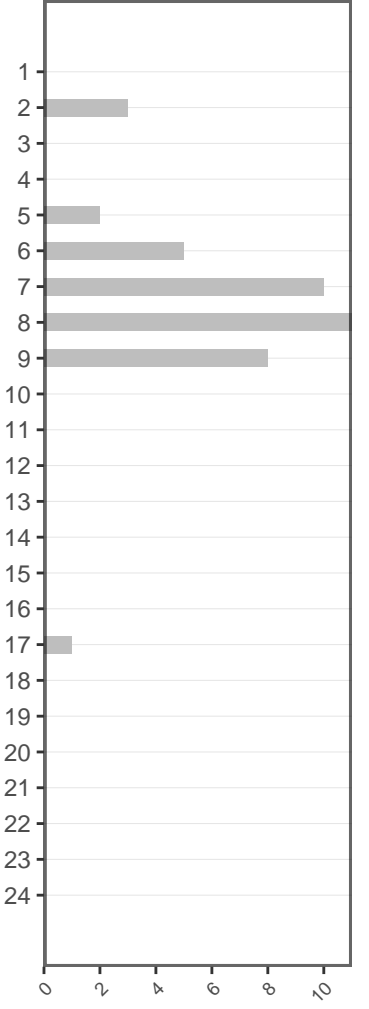
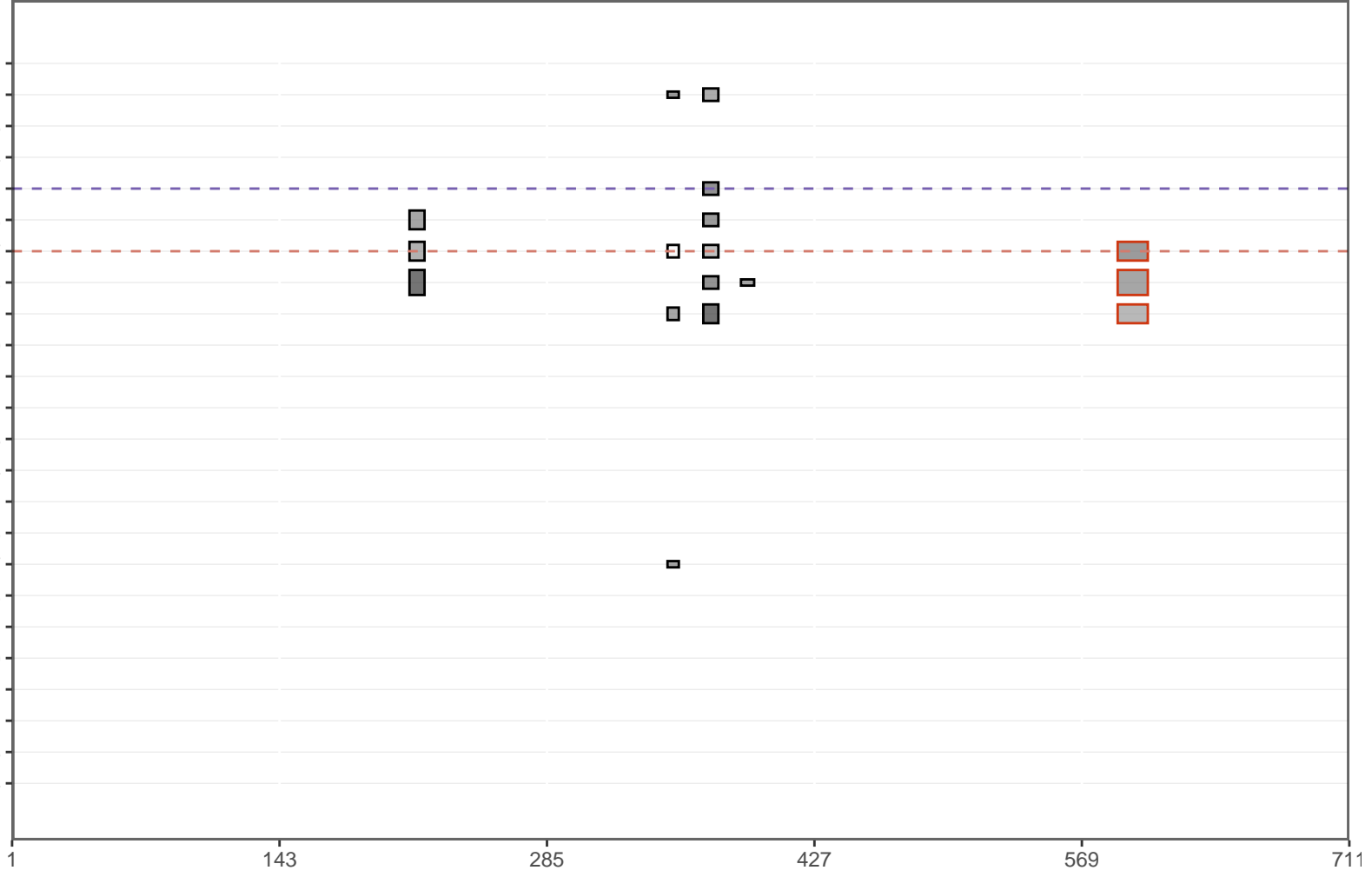
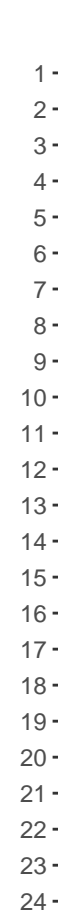
MW indication



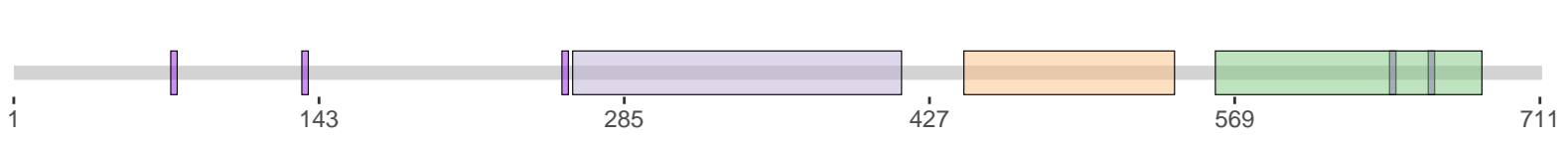
Molecular weight



Gel Slice

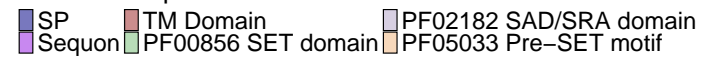


Protein length



Pfam domains

Pfam Description

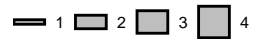


Protein sequence:

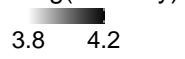
TQKLERGNLALEKEMHRGMEVIRVIRGVIVITNPRGKVMYDGLYRIGESWAEKSLKGGDFRKYKLLRVDPGPEAFLLWKGSGQWRDGTATRVGVLPDLTSGAEGSPVCLWVDVDEKGRPVFTYIPSLKYSKPYMKPNPBMGGGCVGGGGPQGGSTGPGCIQKNGGFLPSSLGLVLSVYKTLHEGGASCSGPPNCRERMRM60AGPKARVEVFKTKNRGWGLRSDPHGGGFCEYAGEVVEEARVDELGNEGDDVFDATRVPELPEVLRDYNDEGKVPYSLVISAQK

NbL13g22350.1 nascent_polypeptide-associated_complex_subunit_alpha-like_protein_1 [MW = 21.84 kDa]

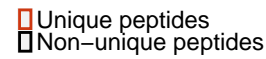
No. of times detected



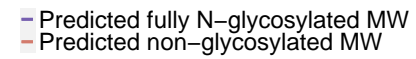
log(intensity)



Values from



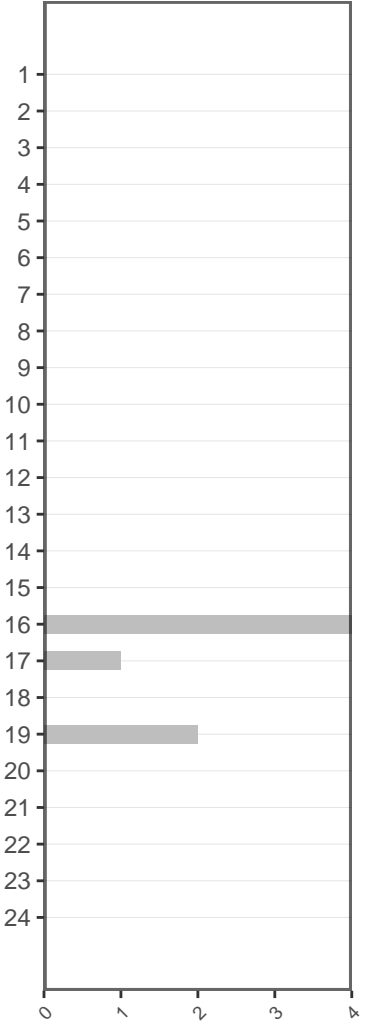
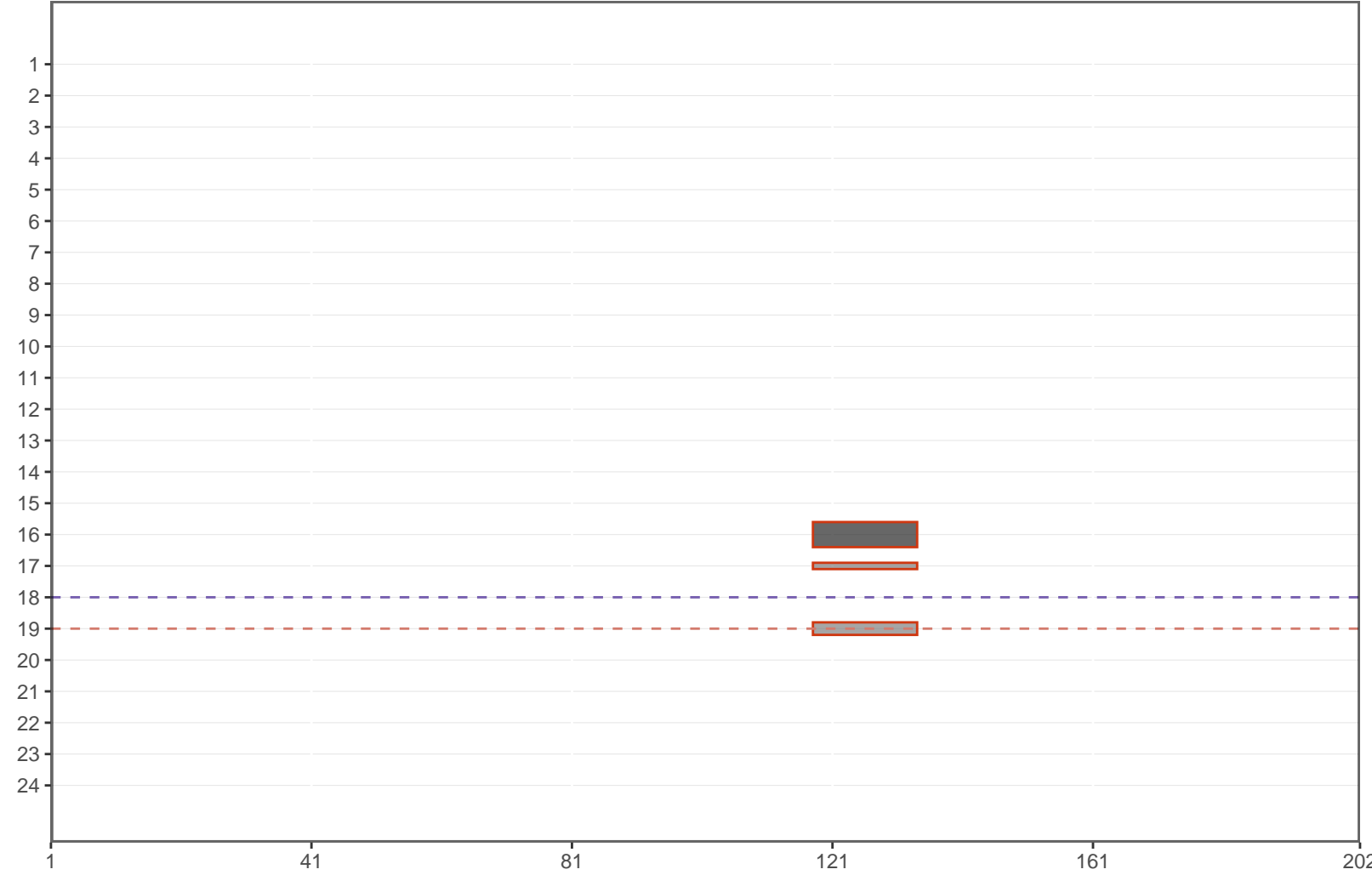
MW indication



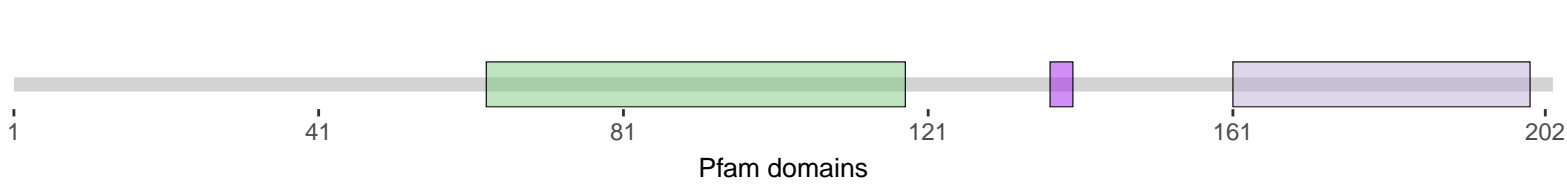
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

AKSKNLFYISKPDVFKRPSADTYVFGAENKIDLSGQLSSGAAEGFKAPNLNWKPKPEPTVAGDDEVDDETGVPEKIDELVMTGAGVSRKAKKAKGADGDIVSAMELTN

NbL13g22160.1 L-type_lectin-domain_containing_receptor_kinase_IX.1-like [MW - SP = 76.02 kDa]

No. of times detected



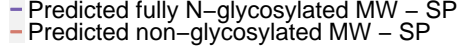
log(intensity)



Values from



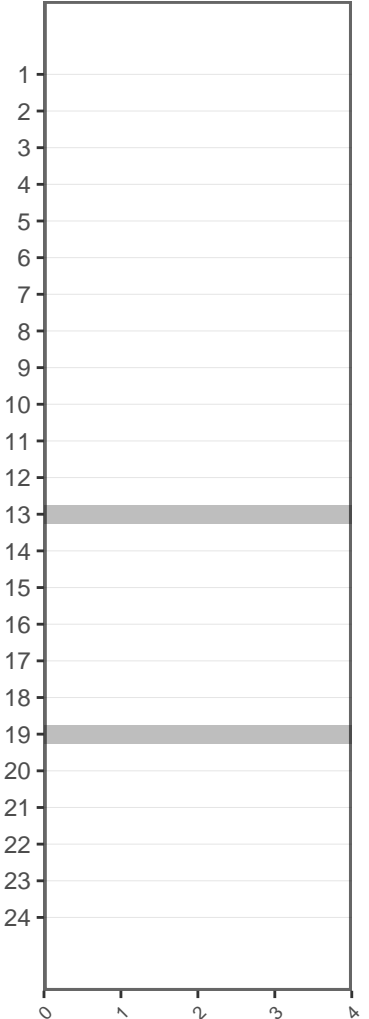
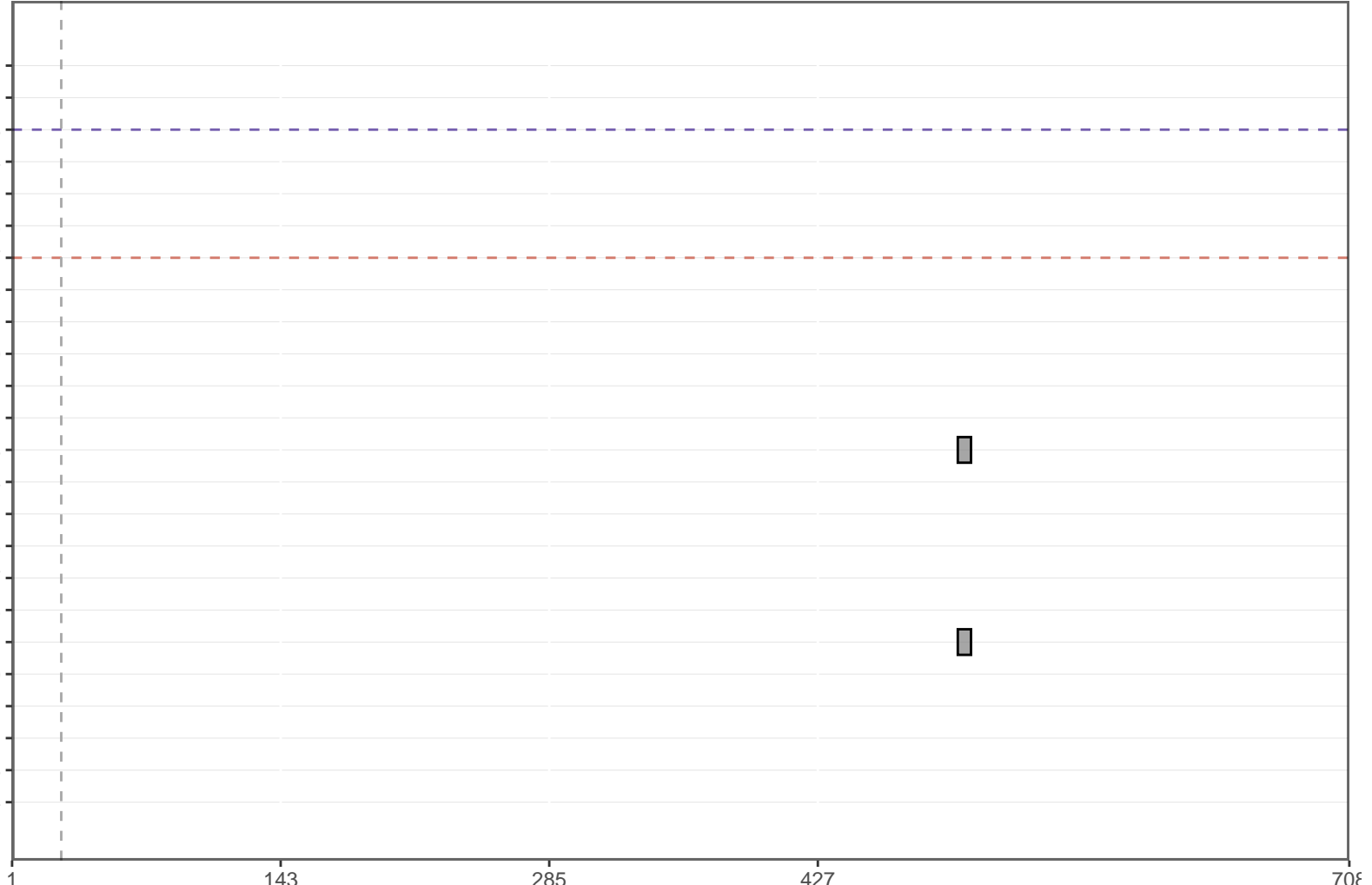
MW indication



Molecular weight

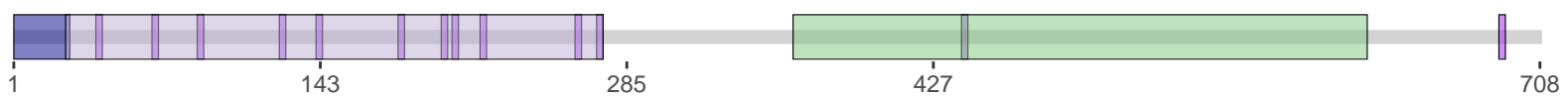


Gel Slice



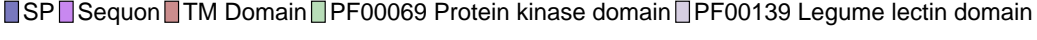
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

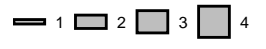


Protein sequence:

STGPKFLYKELARCTKSFANHEKLGEGGFGGVYKGFIREGNSVYWKRIREKGGKKEVASEVRIISRLRHRHLVQLGWGCHKEKRELLVYEFMNSGLDFHLFKGKGLTWPYRKYADGLASALLYHHEEVEGGVYHRDKSSNIMLDSNFKALGDFGLARLVDRHEKSGDTTVALAGTRGYMAPEGFTGKASKETDVSFGGVWALEIAGGRKAIDPKAEHNGENLVQWVWVSLYGMGNLNEAADPKLSSEFNEMEMHLLVGLGWGAPRDKGRPEIROAHVLFNFAPL

NbL13g22150.1 heat_shock_70_kDa_protein_mitochondrial [MW = 73.22 kDa]

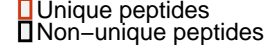
No. of times detected



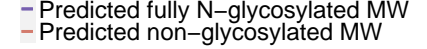
log(intensity)



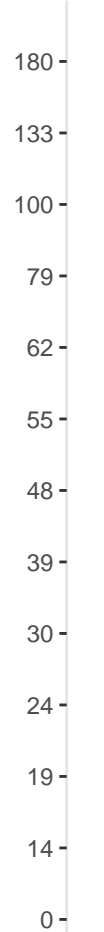
Values from



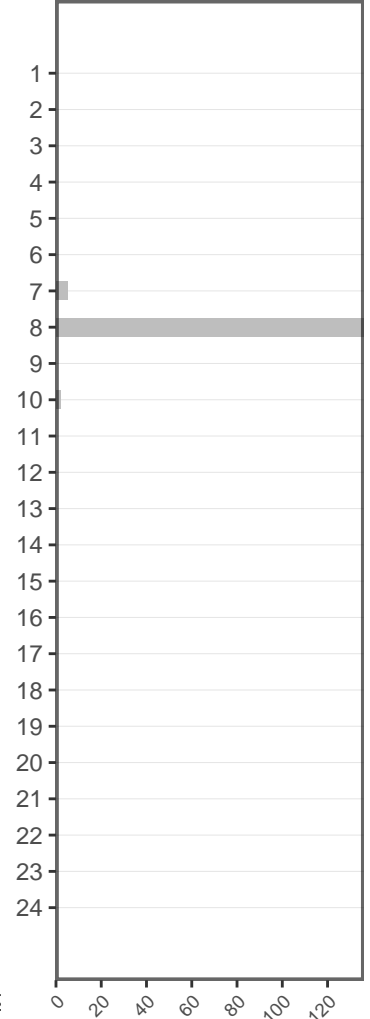
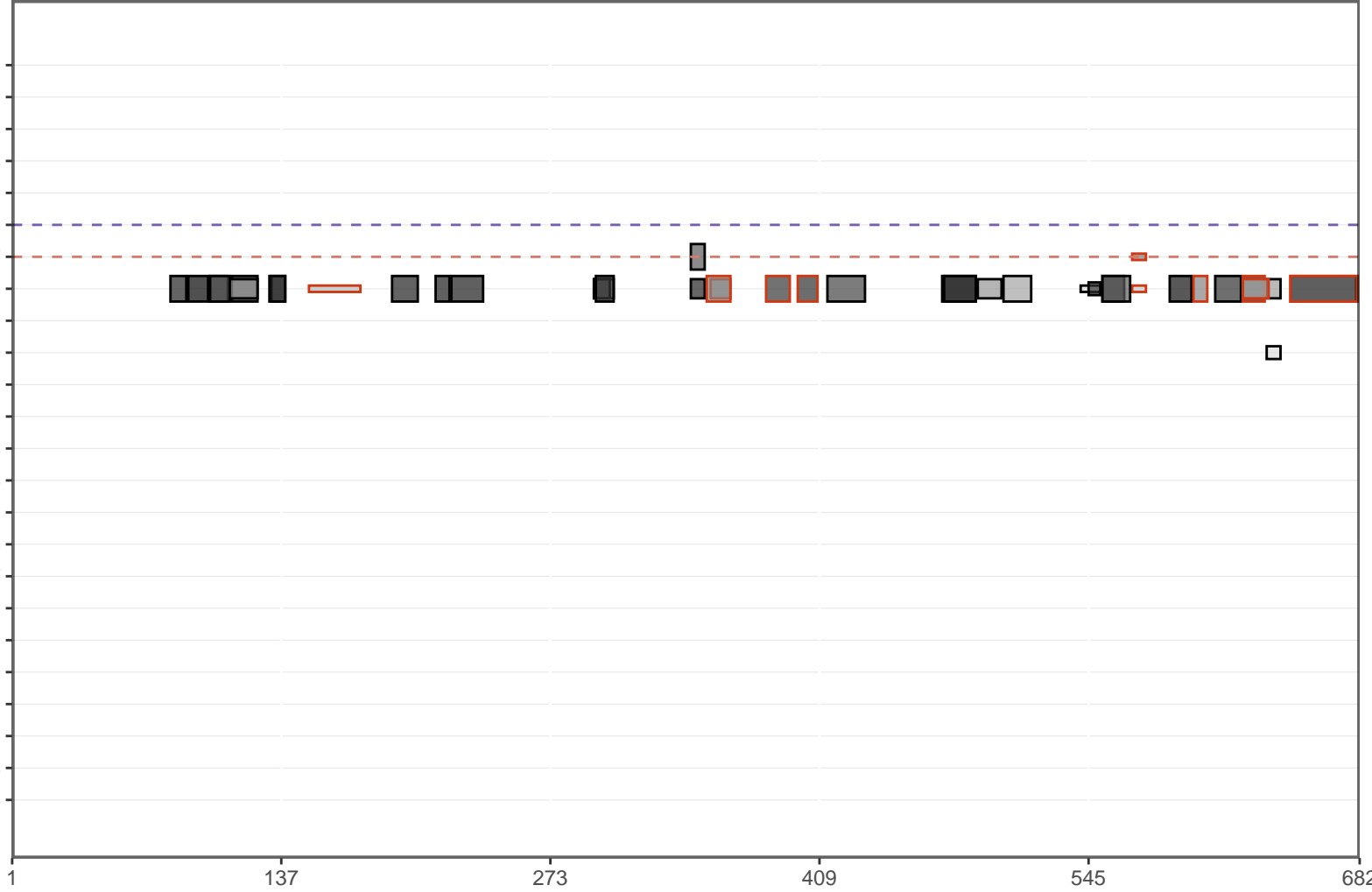
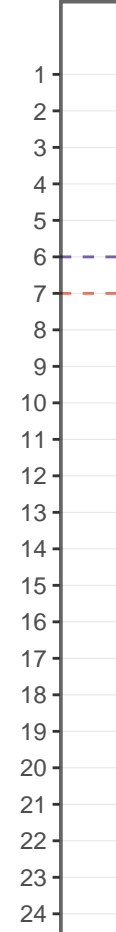
MW indication



Molecular weight

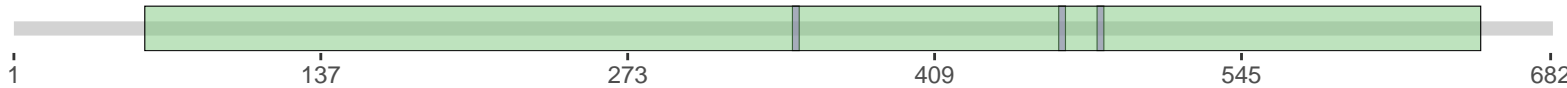


Gel Slice



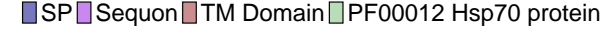
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

QTEINLPFTTADASGAKHLNLTFRSKFENLVNLSIERTRDPCKNGLKDGISTKDVDEVLVGGMTRFVPKVQGVSEIFGKSPCKGVNPDFAWMAAGGGILRGVQKELLVLTPLSLGIGETLGGIFTRLRNNTTPTPKKGVSTADNGTQVGVKVLGGEREMASDNKMLGFEFLVGPAPRGLPQIEVTFDDIDANGLVTVSAKDKATGKGGQITRSGGGLSEDEIDKMKAEELHAGRDQERKALIDIRNSADTTYSIEKSLNEYKDKVPEKATEIETAVSOLRTAMGGC

NbL13g22130.1 soluble_inorganic_pyrophosphatase_6_chloroplastic-like [MW = 32.65 kDa]

No. of times detected



log(intensity)



Values from



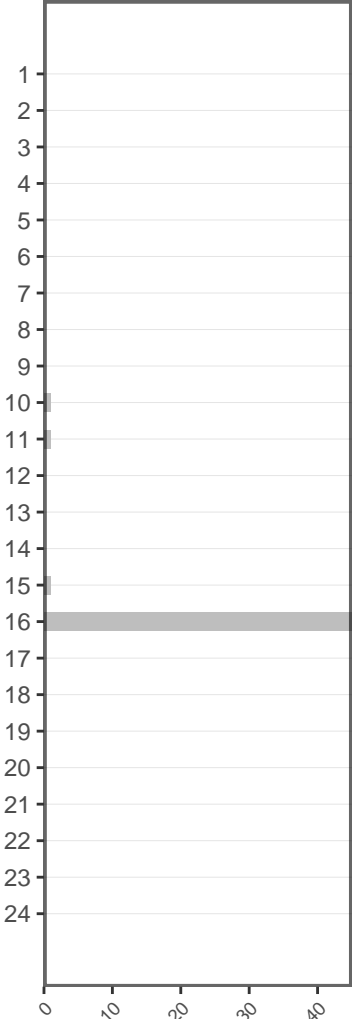
MW indication



Molecular weight

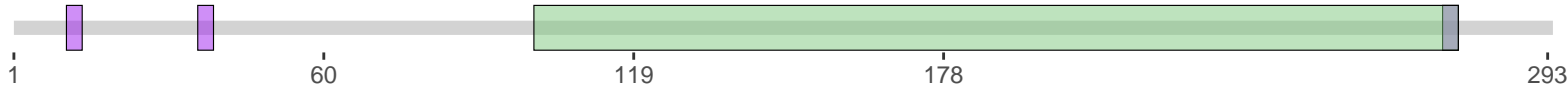


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

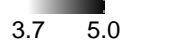
PYNHWNYGLLPQTWEDPSFANAIEVGFAGDNDPVDVVEIGSRANKIGVLRKPLAALAMDEGELDWNVVMSLDDPRASLVNDIDDKVHFPGTLTAIRDWFRDKIPDGKPKNFGLGNKPKNKDKALKITETNESWAKLWRSVPMGDLV

NbL13g21930.1 protein_ABCI7_chloroplastic [MW = 53.84 kDa]

No. of times detected



log(intensity)



Values from



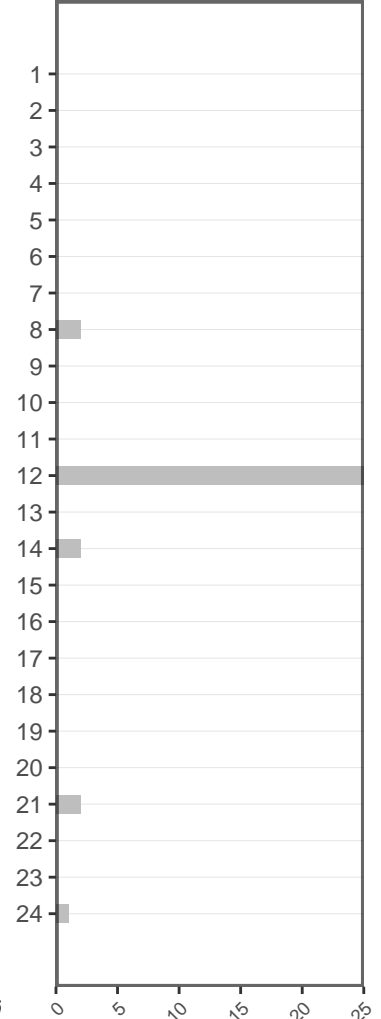
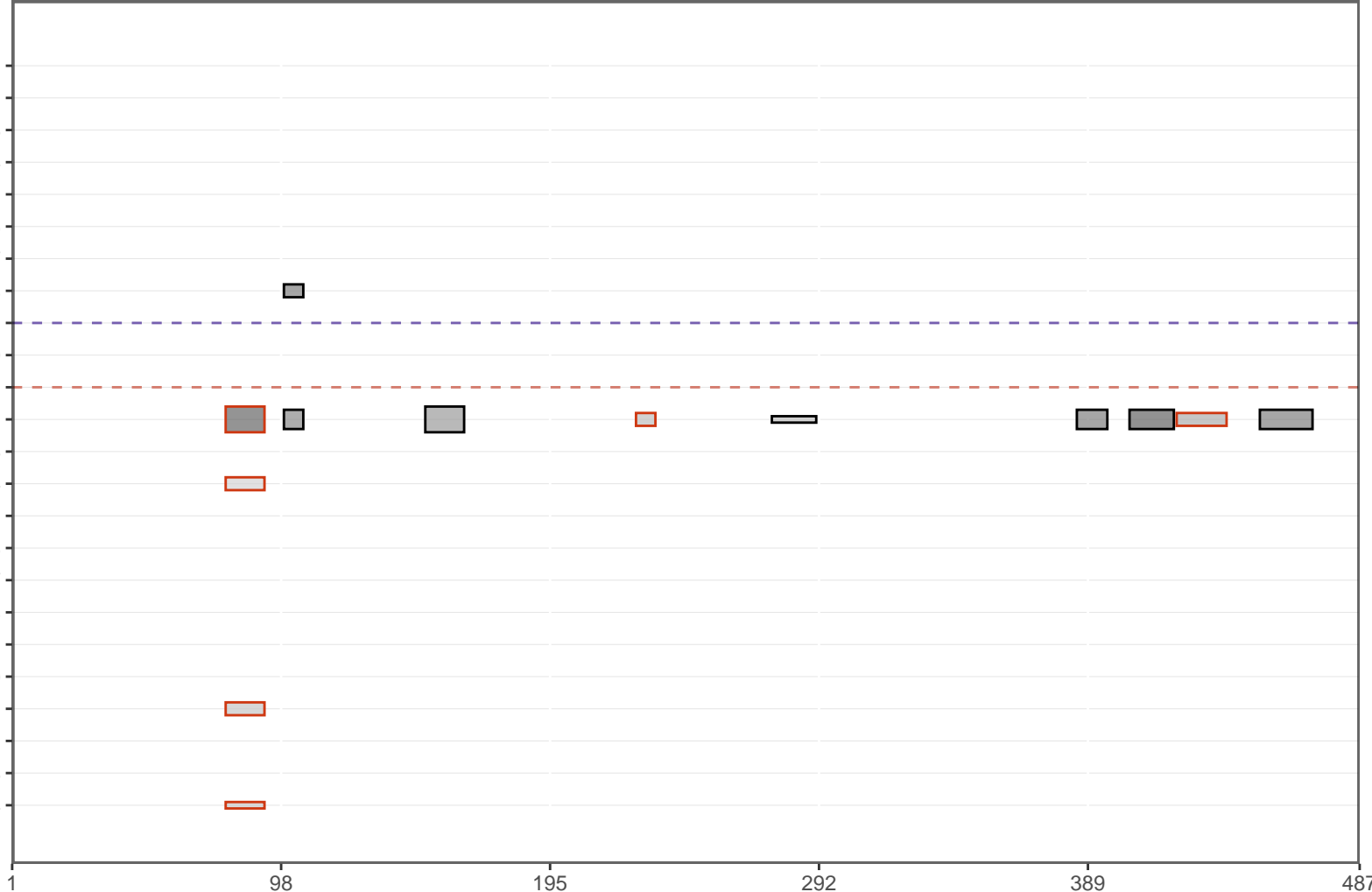
MW indication



Molecular weight

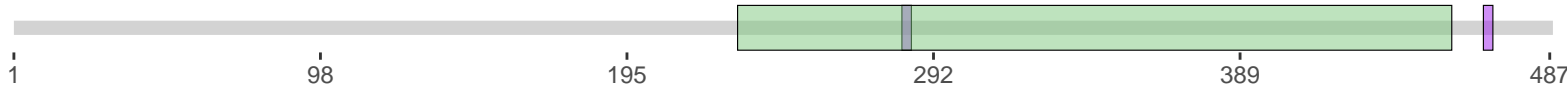


Gel Slice



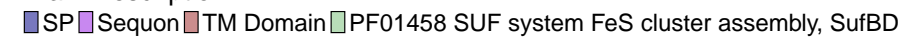
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RLVLLVEKGGESIVVEEYVGGDKDKYWSNBSIEVWVGGAGVSHVYLNQSLNAAHKWTWVGGESTSTYEHVEVSTGGKLSRNIHQGVGPDYTELSTFHMCSGDTQDLHSTLVLYPRGVSGQHKGVVAHSQGVAFDGNVGVNRYAGDTAGGLRSLLEPRATVANKPLQIADGVKSGHGAISDLEEDQLYFRARGVDIETARKALFSAFAEVDKRFNARSKKVVETHRELLDPRP

NbL13g21860.1 glycine_cleavage_system_H_protein_mitochondrial [MW = 17.5 kDa]

No. of times detected



log(intensity)



Values from



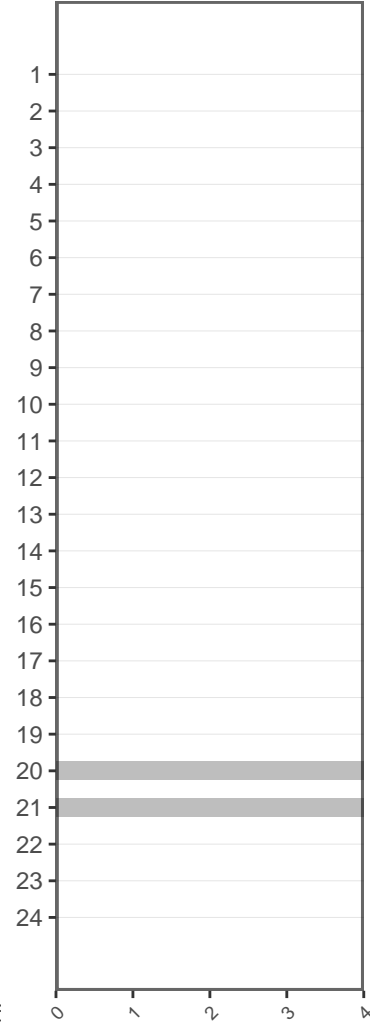
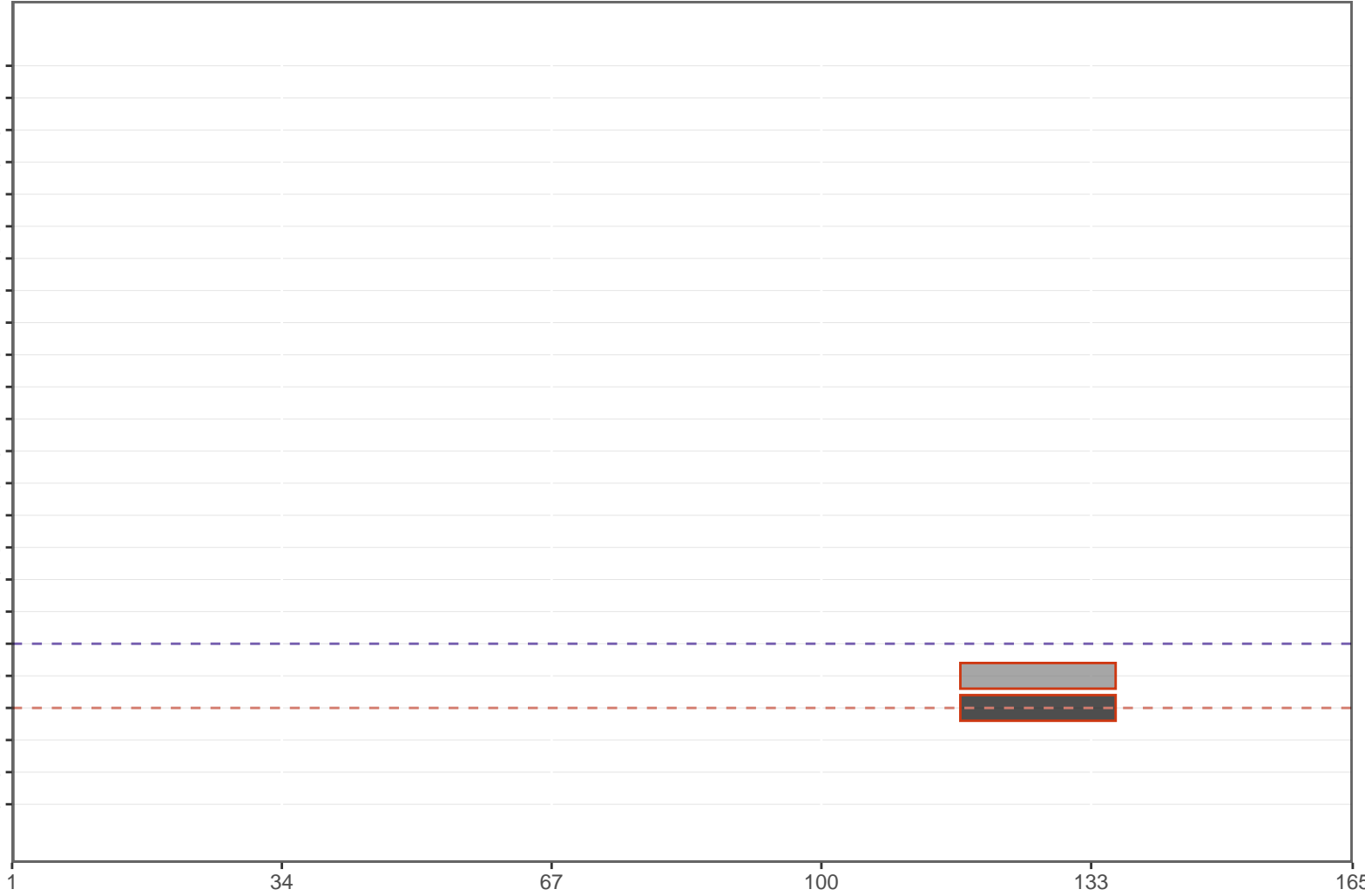
MW indication



Molecular weight

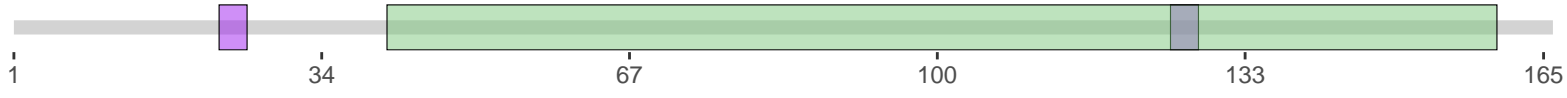


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GEVVFVLDLPETGAAVS6GSSFGAVESVKATSDINCPIG6GEVEVNTKLTGTPGLVNSPVEYEDGWMKVKPSSPELESLSMGSKEYTKFGEEDSH

NbL13g21680.1 LL-diaminopimelate_aminotransferase_chloroplastic-like [MW = 50.07 kDa]

No. of times detected



log(intensity)



Values from



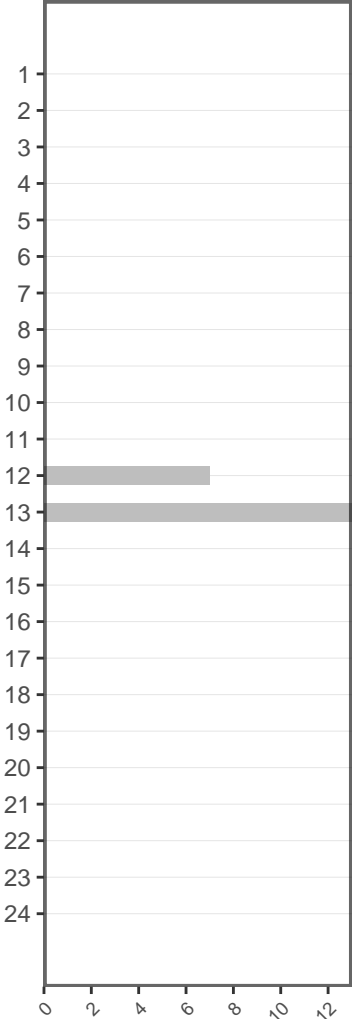
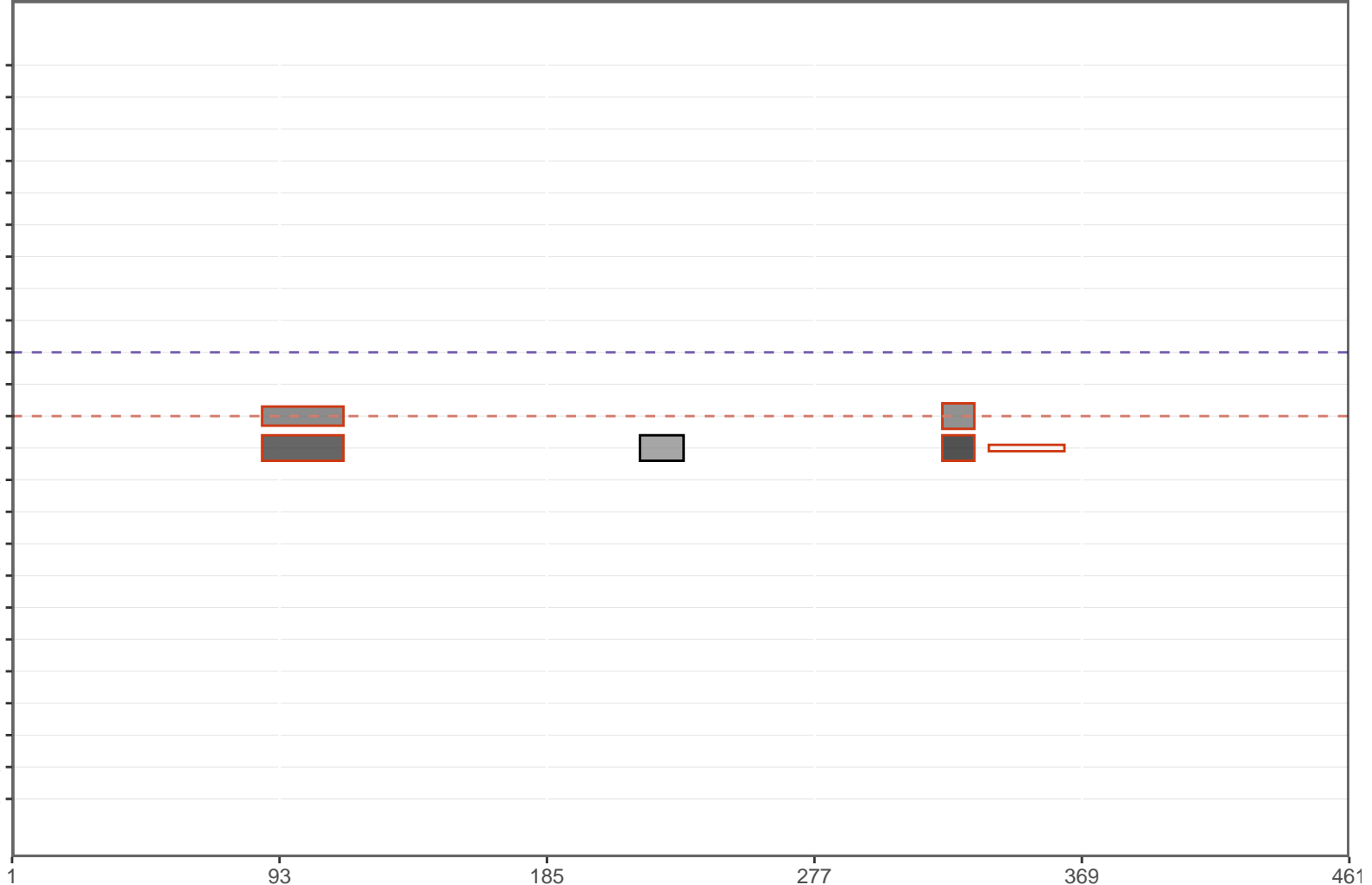
MW indication



Molecular weight



Gel Slice



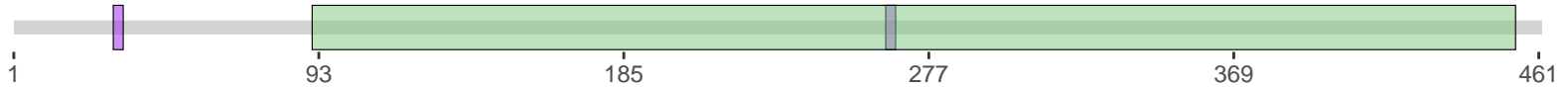
Protein length



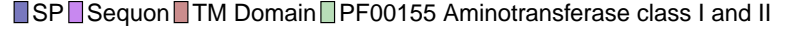
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

TPENGFFDLSVYPRDIFFGSPNPTGAAAGREGTLKLVHFAKNNGSLVDSAVAMVGDDEPKBFEIPGAKEVIEVVSFQVYAGFTGVRLGWTAPKALYSDGFPVAKDFNRIVCTSFNGASNADAGLGLSDGFKAMKNVSYKENTETHEIMETFKELGKYYVGGKNAPYVWVHFGRSBWEVSELEKTHVITTPGGGFGPGGEGFVRYVSFAFGHRDNYVEAGRFRKELYK

NbL13g21410.1 subtilisin-like_protease [MW = 77.95 kDa]

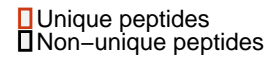
No. of times detected



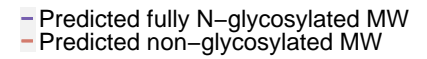
log(intensity)



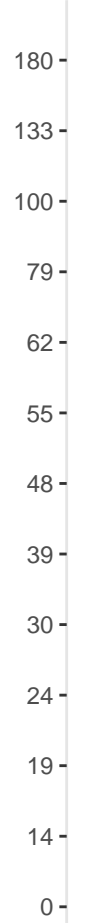
Values from



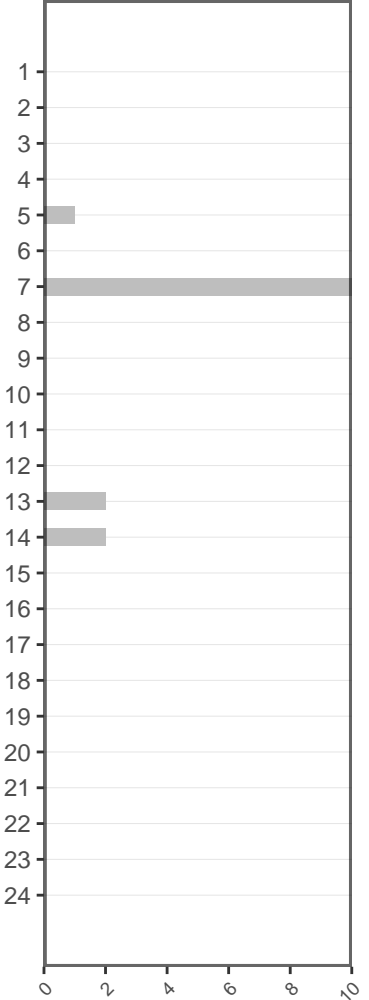
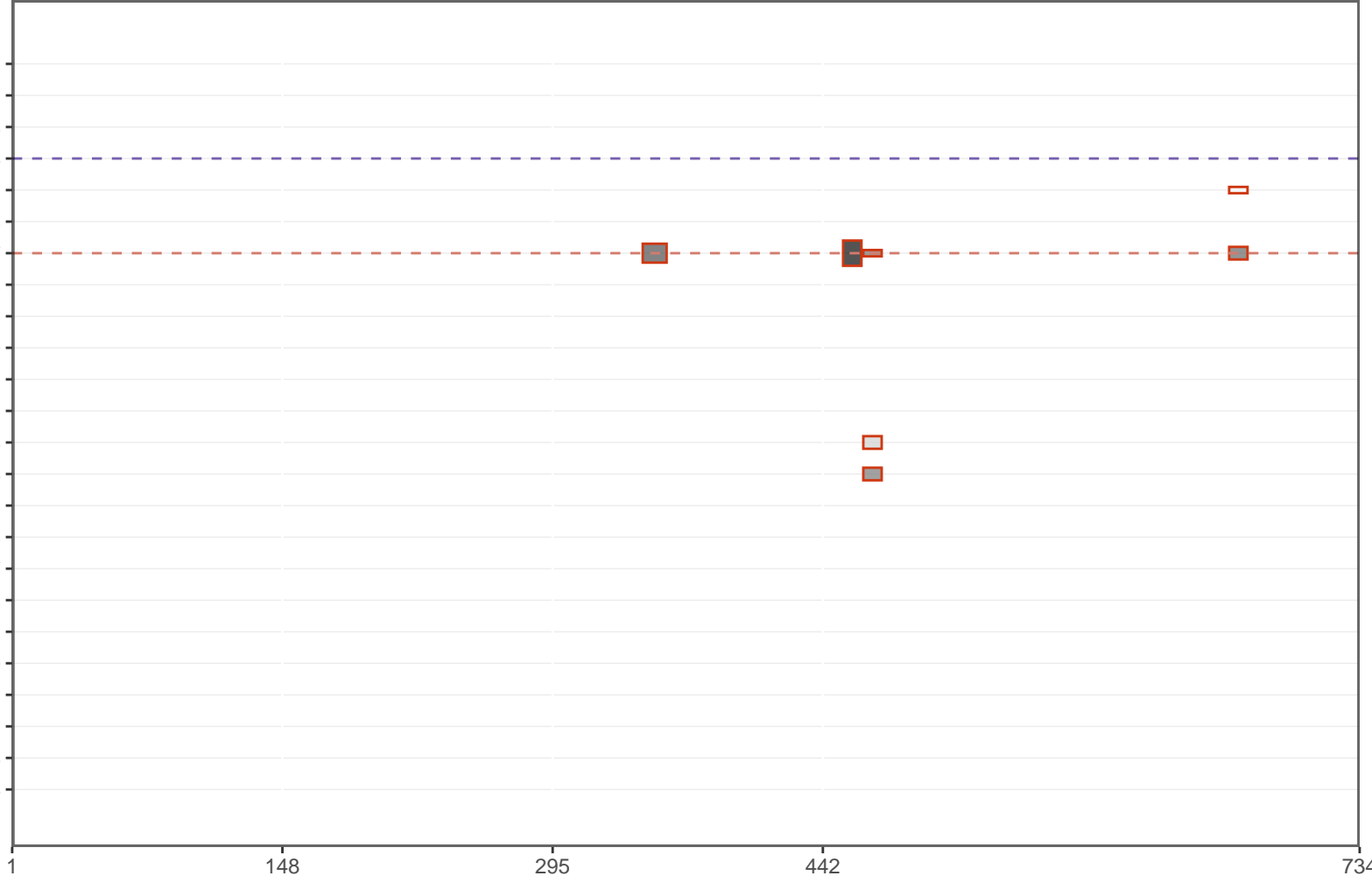
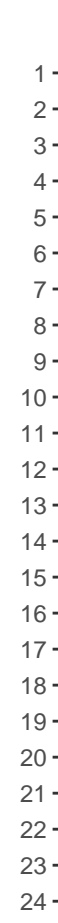
MW indication



Molecular weight

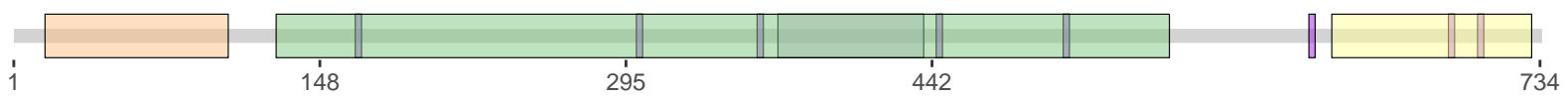


Gel Slice



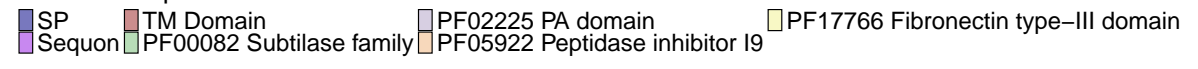
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

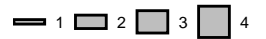


Protein sequence:

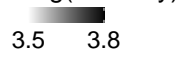
LFDPKNAASDFGSPVGGTGLTLPKIKGKIVLGMAGGGYTRIGKGAVKDAGGVSMIYNGLKEYGVTTLADAHVLPALDVTYADGKILDYMNSTKPKVARITGGTIGDRNAPVVASFSRGRFVASPGILKPDVHGPGVNIILAAWPDGVEVNTNKGSTFNISGTSMSGPHLGGVAALLKSAHPTWSPAAKKSAMTDTNVLNANDLILDETLRPSAIFAGAGHNPSPRANDPQLYDTPIDDPVPLGLGGLHYTNRQAGNLLGRKVNQSEVKBIPEAGLNYPFSITLGTDTDT

NbL13g21150.1 protein_disulfide-isomerase-like [MW - SP = 56.02 kDa]

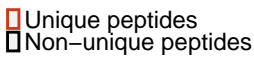
No. of times detected



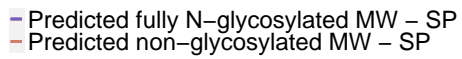
log(intensity)



Values from



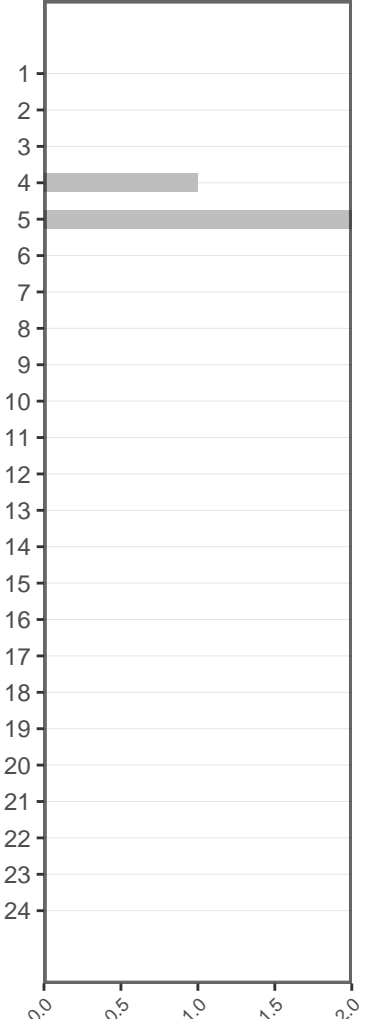
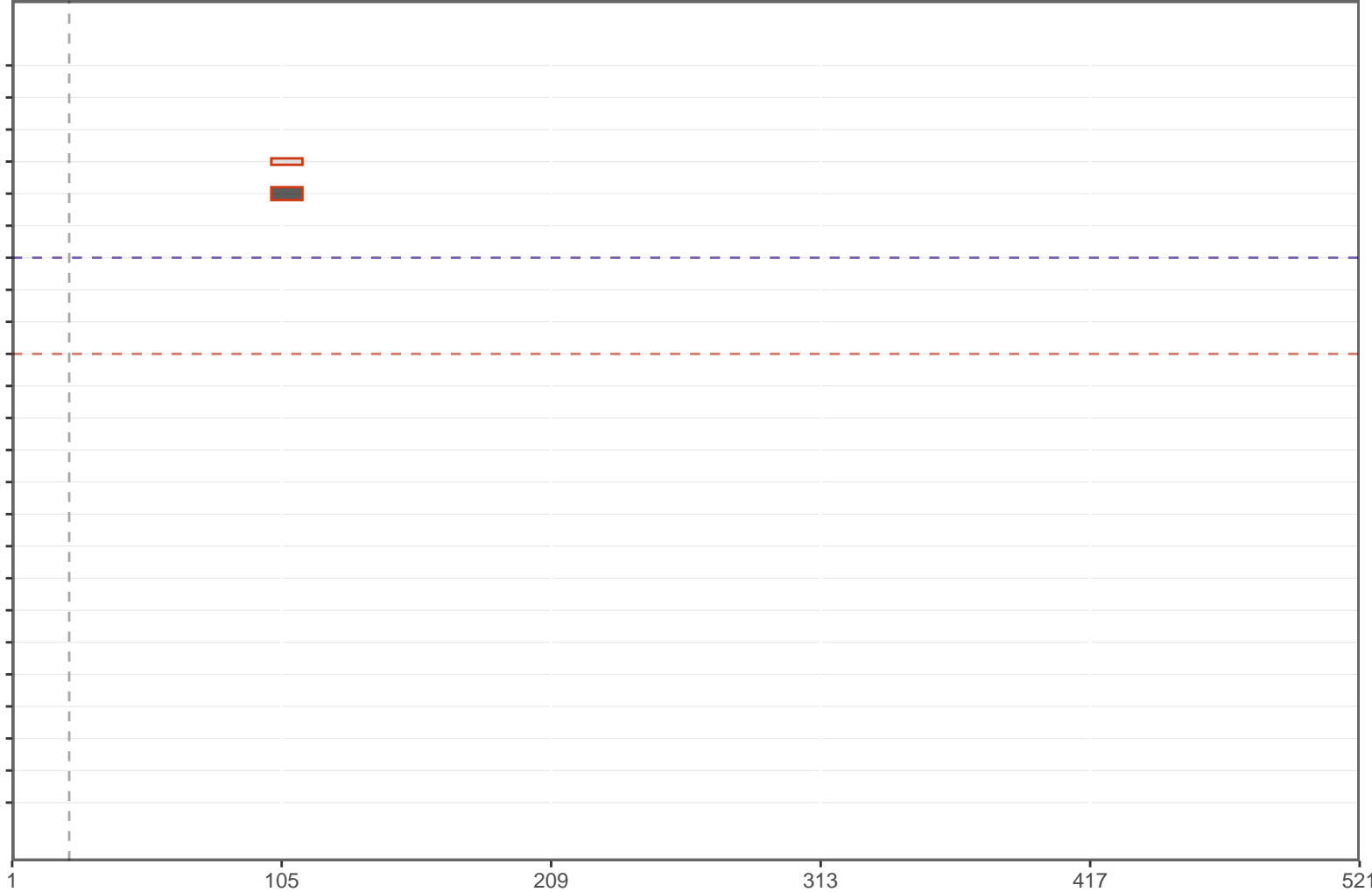
MW indication



Molecular weight



Gel Slice

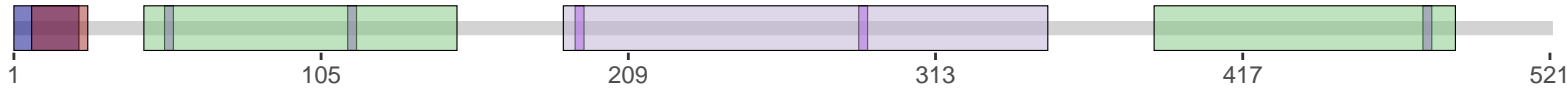


Protein length

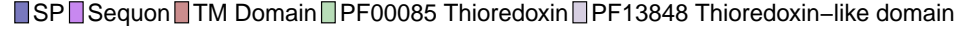


Peptide counts over 4 repeats

Pfam domains



Pfam Description

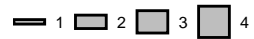


Protein sequence:

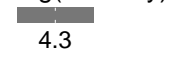
FEETSVPIMALDDKPKENGAFLNHLHSPGDKVFLFNFTTDLDFKSKYVLAASYKGEANFLFLGDAETGKRALEYFGLNTDQVFLIFVLAAMDGKYVQRHVGPDGLGVWLDKDFDKLKPFLKSGPIPEVNEPQVWVAETLEDMEFNSGKDVLEFYRLGKGYCEEFAPVLEALSFEFNDADVLAKIDGTENDIPRERFEVGGFFTLVMISTAGSLRFEGNRTKEAVIEFQITNRGTRAFNPNFANDLTASEHAGTDSMKDEL

NbL13g21110.1 V-type_proton_ATPase_subunit_E-like [MW = 27.71 kDa]

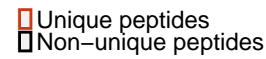
No. of times detected



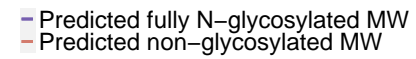
log(intensity)



Values from



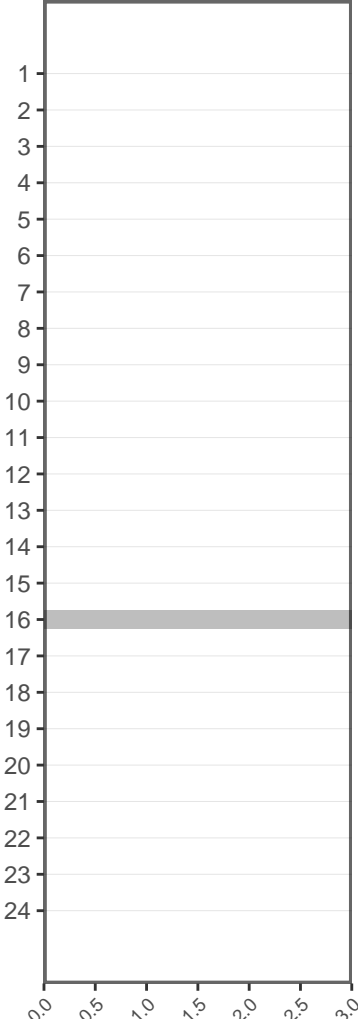
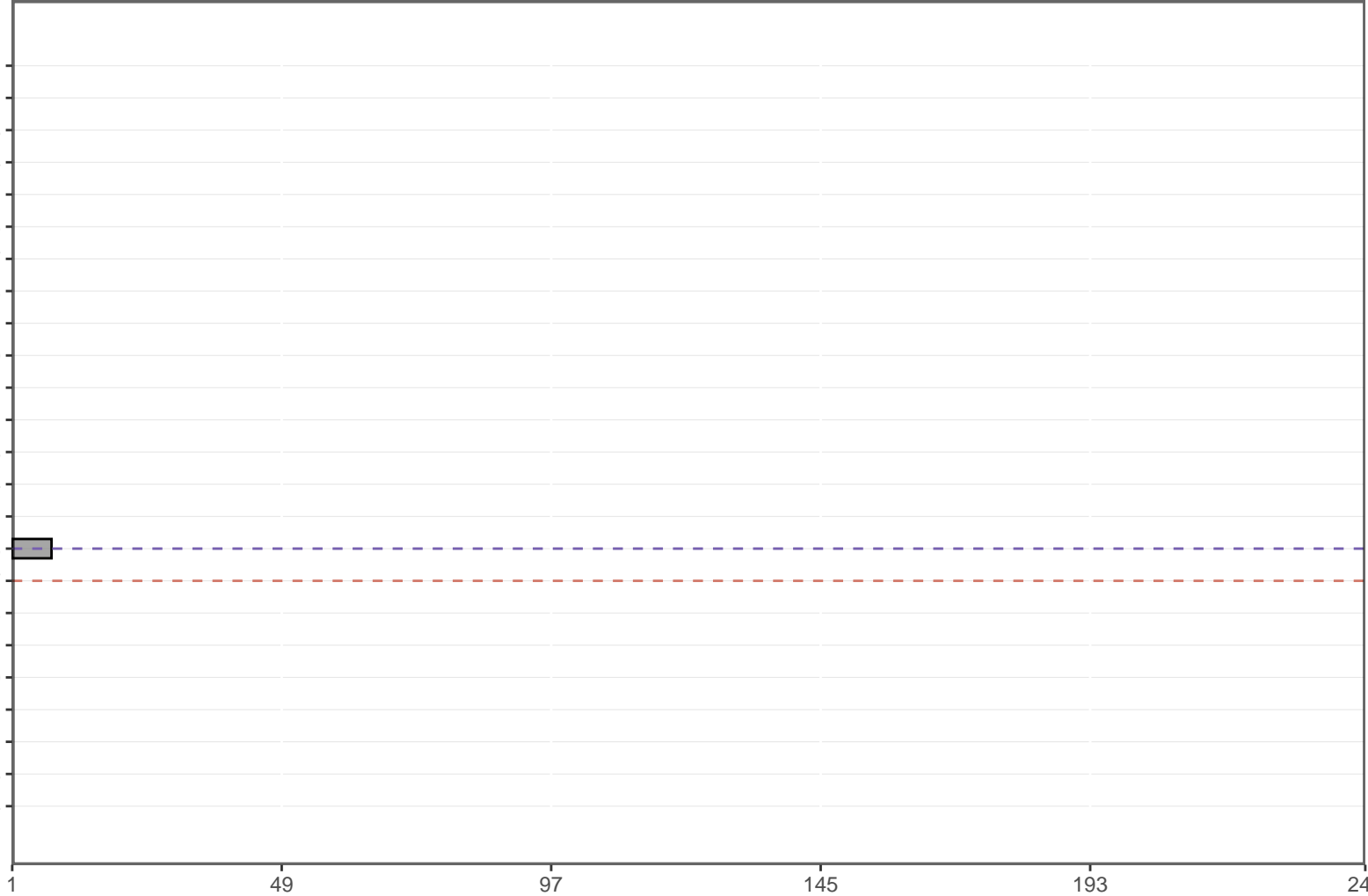
MW indication



Molecular weight

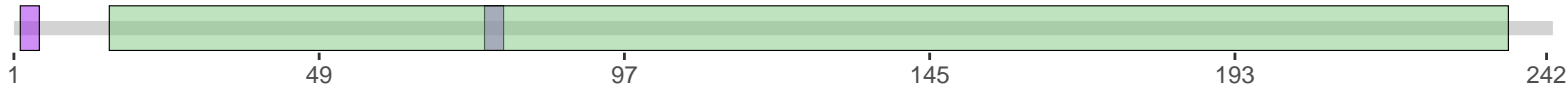


Gel Slice



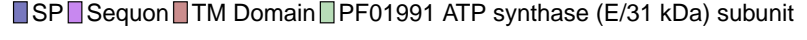
Protein length

Peptide counts over 4 repeats



Pfam domains

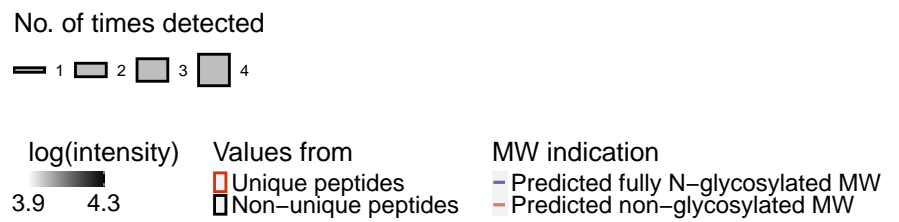
Pfam Description



Protein sequence:

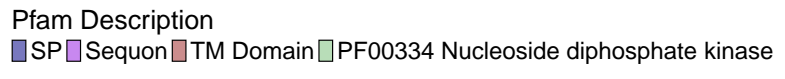
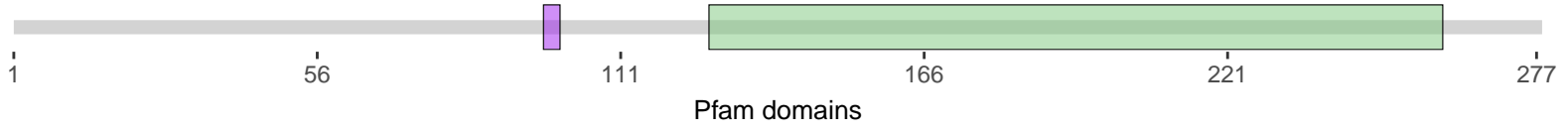
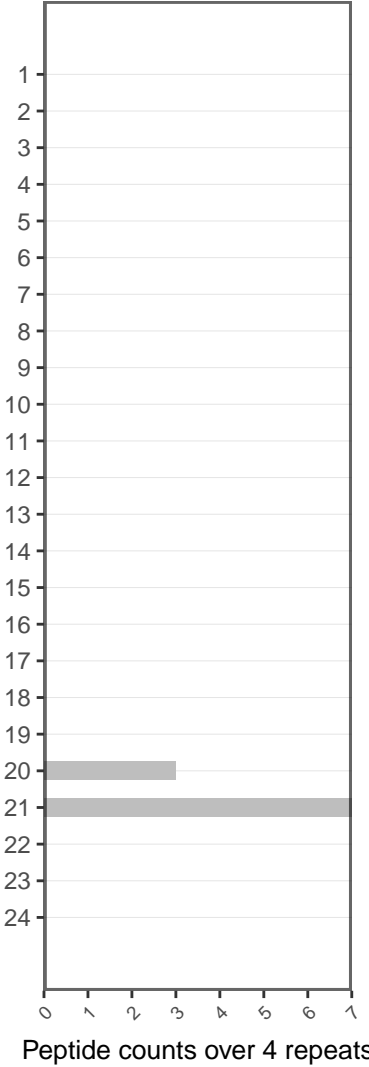
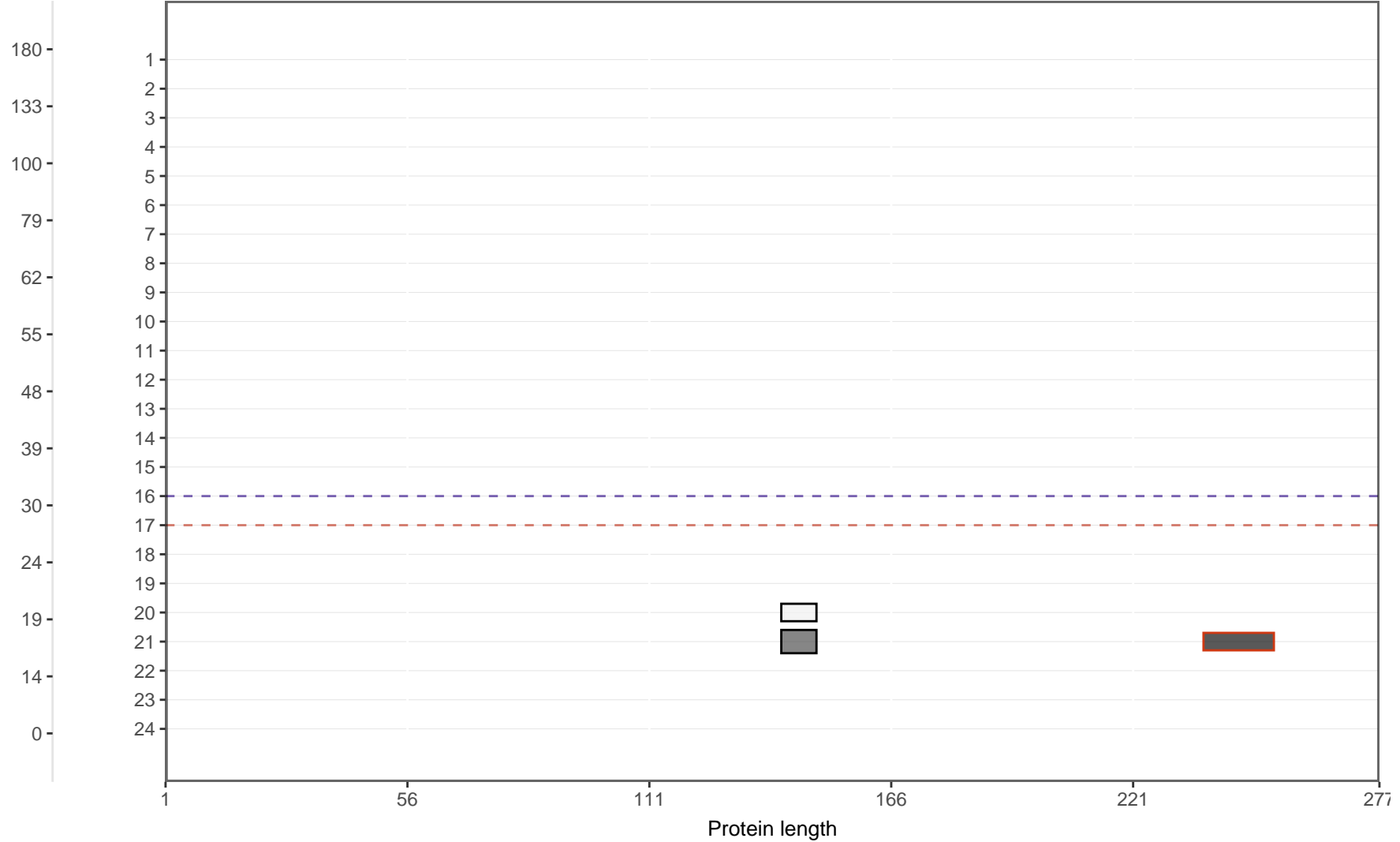
HNELVEILPPIIKQDSYKGLLHNLIVGSLRLRKEPVLRLCRKHQVHVEHVLDAAKEEYAEKANKVHAFPIIVDDHLPKPKHINMHPGPGSGGVWLABRDGKICENTLQARLEVVFRKLPKIRKLFQGVTA

NbL13g21010.1 nucleoside_diphosphate_kinase_3-like [MW = 30.48 kDa]



Molecular weight

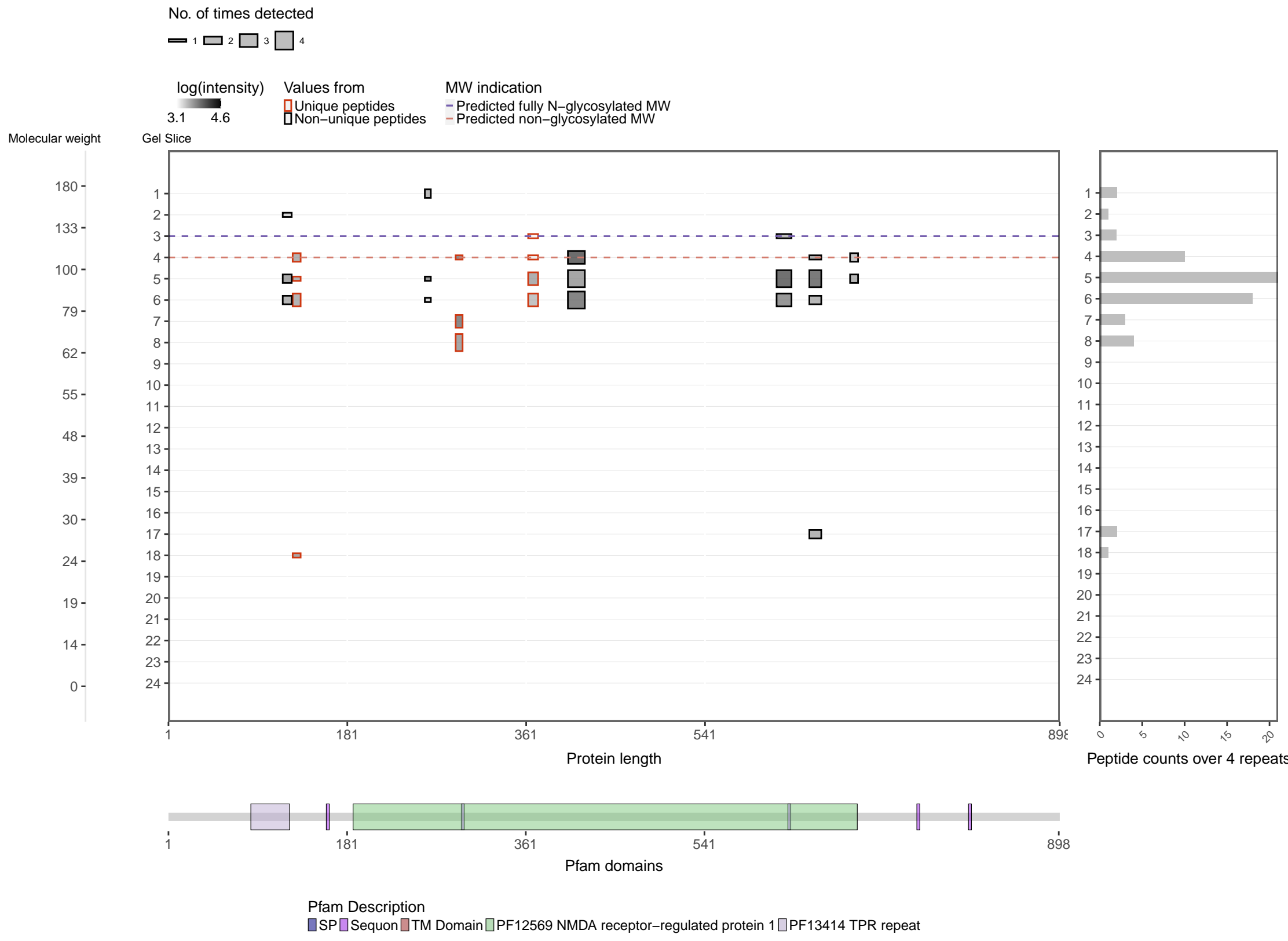
Gel Slice



Protein sequence:

MEKTRIAKPDGVQRGLSEHSRFEKGFKLAVKIVPSKDFAGKHVHDLKERPFPTGLGDFLSSGFLAMVWEQEGVIRYGRKLGATDQKSEPTIRGLDLVAVGRNIHSGSDGPETAKDEKLVKPEELWYTSNDEKWIYGVN

NbL13g20920.1 N-alpha-acetyltransferase_15_NatA_auxiliary_subunit-like [MW = 102.26 kDa]



Protein sequence:

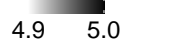
YEARCMGLADRYVNSEGVKRMIGADGVFLAECTAVLFTKDDGDDHNNVMDGGMVYELASGEVYFRDQELGRALKXFLAVEKHVADITEDGDFDHSYGLRKMRTLRTYVEMIKFDQRLHSHYVFRKAAGGARGYLYKLYDFPKBASEEEDKMKLPPSQKKLKKQLRKAERAKKEADYVNEESNAANVTKSGKRHKVFPVDFDPHGEKLIQIEDPLAEASKYLLKLLKHSSDGLLEHLLSFEVNMRRKQKILLALGAIKYLMLDADDPKSHLCLKFRIKIDSLPTPTDTE

NbL13g20880.1 protein_CDI-like [MW = 32.12 kDa]

No. of times detected



log(intensity)



Values from



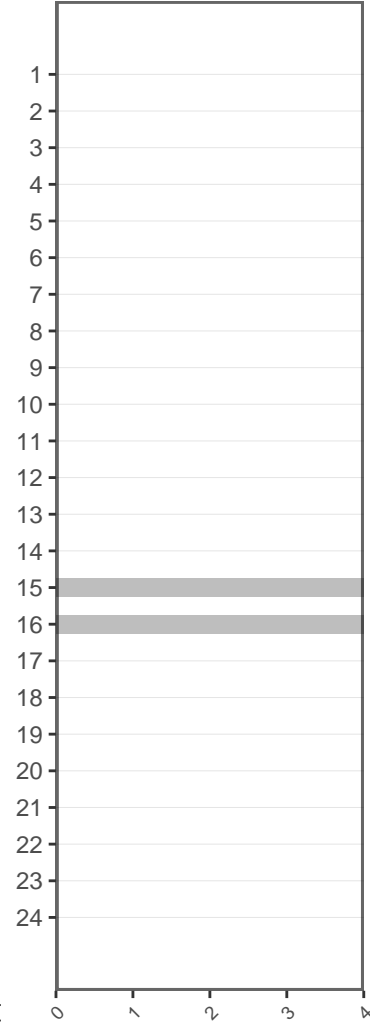
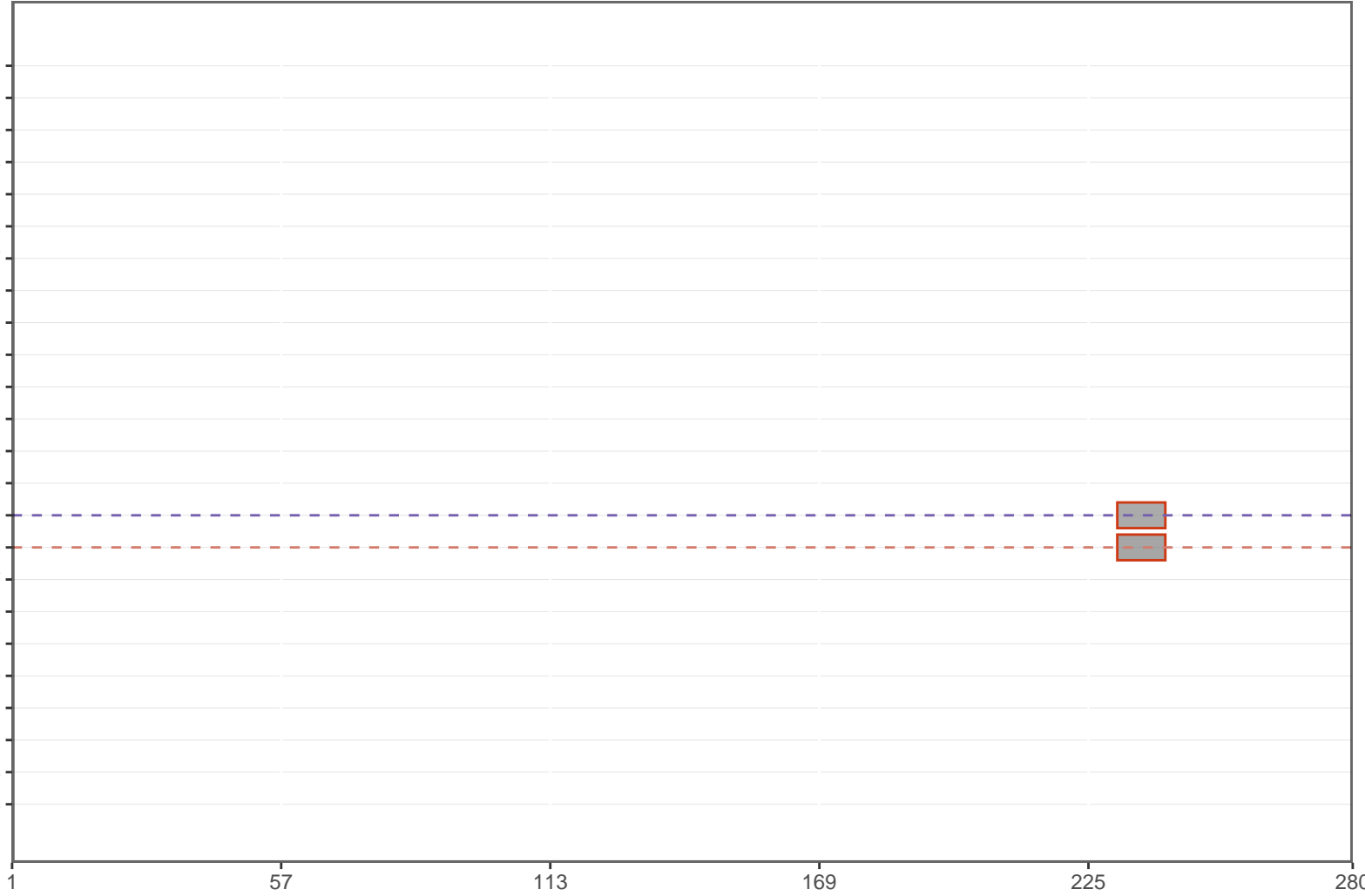
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

LYLEDKELRDLVDDKVALMCSVGHDTPKETTKMDGAVQTVPYPRKNWSSMLVYNGGHPKRNALTRFEVNVSEGGALHFRFMWLEDKKEIGEVPFVWFLVGHNKVVEGDPTFFPKAHHYTLGGPWFEAWNDGDFGDLWKELEEGEKAKELG*

NbL13g20870.1 D-glycerate_3-kinase_chloroplastic-like [MW = 51.26 kDa]

No. of times detected



log(intensity)



Values from



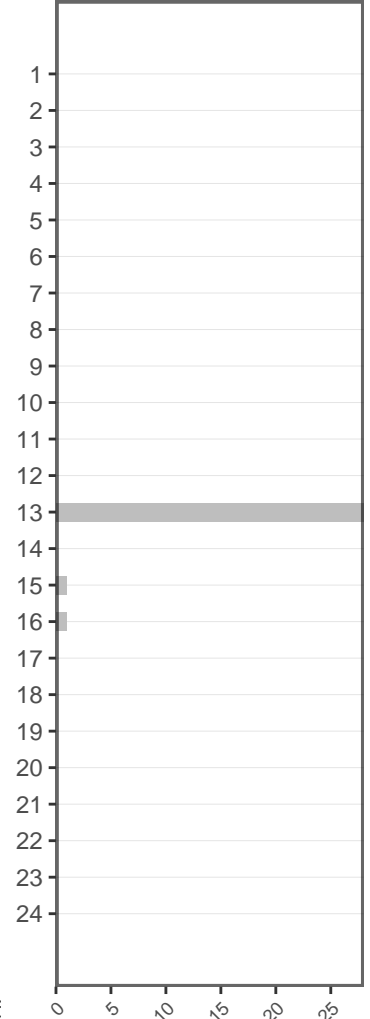
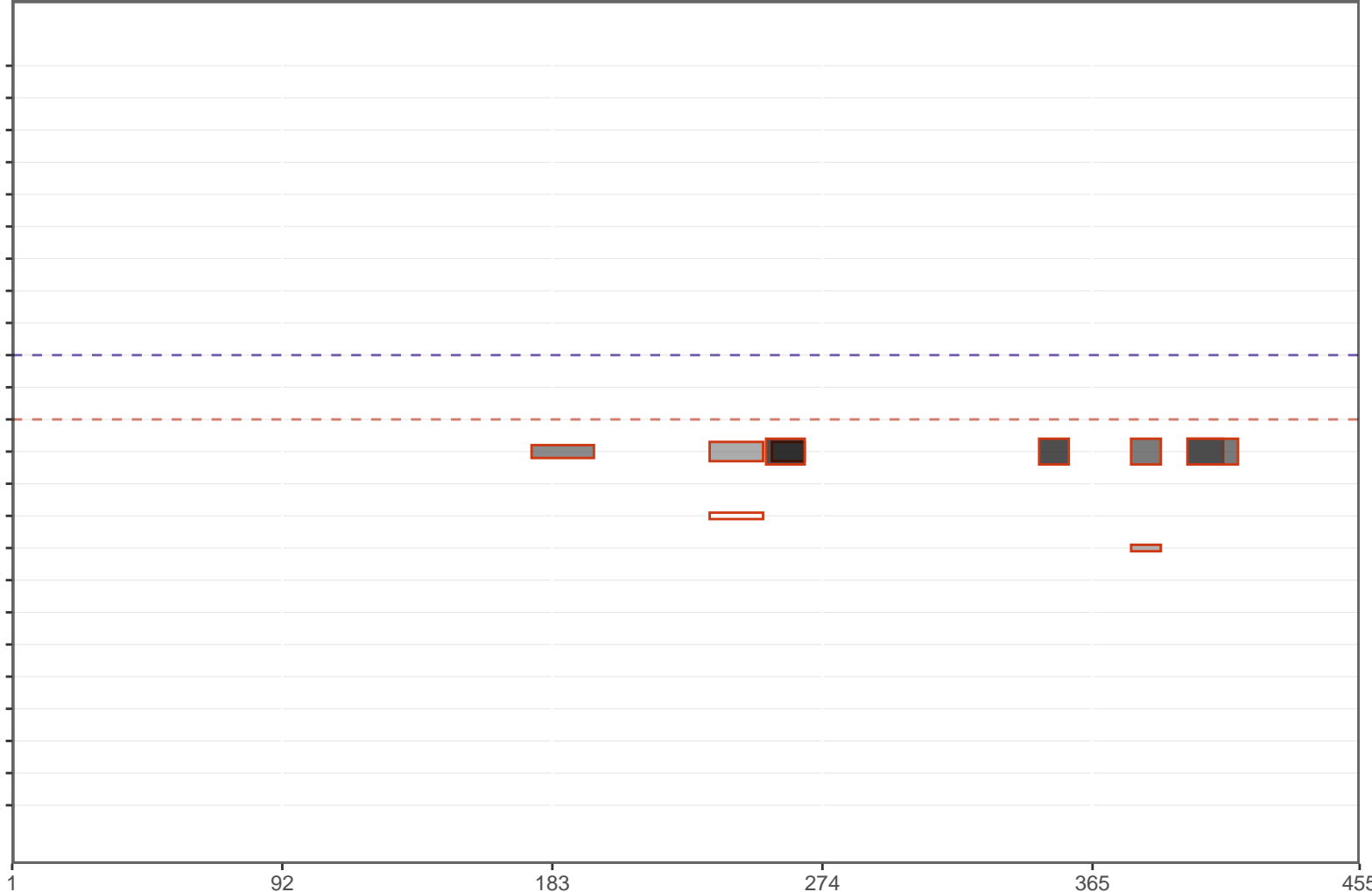
MW indication



Molecular weight



Gel Slice



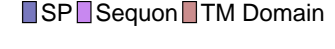
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

CCGCKTLVFALEYLTKITGRKAATLSIDDFLTAEEGARLRREDNPENLLEFRGNAGSHDLSEVETLSEKVTKEGVKMLPRYDKSAVNGRGRADDPSTWPEVEGLVSLFEGWMLGFXPLPVEVYKAVDPOLETNNKLEAYDAWKKYVESWIKIHDPVYVQWRLGAEIMRADGNLGMDSDEVRDFVSRVLFVYKAVLPTLVSEGPPGADPEHLLIEDEGRNPLGS*

NbL13g20850.1 aspartate_aminotransferase [MW = 43.28 kDa]

No. of times detected



log(intensity)



Values from



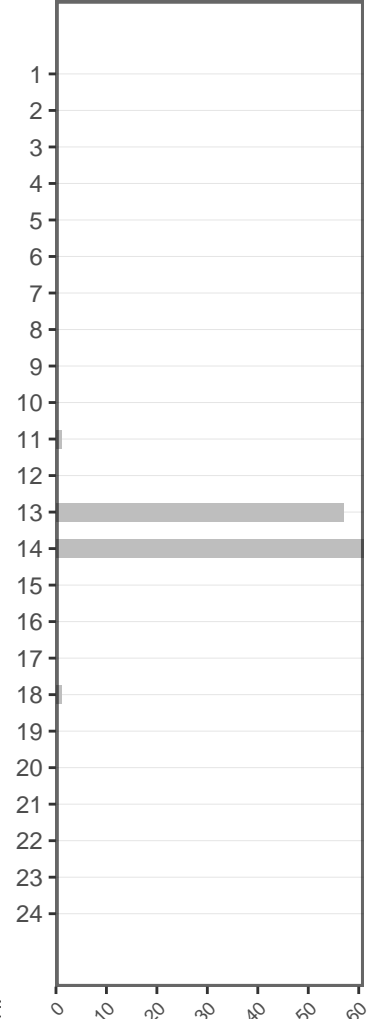
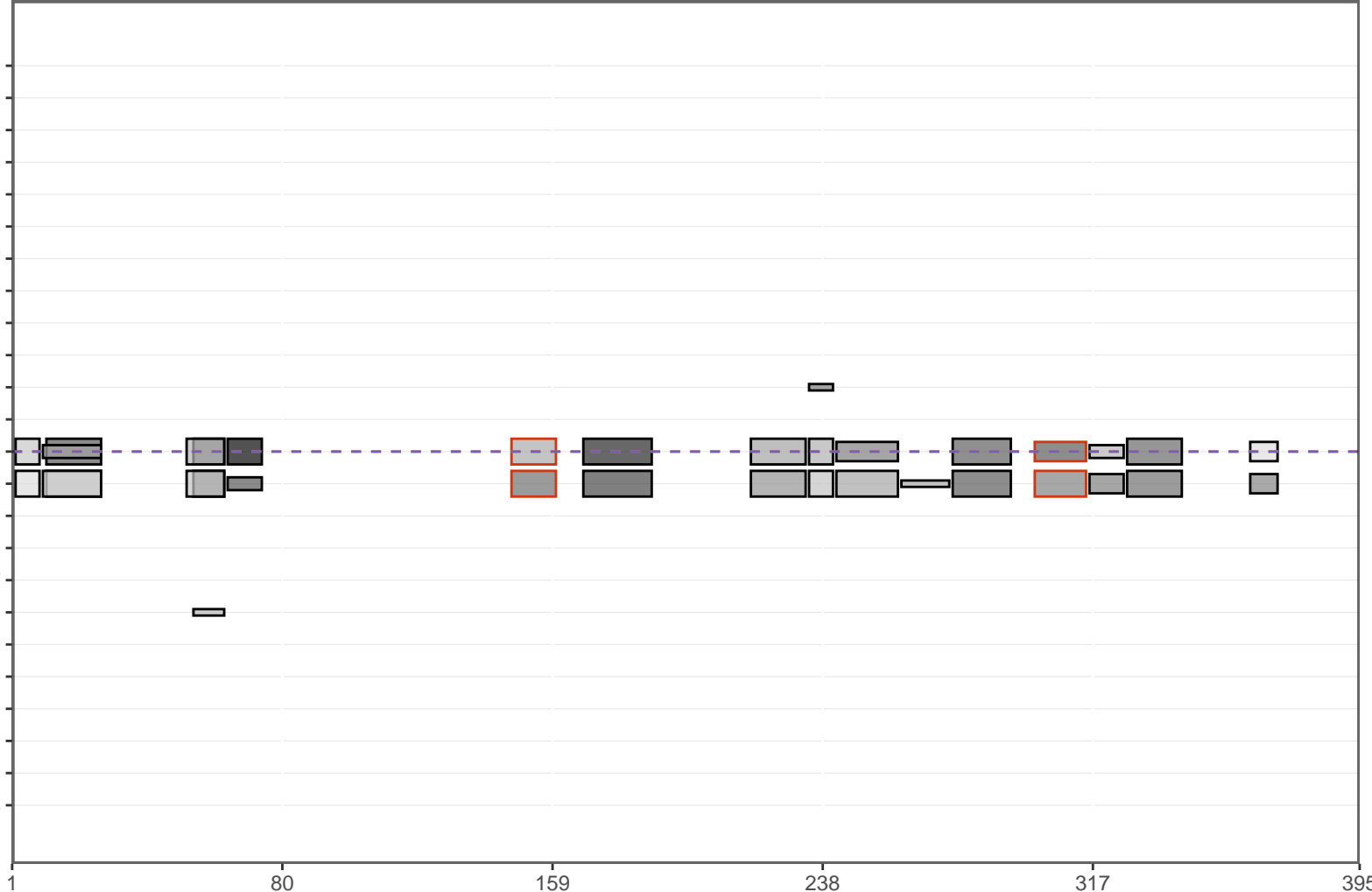
MW indication



Molecular weight

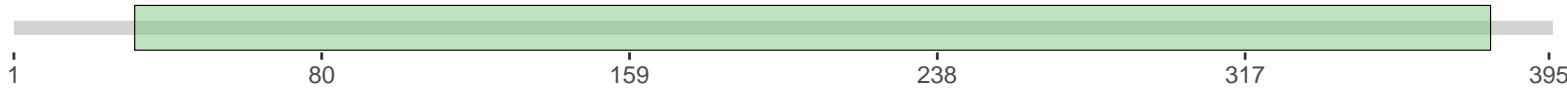


Gel Slice



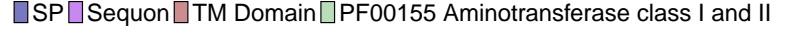
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ESLLKRISDICEAGDWLVDFNYEFMYDORRHVDEGNHVFNFPSKAYGMMGWVGVYAVPSEVEGLAALLKLVQDNIPICASISGRRLALYSMEMGPEWVTDQVWVWLVNRRDLLLEALSPLEGAVVGGEGANLWAKLPDKYENDFEVVHWLAKRHGIVLPGSSGGCPCHVRISFGGLEKDKRVAERLRKGLLELVNNGMIS

NbL13g20800.1 zinc_phosphodiesterase_ELAC_protein_2-like [MW = 107.82 kDa]

No. of times detected



log(intensity)



Values from



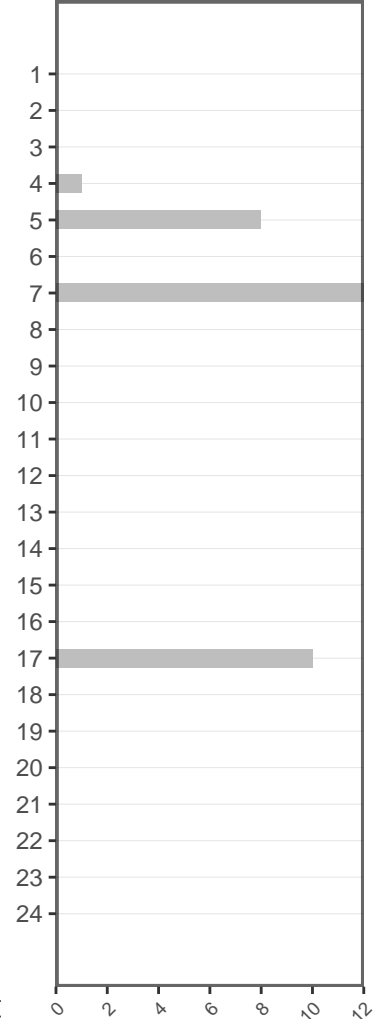
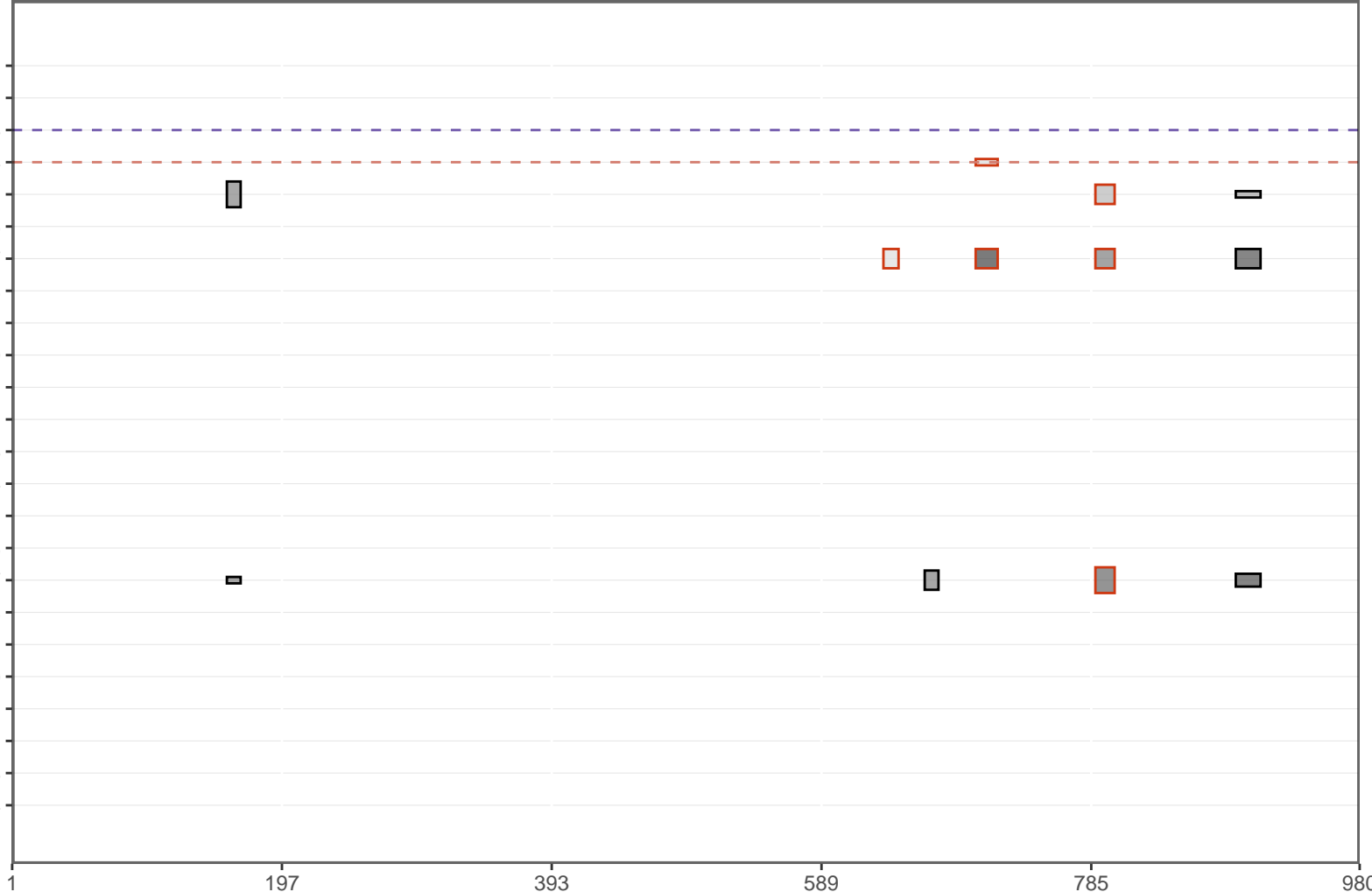
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

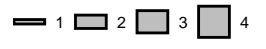


Protein sequence:

KSSARIASRLNYLGPQFFPAPGFWSLPLKSLPVSVKTPBEFSSGQVTAENLNFHLRPVWQLGDRSGIPETSRPKIEELSEIPELDASEHTQMLHGNVNTNGSGATMGVNVKMEESLHETALPSCLEGTREDDVEVLLGTGSGSPKRYNVSSIFVNLFSKGSVLLDGGEGTLGQKRRFGIEGADAVKGLRGIWBIHHDHHTGLARILALRRDLLNETPHEPLVNVGPRQLKRFLDAYQKLEEDLMDPFLDGRHFTFASLKTFFESNGDKDSESACVGSQDKK

NbL13g20740.1 4-hydroxy-3-methylbut-2-en-1-yl_diphosphate_synthase_(ferredoxin)_chloroplastic [MW = 82.08 kDa]

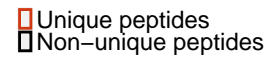
No. of times detected



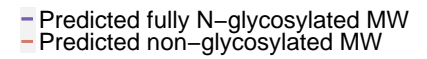
log(intensity)



Values from

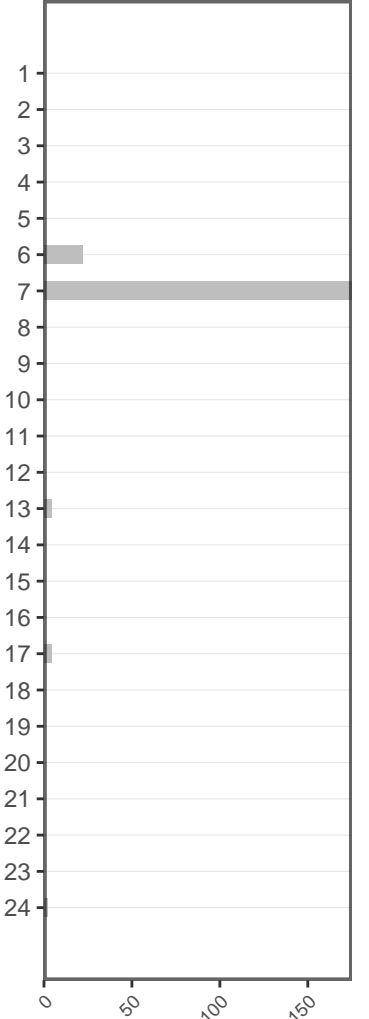
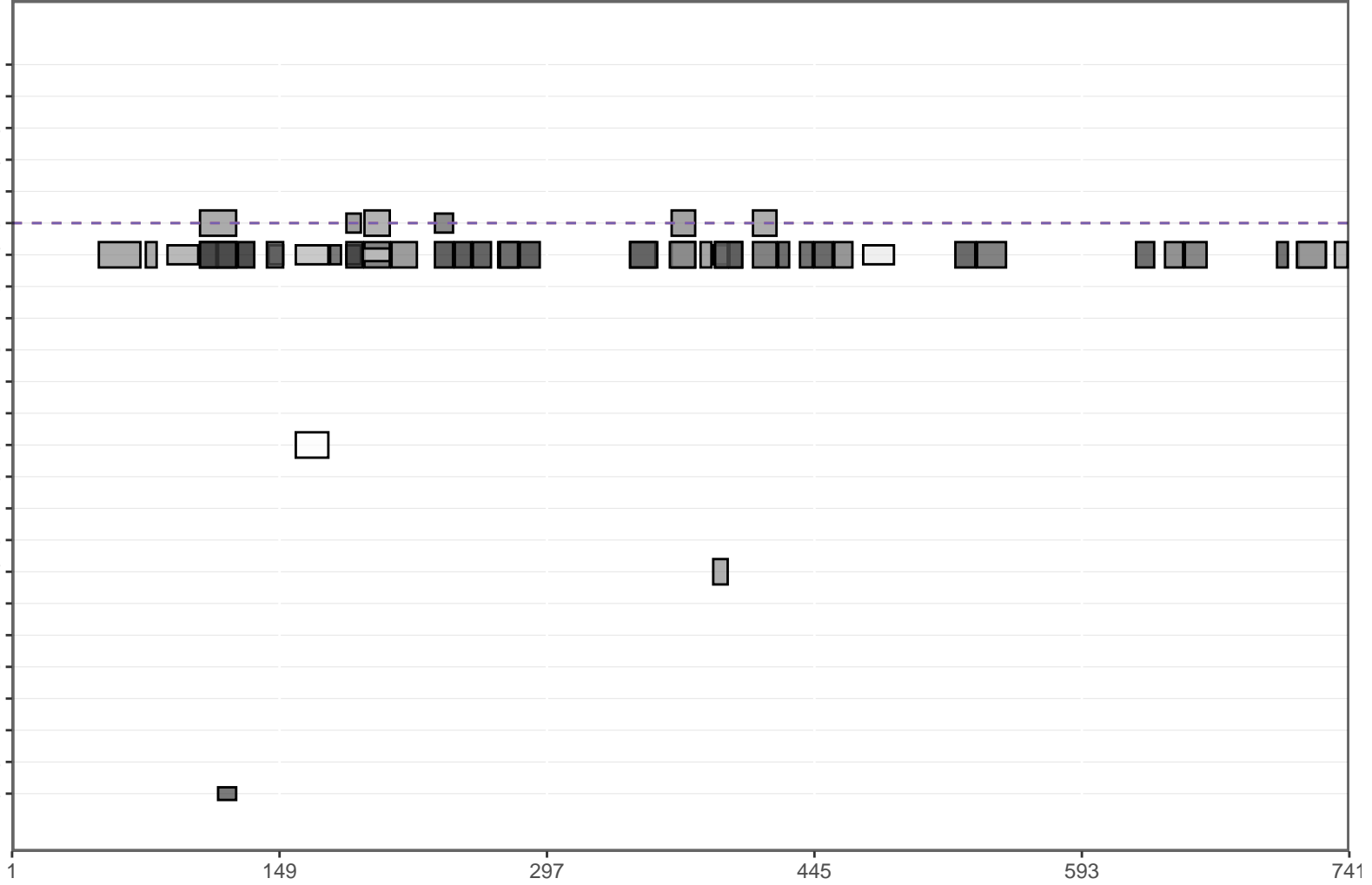
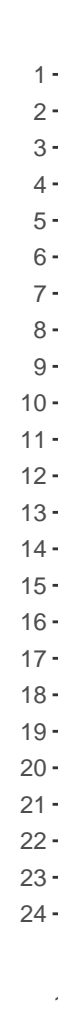


MW indication



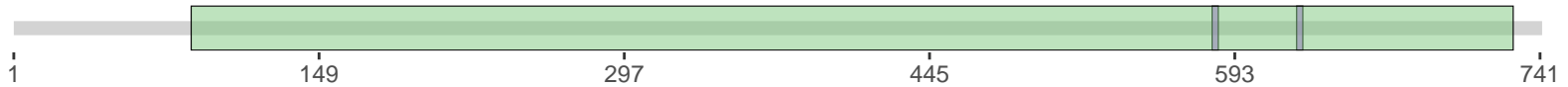
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RLANLGRKRAAELGGVAAFEENRNRVDFDRRSGELPMQKEGDEVYRGLVHRDGGVLMSEVSLDQLKTFELLYRSLAAKLVGMPEKDLATVDSLLRELPPVDDKDRSLGKRLVDSIMGVITFFSEQLTKPLPNAMVLTLEKELSGGSKLLPEGTRLVSVYRSGDESKDELEKSTDTMLLNLPVTEEKTRGVHAAARLFEVLSGENLNFVVIHIFPNDTHRDLLVIGAGANAGALLVDGLGGILLEAPDGGDFDLRNTSFNLGGGRMRNTRKTYISCPSCGRTLF

NbL13g20720.1 probable_inactive_nicotinamidase_At3g16190 [MW = 22.37 kDa]

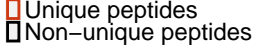
No. of times detected



log(intensity)



Values from



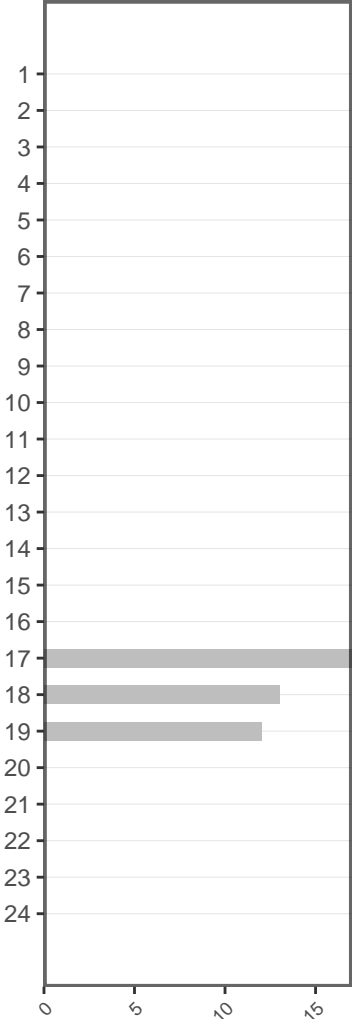
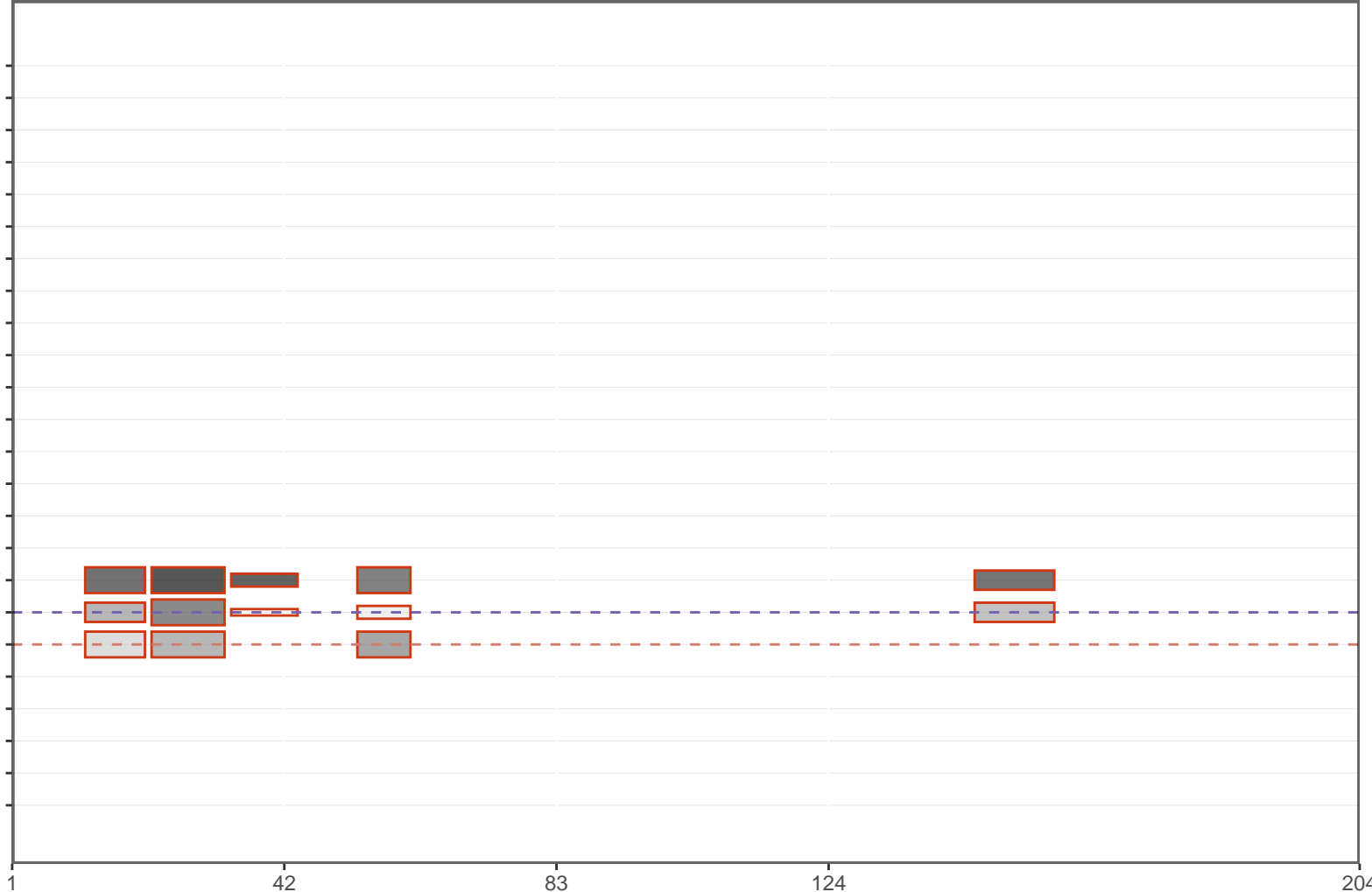
MW indication



Molecular weight



Gel Slice



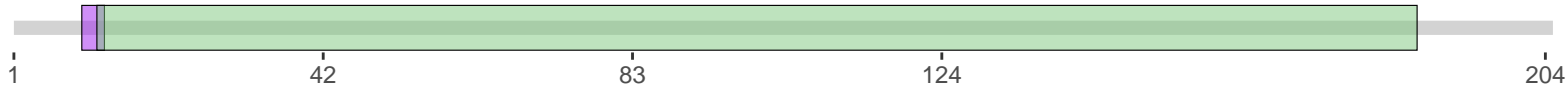
Protein length



Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

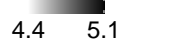
IKGSVGAELVDLVEEDDQKVKTRFSAFRNTNLSHSLGGIGTNLVHVGQTPNGIRGTVDVALEHVERTVSDATAAATPDVHIANFMFMKNNVGVATPTLDEWGSSTEGWAKD

NbL13g20660.1 30S_ribosomal_protein_S17_chloroplastic-like [MW = 17.38 kDa]

No. of times detected



log(intensity)



Values from



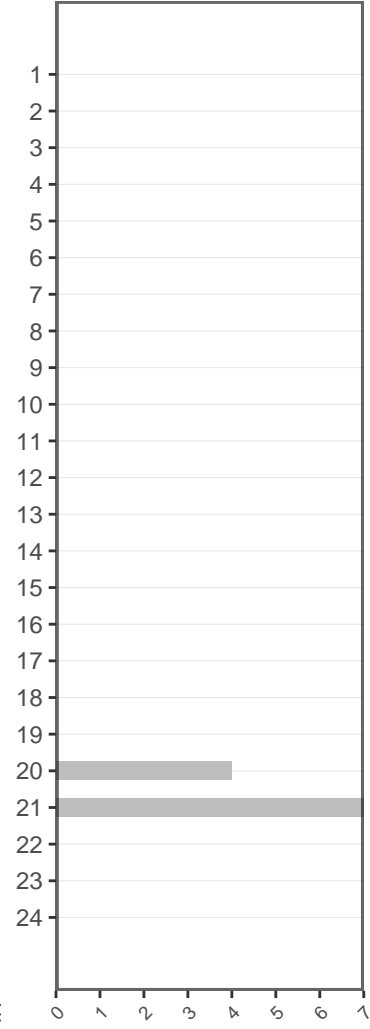
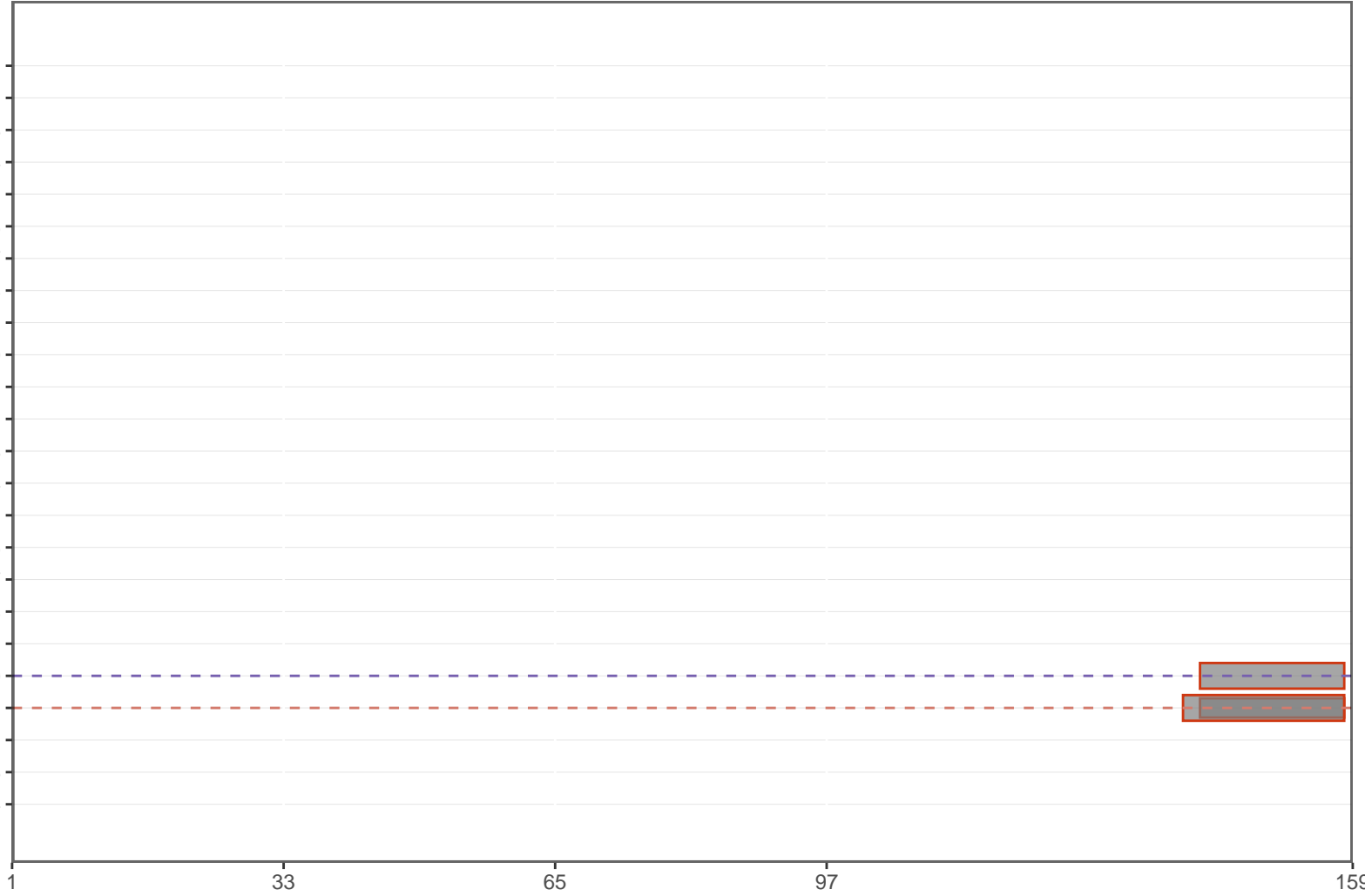
MW indication



Molecular weight

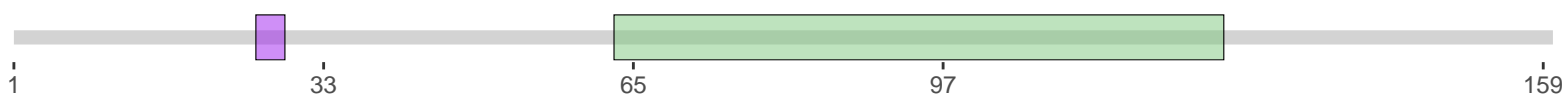


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

STNDKTVSEVETRLAHPKPKRRVRRKKKKYGAHDPLNGFQVGFQLEKTAPIKTKTKFLAVFVPRRNGPKPKGEGDDELGLFLESSLQSL

NbL13g20640.1 photosystem_I_reaction_center_subunit_VI-1_chloroplast-like [MW = 15.32 kDa]

No. of times detected



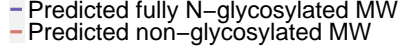
log(intensity)



Values from



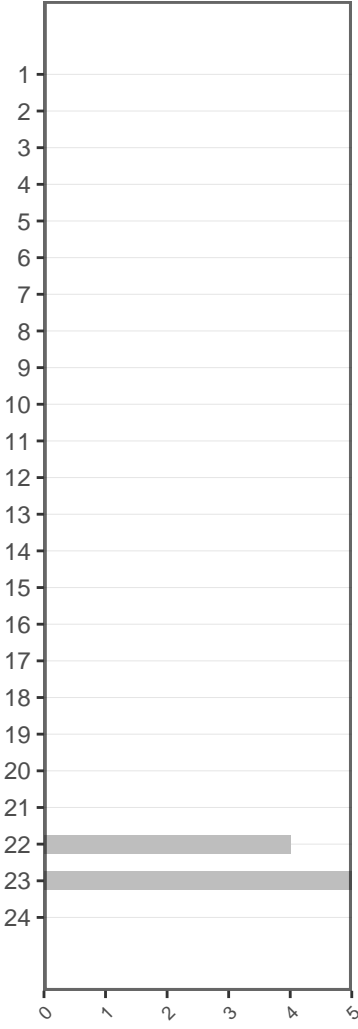
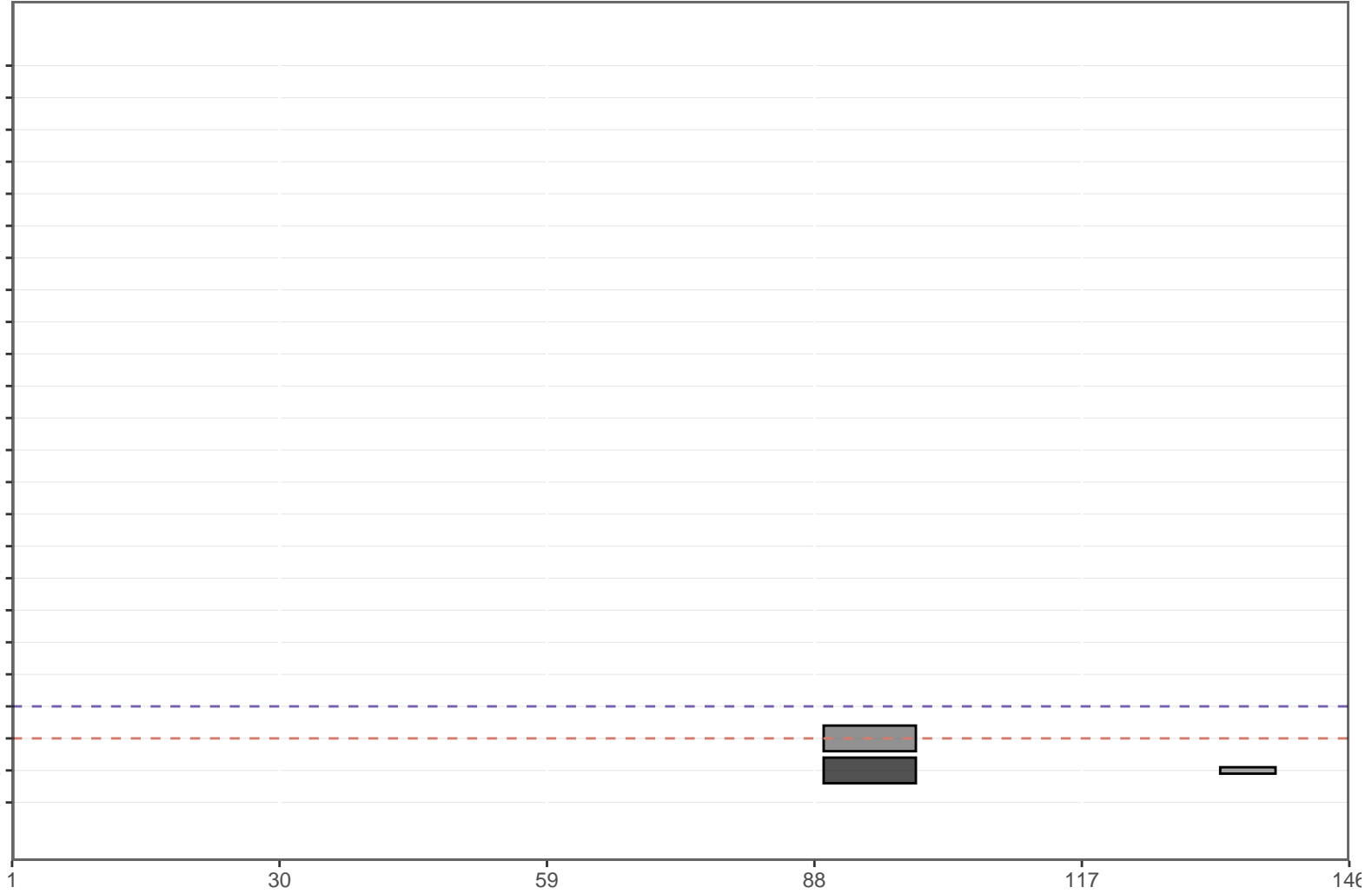
MW indication



Molecular weight

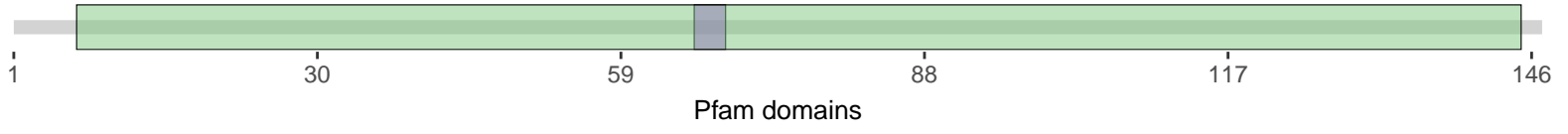


Gel Slice



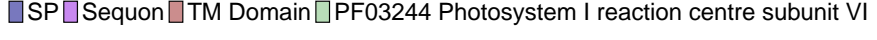
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DLELDGNTTGOVBNLGVGSDAPSPYNLSLGSKFFETFAPEFKRGLLKLFLVGGGSLAYFSSTAGDILPKKGPDLPPKLGPRGKIP

NbL13g20620.1 D-3-phosphoglycerate_dehydrogenase [MW = 34.47 kDa]

No. of times detected



log(intensity)



Values from



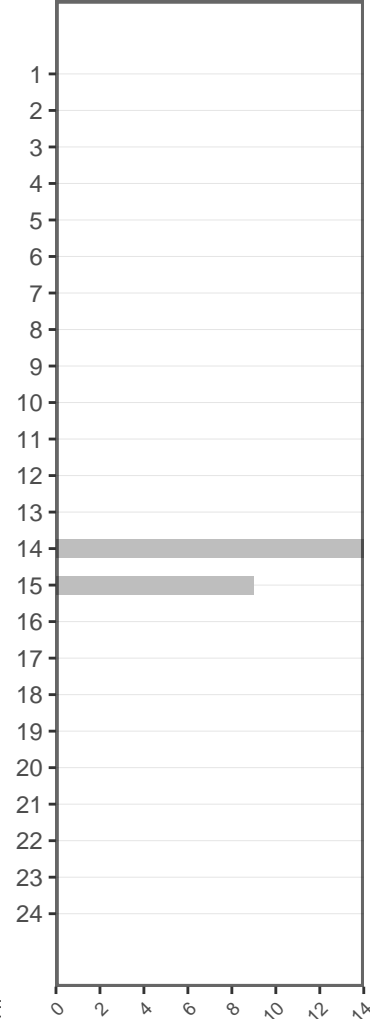
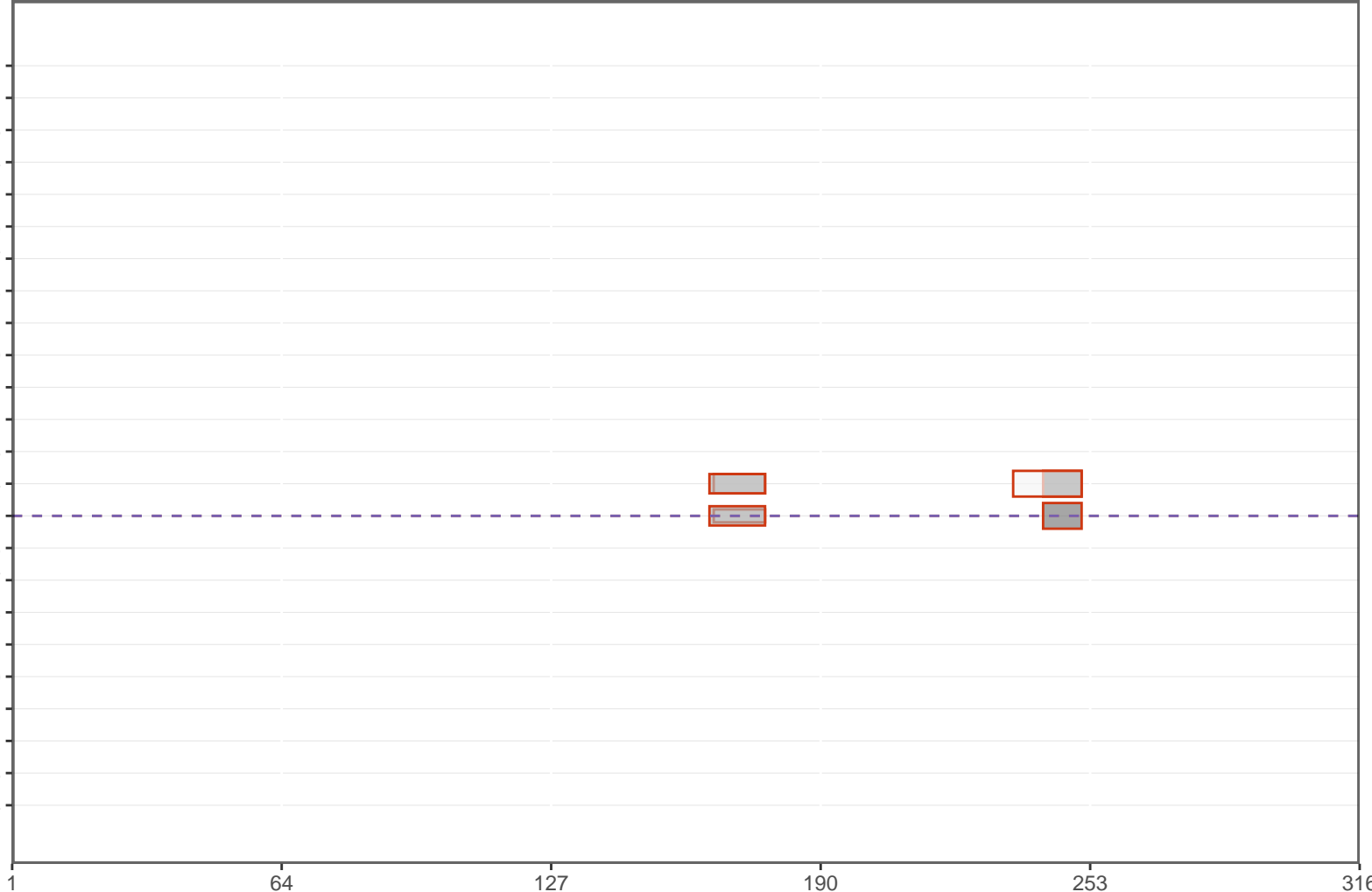
MW indication



Molecular weight

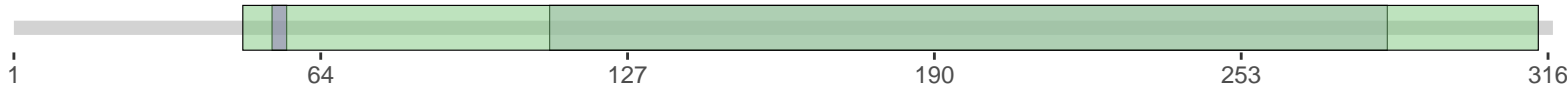


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00389 D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain
- PF02826 D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain

Protein sequence:

IGKSYGIGLGRIGLAKRAEAFGLSEVHARSQKPNTHYKYYPSPVELASNGQIVVAGALTPETRHVNRVEIEALGSKGVLINIGRGPVHDEKELVAVLVEGRLLGGAGLDFENEPVPEQLFGLNLYLLPHVGSSTVETRKAMADLVLGNLEAHFLNKLPLTPV*

NbL13g20570.1 ras-related_protein_Rab7 [MW = 22.98 kDa]

No. of times detected



log(intensity)



Values from



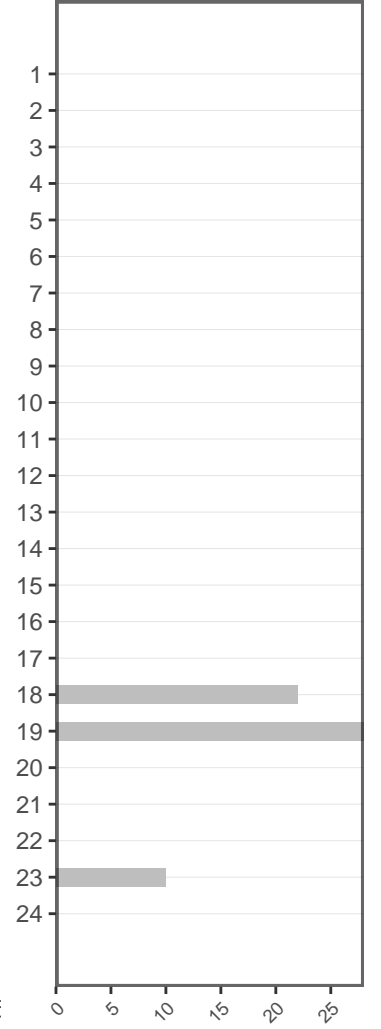
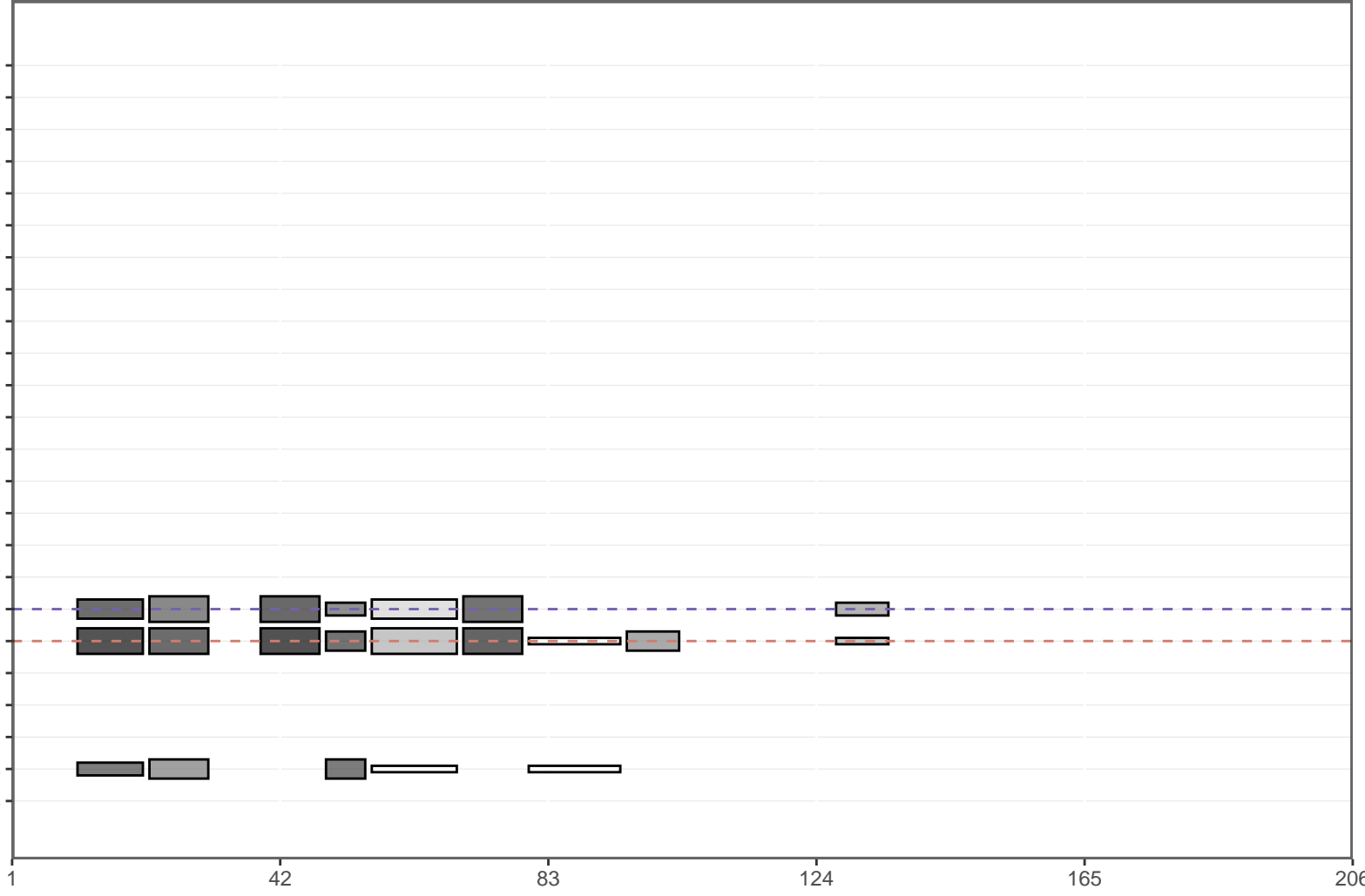
MW indication



Molecular weight

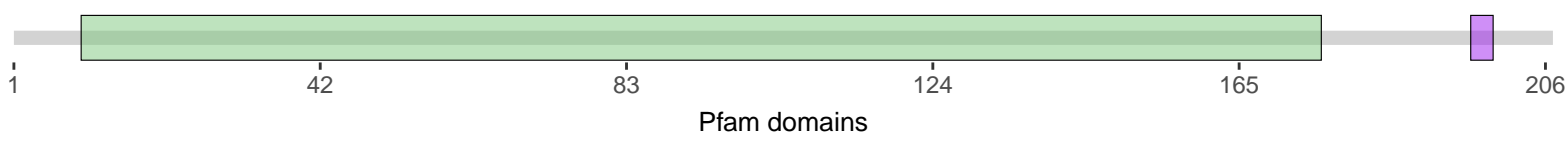


Gel Slice



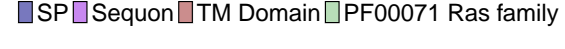
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

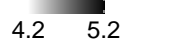
NYMKSFENLNNVREEFLIGASPEDPENFFVVLGNKIDVDGGNSRVRSEKNAKAWGASGIPYFETSAKEGRVDAAFQGIKNAKLNKEPEEMVLPDITDVAAGGNGSRSTGGEC

NbL13g20460.1 ruBisCO_large_subunit-binding_protein_subunit_beta_chloroplastic-like [MW = 64.95 kDa]

No. of times detected



log(intensity)



Values from



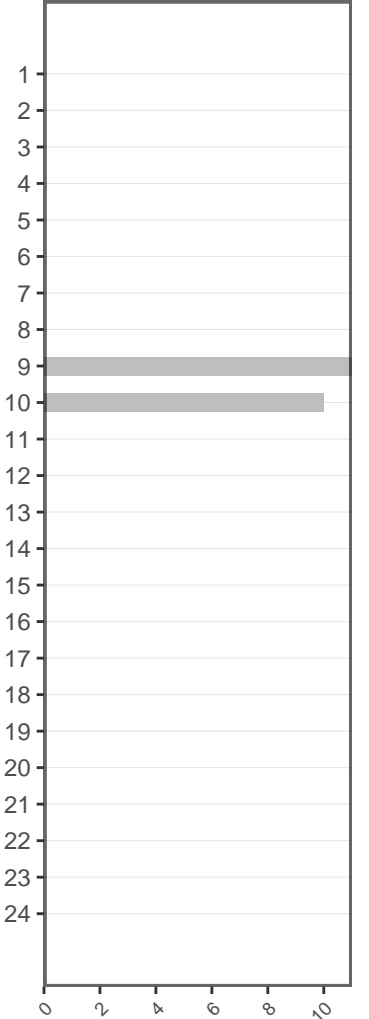
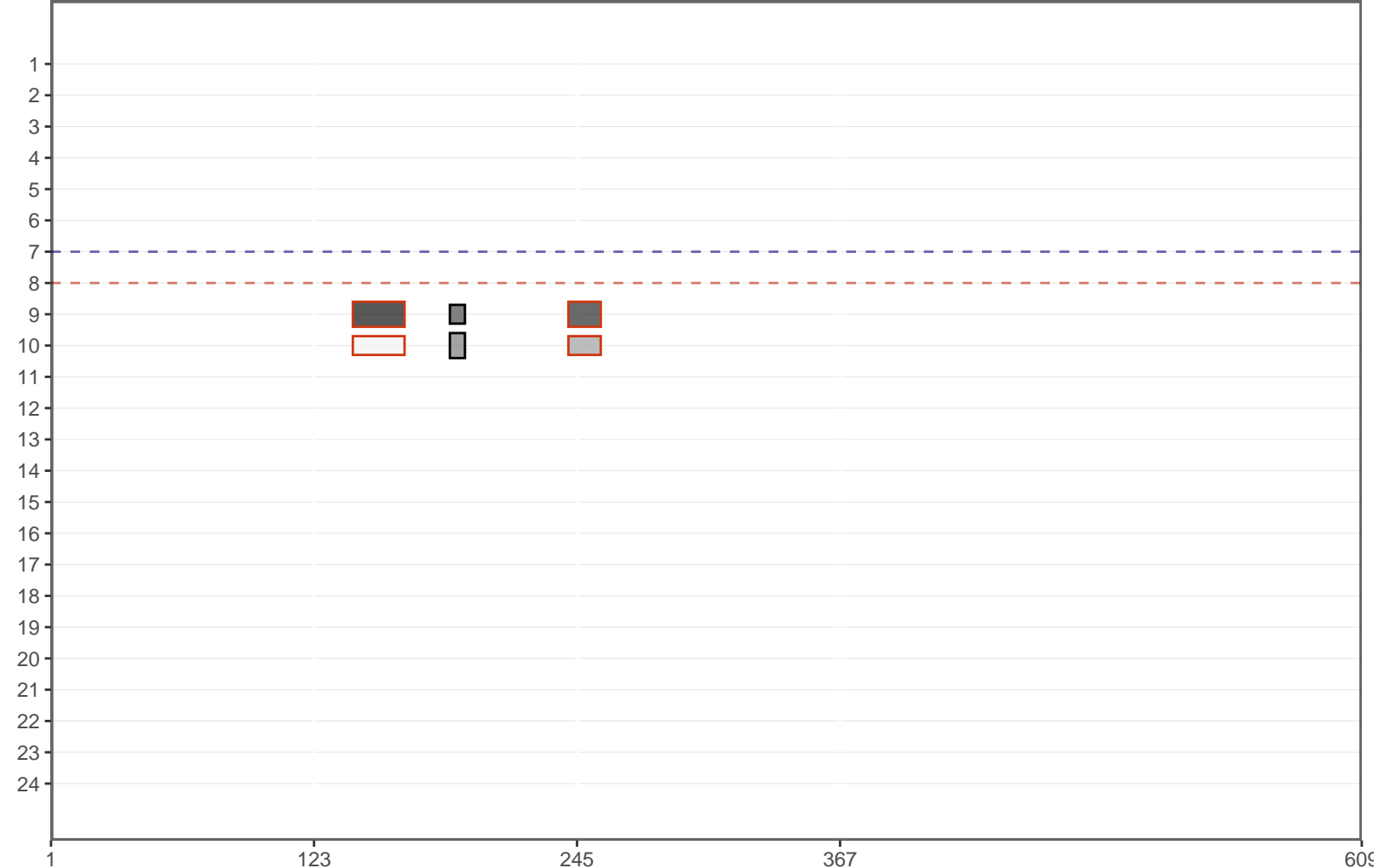
MW indication



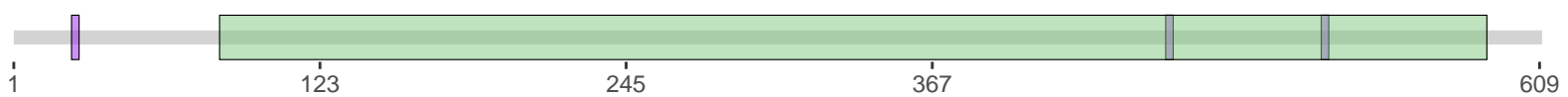
Molecular weight



Gel Slice

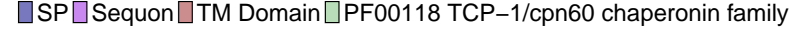


Protein length



Pfam domains

Pfam Description



Protein sequence:

ARDLVNYLEEARGGYPLIHAEDIEQEALATLVVNLKRLGTLKIAALKAPGFGERKSGYLLDIALTGGTVIREEVGLSLDRAGSEVLGHAGKWLISKDSTTIVDGGDTEQAVNKRIAGIKRIVEATEEQDYEKELNERIAKGGVAVIQVAGQTELEKEKLRVEDALNATKAAVEEGVYVGGGTLRLAAKVEDIKGTLDDEQKIGADVVKRALRYFPMKLIKAKNAGVNGSVVIEKGVNKLVDNPKYGVNAATGKYVEDMAAGHDPTKVRQGLEHAASVARTLTSDAVITEN

NbL13g20300.1 clavamate_synthase-like_protein_At3g21360 [MW = 36.24 kDa]

No. of times detected



log(intensity)



Values from



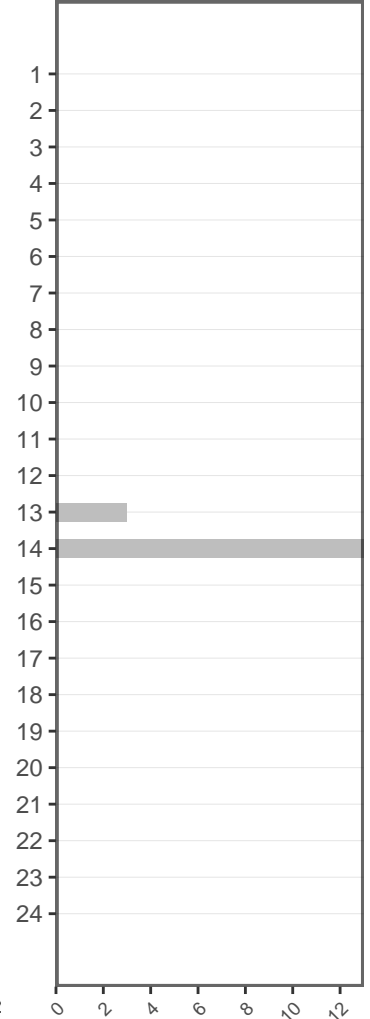
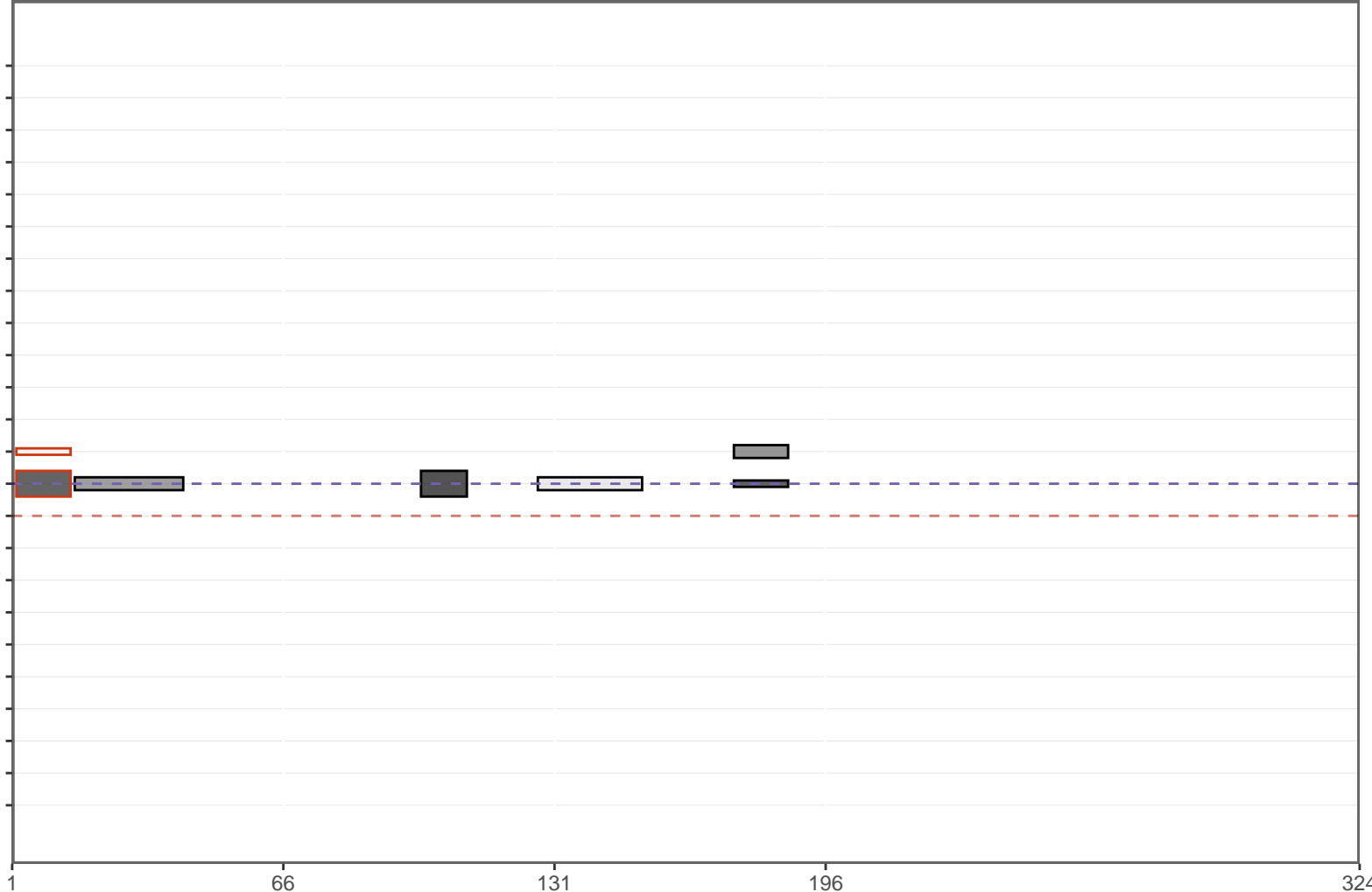
MW indication



Molecular weight

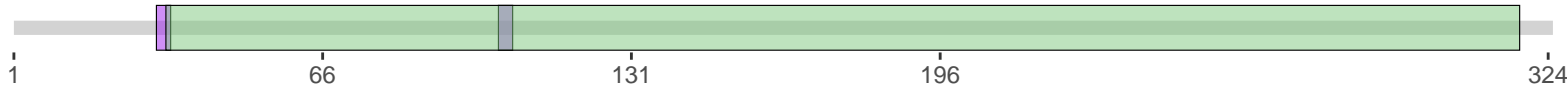


Gel Slice



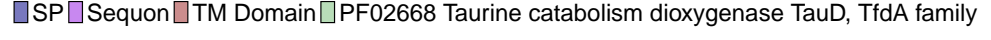
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YYEKMKNYPDFVERLEEHLVIRVLGEDDDPSSPIGRGWKSTFLTKKSAEERAAKLGMLEWEDGVKTVMSPIPAIKFNDRGQKIWFNSMVAAYTGWKBARDNDPKVAITFGDDGPLPAEVIHDCRLREDESVAIPWKKGDVLLIDNLAVLHGRKPFNPPRRLASLCK*

NbL13g20290.1 lysM_domain_receptor-like_kinase_3 [MW - SP = 70.16 kDa]

No. of times detected



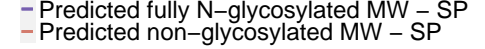
log(intensity)



Values from



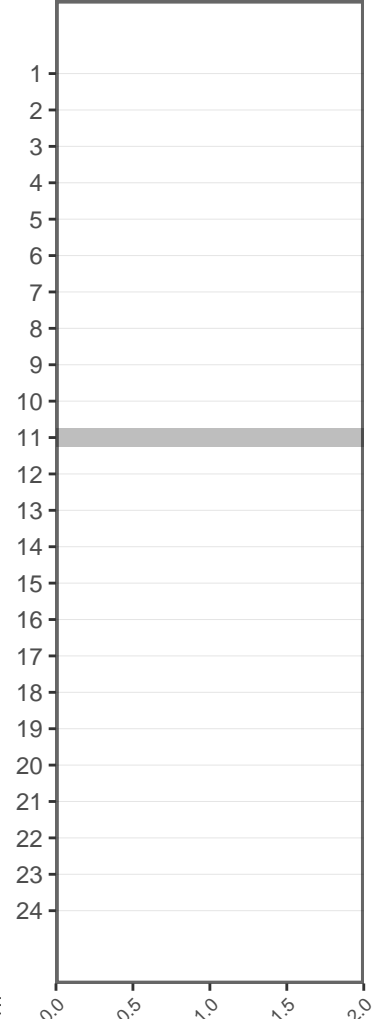
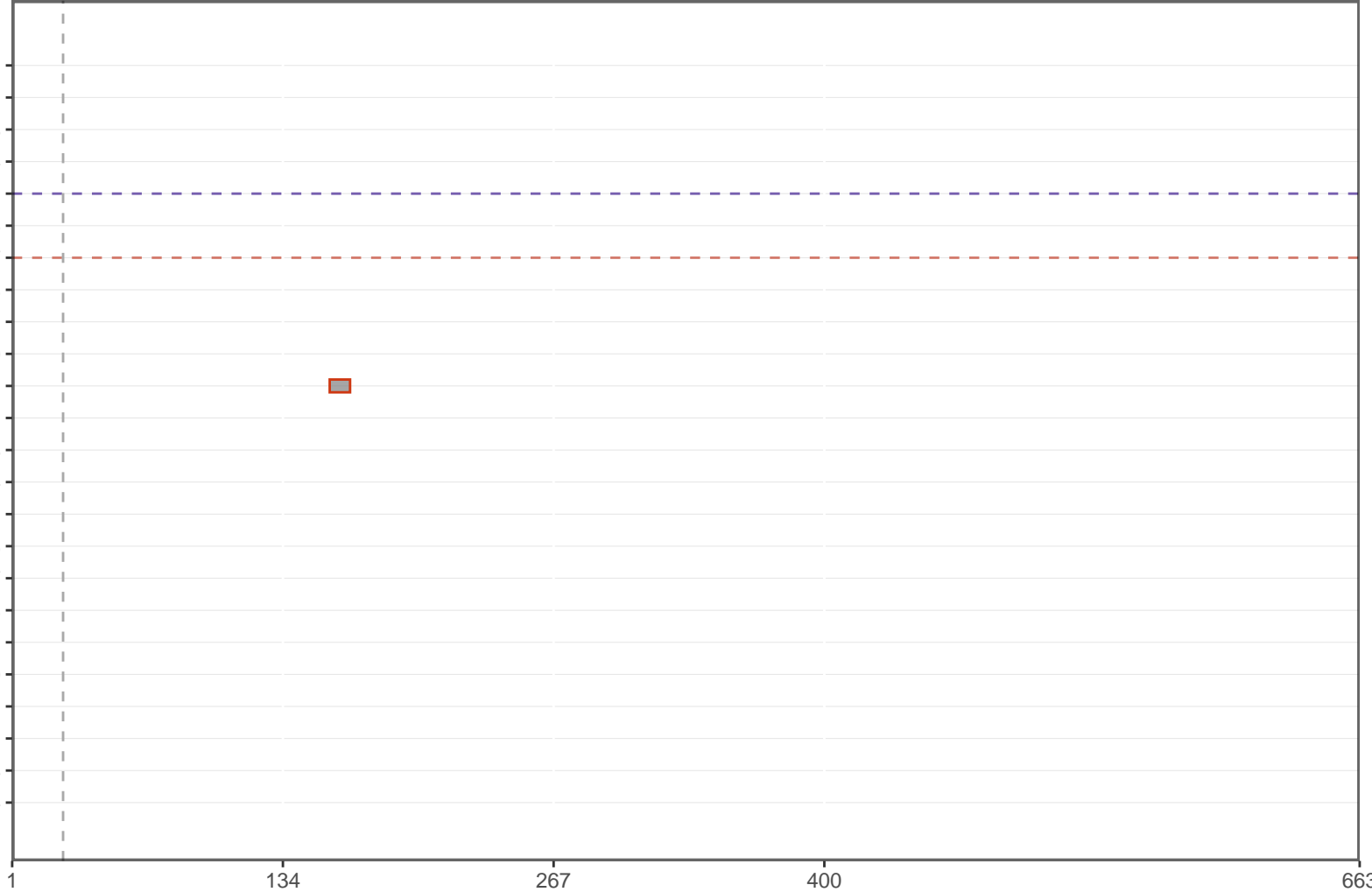
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DQQINPKYIGTDVFDMEKPLVFIYEDLSSDFGSDENLGHGTYGSVYYAIRNNGEVAIKRMATKTRFEFTAEMKVLGKVVHNLNVELHGVAVSNDELVLVEYVQKGSLSKSHLHDPQNKGHHTPLSMVRGIALDAARGLEYIHEHTKPHYVHRDKTENILLDDSFRAKISDFGSKLMGFTNDGEASATRVVGTGYVAPEKVELRDGLATKTDVYAFGVVLFEMLTGKEAVTRTEGNVMTAERRBLVSLMLAALRNSPDSTMTSLKDDLPMLDLYPSDCYFKVAMLAKE

NbL13g20270.1 hexokinase-1 [MW = 53.89 kDa]

No. of times detected



log(intensity)



Values from



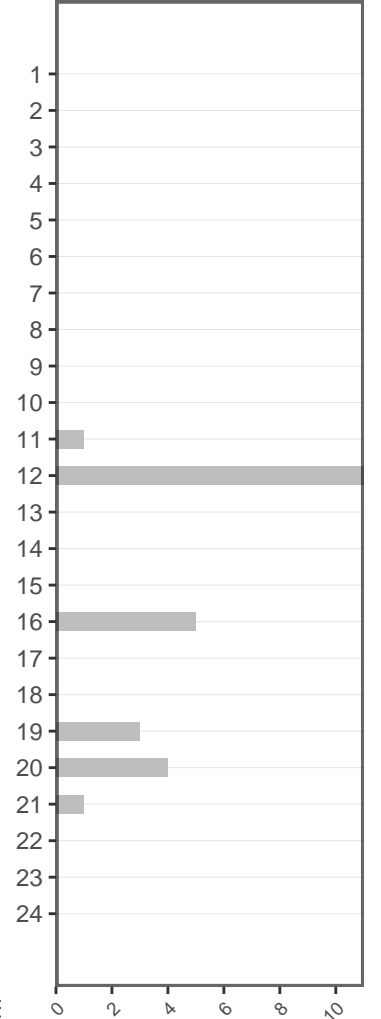
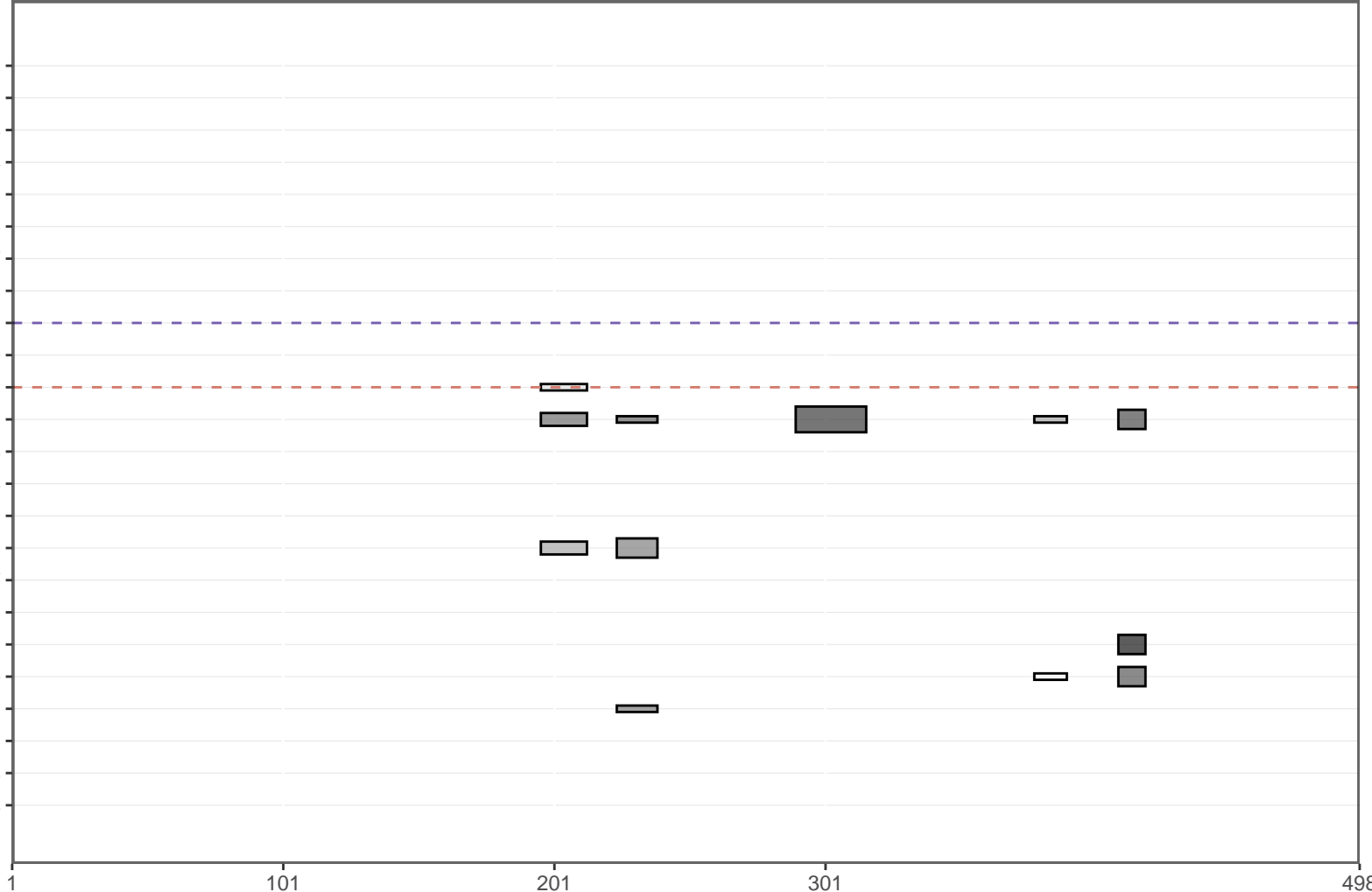
MW indication



Molecular weight

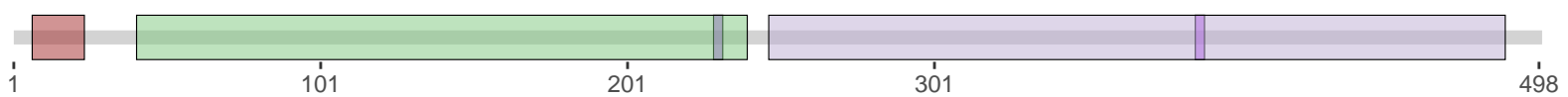


Gel Slice



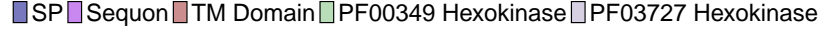
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGGKYTHINDVAIVLGTGTNAAYVERVQDAIPKWHGPMKSGEMVINMEVGNFRSRLPLTQYDHALDITNLSNPDGDFEKMTSGMYLGEILRRVLLRMAEEAGIFGDEVPKLLKSPFLRTFQMSAMHHDTSSDLRVVGDKLDKLEISNTSLKTRRLVVELGNVATRGARLAAAGVGLKXKMSRDTFRGGGPKQKVVAMDGGVLYEYAEVYRTGLENTLKELLGDELATGVFEHNSNDGGGGAALLAASNMVLEDKS

NbL13g20240.1 acid_phosphatase_1-like [MW - SP = 27.08 kDa]

No. of times detected



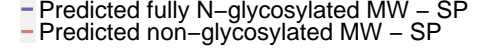
log(intensity)



Values from



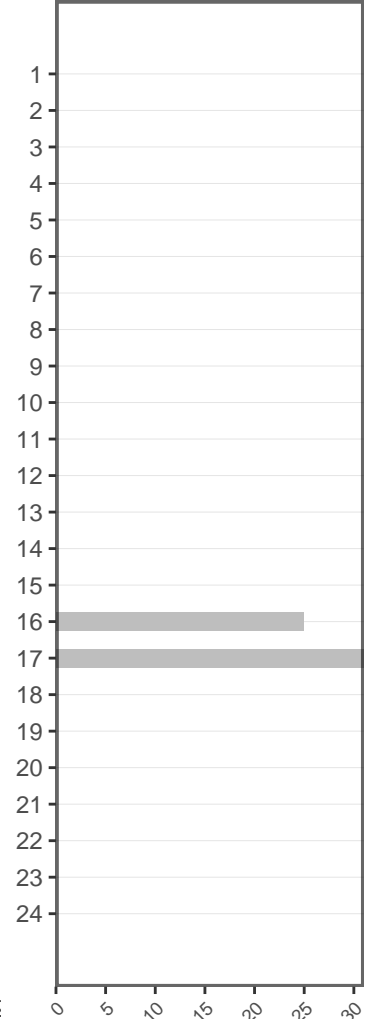
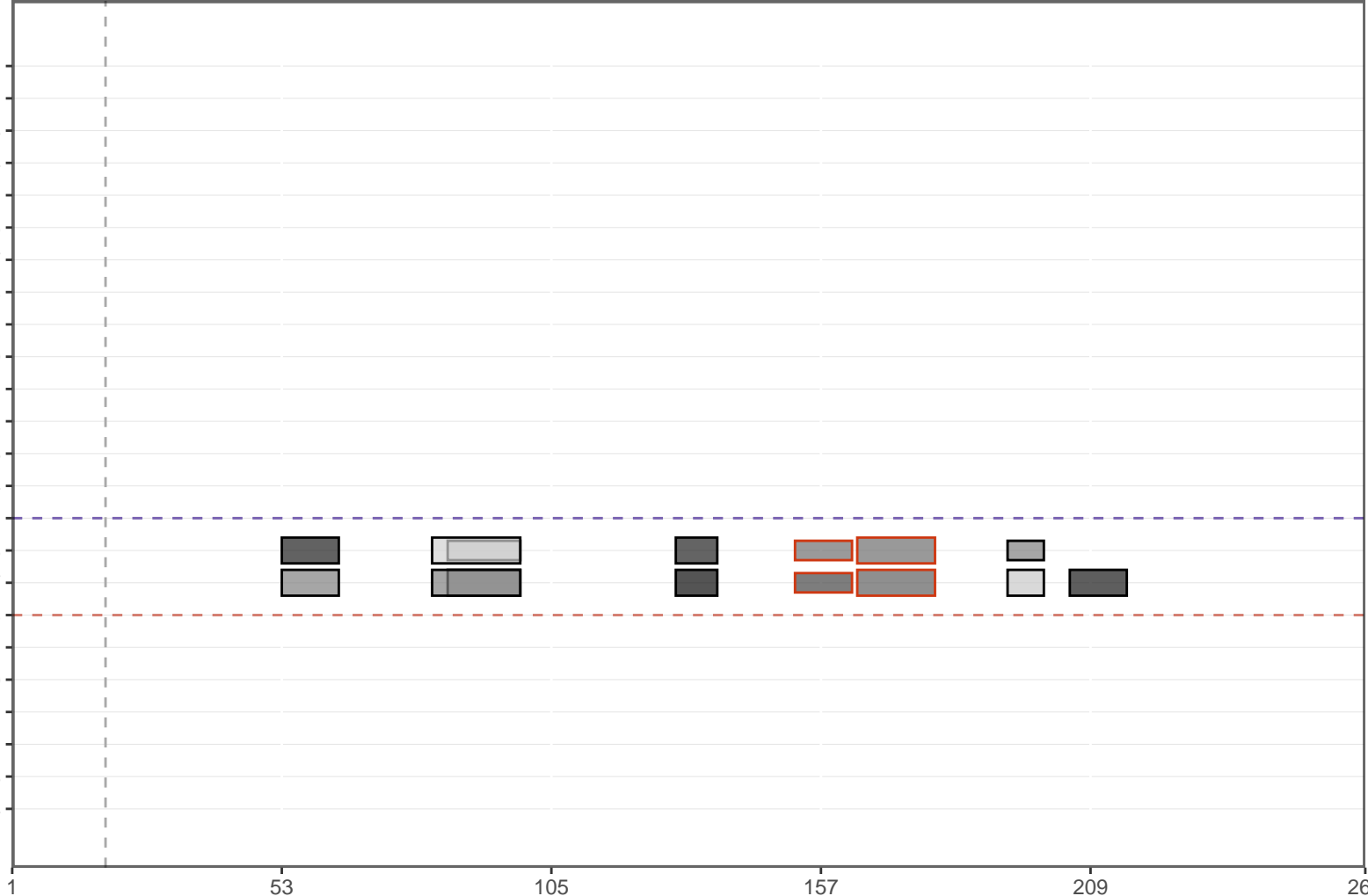
MW indication



Molecular weight



Gel Slice

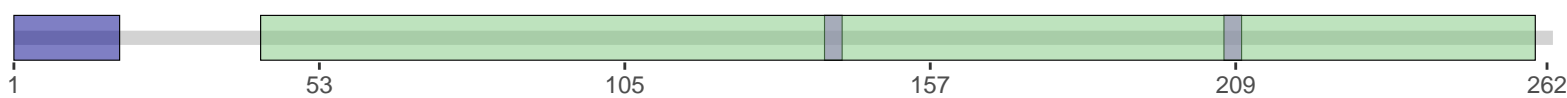


Protein length

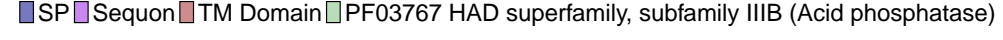


Peptide counts over 4 repeats

Pfam domains



Pfam Description

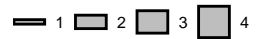


Protein sequence:

TLNLPYARSDVAFGATKFNQTKFDEWTRREGKARVPGALFLYRLLGMDGKPVFTGTKEEFRQVRIANLKKVGVHSWVLLKGVNDTGSVMMKSKRAELVYKAGVRIYVNGDQWSDLLGDFVGDRTFKLPDPMVYK

NbL13g20200.1 GDSL_esterase/lipase_APG-like [MW - SP = 36.29 kDa]

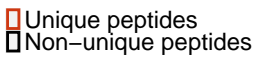
No. of times detected



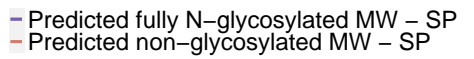
log(intensity)



Values from

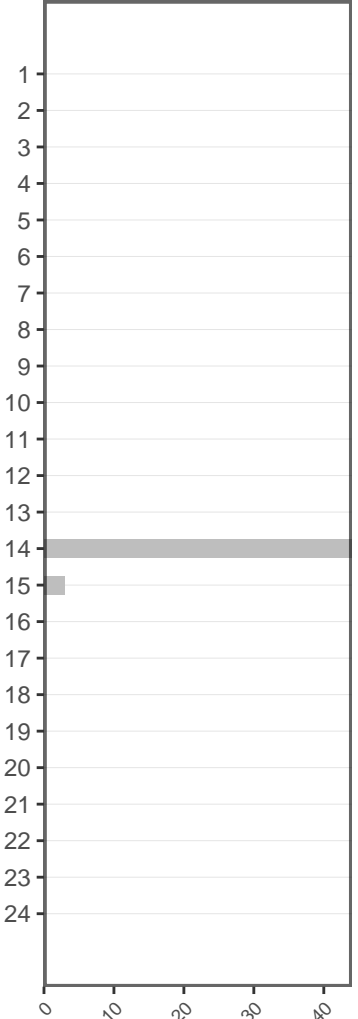
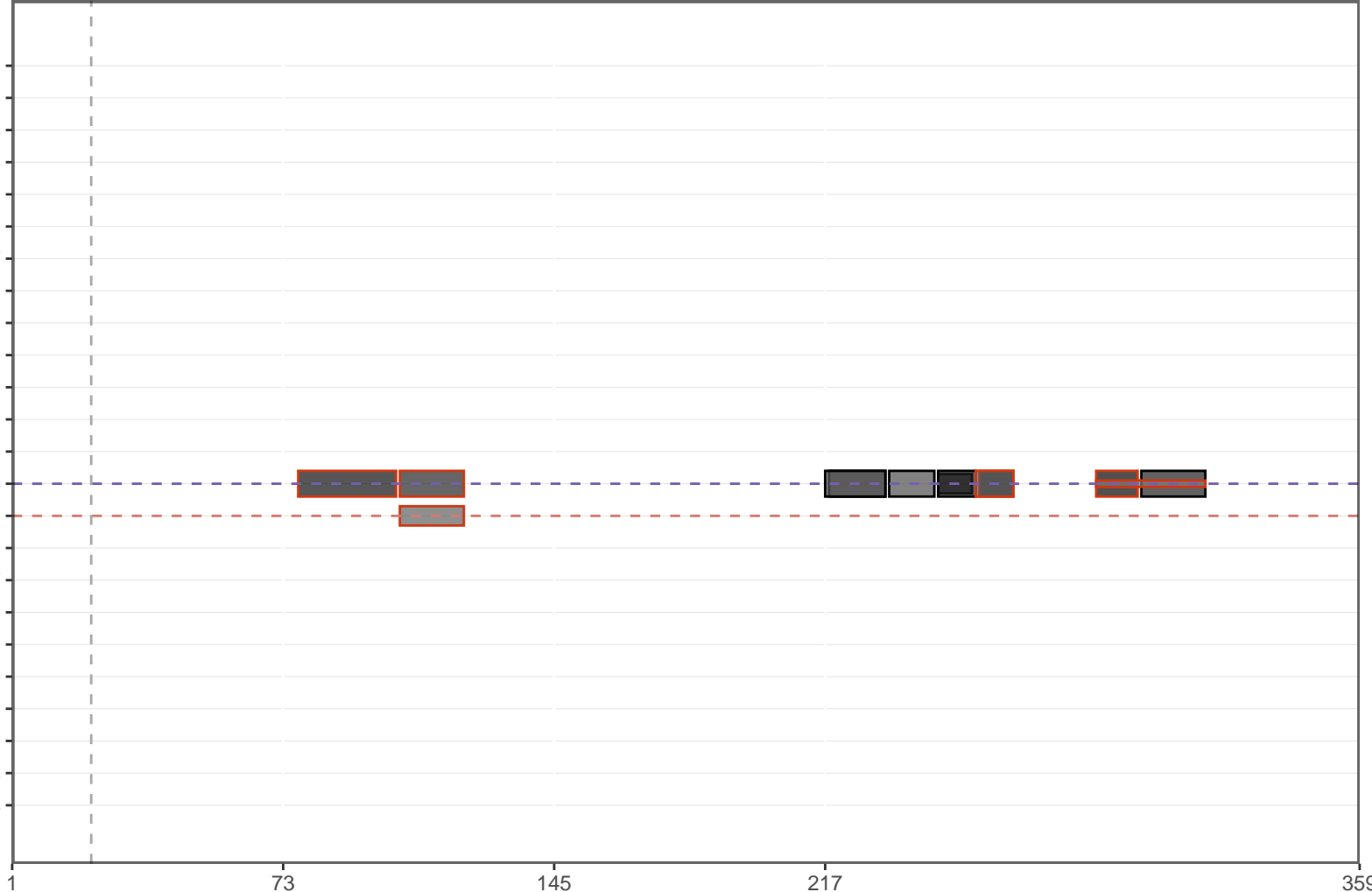
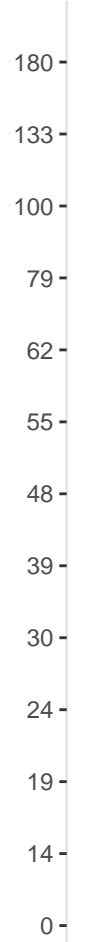


MW indication



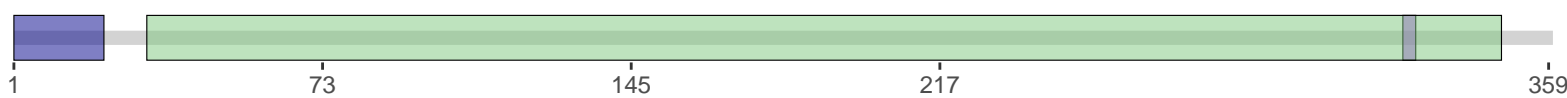
Molecular weight

Gel Slice



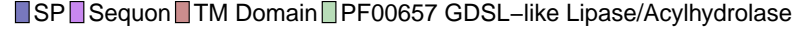
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ILSAGSSDFLQNYINIPYKQLYTPDQYGSYLGIQIFSFVKDLHAGDARRIGVTSLLPPLGCLPAAITLFGFHESGGVSKINTDAGGFNKKINSAATQLGKGLPLGIKIAFDIFQPLVDLWKSPEHNGFTEANKGGGGTGTVETTSLLGNPKPPTGTSNATQVYFVDSVHPSEAANGVLDLGIQGINLIG*

NbL13g20110.1 uncharacterized_RNA_methyltransferase_BH0687 [MW = 63.51 kDa]

No. of times detected



log(intensity)



Values from



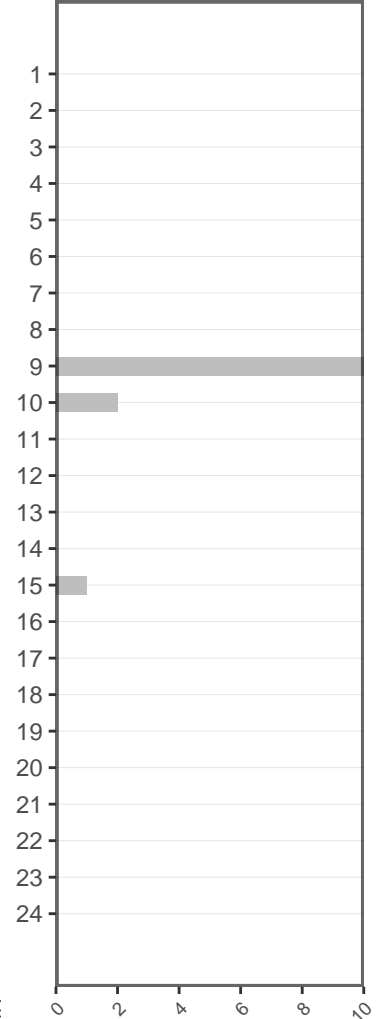
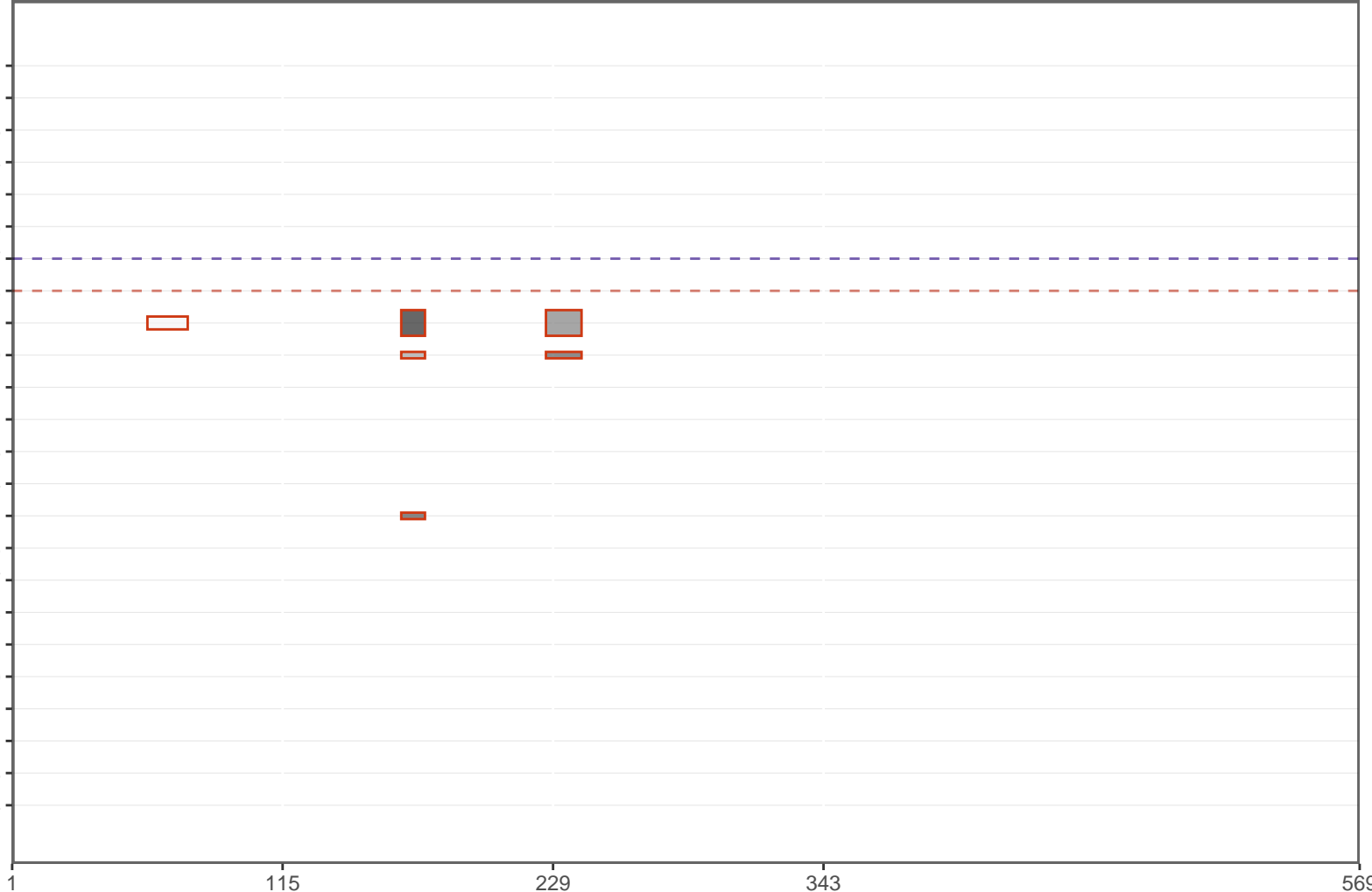
MW indication



Molecular weight



Gel Slice



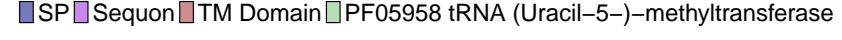
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

3SGNEVLEVYVORCWRIDPELGLSPVDVHSHSGFLKHLMLRTGRNVETGLPELMMVNFYTSVNPPEGLRPRVVENKSAIPEVVTWNNVNTSNGTNSIGEKEYTLVYKGTTEIRLGLTFQISANFFDTNTHQAEILKLEDCAFKKGDSSEVLDLFGTGTGTLGLAKRKHYYGFEVADGAVSDARQNAKLNCGDATTFFEGDLNKIDLNFASNLKPKPDWITDPNRPDMHKLKFLKQKATRIYVYVSNPATGARDLNLVGYGVPEQNEGNYRLSSGQPVDMFPHITPHIECVCLLEL

NbL13g20100.1 IAA-amino_acid_hydrolase_ILR1-like_4 [MW = 57.9 kDa]

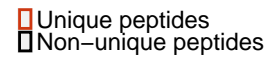
No. of times detected



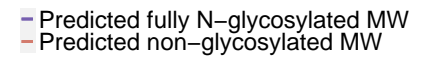
log(intensity)



Values from



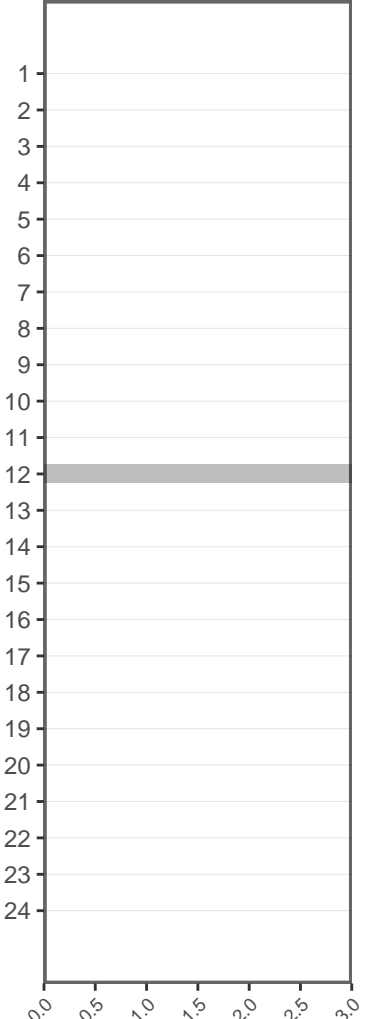
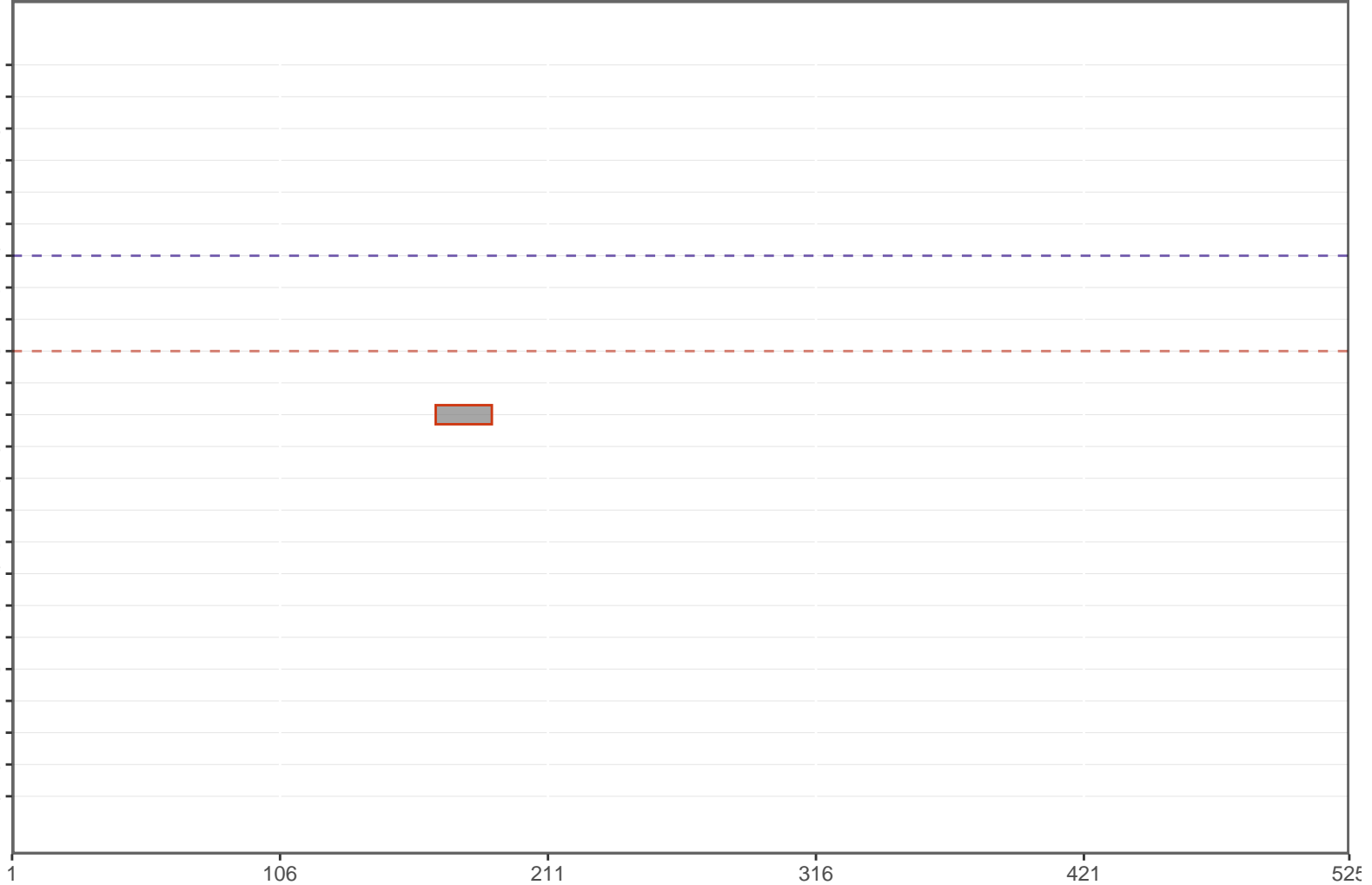
MW indication



Molecular weight

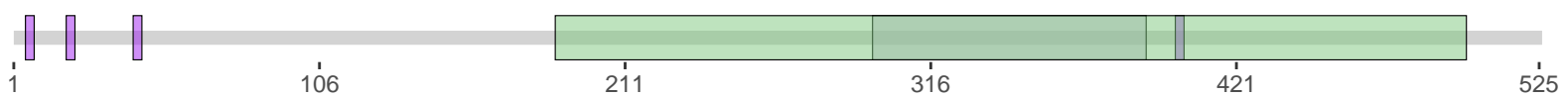


Gel Slice



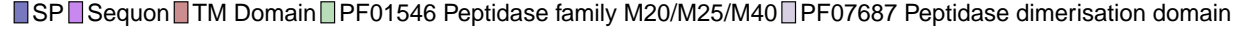
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

GGGAXXMDAGALENEAIFGLHVNPOFPLGKIVSRBPFLAGSDFEAWISGKGHAAIPGHISDPLAASNIVSLQLVSRADPLDGGVTVAKFGGGAFNVIPDSEVTIGGTFRAFSKESFQQLRQRREEVIVGGAAYDRGNATVDFLTKKPPFFPTVNDKLNHWIFQRVASDMLGNDHWKDMPLMGSGEDFAFYQVEVPEVYELLGMODETNEKLVSHSPYFKINEEALPGALQASLAIRYLEAQSLVPSSESDHNDLV

NbL13g20060.1 RWD_domain-containing_protein_1 [MW = 28.06 kDa]

No. of times detected



log(intensity)



Values from



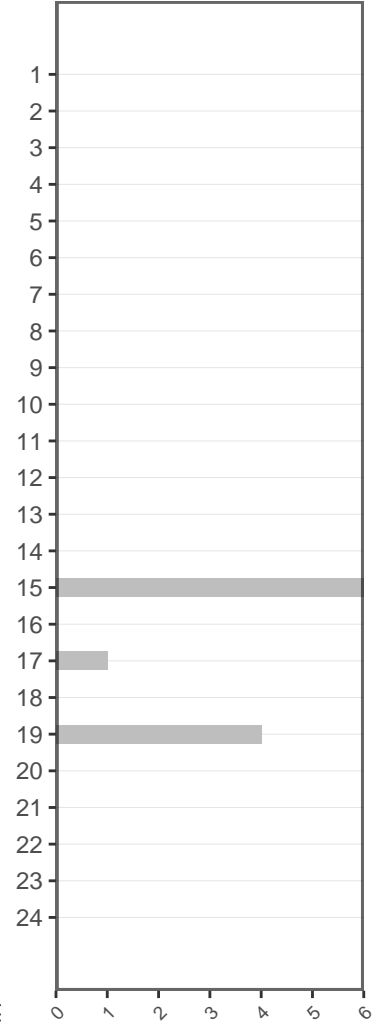
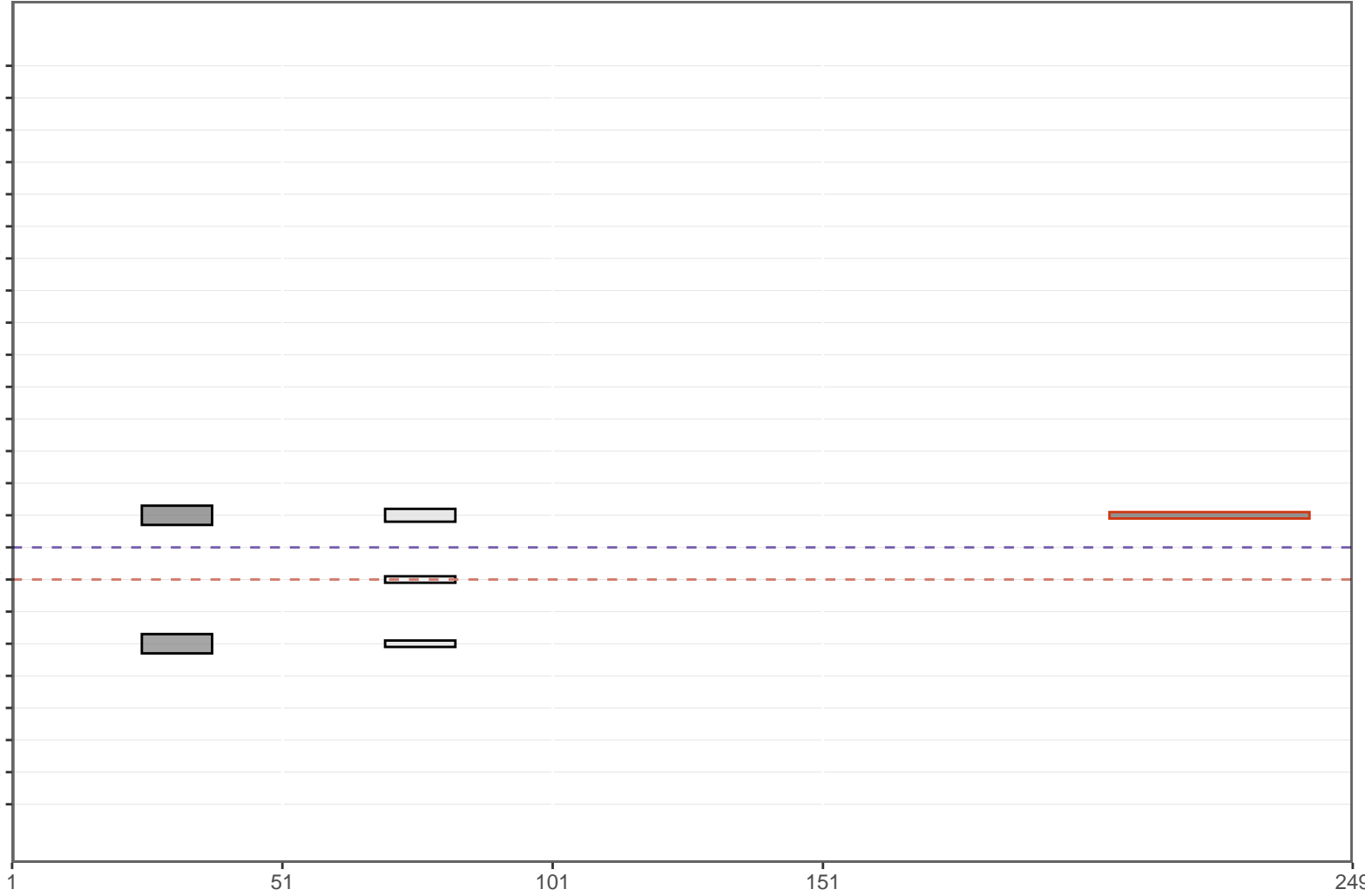
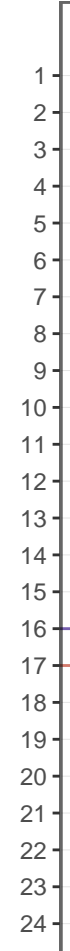
MW indication



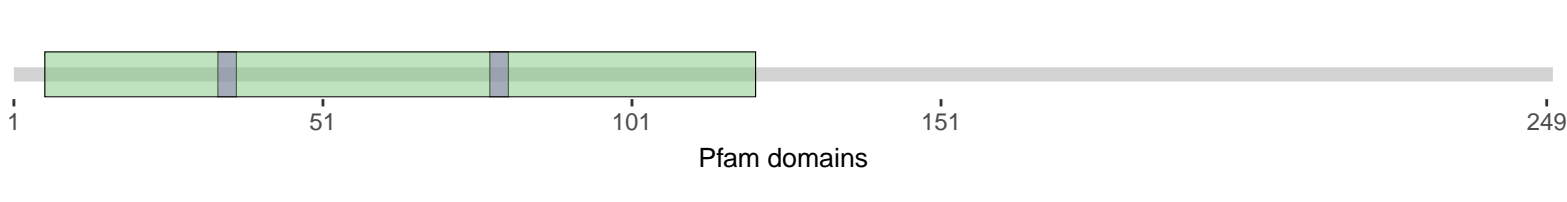
Molecular weight



Gel Slice

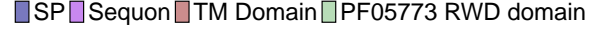


Protein length



Pfam domains

Pfam Description



Protein sequence:

VTSAKDVLSEKFAEETGAEADDEADKKEEVIHPGEPVITDTFLAWRFEAEALERAKLMPDGLNAPKEKILTRGWFEGRASGKAKAAIAEESDEDEDDIFDDDDDFEDEDDEMLLEHYLAETDSSSHG

NbL13g20040.1 60S_ribosomal_protein_L28-1-like [MW = 19.79 kDa]

No. of times detected



log(intensity)



Values from



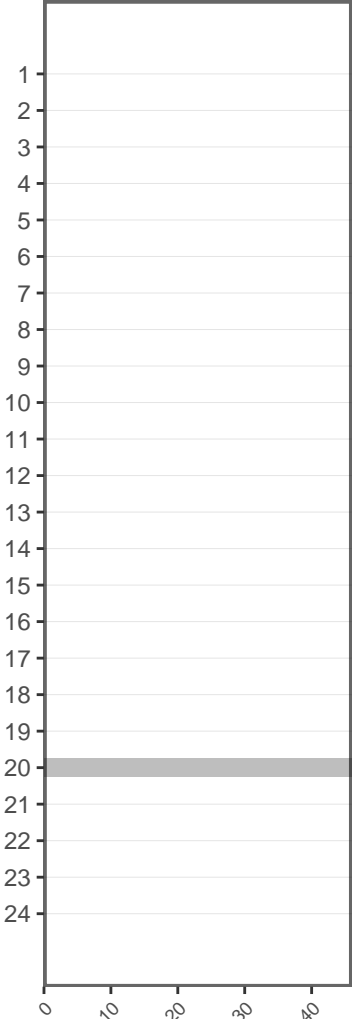
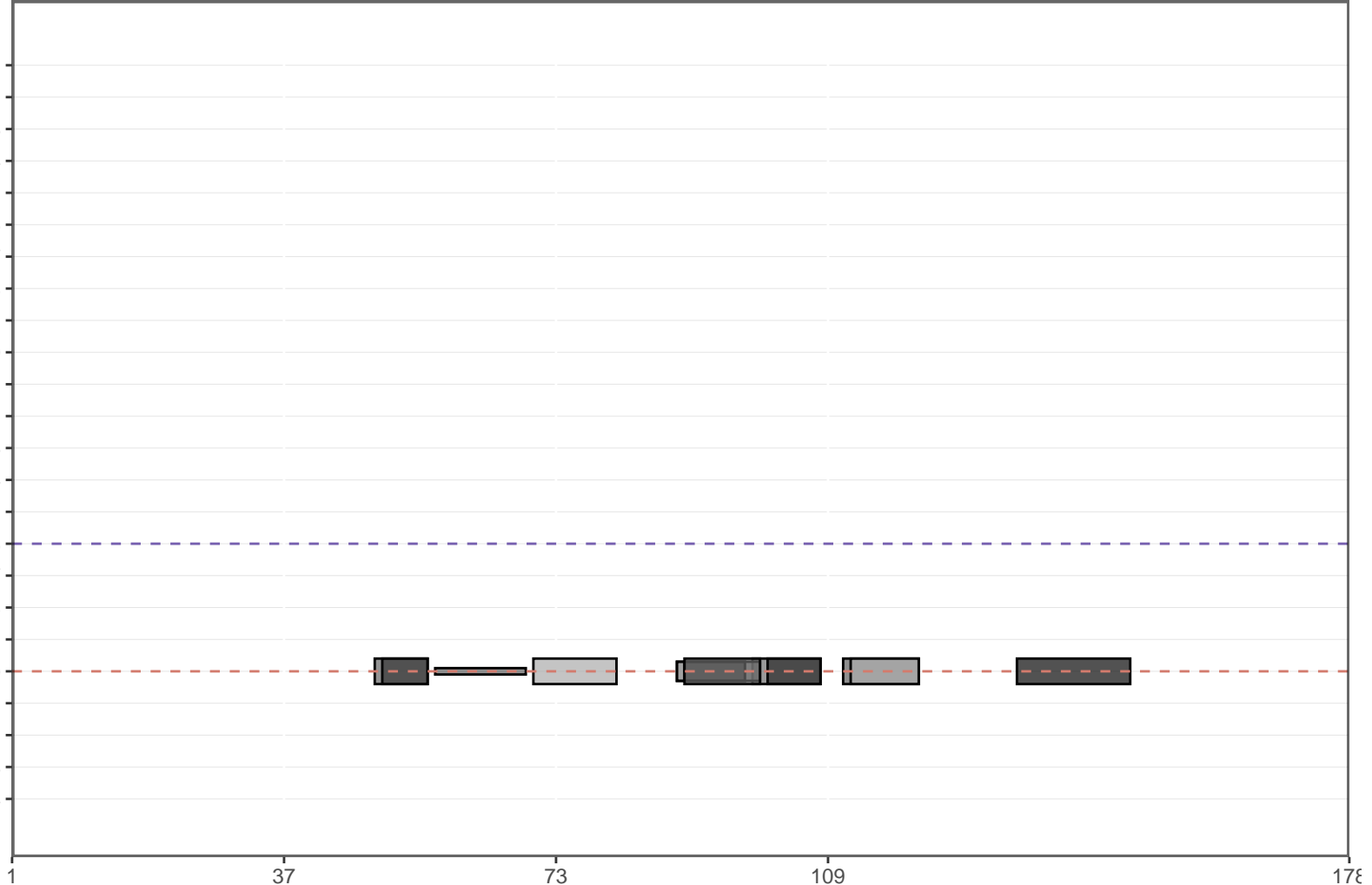
MW indication



Molecular weight



Gel Slice

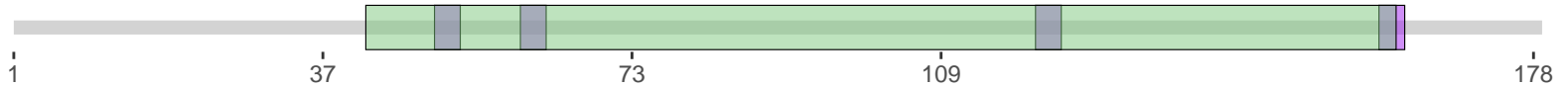


Peptide counts over 4 repeats

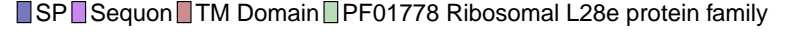
Protein length



Pfam domains



Pfam Description



Protein sequence:

JHSYKHSGLANCKTVTIGAEQKDKSVLLATSKTKGNKPFSTLLNKGVMKKEFRMAKAVTNGVADNYRFDLKKALARLSAVNRSUKVAKGKVKKKRQAI

NbL13g20010.1 ESCRT-related_protein_CHMP1B [MW = 22.7 kDa]

No. of times detected



log(intensity)



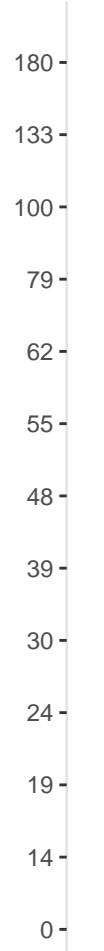
Values from



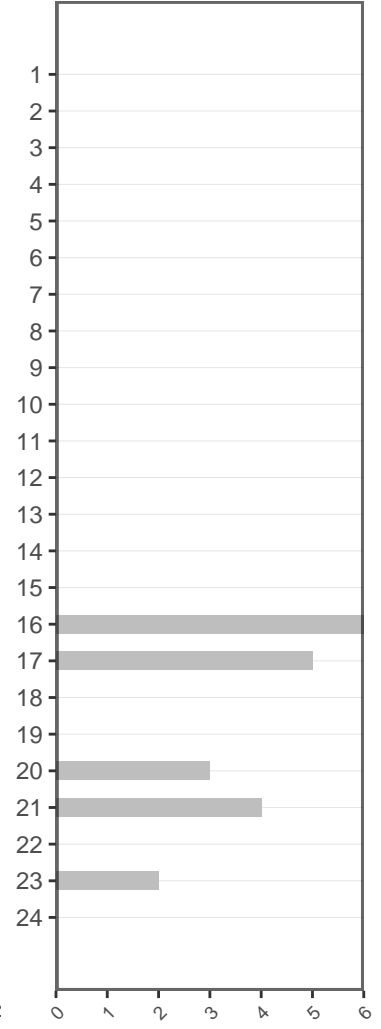
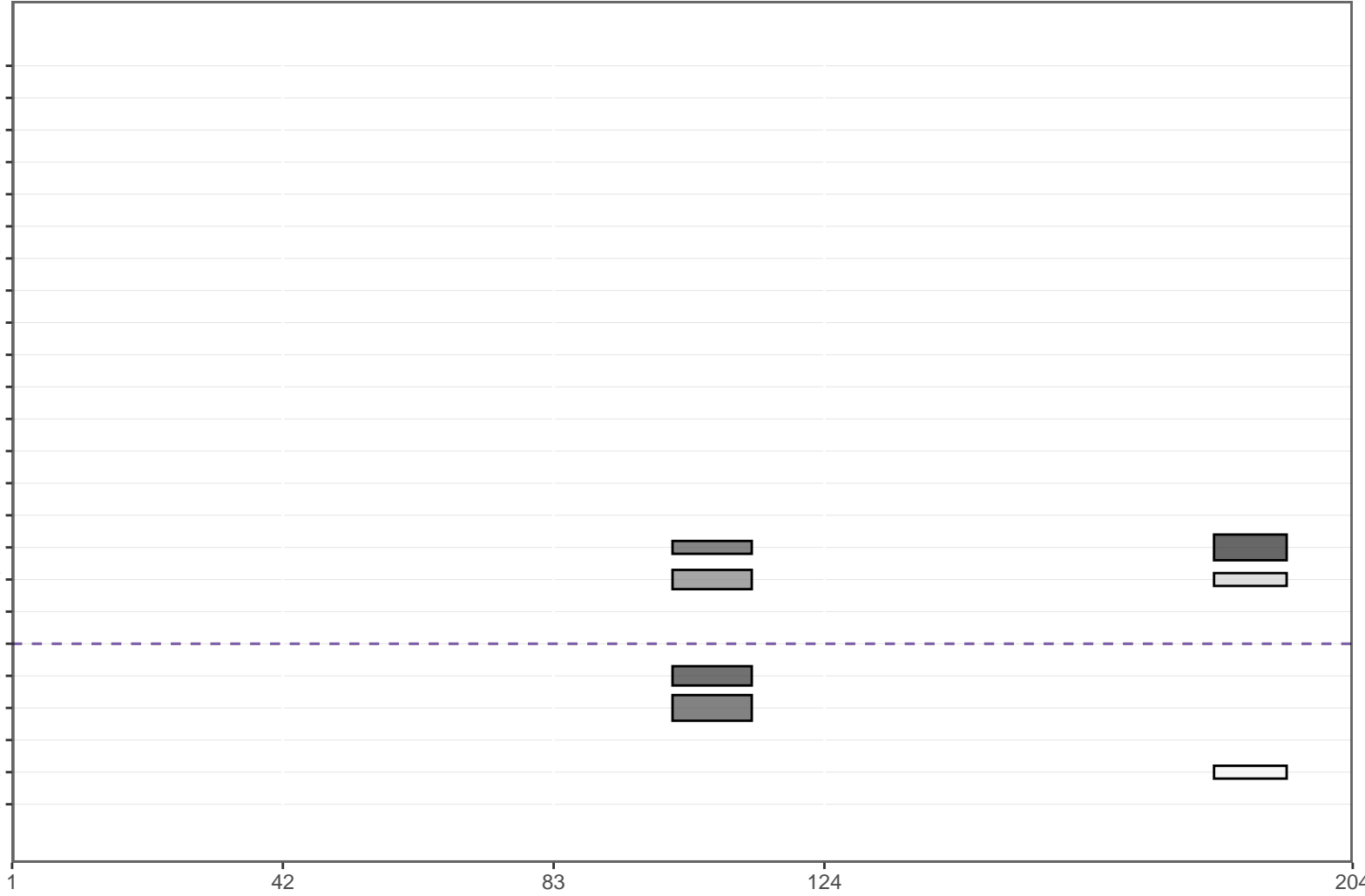
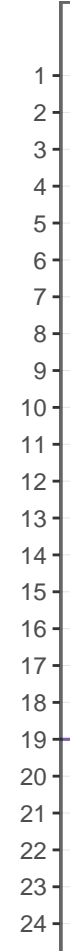
MW indication



Molecular weight



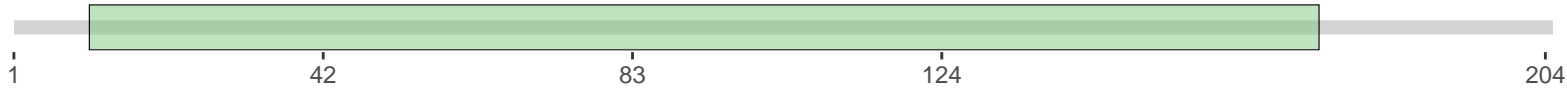
Gel Slice



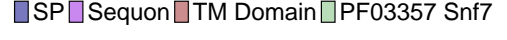
Protein length



Pfam domains



Pfam Description



Protein sequence:

TISKSMGNVKSLESLATGNLQKMSKEMDKFEGGFVNMVEVGAEFMSSMAGSTSLSTPFDQVNSLMHQVADYGLVSVGLPQAAGHAPTKDSEKVEDDDLRRLAEUKARG

NbL13g20000.1 40S_ribosomal_protein_S15a-2-like [MW = 14.75 kDa]

No. of times detected



log(intensity)



Values from



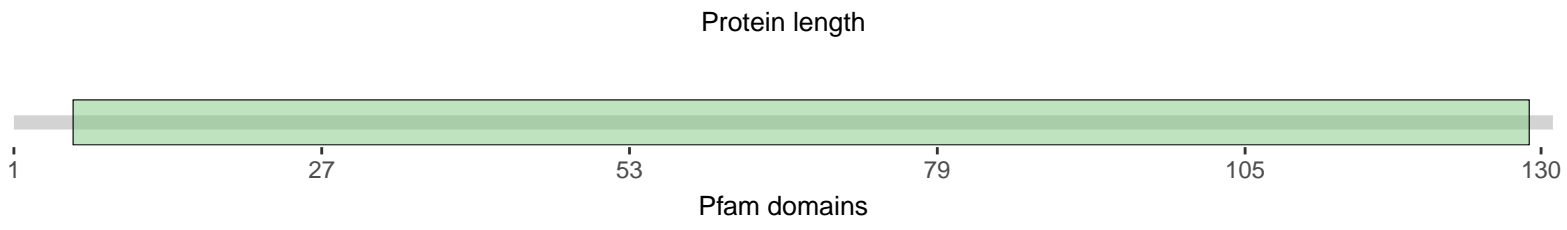
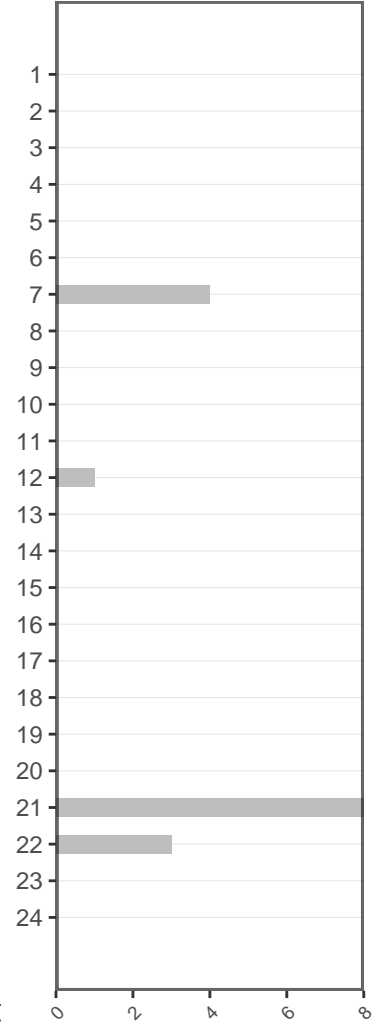
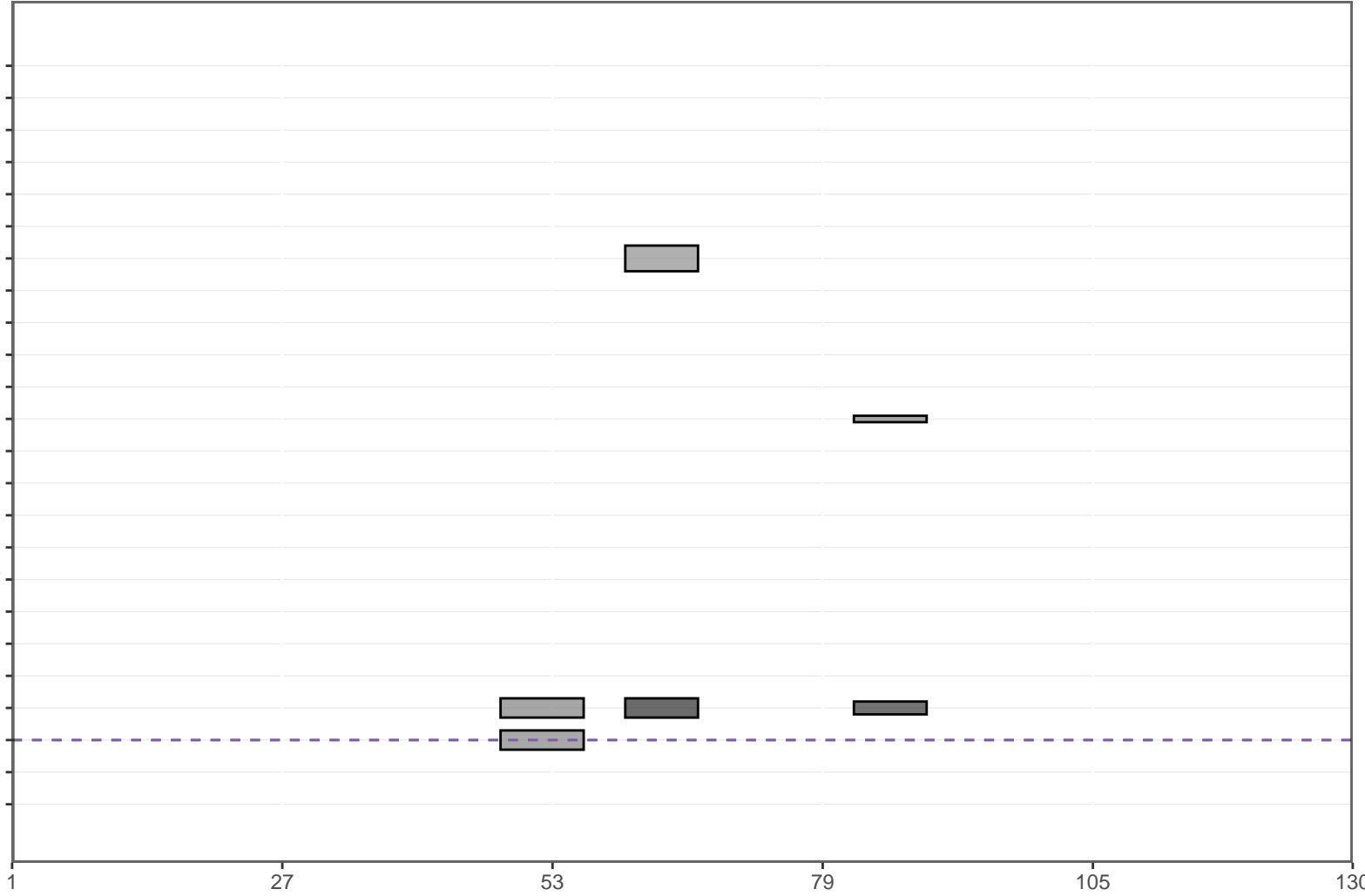
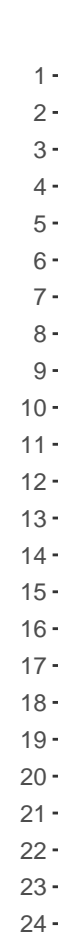
MW indication



Molecular weight



Gel Slice



Pfam Description



Protein sequence:

DPHRVQKTVQLLGRVNDGRALTYRQDKAAISIEQYKTRALPTRQWGFVITTPNSVLDHEEAGRQNVGGQVGFY*

NbL13g19950.1 serine/threonine_protein_phosphatase_2A_55_kDa_regulatory_subunit_B_beta_isoform [MW = 57.46 kDa]

No. of times detected



log(intensity)



Values from



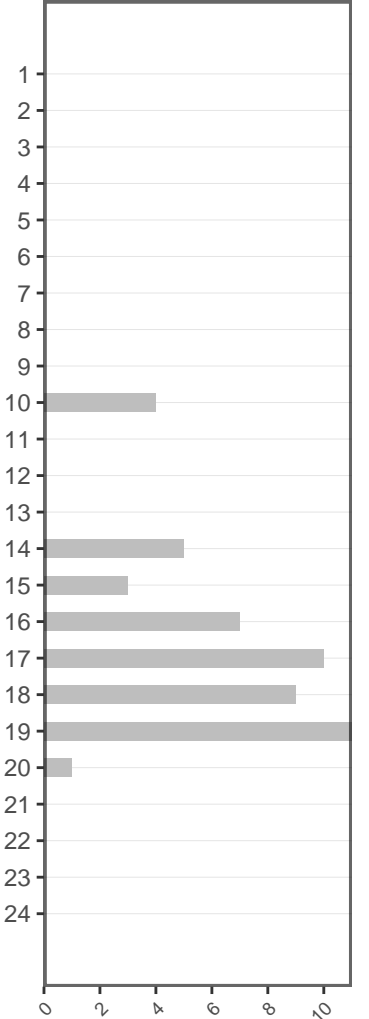
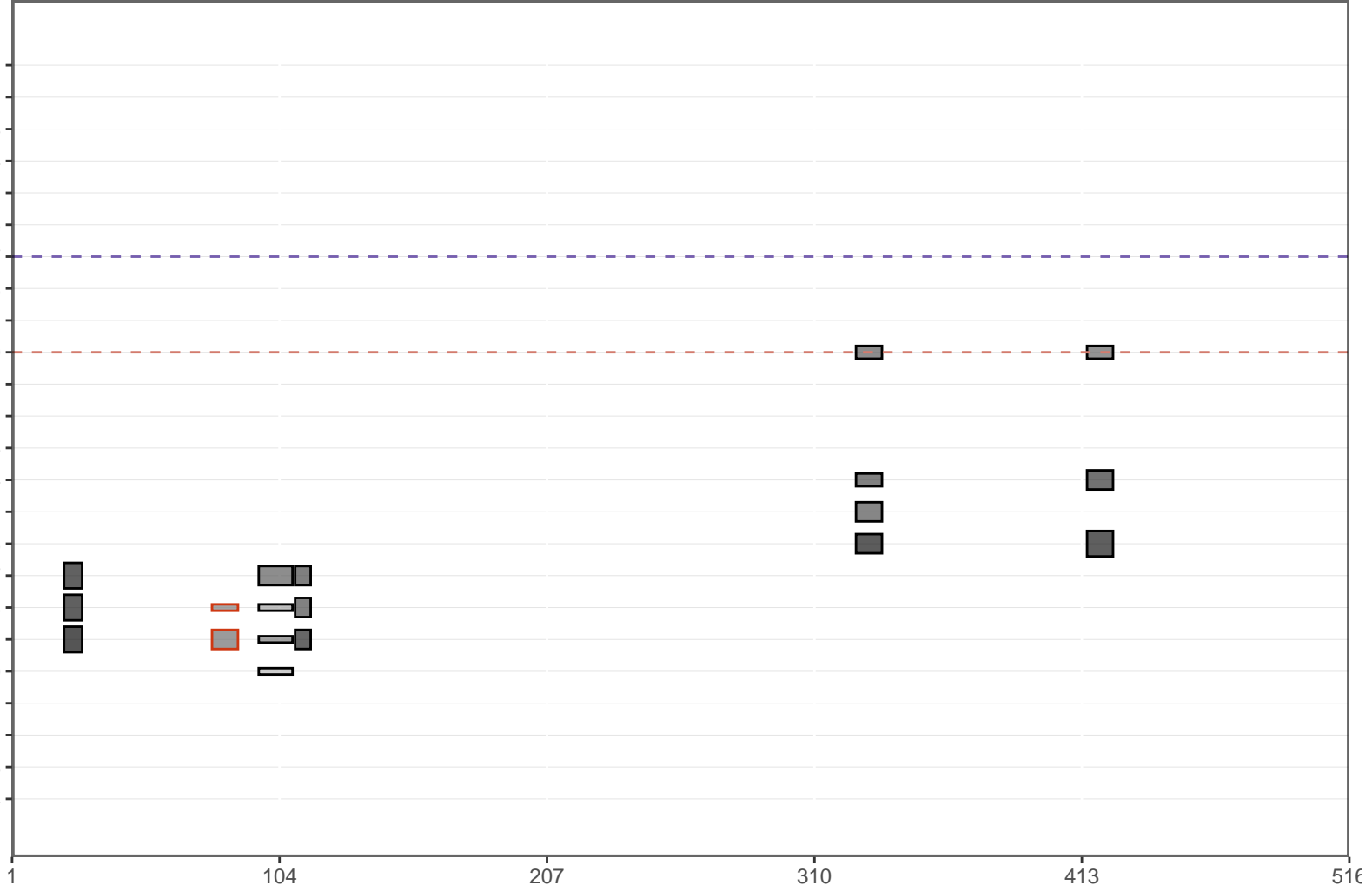
MW indication



Molecular weight

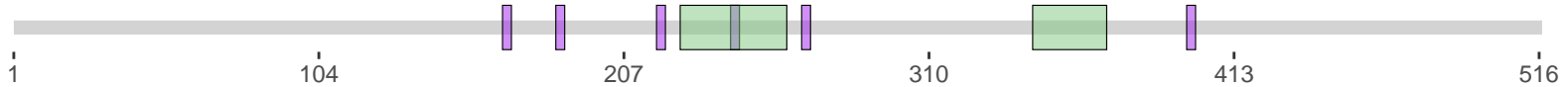


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

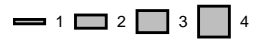


Protein sequence:

NSDGETFSADDLRINLWNLSEISNGSFNIVDVKPTNMEIDTEVITSAEFHPTHTNLAWSSEKGGSRILDLRQSAICDSEKLFEEGEAPGSRSFTEHAISGIDKFSKDRVYLSRDYMTLKLWDMDDPVSFTQVHEVLRPKLGDLYENDSDFDKFECCLSGDLRATGSGYSNLFRVFGGAAGTTEATLEAKNPMRRQVQTPSRPRSLSSGIFRVVRRGSESPQVANGNSDFDTTLLHLAWHPTENSIAGAAANSLVMYVA

NbL13g19810.1 beta-galactosidase-like [MW = 67.48 kDa]

No. of times detected



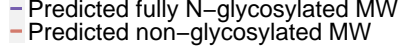
log(intensity)



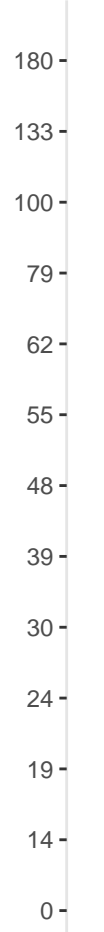
Values from



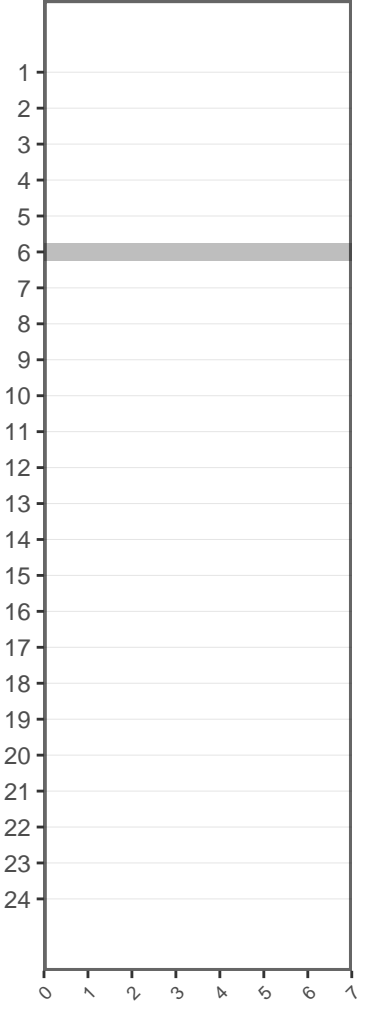
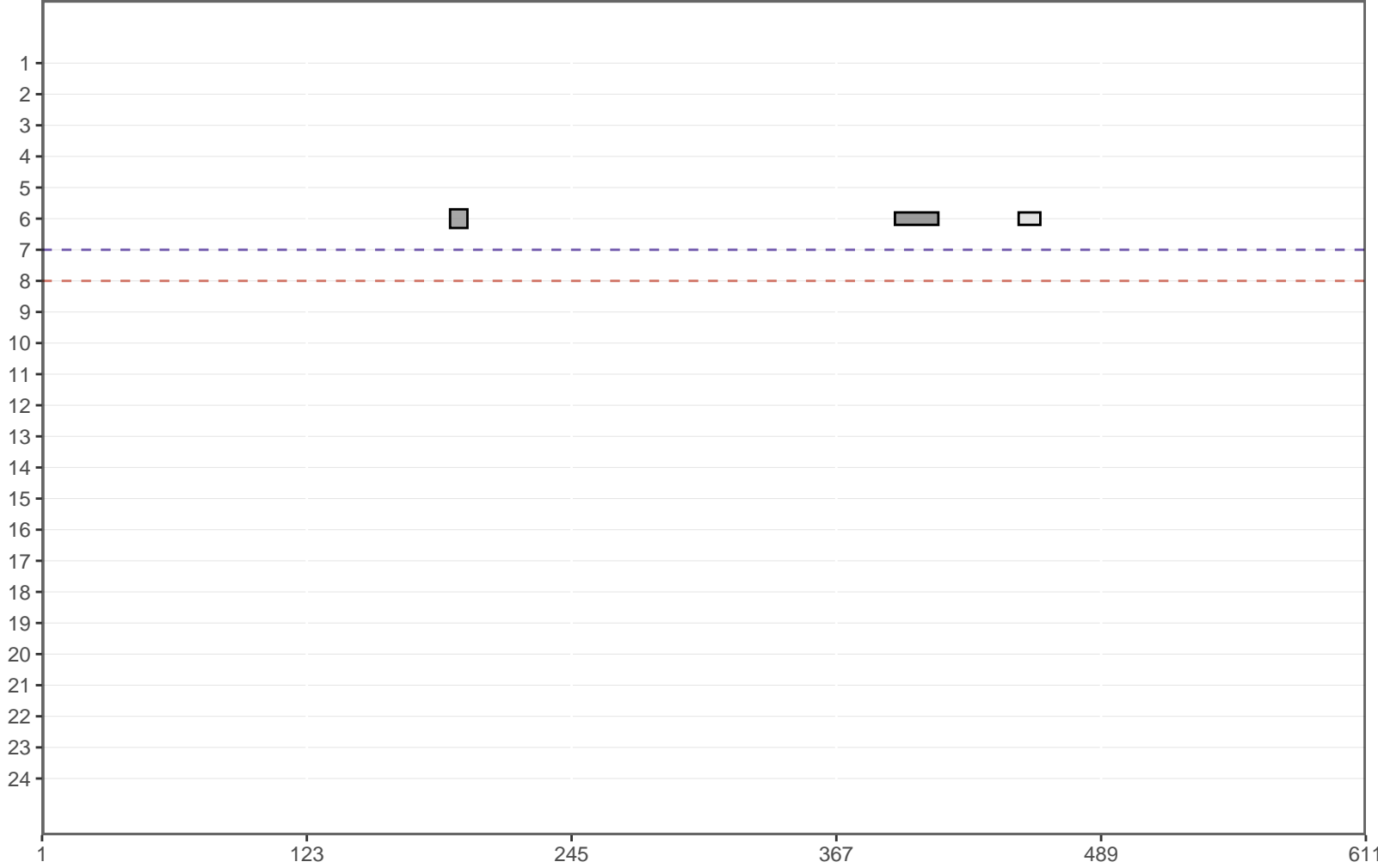
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

KAVNLRAGVNGISLSL6IAVGLPFGPIFETWAGVIGPVLISGLNEGKRDLETWGWYKVKLKGALSLHLSGSSSEVWEGSFVAGREPLTWYKTFNAPAGNEPLALDNTMKGKGVWINGGSGRYPWPGYKASNGACNYAGWVFEKIKLNSGGEASQRWYHPRWLYPTGNLLVFEWVGGEFHGISLKRIVASVGDADNEWGPOLYVWGMGASGVDRPLRPAKHLSCASGGKISIKFASFGTPOGVGGEFREGSGHAFHSYDAFYERYCIGRNSCI

NbL13g19780.1 WD-40_repeat-containing_protein_MSI4-like [MW = 47.62 kDa]

No. of times detected



log(intensity)



Values from



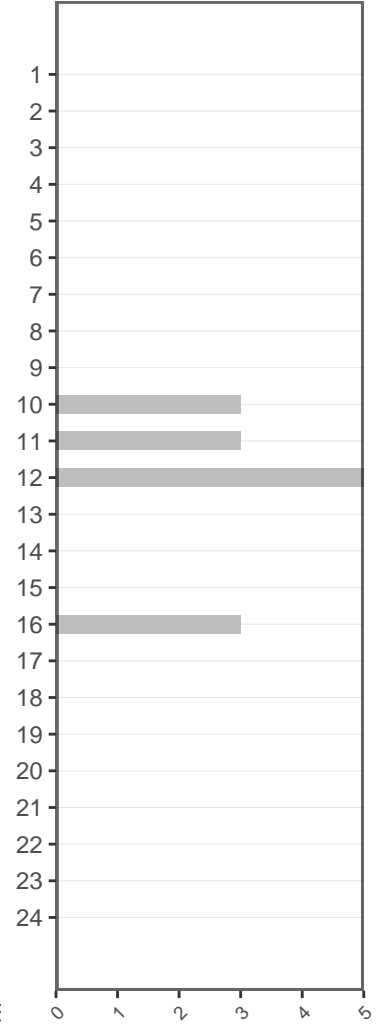
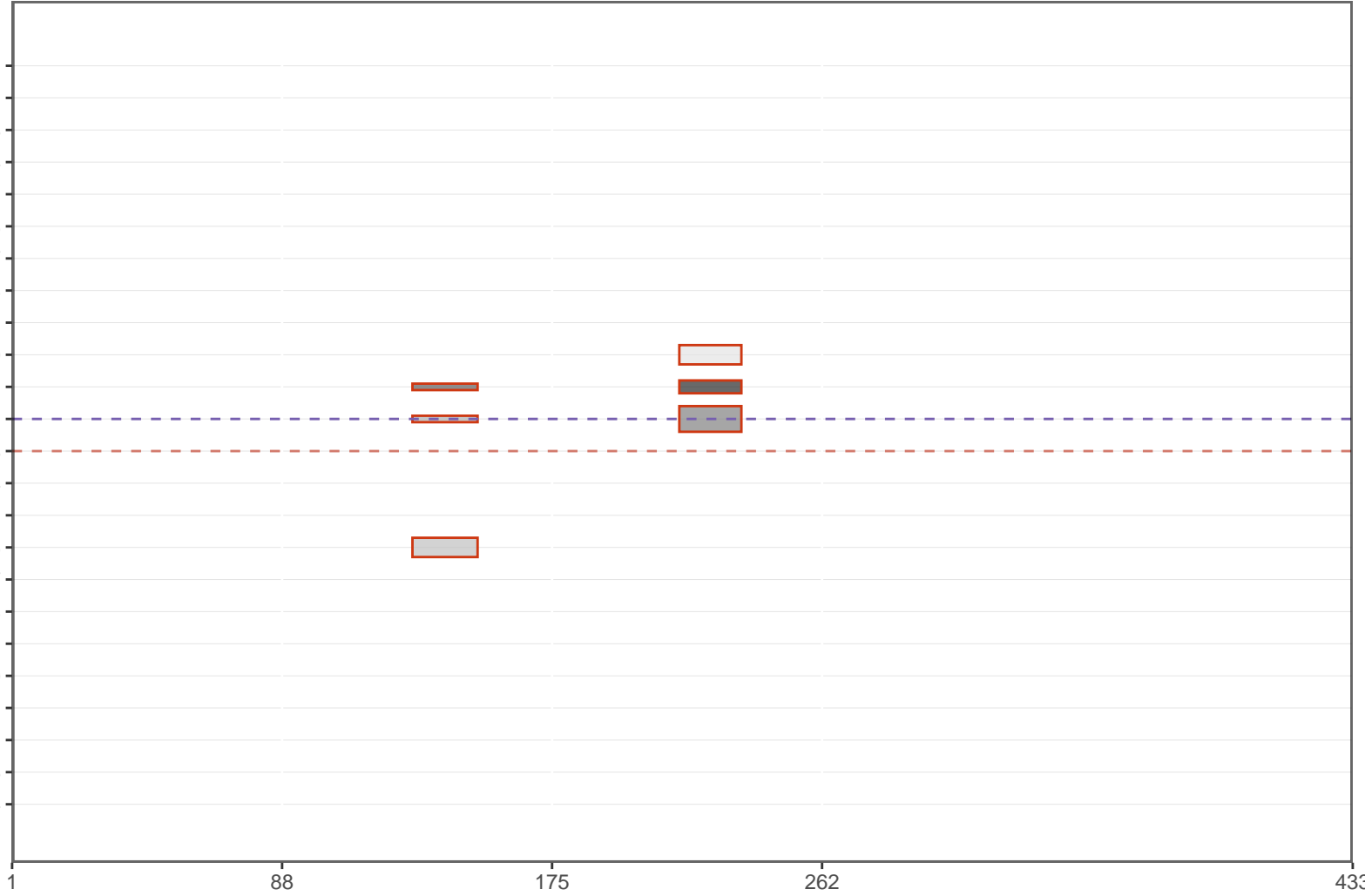
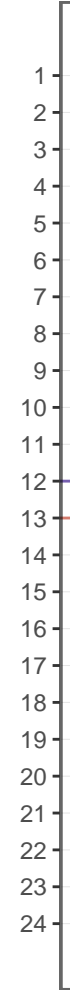
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

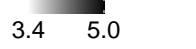
STLAADGATKSPGGGASBNKPAEGPTVARGIFQGHDDTVEDVGFQPSASQEFQVGGDDGCLLWDARTGSSPAWVKEKANNADLHGVDFWPHDNLHVTGSDNTRIMFDRRLKLTGGVGSPIHFEGHTAAVLGVQWSPKSSVFGSSAEDDGLNVDHEKIGKIMEDSAGRIKASTSPGLFFRHAGHRDKVVTSTGMQGHGFLVSGMMKVKVLEVVHRYGE

NbL13g19760.1 protein_HOTHEAD-like [MW - SP = 61.68 kDa]

No. of times detected



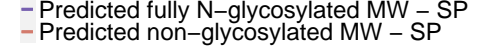
log(intensity)



Values from



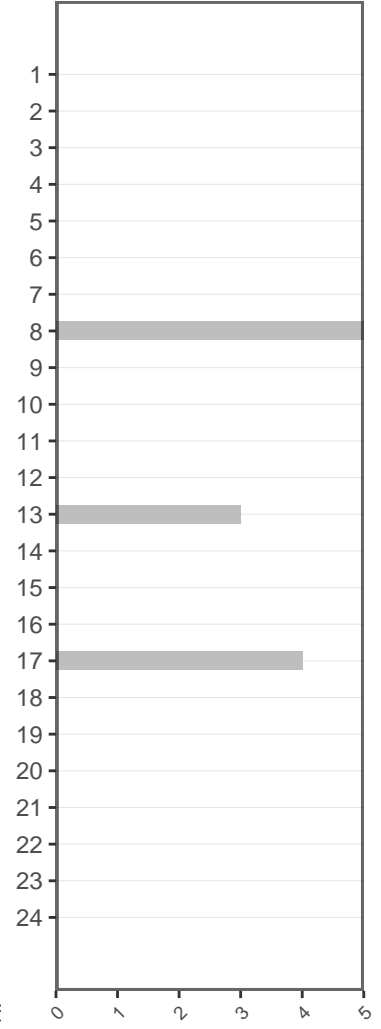
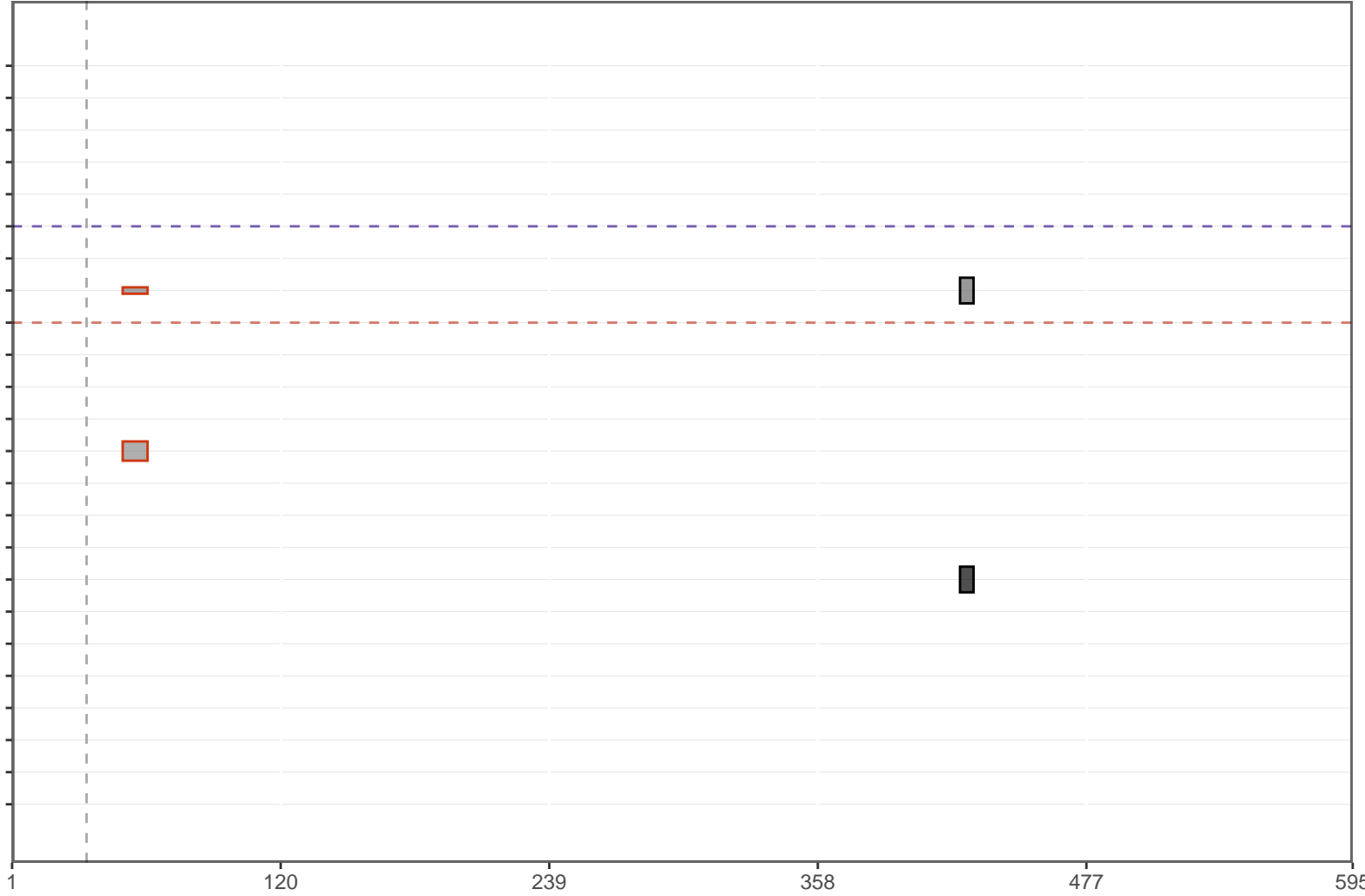
MW indication



Molecular weight

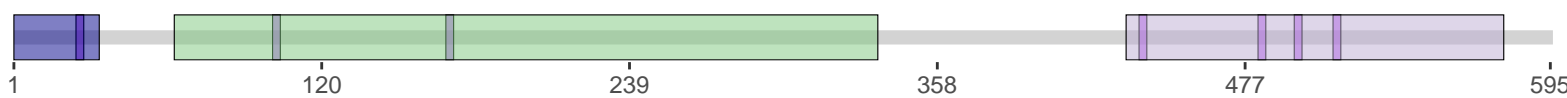


Gel Slice



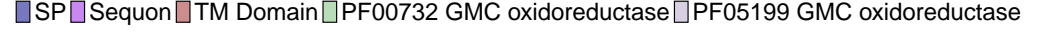
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

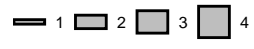


Protein sequence:

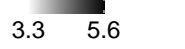
RKGSIIIVSSGAIQSPHLMBSGIGPKAELEKLNIPVLDNKYYVGGGMSDNPNTIFVFTNRHVEQSLHDTVGTKEGVHEASSGFGGSGSDSHGNHGVAEAGKGLSTPFPKQRTFEAEAYRRSKKNIPHELFKRGFLEKIKATPLSRGNISLVITNADNDNPLITFNYSFHPKDLKRCVDSGIRVKKAKSKHFTNYTQCDKETLHLNMEVQANNLIPKHTNNTQSLQFGKDTVITWHYHSGGHVGVKVAAPDVRVLGVHRLRWVDSSTFEESPGTNPQATVMMGRYMGV

NbL13g19680.1 chaperonin_CPN60-like_2_mitochondrial [MW = 61.07 kDa]

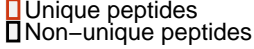
No. of times detected



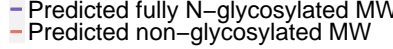
log(intensity)



Values from



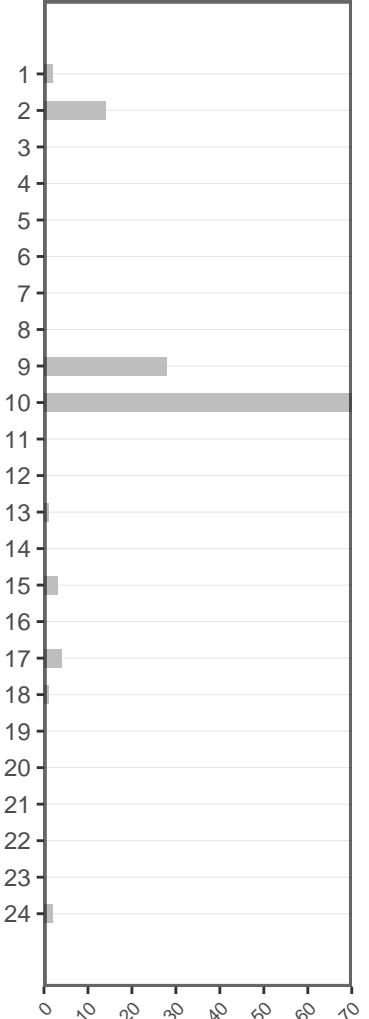
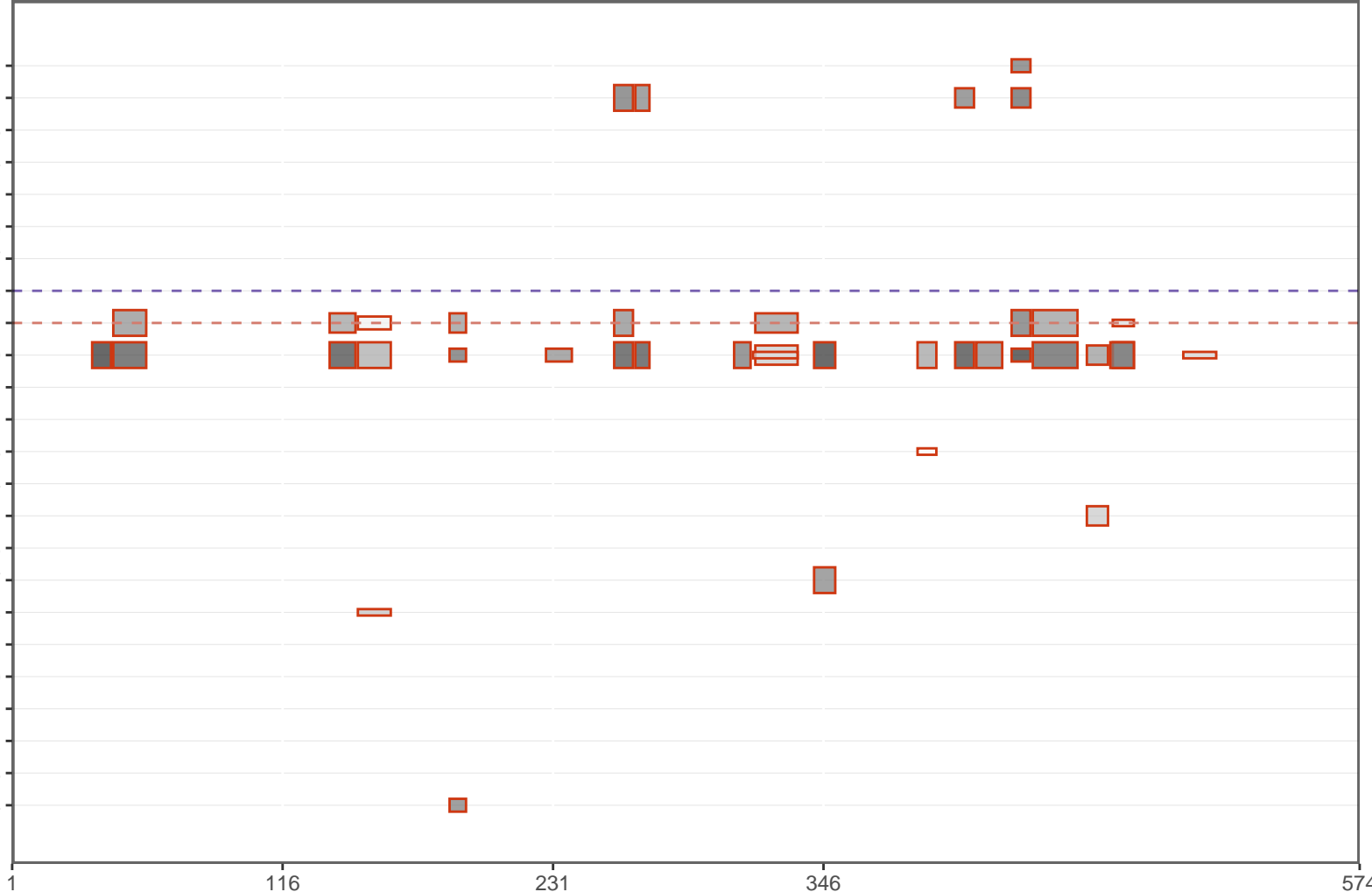
MW indication



Molecular weight



Gel Slice

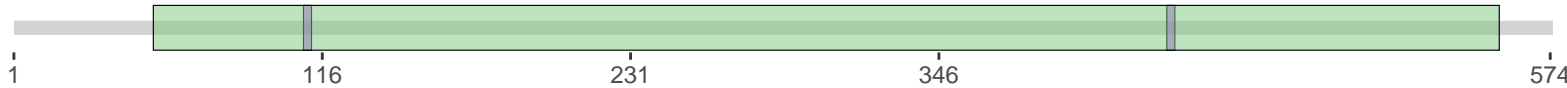


Protein length

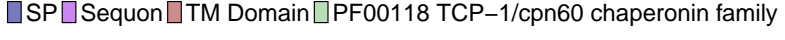


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IPLLIVAEIVESDLSMLNKHAGVKKVCAKAPGFGNRRANLEDLAVLTGGVISEERGLDNKVFQDMLGTAKKTVSLDDTLVHGGDGLKLEERCEGLRIAKEKSSAMFDKEKAGERLSEKLGSGVAVFKVGGASEAEVSEKRDVTDALNATRAAVEEGVPGGGVALLVATKGLKDLGTANDGGKQKVEIENAKAPFTIASNAGVDGALVGLKLEGGDNLGFDAAAGTYRHMVKAGIDPLKVVRTALVDAASVLSLLTTEAAIVDRGKKNPLNRFPMGDC

NbL13g19600.1 glyoxylate/succinic_semialdehyde_reductase_2_chloroplastic-like [MW = 38.9 kDa]

No. of times detected



log(intensity)



Values from

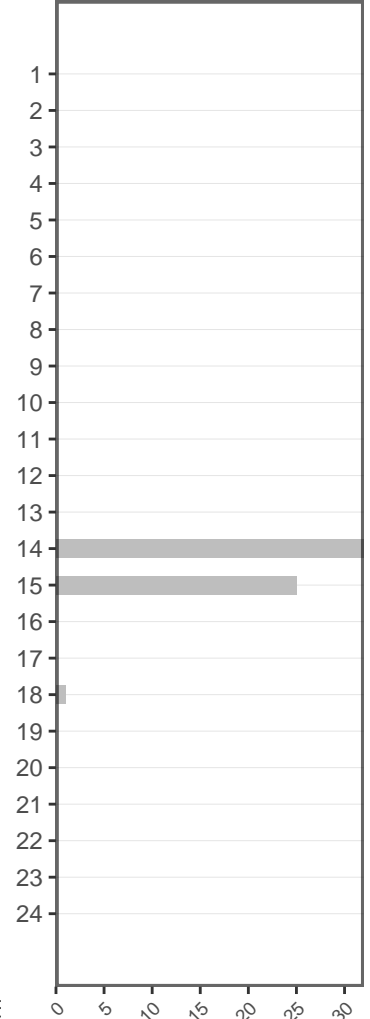
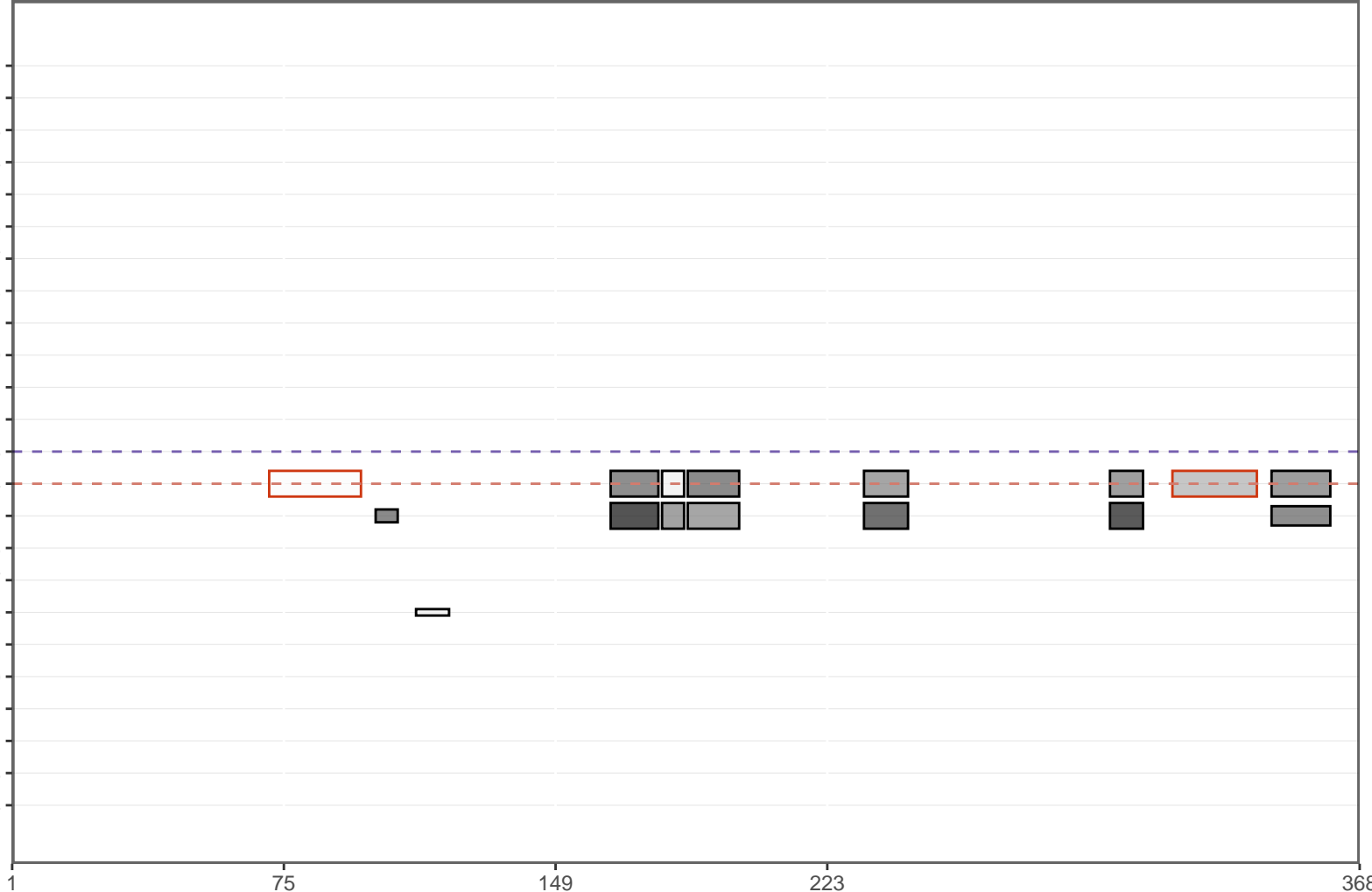
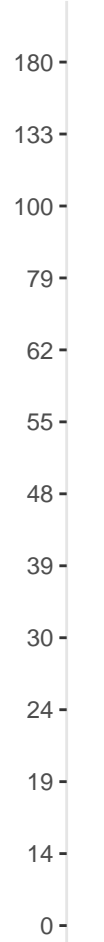


MW indication



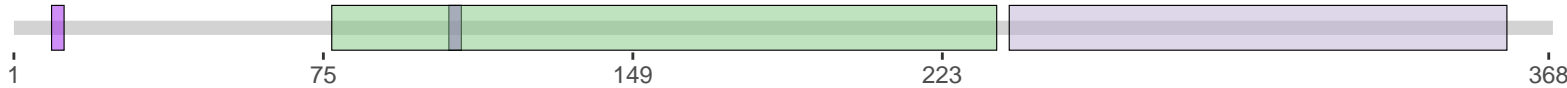
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF03446 NAD binding domain of 6-phosphogluconate dehydrogenase
- PF14833 NAD-binding of NADP-dependent 3-hydroxyisobutyrate dehydrogenase

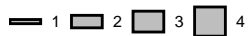
Protein sequence:

ITVDGETSKLICEHRATGAHFLFAPVSGSKKPKEDDGLFLTAGDNLVLYETVAPLLDLMGKSRFYLGEGVNGAMKLVVNMVMGEMMASFSEGLVYSEKVGLOPSPVLEVISLGAISAFPMYAMKGPSPMVKSLVPTAFPLKHDQDKDLRLALGLAEGVSGPTFAAATNEIKYKAKSHGLSDGDFSAVIEALKMKLQRET

NbL13g19480.1

dihydrolipoyllysine-residue_acetyltransferase_component_2_of_pyruvate_dehydrogenase_complex_mitochondrial-like [MW = 38.23 kDa]

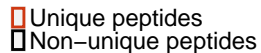
No. of times detected



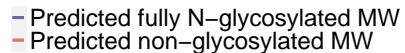
log(intensity)



Values from



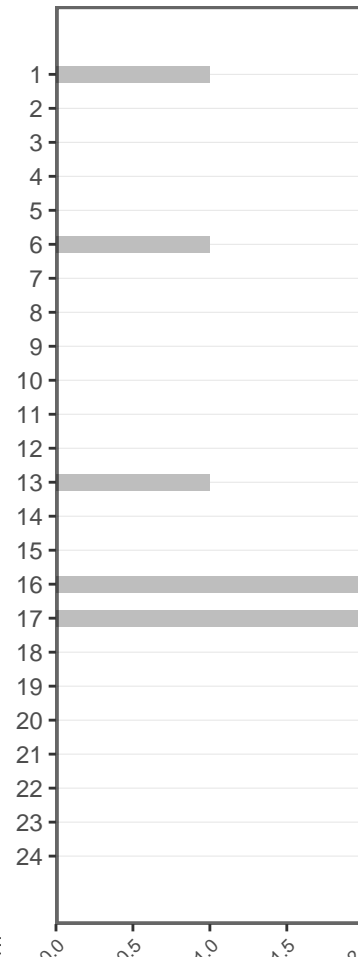
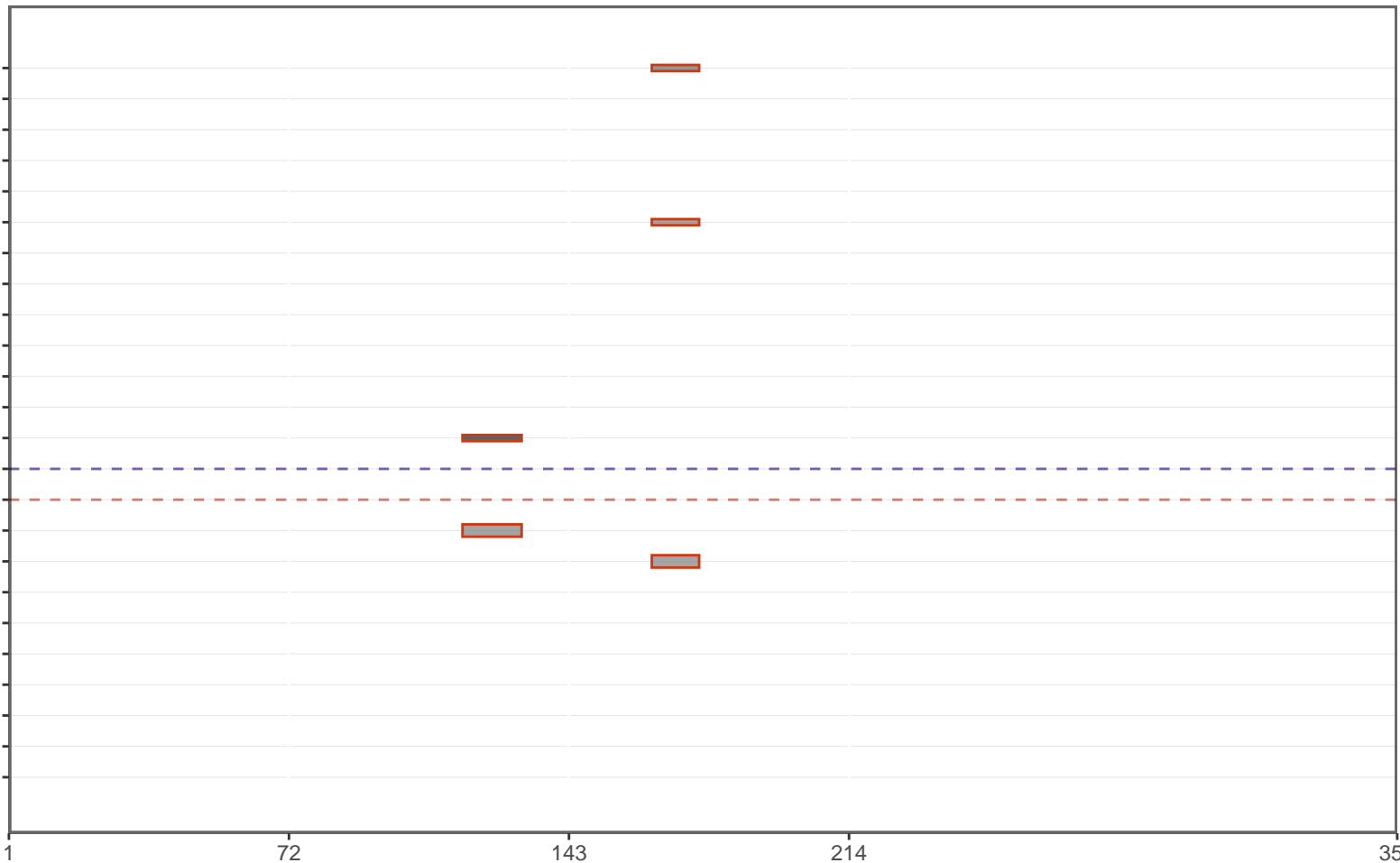
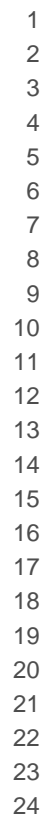
MW indication



Molecular weight

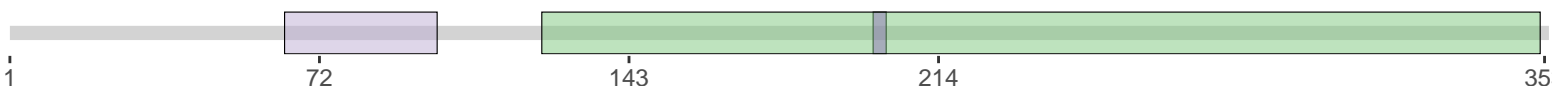


Gel Slice



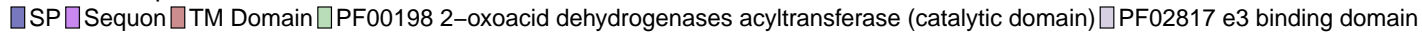
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LNLSYQEASGGKXLSVNDLYKAAALRKYPCNSRWTFYRQYHININAVQTDNGLYVYVVRDADKKGLSTIAEEVKSLAKAKENSLKPDQYEGGFTFVSNLGGPFGKQKFCANIPPOSALAVGSAERRVPIGTGDDYKFKASMMISVTLSCDHRVIDAVGAEWLKAFKGYEVSPEMLL*

NbL13g19410.1 threonine_synthase_chloroplastic [MW = 57.7 kDa]

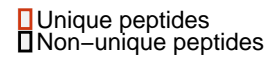
No. of times detected



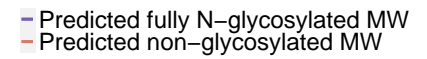
log(intensity)



Values from



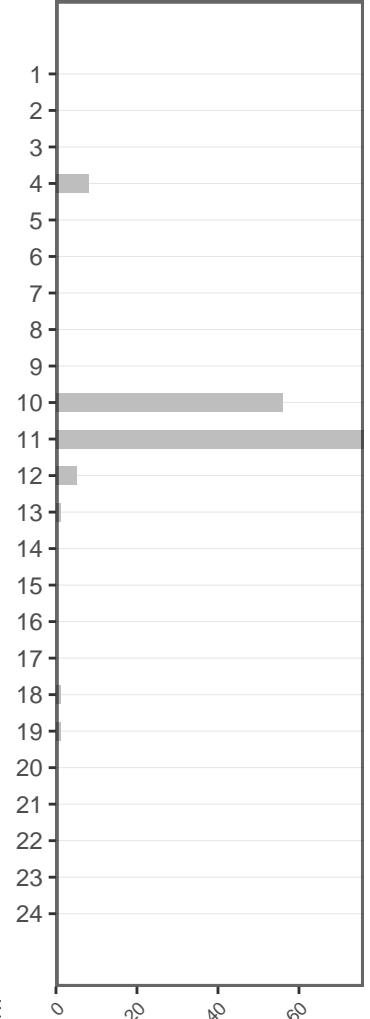
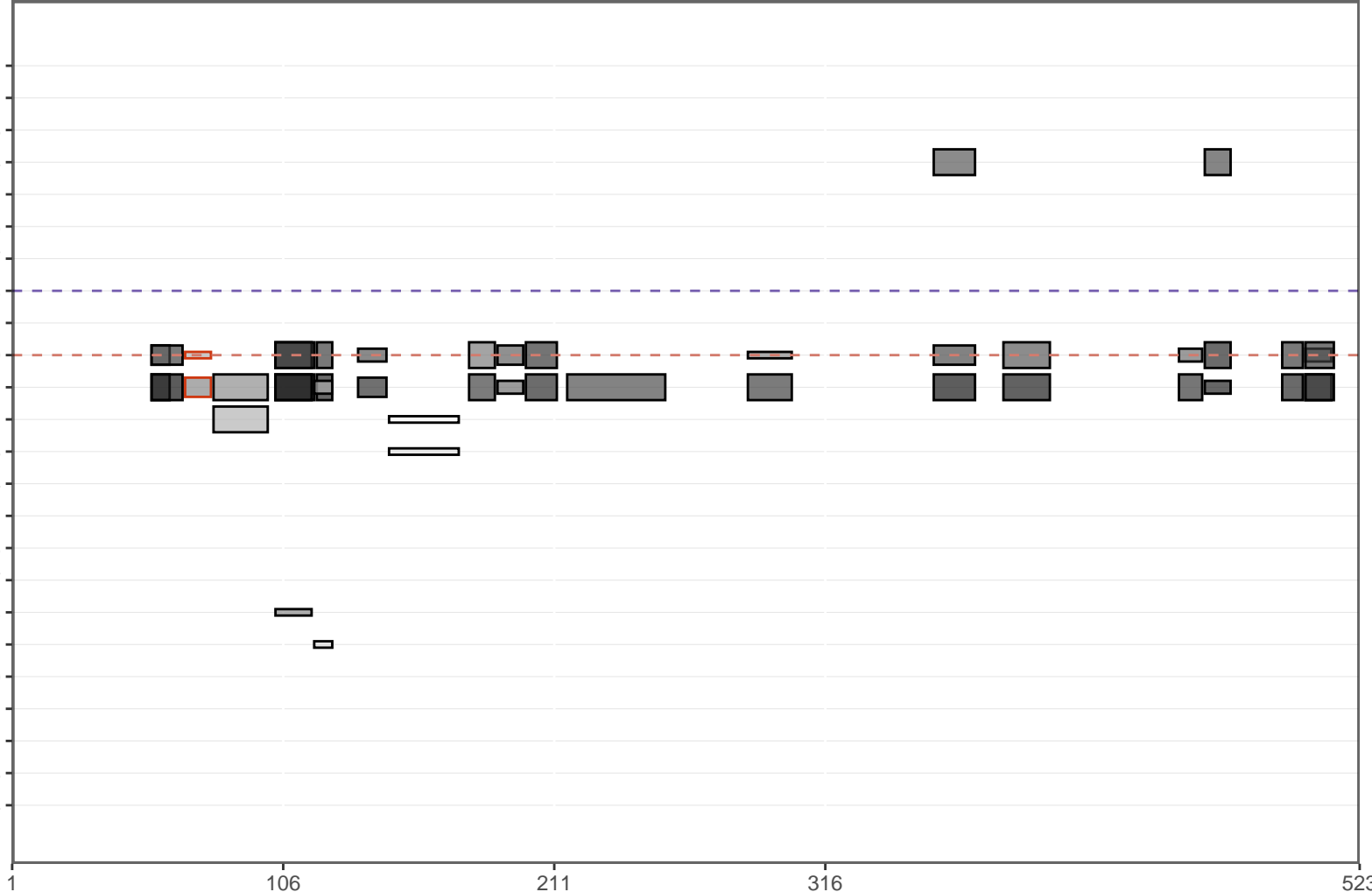
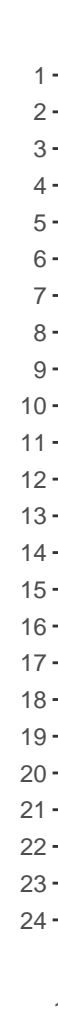
MW indication



Molecular weight

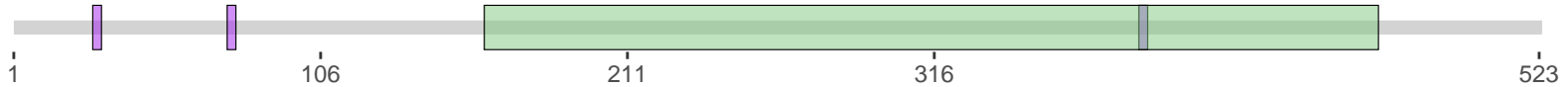


Gel Slice



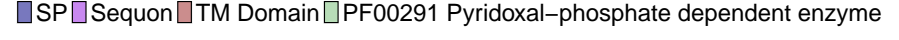
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PSIVFLPANKISMQLVGPANGAFVLSIDTDFDGGMLRREVTALPLHLNBLRLEGGKTAIEILGGDFWQVDPWVIVPGGNLGNVAFYKGFMMKELGLVDRIPRLVCGAANANFLVLYHKSGWKFQPKYKANTTFASAKIGKQDPVSDRAVFAKLNKGGVEEATEEELMDAMQADSDTGMFICPHTGVALTALFKLRNSGVIGVNDKTVVSTAHGLKFTGSKDHYHKEIKDKMKGKRFANPPVEVKAQDFGSMQVLDLKKVLLSKNAKHP

NbL13g19370.1 phospholipid:diacylglycerol_acyltransferase_1-like [MW = 74.19 kDa]

No. of times detected



log(intensity)



Values from



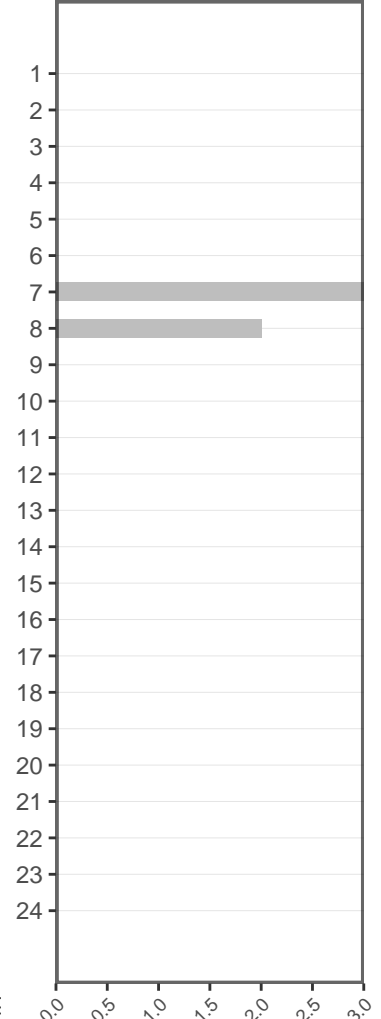
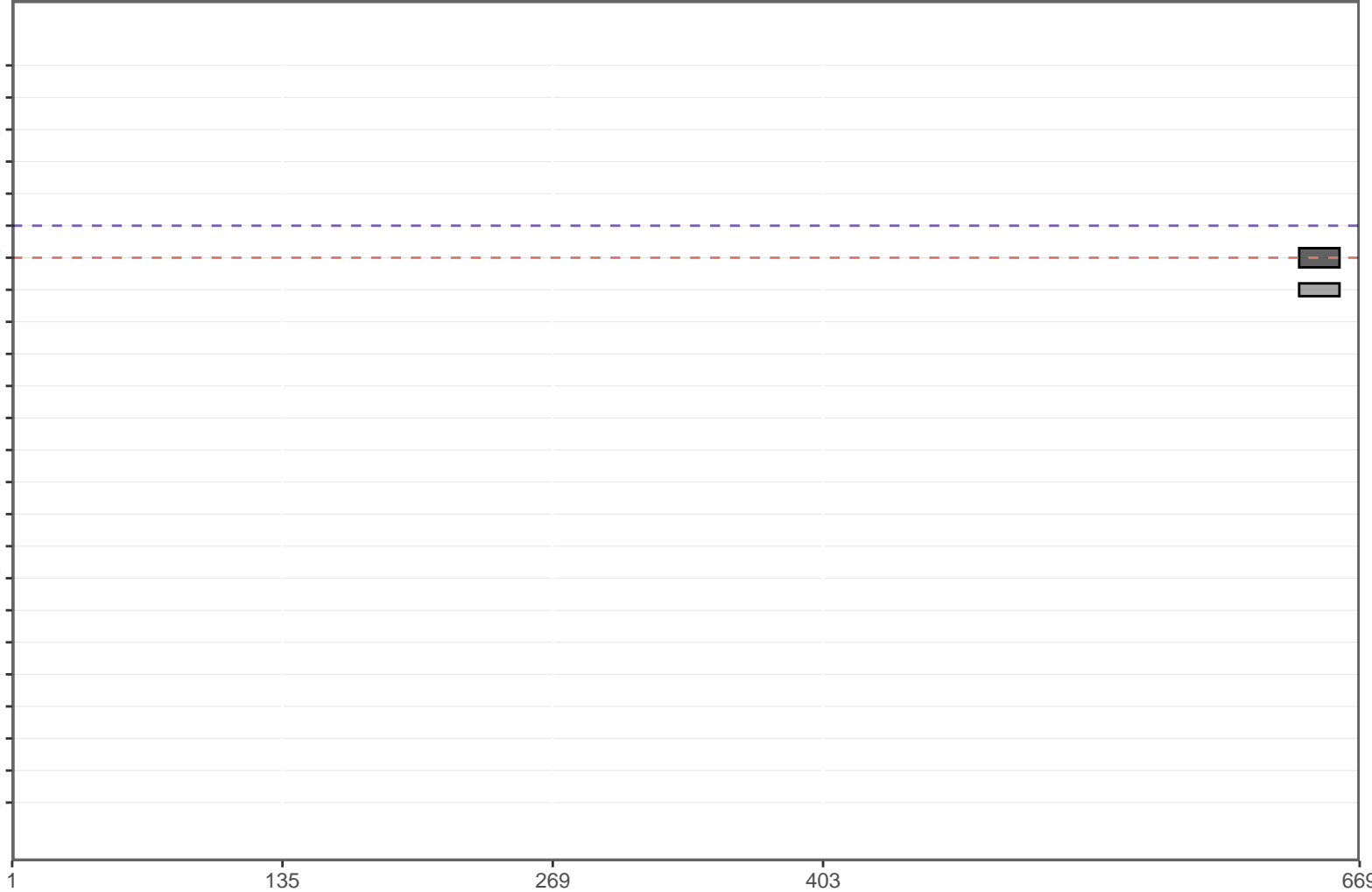
MW indication



Molecular weight



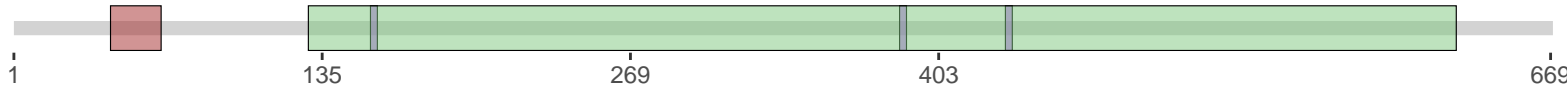
Gel Slice



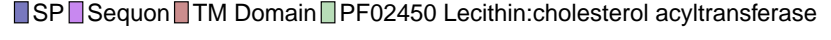
Protein length



Pfam domains



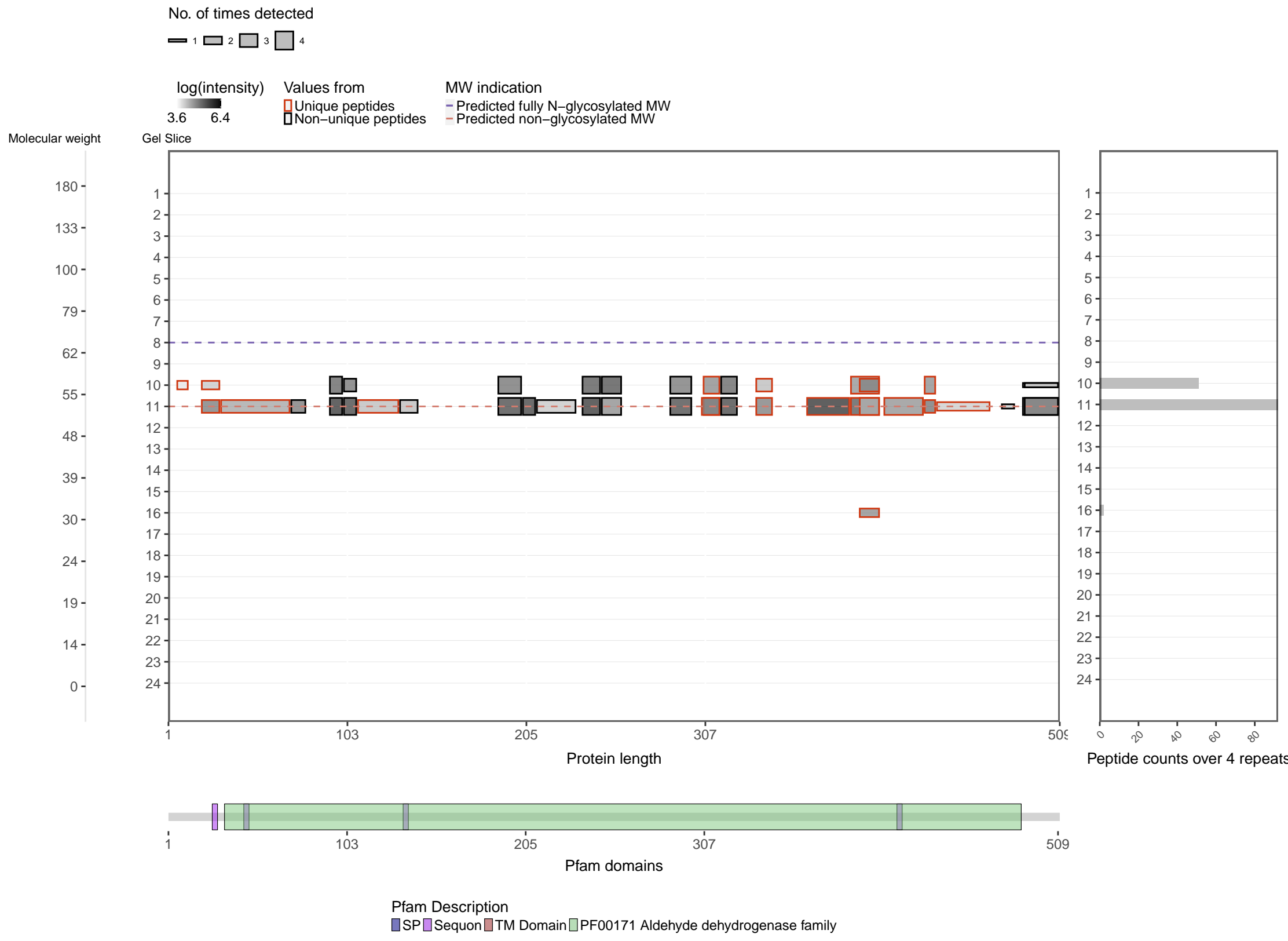
Pfam Description



Protein sequence:

DLFHFQTLLEHMKMTRTWSDTMSMIFRGGGTTWGDLEWSPREGYSPCKSKSKDAAGISGSDENRTTDSNAKYKYVYGRMISFGKDAKAKHSDLKRDFRGAIVKGSNVAANSQDVAWNEHYHDMGVSGAKAVEEKVYTAGIELLDDFVAPKMMARGSAHFSYGIADLDLKYSHYKYVSNPLETKLDPADPMEIVSMYGVGIGTERAVVYRRMPTAGCNFFQIDASVDEEDEDGLKSGVTVDDGETVPALSAGFMKANGWRGRTRFNPSSGKTYIREYTHAFPA

NbL13g19170.1 aldehyde_dehydrogenase_family_7_member_B4-like [MW = 54.57 kDa]



Protein sequence:

TGSSKYGLAVQDTYNGRFGKLELLESGNNAHMDADIELAVRELFVAAGTAGDRTTORRLLVHETVYEVKLEPLVDYKQVKGIDPLEKGLLPLHTRTSRENFQKGNKSGGGKLTGGSHSEGNFVHPTVEISKAEVVKELFAPLVYMKPKSFEAEVNNVPOGLSSSIFTRNPGVMPKRWGAQSGDGGVNNIPTNGAEIGGAFGGKGTGGREAGSDSWSKQVMRRSTCTINYGNELPLADGIFG

NbL13g19160.1 subtilisin-like_protease_SBT1.4 [MW - SP = 79.67 kDa]

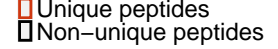
No. of times detected



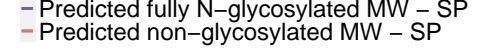
log(intensity)



Values from



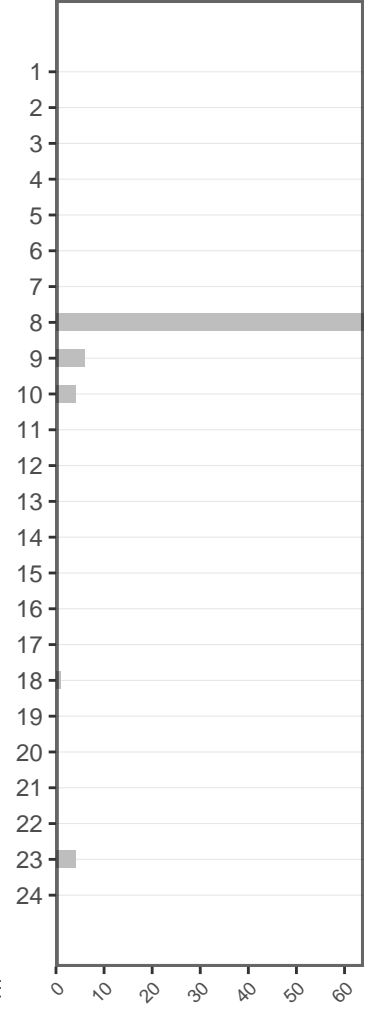
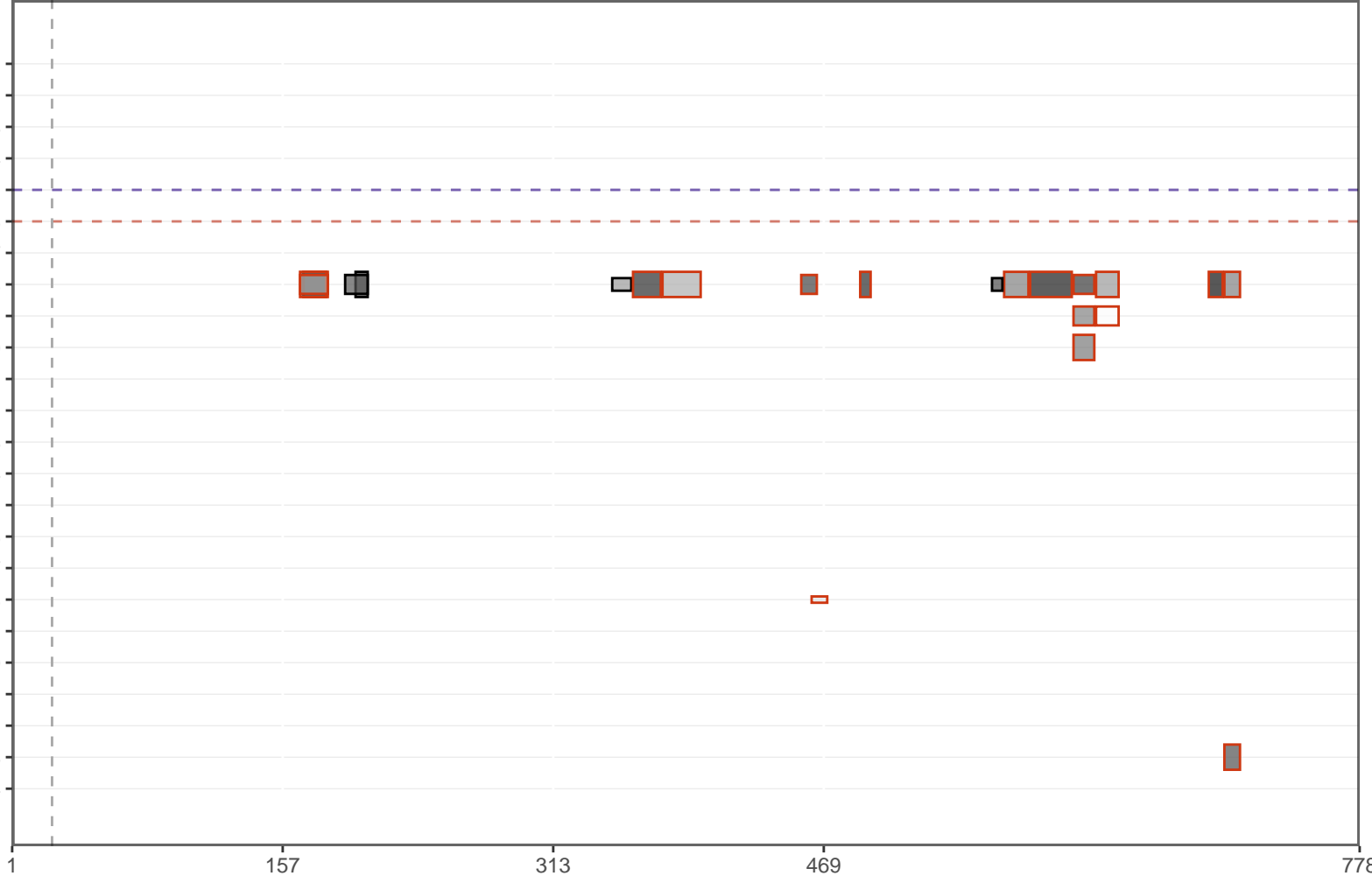
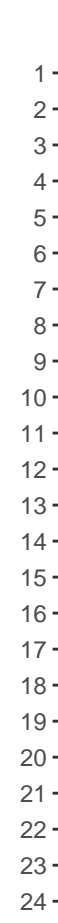
MW indication



Molecular weight

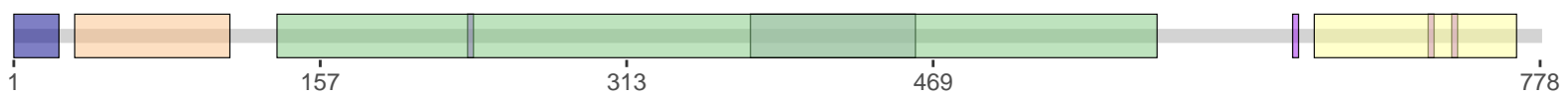


Gel Slice



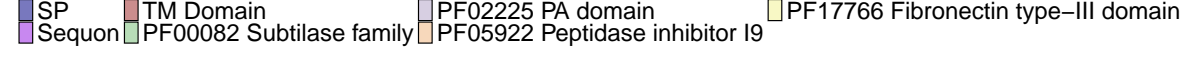
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

.PLVYSGDCSSQLGYPGMLDPSKVGKIVLGDRRGNARVEKGSVAVLAGGAGAMVLANLADSGEELVADSHLLPATMVGKAGDEIRDYVKSDDSPKATVFKGTGKIGKPSARVIAAFSGRGNHYTPPELKPQVAPGYNLAVGTVGSGIPTDLEIDTRVFEVNIISGTSMSGPHVSGLAALLKAVKPVWTTAAKKSALMTTAVHVDNSGKTFDLDATGQESFPVHGSGHVDPNRALDPLGLVYDIDTKQVDFLGAIGYDKRISPFVKDTSSEVNGSEKNLVSPGDLNYPFS'

NbL13g19070.1 auxin-binding_protein_ABP19a-like [MW - SP = 19.57 kDa]

No. of times detected



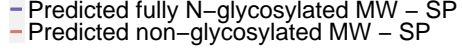
log(intensity)



Values from



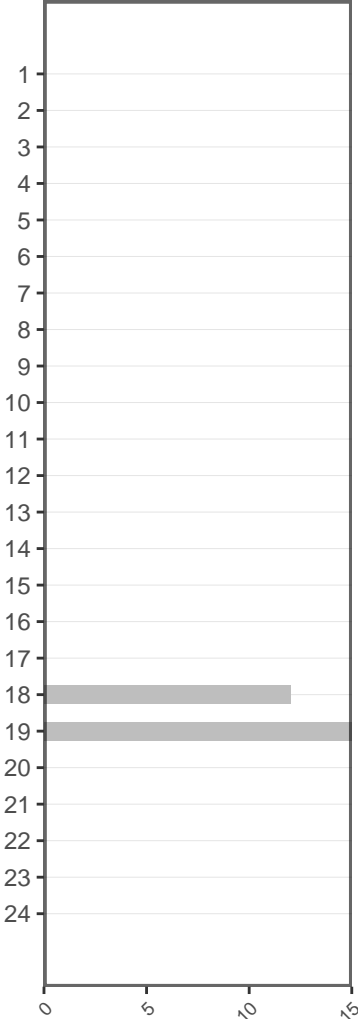
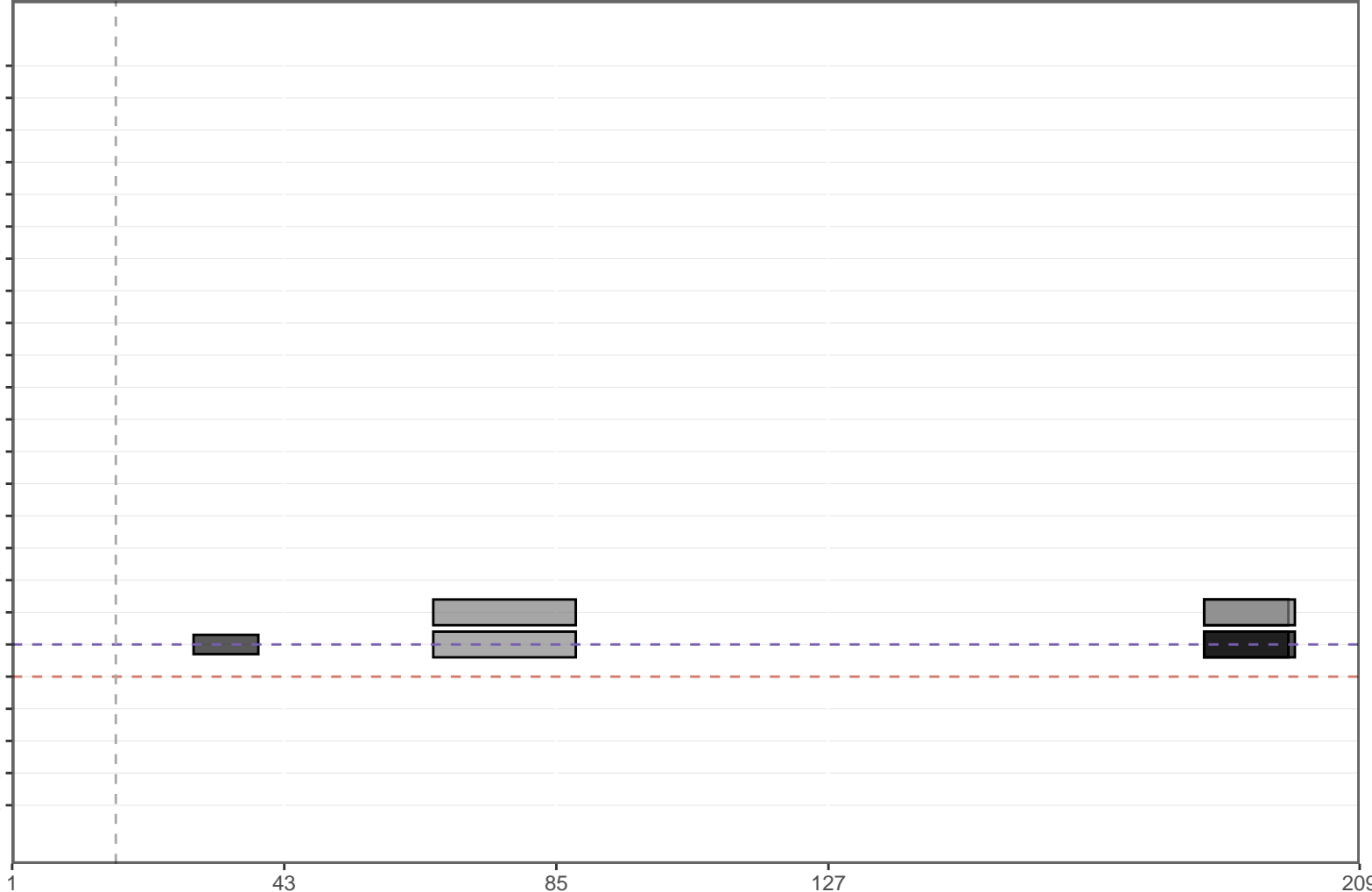
MW indication



Molecular weight

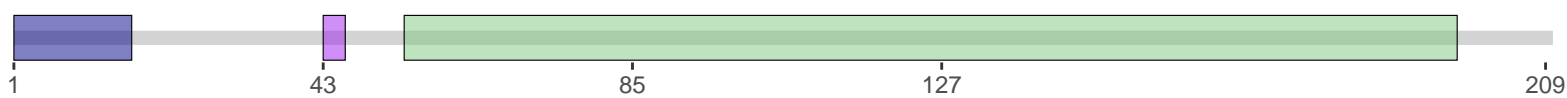


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

APGGVIFPIHTIPGASEVLLVVGGSITAGFVSSANAWLKLKKGDLMEFPQGLLHFQVSDAGYTSVGFVFFSSSSPLQIGTDFALFANDLPTKILVEATTFLDEATKIKLKGVLGGTN

NbL13g18960.1 phosphoinositide_phosphatase_SAC2-like [MW = 92.65 kDa]

No. of times detected



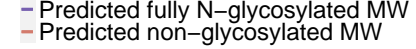
log(intensity)



Values from



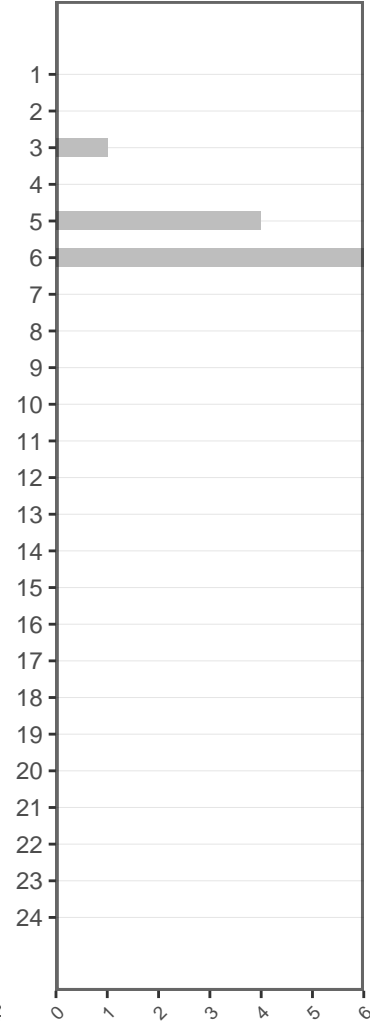
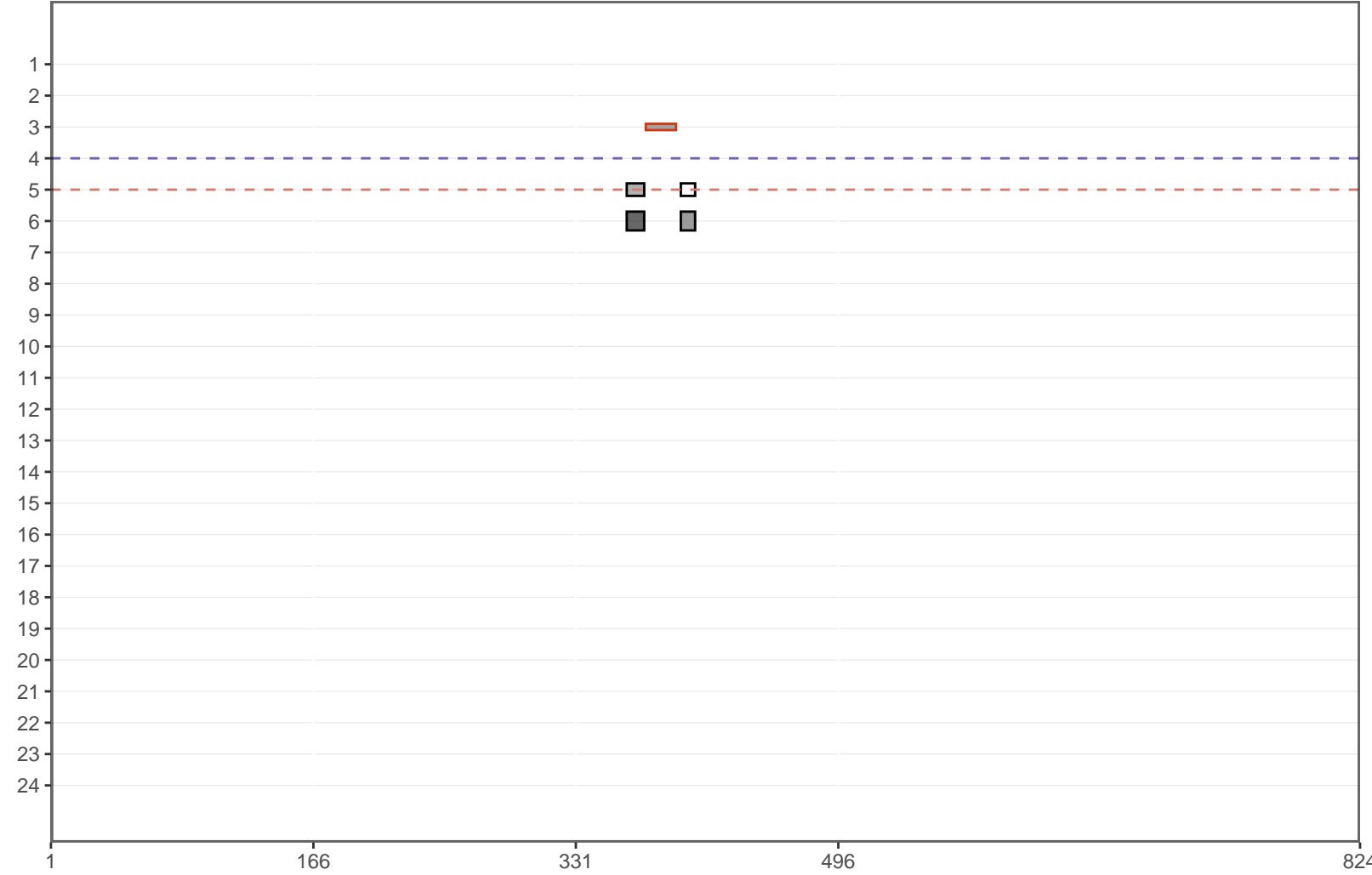
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

GKVAATALDLDTGLFHQQLPAEKSGKLLKFSBTGNTGDDAGKDLGEVGAEPNSGGDLGGDHYKLESLRGRVLRITNDDGLDRTNMAGYVGLVAGLHQLHALGFIDVENLDLADNLMLKLYEAMGDTLALGVGSAANIKFSERRGGWKAATGSGELFRLLGRVYSNAYMDAEKGDANVFLGHFRPQEGKPAWELDDQHYNVGHHGSSLAMETSRSFIKRSLSEGNLKGSSSPVKETETEGTDDSDPLPASAKGGSKLSESTPEIQTCTDSIFTRYTPS

NbL13g18780.1 protein_STRUBBELIG-RECEPTOR_FAMILY_6 [MW – SP = 44.83 kDa]

No. of times detected



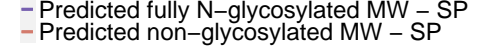
log(intensity)



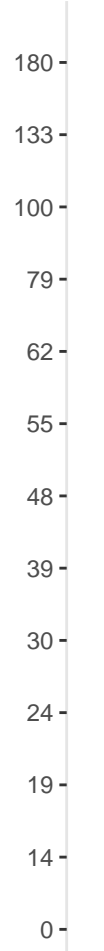
Values from



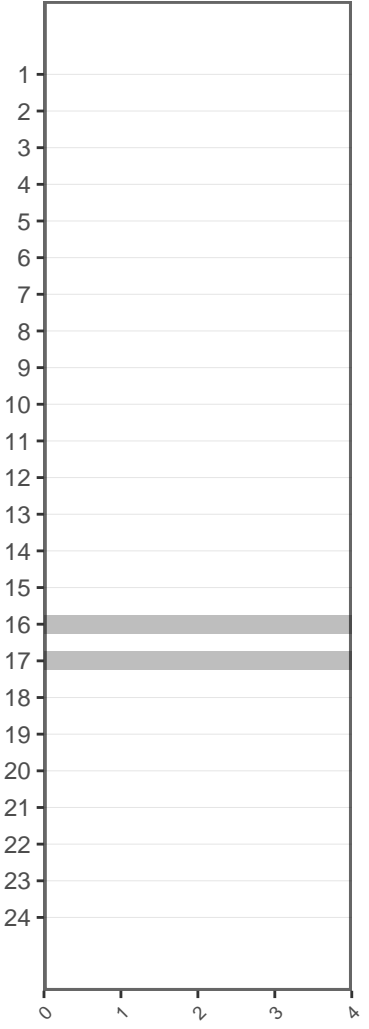
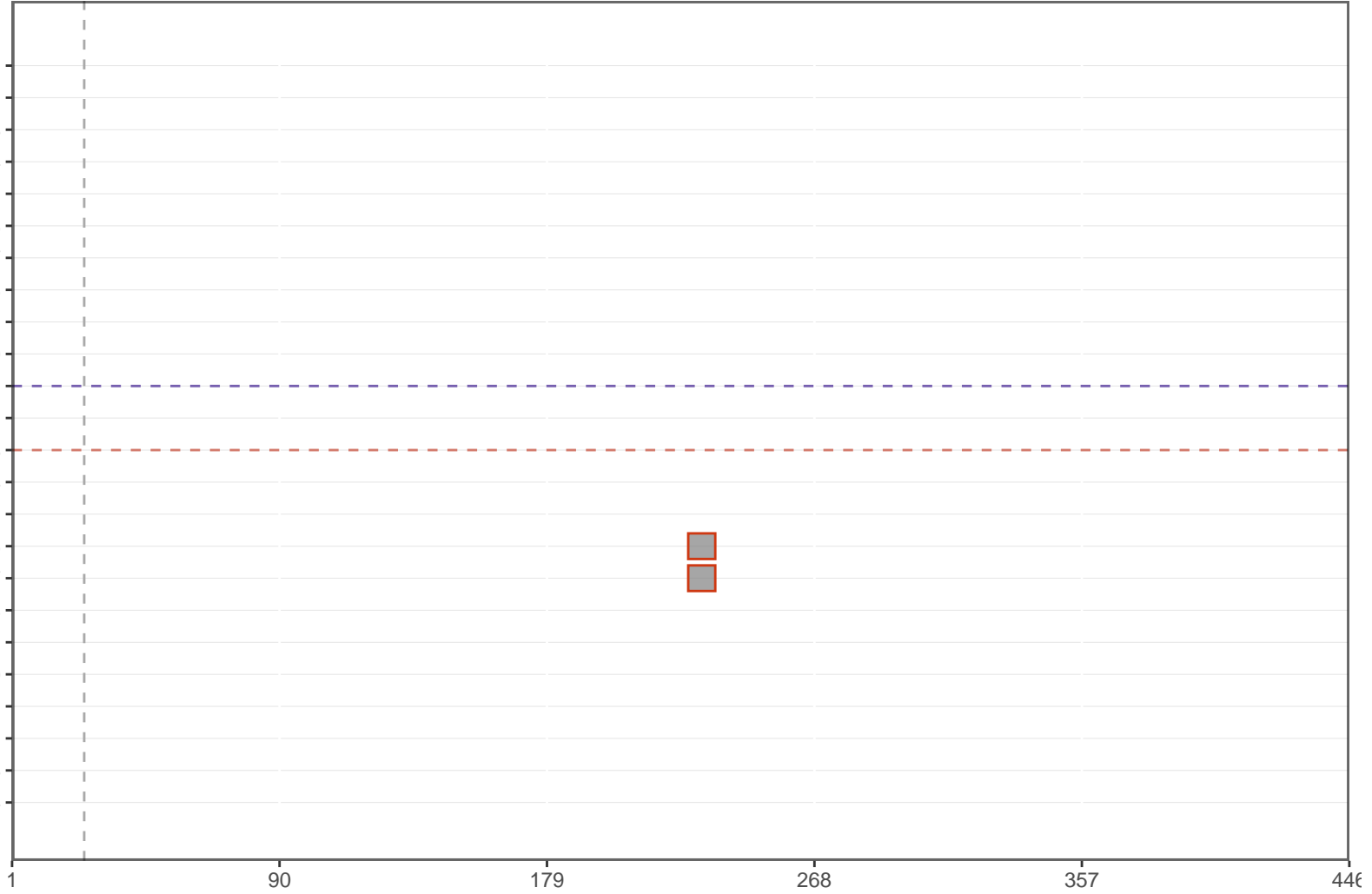
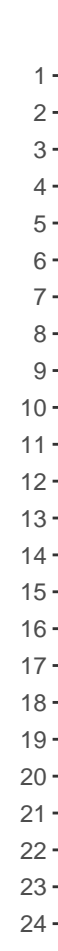
MW indication



Molecular weight



Gel Slice



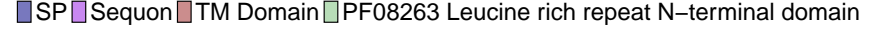
Protein length

Peptide counts over 4 repeats



Pfam domains

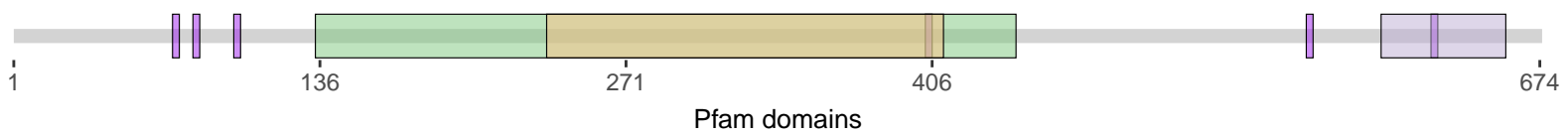
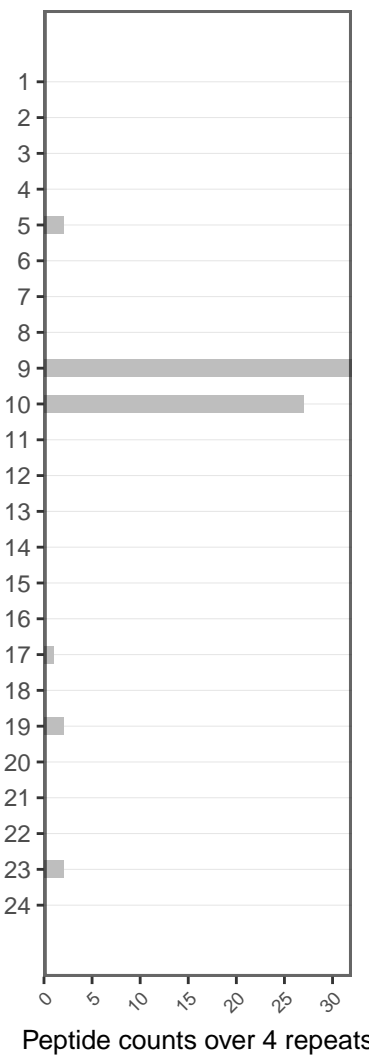
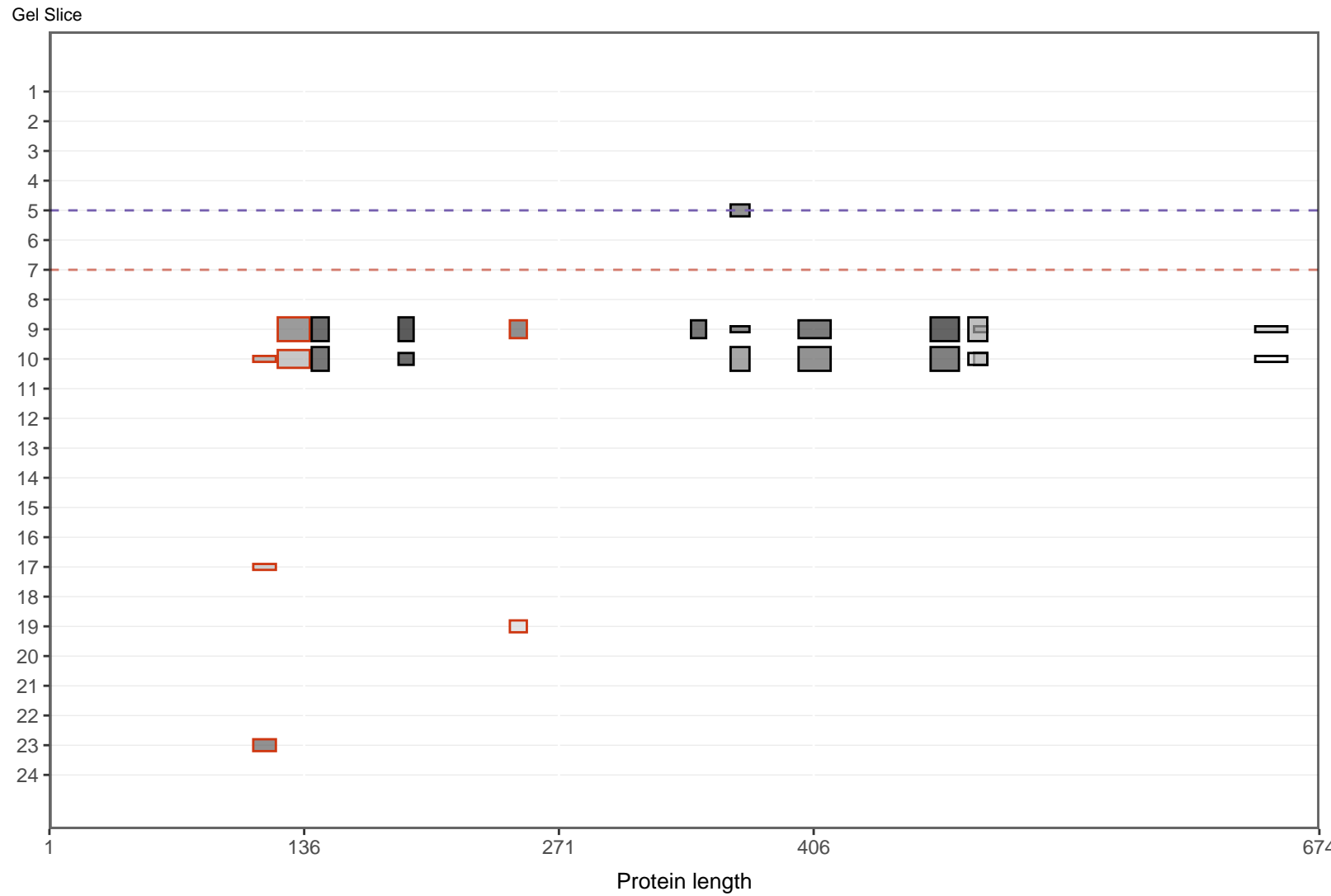
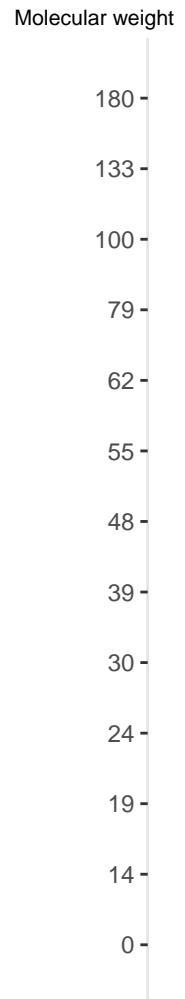
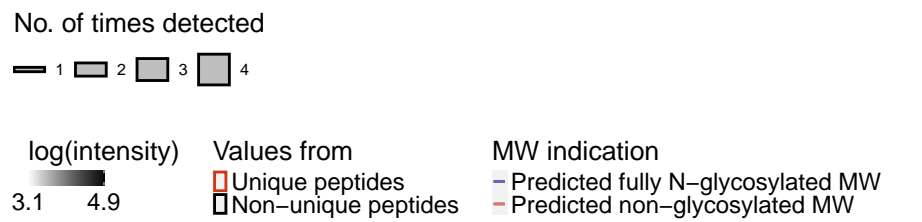
Pfam Description



Protein sequence:

VLANPLDNLNENRFTGWVFDQLKGFVKSNGSNWNSGFAFPFPPPTPASRFDRIHHSKGNNSPFGSGGGGGKGGKGGGAGVIBLVGVAVFFVYKRRSRSSSTDEKHQNGPFAFLASEEVEQEMKTNQASSAPSWKTFEAPVAVLRPPPIERHKSFDEDDIAAKPIVPPKAVNTAKINARQVSIADLGMATDFSDNLGEGSGFGRVYRAGFDGKVFCLPKV

NbL13g18700.1 D-3-phosphoglycerate_dehydrogenase_2_chloroplastic-like [MW = 71.54 kDa]



Pfam Description

- SP
- TM Domain
- Sequon
- PF00389 D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain
- PF02826 D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain
- PF01842 ACT domain

Protein sequence:

VTADFYSLHIMPLTPATKKVFNDDTFAKMKNVRLINVRGQVDEDAVLRALDGGVQAALDFVTEPPPTKDSKLVGHENVTVTPHLGASTKEAGEGVAIEAAVVGALNGELSATVNAFMAPEVLSSELAPVYVLAERLGRLLAVQLVTGGGQGNWYVYKSGRDPDGLDTRLLRAMVTKGIEPIDTINLVNADFSAKGGKLRISEERYVVDSSPEYVPEISQVQISNVQSRFASALGENGNISIEGKVKVGVPHLTRVGSFSDVLSLEGHLKGVQDPQMGVQGNLGI

NbL13g18490.1 photosystem_II_5_kDa_protein_chloroplastic-like [MW = 11.6 kDa]

No. of times detected



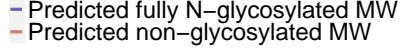
log(intensity)



Values from



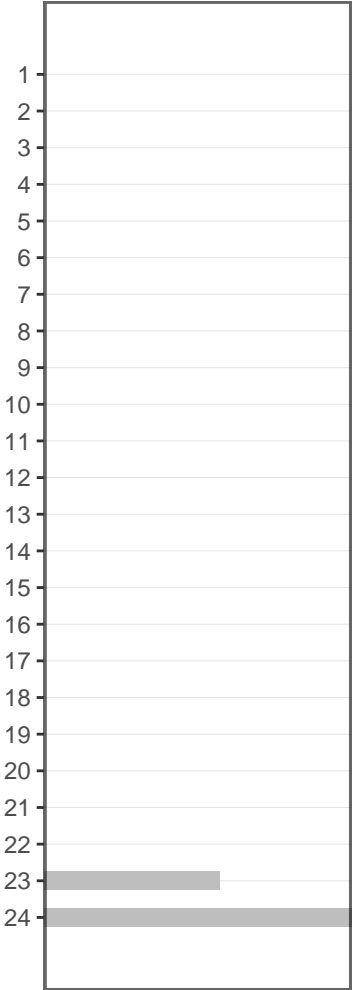
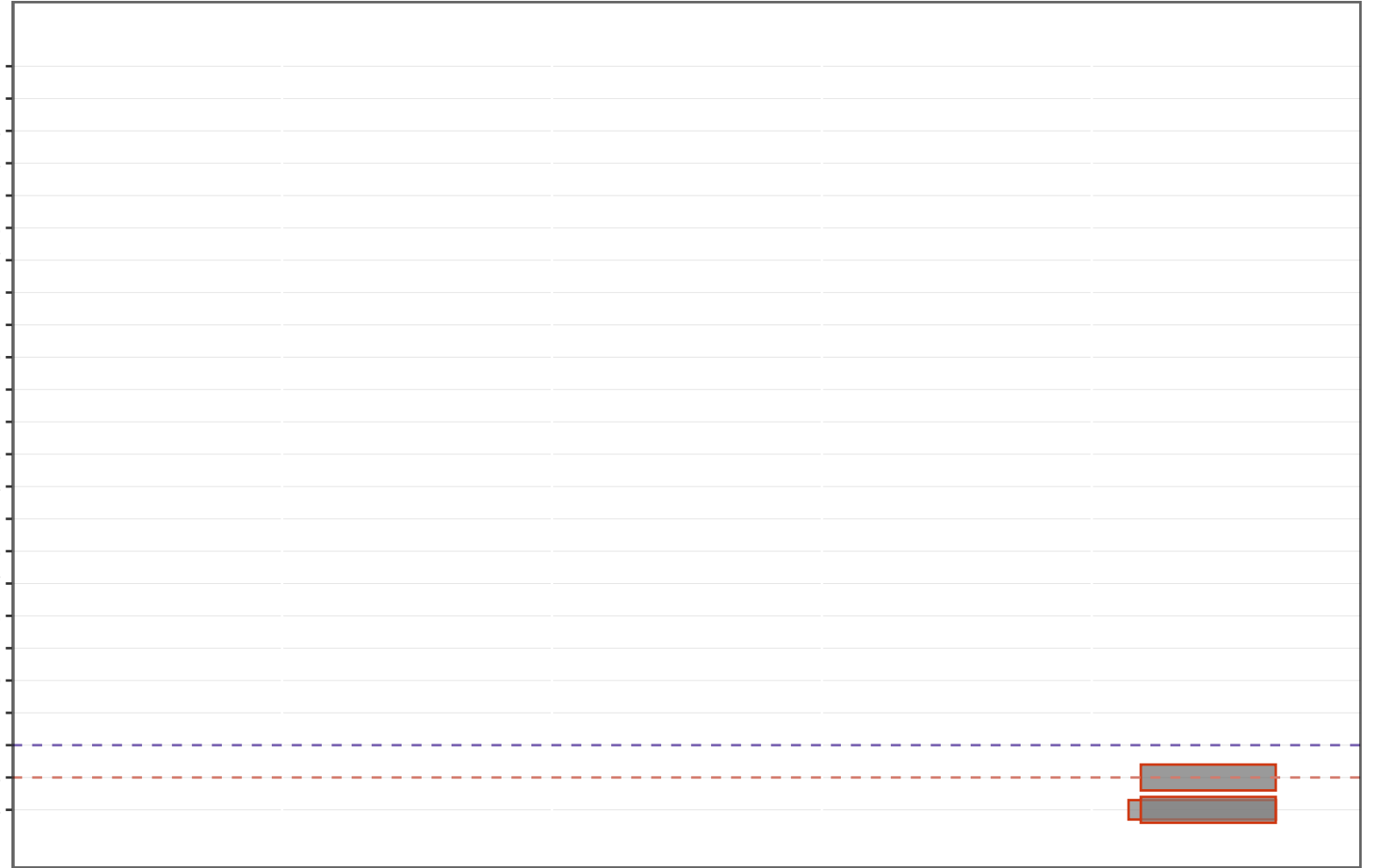
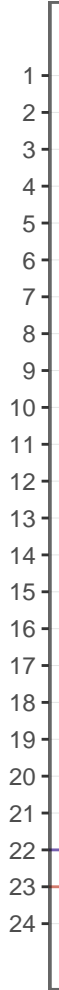
MW indication



Molecular weight



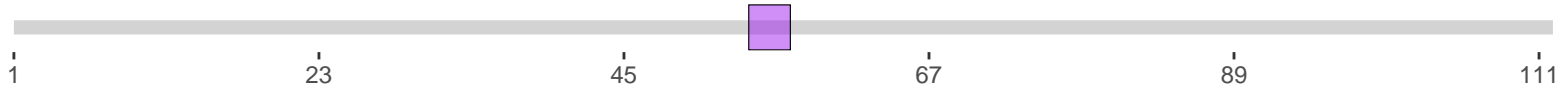
Gel Slice



Peptide counts over 4 repeats

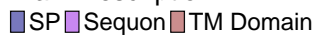
1 23 45 67 89 111

Protein length



Pfam domains

Pfam Description



Protein sequence:

ENVVMSNKKESNNGRRELFAMAAVAASVWAKAAEAEPKRGPEAKKYYGIVSNPTARIGHNAN

NbL13g18310.1 39S_ribosomal_protein_L47_mitochondrial-like [MW = 19.11 kDa]

No. of times detected



log(intensity)



Values from



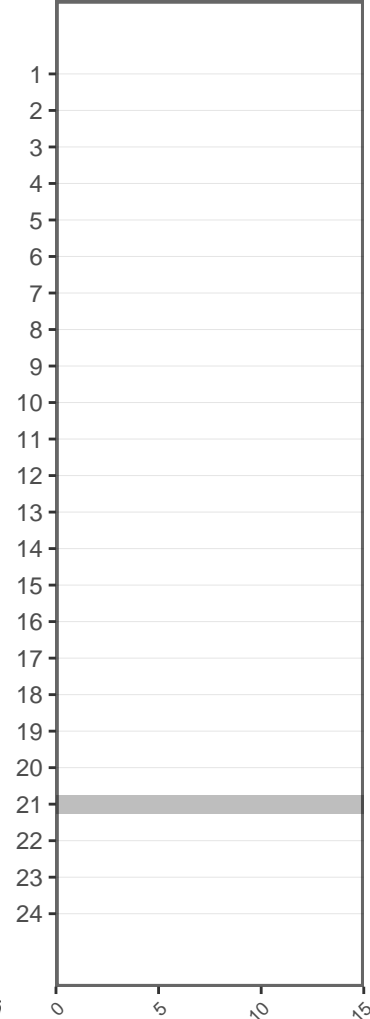
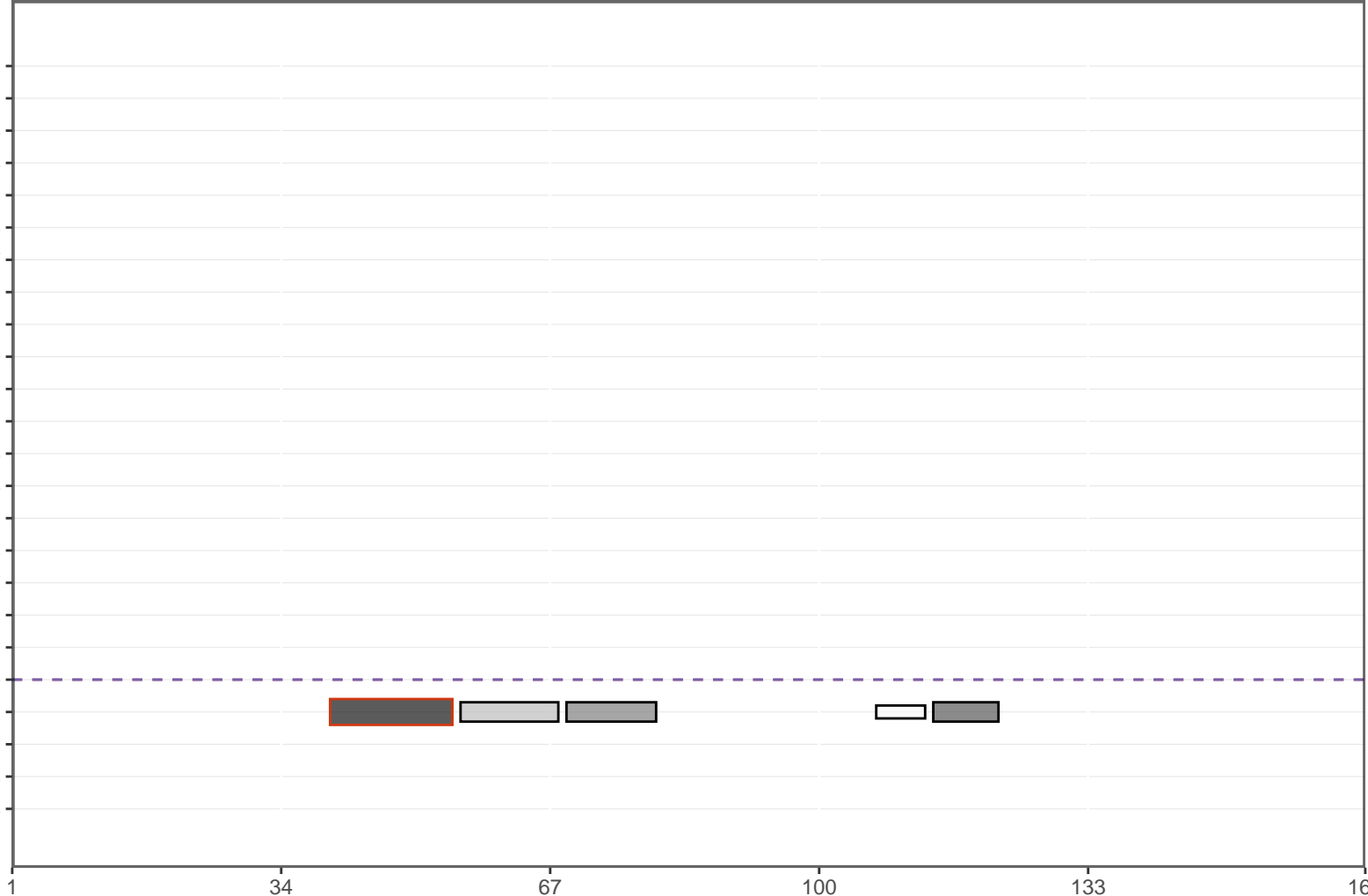
MW indication



Molecular weight

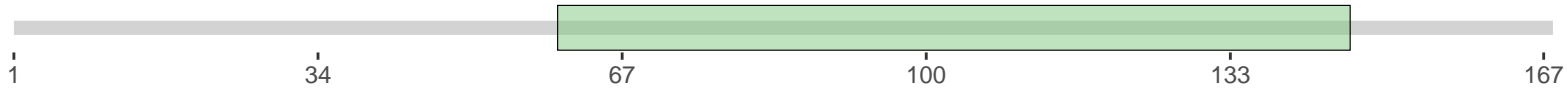


Gel Slice



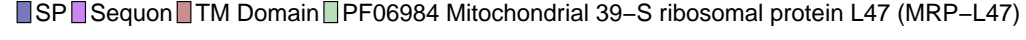
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL13g18160.1 betaine_aldehyde_dehydrogenase_chloroplastic-like [MW = 55.66 kDa]

No. of times detected



log(intensity)



Values from



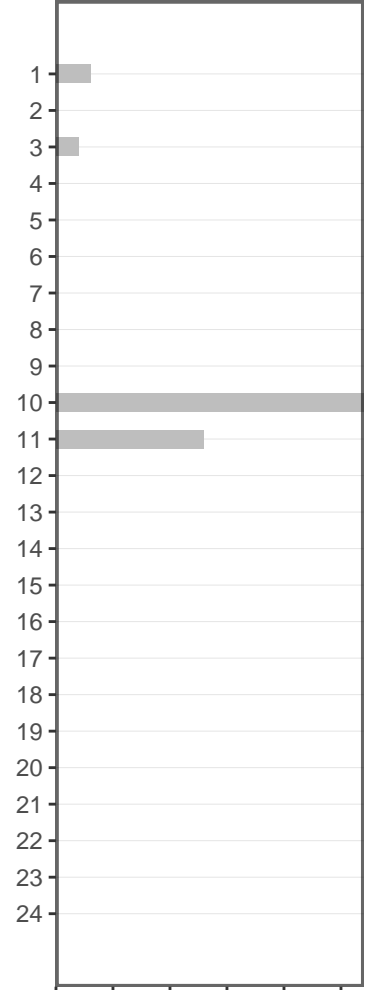
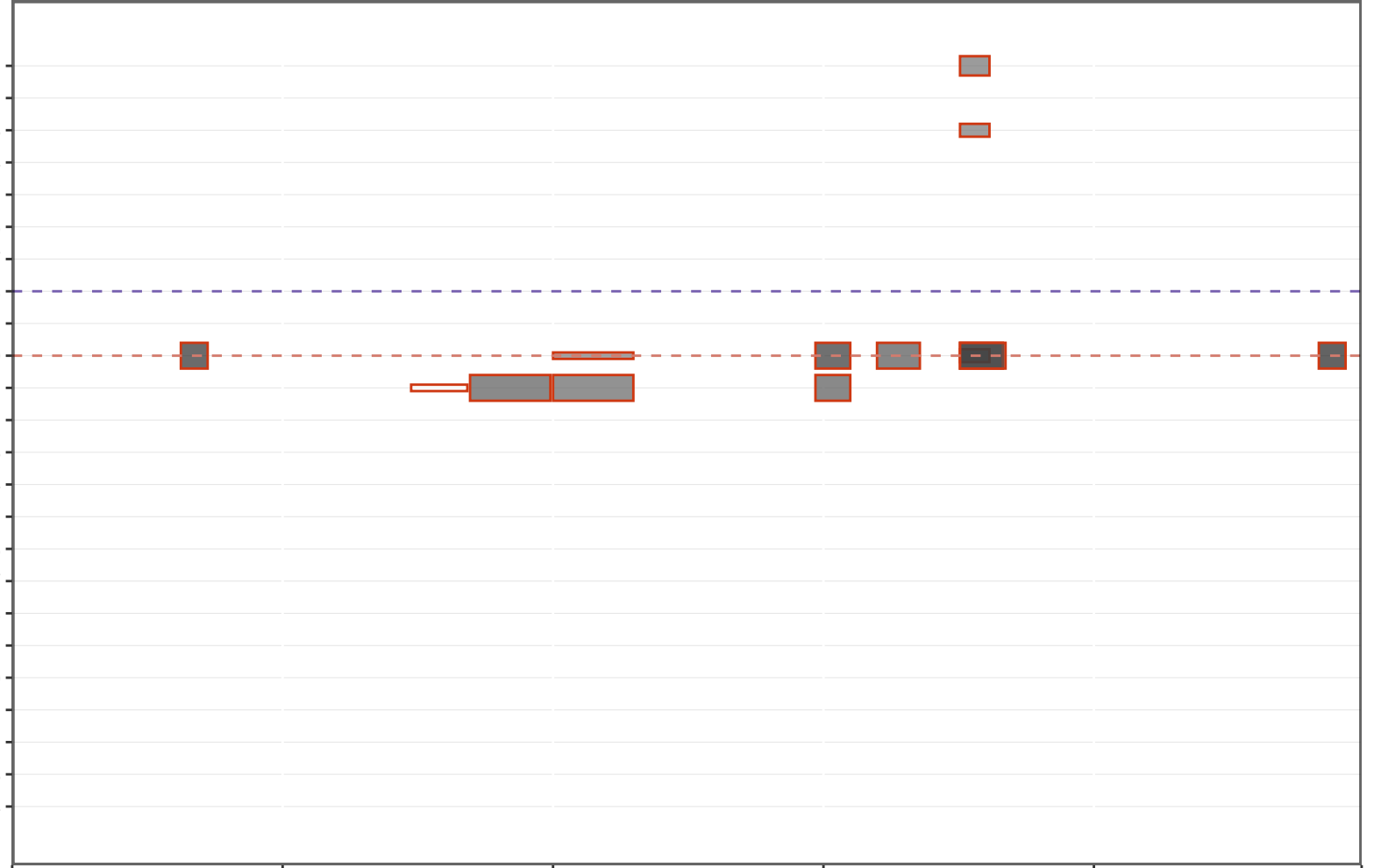
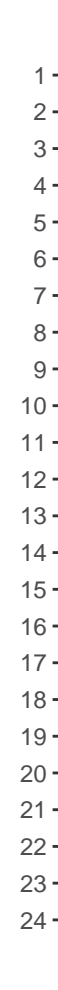
MW indication



Molecular weight



Gel Slice



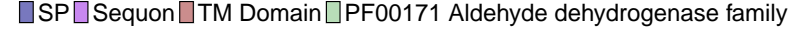
Protein length

Peptide counts over 4 repeats



Pfam domains

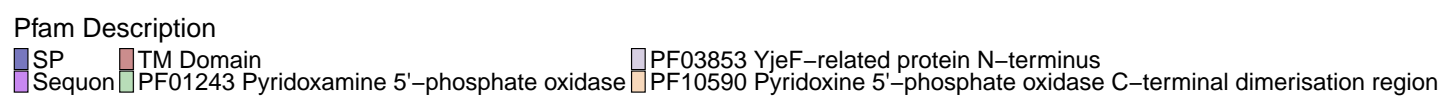
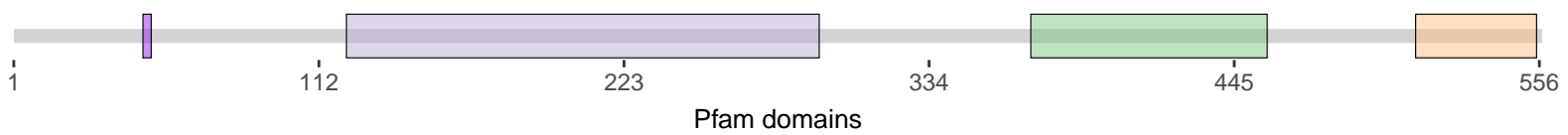
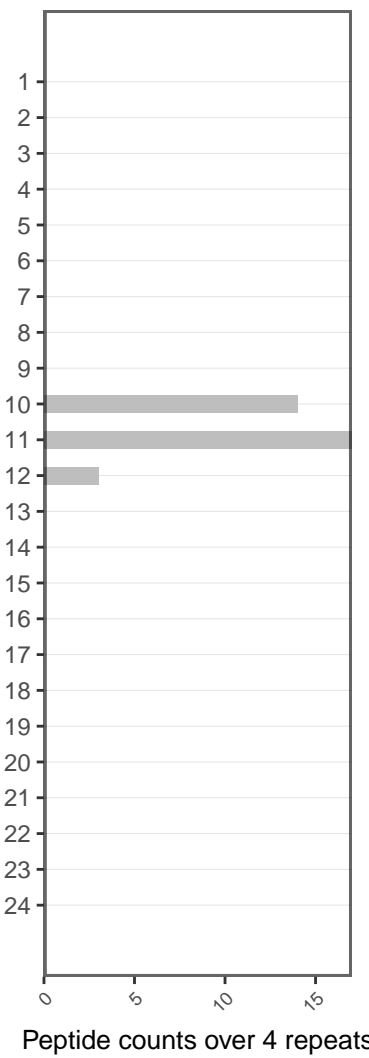
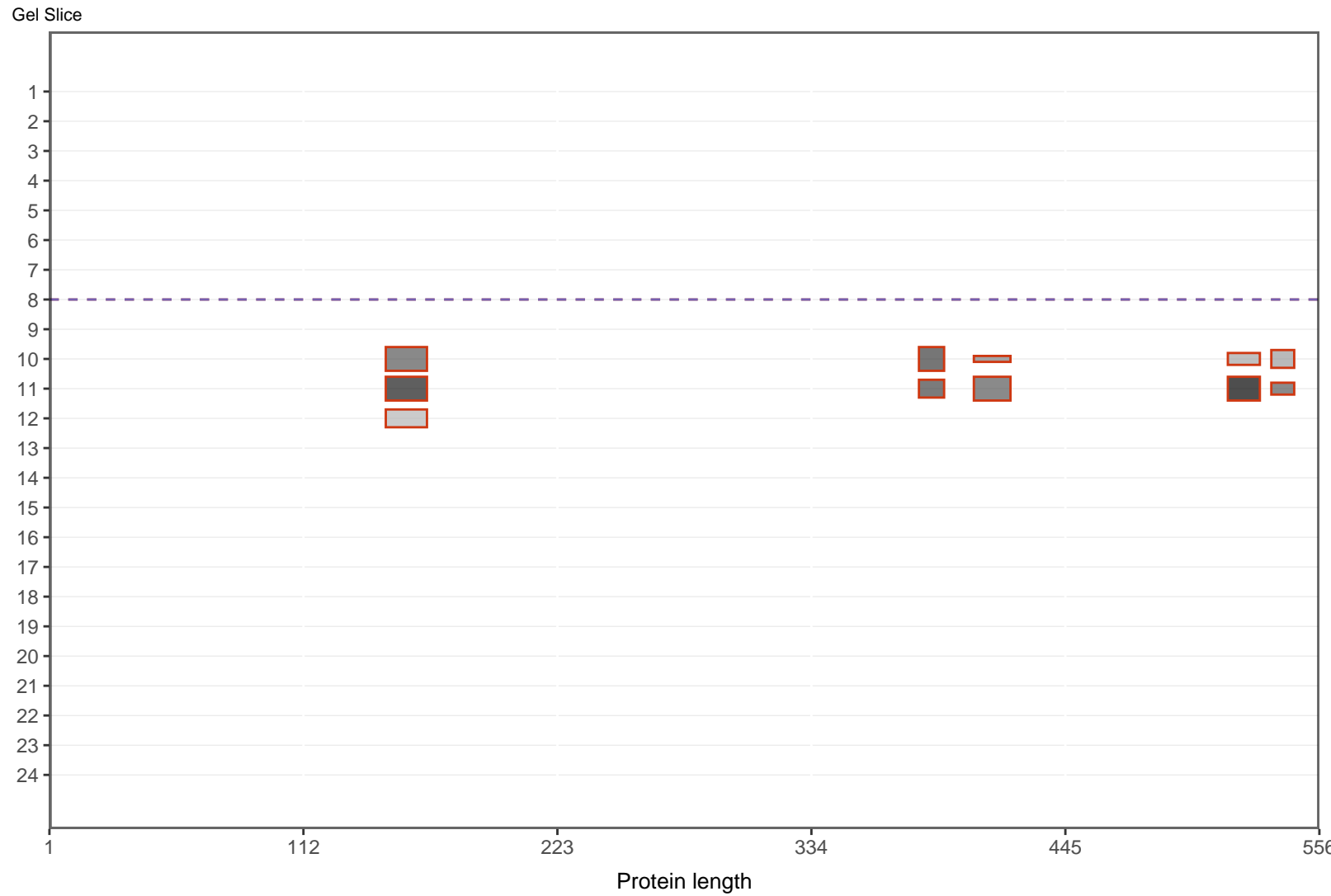
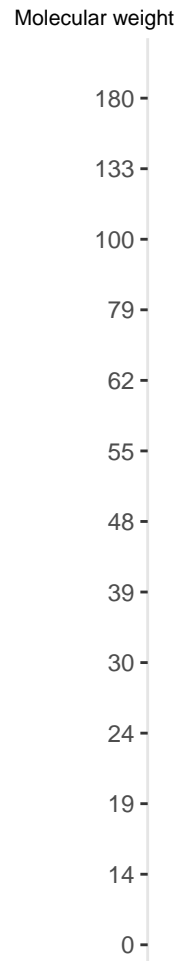
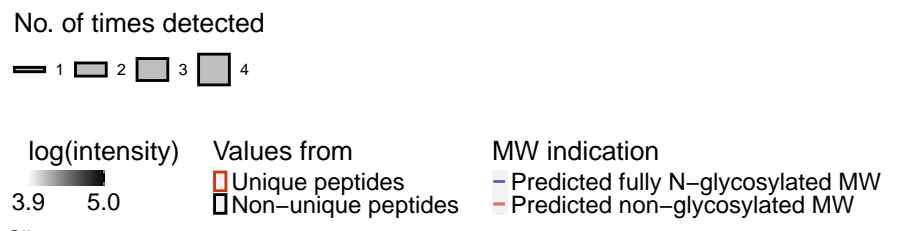
Pfam Description



Protein sequence:

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NbL13g18130.1 pyridoxine/pyridoxamine_5'-phosphate_oxidase_1_chloroplastic-like [MW = 62.08 kDa]



Protein sequence:
 VEEGDLSGEGYKPDMLVSLTAPKLGAKSFGSTHIFLGGRFVPPGIRNKNFNQLPVPPTGTCMCYRIGKPKFDISMSRENYISPLLEEVEVADPDFDQGFQWFDAMTATGLKELNMMALSTTGKDKSPSRVLLKGFDFNDGFVYTNVYEGSGGGGAENPHAAFLFYWDDLNRGVRIEGPVEKVSDEESEGYPHSRPRGSQLGAAKSGSTVIPRQGLIDEYKHLEAKYADGNLIPKPKHWGGVYRLRPEMFEFWGGGSRLHDLRGLYIPETVDRGRIERLAP

NbL13g17830.1 HIPL1_protein-like [MW - SP = 72.58 kDa]

No. of times detected



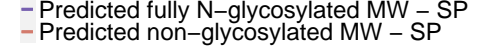
log(intensity)



Values from



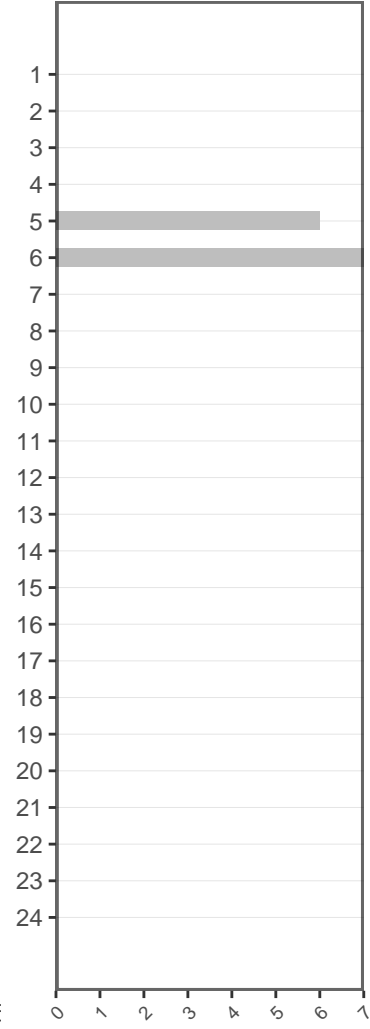
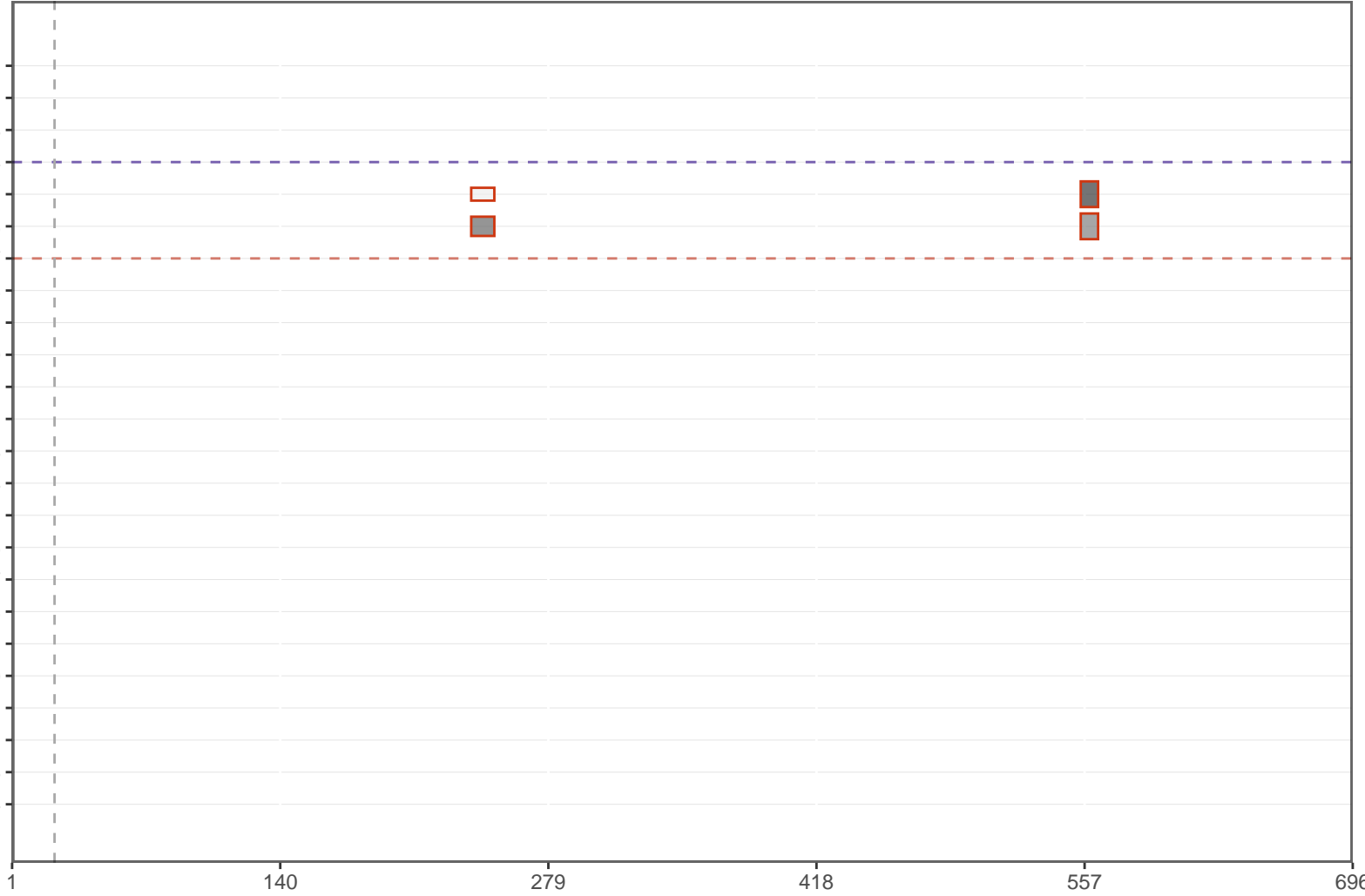
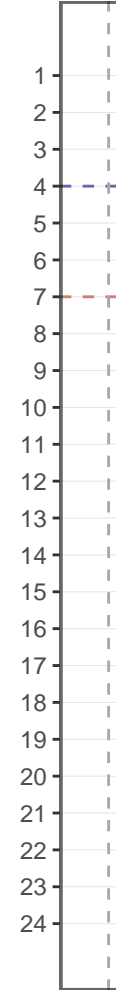
MW indication



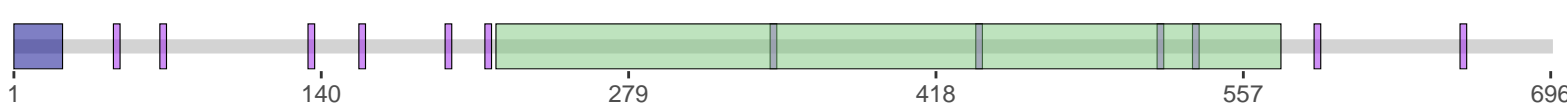
Molecular weight



Gel Slice

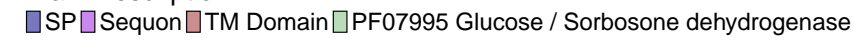


Protein length



Pfam domains

Pfam Description



Protein sequence:

SYQSVIAEFTANGTASGPGDAKTASAEIRIRIFMGLPFTSHHGQGLFGPKDGLVLFMMGGGGTGDANFAGNKKLLGKIMRFVDVSTSAEEISGLGLWGNVTFPKDNPYIEDEKLGPEWALGMRNPNWRGDFDARSPVFMGADVGGDHVEEVDITKGNVGNWYEGAHFFAPFKSPGKNTSTSGINPFPVMEVNHSEVKNKEGASITGGYFYRSTTDPGMDGRVLFADLYAGAMWAGTSEPNSENGIFNTEIAFTGAGNSPINCALVPGSSVPLGYIFSGLI

NbL13g17680.1 short-chain_dehydrogenase_reductase_3b-like [MW = 27.89 kDa]

No. of times detected



log(intensity)



Values from



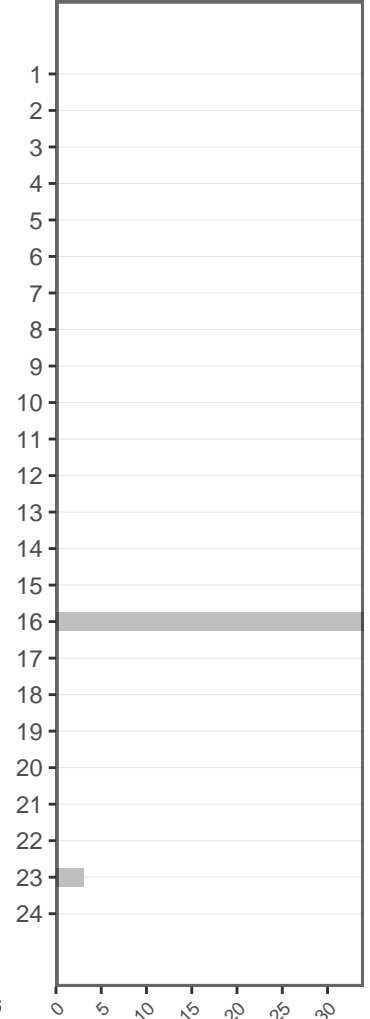
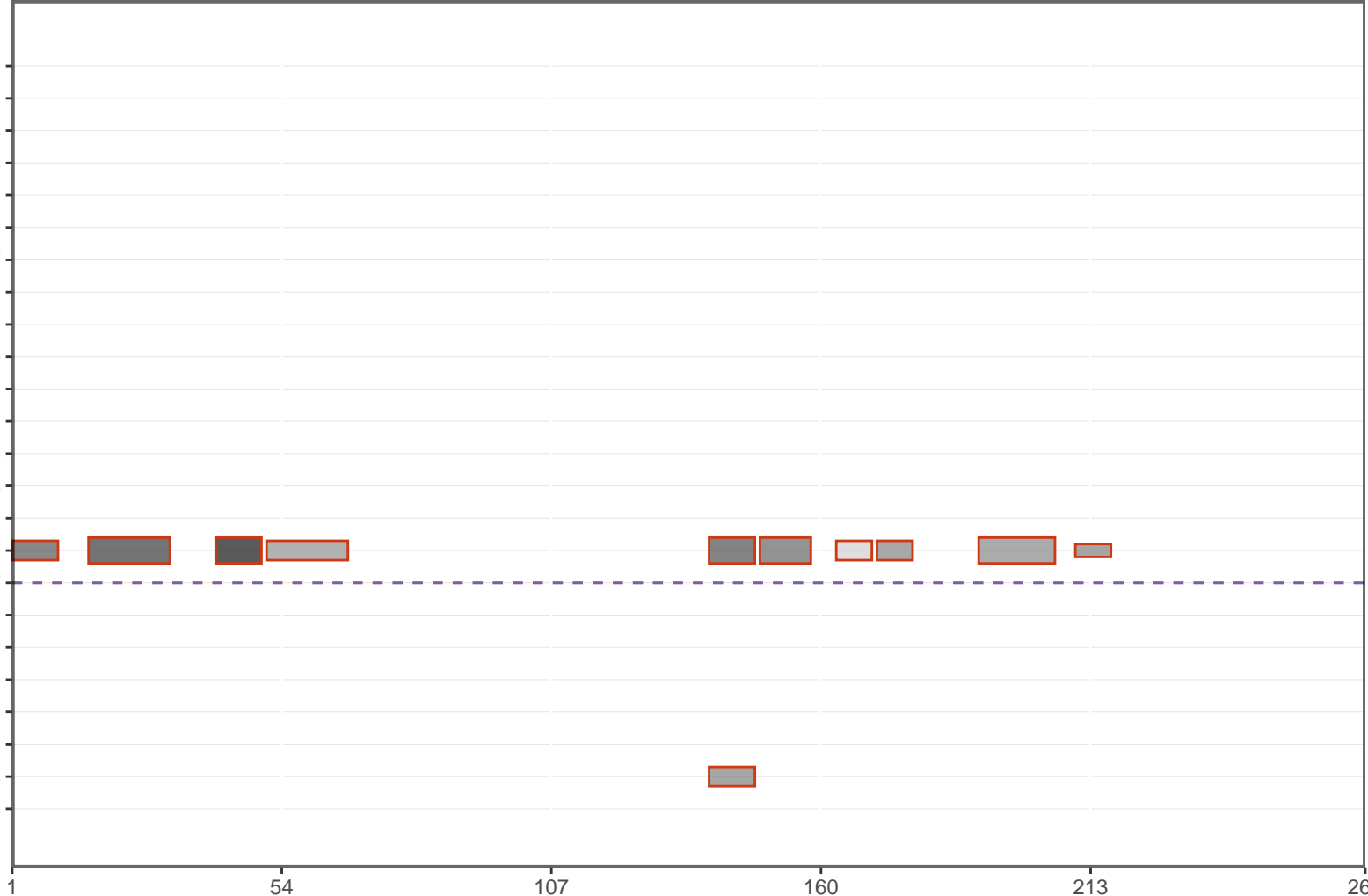
MW indication



Molecular weight



Gel Slice

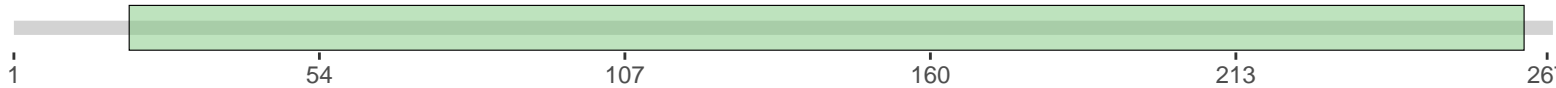


Peptide counts over 4 repeats

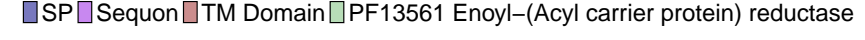
Protein length



Pfam domains



Pfam Description



Protein sequence:

AINVRGSVACVQIVAKAMVEGGVGGKICTGSVTATKGVTKGIDWAMSKHAILGLVKSASKGLGKYGIRVNCVSPMAWATPLLEKSMKMSVEIEIKLFNSFNLKTGAIAKASNAADVLFLLASDDSGFVGHNLVVDGGFHPV

NbL13g17640.1 uncharacterized_LOC107771029 [MW = 19.97 kDa]

No. of times detected



log(intensity)



Values from



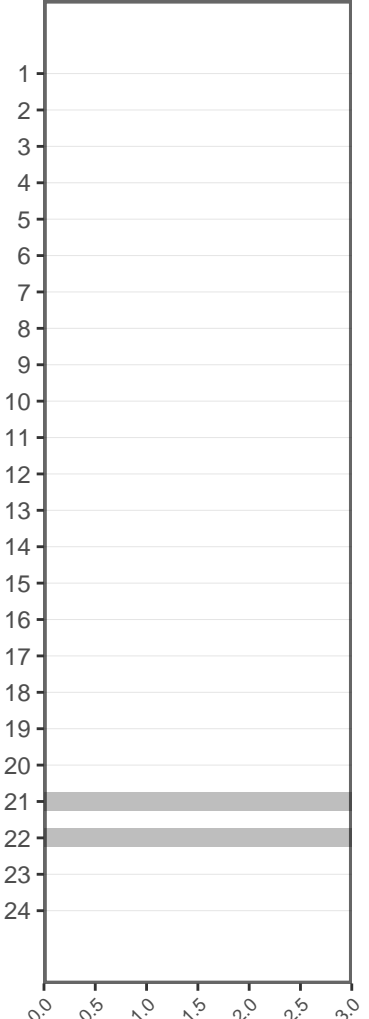
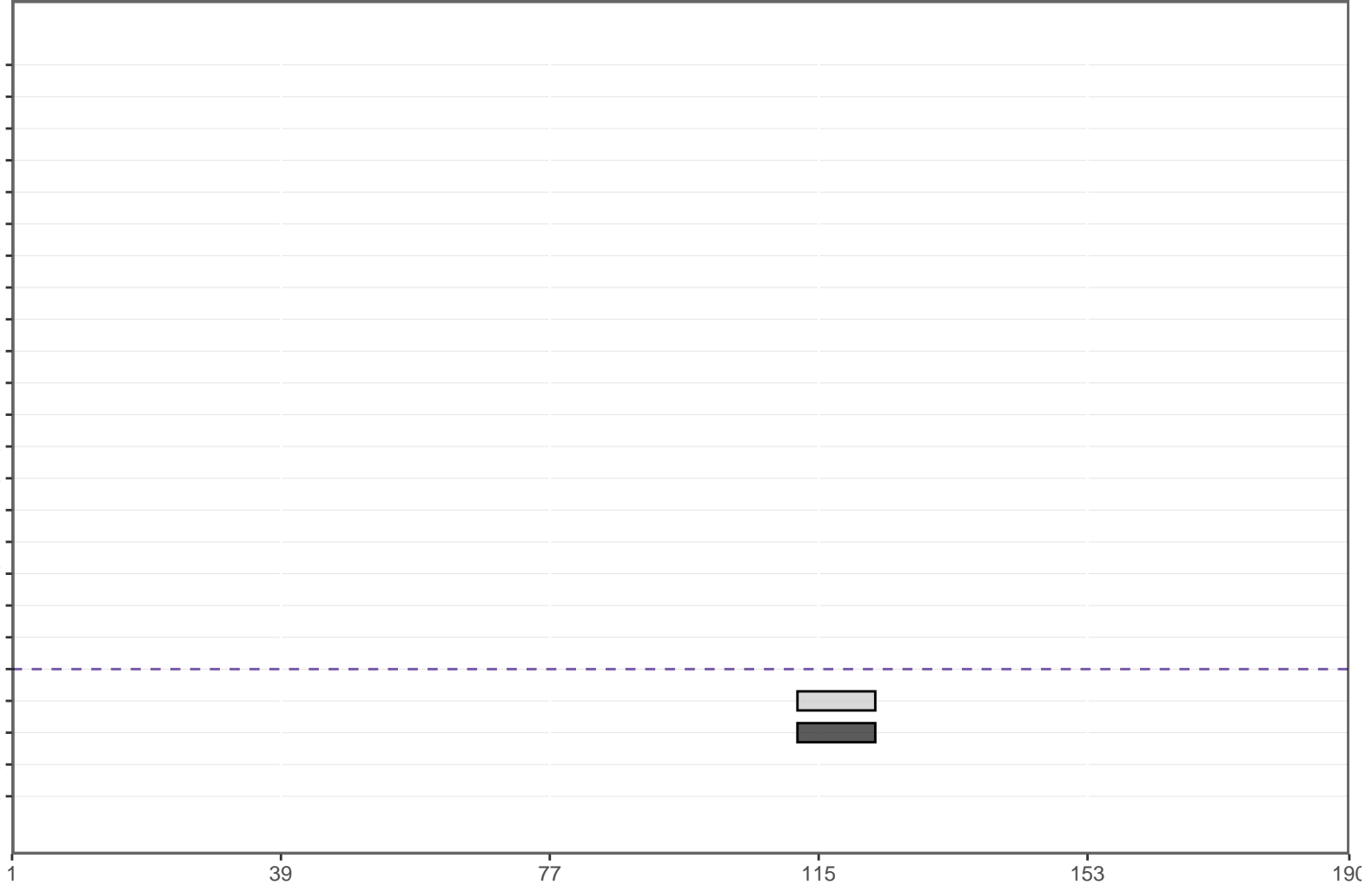
MW indication



Molecular weight



Gel Slice

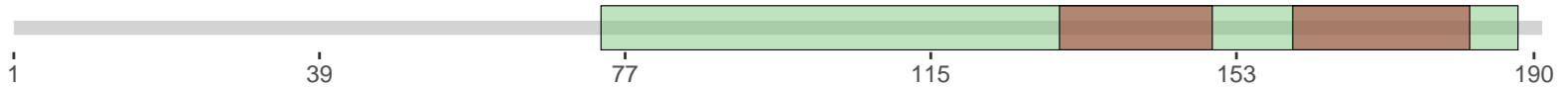


Peptide counts over 4 repeats

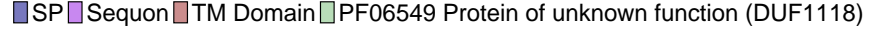
Protein length



Pfam domains



Pfam Description



Protein sequence:

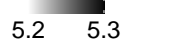
KVLSLTVKAGLLSKAEELGFTLSSEIKLGVFSKAEELGLLLEKKAASFPSALASALPIEVAITIVIPDPSAGLVVGVLAGALGLGAVGLLVGSVLDLGLQEADE

NbL13g17570.1 ubiquitin-conjugating_enzyme_E2_2-like [MW = 17.3 kDa]

No. of times detected



log(intensity)



Values from



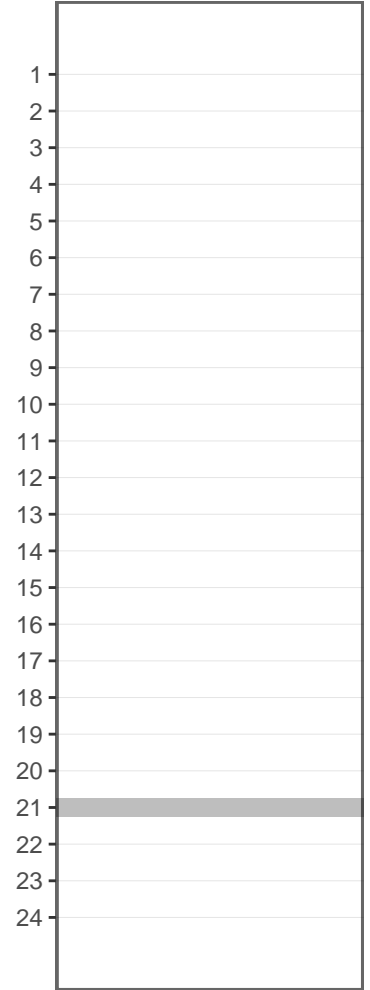
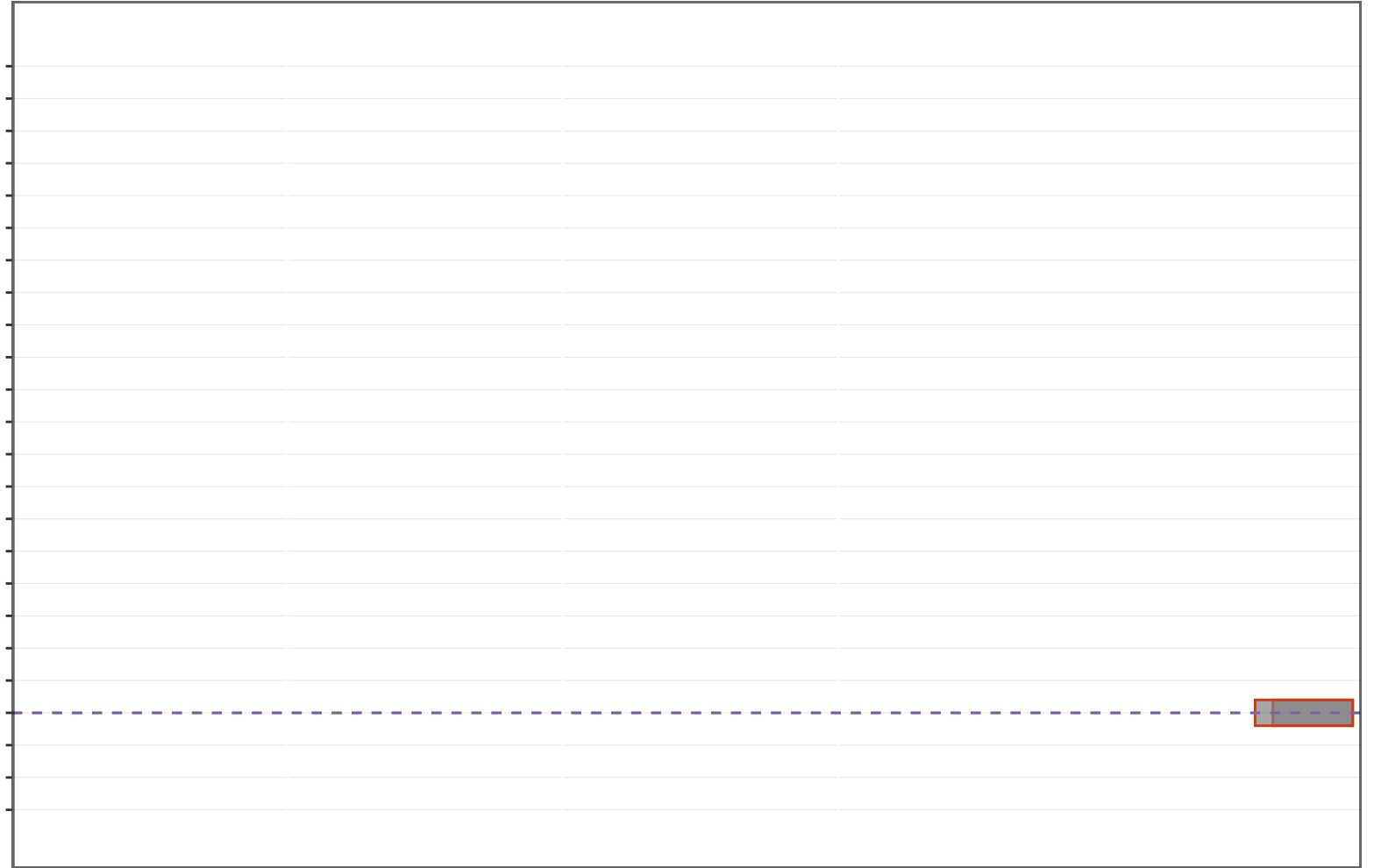
MW indication



Molecular weight



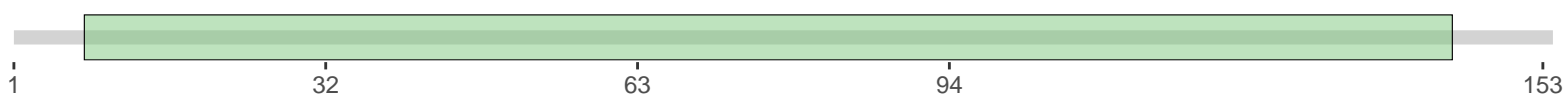
Gel Slice



Protein length

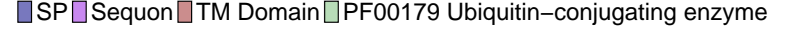


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YFNKPPTYRFLVSRMRFNIVADGGIDLDLGNQWSPVDAALTSIGSLGDFNPNNSRNSAEARLFSENKRDNRNRVREVEGQWTD*

NbL13g17510.1 aldose_1-epimerase-like [MW - SP = 36.56 kDa]

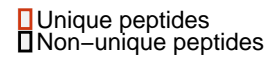
No. of times detected



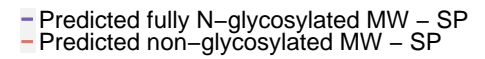
log(intensity)



Values from



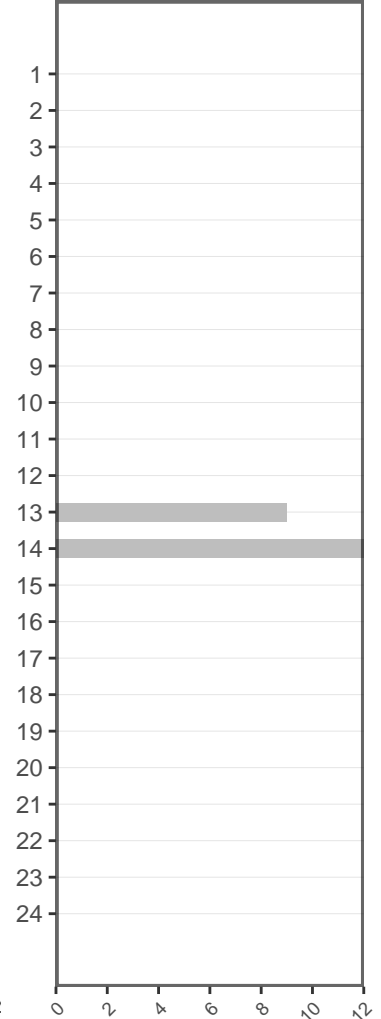
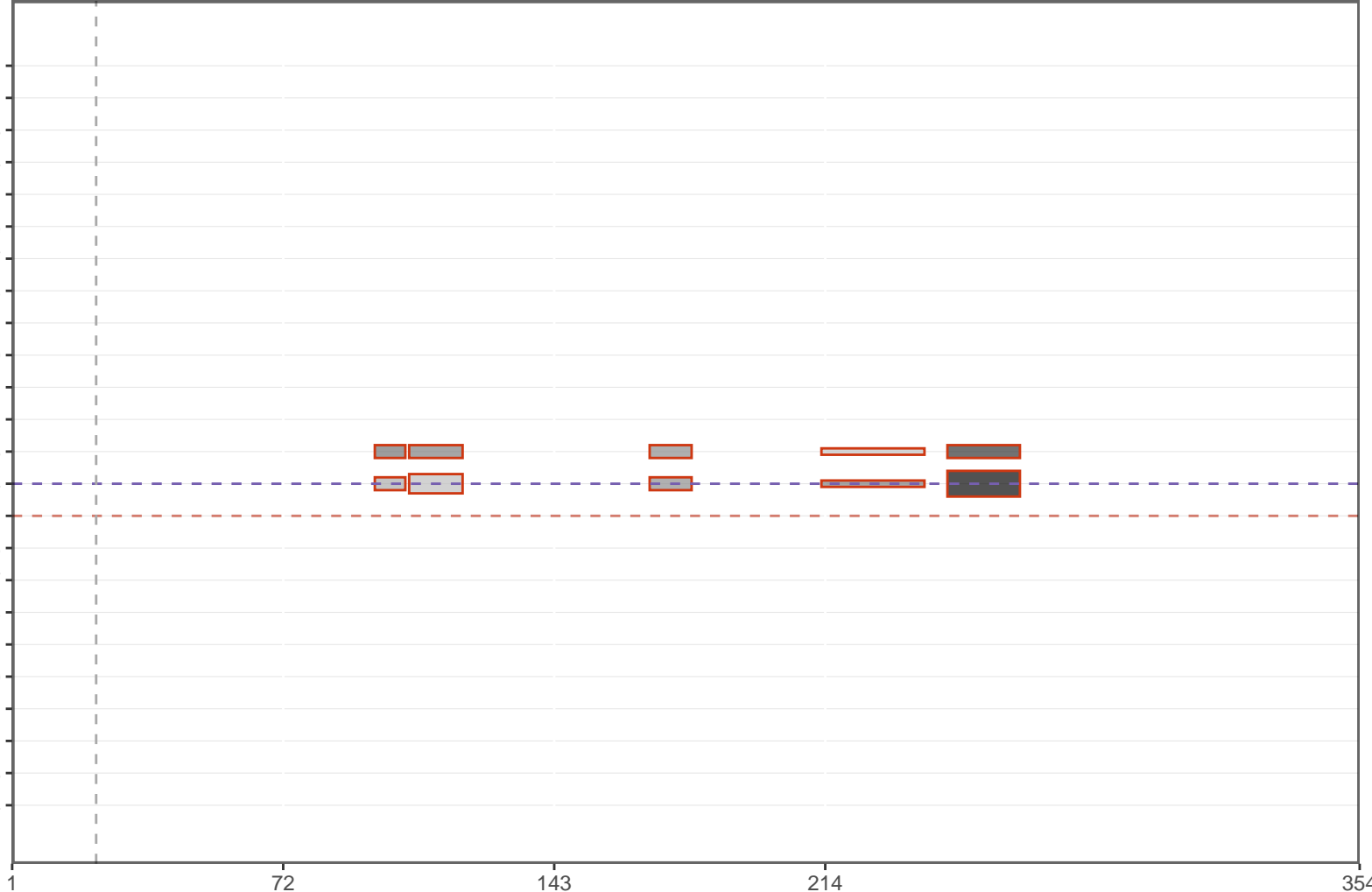
MW indication



Molecular weight

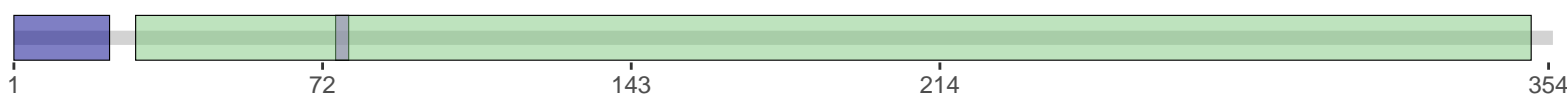


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKLAINMQATPLNKATPVALASHYVWNLGGHTSGNIFSHHTQLFGKTFVDDKLIPTGGITFVEGTAVDFLKPRTIGSKFSDIPGGVDINVLNTEGKHQRVATVQESRSGKMLWTKNPGVGFYTSNMLENAKGGKGFVYSKVALGLETOGFPDGVNHNPNFPGVNPGETYKHIMVRFYV

NbL13g17500.1 vacuolar_protein_sorting-associated_protein_29 [MW = 21.06 kDa]

No. of times detected



log(intensity)



Values from



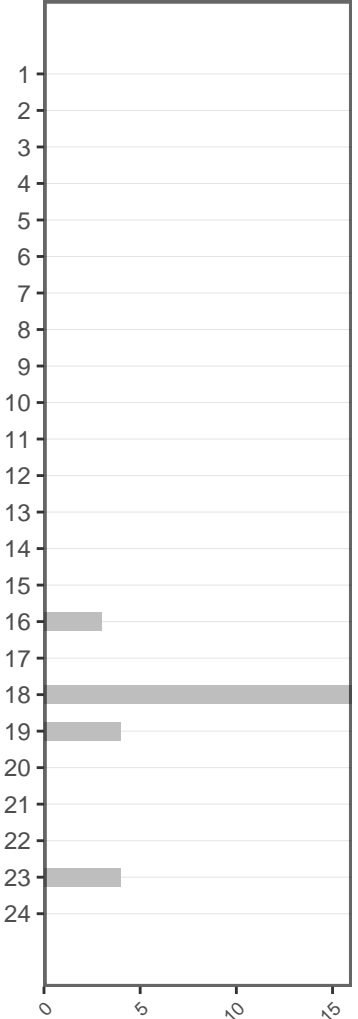
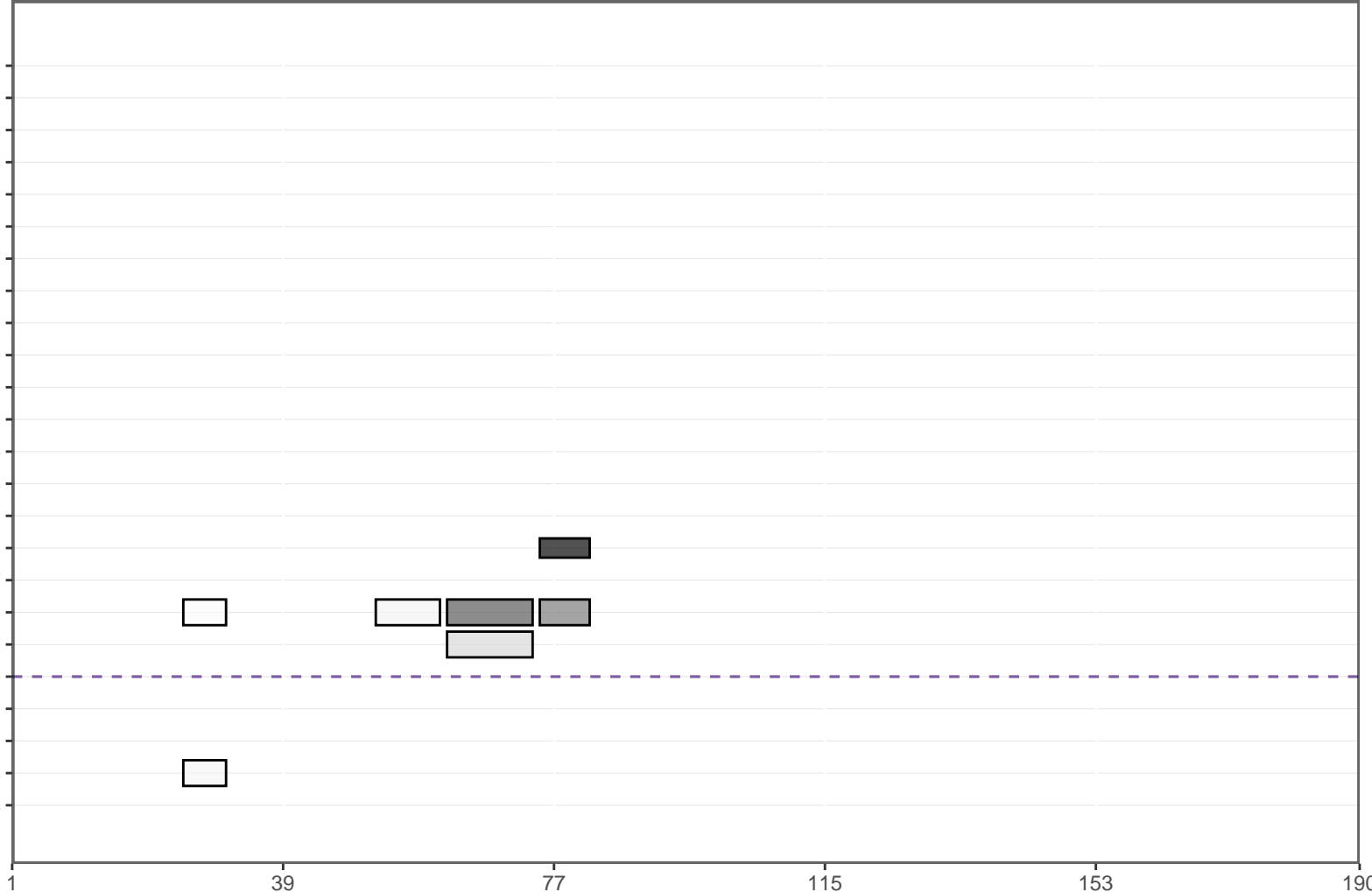
MW indication



Molecular weight

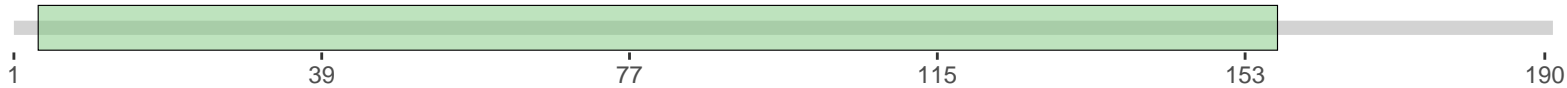


Gel Slice



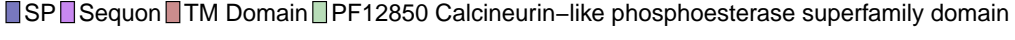
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

.GLCHGHQVPIWVGDLDLMLGRGLEVDLVTGHTHTQFTAYKHEAGVWVWVPSGATGAYSSITYQVNPFRVLMDDLRVWVYVELIDGKVKDKIDFKTKTQNAV

NbL13g17400.1 pantothenate_kinase_2 [MW = 100.02 kDa]

No. of times detected



log(intensity)



Values from



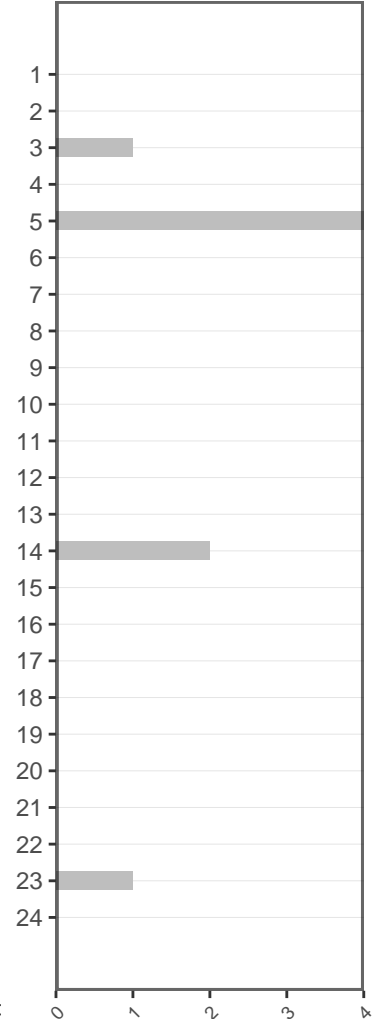
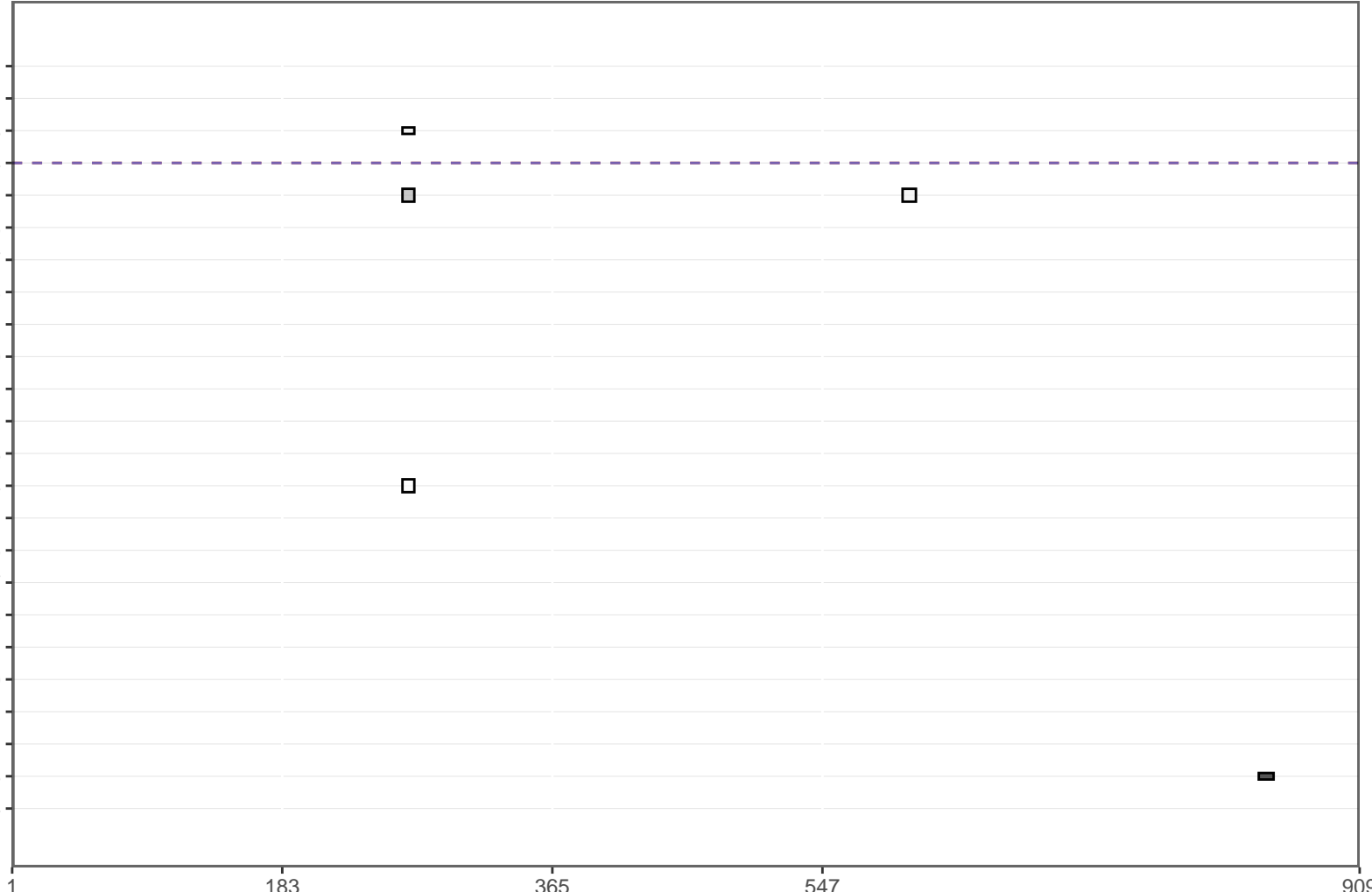
MW indication



Molecular weight



Gel Slice



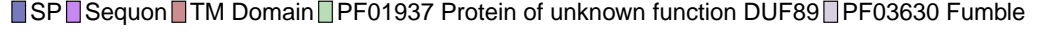
Protein length



Pfam domains



Pfam Description



Protein sequence:

VHQLVERFPMGAPVHGNGHNPPLGDLNENISWMEKFKVKGTEETAPVPMAPRDTGLGGFEVPSKGVLRPDAKLNVDVHLVPSLEVFLLADPRTYEPTDQLSDHSELEVWFTVLGEHLSDLVKVAASEGGTDDAKRRGAAFARAFSAHLARLMEERPAVYKLGKLANLELREECLREFHFDVAVRTKRENEASLAVLPDLLLELDSMTEDMRLLTLEGVLAANFDWGSRRACVBLVHKGTIEIYRMSRKKMGRPRVVDVDFKERMLEGGMKRPQPKRAL

NbL13g17280.1 glutaredoxin-like [MW = 13.57 kDa]

No. of times detected



log(intensity)



Values from



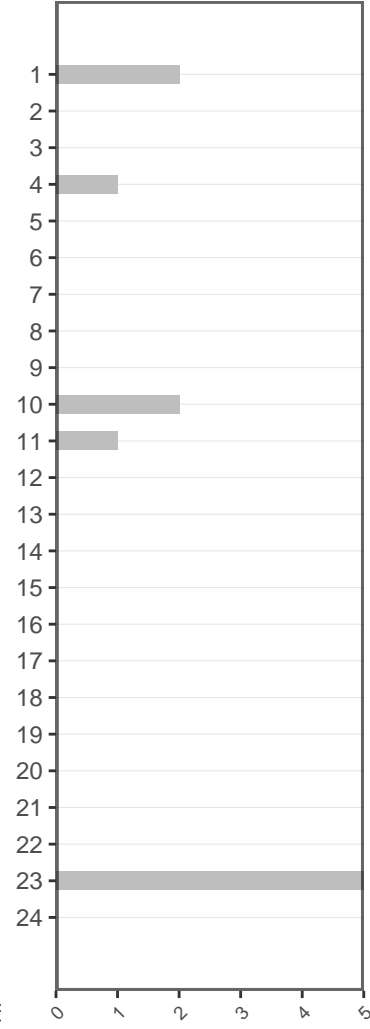
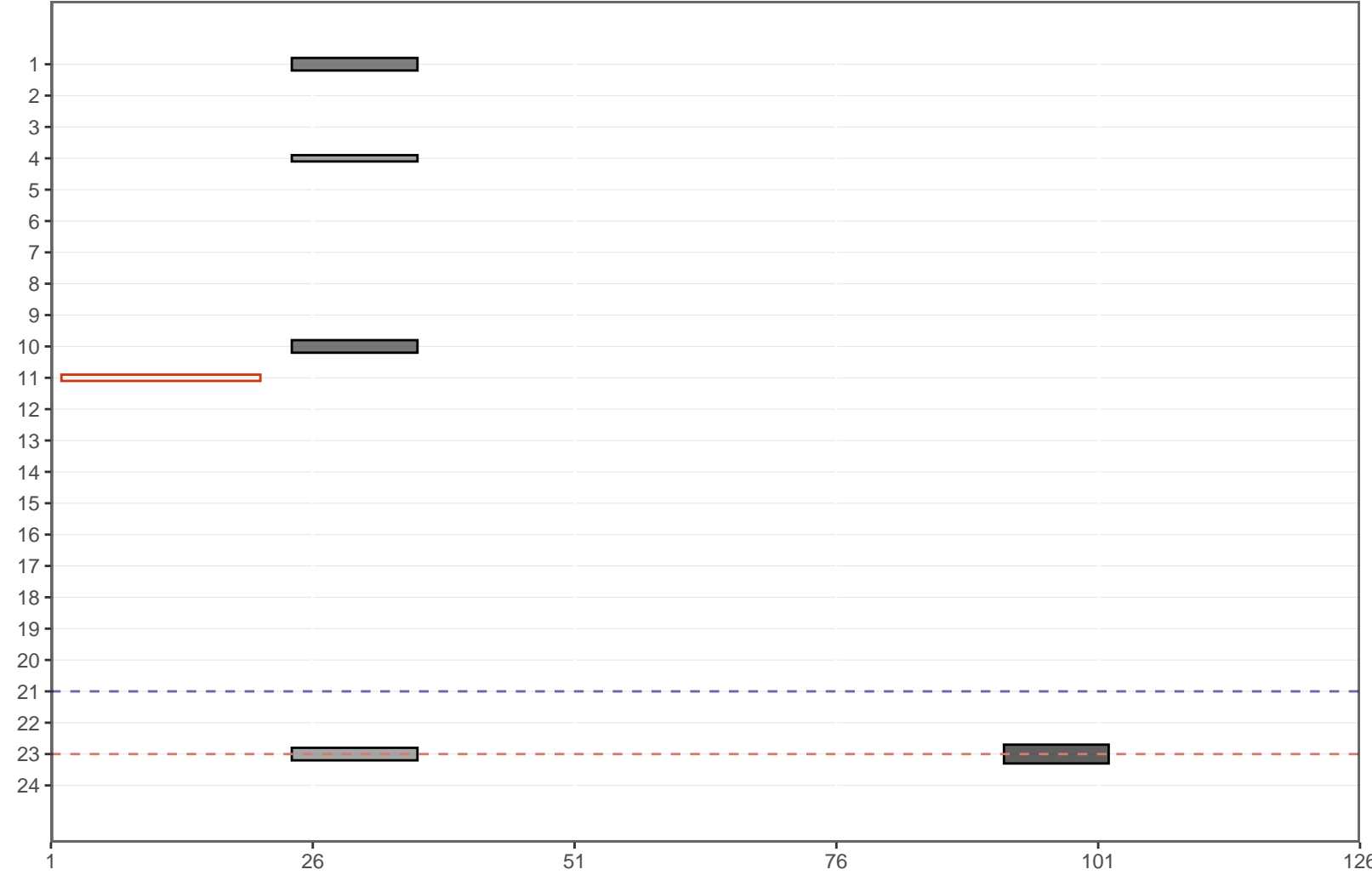
MW indication



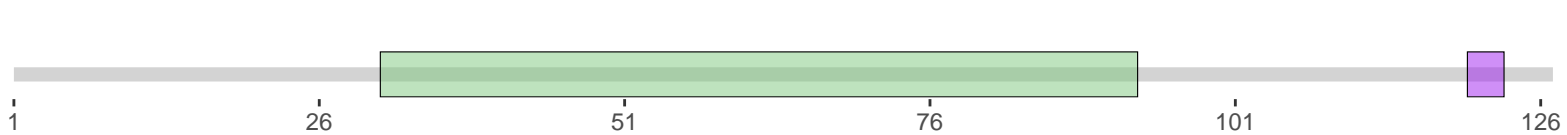
Molecular weight



Gel Slice

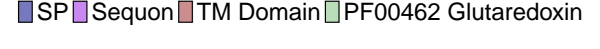


Protein length



Pfam domains

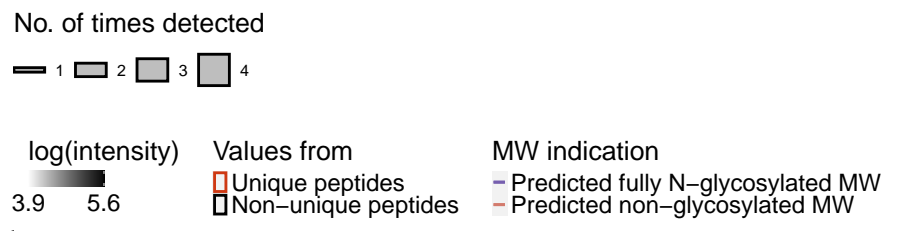
Pfam Description



Protein sequence:

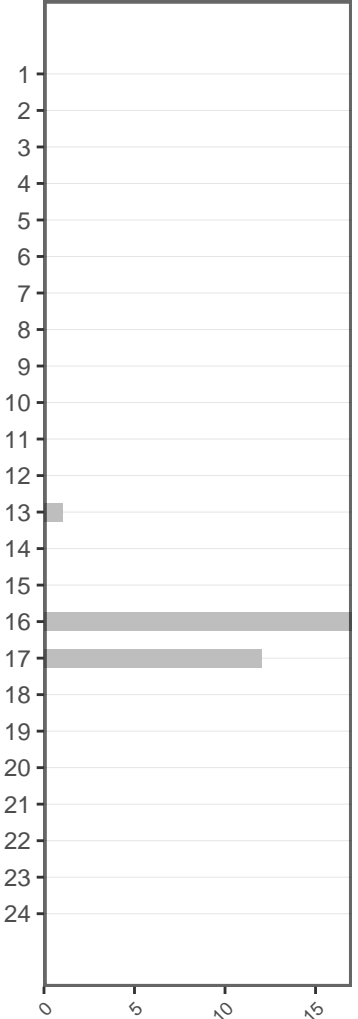
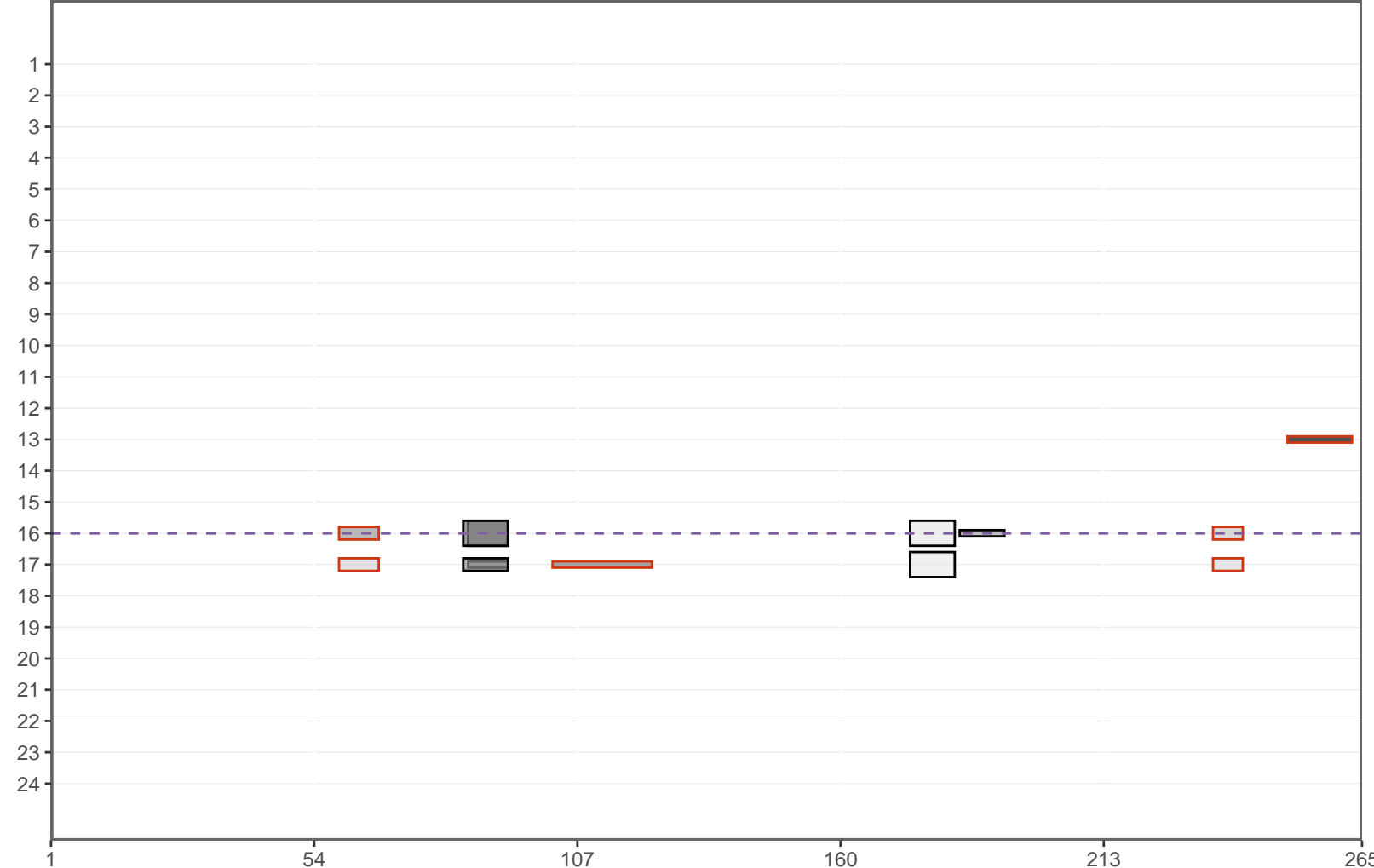
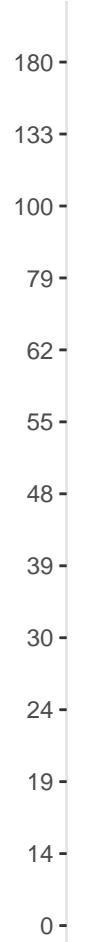
IQLGATFKYIELDQSSGGNEVQGLLEWFGQRTPVNFVIGGKHYGGDSRVEKHQGGKLLPLKIDAAVPTSAKVV

NbL13g17190.1 motile_sperm_domain-containing_protein_2-like [MW = 30.51 kDa]



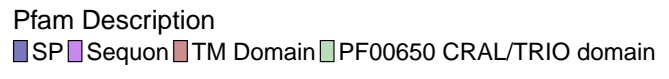
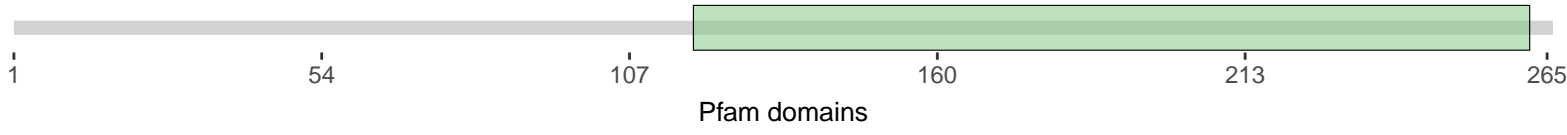
Molecular weight

Gel Slice



Protein length

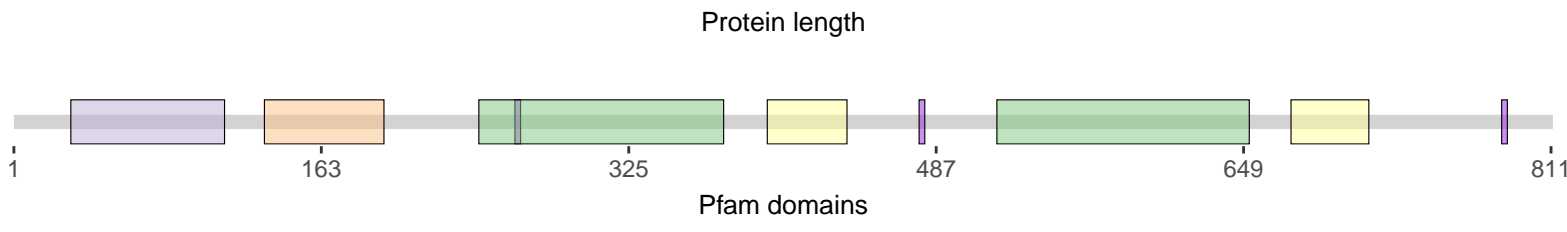
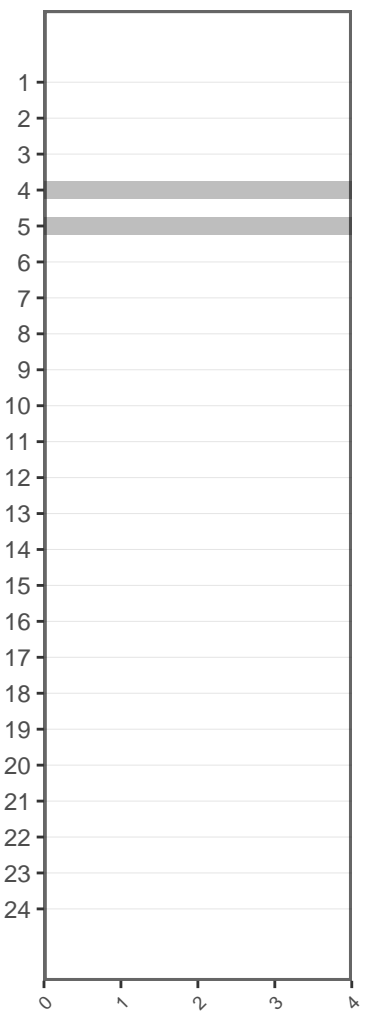
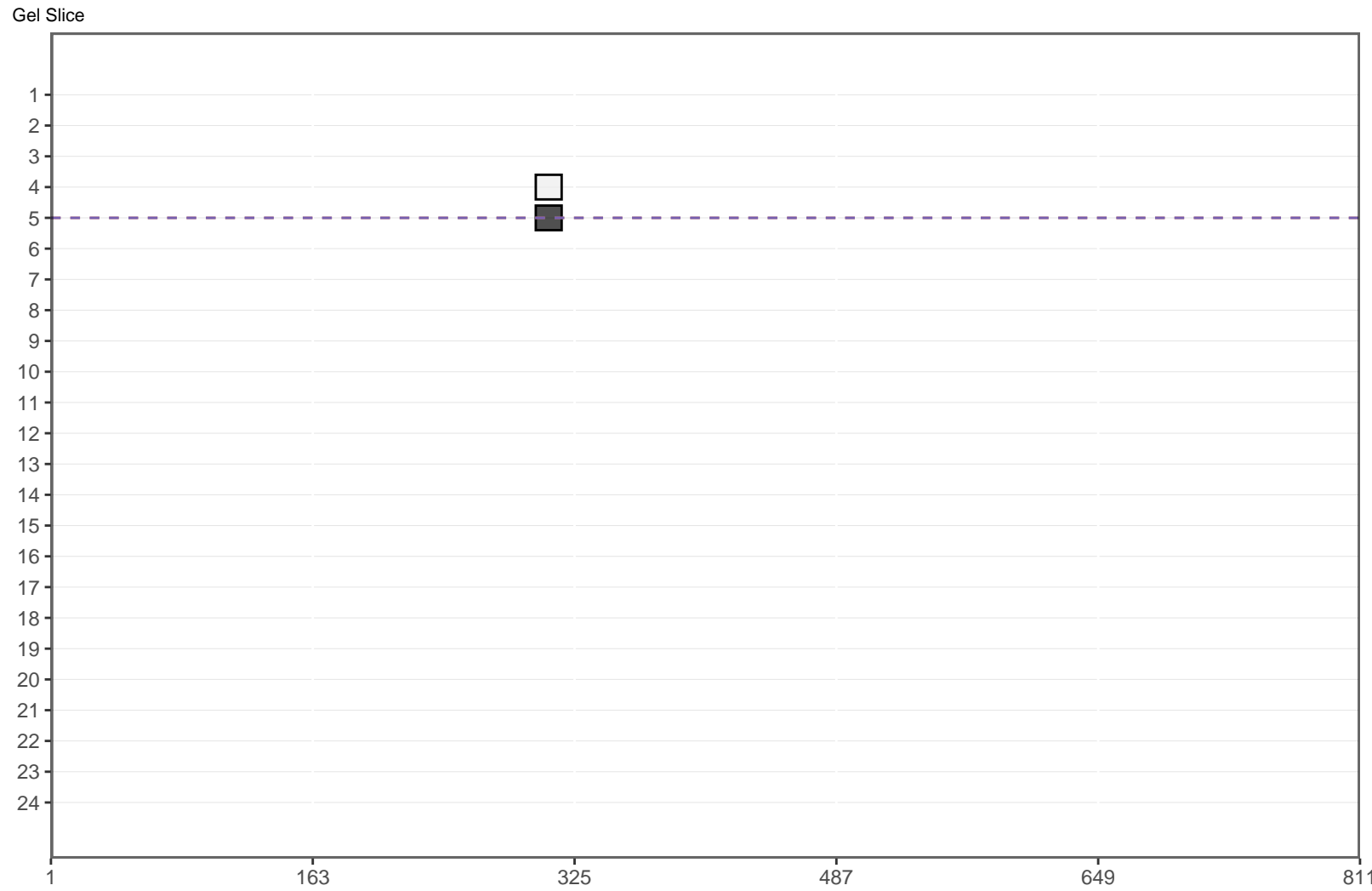
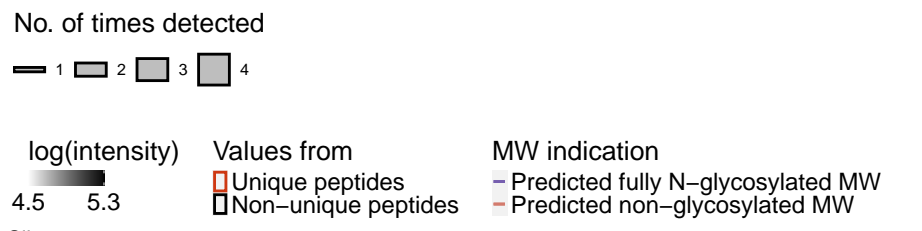
Peptide counts over 4 repeats



Protein sequence:

ETGKAYVHDCFDVAGRPVLVEASKHFGKGDPEDEKLVLEKALSRIPPGKGDILGFDLRFGTENADLKFLLTFMDFVYYYYPRRLGGVLDVADPFVKPLWGLVKPKLKSYSLSVRFCSANDVREYFTEETVWTRK

NbL13g17140.1 cell_division_cycle_protein_48_homolog [MW = 90.02 kDa]



Pfam Description

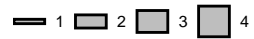
- SP
- Sequon
- TM Domain
- PF00004 ATPase family associated with various cellular activities (AAA)
- PF02359 Cell division protein 48 (CDC48), N-terminal domain
- PF02933 Cell division protein 48 (CDC48), domain 2
- PF17862 AAA+ lid domain

Protein sequence:

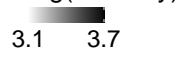
MKLDNVDLERVARDTHGVGADLAALGTEAALGQIREKMDIDLEDETDAEVLNSMAVTHNEHFDLALGASNPALRETVAEVFNISWEDIGGLDNLVRELGETVGVYVPEHPEKFKFGMSPKGVLFYGPQGGKTLAKAIANEQGANFISVKGPELITMWFGESEANREIFDKARGSAFQVLFDFDELDSIAMQRGHVSGVDAGGAADRVLNQLLTFEMDGMFAKKTVFHIGATNRFDIDPALLRFGRLDGLIYPLPDEASRLQPKAQLRKPVSKEVDLAALSRYTHGF

NbL13g17130.1 elongation_factor_Tu_GTP-binding_domain-containing_protein_1 [MW = 112.78 kDa]

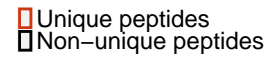
No. of times detected



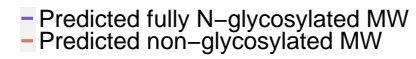
log(intensity)



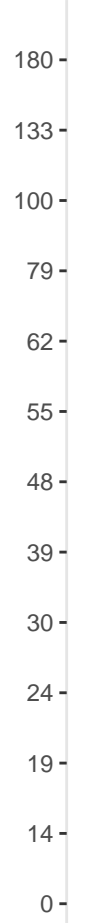
Values from



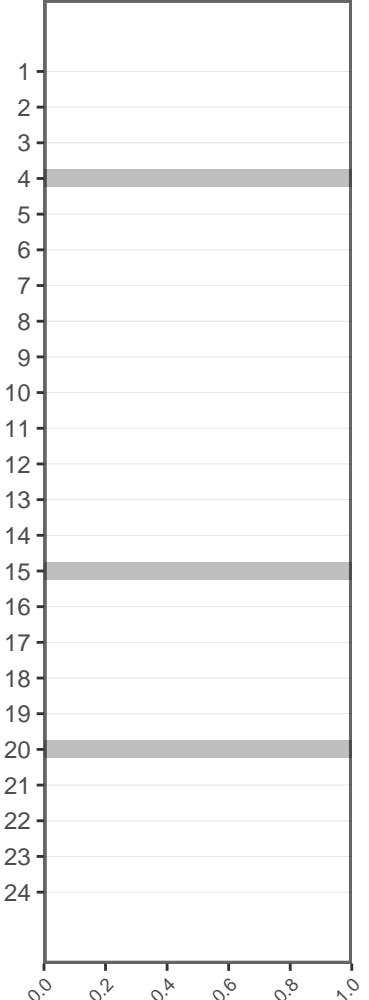
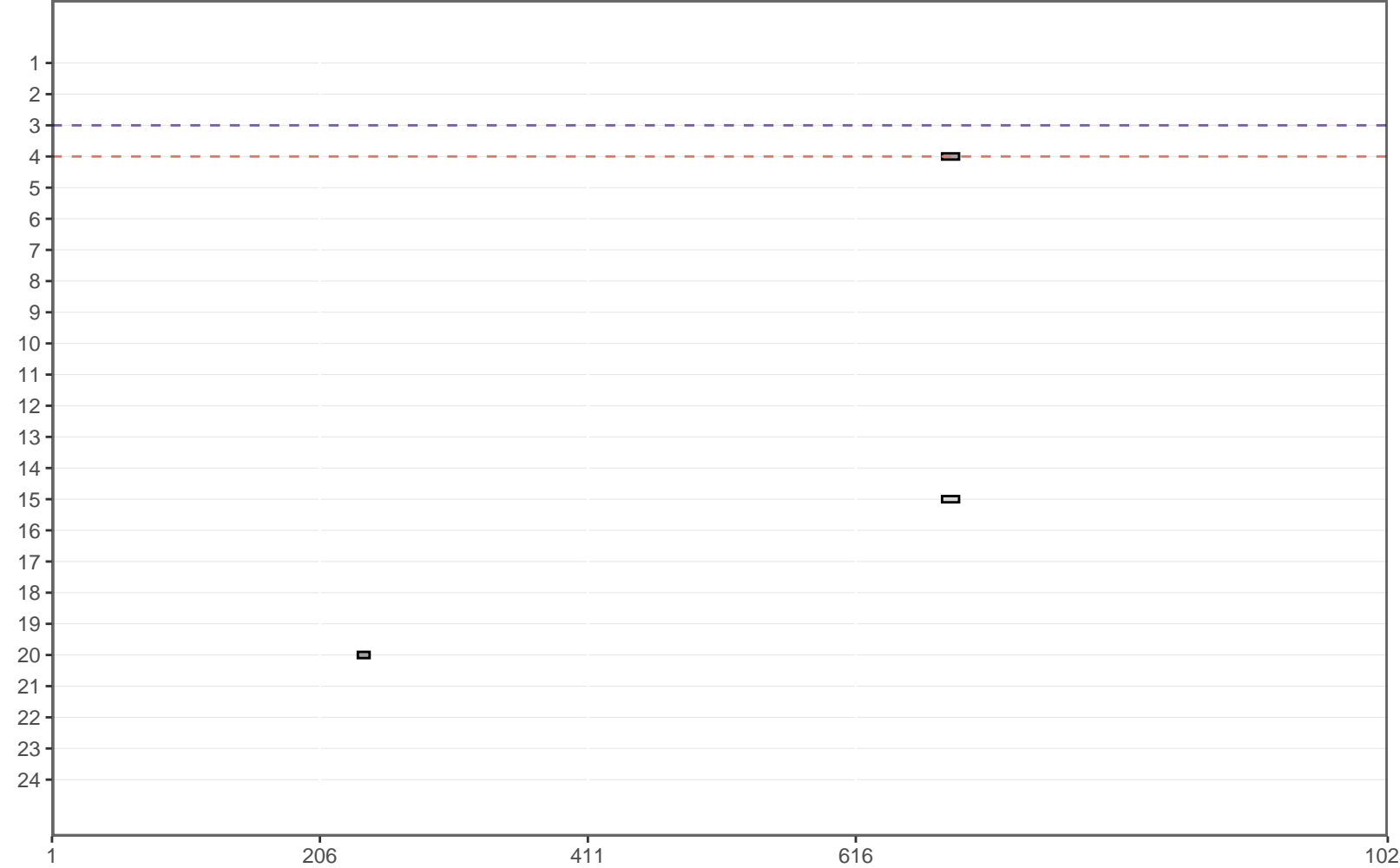
MW indication



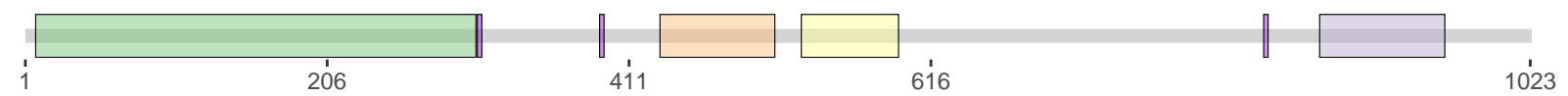
Molecular weight



Gel Slice

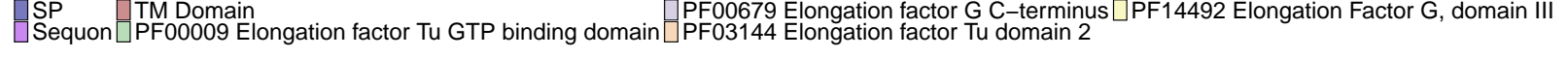


Protein length



Pfam domains

Pfam Description



Protein sequence:

SLAQHLKSATLSSTLNDGWPLSSMVFQVSPMLKVAIEPESDADMGALIKGLRLLNRRADPFVEVSVSARGEHVLSAAGEVHLERCGKDKLKERFAKINLKVSPPLVDFKETEIEGDTANPLENKLKLRSEFELEKATPNAGRVIRVIRVMKLPALTALIKLLDENGLLDGHHGKVLGACRILETLFRGNIVEDENPIEALKRLIDAVEESDSSTGFATETEEDRIDKGGKMMWQKFLKRWALGPRQMGFNILFTPDVWKGKSDDAEVLKGGPPVSEKLGFMGDSGNNGSTRESSTSVYDITLLI

NbL13g17050.1 notchless_protein_homolog [MW = 53.15 kDa]

No. of times detected



log(intensity)



Values from



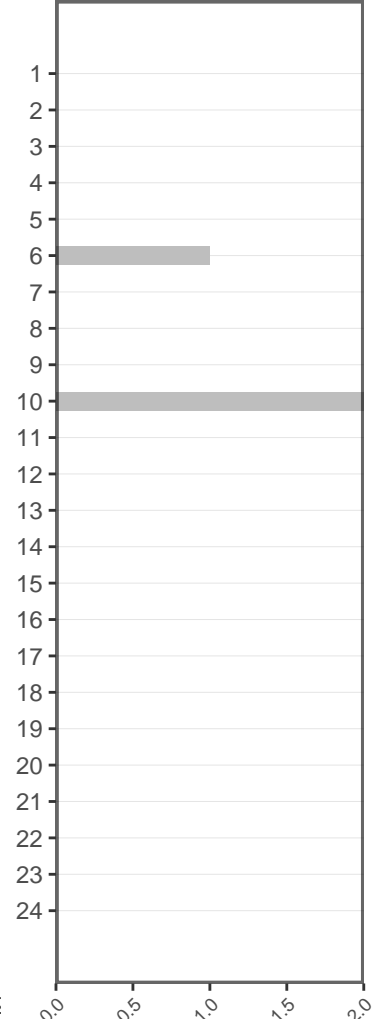
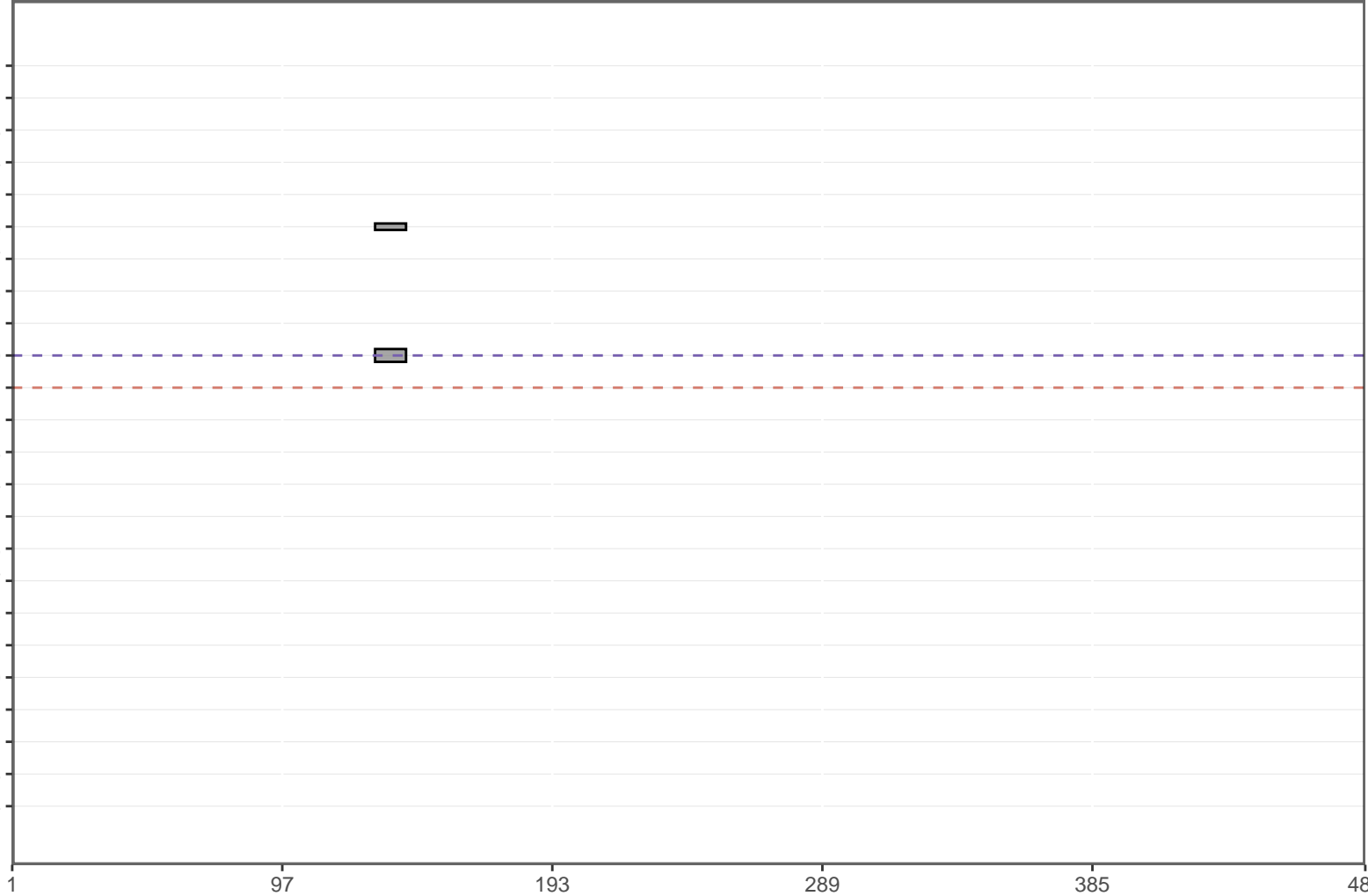
MW indication



Molecular weight



Gel Slice

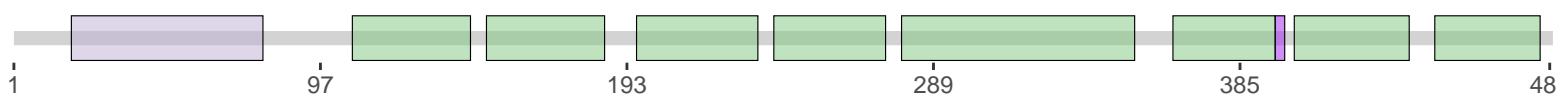


Protein length

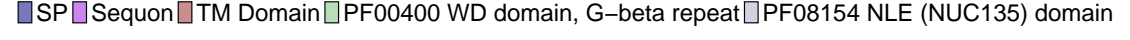


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IRIWDITTRKLCICLGGHTLAITGVKGGDGVYTGSGDCTKHWETLGGKLIRELKGGHGVVNSLALSTEVYLRGGAFDHTGKGVSSPEEMKVALERYNKMKGNAPELIVSGSDDFTFMLWEPVRSKHPKTRMTGHDGQLVNHVYFSPDGGVWASAFDKVYKLVWNGTGTGKFAAFRGHVGPVYQISWASADSRLLLSGSKDSTLKVWDRITKTKLKGDLPGHADEVFAVDWVSPDGEKVASGGKDRVLLKLMWG*

NbL13g16870.1 histidinol_dehydrogenase_chloroplastic-like [MW = 52.8 kDa]

No. of times detected



log(intensity)



Values from



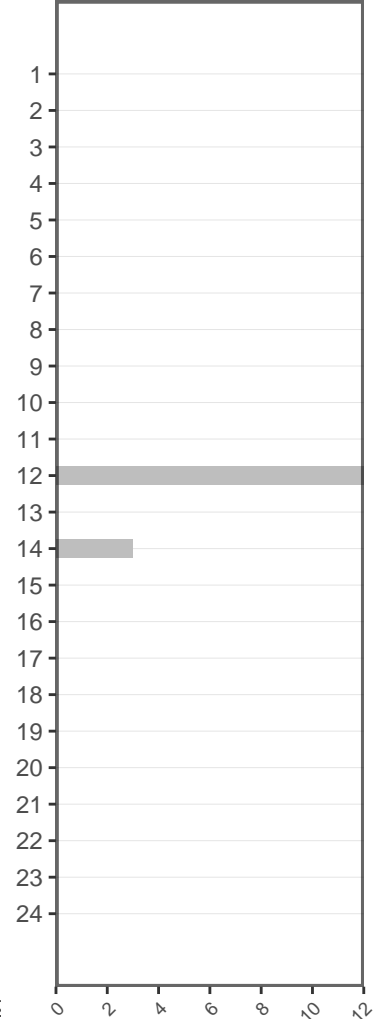
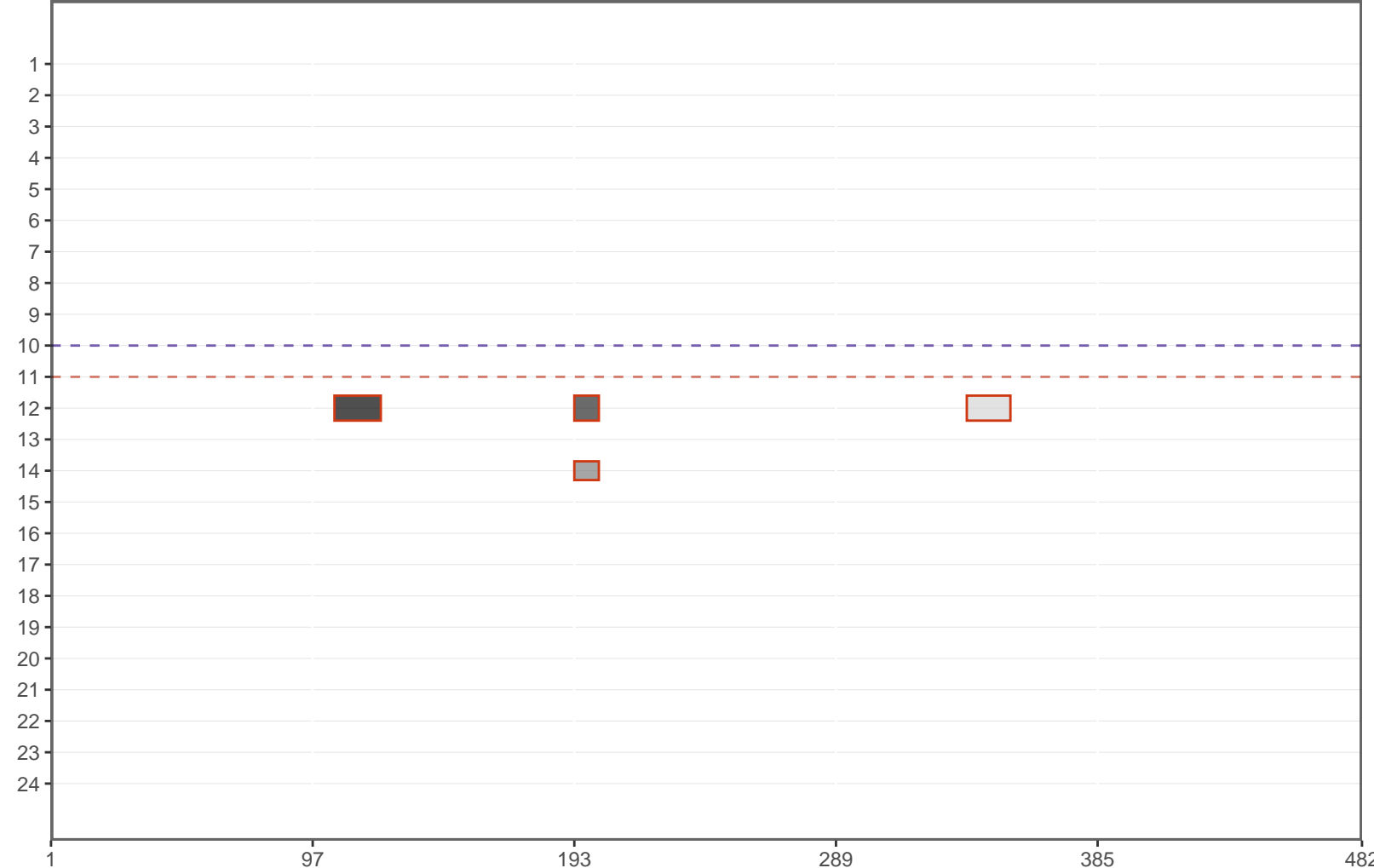
MW indication



Molecular weight

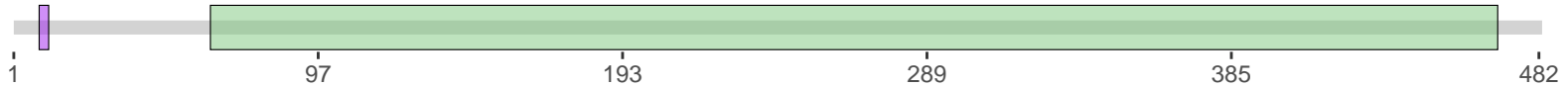


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL13g16810.1 elongation_factor_TuA_chloroplastic [MW = 51.96 kDa]

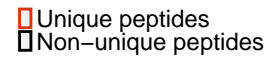
No. of times detected



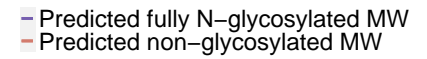
log(intensity)



Values from



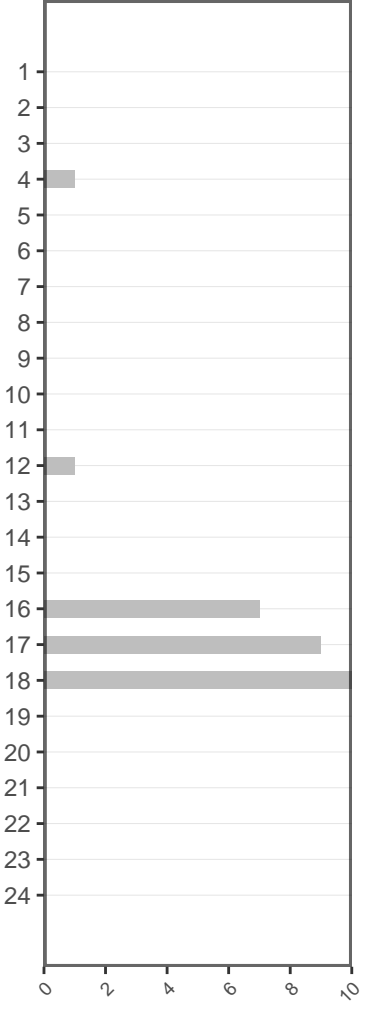
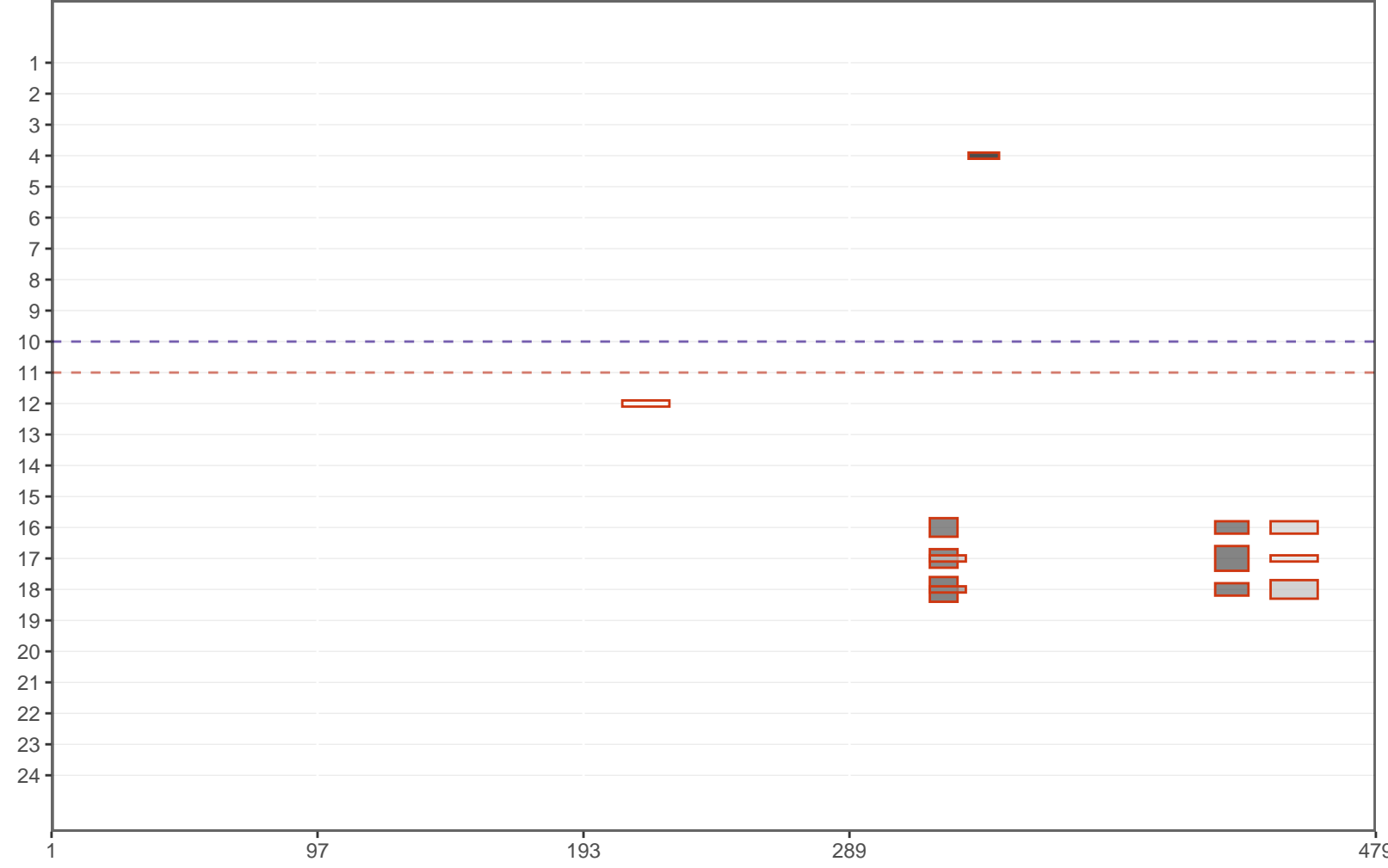
MW indication



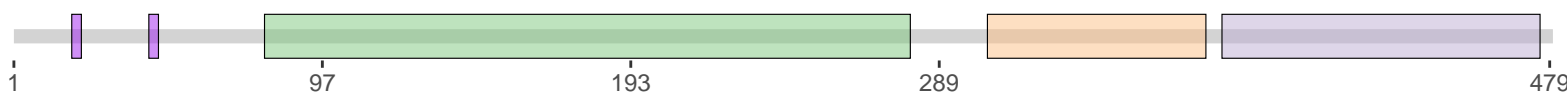
Molecular weight



Gel Slice

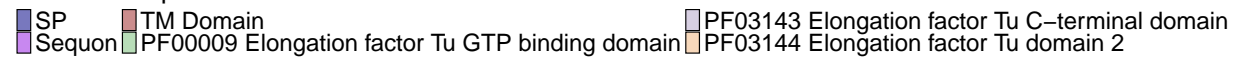


Protein length



Pfam domains

Pfam Description



Protein sequence:

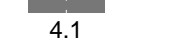
LLSSYFPGDCIPISGGSALLALEALMANPBIKRGENDWQDKVELMDVDSVPIPIVROTTEFLFMAIEDVFSITGRGTVATGRVGRGTVRIGDITDVLQKDTSTTGTGVEVMPQKILDEAMAGDNVQLLRGKIDKIQKGMVLANPCTTPTHTKFEANVYVKKEEGGRHSFFFGVIRPQFYMRITDVTGKVSFTDKGEESSKMMVPGDRVNLVVELMPVAGEGGMRFAIREGGKTVGAGVQKIEI

NbL13g16750.1 manganese-dependent_ADP-ribose/CDP-alcohol_diphosphatase-like [MW = 35.78 kDa]

No. of times detected



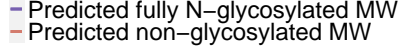
log(intensity)



Values from



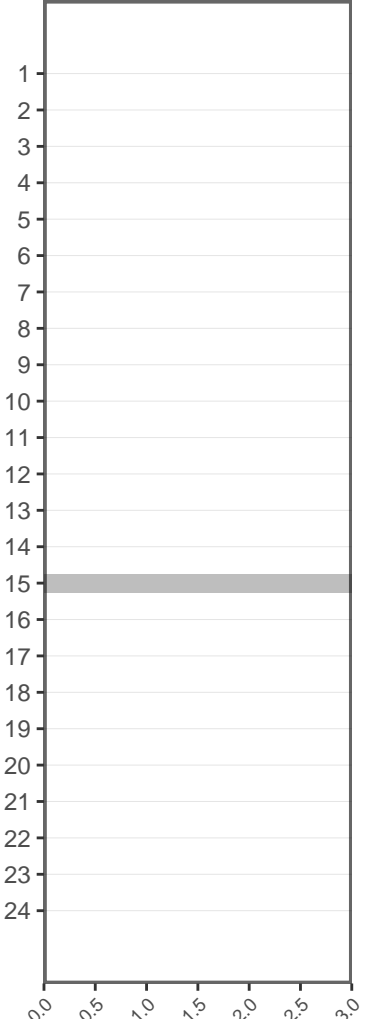
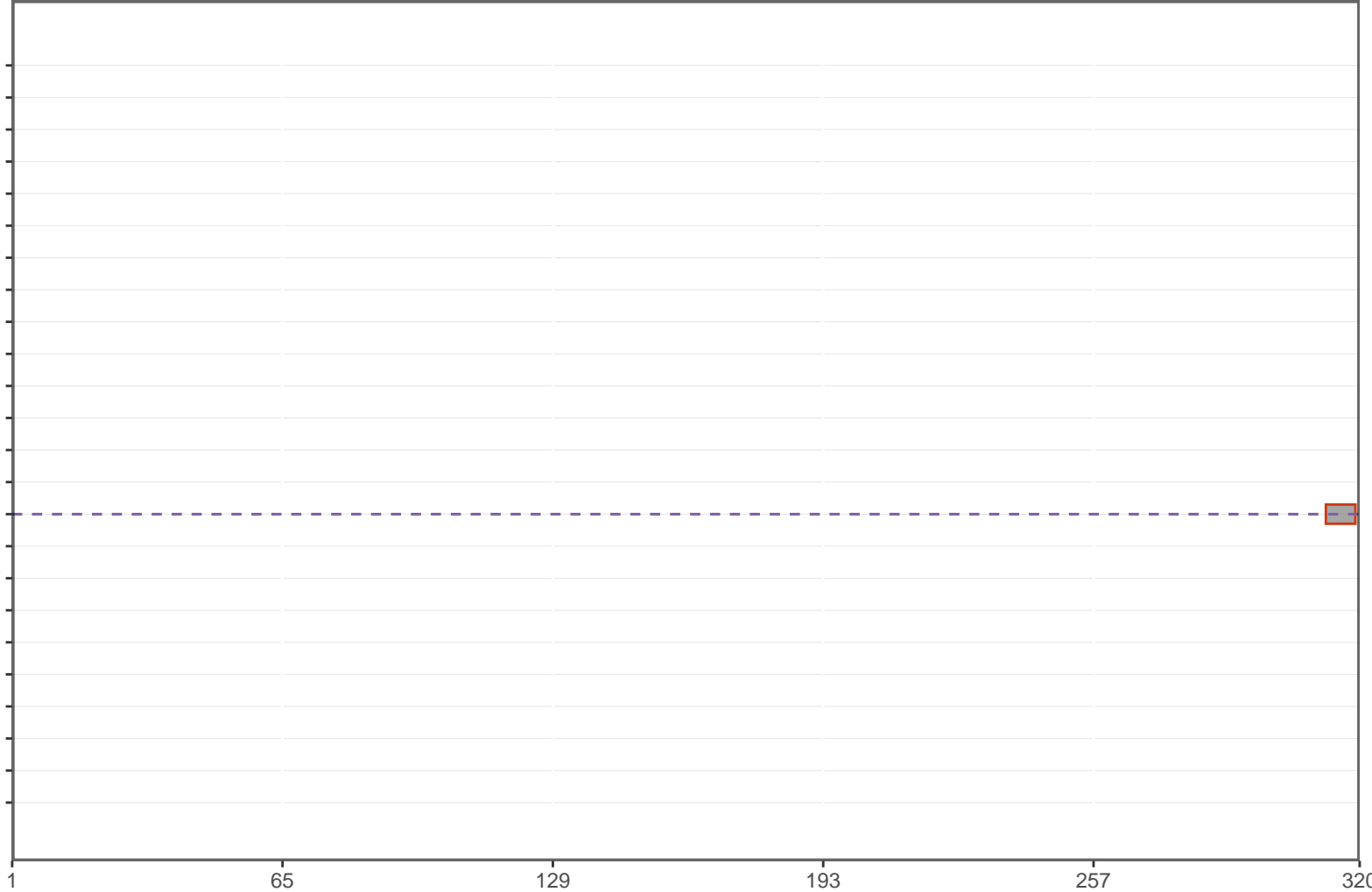
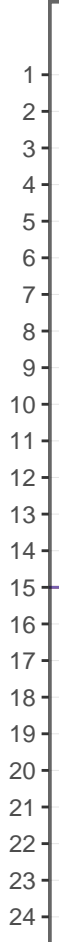
MW indication



Molecular weight

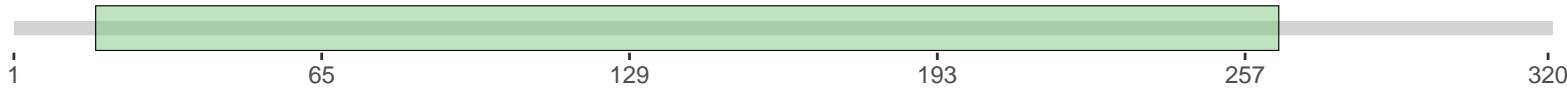


Gel Slice



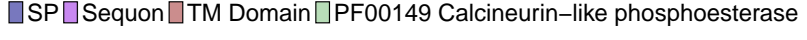
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AIGWPEIHPNTLKALKVIGERNFNSKNSPGLVGLERRFLKFNQGVKQEGLEWLDHVLGEATELNGNIVVCGHLPLDPGASSFAALLWNYDEVMDVHRYSQVYKVLGGHAKKGGQVDSHGVRHRYLEAALEGPPGTDVAFGHIDAFNDRLSLFGNDRMKSSSEMVFQHP

NbL13g16740.1 quinolinate_synthase_chloroplastic [MW = 78.24 kDa]

No. of times detected



log(intensity)



Values from



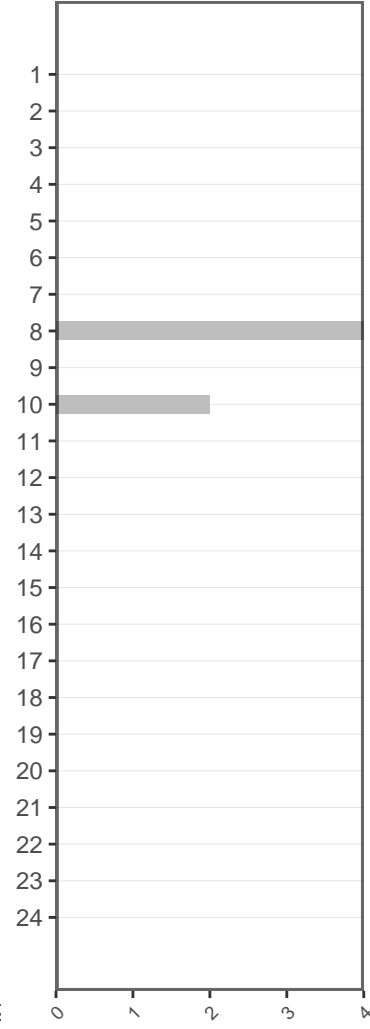
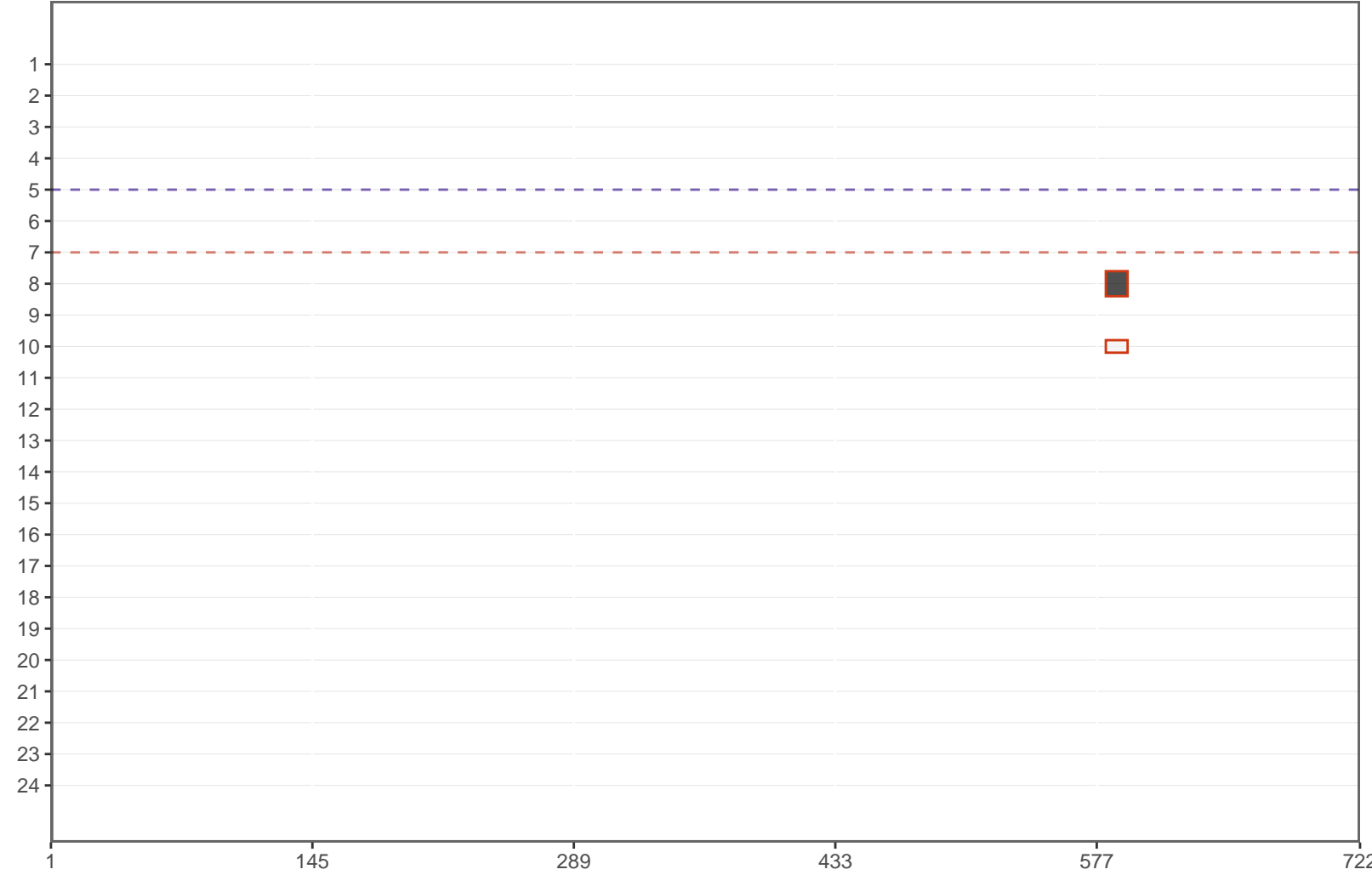
MW indication



Molecular weight

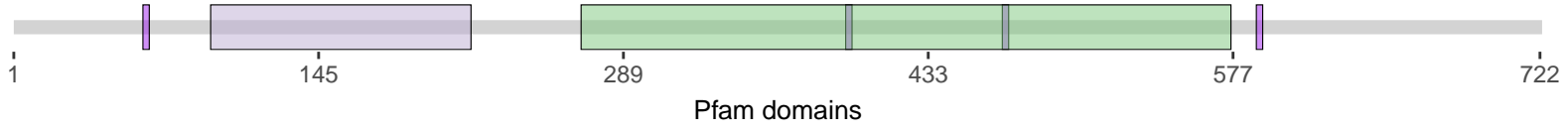


Gel Slice

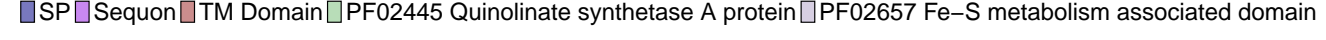


Protein length

Peptide counts over 4 repeats



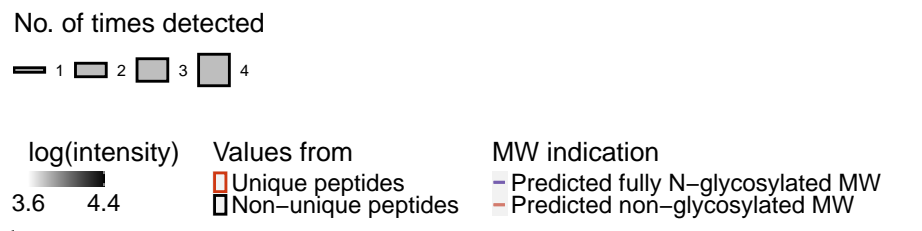
Pfam Description



Protein sequence:

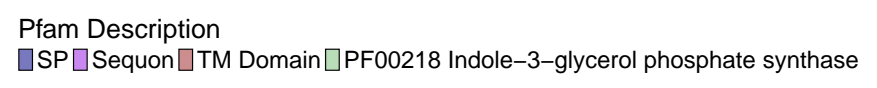
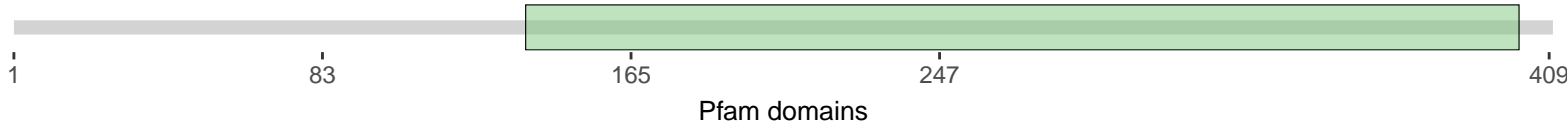
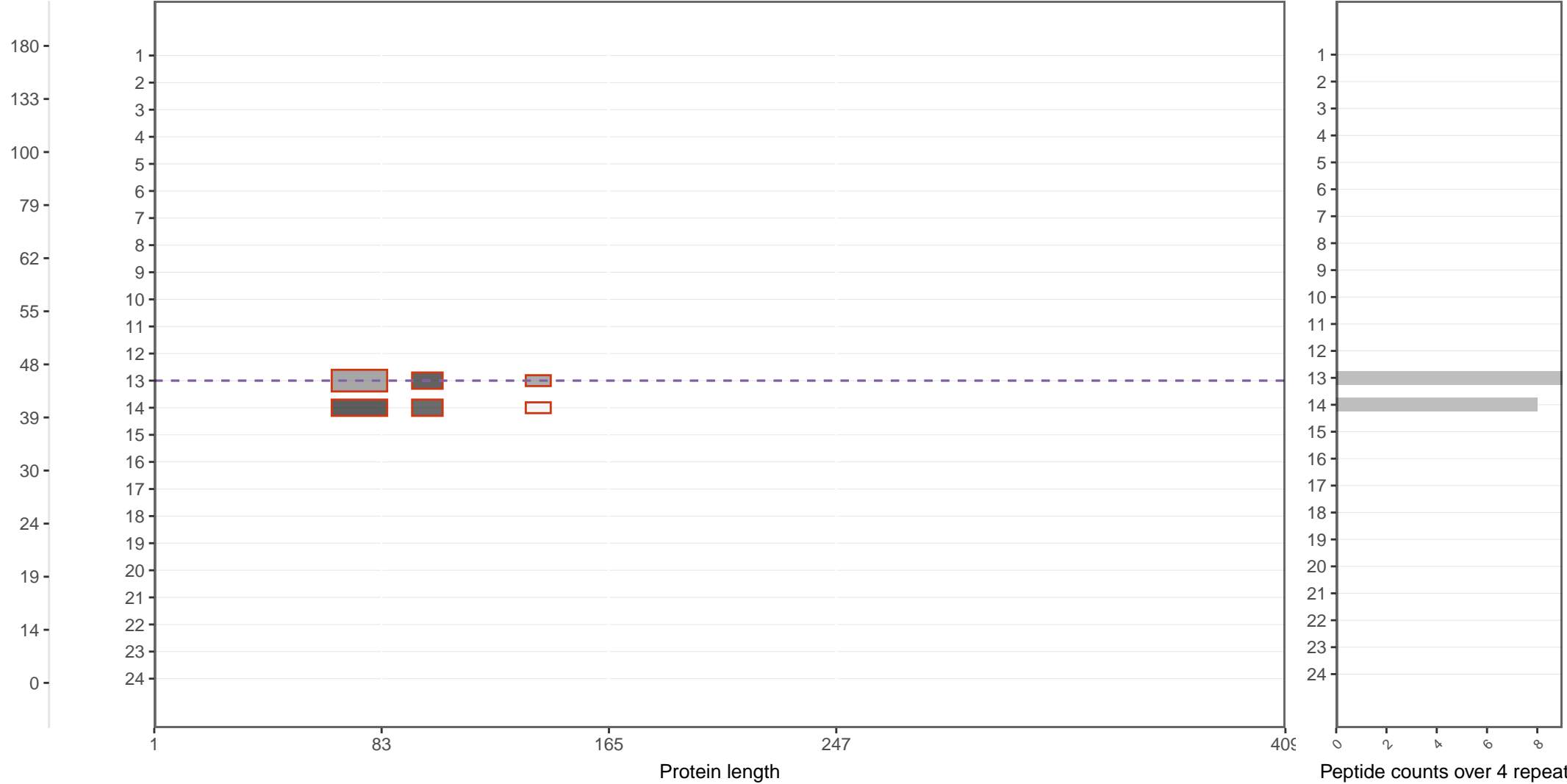
IGPFEVGVYRMSDERIGGLADAAAPRYLDDHAKTASTSSPSLHVHINTSLETKAVSHELVPYTTTGTGSNNVQTLGAFVAPDLEVALVGPDTYMGSNLIELFTQMTMTDDEEISEHPLHNRSSKSLPLRLHYFDGDTGVHHLFGHEVVENNEMYGDAFLTAHFEVPGEMFSLAMEAKRKGMGVVGSTENLDFIKERVEEALDRNVDEHLOFVLGTESGMITAAVAAGKLLGSDANSGGAKVSEVEFPVSSSEVTRTSTGSSLEQNKINIPGVASGECCLSHGGCASC

NbL13g16690.1 indole-3-glycerol_phosphate_synthase_chloroplastic-like [MW = 45.03 kDa]



Molecular weight

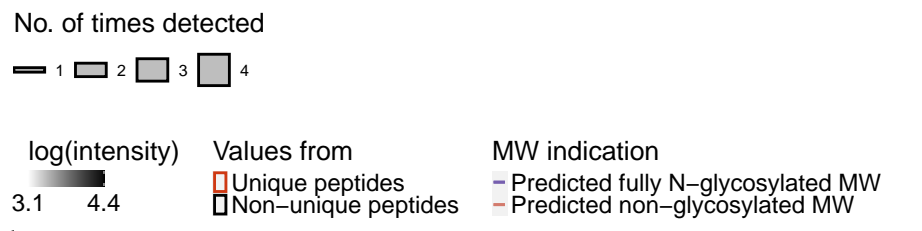
Gel Slice



Protein sequence:

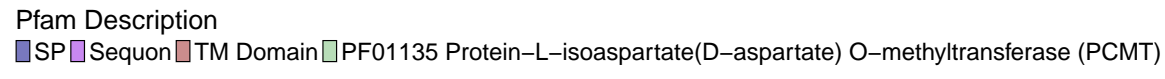
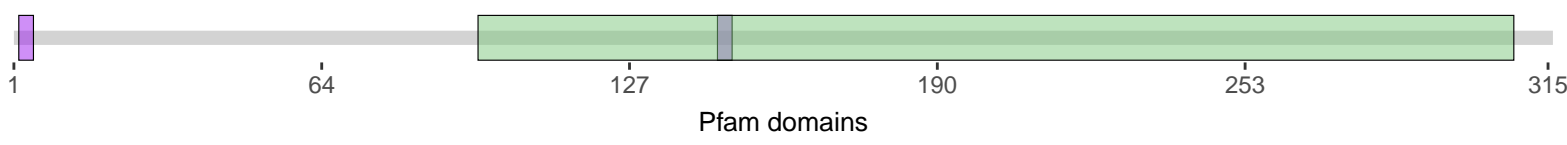
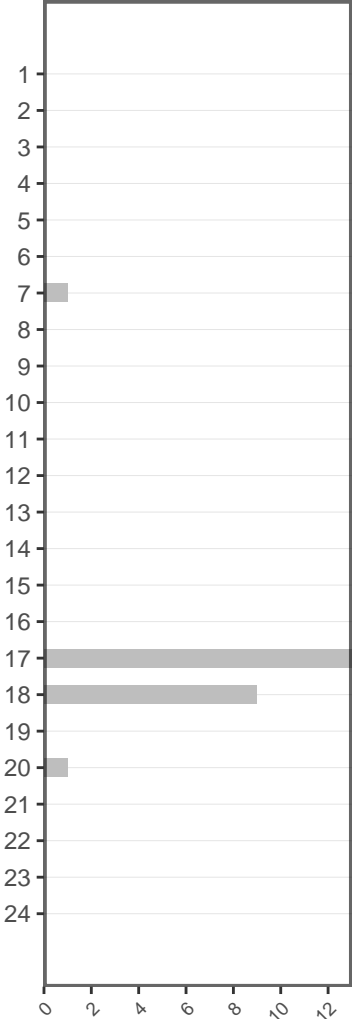
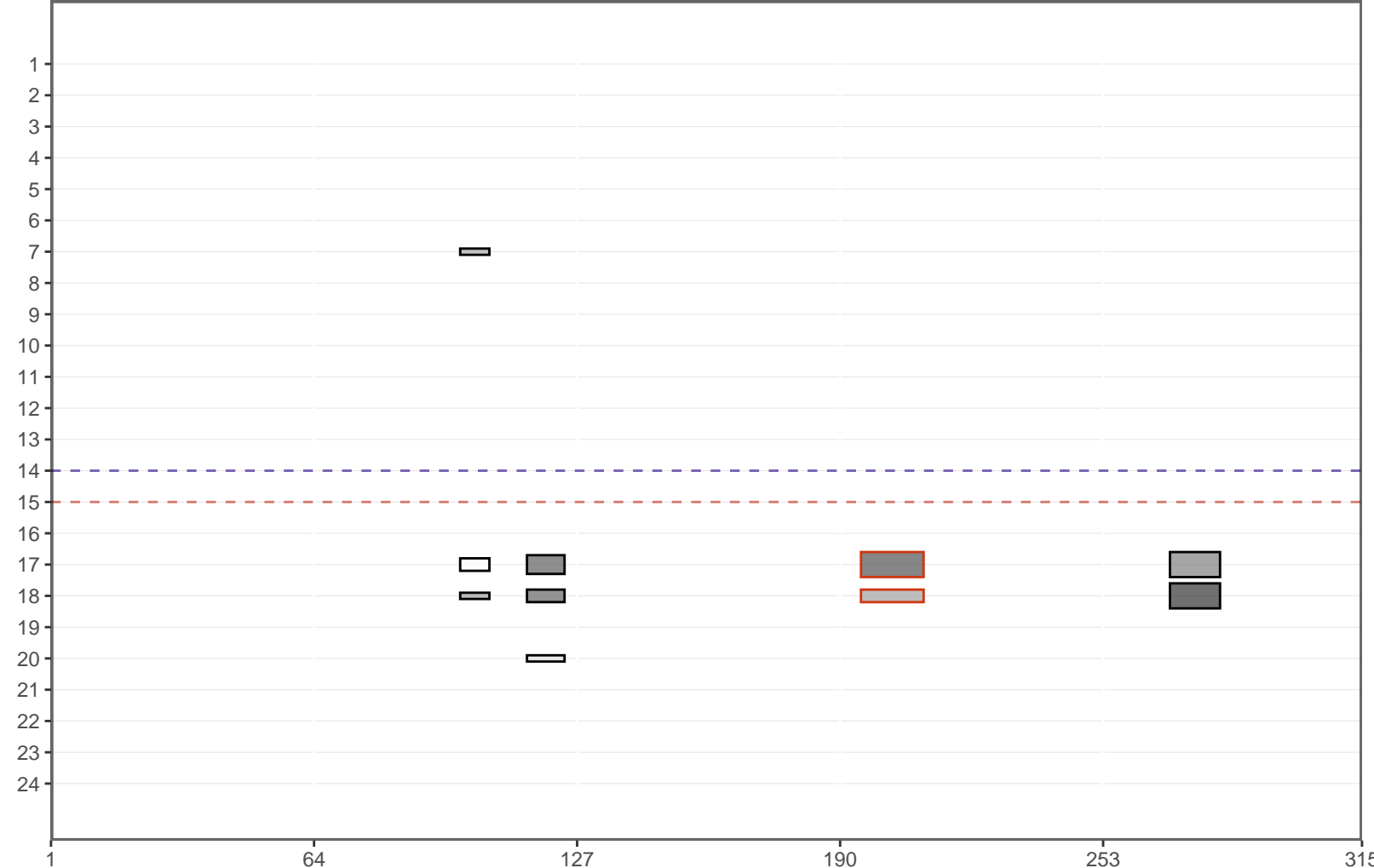
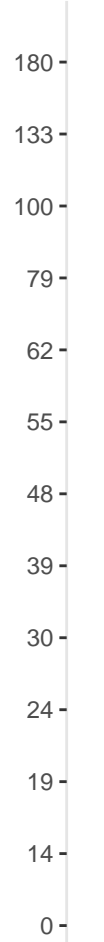
IAEVKASPSRGVLRDFNVEIAKAYERGGAGLGLVLRDQKYGQSFENLEARNAGVECPLLKQEFVIEAWQLYARVKGADAVLLIAVLPDLIDKYMKKICKLGLTALVEVHDEREMDRVLGIDGVELGNNRDLGTFKVDISNTKILLEGERGERREKGIHVGEGLFTRDAIVQEAQVAVLVGSELVWQDPQPTKGRLELFGKDISG

NbL13g16670.1 protein-L-isoaspartate_O-methyltransferase_1-like [MW = 34.57 kDa]



Molecular weight

Gel Slice



Protein sequence:
 ITISAPMIMAMCLELLEDRLGPMHALLDVGSGTGYLTAGFALMVGPDGRAGVVEHPELVAWSTKNVERSAAPLLKEGSLHVGDRKRWPEHAPYDSHVGAAAAADVPQDLDLQKPGGRMVPVGTFFQDKKVIDKNLDGVSVRSETSVRVVPLTSREQLKGT

NbL13g16650.1 protein_ABHD17C-like [MW = 42.59 kDa]

No. of times detected



log(intensity)



Values from



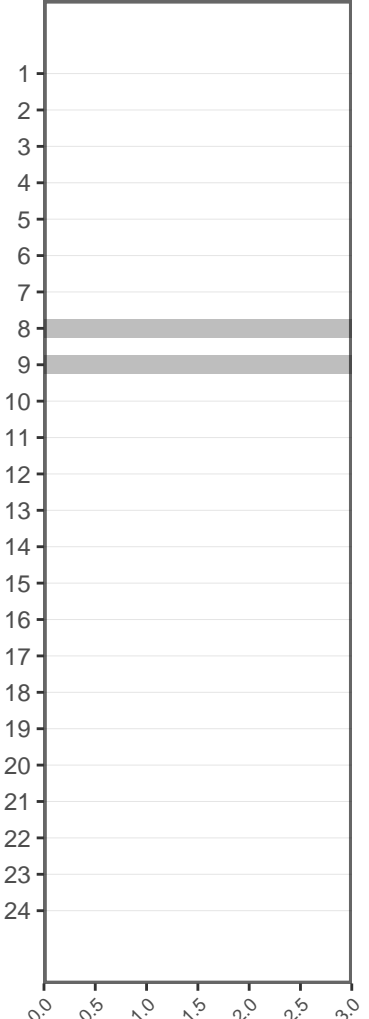
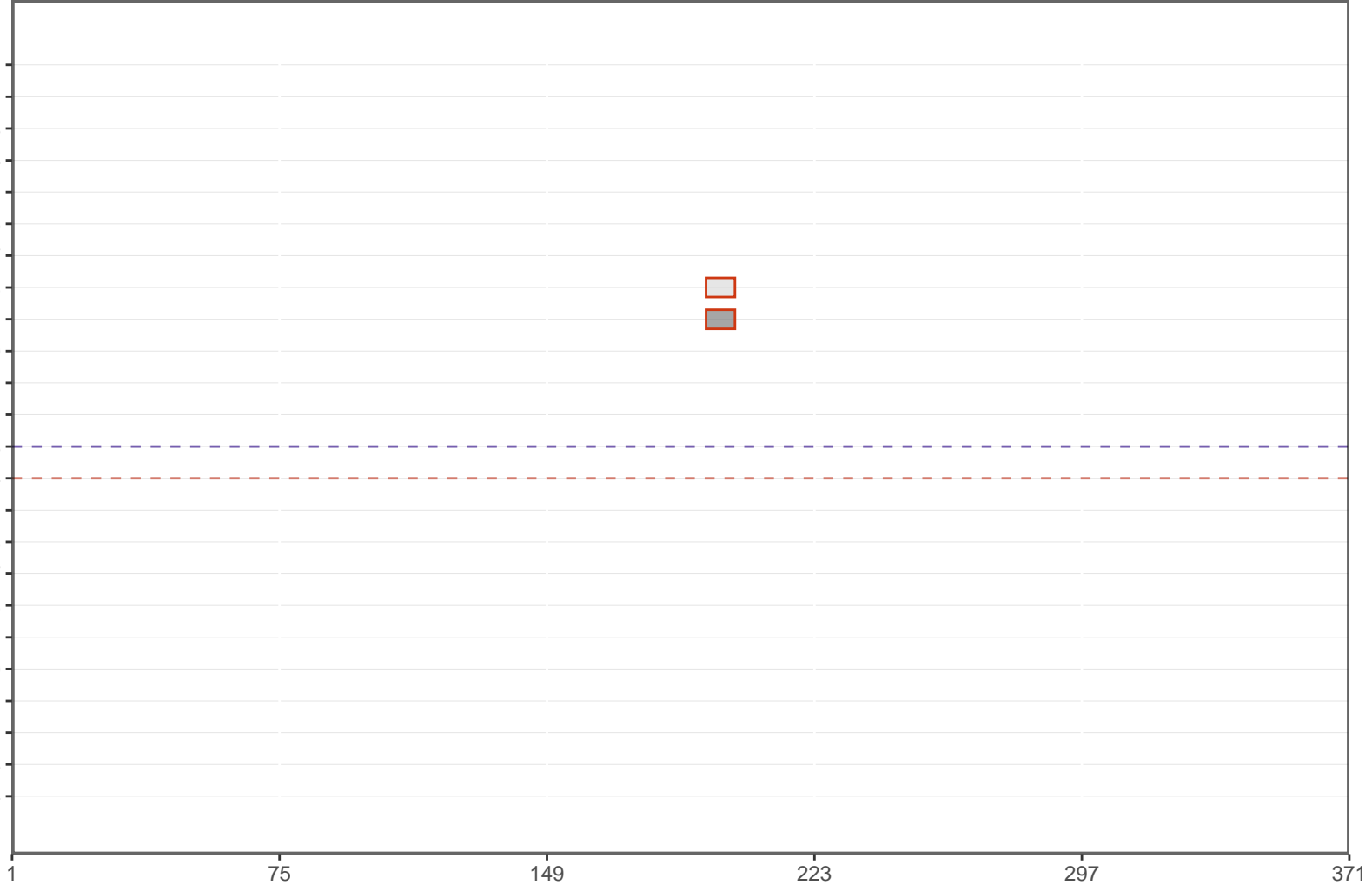
MW indication



Molecular weight



Gel Slice



Protein length

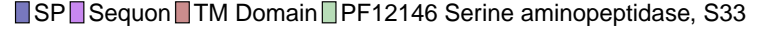


Peptide counts over 4 repeats

Pfam domains



Pfam Description

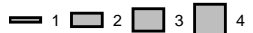


Protein sequence:

ILRVVYFVWRTYVFDIYKNDKPLKGPVLIHGTSDSEVVDGSHGKGLWELDGEKYEFLWIKGTHDLELYPEYRVLKKEFVSTVEKPPDGRNLSRKSISDRFEGSRKSTDFEGPRKSTDWREKPKRSTDKPENFKNYDYKFSIEDNIGKLRMSFDQVVERGARVSEFFEKPRRSDQOMEKARKSEVDWLDRIKAG

NbL13g16620.1 vignain-like [MW - SP = 38.25 kDa]

No. of times detected



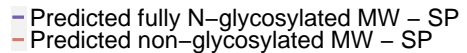
log(intensity)



Values from



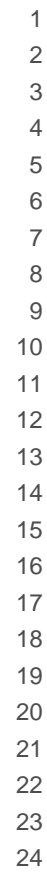
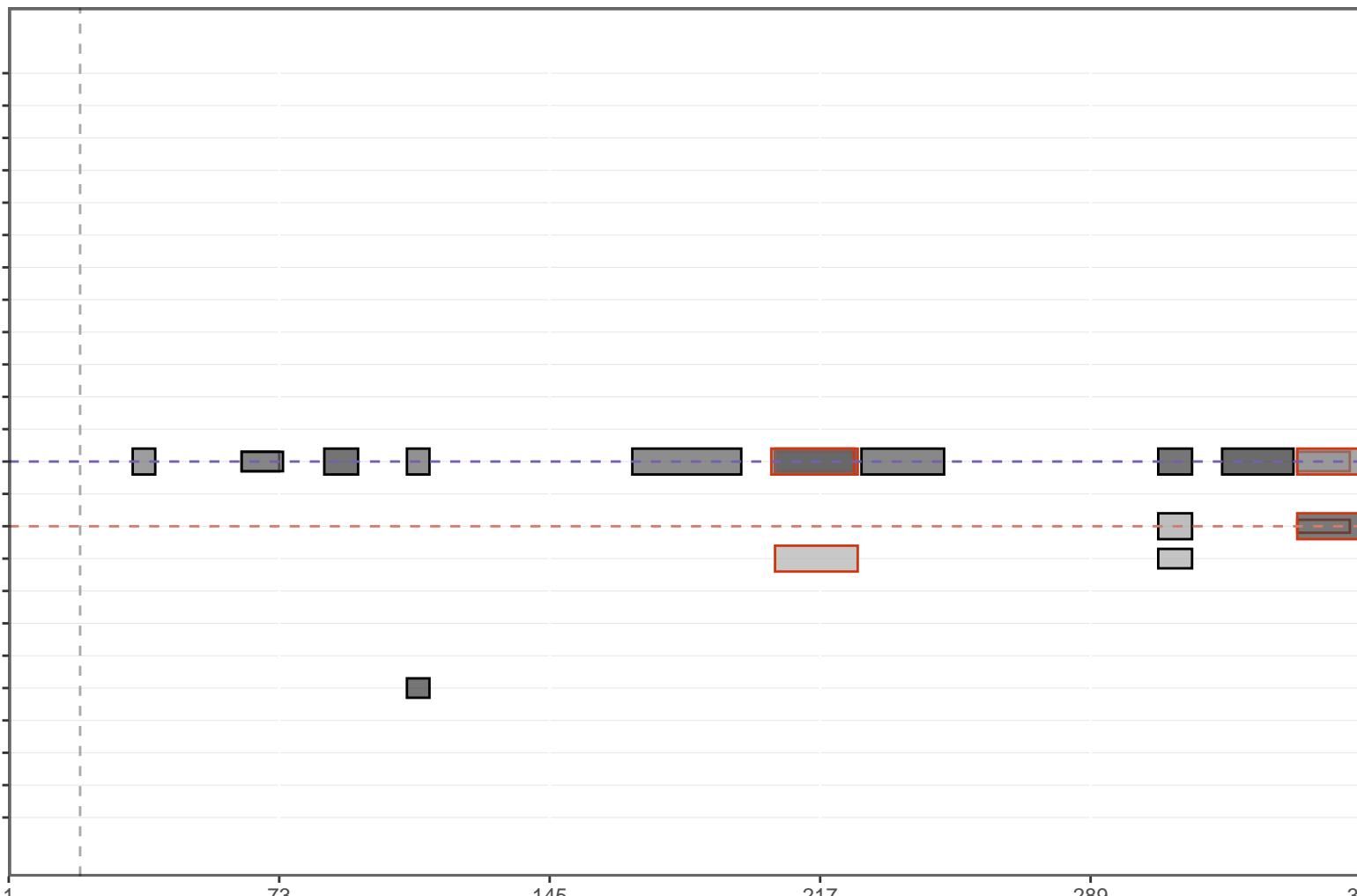
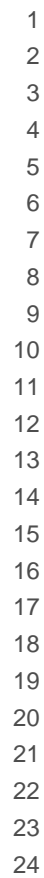
MW indication



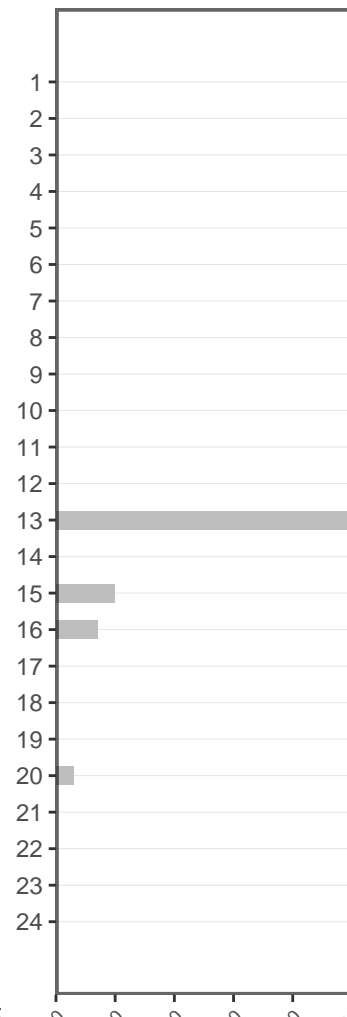
Molecular weight



Gel Slice



Peptide counts over 4 repeats

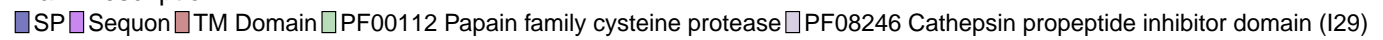


Protein length



Pfam domains

Pfam Description

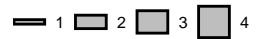


Protein sequence:

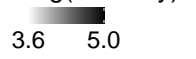
IELVLSSEGLVDCDFGNGGNGGLMDKAFERFKKGGINTEDNYPYMAEDGEGCDGKRNSPVSIDGHEVPPNDEGGLLKAVANQPVSVAIGASGSDFGFYSEGFTGDDGTELDHGVAIVGYGTTLDGTYWIKNBNWGPPEWGEKGYRMRQREDAEEGLGIAAMPQSYPIKTSSENPTGSPATTKDEL

NbL13g16610.1 peptide_methionine_sulfoxide_reductase [MW = 22.1 kDa]

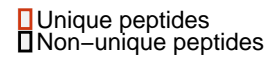
No. of times detected



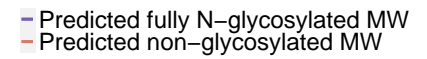
log(intensity)



Values from



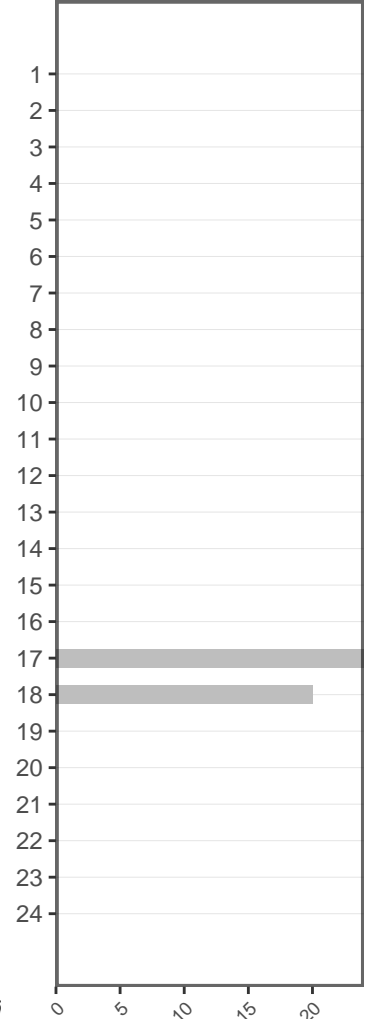
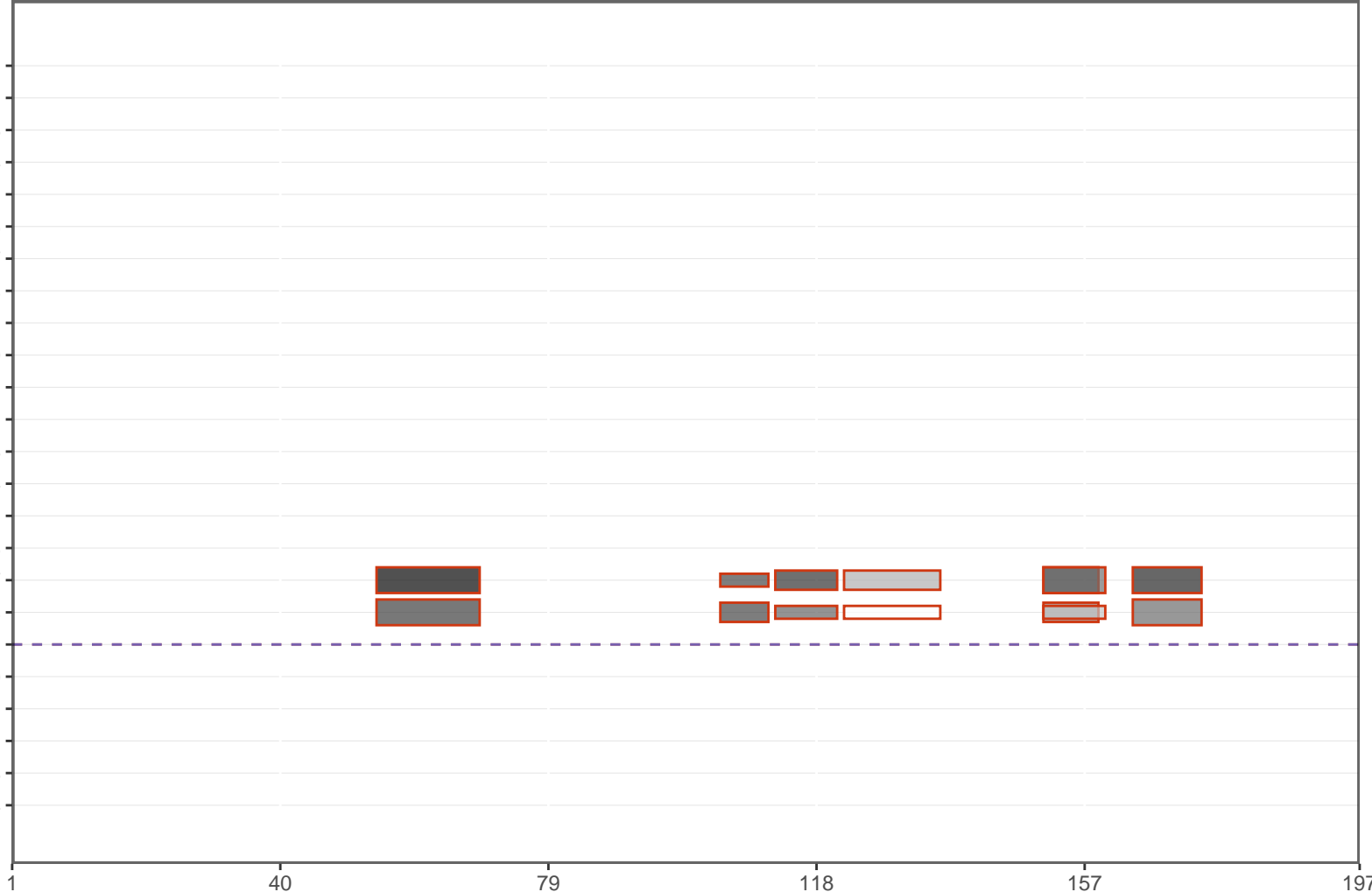
MW indication



Molecular weight

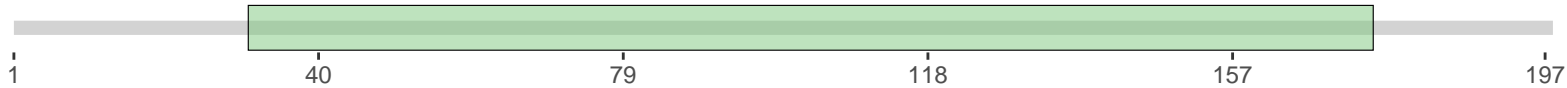


Gel Slice



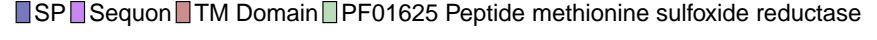
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

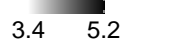
FDPNVCPYTNLLSLFWSRIDPFTLNROGNDVGNQYRSGIYYNEAQAQLAREBLEAKQKFAFKKIVTEILPAKRFYRAEEYHGGYLEKGGGRGAKGSAKGNDRPQYV*

NbL13g16460.1 GDSL_esterase/lipase_At3g48460-like [MW - SP = 38.72 kDa]

No. of times detected



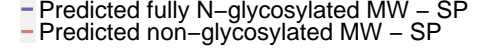
log(intensity)



Values from



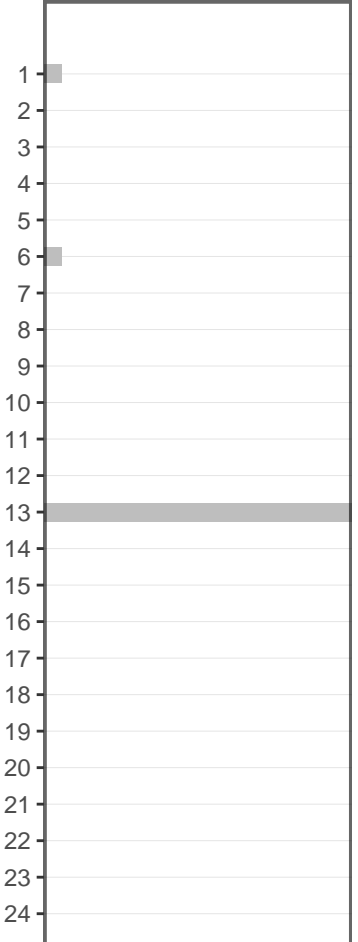
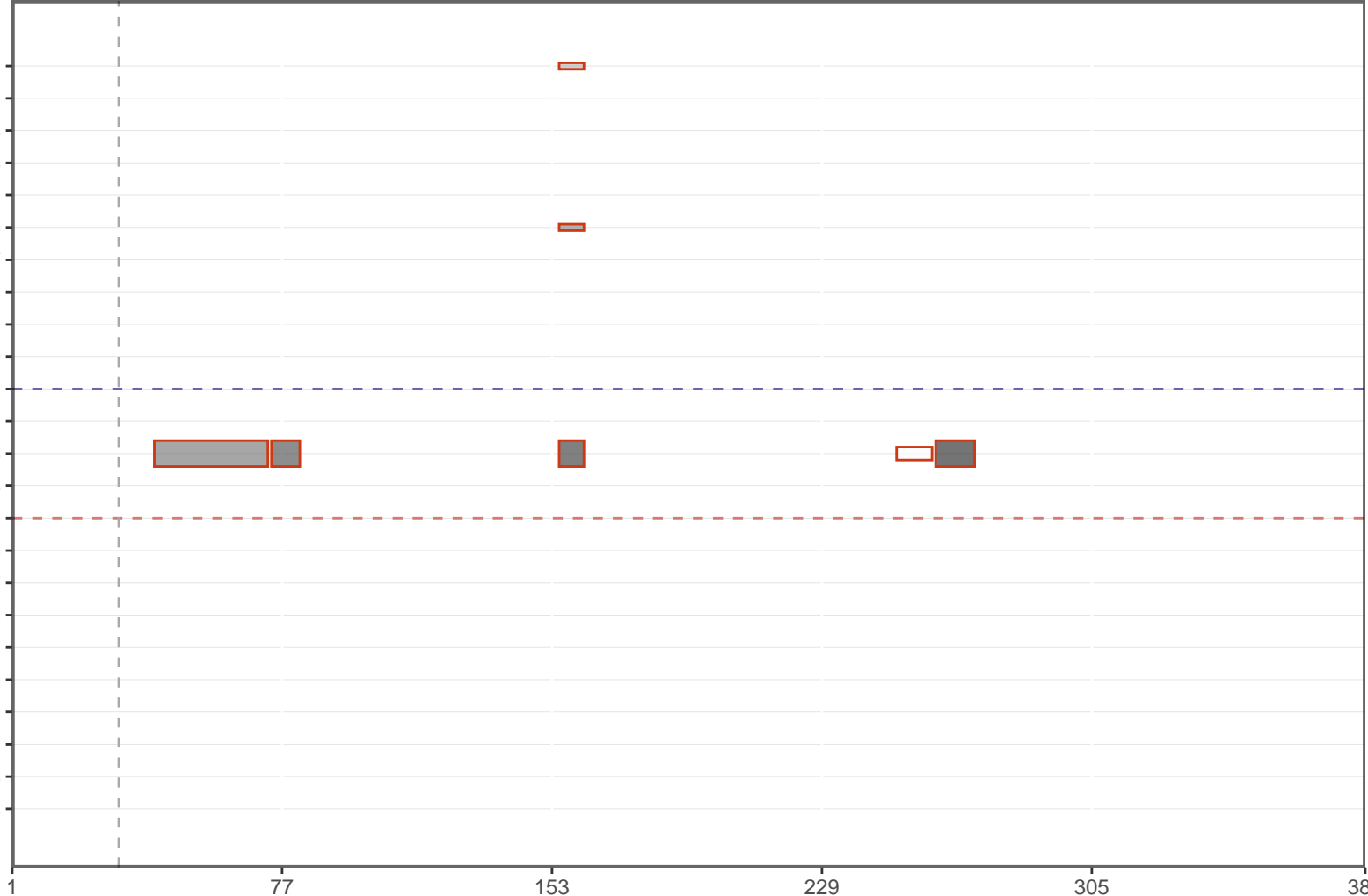
MW indication



Molecular weight



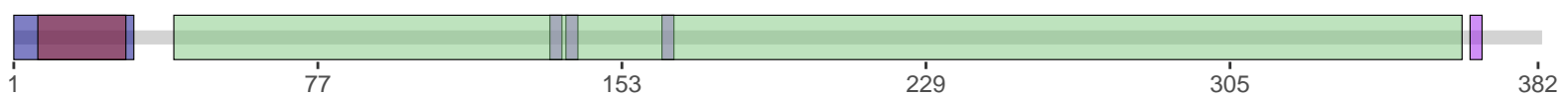
Gel Slice



Protein length

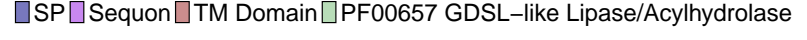


Peptide counts over 4 repeats



Pfam domains

Pfam Description

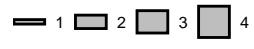


Protein sequence:

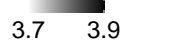
FWVGEIGANDYVYVYFSGSSEVSPNTHQLATLSTLFLQVLLKNGAKYVYVGLPPTGGLTFLMFLAPETDRDDMGVGVSDKGSNLHNNIGTKLDSFRKGFQAVIADYVWYAVSTVYVYGANKYGFKEIFKBSGGGGGNYNFDVFNTCGSPRATSGPDPDSQYINWDGVLTEAMFKAMANLFLNGTFCKPFFSYLLAKKQ

NbL13g16370.1 ubiquitin-like_modifier-activating_enzyme_5 [MW = 46.84 kDa]

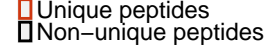
No. of times detected



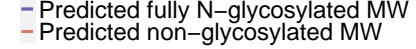
log(intensity)



Values from



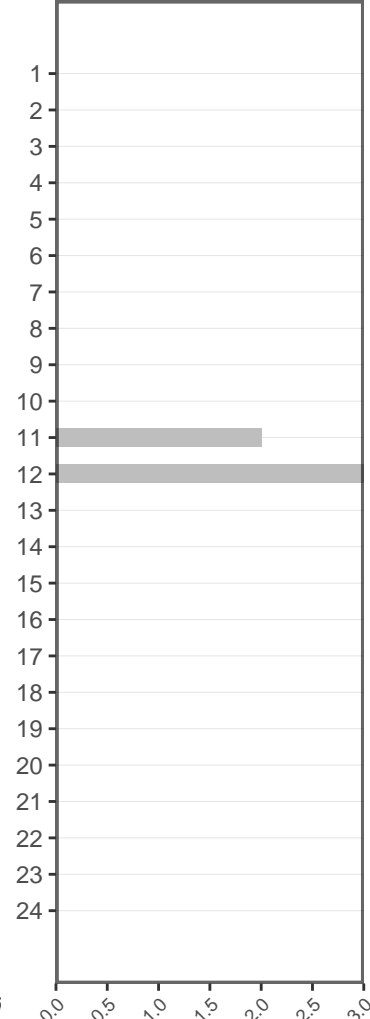
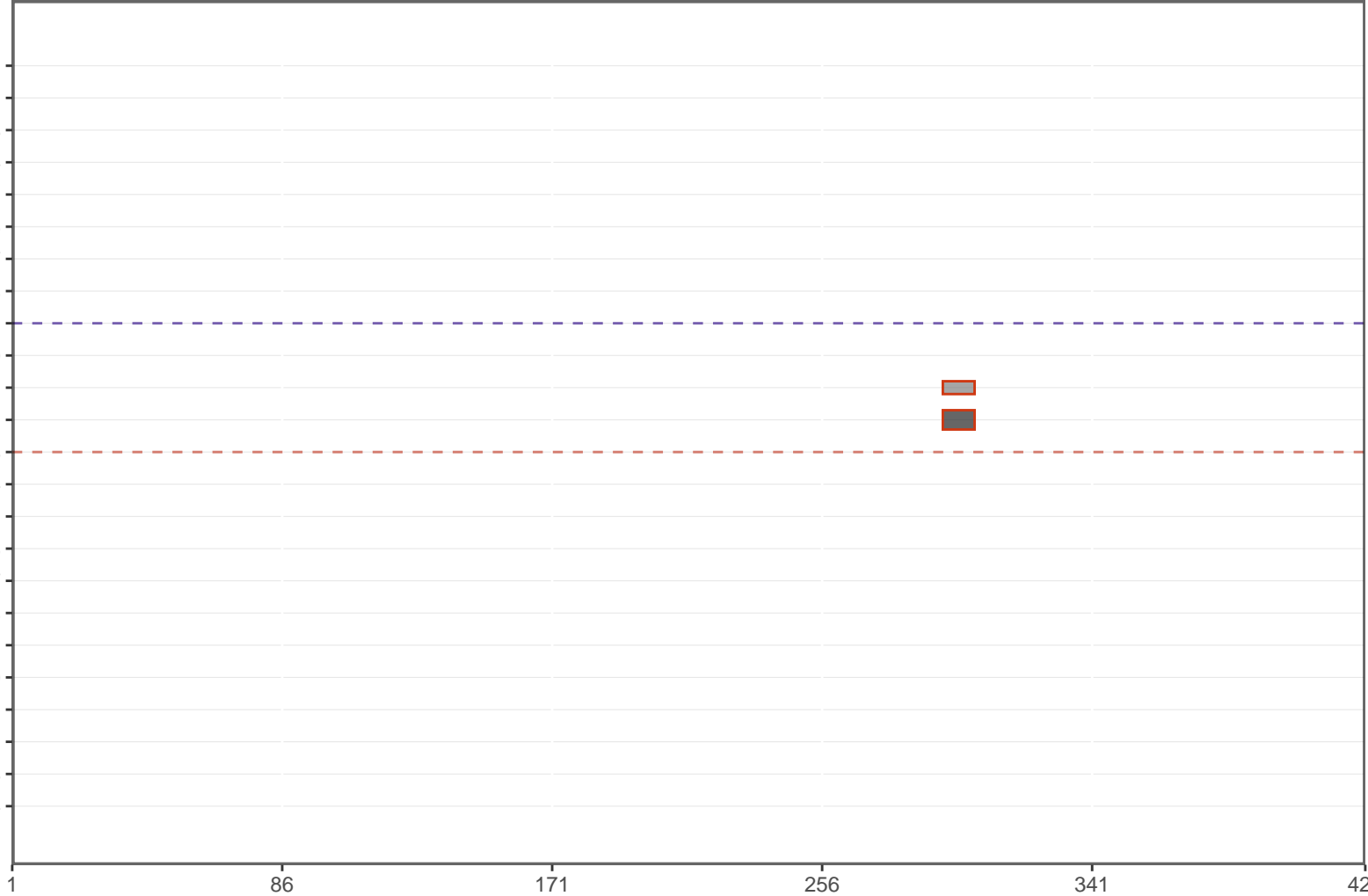
MW indication



Molecular weight



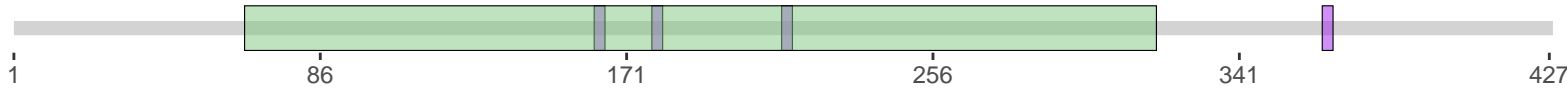
Gel Slice



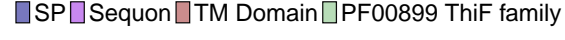
Protein length



Pfam domains



Pfam Description



Protein sequence:

IARMLVYDQACNELNDQTMMEISGVSEDAVSGHQLIPGESAGFAGVPLVVASGIDERTLKRREGVCAASLPTFMGVAGLLVQNTFLKYLKFRGRVSPVLYGNALNKDFPTMEMKPTQGGSNVAGLERQKEYLAKPTRDAVAKAKADKEALSTPENPVHADNEWNIISVLDQNEVDLISRHSGLVPEGIHVHELPADEVPKPAITEVGNPHDLEELRQLEALNAD

NbL13g16360.1 UPF0235_protein_At5g63440 [MW = 25.8 kDa]

No. of times detected



log(intensity)



Values from



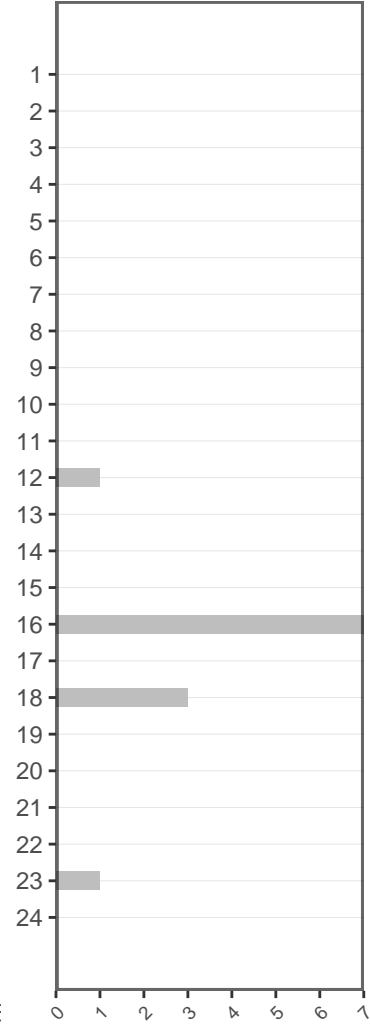
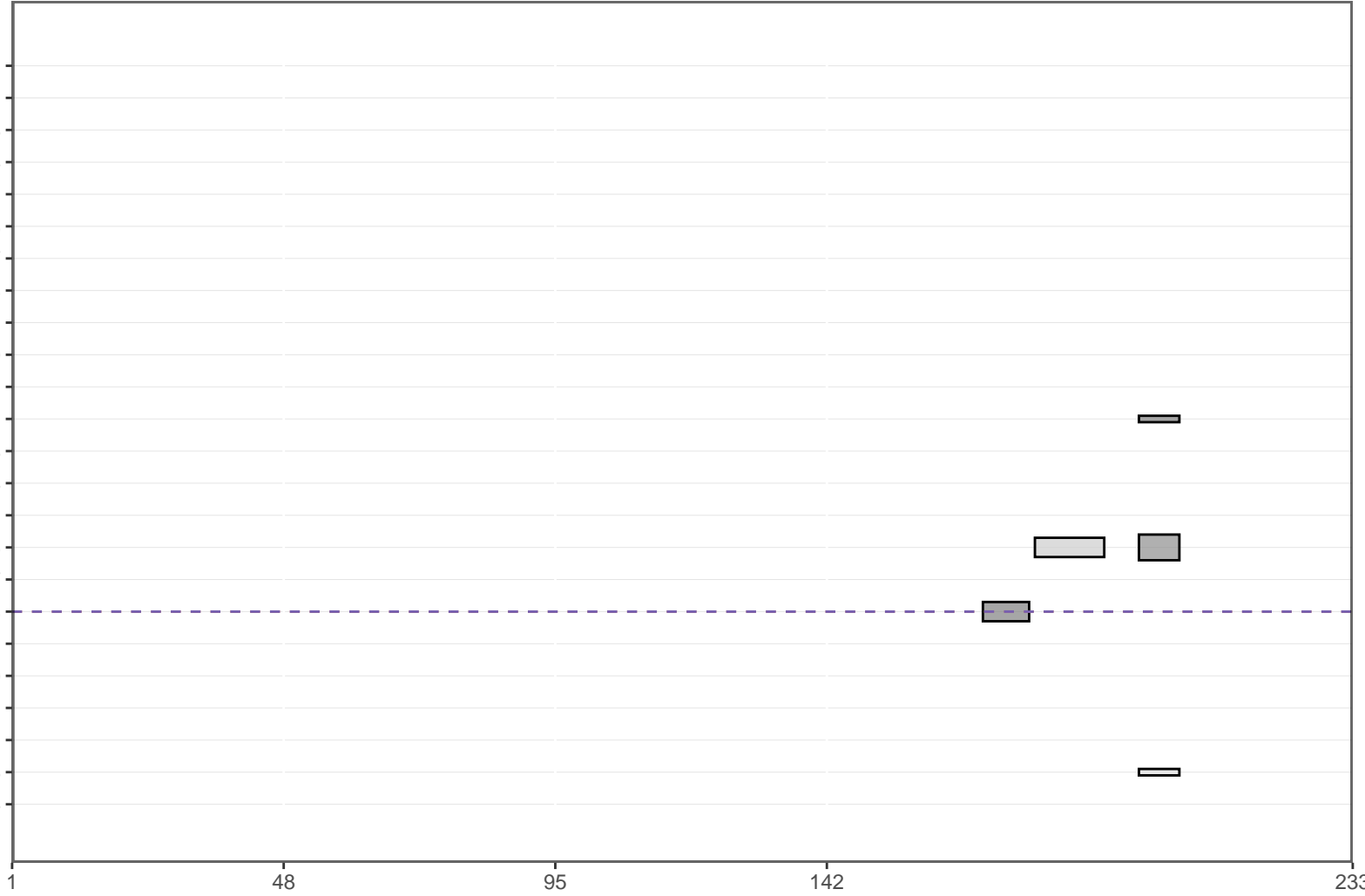
MW indication



Molecular weight



Gel Slice



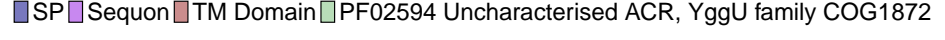
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IEDLETAFTFYVYDGAISAAETNPQDAVPPQISGLEGLVQVAIEVEDRAGRSATFRVNDADRVTVSAPARGEANNELMEFMGRVLGKLGQMTLQRGWNSKILLVVEDLTARQVYKLEEAQD*

NbL13g16290.1 60S_ribosomal_protein_L17-1-like [MW = 19.87 kDa]

No. of times detected



log(intensity)



Values from



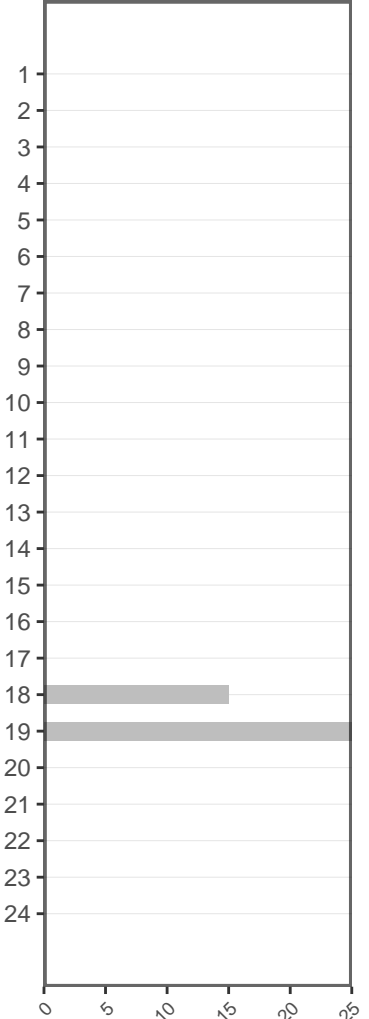
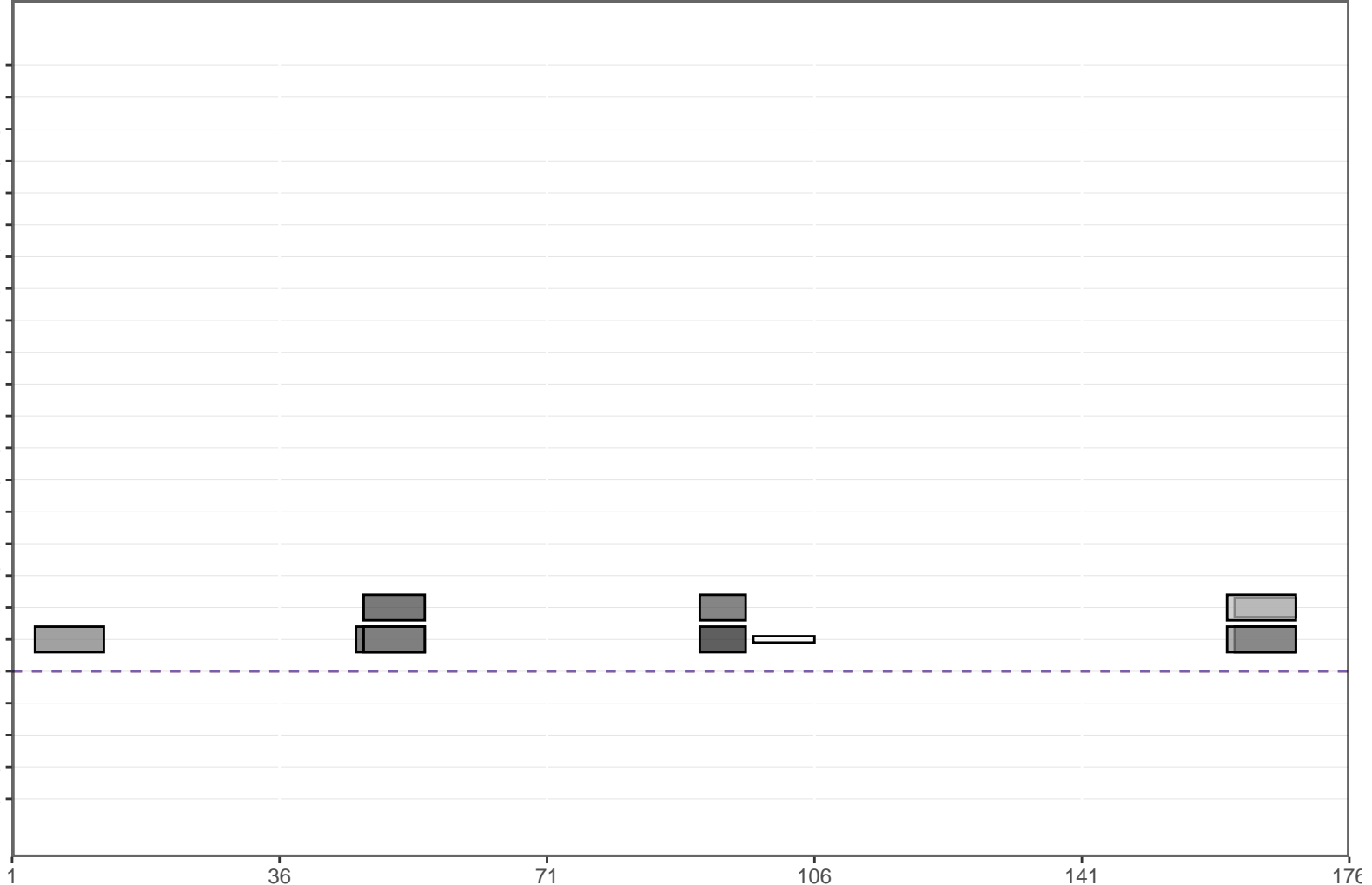
MW indication



Molecular weight

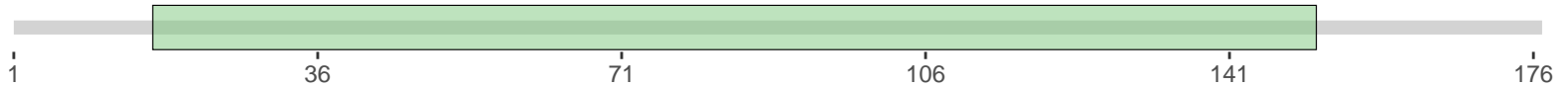


Gel Slice



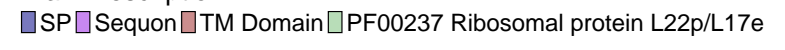
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

HRHSNGQGRVYPVMSANILLKNAEENAEVKGLDVDSLFIHQVNGAGKQRRRTYRAHGRINPVMSPHCHVELTLSEKEESVYKKEPETQLAPRWAKASS*

NbL13g16270.1 adenylate_kinase_4 [MW = 26.6 kDa]

No. of times detected



log(intensity)



Values from



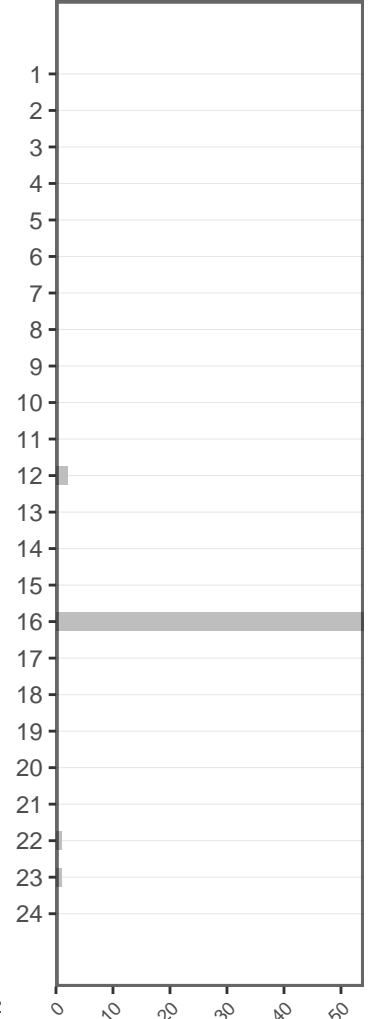
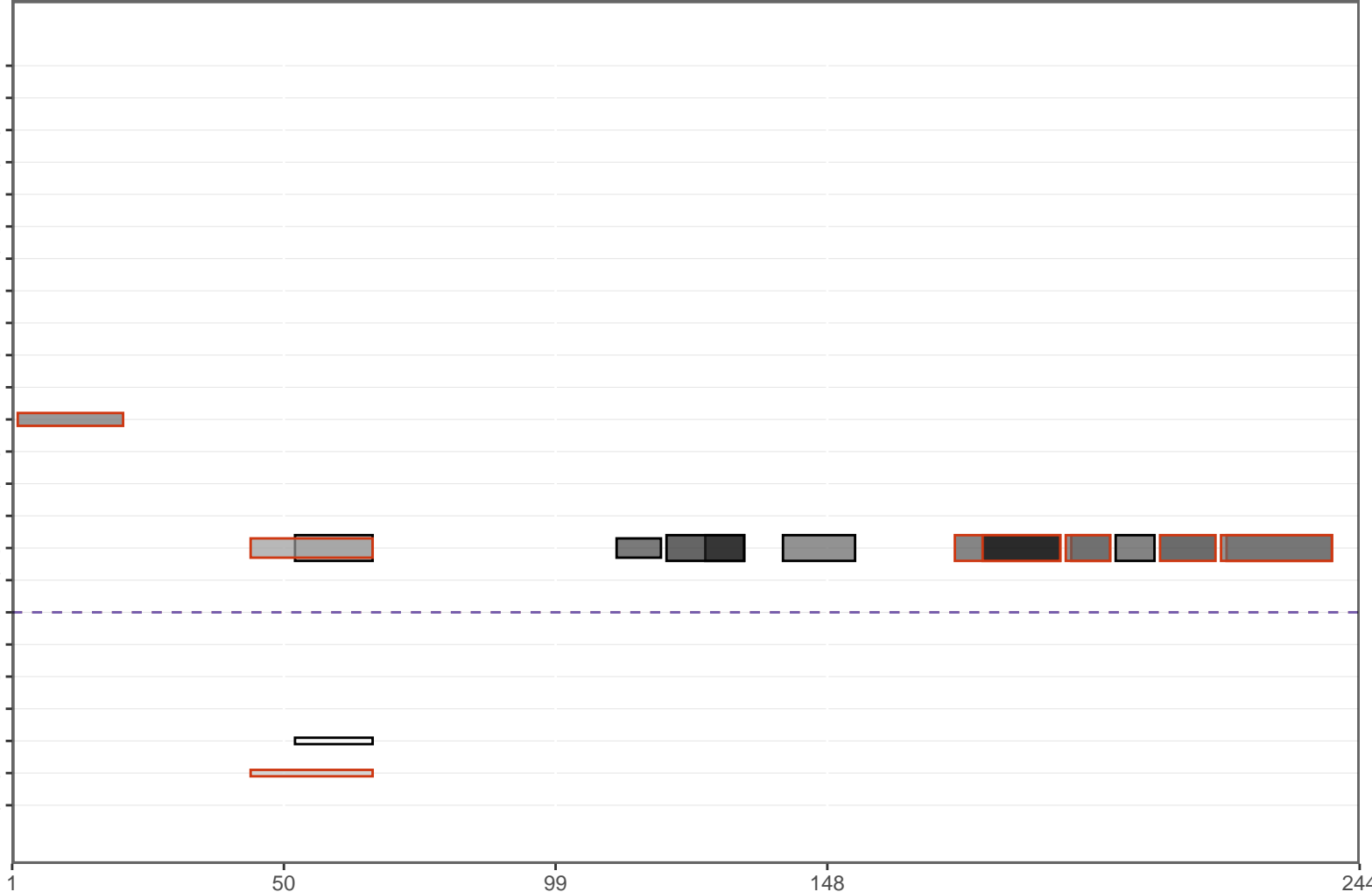
MW indication



Molecular weight



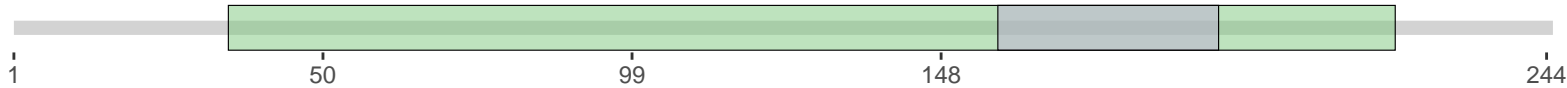
Gel Slice



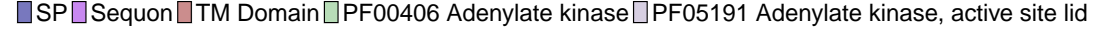
Protein length



Pfam domains



Pfam Description



Protein sequence:

GGFLDGFPRTVVOAEKLEDEMLGNRGTQKVKVLFNFAIDDALEERITGRWHIPASGRSYHTKFAFKVPGVDDVTGEPLIQKDDTAWLKRLSEFHRGTEPIDYAKKGNVNLPAKPKPGTVTAEEVKKALS

NbL13g16240.1 probable_aspartyl_aminopeptidase [MW = 52.74 kDa]

No. of times detected



log(intensity)



Values from

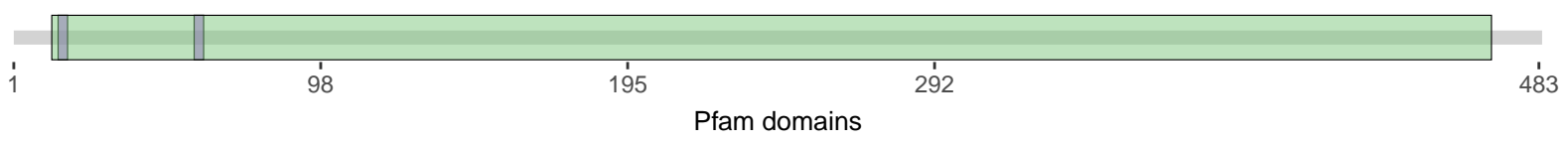
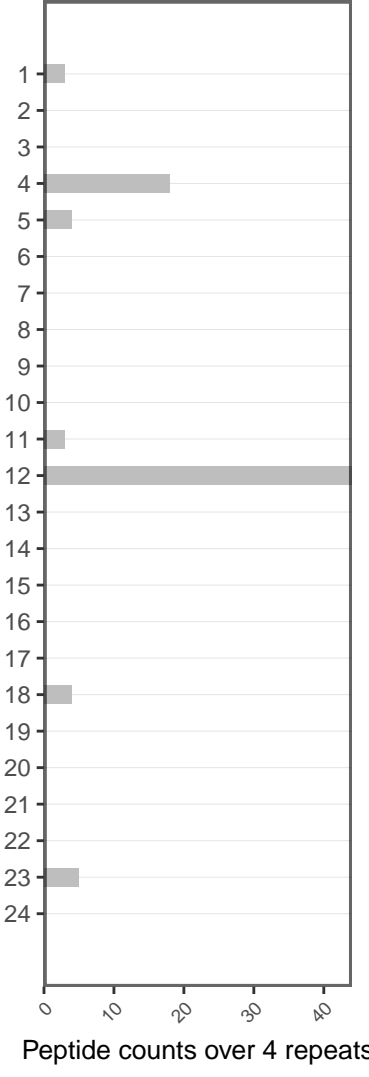
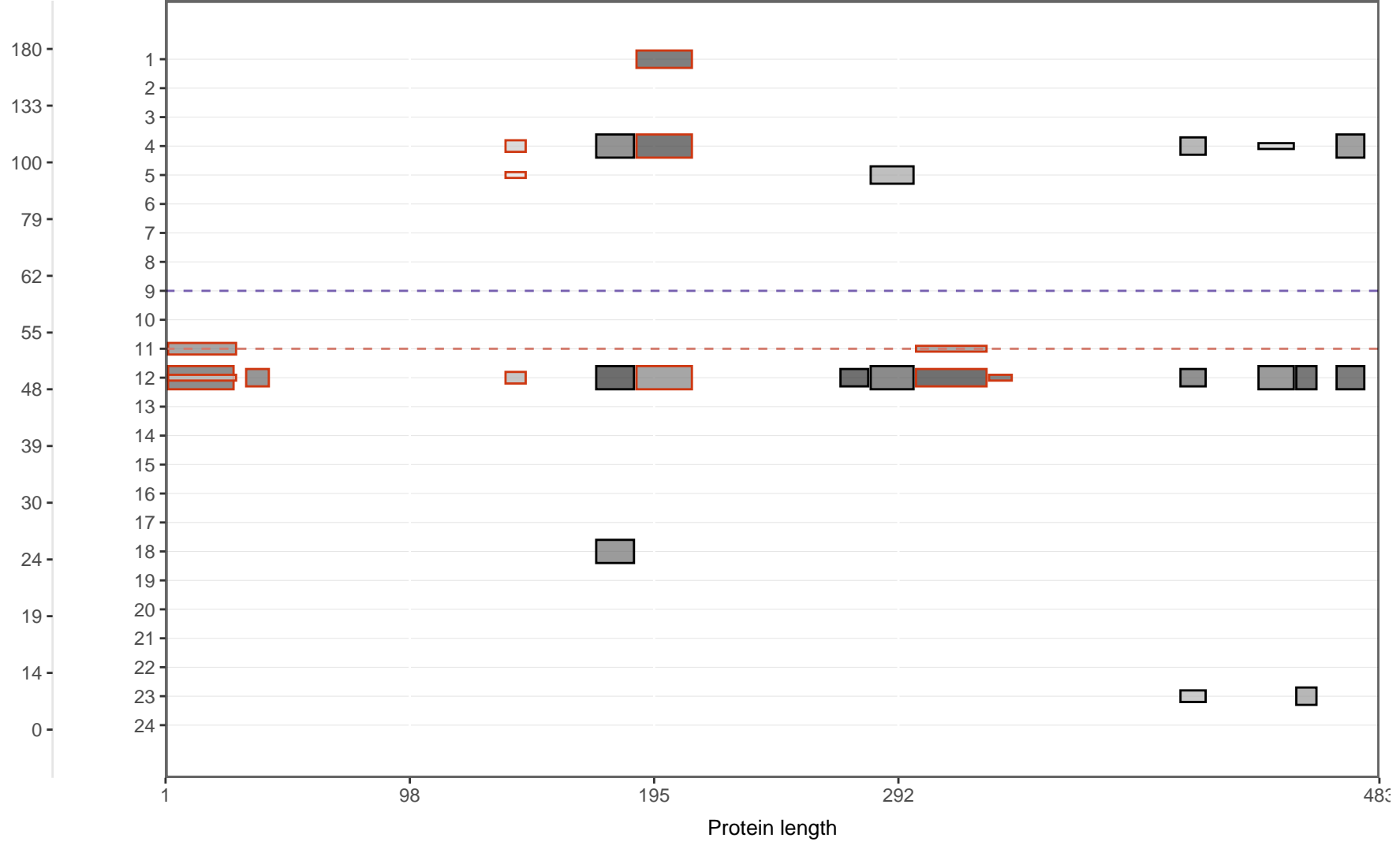


MW indication

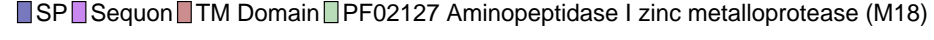


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

LLLAQAGCEPSDGDGDFELGAGDTQPRVIAAGANKEFVFGRLDNLGSSFCBLKALIDATSONSLEDEVGVRMVALFDHEEYVGSNAGGAGSPVDFDLGRITFTTFDEKLPKAGRFLVSADMAHALHNFYDPKHEENHGPKFHGGLVKKHANGRWATNAVTFIFREIAAKHNIPQDFVIRNDMPCCGDTGLPLASGIGRTVGVGAPQWSMHSIREMCAVDDKHWYDHFKAFFGDFSHLDAKIAVDV

NbL13g16230.1 4-coumarate--CoA_ligase-like_9 [MW = 59.65 kDa]

No. of times detected



log(intensity)



Values from



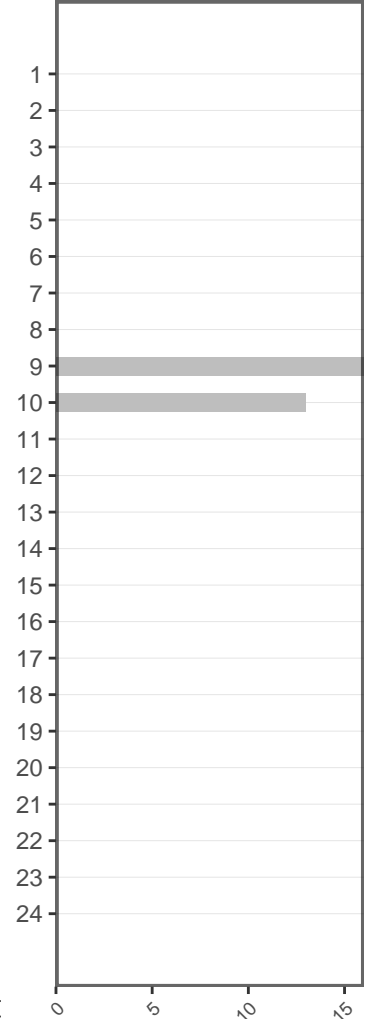
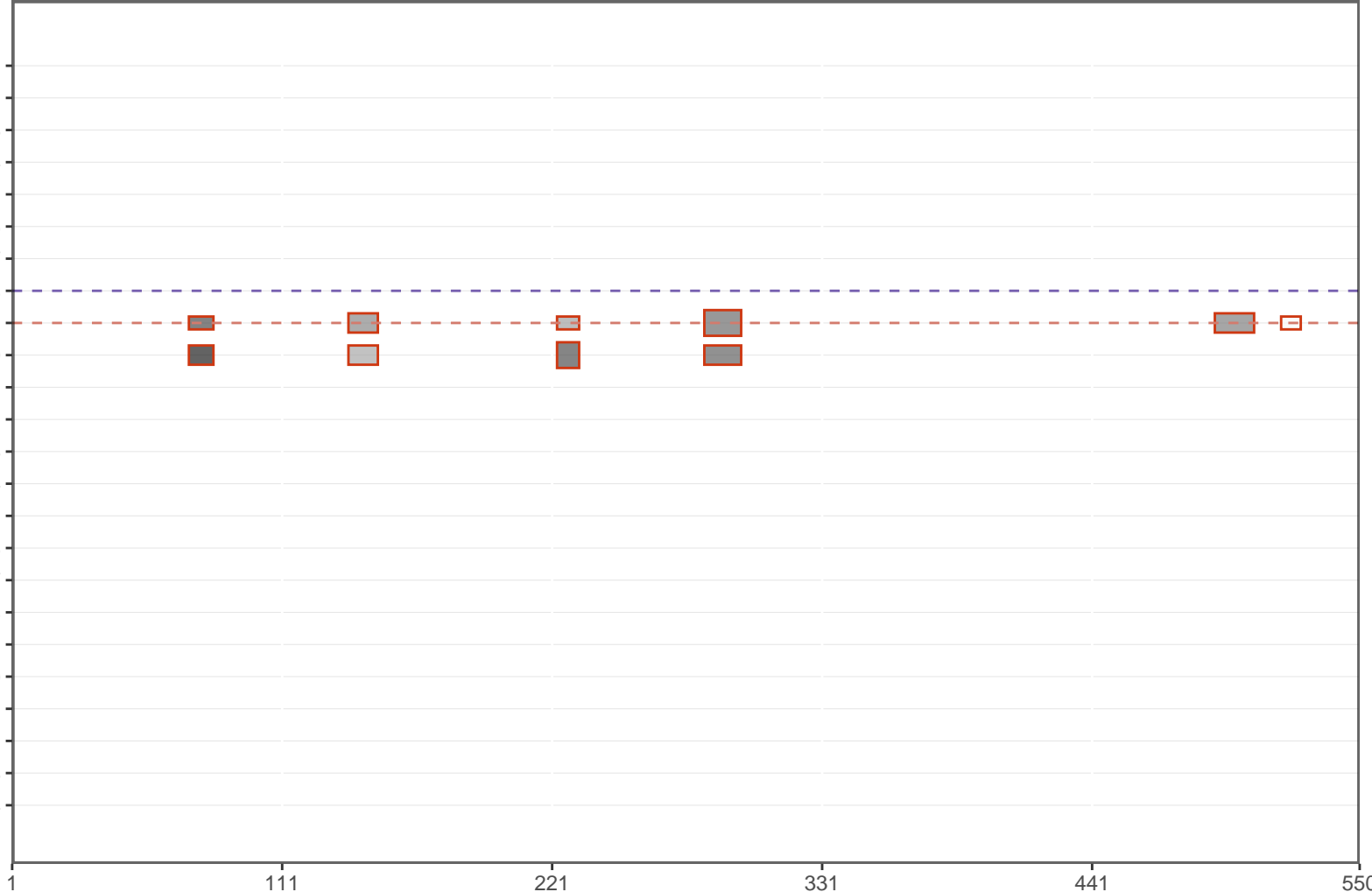
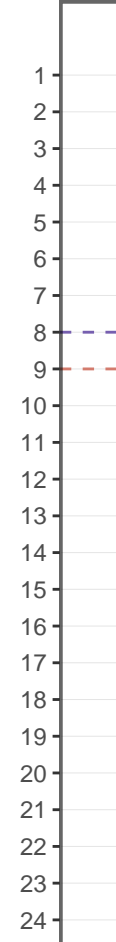
MW indication



Molecular weight

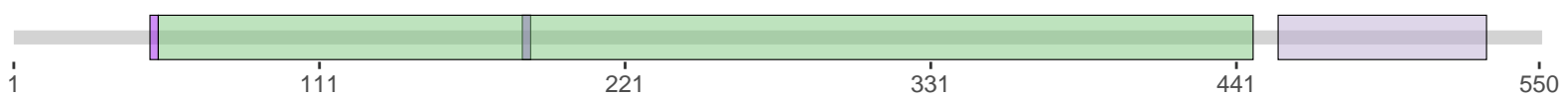


Gel Slice



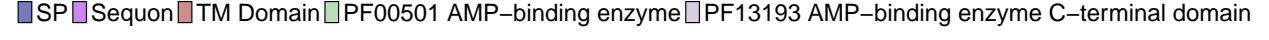
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VTIERFDKMLLEAVEKYRVTYIPVSPPLVAMAKSDLAKLHDLVSLKLLACGGAPLGLKEVAERFKSRFFNVHGGVGLTETTGGATGMSGPEESDRYGSAGRLSNVNAKIVDPDNGETLPPQGRGELWIRGPTIMKGVYGDKQATSATLNSGWLKTGDLGYFDADGFLVHDLRLKELIKYKAYGVPPALEHLGSLSPVADAAVPIYVDEAGEIPMAVYVRRPGSTSESGHDMAXGQVAPYKIRVAFHAIKPKSPAGKILRIELVNHASSGASARL-

NbL13g16130.1 glyceraldehyde-3-phosphate_dehydrogenase_cytosolic-like [MW = 36.73 kDa]

No. of times detected



log(intensity)



Values from

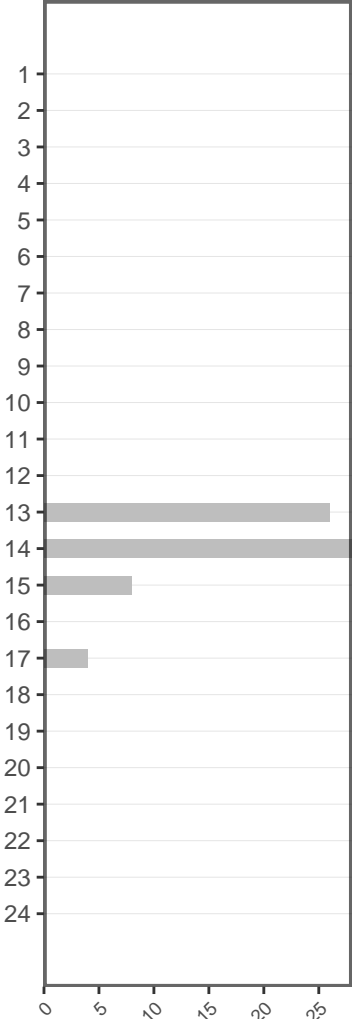
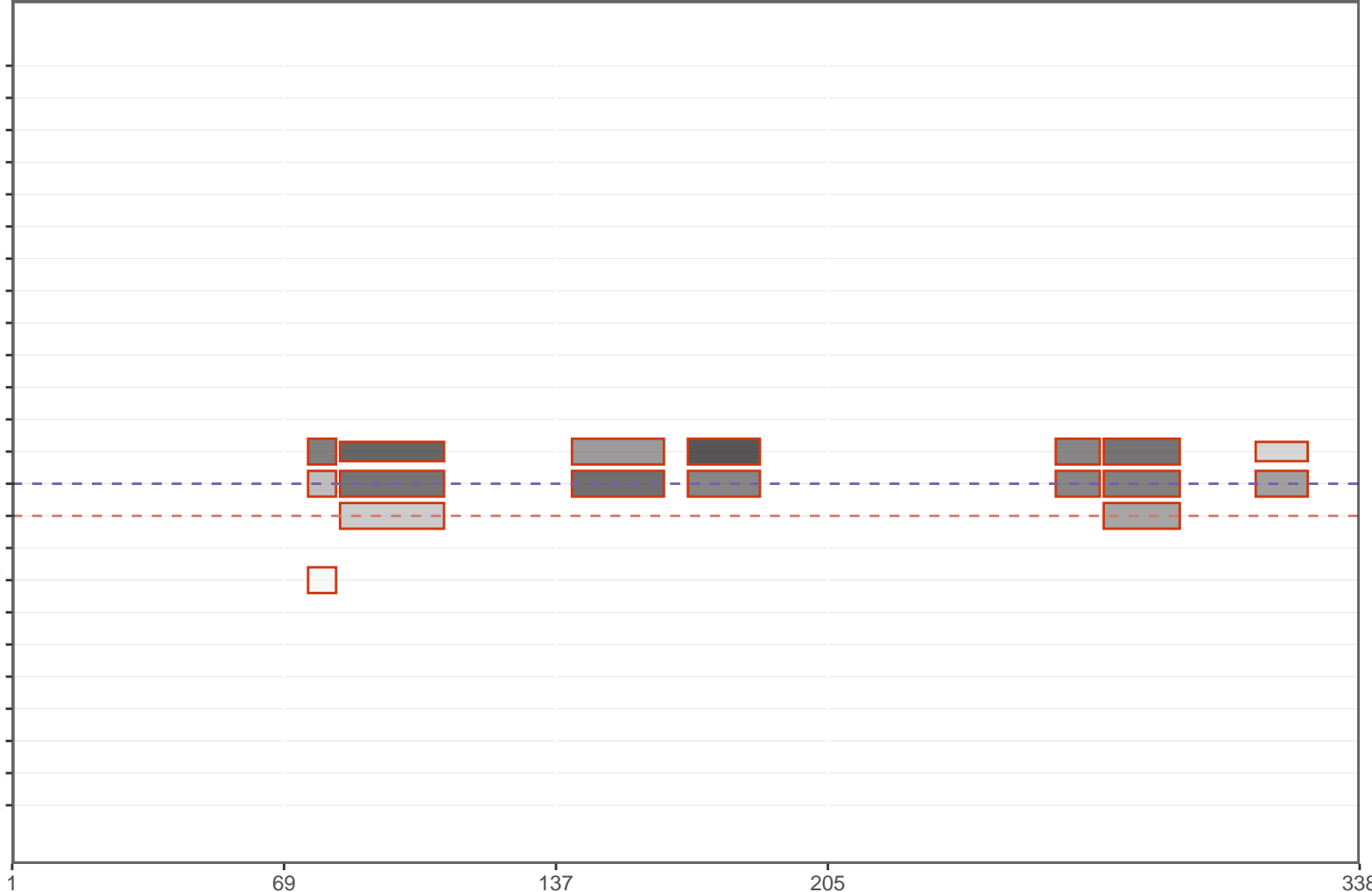
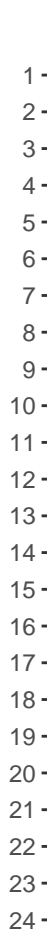
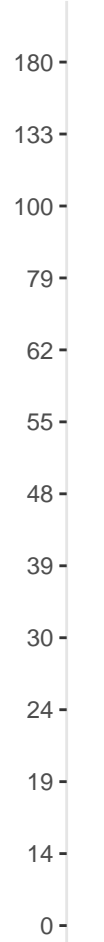


MW indication



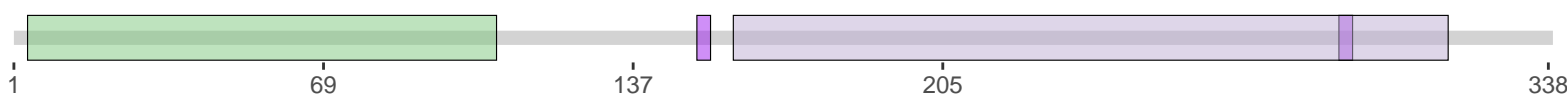
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF00044 Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain
- PF02800 Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain

Protein sequence:

ITNCLAPLAKVINDRYGVIEGLMFTVHSITATQKTVDPGSAKDWRRGRAAGFNIPSPSTGAAKAVGKVLPAIINGKLTGMFRVPTVDVSVVDTLVRLEKEATYDEIKAAIKESSEGNLKGILGYTEDDVAVSTDFVGNRRSIFDAKAGIALSKNFVKLVSWVDNEWGVSTRVVDLKHMASVDQ

NbL13g16100.1 nucleoside_diphosphate_kinase_2_chloroplastic-like [MW = 26.2 kDa]

No. of times detected



log(intensity)



Values from



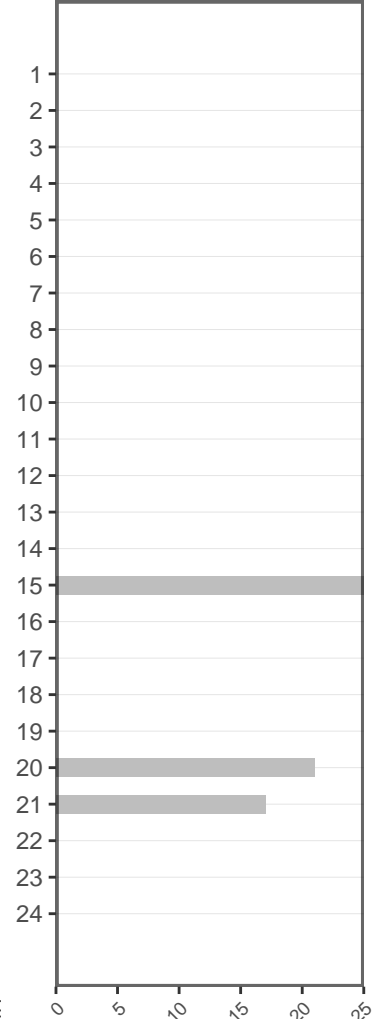
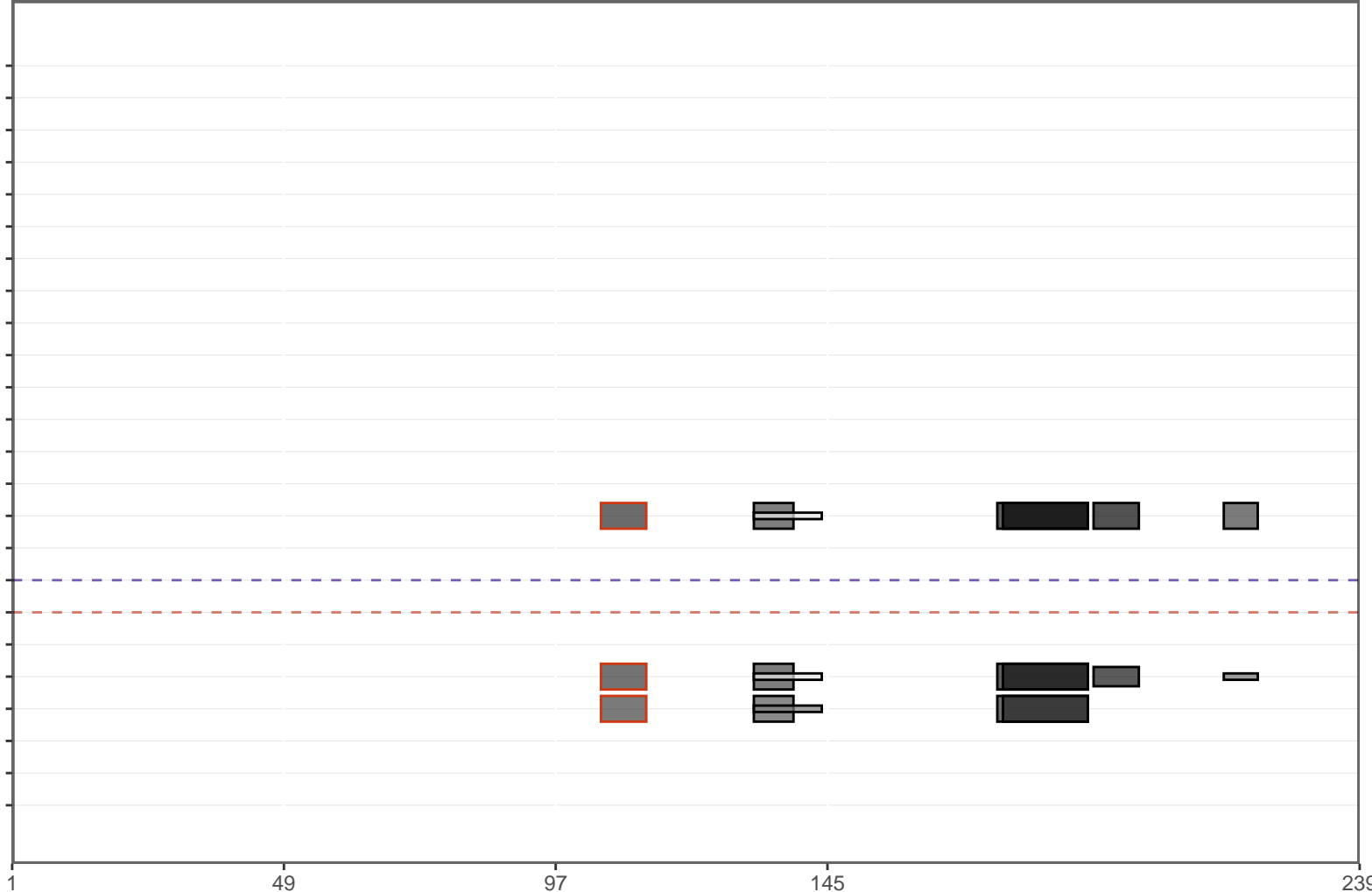
MW indication



Molecular weight

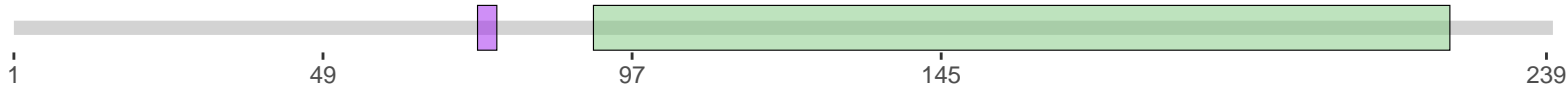


Gel Slice



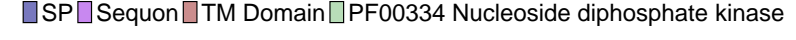
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VGEISRFEXKGFKLGGKLFHCPKELAEHNYKDLGKGFYKLDVITSGPVMAMVEGIGVVASARKLIGATNPLNAEPTIRGDLAVGTGRNVVHGSDSPENGRKRIALWFRREGELGSWTPVQEPWLIE

NbL13g16010.1 nuclear_transcription_factor_Y_subunit_C-1-like [MW = 25.05 kDa]

No. of times detected



log(intensity)



Values from



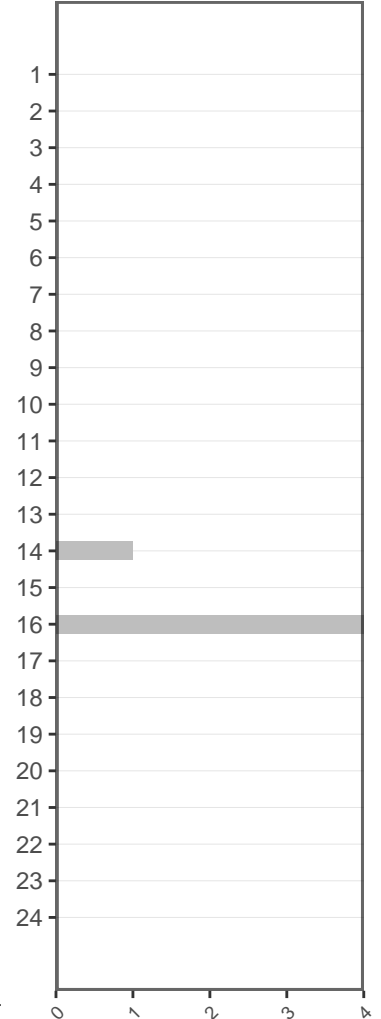
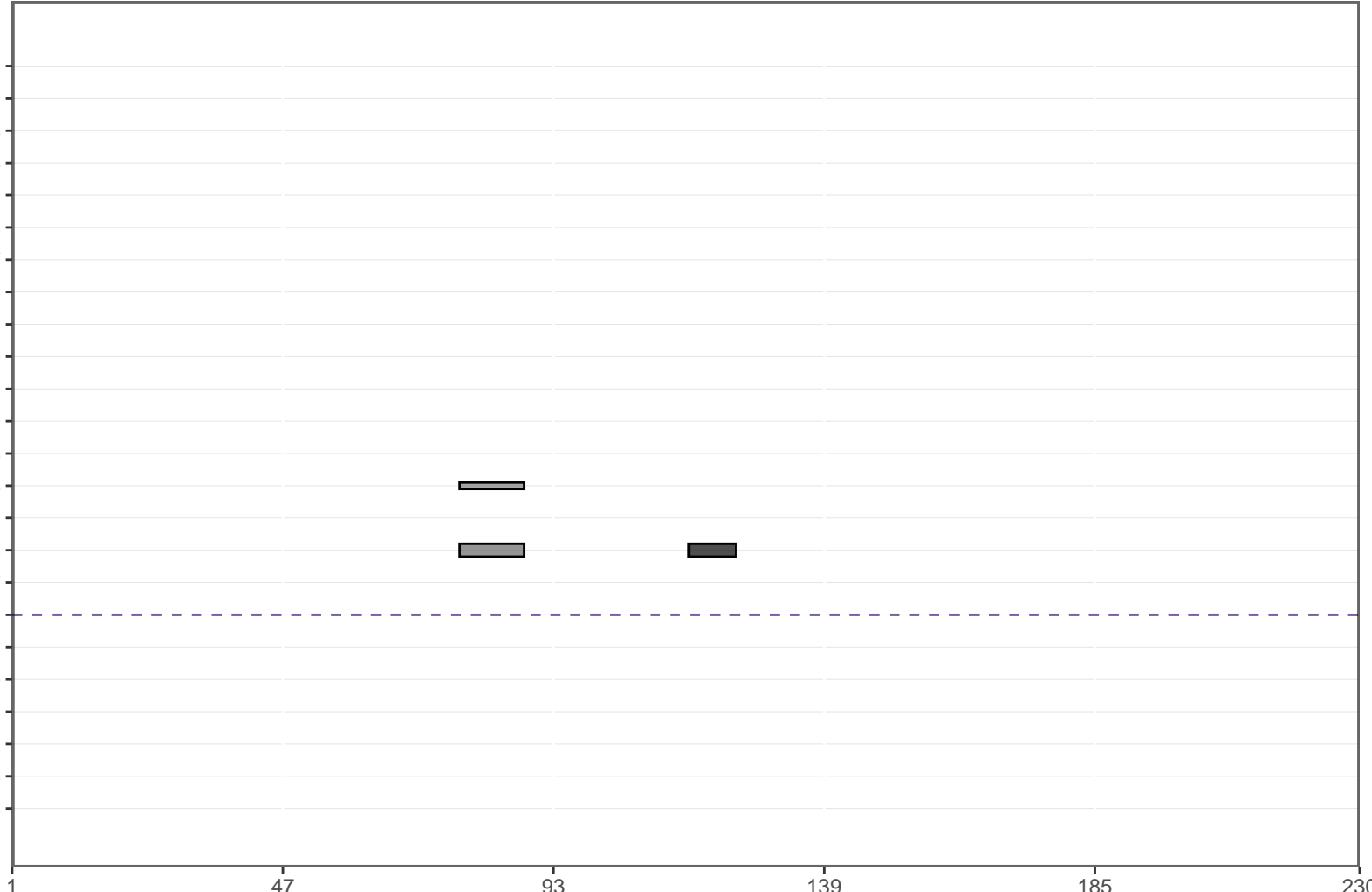
MW indication



Molecular weight



Gel Slice



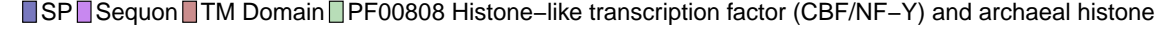
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

JHAEENKRRRLQKNDKAAANTRFDLVDIVPRDEIKEEGGVGLGPGIVGSGTASGVPPYPPMGGPAPPGVMMGRPMFPGVDPSMVGAPPPPGAWGSAWGTAEENVAASGGSSGQNLDDGS*

NbL13g15930.1 thylakoid_luminal_17.9_kDa_protein_chloroplastic [MW = 25.1 kDa]

No. of times detected



log(intensity)



Values from



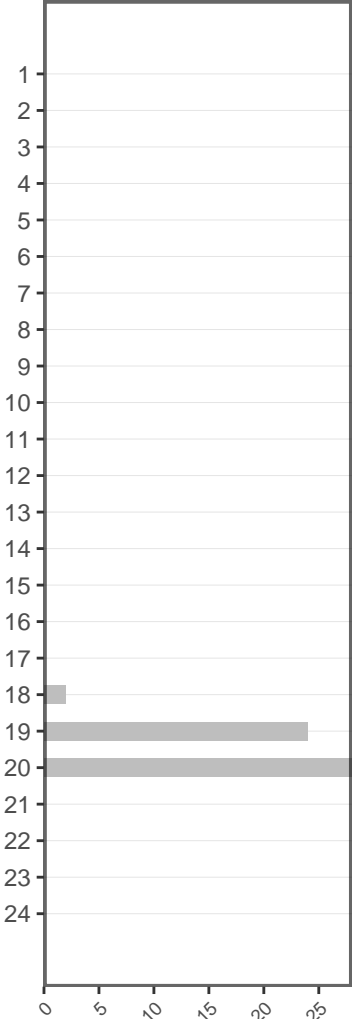
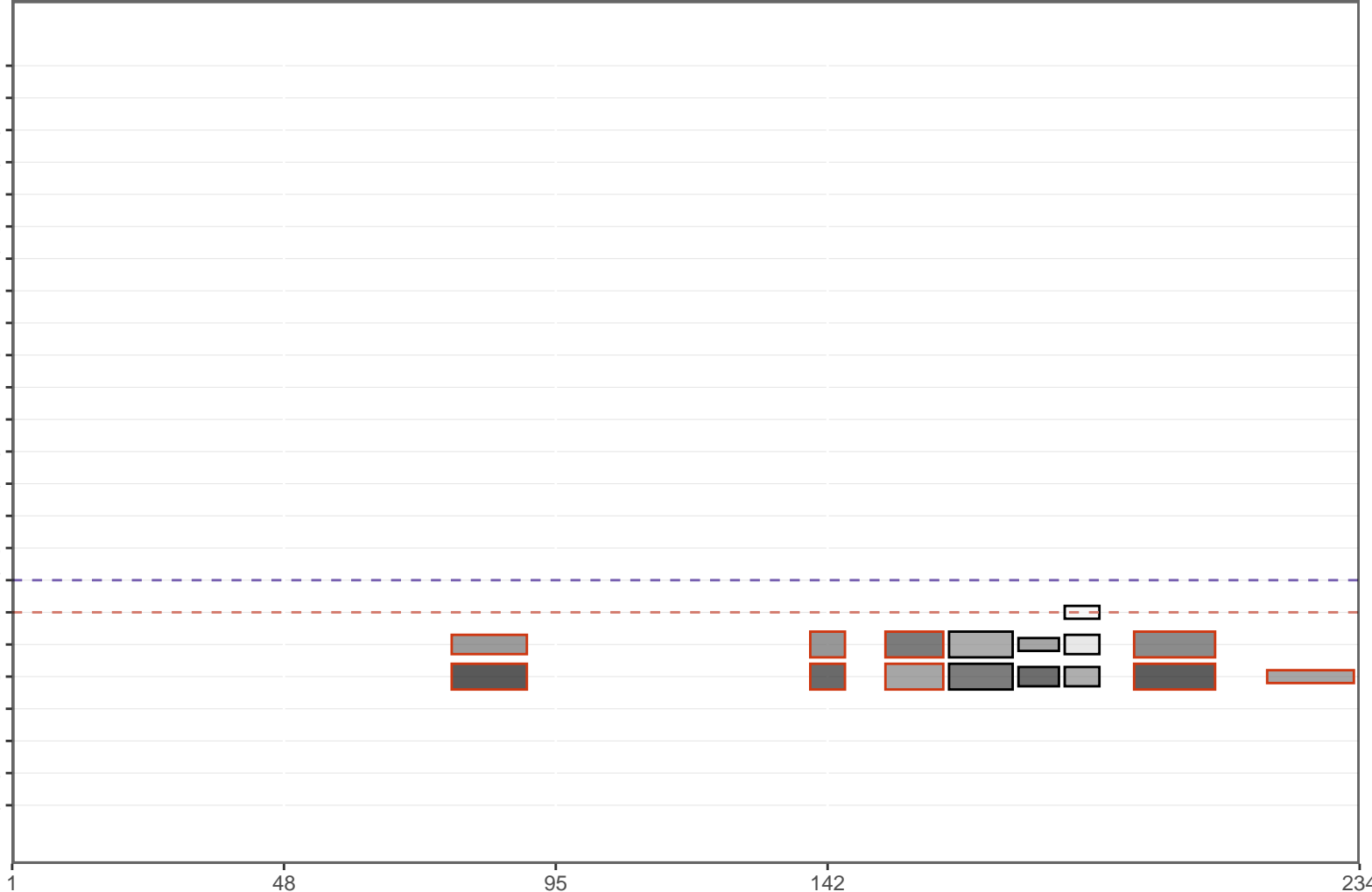
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

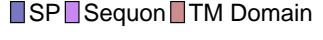
Protein length



Pfam domains



Pfam Description



Protein sequence:

PSVYVPCVYSTNPQSSSFAFWTIPQNETGNAMRLQDALKTKGNNAKQVIEDSDGKYLQAEVDGDFGRDYLEFLVKGDSVAVRAMATKVTYVYFTALGDGKQGEERMKITEELGWYAPSLDSMDP

NbL13g15880.1 SUMO-activating_enzyme_subunit_1B-1-like [MW = 40.31 kDa]

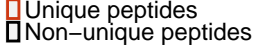
No. of times detected



log(intensity)



Values from



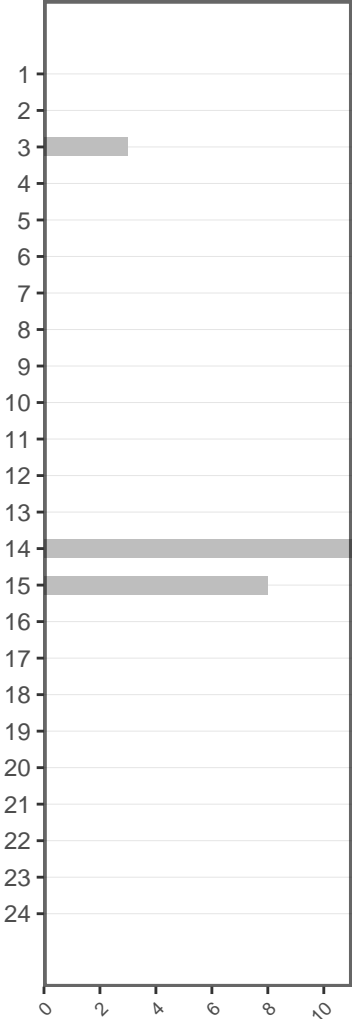
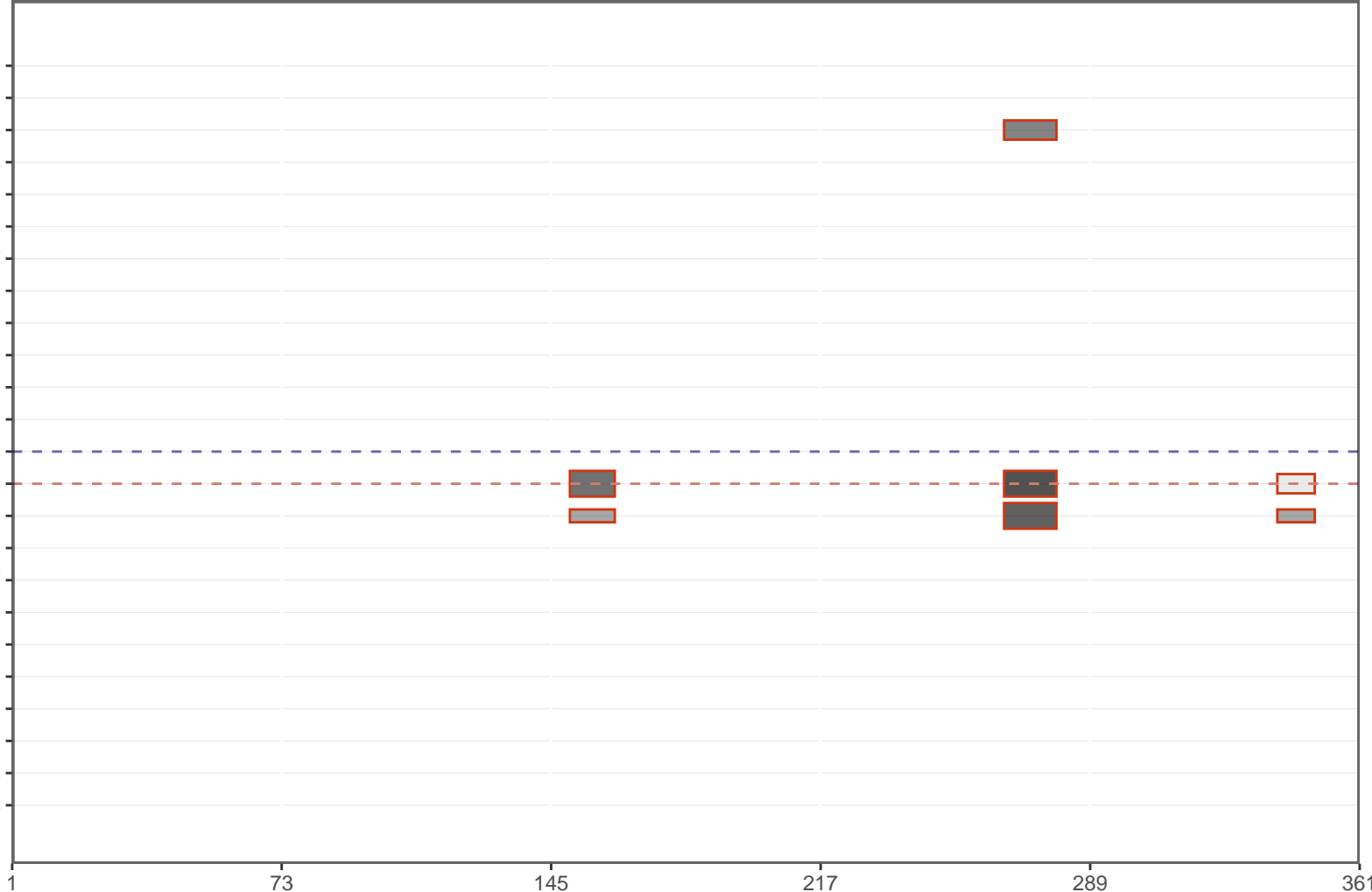
MW indication



Molecular weight

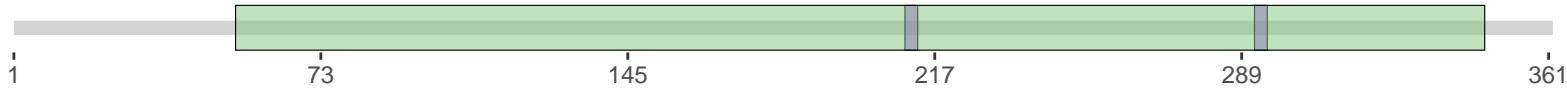


Gel Slice



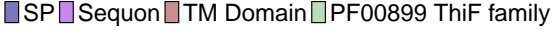
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VVYSCCTLLTKKSIINAKGCHKLRVAFYEVVEGRDSDGSEIFVLDLGNVSEYKQKKNKMETMEGILLYPFEEAAVFWRLPKRMKLYFAMRVERFEELGRNPGSETSDADLPNVQIKRLKELGEAHLNLESGIPDGLLQRLIARSRSEFPMDAHHGHLGGEVKAISGKGDPLNFFFFDAMDGKGIHEDISAVNS

NbL13g15830.1 alpha-galactosidase-like [MW = 48.41 kDa]

No. of times detected



log(intensity)



Values from



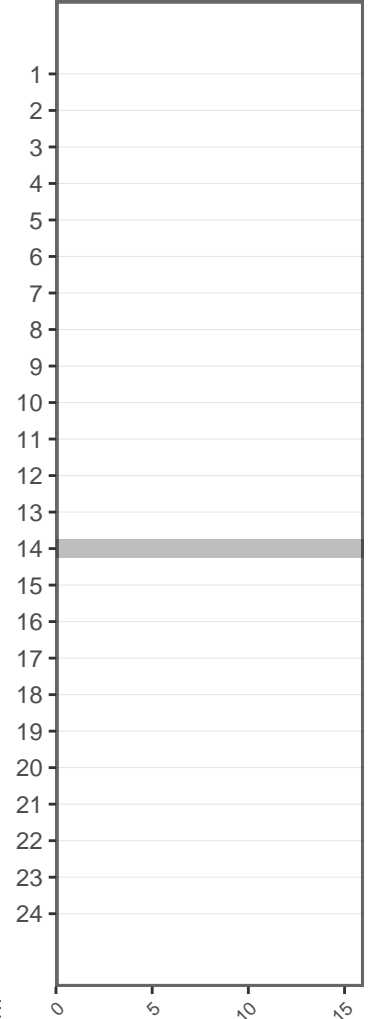
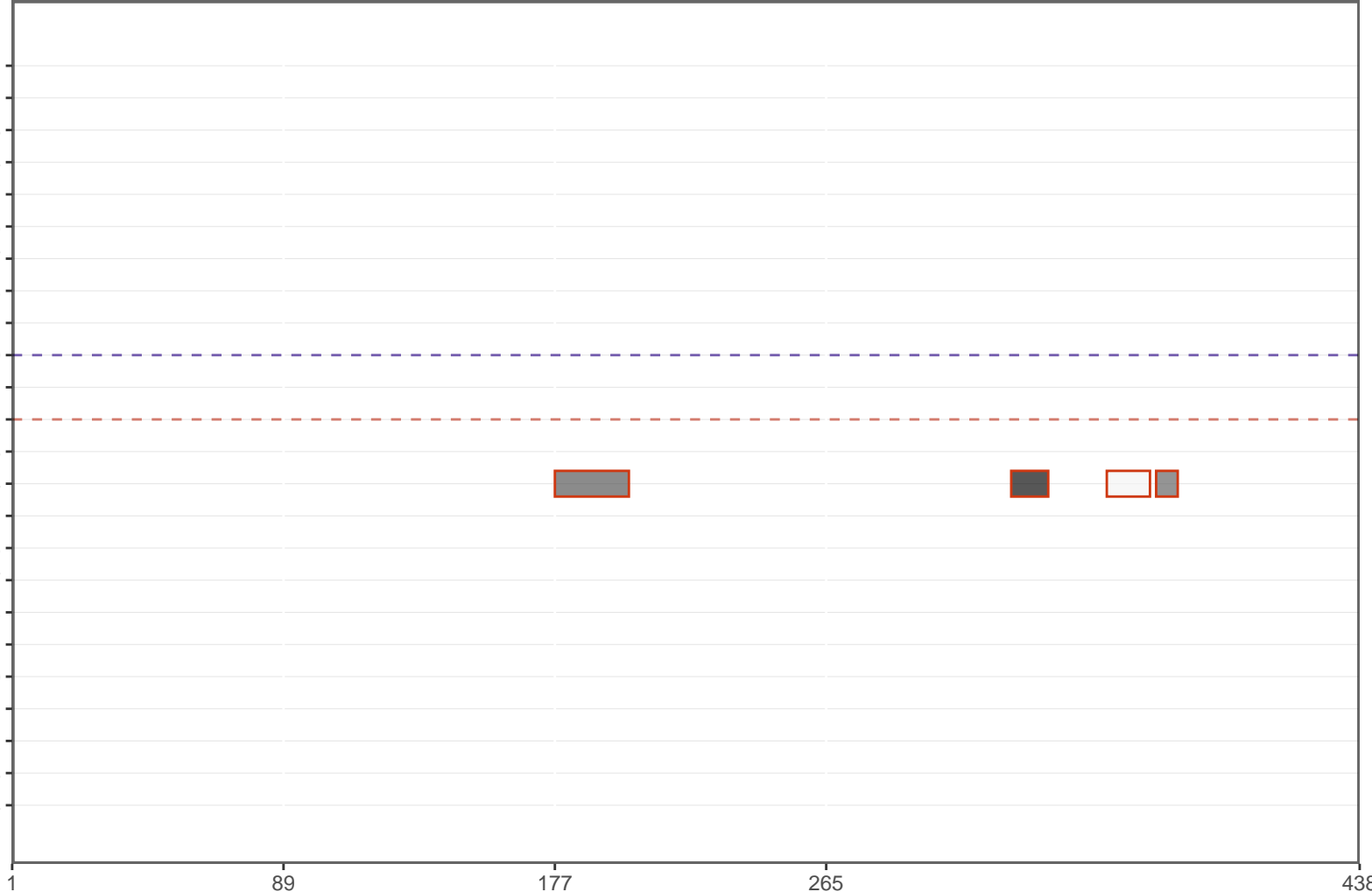
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

NENRSPKERYPIIMSKALQNSGRAIFSLGEWDDDPATVAASSIGNSWRTTGGDSNWDGMSRAEMNDKWASVAGPGGWNDFDMLLEVGNNGMTAAEYRSHFISWALAKPLIGIGDRLRSMDDGTHIELSNKEVIAVWQDKLGVGGKVKVQNGSELEWAGPLSGKRWVAVLWNRSSKADITYWSDGLDSSVTVBARDLWAHSTKGGKGGISASDSHDCRMVYLTFRK

NbL13g15700.1 asparagine--tRNA_ligase_chloroplastic/mitochondrial [MW = 64.14 kDa]

No. of times detected



log(intensity)



Values from



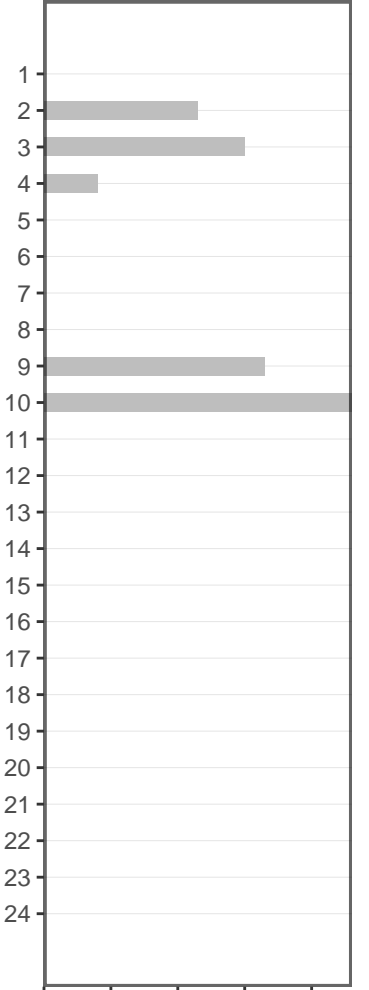
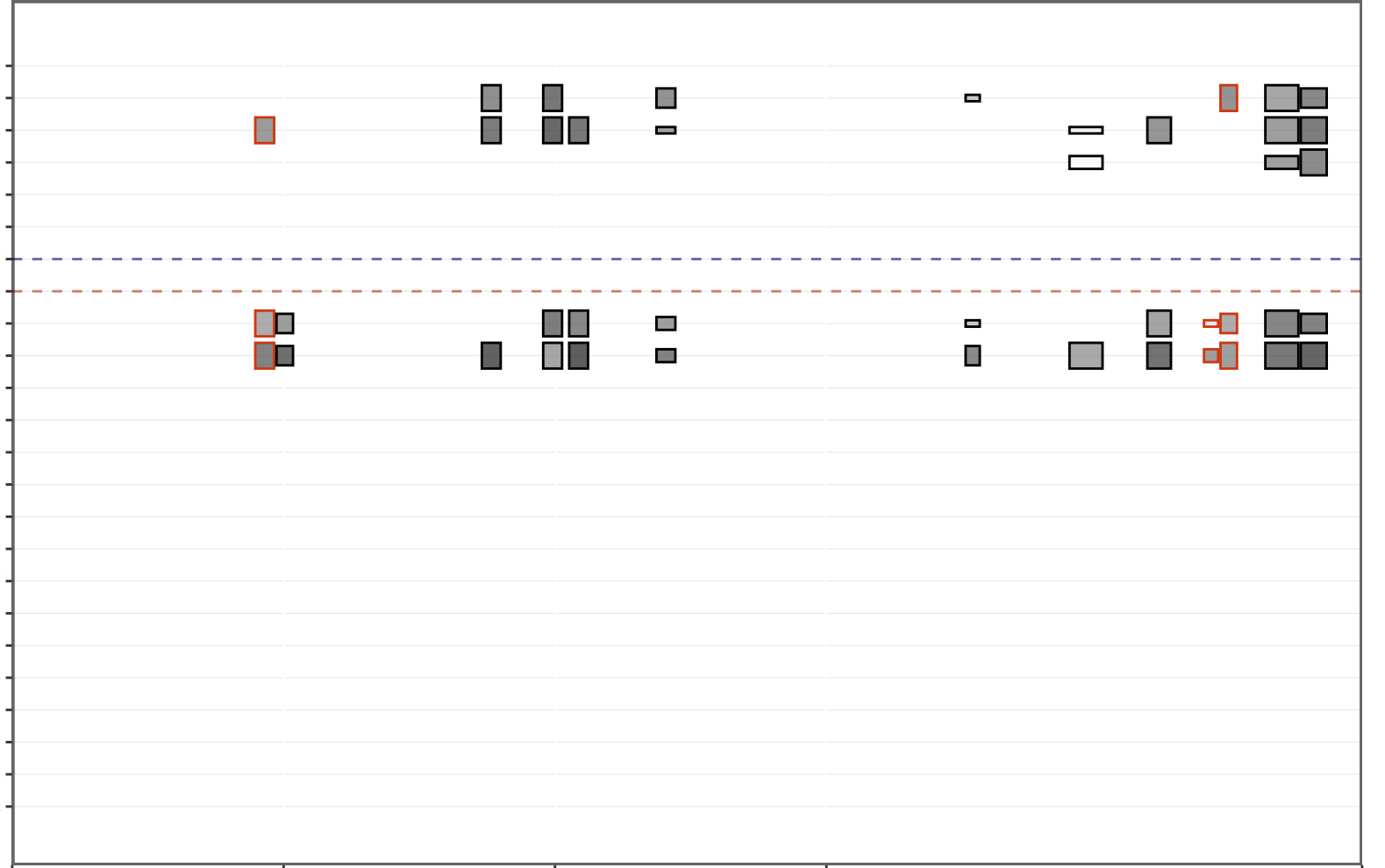
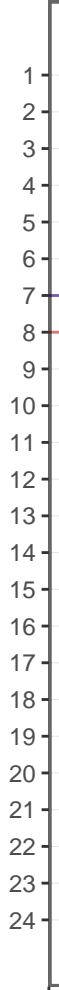
MW indication



Molecular weight



Gel Slice

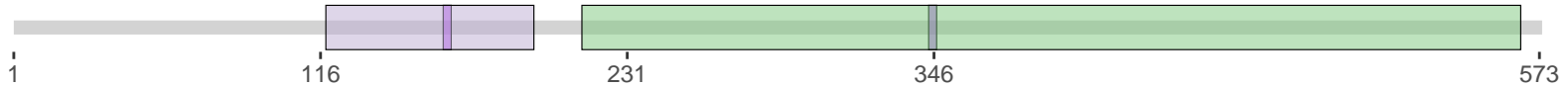


Protein length

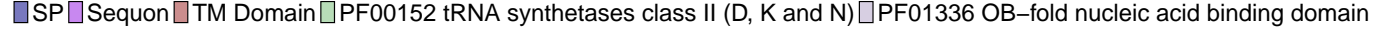
Peptide counts over 4 repeats



Pfam domains



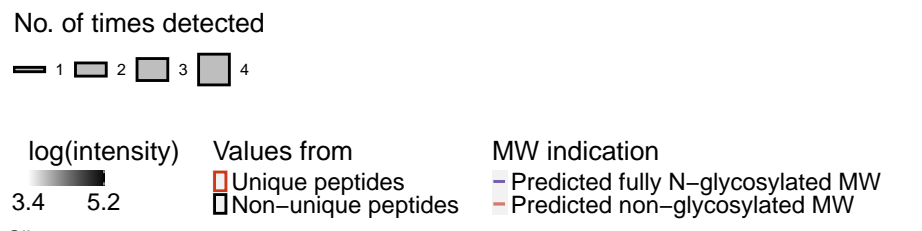
Pfam Description



Protein sequence:

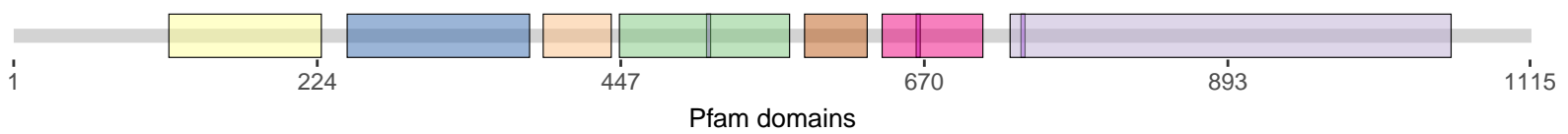
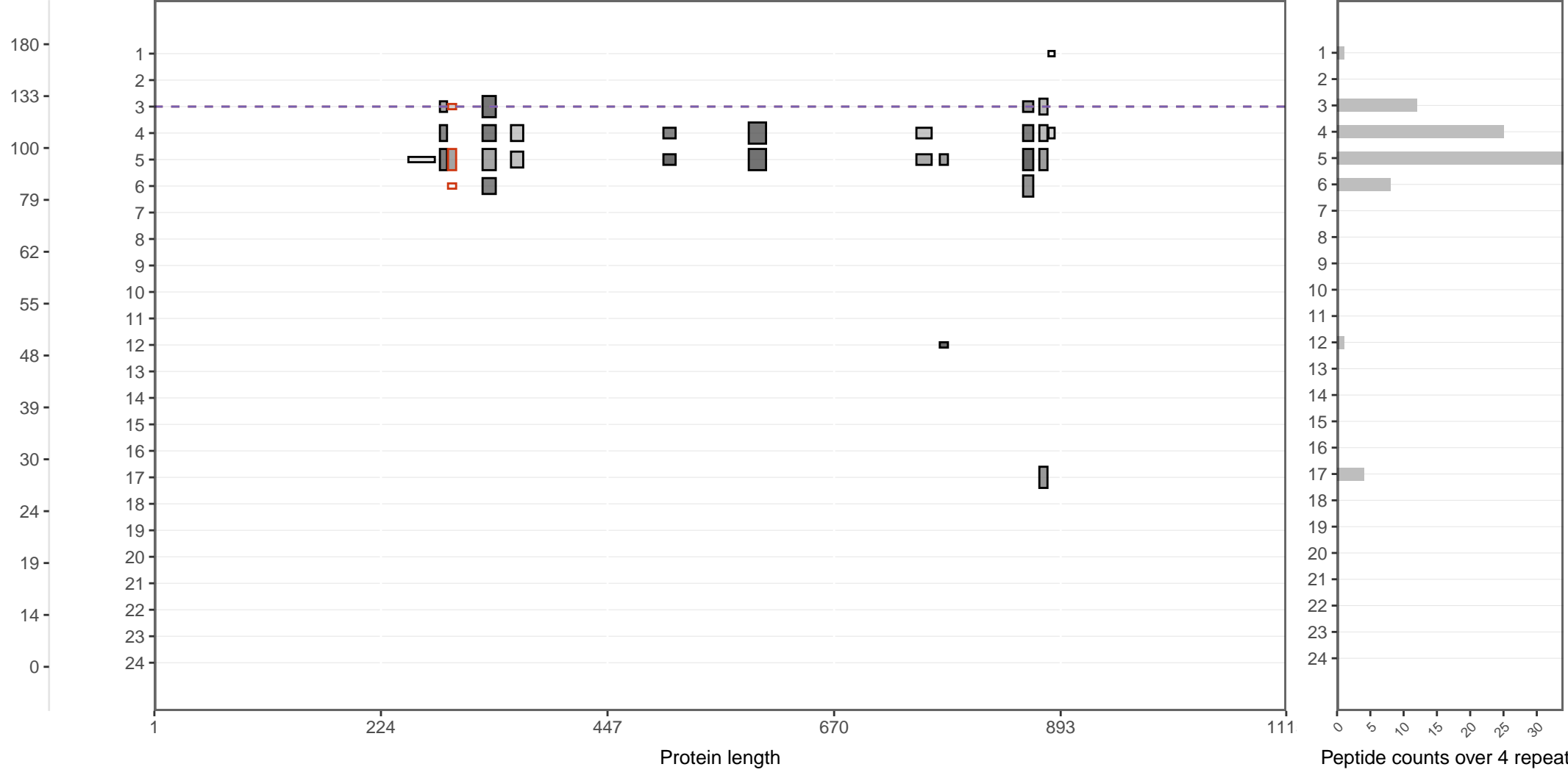
I/T/L/P/T/K/E/G/D/S/P/N/A/R/T/E/S/G/S/V/W/S/D/F/F/G/K/A/L/T/V/S/G/L/N/G/E/T/V/A/S/D/I/Y/T/G/T/F/R/A/E/N/S/T/R/H/L/A/E/F/W/M/E/P/L/A/F/A/D/L/D/D/M/A/G/A/T/A/L/G/V/V/V/V/L/E/N/K/E/D/M/F/F/T/W/E/K/G/H/S/R/L/S/D/V/E/K/N/V/L/T/Y/D/V/E/L/L/K/A/K/K/F/D/F/P/K/W/G/D/L/G/S/E/H/E/R/Y/E/E/A/G/G/C/P/V/I/R/D/P/K/D/K/A/F/Y/M/R/N/D/D/G/K/T/W/A/M/D/M/L/V/P/R/V/G/L/G/S/D/R/E/E/R/L/E/V/L/D/E/R/L/D/M/L/N/K/S/F/W/V/L/D/L/R/R/V/G/V/P/H/A/G/F/L/G/F/E/R/L/V/G/F/A/T/G/D/N/R/D/A/P/P/R/P/T

NbL13g15390.1 protein_argonaute_1-like [MW = 122.85 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF02170 PAZ domain
- PF08699 Argonaute linker 1 domain
- PF02171 Piwi domain
- PF16486 N-terminal domain of argonaute
- PF12764 Glycine-rich region of argonaute
- PF16488 Argonaute linker 2 domain
- PF16487 Mid domain of argonaute

Protein sequence:

.GVGNGOQRPNYLPMVEVKVVEGGRYSKRLLNERDITALLKVTGQRPQGERDILETVHINWVANDPVAKEFGKISDLAGVEARILPPRLKVKYHNGREKDKLQVGVGVMNMMNKMMVNGGTVAHWGDFSRNVQDSVAHFGFSELAMDGISGMNFNPVFPSSAHPDQVEVLKTRFDAMTKLGGHGRLELDLVLVLPDNNGLSYGLKRIKRIETELGVVGGGLTKHVFPMKQYLANVALKINWVGGGNTLVLSAISRRLVSDRPTIFGADVTPHPGDESS

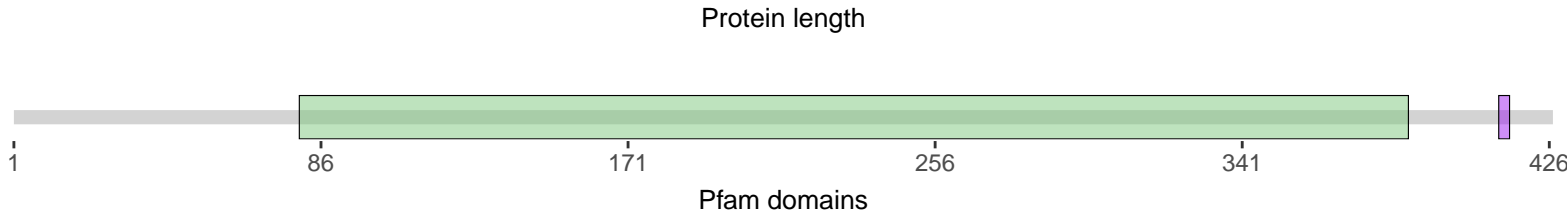
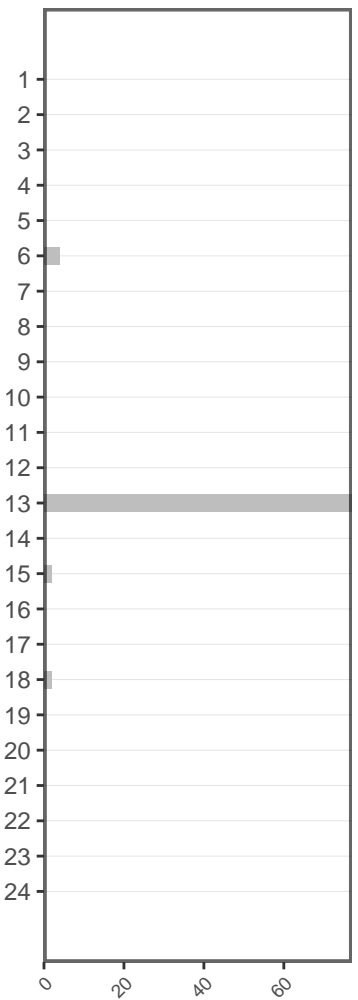
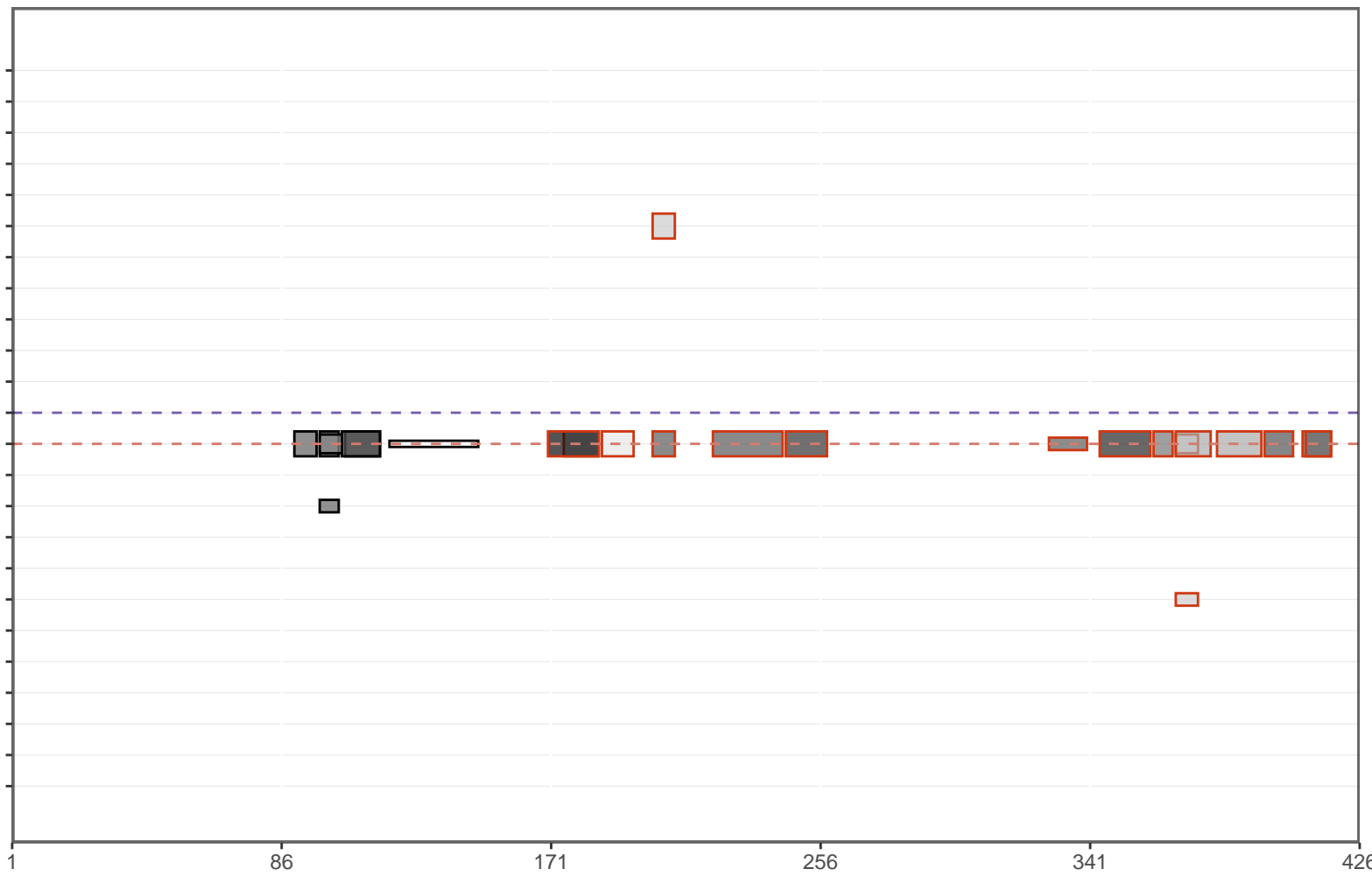
NbL13g15360.1 bifunctional_D-cysteine_desulhydrase/1-aminocyclopropane-1-carboxylate_deaminase_mitochondrial [MW = 46.84 kDa]

No. of times detected
 1 2 3 4

log(intensity) Values from MW indication
 3.8 5.8 Unique peptides Non-unique peptides
 Predicted fully N-glycosylated MW Predicted non-glycosylated MW

Molecular weight
 180
 133
 100
 79
 62
 55
 48
 39
 30
 24
 19
 14
 0

Gel Slice
 1
 2
 3
 4
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 6
 7
 8
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 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24



Pfam Description
 SP Sequon TM Domain PF00291 Pyridoxal-phosphate dependent enzyme

Protein sequence:
 AKYVSEALTKLLKERLLNEGRKPVVIVVGGNBLGTWGYIEAIRVEVQQLGHSSEVWFDDVAVGGSGGTVAGLSIARLGLKAKVNAFCVDDPPDYFYEYVQGLLDGNGVSSRDVSKNAKGLGYMSTADELKFVQVQVAETGVILDPVYSGKAAVGMKMDNENFTKWEGRKILFIHTGGLLGLVDKADEMGSLMKWIKMDNESIPRGDGIKMF

NbL13g15240.1 calmodulin [MW = 16.93 kDa]

No. of times detected



log(intensity)



Values from



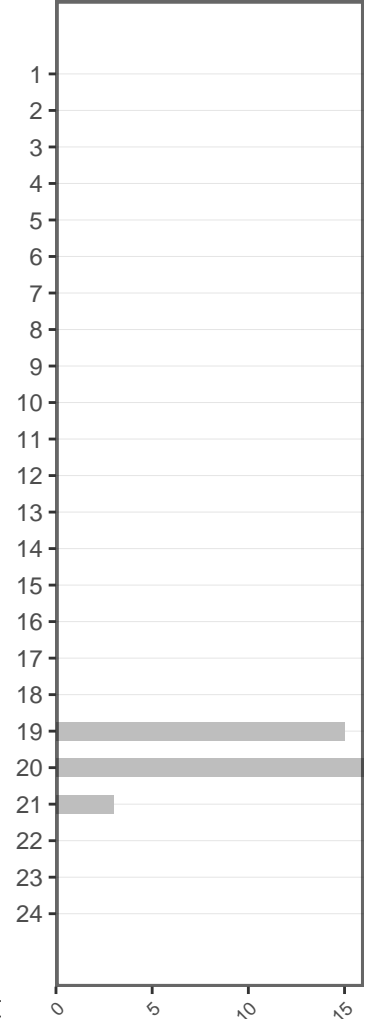
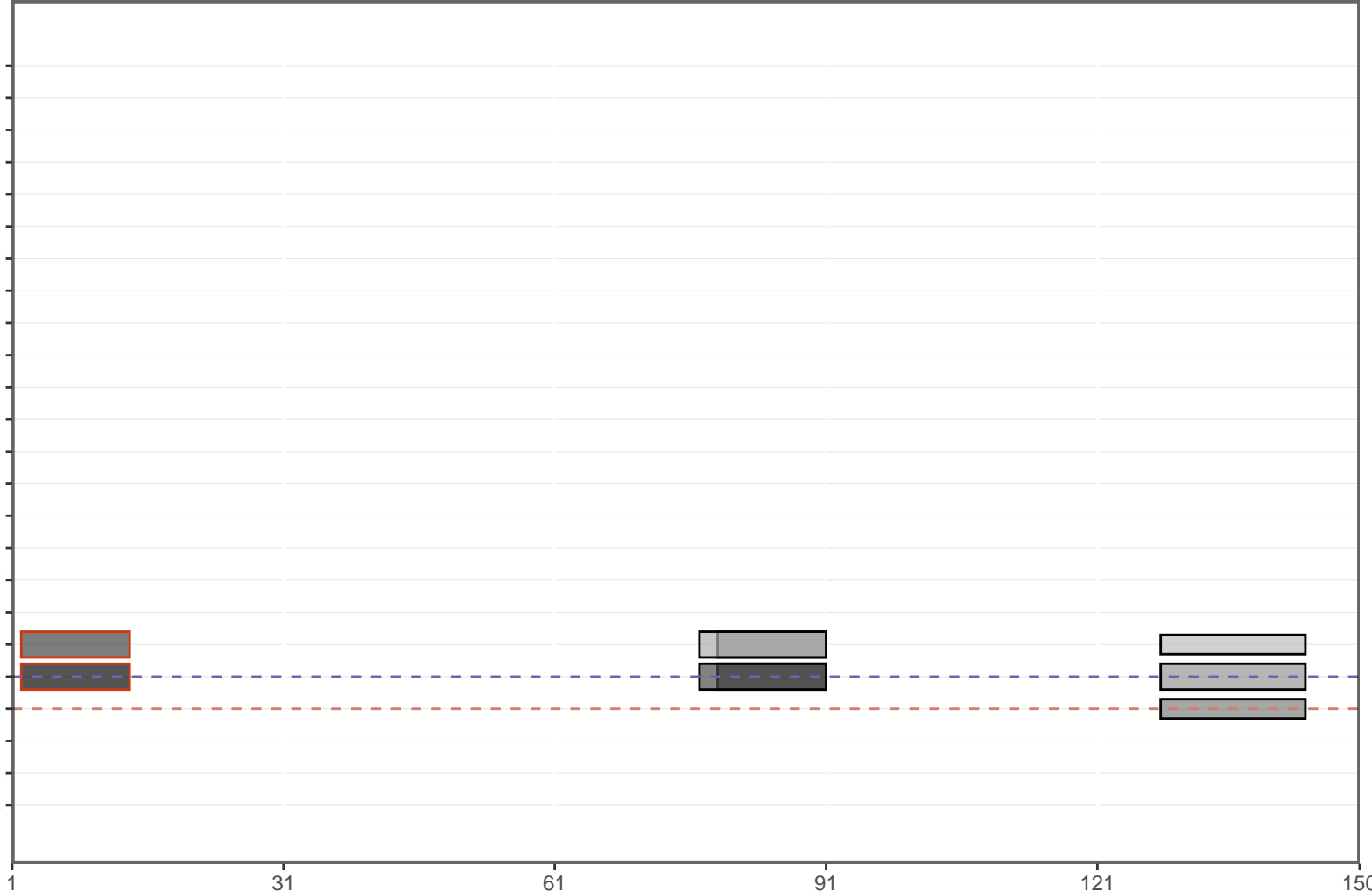
MW indication



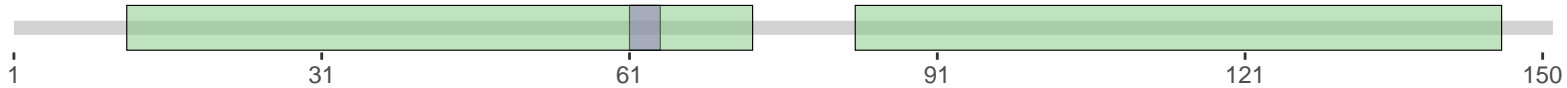
Molecular weight



Gel Slice



Protein length



Pfam domains

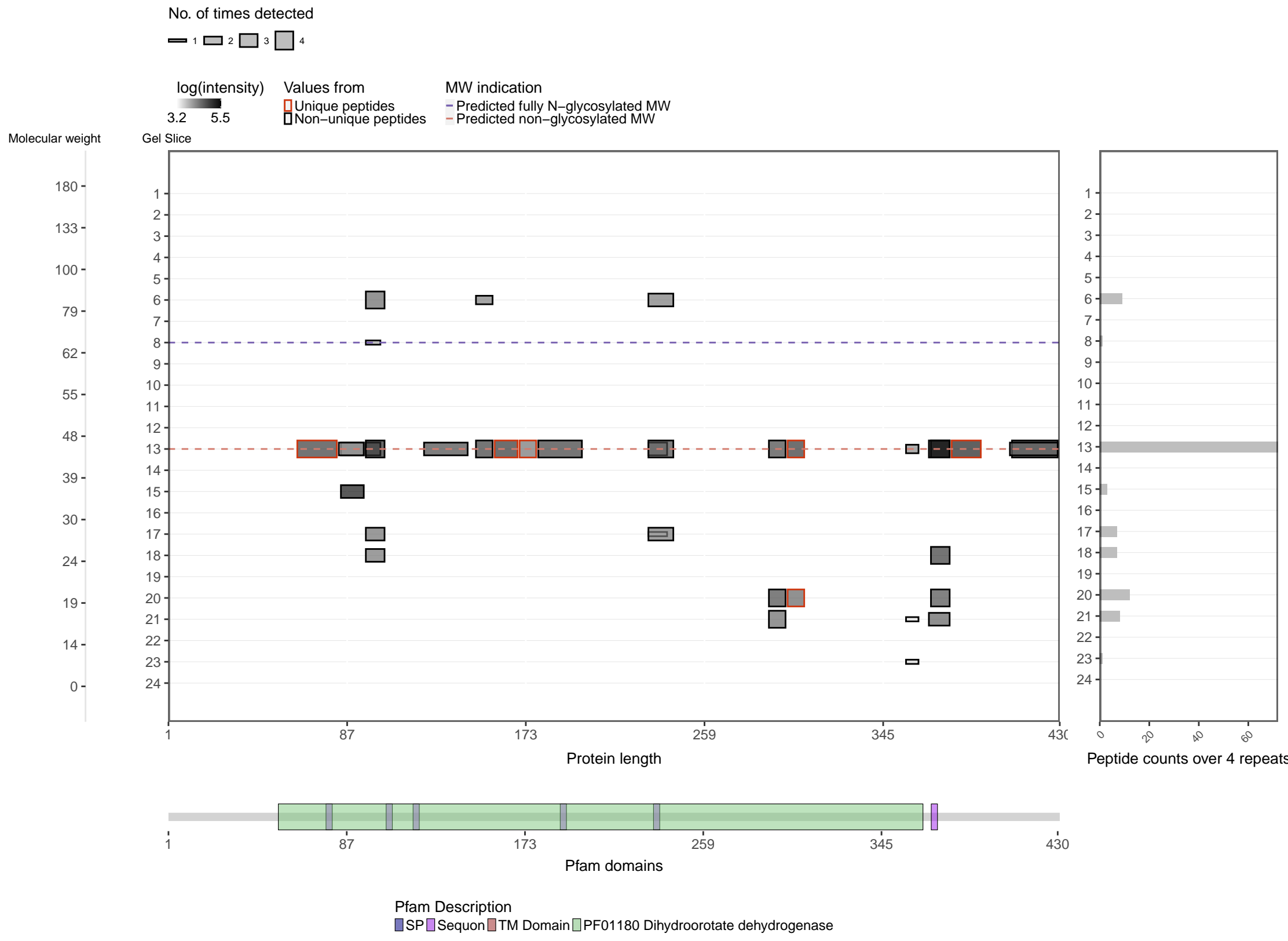
Pfam Description



Protein sequence:

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NbL13g15130.1 dihydropyrimidine_dehydrogenase_(NADP(+))_chloroplast-like [MW = 46.79 kDa]



Protein sequence:

GAAVGGDDCLLEEVGGWVWVATVPVWAWMTFNTDTKPARVSLNGGGEGVSANTIMSVMGINLTLRPEPVEGYSFRGGYSAAVAHPALAAVWVWVMMKKEFGDKDYSLSAIGVETGGDAEFLILGANTVGVCTGVMMHGVGLVKTLSSELKDFMRKHNFSSIEDFRGSSLEYFTHTDLVKRQGEAIRQRKAIRKKGLOGSKDWTFGGDFVGETESMVEN

NbL13g15120.1 40S_ribosomal_protein_S3a-like [MW = 29.73 kDa]

No. of times detected



log(intensity)



Values from



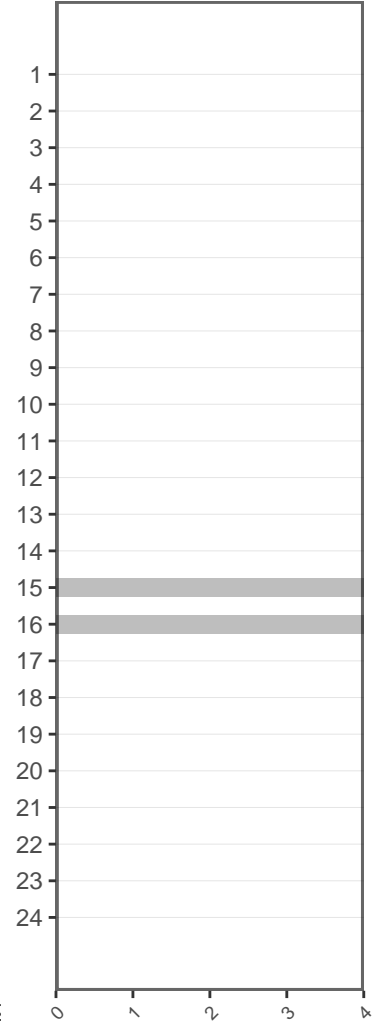
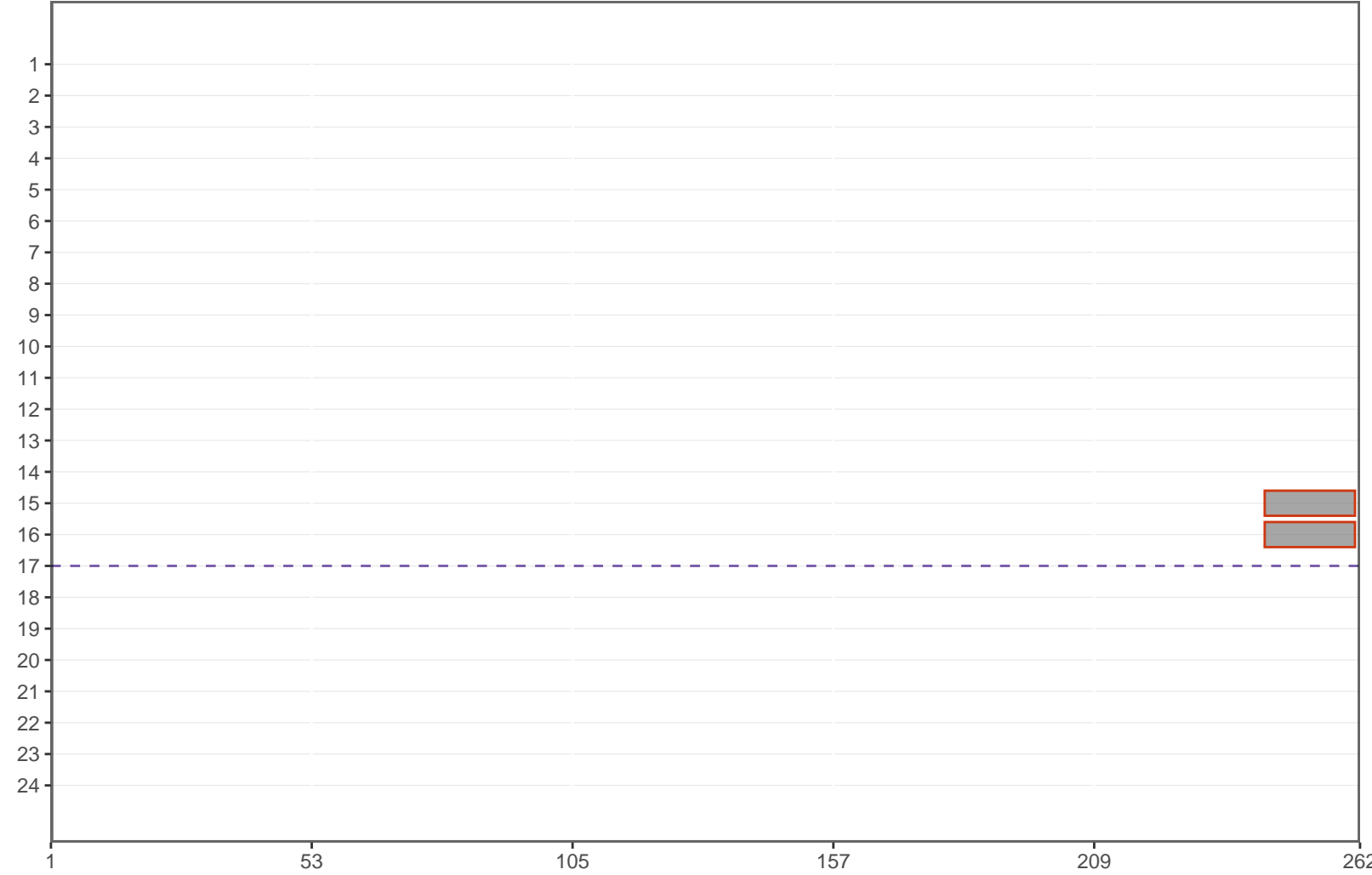
MW indication



Molecular weight



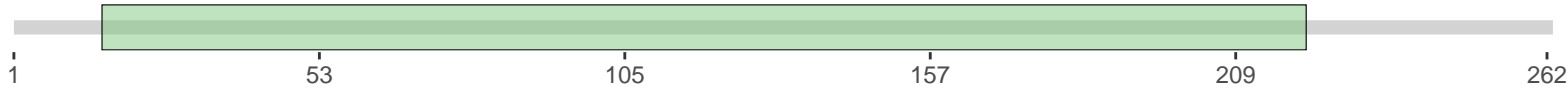
Gel Slice



Protein length



Pfam domains



Pfam Description

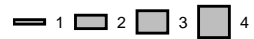


Protein sequence:

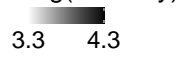
WGQTLEAHVDYKTKTDEYTLRFMGAFTRKRPNGGKRTGYAGSSGIRGIRRMVEMIRNGASSCDLKELVAKRFPESGRIEKATSSIFPLGNVYIRKVKLAKPKFDGKLMMEVHGDQSEEDGVKLRPQDETVAEAEPEVPGA

NbL13g15050.1 V-type_proton_ATPase_subunit_C-like [MW = 42.86 kDa]

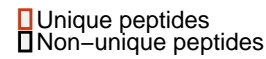
No. of times detected



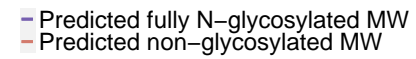
log(intensity)



Values from



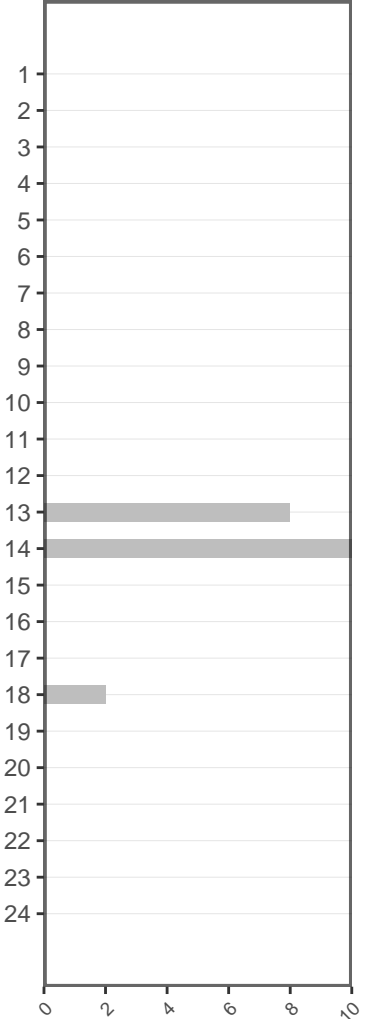
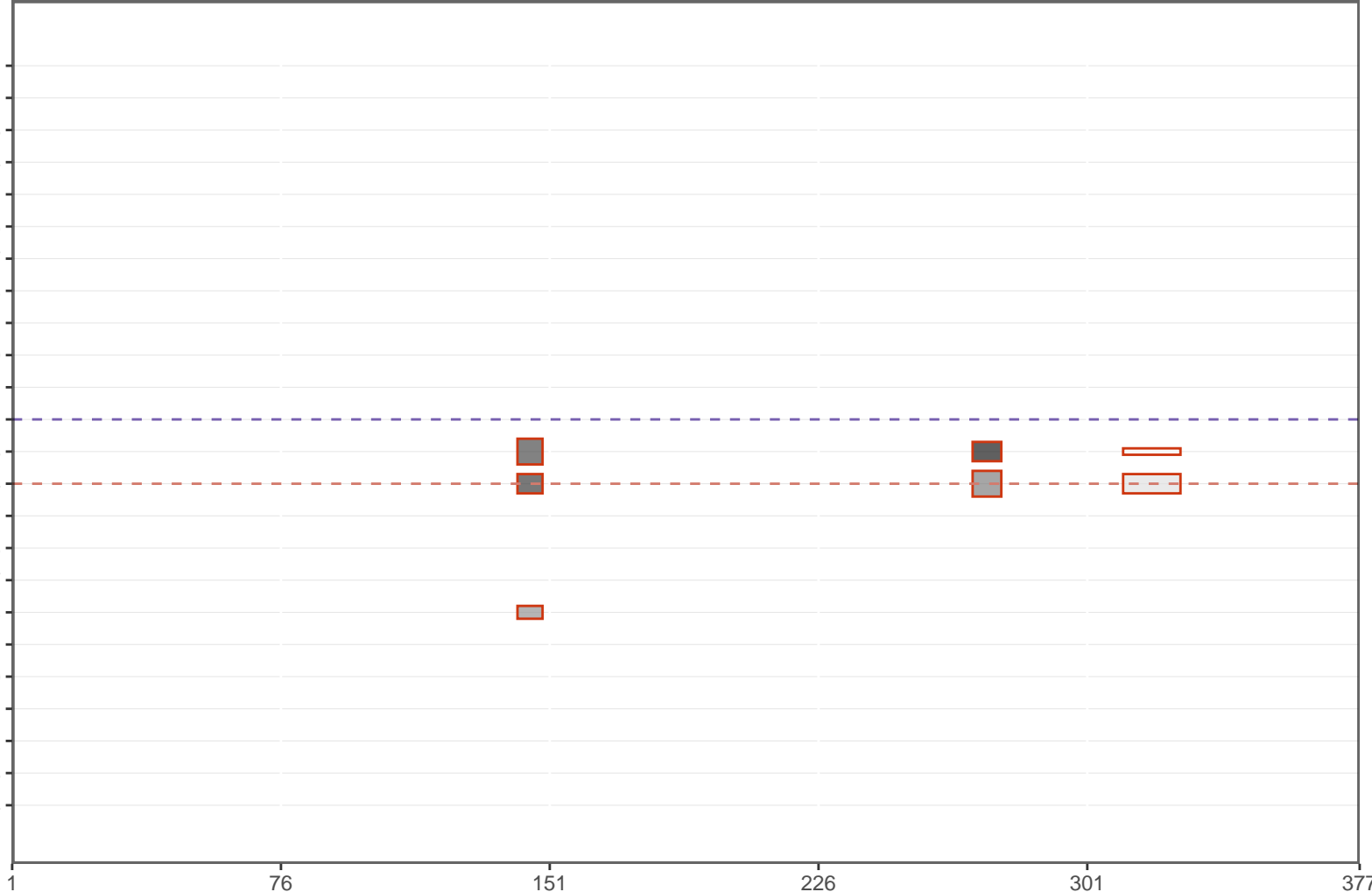
MW indication



Molecular weight

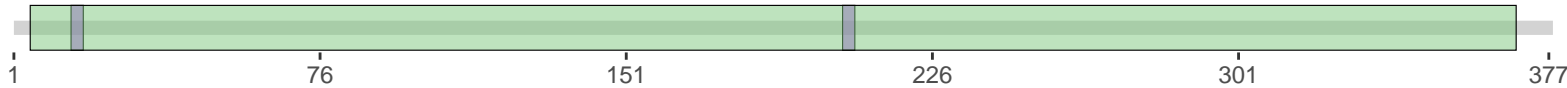


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL13g14950.1 pyruvate_dehydrogenase_E1_component_subunit_beta-1_mitochondrial-like [MW = 40.56 kDa]

No. of times detected



log(intensity)



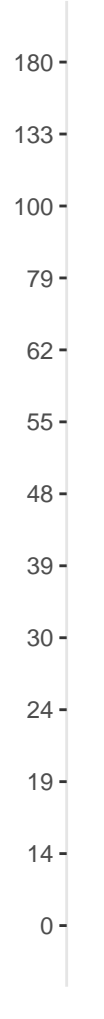
Values from



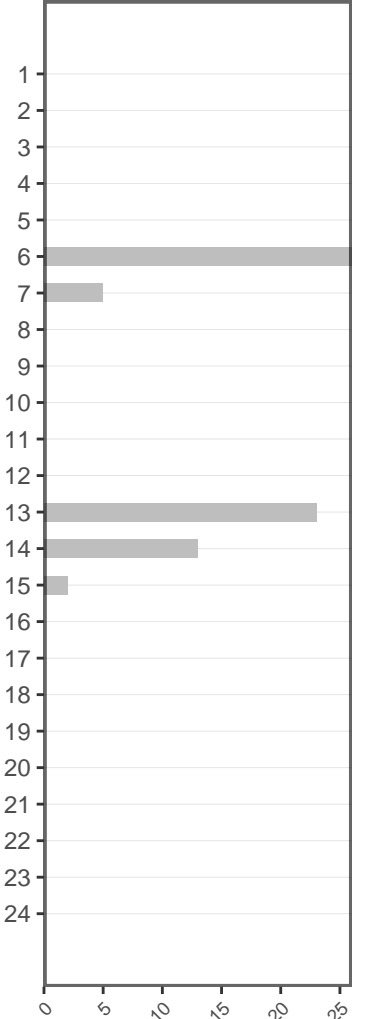
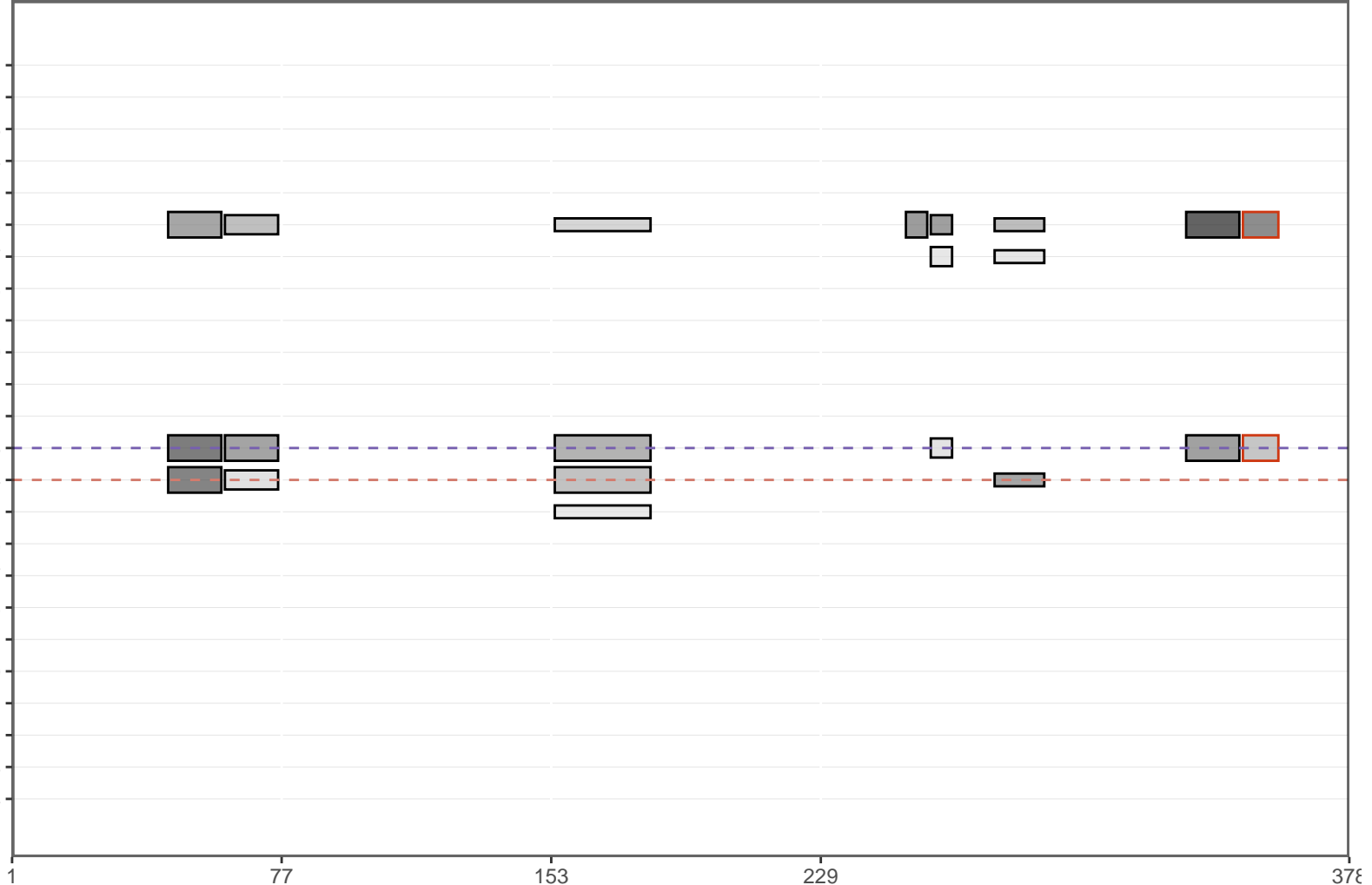
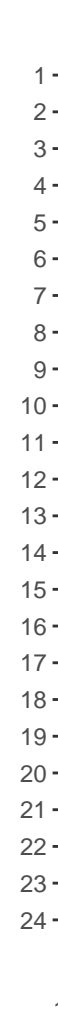
MW indication



Molecular weight

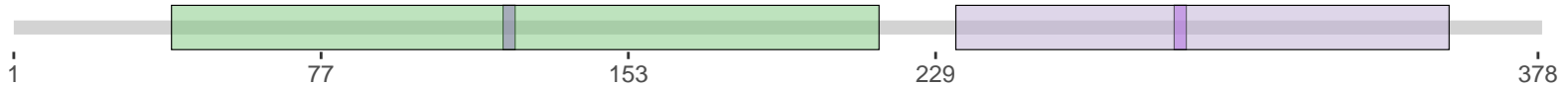


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF02779 Transketolase, pyrimidine binding domain
- PF02780 Transketolase, C-terminal domain

Protein sequence:

MGACPLGLVLPAPYSSEEDARGLLKAIRDPPVAVFLENELLYGESFPVSAEALDSFQLPIGKSKIEREGKQVTTTFSEKMGVYALKAAEILAKEGIAEVLNRSRPLDRPTINASVRKTNRLVTVVEEGFPQHGVAEIGASVVEESFEYLDAPVERISGADVFMPPVAANLERMAVPPQVEGIVRAAKRACYRAAKSVPKATAV

NbL13g14730.1 3-oxoacyl-[acyl-carrier-protein]_synthase_3_A_chloroplastic-like [MW = 46.65 kDa]

No. of times detected



log(intensity)



Values from



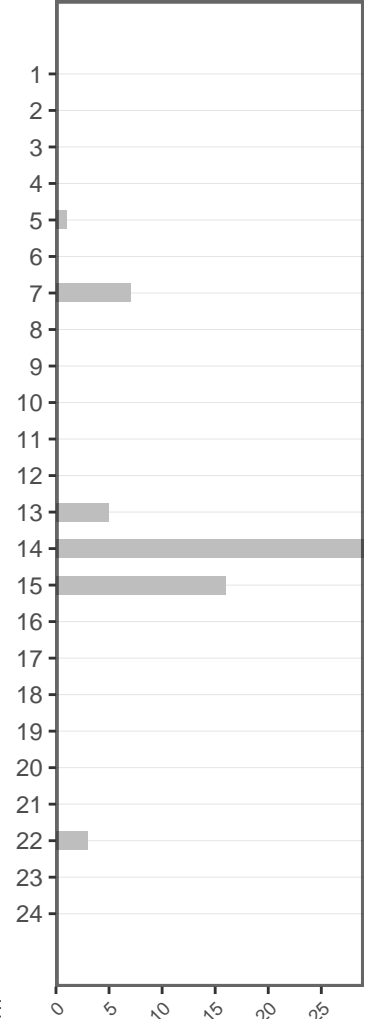
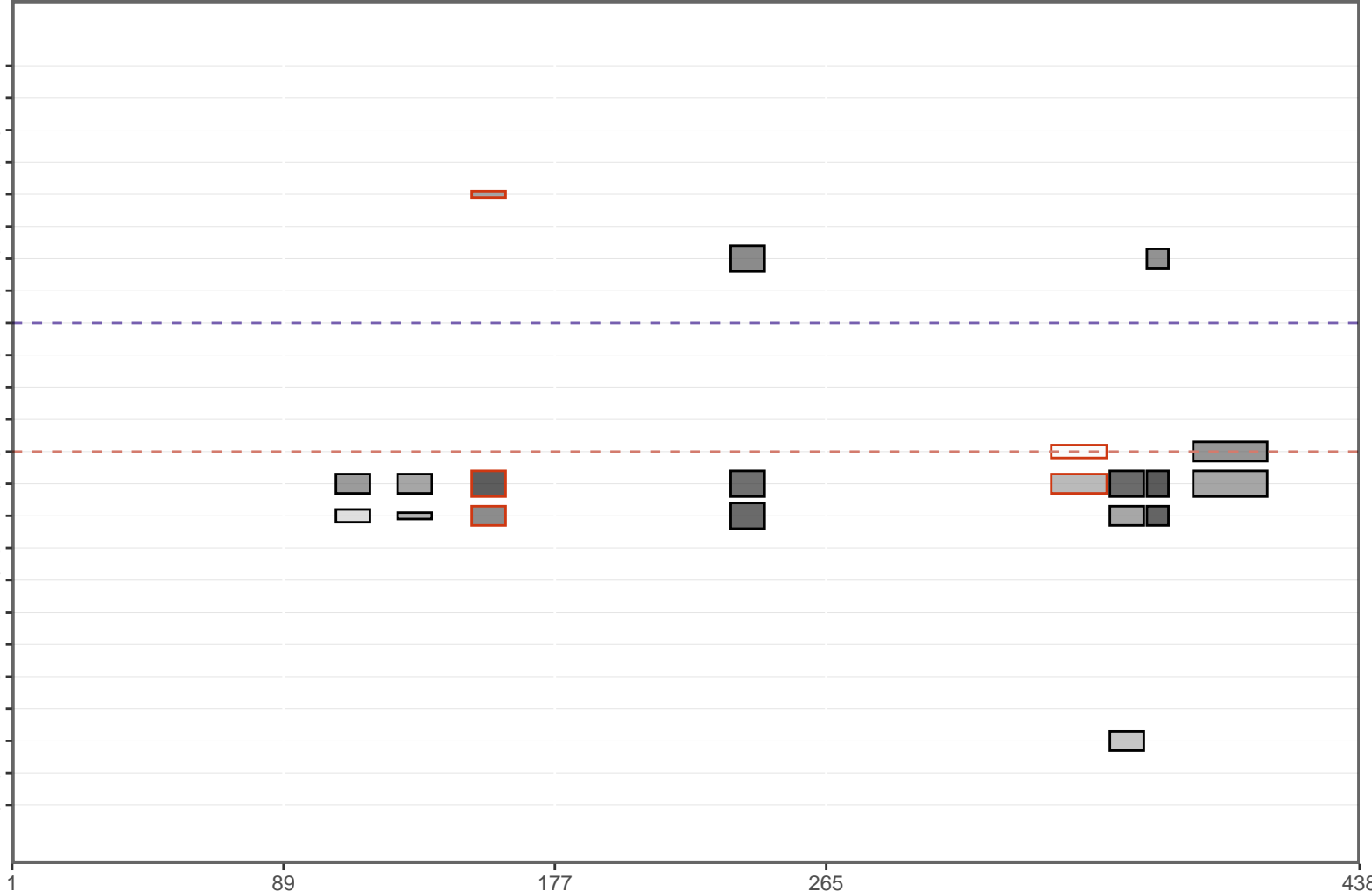
MW indication



Molecular weight

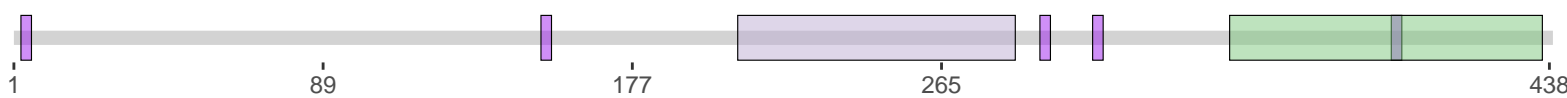


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF08541 3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III C terminal
- PF08545 3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III

Protein sequence:

DTAACSGFMLGLVBAADYRGGGFKNLYIGADALSRVVDWTRDGTGLFGDAAGAAVMQAGDQIGEDLGFDFLHSDGEGGRHLNASKIKENEADHFGTNGSVDFPPKGSVSGIQMNGKEVFRFAVRVYVQGEIAALENAGLPGSKIDWLLHQAQNGRIDGWTRLEVPSEKISALANYGNTSAASPLADFAVRSGNVQAGHWAAAGFGAGLTVGSAALRWG

NbL13g14600.1 DNA-binding_protein_SMUBP-2 [MW = 111.43 kDa]

No. of times detected



log(intensity)



Values from



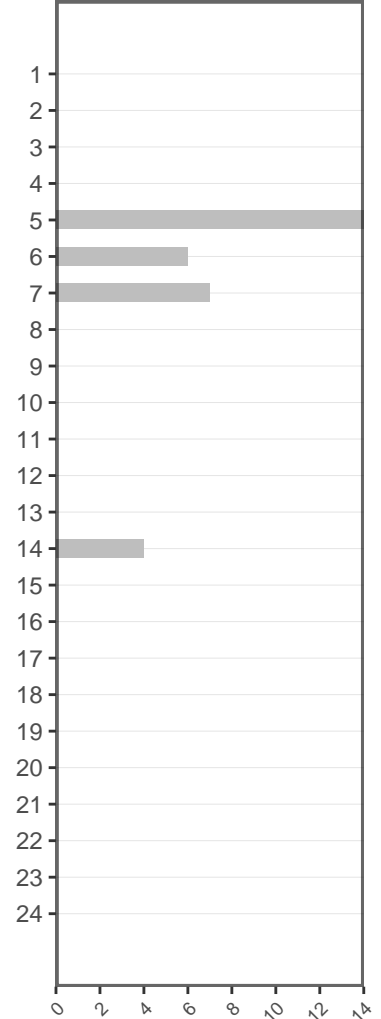
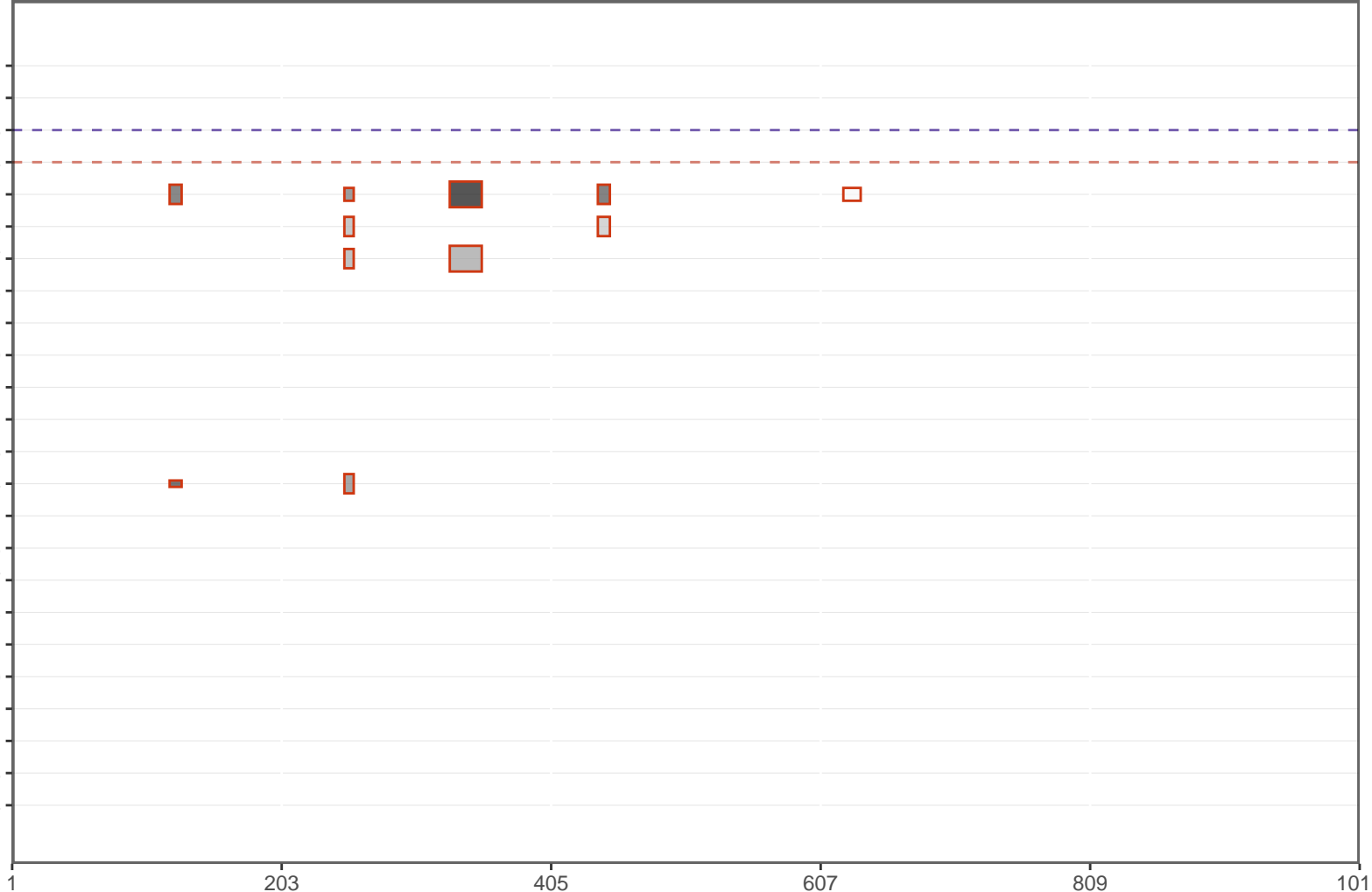
MW indication



Molecular weight



Gel Slice



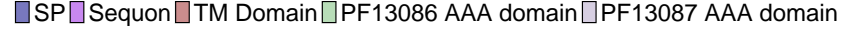
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKKGLIKKIPSVLVWLFQDKEDLWLEENGMDWSEVELPDSITDKSYDASGRKKAALGLNKRPRIMIGDPPGTGKTKMLKELISLAVKGGERYVTAPTNAAVDNNVEKLSIDGILNIVRVGNPXRISPAWAKSLAEVNTLADFRAEIERKKSGLRRDLRYLQKDDSLAAGIROLLKQLGSKIKREKETVKEILSSAQVYLATNGAADPLIRWLDTFDLVIDEAGDAEIPSCWIPILLGKROLAGDQGLAPVLSRKALEGGGLGVSLERAASLHDSMLSTKLTQYRMR

NbL13g14590.1 uncharacterized_LOC104222403 [MW = 17.24 kDa]

No. of times detected



log(intensity)



Values from



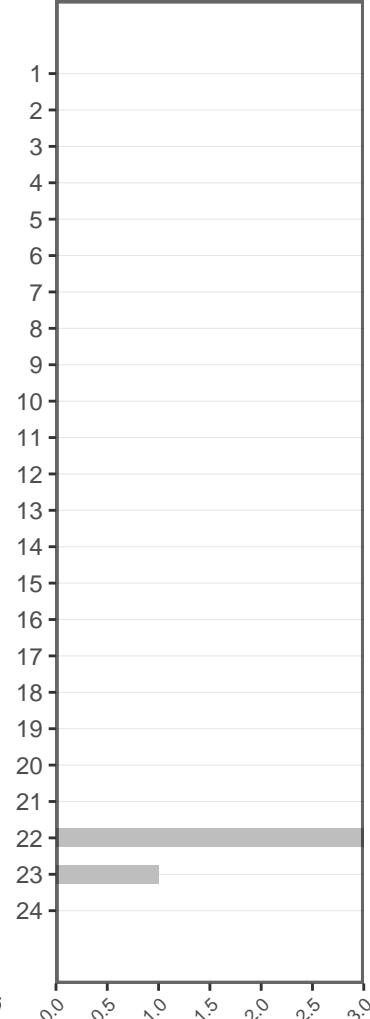
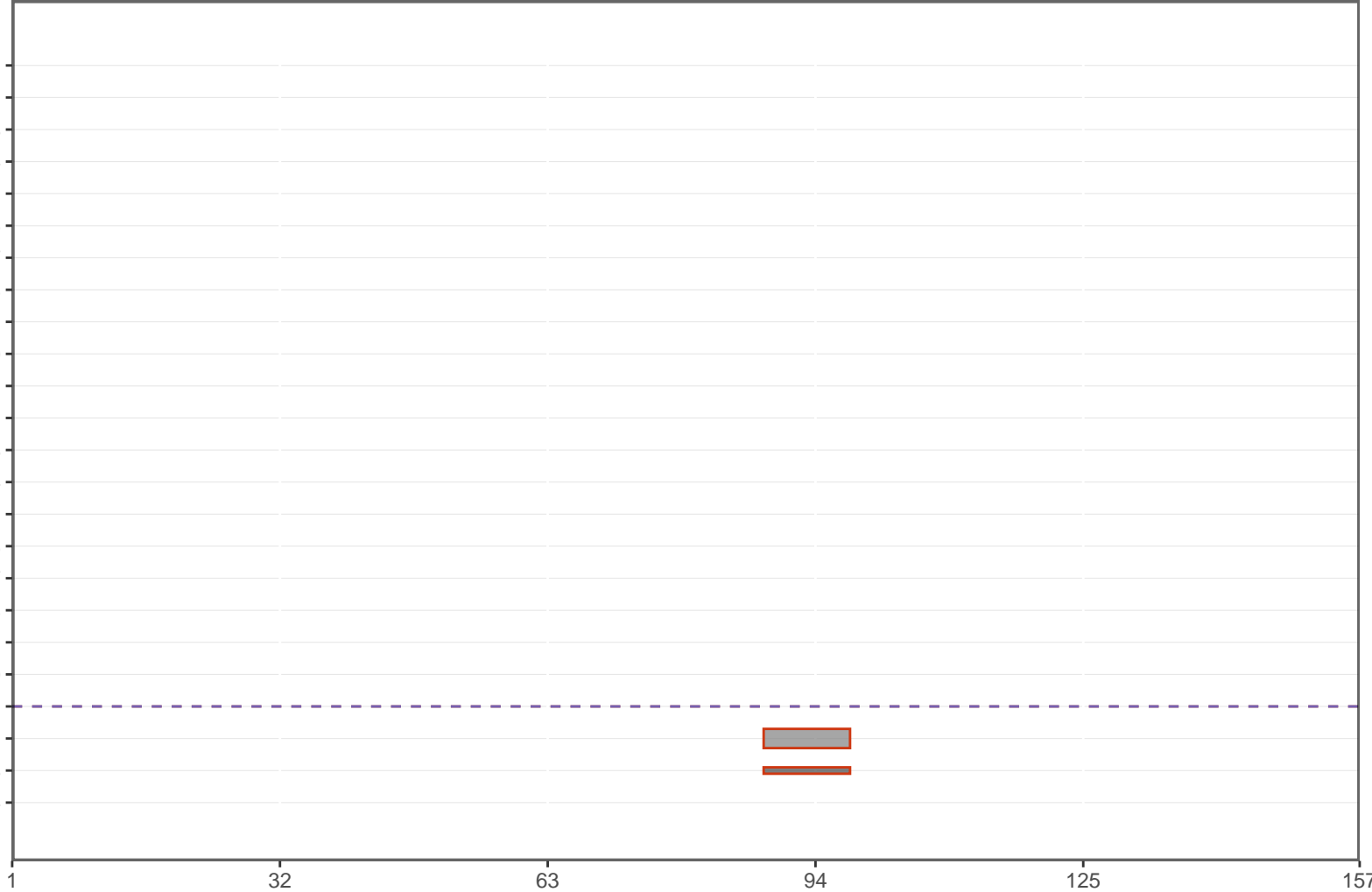
MW indication



Molecular weight



Gel Slice



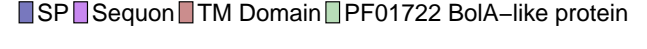
Protein length

Peptide counts over 4 repeats



Pfam domains

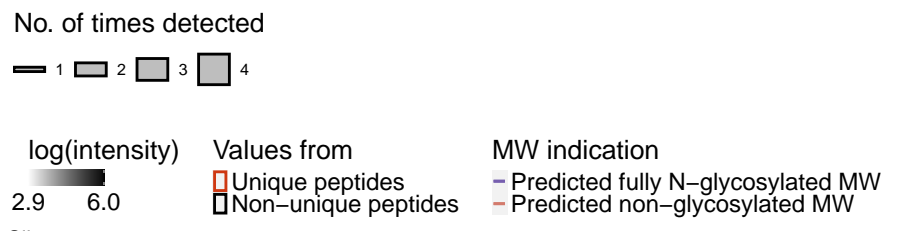
Pfam Description



Protein sequence:

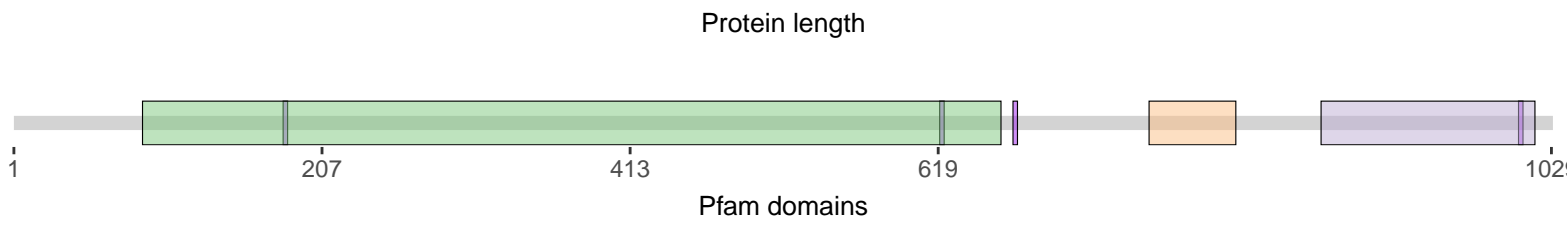
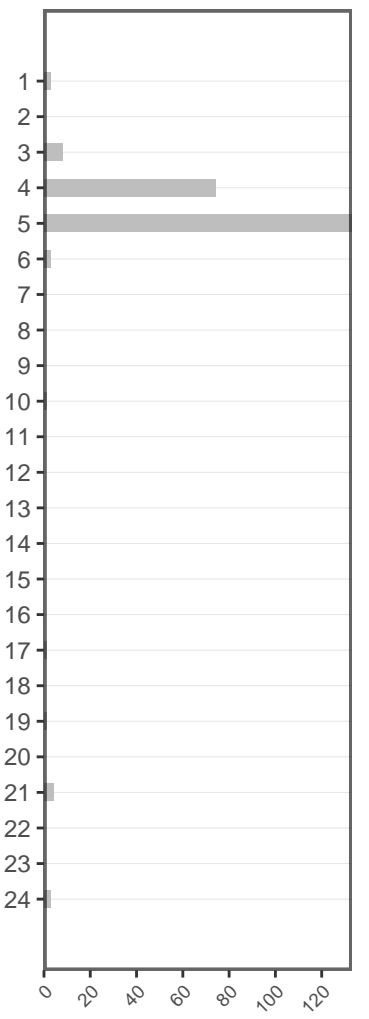
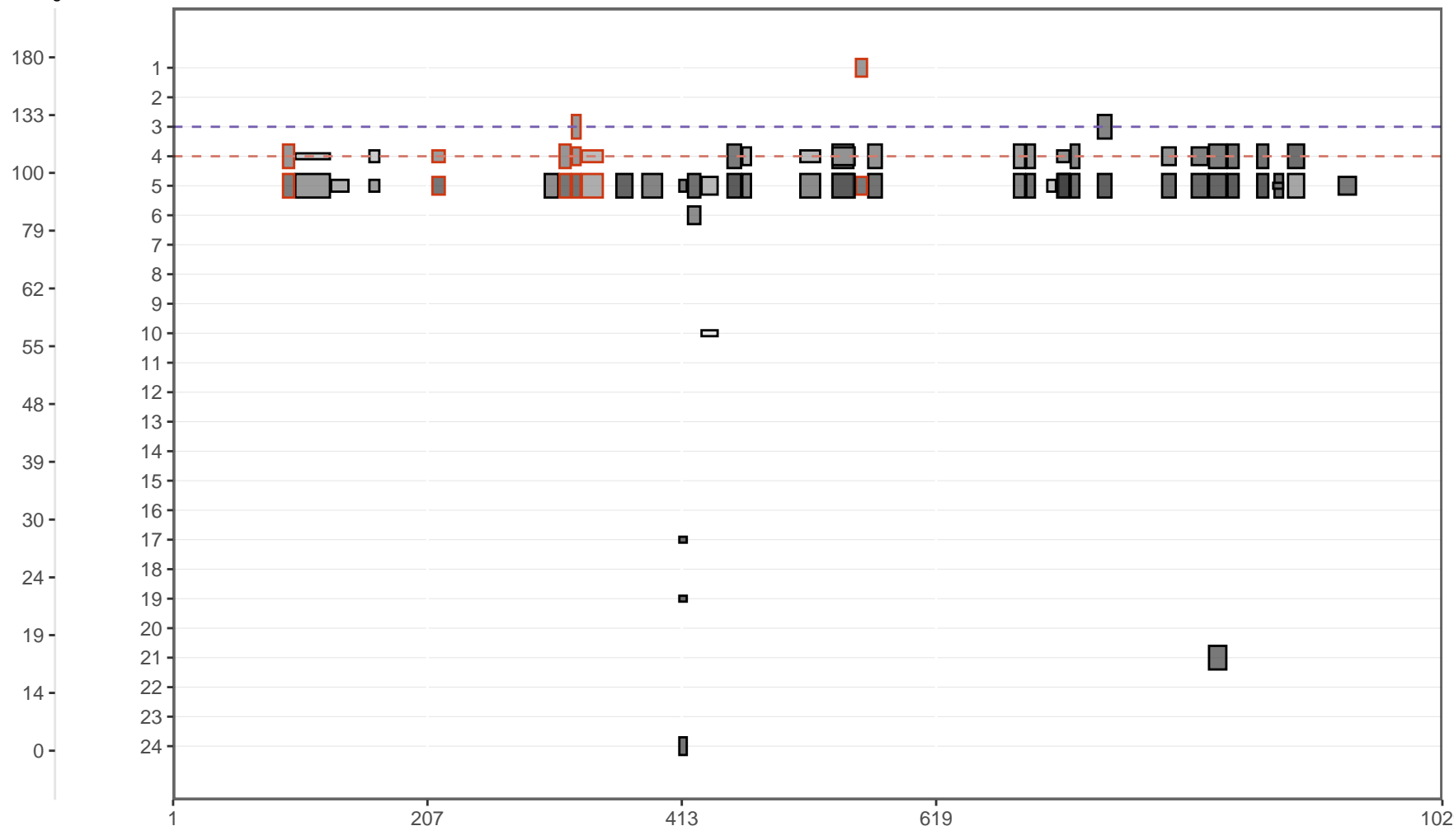
ITSDTGSIDSPLMESMGKRLKEQLNADTFVAKDAVGGGRHVSIDVSSAFEGGSAVNRGRMVKAIWEELGNTVHAVDGMTRKTPTEAGK

NbL13g14540.1 alanine--tRNA_ligase-like [MW = 112.91 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP (blue), Sequon (purple), PF01411 tRNA synthetases class II (A) (green), TM Domain (red), PF07973 Threonyl and Alanyl tRNA synthetase second additional domain (orange), PF02272 DHHA1 domain (grey)

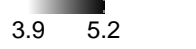
Protein sequence:
 QLMAEERGLVYDQGNVAMDAARERSRNAGSRKNAAGGAIAMDATALHKKGVAAINDKFKFTWFDQHESEKAIYQNEFLESAAAGDVEGILESTSFVAGGGGGYDTGSLSPNGSFDVSNQVYGGFVLIHGSGSQAHKFSGVGDVWVYRRTLAPNHCTHMLNFALKEVLDGHDGKGGSVLPEKLRFDHFHGPVPEELRKHESIVNEQKSELDVFSKEAKLSDAKSKGLRAVFGEVFDPVPRIVSIVGRKVEDLLNPENEWLSYSALCGGTHIS

NbL13g14530.1 cysteine_proteinase_inhibitor_6 [MW – SP = 25.01 kDa]

No. of times detected



log(intensity)



Values from



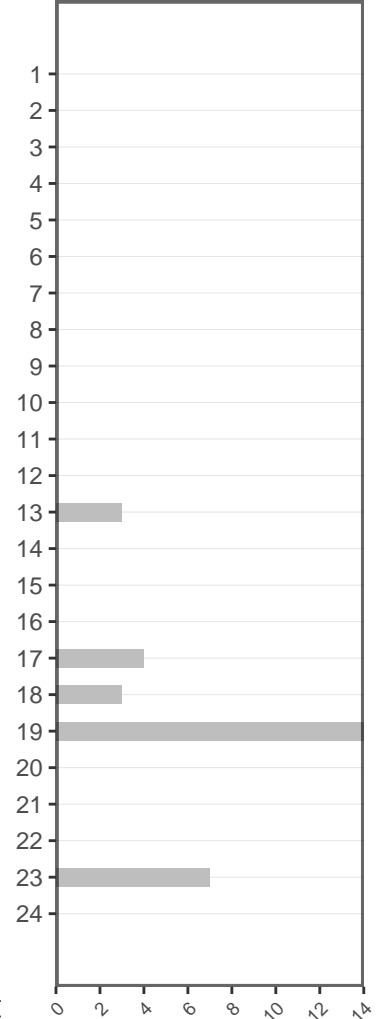
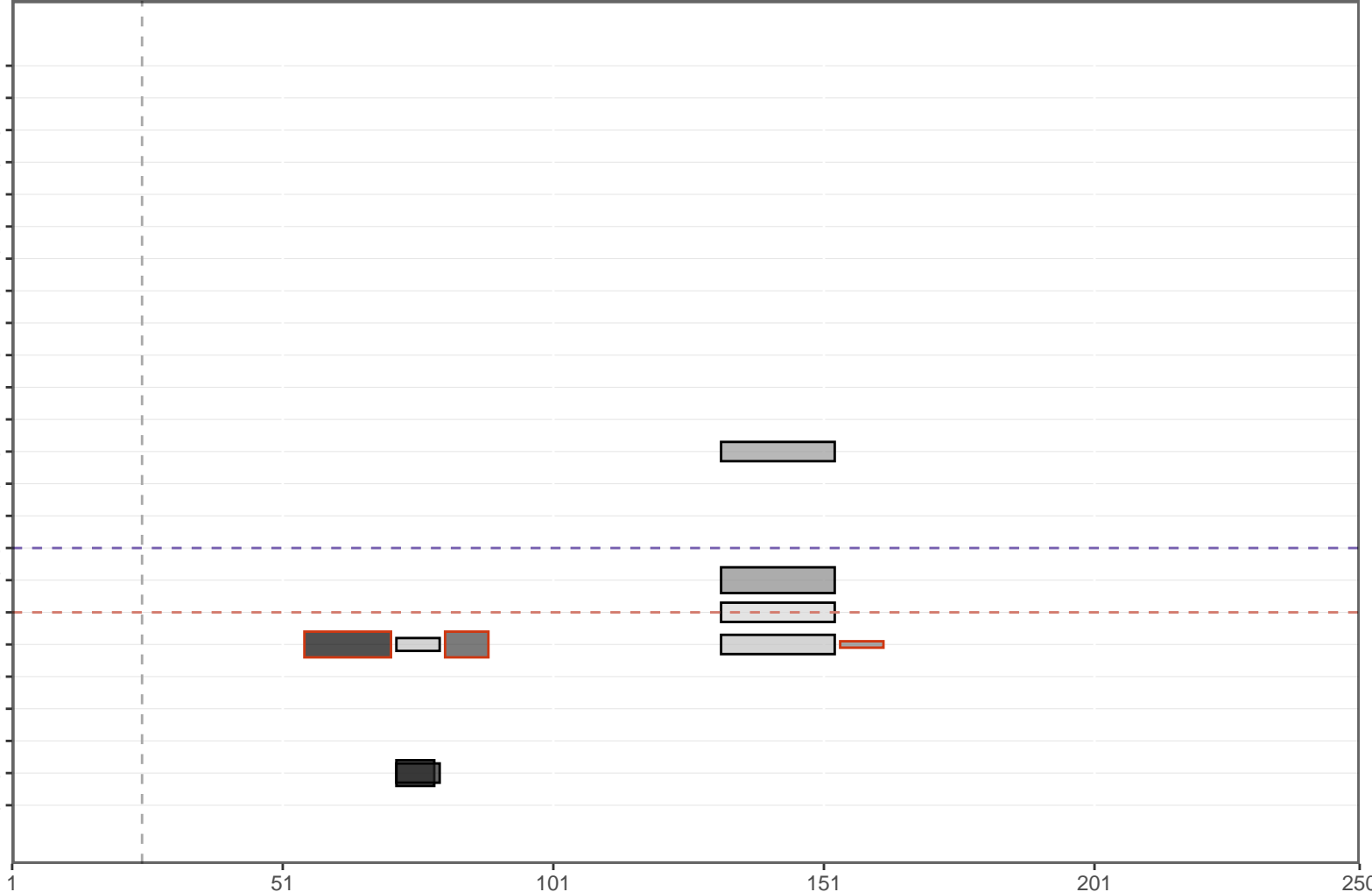
MW indication



Molecular weight

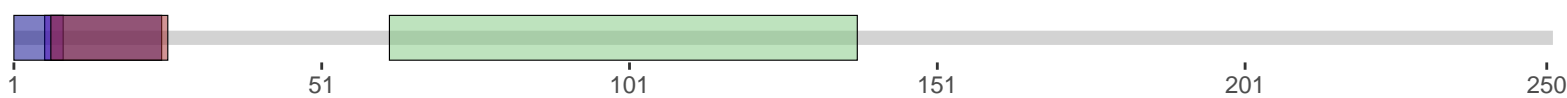


Gel Slice



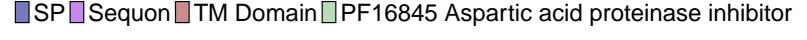
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKKKLYEAKVWYKPKALNFKELGEFTHEEDVPTLTSDDLGVKQEEEGSSGLKSPVHDPIVVDGEAAEHAHKTIGQRSNLLLLYELQERVHANAIEVIGEDNMKHLMLIKTRGDKREKFKVGVHNNEGAFQLNHEPDS

NbL13g14510.1 uncharacterized_LOC104097028 [MW = 14.26 kDa]

No. of times detected



log(intensity)



Values from



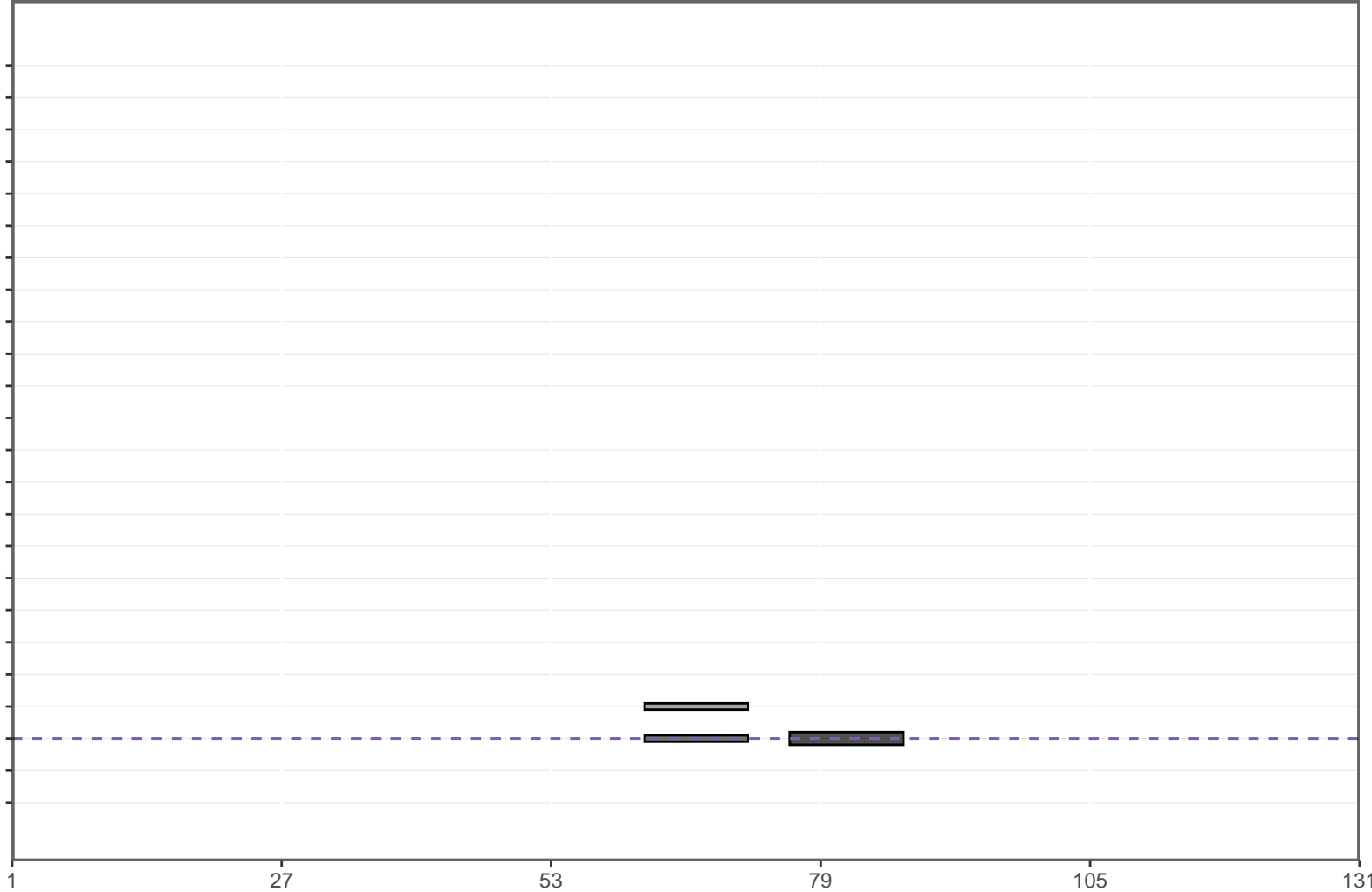
MW indication



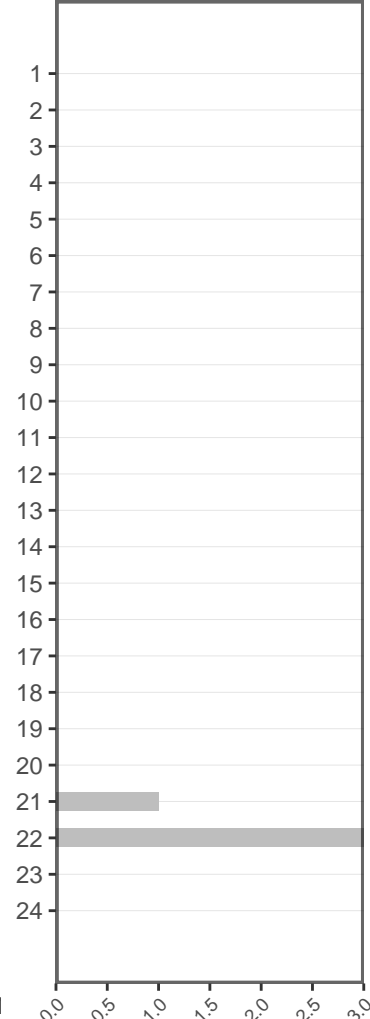
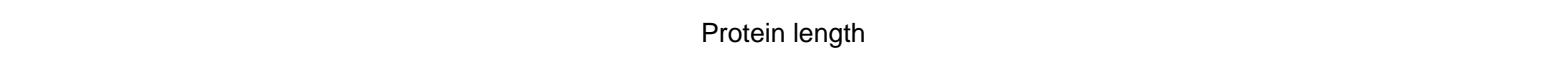
Molecular weight



Gel Slice



Protein length

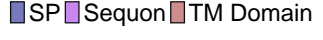


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

YIFAPQIRRSLLNDEEYGFRRAKRPIWHYDEGLEKTRGLNKKLDQLNSAIDKVSRLRGGNMPVPIVETDPEEATM

NbL13g14450.1 WEB_family_protein_At3g02930_chloroplastic-like [MW = 109.68 kDa]

No. of times detected



log(intensity)



Values from

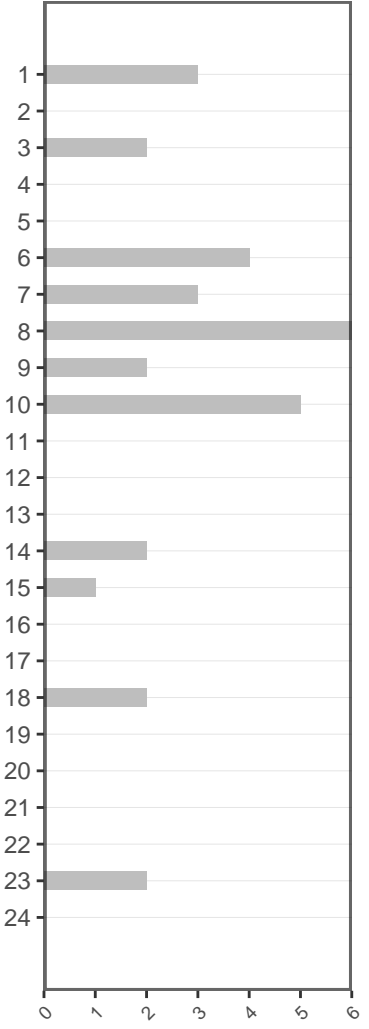
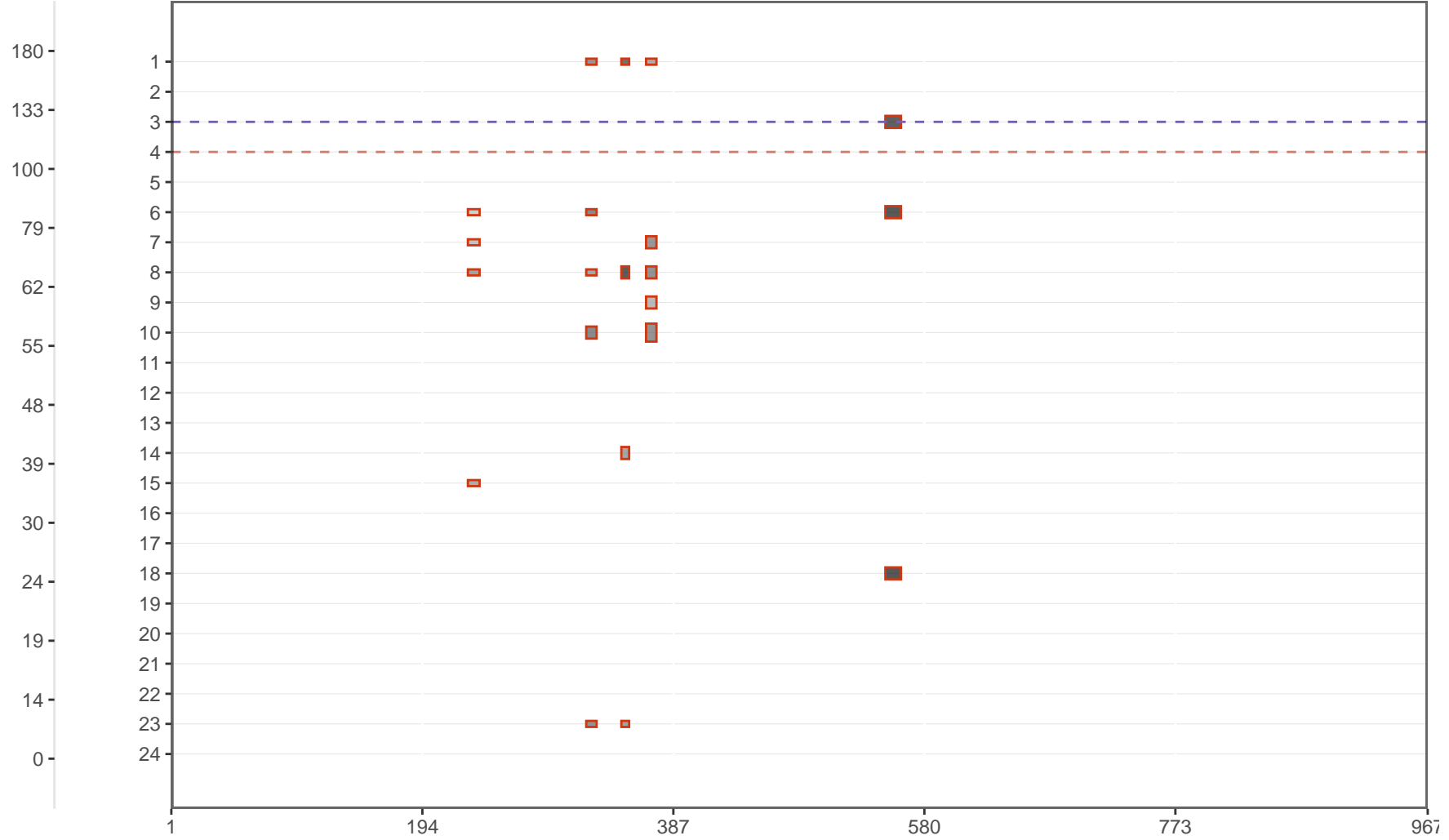


MW indication



Molecular weight

Gel Slice



1 194 387 580 773 967

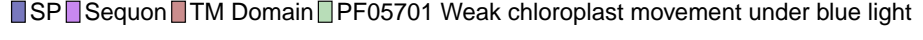
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGSNDLLDAAESEASLKEKLVOLLEMTTRKGDLEESERRRAGIAKEEASEMANKVESLITELETVYKKEKTKQAEHEKLAEEVQGLLEKKNLNELENSREEEEKSKKAMESLASALHEVSSERAKERLLSSQAHEHYETQIEDKLVKATNKVYESSLLDAAEKEDDLTTSVEQSKNEHHKKAWEVDRLLHLMNDVKKTEEENSSMEKEINRLVNLKKEAEGEVSPKKEAVQLKNSLHEAESEVTKYKEVLGEAKGESMKLKEBLDKENEVQNLQENEELRSRA

NbL13g14360.1 binding_partner_of_ACD11_1-like [MW = 29.39 kDa]

No. of times detected



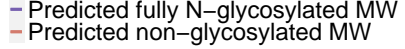
log(intensity)



Values from



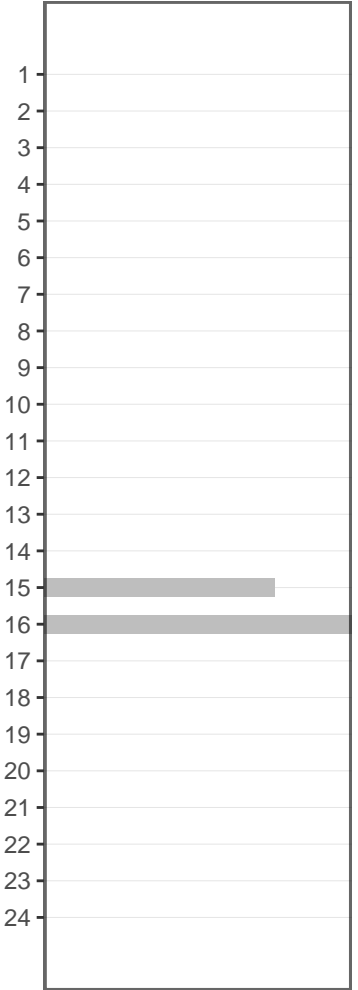
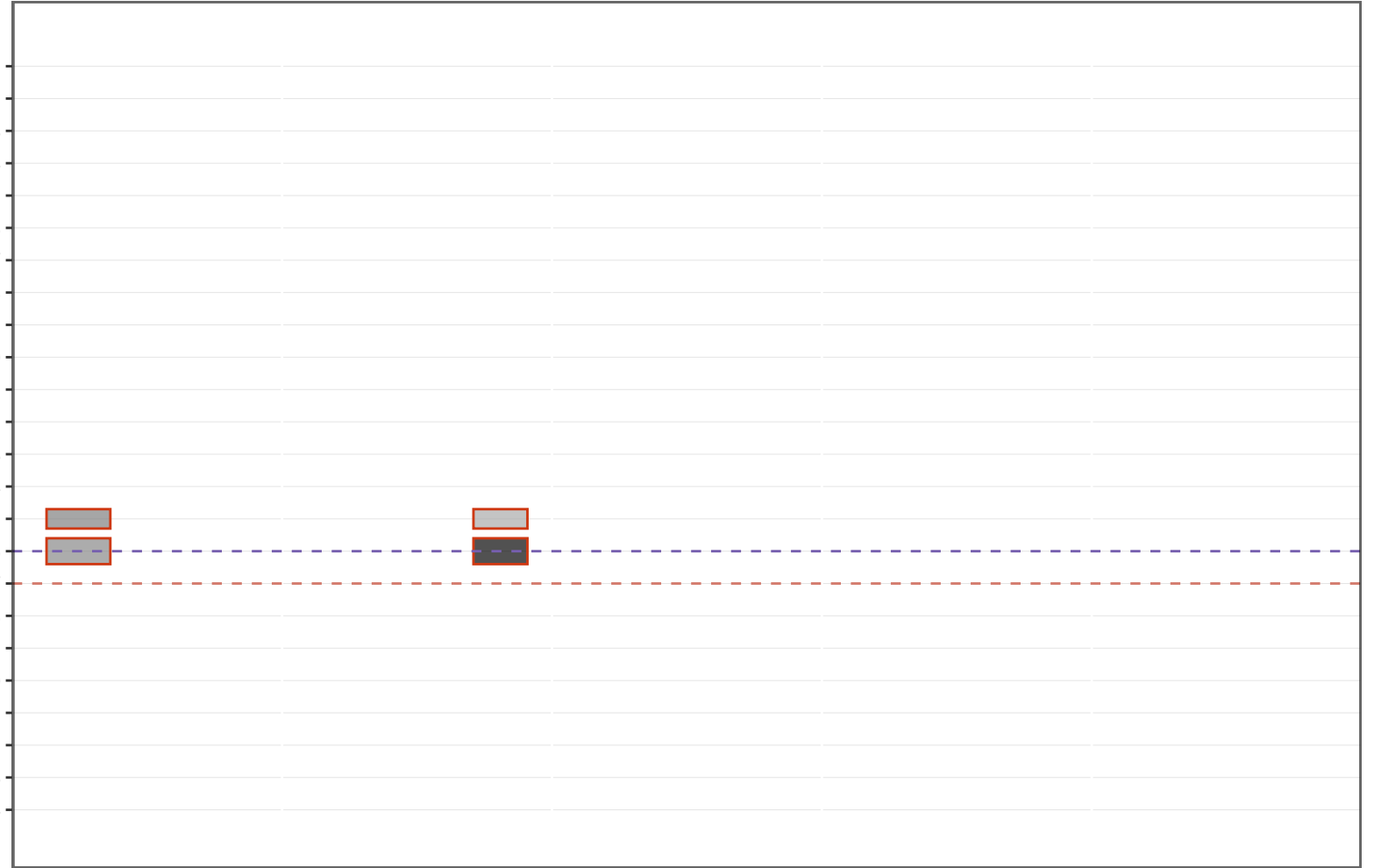
MW indication



Molecular weight



Gel Slice



Protein length

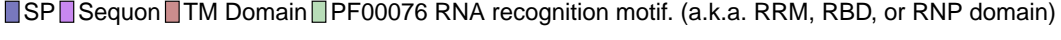


Peptide counts over 4 repeats

Pfam domains



Pfam Description

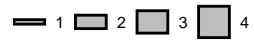


Protein sequence:

NKAKTTFDEKHQFISTASAKWASLDQKIGLSEKINMGTTIVNDKVKEMDQKFDVTEKTSKSAFAAAEQGVSTAGEAIMMKRNVYLTGASVWTFGANVYTKAAGEVGGKTKEMKEEEQGRSSAAGVYPIHAFSESPKASKTEERANPLHLRT

NbL13g14210.1 ADP-ribosylation_factor_1-like_2 [MW = 21.86 kDa]

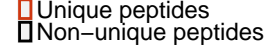
No. of times detected



log(intensity)



Values from



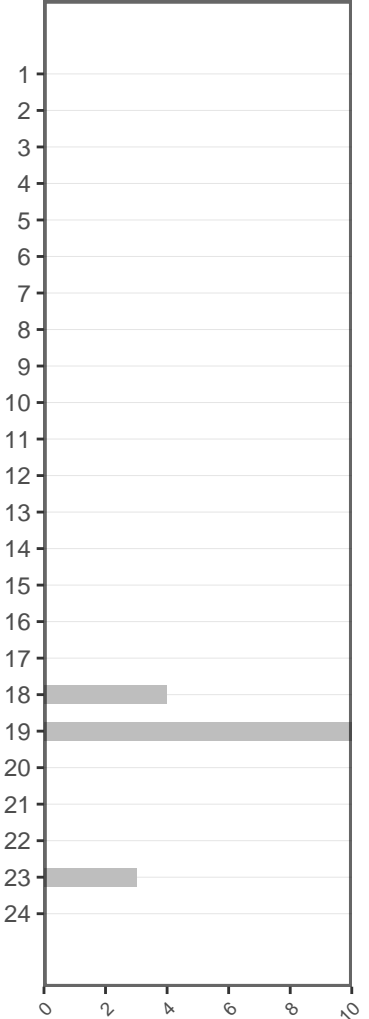
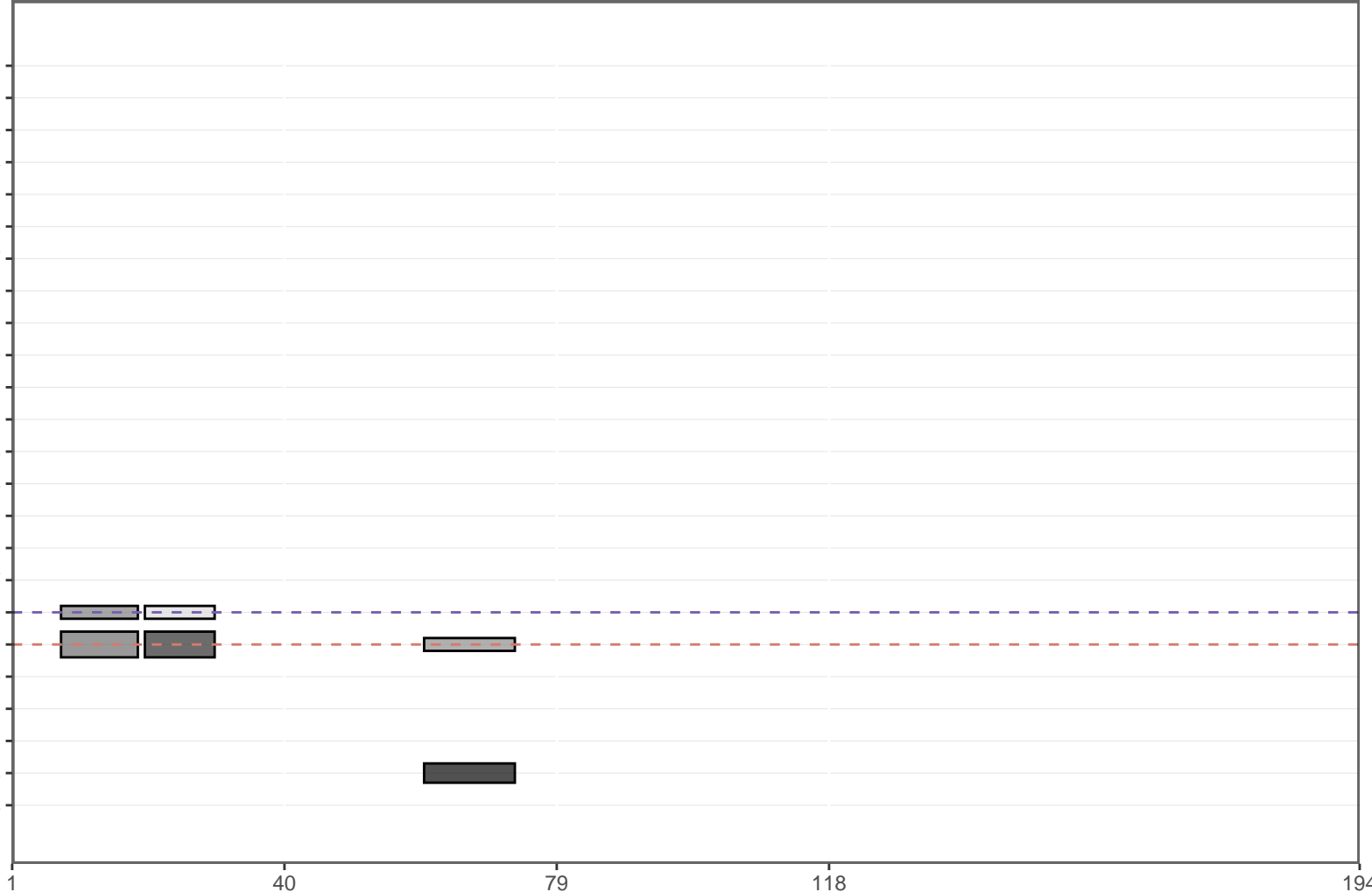
MW indication



Molecular weight



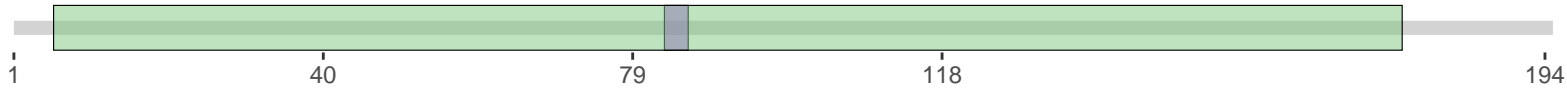
Gel Slice



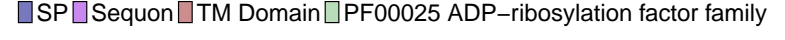
Protein length



Pfam domains



Pfam Description



Protein sequence:

INTDGLIYVYDSDLDRERIGKANGDFGAIRDPFMLNAILFANKGDMKGMATPMEVCEGLGLVELKNRKHWHGGTCLARGDGLVEGLDMLASTLKEHKAVGYSIGPSPF

NbL13g14070.1 uncharacterized_LOC104210248 [MW = 13.81 kDa]

No. of times detected



log(intensity)



Values from



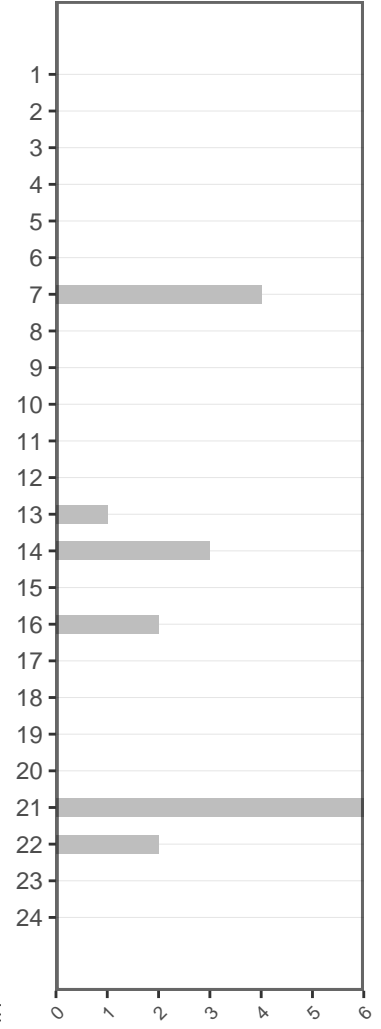
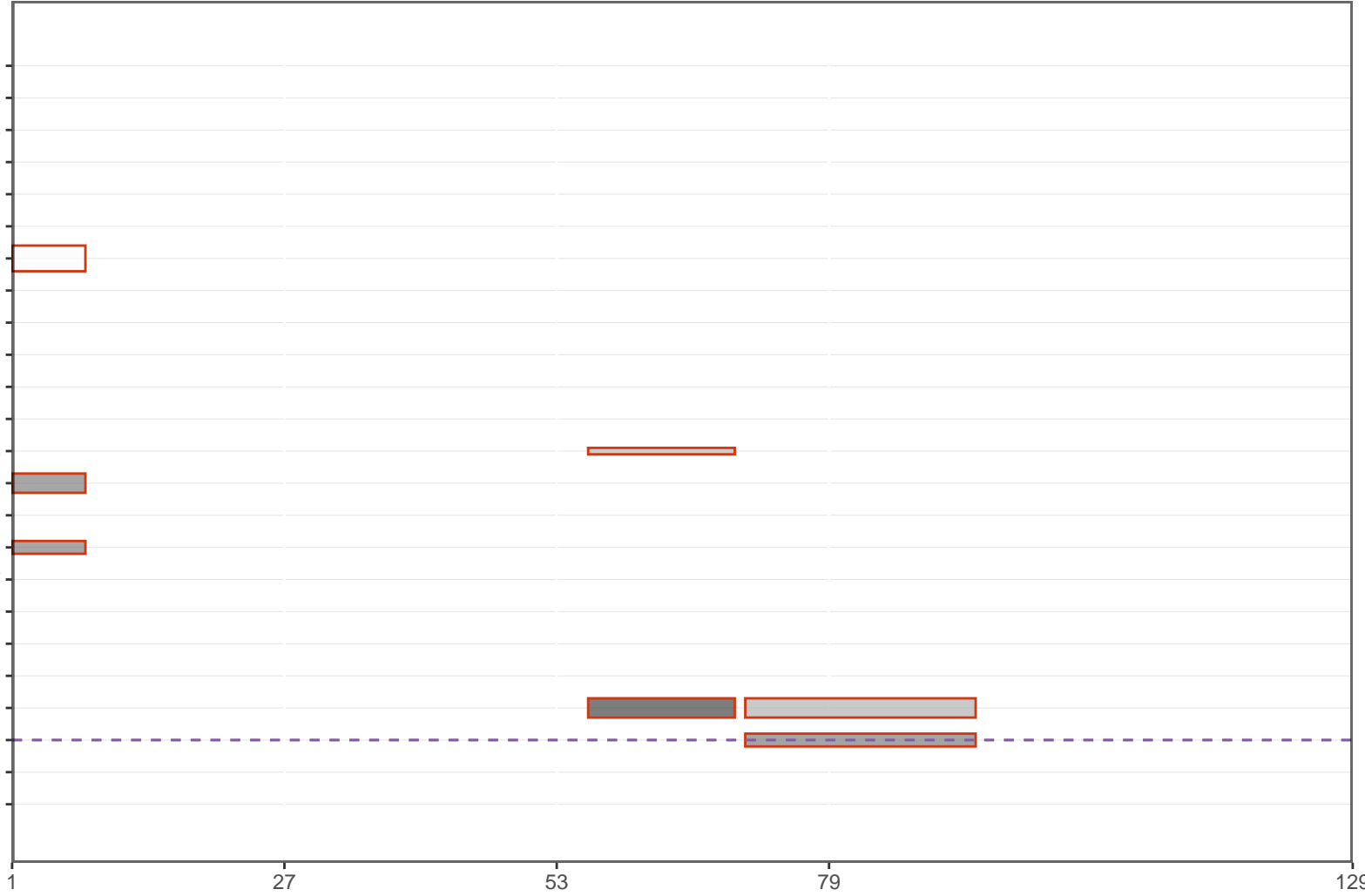
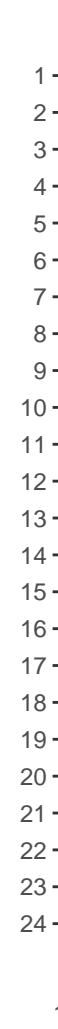
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

DHVRDSVYDVEIELGSEKYGPHQGTGVFGPATNSAGGERGFHHSPTAAAAAESILEKQTFRRPLEDLKPGHAY

NbL13g13970.1 DNA-binding_protein_BIN4 [MW = 44.52 kDa]

No. of times detected



log(intensity)



Values from



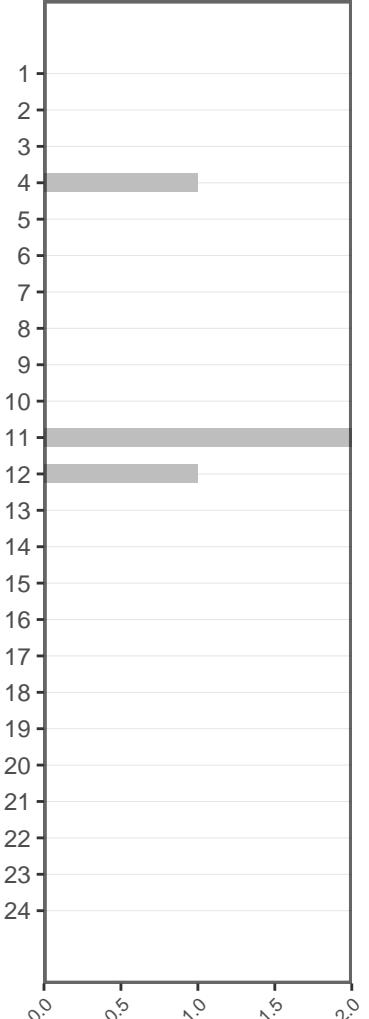
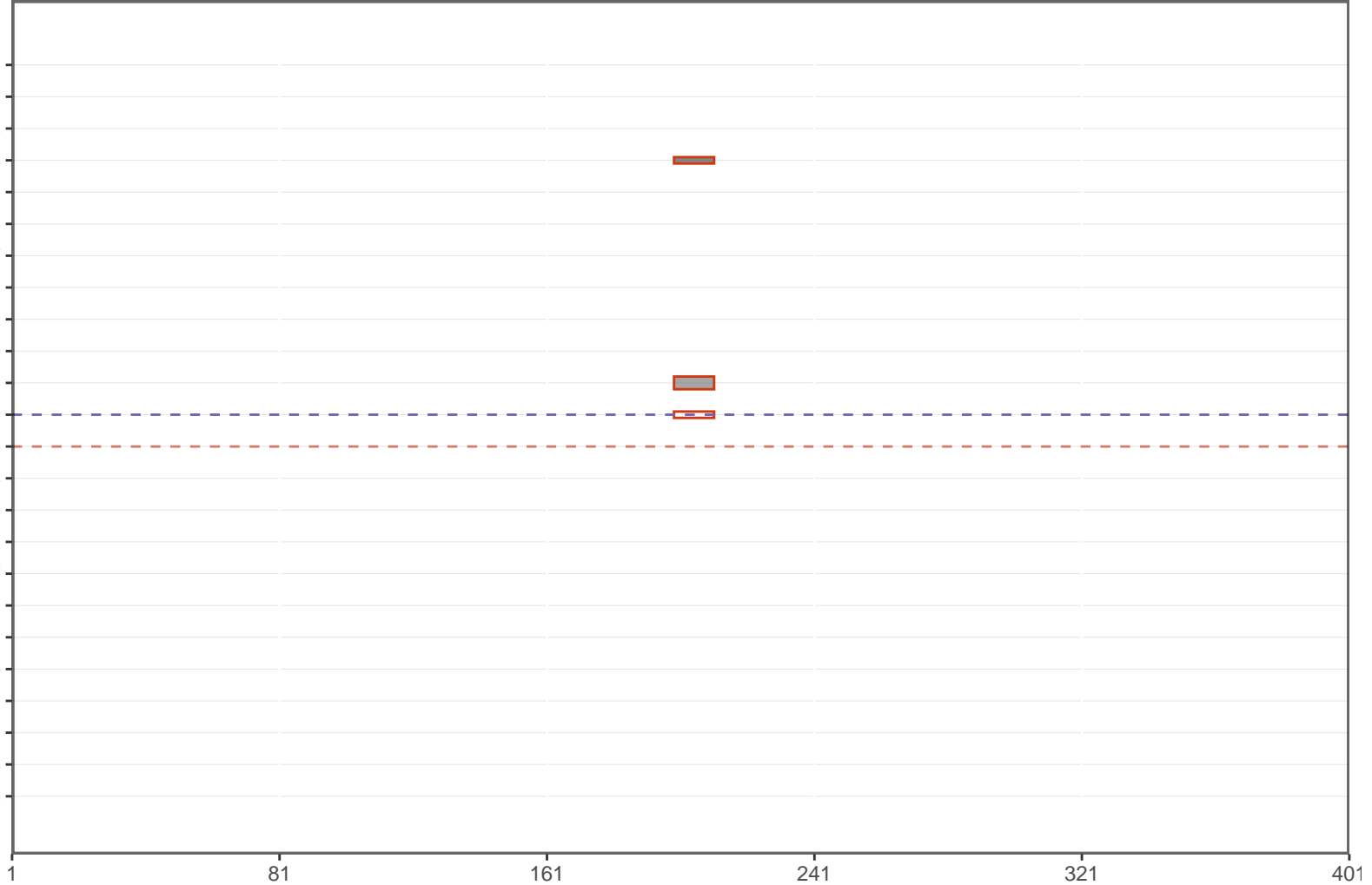
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains

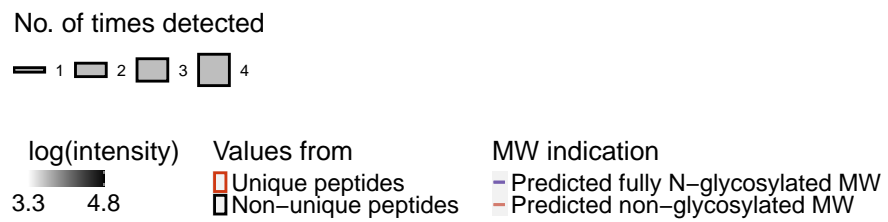


Pfam Description
 SP Sequon TM Domain

Protein sequence:

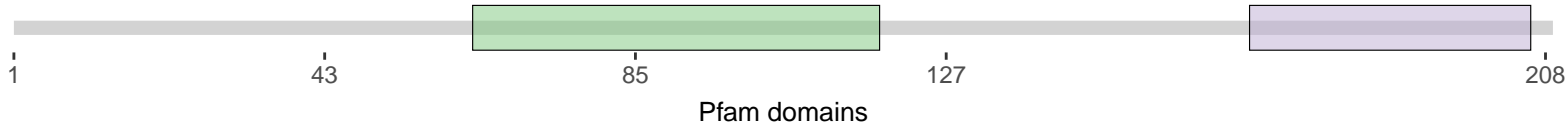
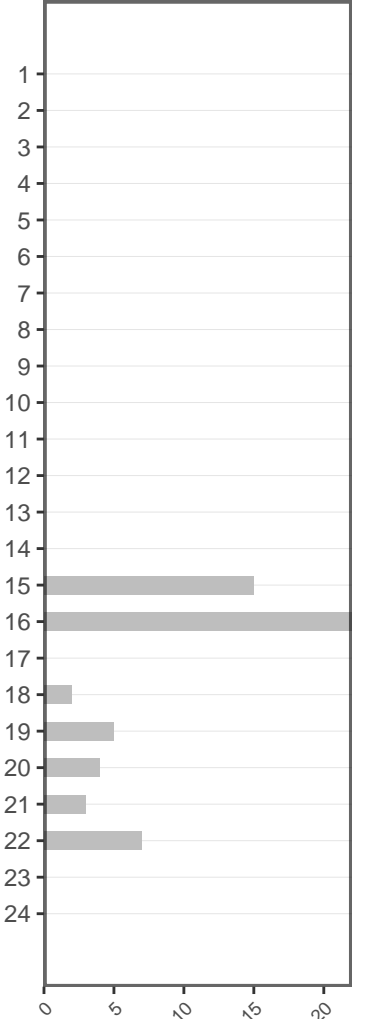
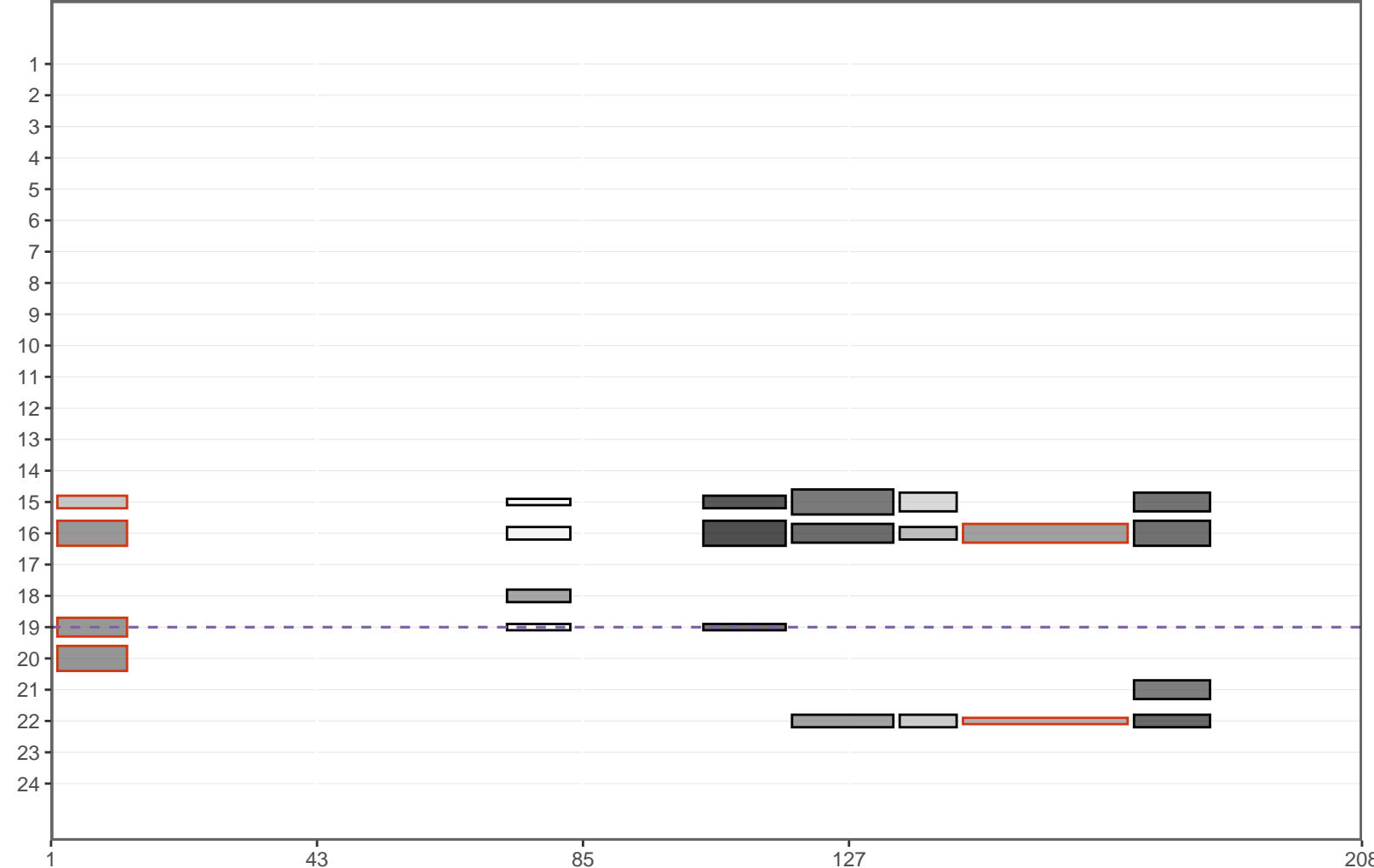
KKKLESQKKEEKEDMDAVEENPEKGGVPLNLSFRLLPLPEKVGQRTHKALVEEGEGDSHLDSGDMGAGRIVISDGPGGKHEMLFDLKGTHYKTTLSRRTFVYVSGQTGAKVYAMNDFQITPQSNVYEATMVEGTLGGFTTFDSEEAENLRPAPSGGGDNENADHGINGNKKAKAKKASATEGKGGKGGKVKIPKVKKKKPAKPKKGGK

NbL13g13840.1 nascent_polypeptide-associated_complex_subunit_alpha-like_protein_2 [MW = 22.66 kDa]



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain PF01849 NAC domain PF19026 HYPK UBA domain

Protein sequence:

KNVLFISKPDVFKSPNSETYVIFGAEKEDLSGQLGTGAAGGFRMPDMGSMVMAKSDVSRPTAAAEADEEEEEVDETGVFRPRDILVMTGAGVSRKAWKALKGHNGDVSAMELTPT

NbL13g13820.1 caffeic_acid_3-O-methyltransferase-like [MW = 39.74 kDa]

No. of times detected



log(intensity)



Values from



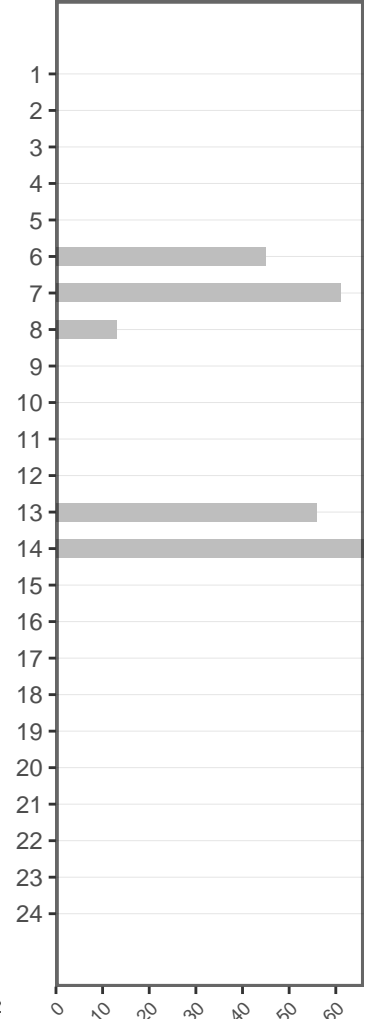
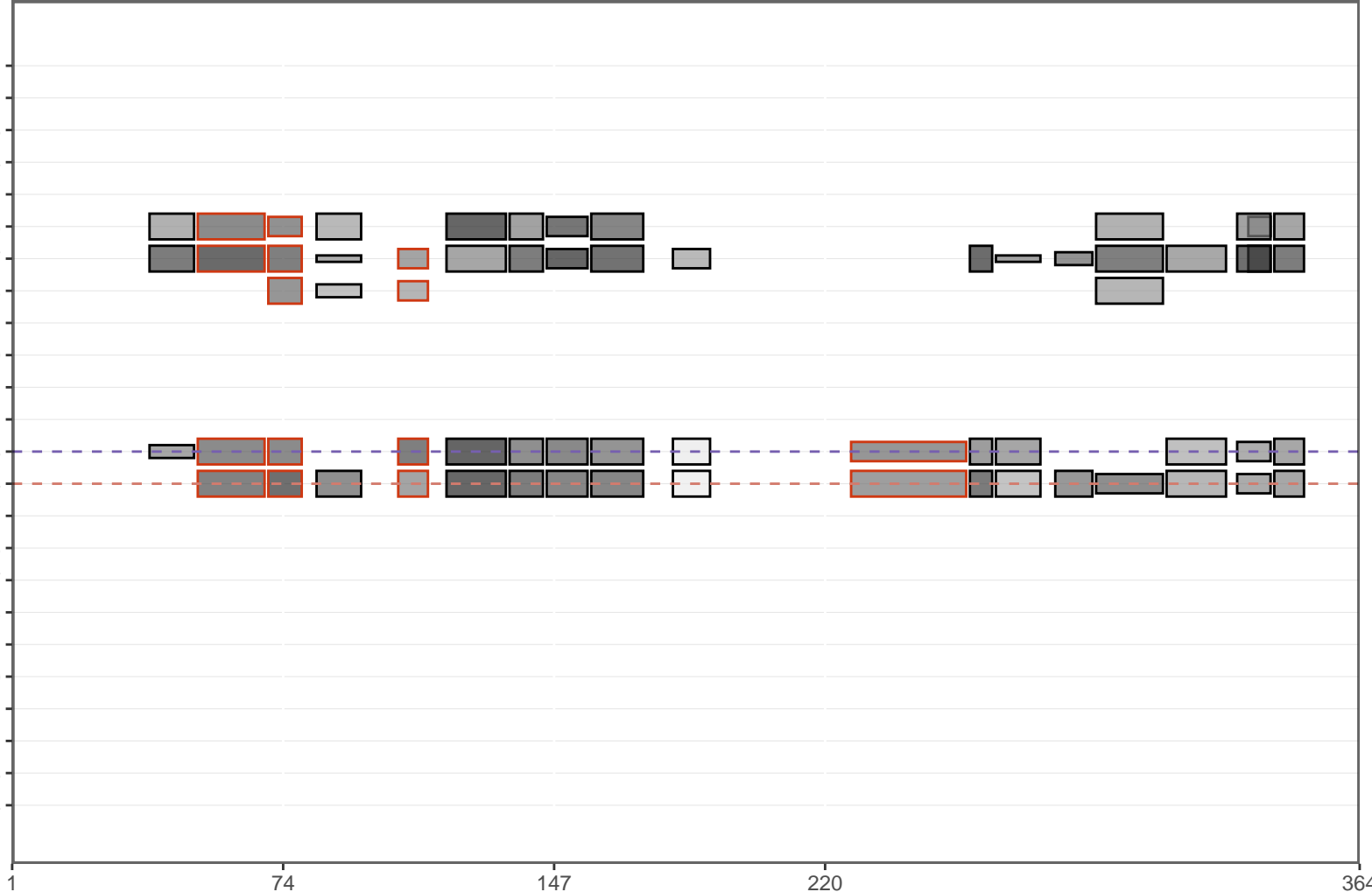
MW indication



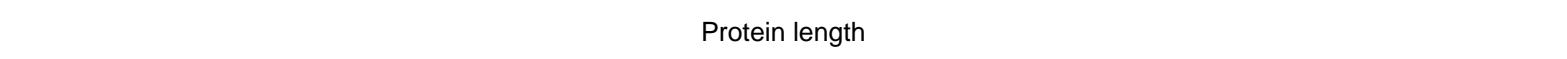
Molecular weight



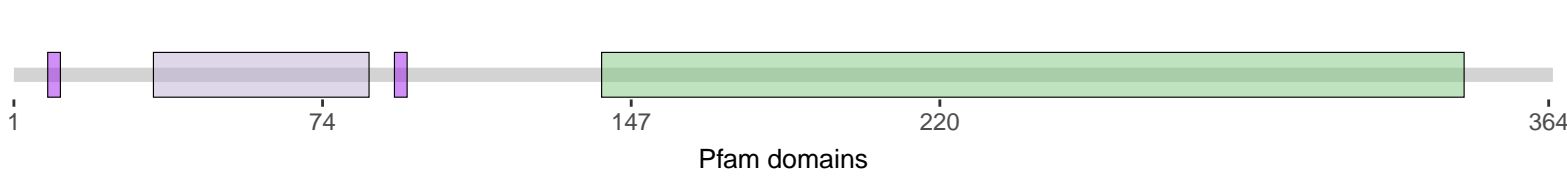
Gel Slice



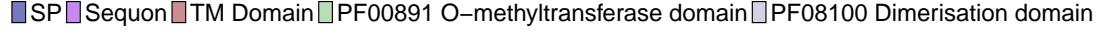
Protein length



Pfam domains



Pfam Description



Protein sequence:

DPRFNKYINRGMSEHSTMEMKLEEDYKGFEGLSNIVVGGGTGATVNMIVSKYPSIKGINFLPHVIEDAPVPGVEHIGGDMFASVPKADAFMKWIGHDWSDEHGLKFLKNDYEALPANGKVVVAEGLPEAPDTSLATKNTVHIDVMLAHNPGGKERTKEFQALAKAGFTGRHKAGAYNTWVMEFNK

NbL13g13800.1 uncharacterized_LOC107802109 [MW = 31.37 kDa]

No. of times detected



log(intensity)



Values from



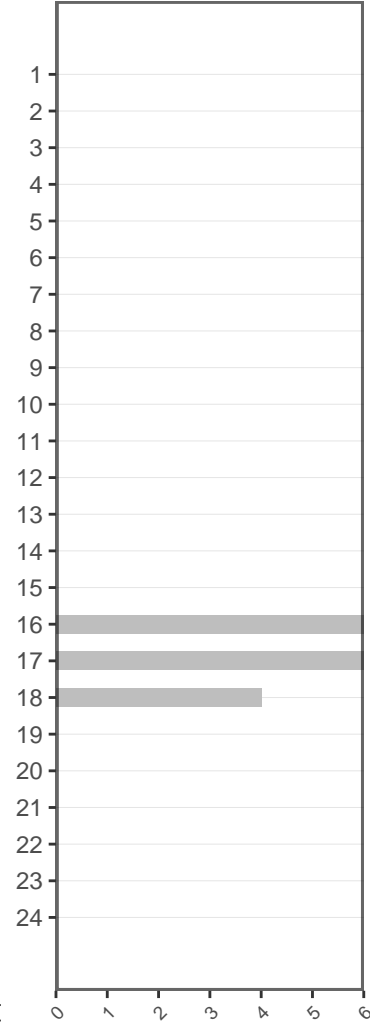
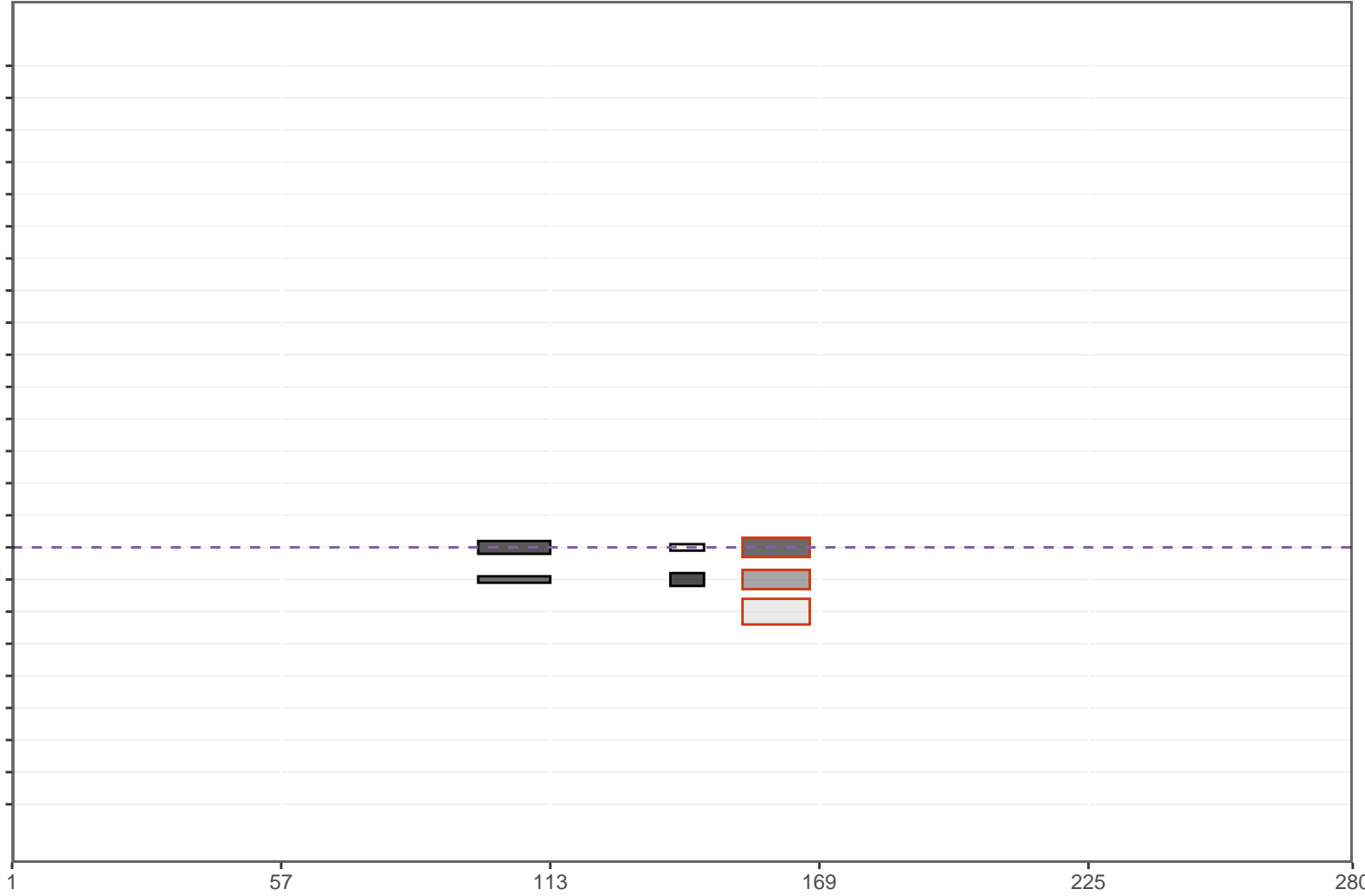
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

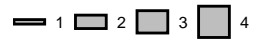
Pfam Description
 SP Sequon TM Domain

Protein sequence:

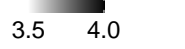
LLADSTPPVRTVEVMVAVRVGDKNKILVESHGELSNQVVRQGRPLSEKMKPGETVDDAVFRVWKEELGSSIKILPNVSTKVEERVSASYPGLFACVWVHTVDVVVDGLPEEETFETEDVEYDSEKRLADGAVSGKHVWVVDADSL

NbL13g13680.1 protein_GPR107-like [MW – SP = 47.59 kDa]

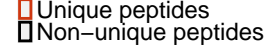
No. of times detected



log(intensity)



Values from



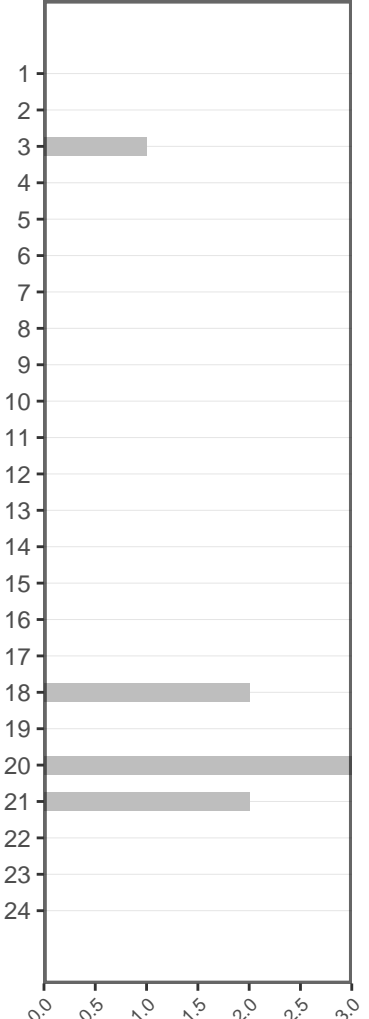
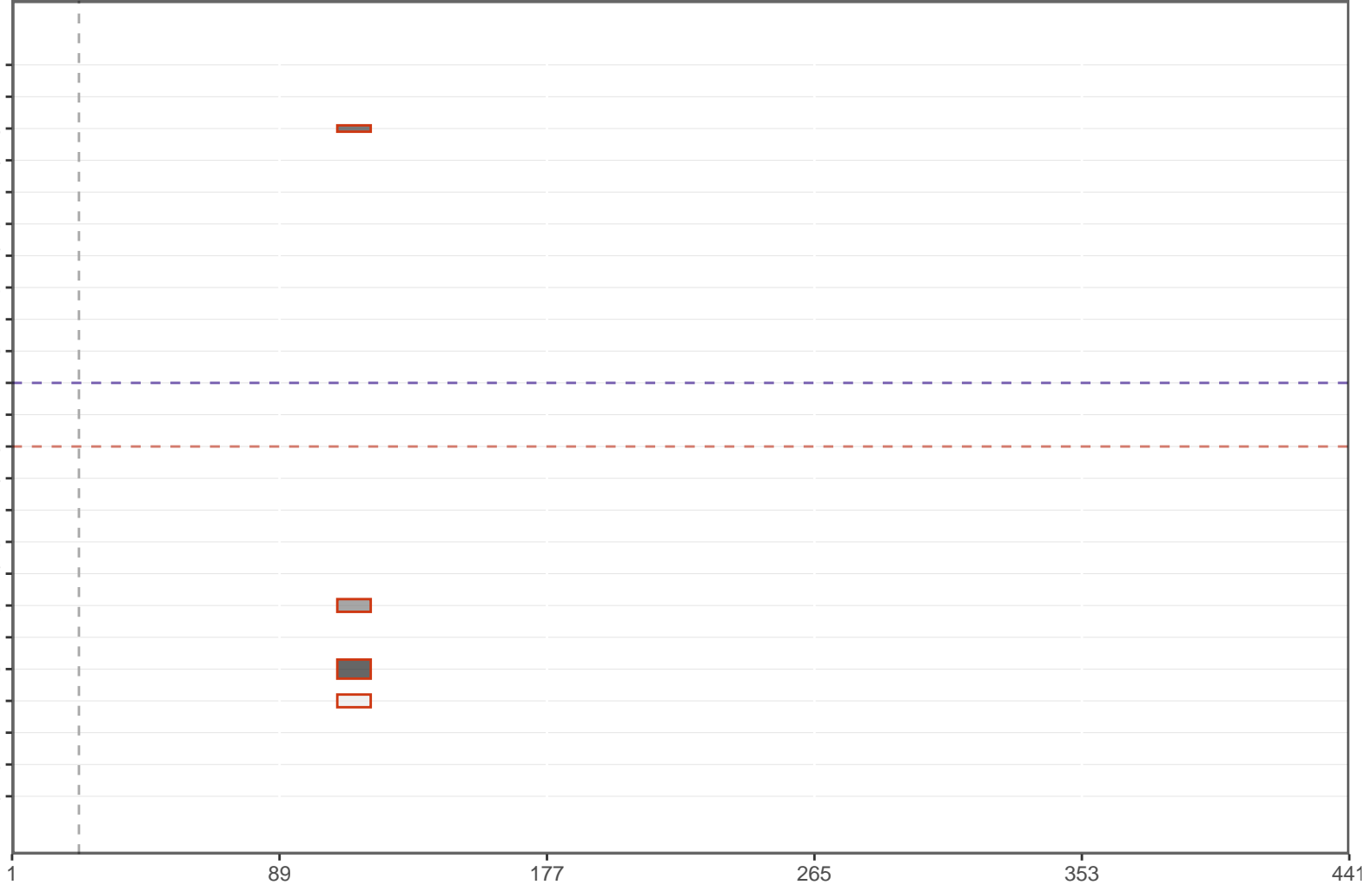
MW indication



Molecular weight



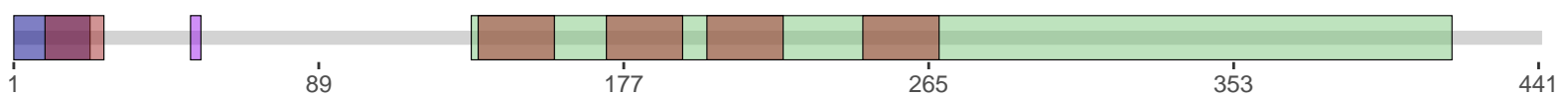
Gel Slice



Protein length

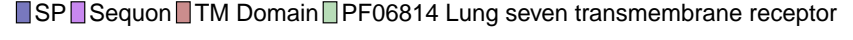


Peptide counts over 4 repeats



Pfam domains

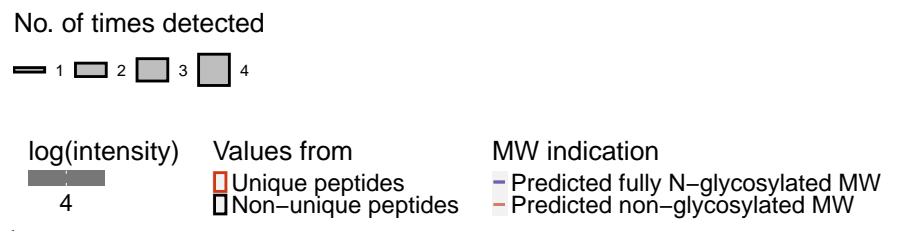
Pfam Description



Protein sequence:

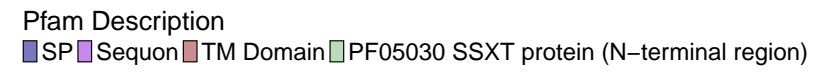
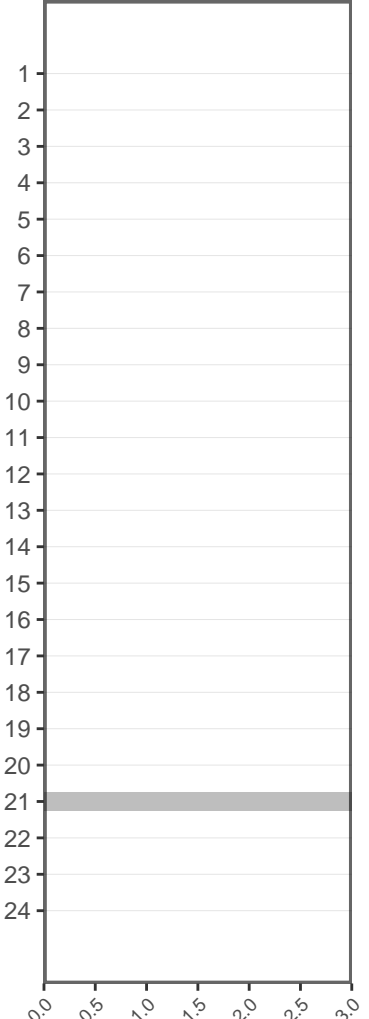
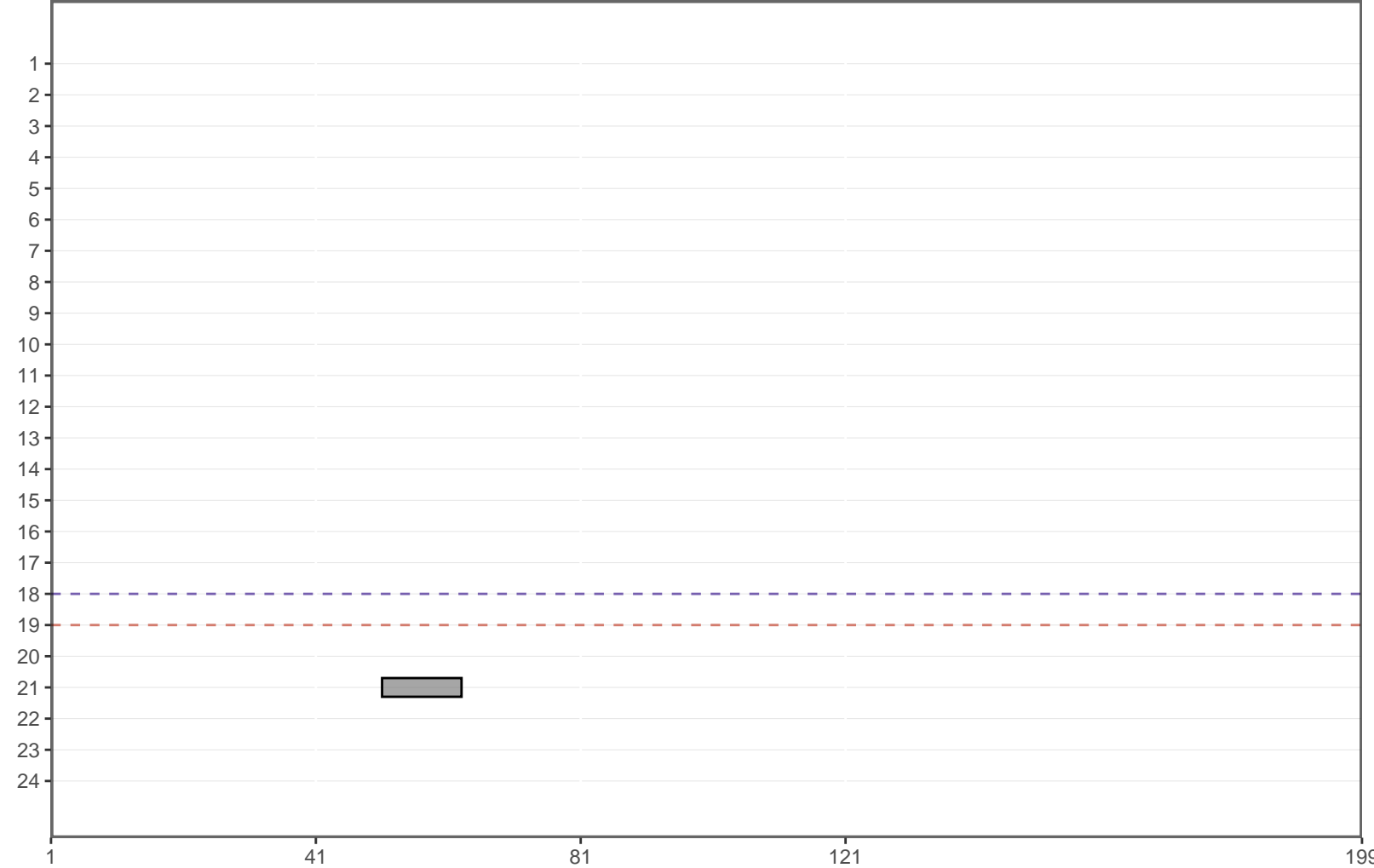
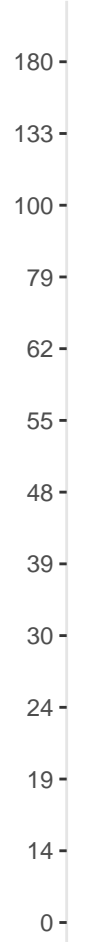
IHFFLAVVVLKALNLVGEAEKSKYKKTGTAHGWDVLFYFSLKGTILFLVLIGTGWVSLKPYLQDKENNVLMVPLQVWVNLQAVVIDETGPFSENSYTWKGVFLVDVDCGAVLFPVWISKNLREAAKTGKAAVNLMLKTLFRQYVWVIGVYFTRVAVVALETTFYRYGWTFSVAAEAATLAFVYFTGYNFRPKAHNPYFAIDDEEEAAASEALKLEDEFV

NbL13g13660.1 GRF1-interacting_factor_3-like [MW = 21.62 kDa]



Molecular weight

Gel Slice



Protein sequence:

IPGSDMGGTAAALGGGPGVPIKLPFQNLKPFGEQGGQMLHFQGGGGGGFGGGVGFQPTANNAMHQLMDFGLNSGGFLDARGNGKGNLEGNPFDGLGKSAARIHNSERE*

NbL13g13530.1 cytochrome_b5-like [MW = 15.04 kDa]

No. of times detected



log(intensity)



Values from



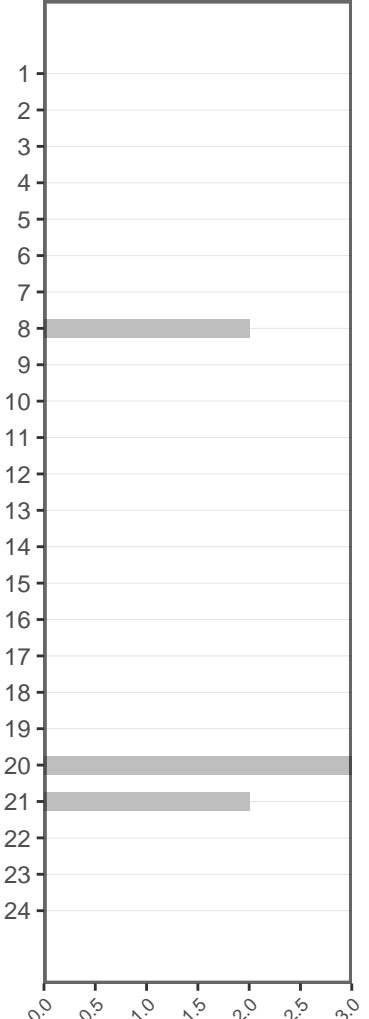
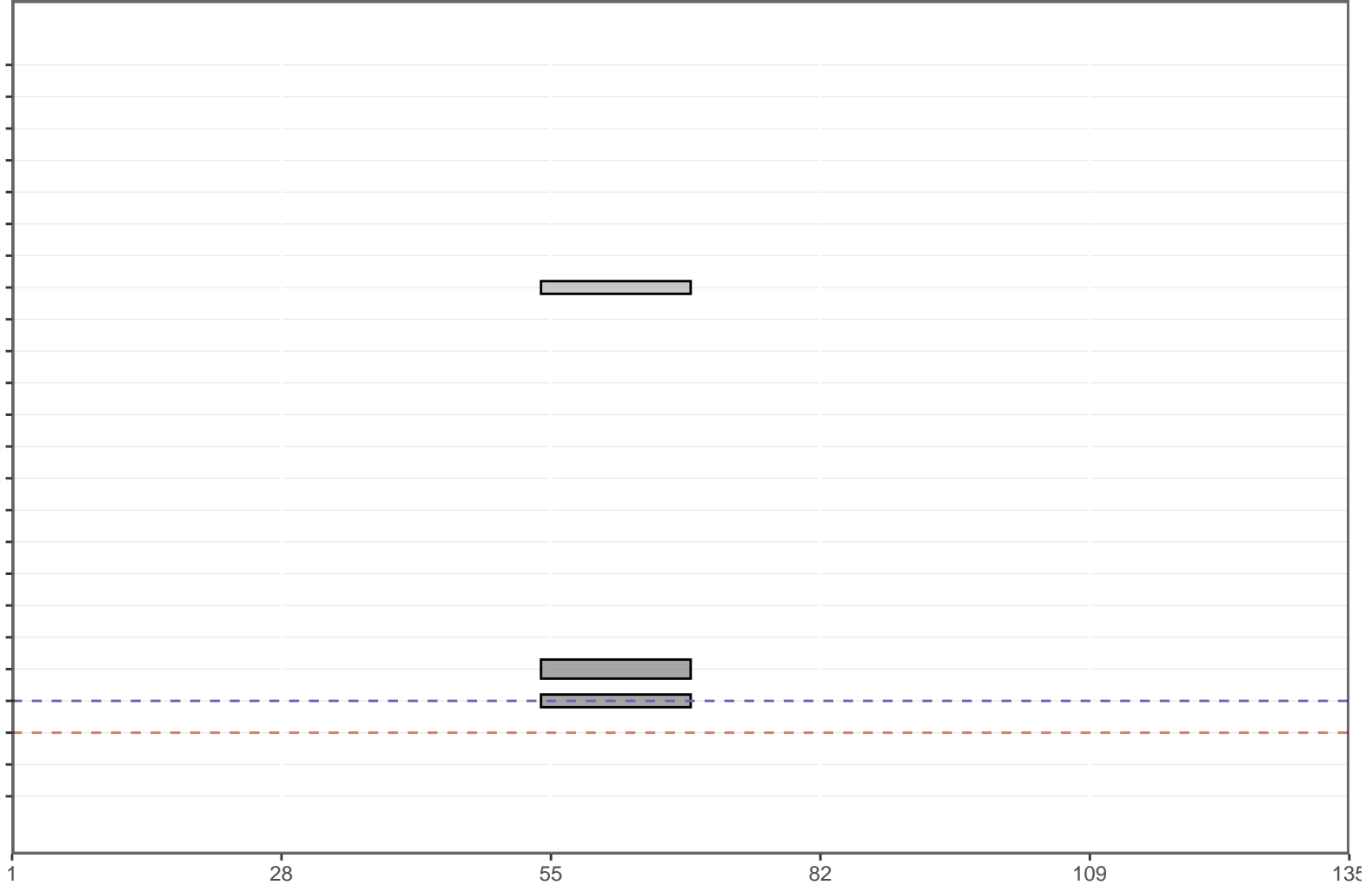
MW indication



Molecular weight



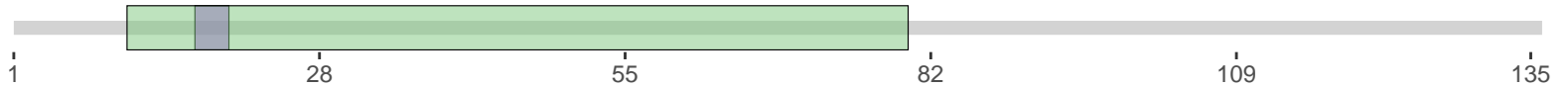
Gel Slice



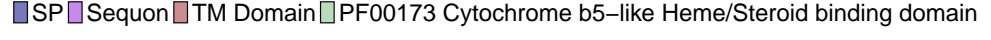
Protein length



Pfam domains



Pfam Description



Protein sequence:

QATNDFEDVGHSDSAREMMDKYVIGDIDVSTVPLNRISVYPPQGAPYVNPDKTPEFIRKILGFLVPLLLGLAFVRRHYTKK

NbL13g13250.1 luminal-binding_protein_5 [MW - SP = 70.7 kDa]

No. of times detected



log(intensity)



Values from



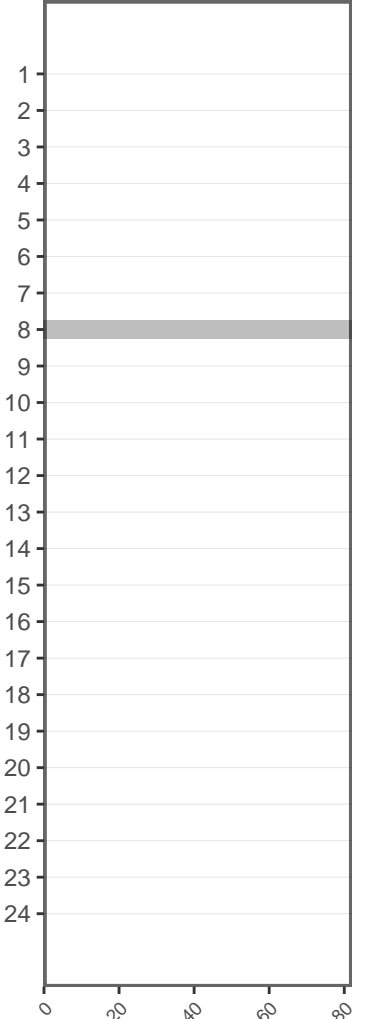
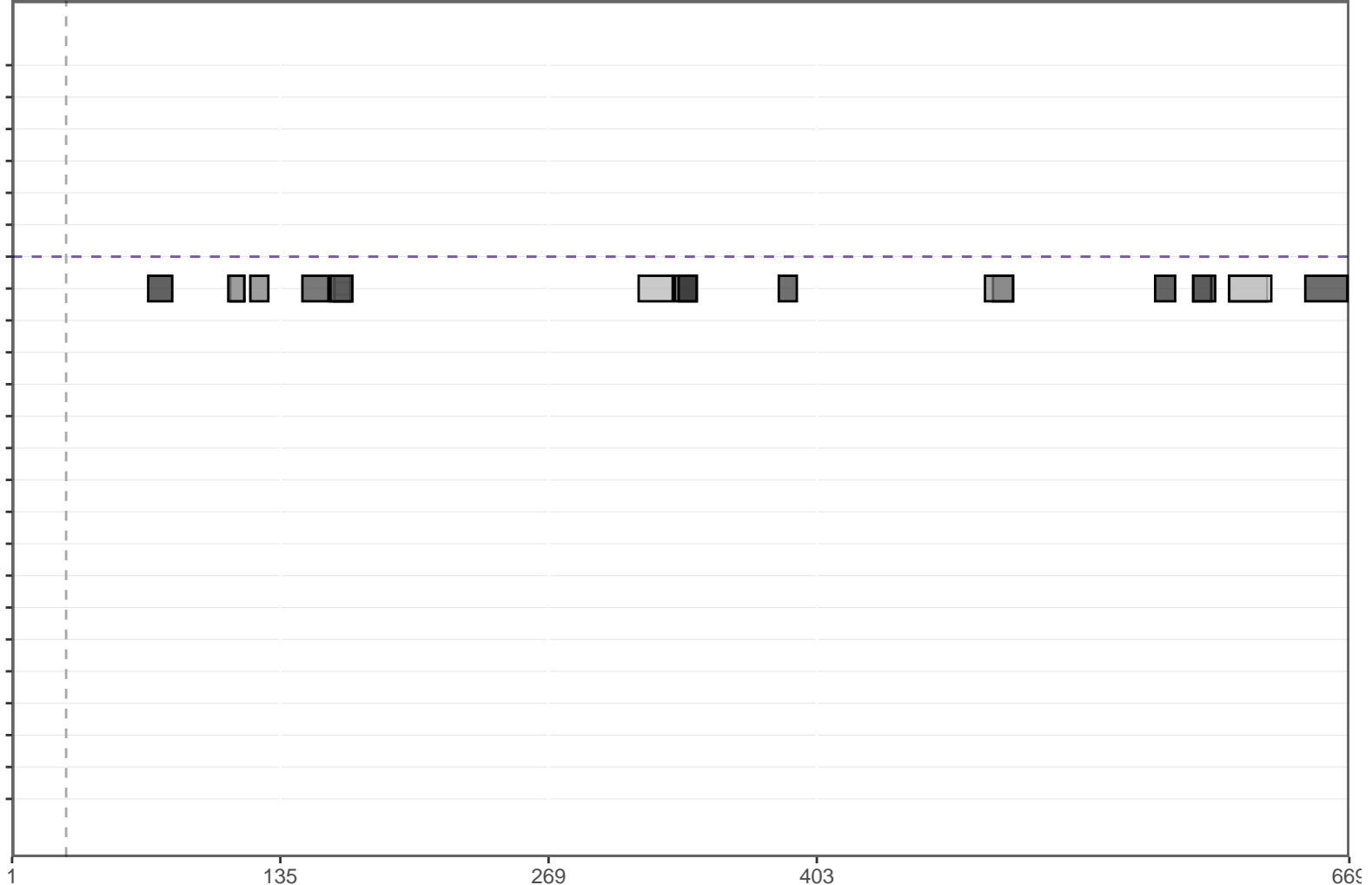
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

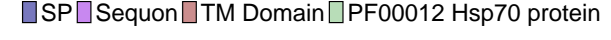
1 135 269 403 669

Protein length



Pfam domains

Pfam Description



Protein sequence:

MFSEPLTRARFEELNNDLFRKTMGPIWKKAMEDAGLEKNQIDEVLVGGSTRIPKVGQLKDFDCKENKGVNPEAWAYGAAVGGILSGEGGDETKDLLLDAPLTLGIEIVGGVMKLIPIRNTVPTKSGVFTTYGDDGGTTVTVISVFEGERBLTKDCRLLGKFDLTGIAPAPRGTPOIEVTFEVDANGLNVAEDKASGKSEKITTNDKGRLSGEEIERMVAEAEFFAEEDKKVYKERIDARNSLETYYVMRNGINDKDKLADKLESGDEKEKETATKEALEVLDNDSAI

NbL13g13030.1 CLP_protease_regulatory_subunit_CLPX1_mitochondrial [MW = 61.89 kDa]

No. of times detected



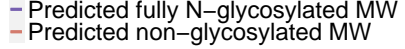
log(intensity)



Values from



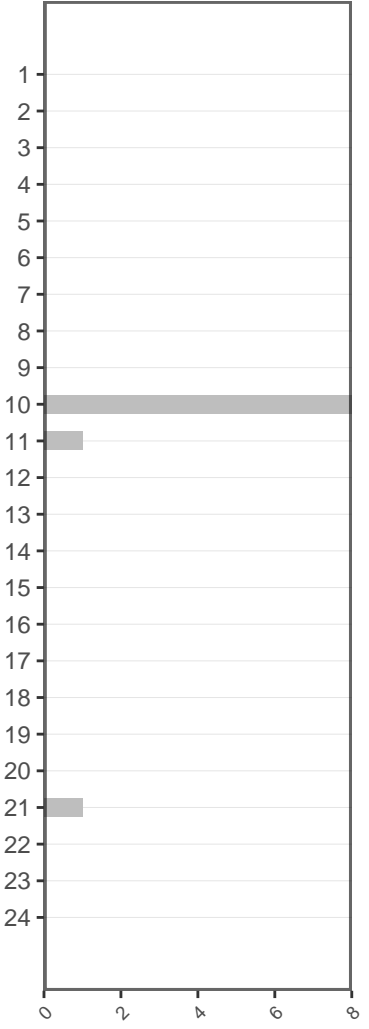
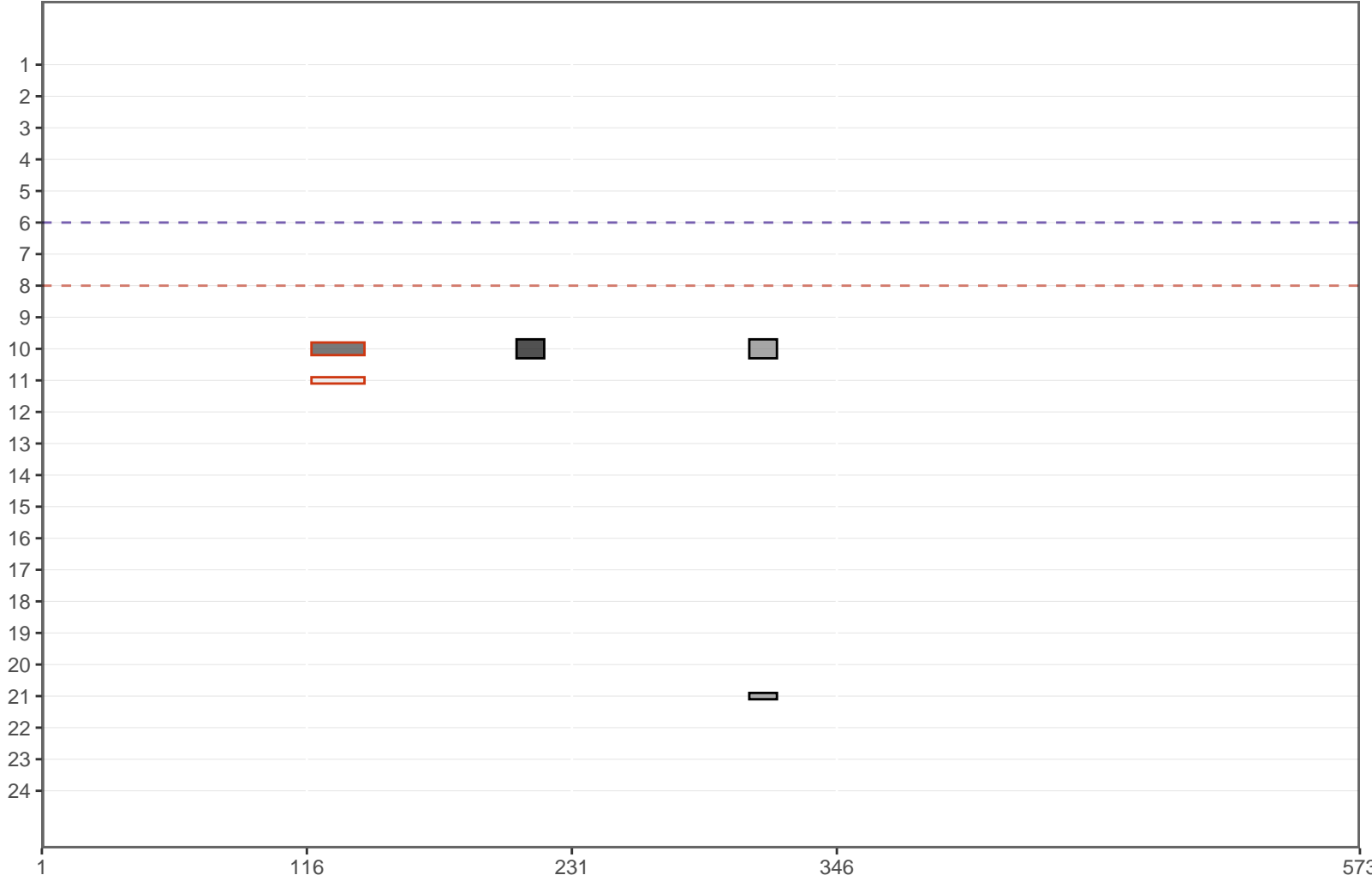
MW indication



Molecular weight

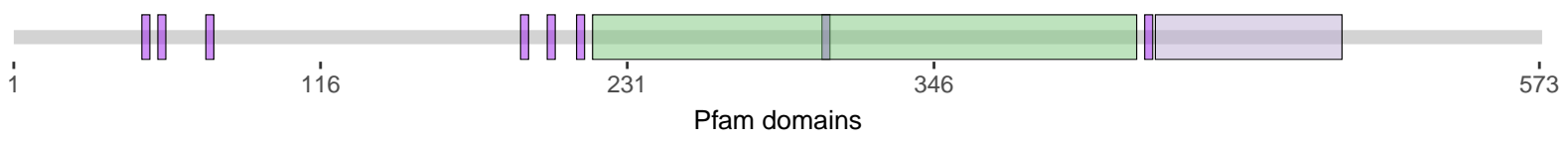


Gel Slice



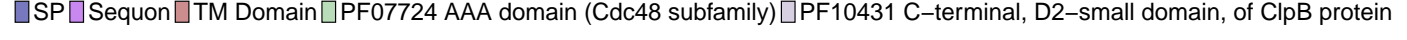
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ILYKLTADYINVAAGQGGVYHDEVDKTKKAEELNISRDSGEGVQDALKKMLEGTTNVAPEKGRARHFRGDNIGDITKDLFCGAFIDLEKTSERRRQDSSGIFGAFVARNMRTGGVTSAAVTSLSLEVESDLSYGLIPEFVGRFPILVNLISALTENGILVQLTEPKNALGKQYKMFQMGVYKLFHTEDALRLIAKKAISKNTGARGLRGLLESLAMDAMYEIFDVRTGDDNDIAVVVDEESVGAEGRGGGAKILYKKGAFDRHFPGNRPKDYETNLEGSDDGHEAELELI

NbL13g13010.1 pentatricopeptide_repeat-containing_protein_At3g49240-like [MW = 73.88 kDa]

No. of times detected



log(intensity)



Values from



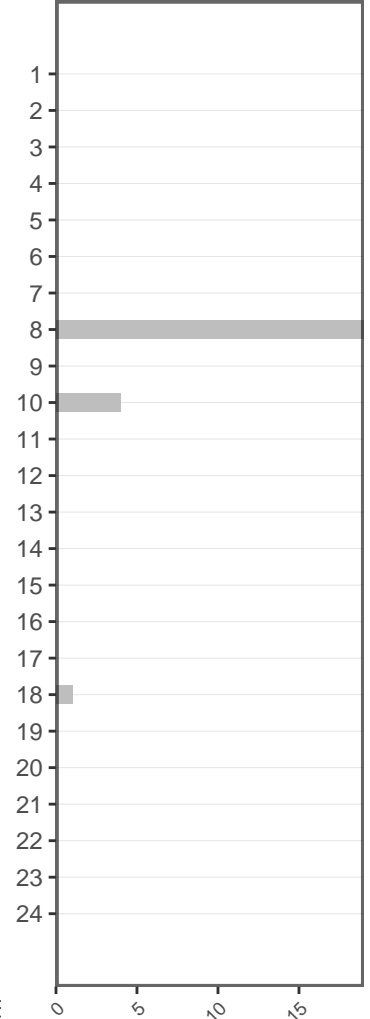
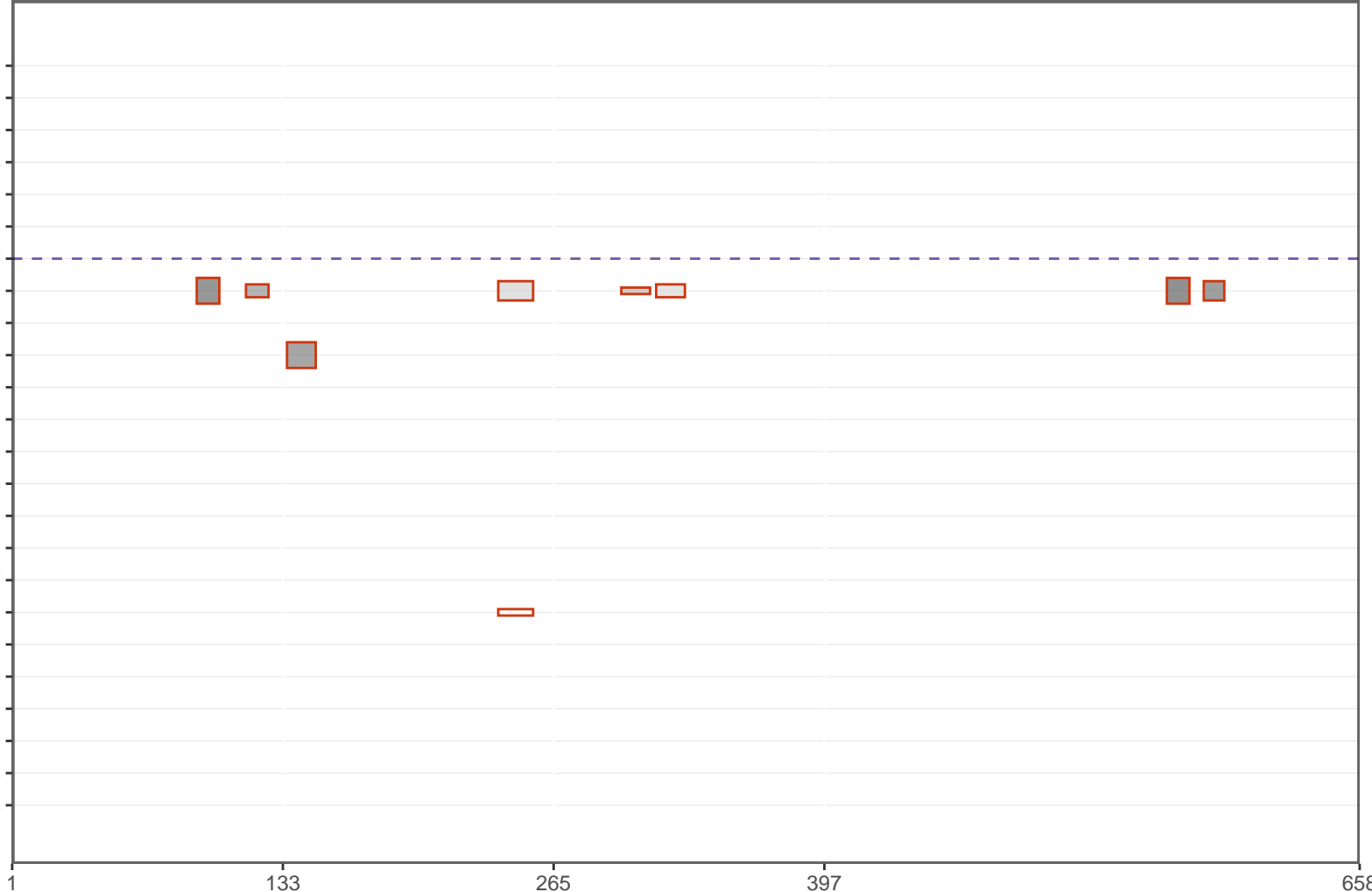
MW indication



Molecular weight

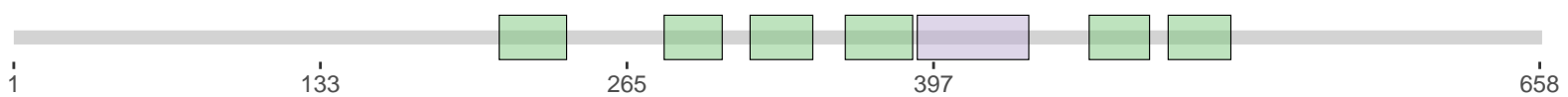


Gel Slice



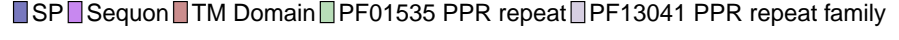
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FNYYLDLSKNGKFDKALKFDRLMLNEHDPKRLFTVNLGFSNVMVDGYCALGRFKDAIDVFNEMSEKRRRFDPTLGVNNEGLCKNDLLGAEADLYKDMSEKGVSPDEFETFLVLLMDTGFKNRPPDAAAMVFKTMVDALRPLNGLVYNRILVDGLVYKGVKDEAKGFFDLMMGKLRMNDGSKYKFMNNALEFKGHDEVLKIVDRMLREDDPDTDDAGEFREAFRKEGRDEELTLMLMDIEREKKEAAAAEAAERAKASARAAYVSLINPKLFGNKEPEEOSTAGEP

NbL13g12940.1 dipeptidyl_peptidase_9 [MW = 87.3 kDa]

No. of times detected



log(intensity)



Values from



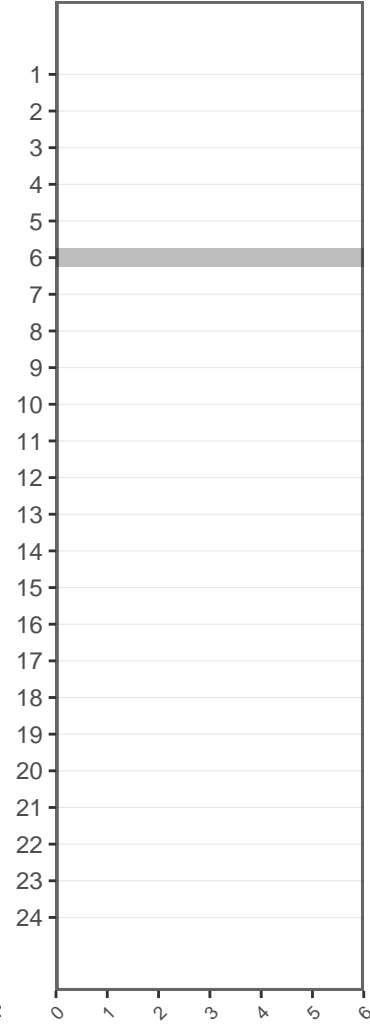
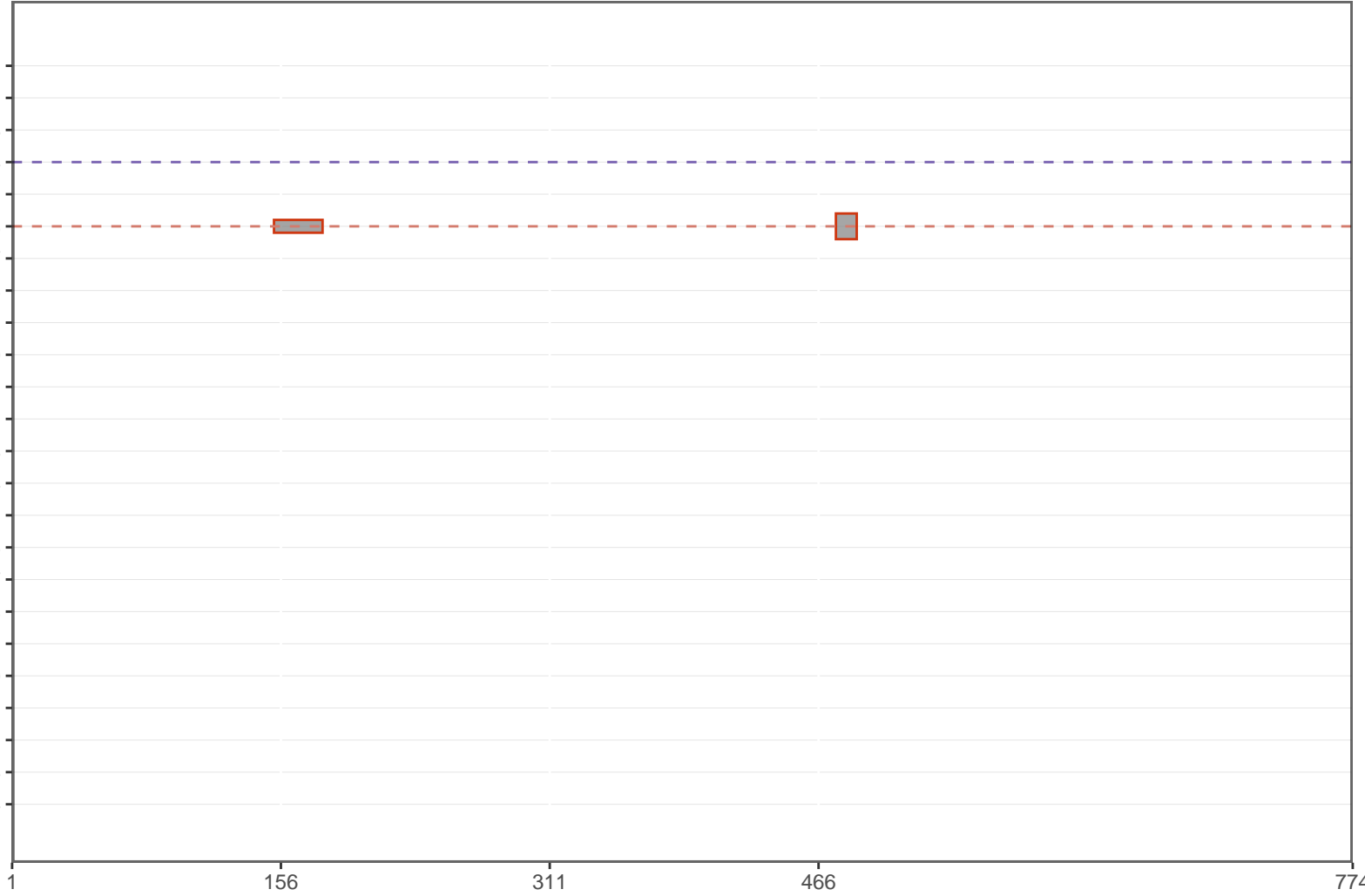
MW indication



Molecular weight

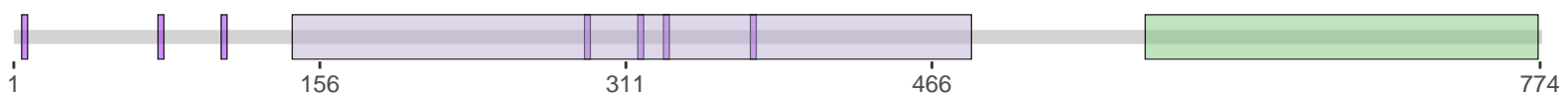


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00326 Prolyl oligopeptidase family
- PF00930 Dipeptidyl peptidase IV (DPP IV) N-terminal region

Protein sequence:

TTNGAFWASEKTFGRHLVLDHTNGVGLGPTGGDMLVEQWGVNEVTGLVYFTGTLGDFLESHLYCAKLFDAHSPLOSPLRLTNGRQGHAVLVDHGMORFDIDHSLVFPRIKLSLHDGSLIMHLFDQPVSVFRFRKHLLESPEHQIAGDGTALYGQYKPDFPKFGPPVYRIMEVYGGPQVQLVQDSWNTFVDMRAGYLRKSGILVWKMDNRGARRGFVFEQALKYNGGLVDAEDQLTGAELVKKGLAKGHLGYSVGGYLSAMRLARFPEVFKAVSI

NbL13g12920.1 probable_pectinesterase/pectinesterase_inhibitor_61 [MW = 65.57 kDa]

No. of times detected



log(intensity)



Values from



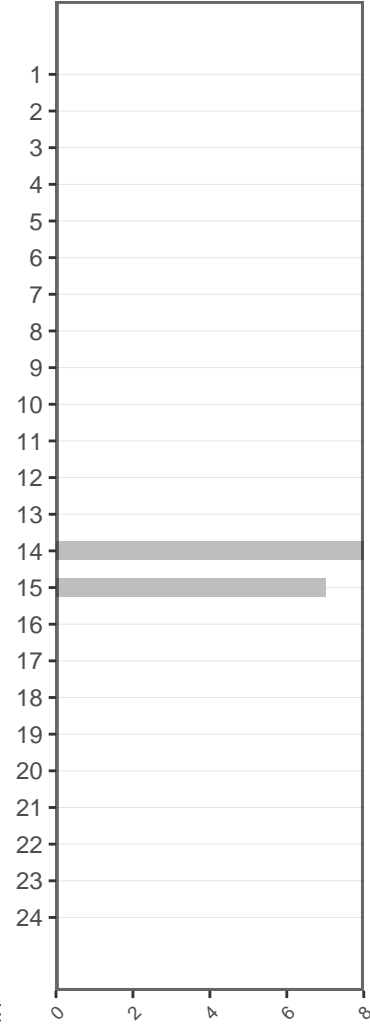
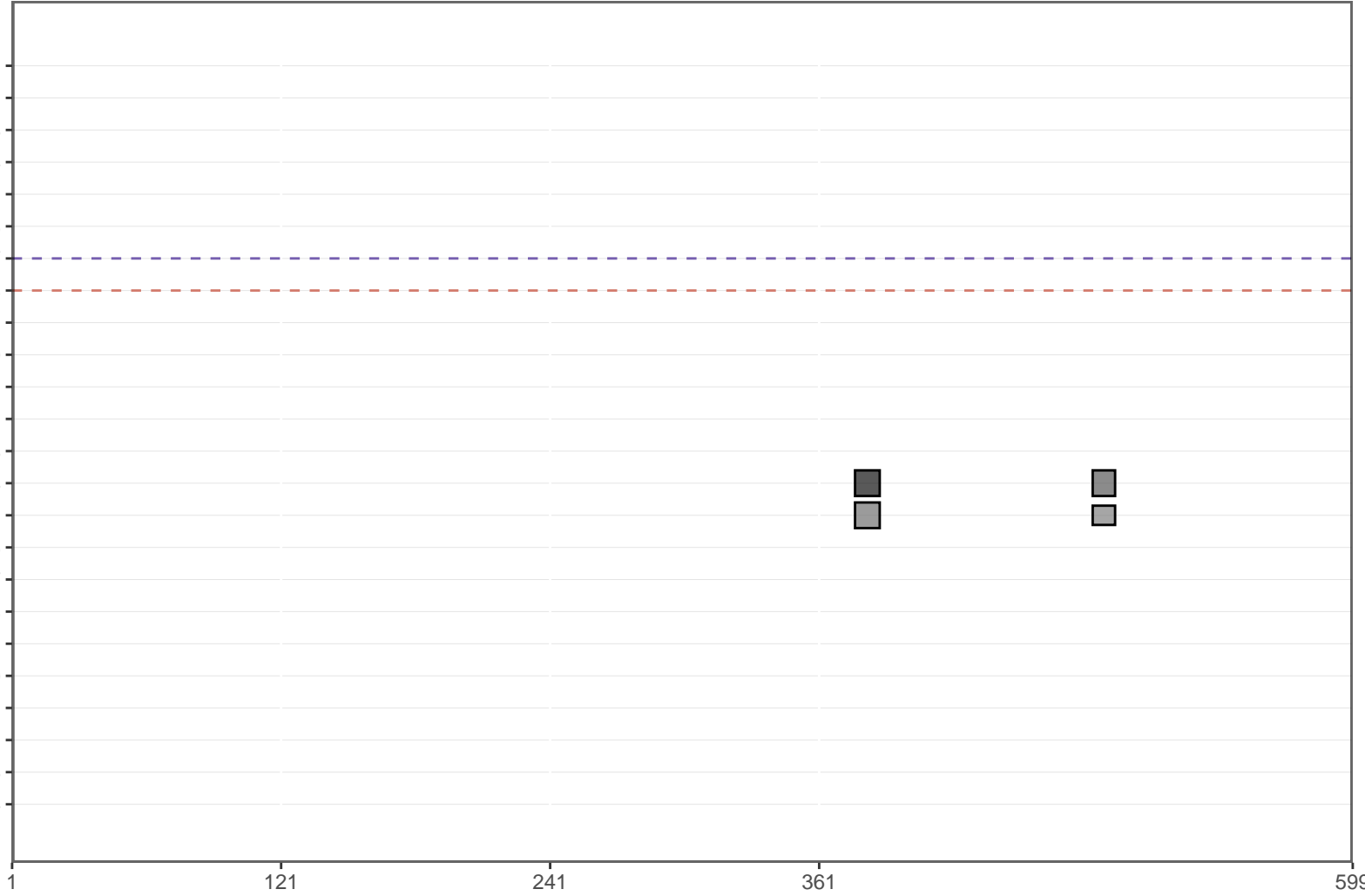
MW indication



Molecular weight



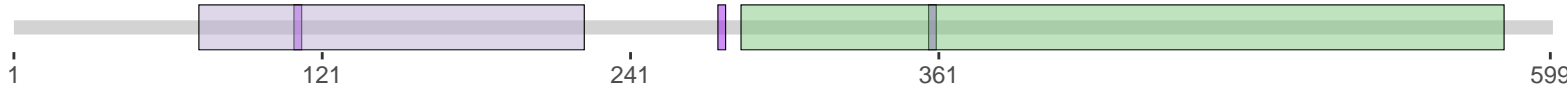
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

KDGSQTVKTLAEAIKKVPEKSNRRITVYKAGRYEENMLKVRKKKMLMFIQDGGKGTVTGGKNGQNTFFHTASFAATGAGFVARDMTFENYAGRPKHQAWALRIGGDHAFVRCNIGYQDITLVHSGRQGFYRREGDIYGTVDHFIGNAAVLLGNCNIVARKPMANGKNTTAAQNRKDFPQNTGISHACKILATPDLAASKGFFPTYLGRPWKMYSRVAVYMLSNMGDHPSPGWLEWNGDFALDTLVYGEVMNFGPGAANGKRVTPWQYRVRKQVEEASKFTVAKFYQSS

NbL13g12900.1 protein_BOBBER_1-like [MW = 33.87 kDa]

No. of times detected



log(intensity)



Values from



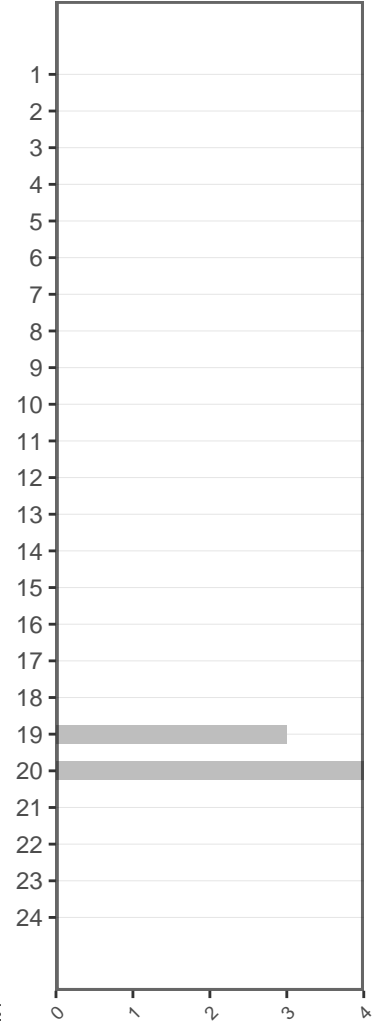
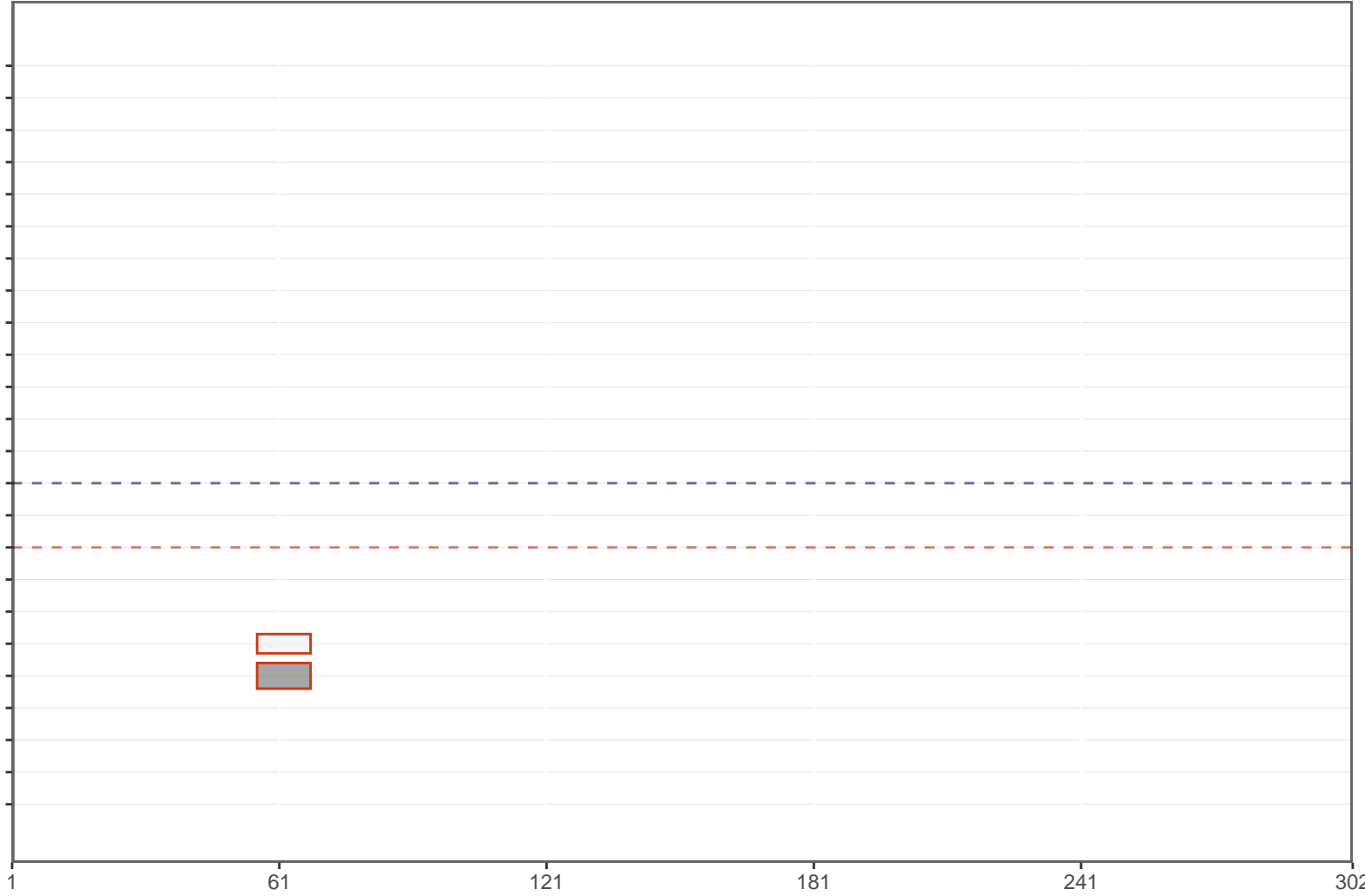
MW indication



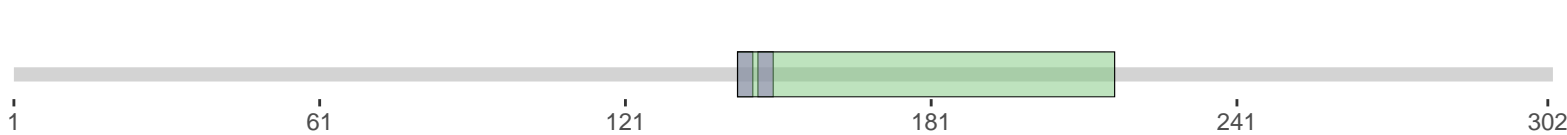
Molecular weight



Gel Slice



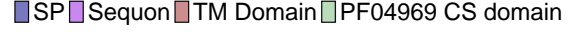
Protein length



Pfam domains



Pfam Description



Protein sequence:

LDLENSYVNGSLQEVNINIPVPGTKSRFRIVDDISKRNRLKVLKGGPPIDGELYRPVYVDDCFVWSLEDQKSHVLLTKKDGMDWVWKGCYKGEPEIDTQKAEPESSKLDLDPETRSTVENMMFDQRGKSMGLPSTDETQKGEILKRFMAEHPMDFSKAKG

NbL13g12830.1 glutamate_synthase_1_[NADH]_chloroplactic [MW = 242.8 kDa]

No. of times detected



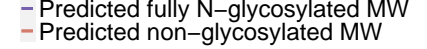
log(intensity)



Values from

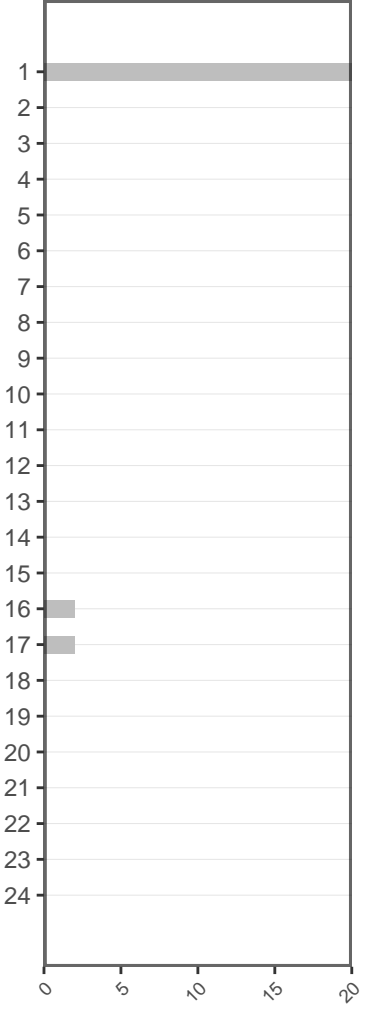


MW indication



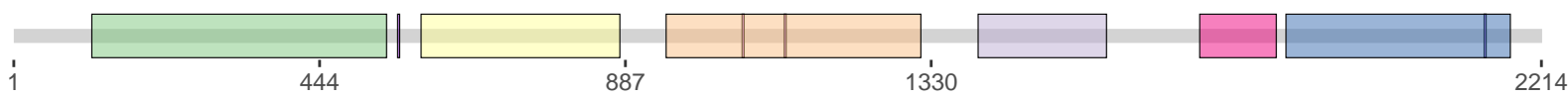
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

tion

Domain PF01493 GXGXXG motif PF04898 Glutamate synthase central domain PF14691 Dihydropyrimidine dehydrogenase domain II, 4Fe-S
 00310 Glutamine amidotransferases class-II PF01645 Conserved region in glutamate synthase PF07992 Pyridine nucleotide-disulphide oxidoreductase

Protein sequence:

IQQAKPGEGLPGHKVIGDIAVTRNNTAGVGLSPRPHHDVYSIEDLADLIHDLKNNANPCARVSVKLVSEAGVGVASGVAKGHADHVUSGHDDGDTGASRWETGHSAGLPWELGLAETHQTLVANDLRGRITLQTDGQKTRGRDVAWALLGAEFFGFSTAPLTLGCIIMRKGKHNKTPFVGIATGQPLREKFAPEPEHVINFFFMALAEVEIMSGLGRFTLTEMVGRREDMLELQKDLTKNNDKLNKIDLSLLRPAADRPEAAAGYGVKGGDHGLDMLDNNLJLSKAL

NbL13g12770.1 probable_protein_phosphatase_2C_76 [MW = 38.79 kDa]

No. of times detected



log(intensity)



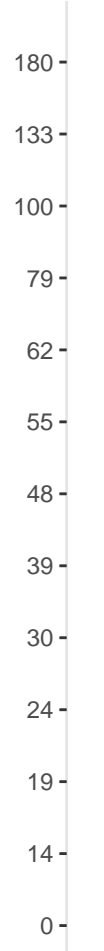
Values from



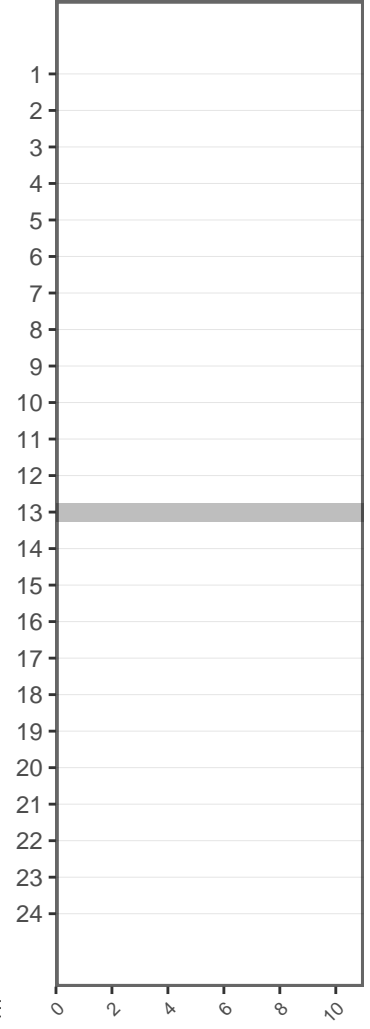
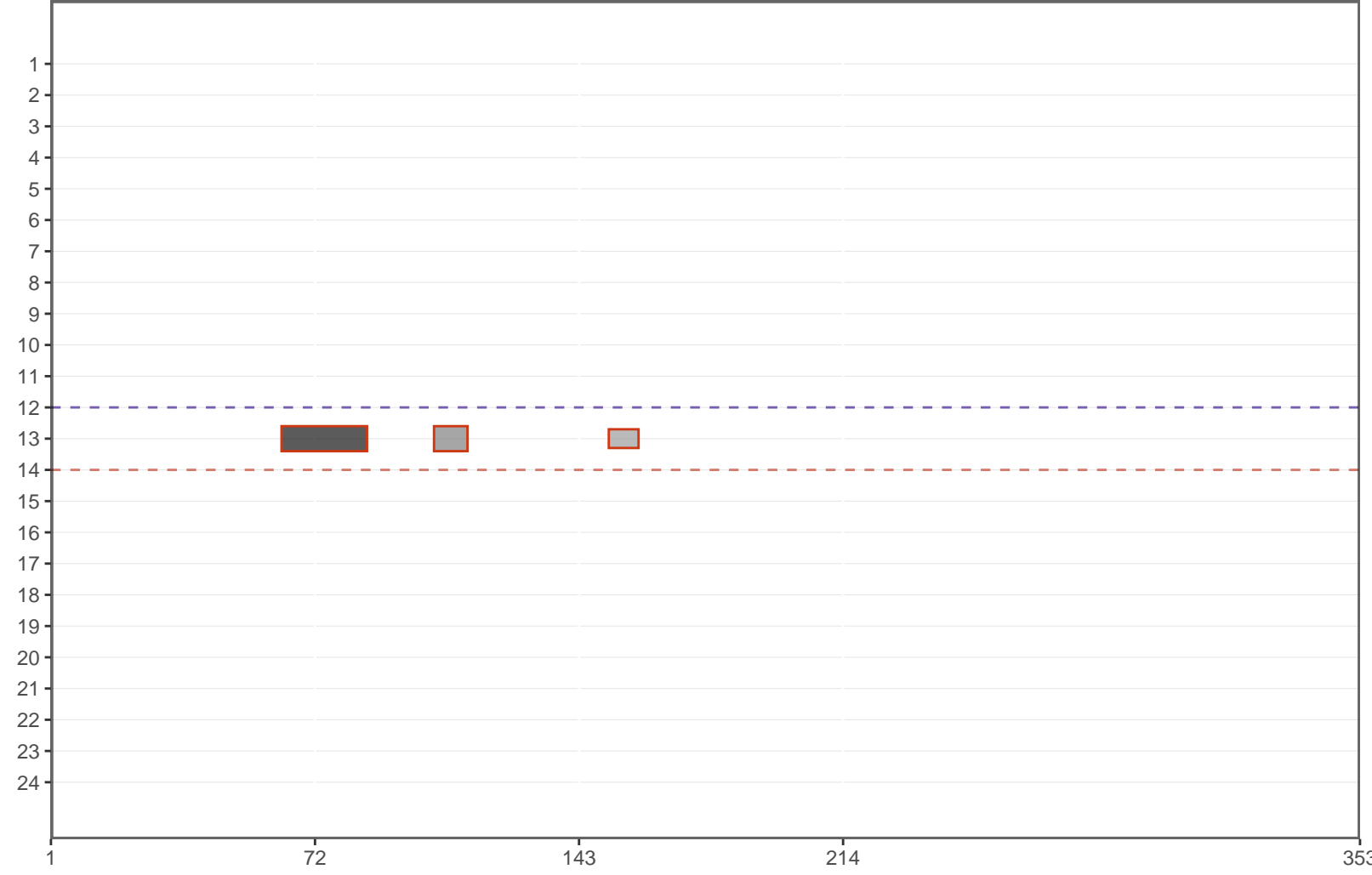
MW indication



Molecular weight



Gel Slice

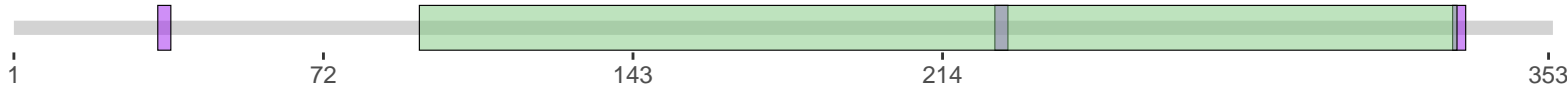


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

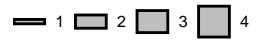


Protein sequence:

SETYQGTDMDFLDSEKDTFRDDGSGTAVLVGNHLYVAVVGDSTRTHSGKGAALGSDHKNPNRTERKRIESAGGVVMMWAGTWRVGGVLAAMRAFGRNRMKGFVVAEPEKDDGDEDELELLVLSADGLWVVPNEDAIISLAGAEEPEAAARKITETAFTFRGSAINTGVVVFHKKVVEPGSGGG

NbL13g12740.1 probable_inactive_purple_acid_phosphatase_1 [MW – SP = 66.91 kDa]

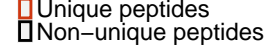
No. of times detected



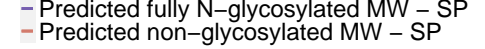
log(intensity)



Values from



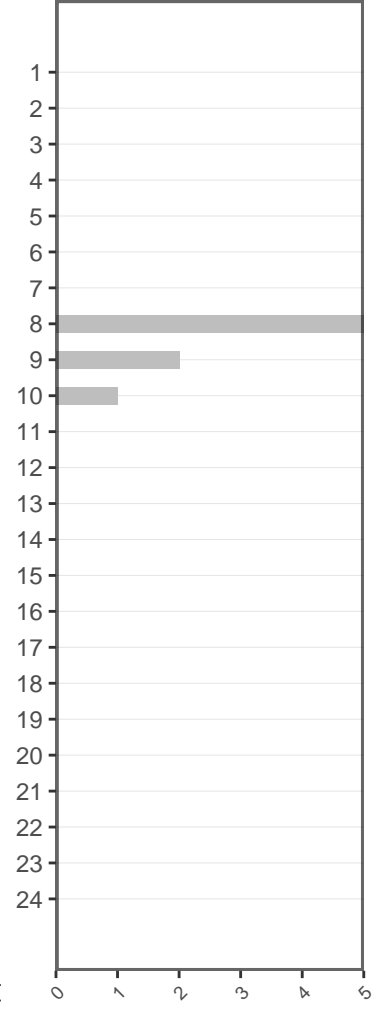
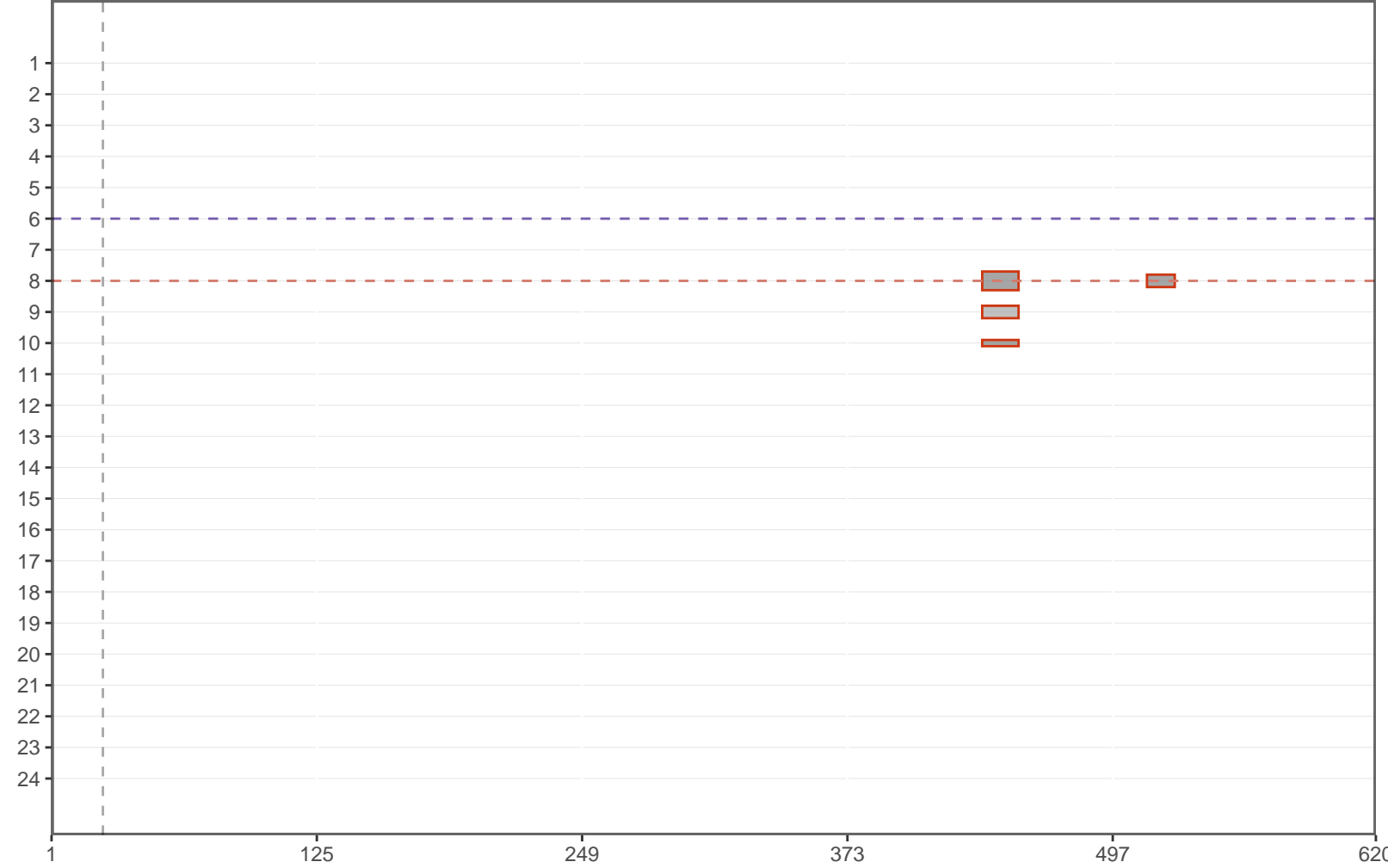
MW indication



Molecular weight

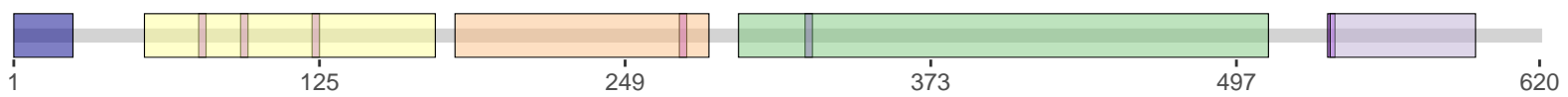


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

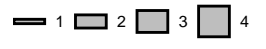
- SP
- Sequon
- TM Domain
- PF00149 Calcineurin-like phosphoesterase
- PF16656 Purple acid Phosphatase, N-terminal domain
- PF14008 Iron/zinc purple acid phosphatase-like protein C
- PF17808 Fn3-like domain from Purple Acid Phosphatase

Protein sequence:

*GDMCKDEADGSENYNGFGPAGLNTFTNGLNDLKNIDNFHIGDQYANGHIGDWDGFTSQIEPASTPVMILASGNHERDWPCTGSGFYGNMDSGEGGVLGNMFMVPTENRDKFWYSTDYGMFRFGADTEHDWRGTEQYHFIEHGLASVDKQKQVWILFLAHRVLYGSSDSVYANEGSFAEPMGREGLQKLVGQYKVDIAFGHWHNYERTGPIYQNGTNNKHFYKYGALNGTHVAAGGAGASLSDFTPIQTTFWIFRDVHGDFVLTAFDHSNLLFEYKKSDDG

NbL13g12590.1 probable_inactive_receptor_kinase_At4g23740 [MW – SP = 65.71 kDa]

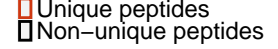
No. of times detected



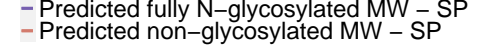
log(intensity)



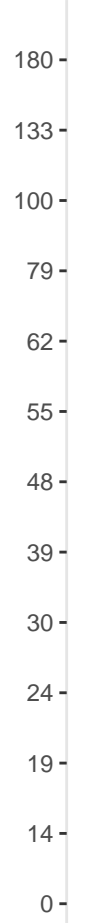
Values from



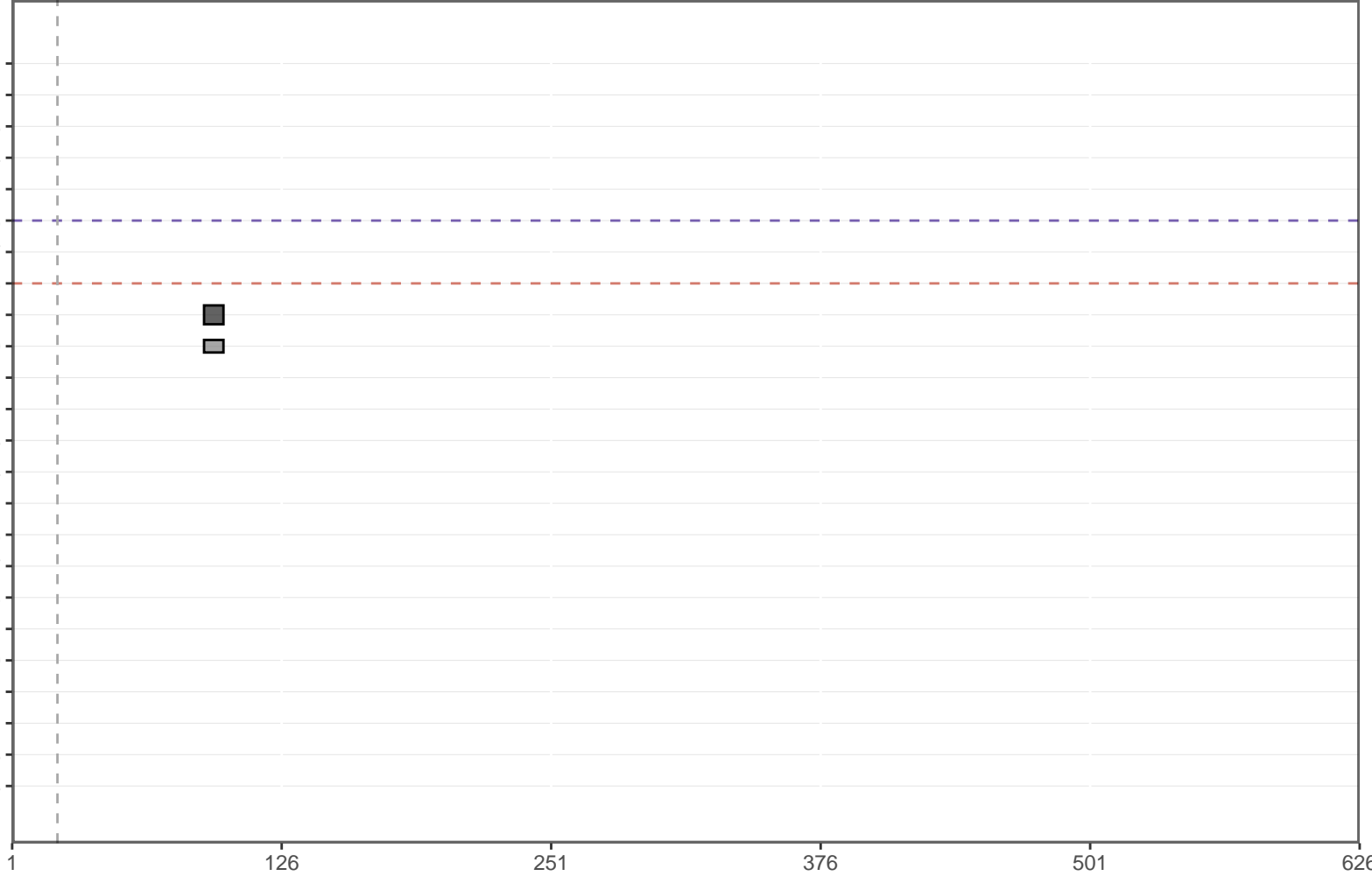
MW indication



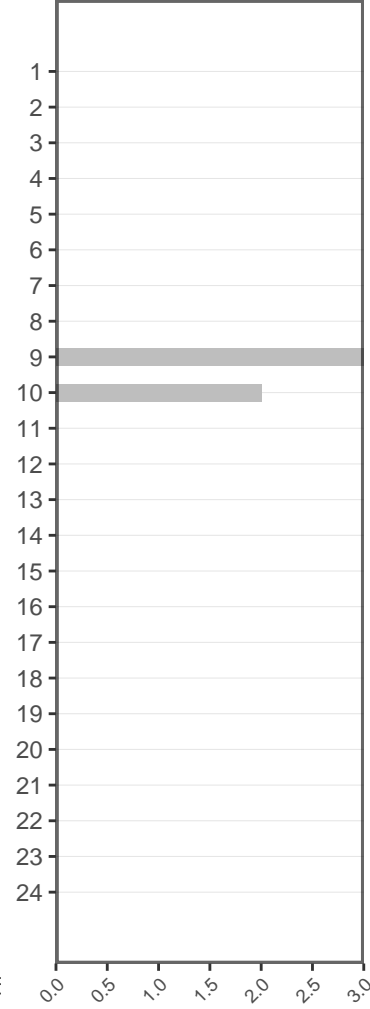
Molecular weight



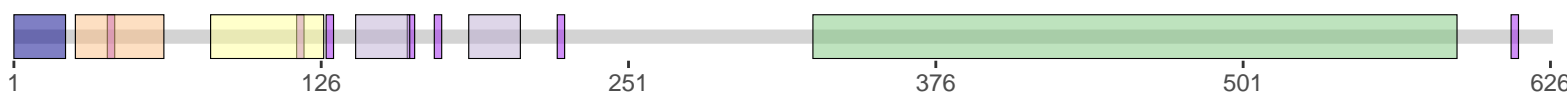
Gel Slice



Protein length

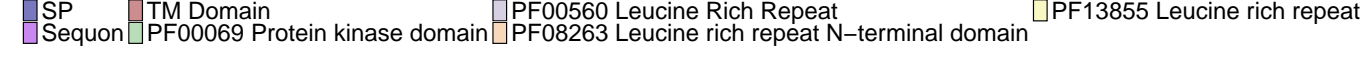


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IERNLVFFEGCNLAFDLEDLLRASAELVKGKTFGTAYKAALEDGTTVAVKRLKESVGRKDFEQGMEVVGNIHENVPLRAYVYKKEEKLNVYDFYGGGASAVMLHAKRVSDRIPLEDWDRLRHAIAGAAAGIAHHGGTGGKLVHGNKESNIFLNSGGFGGDISDLGLATIMSPLVPPVMAAAGVOPPEVTDGRKVSQASDVIYDFGVLLLELLTGKSPHATGTNEVHLVRRWVHVSIVRREEWTAIEVDFDELKYPNIEEEMVEMLGTGLGVARMPDQRPKMSOVVVMVEGVF

NbL13g12560.1 uncharacterized_LOC107819525 [MW = 29.49 kDa]

No. of times detected



log(intensity)



Values from



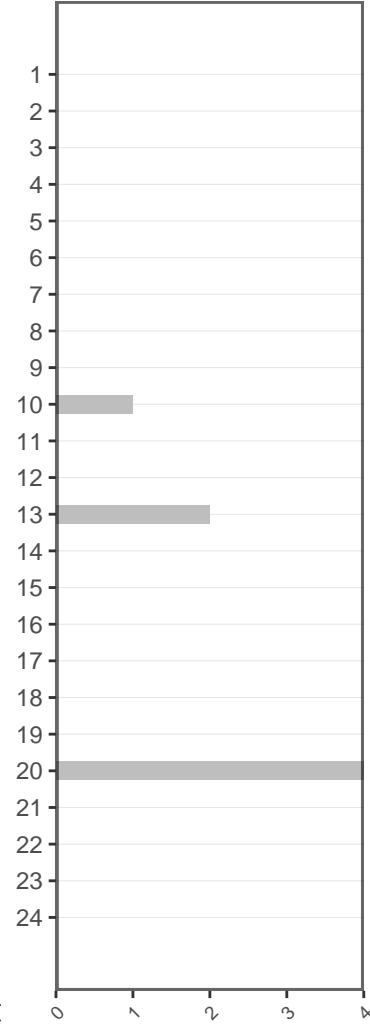
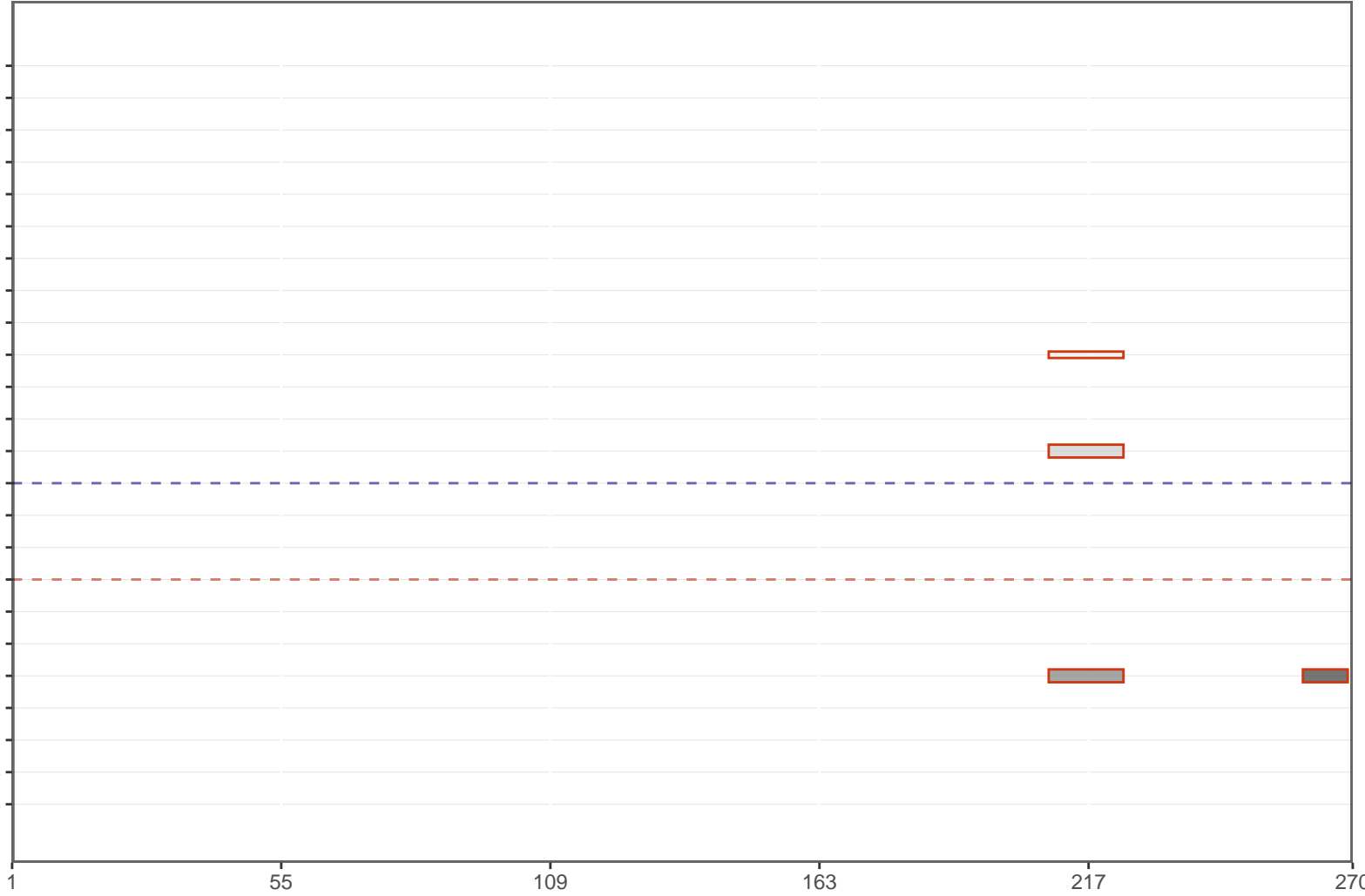
MW indication



Molecular weight



Gel Slice



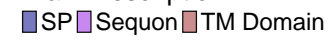
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SVGIRVAIKPEYRITPPPLSTQVGDIPRSTFNDFDFEKILAEAEKESQNWRLGLENLPRRLPEQNTFGSTGDEVINNYTAFGFNREAWAIAWVYGDNPPIKVKFAERYTRLKEEMGFSSNSVADALLNDNDTKAISHLIGNSP

NbL13g12280.1 plastidial_pyruvate_kinase_2 [MW = 72.24 kDa]

No. of times detected



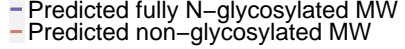
log(intensity)



Values from



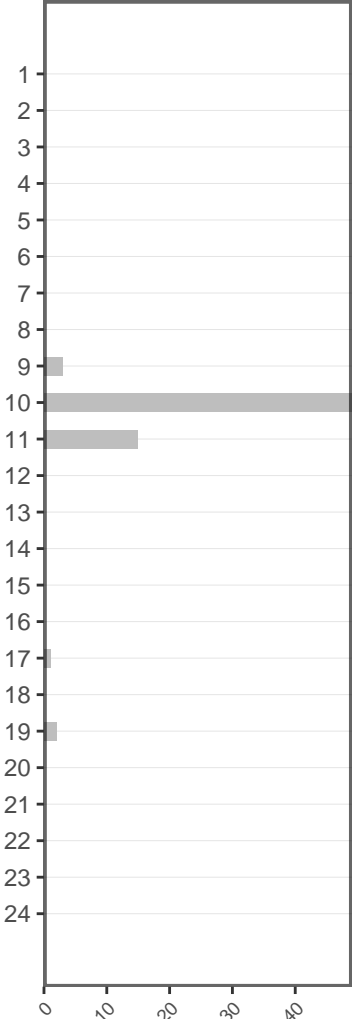
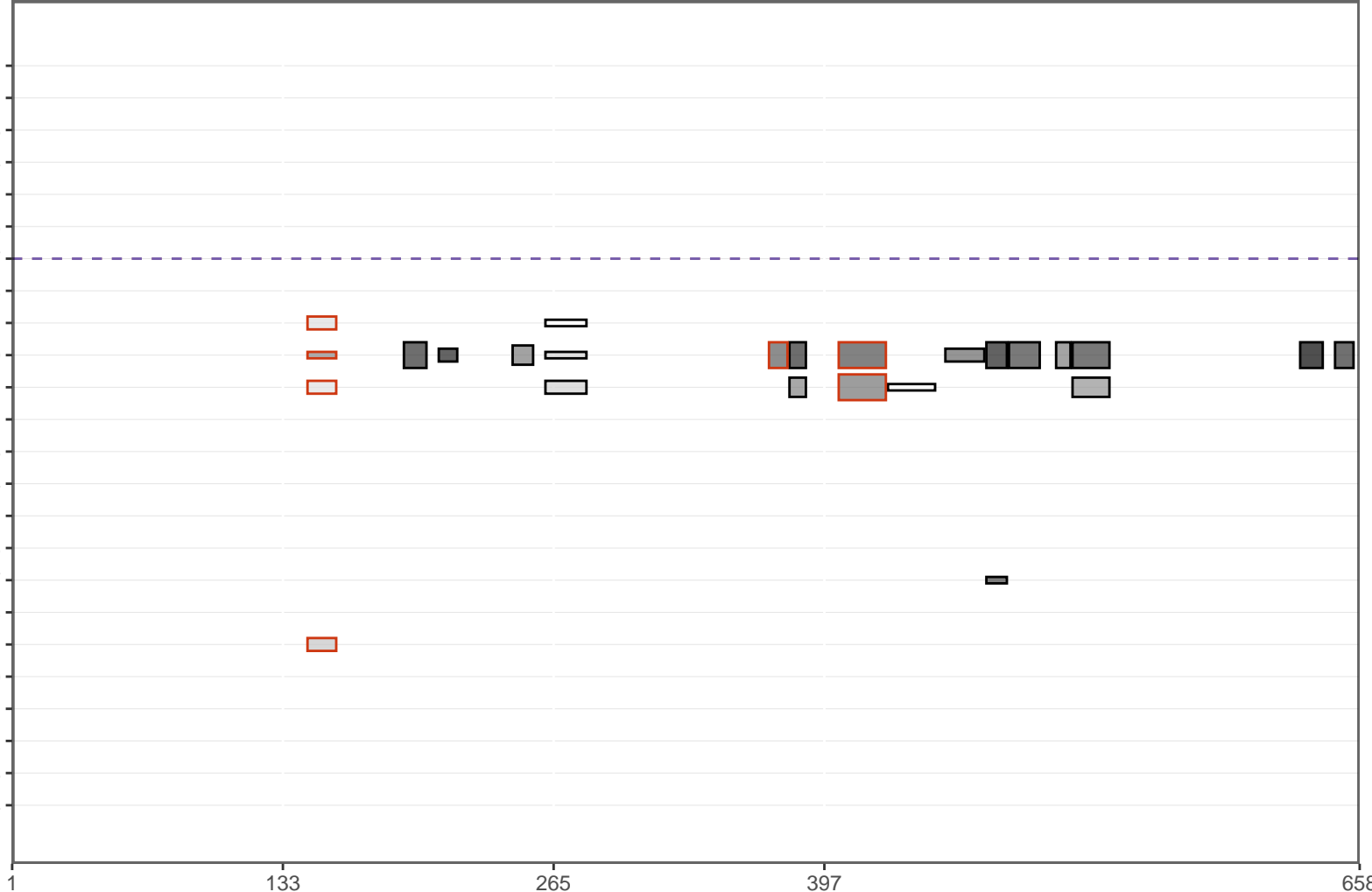
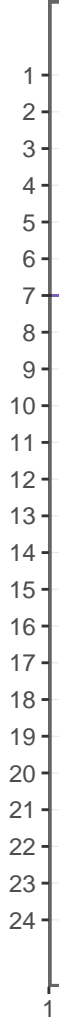
MW indication



Molecular weight

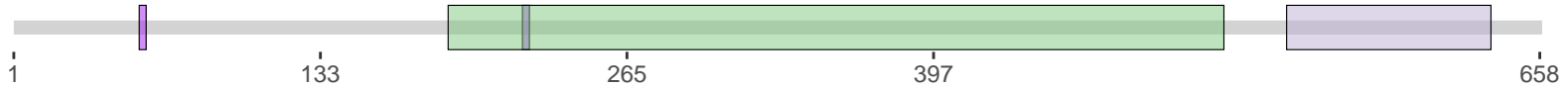


Gel Slice



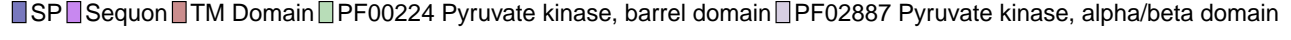
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SLSQVTSKTEESVYGEVVDGGELKSRRLNVRGKSAFLPSITEKDWDDIKFGVDNKIDFYAVSFVQDAVAVHELKNNLKGSDADHVVVIEGADGIPNLHSITFSDDGAMVARGDLGAELEPVEVPLGEEINGRGMSKAVVATNMLSESMVHPTPTRAEVSQDAIIVREGADAVMLSGETAHGGKFLKAVKVMHTVLSRTEATIVSGGETPNLGGAFKNHMSSEFAFHATMMSNTLGTSSVVFTRTGFMAILSHYRPGGTFAFTNDKKVGGORLALVGGLEPIYMEFSGAEET

NbL13g12170.1 glutamyl-peptide_cyclotransferase-like [MW - SP = 29.71 kDa]

No. of times detected



log(intensity)



Values from



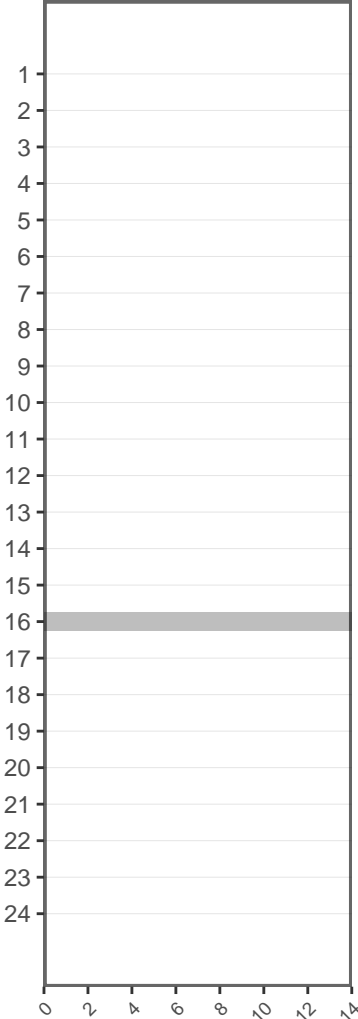
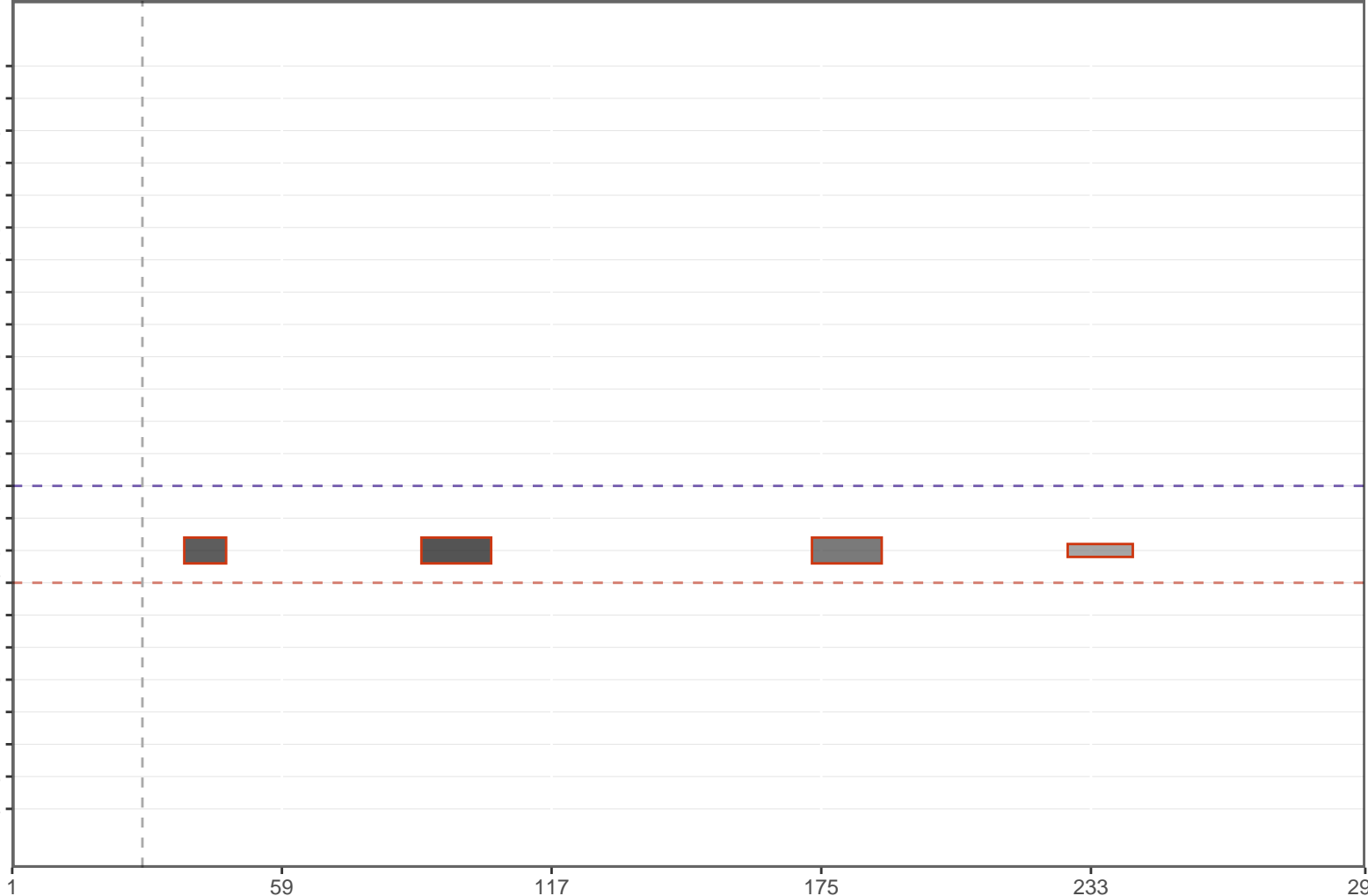
MW indication



Molecular weight

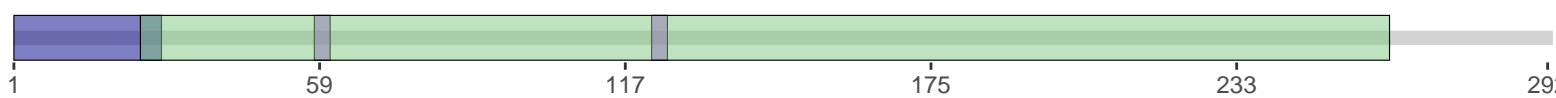


Gel Slice



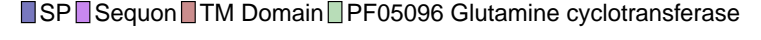
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IMQDQGLATDGGALFGSDGTSLEIDPQTKMKVIRKRVKSGDGEVPLYLEVYKNEIWANVYVTDQIARISPKDGTVIGWILLGSLREDLISRGYKDFEVLNGIAWRDGDRLVTGKLVKPLFEKLLLPNAPLIGEWNLCIPKFFLGELES

NbL13g11970.1 BAHD_acyltransferase_DCR [MW = 50.16 kDa]

No. of times detected



log(intensity)



Values from



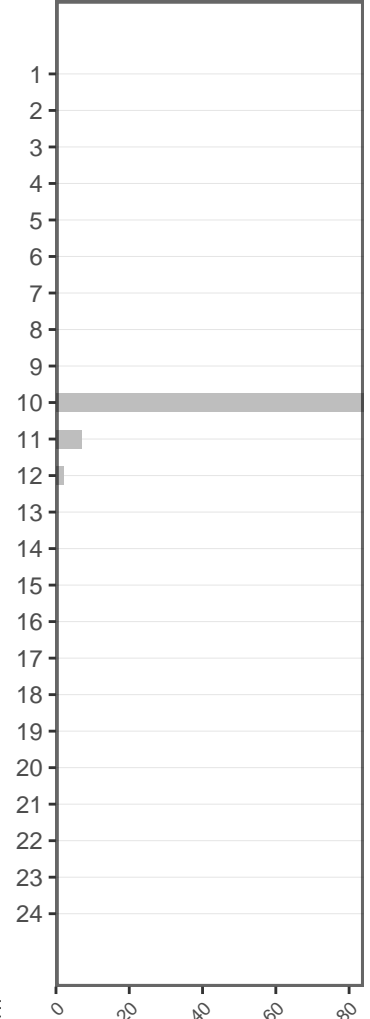
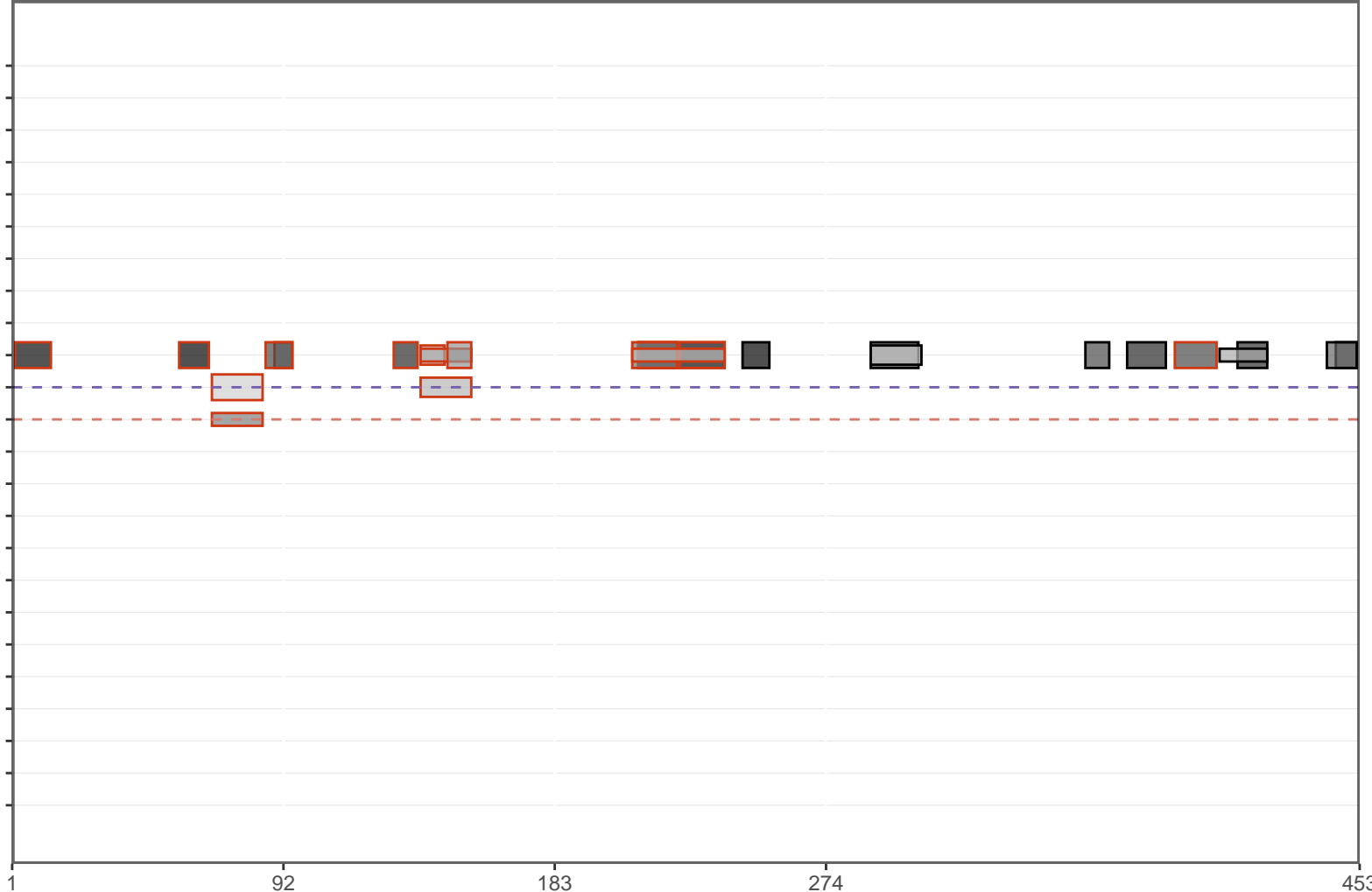
MW indication



Molecular weight

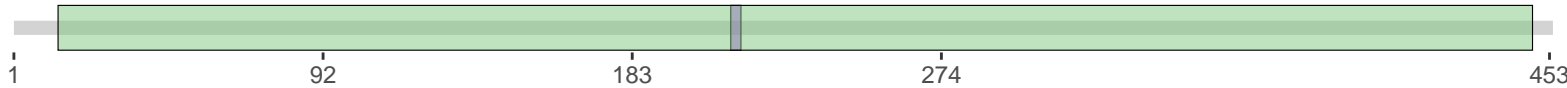


Gel Slice



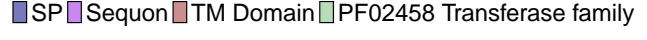
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PPSDATEPKSAPNGDVAEVDPLRERIFKFSBDAIDQKSKVYANRPGESGPFSTFGSLSAHWLAIIRARQKPKEDVTVTVFADGRKRVRDPPMPPEYFGNLQIAFTVTAAGLLSGPEFAAGMIDQAIWVHDKAIDERKKEWESNPKIFGKYDAGVNCVAVGSSPRFRVYVDVDFGWGKPEGRVRSNRRFDGMVYLVGQKSGGRSIDVEISLEANMERLEKDKELMEV

NbL13g11960.1 WW_domain-containing_protein_C11B10.08-like [MW = 32.91 kDa]

No. of times detected



log(intensity)



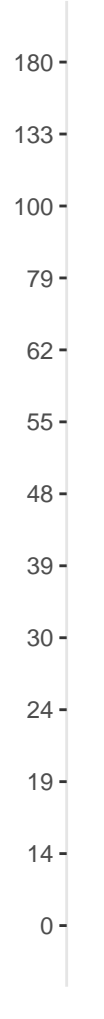
Values from



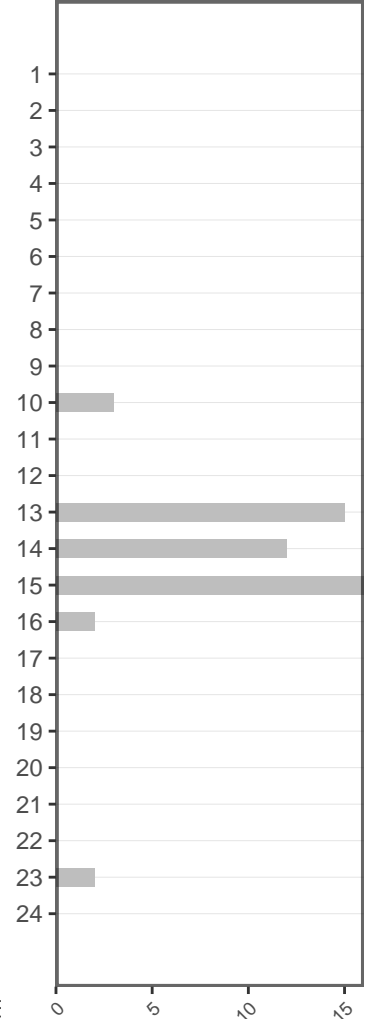
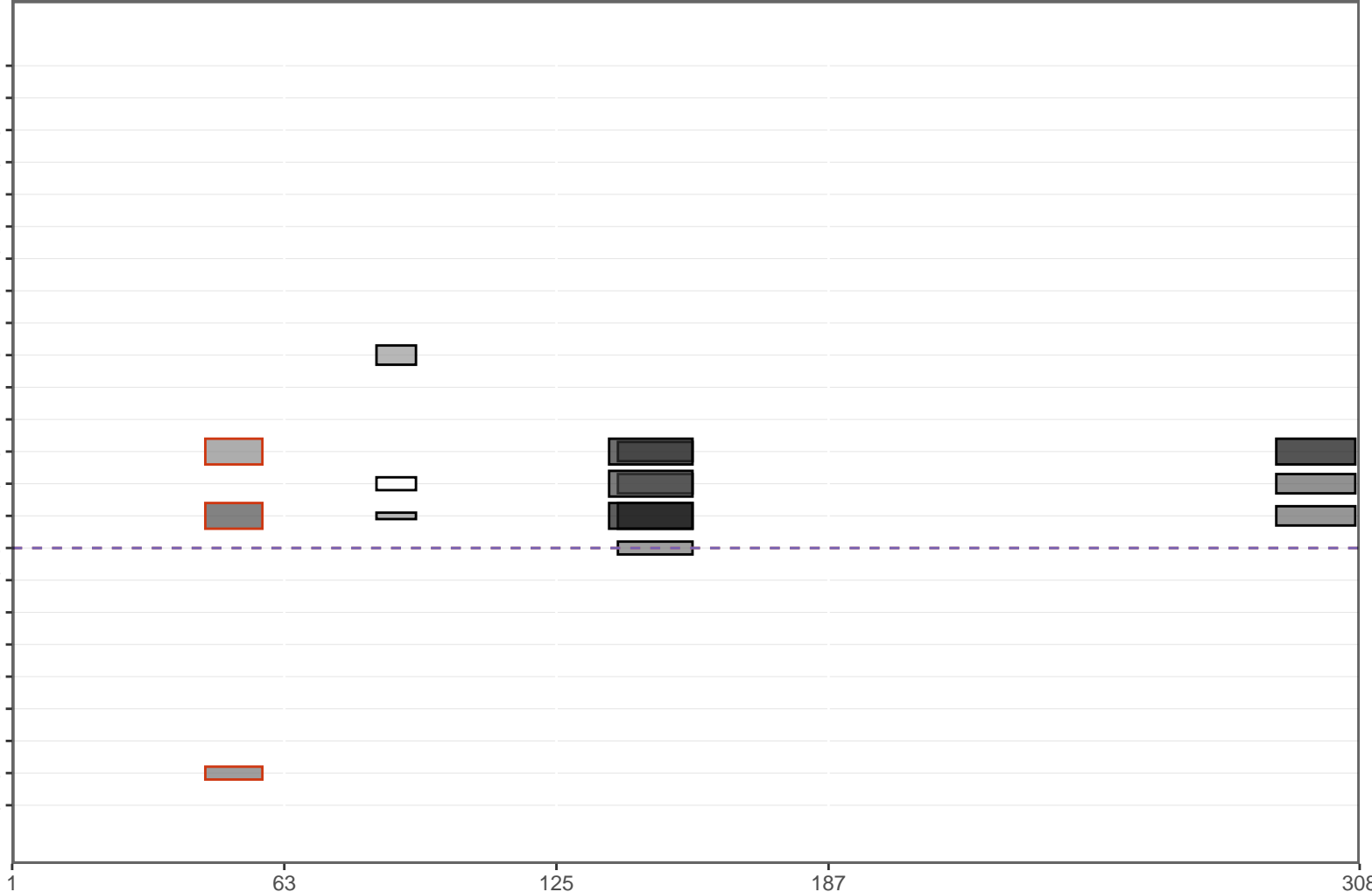
MW indication



Molecular weight



Gel Slice



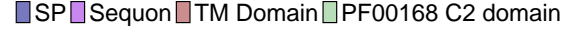
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AAPPYGVPPPGSRDPAAPPQRYGGVYGAAPPAAPRGGYPPYSAAPAPAPYGGGGPEYGAAPAPYSGDSEYGPYSGGSEYGGGGNYGAAVYGGGGYKYEKKGKFGMGLGAGLAVGAVAGLGLAISEGIDHEDNADKAAEKVEDLADDVDDGDDP

NbL13g11800.1 60S_ribosomal_protein_L36-1-like [MW = 12.1 kDa]

No. of times detected



log(intensity)



Values from



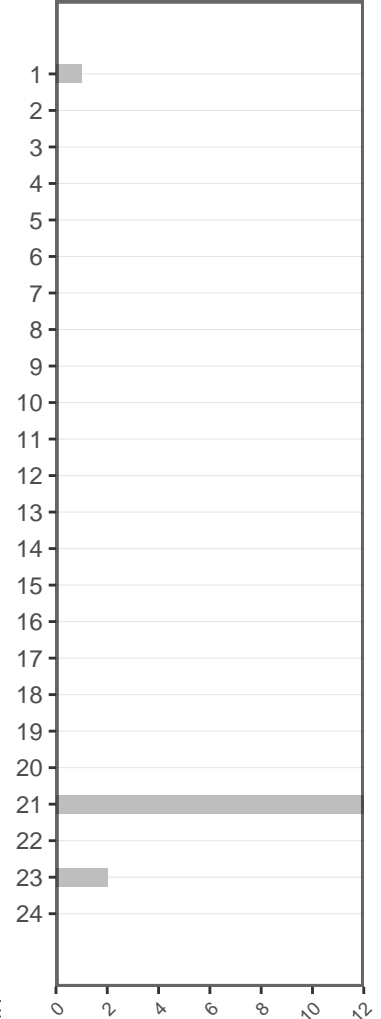
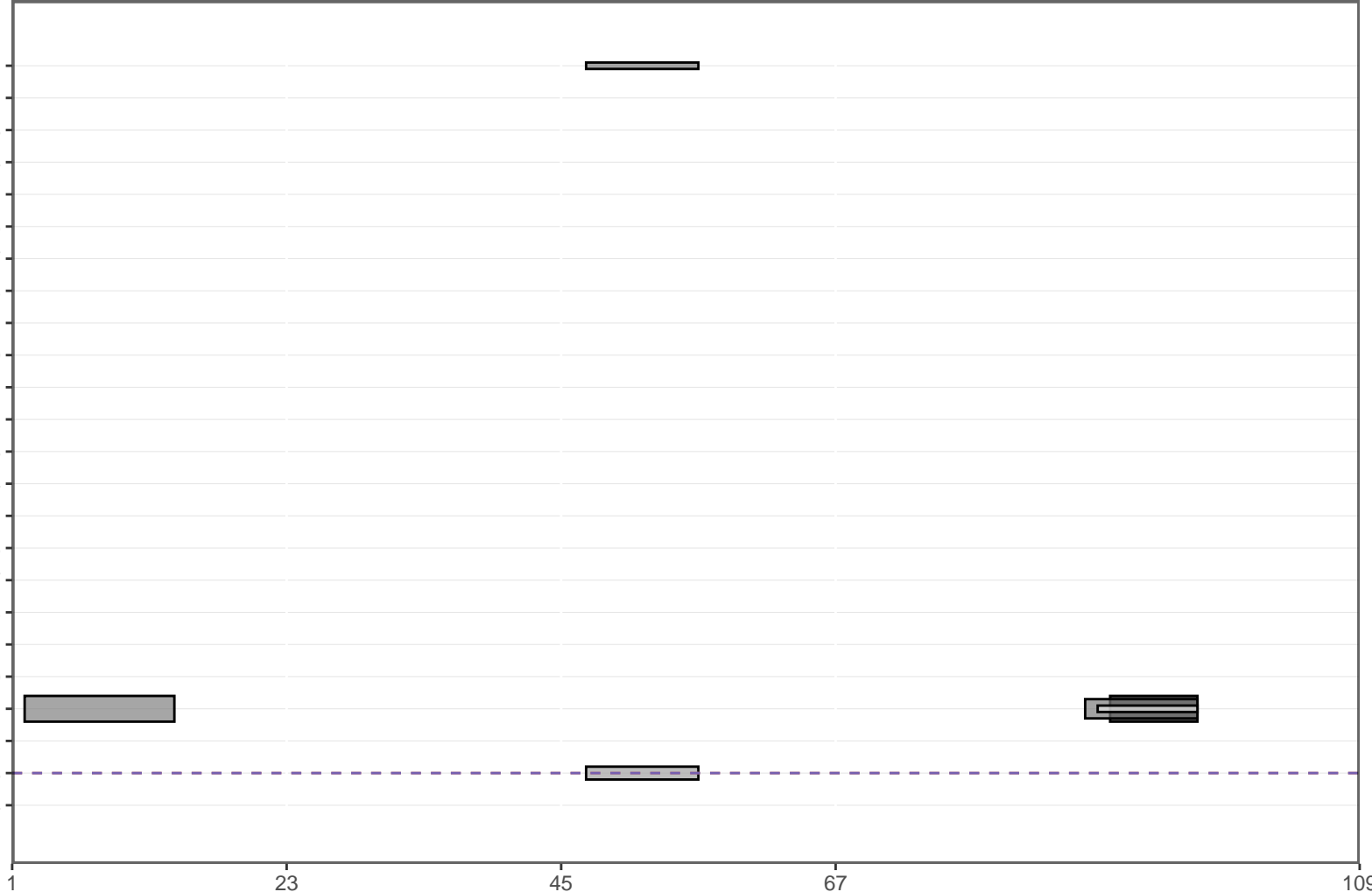
MW indication



Molecular weight



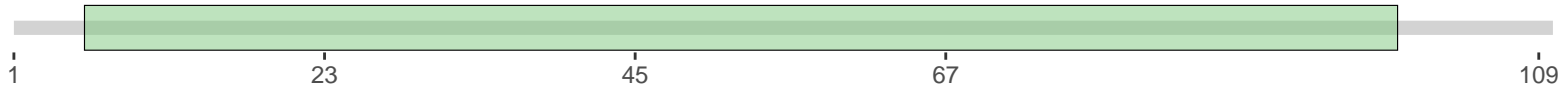
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

IRSLIREVAGFAPYEKRTFELLKVGKDKRALIKVAKRKLGTHKRAKKKREEMSVLRKMRATGGAEKIK

NbL13g11780.1 cleavage_and_polyadenylation_specificity_factor_subunit_2 [MW = 81.52 kDa]

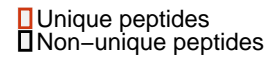
No. of times detected



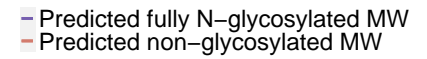
log(intensity)



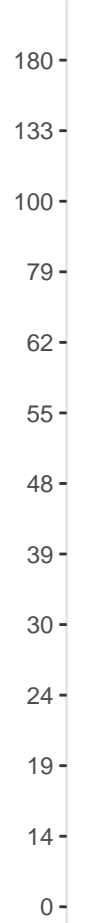
Values from



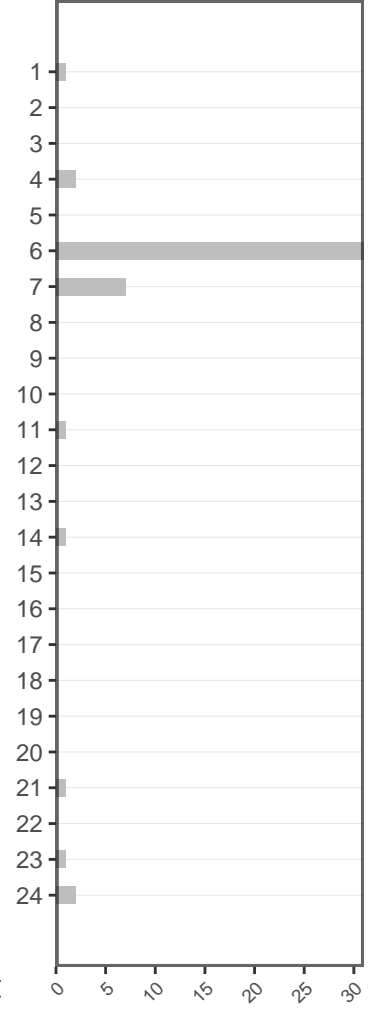
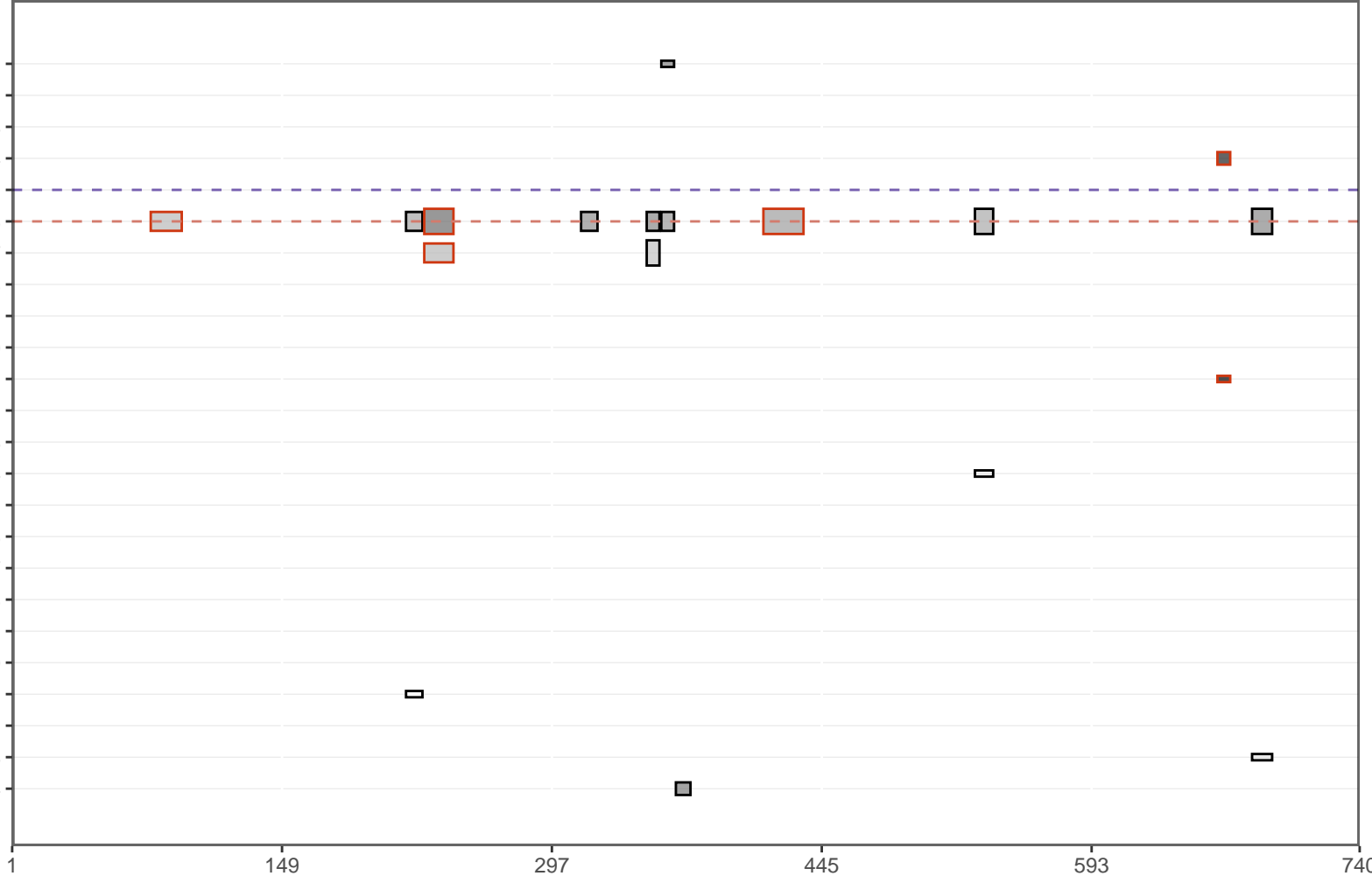
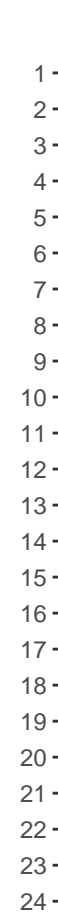
MW indication



Molecular weight

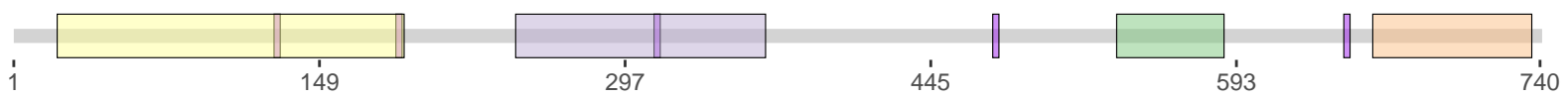


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- TM Domain
- PF10996 Beta-Casp domain
- PF16661 Metallo-beta-lactamase superfamily domain
- Sequon
- PF07521 Zn-dependent metallo-hydrolase RNA specificity domain
- PF13299 Cleavage and polyadenylation factor 2 C-terminal

Protein sequence:

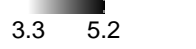
IQFGTLRILOSNFPPKAWKVTMSRRIPLVGEEIWAEEEGINRKRREKATLVKEEESKAPIGAEVHSGDPMVIDARVTHASNAAGPYSGAFKIVLIDGIVPPSSGVAIPFFFYDNTSEWDDFGEVINPDQVVKIDNMEQGSIMHYDGDNLGNLDEGSANLIDSTPEKVVSEELFVQVKGSLLYVDFEGRGDRSKSLAHVAPLKLIVHSGEAEATEHLKQHLKGVCPHYVAPQLEETIDVTSDLGAYKVQLSEKLMKVLFKLLGDHFEIAWVDAEYVKITENTGTSLLPI

NbL13g11710.1 oxalate--CoA_ligase-like [MW = 56.17 kDa]

No. of times detected



log(intensity)



Values from



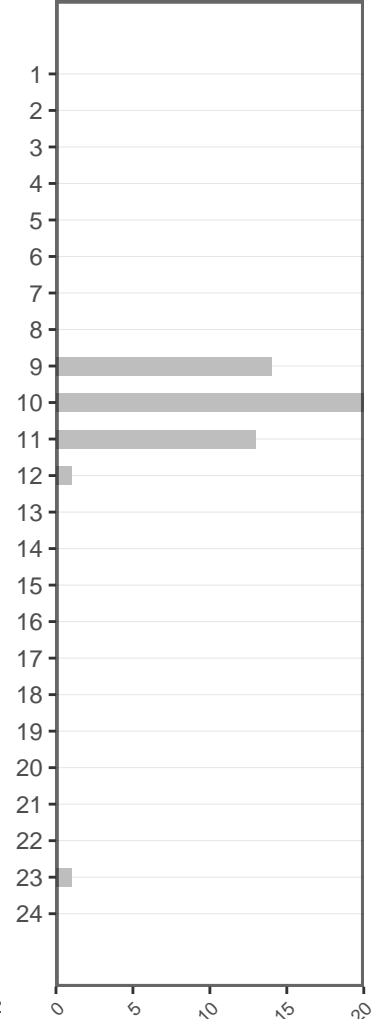
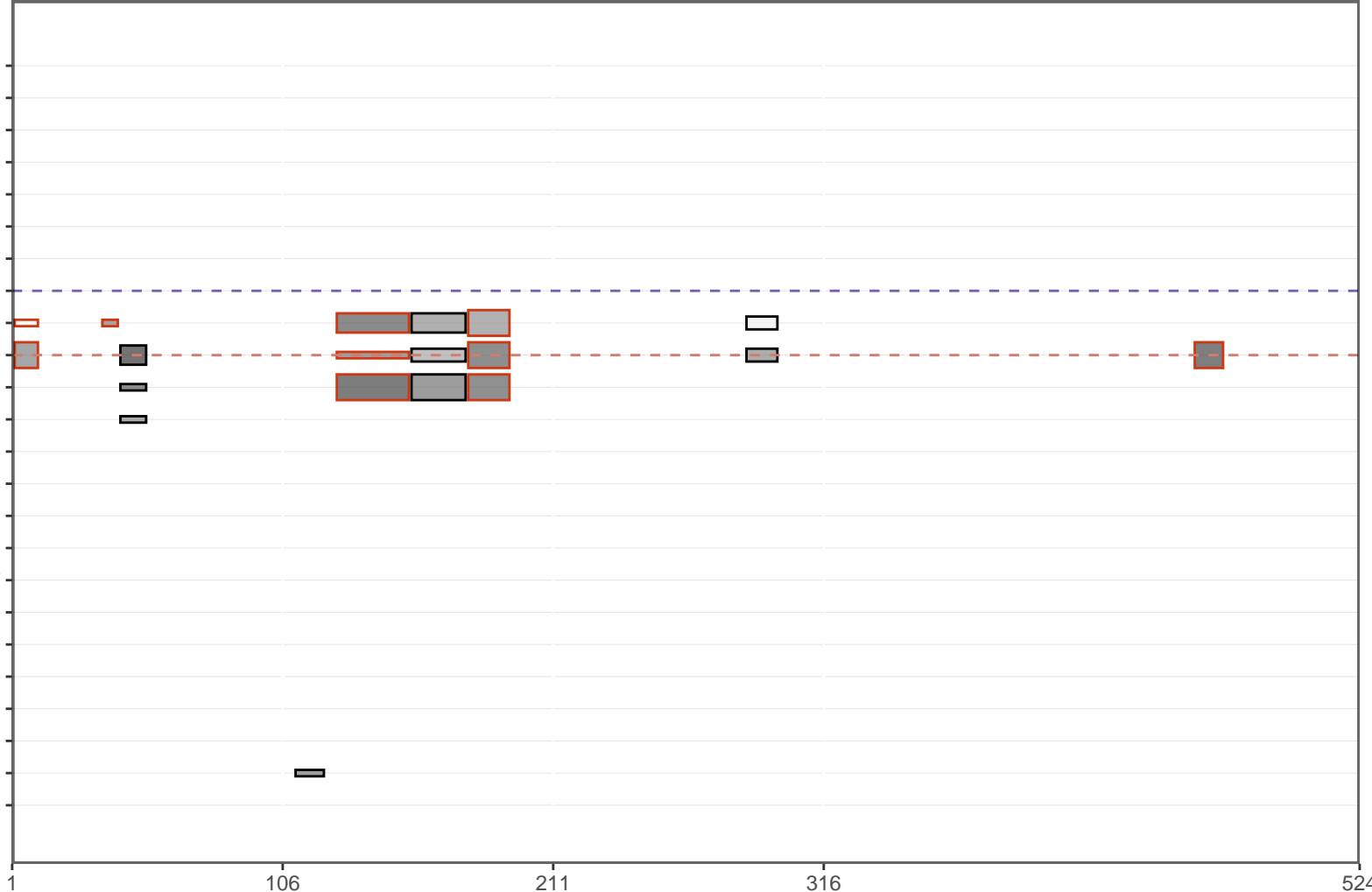
MW indication



Molecular weight



Gel Slice



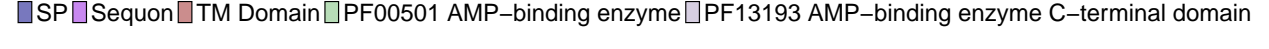
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NATVYTVPTTHQLLDGHLKSPESDYKLRFRIRSCGAALAPGVMMARLEEAFGAPVLEAVAMTEATHLMAENFLPENGPHVPGSVKPVGDEMAILDENGNGVGGPNKAGEVDRGPNVTKGVKYNFEANKSAFQGFVWFHTGDVGYLDSDDGYLHLVGRKELNRRGGENSPREVDAVLVSHAEIADAVAFGVPDDKYVGGEEINGAVIPREGNDIEAEVLRFGKKNLAAFKVPKVFMDSLPKATATGKIGRRLVAEHLAIGETAKVPKFGA

NbL13g11700.1 tubulin_beta-1_chain-like [MW = 50.45 kDa]

No. of times detected



log(intensity)



Values from



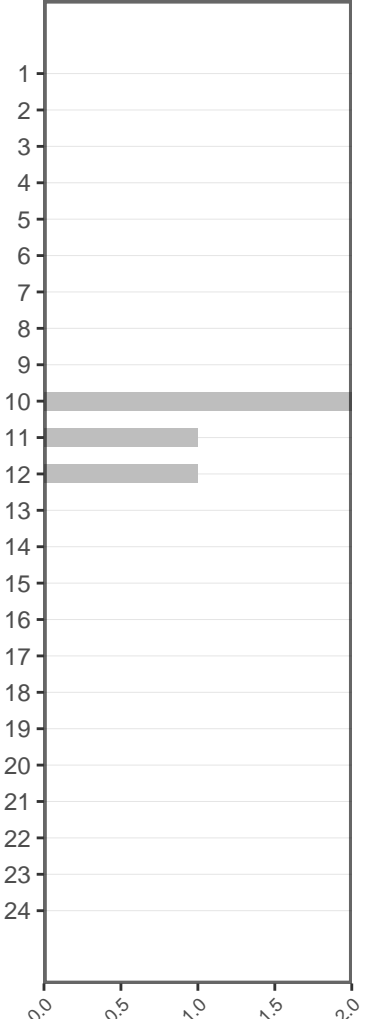
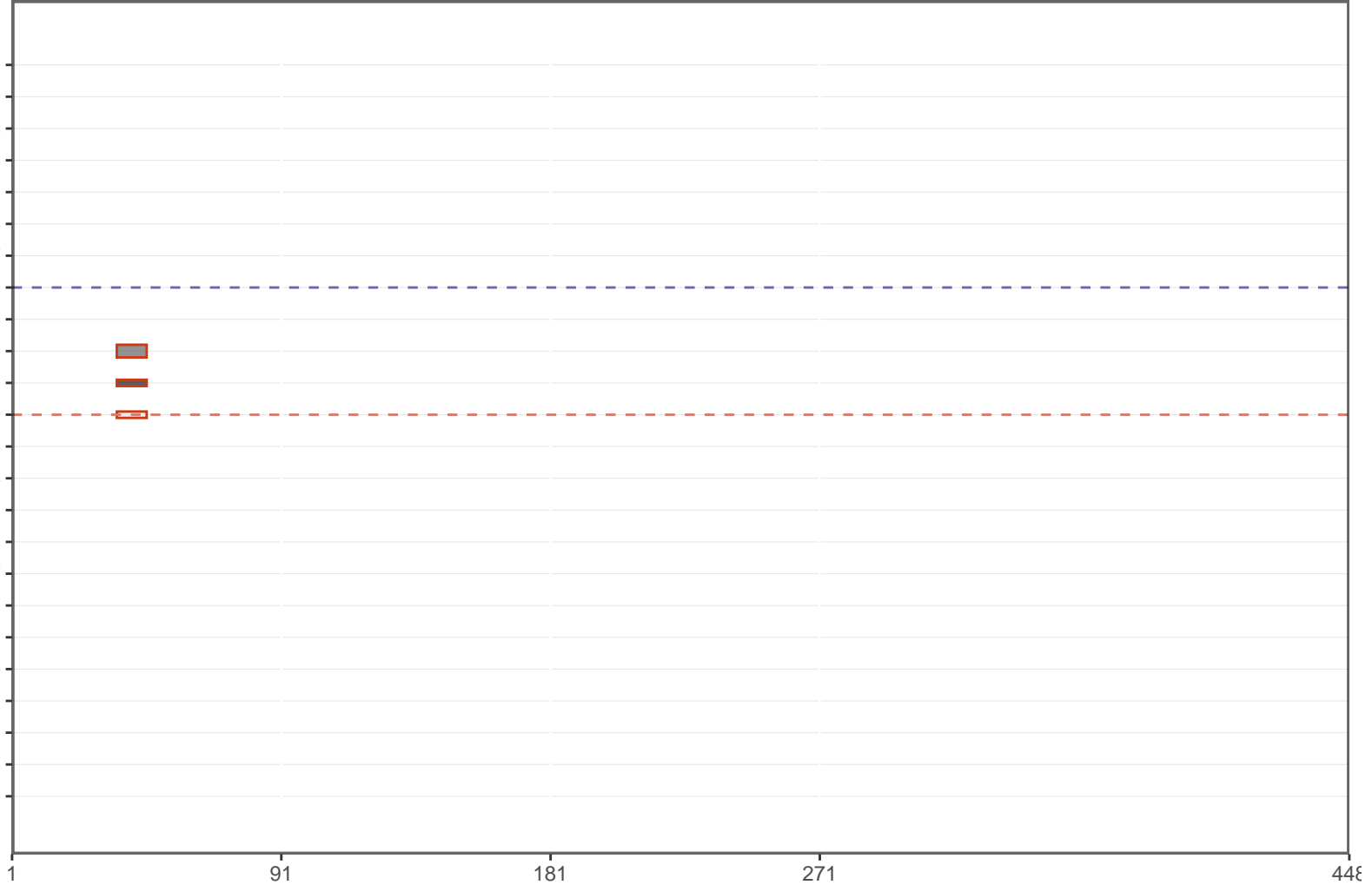
MW indication



Molecular weight



Gel Slice



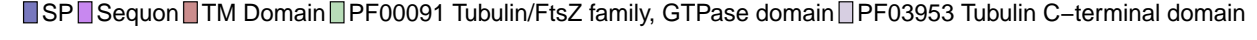
Protein length



Pfam domains



Pfam Description



Protein sequence:

MFRTLKLTPSFGDLNHLISATMSGGVTOGLRFPDGLNSDLRKLAVNLPFPRLLHFMVGFAPLFRGGQYRNLTVPELTQGMWDSKMMGAAADPRHGRVLTASAMFRGKMSKTEVDEQGMNQNNSSEYFVWIPNWKSTVGDIPPTGLRMASTFRGNSTSGEMFRFRVSEQGTAMFRKKAFLHWYTGEGMDMEFTFAESNNDLVSEYQYQGDATAESEYDYDEDEEEGGEA

NbL13g11630.1 transmembrane_ascorbate_ferrioreductase_1-like [MW = 25.42 kDa]

No. of times detected



log(intensity)



Values from



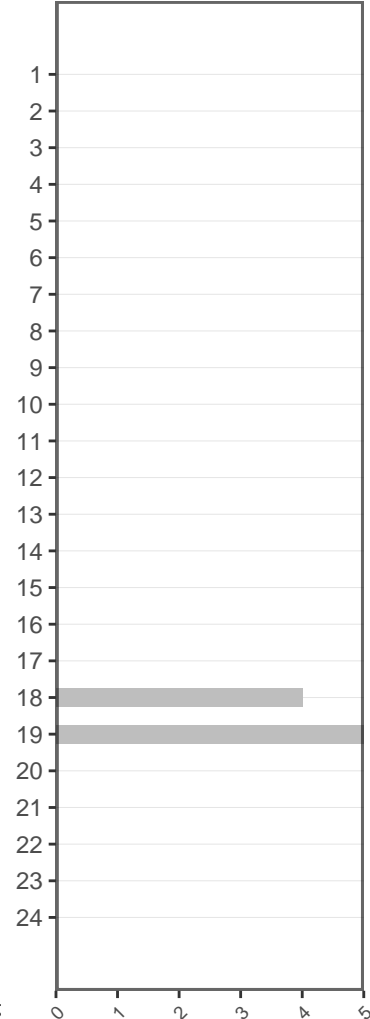
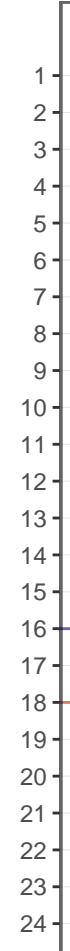
MW indication



Molecular weight

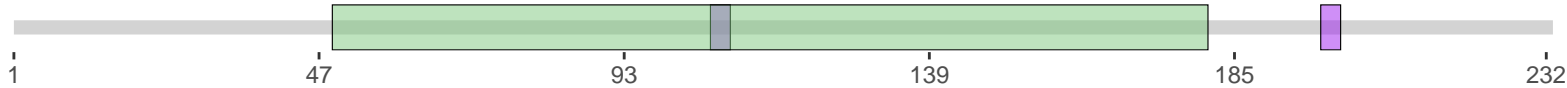


Gel Slice



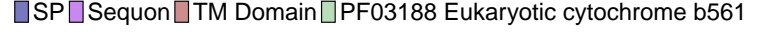
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MNESINPMYSLHSEWVGVVLYLGGWVGFVFFYPGSSAEVRRDLPWHVLFQMFVYVMVGNAGLGLLEKLFLEVNGLAKYGEAFLNFTATVLYGVFVFLTLGGAPTEDDVSYSAE

NbL13g11620.1 remorin-like [MW = 22.85 kDa]

No. of times detected



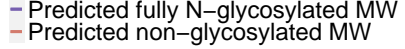
log(intensity)



Values from

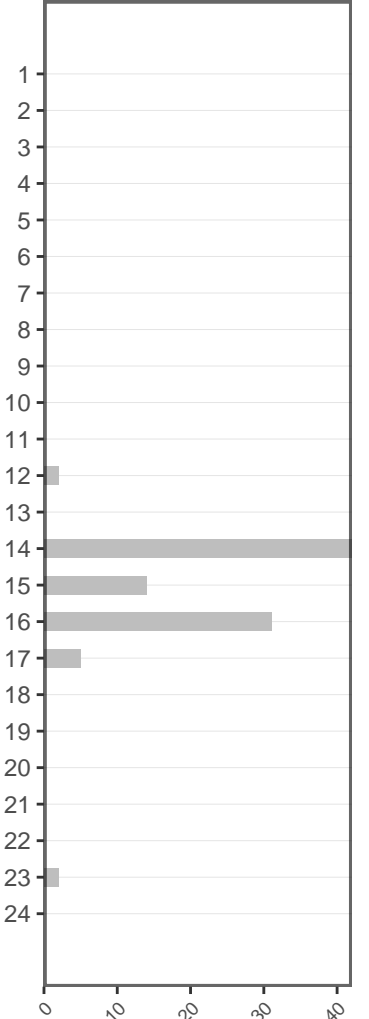
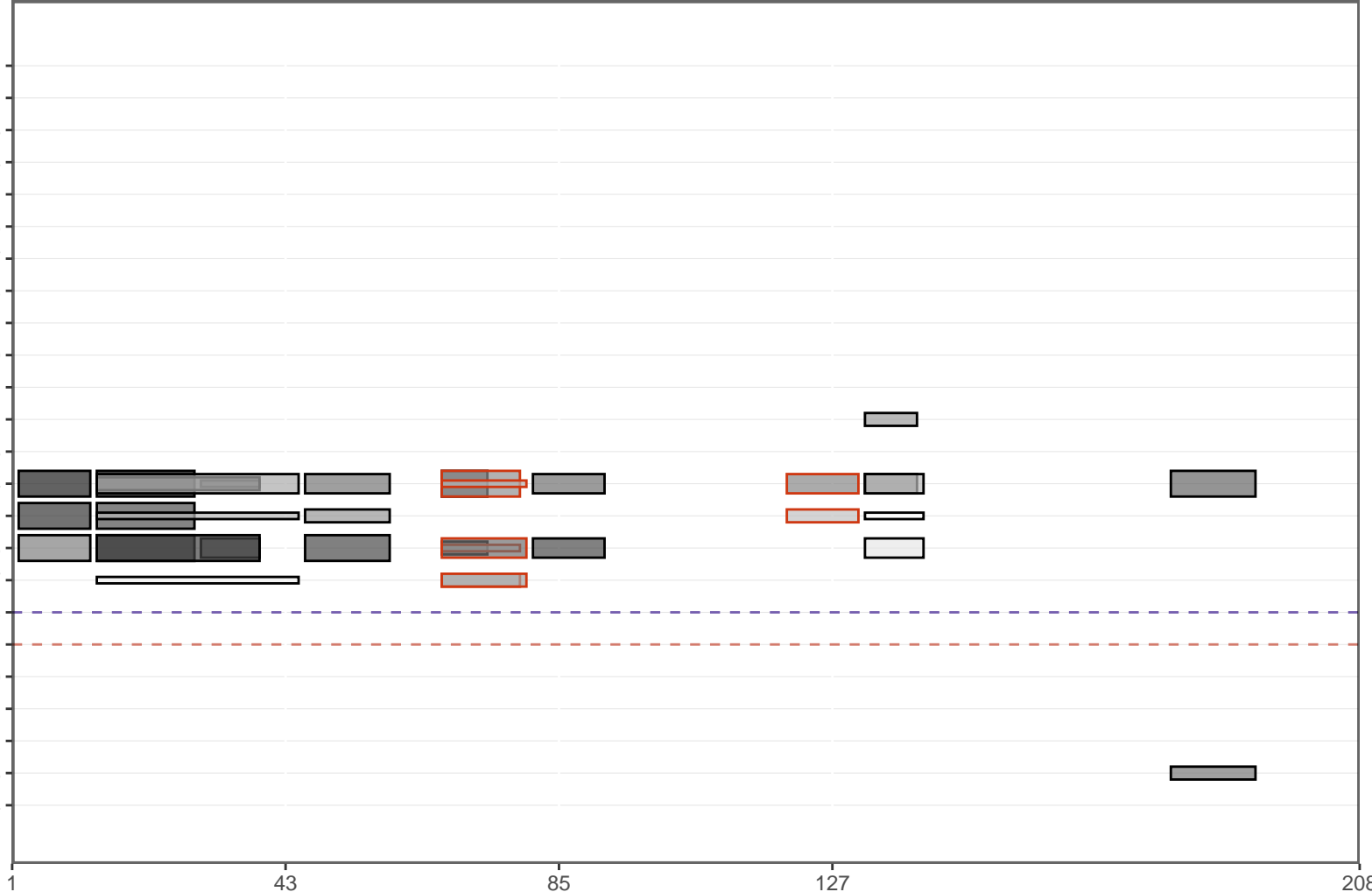
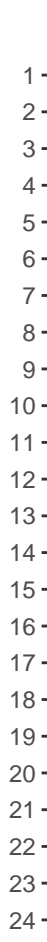
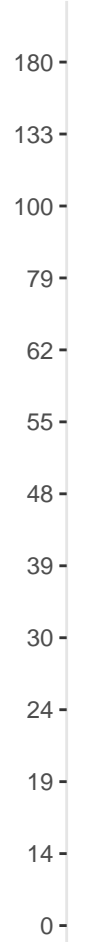


MW indication



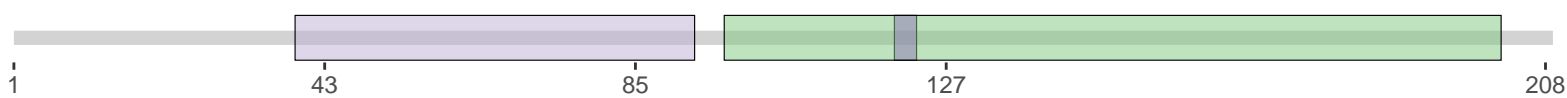
Molecular weight

Gel Slice



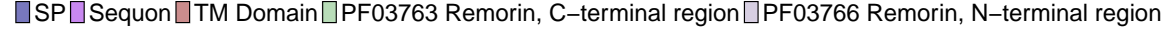
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

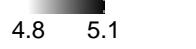
IRVATEKRLSLKAVVEESEKSKAENKAGKNSVIAAWENSKKANLEAELKMMEEQVEKKAAYEIKMKNKALLHKEAEKRAMIEAKRGEDLLKAEELAAKYRATGTAPKLLGGF

NbL13g11590.1 probable_acetyltransferase_NATA1-like [MW = 20.81 kDa]

No. of times detected



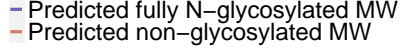
log(intensity)



Values from



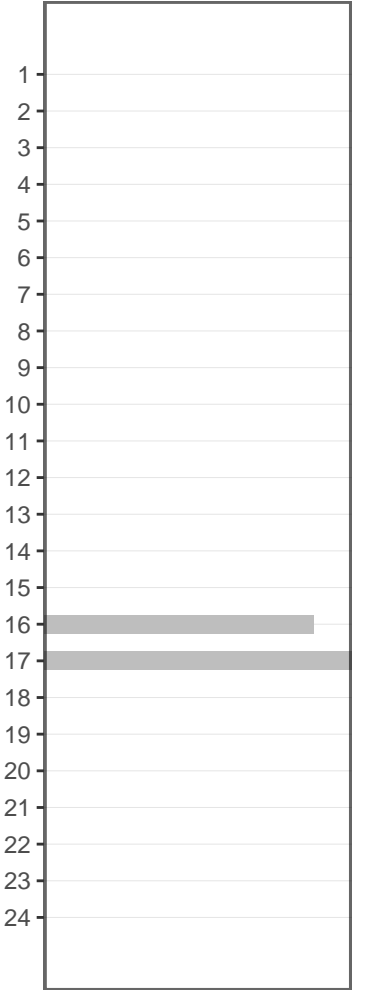
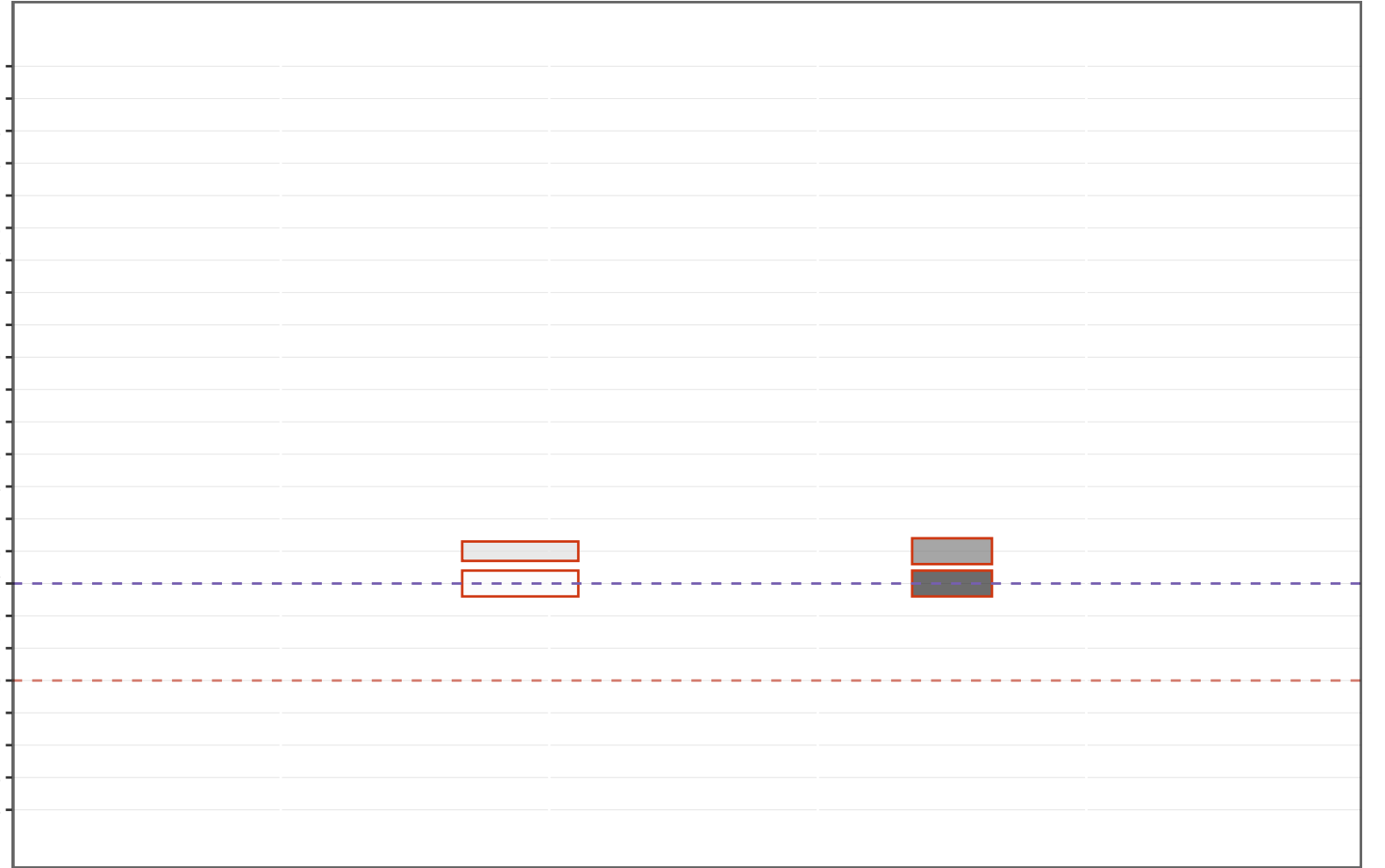
MW indication



Molecular weight



Gel Slice

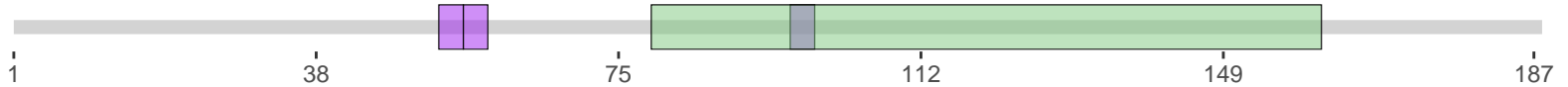


Protein length

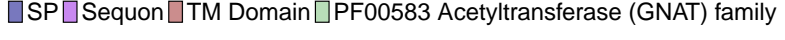


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SNDAVAGFVLFPPNYSFLAKPGFYEDFVREYRRKGFGRLLLSAAVAAQAAMGYSGRVEWVYLDWNNNAKFEEMGADLQEWVRVRLTGGALEAFANVDI

NbL13g11410.1 membrane_steroid-binding_protein_2-like [MW = 24.75 kDa]

No. of times detected



log(intensity)



Values from



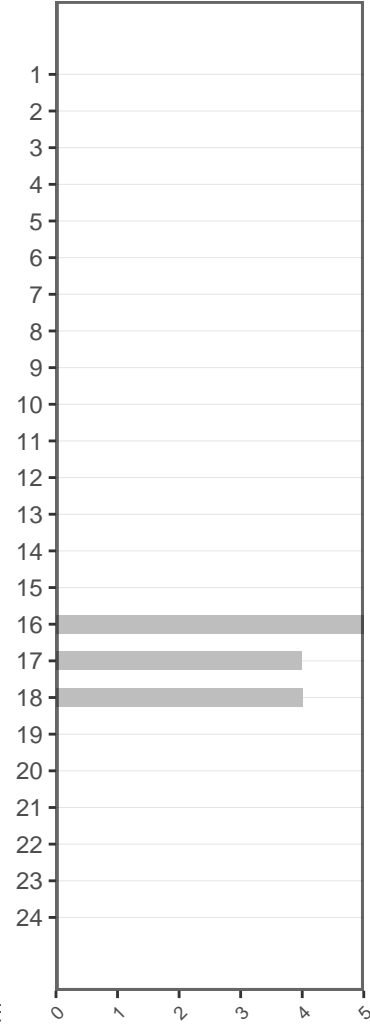
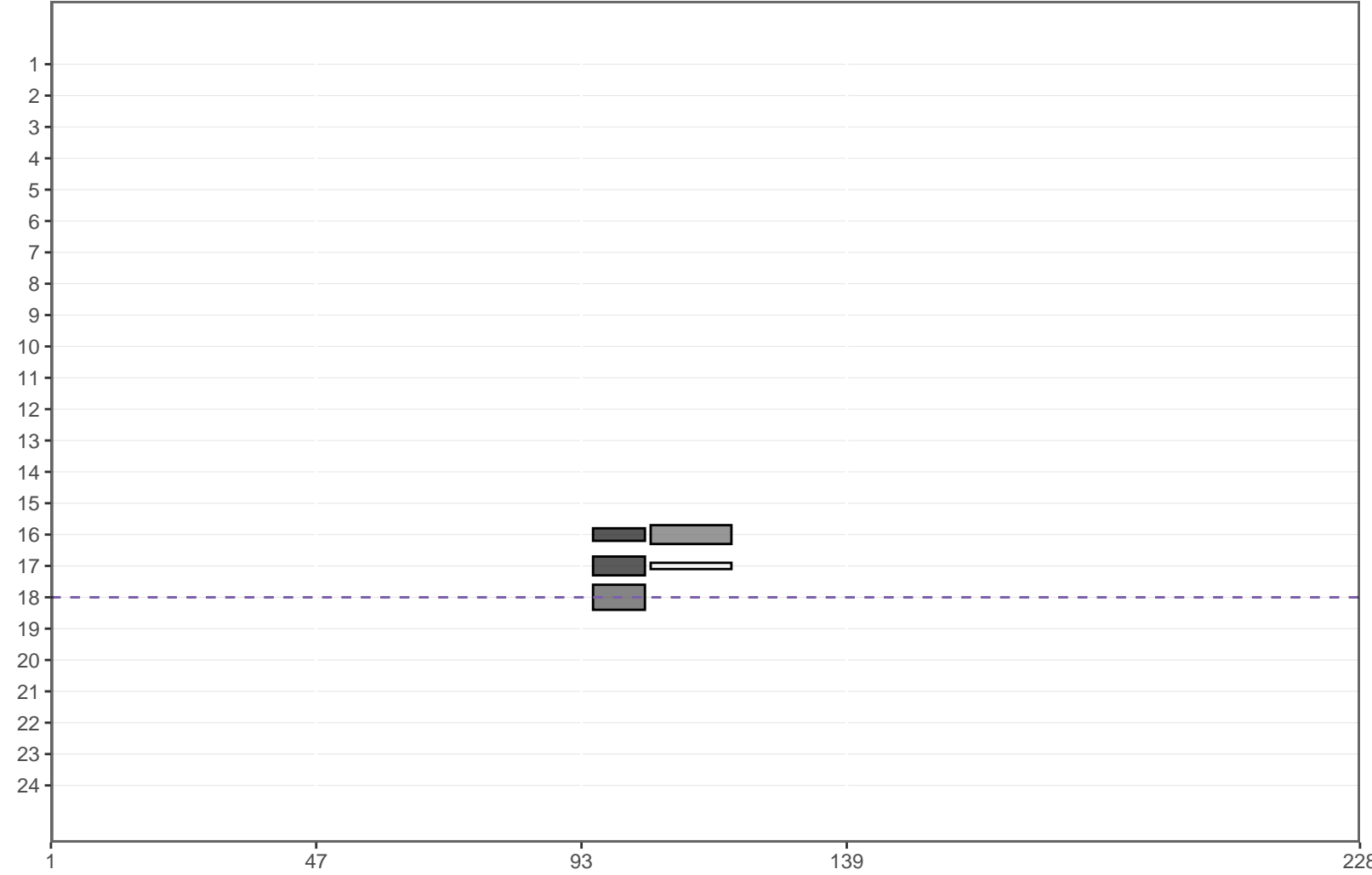
MW indication



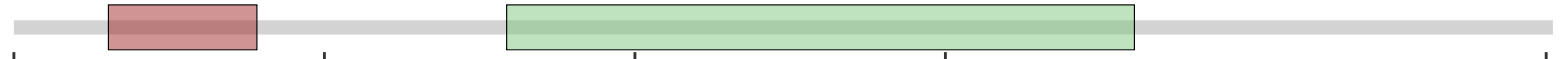
Molecular weight



Gel Slice

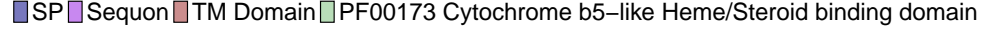


Protein length



Pfam domains

Pfam Description



Protein sequence:

SRMFYGPQGPYALFAGKDAARALAKMFEKDLTGDIGLGPPELEALQDWEYKFMKRYVWGTVYKGTGTPVSDGATNGESVESTDREAKPMEGFSAEAKPSEDGSPSEGAETVQKSDGDAEKKD

NbL13g11340.1 superoxide_dismutase_[Fe]_3_chloroplastic [MW = 30.84 kDa]

No. of times detected



log(intensity)



Values from



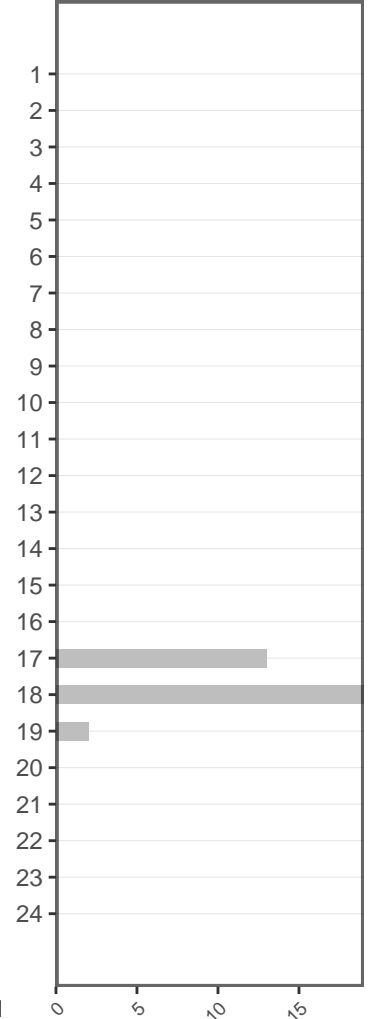
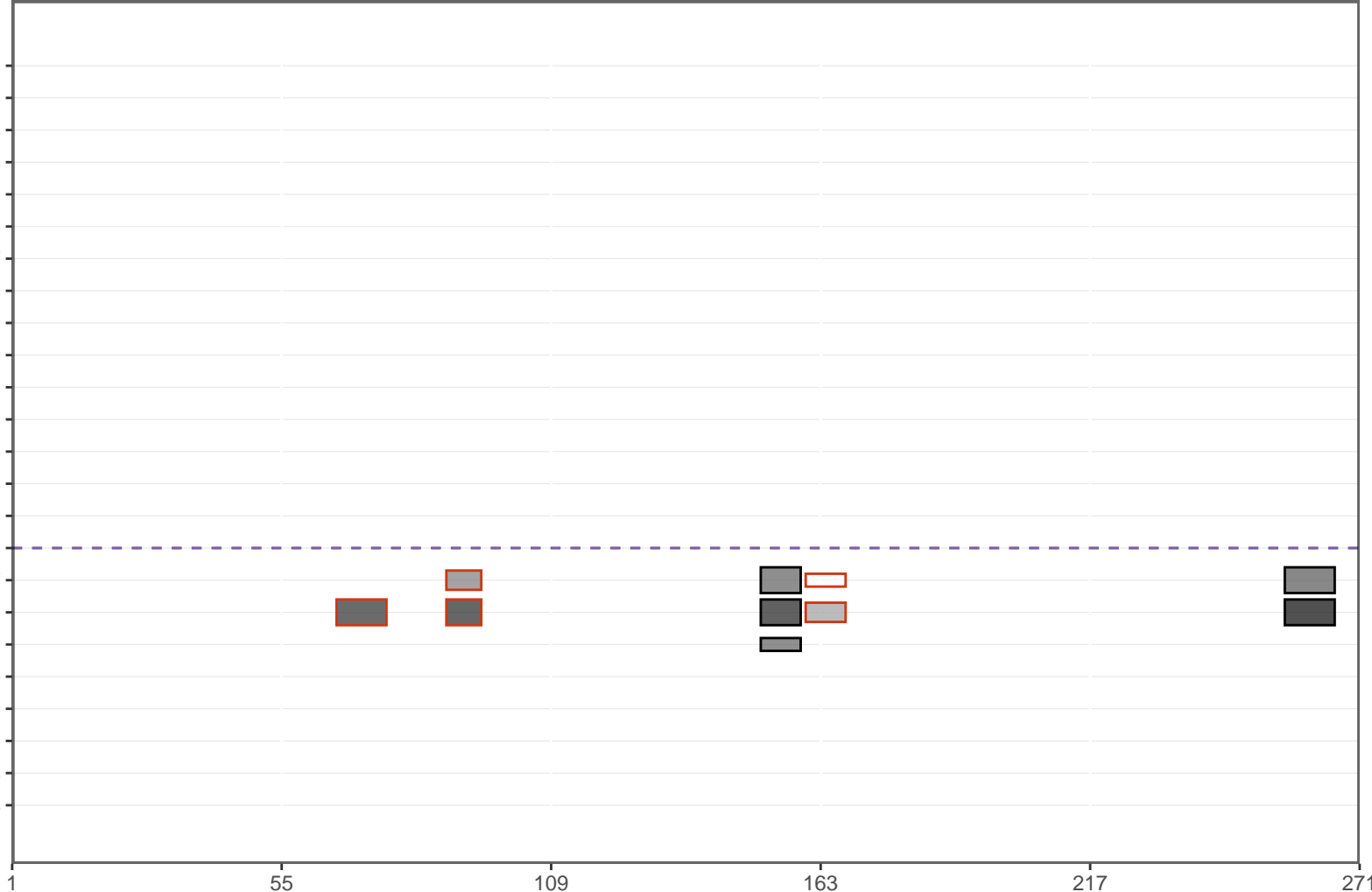
MW indication



Molecular weight

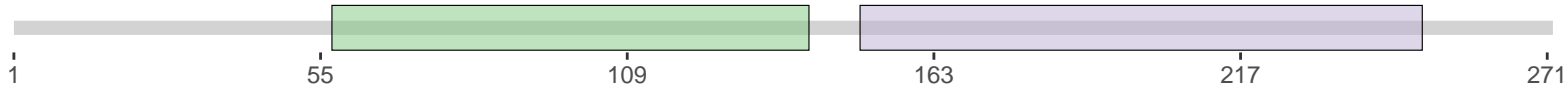


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

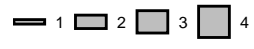
- SP
- Sequon
- TM Domain
- PF00081 Iron/manganese superoxide dismutases, alpha-hairpin domain
- PF02777 Iron/manganese superoxide dismutases, C-terminal domain

Protein sequence:

PEFSDAAQVWNIDFFWESMPGGGMPKLGLLGQIEKDFGFTNFRKFTFAALTLFGSGWVWLVKREERKRLAVKTSNAVNPLVNDIPUGLDWEHAYLQKNDKAKYVNVFMNHLVSWDAALGRMARADAFVNLGEPKIPVA

NbL13g11330.1 ammonia-lyase [MW = 78.23 kDa]

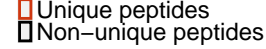
No. of times detected



log(intensity)



Values from



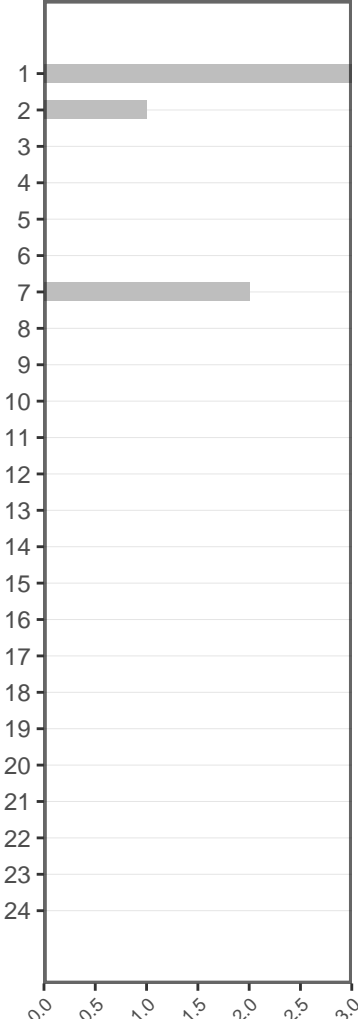
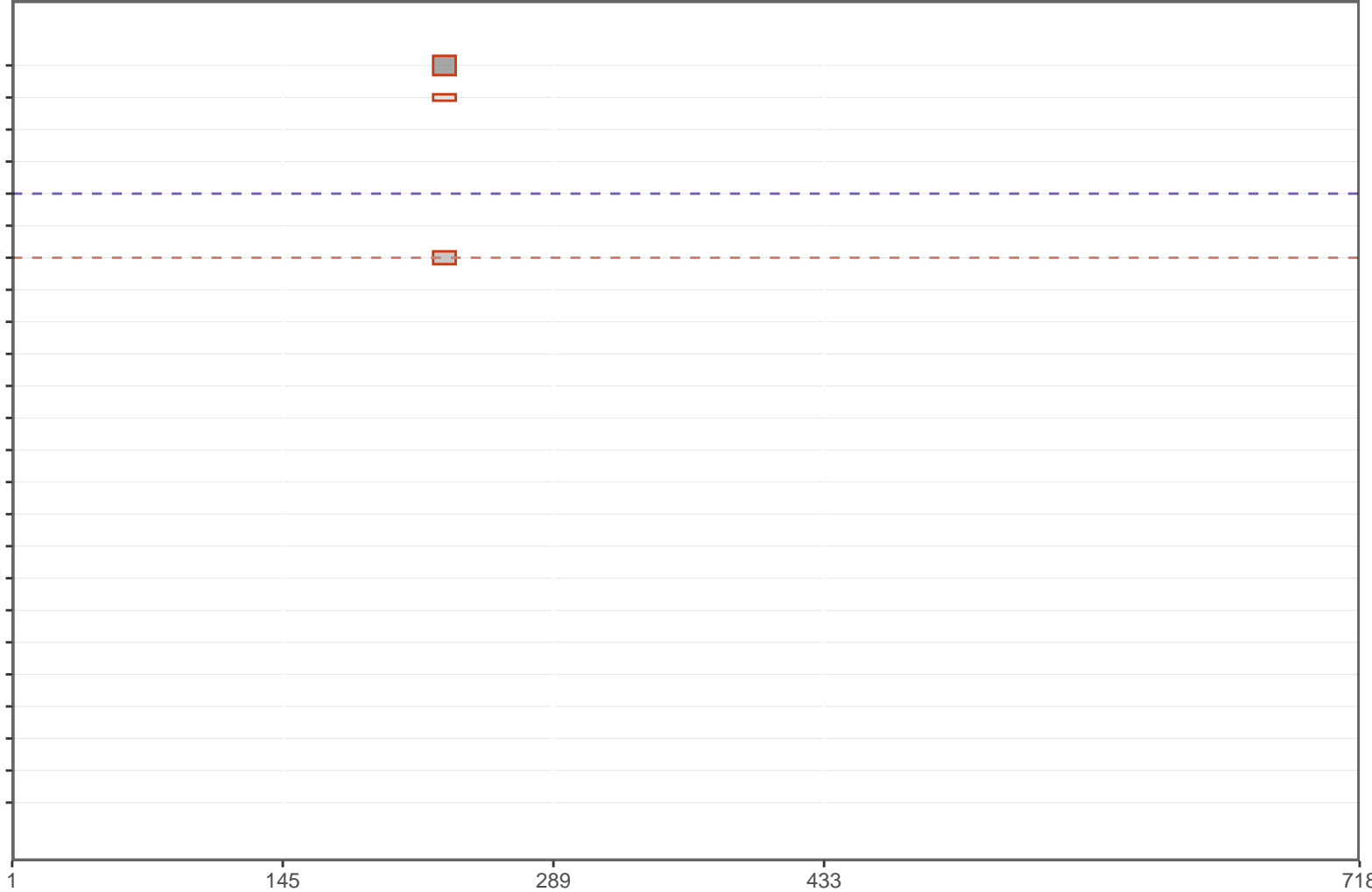
MW indication



Molecular weight



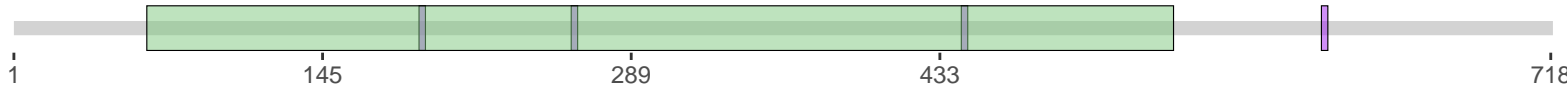
Gel Slice



Protein length



Pfam domains



Pfam Description

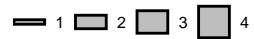


Protein sequence:

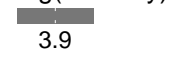
QKPKDRLALRTSPQWLGQIEVIRAAKMERIEINVDNPLIDVSRNKALHGGNFQGTPIGVSMNTRILALASIGKLMFAQFSELVNDYYNNGLFSNLTGGRNPSLDYGFKGAEMMASCYGELGFLANPVTNHVGSAGEQHNGVDNLSGLISRRKTAEAVDIKLMSSTYLVALOGAIDLRIHMEENLKASVKNVYGLVAKKVLITGGNGELHPSRFCEKDLKVVDRVEYFAYVDDPCGCTYPLIQKLRQVLVDHALLNGEGENNSTSIFENISVFEELKALKSEVESARC

NbL13g11080.1 peroxidase_66 [MW - SP = 32.47 kDa]

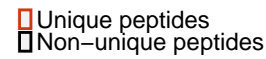
No. of times detected



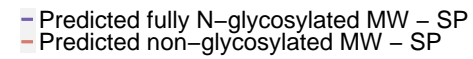
log(intensity)



Values from



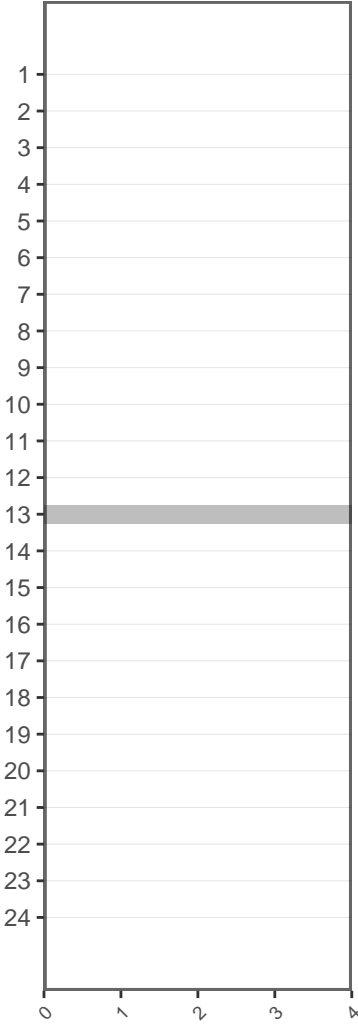
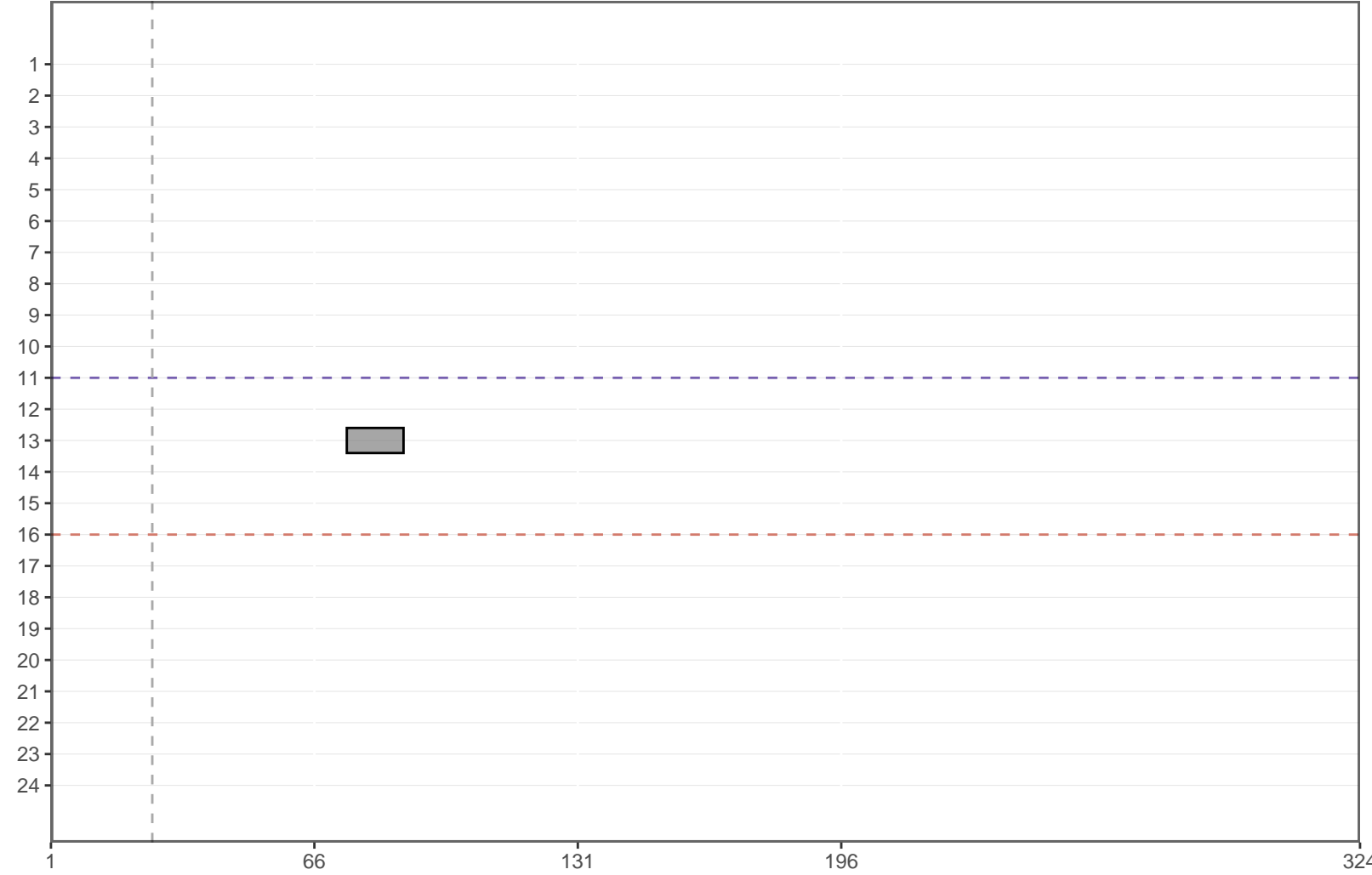
MW indication



Molecular weight

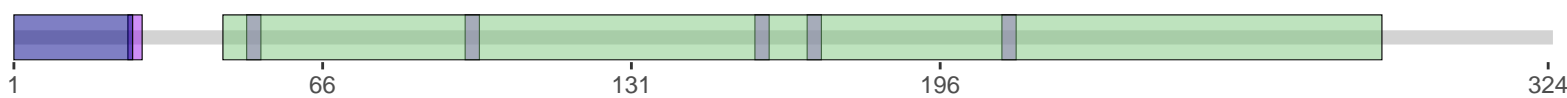


Gel Slice



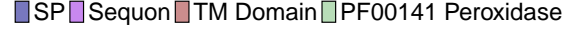
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IRSRANETINLPAPEFTSGLIGSFAKRLGVKDLVALSGGHTLGFSHGGSFEARLRNFSSVHDTDPSELNAVFAEELKKNKPKPNRDSNAGGFLDTTSSGFDNNYKGVAGKGVFAEQDQLLNDVIRTGWVWAFANDQAFSFFVEFAAMVKLGNVGVLENGEVRILNGRAWV

NbL13g11070.1 uncharacterized_LOC107784461 [MW = 26.57 kDa]

No. of times detected



log(intensity)



Values from



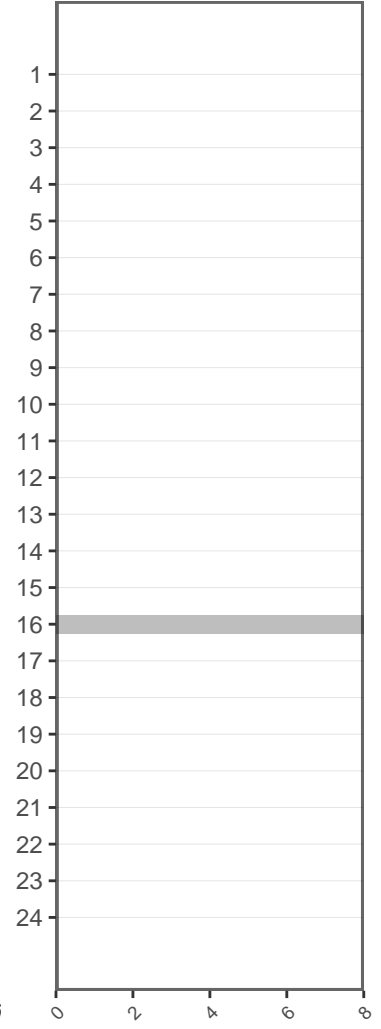
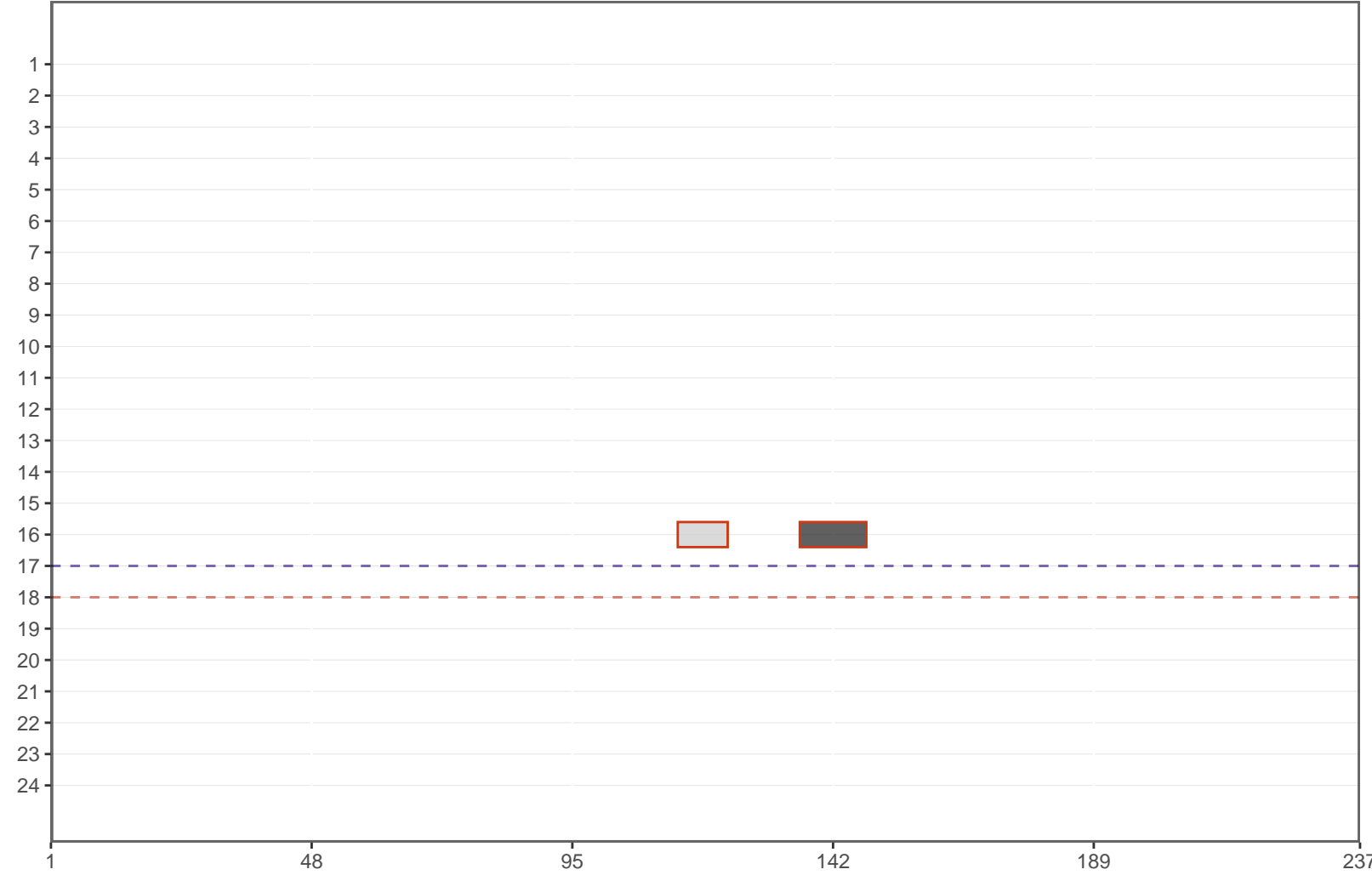
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

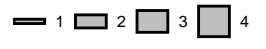
Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

LFSDKIRGRVWGLNPNRFRYYKAGQRFGRHDEVDGEGKRTHYLLVLSGGSKKHKDDKDSGDSVSEILVGETVYFGPRNALVAEVPPTFGMALVHHGDKMLHEARNVTGKQYVLRSDVFA*

NbL13g11010.1 phosphoglucomutase_chloroplastic [MW = 68.69 kDa]

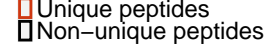
No. of times detected



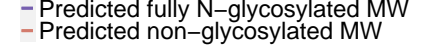
log(intensity)



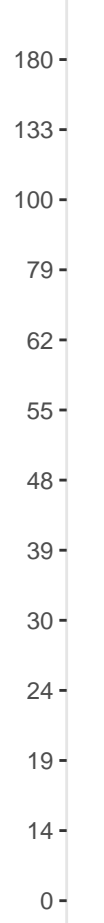
Values from



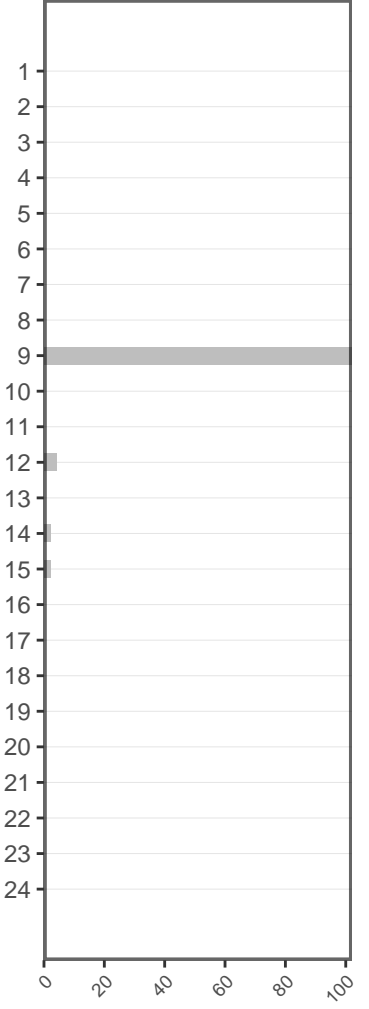
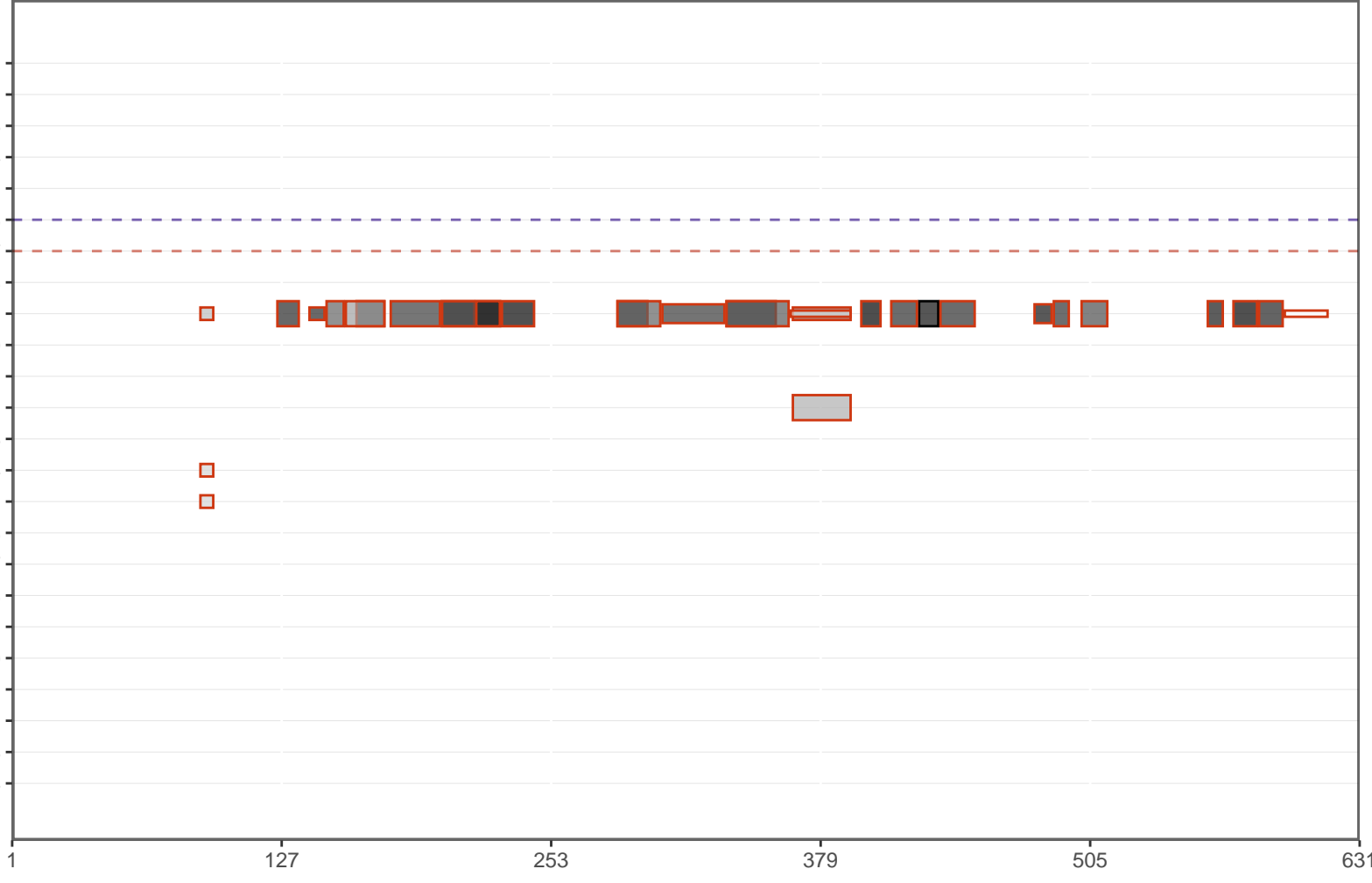
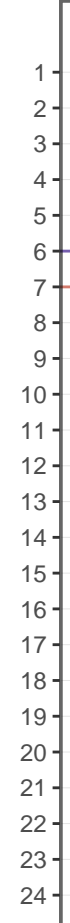
MW indication



Molecular weight

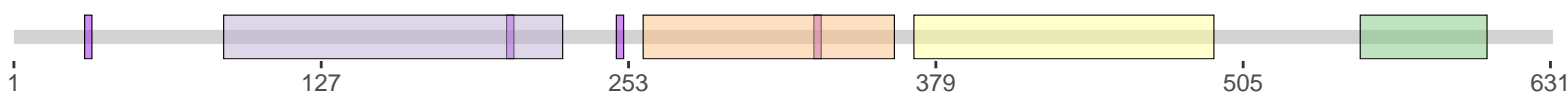


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

PF02878 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain I PF02880 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain II
 Phosphoglucomutase/phosphomannomutase, C-terminal domain PF02879 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain II

Protein sequence:

JASLESIANGEFLDFGHGHPDRLNLYAKDLNLYLVGENGPDFGAASDDGDRNMLGRFFVTPSDVAAIAANAGDAPYFHSGPKGLARSMPTSGSLDRWQKLNLPVEVPTGWKFFGNLMDAGKLSGCEESFGTGDHREKDGWAVLAWLBIAYRNKDKRSGEKNLVSADVAREHWATYGRNFFSRVYVEECEGEGANKMEIVLRDLISKAKAGDEYGNVYLDFADDFTYTDPRVDGSAKGGVRFVPSDGRIFRLSGTGSAGATRIWEQFEPD/SKIIMD

NbL13g10910.1 subtilisin-like_protease [MW - SP = 81.23 kDa]

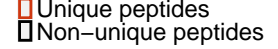
No. of times detected



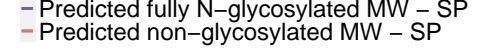
log(intensity)



Values from



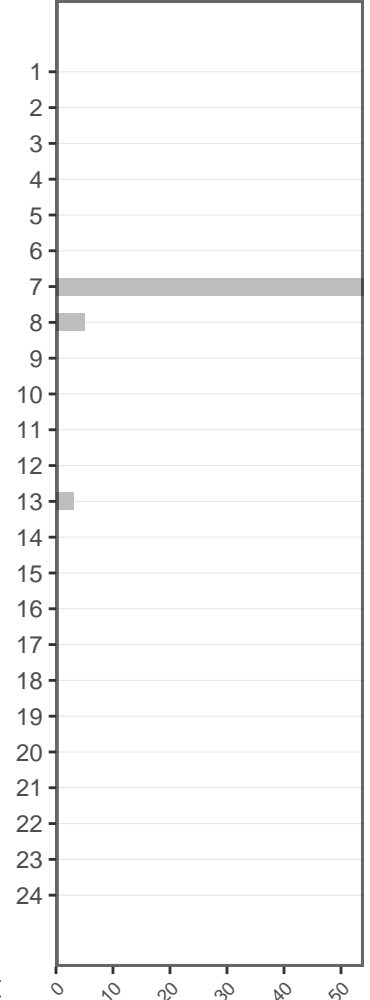
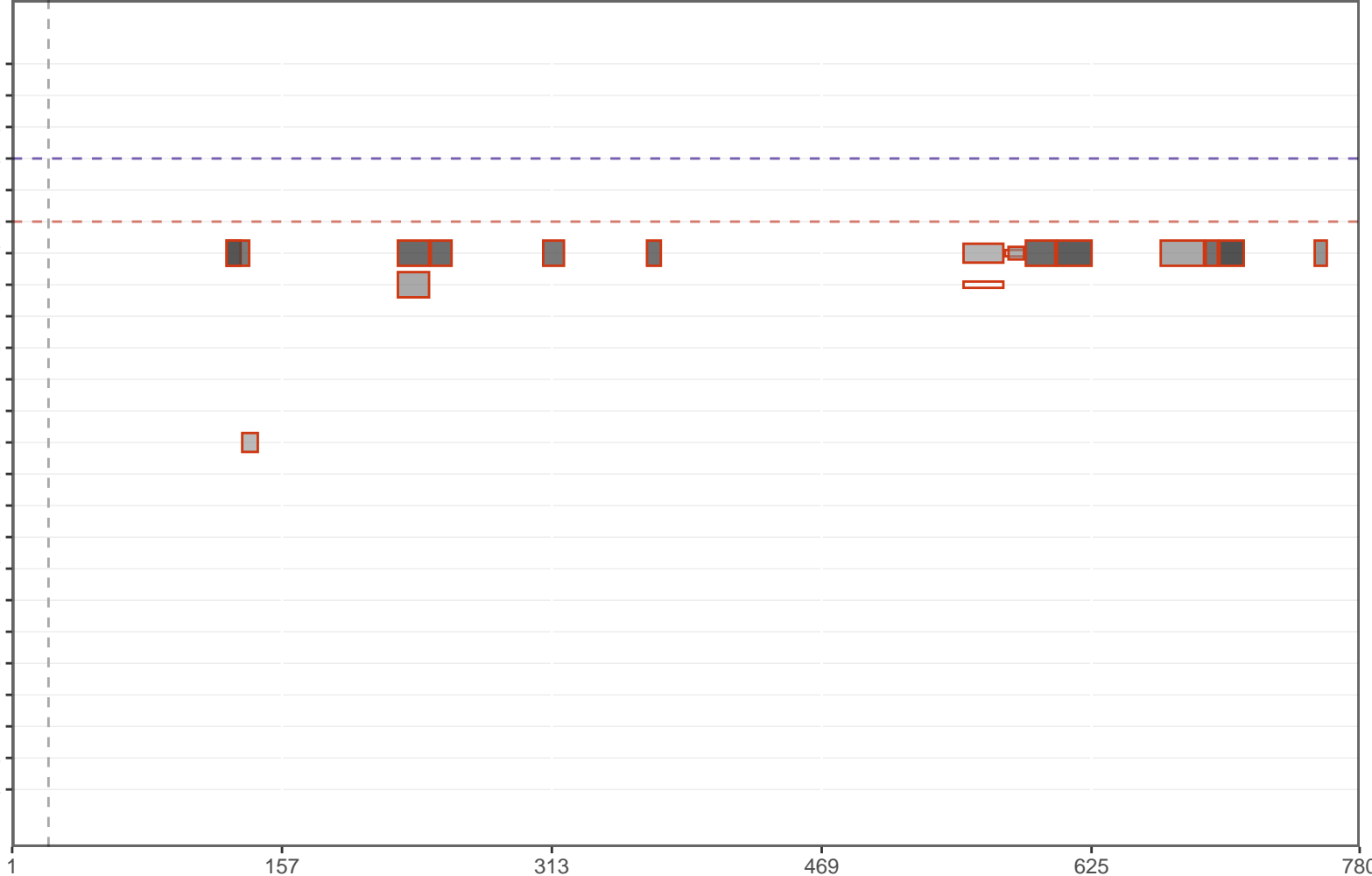
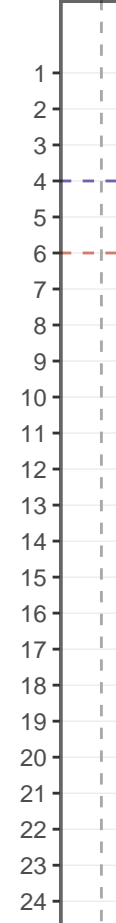
MW indication



Molecular weight

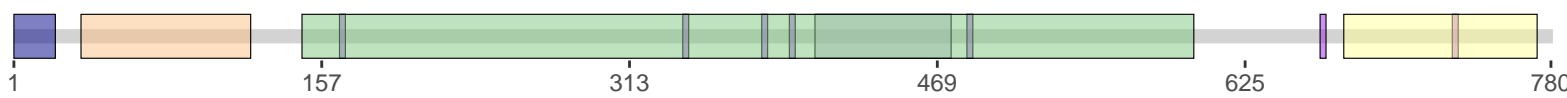


Gel Slice



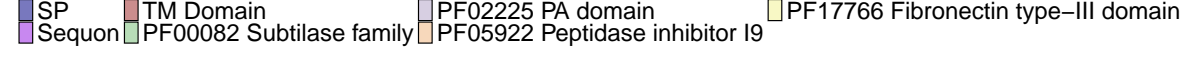
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LYKGRRLSTEKQVSLVYLGANNSSPMPSSLGLEGLDGDADIAQKIVKDRGISPRVQKGVVNDAGGVGMLNTANGEEELVADSHLPWAVGDERGRAIKHYASARNATATLKFLGTLKGRIPSPVVAVFSRGNPFLLEIKPDMVAPGVNIAAATGALGPSBLPTDQRRTNINLSGTSMSCFHVSQIAALLKARHPDWSFAAKSALMTTAVVHDNTYNLSKDSSTATPSTPVDHGAGHNPRAVDPGLVYDGAQDFEFLCTQGLPSGLTVFGKFSNRCTCHSL

NbL13g10850.1 uncharacterized_LOC107782590 [MW = 44.38 kDa]

No. of times detected



log(intensity)



Values from



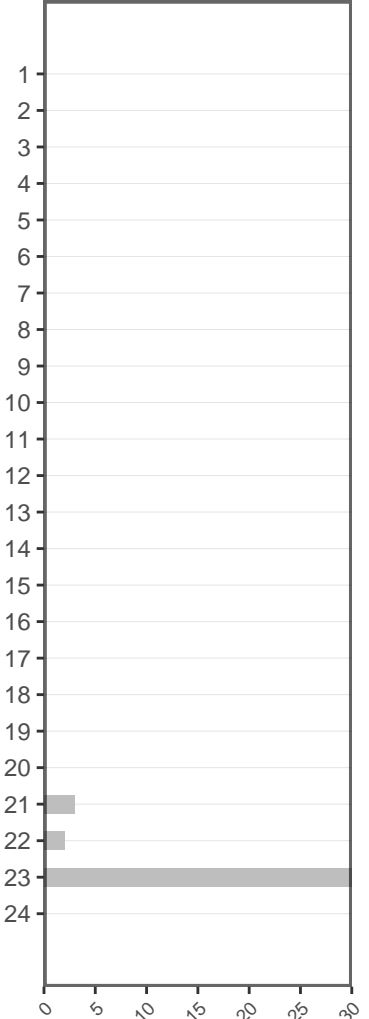
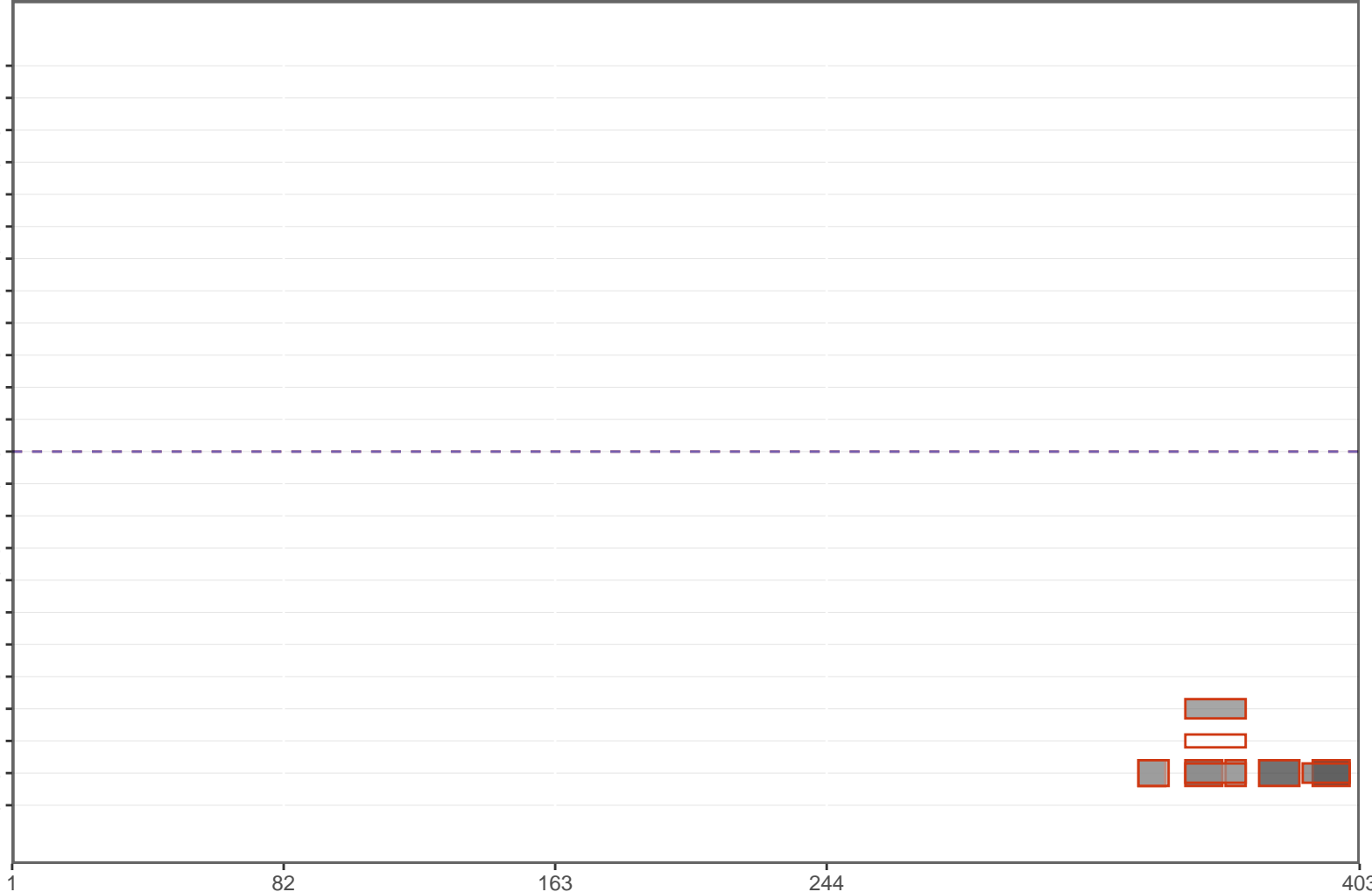
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



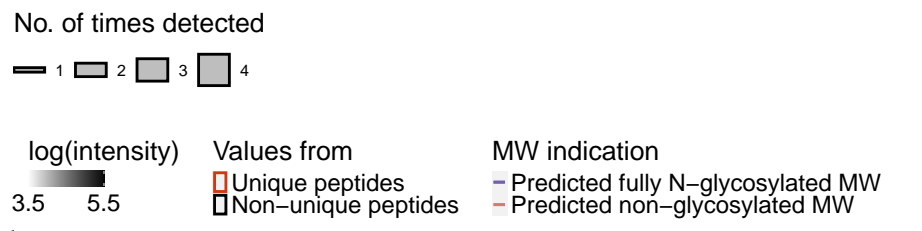
Pfam Description



Protein sequence:

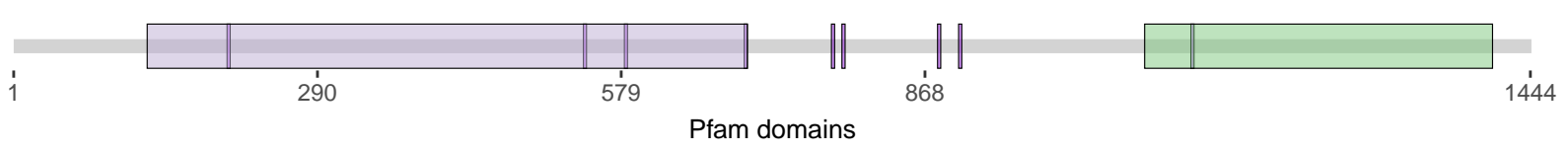
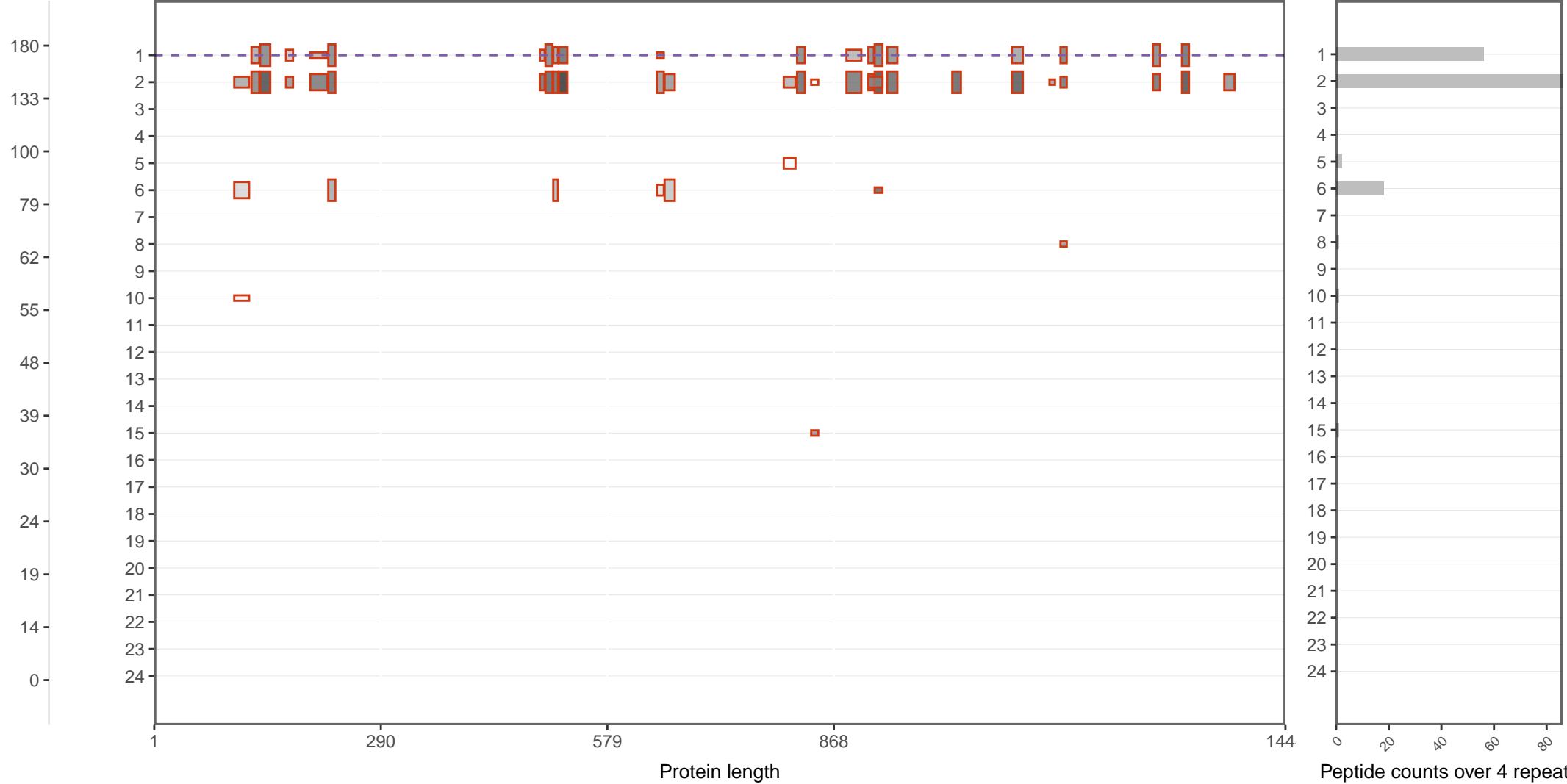
IKARFLQLKAAQCEGRASDTIVNPGTGLVPGNIVTGEPEPDGTRNRMMVWPAKPKPEPEPQTQIDPEPEPDALHPRDLRBLVSLWLGQVSPHKIAFRVLELGMPSLIMNQLMTASASMGAGFSYGGALSEFTARRPRRMVVVRAEAINPKDKKDEAKVDSVIVTELKPLTAVGRQWRSGTFLPLGDGSHVHNKNETGDNVPLLLKKQ*

NbL13g10810.1 cleavage_and_polyadenylation_specificity_factor_subunit_1 [MW = 158.02 kDa]



Molecular weight

Gel Slice

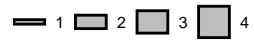


Pfam Description
 SP Sequon TM Domain PF03178 CPSF A subunit region PF10433 Mono-functional DNA-alkylating methyl methanesulfonate N-term

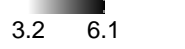
Protein sequence:
 /SVTVPSIFESSKKSIVSAGTLYHDKGPPEPWLKRTSTDAWLSGGMGEANDGADGVTHDGGDVGVCVYENGTLSEFDVNFSGVSVKDFVSGRTHLDTFTIGDPPVNGLKKNTEDVMGPGGKDNANDVKNVVELMMHRWGLYRPFLLGLADGTLGVHAYVFEGAENSKVDSGVSQNSVGLSSTNAGRLRNLRFVRLVPEVYAKEMPSGTPSGRMVFNKNGGSGGLFTGSRPWFVMFRERLRVHPQLGDGPIAETVLIHNNQNHGLIYVTAQGTUKICQL

NbL13g10800.1 ATP-dependent_Clp_protease_ATP-binding_subunit_CLPT1_chloroplastic-like [MW = 26.01 kDa]

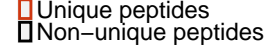
No. of times detected



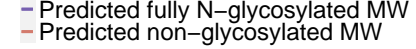
log(intensity)



Values from



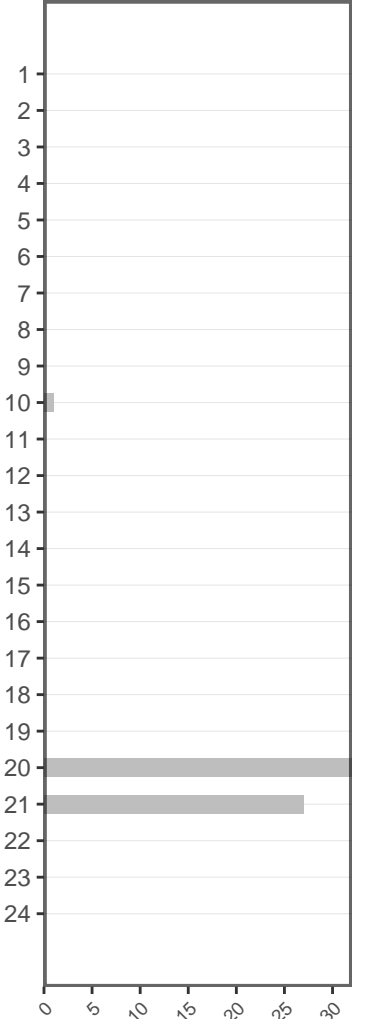
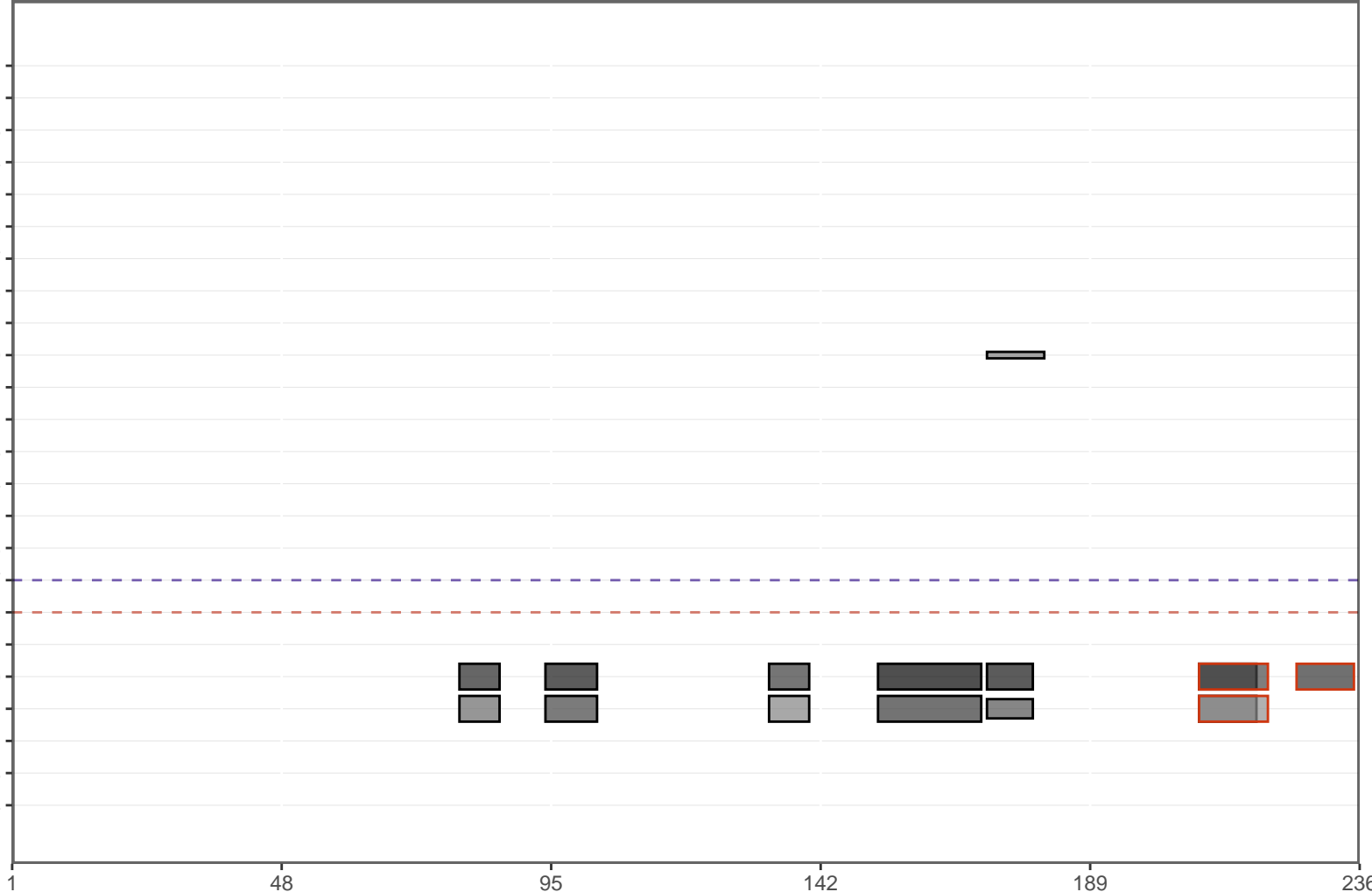
MW indication



Molecular weight



Gel Slice

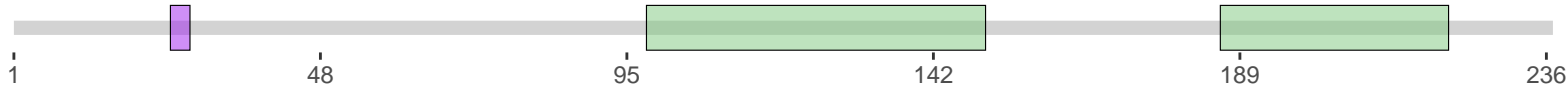


Peptide counts over 4 repeats

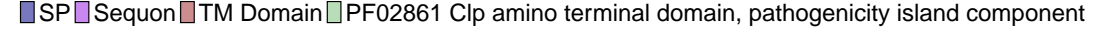
Protein length



Pfam domains



Pfam Description



Protein sequence:

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NbL13g10590.1 21_kDa_protein-like [MW - SP = 18.49 kDa]

No. of times detected



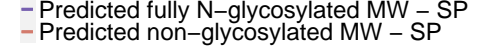
log(intensity)



Values from



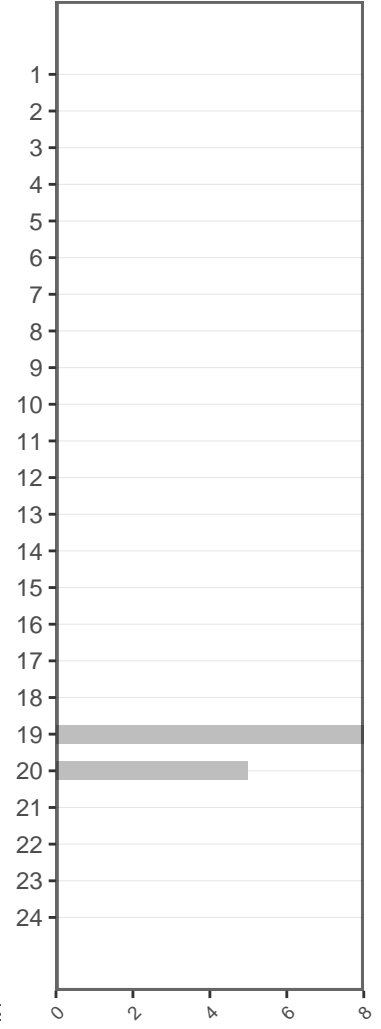
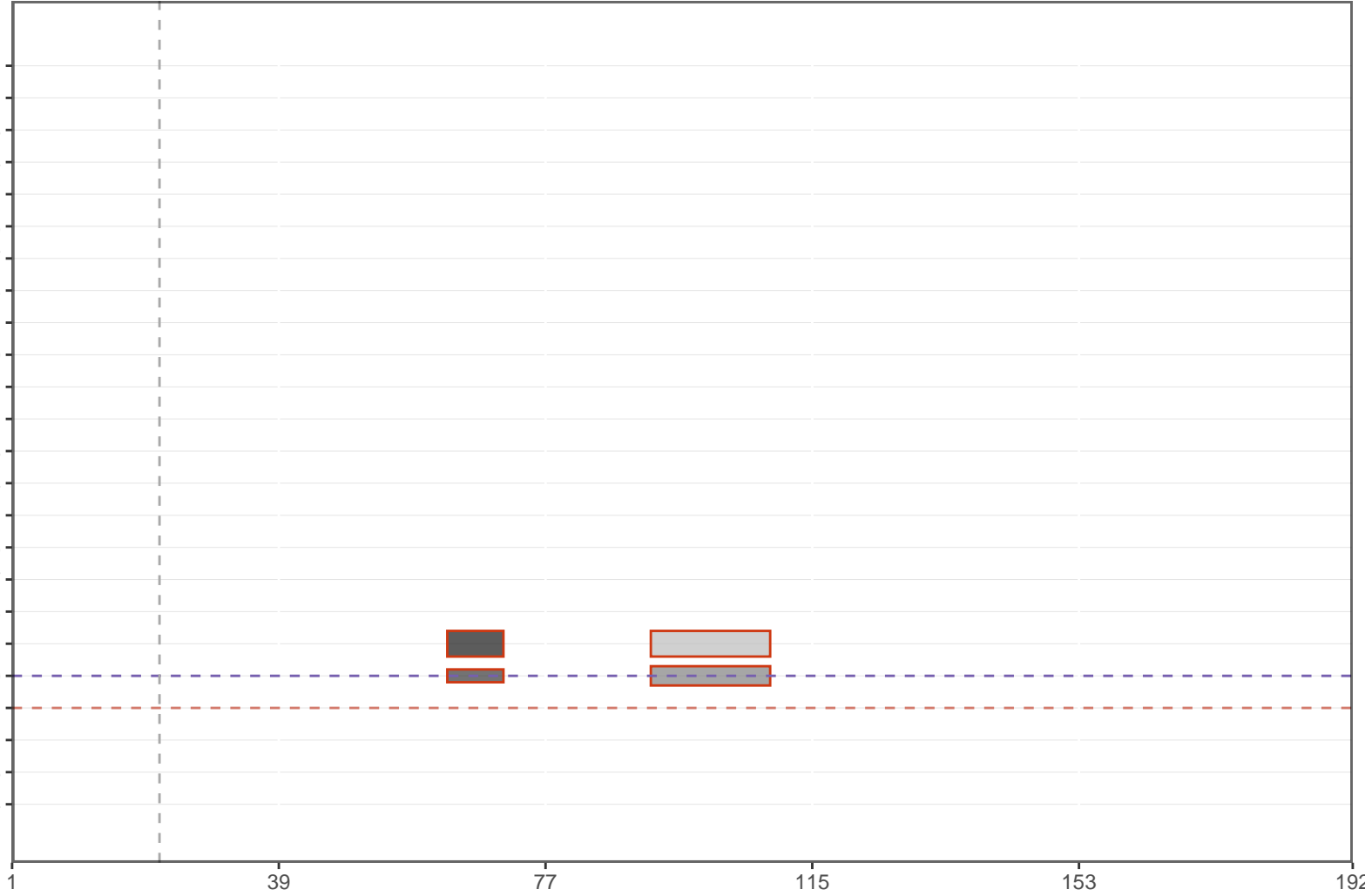
MW indication



Molecular weight

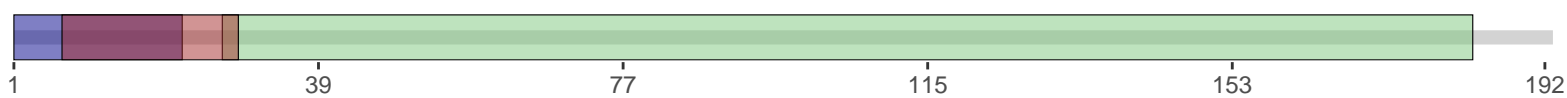


Gel Slice



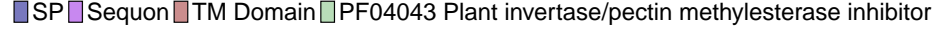
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KFKGLKPREYAAKDCIEETSQVDRLEKGSVELKEVDSRGGKDFLWHVSNVETWVSAATDENTGTDGFAGRALNGRIKASIRNRRIANLADVTSNALALINGVAAKH

NbL13g10550.1 21_kDa_protein-like [MW - SP = 18.58 kDa]

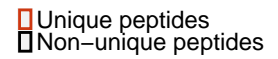
No. of times detected



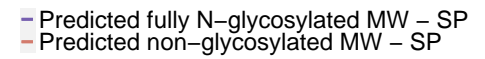
log(intensity)



Values from



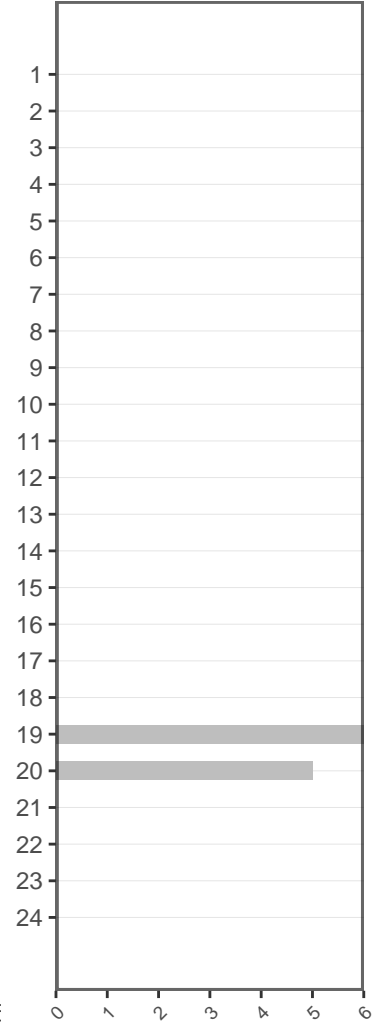
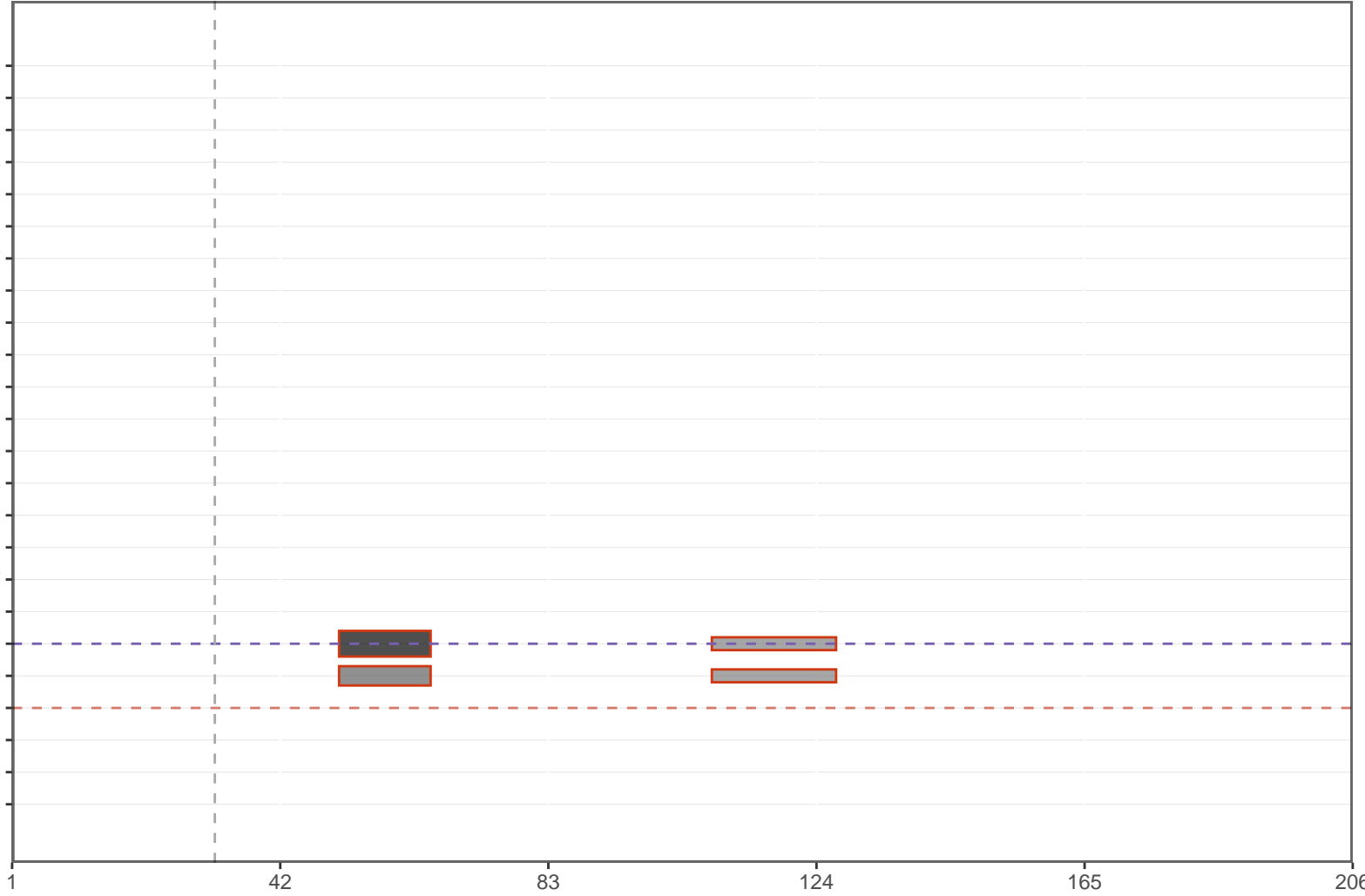
MW indication



Molecular weight

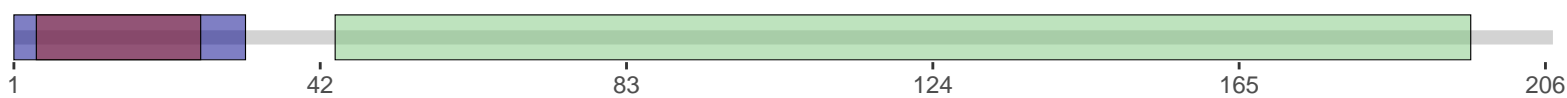


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

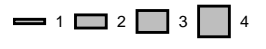


Protein sequence:

AMMLKLAHVRGLTPREVGMHDDVEELSDTVDEMRSKLGEMKQKRGKDFDLKMDNDGTWVAALDDEDTCTEGFAGKVMNGKVKTVVRGKILEVAHITSNALALINSLAAHVA

NbL13g10470.1 monocopper_oxidase-like_protein_SKS1 [MW – SP = 63.57 kDa]

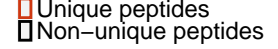
No. of times detected



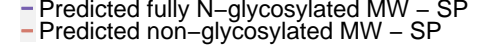
log(intensity)



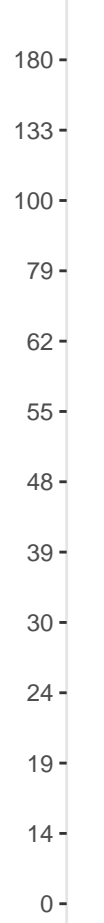
Values from



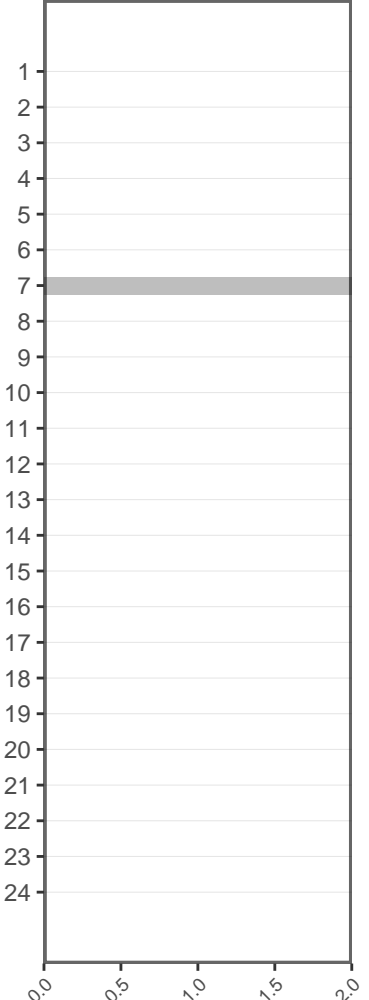
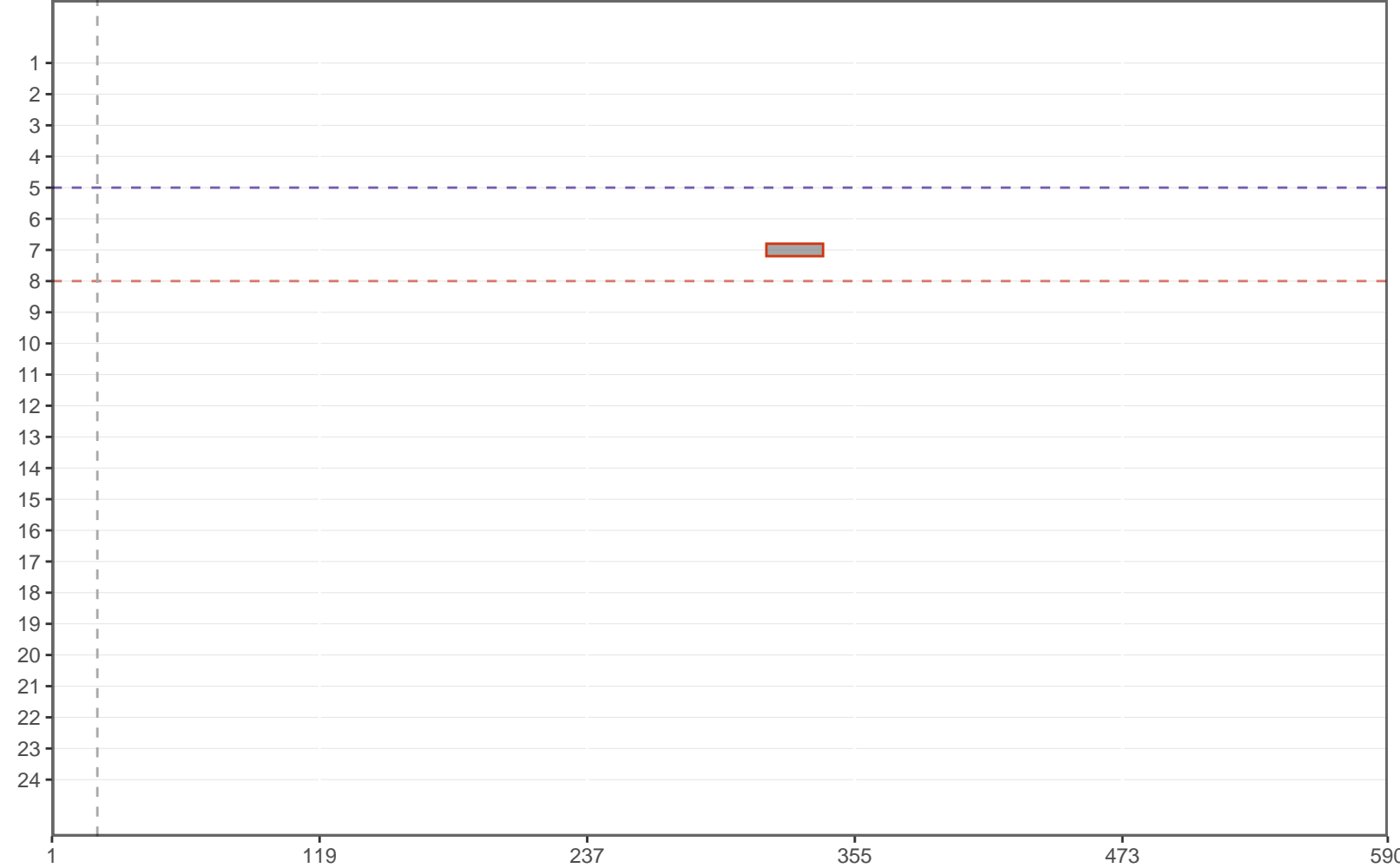
MW indication



Molecular weight



Gel Slice

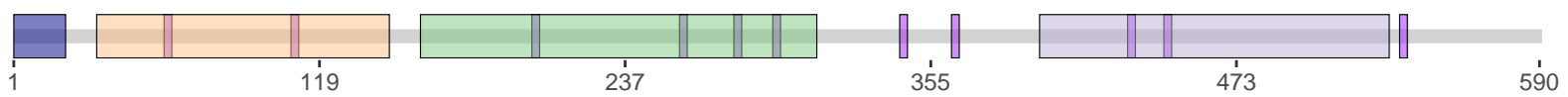


Protein length

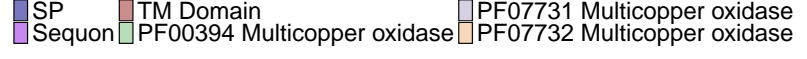


Peptide counts over 4 repeats

Pfam domains



Pfam Description

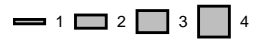


Protein sequence:

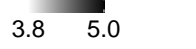
YTVLSPRFVNSLWGVKVTGVAWLHYHNSKGAAGLPDPNDVDTSYALNGMSEIRGNVBAEGARPNDGSPHYGGINVDVYLLKGVPPVVDGKLRATYNGISKNPETPRLADVYHVKGDYKLDFFPKPMNRPPKVDLSLNATYKGRFVILGNNDTAVGSHMDGYSFFVGMGFGEWTEENRGGVNRVWDVIFRSTQVFPGGWTAIMASLDNVVWNLRAENLDRWYLGGETYMRINPEDEHNKTELPVPSNALYGGALASKGPKKSAATIFRSEEM

NbL13g10450.1 acid_beta-fructofuranosidase_AIV-18-like [MW = 72.59 kDa]

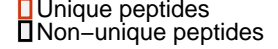
No. of times detected



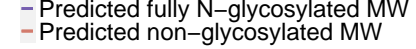
log(intensity)



Values from



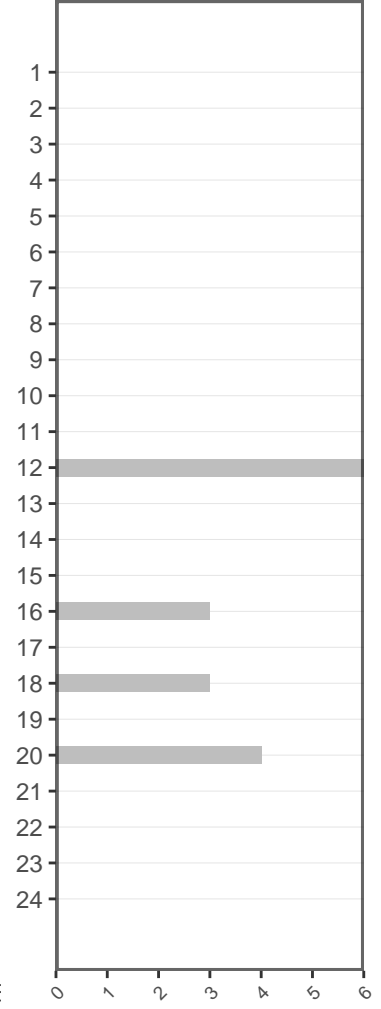
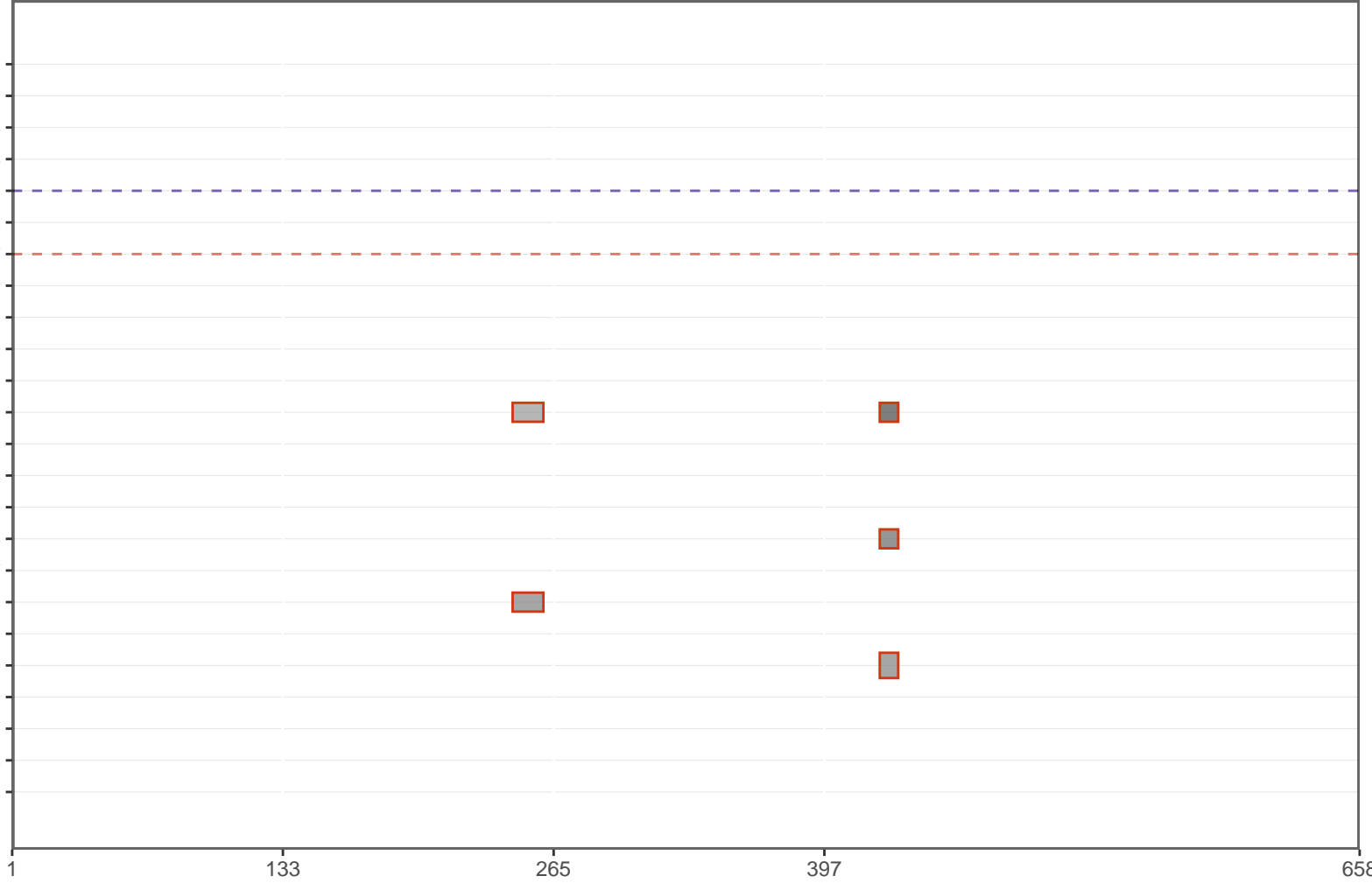
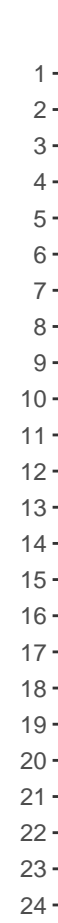
MW indication



Molecular weight

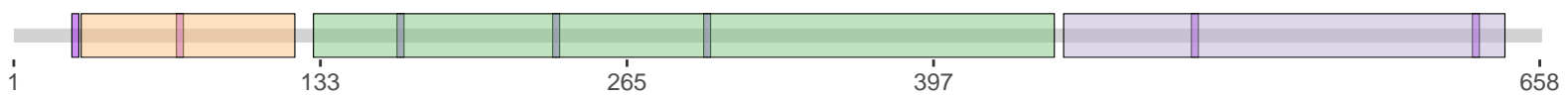


Gel Slice



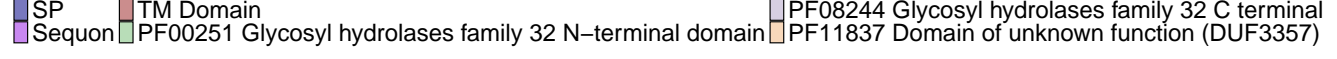
Protein length

Peptide counts over 4 repeats



Pfam domains

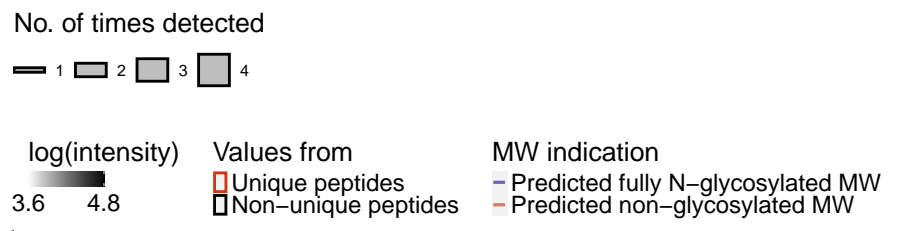
Pfam Description



Protein sequence:

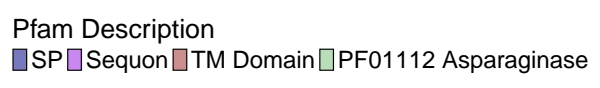
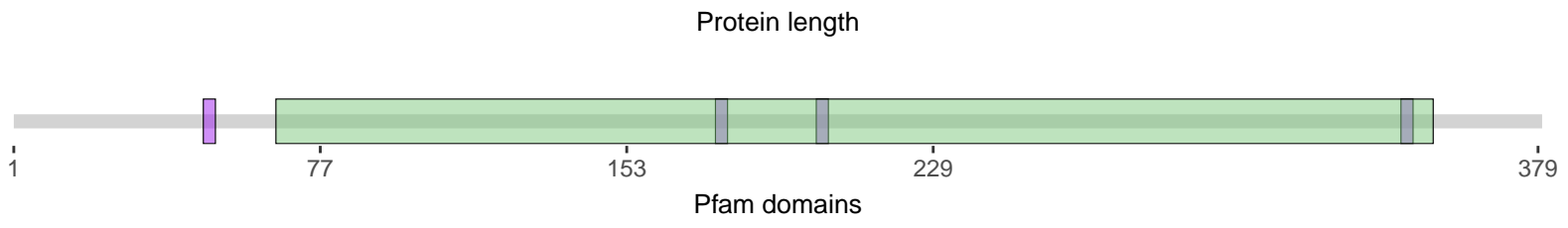
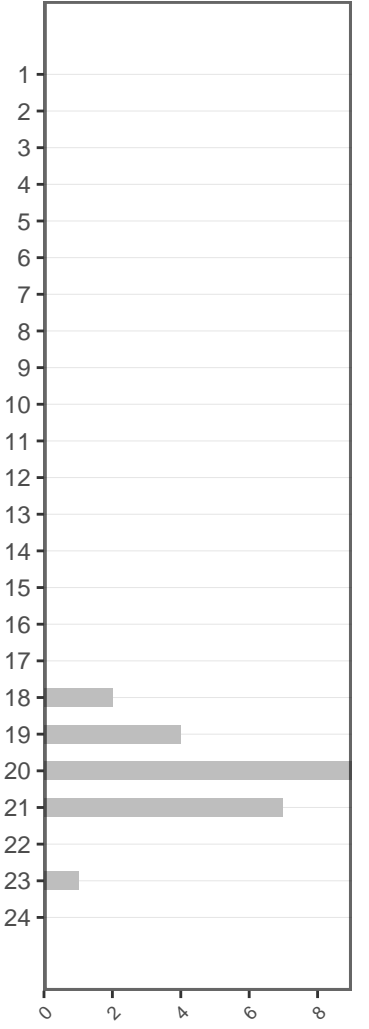
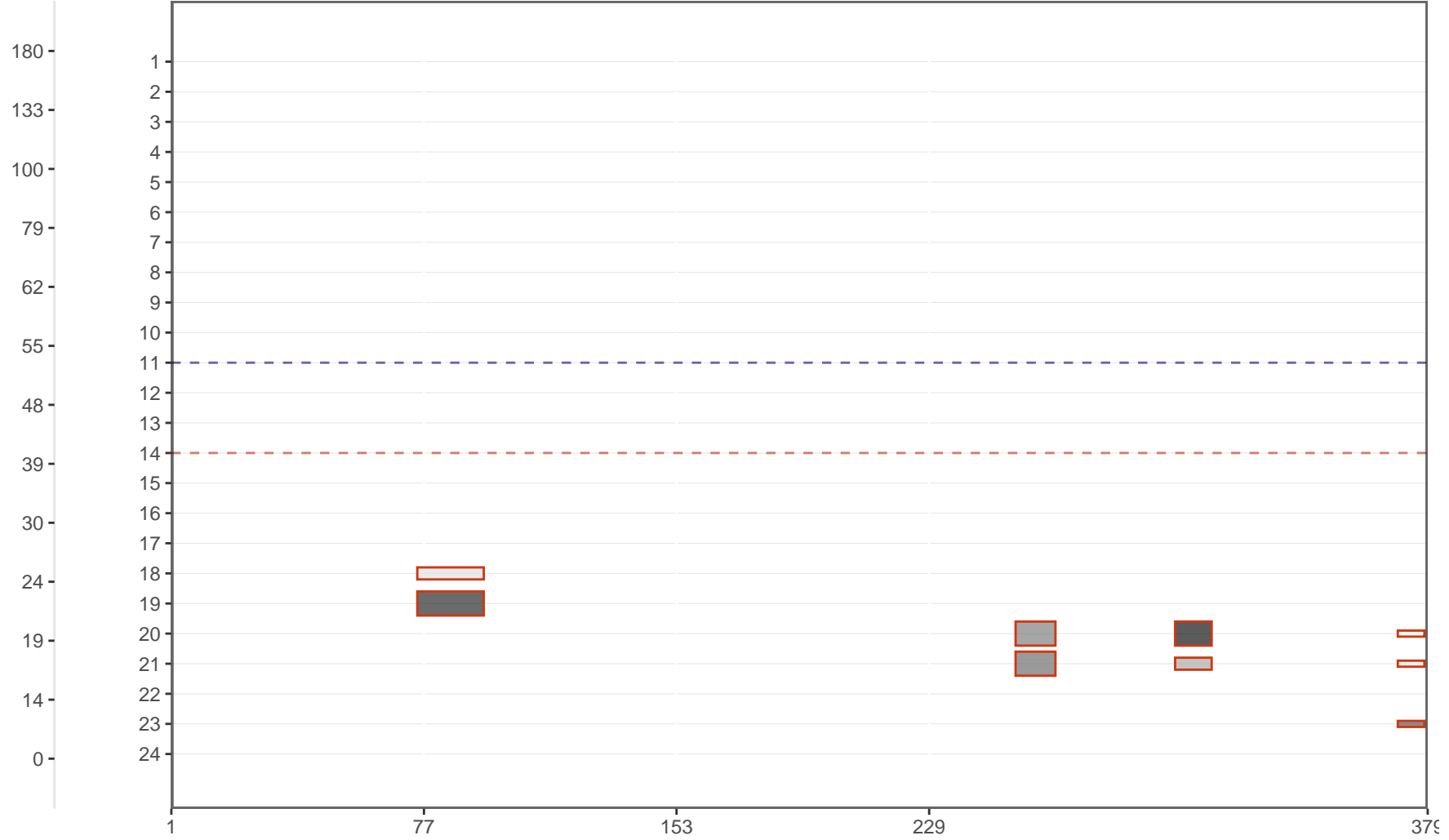
GTGMWECVDFYFVSTVEANGLDTSYNGFGKHVLSKSLDDKHVYAGTVDPKWTFDNPPELVVDGRLRVDGKYAASKTFYDPKEQRRLWGWIGETDSEAAQLLKWASVGSFRTVLDKETRTHVLDGWPKEIESLRNGDPMKQVNLGPGSELVHVDAAQLDVEASFVDDKAALEGTEADVDFNCGTSGGAANKRGLGPFQVVAADQTLSELTLYVYAKGTDGRAETVFCADETRSGSEAPGWAKVYVGSSEVPLDGEKHSMRLVHISIVESFAQGRRT

NbL13g10120.1 probable_isoaspartyl_peptidase/L-asparaginase_3 [MW = 40.51 kDa]



Molecular weight

Gel Slice



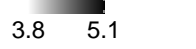
Protein sequence:
 SVSETEKVMKYKENFGQRFNFWNVSPGDNGRPHVHPNGPBGKGLMANELQPNFSGVNVGLHSHDTISMVDEIGRIAWGTSTNGATLKIPRIVGDDGPIAGSSAYADSEVGCAGATGDDGMMRFLPCYQVYVESMRLGMEPKLAAKDAISRARIARKYQDFGALFAVNRSGHAGASHGWTFGYVSRNPNMGKDEVEETVHP

NbL13g10040.1 ATP-dependent_6-phosphofructokinase_4_chloroplastic-like [MW = 64.33 kDa]

No. of times detected



log(intensity)



Values from



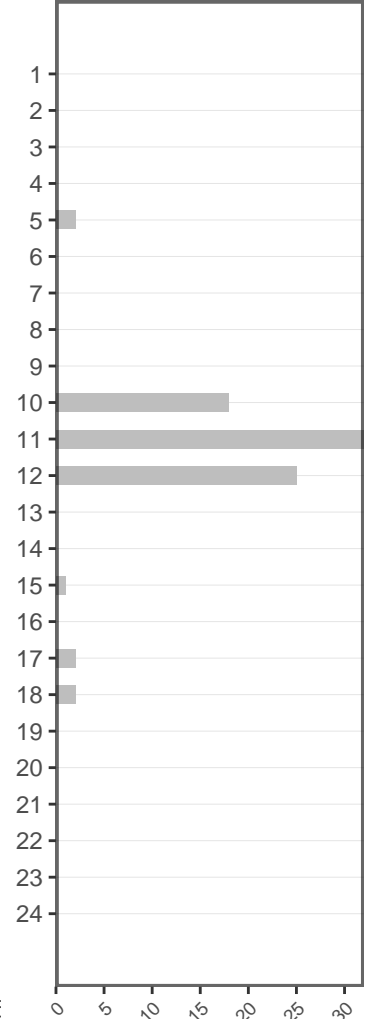
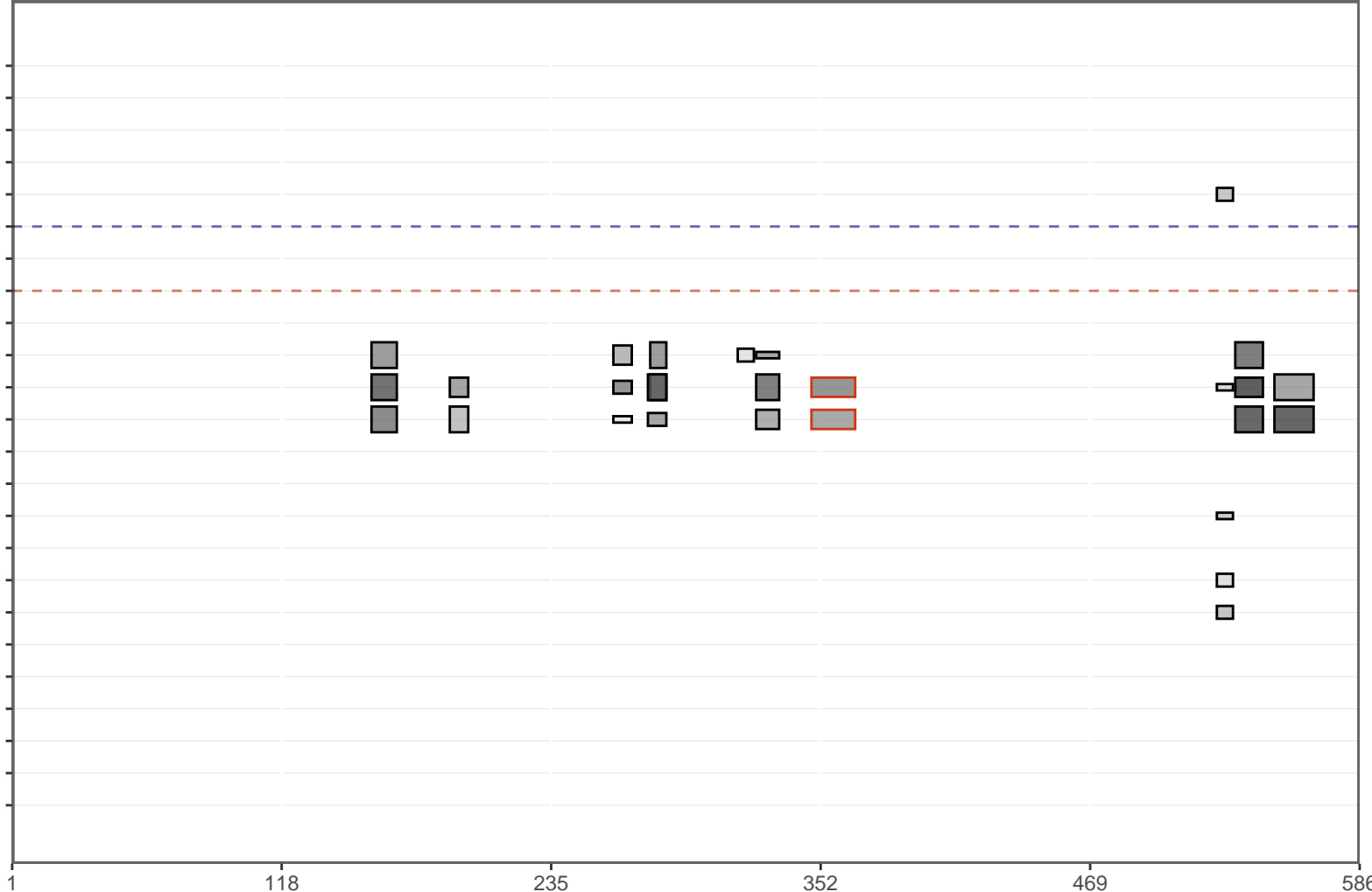
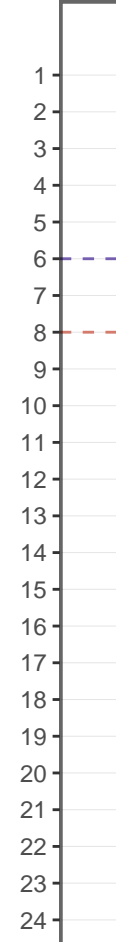
MW indication



Molecular weight

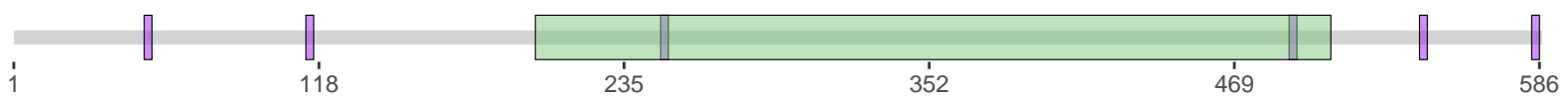


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

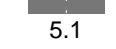
DNIQDRGINQYIIGGGDTQKGAAYKVEKRGKIKVAAGIKPTIDNDVAIDKISFGDFAVEEADRANAAHVEAESMDNGVQIKLMGRYSGFAMLATLGNRRVDGGLPESSFFLEGGPGLYEVYEQRLKENGHVLVLAEGAGGGEYVAQSMGAFQEKDASGNRLLLDVGLWATQHKIDHFTNRIMTKMAYIDPTVMIRAIPIASNDINQVTLLAGSAVHGAMAGFTGFTVGPVNSRHAYIPDRVETETNTVNLFGRMWARLLASTNPFQDFGDSQAVRGSVQKQTDIAI

NbL13g09900.1 protein_mago_nashi_homolog [MW = 17.79 kDa]

No. of times detected



log(intensity)



Values from



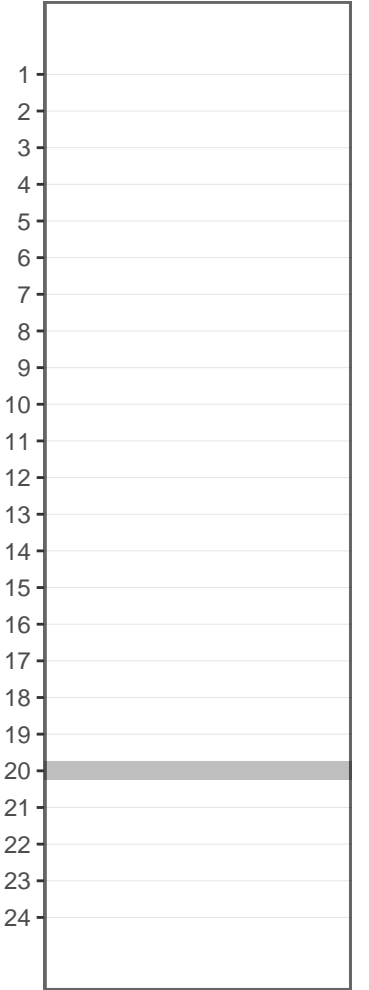
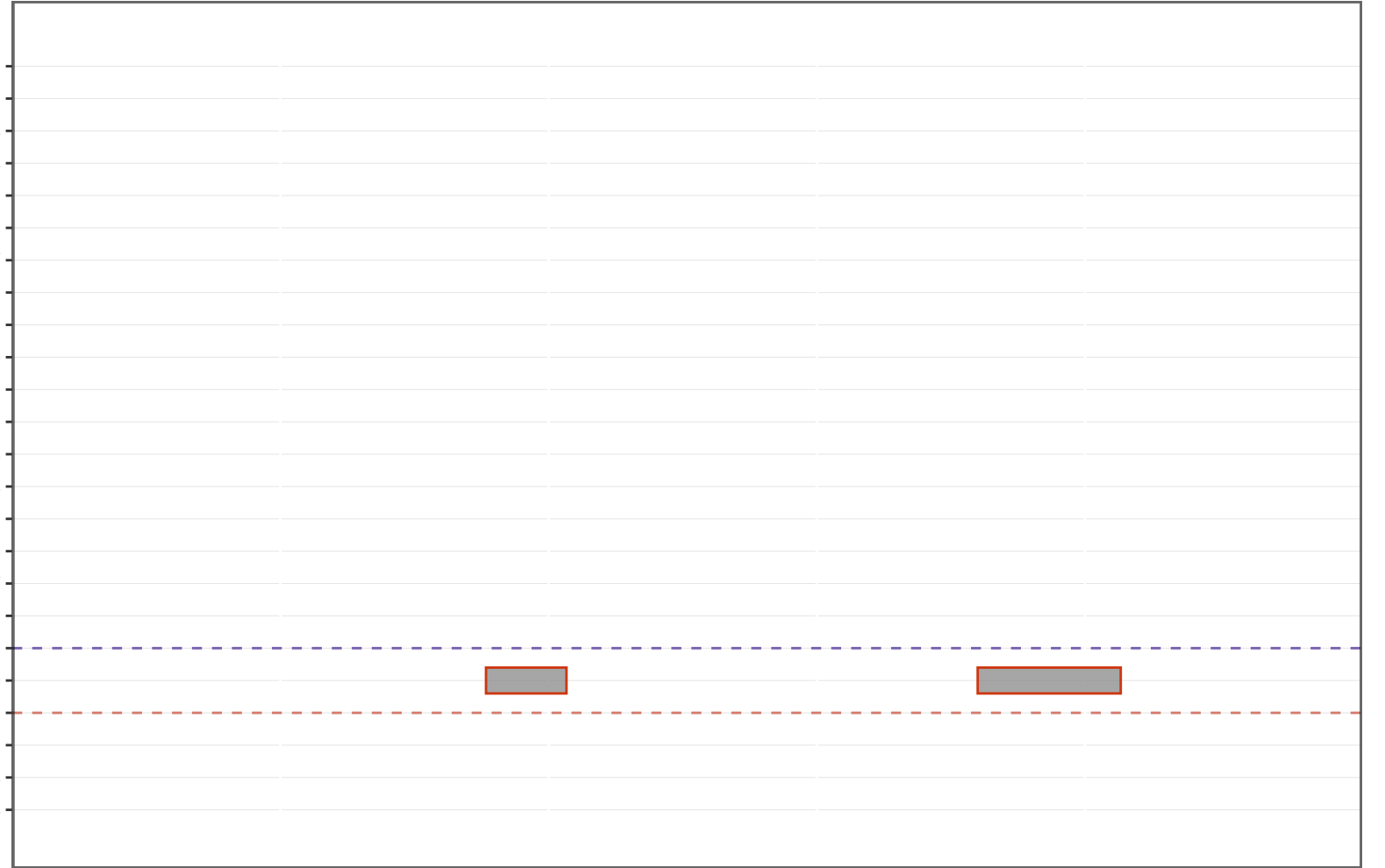
MW indication



Molecular weight



Gel Slice

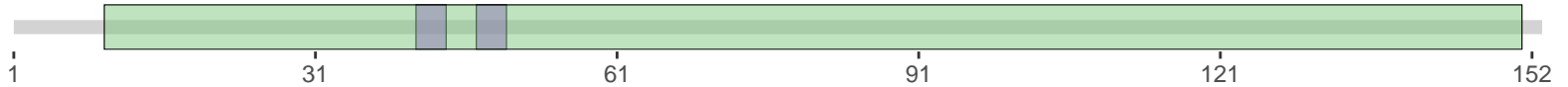


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ILKECRRIVADESIIMKEDDNNWPEPRDRVGRGLEIIVMGNEHSFTTSKIGSLMDVGTENDPEGLRIFYYLVGDLKGFVFSLSLHFNIKPI

NbL13g09890.1 peptide_methionine_sulfoxide_reductase_A1-like [MW = 28.76 kDa]

No. of times detected



log(intensity)



Values from



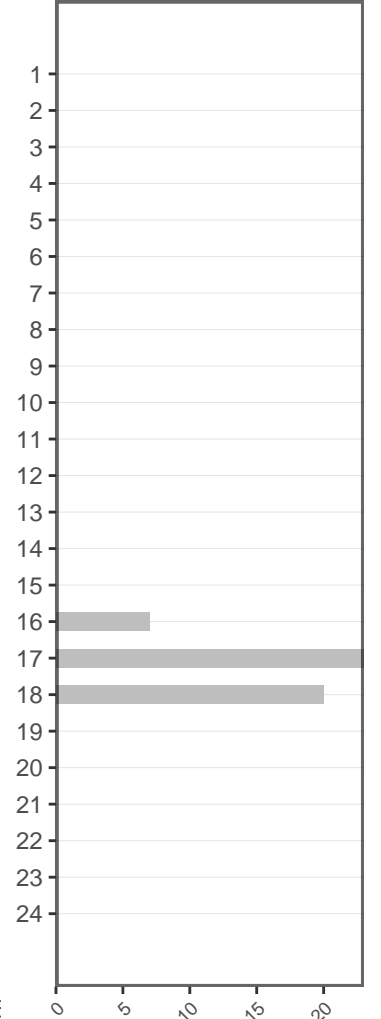
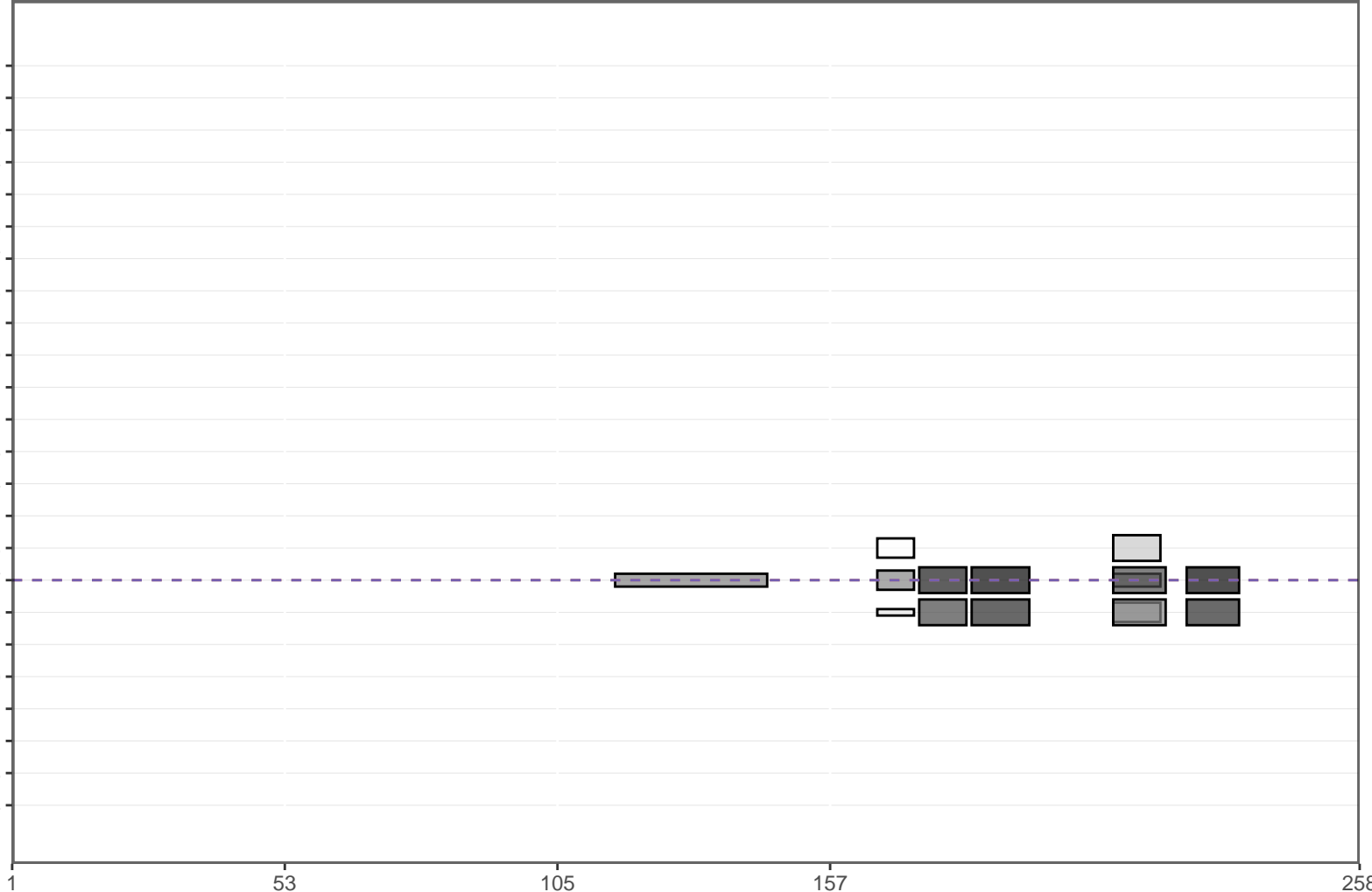
MW indication



Molecular weight



Gel Slice

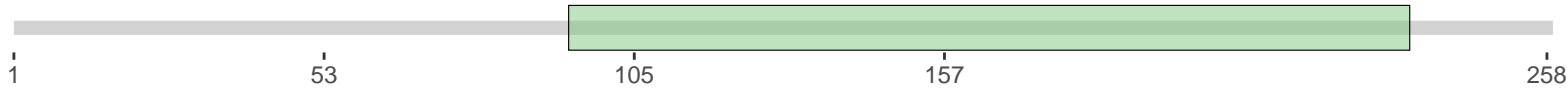


Peptide counts over 4 repeats

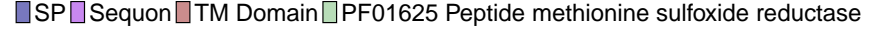
Protein length



Pfam domains



Pfam Description



Protein sequence:

EVGYTGQYLINPQSVEDGSGGTFRHSSEWRVQVDPKECNFDLLQVFWDRHDPFLNRQGNVDGTVYRSGIYFTPEGEKAAIESRDKGQKILNRNIVTELPAKKEYRAEYHQGYLAKGGRFGRSTKGNDRPRQVQ

NbL13g09800.1 glutamate_dehydrogenase_A-like [MW = 44.82 kDa]

No. of times detected



log(intensity)



Values from



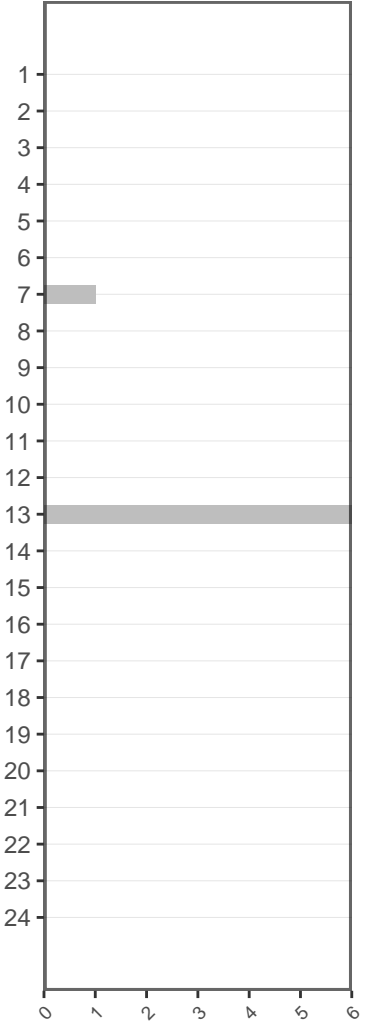
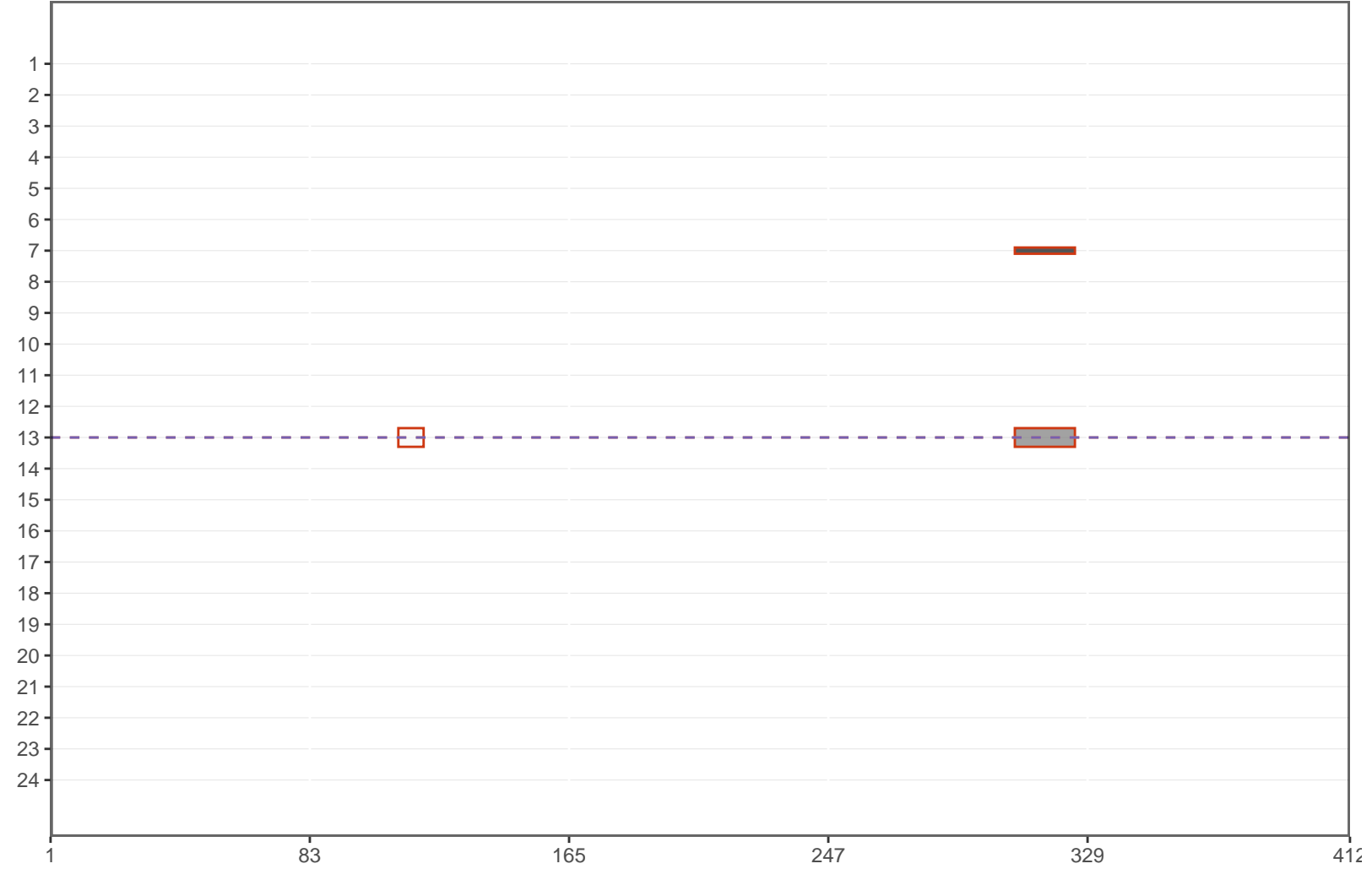
MW indication



Molecular weight

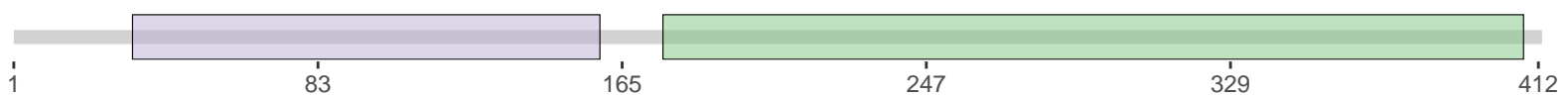


Gel Slice



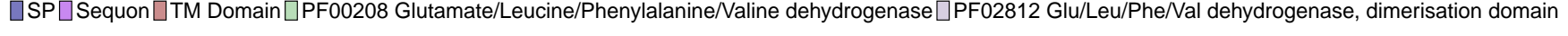
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

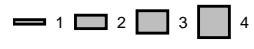


Protein sequence:

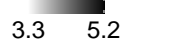
EALLAEYGNKIKLTFAGDGFNGVGAWAGKIHERRGGKVAVSDITGAIKNPNGLDIPALLNHRKRTGKLTDFNSGDVMNSDELLTHECDVLPICALGGVLLNRENADHYAKFEEAANRPTDPADEILSKKGVVLPDIYANAGGVTVSYFEVWVQNGDGFMDDEEKVNAELUKYMTAFHNLKSMCHSHNGLRMGAFTLGVNRRVARATQLRGWEA

NbL13g09770.1 polyadenylate-binding_protein_1 [MW = 25.58 kDa]

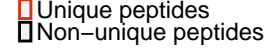
No. of times detected



log(intensity)



Values from



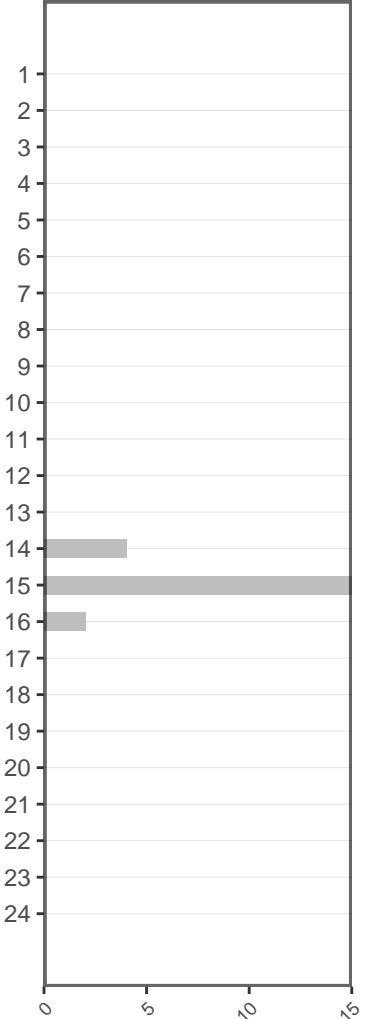
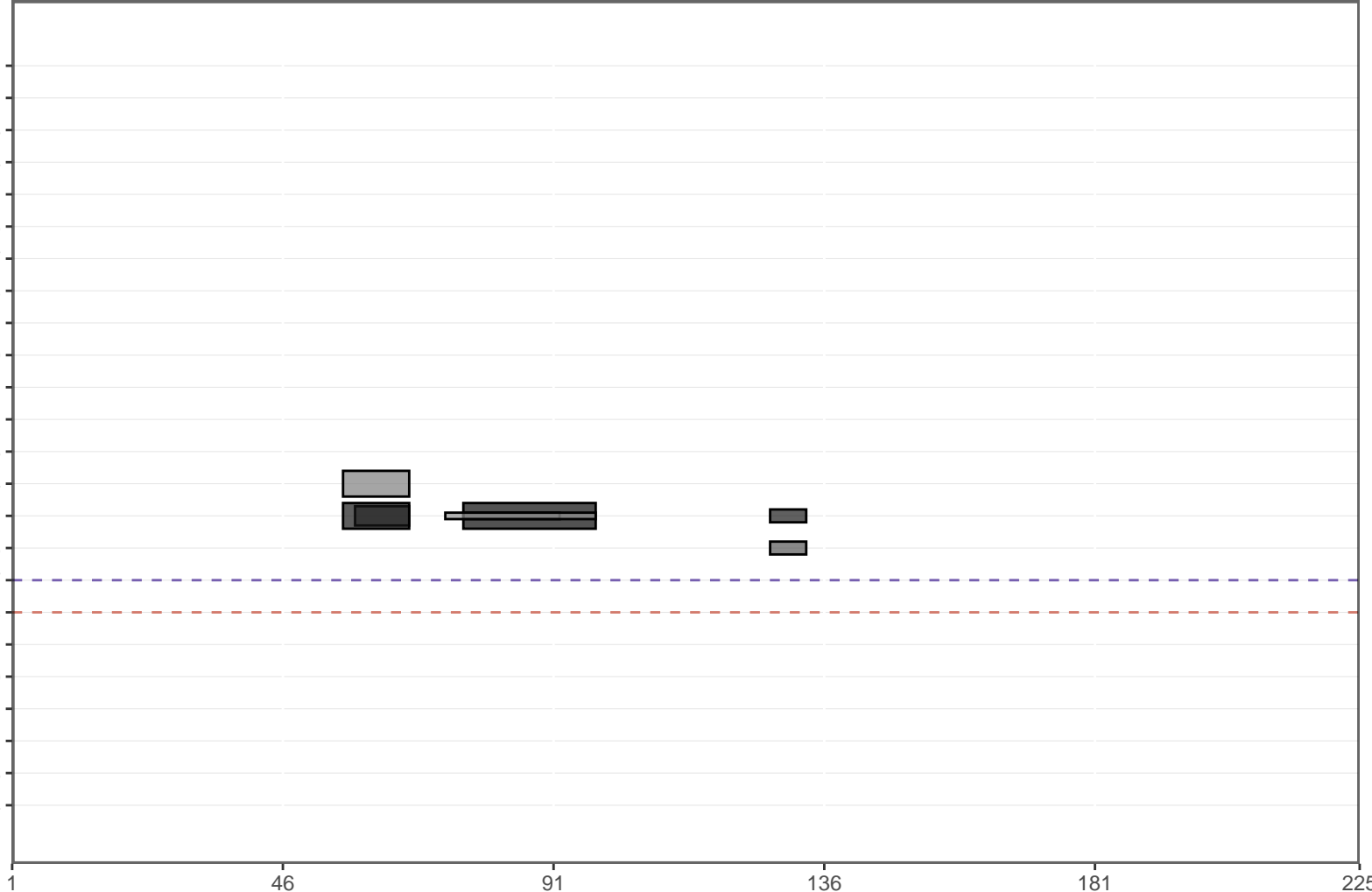
MW indication



Molecular weight

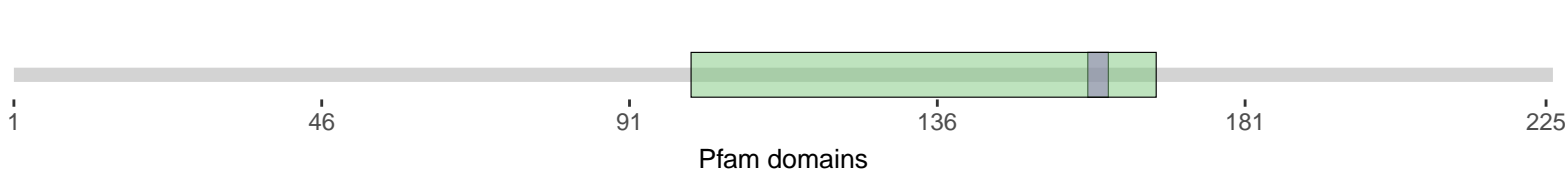


Gel Slice



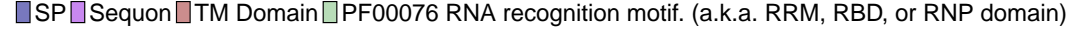
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

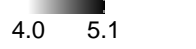
SIVYGNVDYACTPEEEVQGHFQSGGTVNRVILTDKFGQPKGWAYVEFEVEAVQNALLLNESELHGRGLKVSARRTNPLGLKQFRGRFRNFWAGFRPRRRFMPGAPVFPFPGFRPRFRPTFRVRYV

NbL13g09730.1 putative_pterin-4-alpha-carbinolamine_dehydratase [MW = 23.23 kDa]

No. of times detected



log(intensity)



Values from



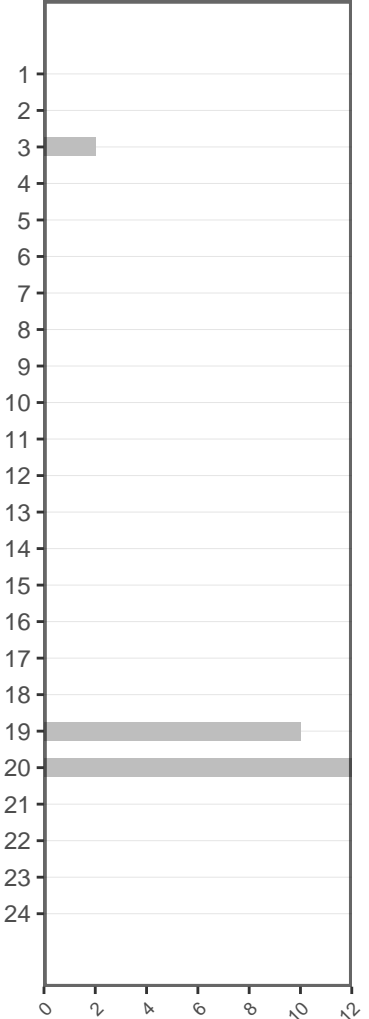
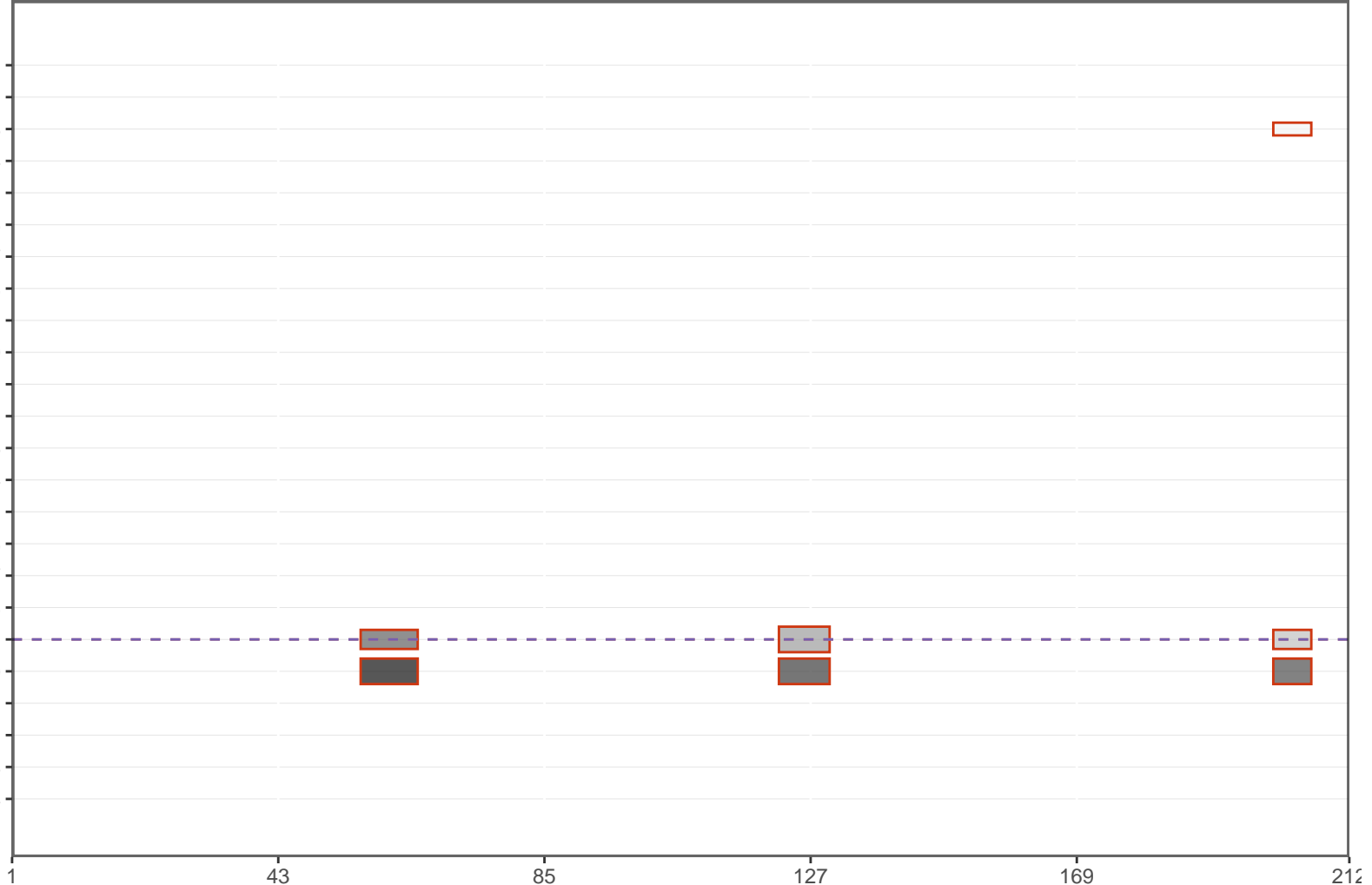
MW indication



Molecular weight



Gel Slice

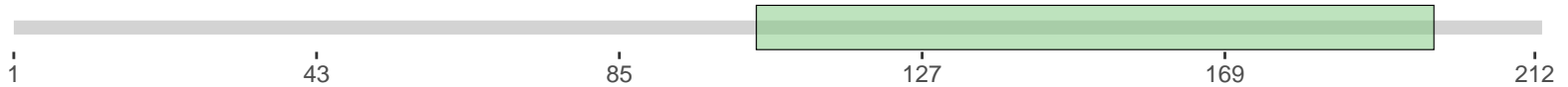


Protein length

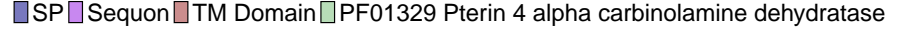


Peptide counts over 4 repeats

Pfam domains



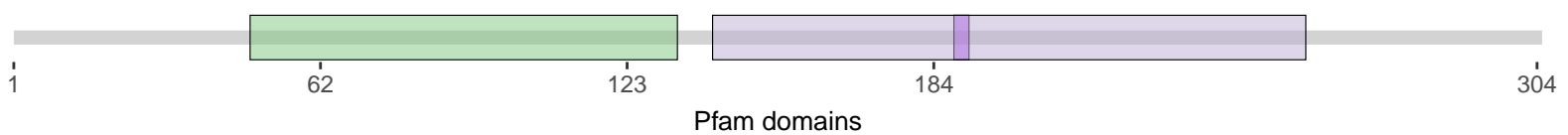
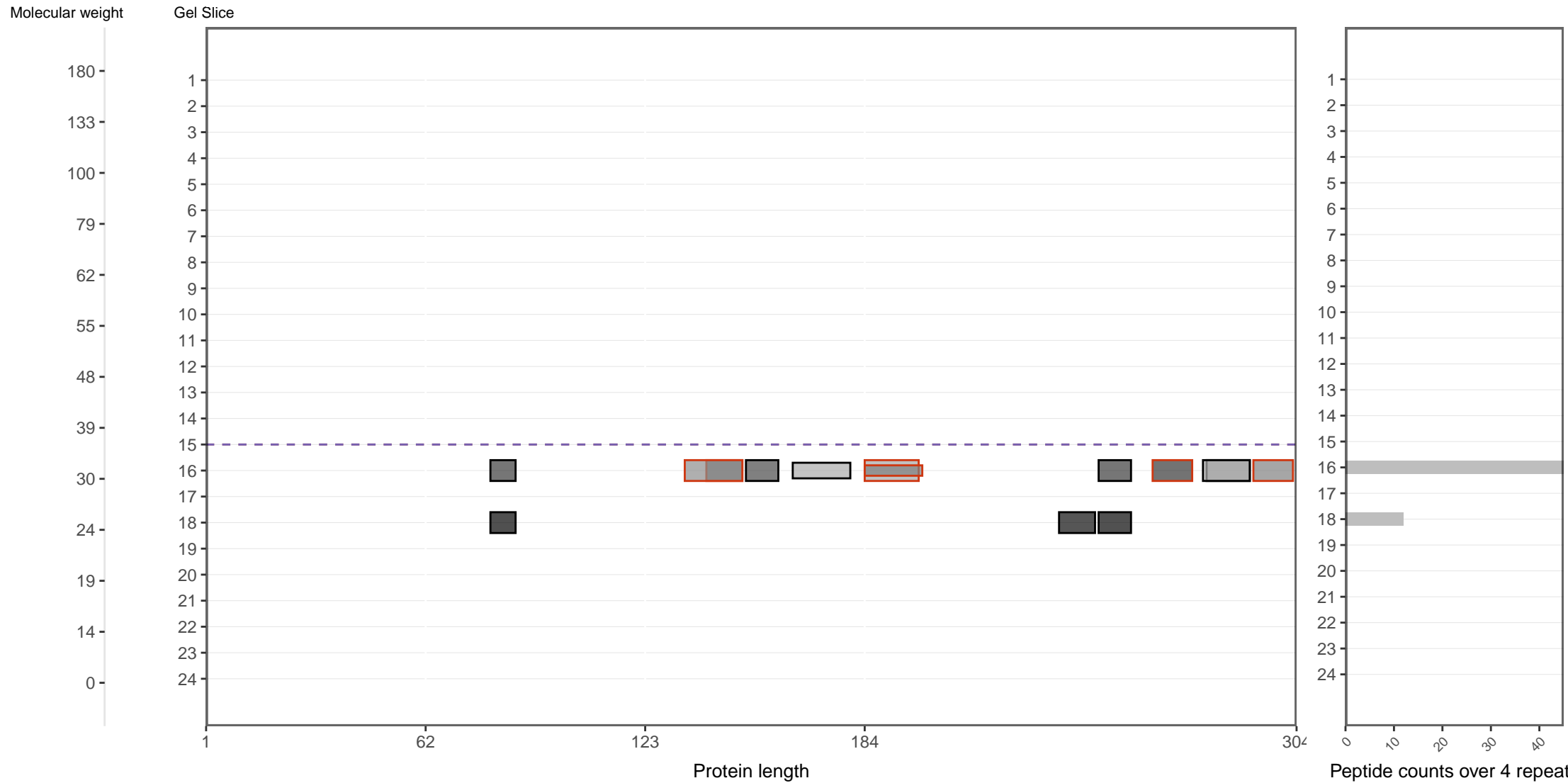
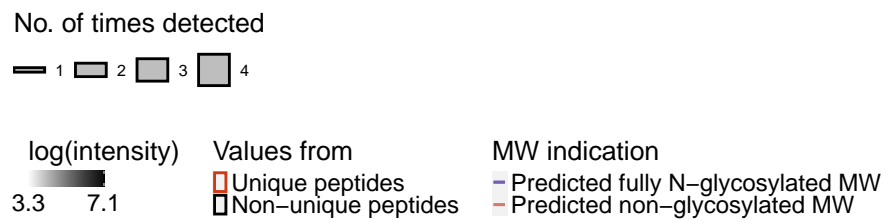
Pfam Description



Protein sequence:

IACIVISPGQTPLSSEVEARGLLFKVVGWRLAHEHGVKLGKGGTWWKLRDFEGGVVELINRIGKVVVEGTGHVPTLLHLEGSNGVRAELWTAEGGLSINDFVAAKIDQIKTSDVPRKRWWA

NbL13g09710.1 superoxide_dismutase_[Fe]_chloroplastic [MW = 34.78 kDa]



Pfam Description

- SP
- Sequon
- TM Domain
- PF00081 Iron/manganese superoxide dismutases, alpha-hairpin domain
- PF02777 Iron/manganese superoxide dismutases, C-terminal domain

Protein sequence:
 IKPSGELFELNIRDFGFEAFVKEPKAAATQFGSGWAWLAKYKANRLVGNATNPHPSNEKLLVVKTPNANFLWDPSPLLTDIWEHAYLDFRNRRPDIYSIFMEKLVGWEAVSRLEVAKAKQAVEREVEEERKREVEEYKAGGEVREMVMVESTDSDAE*

NbL13g09610.1 quinone_oxidoreductase-like_protein_2_homolog [MW = 37.02 kDa]

No. of times detected



log(intensity)



Values from



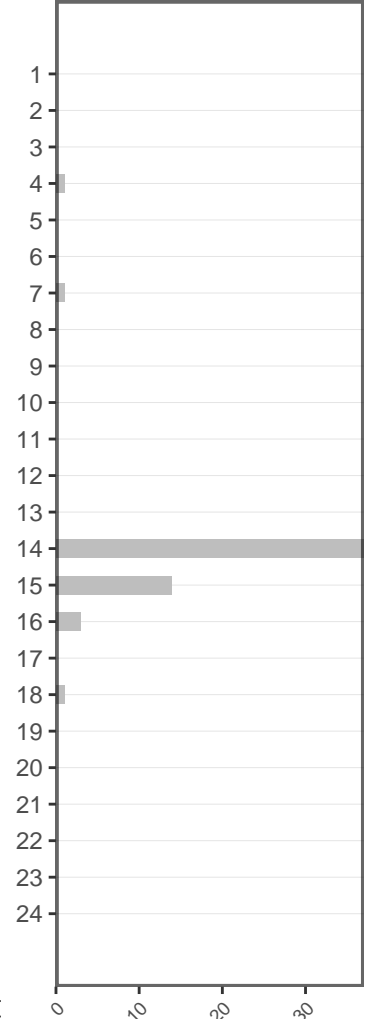
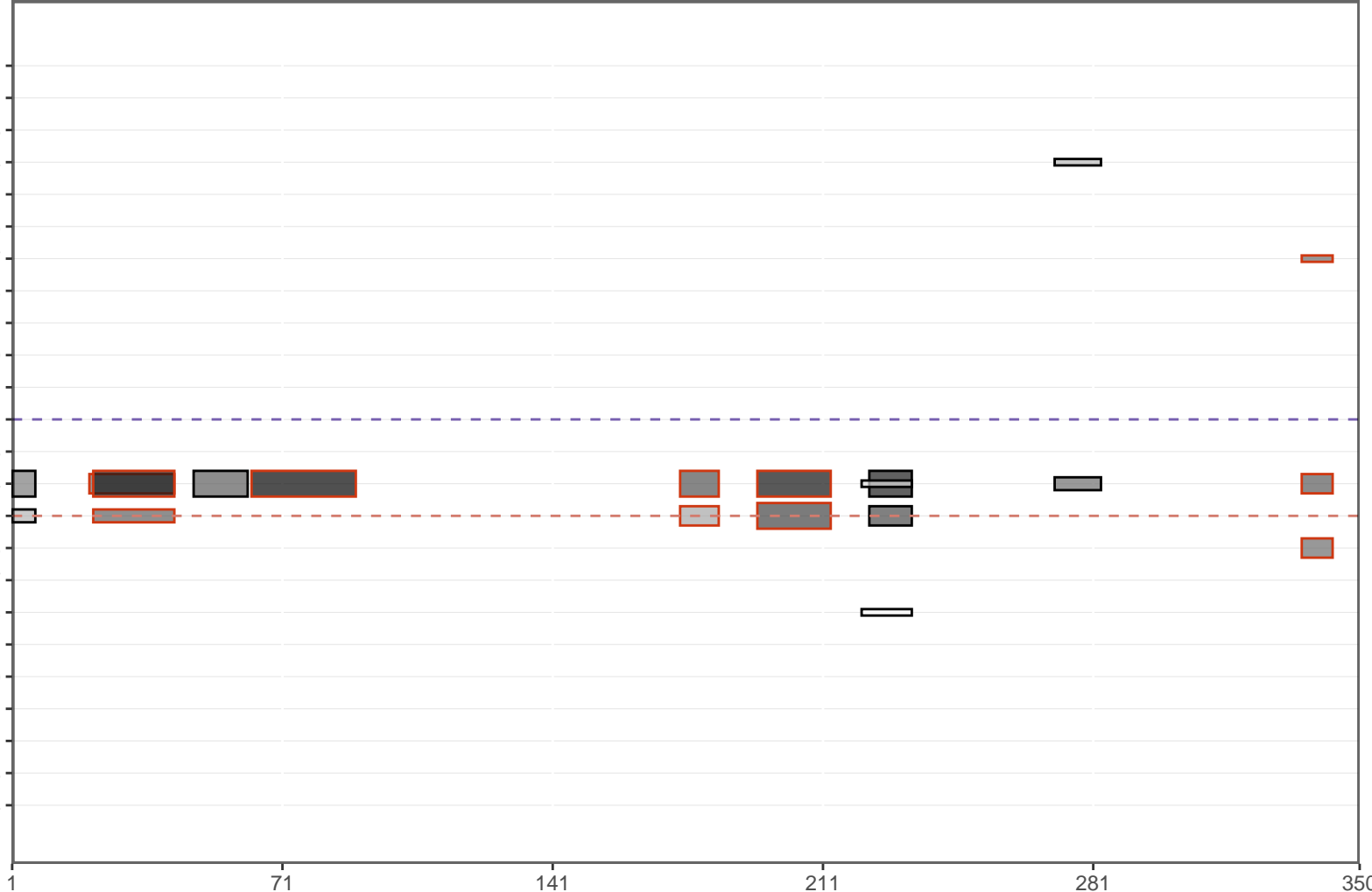
MW indication



Molecular weight



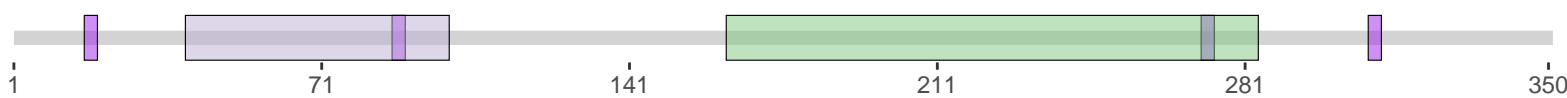
Gel Slice



Protein length

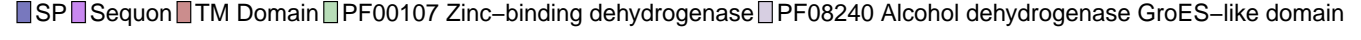


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AGGVLSAVQIGKVGATVWARQNEKVFQFLKSLGVDHVVQLSNANVIESAKGFLKSRKLGVDVYDPVSGKTKDEMQLLNWGAQILVIGFAGGEPVPIRANALKNKWTHTGLVWGHSHKYQPNVLGDLTELLWLSNGLTINISHFLAEHLAFTAKDRRAIKGVMTFFDGRTLKELV

NbL13g09550.1 polygalacturonase_inhibitor-like [MW – SP = 34.4 kDa]

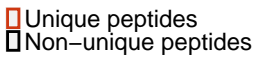
No. of times detected



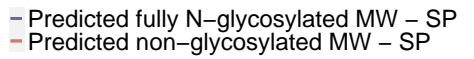
log(intensity)



Values from



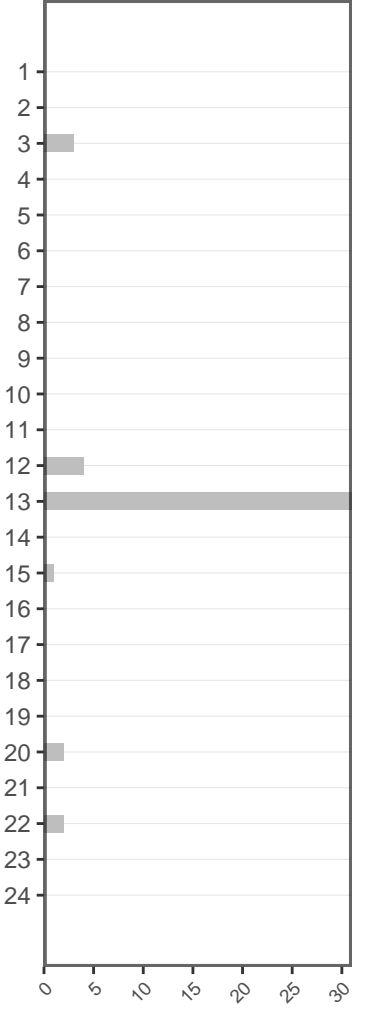
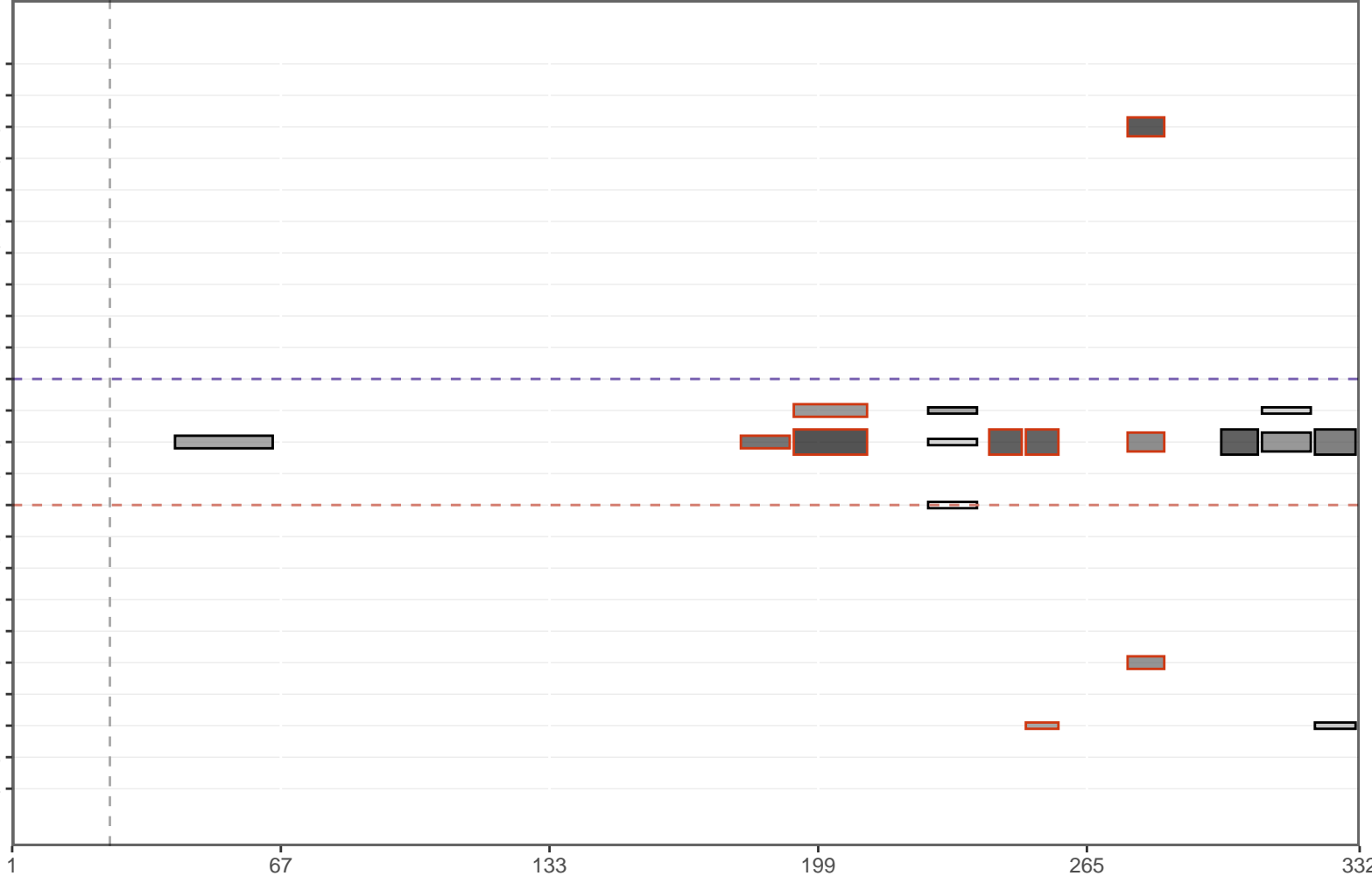
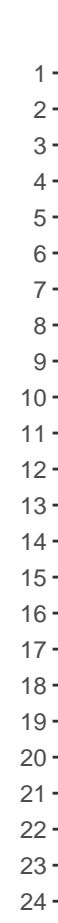
MW indication



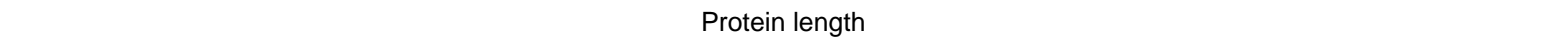
Molecular weight



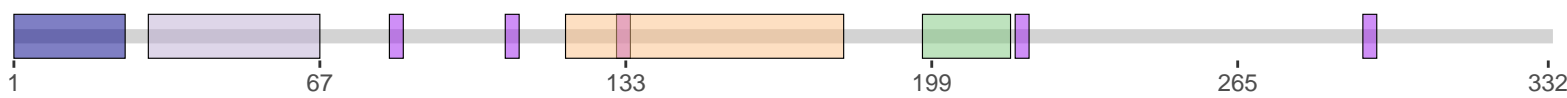
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

NQFTGTIPSSLSLEPNAHLAHLDRNKLKGGPEGFNFRGQIPSLYLSHNSLTPGPKKLSGLNLSFTLDFSRNKLKGGVFLFGKNAKGTIDLSRNLGFDLSKVEFFESLTLWLDLNNHRLFGSLPEGLKDLQGLNLSVSNRLLGGIPGGKLGDFDYVYFPHNKLKGGSLPECK

NbL13g09430.1 UBP1-associated_protein_2C-like [MW = 40.33 kDa]

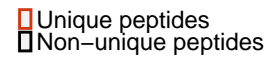
No. of times detected



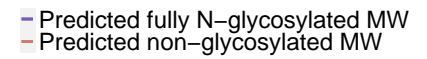
log(intensity)



Values from



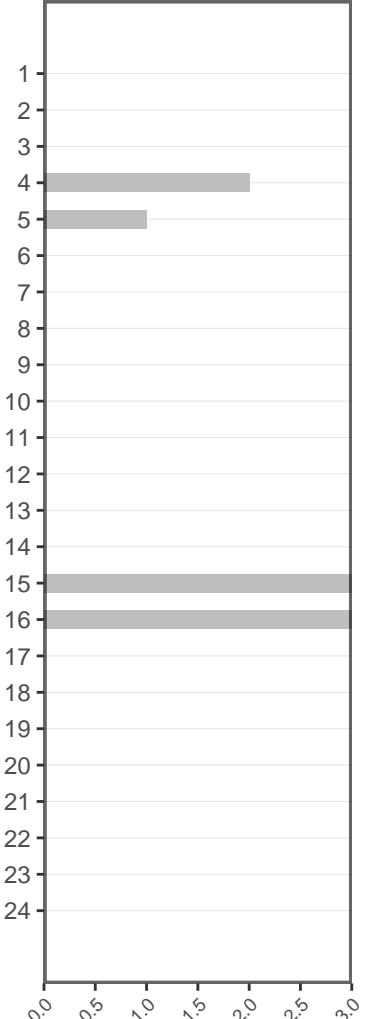
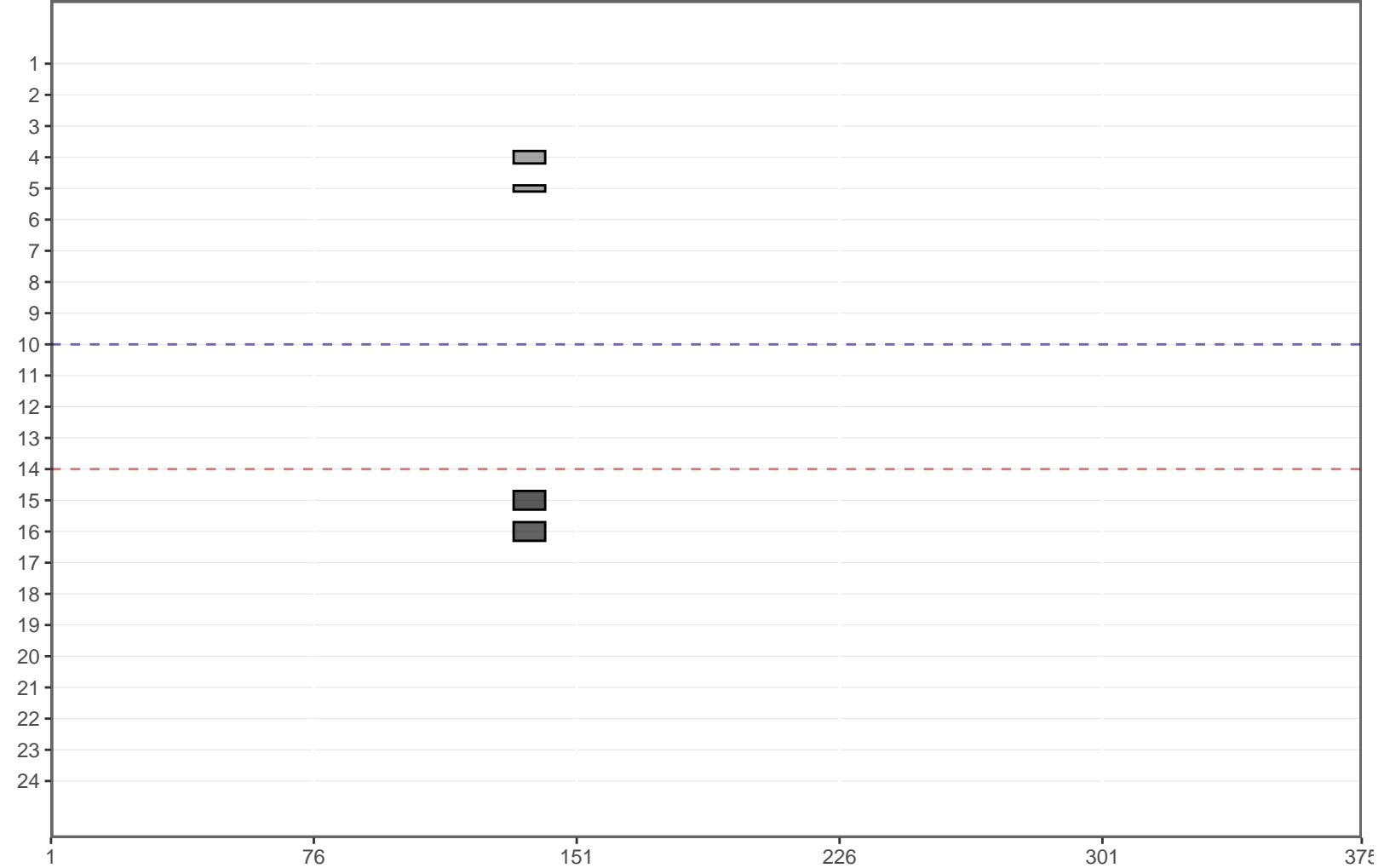
MW indication



Molecular weight



Gel Slice

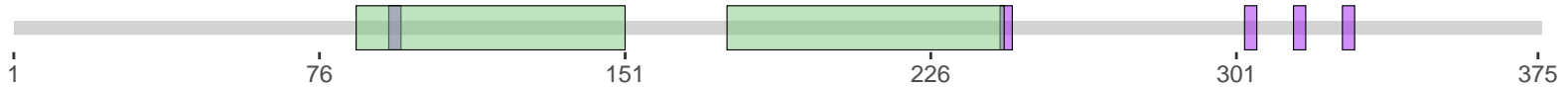


Protein length

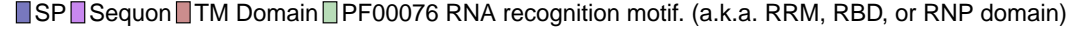


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

YIGLSDDTSEMILFFSRHGEIEEGSWYKDKTKSRGFGFVTKYVEGAKKALNDPQRILGGRLTVKLDNHKGGKIGSQVRATVPMMSMLPAGVPGQAKHHPGPAAPVGYVPGTMAAYTNSTYS6GPAAYTNSTYS6GPAAYTNSTYS6LPGAAPPVGGQDFPPVPGVYFKQESQTTAFSGGYPYVMGKQ

NbL13g09280.1 NA [MW = 14.51 kDa]

No. of times detected



log(intensity)



Values from



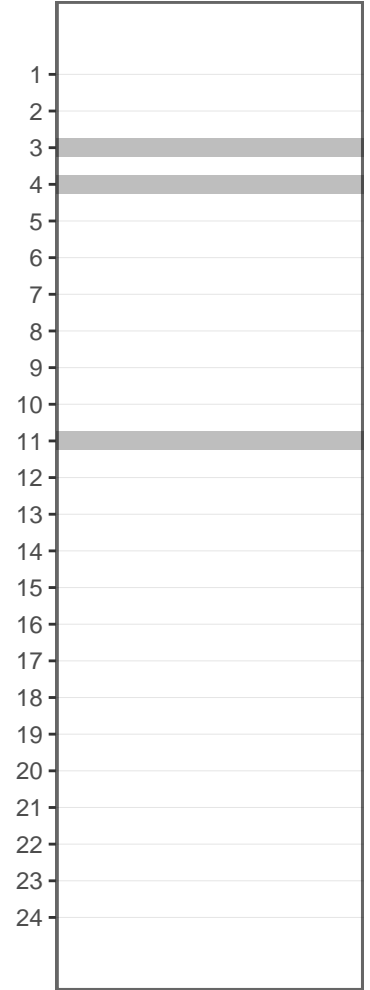
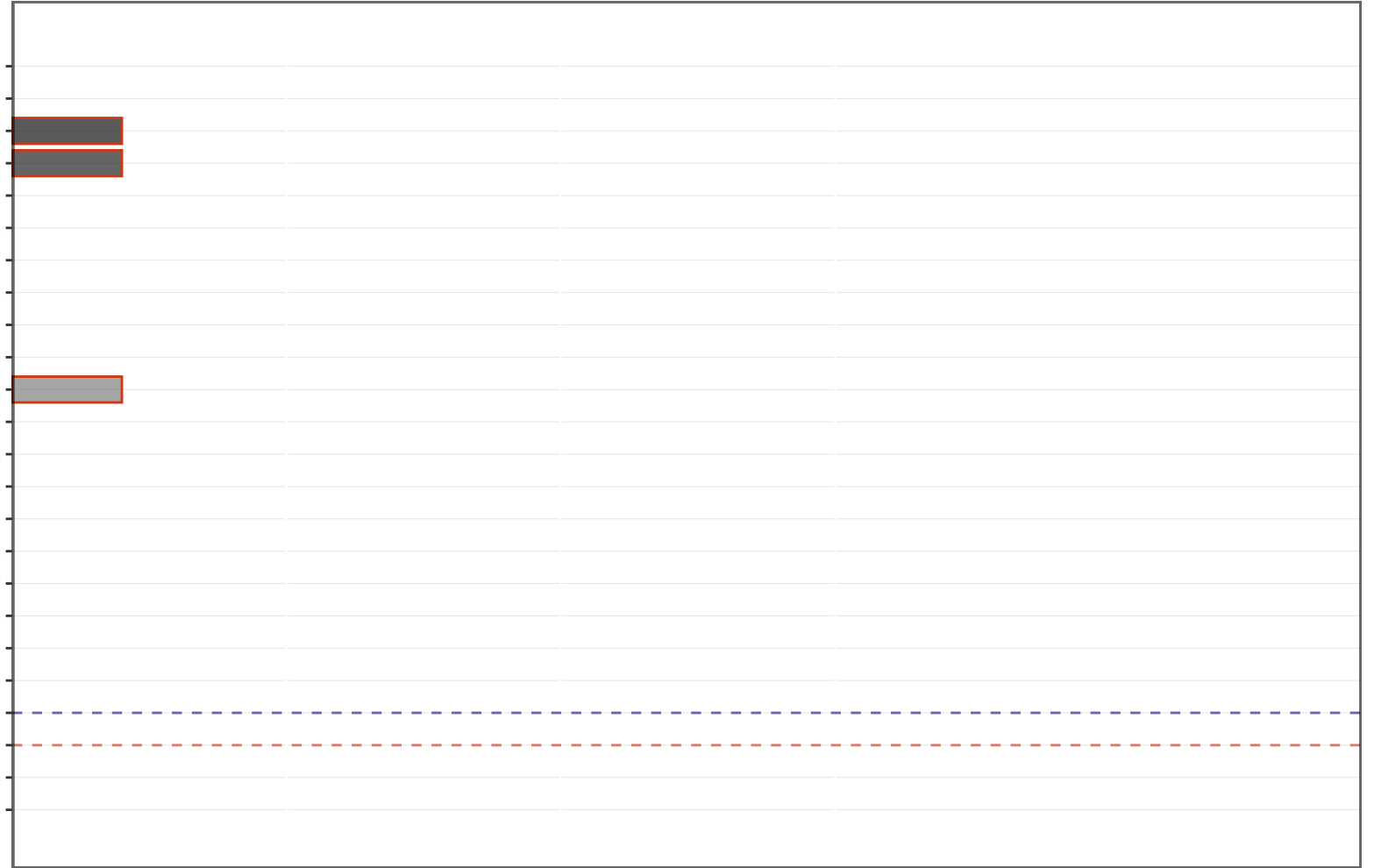
MW indication



Molecular weight



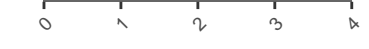
Gel Slice



Protein length



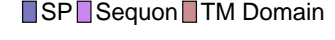
Peptide counts over 4 repeats



Pfam domains



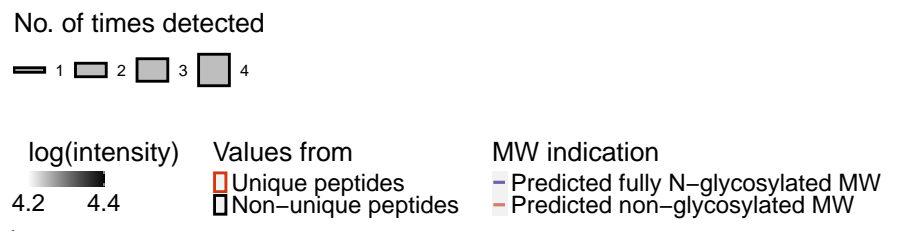
Pfam Description



Protein sequence:

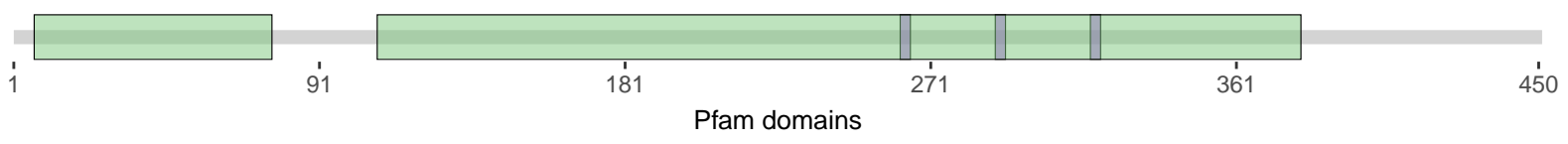
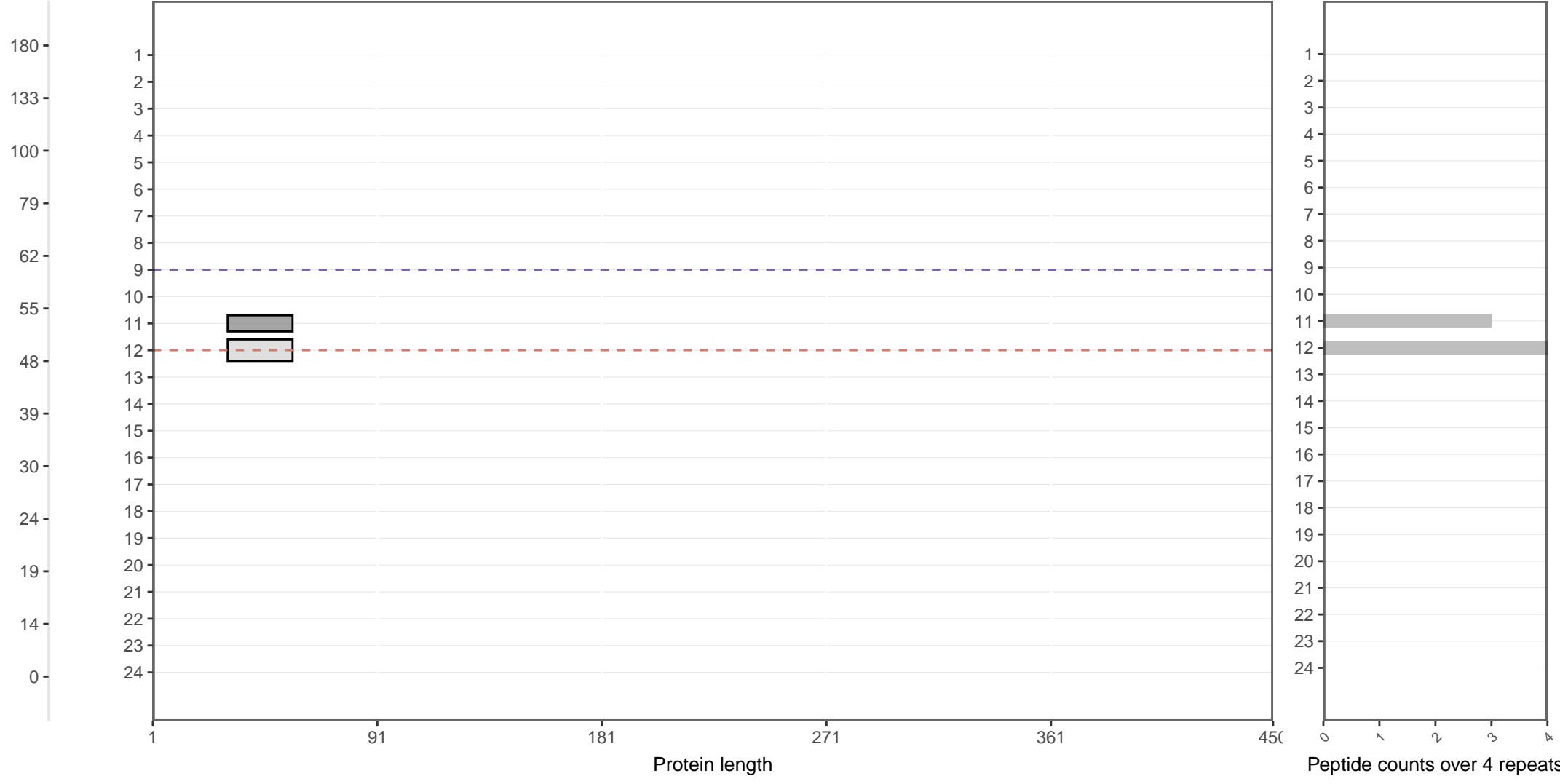
FFFFFFFFLLSSLSFSSRFLFFFLGSSFLSFSHEWSPAKTNIFFFFLFFLYPVGGVSSPMHFVFSVLP

NbL13g09190.1 serine_hydroxymethyltransferase_mitochondrial-like [MW = 49.62 kDa]



Molecular weight

Gel Slice



Pfam Description

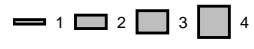
- SP
- Sequon
- TM Domain
- PF00464 Serine hydroxymethyltransferase

Protein sequence:

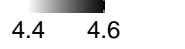
SLRGRGAMIFFRKGLKENKGGKEVMYDYEDKINGAVFPPGLOGGPHNHTISGLAVALKGVRTPEYKAYGEGVLSNGCKFAEELLANGYDLVSGGTENHLVNLTKKIDGDSRVEKVLGSHAAANNNTVPGDVSAMVPGGIRMGITPALTGRGFTTEEDFVKVAEFFDAVKLALKYKAEITGGTKLDFVETLSDDSKIGIEIAGLRDQVEDYAKGFPFVGEKETMKYKDCAGI

NbL13g08950.1 annexin_D5-like [MW = 16.83 kDa]

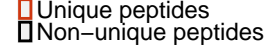
No. of times detected



log(intensity)



Values from



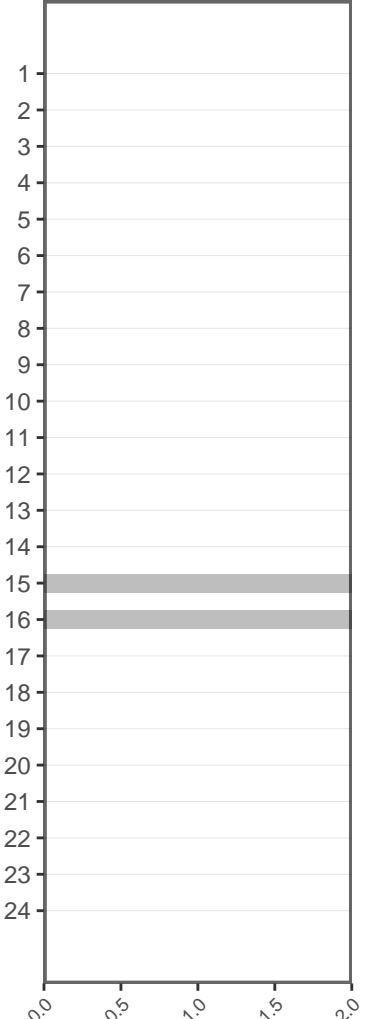
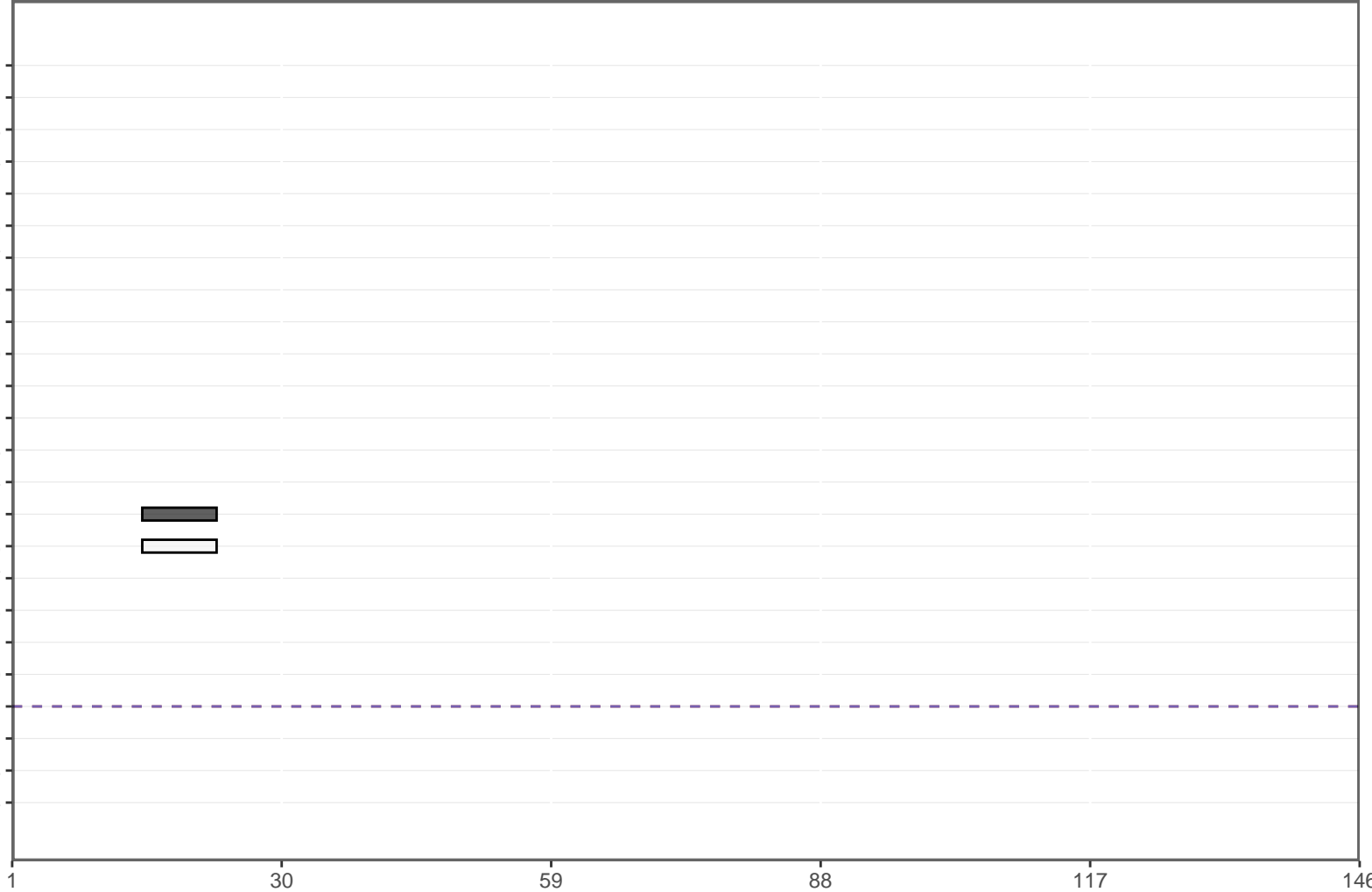
MW indication



Molecular weight



Gel Slice



Protein length

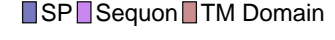


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

CDPRTHFGSNOEKNKNGSFTSFSPHLYVYFHGHVYLPNPIPTFPFATNPNPHHTHSPLLPSTPLRALTPTVATNPPHPTPR

NbL13g08910.1 uncharacterized_protein_At4g26485-like [MW = 21.05 kDa]

No. of times detected



log(intensity)



Values from



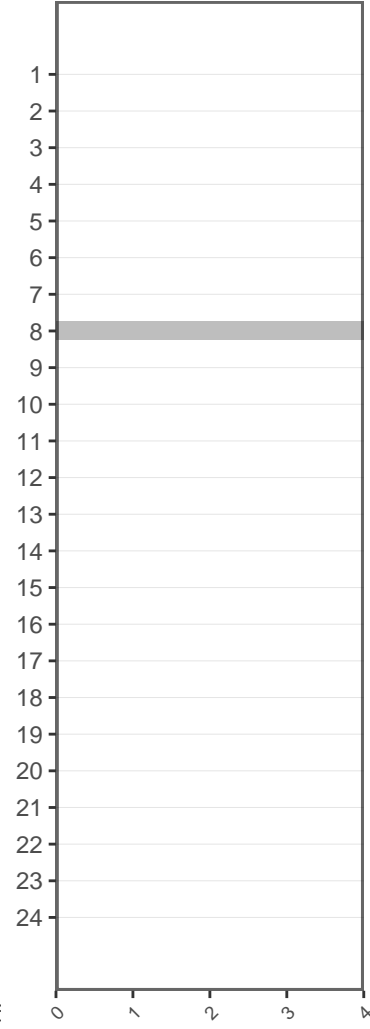
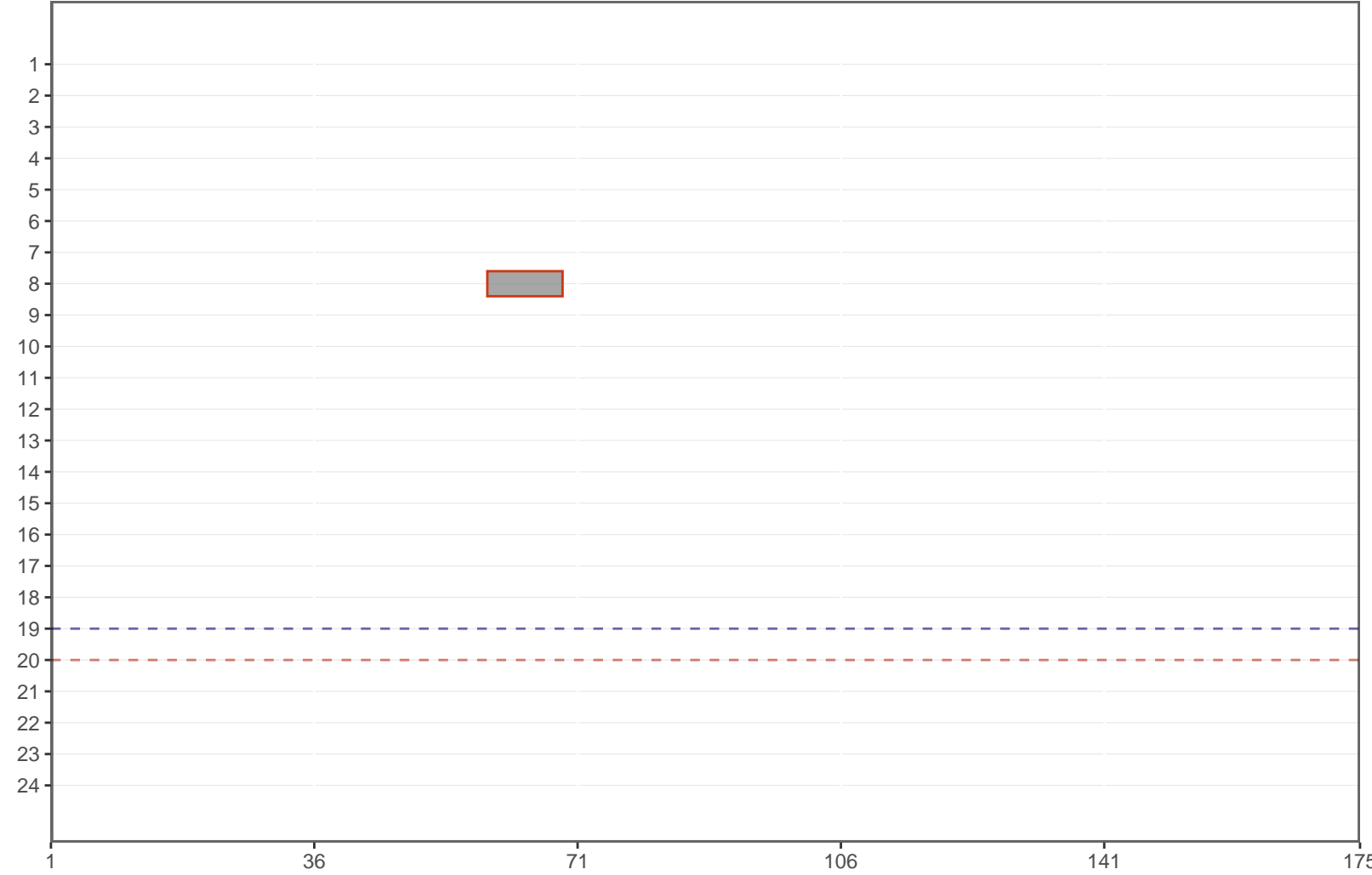
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

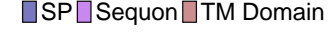
Protein length



Pfam domains



Pfam Description



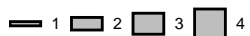
Protein sequence:

GLPARHIDHRISKYFMFFKRNFSYHGQTFGRKDKDEVEVRRKAMQRAASLMFRAENGWLPDPYKILDELGFVWQSRFFRLEGMLLDIDRRRLVEIQGMGQVYL

NbL13g08870.1

enhancer_of_mRNA-decapping_protein_4-like_(LOC104229453)_transcript_variant_X1_mRNA_XM_009782105.1_PREDICTED:_Nicotiana_sylves
 [MW = 153.02 kDa]

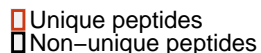
No. of times detected



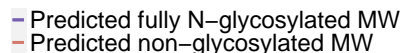
log(intensity)



Values from

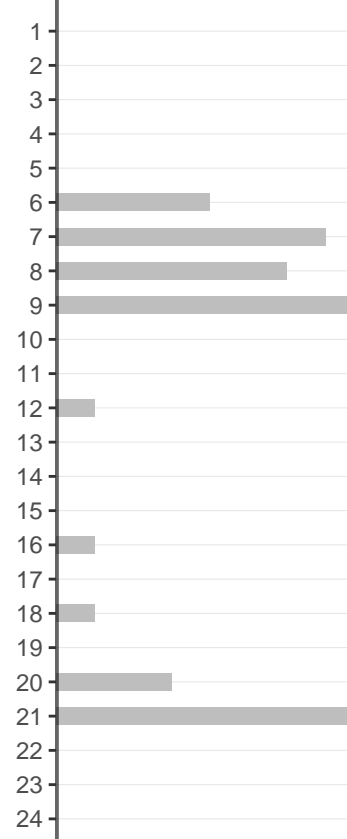
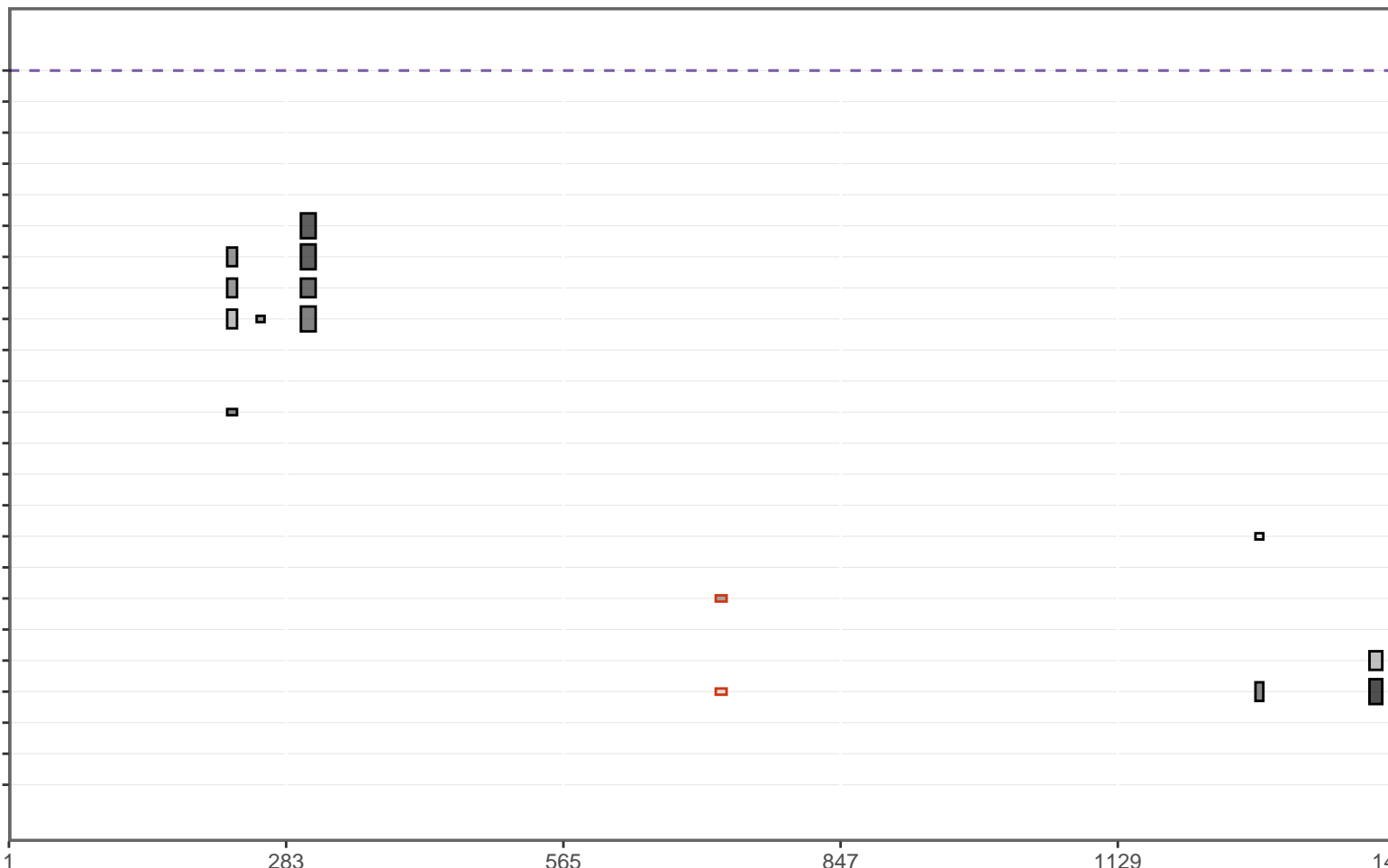


MW indication



Molecular weight

Gel Slice



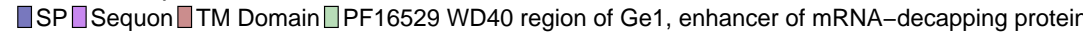
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

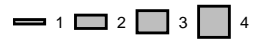


Protein sequence:

PLLSPTLSRKLSGFRGPNISFERGTSYNEQVGDPKVVEVSYDROKEGFTTPNVSDVTSLDDPEKNDESKGSDNDVPSGHSVWFKHPTLHLYPSELMARSSSEVNYNEQKSESELNGDYVNNARNVYEDVYVIGSEAFSGKTDVSGOEEHLHGFVSENEKAFCSQASDLGIMMARECRALSPETYVVEESRDFGAGRSEGPSQPSNLEEDRDSANETSEKDLDSITMSVNYHQAPKPTAKGKQKGRNTQVSGPSSALPSPFNSTDSFNBAGLSSSTPSVEAA

NbL13g08810.1 proteasome_activator_subunit_4 [MW = 203.46 kDa]

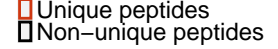
No. of times detected



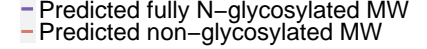
log(intensity)



Values from

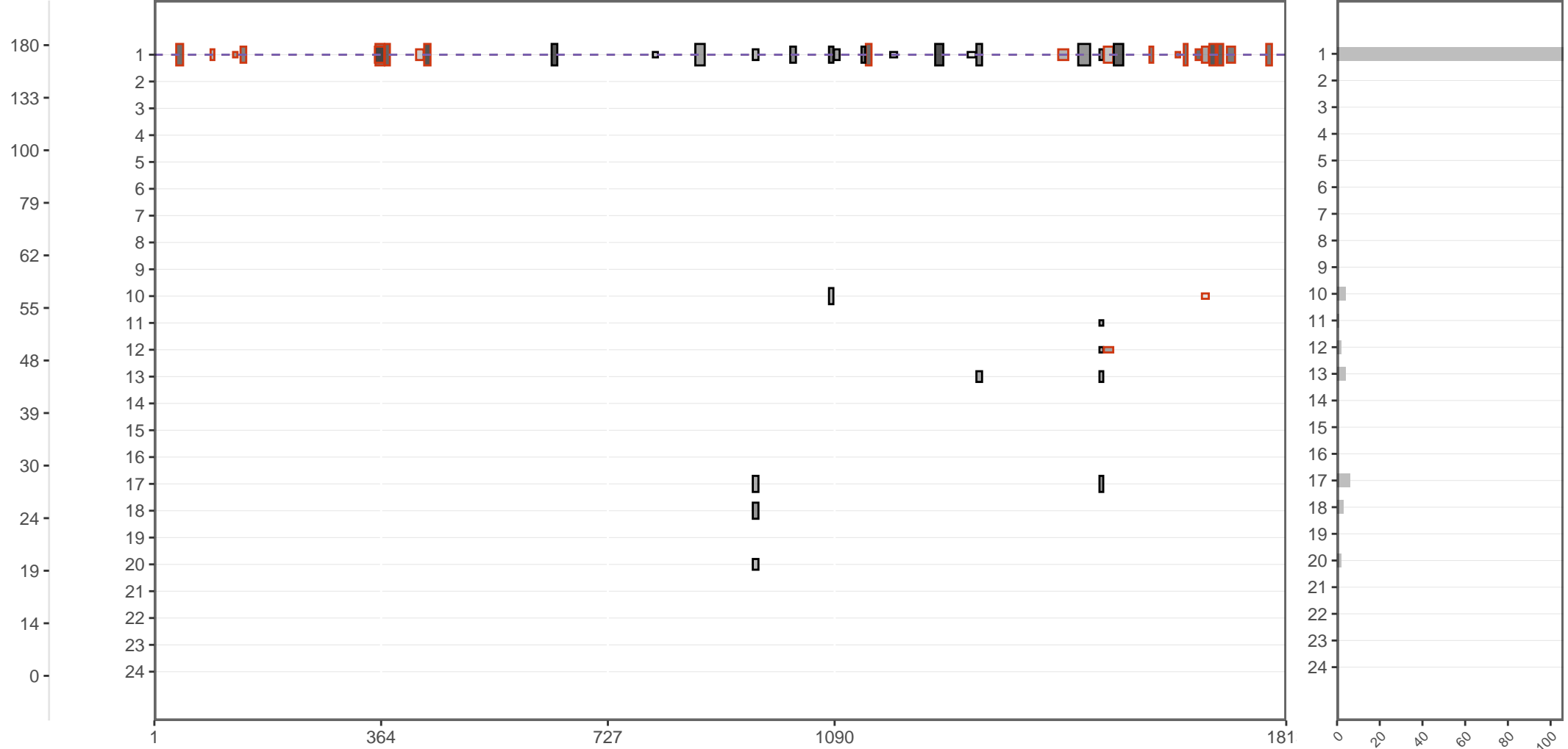


MW indication



Molecular weight

Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF11919 Domain of unknown function (DUF3437)
- PF16507 Proteasome-substrate-size regulator, mid region

Protein sequence:

IRIDSLGNYGSSEYDEWVSNHRGSKLESAHEPPNFWFVSHKSGKRRPRVAIDKGYMHSTWRASQGSYVHFRLSANVSPREHILMDDLLNLSLHGVETVRGLACKSLKMMKRWPFSTKQVLSLQNLKNPSSPEYTLVQSCAVLATQTLKLTDLKALSSFLGLGSSHETLKAQKAINELFKYVNHFFSGVSRNMEKVGNGSEGTDFTLVSEKGLSFEESNLHWRYNLMANRVLALLLSMASRNDPKS66KLS67AGHFLQSLK68QLPOTRILSAISALTL

NbL13g08780.1 THO_complex_subunit_3 [MW = 35.07 kDa]

No. of times detected



log(intensity)



Values from



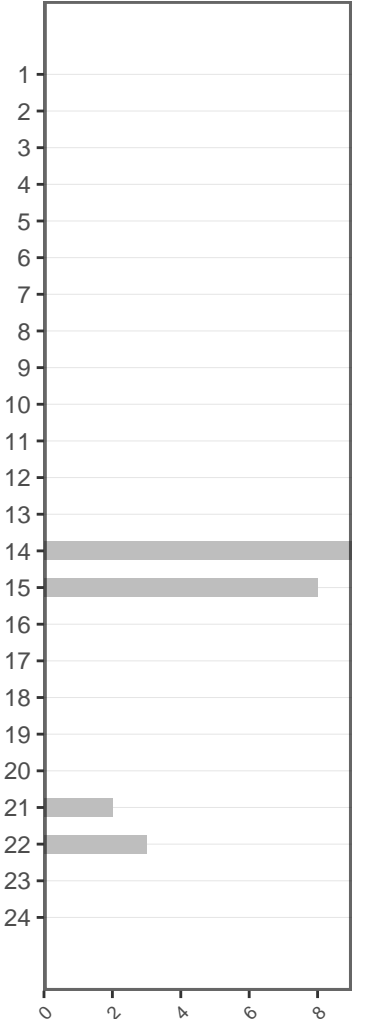
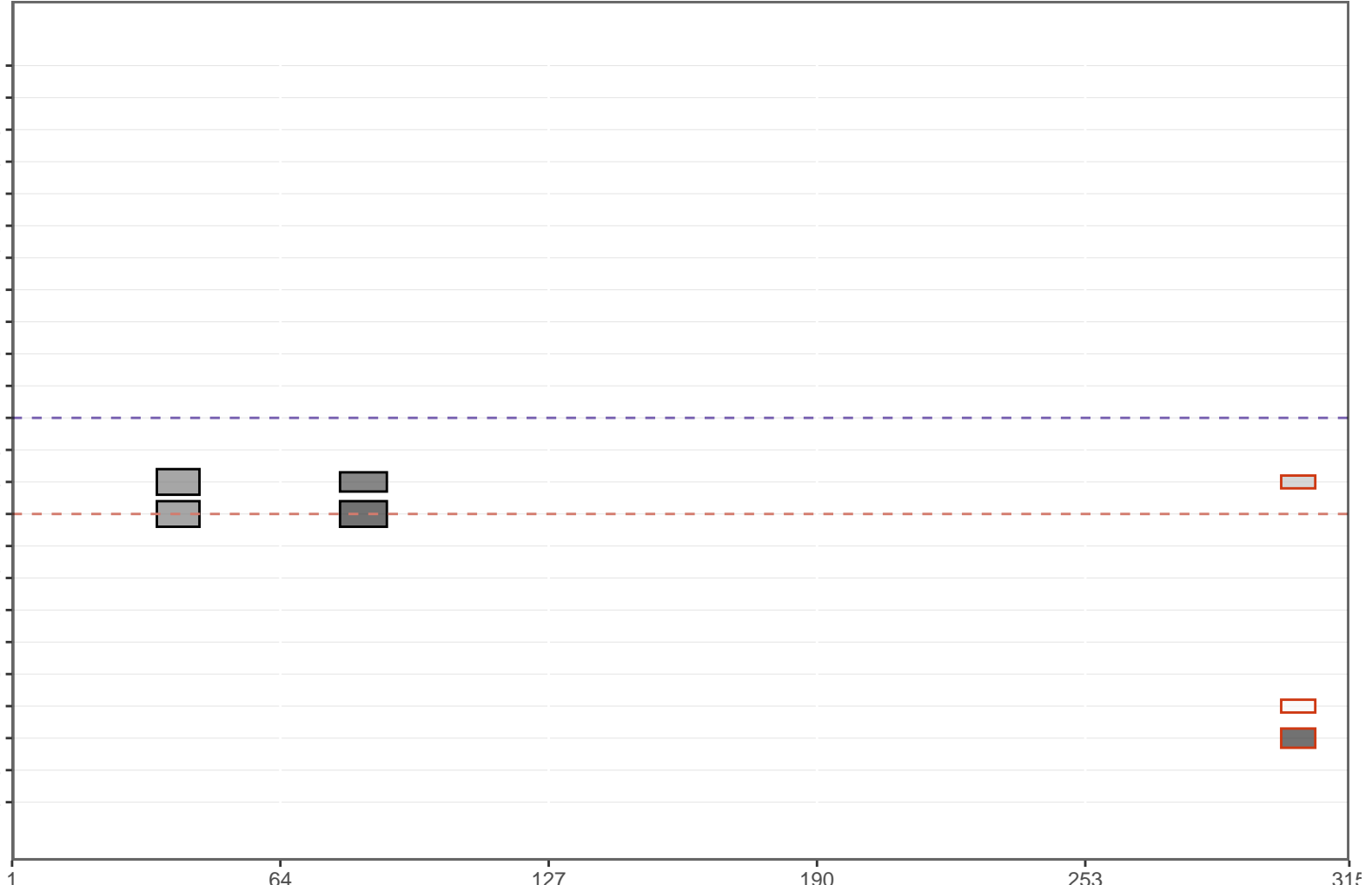
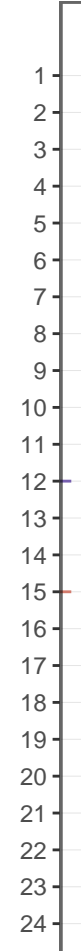
MW indication



Molecular weight

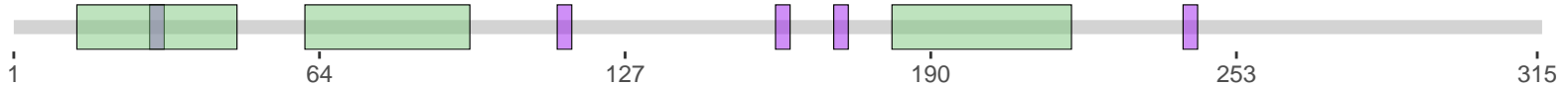


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKRKFNYEVNEIAVWMSGDMFLITGNGTVEVLSYFPLQPVDFLMAHTAGCYGAIIDPLGRYFVAGSADSLVSLWDKMKMLGVRTFTLLEWIPVRTISFNTGDYIAGASELFDIDANVQTRGVHQIPORAMNSVEVWPKCNLLVAGDDKNKYGDEGVFRIFGFESA

NbL13g08590.1 peroxisome_biogenesis_protein_7 [MW = 35.51 kDa]

No. of times detected



log(intensity)



Values from



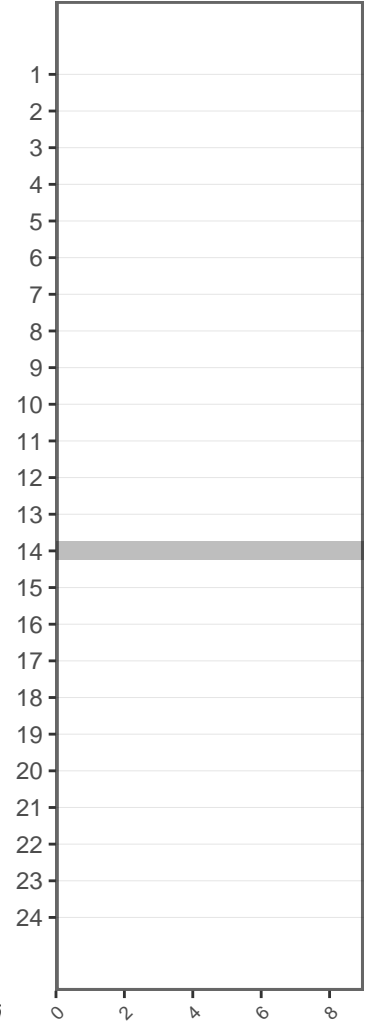
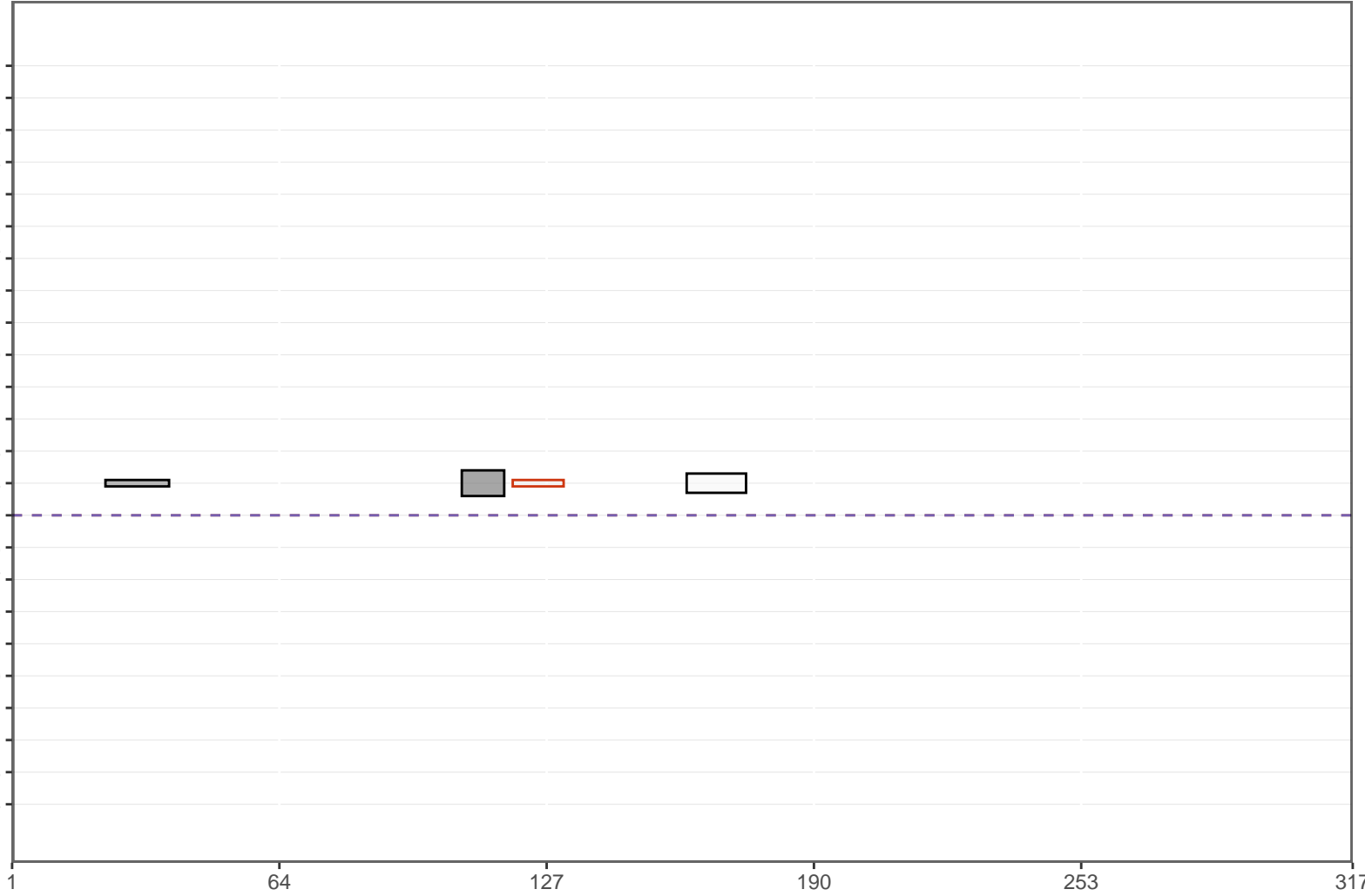
MW indication



Molecular weight



Gel Slice

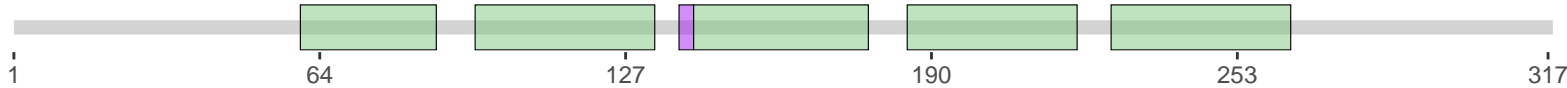


Peptide counts over 4 repeats

Protein length



Pfam domains



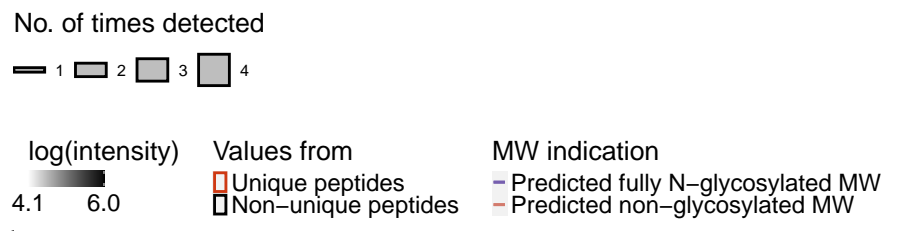
Pfam Description



Protein sequence:

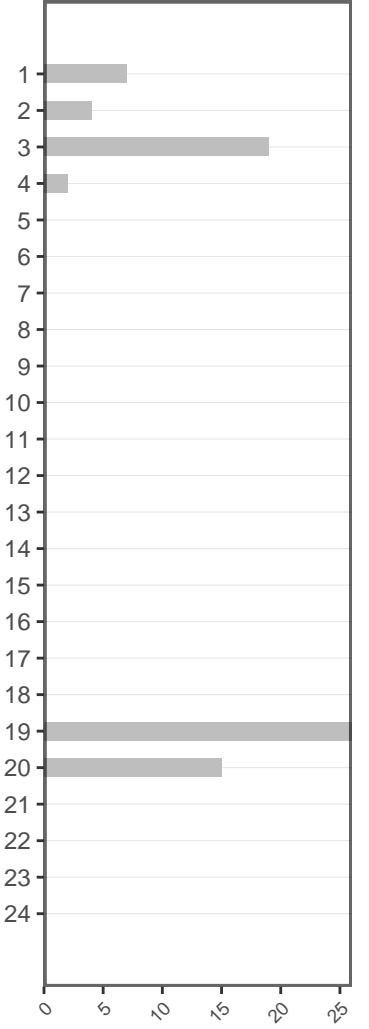
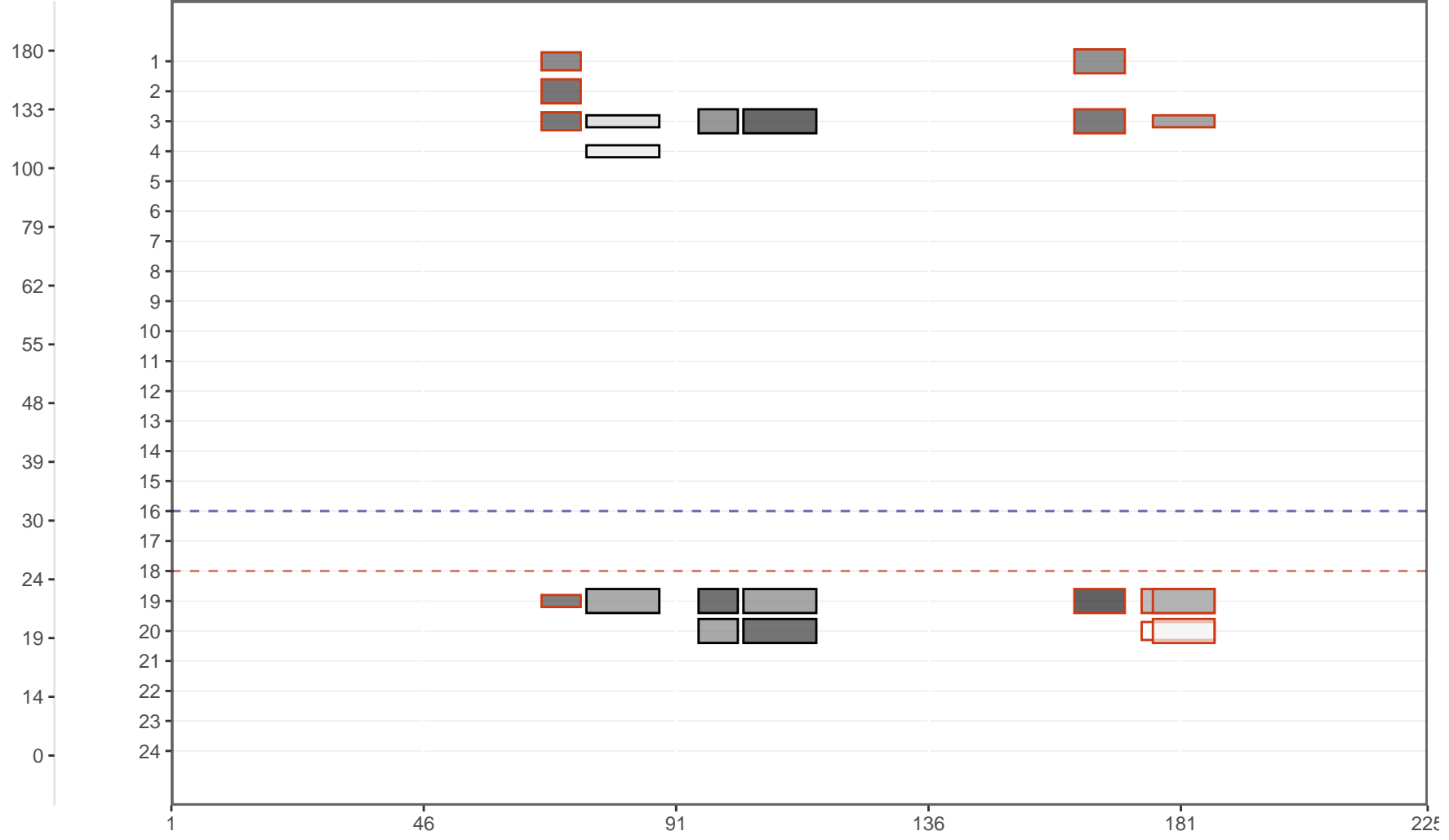
IAVCIYSTWVNPRIHADFASAGDCCTRIWVREPGSTMLPAHFEFELSGDMNKYDDGHATASVDKSRKQVWDRVNYRVPAAVLNHGHYAVRKRFRSPHRASAMVSGSYDMTFCAMWQVMMEDALIGRYDHRTEFAVGVDMSEVLVEGLLASTGWDELVFWVQHGMDPRAPV

NbL13g08410.1 3-hydroxyacyl-[acyl-carrier-protein]_dehydratase_FabZ-like [MW = 24.81 kDa]



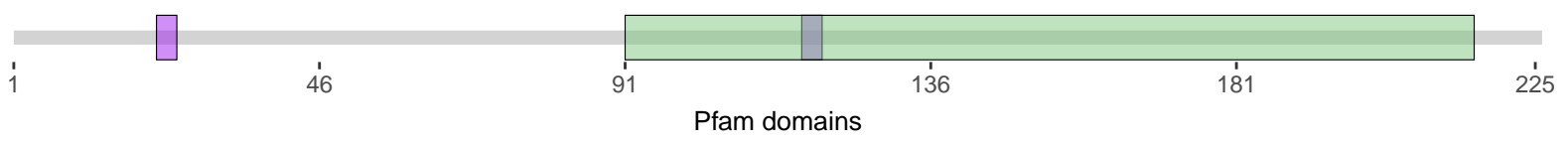
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam Description
 SP Sequon TM Domain PF07977 FabA-like domain

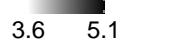
Protein sequence:
 IRVIEYNPGVSAVAKNVTINDNFFPGHFPERRIMPGLMVEAMAGVGGVMLGPEVGGSRNFFFAQGVKVRFRKPVWAGDTLVMRMTLHLGKRFQIAKMEGKAVGVEDVYCEGEFLMMGSE

NbL13g08310.1 peroxidase_43-like [MW - SP = 32.33 kDa]

No. of times detected



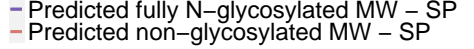
log(intensity)



Values from



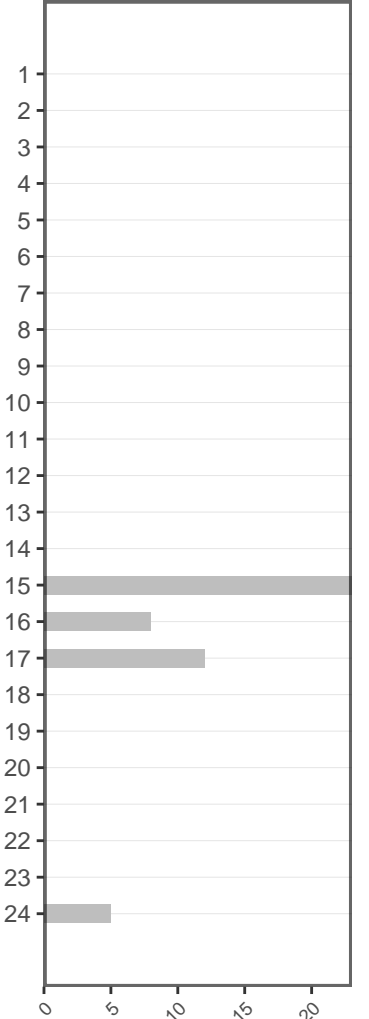
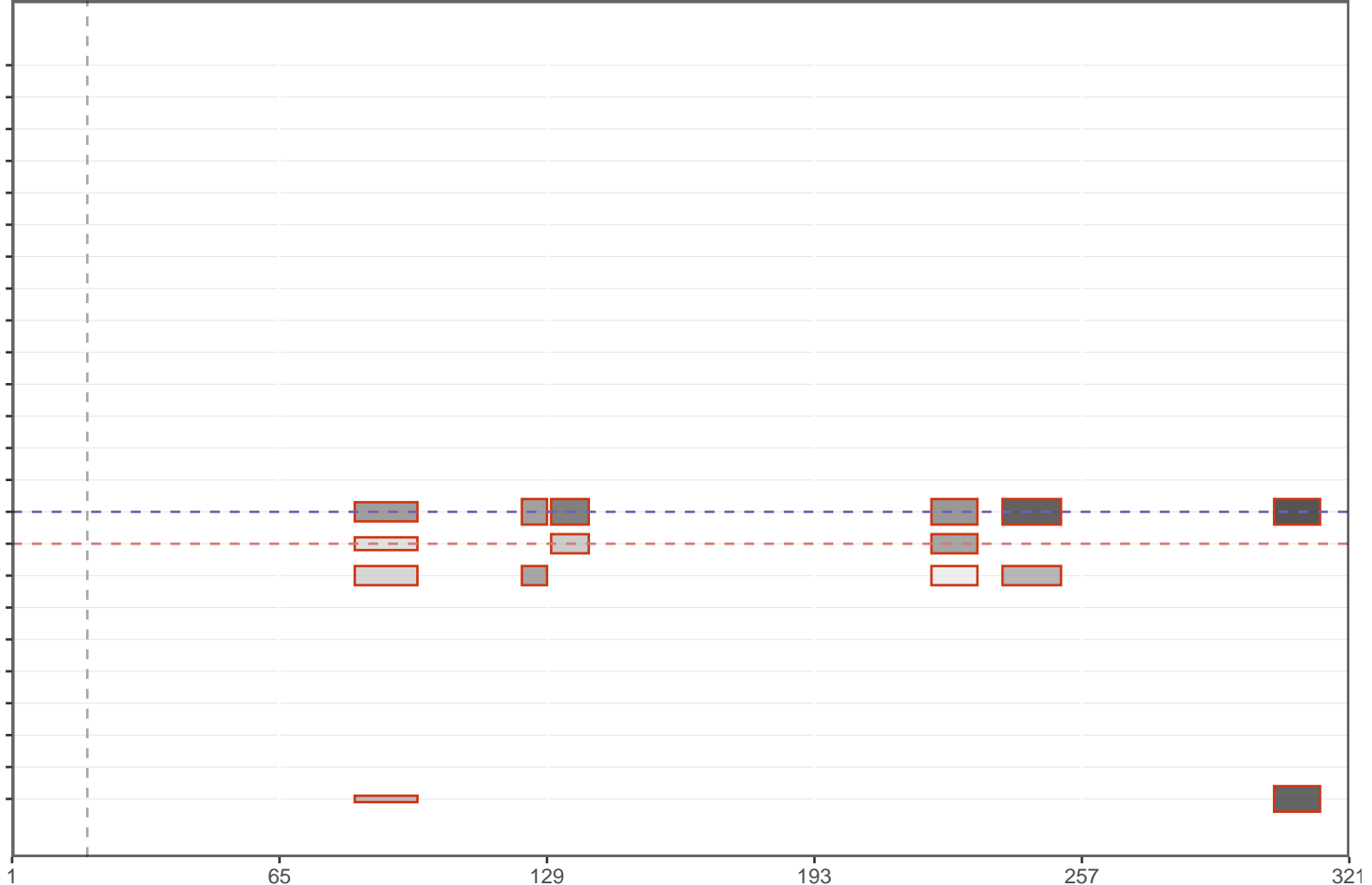
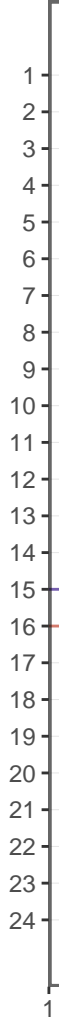
MW indication



Molecular weight

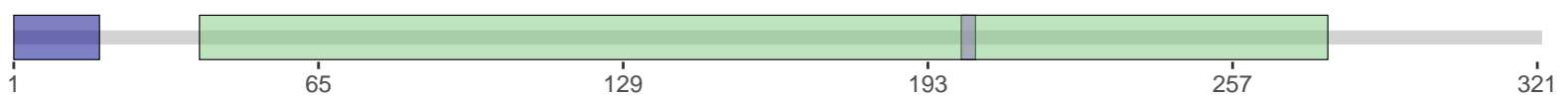


Gel Slice



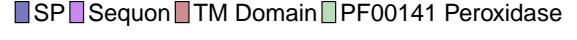
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LAENMPDYEDSIOGLKAKFKLEKLSKDLVLLSAAHTIGTTAGFFMTKRLVNFSPFGGSDPBNFPLPELKATPGNGNINVRLLAMDRLGSGEAFDQHLQNRSGFVAGSDANLYRDETRKRVVDSYFGLSPFLGTSFEADFAHAMKMGRIQVLTGSOGTIRRVCAEFL

NbL13g08240.1 uncharacterized_LOC107822389 [MW = 41.63 kDa]

No. of times detected



log(intensity)



Values from



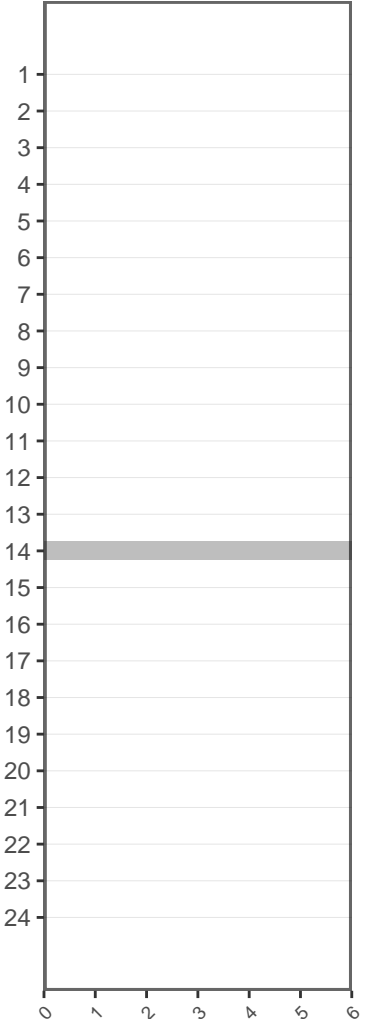
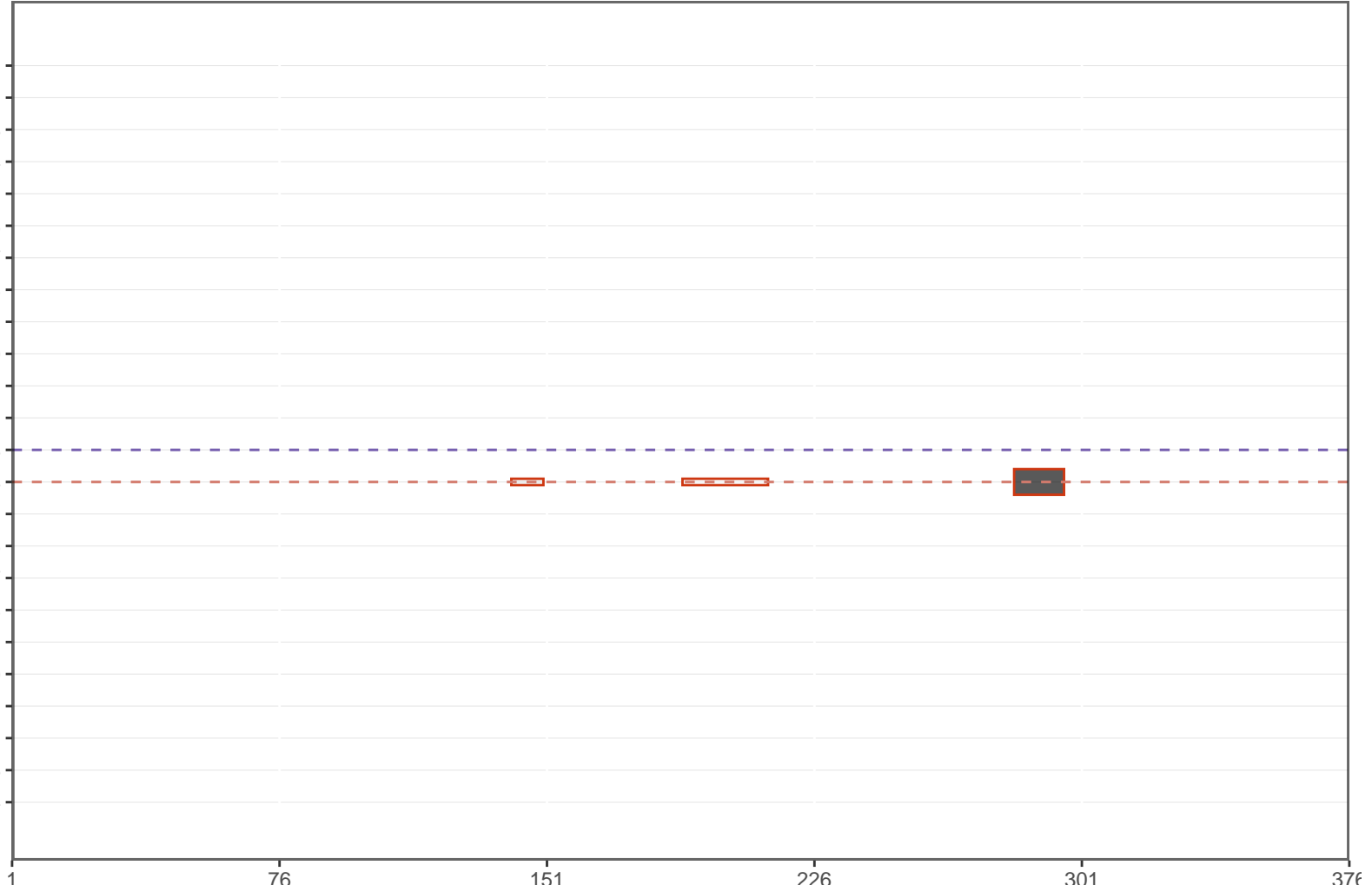
MW indication



Molecular weight



Gel Slice

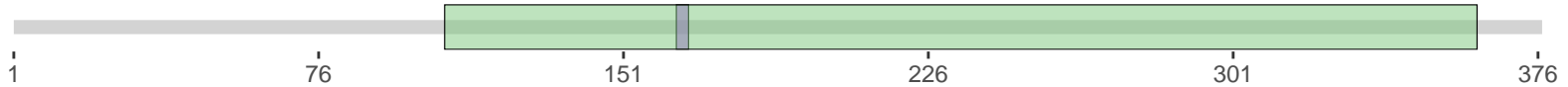


Protein length

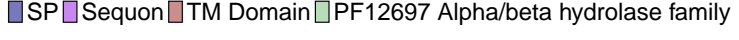


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

GGGHAATIVVRAAKKGLVKTPTAIAAAPTWAGPLPIVFGKDSIMETRYGLLRGCTLRAPAGWMMNVLVLENKESIGSQYKSHVYSDPEKVTDPHESRYALTKRGARYVPAALFTGLDLPVKSREEFQVFAELEGRIPIVLLATAGSPKRSKAEMEALREAKGVSKYEVPGALLPQEEYPEVAEQVYRFLOKFELEA*

NbL13g08170.1 RNA-binding_protein_8A-like [MW = 21.84 kDa]

No. of times detected



log(intensity)



Values from



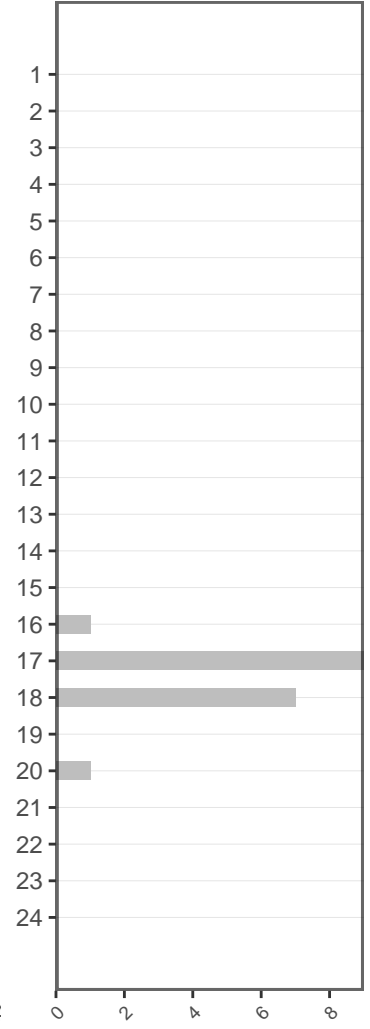
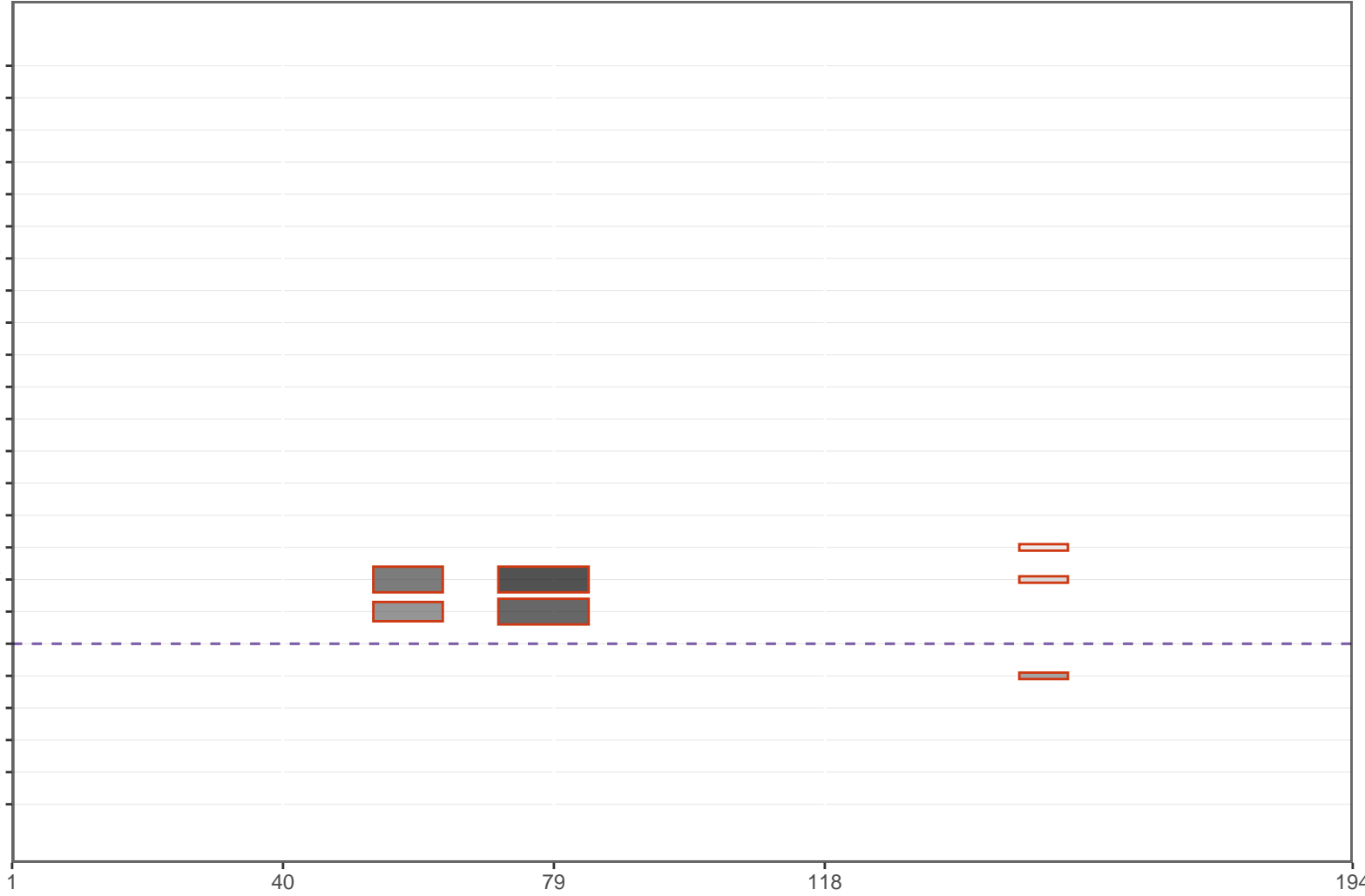
MW indication



Molecular weight



Gel Slice

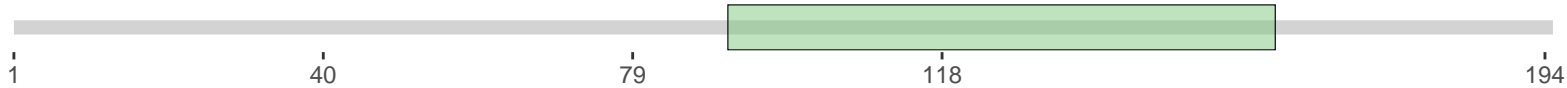


Protein length

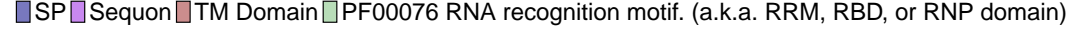


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

RSIEGWLVLTGVNIEAGEEDLHNEFGFGEKKNLHLLDRRTGFVKGVALLEYENFEAEARANEMDGKELTGFPHVDWAFSKGPFRRRNARRRSPHSHRSRPRRRF

NbL13g08120.1 malate_dehydrogenase_chloroplastic [MW = 43.23 kDa]

No. of times detected



log(intensity)



Values from



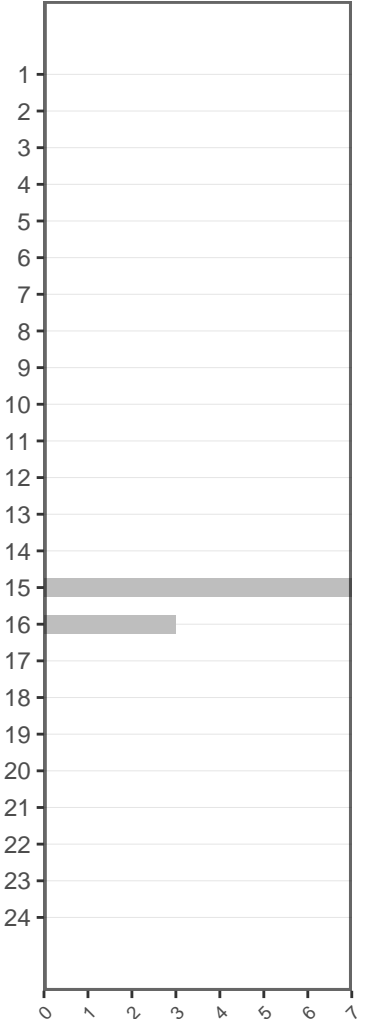
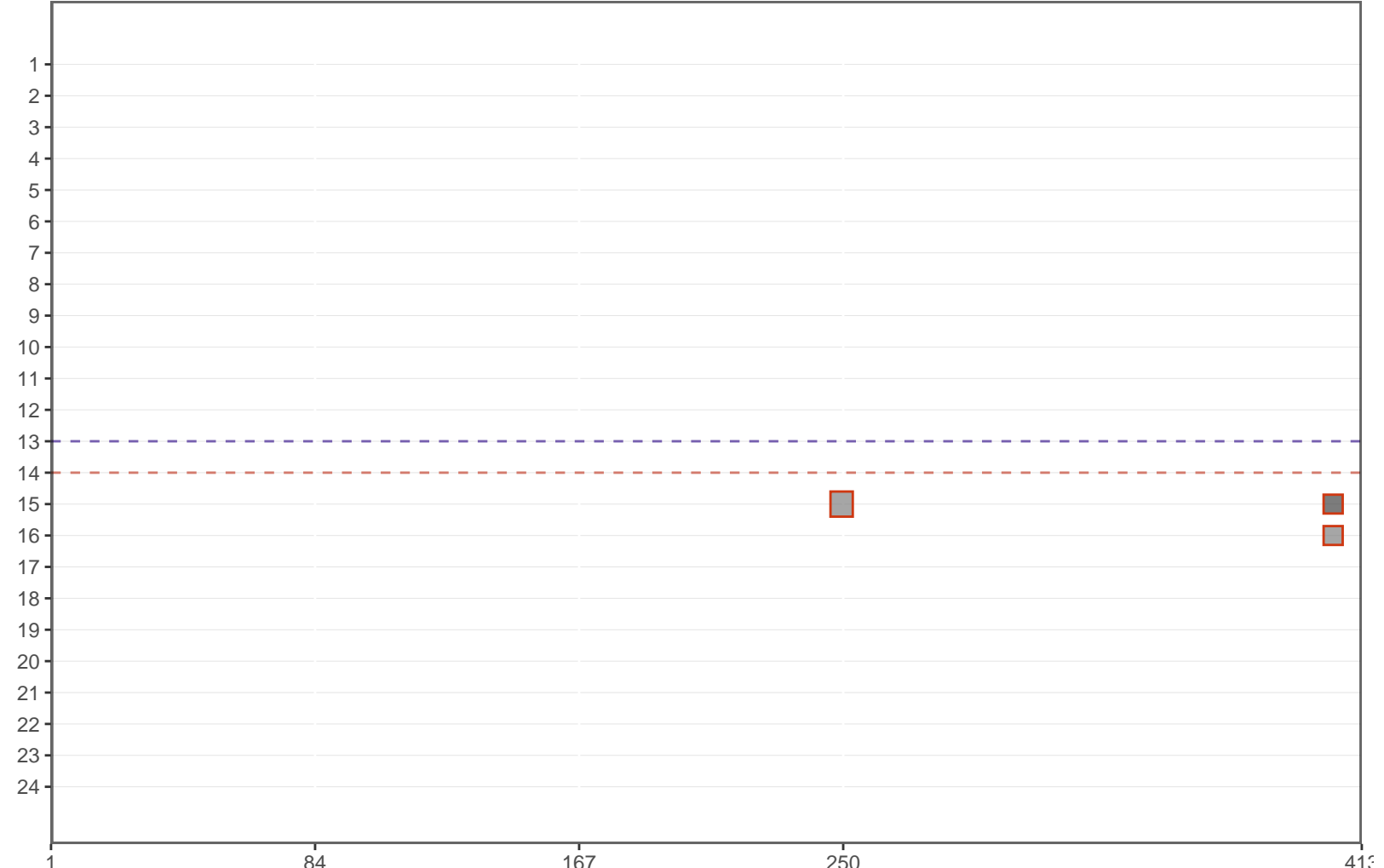
MW indication



Molecular weight

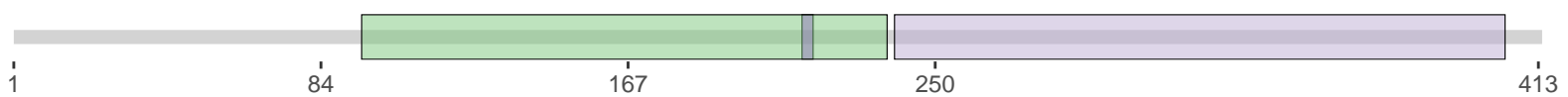


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00056 lactate/malate dehydrogenase, NAD binding domain
- PF02866 lactate/malate dehydrogenase, alpha/beta C-terminal domain

Protein sequence:

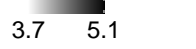
TLLEAVADNCPDAFHIEENPYNSTVPAAAEVLRKRGVVDPRKILFGVTTLDVVRANTFVSGKKNLRLEVDVPPVGGHAGITLPLLSKTKPSTFTTDEEVEQLFVRIGNAGTEVEAKAGAGSATLEMAWAAARFVESGLRALDGGSDVVEGAFVGGSDITLPPFASRIKLGKNGVEALIPEDLGLTEYEQKALDALKPELKASIEKGFVWKEPAAV

NbL13g08110.1 diphosphate_reductase_chloroplastic-like [MW = 51.3 kDa]

No. of times detected



log(intensity)



Values from



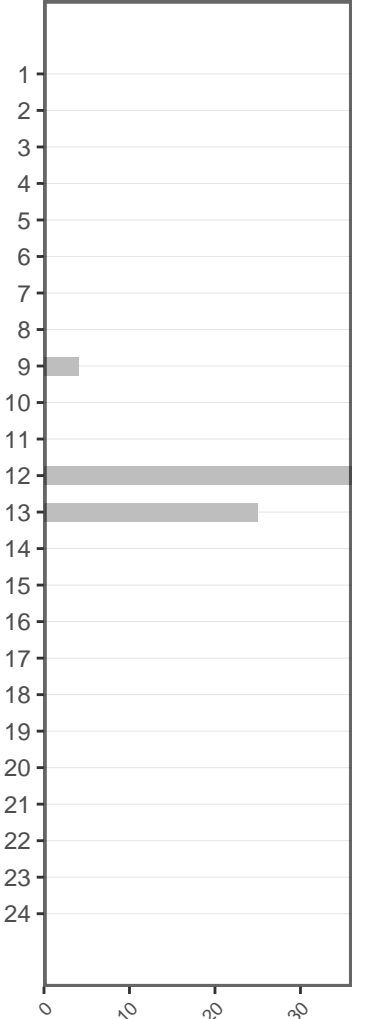
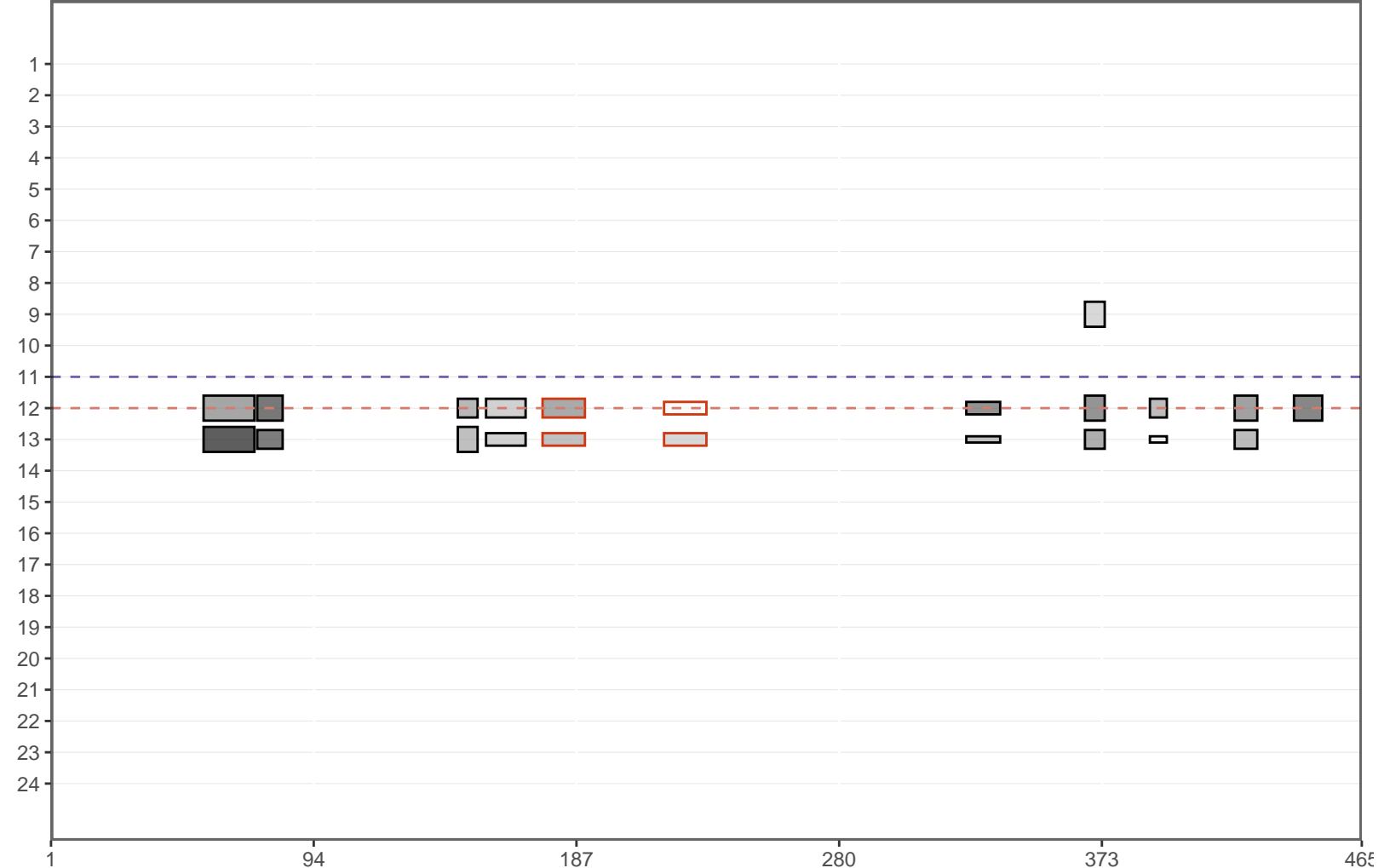
MW indication



Molecular weight

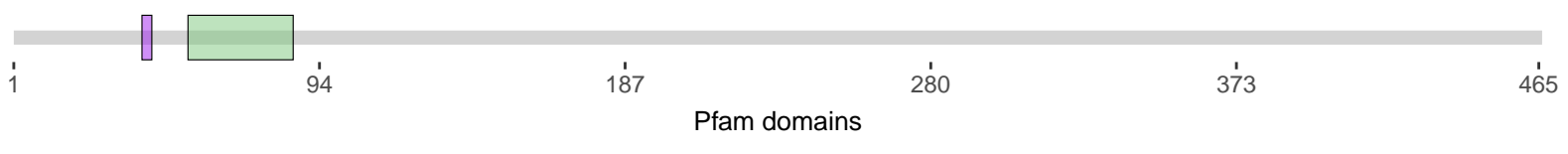


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam Description



Protein sequence:

AGDYEYAAAFQERIRHSDQMKYYENLAEMVGGDVPDFYGVWVFPKGDHWVGTGTVTHKADKKFQLATRLRADSKITGGKIRVEAHPPEHRPRRLGDRVALVGDAGVYTKDGGEGYFAAKSGRMCAEAIVEGSEMGRMVDSEGLRKYLEKWKDKTVPPTKYVLDLQKVFYRGNAPREAFVEMCADEVVQKMTFDSLYLKKVAPGNPIEDLKLAVNTIGSLVRANALREMDKLEV

NbL13g07930.1 vesicle_transport_v-SNARE_13-like [MW = 25.08 kDa]

No. of times detected



log(intensity)



Values from



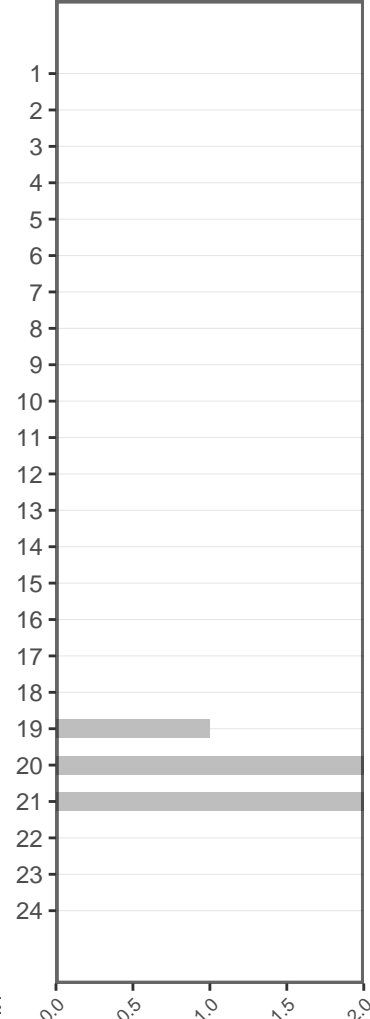
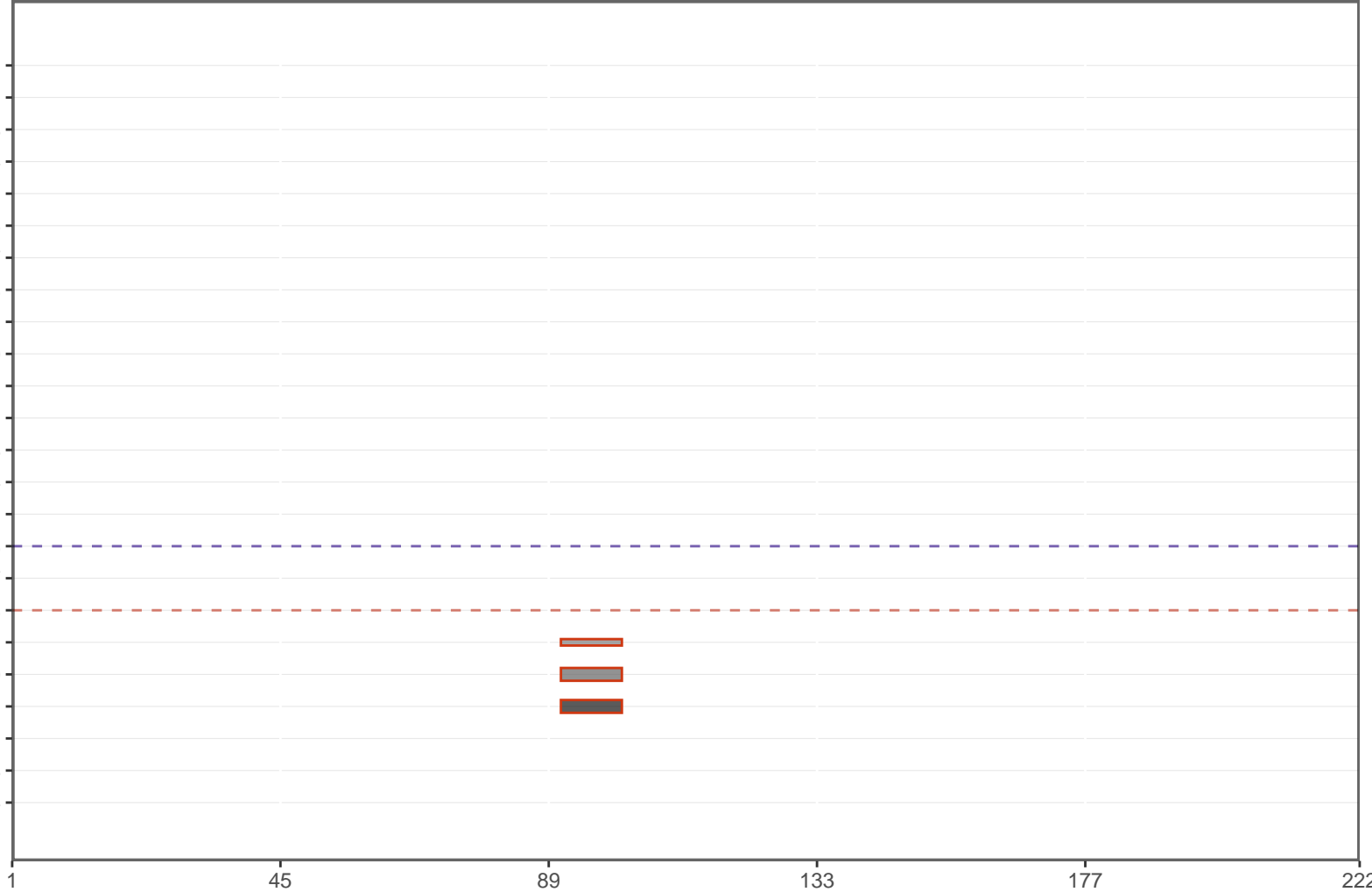
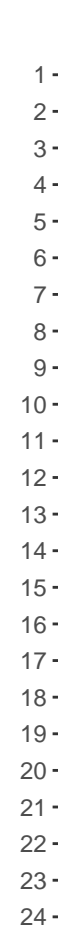
MW indication



Molecular weight



Gel Slice



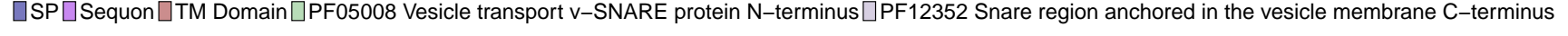
Protein length



Pfam domains



Pfam Description

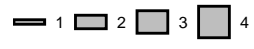


Protein sequence:

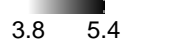
DAARDLLESGMADTMMVNSADGRGRLLMMSTERLNHSGSDRIRRESRKTMLETEELGVSILODLHGGRGSLHAAHDTLHGVDNISRKSKLTMERRRMSRKNWIGSIAVLLALLLVYKLAH

NbL13g07820.1 eukaryotic_translation_initiation_factor_5A-1 [MW = 17.4 kDa]

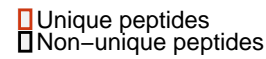
No. of times detected



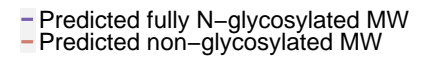
log(intensity)



Values from



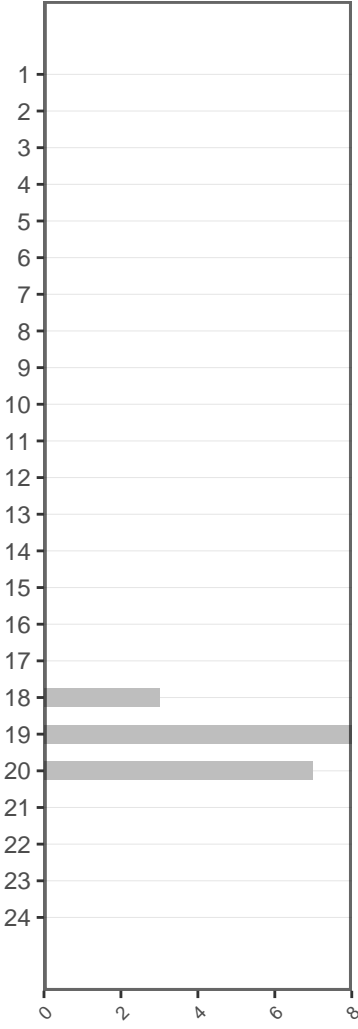
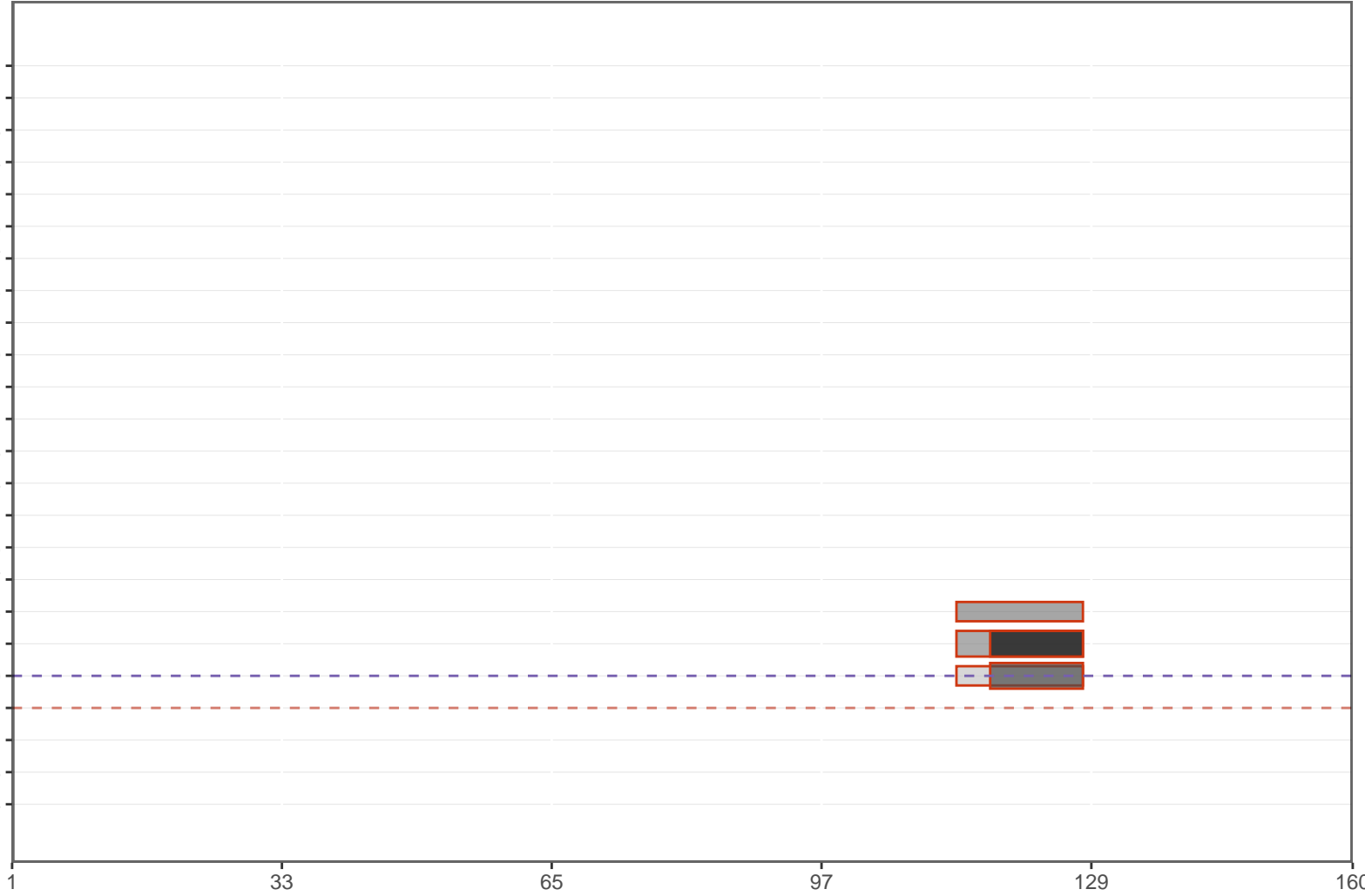
MW indication



Molecular weight



Gel Slice



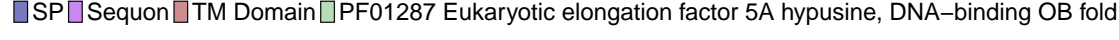
Protein length



Pfam domains



Pfam Description



Protein sequence:

TGKXKLEIVPSSINQGVPHVNRFDVGLIDHSEDDGFVSLTENGNTKDDLRPLPTDQNLTLFNDGFAEGKDLVLEVMEMAMGEEGIGGKIDVGRK

NbL13g07660.1 heparanase-like_protein_2 [MW - SP = 58.45 kDa]

No. of times detected



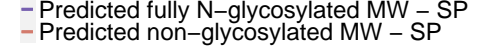
log(intensity)



Values from



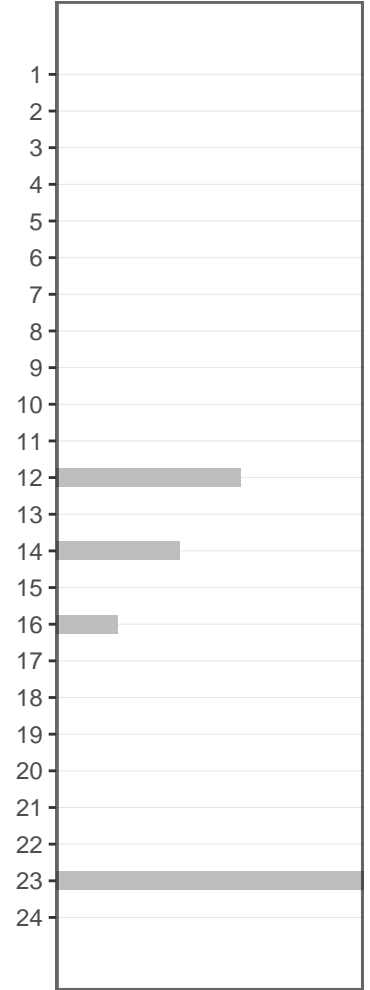
MW indication



Molecular weight



Gel Slice

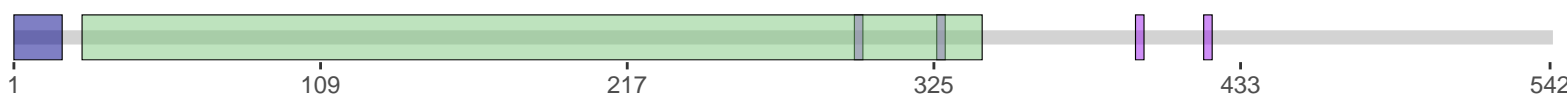


Protein length

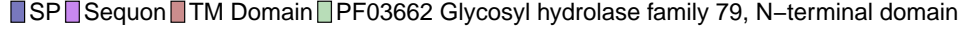


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IIVNLYTHIHYNLGPGSEGSKLVKLNLPQYLNKVSDFDNLTGTRKMGKPVWASAWGEGGAYNSGGPNVSNAFVDFWYLDQLGMAAHHKTKYGRQTLHGQYGLLDTRTFVNPFDYVYALLWRLMGKEVLDVSNASNPYLRVYAHCTKDRAGVTLLELNENQYQYGVNQGSSAYTEVQAGEKKNHKKGSFVHGLKETVSWVSGKSSDVTLYREEYHLTFEGGNGSRMTLNLNKPFLQITETGDSLSPLVLENNKSPVAPLSIKFIAPFNNSPSCR

NbL13g07510.1 phenazine_biosynthesis-like_domain-containing_protein_1 [MW = 31.41 kDa]

No. of times detected



log(intensity)



Values from



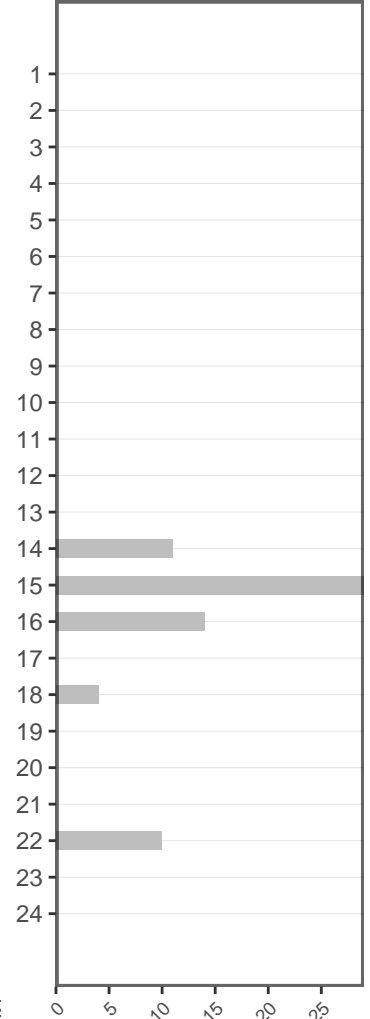
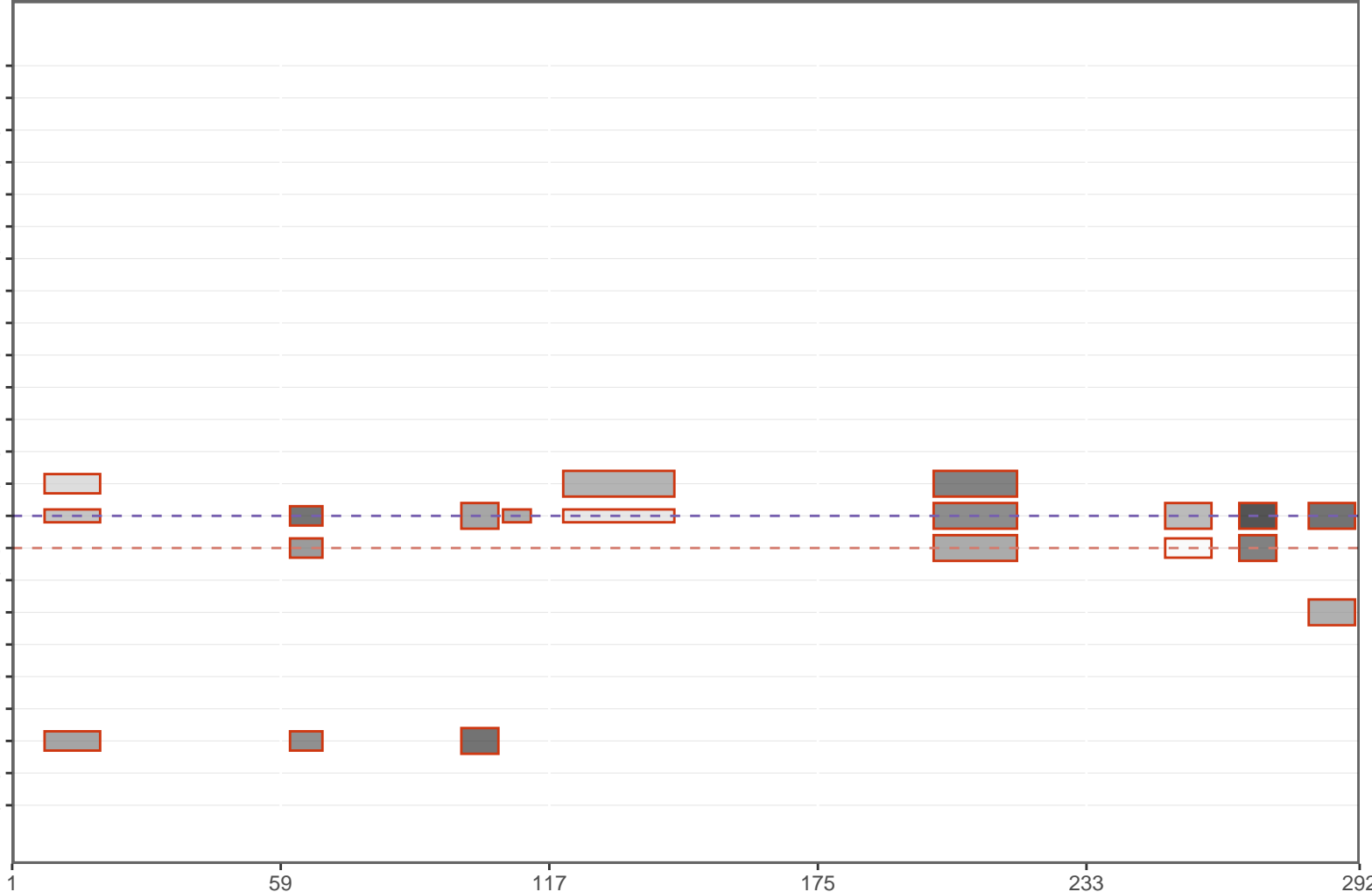
MW indication



Molecular weight

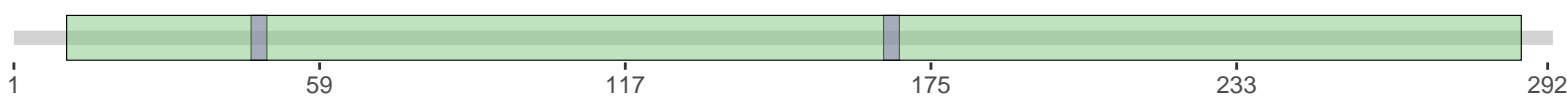


Gel Slice



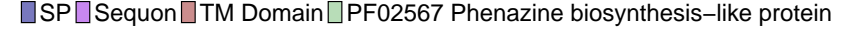
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VELDFPVLQVAKTNSADVTASESFGASMEINETSMDLFIILLPSGEAVVECGPQFDQKNGPCGRGHTGRAPQGGGDFYSRFFGPKLGINEDPHGGSAGCALALVWRKLGKGDVALAASPRGGVWVHLDEENQRVFLRGAATVMEGSLV

NbL13g07360.1 ATP_synthase_subunit_gamma_mitochondrial-like [MW = 38.57 kDa]

No. of times detected



log(intensity)



Values from



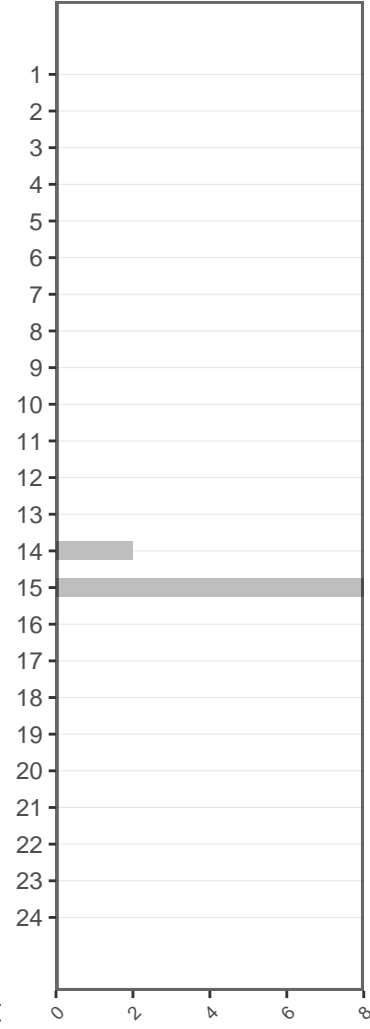
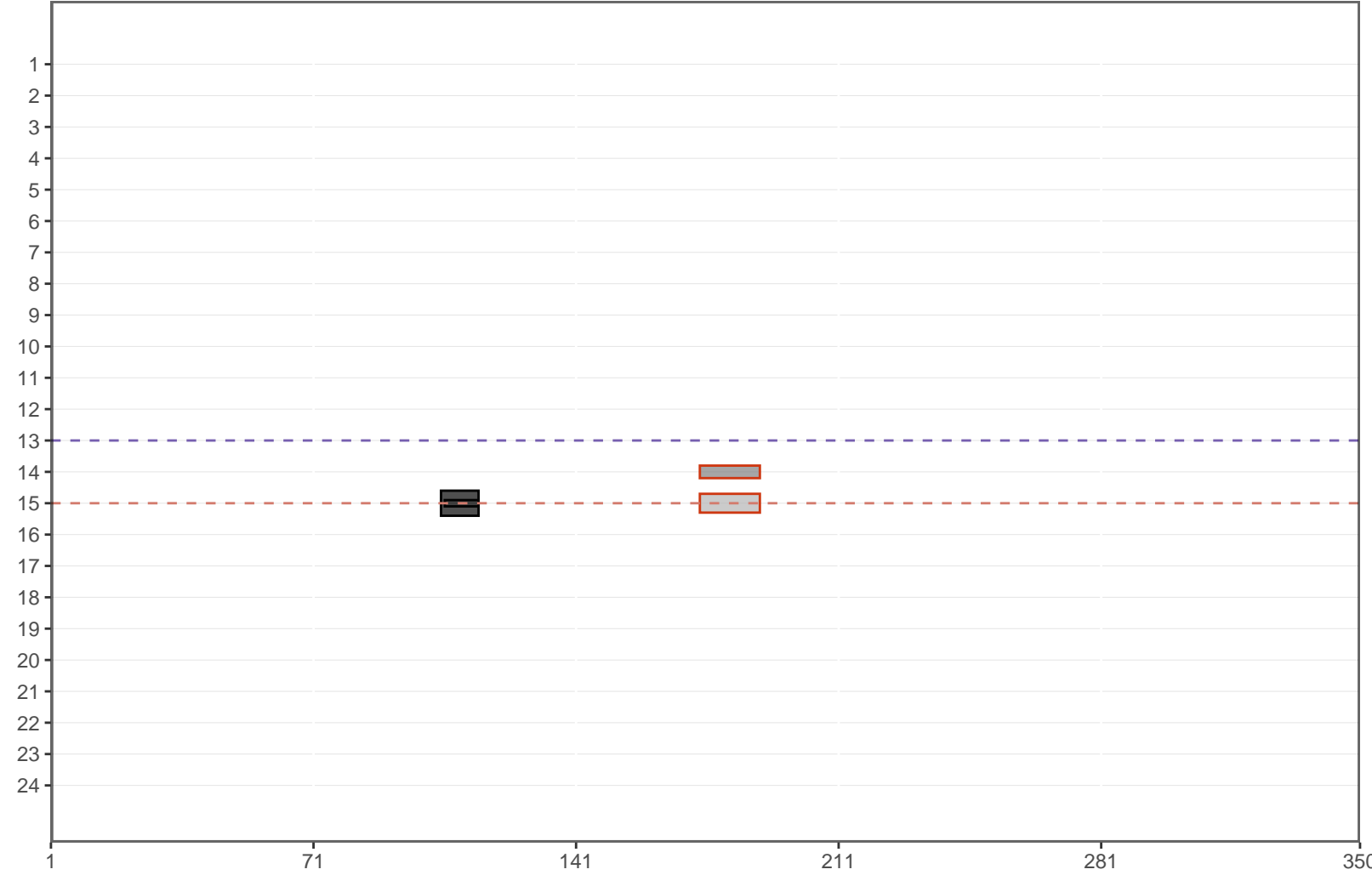
MW indication



Molecular weight

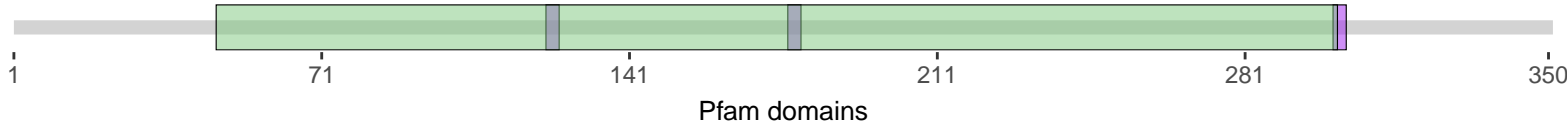


Gel Slice



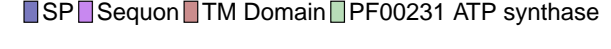
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

◊IELIMTELQKPLNPTQGVSVADDLKNVDFDALRIVYKFGVWVFLPTMSTVLSPFEVVEREAEAGKLGELDSVEVEGAETKAEVLGNLAEQFQSCVMFNVALENAGSEGGARMSAMDSSSRNAGDMLDRILFTYNRVSPLPCLYHHICTVTKLSDMLTQGNRETGFRLKLGHHSSDALLEK

NbL13g07340.1 histone_deacetylase_5 [MW = 72.43 kDa]

No. of times detected



log(intensity)



Values from



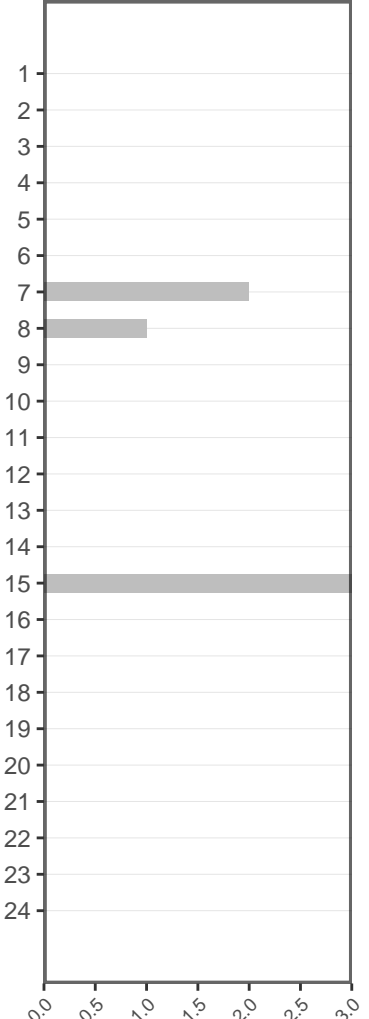
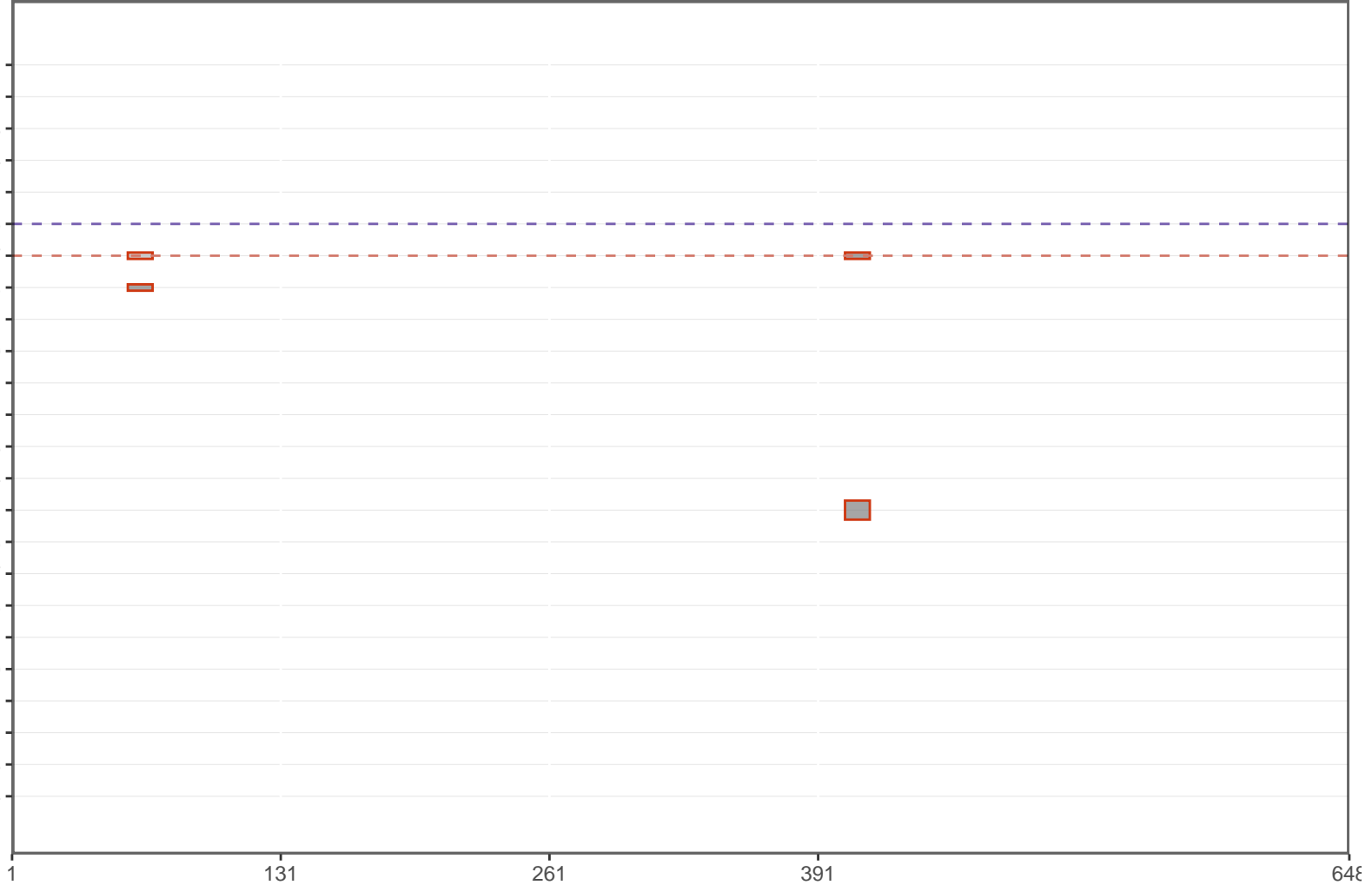
MW indication



Molecular weight

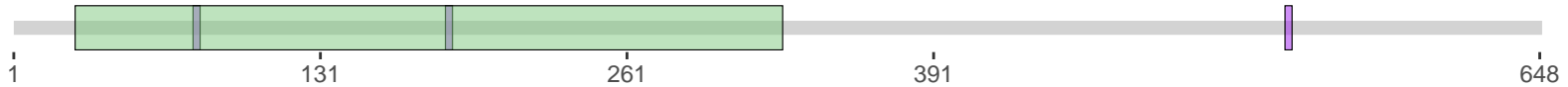


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

.EGSYNLESIANSVKAGIEVLLGQKPIAGSSEAVPFESTWRVWQAVRDKLSAFWQPLAERLTKETKTSMRTPYQAISSDSDEYDTHHTVSGELEKEDIENIQPFSDLKVNDVYHGQACTGHTWRRAELSKIDWYATFGSNMVGSRFLQYIAGGGVEGMQKPGIGLGNKPKKEHWKTFPHRLFFARERTATWGPQGFALFHPESNSEEKAYMGLYRITLQGFNDVLLGENTNFDMISPLFDMTDLHSEIENKGVSAEAWKNGWYHNVLYLQKENSLLLTMTCOLSDIDNFKSGI

NbL13g07320.1 PLASMODESMATA_CALLOSE-BINDING_PROTEIN_3-like [MW - SP = 16.62 kDa]

No. of times detected



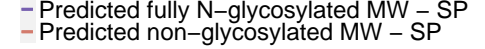
log(intensity)



Values from



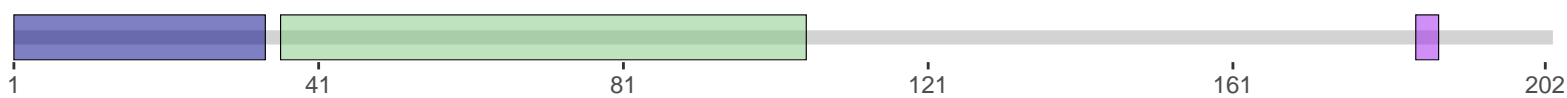
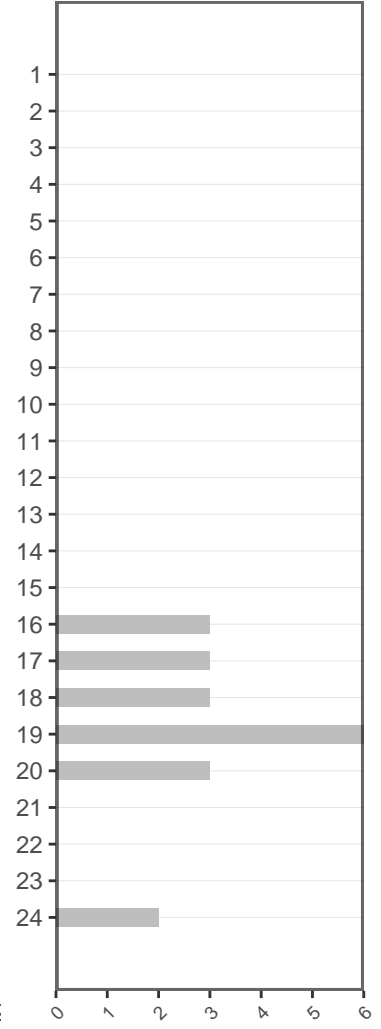
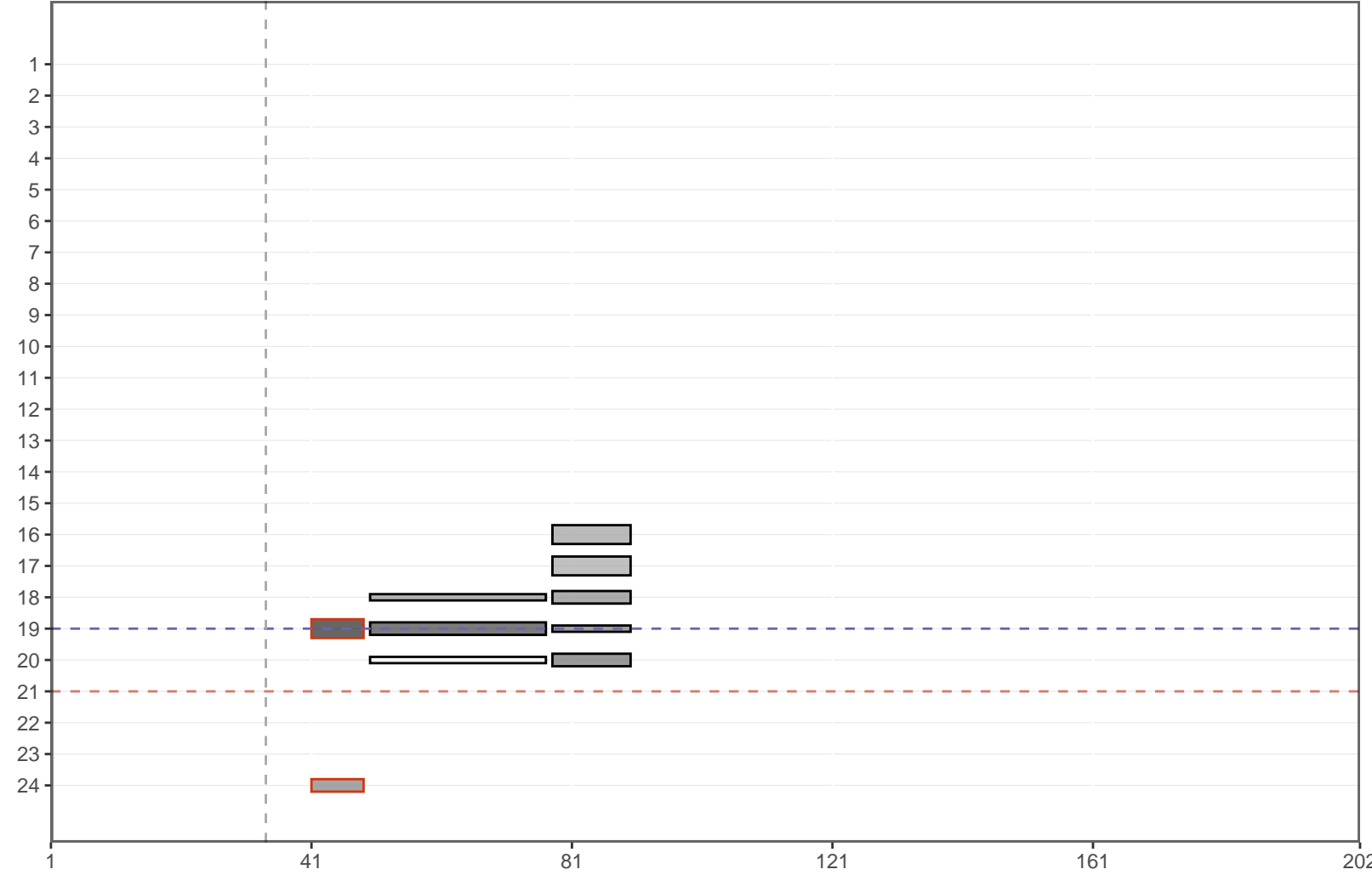
MW indication



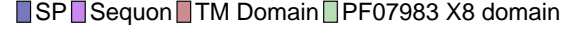
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

YFPQKKGDTSTACDFAGTAVVATDPRSTAGCAVFPVGGSATPTTCTGTSFAIKTPSS6STATGGSPVVNTGILGGVNNGLGPGAGAMNTDISHAGHSIQNA6LFSFAIHSALSF*

NbL13g07280.1 50S_ribosomal_protein_L15_chloroplastic [MW = 28.42 kDa]

No. of times detected



log(intensity)



Values from



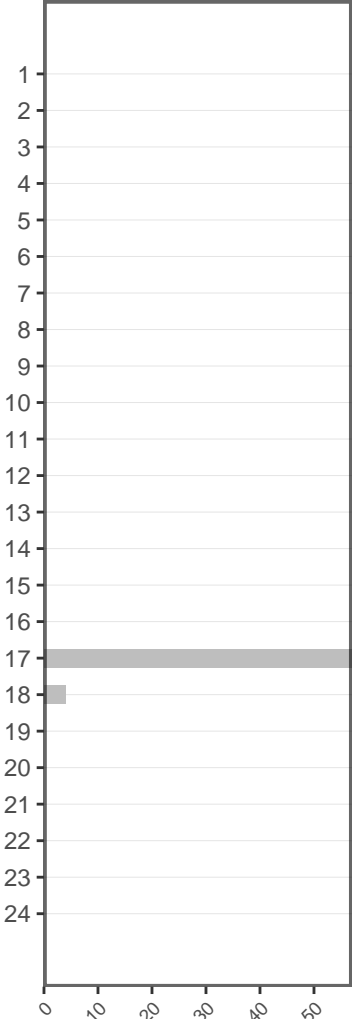
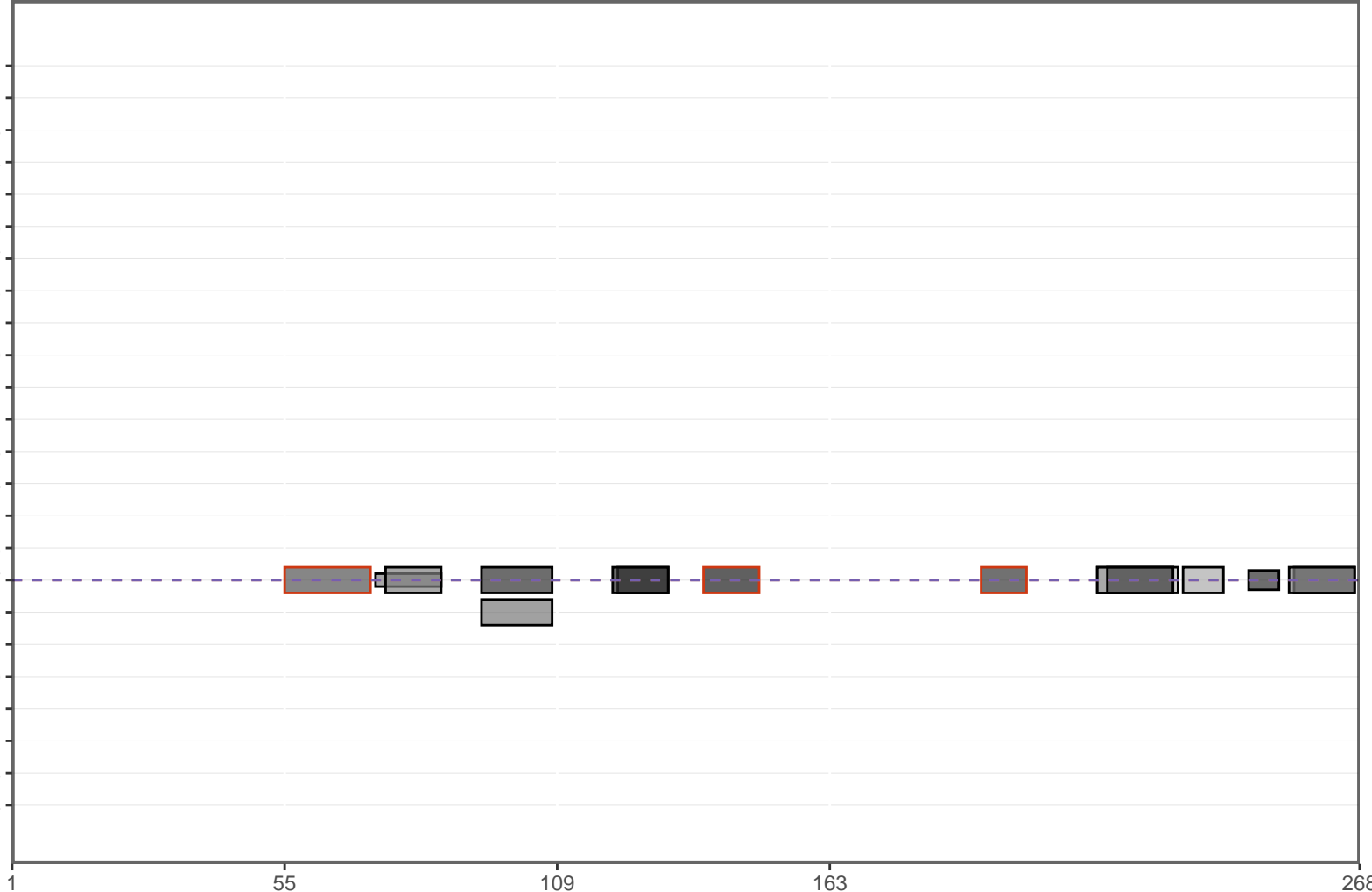
MW indication



Molecular weight

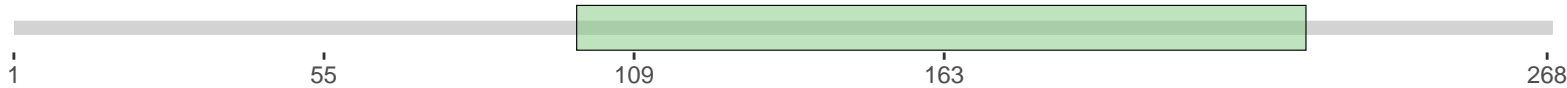


Gel Slice



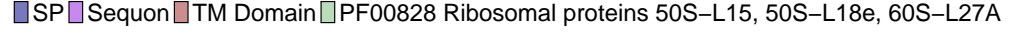
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

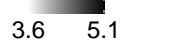
SFEGGQMPLYRRLPKLRIGANGMSAGLPKVVVNLKDAEAGFGECEVSELSLKGKGLINPGRERRRLLPKLGDGELSLKLNFKARAFSTSAKEKLEAAGCSLTVLPGRKRWKWKPEVANKLARADEVFAKRRAAAASEAADPSSA

NbL13g07200.1 UDP-arabinopyranose_mutase_3 [MW = 47.86 kDa]

No. of times detected



log(intensity)



Values from



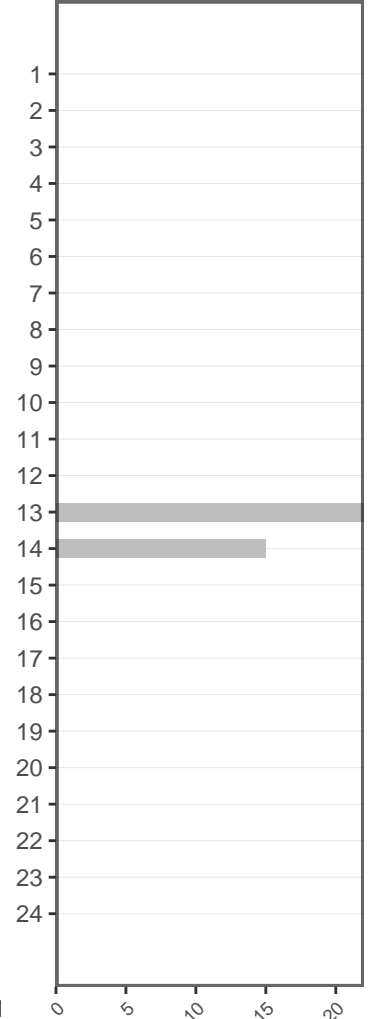
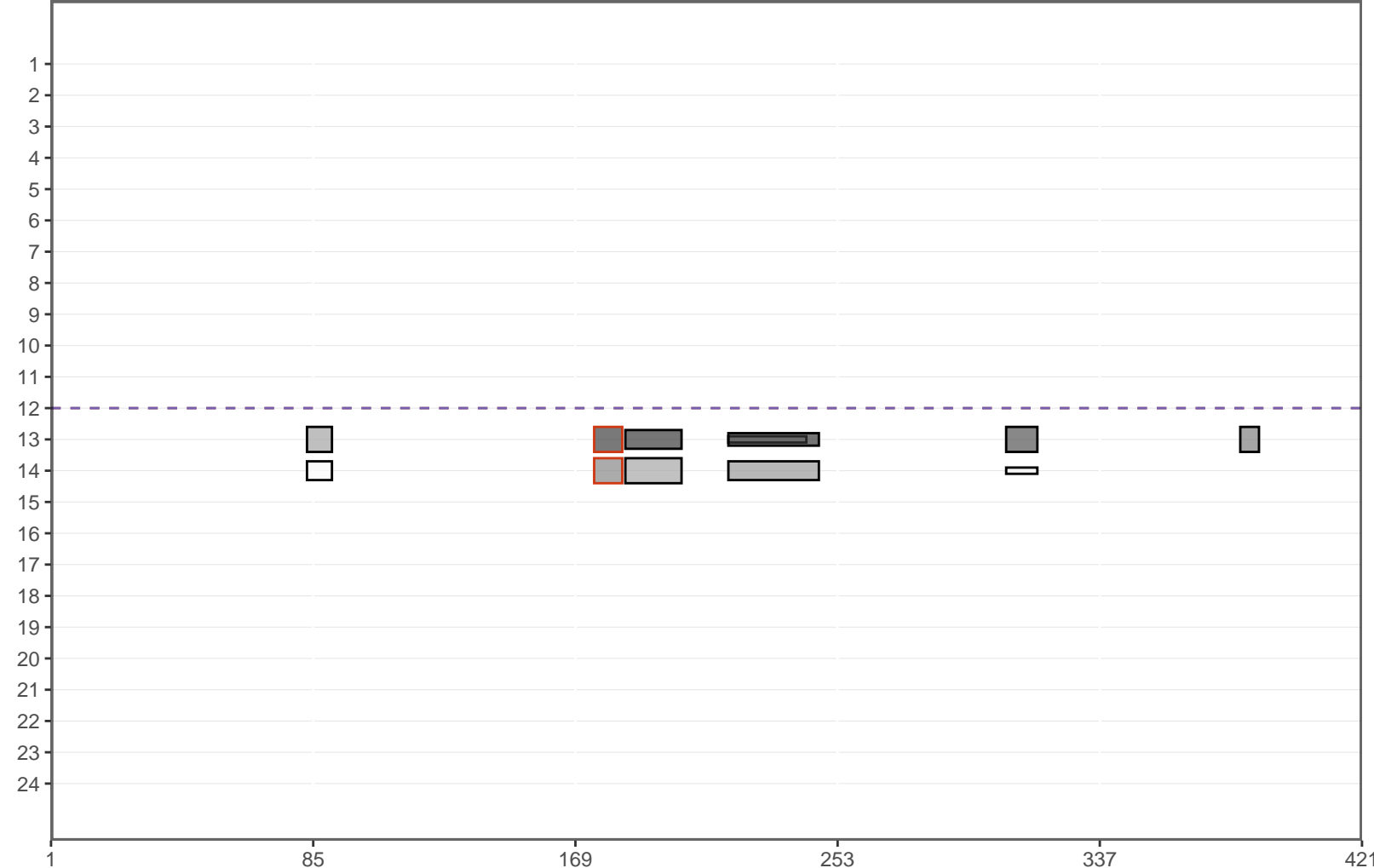
MW indication



Molecular weight



Gel Slice

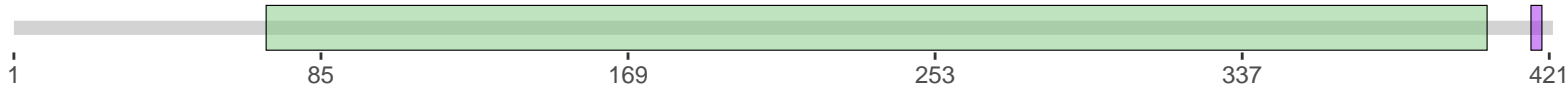


Protein length

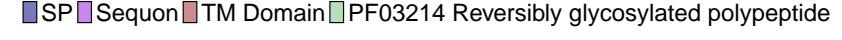


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IRREGADFRGYPFFBLREGVPTAVSHGLWLNIPQDAPFTQLVKPLERNTRYVDAMTIPKGTLPFMCGMNLAFDRELIGPMYFGLMGDGGPIGRYDDMWAGWCTKVKGDHLGLGVKTLGLPYVHSHKASNPFFVNLKKEYKGIYWGDELIPFFQGVALPKDCTSVQKCYLELSKGVKAKLGVKDDVFNKLDAMITWIEAWDELNPASAAAAVAKLPGSSK

NbL13g06990.1 serine_protease_SPPA_chloroplastic-like [MW = 76.98 kDa]

No. of times detected



log(intensity)



Values from



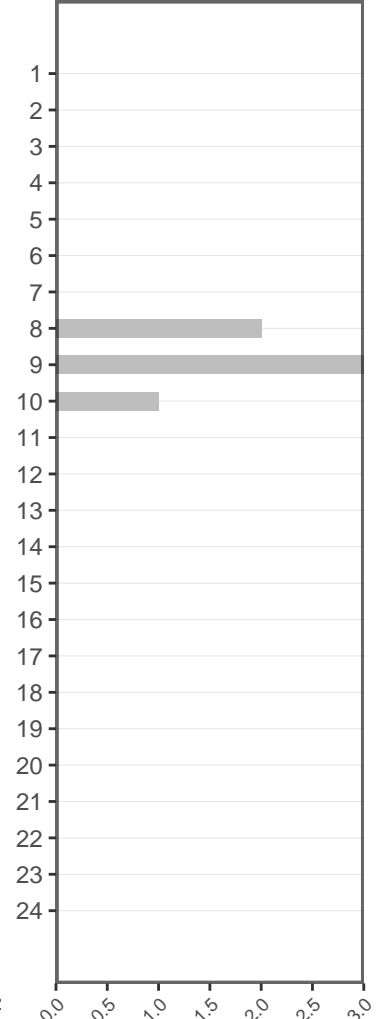
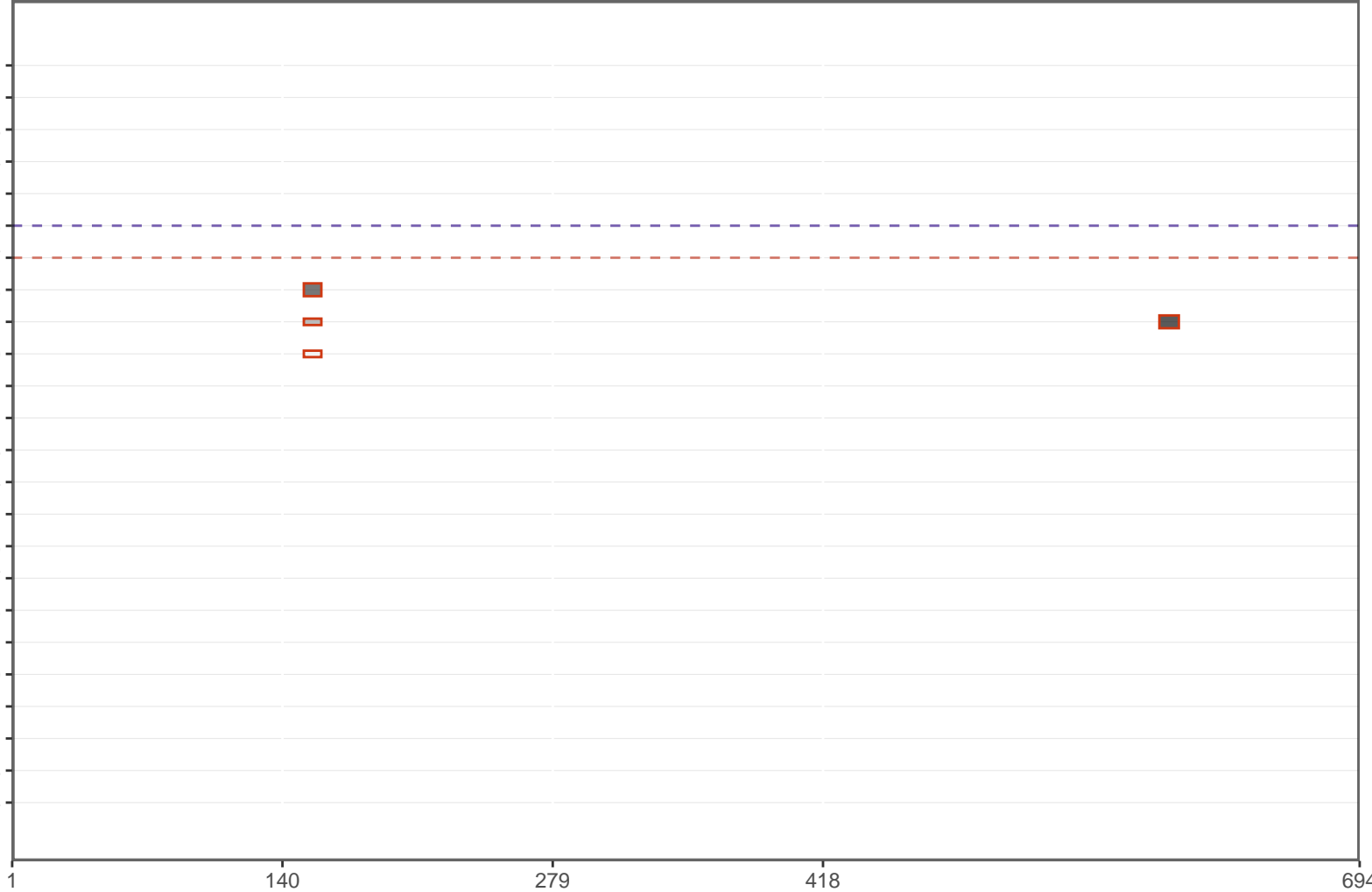
MW indication



Molecular weight



Gel Slice

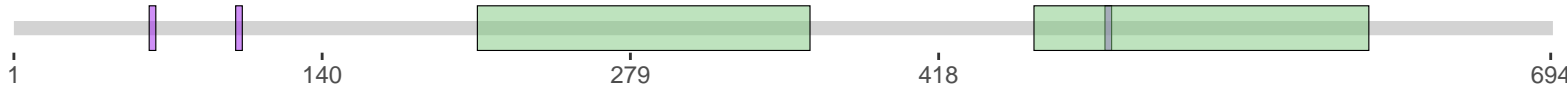


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IVERLKEESWTDIKYDDEVMSMLKERLEIPKDKLPLWIDYRKYRVRVWFLGLTGYKEQWIRASGSSISRTGRFSSSSGGVAEQLEKIRSVRESKRYKAVLVRIDSPGGDALASDMLWREIRLLAETKPLVMSMADVAASGGYMMAMATGAVAEINLTLTSSGIVTGFKNLGNLYEKIGFNKEISRGRVAELTAEGORPFRPEEAELFAKSGAHAYTOFRDKAALSRSMTVDMKEEVAGRRVWTFGNALSRGLVDAIGGLSRAWAIAKQKANIPOEKQVSVVELSRPSASL

NbL13g06970.1 L-2-hydroxyglutarate_dehydrogenase_mitochondrial [MW = 45.77 kDa]

No. of times detected



log(intensity)



Values from



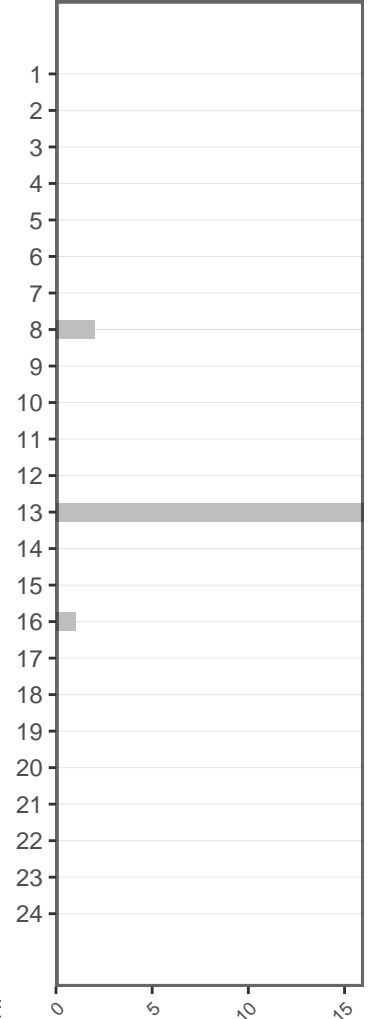
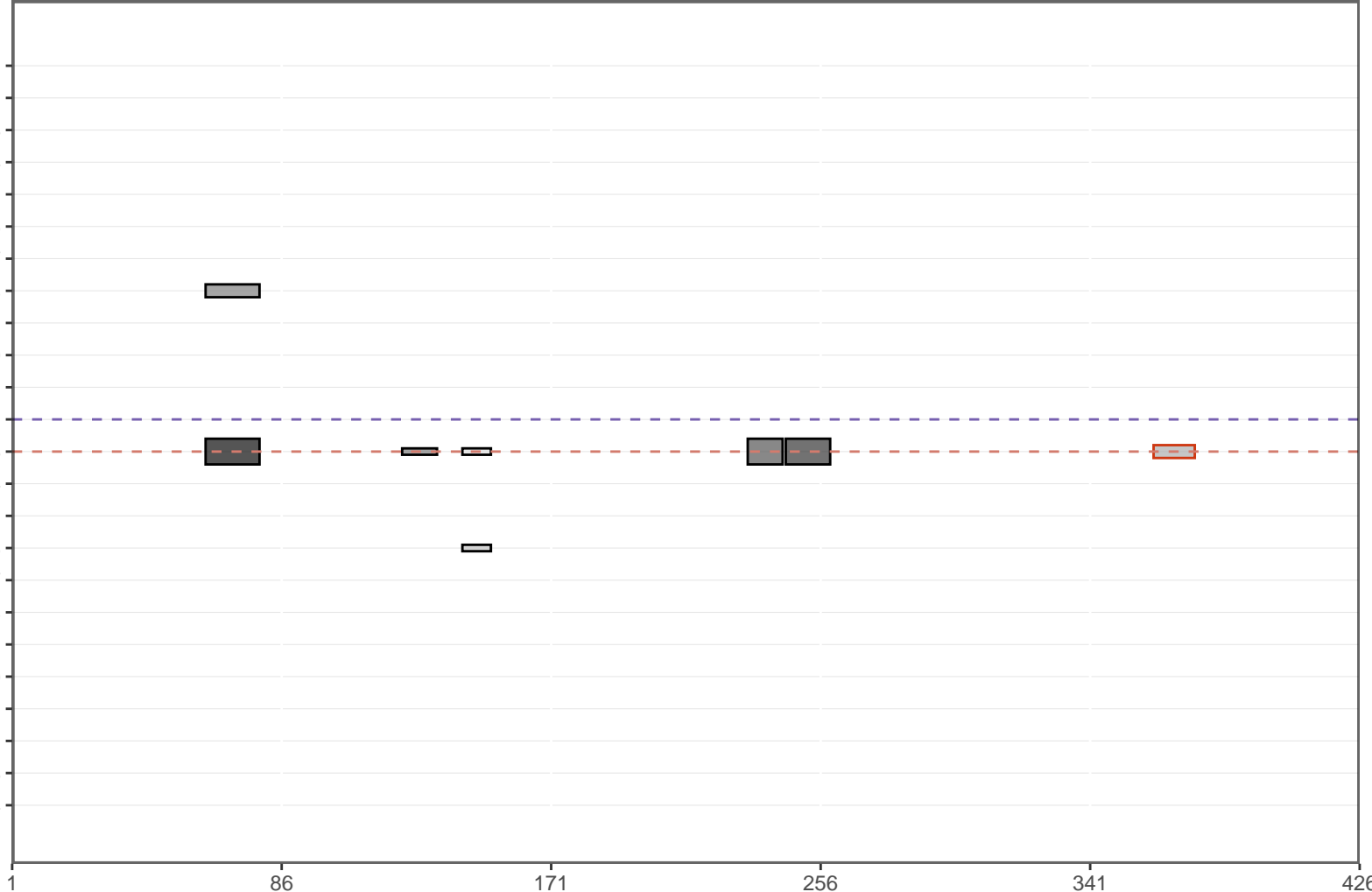
MW indication



Molecular weight

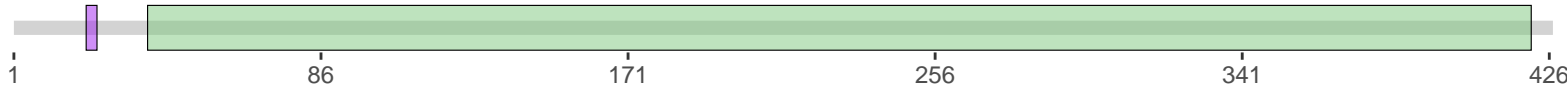


Gel Slice



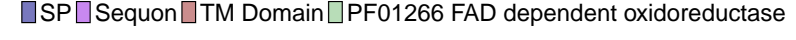
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ITTSYNTAVGGHIEGNGQIHVWGSNANWNGRSELDSELVLRPLVANSAGLSAPAAKRMKGLPDGIPASHYARGGYFTLSNKKSPFRHLVPIPEVGLGVHVTLDLNGVKFGPDVEVWGGCHDIPSFNMFQYVIRREDRAKGFYPAIRKYYPAKDKGSLPEGYAGRPKLGGPEEGTDFVGGEDHGGSLGNLFGIESPGLTSSMAAEHVAALKLK

NbL13g06910.1 enolase_1_chloroplastic-like [MW = 24.4 kDa]

No. of times detected



log(intensity)



Values from



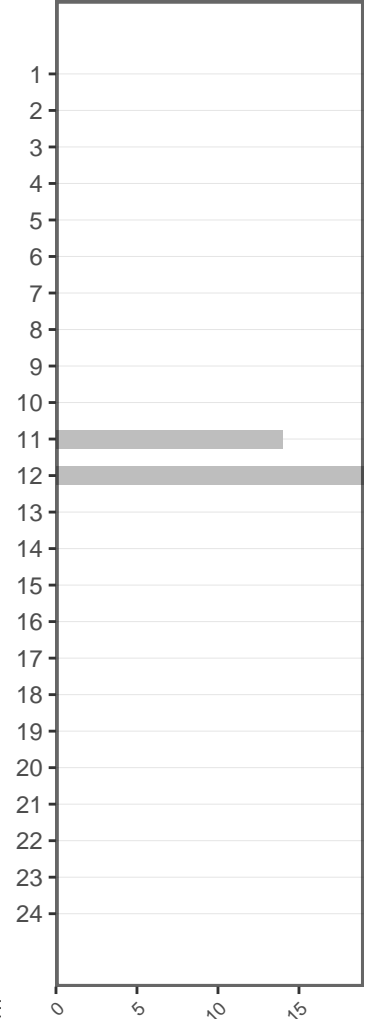
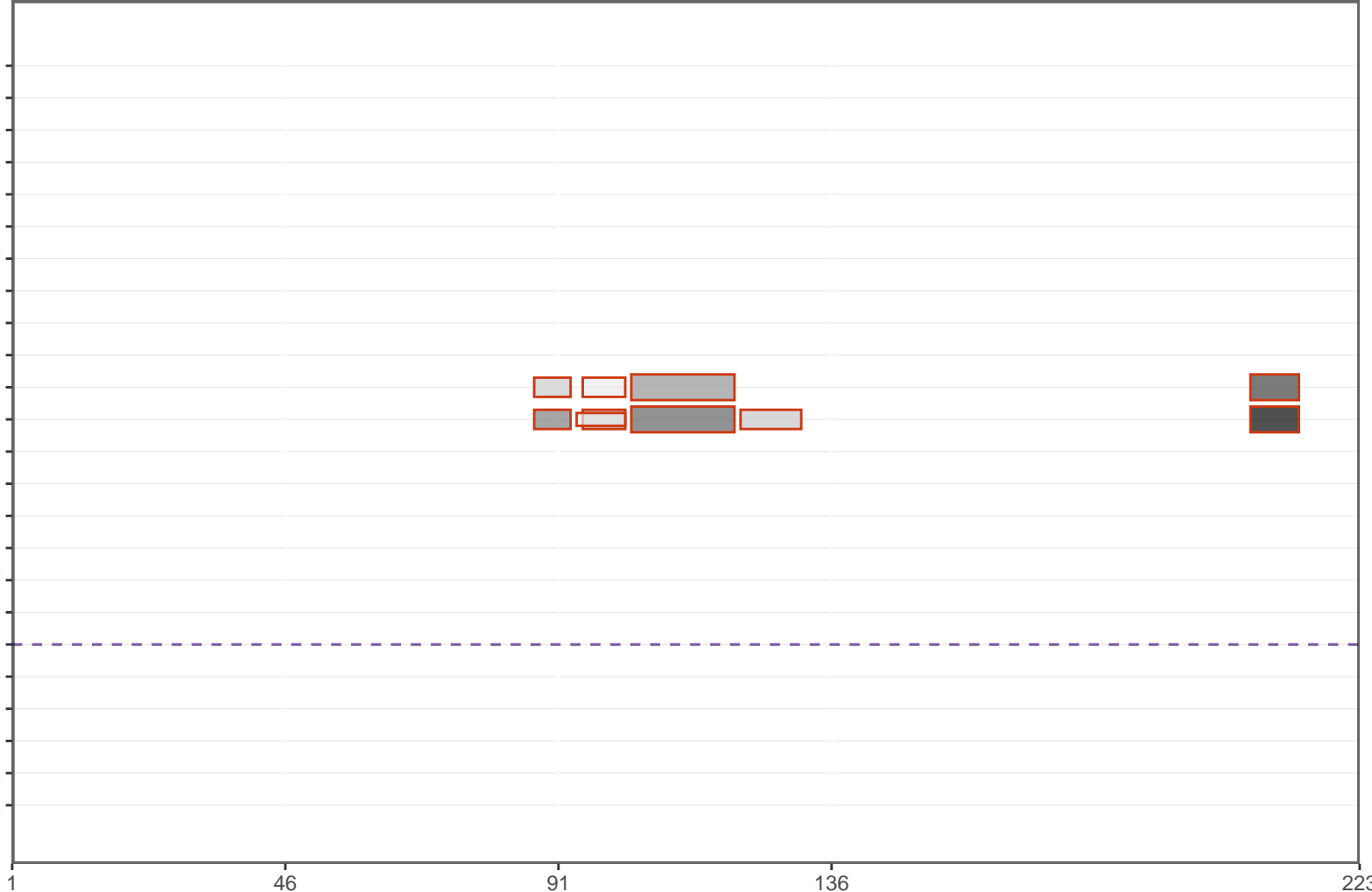
MW indication



Molecular weight

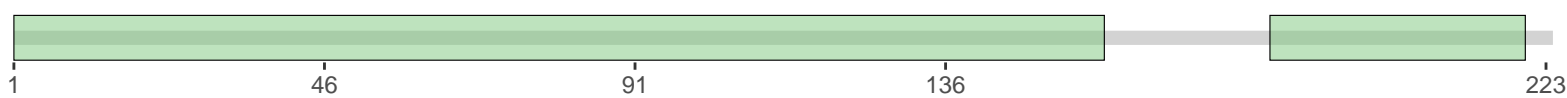


Gel Slice



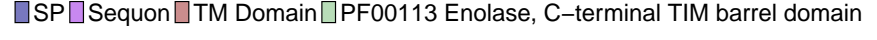
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LLLYKVGIGTITTESGKALDSKAAAGWGMVSHRGGTEDFADLSVGLAGGQVLSSTSSGSLVNLHLSQRHQGHINLLNSPVMQKTAGPCRERLAKYNOLLRIEELGQVRVAGESFRSP

NbL13g06900.1 enolase_1_chloroplastic [MW = 14.76 kDa]

No. of times detected



log(intensity)



Values from



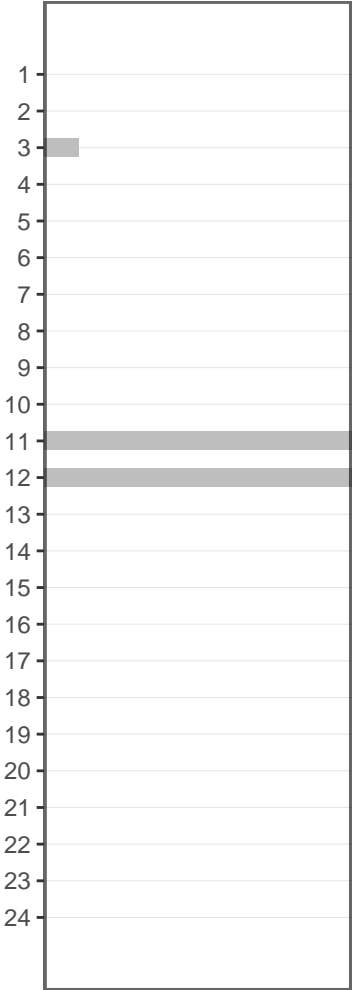
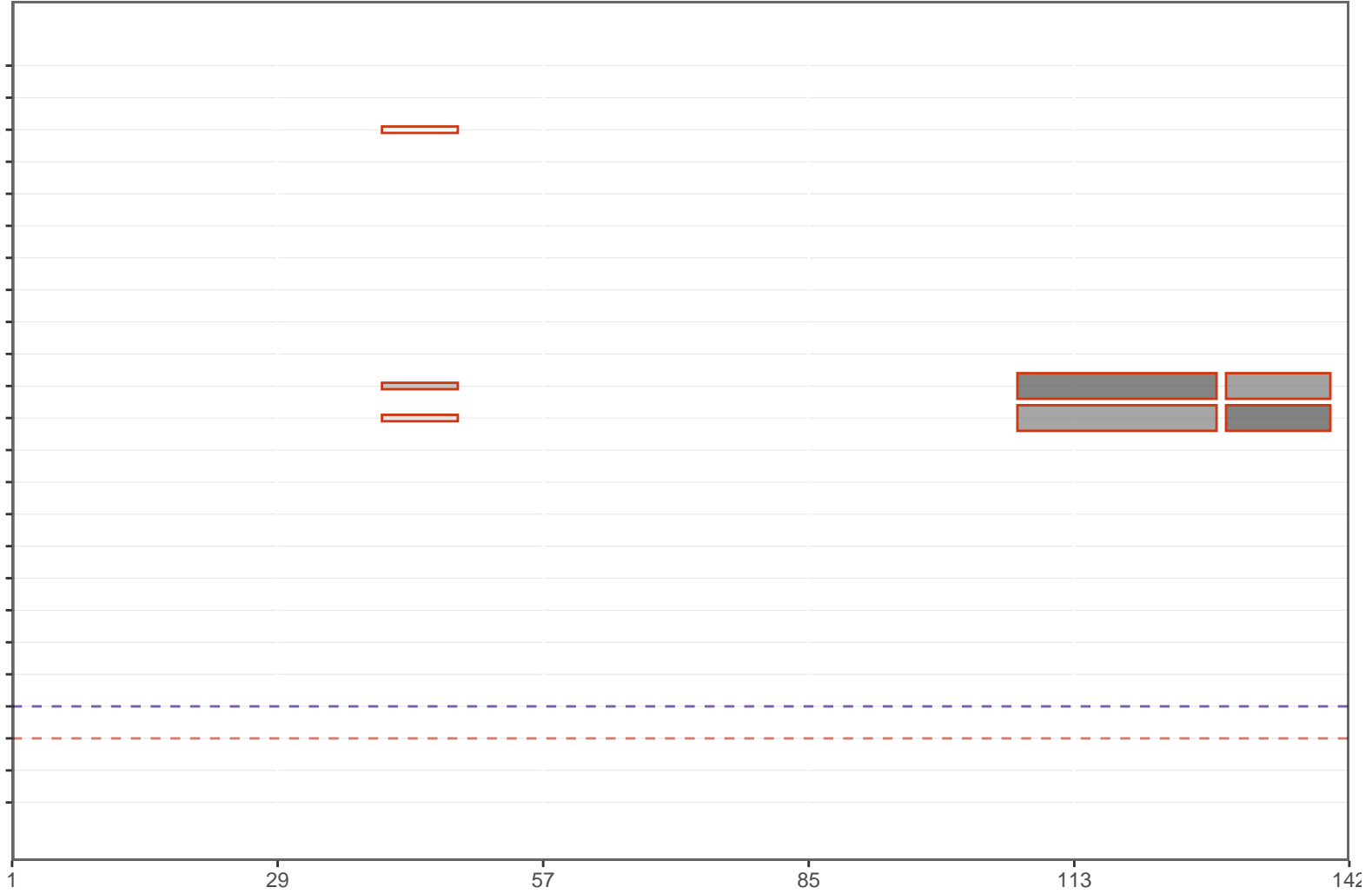
MW indication



Molecular weight

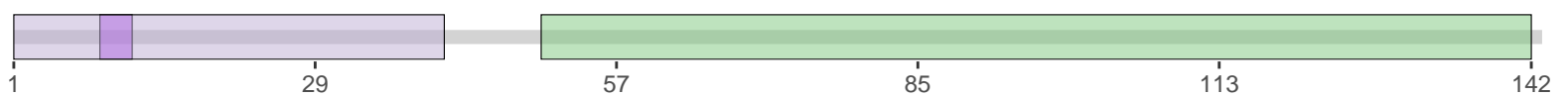


Gel Slice



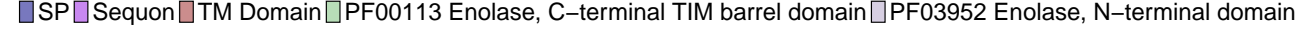
Peptide counts over 4 repeats

Protein length



Pfam domains

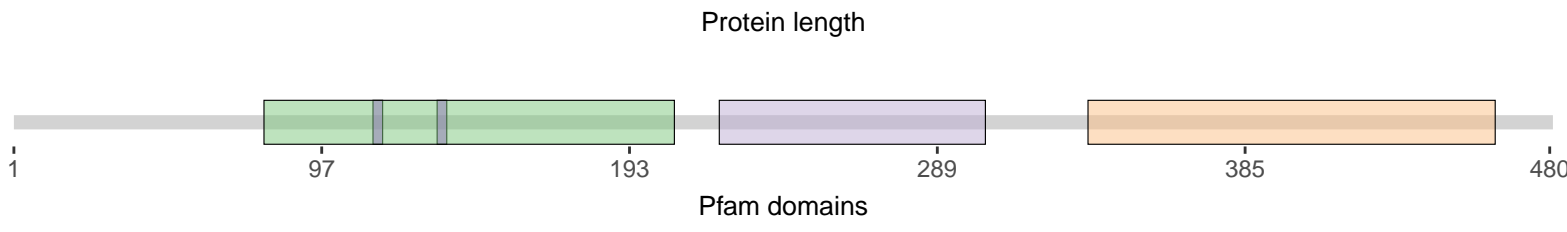
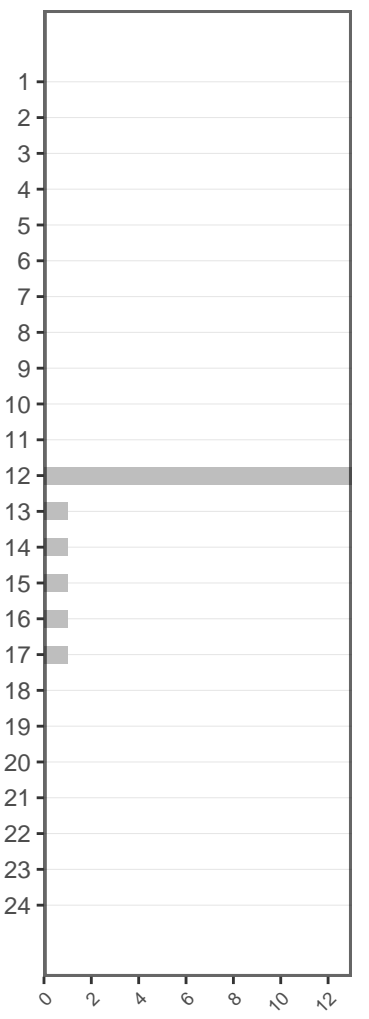
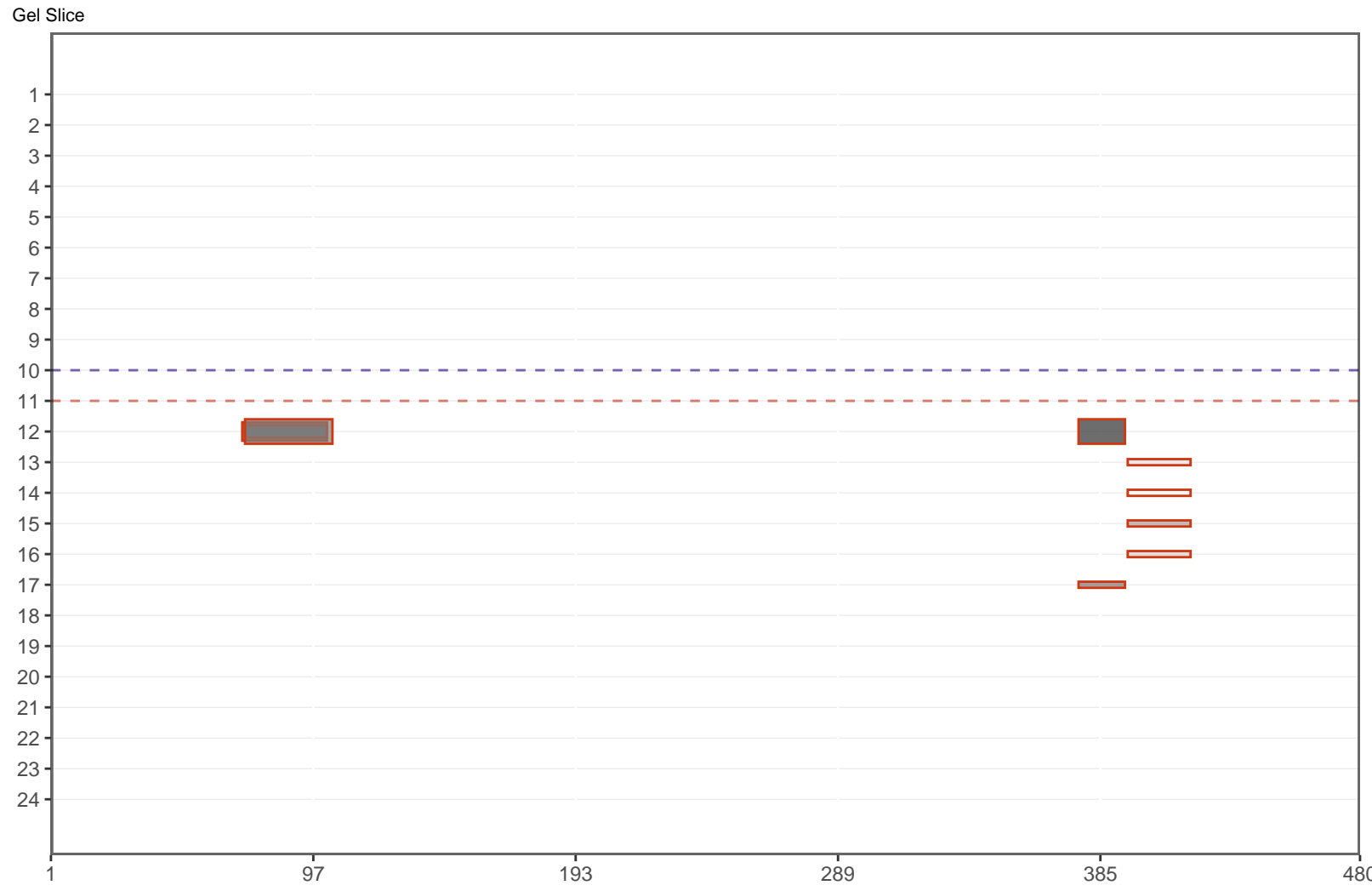
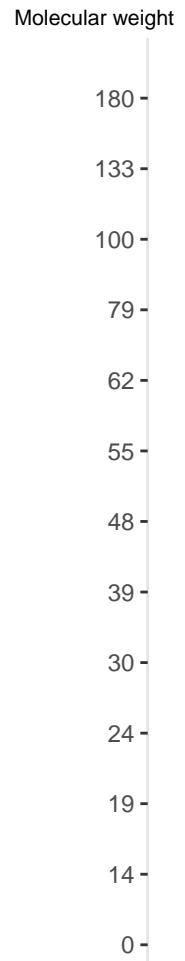
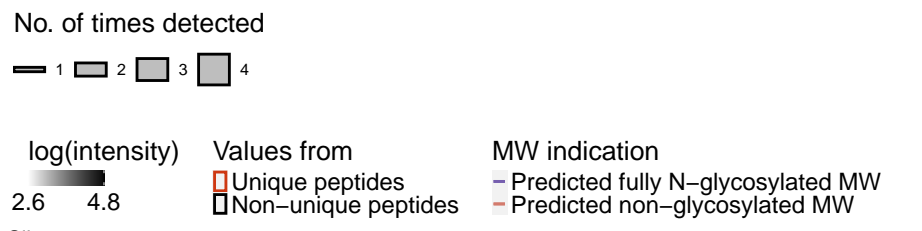
Pfam Description



Protein sequence:

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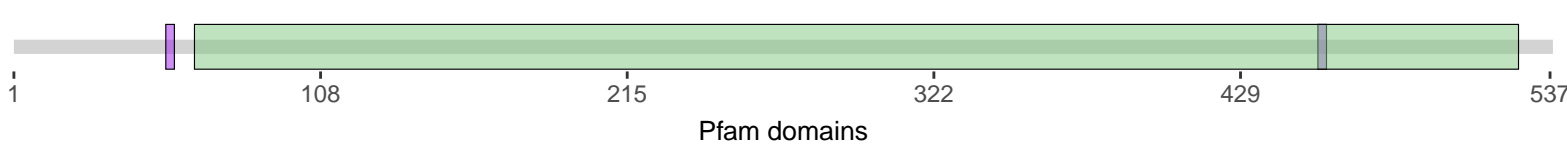
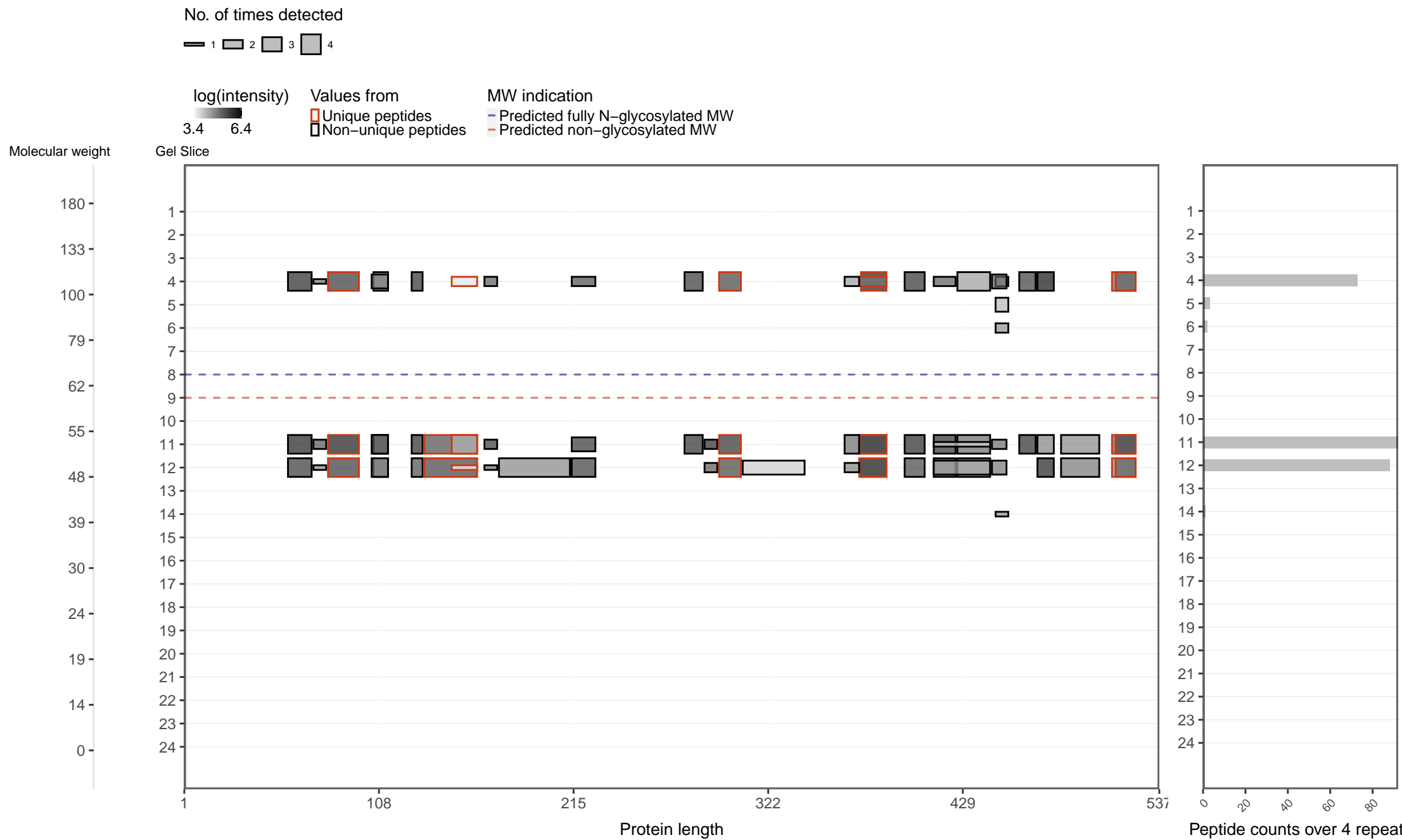
NbL13g06790.1 1-deoxy-D-xylulose_5-phosphate_reductoisomerase_chloroplastic [MW = 52.08 kDa]



Protein sequence:

IEHSALFCCOGLPEGARRRILRTASGGAFRDLPEVKEKVEKVDALKHPNWNMGKKTVDSATLFNKGLVIEAHYLFGAEYDDIEVHPGSHHSMVETQDSSVLAQLGWPDMRLPLVTLGWPDRRYGSEVTVPRLDLKLGLSTFKVPDNNKYPSMDLVAAGRAGCTMTGVLGAANEMAVELFISERICACFRISGLDFIKVLELCAKHKREELVSSPLLEEHHYDLWARDVAASLETTAGFSPALV

NbL13g06590.1 aldehyde_dehydrogenase_family_2_member_B4_mitochondrial-like [MW = 58.47 kDa]



Pfam Description
 SP Sequon TM Domain PF00171 Aldehyde dehydrogenase family

Protein sequence:
 SGFGPTAGALASHMMDVQKLAFTGSETGKTVLELAAKENLKPFTLELGGKSPFICEDADHDHVELAHFALFFNQGQCGGAGSRTYHERVYDFEIKAKARRMRRVYDGFKKGVEGGPQIDSEGFQKLYRIRSGRDSATLEGGDRFGKGYFQPTVFSNFKEDMLAQQDEIFGFPVGVVFKFKDIEKIKRANRTRVYLAAGVFKRNDTANTLTRGLRAGTWWVNCYDVFDAQIPFGGKYMMSGMGRKGGVSLNVLGVKAVVTRPLKNPWP

NbL13g06550.1 aldose_1-epimerase [MW = 36.68 kDa]

No. of times detected



log(intensity)



Values from



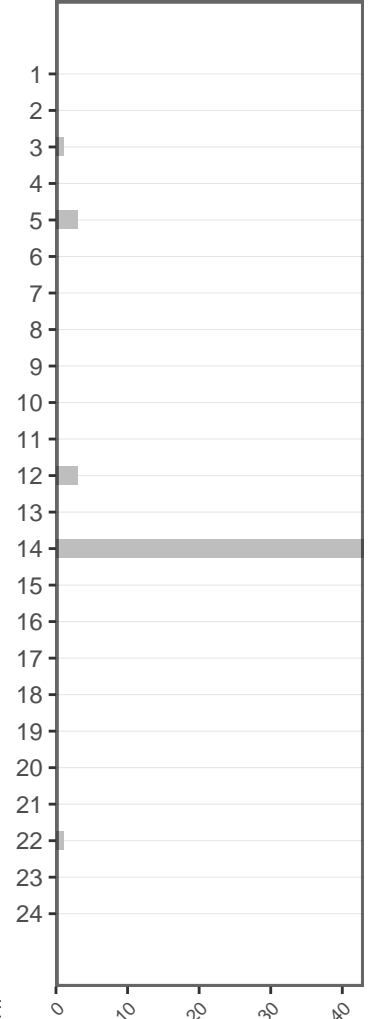
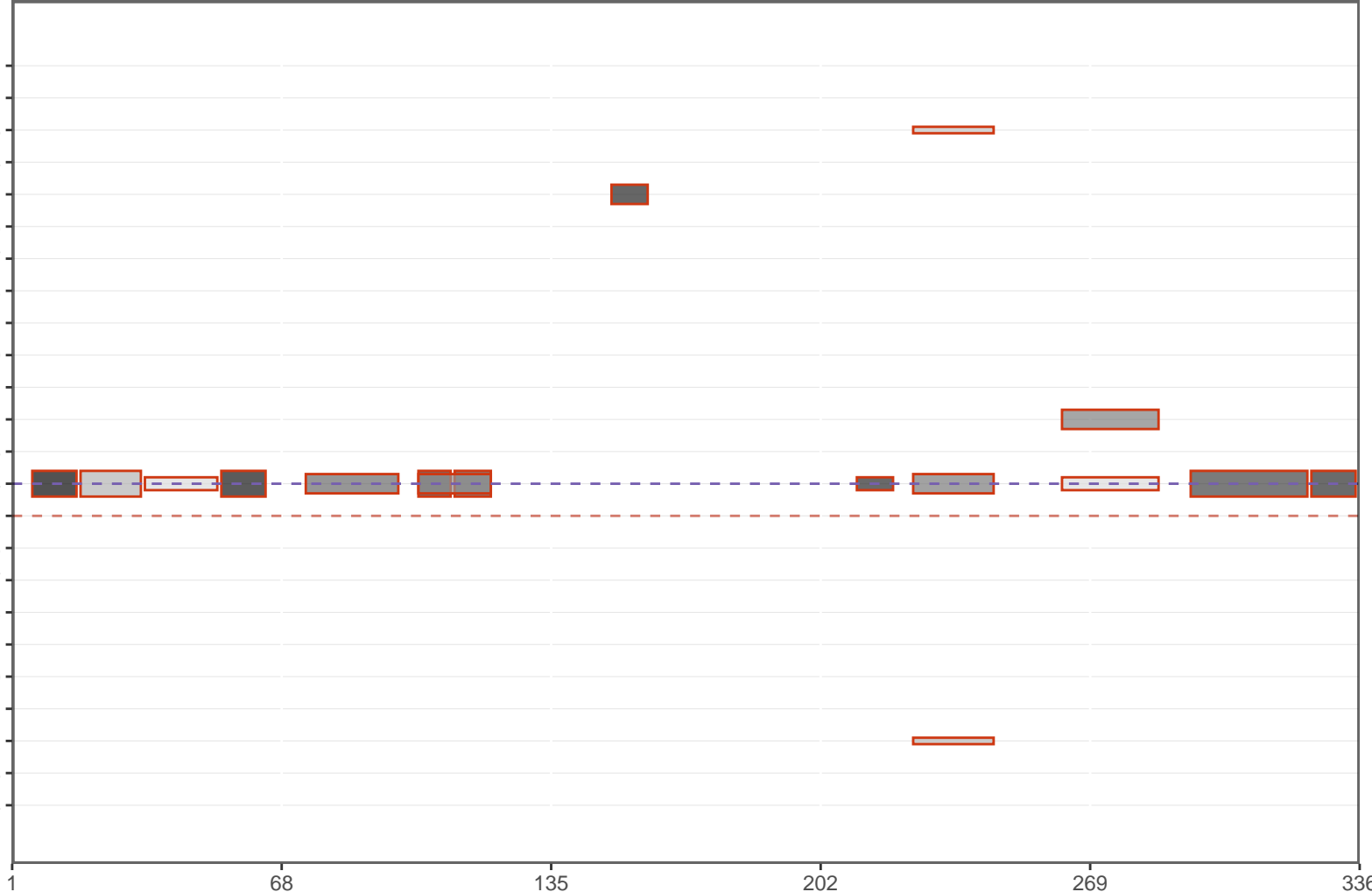
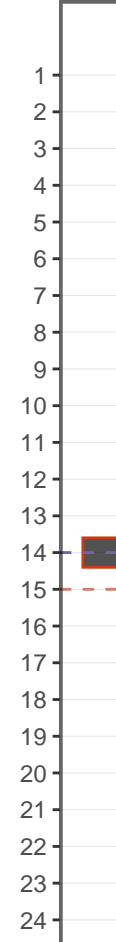
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

/PANKPTVSLAQHFYWNLGGHNSGDLQNTAGIWNHPTVDGNIPTGEMPVKGTDFDFAEKIGRDRDGGVGLGVDHNYVLDGGVKKDGLKHAARKPKSSRVLNLWTPNAPMGFYTANNVNGVYKGGAVYKHKHGVGLETGGFPNAVTPNFPSPVIFQDQKYYHMLYFESIE

NbL13g06510.1 outer_envelope_protein_64_chloroplastic-like [MW = 63.68 kDa]

No. of times detected



log(intensity)



Values from



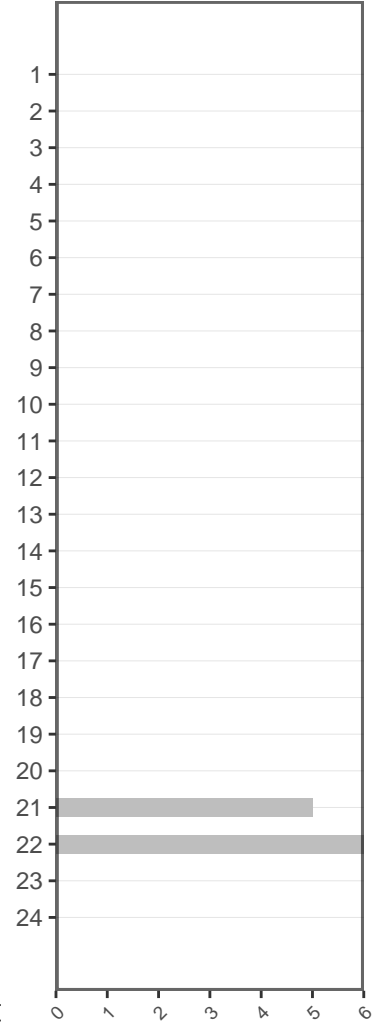
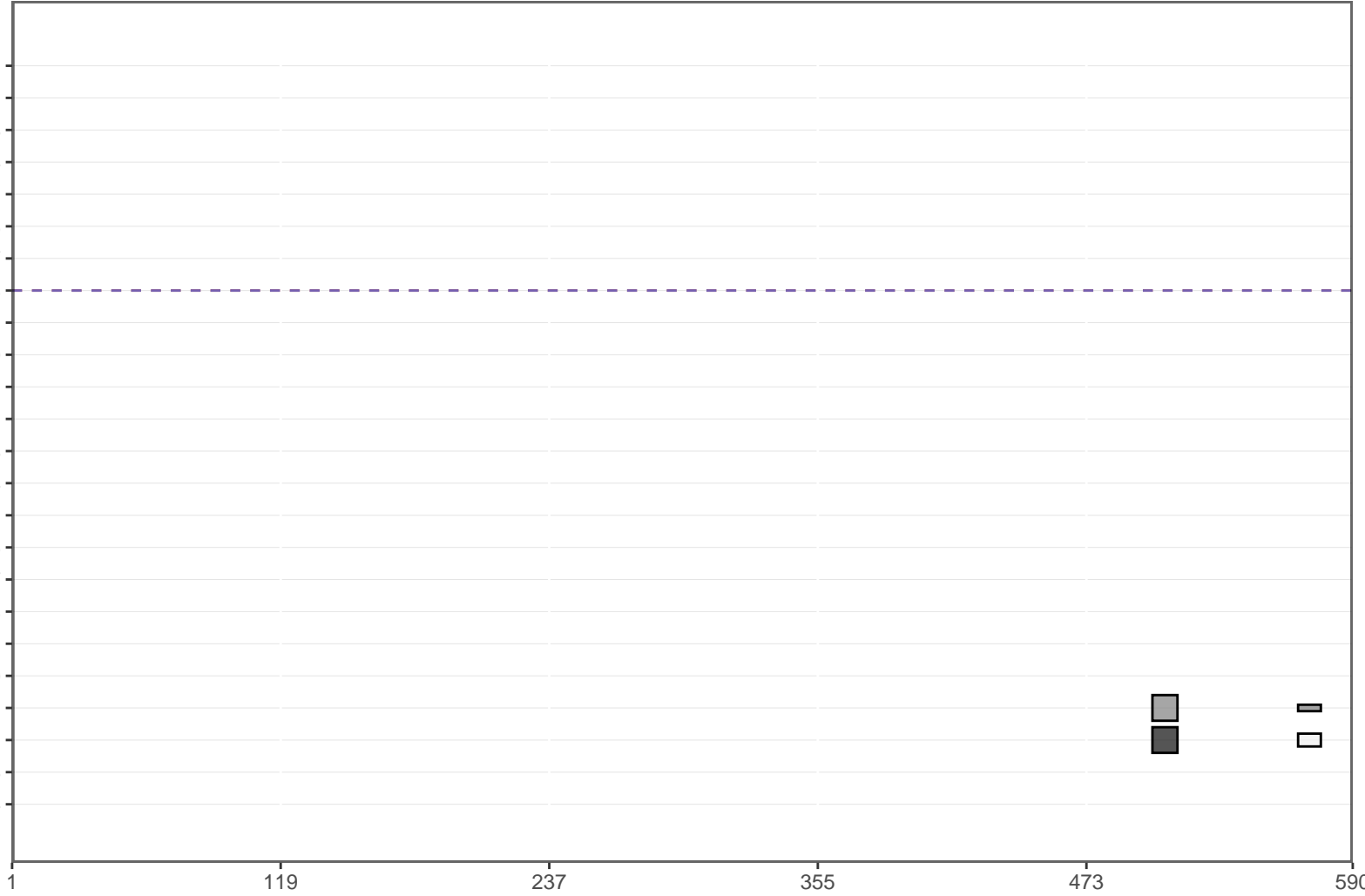
MW indication



Molecular weight

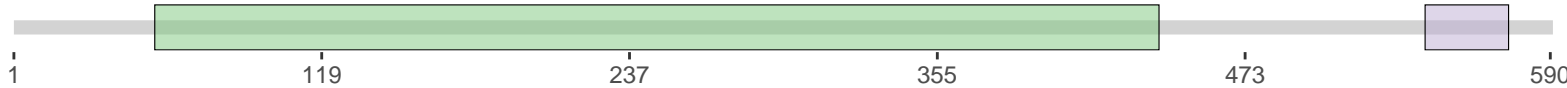


Gel Slice



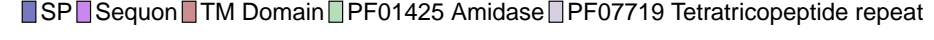
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

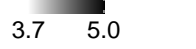
.KQFACKXSDSERKSSSTNLLAYVMHLKRHFQGYHLEWINEAKPNLDPVISAQGGGPEFTDTNENGHAVRNELRSALNDLLKDDGLVPTVSEAPPKGAKIEGSEDEYQIRSGSFSASMSGGGGVCPMGFHDKDKPTSEVSEVARGGGDRFLDITGSMYASLQEQAEVATKSGNIAISKEASAEEMAKEKGNQAYKDKQWQKAIGFTEAIKLNQNTATYFENRAAAVLEMGNFQAEADGSKAIDLKQNKVAYLRRTAREMLGYKKEAIEDFRYALVLEPTNKRA

NbL13g06400.1 splicing_factor_3B_subunit_4 [MW = 38.89 kDa]

No. of times detected



log(intensity)



Values from



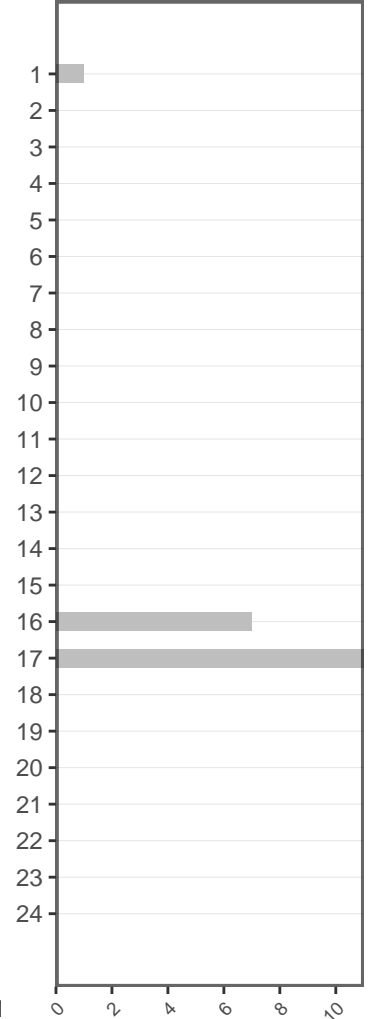
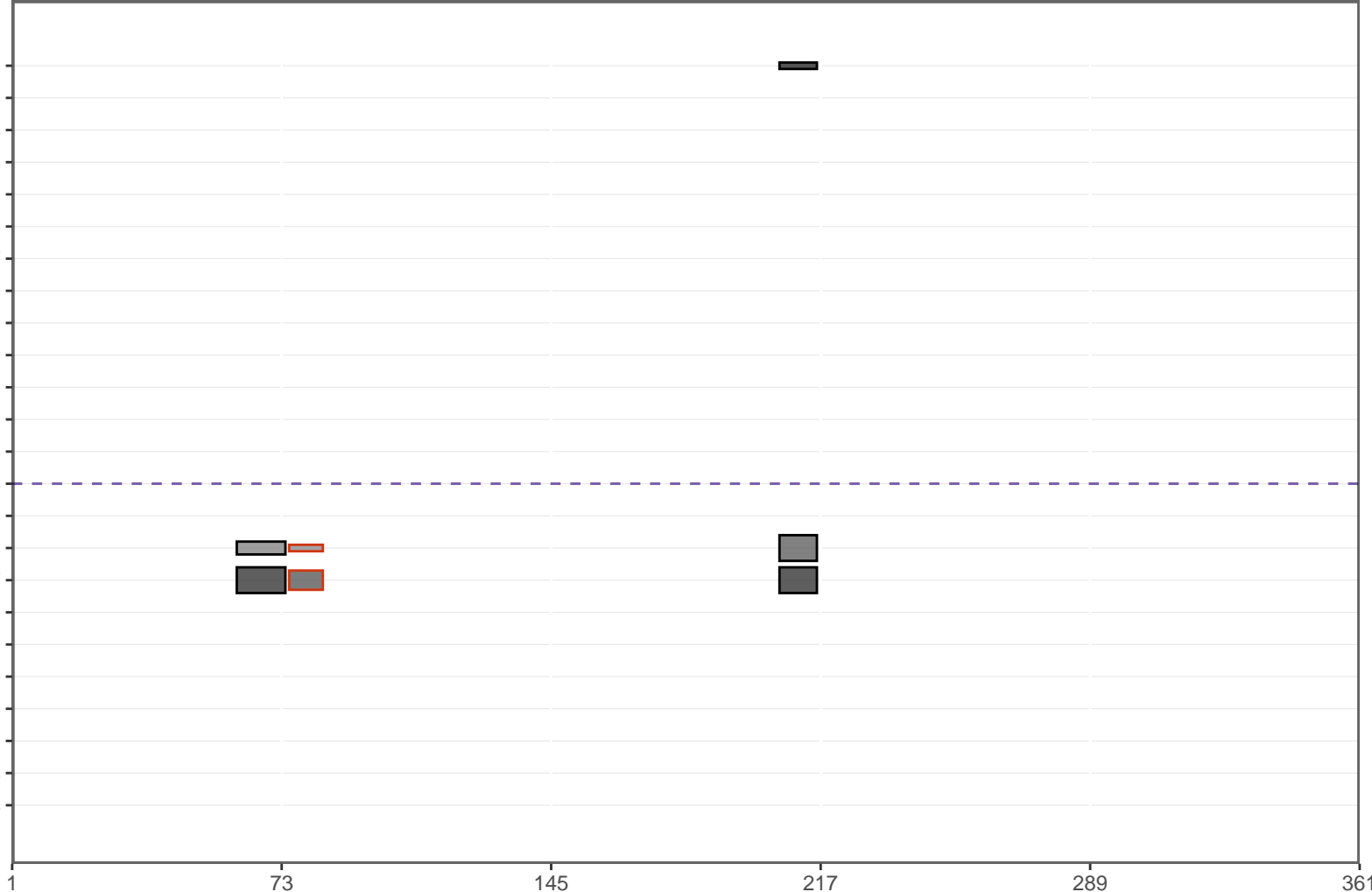
MW indication



Molecular weight



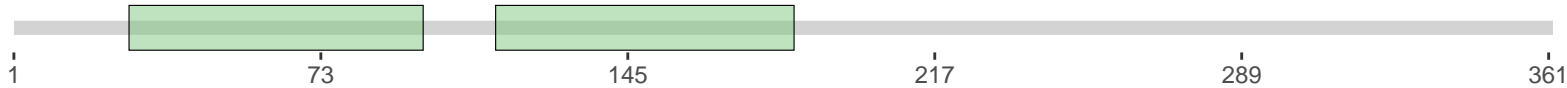
Gel Slice



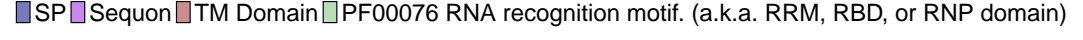
Protein length



Pfam domains



Pfam Description



Protein sequence:

EAMNGQYLNRQFTVSWAKKDTKGERHTPAERVLAAENFGTKNRPHTMFASGPPSPVQANGAVGTPGPPRFETNGPPIPAIPARIPRRPMPQVNVYPPMQMPAPQAWGHPMGPFGAGIPQQGMQFRGMPPPPPPQVAPPLNRPPLPPAAAMAQVWRPPPPPHLNGGPIYHMPHISMGMGPPPPAAGI

NbL13g06230.1 T-complex_protein_1_subunit_delta-like [MW = 57.73 kDa]

No. of times detected



log(intensity)



Values from



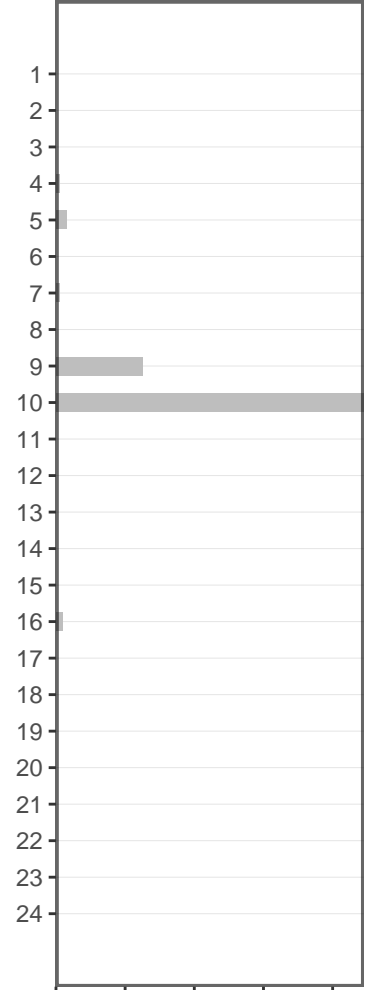
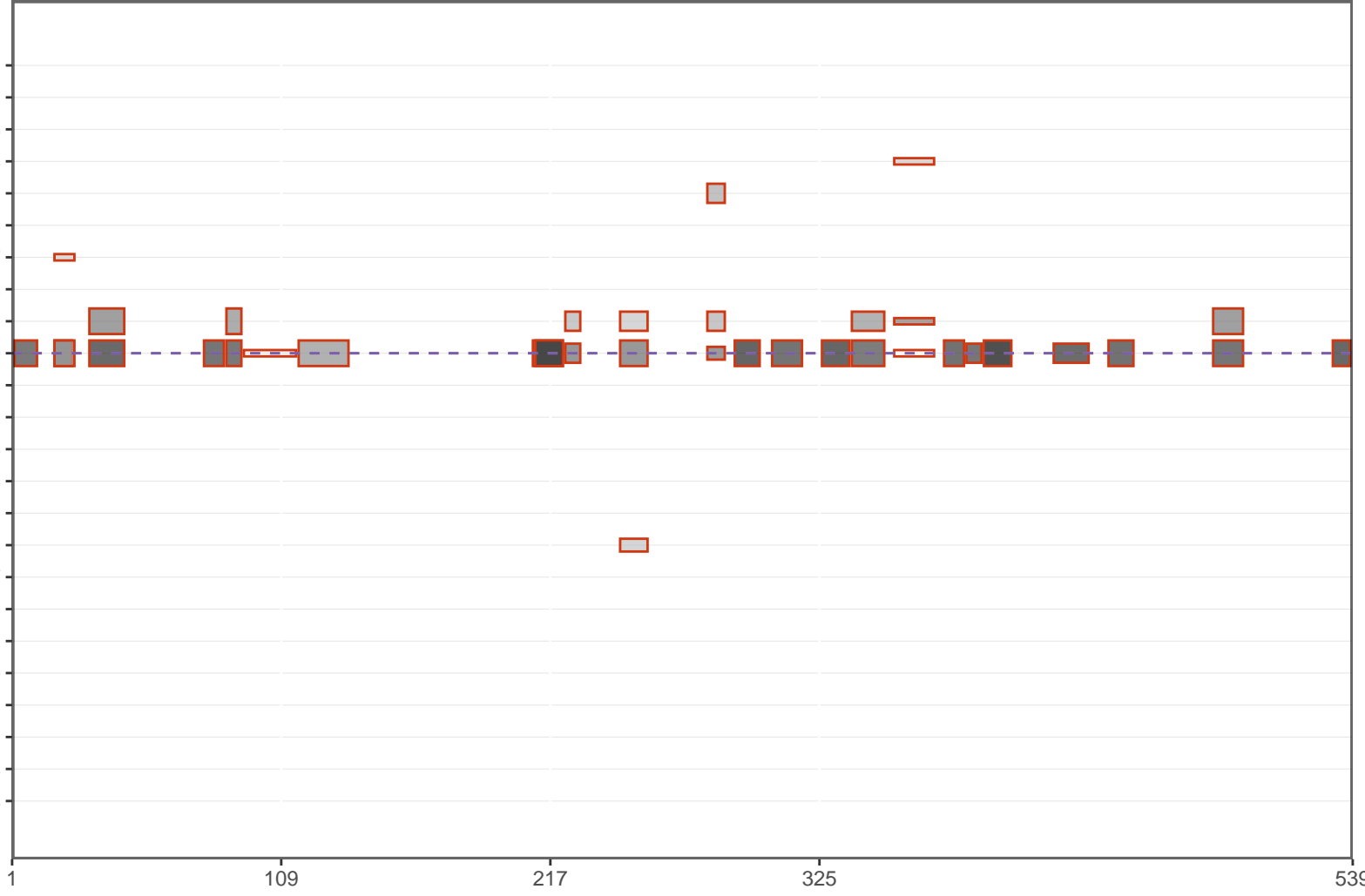
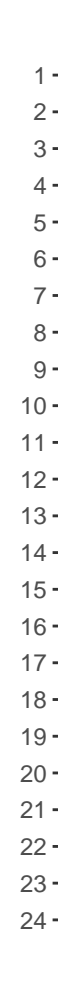
MW indication



Molecular weight

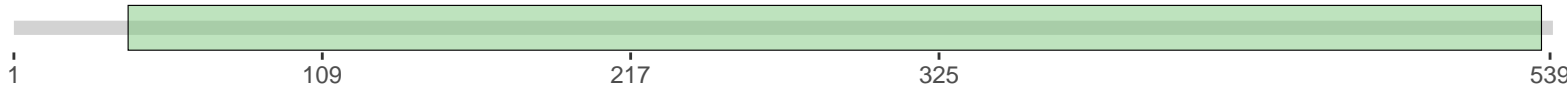


Gel Slice



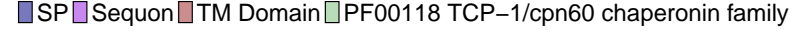
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

PKTDIEQSIIVSDYTGMDRLKEERNYILGMKKIKATGCVNLLIQKSLRDVATELSLHYLAKAKIMVKNVDEIEFRTKLNGLPIANDHFRAEKLGFDLVVEISLGGGGKVIWITGGQDMGRTEFLVIRGEGNQLVDEAERSLHDALGVVRGLVSKRFLIAGGGAPAEIERSQLGAWAKVLQGMGEGYGVRFAGFALELVYPYTLAENAGLNPIAVTELNRNHAGGEINTGNVIRKGDIANLEENVVQLPLVSTSAISLATEQVRLMKIDDIVTVR

NbL13g06150.1 guanine_nucleotide-binding_protein_subunit_beta-like_protein [MW = 39.92 kDa]

No. of times detected



log(intensity)



Values from



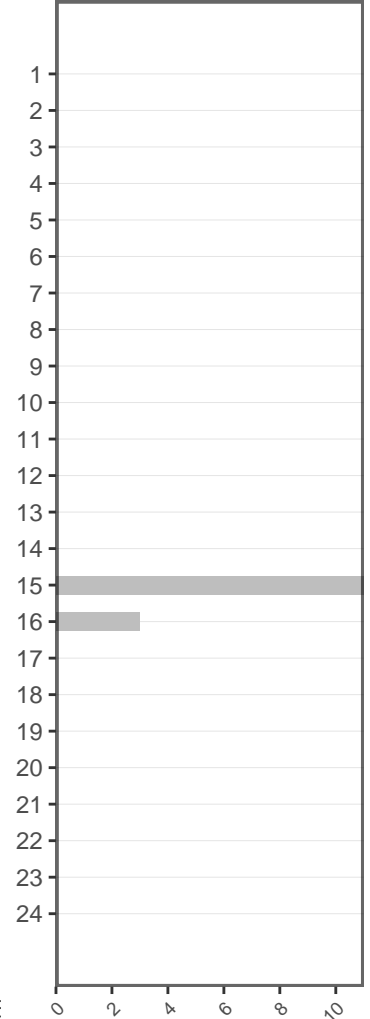
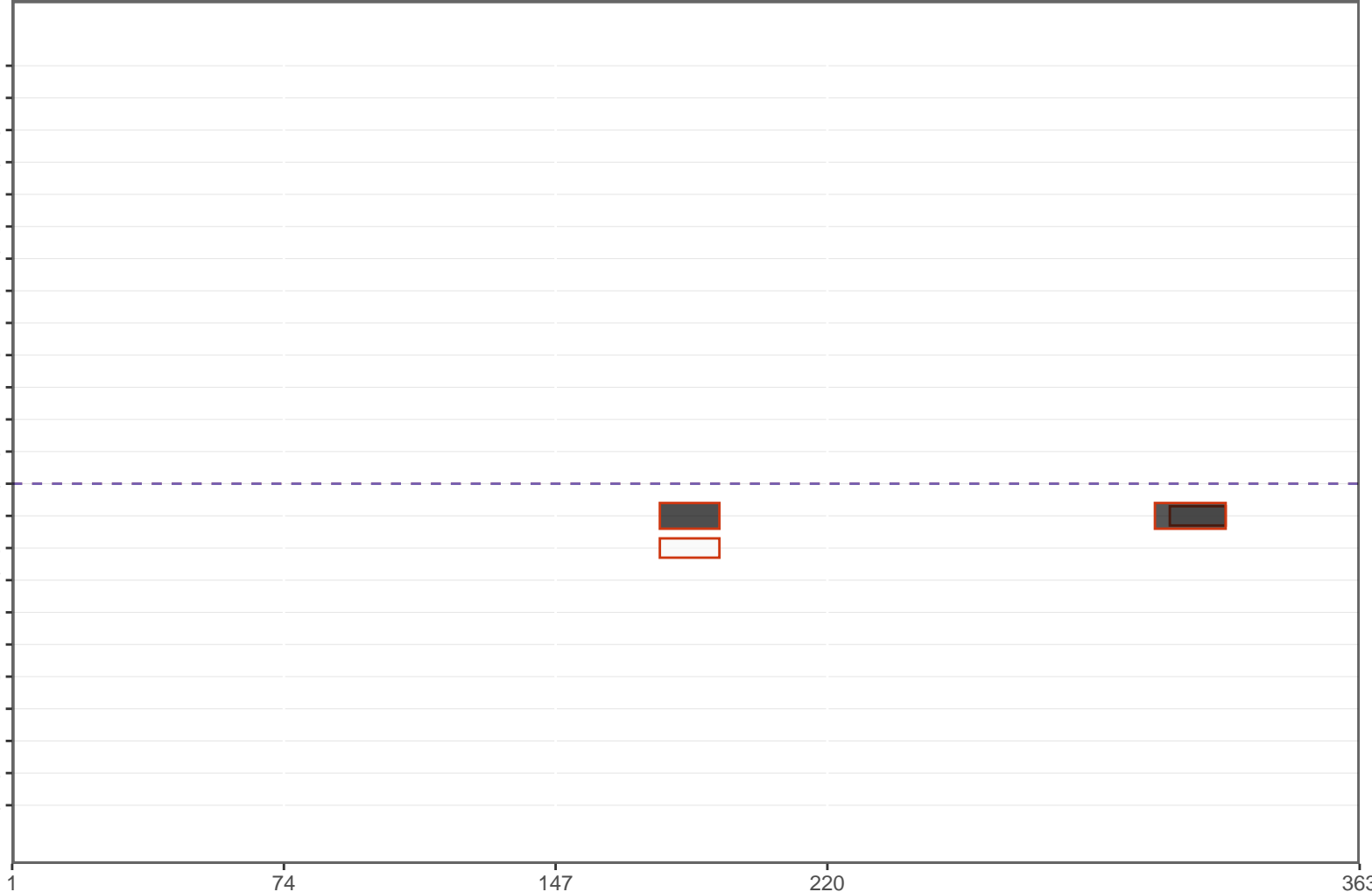
MW indication



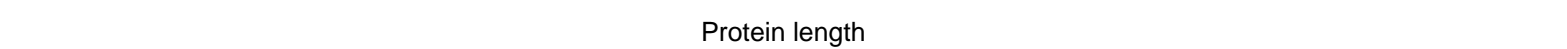
Molecular weight



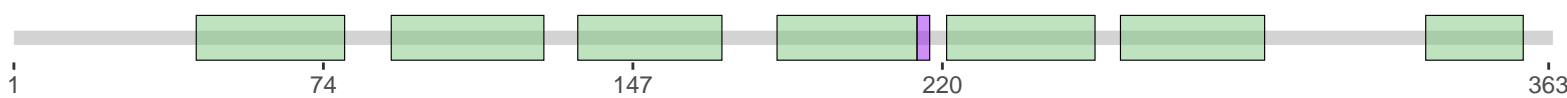
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

NTLGECKYITDGDGSHSDWYSGVRFSPNLTGPTIVSGSDWRTVKWIKLNFCKLRSTLAGHAGYVNTWVSPDGLGASGGKDGITLLWDLAEGKILYSLDAGSHIHALGFSNRYWALCAATETSKIKWLEKSIIVDLKVDLKGESSEMATEGTGSGAKNKIMYCTGLGWSADGSLFSGYTDGLRIRWGIQRYV

NbL13g06080.1 beta-glucosidase_44-like [MW = 60.2 kDa]

No. of times detected



log(intensity)



Values from



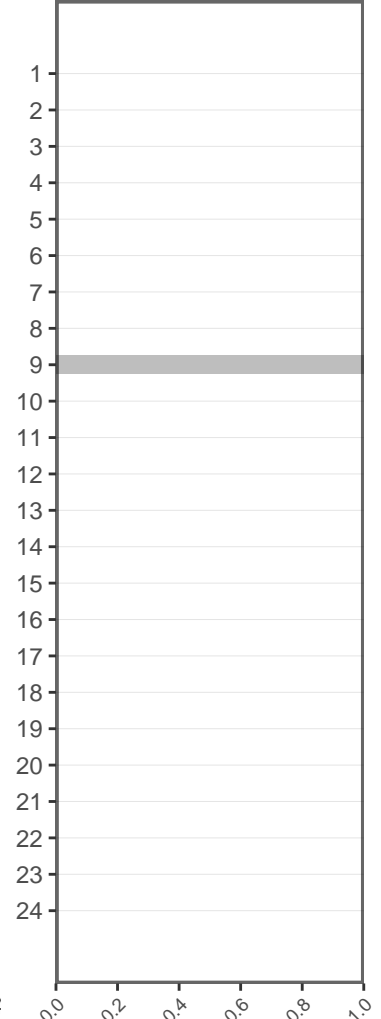
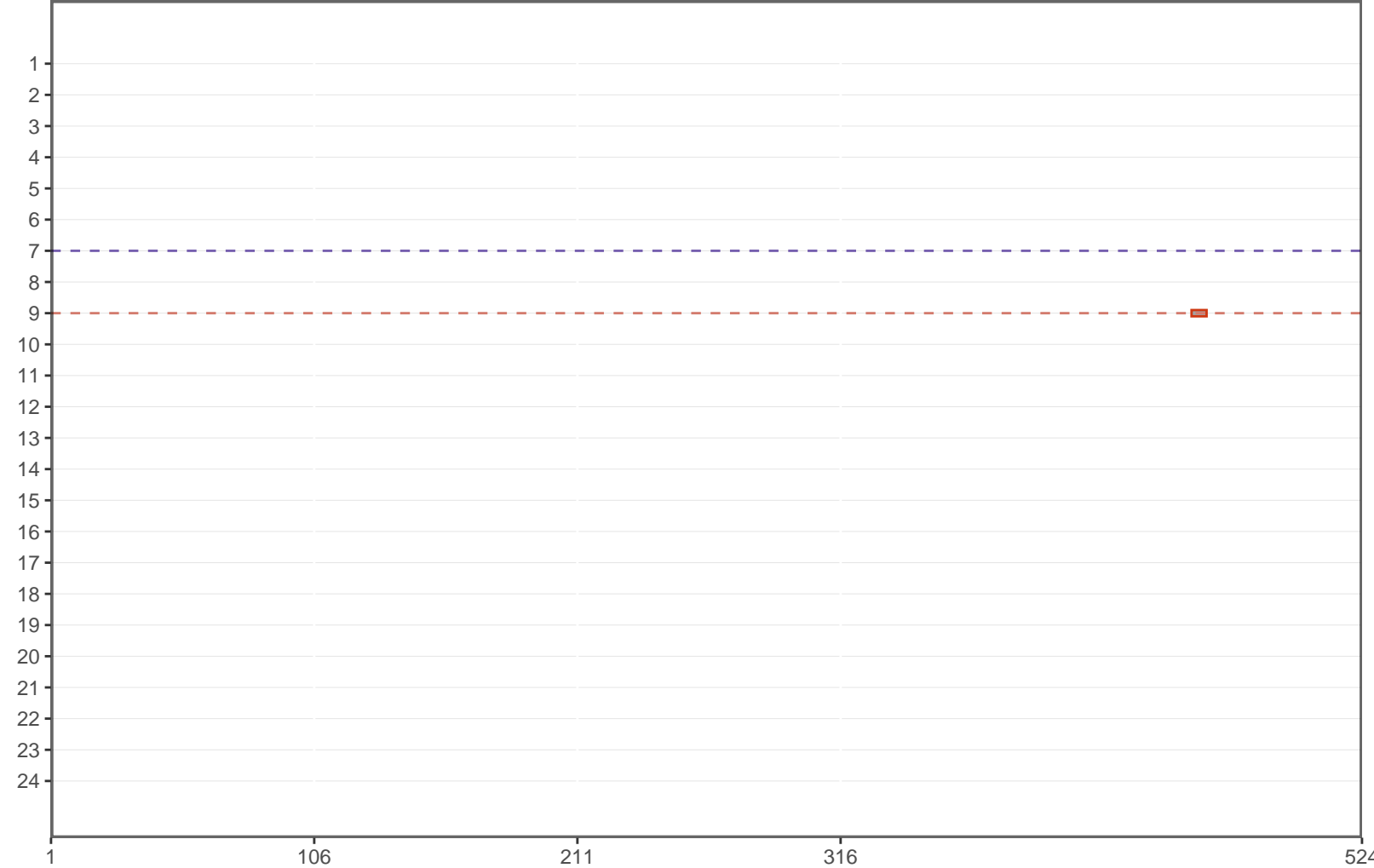
MW indication



Molecular weight



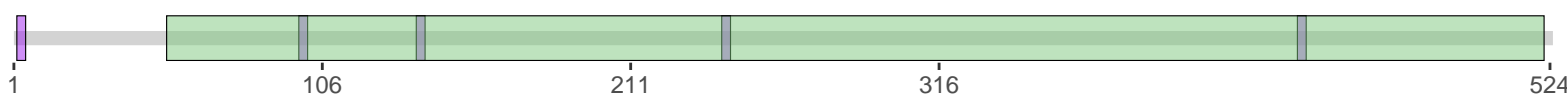
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL13g06060.1 66_kDa_stress_protein-like [MW = 66.1 kDa]

No. of times detected



log(intensity)



Values from



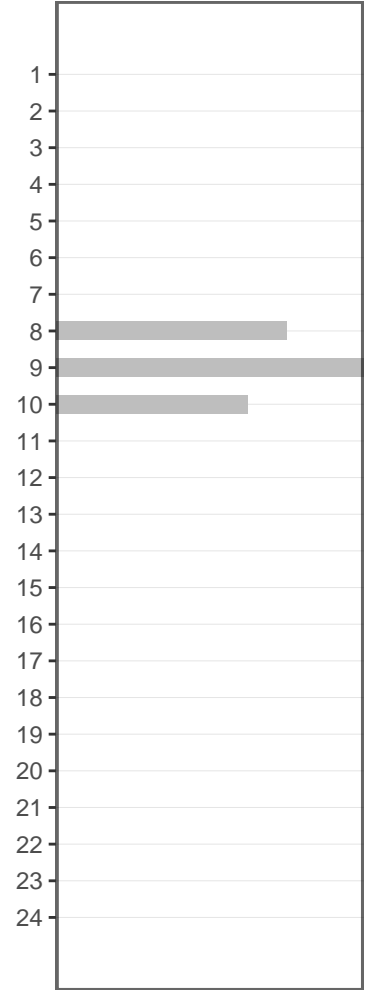
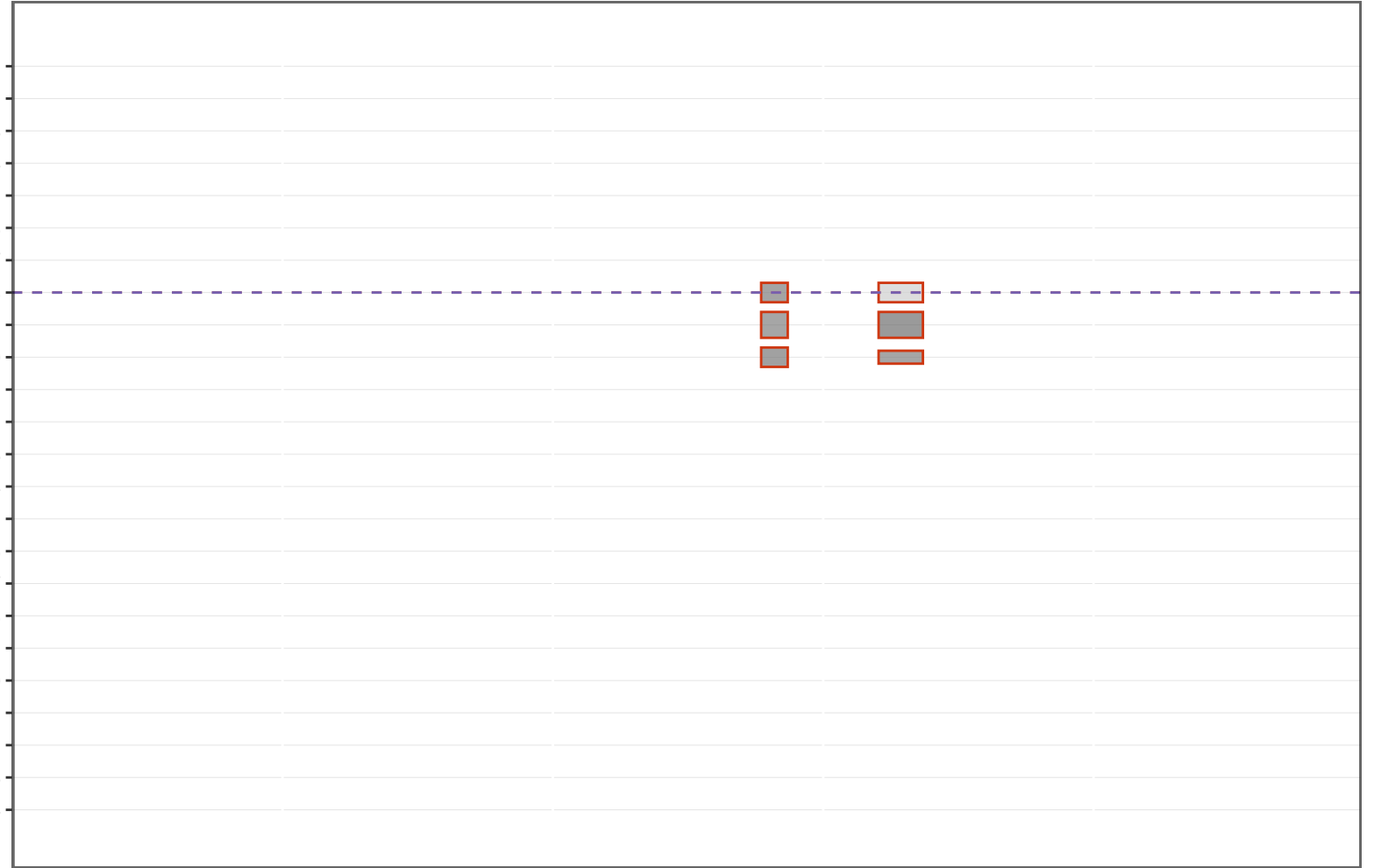
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LWQNDHLVTVSLGGTISFSAIDLEKSPVFSFGHKMNANSLAVLKEPKMLSSSEYDGLVWVWGGIGYSGKLERKVNSSQKGFVAVVEGEIVSCGFDNKKIWRVSLHGGDGGDANSDVNGDPKDLALSSPEVTLVSEFDTGVLIRGTHLLSTDLGGFTVTAASISPDGTEANVGGDGRRLVYSITGDTLNEEAVLEKHRGATVIRYSPDVSFMFASADVNRBAVWDRASGEVQLKNMLYHTARINGLAWSPDMSMATGSLDTGVIVD/SKPAENRITKGAHLGGVYQLAFTI

NbL13g06020.1 histone_deacetylase_6 [MW = 16.29 kDa]

No. of times detected



log(intensity)



Values from



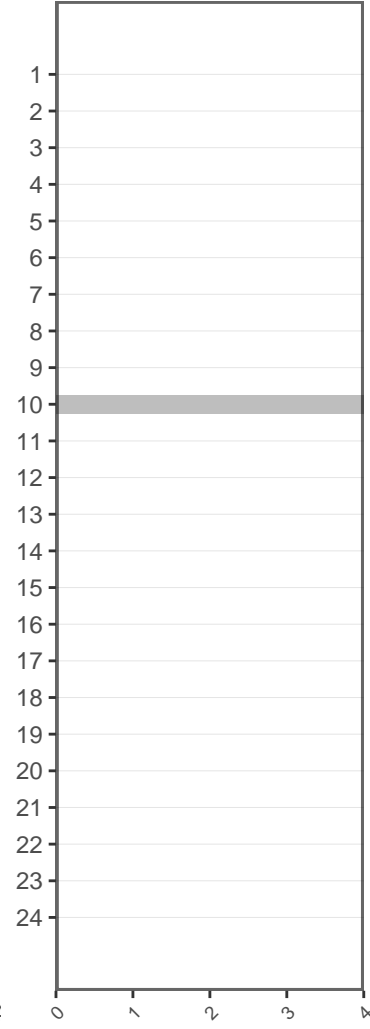
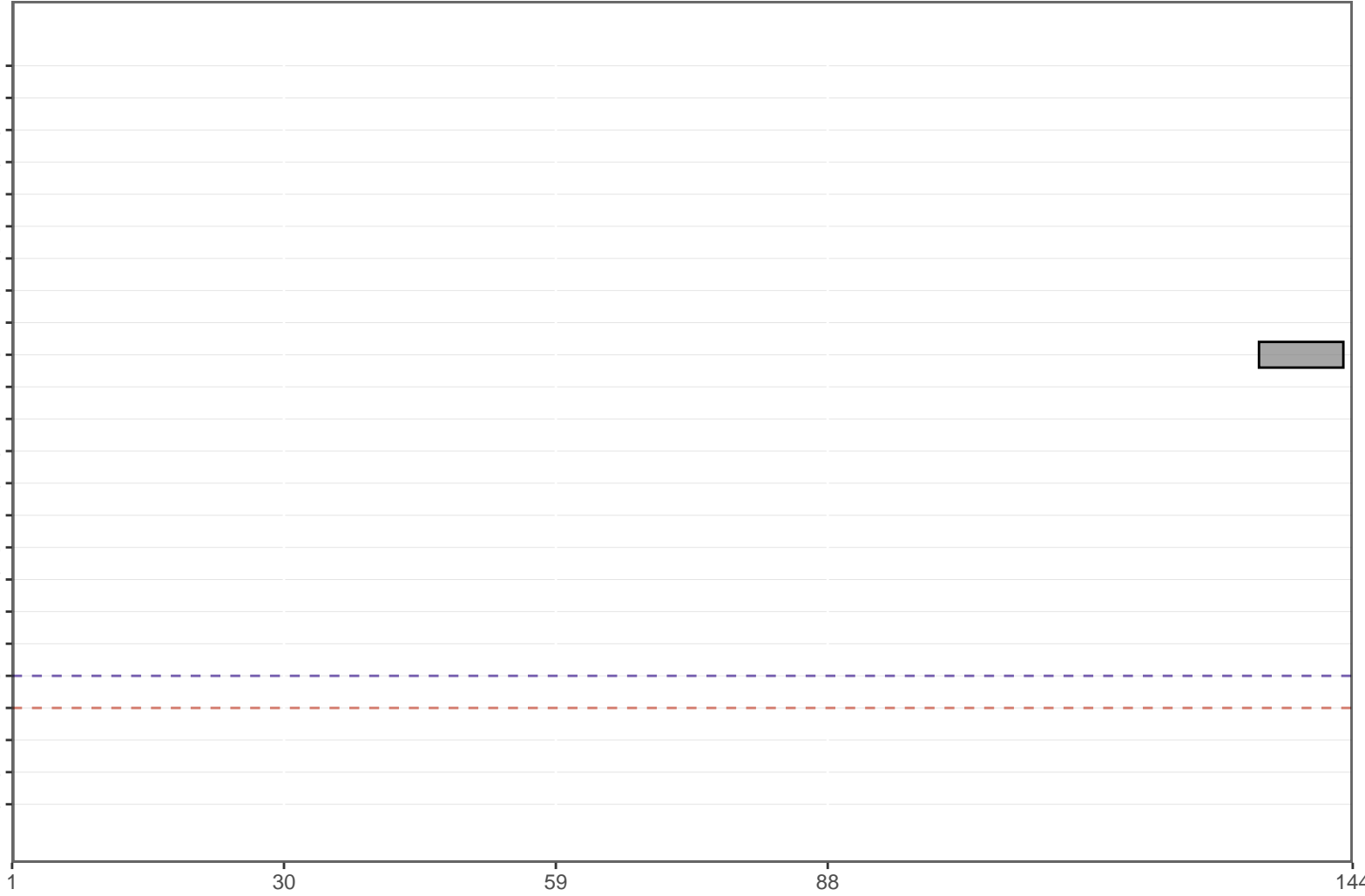
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



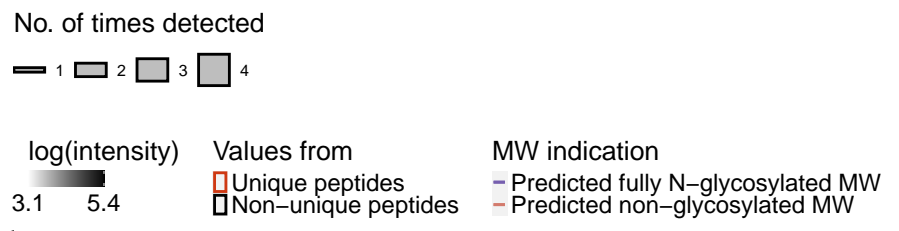
Pfam domains

Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

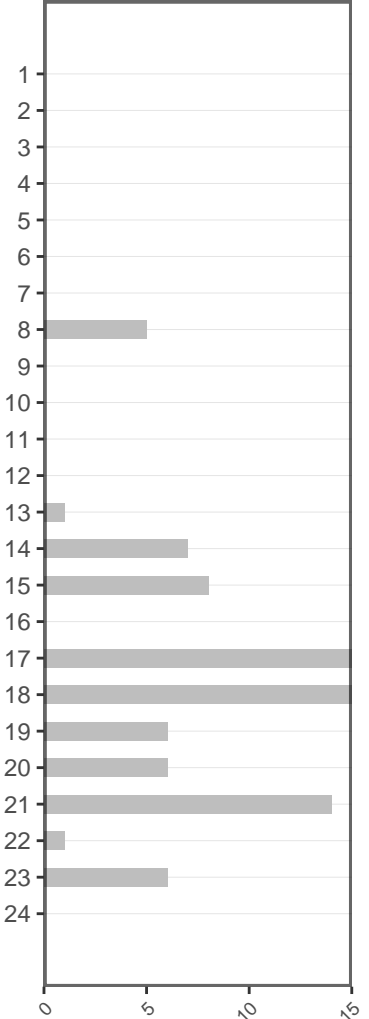
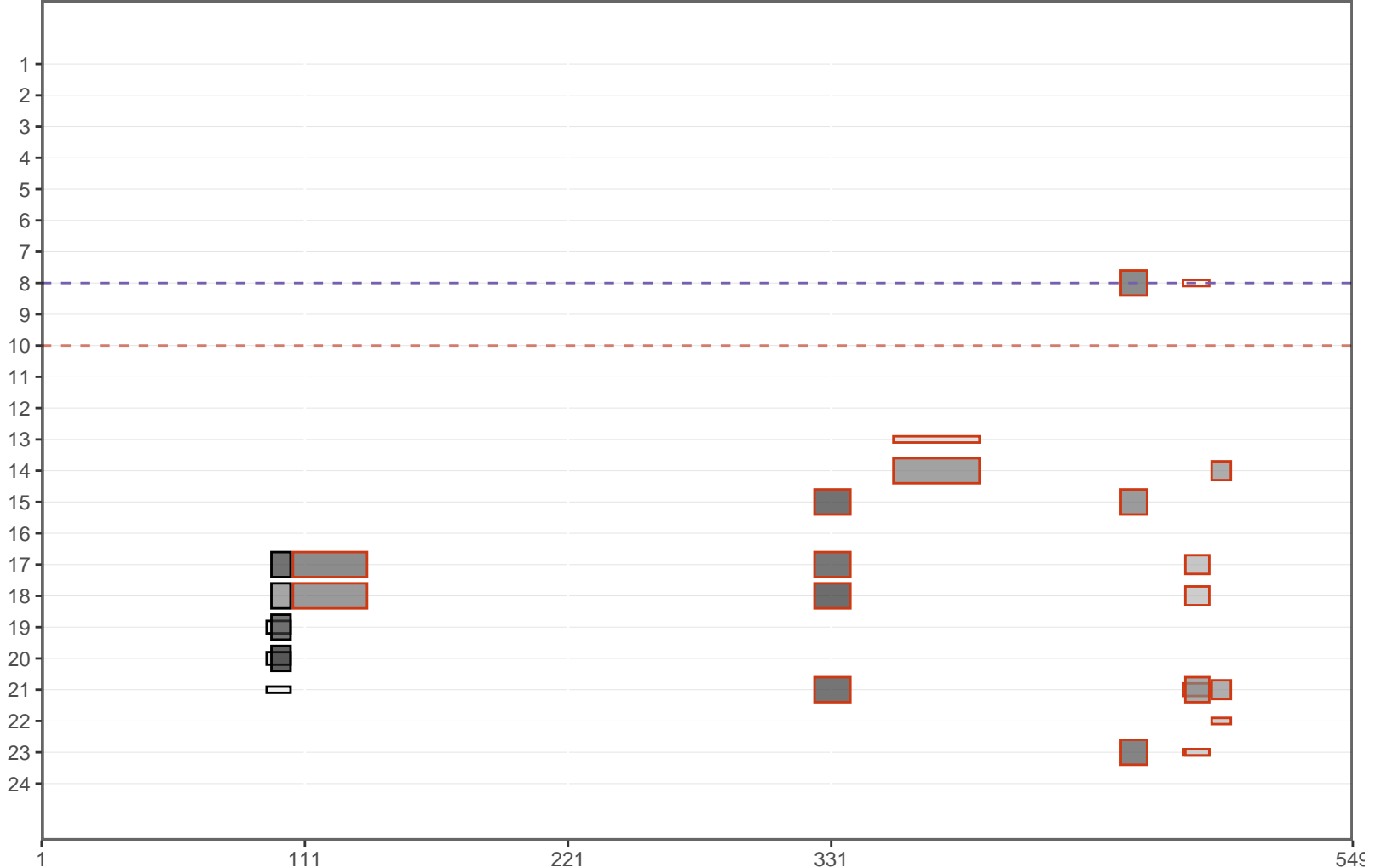
PSVYFGTTPCTTEVPEEEEDMDGRKPSHWNGEDYGSDADEDEHPRGRSSDNLTFVETTTDMRDVDDQAKVDDDMVDADH

NbL13g05940.1 SH3_domain-containing_protein_C23A1.17-like [MW = 58.06 kDa]



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain PF00538 linker histone H1 and H5 family

Protein sequence:

IGPVGVNSFVGLAPAPGAEESTTKRRPGRPRKDDGSTVKKVPEKLPDQSGGTRRRPGRFFKSTTVDAAPQSGAMGTGRGRGPKKNSAPGRRGRPRKNSAVALANGANPFGVANVTNPKAGGVPSGAPFTPKRRGRPRRSGGAPITAVDVTDPPIAAAFETENLPMNAVGVGVTNNGAMPPLGKRRGRPKYSATAAAPTWRPRKLGKPLGRPRKNTFSRWSDPKLMVMAVEELKGLKLEHMOTRIKEAANALPKPLNAESPMALAAALGELEELAAAGDLYQON*

NbL13g05830.1 ubiquitin_carboxyl-terminal_hydrolase_3-like [MW = 26.01 kDa]

No. of times detected



log(intensity)



Values from



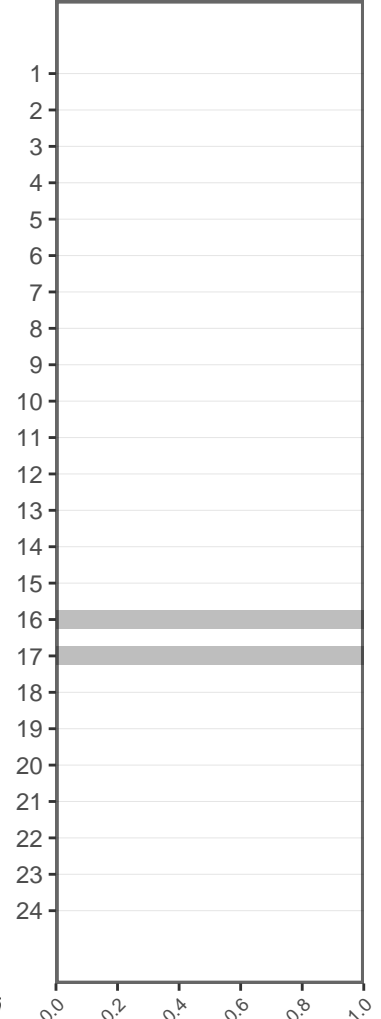
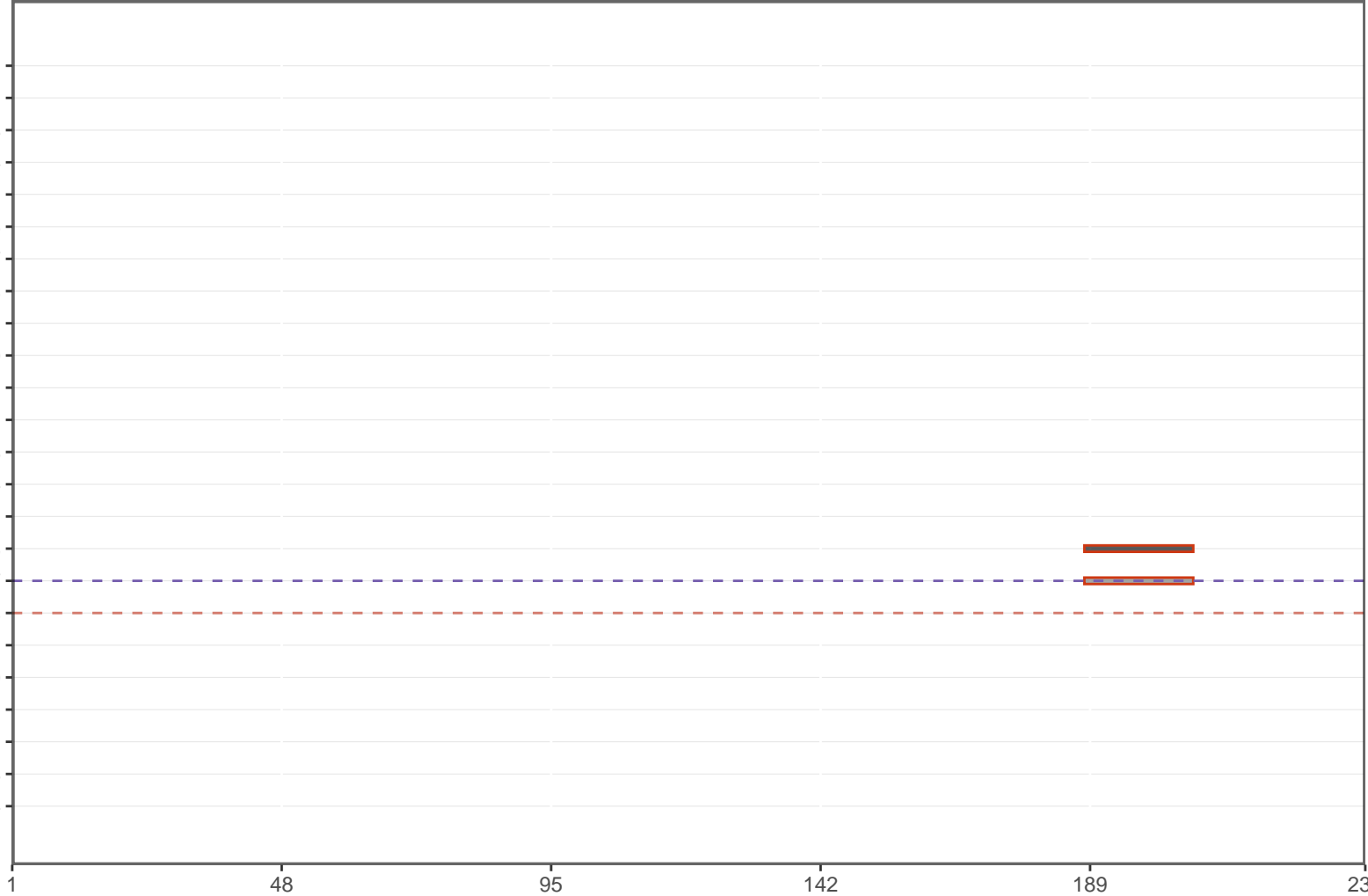
MW indication



Molecular weight



Gel Slice

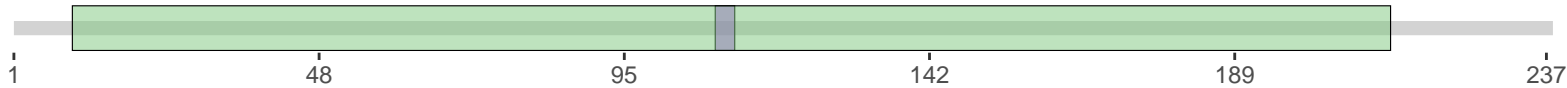


Protein length

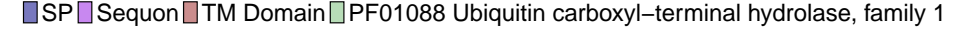


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LHAIIGNITSEIKLDEDGFLKFKFKSTAHMDPMERASFLNDRMEVHSHVAATAGDEAPENVTHFGFTGVGGVYELDGRRGPRHGHGASPTNLGDAAKVEIKMKQKPEINFNVAISKRVKGDAL*

NbL13g05820.1 probable_enoyl-CoA_hydratase_2_mitochondrial [MW = 34.6 kDa]

No. of times detected



log(intensity)



Values from



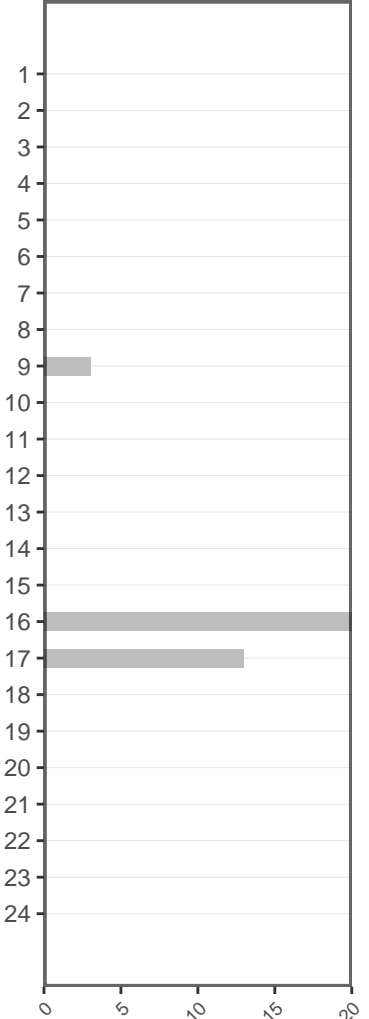
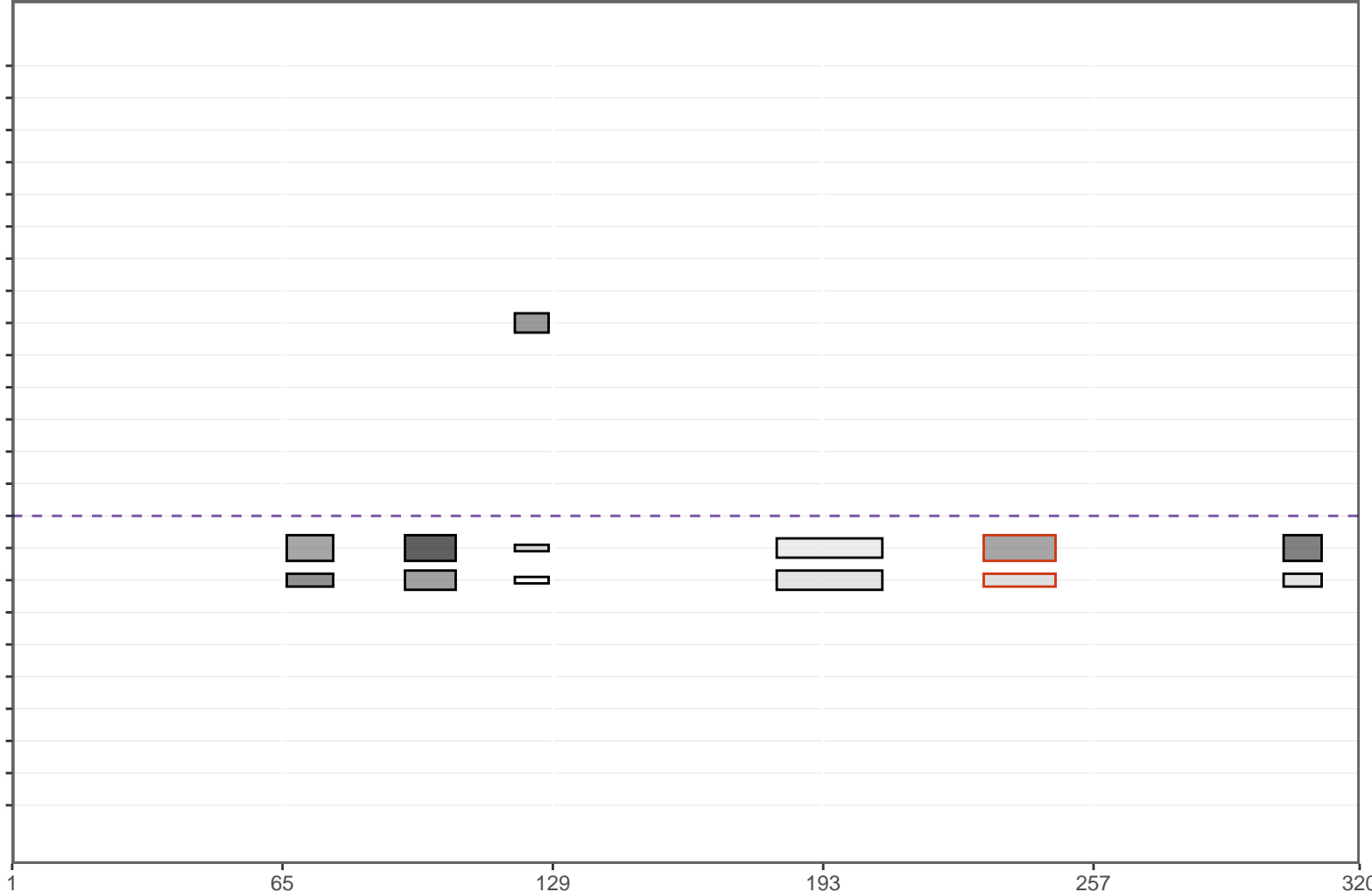
MW indication



Molecular weight



Gel Slice

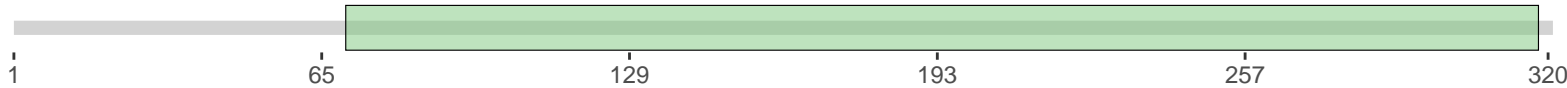


Protein length

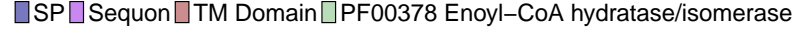
Peptide counts over 4 repeats



Pfam domains



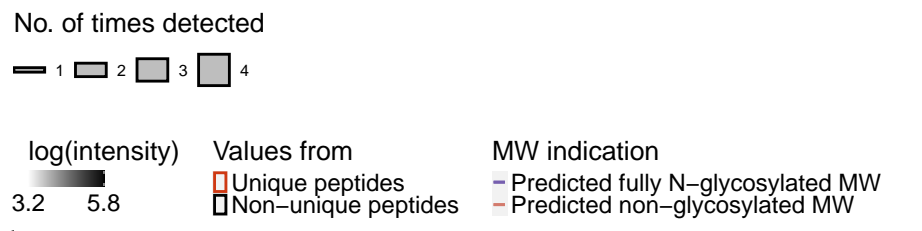
Pfam Description



Protein sequence:

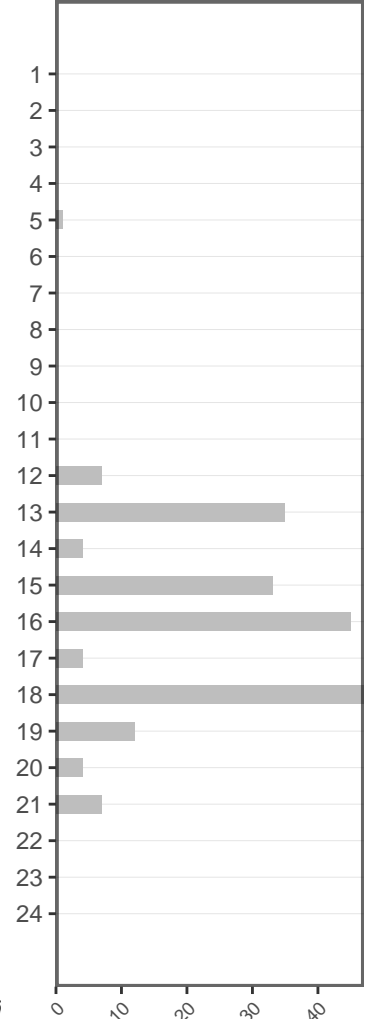
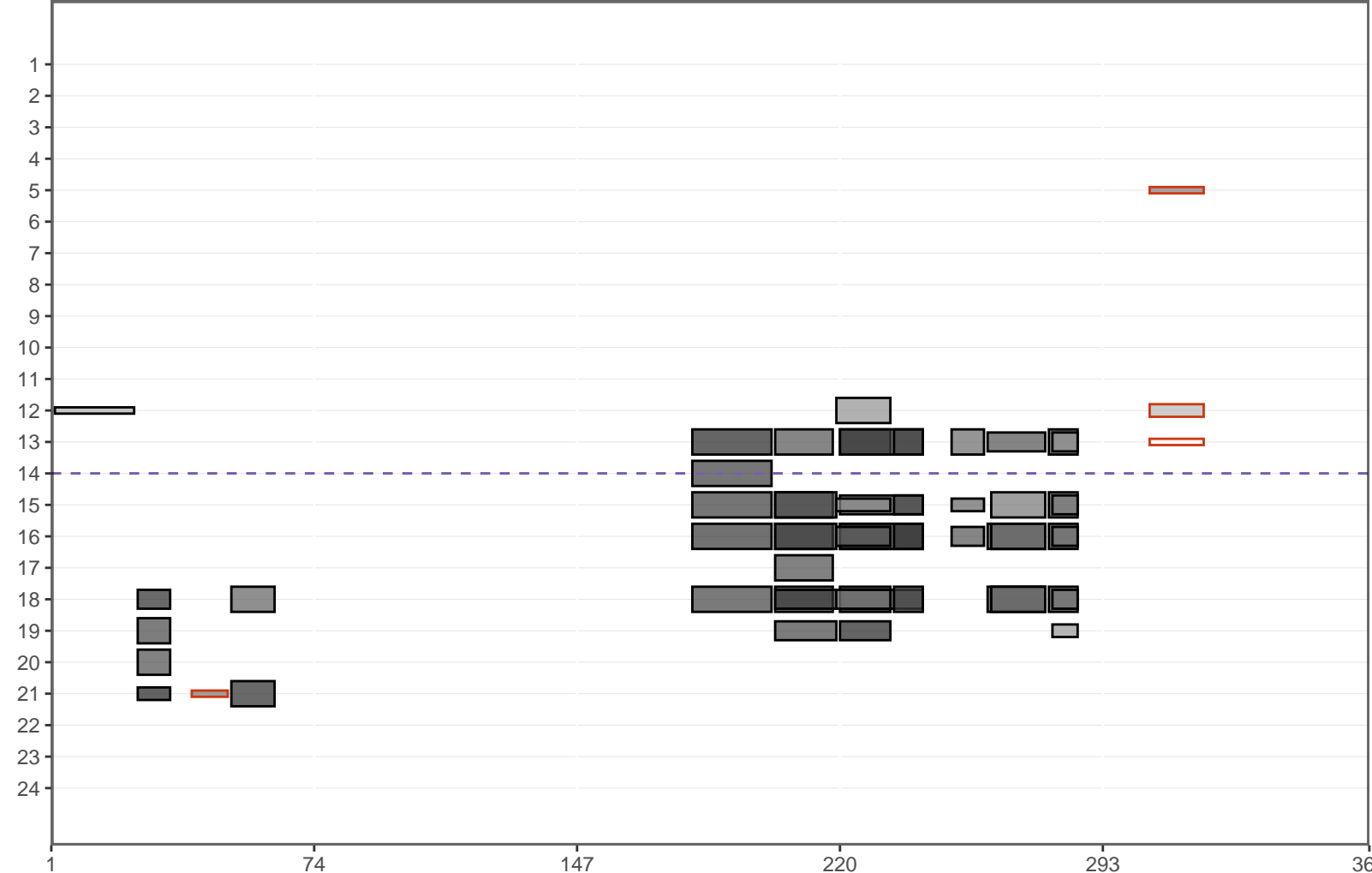
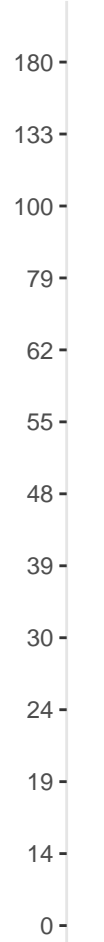
LRSTFSFLEGLHPFAAIEGALGGLEMMASGDIRGCEDAVGLPETGLAVIPGAGGTQRLLRLLVCKSAKDIIFTGRKINGKDAVSHGLVNYCPAGETRKLKALELRDINGKIPVALKMAKCAIKGVELDMESALALEWDCYEQLLDTRLEGLAAFAERRKPRYKGE

NbL13g05780.1 plasminogen_activator_inhibitor_1_RNA-binding_protein-like [MW = 39.51 kDa]



Molecular weight

Gel Slice

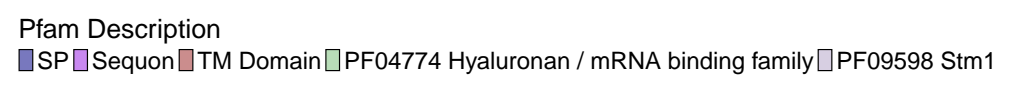


Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:

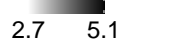
INDFKREGAGRANWGTPTDEAFETEGEKIVDEPKPAGEEDDAGDAKDDSSAAEPEKEPEKEPEKMTLEEYKLEENRKALLAKPFEERKLVLDKDFESMOLLNKNKNEDDDFIKLGAENKDKKEAVEKAKKTKBNEFLKPKAGEGNYRGRGRGGRRGGYGGNGNGSNYSVEAPKIEDVGGFPLGAK

NbL13g05760.1 GTP-binding_protein_YPTM2 [MW = 22.5 kDa]

No. of times detected



log(intensity)



Values from



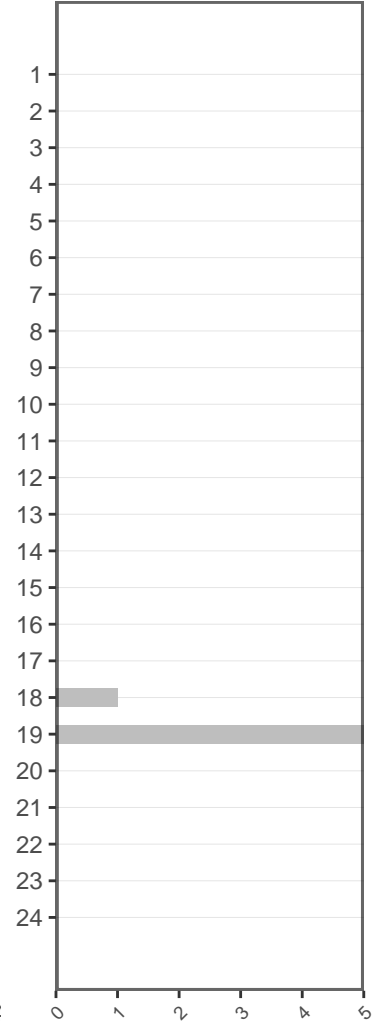
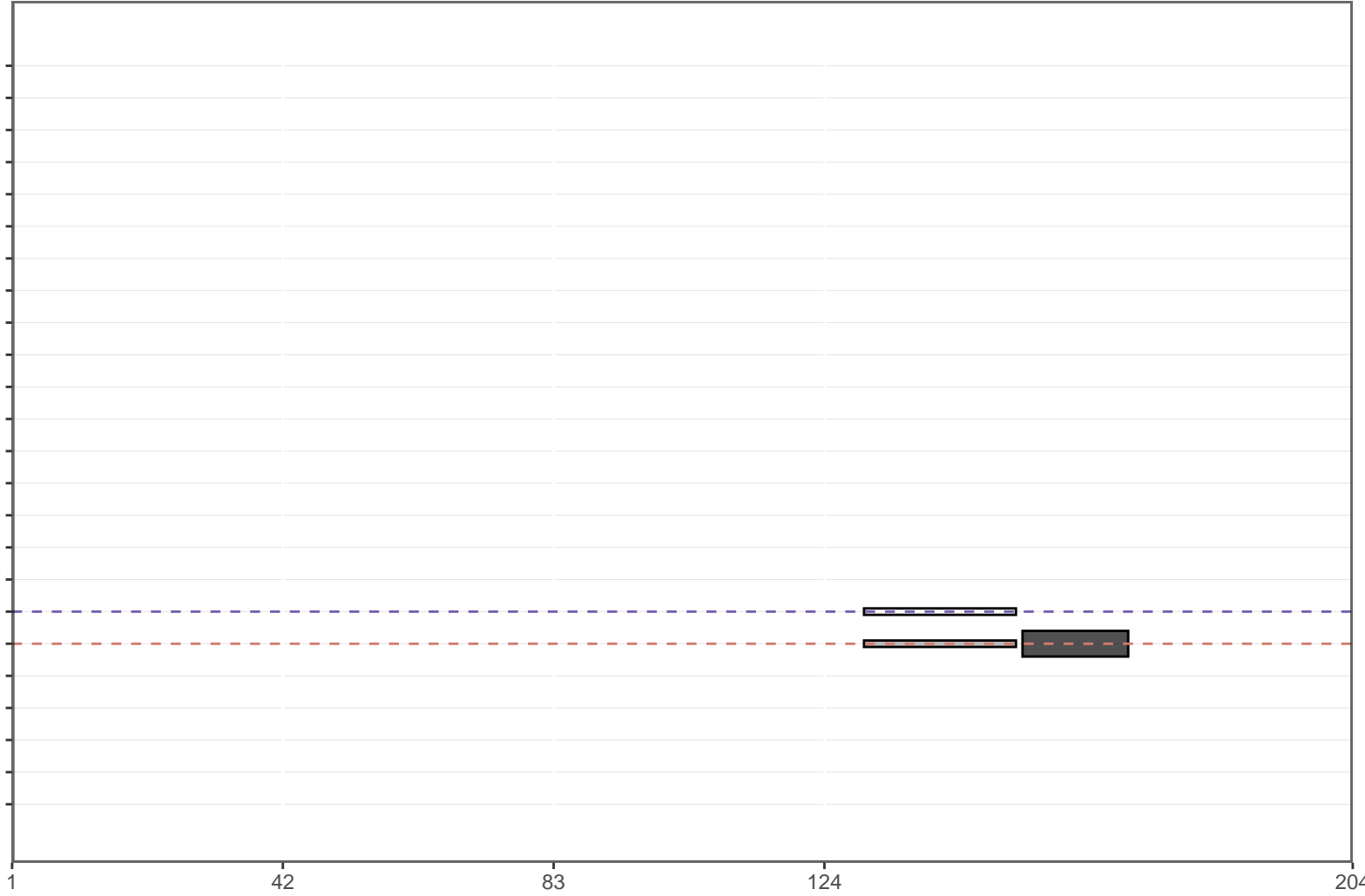
MW indication



Molecular weight



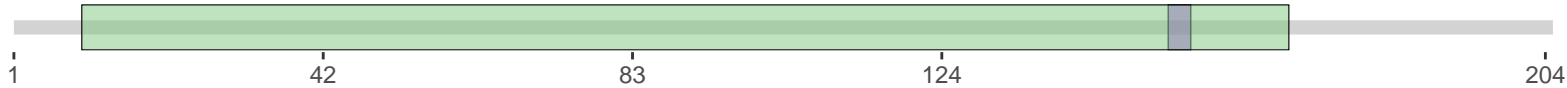
Gel Slice



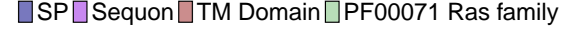
Protein length



Pfam domains



Pfam Description



Protein sequence:

DDDSFNVYGVLEIDRYASDNNKLLVGNKGDITAGKVVSTETAGAFDEIGIPFMETSAKNATNVEGAFMMAASIKNRMASGRASNNRPPITVGRGPPVNGKSGCCGS*

NbL13g05730.1 50S_ribosomal_protein_L19_chloroplastic-like [MW = 24.04 kDa]

No. of times detected



log(intensity)



Values from



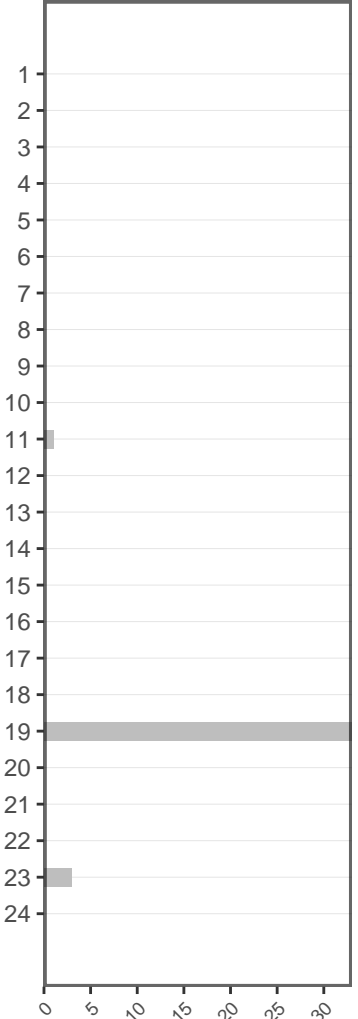
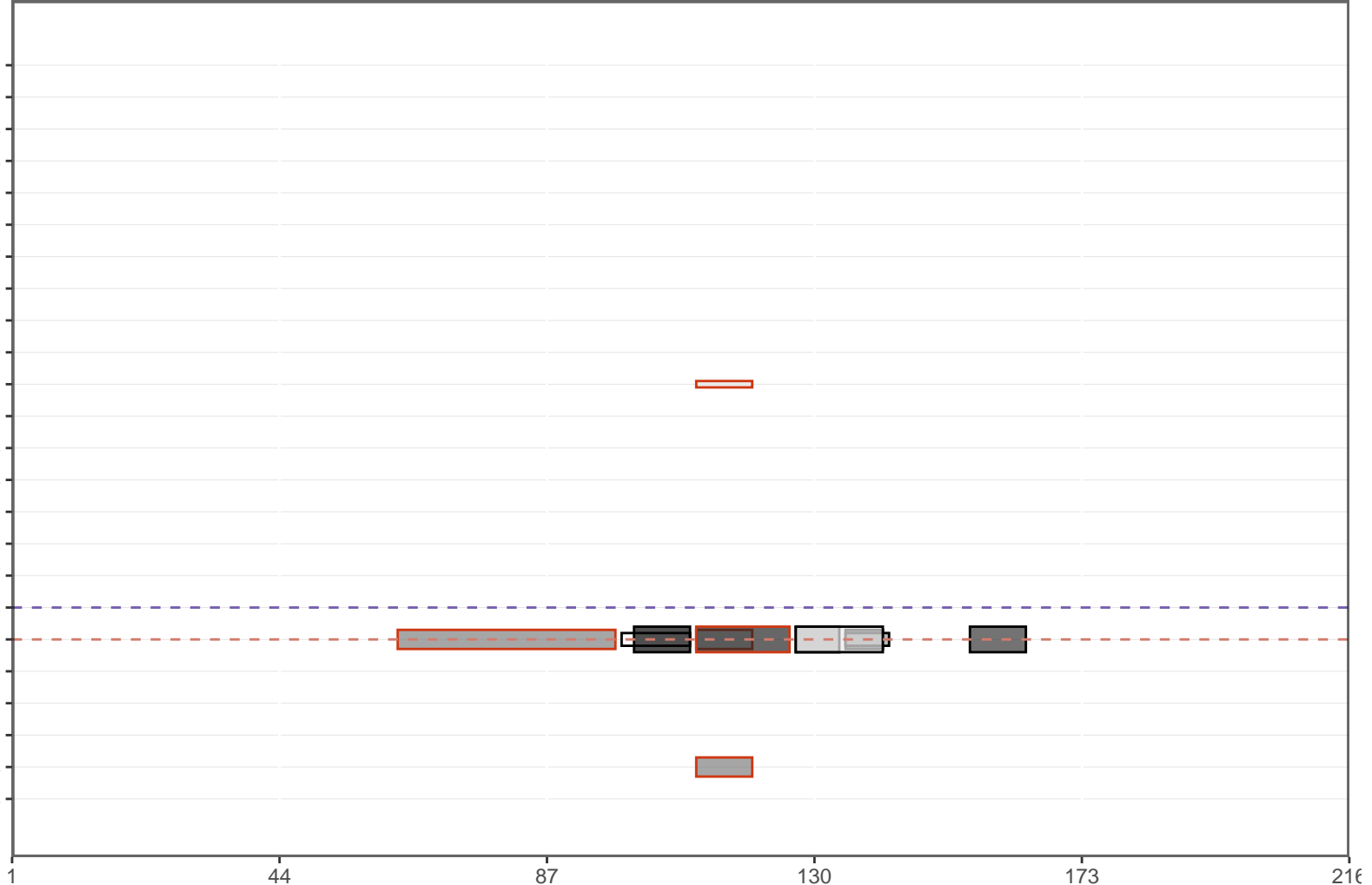
MW indication



Molecular weight



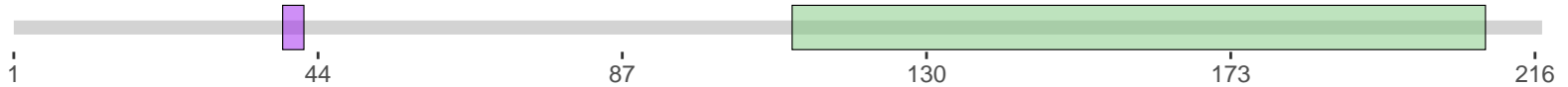
Gel Slice



Protein length



Pfam domains



Pfam Description

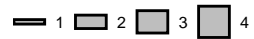


Protein sequence:

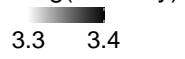
IRPPFKPRAKLGDIMGLNKQIEASDAVRIPDIRTGDVVEIKLEVPENRRRLSGYKGVISKQNGHHTTRIRRIAGIGVEIFPVVSPNIKELVVKHKKVRRARLYLRDKLRLSTFK

NbL13g05700.1 V-type_proton_ATPase_subunit_d2-like [MW = 20.92 kDa]

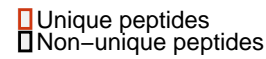
No. of times detected



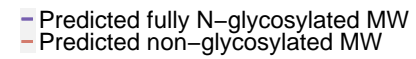
log(intensity)



Values from



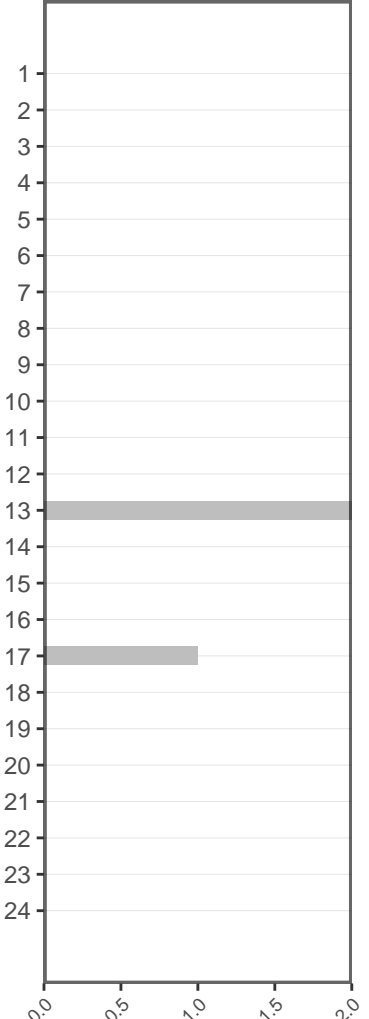
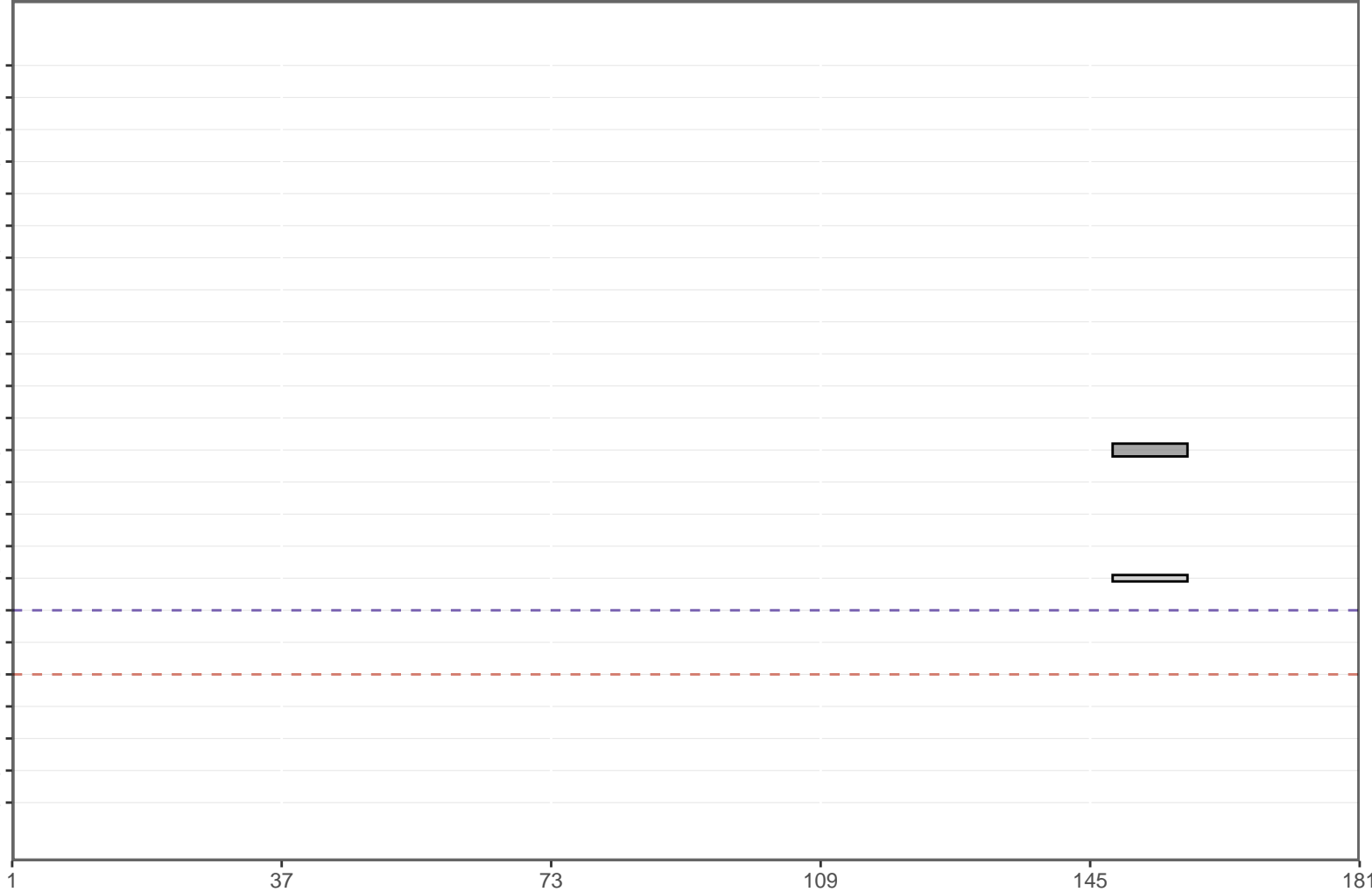
MW indication



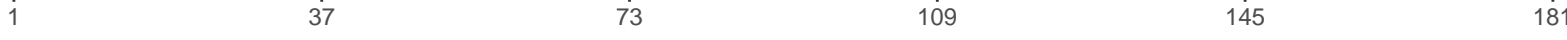
Molecular weight



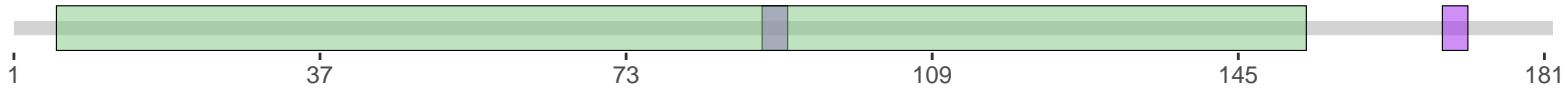
Gel Slice



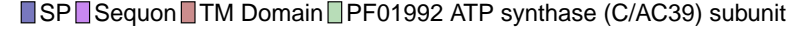
Protein length



Pfam domains



Pfam Description

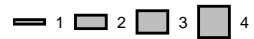


Protein sequence:

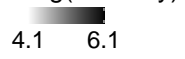
LAFADRRVNTINSIGTELTRDORRKYVSNFGLLYPYGHEELAGEIDIDVGRGVMEKYPYQSFSLAYGEGMLDKRKNTFAWHLNNSSTMVYFLHM

NbL13g05620.1 ATP-dependent_Clp_protease_proteolytic_subunit-related_protein_4_chloroplastic [MW = 33.31 kDa]

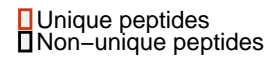
No. of times detected



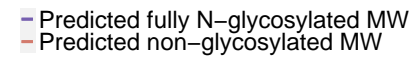
log(intensity)



Values from



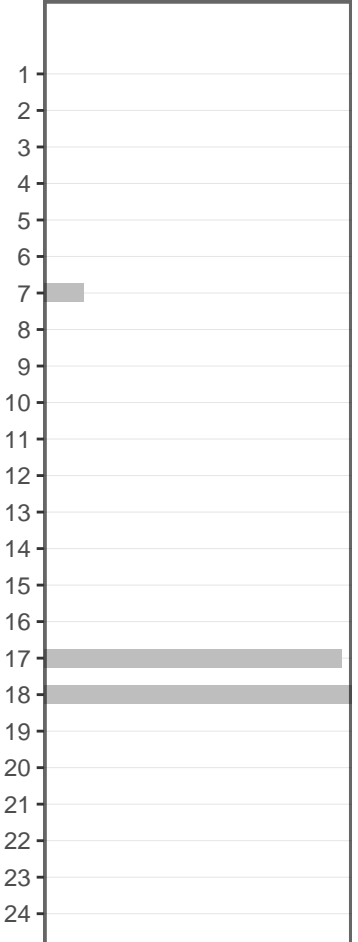
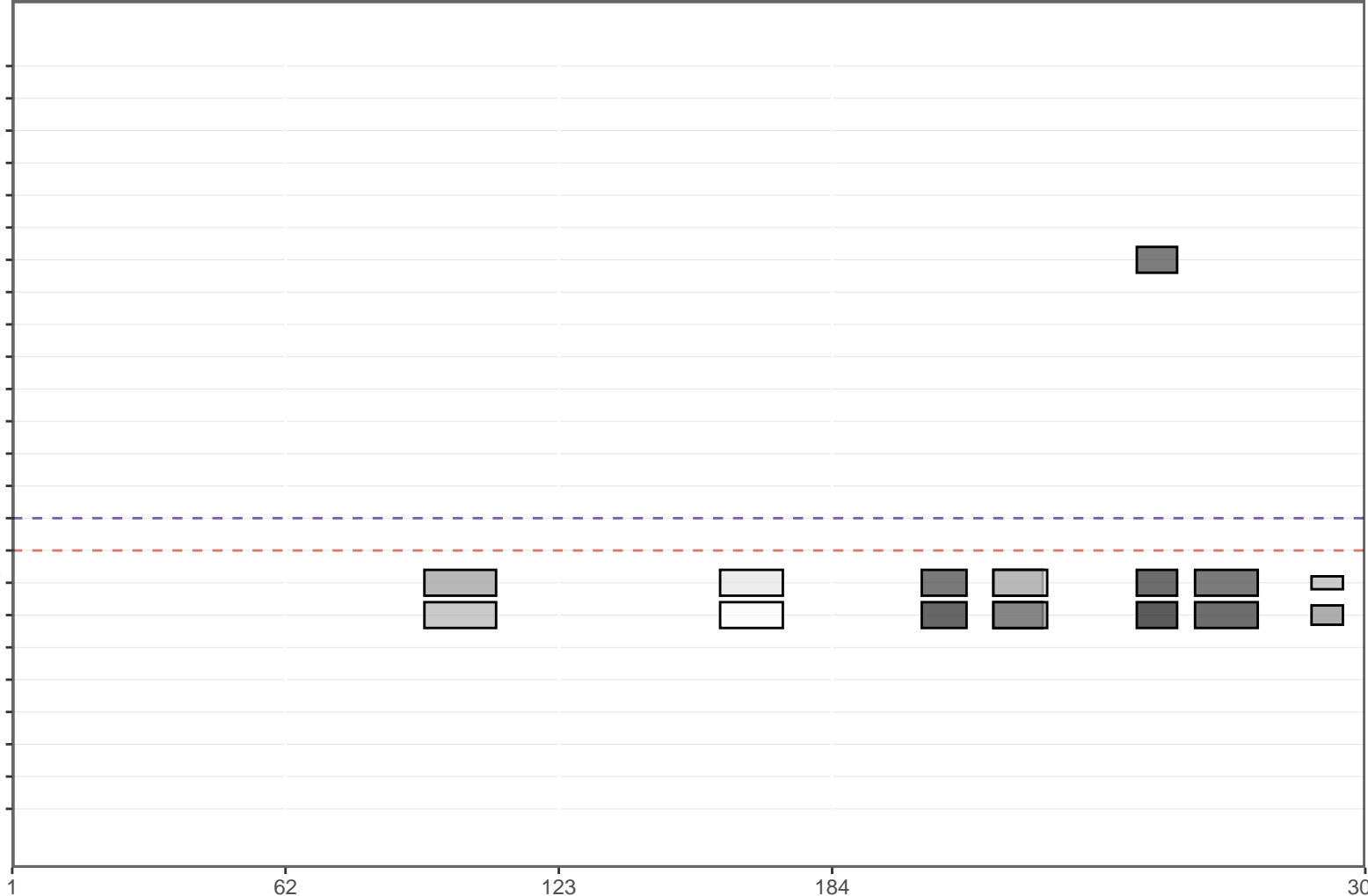
MW indication



Molecular weight

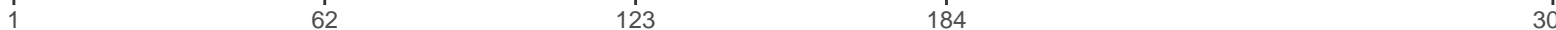


Gel Slice

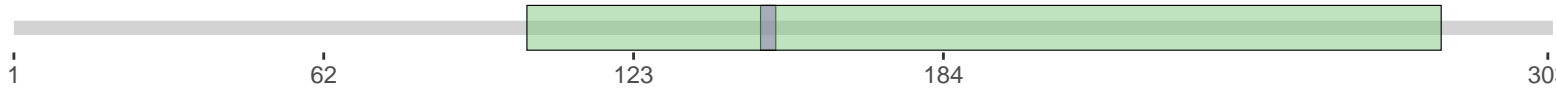


Peptide counts over 4 repeats

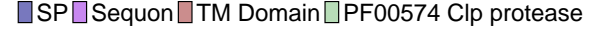
Protein length



Pfam domains



Pfam Description



Protein sequence:

DEEKPIYLNVNSTGTTKGGKELGYETEFAFYDMRYVKRPPIFLGVGNWGEAALLLAAGAKGNRAALPSSTMKQPIARFQGGQATVVELMRKEVKNVAELVKYKSHKSGKSPKEIEADRRPKYFSPSEAVEYGHDKVLYNERGREDRGVSDLKKAKLQI

NbL13g05590.1 light-harvesting_complex-like_protein_3_isotype_1_chloroplastic [MW = 29.71 kDa]

No. of times detected



log(intensity)



Values from



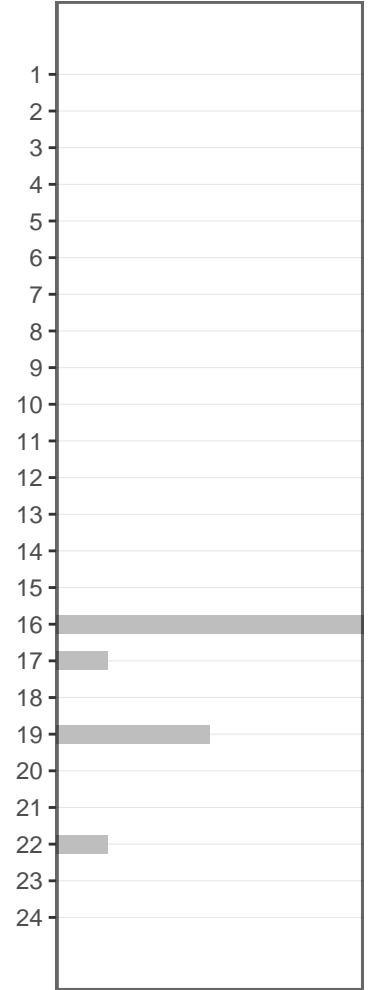
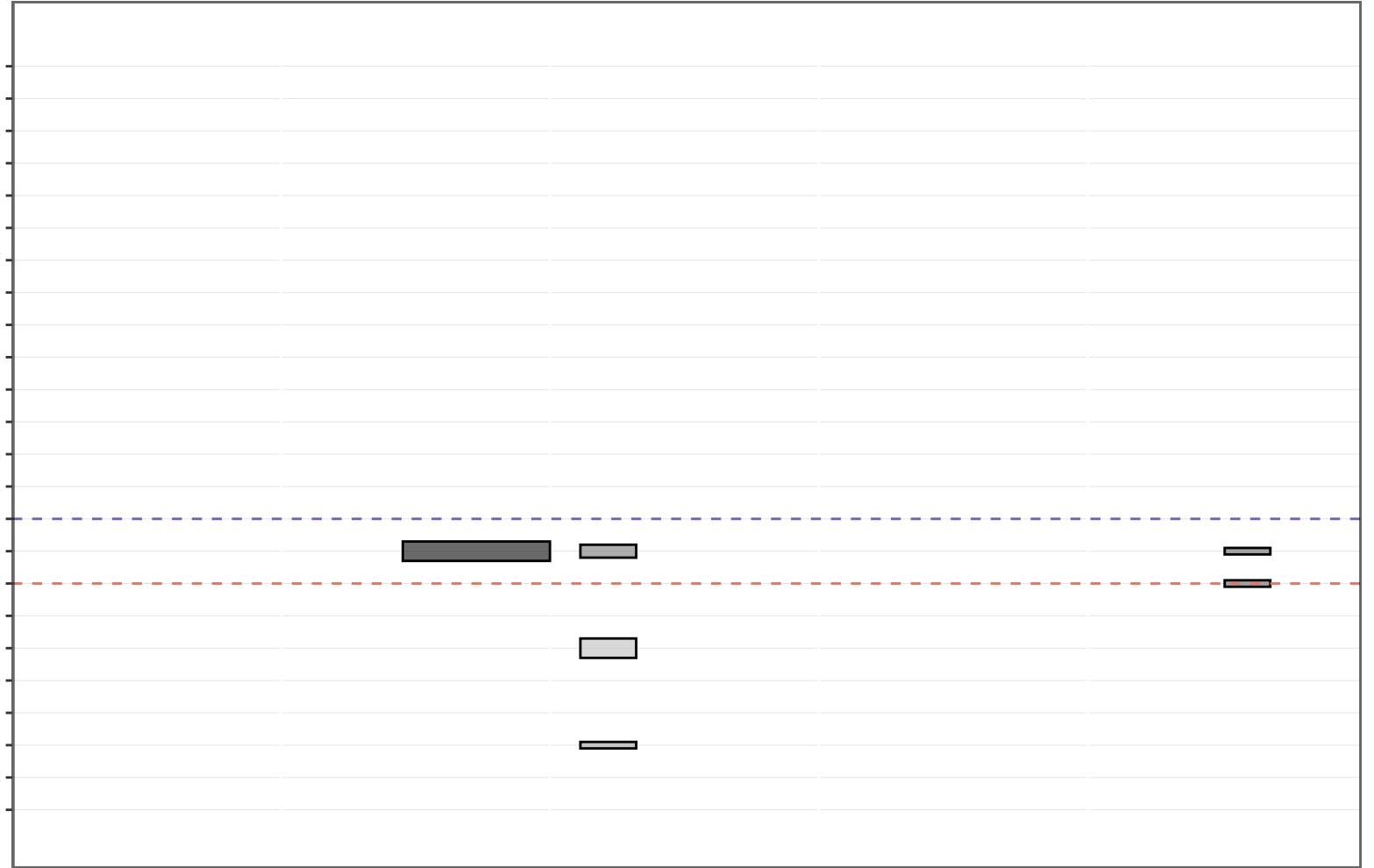
MW indication



Molecular weight



Gel Slice



Protein length

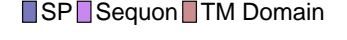
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

NGFXXDGETHYDSDVDEVRRRKLEEDNPESSNEEPFLFDTISIPFWAWMKRFLPEAELLNGRAAMVGFMAVFDVBLTGVGLVDQMGNFQKTLFLFAVAGVLLIRKNEDETWKLEESTFYDKGWGASWKDENSBSKSDS

NbL13g05560.1 (S)-ureidoglycine_aminohydrolase [MW = 36.76 kDa]

No. of times detected



log(intensity)



Values from



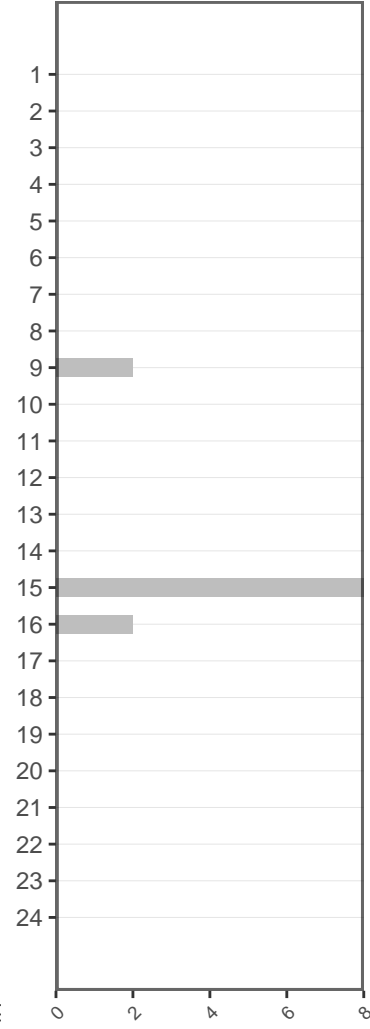
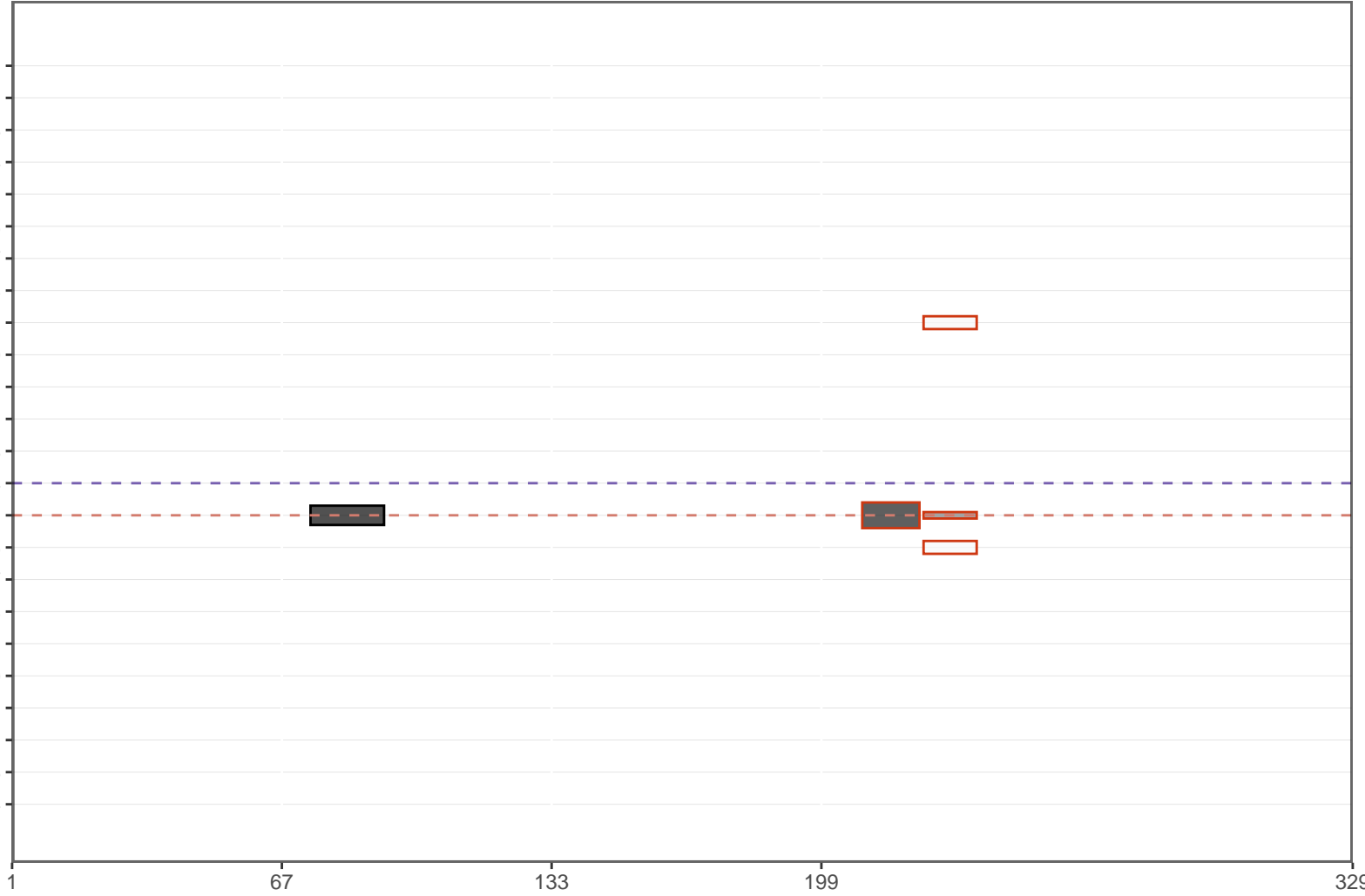
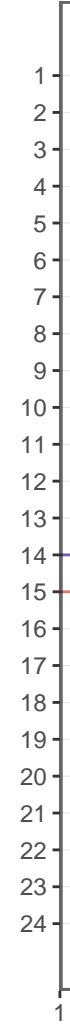
MW indication



Molecular weight

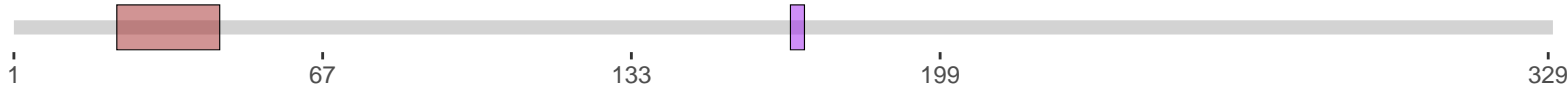


Gel Slice

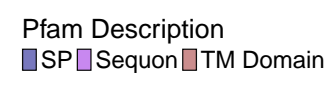


Peptide counts over 4 repeats

Protein length



Pfam domains



Protein sequence:

VERFIFVVOGSVVTNNSGNHKLTVDSWALPPNFDHVAETDAATLVFERRYGRLENHTEQVGGSTKGPLETPGGEIFELRKLPTSLAVDFNHIMDFQGEFLNKEVHYNGHGLLLEGGQGYRLSDSWYPIGAGDAIWMMAFPVQVYALGKTRSRVLYKDVNRNPL*

NbL13g05190.1 expansin-like_B1 [MW - SP = 29.79 kDa]

No. of times detected



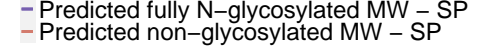
log(intensity)



Values from



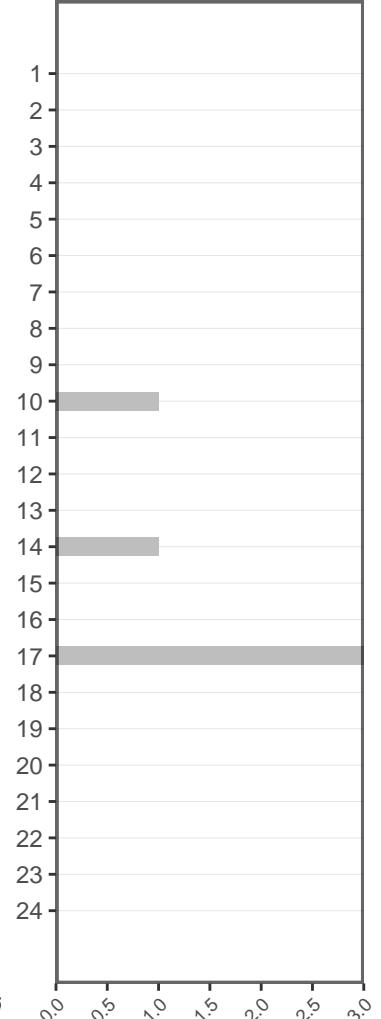
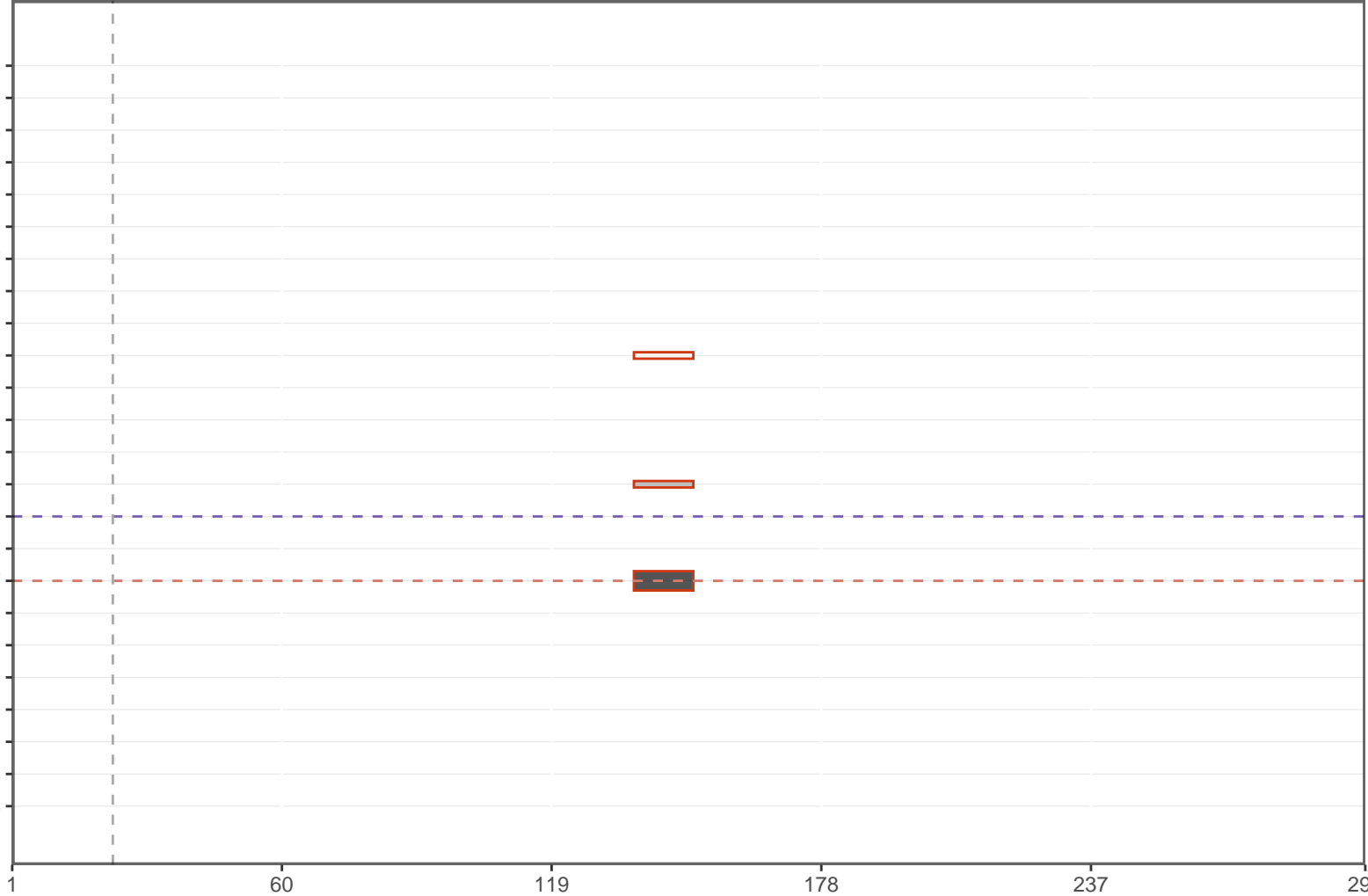
MW indication



Molecular weight



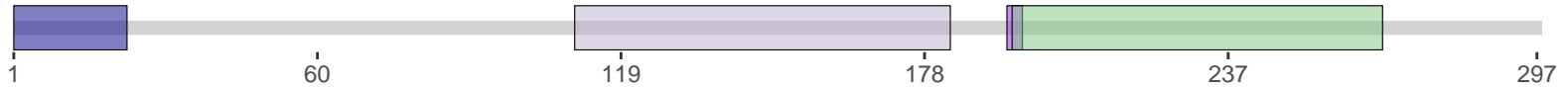
Gel Slice



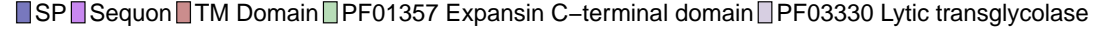
Protein length



Pfam domains



Pfam Description

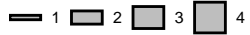


Protein sequence:

KGGTVVITDGGAGDRITDFLGRFAFMAGTTDAASALLSLGIVVDIEYTRVSGCVPKNITIKKESSDNPYFLAFVWYQGGKKDITAVQLCETGDFECHKVLDRTIRGAVWTATSPFRPLQIRMLLGVDDGDEWFPVNNIPENWKAAGDTYDGGIGQVDA

NbL13g05120.1 phosphoacetylglucosamine_mutase [MW = 60.4 kDa]

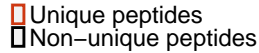
No. of times detected



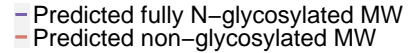
log(intensity)



Values from

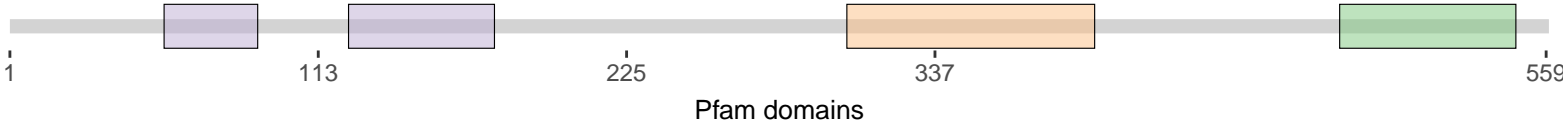
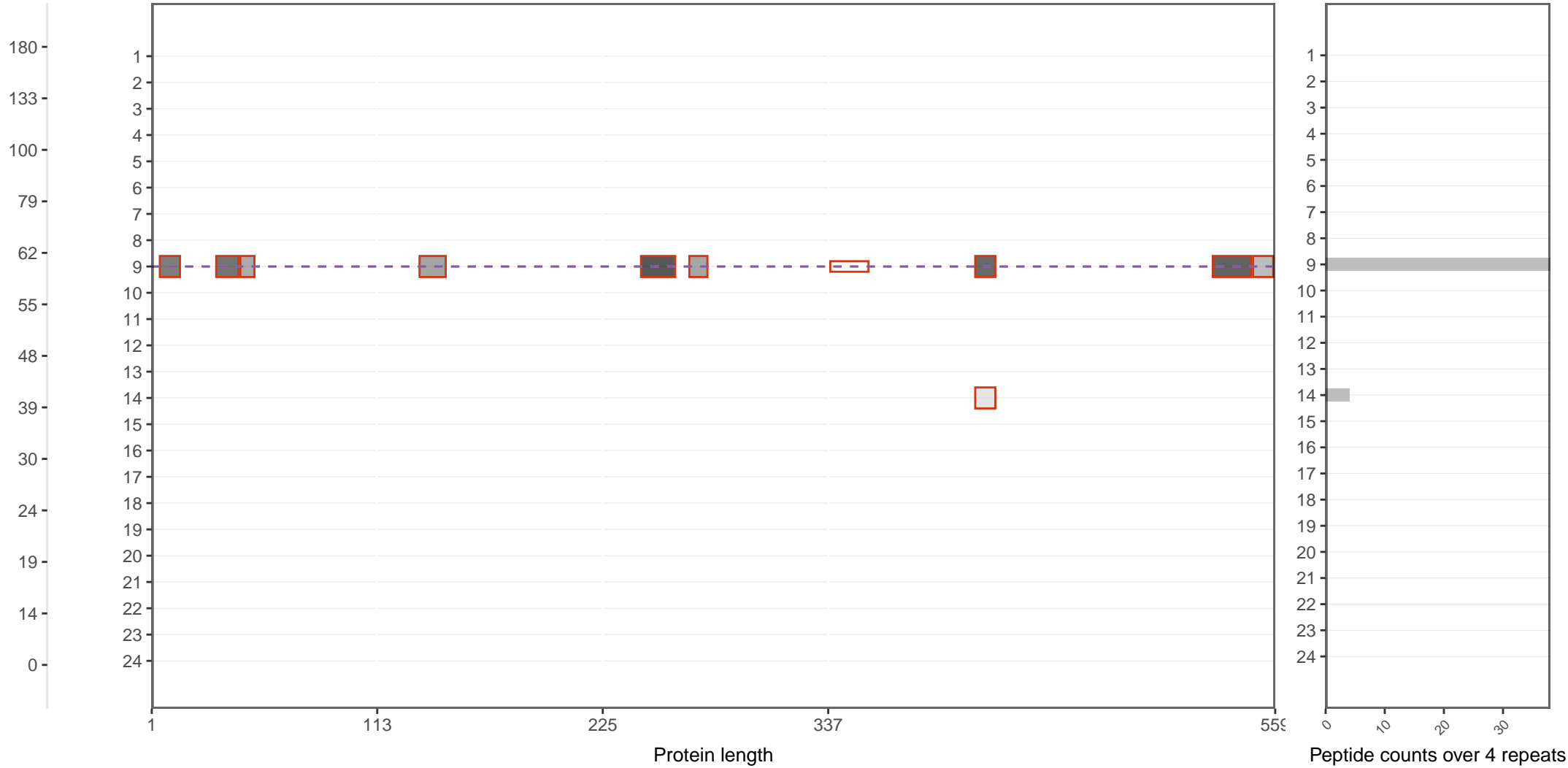


MW indication



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00408 Phosphoglucomutase/phosphomannomutase, C-terminal domain
- PF02878 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain I
- PF02880 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain III

Protein sequence:

/APRSPGSDAQLRCASLDGSDRLVYFVLSNENKIELVDGDKLSLFLFKELSLNEGEDKKGHDBVYKAHLGVVDTAWANGASTDYKEMGLVLTPTGDKYKHEKASEFDGIFEANGHSTLFSSEAFLGWLLETSHKMLLSTSEGSANQKAASRLLAVSGLINGVGDALSGLLLVEVLKYMGSBHRWNLVYDLPSRQKVKVFDRTAVTANAEVTVVQPIGDEINAEIAKYPGRGFRPRSGTEDEVHVVAEATFGDAADALASSVRLVDDYLGFS*

NbL13g05030.1 D1-like [MW = 20.01 kDa]

No. of times detected



log(intensity)



Values from



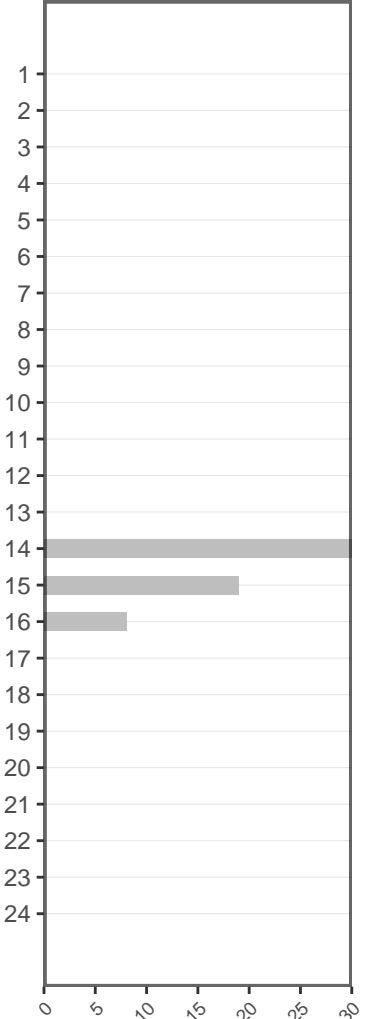
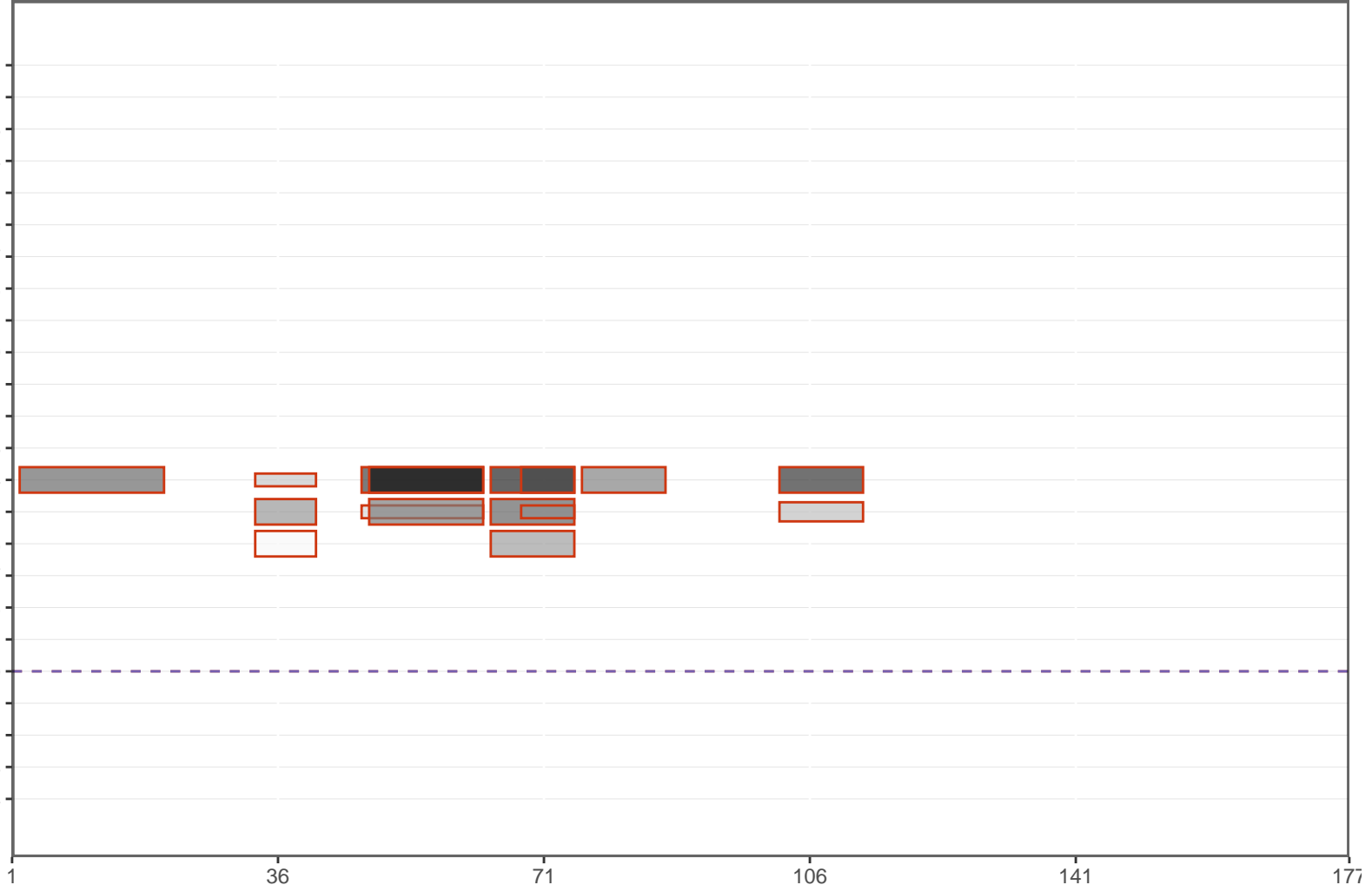
MW indication



Molecular weight

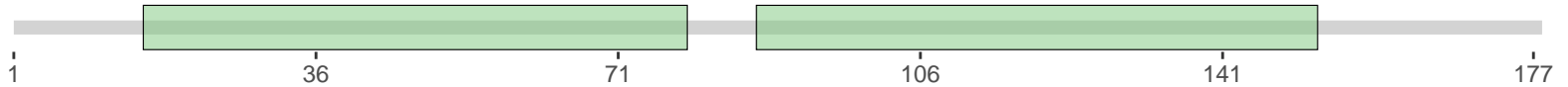


Gel Slice



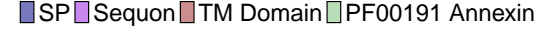
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

...VVVTLDPPEKDWLANEATKRWTKENFVLELAGTRSPKELVLRGVVHARVWVYKYLEEDVAWHITGHRKLLVALVSEVRYGRDRAATAFGVIGGVWWT...

NbL13g05020.1 probable_caffeoyl-CoA_O-methyltransferase_At4g26220 [MW = 32.86 kDa]

No. of times detected



log(intensity)



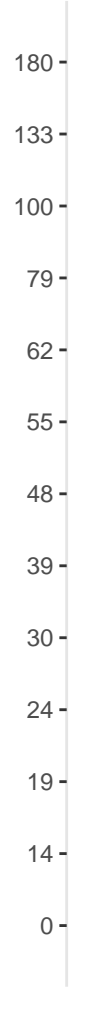
Values from



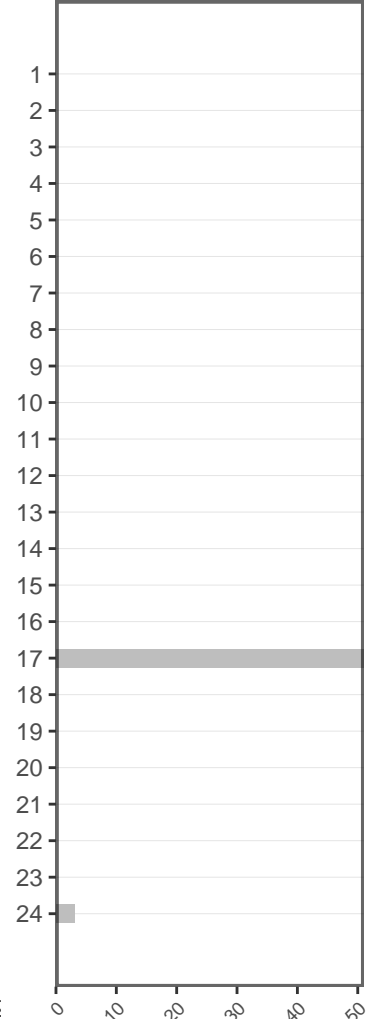
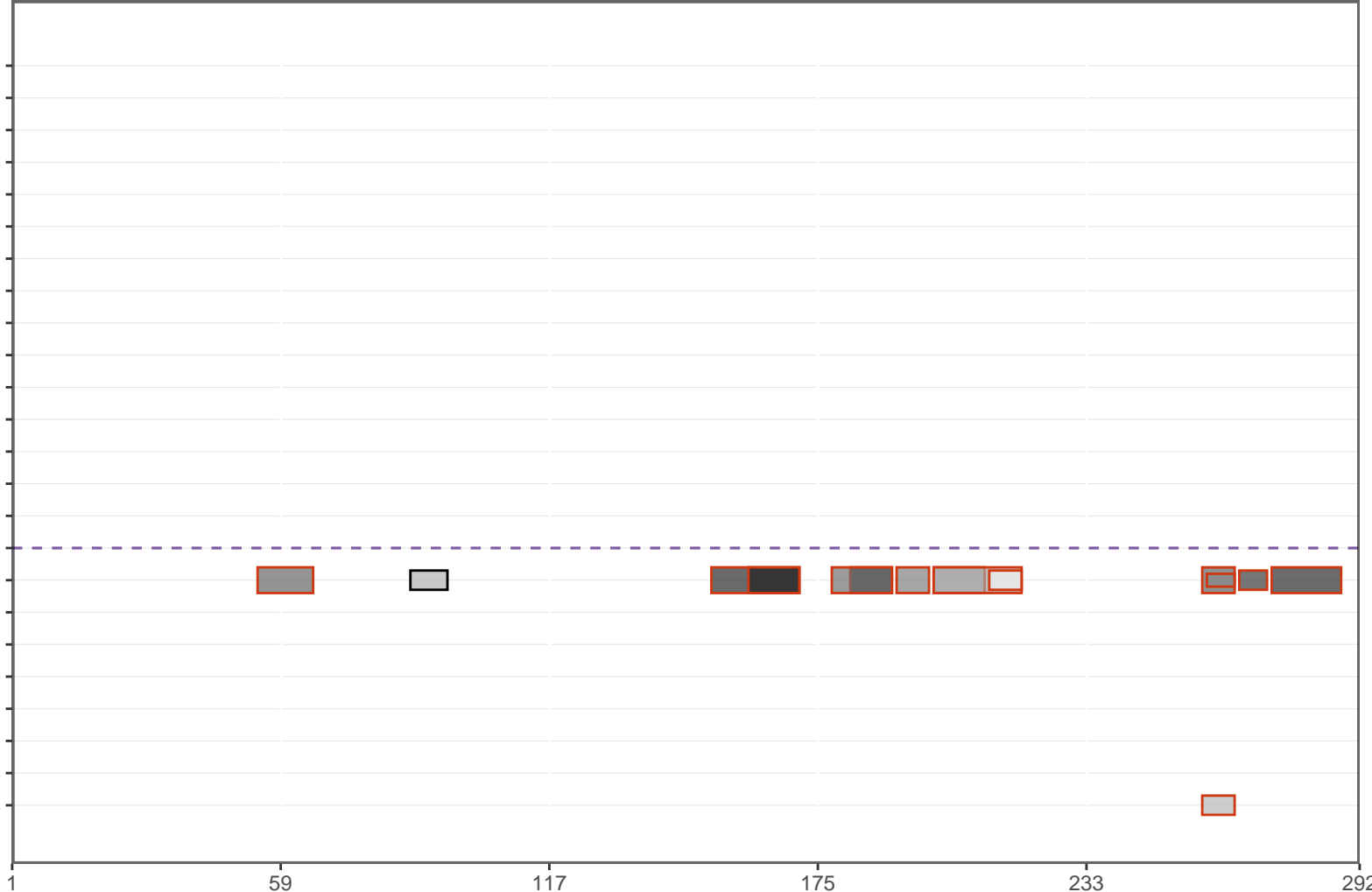
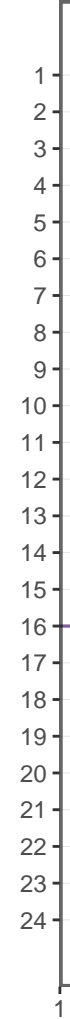
MW indication



Molecular weight

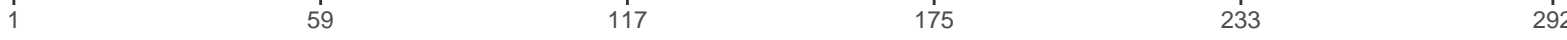


Gel Slice

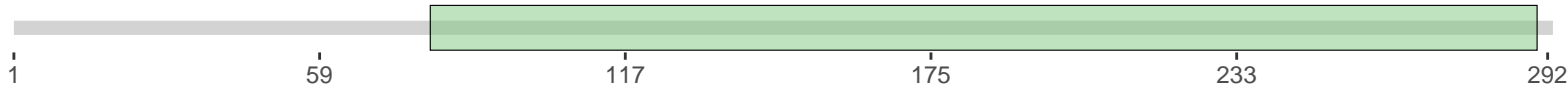


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

SVFTQYSVLLTALTPDDGKIMDPDRGGVELGLPVGKAGVEHKIDKIDSPALPVLDKILLEDSENRDFDFAFVDAQKTYGNVYHKLMLQKLVKGLIYVQNTLWYVGLVMPDEMVDLLRTERKYFLELNRFASDTRIGISGVTVGGDMTHRRLLF

NbL13g05010.1 probable_caffeoyl-CoA_O-methyltransferase_At4g26220 [MW = 26.5 kDa]

No. of times detected



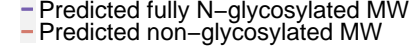
log(intensity)



Values from



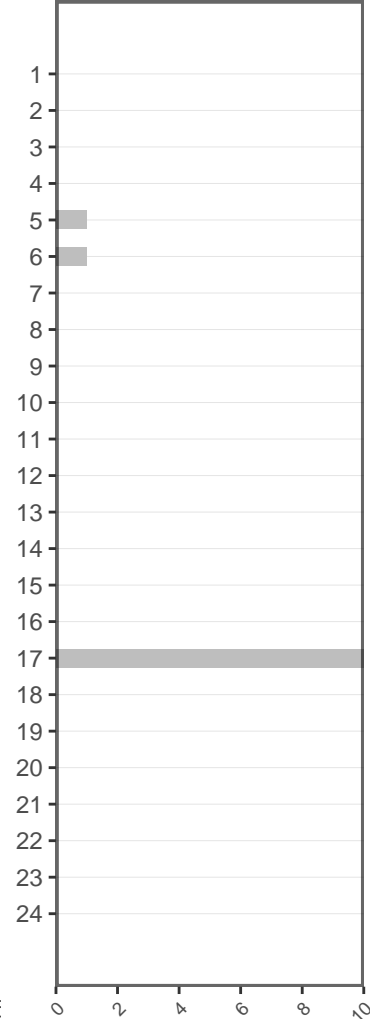
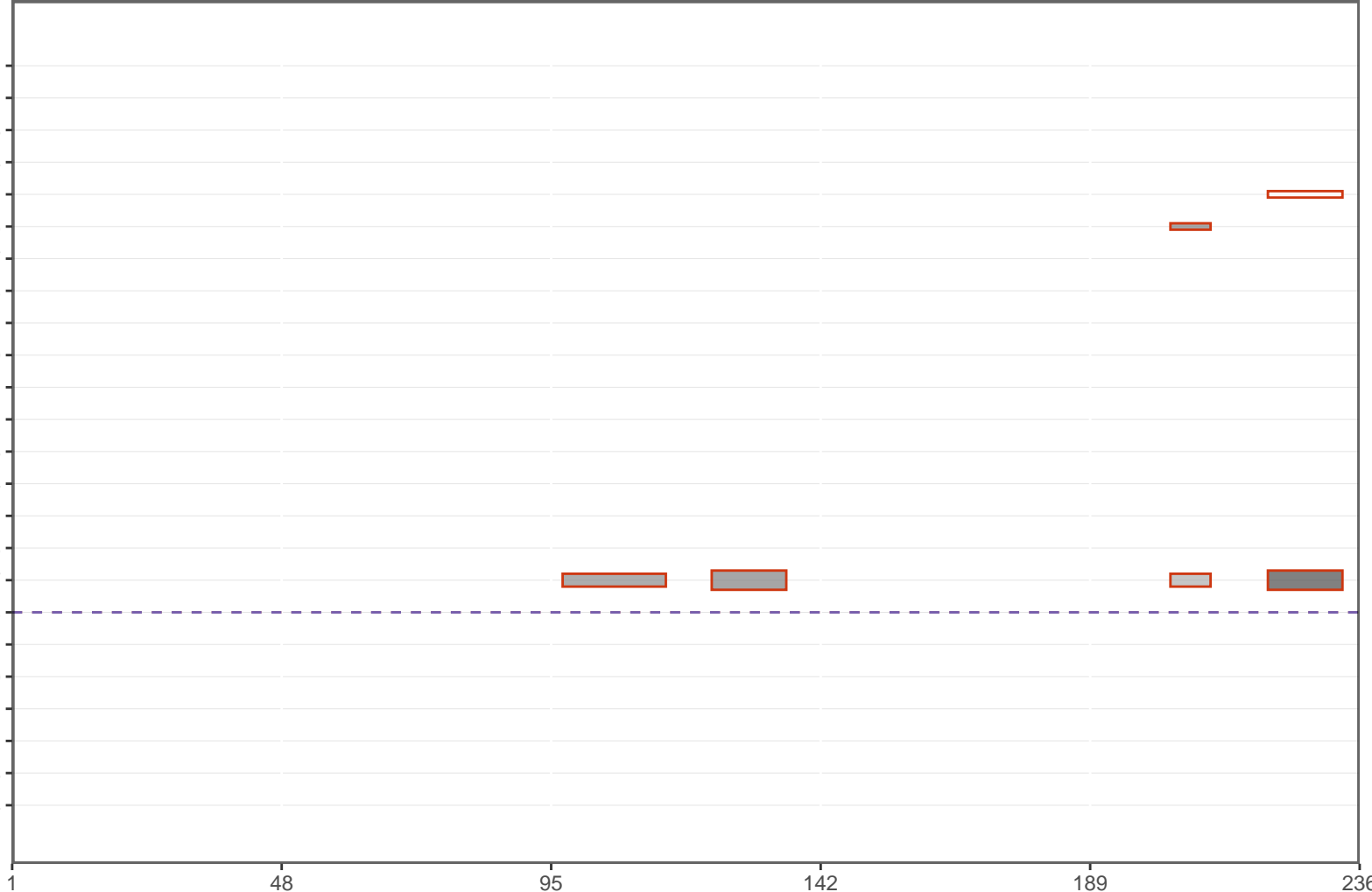
MW indication



Molecular weight

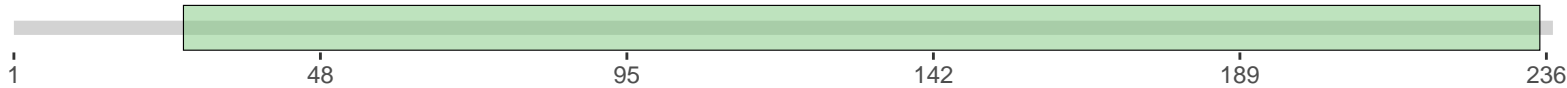


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

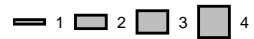


Protein sequence:

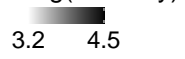
AYEMGLPVIKKAGVEHKINFGSSALPVLKLEEDNNKESFDFAFDADKWAYGKYHERLLQMKVGGHVDNTLWSGTIAMPESVPEGLKAVRHHTIEFNKFLAADRIRLGGVPLDGGITICRLI

NbL13g05000.1 histone_acetyltransferase_type_B_catalytic_subunit-like [MW = 53.06 kDa]

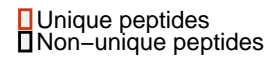
No. of times detected



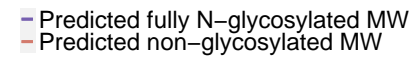
log(intensity)



Values from



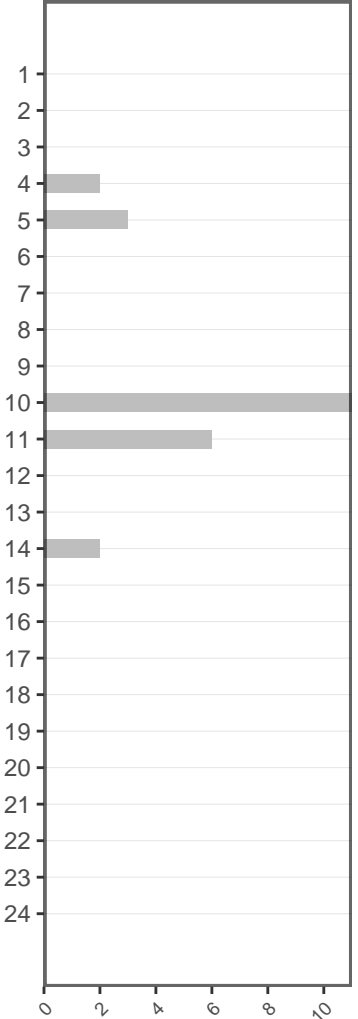
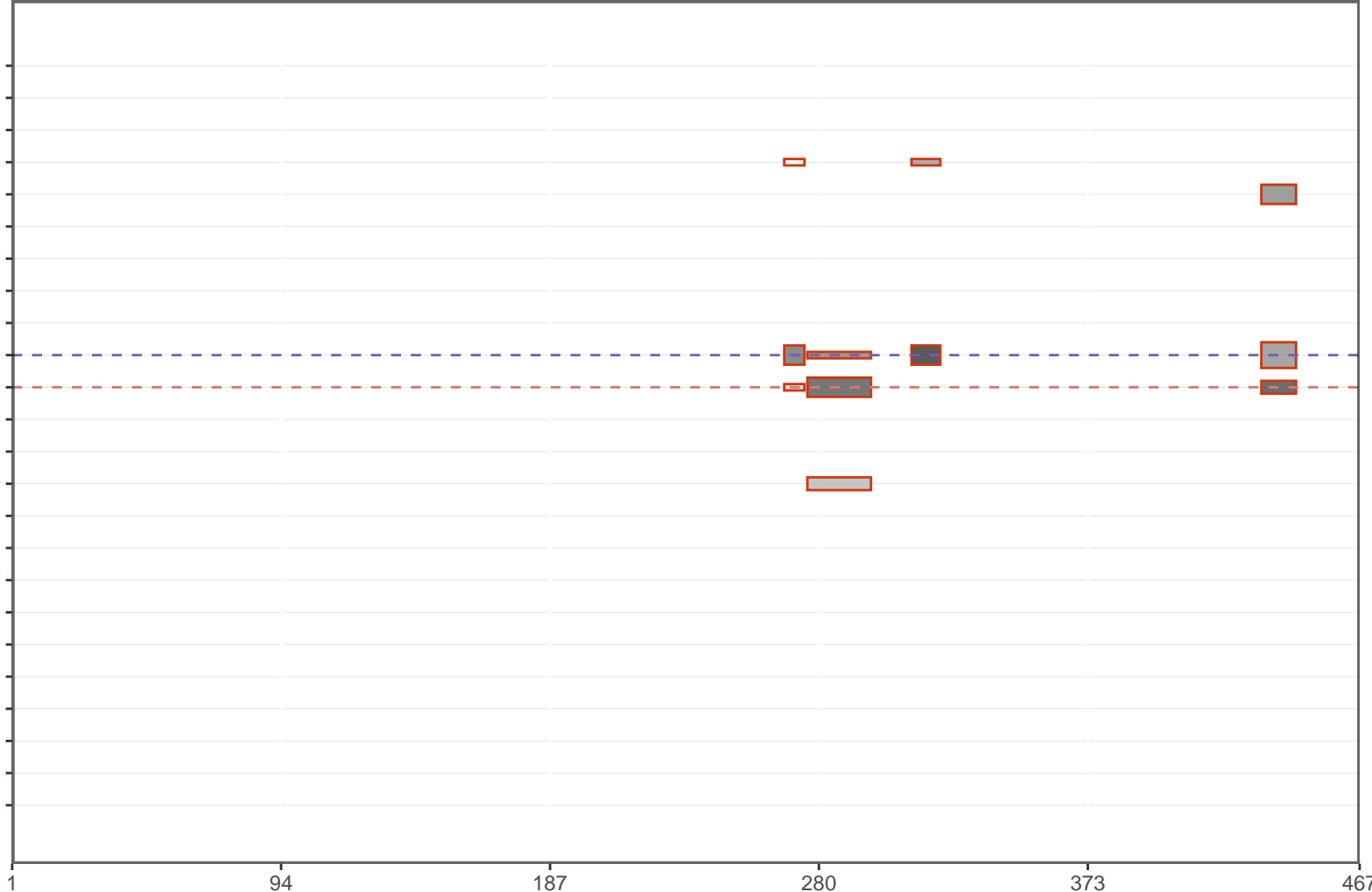
MW indication



Molecular weight

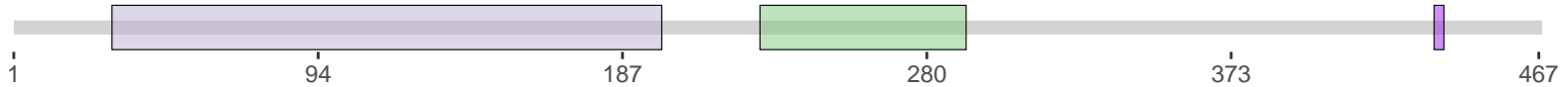


Gel Slice



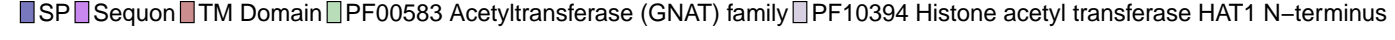
Protein length

Peptide counts over 4 repeats



Pfam domains

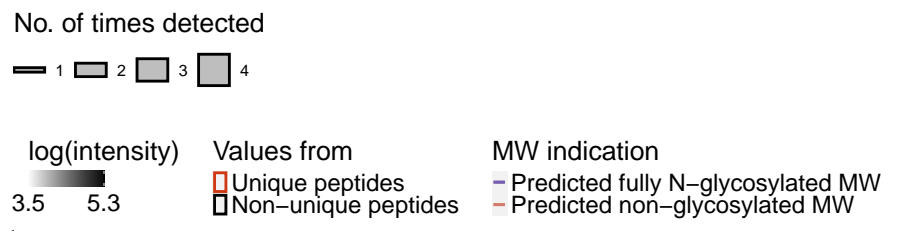
Pfam Description



Protein sequence:

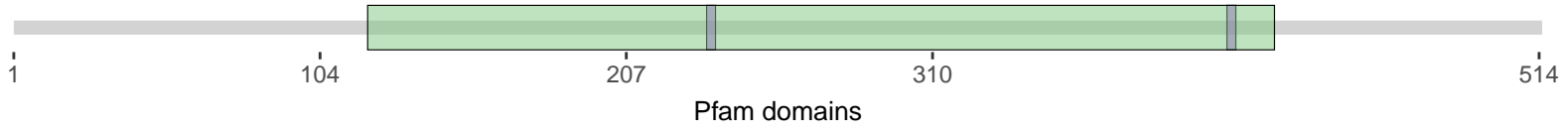
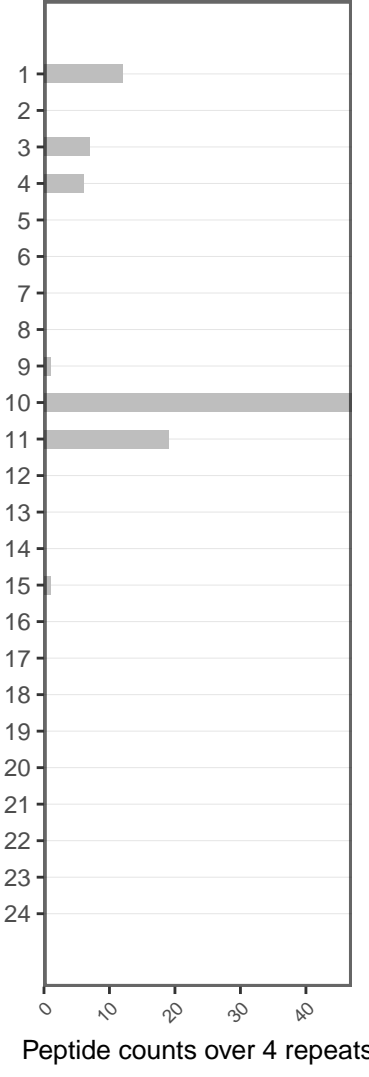
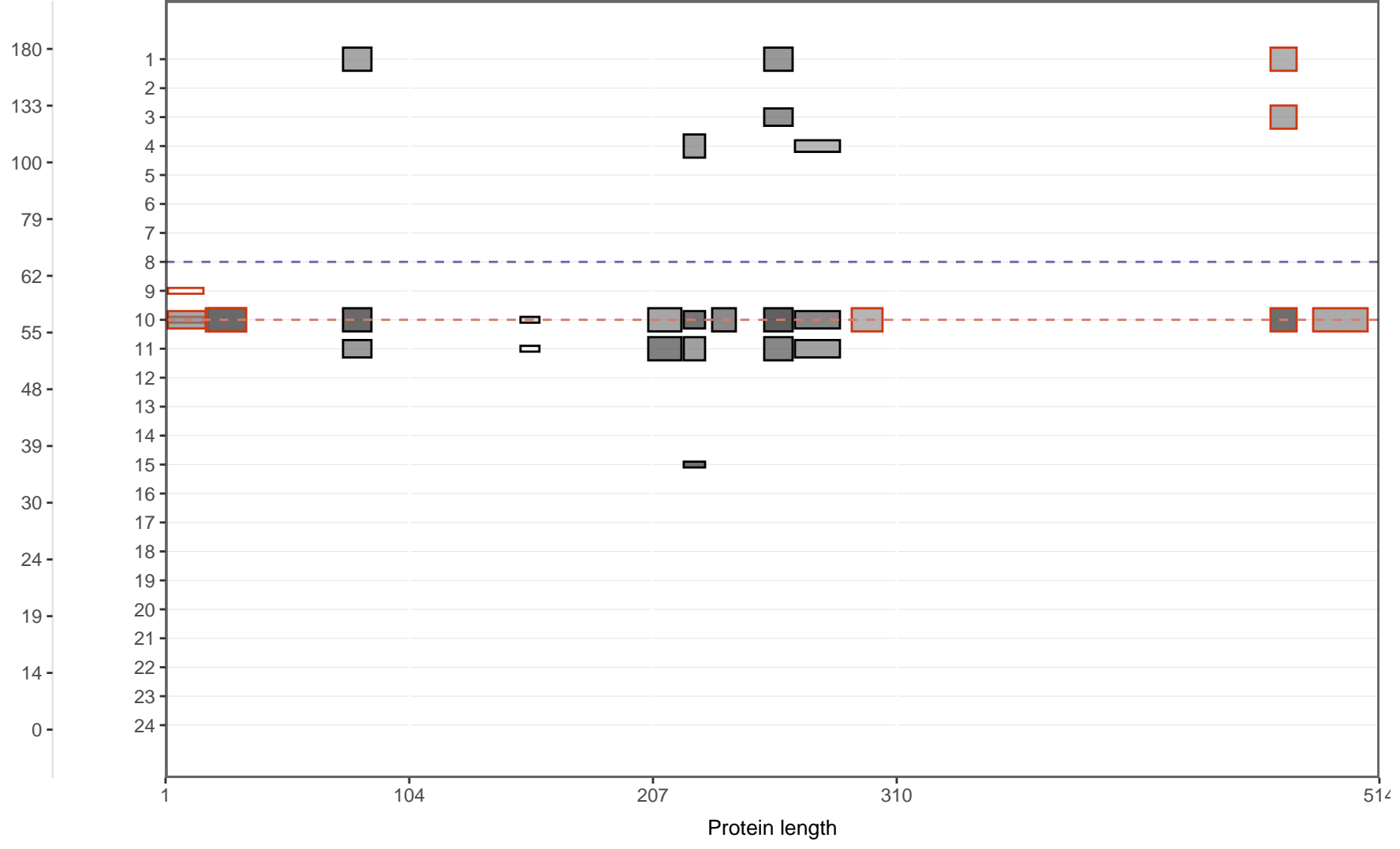
DTQEECSRLLGFANVRFHRYFESKRLRLGGILLPPYQKRGVGRLLLELVNFRVAISENYDITVEEPEDSLQHYRSGIDVERLLVFDRIQQALDSVSRLLKHENPSKSKYTKYGPPLSAVEDVRKTLKLNKKYFEGDWELLYLSLNPIDKYMETYRTVLVHRVKAEEVGGKDEGNGKGVDPVPTHEHDEGMSFVFKSGNGESSEIEKADNDGSIVEEQLGKLVDERLNDKILAEKVSVHRQ

NbL13g04930.1 ATP-dependent_6-phosphofructokinase_6-like [MW = 56.56 kDa]



Molecular weight

Gel Slice



Protein sequence:

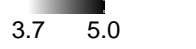
ITDNDIPVLDKSGFDBSAVEEAGRAISAHVEATSFENGIGLVKLMGRDGGFIAMVATLARSVDVDCGLPEPSFYLEGHGGLFEVIEHRLKENGHMVIVAEAGQELVSESLRGTSGKQDPSGNKLLQDVLGWSERKEHFKGKKMLINKYDPTFYMRAIPENASDNVYCTLLAGSAVHGAMAGYGFVGPVNGRHHVYIPNRFETQNKVITDRMWRLLSSTNGPSFLRTRDIKAKHKEEPPQLSDDGTDNDLMEKQVLD

NbL13g04910.1 leucine-rich_repeat_extensin-like_protein_4 [MW - SP = 41.64 kDa]

No. of times detected



log(intensity)



Values from



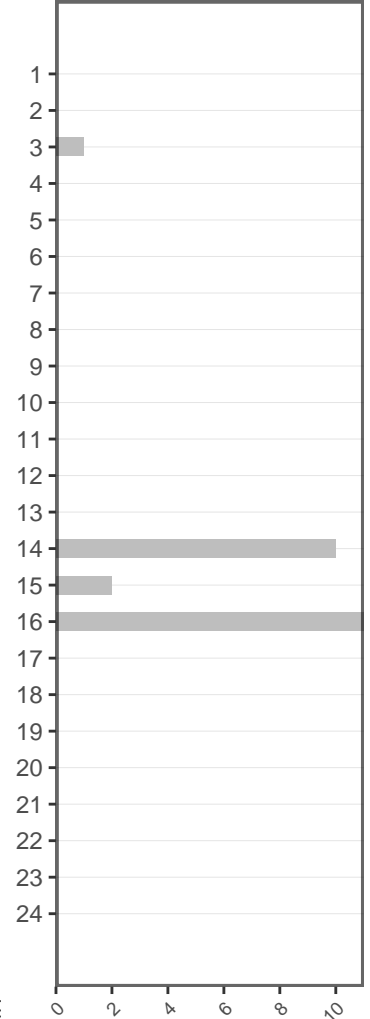
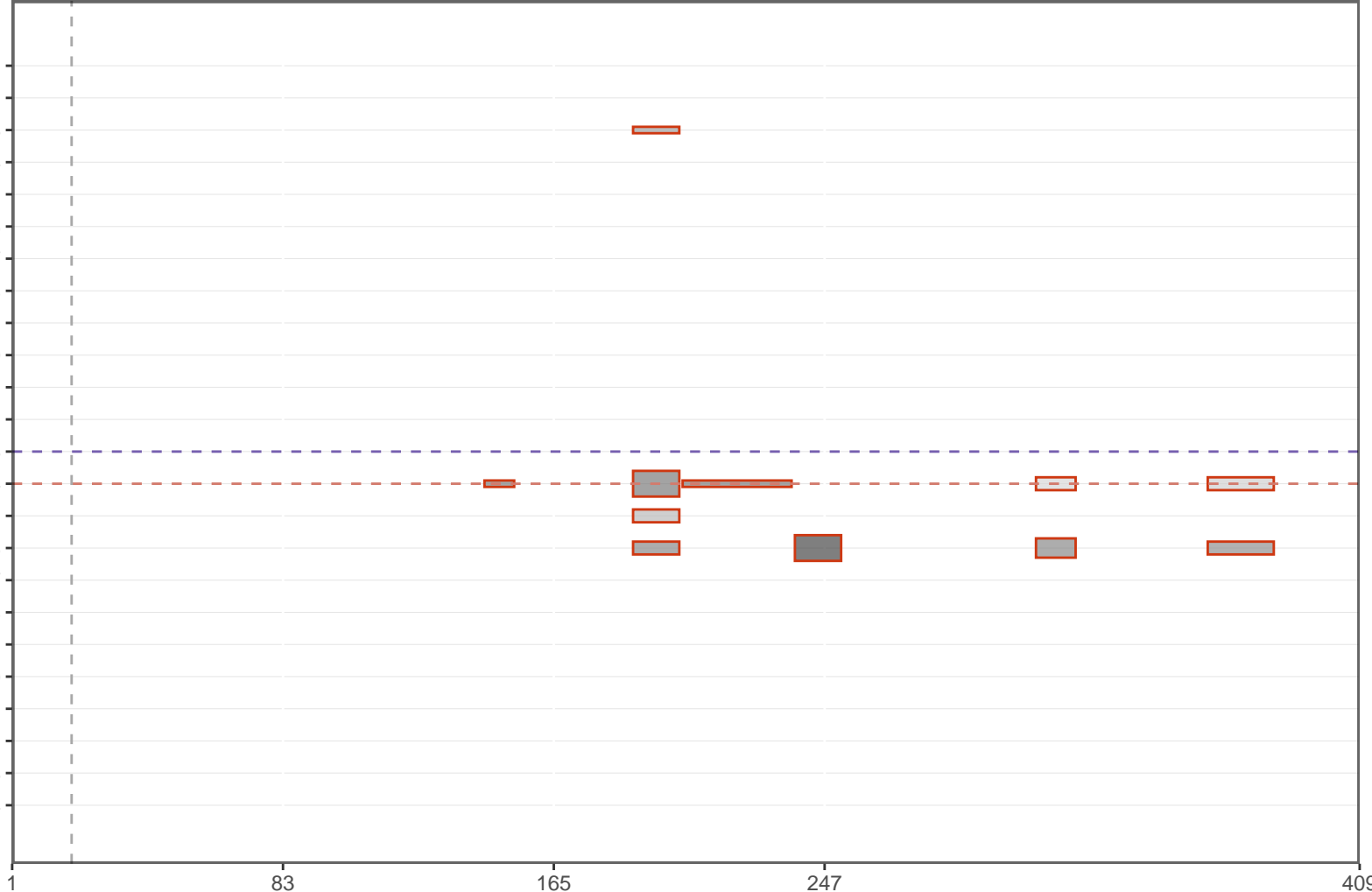
MW indication



Molecular weight



Gel Slice



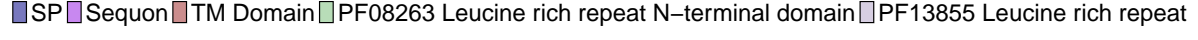
Protein length



Pfam domains



Pfam Description



Protein sequence:

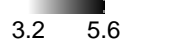
SFSGPIPEDLFNKKLDAFLNNGDFGELPQNLGNPSGIVNLANNKFTGNPFSLGYMGRPKKEIFLNLNQLTGGPEGVGMWTDLGVLDVSNFNLHLPDLSGLSGIEVNLANNKLSGLDLPVLCGLRLSUNLTLTYNFFSGLGGDDKLYPRNVCDFSLNCPGKGMQRPPQPECSLIPGGLSGLRLPAAKPLVCGSHSEEEIVSTPPGH

NbL13g04760.1 ATP_sulfurylase_2 [MW = 54.74 kDa]

No. of times detected



log(intensity)



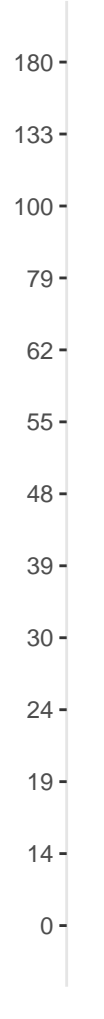
Values from



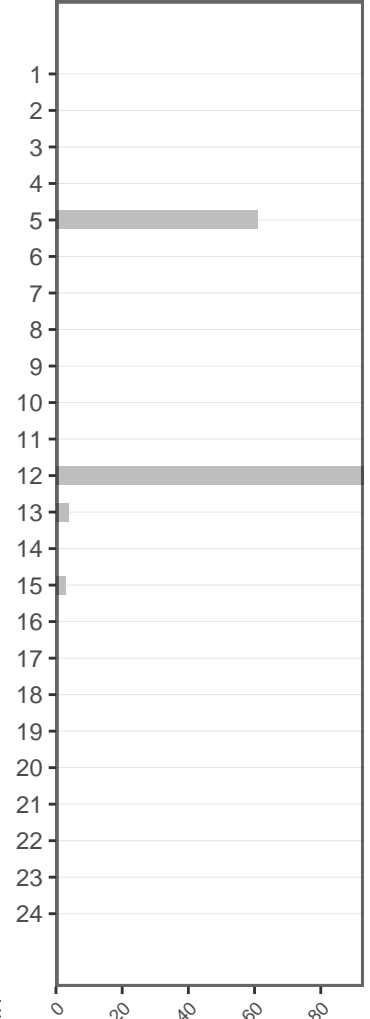
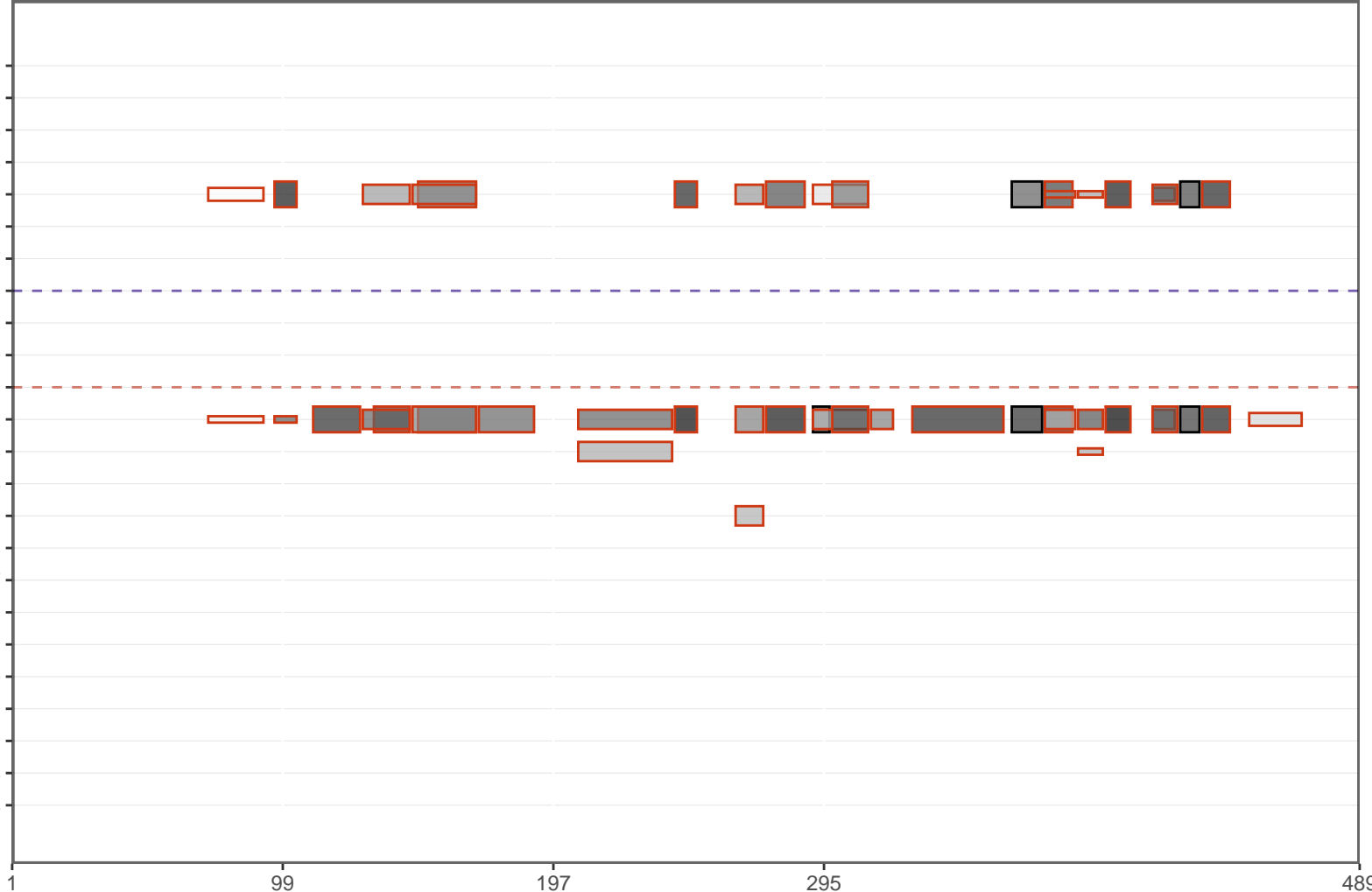
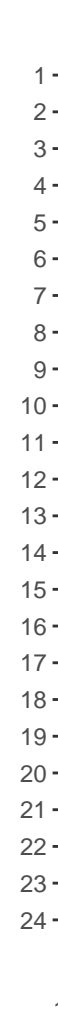
MW indication



Molecular weight

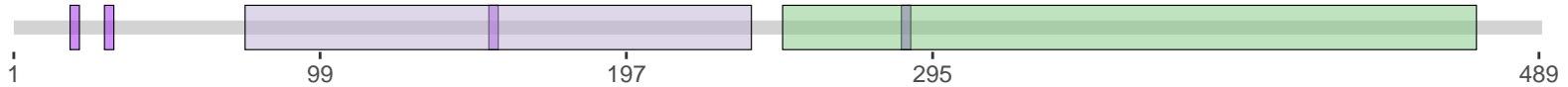


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

/KPKYNDGLDHYRLSPQGLRDEFDRREADAVFAFQLRNPVHNGHALLMNDTRRLLEMDYKNPILLPLGFTKVDVPLDVRMEQHSKLVLEDGLDPETTVAIFSPFMHWGTFEYQVHWAKARINAGANFYVGRDRGMSHPTEKRDLVDFPHGKVKVLSMAPGLEKLNILPFRVAAYDTVDKMMAFFDPSRAGEFLFISGTMKRYTARTGENPPOGFMCPGQWEVLVYKYYEQLGAEQVNSALSAR

NbL13g04750.1 rab_escort_protein_1 [MW = 60.71 kDa]

No. of times detected



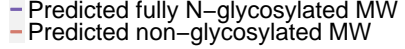
log(intensity)



Values from



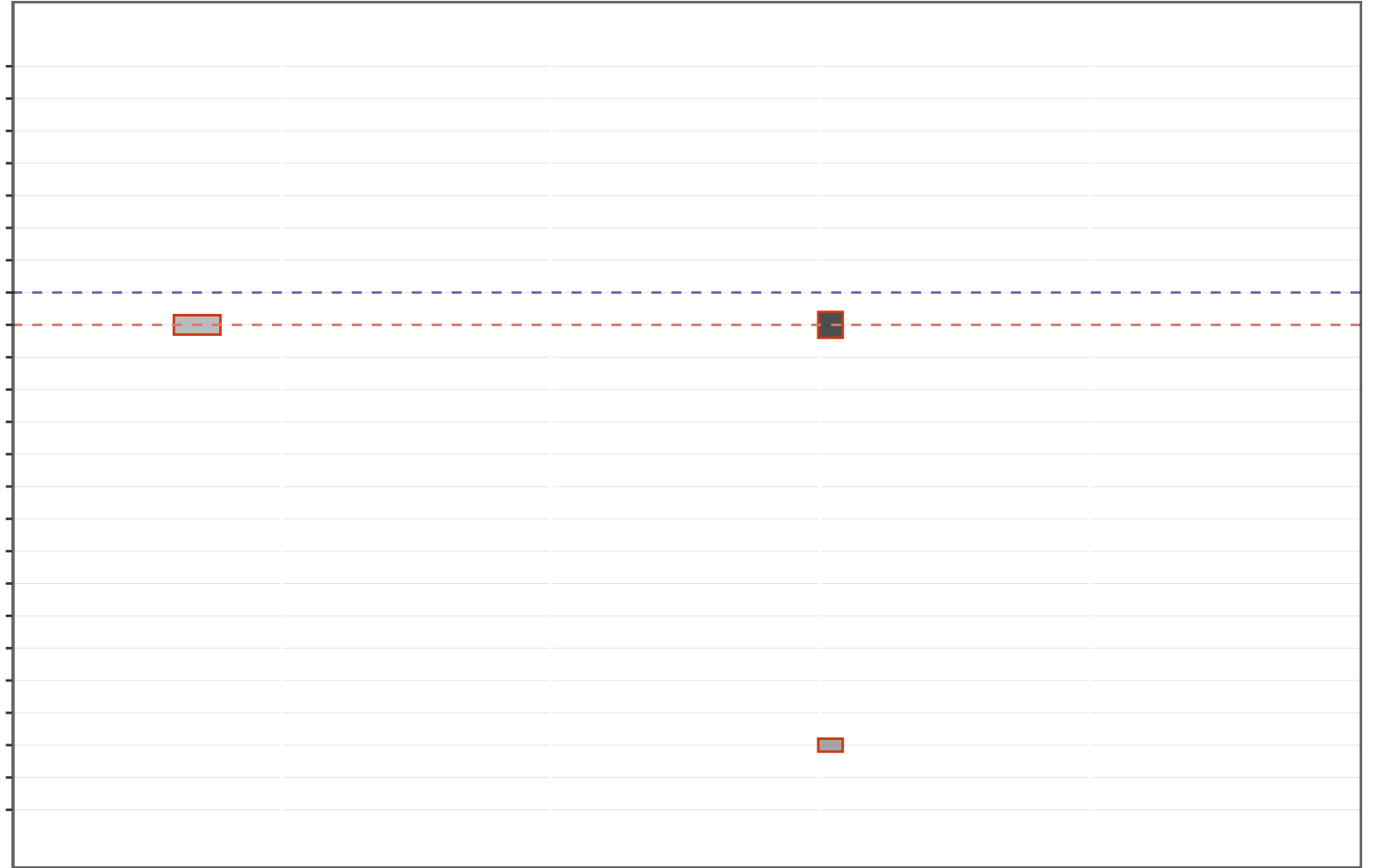
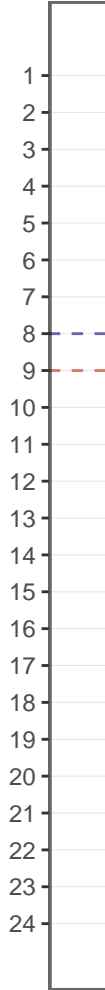
MW indication



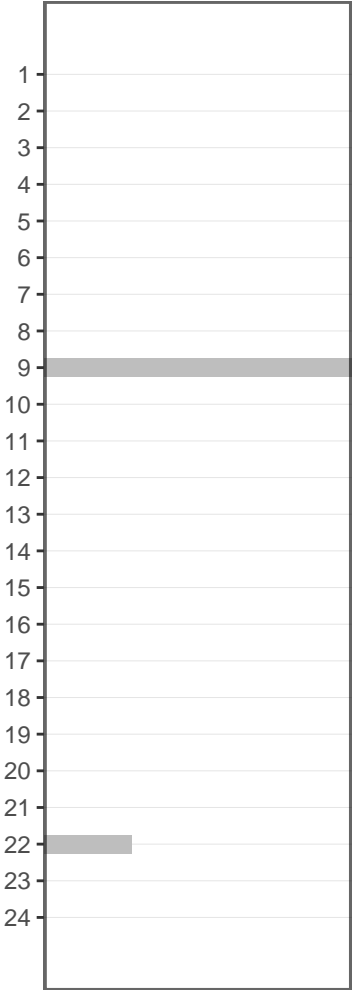
Molecular weight



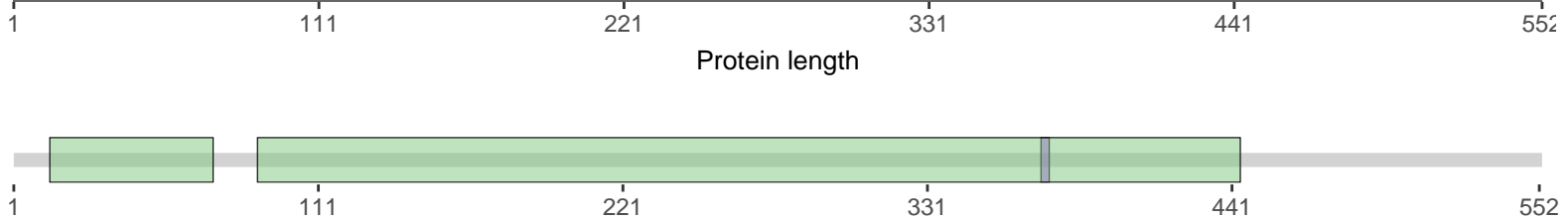
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LLALYHSSVGRFPNAPGAMVPIYGGELPQAFORRAAWGGQHLRMPVHLLMDKATGNVYGVRLASEGEVYSHKILAPSFVQLPPPHSPDAGQNYVDGFLKNTTEKLARSVGTGRHSLKLDKANCLASFPFRSLFPEQVTAHVLQLSGNWVCPGSMFLVLSAICEDDVGQKLLHAANALFGIPVGGSSSENDNSAKKGETRDAKPAALLWSVLTQELTKFDVLDNISASMPDGGSPVYHDLGATEKIFEEVYSGEVFFPKTASSEEGAVEEED

NbL13g04730.1 uncharacterized_LOC109242911 [MW = 34.33 kDa]

No. of times detected



log(intensity)



Values from



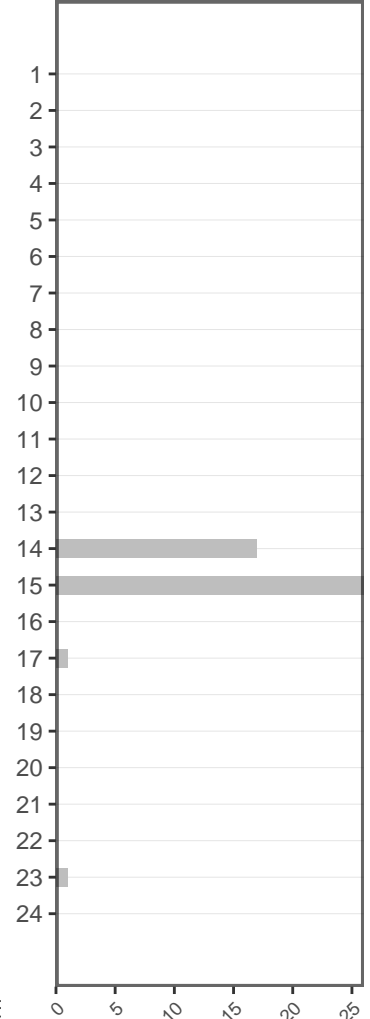
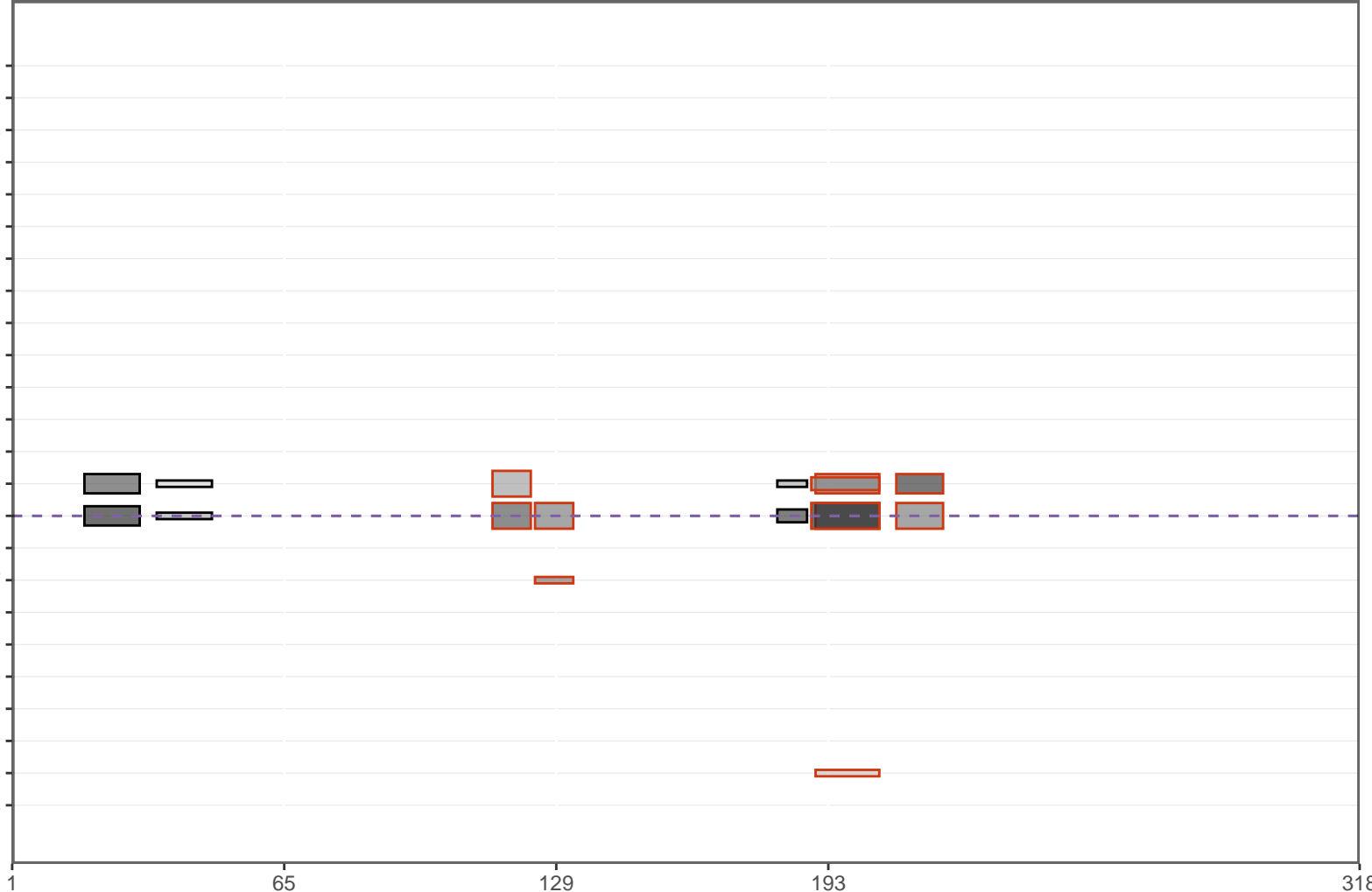
MW indication



Molecular weight



Gel Slice



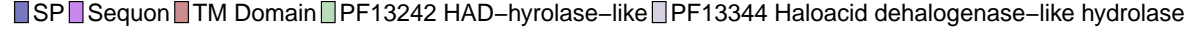
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

/ENAGAEANFLAHGTEALGLSSGAALPMKLLDLEKLEEQCAAKKIPMVAANPDFVTVEARALRVMPGTLAATYEKLGGGKWKMGKPKIKYKSAEMEMADVDVSDGVAVGDSLHHDKKGANAGIASAFITGHHATELGLSKFGEVADDNSHALALGNNAVPTVYLPSTFW

NbL13g04670.1 uncharacterized_LOC109239937 [MW = 29.1 kDa]

No. of times detected



log(intensity)



Values from



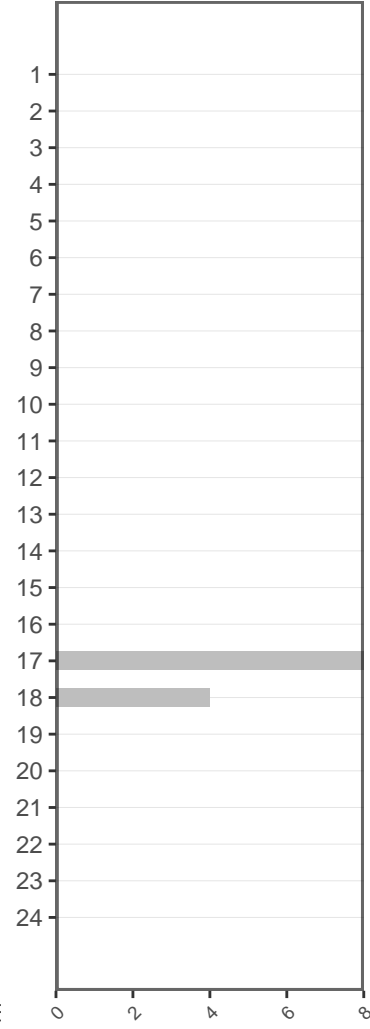
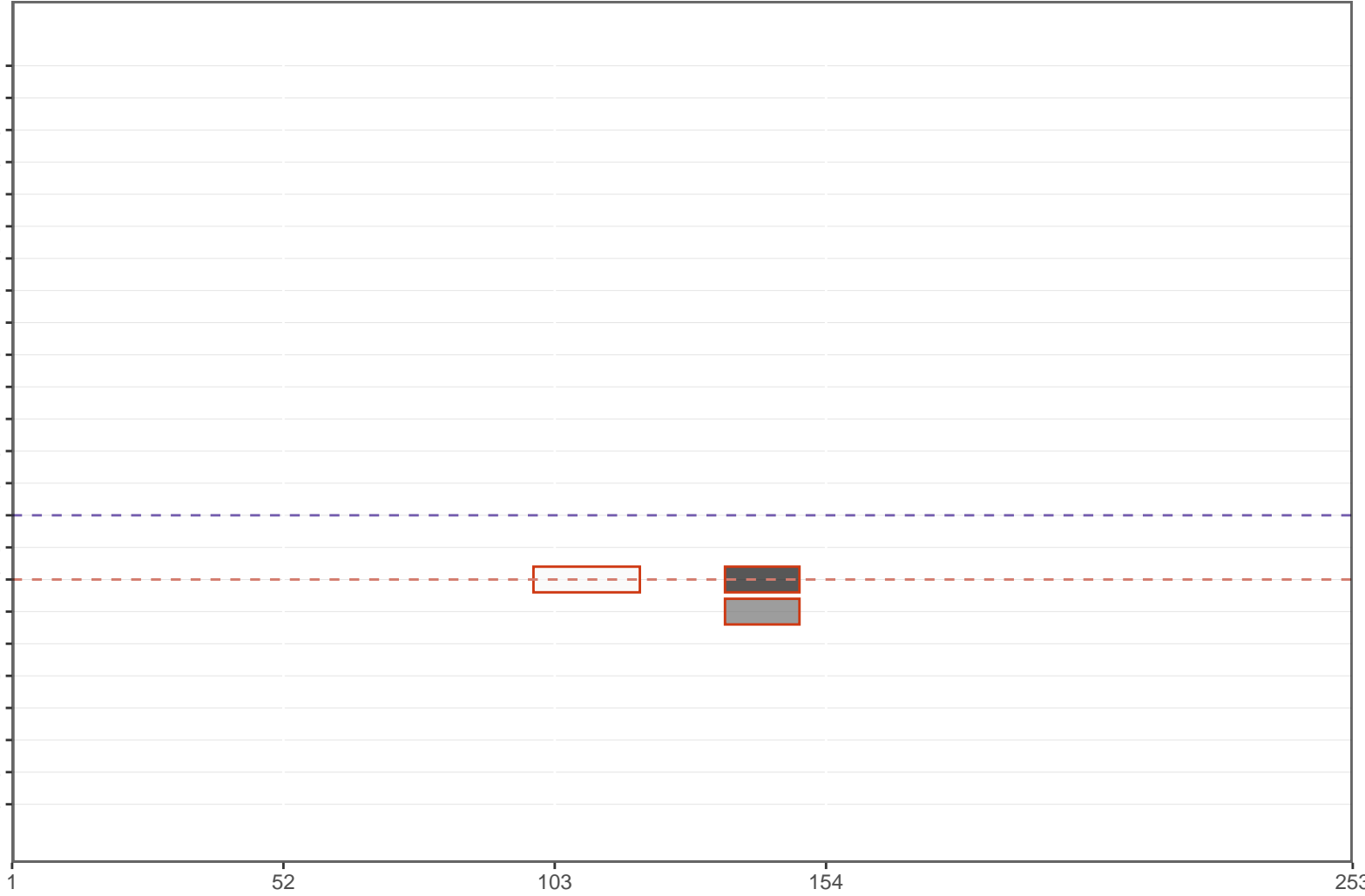
MW indication



Molecular weight

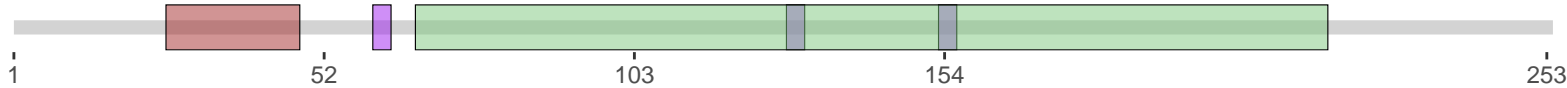


Gel Slice



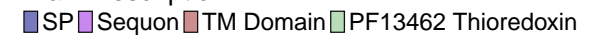
Peptide counts over 4 repeats

Protein length



Pfam domains

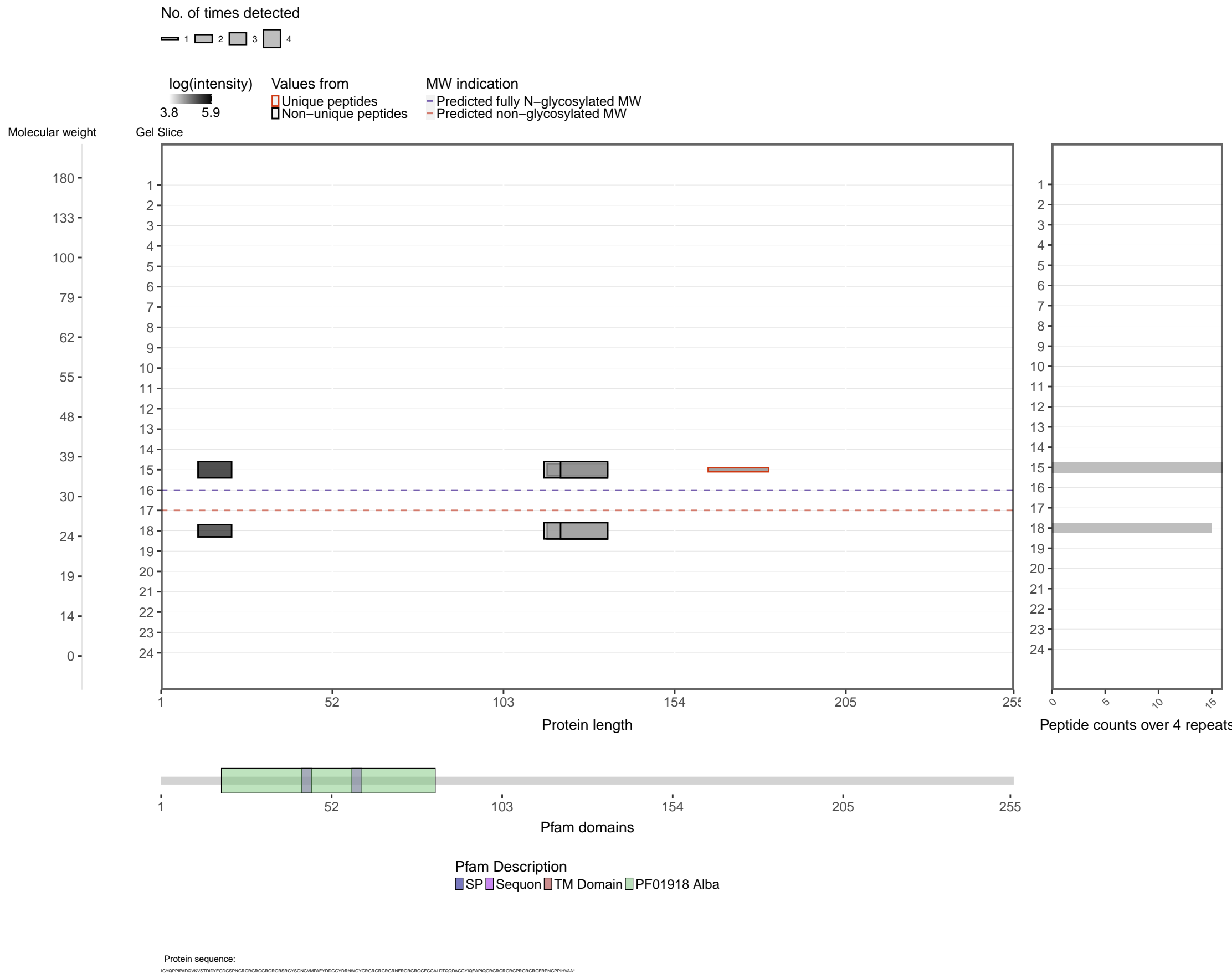
Pfam Description



Protein sequence:

FLTSRALHIVNKLNASATYKLLSEFFDHOEEFYNAKATPFLSRABVIEKVRGFGTMAIGNSNVYKAGFDYKTDGSTRFSEFKYGGVGVGTFFFFVNGFLPDAGSADVNGWRRVLDPLVHGGDTGRNDLLHFFL

NbL13g04660.1 ribonuclease_P_protein_subunit_p25-like_protein [MW = 27.96 kDa]



NbL13g04590.1 subtilisin-like_protease_SBT5.3 [MW - SP = 78.45 kDa]

No. of times detected



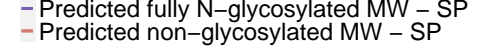
log(intensity)



Values from



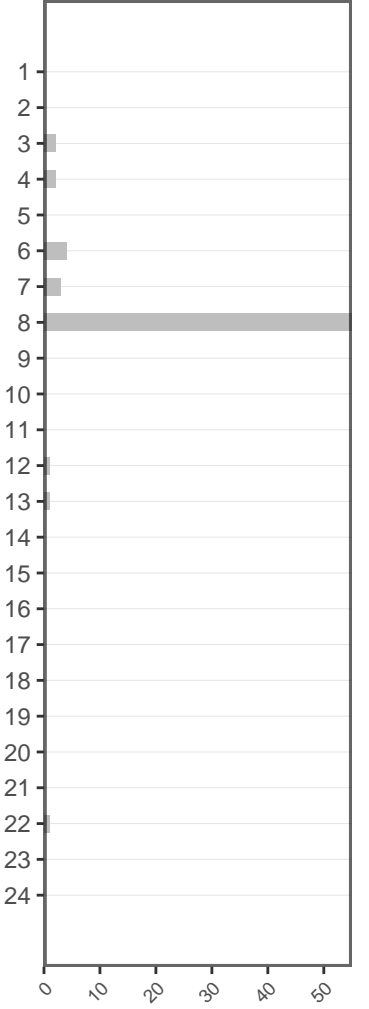
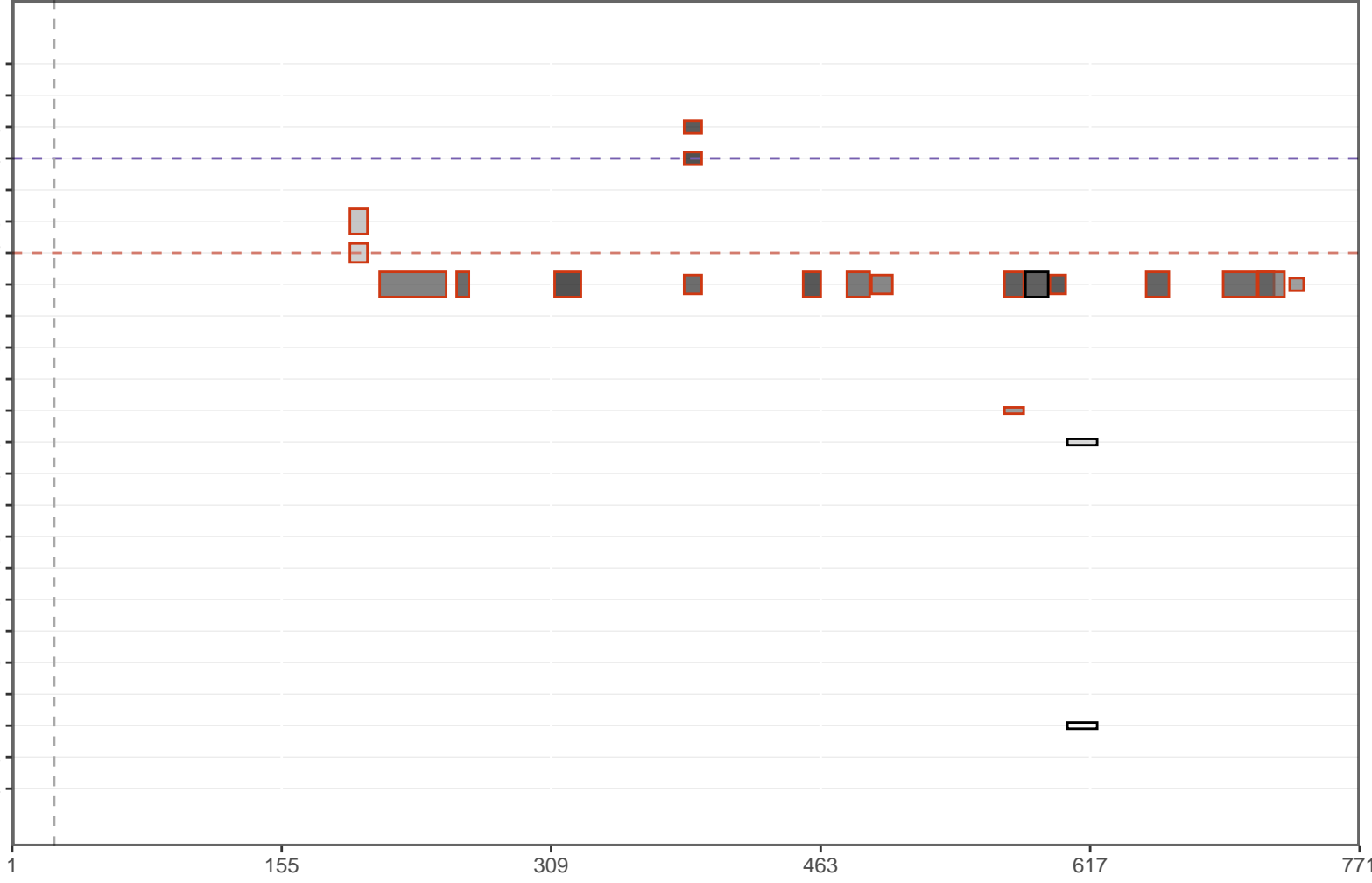
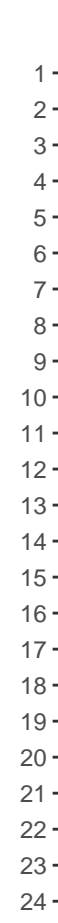
MW indication



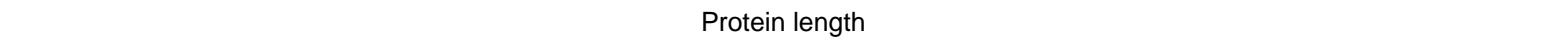
Molecular weight



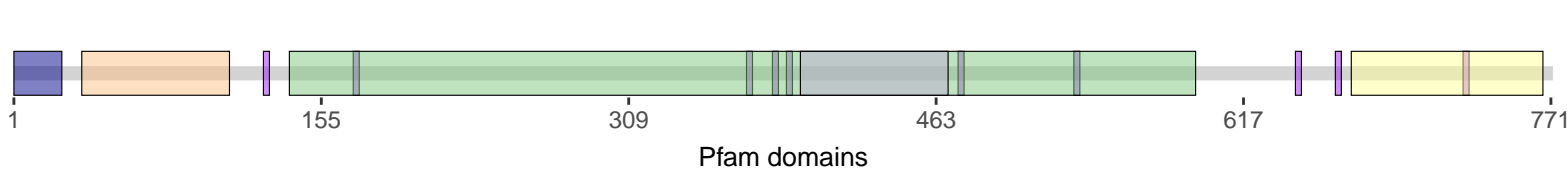
Gel Slice



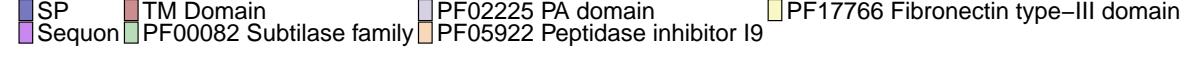
Protein length



Pfam domains



Pfam Description



Protein sequence:

ITKSSVYPLIHGNSIKSNENVSEADARSGVPGELDENKYGKIVLGENLDDGEYFPSDKLDEVKSRGQVGFILDDDERTVAPKFNFSAGVGVSKKDKGNELAVINSTRNPVASILFTVBITKTKKPPVAWVFSRSGRPWNTFPLNKLPDITAPGVAILAAWPGNDTSEALPGGKPPFNLLGGTSMSCPHVSGIAATVKAWNPVWFSRAVKSAMFTAGTGNLKKAPITVGGSKATPYDVGAGEASTSGPLKGLVYETDADVLQFLG6GVGFNSGKILSIFVPEDFSCPKNSTSELV

NbL13g04550.1 endoplasmin_homolog [MW – SP = 90.82 kDa]

No. of times detected



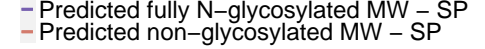
log(intensity)



Values from

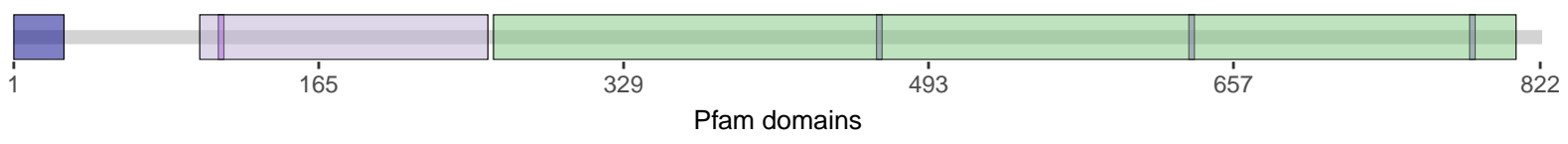
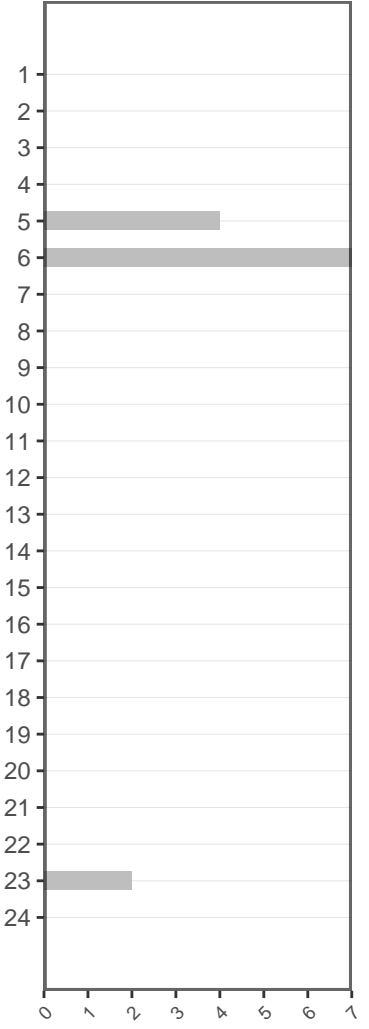
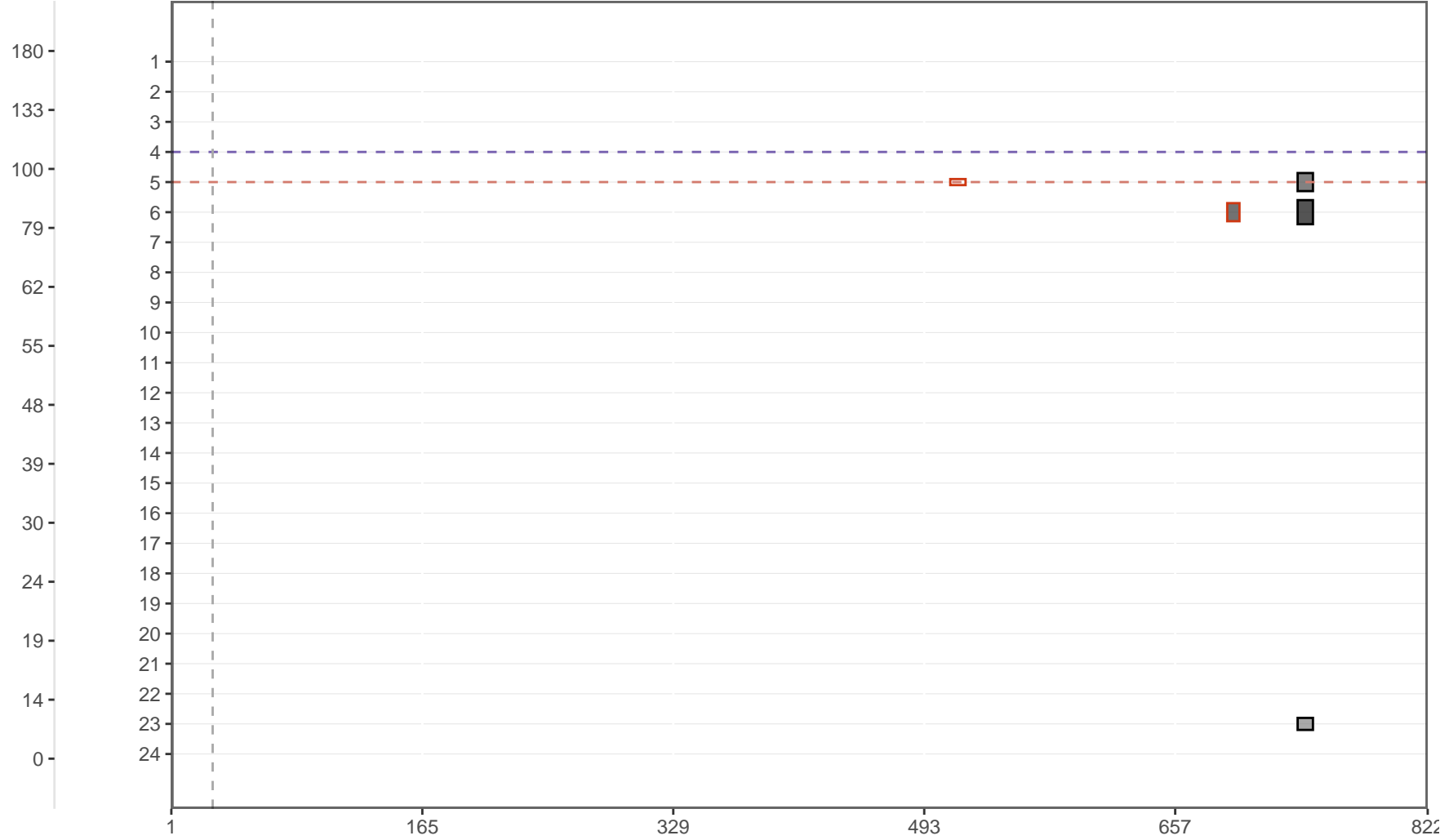


MW indication

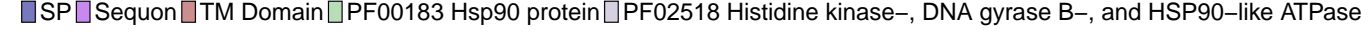


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

DVFEKALVYPPKAPHDLVDEYFNKKNLKLVRVRFISDFDELLPKVLSFLMLGVDSDTFLNLSREMLGQHSLSKTKIKKLRKALDMIRKIADEDPDESNDKDKKKVVEESGADNEKKGVYKVFNEFGKSVLGHEDATRNRLAKLLRFETSKSDGKILSLDQYHSMKAGGKDFVITGASKEGLEKSPFLERLTKKNVEVIFFTDPVDEKLMQVLMDFEDHFGQVNSKEGLKLGKDSKAKELKESFKELTRWWWKALASDNVDDVWISNRLADTPCVVVTSKYGV

NbL13g04470.1 prolyl_endopeptidase-like [MW = 92.1 kDa]

No. of times detected



log(intensity)



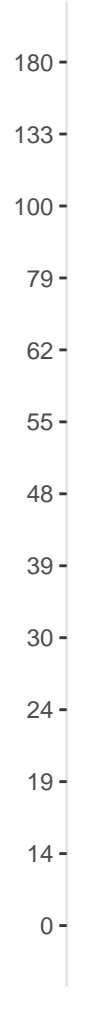
Values from



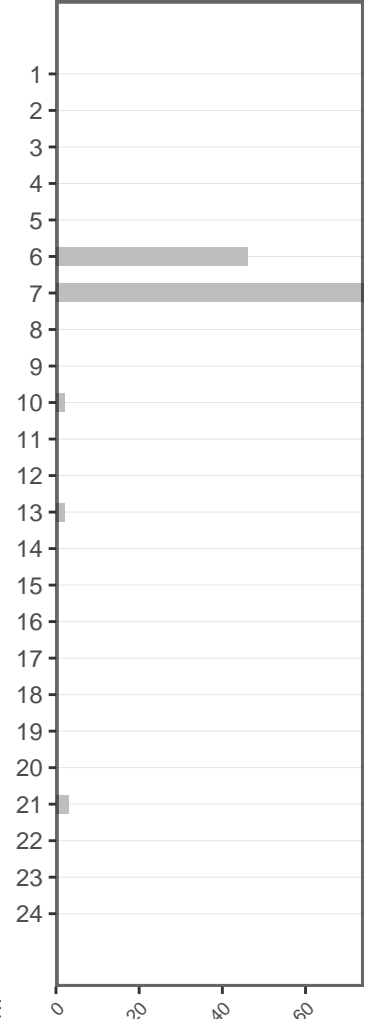
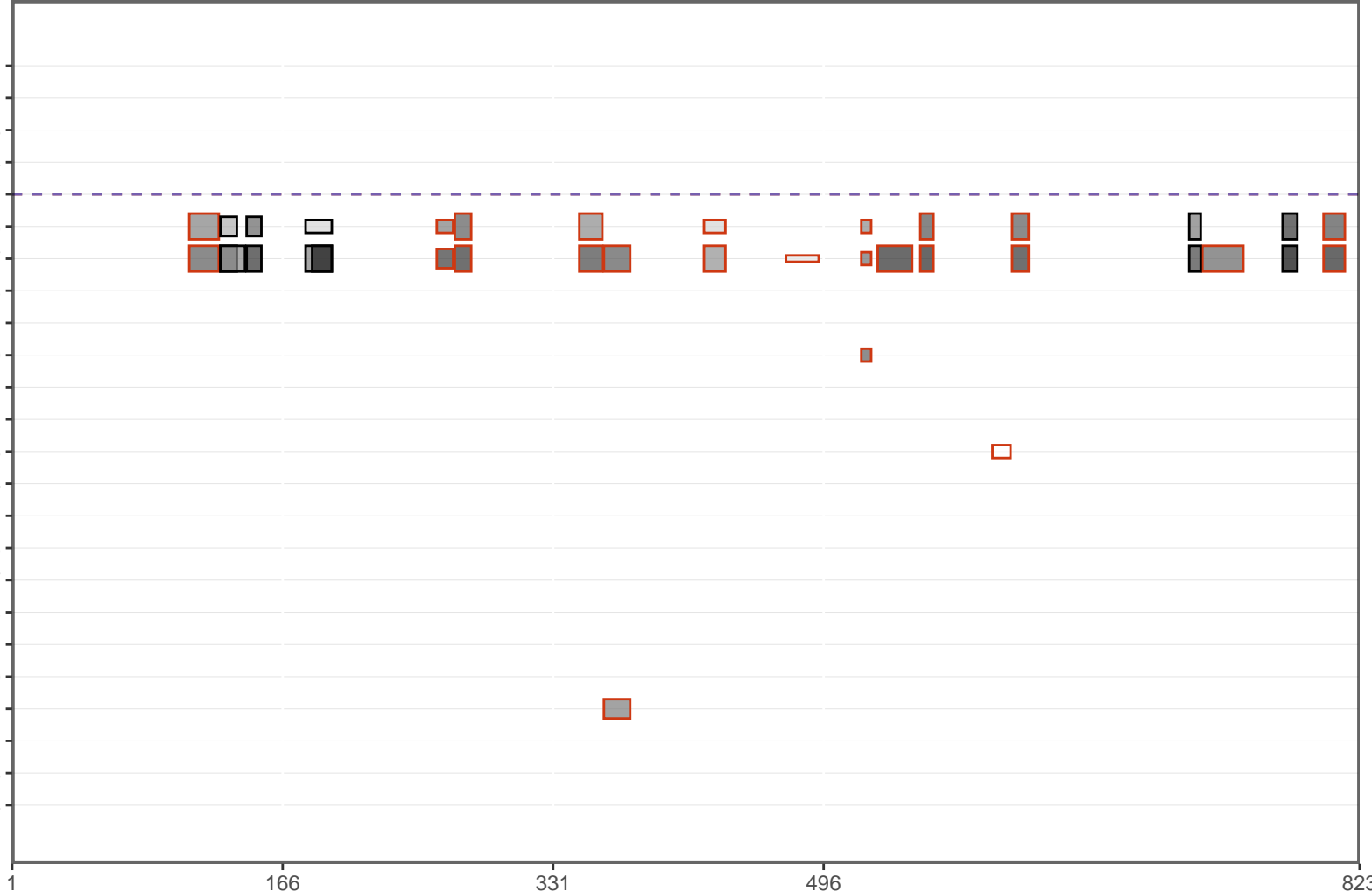
MW indication



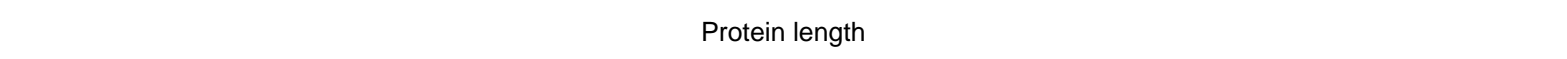
Molecular weight



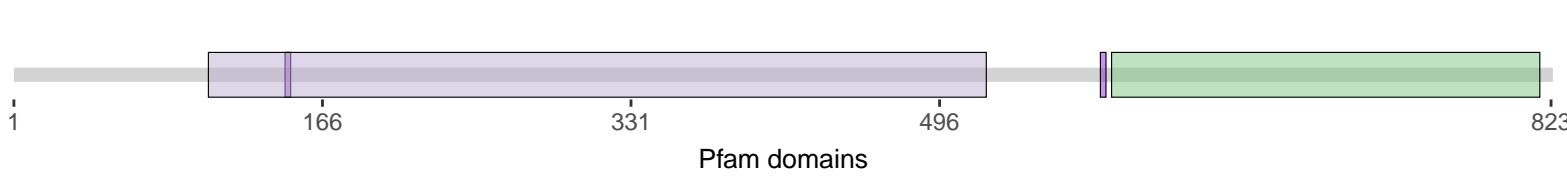
Gel Slice



Protein length



Pfam domains



Pfam Description

- SP Sequon
- TM Domain
- PF00326 Prolyl oligopeptidase family
- PF02897 Prolyl oligopeptidase, N-terminal beta-propeller domain

Protein sequence:

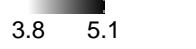
YDCVANDGTAFTFRNKDAPKYLVRVLDLKEPEFESWSDIREDEKDVLESAAVNDNDQNLVYVYLSDDWNYLQLRDLKYGVLHLLHPIDIGTVSGISARRKDTSTFIFGFTNLFIPGRIYEGDLKAEVPLDKVFRRETVVPGFDHTEFQVNGVYVPSKDGWIPMFIWAGKDFLGGSPDLLVGYGGFNISITPYFVGRVYAKHLGVFQIANIRGGEGYEDWIKAGLSLKKQNGDFDFISAAEYLVTAGYQPEKLIIEGGNGGLVAGINRPPDFGALAIYGVMDMLRFHK

NbL13g04400.1 probable_acyl-activating_enzyme_1_peroxisomal [MW = 60.91 kDa]

No. of times detected



log(intensity)



Values from



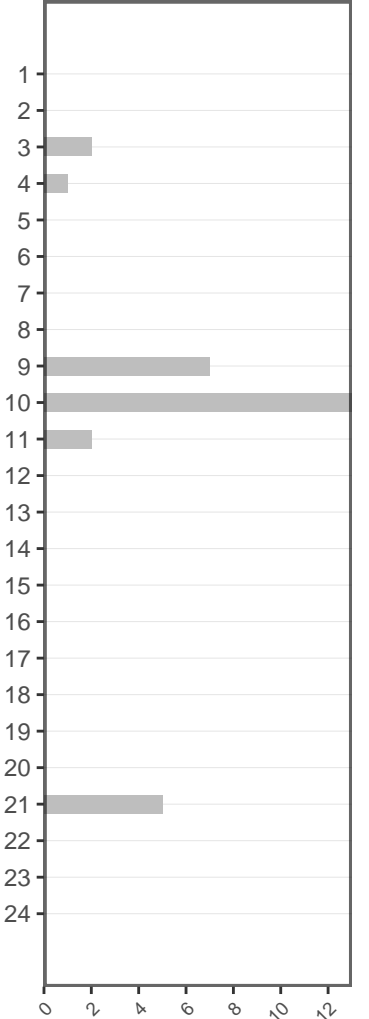
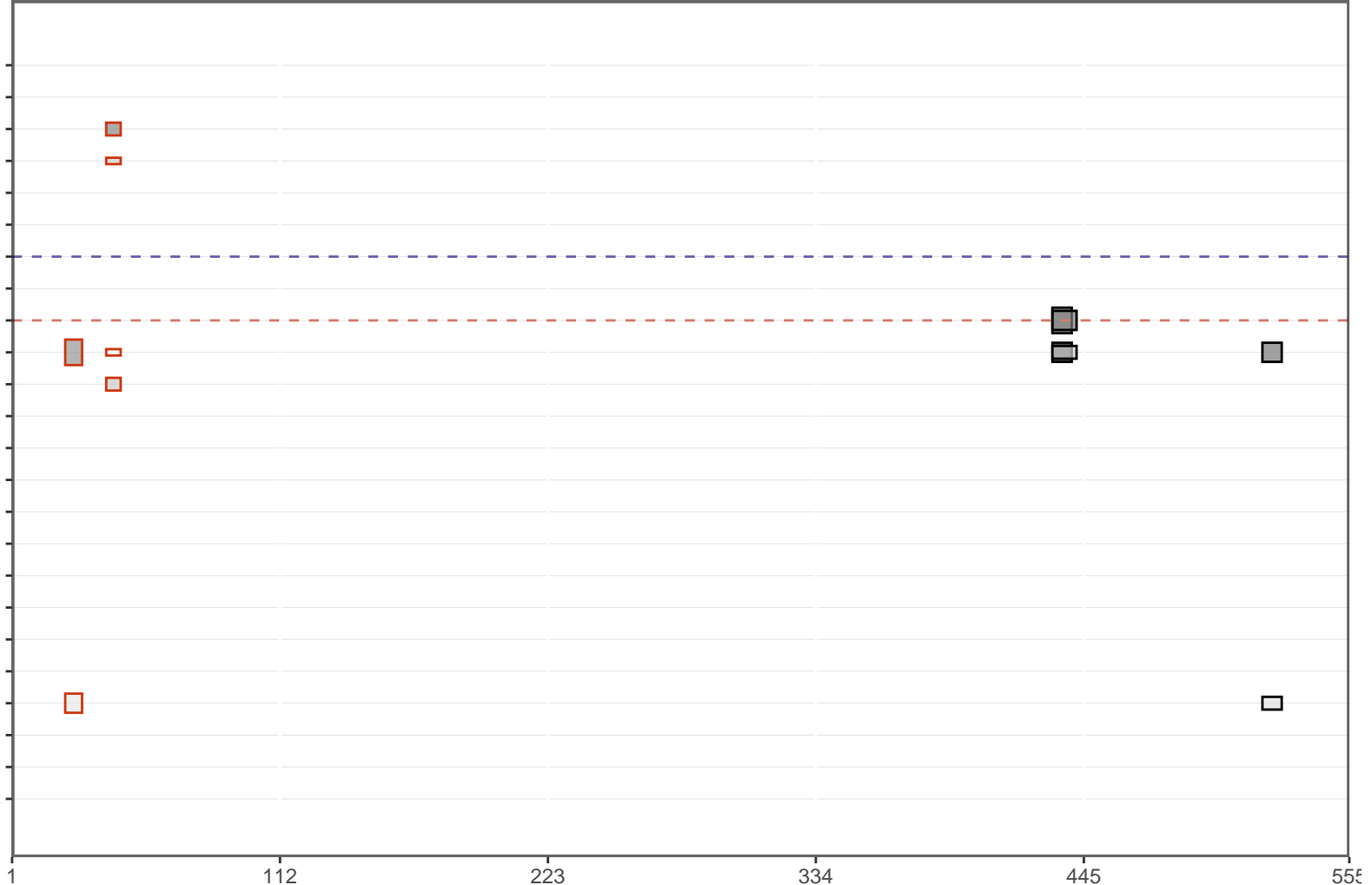
MW indication



Molecular weight

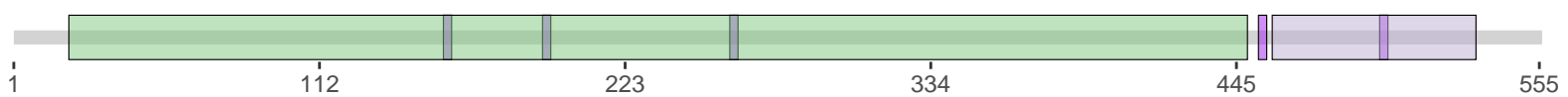


Gel Slice



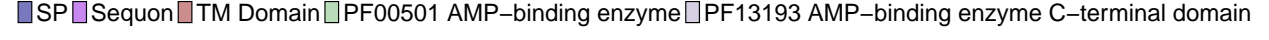
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AGIFTSIAGHGVSHMGGAPTVLNMINAPRVRRLPRKVAWMTGGAPPPQVLFKMEELGFDVHSHYGLTETVGPDTVCTVKPEWSTLSPDGEANIKRGGHHSMEEVVDKPTMKSPDPDAKTMGEVDFRGNVTMNGYLNKUKATEDAFKRGWFRSGDLAVKHPDGVYELKDRAKDHSGGENSTIELEGVFGRHWLEAAVGRPDQWVGETPCAFVKLKDGDMTADENYGRDLRPRYMAPKTVIFDDLPKTSTGKTQKFLRQKAKAMCSISKSL*

NbL13g04380.1 catalase_isozyme_3-like [MW = 56.84 kDa]

No. of times detected



log(intensity)



Values from



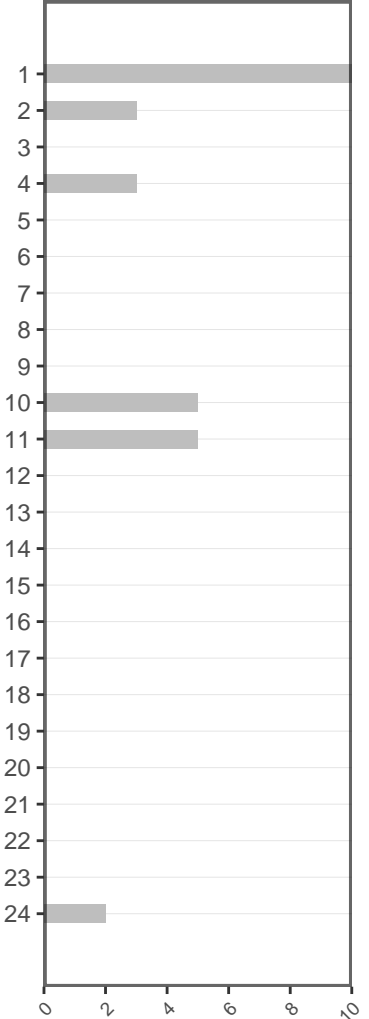
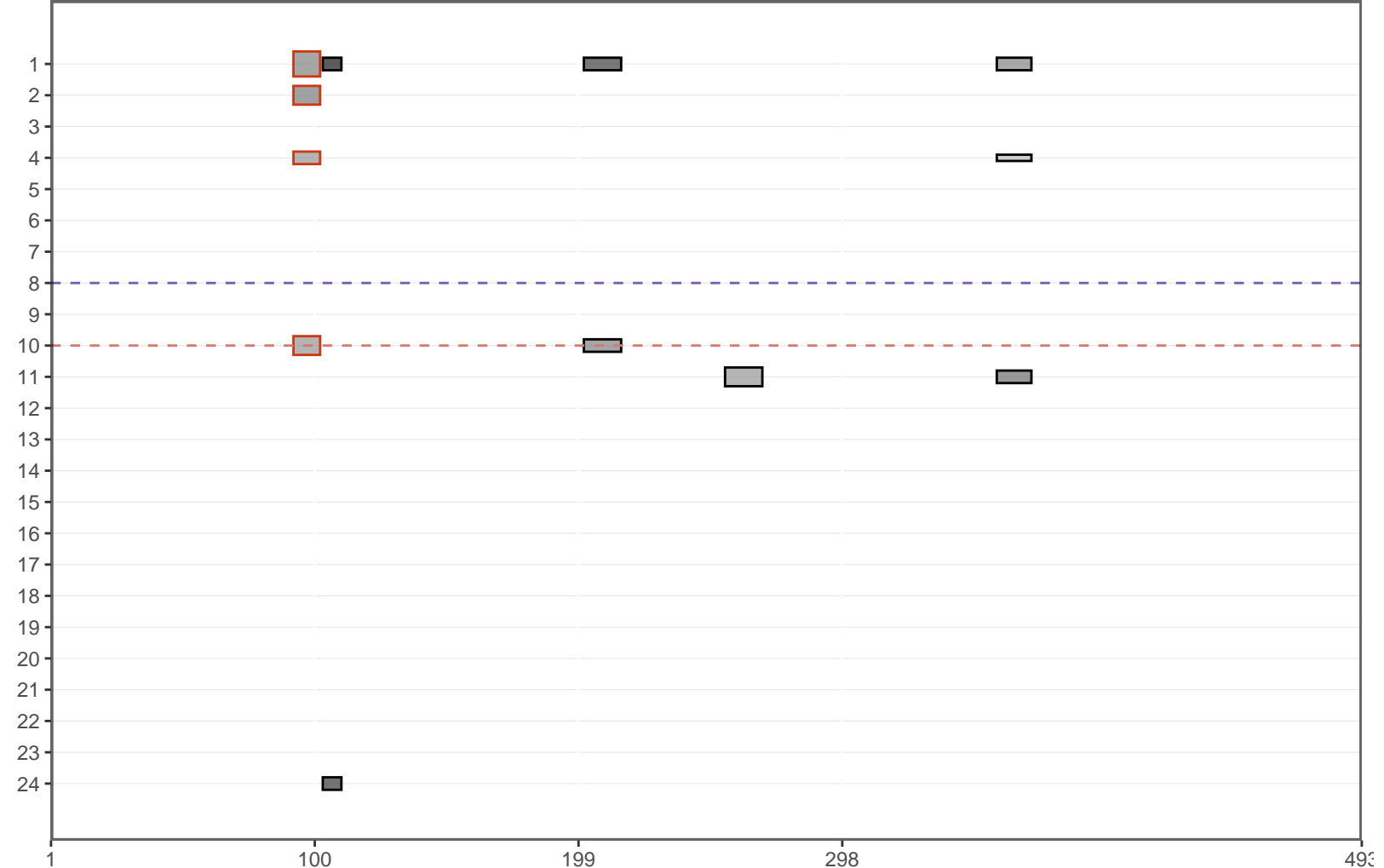
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

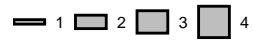


Protein sequence:

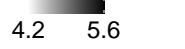
EVXCLLEEVAKVGGANHSATKQLYDMAAGNYPEWKLFIQTIDPDHEDRFDFPLVTKTWFEDLPLGPIVGRLLVKNKNDNFAENEGLAFGPAIVPGIHYEDDKLGRIFSYSDTQRHRLGPNYLQLPVAAPKGAHNNHHEGVNFMHRDEEVNYPGDFPCRHAEGYPIPRIVTGKRDRCHEKENFKQDGERVRSWSPDRGERFICRWISALSOPRVTHERTIWIISWEGADKSLGKIAERLNVKPTM

NbL13g04140.1 probable_steroid-binding_protein_3 [MW = 10.89 kDa]

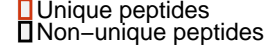
No. of times detected



log(intensity)



Values from



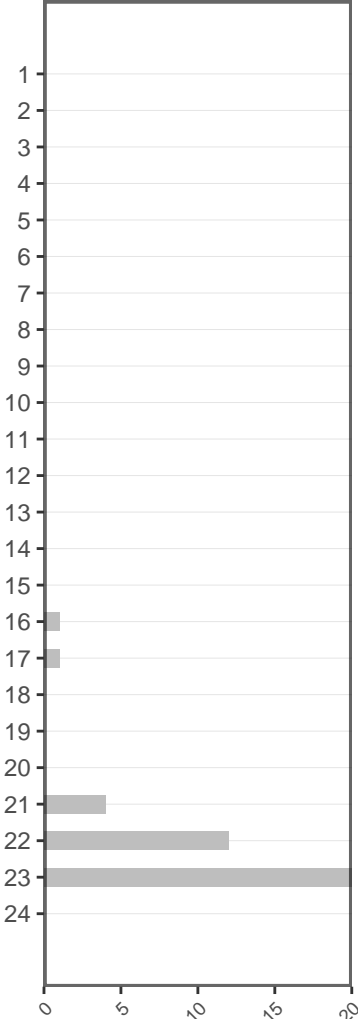
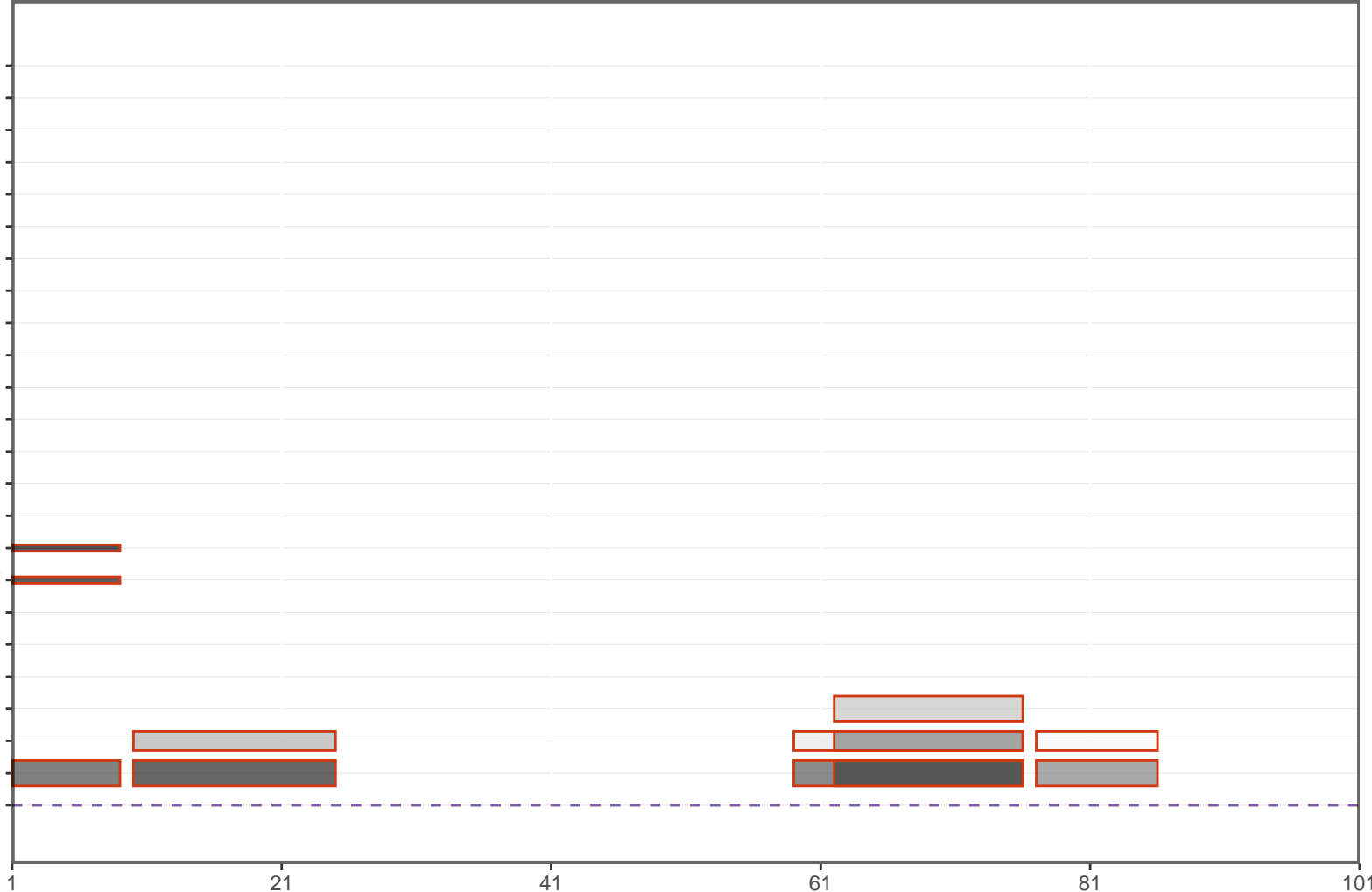
MW indication



Molecular weight



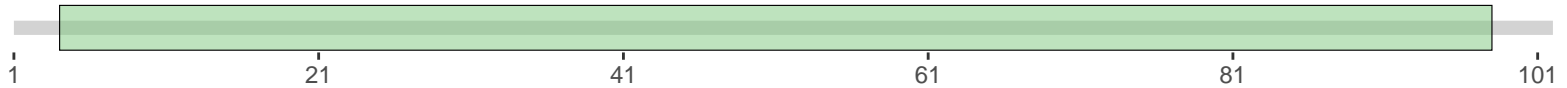
Gel Slice



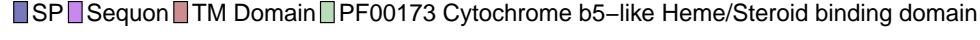
Protein length



Pfam domains



Pfam Description



Protein sequence:

SFGGAYCMFACKDASRALAMSKNNEEDVTPSLDGLSEKEMGVLNDWEKFKQAKYPIVGVTSIS

NbL13g04130.1 cysteine--tRNA_ligase_cytoplasmic [MW = 65.04 kDa]

No. of times detected



log(intensity)



Values from



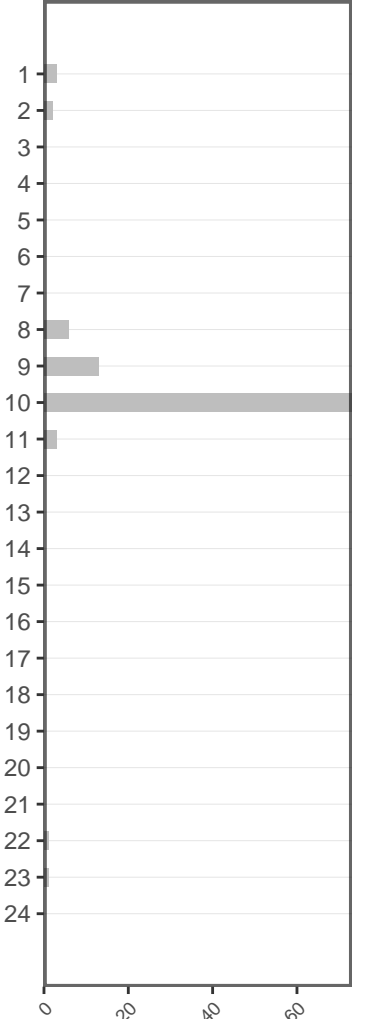
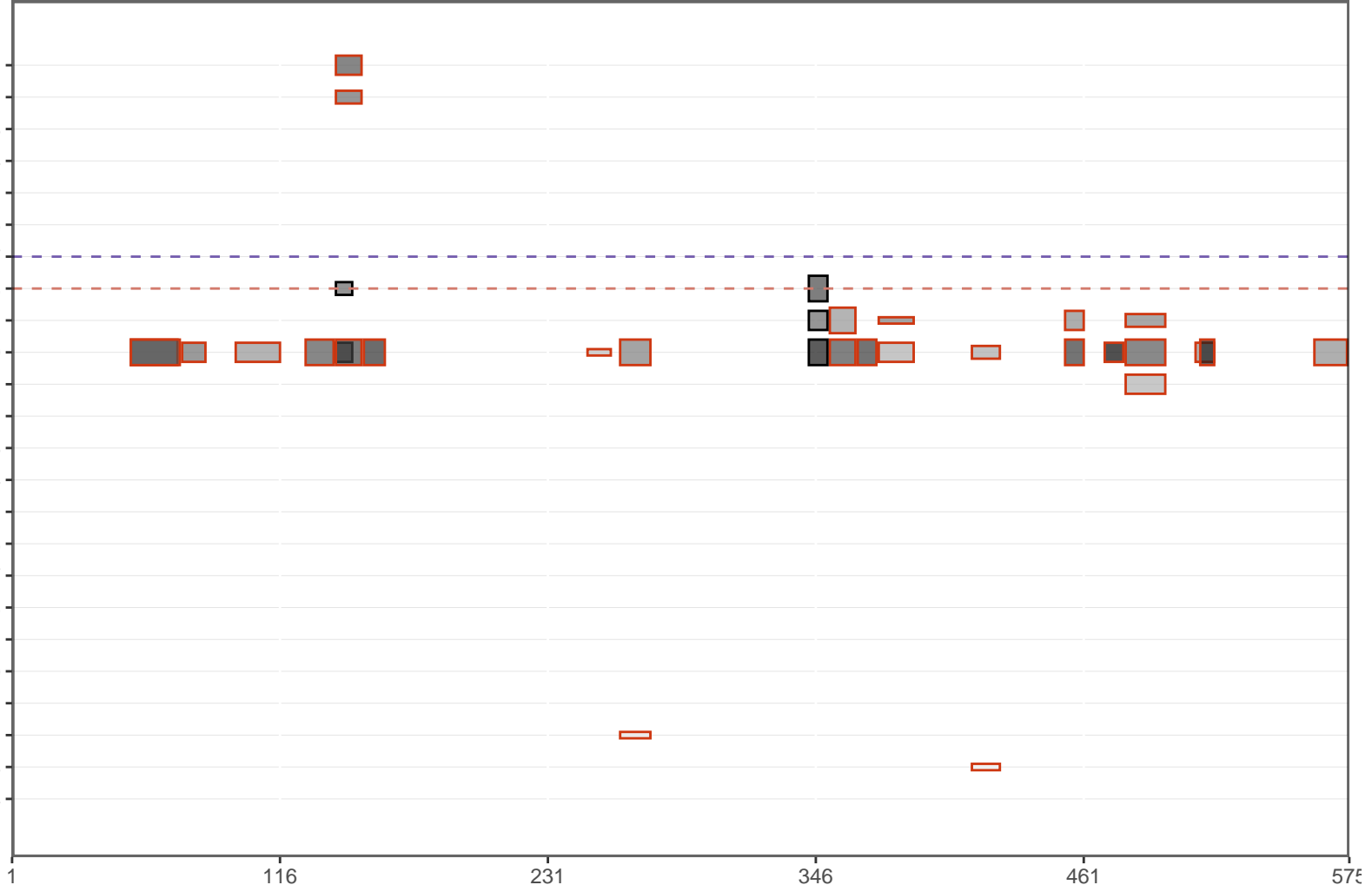
MW indication



Molecular weight

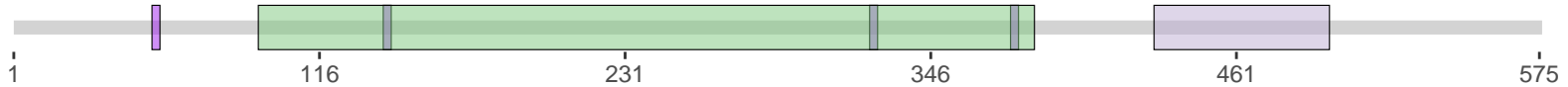


Gel Slice



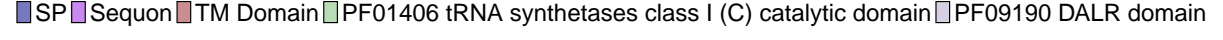
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGPGRPGVWHECSAMSAARLVGYSFDIHGGMDLVFPHHEHNEIAGSGAACKKSNITYWHNGFVNDSEKMSLGNFFTRIGVDLVHPLALRLFLGTHYRSPINVTIAGIESASDRLLFYHQALYDGGVILSGHDEASRKKDSIPAGTACGINKFQDEFIVMSDDLHTPVALAAMSDPLKLNLDLHTRKGGKQGLRIEGLAALKERTITTSGLLEILGLVPTSEYKALHELREKALKRAKLTEDQVRRKITERDPTARGNKEYERSDAIRKELAAVGIAMDSPEGTTWRPKPLALQEECV

NbL13g04050.1 signal_recognition_particle_subunit_SRP68-like [MW = 68.37 kDa]

No. of times detected



log(intensity)



Values from



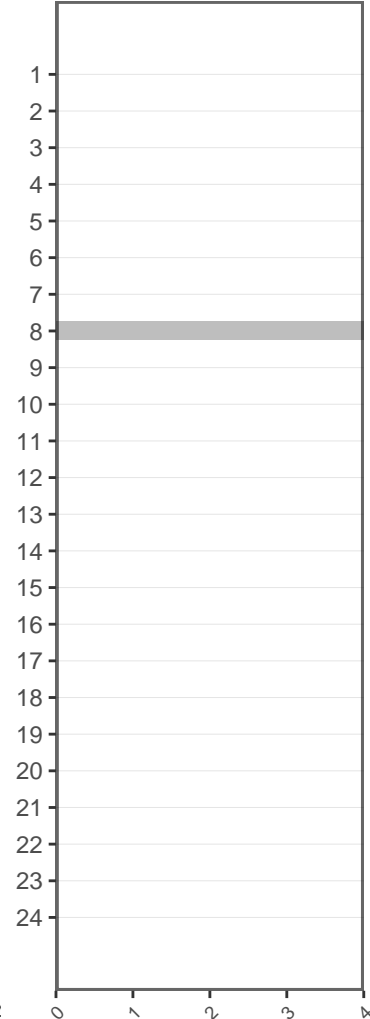
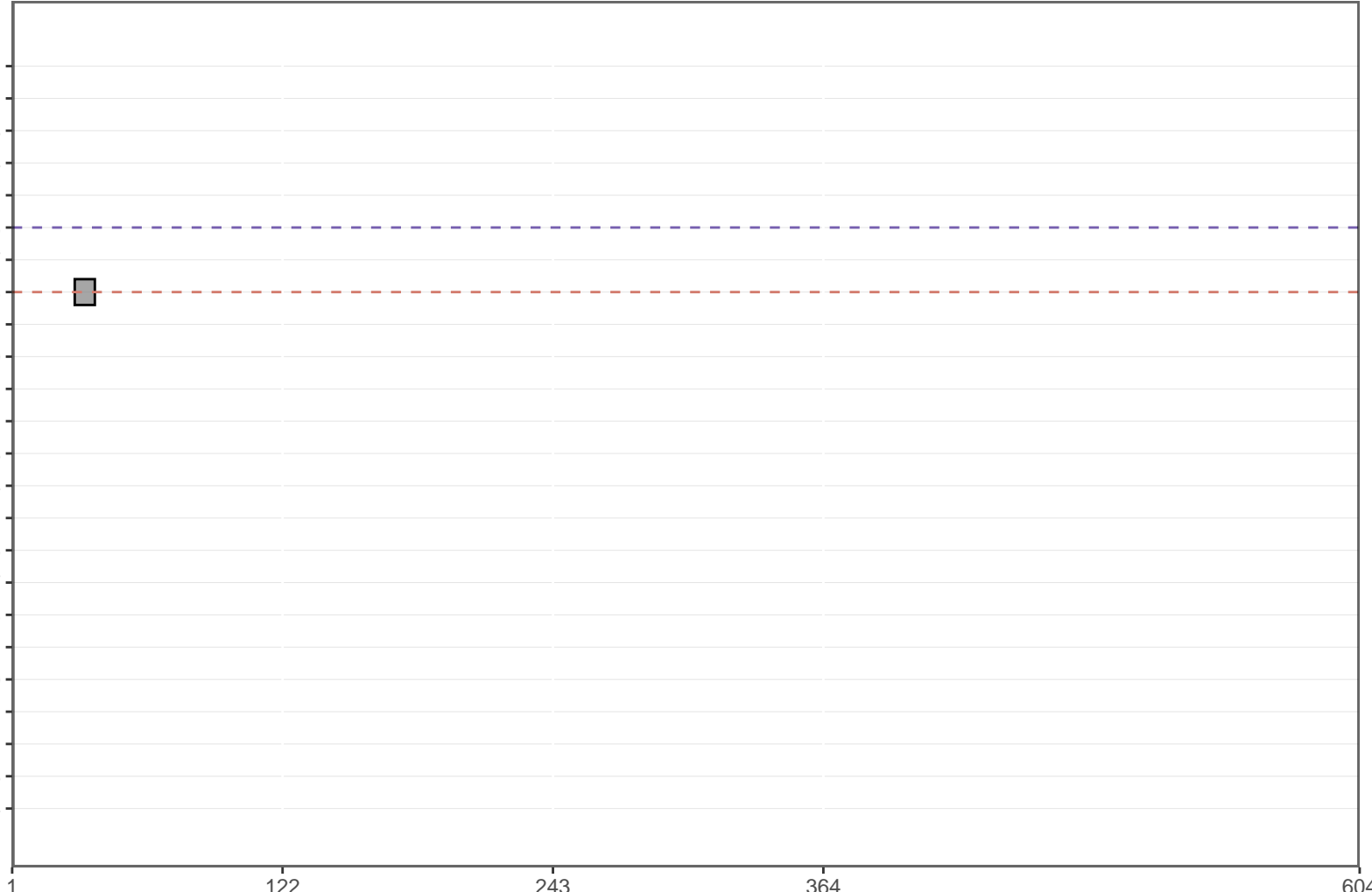
MW indication



Molecular weight

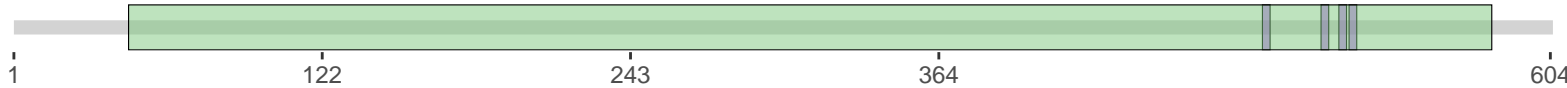


Gel Slice



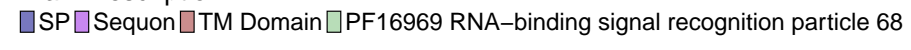
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILKAQELKDIHGSAADBLLAEKLLVYDKFAHYHEARSGIRNDLVTAANSENKDELGSLDKAGAILGGRTIERNQLLVIAAKKLNKVRDDKNEKVTYKPEELVRLYDILLQNTADLFDLVSSGRDRKMEVEVLAEEGELRSMVFRARFCFYLAQVYSSAGKRTYALVYQGARLADAKLRKLRHNDADQVMKELKLTLYNEBRSNGIEHAKGIMEEEKAPENLSKKISNLSNGSDKKVREKLLMEKMDTYESAVGEANVAVPRIETFPFAFGVPRNPVYLDLAYNLVFPF

NbL13g04040.1 protein_MEMO1-like [MW = 33.17 kDa]

No. of times detected



log(intensity)



Values from



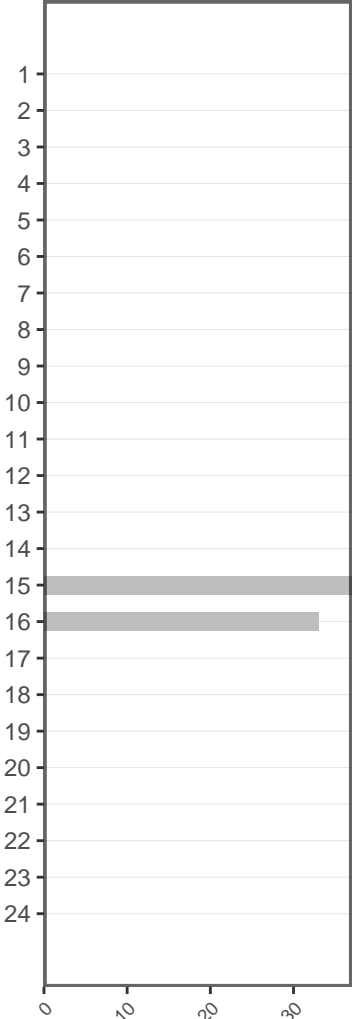
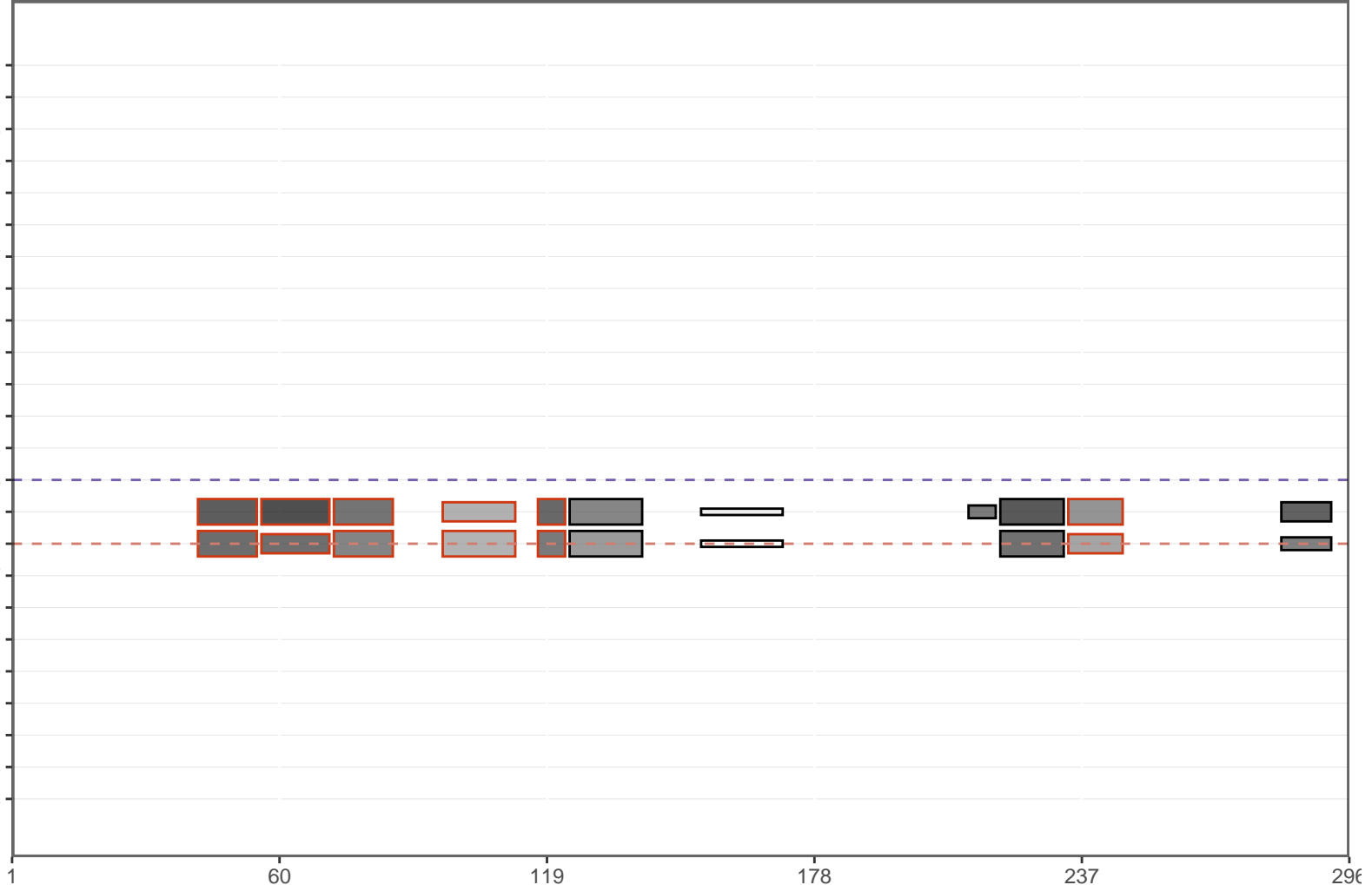
MW indication



Molecular weight

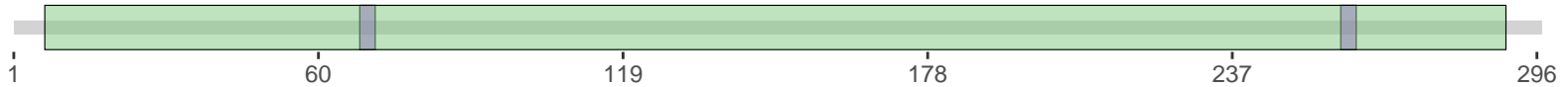


Gel Slice



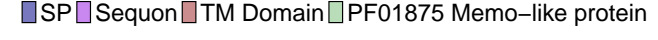
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

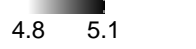
IIKPYLAKYFDGYIDRYIPKIVPLVGLSASEALYGRLLAKYADDPKKNFFSIVSDFCHWGRFNMHYDKHGAVYKSIKALDKMGMDIETGDPDFKGYLSETDNTICGRHFISVFLHMLKNSIKKIRFLRYEQSSGCKMRDSSVYASAVGHDAI

NbL13g03980.1 40S_ribosomal_protein_S11-like [MW = 17.69 kDa]

No. of times detected



log(intensity)



Values from



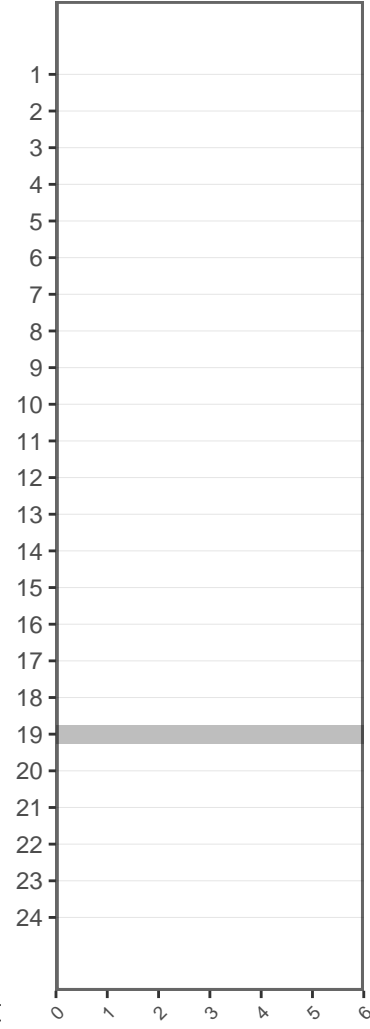
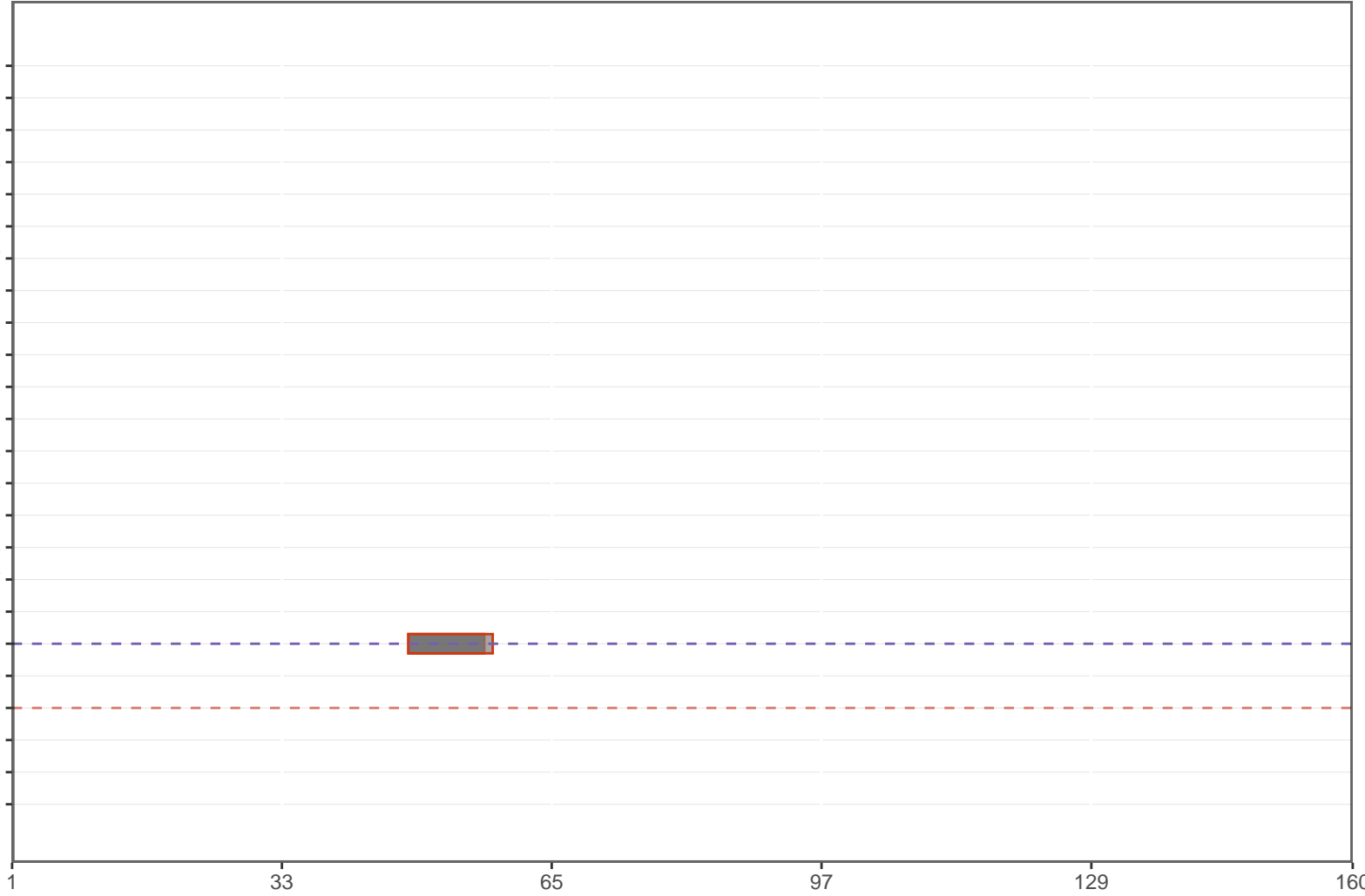
MW indication



Molecular weight

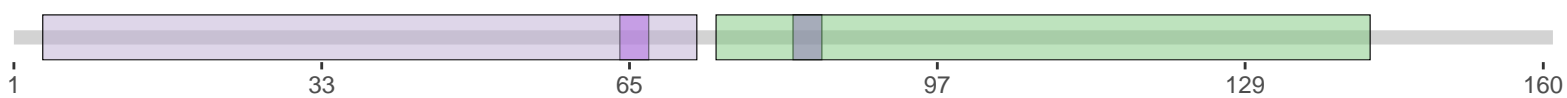


Gel Slice



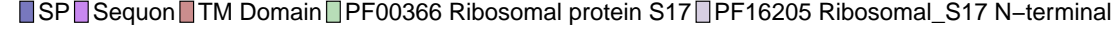
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

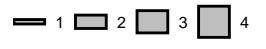


Protein sequence:

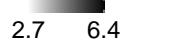
SIRGRILAGTCHSAMNRTIVRRNLLHYVKKYQRYEKRHNSIPAHIPGCFRVKEGDHVIGGCRPLSKTVRFNLKLVIPMGSAAGGKKAFTEM

NbL13g03840.1 aspartate_aminotransferase_chloroplastic-like [MW = 50.77 kDa]

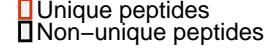
No. of times detected



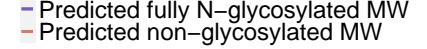
log(intensity)



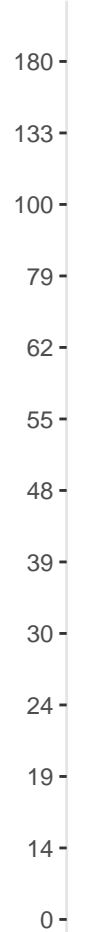
Values from



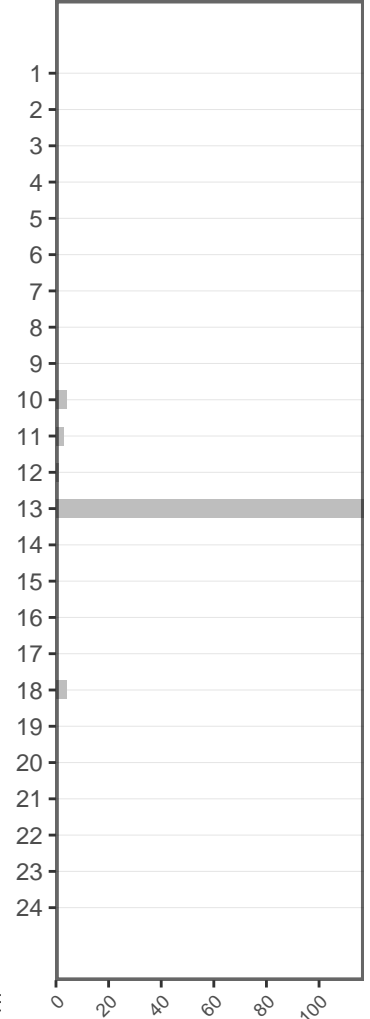
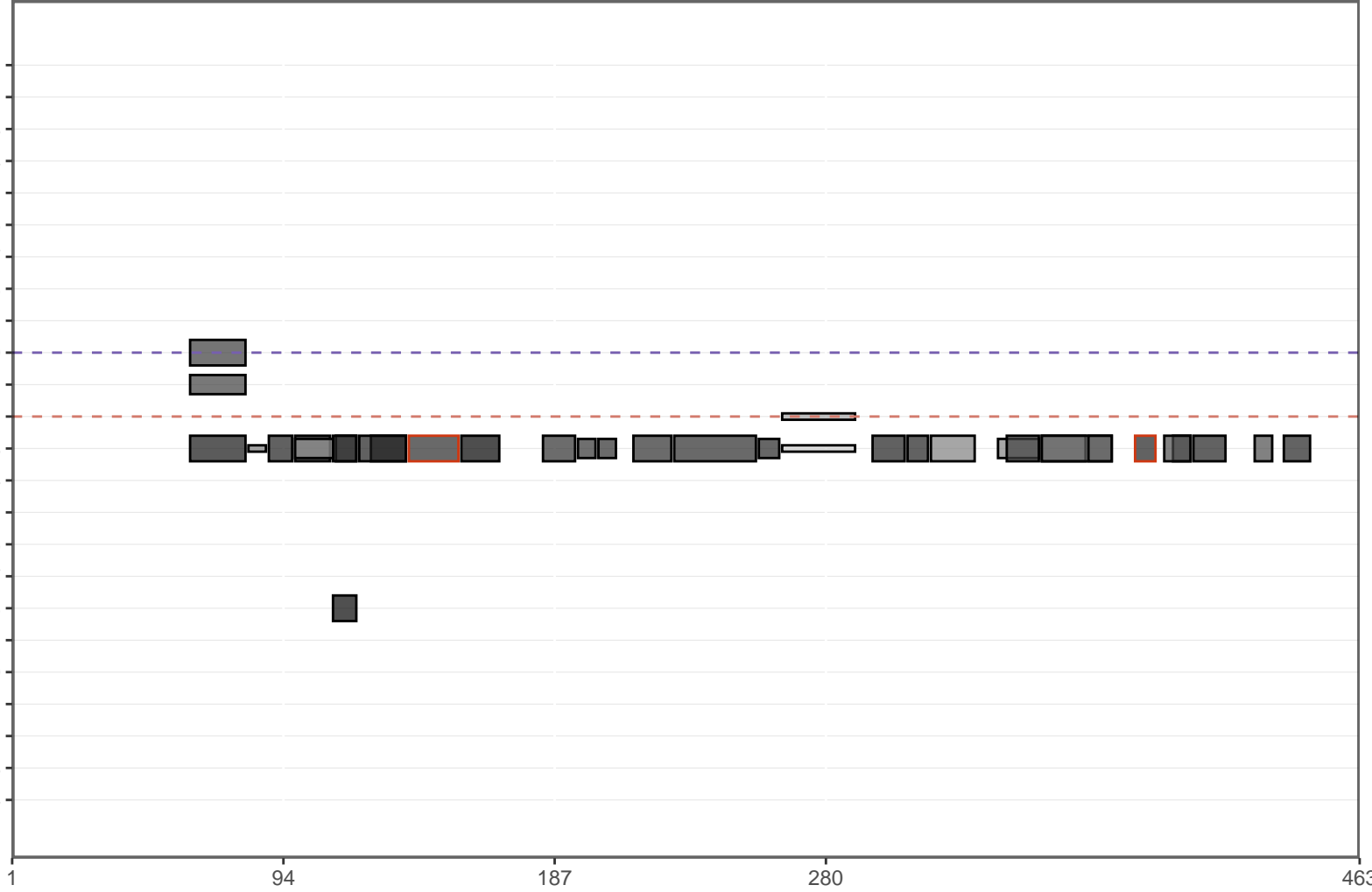
MW indication



Molecular weight

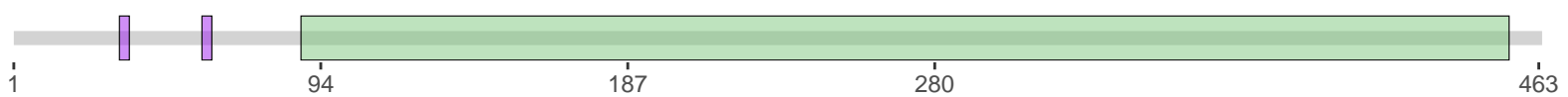


Gel Slice



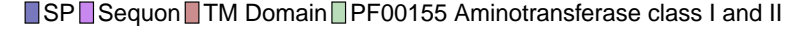
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DFAGMIEDKAAPEGGFILLHGCAHPTGDPTTEGWEKIADVQENHPFFDVAVYGGFAGSLDEDASSVRLFAARGMELLVAGDYSKNLGLYGERIGAINVLOSSADATRVKSGLKRRLARPMYNSPPHIGARIVANVYGIPEFFDEWVQEMEMMAGRIKRVROKLYDLSGSKDKSGDKDWSYIKDQIGMFSFTGLNKAGSENMANKWHVYMTKDRISLGLSAAKGEVLAADIQSYNNV

NbL13g03780.1 glucan_endo-13-beta-glucosidase_4 [MW - SP = 52.53 kDa]

No. of times detected



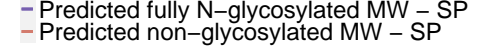
log(intensity)



Values from



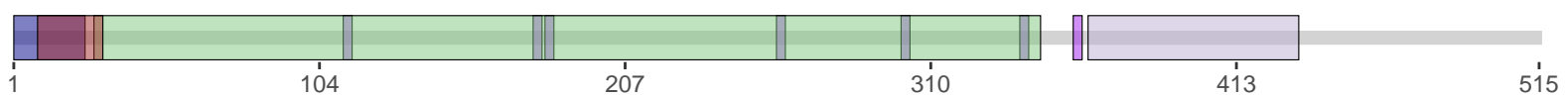
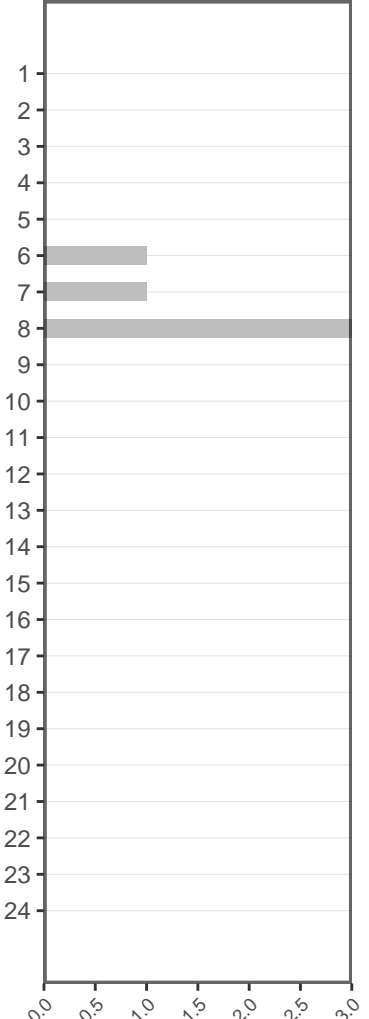
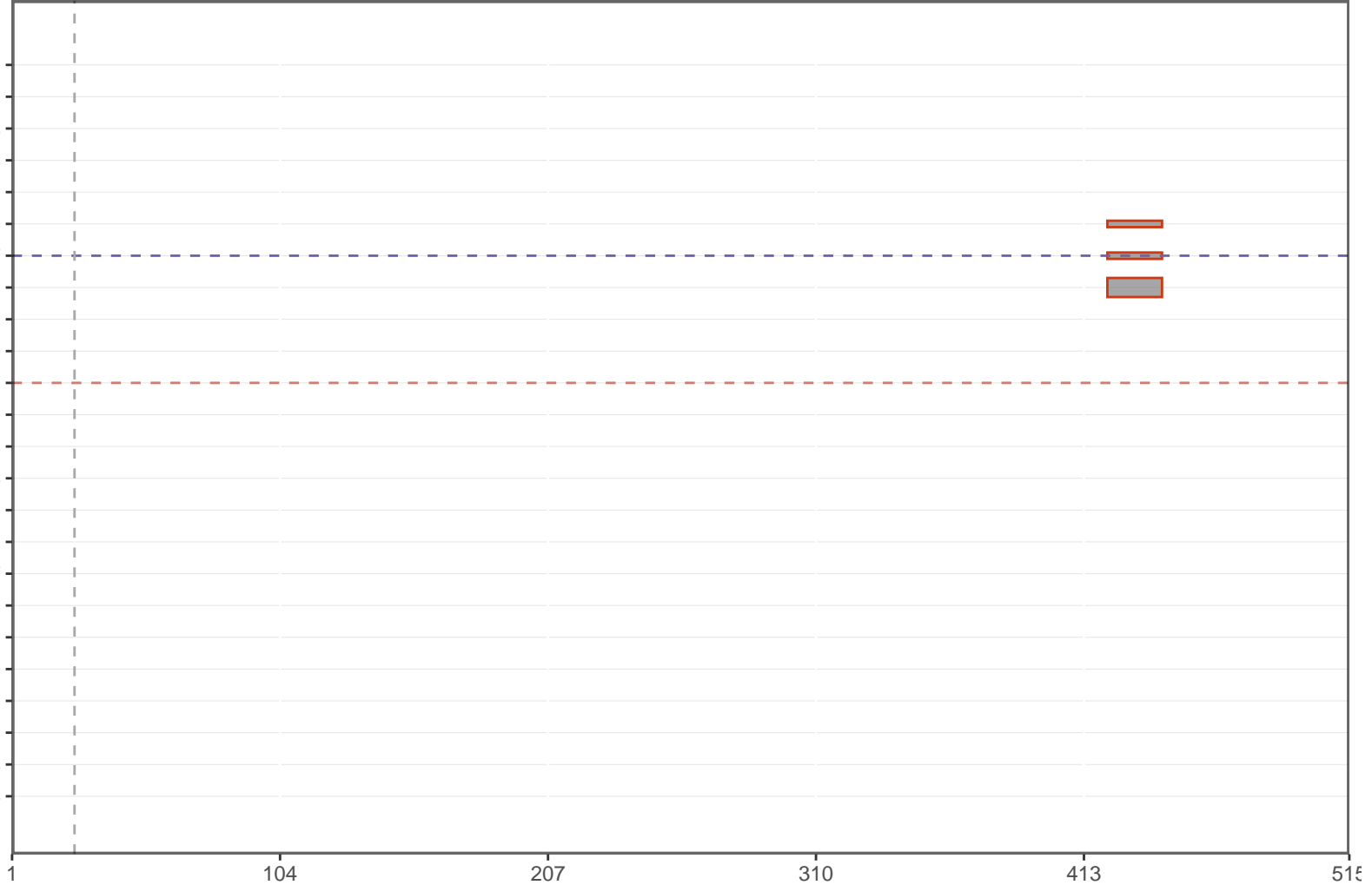
MW indication



Molecular weight

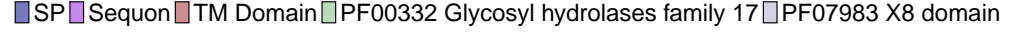


Gel Slice



Pfam domains

Pfam Description



Protein sequence:

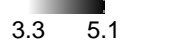
AAVNSIAAFNFSDIPVVTETGWPWDDGANEDPATKENAETFRNNLRHVSNDTGPFPSPKPNPNTFRVYEMFNEDKRPGPSERBWFSTNGSDVYSLGLGSSAGISDNSTAVFGIAKPGADGNLGDGINWAGDGGHANGIAIGSGGPPYFDLQNHASVAVNDVYQRMRLGGTDFDGTATTTTQDPSLKTCKFTGSGTSGGLFPPAAFGPSPTSGGSTRRAVIVYTLAVFSALLMLDENVVGGQGLPBLPPGGWGG

NbL13g03570.1 uridine_5'-monophosphate_synthase [MW = 51.62 kDa]

No. of times detected



log(intensity)



Values from



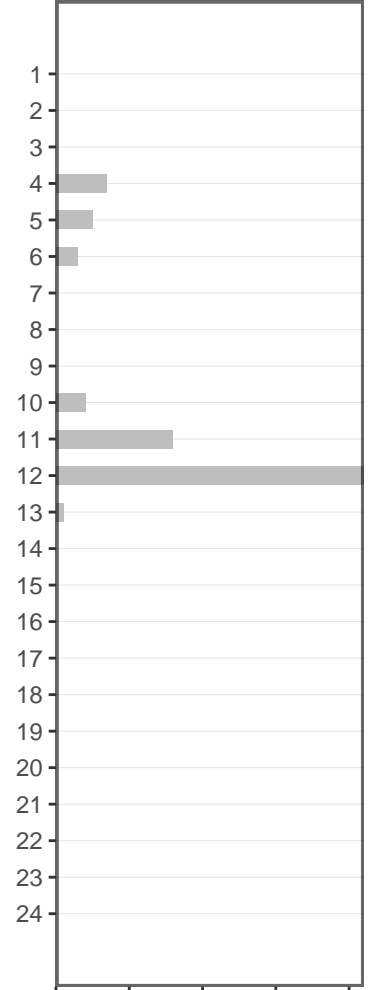
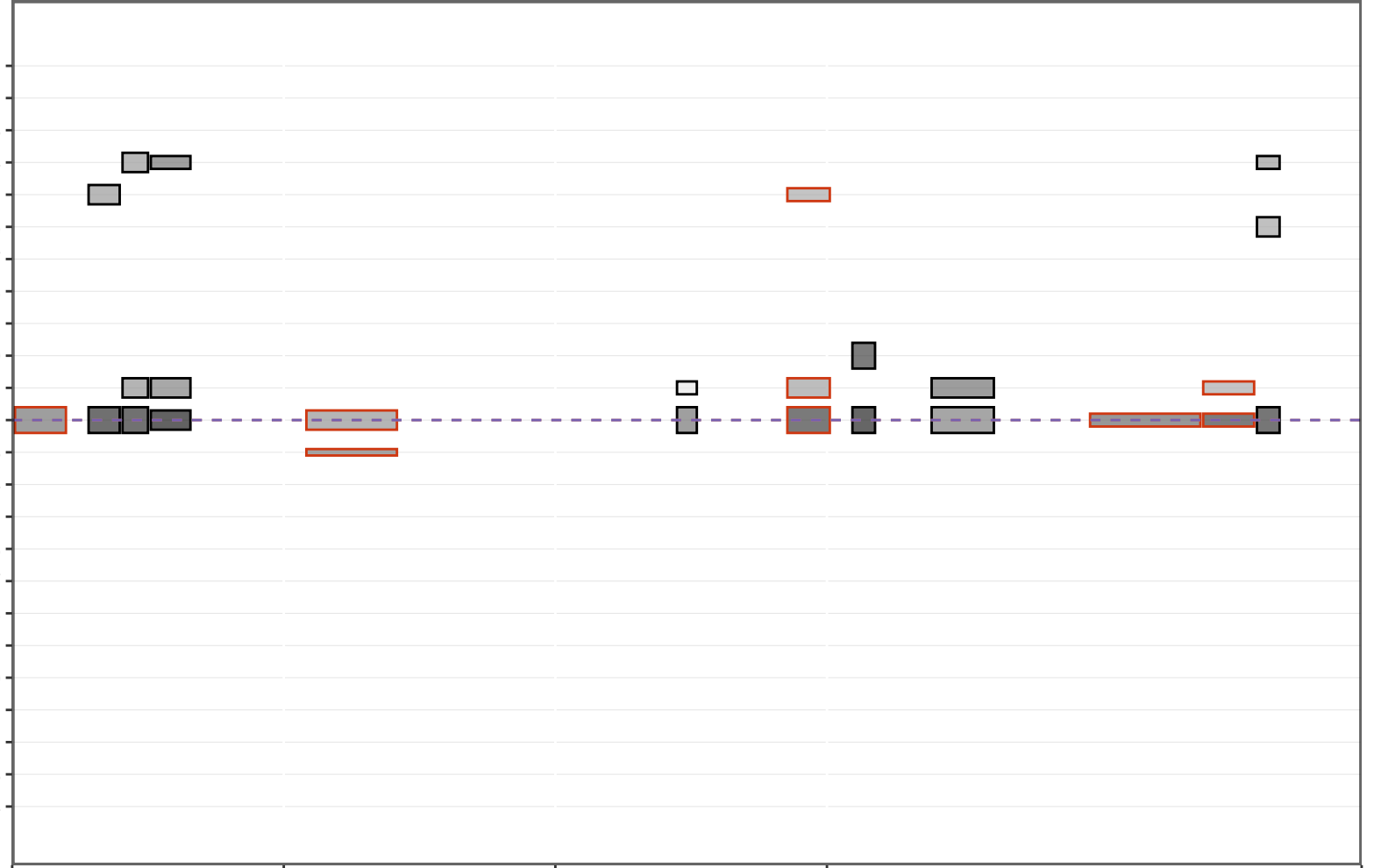
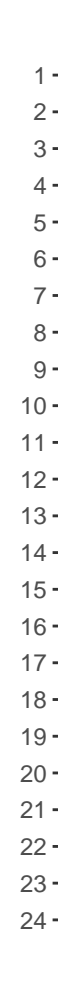
MW indication



Molecular weight

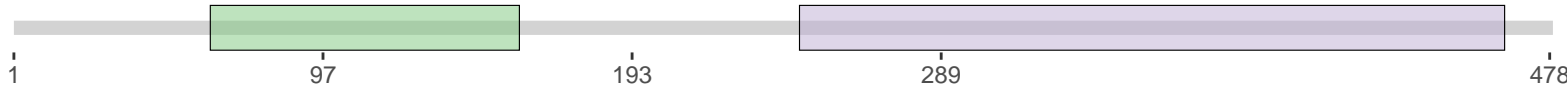


Gel Slice



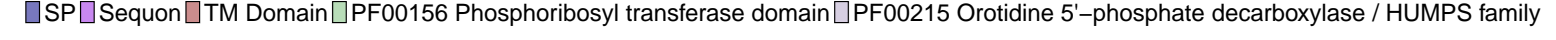
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KIAKNPTGKLFEMVQKETHLGLSADVAIAAELELDADKVSPEICMLKTHVDLPDFTDFGSKLRSIADKHNFLFEDRKFADKNTVTMGVEGGIFRILDWADITNAHIIISGPGVIGLKLKGLSRGRGLLLLAEMSSGNALATGAYTAAAKIAEDHSDFVIGFISVNFQVWPNQNGPNSLIHATPGVQLKGGDLAGGGVYTPSAVIADRGSDIIVRGRIKAAKAPAEAREYRLGGWDVAVLNCK

NbL13g03490.1 methionine--tRNA_ligase_cytoplasmic-like [MW = 91.19 kDa]

No. of times detected



log(intensity)



Values from

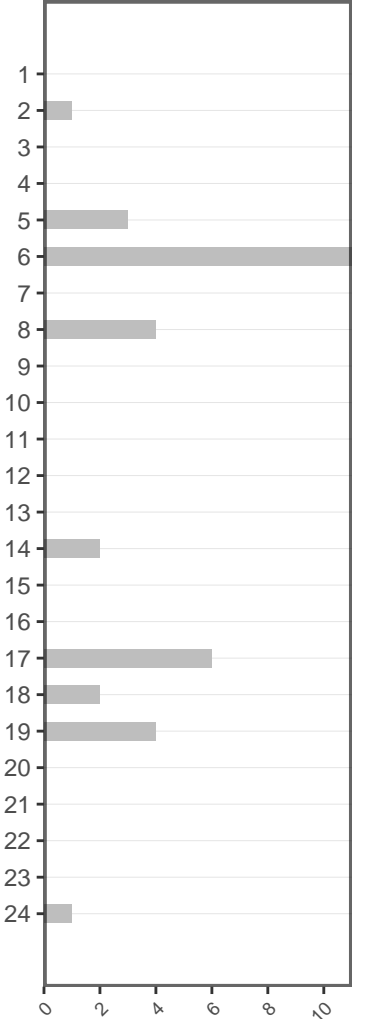
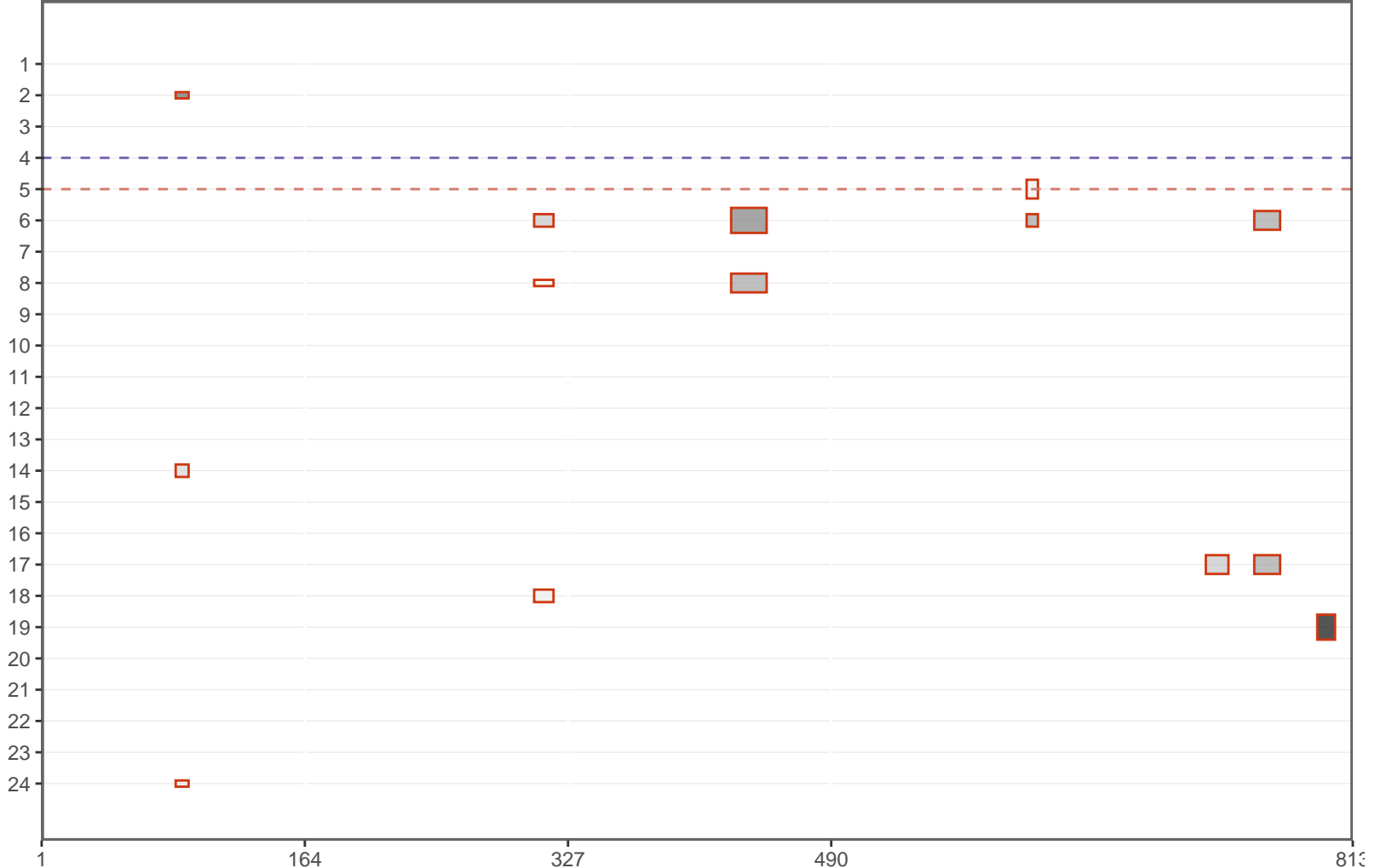


MW indication



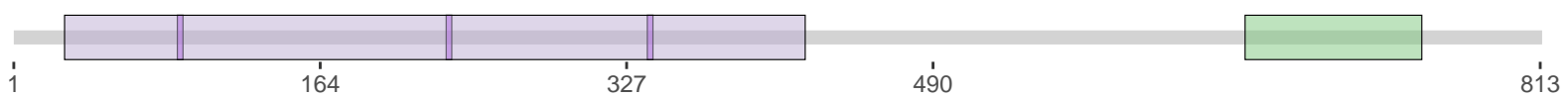
Molecular weight

Gel Slice



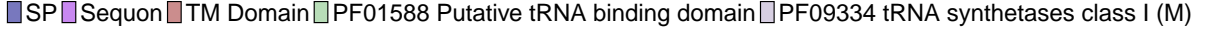
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

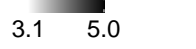
RPEVSDTLFSDVADLQAKLNSELLNLSNGFNIRVLSFIAKDPVGGYDSHPNPEGASHPLTKALGEKVGNYVEQVIEAMEKVKLQKGLKIAMBSISGEGNGVYGEISGFVKLYKEDKPFSGCIVMSTAGLVYLLAGLLEFPMPFSREIVLKGILNFPPEQVSLADERGDIKSKRPWHLPAGHKGGIPALFLKELKDEVEVFYREKFAAGSADRNLKAEAEAKKTDGLNKAKISDANKKKEKATKPSVAKSKGSABVEAEISGALDRVGLITRAKQHPDADSLYEEIDVGEAQR!

NbL13g03440.1 subtilisin-like_protease_SBT2.5 [MW - SP = 85.1 kDa]

No. of times detected



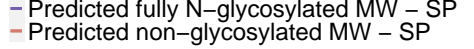
log(intensity)



Values from



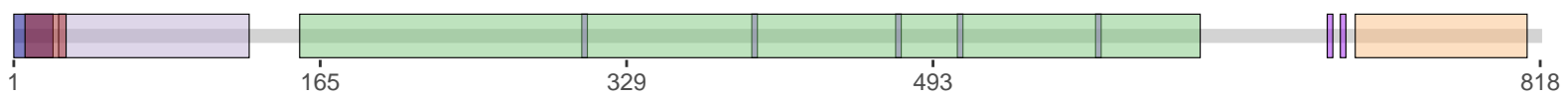
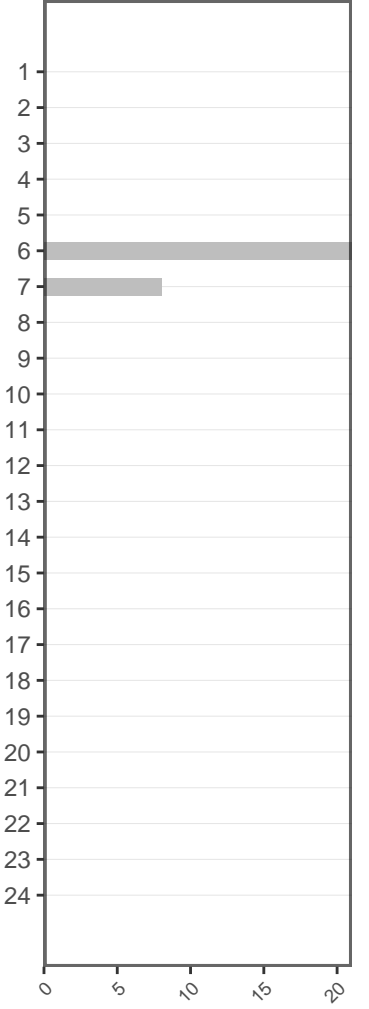
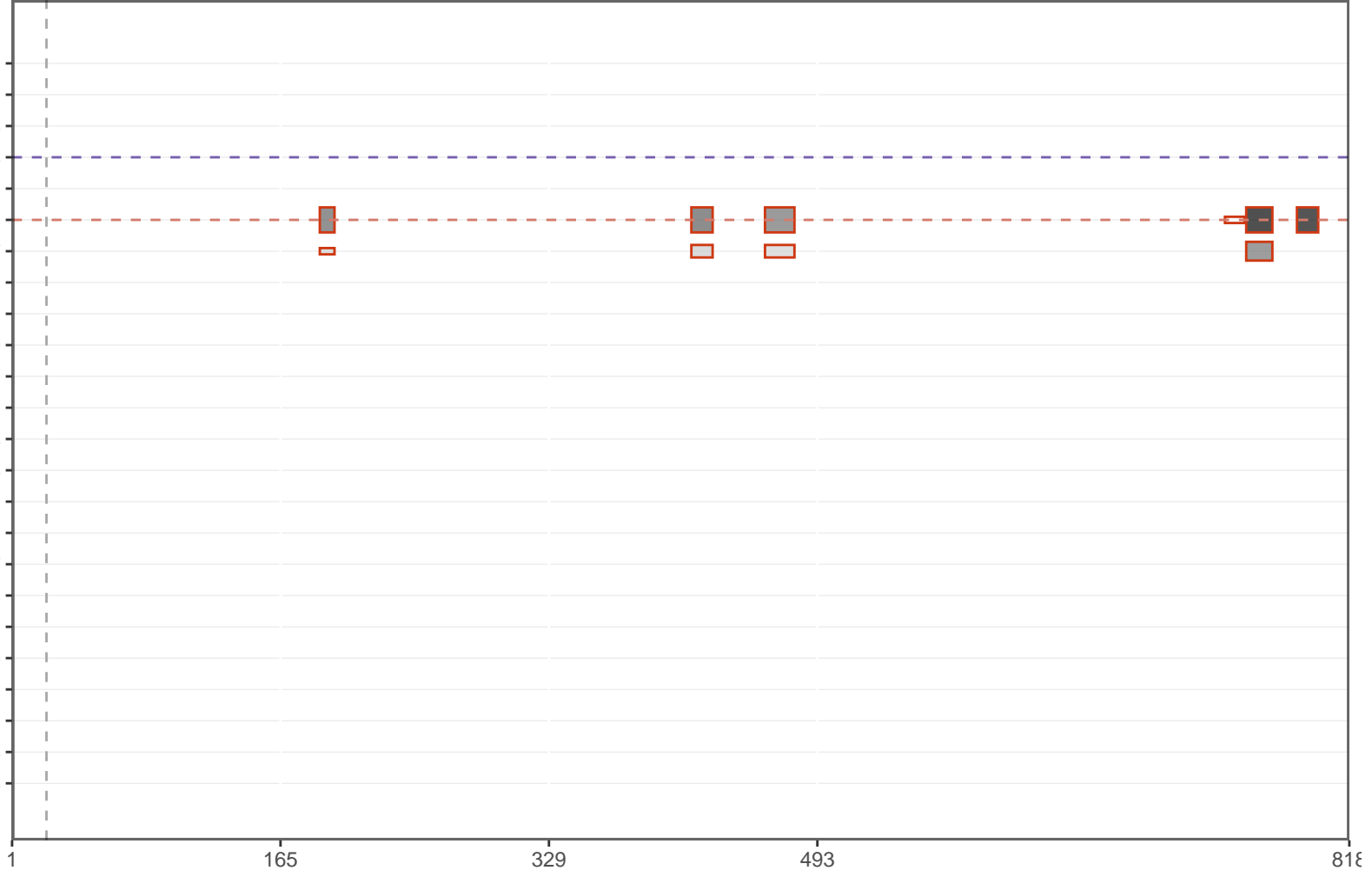
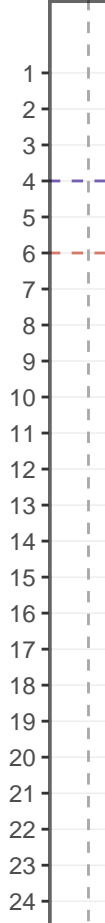
MW indication



Molecular weight



Gel Slice



Pfam Description



Protein sequence:

*NQTTMVAANDVLEDSVTRKYSFADGQKPEVLNKNLVEGNLLGGYSFNFVGTASKKVWETAKVLAAGGFVLAENASPGTKFDPVPSIPGILFDASGSMELVDYVNTTSRDVWTRVWSEKSTGSGINGLRPLHKAPQVWFVARGPNKIDVYFQDADLLKPDILAPGLIWAIAVWVNGTDEANFCGEGFALISGTSMAAPHAGIAALIKGHIPIHWSPAAIKSALMTTSSITDRAGRPLGADGYSGSETMTLVFATPFDFVSGGHVNPRAALDPLIFNAGYDYDLGLC

NbL13g03390.1 inosine-5'-monophosphate_dehydrogenase_2-like [MW = 53.4 kDa]

No. of times detected



log(intensity)



Values from

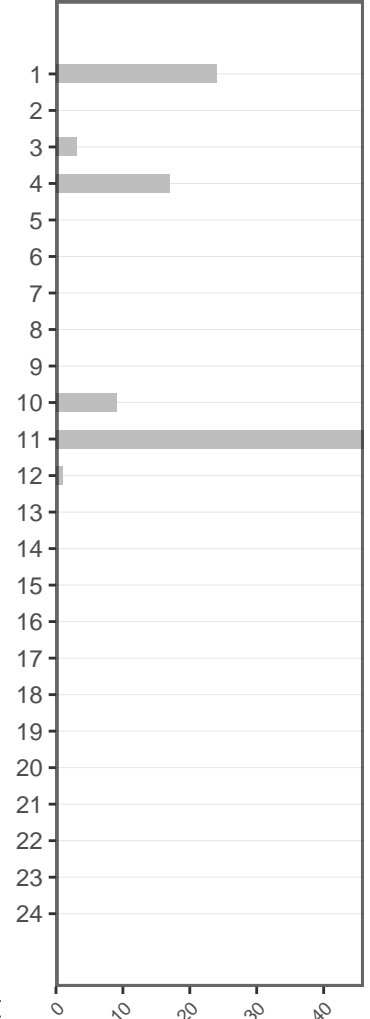
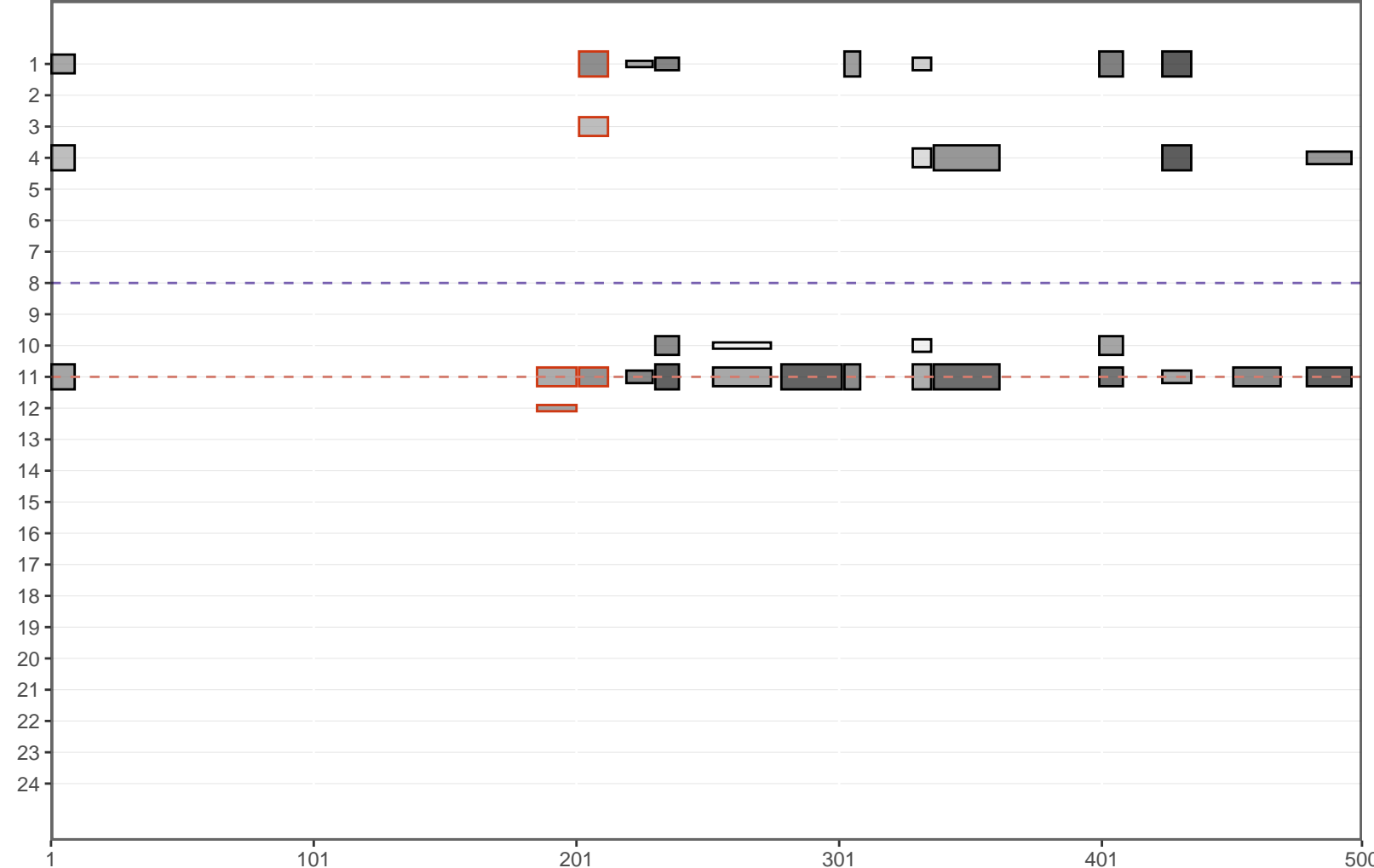
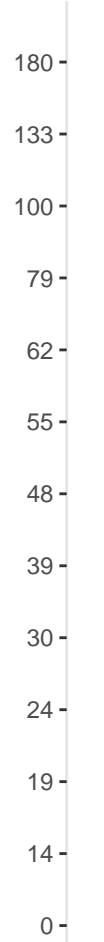


MW indication



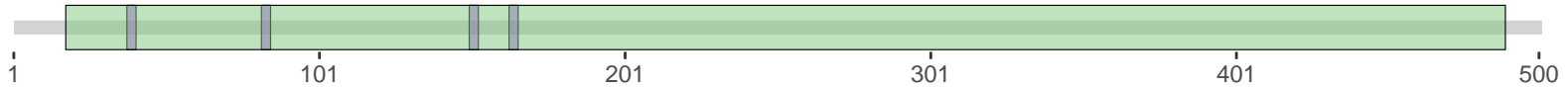
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TRSDKERLEHLVNEGIMAVHDSGGNSLYGNMKHVMHTYPHLEIVGSMVVTNYGAENLKKGVVDGLRVGSMGSSGCTTQEVCAVGRGATATVYKVSIAEGHGIPVADGGHNSGHVYKALSLGASTVMMSSFLAGSNEAPGTVEYKNGLRVKKYKRGMSLEMTKGSQDARYLGDATLKIAGQVTVGVSDKGGSLKFPYFMQAVKGGQFDLGSLSLQSAHLLKSGKLRLEVRTGAQVEGGVHGLVGYEKRYF

NbL13g03170.1 nucleotide_pyrophosphatase/phosphodiesterase-like [MW = 74.73 kDa]

No. of times detected



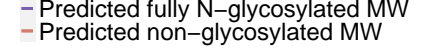
log(intensity)



Values from



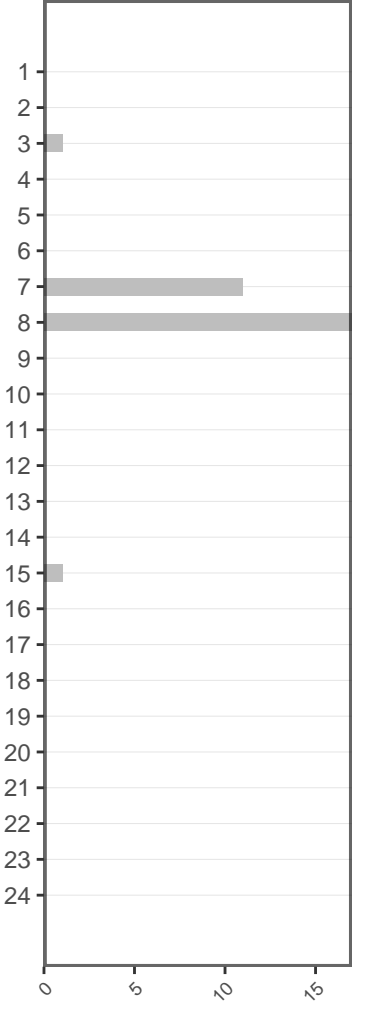
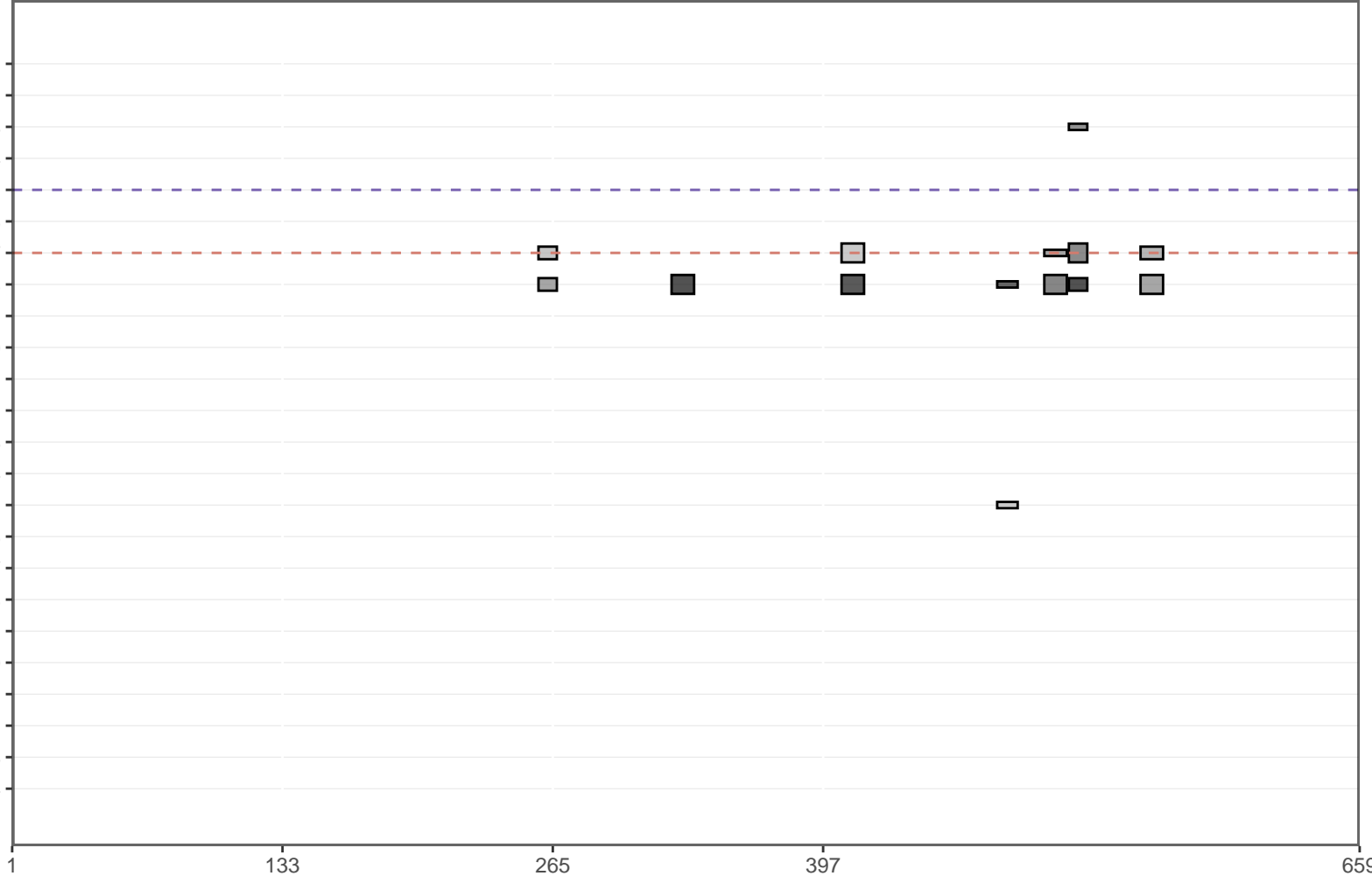
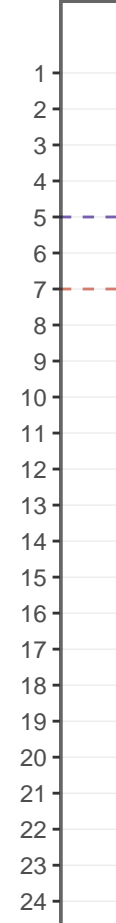
MW indication



Molecular weight

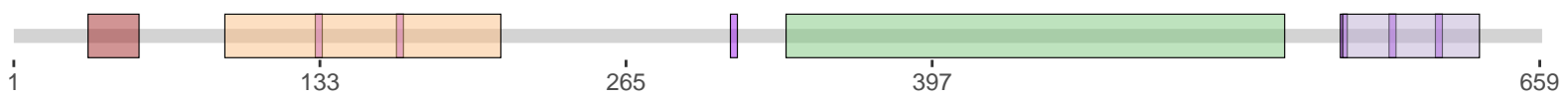


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00149 Calcineurin-like phosphoesterase
- PF17808 Fn3-like domain from Purple Acid Phosphatase
- PF14008 Iron/zinc purple acid phosphatase-like protein C

Protein sequence:

/SFKSPFPFGQESLQRVVFQDMGKGERDGSNEVANYQPSLMTTDTLKLKLDNDIVFLKGLPLVANGYHSQWDGFTAQVPEPTKVPFMAISGNHERTWENSGSLYGLDSSGEGGVPEITLYYPAENRAKFWAADYGMFHFQIGDTEHDWREGSEQYKFIIECFASANRHKGPWLFSARHVLGYSSNDWYAKEGSFEFPMGREHLGKLVQKYYKVDMAFFGHVHNYERVCFYQNGGVNKETSHYSGVANGTHVAVGGGGHLDGFTPNTTWSYFKDYDYG

NbL13g03150.1 poly(rC)-binding_protein_3-like [MW = 50.02 kDa]

No. of times detected



log(intensity)



Values from



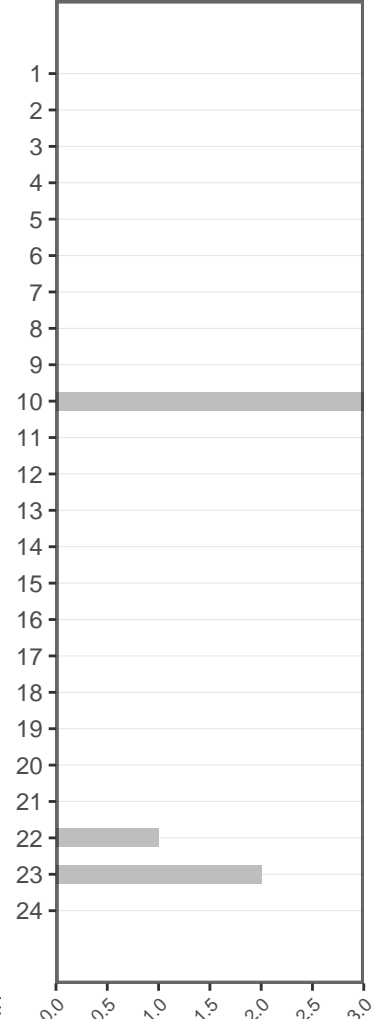
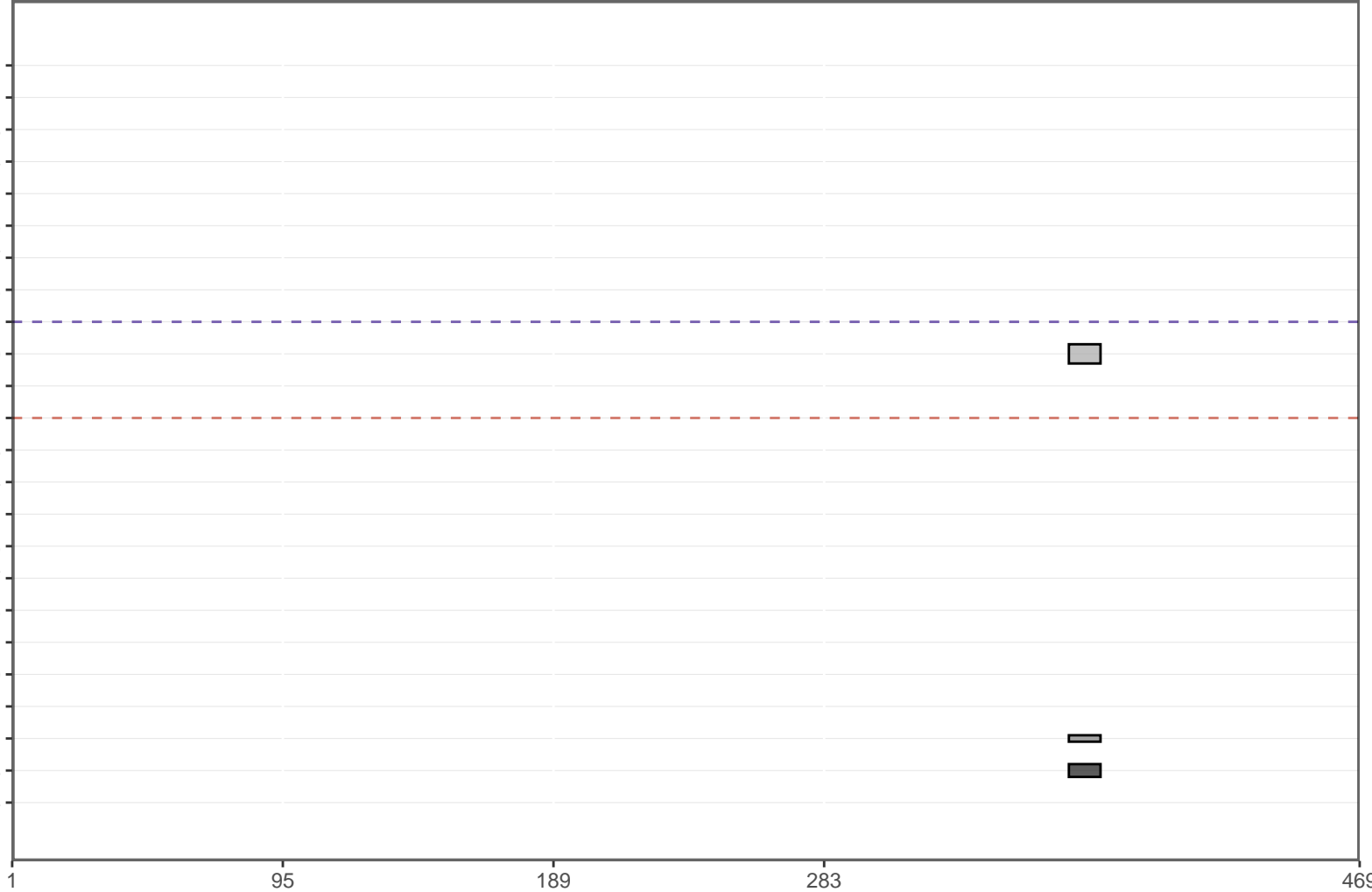
MW indication



Molecular weight



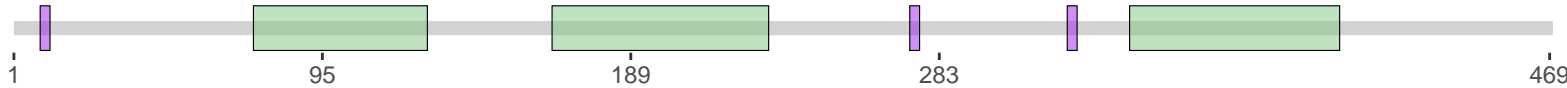
Gel Slice



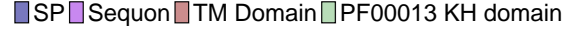
Protein length



Pfam domains



Pfam Description



Protein sequence:

YLVKALEAVIGHLRKFVLDVHSLPLFEKSNTPATGTGERPEPEPWISERTMLNMSRPLGMDVPPPLKRDLSFSERESGLDGGYHPPGLSLVGGDPGLSANRSTGLGRAGNPFVTGIGSTVGMQPLAVEIDIGGGANAVIRRTSGALITVQESRGLPDEITVEIKGTSSEVQTQQLGDFMGGHKEASLSSVGGQLDTGLRQSSVSNLGGGSGVSSSSVGGQVGGGGGGGGYGFAGGYSVRS

NbL13g03130.1 macrophage_migration_inhibitory_factor_homolog [MW = 12.21 kDa]

No. of times detected



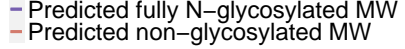
log(intensity)



Values from



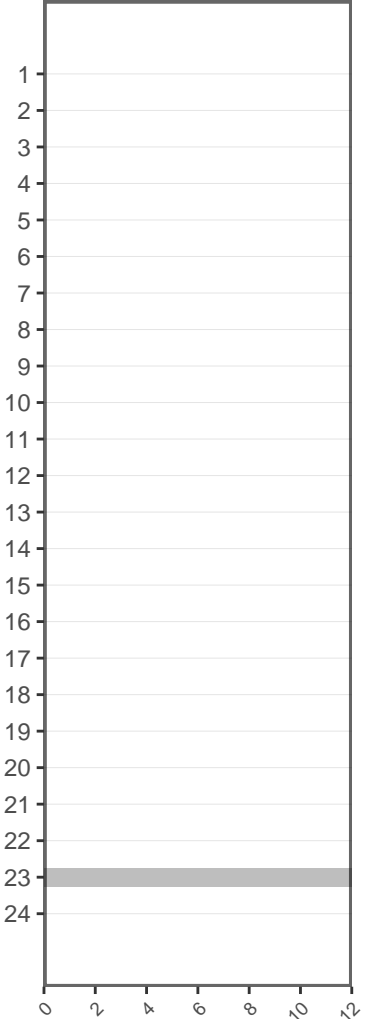
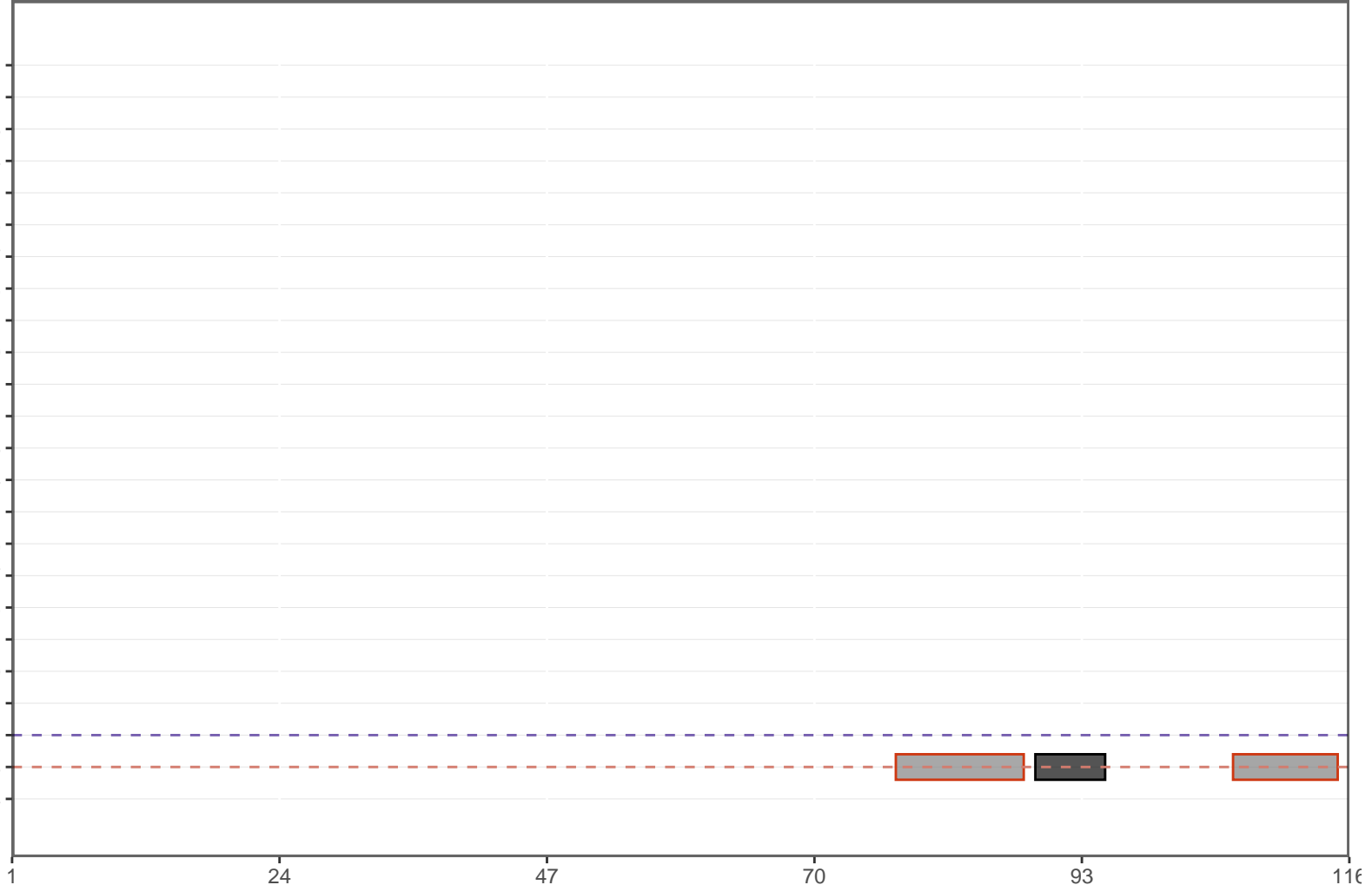
MW indication



Molecular weight



Gel Slice



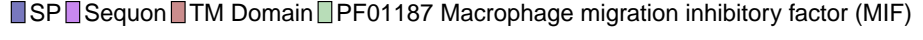
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SGVPIAFAGTEAHAAVAGELISGGLGPGVNGKLSHAEIQLTSLSDSNRFYKFKYDPSRQFFGFNGSTF*

NbL13g03030.1 choline_monooxygenase_chloroplastic-like [MW = 48.66 kDa]

No. of times detected



log(intensity)



Values from



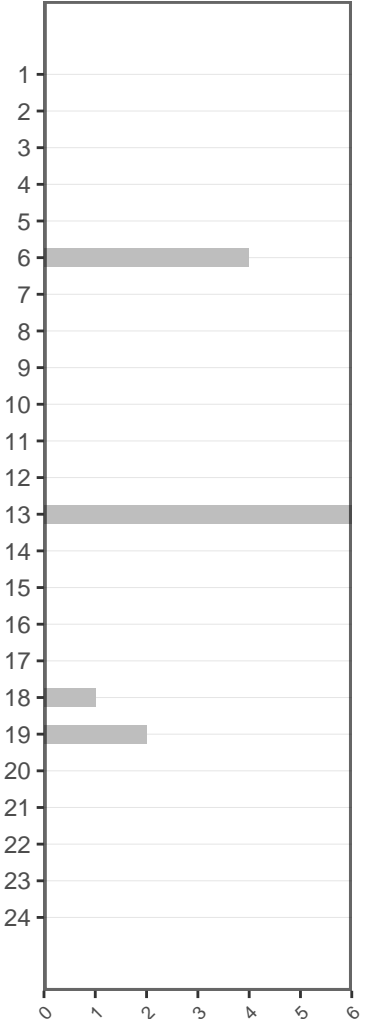
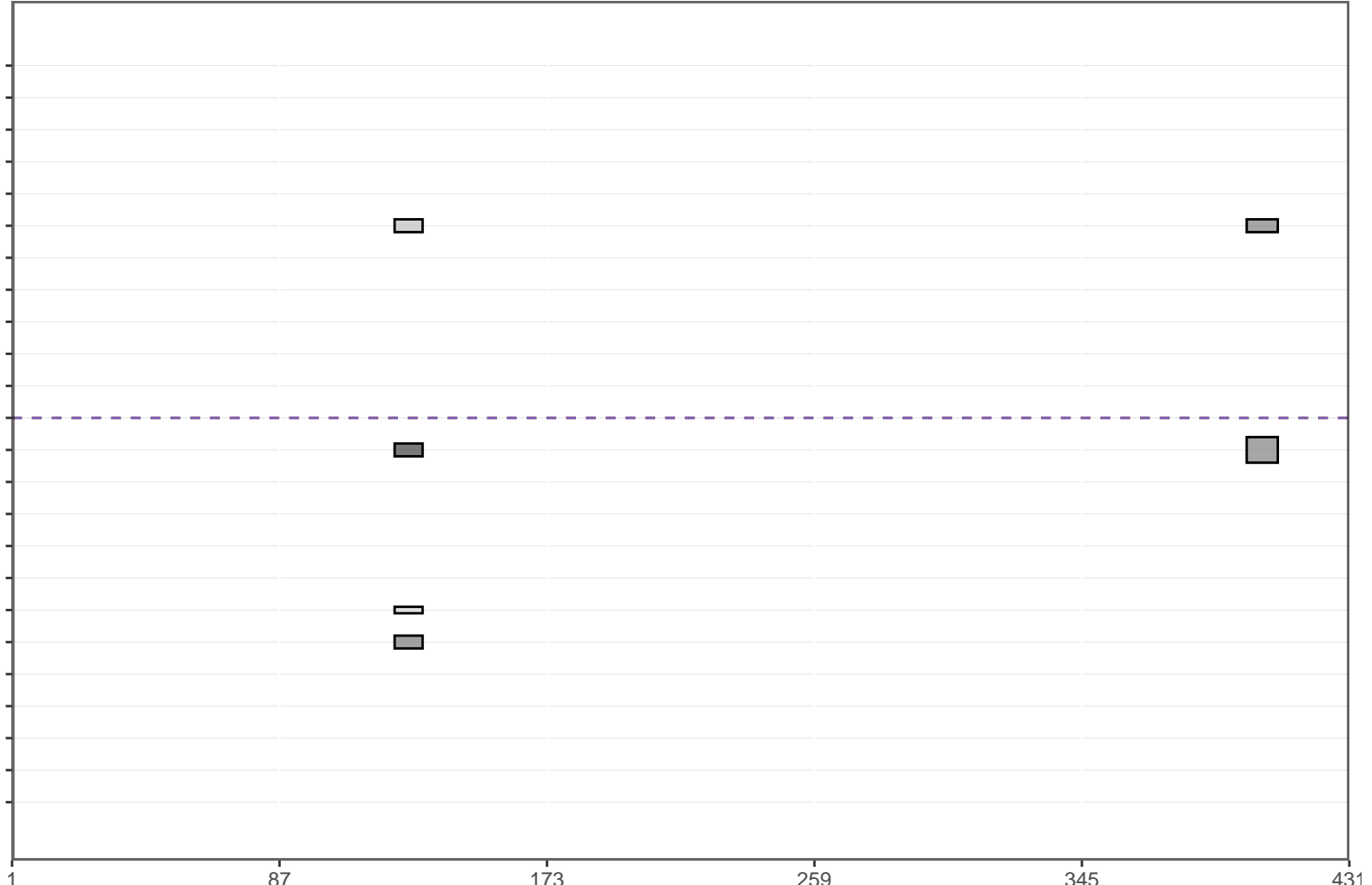
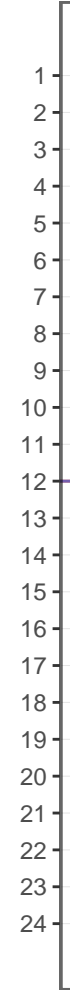
MW indication



Molecular weight



Gel Slice



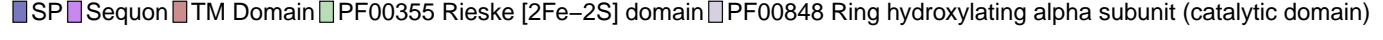
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

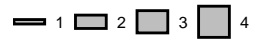


Protein sequence:

LVAVGGPILLNFENGLSERESGDFDLVGEWLGTSQQLAEGGVDSLSLFLGRKRYTIEGNWYVFDGNYLDGGYHVPAHKLGLASGLTGLGYSFTILEKVSQRGETGSAEKGEYDRLGSKALVAFYVYVPMNRYGPPMDTNLVLPGGPRKGLVFDVFLDASLKGDDDFIAGSLGDSSEIVGMEIKLCEAVGRGLESPAVNSGRVAPQVEKAMHFFHLLYENLN

NbL13g02910.1 methyl-CpG-binding_domain-containing_protein_10-like [MW = 55.55 kDa]

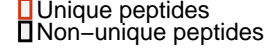
No. of times detected



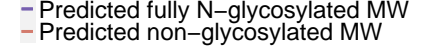
log(intensity)



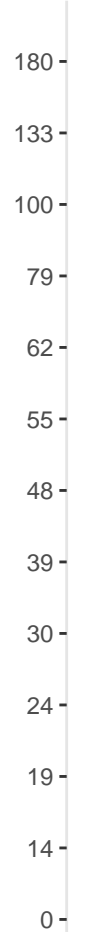
Values from



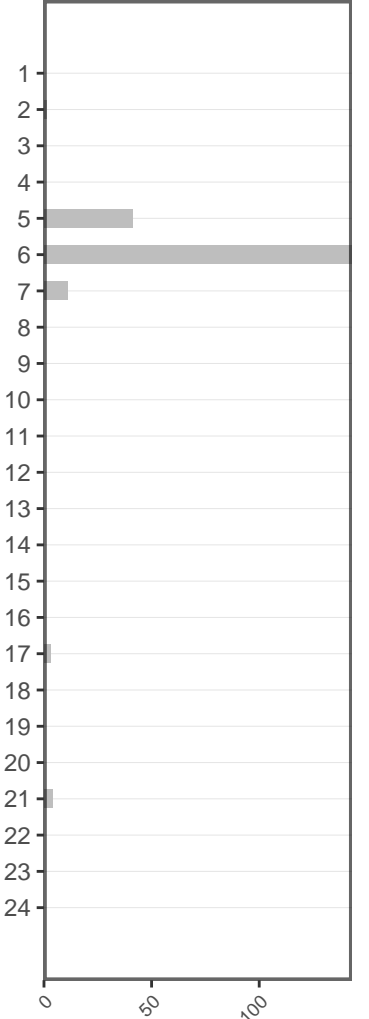
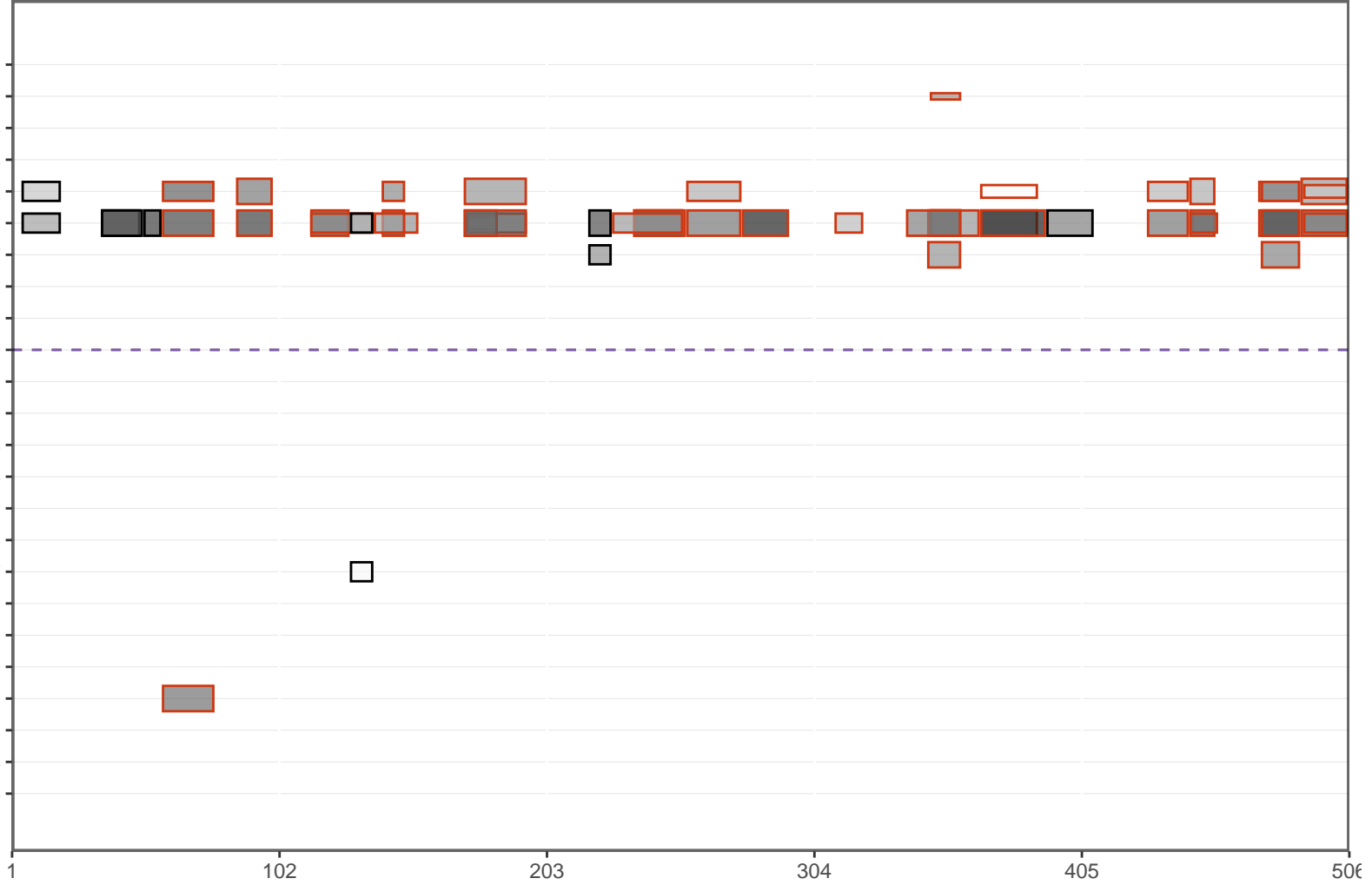
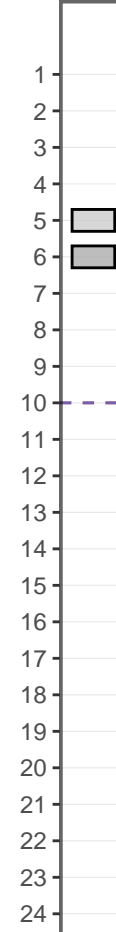
MW indication



Molecular weight



Gel Slice



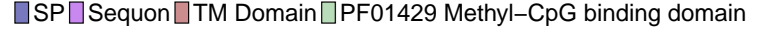
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PSNVDVVEENQADRKIDGGTDEGKAEAEAGDGKDKVMADNFQHPEDAGEASVYKKEAPLEKEFEATKDEEGKDVLPESVVEGKLTETKKEAAVEKDKVMADNAEKKDEHSSNVDVVENQADRKIDGGTDEGKAEADAPPEAAEGDKDKVMADNFQHPEDVEEASVYKKEAPIGKEADVFEATKDEEAKDVGVGVEGVEKPTETKEDFSAEEKKHQPEGERRDENGAARKSTGEGDAMNSAISKVGVGEEVTEENGNEADEAVP

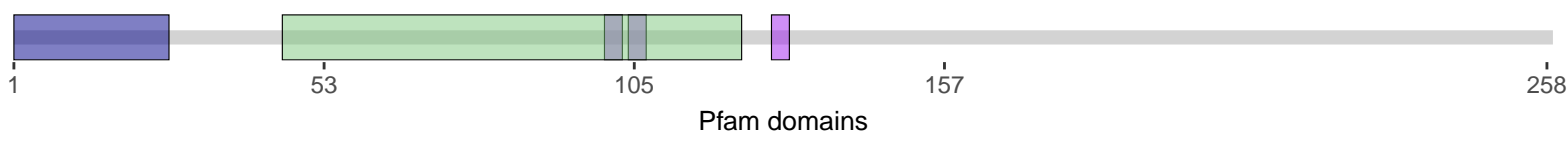
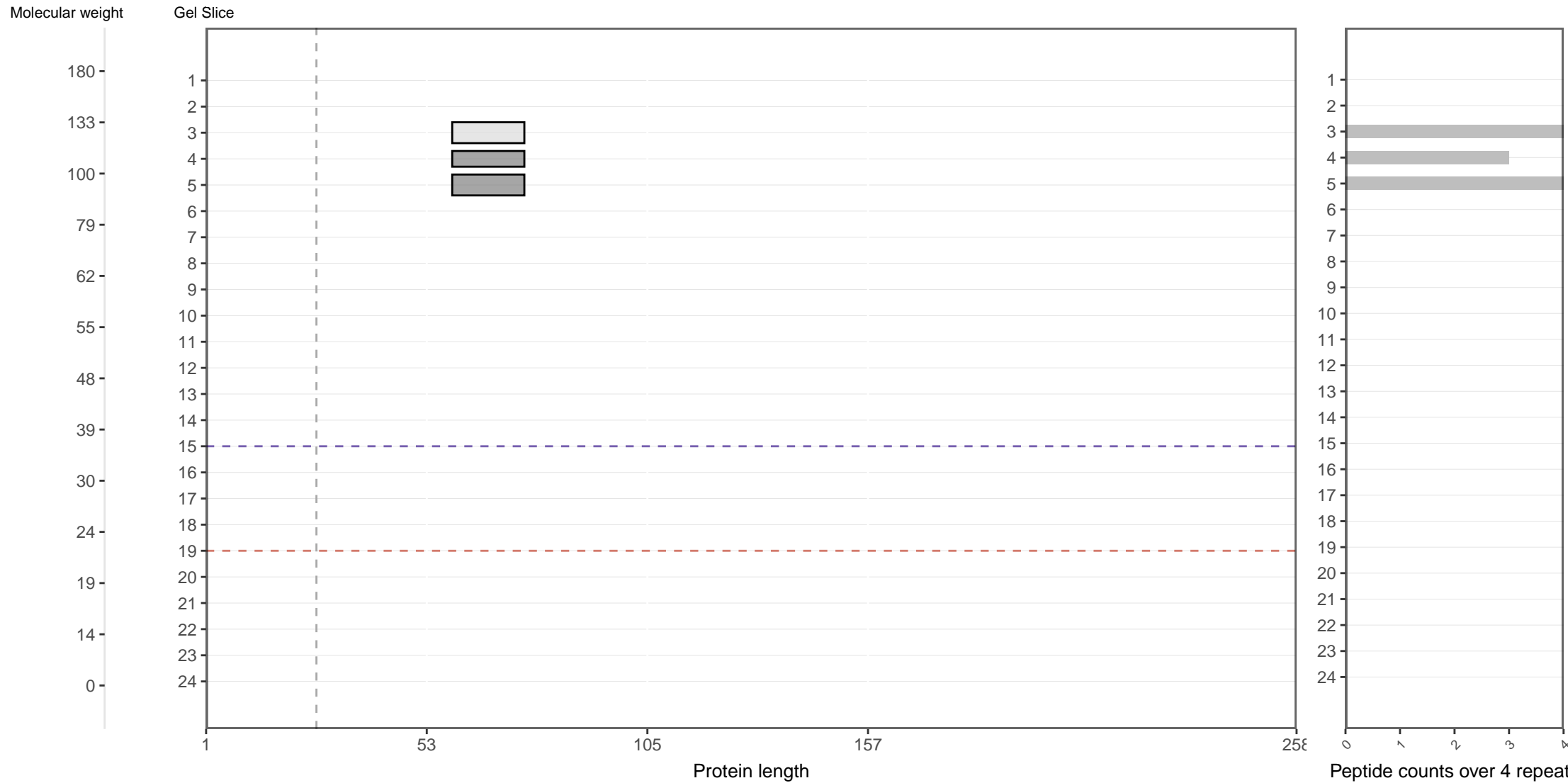
NbL13g02890.1 cucumber_peeling_cupredoxin-like [MW – SP = 22.9 kDa]

No. of times detected
 1 2 3 4

log(intensity)
 4.5 4.7

Values from
 Unique peptides
 Non-unique peptides

MW indication
 Predicted fully N-glycosylated MW – SP
 Predicted non-glycosylated MW – SP



Pfam Description
 SP Sequon TM Domain PF02298 Plastocyanin-like domain

Protein sequence:
 SQHCSAGQKLAIVTASSTSSPAPSPPTTTPSPSPVPTTPTTPTTPTTTPAPSAPSPPTMSTATPTTSPSPSMGSPAPTPTTSGGAGTSPSSSPTSSPTTPTTPTTPEGLPPPAPSPAPRNVFAPALIMFMGIAISLW

NbL13g02870.1 blue_copper_protein-like [MW = 39 kDa]

No. of times detected



log(intensity)



Values from



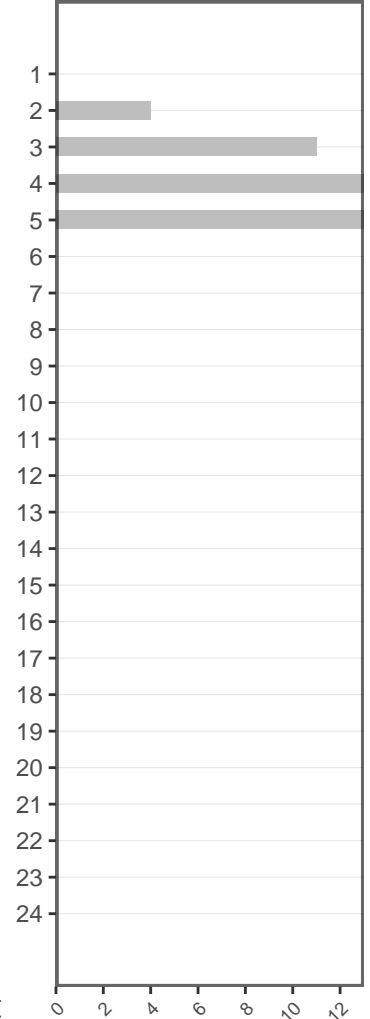
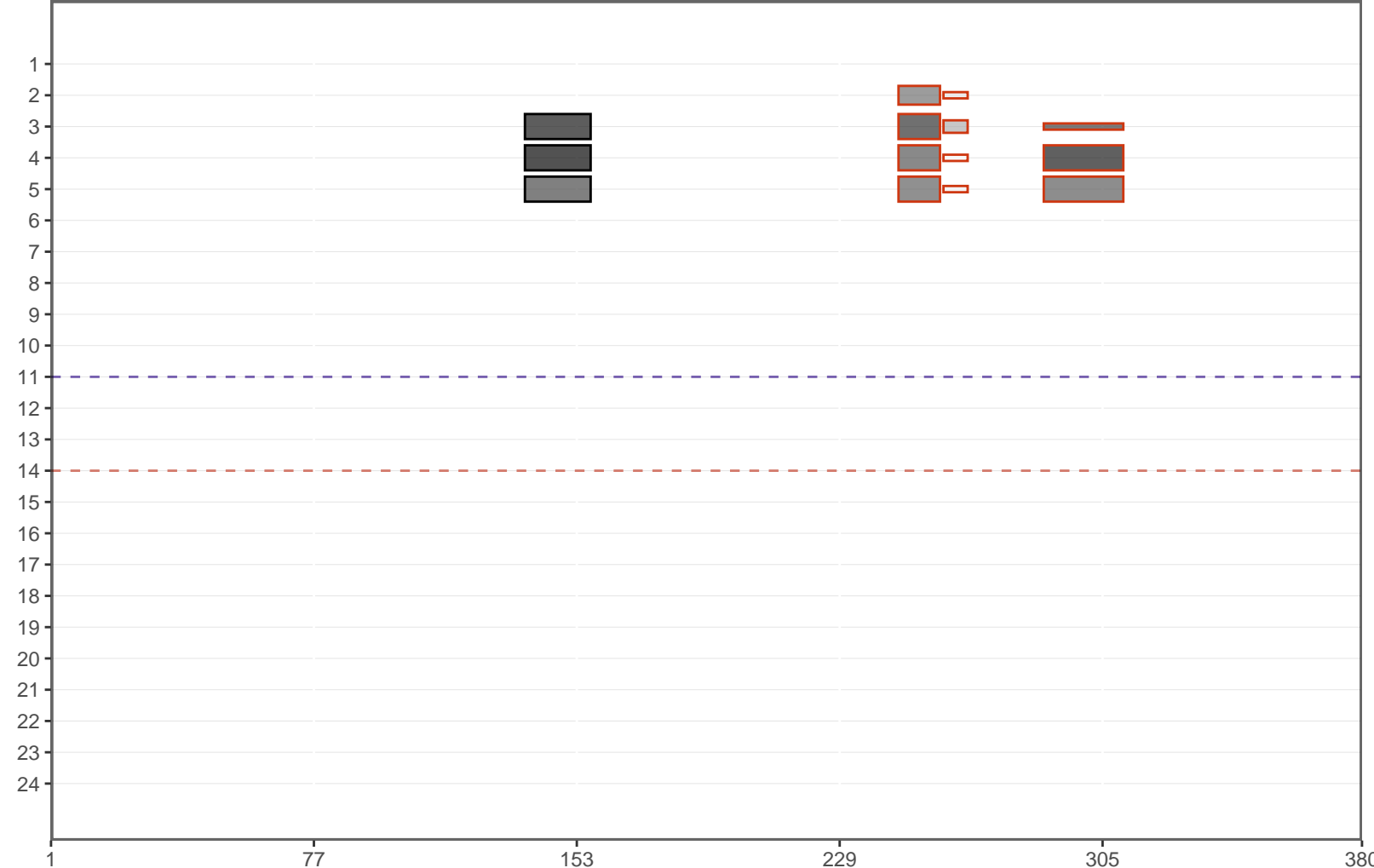
MW indication



Molecular weight



Gel Slice



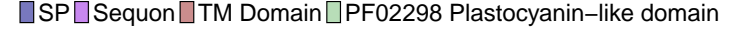
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PPTAAPVTPASASPSIAPTPEVAATPEAPAPVAAGTFIVGDNMGWNPPTGGPNWGTWANGKFKYGDGLVFNFNVNGRHNVMVSKAAYDSCNTSSPINTISTGPARIFLNSGENYVMCTFFPHDGLGKLIANNVTGTSAAAPTSPSIAATPSGGETVPSIPSGDSEPVTSPPPPPSASPSLVLAALPVTFLSLAFARLN

NbL13g02810.1 topless-related_protein_4-like [MW = 125.14 kDa]

No. of times detected



log(intensity)



Values from



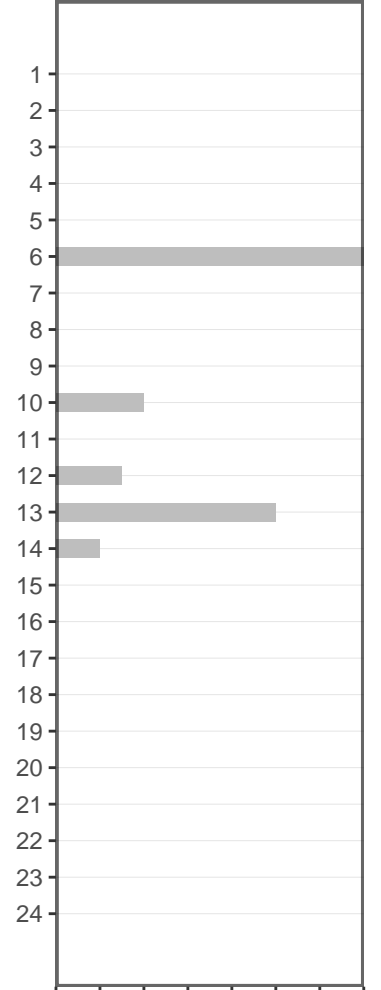
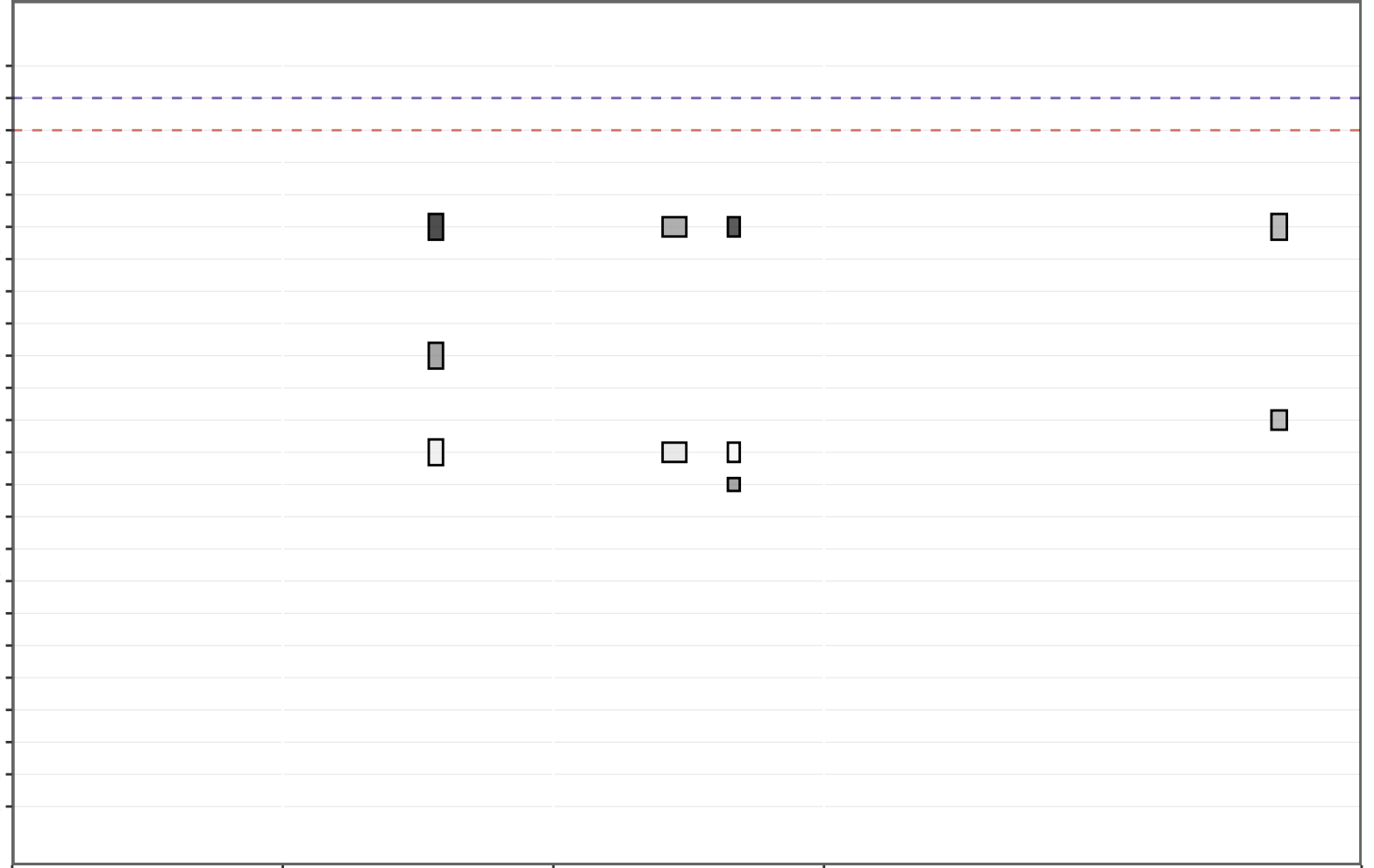
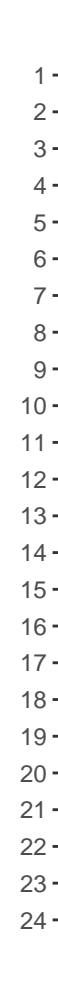
MW indication



Molecular weight



Gel Slice



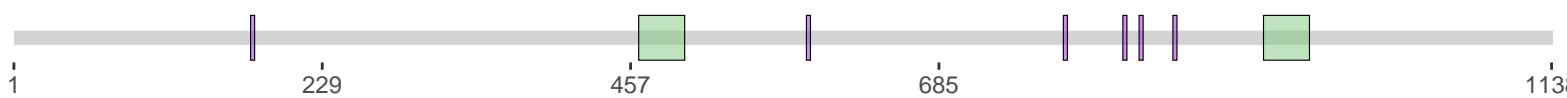
Protein length



Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

HSSTTMAYSDGTRLFSGGTNGKESVLEWVNESEGAVKRTFFIGLGRAGGVVQFDTRNRFLLAAGDEFMKFWDMNINMLTSTEAEGGIPASPLRFNKEGLLAVSTSDNGIKVLANADGLRLLRSMENRQGFDRVASAGVKKPPTLGGFGPPSTVAASFVDRGVPMTSMVGMINGENRNLGDVPRAAEETVYDKRIRWKPTEINEFSQKSLKLPDNTITRISRLRYTNSGLAILALASNAVHKLKWKWPRNERNPTGKANASVPLQWQSPENGLTMDTDTNPI

NbL13g02660.1 12-oxophytodienoate_reductase_3 [MW = 40.54 kDa]

No. of times detected



log(intensity)



Values from



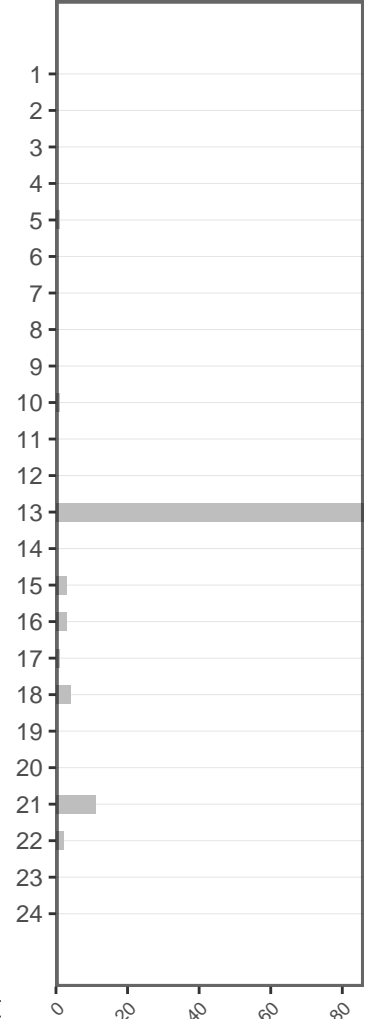
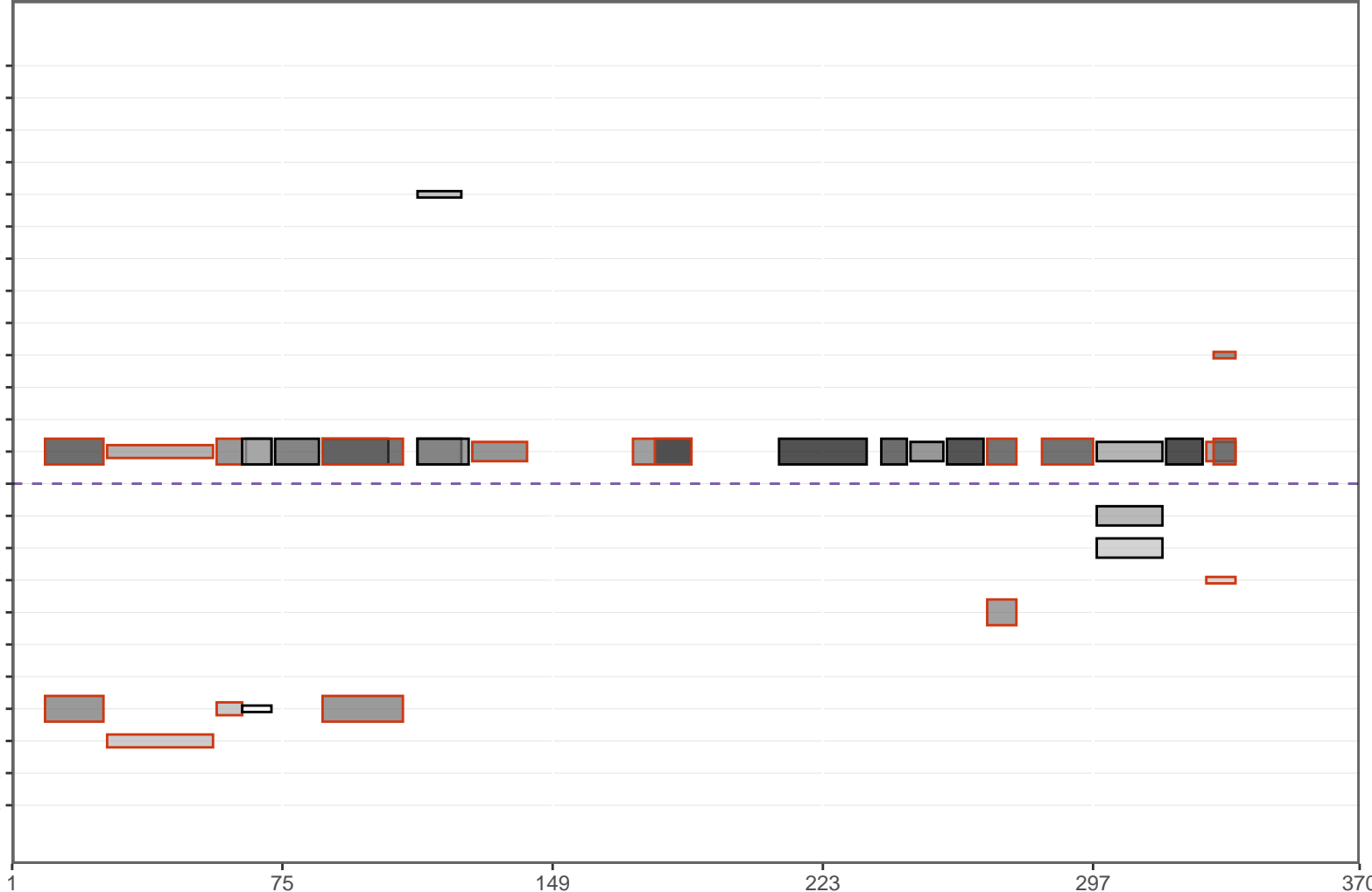
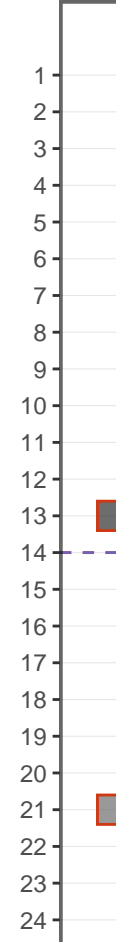
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

INDRTDEYGGSLGNRCKFMQVVEAVTAIGVDRVGVVMSPAIDHLDAMDENPLSLGLAVVERLNKQLHFGSKLAYLHVTQPRVAVYGGTEAGRLGSEEEEARLMRLRNNAVQGTFCISGGYTRRELGEAWAGDADLVSYGRFLFISNPLVLRLLKLNAPLTKYNRKTEFTQDPVIGYTDYDFPLOGNGNIPSSRLV

NbL13g02600.1 probable_sucrose-phosphate_synthase [MW = 118.8 kDa]

No. of times detected



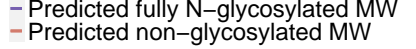
log(intensity)



Values from

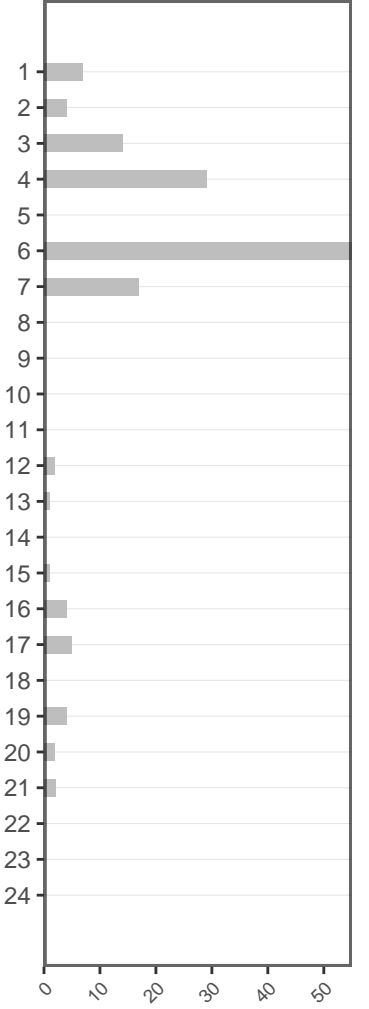
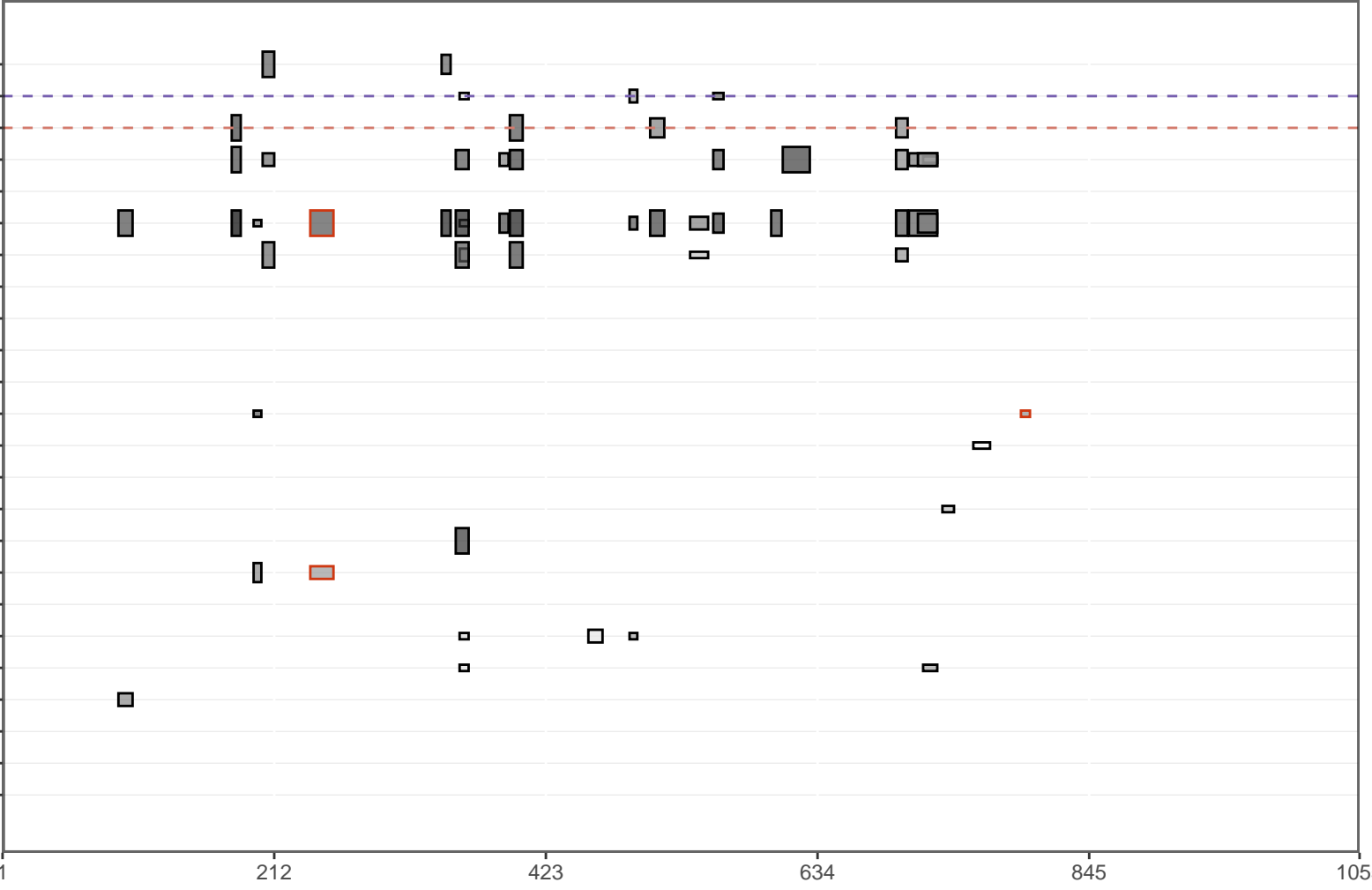
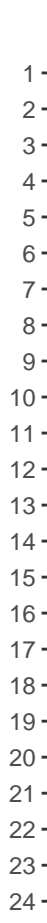
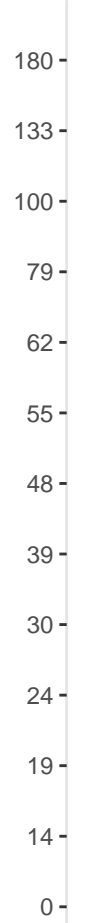


MW indication



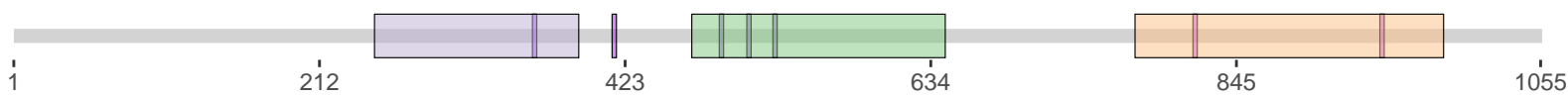
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00534 Glycosyl transferases group 1
- PF00862 Sucrose synthase
- PF05116 Sucrose-6F-phosphate phosphohydrolase

Protein sequence:

IMGNRDNDIEMSSSTNSGVALLEKIMDKYDLVGGVWPKHKHKGADVPDWRLAANTKGVFNRFIEFPGTLIEAAAYGLPMWATKNGGSPVDIHRVLDNGLLVDPHDQQAADALLKLVADKHJWAKRANGLKNHILFSWPEHKCTYLSRIASGKPRGPRFRLWRTDDDDDDENSETSPSGLRDHDSINLRFSLDGEKNDNKENADNTLDFEVRKSKLENVLSWESKGVKSTPKAWSSDKGDDNSGAGKFPFARRRRHIFVAVDGDASGGLSEVRKFEVEXERAEGLI

NbL13g02570.1 bifunctional_purple_acid_phosphatase_26-like [MW - SP = 52.74 kDa]

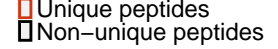
No. of times detected



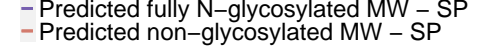
log(intensity)



Values from



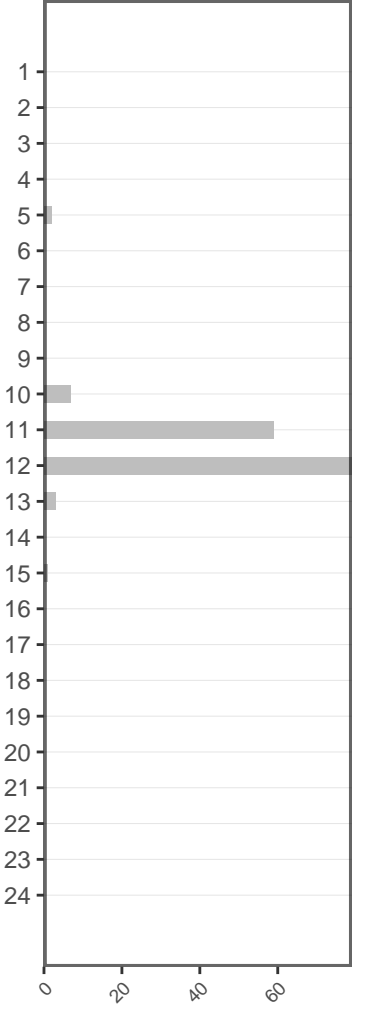
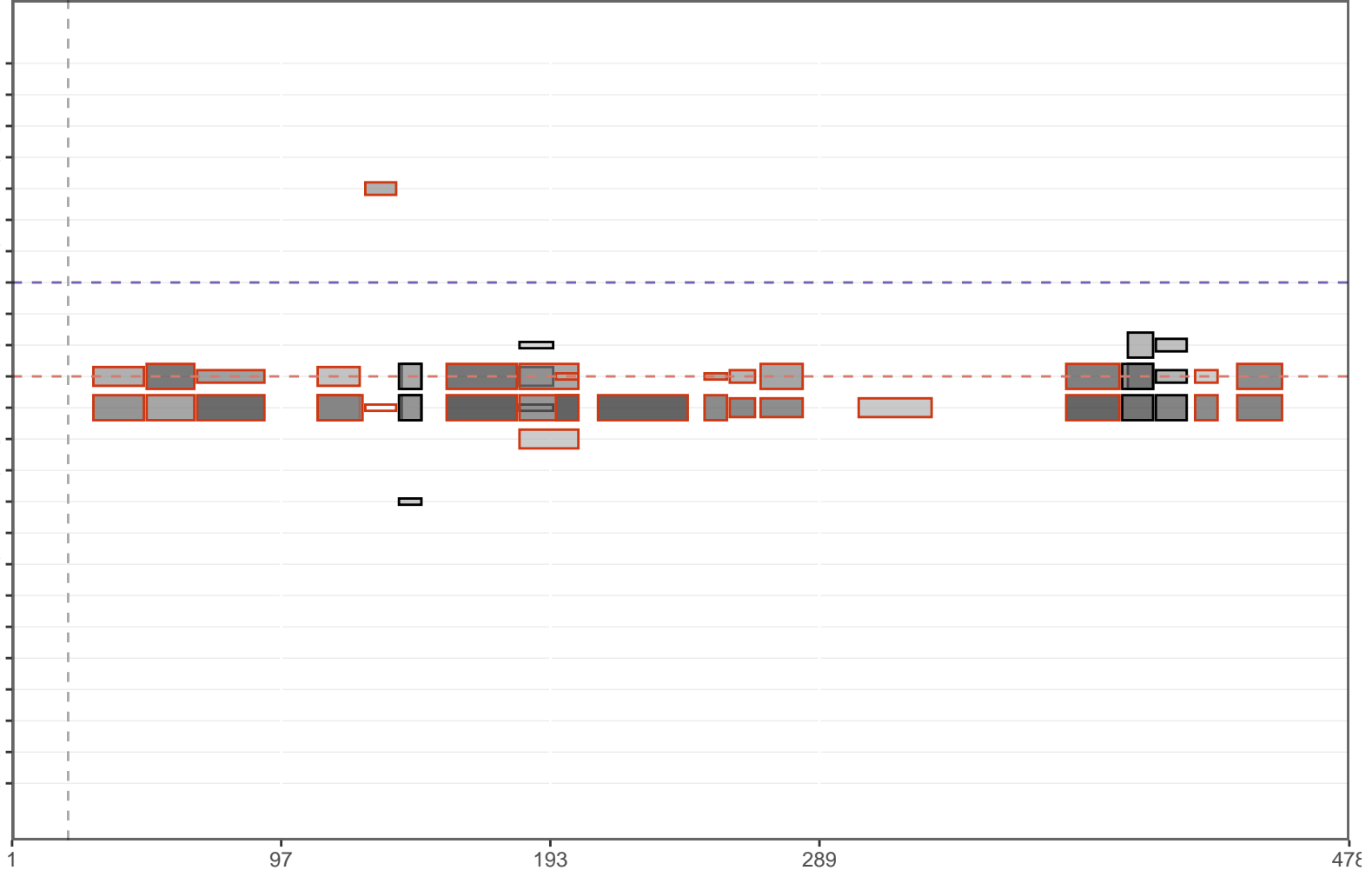
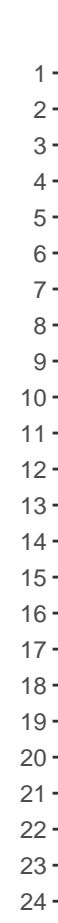
MW indication



Molecular weight

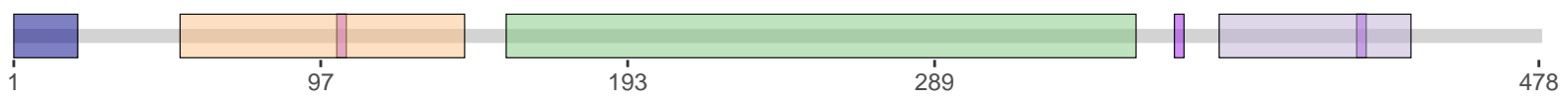


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEIEYFPNMGELVDFKSFILRYPTTPGVGRSSNPLWVAARRASTHIVLSGYSDFKYPQWHLVKGELNNVNRGKTPWLVLMHVPVNSNEAHFMEGEMRSVFERWFKHRVDVIFAGHVAVERBYRISNHYNVSGGDVFPVDPKTAPIYTVSGDGGNGEGLASRFDPQDPVSAFREASVYGHSTLEIKNRTHAFYHWRNDDGNKVTVDGFTLHNQYWGARRRRLLKNNHLHVSERPSAVRF

NbL13g02470.1 pyrophosphate-energized_vacuolar_membrane_proton_pump-like [MW = 80.02 kDa]

No. of times detected



log(intensity)



Values from



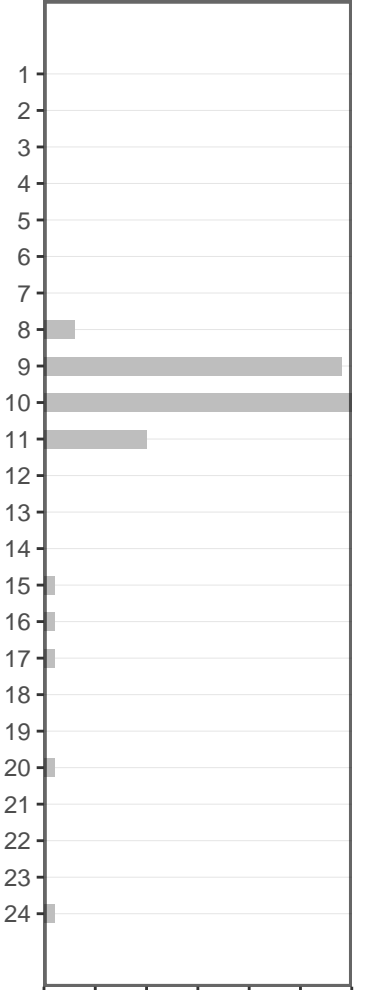
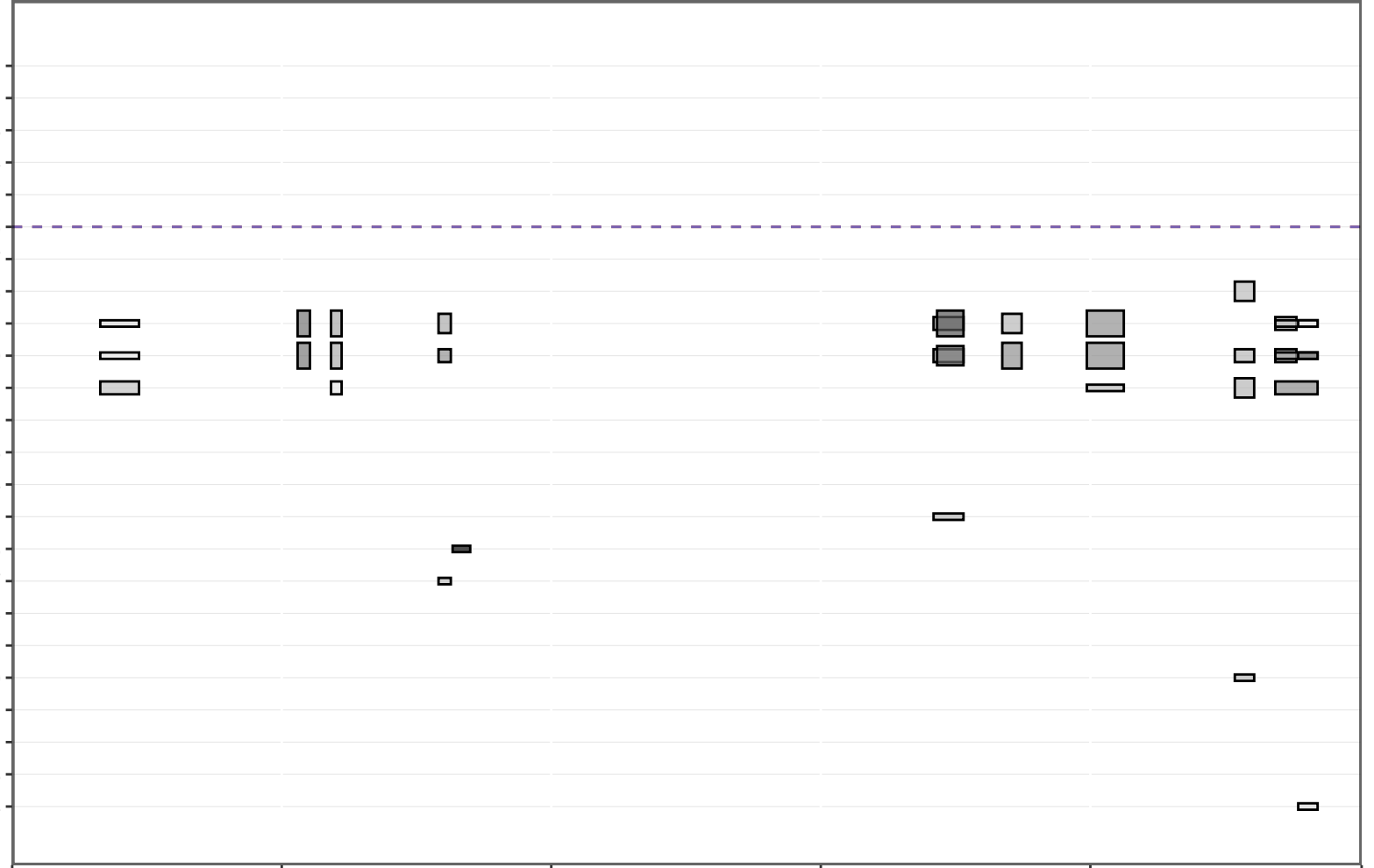
MW indication



Molecular weight



Gel Slice

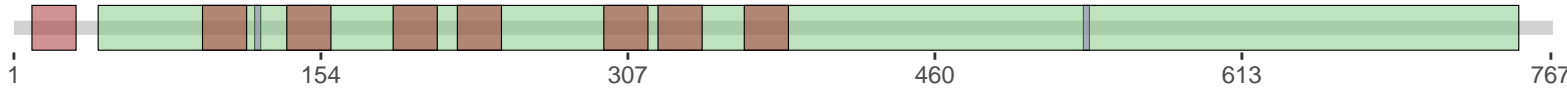


Protein length

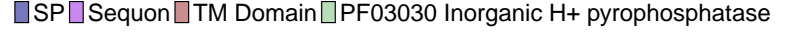


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ALMTVGIIVYTWALPSTFTIFNFAGKEVKNWOLFVGVGVLWAGLHGFVTEYTSNAYSPVGDVADSCRTGAAATNIFGLALGYSVIRPFAWISFVFSFAMFYGVAALGMLSTIATGLADVYGPISDNAGGIAEMAGMSGRIRERTDALDAAGNTAAAGKGFAGSAALVSLFAGAFVRAAISTVDVITPKVFIGLLVGMALPVWFSAMTMKIVGSAALKMVEEVRROFNTIPQLMEGTAKPDVATGVNIGTDAKEMIAFGALVMLTFLVGLFVETLSGVLAGSU

NbL13g02460.1 arogenate_dehydrogenase_2_chloroplastic-like [MW = 42.86 kDa]

No. of times detected



log(intensity)



Values from



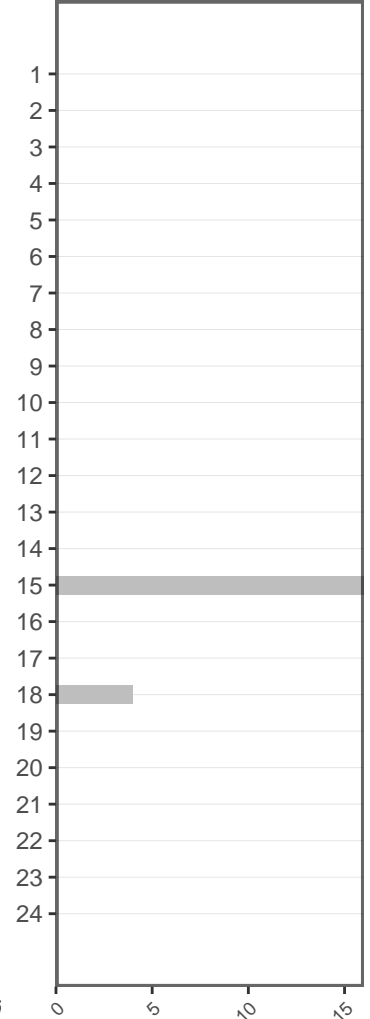
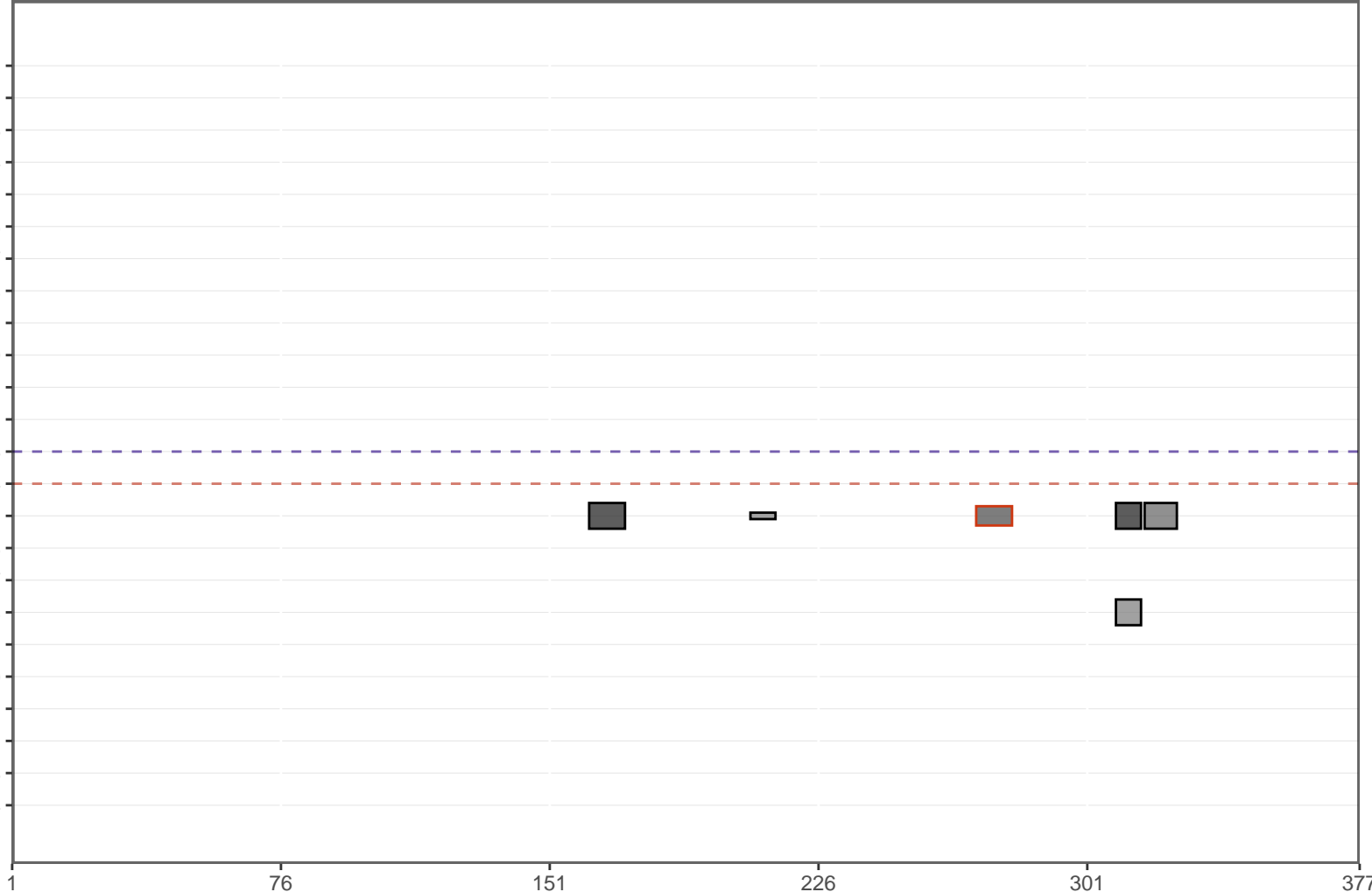
MW indication



Molecular weight

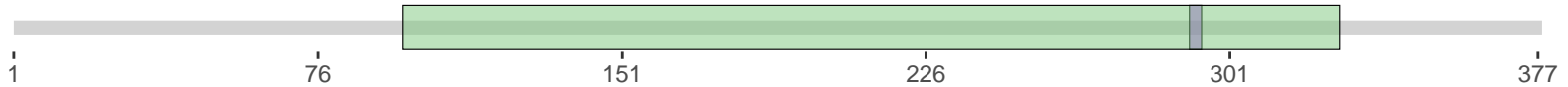


Gel Slice



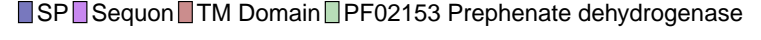
Protein length

Peptide counts over 4 repeats



Pfam domains

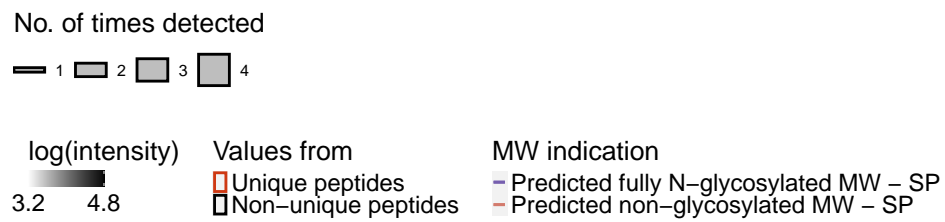
Pfam Description



Protein sequence:

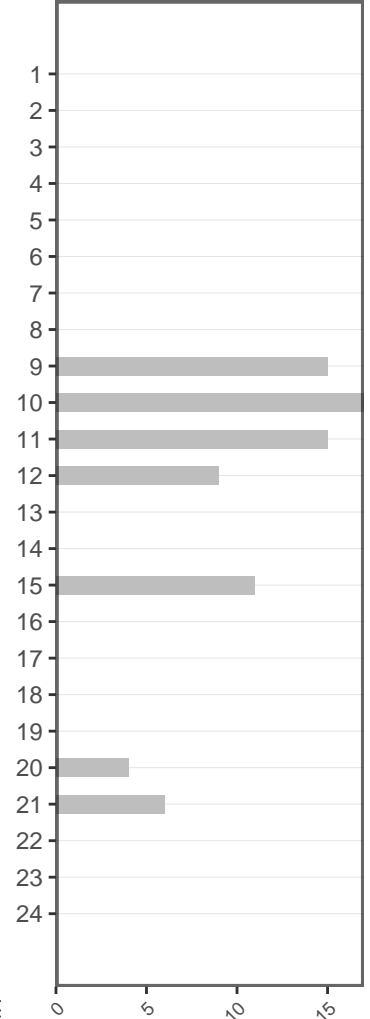
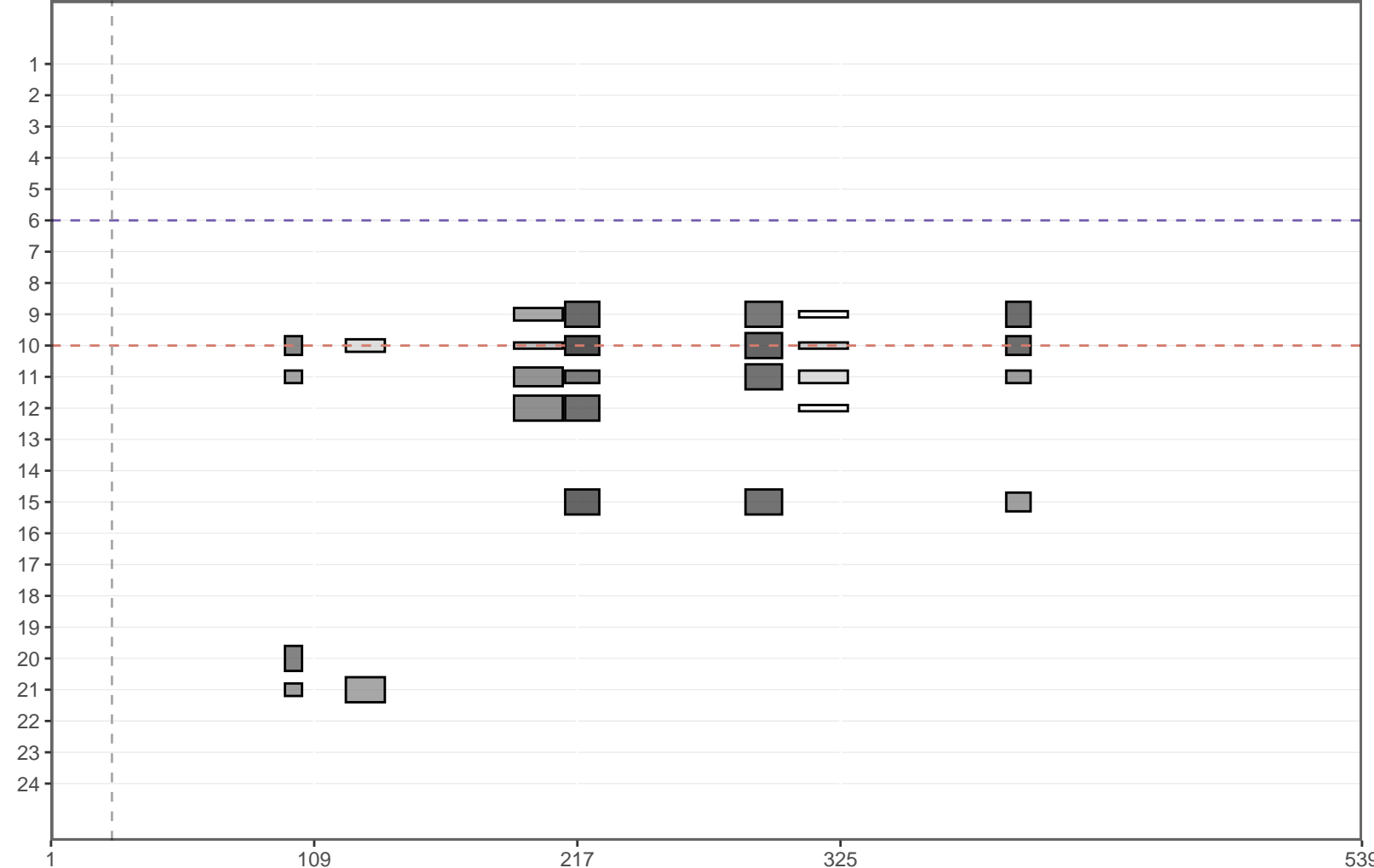
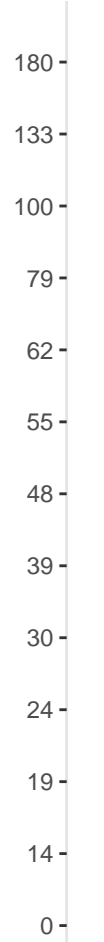
VFLOVLP SHFDLCTHPMF GPEGGKDWKDLAFVFDKVRIGEGESRKRGRVDRFLHFKEKGGRMVQMTCAEHRVYAGSQFTHMGRVLEKLELETTPTNKGYETLNLNIVENTSSGDFDLYYGLFMVYKNNAMEQLERLDLAFEALNKELFGHLHEVLRKQLFGKAAEAGQRRLTKPKNGVLPAPSSSEAVKSENY

NbL13g02440.1 heparanase-like_protein_3 [MW - SP = 56.34 kDa]

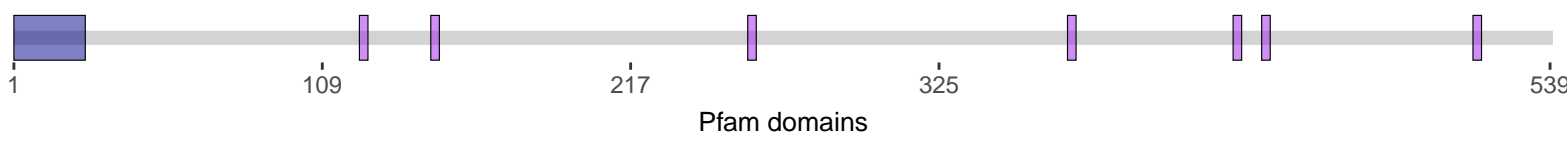


Molecular weight

Gel Slice



Protein length



Pfam Description
 SP Sequon TM Domain

Protein sequence:

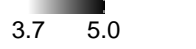
ILNKTGKSFDAITHHYNLGPRGRDEHLVDKLDPSVLDGEADTFKLGNYLKTSGTSTVAWVGEAGGAYNSGRDHYTNVAFSEWYLDQLGMSAAVDYNRGRTLGGNYGLLNTFTTFVNPDIYKALLWRLMGRNLYTSFSGSKIRAWAHGAKQSGGTLLINLDGNTTISANVAFNGTTLRHKHSHRHSKHSKSSRLPKGRKIAENRQGEYHAKDGDLSGQTMLLNGKPLTDSGSGNIPLEPIFVNSTEPLTAVPFSIVFVHPVWLRGSP

NbL13g02430.1 triphosphate_tunnel_metalloenzyme_3-like [MW = 28.14 kDa]

No. of times detected



log(intensity)



Values from



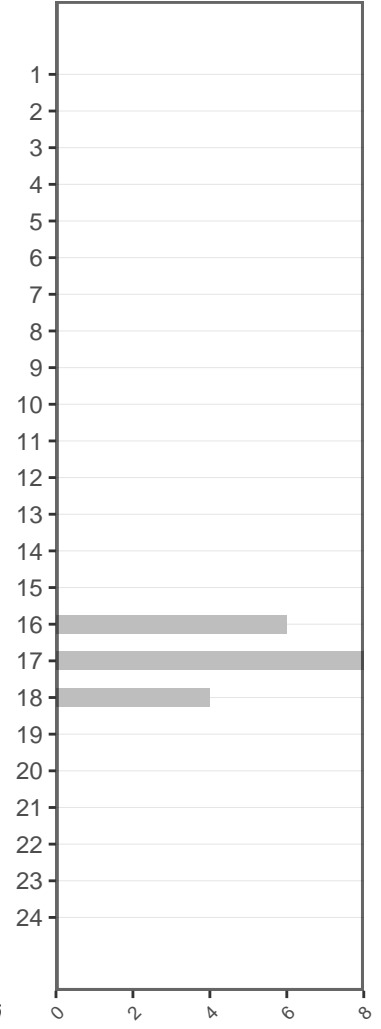
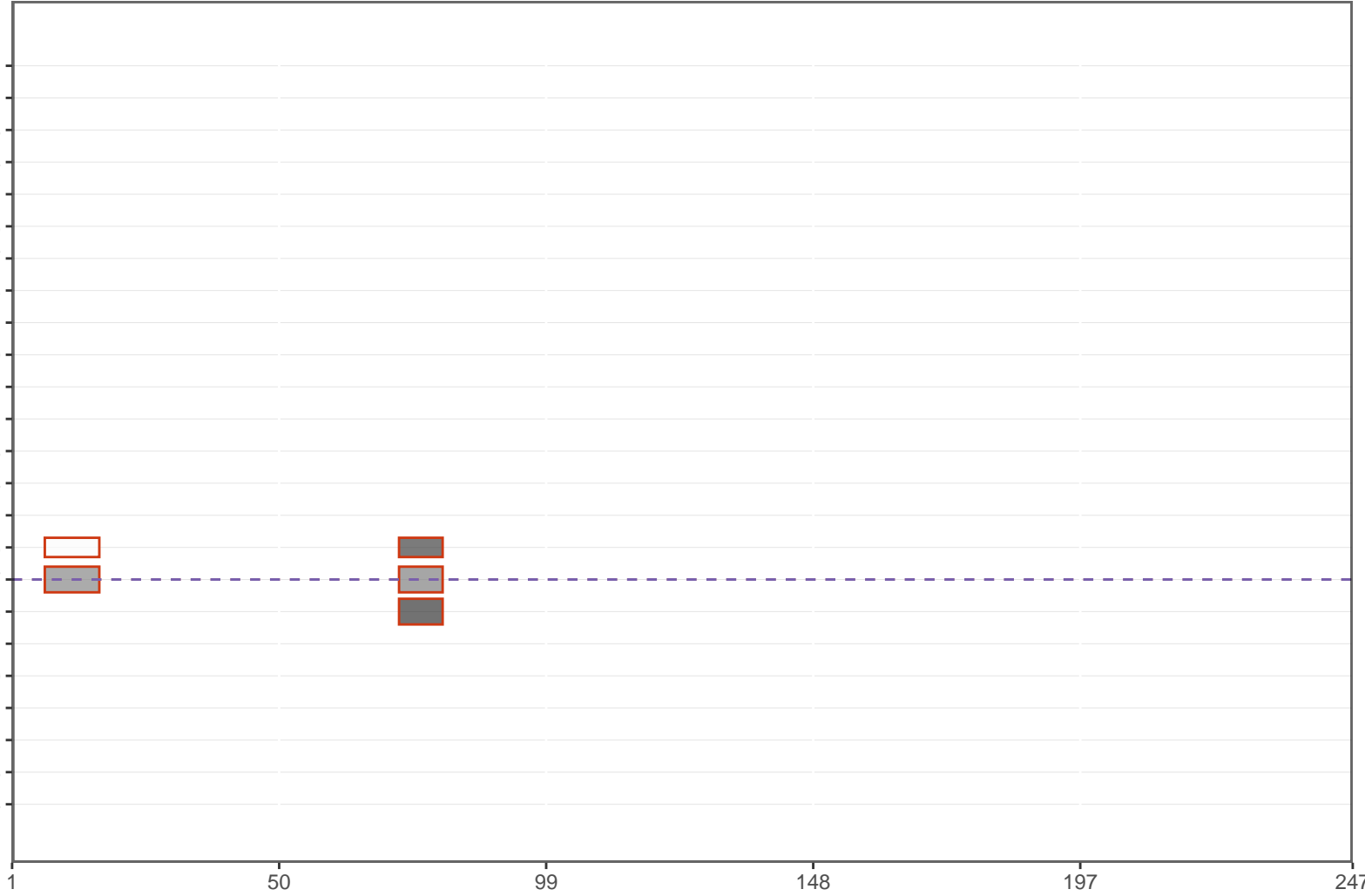
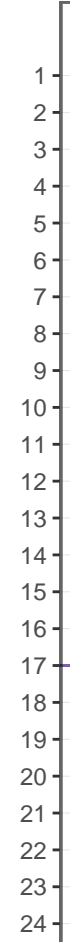
MW indication



Molecular weight

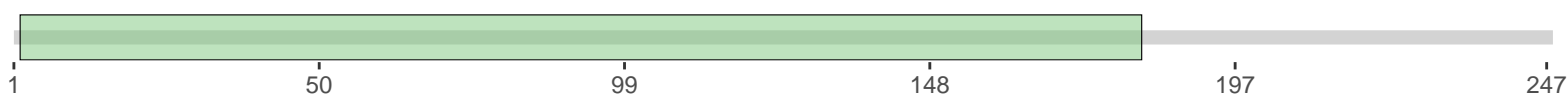


Gel Slice



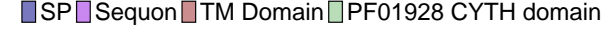
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RVLKRAKEEFDVAEEGFHGLGDFNNRVNFWQWNGLELEVDETYDFGTQYEIGGSETEPEEAKAMEALLKENDIDYSYRSVKFATFRAGKLPQCTSLAPLYLEGPKSSPQYAMKSHYLAVFRKELPCGDFVVS*

NbL13g02200.1 protein_CHLORORESPIRATORY_REDUCTION_6_chloroplastic [MW = 29.23 kDa]

No. of times detected



log(intensity)



Values from



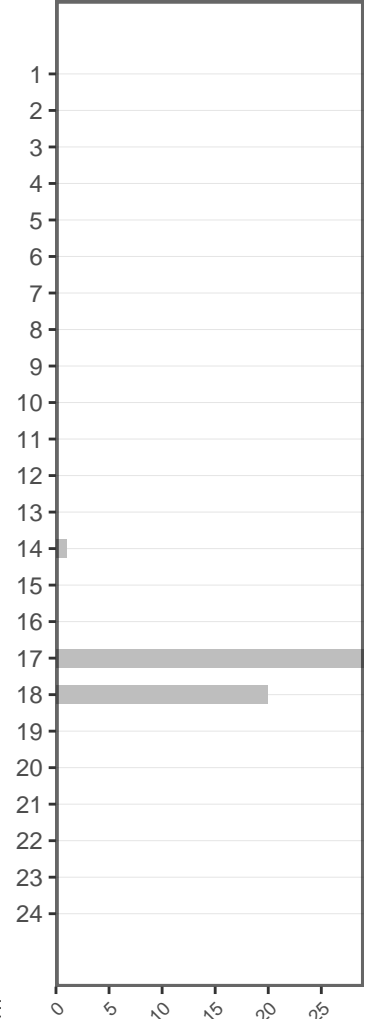
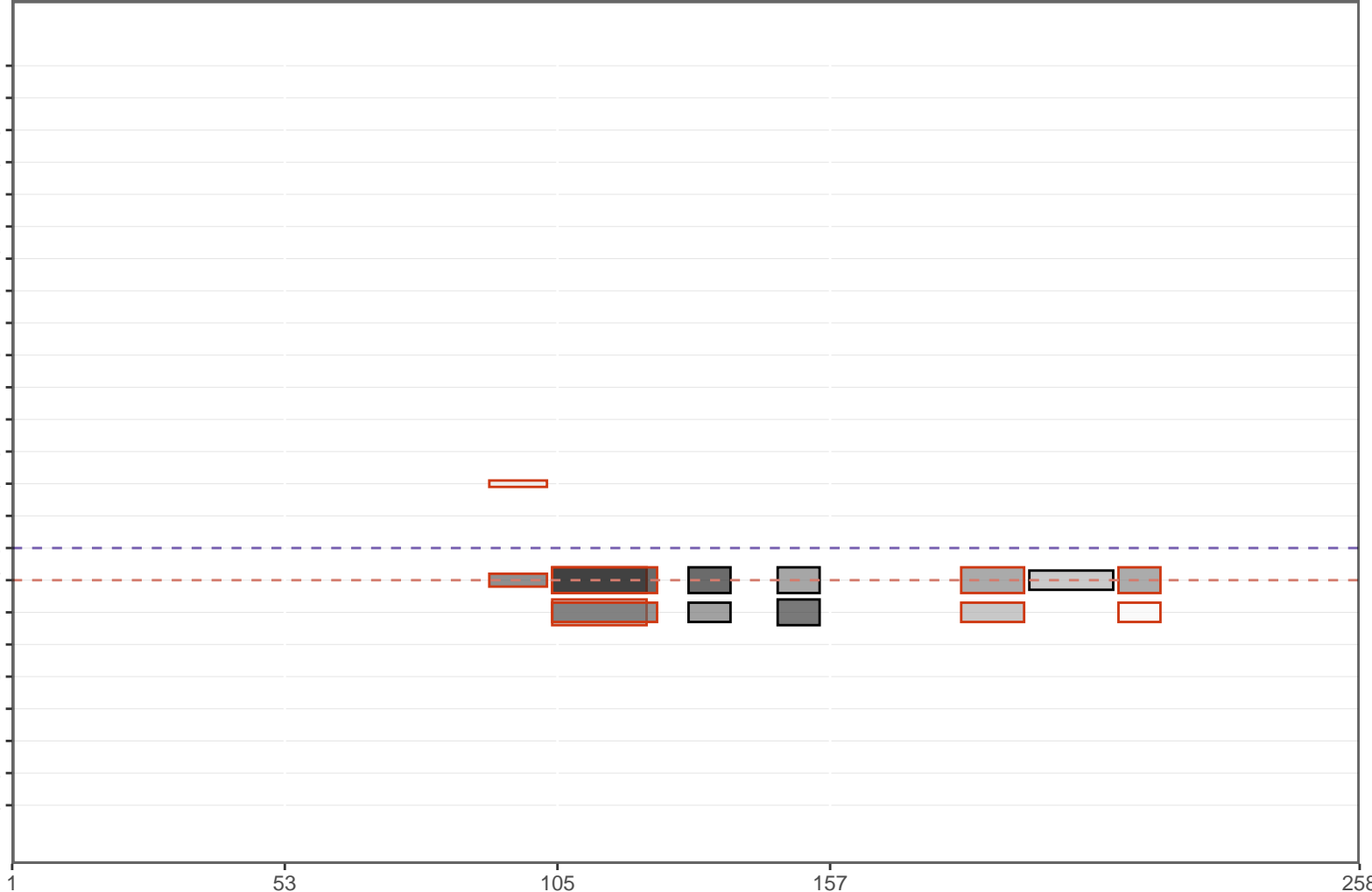
MW indication



Molecular weight

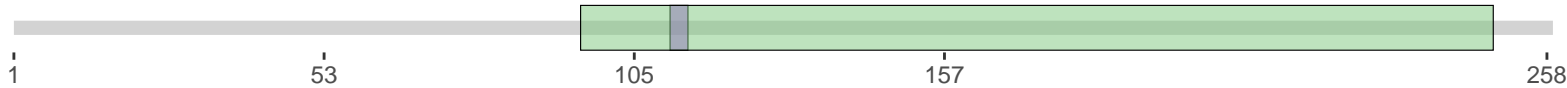


Gel Slice



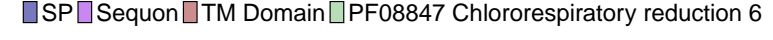
Protein length

Peptide counts over 4 repeats



Pfam domains

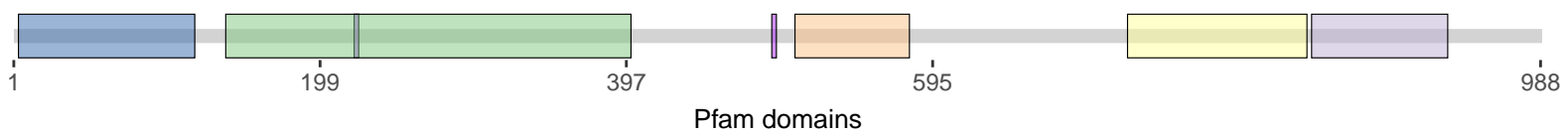
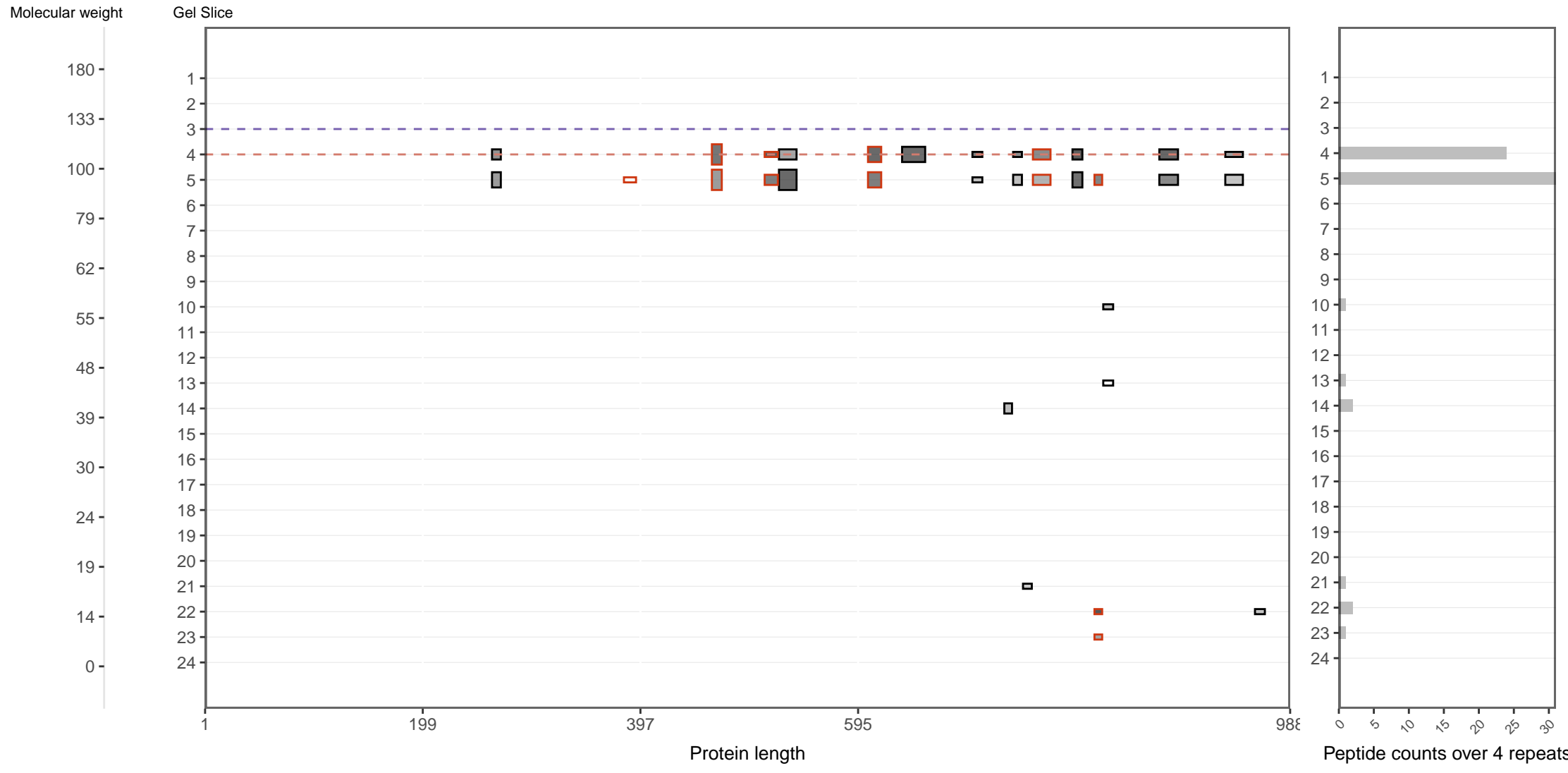
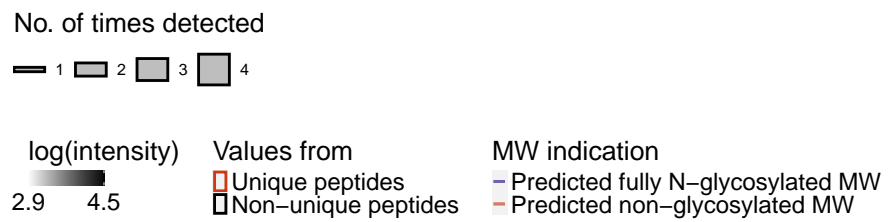
Pfam Description



Protein sequence:

ISPLSAKPKFELERKIGFTNFKREDKVDPRELSEFFDRIILWVRLDQTYWPLVLLDWKAGELARYAAMLVPHQMSMMGVFNPEALELFAVNNKVFVYVSWLKGNEIPMRLKTKDMARMLGFGGDELFDLIDKHHDT

NbL13g02130.1 110_kDa_U5_small_nuclear_ribonucleoprotein_component_CLO [MW = 110.41 kDa]



- Pfam Description
- SP
 - Sequon
 - PF00009 Elongation factor Tu GTP binding domain
 - TM Domain
 - PF03144 Elongation factor Tu domain 2
 - PF00679 Elongation factor G C-terminus
 - PF03764 Elongation factor G, domain IV
 - PF16004 116 kDa U5 small nuclear ribonucleoprotein component N-terminus

Protein sequence:
 ICDSAGPLMNVNITKLYPKNSDGVFDAGRVYSGEIMAGQTVRVLGEGVSPFDEEDMTVKEVTKLWVYQARYRIPNSKAPDGAWVLEGVDAISIMKATLCSNFEFGDYYIFRPLGNTPLVYKATEPLNPSLPLKMWVEGLRNIKSKYPLAIVKVEEGEHTLGTGELVLDISIMKDLRELYSEVEKVAADPVVDFGETVVEGSSMKGFPAETPNKKNKMTMAEPLERGLAEDNENSVVSDWPRKVLGDFDFTKYDWDLLAARWAFGPDKGGPNILLDDTLLSSEVYDKSLLNVAI

NbL13g02030.1 peptidyl-prolyl_cis-trans_isomerase_CYP28_chloroplastic-like [MW = 34.78 kDa]

No. of times detected



log(intensity)



Values from



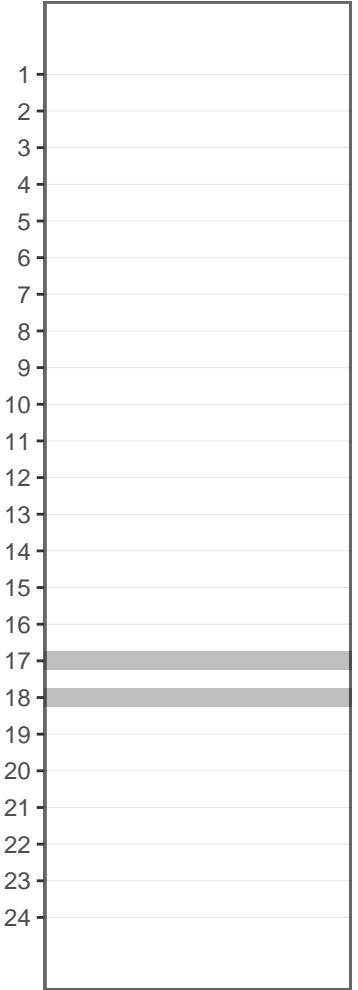
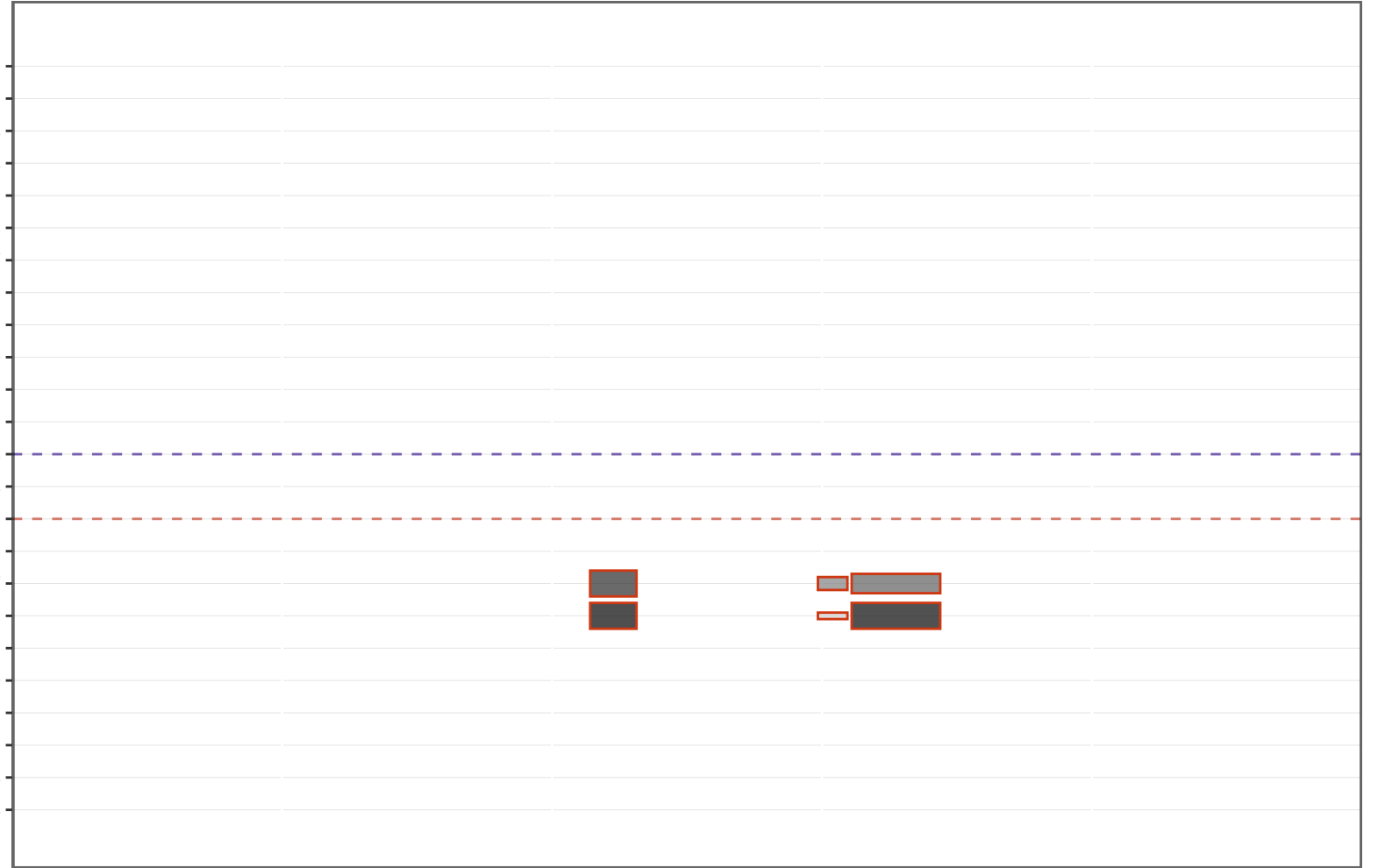
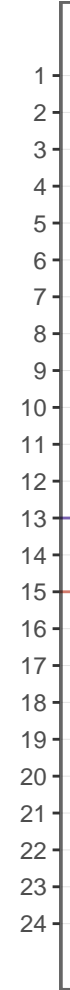
MW indication



Molecular weight



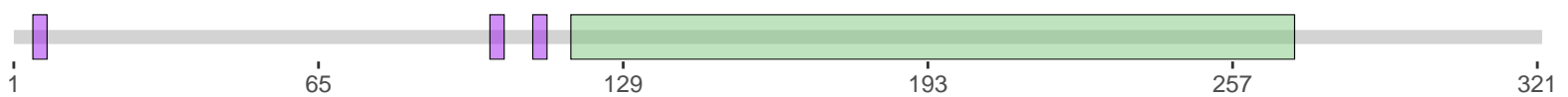
Gel Slice



Peptide counts over 4 repeats

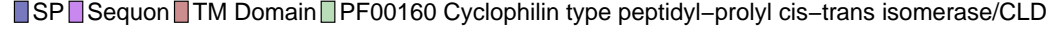
1 65 129 193 257 321

Protein length



Pfam domains

Pfam Description



Protein sequence:

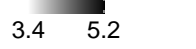
GTLVQKIFPGQFFMAGRGGRDRDKGEVYKPLSENDSDDDMLNPKYHNVFLITGPGVPLQDKNVFGTVLEGMDVFTTAAIPTYKPSENRQVYNGFAELLDGGRAKTARAANNKPKQTVYISDGGELKVTXPTLSPGLP

NbL13g01870.1 3-isopropylmalate_dehydrogenase_chloroplastic-like [MW = 40.15 kDa]

No. of times detected



log(intensity)



Values from



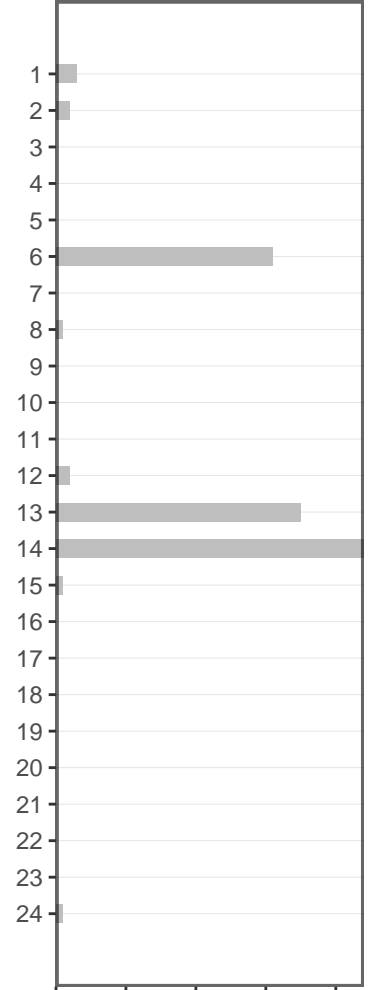
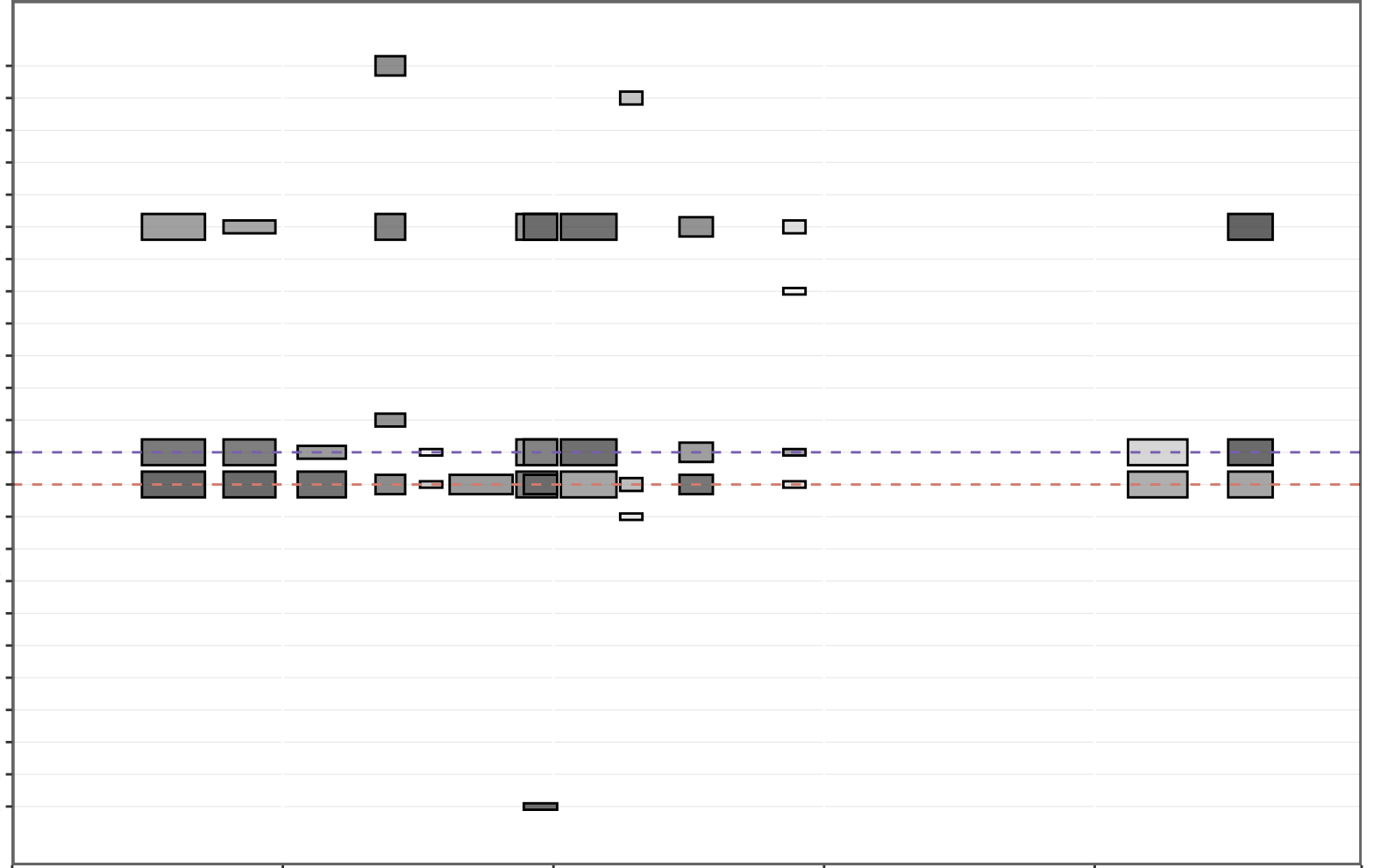
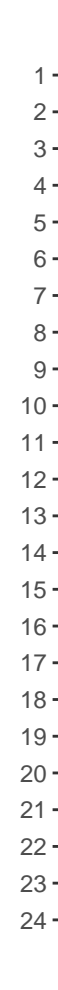
MW indication



Molecular weight

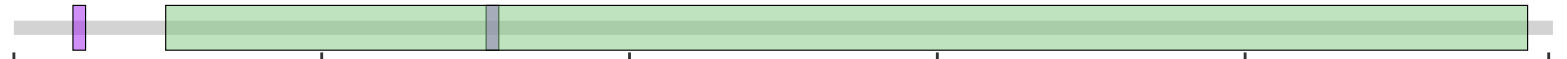


Gel Slice



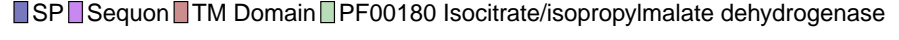
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

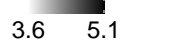
ESLKIITRQASLRVAEYAFHYAKANGRRERVAHKKANIMQKTDGLFKGGRVAEKYPEIKYEEVVIDNDCMMLVKNPALFDVLMVNPINLYGDISDLCAGLGGGLGTRFPCNIGEGGIALAEAVHSSAPDIAQGNLANFTALLLSAVTMRHLELHDKADRIQGVAVLNTIAEGKYRTGDLGGTSTDFTNAGDHL

NbL13g01840.1 chitinase-3-like_protein_1 [MW - SP = 39.78 kDa]

No. of times detected



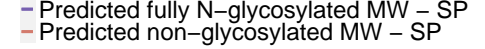
log(intensity)



Values from



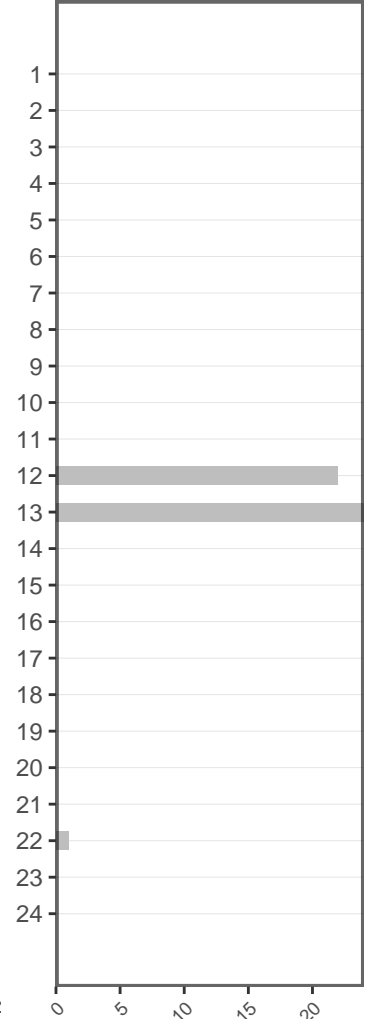
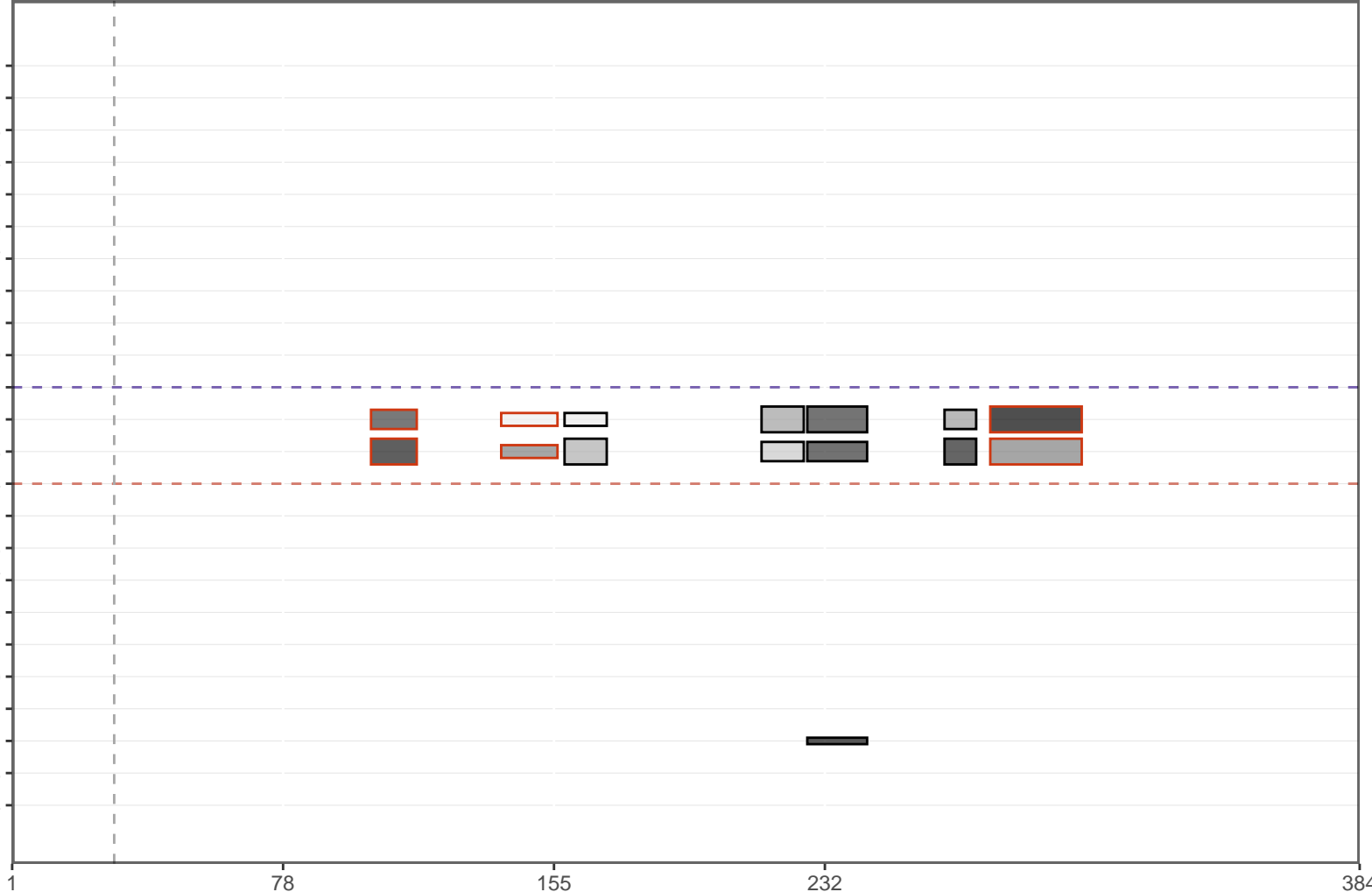
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TKKQPLLTAAVYFSDVDFLSEDFRBYVHSHINKLQWLNLMQVDYRGSWDTSATGAPALFDTKSNISTVYGLSSWIKAGAIRSKMLMLPLVGRTRWIKLDPNVHIGIGAPGIGPGDGGTMTFYREVKEFNEENNAKVVFDATVSTYSVAGNSWIGYDDRSVAMKRYAQARLRGFFVWVAGDLQWIKRITAKQLWIS*

NbL13g01820.1 uncharacterized_LOC107807700 [MW = 37.58 kDa]

No. of times detected



log(intensity)



Values from



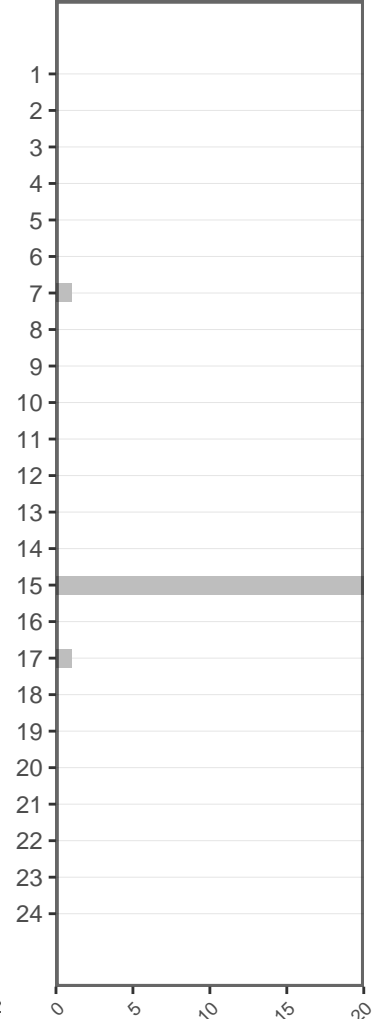
MW indication



Molecular weight

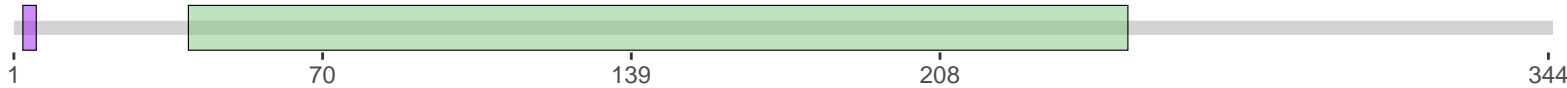


Gel Slice



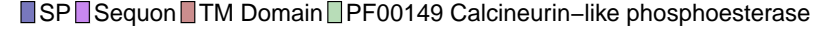
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RKOLLKARYGVYIDMDRSTERLGAAMGTPEDEHSIFLAHNGPTGLGANIDIDGGRDWFVGGDGHGDPDLAHLAQLKEAAPYSVPLVFGHMHKGLALGNFRKIMVVGNDNTYLNGANVPRVTRTALAESEGTSAFTFAEISGNRVEKIAETWISVIGDETRLEEEHLNTRPRGVTASLL

NbL13g01510.1 S-norcochlorine_synthase_1-like [MW = 17 kDa]

No. of times detected



log(intensity)



Values from



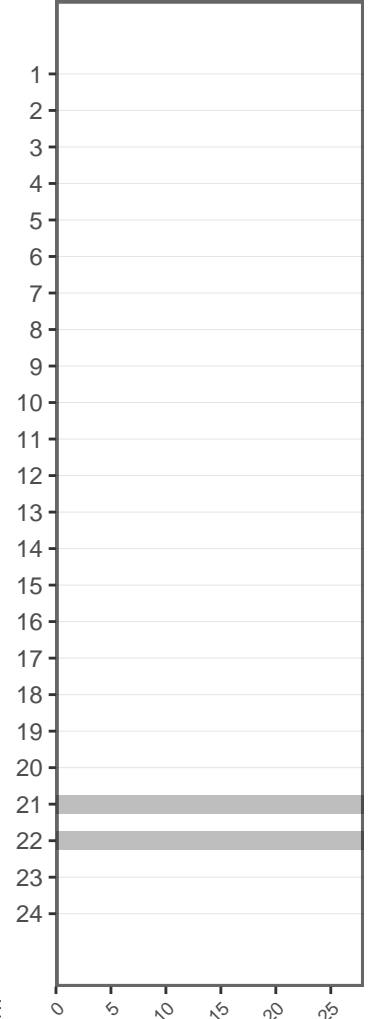
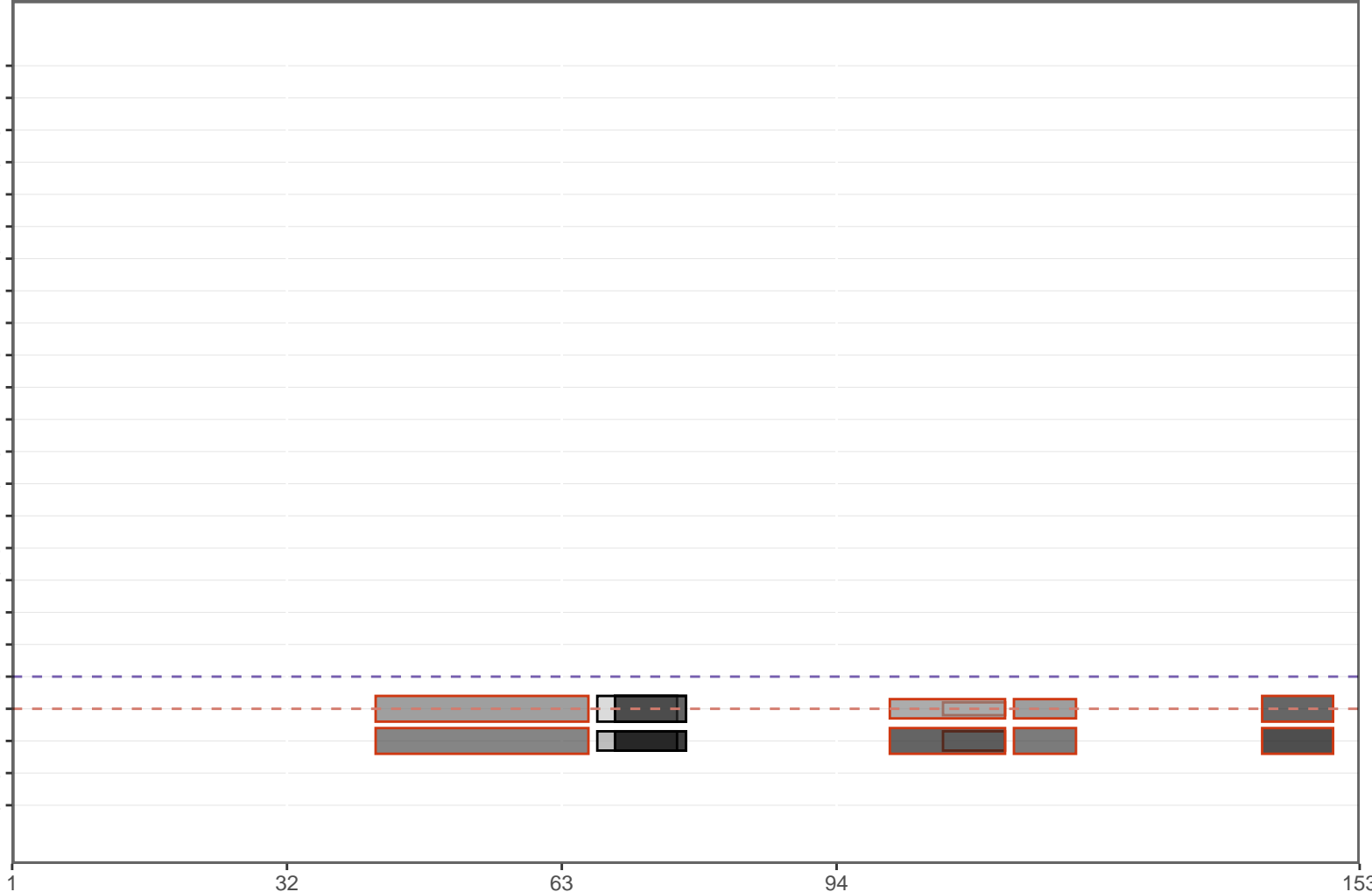
MW indication



Molecular weight

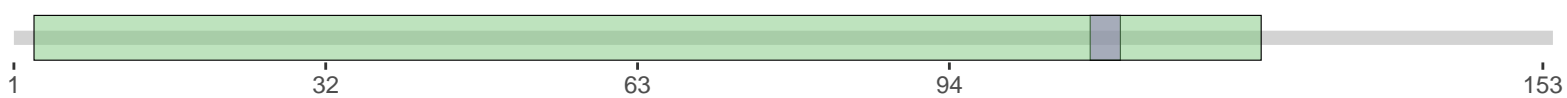


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

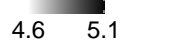
NAAYKEKFYSDDEKRWKVEVEGGVLDLGGFYGKFEVIEKDDNLGIVKISIDFETHDAENHLTVGLQAFIAMKATVEYFNGKSKY

NbL13g01500.1 S-norcochlorine_synthase_1-like [MW = 17.21 kDa]

No. of times detected



log(intensity)



Values from



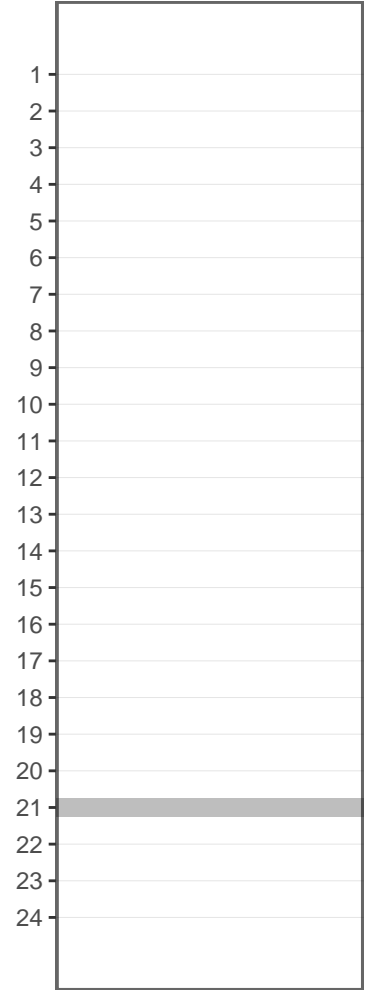
MW indication



Molecular weight



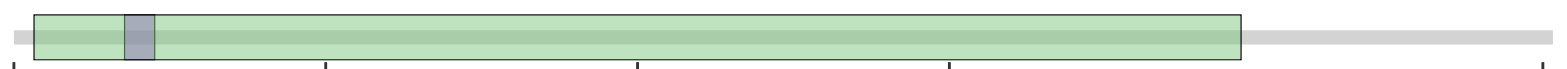
Gel Slice



Peptide counts over 4 repeats

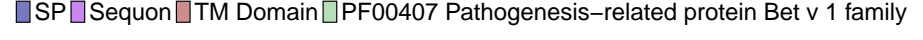
1 32 63 94 153

Protein length



Pfam domains

Pfam Description

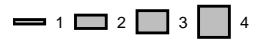


Protein sequence:

YKEKPYSIDDEKRWKEEMVEGGYLDLEFSYGGKFEVIEKDENSGIVWITGSETKDAENHILTGNPTVFAIKATVEYFENEKNGM

NbL13g01480.1 NADP-dependent_glyceraldehyde-3-phosphate_dehydrogenase [MW = 53.27 kDa]

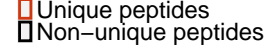
No. of times detected



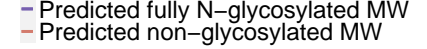
log(intensity)



Values from

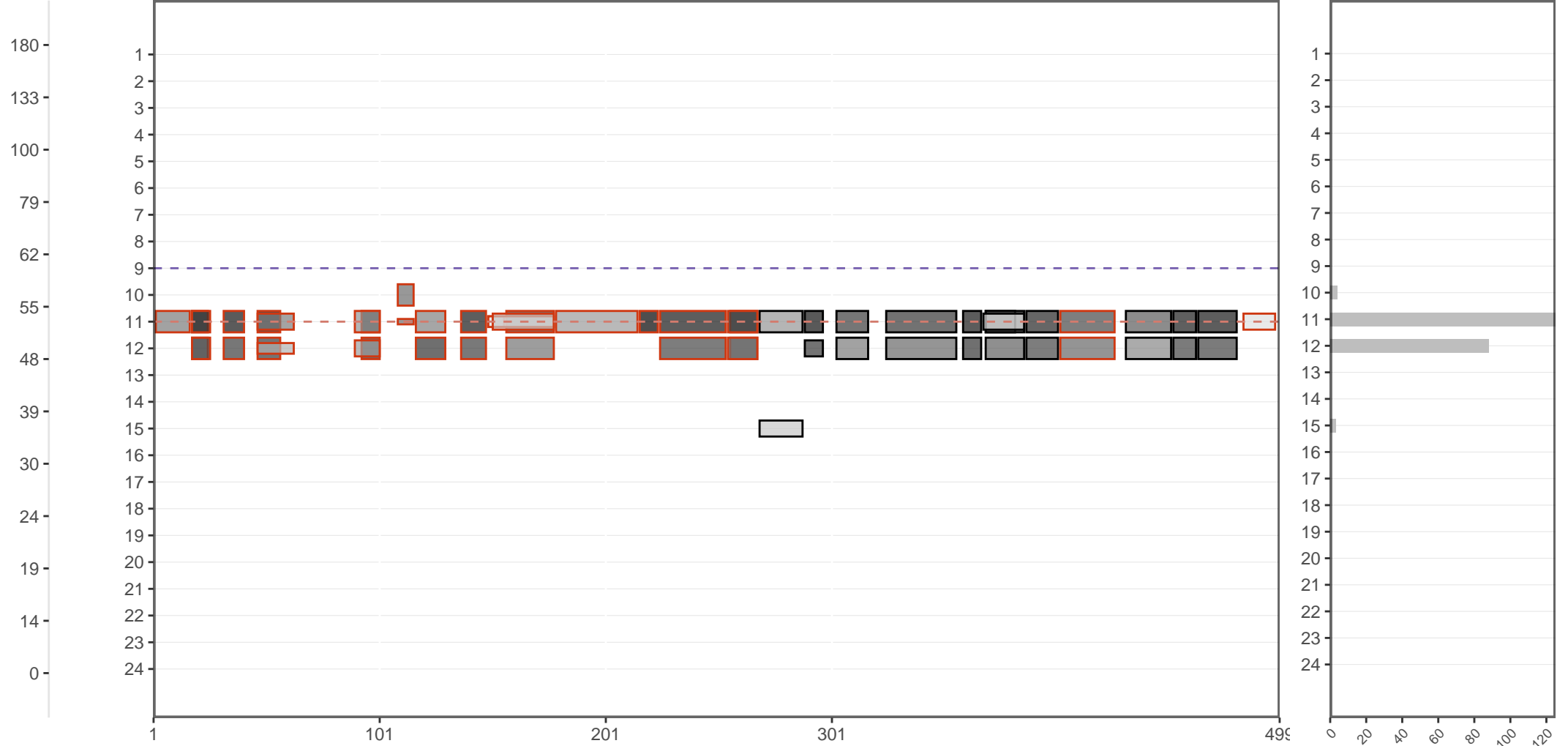


MW indication



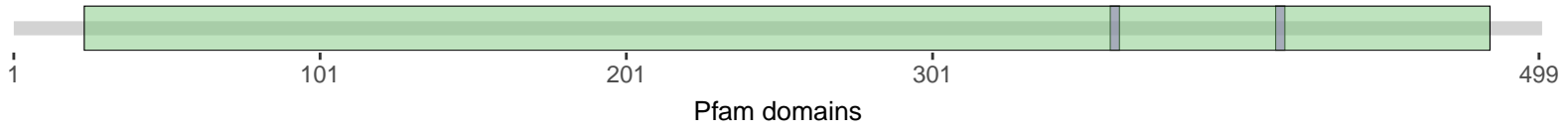
Molecular weight

Gel Slice



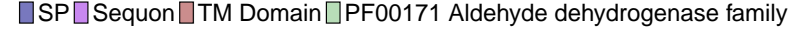
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IVHCISFTGGDTGVAISKKAGMPLQIMELGGKDACVLEADLDLAAAGSIVKGGFYSGGRCATKVVYLVMSGVADALVEKVAKVKVLTGVPPEDDDDITPVVSESSANFIEGLVMDAKKNTATFGQYKREGNLWPLLDLNVRPDMRIAWEEPFGPVLVIRISVEEGRHONANFNLOGGVFTDKNKALISDAMETGTVQVINSAPARGDHPFFGQIKDGGGGGGTNSINMMTKVKTFTVWNLPTPSTYTMGKL

NbL13g01230.1 serine_carboxypeptidase_24-like [MW - SP = 49.48 kDa]

No. of times detected



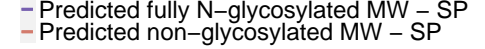
log(intensity)



Values from



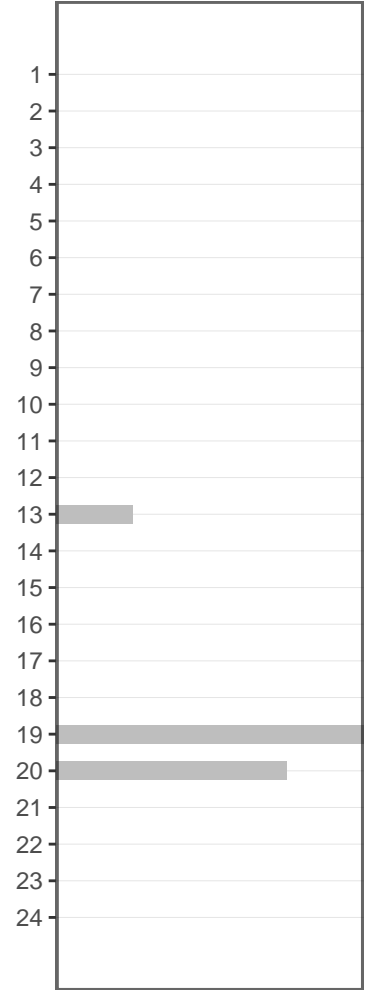
MW indication



Molecular weight



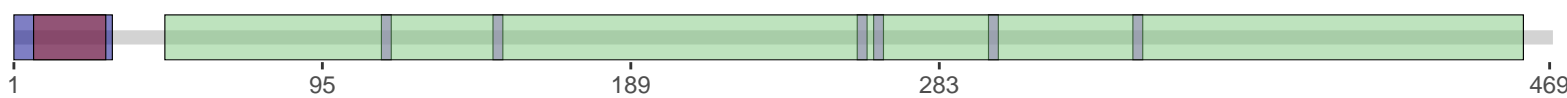
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

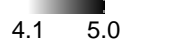
TDNKYDGGTYTYWWSHSMISGDNITKIMHSGNFTSEMSKQCDNAVTVWSHEFGIDGYSIKTSPGKVEQNETGKYVRFKNTIHRKLGSDYDPCENYAEKYYNRADVGRAMHANTTGGISWTCAGDITLLKNWKGSDSDMLPIYKIKLMAAGLRHWVWFGSDTSGVVPVTATRFSLKHLNKKIKTPIWYFVYVSGGQVGGWTEVYDGLTFATVRGAGHEVPLFQPRRAFILFQSLAGKELPKV

NbL13g01170.1 shikimate_O-hydroxycinnamoyltransferase-like [MW = 48.36 kDa]

No. of times detected



log(intensity)



Values from



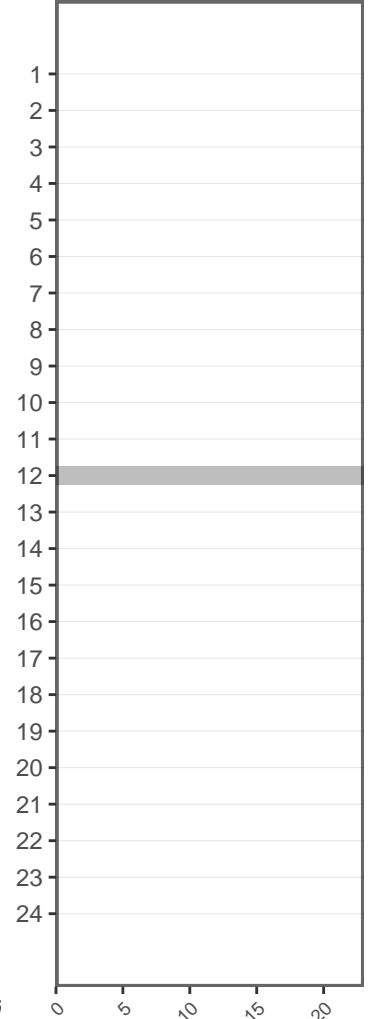
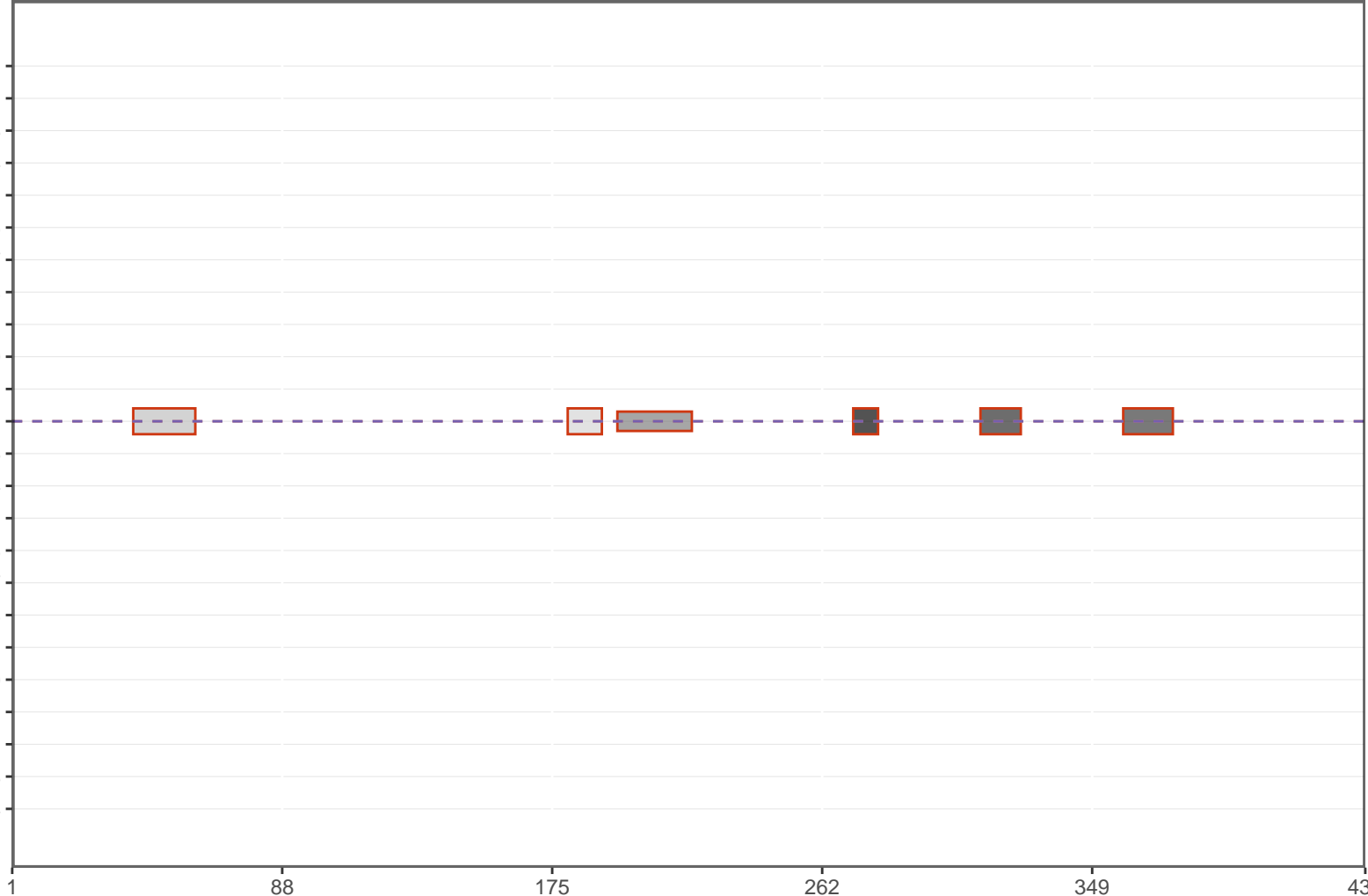
MW indication



Molecular weight

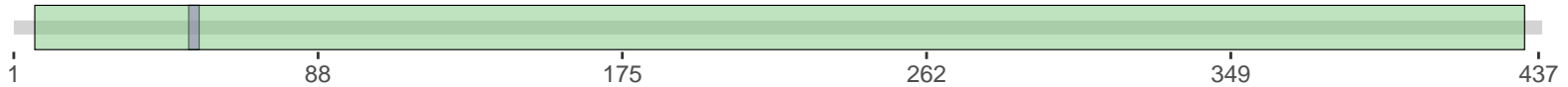


Gel Slice



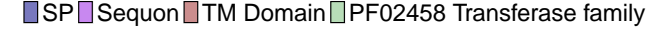
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VEYHPPPSLSSSKTKKESTSPKPTTAMFKFSSDQLGLLKSKEHEGTYEILAAHWRCTKARALSDDQLTKLHWATDGRRLCPPLPPGYLVNVTATPKMAKSSLEELLEPTNSAKRHSSLSKMDNDNYLRSALEKLELQPDLSALIRGPVAFASPILNINSWTRLPVHDEDFGWRPPIHMGPGILVGGTYVILPSPNKKDRNLRLVAGLDAHIMPLFEKYLVEF

NbL13g01120.1 eukaryotic_translation_initiation_factor [MW = 85.01 kDa]

No. of times detected



log(intensity)



Values from



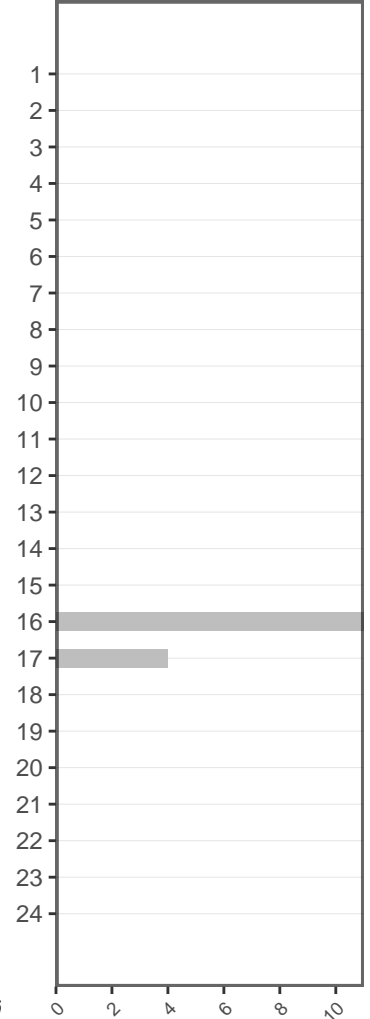
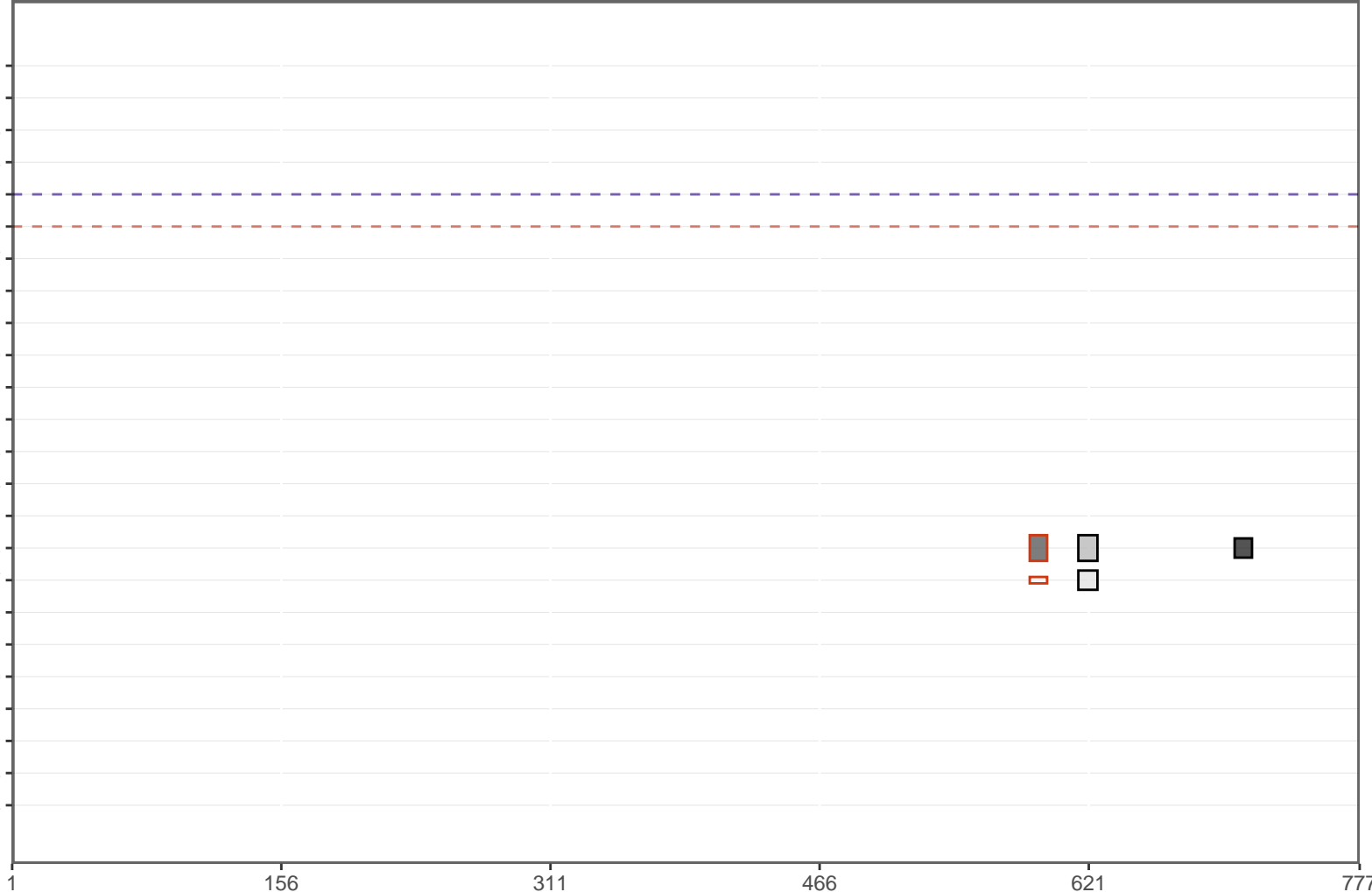
MW indication



Molecular weight



Gel Slice

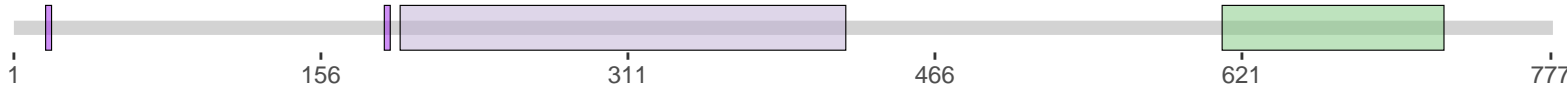


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

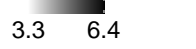
.DENOKSRRLNDVYFNRLKELSTNPQLVRLSFMVRLDLRLSNVWVPRREEVWAKTTEHTEAEKTLGLRPGATASMRNSRGPPSPQGSLSGGYVPMNRPTGGMMMPGMPGARKIPGMGMNDNDNVEVPRSRMPPRNGPMVQPGGRGPPPLVKGPSLNPRLLPQGGGGVSGRPSALLGGGGAPNRPGLGYGFMERFASGVPVRSPTTSPVAEKAPQAPARSNPDELKRKTASLLEEVFVRLLDGALQGVLEELKSPVHPVWKEAISGLDKSPRR

NbL13g01090.1 translation_initiation_factor_IF-3_chloroplastic-like [MW = 30.09 kDa]

No. of times detected



log(intensity)



Values from



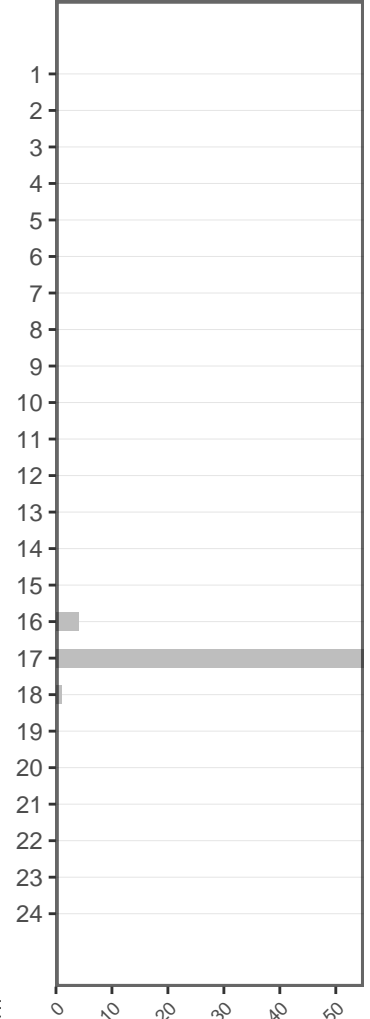
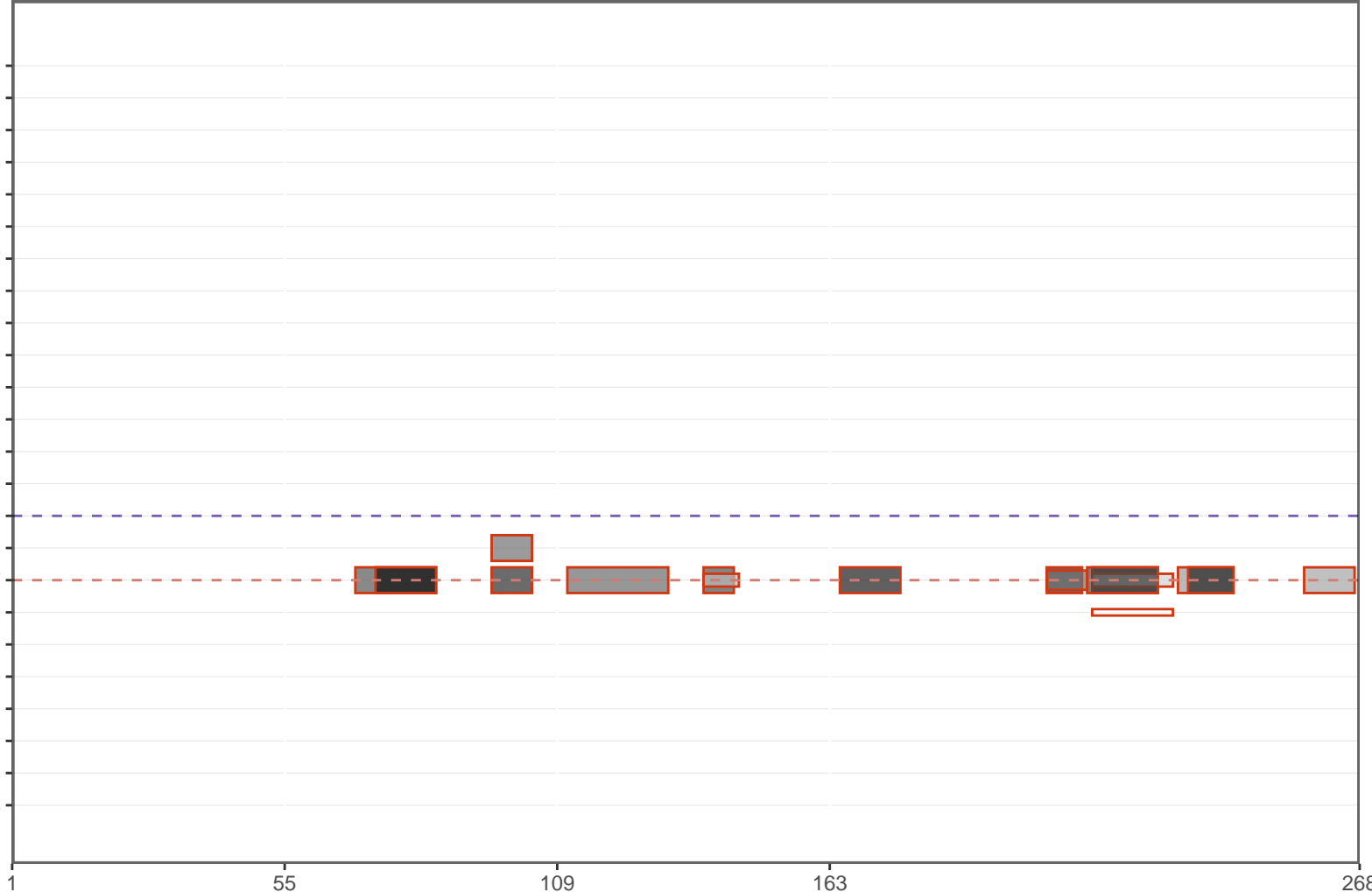
MW indication



Molecular weight



Gel Slice

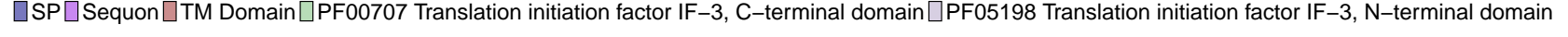


Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

IPKADPPVYKMDYKRYKVELGKRRKGGKKNAAAGRMDLKELKMGVYNDSDHYVRLRAAGKFLKDGDKWIKVNLKGRNEFRNNAELIKRFQNDIGELATEENKSFDRDMMFVLPNKAIVKQKGGKPKKESKATEVSAASV

NbL13g00950.1 serine_carboxypeptidase_II-2 [MW - SP = 50.12 kDa]

No. of times detected



log(intensity)



Values from



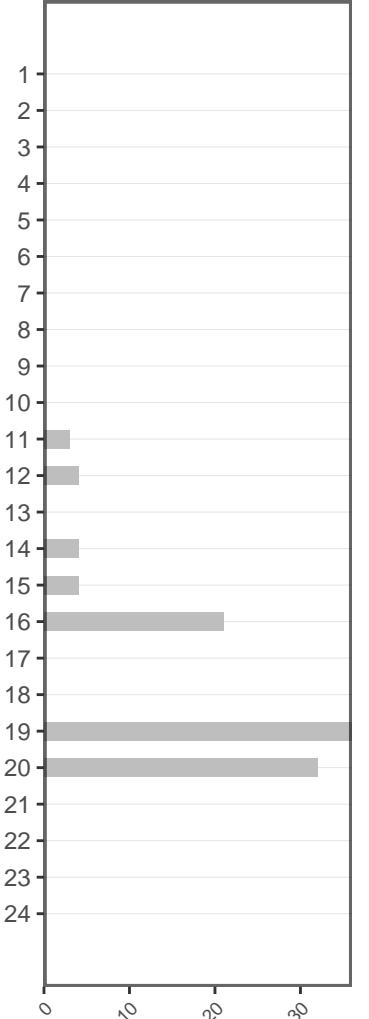
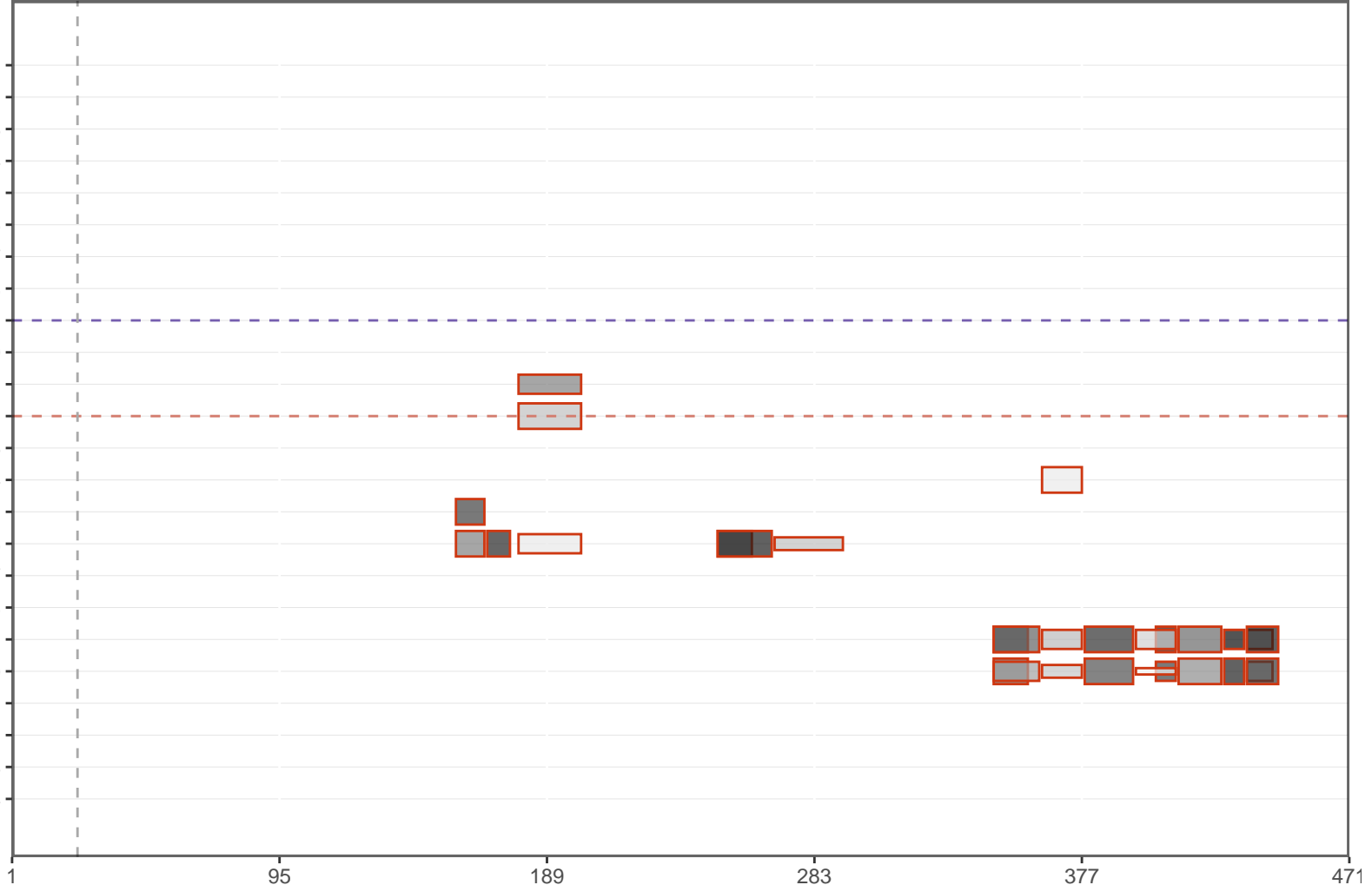
MW indication



Molecular weight



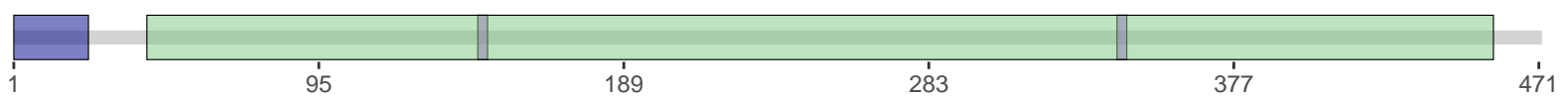
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

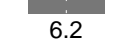
LTDDYIHILGLFCFMVBSGAMISDGTFRKANALGDYQSRIRPSEGGDKLDAQANEEVGNIDSYIFPTGTAKFSLANLLKRSSKVGHLRRSDVDPCTEGHGVYFNLPEVQGLHVKRNSFKWVTCSEEVSSGVDKSPKGVLDVYHEHLHSGLRWVFSGDTDSKVPVSTRYSIDALKLPTVGPWRWVAYDGGQVGVGWVTEYKGLTFVTRGAGHEVALHRPKQALTLVKVFLAGAMPFLGGISDS

NbL13g00890.1 50S_ribosomal_protein_L35_chloroplastic [MW = 17.15 kDa]

No. of times detected



log(intensity)



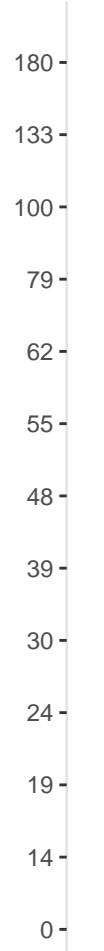
Values from



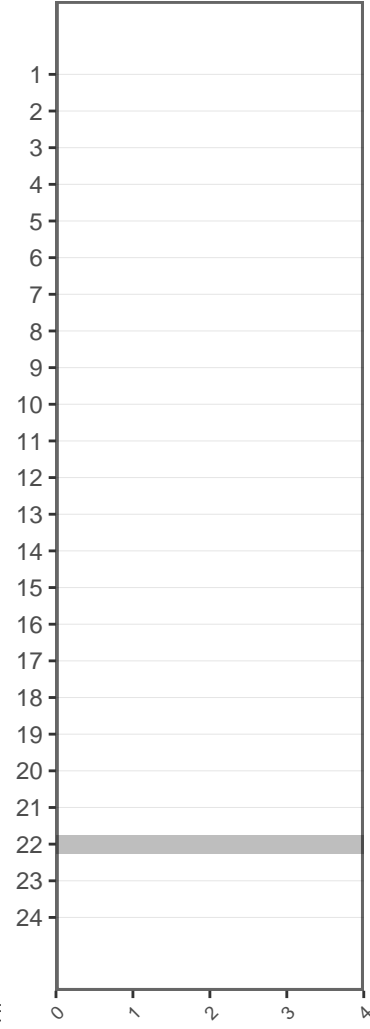
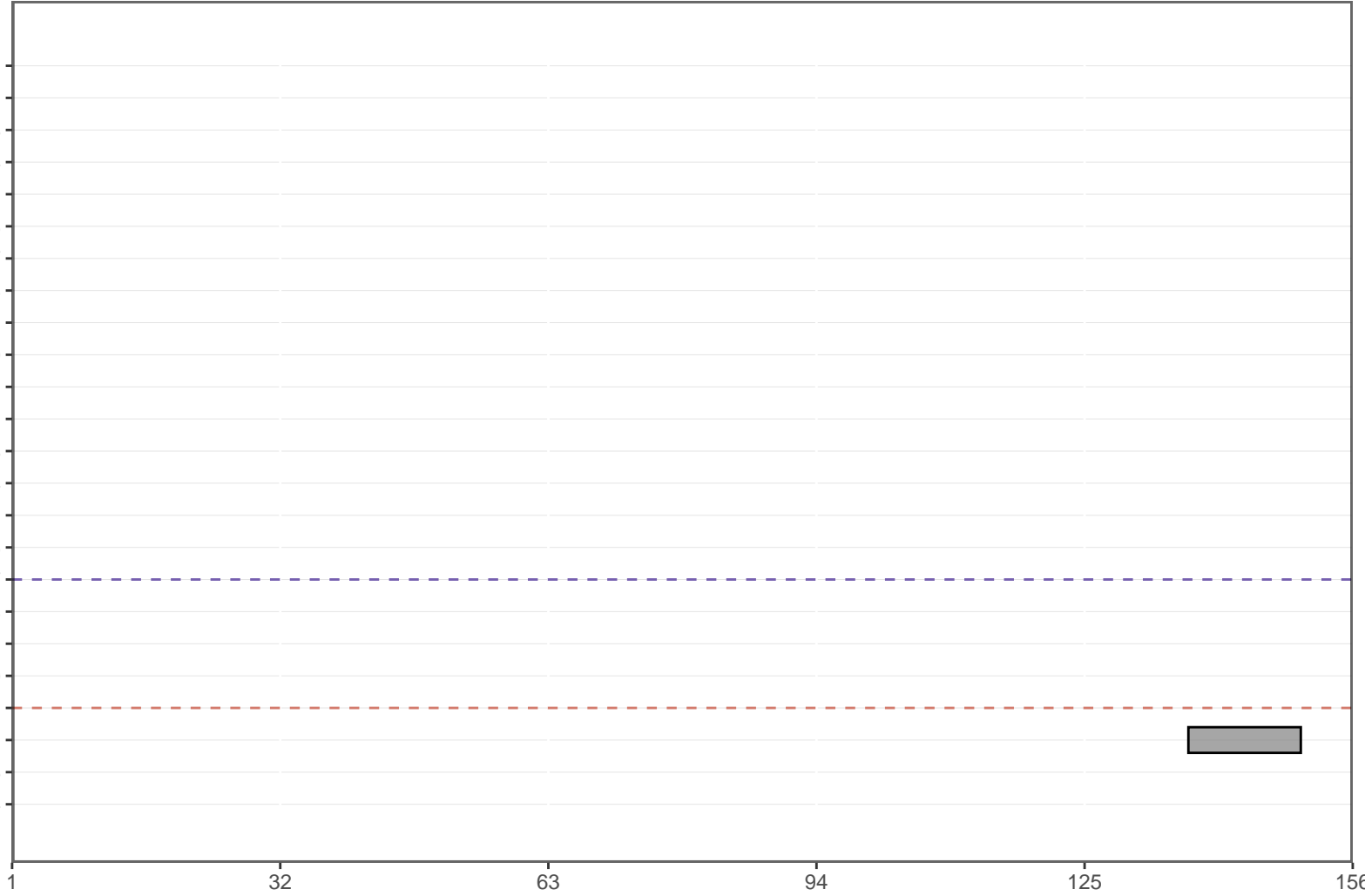
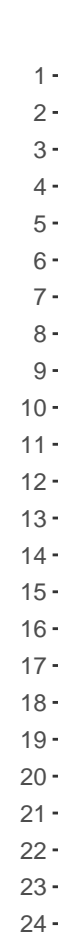
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

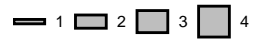


Protein sequence:

ATPTSGNPLPLTVVCAKGGYKMKTKKAKAKRFKVGSTGKILRRRAAGKHLRKKNAKRRNRRLSKTVGVDRSDYNNVIGALPYLKVNRAN

NbL13g00860.1 clustered_mitochondria_protein [MW = 202.18 kDa]

No. of times detected



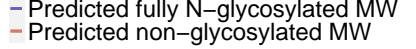
log(intensity)



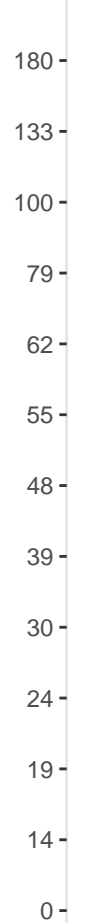
Values from



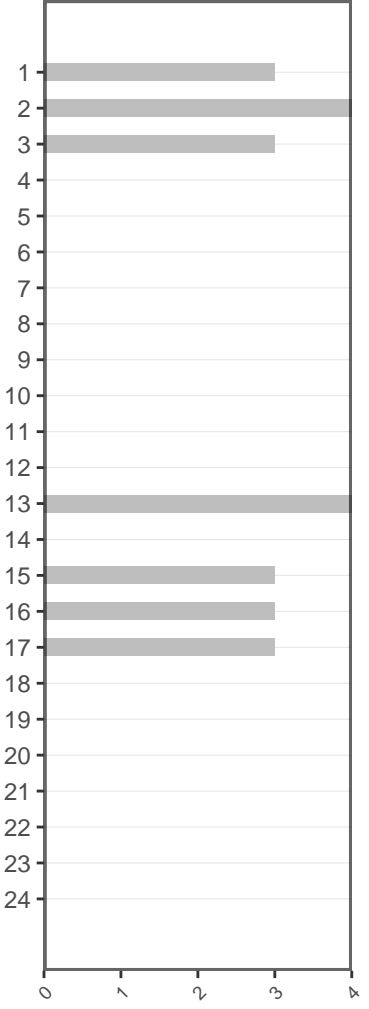
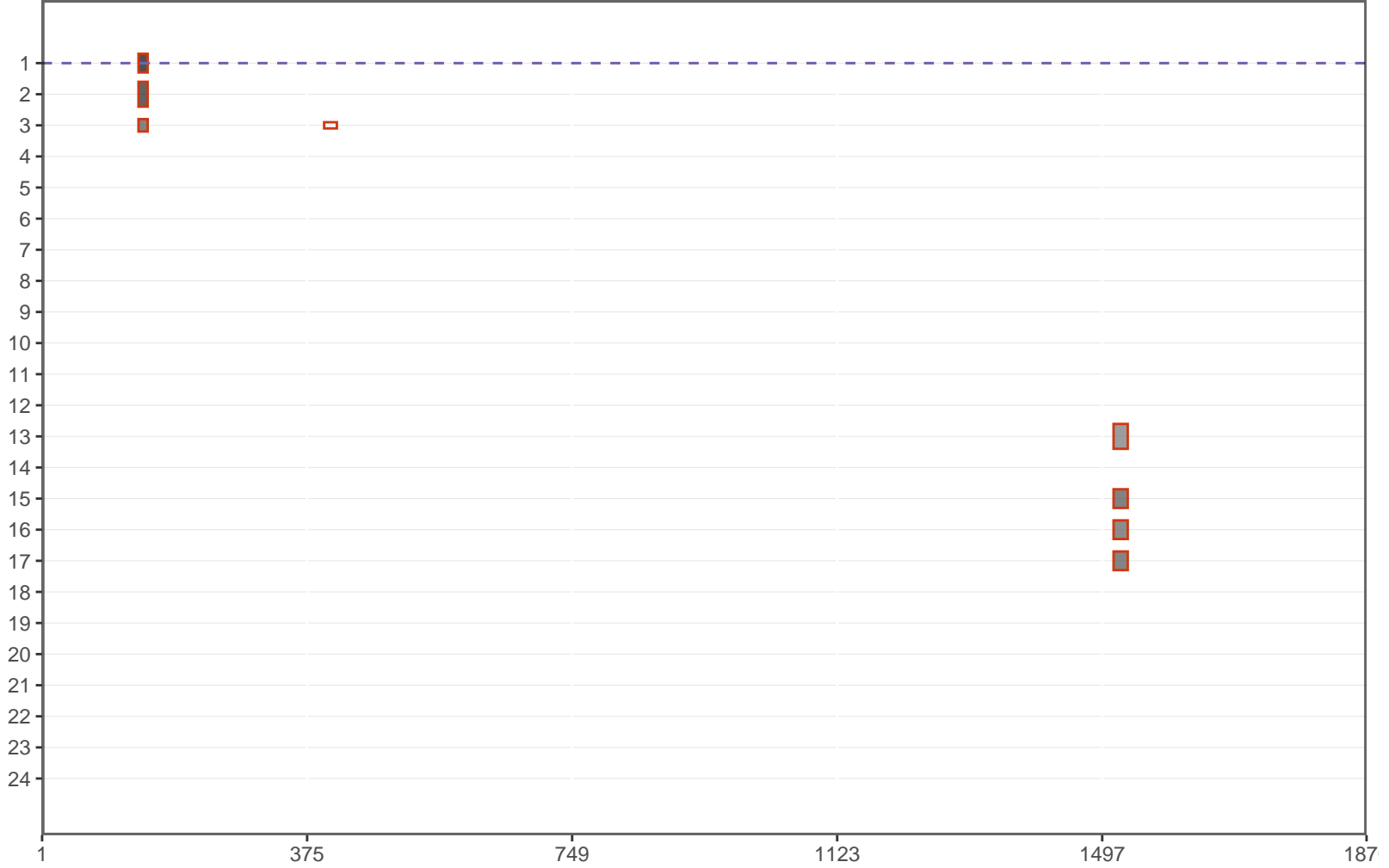
MW indication



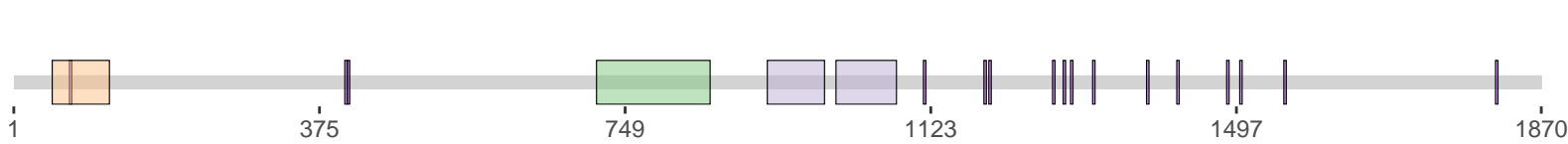
Molecular weight



Gel Slice

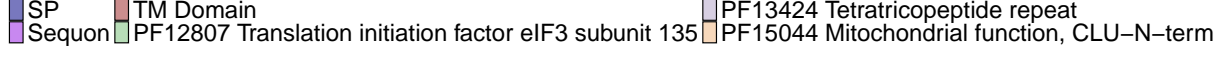


Protein length



Pfam domains

Pfam Description



Protein sequence:

IGAYSLAVLYHTGDFNATHYGGKALDNERELGLNHPDPTMKSYGSLAVFYRLGHTLALKYVNRALVLLHLTGGPSHPNTAATYVNWAMMEGLGNVHVALRYLHEALCKNGRLGADHGTAAVYHAAALSLMEAVSLVQVHEGFTLQILQAKLGPDDLRITGDAVAWLEYLESKALEGGEAARNGTTPKPDASISKGLHLSVDLLELYAPDAEMKAREADKKQARTKVKGKAGNGGATDEFEKDELLSPVWENSSDKENKSELNKGELQADSTPKPSDHL

NbL13g00810.1 putative_GDP-L-fucose_synthase_2 [MW = 37.46 kDa]

No. of times detected



log(intensity)



Values from



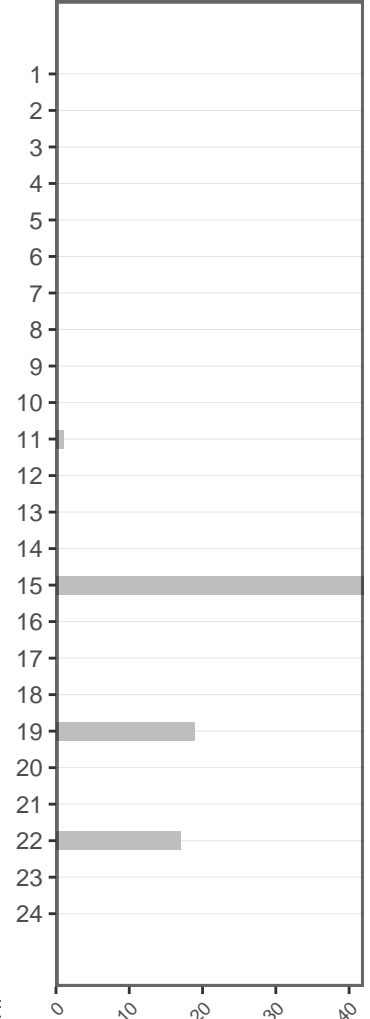
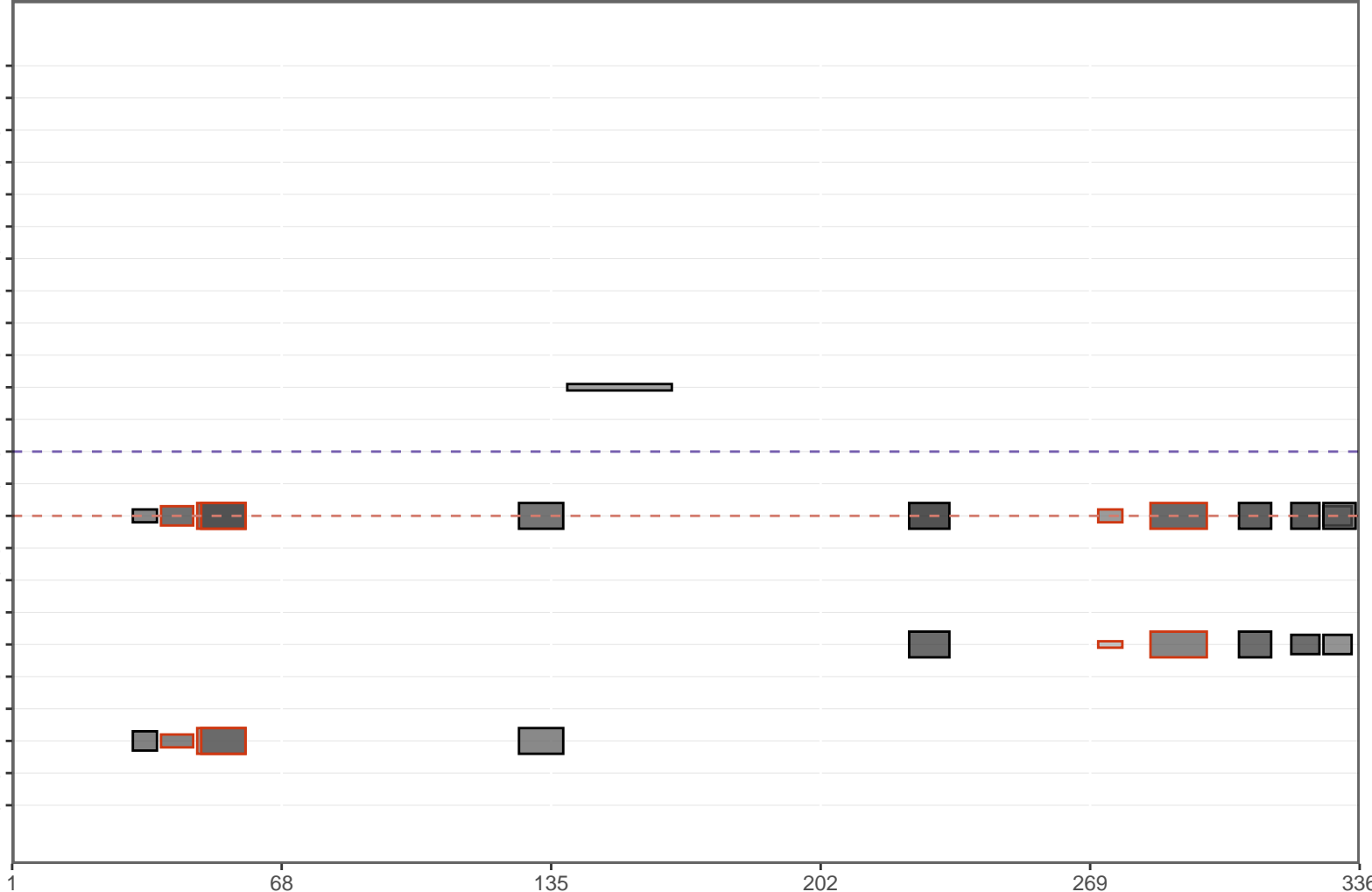
MW indication



Molecular weight

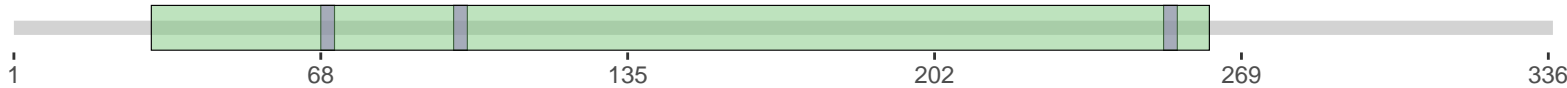


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

NEWYAAKAGKAGAGYRLQHFDAEMPTNLVGTNDNFHPENSHVLPALLRRFHEAKINLQKVVVVGTGSPFLREFLHVDDLADAVIFLLENYSDLEHNVYGGSEVTKELAEIKEVYFGKGLVDSKPDGTPRKLMDTEKLVGLGWTPKIKLRDGLVDYKWLLENYGGQ

NbL13g00690.1 tetratricopeptide_repeat_protein_1-like [MW = 30.94 kDa]

No. of times detected



log(intensity)



Values from



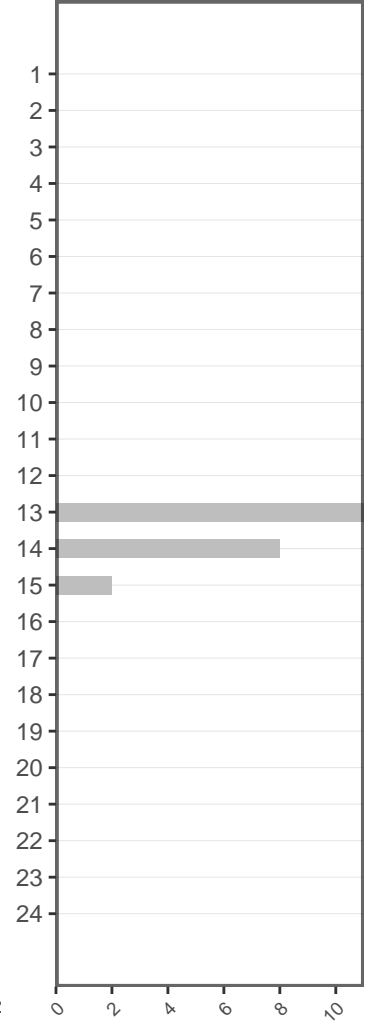
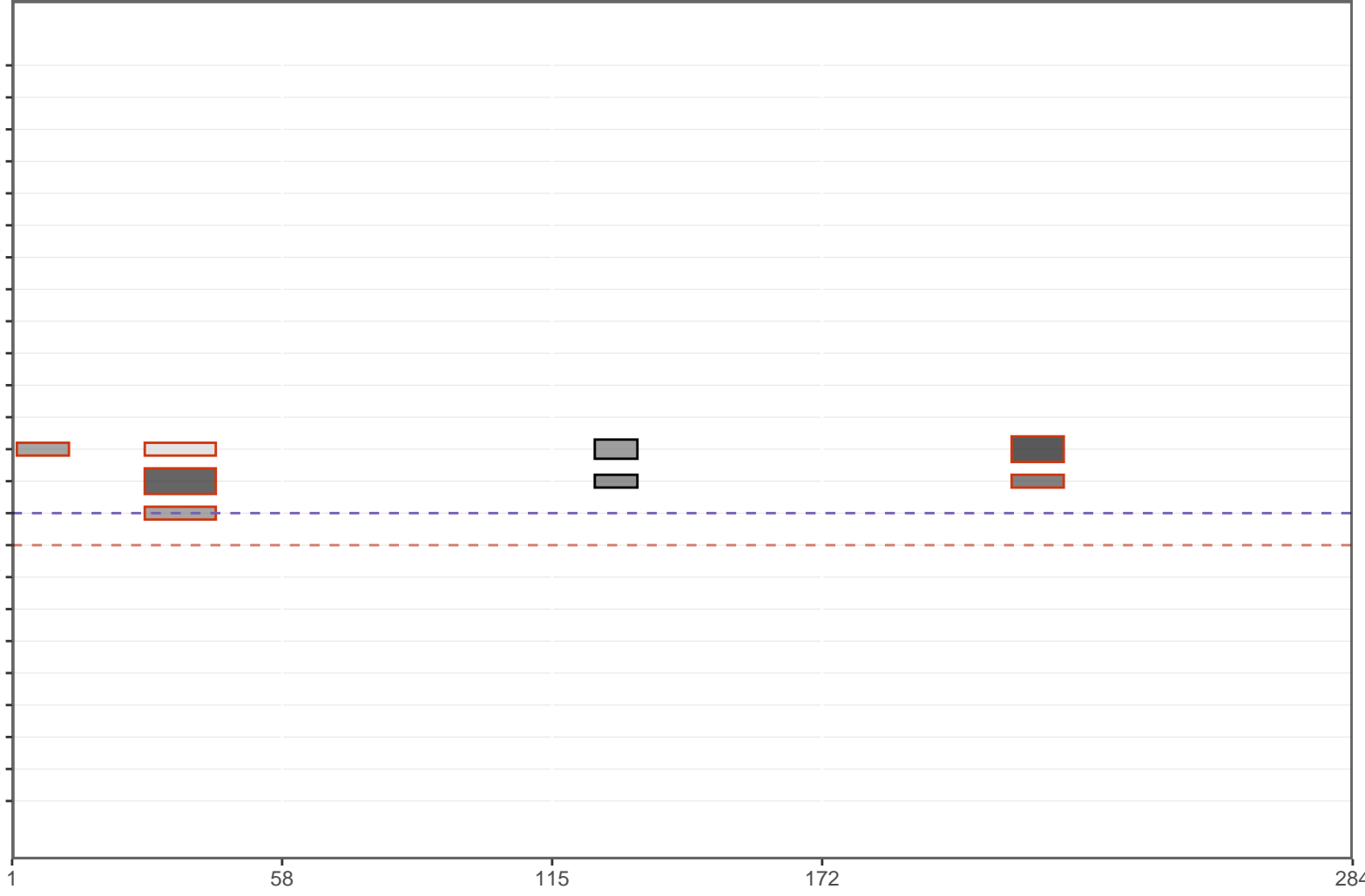
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

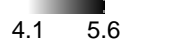
EEALSKYELAQVADIPGSTEIRBIGHANRAAGFSKLGKHGETKECTKALELNPTYMKVALVRRAEAEHEKLEHYDEATDMTKILELEPNDQVRRSVMRLKPLADEKREKMKKEEMIGLKEKMGNSILGRFGMSVDNFKAVKDPNTGVSVSGFK*

NbL13g00670.1 HD_domain-containing_protein_2 [MW = 29.64 kDa]

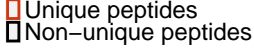
No. of times detected



log(intensity)



Values from



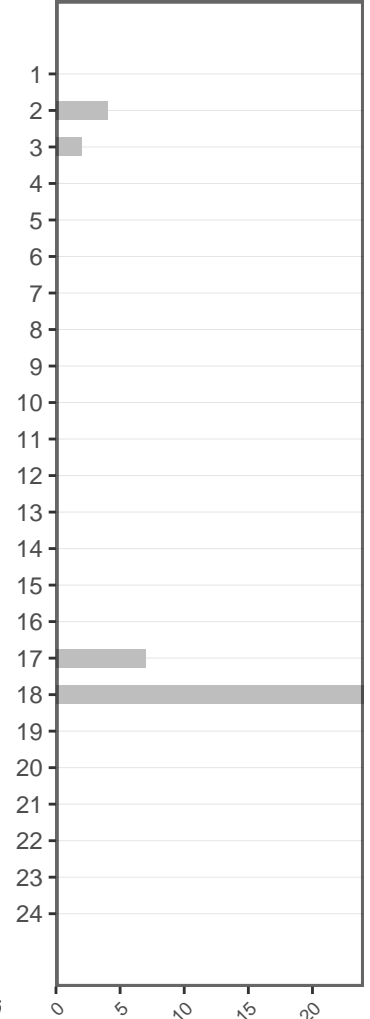
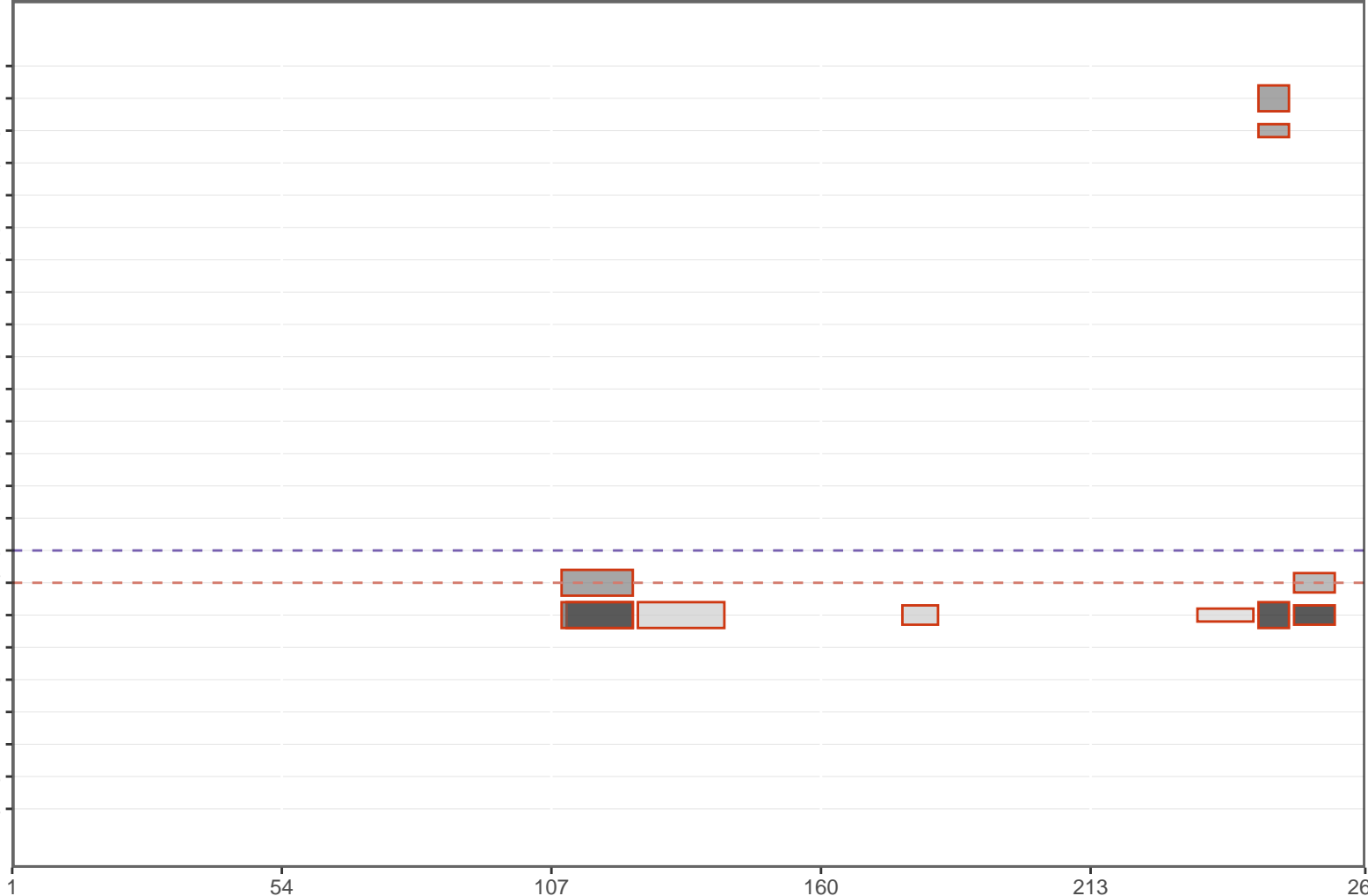
MW indication



Molecular weight

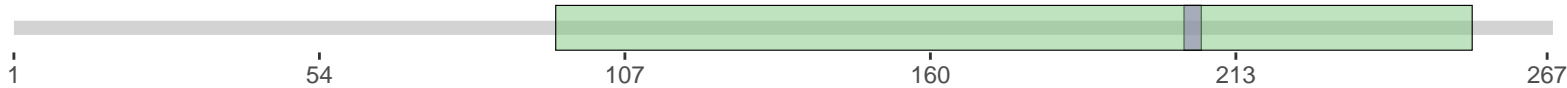


Gel Slice



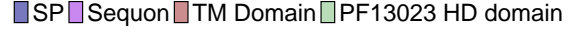
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MYRIMGVMAIIADLPGVDRDKGVMAIVHDIHEAVIGDITPADGHSKDEKSRERRAALEDMDCKLLGGGFRAKEISDLMVEYENSLEAVVDFDKVEMILQALEYENEGGKLEEFFGTAKGFDVGVKAAVEVASRRKKSN

NbL13g00490.1 defensin-like_protein [MW = 18.28 kDa]

No. of times detected



log(intensity)



Values from



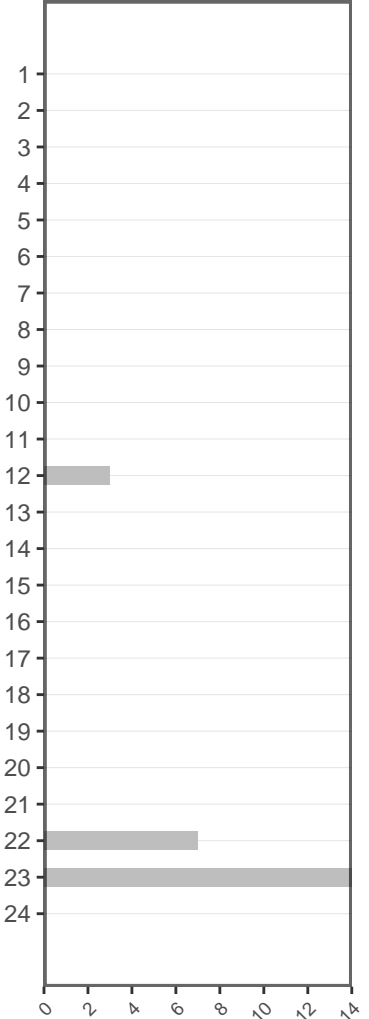
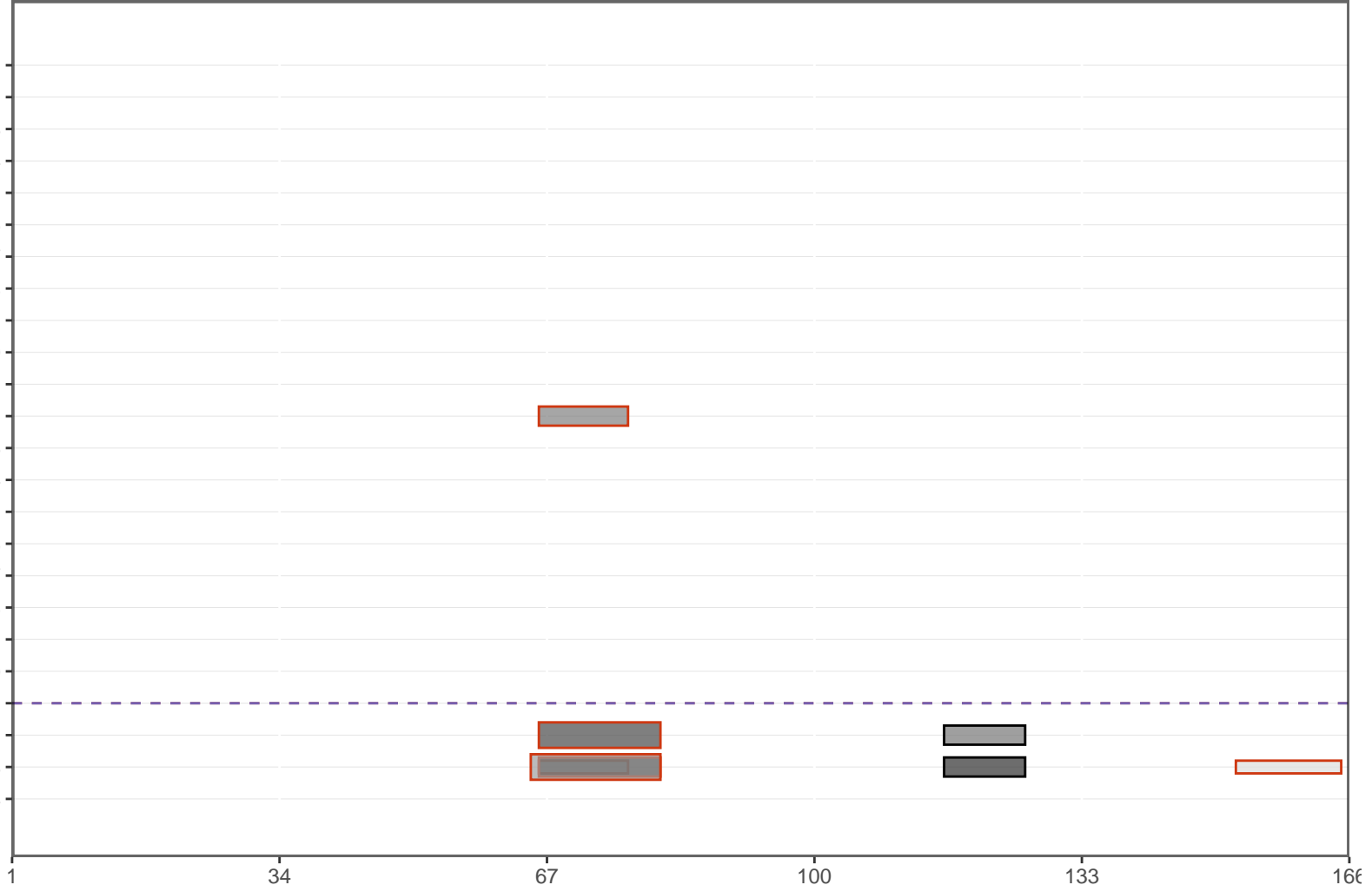
MW indication



Molecular weight

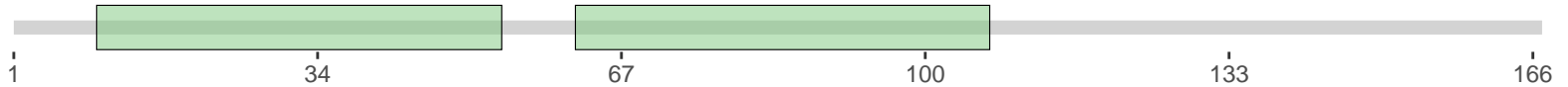


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

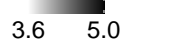
FFPGICLTQPPCRKAGISEKFTDGHGSKILRRGLGTQPCVDFDEKMKITGAETLAEAEAKTAAALLEEEMKKTGAETLAEAEAKTAAALLEEEMDN

NbL13g00410.1 adenylosuccinate_lyase-like [MW = 61.29 kDa]

No. of times detected



log(intensity)



Values from



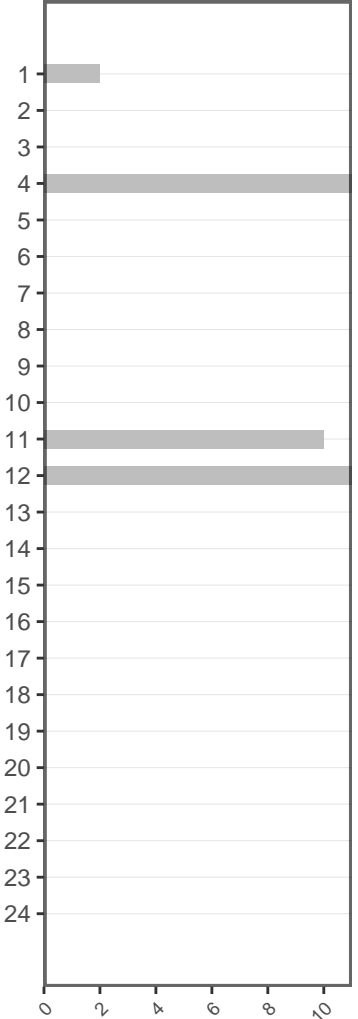
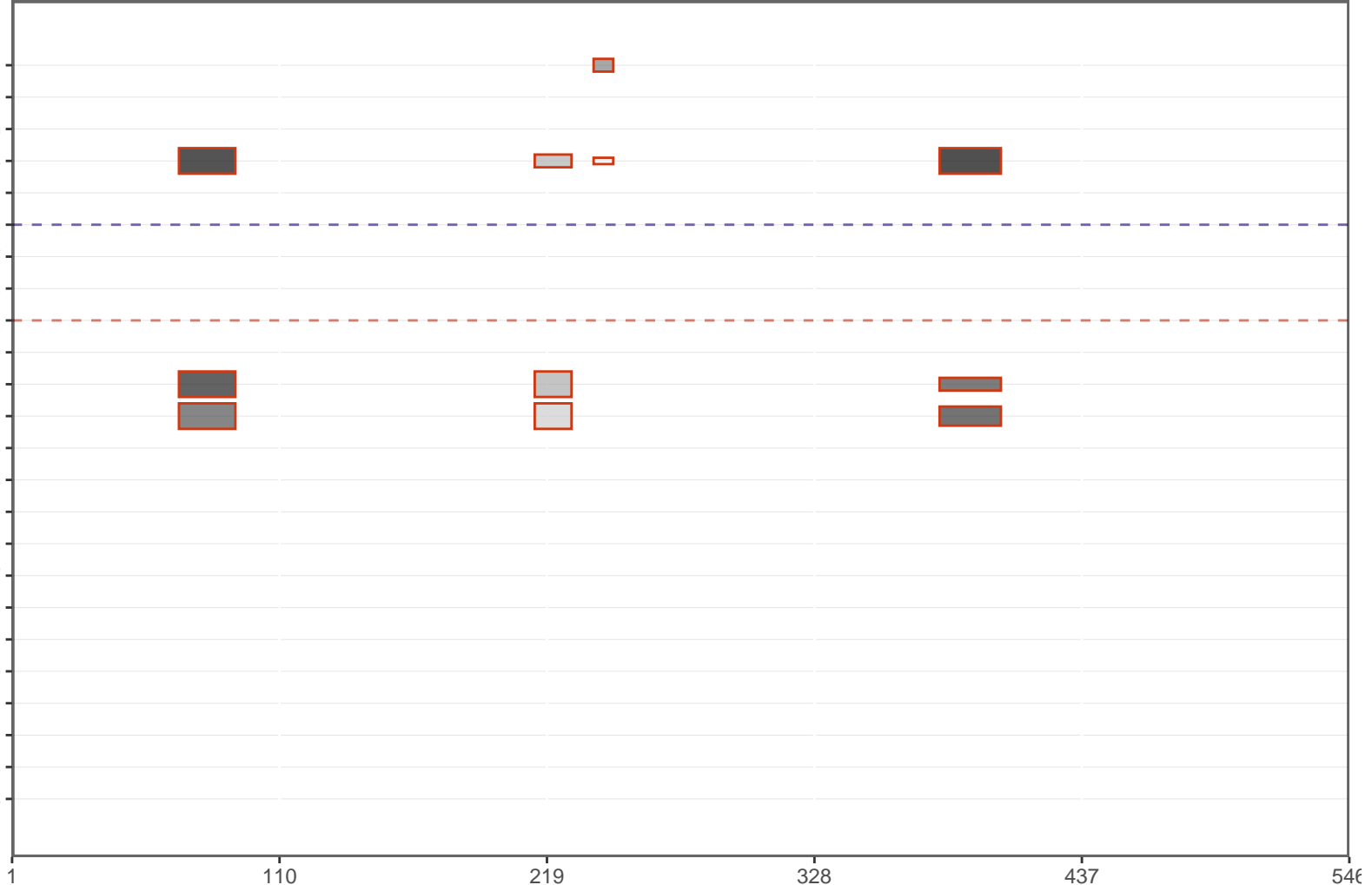
MW indication



Molecular weight

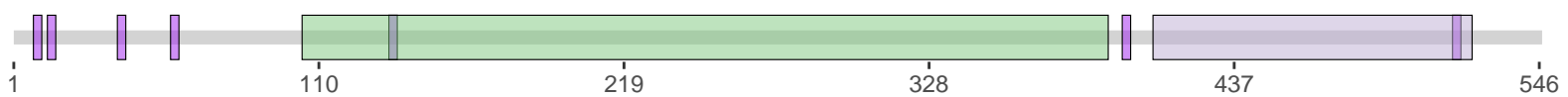


Gel Slice



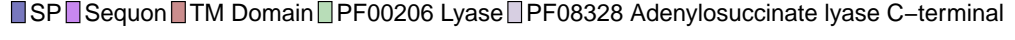
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IMAFYRLSRERKEISQEMLKGKAGVGNYNNAHVAAYPEVNWPKQAEFVMSLGLKFNFPYVQIETHDYMALFLHSIVGFNLLVDFDRDVAWGYSLSLGYFKGQTKKAGEISSTMFHKVNPDFENSEGNLGVANGNLSHLNKLPSRWQRDLTDSFLRNMGVGLGHLAYRSALGGQIKLGVNEAALSEDLKQWEVLAEPQGTVMRRYGVPEPEYKLVKTRGRVTYKIEKREFIKLQIPADAKTALLNLRPHYVGGAAELAKNNVAINLENGAQIF

NbL13g00400.1 50S_ribosomal_protein_L22_chloroplastic-like [MW = 30.11 kDa]

No. of times detected



log(intensity)



Values from



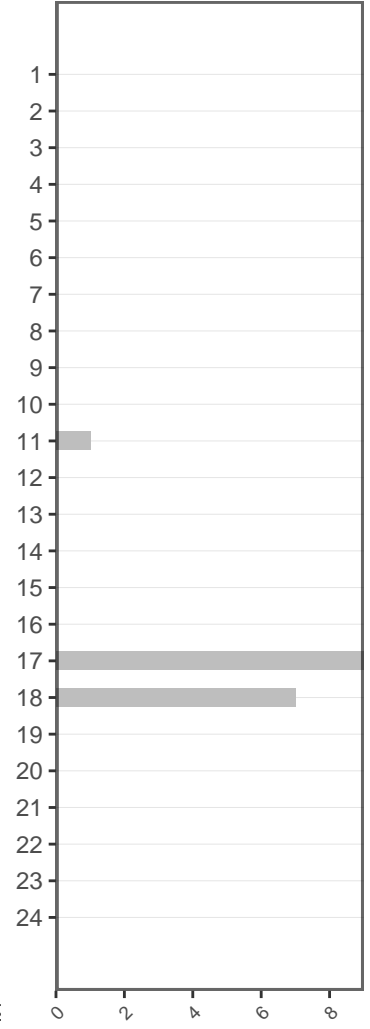
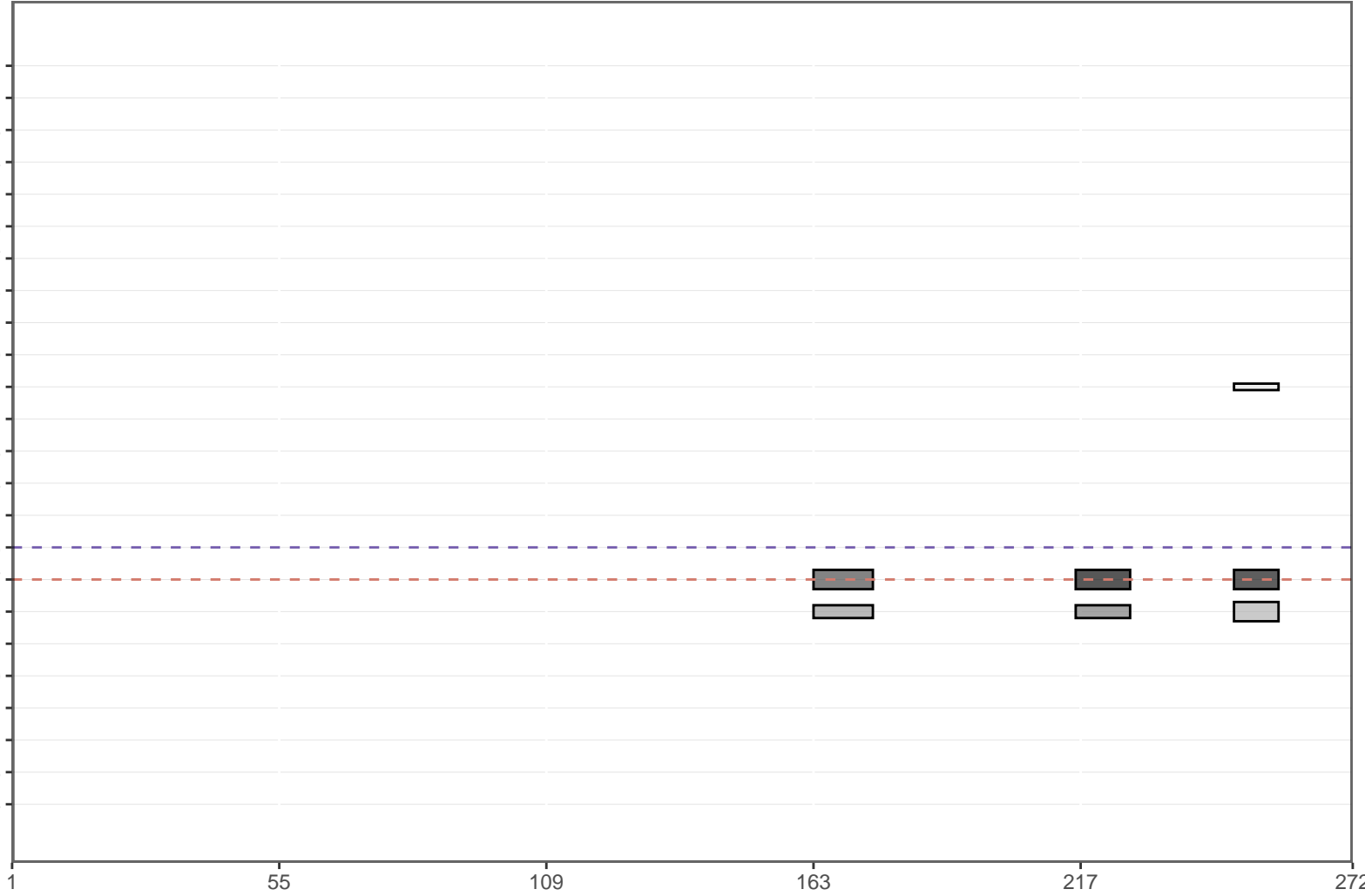
MW indication



Molecular weight

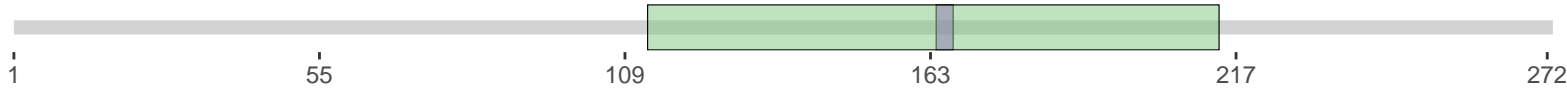


Gel Slice



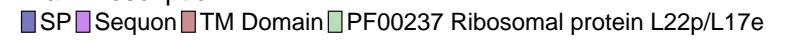
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

MSKLNLAALVLRGMREDEALLGLGWVKKRASKTYVQVHISARANATHNYGFDPPDRLLWAEAFVGGKGLFKKRVSYHAAGKGGKRVPECDRLTVVREITPEEEAEAKLRVHNFKRLTKRERRLVPHKLIETTPVWDRKGRAKNGSPGAAVA

NbL13g00280.1 xylose_isomerase-like [MW - SP = 50.72 kDa]

No. of times detected



log(intensity)



Values from

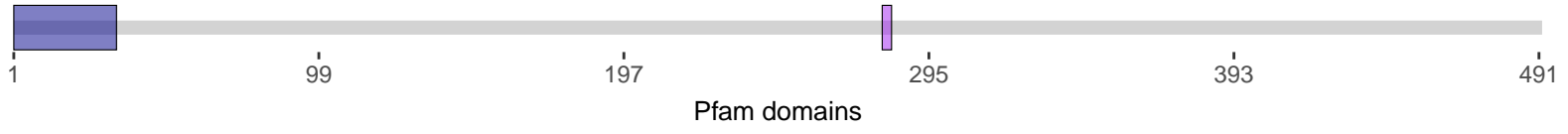
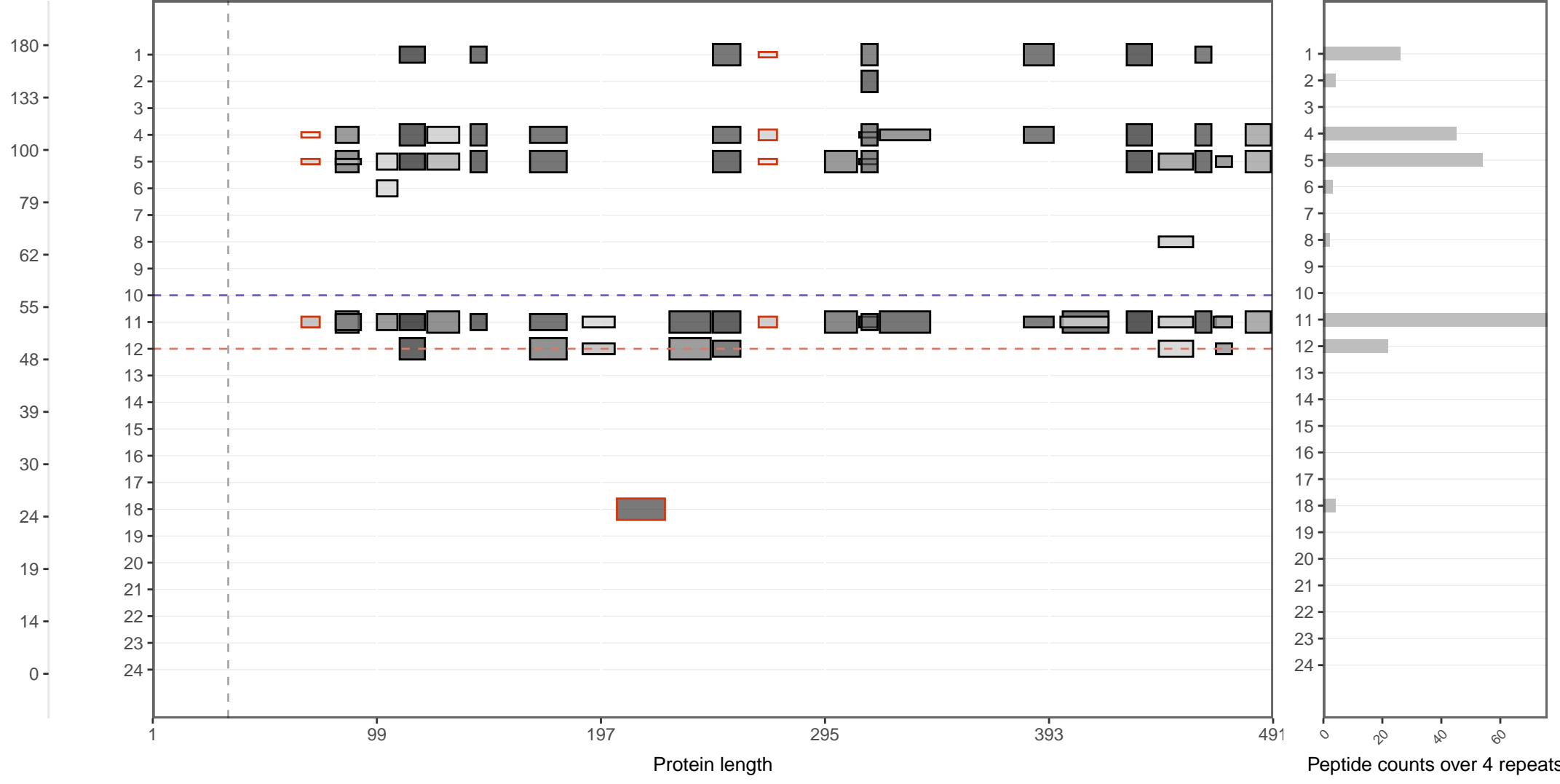


MW indication



Molecular weight

Gel Slice



Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

YLLGENYFVVGREGYQSLNLTDMRELDHMARFMEVAVWAYKKIKFNGTLIEPKPGEPTRKHQVDVDAASANFLRKYGLHGEFKLINECHATLHAGHSCHHELETARINSLGNDANTGDPQVGVWDTDFLMDVAEATLVMGTVIKNGGLAPGGFNFDAKLRRESTDVEDLFIHAGMDTLARGLRNAAKLHEDGSLGELVNRKRVGSDFTELGAAIEAGKADFELLEKKALEWGEPKVPSGKQELAEVFGSAL

NbL13g00260.1 salutaridinol_7-O-acetyltransferase-like [MW = 49.37 kDa]

No. of times detected



log(intensity)



Values from



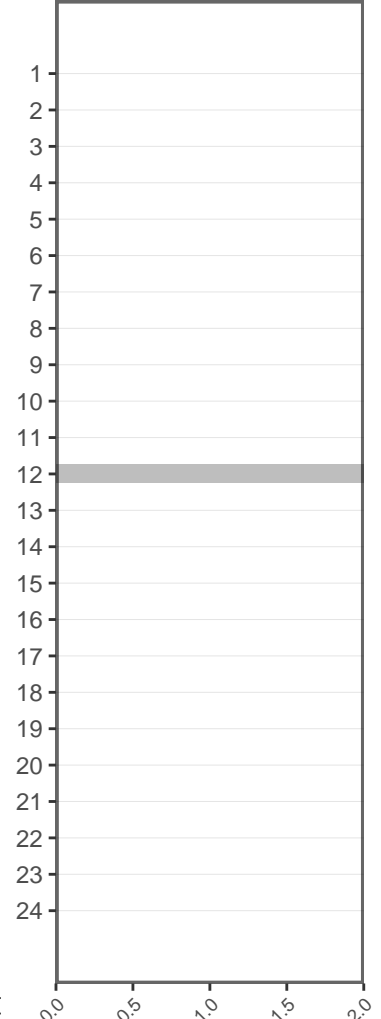
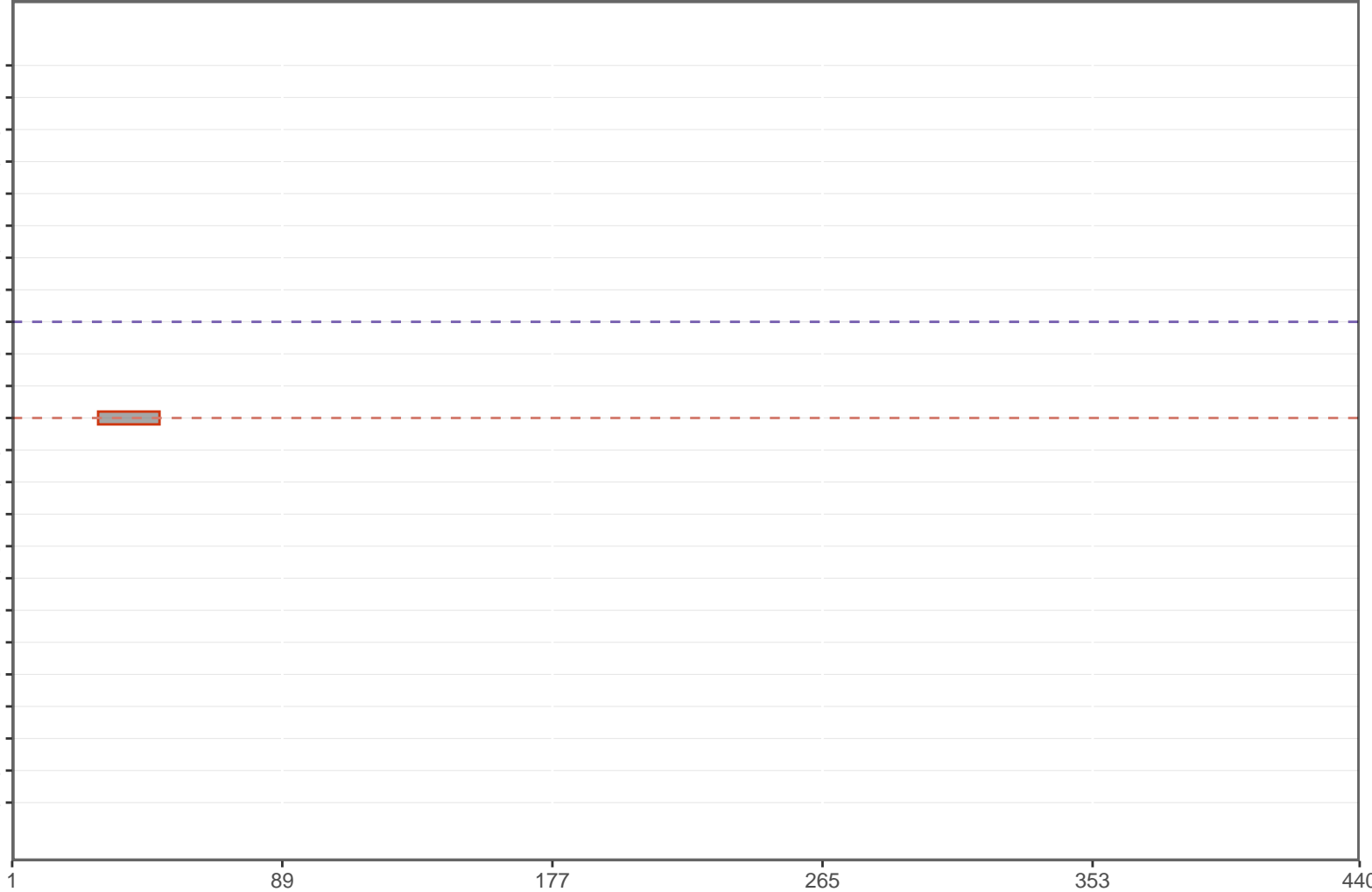
MW indication



Molecular weight

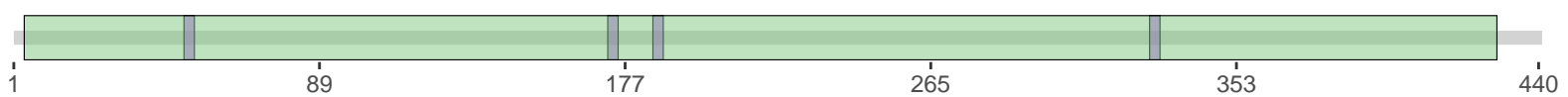


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KCAAIEPVVEKLVWRRIITASNIVMKSKVINSYGNKIKRERTRVEVITALLWGFMAKGCNSIAVLPVNRKRVKIVPLPENSGNFFLVSSAIGNVENEWFSLVGRKIKLIERIDGNYTEKIRGRNGFEFVYNNFKVGVKLLSGDDDKVLRIGSWNFPNGVYVFGWGEILPVALGVKDKHVLDSLSKYGGGIEAWVMTDQEMALFEQDKELQDFTSLDVSLL*

NbL13g00060.1 probable_xyloglucan_endotransglucosylase/hydrolase_protein_23 [MW – SP = 28.39 kDa]

No. of times detected



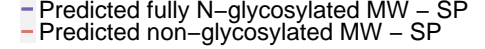
log(intensity)



Values from



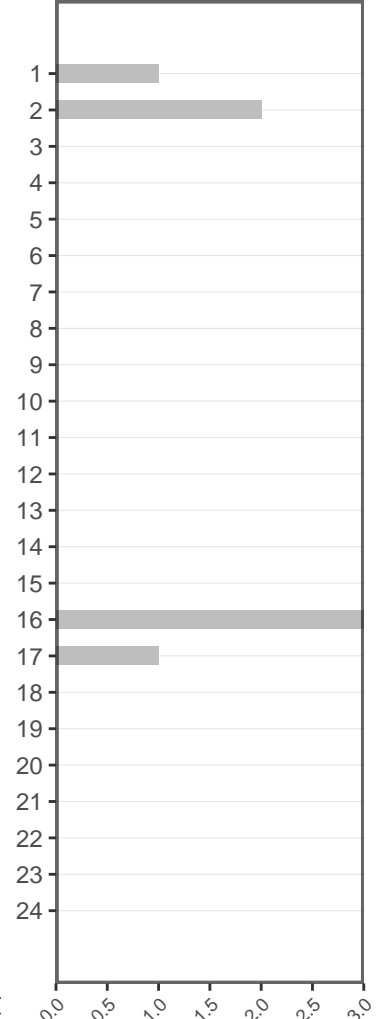
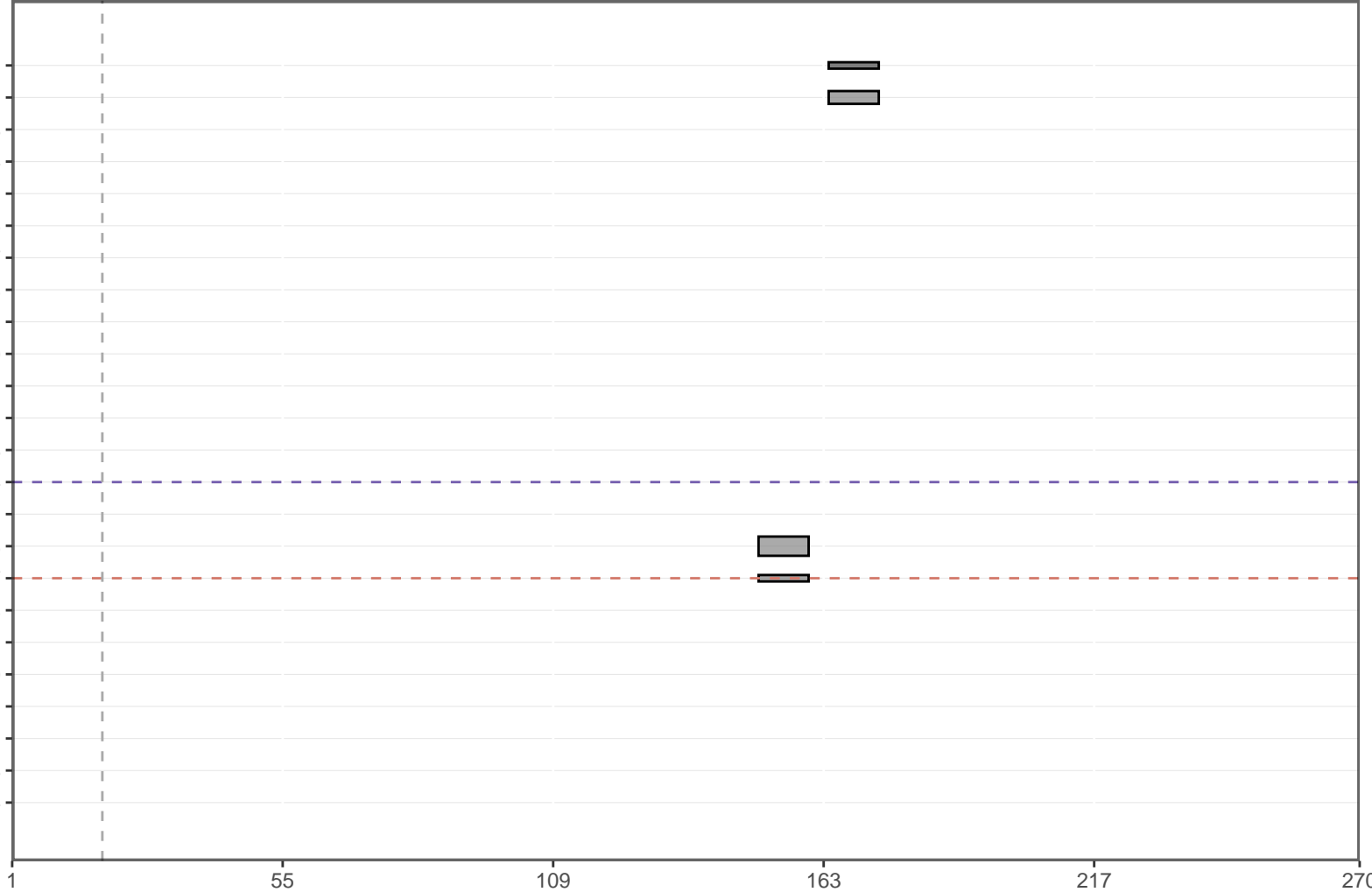
MW indication



Molecular weight



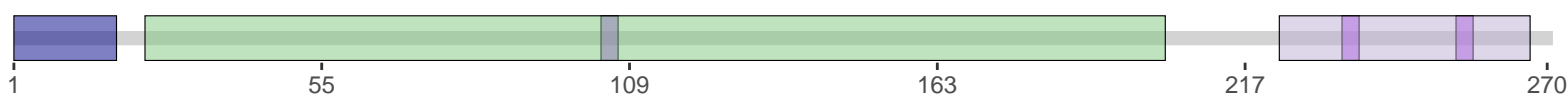
Gel Slice



Protein length

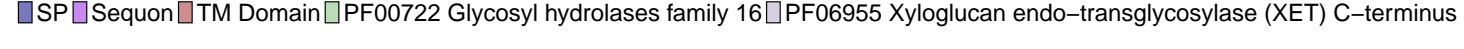


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

REQQFHLWFDPTADPHYSLGNPGRIFVVDGTPREYKNAESVGVGVYKPKNPMIRYSSLLWNADGWATRGGLIKTDWSKAPFSASVYRNFKVTSAASATNSWLNELDNTSGERLKWGKVMVNYGNDKSRFPQGFPAQCAM

NbL13g00040.1 calmodulin-binding_protein_60_B [MW = 71.67 kDa]

No. of times detected



log(intensity)



Values from



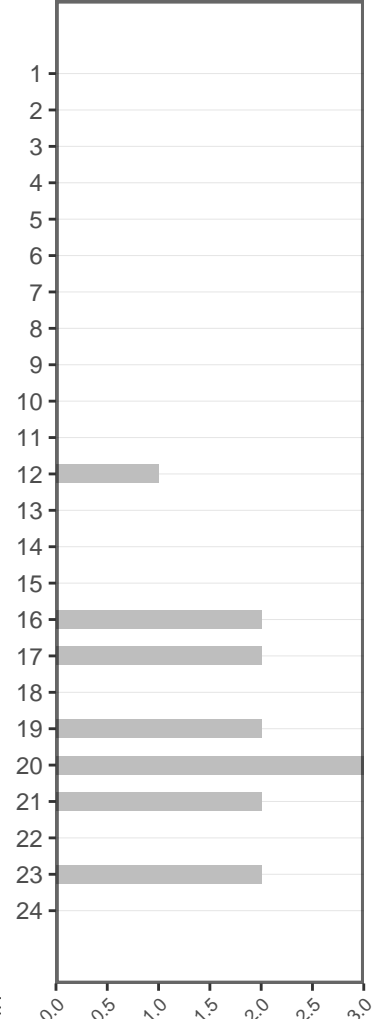
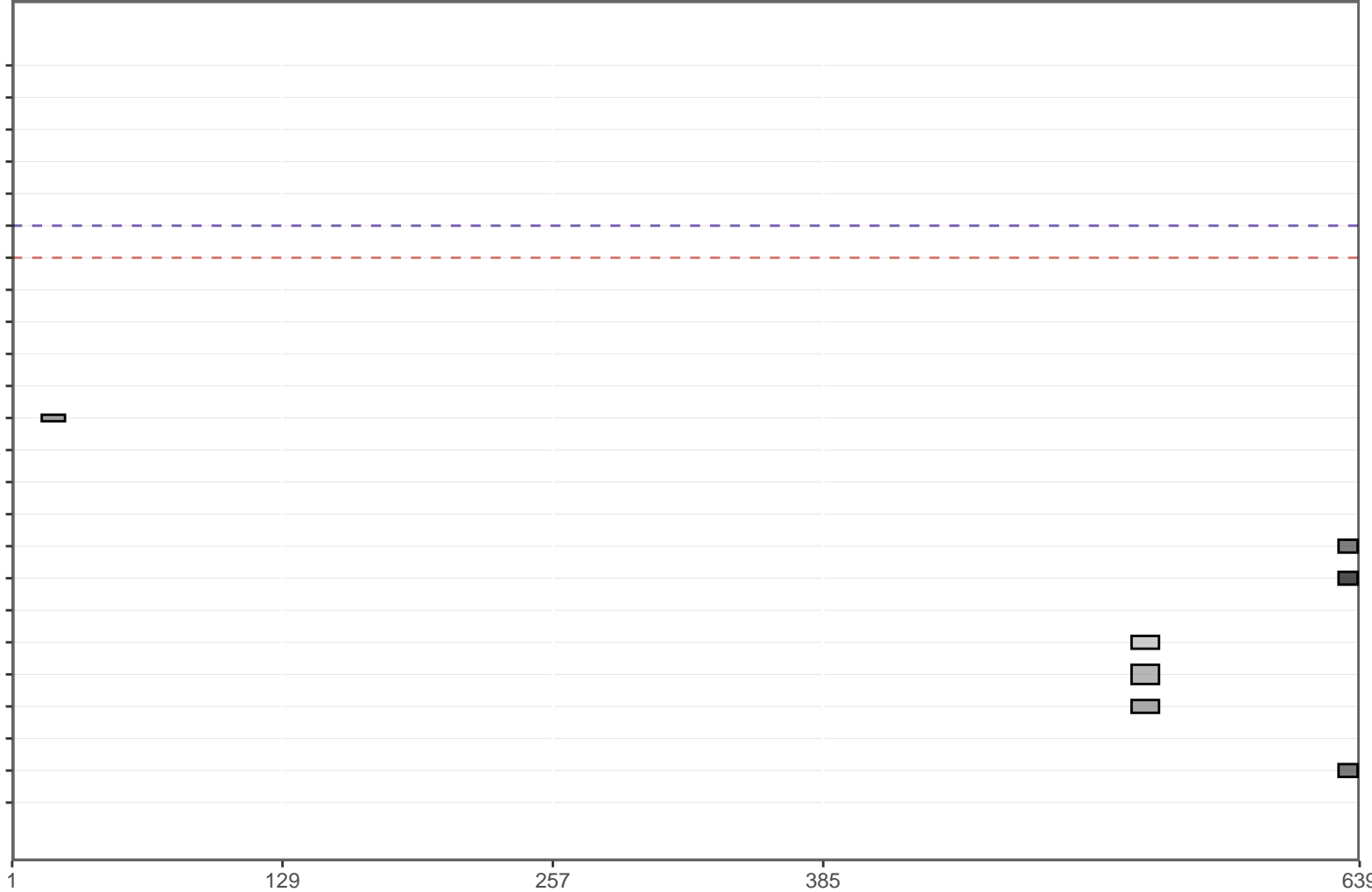
MW indication



Molecular weight

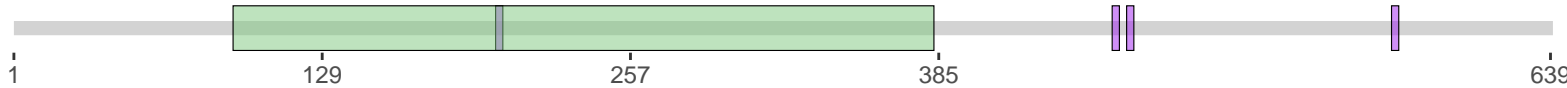


Gel Slice



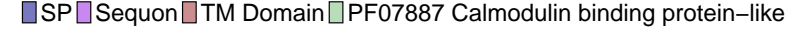
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



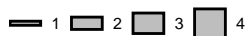
Protein sequence:

...LIEHAKTCVLSGKLVVYVSDDRNIGVFNENYELNGLAGEGYVADSLSDSGKVVYVDSLKVKAYDQWNGVVEYDQKSLNIKQNGKAGSLRNLPLVGPVDPYNNMVGKLPGRPLPVSQEGESMDPNFLIGGAGVNDGIWARMFNGSGMMNSGSRSGFESTPTFAQGGQINTHQLQSTGYDNNVGLALGPPQ66SYGTMTSGLPQTNLHPFEDWSHNRDKVDFLSEEEIRMRSHLELENDMDQHLRLFSMGGGHGSVNVSEDEYGFSPFMPSPPTFGYI

NbL13g00020.1

dihydrolipoyllysine-residue_acetyltransferase_component_2_of_pyruvate_dehydrogenase_complex_mitochondrial-like [MW = 58.6 kDa]

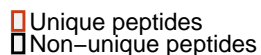
No. of times detected



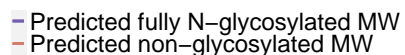
log(intensity)



Values from

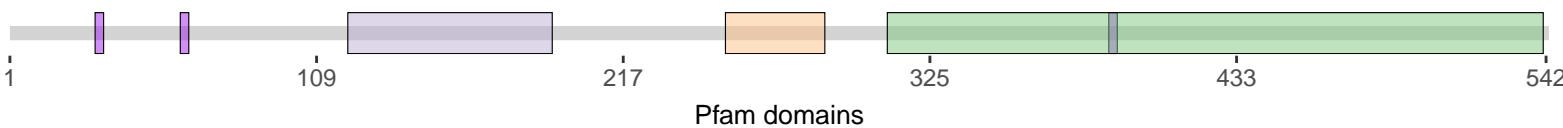
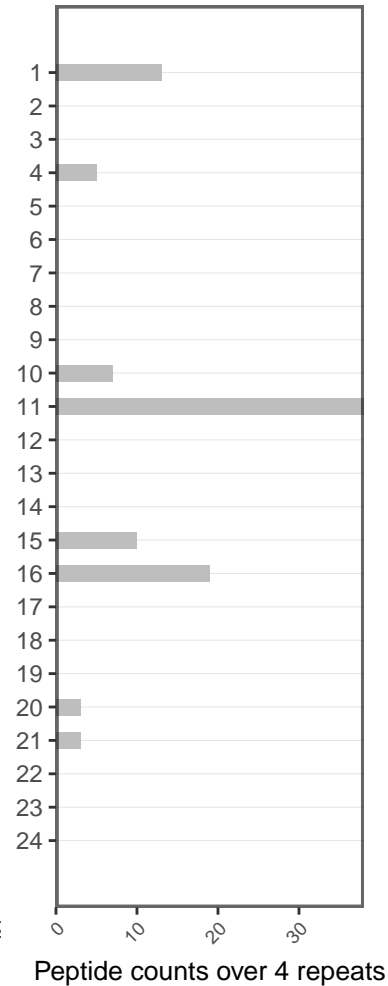
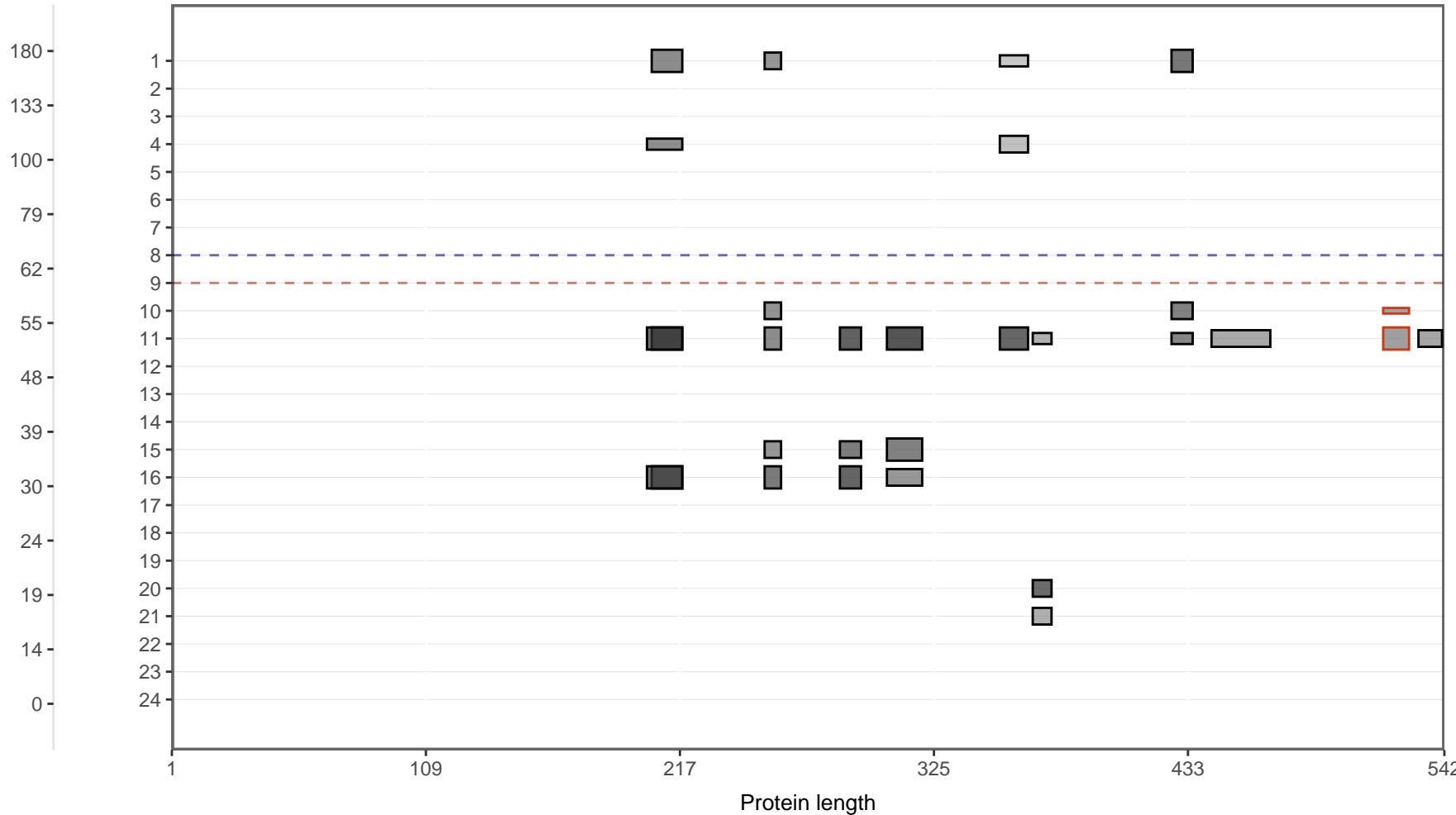


MW indication

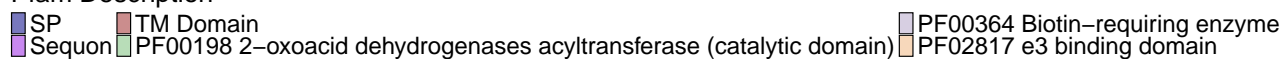


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

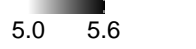
SPLARKAIEDHNPISLSSKGTGPEGRVYKADIEDYLSGRGKEALAPPKAEASLDYTDIPVSRKVTASRLLLSKOTPHYLYTDAEYDKLMELRSQLNSLDEASGGKLSVNDLYKAAALRKYVPCNSWYTDYRQYHNININAVQTDNGLVYVYRDADKKLSIAEAEVQLADKAKENSLKPDYEGGFTFVSNLGGPFGKQFCAINPPQSALAVGSAERRYPGSGGDDYTFASMSVYLSGDHRVIDAIGAGWLKFKQYHESPEISML*

NbL12g22790.1 14-3-3-like_protein_F [MW - SP = 28.98 kDa]

No. of times detected



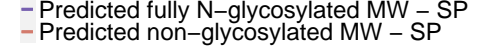
log(intensity)



Values from



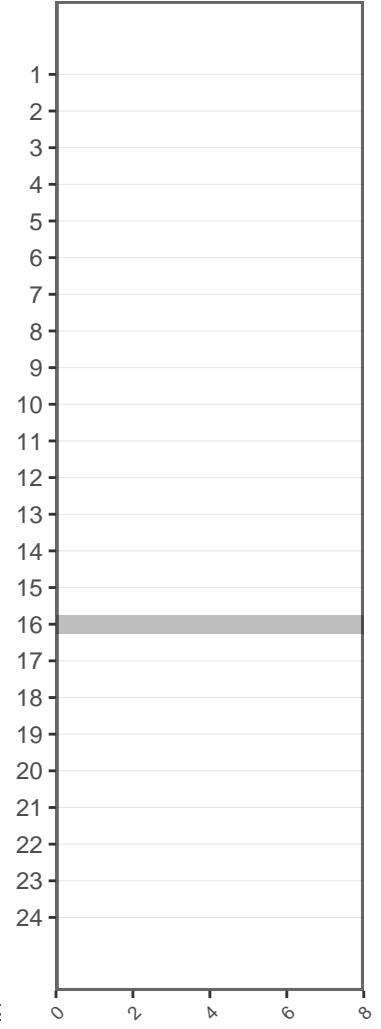
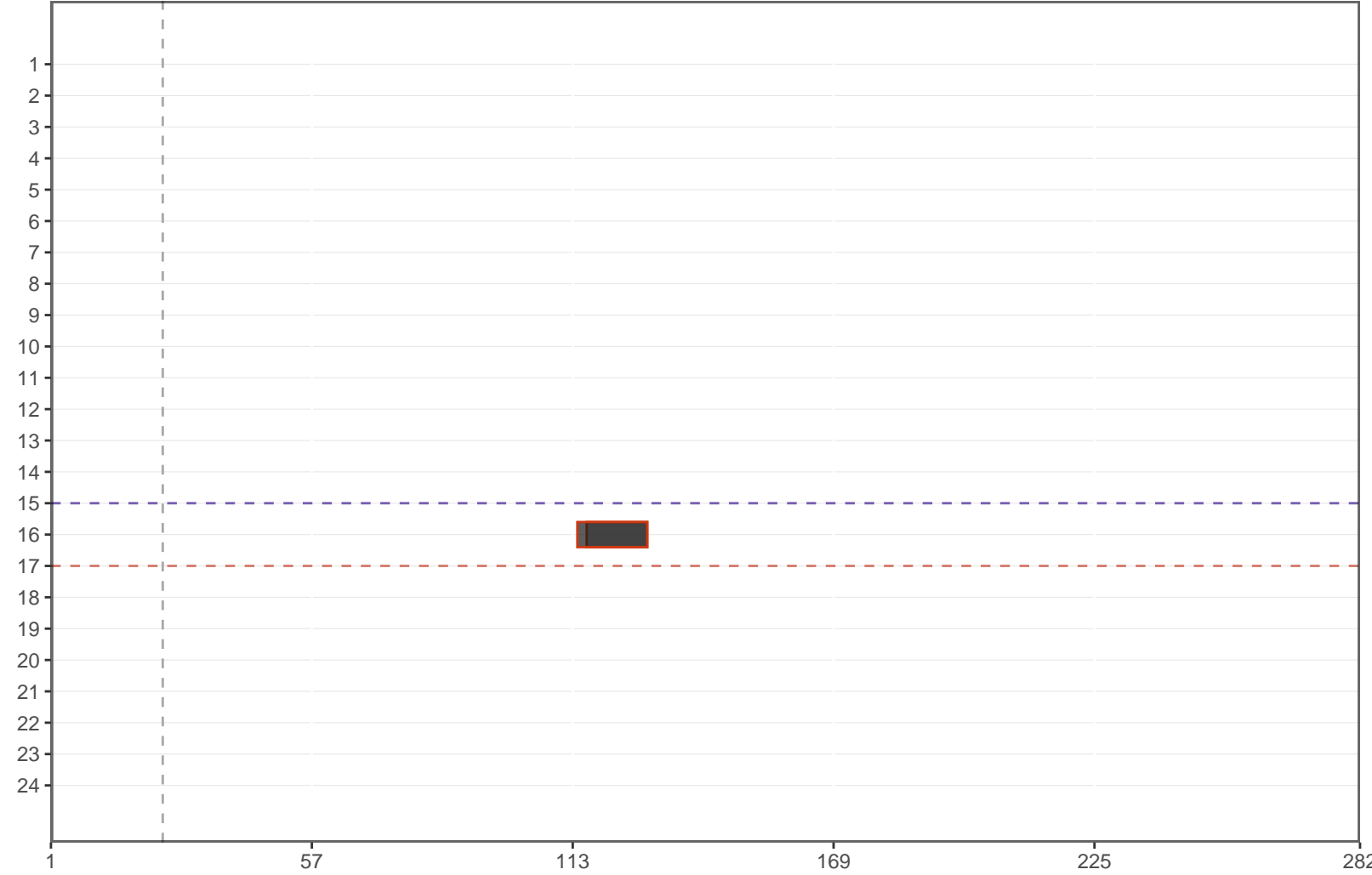
MW indication



Molecular weight



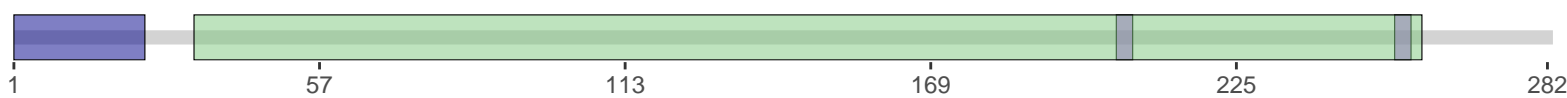
Gel Slice



Protein length

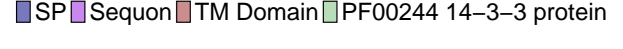


Peptide counts over 4 repeats



Pfam domains

Pfam Description

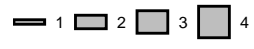


Protein sequence:

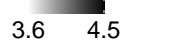
CLLDSNLGAASIGDSEKVFYLLMMKGDHRYLAEFKTGAERKEAAENTLSBYKSAQDIAAEALPFRILGLVLFNSVFYFEILNSPDRACNLAKGFADAEIAELDTLGEESYKDGSTLMLQLLRDNLTLWTSMDQDEGTEDMKEVAKPENEEH

NbL12g22710.1 polyadenylate-binding_protein_2-like [MW = 24.84 kDa]

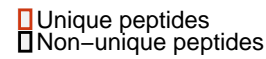
No. of times detected



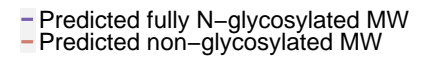
log(intensity)



Values from



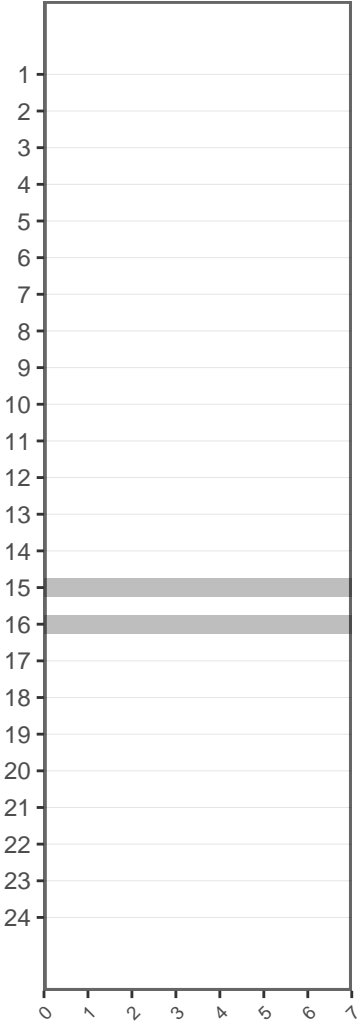
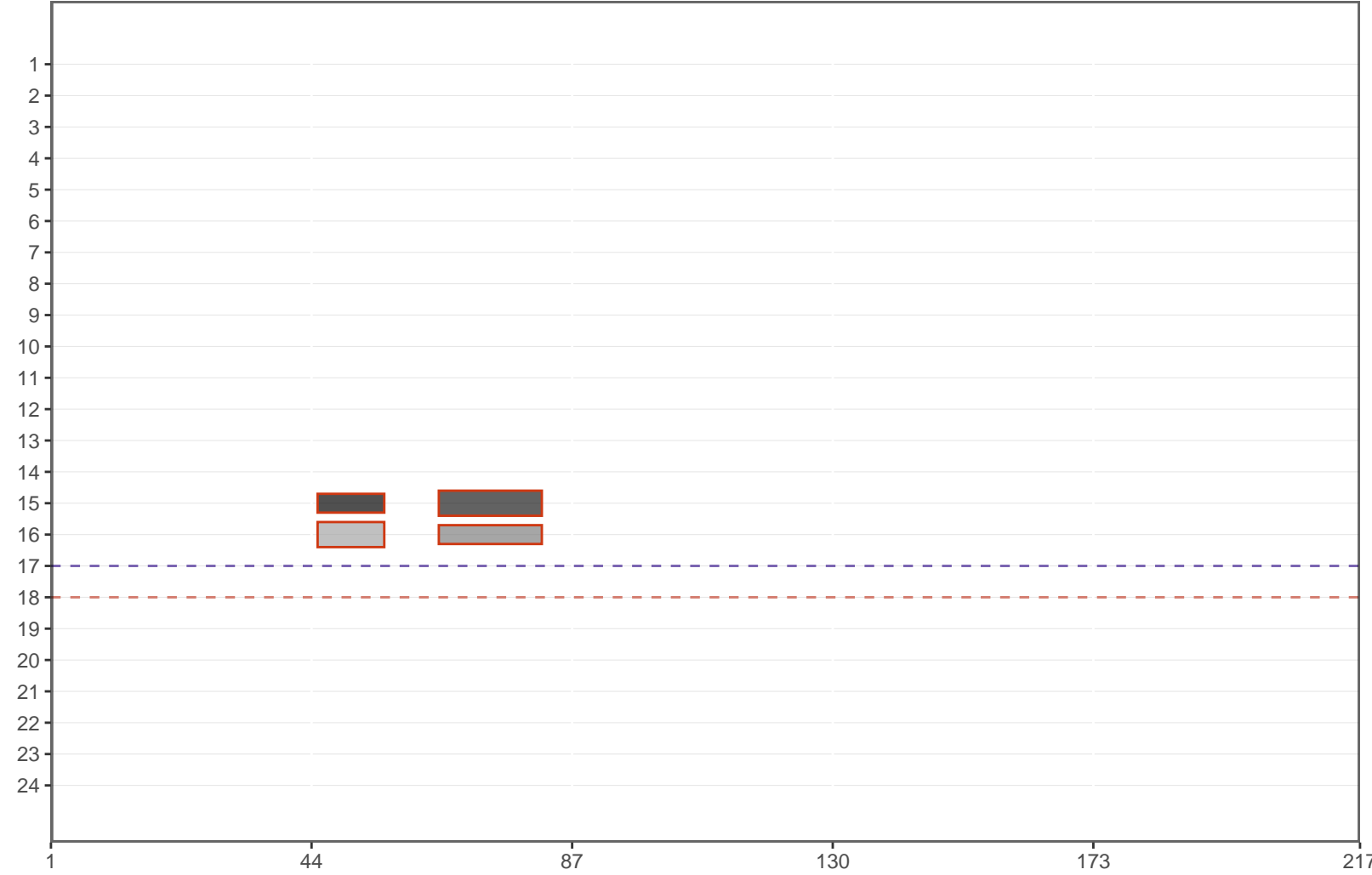
MW indication



Molecular weight

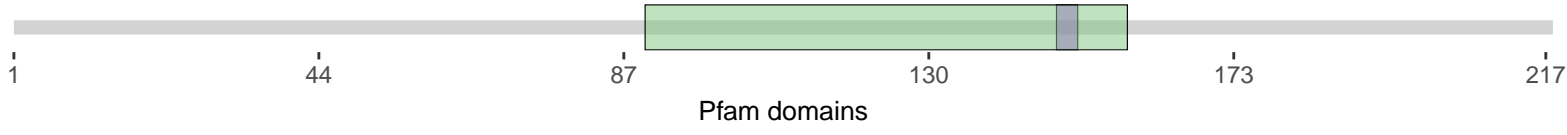


Gel Slice



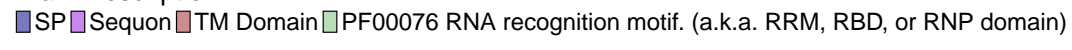
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

/D/ACTPEEVOQHFGAGGTNVRVLTDFGDFKGFVAFVFEDEGAIEALQLNESELHGRGLKVMPKRTNVPDMKDFRGRFNPVMVGFRRPVPPLVSPYFGKVPFRFRFRMRMPVY

NbL12g22460.1 gamma-glutamyltranspeptidase_1-like [MW - SP = 59.45 kDa]

No. of times detected



log(intensity)



Values from



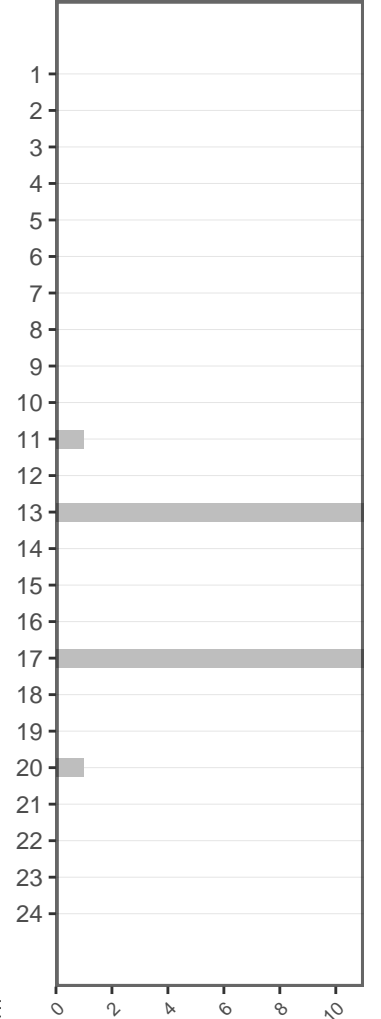
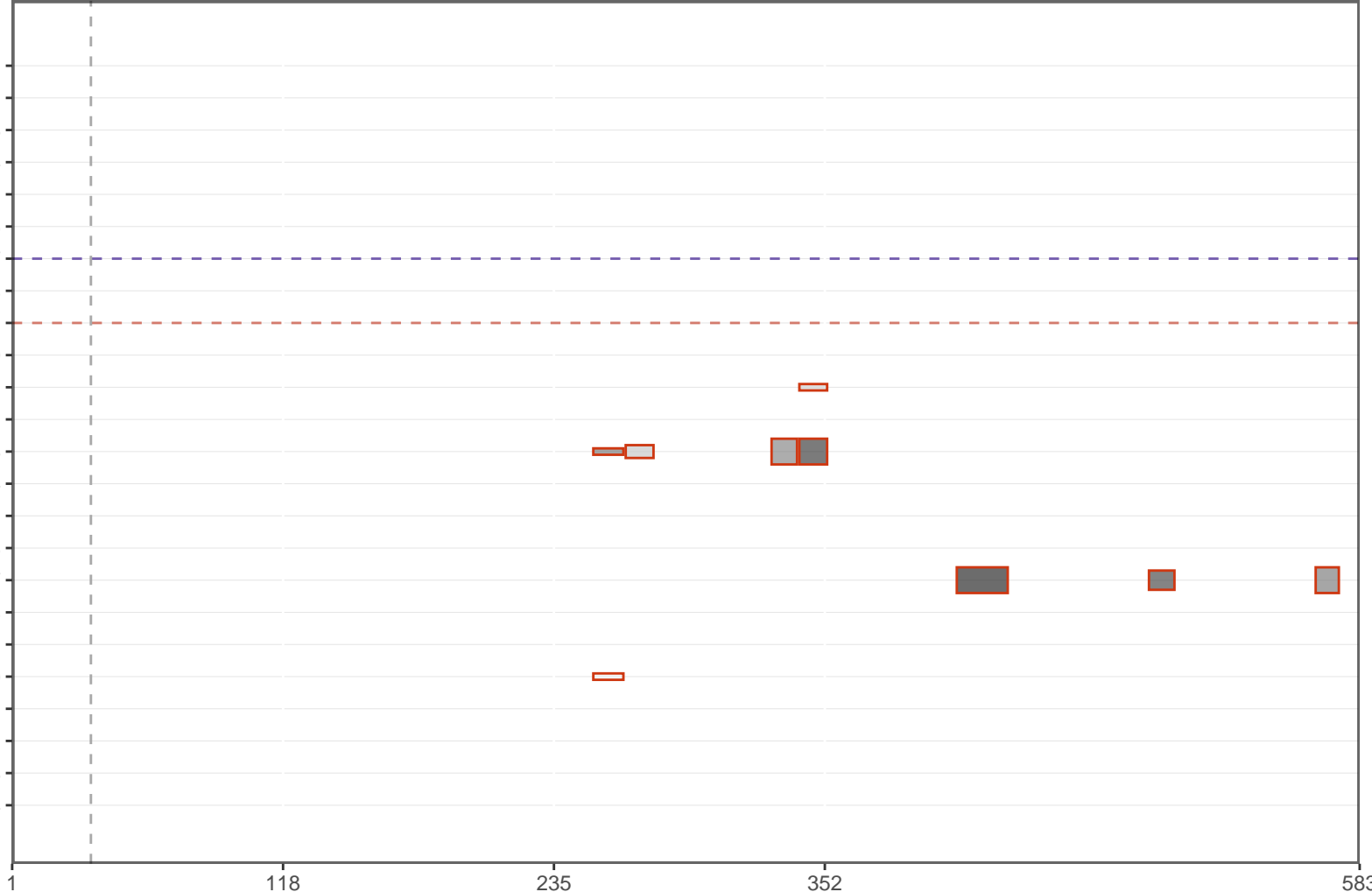
MW indication



Molecular weight



Gel Slice



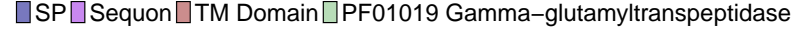
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LMPPPSAGGAAMVLLNLADYQGMIEGPRLLIHRGIEALHAFALRMNLGDDPFNKKVINDMLSTEFAGLKKTKTYDNTMTFSPNHYGGKWNQHDHGTSHMSVDSDDRNVAHMTSTVNAVFGAKYLPSTGVLNEMDDFSPEKREBNVPPDPAANFRPGRKRLSSMTPTFLKGEQLRAVIGASGGAMIAATTEVLNHFARGMDPFSVMAFR6YHQLPVLGVYENWTVTGDHEVFPVXTRALQKKGHVLSQSIAGGTGGFVWGEFKSKLGEUVASDPRK

NbL12g22410.1 RNA-binding_protein_39 [MW = 66.46 kDa]

No. of times detected



log(intensity)



Values from



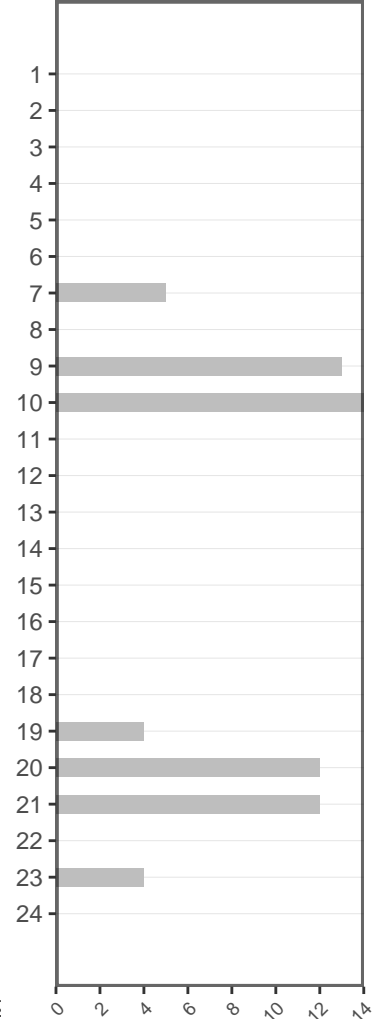
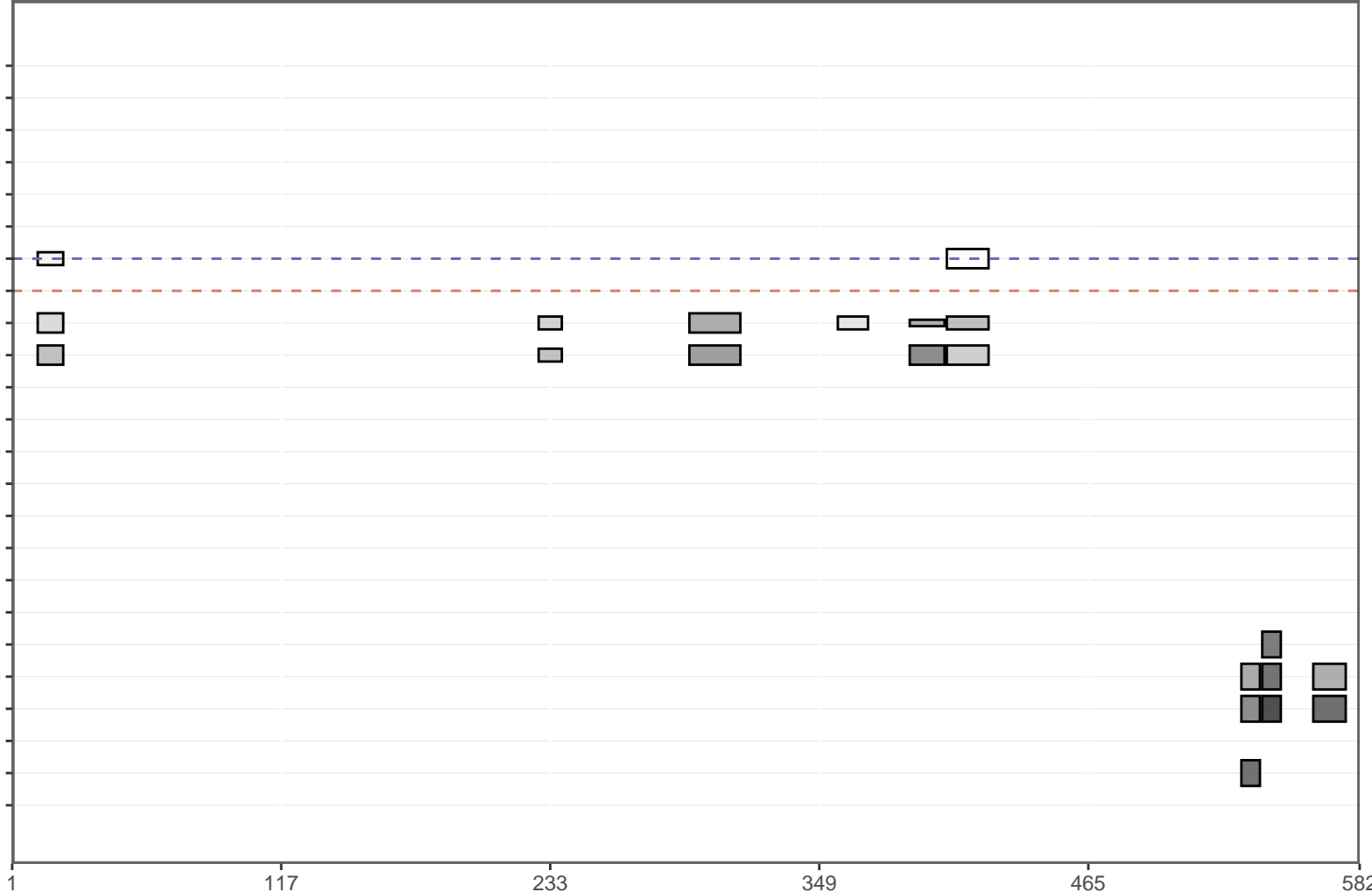
MW indication



Molecular weight



Gel Slice

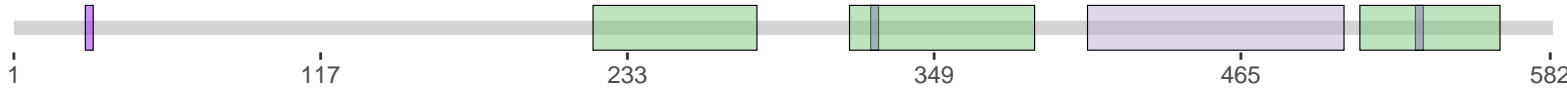


Protein length



Peptide counts over 4 repeats

Pfam domains



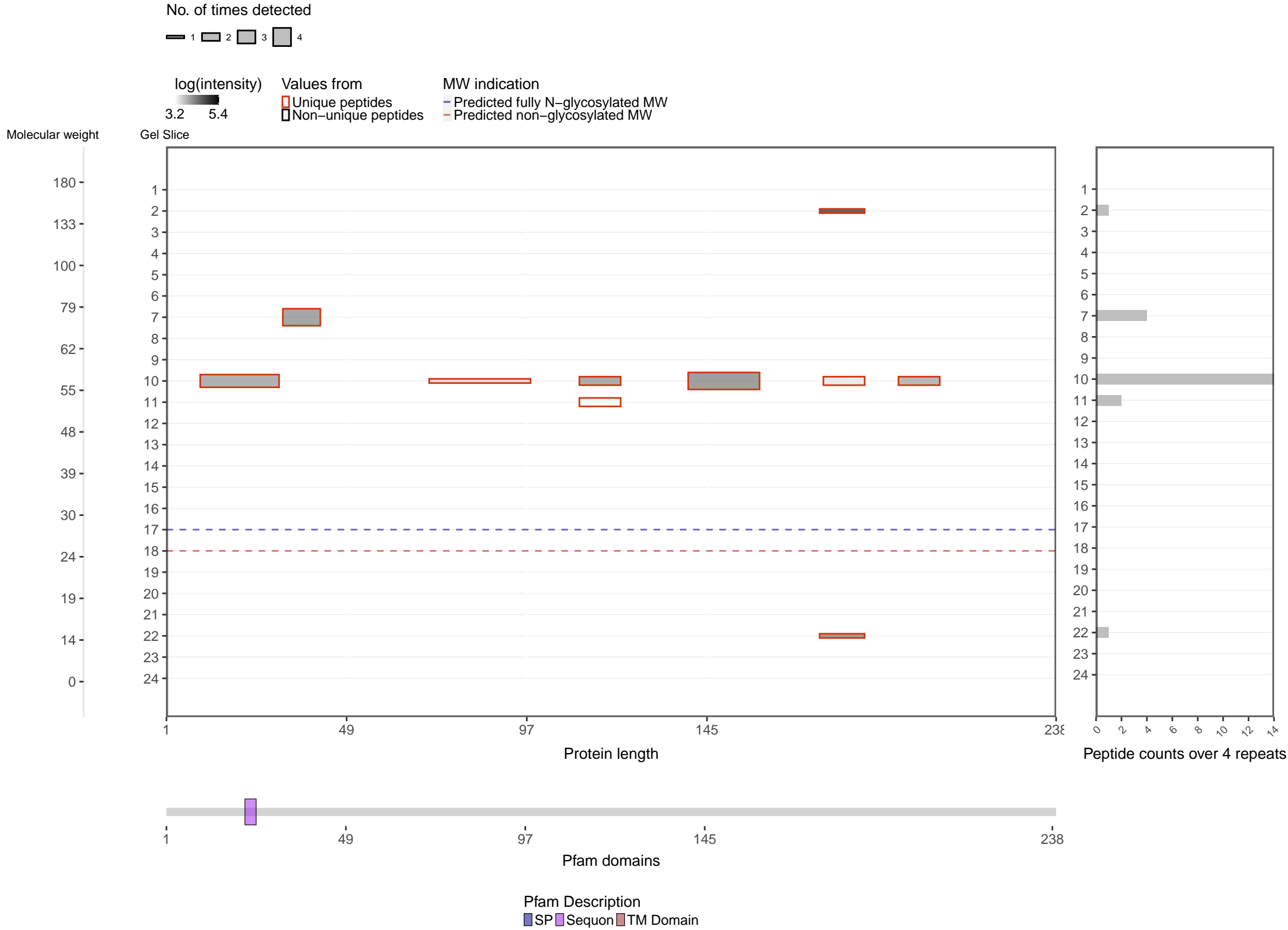
Pfam Description

SP Sequon TM Domain PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) PF15519 linker between RRM2 and RRM3 domains in RBM39 protein

Protein sequence:

SRLLFGQPVLYKPSAEKNIYDGTASGGGGSLAGPNAASERKLYVGNLHFMTELQLRGFQFAFGPVELVQLPTDRETGHKGGFGFVQFAGLEHAKAAGSINGKLEIAGRTRKIVSSVTEHVGVDGAKATAFDDEEGGLALNAGSRAMLMAKLRDGVASSVAGTLGVYALNGAAPAGMMPGIGATAPNMLPTQVLAAMAPERIGPSEHLLKNMFDPTETDPEFDLKDQDKKECGKYGKRVKHHVQKNSSGVYVLRFRDSEVGAARAGQAMIKRWFAGRSIS

NbL12g22060.1 serine/threonine-protein_phosphatase_4_regulatory_subunit_2-like [MW = 25.37 kDa]



Protein sequence:

VRVTEKALQVYSTGAPKAETSEEKWEIEVKSETKTPAENKVEEVTWVETPAEKNEIEVTWVETPAEKMEEFAPATEAGKSVWVPEIKAEKHPVATEAPKGEAPVFTKAENKPAEAELKVIDEKKSQKPS

NbL12g22000.1 60S_ribosomal_protein_L13a-4-like [MW = 23.53 kDa]

No. of times detected



log(intensity)



Values from



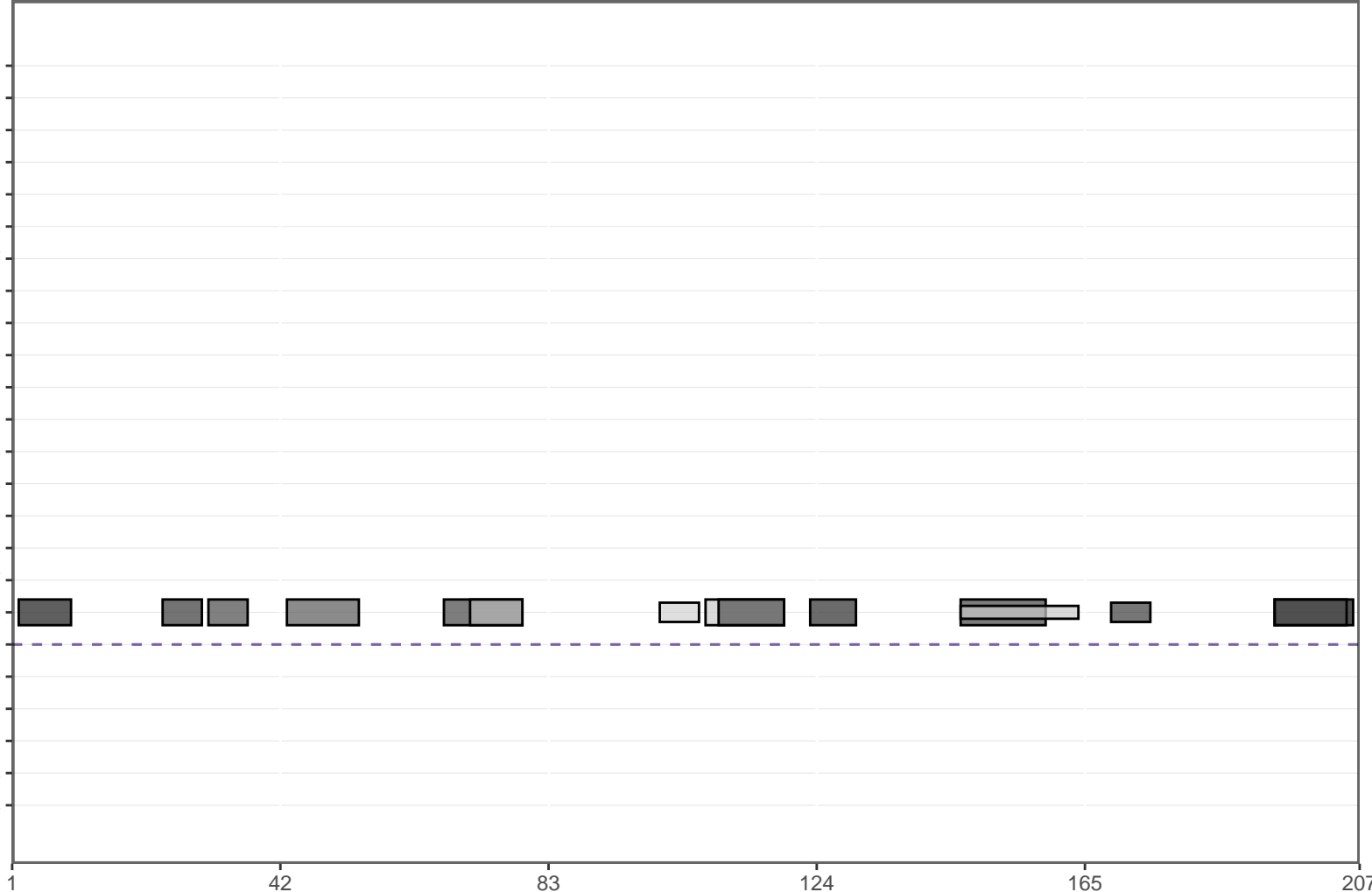
MW indication



Molecular weight

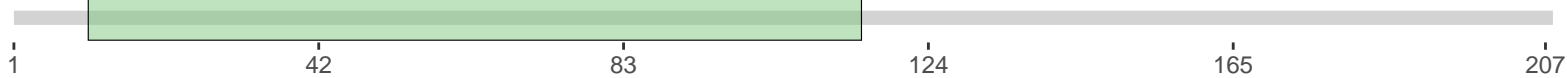


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

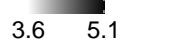
IGMIPHKTRGAAALARLVKVEGVPPVYDKIRKRMVDPALKVLRLQAGHKYDGLGKLSSEVGNWVHYDTKELENKRKERAGVYERRKQAKLRLVKAKEAAEELGQQLAVIEPKY*

NbL12g21990.1 U6_snRNA-associated_Sm-like_protein_LSm3 [MW = 13.91 kDa]

No. of times detected



log(intensity)



Values from



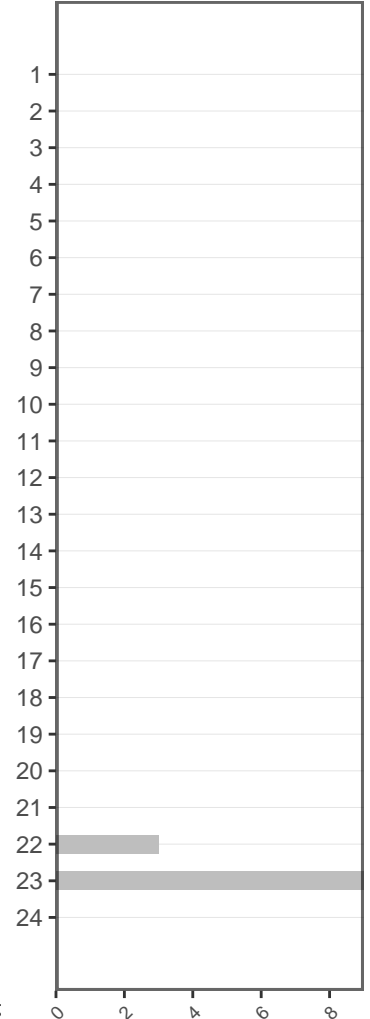
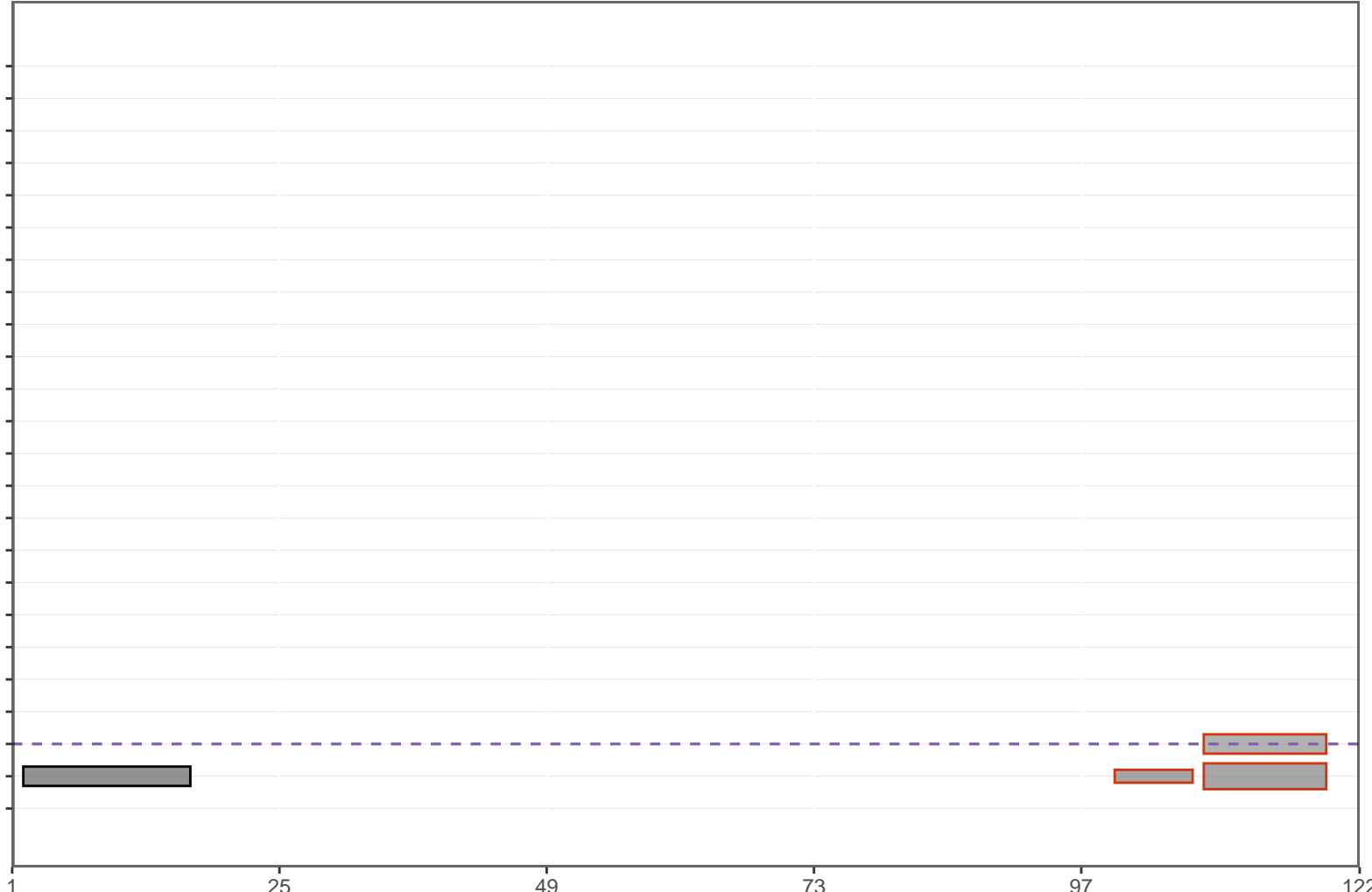
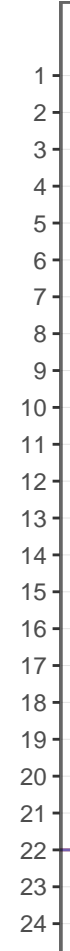
MW indication



Molecular weight

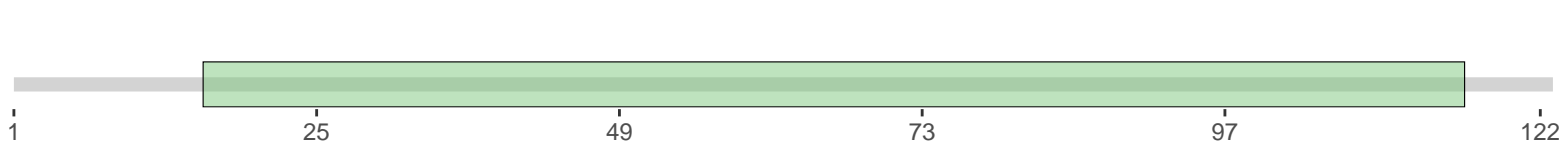


Gel Slice



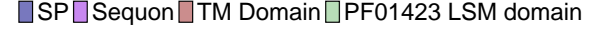
Peptide counts over 4 repeats

Protein length



Pfam domains

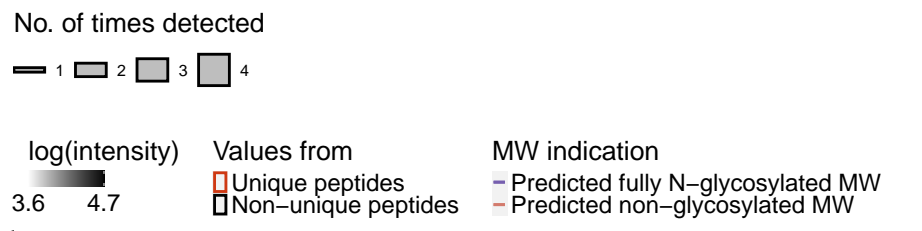
Pfam Description



Protein sequence:

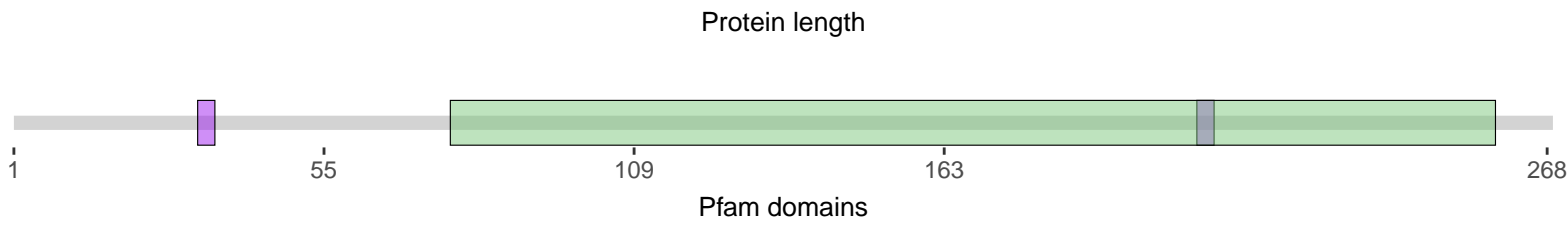
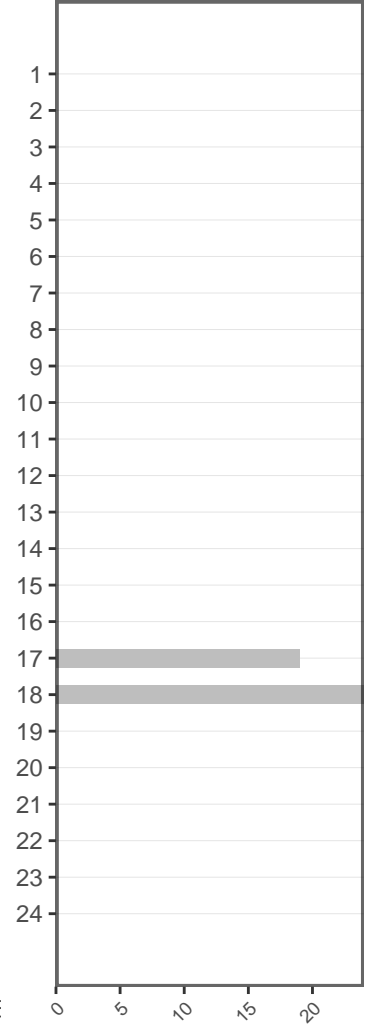
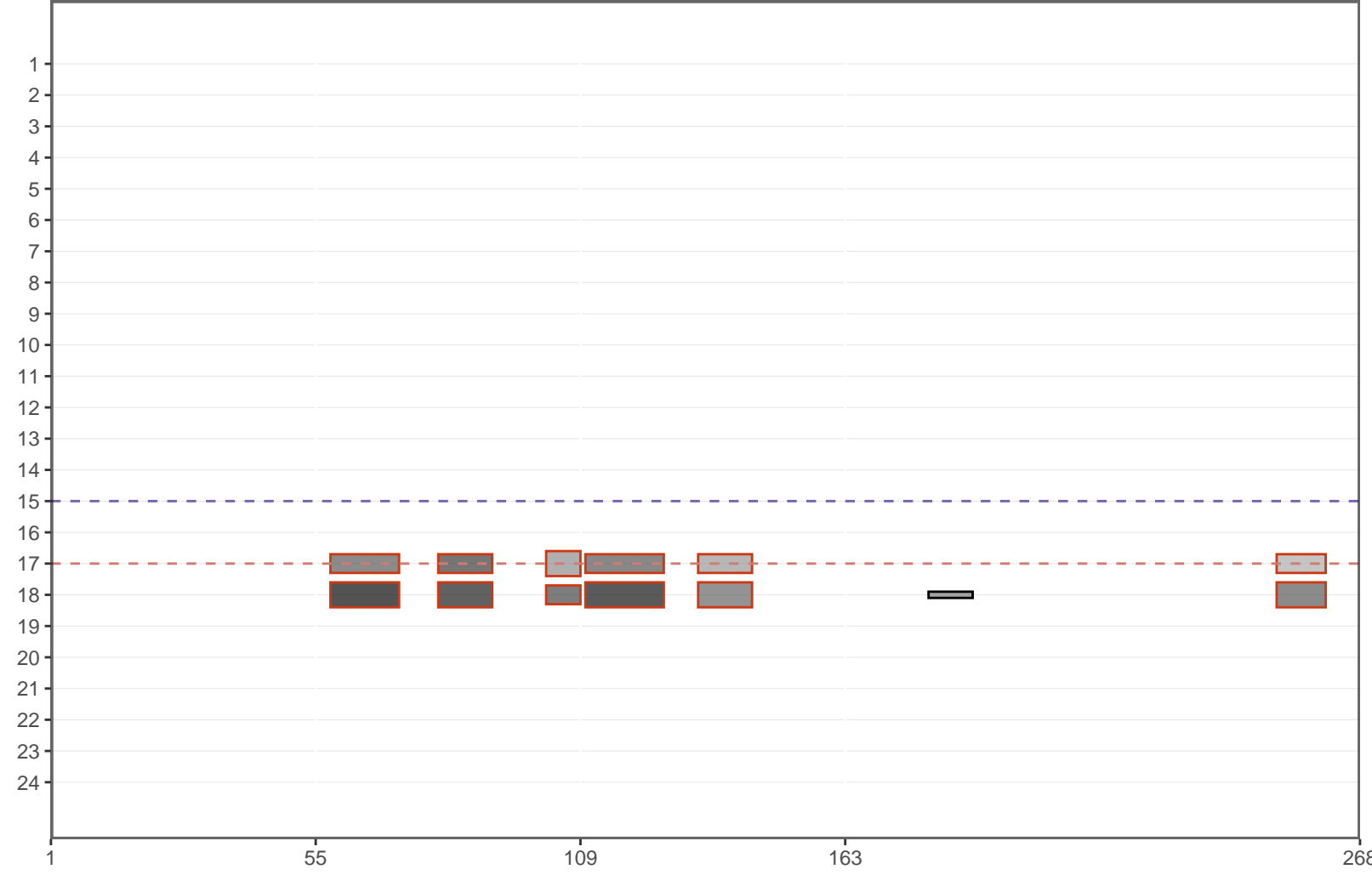
MLGDVEEVITTVVDEDDETVEEIVRTHYSGSGMGLFWAFKSGSLKTKTRRTHFLFVRGDGVLVSPPLRTV

NbL12g21970.1 probable_plastid-lipid-associated_protein_7_chloroplastic [MW = 30.03 kDa]



Molecular weight

Gel Slice



Protein sequence:

PTLSLDKAGSIVKLYSTISIGSRRTKLGIRDFTLGGDLYQNDISEGKAVNKKFNARGLSLLSGELRIEATFNASKSRVDFVYNSAFTDQLMNVFQKNYDLLLGFNPEGWLEITYVDENLRIGRDKGKNFVLERGDEKLV

NbL12g21960.1 actin-7 [MW = 41.73 kDa]

No. of times detected



log(intensity)



Values from



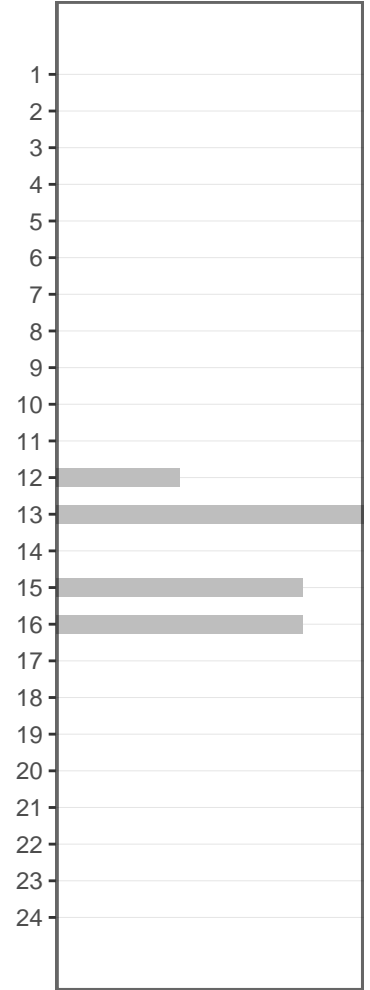
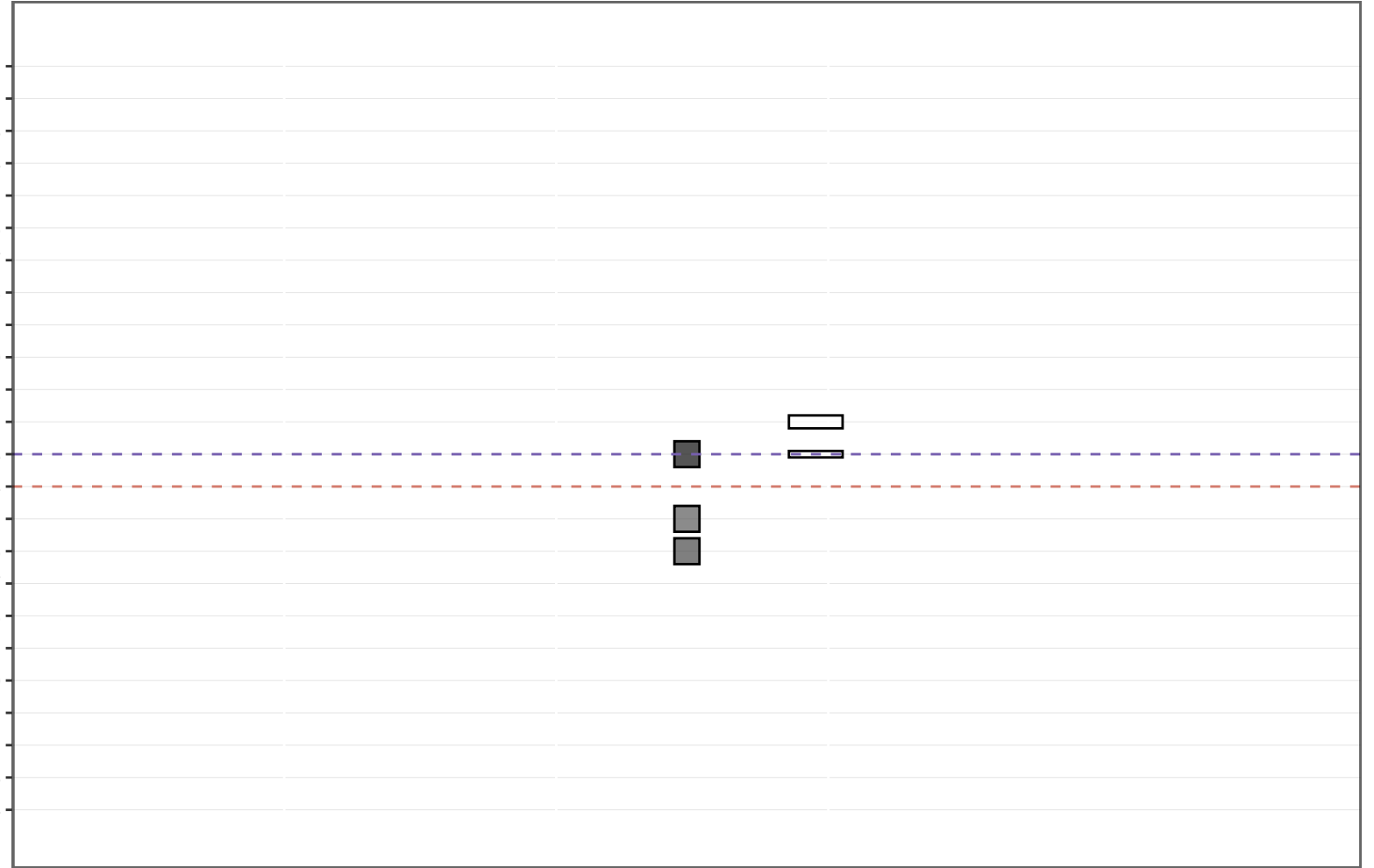
MW indication



Molecular weight

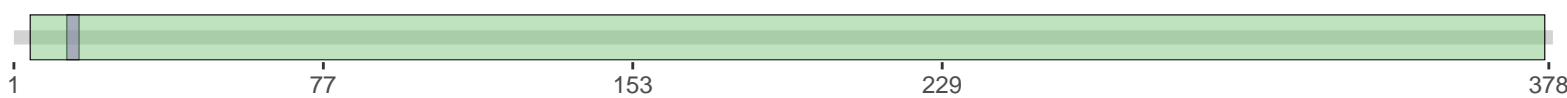


Gel Slice



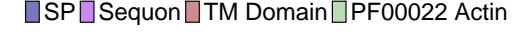
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

2HALRLDLAGRLDLDNLMKILTERGYNMFTTAERERIVRDMKEKLAVALDYEQEELDTAKSSSSVEKNYELPDGGVITGAERFRCPVELFQPSMGMEEAAGHETTYSIMKGDVIRKDLVGNVLSGGSTMFPGIADRMKEITLAPSGMKIKVWPPERKYSVHWGGSHLASLSTFGQMWSKGEYDESGPISVHRKGF

NbL12g21880.1 acetylglutamate_kinase [MW = 36.4 kDa]

No. of times detected



log(intensity)



Values from



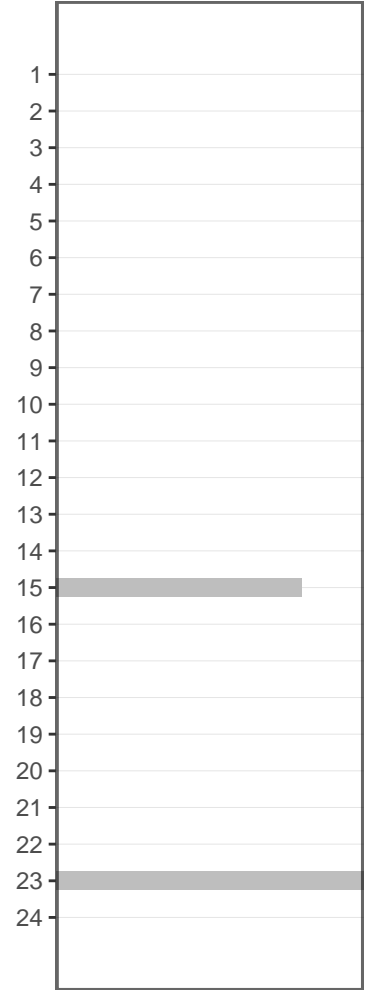
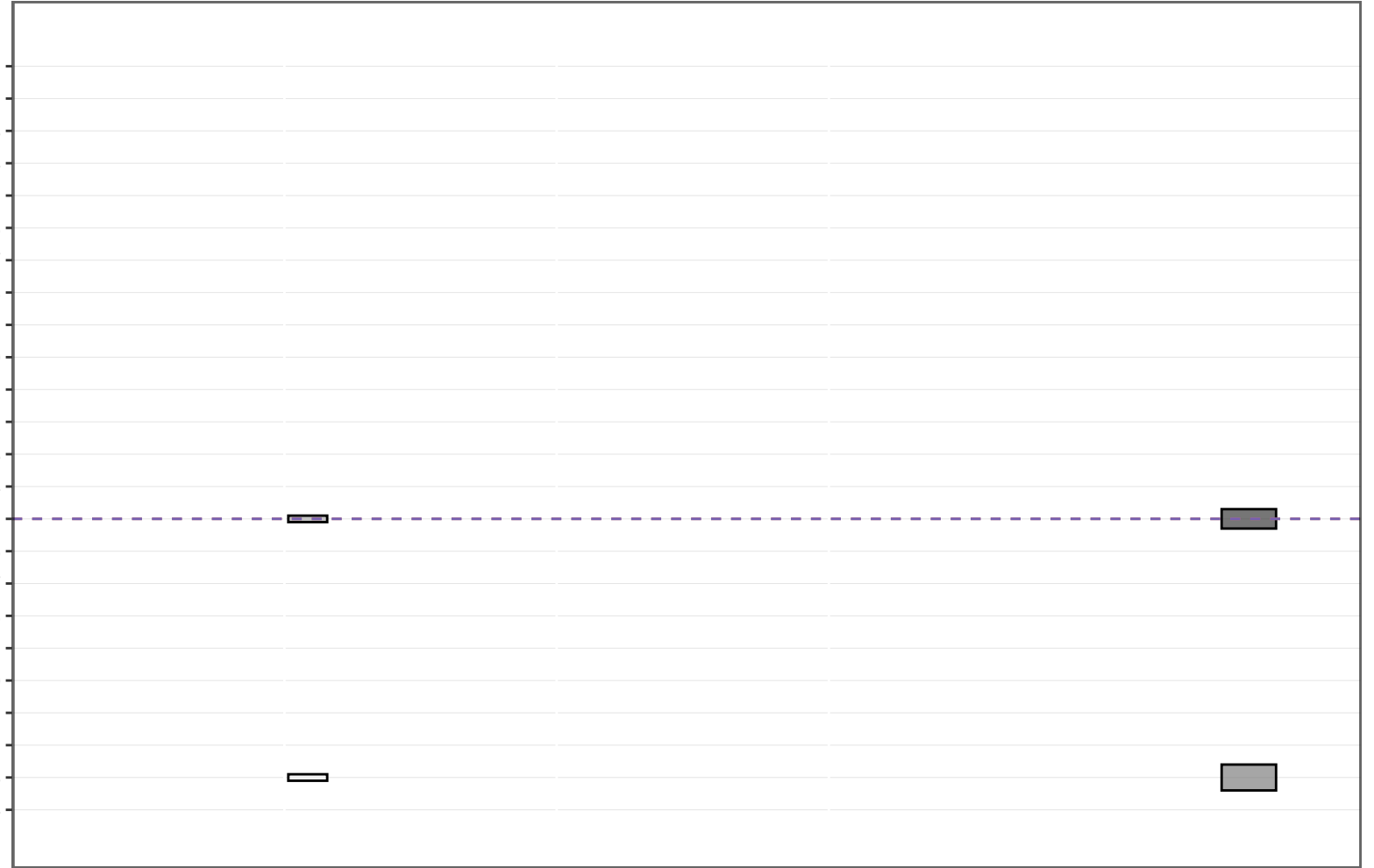
MW indication



Molecular weight



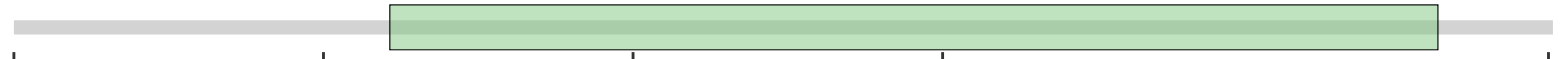
Gel Slice



Peptide counts over 4 repeats

1 71 141 211 281 348

Protein length



Pfam domains

Pfam Description



Protein sequence:

ILLVGKYNQLEVSLINKAGATAVLGGIDGHLLTARSPNADQLGFRVGDIAVDPVLRPLDNYHIPVAVSVAADIKTGGSYNNADTAAGELAAALGAENLILLTDVAGLEDRNDPGLVKQIDKGVKMTDDGKVAAGMPKVNCGVRLAGGVTTASHIDRGLGHSLLLELDEGAGMTG*

NbL12g21860.1 40S_ribosomal_protein_S18 [MW = 17.54 kDa]

No. of times detected



log(intensity)



Values from



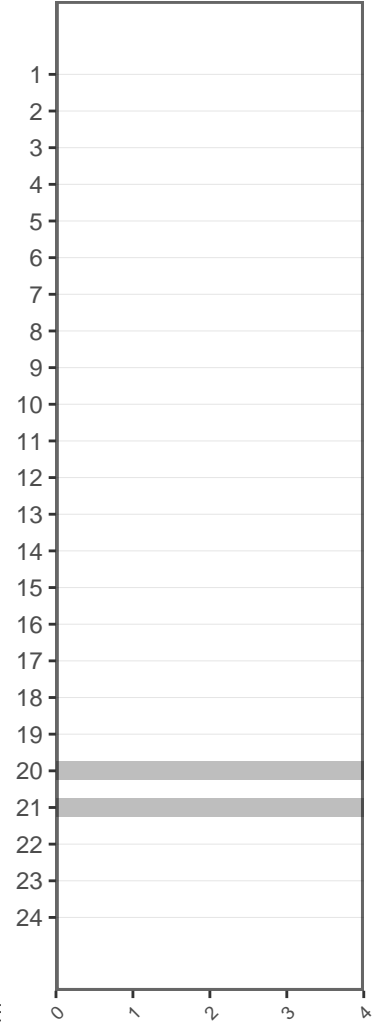
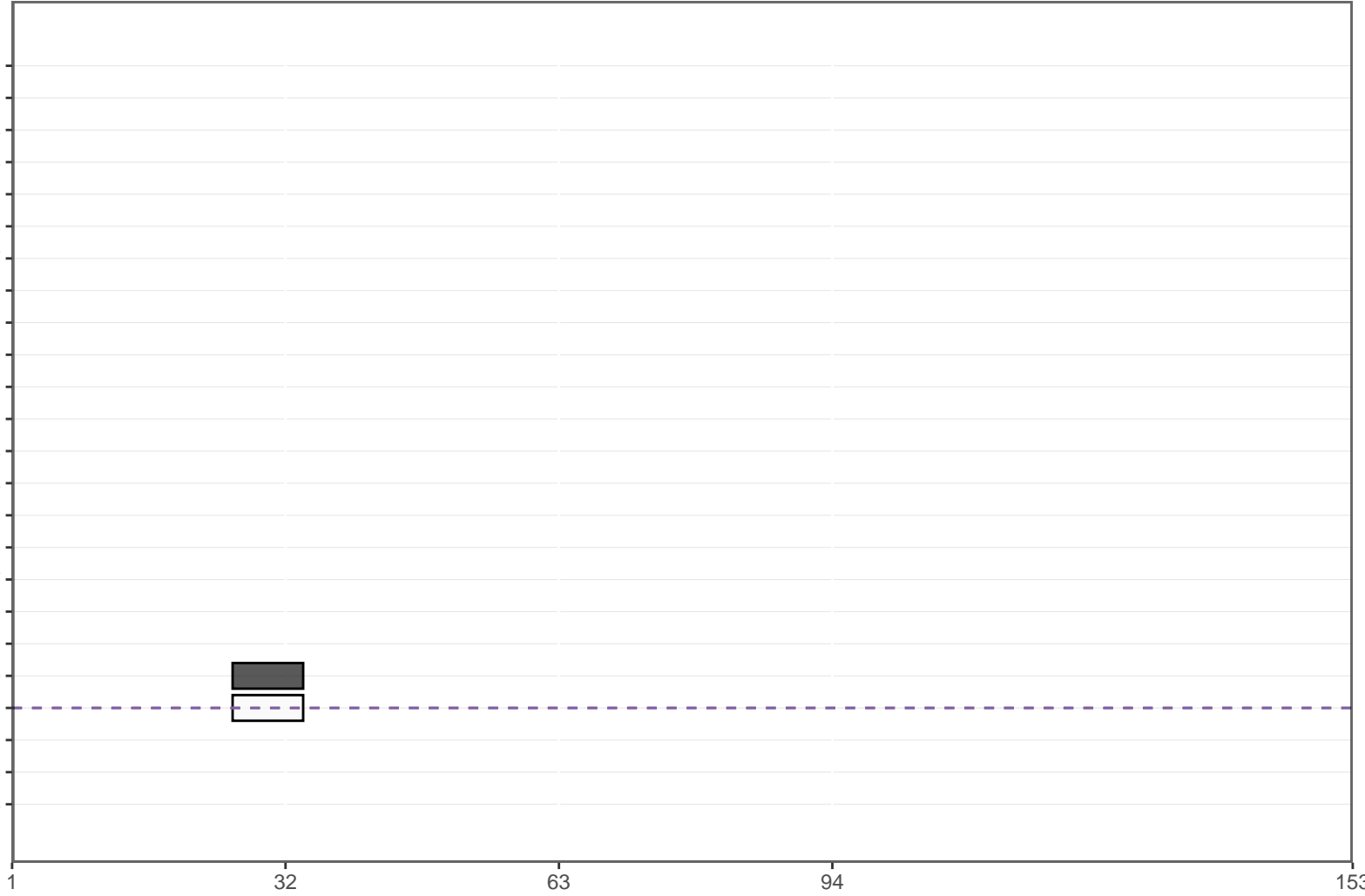
MW indication



Molecular weight



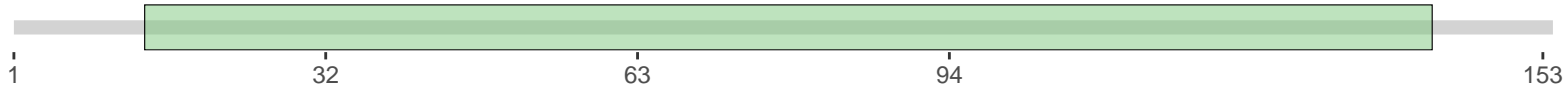
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

ISLMVVANPRQFKIPDWFNLNRGDKYKDKGKFSQVTSNALIMKLRDDELRKLRNHRGLRHHYGLRVRGQHTKTTTGRGKTVGVSKR

NbL12g21760.1 probable_pectinesterase/pectinesterase_inhibitor_51 [MW = 61.53 kDa]

No. of times detected



log(intensity)



Values from



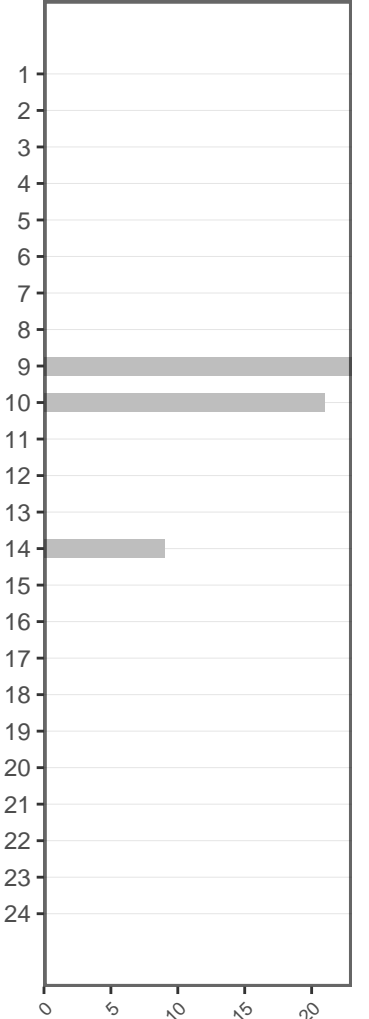
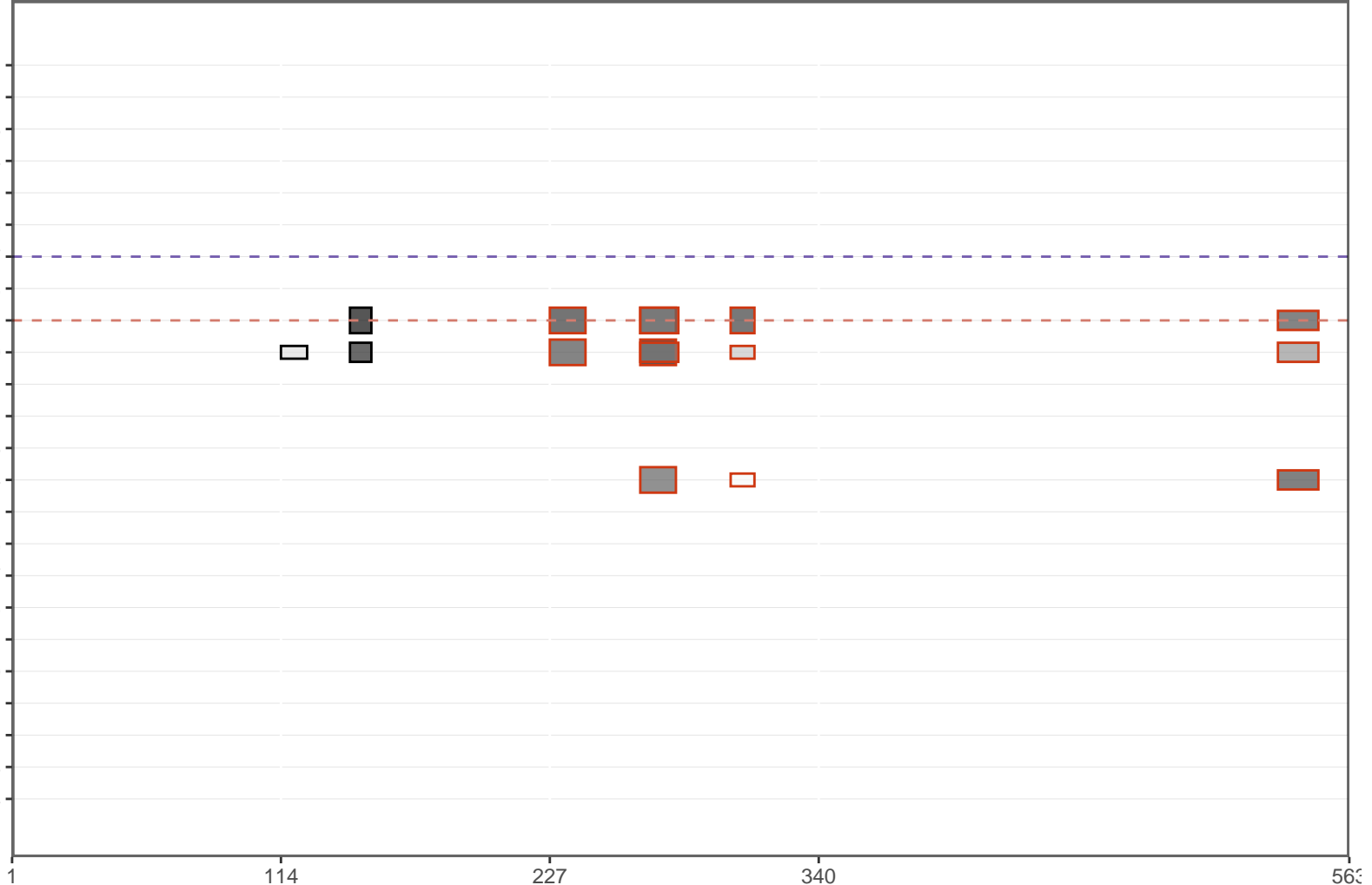
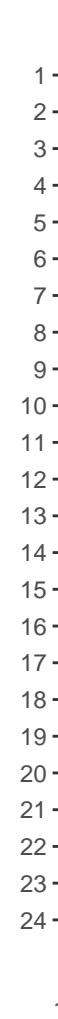
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

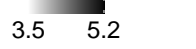
IQEA/NAAPDNEVTRKFWKAGLYEEKVRFPLEKKNVFLDGGIGKTVTGSLLNIGMAGVTTTETATVGVAGDGFMAISGTFQNTAGPVAHQAVAFRSDDSLVHENGDFRGNQDTLVYHALRQVYKSGRIGQNVDFIFGNSAAFFDGEDDLAPRGLNPEKGEKNVTAHGRADPAGSTGFVFNQLNGTRKYMALVYKPKVHNKHLGRPWKEYSRTVFECTLEALVLDGWLNPWSDGFALKLVYGEVNTFGAGANTAGRVPWSSGQPEHWNDSIRNFIQGDQWIT

NbL12g21620.1 guanylate_kinase_2_chloroplastic/mitochondrial-like [MW = 34.17 kDa]

No. of times detected



log(intensity)



Values from



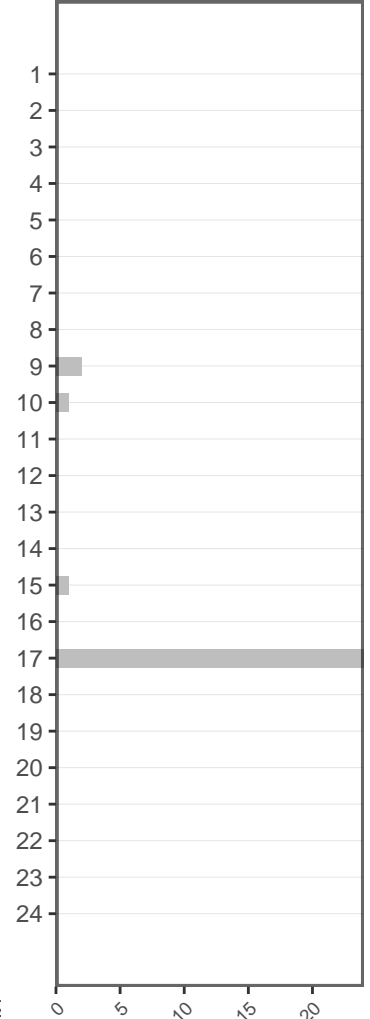
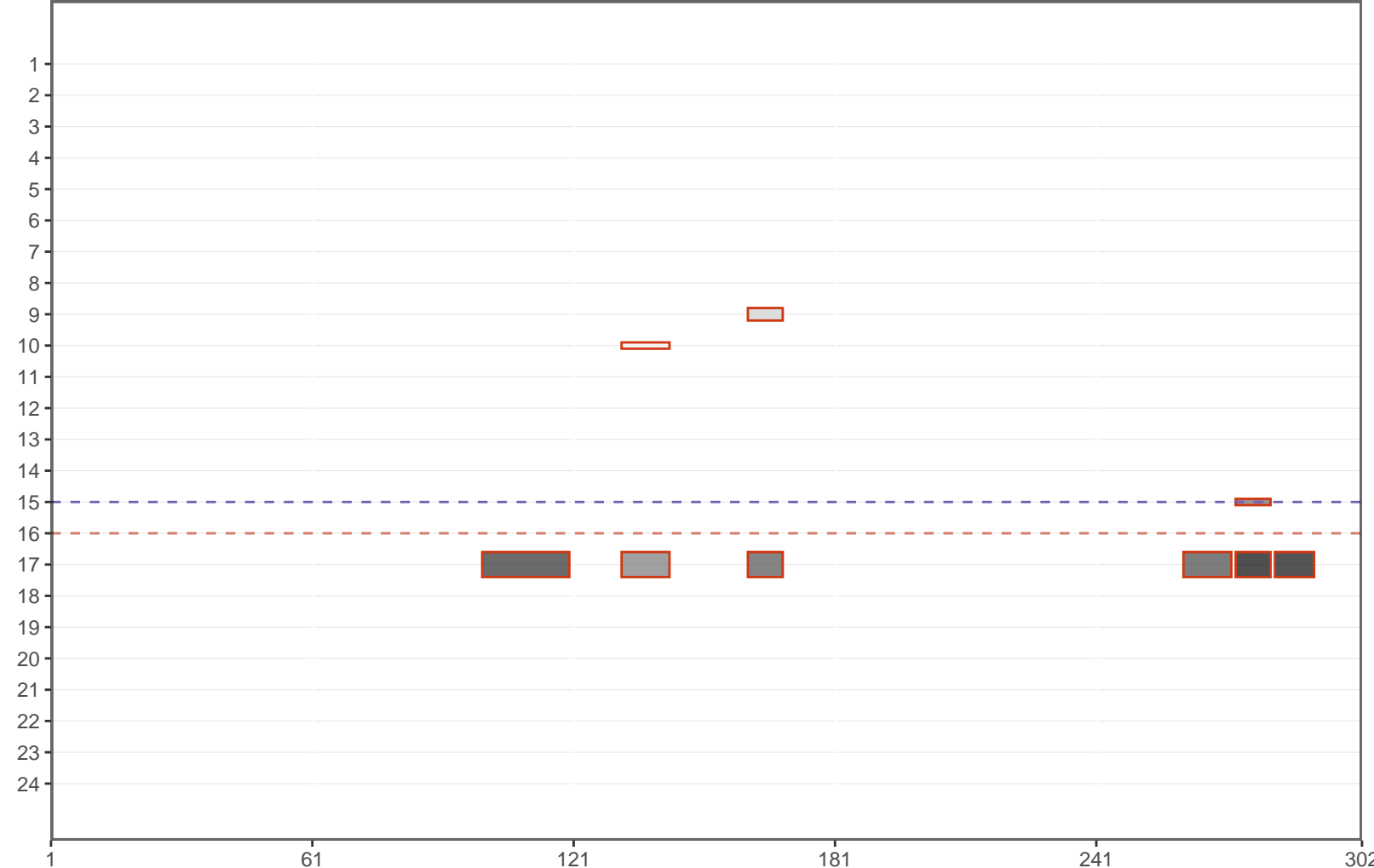
MW indication



Molecular weight

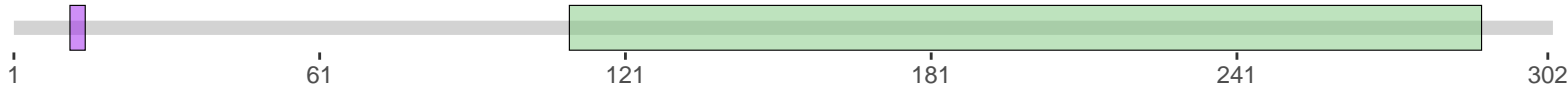


Gel Slice



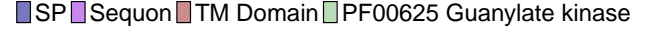
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VVATSRGKRSGEVDDGKDFVFFVSKKEEFTMIERHELLEVALVYGDYKGPKGQIRDGMKGLDVLRVDDGGAATLKRILGKSAVFLVAEGEDALVKRLDRKTKETKELLRVATAREEVKHMEEFDYVVVNRREGELNSVKLMESGIDAEKAVRQRATPI

NbL12g21530.1 probable_polyamine_oxidase_5 [MW = 58.63 kDa]

No. of times detected



log(intensity)



Values from



MW indication



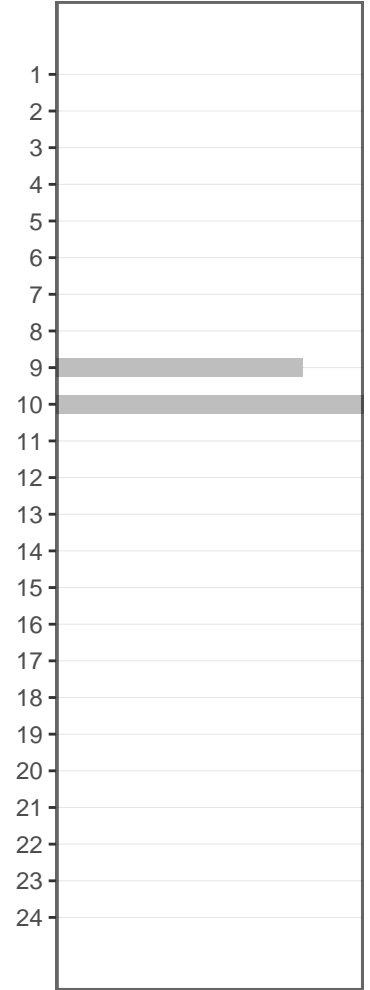
Molecular weight



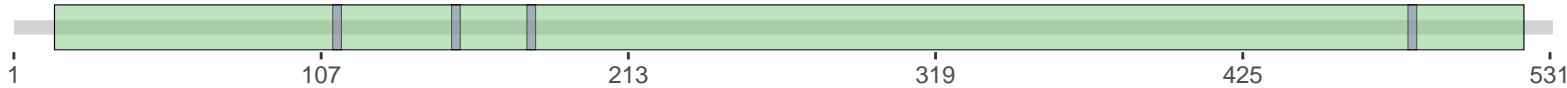
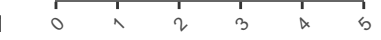
Gel Slice



Protein length

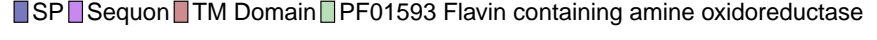


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEIWPDDGGFLDVENGGDTPKVLHFYDGSVMYADHWIVTVLGLVKREIRDGSGMFSPLPFSKTRAIKILGFGVANKLFLGLSPTKDEDAMKFPYLGOMVHFQPDKLRHPKTPWMMRRTASLGPYVGSNVLGWFAGAEALEGLDNEEHDGFSMTMISDFLVNKHNLKLNGLHAEISCFKFDKVLKSGWGTDPFLFGSYSYVAVGSSGDDLTMAEPLKRSNYSQGISPLQVLFAGEATHRTHYSTHGAYFSGLEARNRLGHYHRDIP-

NbL12g21370.1 PI-PLC_X_domain-containing_protein_At5g67130 [MW = 49.01 kDa]

No. of times detected



log(intensity)



Values from



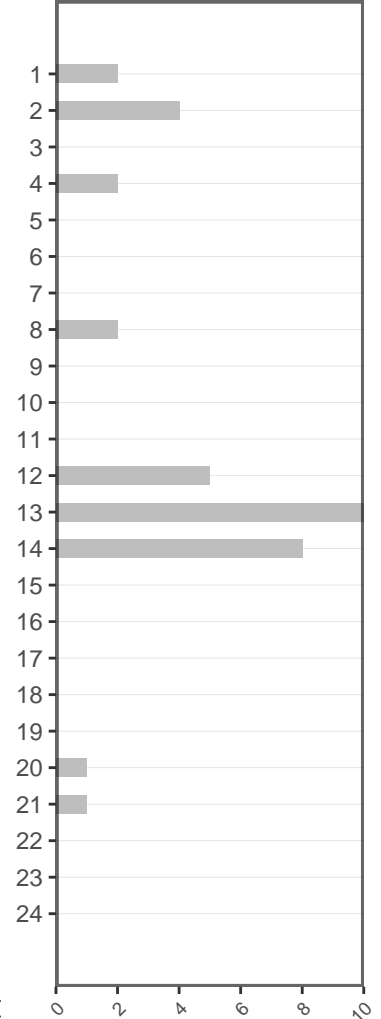
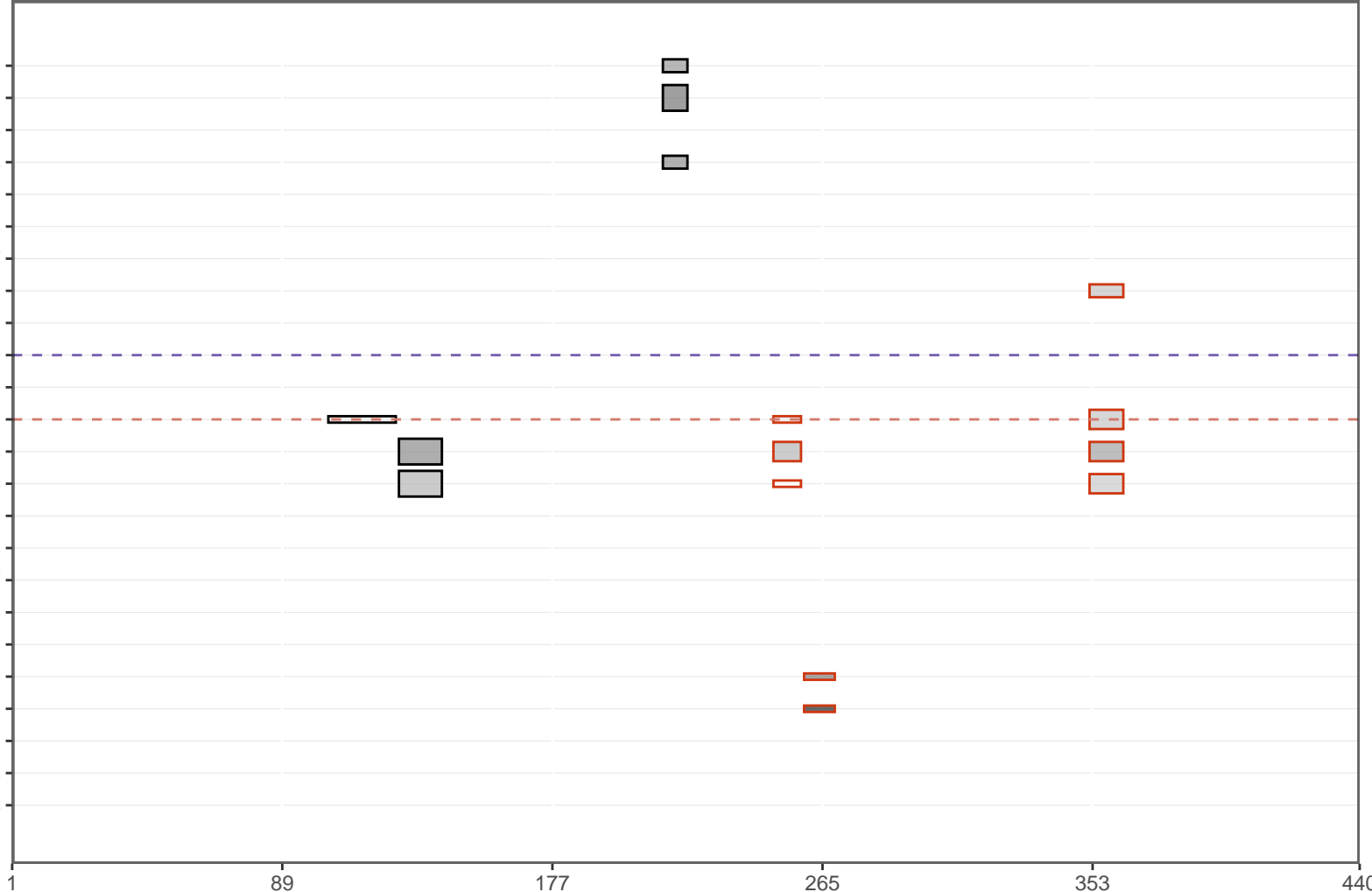
MW indication



Molecular weight



Gel Slice



Protein length

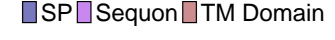


Peptide counts over 4 repeats

Pfam domains



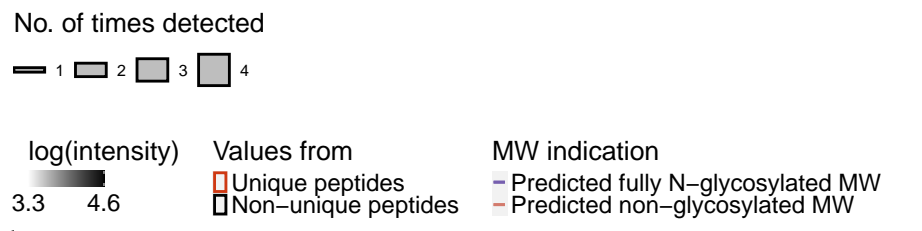
Pfam Description



Protein sequence:

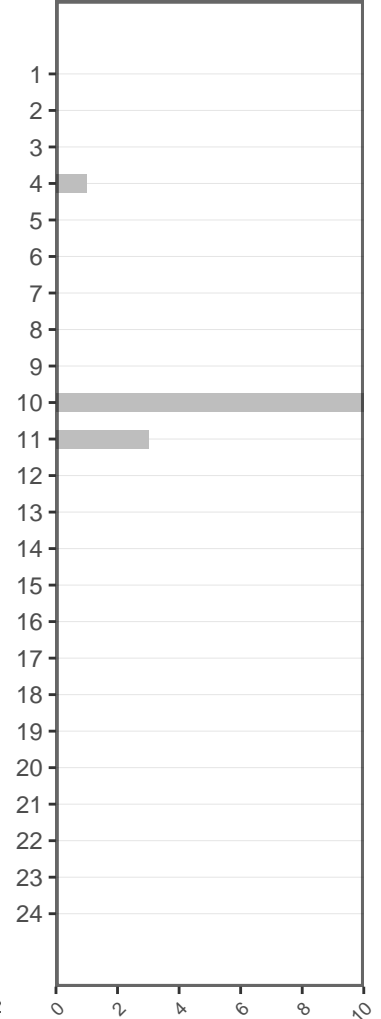
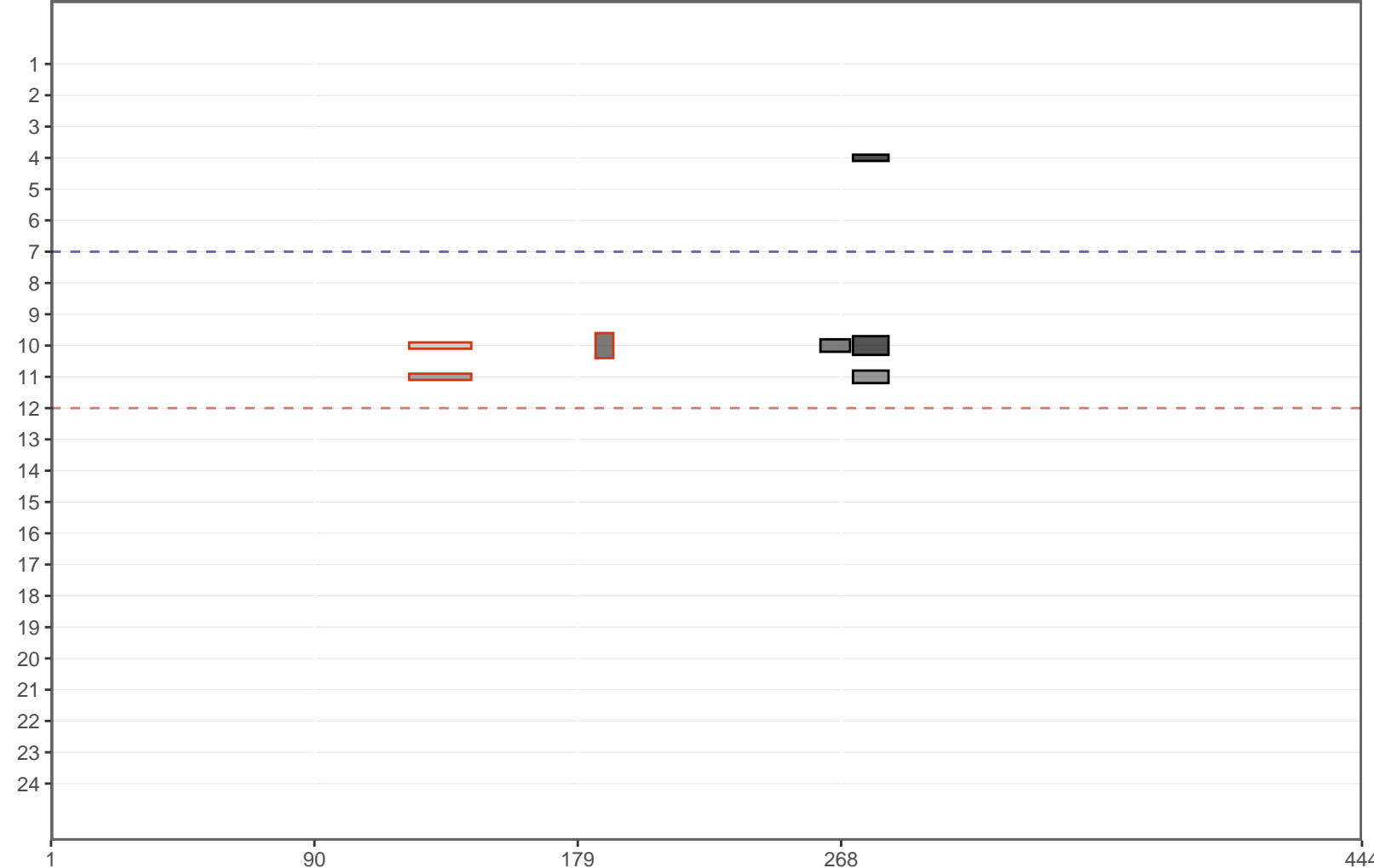
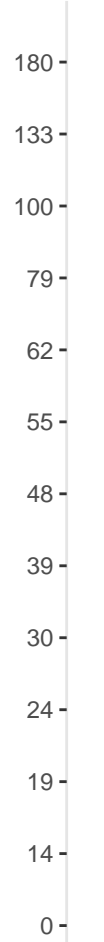
LTRVFTDAGLDKYRFFVSKMPKGGDDVPTVNDMWKKNHRLVFTSDSKEAAEGIAWQWRYMVENEPGDPVMPGACSSRKEKPLNRSASLFLMNYFTVAQNGVCKEHSTQLVDTVGACFKAAAGNLMFNYYWVNFYMRSDGGGVFDVLDRMNGETLGGGPTVTAGGGERFGVGRNITANATPTATNAAGSFSGSVQLGTHASAHFSSIRYFLLSVWLYLF

NbL12g21270.1 PI-PLC_X_domain-containing_protein_At5g67130-like [MW = 48.69 kDa]



Molecular weight

Gel Slice

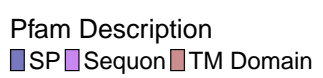


Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:

VFNASGLNKYYWTFVSRMPKKGEDWPTVDDMYKGNRILVFTFSKSKSEAGIYEWRYVYENGNGGDMKVGSGPSRSESPPMSTSSISLVGNFYDPNINTAACVDNSAPLVNMTKTCFEANGKRWPNFIAVDFYKSKSDGGGAPAVDEANGQLGGNCSSIAVYKASGTHKCEAPMLSPRRPAGATTAGTSGGGNENKNSHRRKPLHLWJSTFAALLLRV

NbL12g21160.1 zeaxanthin_epoxidase_chloroplastic [MW = 72.56 kDa]

No. of times detected



log(intensity)



Values from



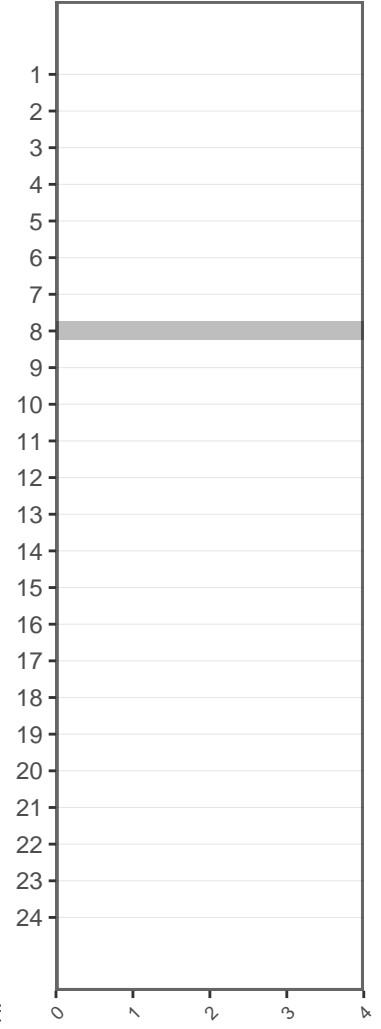
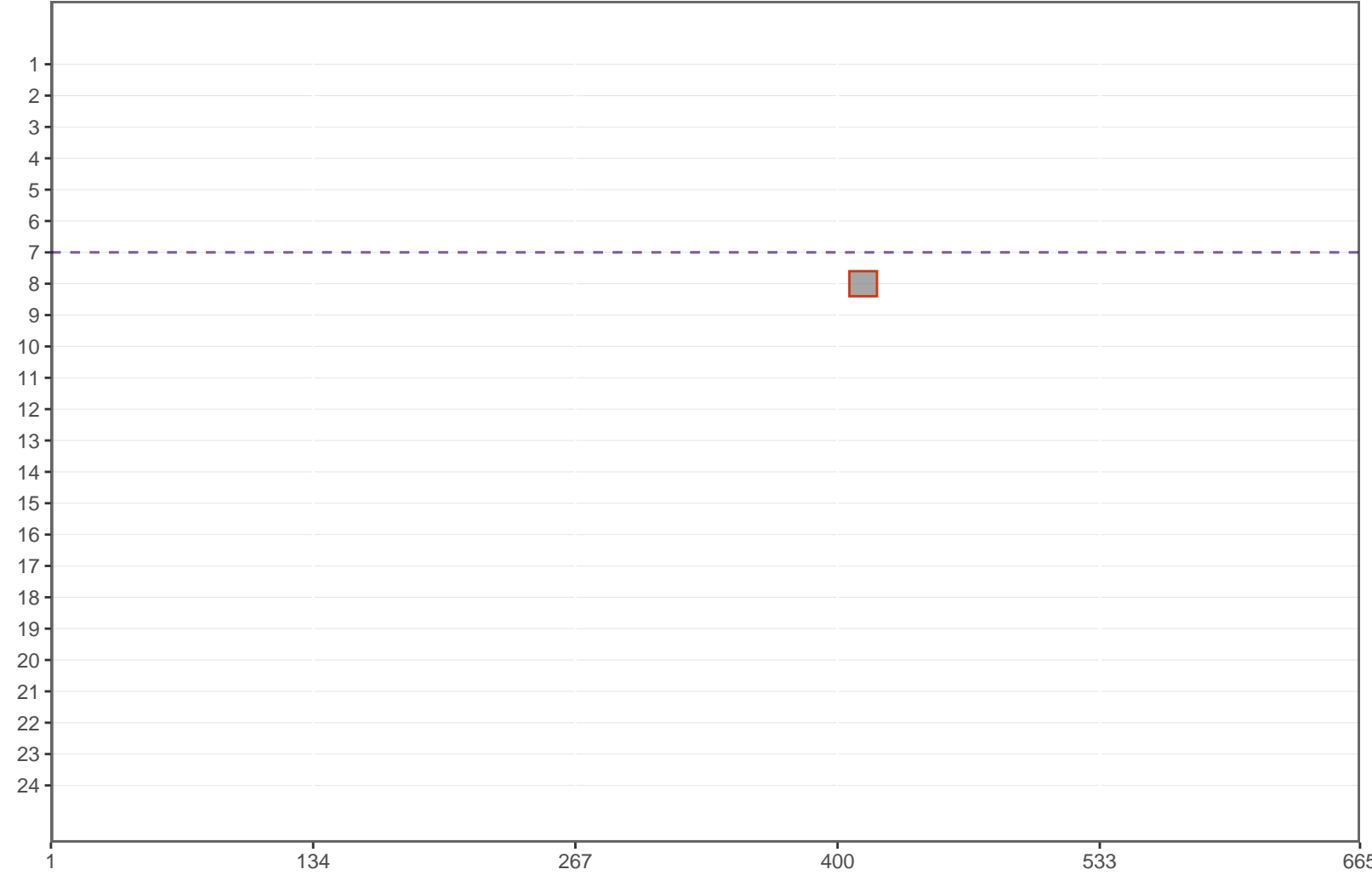
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IKKARLLKFEIGVCINVIDLVAITNEDAILRRDIYDRPPTFNWVKGRVTLIGDSVHAMQPNIGGGGMAEDSVQLALELDELKLSRSTEGSTPYDIISLRISYESSRKLRYGVHIGLARMAAMASTYKAYLGVGLGFLSFLTKFRIPHPGRVGGRRFDLGMPLMLSWVLGNGENLEGRKIKRILSEKANDQLRINWFEDDDALERATDAEIVLLLPAGNGNAAAEALVLSRDEDPTPTGTGVSHTKIPGKSVIPLQVSEM HARISYKGGGAFFYDLRBEHIGTYITDNEGRR

NbL12g21050.1 uncharacterized_LOC109225879 [MW = 178.96 kDa]

No. of times detected



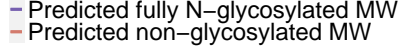
log(intensity)



Values from



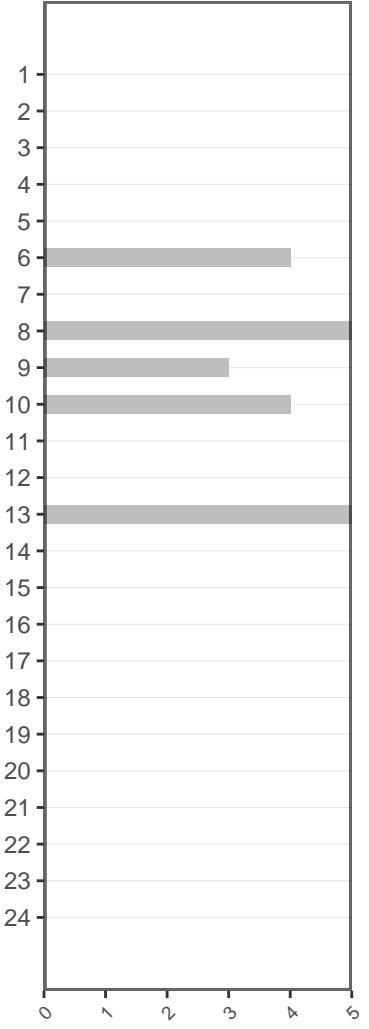
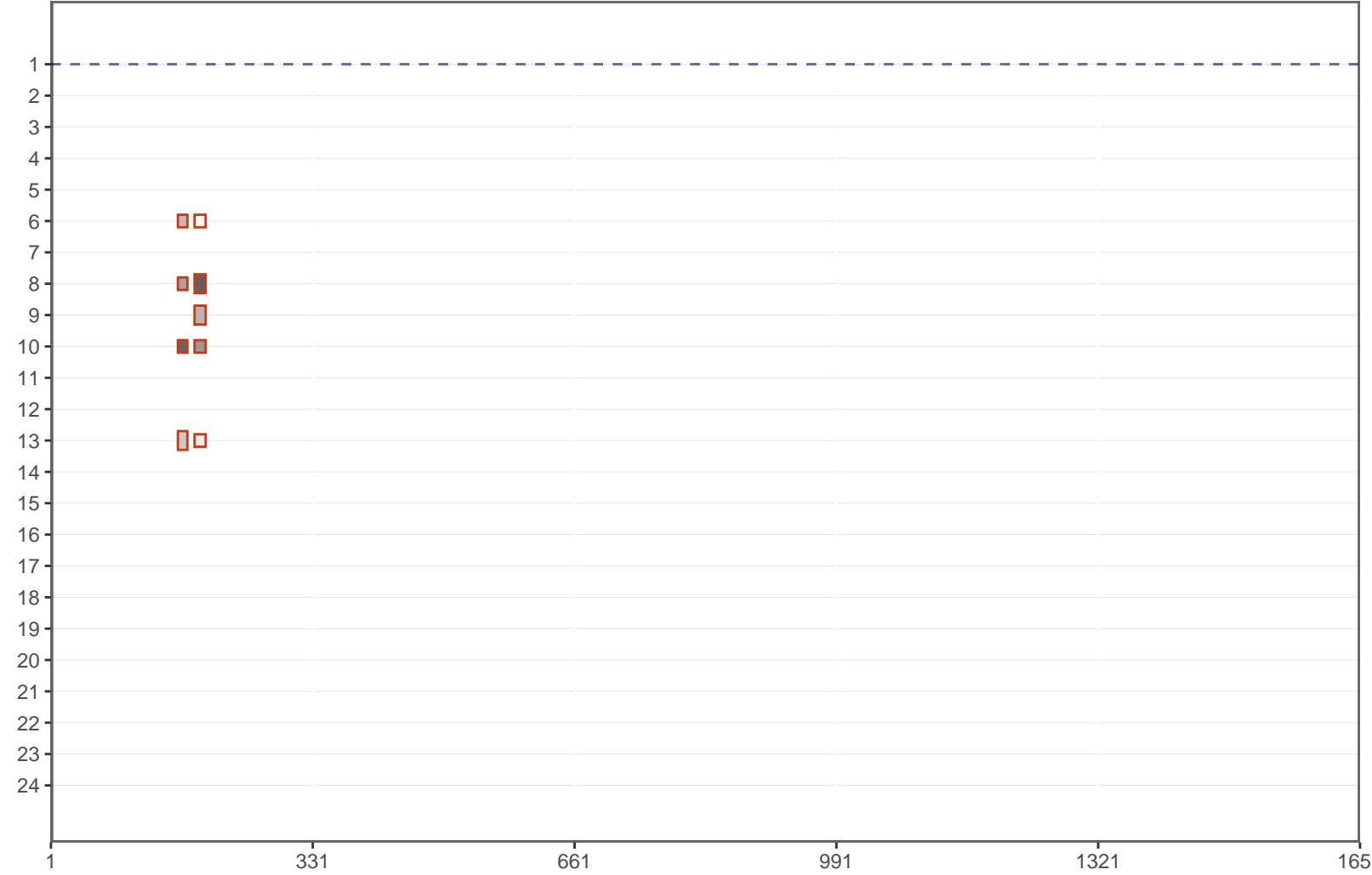
MW indication



Molecular weight



Gel Slice



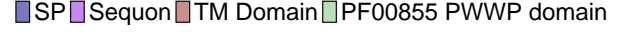
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AATADKMSIEENLNVEGAIKSGTIVNSGADVPPPVEENTFNVEGAIKSGAVTNSGADVPPSGDQTVEVGSHTSNAETNGANEVQDSSKADEGLVFRRAHAEMKVADEPEKGEIETGISHASNAETNGANEVQDTSKADEGLVFCADAAEMKVADEGEKGEVLEKLDADTVGESSSEQDKGTEEVAKTSHTVMLNEKPVBLKMGPGYLIIPQTDDEGYSISDLVWGVKVRSHFVWPGQIFDPSDAEKAIRYKKKDFLWYFGDRTFANDBAVLRFPCSNFSQIEKG

NbL12g21020.1 uncharacterized_LOC107785953 [MW = 29.11 kDa]

No. of times detected



log(intensity)



Values from



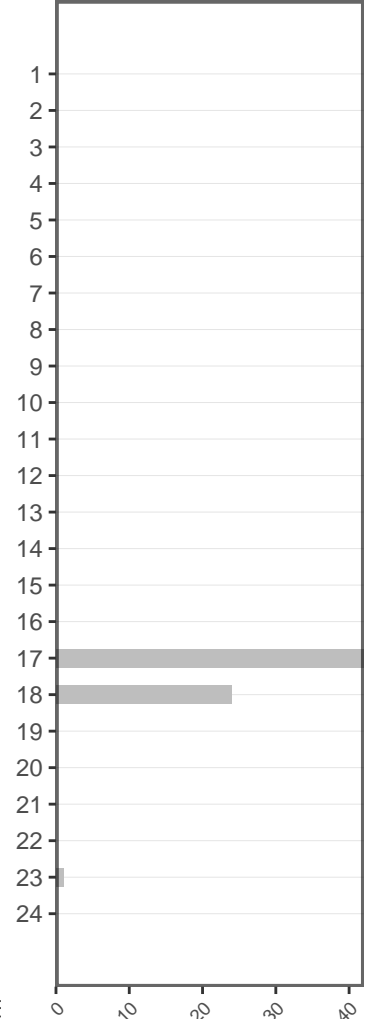
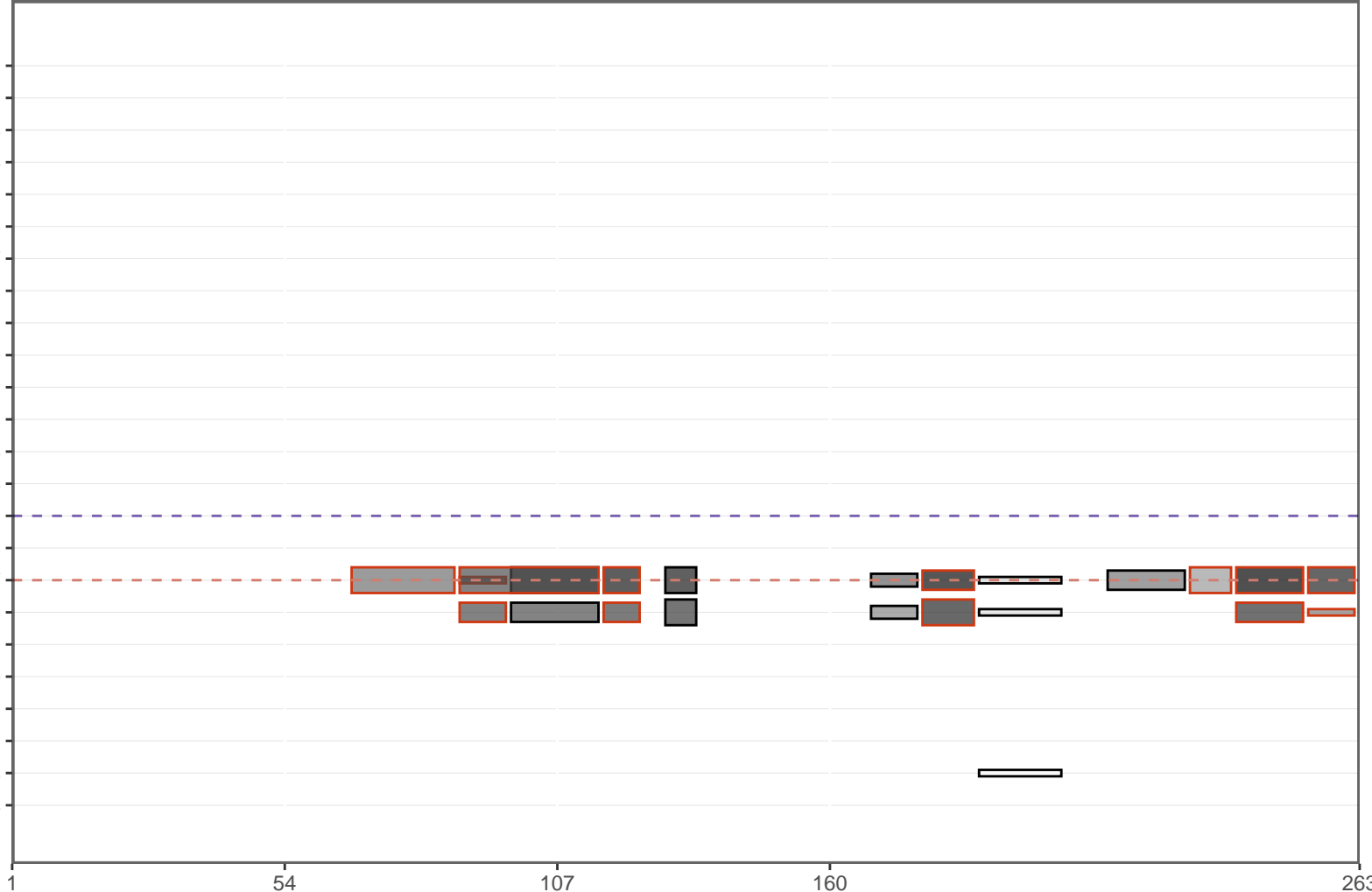
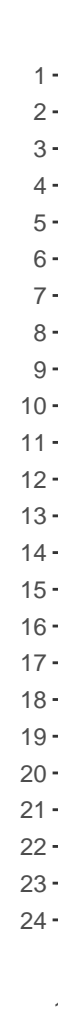
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

LDLSRGIPRFYIMQLKDRSLRFSNTHANVTGCLGSGGNWYLGWAKPVDPAIDKGAUADNDSRGHFYPPVADEVQAFRISGPKFKLNHGTHWAGPLEFTDDKMDYFVLELNKNTNVDHTTHDFWKNVEVFLDDP

NbL12g20890.1 vacuolar_protein_sorting-associated_protein_26A [MW = 35.66 kDa]

No. of times detected



log(intensity)



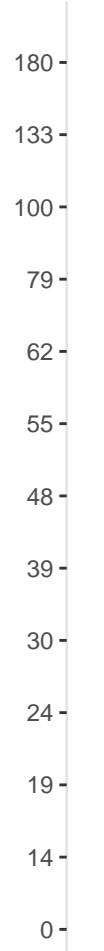
Values from



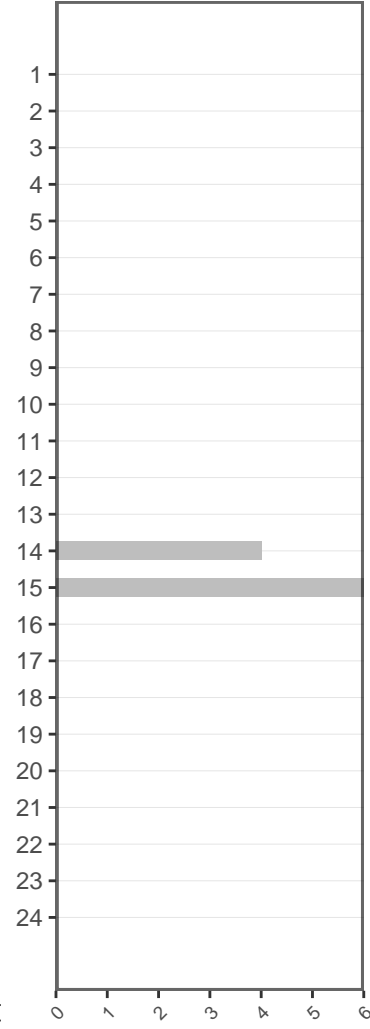
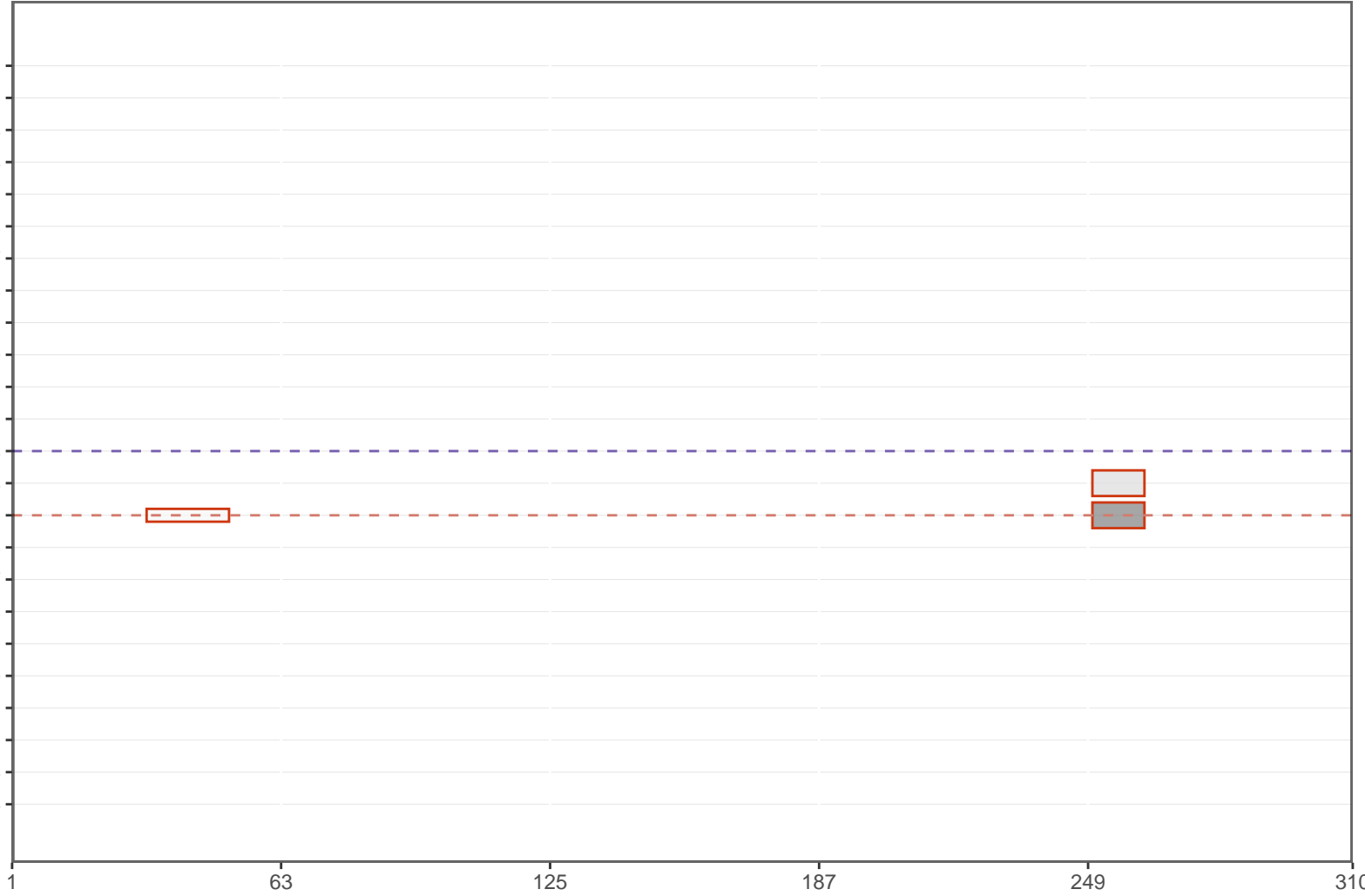
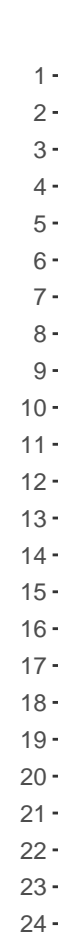
MW indication



Molecular weight



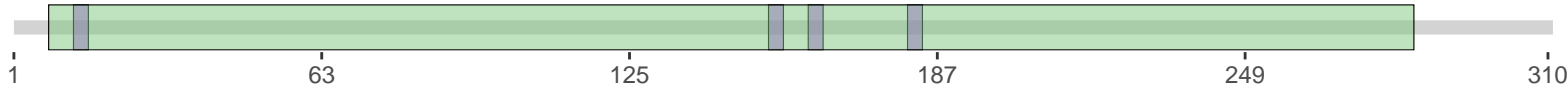
Gel Slice



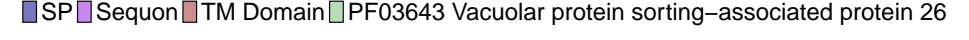
Protein length



Pfam domains



Pfam Description



Protein sequence:

GSIVIEYQYFVVRNYSPPPSNNSKMEVGEDGLHIEFVYKSKYHLKDKVIGKIVFLVRIKIKKMDLEIRRRESTGSGANTHYETETLANFELMDGAPVRGSEPIRLFLSPVELTPTVIRNINNFQSKYYLNLLVDEEDRRYFKQGEITMFLRAETSVINQAVGAT

NbL12g20750.1 GDSL_esterase/lipase_At5g33370-like [MW - SP = 37.25 kDa]

No. of times detected



log(intensity)



Values from



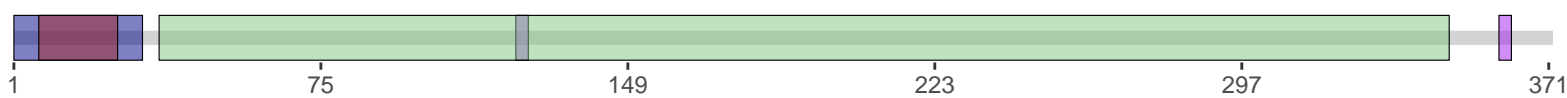
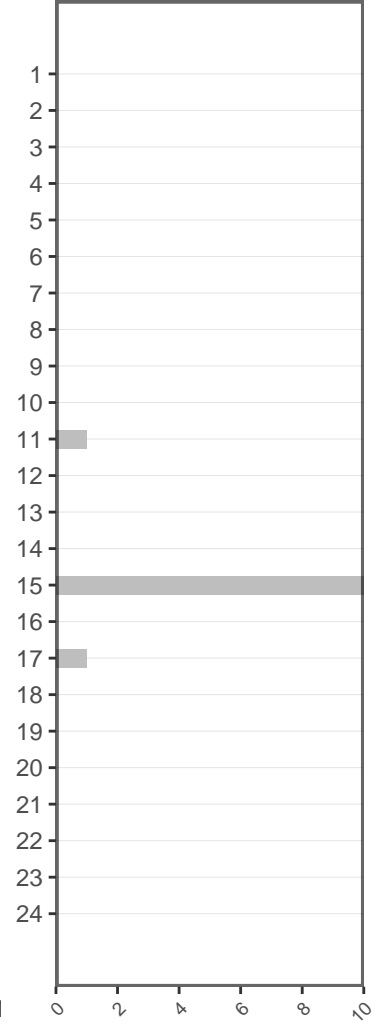
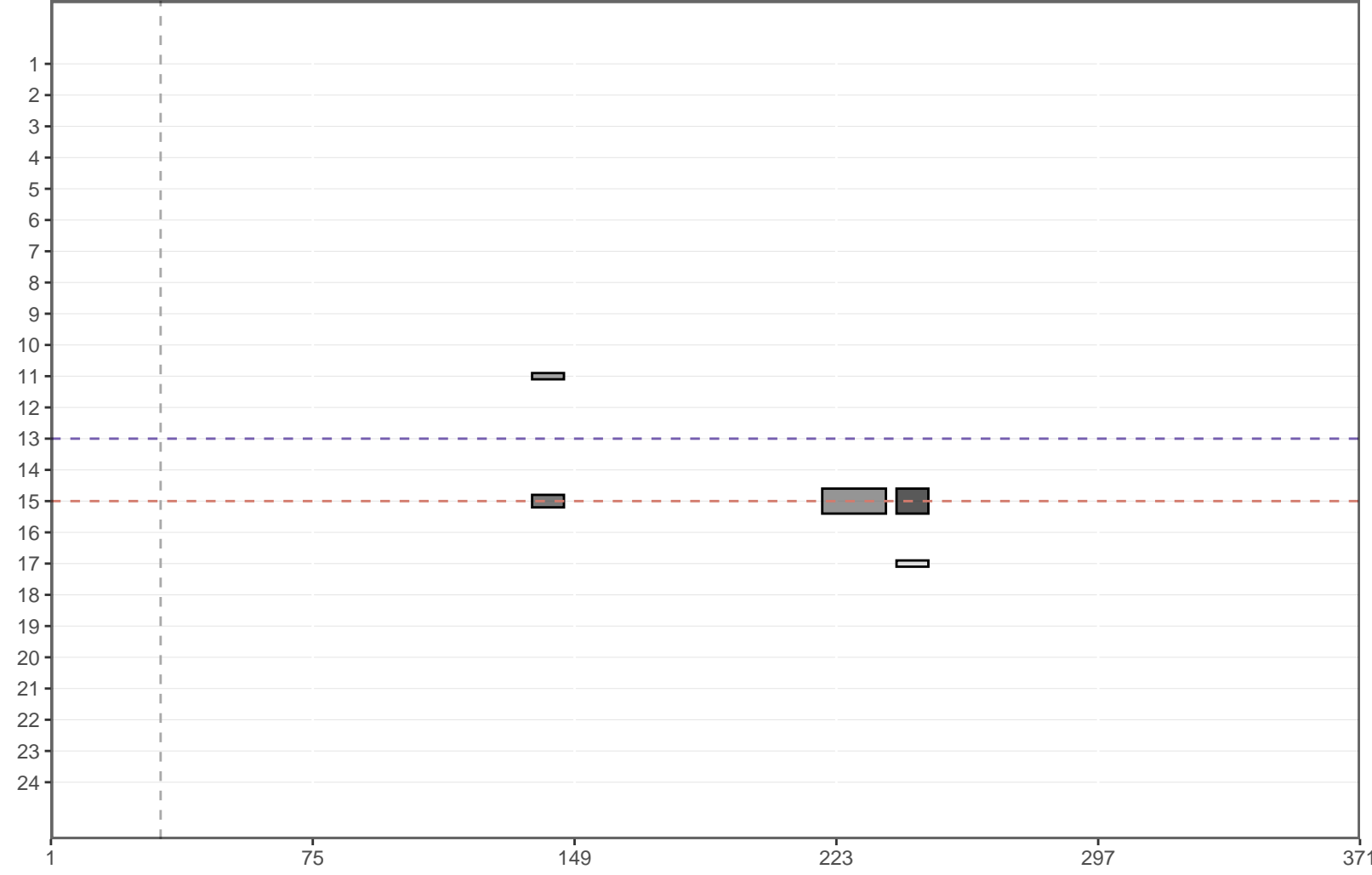
MW indication



Molecular weight

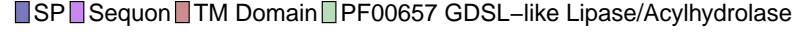


Gel Slice



Pfam domains

Pfam Description



Protein sequence:

MFVNYLYPFSARERGFALPDVRYRYSSEYRKLQKLVLDGARRVLTGTGPMGCVFRELADRRTGEGCEVLRGAASLFPDLTQLLSLNAQLAADVFAANTYTMHMDVFNPAQAFGVTSKMACGGGGPYNGIKLCTPLSNLCPNRNLYAFVDFPHPEKANRIVGGIFGTSSEYVMPNMLSSIALDSRT

NbL12g20700.1 uncharacterized_LOC104249736 [MW = 25.63 kDa]

No. of times detected



log(intensity)



Values from



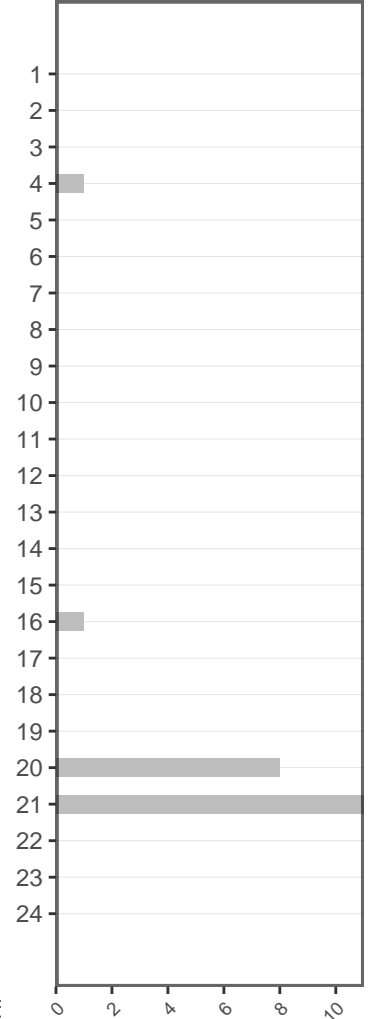
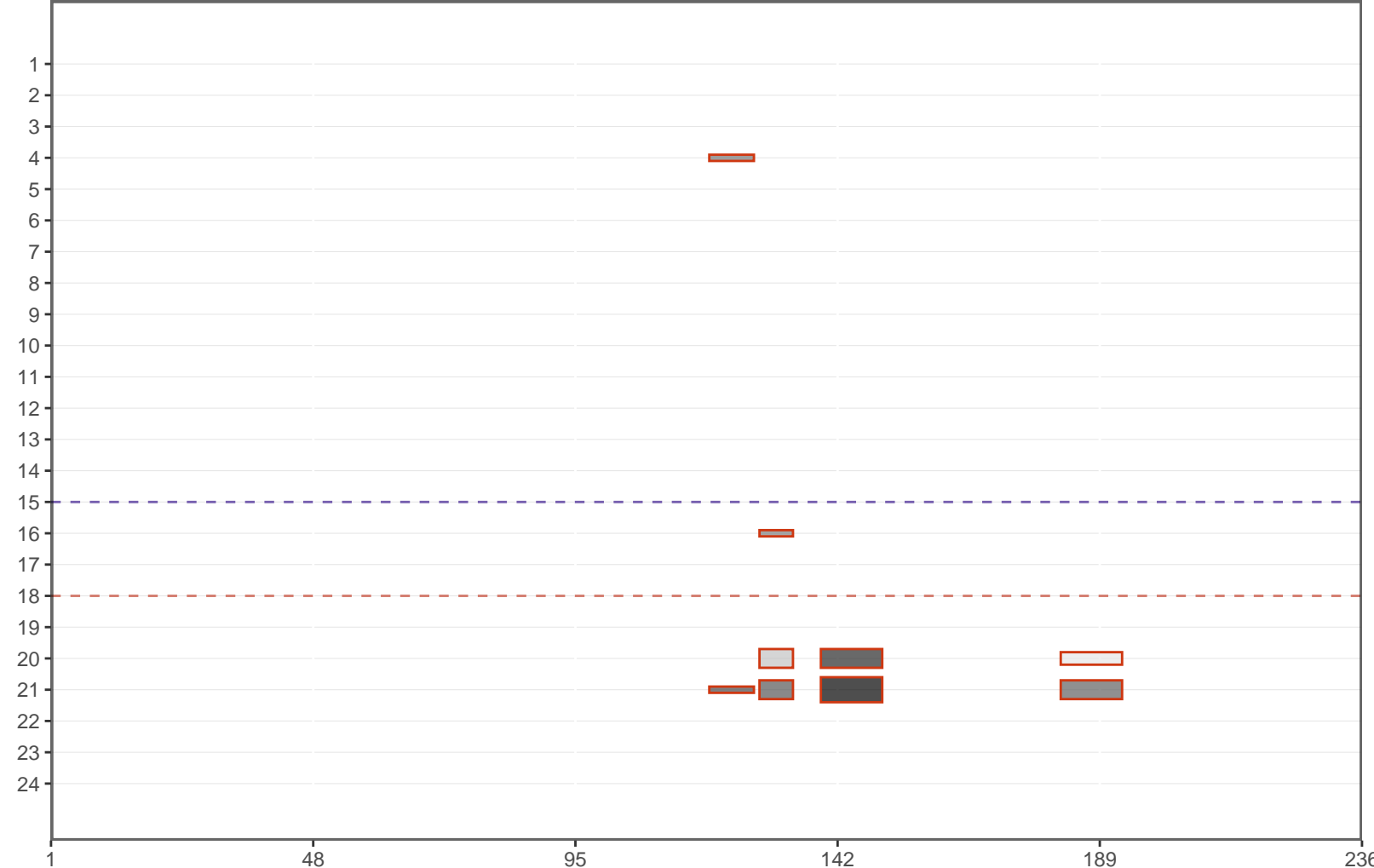
MW indication



Molecular weight



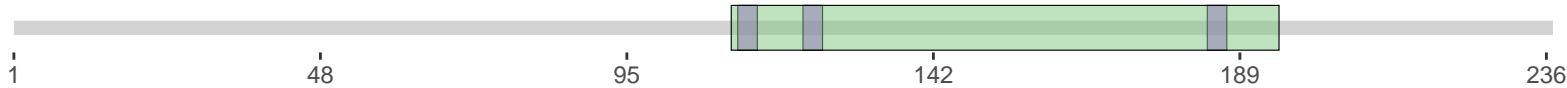
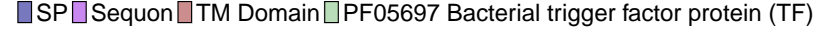
Gel Slice



Protein length

Peptide counts over 4 repeats

Pfam Description



Pfam domains

Protein sequence:

IFEDFSVTTSGVNGENKLIKISVNVSGAKTEEIFGKVFRRMVEDAGPIPGFRFRVKGKGTNPRDLIELLGYSKVYKQVKKINSTISEYVEKVDPLPSPSLGISVLHHTLLLKLDLDRVRIKVGCF

NbL12g20610.1 PHD_finger_protein_ALFIN-LIKE_4-like [MW = 27.77 kDa]

No. of times detected



log(intensity)



Values from



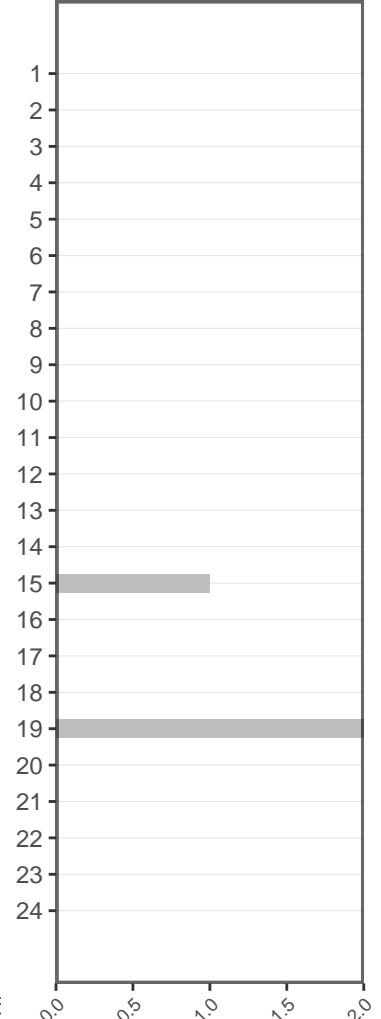
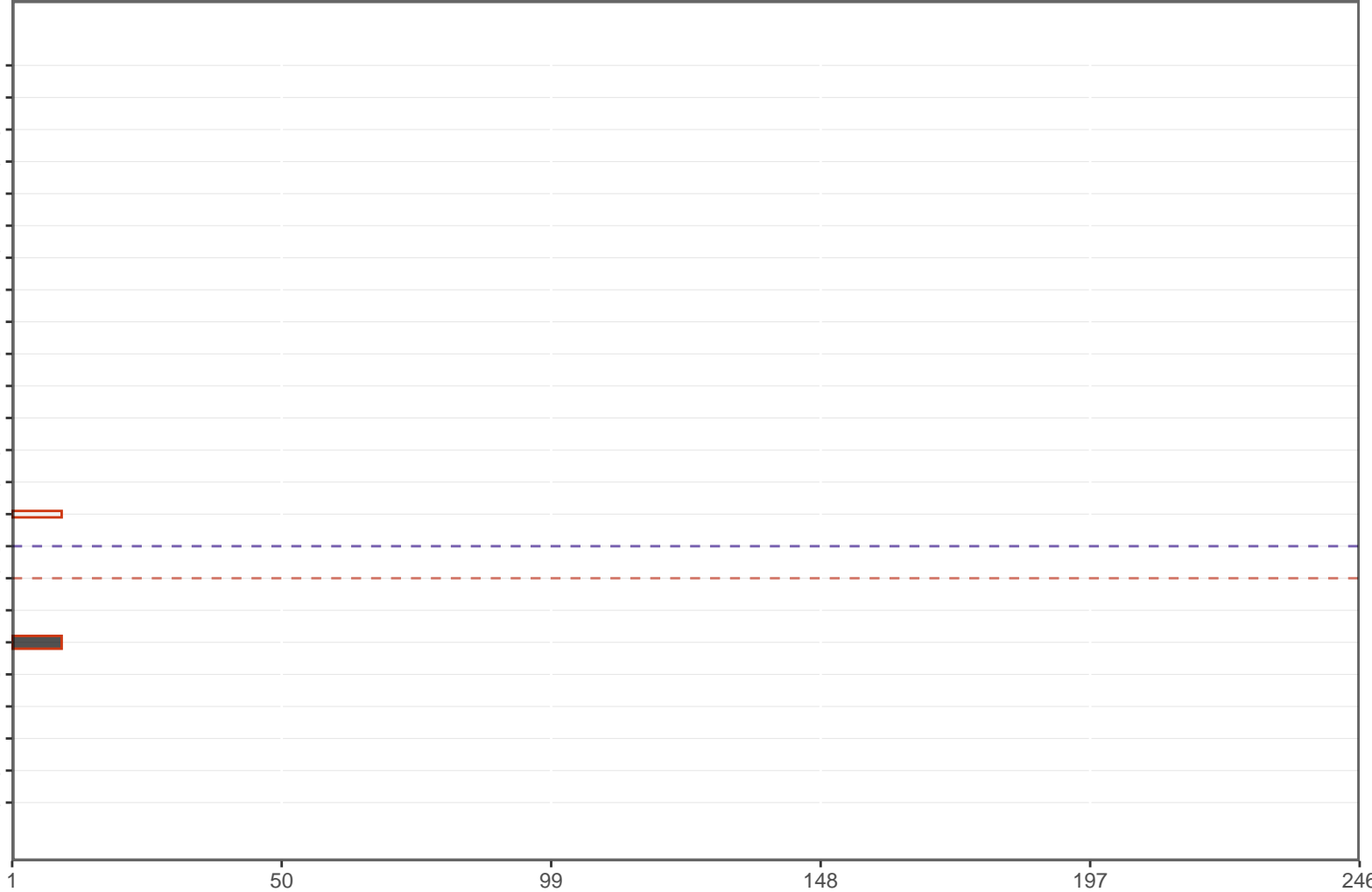
MW indication



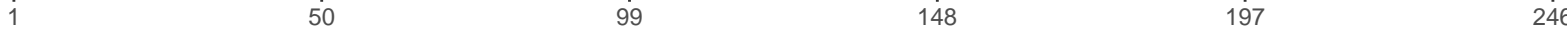
Molecular weight



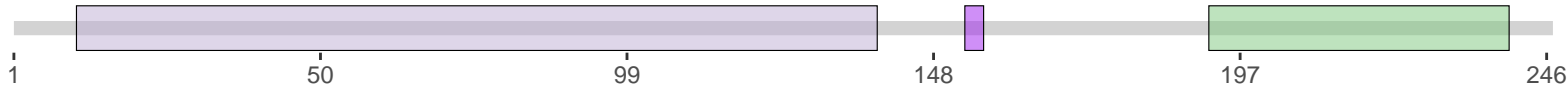
Gel Slice



Protein length



Pfam domains



Pfam Description

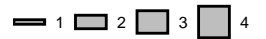


Protein sequence:

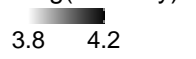
ARFGDKADRRKLFENMINDLPTTVEVVTGAAKKQVWRKRSVSNH66TKR66SKVSKYKVEVDEDDGLDEEEEEHGDTLGGAGGENYASDFEWWGGDIDGERWFRHKGKVKITPAEAHKGKYGKPTGSNKRPRP

NbL12g20600.1 threonine_synthase_chloroplastic-like [MW = 54.34 kDa]

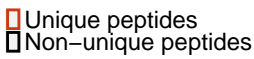
No. of times detected



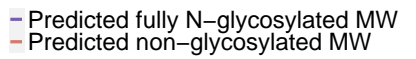
log(intensity)



Values from



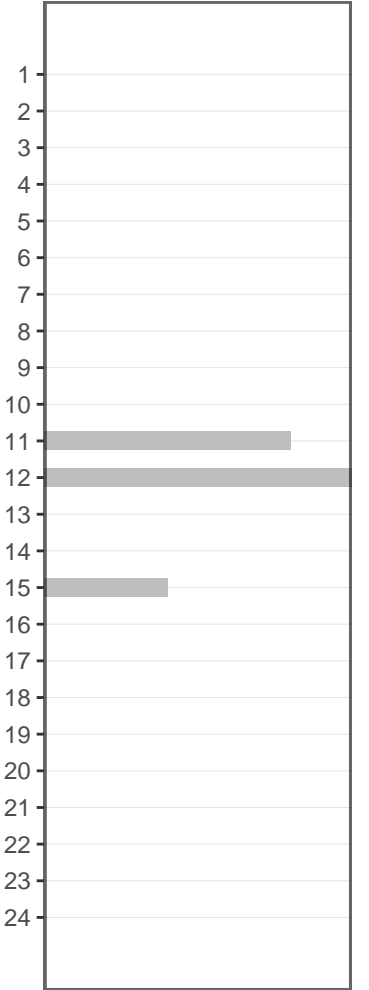
MW indication



Molecular weight



Gel Slice

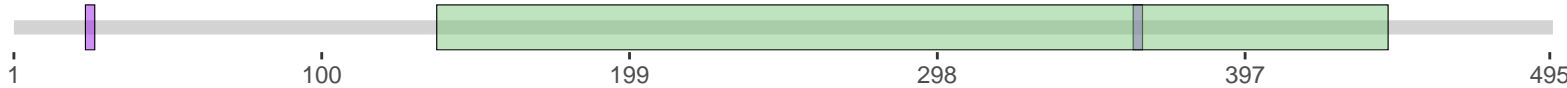


Protein length

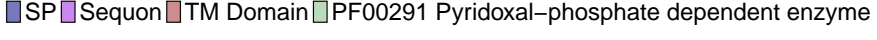


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

AAQLVQPIANGAFVSDTDFDGMKLRVETSELPRVLANSLRLLEGOKTAIELGGDFVEVFDWVHPPGGNLGNVWFYKGRKMGEMGLVDRIPLRVCAQAGAAANPLVMYKSGWTFNGFQPKANTTFASAIGKDFVSDRAVYALKNNGNIVEEATEEELMDATALADSTGMFCFHTGVALTALMKLRNSGVIAPTERTVWVSTHGLKFTGSKIEVHSEKIKDMSRFANFPVQVKAADFGSVMDLVNLYLKSKE

NbL12g20510.1 CBS_domain-containing_protein_CBSX1_chloroplastic-like [MW = 26.28 kDa]

No. of times detected



log(intensity)



Values from



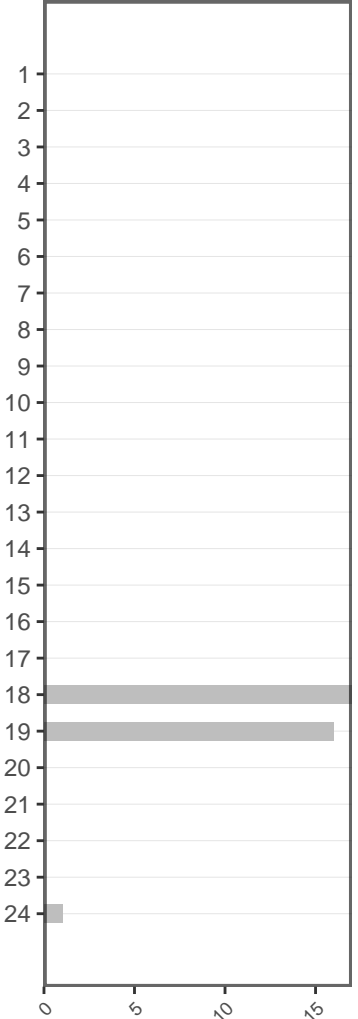
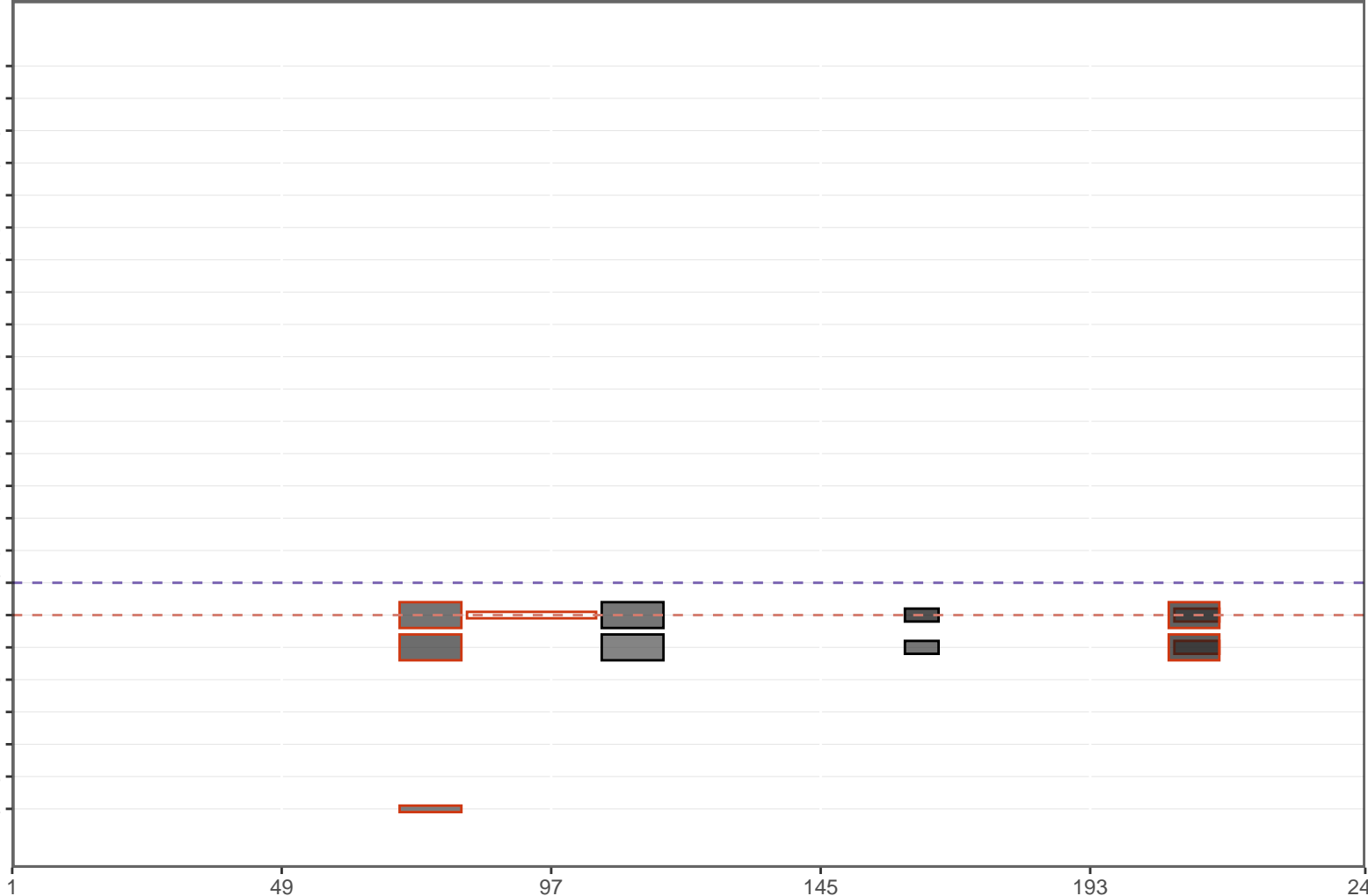
MW indication



Molecular weight

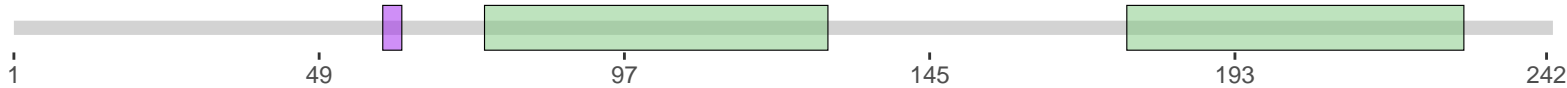


Gel Slice



Protein length

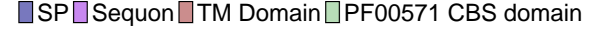
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

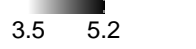
GFPVDDNWKLVGLVSDNLLALDSISVQILLGGTTDADMPFEVDNKNWTFNIEQKLLGKTKGKVVGDMLTPAPLVVRETNLEDAARLLKTKYRRLPVVDGDKLVGHTGRNVRAALGVKRNEMEG

NbL12g20150.1 kinase_II_subunit_alpha-like [MW = 39.33 kDa]

No. of times detected



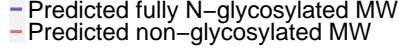
log(intensity)



Values from

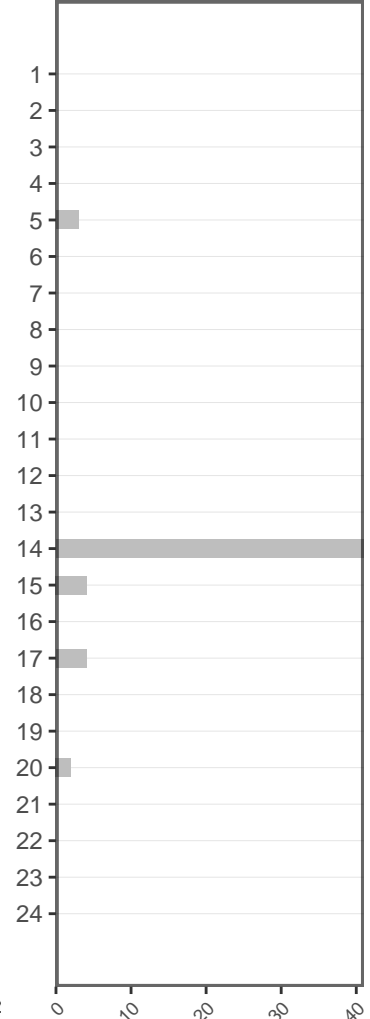
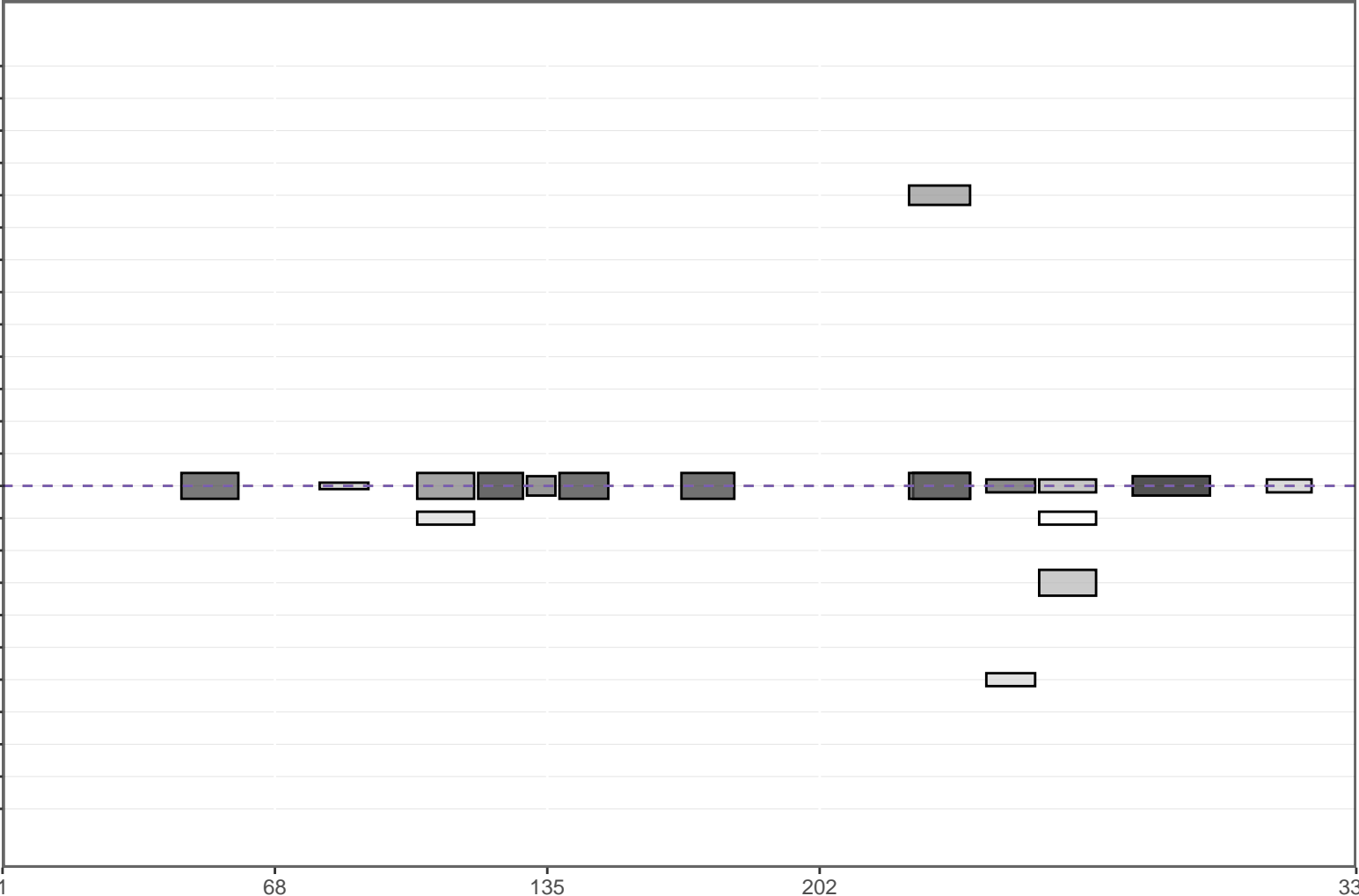
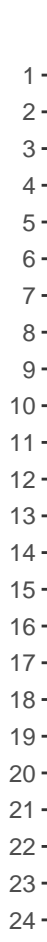
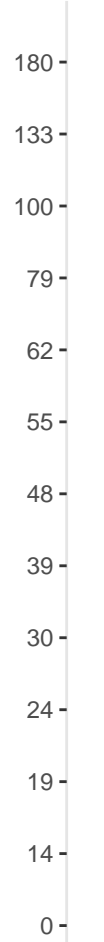


MW indication



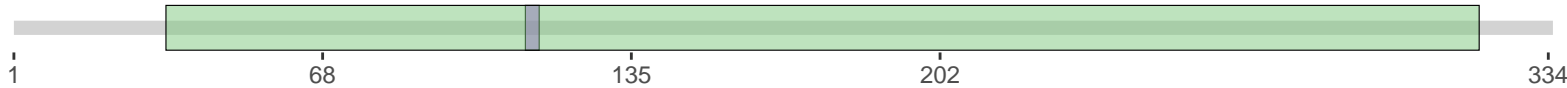
Molecular weight

Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

VMDHELRLRLDVGWLAEFYHPGKEYNVRVAGRYFKGPPELLVDLDQYDYSLDMSLGGMFAQMFYKPEFFYGHNDGDLVQAKVLTGDELNAVLRHKYGLLEDPGLEAMVGRHSRKPWSKFNADNGHLVSPFAIDFLDKLLRYDHSRLTAKEAMAHPIFLGVRAAETSRRMAGI

NbL12g19960.1 60S_ribosomal_protein_L26-1-like [MW = 16.71 kDa]

No. of times detected



log(intensity)



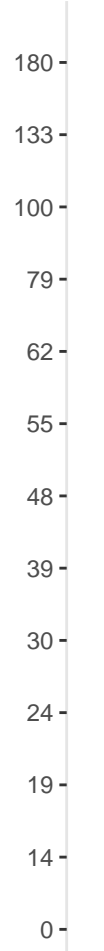
Values from



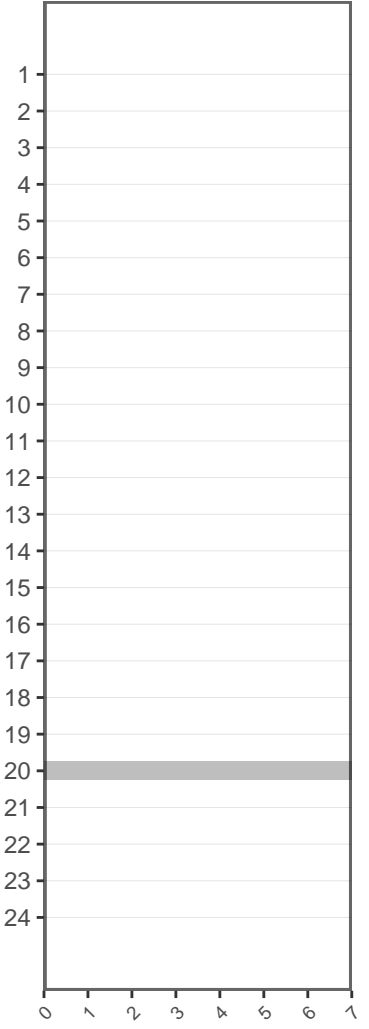
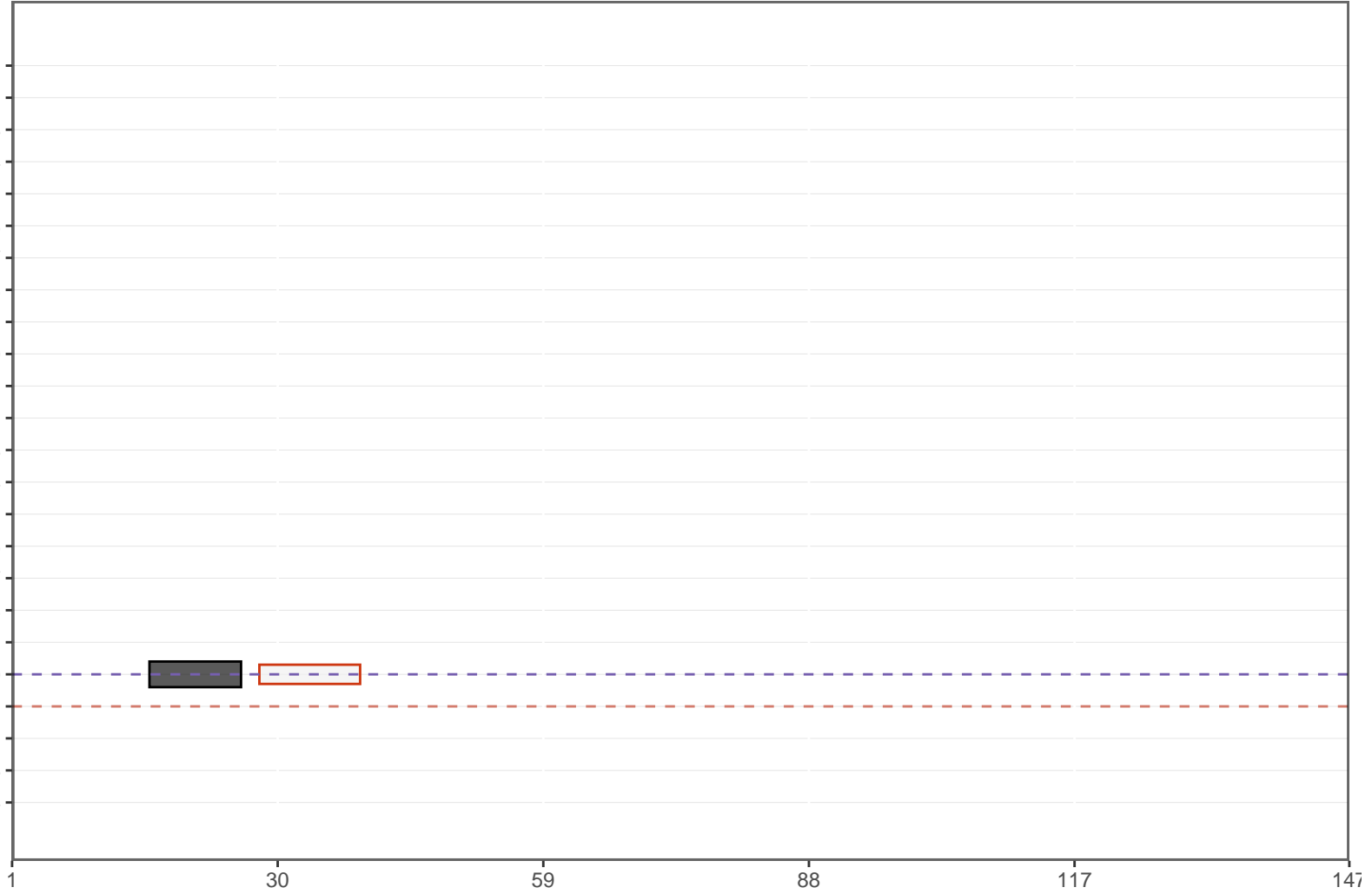
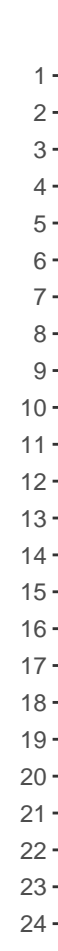
MW indication



Molecular weight

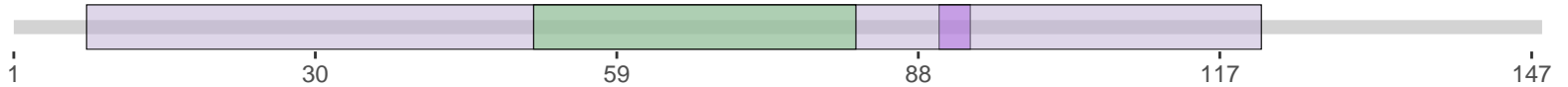


Gel Slice



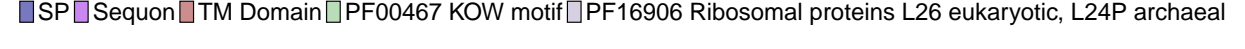
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

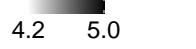
GTYYGREGKLVQVWRKRWIHERITREKVNQSTFVWGHIPKVAVTKLRLEKDRKLLDRKAKGRAAAADKDKGTFKTAEDIMGTVDI

NbL12g19640.1 superoxide_dismutase_[Fe]_3_chloroplastic [MW = 22.96 kDa]

No. of times detected



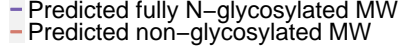
log(intensity)



Values from



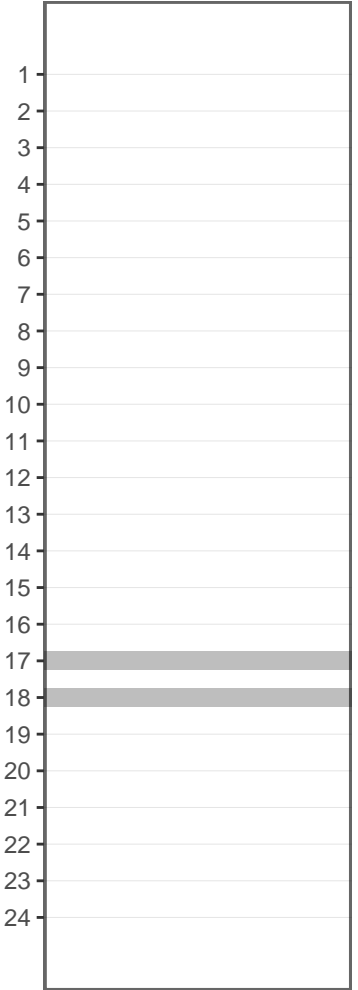
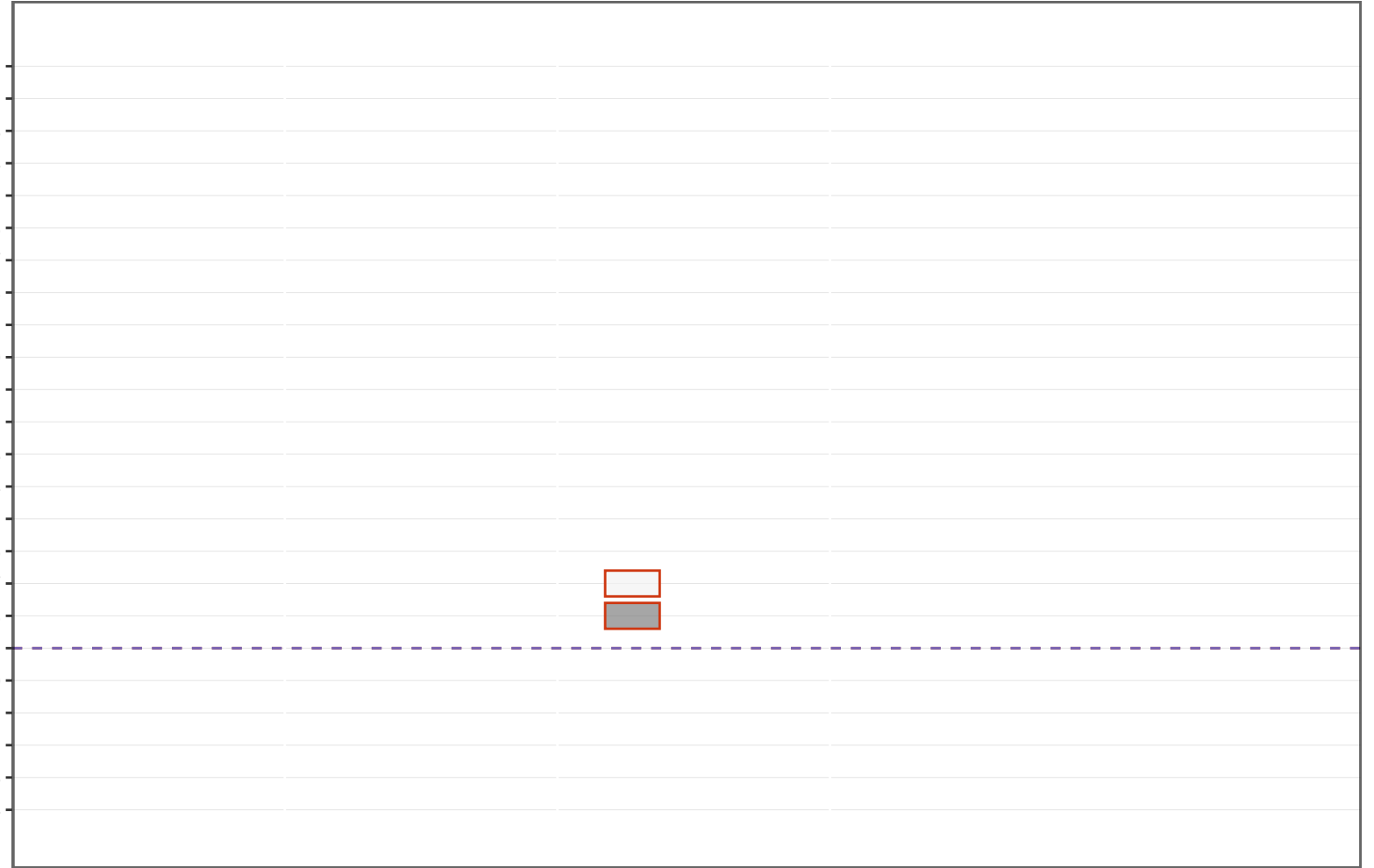
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains



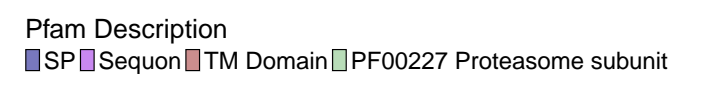
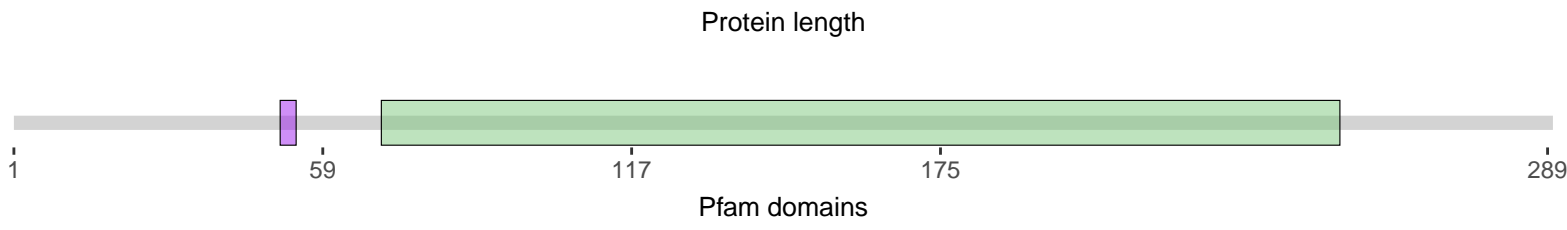
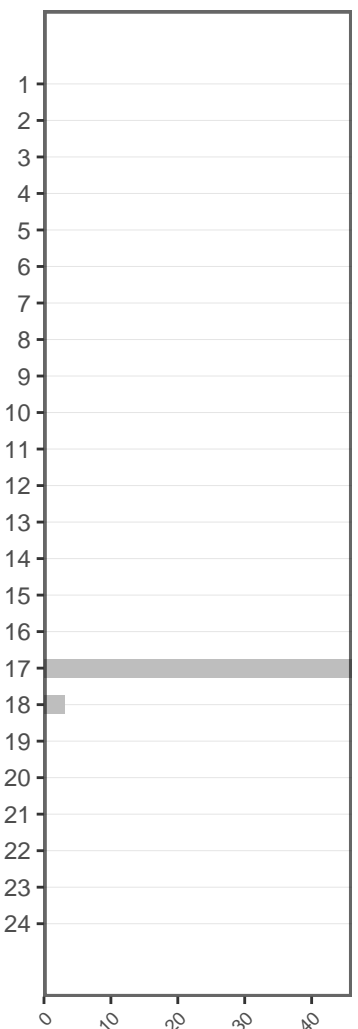
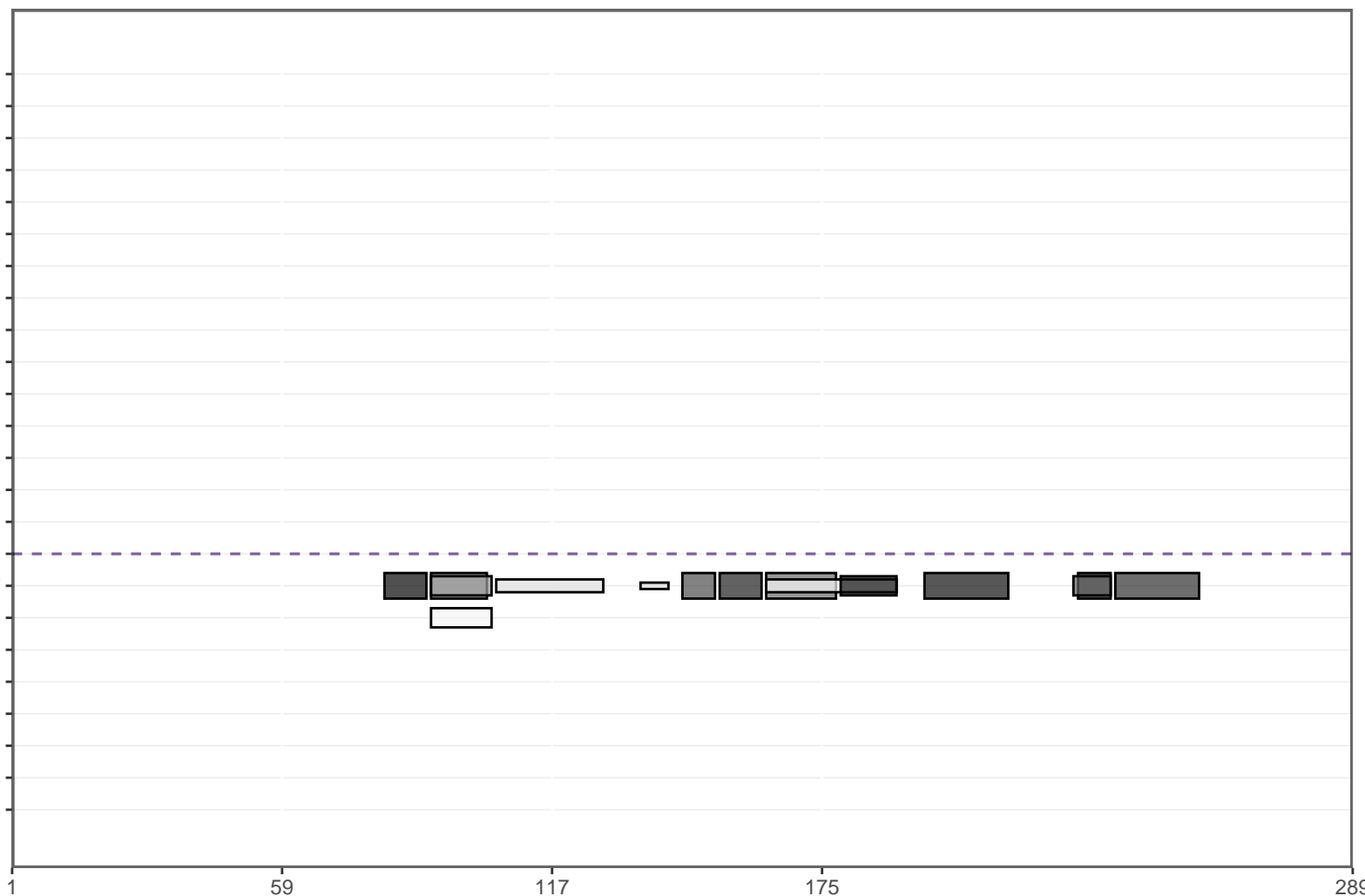
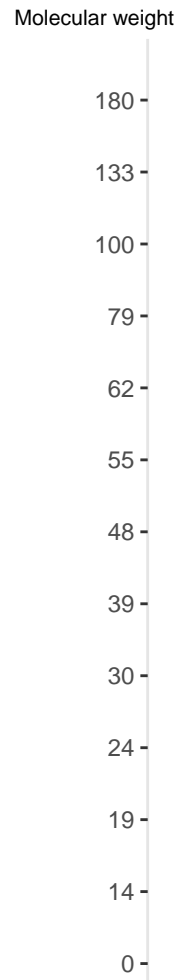
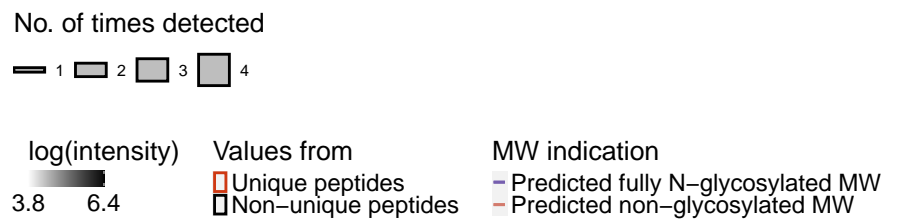
Pfam Description

- SP
- Sequon
- TM Domain
- PF00081 Iron/manganese superoxide dismutases, alpha-hairpin domain
- PF02777 Iron/manganese superoxide dismutases, C-terminal domain

Protein sequence:

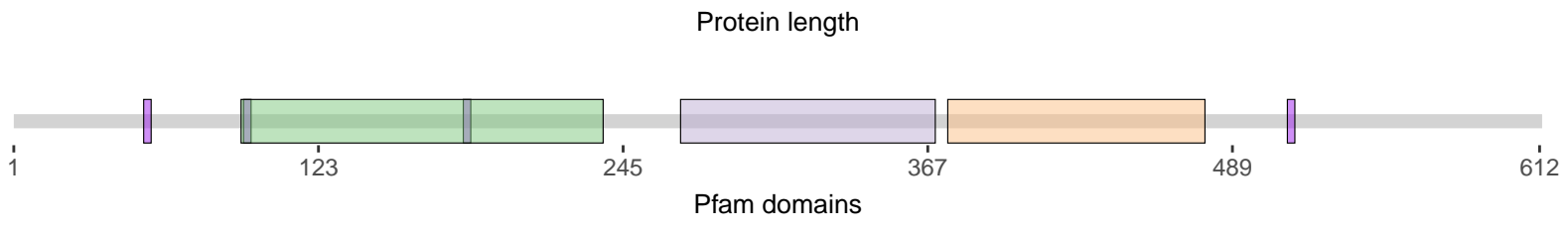
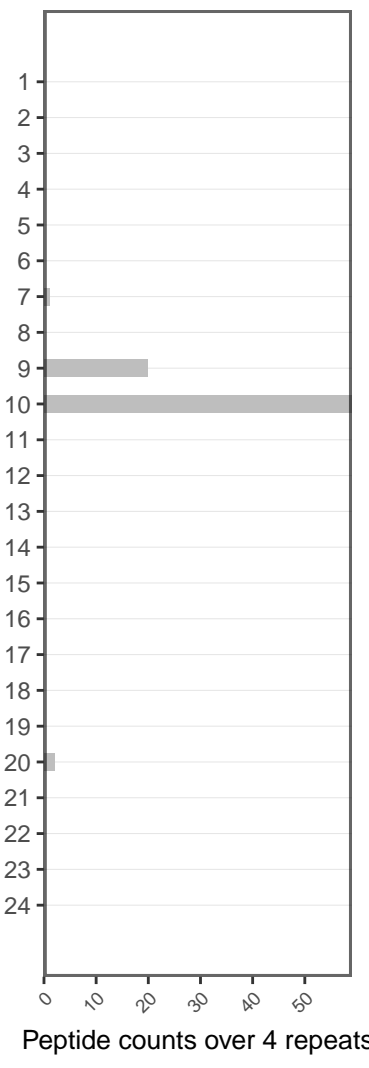
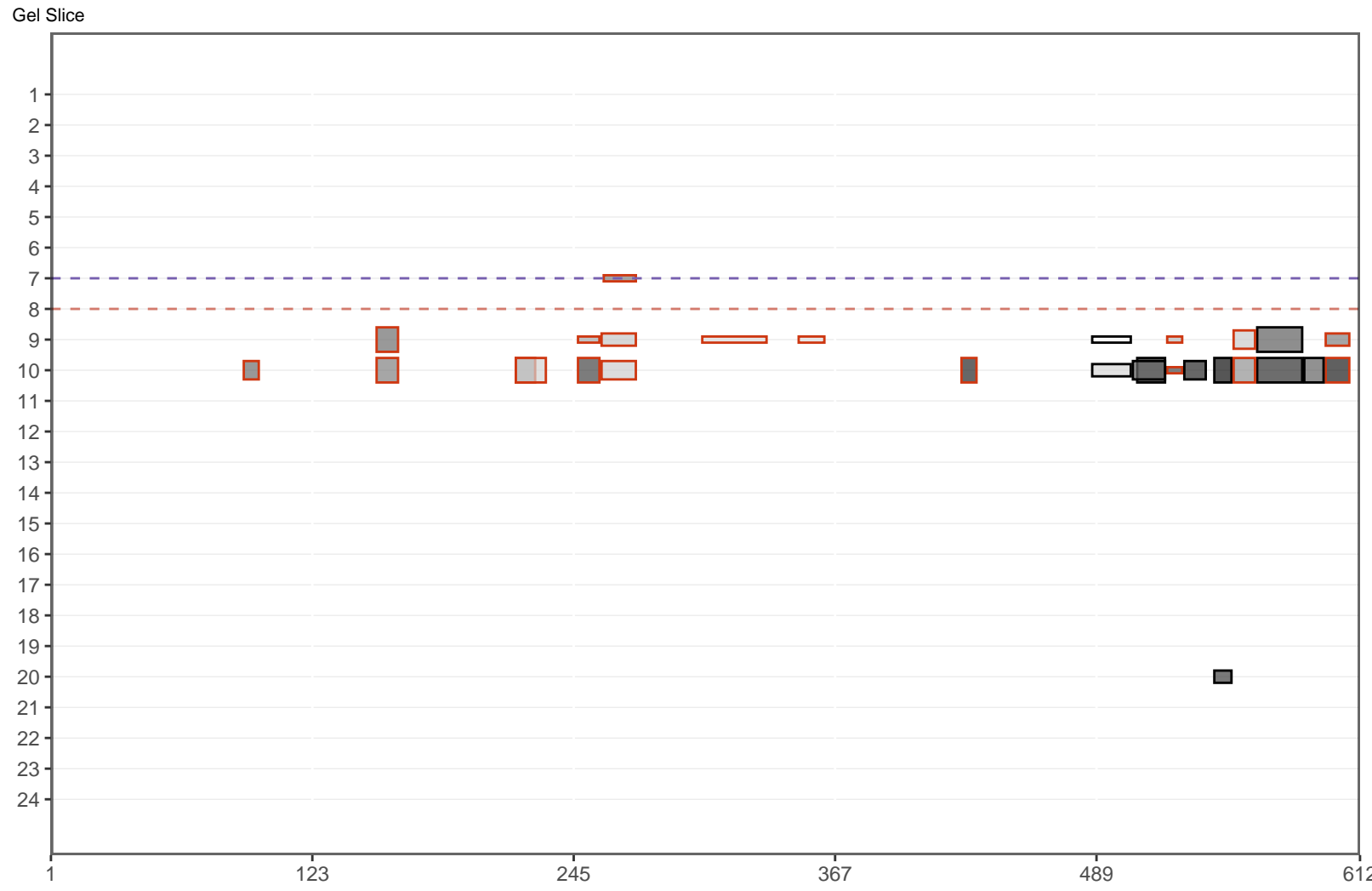
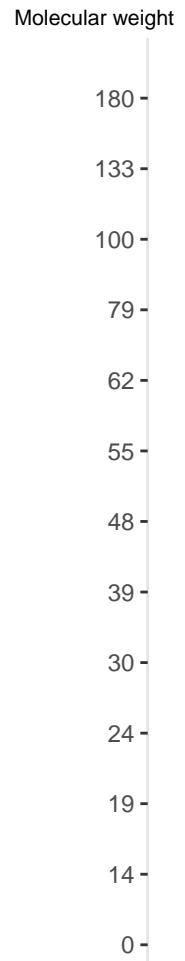
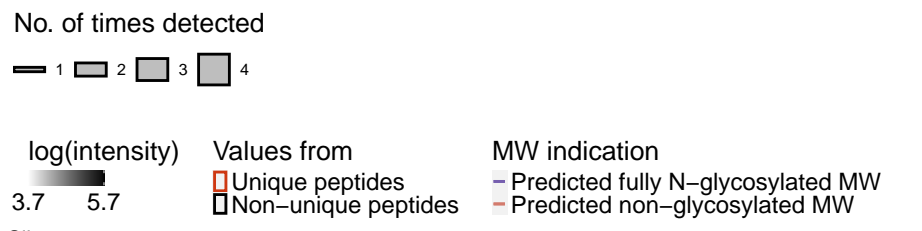
IEKDFGFTNYREKFTFAALFLFGGWWLWLRKREERKRLAVKTSNAVWPLVNDIPLGLDLWERAYFLDKNDKAKYVNVFMNHLVSDAALGRMARAGAFVNLGEPKIPVAI

NbL12g19580.1 proteasome_subunit_beta_type-5-like [MW = 31.11 kDa]



Protein sequence:
 [CR]LHELANKRRISVAGASKLLANLYSYRGMGLSVGTMGAGWDEKPGLYYVDSGGRLKGNRFSGVGGSPYAVGVLDGGVRFDLSEEAELARRAIYHATFRDAGSGGASVYHVGFGWKKLGGDDVGGELHYNVYFVELESVEGEMAEVPA*

NbL12g19410.1 phosphomannomutase/phosphoglucomutase [MW = 65.64 kDa]



Pfam Description

- SP
- Sequon
- TM Domain
- PF02878 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain I
- PF02879 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain II
- PF02880 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain III

Protein sequence:
 AGNGAGFFVCKVLEPLGATSGGGFLEPDGLFNNHNPEDKTKMKATKAVLQNRADLGIQFDIVDRSAAVDSGGREFNRRILALMSAVLLEHPGTTVTDVSTSDGLTTFEKLKGGKHFRFKRQYNNVIDEARLINSVGEAAHLAIETSGHGALKENHWLDDGAYLMLKLLKASARTSGGGSGKVALTMVEGLEEPWVAVELRLKIDQNHSDLHGSGFRDYGAVLKGLENTVDSDAKLLKAPVWYEGVVRVGGYGGWFLRLSLHDPVLPUNIEAPSNEAVKLAJ

NbL12g19340.1 acetylornithine_aminotransferase_mitochondrial [MW = 49.27 kDa]

No. of times detected



log(intensity)



Values from



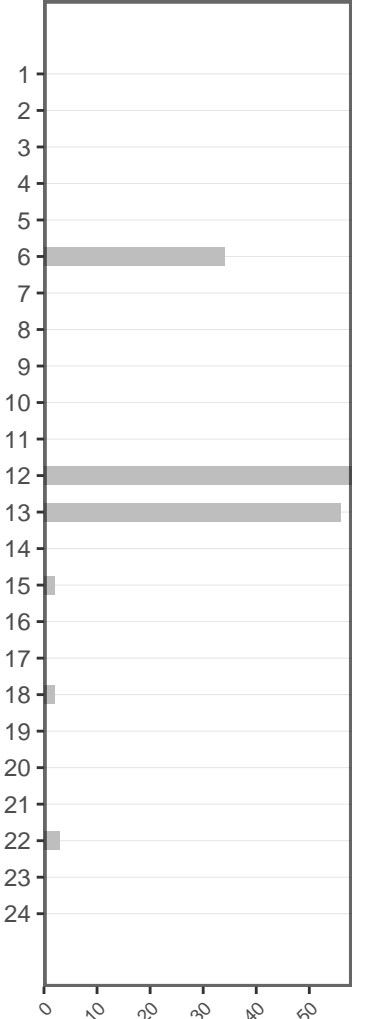
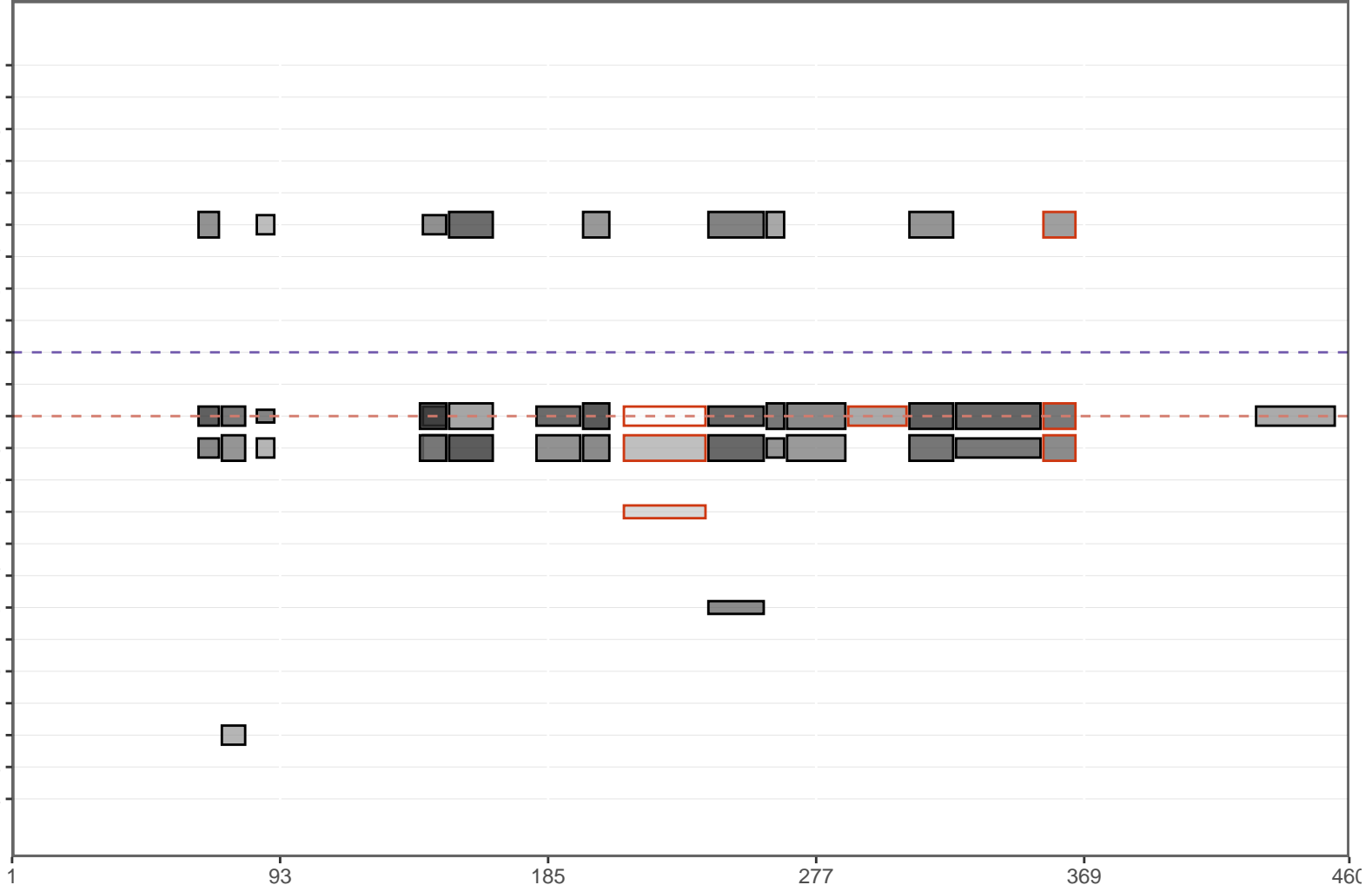
MW indication



Molecular weight

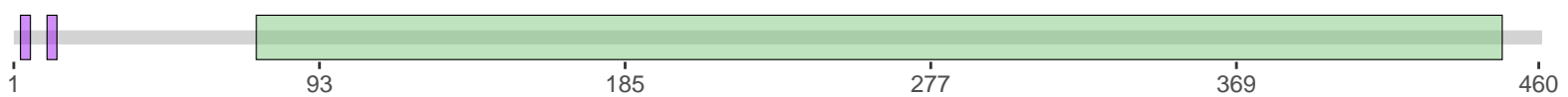


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IPVMPGVTFLEYSGQATELHQSGKIAWVFEVPHQGGGGYSATKEFLGALRTSGDVGSGLLVFDEVGGGLGRTGHLLWHEAVGYPDMFLAKPLAGLPGVAVLTERVAANVYGHGSGTFAAGGFLVQNAVAWLNKIAEPLAVSTKGGVYFRELLVKKLGGNSHWKEVRSVGLIGIDLPVPSPLVDAGQGSGLLVITAGKGNVRLVPLPTTEQELDHAAEILFNLPLVLDKTKNY

NbL12g19140.1 uncharacterized_LOC109205533 [MW = 11.93 kDa]

No. of times detected



log(intensity)



Values from



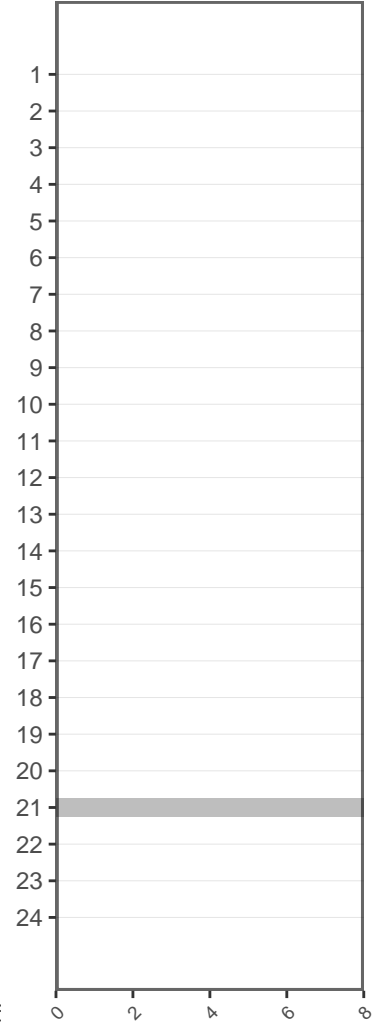
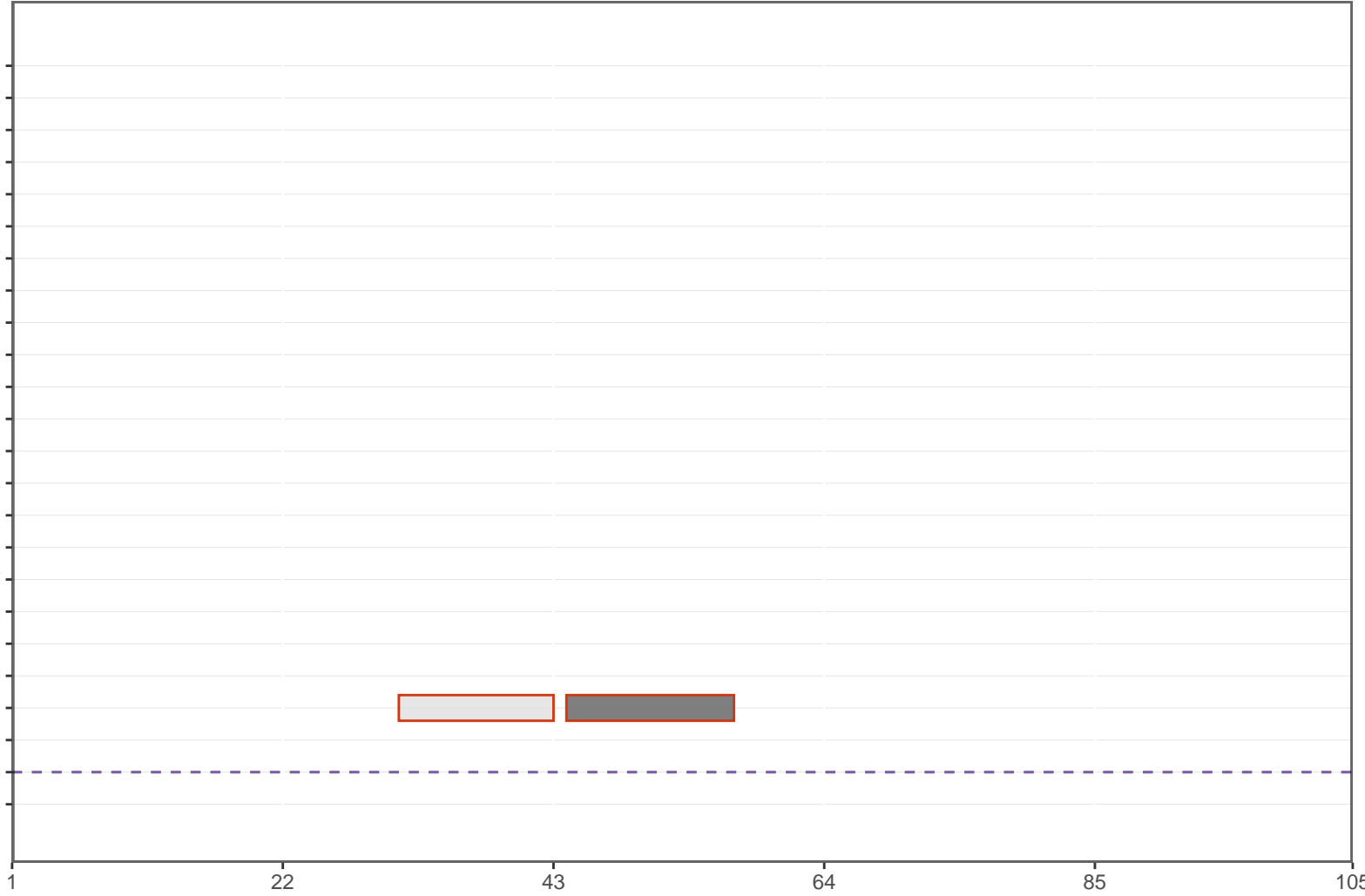
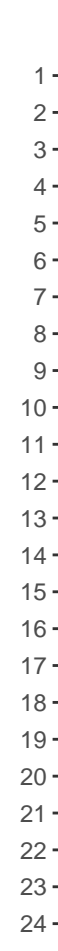
MW indication



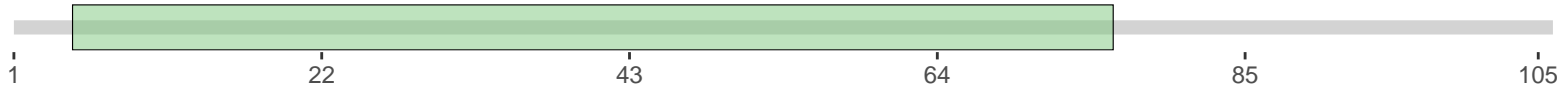
Molecular weight



Gel Slice

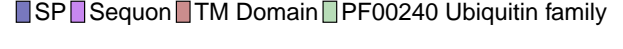


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IQDRLLVATGDVLDGKELADQKVENDAVALFLRKDNEFEEDANVRPNDFYQGRDAEGGASW*

NbL12g19130.1 chlorophyll_a-b_binding_protein_6A_chloroplastic-like [MW = 26.24 kDa]

No. of times detected



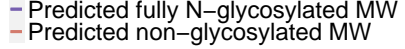
log(intensity)



Values from



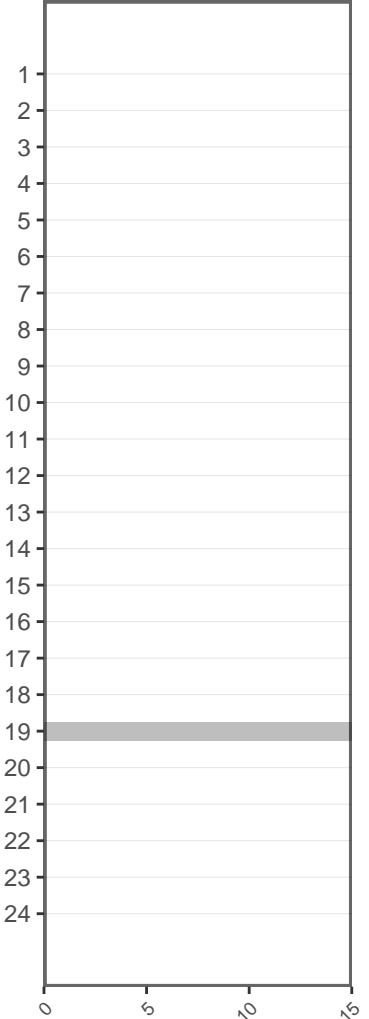
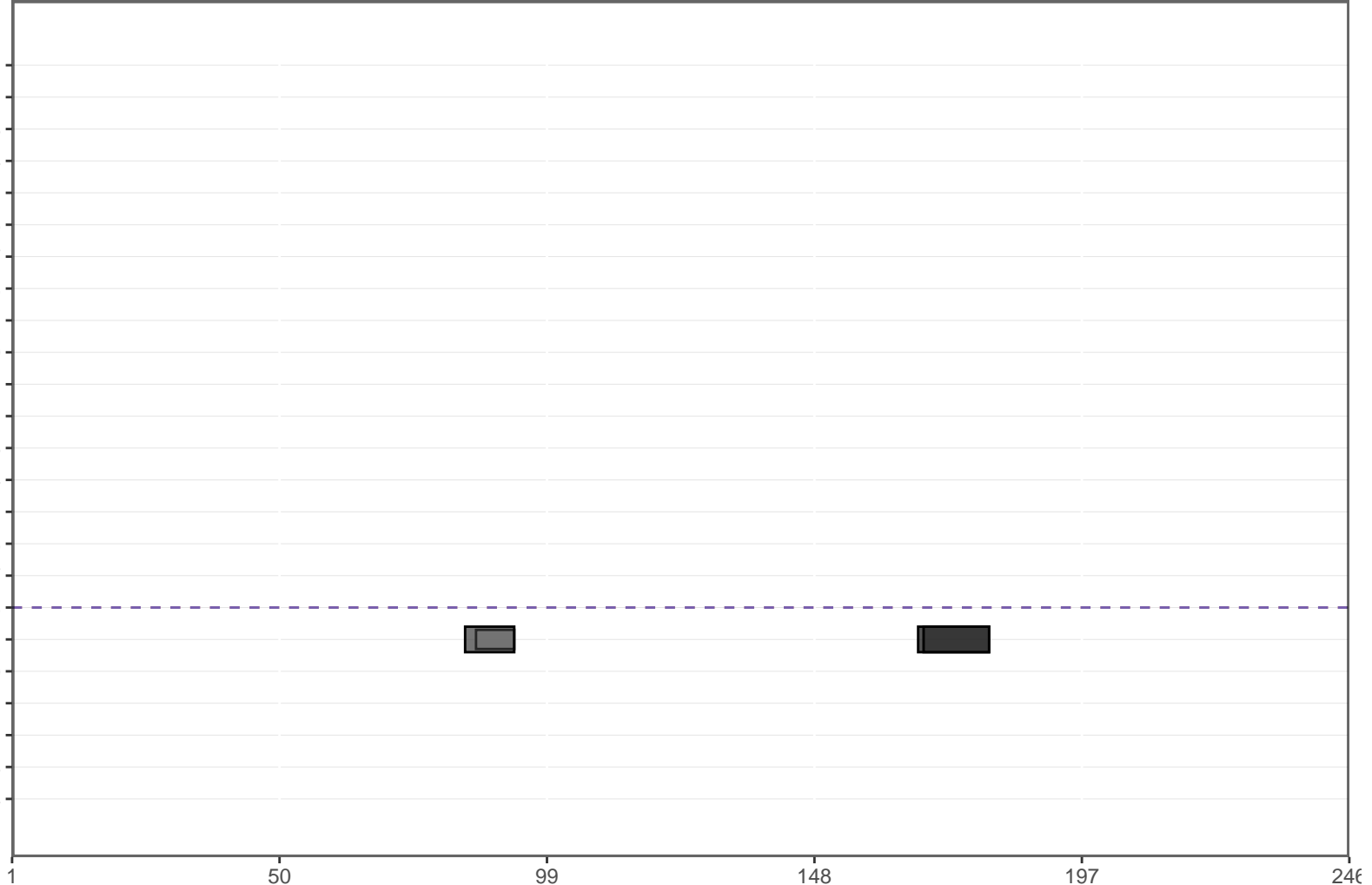
MW indication



Molecular weight

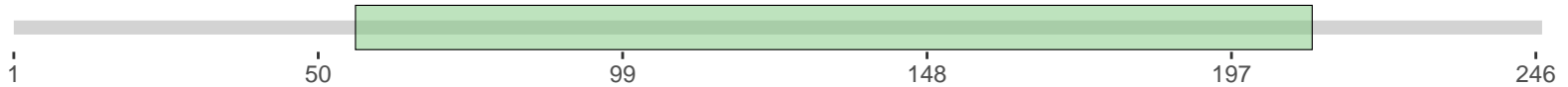


Gel Slice



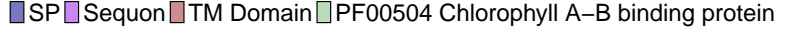
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SLGNWYKAEQWAIIPGGGATYLGQPPVWGTLPFLAEFLAAAFVHEHGRSMKDPENKKYFGGAFDPLGYSKDPKFEELKVEIKNGRLAALAFVFGVGGSAVPGTGPLNLAHLADPWNINNGDNIIRGLP*

NbL12g19100.1 chorismate_synthase_1_chloroplasmic [MW = 20.84 kDa]

No. of times detected



log(intensity)



Values from



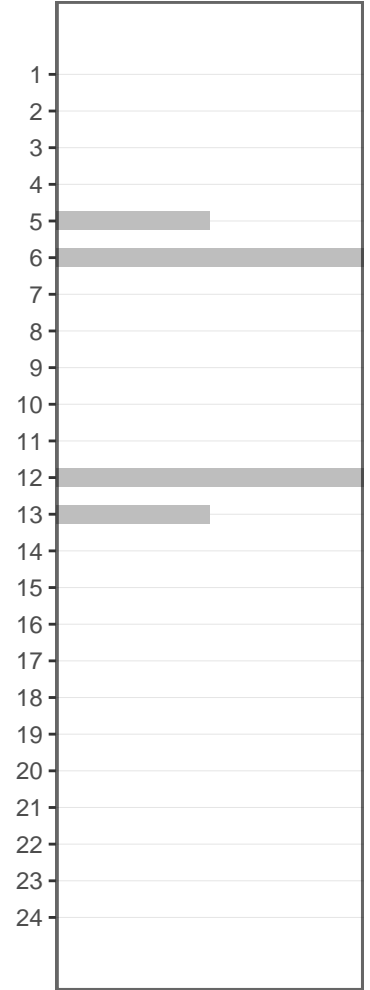
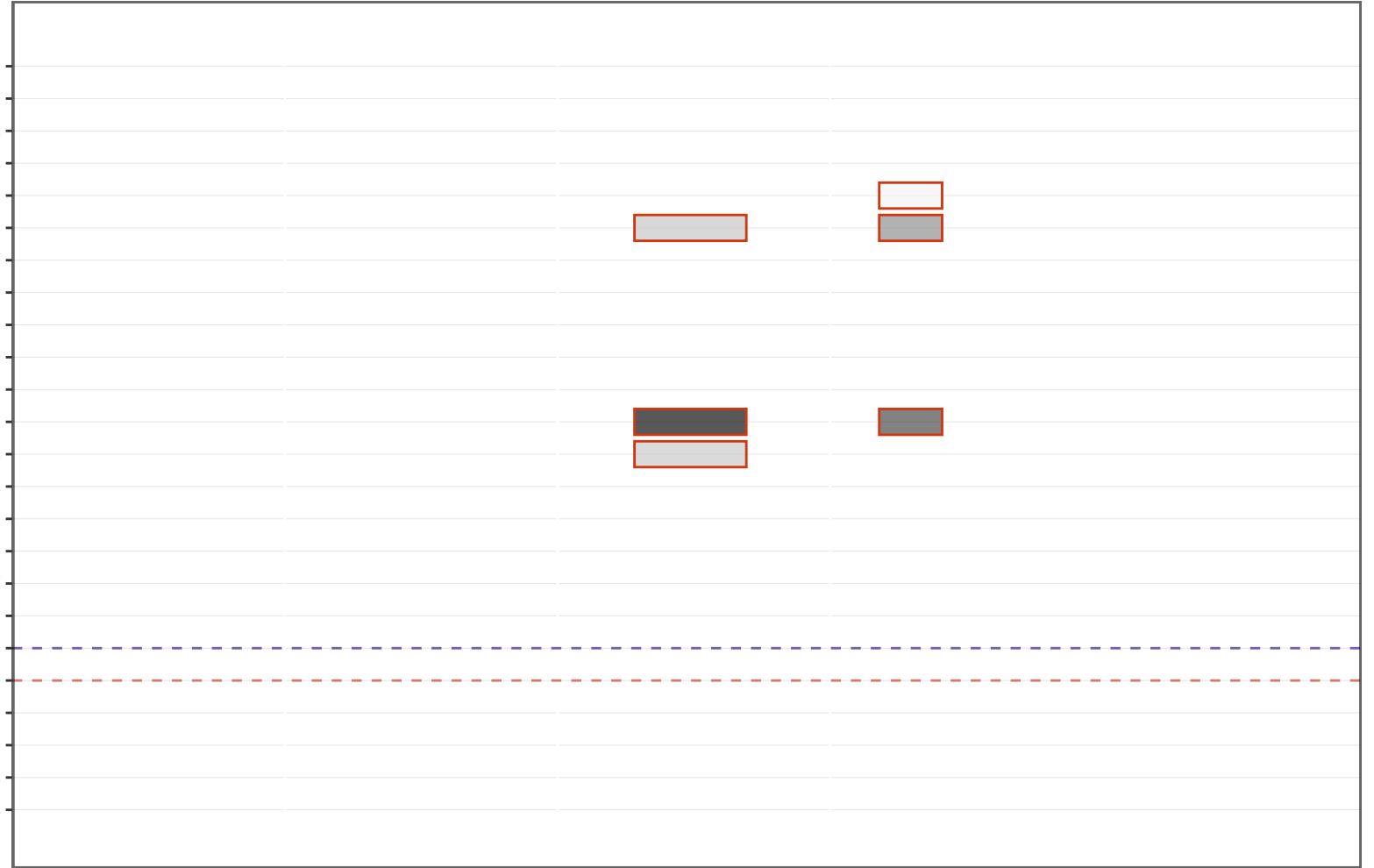
MW indication



Molecular weight

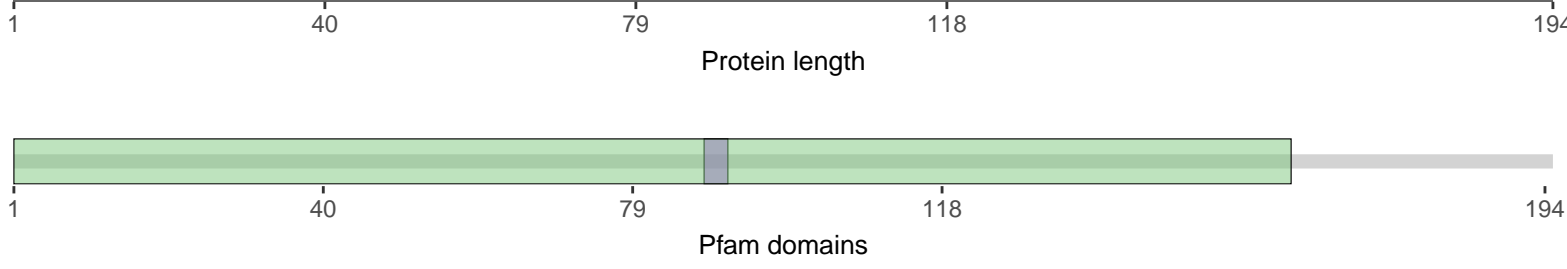


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

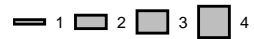


Protein sequence:

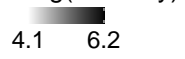
IRTRKTRNSGGIGGSHNGEVNINMIAFKRPTSTIARKGGQVTRDKHDTELIARGRHDPGVVFRVAVPMVEAMVALALVDGLMAHYAGQMLFPINPALGEPLGSGSTPESAEVTL

NbL12g19050.1 V-type_proton_ATPase_subunit_G_1 [MW = 12.33 kDa]

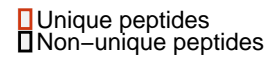
No. of times detected



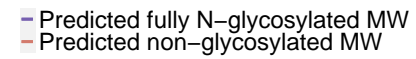
log(intensity)



Values from



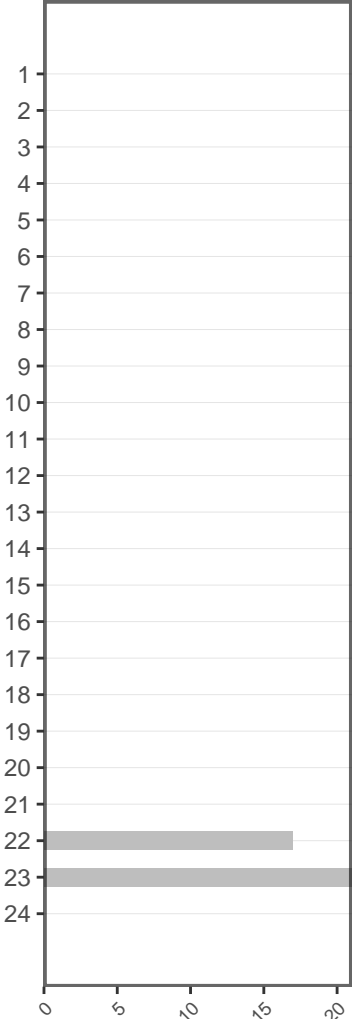
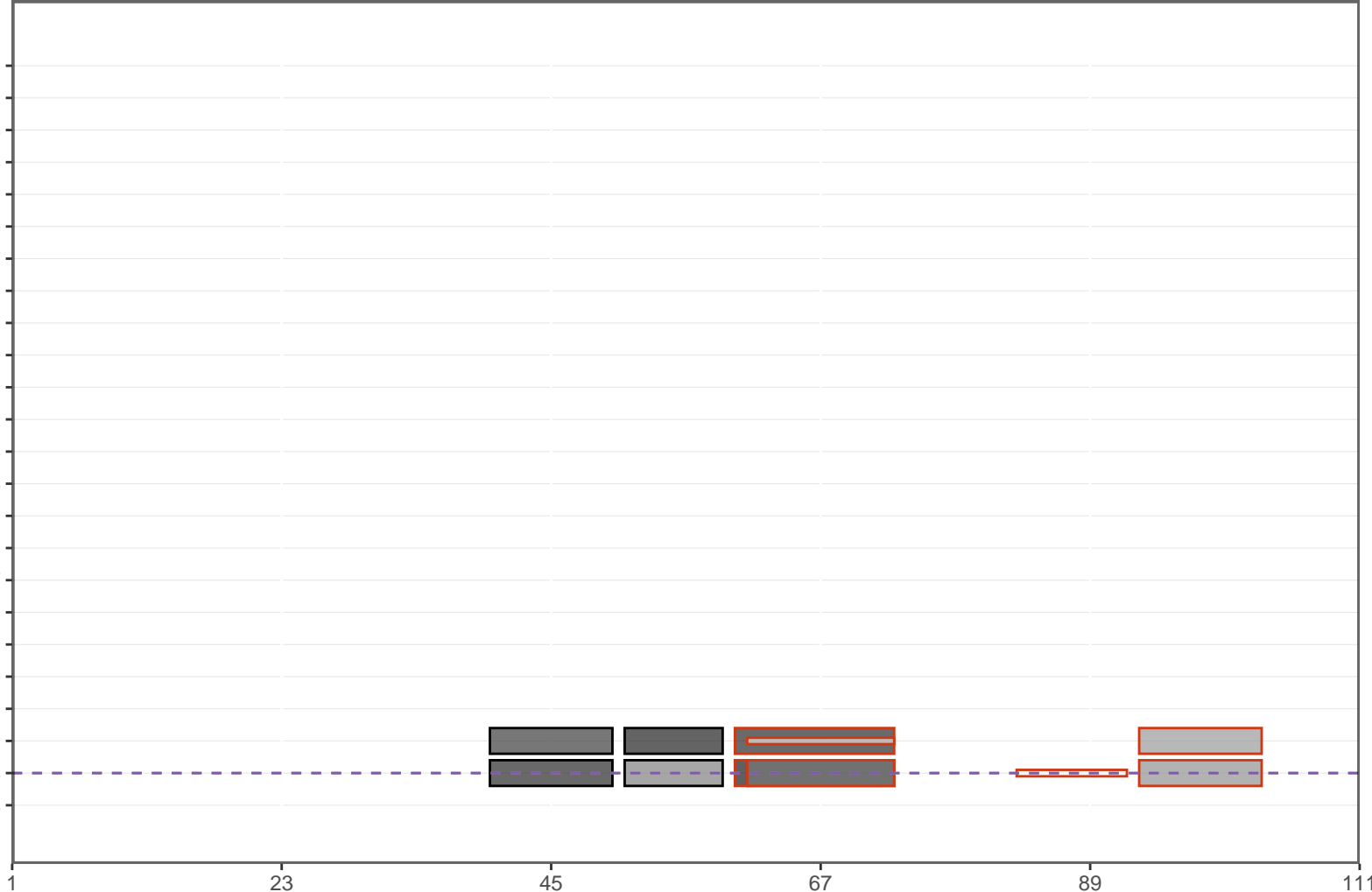
MW indication



Molecular weight

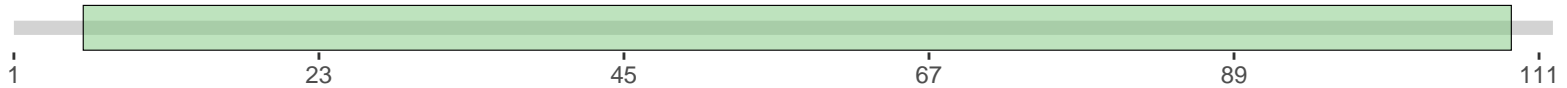


Gel Slice



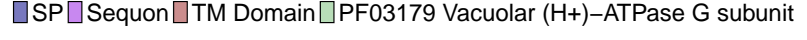
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EKEIAEFRAYMEAFGRKLEQTSDDSGANVKRLEGETDAKIEHLKTEAERVSPDVAQMLLRHVTYKN

NbL12g19020.1 protein_disulfide_isomerase-like_1-3 [MW - SP = 61.17 kDa]

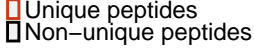
No. of times detected



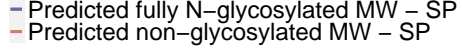
log(intensity)



Values from

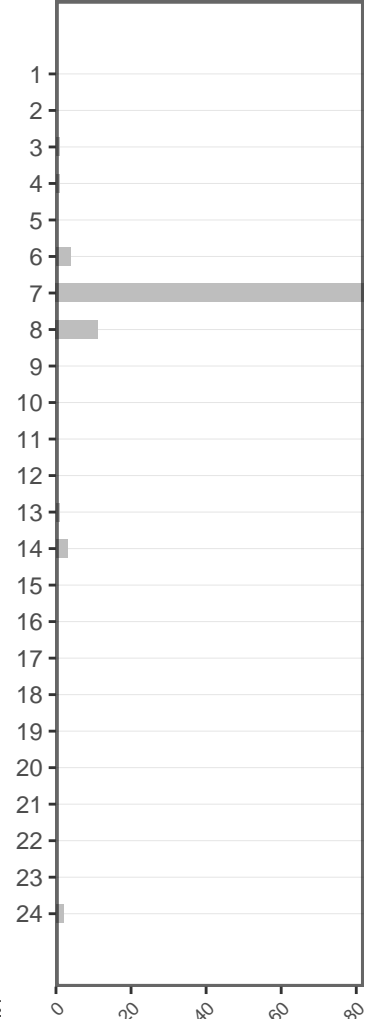
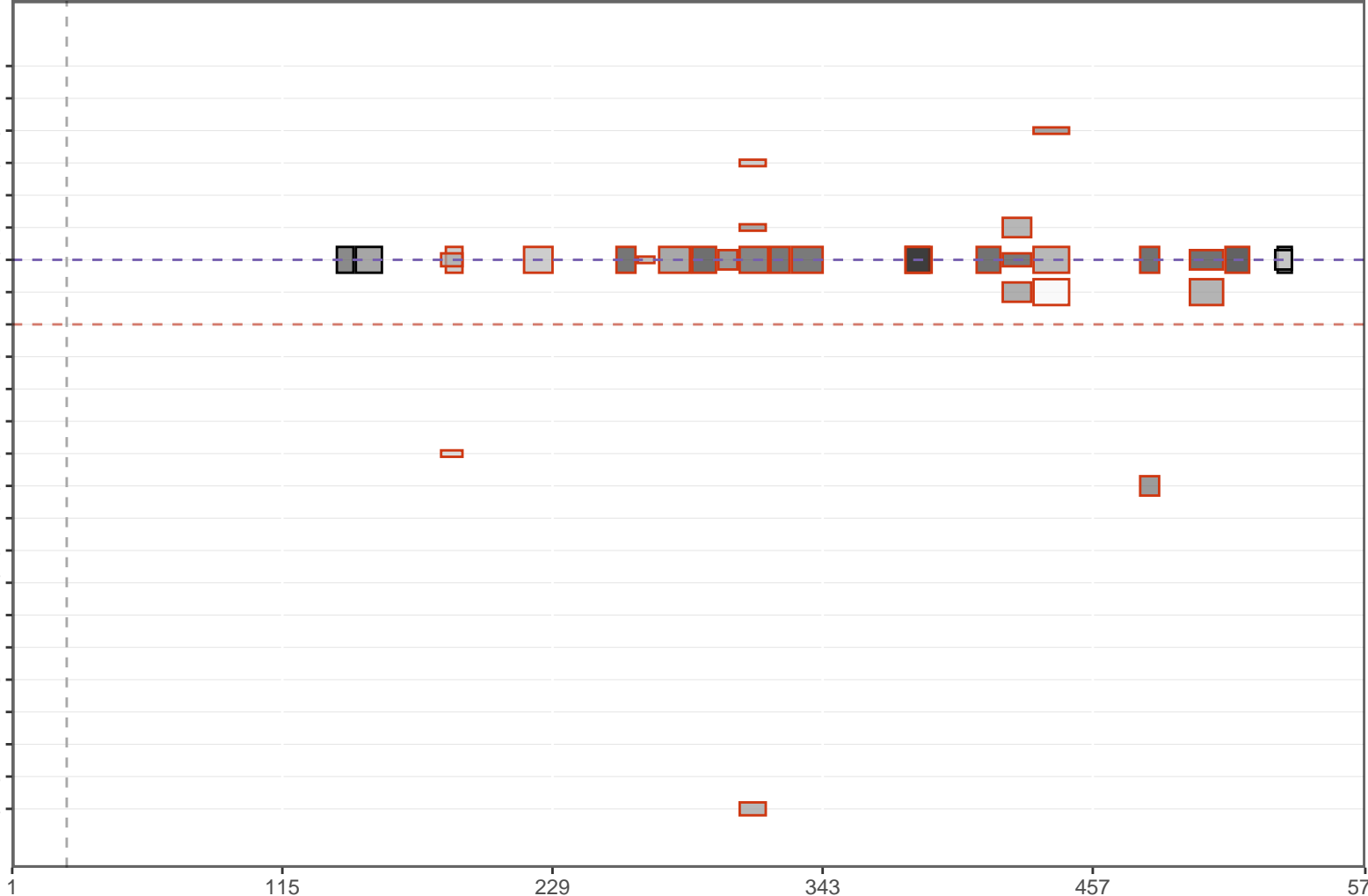
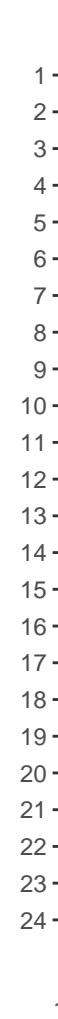


MW indication



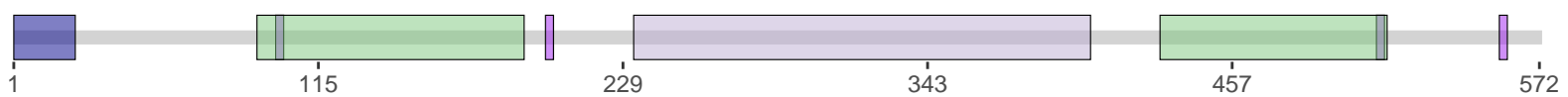
Molecular weight

Gel Slice



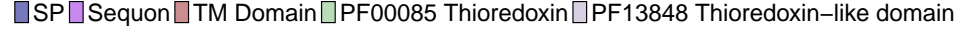
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKKEAZNNHFGGGEFTKSAAEFVFNKLPVLYFTRESASEFENPKKQLLFATKDDKFLPFQGAVKAFKGLKLVVVEIKNEDGKPKVSEYFGIGGGDAPRRLAVYTGNEGRKPFLESEITLDSVKVGFGEKFLDNLKPFYKSDPIPETNDGDKVYVGNVFNDEIVLDESKDVLLEHAPWQGHGDSLEPIYKHLGHLRQIDSLVIAKMDGTNEHPRAKSDGFFTLFFPAGNKGFDPITVQDRTVVAFYKFLKHASIPKIKKPKASTGKPFTEFANSPSESTIDVYDEL*

NbL12g18780.1 leukotriene_A-4_hydrolase_homolog [MW = 68.54 kDa]

No. of times detected



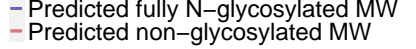
log(intensity)



Values from



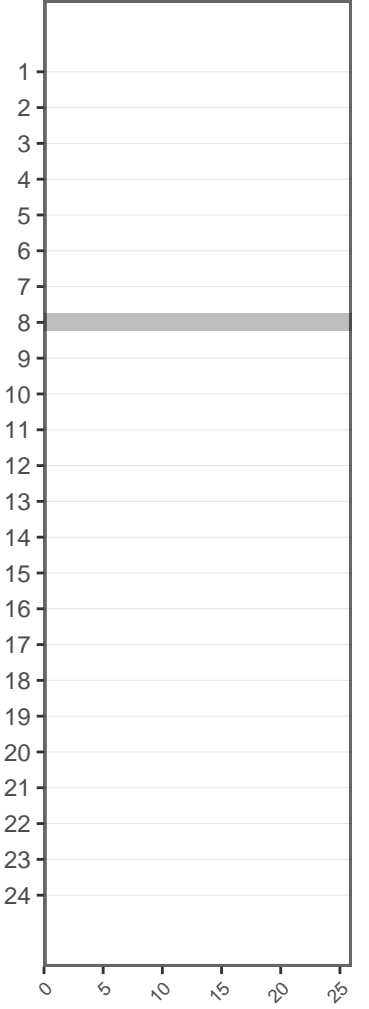
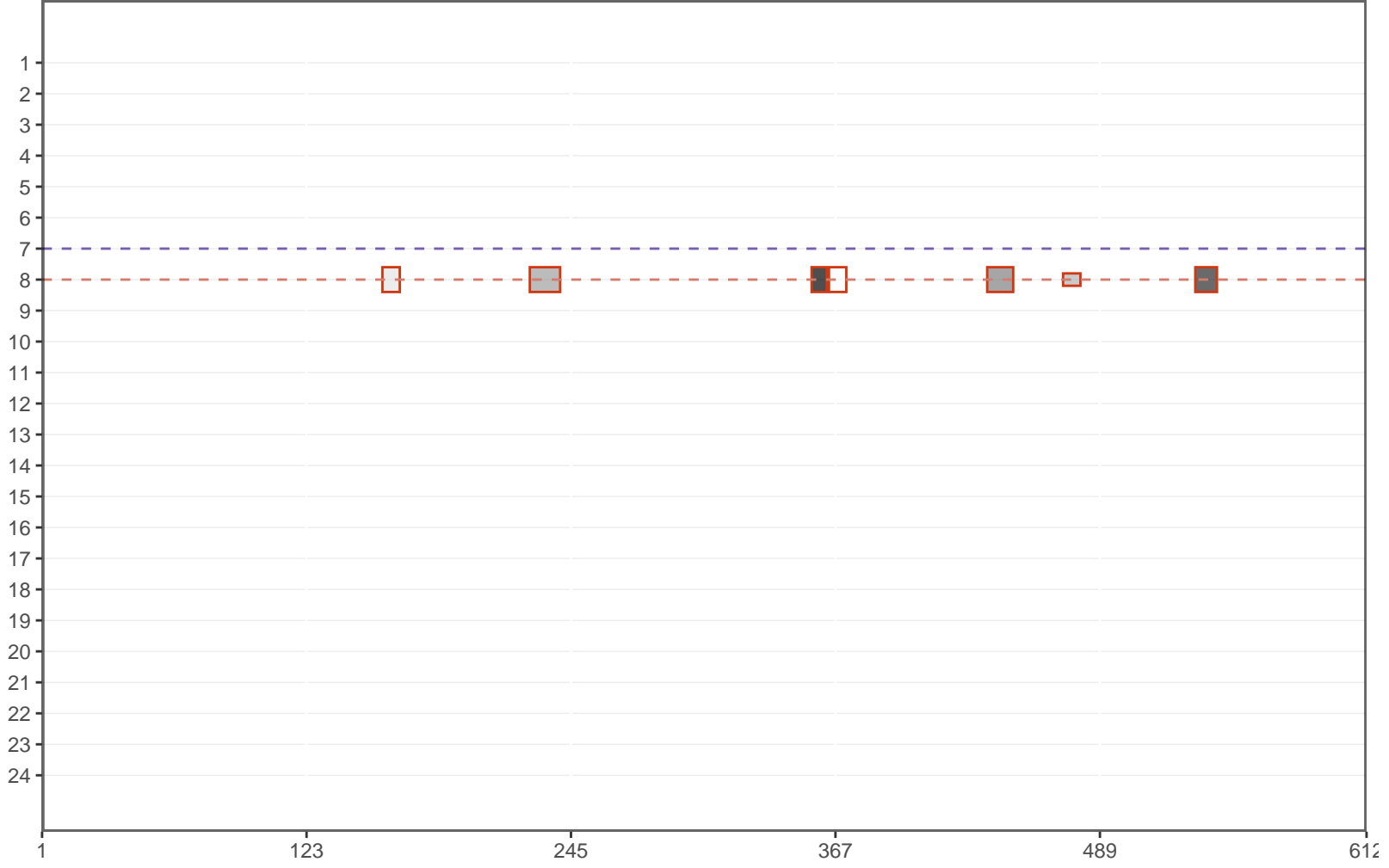
MW indication



Molecular weight

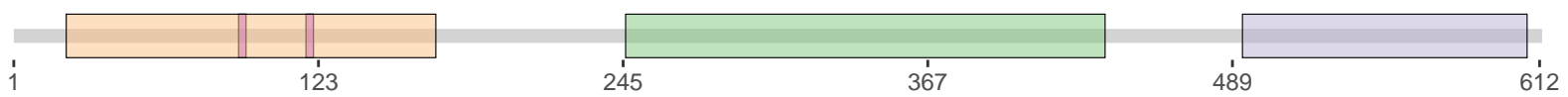


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISGAGVVAHELAIHSWTGNLFTKNNKHFWLNEGFTTYAERRRIVEVVGEGDIAALNIGHWKRLVEEMERFKDNMELTKLKTNGAGVDFDDVYSGVVPYKQKGLWRRIERQTRGPAFDLKKYATKFKGSDTDMFLNFKANVPGIENIDLKLWTEGTGIPPDAMEFVSNYKSKVSLATEFKLGRMPREDEVDKWKGGWELVYENLPKSVEASQVATLADARYHLSEKQVEVRAVFLQLATSARGDRDYGEVEKTLKEVGRMKYLRPLVYALVGGAKKEEKVYARRVI

NbL12g18630.1 uncharacterized_LOC107816357 [MW = 265.67 kDa]

No. of times detected



log(intensity)



Values from



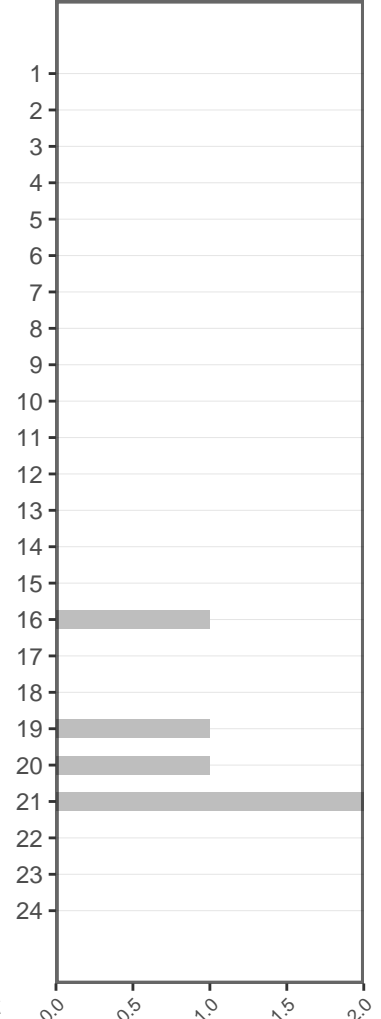
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

NRVQETAKIMCESEFRVSTEPHSAANLLDGVDDVYCGPSCAQQTFSLSLGTSPSSIGQTSVBSLTS6SGPDLPLVLFQGLFGPFLPSPVPAQIGSGMPPHLPVPGVSLTHHPGPPFQFGQLRYSSNVGGGCPHTAGSMFQGNVGAHNTSGNS6SGVPPQALDASALVMMKDNVGSLSANGEHASVLRPPGHNDKPKVGGSAEKALFTNTGTGAGASDRKLISEEALQAEAKGLTNADRIHVQPSKGGKGGDQK66VLPSTQGVENEKNYAGGRAQGGAA

NbL12g18540.1 methionine_aminopeptidase_1D_chloroplast/mitochondrial [MW = 33.77 kDa]

No. of times detected



log(intensity)



Values from



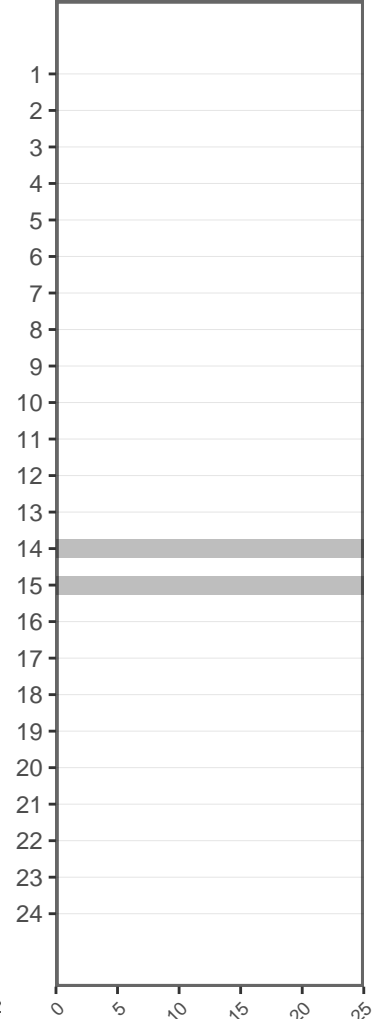
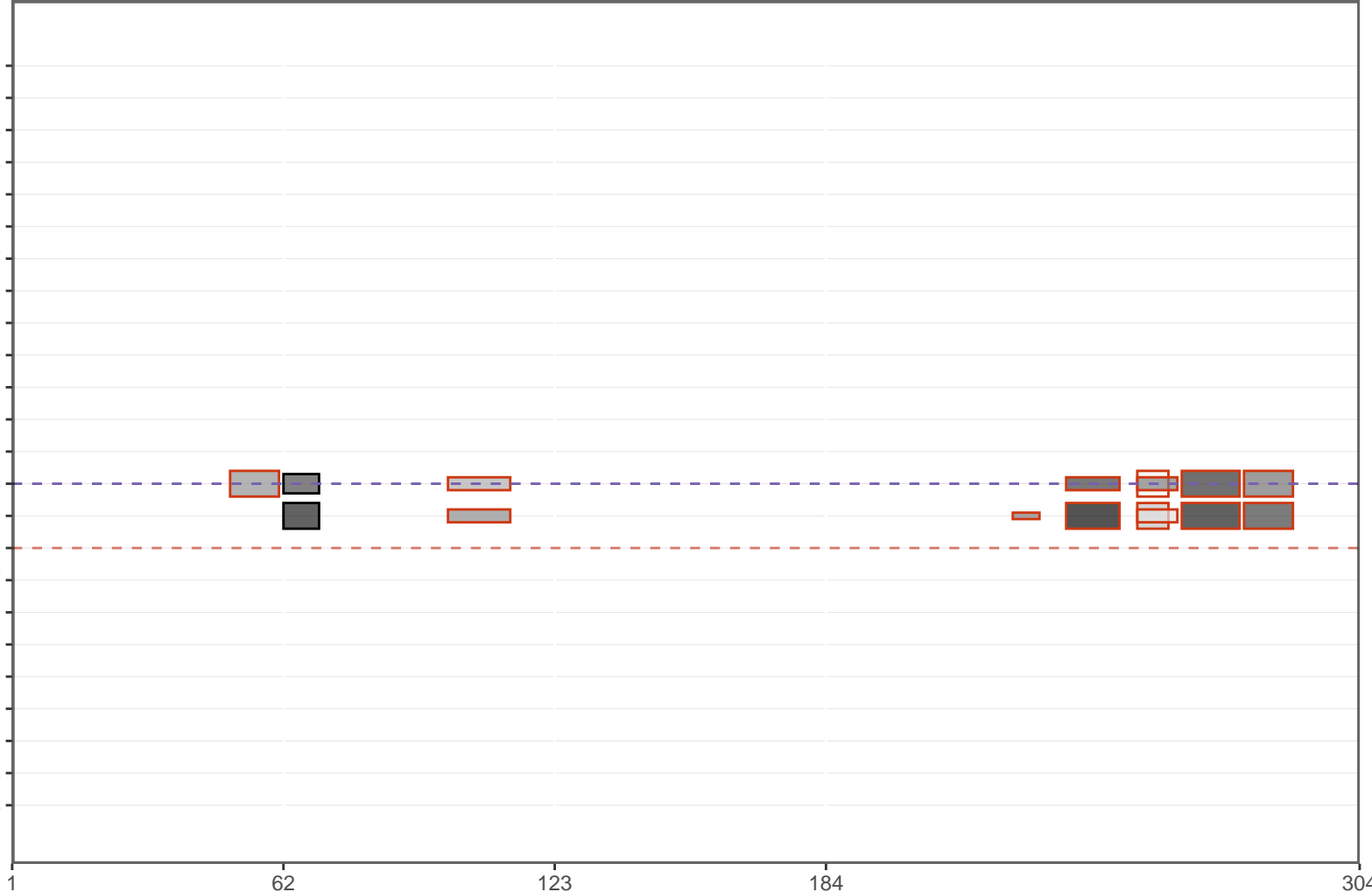
MW indication



Molecular weight



Gel Slice

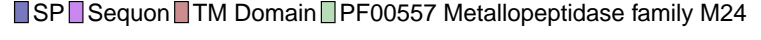


Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

STMTDEIQAVHQMIDNGAVPSFLVGGFKKGVGTGVNEGKGGIPDRPLEDGGVNDVTVYLVNGYHGDTSAMFFVGNVDEEAKNLVQVTRKELDKAISKAPGVFEFKKGTIKHDLADKIRYGVVEGVGKGRSHFSDPWLHYRNNRSGQMVLNGFTI

NbL12g18430.1 3-ketodihydrosphingosine_reductase-like [MW = 28.79 kDa]

No. of times detected



log(intensity)



Values from



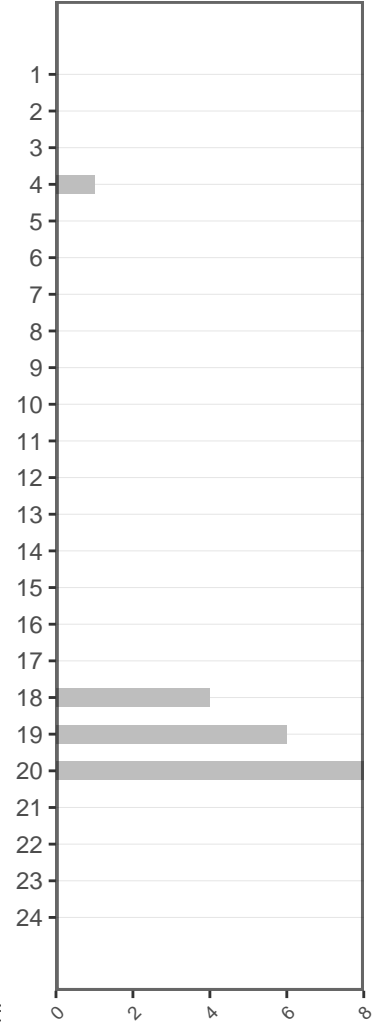
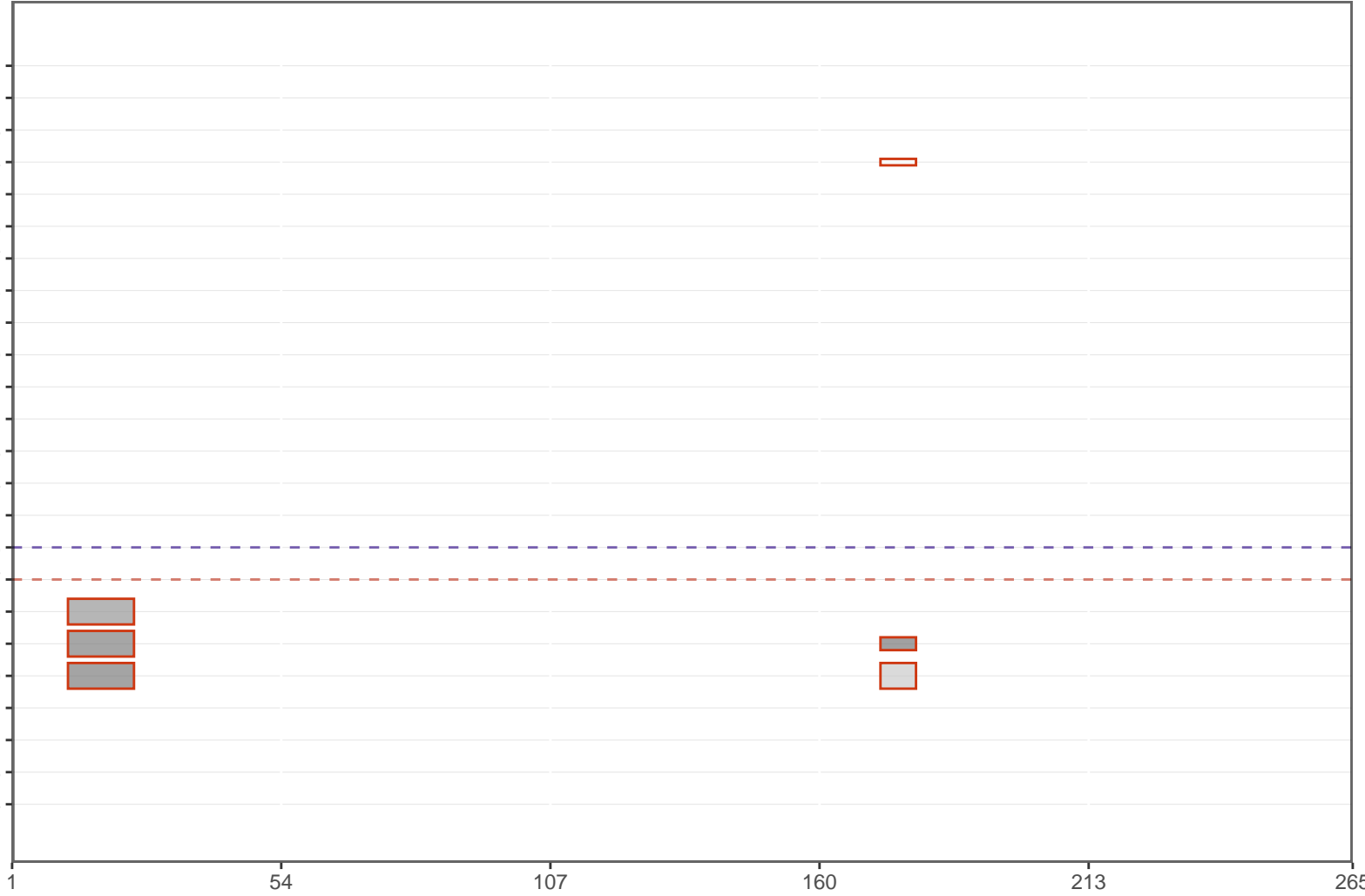
MW indication



Molecular weight

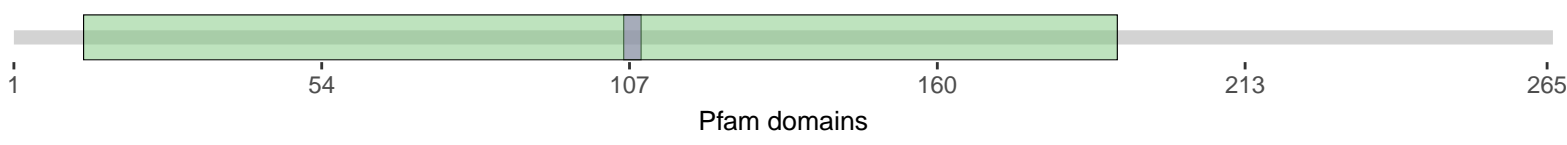


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SVGAFHCAQQVLPGMVERGRGTVLFSGGSASLNGIAGYSELGGCKFAMRALGGCVAREFQPLGSHVAVVHNSGVGAPRGSMTSGNRLLVGEGGGGGGGSGRDLMDPDLAGEYVHLLHQDRBAWTTGEIDHPSNRYM

NbL12g18370.1 peroxidase_10-like [MW - SP = 32.89 kDa]

No. of times detected



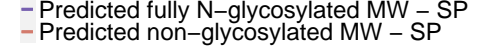
log(intensity)



Values from



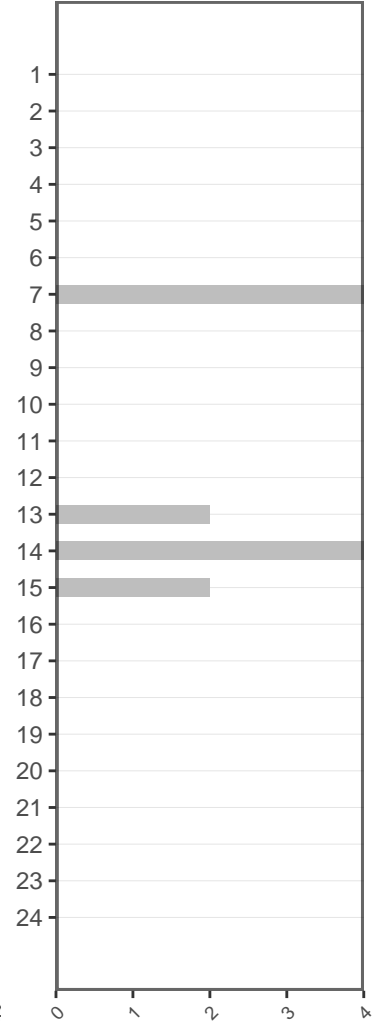
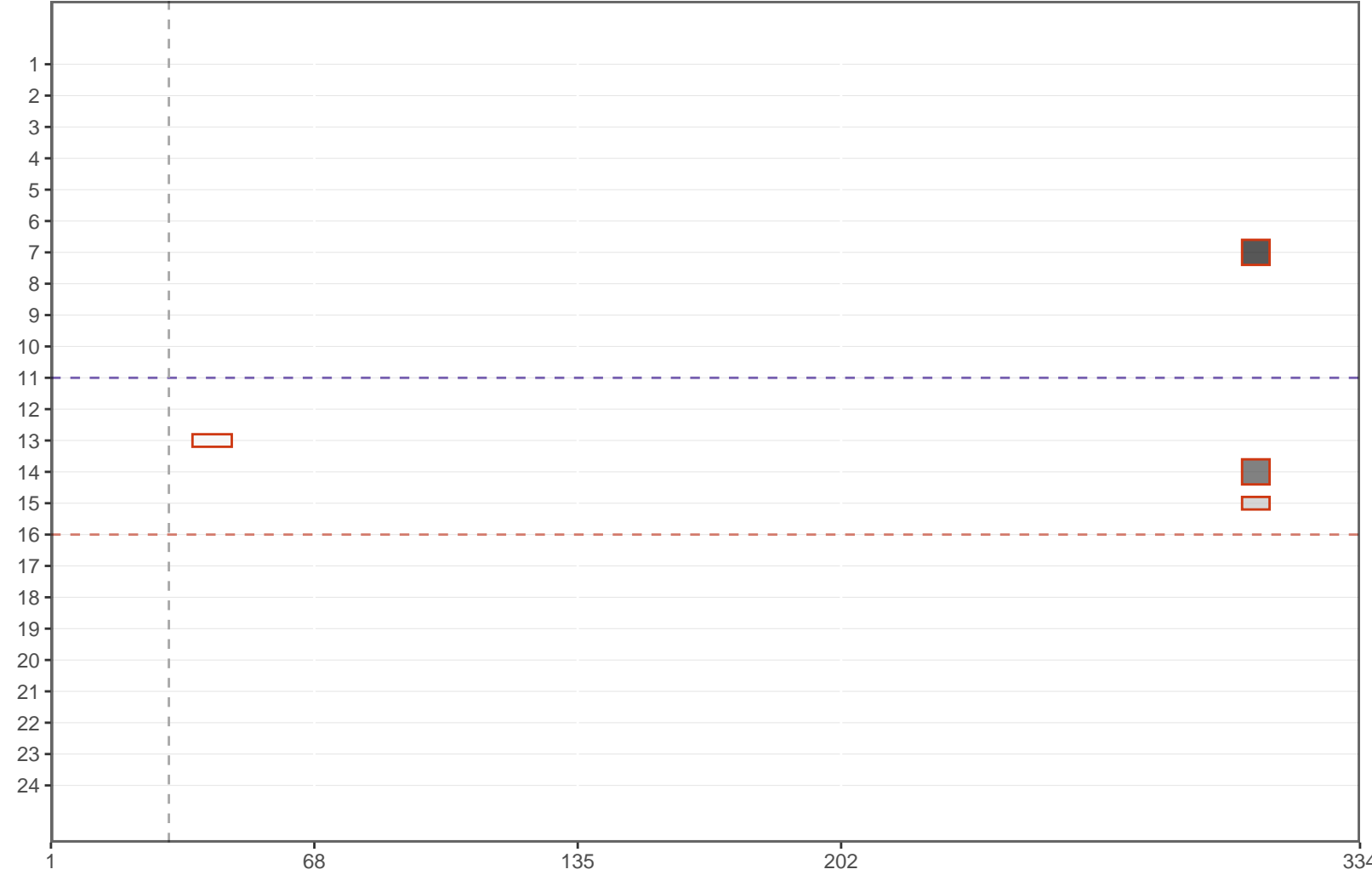
MW indication



Molecular weight



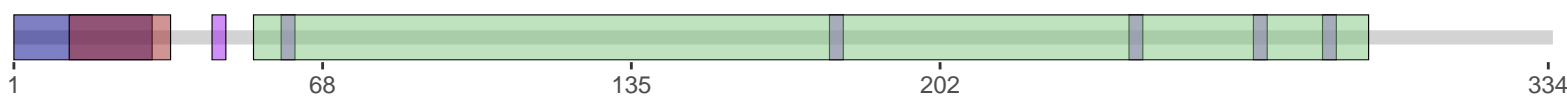
Gel Slice



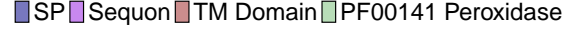
Protein length



Pfam domains



Pfam Description

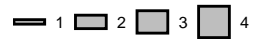


Protein sequence:

IDSLSIASQSAANAQIPSPFPELQNTAKFVSKGLGVKDVVVLGSAHTGTFAGQFTFKGRFLDFDGGGNPDPFLDSSLGNLRVCFPNQNDSDSNLAPLDVATINKFDNVYFRNLMNNSGLLGGDGLMNDNTASMVSTYKYPVLFKFAFASMKLTNLGVLTDGDCERKNGRLMNV

NbL12g18290.1 proteasome_subunit_beta_type-6-like [MW = 25.17 kDa]

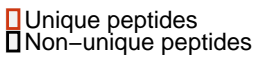
No. of times detected



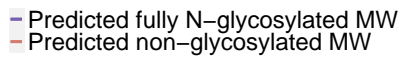
log(intensity)



Values from



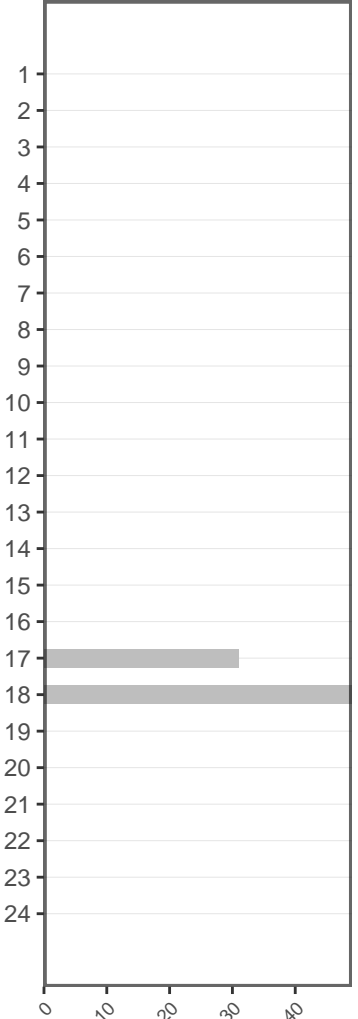
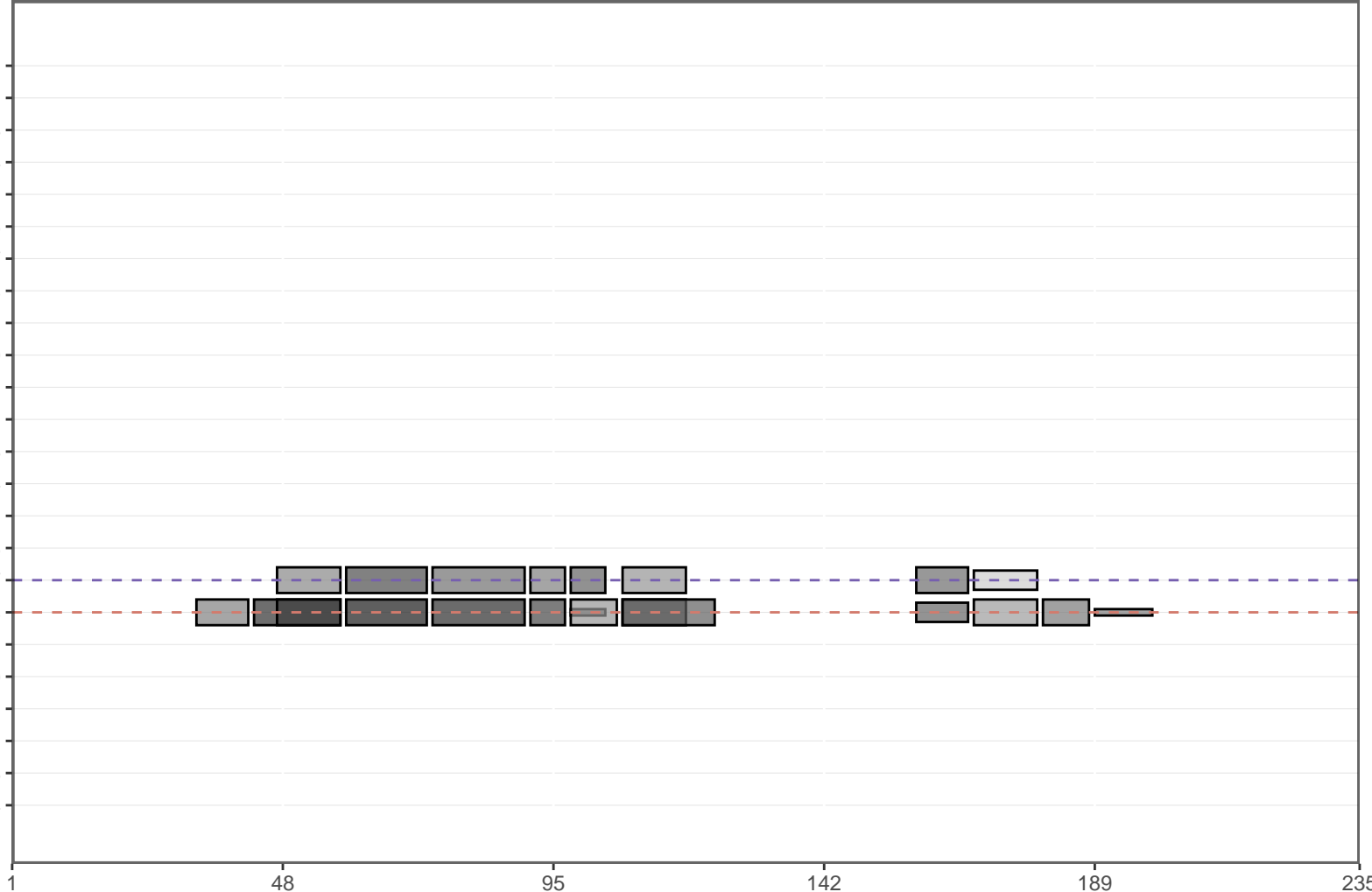
MW indication



Molecular weight



Gel Slice

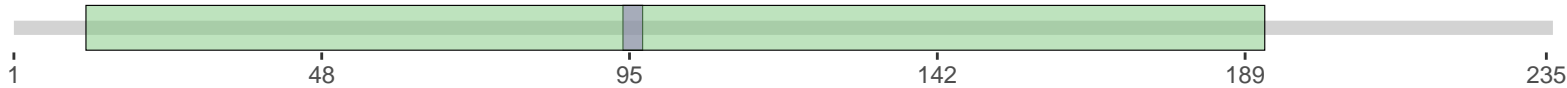


Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

DRLOTGMIGGWDKYEKGGKYGIPGLGTTLEQFPFAIGSGSGSGLYGFDFGAWKEGMTGEEAEKLVITAVSLAIARDGASGGVVRTVTINKDQATRKEYPGDLSGLWHEELEPNLSLDDVASESPDMVQ

NbL12g17850.1 alanine--glyoxylate_aminotransferase_2_homolog_1_mitochondrial-like [MW = 42.22 kDa]

No. of times detected



log(intensity)



Values from



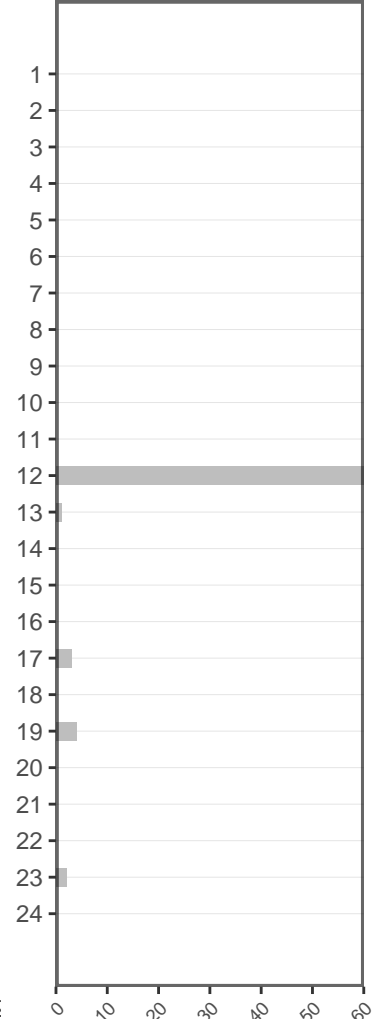
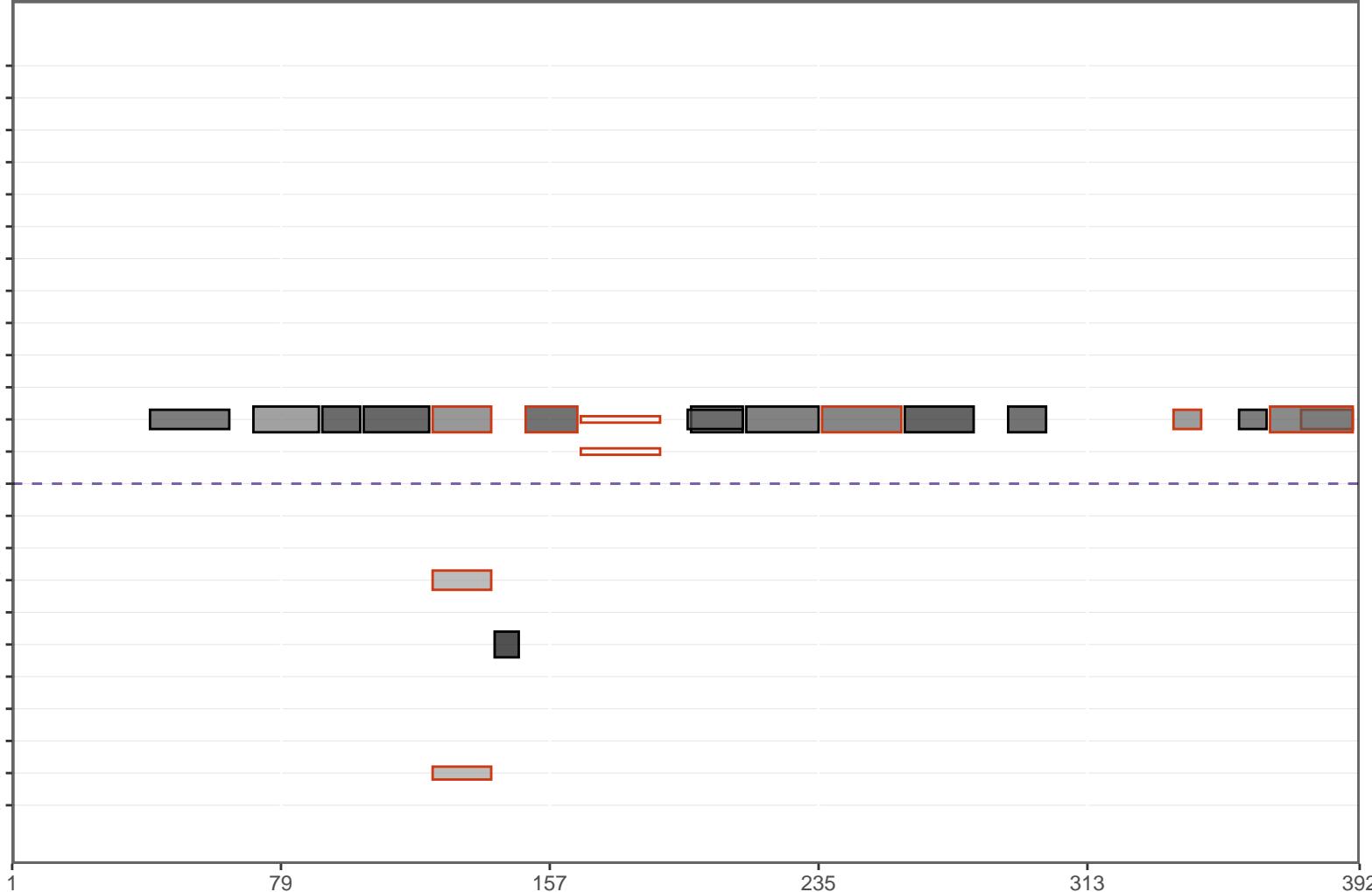
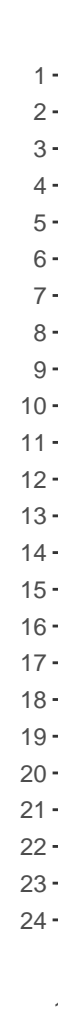
MW indication



Molecular weight

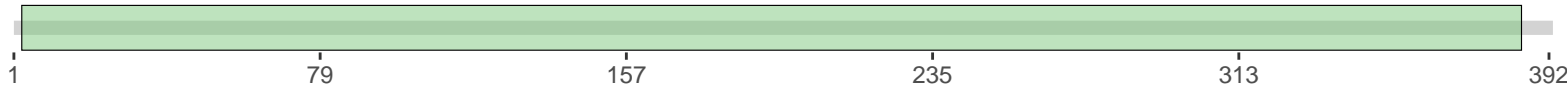


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LAPGYLKYDYVRKAGGVGIADEVGTGFGRTGSDVWFGDTGVDVITMAKIGVGNLPLGAVVTPPEIAEVMAGKIGFTYGGNPNVCSAGGHAVLRVLDKEGRQKHDAEYVSHLIGLRDLQKRHDIDGVDVGRGLMVGIELVTDTKETPAWAETGVLFKELRELGLVGVKGLHGNVFRKIPPMFGFGKDDADFLVDALDYSIKL

NbL12g17760.1 uncharacterized_LOC107825767 [MW = 65.74 kDa]

No. of times detected



log(intensity)



Values from



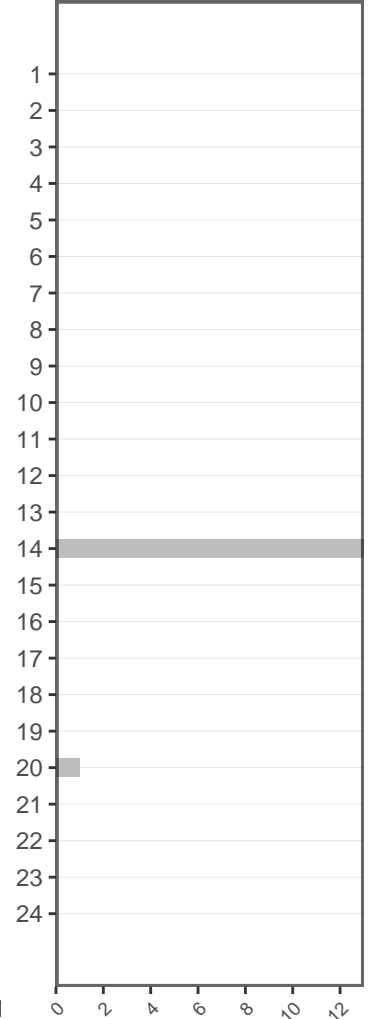
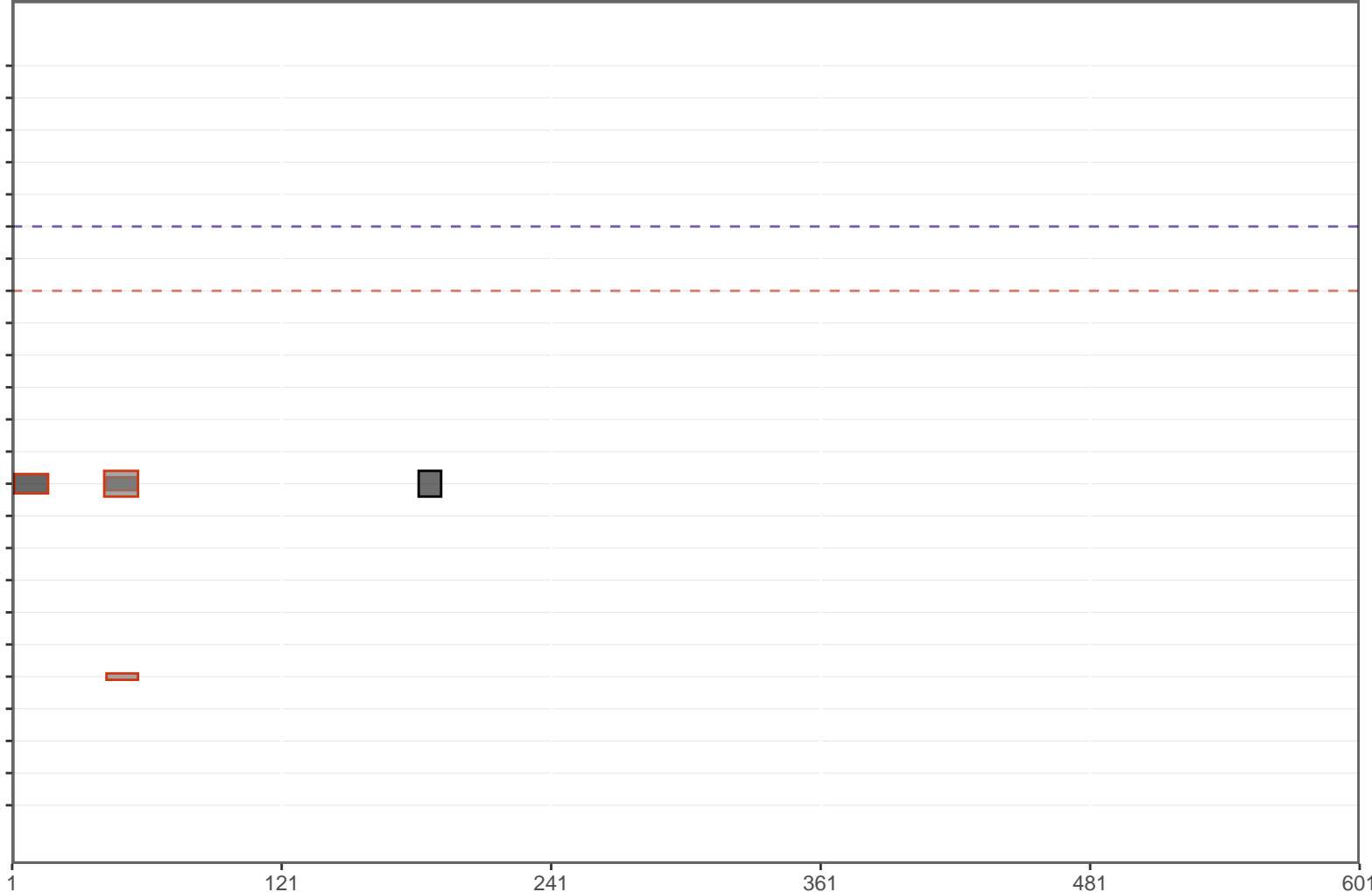
MW indication



Molecular weight



Gel Slice



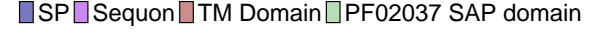
Protein length

Peptide counts over 4 repeats



Pfam domains

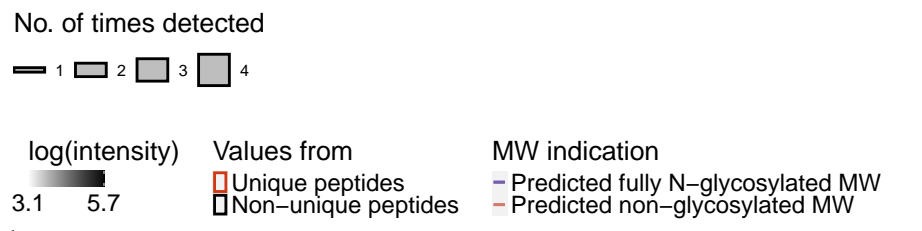
Pfam Description



Protein sequence:

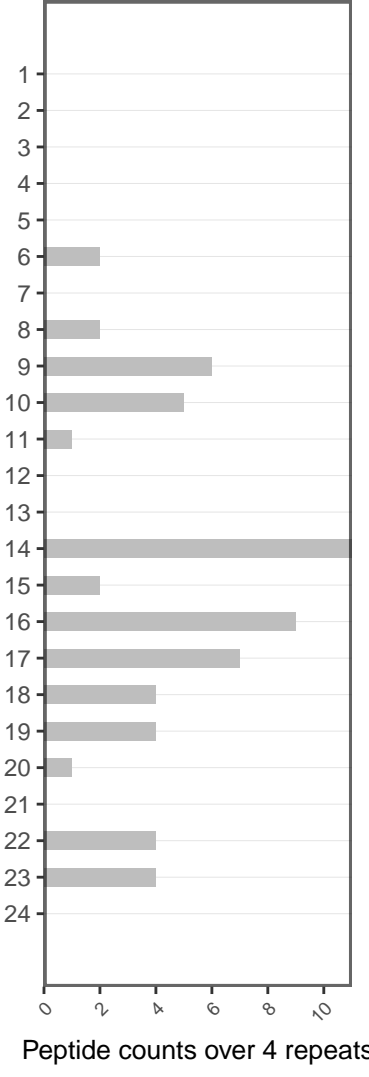
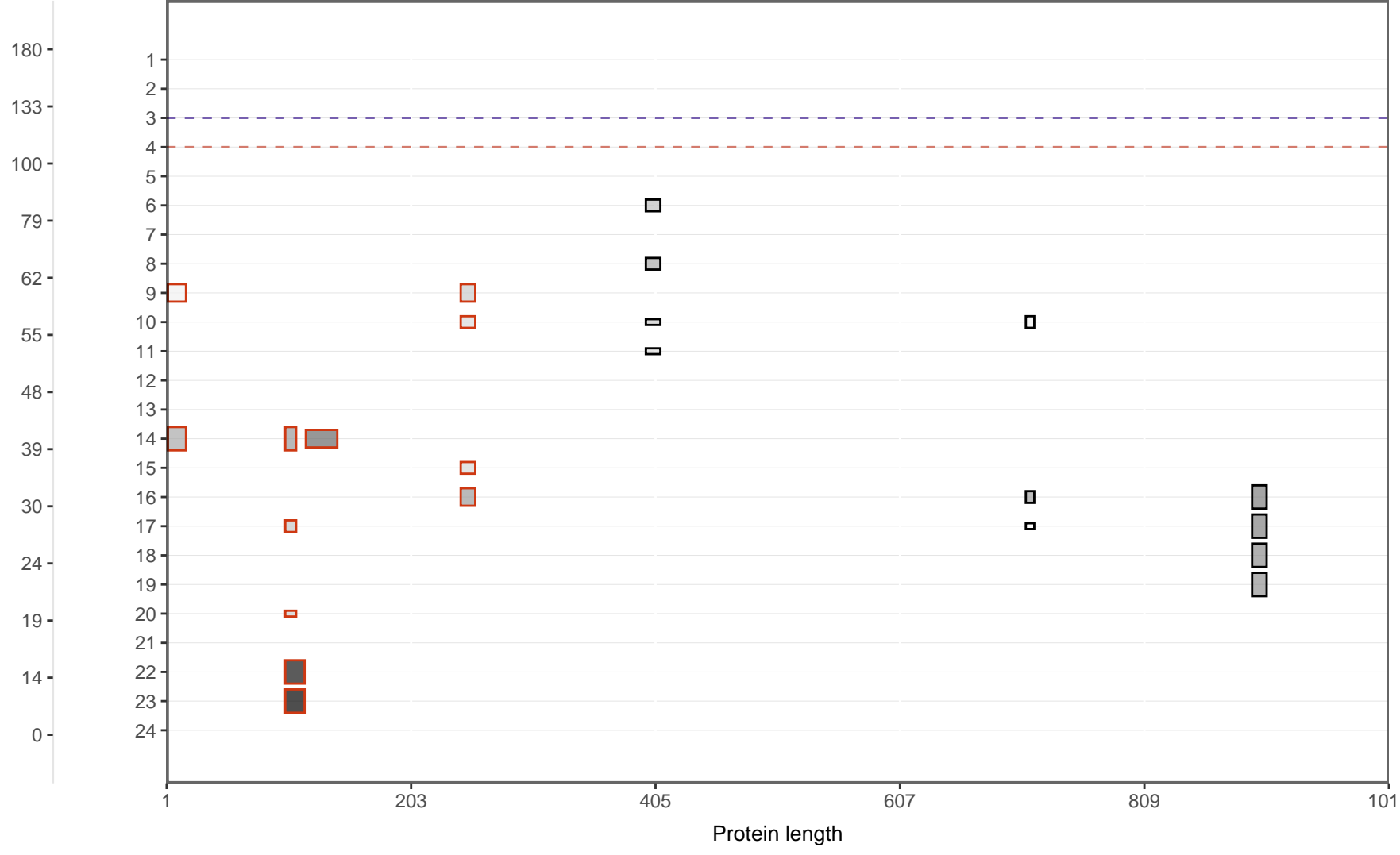
EPHDKXKSTTEEPGNKNDKYPVSVYVGTSDPVGVGVESEDALRGDDLQKYETQNEEEDKKEGLENHHSISVDEAKVSSNLETQVSDLSPLVGFQVKSQDVSADVSDSEKELMDTVIADQVKIELDVKPQNVQLSSISVDPDQDQKSGPQVVEEPYDEKVSVEEPEENENKDFVDMKTDGNGDSEAKLGLDRSPGDDETEEEVSEKELADPKLDSANKIDGKKEIEVNTSRGVGVSVTSLDDARVAVHIDTNVEDDGPVKSVRKPKHGKFSKICFALHIFVYMALQFSFYDS

NbL12g17750.1 apoptotic_chromatin_condensation_inducer_in_the_nucleus-like [MW = 110.72 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF02037 SAP domain PF16294 RNSP1-SAP18 binding (RSB) motif

Protein sequence:
 VSTEEPCKENDKYFEVSVYVGTSDPVGVSVEGATALSGDDSGKYEQNEGGDLKEGRENHISNSVDETKVSSSNLETQISELSPILGGQVKSDVSPDIBDEKIELKDNVANDVKLELDNPKPEMVQLLS66SDVPDAKLFPMDEVEEPDKKIVSTEEPCKENDKYVDIMKTGNGNSAEKLGQLDRPCEDEHMEEDVSEGLADSKLGSVKEIDGKKEIEVDNTRREVGFVASVDDARSAAHDTDVEDDSPTVLSLKRKLIHQRTATGNAIGKRGRRRVNSDELKIPDNKKI

NbL12g17690.1 photosynthetic_NDH_subunit_of_luminal_location_4_chloroplastic [MW = 22.09 kDa]

No. of times detected



log(intensity)



Values from



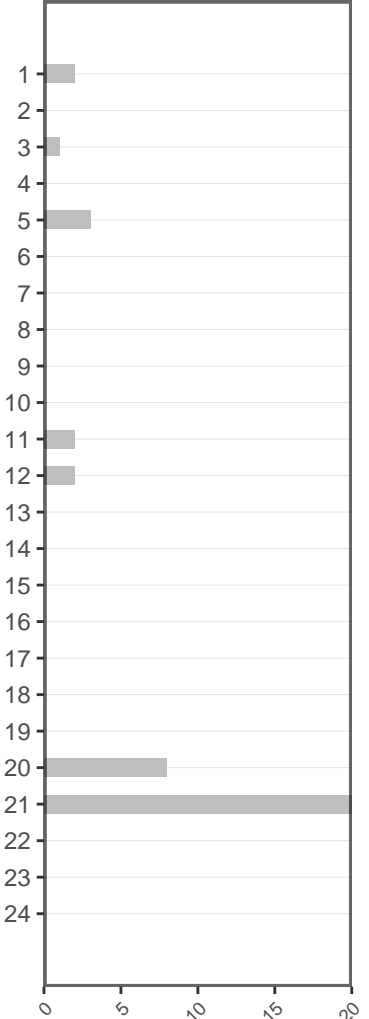
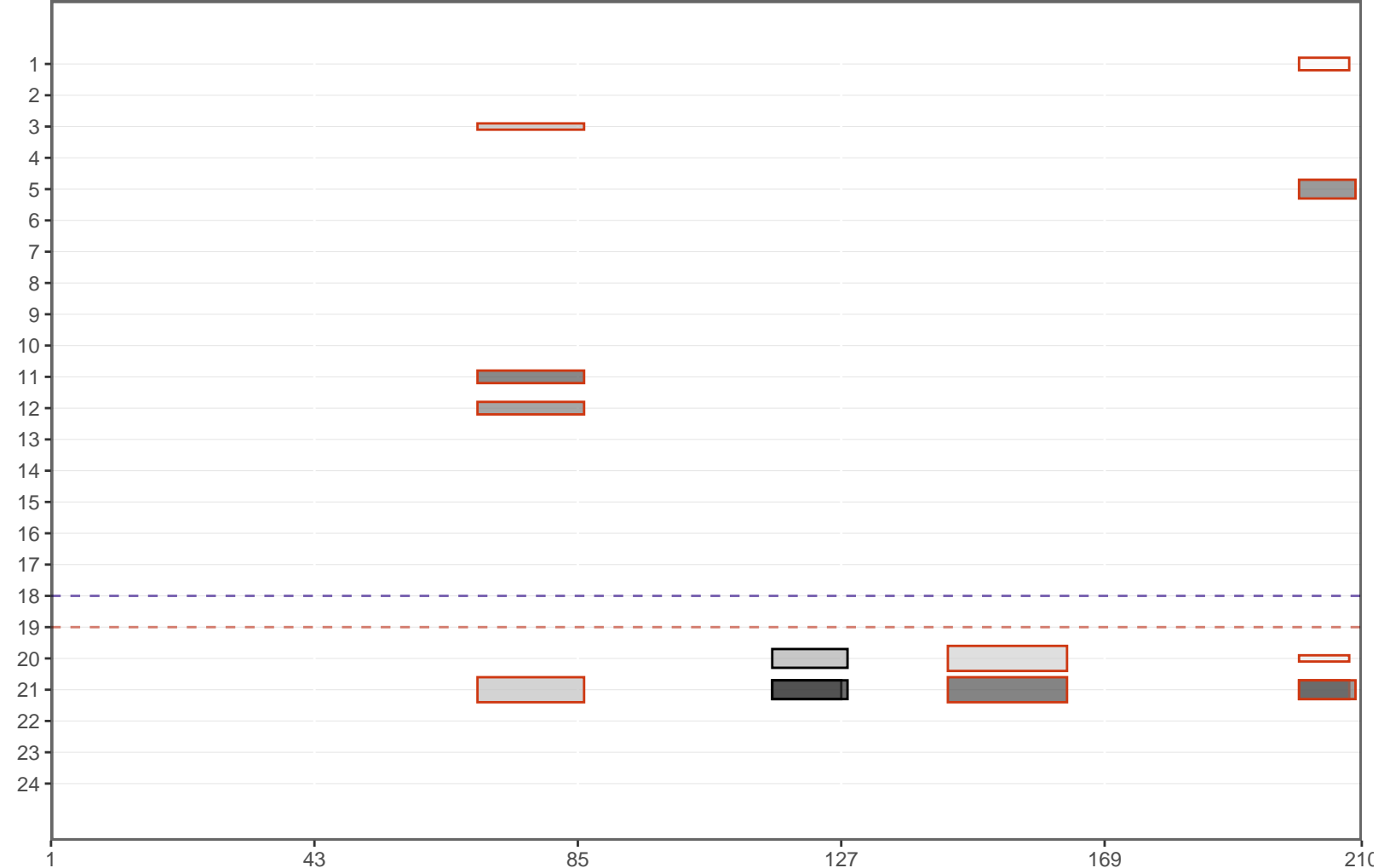
MW indication



Molecular weight

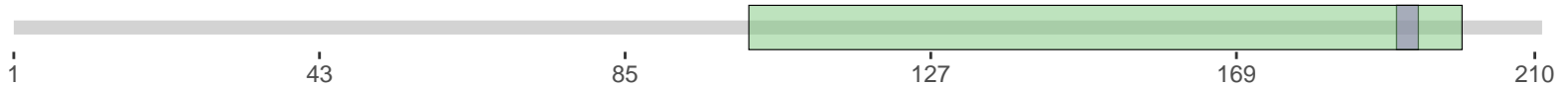


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IAVSGQSEAPYNQLNHHYFARFGDGFVDSBYKRGRRPLETMRLLGMGKVKGLDGGLOGEGVPPMHGGKRLGPPHLLAYGPERFAGDFSGDGNIPGNATLVYDKFVDFVYSGNRK

NbL12g17670.1 L-ascorbate_oxidase [MW - SP = 61.41 kDa]

No. of times detected



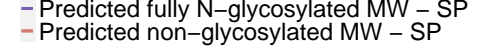
log(intensity)



Values from



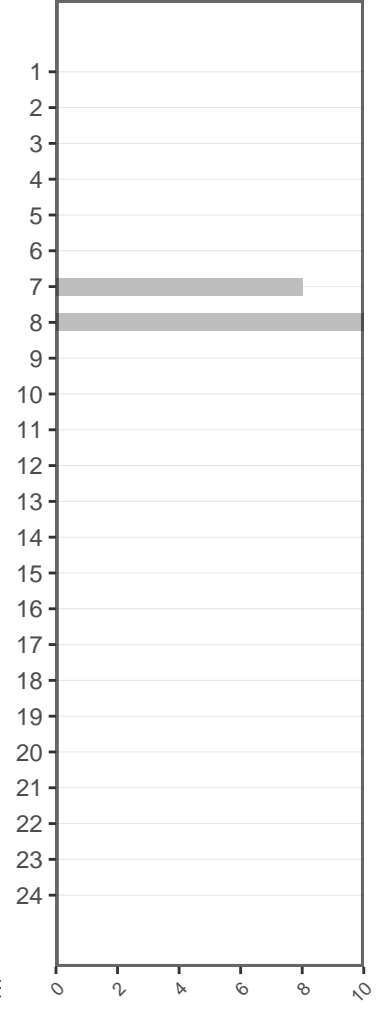
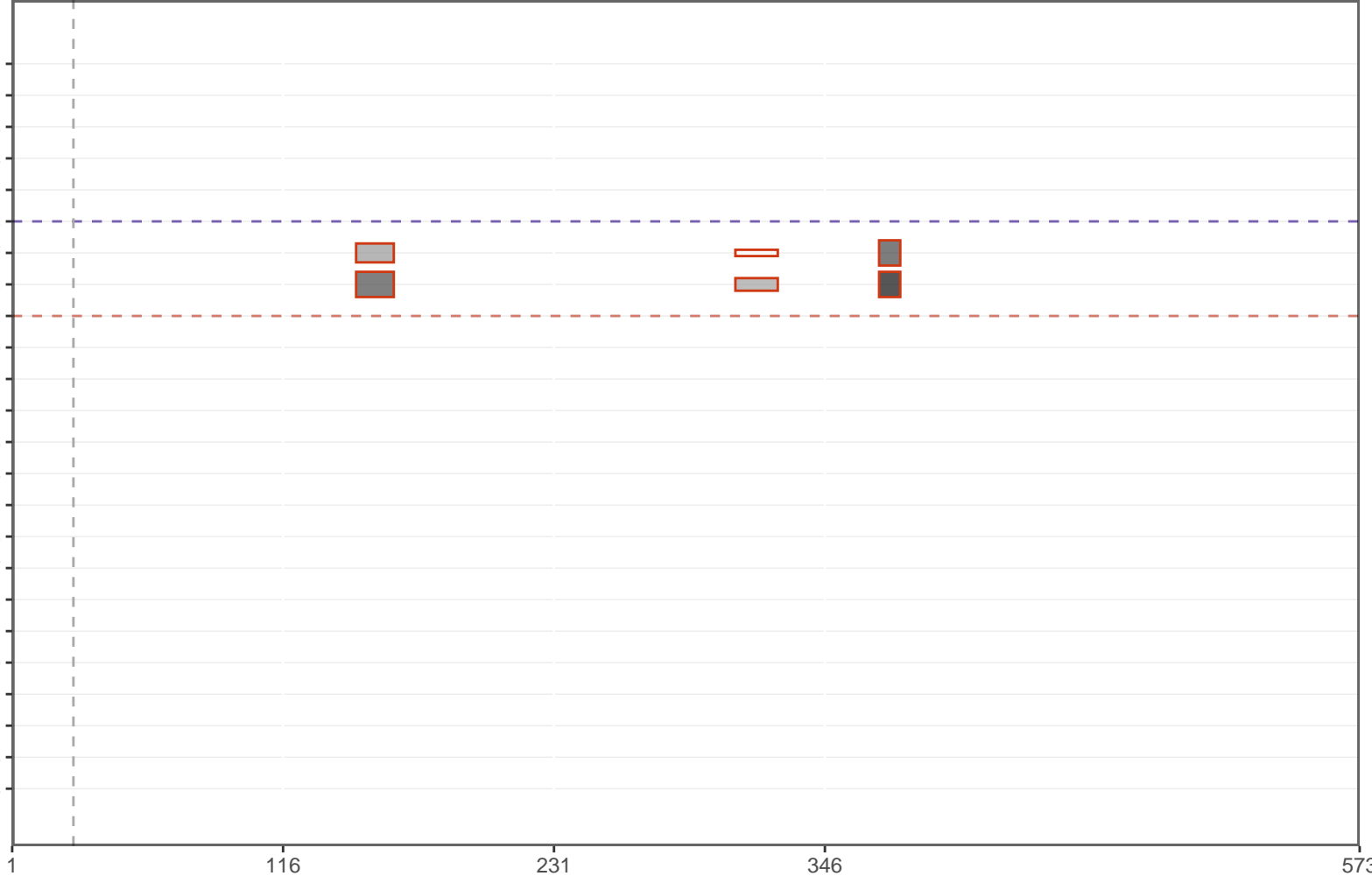
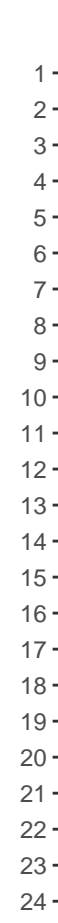
MW indication



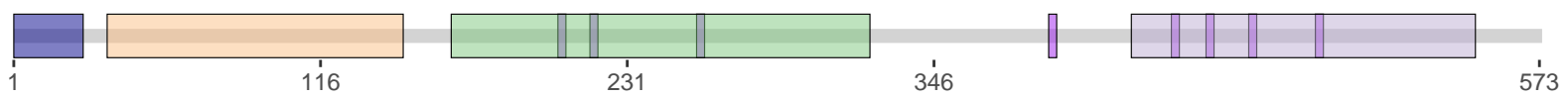
Molecular weight



Gel Slice

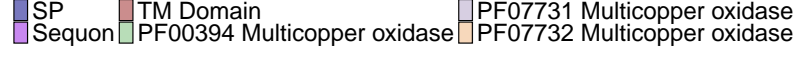


Protein length



Pfam domains

Pfam Description



Protein sequence:

NLFLYSGETYSVLKHADQDPERNRYWASTKIVSRPSGATPNGLGHSYYPNHPRRAPPTIPDAGPHWVNDVAPRVAGSVAIKSHKDFHAPPKTSDRIVMLNTQNRINGEVRWISNNVSNMHPHTYLAALKHNLHTEFQTPPENVNDENYDFVQKQVWATTSNSYRLKFNFTTVDLGNANTMNPNSSETHPWHLHGHDVWVMGVYNGKFNQSDPKNYLVNFMKNTIPVHPYGVWTLRFRADNPGVWAPRHGHIESHFFFMGMGVVFEEDGKVKLPTSIMGCCDSP

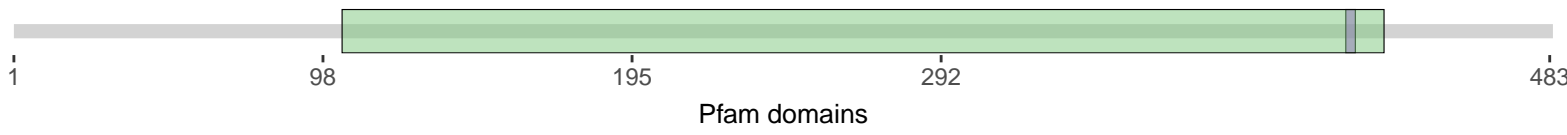
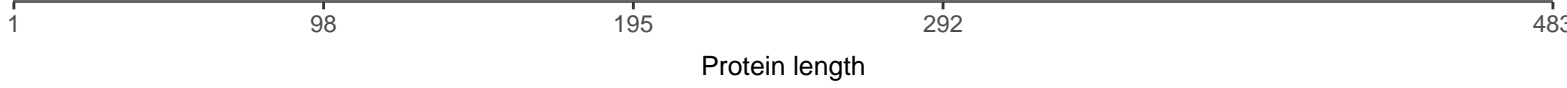
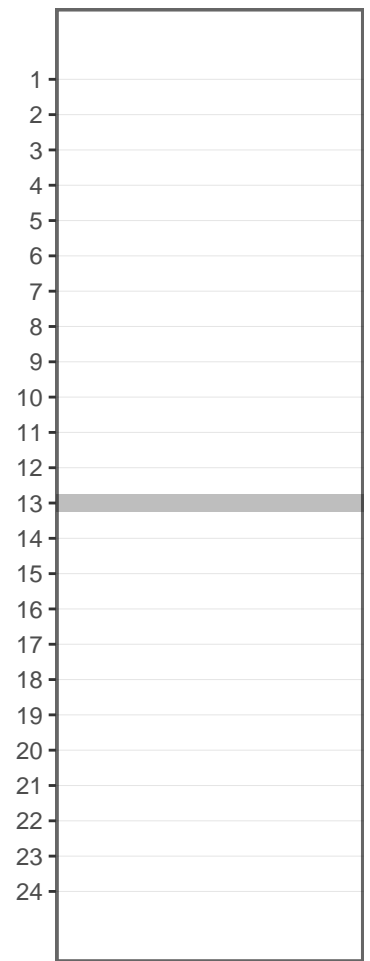
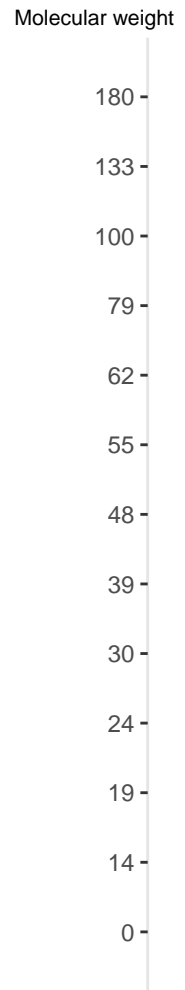
NbL12g17630.1 bifunctional_aspartate_aminotransferase_and_glutamate/aspartate-prephenate_aminotransferase-like [MW = 52.49 kDa]

No. of times detected
 1 2 3 4

log(intensity)
 4.8 5.4

Values from
 Unique peptides
 Non-unique peptides

MW indication
 Predicted fully N-glycosylated MW
 Predicted non-glycosylated MW

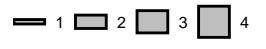


Pfam Description
 SP Sequon TM Domain PF00155 Aminotransferase class I and II

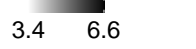
Protein sequence:
 ESKLTKSRLLLLCSPNPTGCVYPRKLEEEIAEIVARHPRLLVGDEVEYHIVAPATHISFASLPCMVDRITLTNGFSKAFAMTGVRLGYIAGPKHIVSAGNKGQGGFTSGASSISQKAAVAALGLGYAGGEAVATMVKAFRRERRDYLVKSFGEIDCVKISEPRGAFYLFIDLSVYGVVEVDGFGDNDSESLGRYLLDKAQEMHLMGTHAVSVPMDQHPSPRCQDQWRERKHWLLLDGMSQFKTSNYAD

NbL12g17590.1 inositol-3-phosphate_synthase [MW = 56.46 kDa]

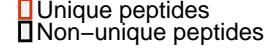
No. of times detected



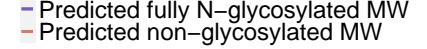
log(intensity)



Values from

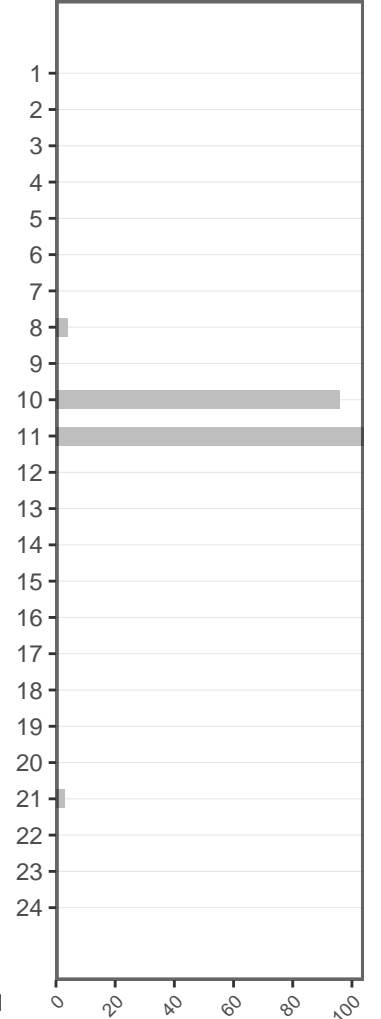
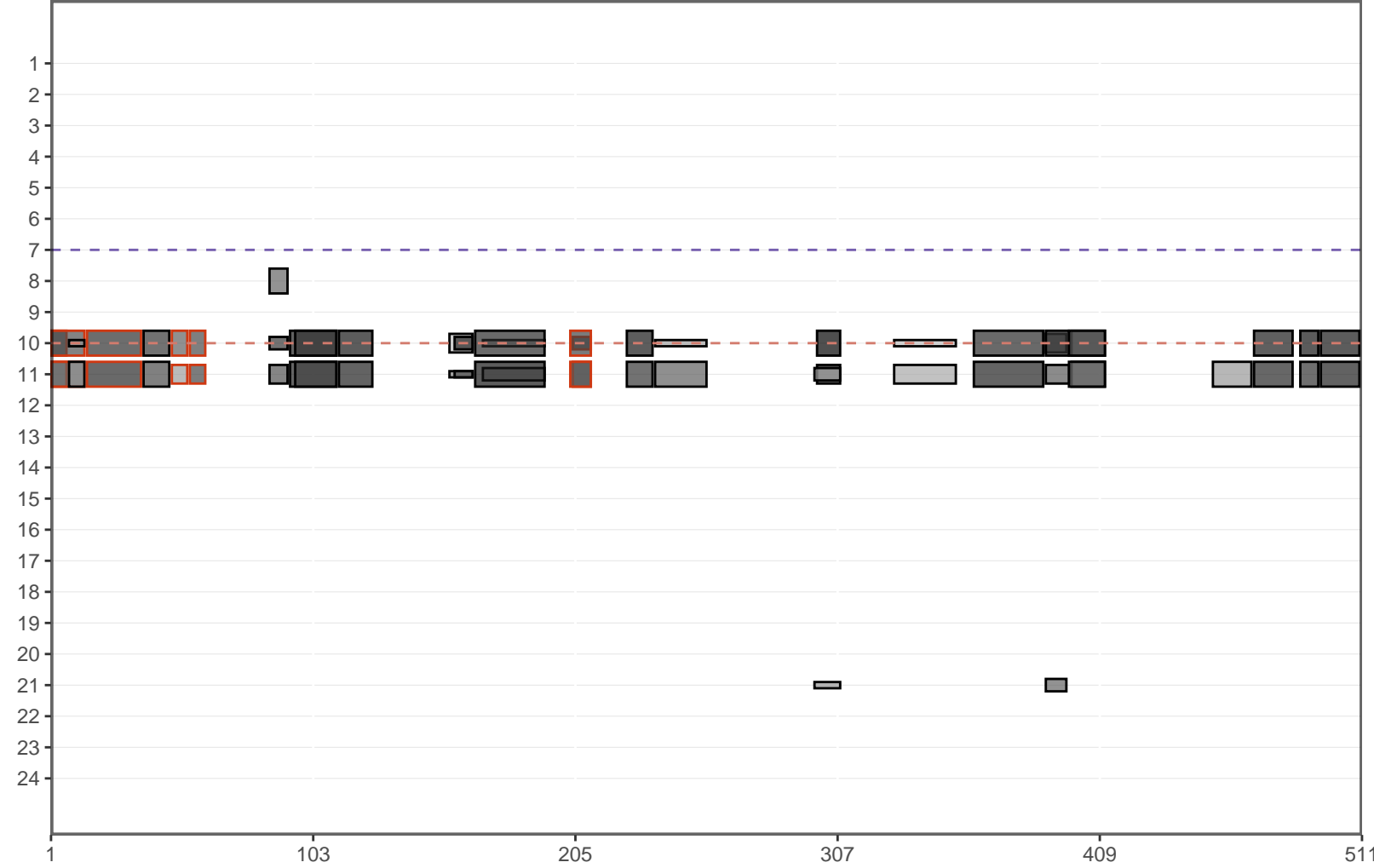
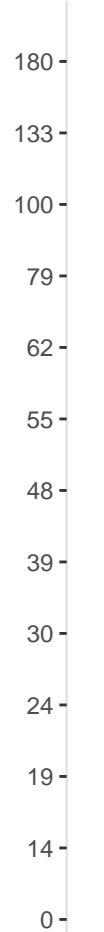


MW indication



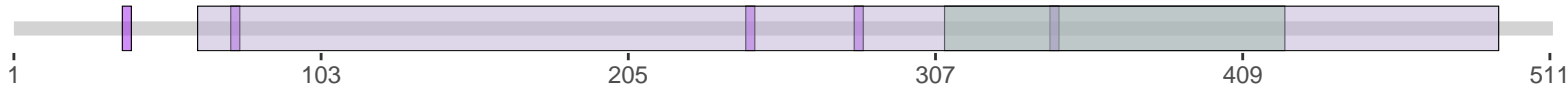
Molecular weight

Gel Slice



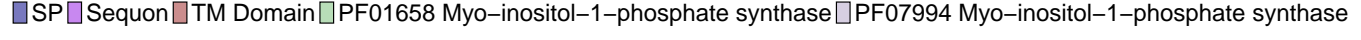
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

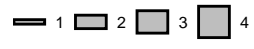


Protein sequence:

VVVLGNDTMEILFADVDRIEAEISPTLVIAQILENVVPIFNGSPQNTFTVPLGLDLAKRNTLIGDGFKSGGOTRKRKSVLVDLVGAGIKPTSVIVSNHLGNDGMMLSAPQTRFRKEIKSNVYDDMVSENALVPEPGEHPHVVVKVVPVYVGDGSRAMDEYTFSEIFMGDKNTVLRHTCEDSLAAPIILDVLLLAELSTRIGLKAEGEGKHFHSPWATLSEVLTAKPLVFPFGTPTVWNLKSGRAMLENLRACVGLAPENMLLEYK

NbL12g17270.1 annexin_D2-like [MW = 35.91 kDa]

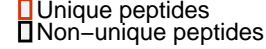
No. of times detected



log(intensity)



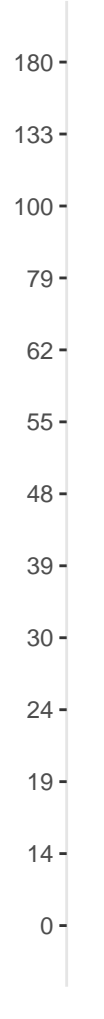
Values from



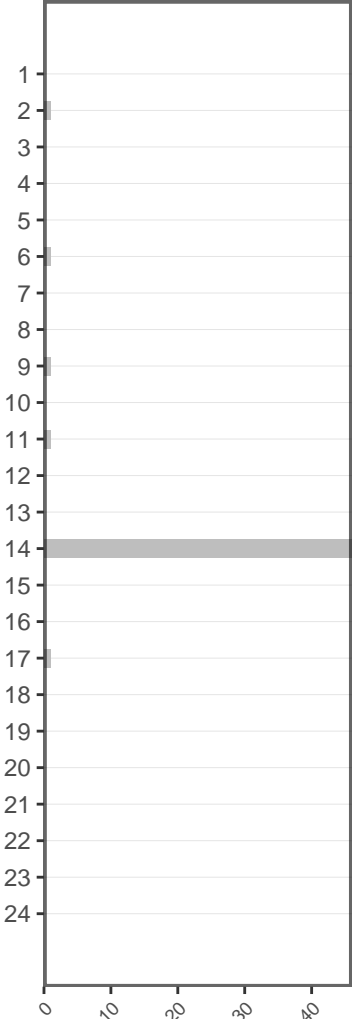
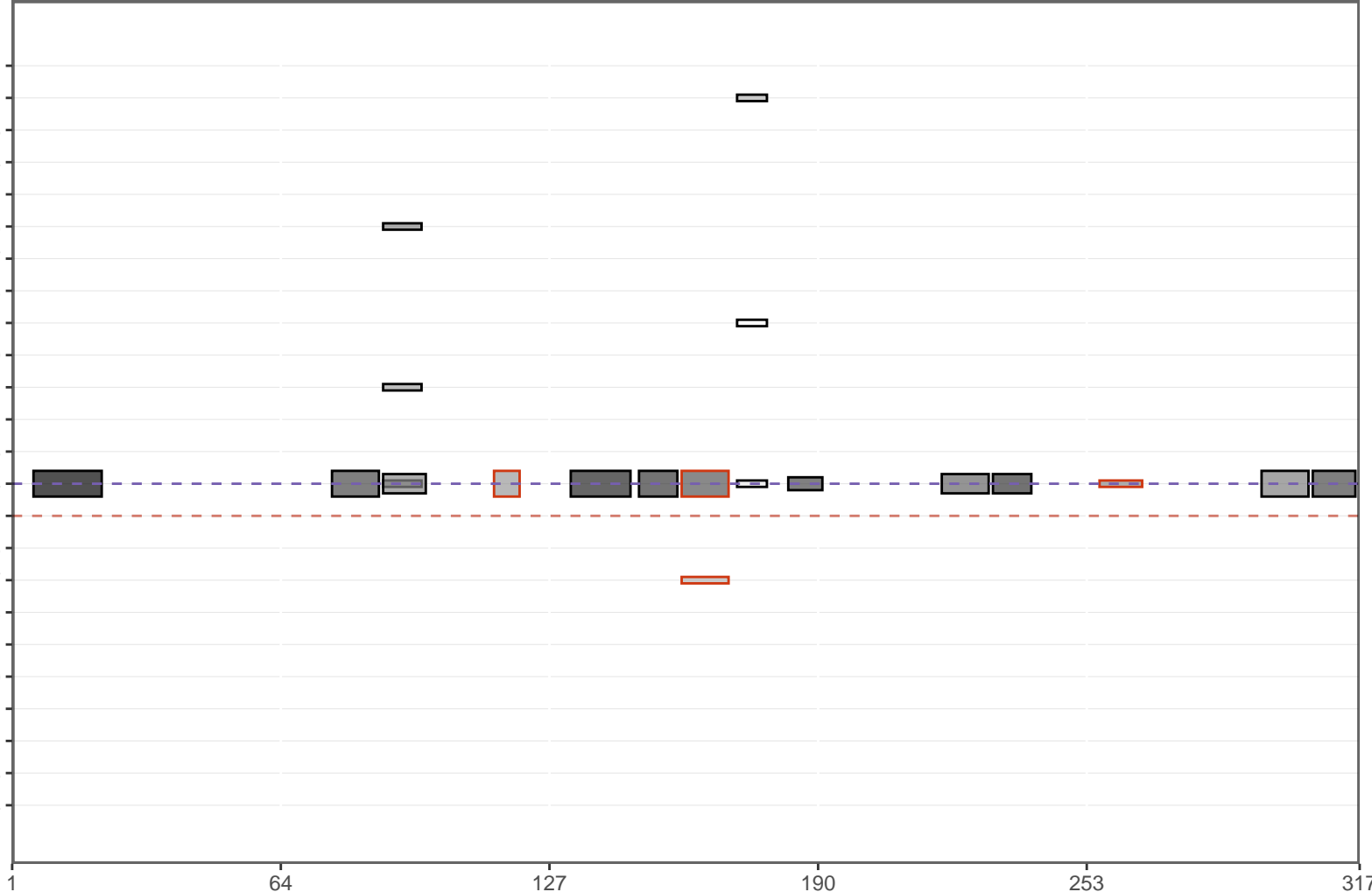
MW indication



Molecular weight

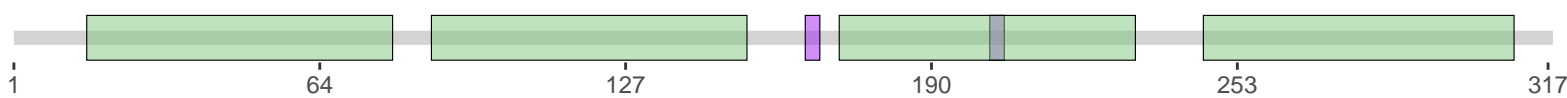


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

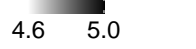
RKLLPLVTAFRYEGAEVNMFLARKEANLHKEKSDKAVNDELIRLSTRSKAQLNATFNHYLDQHGSEINKDLETDSGDEYLVKLSAAIEQLKTPKFKVLRVLGKGTGTGDEWDLTRVVTTRAEVDMERIKEEYQKRNVFLDRDAAGDTSGDYERMLLAIGHGDA

NbL12g17250.1 asparagine_synthetase_[glutamine-hydrolyzing]_2 [MW = 67.91 kDa]

No. of times detected



log(intensity)



Values from



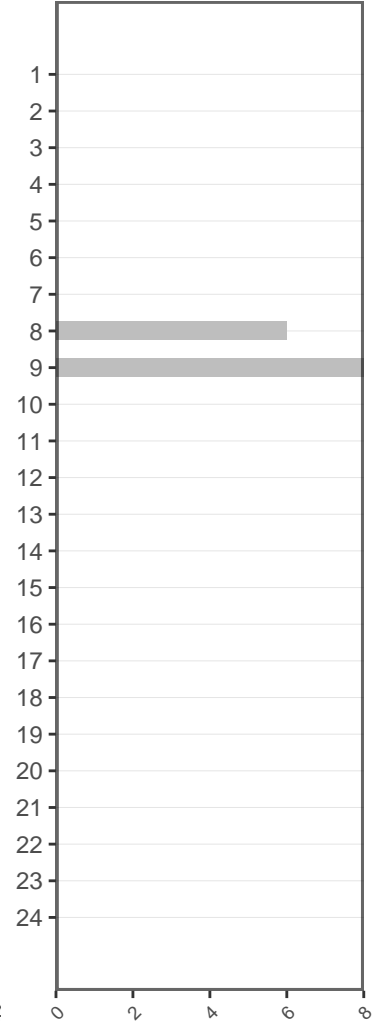
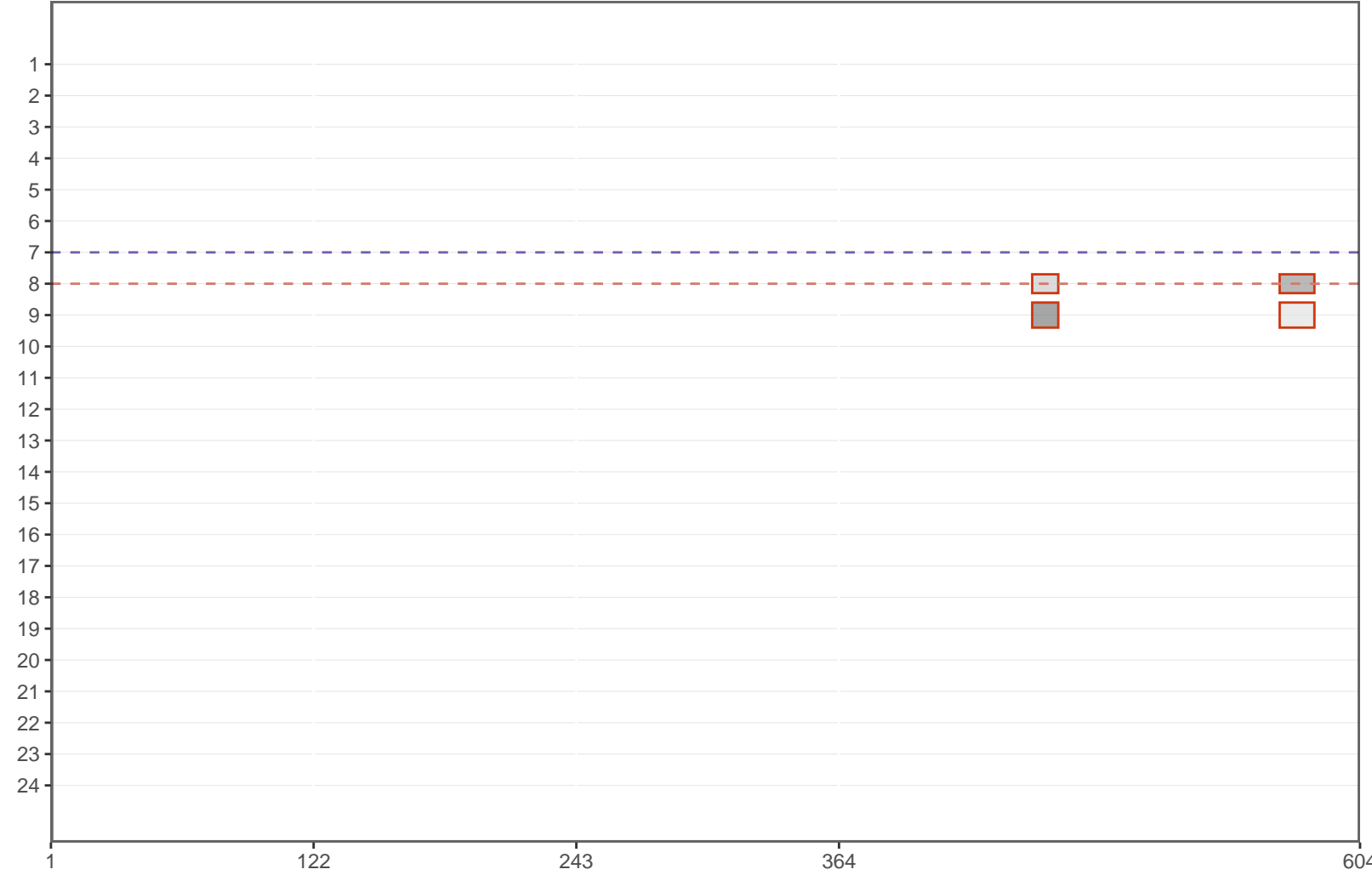
MW indication



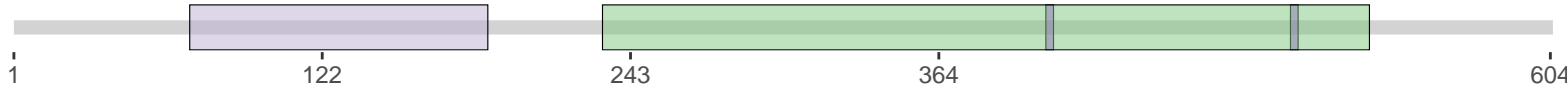
Molecular weight



Gel Slice

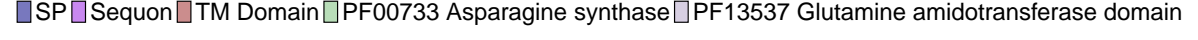


Protein length



Pfam domains

Pfam Description



Protein sequence:

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NbL12g17060.1 aspartic_proteinase-like_protein_2 [MW - SP = 49.84 kDa]

No. of times detected



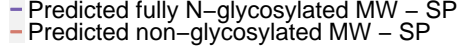
log(intensity)



Values from



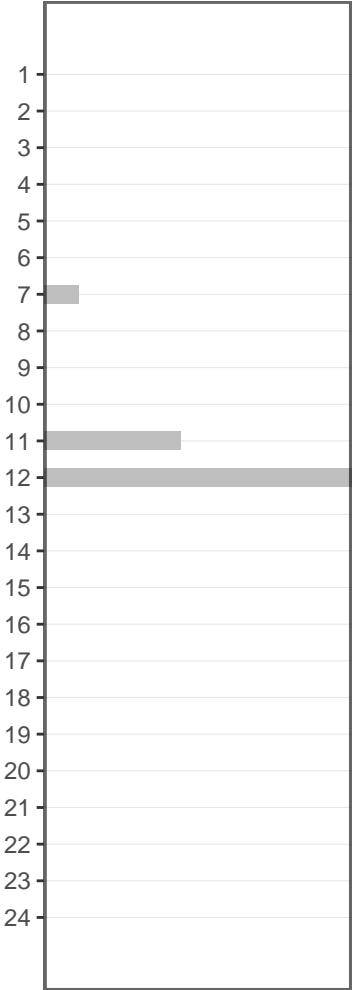
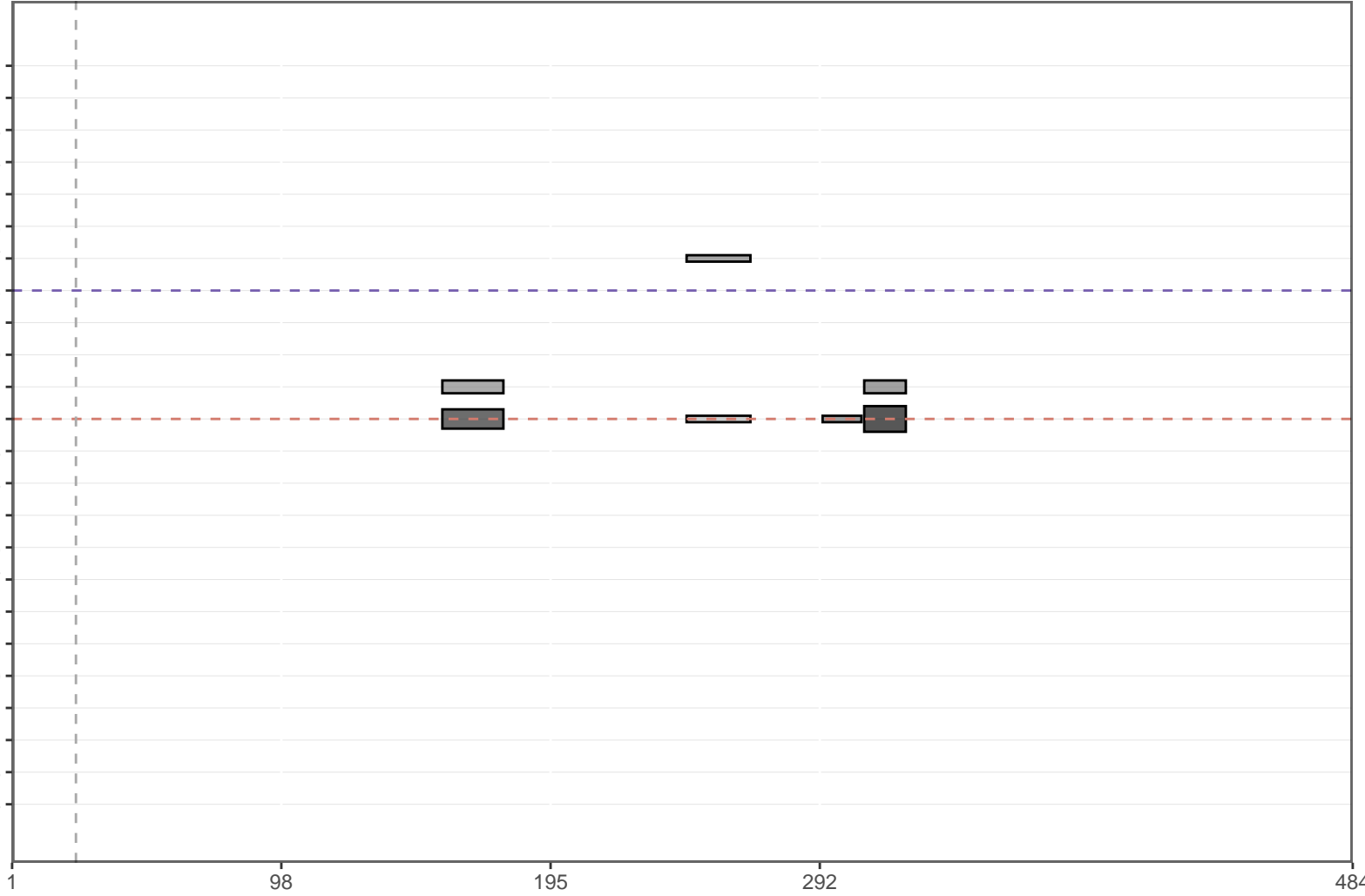
MW indication



Molecular weight

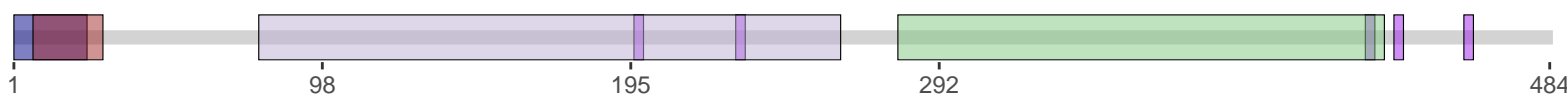


Gel Slice



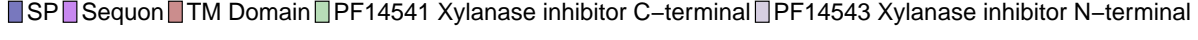
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

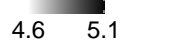
MANSLSLSLSLSSQKWKVFAHLDGNNNGGIFAIGGVGPKVKGSTPLVNPNEPHYVVMKGEVNGKALDIPITTFDAGSNRGTIDSGTLLAVLPNKVYNALMSKLMVKGPDLPHTLVEGFSHFYFSGKVGDDGFPVYVTFQFANSLVLTVPYHDLFGVNDDEWGIWGGSGMGNDGKETLLGLDVLNKLVLVLDLENGSGWTEVNGSSIKVRDETSGKDYIAAHNISAWNGNSRMVFAFVLIHSLGNV

NbL12g16930.1 uncharacterized_LOC104214608 [MW = 75.67 kDa]

No. of times detected



log(intensity)



Values from



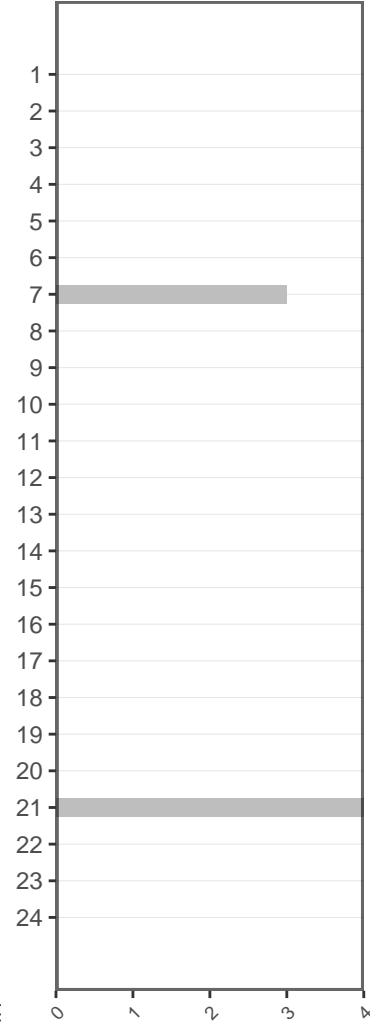
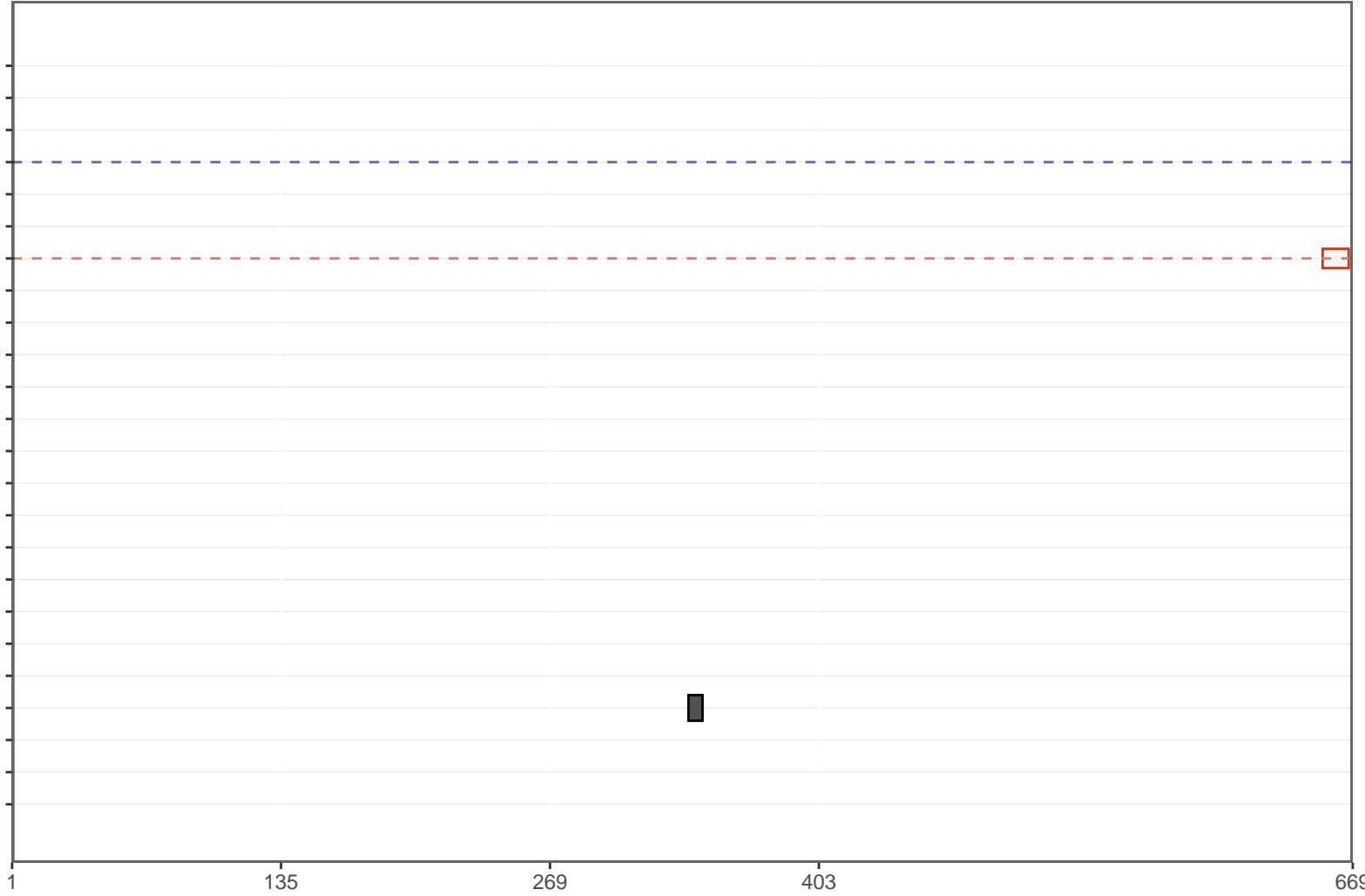
MW indication



Molecular weight



Gel Slice



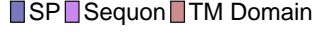
Protein length



Pfam domains



Pfam Description



Protein sequence:

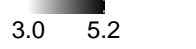
LRNGSNFDNKPVTFRGLTFLNLFKFFRMVYHNLHDLRLIGPLLHEFLPSSFNEISQLQASVQRPNDDLNTFLVYFLSSVVEIKNQNVLGPVSLADLGGYIGISIGLFFYILVQCEYRIKRLNEDCVMRKVRSRKADDRWDKLRKYVMYTFAPNQLLEEVDMRNDGGCTGVKMEGLNRKSSVVRGRGSTRLDTRFGRKVLSPSEKRAISEGIDTGGATHFLPESAADRKRKSTRLKEERFQENAVPPSTENSKPEDLDWVIGSPVFSAADNLTPPPPLESAAADHII

NbL12g16900.1 probable_UDP-arabinopyranose_mutase_5 [MW = 39.11 kDa]

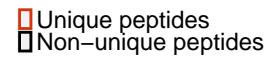
No. of times detected



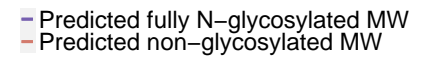
log(intensity)



Values from



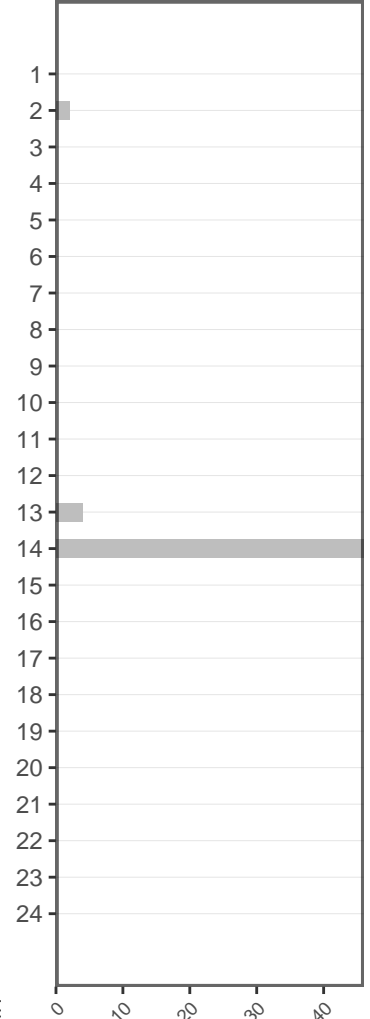
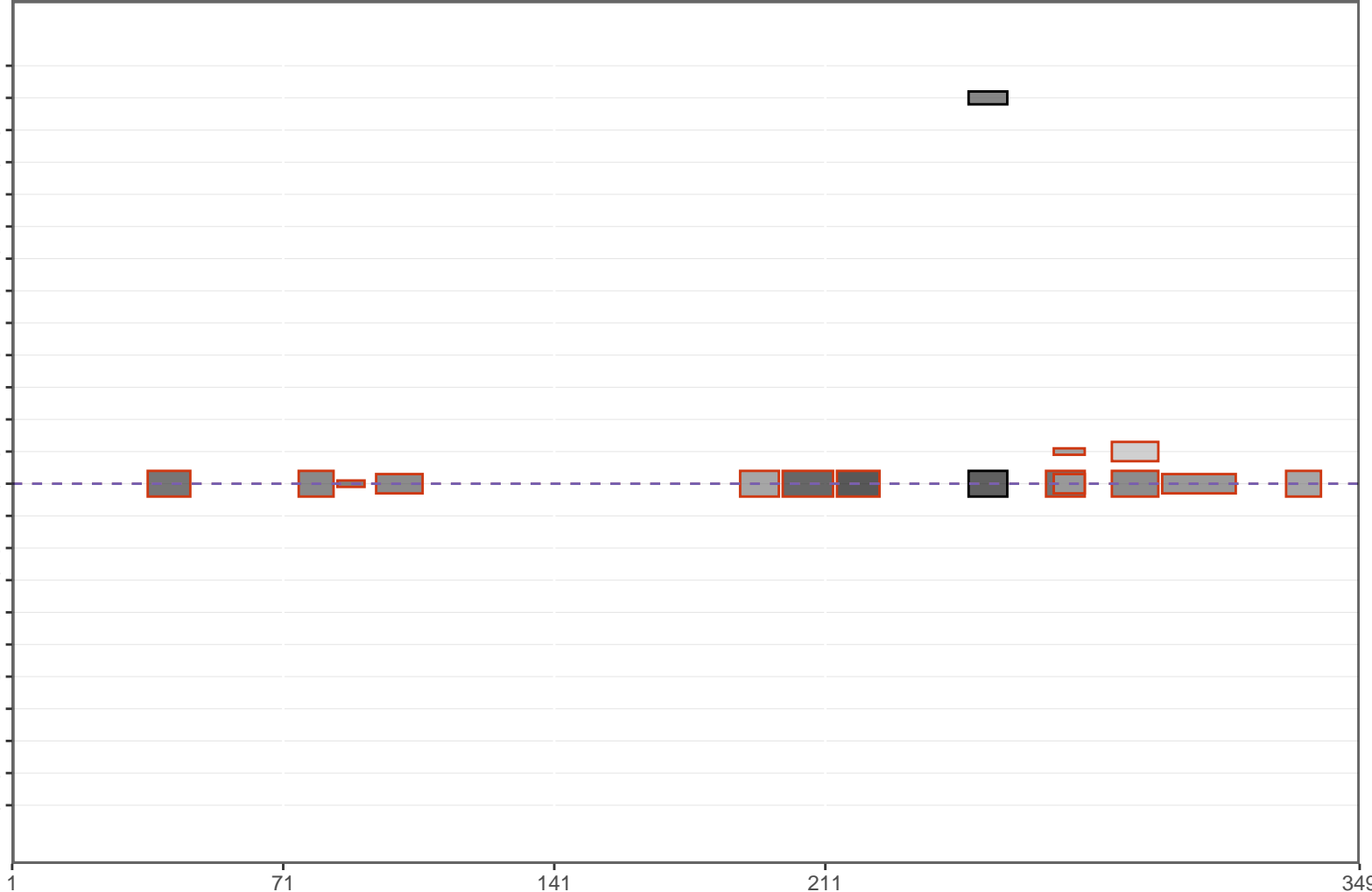
MW indication



Molecular weight

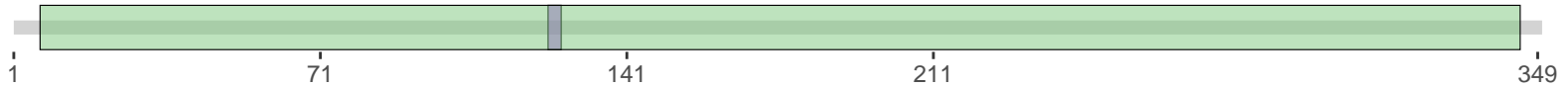


Gel Slice



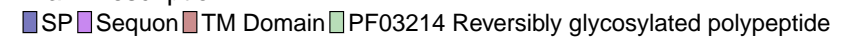
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

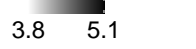
LCLNLAADLDAPTDQALPKALNTRVYVDWLVTPARAMPLSLGNAFDRELVSPALLPSFRLAKEQKFRVETWDTGMGVKVVCDHLGYGKTKLPLVYWRKERGDVESLKKKEWEGKLMEEVVPFFQGMRLSPNATAEDCVVEVAAMKEQLGRDIPVFTFRADSMVEVWKLWMMKGTG

NbL12g16800.1 violaxanthin_de-epoxidase_chloroplastic [MW = 54.82 kDa]

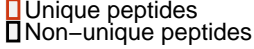
No. of times detected



log(intensity)



Values from



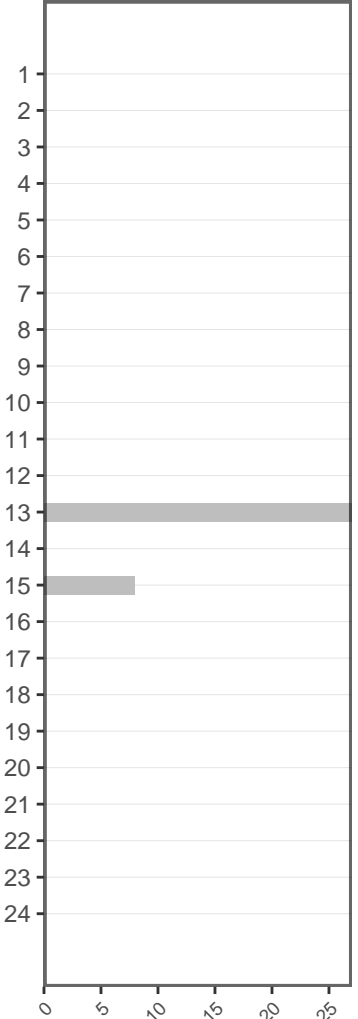
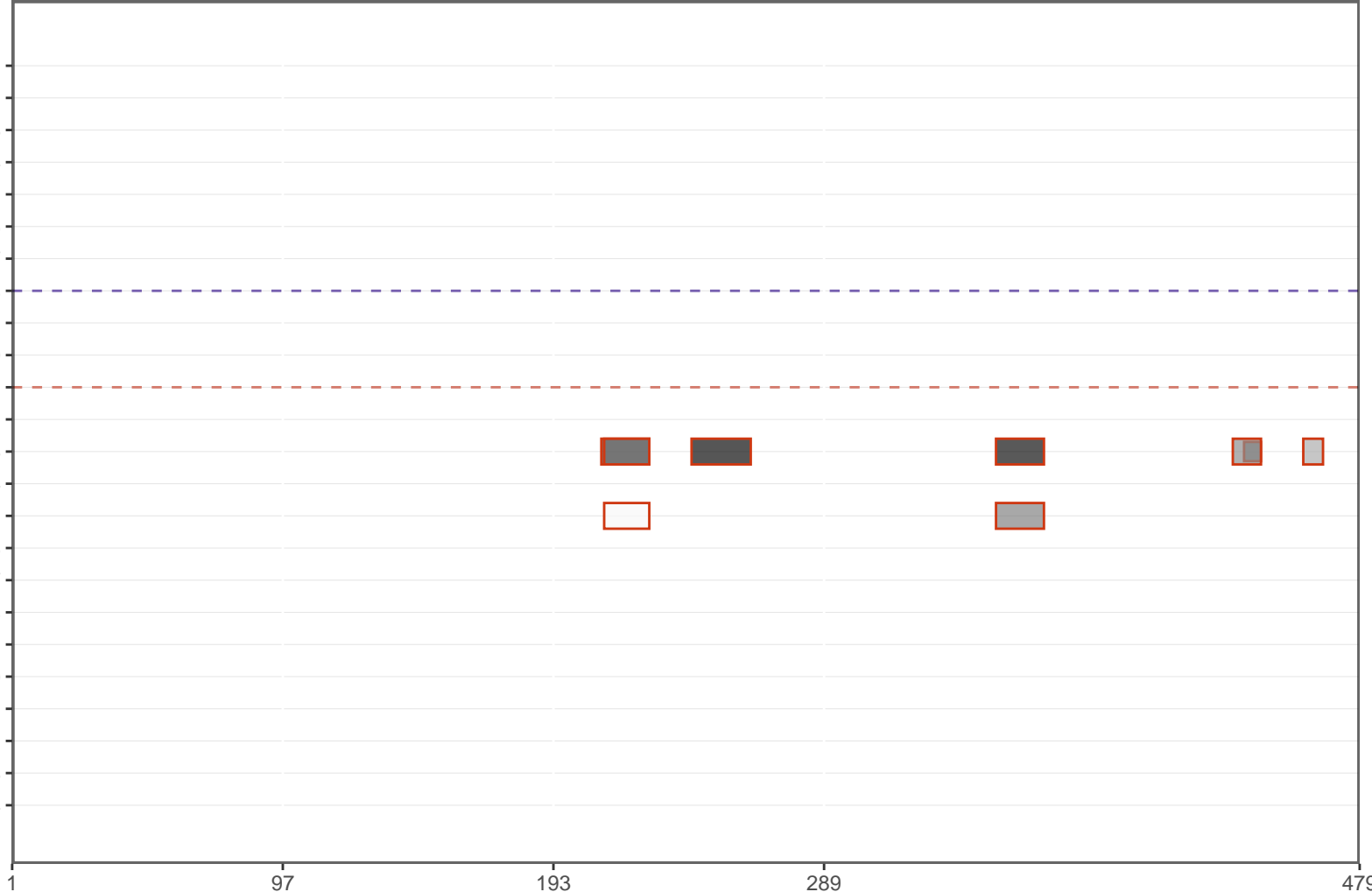
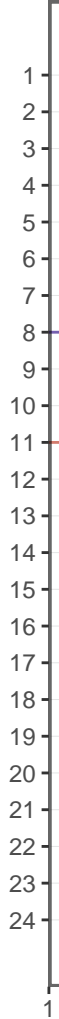
MW indication



Molecular weight

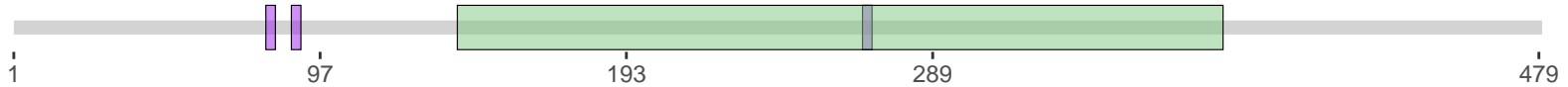


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KFTDMKDFSGKWFTRGLNPTFDADFGLHEFTEENKLVLSWRIRTPDGGFFTRSAVKFVQDPKYPGLNHNENEVLYHQDDWYLLSKSVENSPEDVIFVYKGRNDWDGYYGAALVTRSAVLPESIPELQTAGKVRGRDNTFKTNTGCGPEPLVLERLEKKEVEEGERTIREVEEIEEVEKVRDKEVTLFSRLFEQFRELGRDEENFLRELKSEEMDVLQGLKMEATEVENLFGRALPIRKLK

NbL12g16720.1 peroxiredoxin_Q_chloroplastic-like [MW = 24.04 kDa]

No. of times detected



log(intensity)



Values from



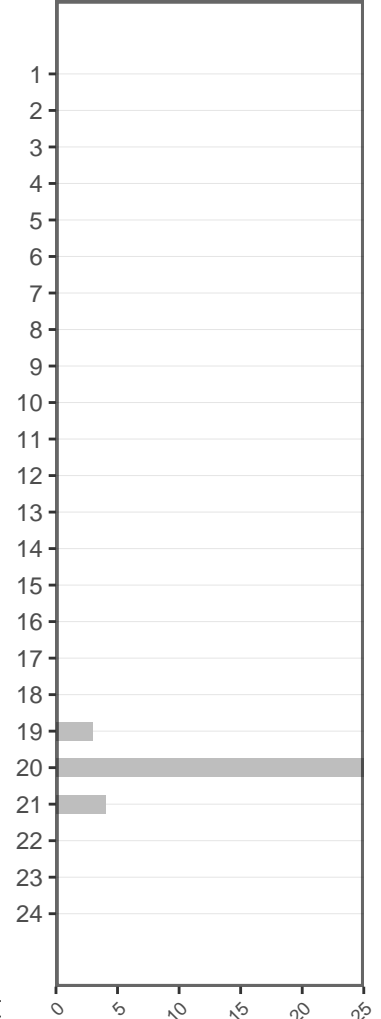
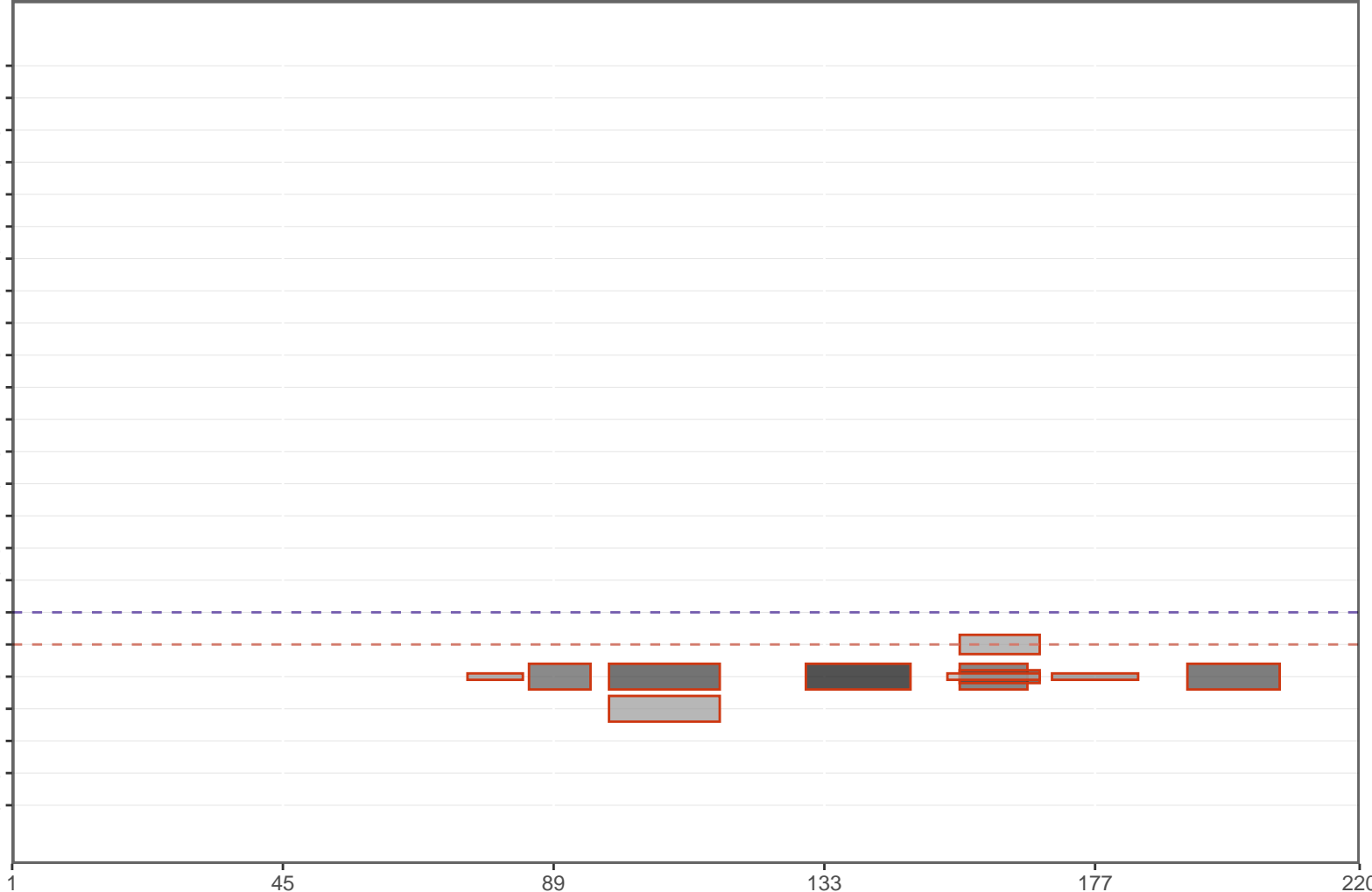
MW indication



Molecular weight

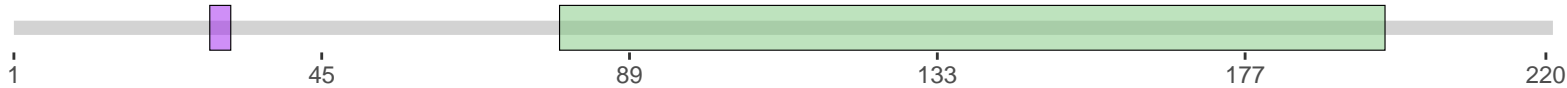


Gel Slice



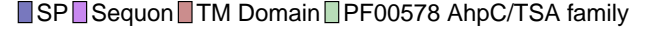
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

CPVVVYFPADESPGCTKAGSFRDSEYKFKGAGAEVVGISGDDPEGHKAFKKYRLPYTLLEDEGDKVKEWGVPAIDFOTLPCGRTYVLEKNGVWVQVYNNQFQPEKHDETLKLLGEL

NbL12g16640.1 uncharacterized_LOC104113886 [MW = 107.6 kDa]

No. of times detected



log(intensity)



Values from



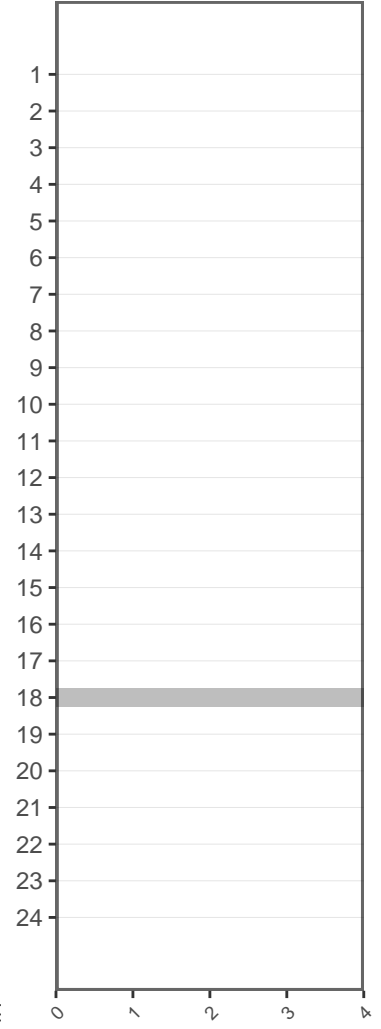
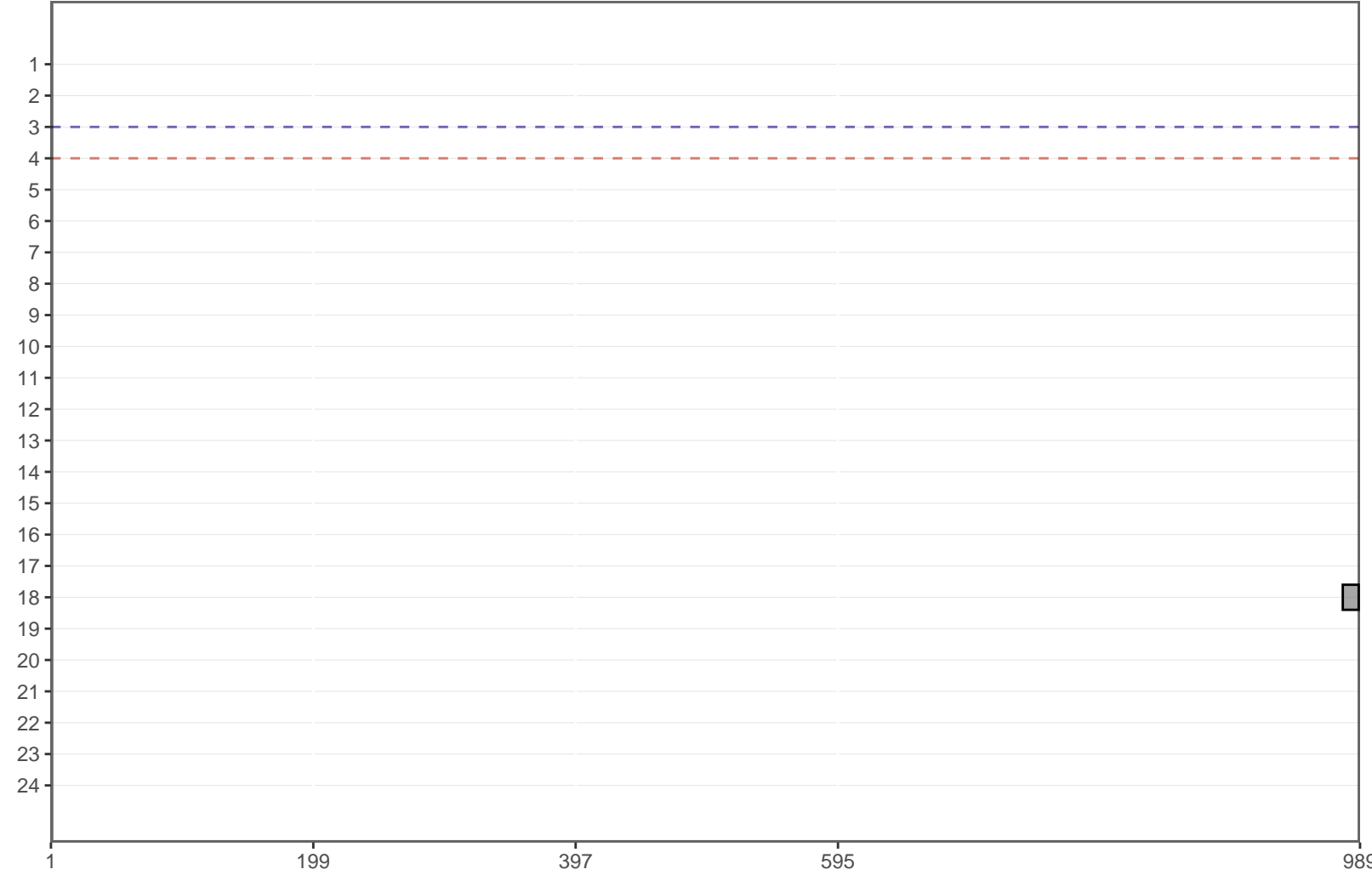
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

ISASDPKSAALALDRMVGAAWVFLGENNYAAASEYAWESGATPPGTALMMLDADKMWAAASGRNPTLGGALTRLRGCAFNQSGWEVRIAGALTIARSGEPYRLGIYEFLLHALGGVQSGQSDMHNSNGEDOGASGTGLGSLSPMLKVLDEMYSGVDELKEMRNHNAAKKEWTEDEELKLYETHERLLDLVSLFCVYPRSKYPLPGPTEAKGLIDYRTRHNISASTGLSDRPWATGSDLMYETTKAGAAEPETIDDDLVNFWAANLGGDDLNNAPNRVYQFLAGAGTC

NbL12g16630.1 glucan_endo-13-beta-glucosidase_6-like [MW - SP = 50.11 kDa]

No. of times detected



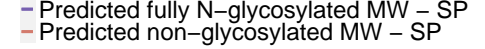
log(intensity)



Values from



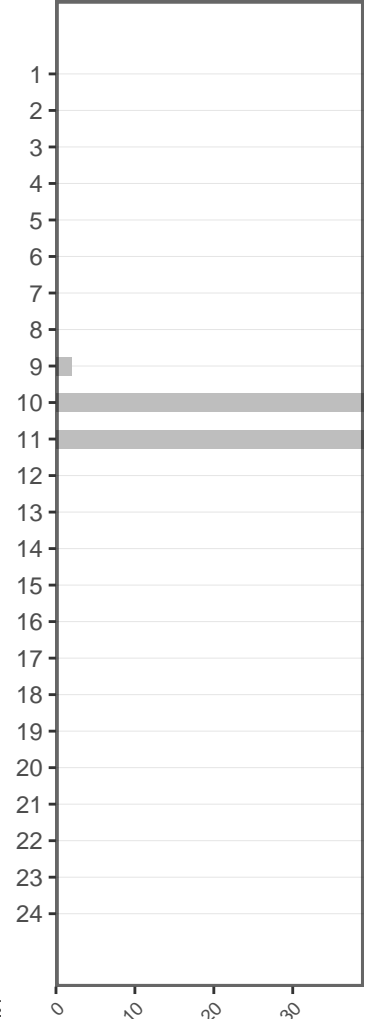
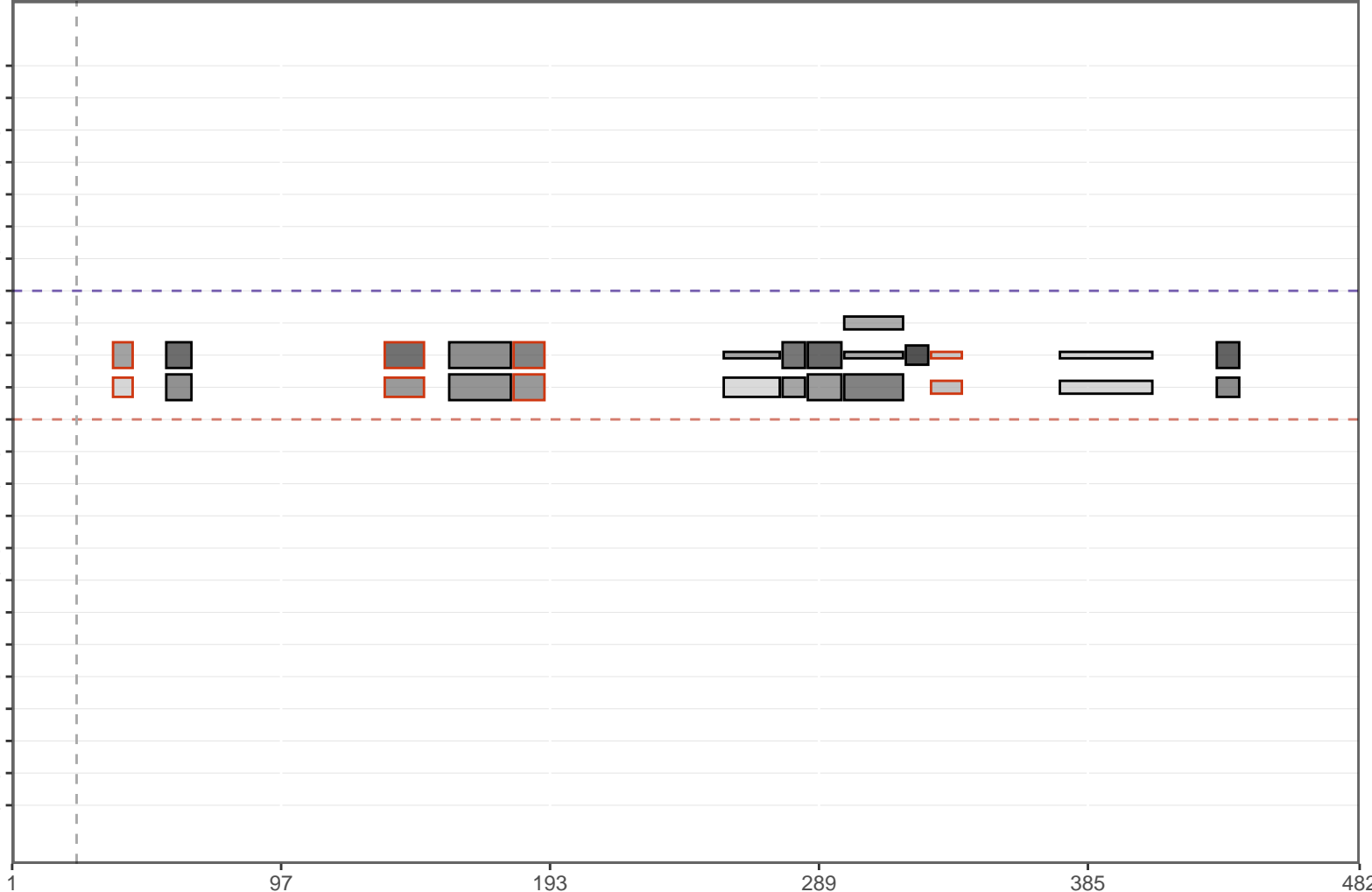
MW indication



Molecular weight

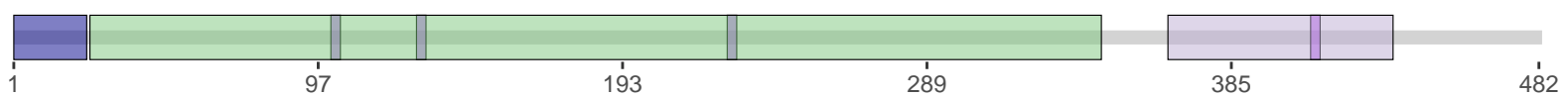


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

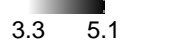
IDGGTTYTNMFDANHDITLWALGKNGFVPHIGEGWPTDGDGRNANAGLGRFNGFMQHSIEGKGTPTMRPGIDAYLFLSLEDKASIQPGRFHWGFTFYDGLPKYSNLGTTNSGALVQANNRYLERKRWGVFKPNKAVDDPQIAPSMYAGGLADCTSLGYGTSCGGLDARGNSIYAFNSYQINQLDDACKFQGLGTVTKSDPSTGTGRYGLMIEPIYGGADRGLGYTRMALALLFMWTLI

NbL12g16420.1 uncharacterized_LOC109231956 [MW = 37.8 kDa]

No. of times detected



log(intensity)



Values from



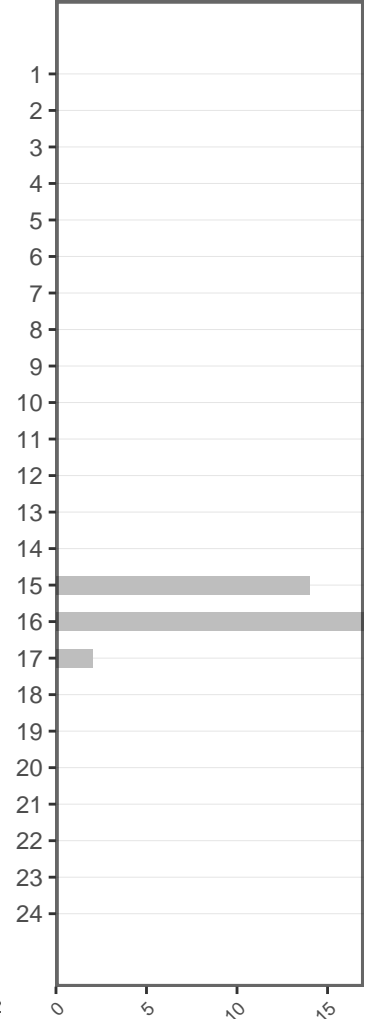
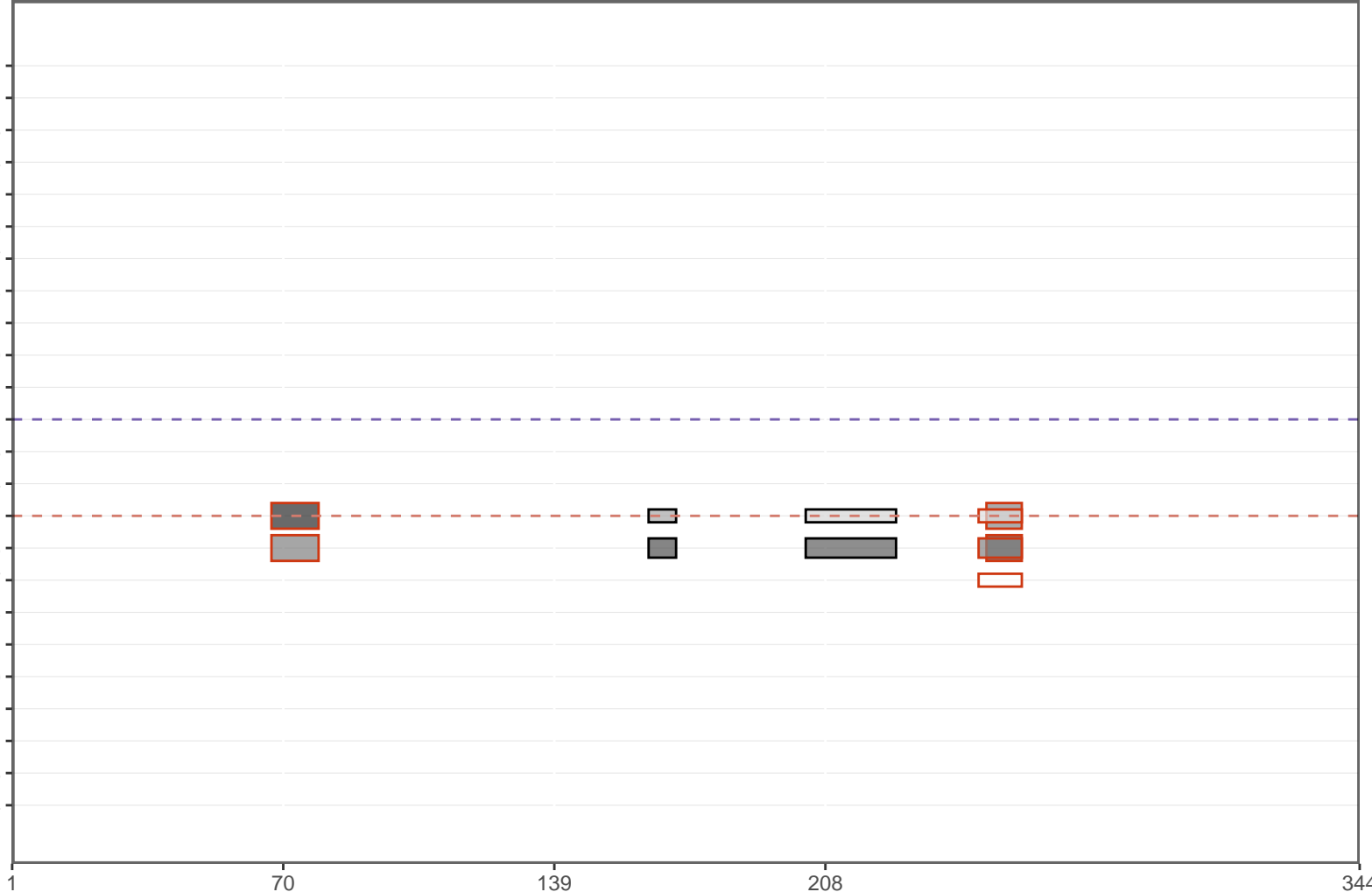
MW indication



Molecular weight

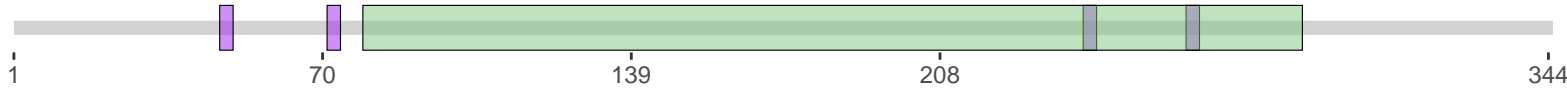


Gel Slice



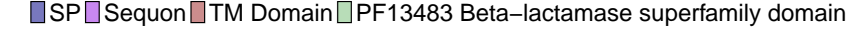
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PNLRVATPNAXKTLIDPLFNFVWYLEPGDDEIEVSNGLGVNKKATAGPVLGPPWDRPENGVLVTSRPGKALTYVEPHCVNKTFLKWKYKADIVTPVKKOLLNFTLVSGGDGDAVLAKLLSARFVWPMKNGDLSKGLASIHSEGTMESEFKELLSKELPDAKYLEPVPGEPLDISAVGGD

NbL12g16410.1 phenylalanine--tRNA_ligase_chloroplastic/mitochondrial-like [MW = 54.19 kDa]

No. of times detected



log(intensity)



Values from



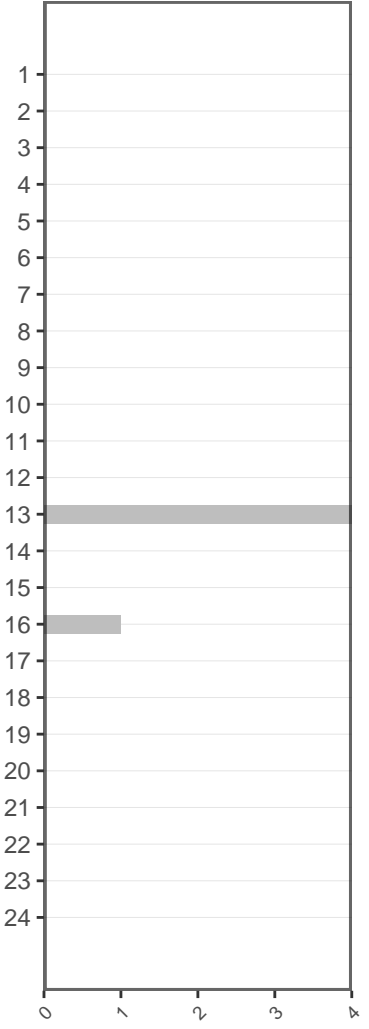
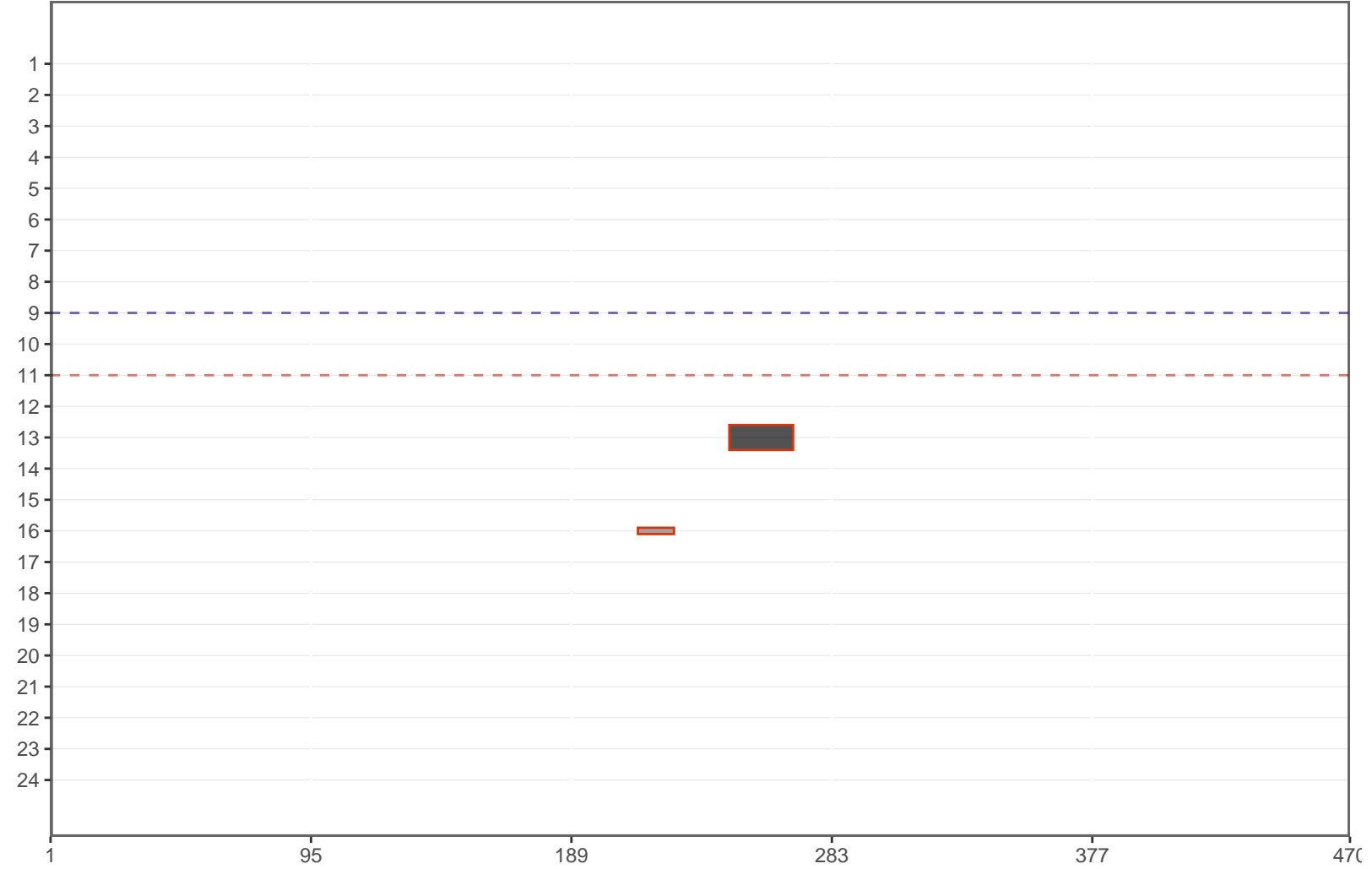
MW indication



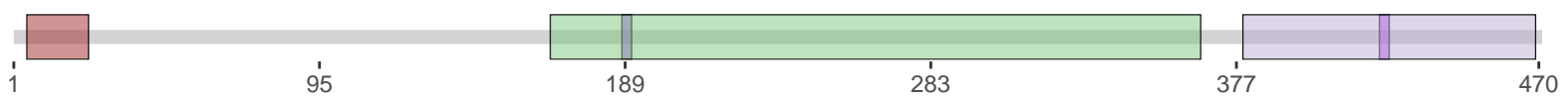
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01409 tRNA synthetases class II core domain (F)
- PF03147 Ferredoxin-fold anticodon binding domain

Protein sequence:

RRRDSIDATHYYPVTHQMEGVRRVFAPNDWEGSGADATSHAADLKKKLEGLARHLFGGVEMRWVDYFPFTNPSFELEVFQNEWMEVLGGGVTEGELKRGRTDNWAWFGLGLERLMAVLDNPDRLFWSTDERFTSQFSSGRLLGLKPKPFSKYPPCYKDMFVWDSFTENLGEVVRGIAGDLAEELKLDNFTNKKKGMTSHQYRIARRSMERBLTDEEINDLQWVKVREGVESKLVVLR

NbL12g16130.1 SAL1_phosphatase-like [MW = 44.32 kDa]

No. of times detected



log(intensity)



Values from



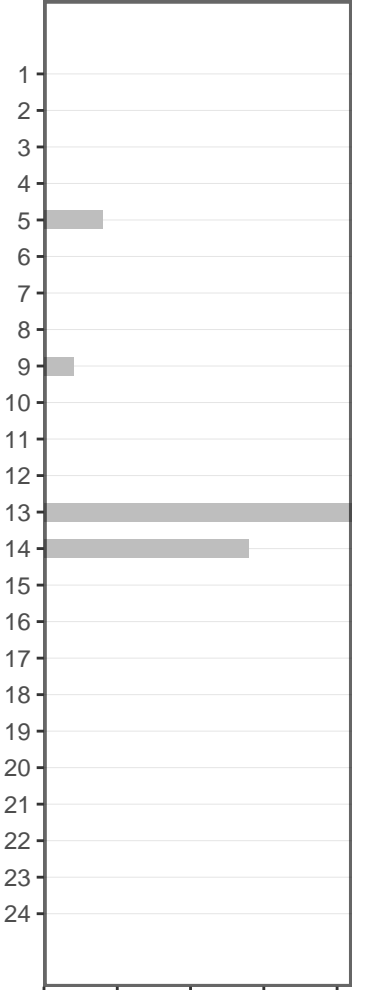
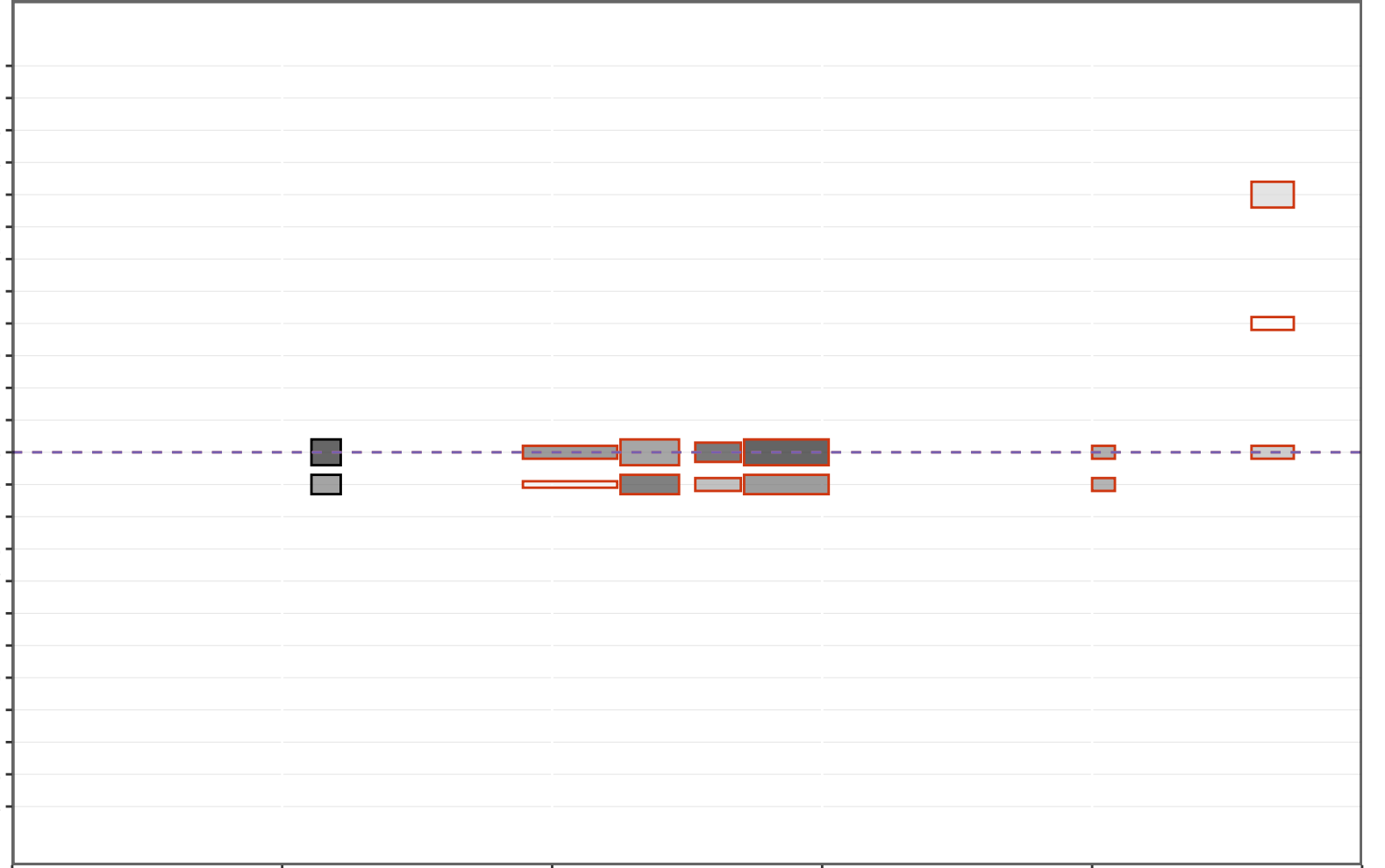
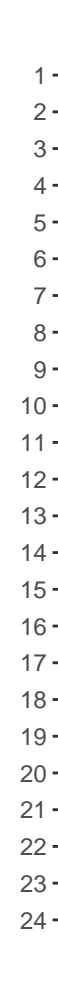
MW indication



Molecular weight



Gel Slice

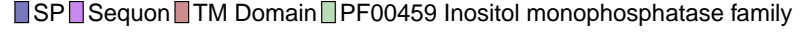


Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

HWYLDPDGDTKGFVRGGVYALALLDEGKAVLGVLAGPNLPLSVAASHNPDGSGEKVGLFYAQVSSGTYMDELGGSTLKVHVTDLNPEEASFEEFEAAHSLHDLSSIAKLGVRAPPVRRISGAKYCALSRGDGAVLRFPHKGVREKIVDHAAGYLVVAEAGGVVSDAAGNPLDFSRGKYLDELHEGIVTNGKLMPLALKAVKEELNEKSSSL

NbL12g16060.1 alcohol_dehydrogenase_1B [MW = 36.82 kDa]

No. of times detected



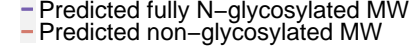
log(intensity)



Values from



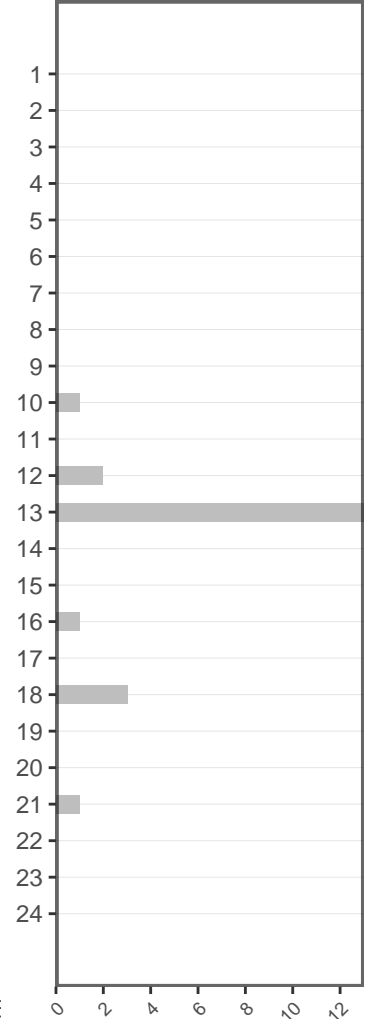
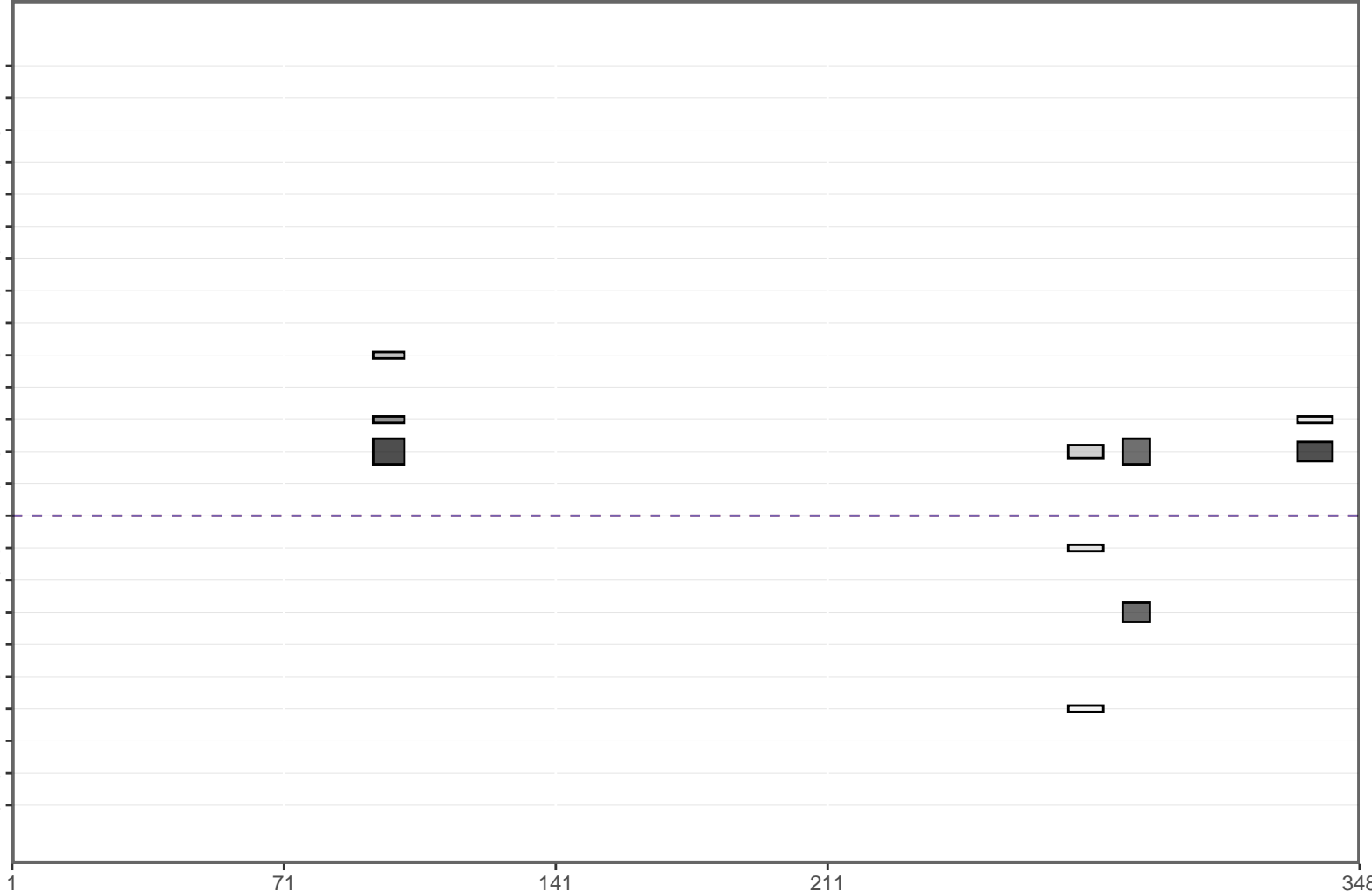
MW indication



Molecular weight



Gel Slice



Protein length

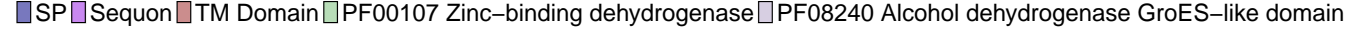


Peptide counts over 4 repeats



Pfam domains

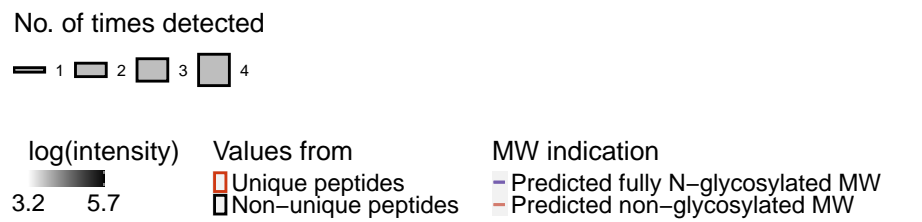
Pfam Description



Protein sequence:

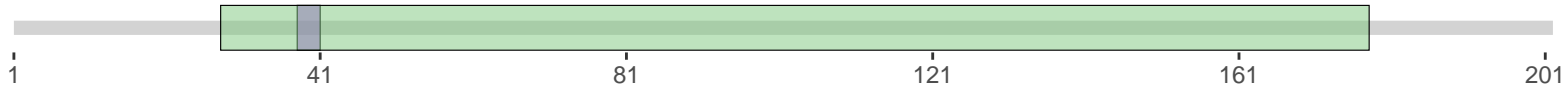
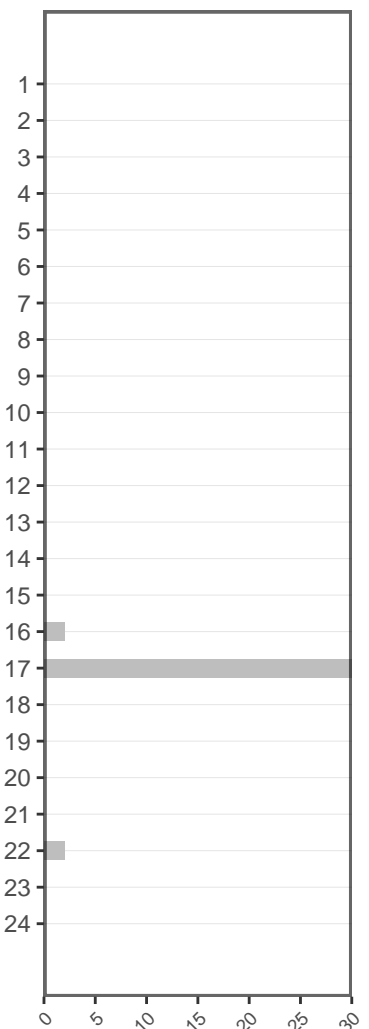
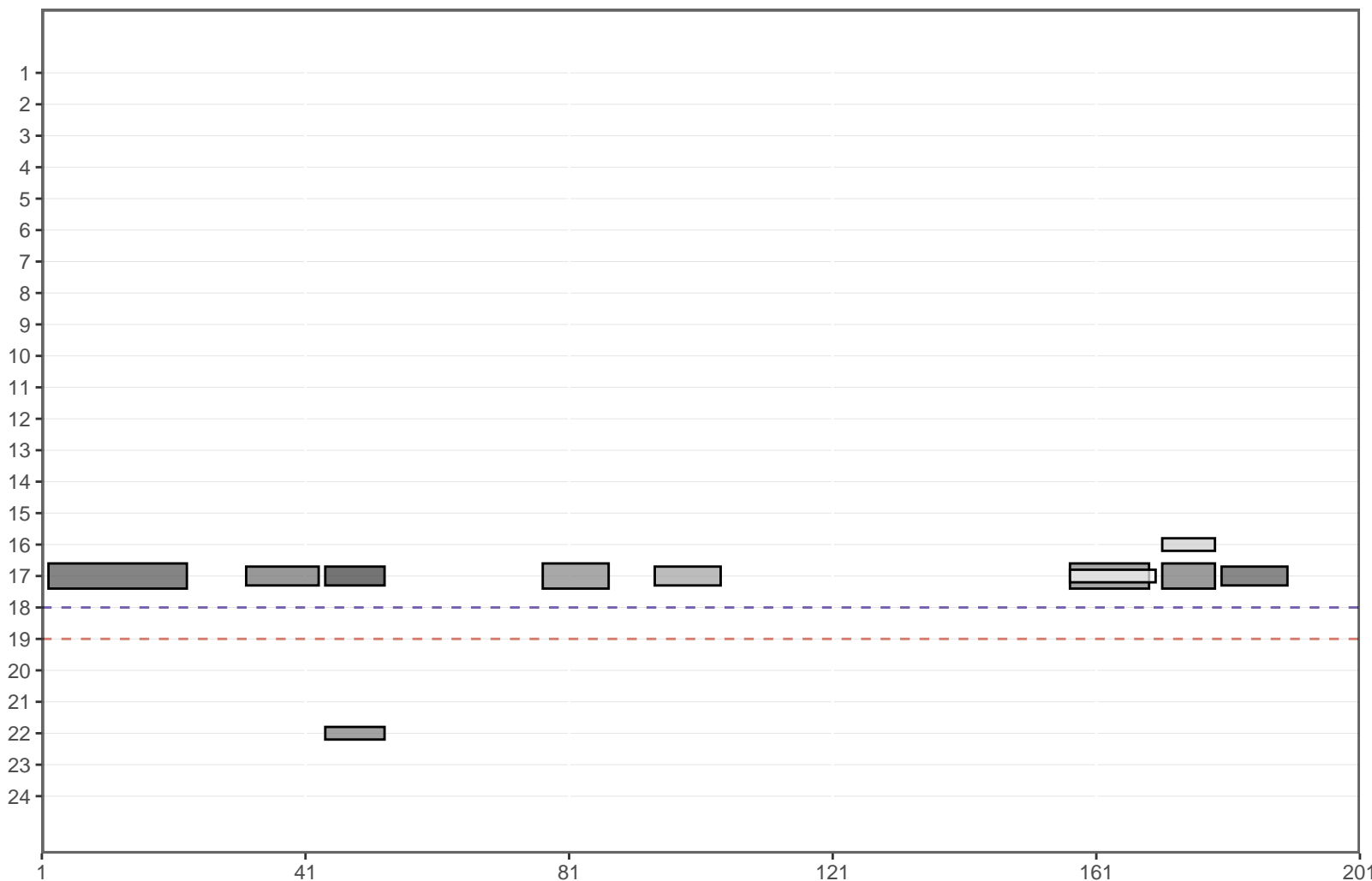
AAEVRPGAAUAVGIGGVGSSGLGARAFGASEIIAVDVGDEKLGKAKMFGATHGCVNAEKEDAVKRKIDTGGMVDVAWEALGKPTOTFLGGVGVSRDGGKAVMIGLFLSGAKGEVDNHLVRRGKIVGSGYCARARQDLPLKLNLAESGFDLSAAVSRTKCFEEAGGAYKDLQGAISGRGVVEIM

NbL12g16050.1 eukaryotic_translation_initiation_factor [MW = 22.85 kDa]



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain PF01652 Eukaryotic initiation factor 4E

Protein sequence:
AGIEPKWEDPFCASGGKWTVTSSRIKANLETMLLETLMALVGGEGFDESEIEGGVAVSVRRSGDKLSLWTKTASNEAIGMSGRKWKHEIDAEKISVFSFHDGSKRERAKGRVTV

NbL12g16020.1 calcium-dependent_protein_kinase_SK5-like [MW = 62.55 kDa]

No. of times detected



log(intensity)



Values from



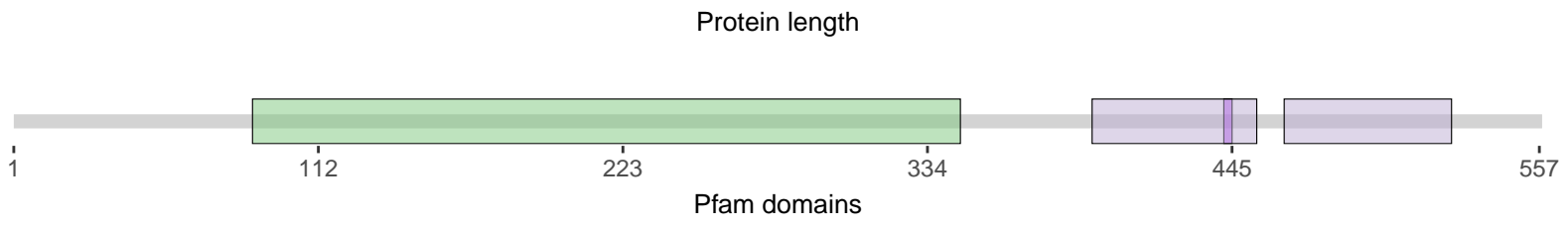
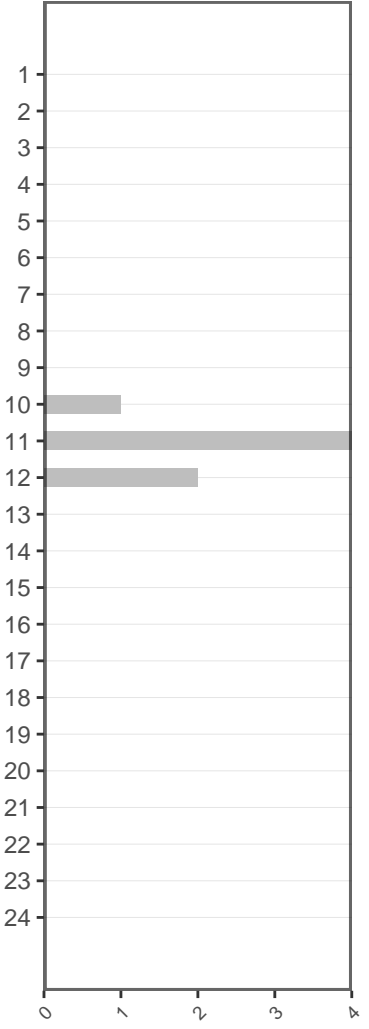
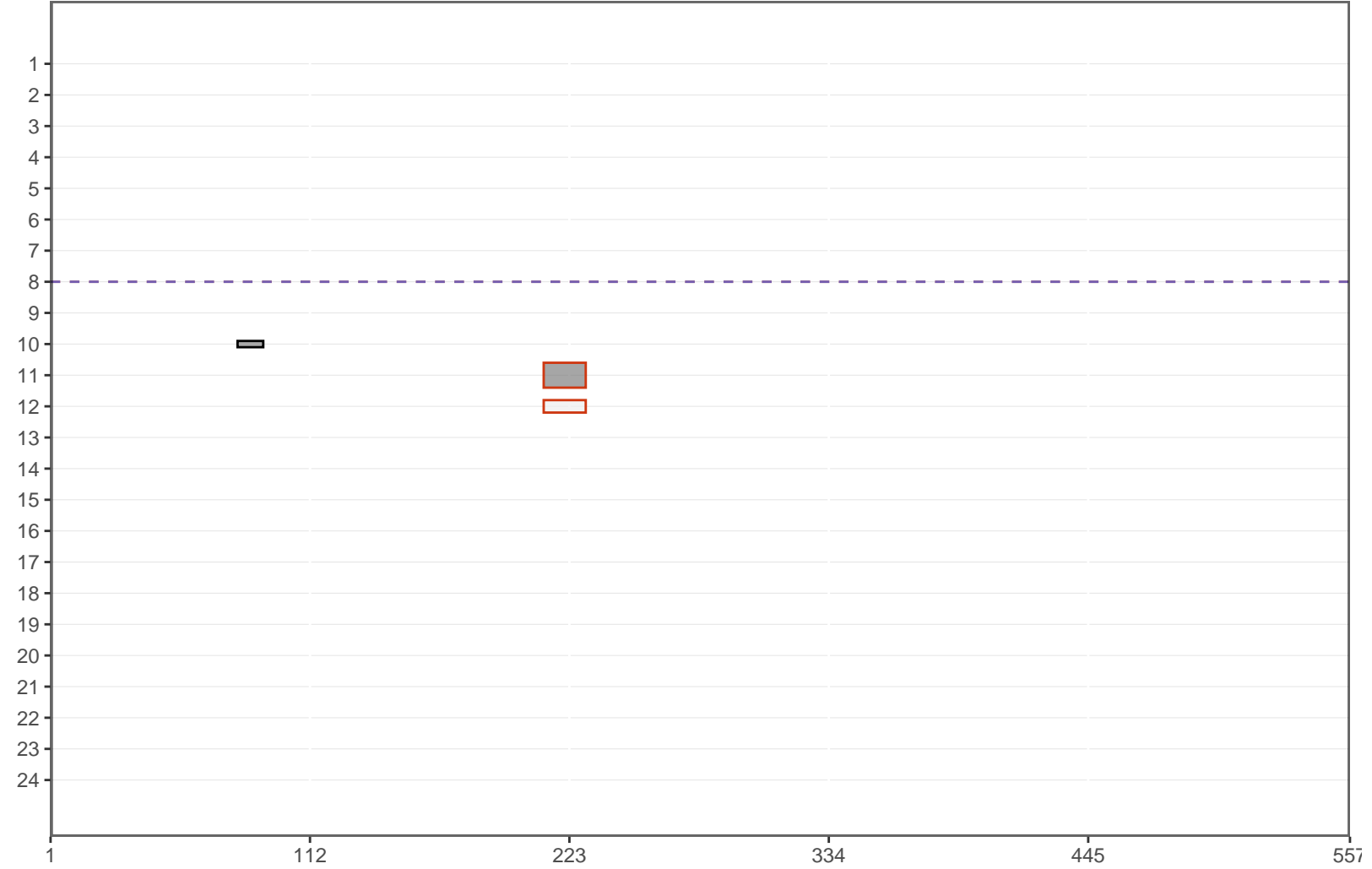
MW indication



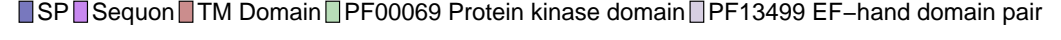
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

YGHESDLYSAGVYHLLSGVPPFAETDMGFRQLRGLDLESEFPWPGISDSAKDIRKILDRNPKRRLTAEHLGHPWIVDITMAPDKPLDSAVLRSLKGFSAAMNKKMLKALRVAERLSEEEIGGLKELFKMLDIDNNGTIDYGEFIATVHLNKLEREENLSAFSYFDKDGSGYTEELGGACKFGLSELNLDKIKDDQDNDGGIDYKFEFSAMMRKGTGGGVRRTIRNNLGEALGLVQSEENL

NbL12g16010.1 acyl-coenzyme_A_thioesterase_13-like [MW = 18.35 kDa]

No. of times detected



log(intensity)



Values from



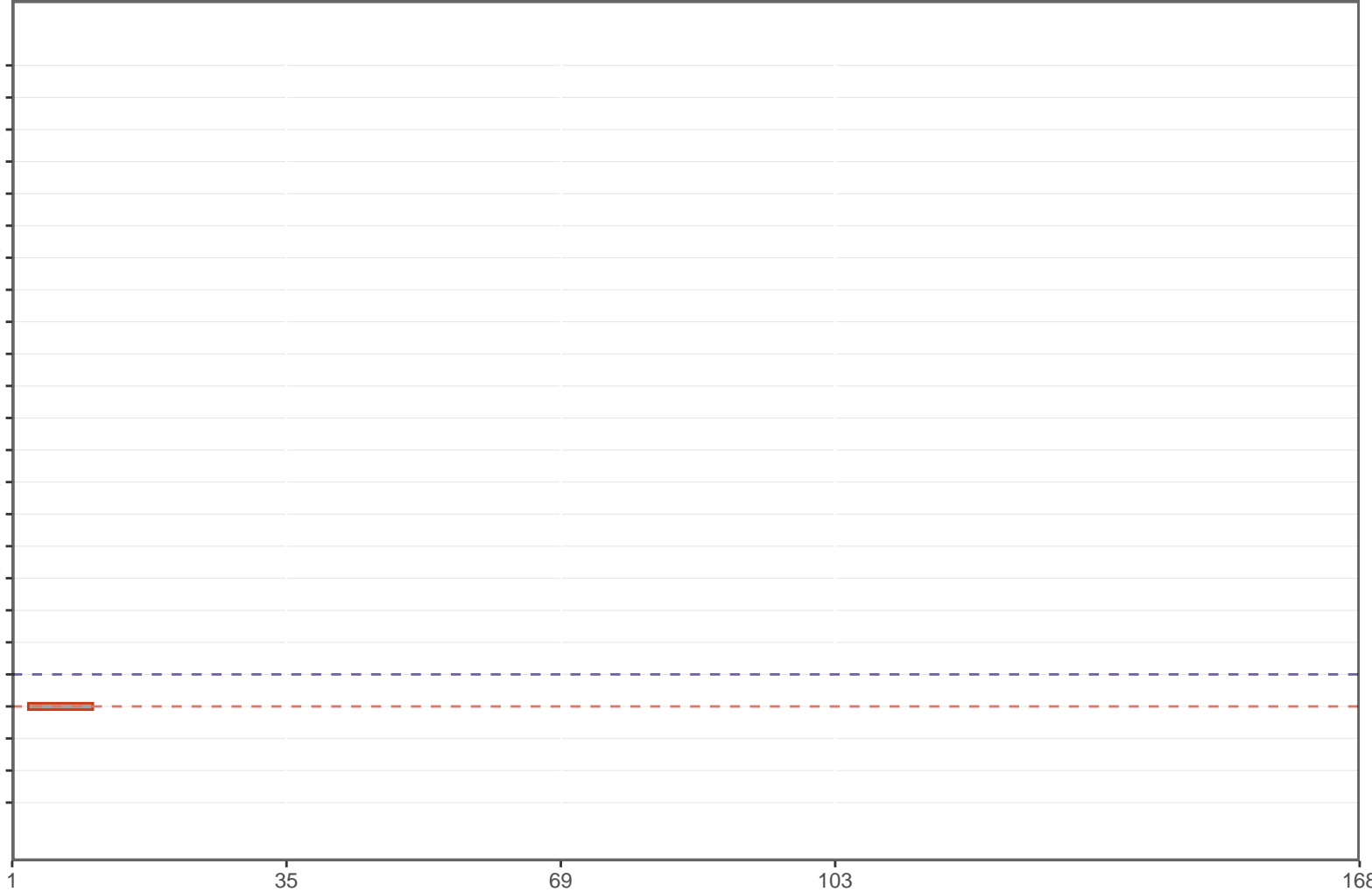
MW indication



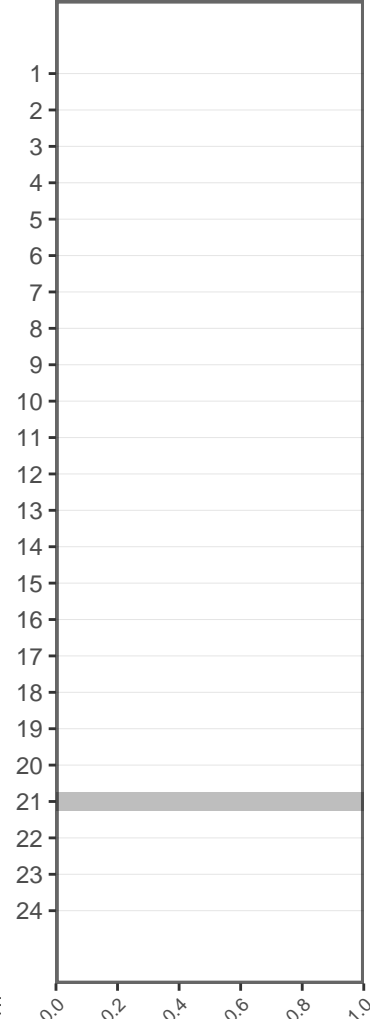
Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGATATLVLDLGSVAIHTVGAFFTGVSVENVSYLDAAFIGVSGPLSGFSDLNIVHFLNTELLNTGMRHFLADPQLWDCGFVWVKLGGELALFFSP

NbL12g15990.1 probable_methyltransferase_PMT26 [MW = 89.94 kDa]

No. of times detected



log(intensity)



Values from



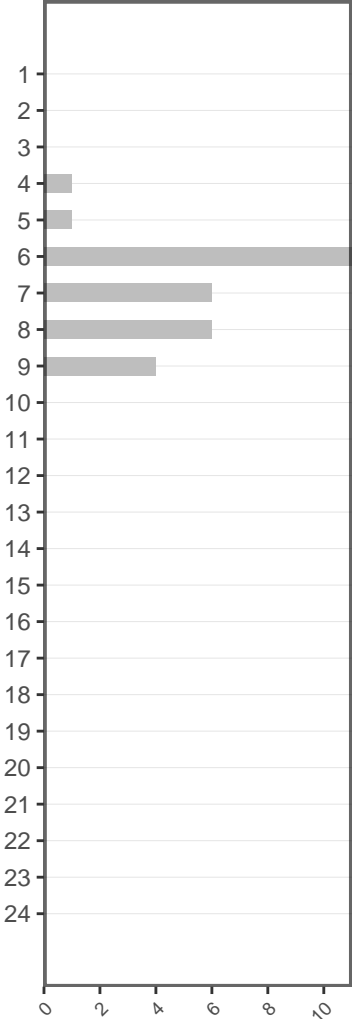
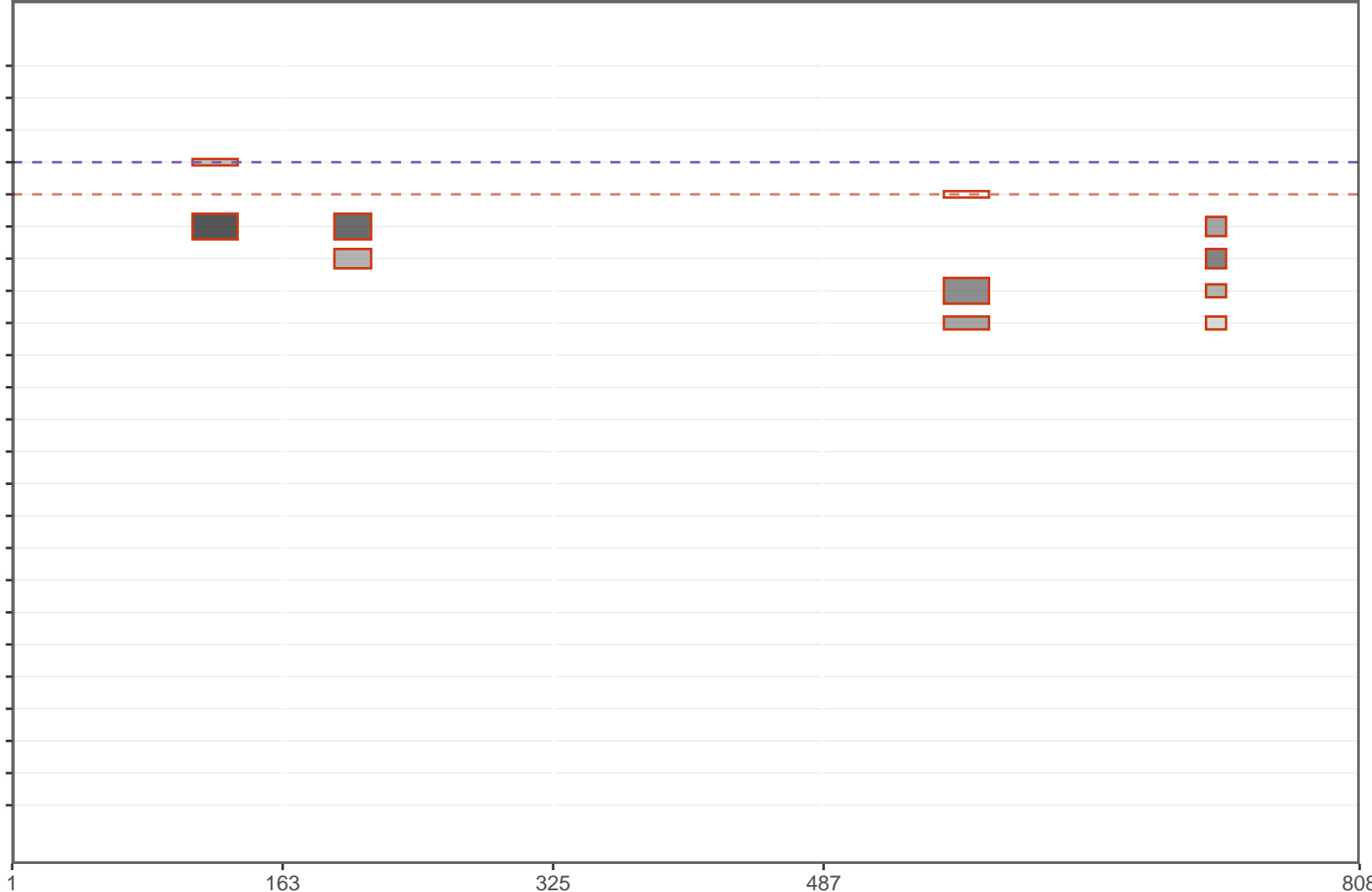
MW indication



Molecular weight



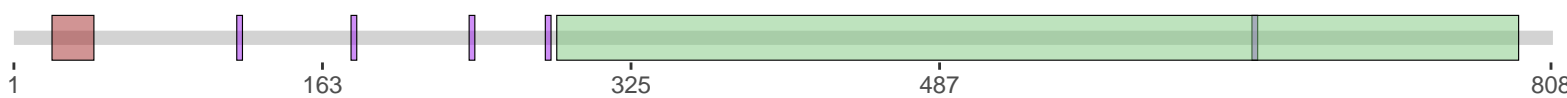
Gel Slice



Protein length

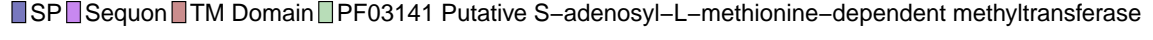


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

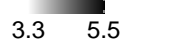
FDQSFDDAWQKRRIVLELVGGVAFSGVLFDRDVLAMSLAPKDEHEAGVGFALERGIPNSAVMGTKRLLFPFSRIVFDVYHVCARCRVPVWHEGGKLLLELNRLLRPGGLFVWSATPVYQKLPEDVEIWEAMKRLKAMQWELISGKTKDRVNGVGVWVYRKPMDNECYEQRSEDAAPLQGESDDPNAAWNPVPLGACLHKAPAATSERGGQWPEGWPARLSEKSPYLLSSQGVVYKPKPAPEDTADVEHWHKHWKNEVINGMGNWSTVRNVMMDMRAIYGGFAALRD

NbL12g15920.1 4-hydroxyphenylpyruvate_dioxygenase-like [MW = 49.26 kDa]

No. of times detected



log(intensity)



Values from

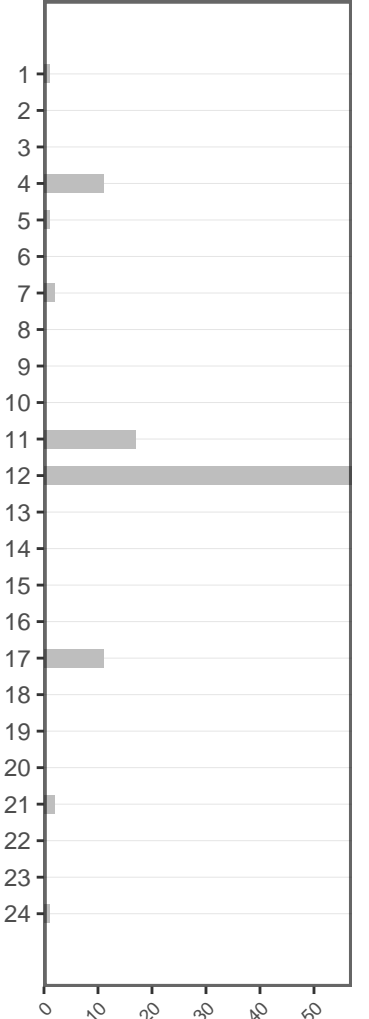
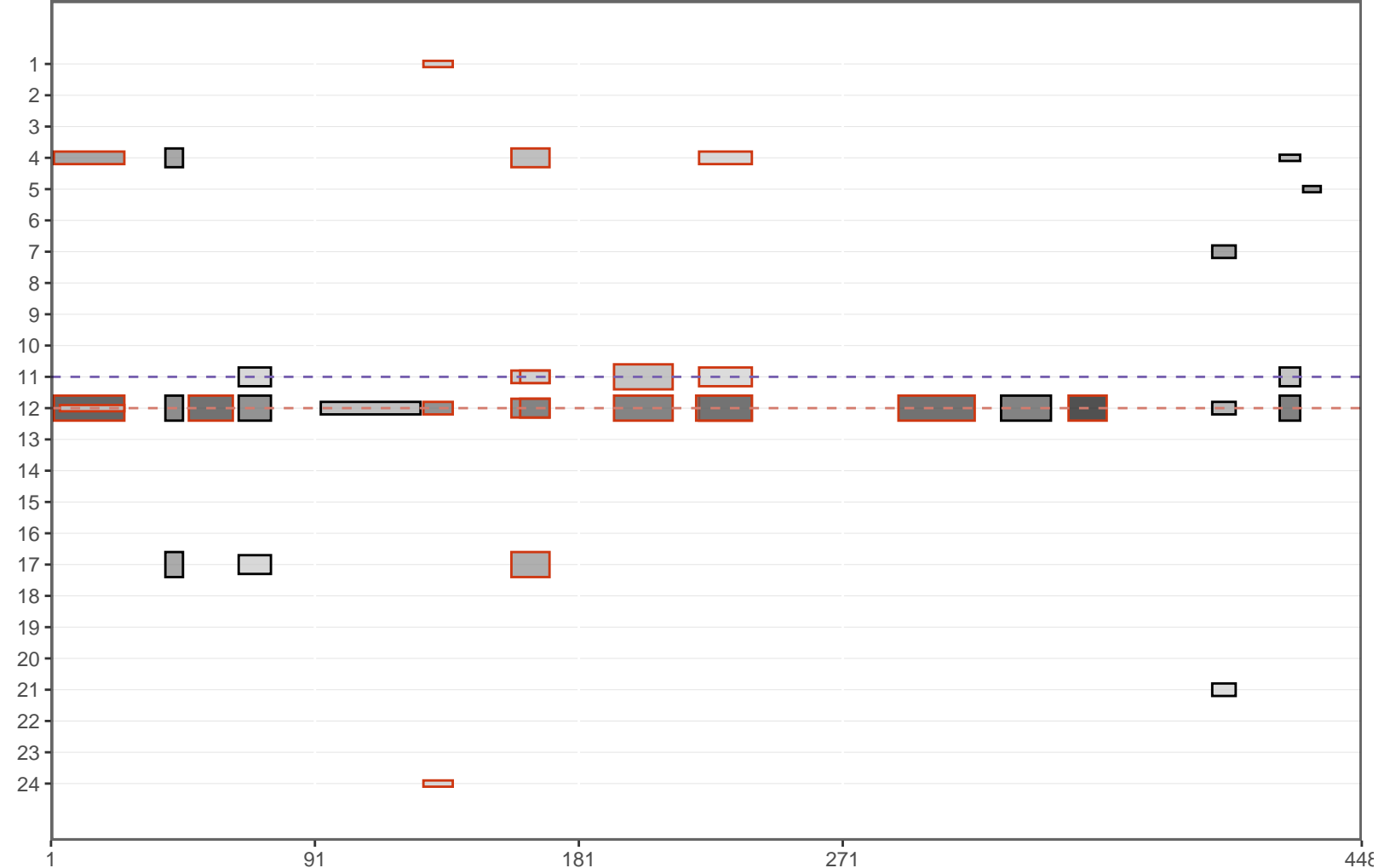
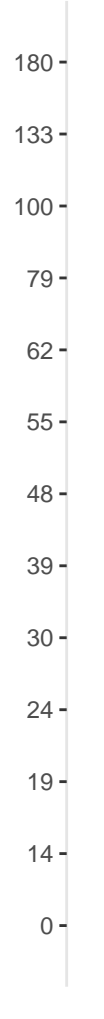


MW indication



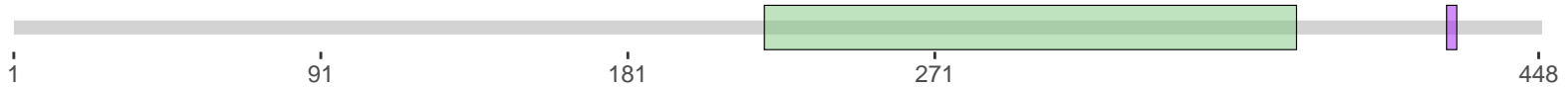
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

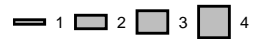


Protein sequence:

YKELYGIRRLDIHWGNVPELGRVVDVIRKRFTHGHEFAETAEVDVGTAESEGLNSMVLANNDETLLVLPNEPYYGTRKRSGIGTYLEHNEGAGMQLHALVDEDFKTKLTEMKRKSGVGGFEFMPSPPTFYNNLNKRAGDVLTDGEGQACKELGLVDRDDGGTLTGFTKPVGDRPTTFEIKRIGMUKDEKGVVYQKGGCGGFGKGNFSELFRBIEEYKTLKAGANPVTA*

NbL12g15830.1 WD_repeat-containing_protein_26-like [MW = 27.03 kDa]

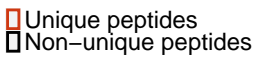
No. of times detected



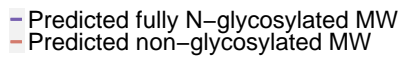
log(intensity)



Values from



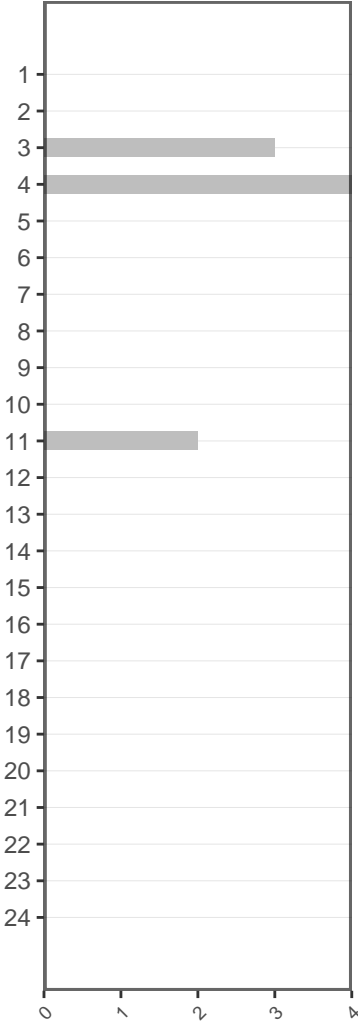
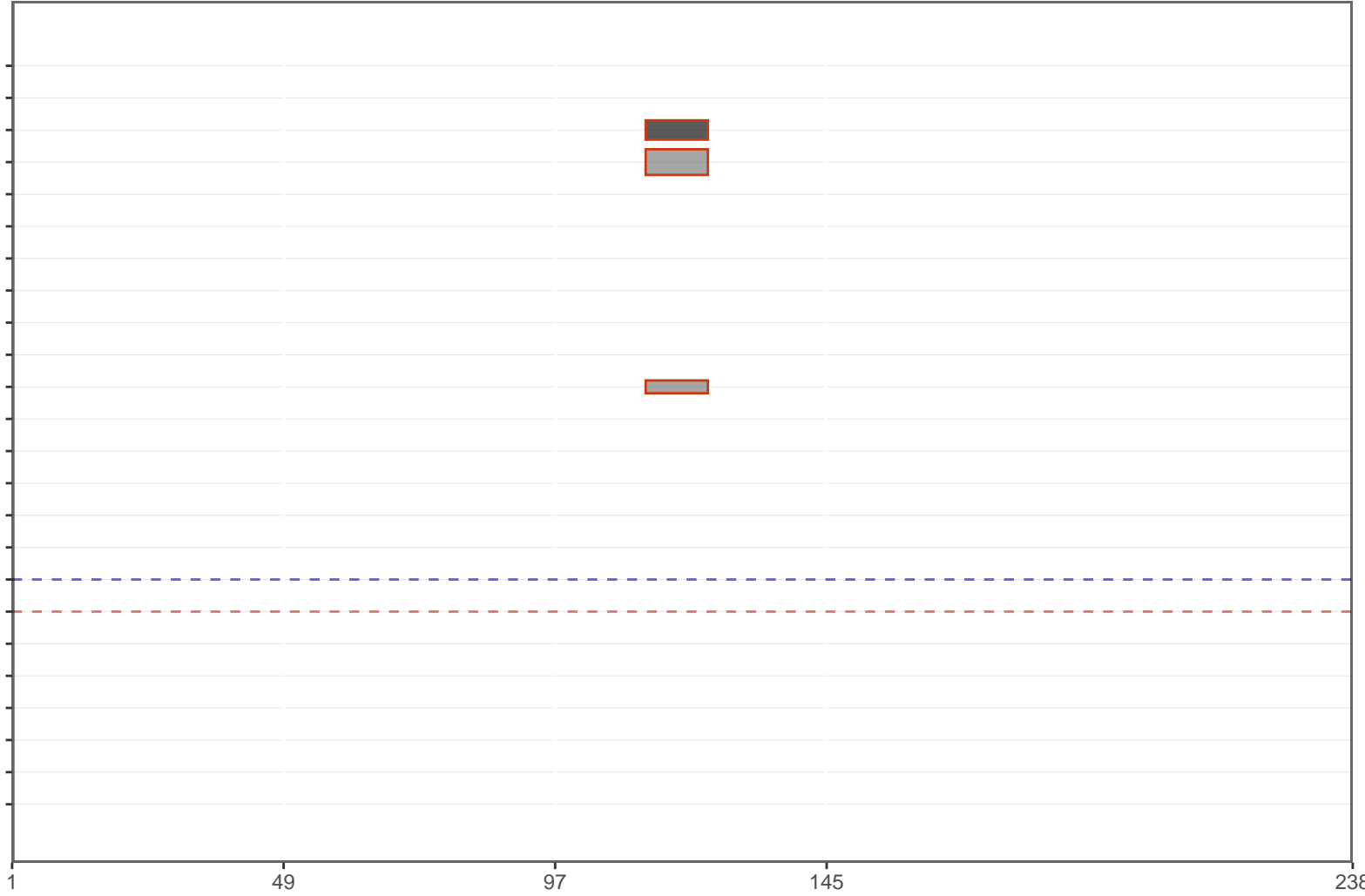
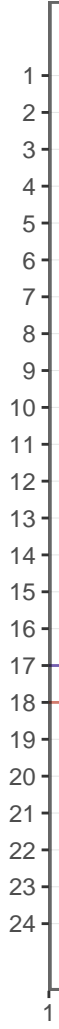
MW indication



Molecular weight



Gel Slice

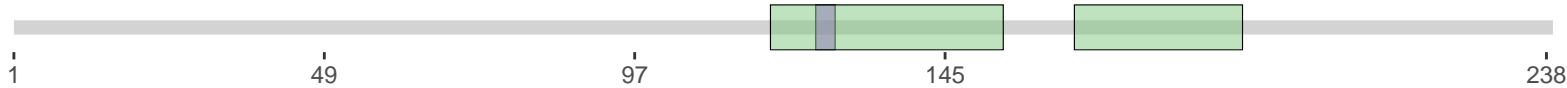


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

CCGRDQIPSTLQRLRNHSDEVWFLGFSDKGLASSAANDGVHVEVKLDGLFLKHKDFSGHGKPKVSYMSVSPDDHQLLTCGVEVRRRWVDESGEGVHFENKGLGLSGGWAFDGRILRWRCYGGEH

NbL12g15820.1 oxygen-evolving_enhancer_protein_2-2_chloroplastic [MW = 37.57 kDa]

No. of times detected



log(intensity)



Values from



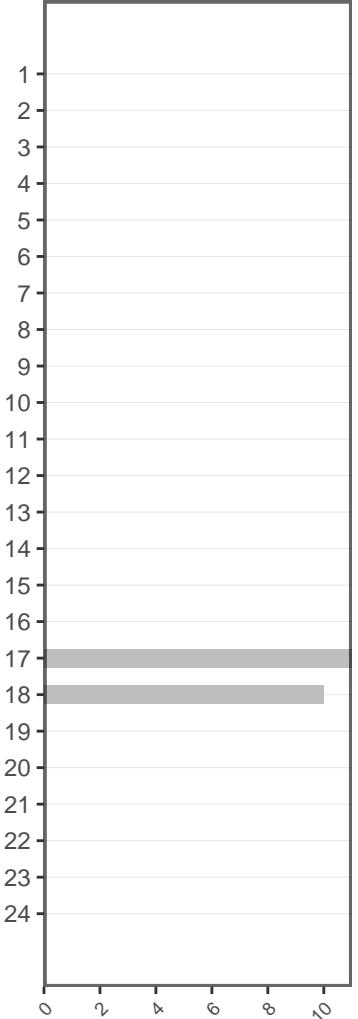
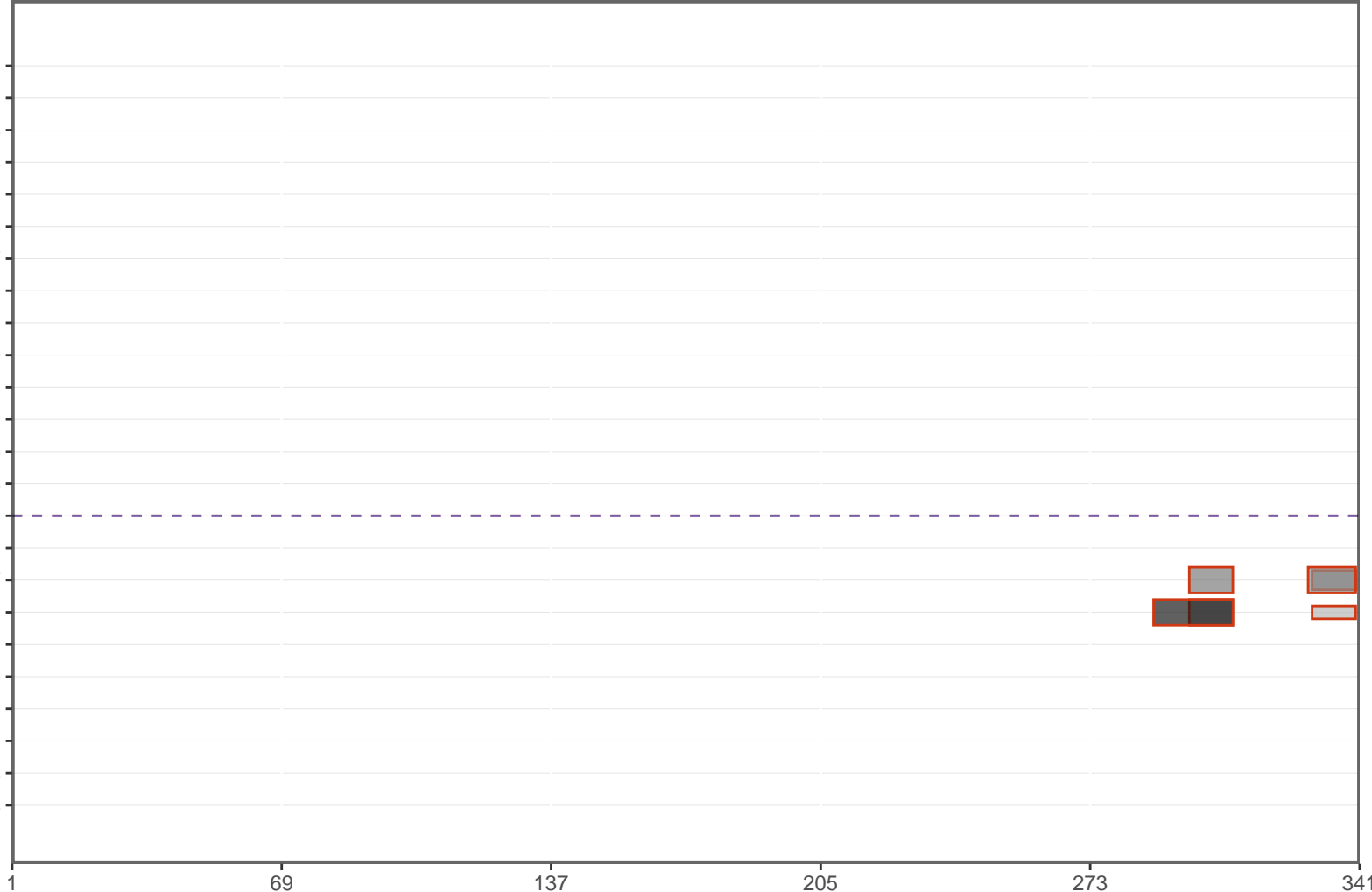
MW indication



Molecular weight



Gel Slice

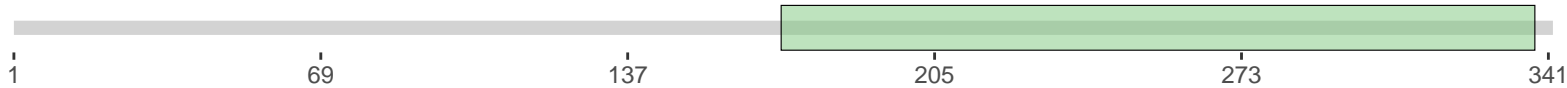


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

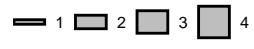


Protein sequence:

EAANVFGKPKTDTDFGTYNGDGFKLGIPSKWNPINKEVEYPGGVLRFEEDNFDAISNVAWPTFDKKSIFDFGSPGQFLSGVDKLLGRQVYSGKTDSEGGFESDVAIAIIVLETSSAEVGGKPYLYLVLRTRADNGEGGKHLQITATVNNKSLYKIKADAGKRWFKGANKFVENTATSFSLA*

NbL12g15730.1 V-type_proton_ATPase_subunit_G_2 [MW = 12.5 kDa]

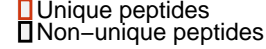
No. of times detected



log(intensity)



Values from



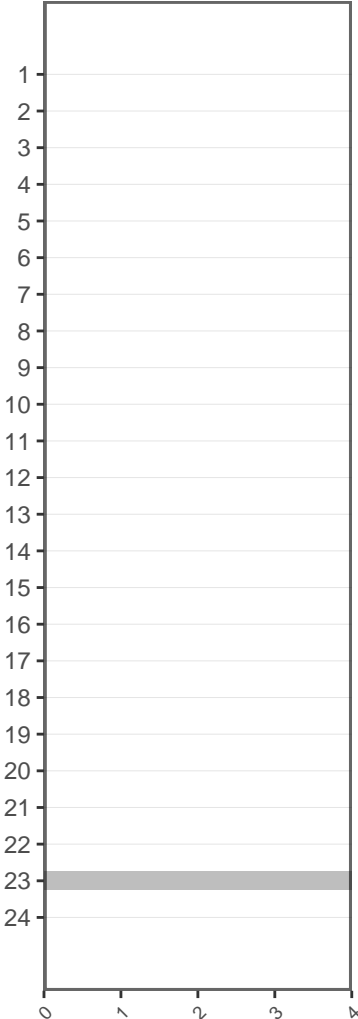
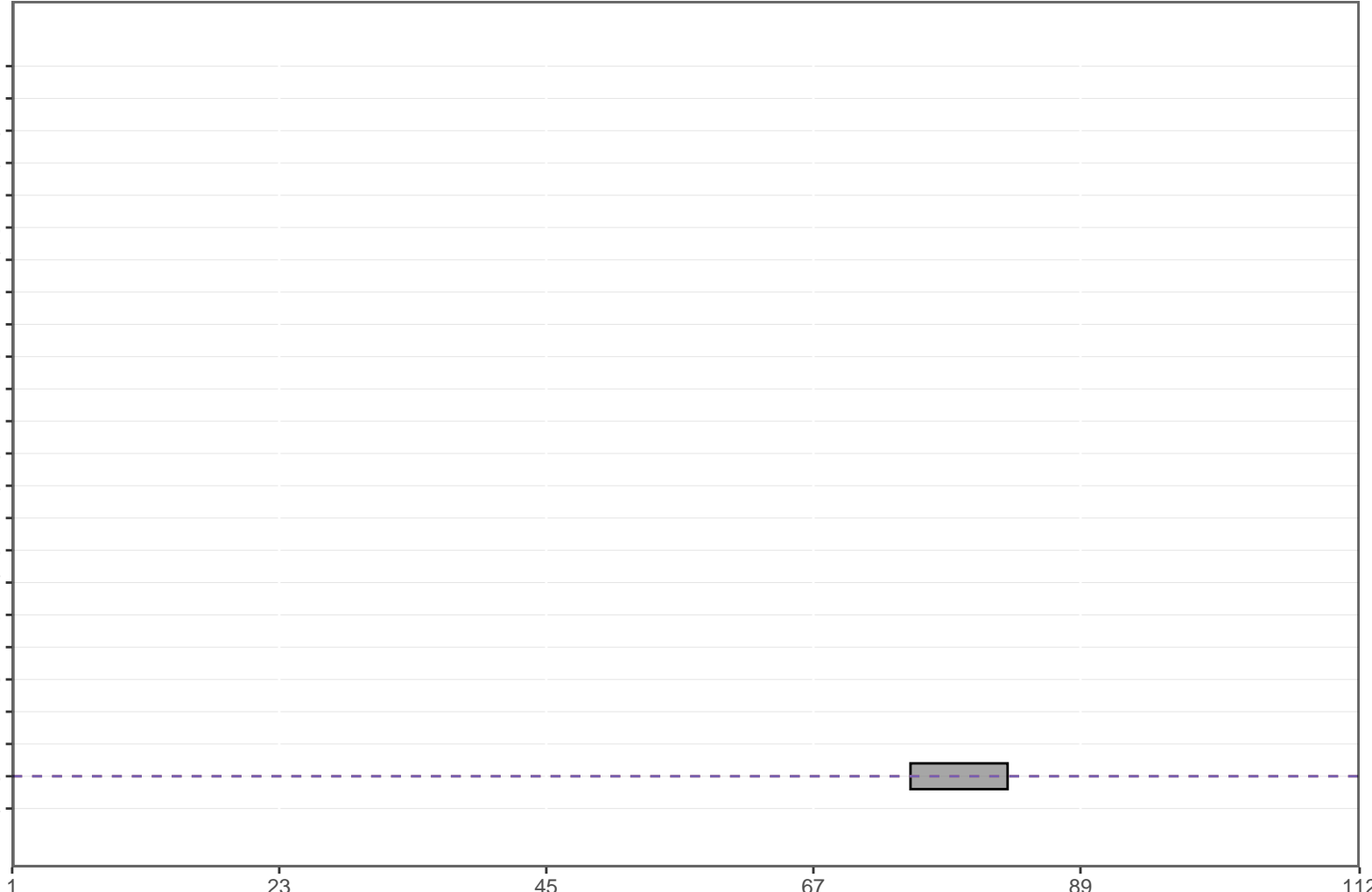
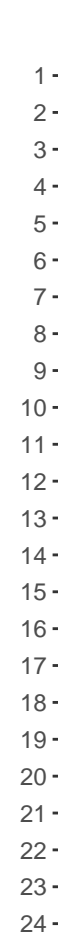
MW indication



Molecular weight



Gel Slice

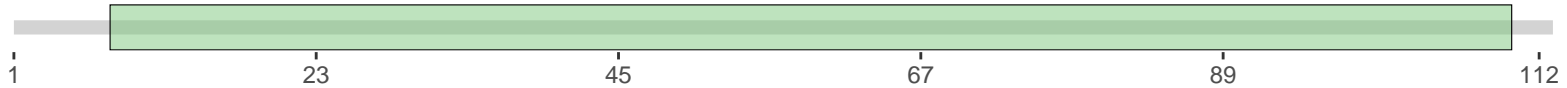


Protein length

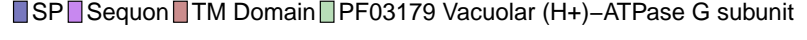


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

AEKEIAEFRAYMEAEFGKRVKVEGTSGDGGANVWRLEGETTFAHQHFKTEAESISHVQVOMLLRQVTVKVP

NbL12g15550.1 proteasome_subunit_beta_type-3-A-like [MW = 22.67 kDa]

No. of times detected



log(intensity)



Values from



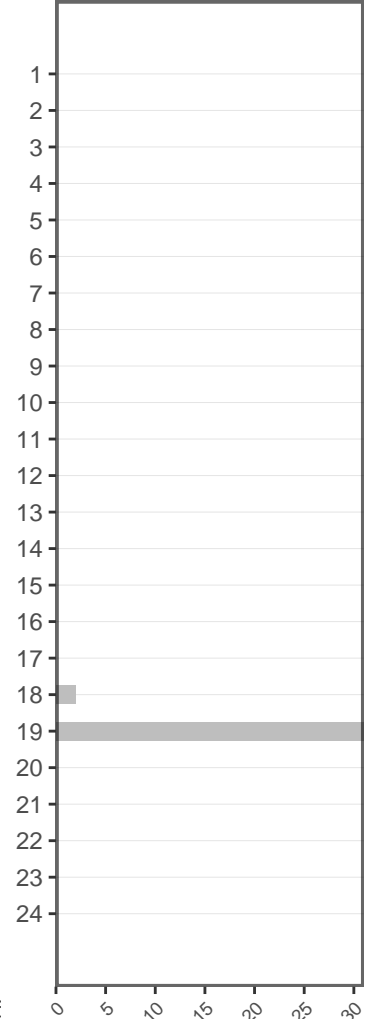
MW indication



Molecular weight

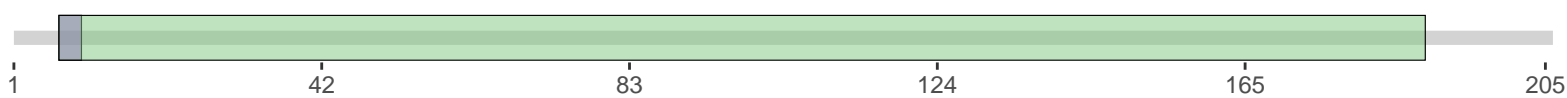


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VSALLYEKRFQPYFGQPIVAGLGGDDKPFICTMDSIGAKELAKDFVAVGTASESLYGACEAMFKPDMGPEELFETHGALIASVDRDCLSGWGGHVAVVTPTEVTEKILKGRMD

NbL12g15520.1 uncharacterized_LOC109225451 [MW = 29.8 kDa]

No. of times detected



log(intensity)



Values from



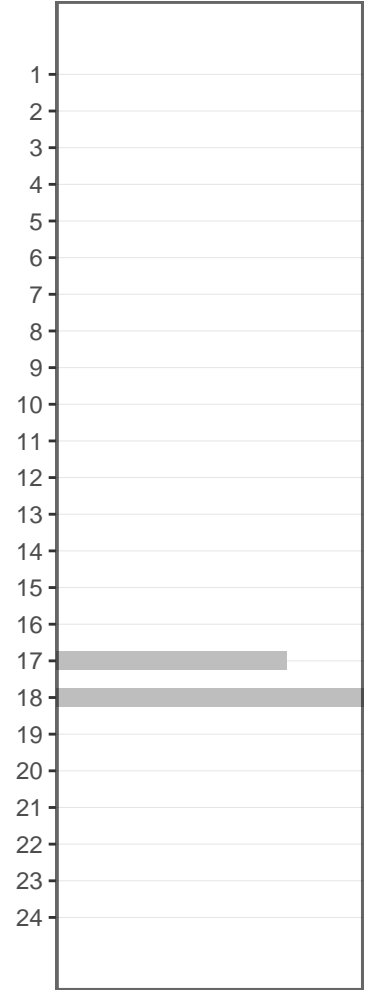
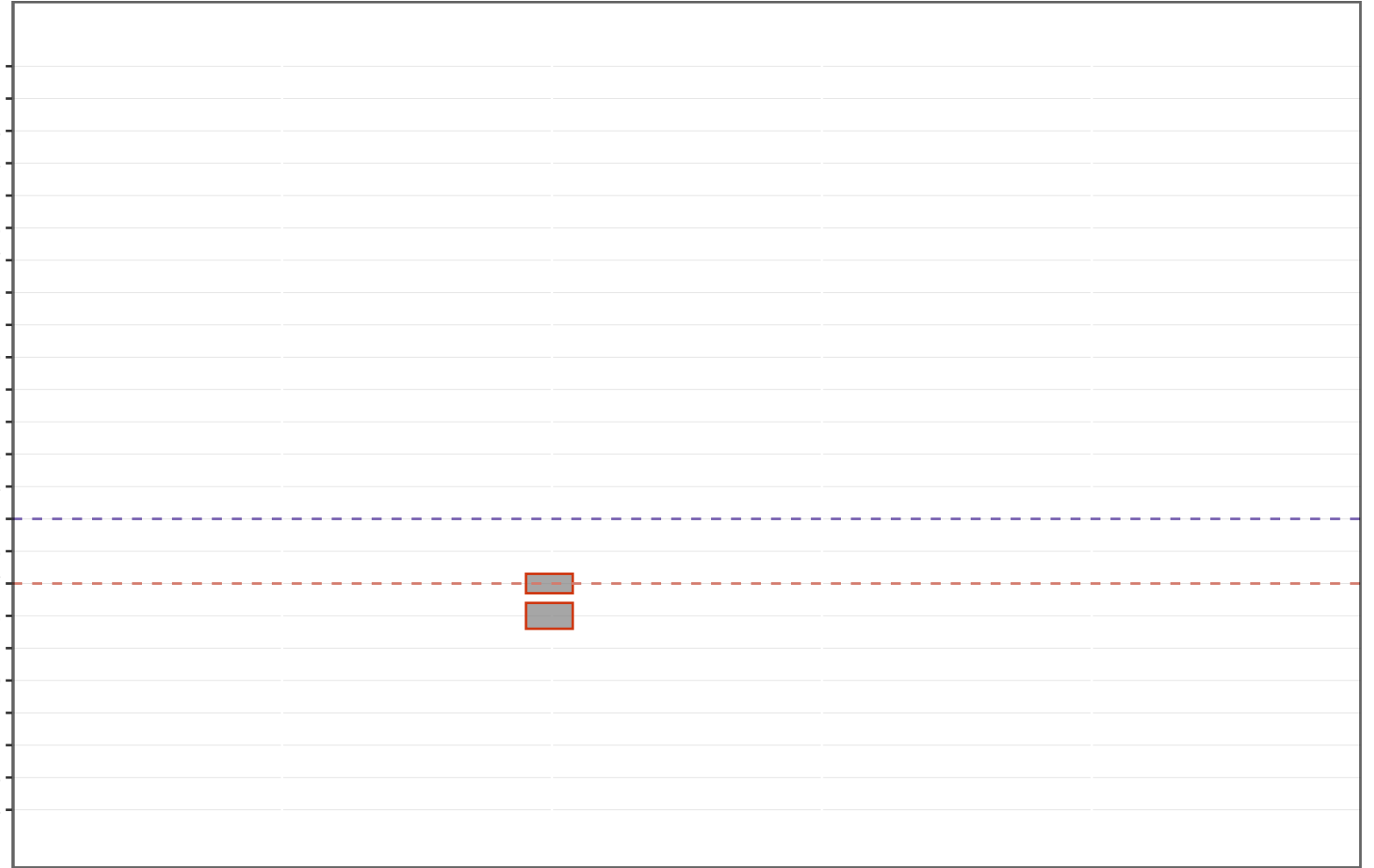
MW indication



Molecular weight



Gel Slice

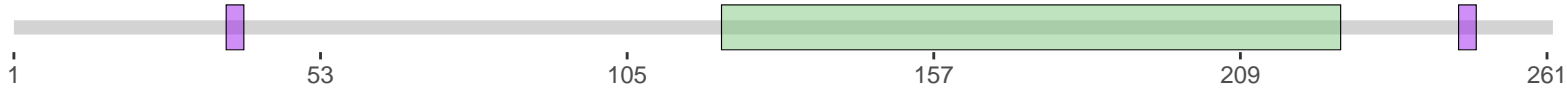


Protein length

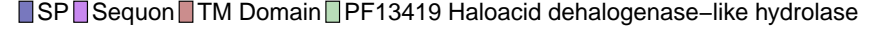


Peptide counts over 4 repeats

Pfam domains



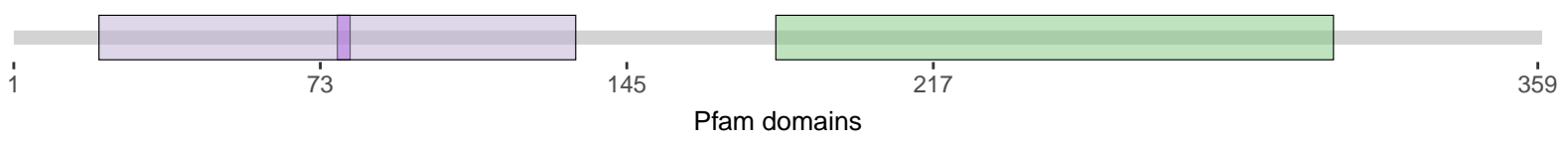
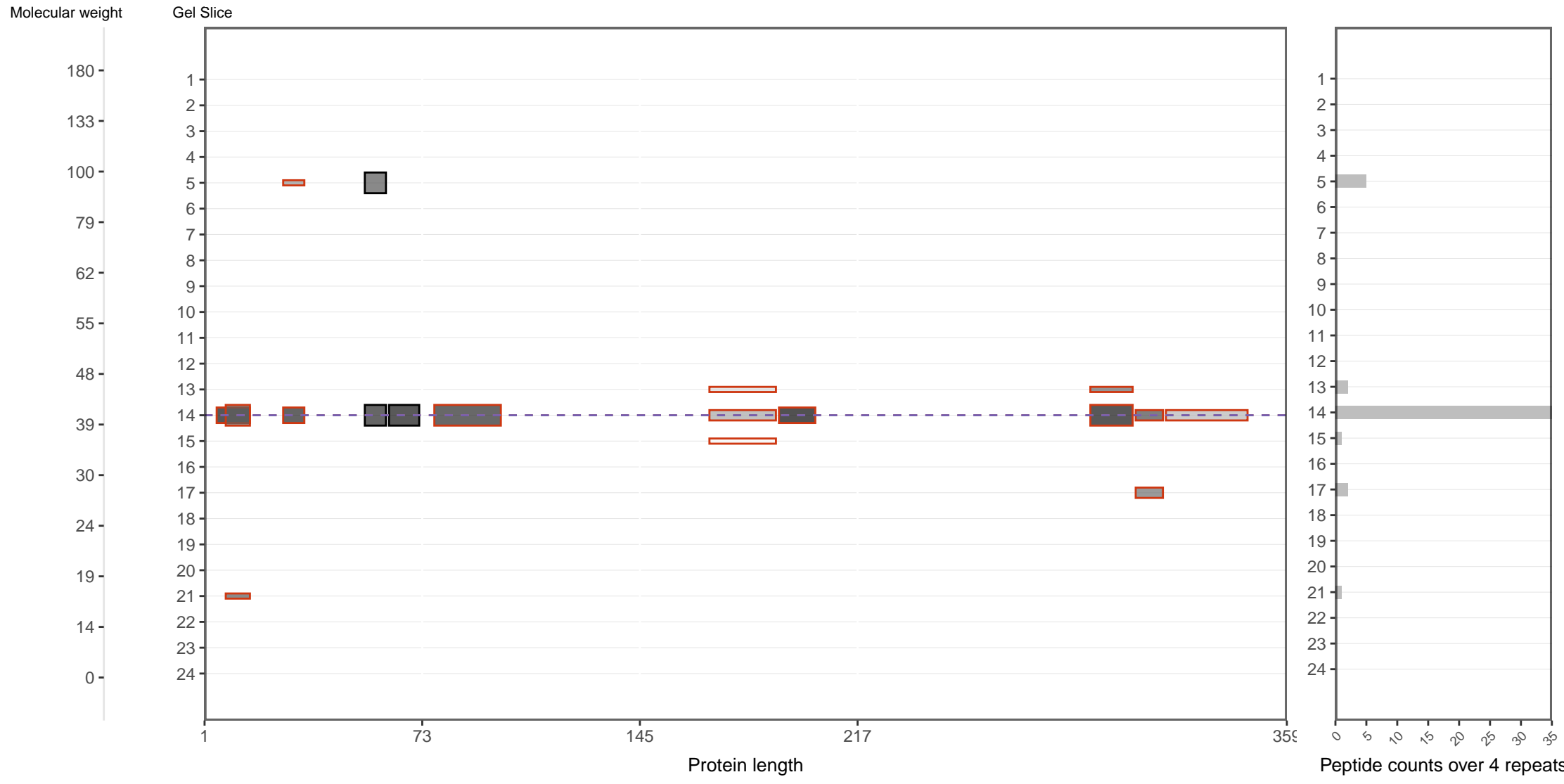
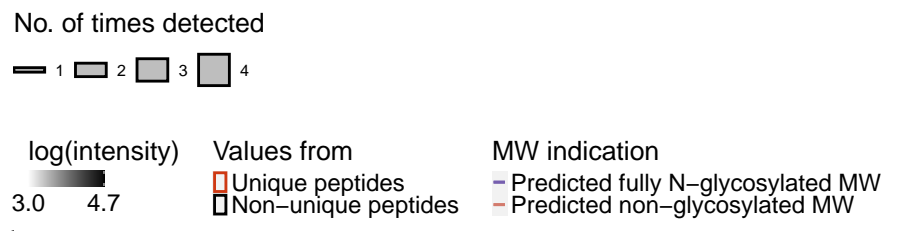
Pfam Description



Protein sequence:

FDLEGLNCKMCRANWVYEGVEGLNLSKENGVEIHFATNYPWVGMIEDKLSNLSWTFGSCIFGKRKPPDPFLYLVKHLNVEASSGCFVDDRMNRVEAVVEVGLNGLQFNADLLRKLDELGLVGNISTNEPDLAEGSI

NbL12g15370.1 2-alkenal_reductase_(NADP(+)-dependent)-like [MW = 39.52 kDa]



Pfam Description

SP Sequon TM Domain PF00107 Zinc-binding dehydrogenase PF16884 N-terminal domain of oxidoreductase

Protein sequence:

IRGEYVYSAASGAVGSLVGLAKLHGIVYVGSAGSGKQKVDLMDKLGFDGAFNYKEEADLDKALKRHFPGIDIVFDNIGGSMLEDAALNMRINGRIAGGMVSGQSLSDPQGHNLQILTKRVMQGFLOGSDYHLFPRRLEFDVTSLKQGEETYLEDMNEGLESGPEAFVGLFSGKNGKQVIRVAHD

NbL12g15350.1 probable_methylenetetrahydrofolate_reductase [MW = 67.13 kDa]

No. of times detected



log(intensity)



Values from



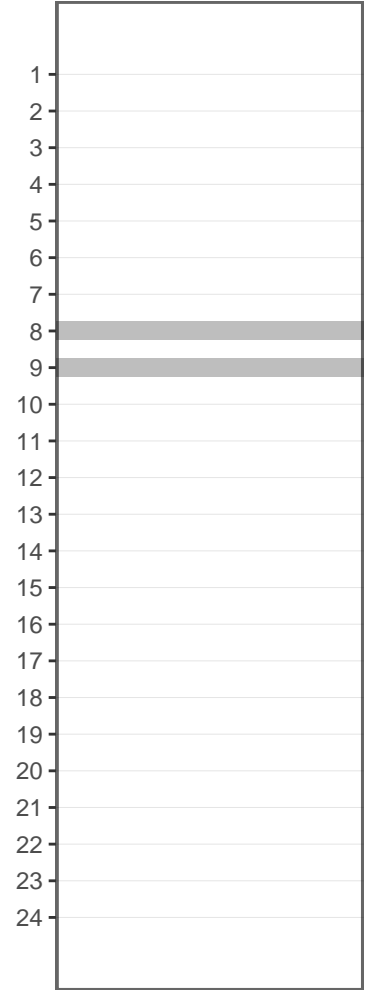
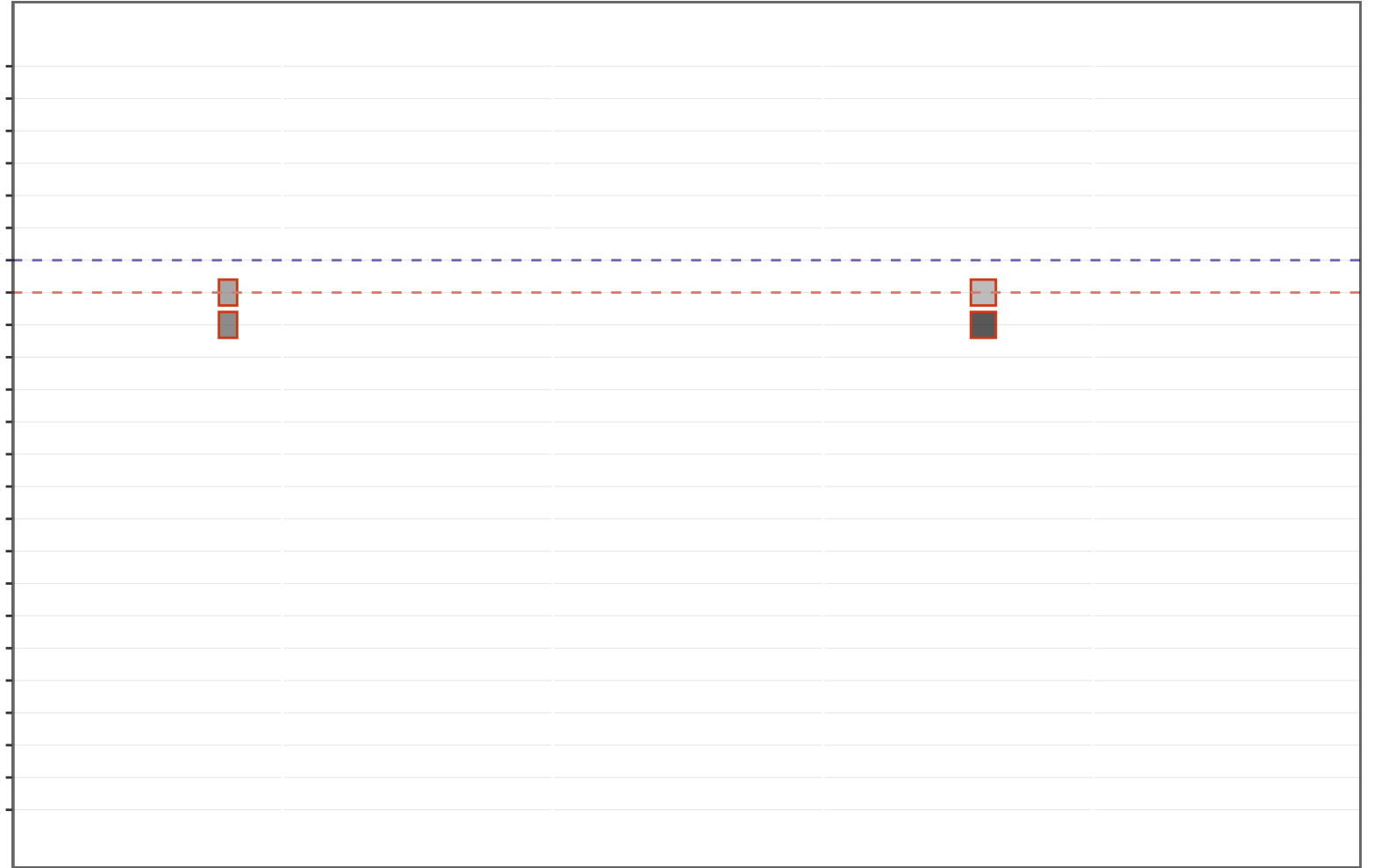
MW indication



Molecular weight



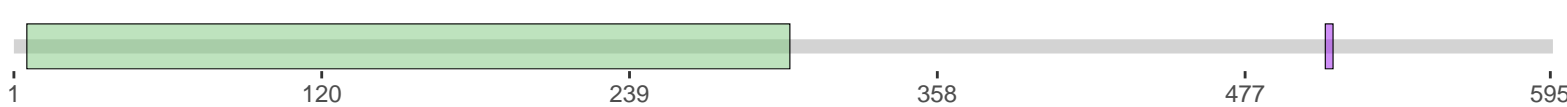
Gel Slice



Peptide counts over 4 repeats

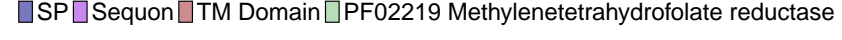


Protein length



Pfam domains

Pfam Description



Protein sequence:

IMKSAALAILMLGLIEESKSRPLPWRPRTNIVFRVKEEDVRPFWANRPKSVSRITGWDDEYPHGRWGNAGNPNFYGALEDYGFMRARBRKKLQEEWAWLNSVEDYERFMNYGLKLRGSPWSELDELGLPETRKHDEHLGNINTKGFLTINSQPAHWGAKSDAPSGDGGYYGKAWLEFFGSHKLNALVEKKAFFPLEYMAVNEKGNWENANGTINVAVTWGWVFGKKEIVQPTVYDRPASFVWKDEAFESWRSRWAGLYGESDPSRRLLEQVQNSYTLVSL

NbL12g15300.1 isopentenyl-diphosphate_Delta-isomerase_I [MW = 27.12 kDa]

No. of times detected



log(intensity)



Values from



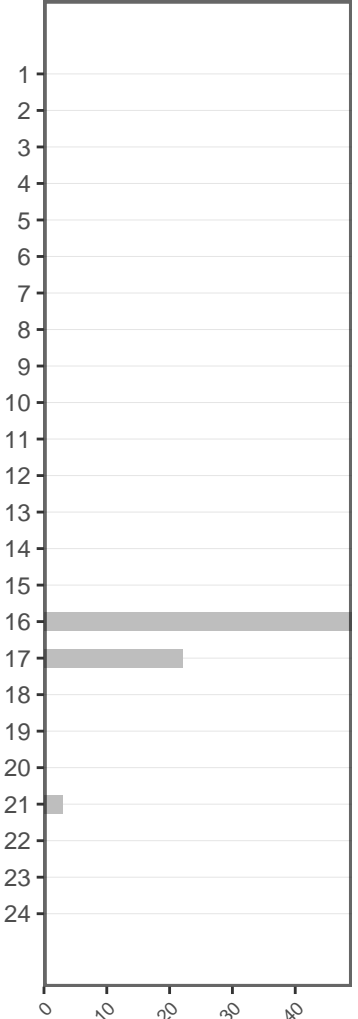
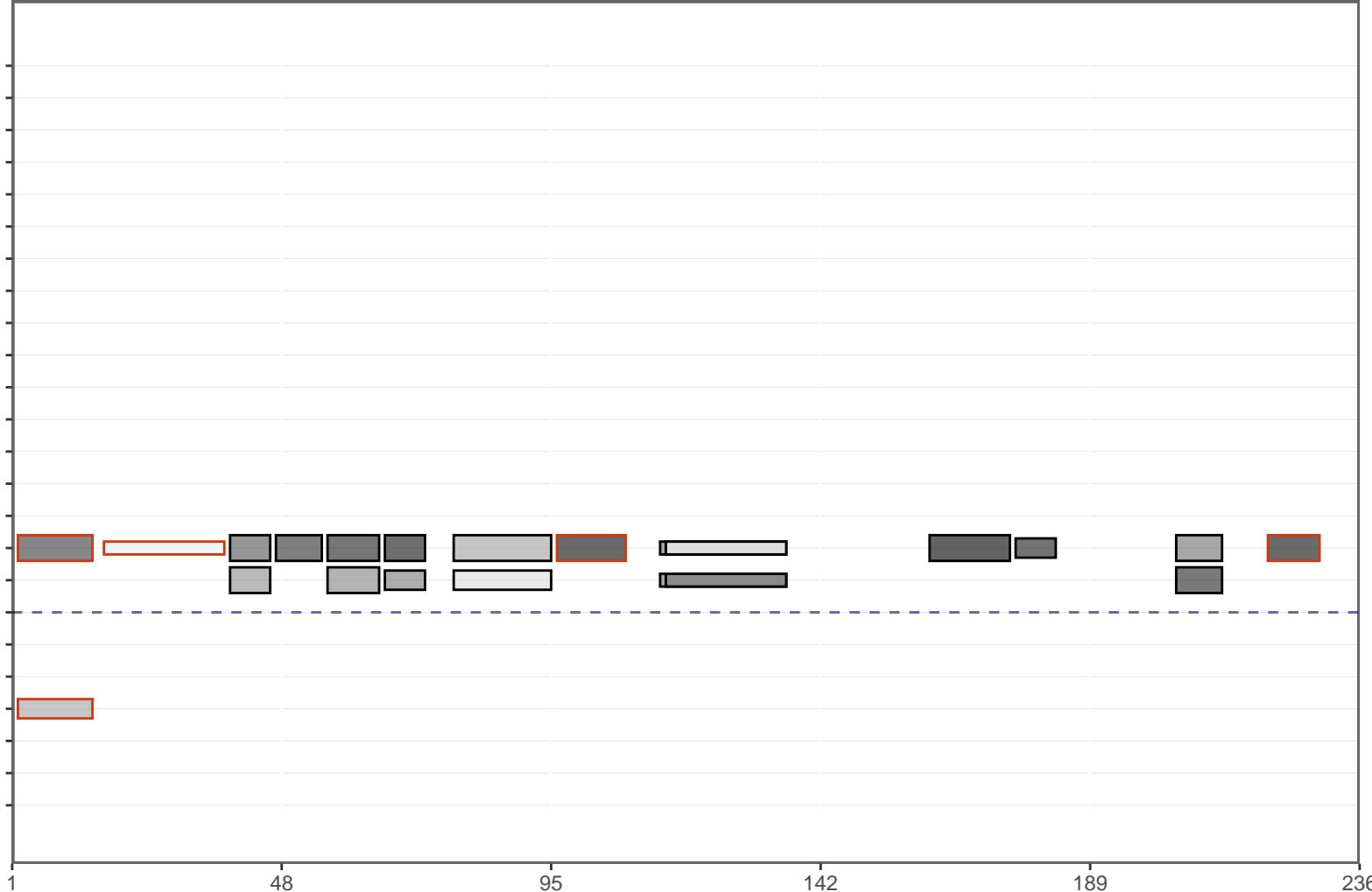
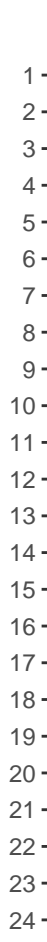
MW indication



Molecular weight



Gel Slice

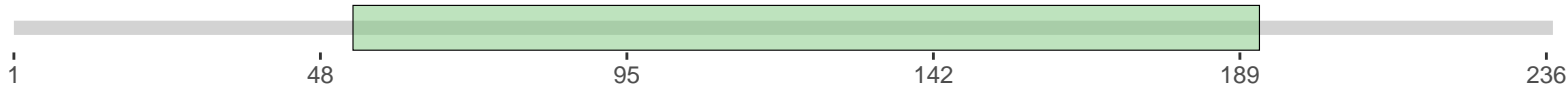


Peptide counts over 4 repeats

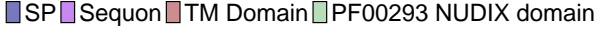
Protein length



Pfam domains



Pfam Description



Protein sequence:

GVRNAQRKLLDELGPAEDVPIVDFPTLGRMLYKAPSDGKHWGEHELHLLFVRDWNVNPDEVDKYYNDEGLKDLRKADAGEEGLKLSFWFRLLVDFNLFKRWVGHVEKGTIDGAAAMKTIKGLT

NbL12g15270.1 uncharacterized_LOC107805381 [MW = 23.48 kDa]

No. of times detected



log(intensity)



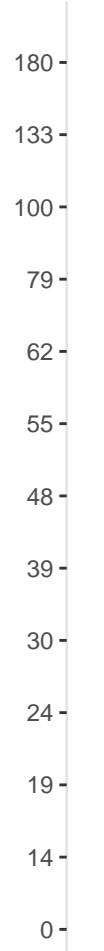
Values from



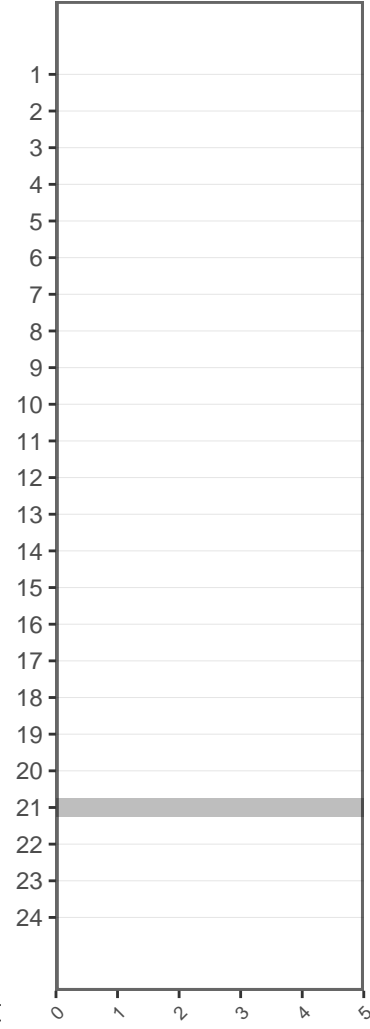
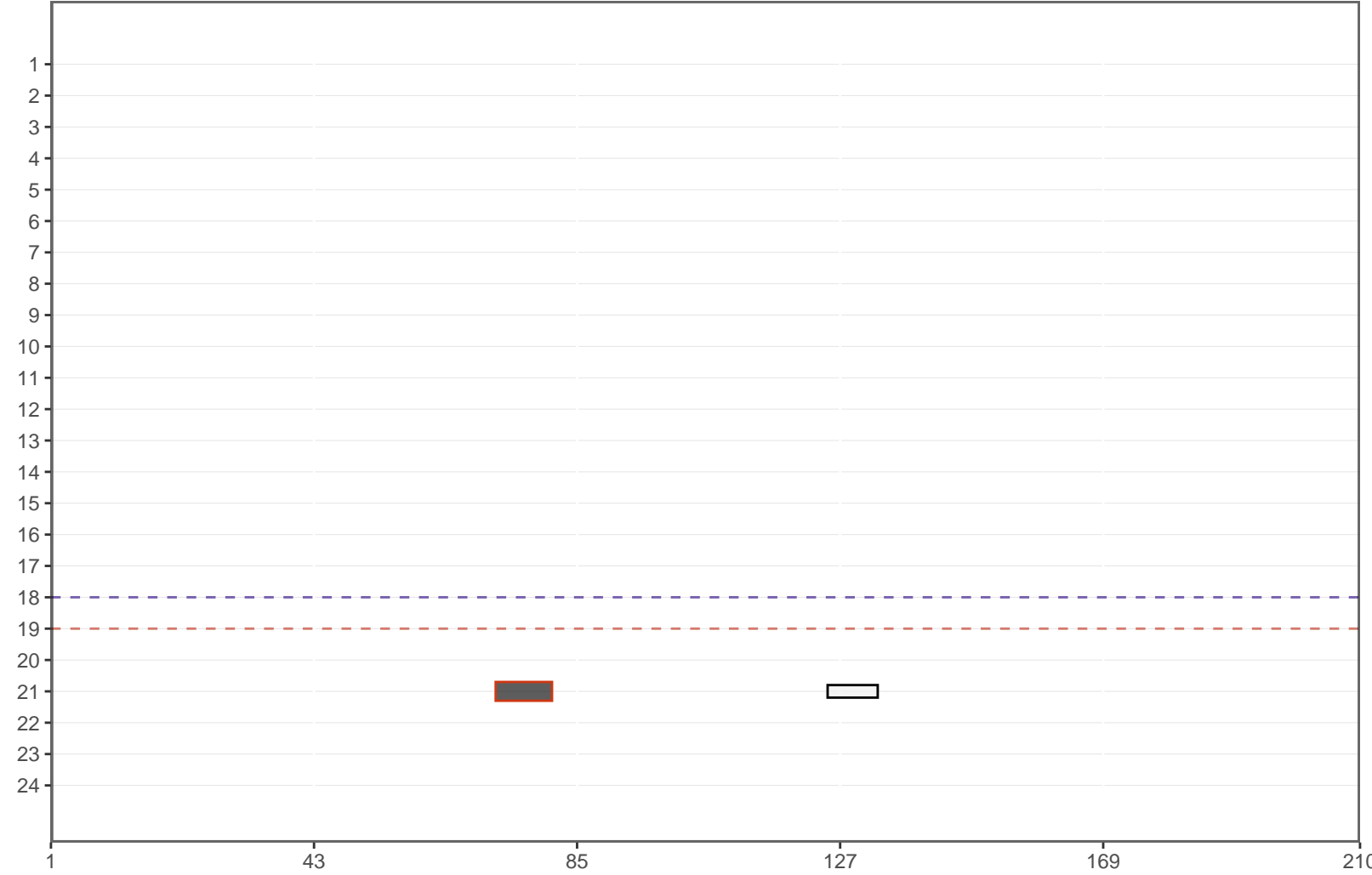
MW indication



Molecular weight



Gel Slice



Protein length

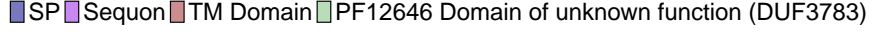


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

EVVEAAKQOQLKEMDGEFLQVIFCTEDMRRLWEAMNTKQPNLDAKIAKQLPRICFLSGLTGEEMMFIDAFEESELEDVFAALVENSADKPLQELDEIMGDHELLSARNSSP

NbL12g15170.1 protein_BTR1-like [MW = 35.87 kDa]

No. of times detected



log(intensity)



Values from



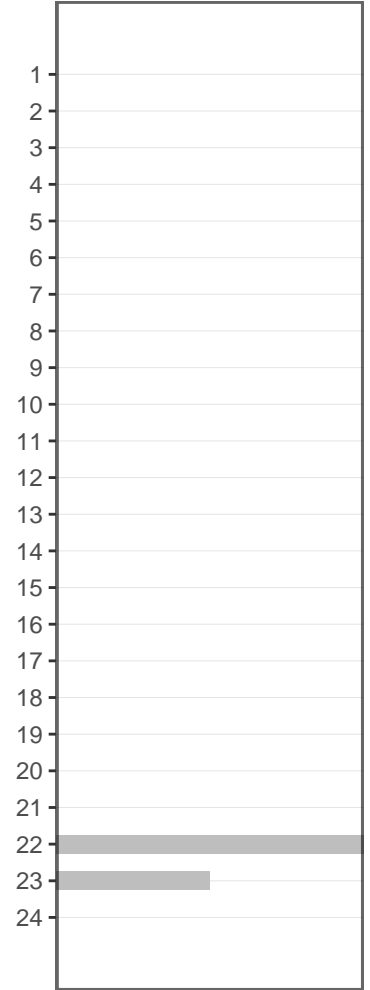
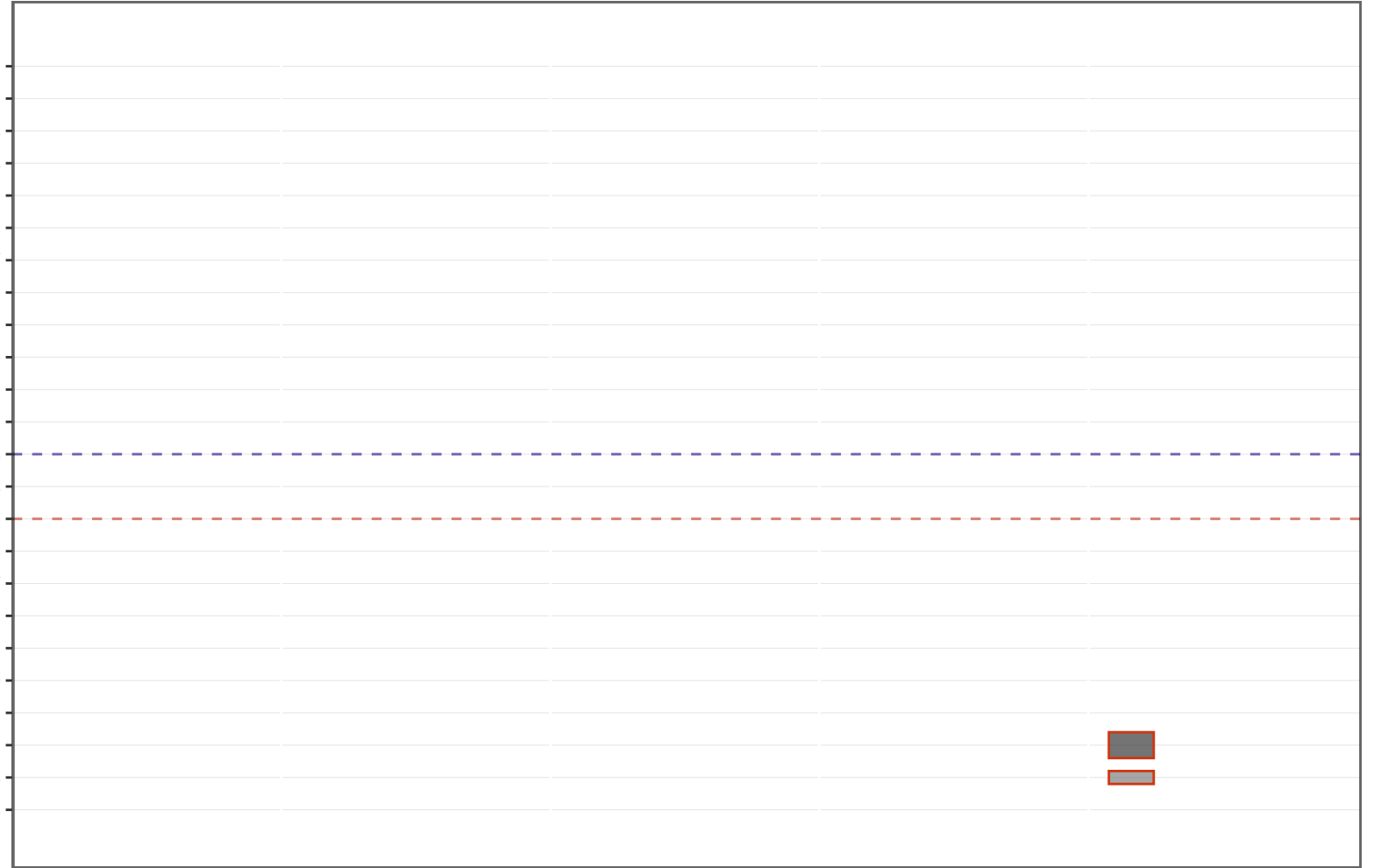
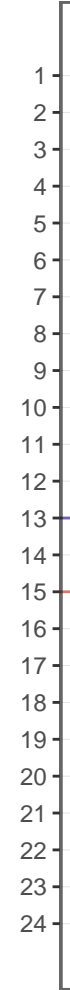
MW indication



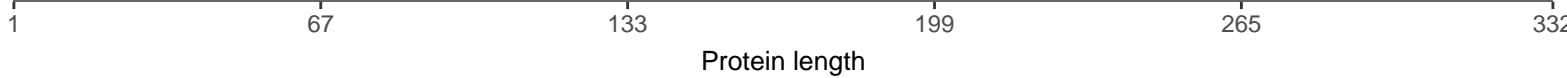
Molecular weight



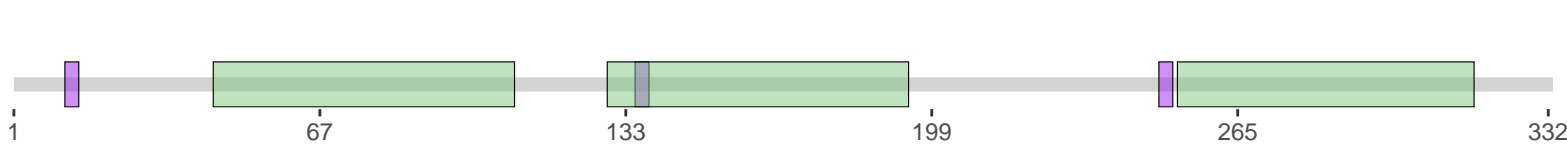
Gel Slice



Peptide counts over 4 repeats

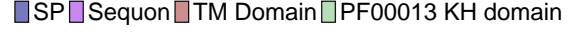


Protein length



Pfam domains

Pfam Description



Protein sequence:

1EEDSHAGIKISSODDNFPLGHRDLVVTGTLEEGMRAEILHLKLAEDSHYIGNMNAPEFVWVYGMVYSPRNGVGRYPNRRYGNVGNSEDRNNSVTIGVADEHVLGLGRNGRSHIEISGQSGGARIKISDRGDFISGTSDRKVTITGSGRAIMAEISMISGLARVSEDEFVYK*

NbL12g15020.1 copper_transport_protein_ATX1-like [MW = 12.87 kDa]

No. of times detected



log(intensity)



Values from



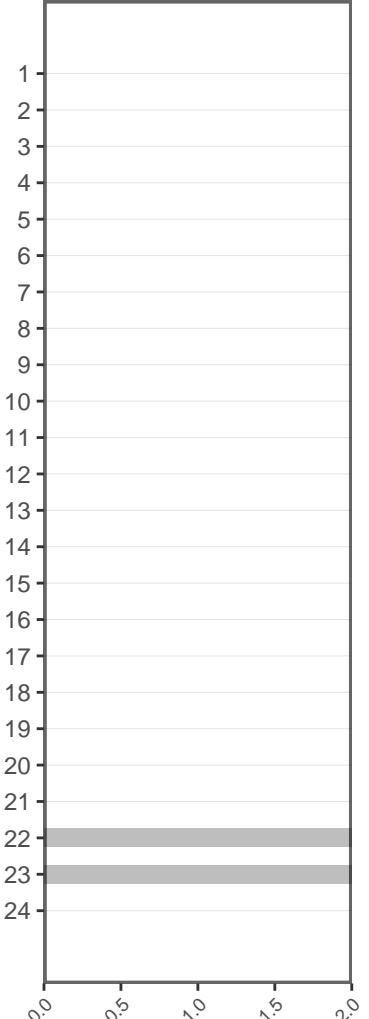
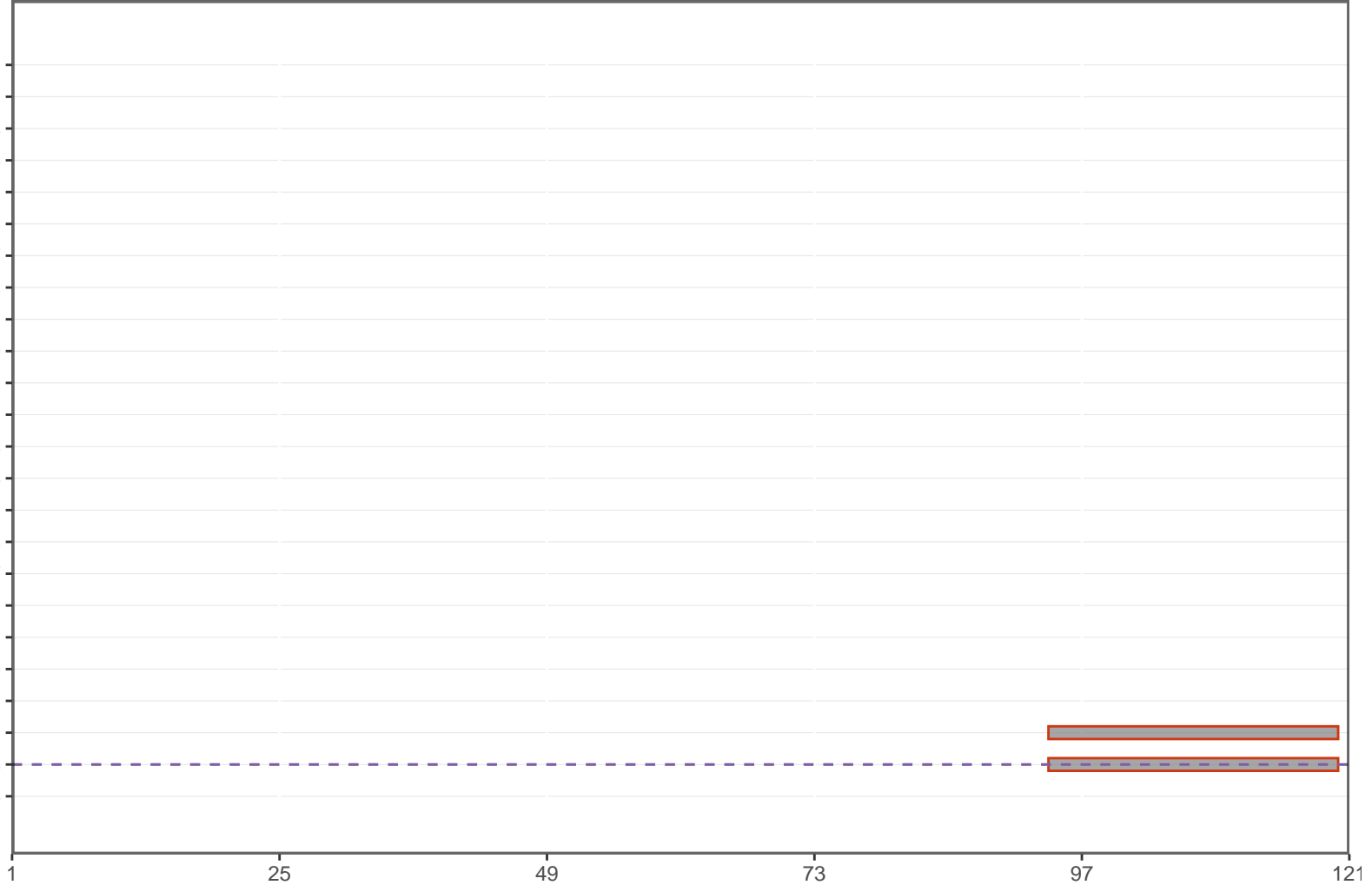
MW indication



Molecular weight



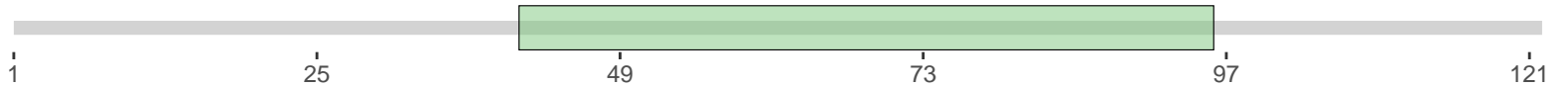
Gel Slice



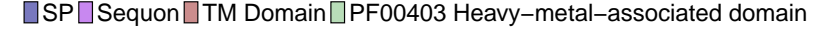
Protein length



Pfam domains



Pfam Description



Protein sequence:

IGCYGAVKRVLGKMEGVENFDIDLEKQKVTYKGNVQPEAVLQTVKTKPKPWFWEAGEPAQTEKPKPEAVGTA*

NbL12g14900.1 dnaJ_protein_homolog [MW = 46.66 kDa]

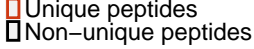
No. of times detected



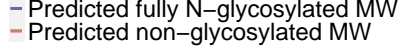
log(intensity)



Values from

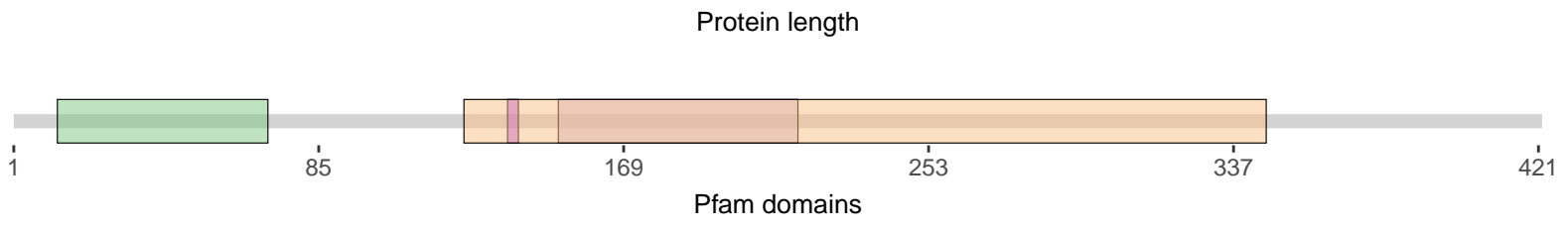
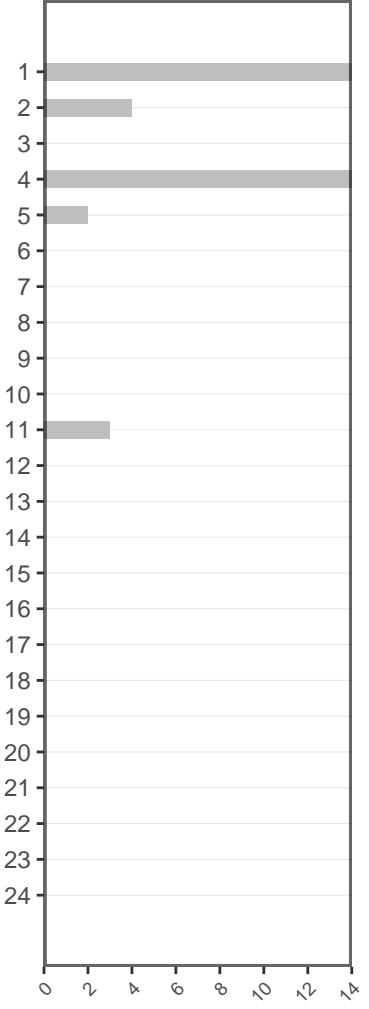
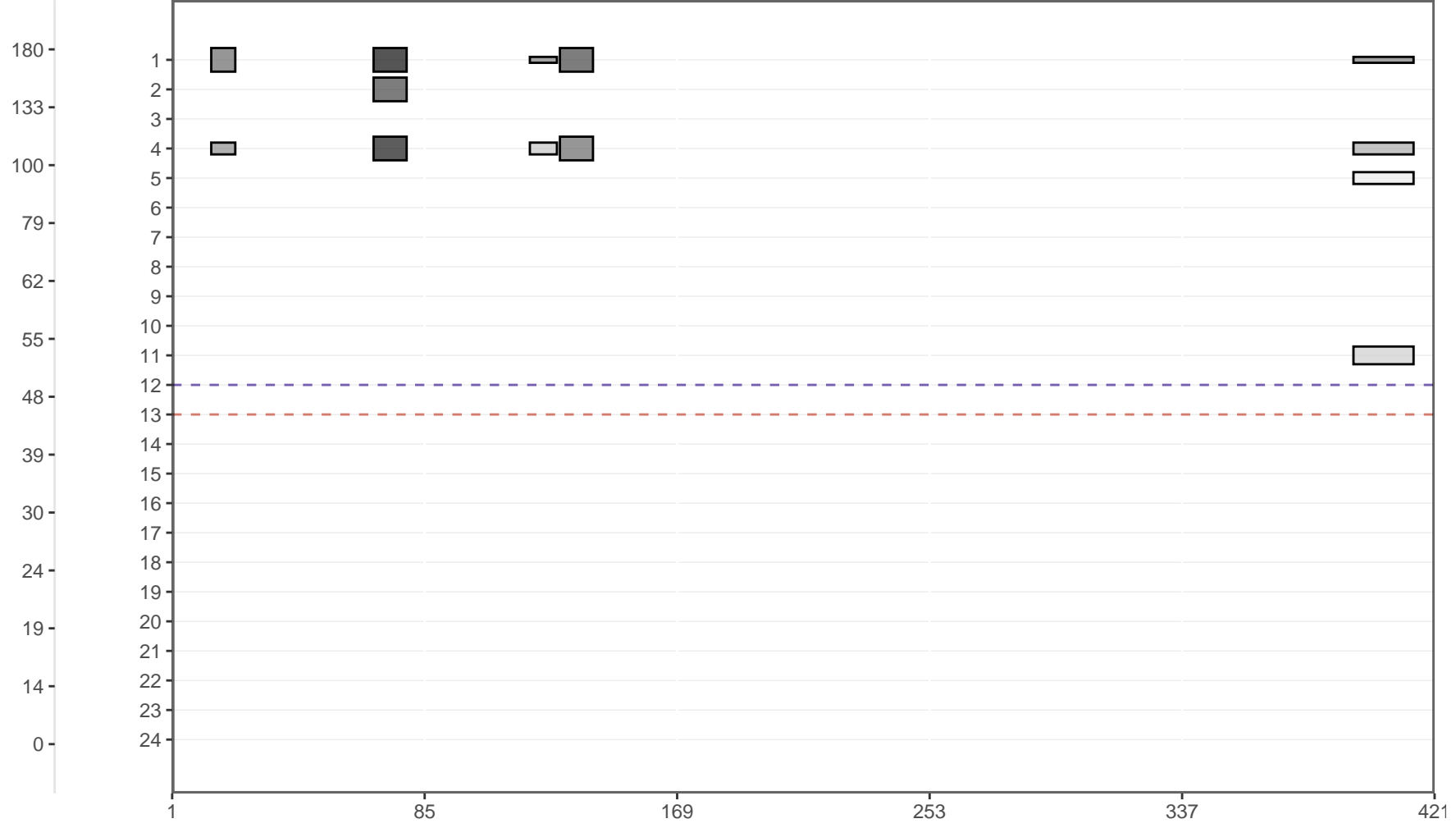


MW indication



Molecular weight

Gel Slice



Pfam Description

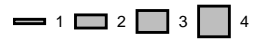


Protein sequence:

ICKGTGETISDKDRGGGKGDVVEKMKVLEVVVEKGMQNGKNTFPGEADEAPDTTGDVFLQKKEHPKFKRGDDLVEHTLSLTELALOGFQIFLTHLQNRQLLKSGPGEVWVFDQFKANDEGMPMYGRPFMRGKLVHFTVDFPETLSLEQCKNLEAVLPPKPKTKMTDMELDEGEETFLHDVNIIEEMRRKQGGAGEVDEDEDMHGGAQRVQCAQQ

NbL12g14860.1 ubiquitin_carboxyl-terminal_hydrolase_12-like [MW = 139.89 kDa]

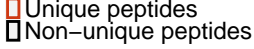
No. of times detected



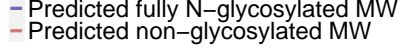
log(intensity)



Values from

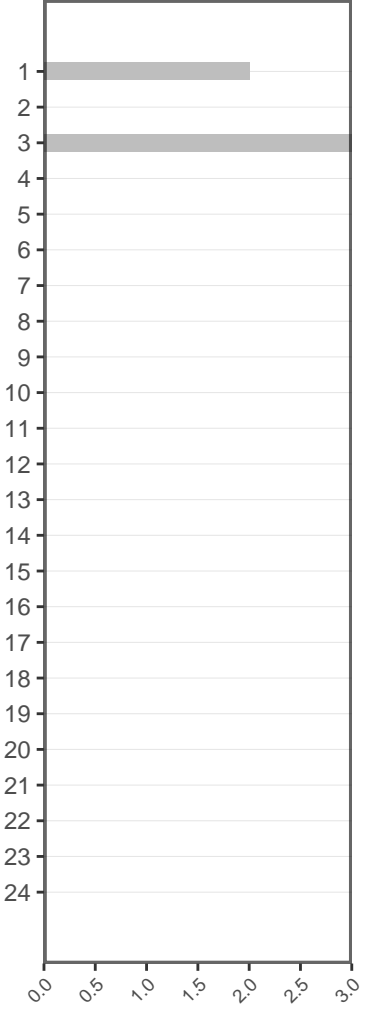
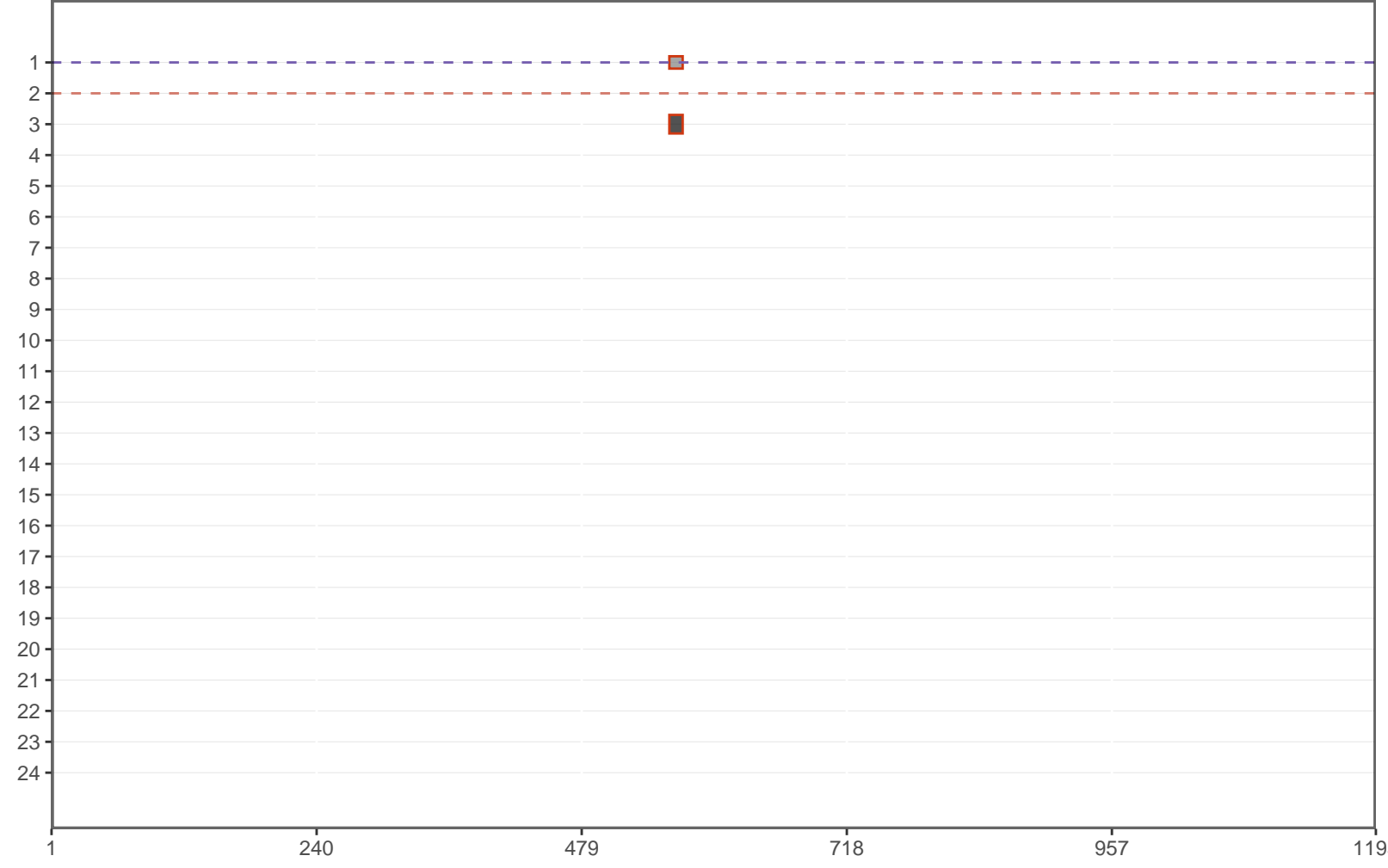
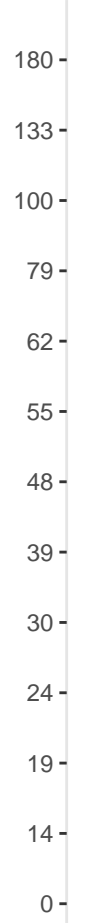


MW indication



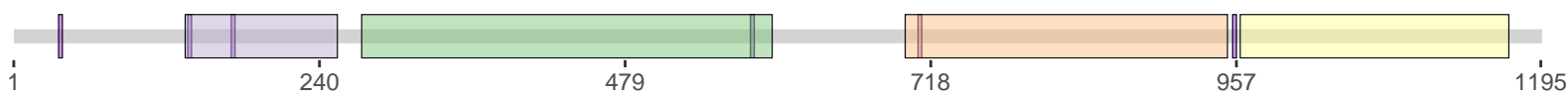
Molecular weight

Gel Slice



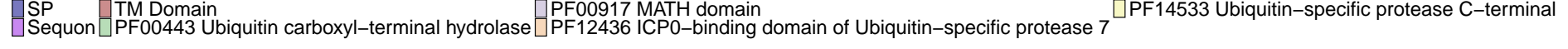
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FKFTKYSNAYMLYHRESGDKIKICNVDEKDAEHLRLRLKKEGEKEQKKEKAEAHLYTIKVARDEDLGEGIKKEIYFDLLDHDKVRFRIRKGMPTFGFKEEVAKELGIPVGFGRYVLLWAKRONHTYRPNRLTAQEEVQSGQLREVSNNANNAELKLFLEVEFGLDLQFPFFPEKTEKIDLLFFNLYDPLKEIRYVGRVFKVGGGKPLELTLNELAGLFPDEEELFEEKFEFNVMGEHIDWLSFGGSGLEDGDHGFQKSLRNQDREGYRFRVPLFLEYVYNRQV

NbL12g14810.1 serine/threonine-protein_phosphatase_PP1-like [MW = 37.95 kDa]

No. of times detected



log(intensity)



Values from



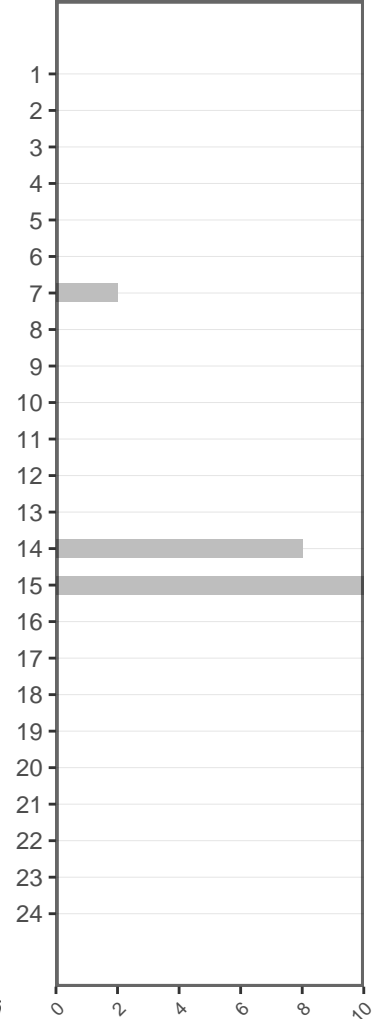
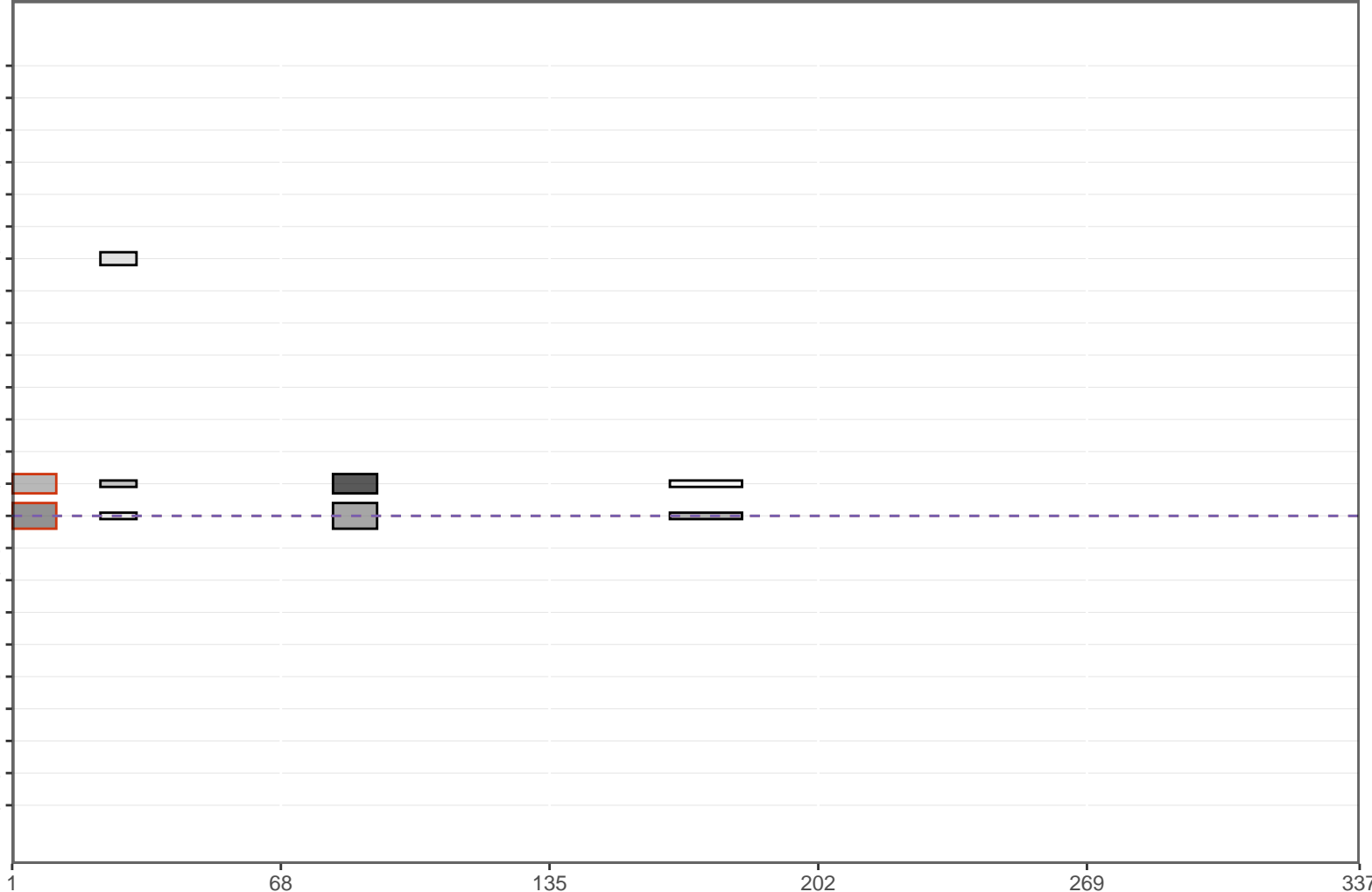
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00149 Calcineurin-like phosphoesterase
- PF16891 Serine-threonine protein phosphatase N-terminal domain

Protein sequence:

LDDEKLCMIGGLSPDLNLDGRNLRPTDVPDAGLLGDMWSDPSKDVGGWGMNDRGVYTFGADKVFTEFLKQDLIDGRAHGVVEDGVEFFANRGLVTFISAPNYCGEFDNAGAMMSVDEFLMCSFQILKPAEKKRFNFQSGTTAKPQSGFTGMSFLVYVVGEPKSGGGND

NbL12g14740.1 cysteine_desulfurase_1_chloroplastic-like [MW = 52.13 kDa]

No. of times detected



log(intensity)



Values from



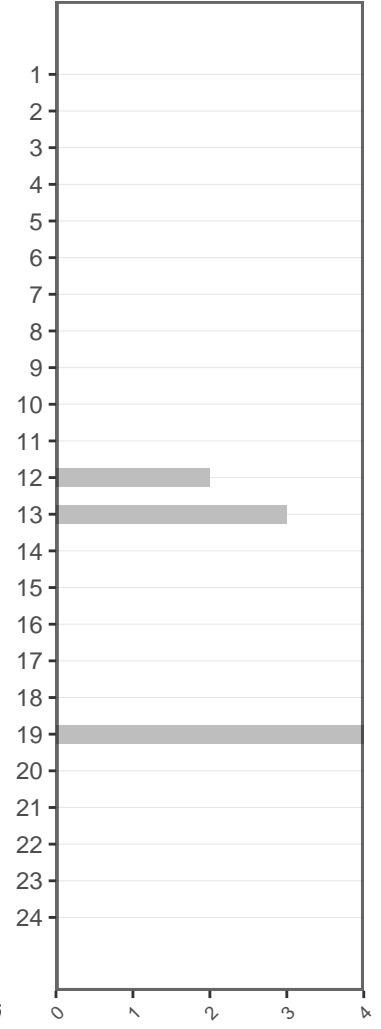
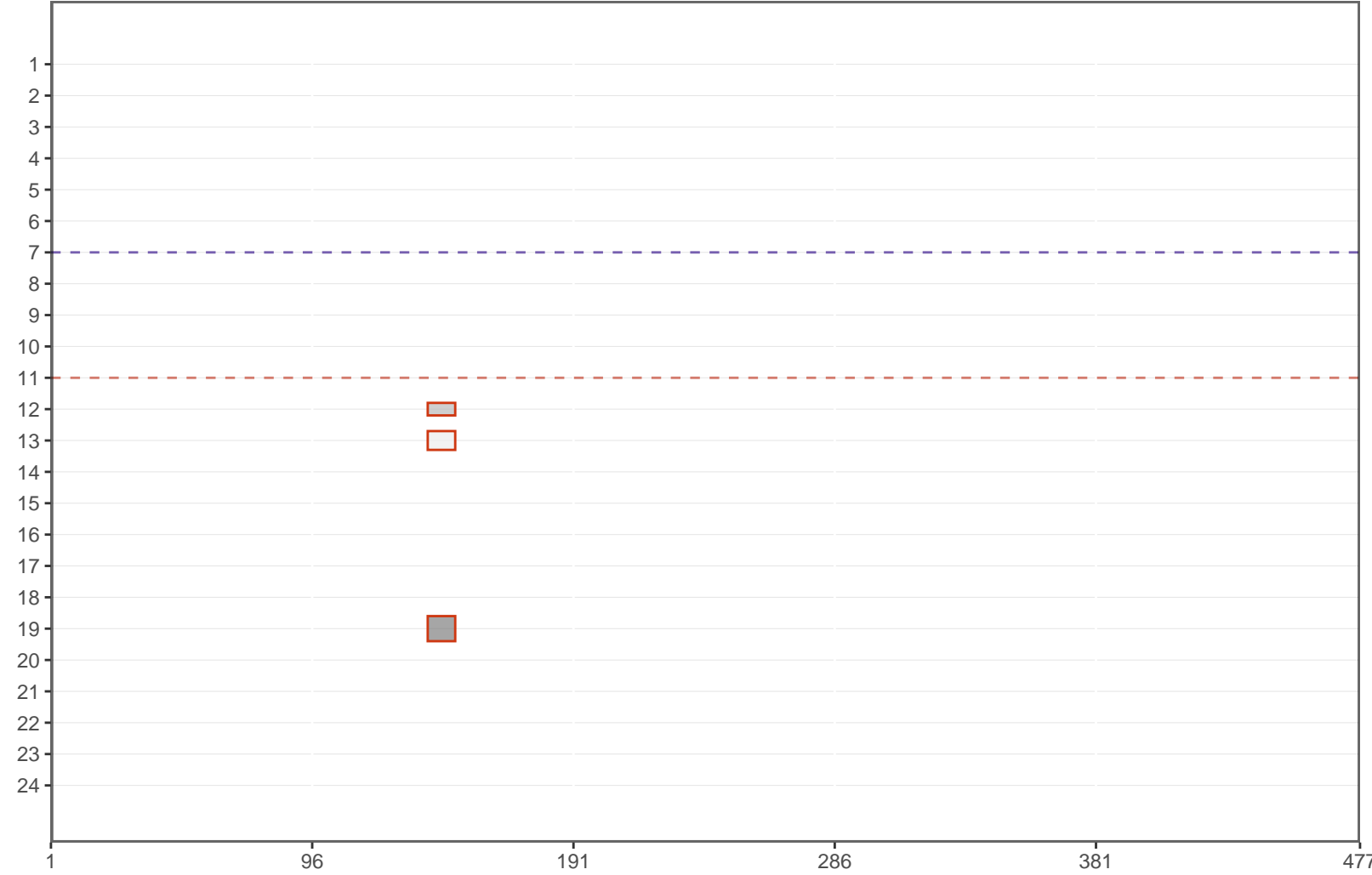
MW indication



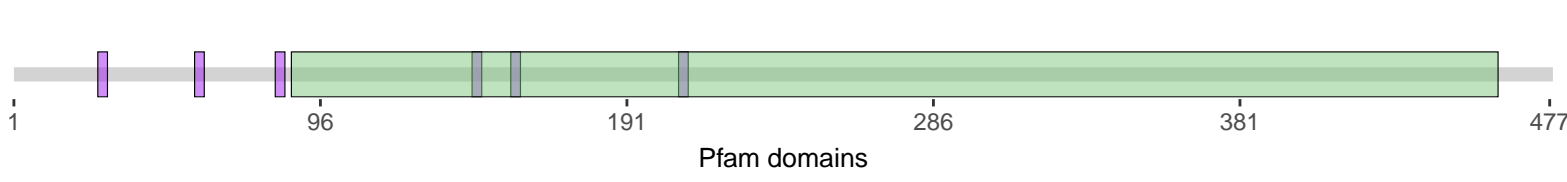
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

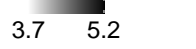
TKLLVHIVSNMLASVLFMDEVISWANDVGAKVLVDAGQGVPHMVVDVKTLDDFLVASSHKMGCPPTGVFLYKSEILSAMPPFLGGGEMIAADVLDHSTYAEPPRFREAGTFAIGEAGLGAANDVLSSEIGMQGHVDVEMELANLYDLSVSDVRIKGPAPRAVKRAALGSFNKDVHPTDQATFLDQGHGVAIRSGHHGAGPLRHLGSSSARASLHFYNTKDDVDRFEALKDTISGFTFSK

NbL12g14680.1 nitrilase-like_protein_2 [MW = 35.68 kDa]

No. of times detected



log(intensity)



Values from



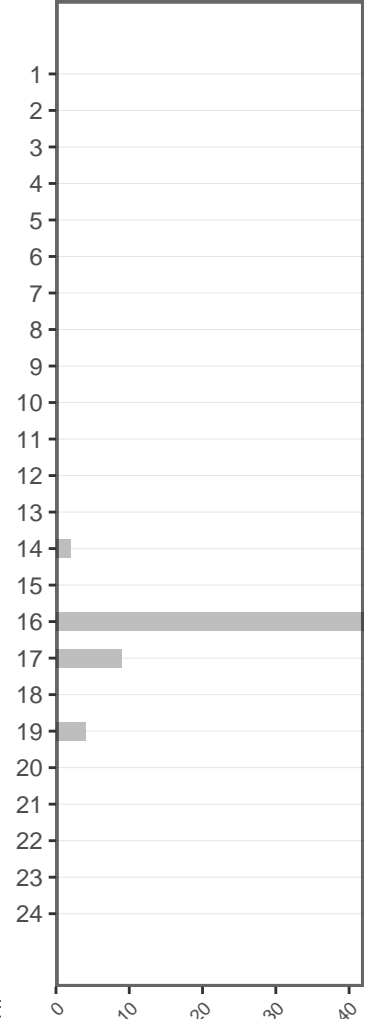
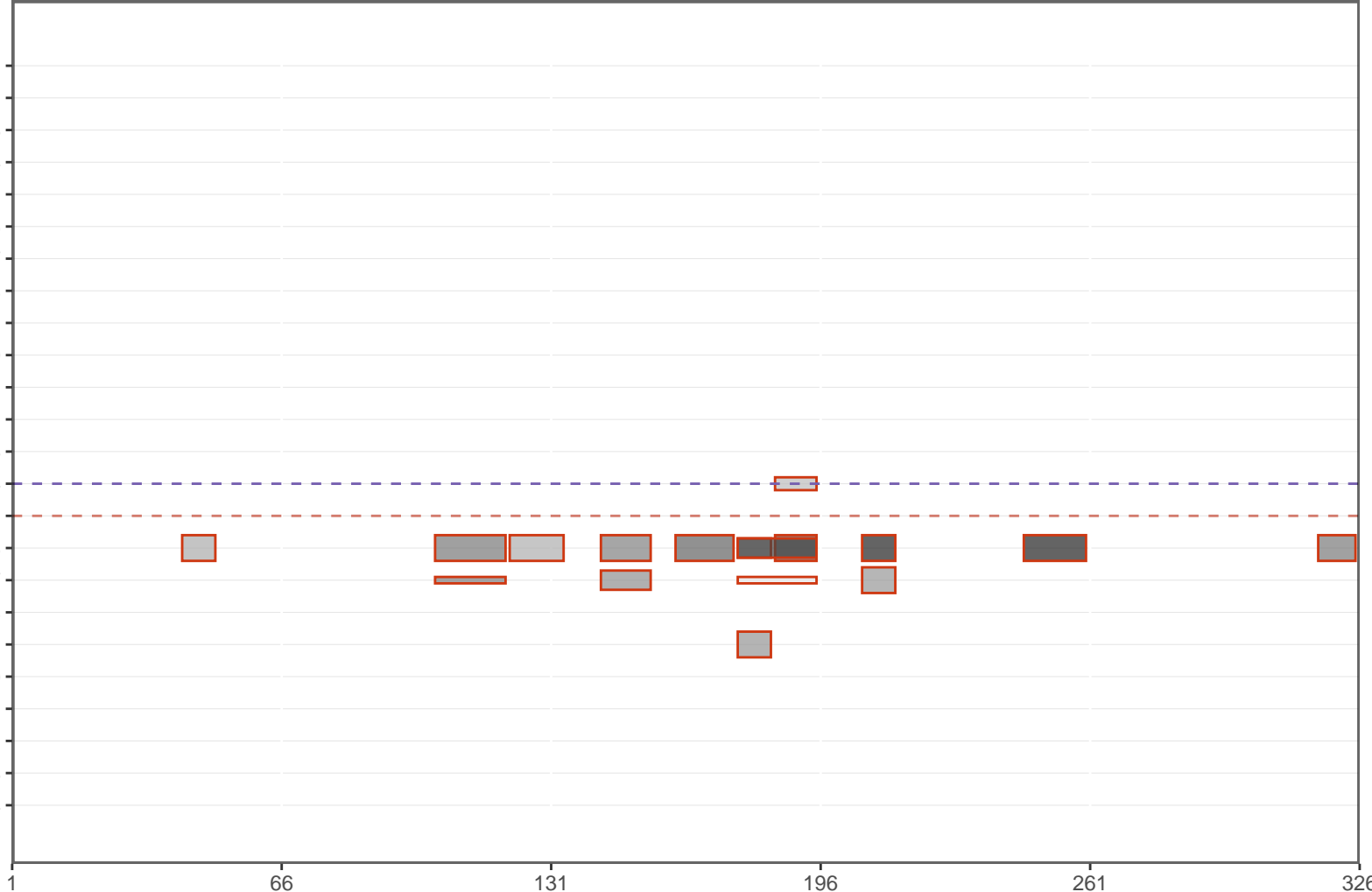
MW indication



Molecular weight



Gel Slice

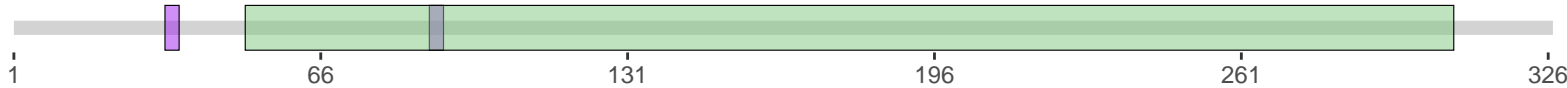


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

INGIRSTYSKMLFDQVDPGGAWYKESFTEAGKDIVVADSPQRLGLTVGVDLRFPELYGQLRFNHDMLLVPAFTMVYGGAAHWEILLRARRAETGGYVAAAGAGKHNEKRESYGDTLIDPWGTIVGRLEDRSSTGTVDIDFSLSDSVRAKMPVSKHRKPAEFVNHQP

NbL12g14610.1 putative_uncharacterized_protein_DDB_G0270496 [MW = 48.61 kDa]

No. of times detected



log(intensity)



Values from



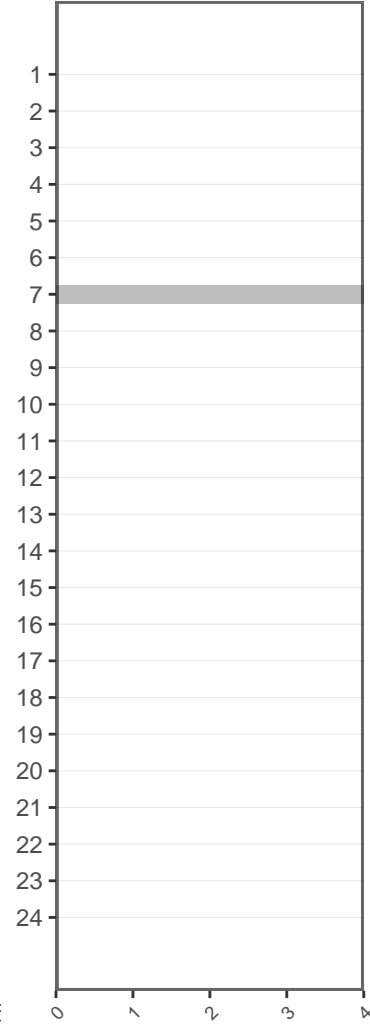
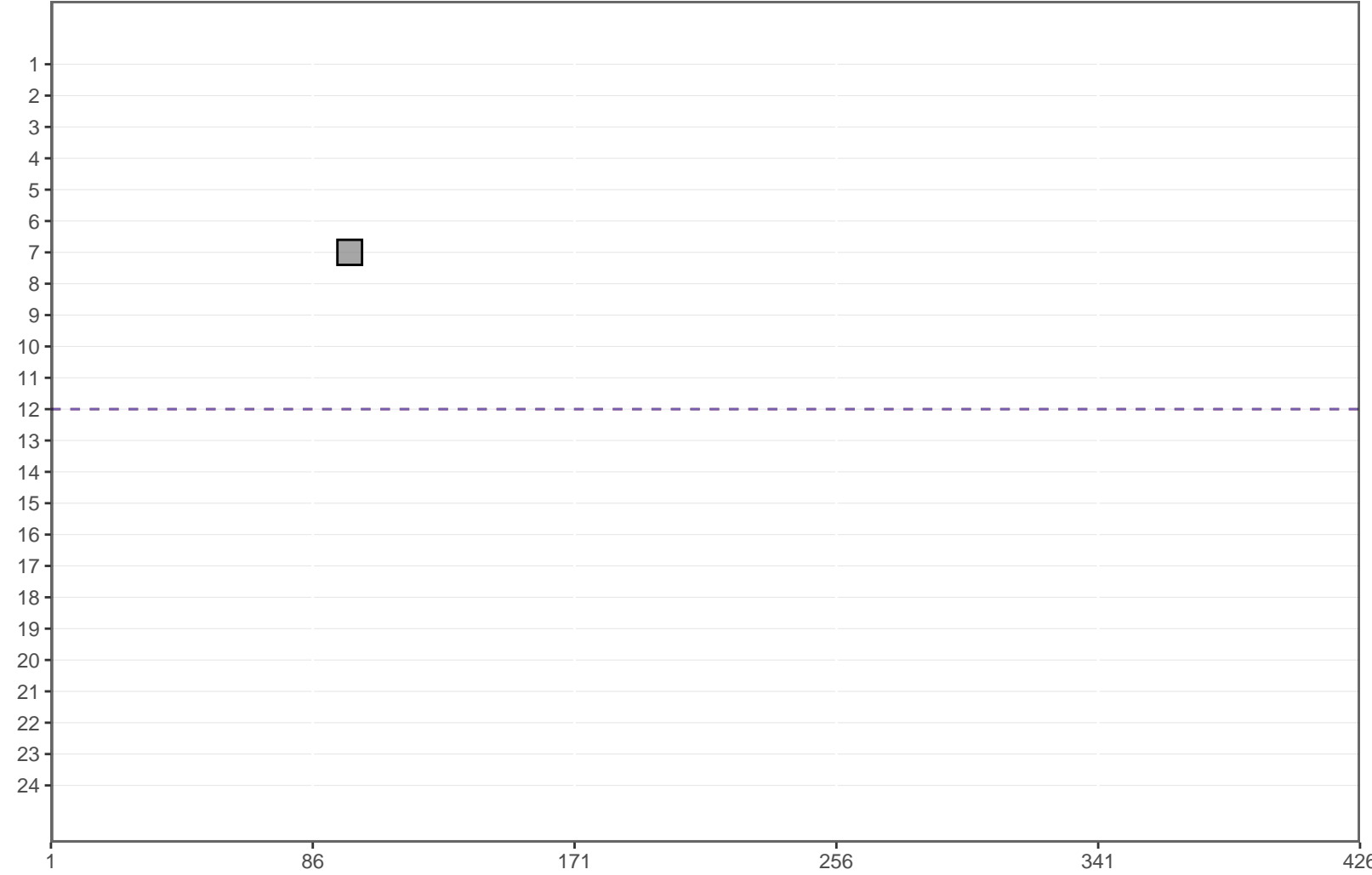
MW indication



Molecular weight

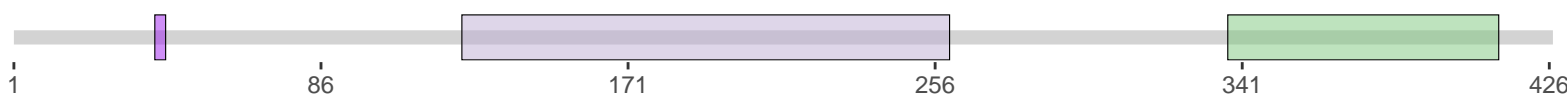


Gel Slice



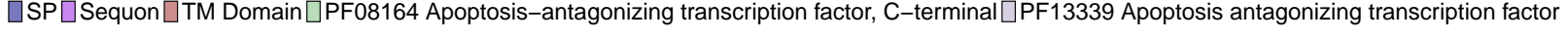
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

...LLEKNPSTGSMVDVNSGKREKLESDVEESNGEVEDDWHKISGMHSRMAAFRDKSIKVGWRKTFQVTSAAAANKGLGFNGDSDGQVAGVMRDPKMKMGDGGREAVLFGTASDATGNGEGFNMDGDPPELLDDSEFYQGLLKEFFEAVDPASSETAFYALKRLGTTKRRKIVDRRASRKRIRYNIHEKIVNFMAGPQVNLPPMAPKLFENLFTGGSTHRPNNLH*

NbL12g14540.1 60S_ribosomal_protein_L35 [MW = 14.32 kDa]

No. of times detected



log(intensity)



Values from



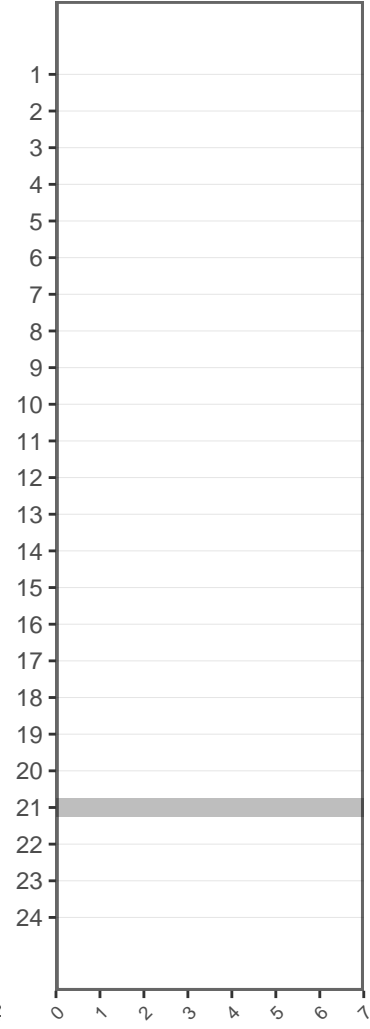
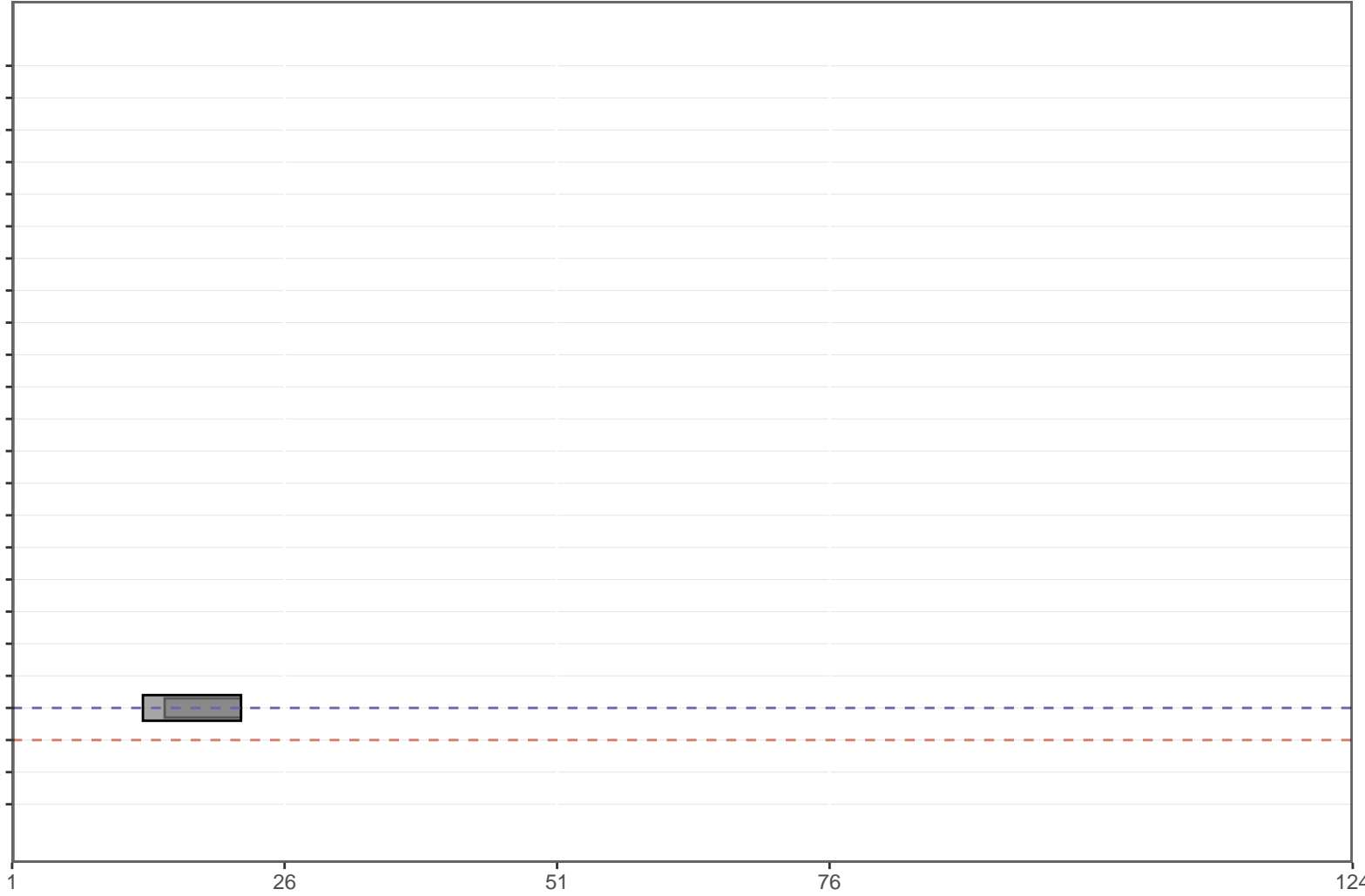
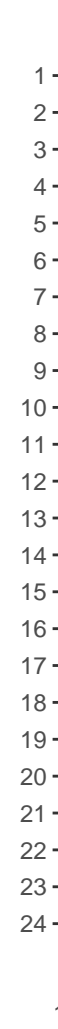
MW indication



Molecular weight

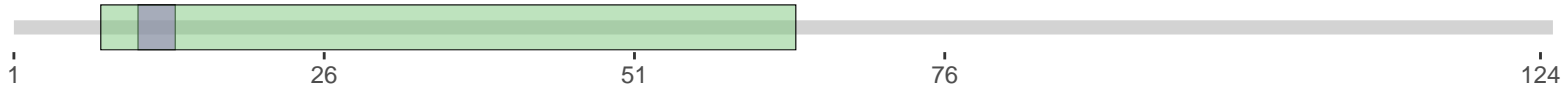


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VVRLSIAQVLTVISGKIKTALREAYKNNKYLPLDLRPKIKTRAIRKRLTHQVSLKTEREKKEMFFPKYKAVK

NbL12g14460.1 glutathione_S-transferase_DHAR2 [MW = 23.79 kDa]

No. of times detected



log(intensity)



Values from



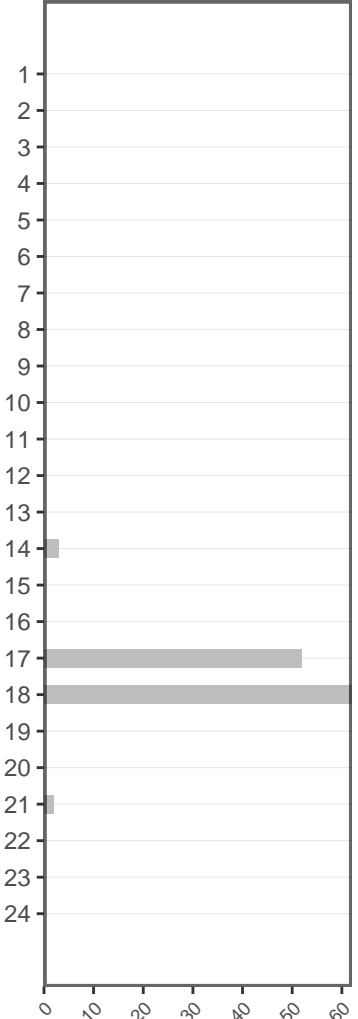
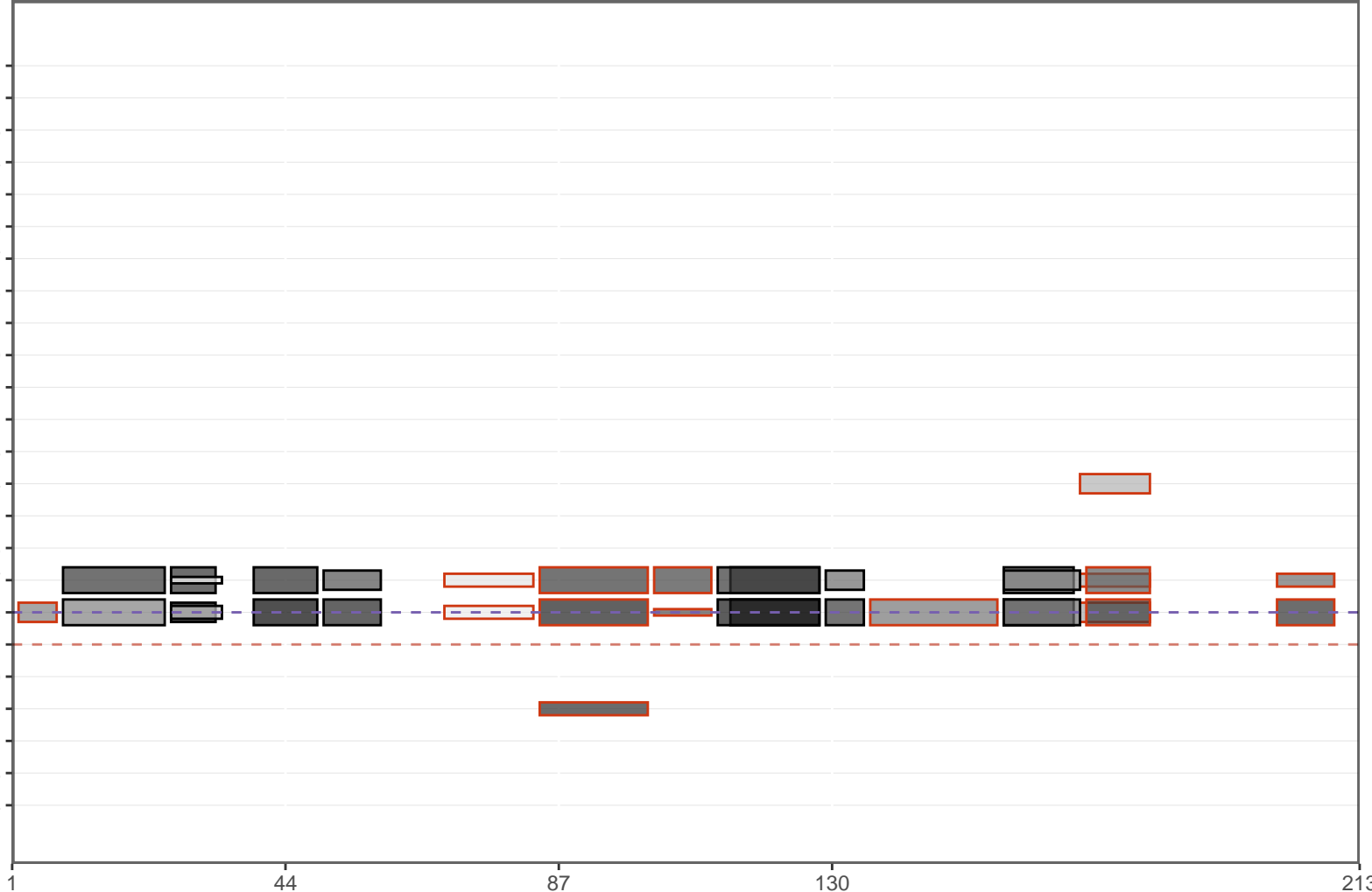
MW indication



Molecular weight



Gel Slice



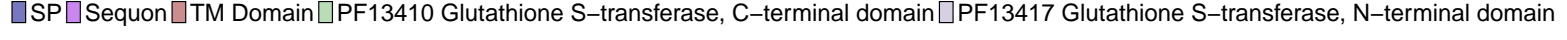
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EFASVGSKIFPTTVSFLKSKDASDGTGALLDELKALEEHLKAHVPYVNGENICGVDLGLAPKLYHLEVALGHFKKXWVPEGFSHVRNVMKLLFERESFGKTKCAKEYVIAGWAFKVPNP

NbL12g14340.1 2-oxoglutarate_dehydrogenase_mitochondrial-like [MW = 115.63 kDa]

No. of times detected



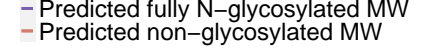
log(intensity)



Values from



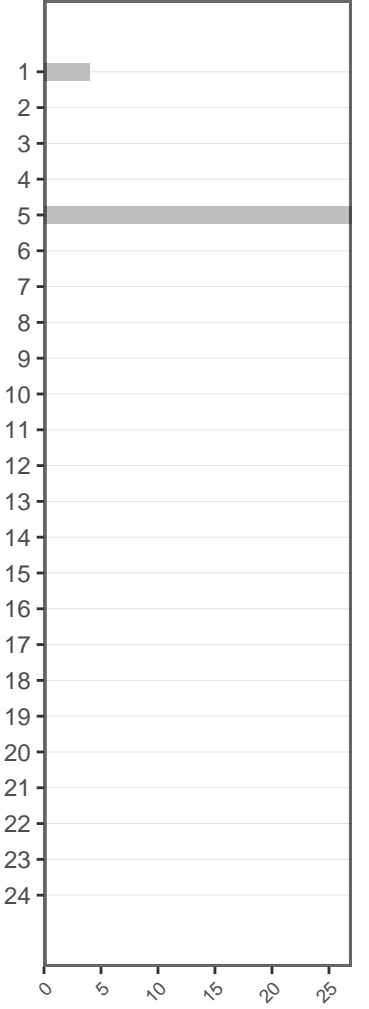
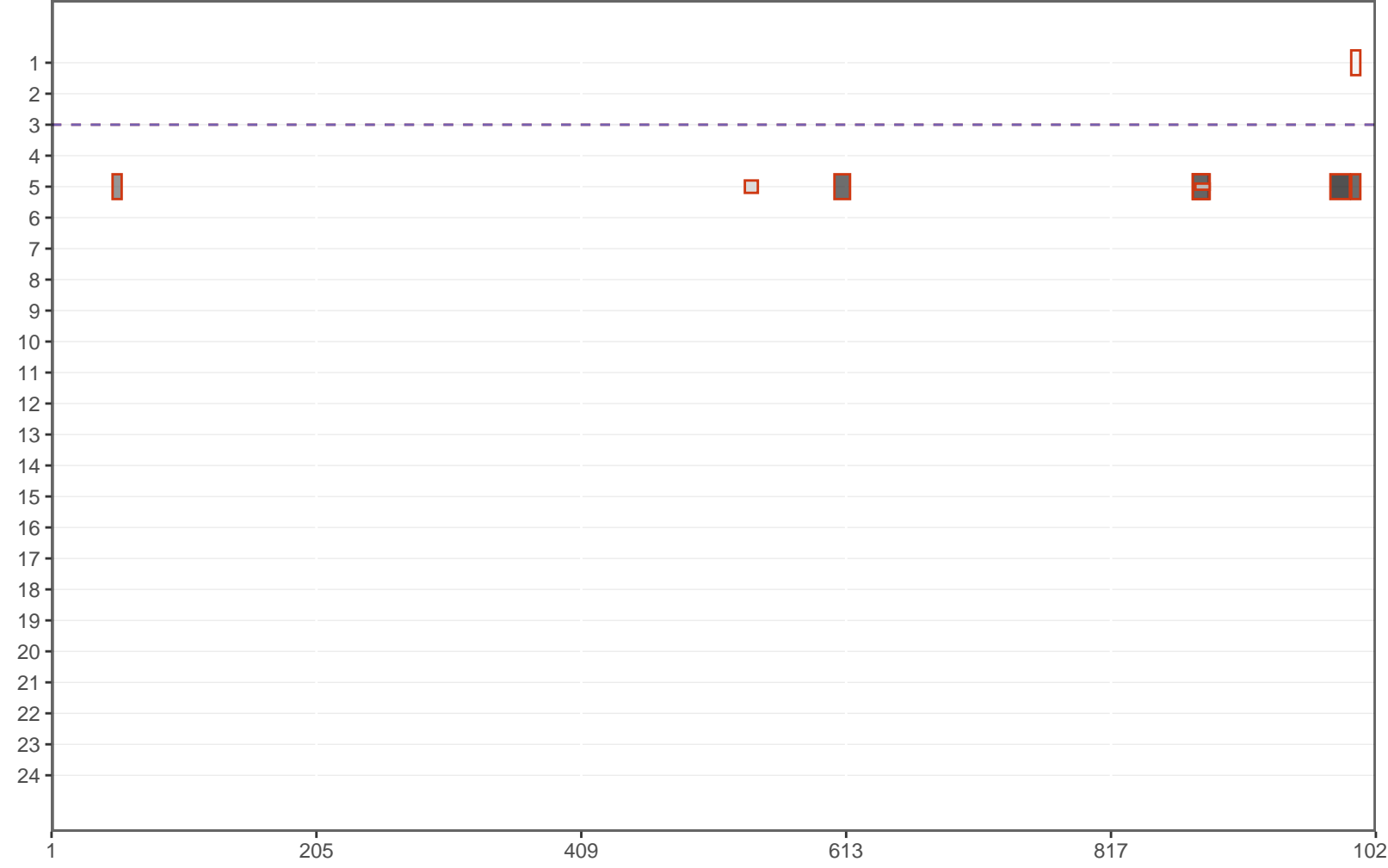
MW indication



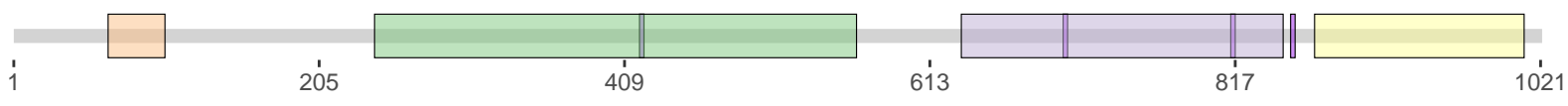
Molecular weight



Gel Slice

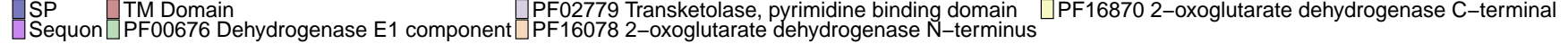


Protein length



Pfam domains

Pfam Description



Protein sequence:

RFQIHEIDEPSFTQPKMKYKIRNHPSSLEINQNKLLKSGQVTKDDVKEIKINRILNEEFVASKDVPQKRDWLSAFWAGFKSPQGLSRVINTGVKPEIKNKQKATMLPDDFKPRAVKRFDDRKMETGEGVDVWVGEALAFATLVEGNHVRLSGGDVGRTGFHRHSHVLDQGETGAGYCFLDHVMNNGNEEMFTVSN6SLSEFGVLGFEFGYSMENPNSLVLWEAGDFDFANGAGVIFDQFV6SGEANWLRQ6GLVLLPFGYDGGDGFHSSGRLERFLOM

NbL12g14310.1 histone_H4-like [MW = 11.43 kDa]

No. of times detected



log(intensity)



Values from



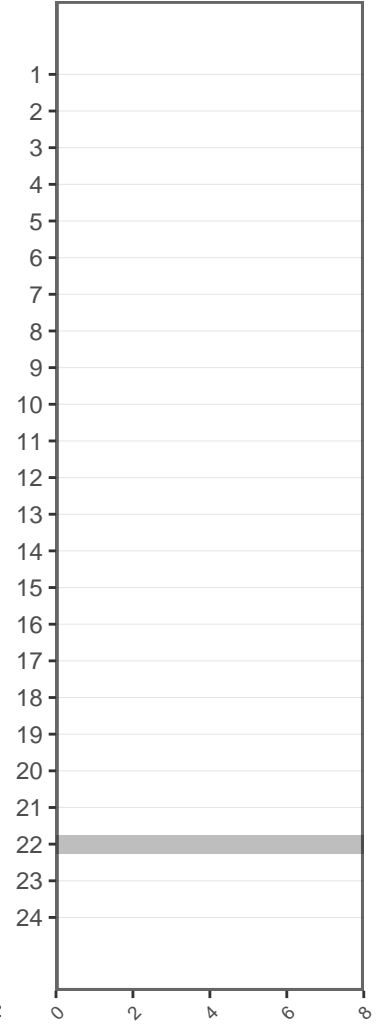
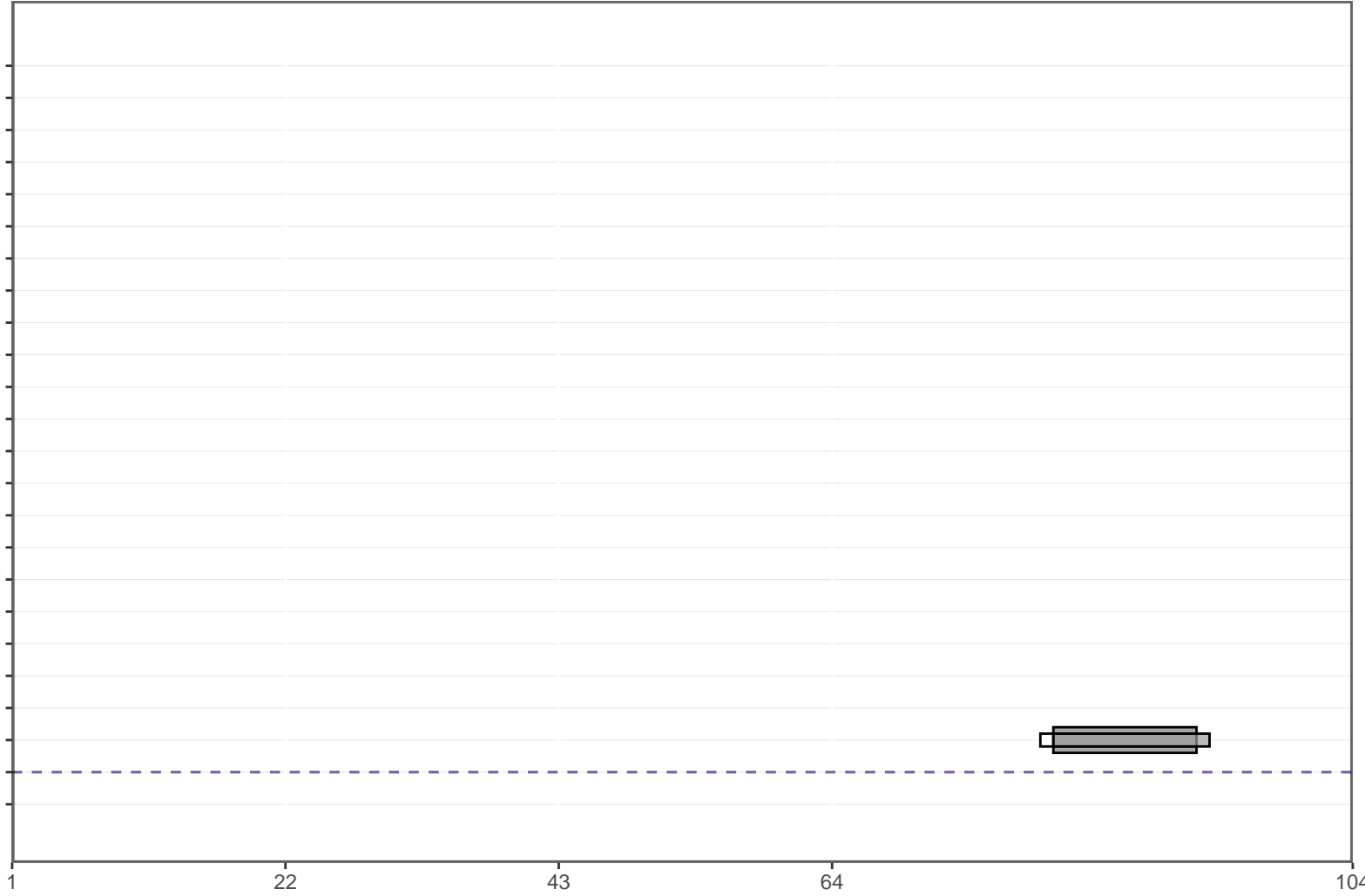
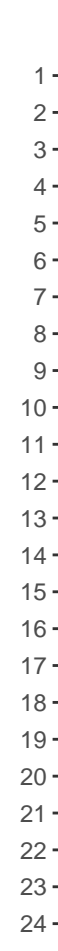
MW indication



Molecular weight

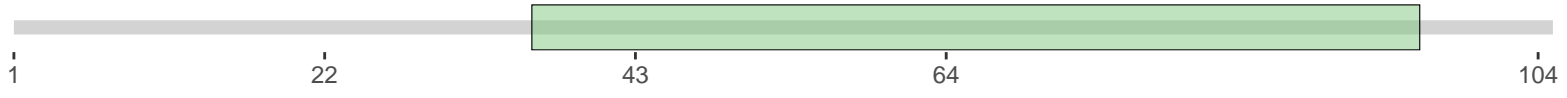


Gel Slice



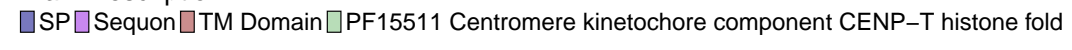
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ARRGGVXRISGLIYEETRGRVLFKIFLENIRDAVITYTEHARRKTVTAMDVYVSLKRQGRITLYFGGQ

NbL12g14280.1 UDP-glucuronic_acid_decarboxylase_6-like [MW = 38.65 kDa]

No. of times detected



log(intensity)



Values from



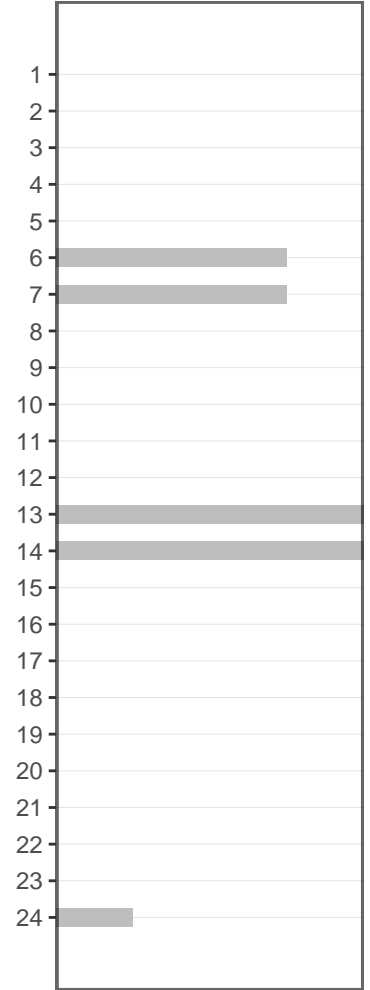
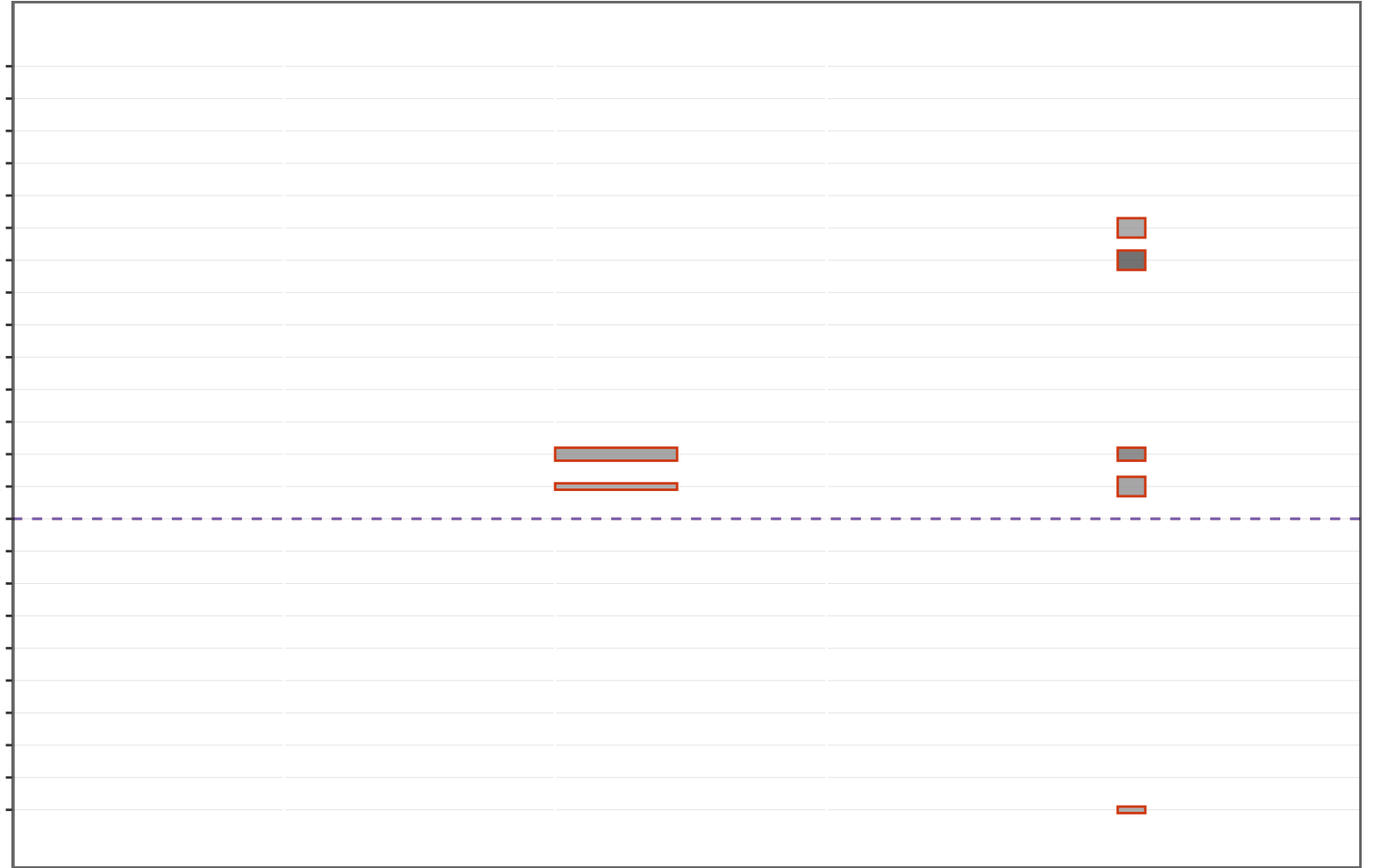
MW indication



Molecular weight

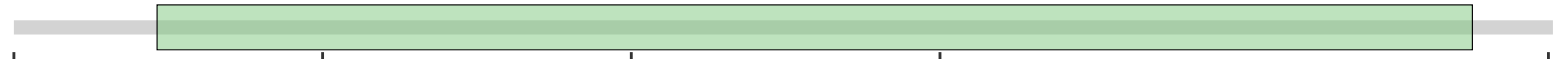


Gel Slice



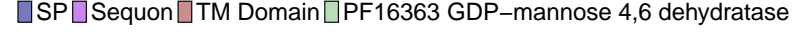
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ITYYWGNVNPICVRSCHYDEGRVAETLFDYHRGHGIERIARIINFTYGRPMNDGRRVSNFAGARDEALFVLPQTQTRBFCYVSDMVDGLRLMEGDITGPNKGNPGEFTMELAEVYKELNPGVNIITVENTPDGPRGRKPPDITKAKELLGWEPKRLRDGIFLMEEDFRGLGIARKK

NbL12g14240.1 ubiquitin-conjugating_enzyme_E2_7 [MW = 18.81 kDa]

No. of times detected



log(intensity)



Values from



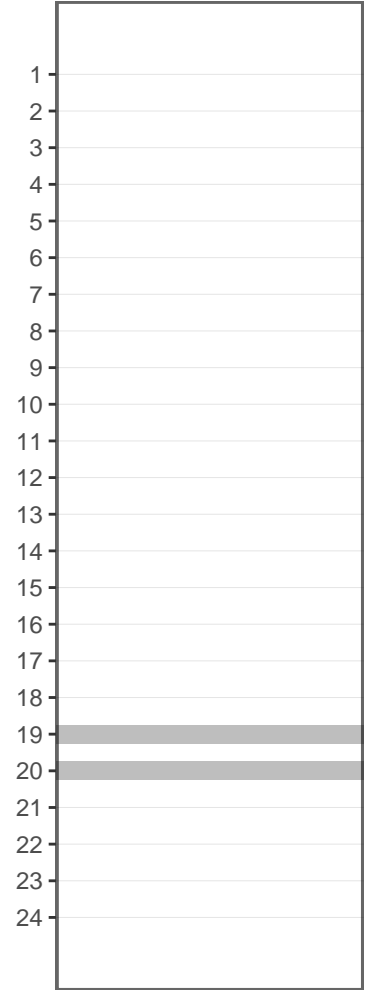
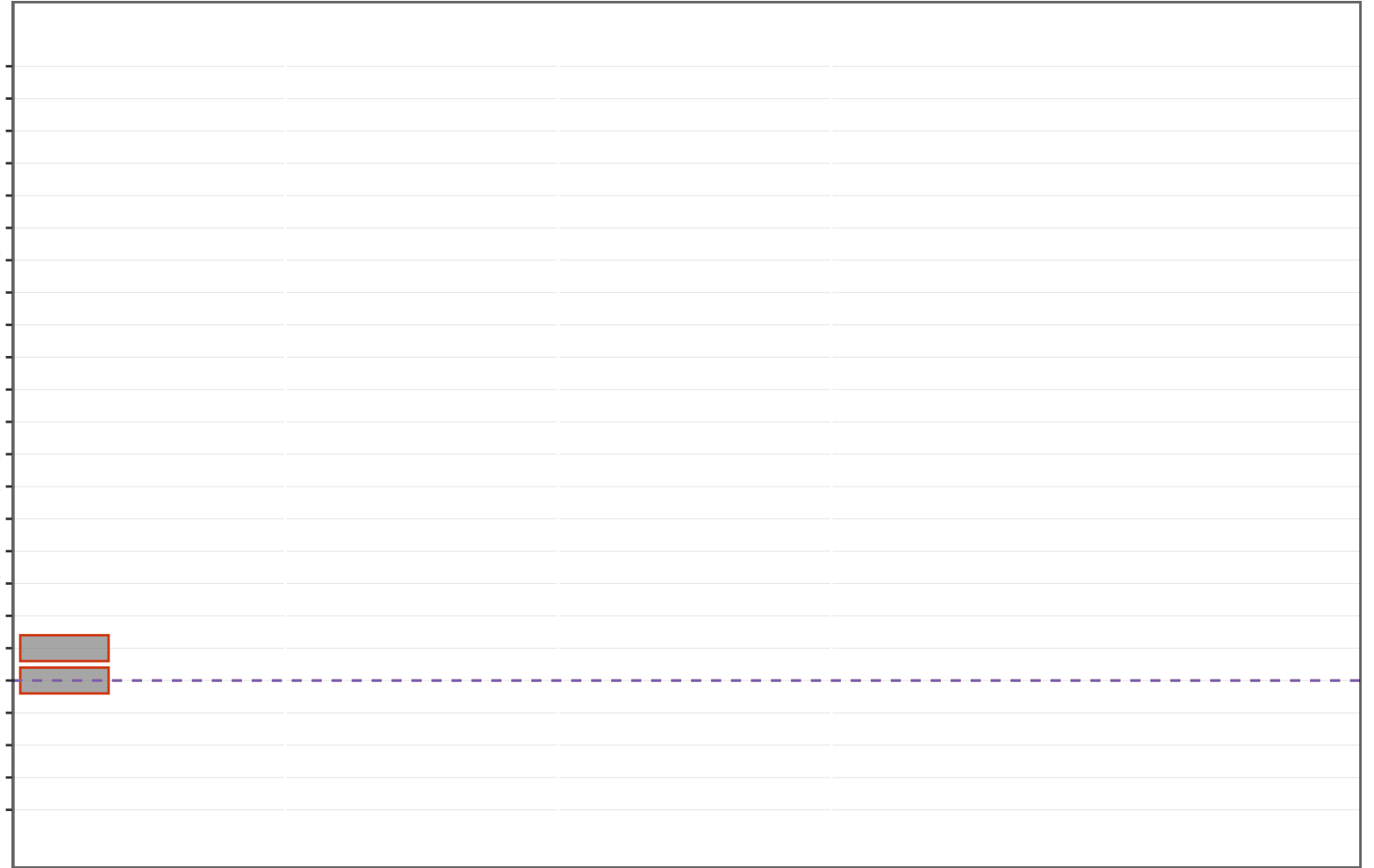
MW indication



Molecular weight



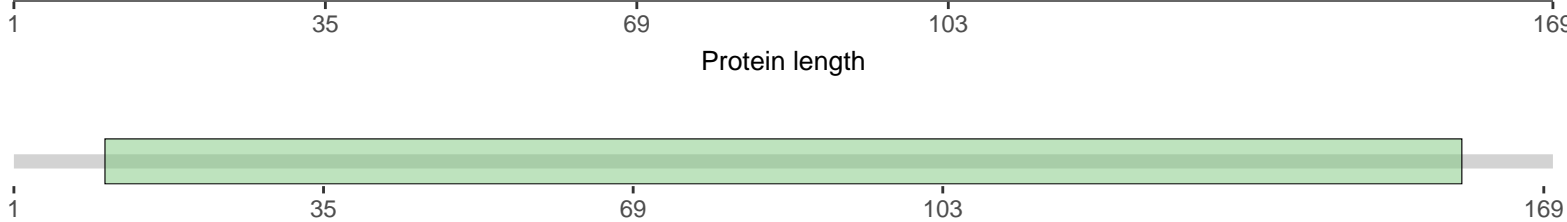
Gel Slice



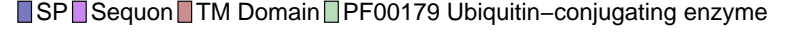
Peptide counts over 4 repeats

Protein length

Pfam domains



Pfam Description



Protein sequence:

TRFTSEVWHPNLYSDGKVCISLHPGDDPNDGVELASERWSPVHTVESILSHEMLSPNDESPAVEAAXEWRDNRDFKPKVSRGVRRSGEMT

NbL12g14020.1 pathogenesis-related_protein_STH-2-like [MW = 17.72 kDa]

No. of times detected



log(intensity)



Values from



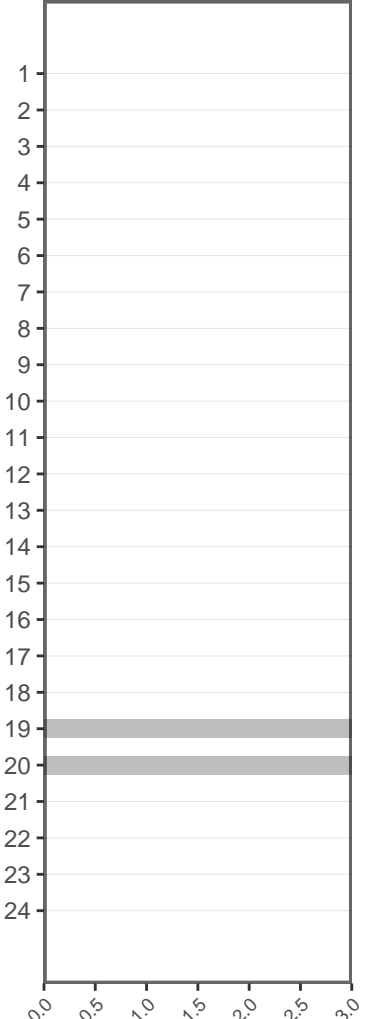
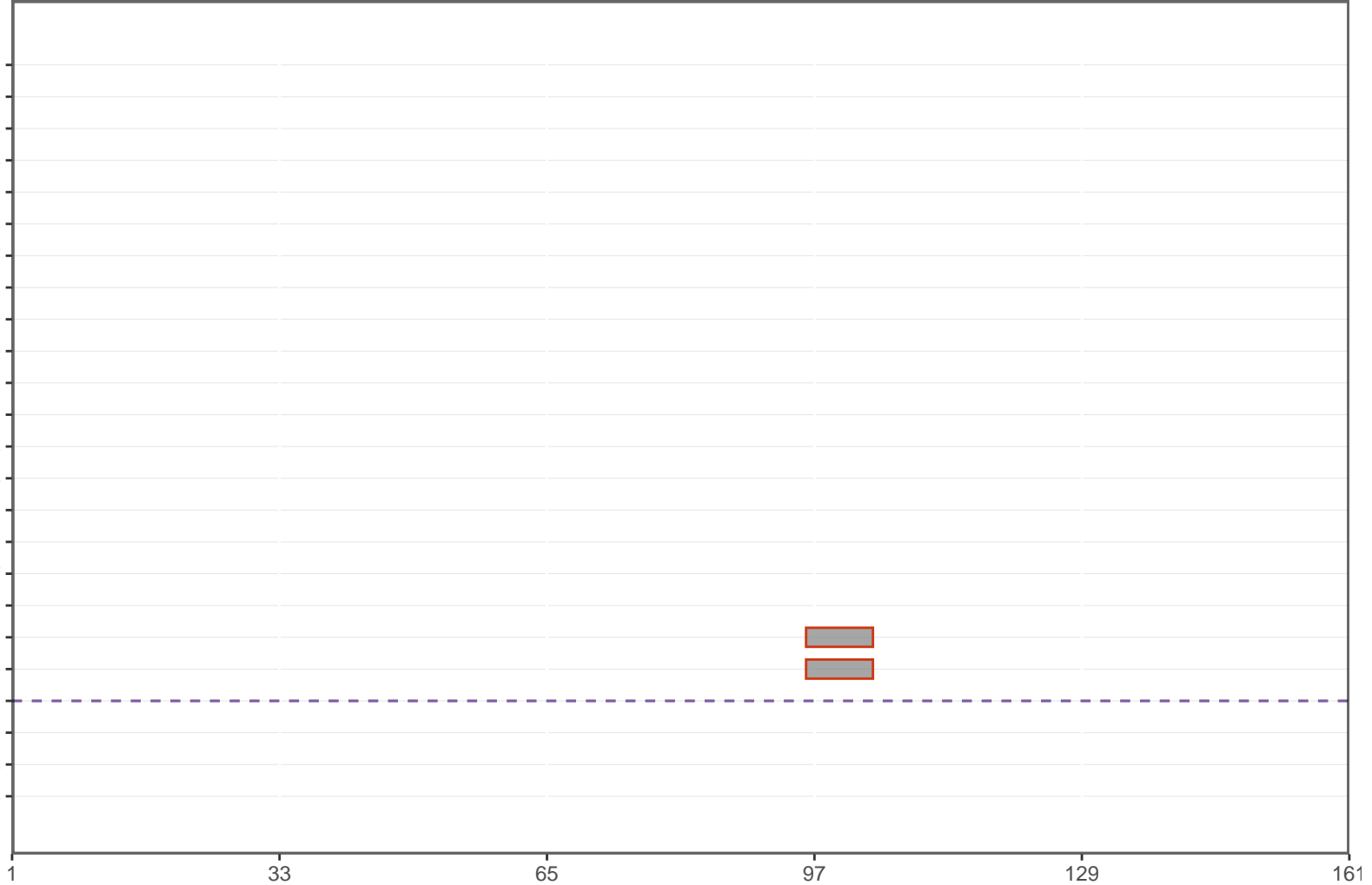
MW indication



Molecular weight



Gel Slice

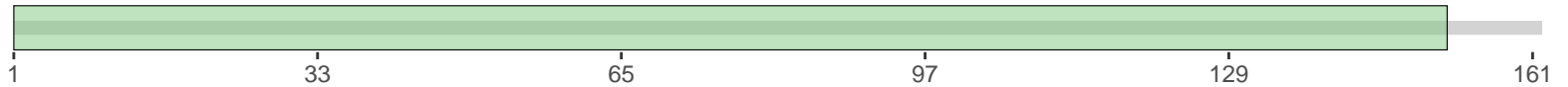


Protein length

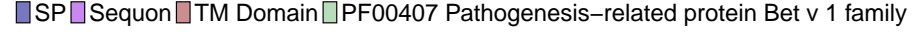


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VKHRIDEVQEKEMVQKYTMIEGNALRDKLDISIVYKFEESNNGGGGDKMTRKYGGDFVKEEIKAGKDGATGIVKAVESHLPNPSLW

NbL12g13940.1 50S_ribosomal_protein_L7/L12 [MW = 23.86 kDa]

No. of times detected



log(intensity)



Values from



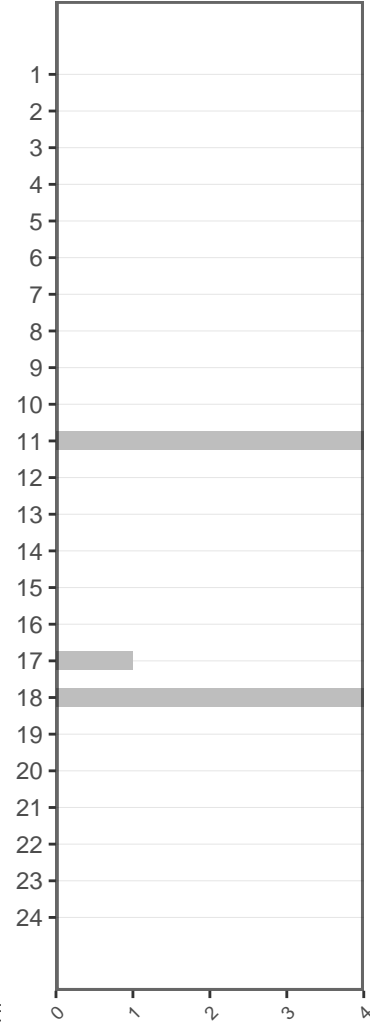
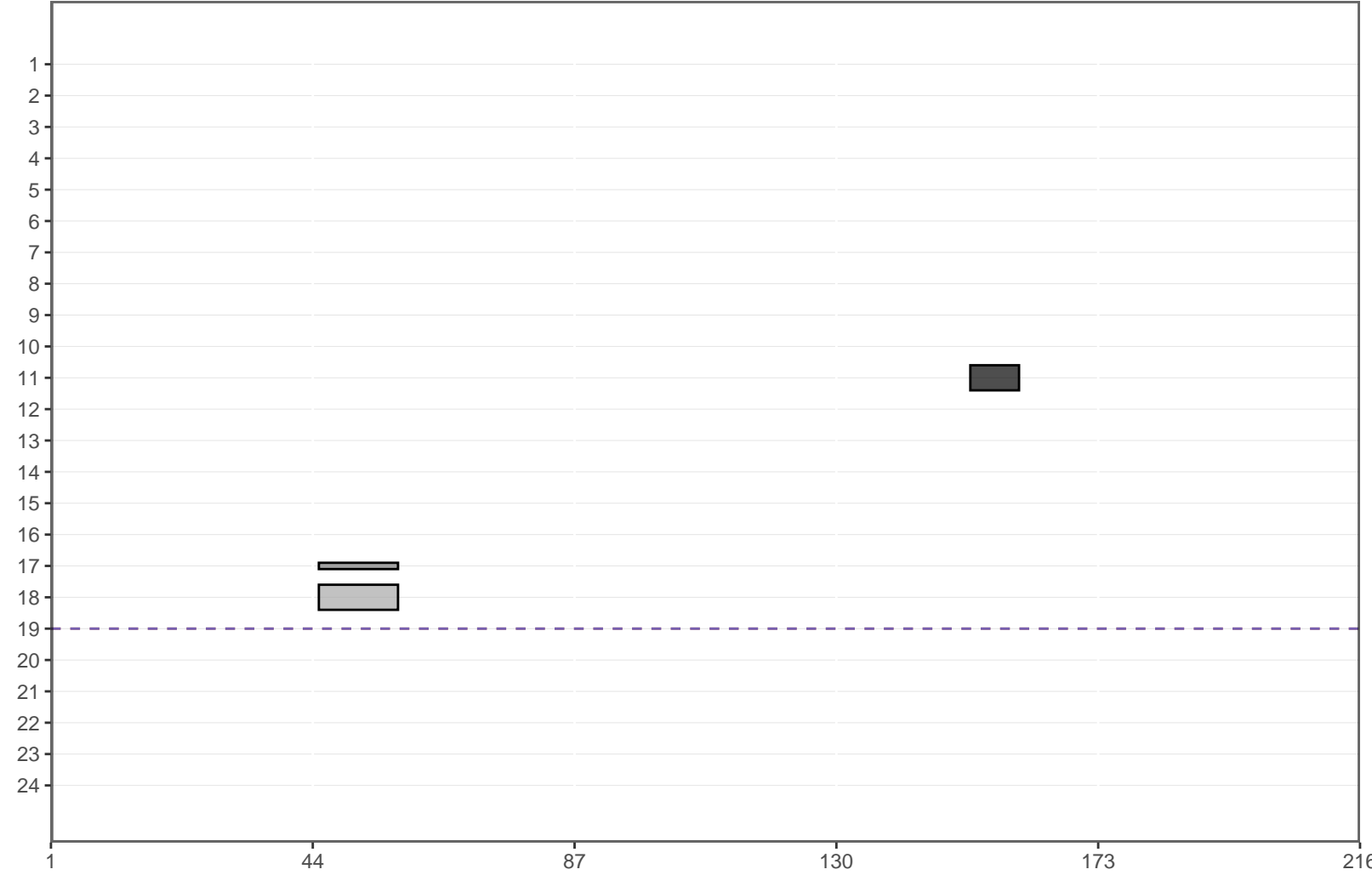
MW indication



Molecular weight

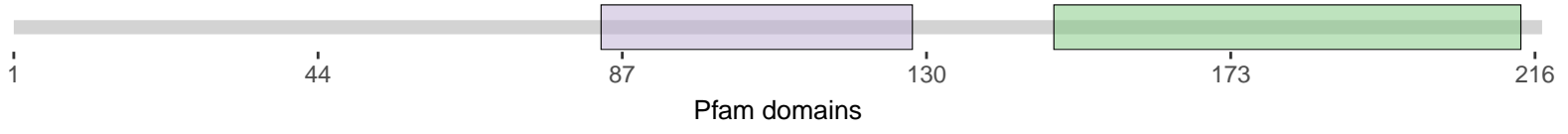


Gel Slice



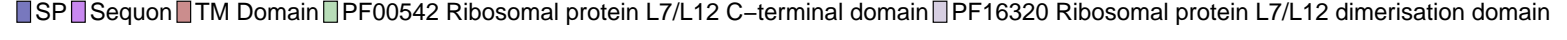
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LVEVAELSSIIIMKRLGMTEGPMVGVMMKAGAGLAAAIKGGSEAAKEDNKPEKTVFELKLESFDAAGIKRIKEVRSGCTELGLKEAKELVEKTRPAIFKIKGVSKVEEGEIQIEKMKAVGANVLE*

NbL12g13890.1 probable_histone-arginine_methyltransferase_1.3 [MW = 59.13 kDa]

No. of times detected



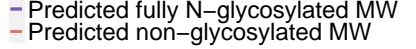
log(intensity)



Values from



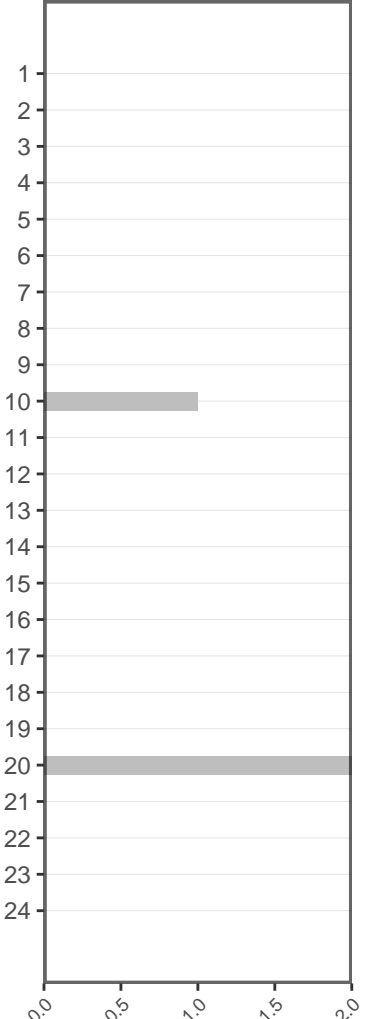
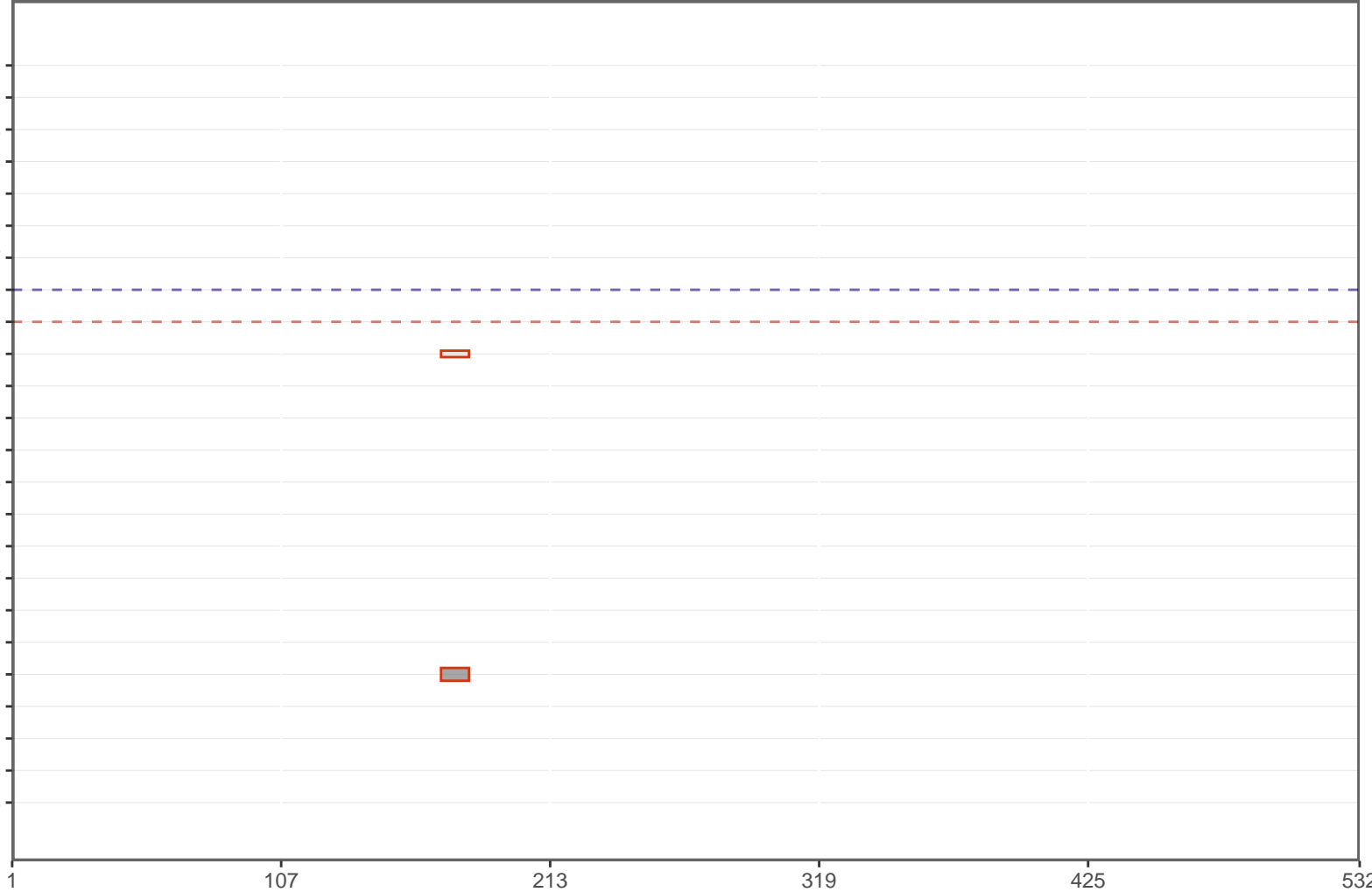
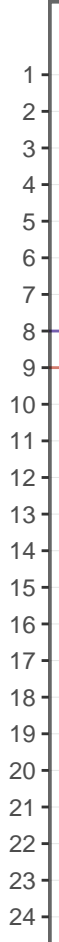
MW indication



Molecular weight



Gel Slice

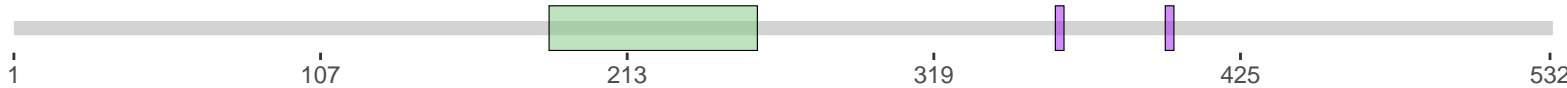


Protein length

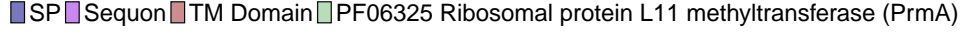


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

CADLSEPMGTLTYNRMLESYVARDRLVNGKMFPTVGRHVAPESEDELYMEIANKAFWGGGQYFGVDTLPLGRSAVEGYFSGPVDAFDPRLLVAPMISHVINFTSKEEDLYEIDPLRFTSSASTRIHGLAGVDFVDFNGSETVPRLLITAPGAPTTTHVQLRVDLGGPLVYMPGQETGGLRLVAHAKGQVTVLFLSATVGLGTSSGKLDLKEPYRMSPQSGYSVADGQGPVQLLQAGDILTQSRDEDEGSPVVGQSPFNSGVALHSL

NbL12g13710.1 induced_stolen_tip_protein_TUB8-like [MW = 20.91 kDa]

No. of times detected



log(intensity)



Values from



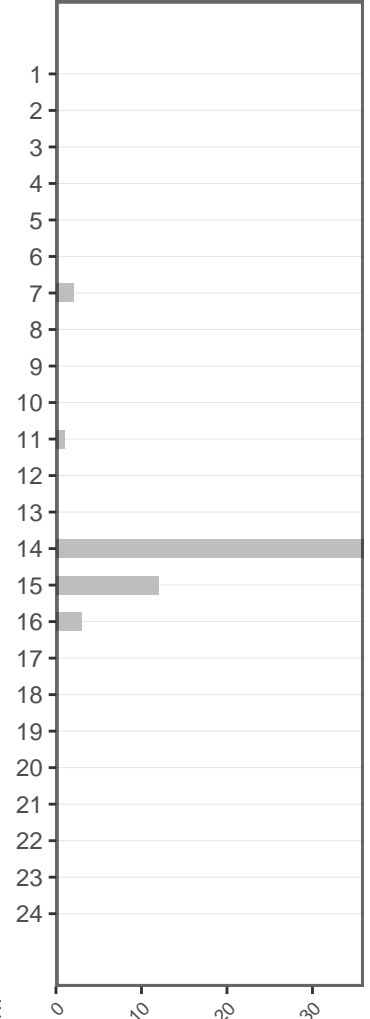
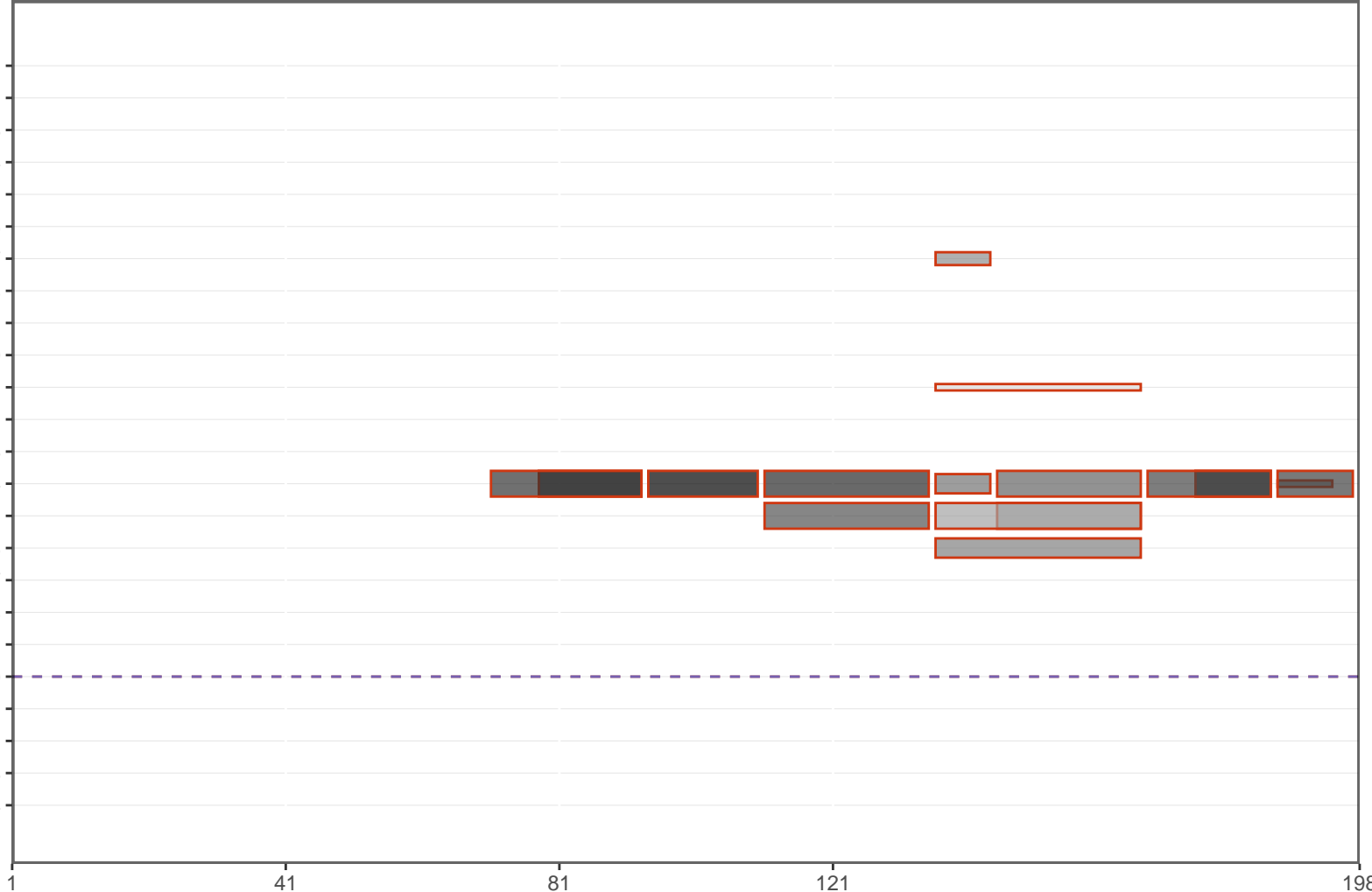
MW indication



Molecular weight



Gel Slice



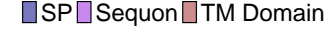
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KEENVAEKVAETTRAEETAPFVEEKAAPAAEYTVAGEEATFVETEARVAKETVAEEAAKAETVTVAAMAVETPVELAEVKTEAEEGKAVETTEAPAANKATTEVPVKEIEE

NbL12g13680.1 60S_ribosomal_protein_L6-like [MW = 27.78 kDa]

No. of times detected



log(intensity)



Values from



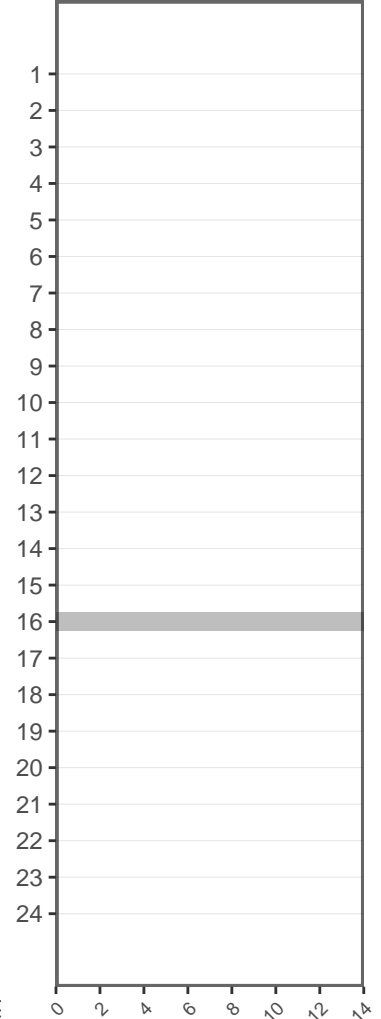
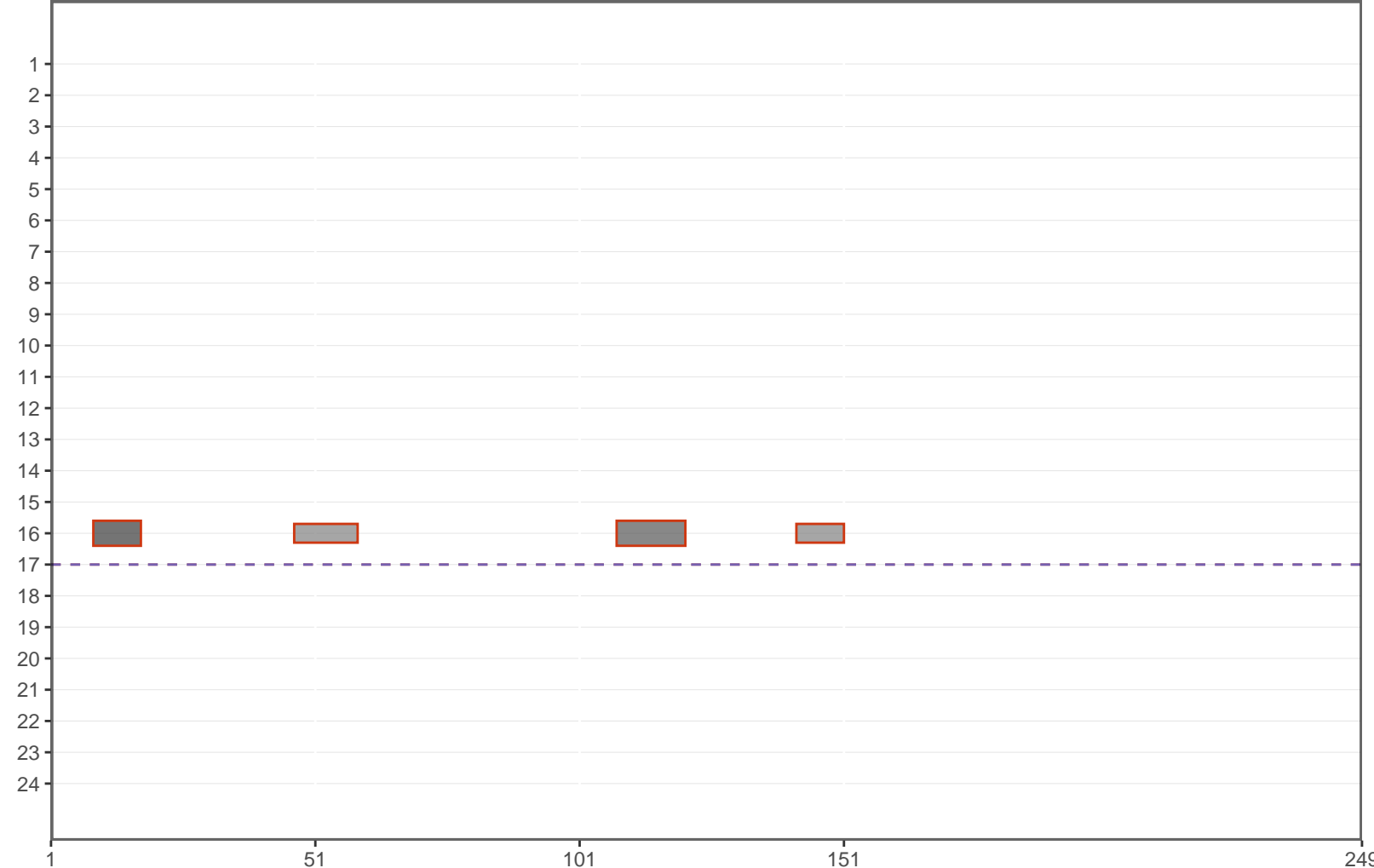
MW indication



Molecular weight



Gel Slice

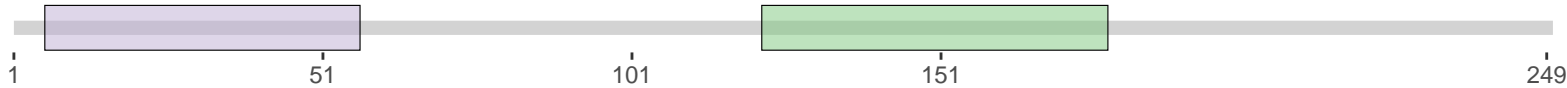


Peptide counts over 4 repeats

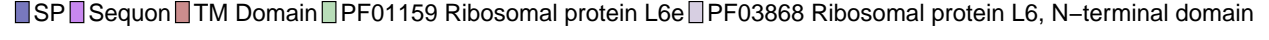
Protein length



Pfam domains



Pfam Description



Protein sequence:

SLLLVGGPKLNGVPLRRVNGAYVGTSTKVDVSGVWVEKFDKVFYAKGVKKGKGGKEEEFFDKKEVWFLHYVGDVYKSKAMGHLYNIGARGHAGGRRRPFQNYLGLFTEVANSLSIEVRLGLCMACAGD

NbL12g13660.1 UTP--glucose-1-phosphate_urydyltransferase-like [MW = 51.91 kDa]

No. of times detected



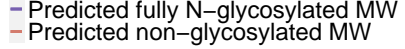
log(intensity)



Values from



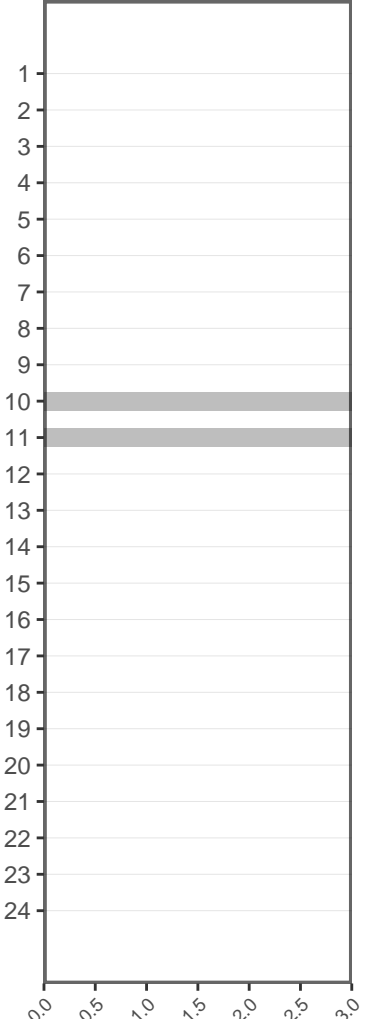
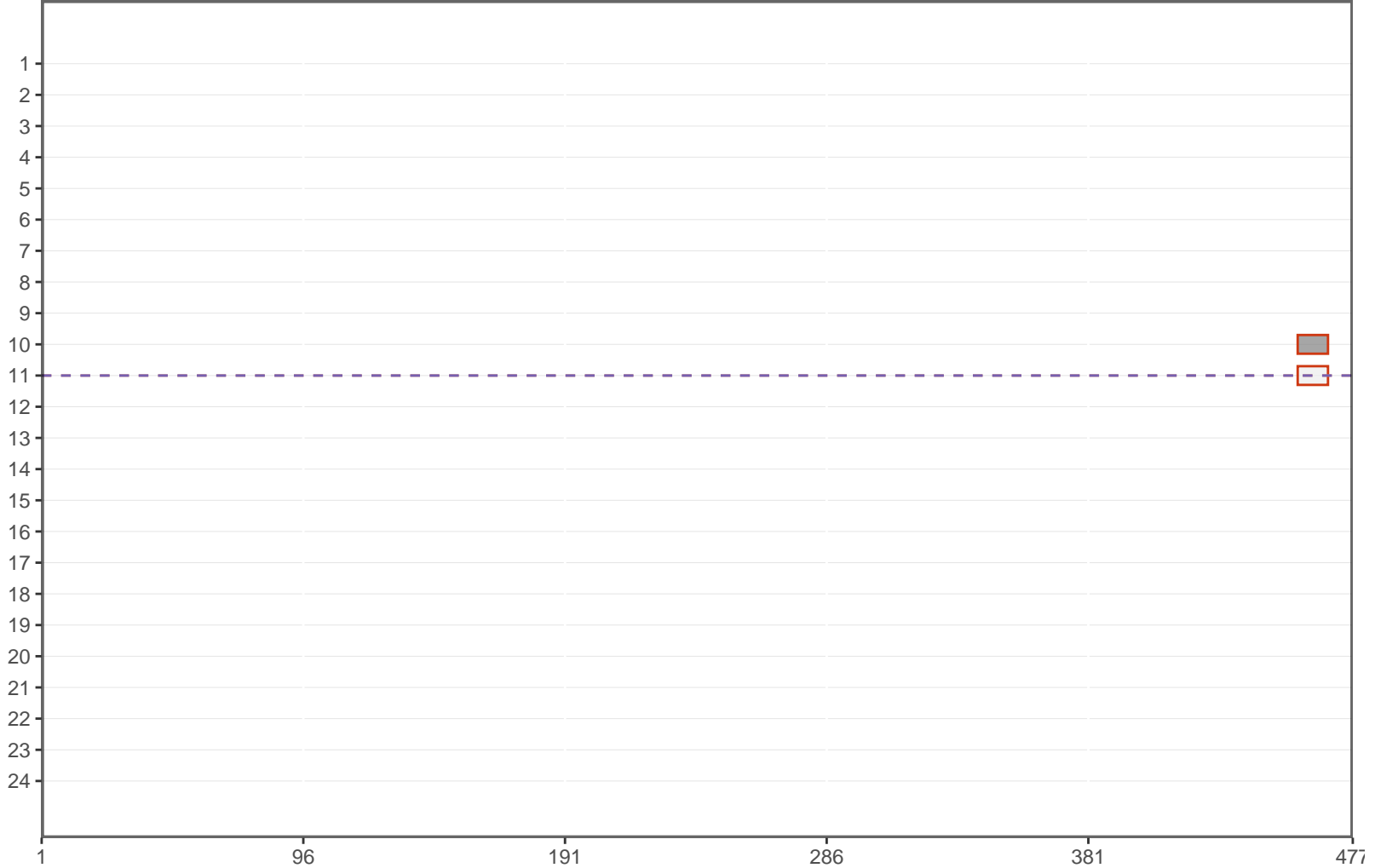
MW indication



Molecular weight



Gel Slice

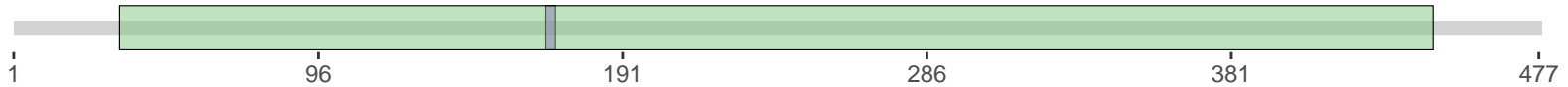


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

FVANSNDLGAIVYDQIKILNHLGKNEVMEVTRKTLADYKGGTUSYVEGKVLLEIAGVDDGHNEFKSIEKRFNFTNLLWNLKAKRRLVEADLKMIEFPNKEVDGKVLGLETAGAARFFDRAGANVPRRFLPKWASSDLLLVQSDNLTLDGGVYIRNPARTNPENPEIELGPEFKKXVNFLSRFKSPISHELDLKVYTGDFYFGAGTLKGVVAAKAGVKLEIPDGAVALANKDNGSPED

NbL12g13650.1 glutamate_decarboxylase-like [MW = 55.96 kDa]

No. of times detected



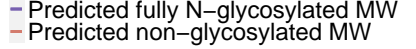
log(intensity)



Values from



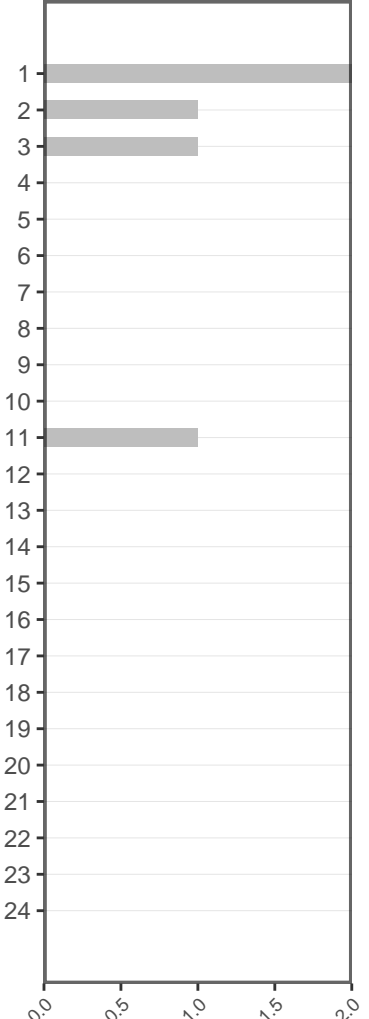
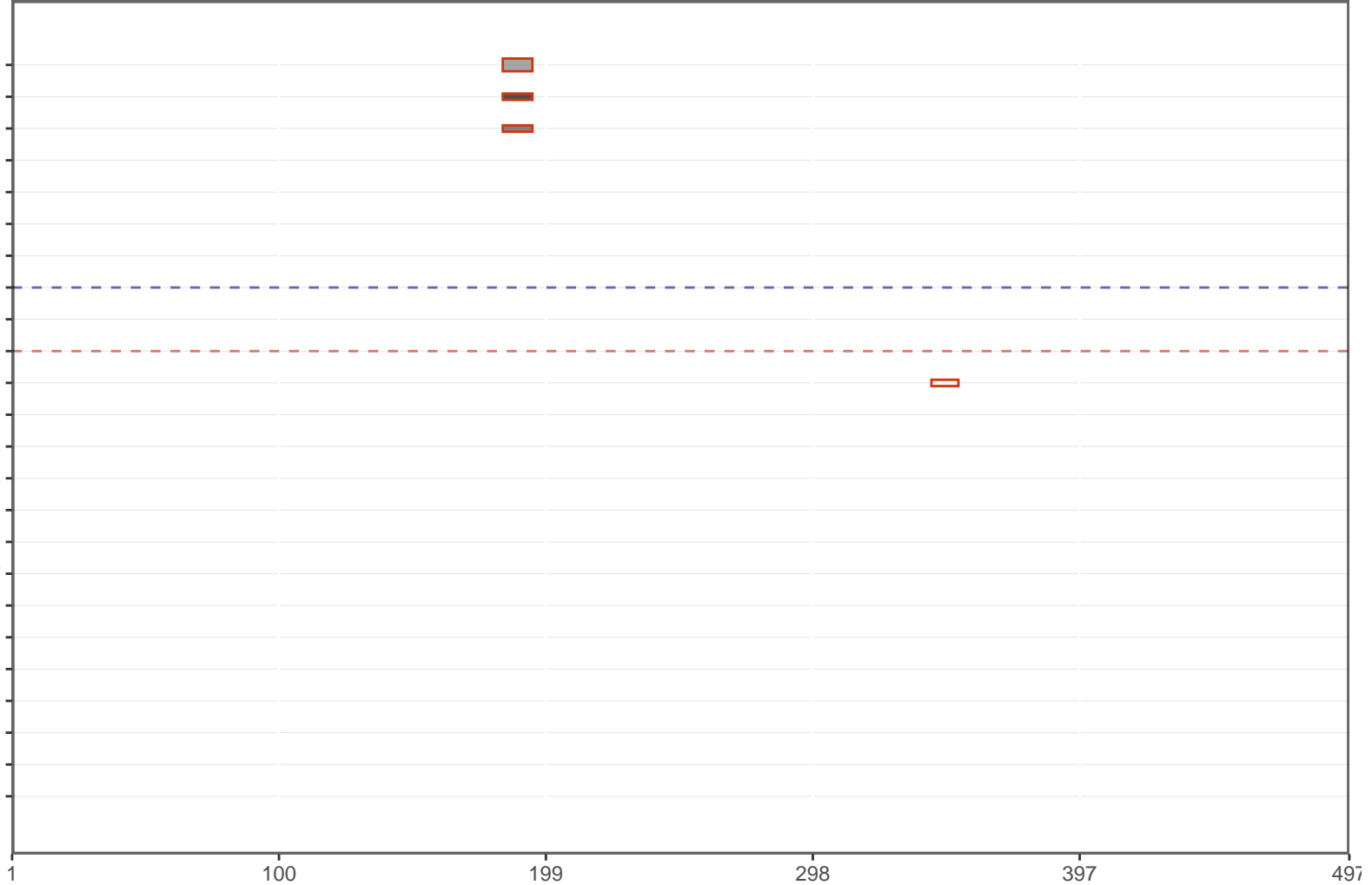
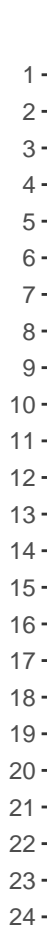
MW indication



Molecular weight

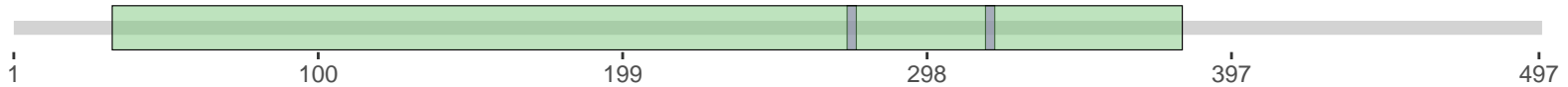


Gel Slice



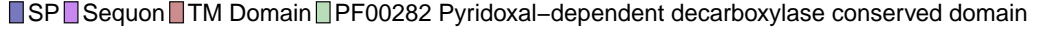
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ETGWDTPHVDAAAGGGIAPFLYPELEWDFRLPLPKSINVSCHKYGIVAGIGWVWRNKEDLPEELFPHNYLGADPTFLNFSKSSGVAGYQDLRLGVGYGRYRNMENGENANRVLEEGLEKTKGFNYSKIGVPLVADSLKDKSKHNEFEVSDHLRRFGWVWPVTPMPPNAEHVTVLRVIVREDFSRTLAERLVADIKVVLHELDSLPARVSAKLAEESSSGVQKKSAMEVQLEITNWWKFFAENKIKTKNVIC

NbL12g13600.1 pre-mRNA-splicing_factor_ISY1_homolog [MW = 35.21 kDa]

No. of times detected



log(intensity)



Values from



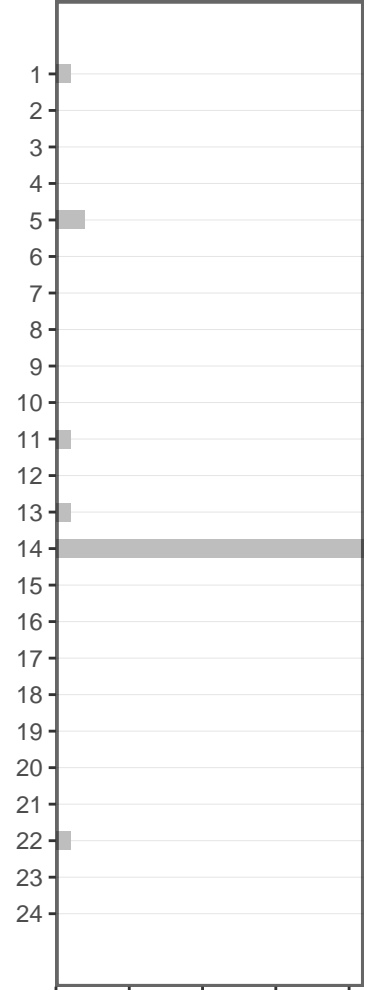
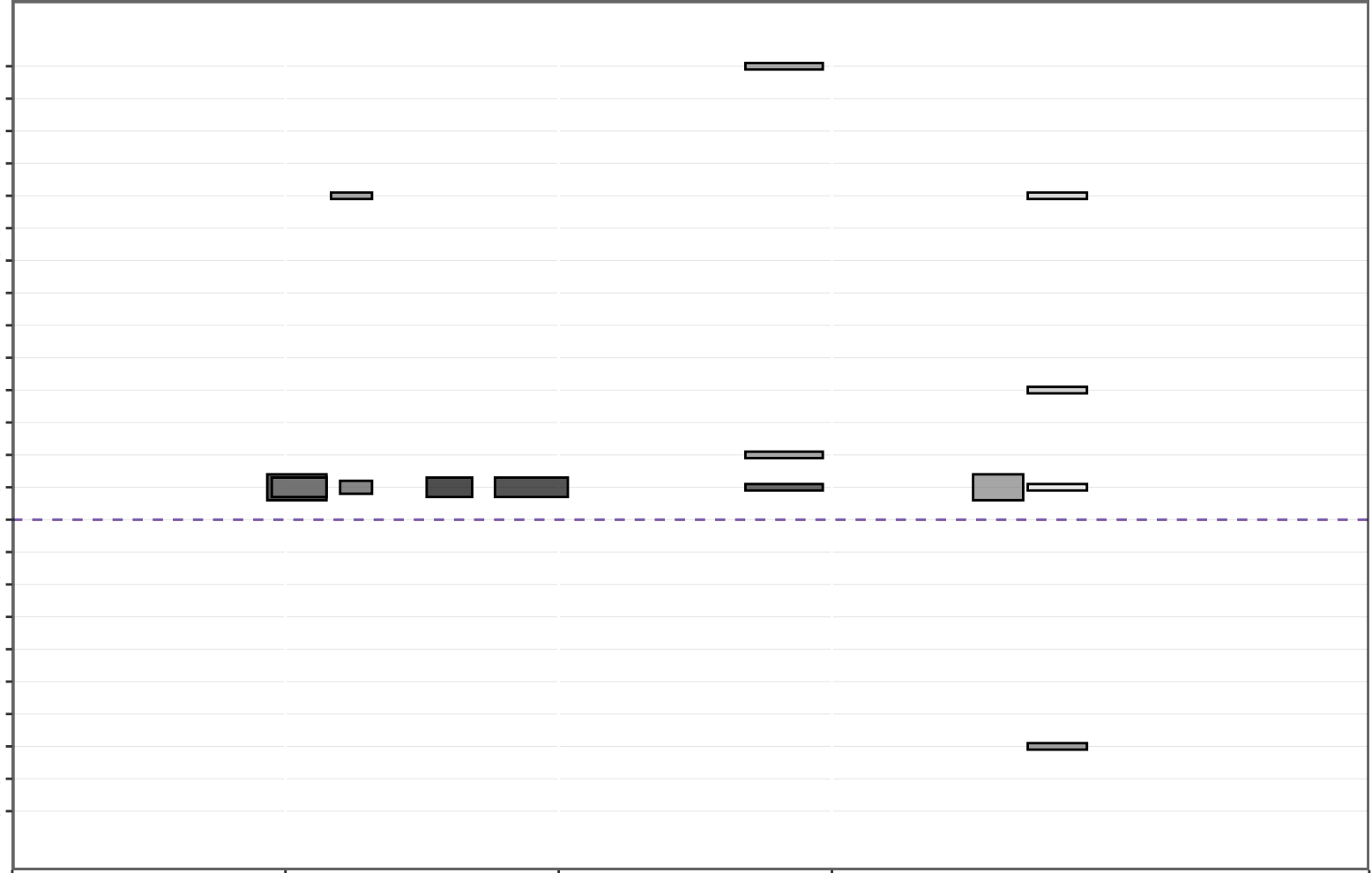
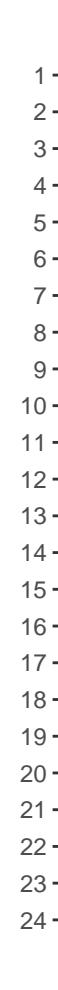
MW indication



Molecular weight

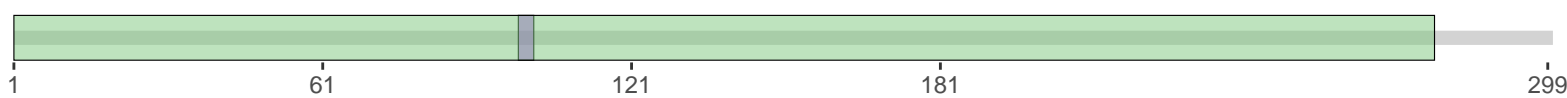


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LPGVRELFEKPELAKRRFRFDYDKRIDASGYGYRDEEDGILEKLEGPAEKMGAAAKKEMEMEEKREARKAVKSGEVEVGLGSKILFEEDDVEIEERROKEREKEKEFEVHHPLPDEKEIEMVDEGKKMELLKSYASEDLMEEGMEAKMLNQR

NbL12g13520.1 HMG-Y-related_protein_A-like [MW = 21.68 kDa]

No. of times detected



log(intensity)



Values from



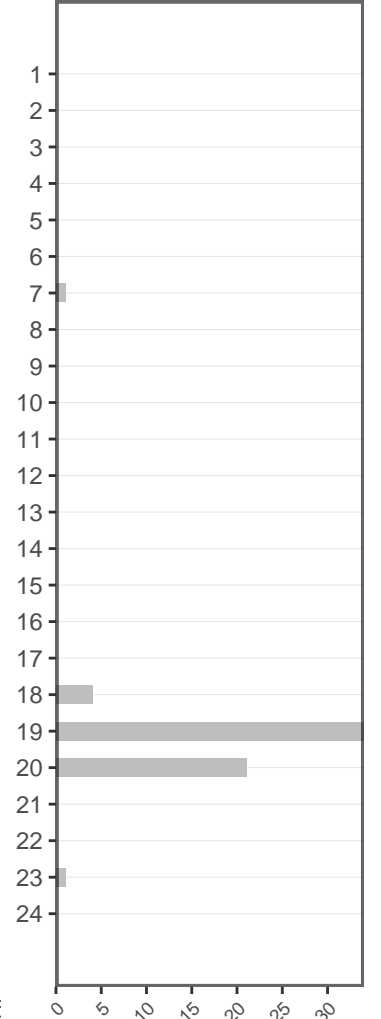
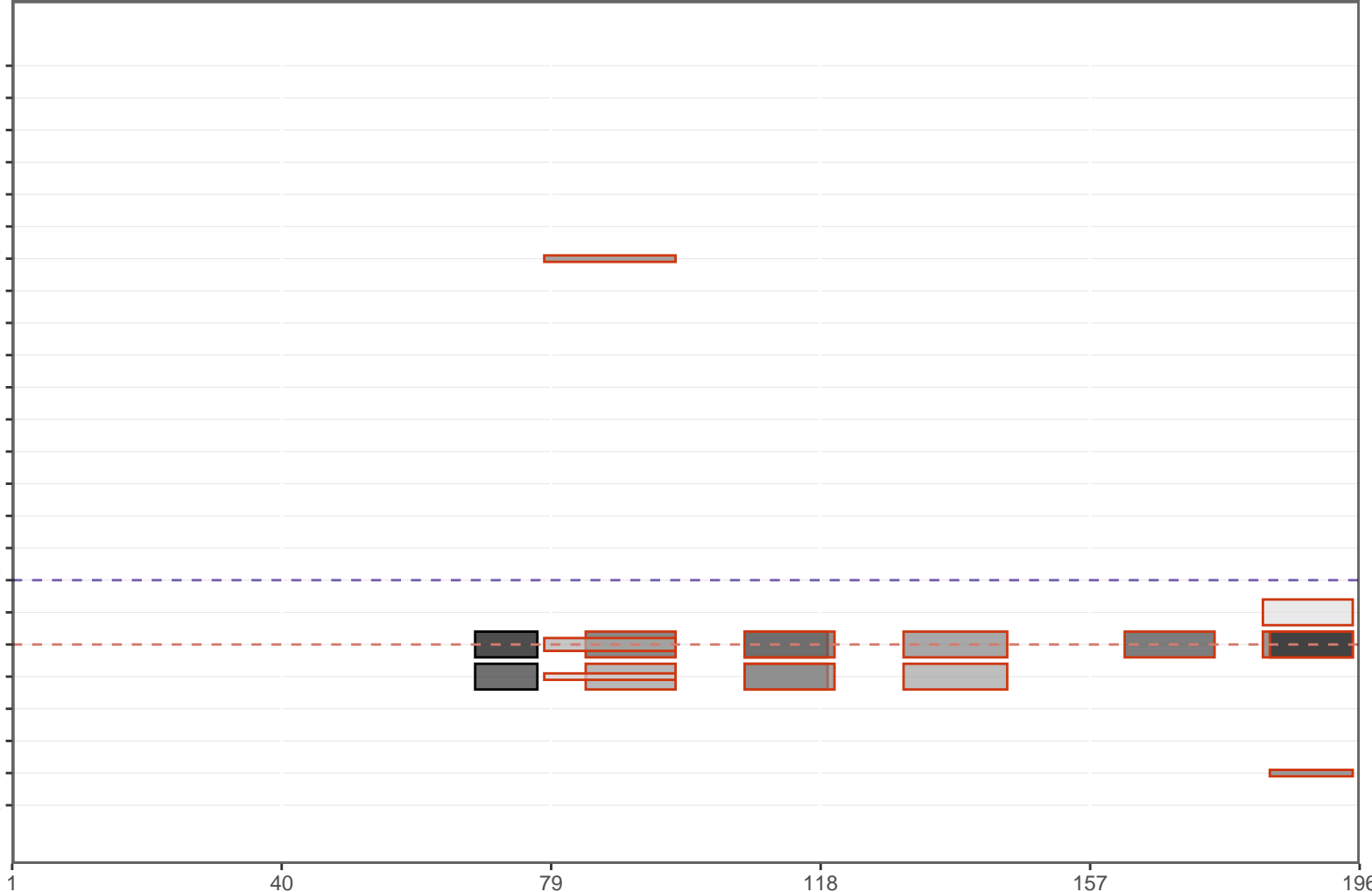
MW indication



Molecular weight

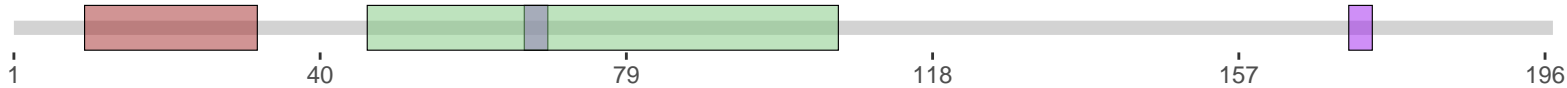


Gel Slice



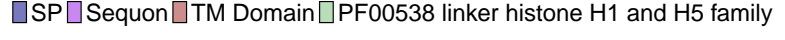
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ERLTLNLDNMKQTGELFLKNNYKPGTDVPOKRRGRGRFRPKFKTLLPPGAESAIEASPRRGRPRKEDNAPFTSKKPKPTAAPNSTGRPRGRPRKVRPQAGDDVEE*

NbL12g13510.1 uncharacterized_LOC104103198 [MW = 49.69 kDa]

No. of times detected



log(intensity)



Values from



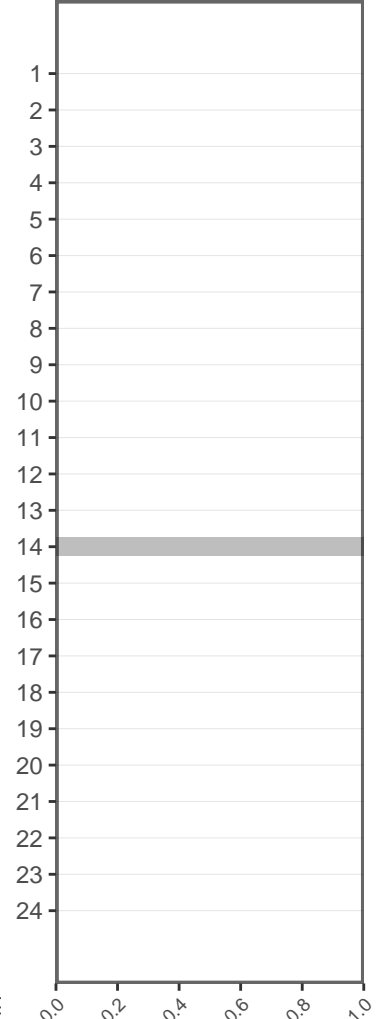
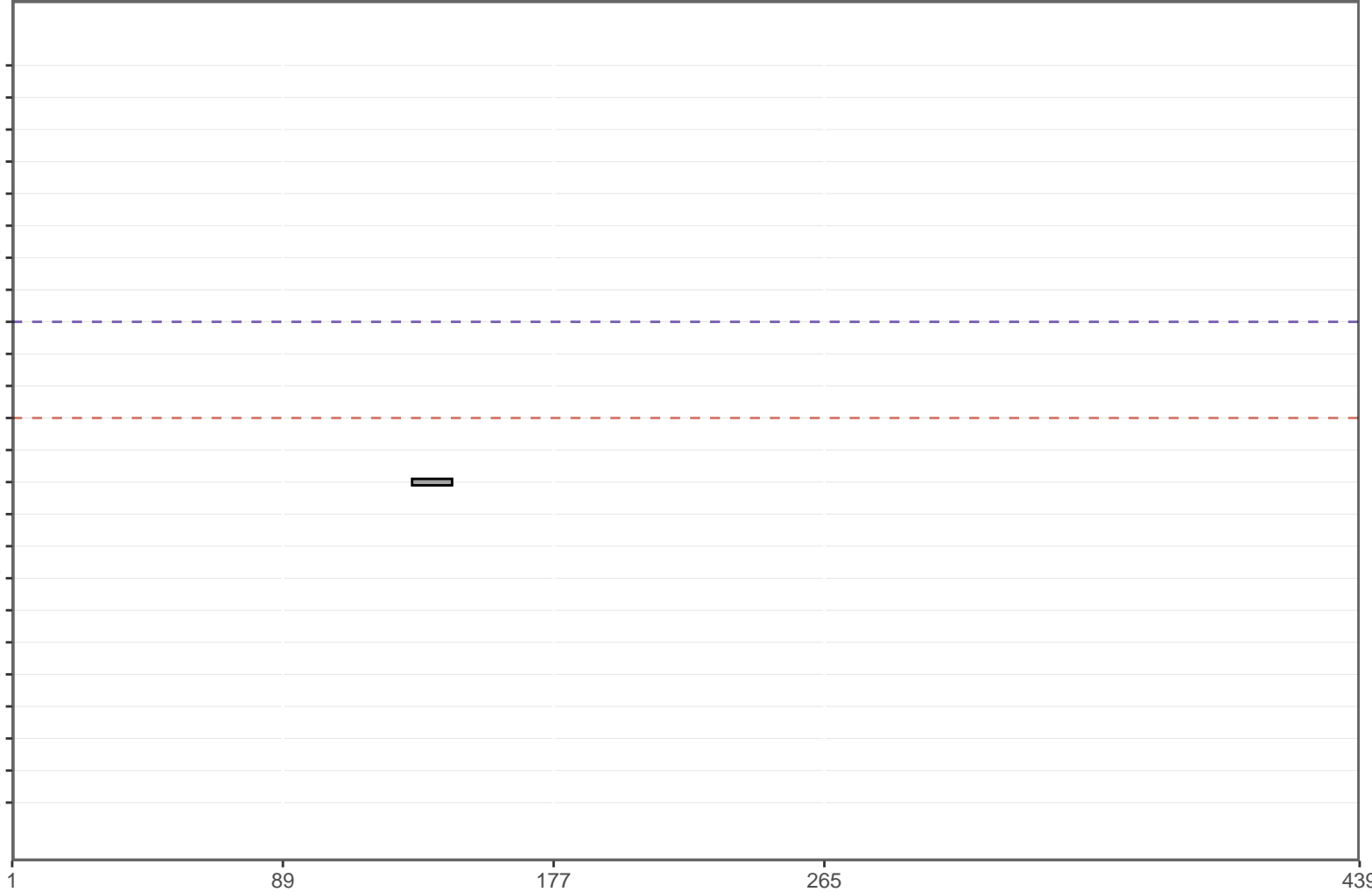
MW indication



Molecular weight



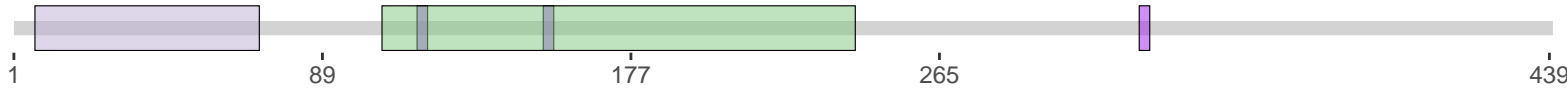
Gel Slice



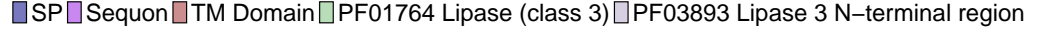
Protein length



Pfam domains



Pfam Description

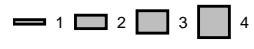


Protein sequence:

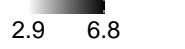
RCYAVAPRMCMSLNLAVKYADHSVVLGGDFLRATPTLEDFKSFGLPLCLFLVGLRDTFPEGRKLGDPRLRYAPGRMYHIVERRFCRGRYPDPVTRAPVVDGRFEHVLGSHNATADHGIIWERESEKALARLKEASAEITTTTPKVPKIERLKTLEKEHKDALERAVSLNFPVAVAEDEEESAESKTEESGGKGEEDAMTNKAGGSDARTNWDVEVVKLFNRDESGK

NbL12g13340.1 NA [MW = 28.57 kDa]

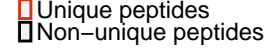
No. of times detected



log(intensity)



Values from



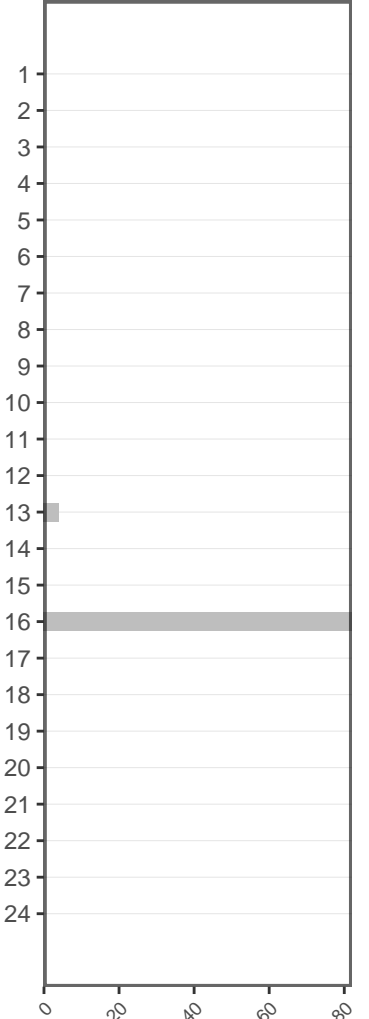
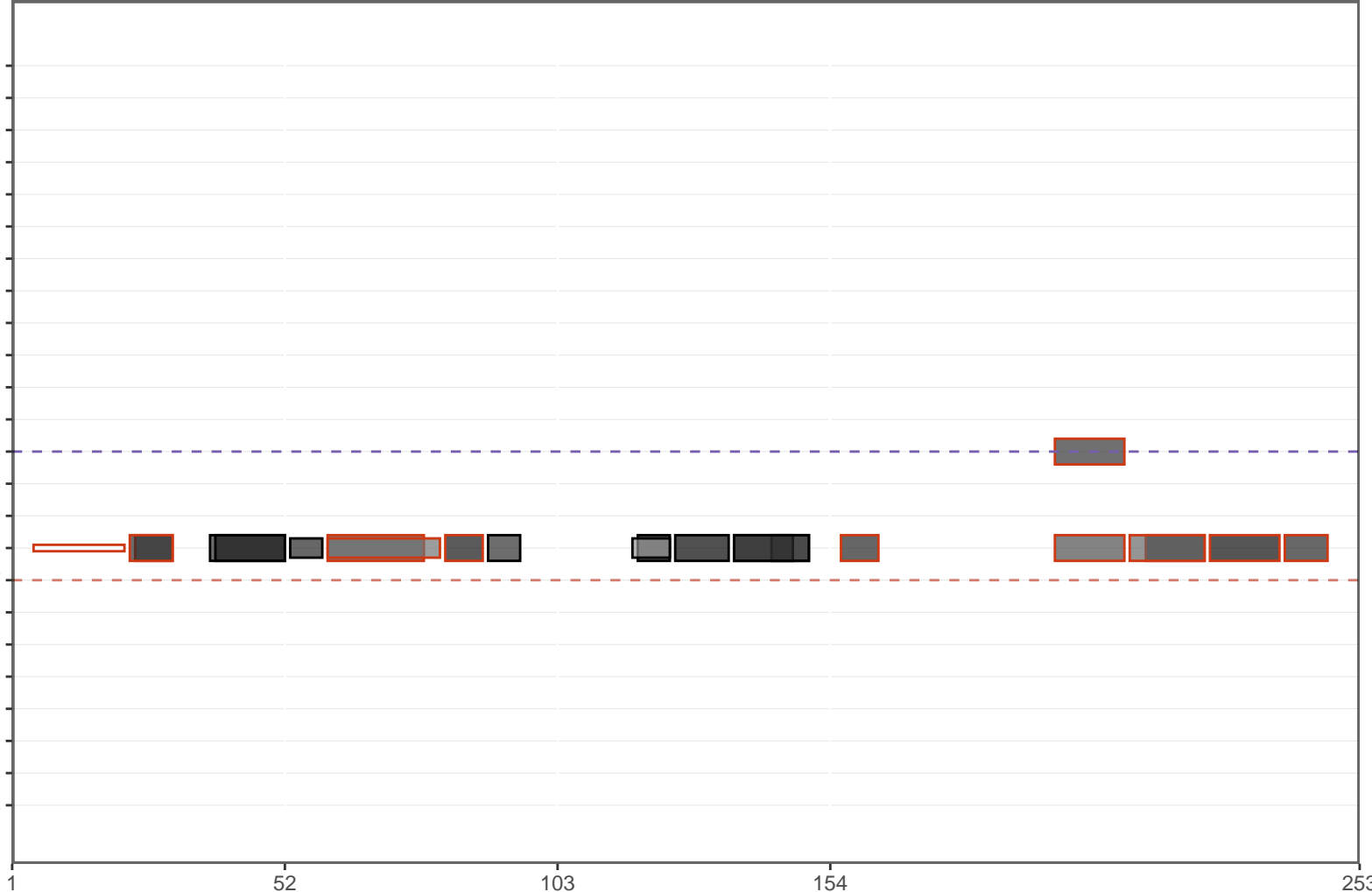
MW indication



Molecular weight



Gel Slice

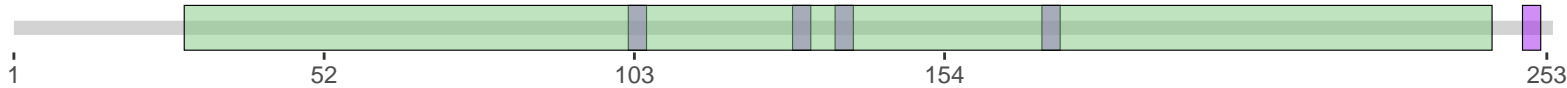


Peptide counts over 4 repeats

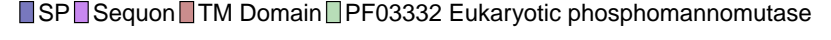
Protein length



Pfam domains



Pfam Description



Protein sequence:

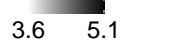
KRQTTIEFRSGMLNVPGRNCSGQERDEFKDYKVVHRRQTMVSLVREKFAHLNITFSIGGGSFDFVPGQWDTYGLRVLEEFNEHFFGDKTYKGGNDHEIYESERTVGHYHTVTSFEDTVKQSGEFLGKNGGSS

NbL12g13270.1 probable_polygalacturonase [MW – SP = 49.72 kDa]

No. of times detected



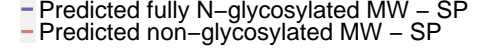
log(intensity)



Values from



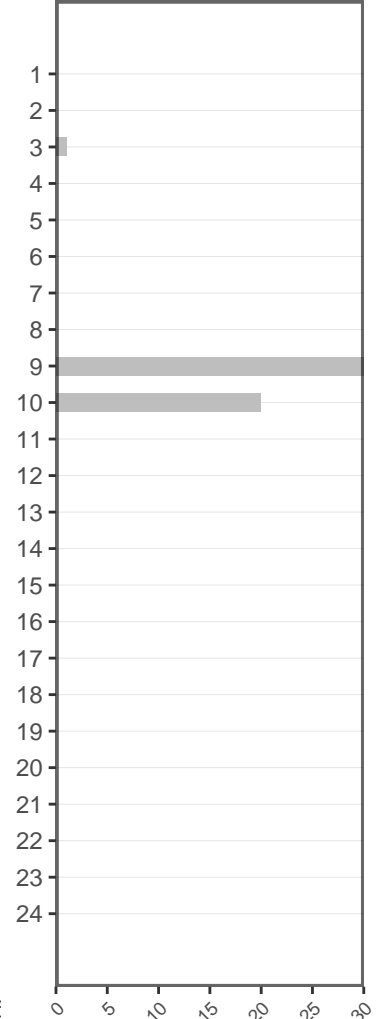
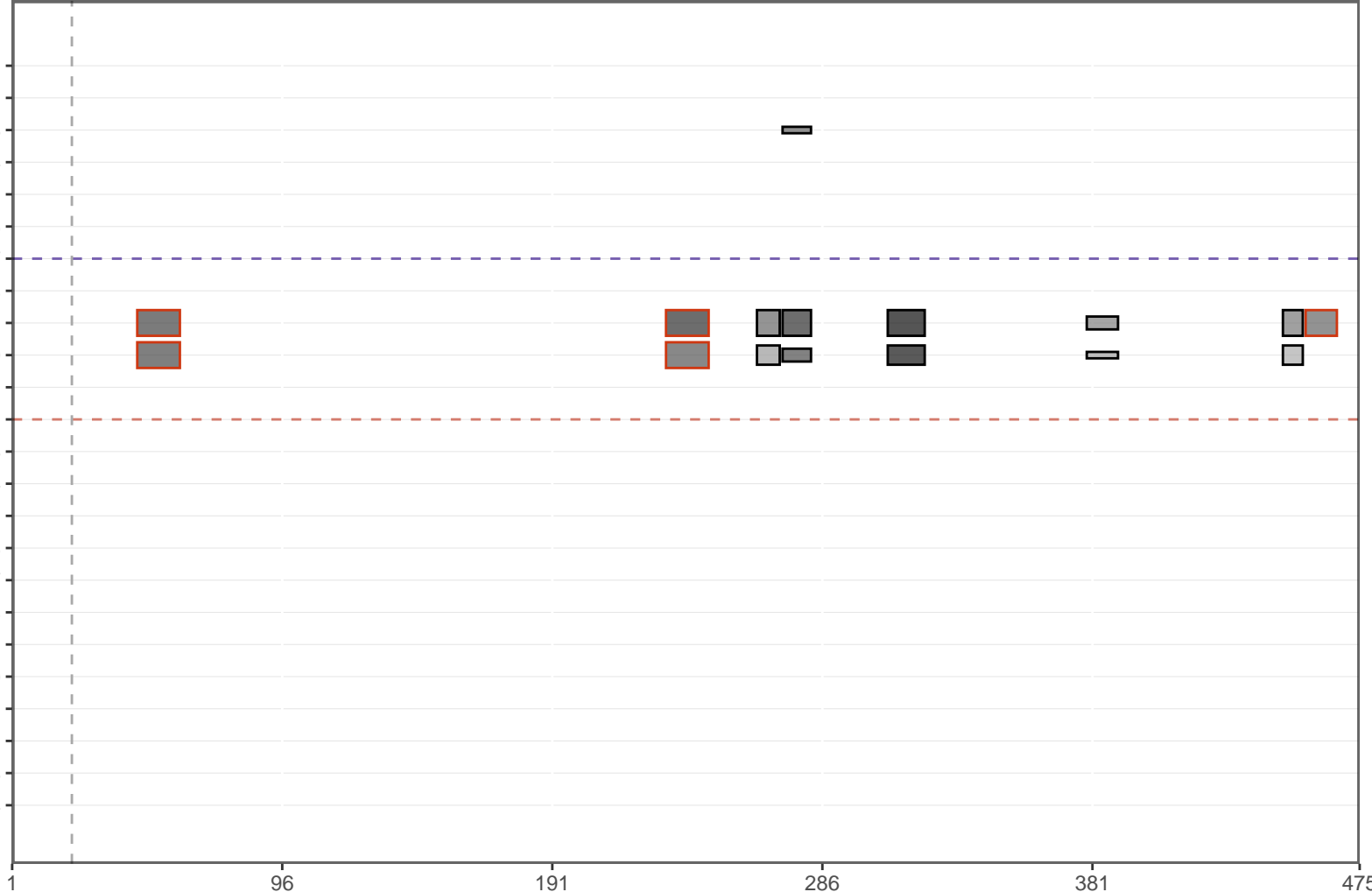
MW indication



Molecular weight

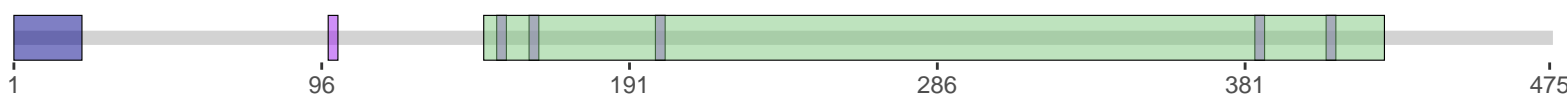


Gel Slice



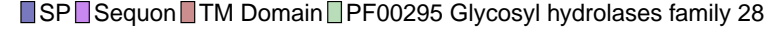
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

*KSPNTDGINPDSGTRLEEDNYVGGDDCVAKKSGWDEYKGYGMPFGSLVIRRLTGISPSAAIALGSEMSGGHDIRAEDITANTESGVRKTAVGRGDFVKDYVYKGMTHLTKMKVFWMTGNVYGHADTHWDPNALPEKGINRYDVAENVSMARLEGISGDPFTGICMSNVTSIMAKKANKYPTWCTDIEGITSGVQPPPPOLLPDGQPEKSEMCGDFRENLPIDNIEMDRGSEYRLNY

NbL12g13260.1 mitogen-activated_protein_kinase_homolog_MMK2-like [MW = 42.94 kDa]

No. of times detected



log(intensity)



Values from



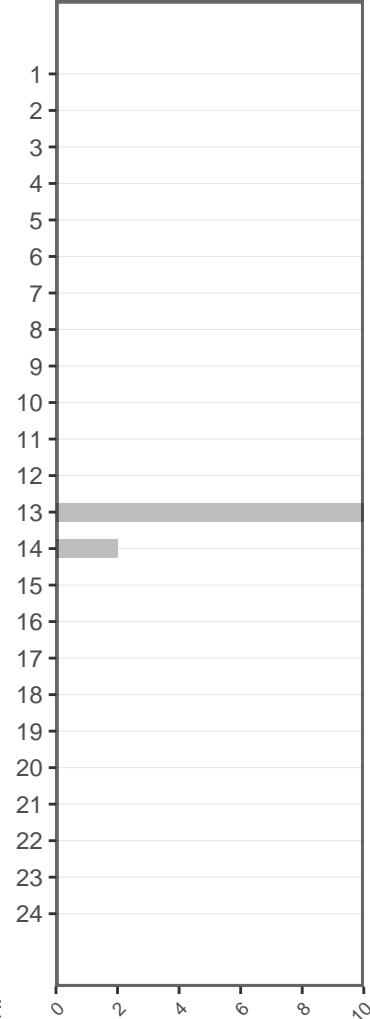
MW indication



Molecular weight



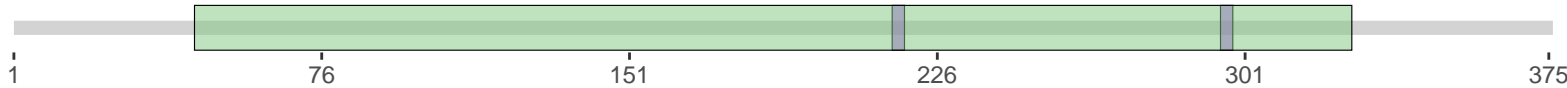
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

/NAKCDLKGDFGLARITTTETDFMMEVGVTRWYRAPELLNNGSEYTSADIDWVSGIGLGEITROPFLFGRDYYHQLRUFELIGSPDDASLGLFRSNRRYVYRQLPRVYRQGFARFNFNSPRAVDLEKMLIFDPSRRITVDEALSHPLYLAPLHDNNEEPVGRPFSLDFEGRFTENKELIWRFAWVFNPDTH

NbL12g12910.1 cyclic_pyranopterin_monophosphate_synthase_mitochondrial [MW = 25.05 kDa]

No. of times detected



log(intensity)



Values from



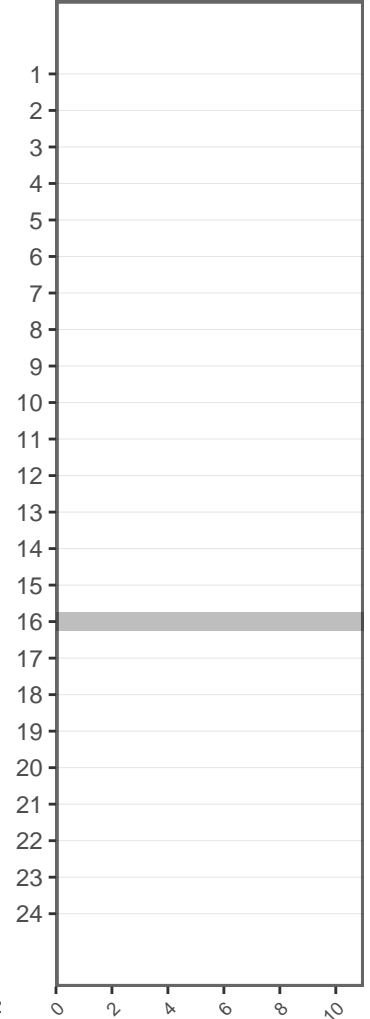
MW indication



Molecular weight

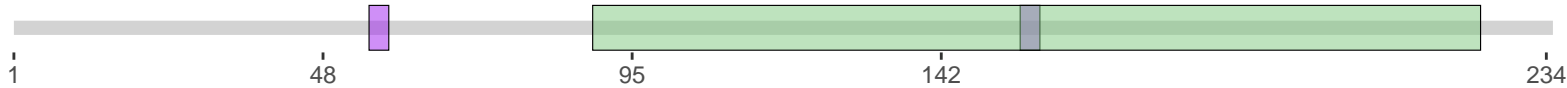


Gel Slice



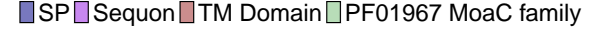
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

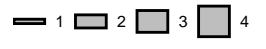


Protein sequence:

AHGKYLGRVFDLVSANQMGKGDVLEVAKLAGICGAKQTSNLPFGHNINLTHRVVDLALNPHDFVSEIEGGAASDGKTVEMEAALTAVTAVGLTVYDMOKAASKYVIGTDIRLERKTKGKSGDWSRDK*

NbL12g12750.1 transketolase_chloroplastic-like [MW = 79.79 kDa]

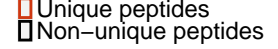
No. of times detected



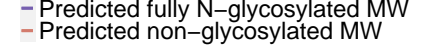
log(intensity)



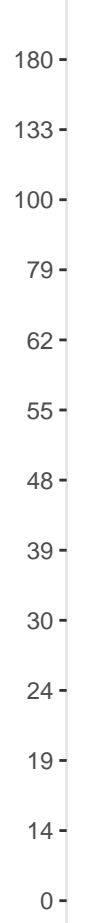
Values from



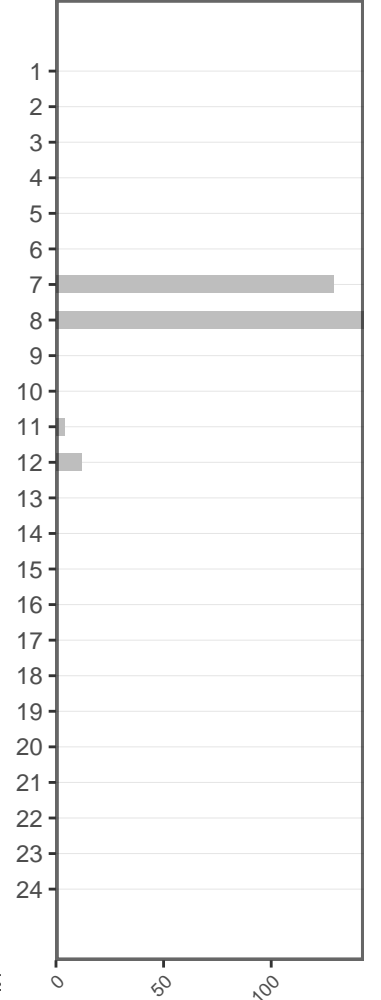
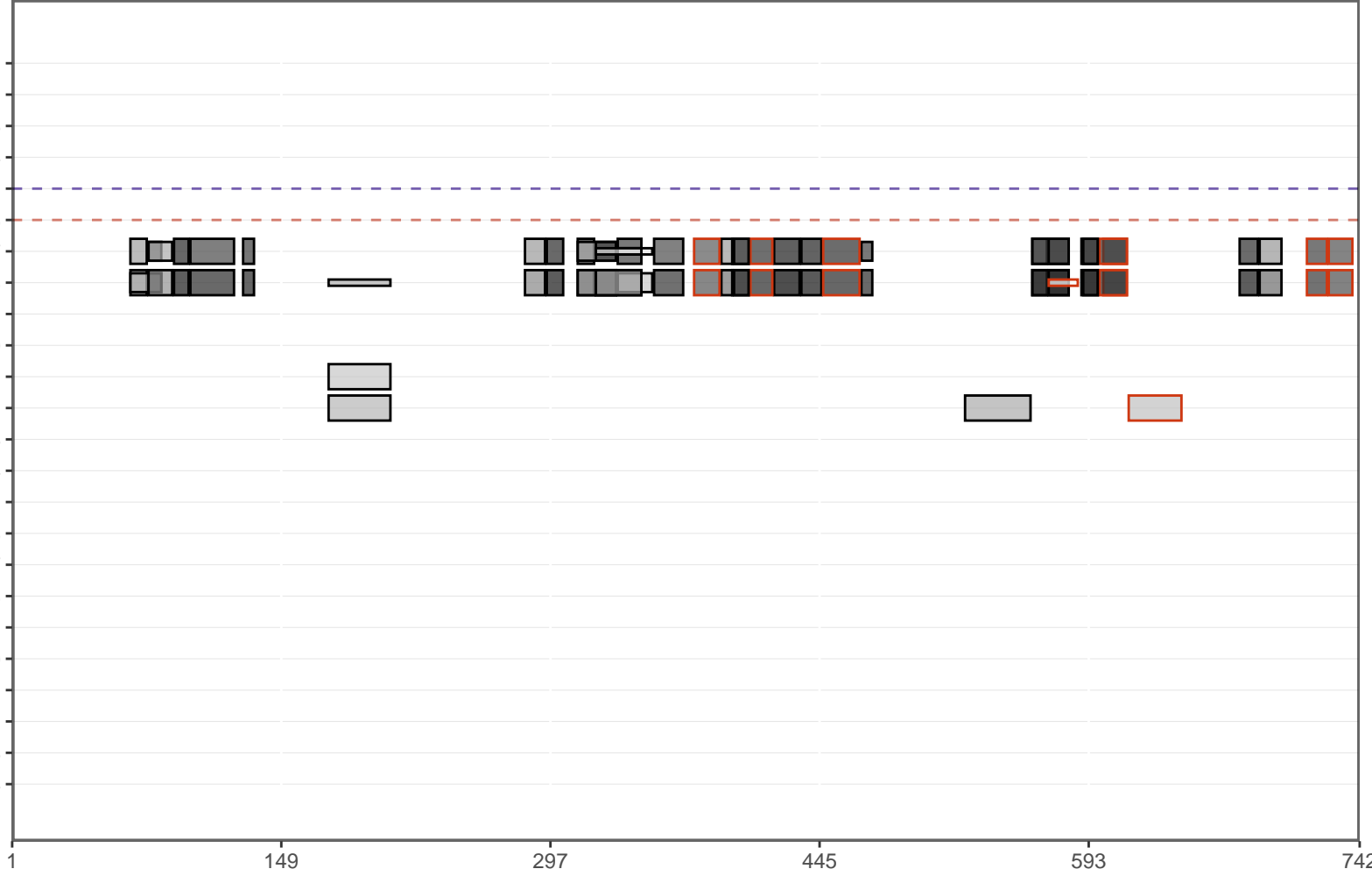
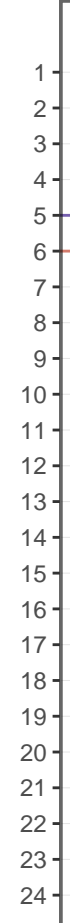
MW indication



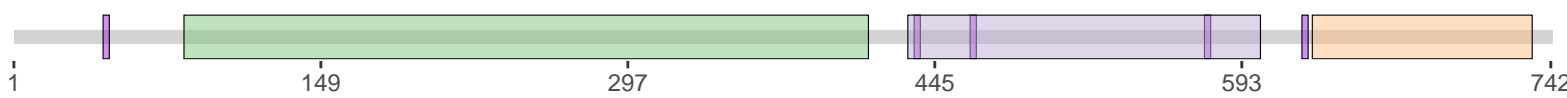
Molecular weight



Gel Slice

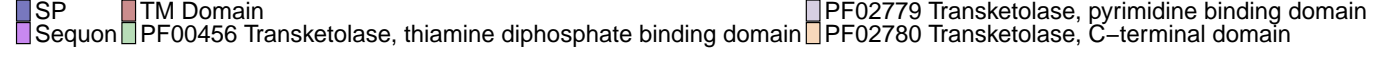


Protein length



Pfam domains

Pfam Description



Protein sequence:

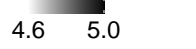
WVYEPFIVPEDVKGHWRSRHPGGALEVGVWNTKFAEYKYPPEAAELKRFITGELTAGWEKALPTFTPEPADATRNLSGGNLSNALAKVLPGLFGGADLASNNMLMMFGDFGKNTPEERNLRFQREHGMGAICAGIALHSPGLIPYCATFFVFDYMRGAMRISALEAGVIVVMTDSDGLGEGDPTHPDIEHLAIFRAMFNLMFRPADGNETAGAYKVAVLRKRTPELALSRQKLPQLAGSSIEGAANKGCYILSDNSGKPKVILHGTGEELEIAKAADELRI

NbL12g12650.1 protein_transport_protein_Sec61_subunit_beta-like [MW = 12.77 kDa]

No. of times detected



log(intensity)



Values from



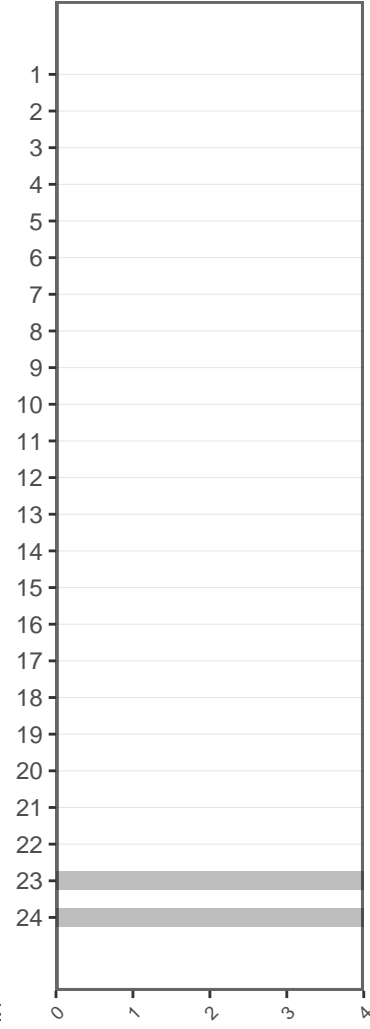
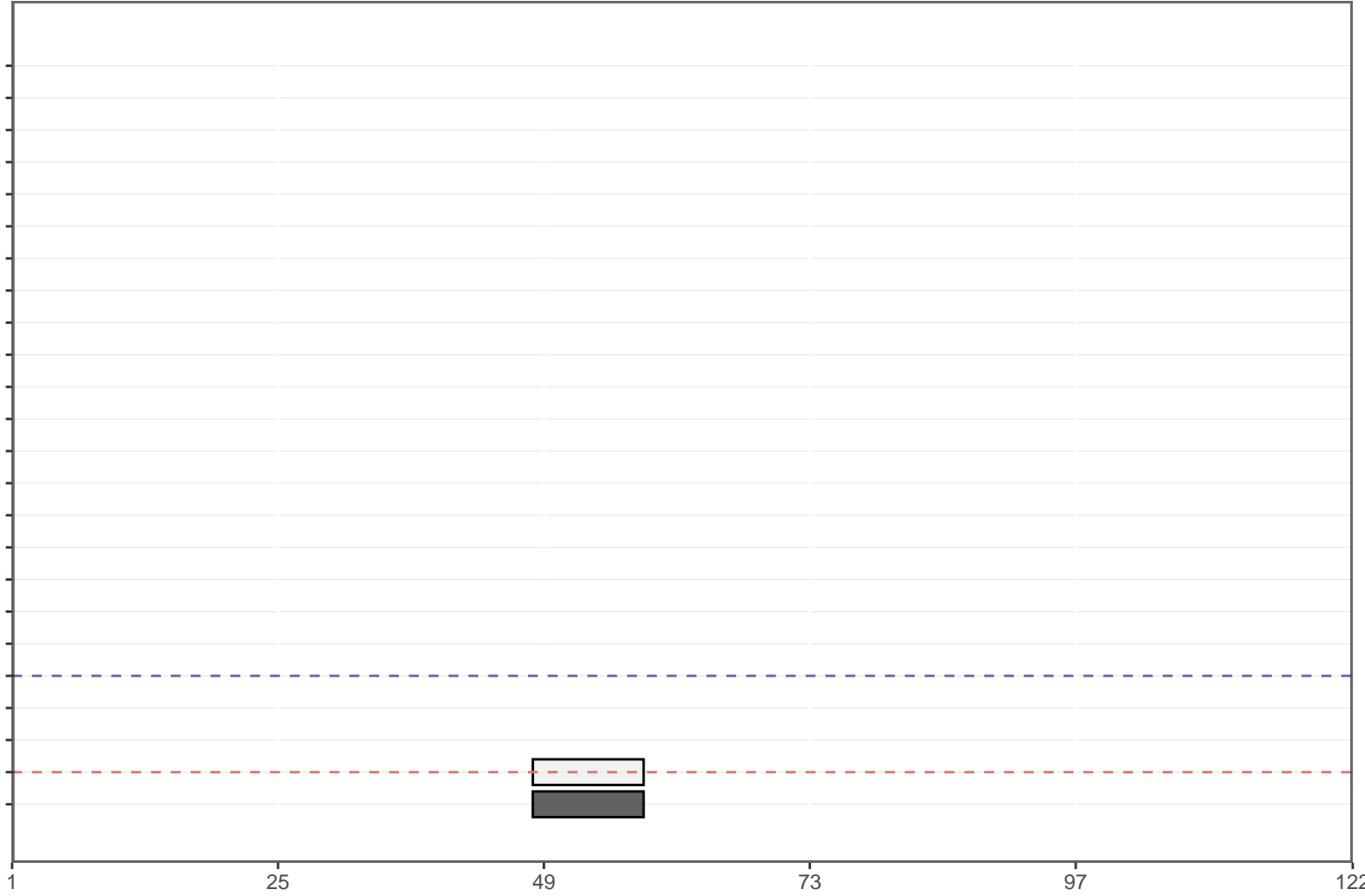
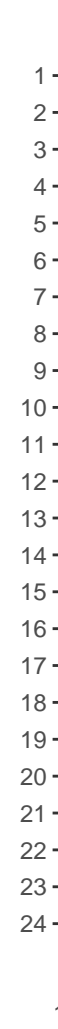
MW indication



Molecular weight

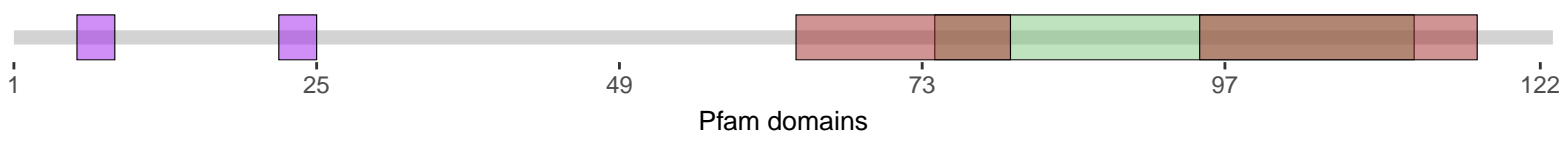


Gel Slice



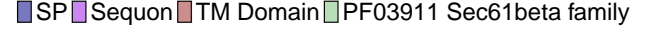
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

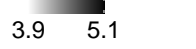
STAAAAANLRRRKTAGGSAAGGAGGNMLGFYDSDPLKISFNVALVMSIGFAFVALHVMKGLFYRREA*

NbL12g12610.1 uncharacterized_LOC109212372 [MW = 28.38 kDa]

No. of times detected



log(intensity)



Values from



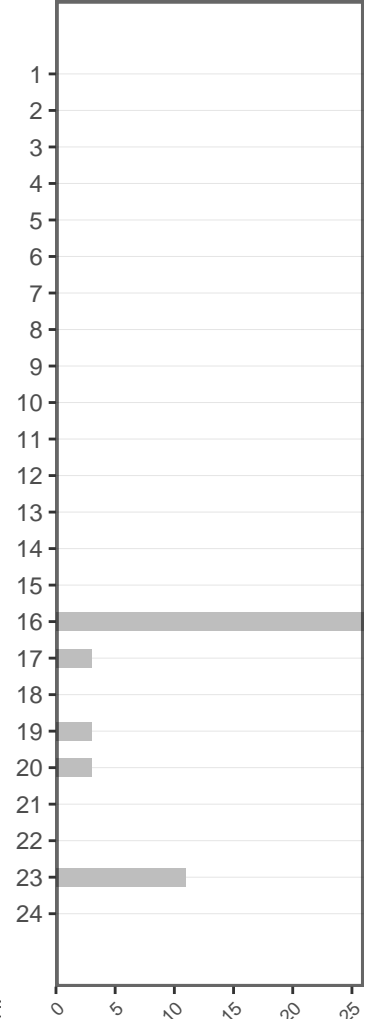
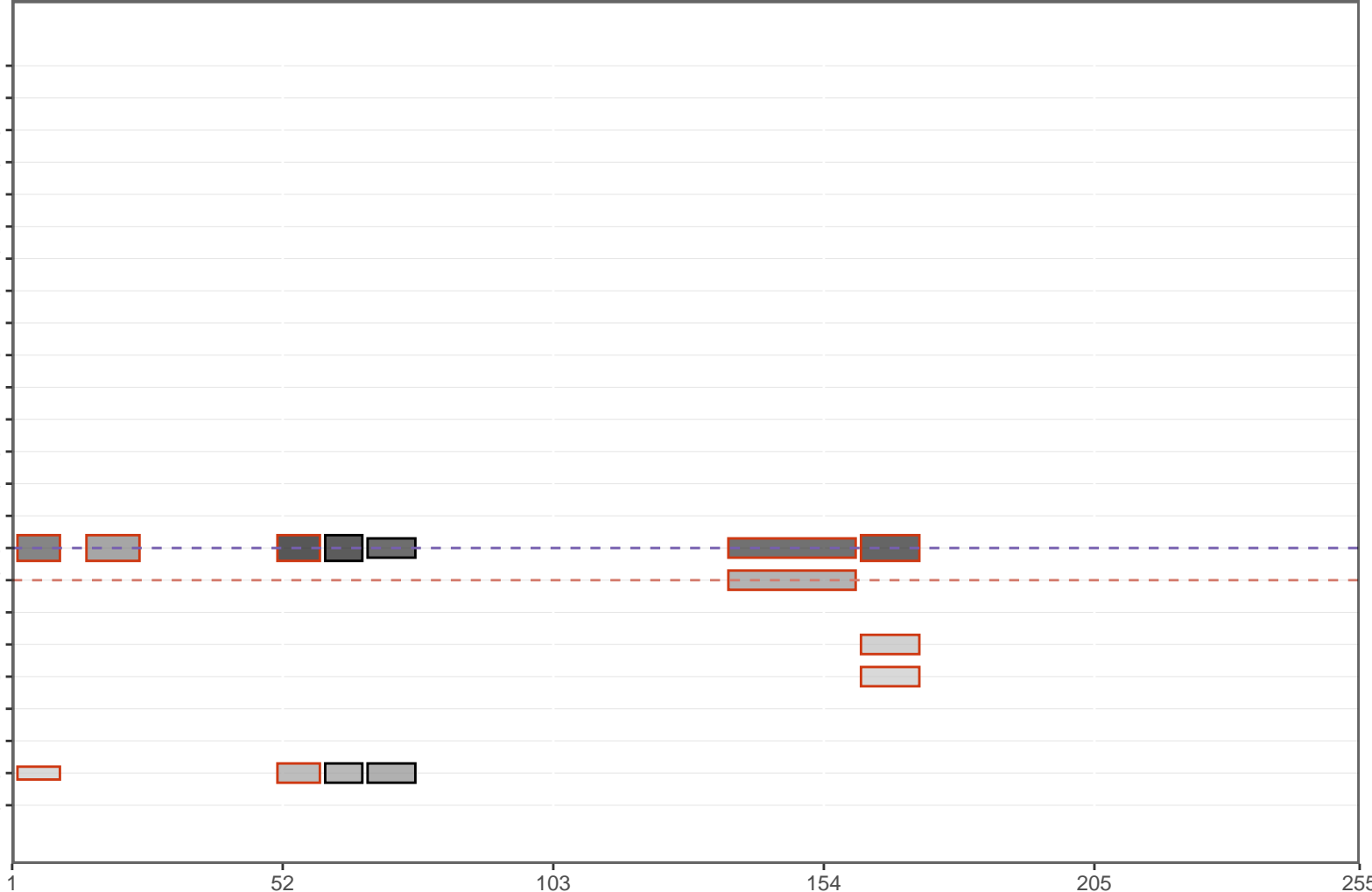
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LCLEMLNLVARSNSAPKDDGDFKFSIGYEAEIPLAGTVDHTVEPVYQKLPWQETLDGARARYVEVVKALADKYPSENLLVTHSGEGVGSFFTELKNDATLVEVYGGHVLAKRSIQDFGNSFTAGEPEVYKGTGLSAK

NbL12g12590.1 60S_ribosomal_protein_L27-like [MW = 17.9 kDa]

No. of times detected



log(intensity)



Values from



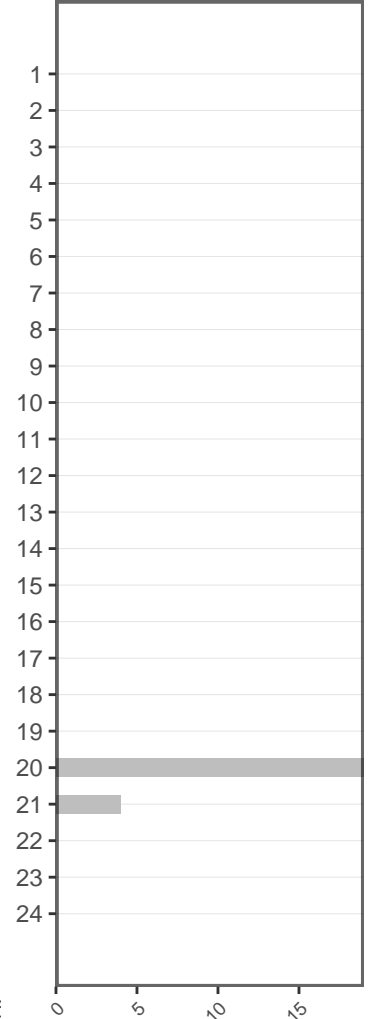
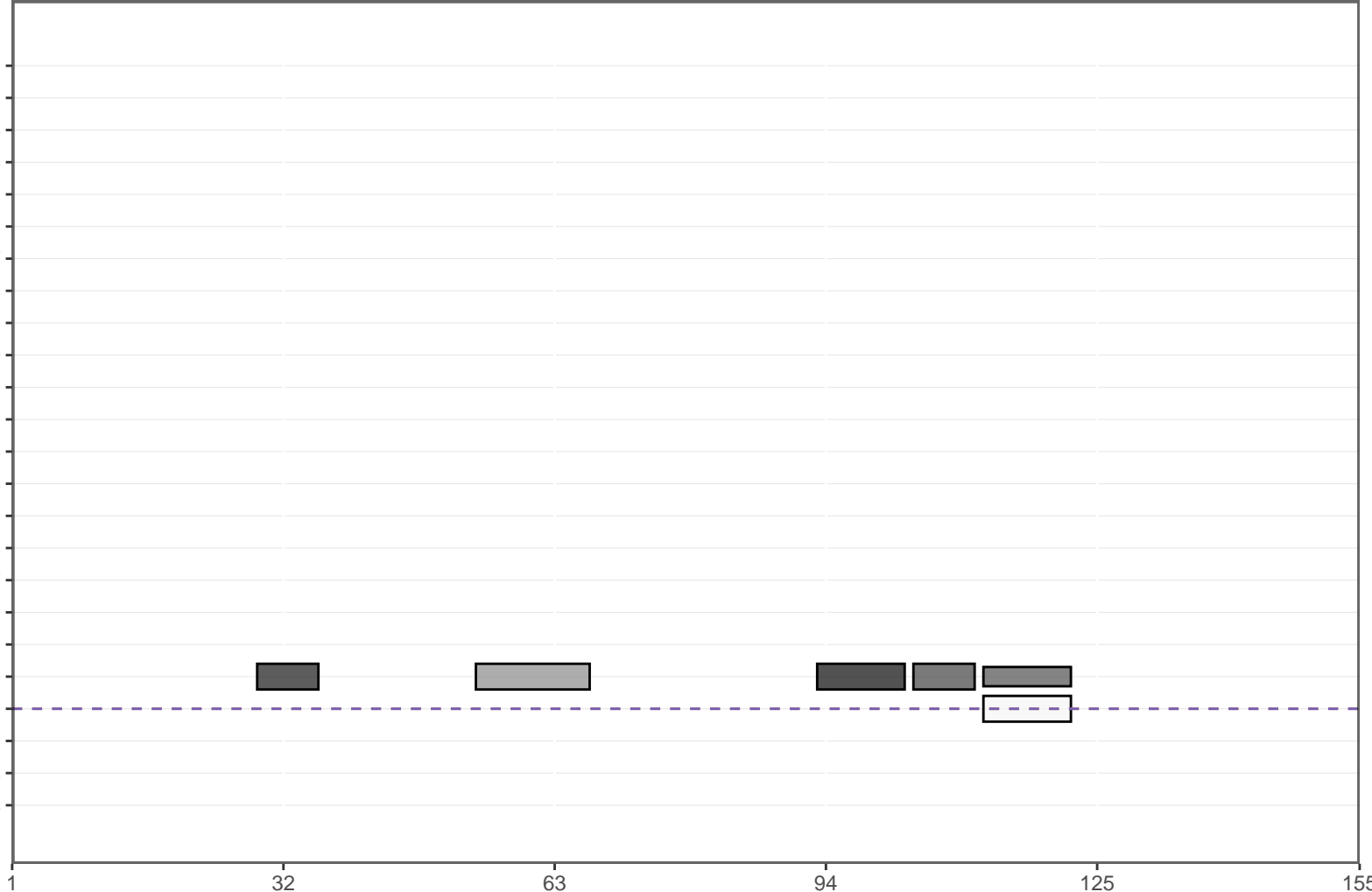
MW indication



Molecular weight

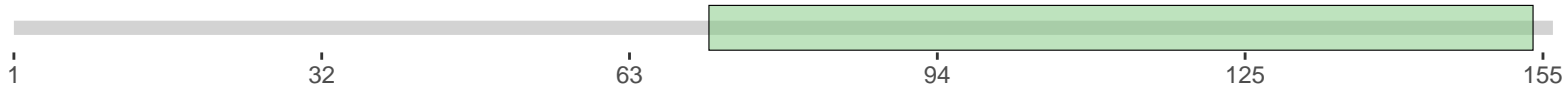


Gel Slice



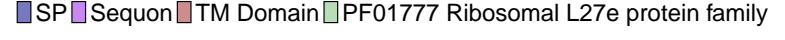
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

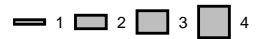


Protein sequence:

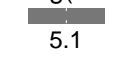
ISKYPQKIVRKDSSAKKGAKKSRVAFKILVNVNIMPTRYTLDDVLDKDVNVVLDVLSRDKKVTAKEAKARLEERFKTGKNRWFFTKLRP

NbL12g12520.1 nucleoside_diphosphate_kinase_1-like [MW = 15.71 kDa]

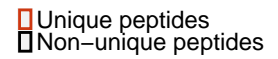
No. of times detected



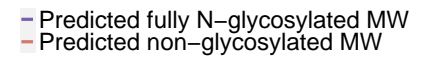
log(intensity)



Values from



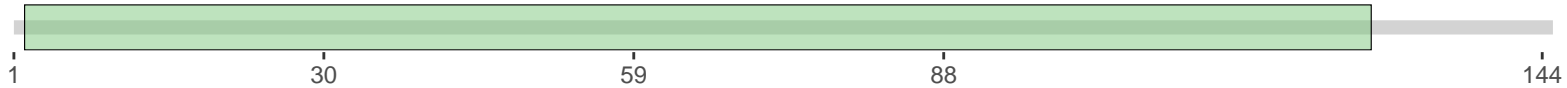
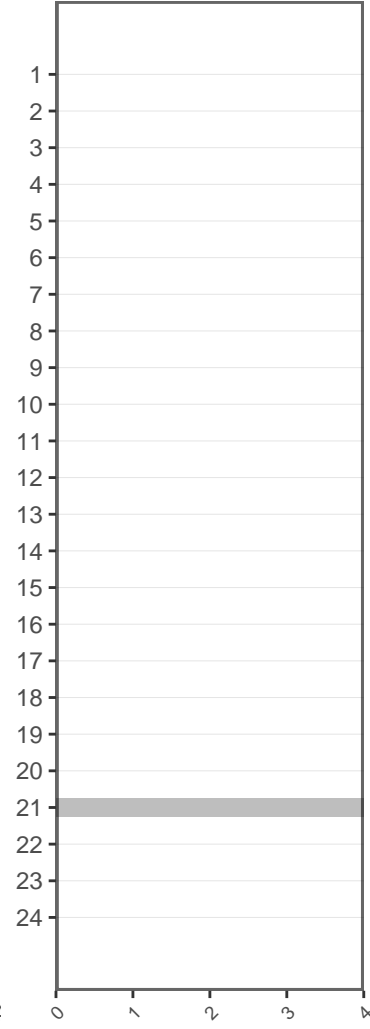
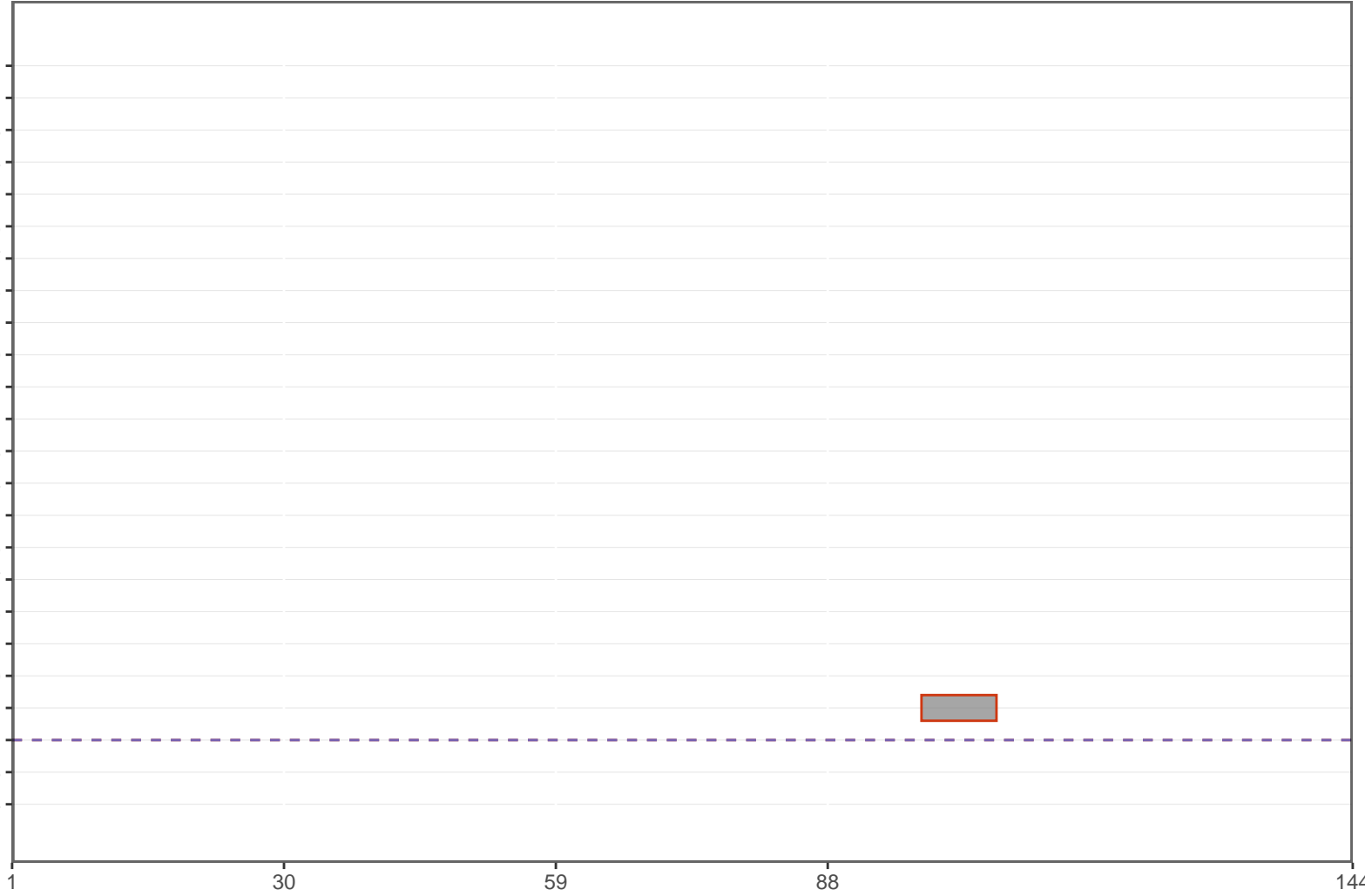
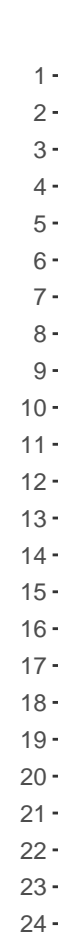
MW indication



Molecular weight

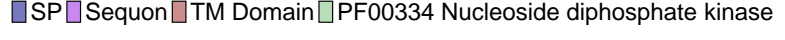


Gel Slice



Pfam domains

Pfam Description

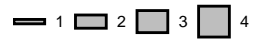


Protein sequence:

TVSGPVAMVRAKGGVSTGRKIGKATNPLESAAGTIRGDVSDIGRNVIHGSDVESAKKEIALWFFEGVYQWQGSLSHWIYE*

NbL12g12390.1 protein_transport_protein_SEC23-like [MW = 85.26 kDa]

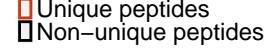
No. of times detected



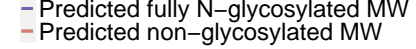
log(intensity)



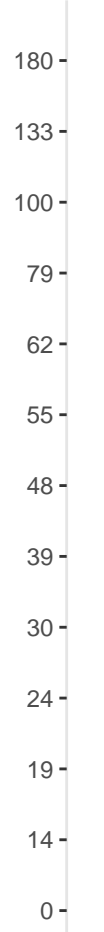
Values from



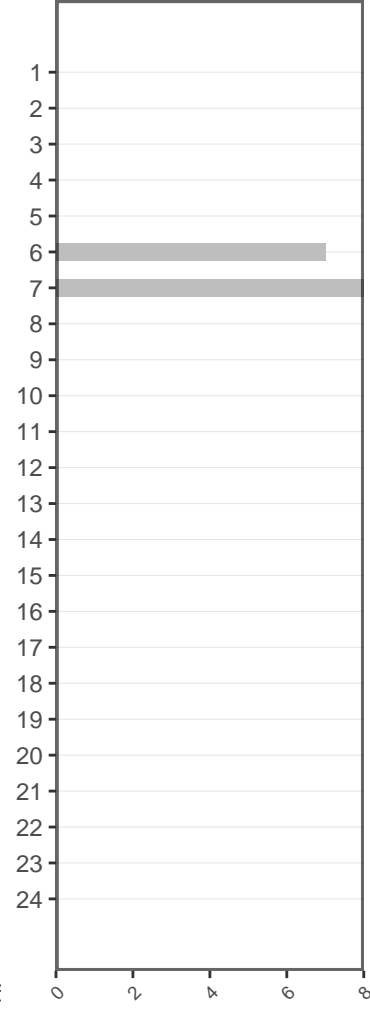
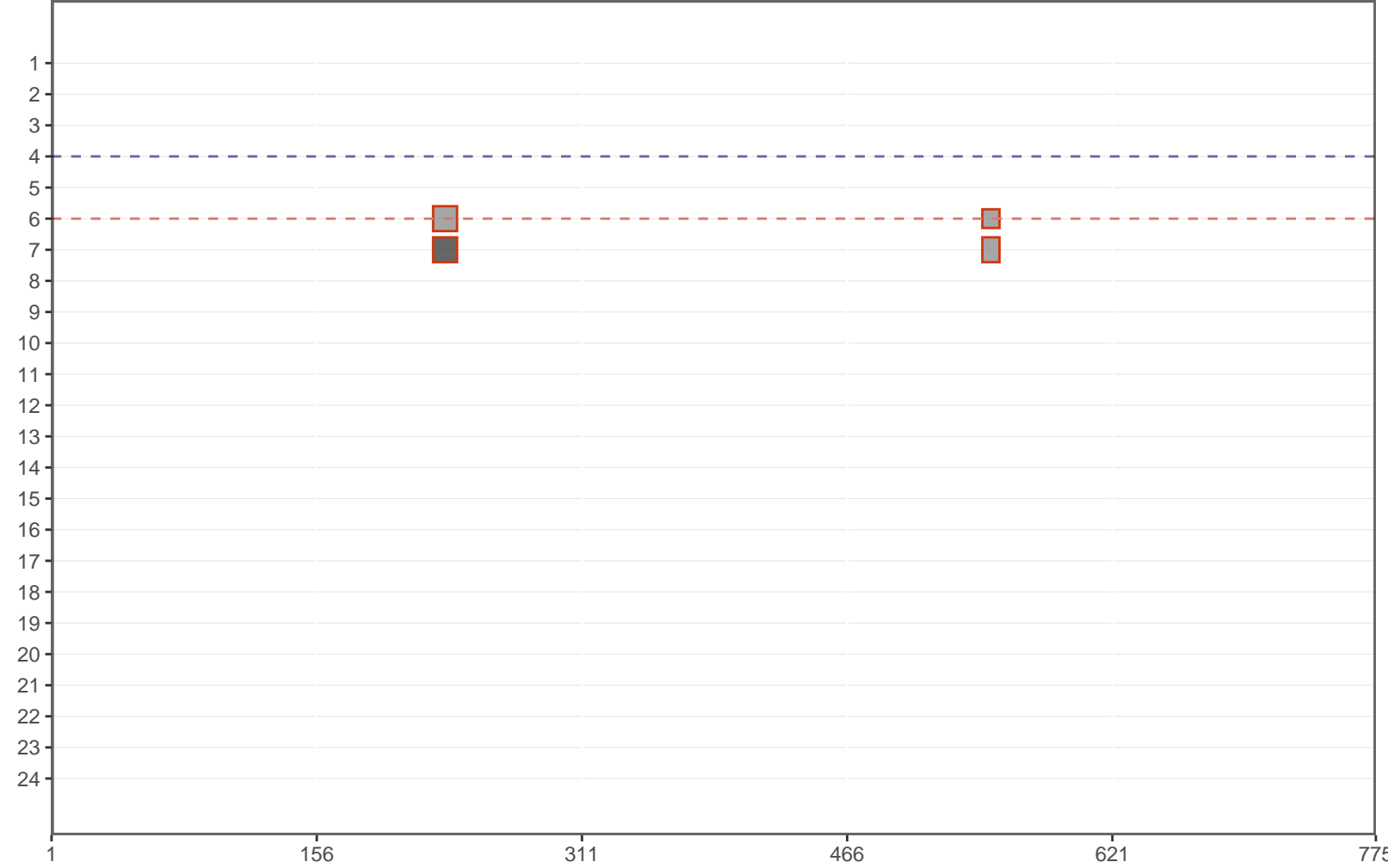
MW indication



Molecular weight

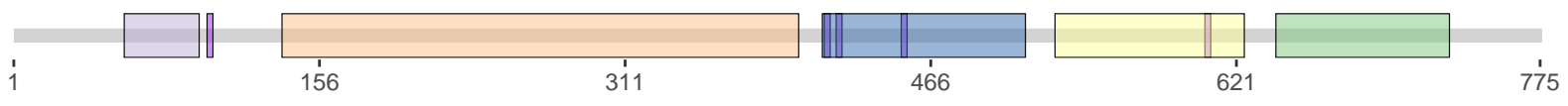


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

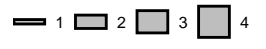
- SP
- Sequon
- TM Domain
- PF00626 Gelsolin repeat
- PF04810 Sec23/Sec24 zinc finger
- PF04811 Sec23/Sec24 trunk domain
- PF04815 Sec23/Sec24 helical domain
- PF08033 Sec23/Sec24 beta-sandwich domain

Protein sequence:

IEKTKGLVLAESFGHSHVFKDFKHIFEDGEGELGLSFGNLTLEINSGKDKKGGHGPCTSEKKGKPVWSTVIGEGNTTAWKLGGLDKNTGLTVFFDVSSSEKSDPSGNGNPQLYKFLTSYGHSHGGTKLKVTTITRHWINDAAWSTEELVGDFDEAAVAVMARLAGYKMEMEEDFDATRWLDRLRLGAKFGDYRKDDPSSTFLNPSFSLFPQFMHLRRSQFLQVFNNSPDEYAFRMLLNREGISNAAVMKGPTLMAFGFNSLPAPLLDDVASIAADRILLDDYFSVYIR

NbL12g12320.1 serine_hydroxymethyltransferase_4-like [MW = 54.44 kDa]

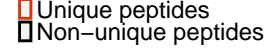
No. of times detected



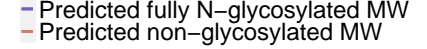
log(intensity)



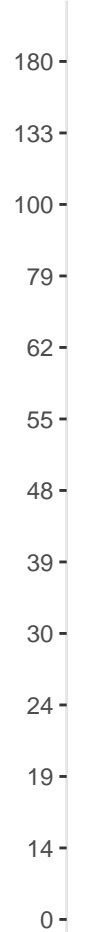
Values from



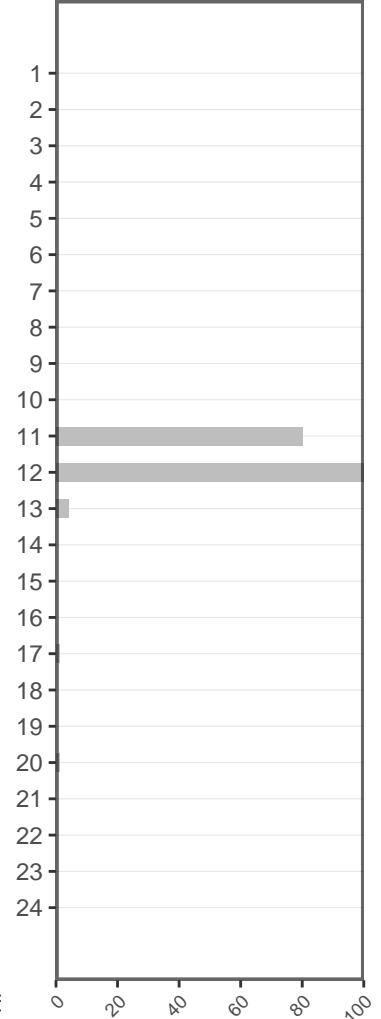
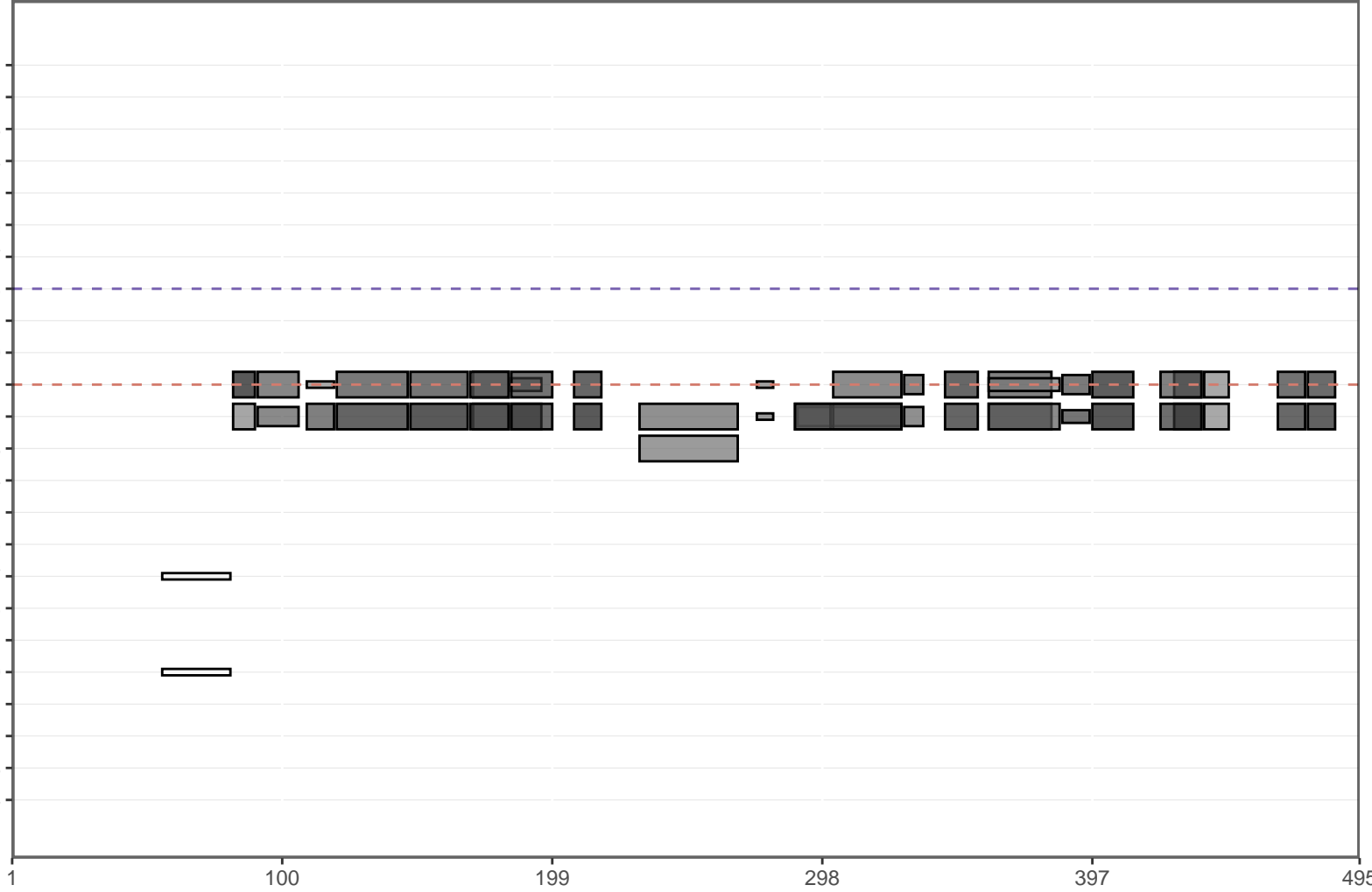
MW indication



Molecular weight

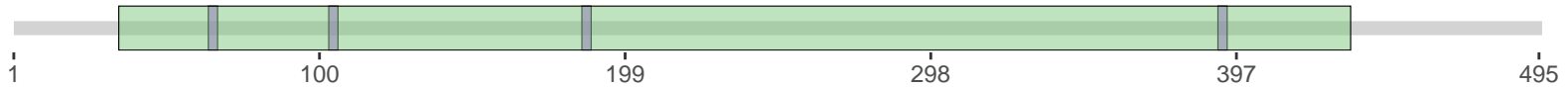


Gel Slice



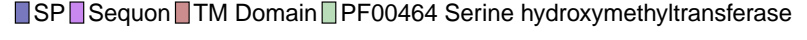
Protein length

Peptide counts over 4 repeats



Pfam domains

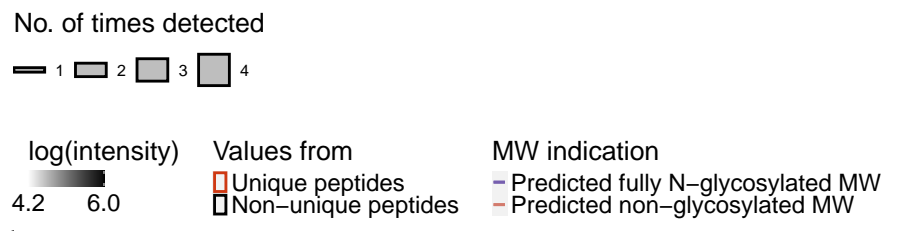
Pfam Description



Protein sequence:

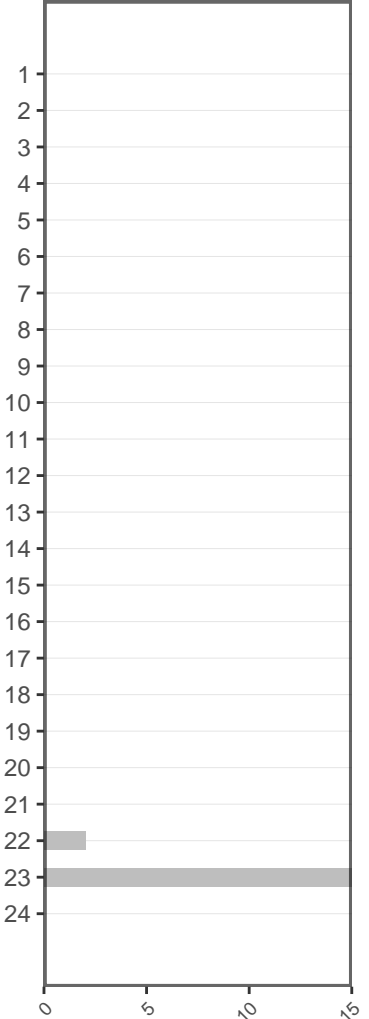
CDMAHISGLVVAQDEAADPFVEYGDVLTFTTHKSLRGRPRAGMIFRYRKGPKPKKGGQPEDAVYDFEDKINFAVFRSLGGGFHNGIGALVALKGAATPGFKAYAKGVKNAVALNGNYLMBKGYKLVYGGTENHLVLDLRLPLGLTGKVKELGDLANITYNKNVAFDGSALAPGGVRRIGTPTMTRSLGVKEDFEGIAEFLHRAVTTITLNIQKEYKLLKDFNKGLVNNKEIEELKADVENKFS66FDMPGFKLSEMKYKD

NbL12g12300.1 glycine-rich_RNA-binding_protein_2_mitochondrial-like [MW = 21.12 kDa]



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

SP Sequon TM Domain PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

Protein sequence:

CMSTKLFIGLSLWGTDDGSLRDAFATFGVVDARVIVDRDSSGRSRGFGFVNFDDDESANEAKAMDGDELGRNIRVSIAGERAPRGGGFGSSGGFGGYYGARDNDGV

NbL12g12250.1 50S_ribosomal_protein_L9 [MW = 24.56 kDa]

No. of times detected



log(intensity)



Values from



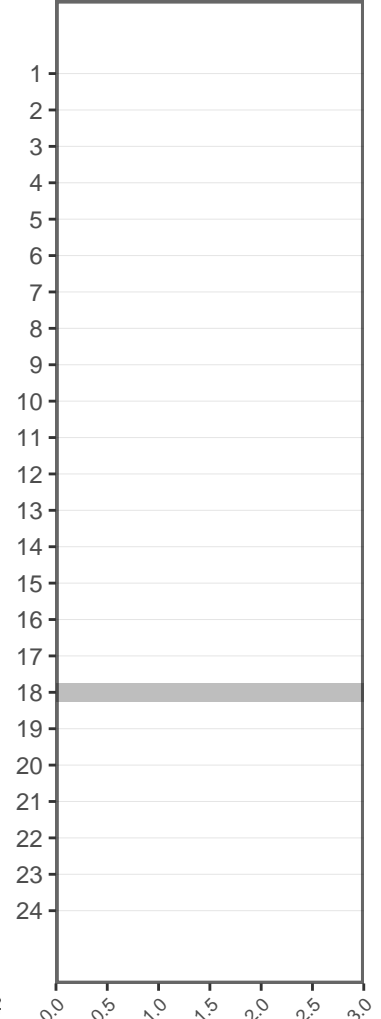
MW indication



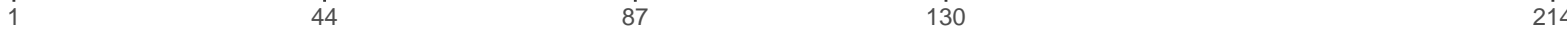
Molecular weight



Gel Slice



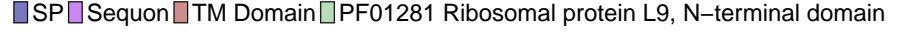
Protein length



Pfam domains



Pfam Description



Protein sequence:

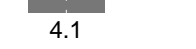
IQREEEVEEYKVPYPTKEDKMEYGMANRLDRTKLVLRKLAANKPKTKDDSGRTSGDEPKDENAEVARGLSVHEPEHVLDTPLHVMGEFDPLMRPRLPEKGVQWLQVNRGR

NbL12g12130.1 cytochrome_b561_and_DOMON_domain-containing_protein_At5g47530-like [MW - SP = 41.15 kDa]

No. of times detected



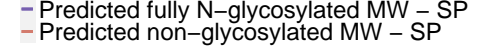
log(intensity)



Values from



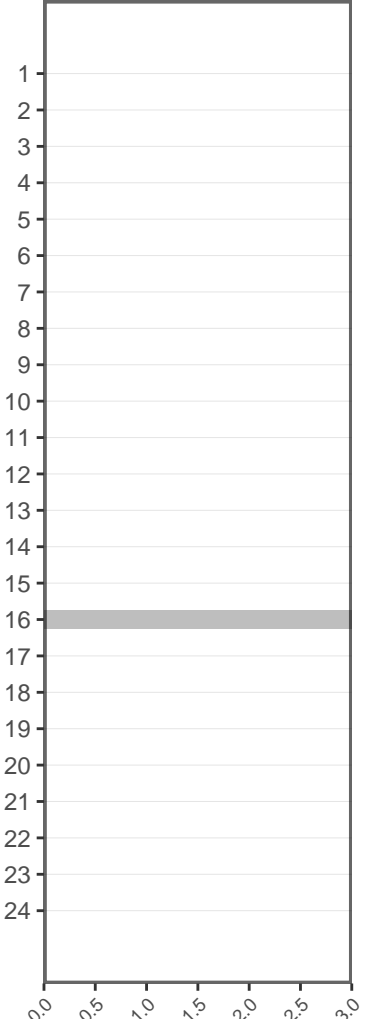
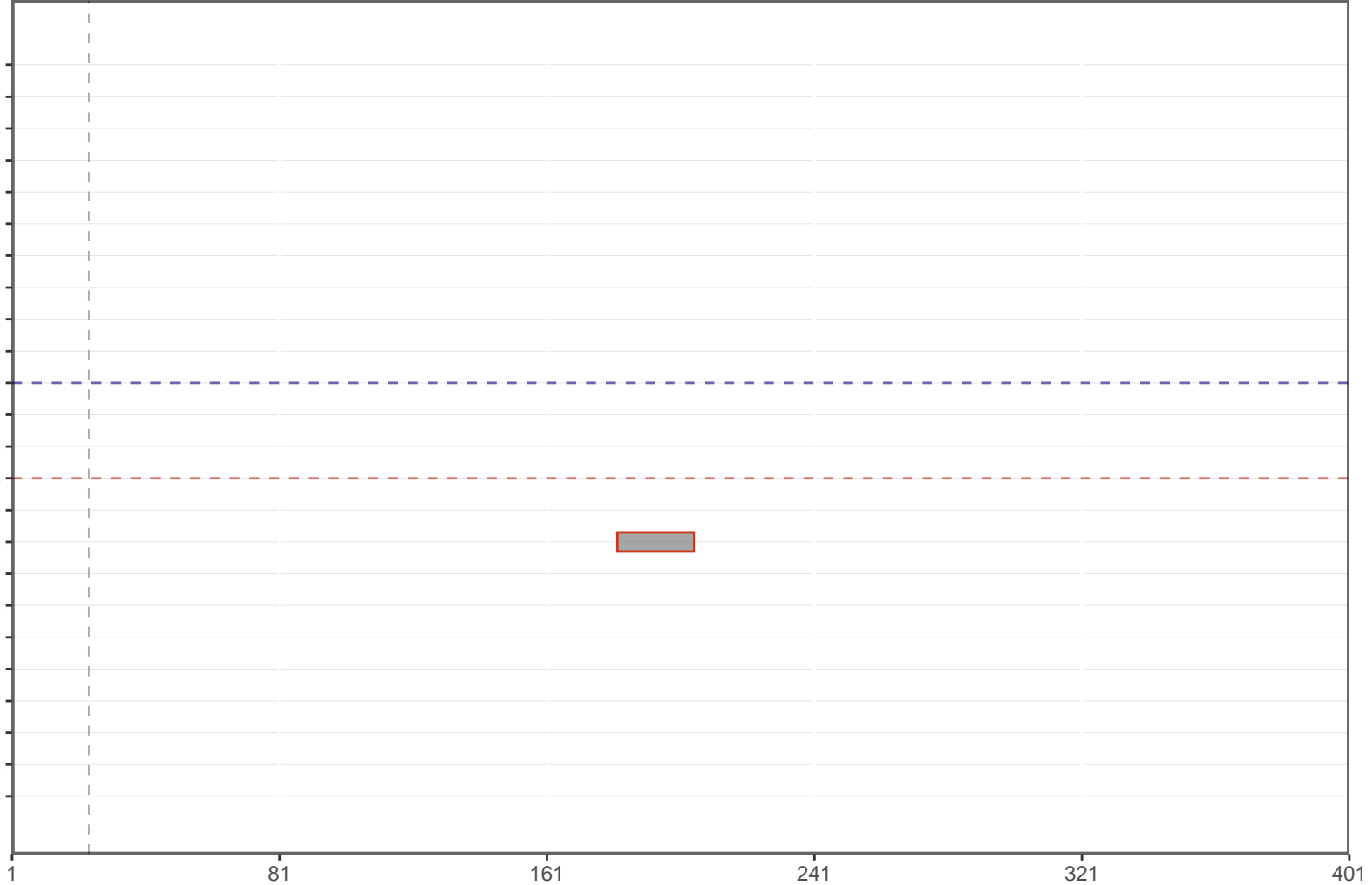
MW indication



Molecular weight



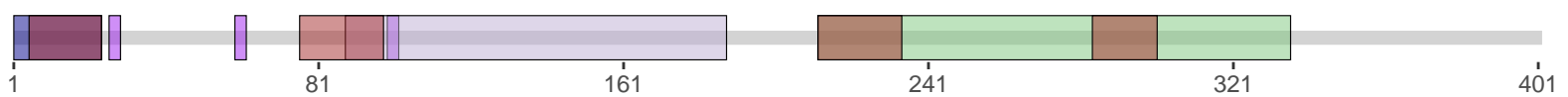
Gel Slice



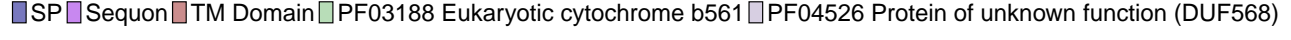
Protein length



Pfam domains



Pfam Description

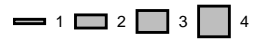


Protein sequence:

IDFASGQTSAAAGSASRRQRNRNTHGLVNAISWGVMMFMGAVFARYLKVFKSANPWYVYHAGDGTSAVAVGVAGWGTLKLGSDSDVGVKFNTRHNGITFLDGLGLQV FALLRPKPKPHKRYLWVYHHTIGFTVILSINVFEGFDALNGGKYWKRAYGVIALGAVALLEAFTVFWIKRKRKTSVSDKYPNGNGANGVNAVANREV

NbL12g11970.1 probable_inactive_receptor_kinase_At5g10020 [MW – SP = 112.45 kDa]

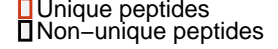
No. of times detected



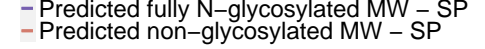
log(intensity)



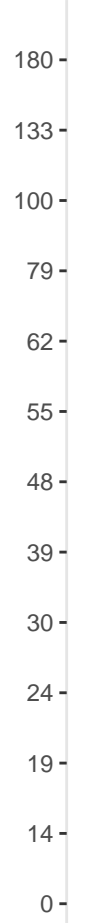
Values from



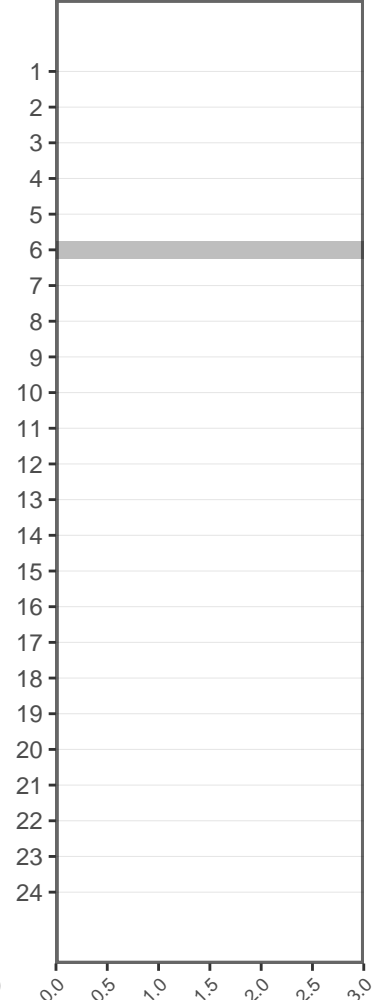
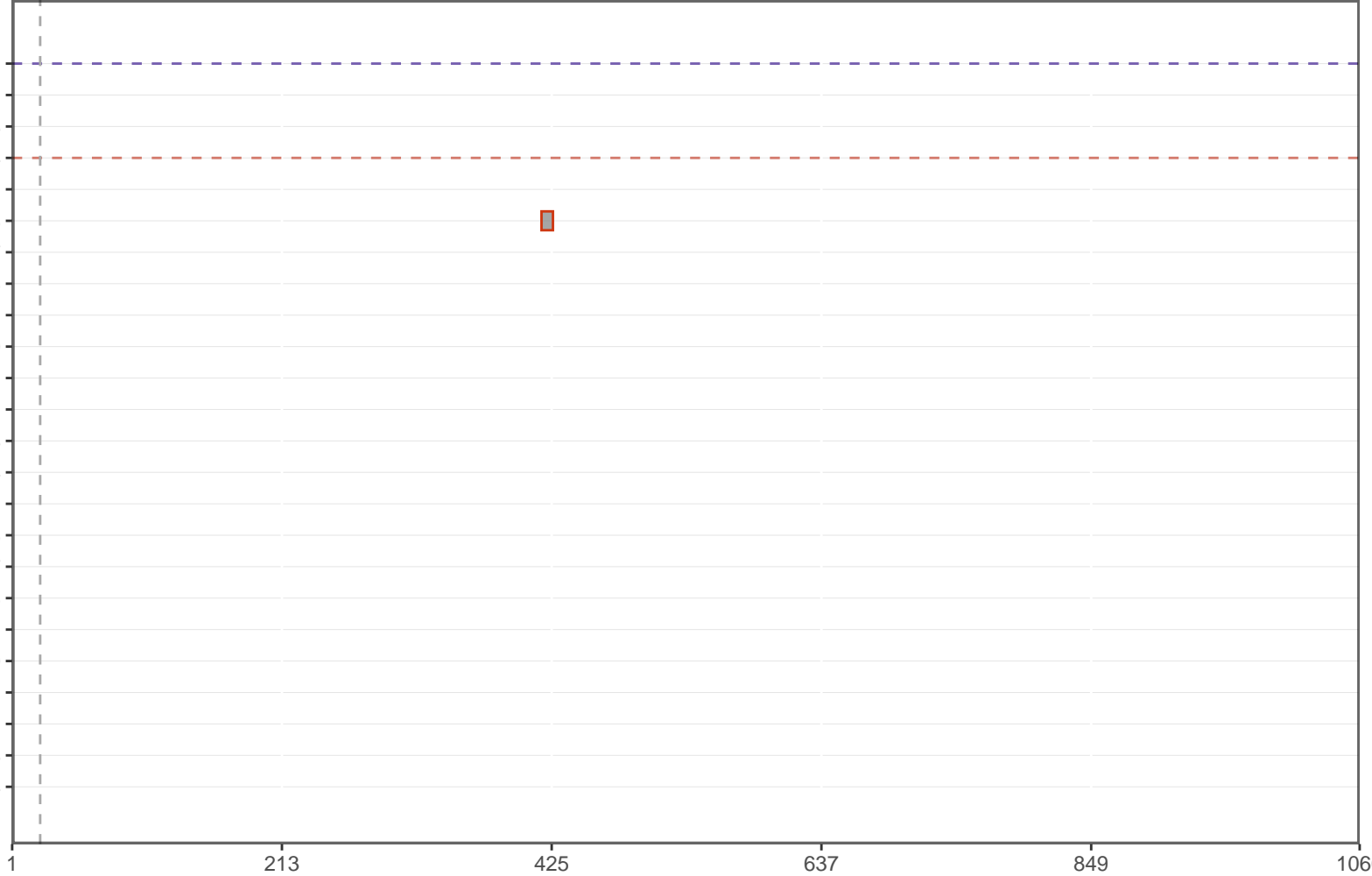
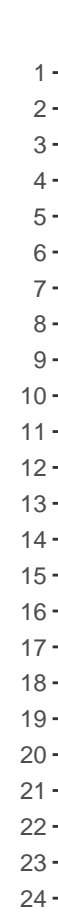
MW indication



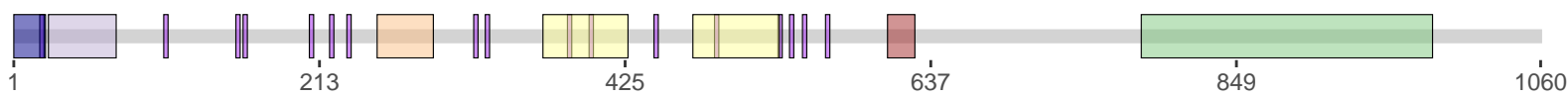
Molecular weight



Gel Slice

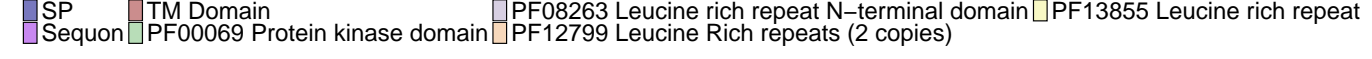


Protein length



Pfam domains

Pfam Description



Protein sequence:

IELGKLSLEFLDYSKNNFTGRIPENLSNLRVFNVGVNDLGGTVPSLKNFSDSSHPGNLSLIFPSNWPNNHGVPOGSPNRHHSKSKKVAIVASVQALLMIAFLVFRAYRAGADARLRSQFNQGGSTGRDVKLGRFNRPKFKHSGSEPPPTSLFSFNDHLLTNSRSLGGQESGTEIVEHVPPEVVTAGSATSHVGNHPATSGRRSSPDSPIGSSPHFDIEGPVTLQVYSPDRLAGELFDDGSLSTAEELSRAPAEVLRGSHGTYKATLNSGHVLTYYKLR

NbL12g11950.1 protein_HEAT_INTOLERANT_4 [MW = 33.76 kDa]

No. of times detected



log(intensity)



Values from



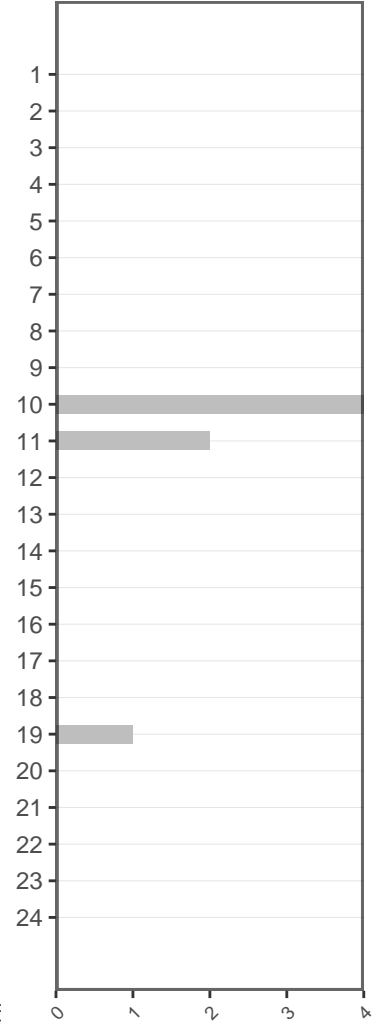
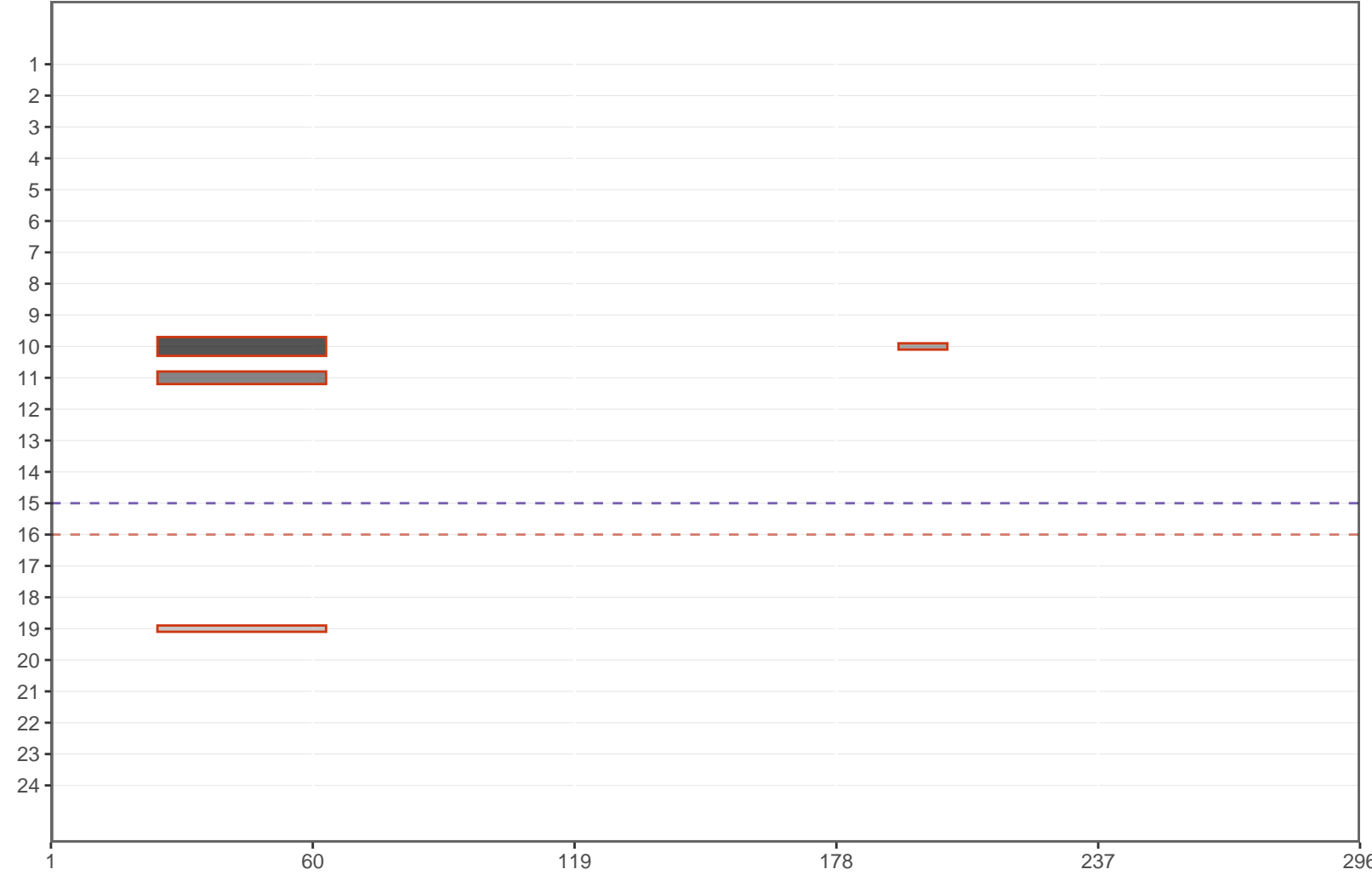
MW indication



Molecular weight



Gel Slice



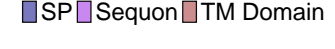
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LEDAFEEGGELHGGKVVYFGCTEPQLVYFGGKVTGIPVAVAVSFPFPPDKIGINSVQREAEELPMNMMDWVVPVPLENREGQVERLKSQIFLRCTGRRAGLKHKLKLRVKKFVGLVYFYQFFAEDELEGSTVQLFRTPEPPVFGQILVDYTAIPQ*

NbL12g11890.1 60S_ribosomal_protein_L35a-3-like [MW = 12.92 kDa]

No. of times detected



log(intensity)



Values from



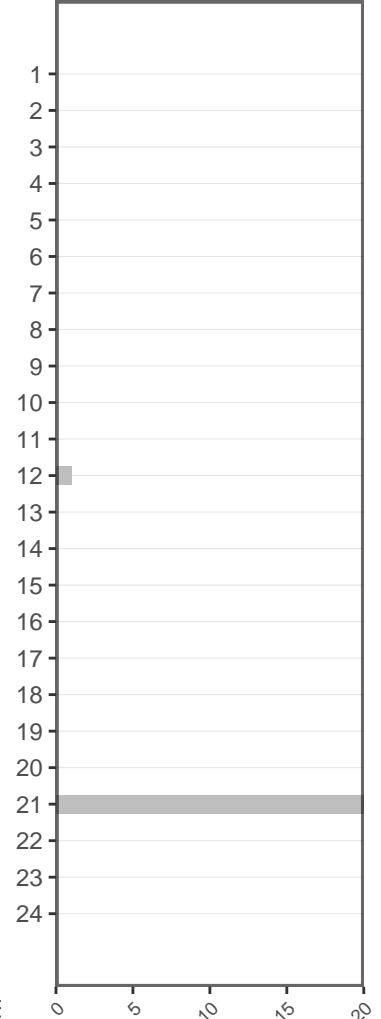
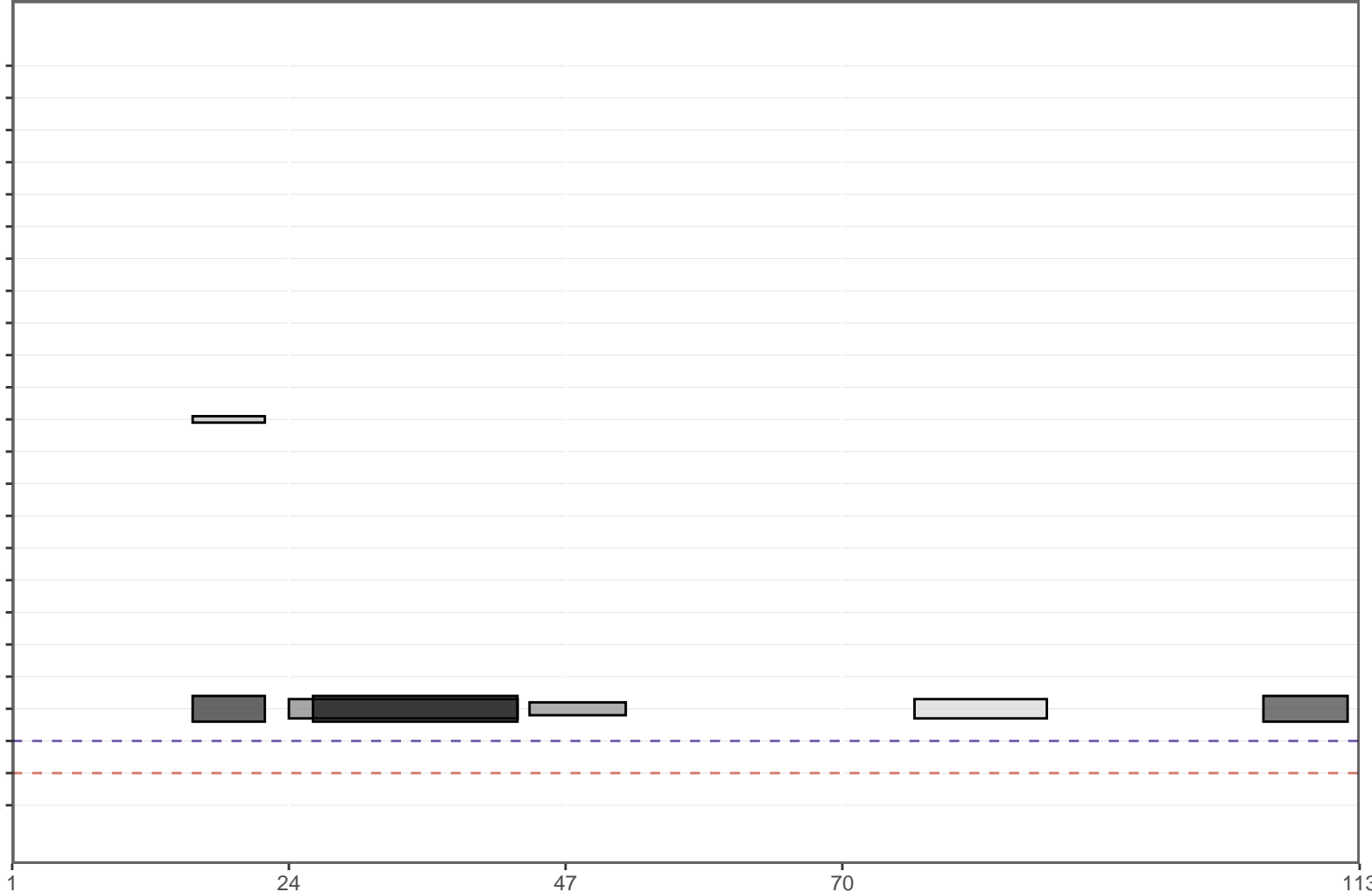
MW indication



Molecular weight

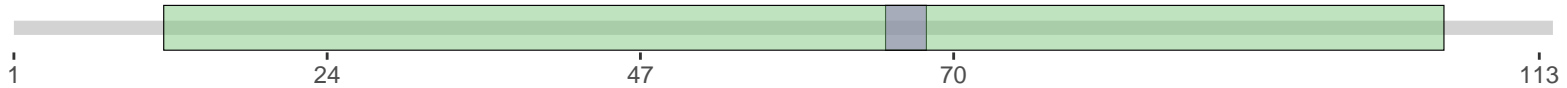


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

EVDVYLGRMAYVYKAKTKKNSHVRDVGKVRPHGNSGVVRAKFKSNLPPKSMGSAKVRVFMVPSNIP

NbL12g11650.1 uroporphyrinogen_decarboxylase_chloroplastic-like [MW = 43.46 kDa]

No. of times detected



log(intensity)



Values from



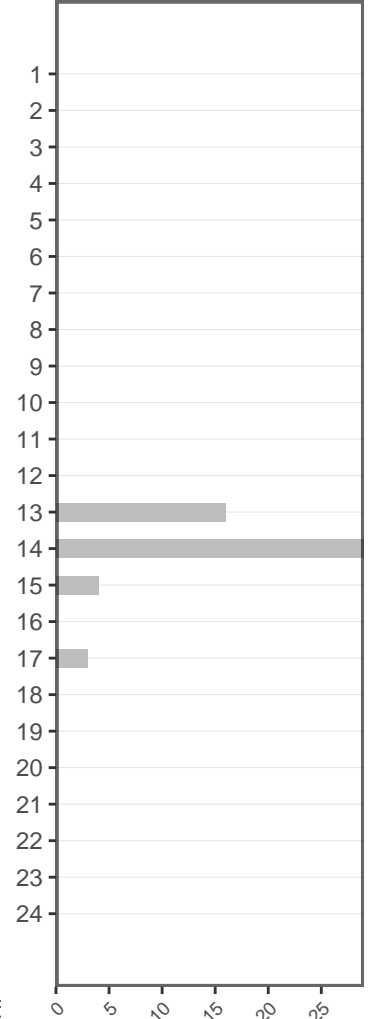
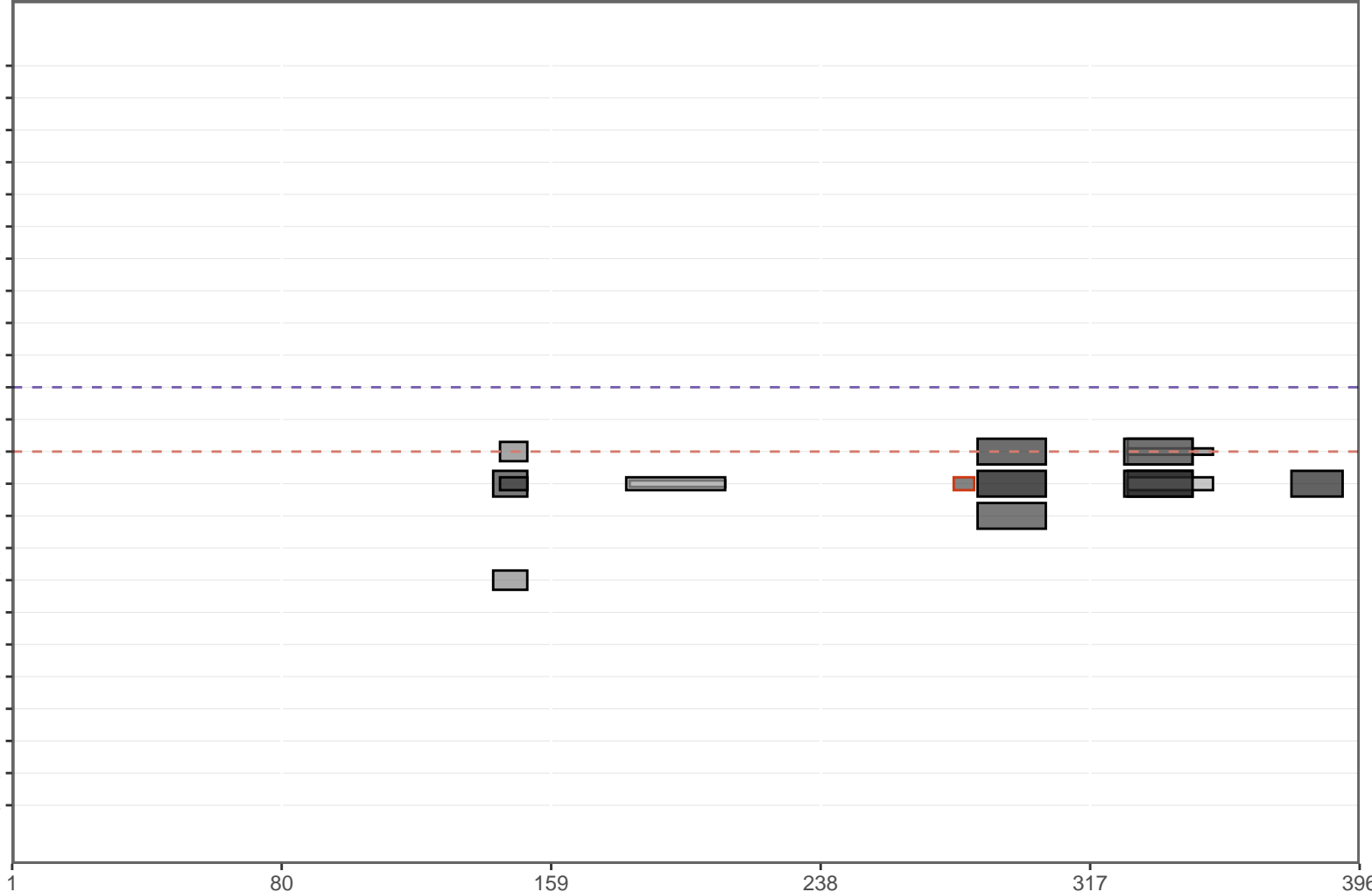
MW indication



Molecular weight

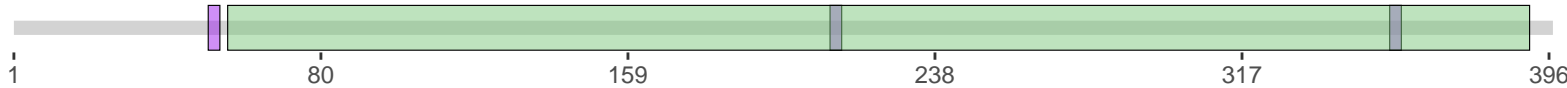


Gel Slice



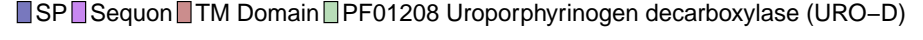
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

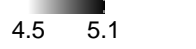
DAAVLGFVGFPTLASVYIEGGSSKFTKIKRLFAERKVLHALLGKFAFSMAKYHYQADNSAQAVQFDWATELSPVDFEESFLPKYKQIVESVKLTHPDLPLILVAGSGGGLLERLHLTGVQVYVSLDWTVDMDGRRRLGPNVAVGGKVDVPGVLFQSGKEFTFRINDTVKKAAGRKHLLNGHGRKVTPEENVAHFVEVAKGLRY

NbL12g11550.1 ABC_transporter_I_family_member_6_chloroplastic-like [MW = 34.54 kDa]

No. of times detected



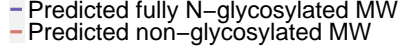
log(intensity)



Values from



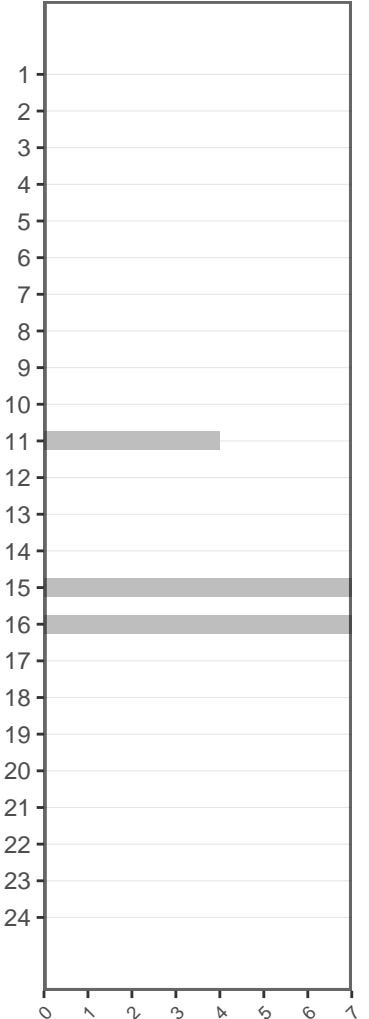
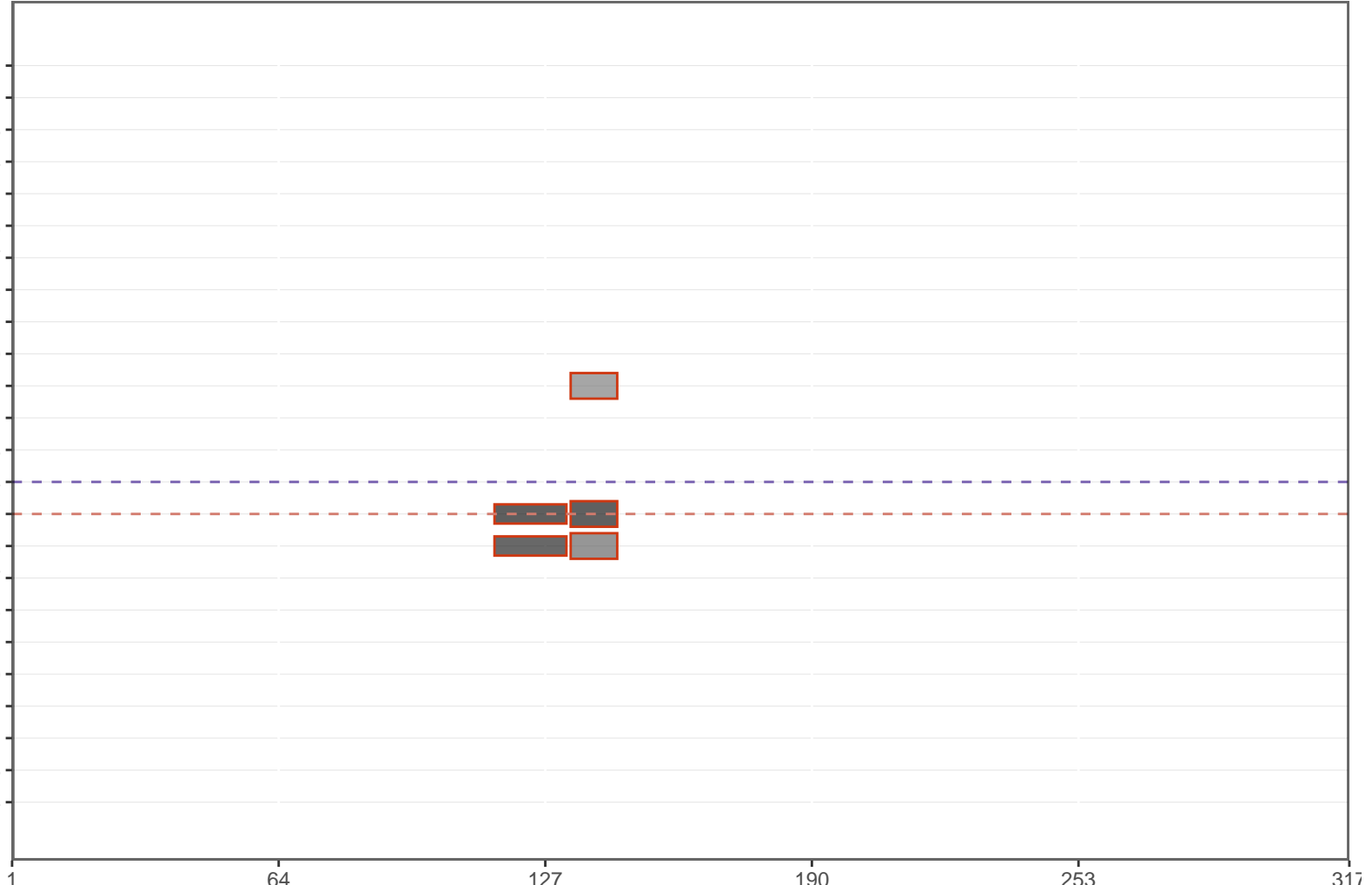
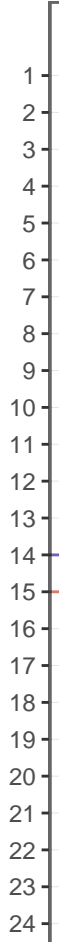
MW indication



Molecular weight

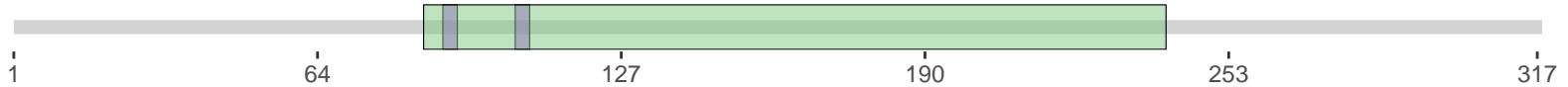


Gel Slice



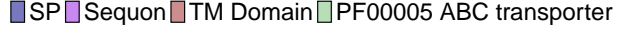
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IRSLAGLFMSFQSPVAIPGVSNDFLNMAYNAGRRIHGLPELPIEFYGVYVPKLELVNKKDFLNRVNEGFSGGERKRNEILQLVLAGADLALDEIDSGLDVLDALRDVAKAVNGLLSPKINVLMTIHYLRLLLEFKPTVYHIMENGRIVKTDGDISIAKVKLEKGYKAISGA'

NbL12g11540.1 hydroxyacylglutathione_hydrolase_cytoplasmic [MW = 34.13 kDa]

No. of times detected



log(intensity)



Values from



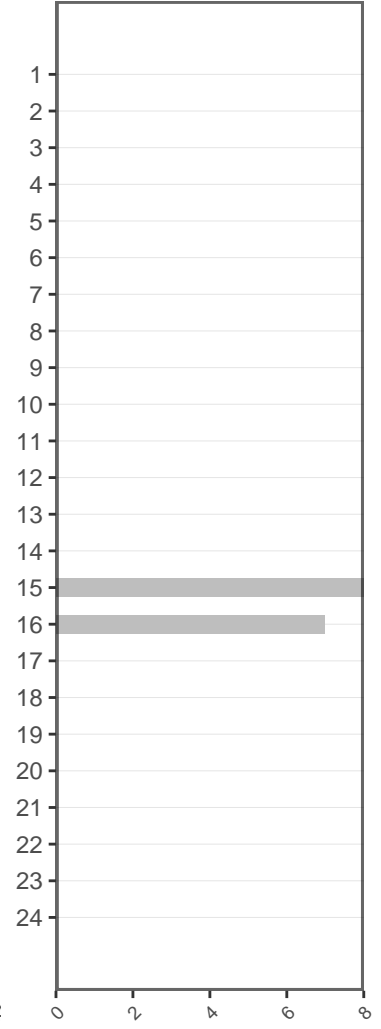
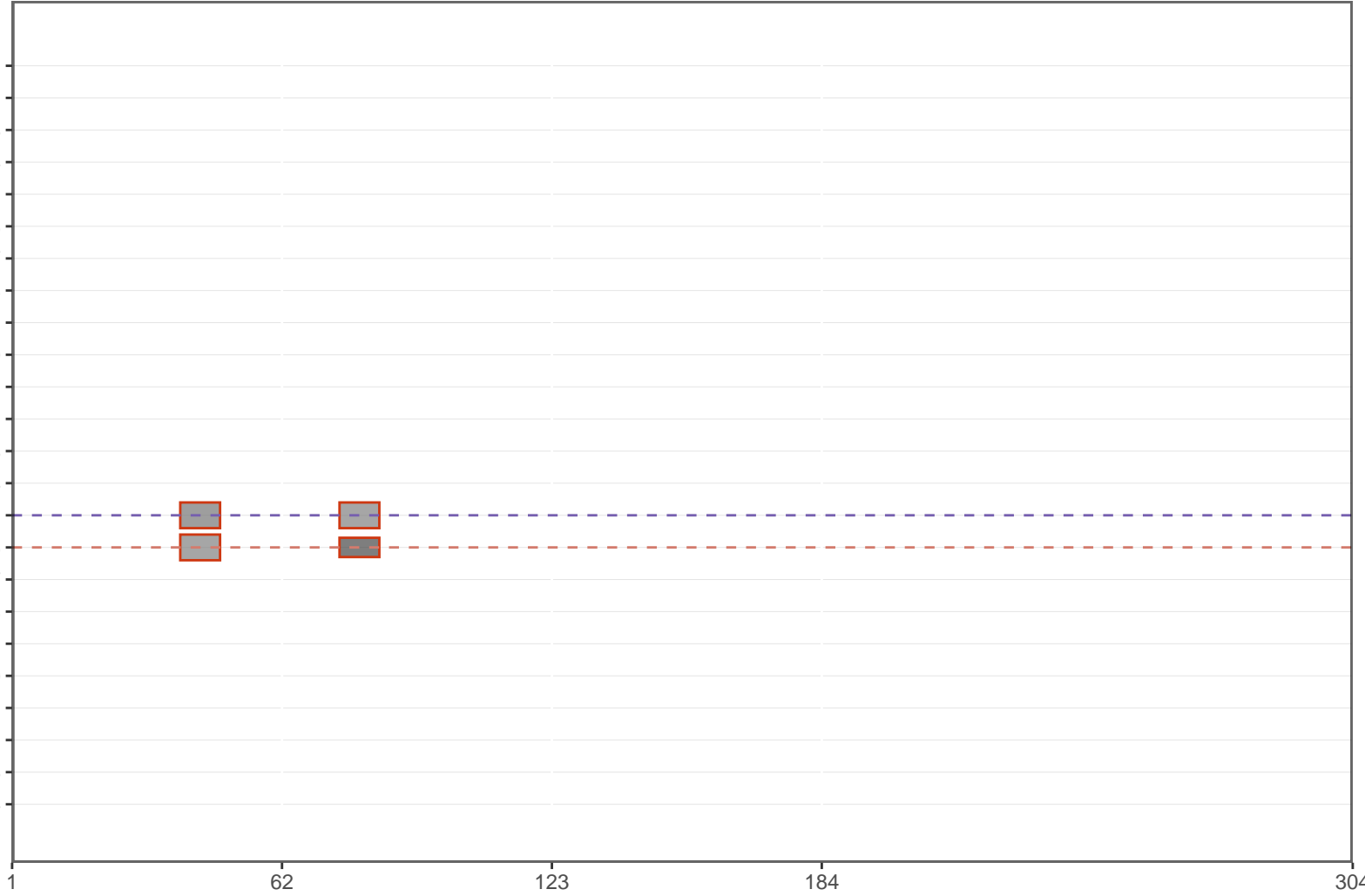
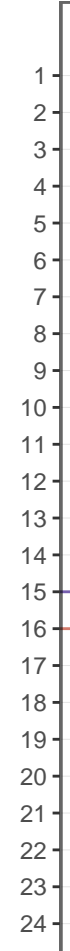
MW indication



Molecular weight



Gel Slice



Protein length

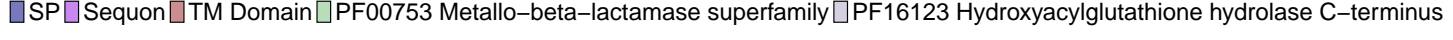


Peptide counts over 4 repeats

Pfam domains



Pfam Description

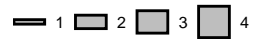


Protein sequence:

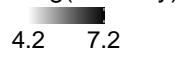
HTLSSVFPDGLLSWGTFLLHFLHFFVSVSRFRFRPMHLSBSPFRAGGGKFFEGTAEQMYSGLVITLALSLPKPTRVYGGHEVTVKNIQFALTVEPDKAKIAGKLTWAEHQRRVGLPTIPSTIEEEMETNPFMRADLPVQEKVGFKSPVEALREIRQRKDNWKG

NbL12g11490.1 superoxide_dismutase_[Fe]_chloroplastic [MW = 27.94 kDa]

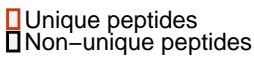
No. of times detected



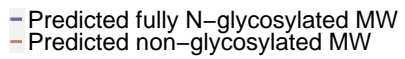
log(intensity)



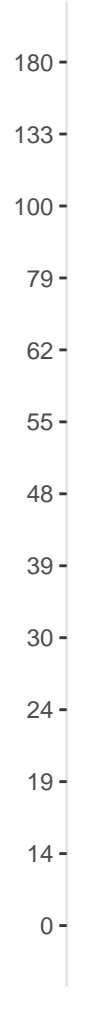
Values from



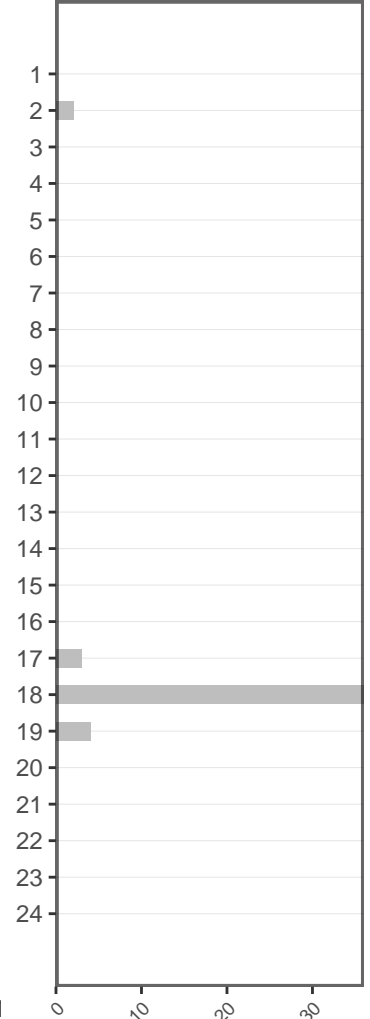
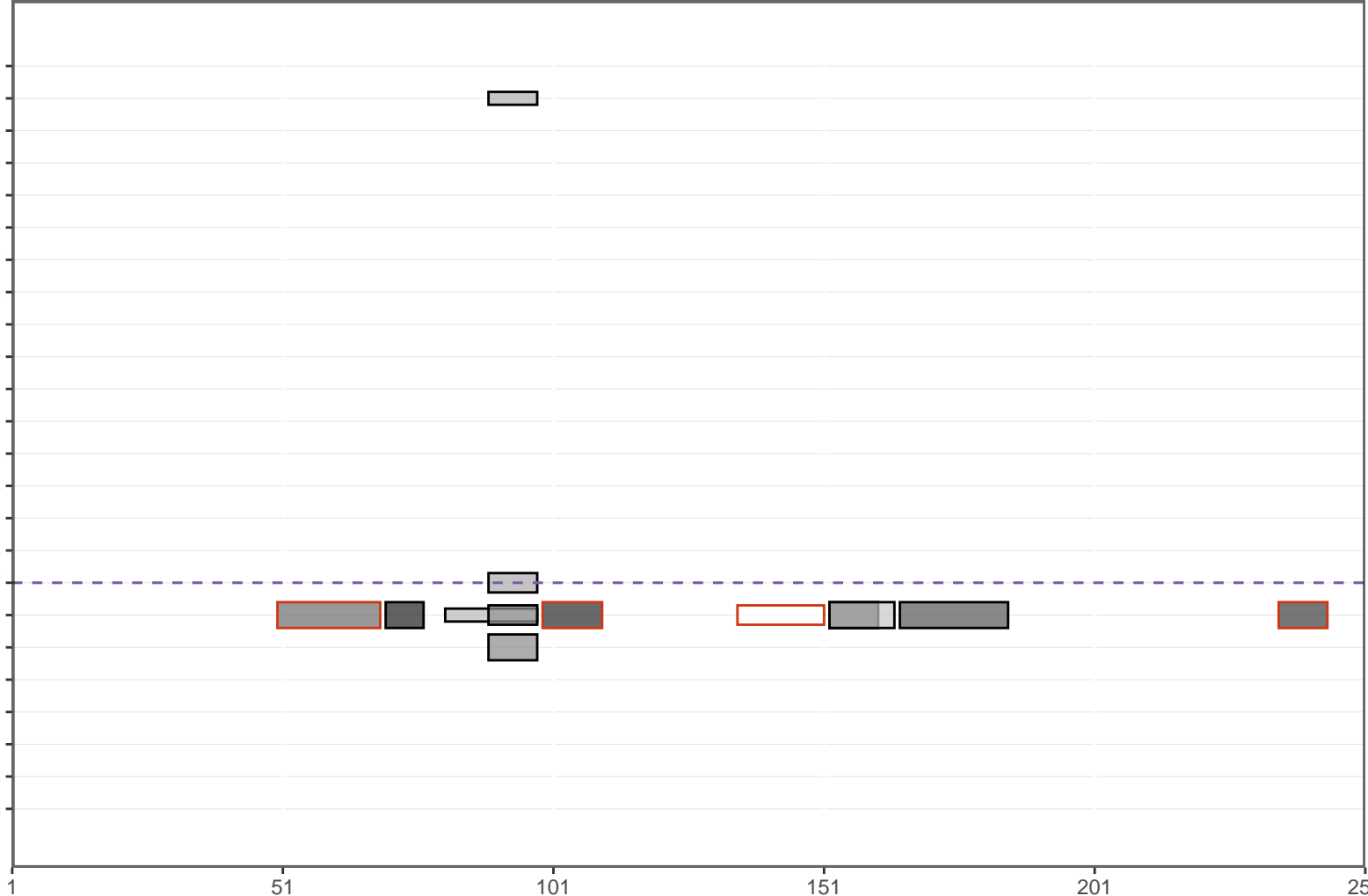
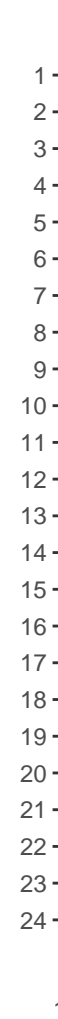
MW indication



Molecular weight

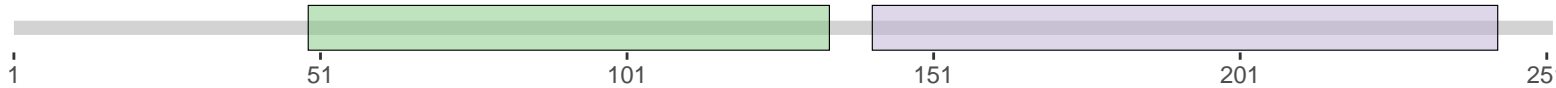


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00081 Iron/manganese superoxide dismutases, alpha-hairpin domain
- PF02777 Iron/manganese superoxide dismutases, C-terminal domain

Protein sequence:

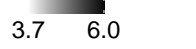
PLPLFNNAAQAVNHHQFFWESMKPNSGGGEGSGDLELHNRDFGSDAFVKEFNAAATGFGGWWLWLYKPEEKLALVKTPEAENPLVLGYTALLTDVWEHAYVLDQNRNRPDYISIFMEKLVSEAVSCRLLKATAV

NbL12g11310.1 probable_carboxylesterase_120 [MW = 36.65 kDa]

No. of times detected



log(intensity)



Values from



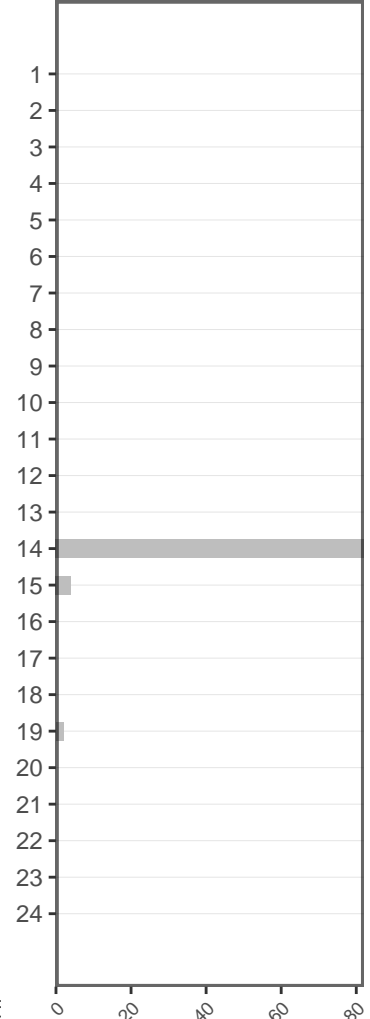
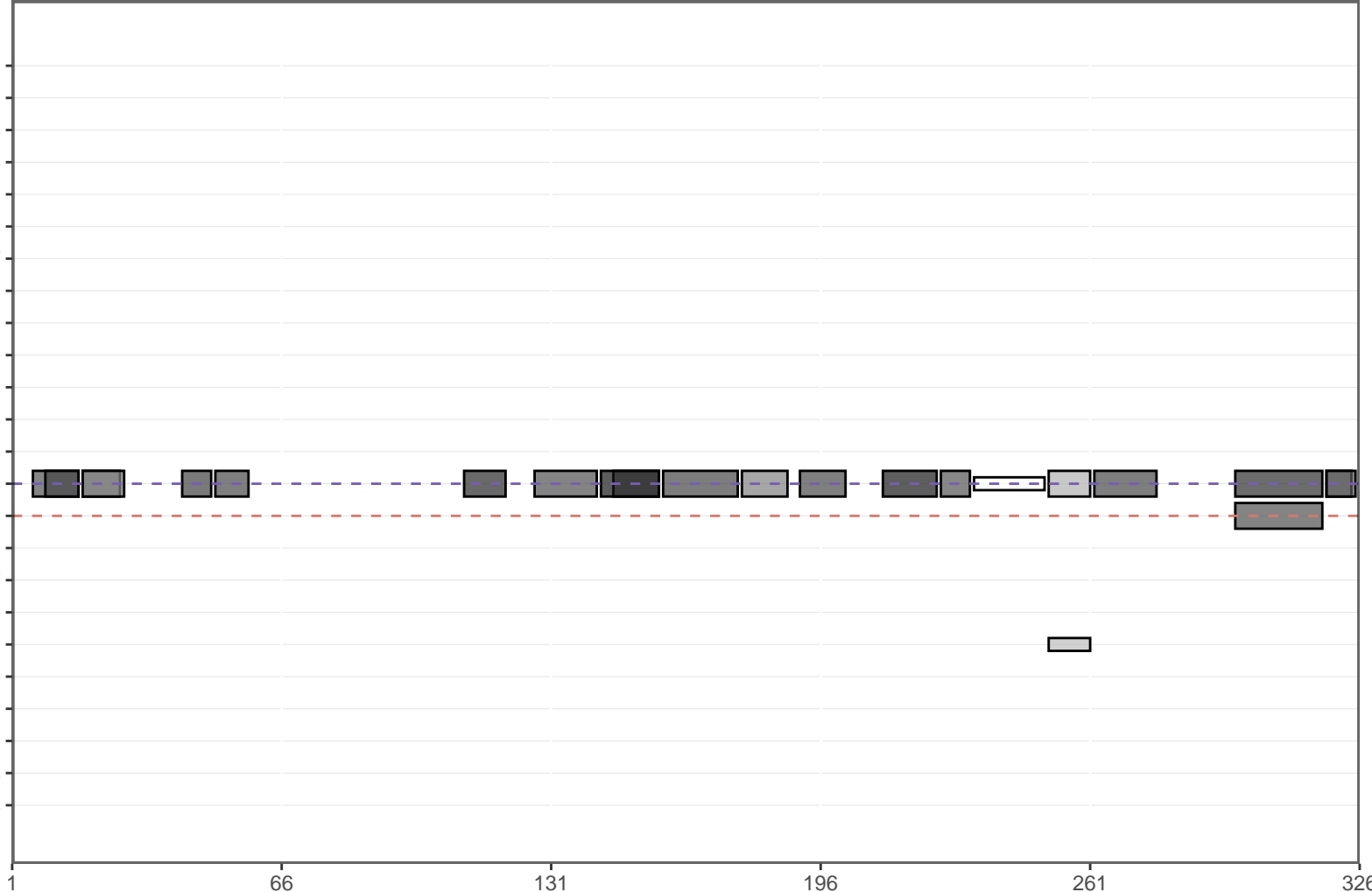
MW indication



Molecular weight



Gel Slice

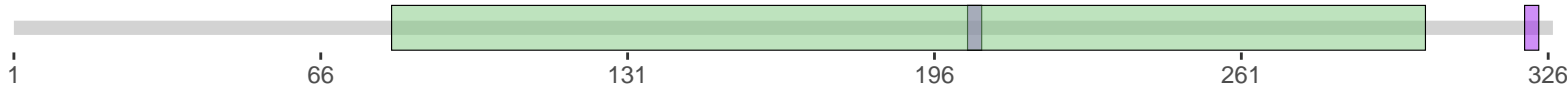


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

YYADLSR^VLYLGT^SAGNLA^YHAGLRA^AAAA^NELE^PIR^IKGLL^H^HPY^FSG^N^R^T^E^S^E^K^L^K^D^D^L^L^P^L^H^A^I^D^K^M^F^D^L^G^L^P^K^G^V^D^H^D^H^E^Y^C^N^P^G^A^N^G^G^S^H^L^D^M^K^E^L^G^W^K^V^L^T^G^V^G^E^D^P^L^V^D^A^G^R^N^G^V^K^L^M^E^E^K^G^K^Y^K^F^R^D^G^Y^H^A^M^E^V^F^D^G^S^T^A^A^L^Y^D^A^T^R^D^F^L^N^A^S^K^V^

NbL12g11010.1 5'-3'_exoribonuclease_4 [MW = 111.7 kDa]

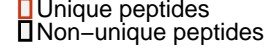
No. of times detected



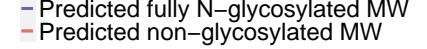
log(intensity)



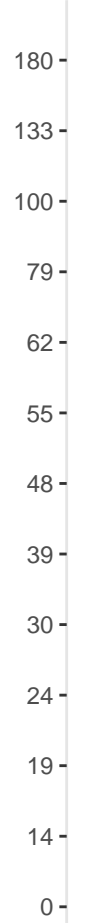
Values from



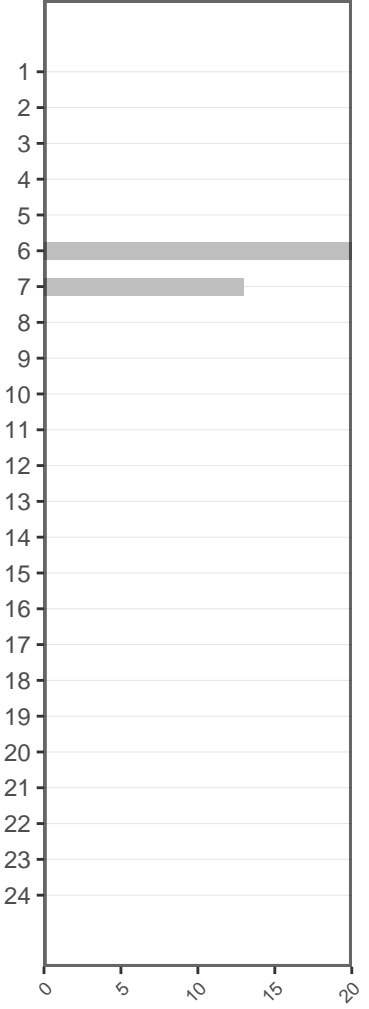
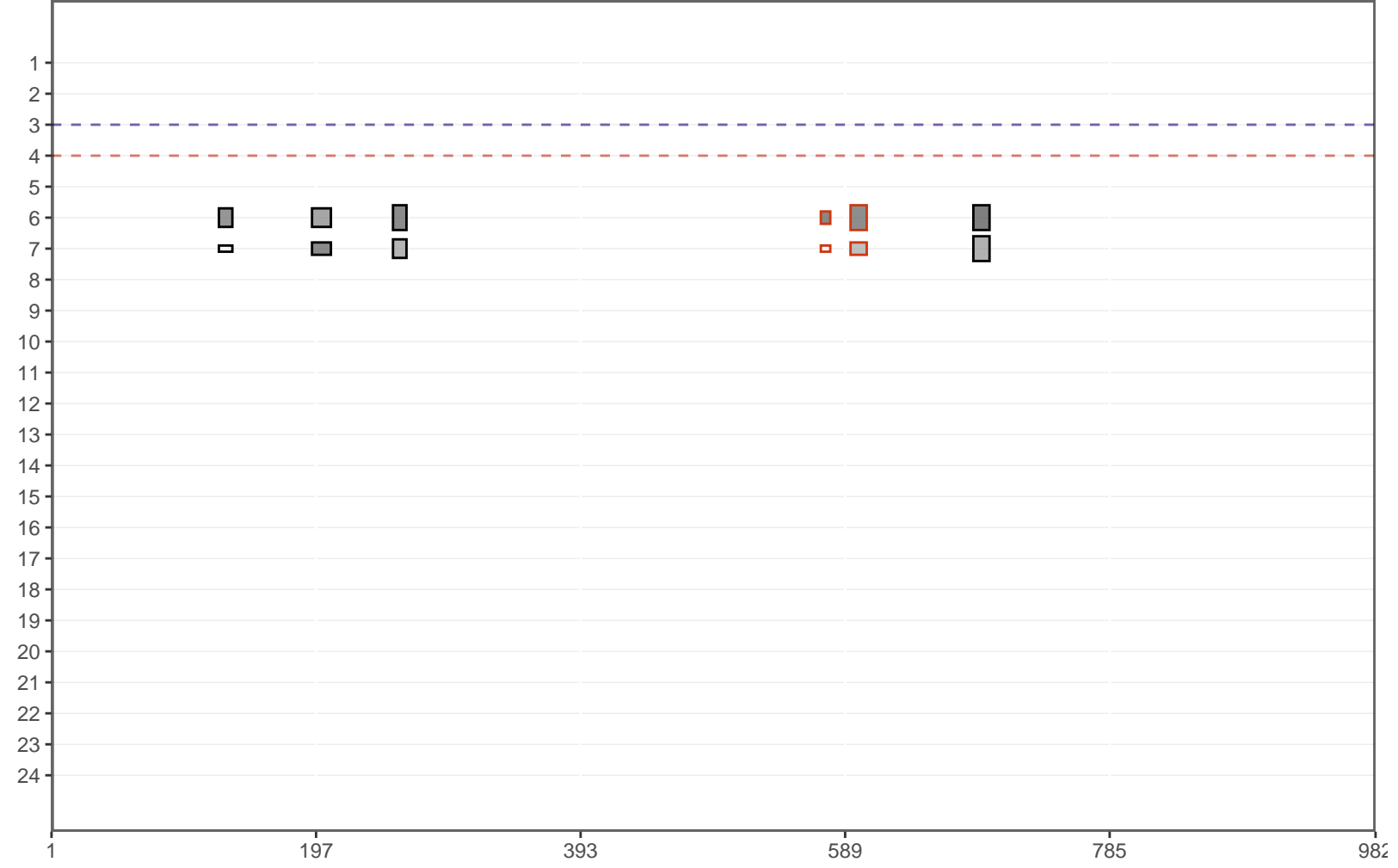
MW indication



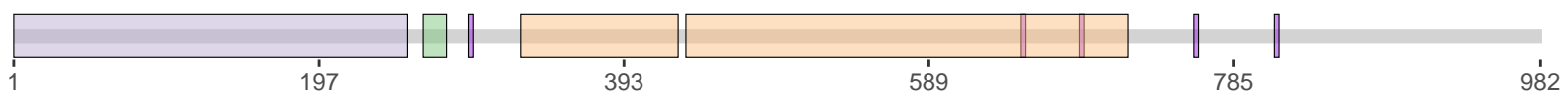
Molecular weight



Gel Slice

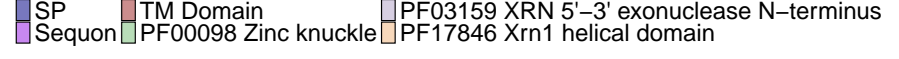


Protein length



Pfam domains

Pfam Description

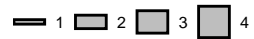


Protein sequence:

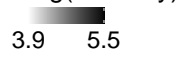
YYQGVCSVQVWFYFVHAFASDLKGLADLEITFFFGEPFRKFDQMGVLPFAASANALPEKYRMLMMDSSSPIDFYPTDFELDMNGKRFVAVGAVKLPFDIEKLLAETKLEDLSEDEGLRNSVLFDLVYVHHHHTLAPYISVYHHNNKVPFGEGRPLWLDANLGGMNGFIWLSEKRLRQDGVCEPLNGLDIEKIKLINTFLNPFVFKHKHPKPEGVYMPKXLRVADKPFPLVWHEDHGTRQLGKDRGPVPGAIAAGPTLGEAAHRLNLTNPKPGGTNSGLI

NbL12g11000.1 probable_glucan_13-alpha-glucosidase [MW - SP = 102.83 kDa]

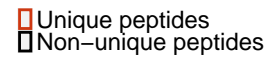
No. of times detected



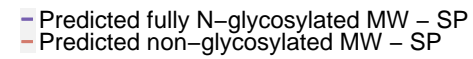
log(intensity)



Values from



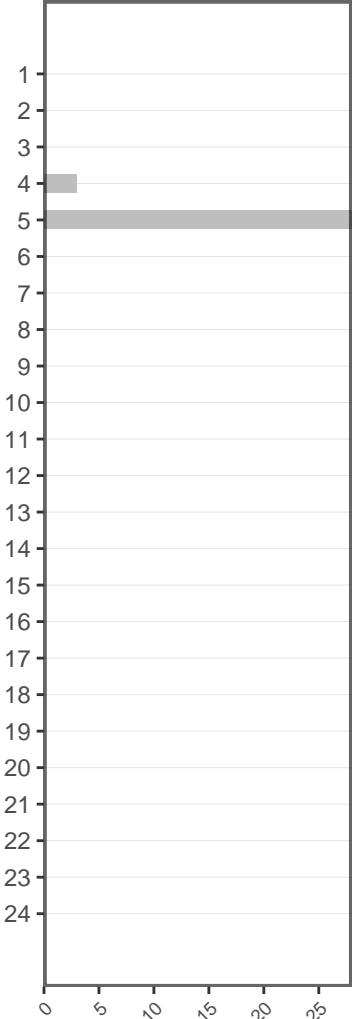
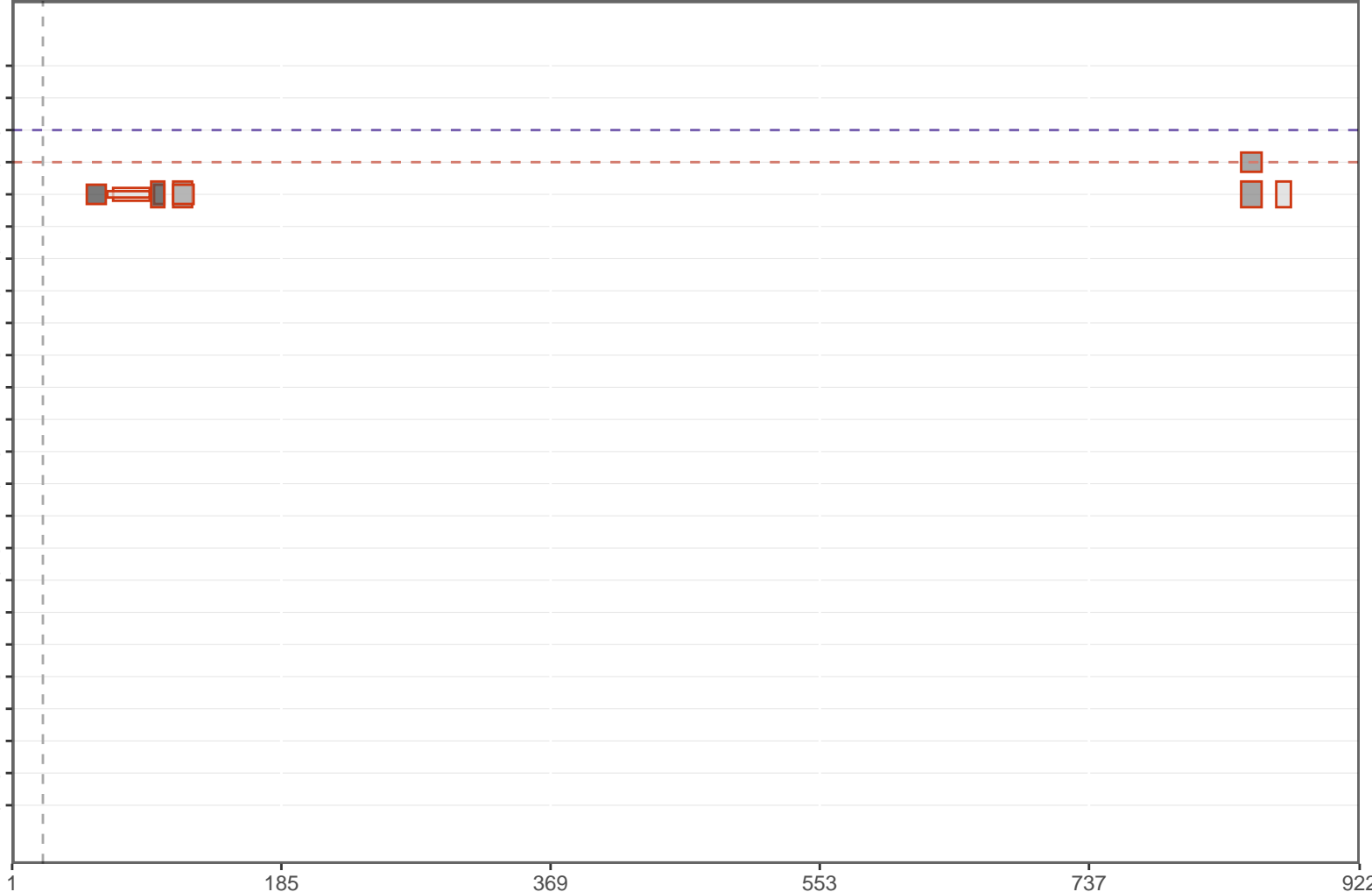
MW indication



Molecular weight



Gel Slice



Protein length

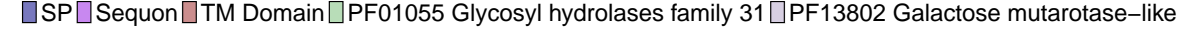


Peptide counts over 4 repeats

Pfam domains



Pfam Description

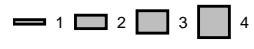


Protein sequence:

HKEASEKYYKDATGNDYDQWGWPGS66YVOLLNPEIRSGWGGKFLSDGYTGSTQYHWNMDMNEPVEVNGPEVTMPRDALHHGGVEHRELHNAYGVYQMATSNGLKRRGGDKDRPFVLRGAFFAGSQRVGAIVTGDNTAEWEHLRIVSWPMVLTLSISGIVFSGADVGGFFGNPDTELLVWVQLGAYYFFRGHAIHDTKRRPELWFGERTQLMREAIHRYMVLPIYFTLFRANSSGTPVAPRLWMEFFDDEKSFNDEAFMVGNGLLVGGIYTERAKI

NbL12g10960.1 aspartate--tRNA_ligase_2_cytoplasmic-like [MW = 60.28 kDa]

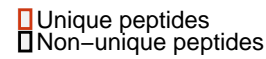
No. of times detected



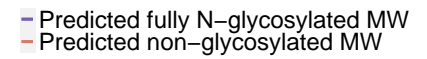
log(intensity)



Values from



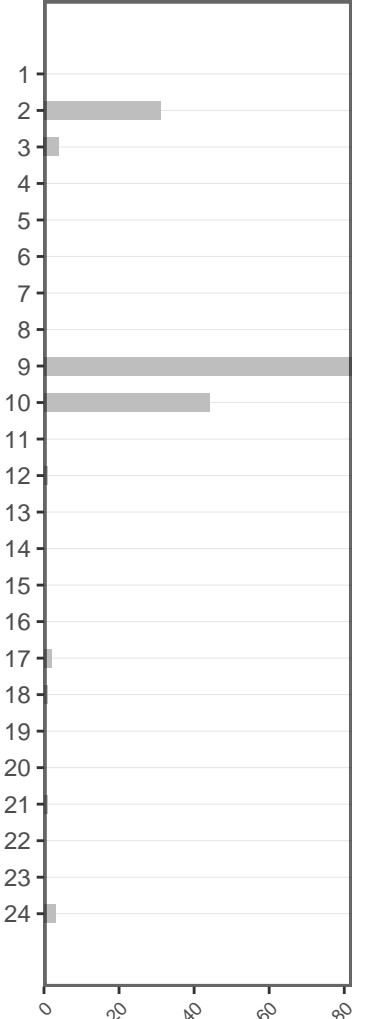
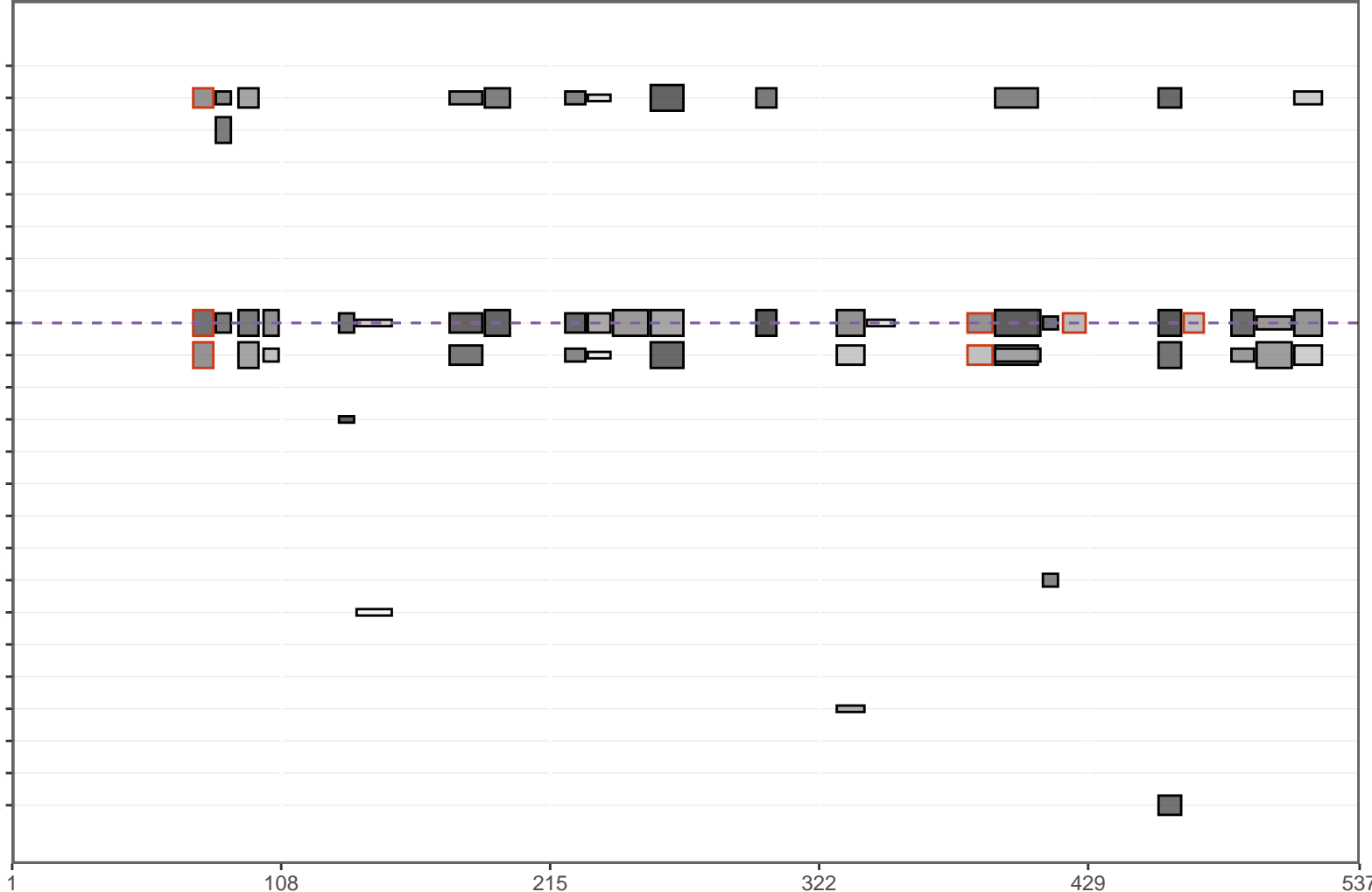
MW indication



Molecular weight

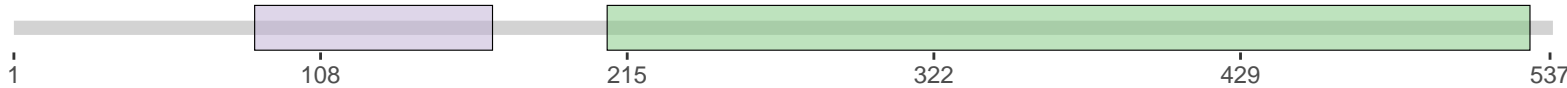


Gel Slice



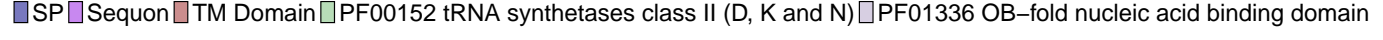
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

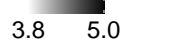
IIGSSSEGGSAVFRLEDPKGGFGLAGSPQLHKQMAAGDGFGRVFEIGVFRADDSFTRHLCEFTGLDVEMEKEHYSEVMIDVDRLEVFVTFDSLNDKKELEAIGRQVYFEHLVYFREDKTLRLTFEEGGVQLKEAGIEVDFPFDLNTSESRNKGQLVAKKYGFTEFYLHKYPLAVRPFYTMPGVDNPNVNSDFVIRGEEHSGAQRVHYVPELEKRAEECGDVKTIISTYIDSFRYGAPRHGFGVGLERVAMFDALNNRKTSLFPRDPQRAPL

NbL12g10940.1 peptide_chain_release_factor_PrFB1_chloroplastic [MW = 51.2 kDa]

No. of times detected



log(intensity)



Values from



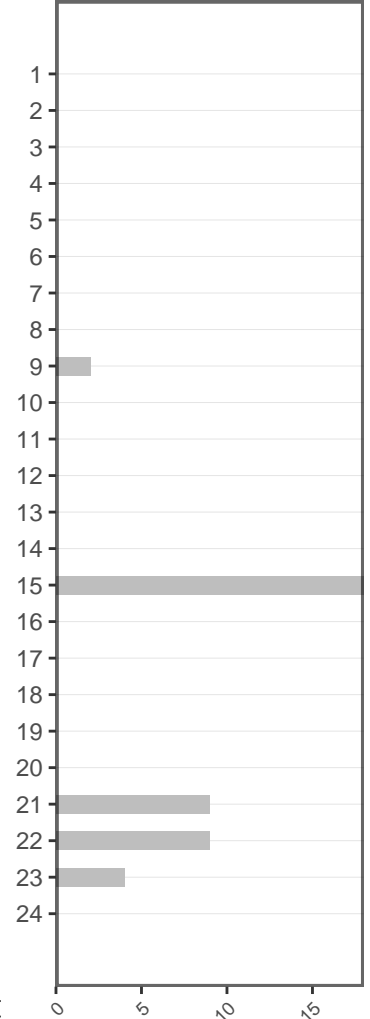
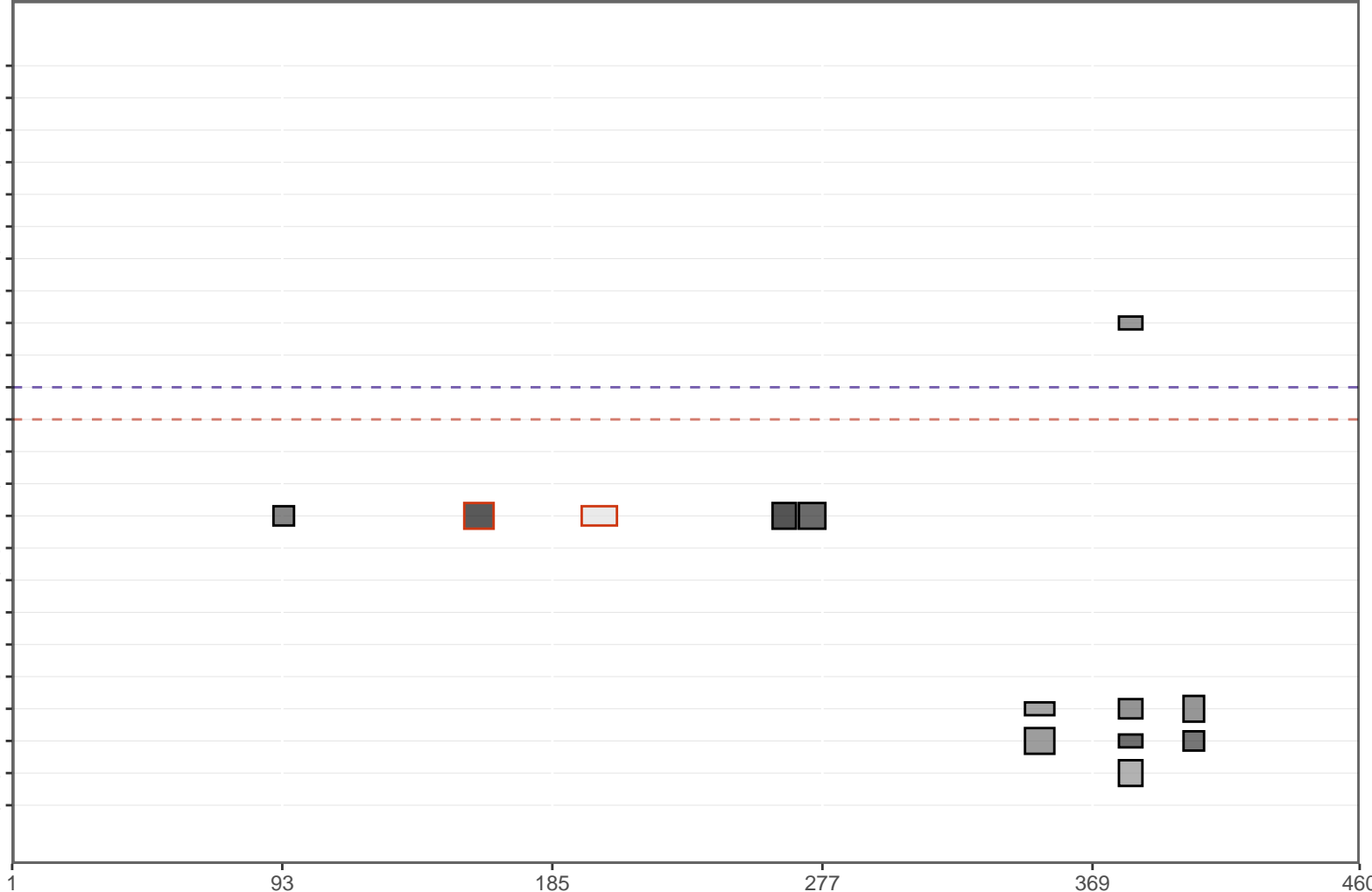
MW indication



Molecular weight

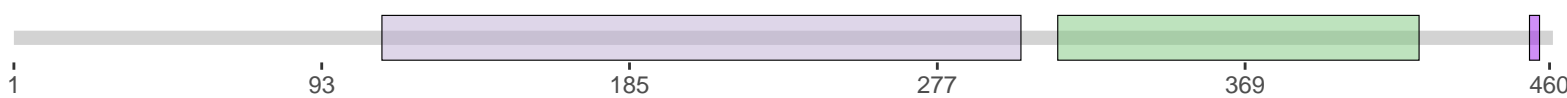


Gel Slice



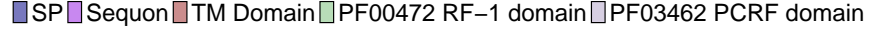
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IGGTDACDVAADMLLRMYVRWGEKGRYKTKVVEKMGEEAGKBTAEIEGRYAYGLSGEKGTHRIVRQSPFNKGLRGTFSGVEIMPLPEDSLVPEIPELDLISFTRAGDKGGQNNKVKYETAVRITHIPTGVAWRCTEERSGQLANKIKALSRKAKLLVIAEGRASEIKQIRGDVAKAEWGGQIRNVYVHPYKLVKDVRTGYETSDDTSVMDGDLDFPKSYLKHKKYSLAANTEVAV

NbL12g10910.1 calreticulin-3-like [MW - SP = 46.66 kDa]

No. of times detected



log(intensity)



Values from



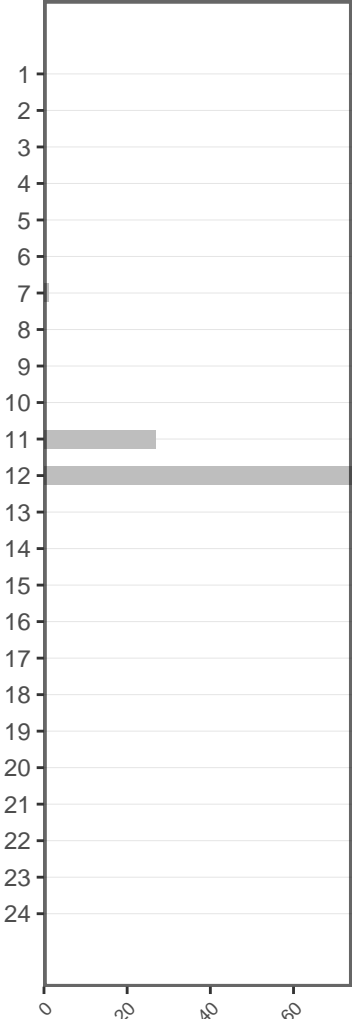
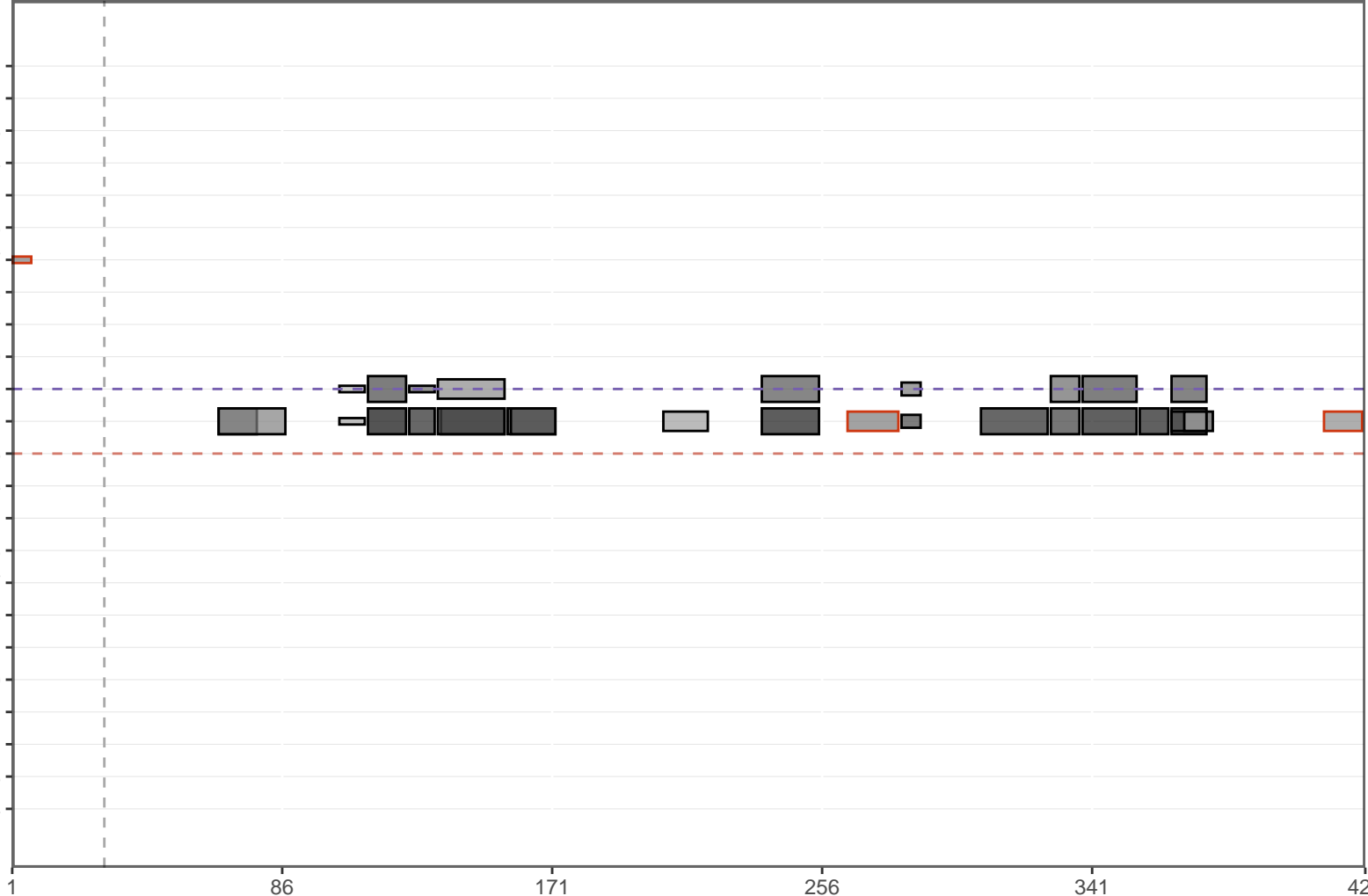
MW indication



Molecular weight

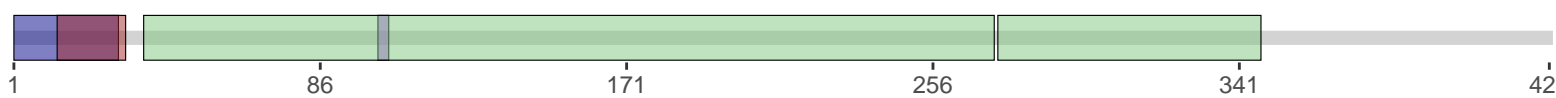
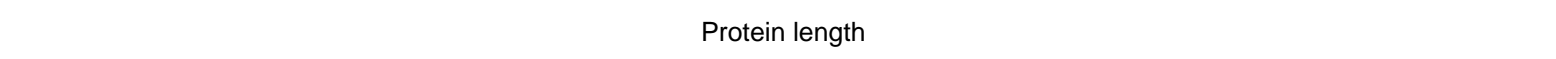


Gel Slice



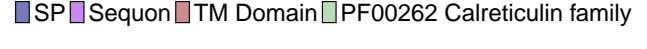
Peptide counts over 4 repeats

Protein length



Pfam domains

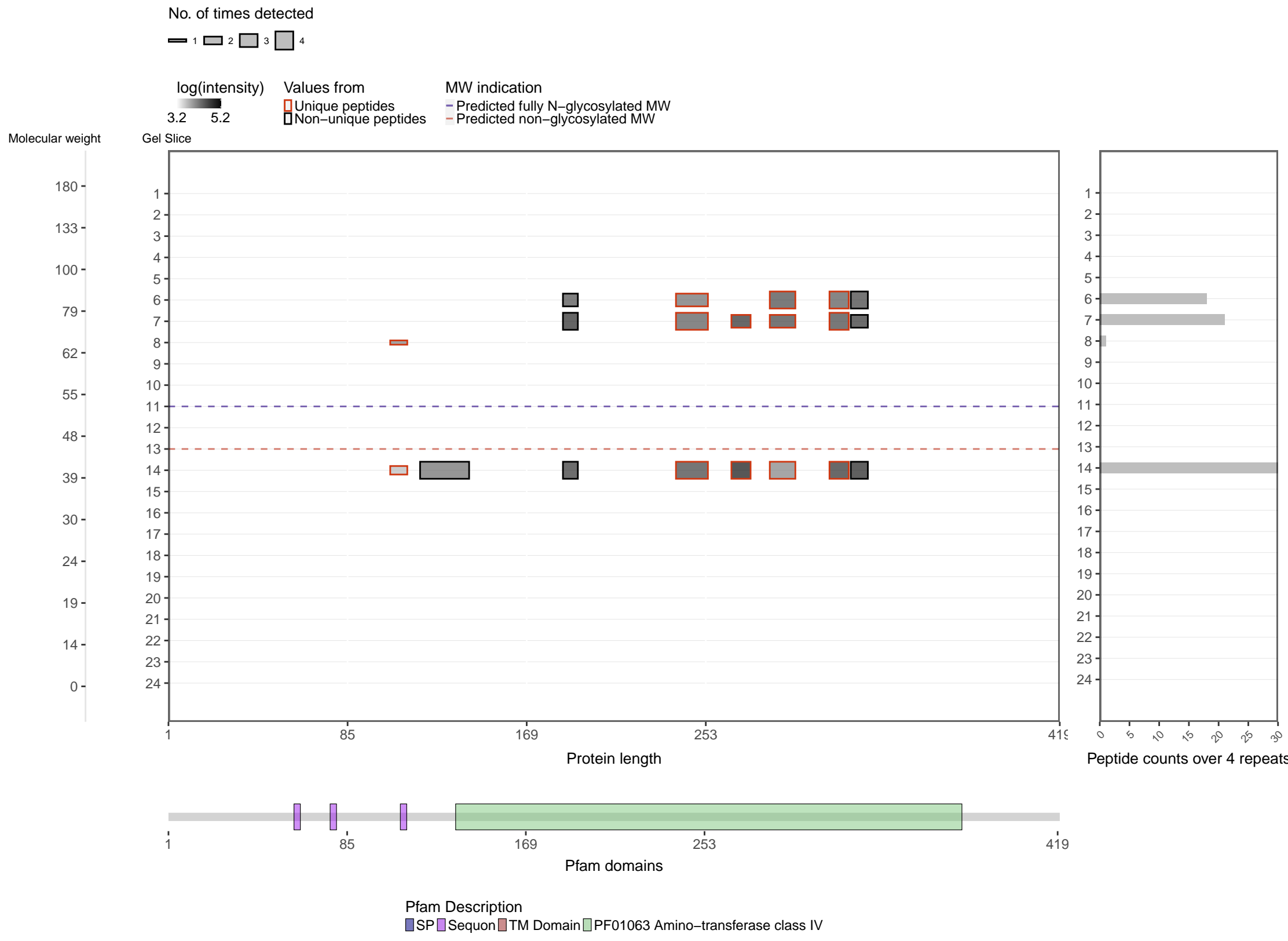
Pfam Description



Protein sequence:

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NbL12g10780.1 branched-chain-amino-acid_aminotransferase_3_chloroplastic-like [MW = 45.35 kDa]

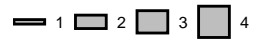


Protein sequence:

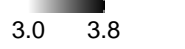
//PPSPGKSLYRPLLMGGGAVLGLAPAEYTFLLVSPVGNVFKKGLAPINIVETEMHRATPGGTGGVKTVDVNVAVLKAQSAKAKGYSDVLLDSVGVQKRYLLEESGNNVFIWGNLIVTAAKGTLPFGITRKHSDVLSGGFVEEERLIVSVDLLEDADEVFGTAVVSPVGSITHQGRKRVTYGNNGVGVGGQQLYSALTSGLQMLAKDKMGWVLEK*

NbL12g10770.1 protein_CROWDED_NUCLEI_4-like [MW = 109.76 kDa]

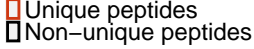
No. of times detected



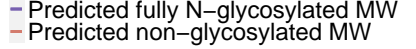
log(intensity)



Values from



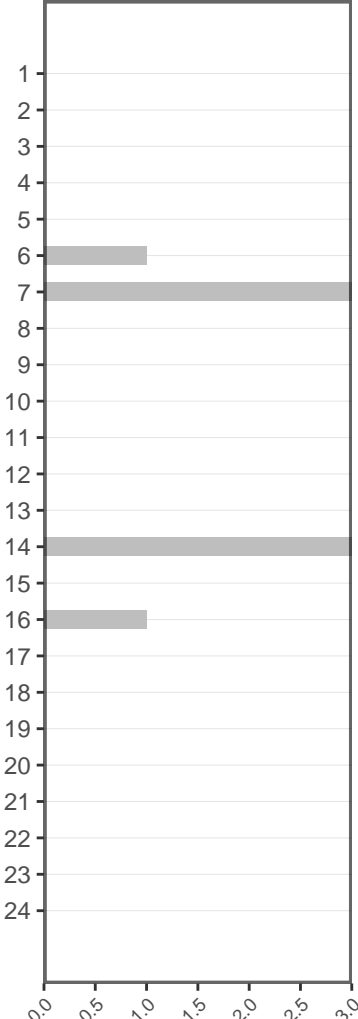
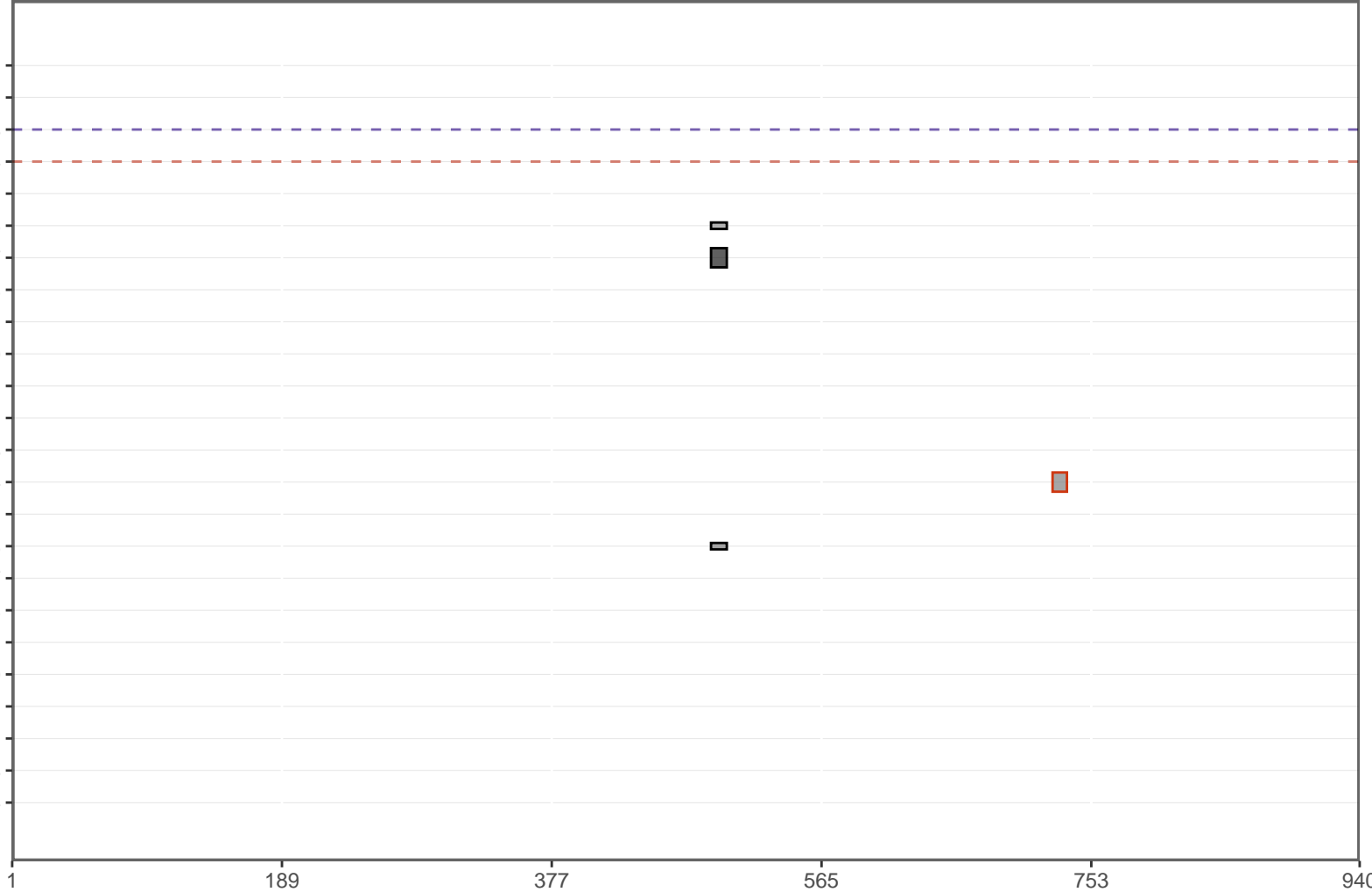
MW indication



Molecular weight



Gel Slice



Protein length

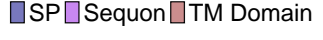


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

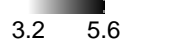
MKNDLEKSAKIMDEKRRKSIDHEEENVEAMKSETQELLILETRLKGQIEDMIRAEKEEKEKADRLKAEKAKFETEWIWEVDEKREELQKEAEGVAEERIAKSLKDSRDLKAEKNAIQEYKGLNLSLSRDRFAFMYEIEGAEAEVWFSKQKEREKFNFLDVMQKKELENIEKRRKEEITDLKEKEKAFEEQKKRELDGASRLRTEKKELEHVGLELKLDAERKDKNLDRERRDKAEWELNNAIEELKVGRLKLEKRELLHADREELAQIEQLKLEEVKIPDRITPTKLL

NbL12g10760.1 lysosomal_Pro-X_carboxypeptidase-like [MW - SP = 55.04 kDa]

No. of times detected



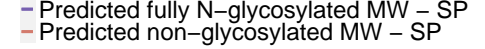
log(intensity)



Values from



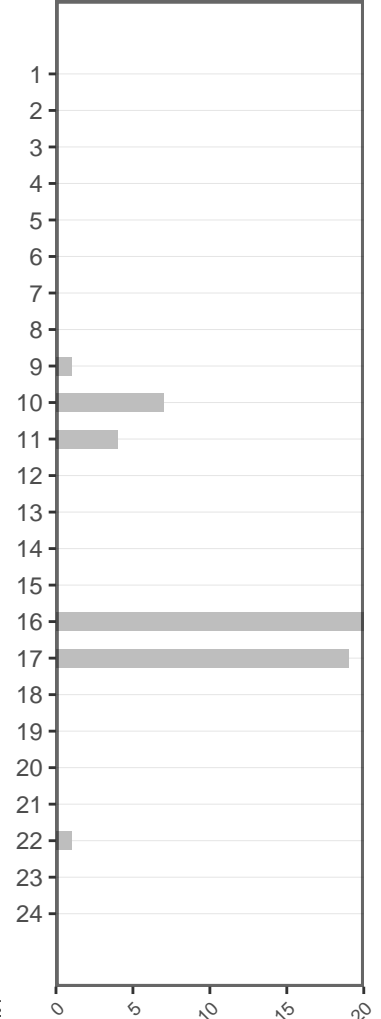
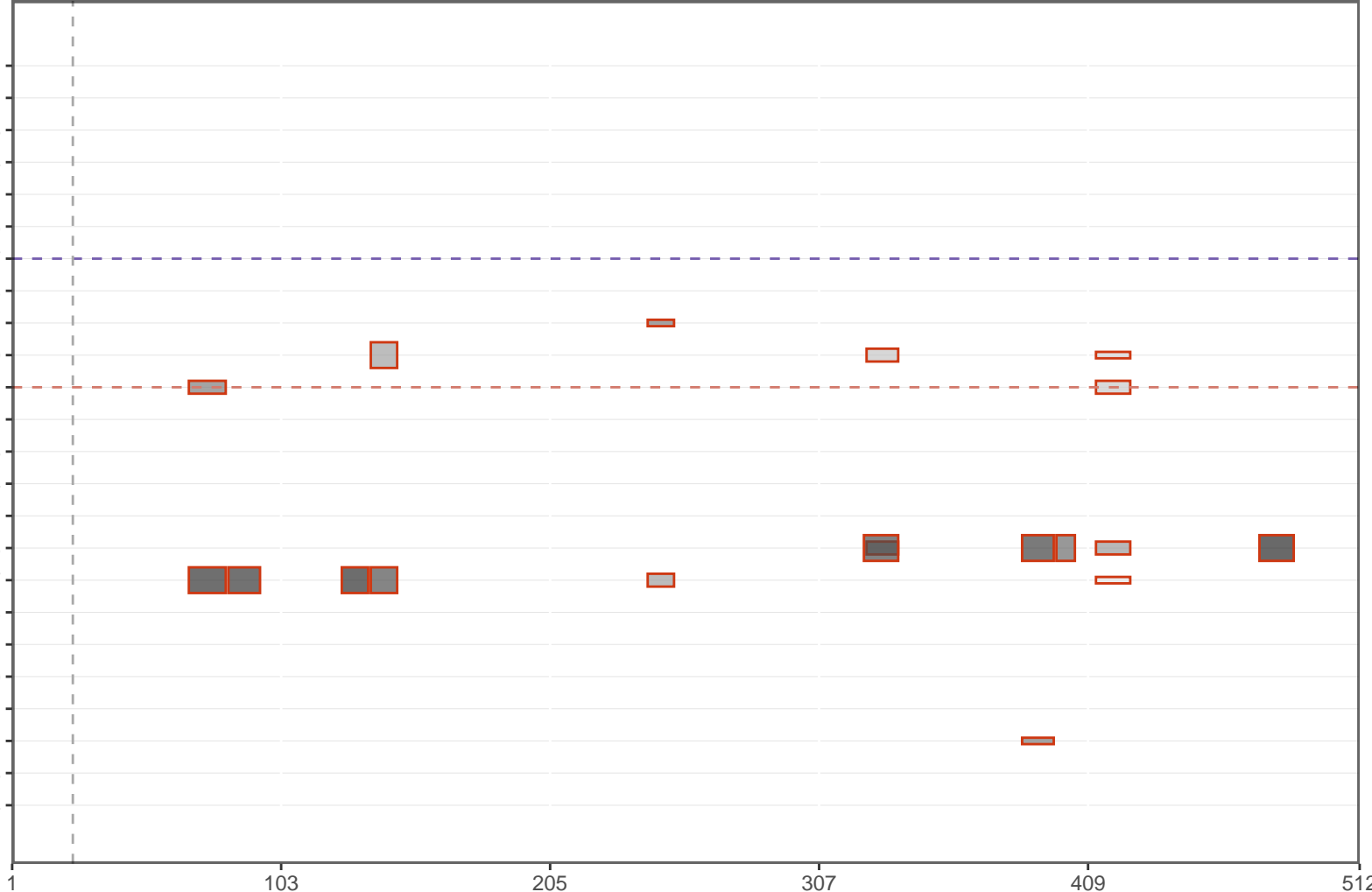
MW indication



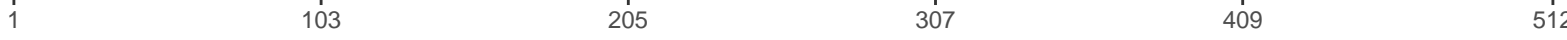
Molecular weight



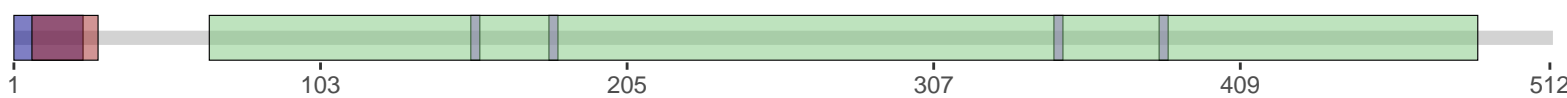
Gel Slice



Protein length

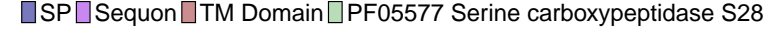


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISCFTHKESVDVINSVEGMNGLADLTKTFHLGRKLEVDVGLSNWLESAYSVLAMANYPVPTGFLMPLPQSPKKEVCRKIDGLPDGASVLRIFRFGNYYNYNTGDKVFNLDDPHGMSGGVDWAGACTEMVMPMASNRRTSMFPEFYDQPKSNEEQGLKDFHKPRPTWITTEFGGHAFKSALKAFGSIHFNGLLDPWGGSVLEDDVSETVALITEKGAHLLDLRAATAEDPWLLEGRSSEIKLRGWLKDYVDEKKATFNM

NbL12g10700.1 probable_xyloglucan_endotransglucosylase/hydrolase_protein_7 [MW - SP = 29.89 kDa]

No. of times detected



log(intensity)



Values from



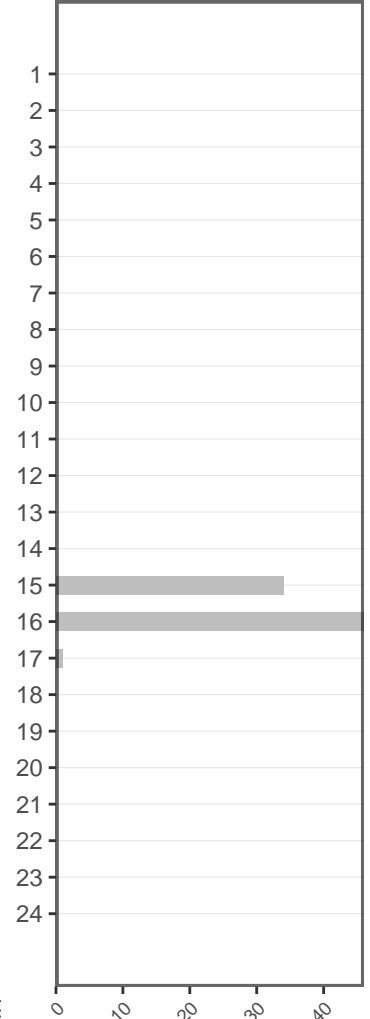
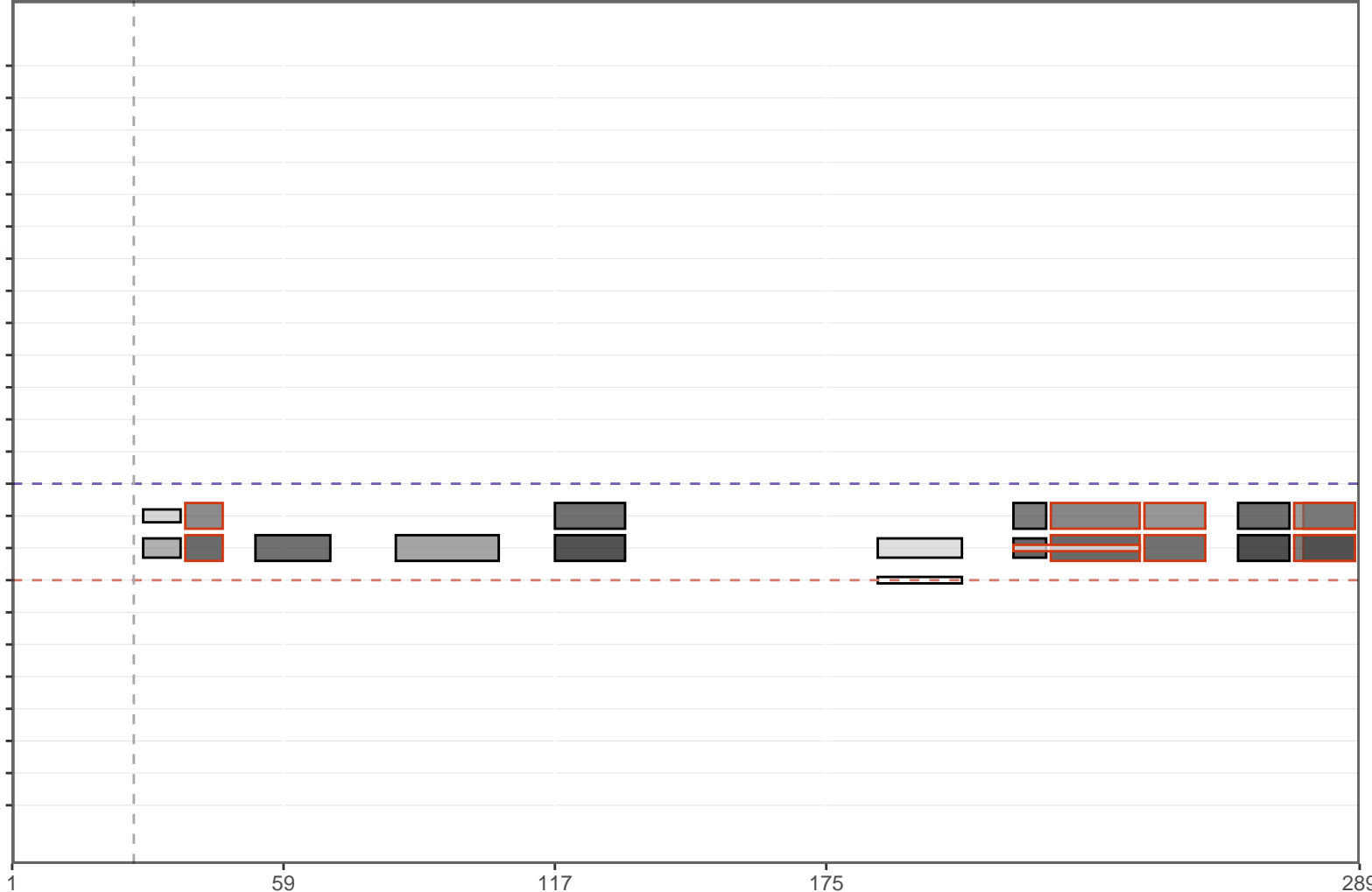
MW indication



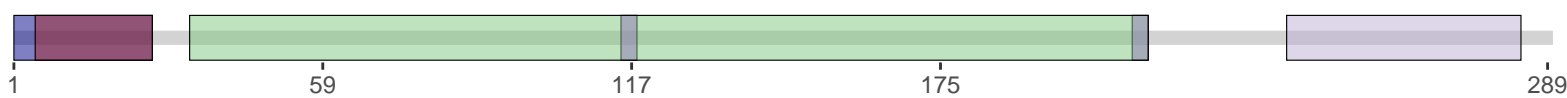
Molecular weight



Gel Slice

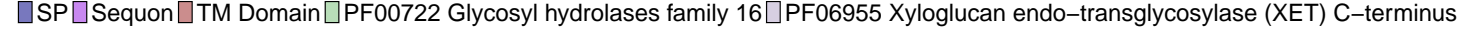


Protein length



Pfam domains

Pfam Description



Protein sequence:

KEQRNLWFDPSVDFHFTLNNHHTVFDVDFRIRVYKNNKAEKGFPPKFGPMGVYSTLWEADDWATRGGLEKINWKSFPVAYYKDFDIEGGAMPSPANGATNPRNWWWEGGGLSAVEAKGYRWRMNHMKVDYCTDKSRNPTPPEGVDDI

NbL12g10680.1 cysteine_desulfurase_mitochondrial [MW = 50.39 kDa]

No. of times detected



log(intensity)



Values from



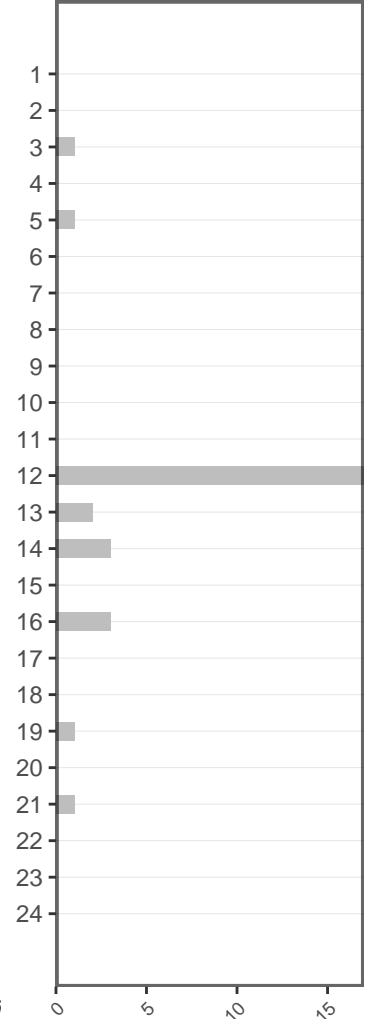
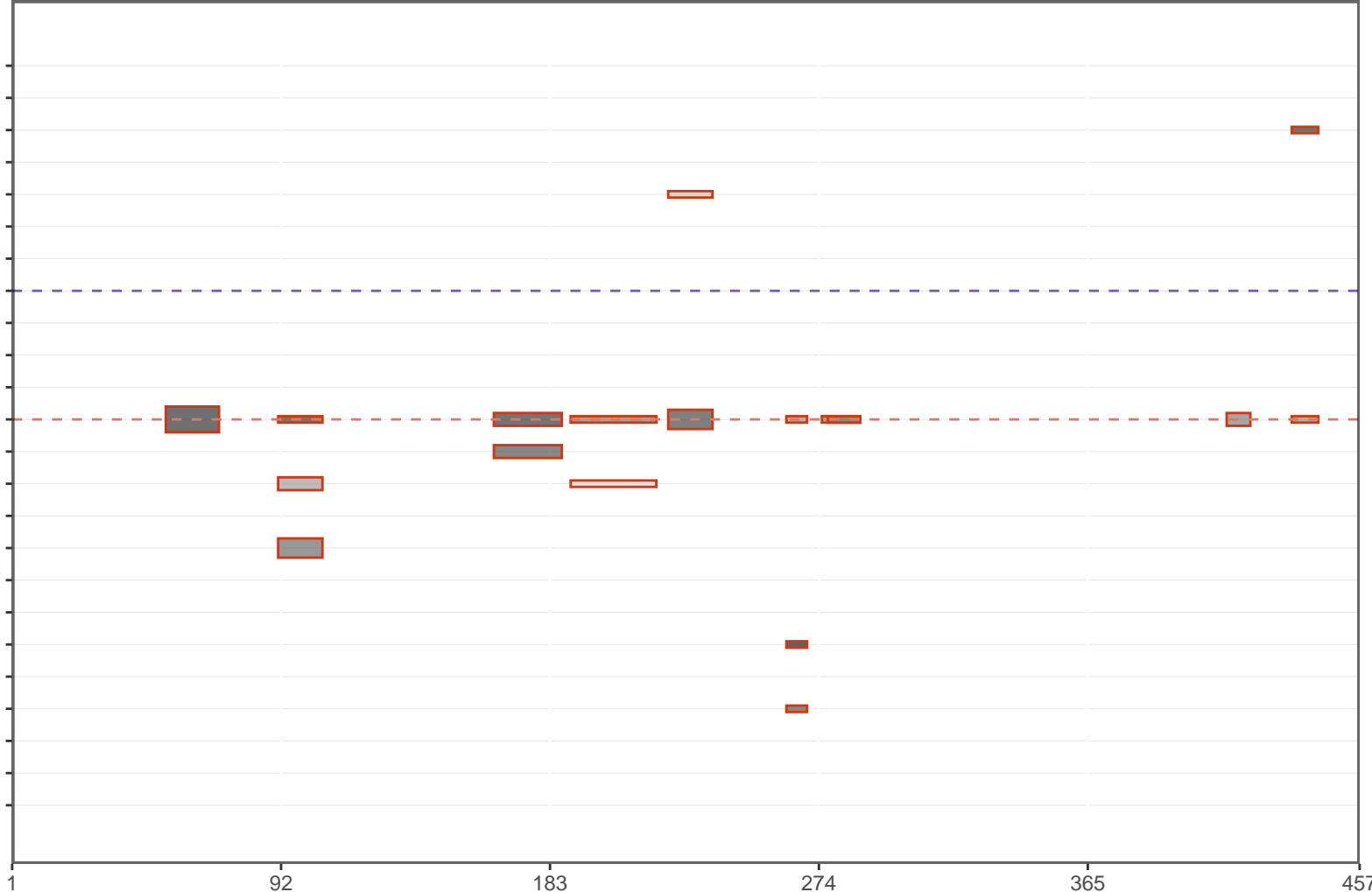
MW indication



Molecular weight

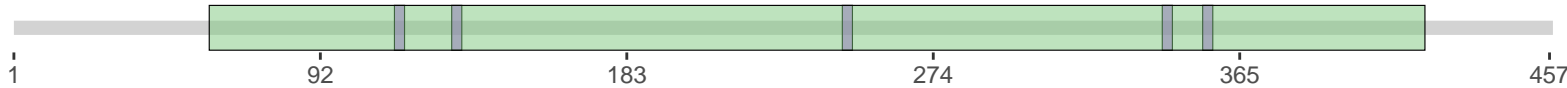


Gel Slice



Protein length

Peptide counts over 4 repeats



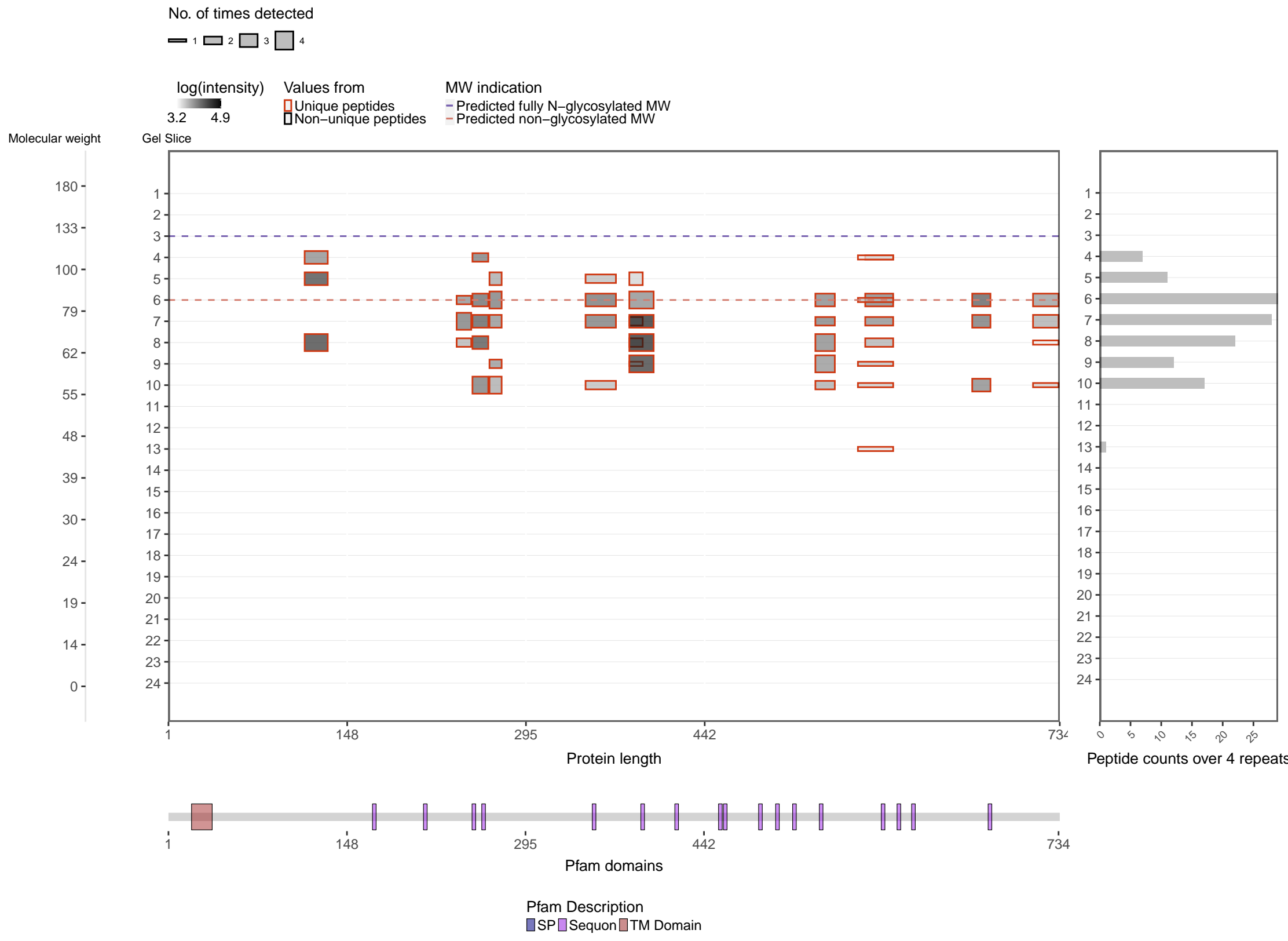
Pfam domains

Pfam Description



Protein sequence:

IEIGKCKEFNVPFHDAAGALGKPKIDVEKMNISLMBLSGHKHYGPKGVGALVIRRRPRIRVEPQMNNGGGQERIRSGTVPTPLVGFGAACELAMKEMEDYDGRKIKLQERLLNGRDKIDGVVYNGSFERRVAGNLNLSFAYVEGELLMLGLKEVWSSGSACTSABLEPSYVLRALGVVEEDMAHTSRIVYIGRFFTEGEIDRAMDLTVKQVEKLREMSPLVEMVKEGDKSIQWQH



Protein sequence:

INLAMNLEEQSKKXGEDELGDRNKNNEASDEGLNKSEADAGENKMKVQSSSSSDNNAAGEASNSGNSGNSGNSDPNAGNEATGQTGTGNAAGETNRINENINNSNSDAAAGTNEANEHOGGNSNSHISHTQENNSSDNENNPAGNENNSGSDNPNAGNENNSGSDNSNAEATNEANKKGGGENDSSTGTTGNENKNSGSDNSAEGTNKANKKQGEDEKNSANEAAASVGGDTGNISNEGQSEKSDNSGSDNNSGNEEVSITGNSGSESVWVVDQGNVSTAGATEKSTI

NbL12g10620.1 40S_ribosomal_protein_S14-2 [MW = 16.34 kDa]

No. of times detected



log(intensity)



Values from



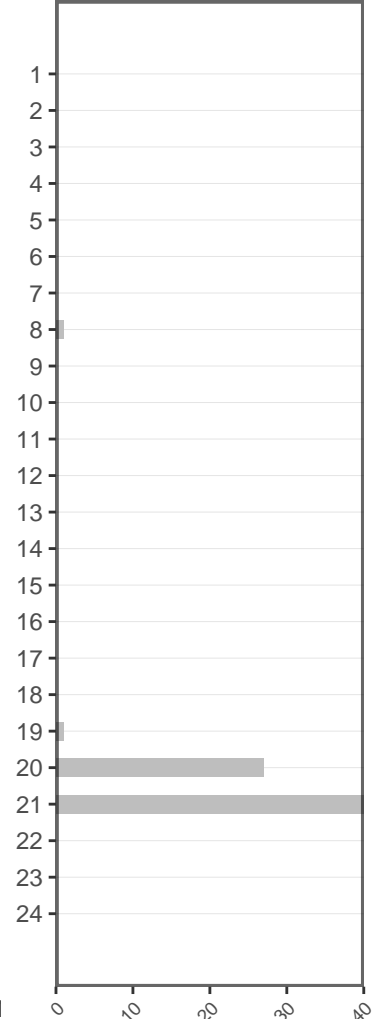
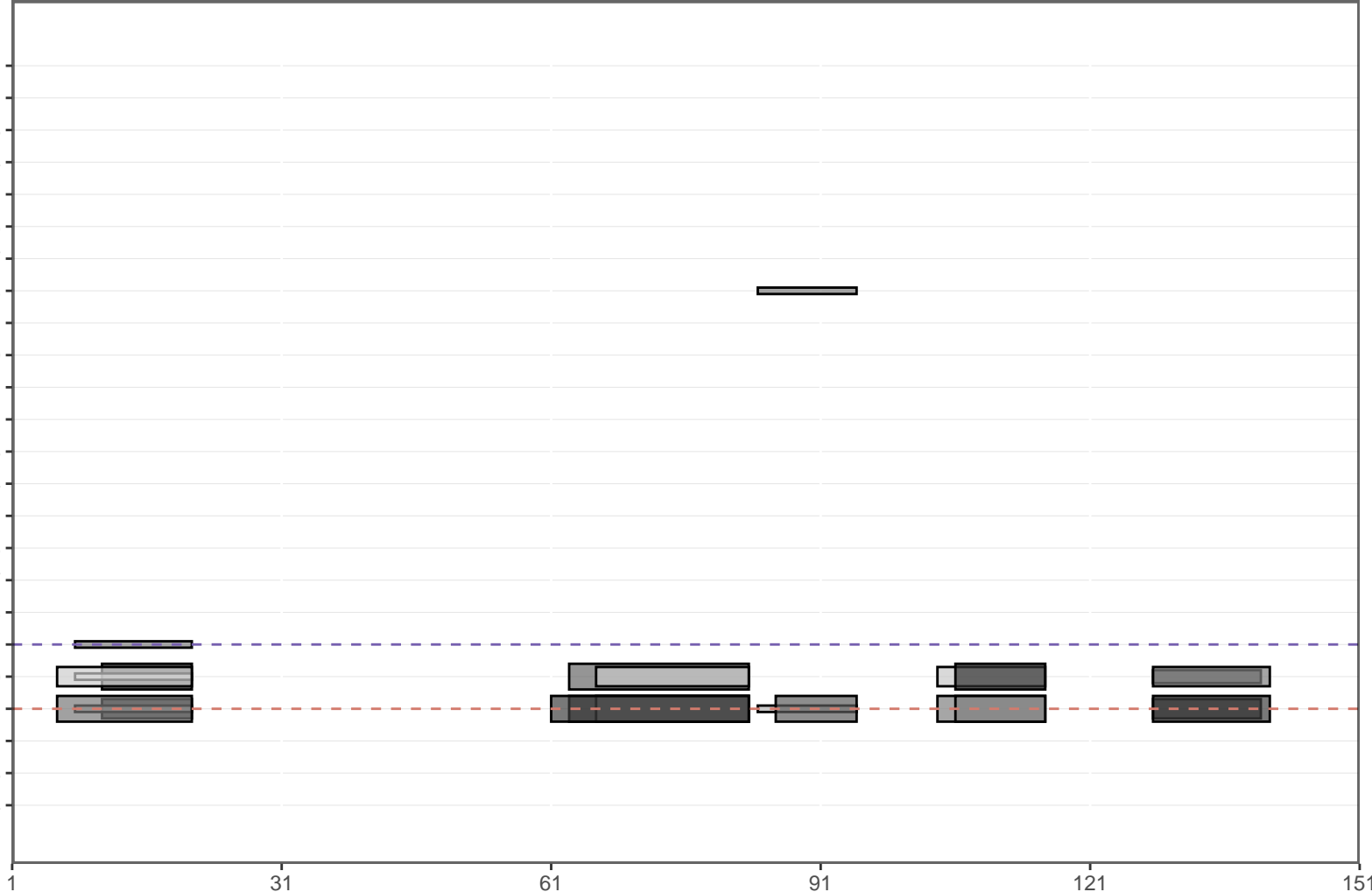
MW indication



Molecular weight

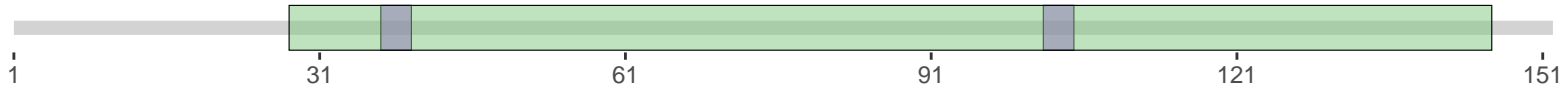


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LDRESSPYAAMLAAGDVGSRKELGINALHKLKLRATGKTKTPGPGQBALRALARSGMKGRIDVYPIPTDSTRKGGRRGRRL

NbL12g10600.1 Ia-related_protein_6A-like [MW = 46.4 kDa]

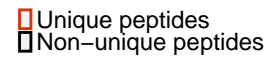
No. of times detected



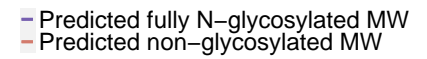
log(intensity)



Values from



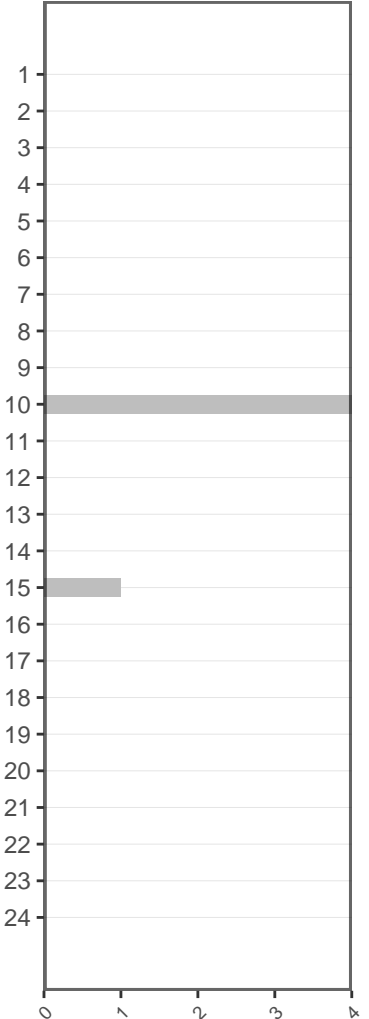
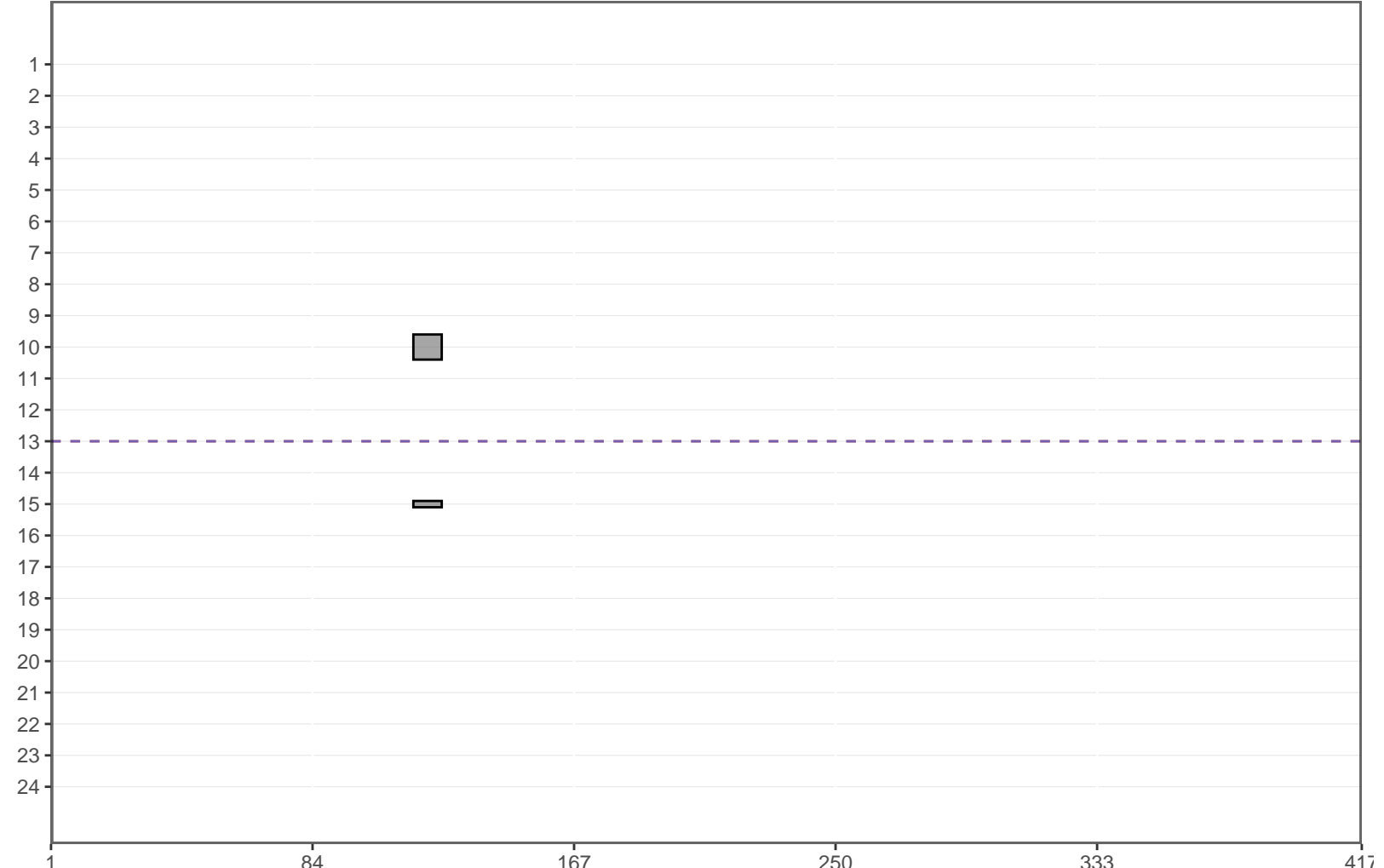
MW indication



Molecular weight



Gel Slice



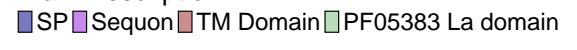
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AELKLSGKLAHALVYENTVEAEKAWALNDEGDWRFGLRVLKTKTKPKPGKNGKWRDPDSDRNMINQASGGAVNEEYHSESHVLRGKPKGSGKGRSDPDSRINTNVGASDLAVNEEHSNHHFVDSPEDEEGDHRKSKETVGEHAGKEKNVHRVQTRNRRGRGRNKRGTNGHGHGTTFTYKNHVESKFPKPRMPDGTGRGFAMGRGPLSSPQ

NbL12g10590.1 uncharacterized_LOC109208446 [MW - SP = 39.86 kDa]

No. of times detected



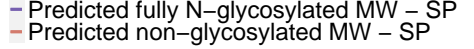
log(intensity)



Values from



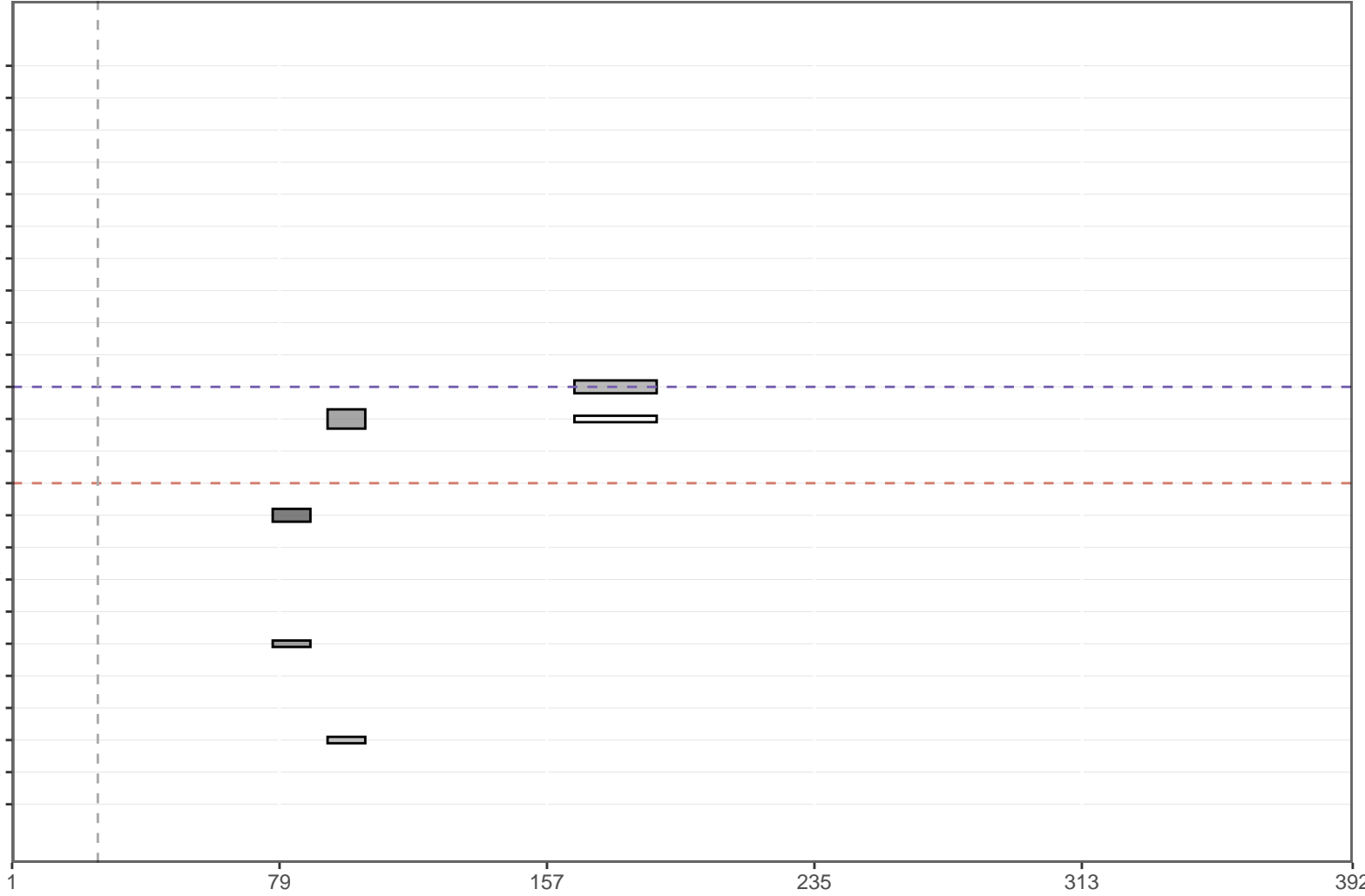
MW indication



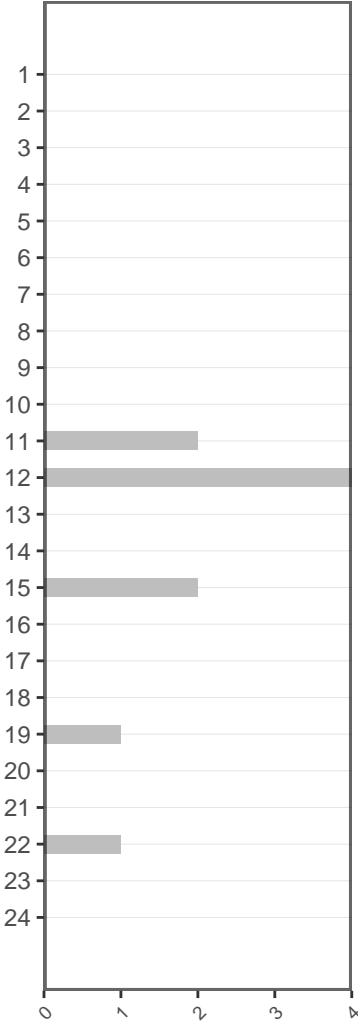
Molecular weight



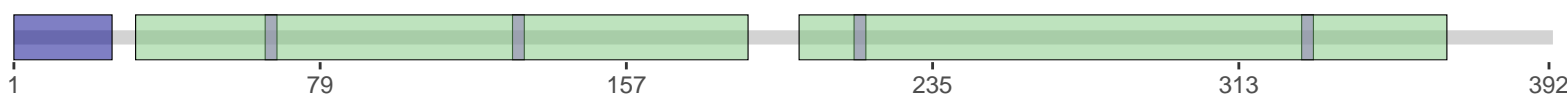
Gel Slice



Protein length

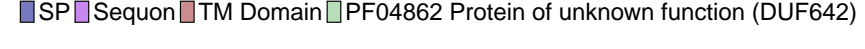


Peptide counts over 4 repeats



Pfam domains

Pfam Description

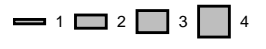


Protein sequence:

MDIAIKLFLNPKSKGNALNGDFEEGPNMFRNANLGVLLPTNLDEETSBLPGWVESNRARVRYDNYHFTVPEGRKRIELLGGKEGHISGMVETKPKPKRYLFLFHGHAGDGGKQPLAVAMFAGDQAGNHHTPNSDSSFGIANKLNTAKADRTWAFYBYNYNTRSDDMSEKGGPVDDKVRVEVSGSSTVRLVGFGLMLWLLVLI

NbL12g10450.1 40S_ribosomal_protein_S4 [MW = 29.85 kDa]

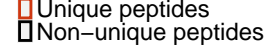
No. of times detected



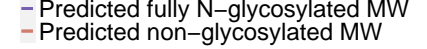
log(intensity)



Values from



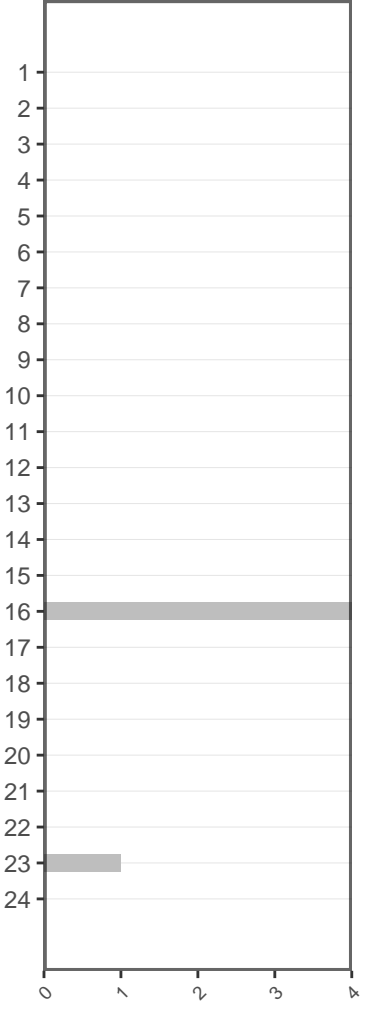
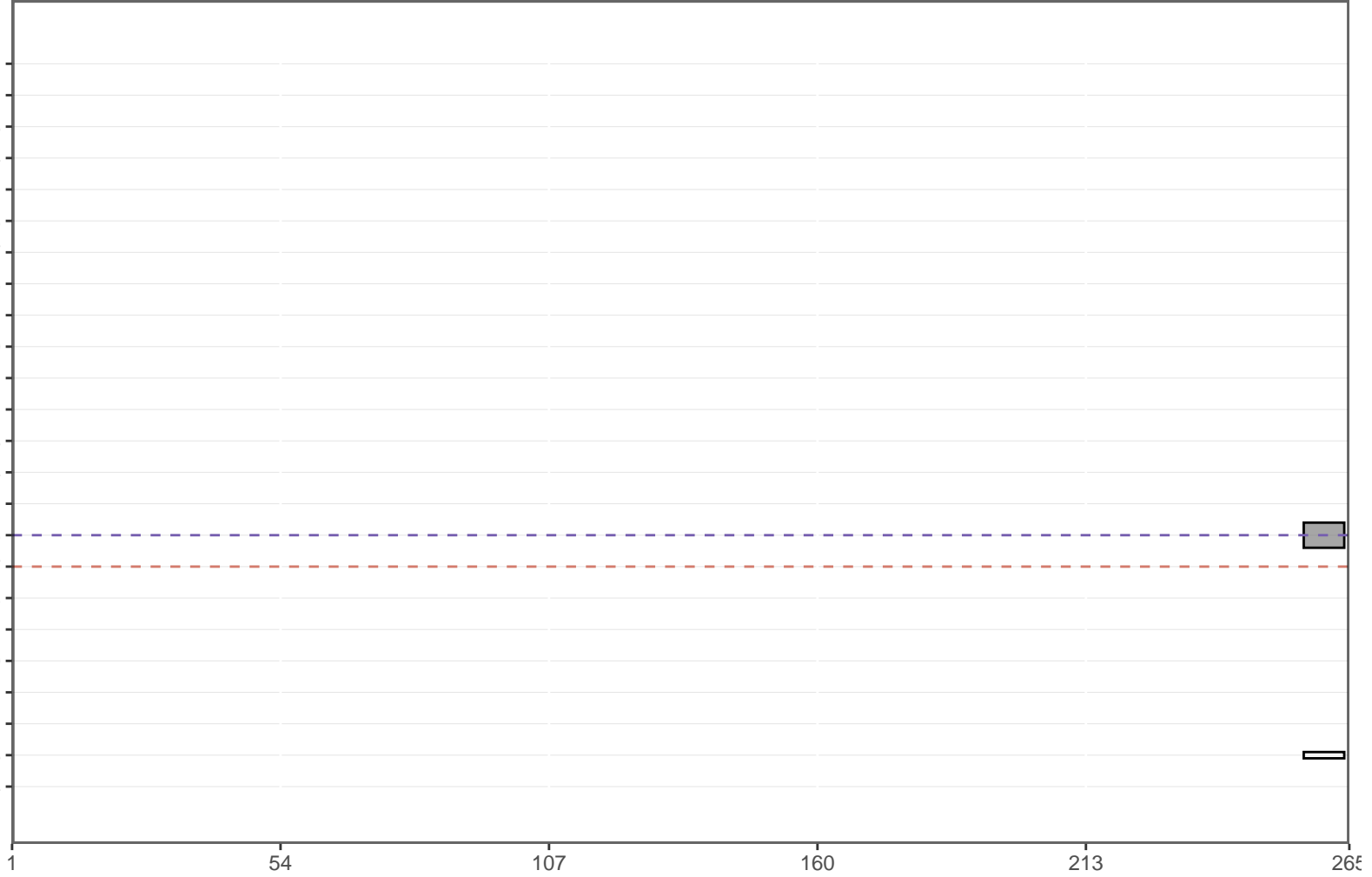
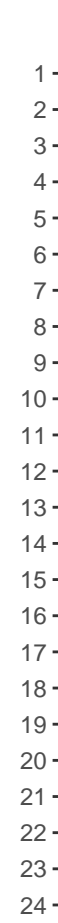
MW indication



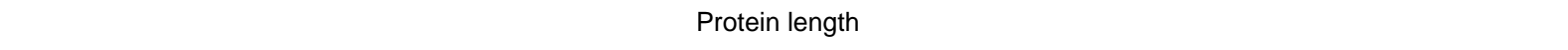
Molecular weight



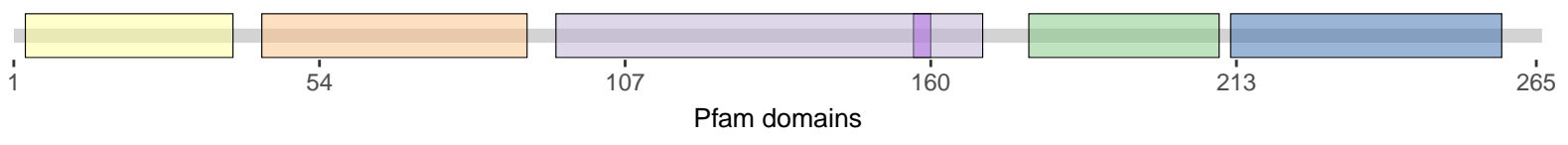
Gel Slice



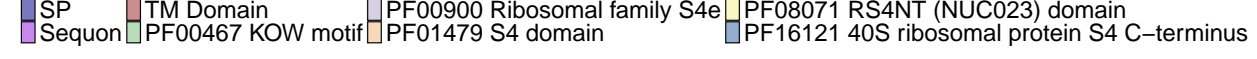
Protein length



Pfam domains



Pfam Description



Protein sequence:

AKFKLCKYRSVDFGGKGIPIKNTFYDGRTRVRYVDPDLKANDTKLDEESNKIVDFIKFDVGNVMMVTGGRRNRGRVGVKIKREKHKGSFETVHGDALGHEFATRLGNVFTLGGTKPKVWVSLPKGKIGKLSIEEARKRLAAGSATAA

NbL12g10430.1 60S_ribosomal_protein_L32-1 [MW = 15.63 kDa]

No. of times detected



log(intensity)



Values from



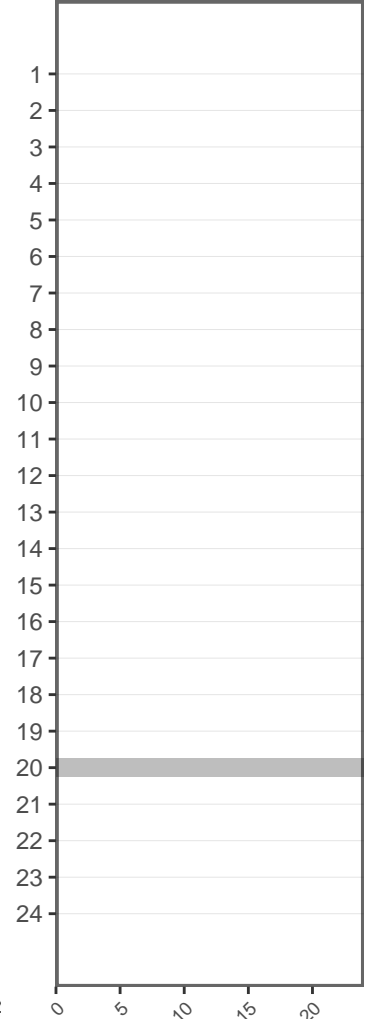
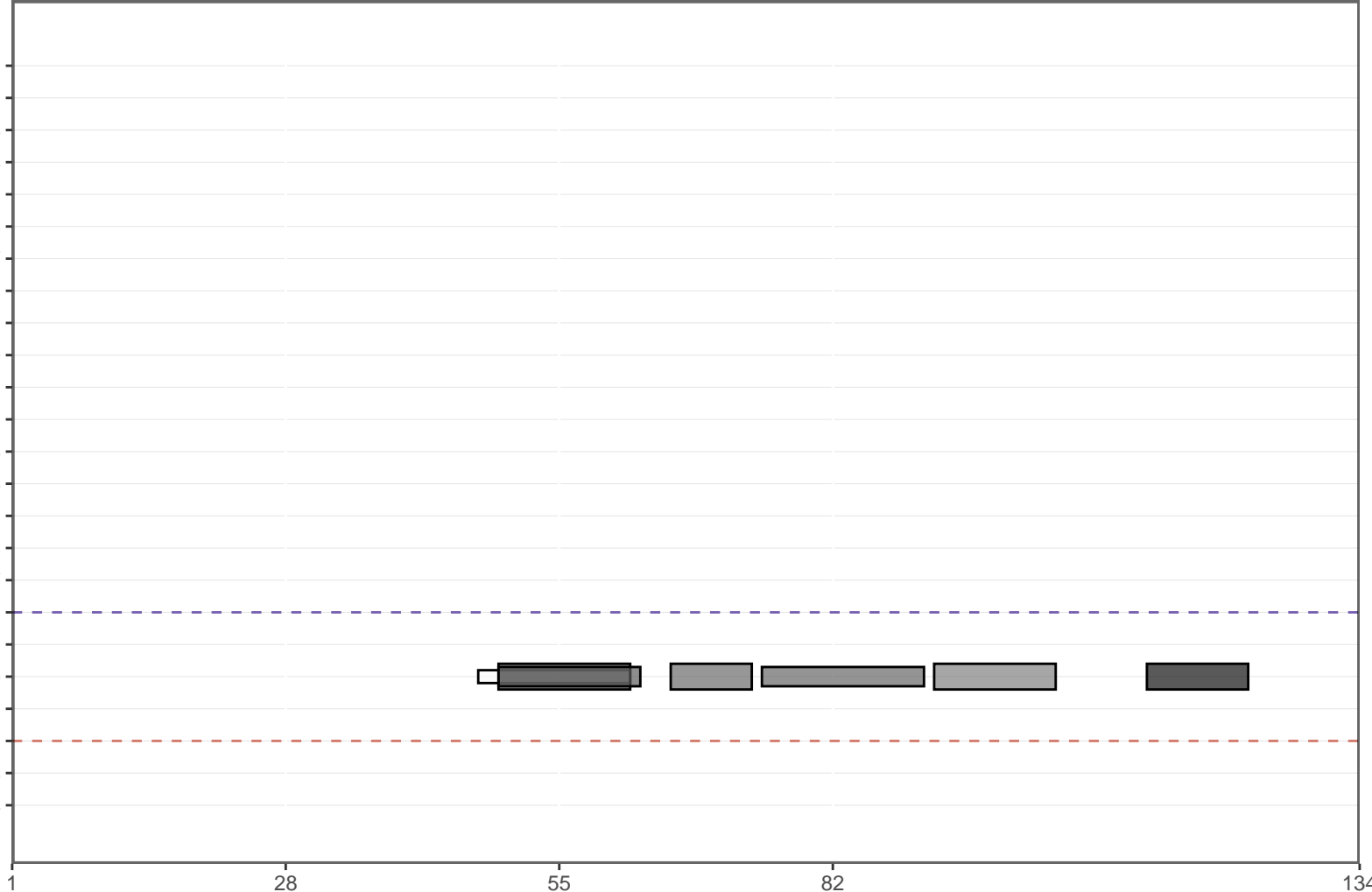
MW indication



Molecular weight



Gel Slice

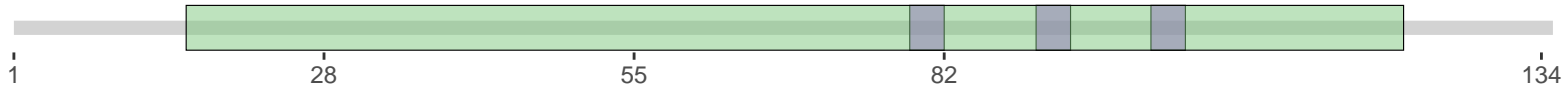


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

NIGYSDKXKTRHYLNGFKFVWNASLEVLMMHNRITYGAEIAHNVSTRKRKEVERAAGLEIVATNKLARLRGGED

NbL12g10370.1 accelerated_cell_death_11 [MW = 23.42 kDa]

No. of times detected



log(intensity)



Values from



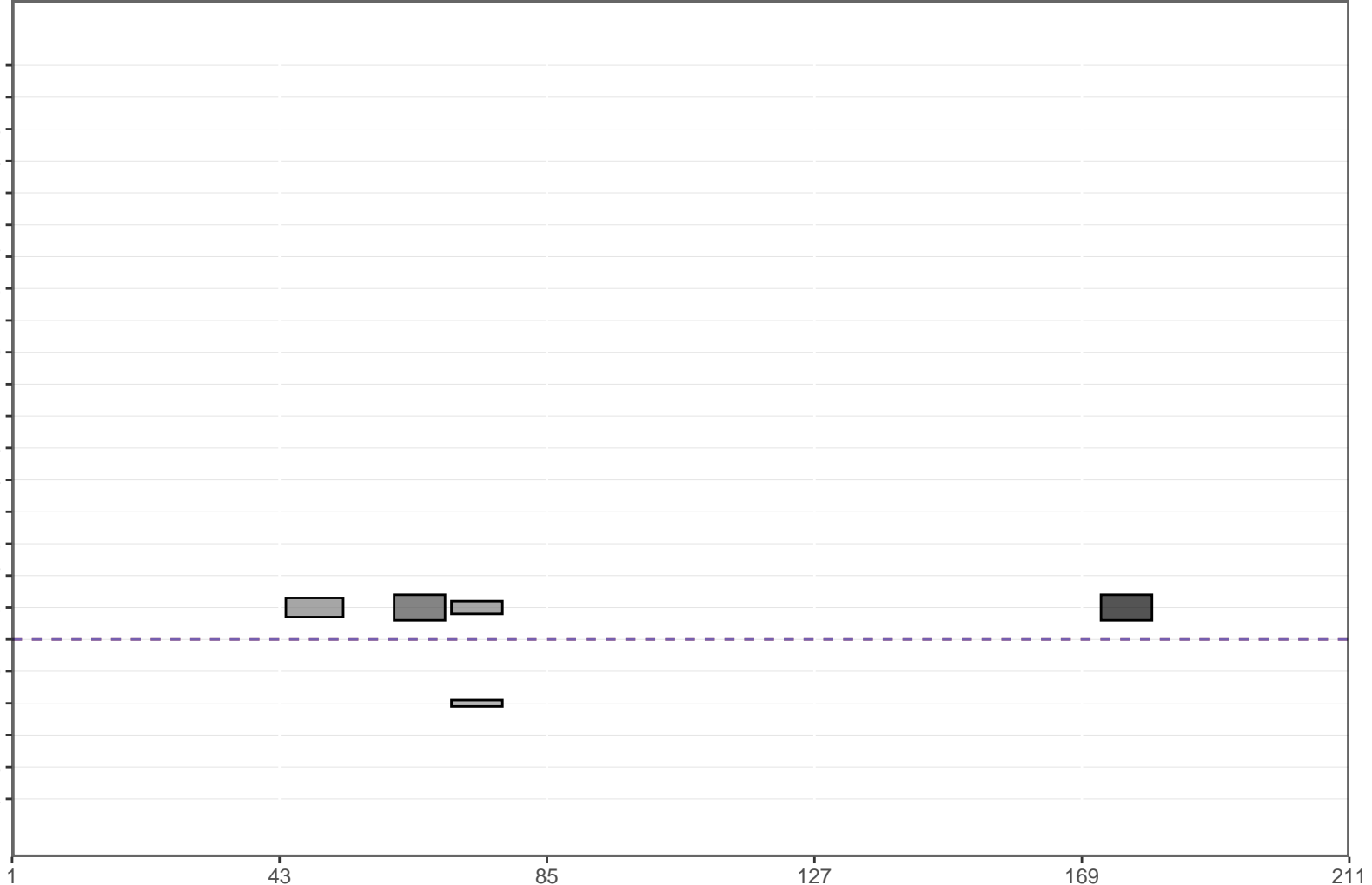
MW indication



Molecular weight

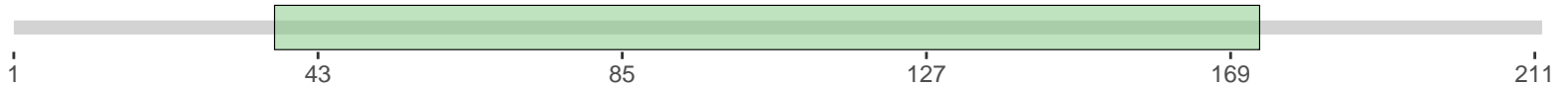


Gel Slice



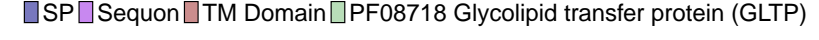
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LDQVRRAGSHTRNLRNRKGLDMKVLFEQIASEGNSLKDPAKAVGGVFAPYHGWAIRKAVSAGMVALPTRGQLMKNLNEDEASARTGMQNYVASGGTILYIDKLFISRLGIDW*

NbL12g10110.1 40S_ribosomal_protein_S25 [MW = 11.77 kDa]

No. of times detected



log(intensity)



Values from



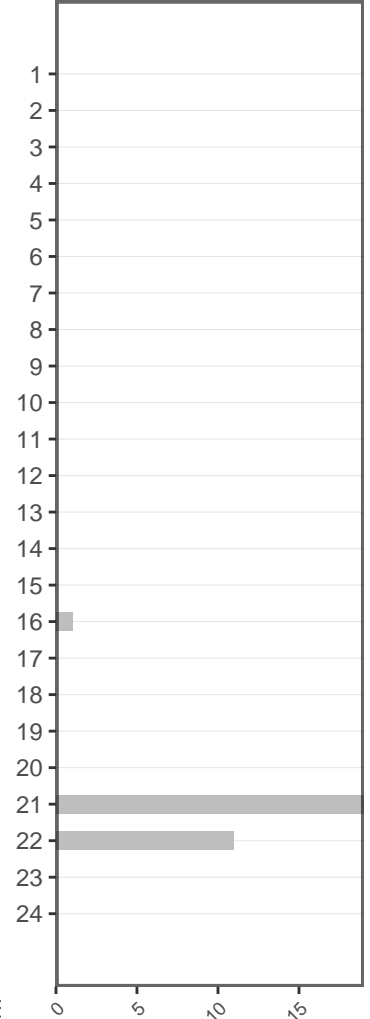
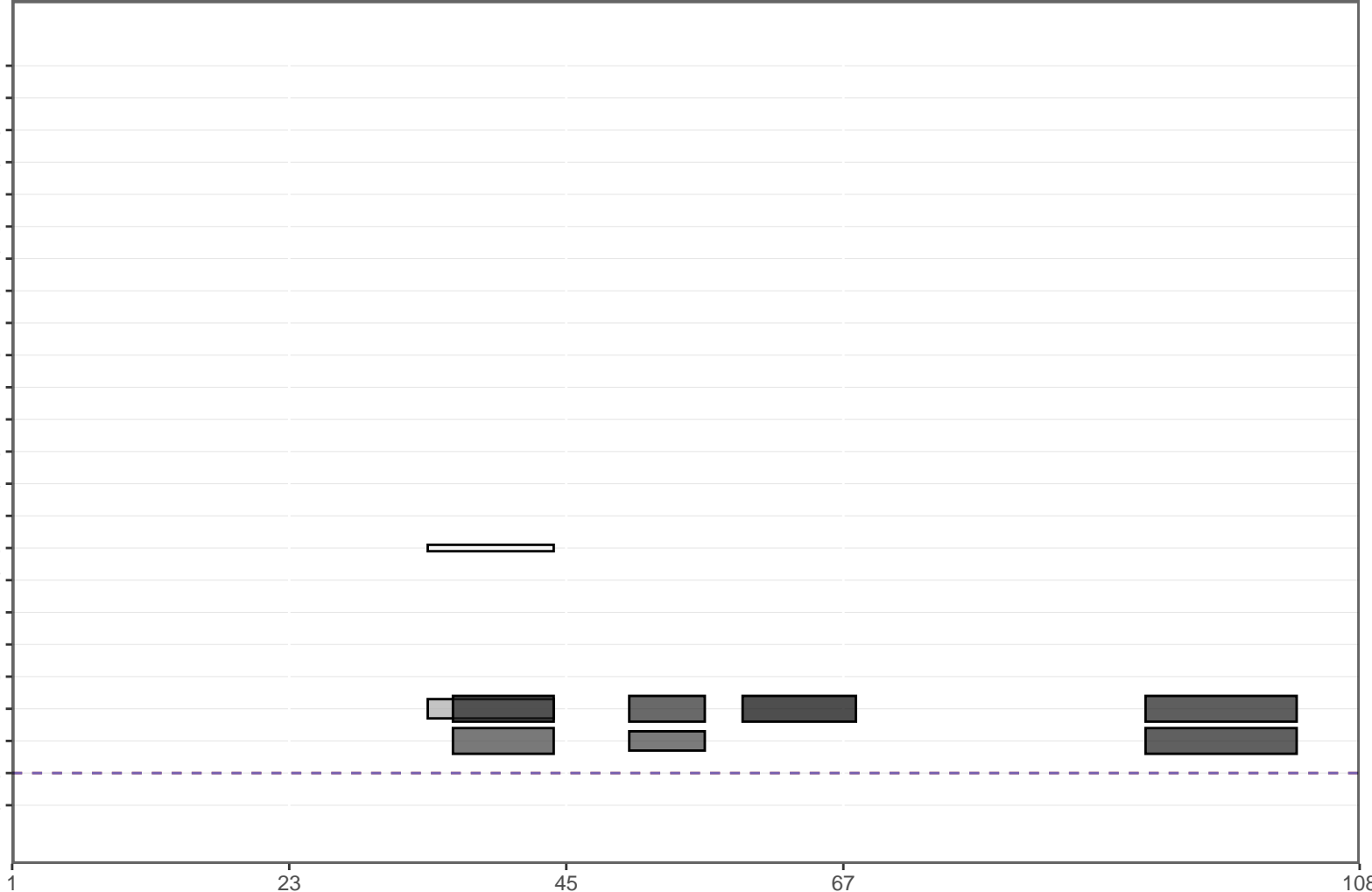
MW indication



Molecular weight

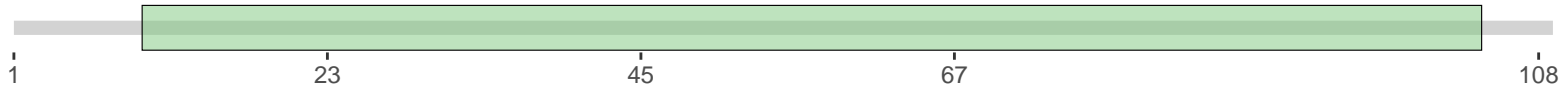


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IVLFDKATYDKLLSEAPRYKLIPTSEVLEDRLRISGSLARKAKRDLMARGSRIMVSAHAGQIYTRATNT

NbL12g10100.1 50S_ribosomal_protein_L20-like [MW = 14.52 kDa]

No. of times detected



log(intensity)



Values from



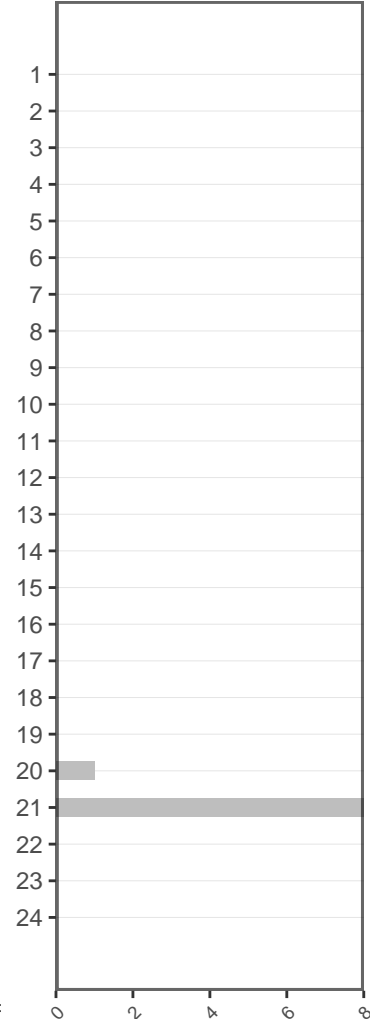
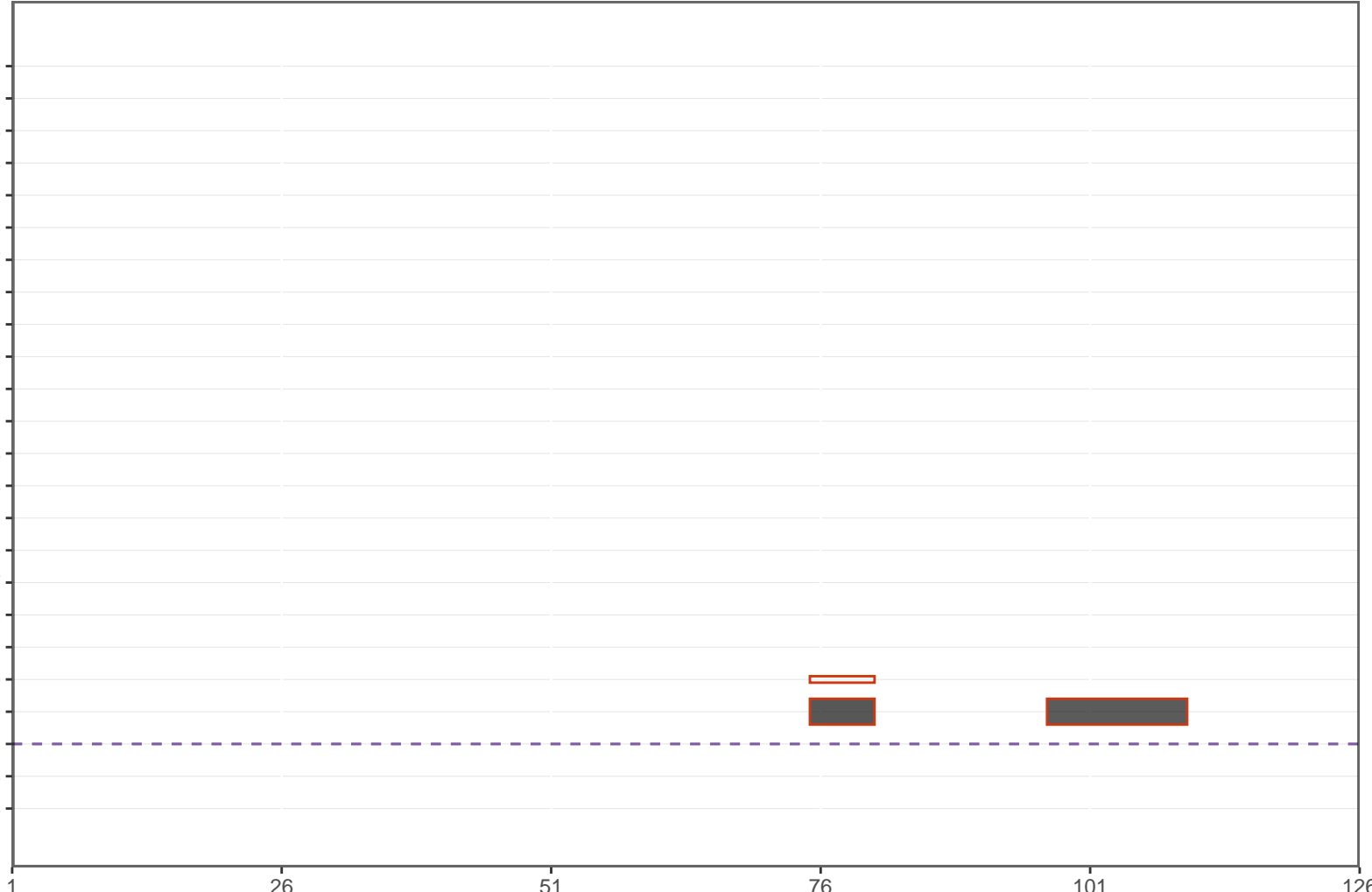
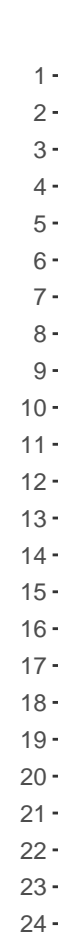
MW indication



Molecular weight

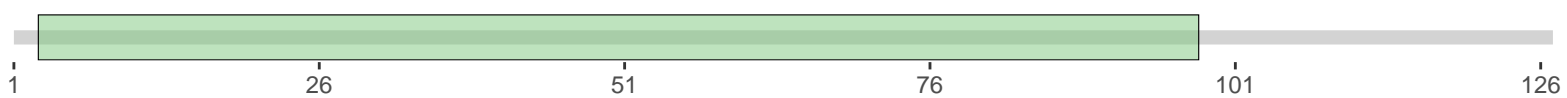


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

WQQRINAGTRCHGVNNGFNFMHGLMKNVQLNRKVLSELSMHEPVSFKALVDSSAFPQNKKAIVPPKKEGLAFL*

NbL12g10070.1 probable_carboxylesterase_17 [MW = 40.96 kDa]

No. of times detected



log(intensity)



Values from



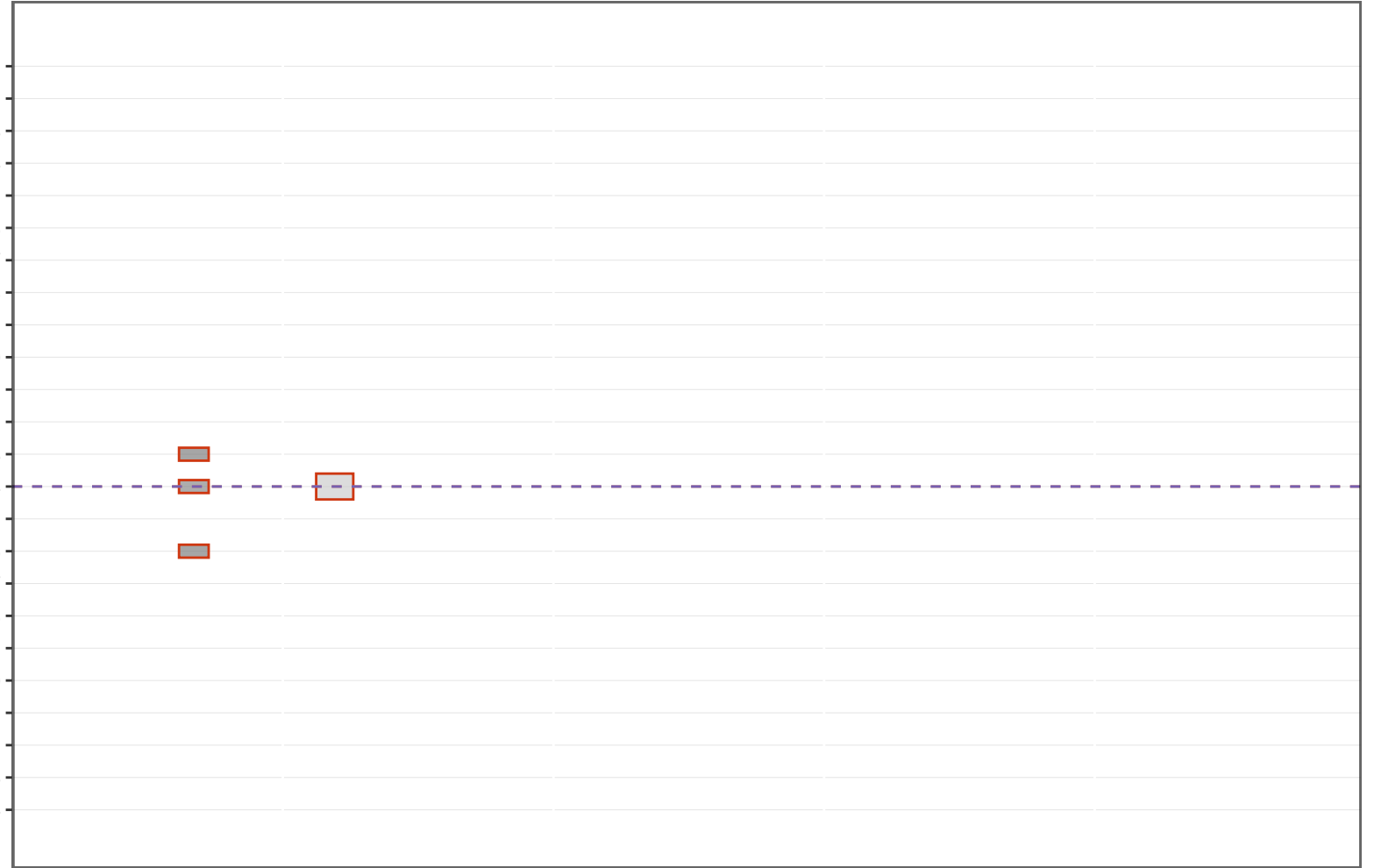
MW indication



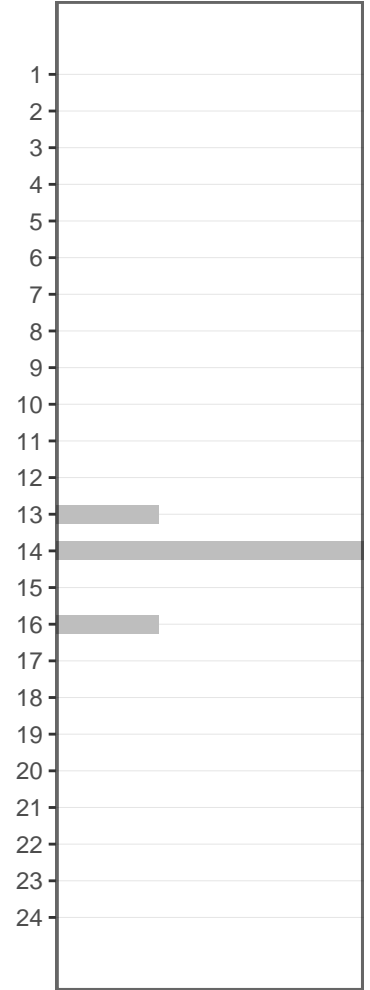
Molecular weight



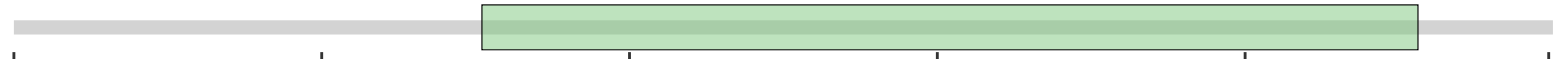
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ALLVLRDLRSROOGYEPWLDKADFNRFVLDGSSGGNVHGVAWRAGEETLSPMRLAGAIPIHGFVRSYRKSSELEGEQTFRLTDMVDKFLALALPIGSKNDHPICPMGDAAPVEELKLPFLVYGAEKDLKDTMEFYEAMKKGKQVLELFINNGVGHSEFLNKIARMDPVTGSETKLYEAWAEFRSKP

NbL12g10060.1 DNA-damage-repair/toleration_protein_DRT111_chloroplastic-like [MW = 42.02 kDa]

No. of times detected



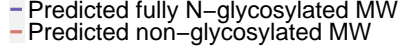
log(intensity)



Values from



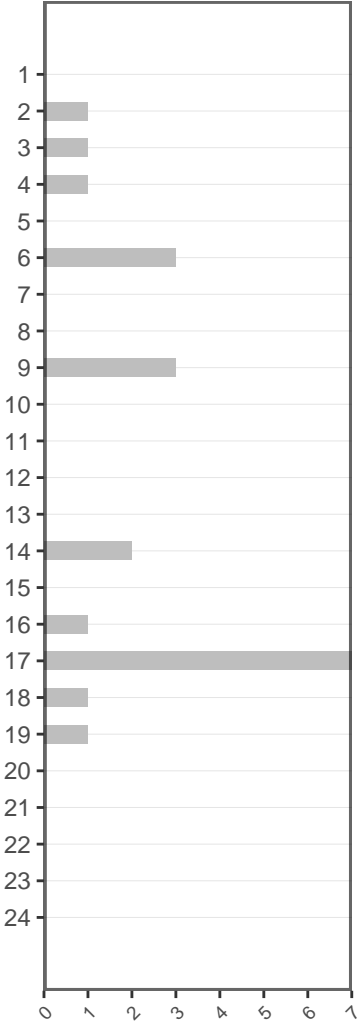
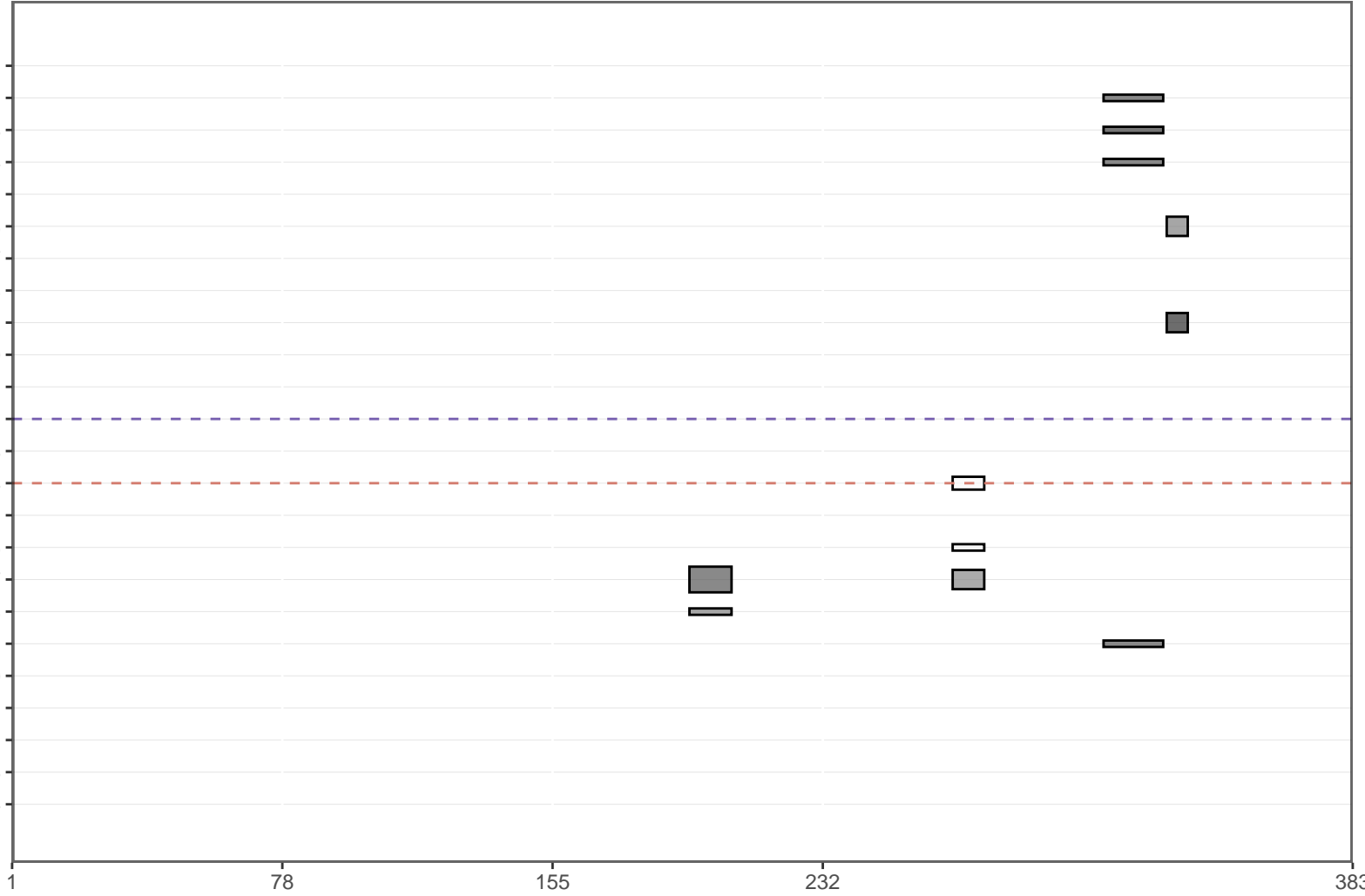
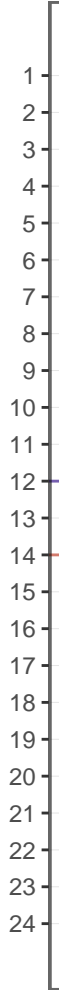
MW indication



Molecular weight



Gel Slice



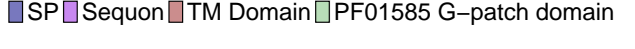
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

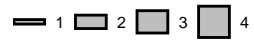


Protein sequence:

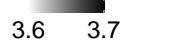
GSPSPSSQNEFSIGRSEGGGLGGAEGKMTAQRMMAMKMGWKEGGGLKLEGGITFLMAKTKDRGIVVASEAKGGGGGGHPEKVKVSNFNPPTRVLLKNNMVGPEVDDLEGEVAEEGTFKGTVTRVLFEITEANFPHHEAVRIFVGFERAEQATKALIELEGRFFGGRVHACFYDEERFSNNELAPMPGEIRGPF

NbL12g10030.1 probable_choline_kinase_2 [MW = 40.48 kDa]

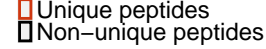
No. of times detected



log(intensity)



Values from



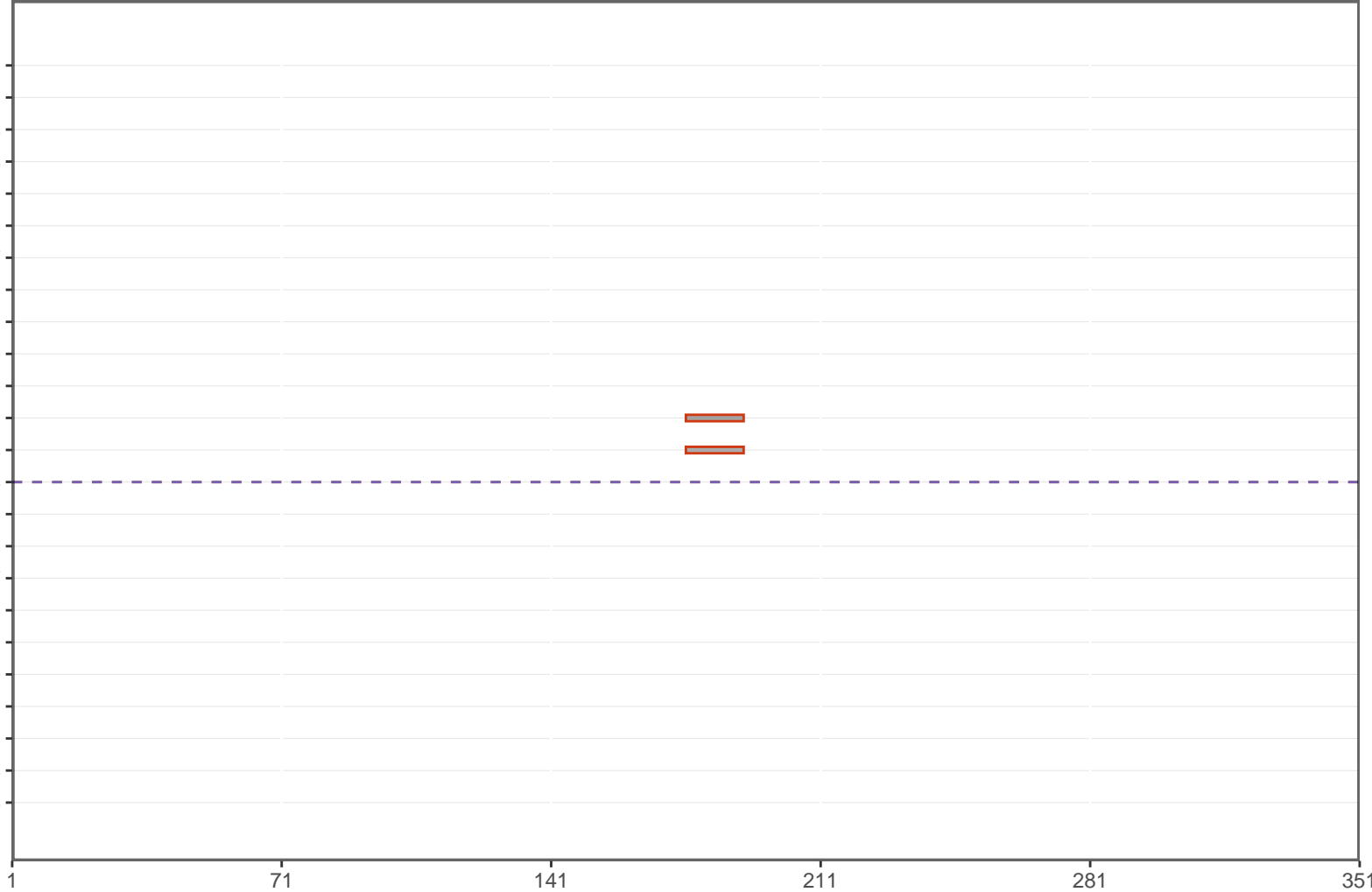
MW indication



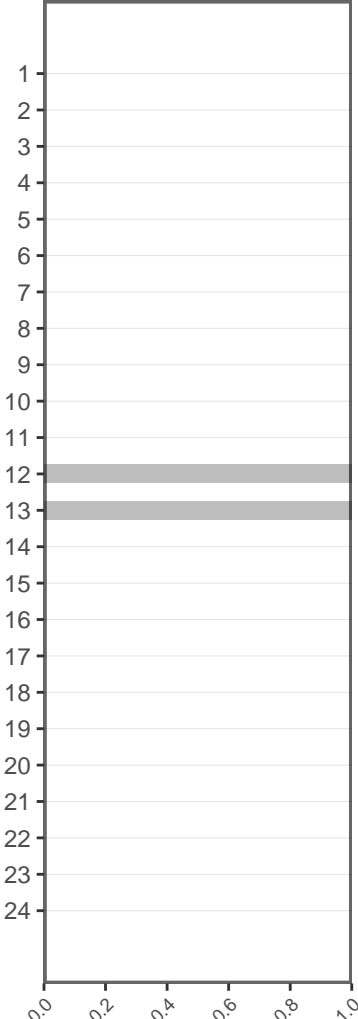
Molecular weight



Gel Slice



Protein length

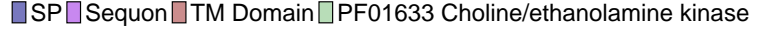


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

.NVAKRLASAEAEAKDFQLDHLGGEISALEKSLAGNHLSMGFCFNDLQYGNMDEERISITFDIYEVAGYVNHVAFDIANHFCEMVAADHTETPHMDFSKYKPLGLEERKRFLSAVLSGGGGSPSEGELEKLADEVKYLASHLFWGLVGHISHHVNKIDFNYLEYARGRFQPYWSKPELLGSSGSKKG

NbL12g09980.1 flavin-dependent_oxidoreductase_FOX2-like [MW - SP = 58.95 kDa]

No. of times detected



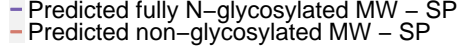
log(intensity)



Values from

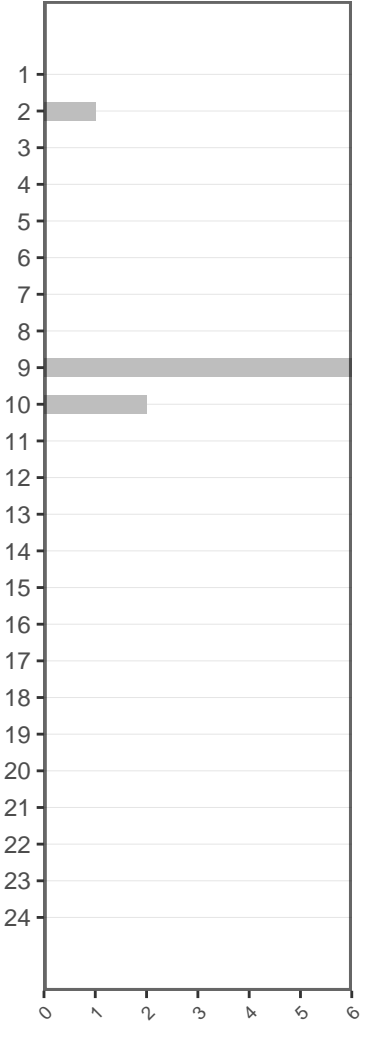
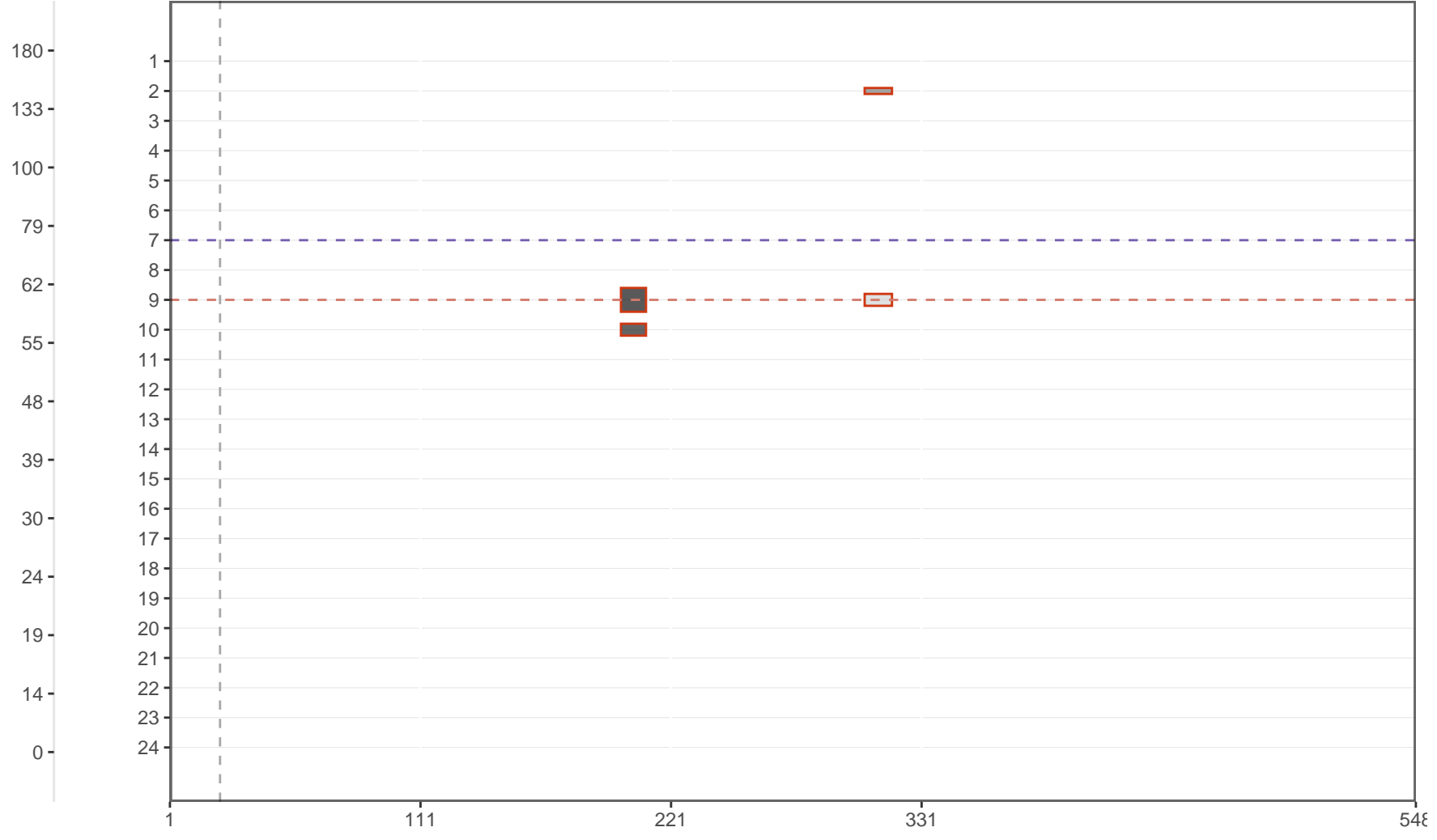


MW indication



Molecular weight

Gel Slice



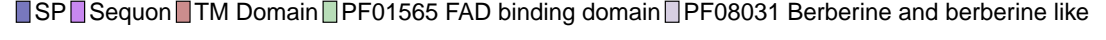
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KTLTGATKILNKWQHWAKMDEDLFRILUTFNSTKGGKTVLTAVQALFLGKTRDLLHVMNHSFPELGLTGKDGEMBWESVYIAGYPSGKPEFLLGGKGLFPPVNFKAASDFLRVPPETGLGEMWKKFLEEDSPMMWNPYGGMMGKISESIPFPHRKGIVCKIDYVLTGWSIEGDKSADKHINWIRELYEVMGTFVSKFFREAVNYNRDLDLGMMNRNANSNLEASVWGKKYFNKNYDRLLVVKTKVDPDPNFFWHEGSLPLPRKVGKDGKGLH

NbL12g09940.1 ATP_synthase_subunit_alpha_chloroplastic [MW - SP = 57.08 kDa]

No. of times detected



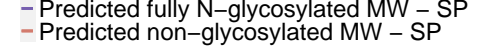
log(intensity)



Values from



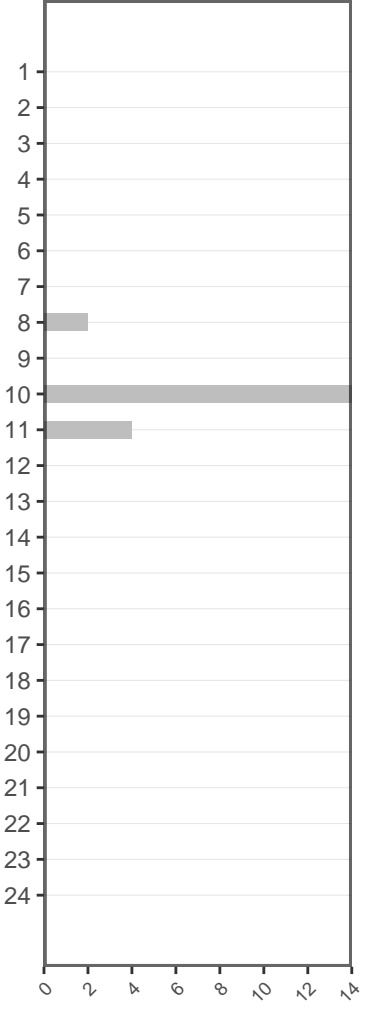
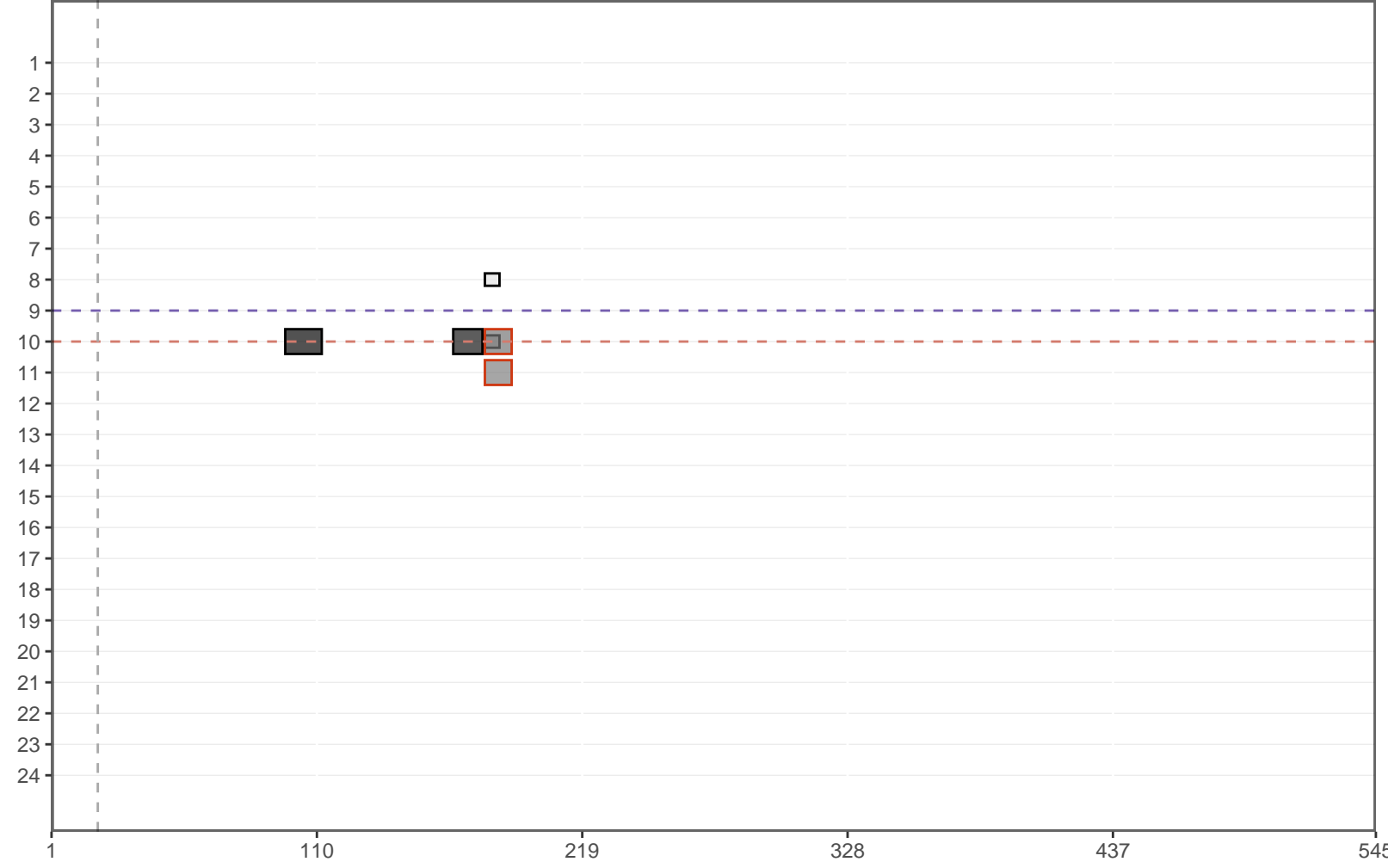
MW indication



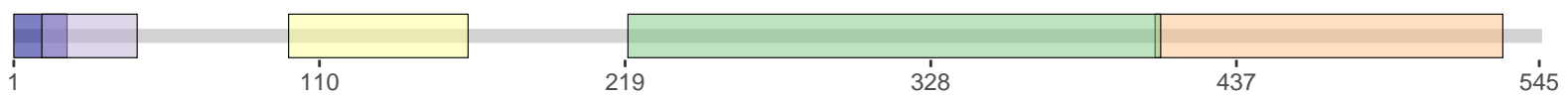
Molecular weight



Gel Slice

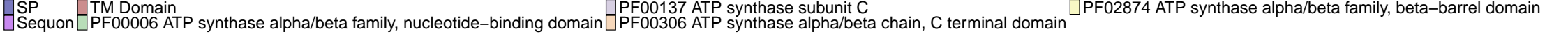


Protein length



Pfam domains

Pfam Description



Protein sequence:

VVICVYVAIQOKASSVAGVAVTFLGERGMEYTHVAETAQDSPTLQYLPAYTGAALAEYFMYRERHTLIVDDLEKAGAGAYRQMSLLRRPPGREGAYPGDVFYLSHALLERAAKLSLSEGGSMALPIVETQGGDVAIYPTNSAAGKAMKQVAGKIKLELAGFAELEAFAGFASDLKATQNLARGGRIRELLKGGSGSAPLTVEEGIMTYTGTNGYLDGLEVDGVKFLVELRTYIKTKPKPQGEHSSTKTFTEEAEPKKEAQEGMDHFLLEGDA

NbL12g09770.1 haloacid_dehalogenase-like_hydrolase_domain-containing_protein_At3g48420 [MW = 41.56 kDa]

No. of times detected



log(intensity)



Values from



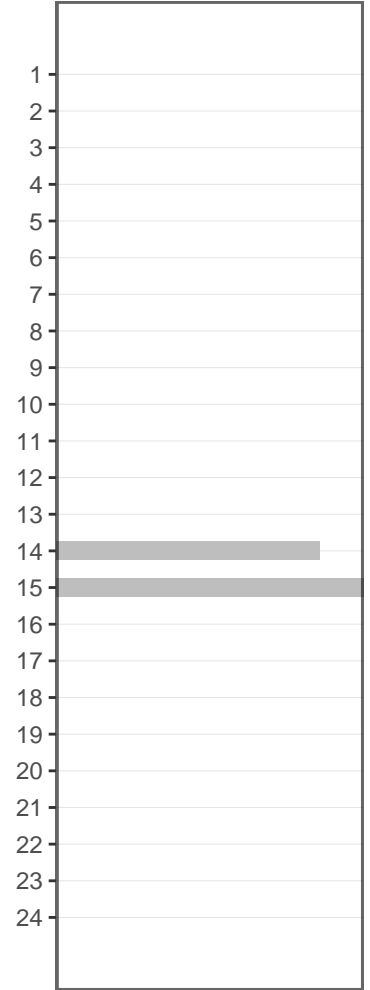
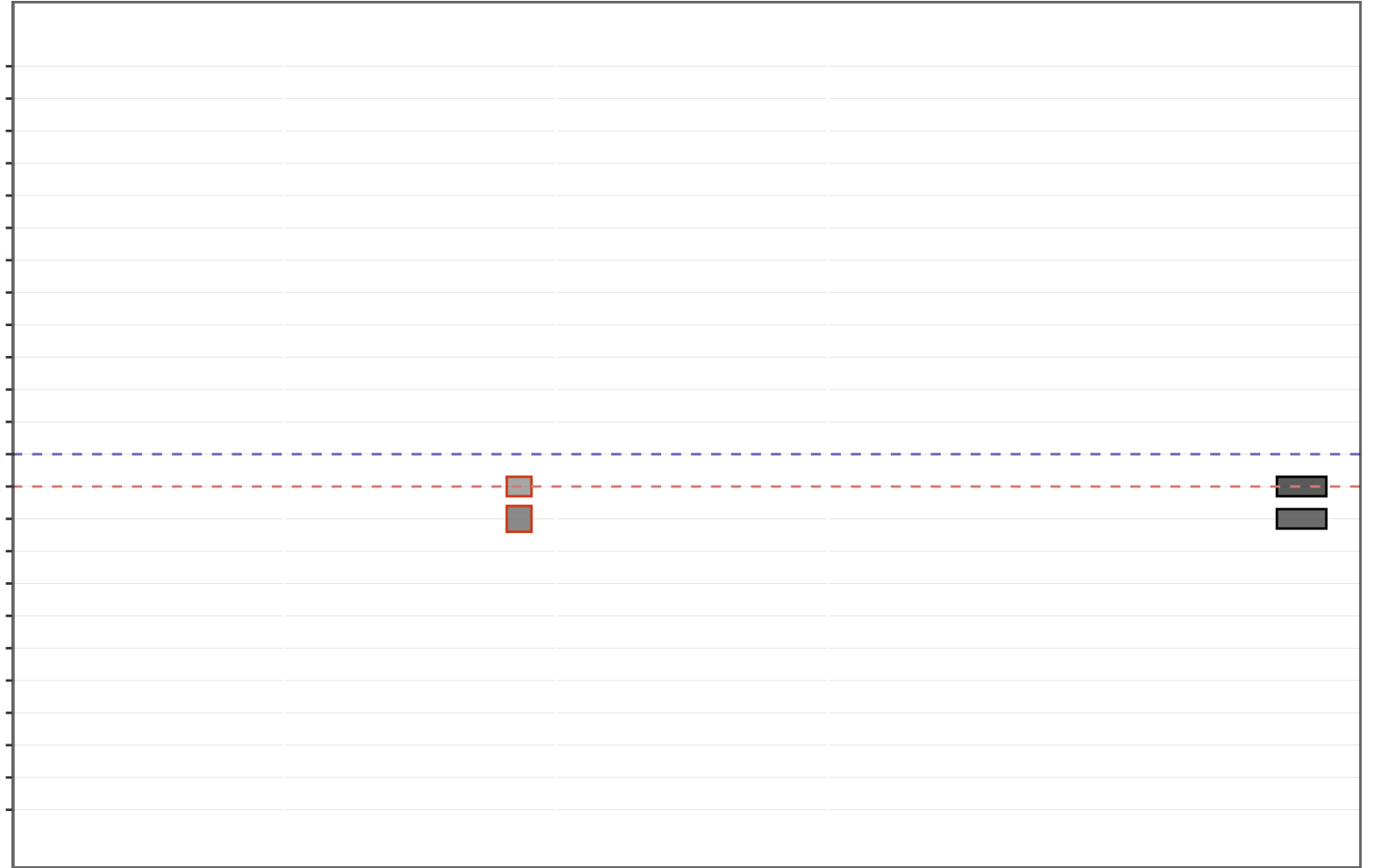
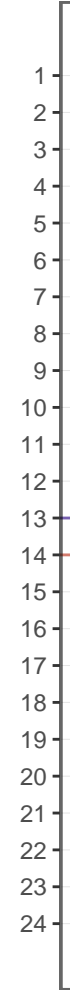
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

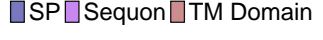


Protein length



Pfam domains

Pfam Description



Protein sequence:

VMSKSLPLRPGVEEFMDEAYEEGPGVPMALTSYKGGKPKPARIIEKLGNDKMARKIKLGMEEVWGSFYGQLVFGEGVADLGEQLAKEARKAASAEQRIAKEVASMILKLSVDIDTTSSEEMKNVVALRAGAEYANVFLDNCVWVAGSGSGVAGAEIRIGMPGVVRSSTARAEFFPKAKIMDFGGGDLISIRLRGQGLDV

NbL12g09750.1 non-specific_lipid-transfer_protein_1-like [MW = 11.18 kDa]

No. of times detected



log(intensity)



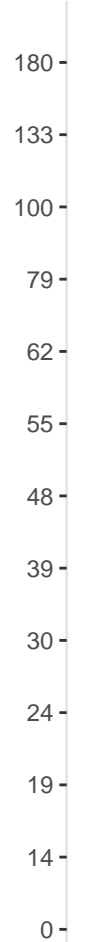
Values from



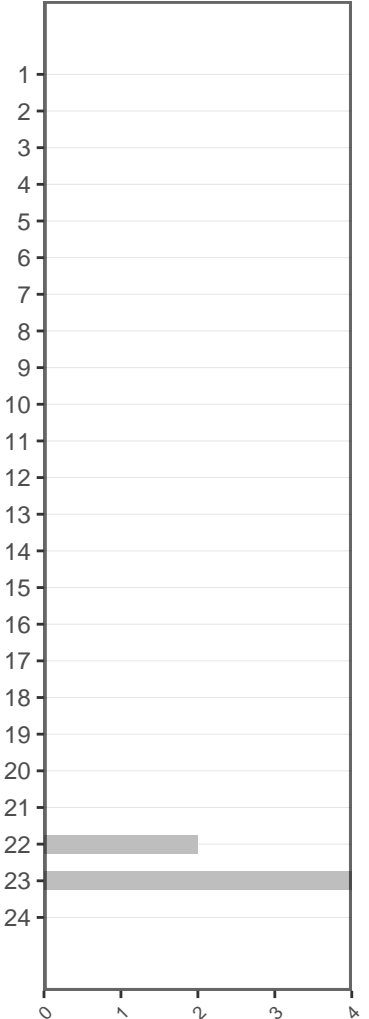
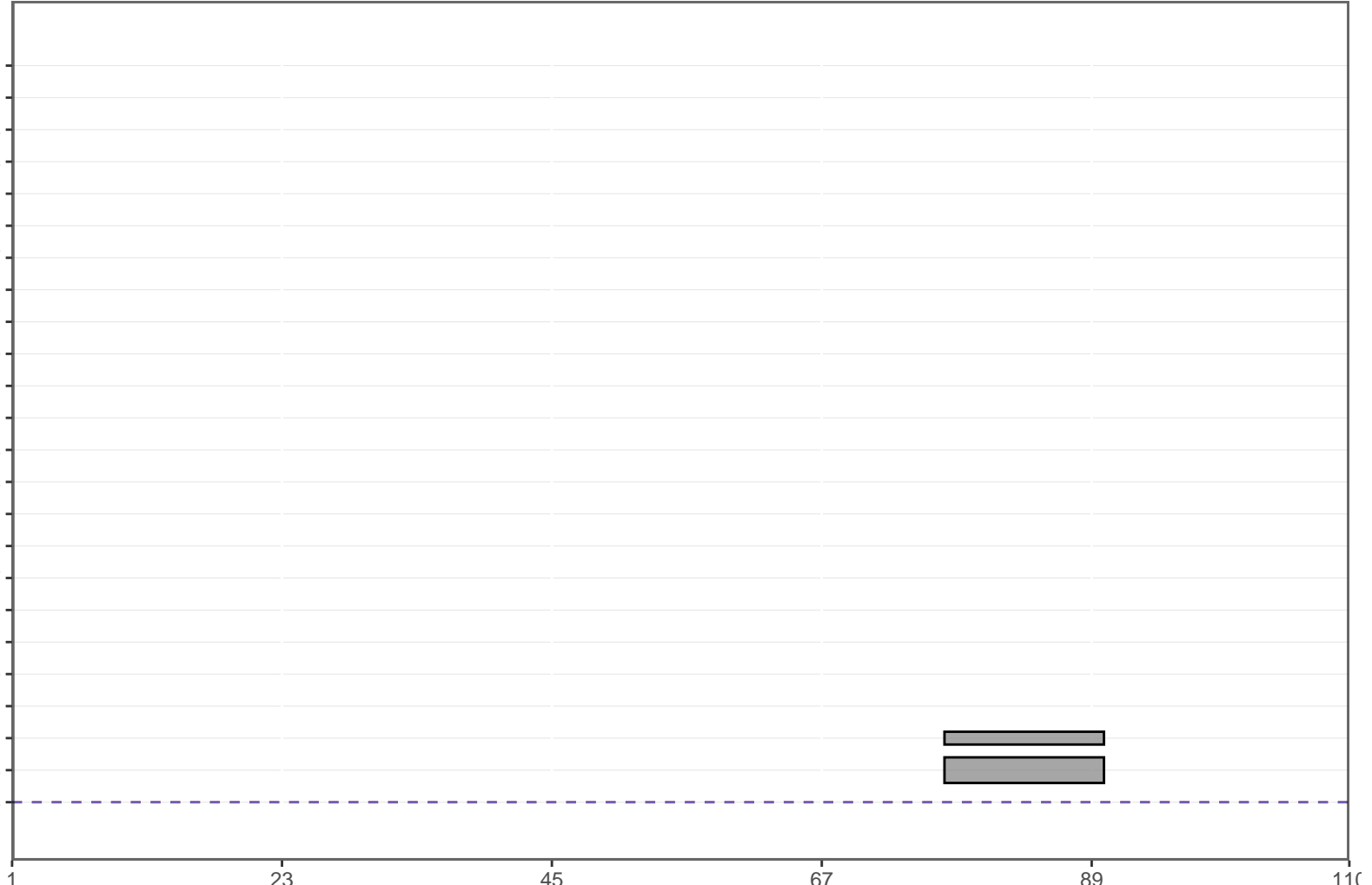
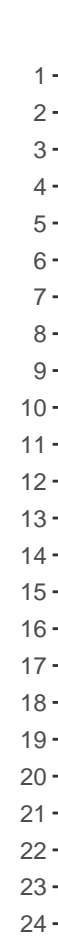
MW indication



Molecular weight



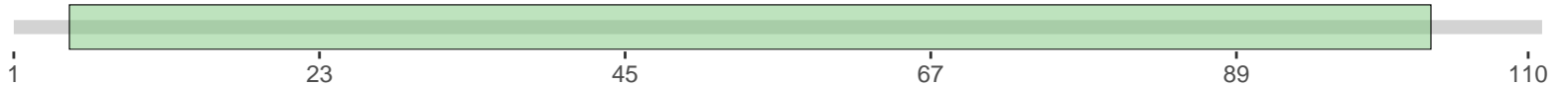
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

ISRKVPYACCCKIRALKLTFKGLGAALESFAANNAGVNPVAVTFPKRGNKRNRFVGRKGGRYVVP

NbL12g09720.1 peptidyl-prolyl_cis-trans_isomerase_FKBP17-1_chloroplastic-like [MW = 23.88 kDa]

No. of times detected



log(intensity)



Values from



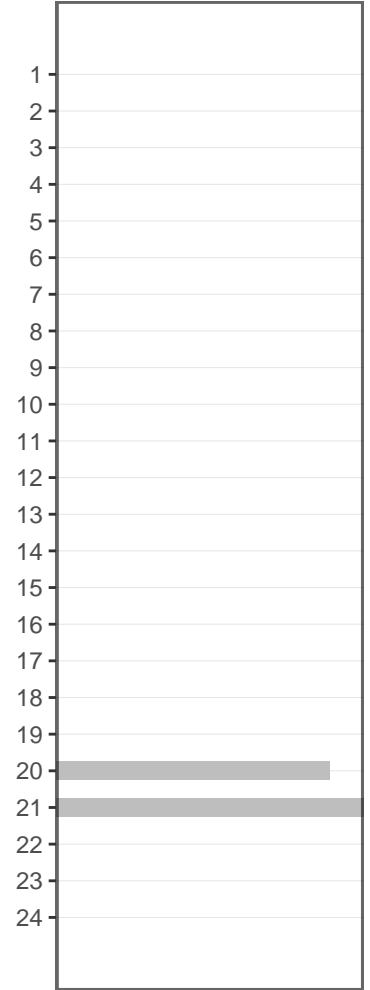
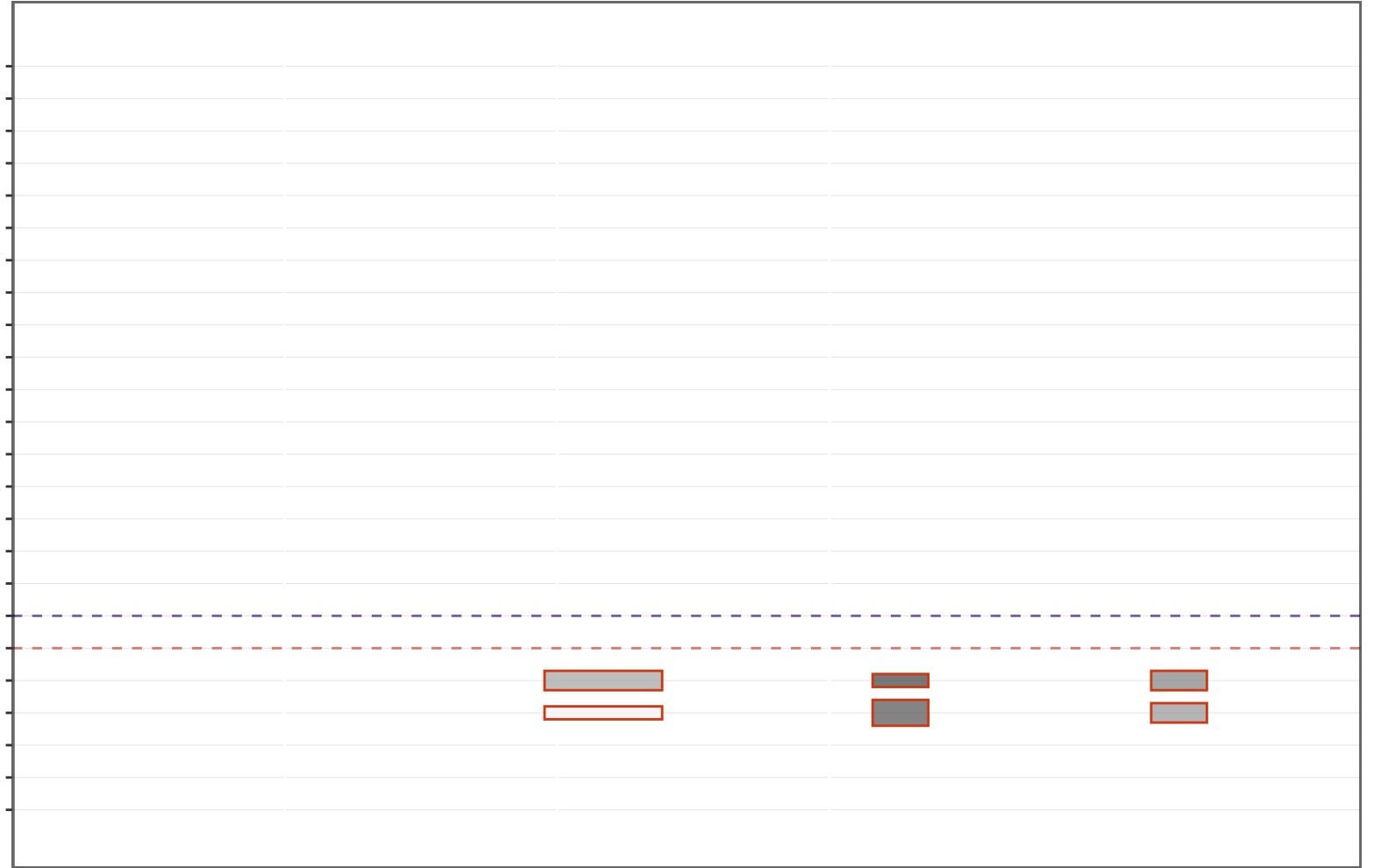
MW indication



Molecular weight



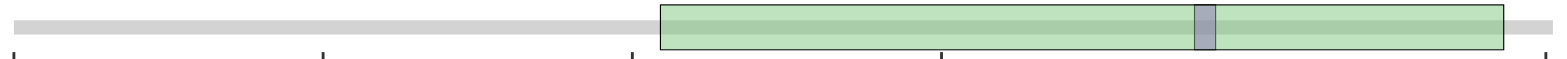
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

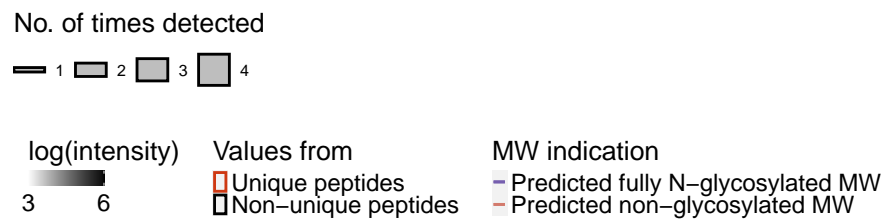
Pfam Description



Protein sequence:

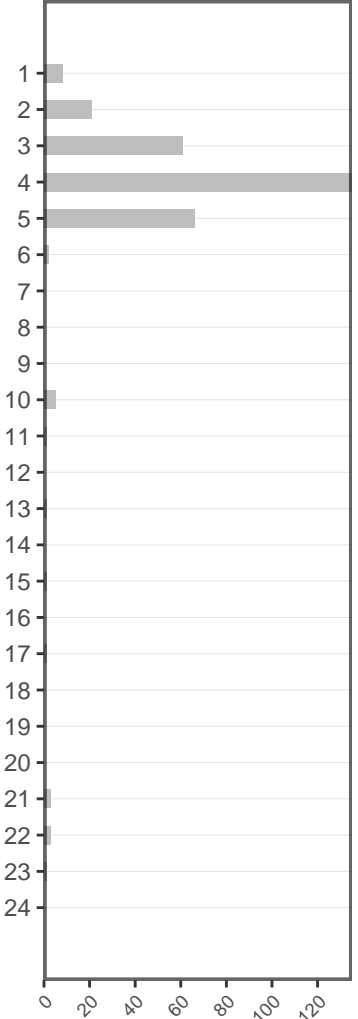
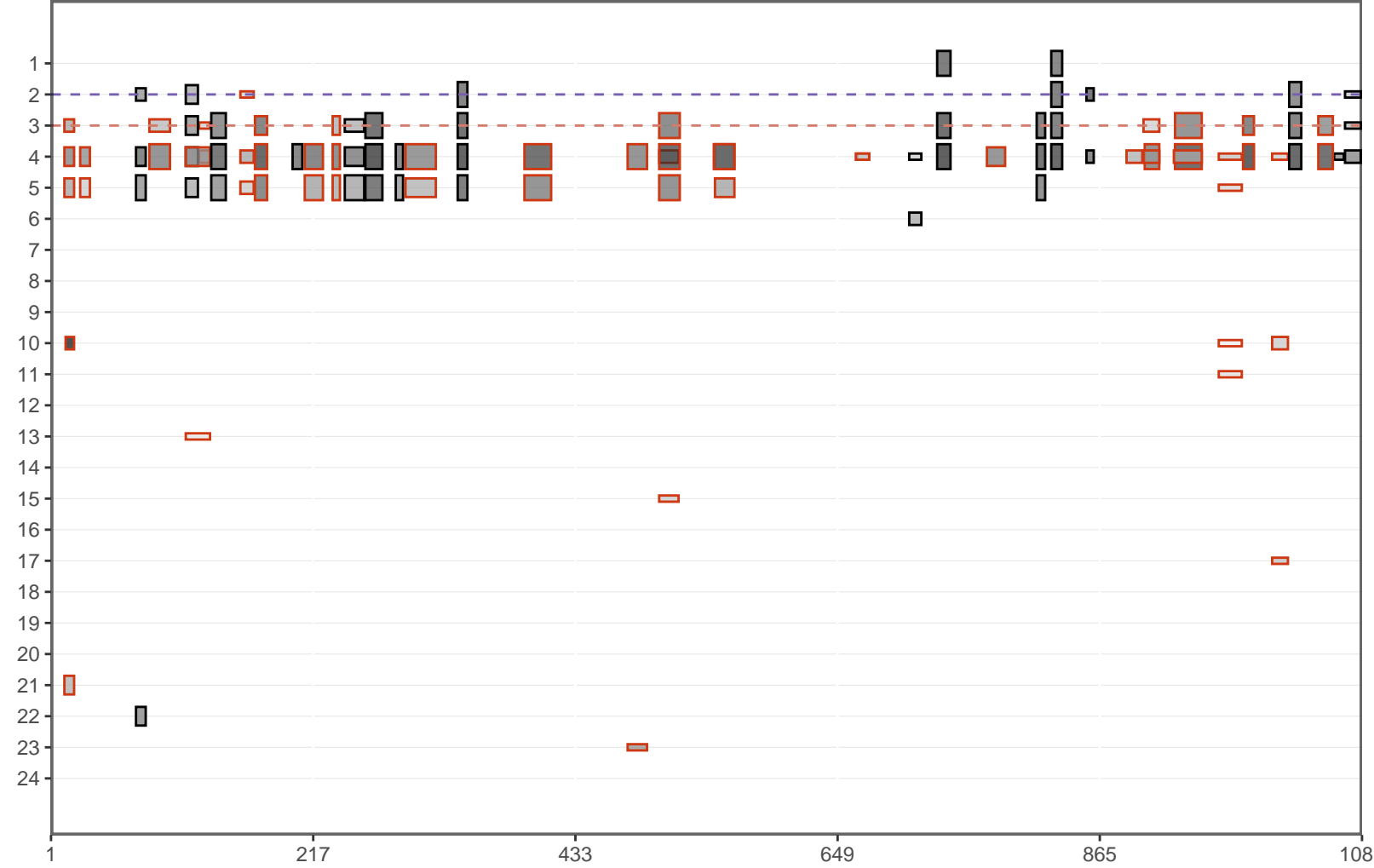
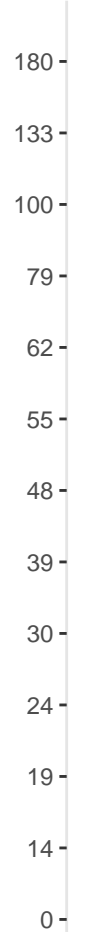
GGVVAHYYGRLLAANGWRFSDYDHDKDETGEPIPSFILGGKVISGIESAVRSMKVGGLRRVIPPSSKGYQNTSGEPLPPNYFDKGRLLFTTFNPTRLNANGEGATLGTVFDEIIVSLRHL*

NbL12g09700.1 leucine--tRNA_ligase_cytoplasmic-like [MW = 122.94 kDa]



Molecular weight

Gel Slice

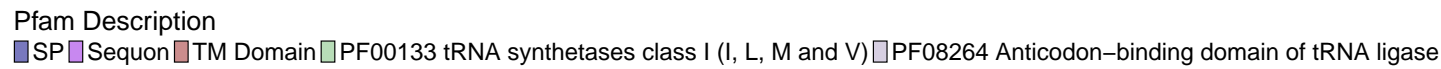


Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:

''VALTDQWYLYTGESEWRKAAEEGLASMLNLYSDTRIHGFEHLTSLWLNQWAGSRISGLGTRIPWDEEFVLESLSGSTHMAVYTAHFLQKGDMMYGTDSHSVKGQLTDEIWEFLFDGPPFNESLSSLLKEMRKEFEYWPFDLRVSGKDLMNHLFGYHHTAIFFEHWWFRGFRNGHMLNSEKMSKSTGNFRTRLQAEIEFSADATRFALADAGDGMDDANFVETANAALRLTKEIAWQEVLAES6SLR6GPPSTYFDCVFAINEINAVRTTEKXSEYMF

NbL12g09640.1 protein_argonaute_2-like [MW = 120.9 kDa]

No. of times detected



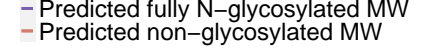
log(intensity)



Values from



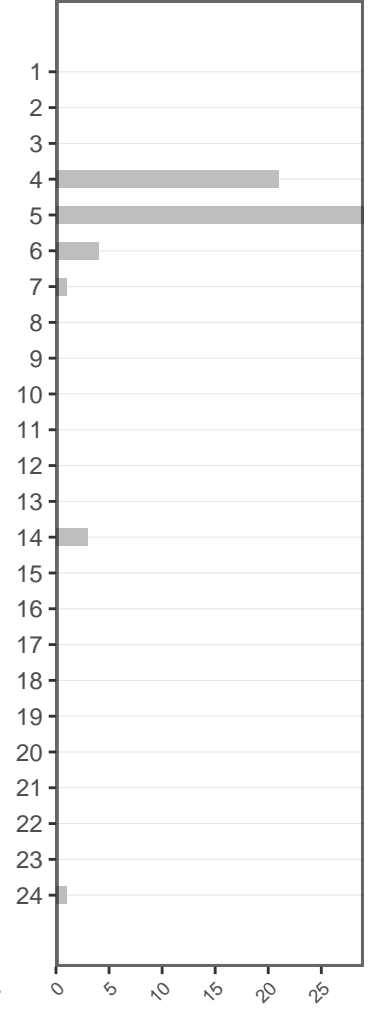
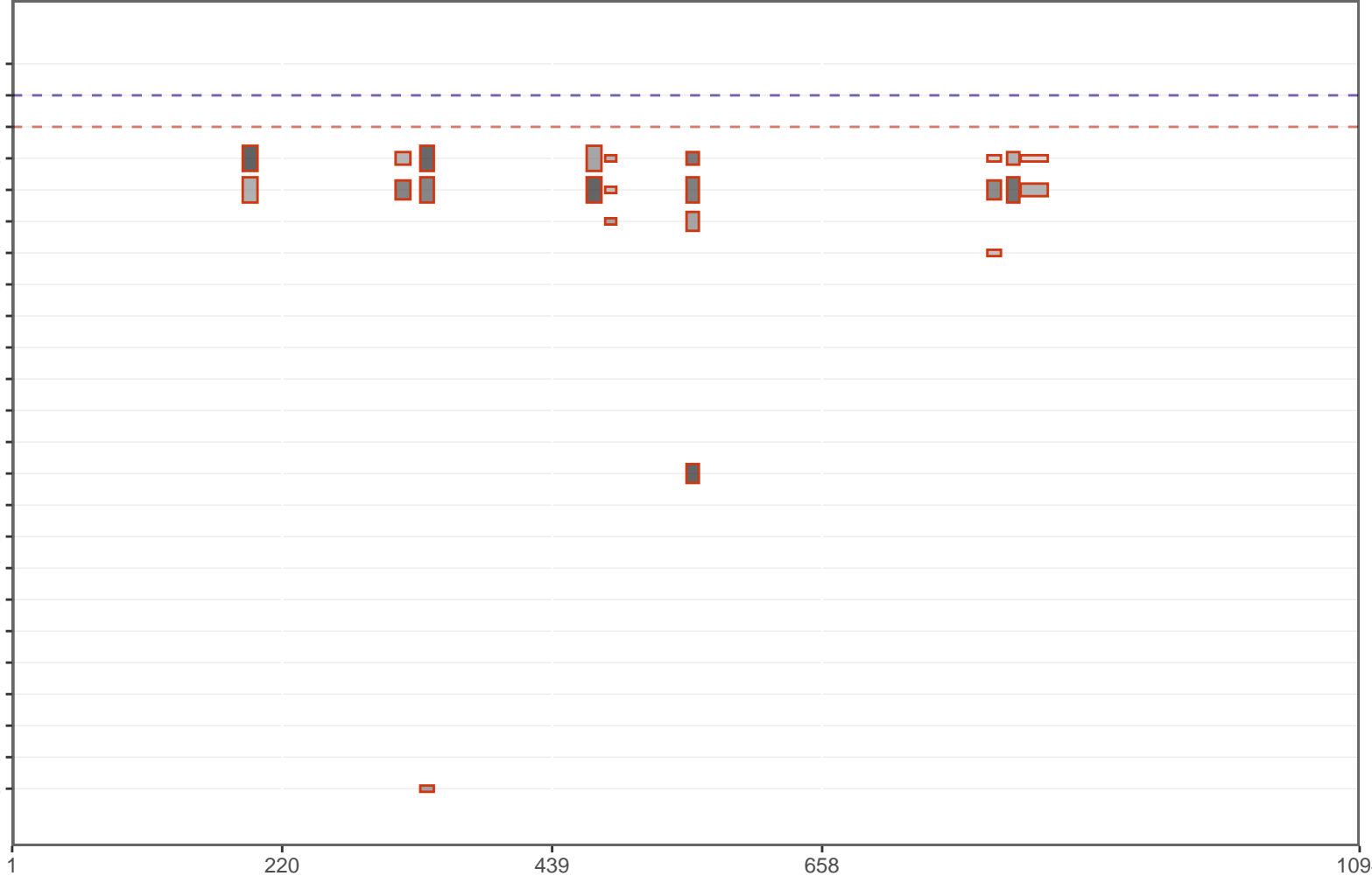
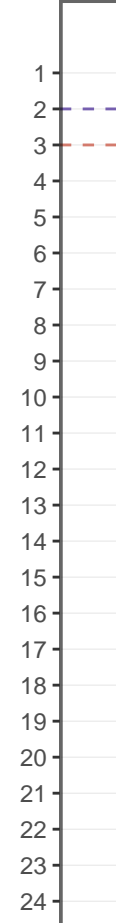
MW indication



Molecular weight

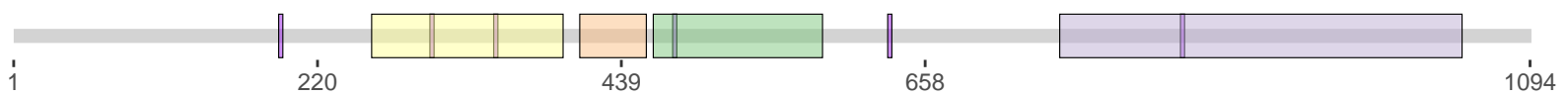


Gel Slice



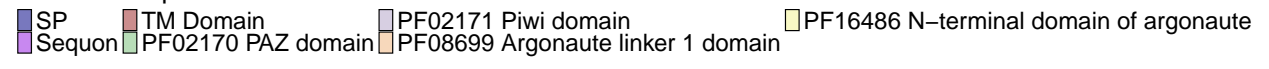
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

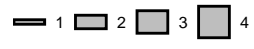


Protein sequence:

DPPKXVFLVDFYREKYQVERIYGNLPELDLGGKGNKNYVMEFQVLEGGDFPKHELDKDALFMKKSILVPPRREREAECEMVRAEDPGGAVTRNFIRVDRNMTGVSGRILPTPOLKLGGLSRVPLDNKQWNLVQKSVVEGKALGRWALIDFSSGQRNPNFRLRTDEFVFLKIKERKKLGNMEEPVTHTFTGMVELSVAEKVEDLLRGVWRAADEKIDRLQMGVQVMAAKHNGYKQKWSEIKGQVYTGQGLSSLANKGGDQGYLANLGIKNAKLGSSNMLTGR

NbL12g09550.1 protein_RABF2a [MW = 21.73 kDa]

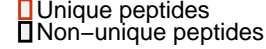
No. of times detected



log(intensity)



Values from



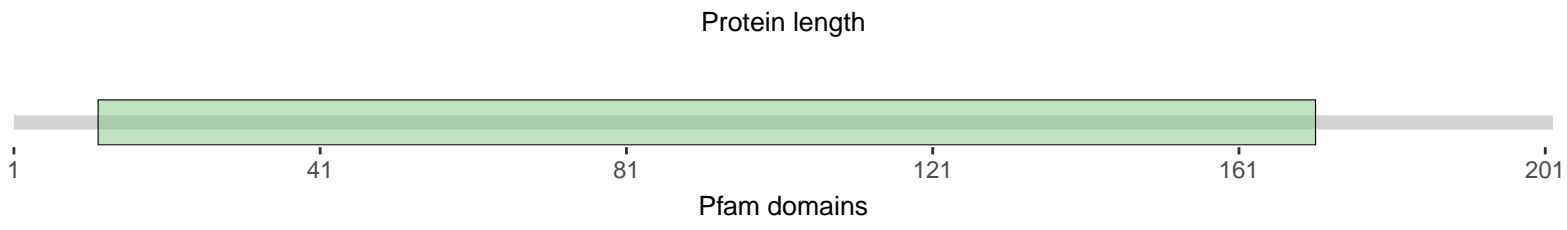
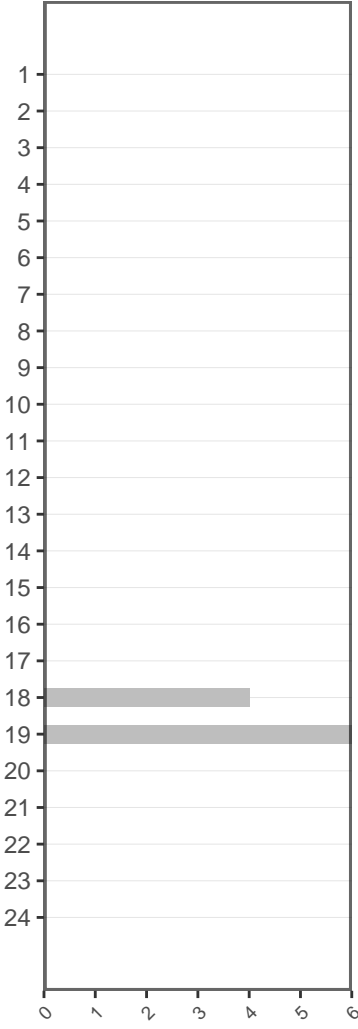
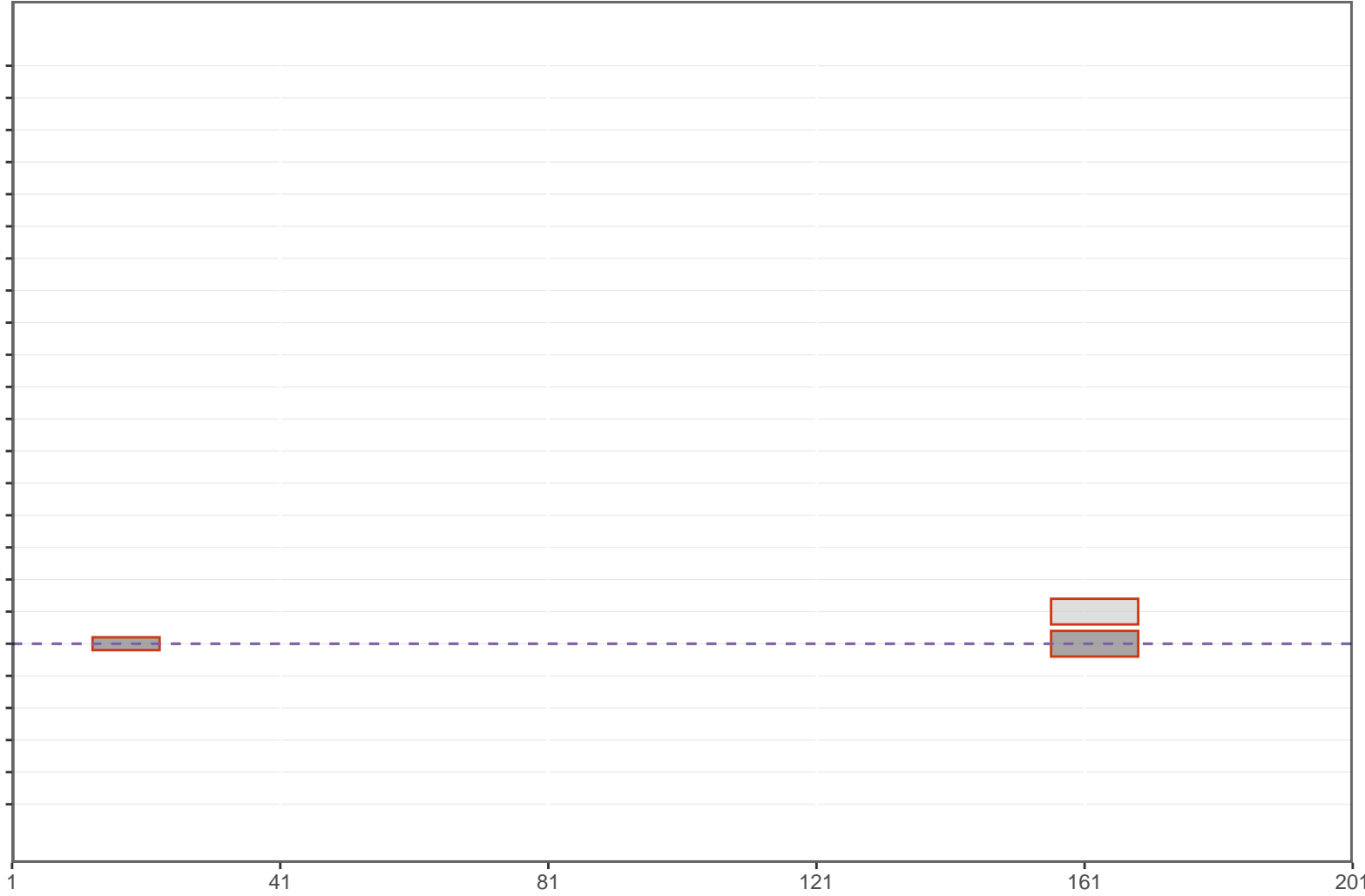
MW indication



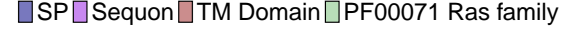
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

FDITNQSFDRAKKWVQELGAGGNFMVMAIAGNKAILLDRKVAEEAGTYAGENGLFFMETSAXTASNNDIFYEIAKRLRPLGPAQNP6GMVLMDRPAGTPASAGCG*

NbL12g09520.1 cathepsin_B-like [MW - SP = 36.51 kDa]

No. of times detected



log(intensity)



Values from



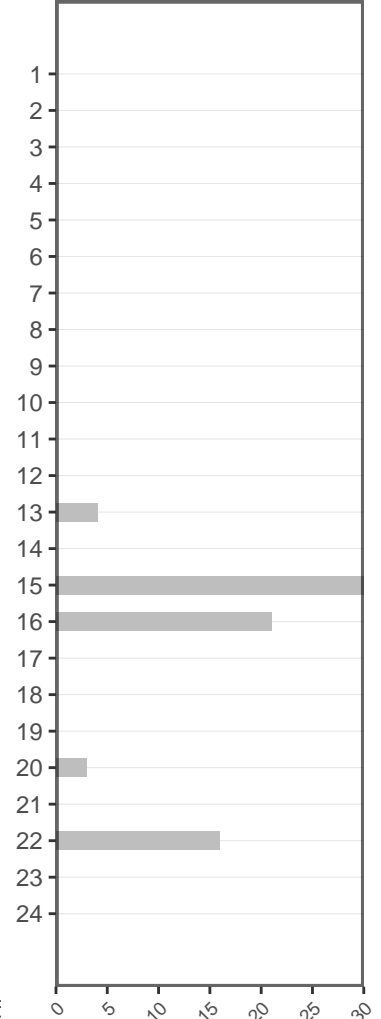
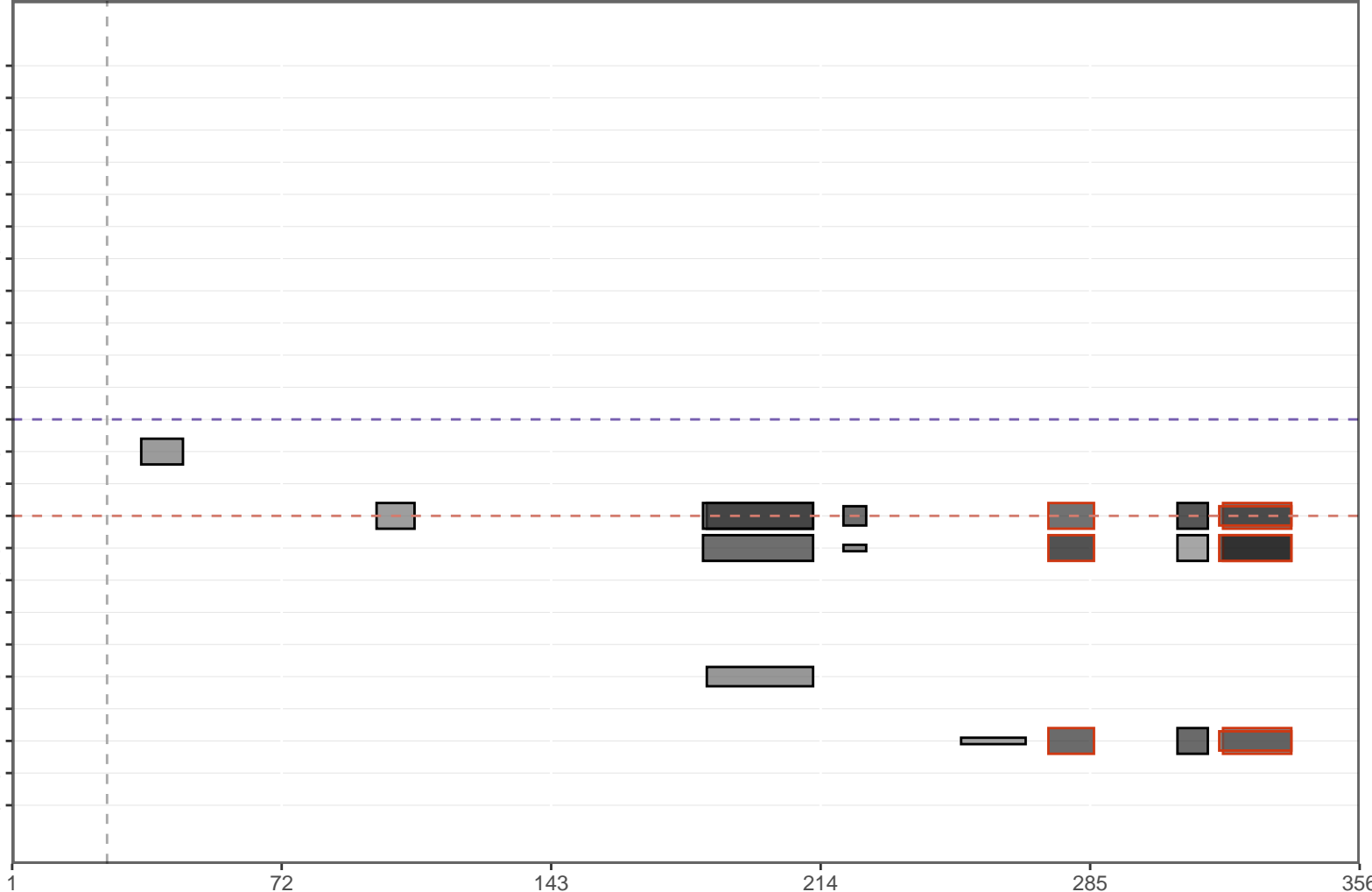
MW indication



Molecular weight

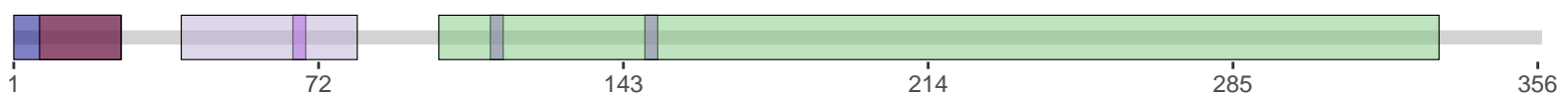


Gel Slice



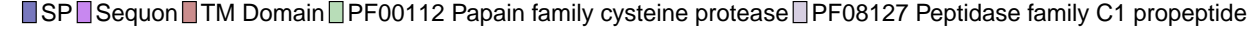
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISGYPLDAWKYFYFRKGVVTEDECDPFDNEGGSHPGCEPAPPTPKHRKGVKGNLWRSKHFQVNVYLSDDPHSMTELYKNGPVEVSTFYVEDFAHKKGGVYKHVTGDMGGHAKLIGWGTENGEDYLLLANGVNRGWGDDGYFKIRRGCTNEGGIEDEVVAGLPSARNLMELDASDAVLDAAI

NbL12g09480.1 phosphatase_IMPL1_chloroplastic-like [MW = 38.44 kDa]

No. of times detected



log(intensity)



Values from



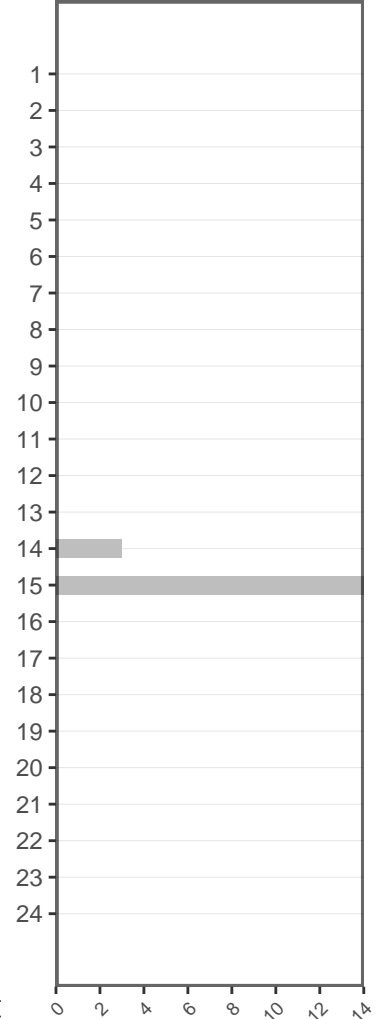
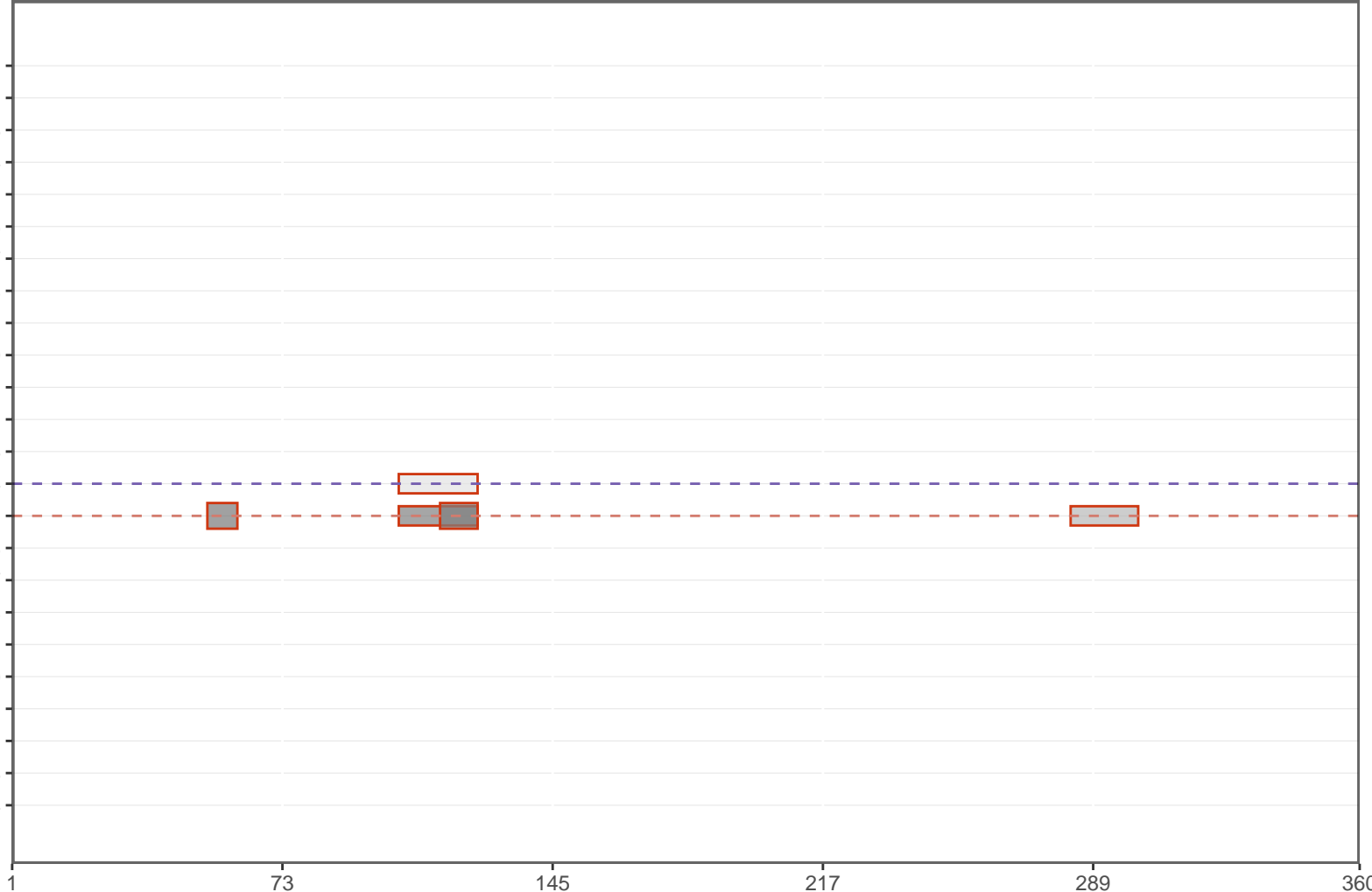
MW indication



Molecular weight

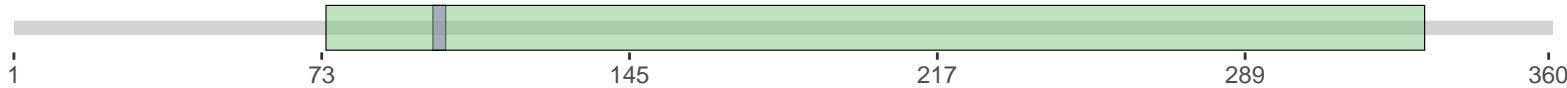


Gel Slice



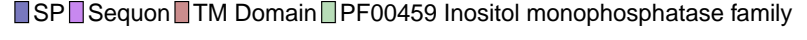
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VSVGVLFRRGKPAATVVEFVGGFMDWTRIFSAAGKGFANGKEKHVSGTDRKVEGSLVITGFGYEHDDPWATNMLFKDFTDVSRRGVRRLLGAAAVDMCHALGIAEAYWEYRLKPKWDMMAAGVLVEEAGGKVFSGMDGGKFSVDRSVLVSNGLLHAKLLEKGPATENLKGKGGDFSVWFKPENHYTEV

NbL12g09330.1 glycine_cleavage_system_H_protein_2_mitochondrial [MW = 16.78 kDa]

No. of times detected



log(intensity)



Values from



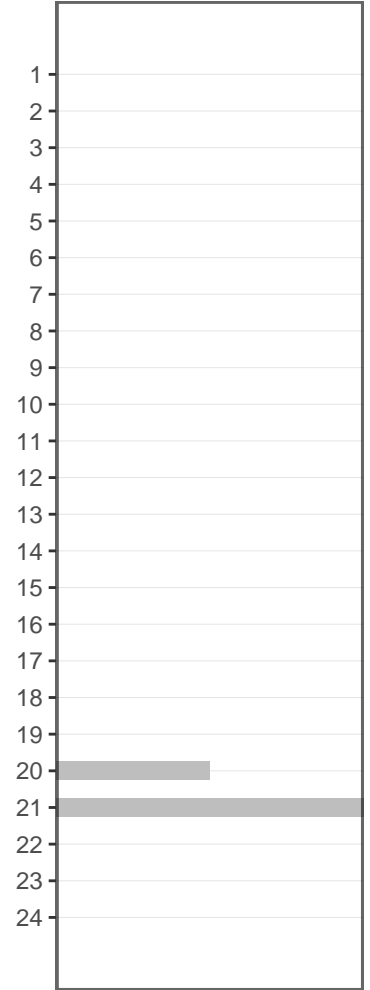
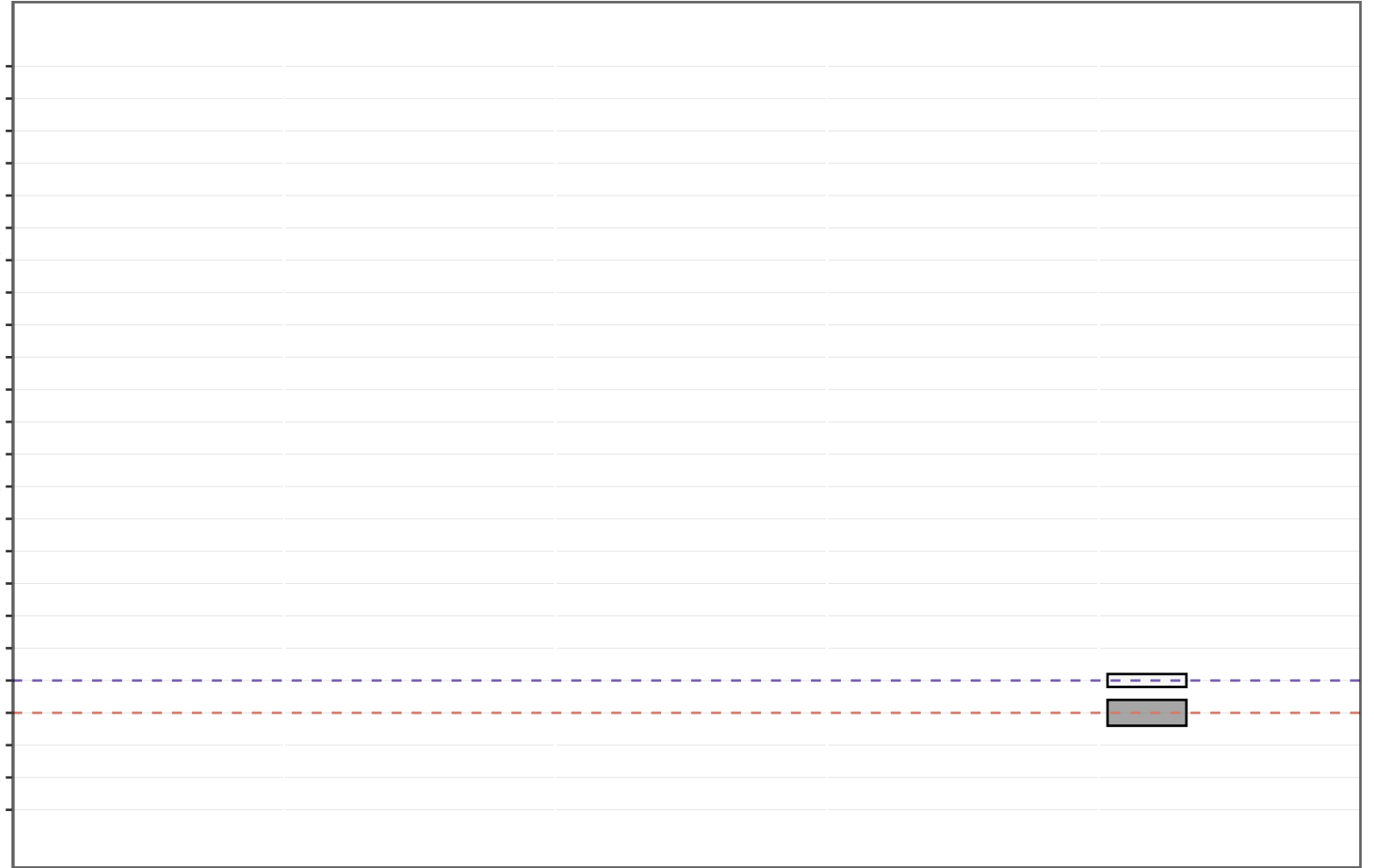
MW indication



Molecular weight



Gel Slice

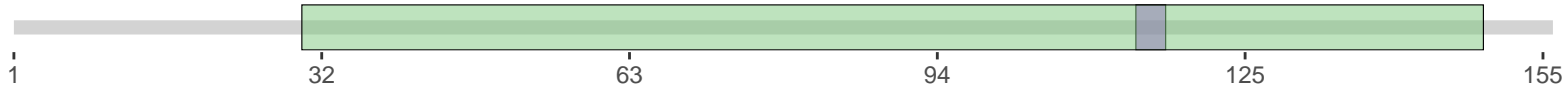


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

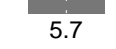
ILPEVIGASVYNOFDSFGAVEGVKATSDINSPVGGKVAEVNEKLDSSPALINGSPYQEGWIKVEMNIPDELKSLMDPKYSSFGDEEDAKH

NbL12g09290.1 14_kDa_zinc-binding_protein [MW = 19.67 kDa]

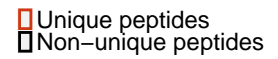
No. of times detected



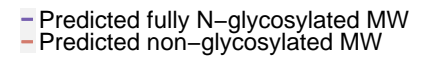
log(intensity)



Values from



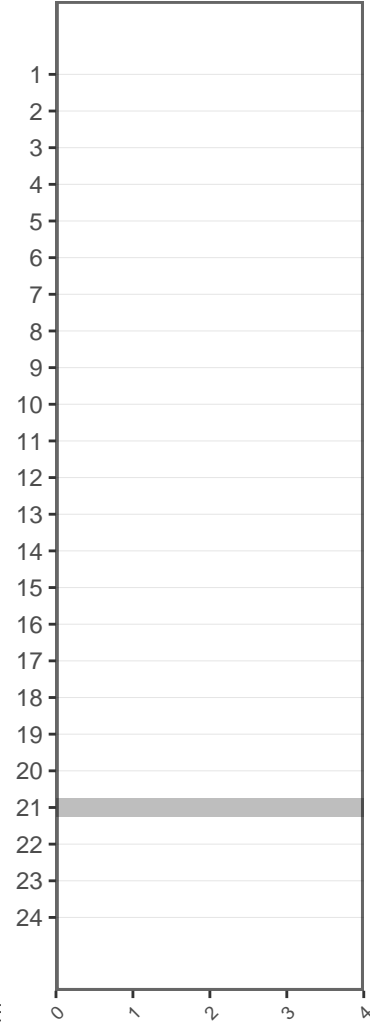
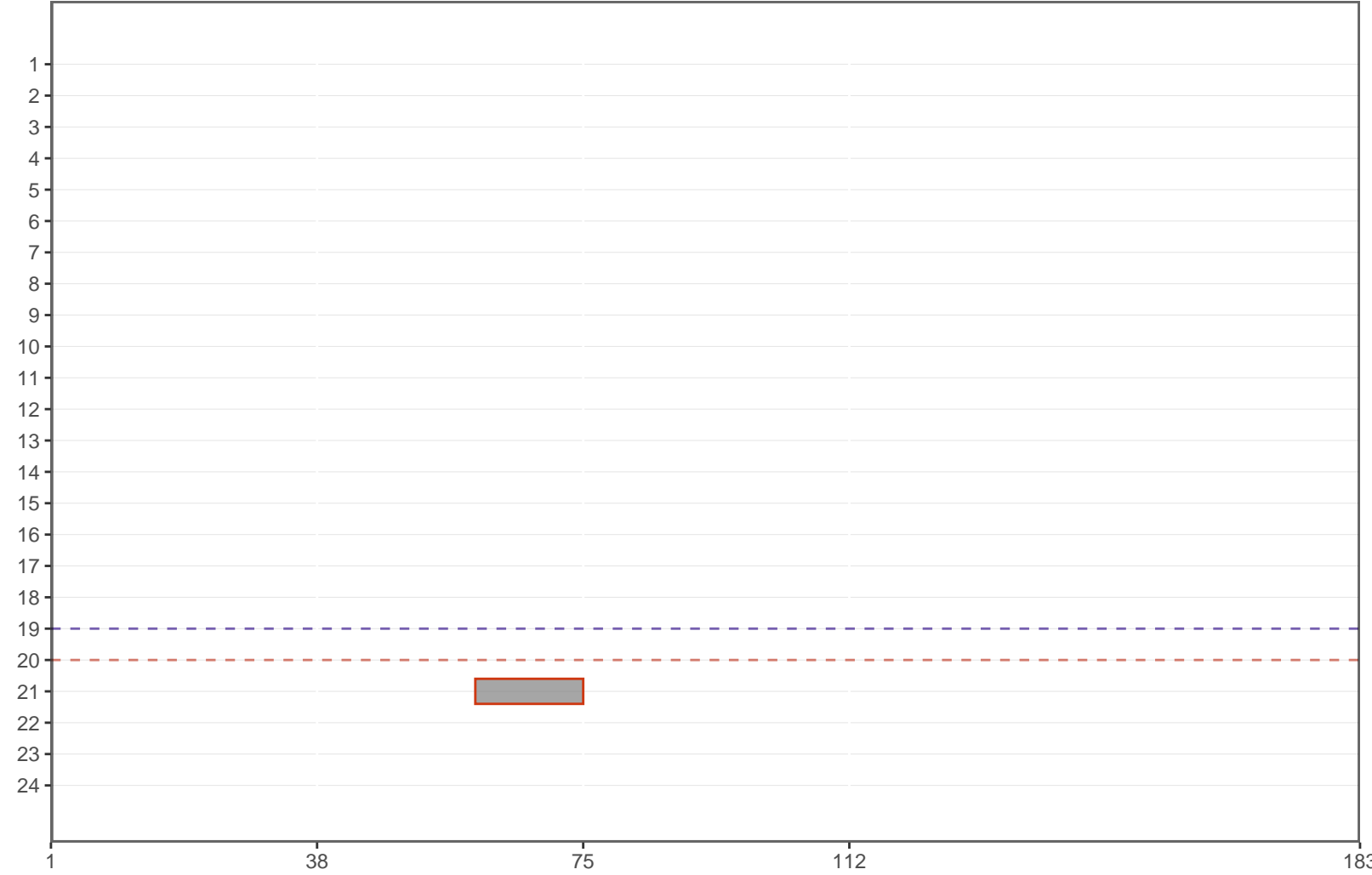
MW indication



Molecular weight

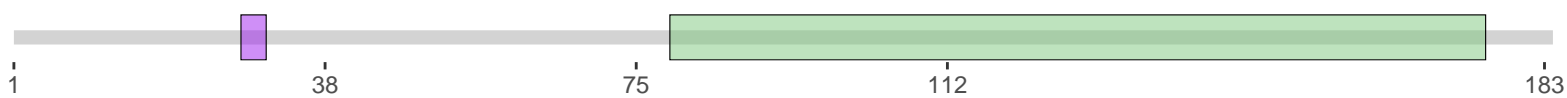


Gel Slice



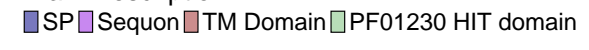
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KEIPASVYYEDEKVLGFRDINPQAPVHLVPIKLRDGLTELKAEGRHEDLGNLLYAAKVAKEKGVDFRIVVNSGSSACGVYHLHLVHVGGRGLKWPQV

NbL12g09210.1 pyrroline-5-carboxylate_reductase [MW = 28.97 kDa]

No. of times detected



log(intensity)



Values from



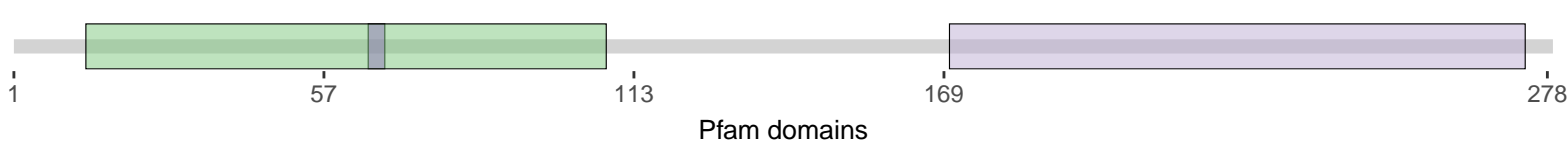
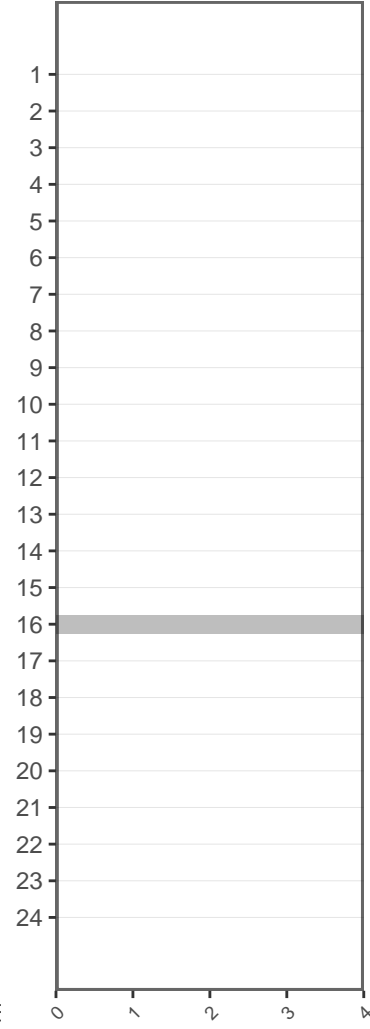
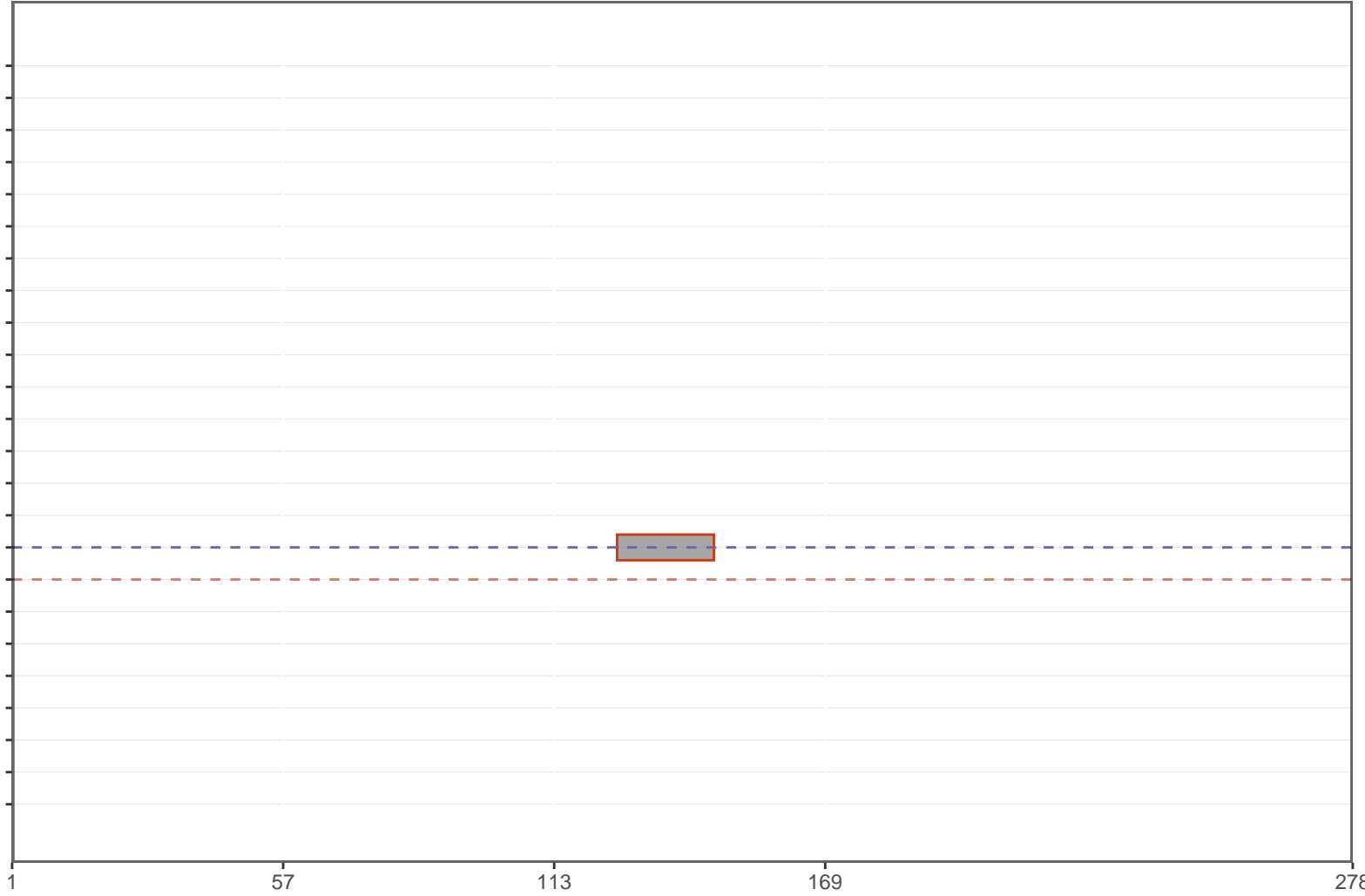
MW indication



Molecular weight



Gel Slice



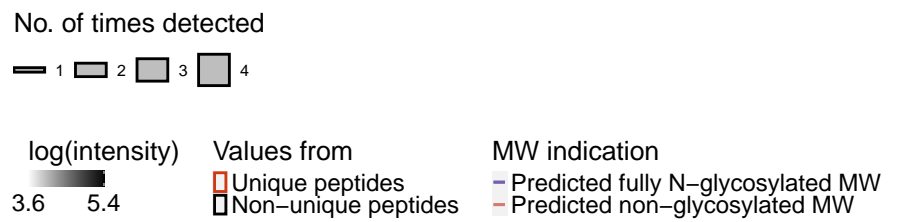
Pfam Description

- SP Sequon
- TM Domain
- PF03807 NADP oxidoreductase coenzyme F420-dependent
- PF14748 Pyrroline-5-carboxylate reductase dimerisation

Protein sequence:

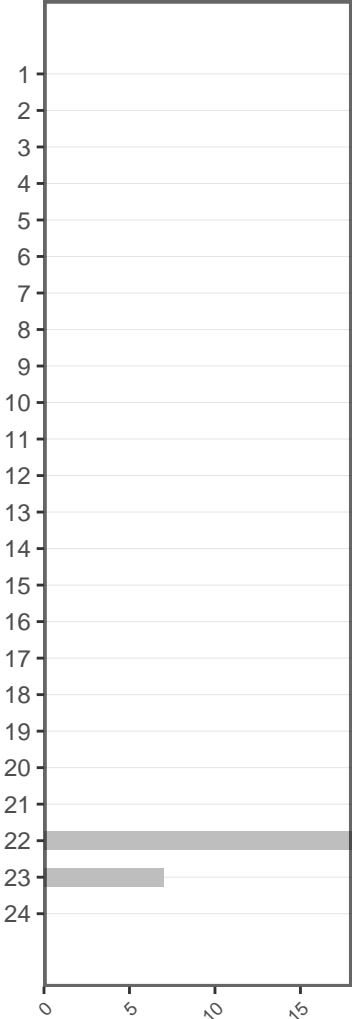
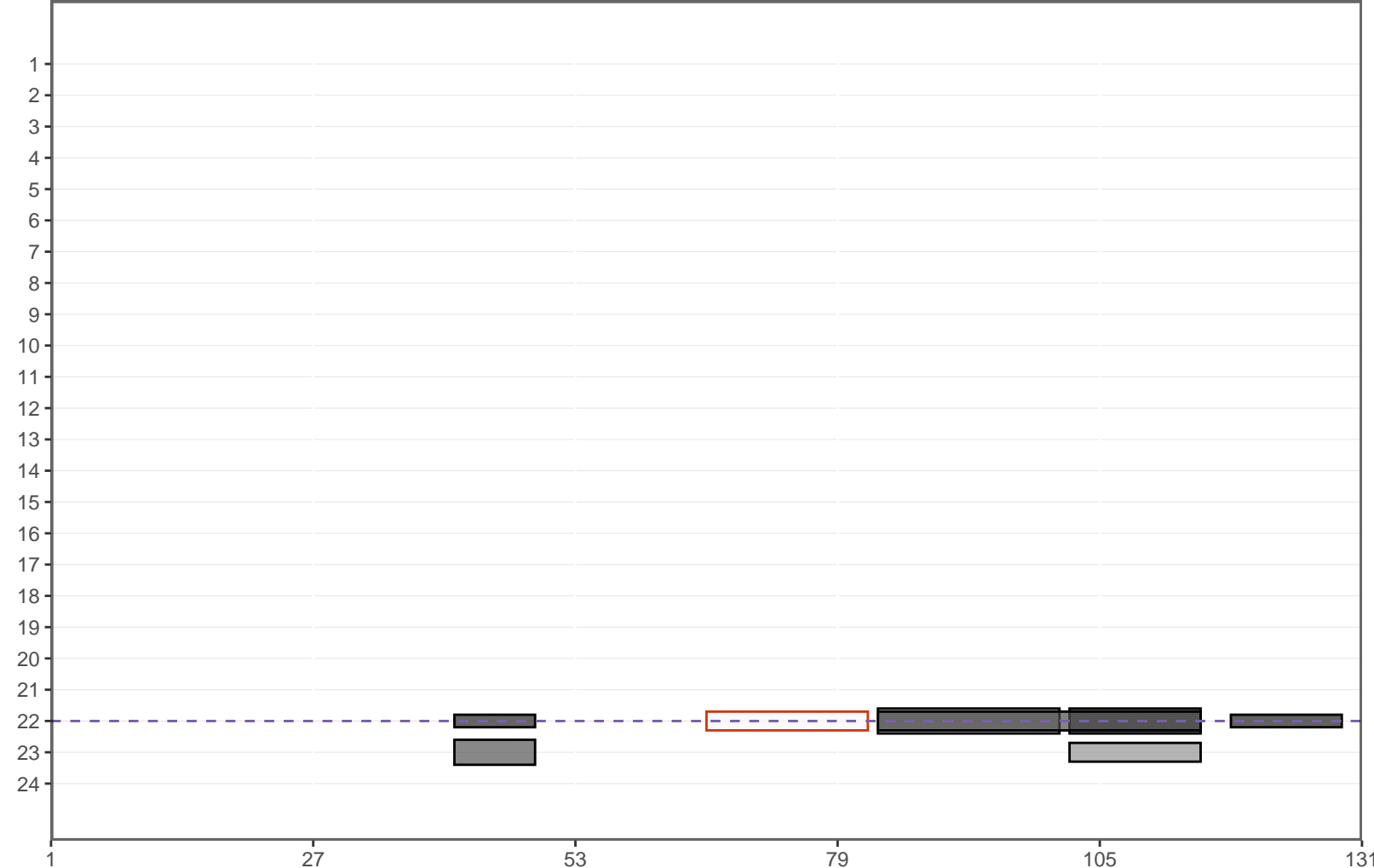
MPNTPSAVGEATVFTLGEKATFEDGELISQLFGAGKWRRADEKLFDAVFTGLGGSGPWFYFLAEALADGGVWAGLPRELALGLAGTFLGAAMVWGMGKHFGDLKDDVSPGGTTIAGIHELEKAGFRGLMMVAWAAKRRELGSN

NbL12g09040.1 V-type_proton_ATPase_subunit_F-like [MW = 14.5 kDa]



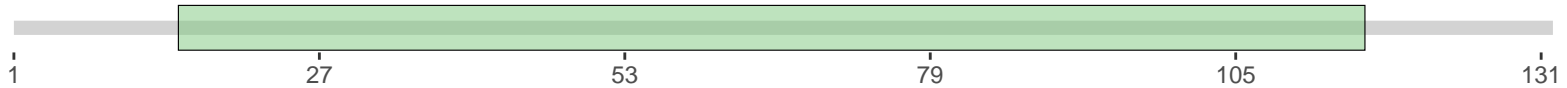
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain PF01990 ATP synthase (F/14-kDa) subunit

Protein sequence:
 YKQIEDAFKFTTREDNAVLISGQYANMIRFLVDSYKPKPALEIPKDKHPYDPAHDSVLSRKYKLFSTEGVASGRR

NbL12g08980.1 allantoate_deiminase [MW = 53.89 kDa]

No. of times detected



log(intensity)



Values from



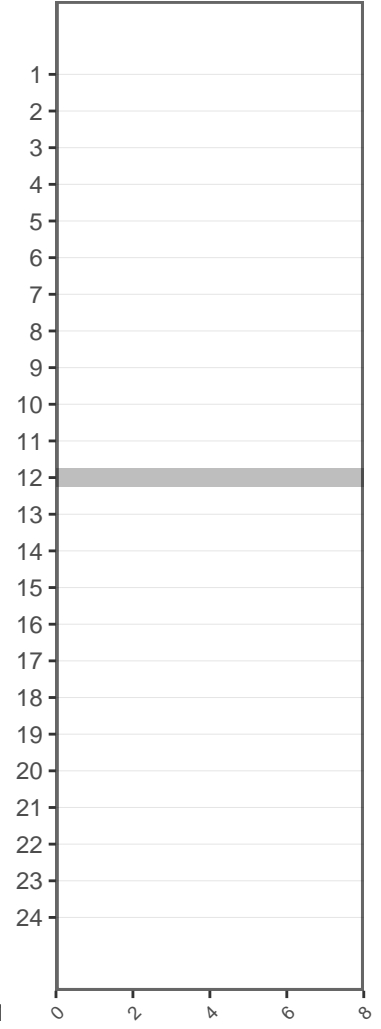
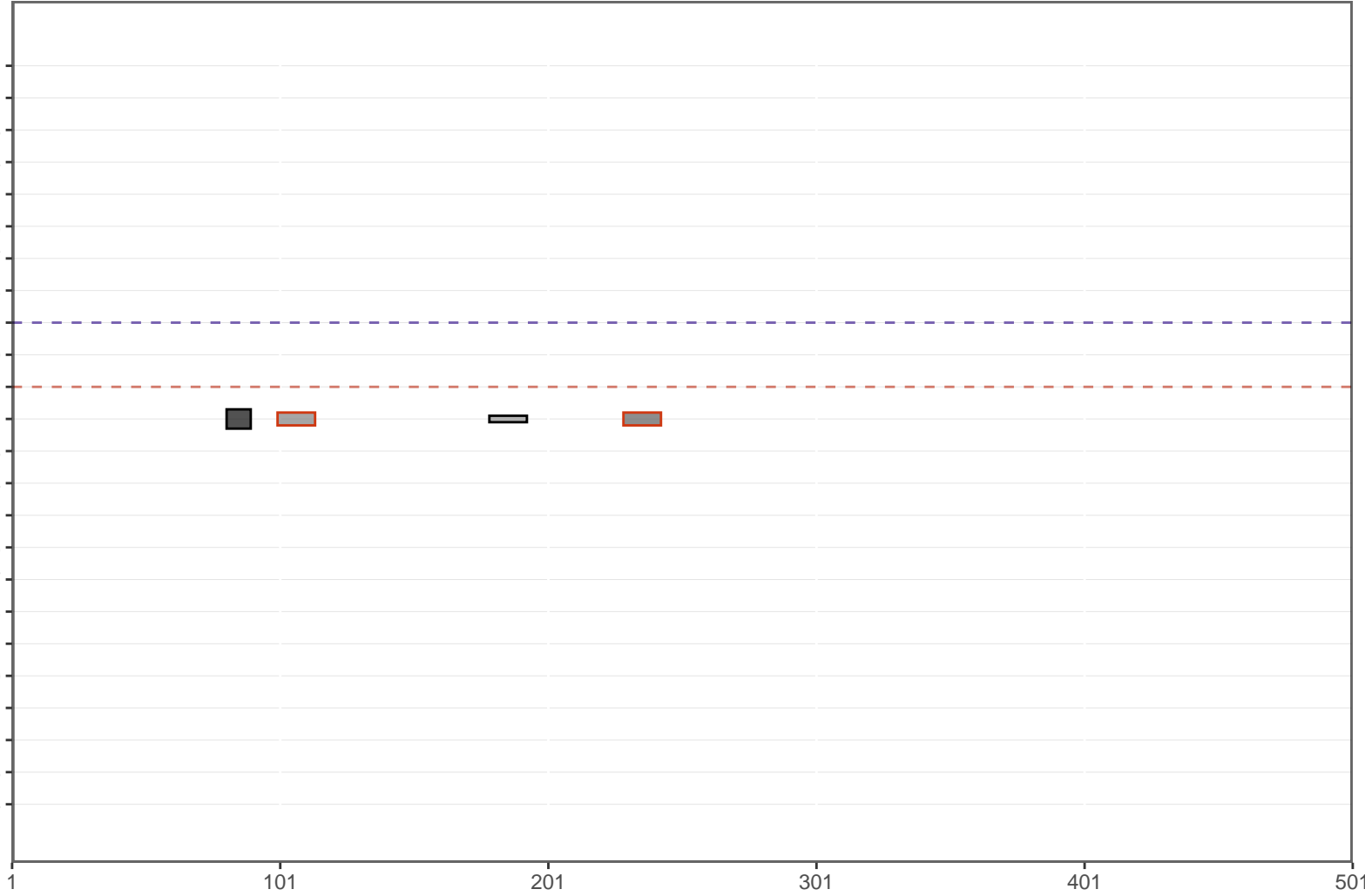
MW indication



Molecular weight

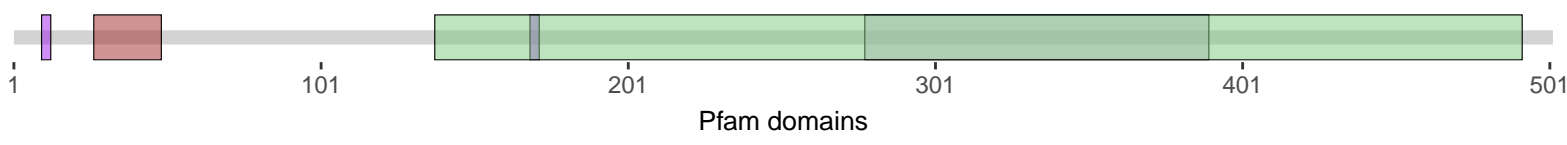


Gel Slice

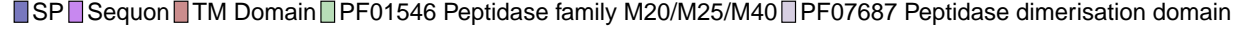


Protein length

Peptide counts over 4 repeats



Pfam Description



Protein sequence:

ILKYEPESVWGYYEVHIEGGPVALENVGLPLGLVKGAGGTRLRKIVRGTGGHAGTVPMNMRQDPMVAALAEIIVFLESIGKDPVYLSYDGGCAGSTVEISLAGSLVCTVGEISGWSASNVFGQVTFYDVRAMDDMGREAIIVEFSNRLVHMDDRRSDFGNVERKHANAVVCDPGLSTELKASGASHAAKRITGDEPQDVPVLMSSGAGHDAMAMEHLTKAGMLFVRCRGGGISHRPEHVLDDDIWAAGMAVLTLETLLI

NbL12g08840.1 protein_transport_protein_Sec24-like_At3g07100 [MW = 115.04 kDa]

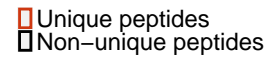
No. of times detected



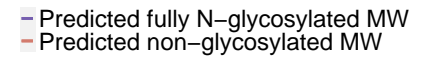
log(intensity)



Values from



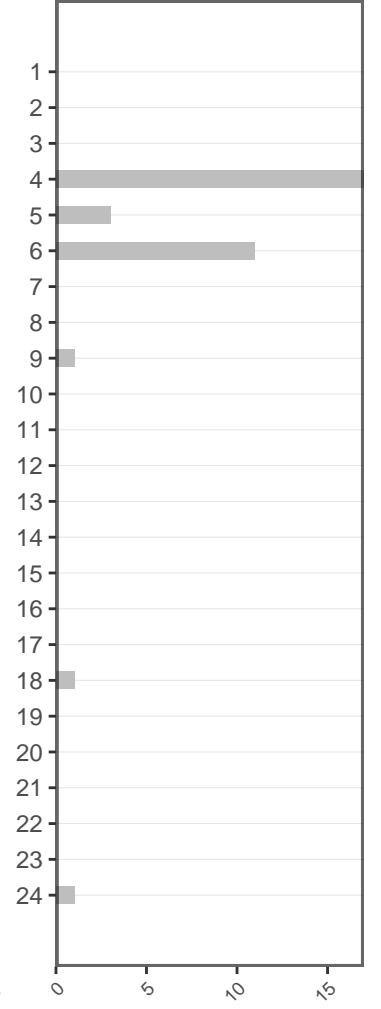
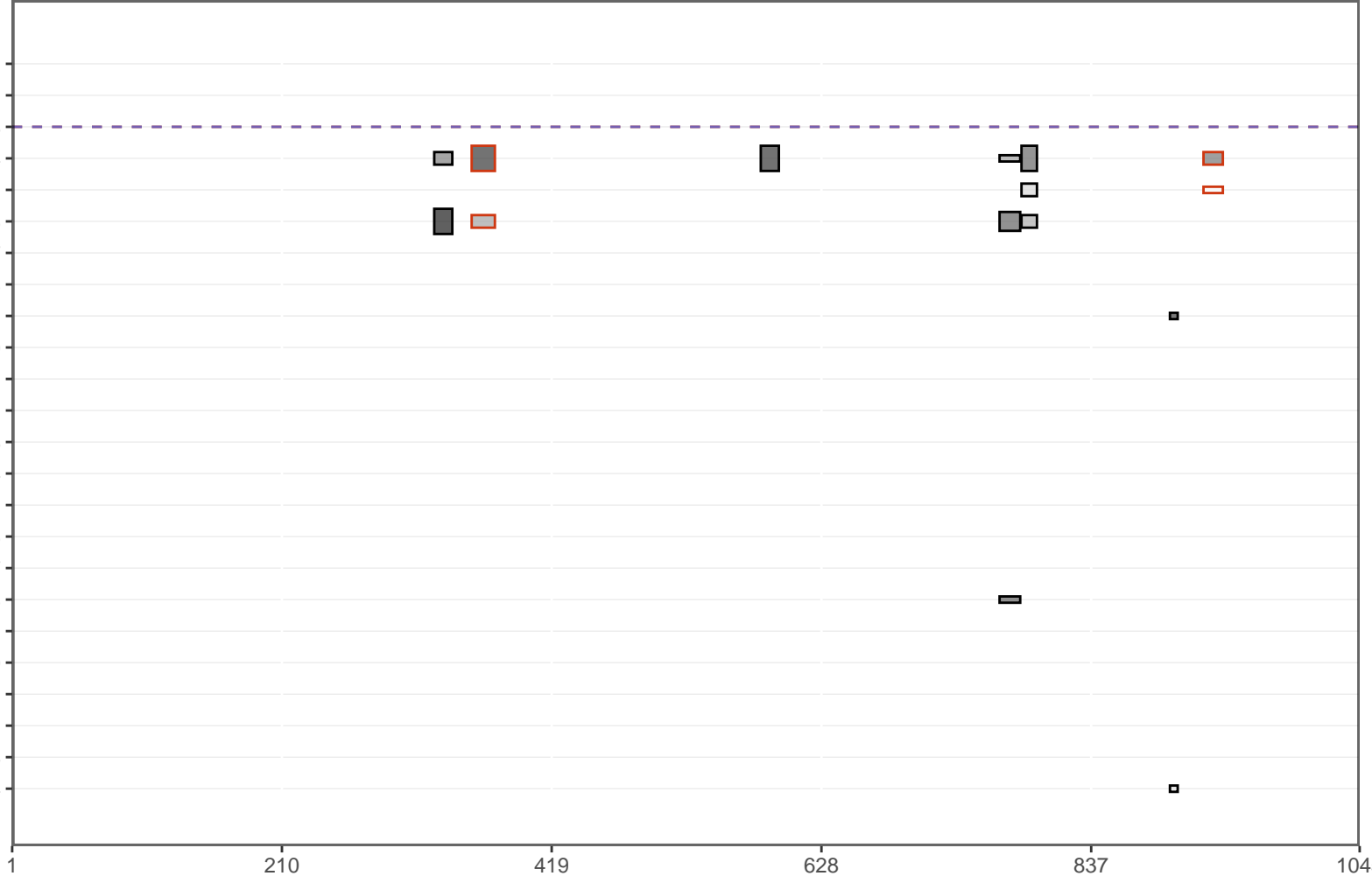
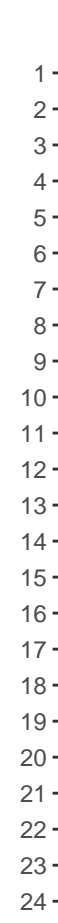
MW indication



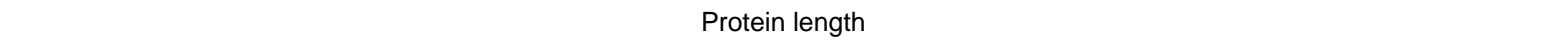
Molecular weight



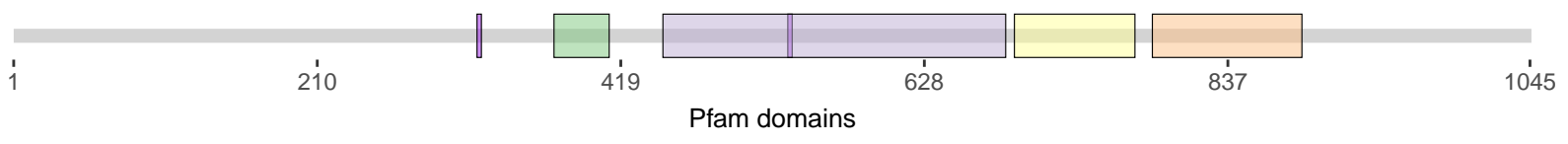
Gel Slice



Protein length

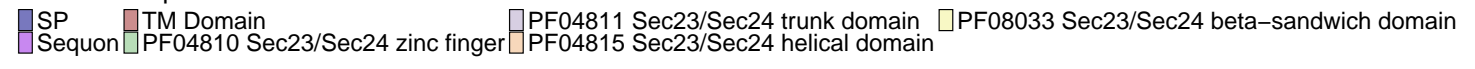


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IMKSSFTQPMVMVMSDLEDFVPLPDDLLVNLSESRITVVDVFLDGLPDMFQDNNVNESAFQPLKAAAFMVMSSQGGKLLFQSSLPGLGVGRLLRGGDLRIGYGTQKEHLRVPEDPFYKQMAADFQYQIANVYAFSEKYTDLATLGLAKYTGQGVYVYVPSFGASHKDRFYHELRDLTRETAWESEVMRIRCGKGVRFETYHGNFMLRSTDLIALPAWDCQKAYAMQLSLEETLTFQTVYFGIALLYTSBSSGERRIRWHTAAAFVVDLGGEMVRLADTGAIISFLRLAEI

NbL12g08820.1 thioredoxin_reductase_NTRB-like [MW = 39.13 kDa]

No. of times detected



log(intensity)



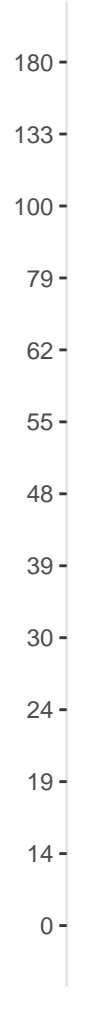
Values from



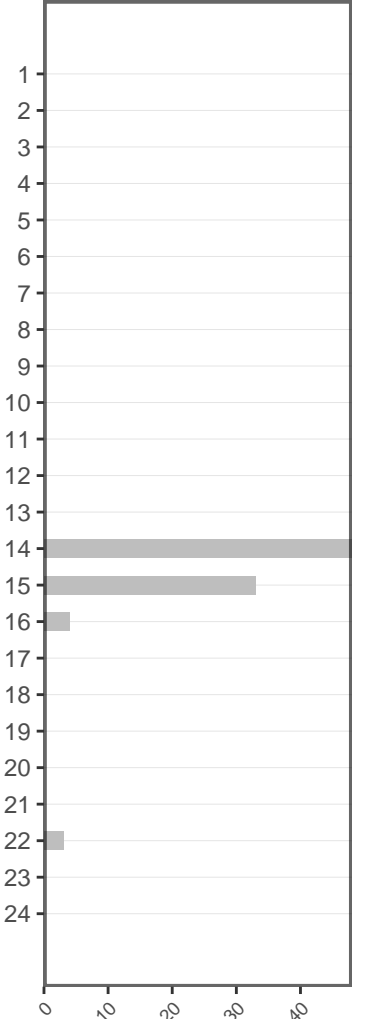
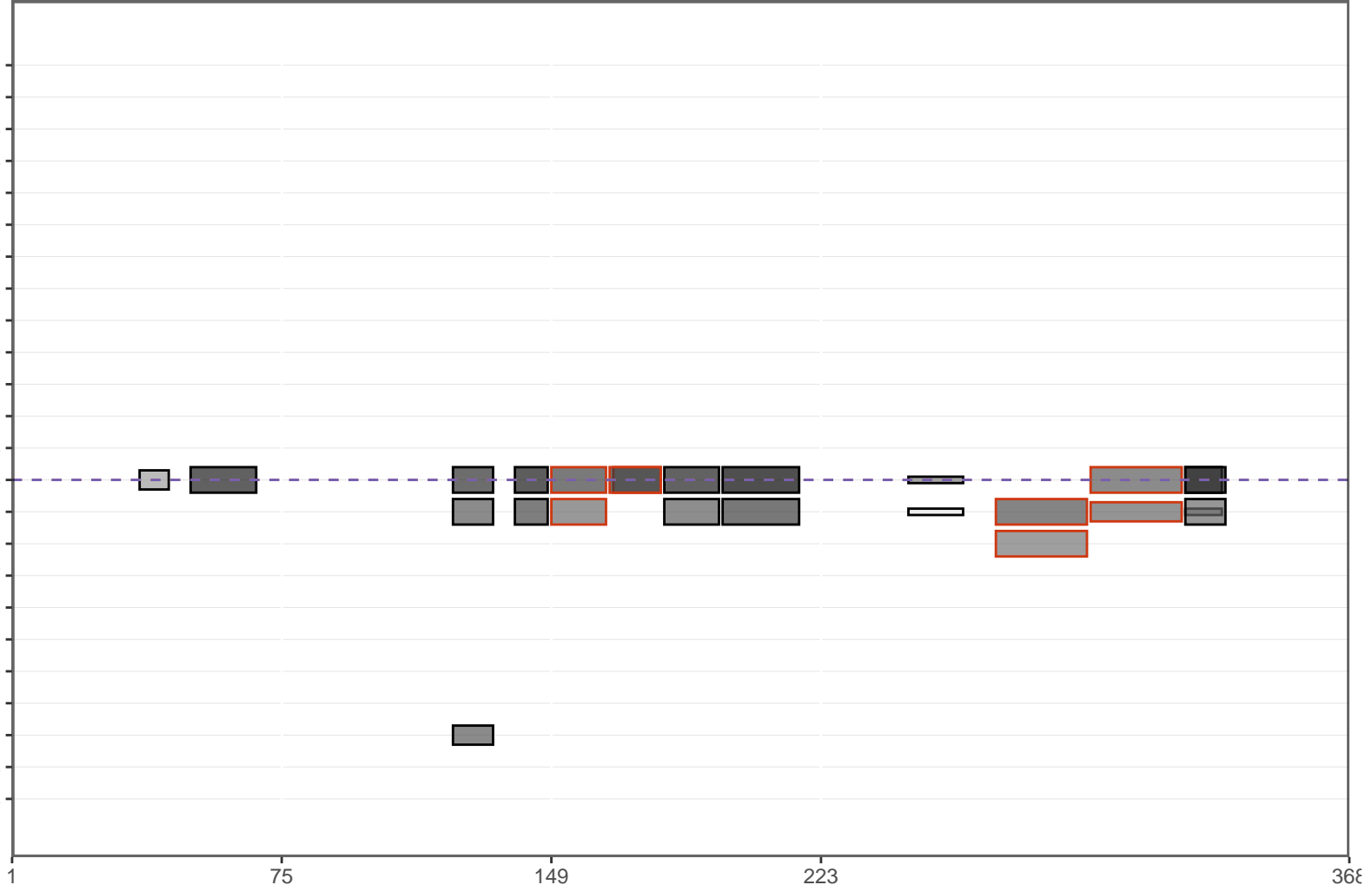
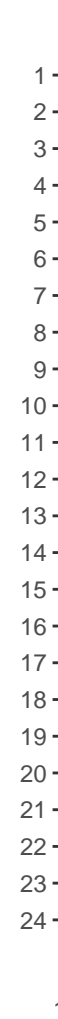
MW indication



Molecular weight

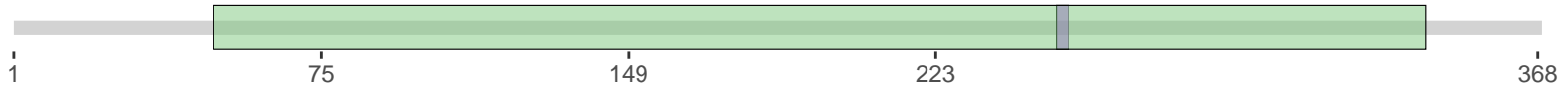


Gel Slice



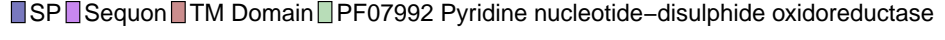
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

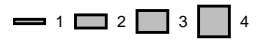


Protein sequence:

INDGFWNRGISACAVDDGAAPFRNKLAVIGGGDSAMEEANFLTKYGGKVIHRRDFRASKMGRALSNPKIEVWNSVVEAYGKELGGKVKVNVTVGEVSDLVGSLFFAIGCHEPNTKFLDGGLELDSDGVVYTKPDTLTFVKGVFAAGDVGDKKYRGAITAGRCMAALDAEHYLOEIGADEGKSD

NbL12g08770.1 MORC_family_CW-type_zinc_finger_protein_2A-like [MW = 83.88 kDa]

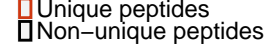
No. of times detected



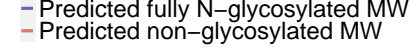
log(intensity)



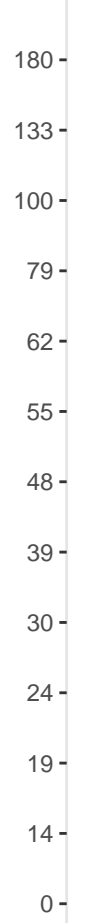
Values from



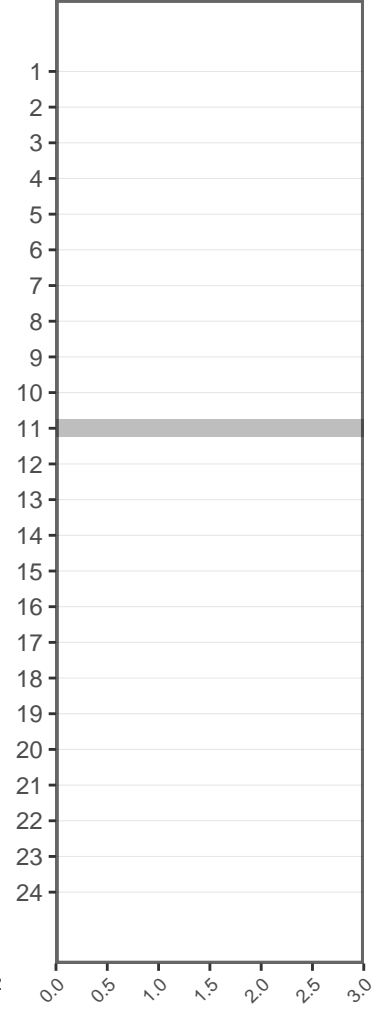
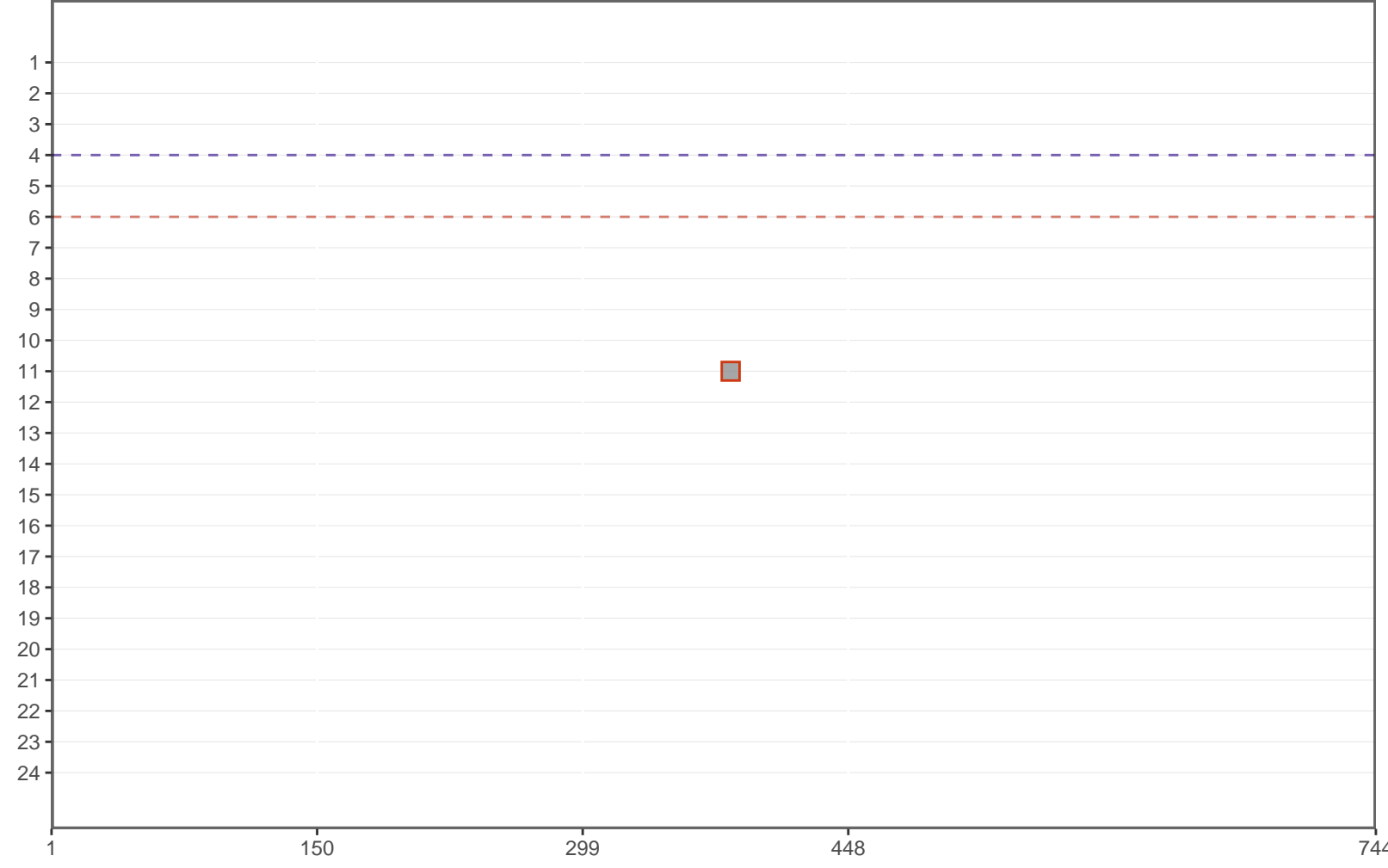
MW indication



Molecular weight

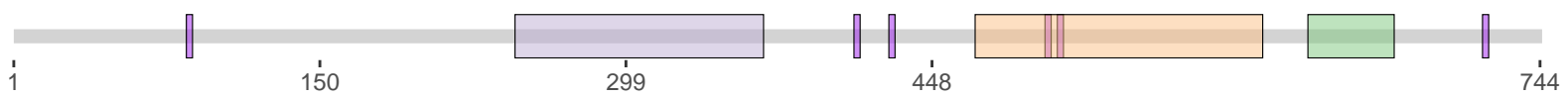


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF07496 CW-type Zinc Finger
- PF17942 Morc6 ribosomal protein S5 domain 2-like
- PF13589 Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase

Protein sequence:

/SYYRNGFMEIDKQNEALFKGNLKAKEFSPFDKYFGEKVLGFSNNGTGTQHYWNLDEWGSNYSLGWESGTTGASFSFHGGDLRSRRVRRRPGMTQMFLDYLRLRLELVFLDPRMKVYVGGSGVKGKPLARSLNKTLENGTIMGKPFVQLTGGGSOLEWEEANSQGMFLYHGRLEIAKRVKRGEMMHNGDNGRGGVIGVIDVTLNLMAEEDNGVWVHNNKGGFGDCEVYVAELEKWLGGKSDRYLDEHVDKVELKAGTGVYKFPDHEWVGGDKCRKWRMLSHGF

NbL12g08650.1 exosome_complex_exonuclease_RRP44_homolog_A [MW = 104.73 kDa]

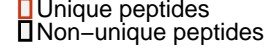
No. of times detected



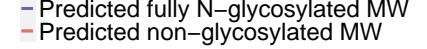
log(intensity)



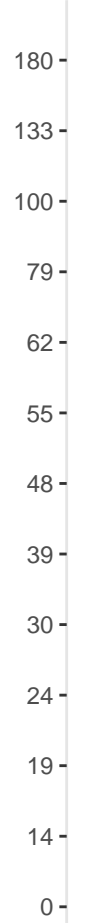
Values from



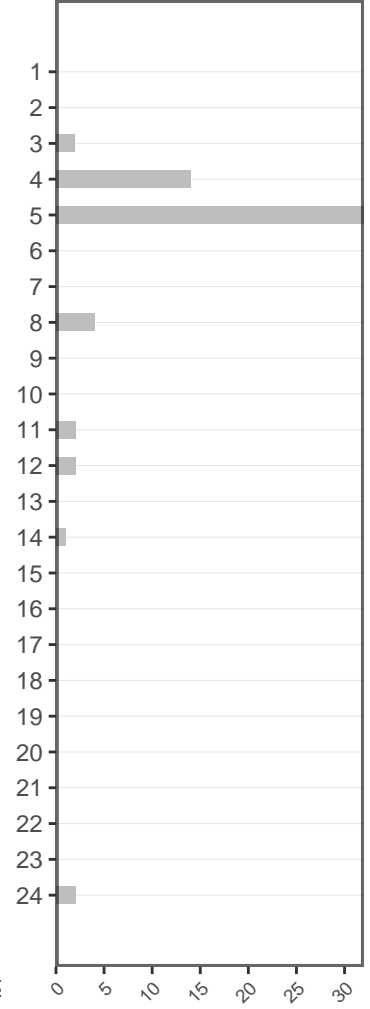
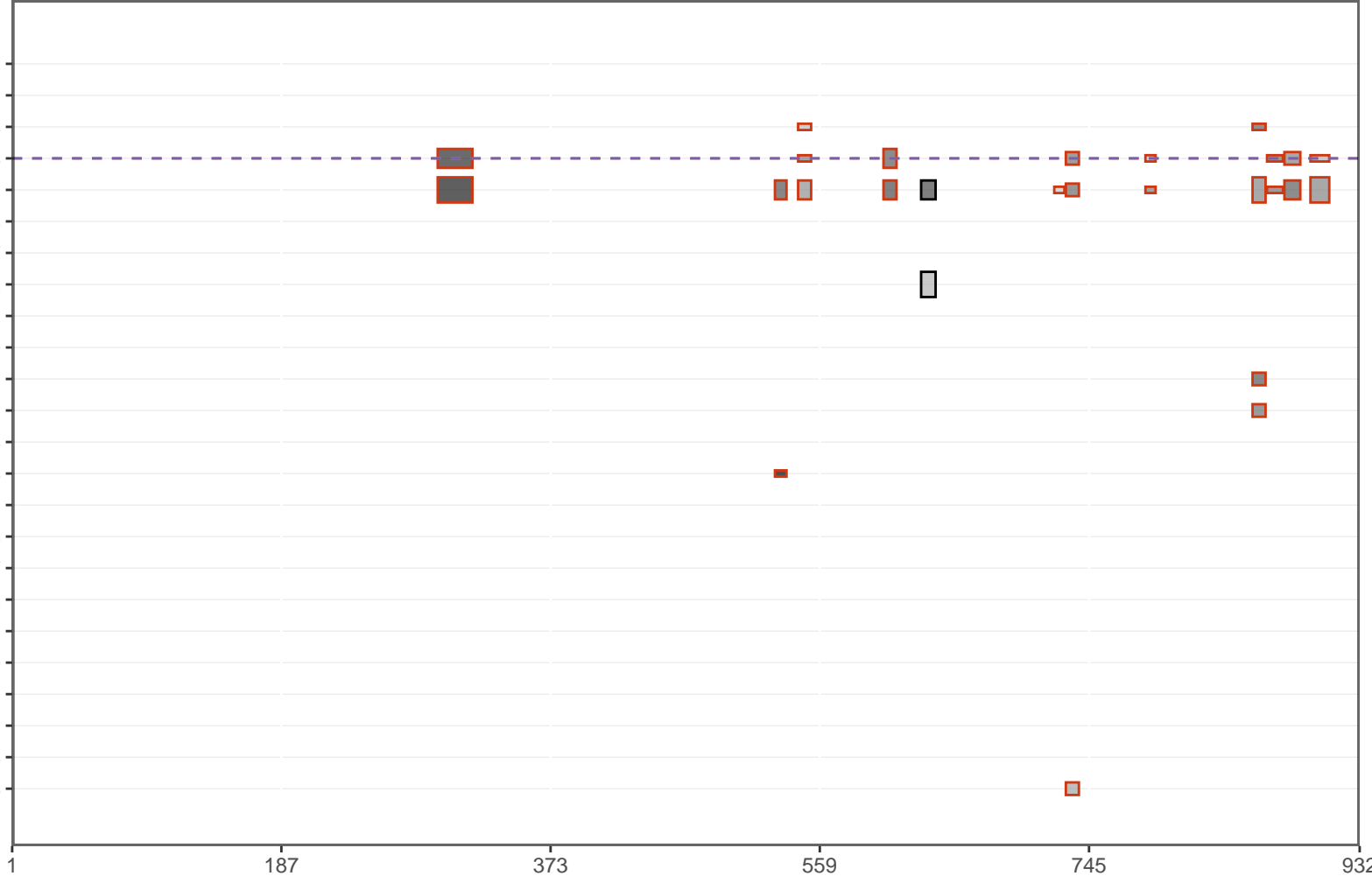
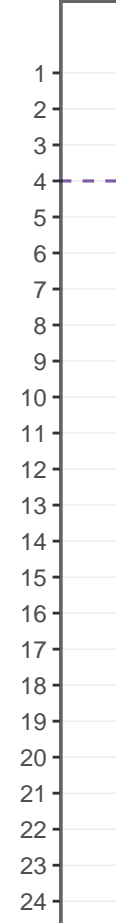
MW indication



Molecular weight

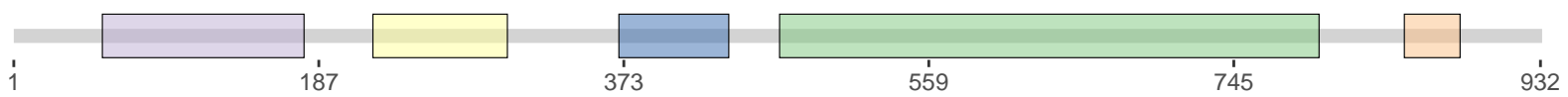


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

.PPLPWSVSSPOLTFNMRGDLRHLRQVSDPPGCRDIDDLHMLPLNGNFVGHADVTNFTVHPGTLDDAASGRGTSVYLVERRIDMLPKPLTDDGSLRADVERLAFVWEMTFDAEISSTRYTKSVKSGAALSYVEAGARMDDSLVDPITSDLRNLNGLAKIMRGRDRGALTLSAEVKGFDITETHDPLDGMVQIREANGMVEEFMLAANVAEKIKHFPFLGSLLRHPSPPTKEMLEPLLRTAEEVGLSLDVTSSKAMADSLDRAGDDPYFNKLRRLATRC

NbL12g08330.1 isocitrate_dehydrogenase_[NAD]_regulatory_subunit_1_mitochondrial-like [MW = 38.87 kDa]

No. of times detected



log(intensity)



Values from



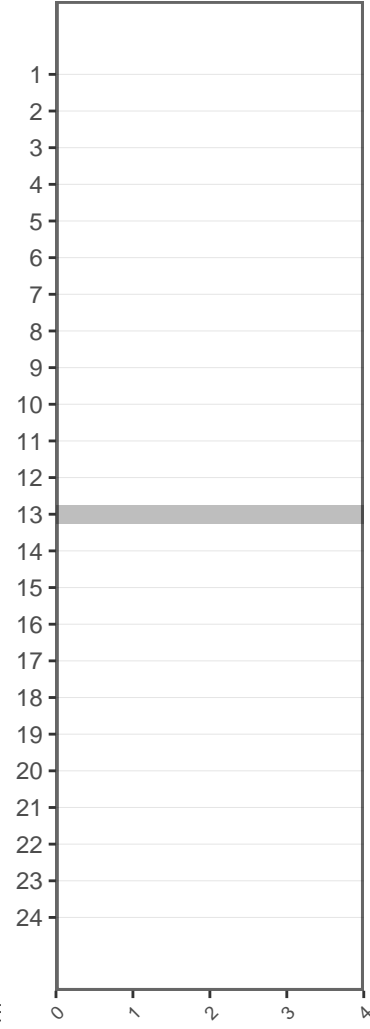
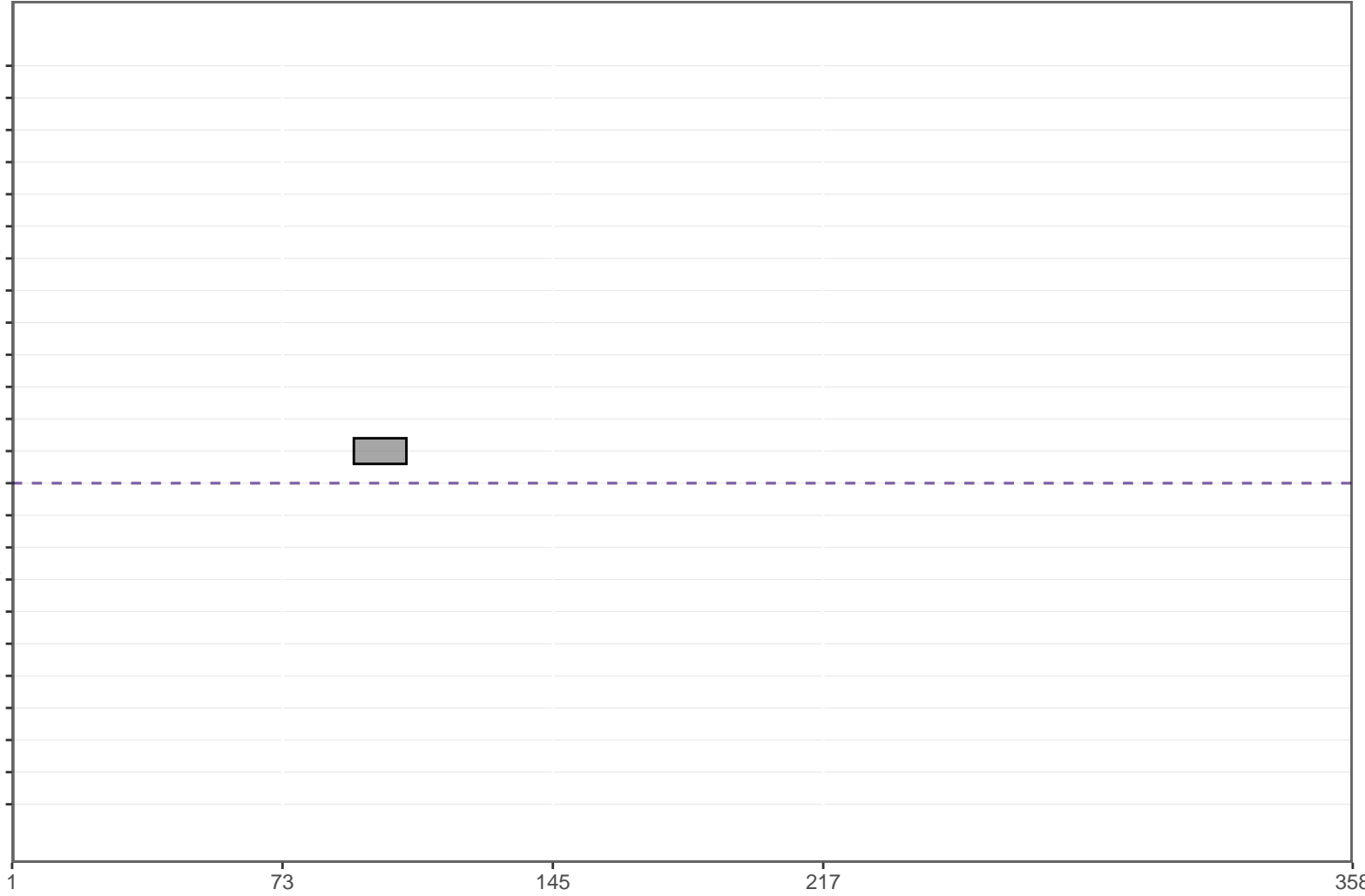
MW indication



Molecular weight



Gel Slice

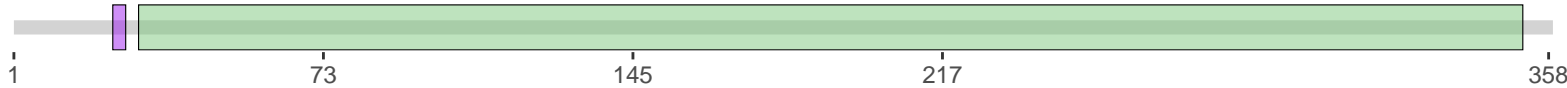


Protein length

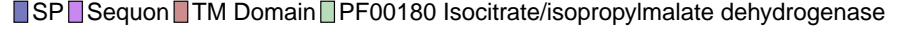


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

CSERIAKFAFEYADVNRKRKKVTAVHKANIMKLADGLFLESGREVAVKYPEIQYEEIIVDNCGMQLVSRPEQFDVMVTPNLVGNLIANTAGLAGGTGVMPGGNVGTGDAVFEQGSAGNVGNEKILKIKKANPVALLLSSAMMLRHLFFPSFADRLLETAVKRVIAEGKVRITKDLGGDCTTGEVVDMAALD

NbL12g08300.1 phosphoserine_aminotransferase_2_chloroplastic-like [MW = 47.45 kDa]

No. of times detected



log(intensity)



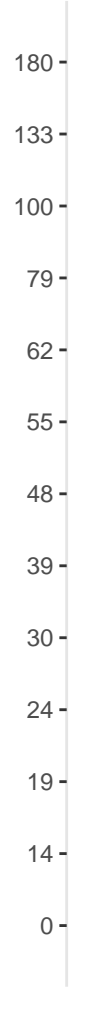
Values from



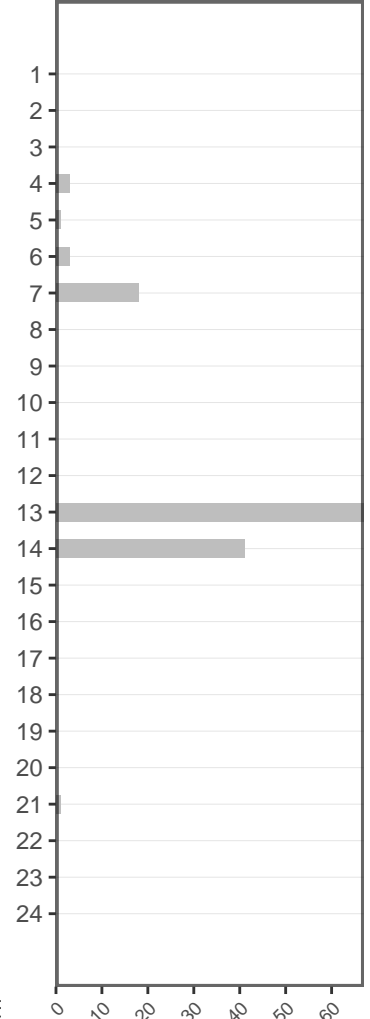
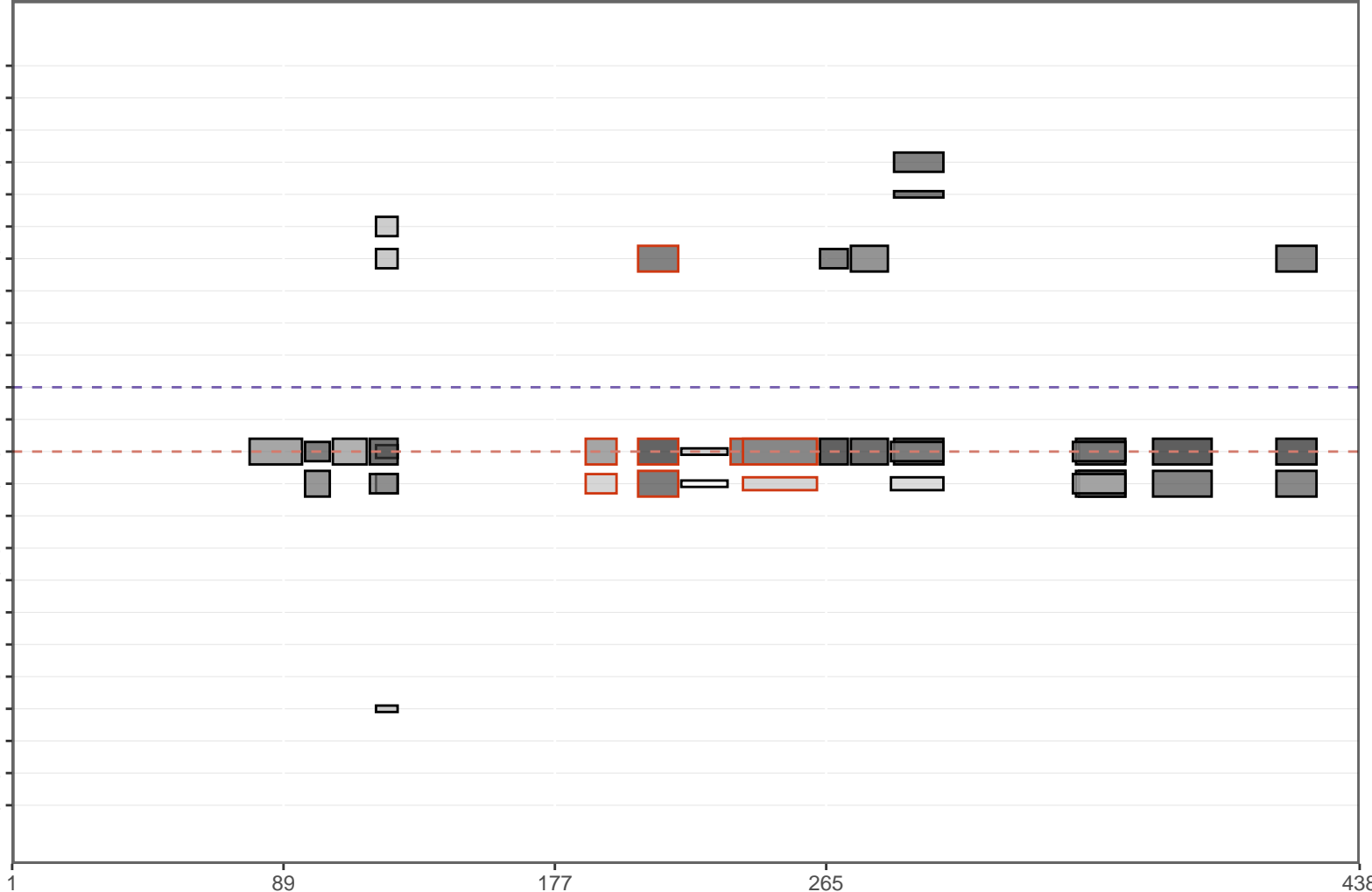
MW indication



Molecular weight

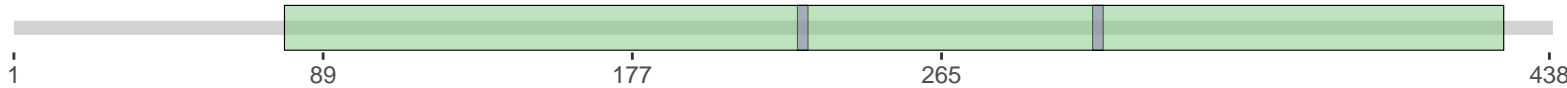


Gel Slice



Protein length

Peptide counts over 4 repeats



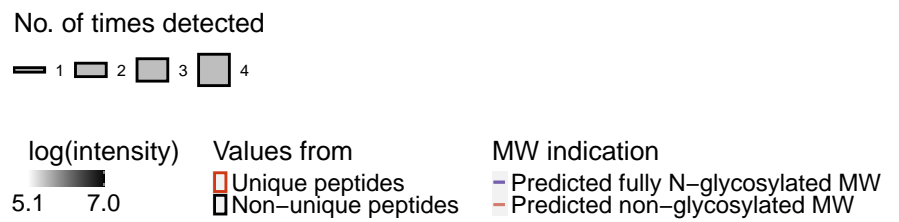
Pfam domains

Pfam Description



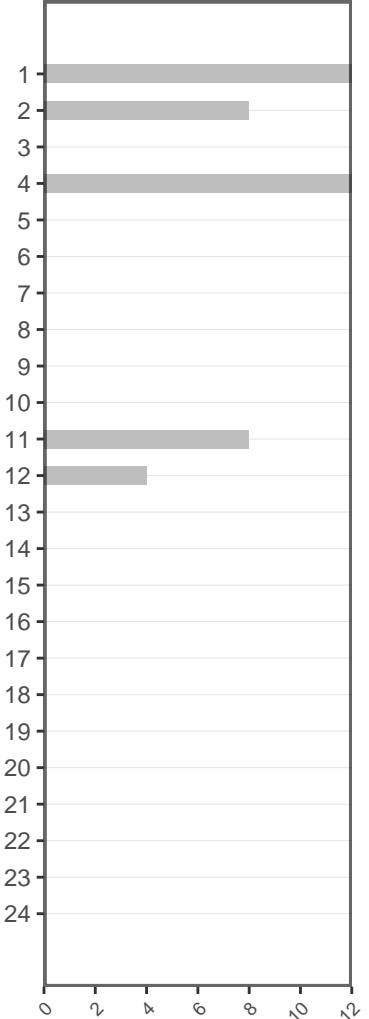
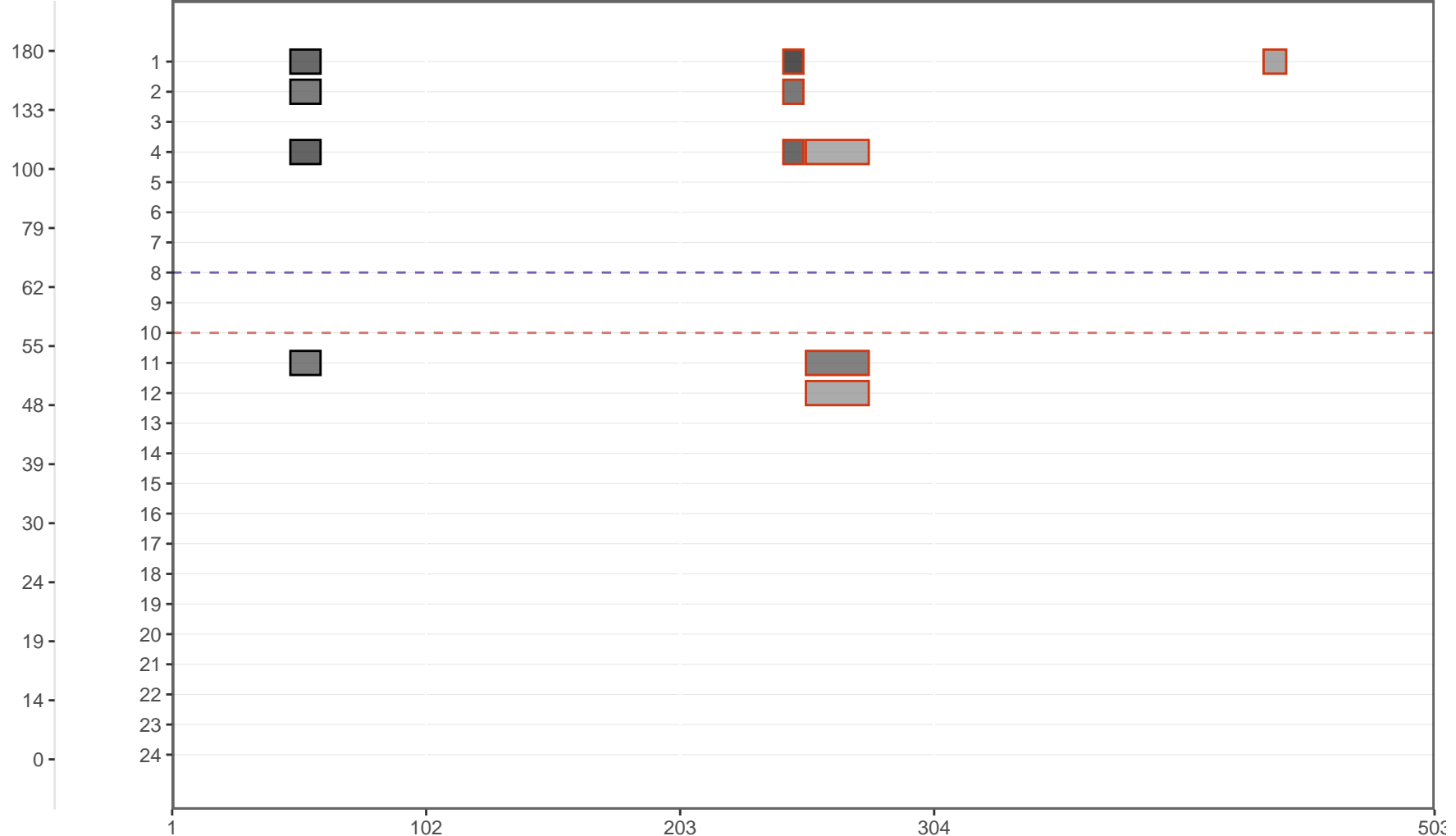
Protein sequence:

AFDSLOOTPGAKYLHIGANETHHGVEFKDYPKPSNANTLLVADMSENFSKSKPVDVSKFGVYAGAGKNNVSPSGVTVIRKDLIGNAQESTPVMLEQKIHAEENSLNTPPCYGVMDGLVFEFLAAGGLVEVEKNNKKKAEILYNADSSNGFFRRGPEKESVRLSMNVPTLAKPELEAEFVAAAEEKMVKLKGHRVGGMRASVYNAAMPLAGVEKLVAFMKDFQAKHAY



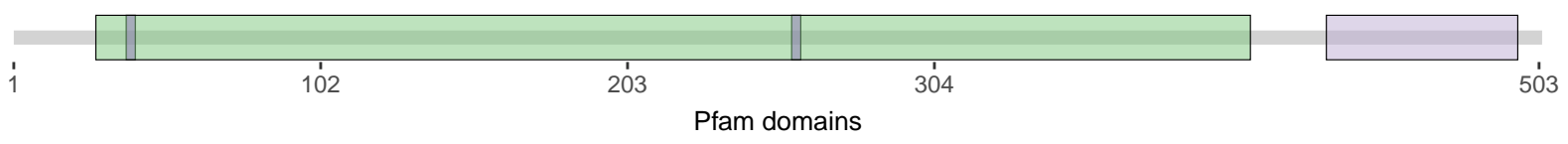
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam Description
 SP Sequon TM Domain PF00199 Catalase PF06628 Catalase-related immune-responsive

Protein sequence:

TCGVKSLLEDEAARVGGANHSATGDGLDYDIAAGNYPEWKLFIQTMDPDHEDRFDFDPLVTKTWPEDLPLGPGVGRILVLNKNDIFFNEGLAFSPGIVVPGVYVSDDKMLGTRIFSYSDTQRVRLGPNYQLFPAAPKGAHNNHYDGSNFMHRDEEIDYFPSRYDFVRLHAEKYPIPMCTMGKREKGVIGKENNFKPGDGRYSFPPRQRERFIRWVEALSDPRITVEKRSIWHISYWSGADKSLGQKLAGRLNVRPDI

NbL12g08140.1 thiol-disulfide_oxidoreductase_LTO1 [MW = 40.07 kDa]

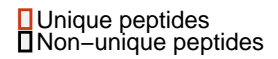
No. of times detected



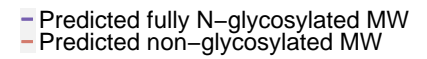
log(intensity)



Values from



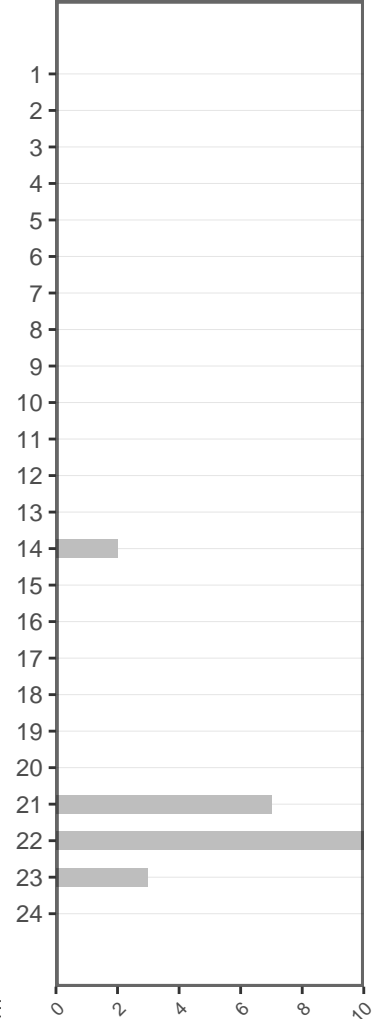
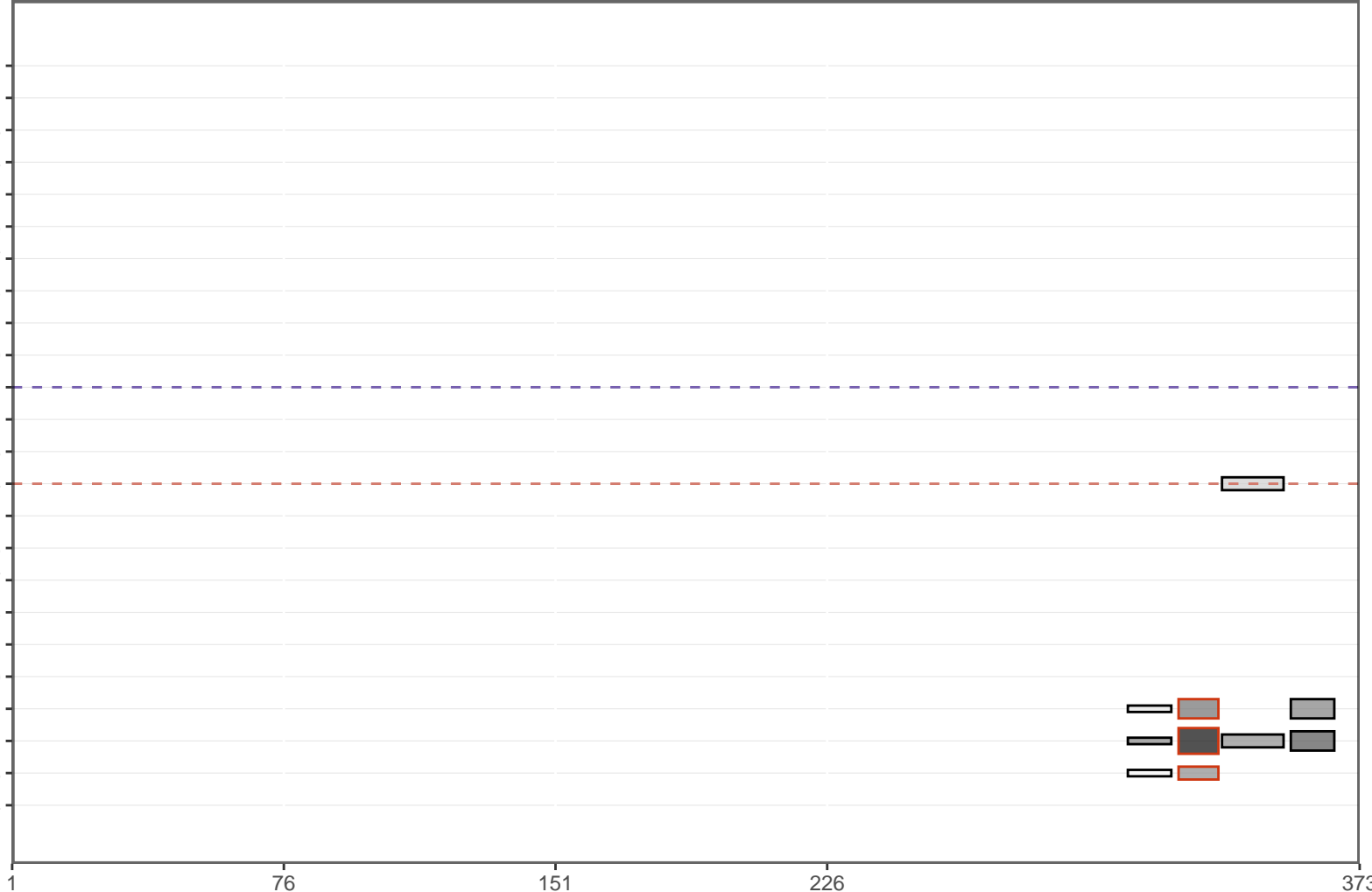
MW indication



Molecular weight



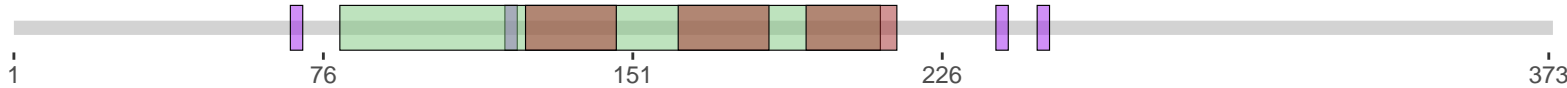
Gel Slice



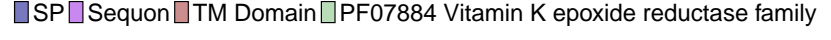
Protein length



Pfam domains



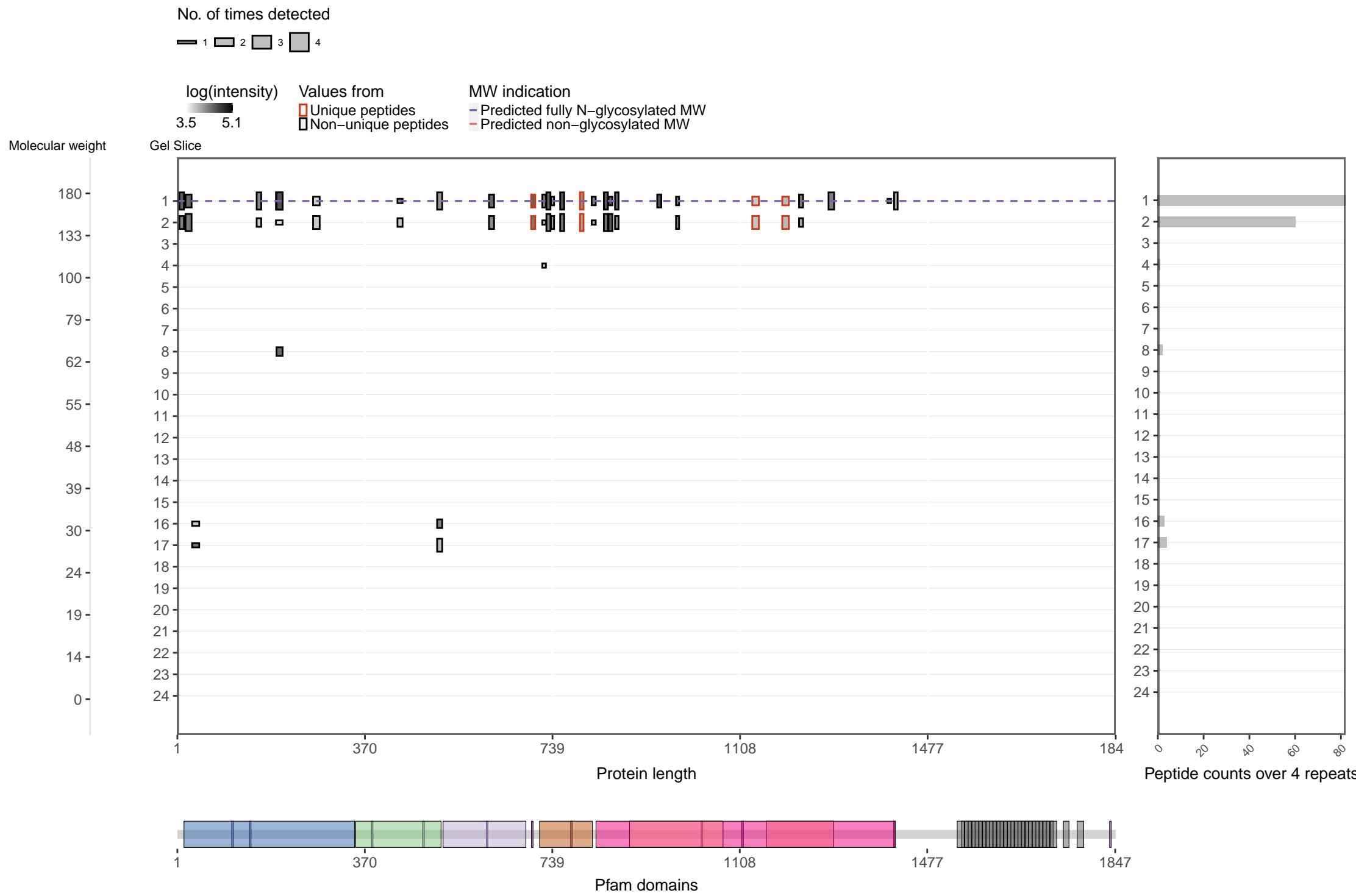
Pfam Description



Protein sequence:

MAAASAYFLYLSTQFSGGEGFLGLASALLGFLGRISBIMGLGDEVEQKEVGLQLLVLLVSTLNNSVYASQPTNTSSAMTELEYFTTEITSPTFFAIBLAKHLRIGIGAKMYGAFVDSHDDGQKEMFGRASKLLDVEGFPDGVKKGIVMANAGDEAKLEGFPTTWINGEVLGGEKKLSELAELEGFTMKELTEAKY

NbL12g08050.1 DNA-directed_RNA_polymerase_II_subunit_1 [MW = 205.42 kDa]



Pfam Description

- SP PF00623 RNA polymerase Rpb1, domain 2 PF04992 RNA polymerase Rpb1, domain 6 PF05000 RNA polymerase Rpb1, domain 4
- Sequon PF04983 RNA polymerase Rpb1, domain 3 PF04997 RNA polymerase Rpb1, domain 1 PF05001 RNA polymerase Rpb1 C-terminal repeat
- TM Domain PF04990 RNA polymerase Rpb1, domain 7 PF04998 RNA polymerase Rpb1, domain 5

Protein sequence:

KSTFDLLVAEIDDPNVAIPSYMLPEAEKDKFREIRSRVDAEYKQLADRKLGKTEVAWTDGNSWPLVWDRVLVNAKTKFKIDFRRRSDMHPMEIWEAVDKLQERLKYVPGDDYLSMEADKNAKTLFFNLRSLASAKRYLKEYRLSREAFDWWIGIEISRFLOSIVAPGEMGCVAAQSIGEPATQMTLNTFHYAGVSANNKTYLGVPRLEINWAKKKTPLSYLKPVEYKTKERAKTYDCALEYFLTRSVTQATFEVWYDPPMSTLEEDVEFYKSYIEMPEDEIDPFKIS

NbL12g07870.1 uncharacterized_LOC107826763 [MW = 23.25 kDa]

No. of times detected



log(intensity)



Values from



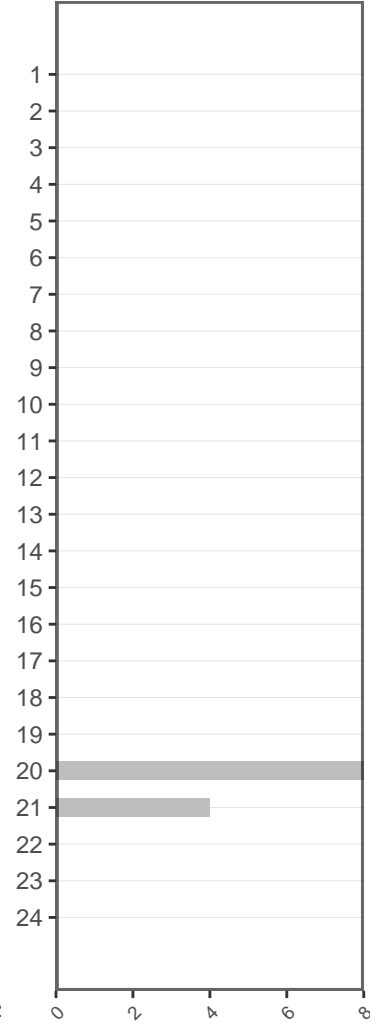
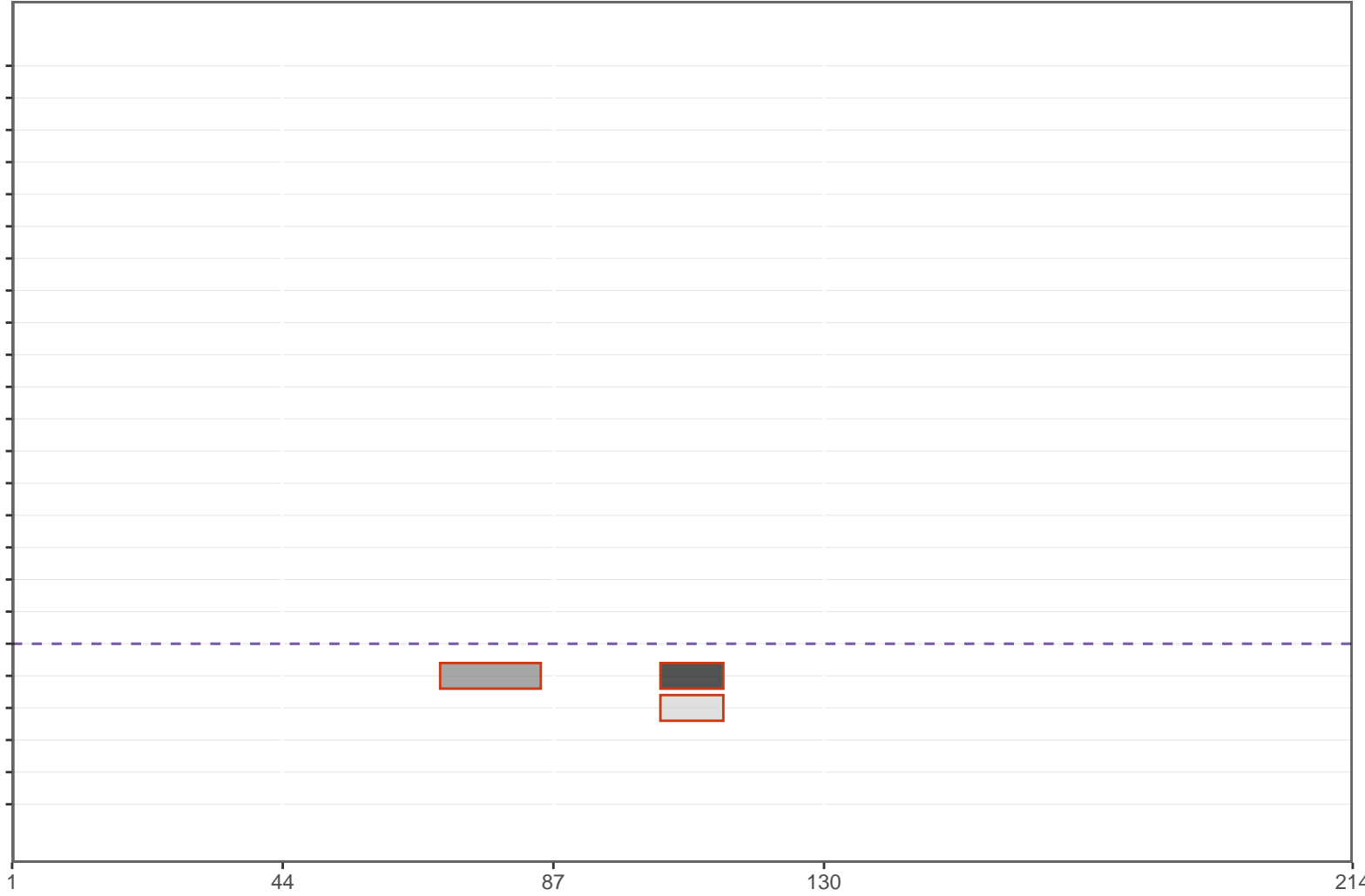
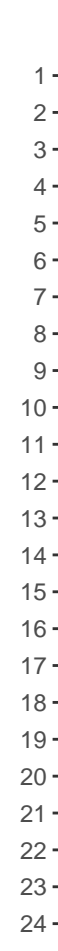
MW indication



Molecular weight



Gel Slice



Protein length

Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

IRNPNYLSGSRQAAATAALAKKYGADITVWVIDEKEKAVPEHETQLASIRWHLSEGGYQEFKLLERLGGESKPTAIGEIADENMLDVAIMSMEAIHSHKIVDANLLAEFPCPVLLLPV

NbL12g07820.1 26S_proteasome_non-ATPase_regulatory_subunit_4_homolog [MW = 42.25 kDa]

No. of times detected



log(intensity)



Values from



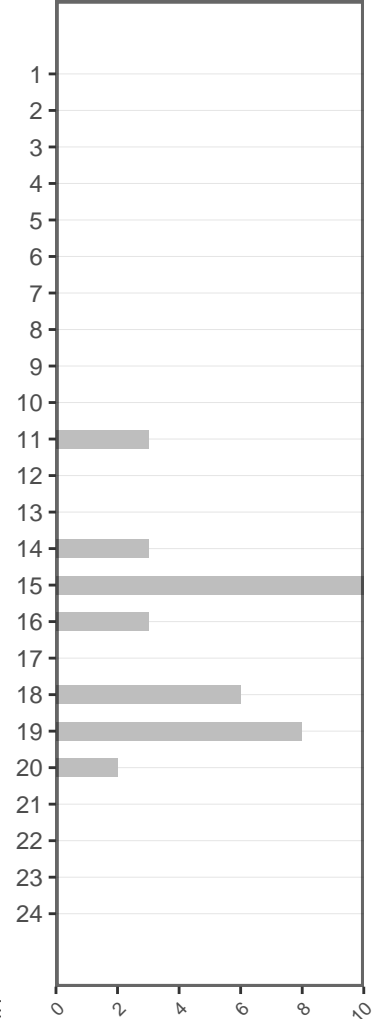
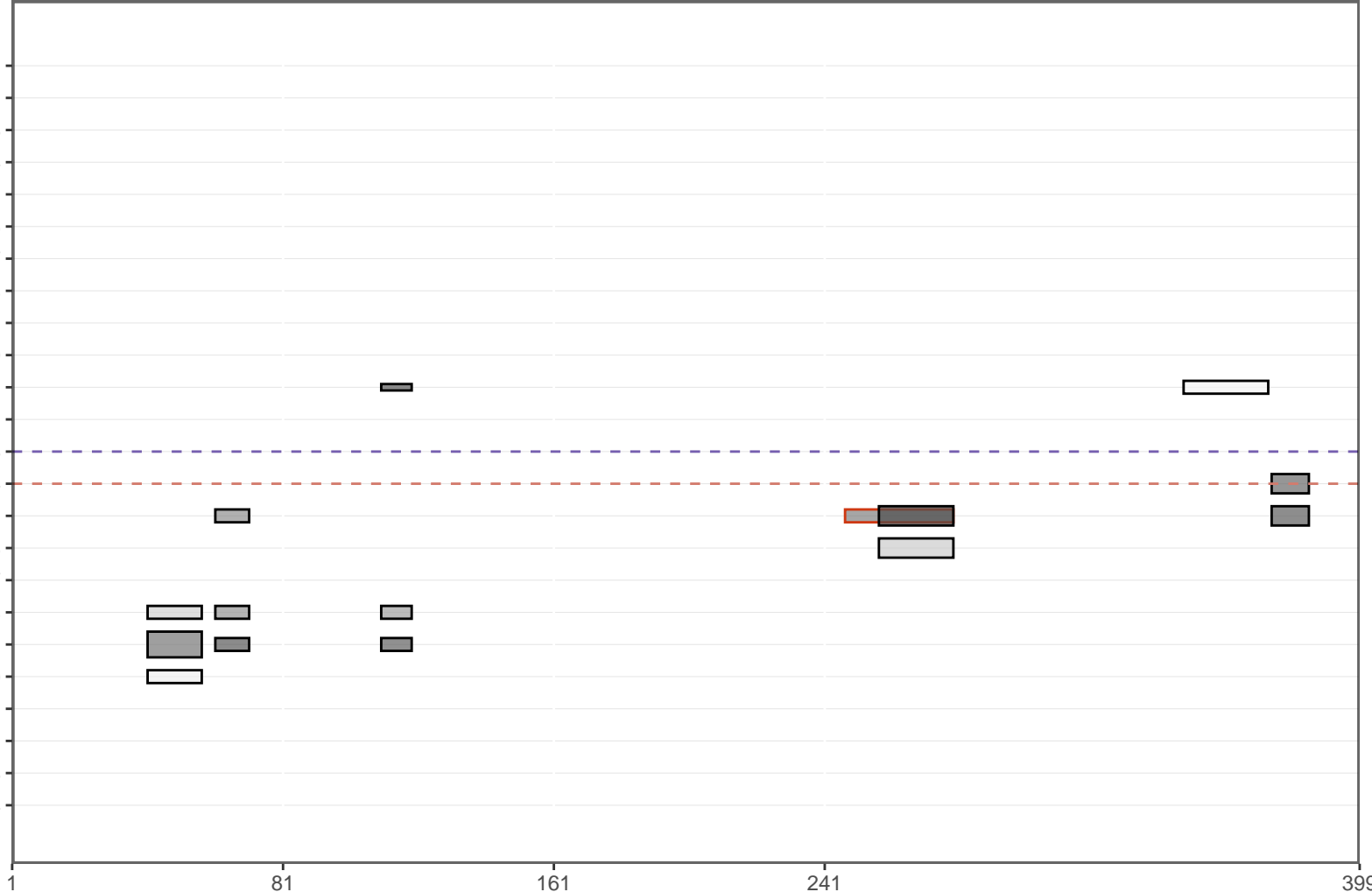
MW indication



Molecular weight



Gel Slice



Protein length

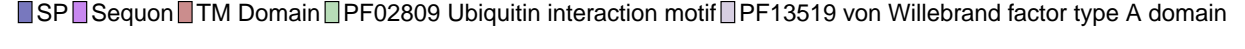


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TGDEGGSGFIAAAMAGGVSDFDVPDNLDELALALRVSMEEERARQEAAMAAKAADETATQEKGETSDDVTMAENNVAGTPPEPKATDLMEDENALQQALAMSMDDASGNVATRTDMSEAASEDDGLALALGLVSGDETNDQSSGDTMSKLLADGFSVSLIASLPGVDPNDFPKDLLASMOGQSEKDEDTDKEGEEKK

NbL12g07810.1 alpha-mannosidase [MW = 34.18 kDa]

No. of times detected



log(intensity)



Values from



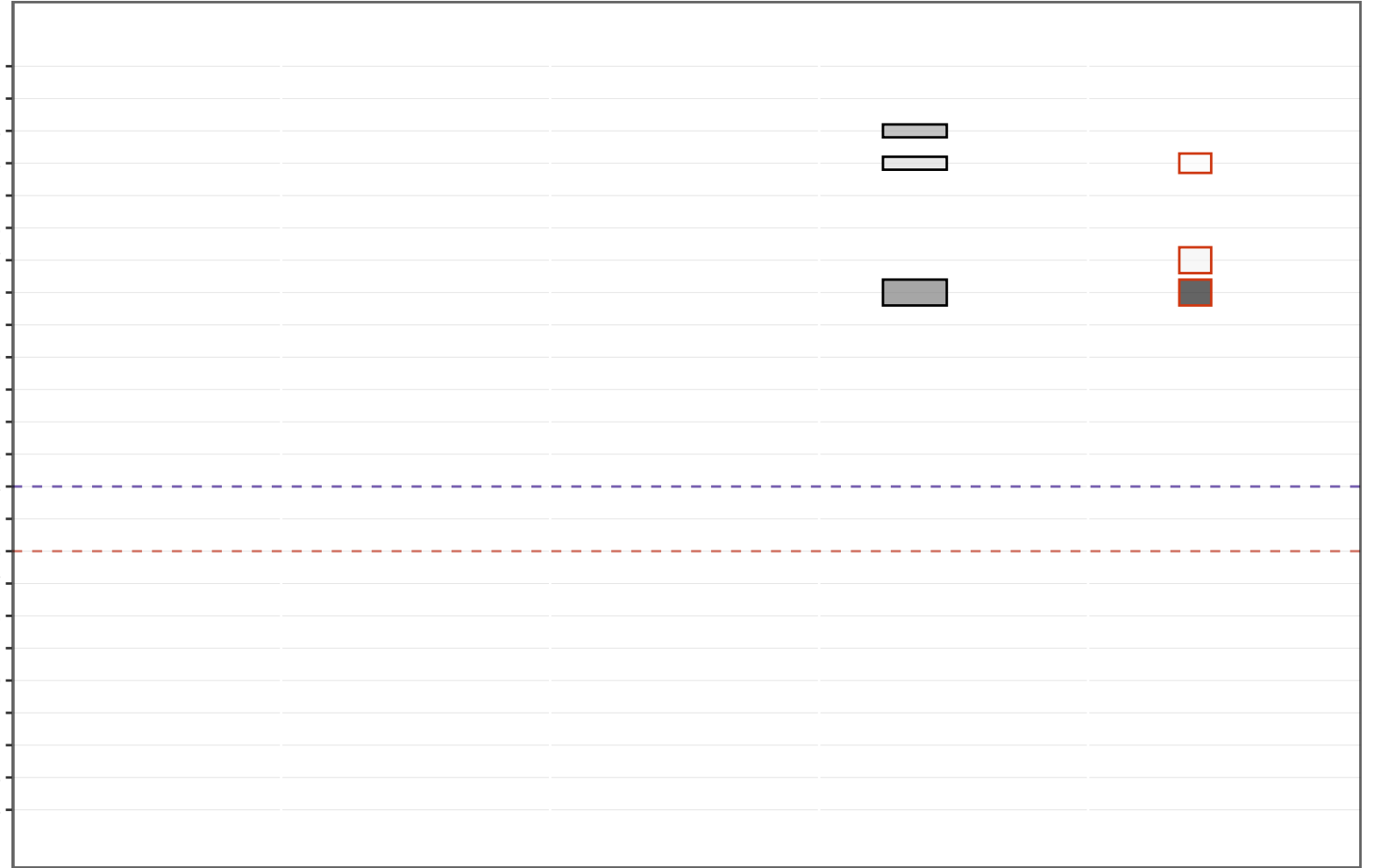
MW indication



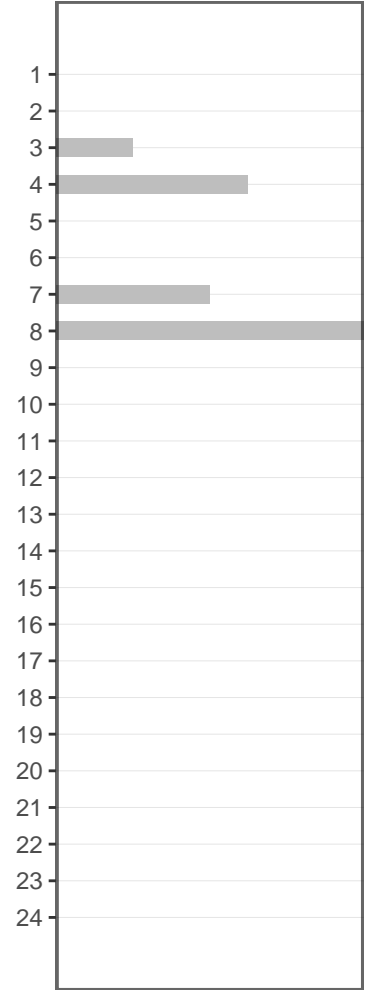
Molecular weight



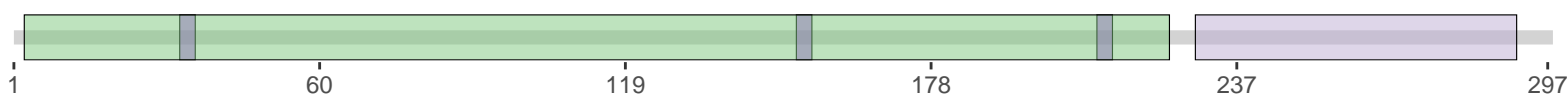
Gel Slice



Protein length

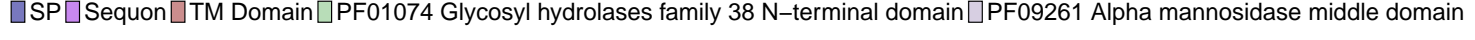


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DIRVNDVNSAISOANVTRRNHMMWTMGDDDFQYGAESGWFKEMOKLHYVVKDGRVNALYSTPSYVDAKHATNGSWPLKTDQDFPVADGANBYWTGFTSRPAKRYVRLMSGYVMAARQLELTGRKSEGNTFSLGDALGVTHDAVDTGTQNSQLM

NbL12g07800.1 alpha-mannosidase [MW = 46.45 kDa]

No. of times detected



log(intensity)



Values from

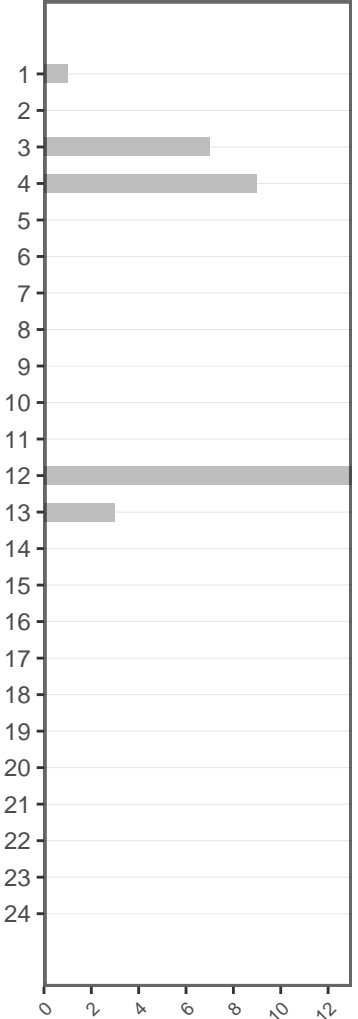
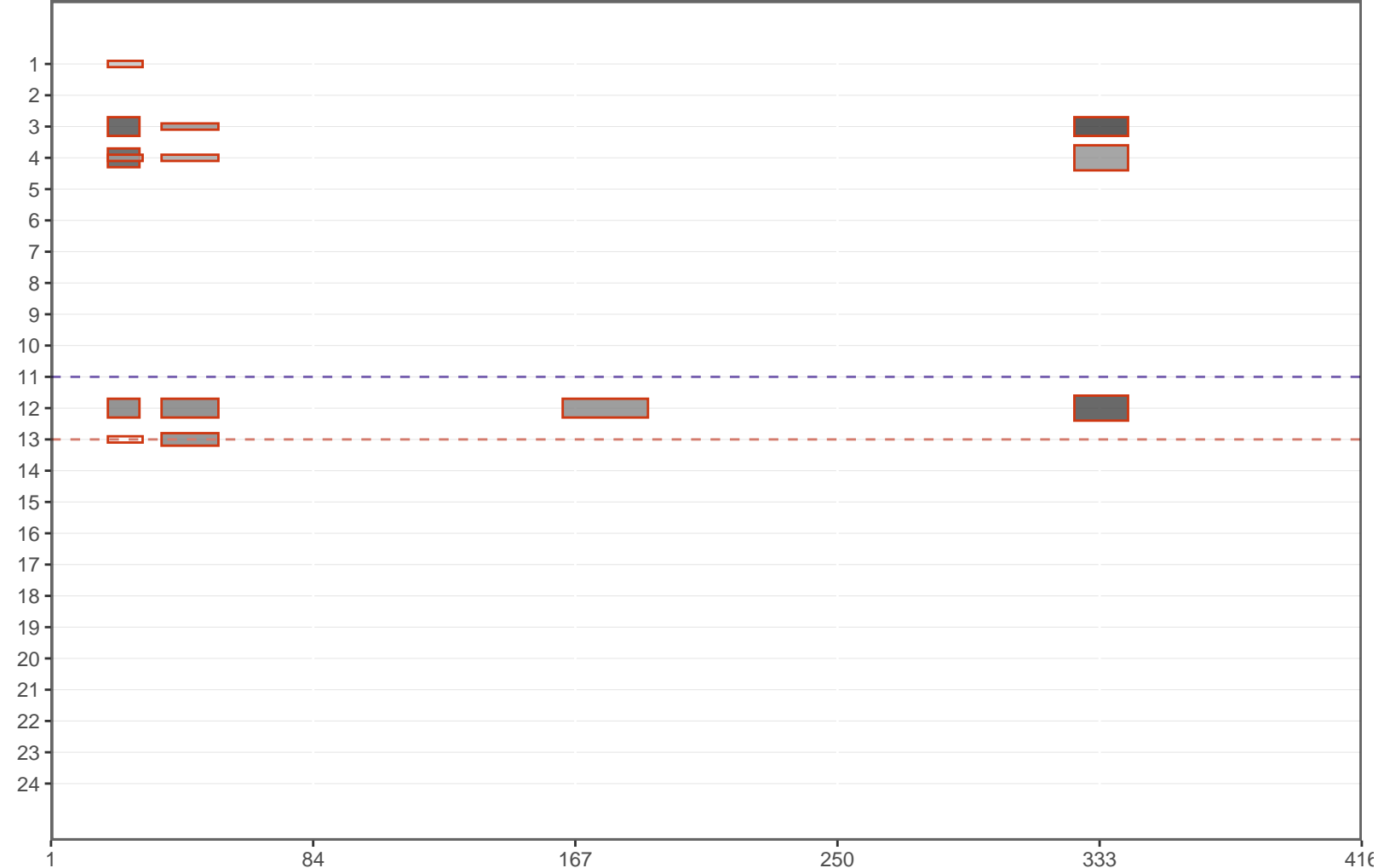
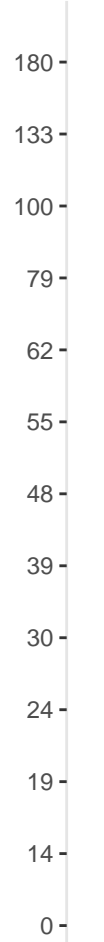


MW indication



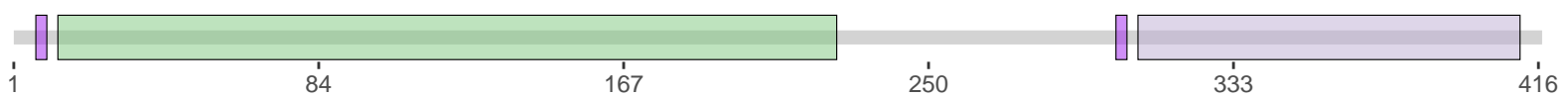
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF07748 Glycosyl hydrolases family 38 C-terminal domain
- PF17677 Glycosyl hydrolases family 38 C-terminal beta sandwich domain

Protein sequence:

/LVDRATGGASINDGEIEMLRRLLYDDARGVGEALDEFVGVGTAGEGLRVRGNYYLGHKNDDGSRWRRTTGGGEYSPVLAFGHEHNGEWRRAHLTKATMNPVLPFNVALTLGELINDGVLLRLHLHVEAGEDTEYSTTKVQLKDMFAGTKTKEIKETLSANOGKNEMKKMSWNEHDTGSEPRGVPVDSISLIVELGPMIEIRTFVVEP

NbL12g07720.1 3-dehydroquinate_synthase_chloroplastic [MW = 47.87 kDa]

No. of times detected



log(intensity)



Values from



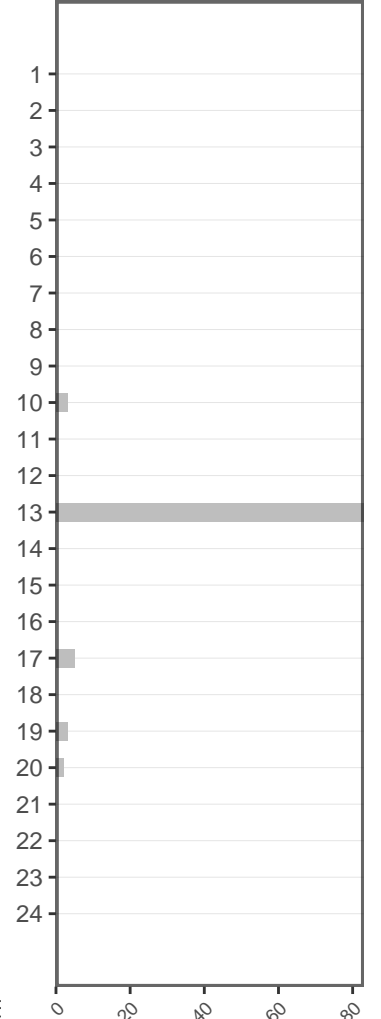
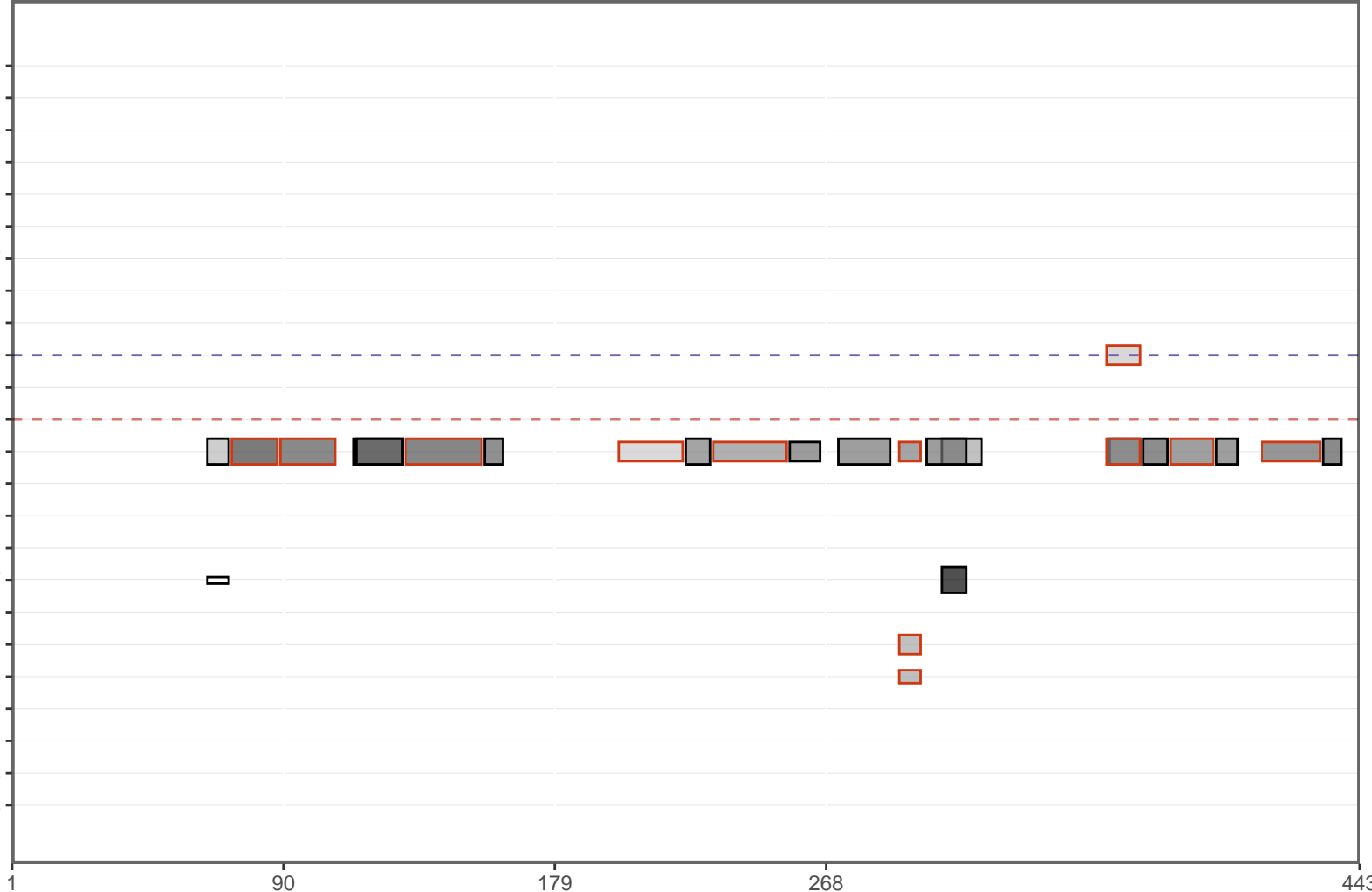
MW indication



Molecular weight

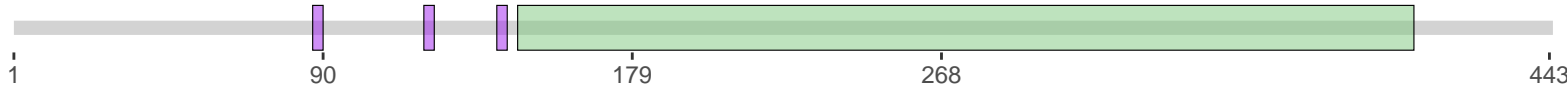


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

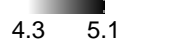
MAQDVSSVGGKIGINHPGKMGTFYQPGVLDVDTDLDPRELASGLAEVIRKGLVRAEFFEWDGEGNMLLLARDRTAFAYAKRSCENKAEVSLDEKESGLRATLNLGHTFGHVAETGFGVGGWHLHGEAAAGTVMAVDMSRRKLGWIDDSLVGRVHNLGGAKLPTAPPPTMTVMFKSMAVDKXKADGKRLRULLEGPLGNVFTGDYDQKALDETURAFSK

NbL12g07650.1 extradiol_ring-cleavage_dioxygenase-like [MW = 30.35 kDa]

No. of times detected



log(intensity)



Values from



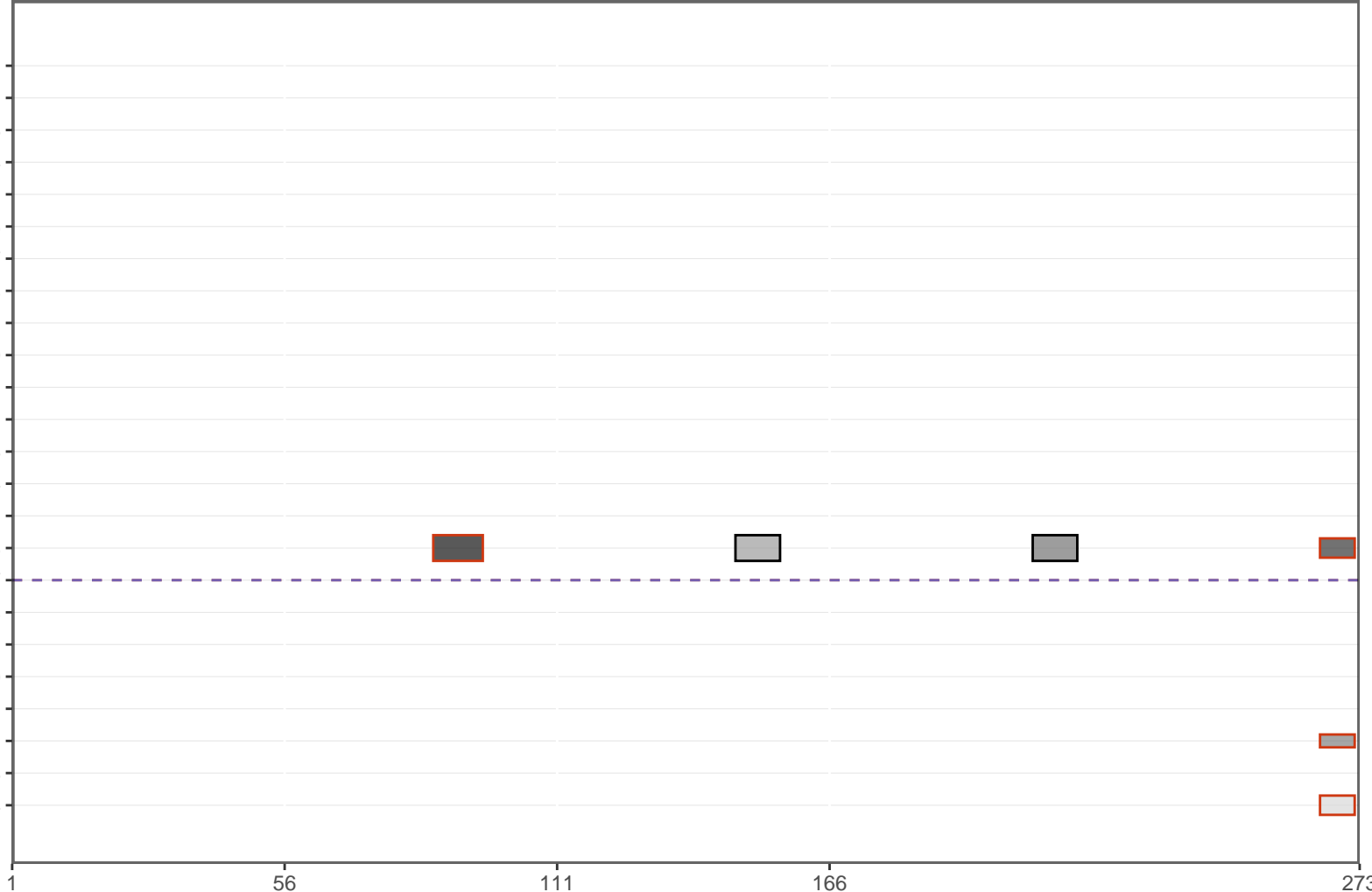
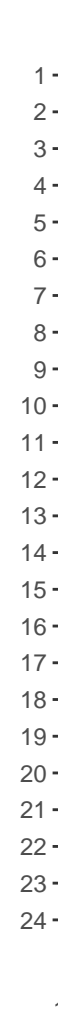
MW indication



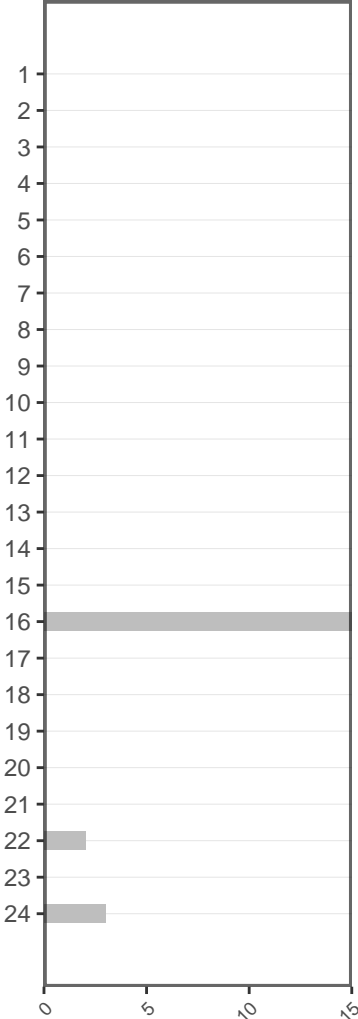
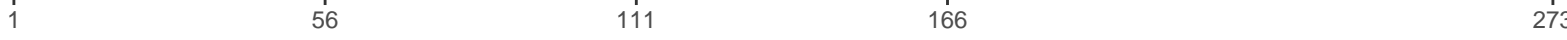
Molecular weight



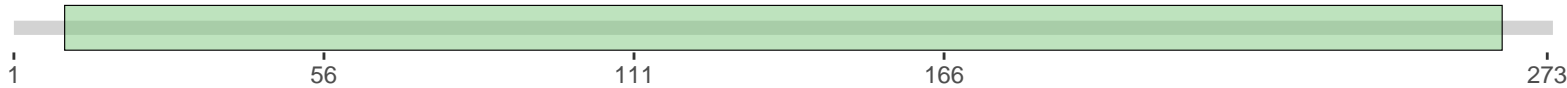
Gel Slice



Protein length

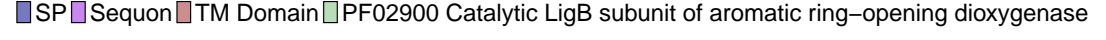


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PLMLMYPEDIPVCGQLSVQPNRDGTTHYHNMGRALASLKDIEGLVHGSGSATHNLRALGSSKSVVSWALEFDNWLKDALLSGRHGDVNNYDMKAPHAKVAHPWFHEHYPLHALGASGEGTNGELIHSWDLGALSVAIVKFSLSLRPS

NbL12g07490.1 ferredoxin--NADP_reductase_leaf-type_isozyme_chloroplastic [MW = 40.32 kDa]

No. of times detected



log(intensity)



Values from



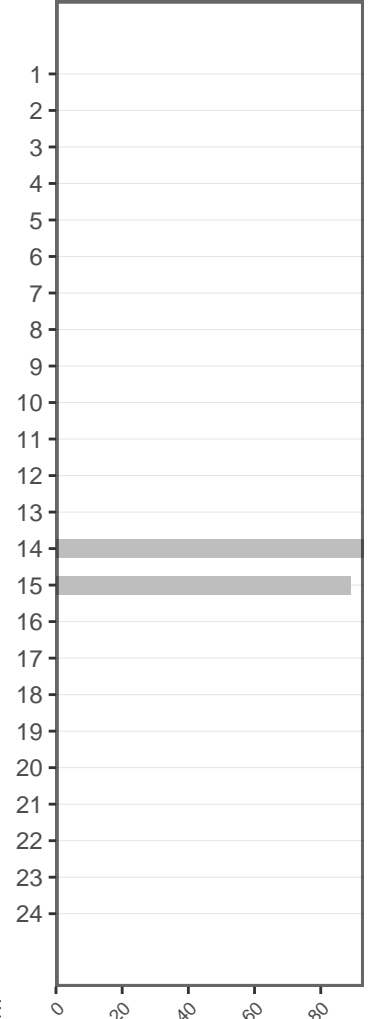
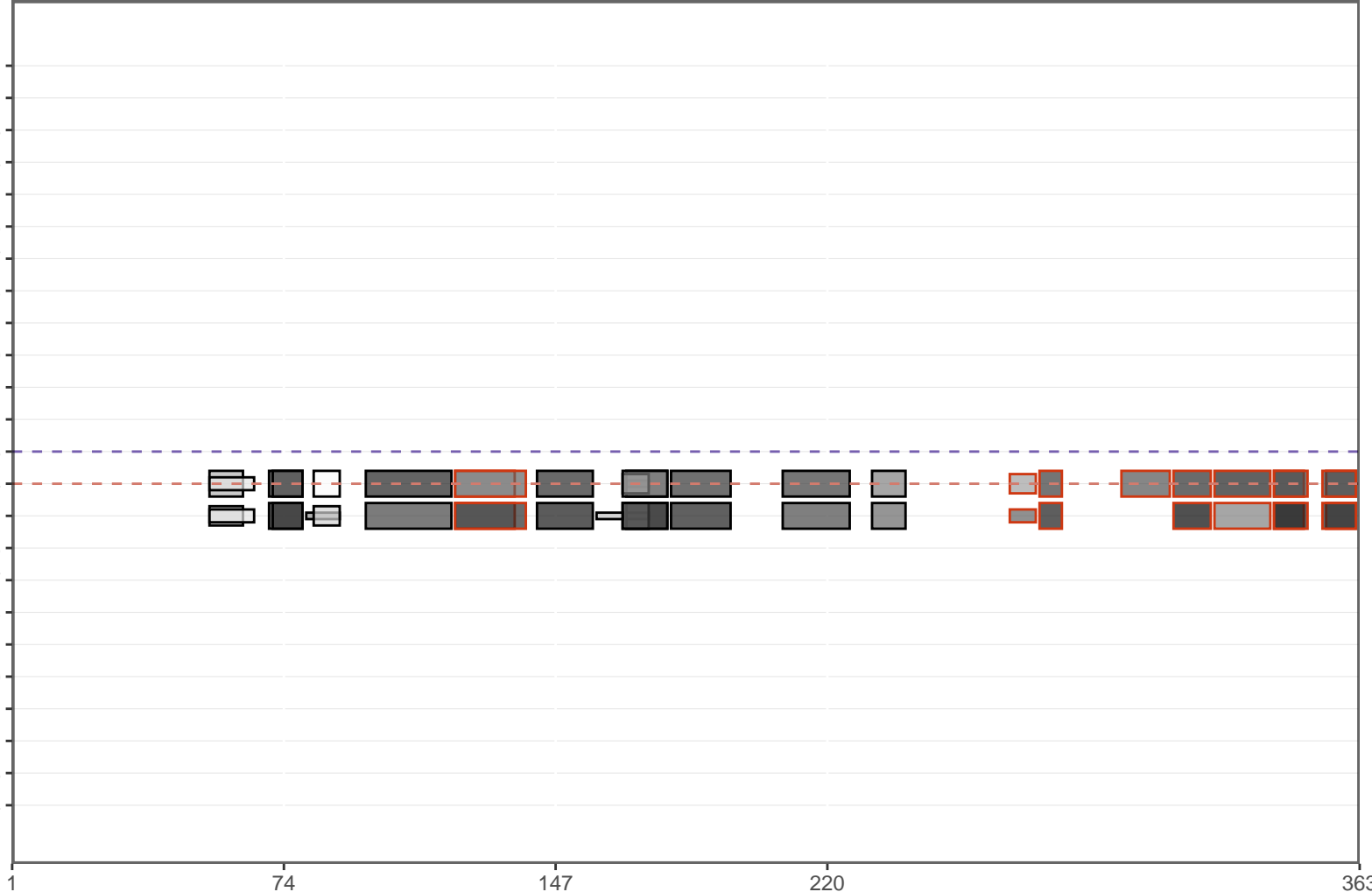
MW indication



Molecular weight



Gel Slice



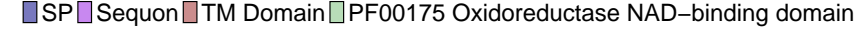
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKGEEVGVCSNFIIGDQKPGAEVWIKGPKVQKEMLMKDPNATVMLATGTGIAPFRSFLWKMFFEKHEDYKFNGLAWLFLGVPTSSLLYKEEFKMKKAPENFRLDFAVSREGQTEKGEKMHQTRMAGYAEELWGLGKNTFVYMGGLKGMESGDDMTSLAARDGIVWADYKGLKKAEGWNEVY

NbL12g07300.1 DNA_repair_protein_UVH3-like [MW = 54.81 kDa]

No. of times detected



log(intensity)



Values from



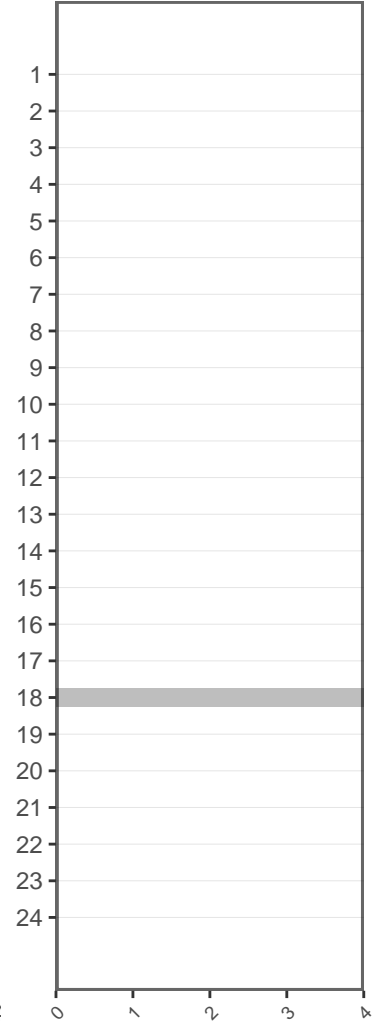
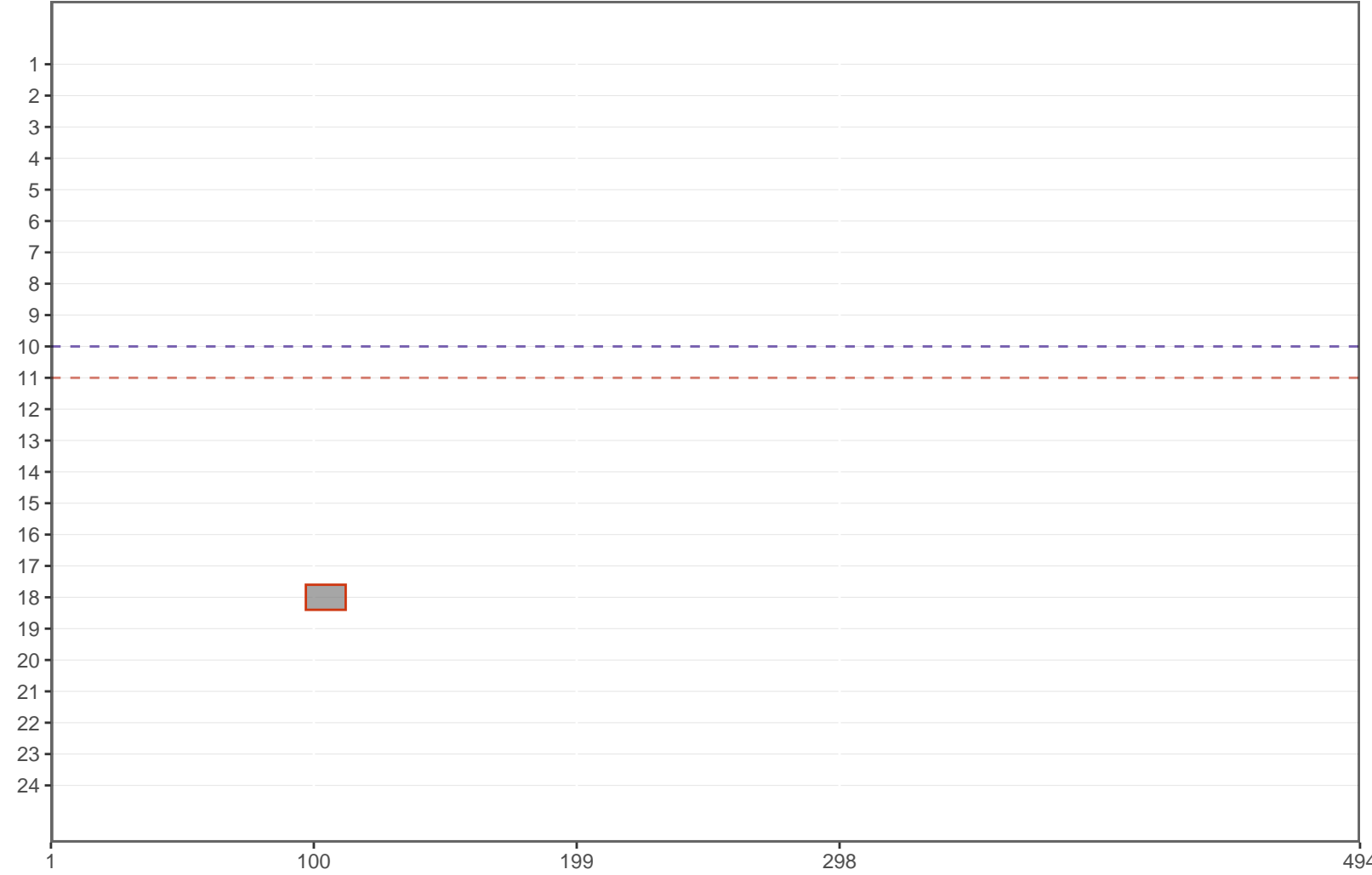
MW indication



Molecular weight



Gel Slice



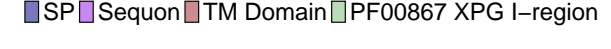
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EREKLGDEORKLERNAEVSSEMFAGEGQELLQMFGLFYIAPMEAEAGCAYMELTNLDGVVTDSDDAFLFGARINYYNFFDDRKYMETYFMKDVENELGLDRKLRMALFLRISYYTEGVSGIGVNAEVLNAPFEEDGLKFRFVVEVSPDPBILGGLDAGVSGSTRKRQSEVGDPMSCSSSNVEGNSSESDENKSEDRVQKLGKQFMNKHRSKSNWHIPSSFFSDAIVSAVASPRVDEKSTEPFAWGGKPDVGVLRK

NbL12g07170.1 mitochondrial_outer_membrane_protein_porin_of_34_kDa [MW = 29.61 kDa]

No. of times detected



log(intensity)



Values from



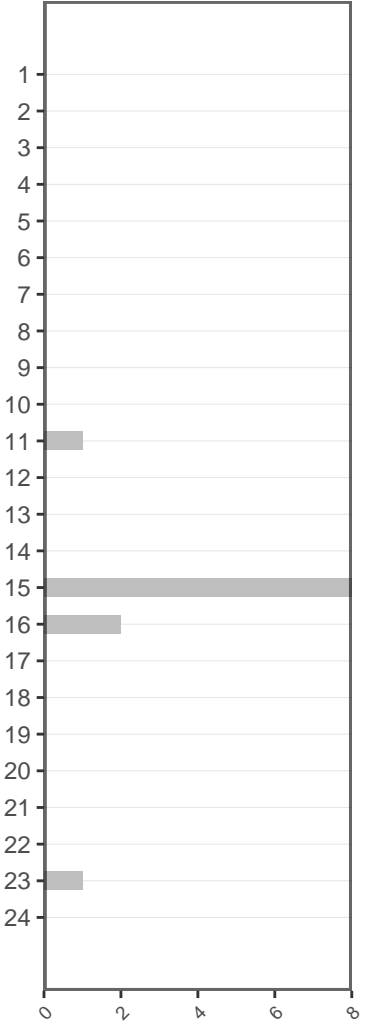
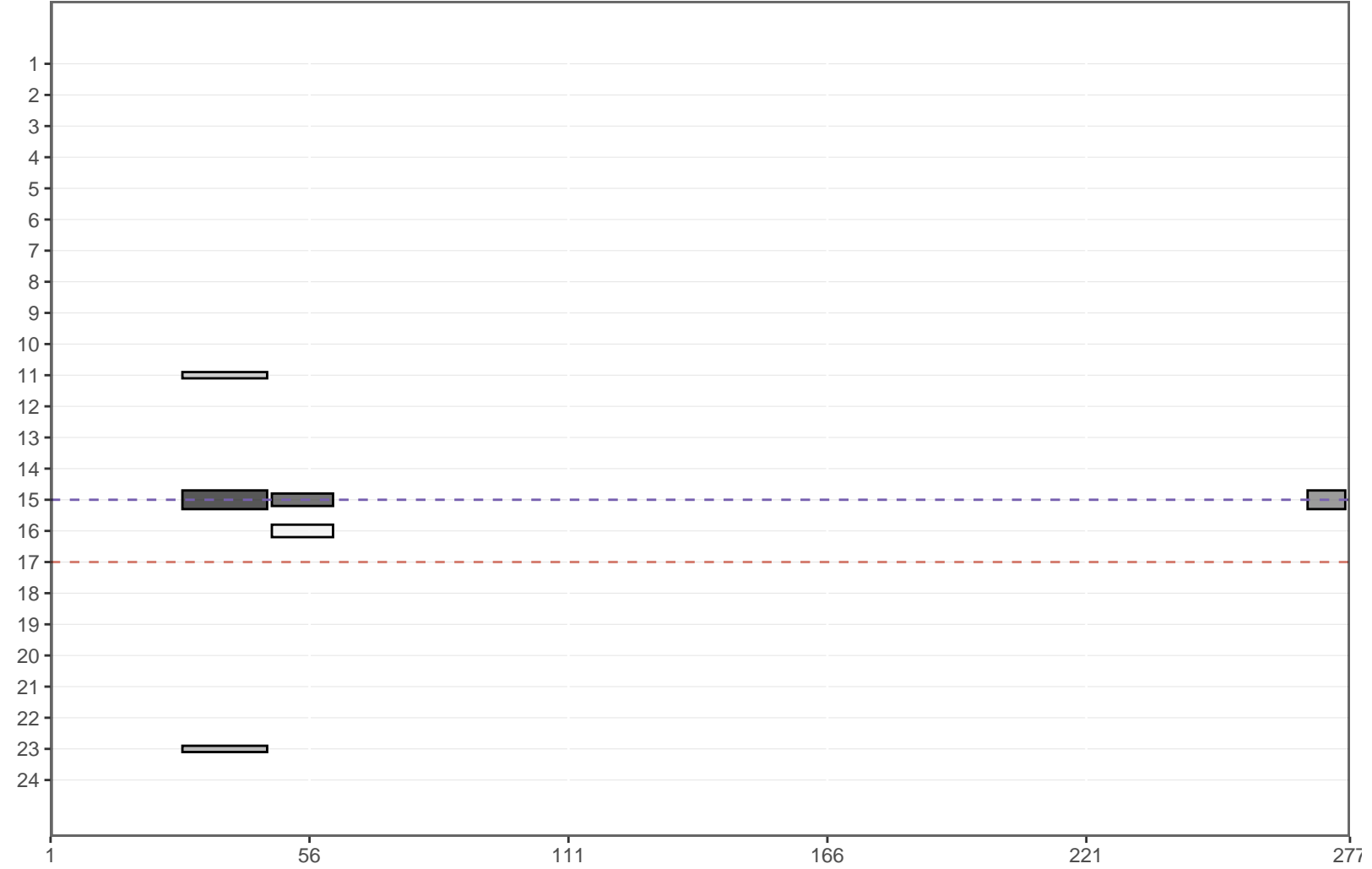
MW indication



Molecular weight

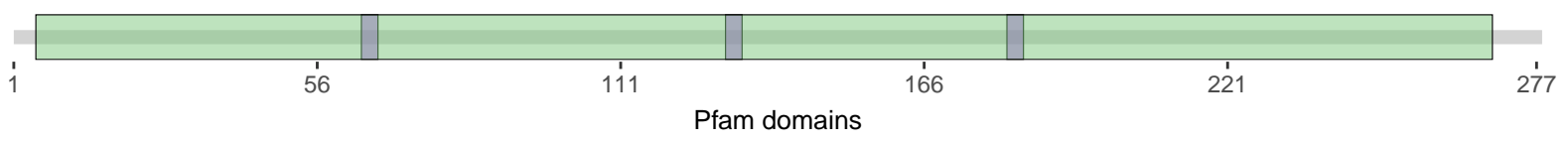


Gel Slice



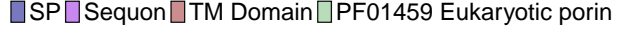
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NFSGGVGTNLALAGTGVSPDTRTKGDFTRKGNAGLSFTNADLWASLNLDKGDNLASBYHTVSPFTSTAVGAEVTHGCFSTNENTITVGTQHRLEDPLTSWAKRVNFFGKASALLGHEWRPKSLFTISGEVDTKSDKGAKFLALAKP

NbL12g07070.1 NAP1-related_protein_2-like [MW = 28.27 kDa]

No. of times detected



log(intensity)



Values from



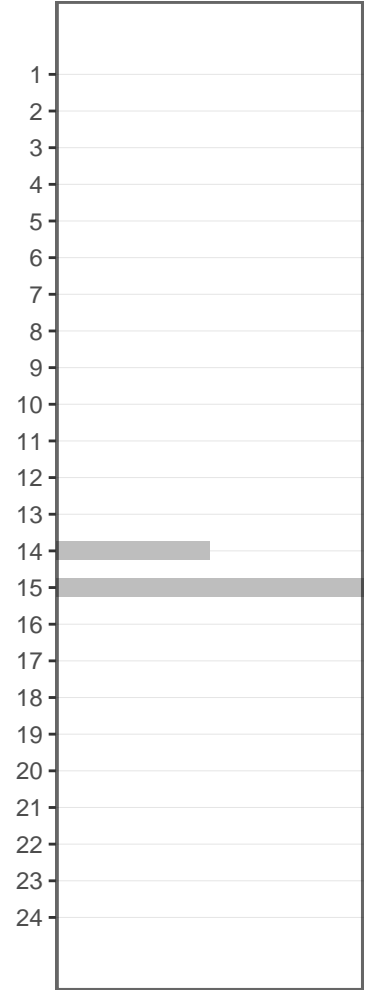
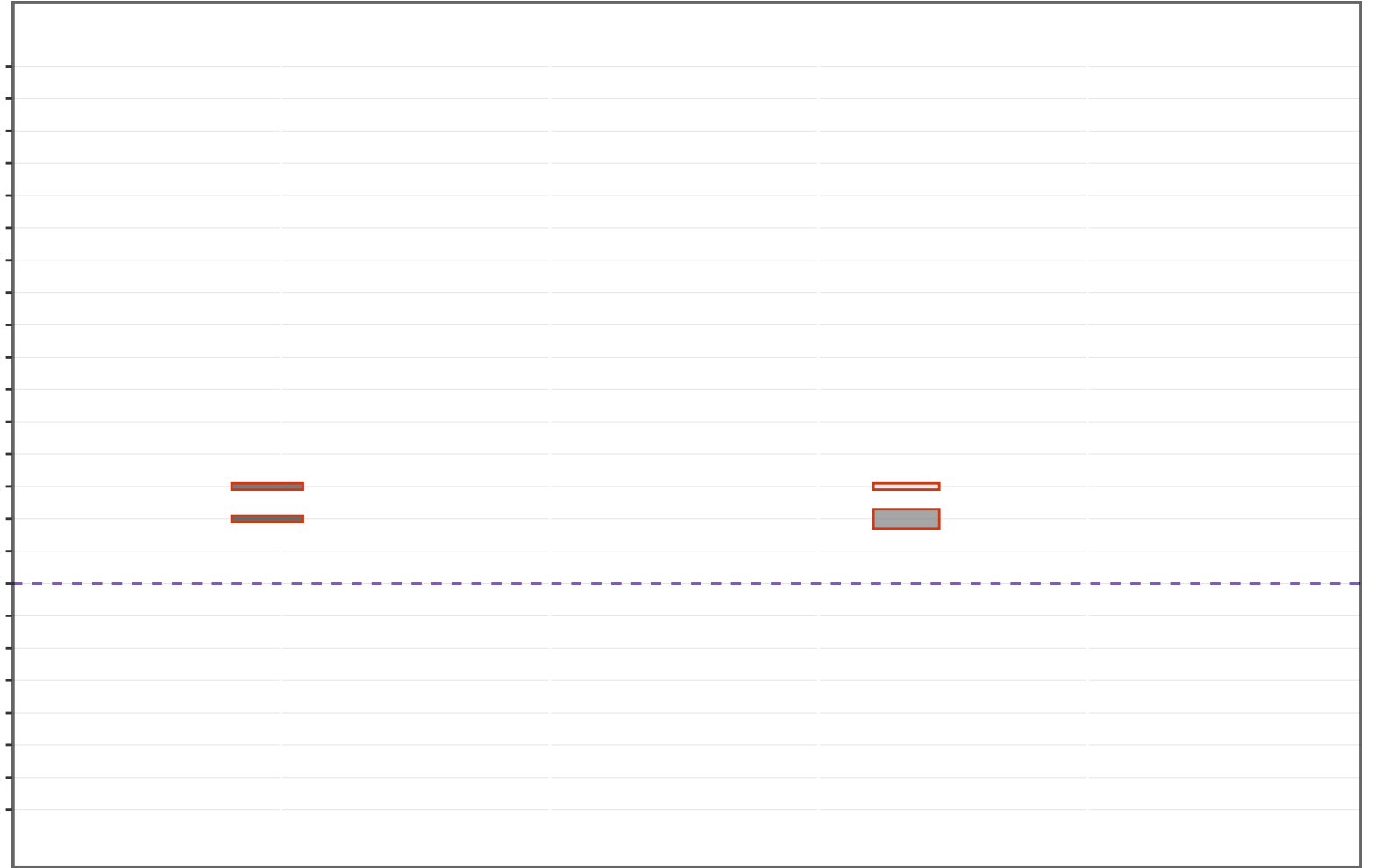
MW indication



Molecular weight



Gel Slice

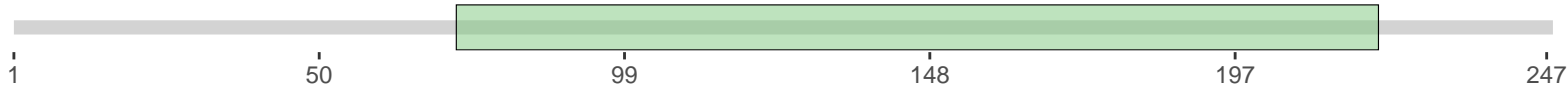


Protein length

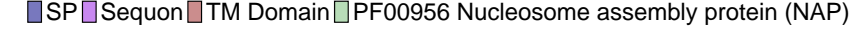
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

3MTSGYSLTFFKPNPFFEDTKLWTKYTFLEDEGTTTFTGMPKWKEGMDAAAGGTPEKKGKRRPPEVESFFSWFSETQLKDIADGLSEVDEIHKDLWPNPLKLYFNNEADEEESDGDDEDEDEDEDEDEDEDE

NbL12g07060.1 protease_Do-like_8_chloroplastic [MW = 54.41 kDa]

No. of times detected



log(intensity)



Values from



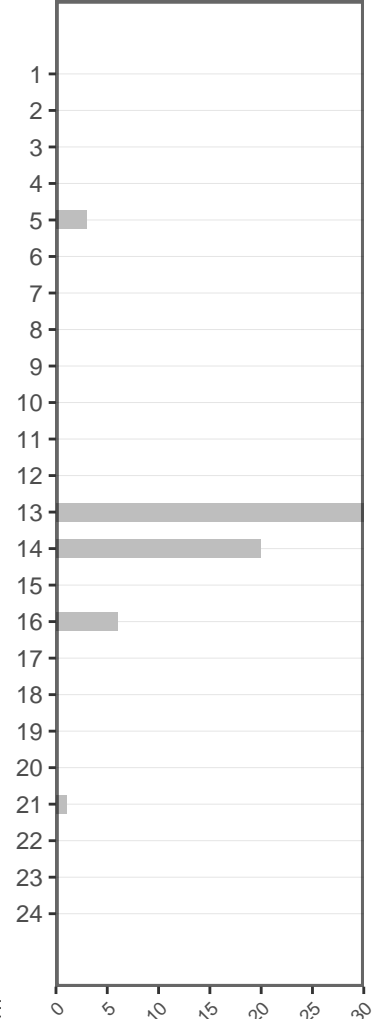
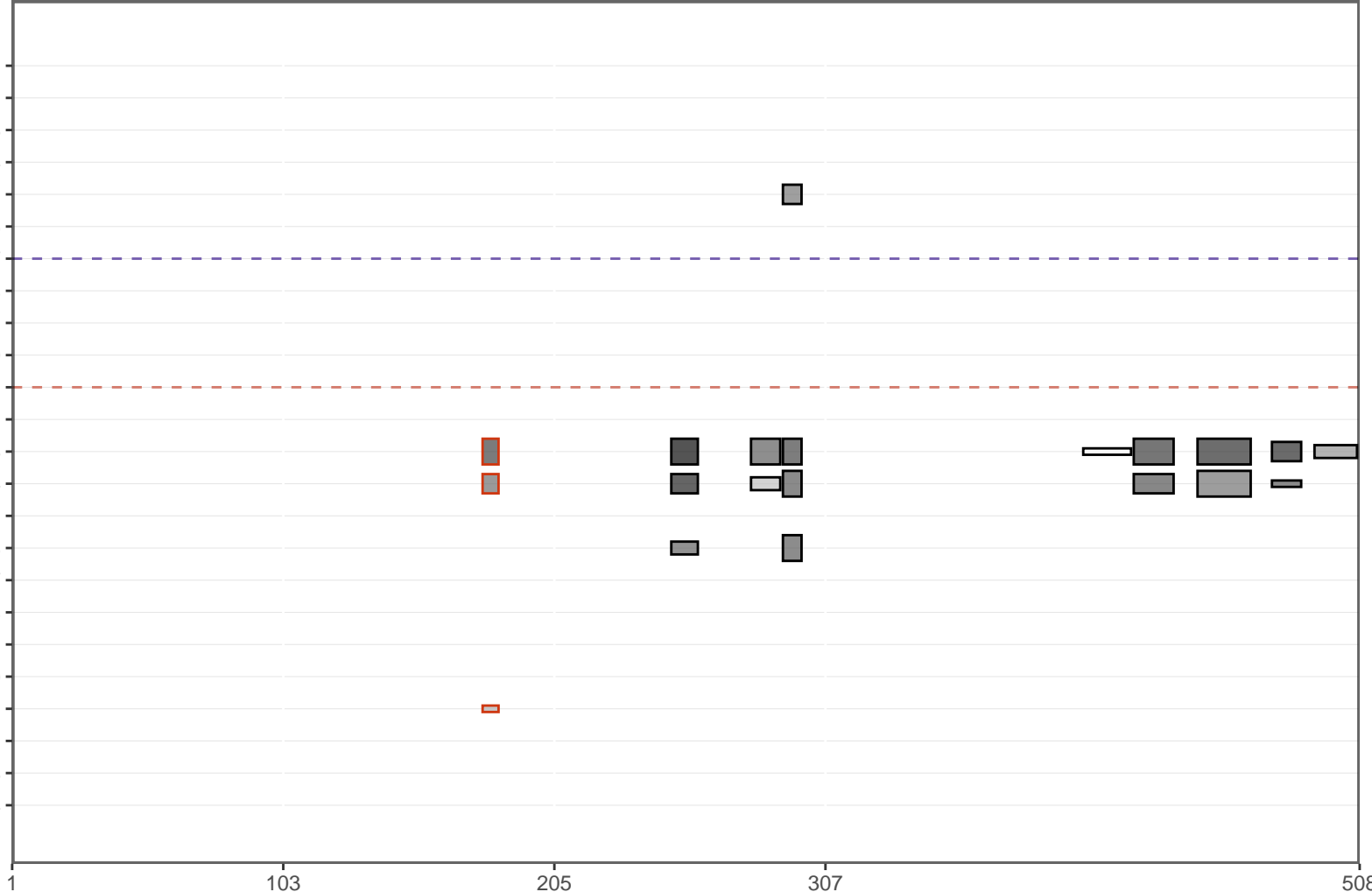
MW indication



Molecular weight

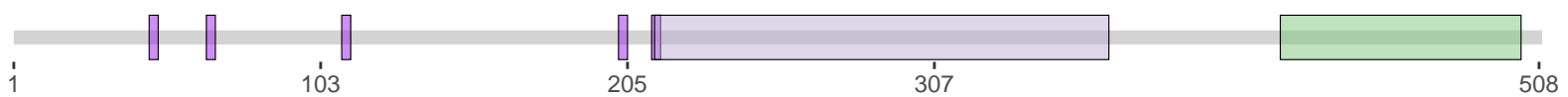


Gel Slice



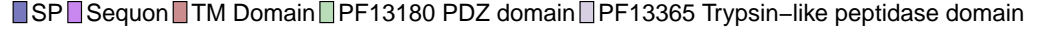
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

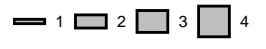


Protein sequence:

NPSRGEVYARVNLAAEGVQKNEFKLIGADRADKDLVAVKVEASEDLRPIRVGESASLRVGGQGLAICAPFGFDHLLTVGVVSGLNRDYSGTGTGTSAGVGFAPSPSTVLRVVPQLIEGKVVVRAGLNIEAPLIANDLNVRNGALVGVPGNSLAAKAGLLPTTRGFAGNIVLGDIEAVDQKPKVRSKADLYKALDNNYNGDEVRLKIRRGNEIMELSALEEKDS

NbL12g06860.1 UDP-glucose_6-dehydrogenase_3 [MW = 52.9 kDa]

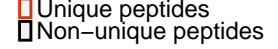
No. of times detected



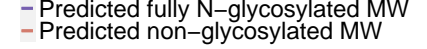
log(intensity)



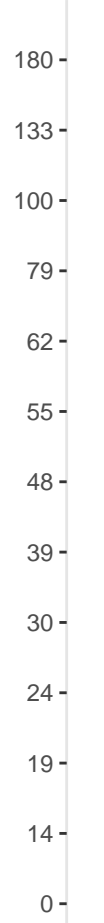
Values from



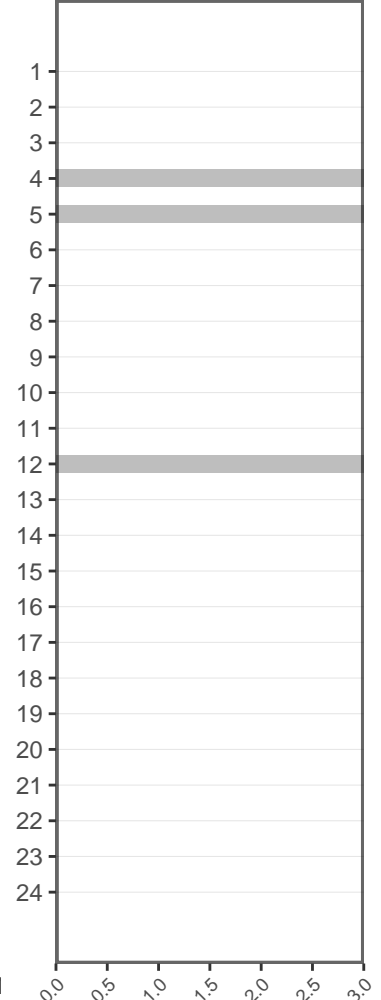
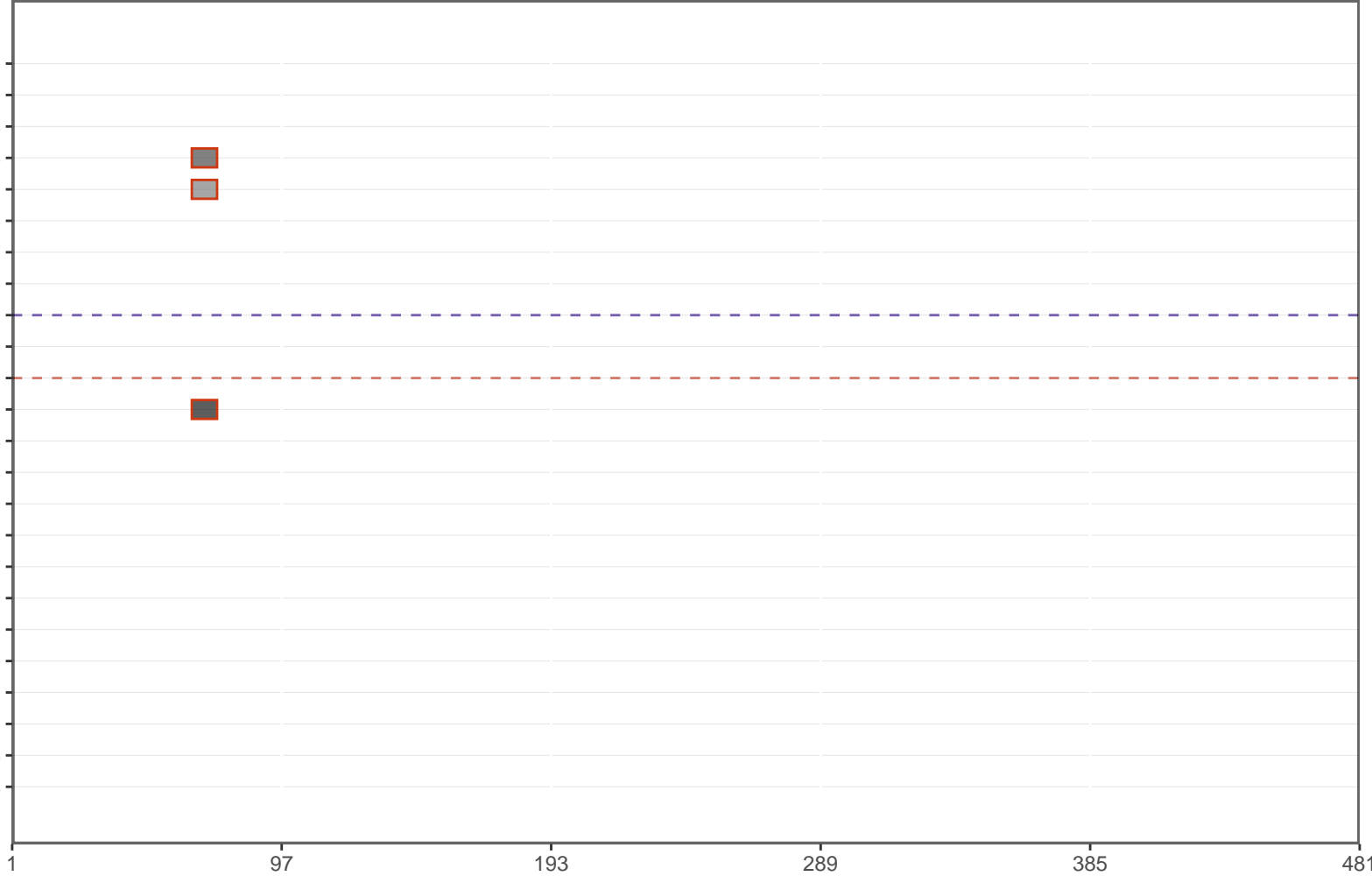
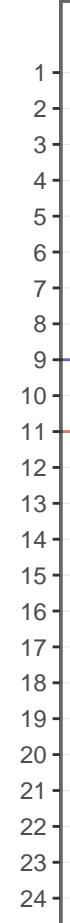
MW indication



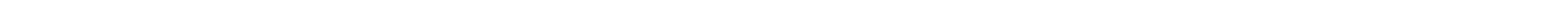
Molecular weight



Gel Slice



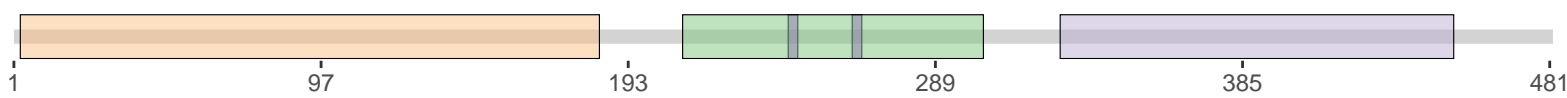
Protein length



Peptide counts over 4 repeats



Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF00984 UDP-glucose/GDP-mannose dehydrogenase family, central domain
- PF03720 UDP-glucose/GDP-mannose dehydrogenase family, UDP binding domain
- PF03721 UDP-glucose/GDP-mannose dehydrogenase family, NAD binding domain

Protein sequence:

VNAMSALCEATGANVSGWAWVSGKDRIGPKFLNABVGFSGGFGKDKLNIVYKCEGNSLPEVAEYWGKVKINDYKTRFVNRVVASMFINVSGKKVAVLGFAPKDKTGDTRETPAADVKGKLLGDKAKLSHYDPGVNEDGQRDLMSMKFRDWHPLHLQPMSPPTTKGVSVVWDAYTATDAHAVALTEWDFEKTLDYQKHVDNMGKPAFFDGRNYYVVEKLRIGFVYSGKPLDAWLKMPAAV

NbL12g06790.1 protein_CHLORORESPIRATORY_REDUCTION_7_chloroplastic [MW = 24.17 kDa]

No. of times detected



log(intensity)



Values from



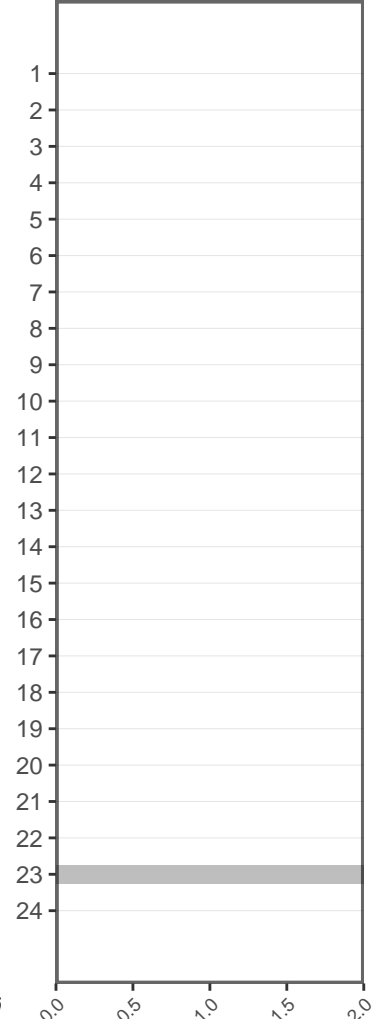
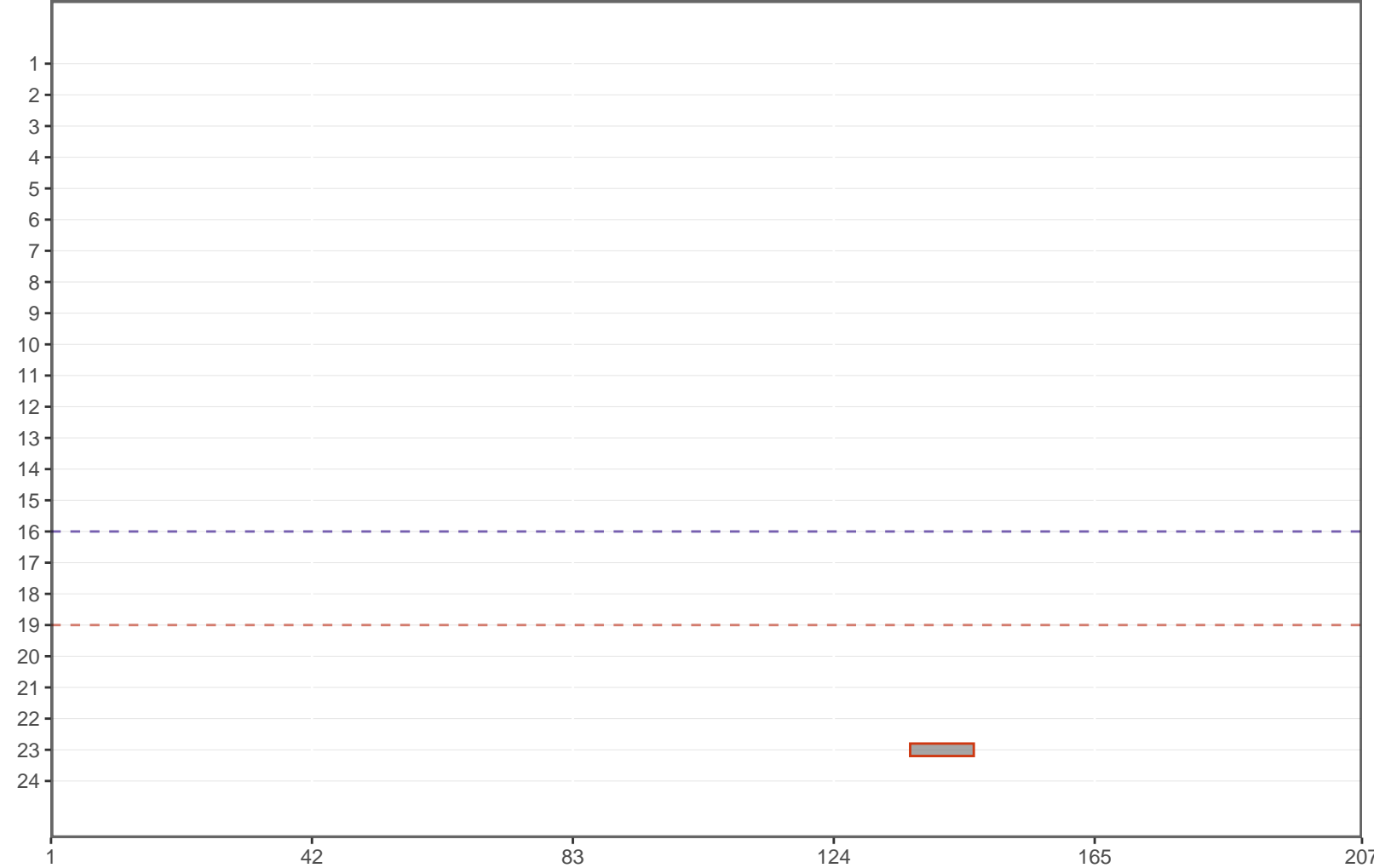
MW indication



Molecular weight



Gel Slice



Protein length

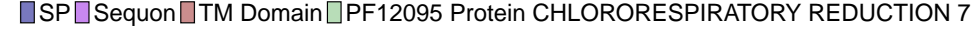


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IQPNSSFTYHSVTCRGLRNGTKLAIRRRRANGTDTYVLMPEPKGSEEFVSEELRERLKGWLENWPGNELPKDLARFEEIDDAVEYLVKSVGELRIDGDSVGIQWVEYRLOGGME

NbL12g06680.1 protein_COBRA-like [MW - SP = 47.37 kDa]

No. of times detected



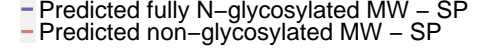
log(intensity)



Values from



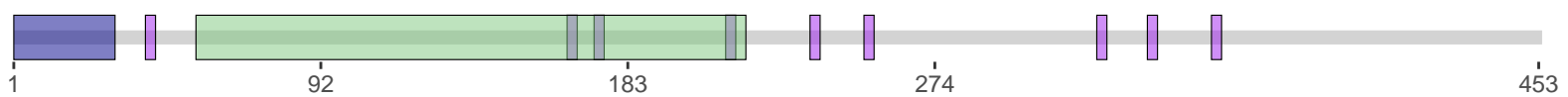
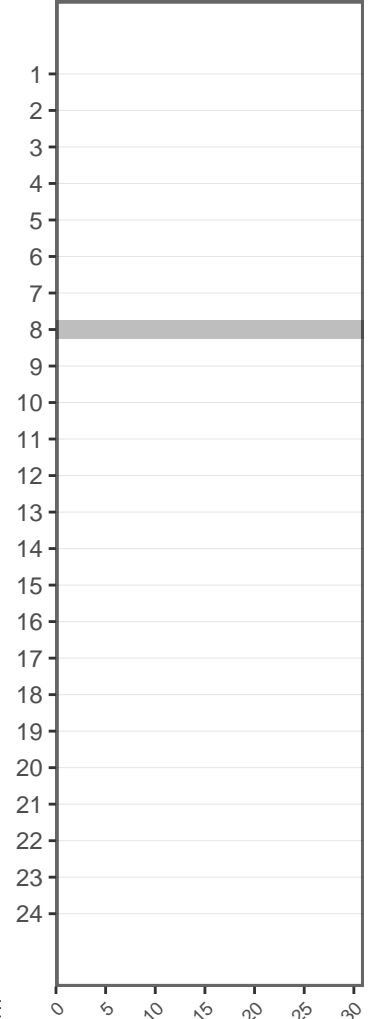
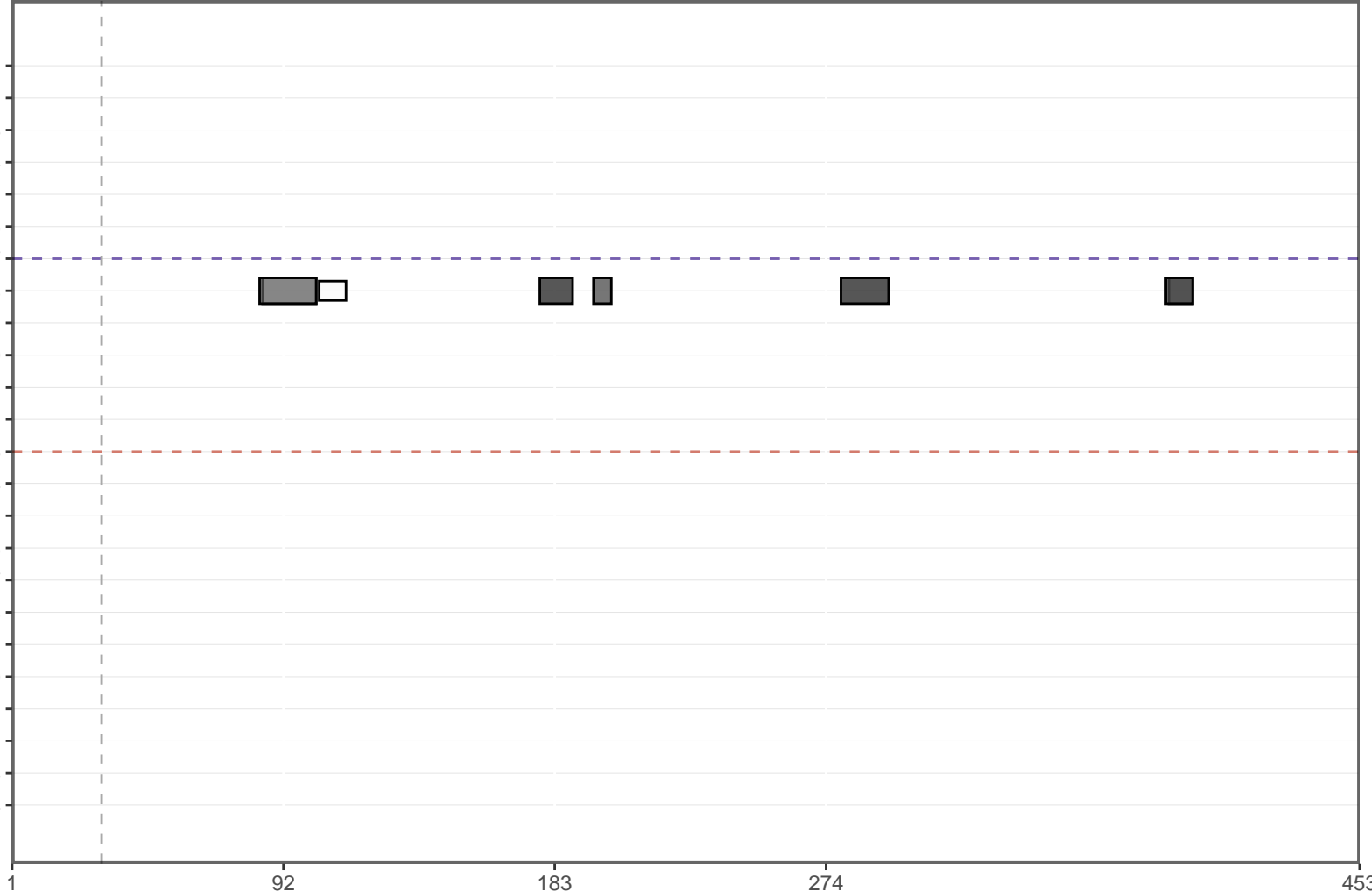
MW indication



Molecular weight



Gel Slice



Pfam domains

Pfam Description



Protein sequence:

TCTYSQFLAQKTPFDGVSSISFYNDRIVPGPTGGGGKNGTGHGNGVDEDEPHLASVSDHGKGNKNTYAPLVGCTNMMSPRIHWHVVKLVKYEYWRVWVYITTFNFMNMYTGWNLVGHNFNQLTGLFSFNKSLTPVGAINDTAMLVGMKFNLDLLMGAGPLGNVGSLELFRKDLSTFTFDKQWAFPRRVYVFNAGNVMPPDQVYVPMNAGTVWVKSLSKLVTLMLSTAFFAFI

NbL12g06640.1 alpha-14-glucan-protein_synthase_[UDP-forming]_2-like [MW = 40.62 kDa]

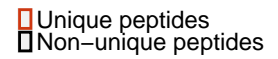
No. of times detected



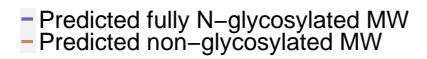
log(intensity)



Values from



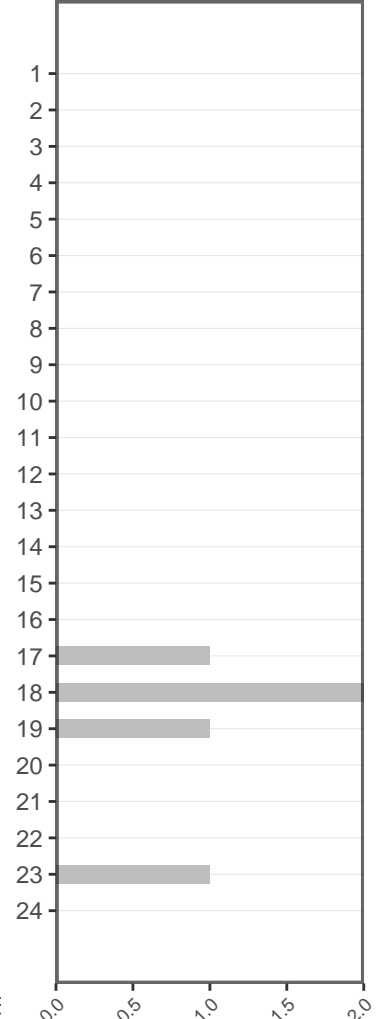
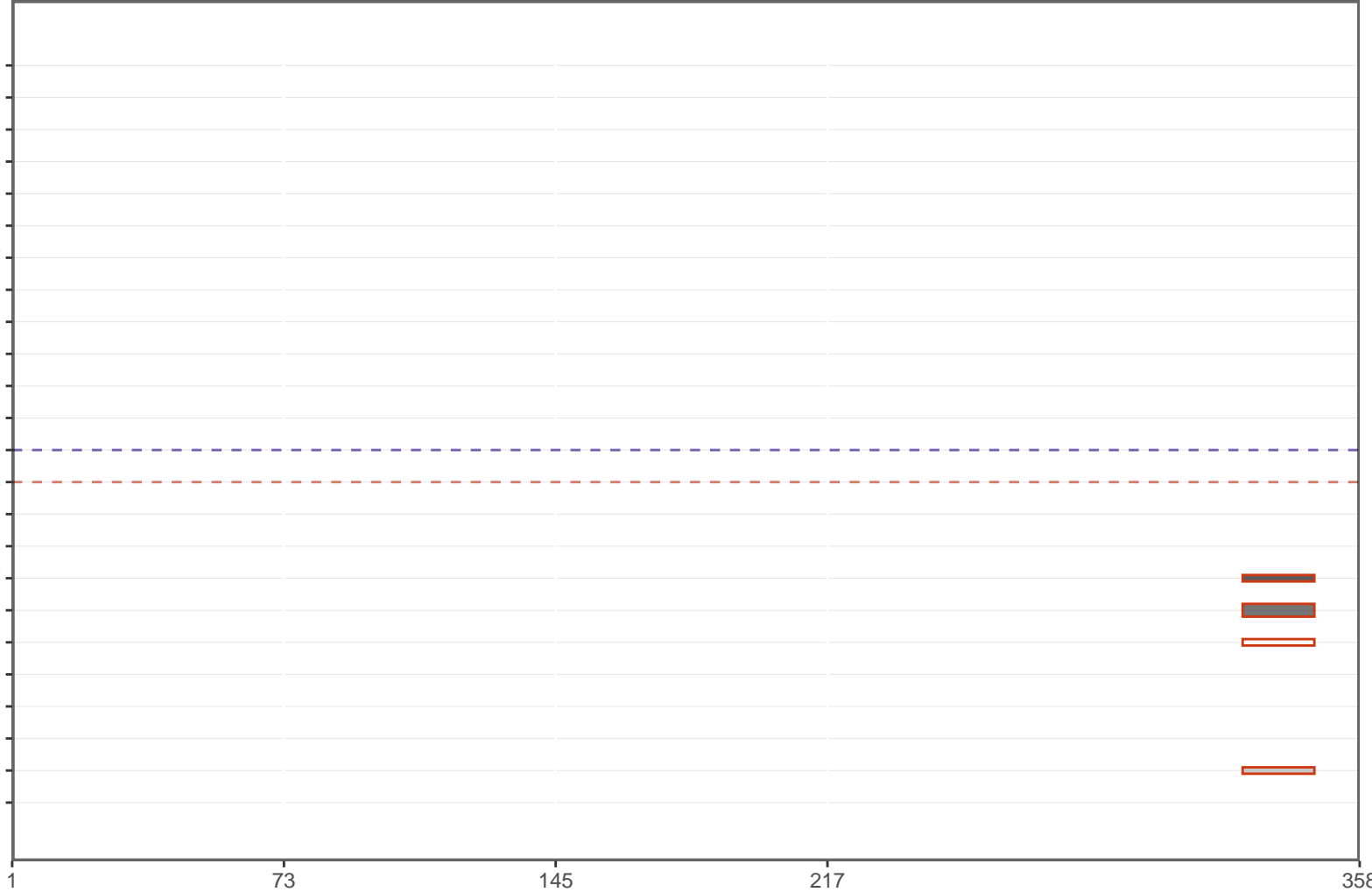
MW indication



Molecular weight



Gel Slice

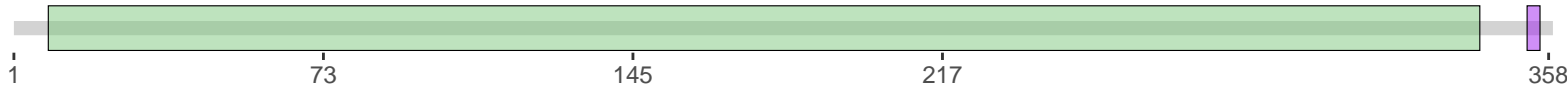


Protein length

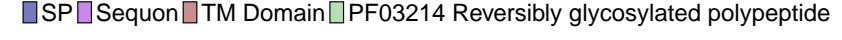


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LNPDYDAFPTOLVYKFLERINRYVDVLRKGTLPFGMGNNLAFDRLEHGPAMYFGLMGDDGPNRVDMMWAGWGGKVCDDLGLGKTKLPLVYHKBANPFLNKKELGIFWQEEIPFFQSHFTSKDCTSVQKQVYVELSKGVYKEHLGKVDVYFVKLADAMITWAEAWMDLNFASKDSSKLPNGSEK

NbL12g06470.1 STS14_protein-like [MW – SP = 17.37 kDa]

No. of times detected



log(intensity)



Values from



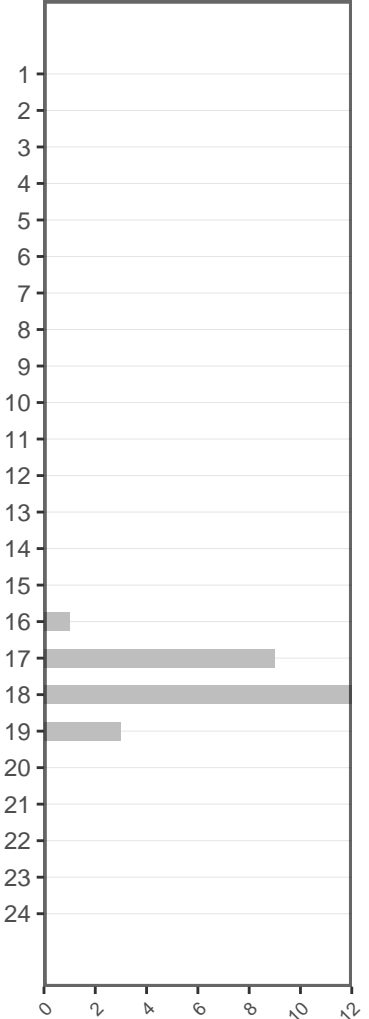
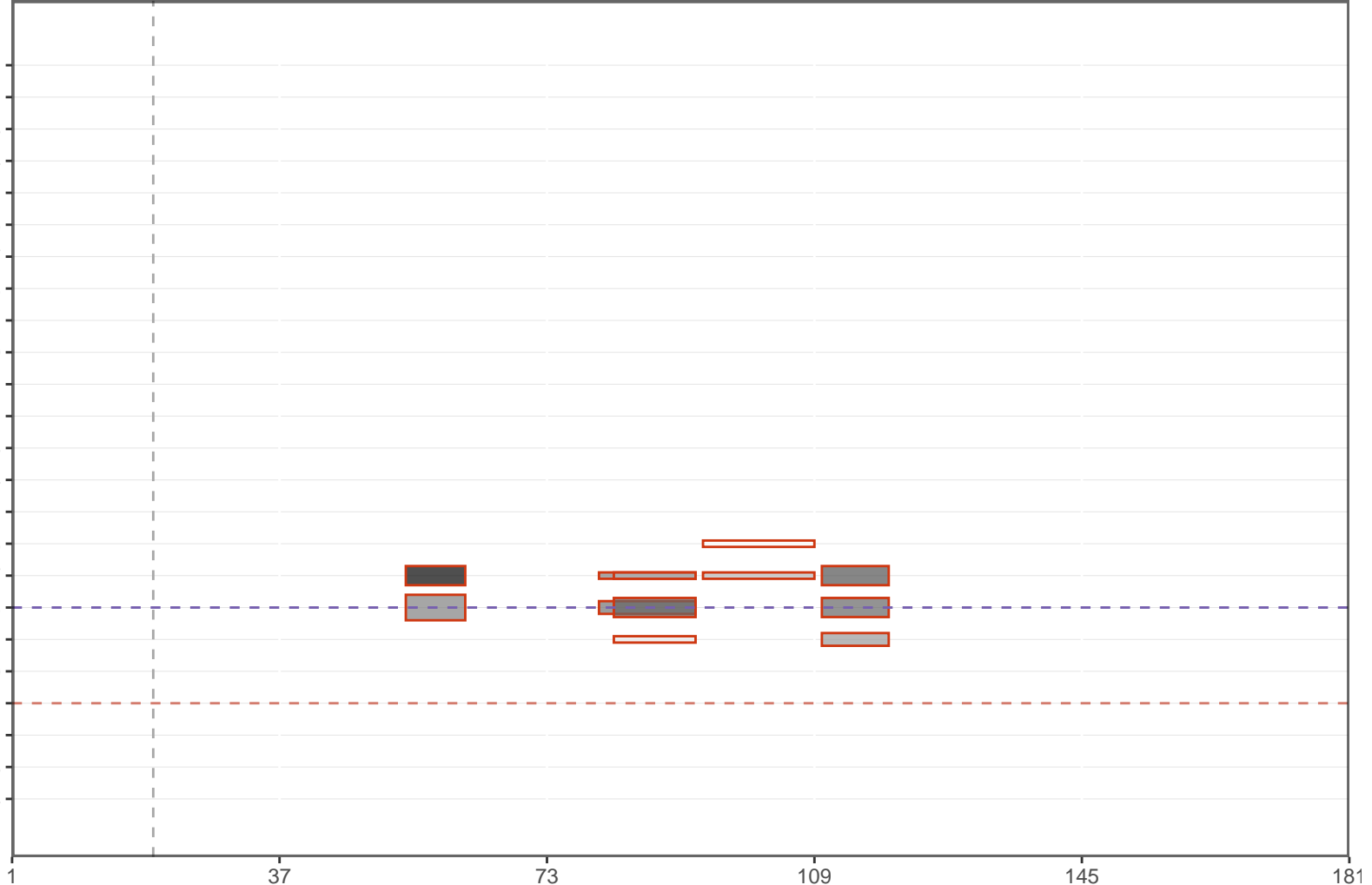
MW indication



Molecular weight

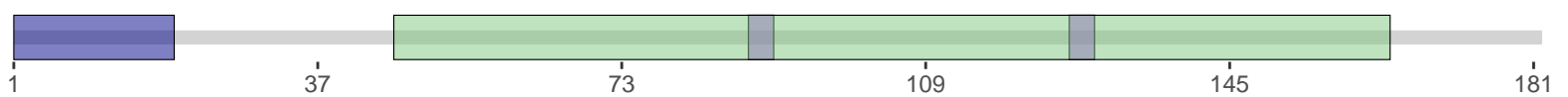


Gel Slice



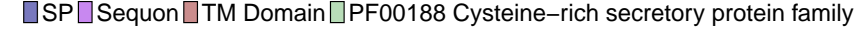
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IKQCNCFANLTSQKYGNGNLWASGMVTRRMVDNWAQEKFFYNVANSQVGDHKGQVYTGIVVWKGSELEGGAGETGGRNPETLTGCFNPPGIVGKPKV

NbL12g06360.1 acid-binding_protein_2 [MW = 29.21 kDa]

No. of times detected



log(intensity)



Values from



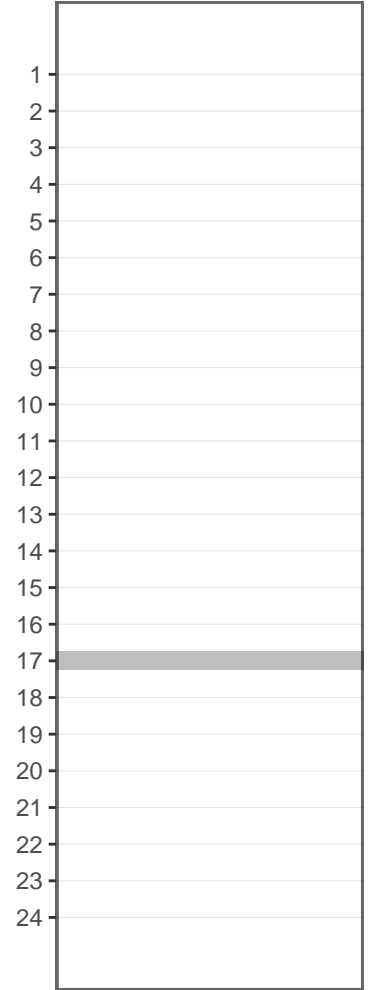
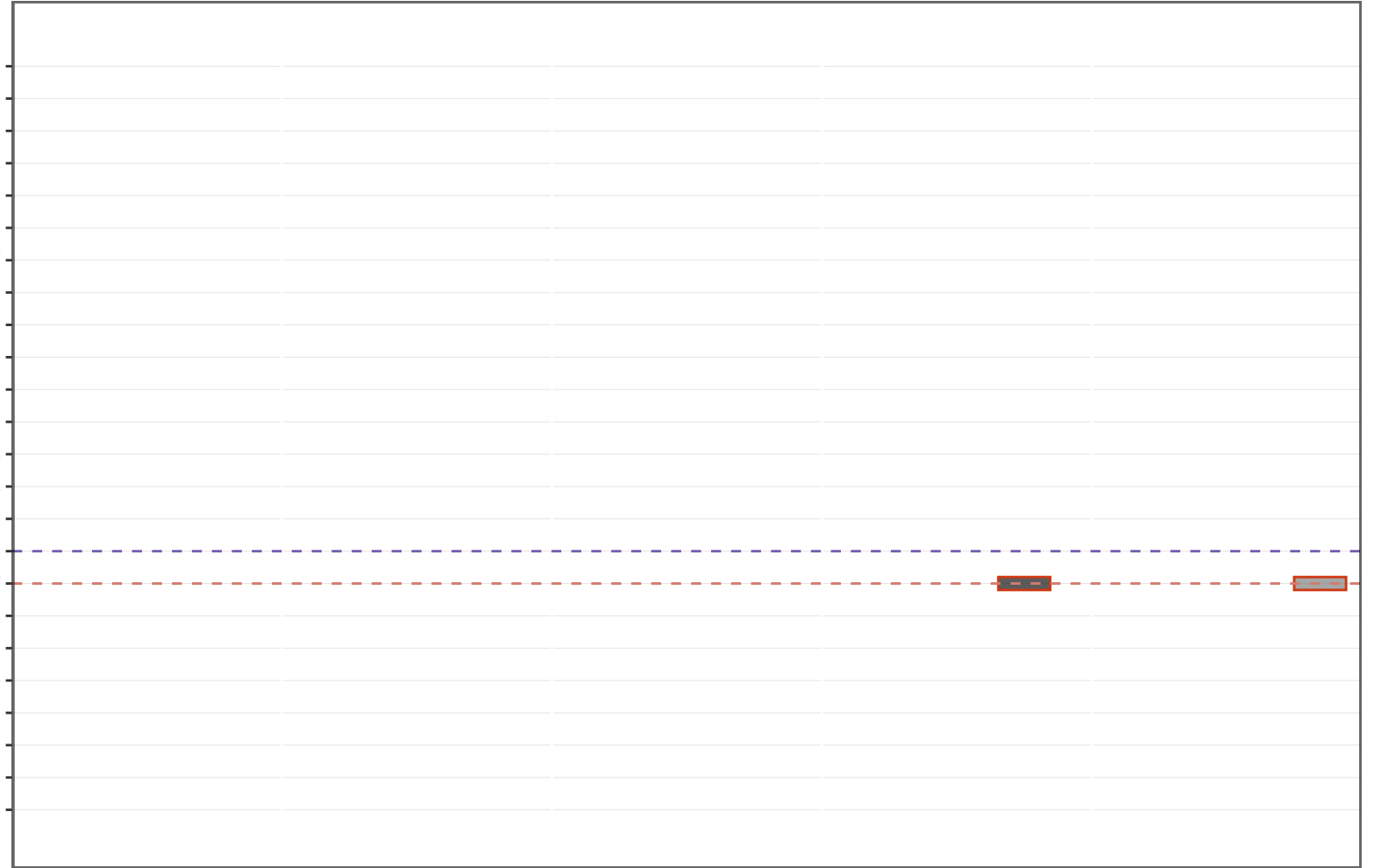
MW indication



Molecular weight



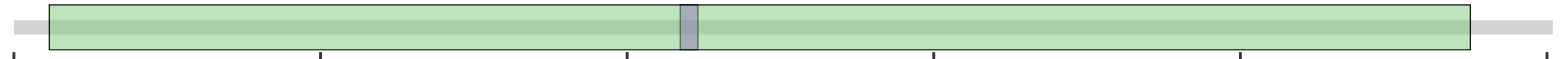
Gel Slice



Peptide counts over 4 repeats

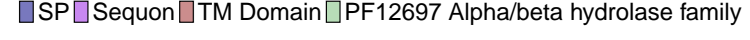


Protein length



Pfam domains

Pfam Description



Protein sequence:

FVLEKYYERTPAESWLGTFPLYPGPFEEPLTSMFFGPKFLAHKLVQLGLEDLALASSILVRPSSLFMEELAKAKYFTDEGFGSVKRVVYVCTEDKAPEEFGQRWQIDNGVTEAIEIKGADHMMMLCEPQKLGALLLEIAHKYV

NbL12g06270.1 patatin-like_protein_2 [MW = 35.72 kDa]

No. of times detected



log(intensity)



Values from



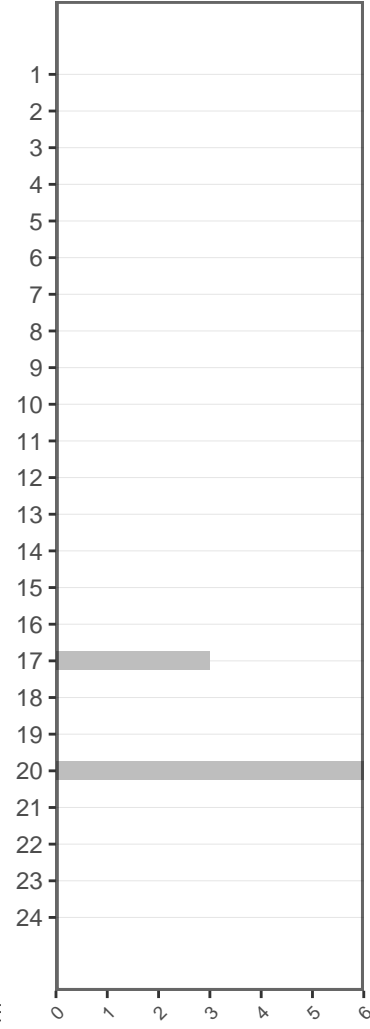
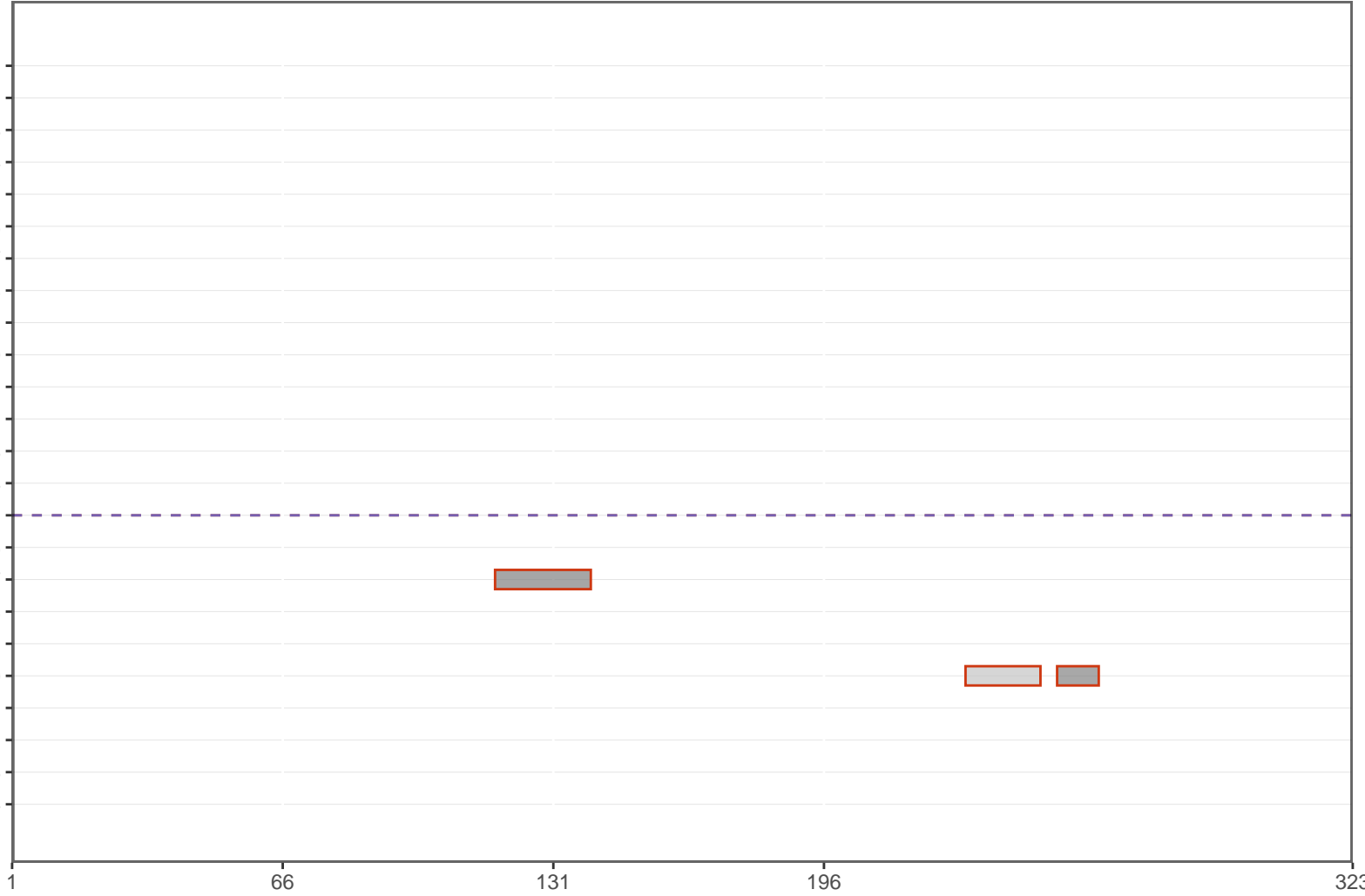
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SMEPMDCKKMLVLSLGTGIGKEEKRYSAVAASTWGVLGWLYNNGASPLDVFQDASADVDHLSSTMFQSLQNEKNYLRIGDDSLTGEAASMDVSTTKMKALVQIGNDLLKPKVSRVNLDTGRVYEEVSGEGTNEEALIRFAKLLSEGRKLRGPFVEEFTSTRNIFQESVWRQ*

NbL12g06200.1 calmodulin-like_protein_1 [MW = 21.21 kDa]

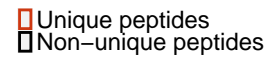
No. of times detected



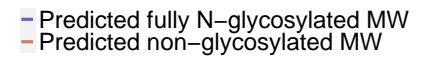
log(intensity)



Values from



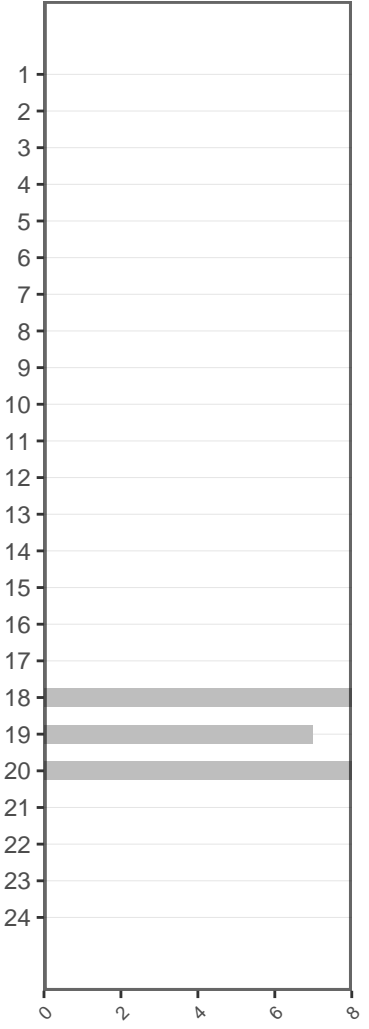
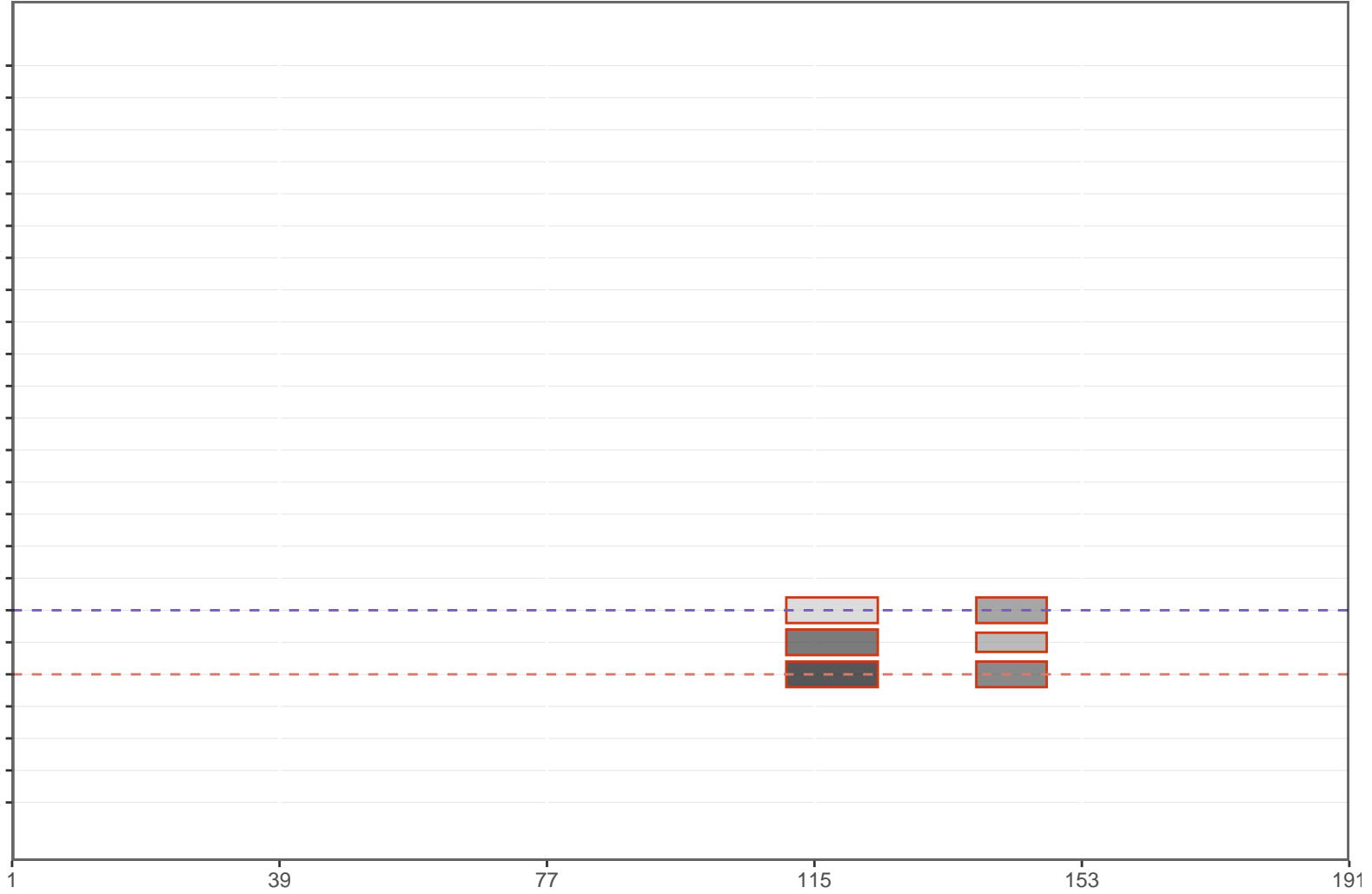
MW indication



Molecular weight

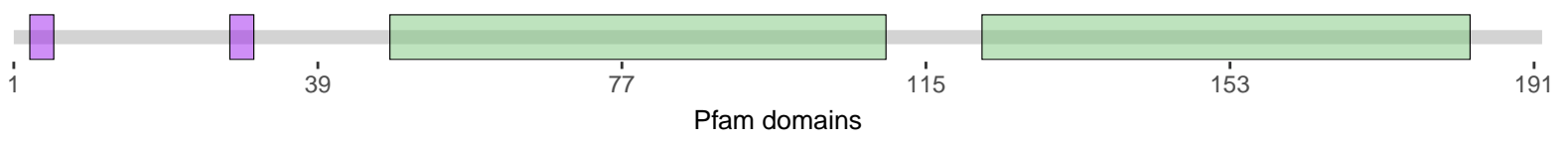


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TKTYDVGDAFGAABTDGDFKFEFFMRVGNLEGGVNPFDKKSAPKAFDLDSGGKISADELLGVQRMLGKGLSLENGKMRVGVDAANGDGLIMDFVTMMTRTKMLV

NbL12g06150.1 CBS_domain-containing_protein_CBSX1_chloroplastic-like [MW = 25.36 kDa]

No. of times detected



log(intensity)



Values from



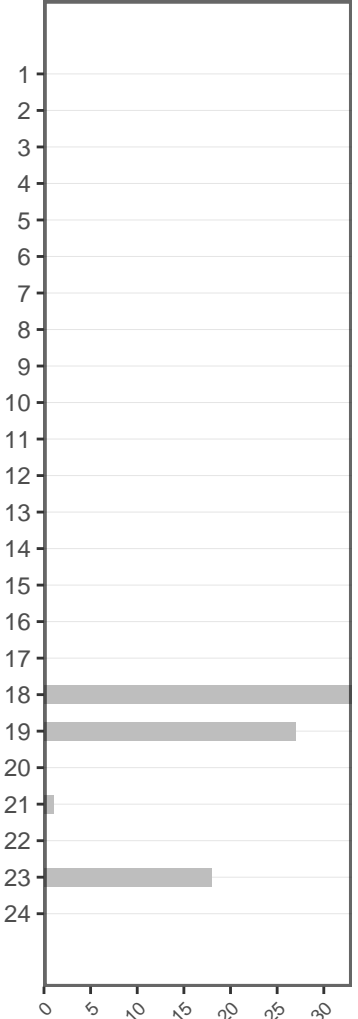
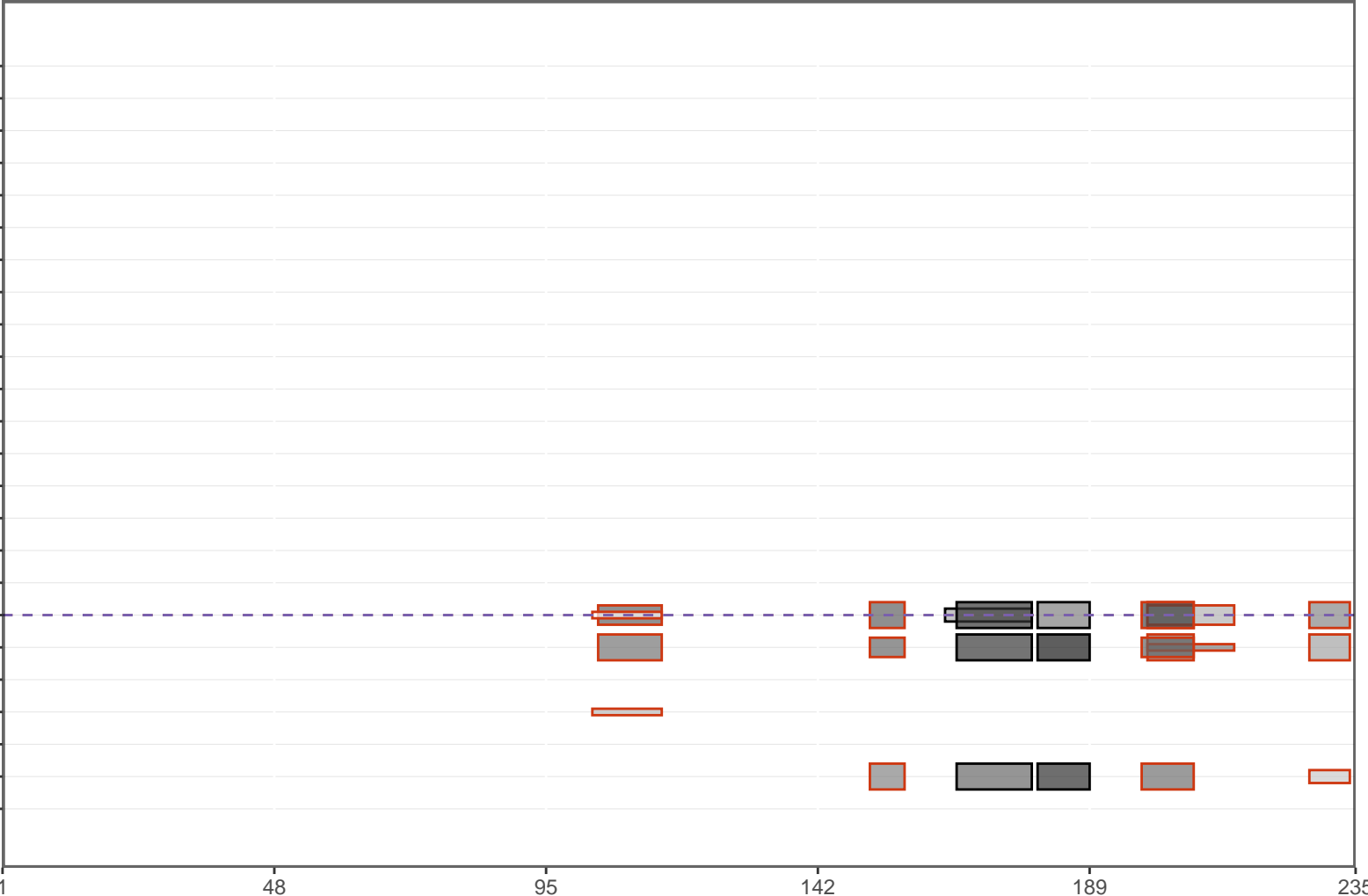
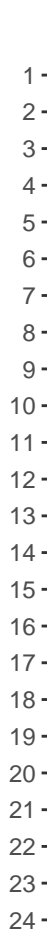
MW indication



Molecular weight

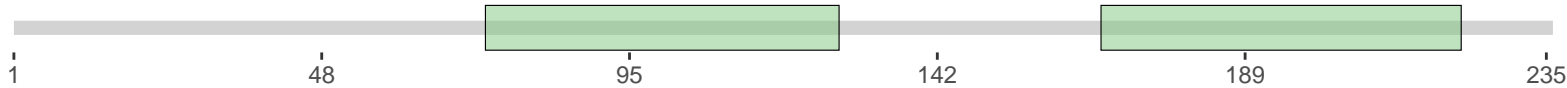


Gel Slice



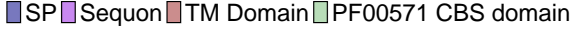
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

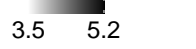
GFPVVDQDWKLVGLVSDYDLDLADDSISGTGGADANMFPEVGSNWKTFNEVQKLSIKTKGKVVGDMLTAPLVRVSTNLEDAARLLIKTKYRPLPVDSDGKLVGITRGNVVRALHKRDIEMEGGQ*

NbL12g06070.1 probable_esterases_KAI2 [MW = 29.97 kDa]

No. of times detected



log(intensity)



Values from

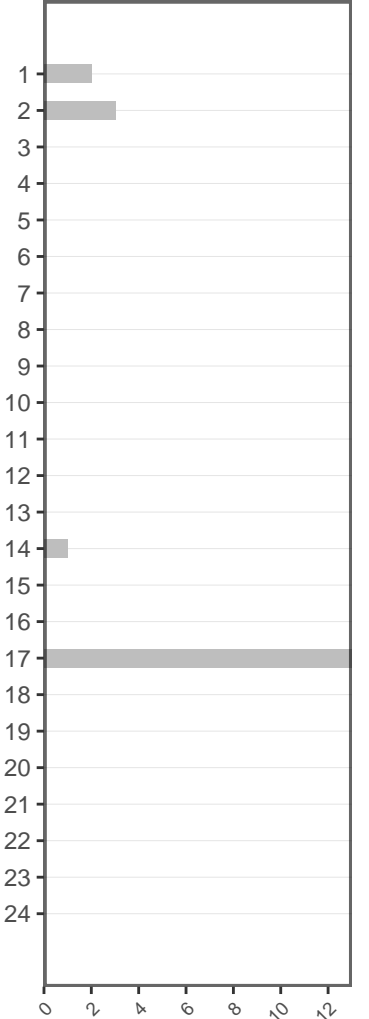
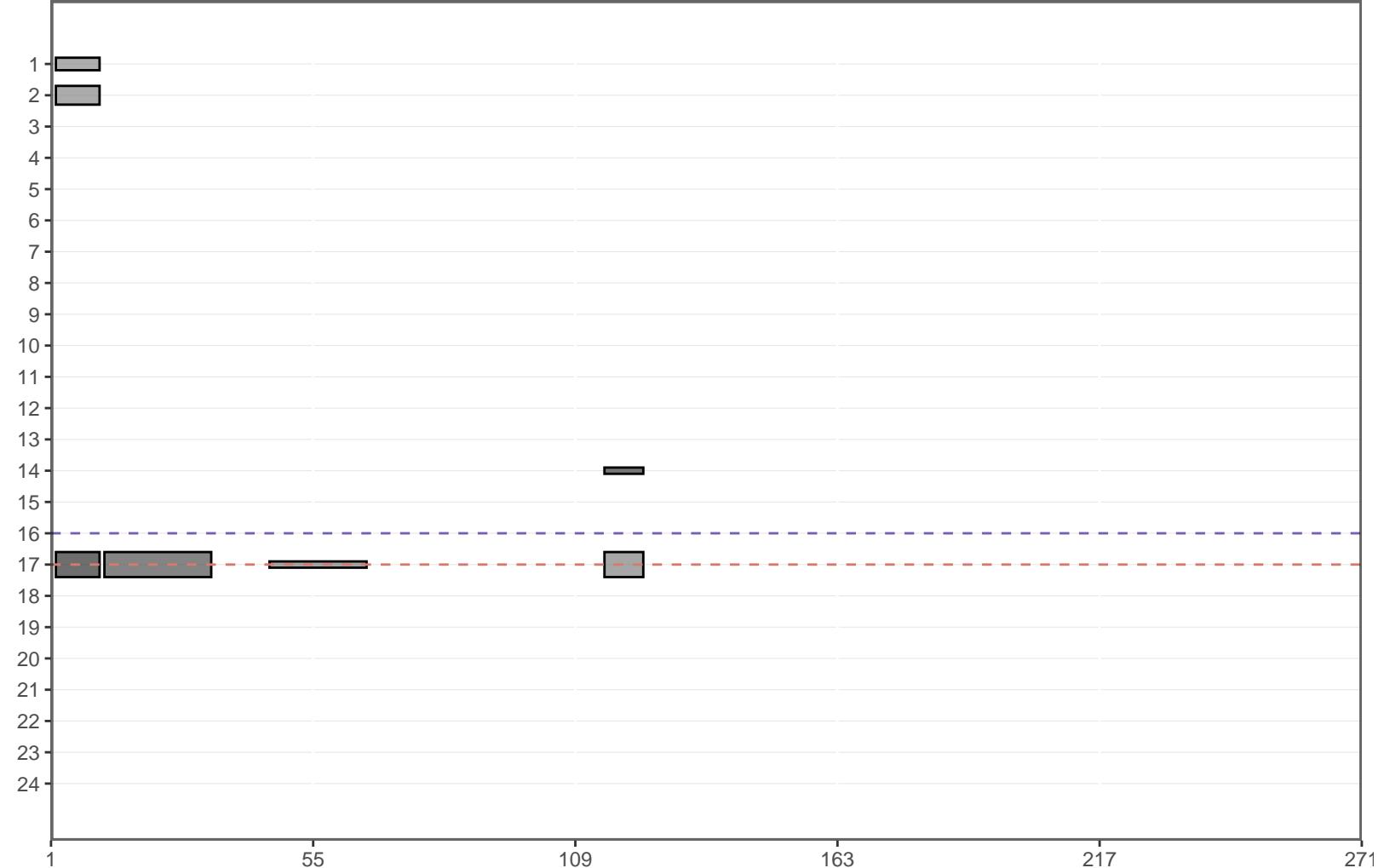
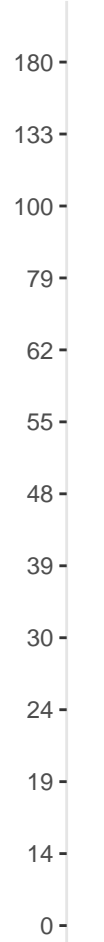


MW indication



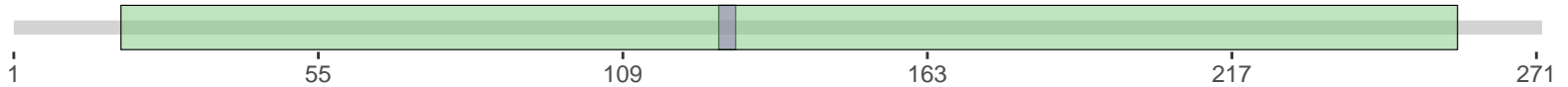
Molecular weight

Gel Slice



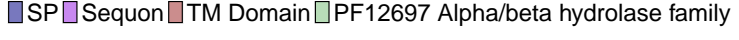
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YLNDSDYGGFEQEDLDLGFAMRSNYKAWGGGFAPLVGGGMDSVAGFGRFLFNMRFDALEVLGIFLSDLRHLHAHTVTPCHLIGGKMLAVPVAWSEYLHQHGGSEVEMSTEGHLPQLGSSPVAIPVLLRHRIHDIVV

NbL12g05960.1 60S_ribosomal_protein_L26-1 [MW = 16.75 kDa]

No. of times detected



log(intensity)



Values from



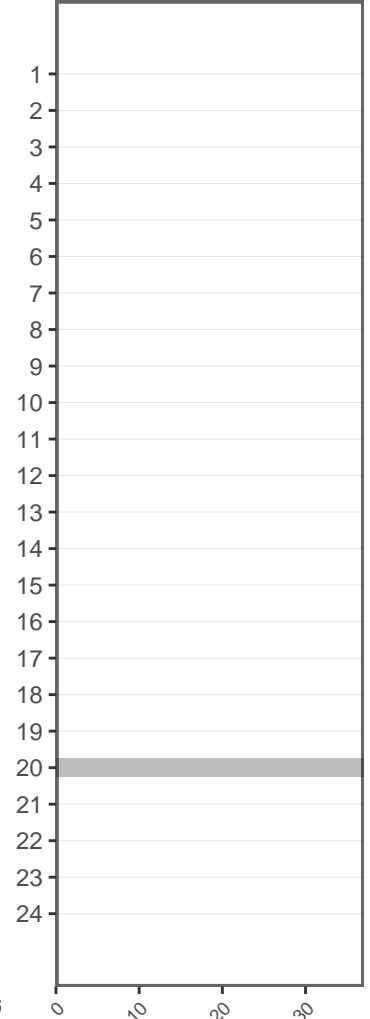
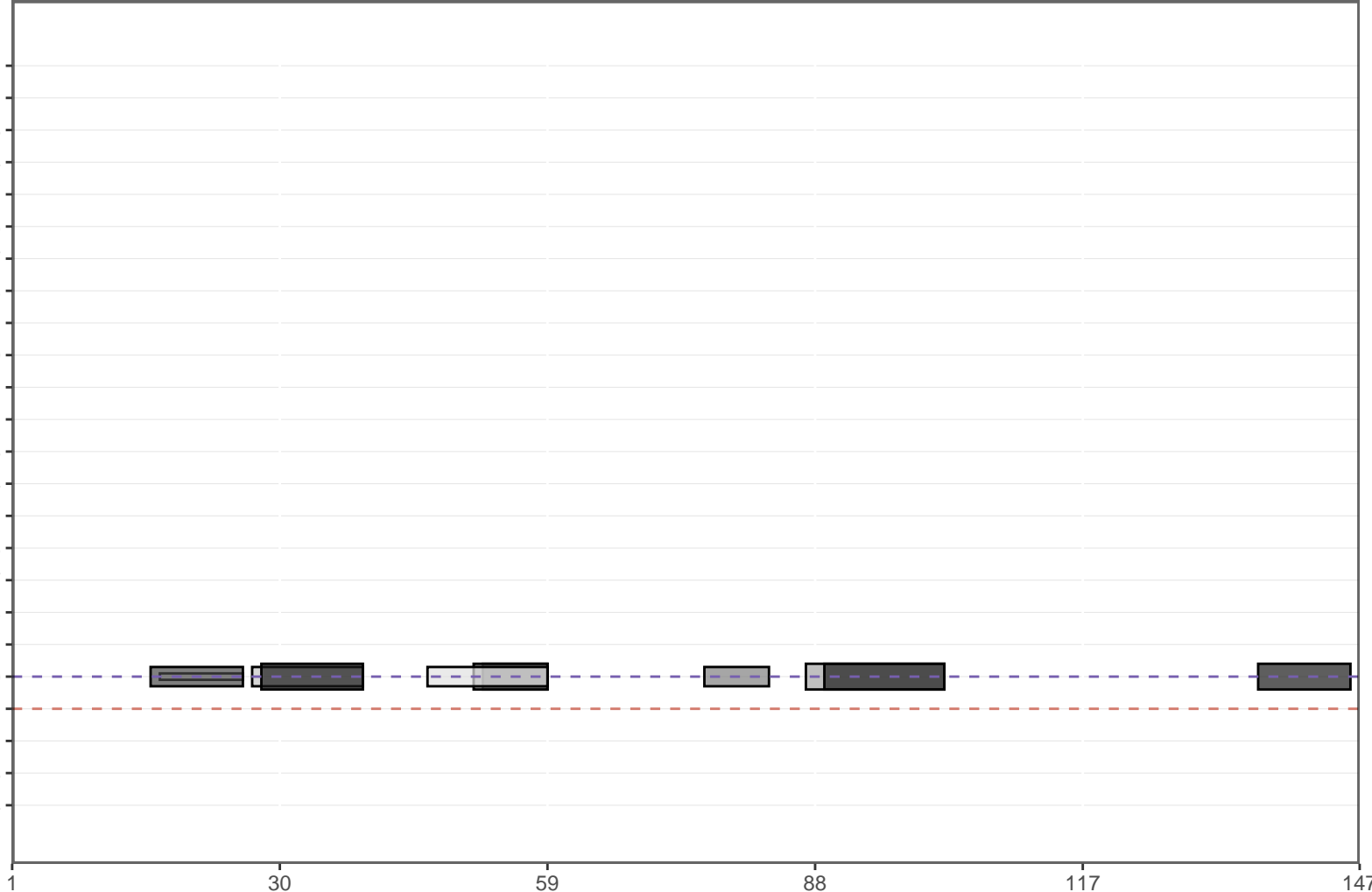
MW indication



Molecular weight

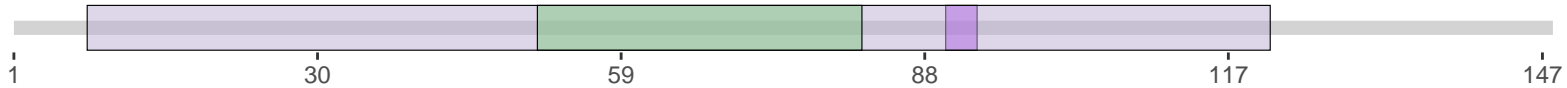


Gel Slice



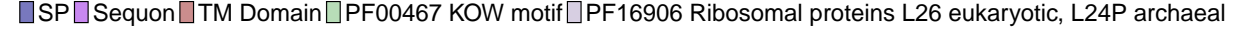
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

STYKREGKYYVWRKWWIHERITREKVNSTVWGHIPKVVVTKLRLDKDRKSLDRKAKGRAAADKDKGTFKTAEDIMQTVDF

NbL12g05890.1 prostamide/prostaglandin_F_synthase-like [MW = 31.47 kDa]

No. of times detected



log(intensity)



Values from



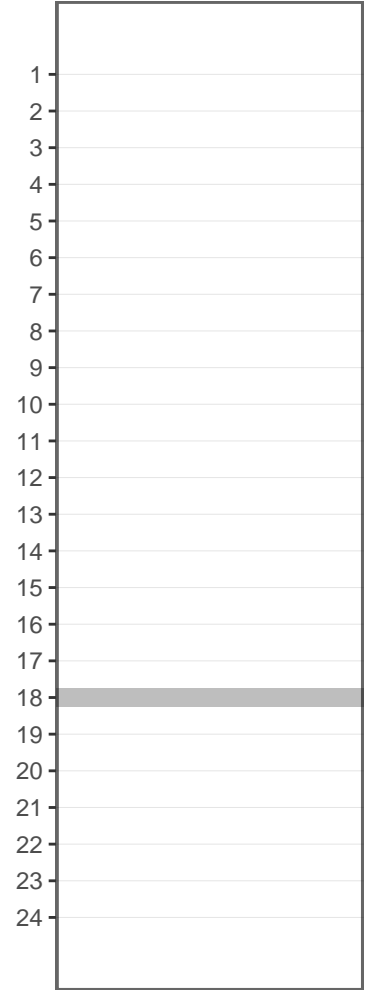
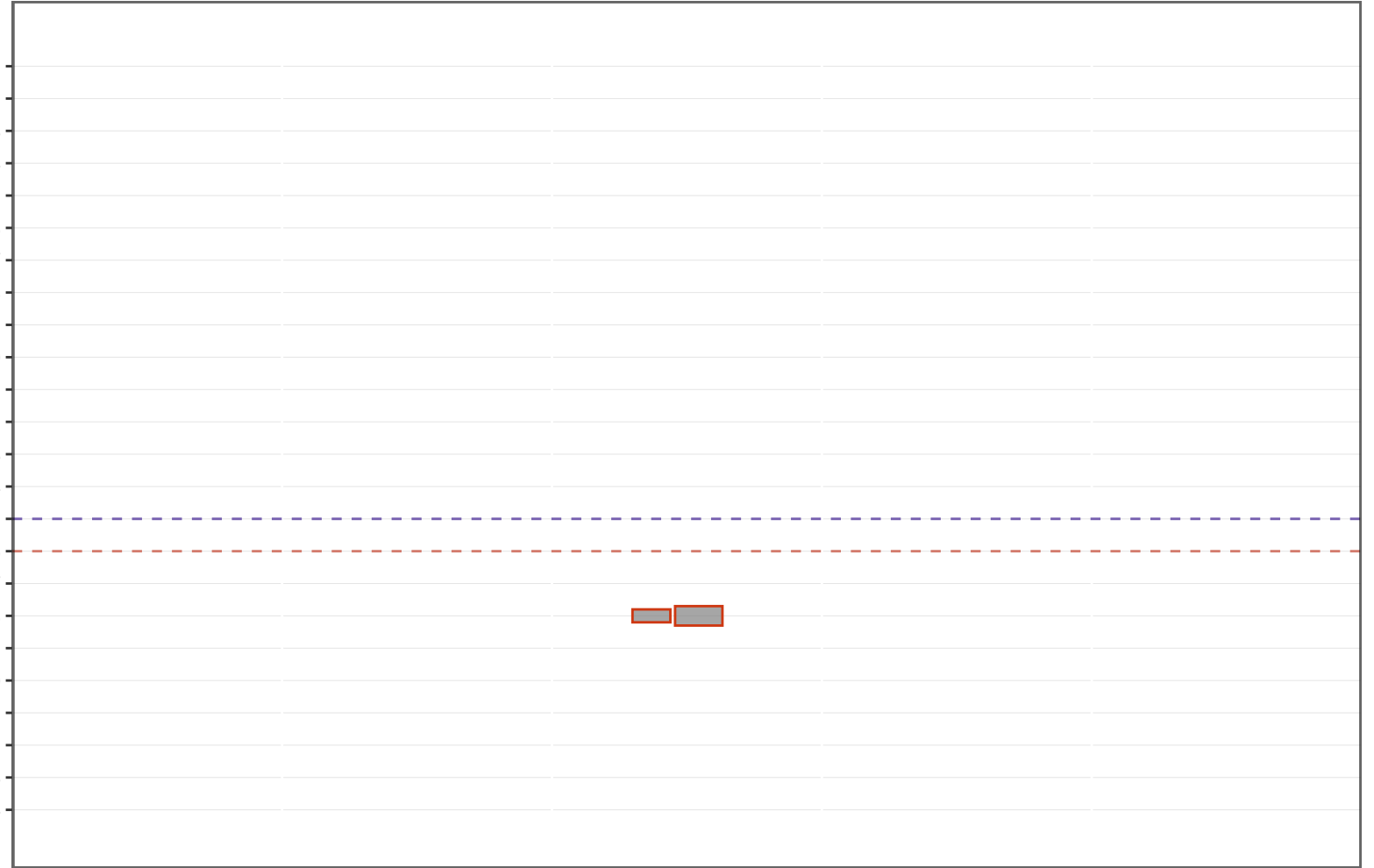
MW indication



Molecular weight



Gel Slice

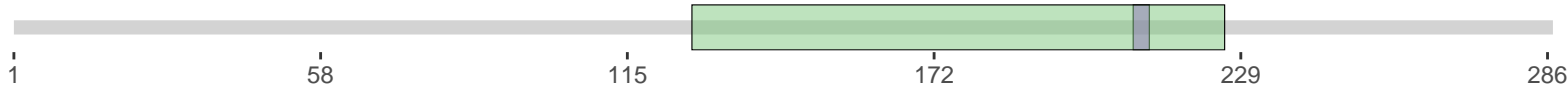


Peptide counts over 4 repeats

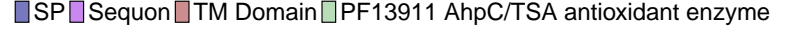
Protein length



Pfam domains



Pfam Description



Protein sequence:

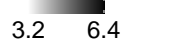
IRERFESAGVYLVAVGIGAPSKARILAEPLPFLDGLVADPDRRAYGVVGLVYVGFRTFFNPSASAVLRFKELQEAATKNTTEATPDDISGLVQGGSDGDMHGRMKEPVYTLFVWVSLMFAAKFLVKAICIPKEVDEYRIKVSFGLGCKSGGRVY

NbL12g05850.1 malate_dehydrogenase_glyoxysomal-like [MW = 37.66 kDa]

No. of times detected



log(intensity)



Values from

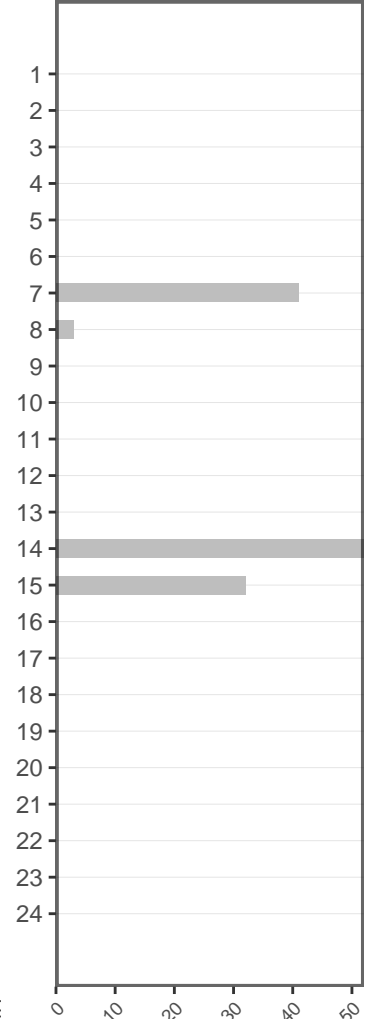
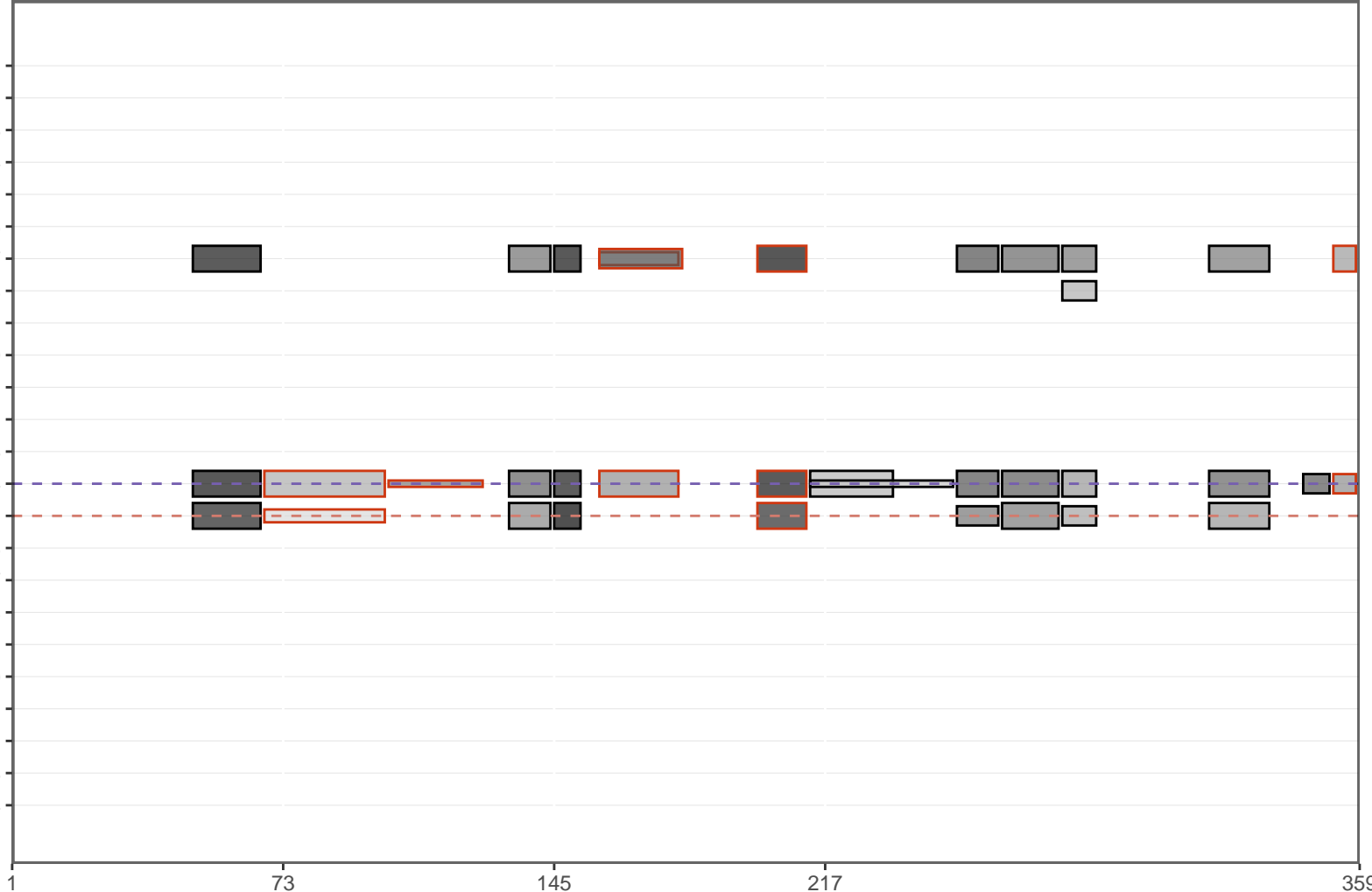
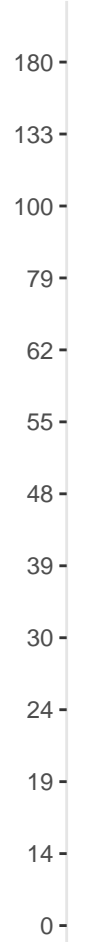


MW indication



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

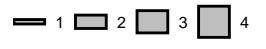
- SP
- Sequon
- TM Domain
- PF00056 lactate/malate dehydrogenase, NAD binding domain
- PF02866 lactate/malate dehydrogenase, alpha/beta C-terminal domain

Protein sequence:

ISTVPIAAEVFKAGTFDPRRLGLVTKLDIVRANFVAEVGLDPRREVDPVVGGHAGVITLPLSGVKKPDSFTPEETEVLTSRQNGGTEVVEAKAGAGATLSMAYAAKFDADLHGLRGDAGIVECAPVSSGVTELPFFASKVRLGRNGVVEIPLGLNEVERSGLEKAKKELATSIQKGVNFVMK

NbL12g05790.1 serine_hydroxymethyltransferase_mitochondrial-like [MW = 57.15 kDa]

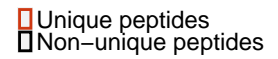
No. of times detected



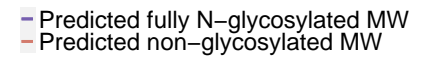
log(intensity)



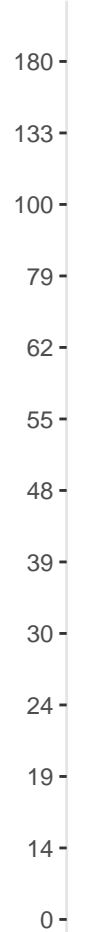
Values from



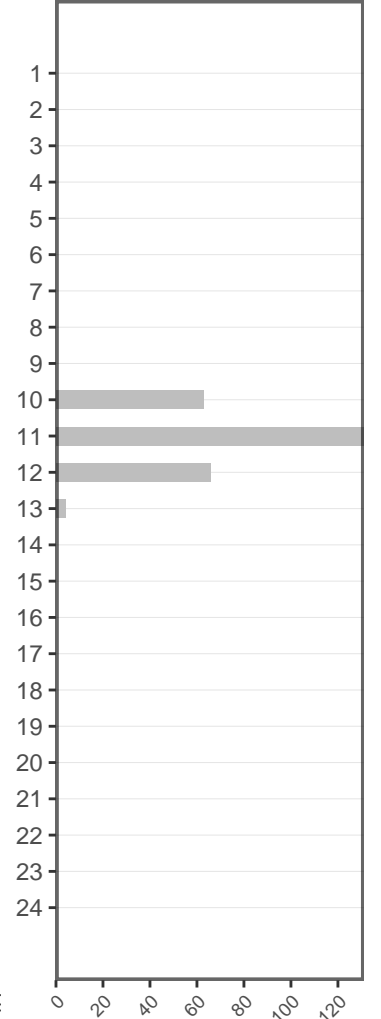
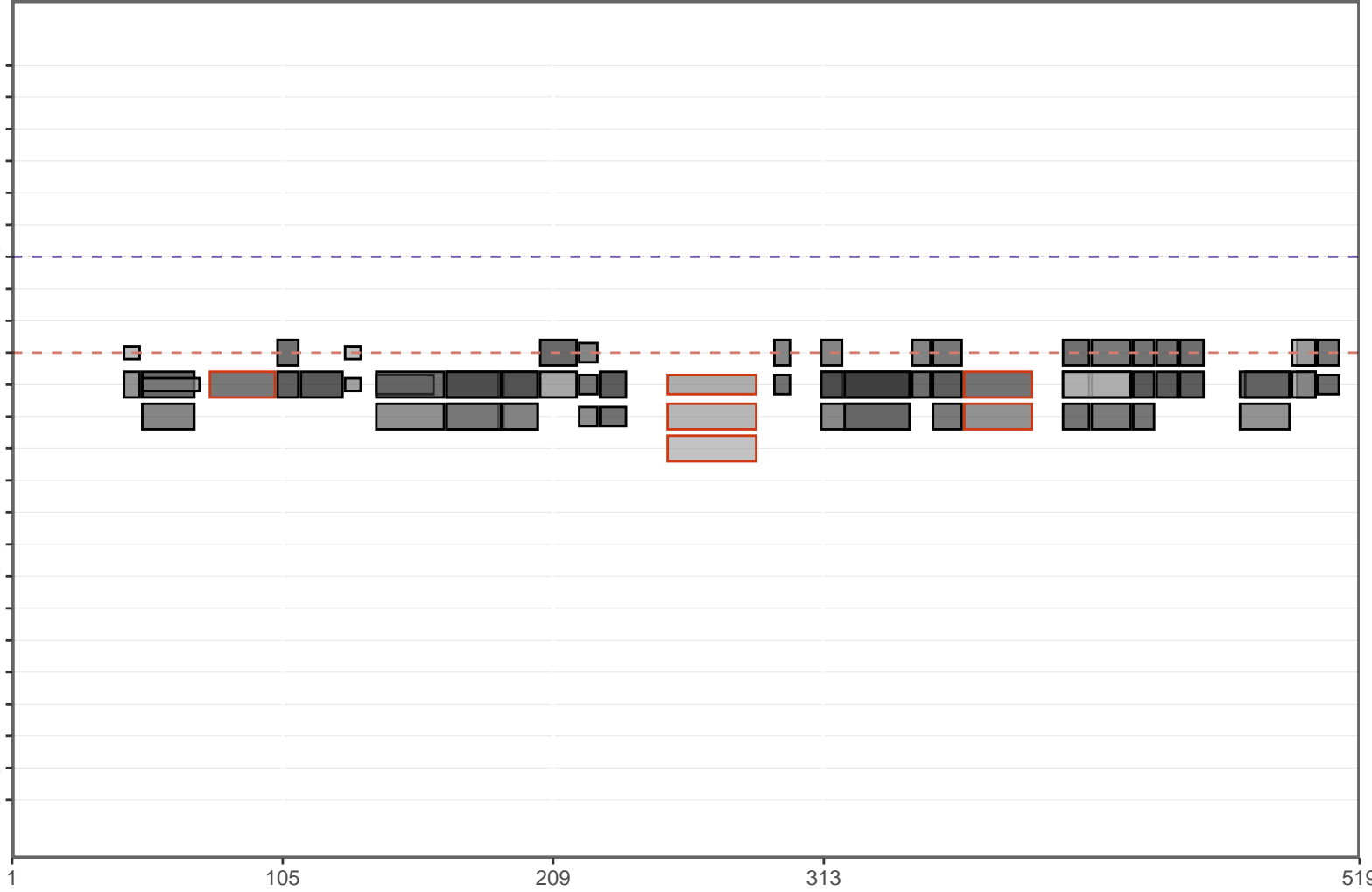
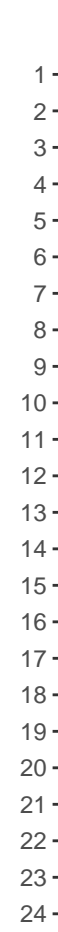
MW indication



Molecular weight



Gel Slice



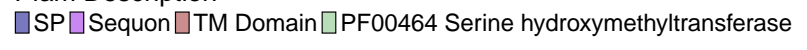
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

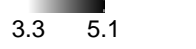
VCDKQKAIMLADMAHISGLVAAGVIPDFADVTTTTTKSLRGRPRGAMFFRRKGVKEVKNQKQKEVLYDVEDKINGAVFPLGGGPHNHTITGLAVLAKQAMTPEYKAVGEGGLNSGSKFADALAGMGVELVSGGTENHLVLLKLNKKGIDGSRVEKLEAVHAAKNKTVPGDVSAMVPGDIRMGTRTALSRGFIEEDFVKVAEFFDAVKKIWKIKGADGTLKDFVTTLQSSASQSEAKLRHGVEEVAKGPFRTGFEKETMKYKK

NbL12g05570.1 ubiquitin_receptor_RAD23d-like [MW = 40.88 kDa]

No. of times detected



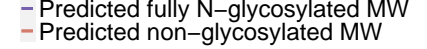
log(intensity)



Values from



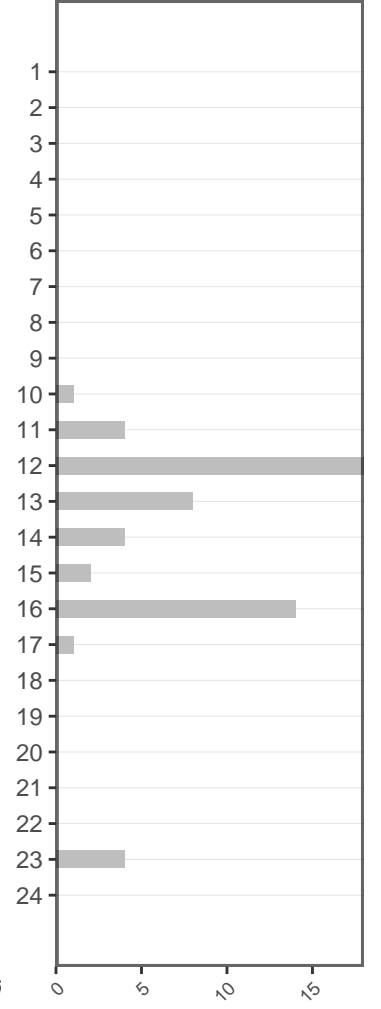
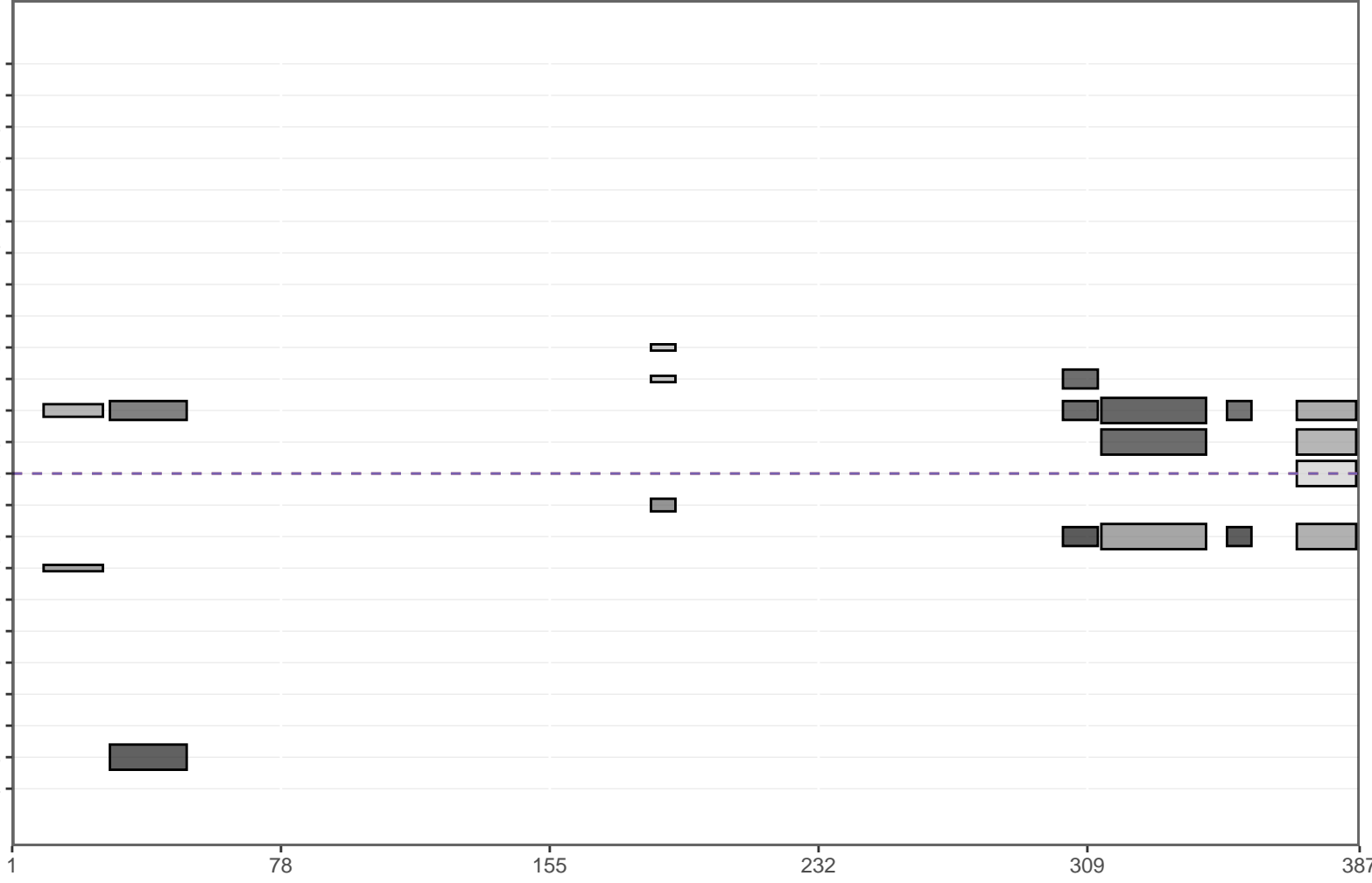
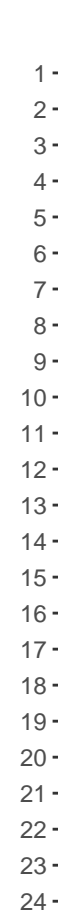
MW indication



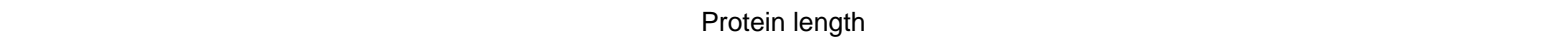
Molecular weight



Gel Slice

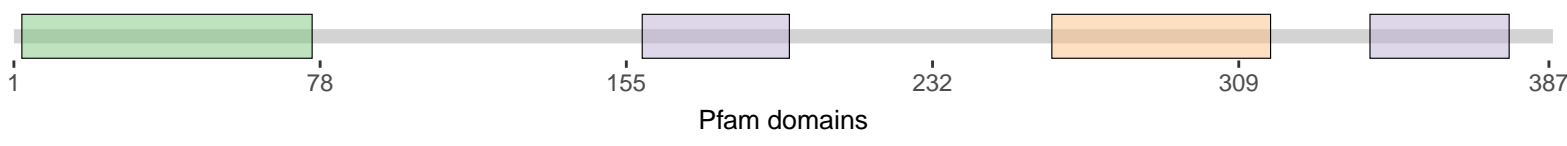


Protein length

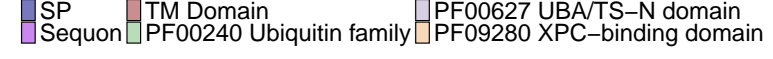


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

.RAAFNIPERAEIYVSGIPEQAEIPPAARALAPASGGAVNPPVQASGQVPSGGPNANFLDFPQGLPNVGSNAGAGNLDFLSNPSQFQALRMVGNPQILQPLMDELGKGNPQLMRIGEHGADFLRLINERFVEGEGNVPGGPQAIQAVTVTPEREIERLEAMGFDRLALVGVFFAGNKEELAAVYLLDHHHEFDEI

NbL12g05560.1 T-complex_protein_1_subunit_zeta_1-like [MW = 58.91 kDa]

No. of times detected



log(intensity)



Values from



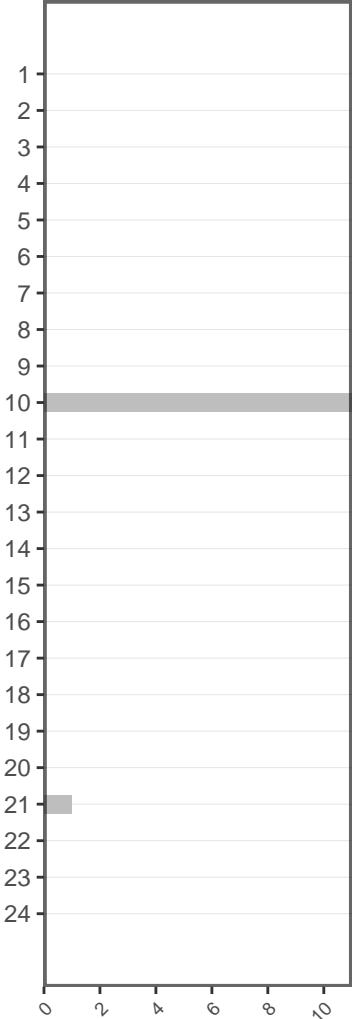
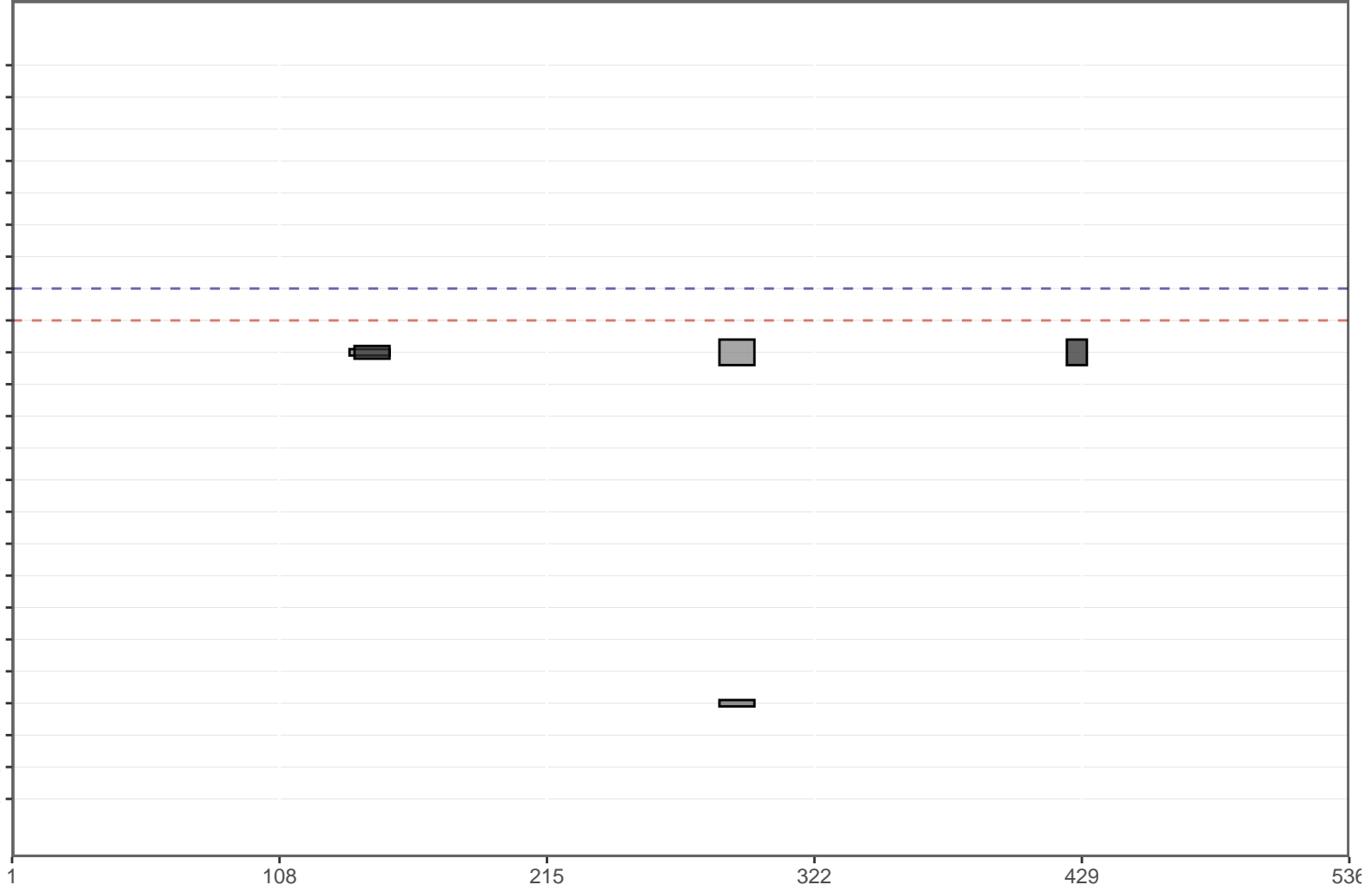
MW indication



Molecular weight

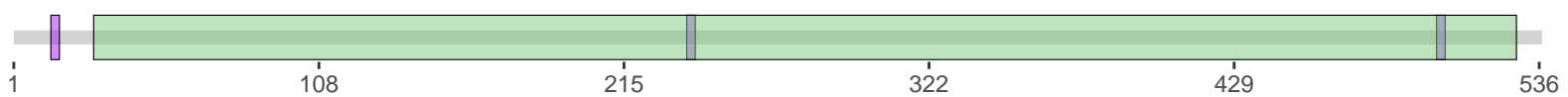


Gel Slice



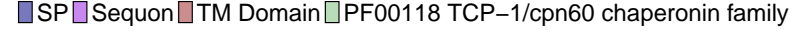
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

INAEQREAMVAERRRVDEIRVQKHIDLNKVKAGNDNNEVINKQKIDPPSLDLARAGIALRAKRRNMRERLVAAGGEAVNSVDDLTPDGLGWAQLVYEHVLSGEEKYTFVENWKNPHSGCTLKGPNIDHTAAGKDAVRQDGLRAWNTHIEDEAVLGGTFEVAWRQLINEVKKTKVGRAGLGVAFANALLVPKTLAENSGLDTDGVIAIATGSHDKGNVVGILNHTGEPDPMGEGIFDNYSVKRGIVNSGPIVAGQLLVDEIVRAGRNRKPN---

NbL12g05480.1 probable_Xaa-Pro_aminopeptidase_P [MW = 72.9 kDa]

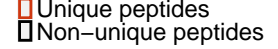
No. of times detected



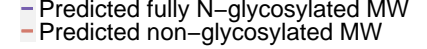
log(intensity)



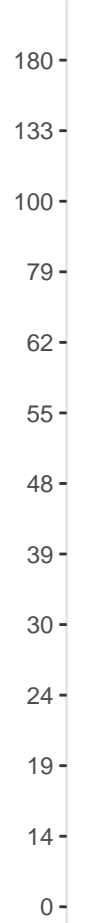
Values from



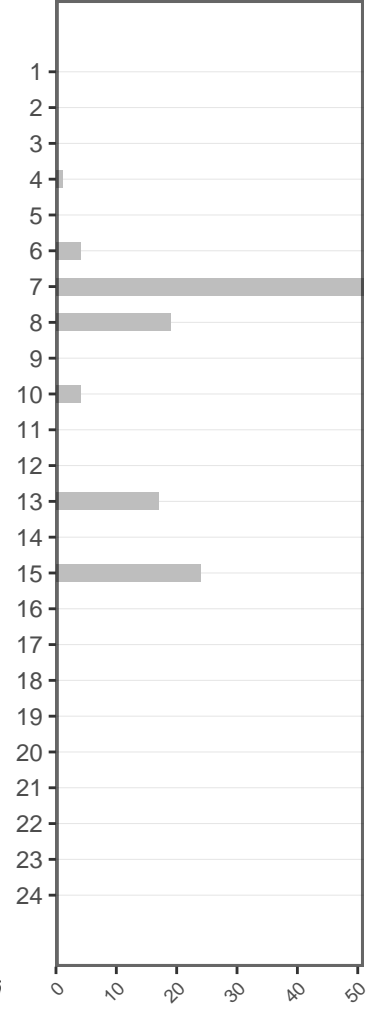
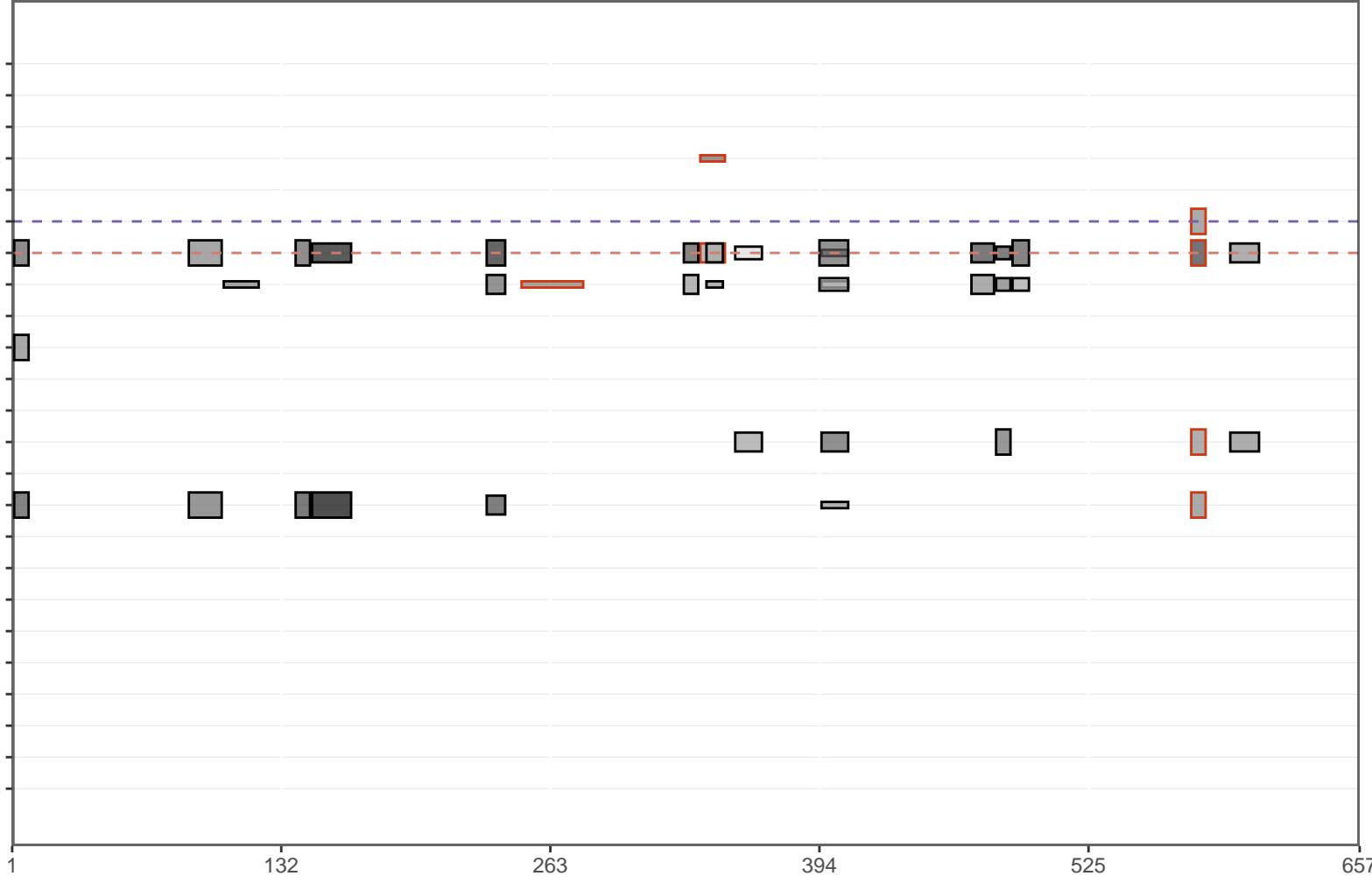
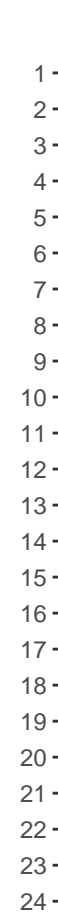
MW indication



Molecular weight

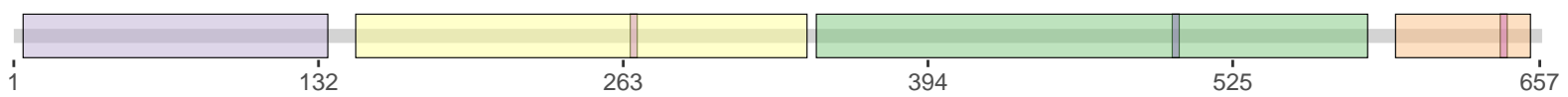


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ALYSKLNADKYLKGGFLALEKALKNFVEMEGLKKAHIRDGAAVQVHLAWLQKMGQENYASGQYFAEASLKNLKDTRKLTVEVSAEDNLEEFRAKSNFRGLSFPYHSVGSNAAHHYSEPAETCAELDPDKIVLGDGGAQYLDGTTDTRTVHFQKPTPEKADYAVLKGHSLGNARFPNGTNGYALDLARTPLWKYGLDVRHGTGHHGGSYLVNHEGPHQISFRPSAQNPLQVSMVTYDDEPGYVEDGDFGIRLENLVIKEGNTKFNFGDKGTYTFEHTWAPYQI

NbL12g05450.1 G-box-binding_factor_1-like [MW = 36.55 kDa]

No. of times detected



log(intensity)



Values from



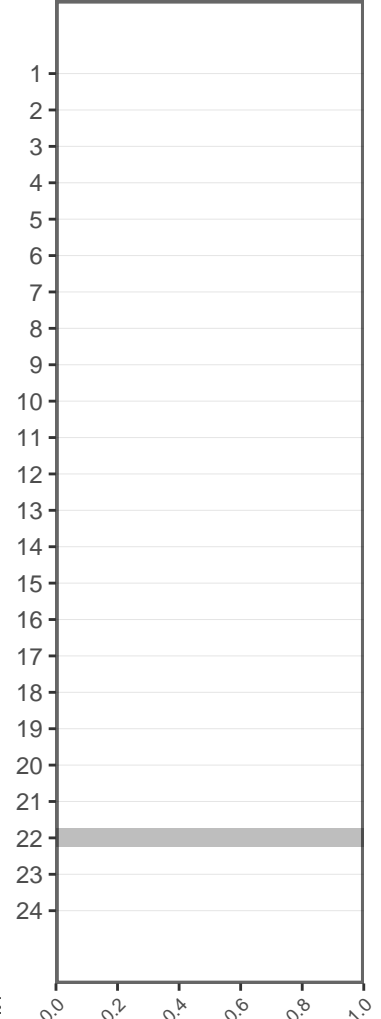
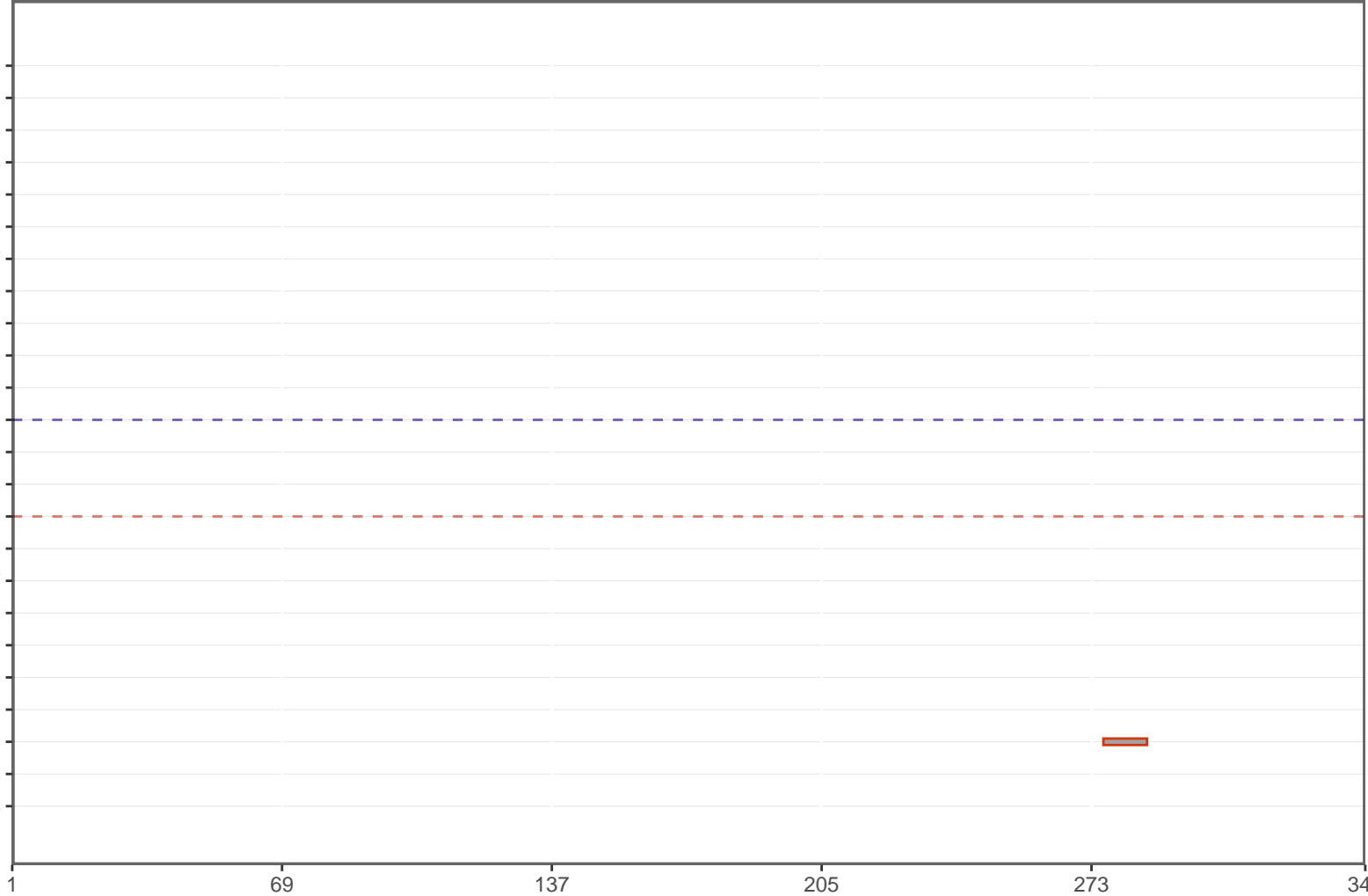
MW indication



Molecular weight

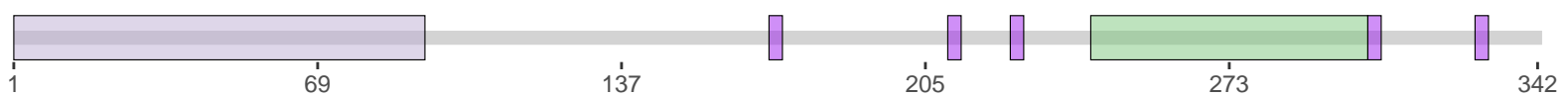


Gel Slice



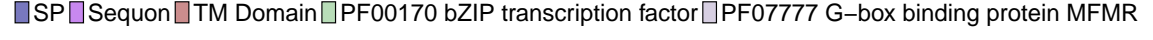
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

MANDENDNHEFSANKSRNFDMLANGASGNNPXTGNPVAAPATLNIGMELWNASSAGCPMKMRSSNGSGVAPAPGIGREWIGDERELKROKRRKGNRESARRRSRLRKAEGEELQQRVETLENIENHALKEEMRKLSEEGEKLTSENNNSKEELTRLGGPEAVSKLESNANATHLQSNLDEANS

NbL12g05210.1 proteasome_subunit_beta_type-1 [MW = 29.12 kDa]

No. of times detected



log(intensity)



Values from



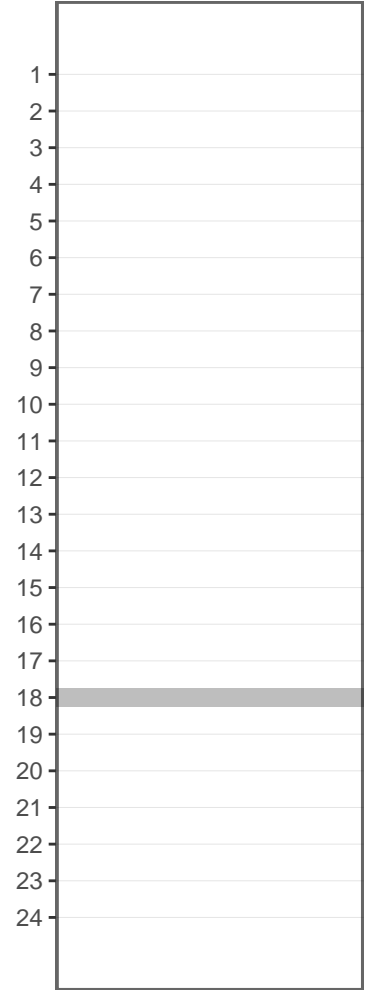
MW indication



Molecular weight



Gel Slice

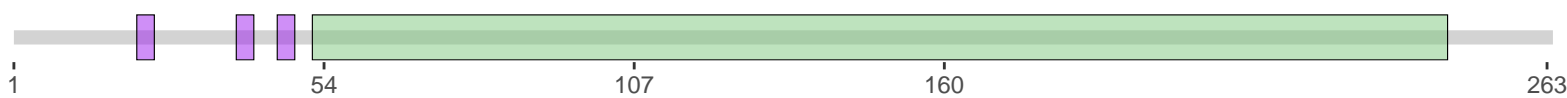


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

LYYHQHKKQKSCFRMAGQLLNTFLYWRFFPYFYSFNLVGLGDSKGGVFTFYDAWGSYERYGVYSQGGGSSFLMPFLDNQKSPKPEFLLLPKKDAVTPLSESAIDLVKTFQFASATERDVTGDRLEIVLNANGIRREEMELKDP

NbL12g05140.1 D-2-hydroxyglutarate_dehydrogenase_mitochondrial [MW = 63.49 kDa]

No. of times detected



log(intensity)



Values from



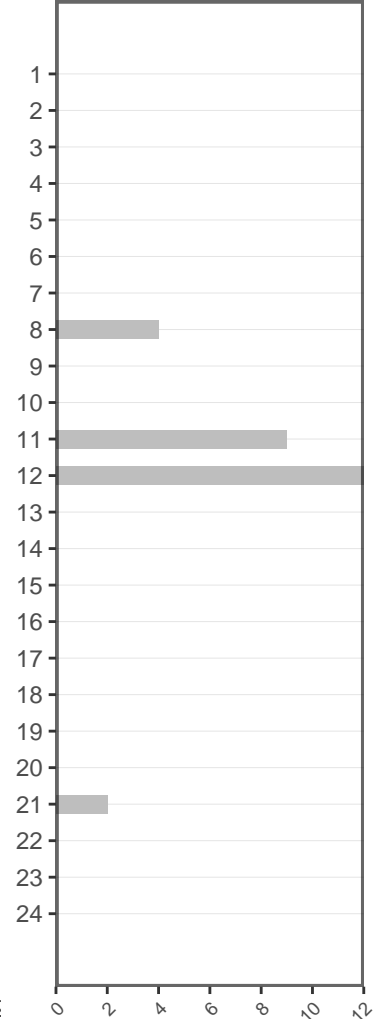
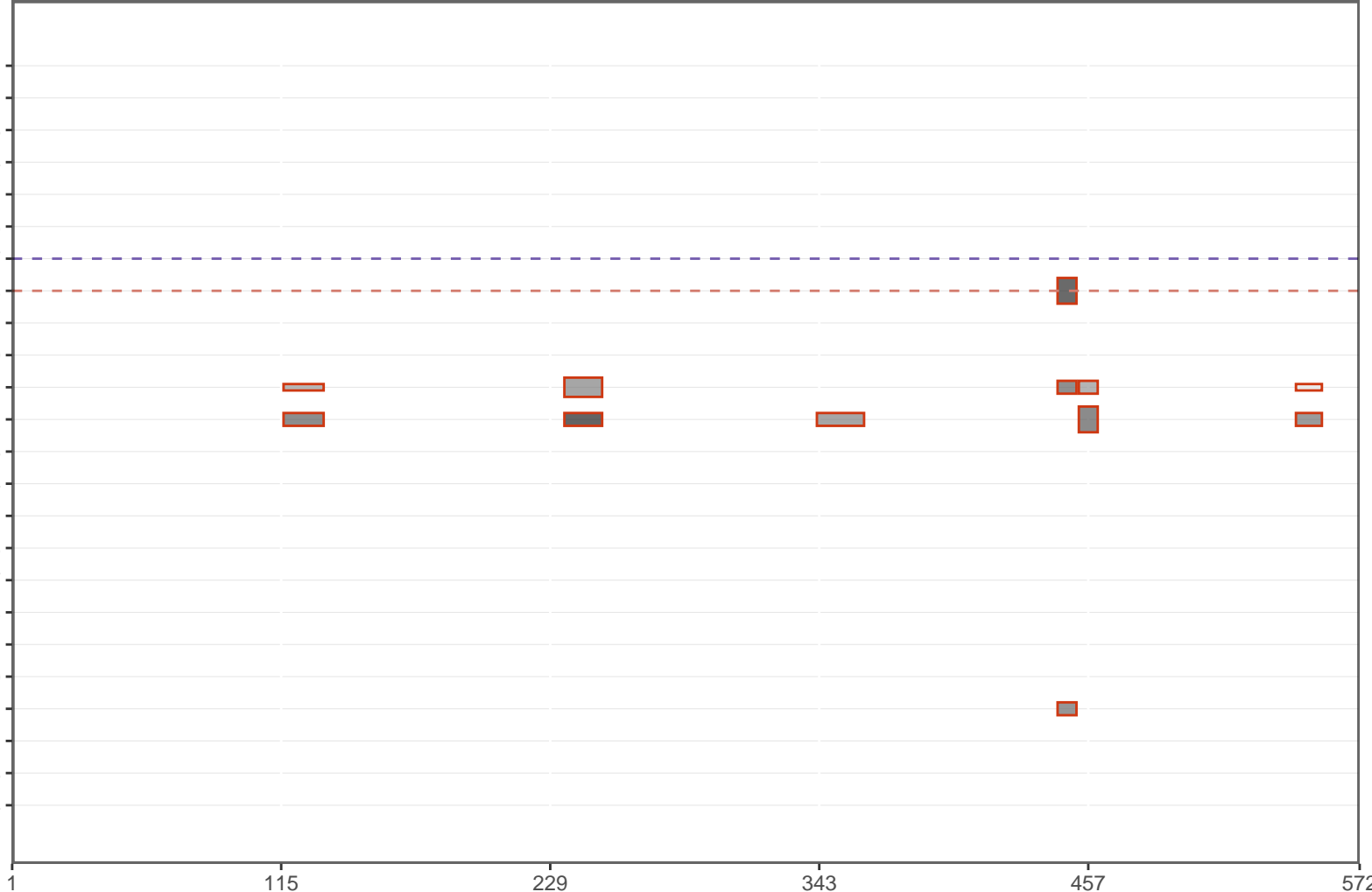
MW indication



Molecular weight



Gel Slice

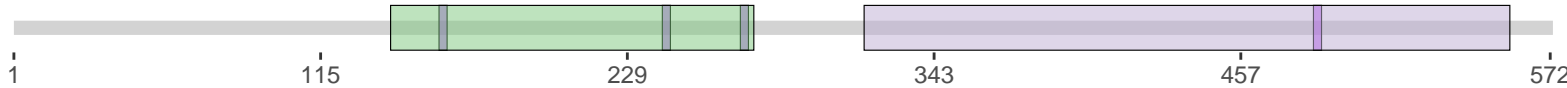


Protein length

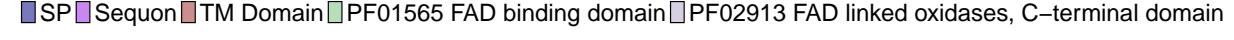


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IGTVLDMGLTLRKNDFGVDLKHLEFGEGELGIVTRVSLTPPKLSEVNVFLACDSDVAGCLLKLDDAKRKLGEILSAFELDHDMDLVLKHLEGVNRPFFSSMNFYVLETTGSSSETYDREKLDLFLHSMENGLSDGVAQDDTGAQSSGWHVREGPEALMKAGGVYKYLGLIPVENMYDLVLEEMRVRLDASAKYVAYGHLGDGNLHLNISTPQYDNDNLGIEPFVYEWTSKHGKSGISAEHGLGLMKANKRHYSKPETVQLMVSIKKLLDPLNGLNPYKLPPLSFSKAE

NbL12g05080.1 fructose-bisphosphate_aldolase_1_chloroplastic [MW = 42.59 kDa]

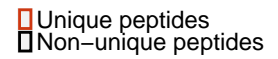
No. of times detected



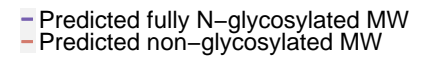
log(intensity)



Values from



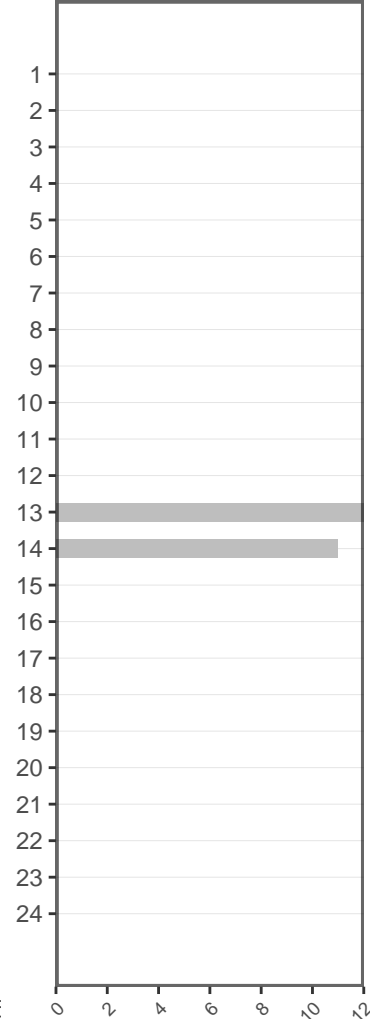
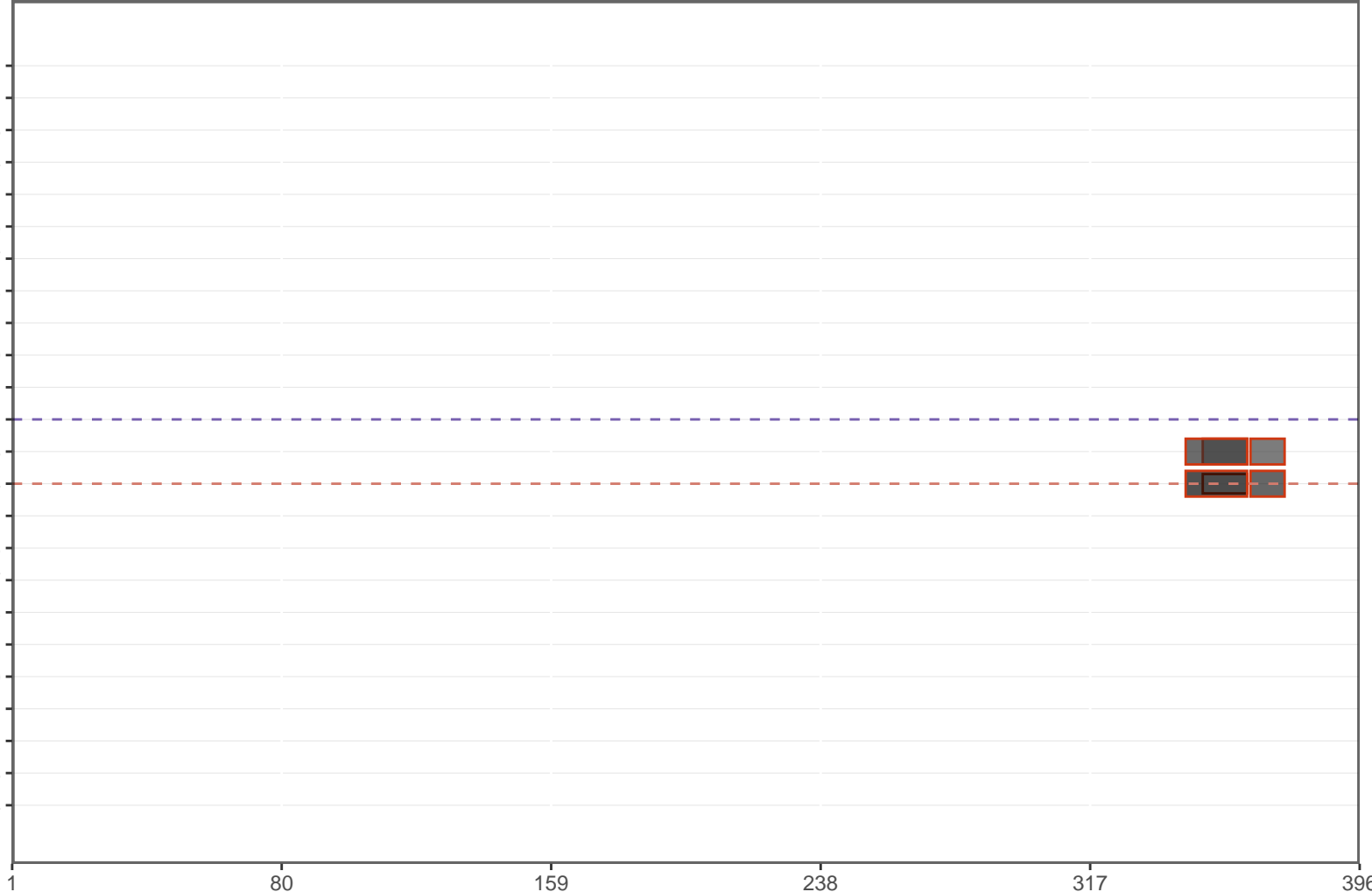
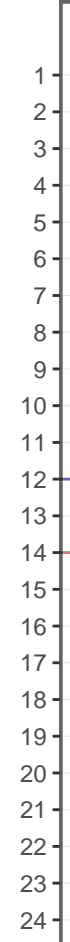
MW indication



Molecular weight



Gel Slice

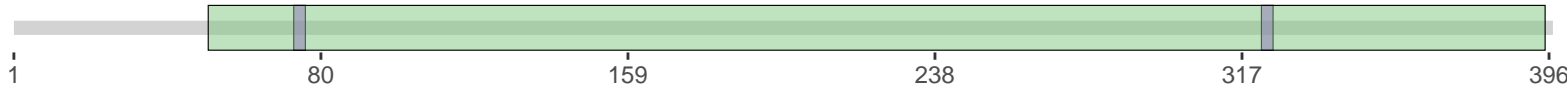


Protein length

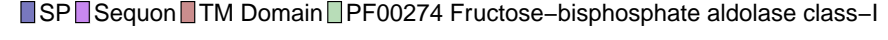


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

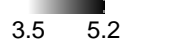
V/SIPNGPSALAVKGAHWGLARVAISGDNGLPIVPEPELLDGEHNDRTFEVAGKVAWEVFFYLAENNVVMEGILLKPEMVTPGAEGKERATPDQVADYTLKLLGRIPVWPGMFLSGGQSEVEATLNLNAMNGSPNPNVHVSFSYARALQNTFKTWGGRPNVEAAGEALLIRANANSLAQLGKYTGEGESEAKKGMFVKGYYV

NbL12g05030.1 nucleolin-like [MW = 128.69 kDa]

No. of times detected



log(intensity)



Values from

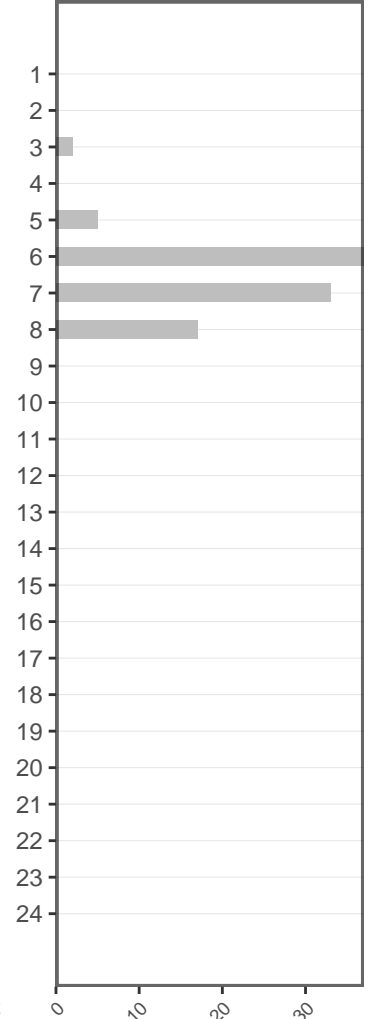
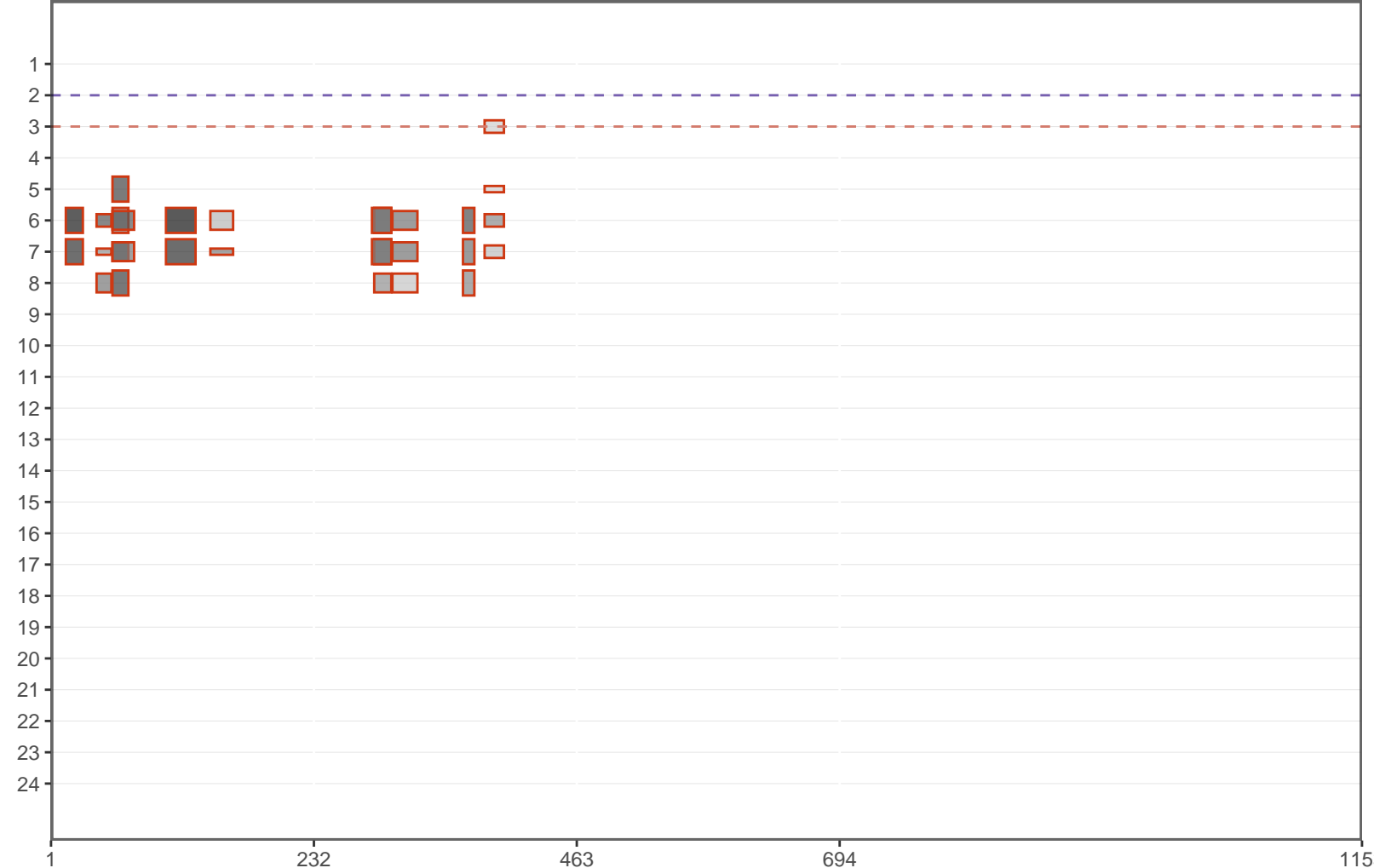
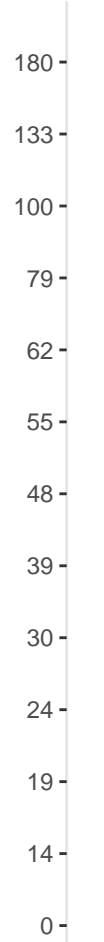


MW indication



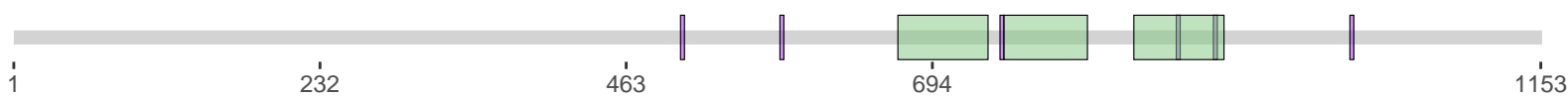
Molecular weight

Gel Slice



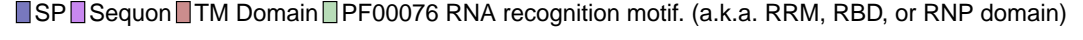
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

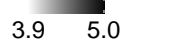
KEGSELMRGKDSNPTPTGDNINANGAEDRMEEEDIKMKKDKDSDVDEVDGKIEAFADGNGEEFVEDGVPEDGCEAEALDDERAQLAAHAKERMKRKKEVFGGLDRDAVEEDLKRIVFGHVEVDVIRMHREMTNKNKGYAFVKFATKEGASRALSEMRNPVIRGKRGGTAPSEEDNTLFLGNICNTWTKAEVIRGKLDKQGVGEGVGINLVADPKHEGLSRGFALFEFFDHTDAMTAVKILGRPDVVFQHSERTAKVAFAPLRDPPDPEVMAQVKSVFDGLPPVY

NbL12g05020.1 peptidyl-prolyl_cis-trans_isomerase_Pin1-like [MW = 13.53 kDa]

No. of times detected



log(intensity)



Values from



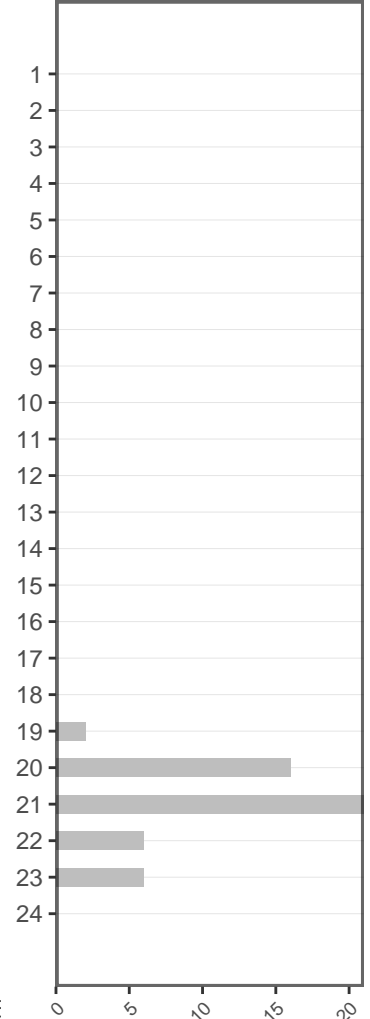
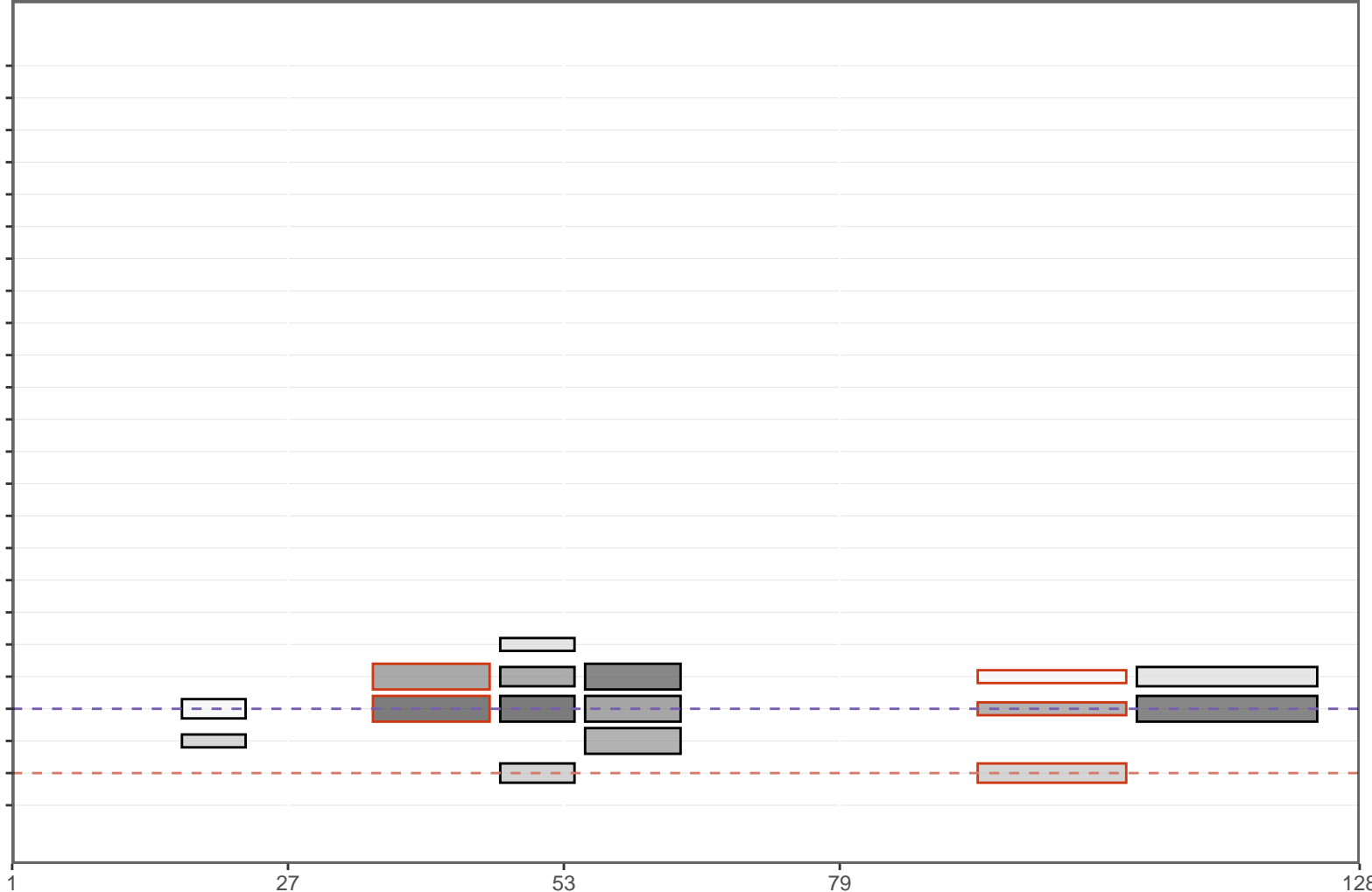
MW indication



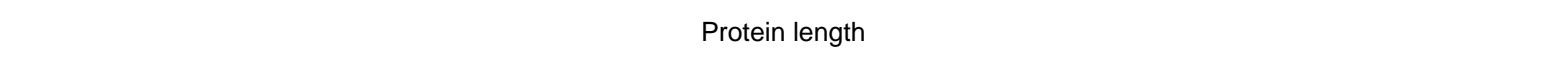
Molecular weight



Gel Slice

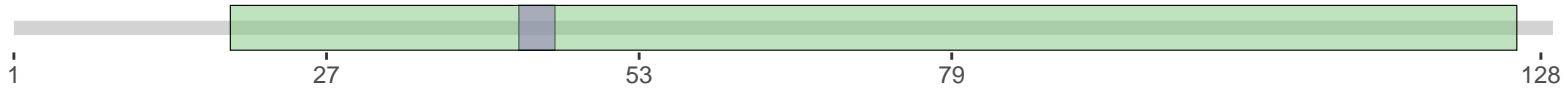


Protein length



Peptide counts over 4 repeats

Pfam Description



Protein sequence:

/SOLKSLREDIVSGKAKFDNAATHSDGSSAKRGGDLGPFKGGGQKPFVATYALKVGEISDVEVDGGVHKRTA

NbL12g05010.1 small_nuclear_ribonucleoprotein_Sm_D3-like [MW = 14.45 kDa]

No. of times detected



log(intensity)



Values from



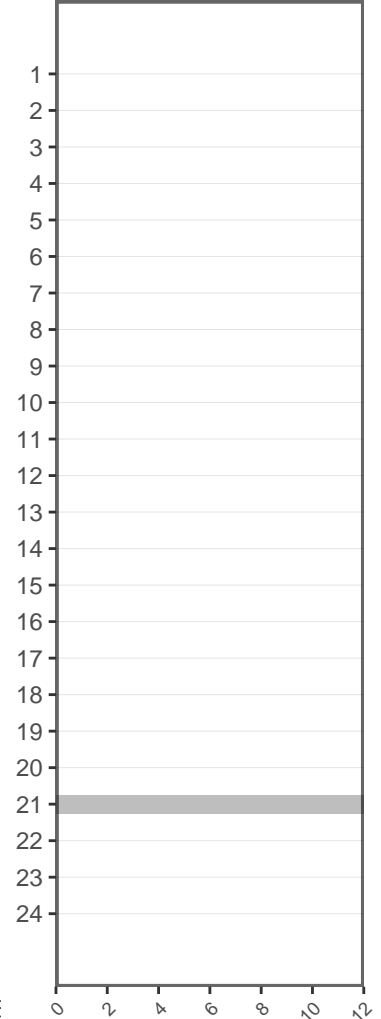
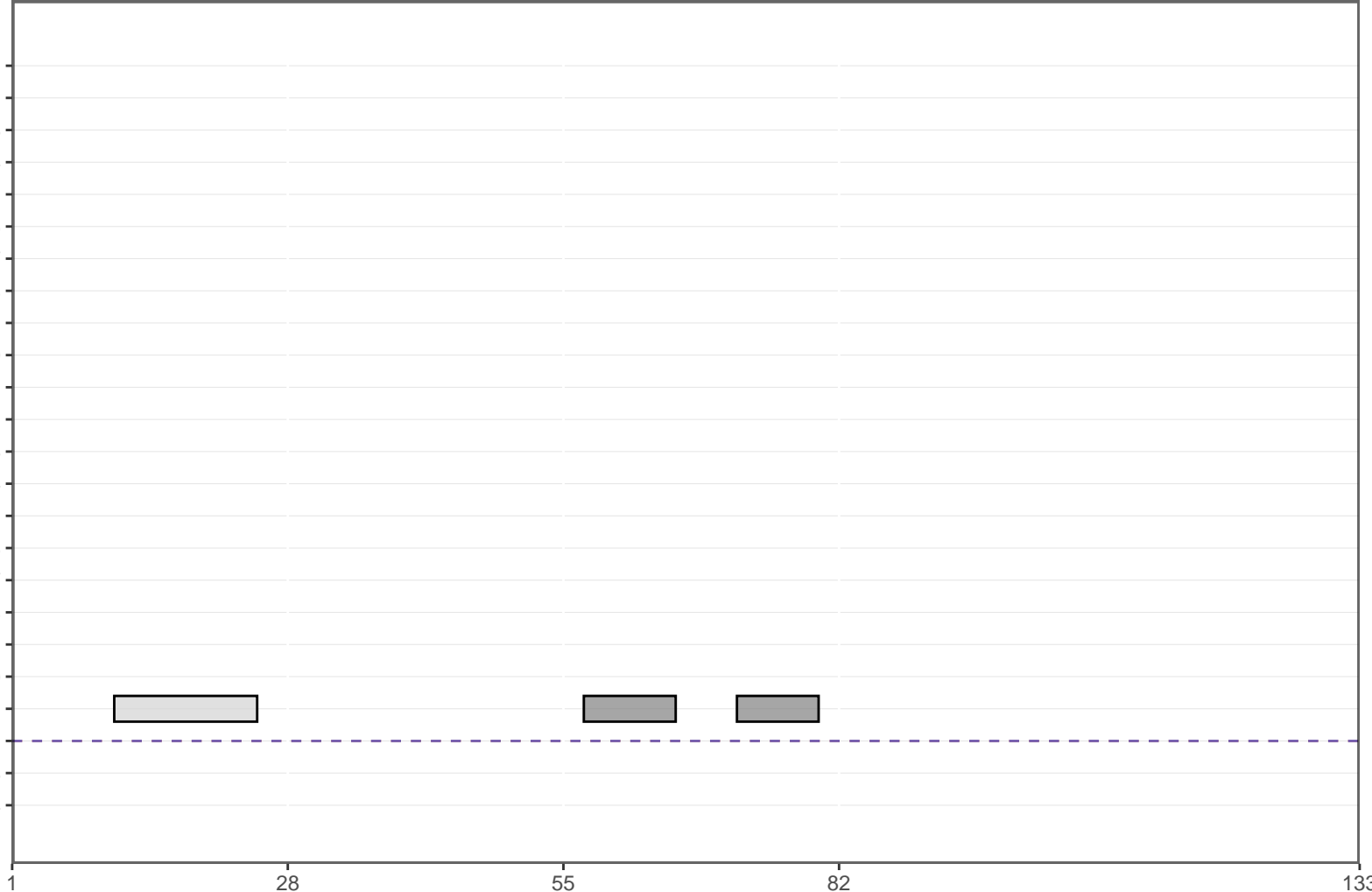
MW indication



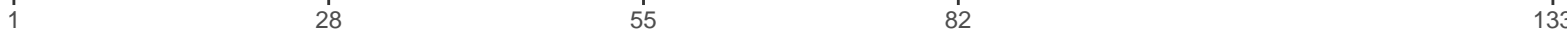
Molecular weight



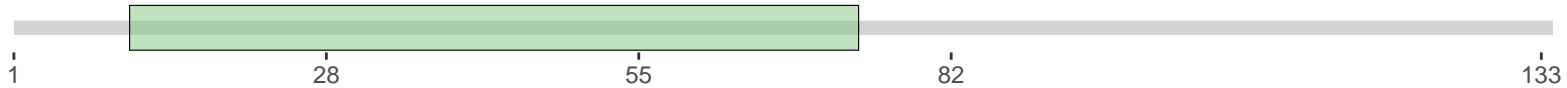
Gel Slice



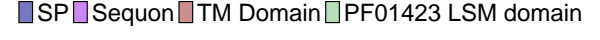
Protein length



Pfam domains



Pfam Description



Protein sequence:

IGRVLSLEHVFIRGKQVRFMIPDMKQNFPMFKRLEARIKGGKTSLSGVRGRAIMRAKAGAAAGRAAPGRGVVPPVRR*

NbL12g04810.1 basic_endochitinase-like [MW - SP = 26.81 kDa]

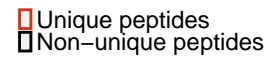
No. of times detected



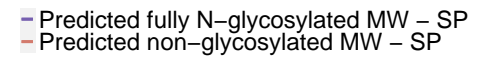
log(intensity)



Values from



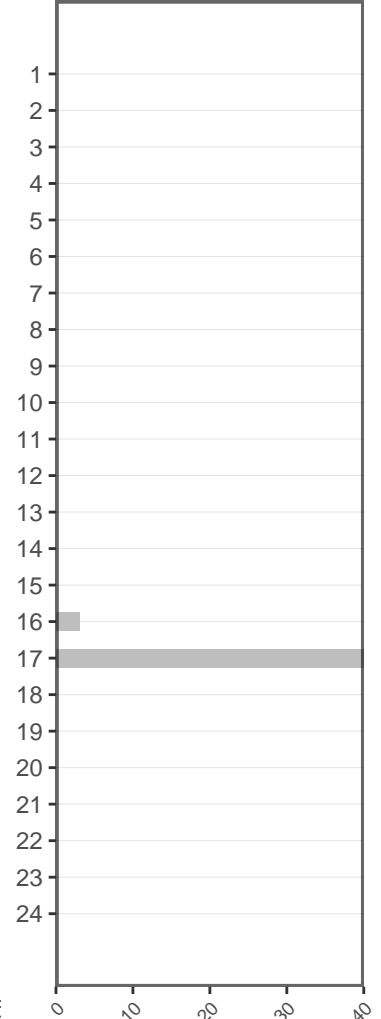
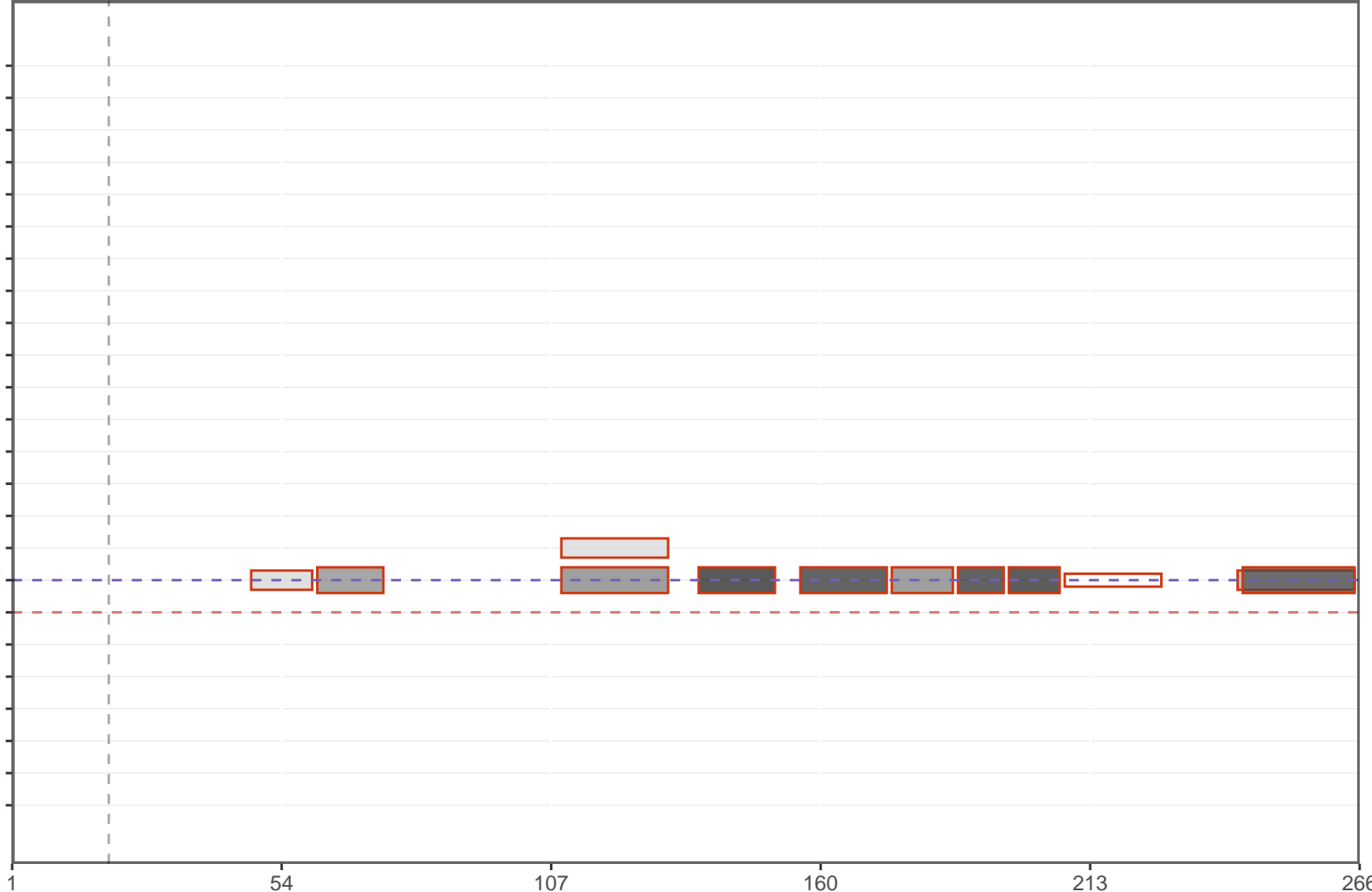
MW indication



Molecular weight



Gel Slice



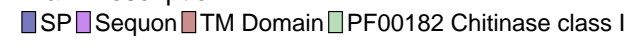
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SIQWPCAPGKSYFGRGPIQIENYNNYRQPRGIRAGRDLNINPDLWANDPVVVFKTLWFVMTFQGGPKPAHGVITGRWTPSAADLAARRVPGFVITNINNGIEGSKSNAGMGRIGFYRRYQGLGVDPGNLDCASGRPFQI

NbL12g04760.1 ubiquitin_domain-containing_protein_DSK2b-like [MW = 58.35 kDa]

No. of times detected



log(intensity)



Values from



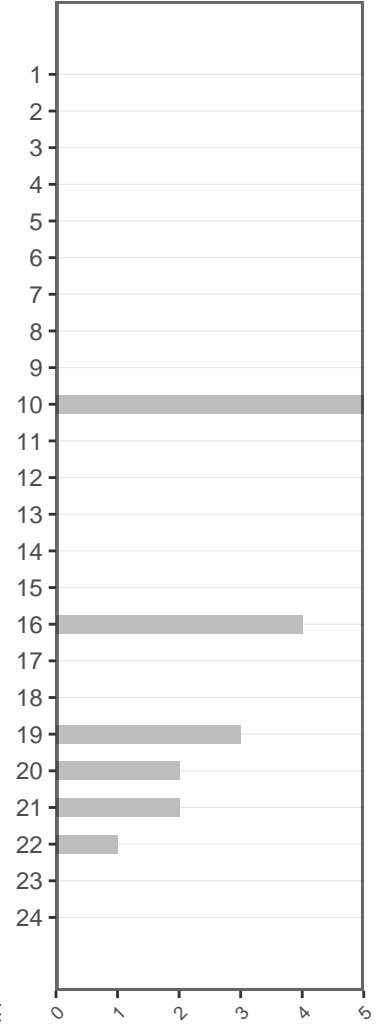
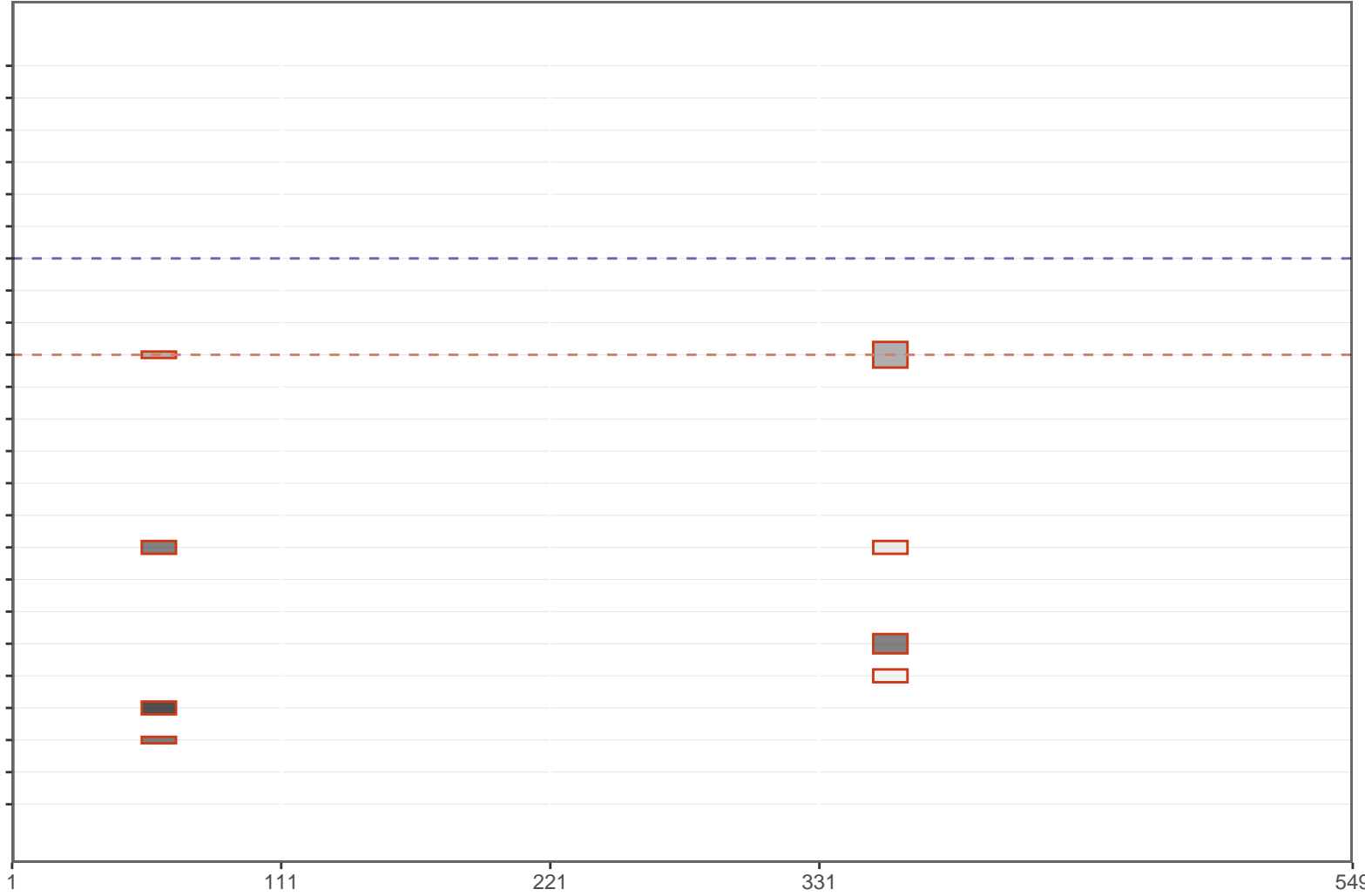
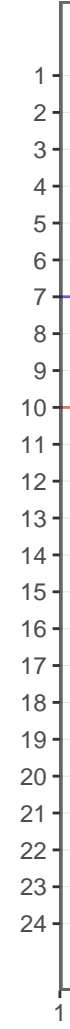
MW indication



Molecular weight



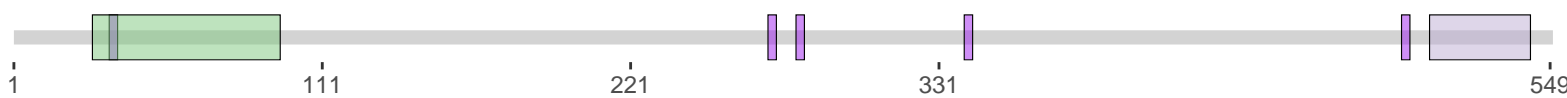
Gel Slice



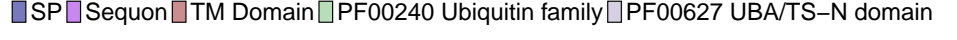
Protein length



Pfam domains



Pfam Description

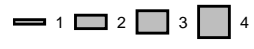


Protein sequence:

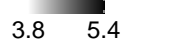
IIVQEPFLNMTTMAQDTRNDSDGNPFALLGADGGGGAGNATSLPVTGSETTANPPAINTNPLNPNWASAGTGAAGTNTSARENAAADTRALPLGGGLGALPOLQRMGGMPDASELNLQMLNQNPAISGMQSLLENPQYVWNGISGLNPQLRMLDNPQLREMMQGNPEFRQLTSPETMDQVMSLQGGLLSGLGRGGTNRGGGGDAGRTAFDNGMMEMLMNFQGLGTGGLGVSNRNPPEELVATQLAQLQEMGFDDTGENIRLATAQNYHAUVERLLGNTI

NbL12g04600.1 eukaryotic_translation_initiation_factor_6-2 [MW = 26.42 kDa]

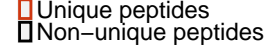
No. of times detected



log(intensity)



Values from



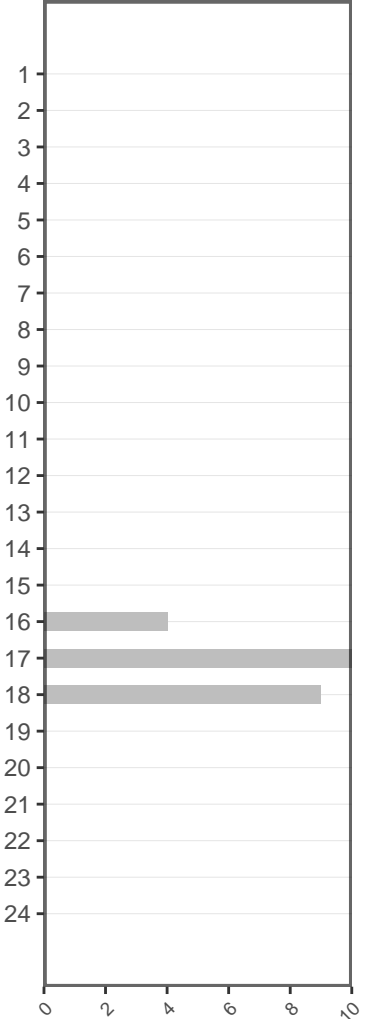
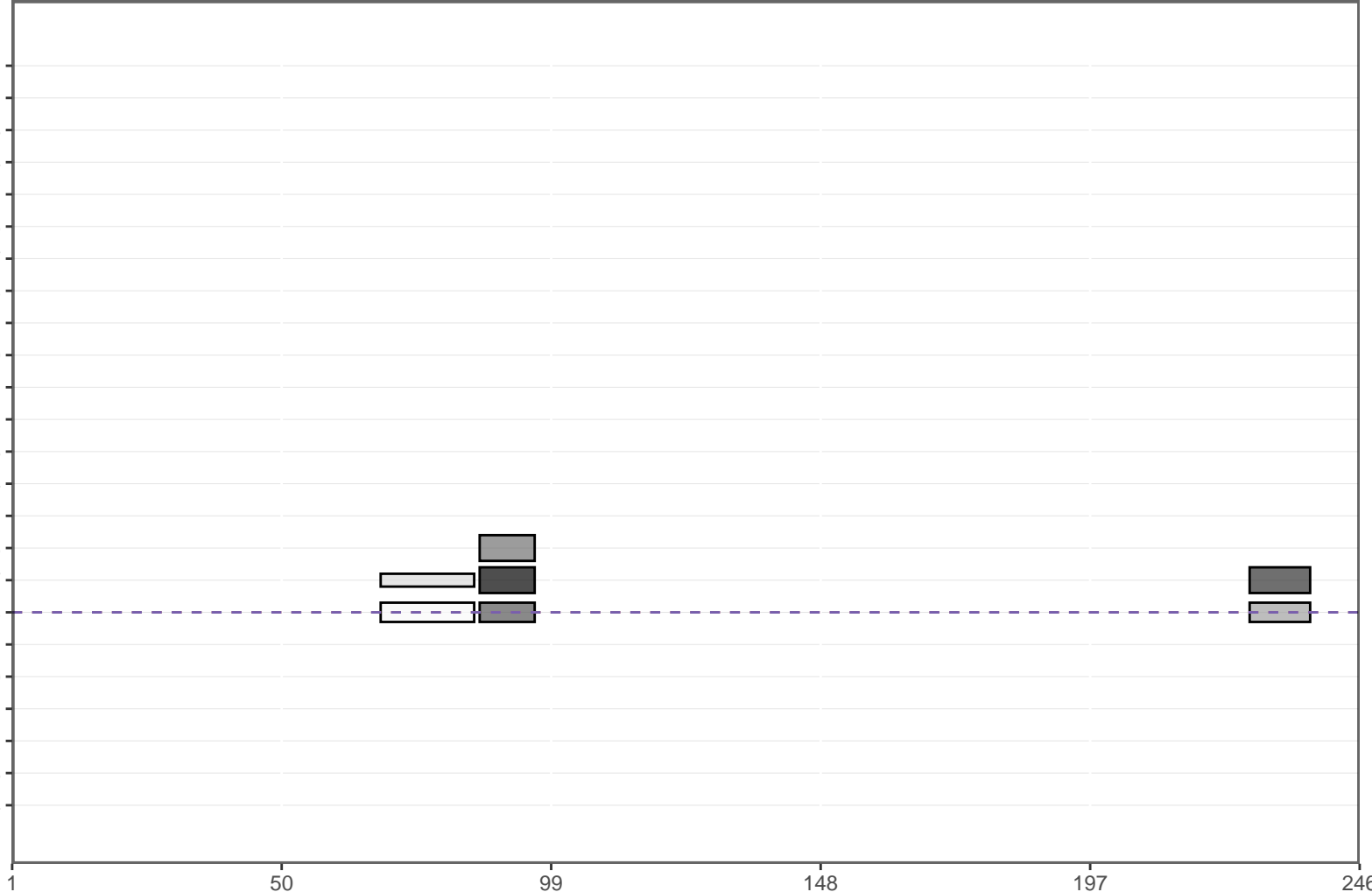
MW indication



Molecular weight



Gel Slice

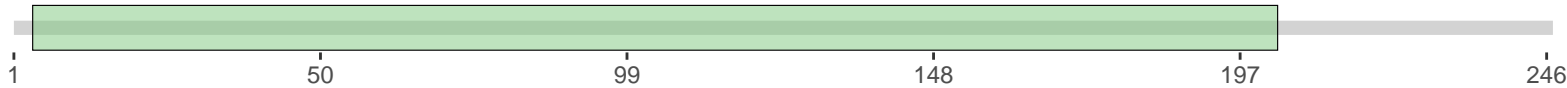


Protein length

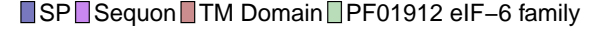


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

NDHVALHTLDLKDKEEEMADLVGVEVFRQTAGNLIYGGYGSFNRGGLVHPHTSIEDLDELSTLLQVPLVAGTVNRGSEVIAAGLTVNDWTFQGGDITATELSVESVFKLRLEAGPSAIVDEMRSKSLIDVYV

NbL12g04470.1 probable_acyl-activating_enzyme_6 [MW = 60.98 kDa]

No. of times detected



log(intensity)



Values from



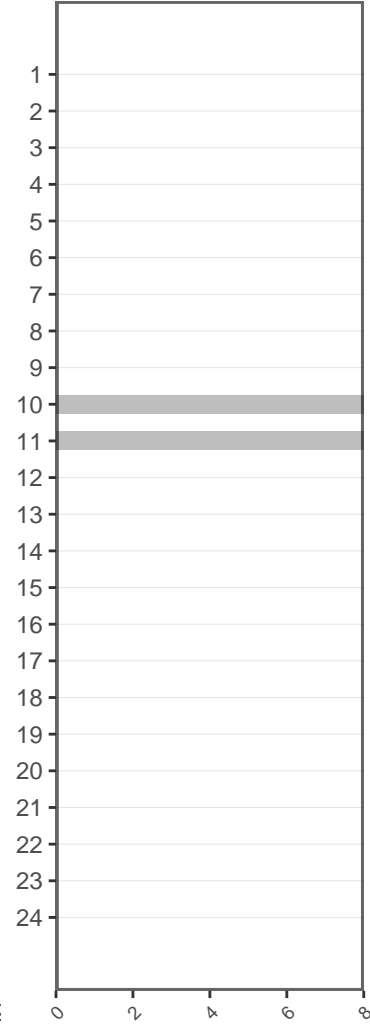
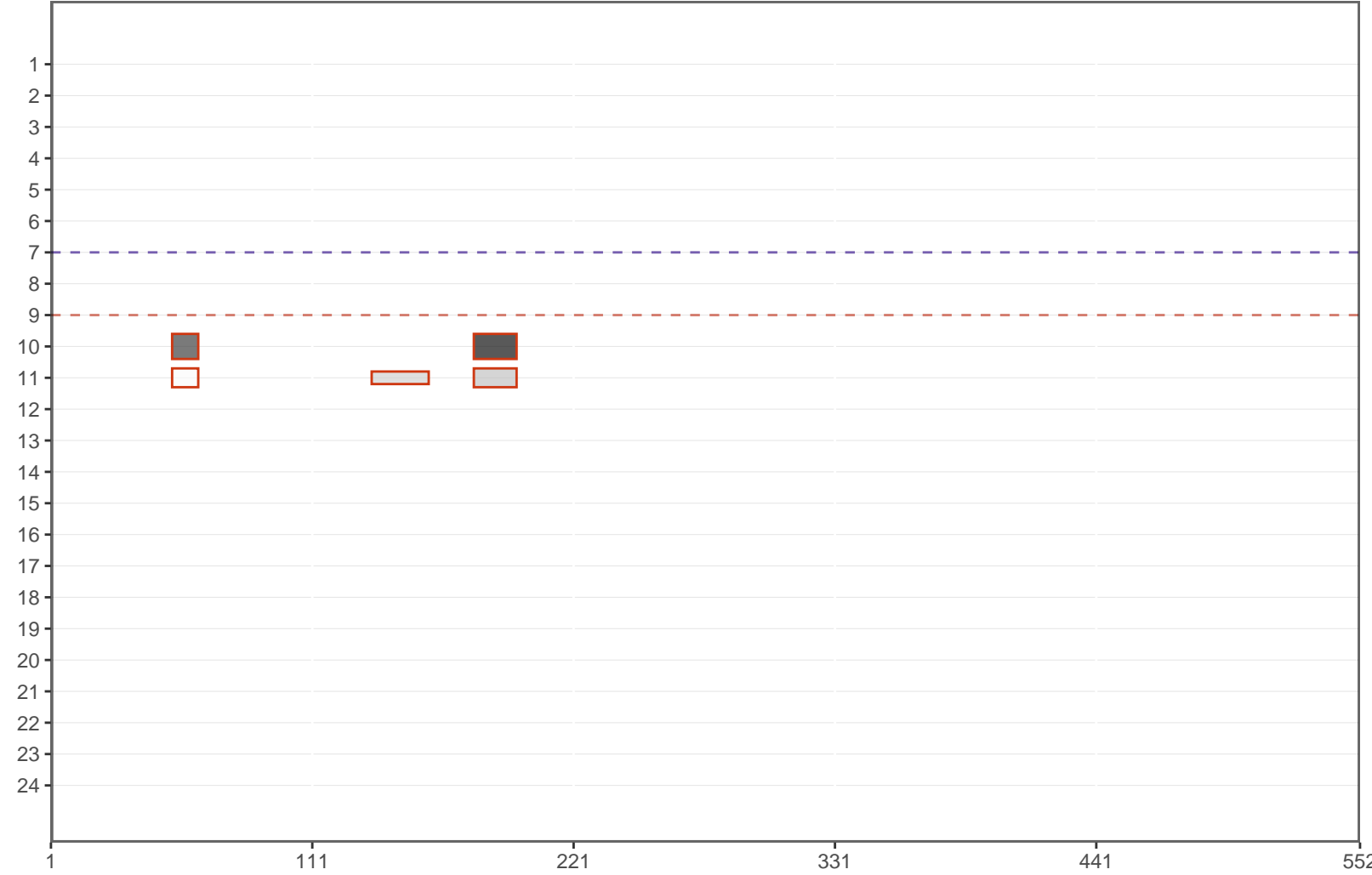
MW indication



Molecular weight

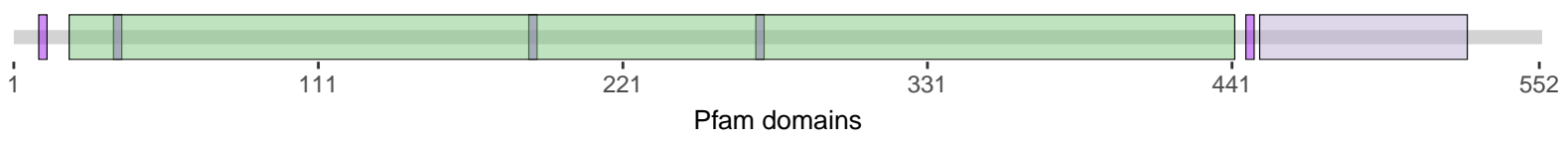


Gel Slice

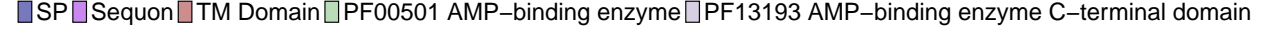


Protein length

Peptide counts over 4 repeats



Pfam Description

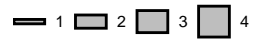


Protein sequence:

00NVTHTCAAPVYVNLMSNPDKPLKHVHMTAGSPPAWLFRTESLGFVHHGVLGLETGGGLVSGCTWNNHYNKLPAEERARLKRGGVRTGMTEVVDPEGGVSVWRDGTFLGELHKGGMGLGLVLDPEGTSKGMKDDGWYFTGDVAVMHFDGYLEIKDRKDVHSGGENLSSEVEGVLYTHPAINAAVWARPPDEFWGETPCAFVLSNGKEKASEKDIIEFCRAKLPHYMVPKTYFKGELPKTSTGKIQKPLVRDAKMSMKTGSLKSKM*

NbL12g04450.1 protein_YLS9-like [MW = 167.14 kDa]

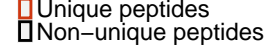
No. of times detected



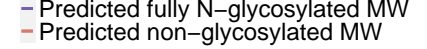
log(intensity)



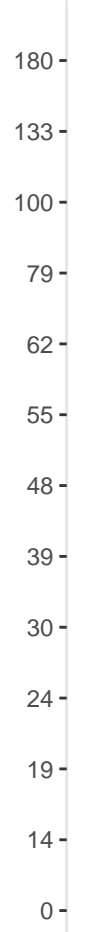
Values from



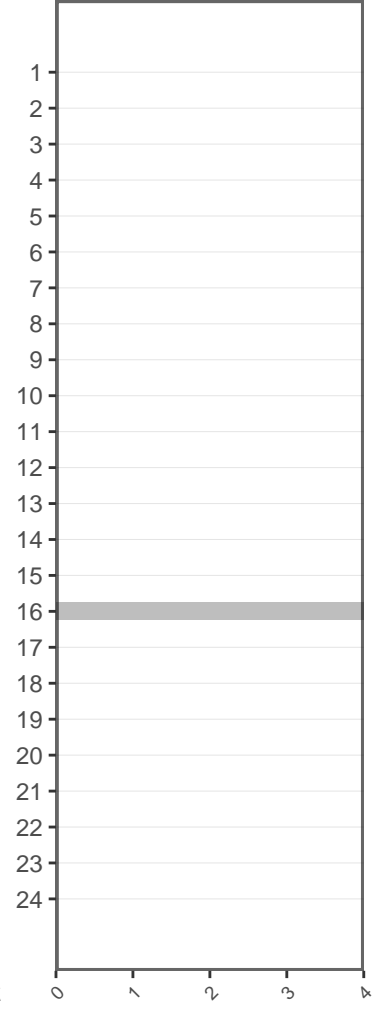
MW indication



Molecular weight

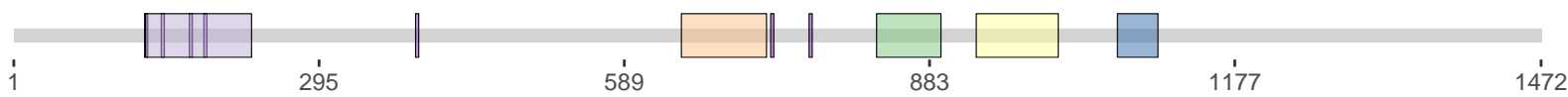


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00078 Reverse transcriptase (RNA-dependent DNA polymerase)
- PF03168 Late embryogenesis abundant protein
- PF08284 Retroviral aspartyl protease
- PF17919 RNase H-like domain found in reverse transcriptase
- PF17921 Integrase zinc binding domain

Protein sequence:

LDMVDFDTCPLSGEGPQVMPVLMFLFMSRLDAWSKIGYLYLAVYVNSSAEVPDSDVPIVREFPRAHFHYAIEYGTAGVERVYKDGQLGDLLEKGRIPRLRIRASGVLKIVFTRIGHYEFVMSFGLTNSPFAFMDLNNRVVSPFLDFFMVIFDDIMVYRSQEEHEGHLRVRAFKWTRRRRLQGRTRDQDPQMLRLTKGKAGDFRWSDEGEVSGFKLKTALSTTPVLLPTGLGPYTVYGDASRIGLGTALMGNRGRVIAVAGRELKHEKNVPHDELEAAJLANRLRLD

NbL12g04430.1 ras-related_protein_Rab5 [MW = 21.87 kDa]

No. of times detected



log(intensity)



Values from



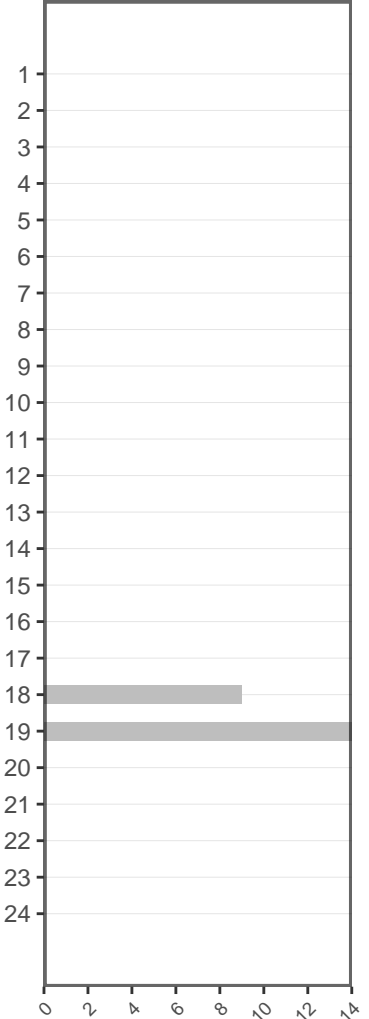
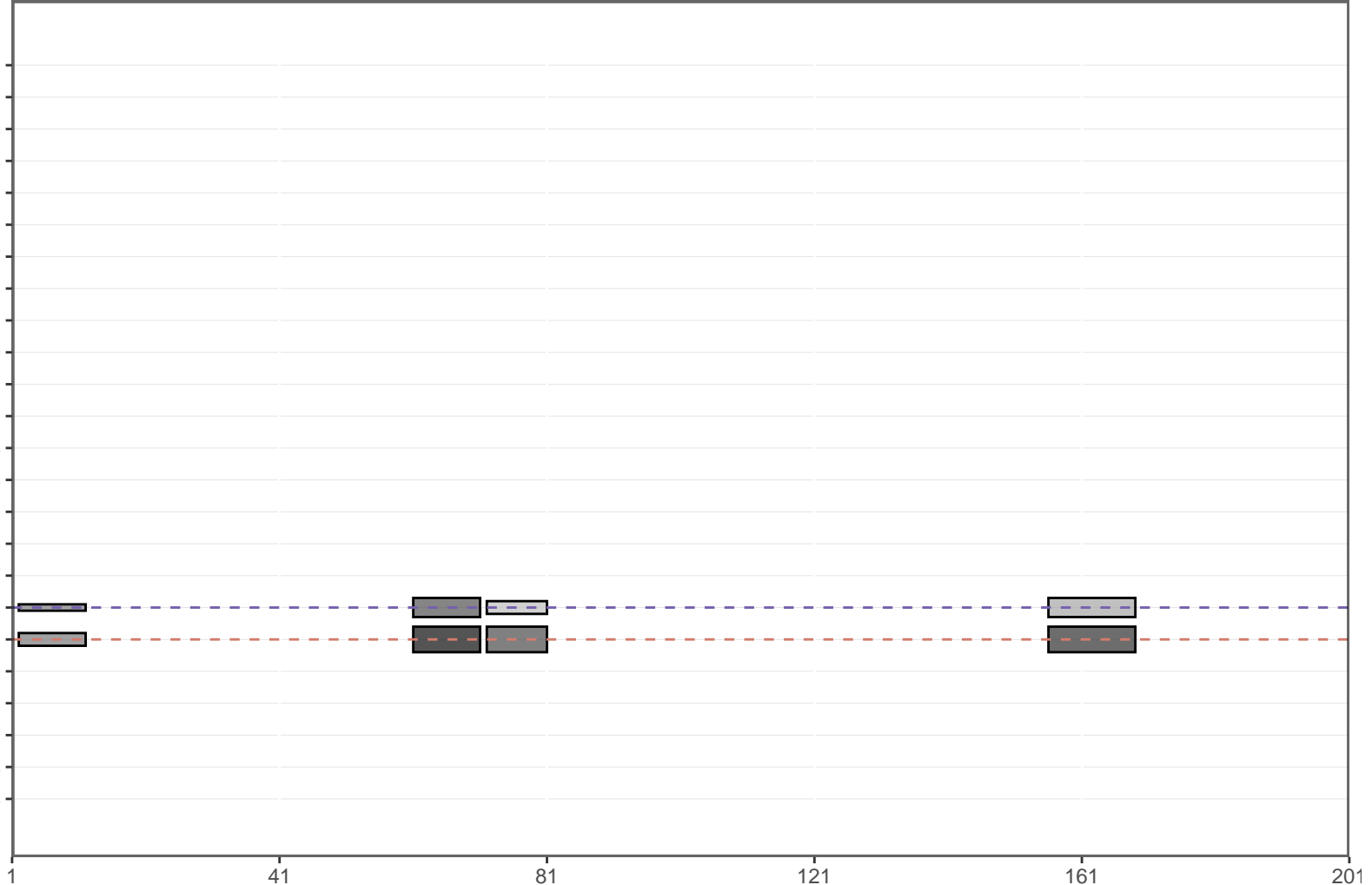
MW indication



Molecular weight

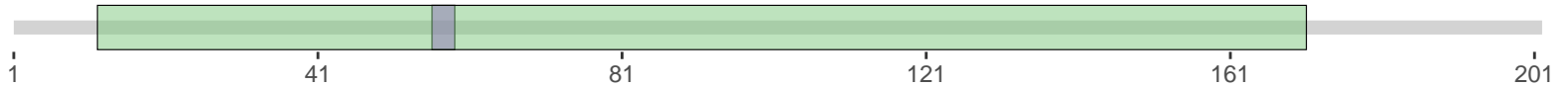


Gel Slice



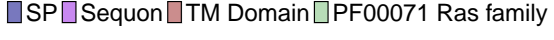
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IVYDITSTESFARAKKVVWDELGKGNPNMVMALAGNKADLEKRRKVTAEEARLYAEENGLFFMETSAXTATNVDIFYEAKRLPRAGPAGNPGMVLVDRPEGGGAAAGCTT

NbL12g03940.1 protein_PHLOEM_PROTEIN_2-LIKE_A9-like [MW = 19.3 kDa]

No. of times detected



log(intensity)



Values from



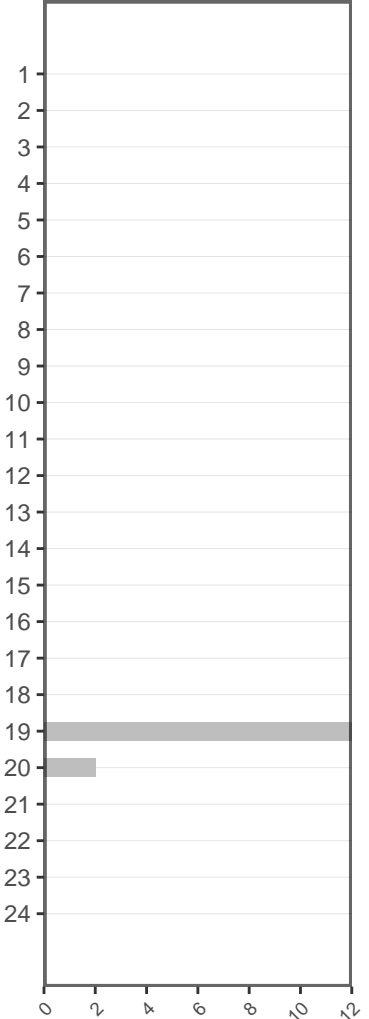
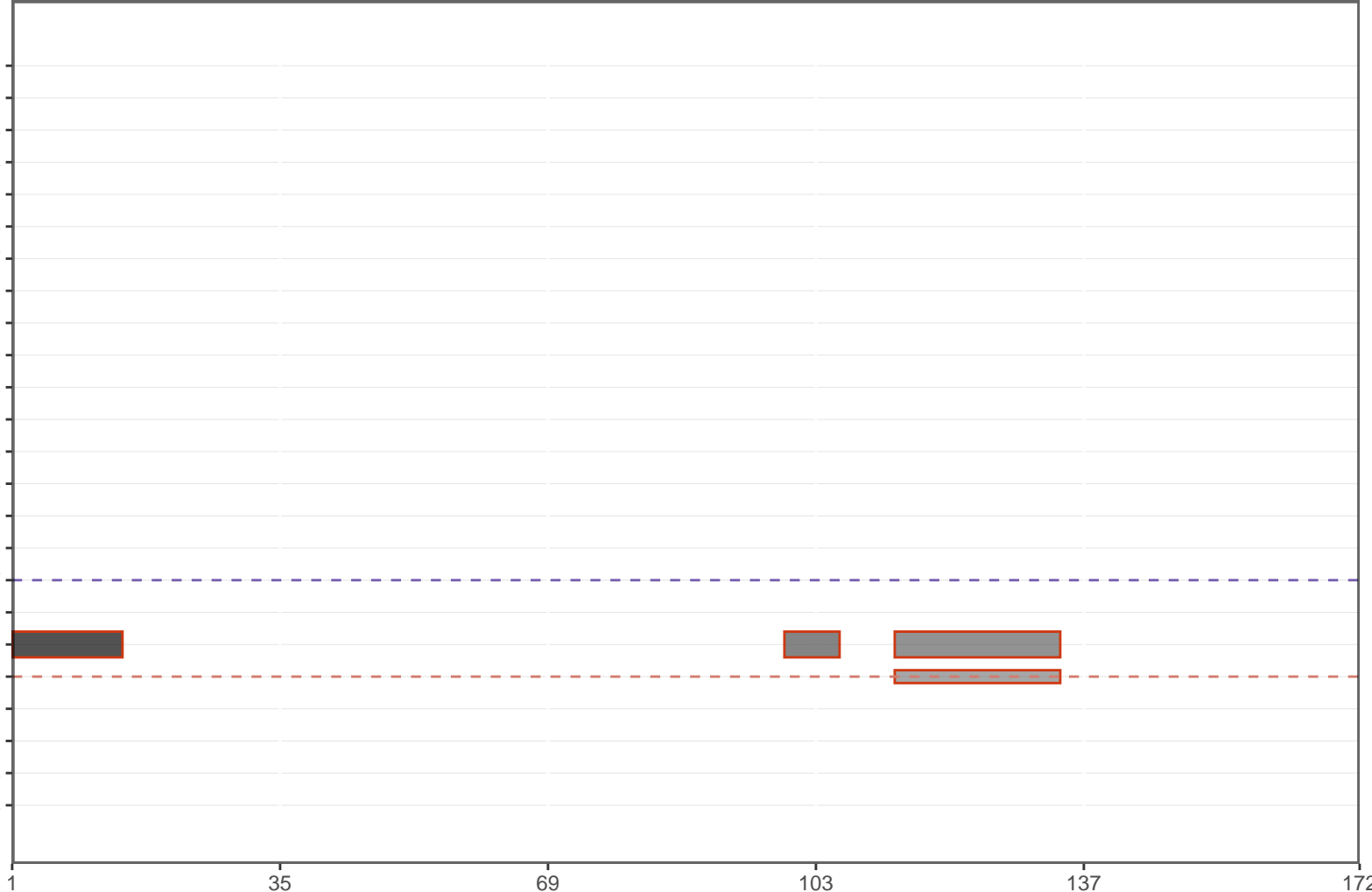
MW indication



Molecular weight



Gel Slice

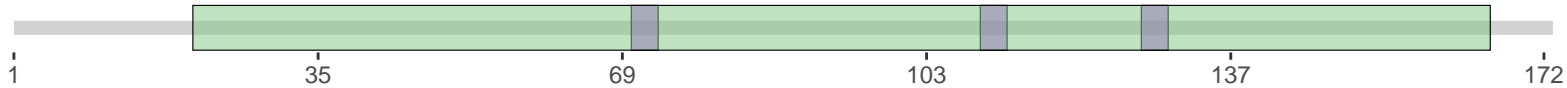


Protein length

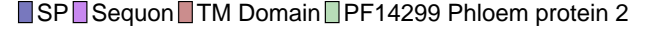


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

DVYFKLKLTDADFQWDLPIYFMKGGGSLWKNLTKDGPINPDGTYYVFNILTVTVGKGGNDENKLYFGLYEVVSGKWKGLRIGKVVTKVEEG

NbL12g03820.1 delta(24)-sterol_reductase-like [MW = 66.11 kDa]

No. of times detected



log(intensity)



Values from



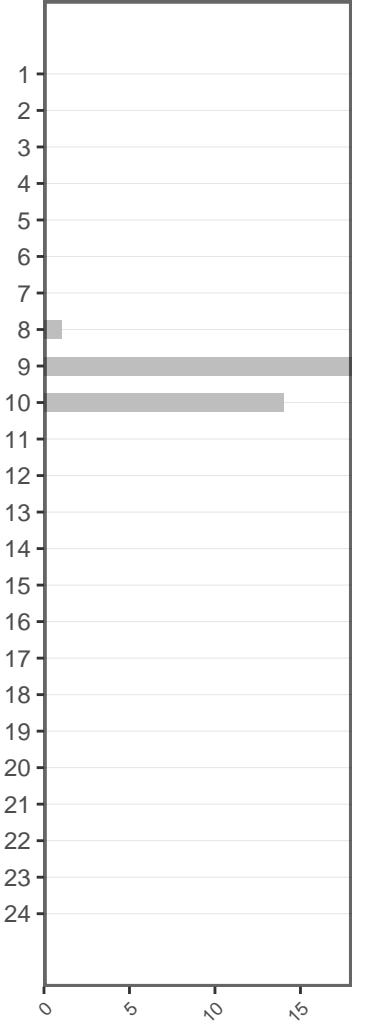
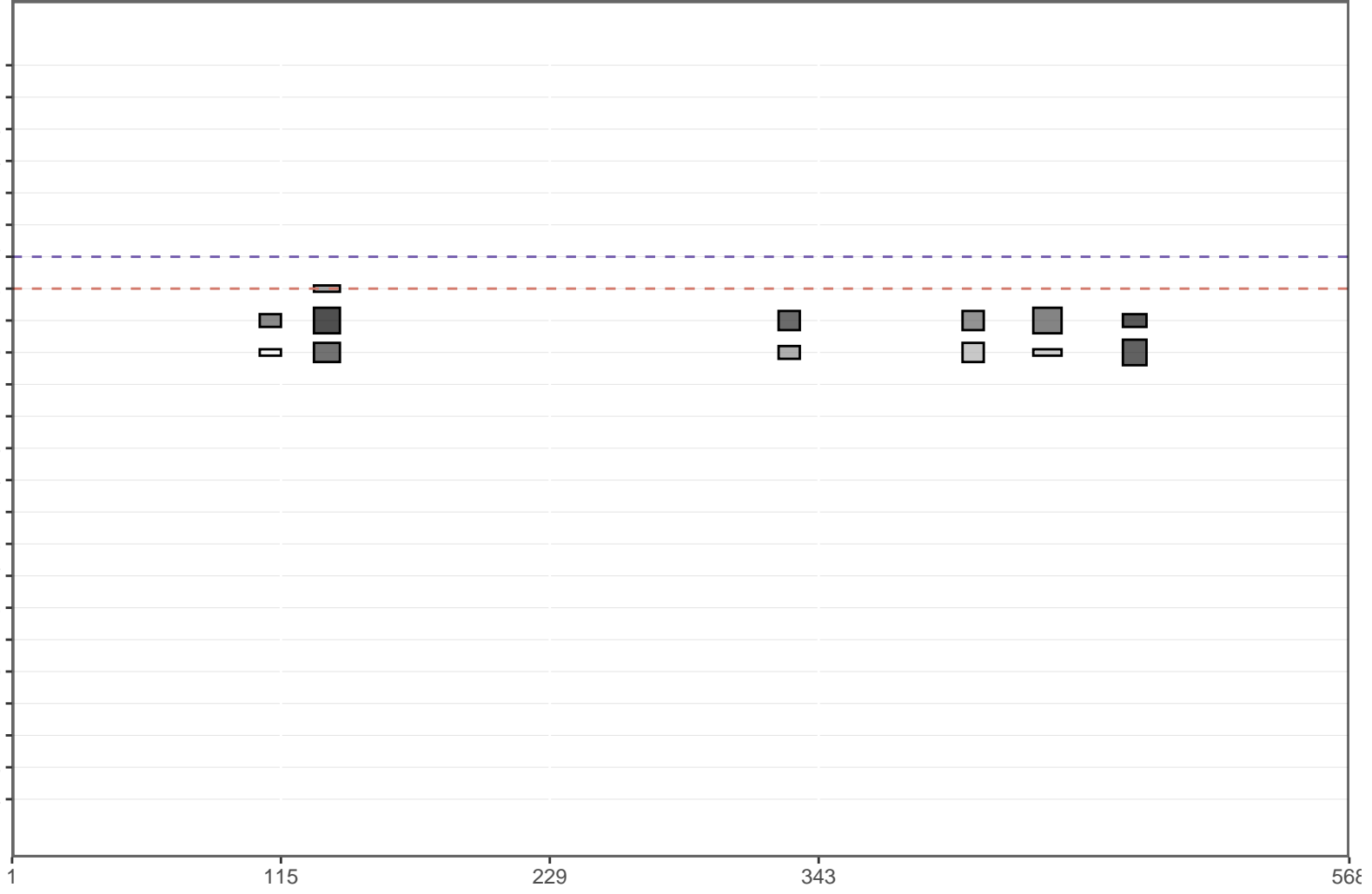
MW indication



Molecular weight

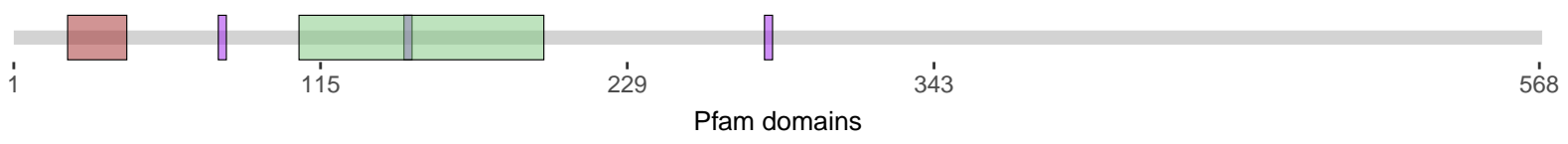


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MVYNSTEAVCMTRGRVASKKEAKKGNVYINBVGWFKPWFYQHAGTALKRGEFVEYPTREYYHRHTRQLYWEGLLPLFGDQWVFRYLLGLWMPKPVSLKATGGEAIRNYYHDMVYDGLLVPYKVGDALEWHHREMEVYPIWLGPHRLYRLPLKTMVYPEPFELHRRGGDTPYAGMYTDVGVYAPKPLRGEVYDGAEAARGLNWLLENHGFQDQVWSELTEKNFWRMFDAGLYEHCRNKYRAIGTFMBSVYKSKGKKEKEVQDAEQETALETPEV

NbL12g03730.1 photosystem_I_P700_chlorophyll_a_apoprotein_A1 [MW = 141.14 kDa]

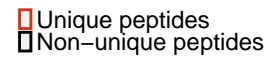
No. of times detected



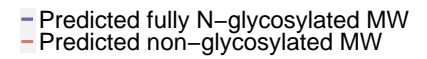
log(intensity)



Values from



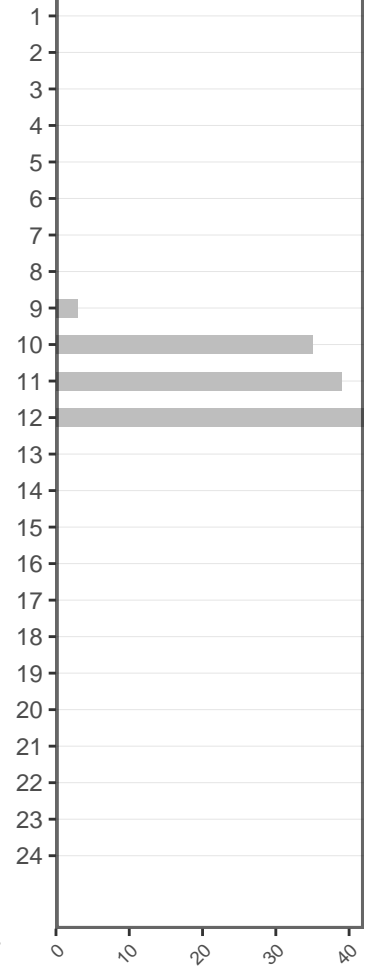
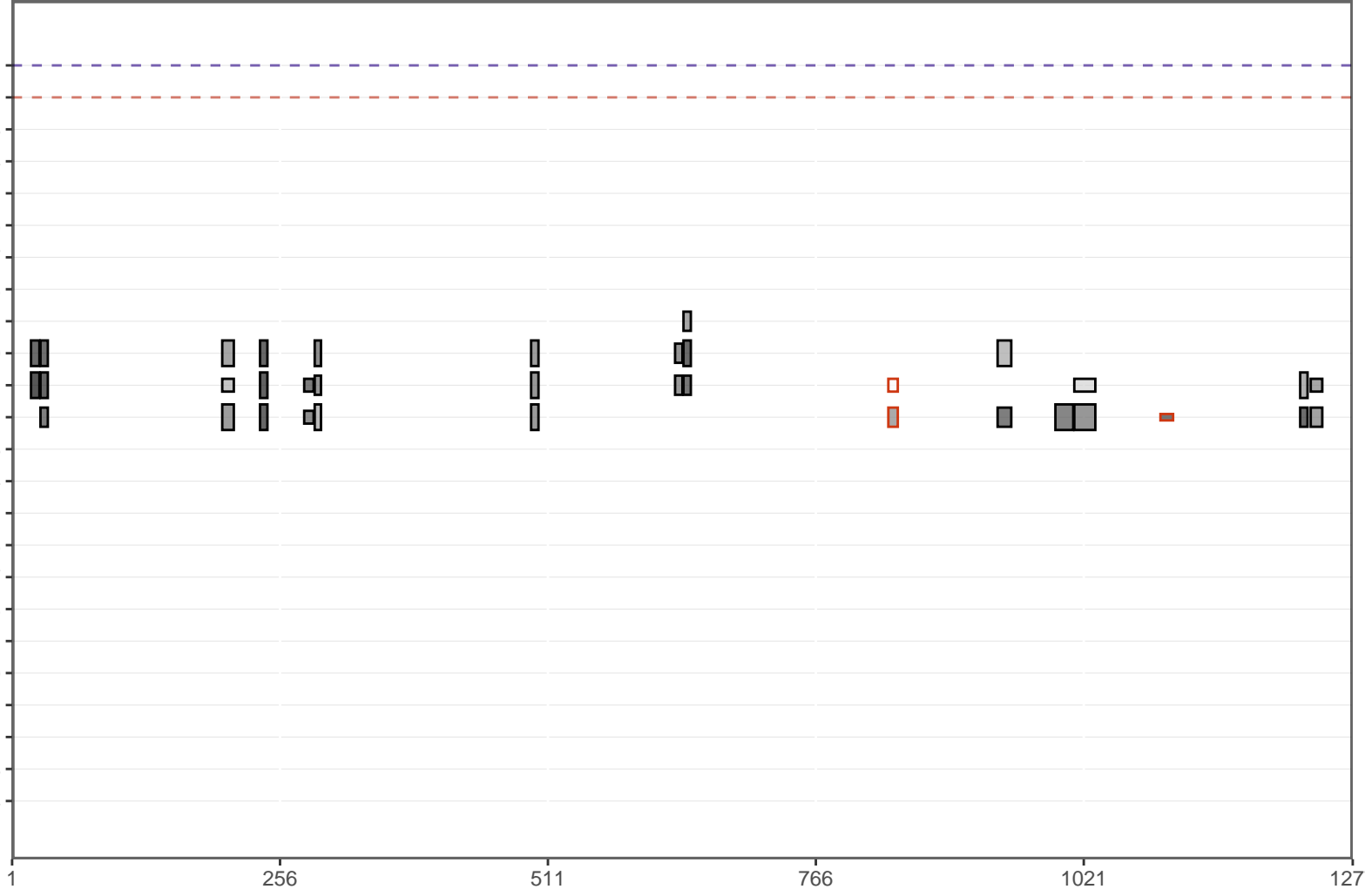
MW indication



Molecular weight

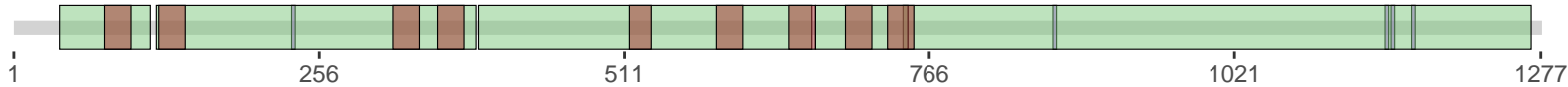


Gel Slice



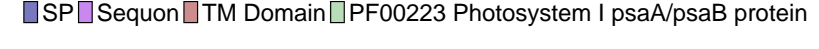
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MAINLKLVAIPATCPRALSIQGRVGVTHYLLGGIATTWAFLLARIADPLHVRPIAHAIWDPIHFGDPWEAFTRGGALGPVNIAYSGVYQWWTYIGLRTNEDYTGALFLFLBAISLIAGLFGVSSLAWTGHLWHVTPASRGESMESLGNPDSSSHLFGTAQAGATLTLGGFHPQTGSLWTDIAHHLAIAFIFLVAQHMYRTNFNGIHEMKDLLEHPPQGRILGRGHKGLYDTNNSLHFQGLGLALASLGVITSLVAQHMYSLPWFVFIADFTTGAALYTHIQYAGFM

NbL12g03720.1 photosystem_II_CP43_reaction_center_protein [MW = 51.98 kDa]

No. of times detected



log(intensity)



Values from



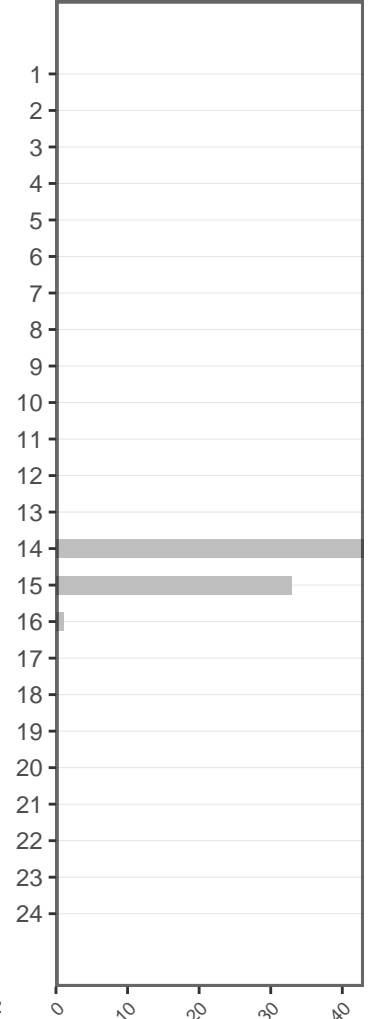
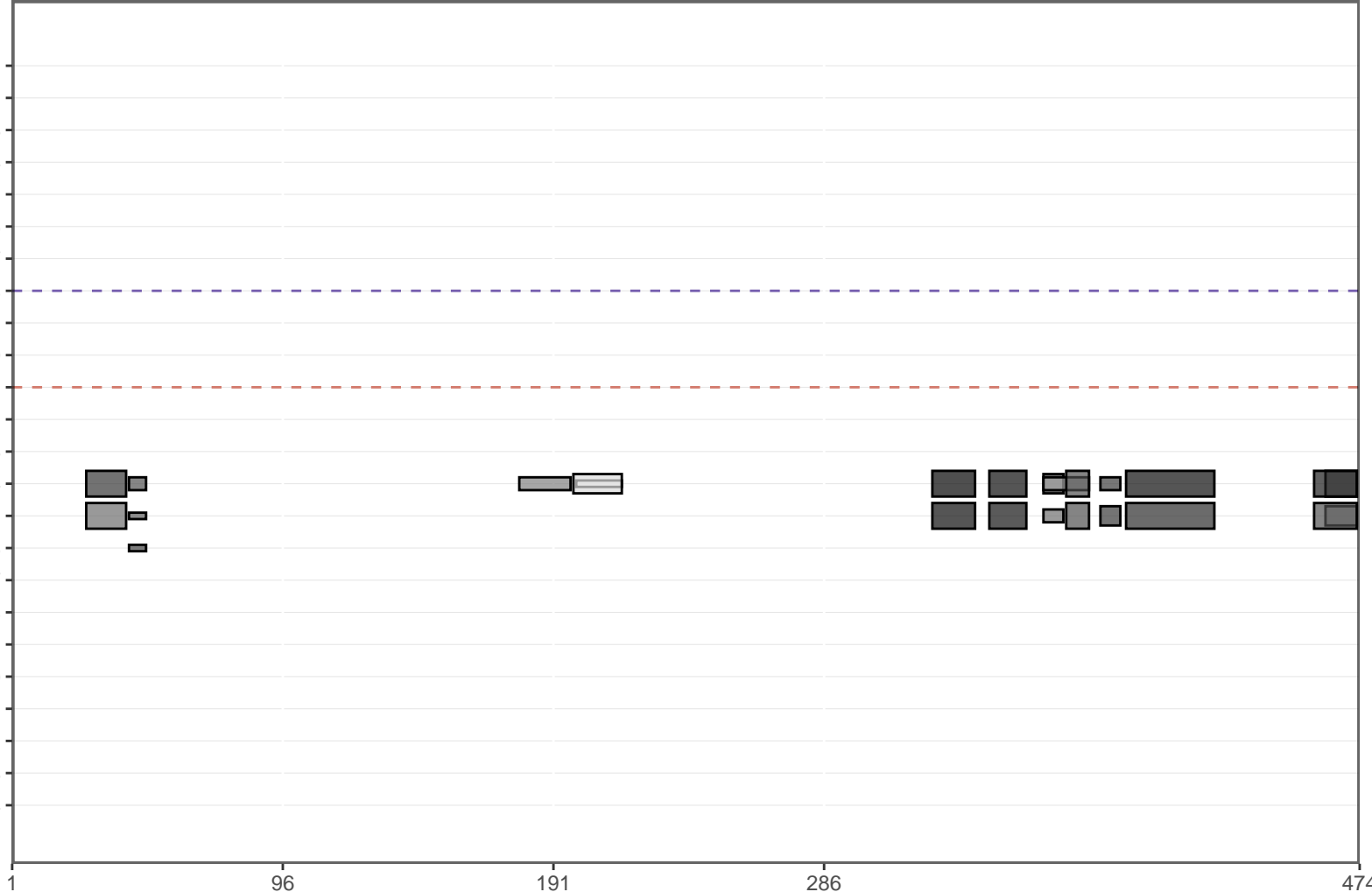
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

VDLEDDIGGHVYLGGSGILGGWHILKTPFAWARRALVWSGEAYLVSILGALSVFGFIAGCFVFNNTAVPSEFYGPTGPEASQAGAFFLVRDRRLGANVGSAGSGPTLGLKYLMRSPRTGEVIFVFGGETMRFWDLRAPVLEPLRSPNGLDLSRLKDKQIPWGERRSAEVMTHAPLGSLSNVGGVATEINAVNYSRPSGLATSHVFLGFLVGHVHAGRARAAAAGFENGIDRDFEPLVMTPLN

NbL12g03690.1 ferredoxin--NADP_reductase_root-type_isozyme_chloroplastic-like [MW = 41.95 kDa]

No. of times detected



log(intensity)



Values from



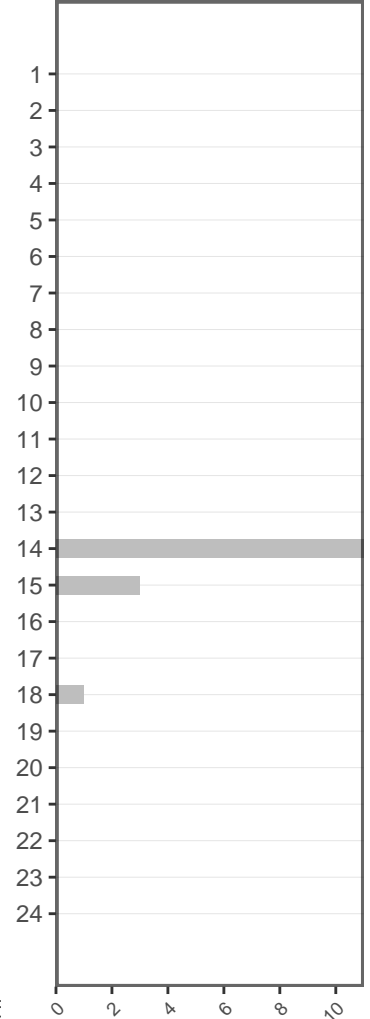
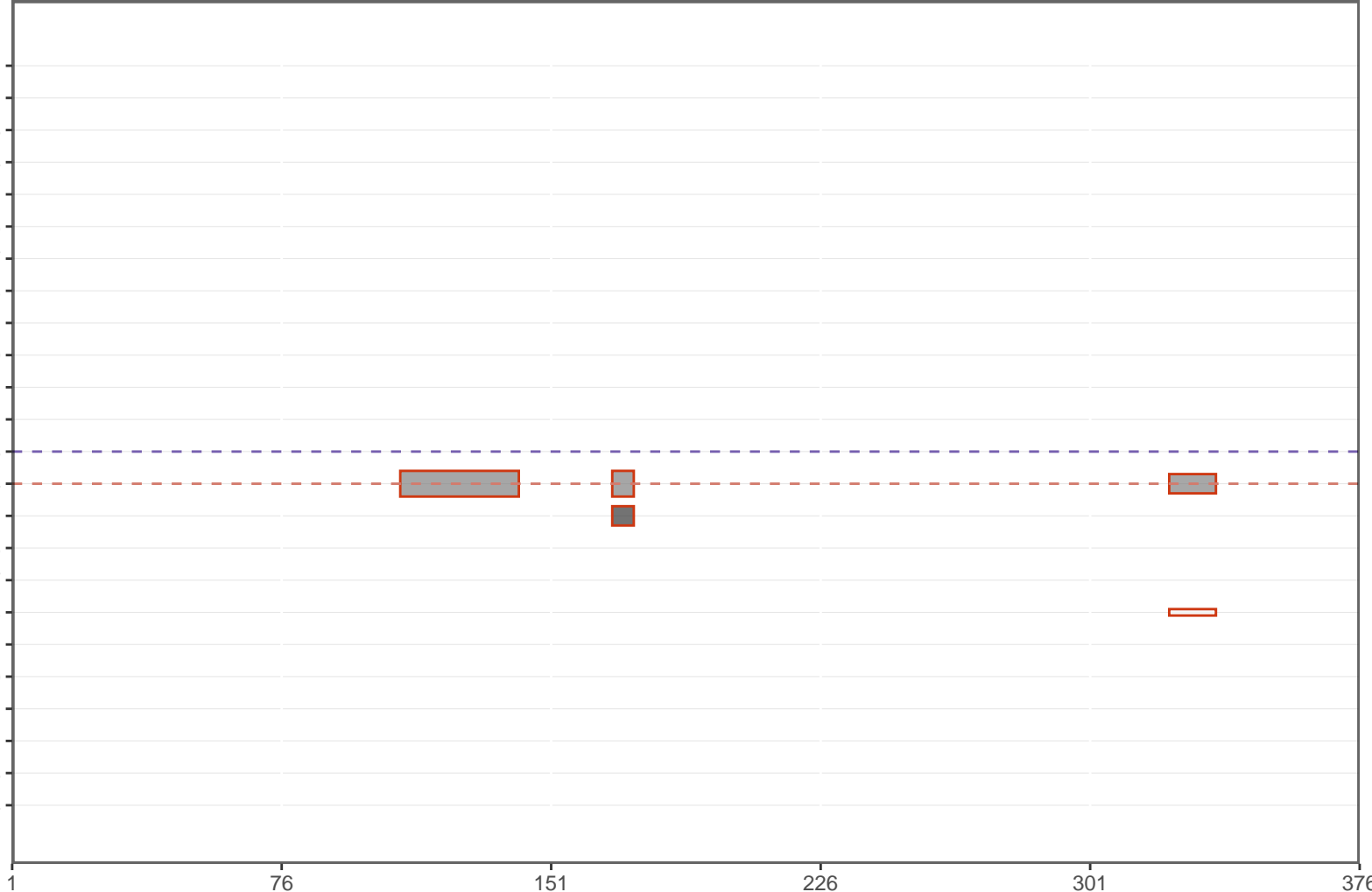
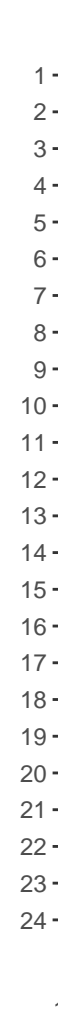
MW indication



Molecular weight



Gel Slice



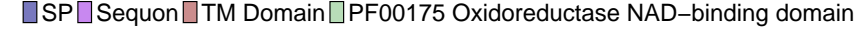
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

YYDPETGKEDPSKNGVGSNLFGLSDSKPGDKVYKTFPSGKMLLPEDFNATHIMGTGTGVAFPRGKYLRRFMESGVPTKFNGLAWLFLGWANTDLSLVDDEFTKYLNDYPCNFRYDRALSREQNKKNGGKMYVQDKIEEVSDEIKLLDEGAHYFGGLGKMMPGHDTLKRVAEGRGSEWEGKLSQLKKKKGWHVEVY

NbL12g03650.1 C-factor-like [MW = 32.61 kDa]

No. of times detected



log(intensity)



Values from



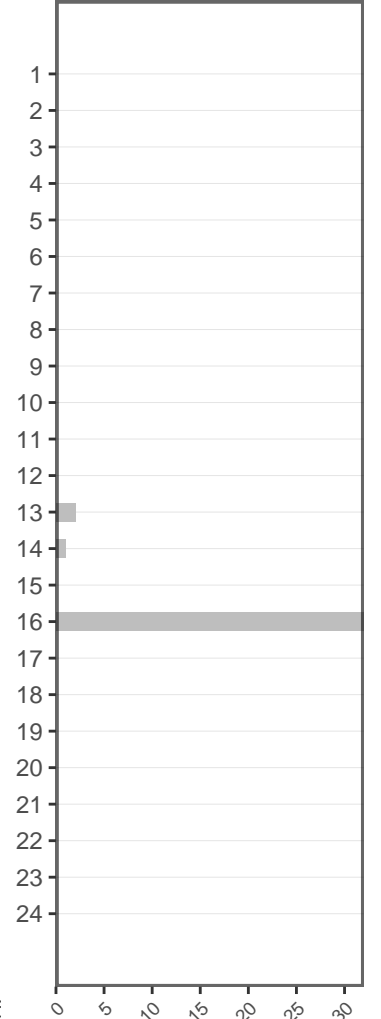
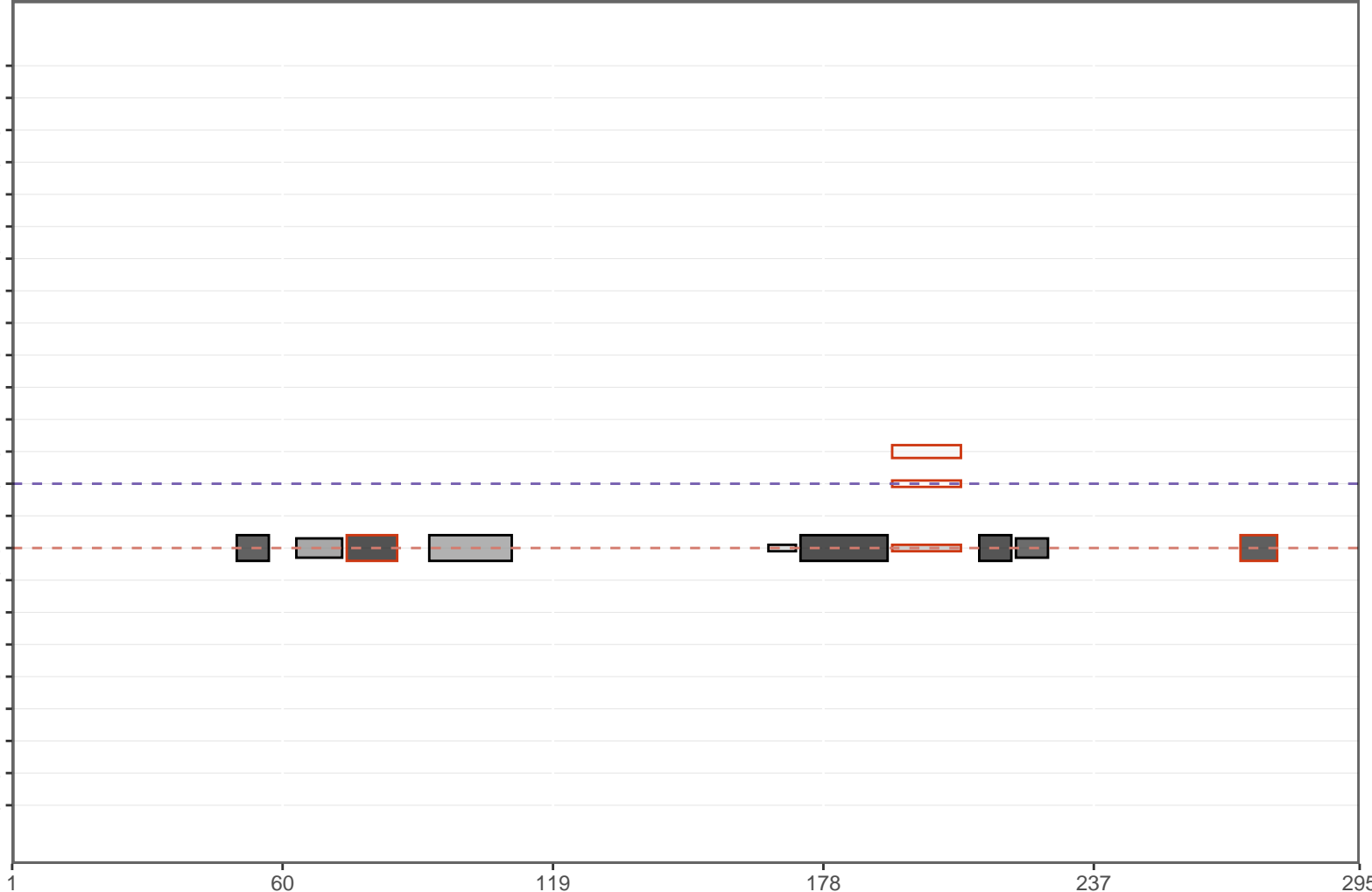
MW indication



Molecular weight

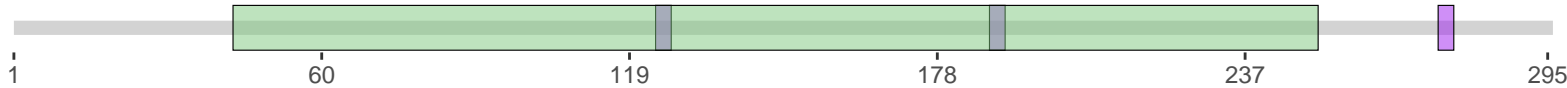


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VMPETTLKSVORBSLLLAYDINAVGFLVIRKHMWPLLKAGGGSGTKDFAVANLSARVGGSDNSLGGWHYRASKTALNGLTKNVAVEFARKKDPKIGLLHPGTVDTDLKPFQRNVPKELFTKEYSVQKLLGIINNTKRDNGKFFFAWDAQGIPIW

NbL12g03630.1 obg-like_ATPase_1 [MW = 44.37 kDa]

No. of times detected



log(intensity)



Values from



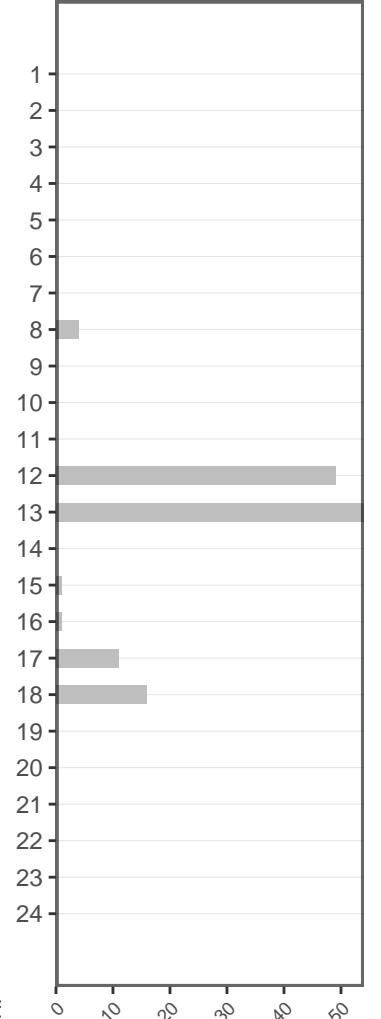
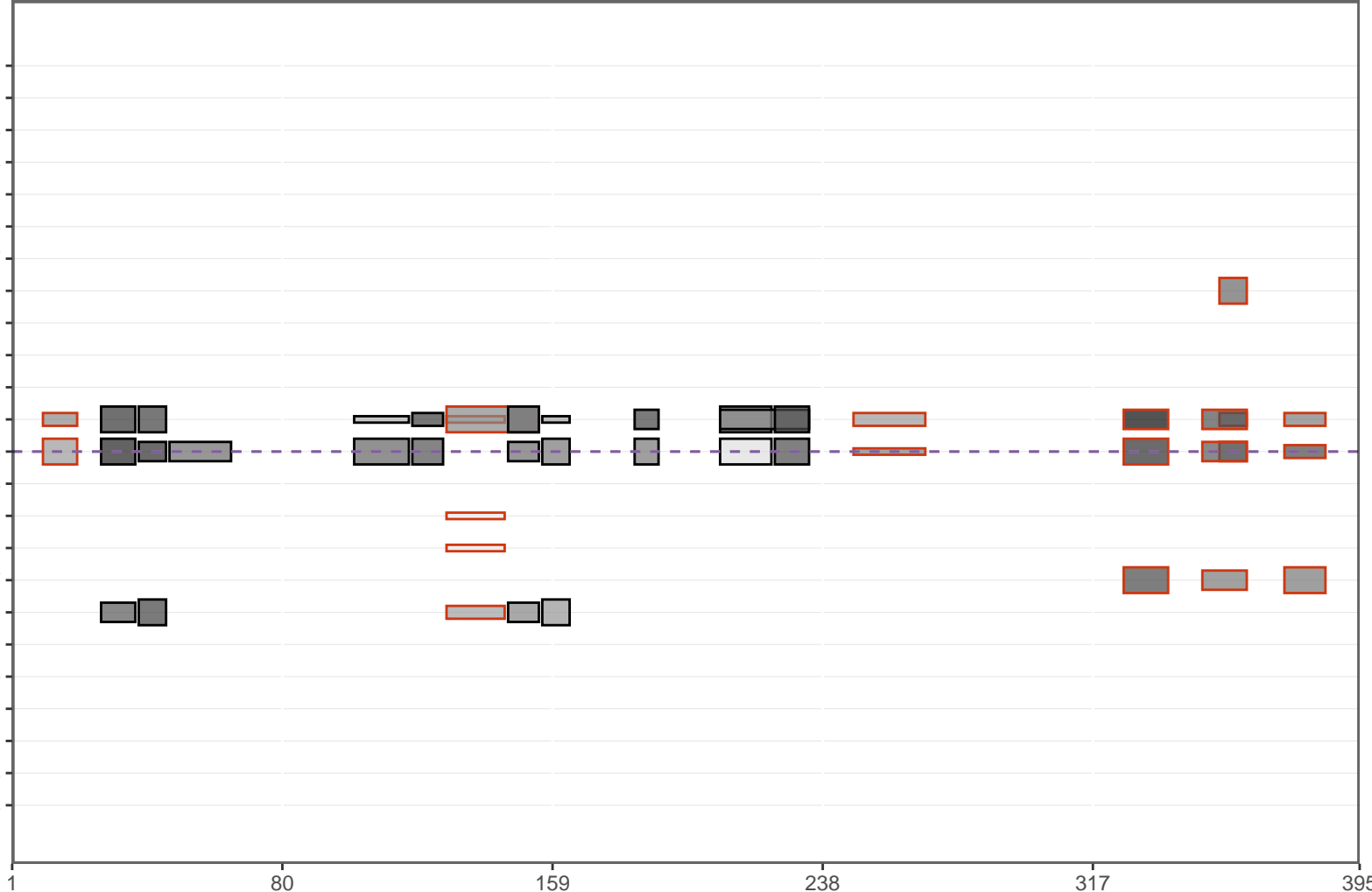
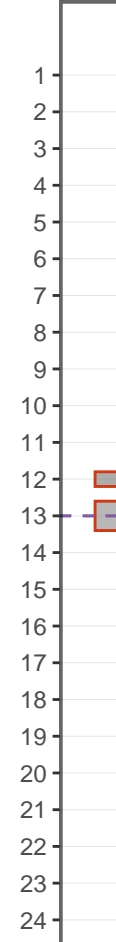
MW indication



Molecular weight



Gel Slice



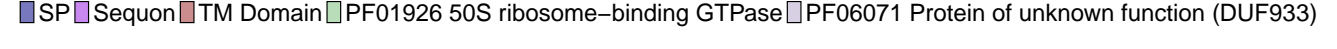
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LSLRVMSLKEGKDRLDGDKAAADVEFLNTFQLTAKPAPVYLVNINNEKDWARKNKKFLPKHAWVQEHGSGEIPFSAVERNLADMPDDEASKYGEENLGGGLPKIKTGFAINLHYFTAGPDEVWQWIRRLMKAPGAAGTHTDFERFGICAEVMKFDLDELGSEAAKAGKRYGEGKTYVVDGDDIFFKFNVSGGGKK

NbL12g03540.1 reticuline_oxidase-like_protein [MW – SP = 58.63 kDa]

No. of times detected



log(intensity)



Values from



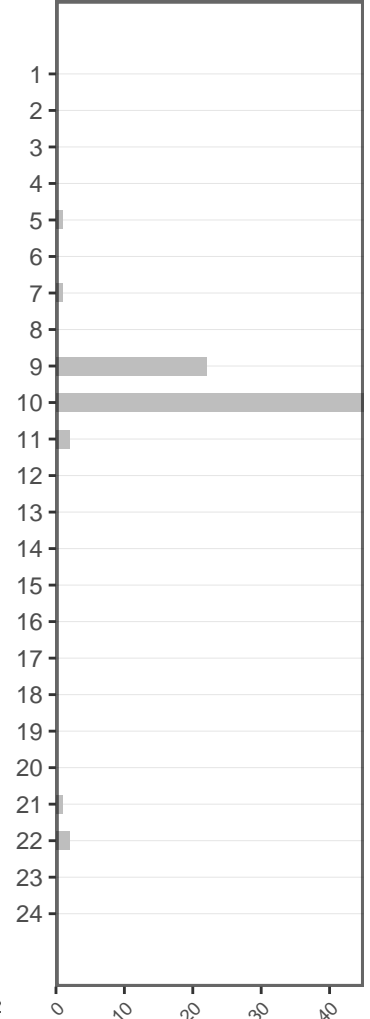
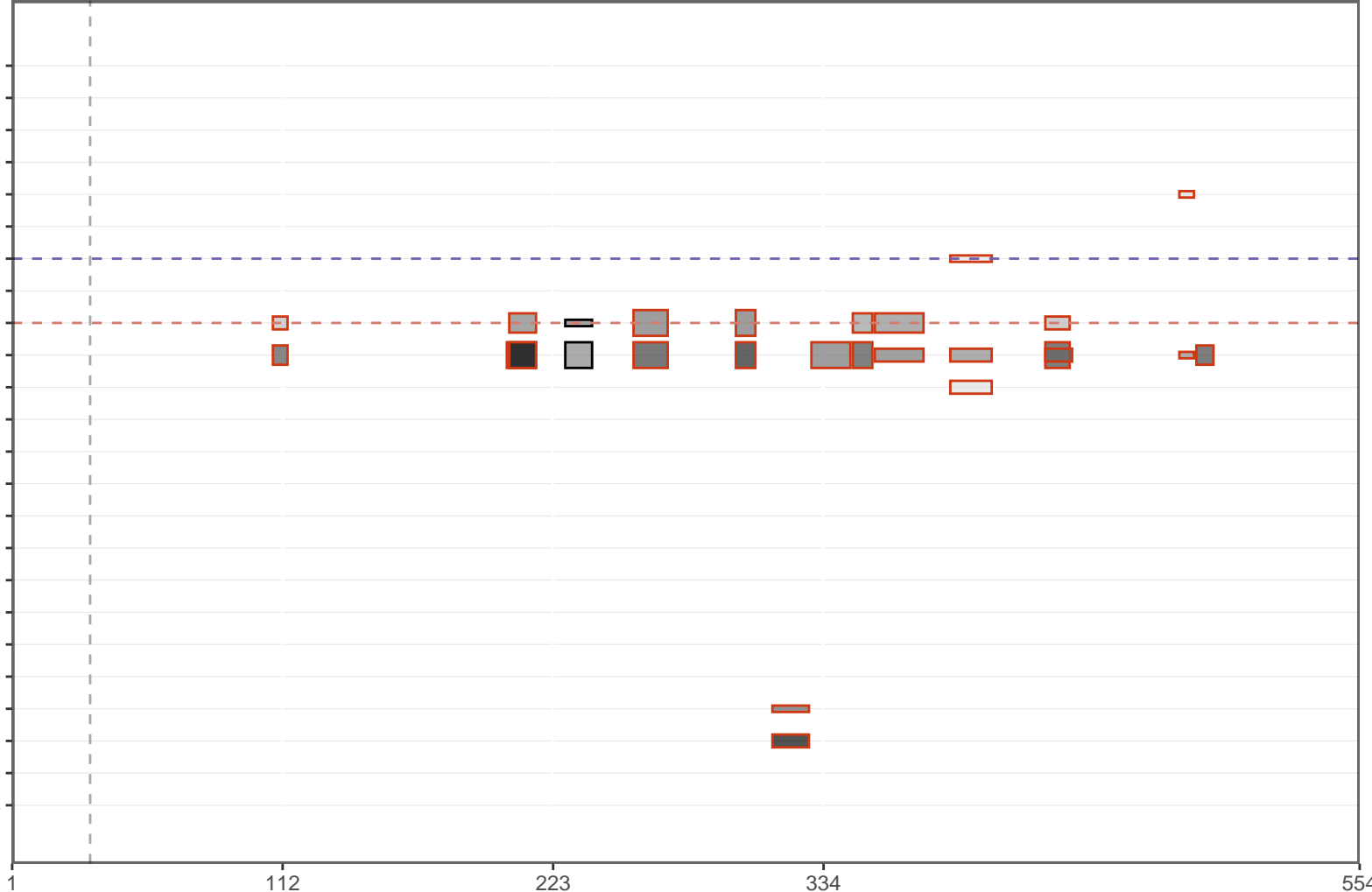
MW indication



Molecular weight

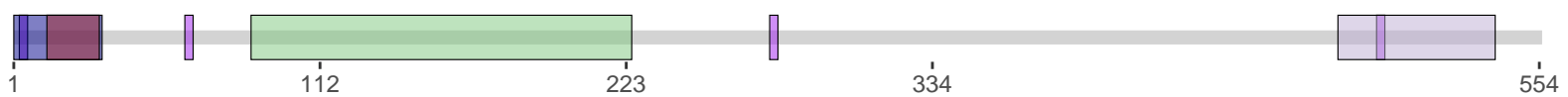


Gel Slice



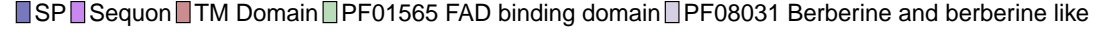
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VFTVPKTLQNGTKIKYKGGVADKIDKDFIRVIMNIVDKKDKKGEKTIQMAVNSLFLGTSDRLLKLEIMNENFELGLTGKDKTEMSWIKSILVAGYDPTPEVLLGKSLFNKFKAKSDPKVKEPIPEDGLEGLWLRKLMEEEDPLMWNPNFYGGMMAKISESETPFPRKGVYIMVQYTLWNPDKELATHFDWIRRLVNYMTPVASMFRQAVVAVRDLDELGNKNGSSSFQASWGNKYFNKDFNRLVKVKTKVDPENYFLHEGSIPTLPIRNGKQKSMVQ

NbL12g03520.1 reticuline_oxidase-like_protein [MW – SP = 58.91 kDa]

No. of times detected



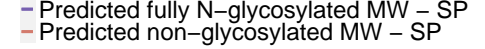
log(intensity)



Values from



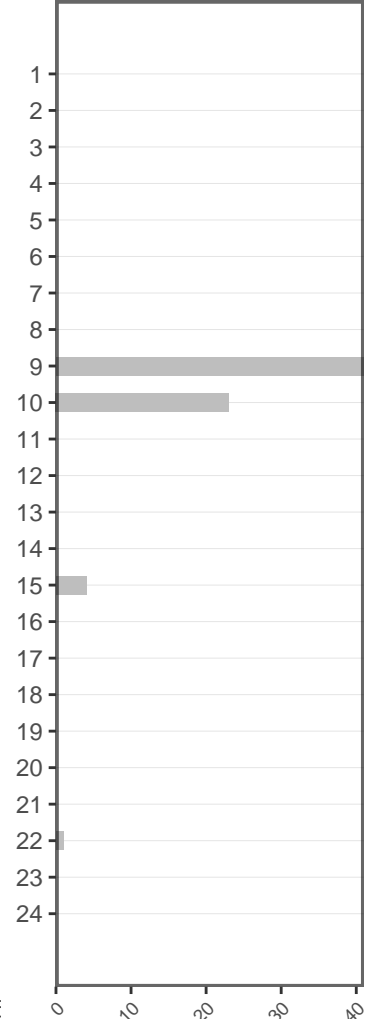
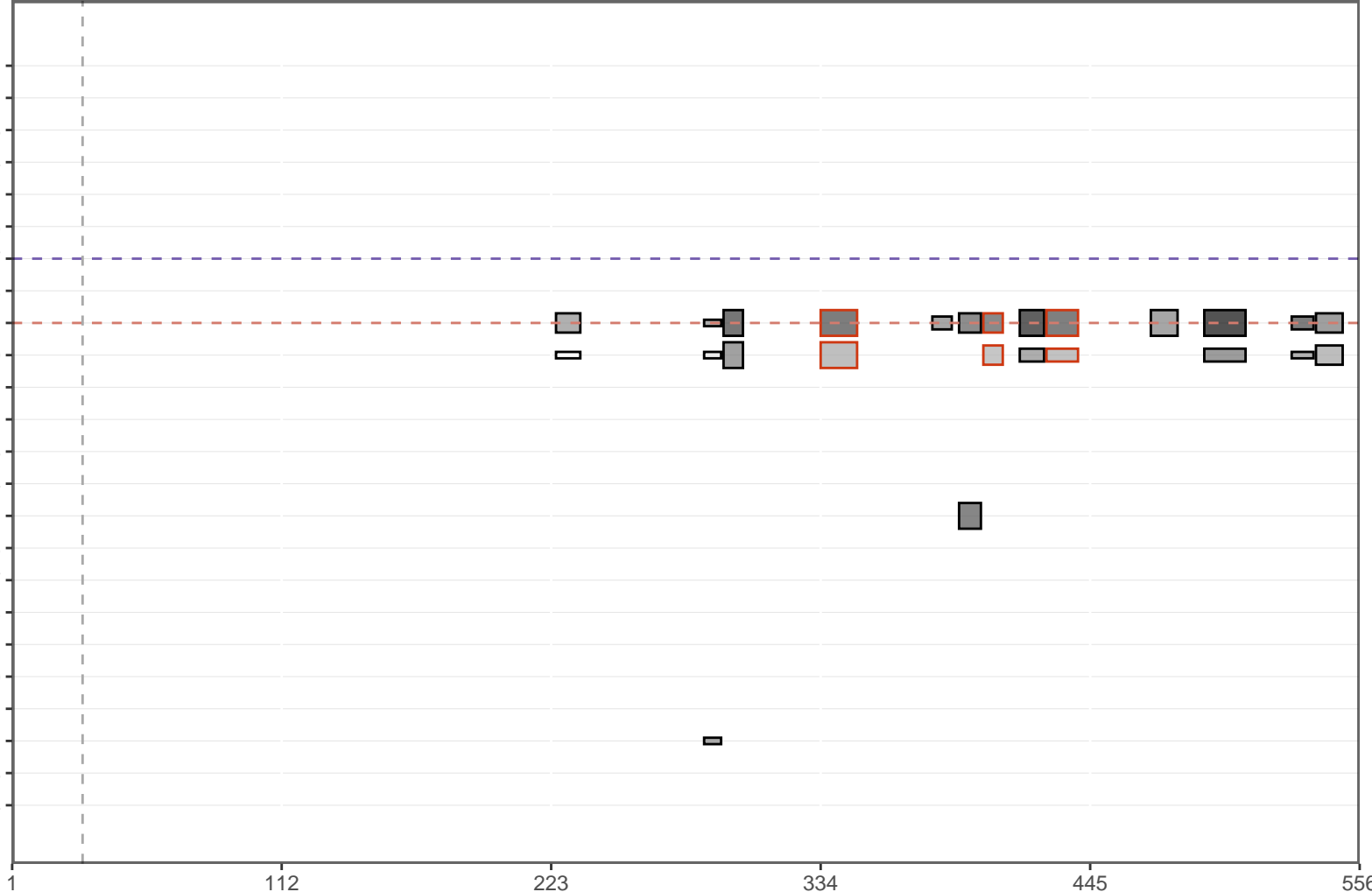
MW indication



Molecular weight



Gel Slice

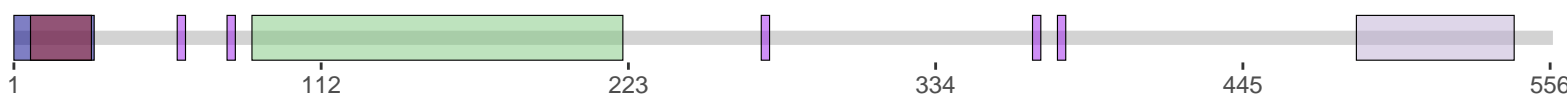


Protein length

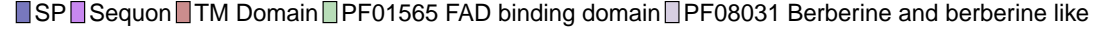


Peptide counts over 4 repeats

Pfam domains



Pfam Description

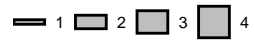


Protein sequence:

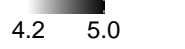
FLDQNTDAVLOWGNYVANKIDNLFIRLLWQPTVKNKKEKVKWGHKNADGKSRIVTFIALFLGDSRLMSLVSNELFALGLTKGDFEMWDSVGLWANFDNFKPIALLNRTSDPLNFKRKSQVYQEPNPRDVLSEIFQKMSLGGKAGLVFNPNYQGRMTEIPEGETPFFPRAGILEFKQGVVWVNEEGAAAEKEYLTKRDLVSMFTFVSKNPRQAVLNYRDLIDGTNDGGFHSLEEGRVYGTMYFNKFNFRDMKVKYKSAVDPTNFFRNESGIPDTGTTKPRXGCE

NbL12g03370.1 DNA_damage-binding_protein_1 [MW = 122.23 kDa]

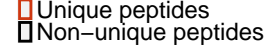
No. of times detected



log(intensity)



Values from



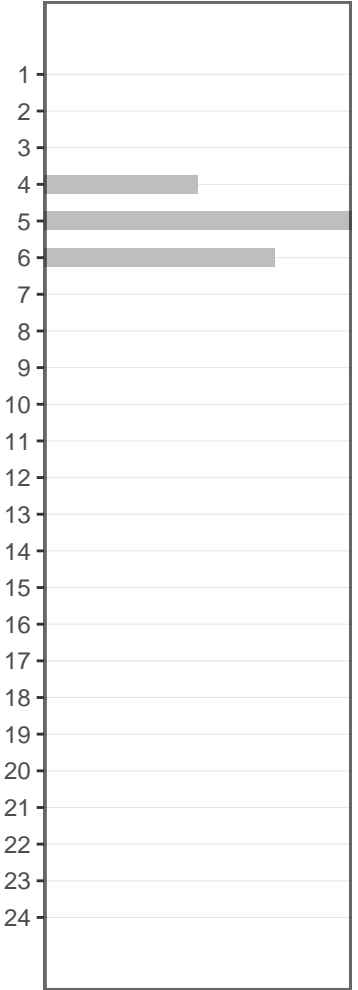
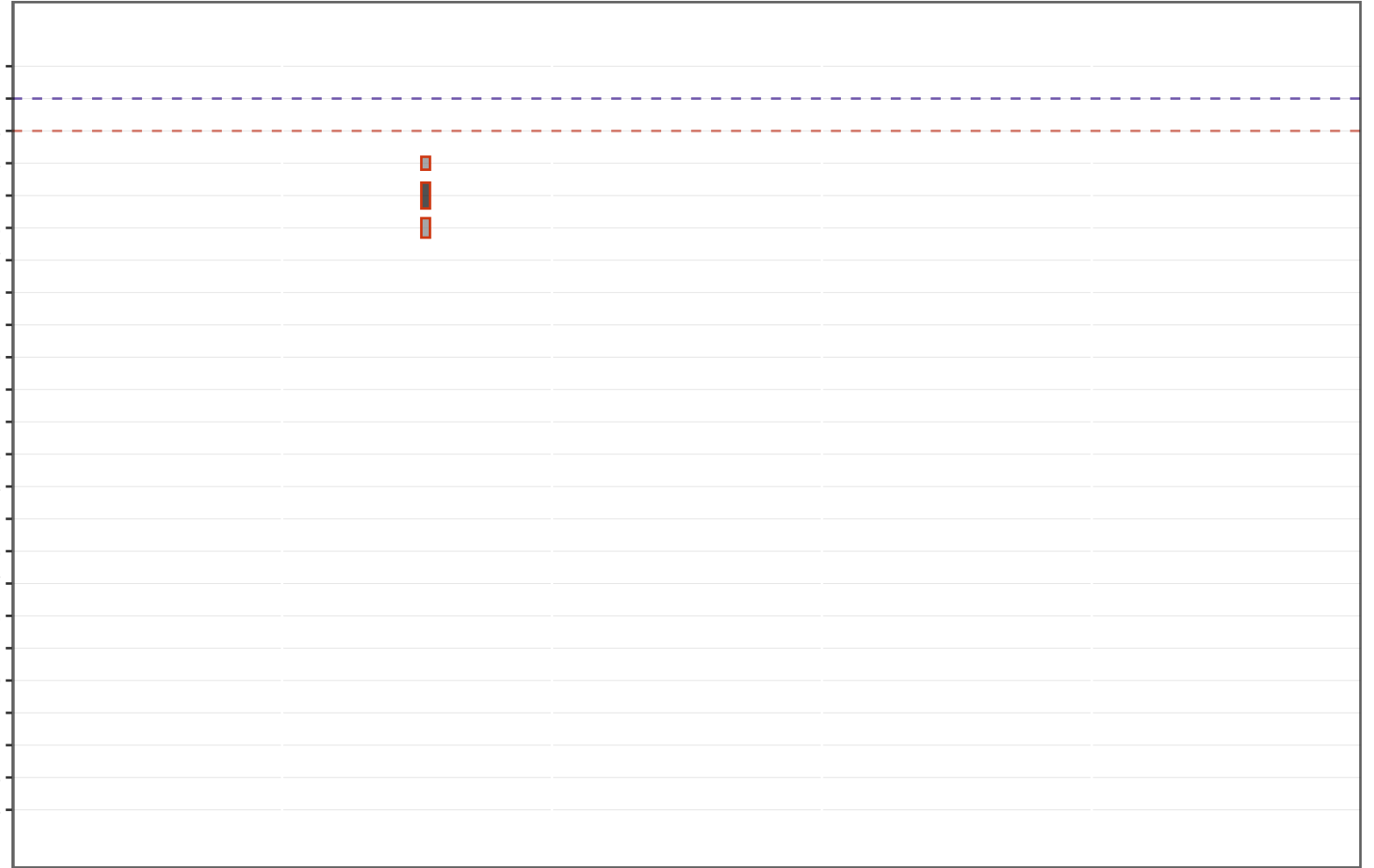
MW indication



Molecular weight



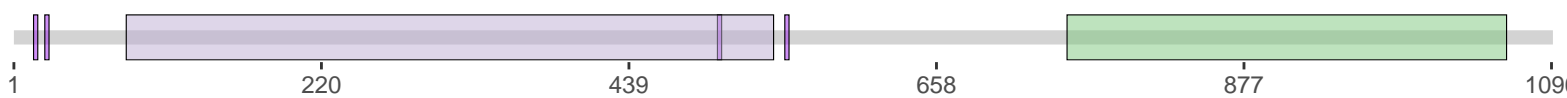
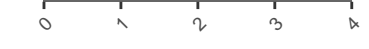
Gel Slice



Protein length

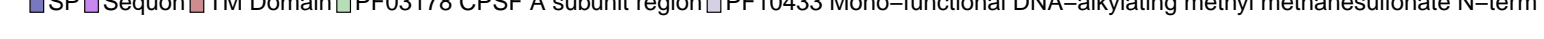


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

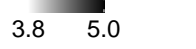
ISCLDNPIDENPNFQGMVGMWTDSEVRYSLPDLNLITKEGLGGEIIPRVLMGSEFEGISYLLCALGDGHLNLYLMSGGELTDRKKVSLGTQPIFLRTFSSKADATHVFAASDRPTVYSSNKLLYENVNLKEVSHMCPFNVAAPDGLAAKEGELTGTIDGKLIHRISPLGEGHARRISHQEGTRTFALGSKWYKTSNADDPVEVHFVRLDDDTFERISTYPLDGFYKGGSLSGFSDDSTVYVGVGTAVVMPPENEPTKGRILVFIVFEDGKLGKLAKEKTKGAVYSLNAFN

NbL12g03330.1 40S_ribosomal_protein_S4-like [MW = 29.86 kDa]

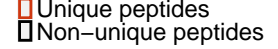
No. of times detected



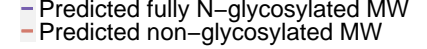
log(intensity)



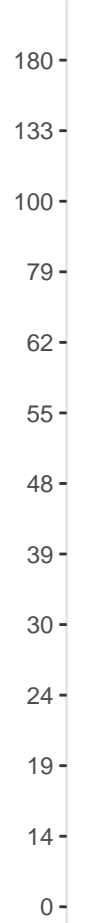
Values from



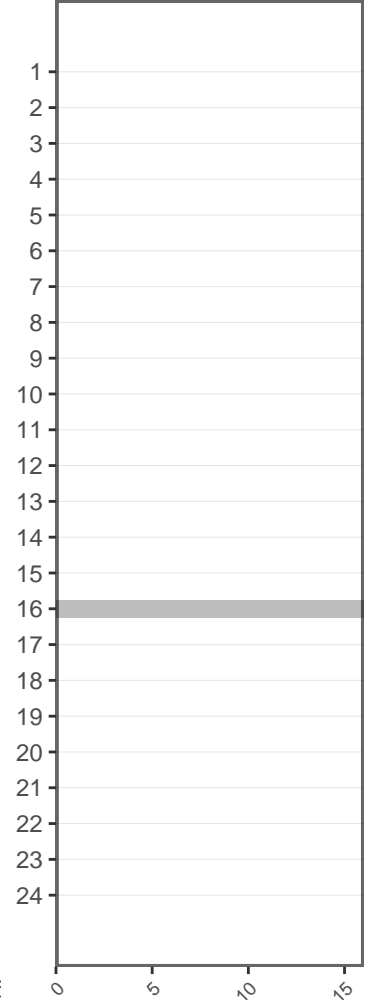
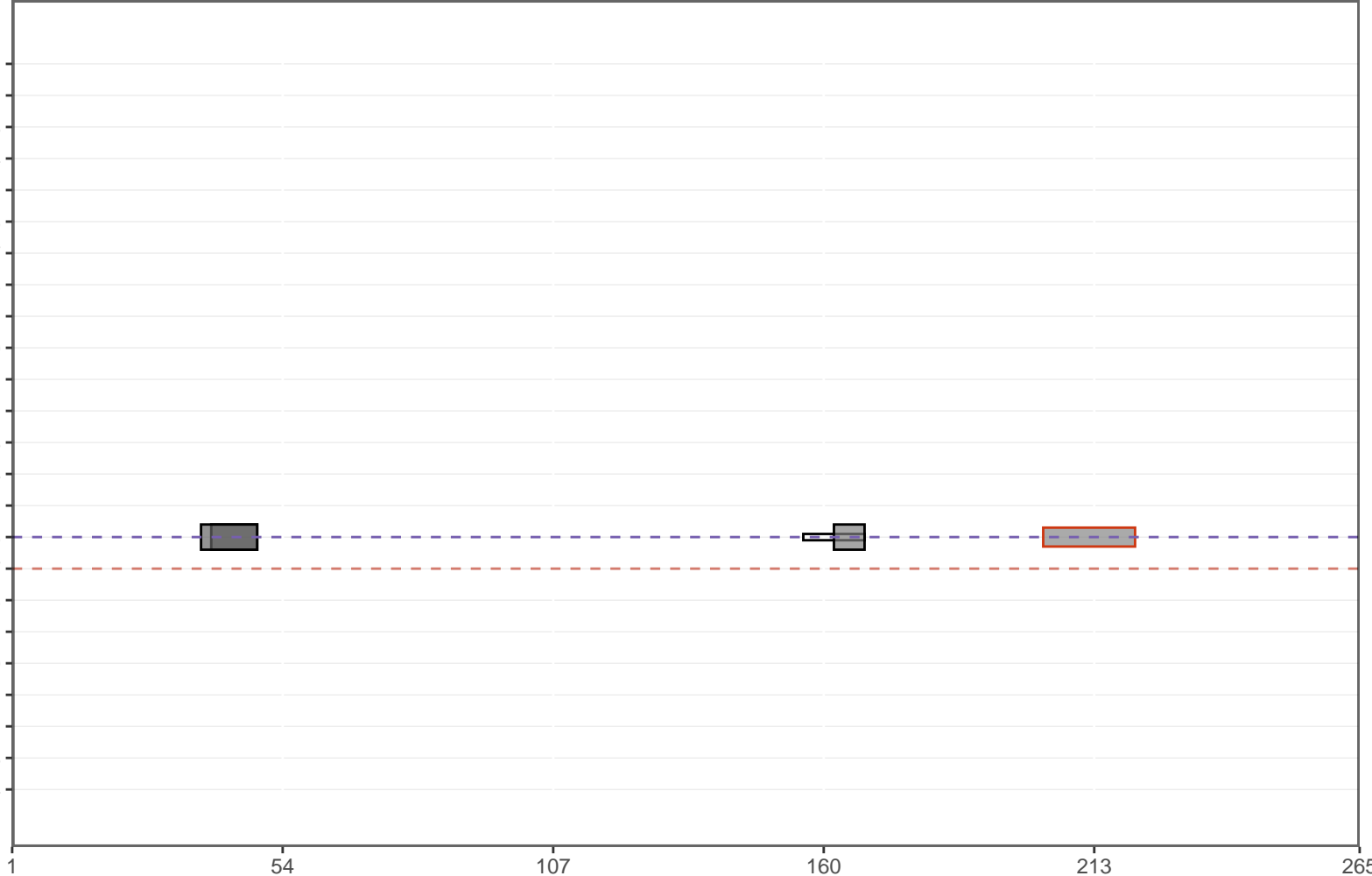
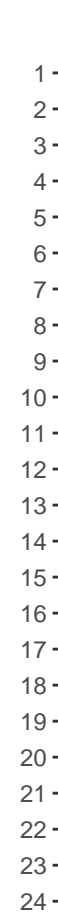
MW indication



Molecular weight

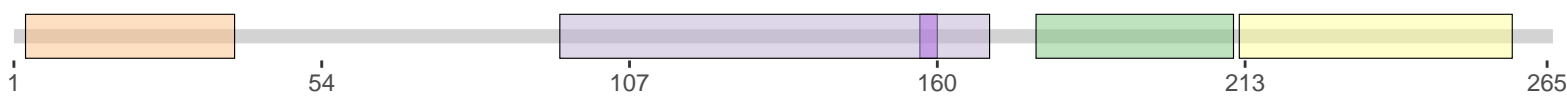


Gel Slice



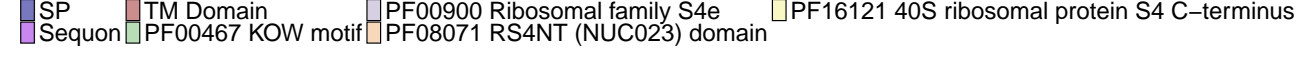
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IAKFKLCKYRSVYQFGGKGPINLNFYDGRTRYPDPLIKANDTKLIDLENNKIVDFIKFDVGNVMMVTGGRRNRGRVGVKIKREKHKGSFETVHHDDAGGHEFATRLGNVFLGKGTQPVWLPKGGKIKLSIEEARKRLAAGSATA*

NbL12g03250.1 UBP1-associated_protein_2C-like [MW = 43.84 kDa]

No. of times detected



log(intensity)



Values from



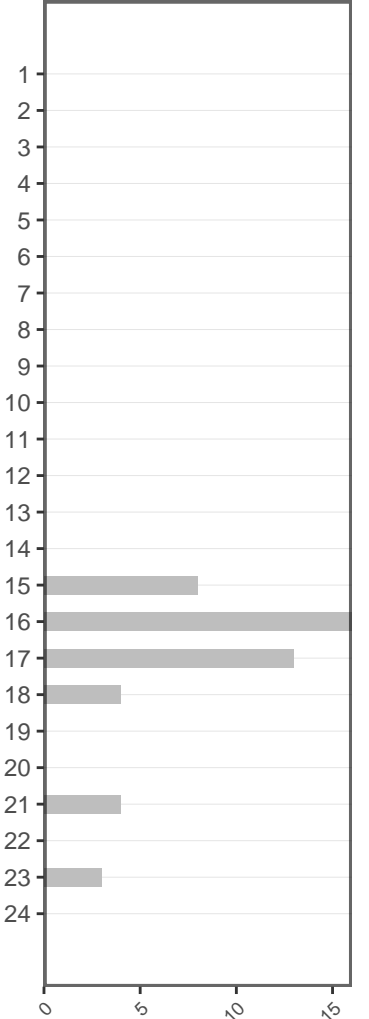
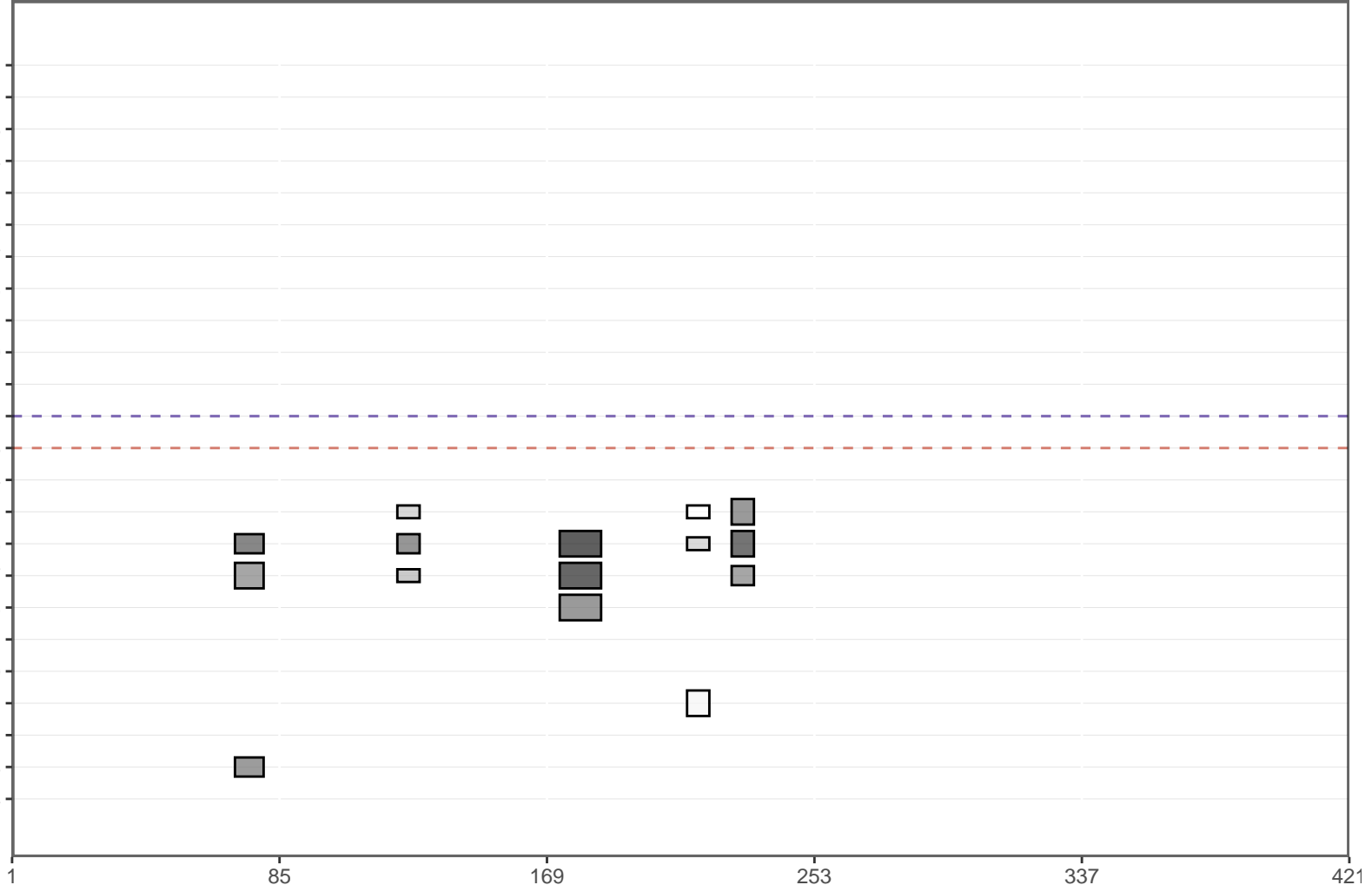
MW indication



Molecular weight



Gel Slice

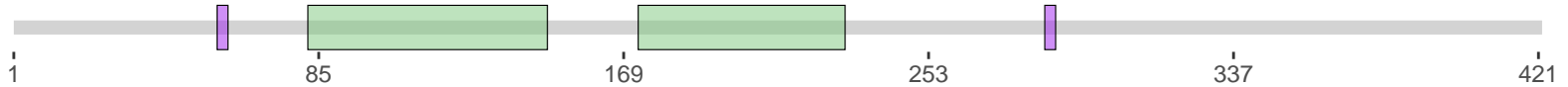


Protein length

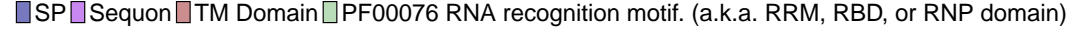


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IQIGKAGFAFFVYKTEEGARASLVDPKVTIDGHVLEKILATDNKKGKPHNTGPGGMPNTHPTGMPGDDRVGTMPGSGNYSVPVSGLGPYVGGGPGMGGPPPPPGMVAHQNHFPVGGVYGNCGPGFTGSAGYAGAGYGGGAGDHTGGLGNAGYRMPQNSAGMPSGGYFDGGNYGLGGYFSGVPPQPGGAVARVPPGGMVGMPFVY

NbL12g03230.1 p21-activated_protein_kinase-interacting_protein_1 [MW = 36.72 kDa]

No. of times detected



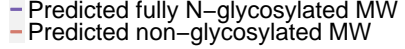
log(intensity)



Values from



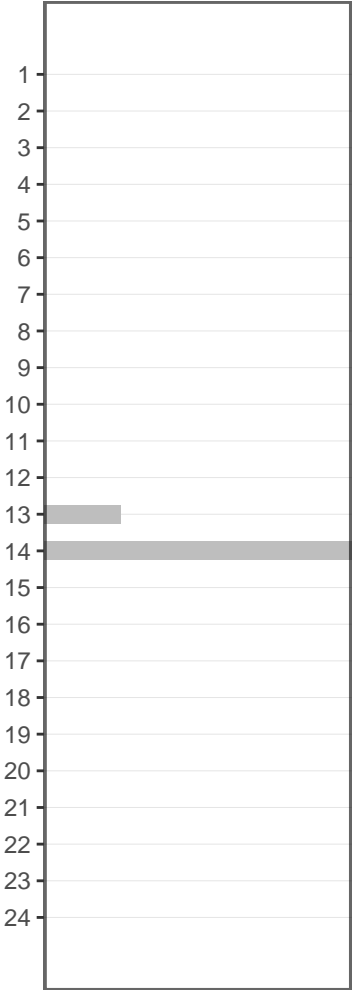
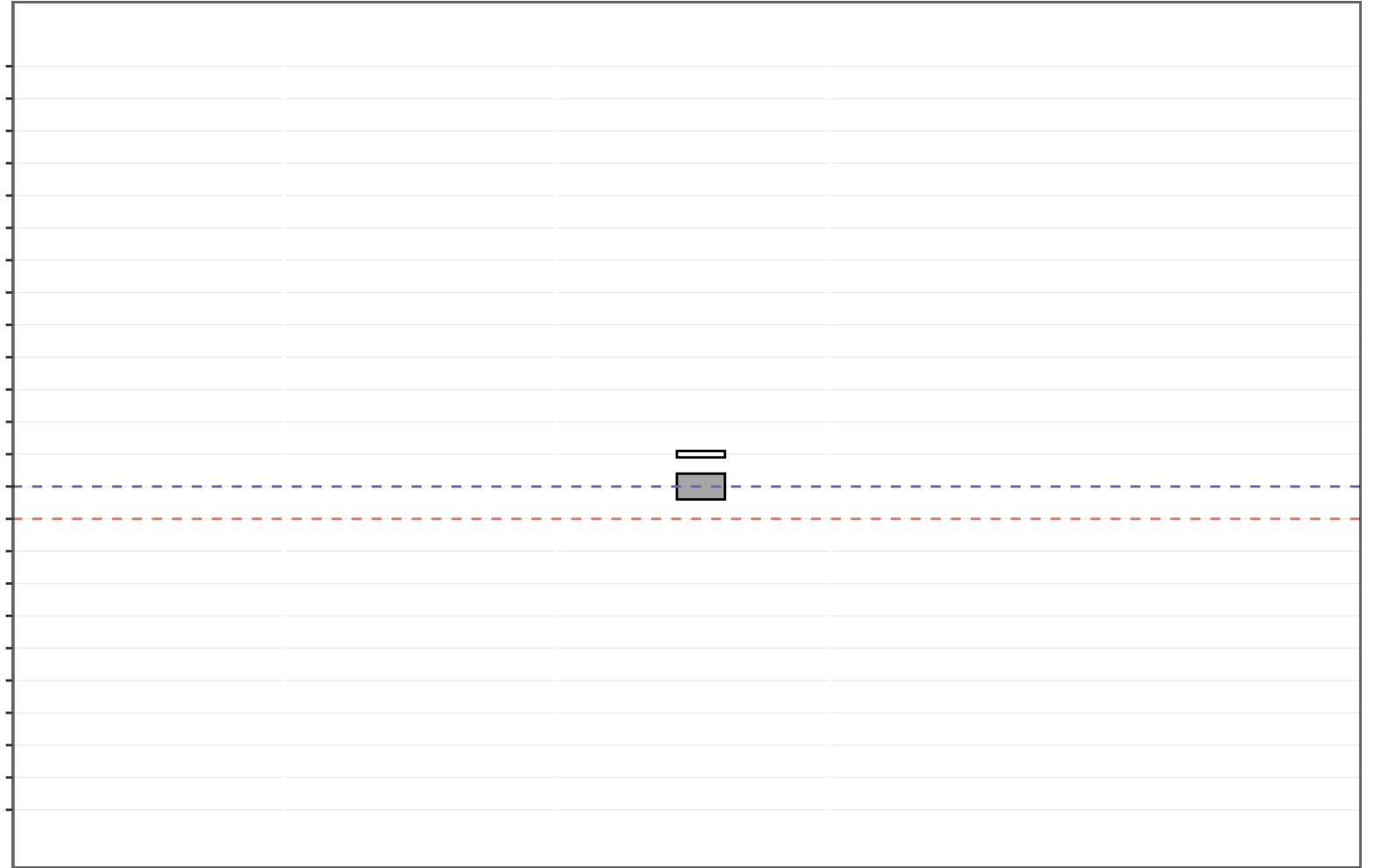
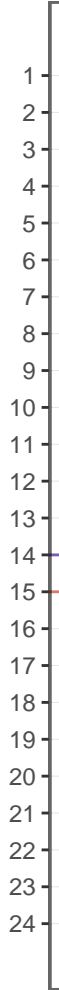
MW indication



Molecular weight



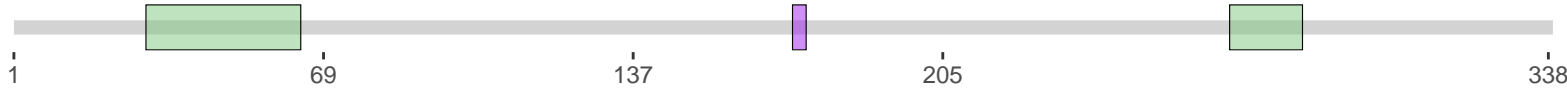
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

IRRSFYCRLLGKEASLVNYSSTGKPKFMVMDKDISVHESEDAKIIELDNKKVLCATPGTHGLFTGGEEIRKAWDITSGKVAVBIEDAHSTRVKGIVLVKNNDDGDAEENGHIVASASGGDIRVWDVIRMTREKPKPLAEANTKSRLLGLAGSSIKVKKRFLVGNATASNGOGLDAGEES

NbL12g03200.1 uncharacterized_LOC107786033 [MW = 24.77 kDa]

No. of times detected



log(intensity)



Values from



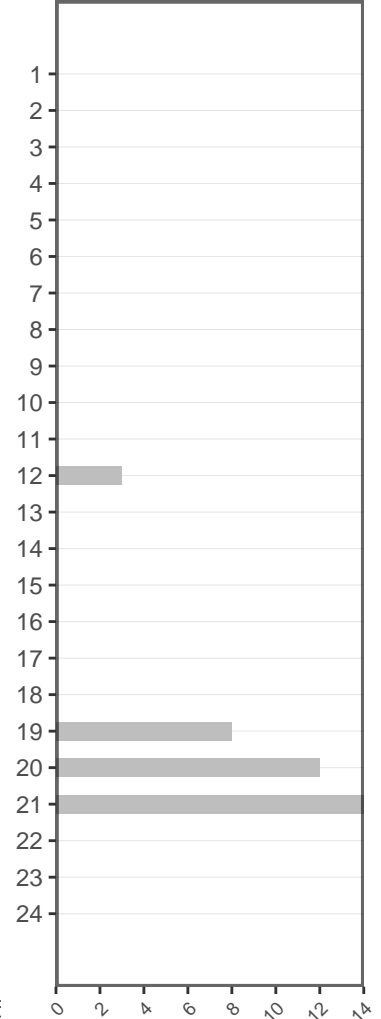
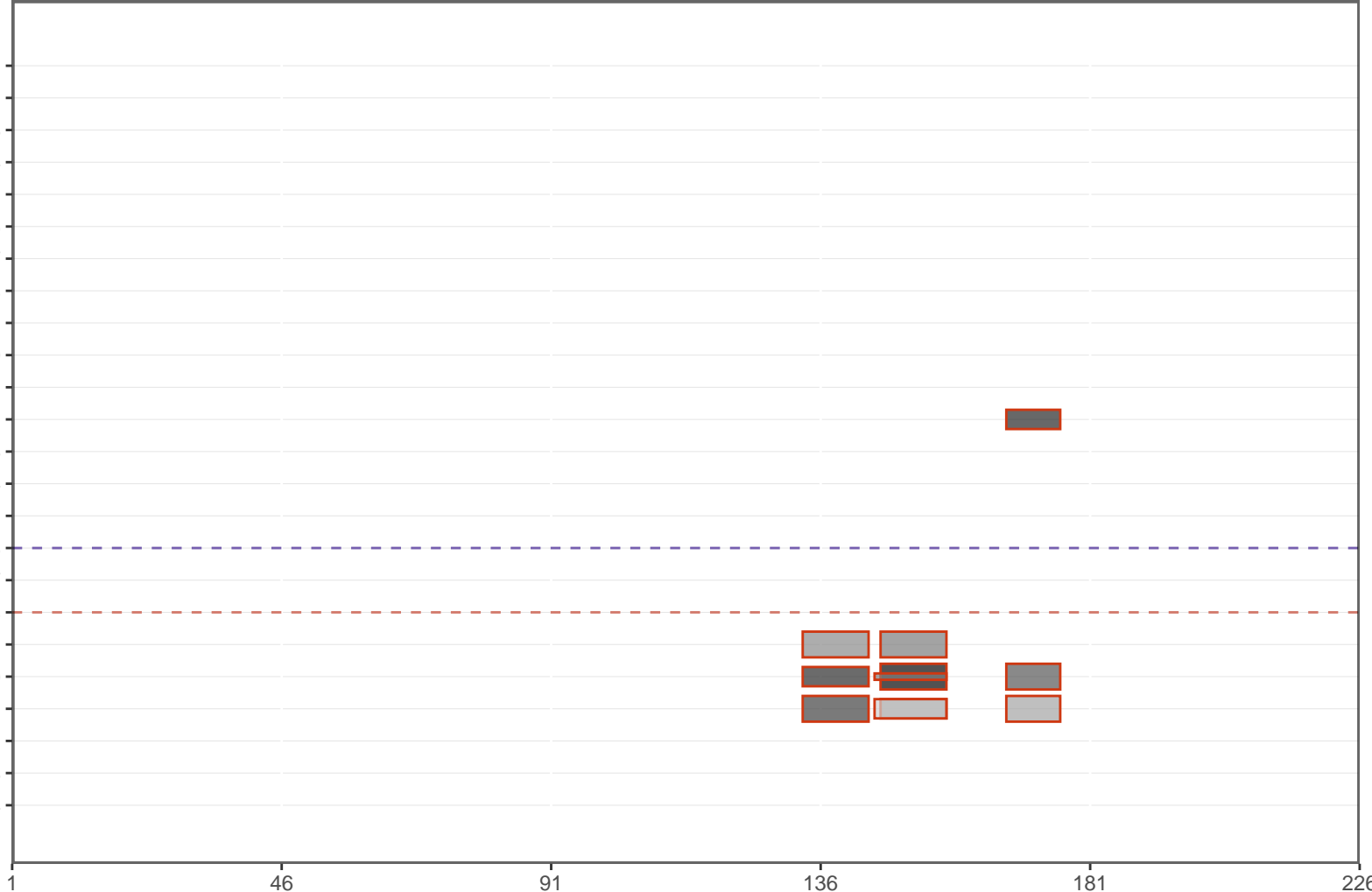
MW indication



Molecular weight



Gel Slice



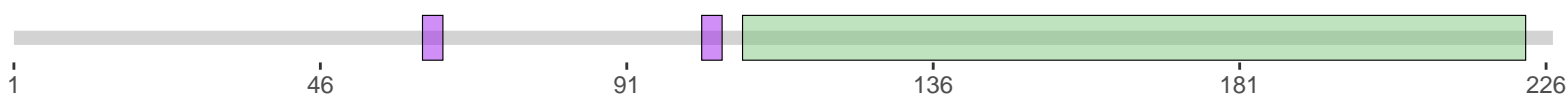
Protein length



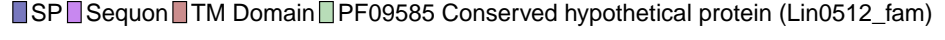
Peptide counts over 4 repeats



Pfam domains



Pfam Description

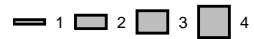


Protein sequence:

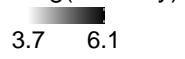
NSSMTLLFVEMGVGVYDQHGDDTSAAAMRACKNAISNBIPAFRRGSPGVSEFQMKLQKLGVRPFLGGSLDLEKVKVFFPYGRLLIEVVDGLICSGGVQVEDMGDKNDGHWNAAYVDY*

NbL12g03170.1 proteasome_subunit_alpha_type-5-like [MW = 26.08 kDa]

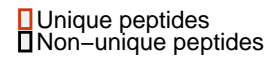
No. of times detected



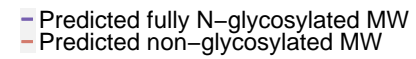
log(intensity)



Values from



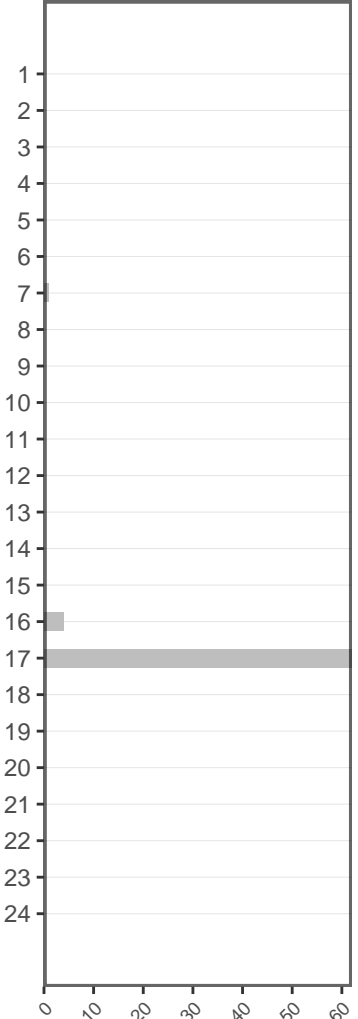
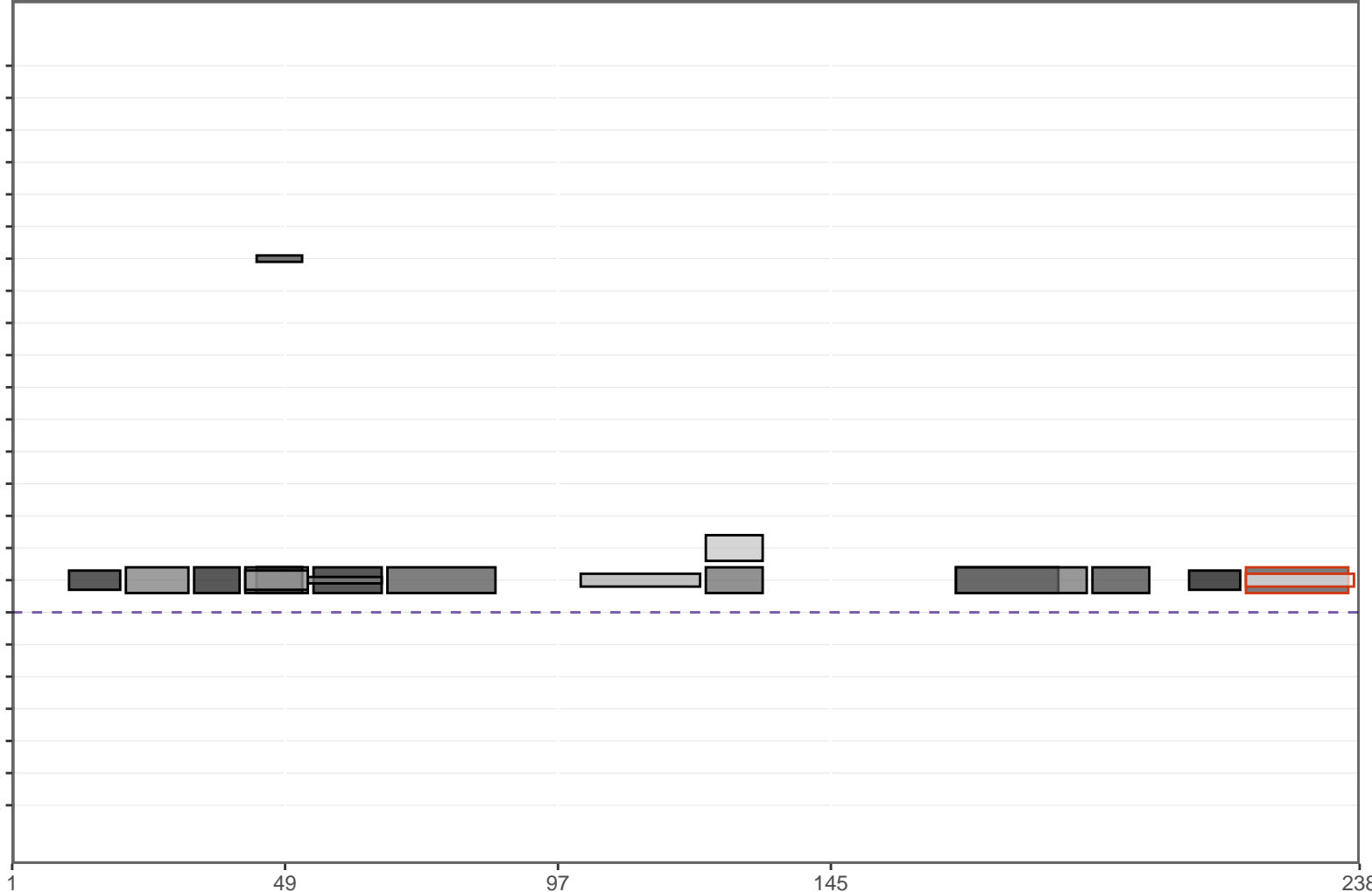
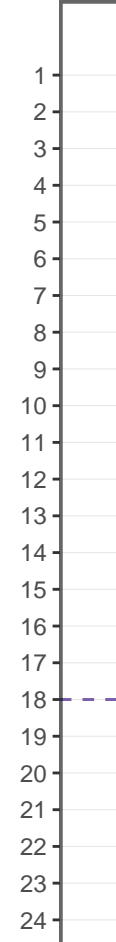
MW indication



Molecular weight

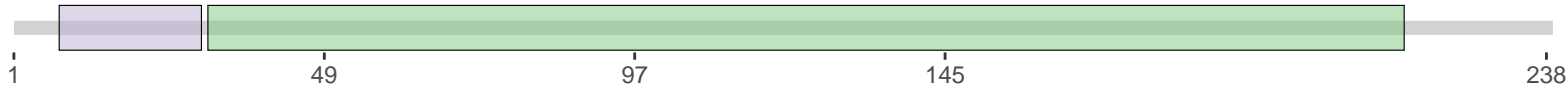


Gel Slice



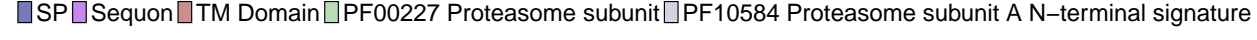
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ITVESTTQALCDLALRFQGGDEEMSRFFGVSLIAGHDENGLNYTDPGGTFWQGNKAKGSSGEGADSSLGEGYKDKLTKEAEAIASLKGVMEEKVTPNNVDIARVSPFTHYSPSEVEDVHRLV

NbL12g03070.1 40S_ribosomal_protein_S11-like [MW = 17.66 kDa]

No. of times detected



log(intensity)



Values from



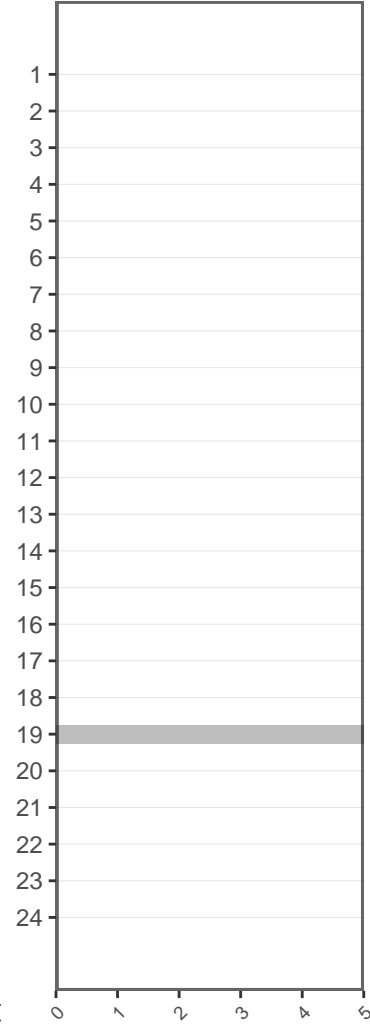
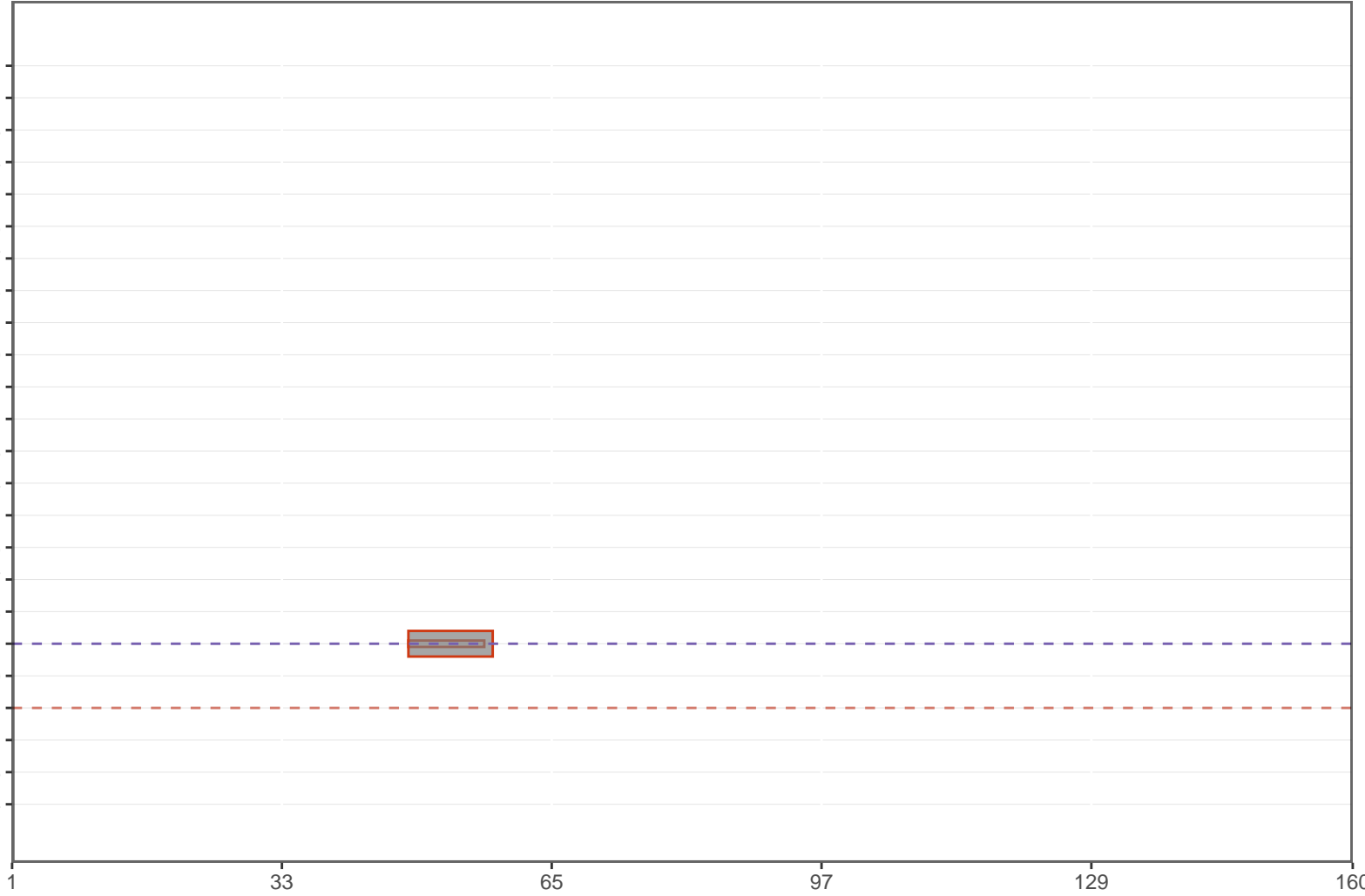
MW indication



Molecular weight

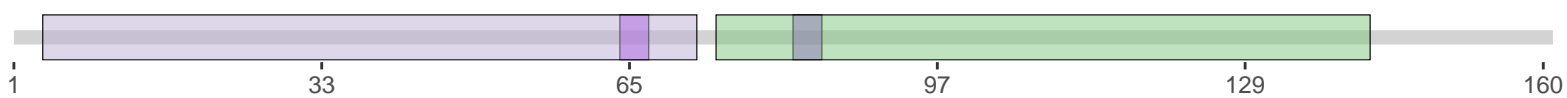


Gel Slice



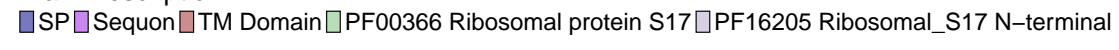
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SIRGRILAGTCHSAMNRTFVRRNLYVWYKQRYEKRHSHNPWHSIPCFRVKGGDHWIIGGRPLEKTVRFNVLKVRPAGSAGGGKKAFTGM

NbL12g03020.1 uncharacterized_LOC109211931 [MW = 33.69 kDa]

No. of times detected



log(intensity)



Values from



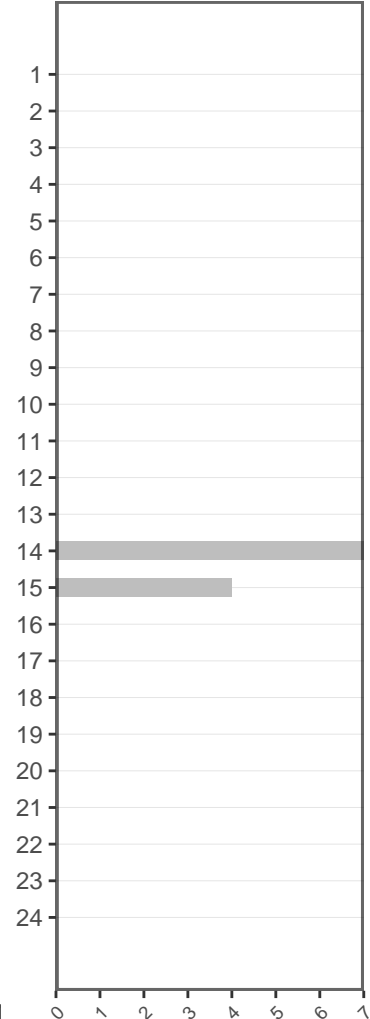
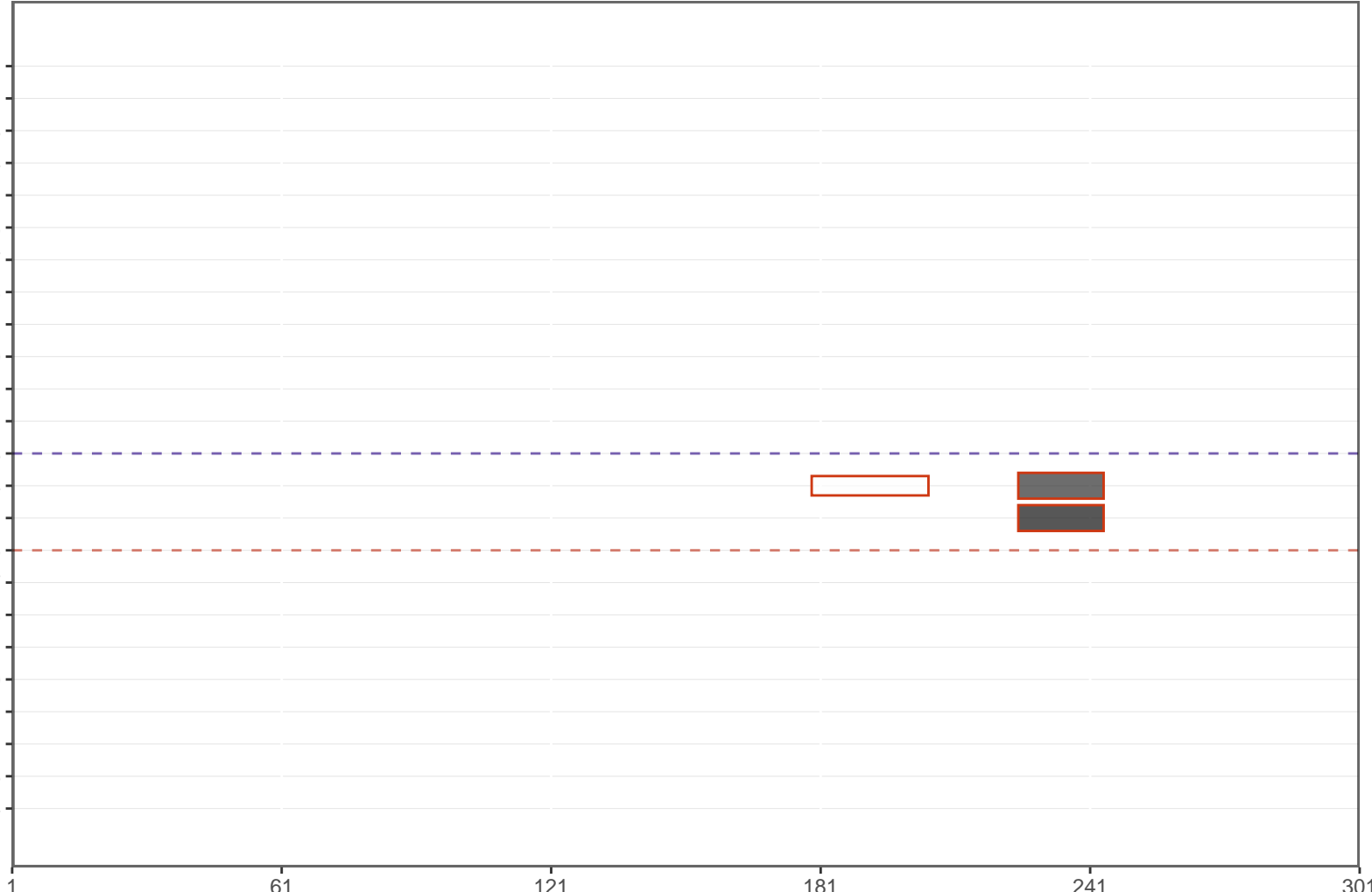
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

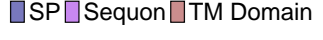
Protein length



Pfam domains



Pfam Description



Protein sequence:

SELGLYAFKTLQVANIQVRRVERLTKNGKTPNMDIEAFSLRYREKLEDEDEVAGSIPNNVLEVSPPGVERVIRIPQDLERFKDRPMVWYVSDVEAEGSSSEHDGVLRLVSNLETNAGIWKGIADVRRNREKAGKPKLKKGRDWRLETSFSLRLVRLYSEF

NbL12g02940.1 uncharacterized_protein_At2g34160-like [MW = 18.29 kDa]

No. of times detected



log(intensity)



Values from



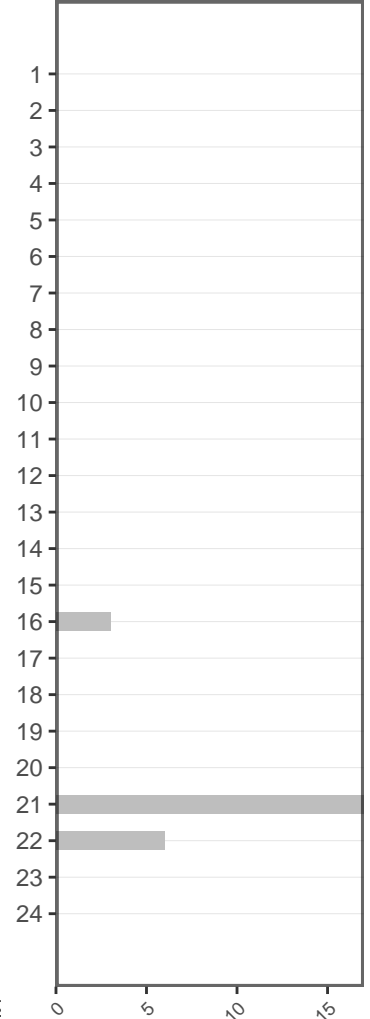
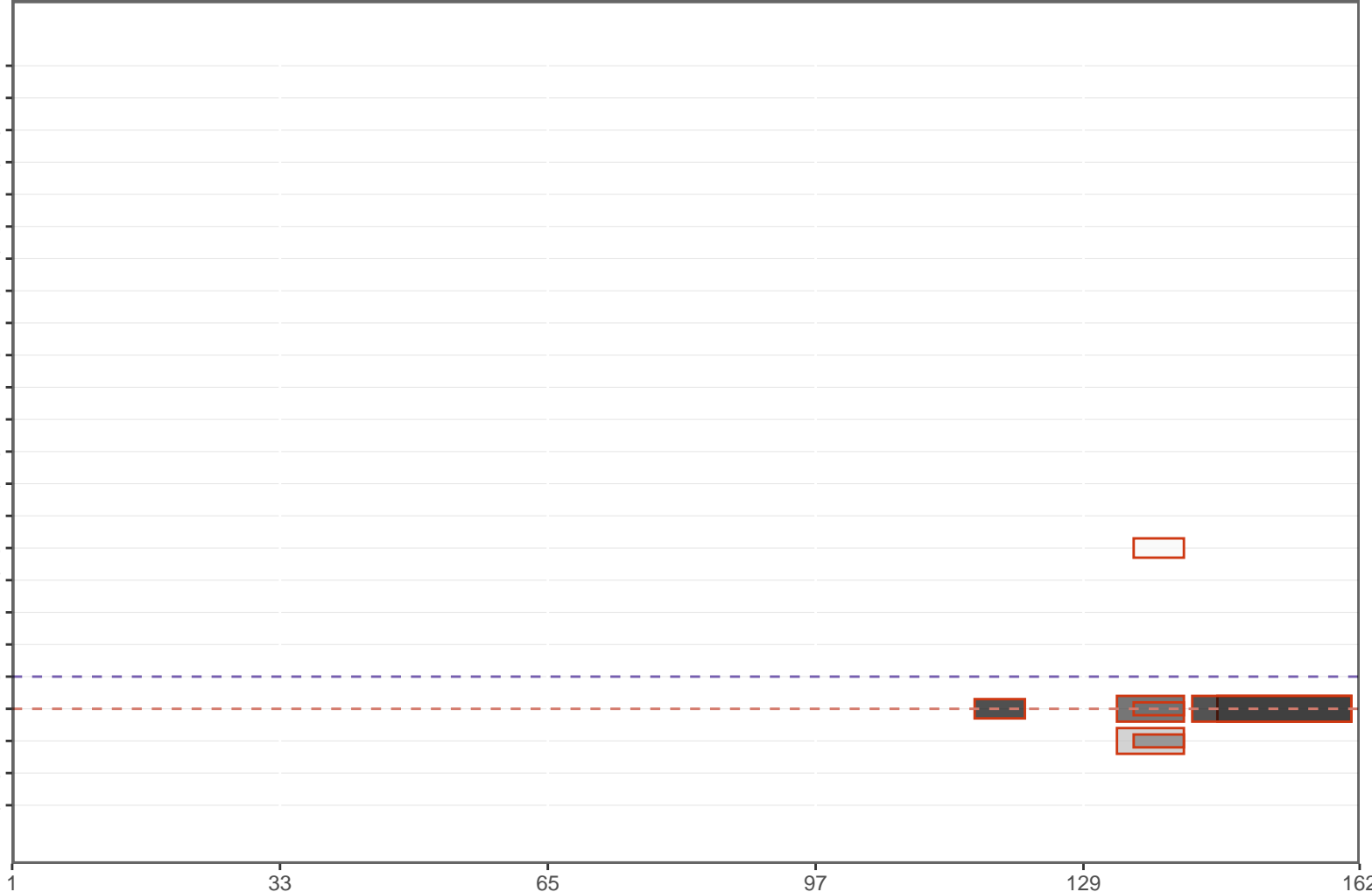
MW indication



Molecular weight

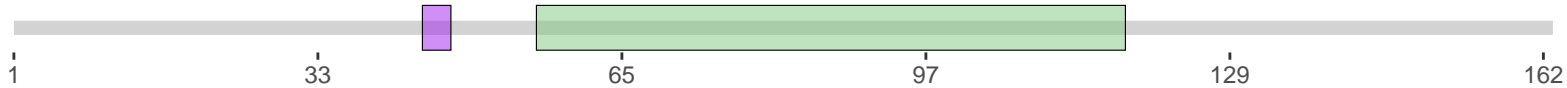


Gel Slice



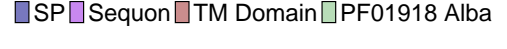
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FFYVNLAKRYMOOHNEVELSALGMISTVTVVAELKKNNGFAVEKIKRTLVDMRDEPGARPIPKAKIEVVMGKTEKFDLMAAEAGNGDNEE

NbL12g02780.1 serine_carboxypeptidase-like [MW - SP = 53.98 kDa]

No. of times detected



log(intensity)



Values from



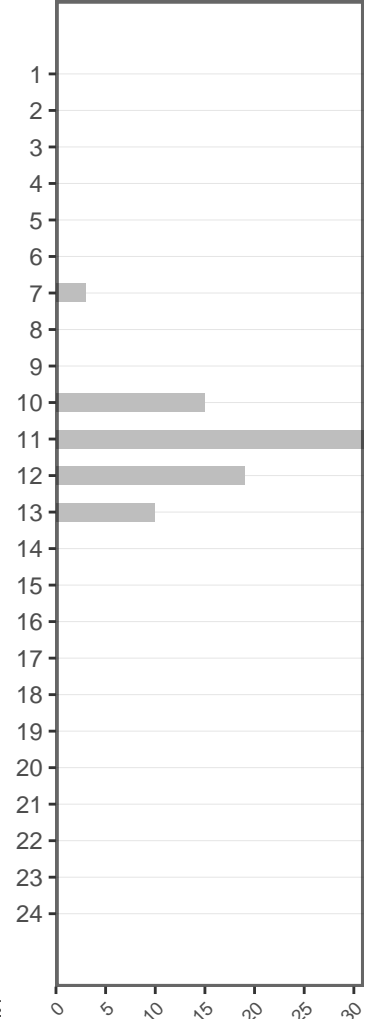
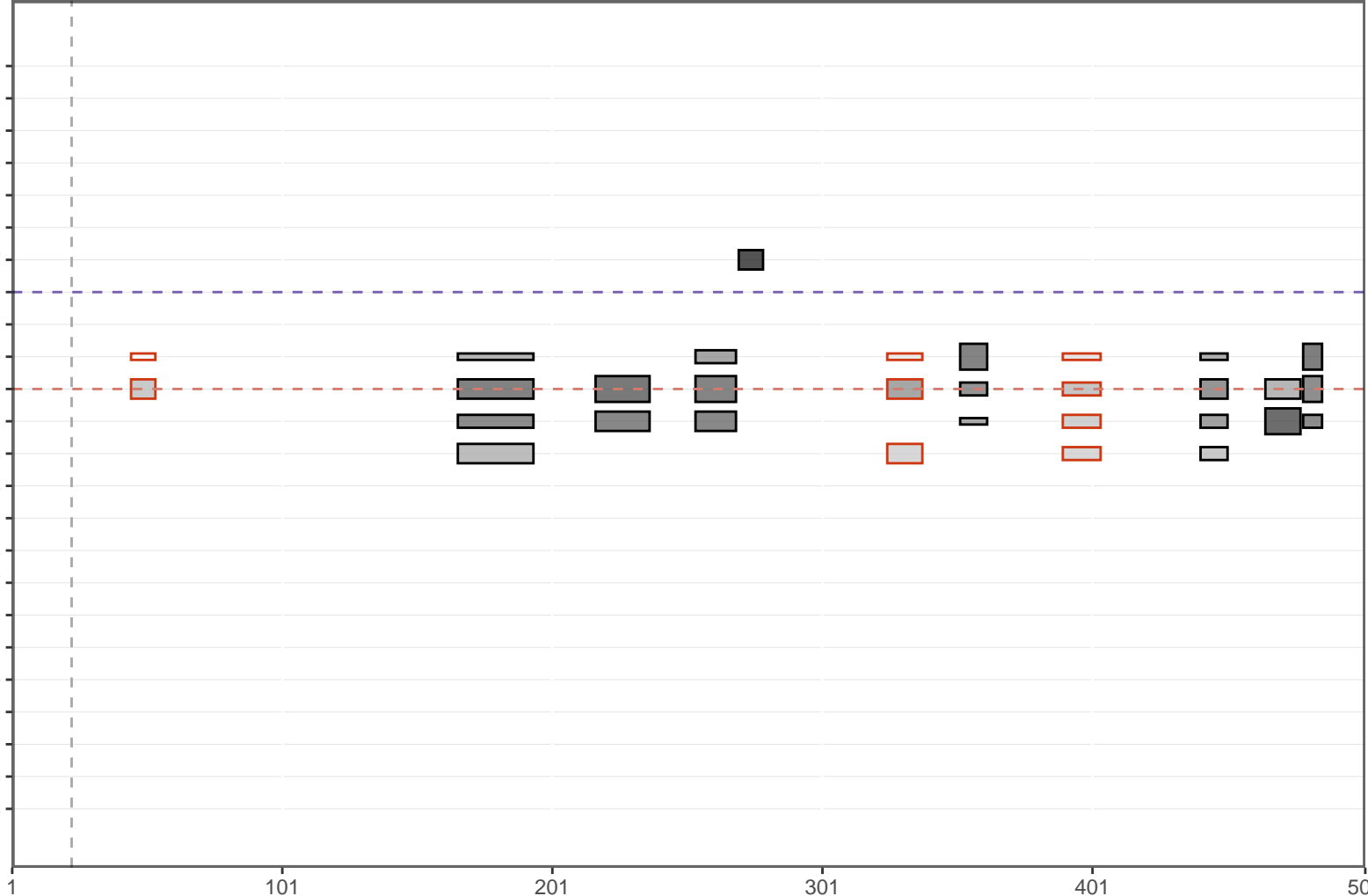
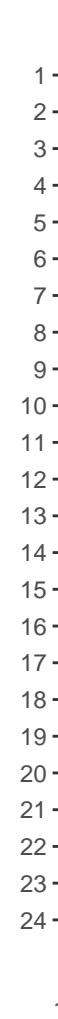
MW indication



Molecular weight



Gel Slice



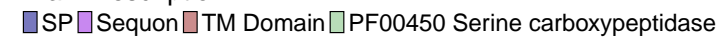
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CGNKNKEGTHNLKGFAGNGLTNPENHYKATFDALDMRLKADYNAIDKSYPKGGQAIRLGGTDGSGSACMAAYLVCTSFNKMMDVAGDKNYDYVRKTKDGLGVDFSKMETLLNDEQVYKHALGVGGDFVSCSSTVYQAMQLDWMRNLKAGIPPLLEDGKLLVAGEYDLGNLGNRWRWHAMEWSGGKDFDGAARVPEVVDGEEKGQKHGSLFLKVDAGHMVPMGGPKAALEMLGRWMMGKLSKEGHFAHM

NbL12g02670.1 protein_DETOTOXIFICATION_21-like [MW = 53.08 kDa]

No. of times detected



log(intensity)



Values from



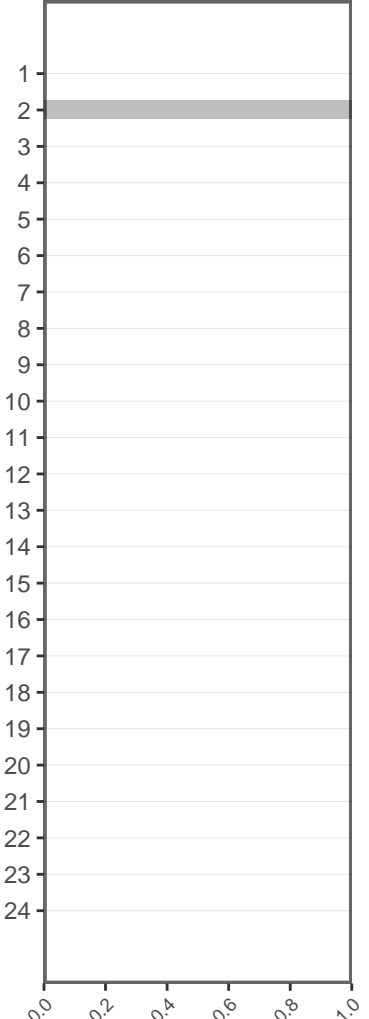
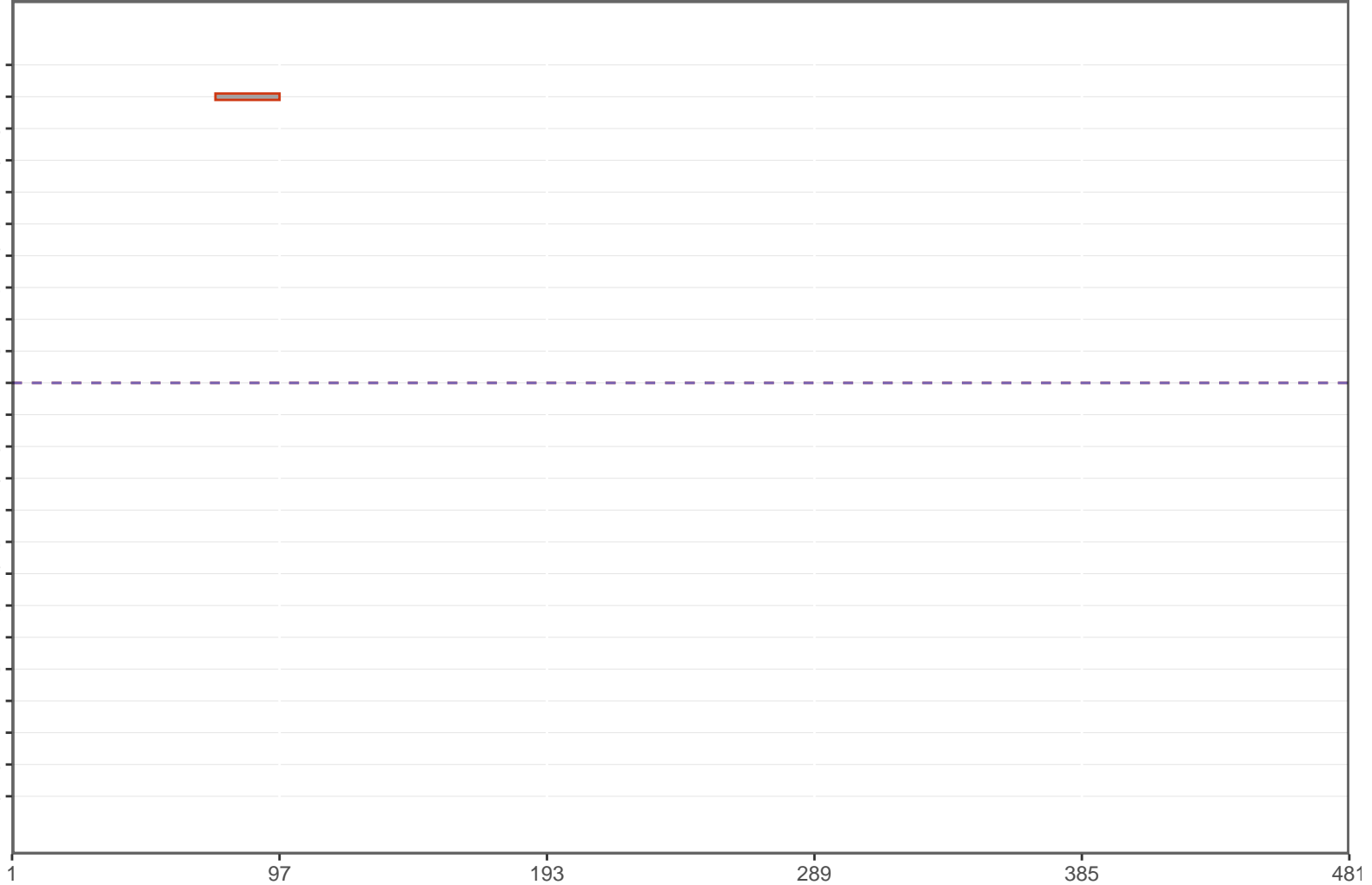
MW indication



Molecular weight



Gel Slice



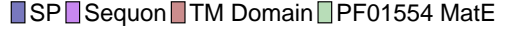
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IGCKETVYKGFSSSLAFKDLWFWVVKLSLSGSGAMLGLPEFVYNSILVLTGNLKNAMVQIDALSIGLNINGWEMMISLGFLLAACVYRVSNELGRGSAKAAARFSLITATTFVIGFLFLFFVFLRGLAYLFTDGDVAKEVEQLSFLLAFLSILMNSVQPLSGVAVGAGWGSIWVYVNGCYVLLGIPVGFVLYVFLGVKGVWVWGMFGTLVGTVLLMIFLRFDWQKLLAQGRVKKRWLVEAETNADSGTA

NbL12g02560.1 60S_ribosomal_protein_L12-like [MW = 17.81 kDa]

No. of times detected



log(intensity)



Values from



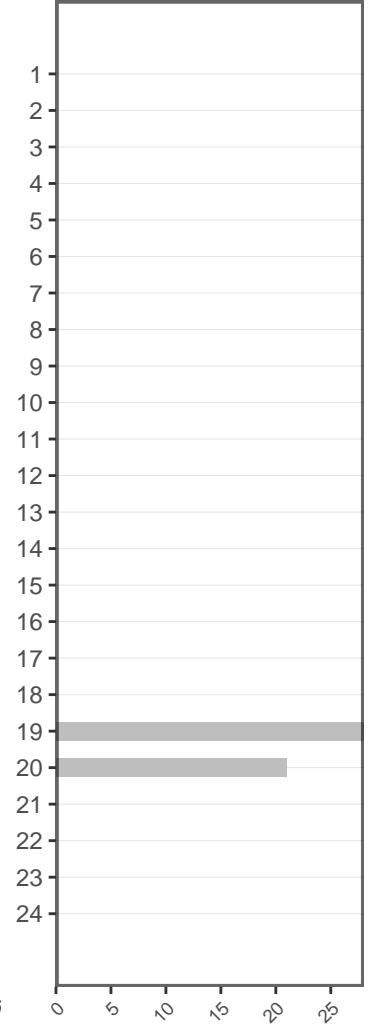
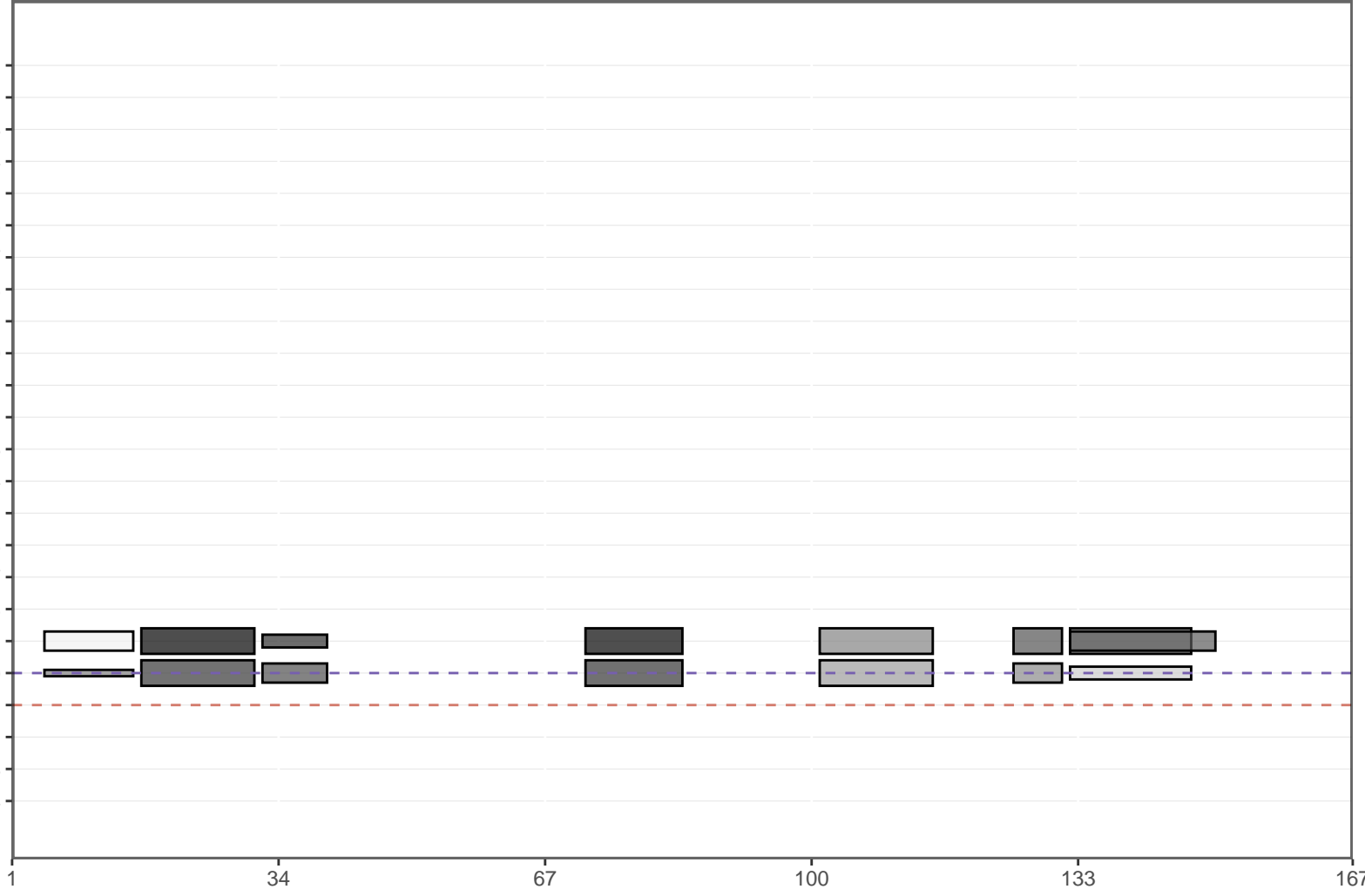
MW indication



Molecular weight

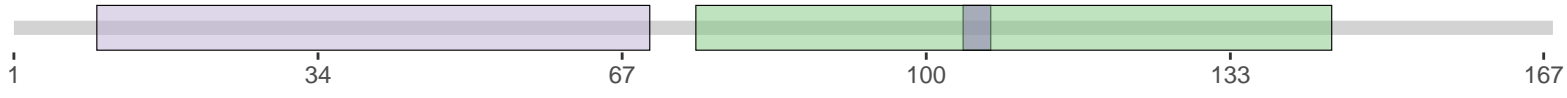


Gel Slice



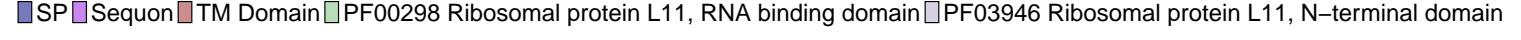
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IAKYISVYVPSAAALVWALKEPERDRKTKRKNKHNKNSLDDWIEIAKVMKPRSMKDLTGTWKEILGTGVVGGTVDGDKPKDLQGEIDGGDVEIFLD

NbL12g02440.1 ATP_synthase_subunit_d_mitochondrial-like [MW = 19.76 kDa]

No. of times detected



log(intensity)



Values from



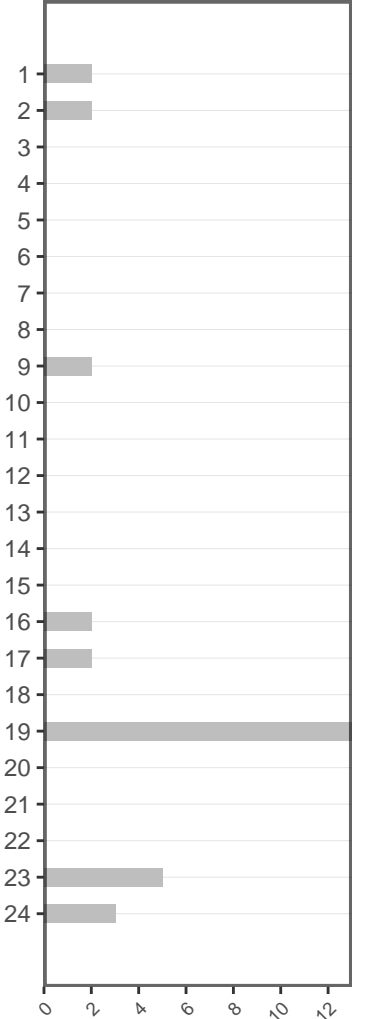
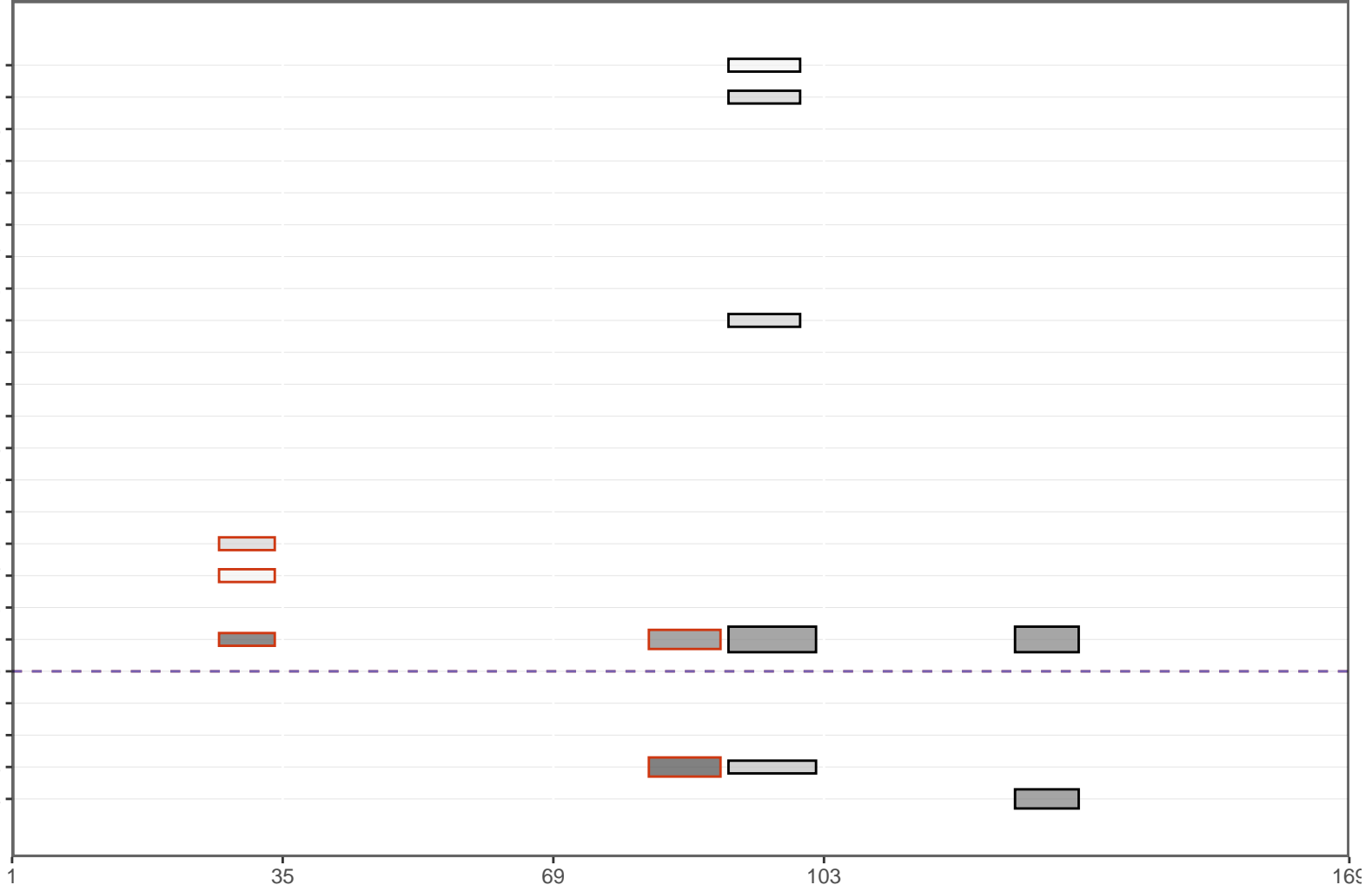
MW indication



Molecular weight

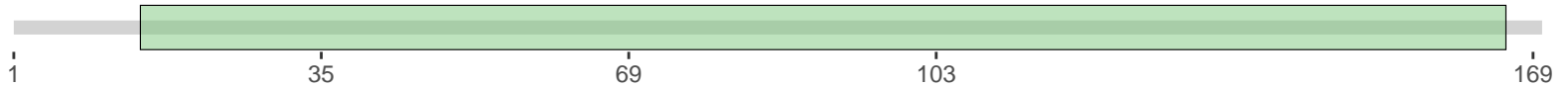


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IIGSRLLVDMYKAYDSIEIPKFDVTVTPQYKPKFDALLVELKEAEQKSLKESERLEKEIADVDELKKKLSMTAAEYFEKHPLELKKKFDIEIRNDYWGVI

NbL12g02420.1 elongation_factor_1-alpha-like [MW = 49.26 kDa]

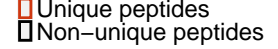
No. of times detected



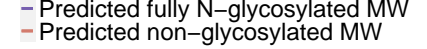
log(intensity)



Values from



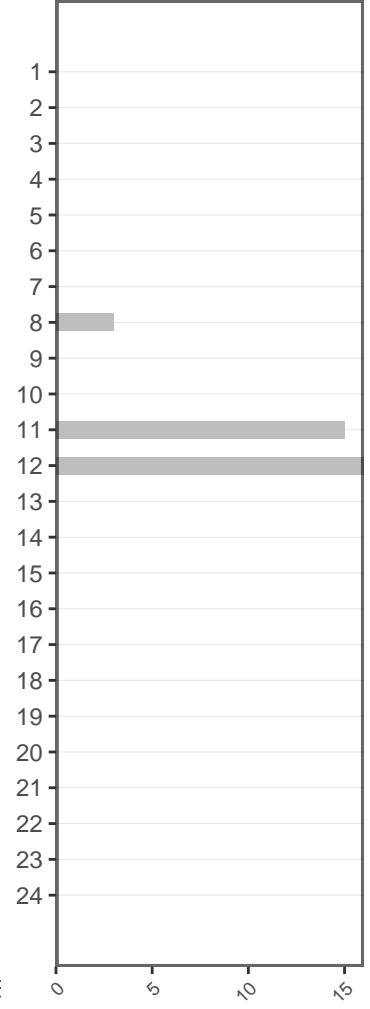
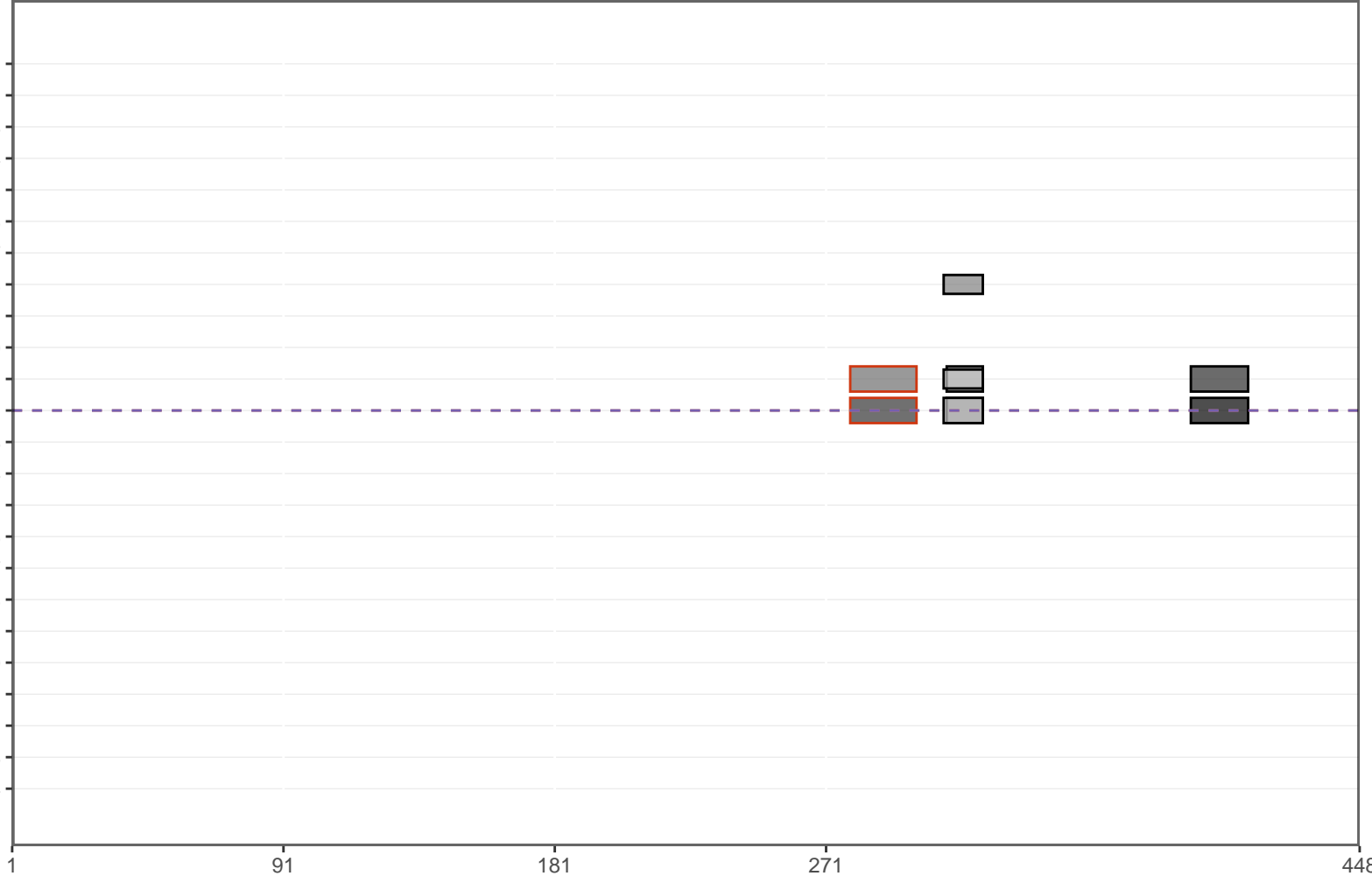
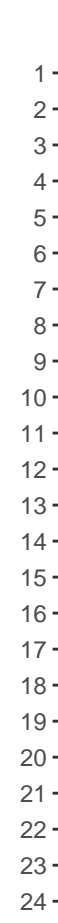
MW indication



Molecular weight

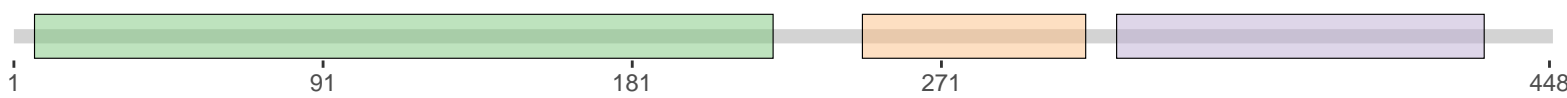


Gel Slice



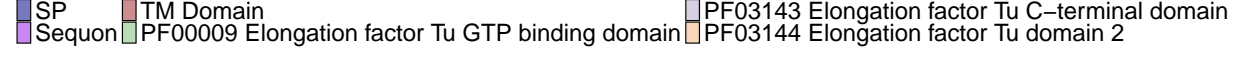
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SPITLLEALDQINEPKRPTDKPLRLPLGQYKIGGIGTVPIGRVETGVLKPGMVFVTFGPTGLTFEYKSEVMHHEALLEALPGDNVGFNKNNAVADUKRQYVAGNSKDDPKGAASFTSGVHMNHPGGIGSNVAPVLDGHTSHAVKFAELTKIDRRSGKELEKEPKFLKNGDAGMVMMPDKPMVVFETFAEYPLGFRFAVRDMRGTWAGVKSVDKDKDPTGAKVTKAAGKKK

NbL12g02390.1 endochitinase_EP3-like [MW - SP = 26.75 kDa]

No. of times detected



log(intensity)



Values from



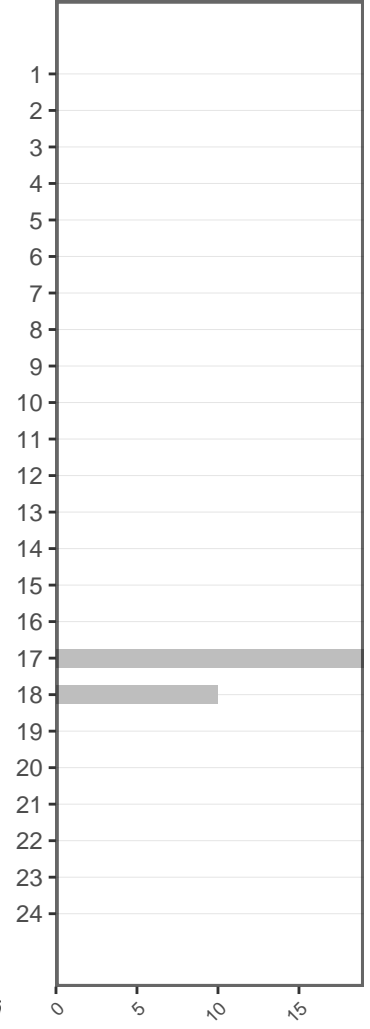
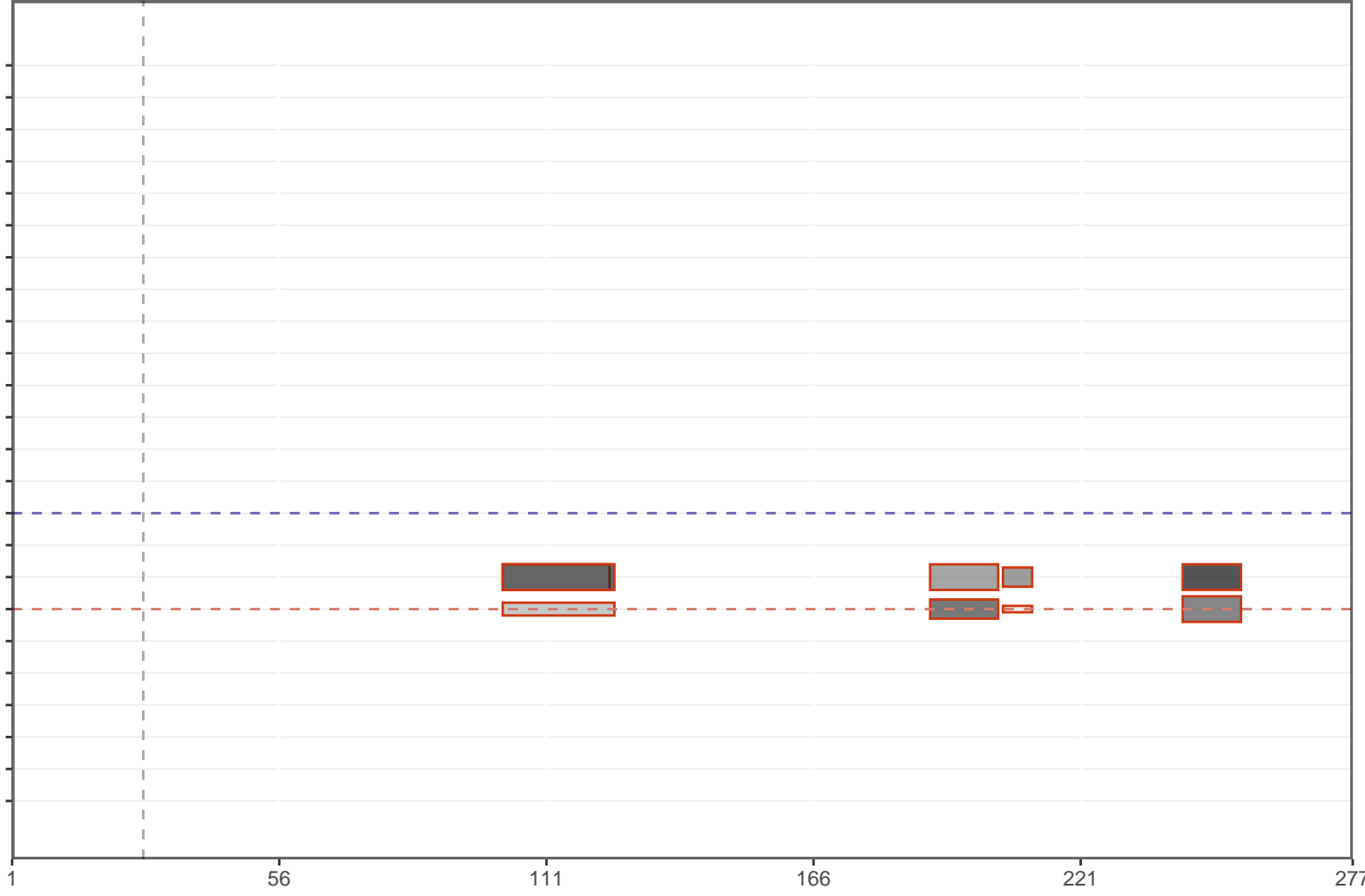
MW indication



Molecular weight



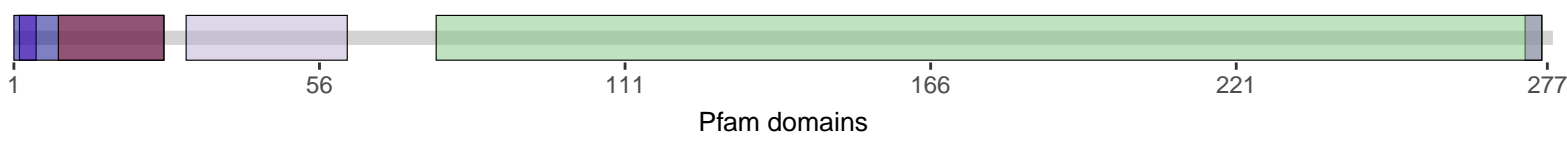
Gel Slice



Protein length

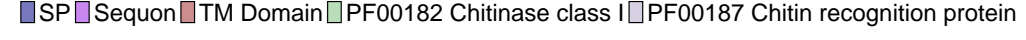


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

REIAAFFAHVTHETGHMCFINEINPESGQVDEENTEYPCVSGKYYGRGPIQLSWNFNYGFGKSGFDGLNDPQVARDVSEFKTALWWMNNGHSLTSGGGGFPTRINAIKEDGNGPQTVARRVEVYETEYGGQLGVETGDNLTG

NbL12g02360.1 mitogen-activated_protein_kinase_3 [MW = 42.89 kDa]

No. of times detected



log(intensity)



Values from



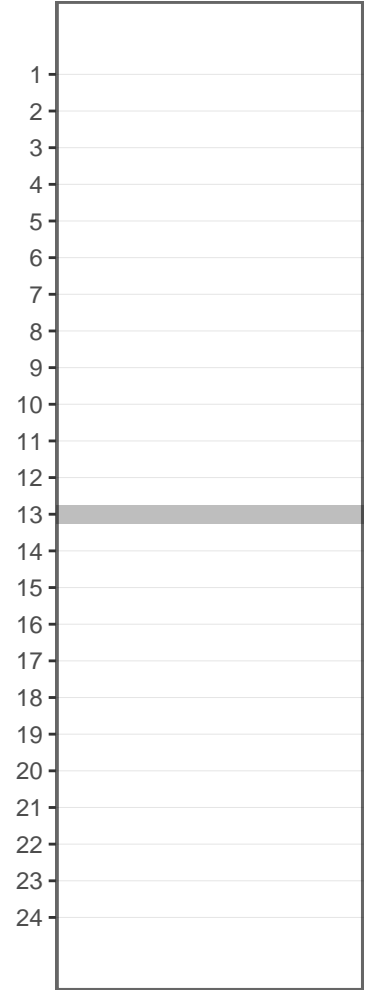
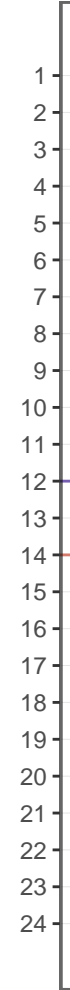
MW indication



Molecular weight



Gel Slice

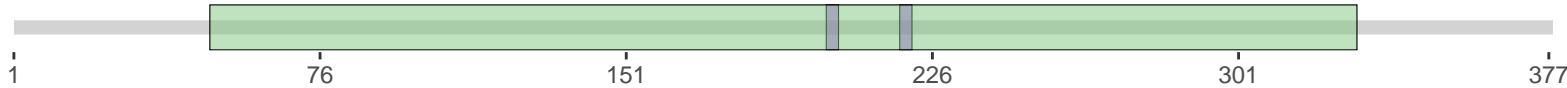


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ILLNANCDLKCDFGLARPNENEMTEYVWTRWYRPELLNSSDYTAADVWVSGVGFMEIENRPLFAGKDHVHGIRLLTELLGTRTEADLGFIGNEDAKRYRGLPQHPRQLANVFHYNPLAIDLVDKMLTLDPTRRITVEEALDHPYLAKLHDAGDEPKGVPVPSFDFEQQGGEEQKDMYGEALSINPEVAI

NbL12g02350.1 peroxidase_2_cytosolic-like [MW = 27.41 kDa]

No. of times detected



log(intensity)



Values from



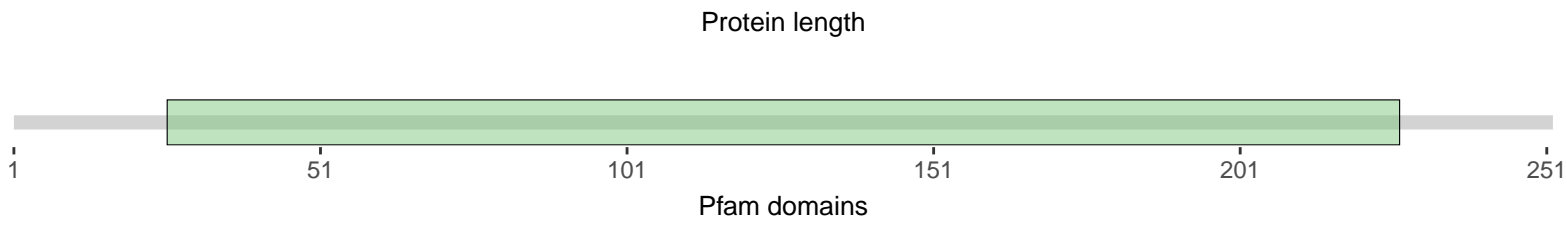
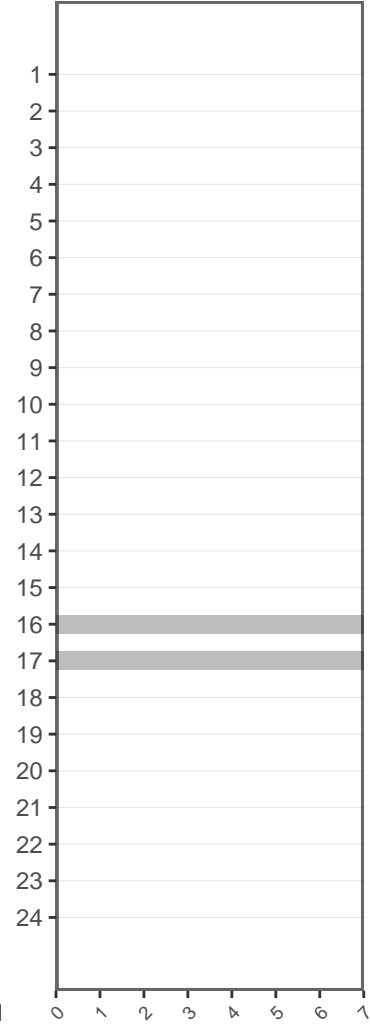
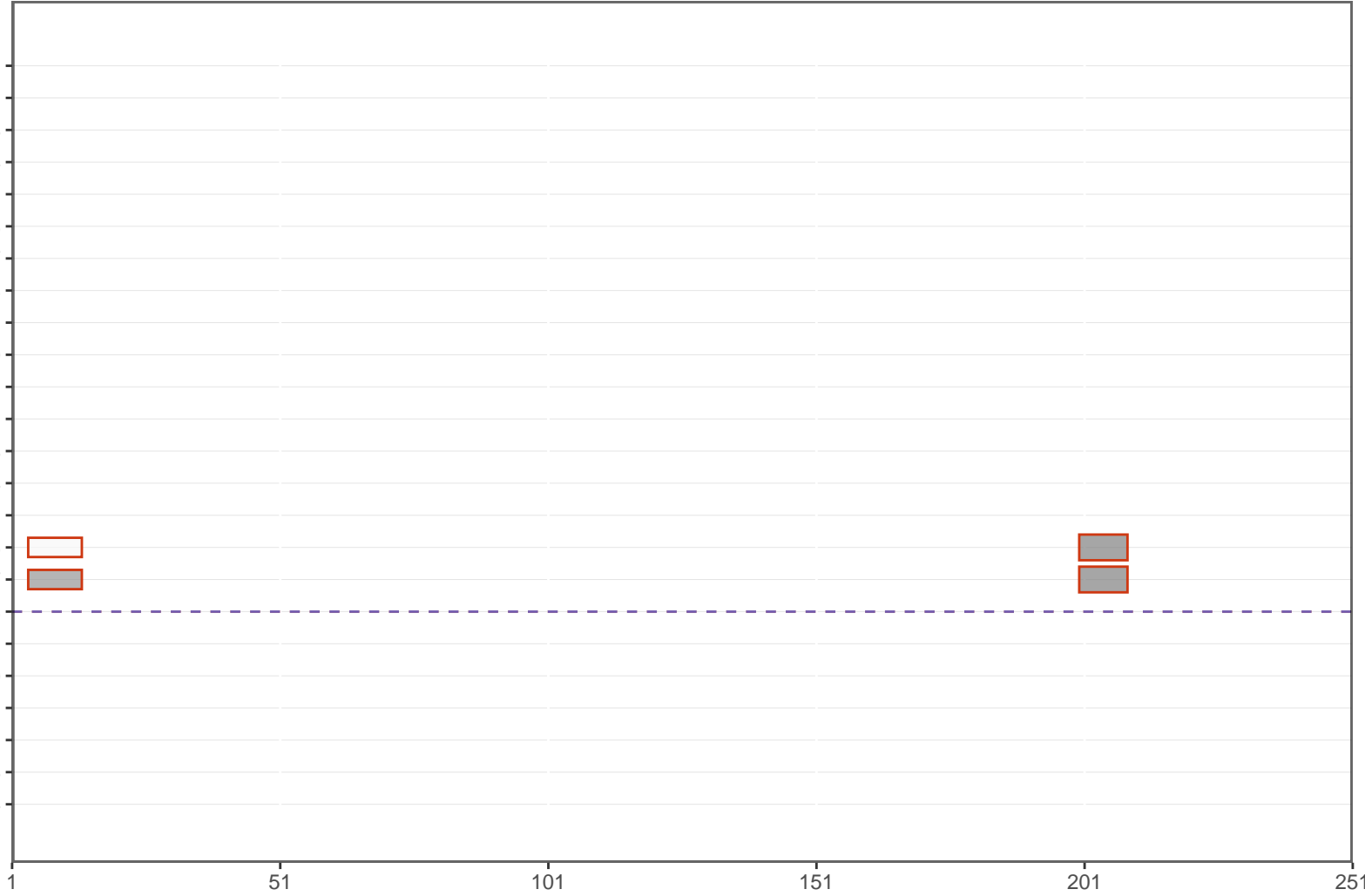
MW indication



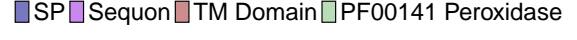
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

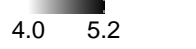
Y/PFHIPGREDKTEPPVEGRLPDATKGSQHLRQVFWQMGSLSDKDIVALSGGHTLGRQHKERSGFEGPWTFNPLFDNRYFTLLSGEKGLLLLPQKALLSDPAPRPLVERKYAADEDAFFADVAEHLKLSLGFQEA*

NbL12g02210.1 histone_H2A [MW = 15.78 kDa]

No. of times detected



log(intensity)



Values from



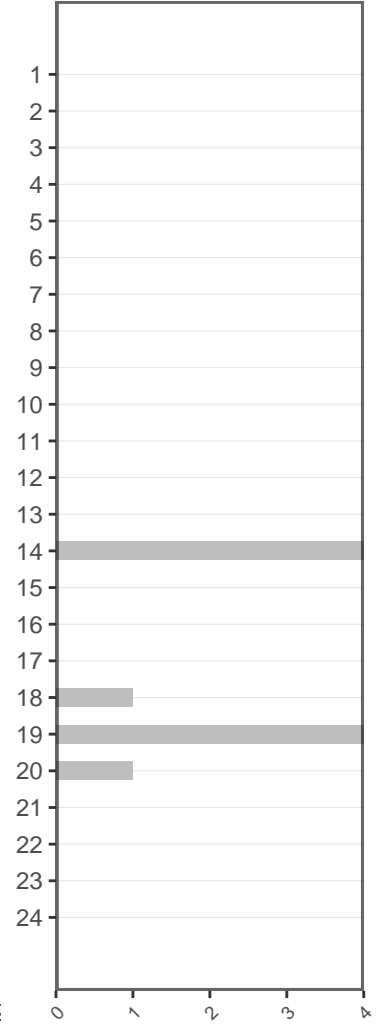
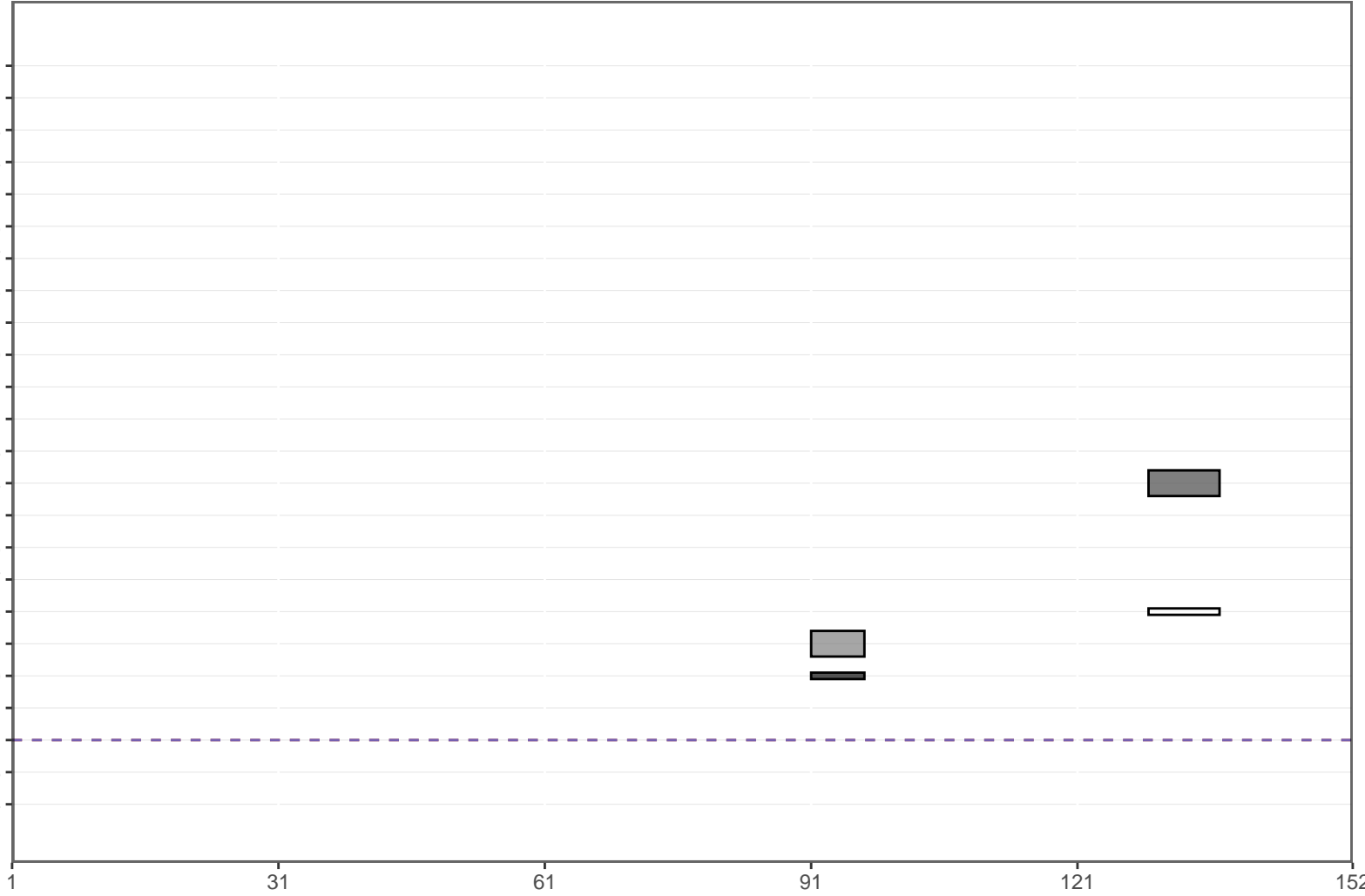
MW indication



Molecular weight



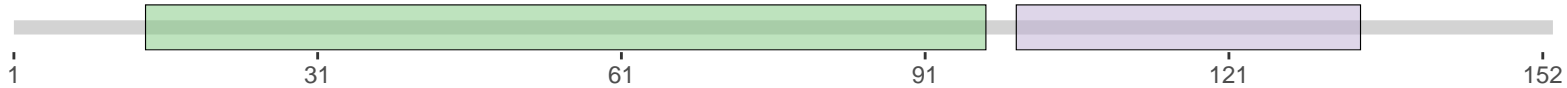
Gel Slice



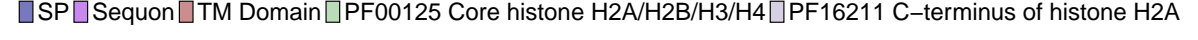
Protein length



Pfam domains



Pfam Description



Protein sequence:

MAVLEYLAEEVLELAGNARDNKKRIPRHVLLAVRINDEELGKLLAGVTIAHGVLFPNINPLLPKKTGGAEKEPKSPAKTKSPKAAAI

NbL12g02110.1 protein_plastid_transcriptionally_active_16_chloroplastic [MW = 54.52 kDa]

No. of times detected



log(intensity)



Values from



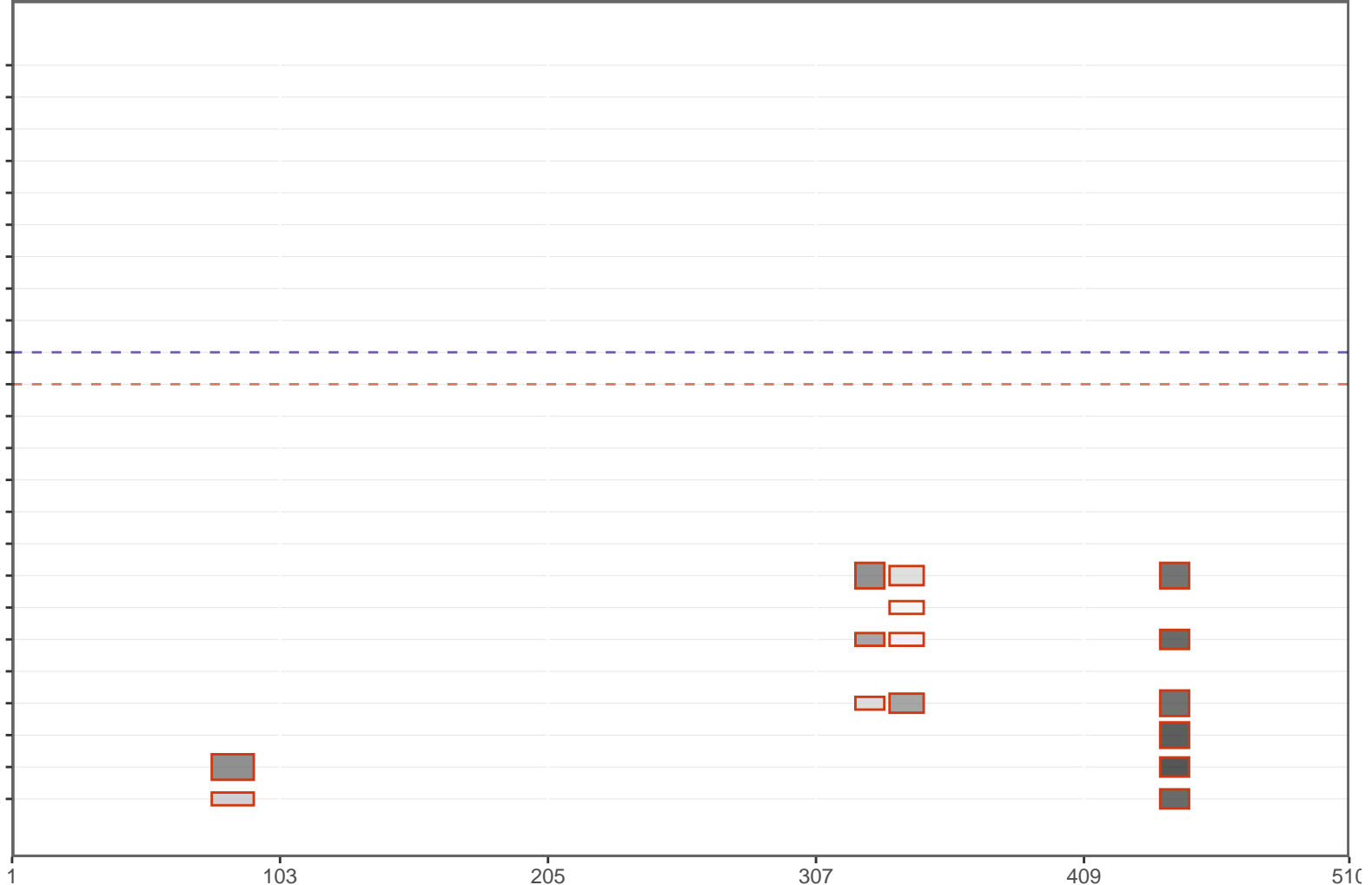
MW indication



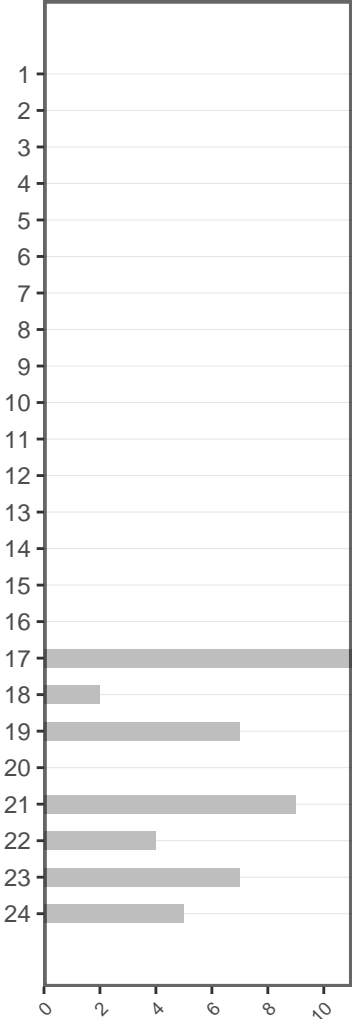
Molecular weight



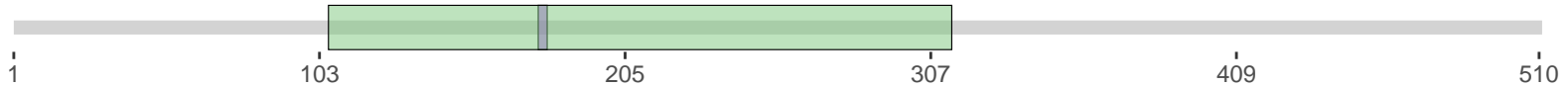
Gel Slice



Protein length

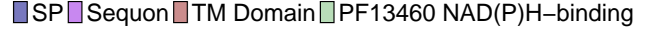


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILFSKSDPLTTEFLGKIVETDVRYLTKLSTLDFSPREBSYNIIVSAEGSGAGENYKWKSEIAKLVVDFSNATAENKVEVFTDPSASRIKTVDEHFSTIPEDGRRKVAEALEKSKAEFEERARGAAEASKRQEEEVKLEKQKAAANVAKAEKDS6AAGPVSLELDDKAKGLSTGDFEFKFS6QLKSAVEKAGEESTQVATIRGDAKARNLPAQKAVIKTPRKRPFASKNNEVPKTKGTETKTRKVFGLFGQETIVDD

NbL12g01970.1 serine/threonine-protein_phosphatase_PP1_isozyme_1-like [MW = 36.28 kDa]

No. of times detected



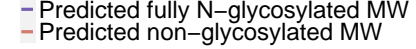
log(intensity)



Values from



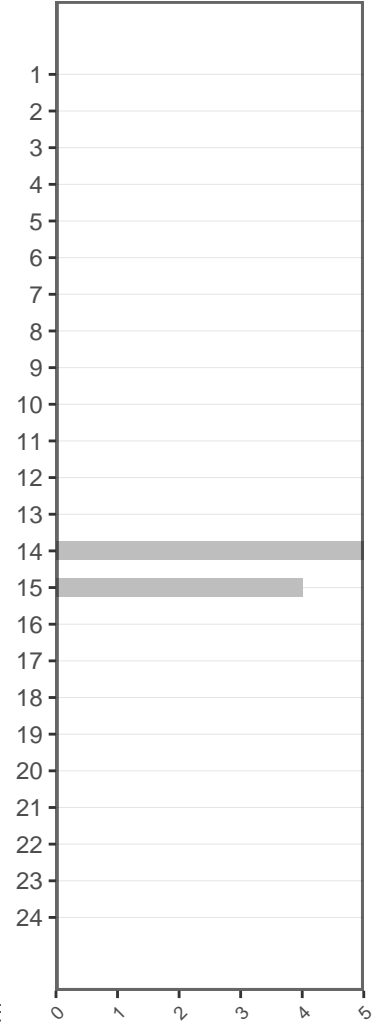
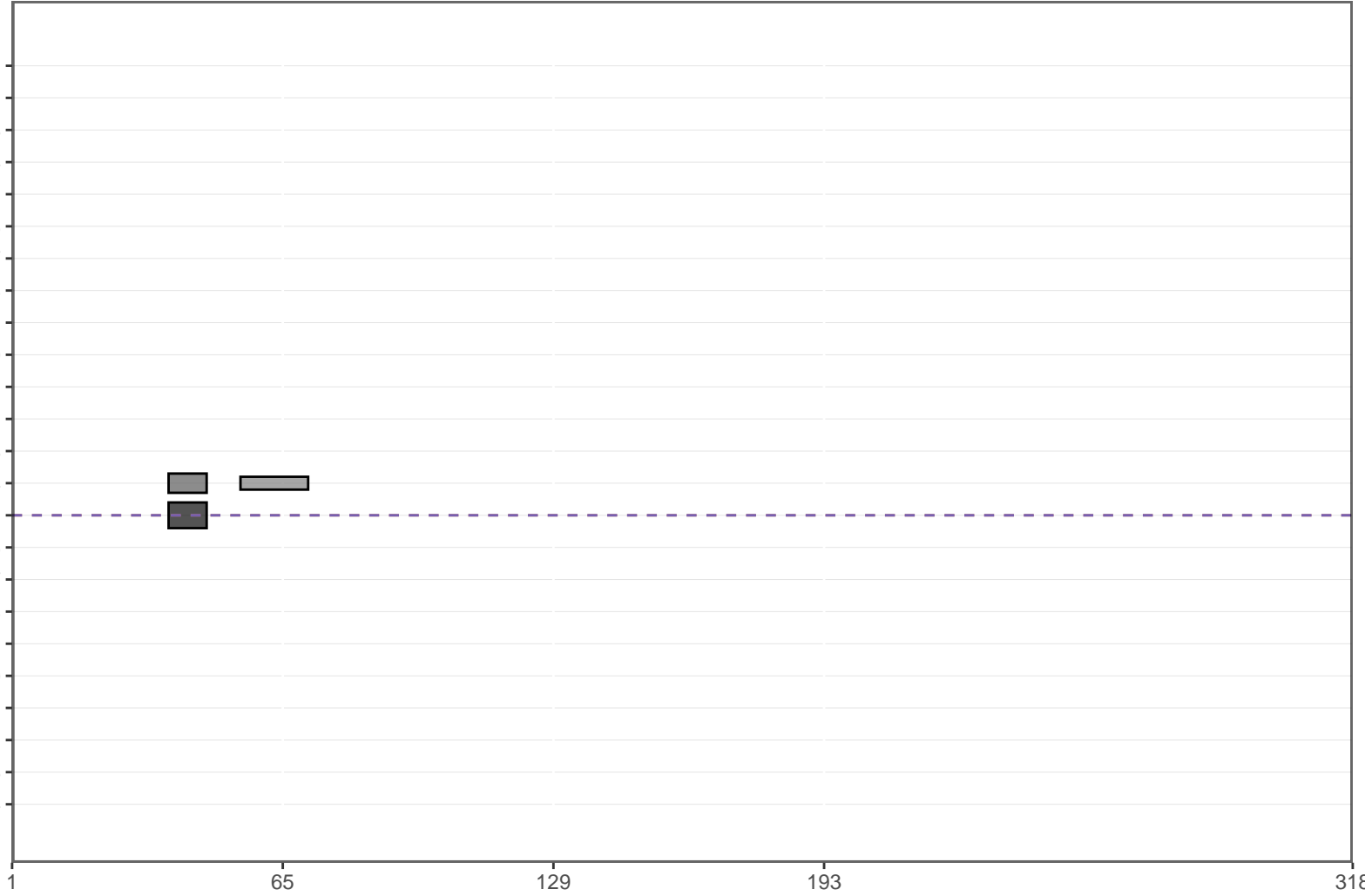
MW indication



Molecular weight



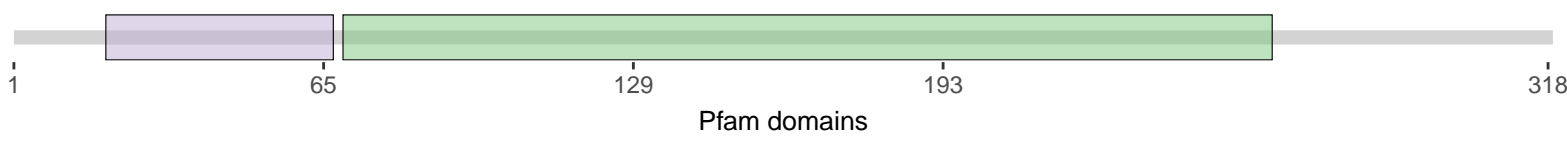
Gel Slice



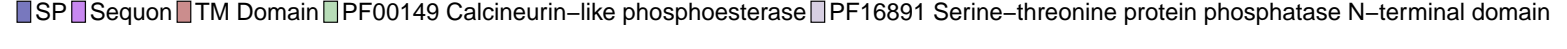
Protein length



Peptide counts over 4 repeats



Pfam Description



Protein sequence:

DECKRRFNVKLVKGFTECFNGLFPAALIDKILGMHGGLSPLTNLDGIRNLPRPTDVPDGLLGDLLWSDPSEKVGWGMNDRGVSYTFGPKWAEFLMGHDMLVGRAGHVEDGYEFAERQLTIFSAFNYYGGEFDNAGAMMSVDEGLMGSGLKPTDRKPRFL

NbL12g01920.1 M-phase_phosphoprotein_6-like [MW = 20.71 kDa]

No. of times detected



log(intensity)



Values from



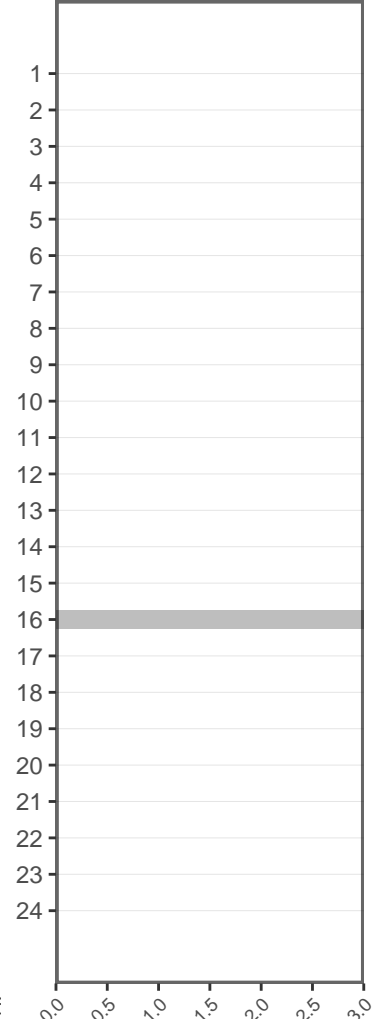
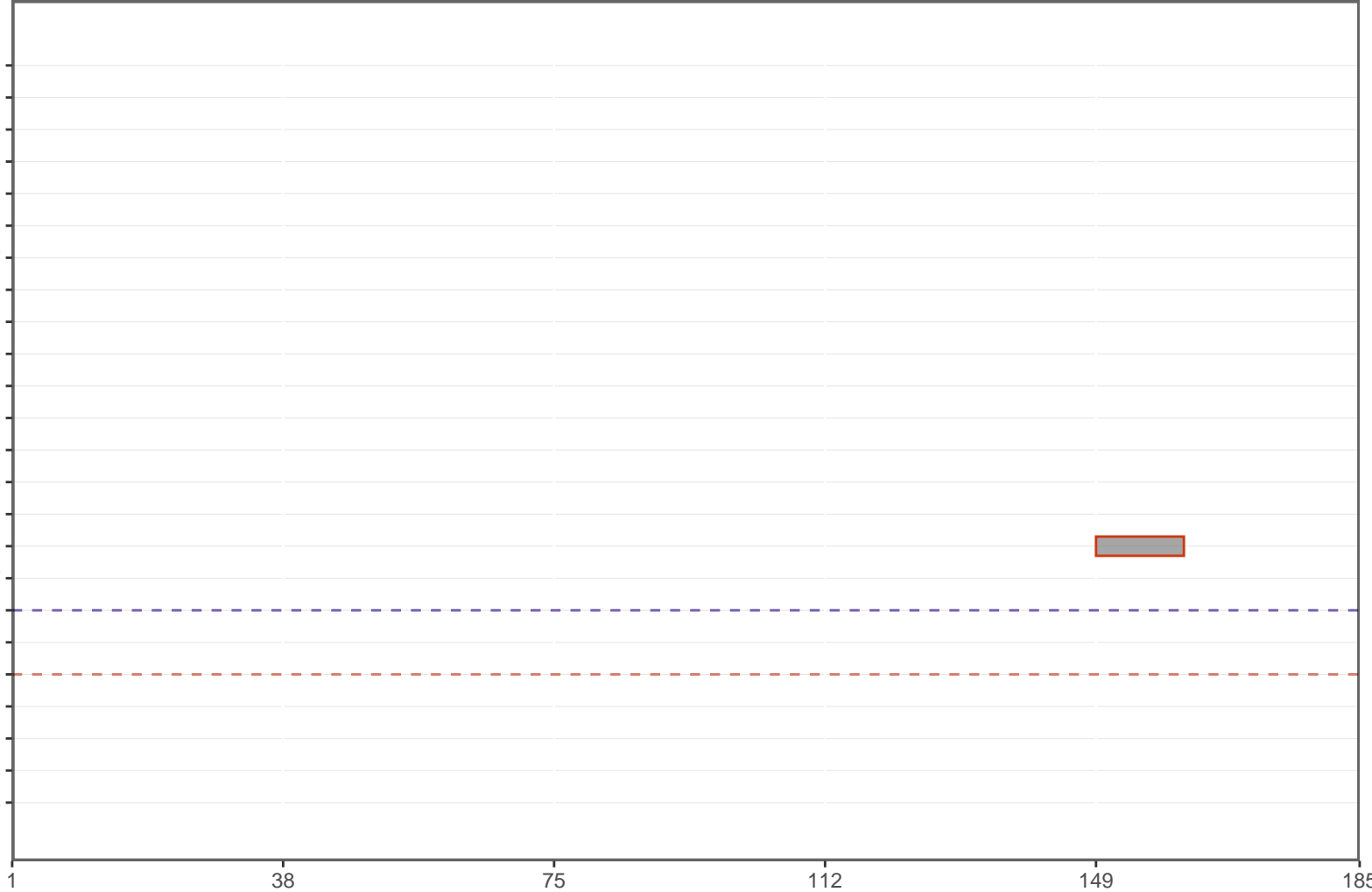
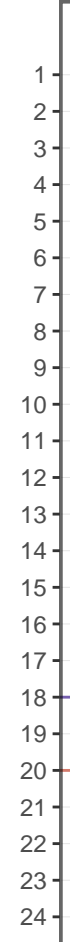
MW indication



Molecular weight



Gel Slice

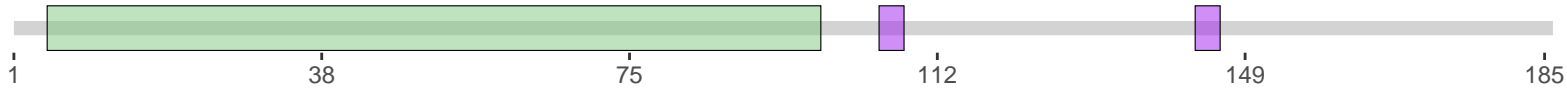


Protein length

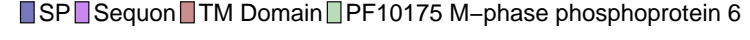


Peptide counts over 4 repeats

Pfam domains



Pfam Description

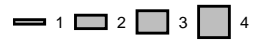


Protein sequence:

LSKPHSEGSAAACSSSETSEINKRENGTSGOGLIENSNMDDSLSPNEDLKRKQDDTSSEVGYPNKSHKRVLGNAESPSRSRSGQKPHLDWVSLKPKPKGQKKQR

NbL12g01790.1 beta-glucosidase_BoGH3B-like [MW = 66.12 kDa]

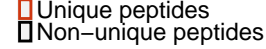
No. of times detected



log(intensity)



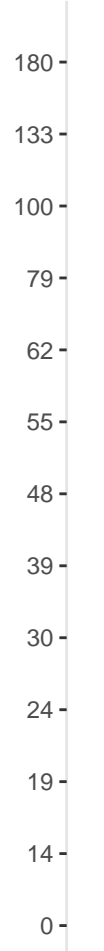
Values from



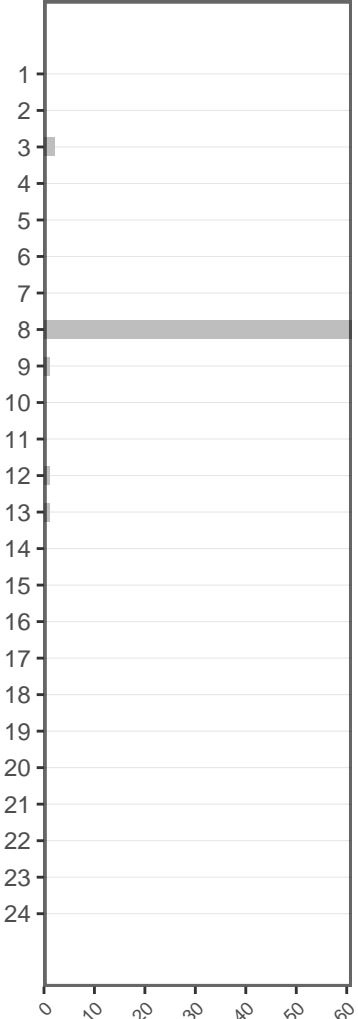
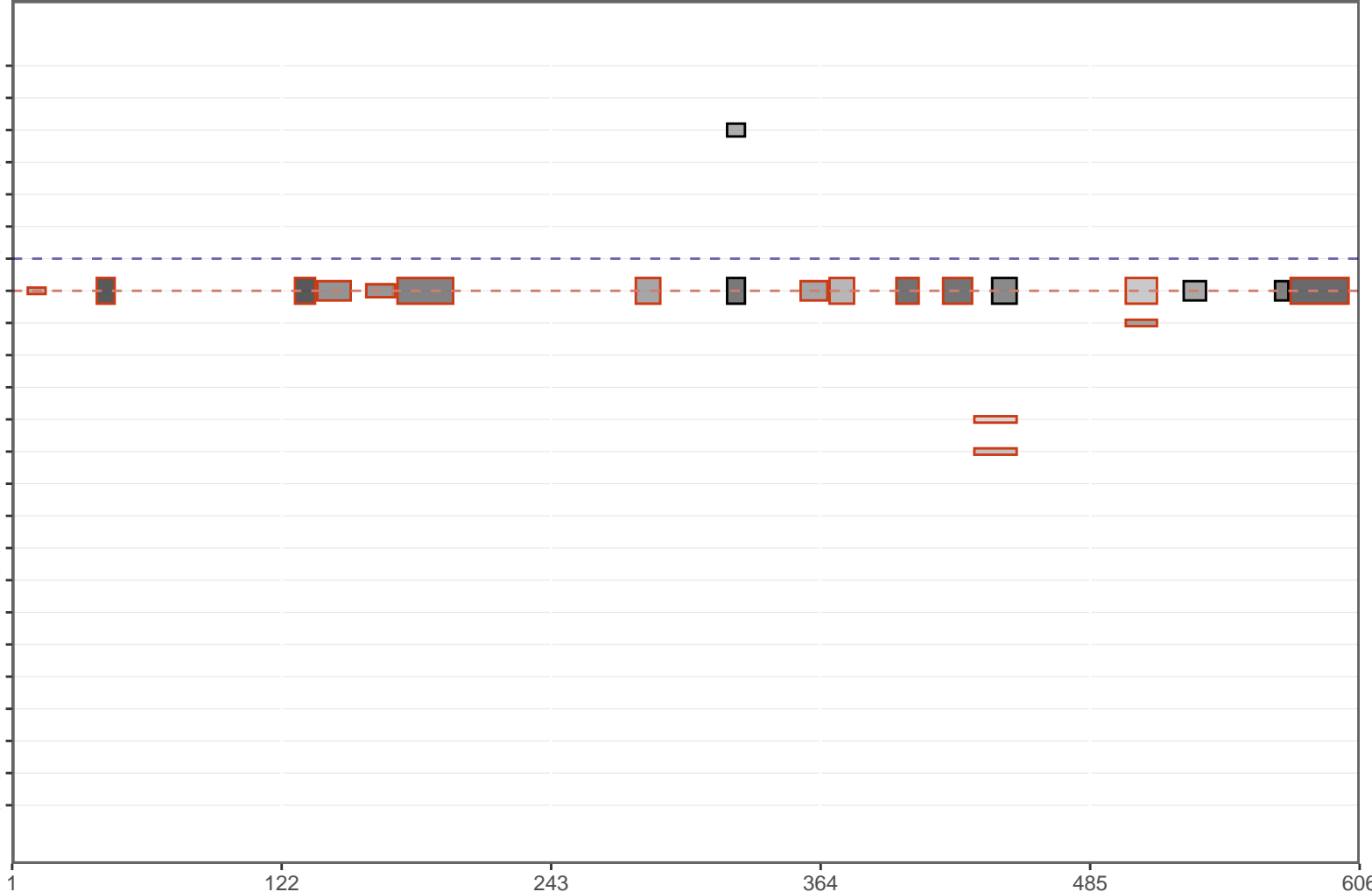
MW indication



Molecular weight

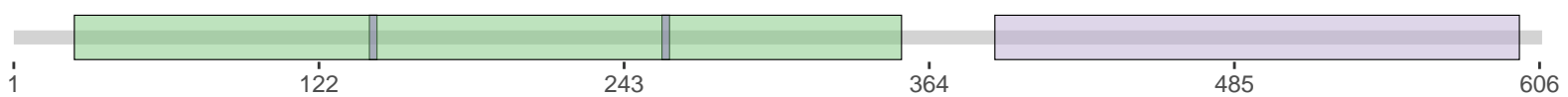


Gel Slice



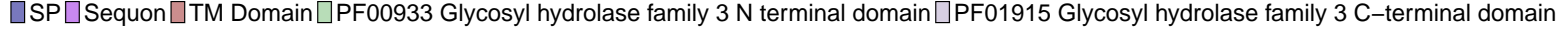
Protein length

Peptide counts over 4 repeats



Pfm domains

Pfam Description



Protein sequence:

LDRLSPHGSIYDGGITANAGIDMMVFFRYVOLFELHRLGLVESGKIPMTRIDDAVERILRLKVFVAGAFEYPLSDRSLLDTVYGGNGHRELAREAVRKSLLKNGSKDVKPFLPLERNAKKILVAGKHADDLFGGGGQWTKTWDGMSGRITGTTLEAKKDAVGGETEVVYEEENPSPETFAAGDFSYISIVVYGEPPYCEGGSDSDLLKIPLGGELISLVADRVPFTLVLSGRPLVIEPSELLEKMDAFVAVLWLPCTEGAGTGVVFGDVEFGKLPMTWFKSYVDLPLHDEQ

NbL12g01760.1 phosphomethylpyrimidine_synthase_chloroplastic [MW = 72.08 kDa]

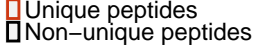
No. of times detected



log(intensity)



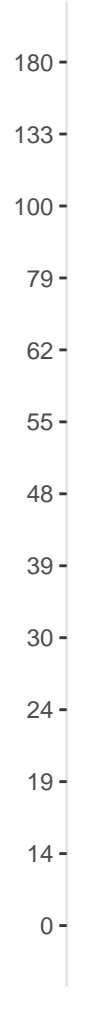
Values from



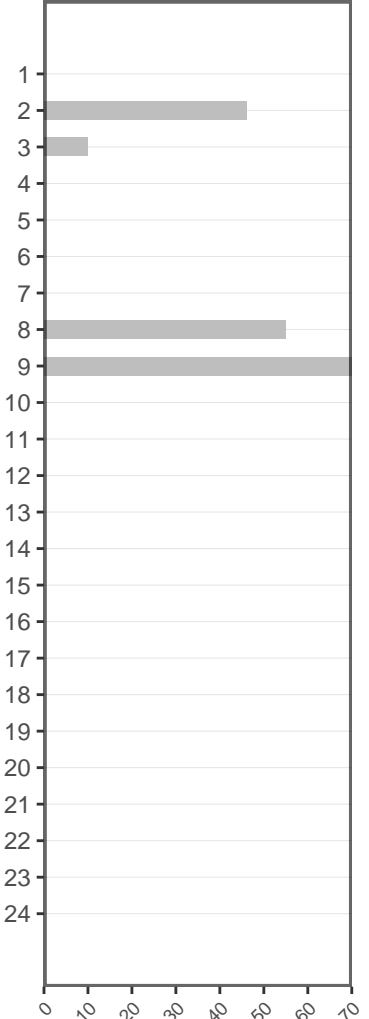
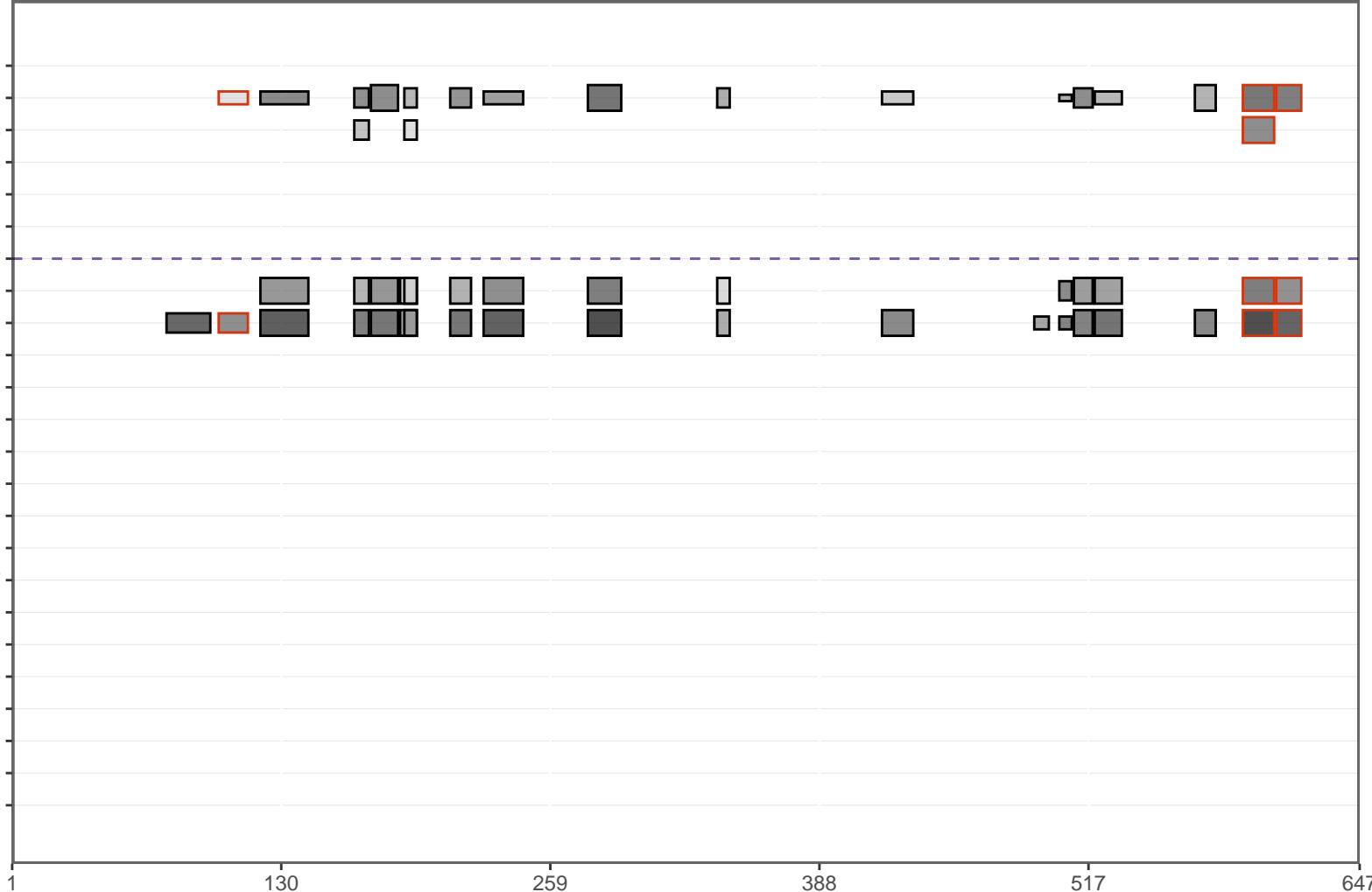
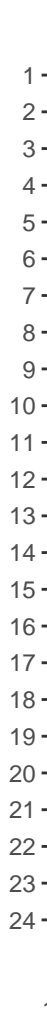
MW indication



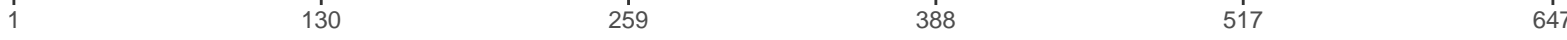
Molecular weight



Gel Slice

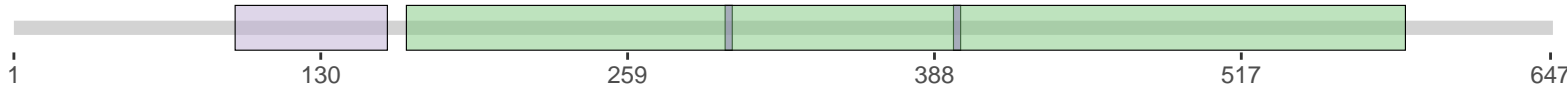


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LIEQAEQGVDDYFTIHAGVLLRYPLTKRMTGIVSRGGSHAKWCLAYHKNFAYEHWDLLDKNGYDLSLSIGDGLRPGSYDANDTAGFAELLTQGLTRRAWKEKDVQVNEGPGHYPMKIPENMKKOLEWNEAPFFYTLGLPLTDAHPGVYDHTSAGIAANGSALGALLGVVTPKHELGLPNRDDVKTGVYKXIAAHAADLAKGHPLSGAWDDALSKARFEFRWMDGFALSPLDPVTALSFHDETLPADGAKVAHFQGMCGPFGFQGMKTEIDRKYETHGYGSAEAL

NbL12g01750.1 uncharacterized_LOC107777172 [MW = 10.76 kDa]

No. of times detected



log(intensity)



Values from



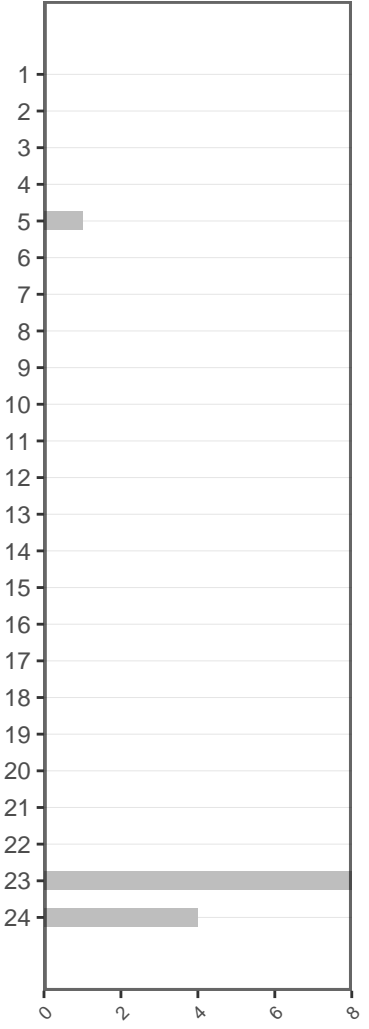
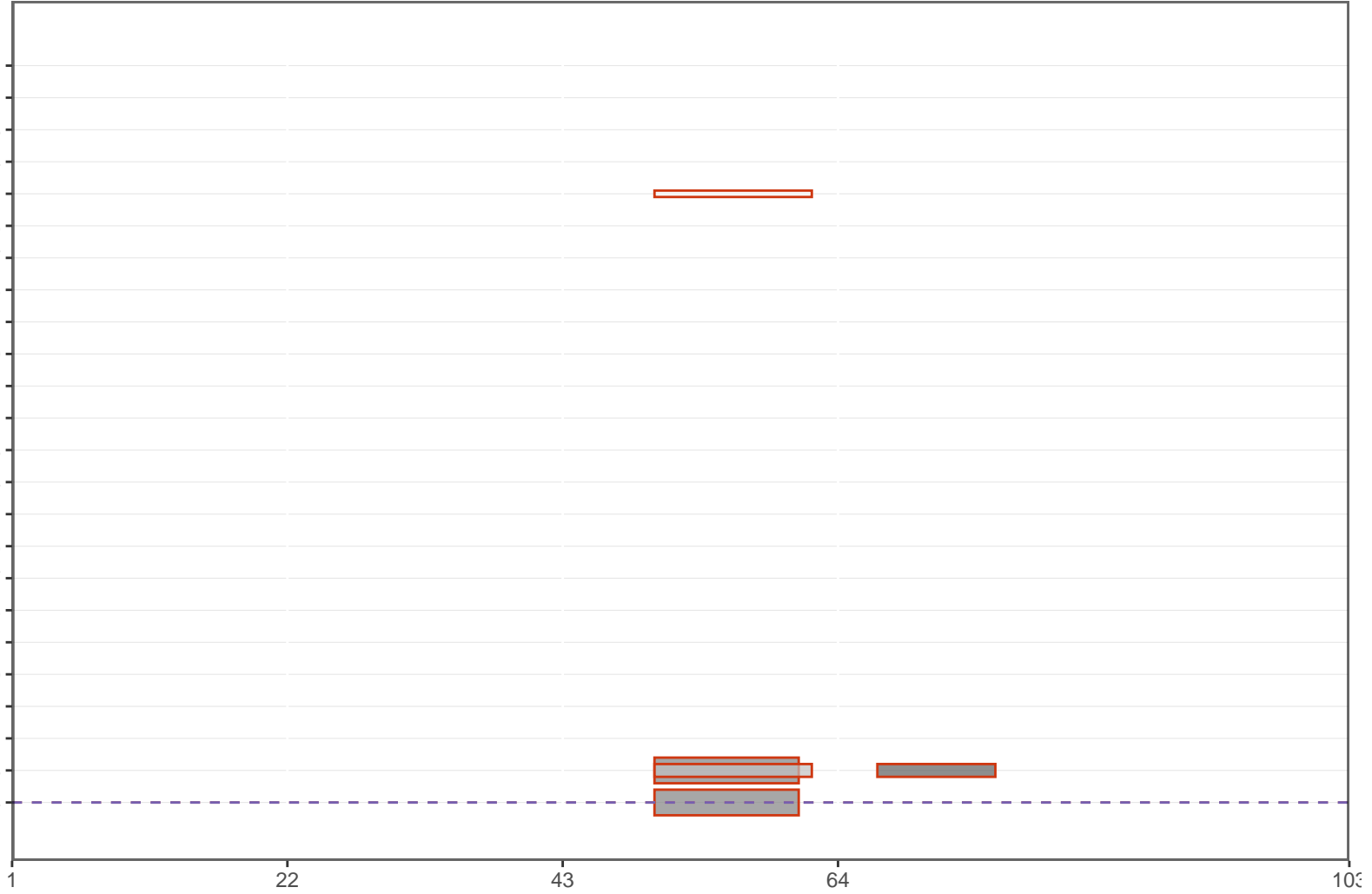
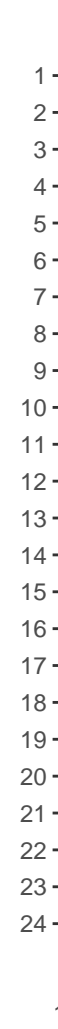
MW indication



Molecular weight



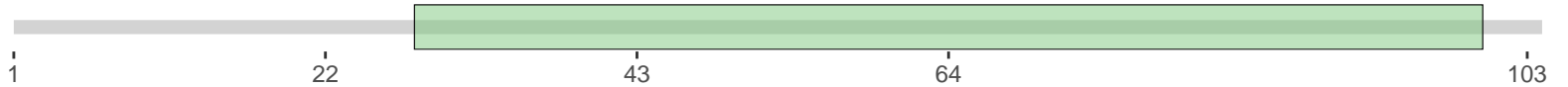
Gel Slice



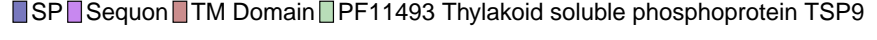
Protein length



Pfam domains



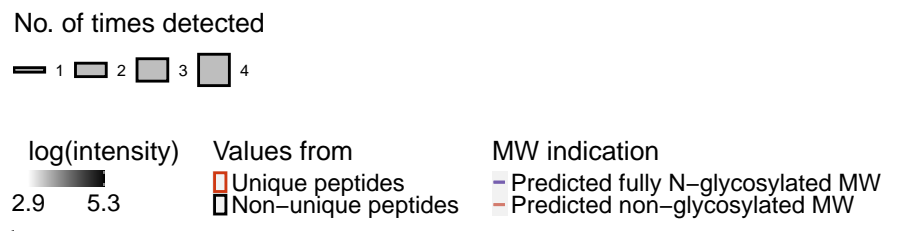
Pfam Description



Protein sequence:

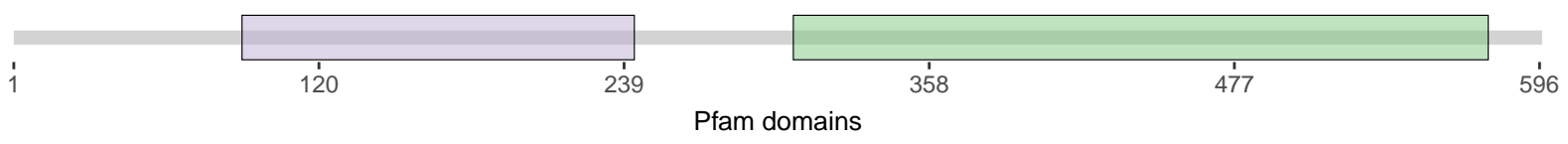
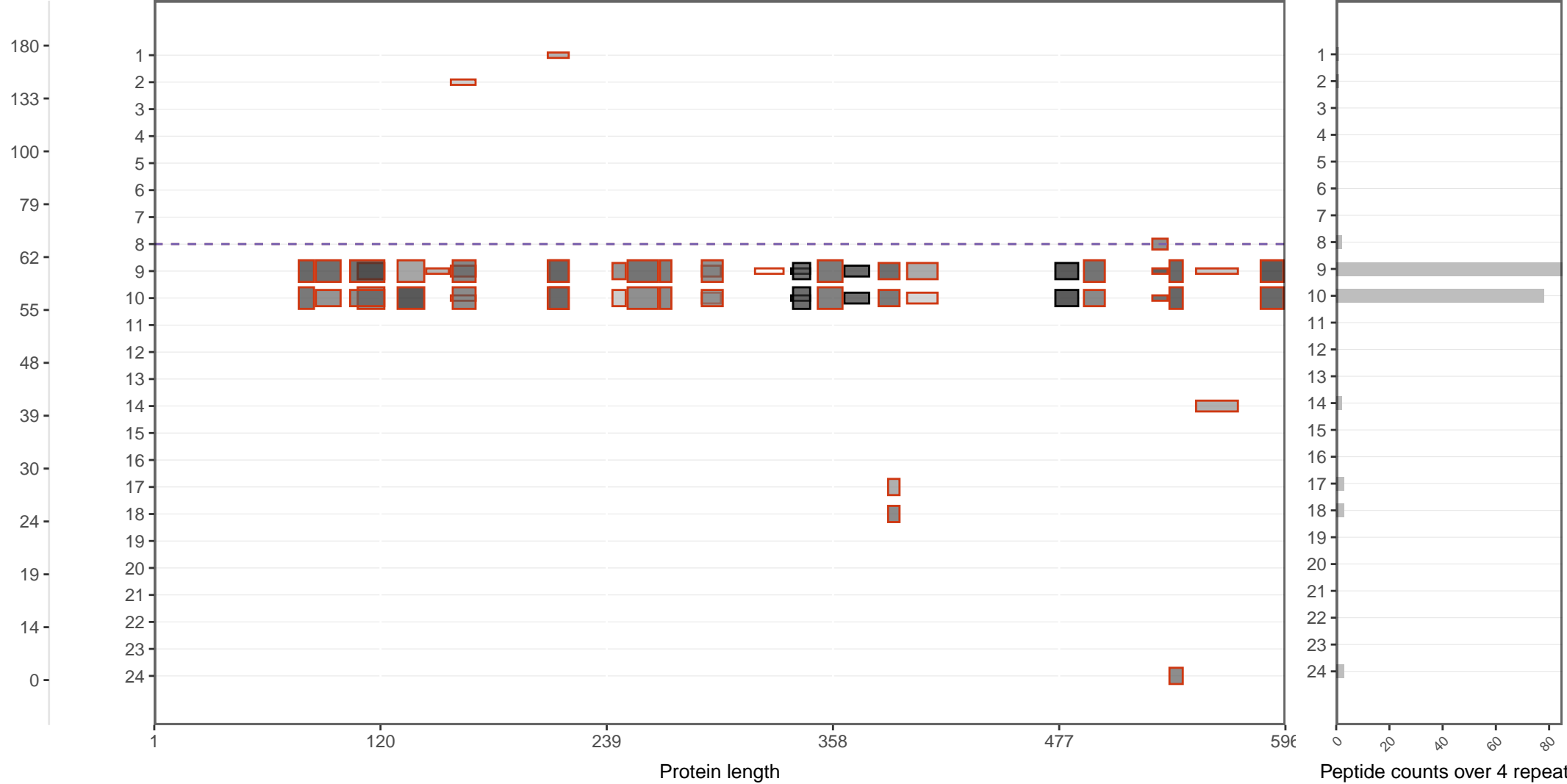
ILDVFLGATKEDQLLETDPILKIKVEKSTGTTTSSKKSIVSPPKKNSSGGFGGGLFAKKE*

NbL12g01730.1 anthranilate_synthase_alpha_subunit_2_chloroplastic-like [MW = 66.49 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00425 chorismate binding enzyme
- PF04715 Anthranilate synthase component I, N terminal region

Protein sequence:

SSIKLHTSGFGTSLKKKSTMTREDYKQKAVLNKKEHLGADFDQILVSRQFERRTFADFEVYRALRVNPNPSPMTYLGARGGILVASSPEILTRVKKKTYNRPPLAGTRRGGKPEEDYENLGNLLHDEKQCAEHLMLVDLGRNDVGRKVPQSGVYKELMNVVERYSYVHHSSTVTGELLDLHLSGWDLRAALPLVGTVSGAPKVKWAMELIDQLEVTRRGPVSGGFGGHSFTGEMDIALALRTVFPFGTRYDTMYSYKDKANKRRDWAHLGGAGVADSDPQDCEORECENKAA

NbL12g01670.1 protein_PMR5-like [MW - SP = 40.5 kDa]

No. of times detected



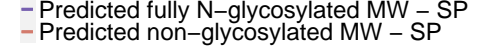
log(intensity)



Values from

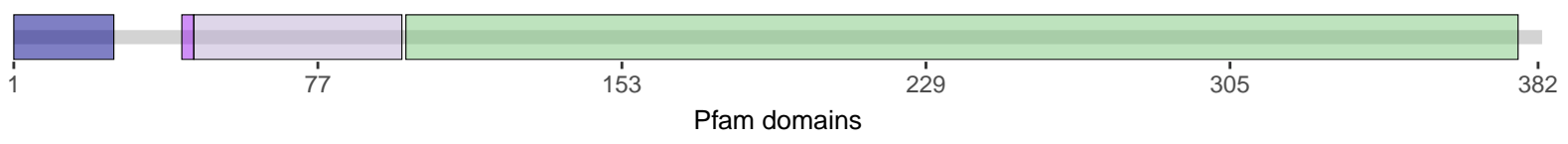
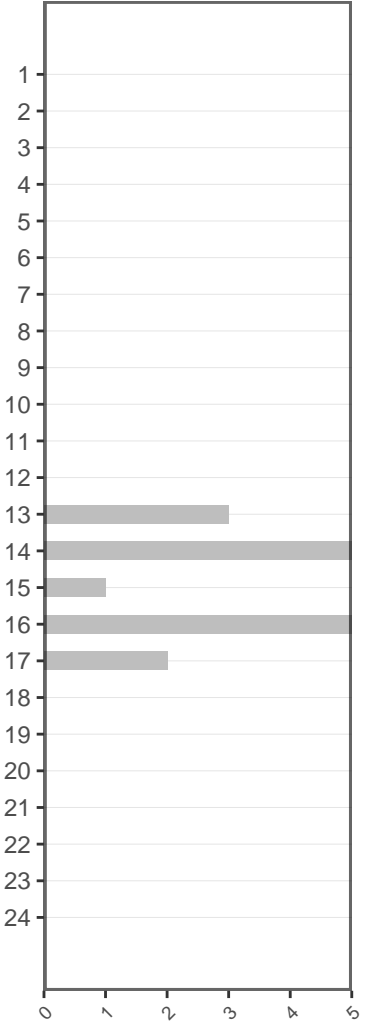
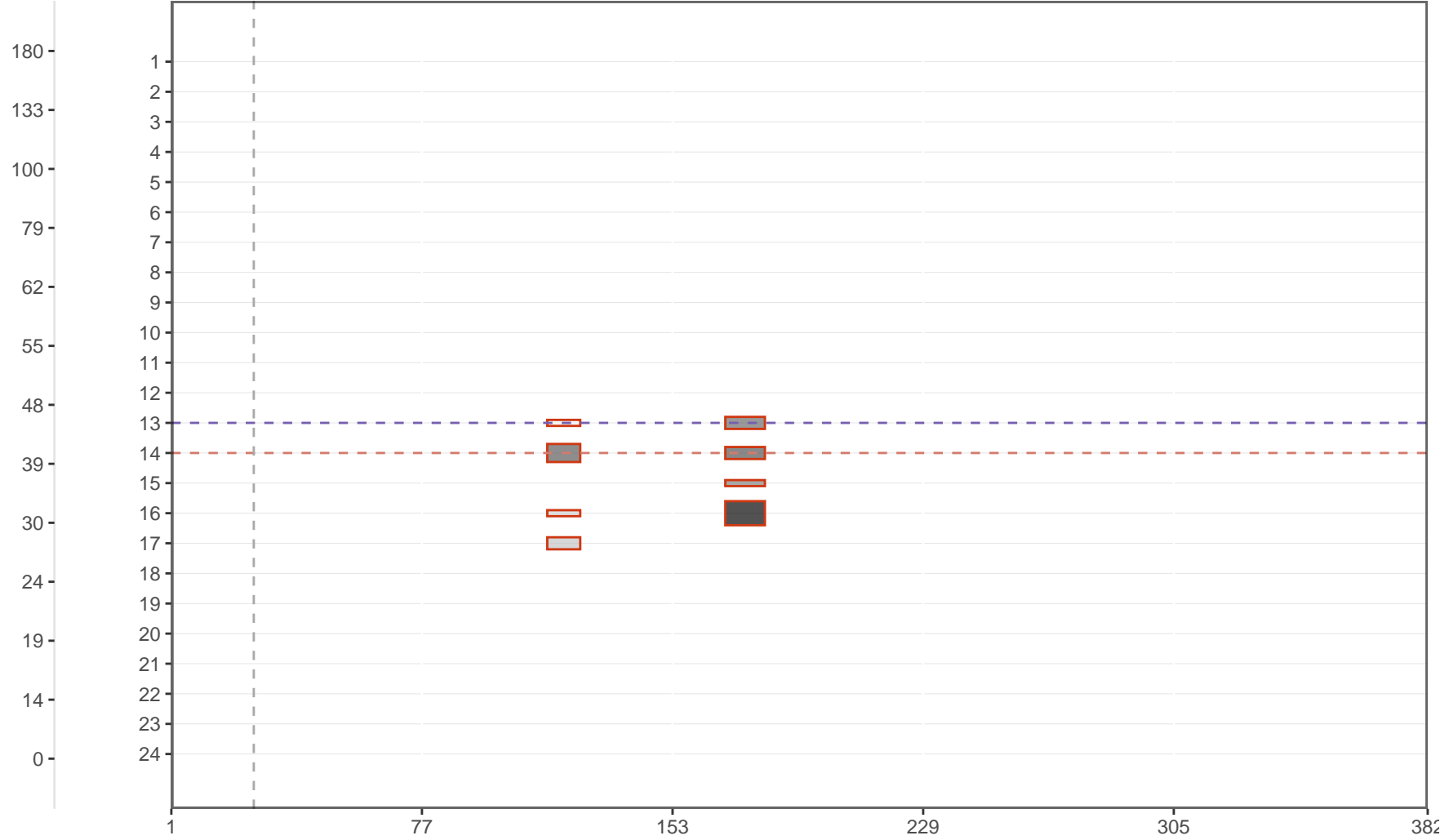


MW indication

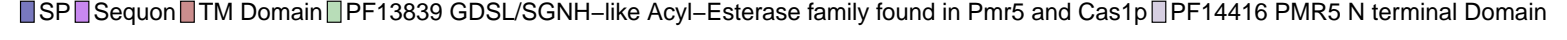


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

IKNVLRLDDISKNSNAWAGVDFLSEFTNGHWTHKSGSLQGWMEAGGTLHQDMNRLVALERGLRTWARWIDANDKSRTRIFFGQISPTHYHNQWNTGTSMATSR6CYGETVPMFTGTAVPGTYPDQMKVLGAVIRDMNPPFLDITFLSAMRKDAPHSIVGGALTSSEGRANPDRHSADGSHWGLAGLPDTWNGLEYTALFF

NbL12g01630.1 ran-binding_protein_1_homolog_c-like [MW = 24.79 kDa]

No. of times detected



log(intensity)



Values from



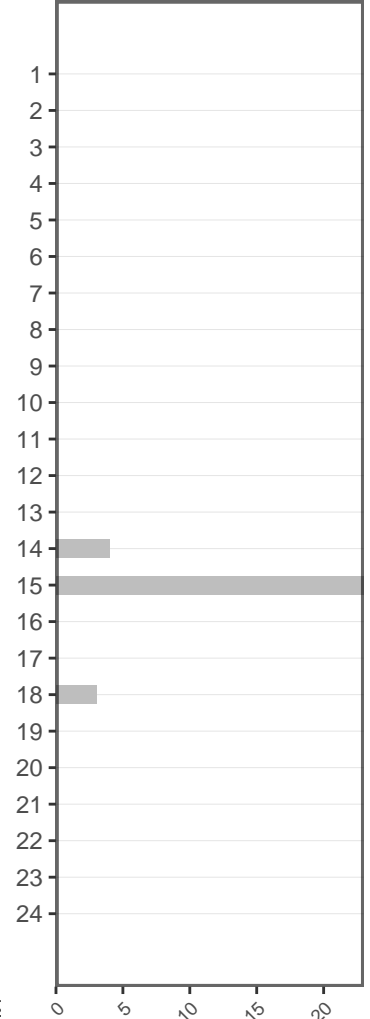
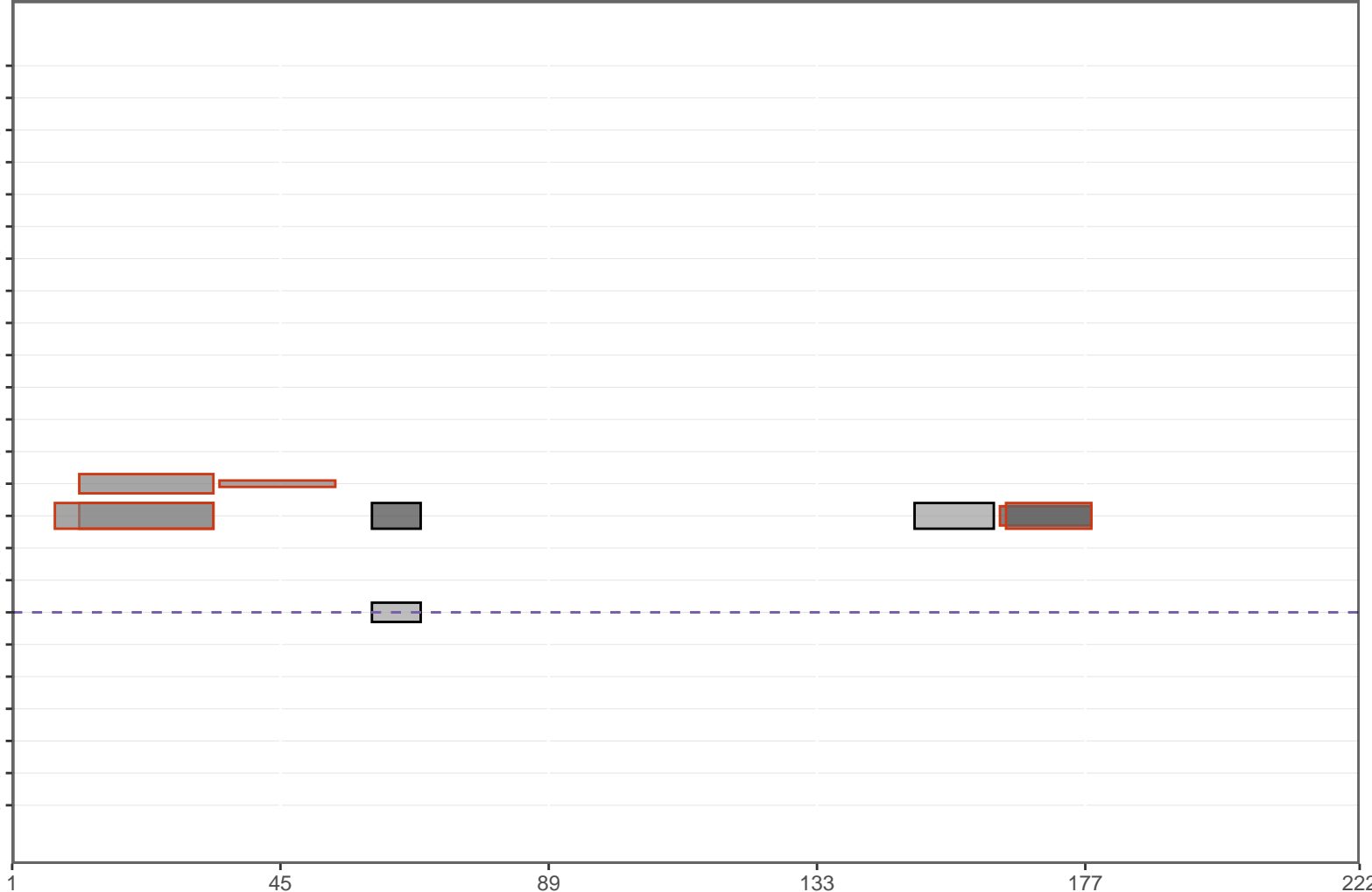
MW indication



Molecular weight

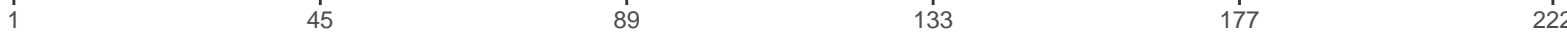


Gel Slice

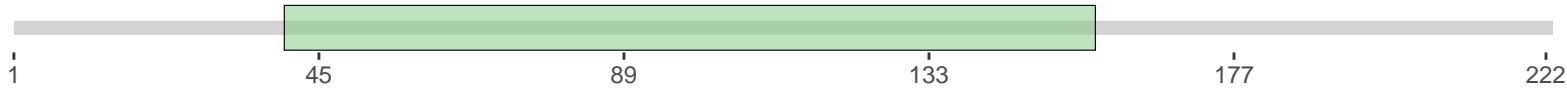


Peptide counts over 4 repeats

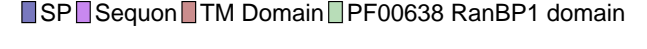
Protein length



Pfam domains



Pfam Description



Protein sequence:

MSANIKLVLPMTLQSHAGNEKSGLIWHPDFADGELKDELFLGRFASIEKIKSFMEFMFOEVAESGQKKVVENEDGDTAAELLEKLVSEDKKSEKSEKDAEDKTHEGGDKDENFSKDKTEKKDESAIA*

NbL12g01620.1 ERBB-3_BINDING_PROTEIN_1-like [MW = 43.52 kDa]

No. of times detected



log(intensity)



Values from



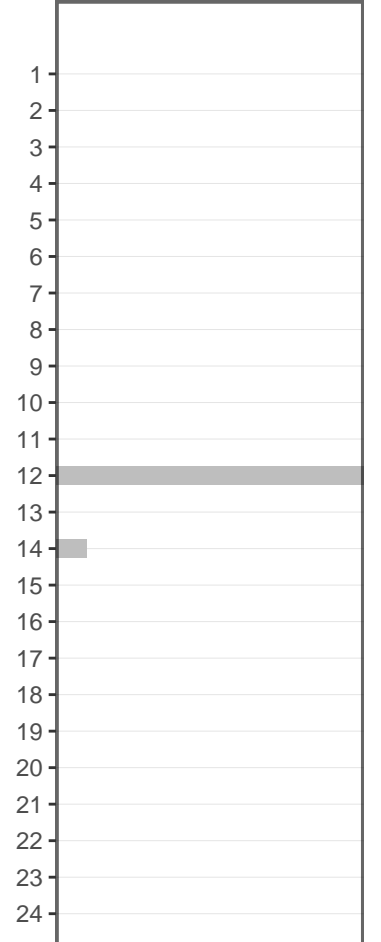
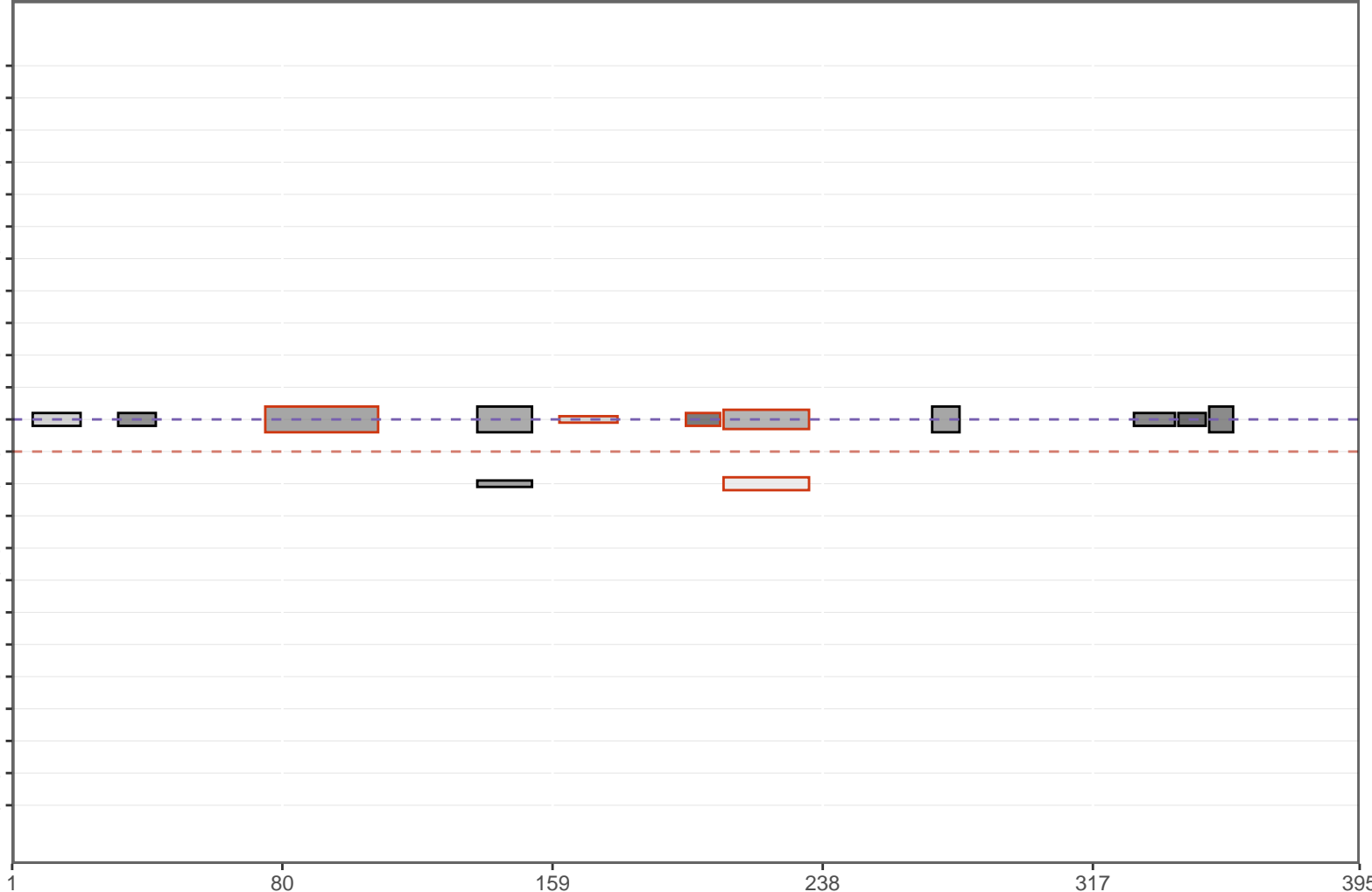
MW indication



Molecular weight



Gel Slice

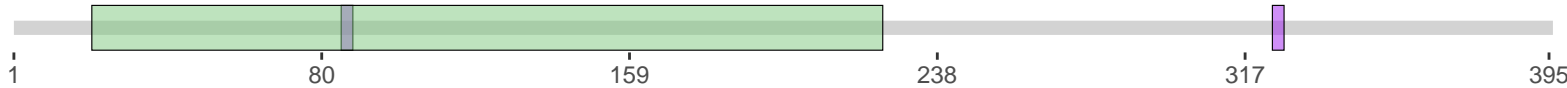


Peptide counts over 4 repeats

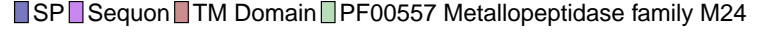
Protein length



Pfam domains



Pfam Description



Protein sequence:

SHQMKQFYIDGNKVLGVSNPETRVEDAEFEENEVYSIDVTSTGEGPKLLDEKGTTYKRAVDKSNLJKMKASRFISESGKFFVMPFTARDLEEKRARLGLVEGVNHELLGPPVPLHEKPGDLVAHFKFTVLLMPNGSDRIFTHLQELKPKTKTIDDEPEKTVLALPLVSKKKKGGKXXXXKXKGEKTEELSGAEPMEGEEGNGAES

NbL12g01610.1 BAG_family_molecular_chaperone_regulator_1-like [MW = 22.68 kDa]

No. of times detected



log(intensity)



Values from



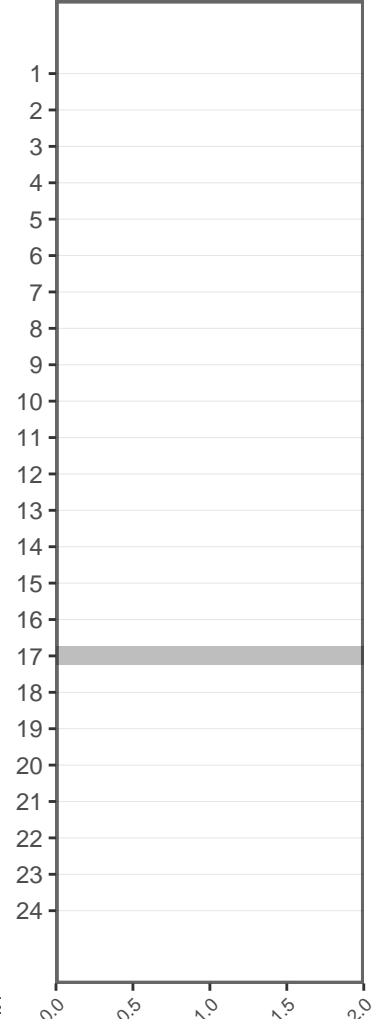
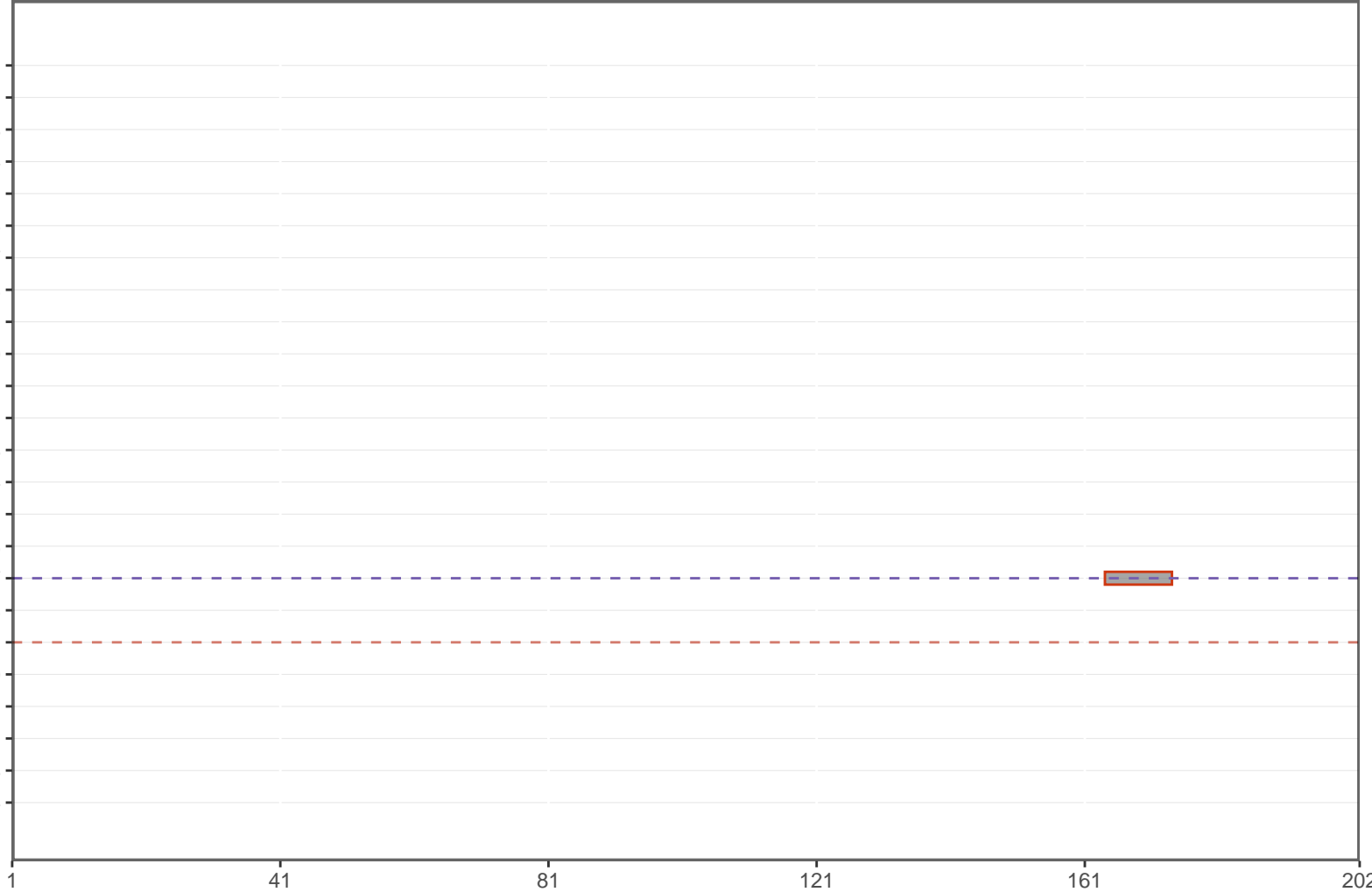
MW indication



Molecular weight



Gel Slice



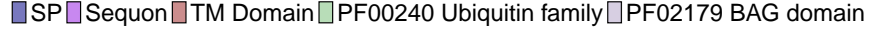
Peptide counts over 4 repeats

Protein length



Pfam domains

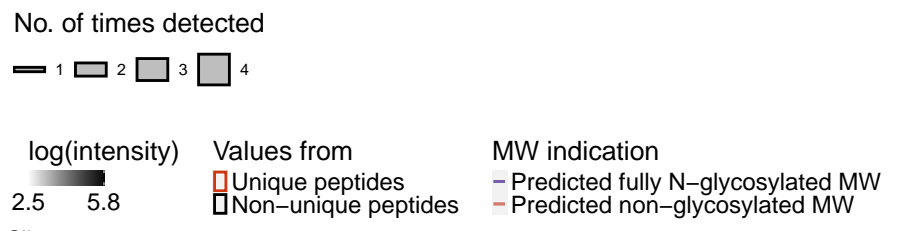
Pfam Description



Protein sequence:

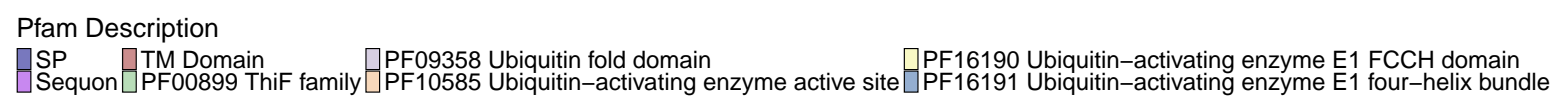
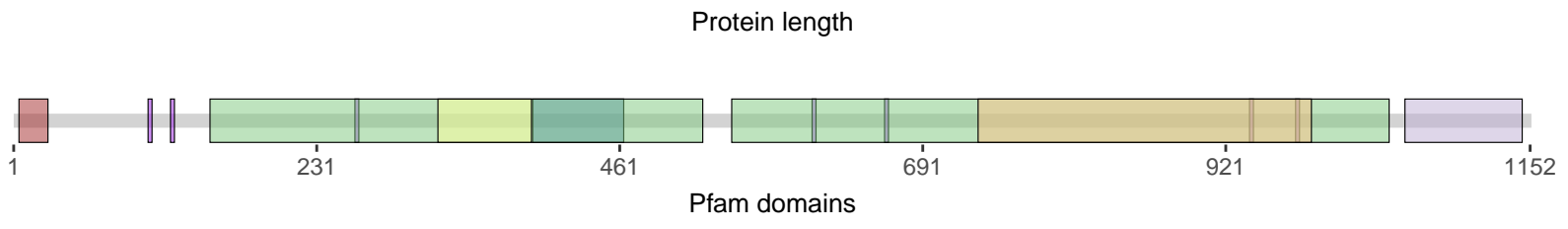
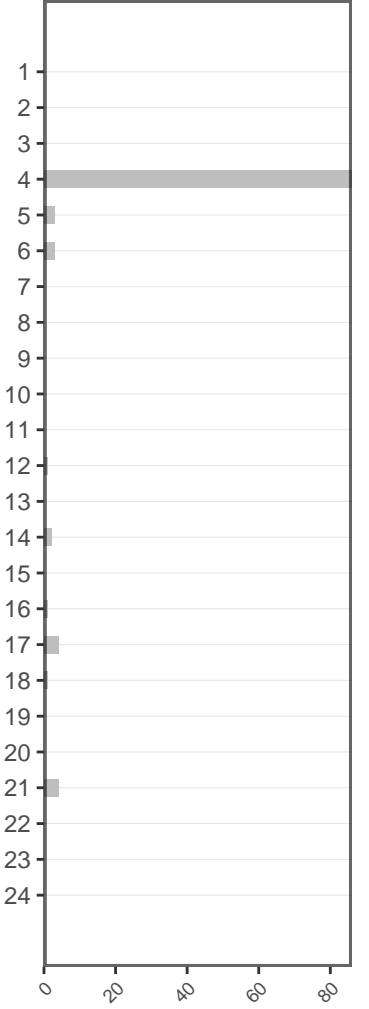
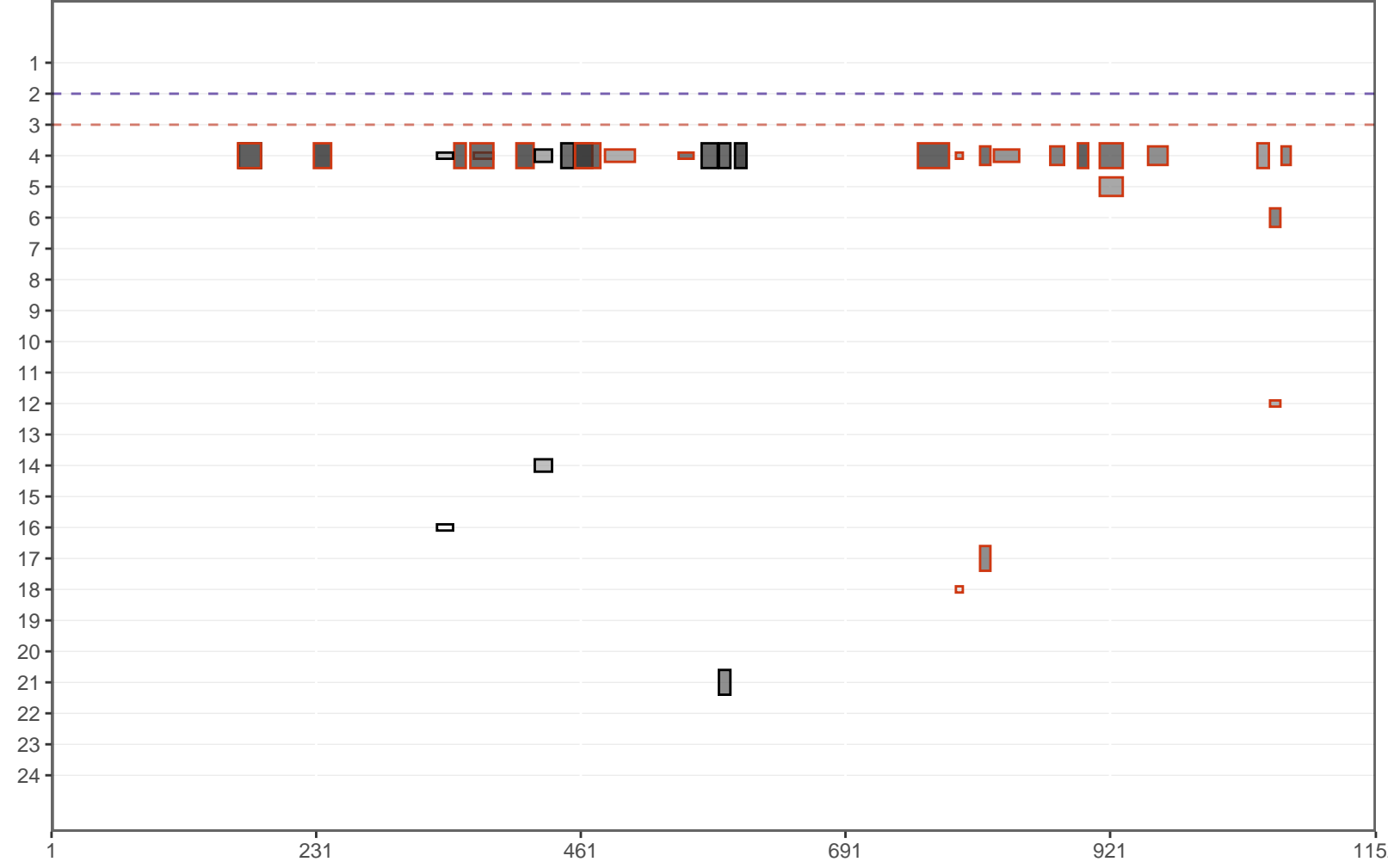
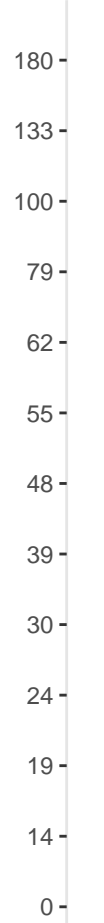
LHIOEDMPNLLLEDPMSEKRNKINQNTFVSGEAWGVVREVDKLSHRLLAEAEAMQGRGTVVEDREFVVLTELFMQLLKLDSIEADGGEARAEARRKEVHRQGFVDMLDNFKARNEKL

NbL12g01580.1 ubiquitin-activating_enzyme_E1_1-like [MW = 128.33 kDa]



Molecular weight

Gel Slice



Protein sequence:
 MKNVFLVGGGALGCEFLKNNLALMGVSGNKKGKLTVDLDDVIEKSNLSRGLFRDWNIGGAKSTVAATAASINSGLQVEALGNRVGPEFENVFDQTRWENLSVYVALDNNINARLYVDGRGLYFQKPLLESGTLGAKNTGMVPHILTENYGSARDPPEKQAPMCTLSHSFPHNDHQLTWARSEFEGLLEKIPAEVNLVGNPSEVTSAGTNAGDQARDNLERVLEGLDRESGETTFEDGIAWARLKFEDYFANRVKGLIFFTFPDSMTS6GAPFWEAPKRFPHLPQFSSTDP

NbL12g01570.1 gamma-interferon-inducible_lysoosomal_thiol_reductase-like [MW - SP = 25.32 kDa]

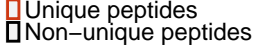
No. of times detected



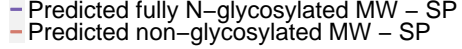
log(intensity)



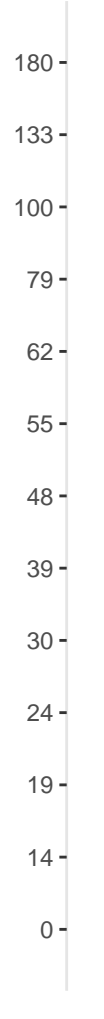
Values from



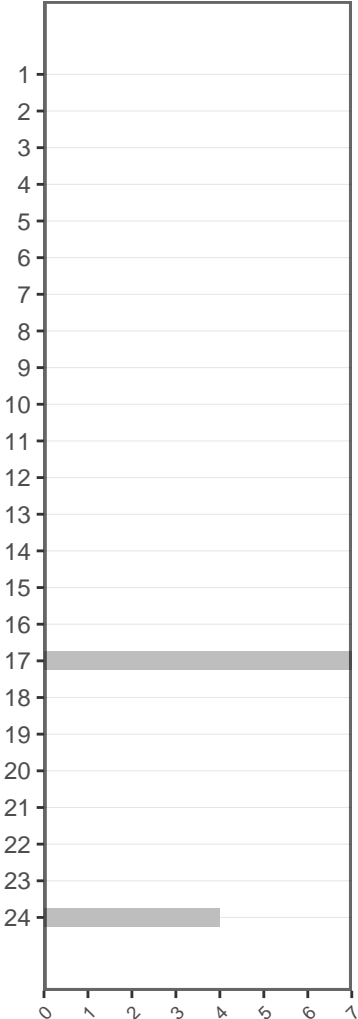
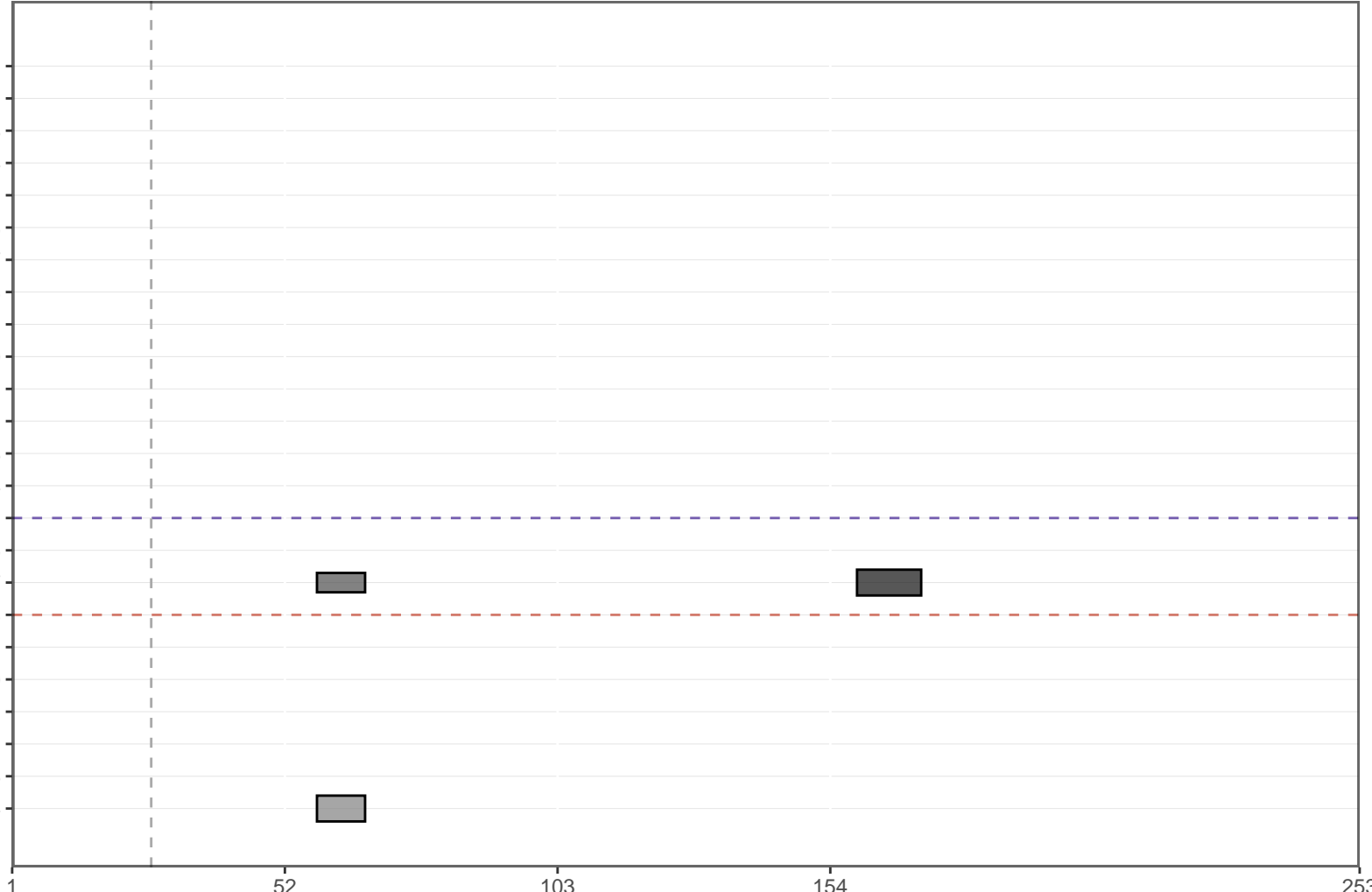
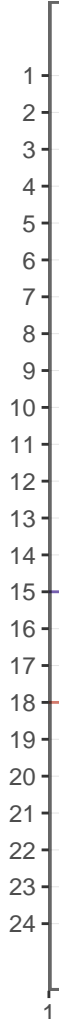
MW indication



Molecular weight

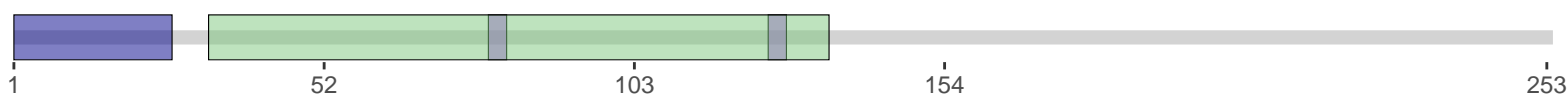


Gel Slice



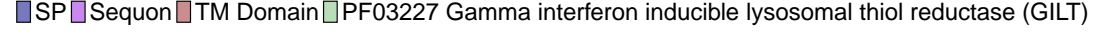
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

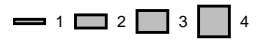


Protein sequence:

CVESLLYIKNYIQWETCFEKLKAKPVDGCVSGRGELELRVAAETNALGPHKIVPVAIVVGGPLVDEYMDFFIYKAYKAGAPVPGG66TVNWKTRKRFPEFLMHTASSKLSITGSAITSWIMNRVNPASA

NbL12g01560.1 40S_ribosomal_protein_S4-like [MW = 32.02 kDa]

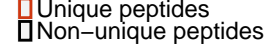
No. of times detected



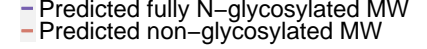
log(intensity)



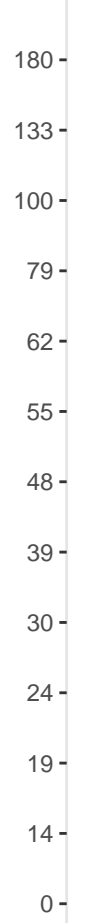
Values from



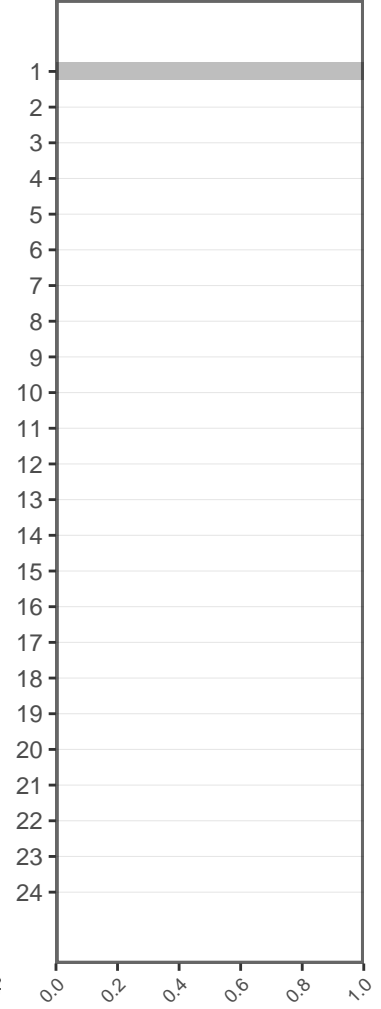
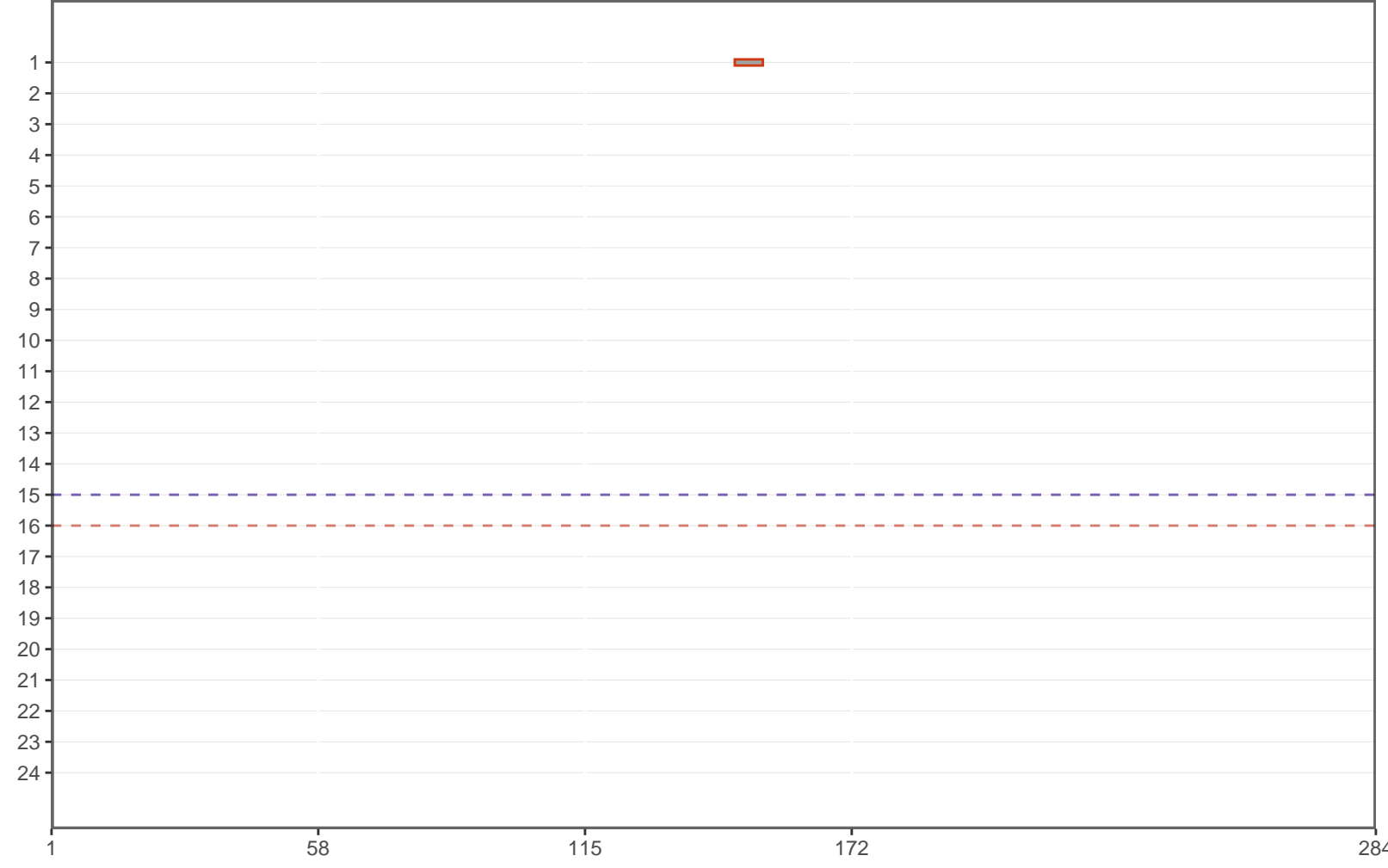
MW indication



Molecular weight



Gel Slice

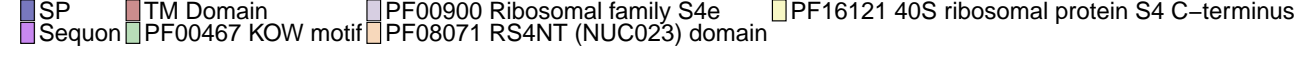


Protein length



Pfam domains

Pfam Description



Protein sequence:

RLHSVYRDEEAQKFKLQKVRISIGFGKGIPIVLYDGRFRIRYDPLIKANDTVKLDLESNKIVDFIKFDVGNVMMVTGGRRNRGRVGVKNREKHKGSFETVHQDLAGHEFATRLGNVFTLQKGTQPVVSLPKGDKGKLSIIEEARKRLAAGSATA

NbL12g01480.1 40S_ribosomal_protein_S8-like [MW = 25.12 kDa]

No. of times detected



log(intensity)



Values from



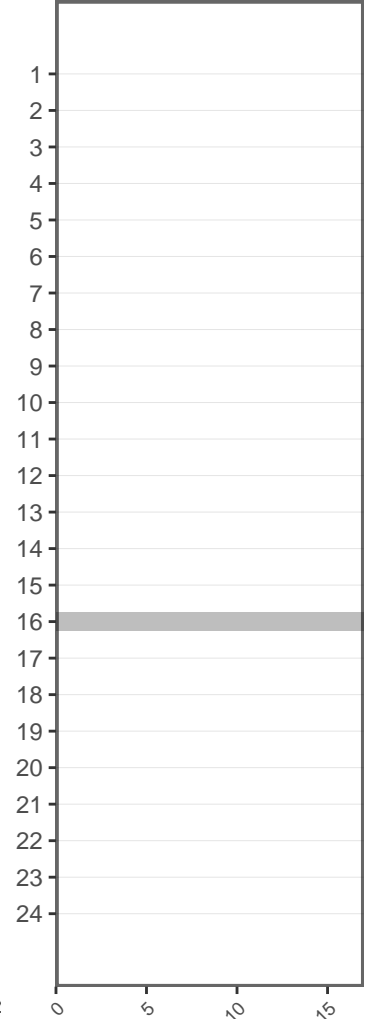
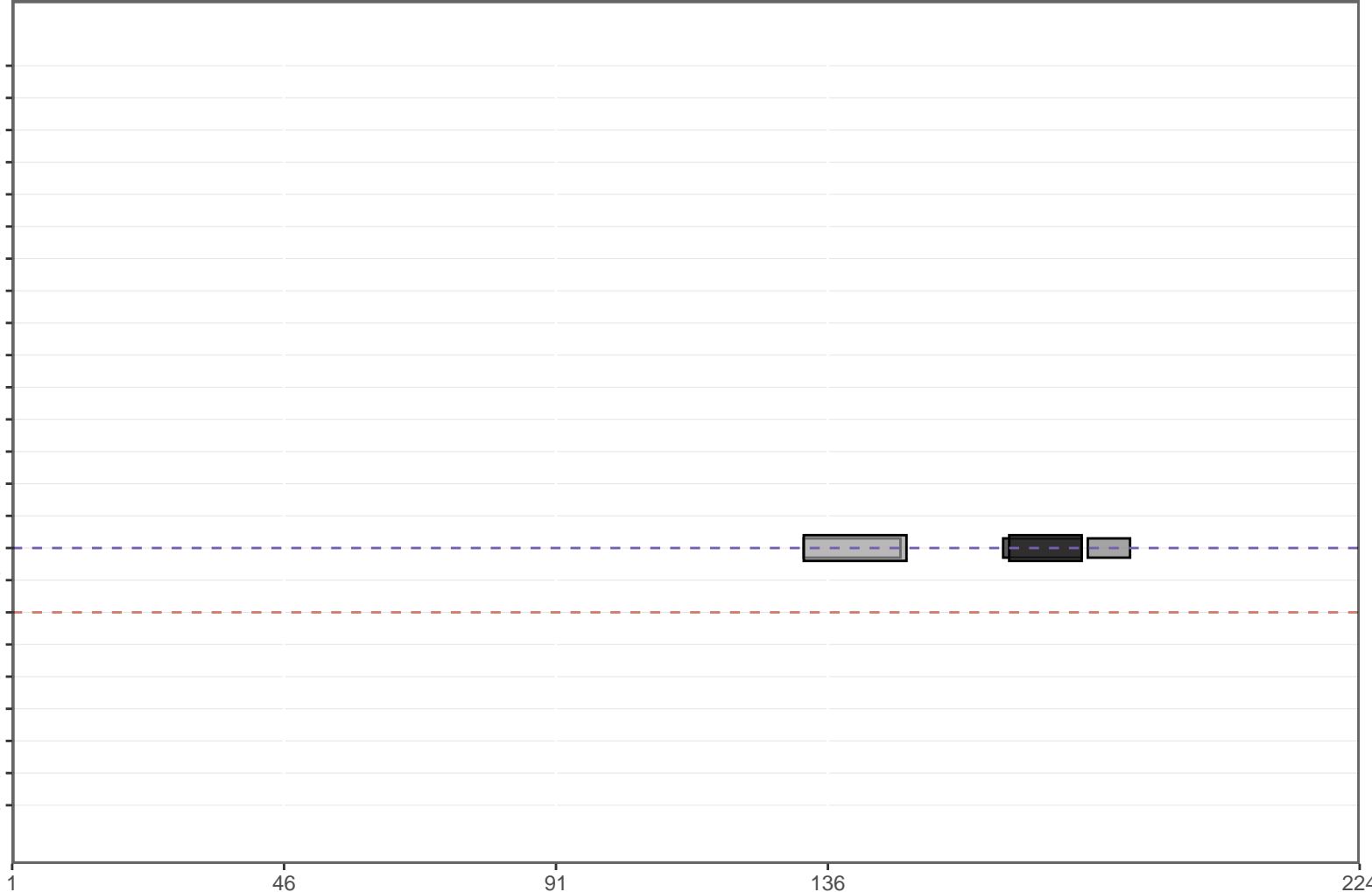
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

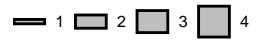


Protein sequence:

ISAVQVDAAPFKQWVFLGHVYDGRKKKGAANKETTEEESGAAAPAAEAAKSNHVARLKRKQKDKLDPHLEEGFSGRLVADISRPQGGGRADGVILEGKELEFYMKLGNKKKKAAGSAAV

NbL12g01410.1 26S_protease_regulatory_subunit_6B_homolog [MW = 46.34 kDa]

No. of times detected



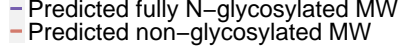
log(intensity)



Values from

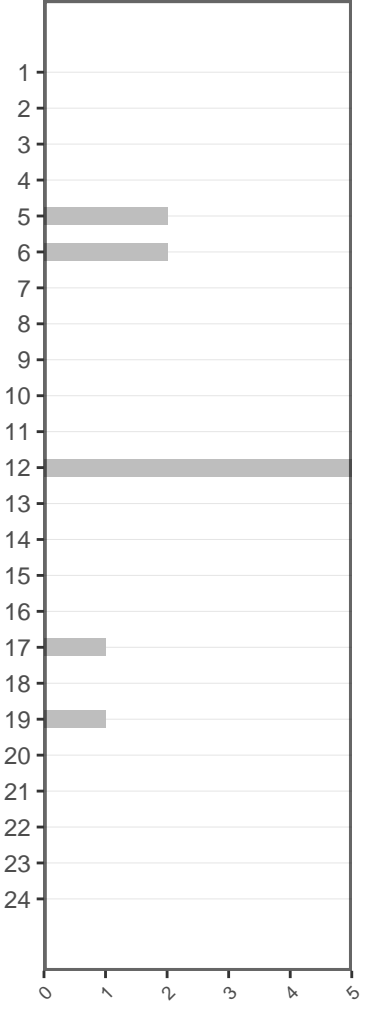
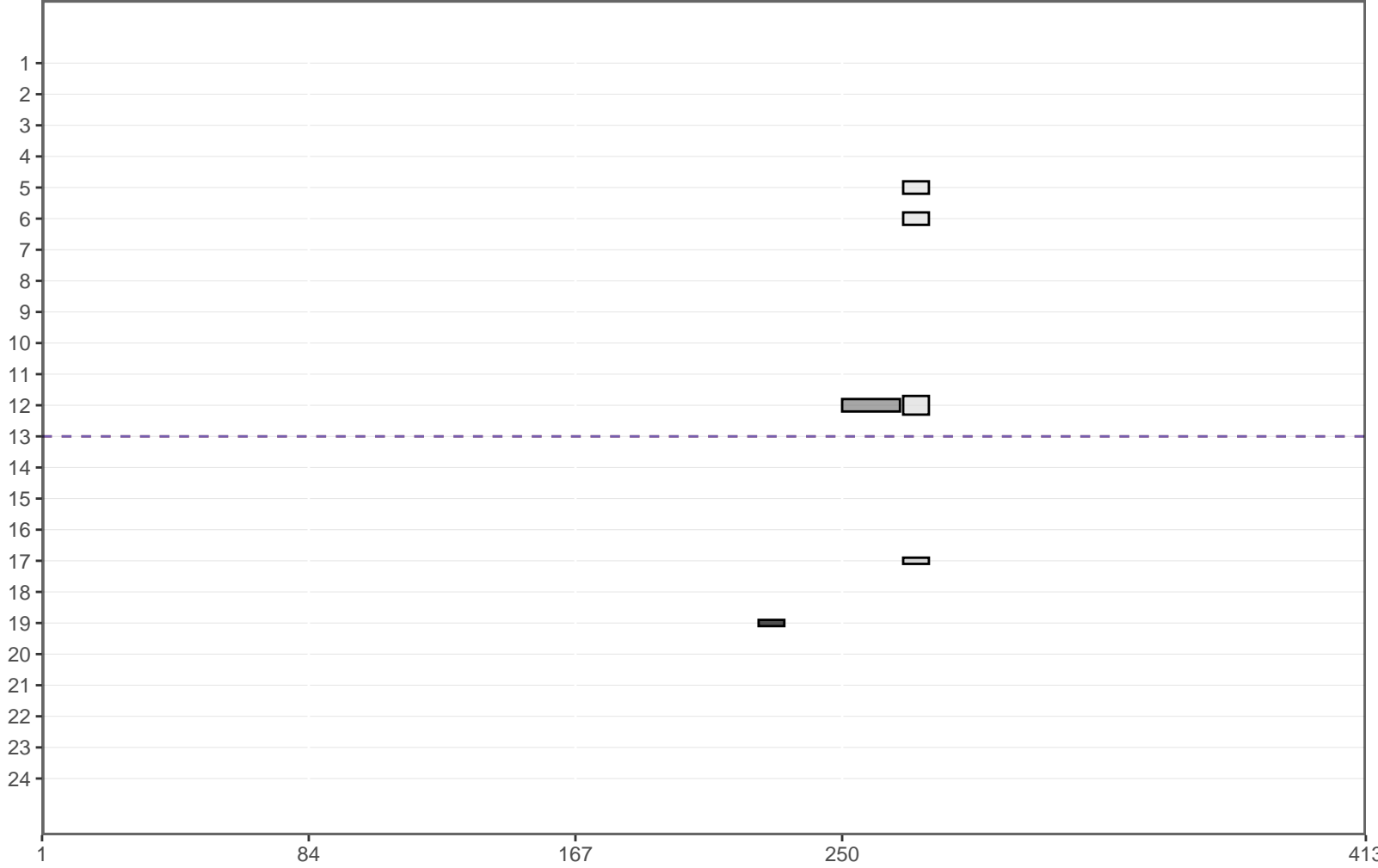
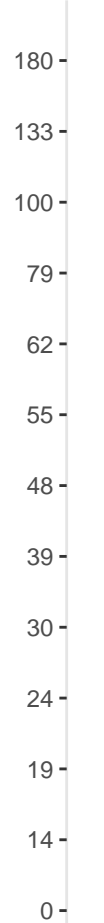


MW indication



Molecular weight

Gel Slice



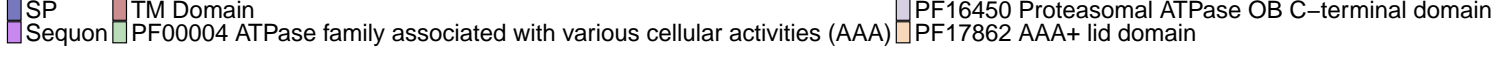
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

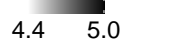
SVLLYGPPTGKTKMLAKAWAHHTAFAIRVGSSEFVQKYLGGPRMVRDVFRLAKENAFIFIDEVDIAATRFDAQTGADREVGRIIMELLNGMDGFDQTVNKKVIMATNRADTLRDLRALPGRLDRIKIEFPLPRRQKRLVFGVGTAKMNLGDEVLDLEDVSRPKISAAEISAGDEAGMHAVRKKNRYLFPKDFEKGVRTNKKKPDQDFEYK

NbL12g01390.1 40S_ribosomal_protein_S26-3-like [MW = 14.48 kDa]

No. of times detected



log(intensity)



Values from



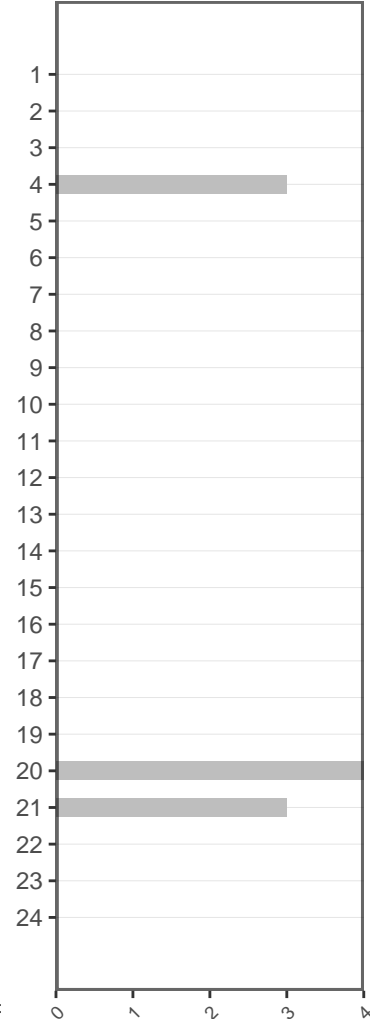
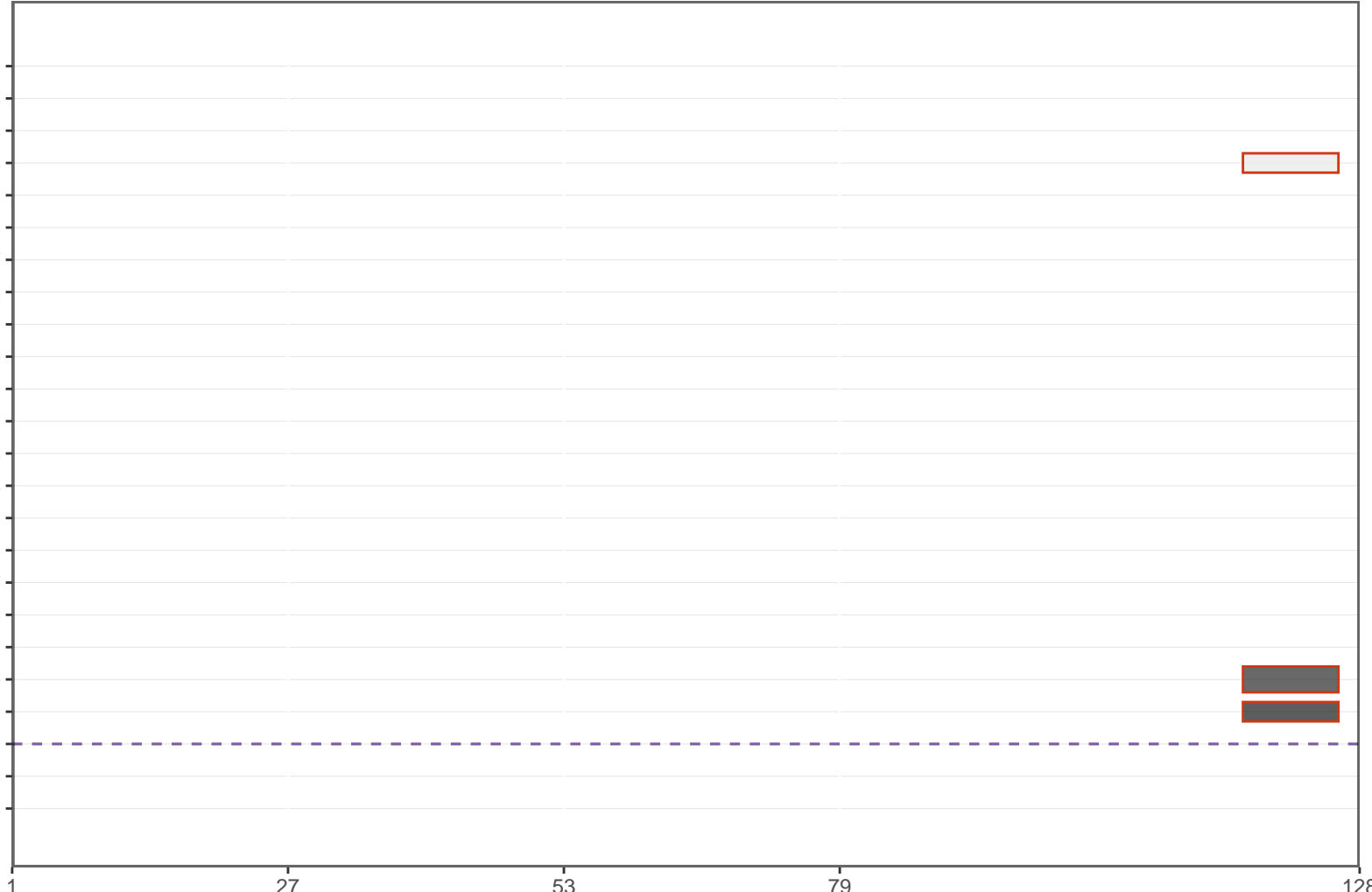
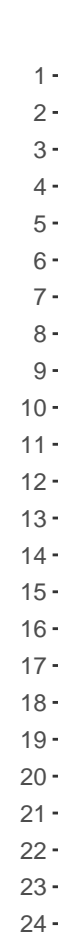
MW indication



Molecular weight



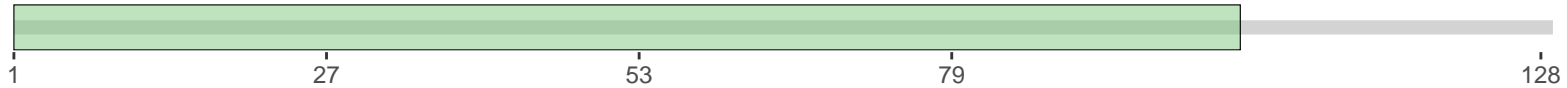
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

IDVQEACAFETYTLFKLKLKMGVGVGSAHKKVWRVRSVTDRRVREPPQFRFRPRDLPKPGDAPRPMGGAPAPRT

NbL12g01350.1 uncharacterized_protein_At5g48480-like [MW = 17.7 kDa]

No. of times detected



log(intensity)



Values from



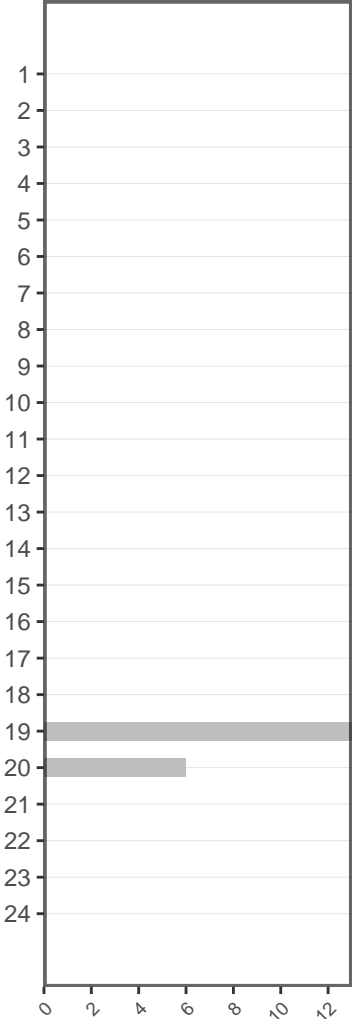
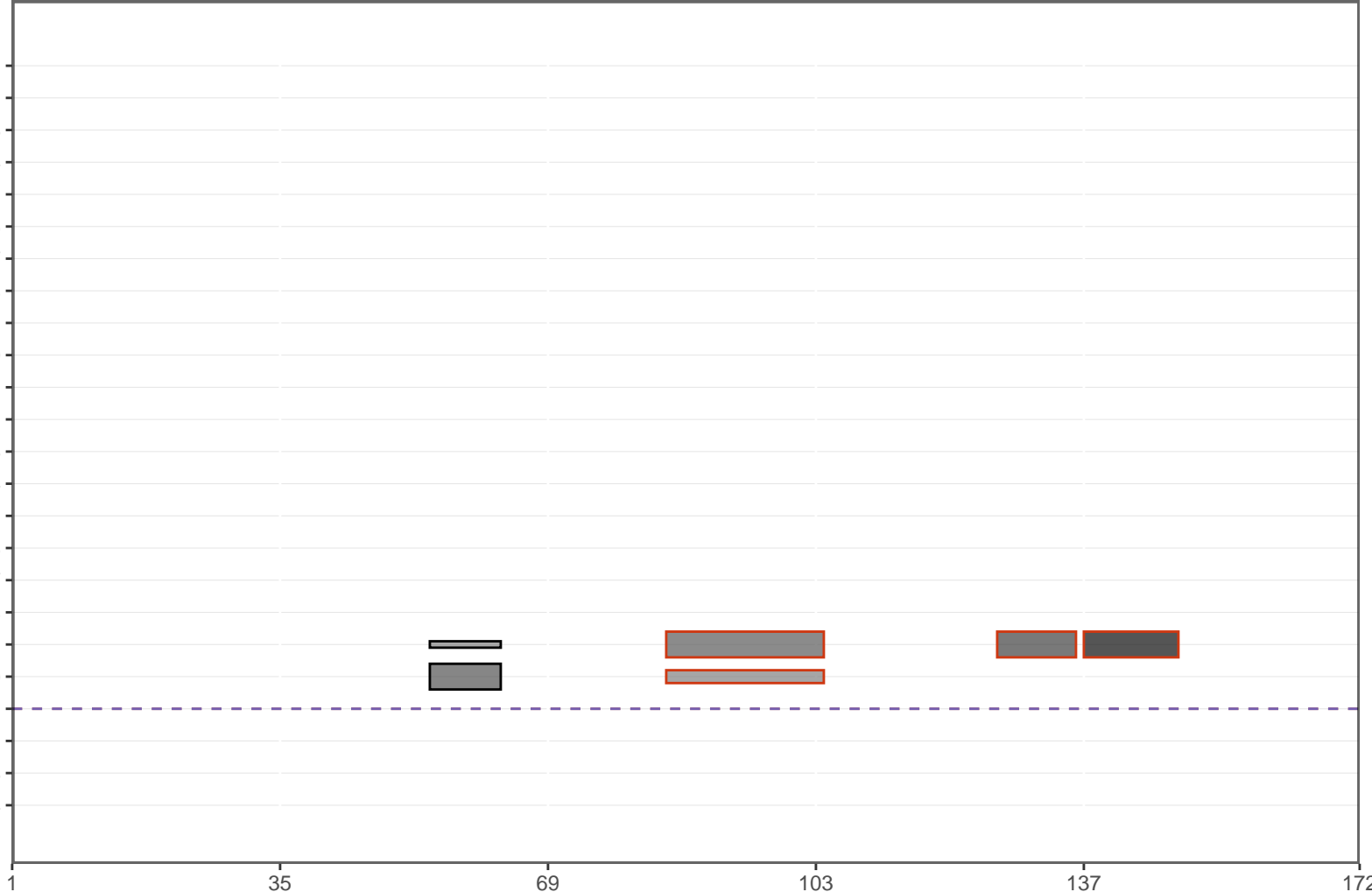
MW indication



Molecular weight



Gel Slice

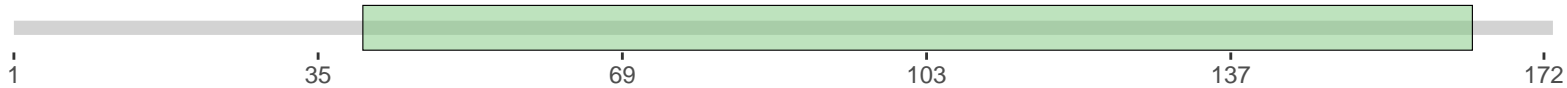


Protein length



Peptide counts over 4 repeats

Pfam domains

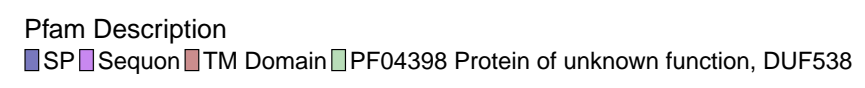
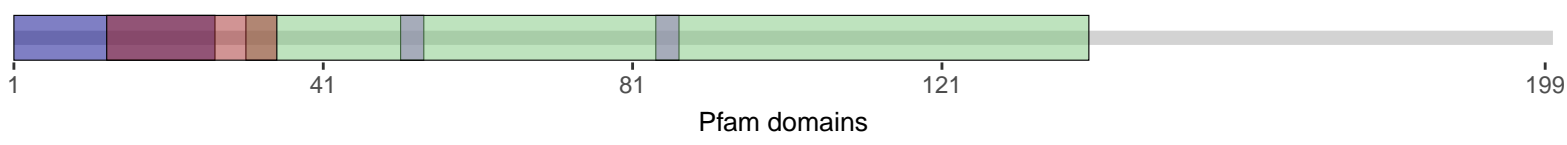
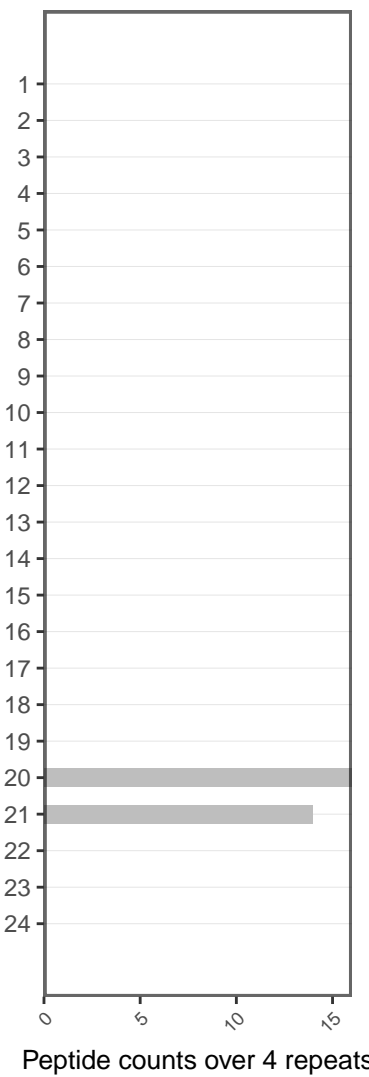
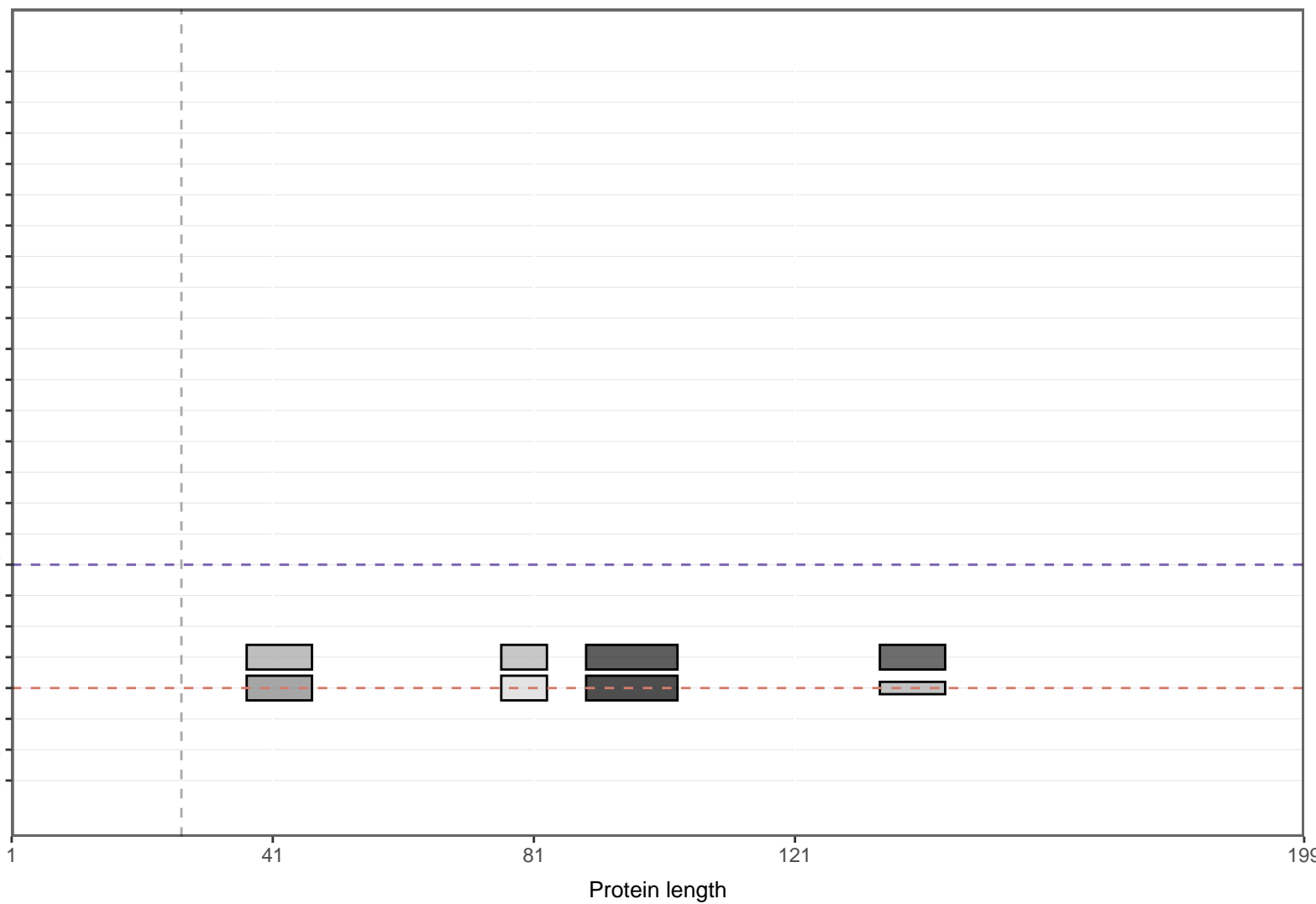
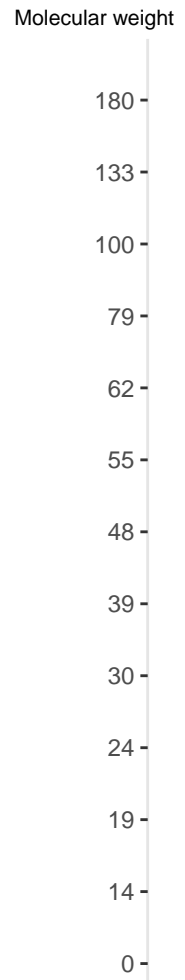
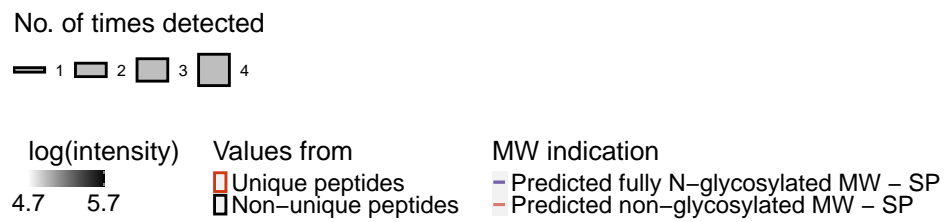


Pfam Description



Protein sequence:

SEIPLISSVELKLGSE6FLVSDLTD0066APVKKWTGGVFLQLETEDEVAAWAKAVAGAGVSEKIAEGDGAAGFGGRVQKLDKDPVGNVMMGSPVKKSGS



Protein sequence:

IRVSDGQIDSYSGISAKDLFLWFGVKKVYVABSSGGVYFDVGVVSKGFLSAFDSPEKCTAVQPTDLEVKVMSGRNSLLGKCTVRLRTTDCGPAAGSEARNLLKIVGT

NbL12g01330.1 adrenodoxin-like_protein_mitochondrial [MW = 17.89 kDa]

No. of times detected



log(intensity)



Values from



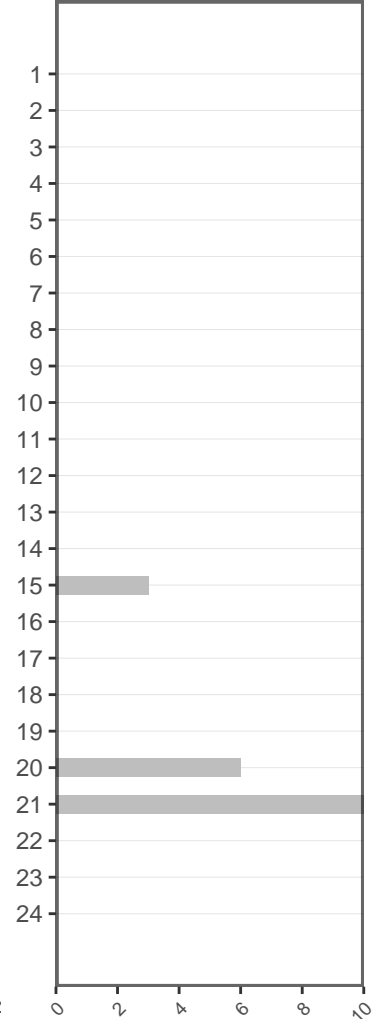
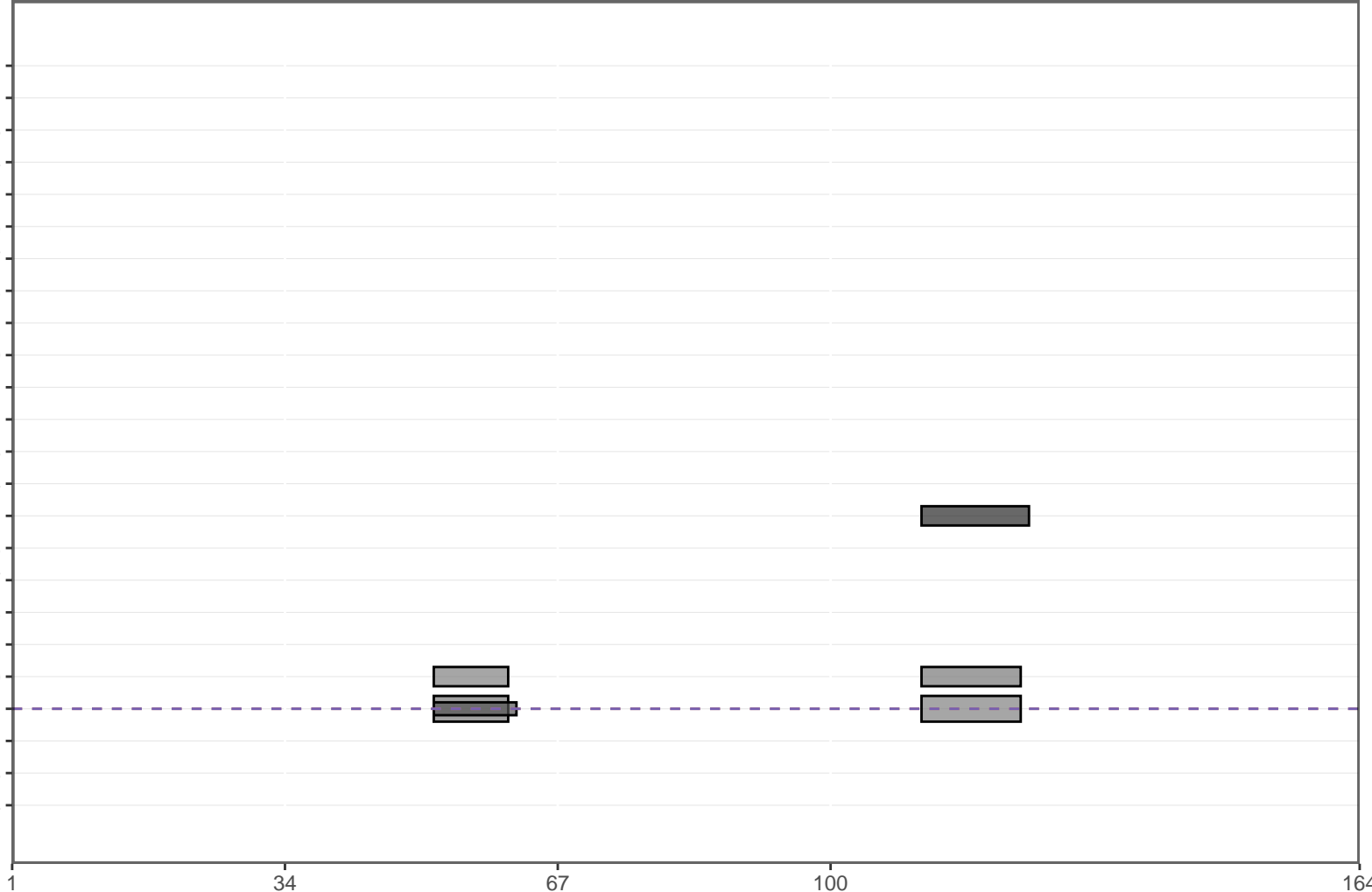
MW indication



Molecular weight



Gel Slice



Protein length

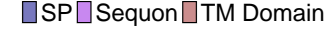


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

QTLKALTNHIGLIDPDHRLIEDIAGSAEGEVHAGEVLEKLPATYDEGVYVKRNSRARVLNKHSRLGGVVLSPLELGMVAIPERKPDIP

NbL12g01280.1 60S_ribosomal_protein_L5-like [MW = 37.81 kDa]

No. of times detected



log(intensity)



Values from



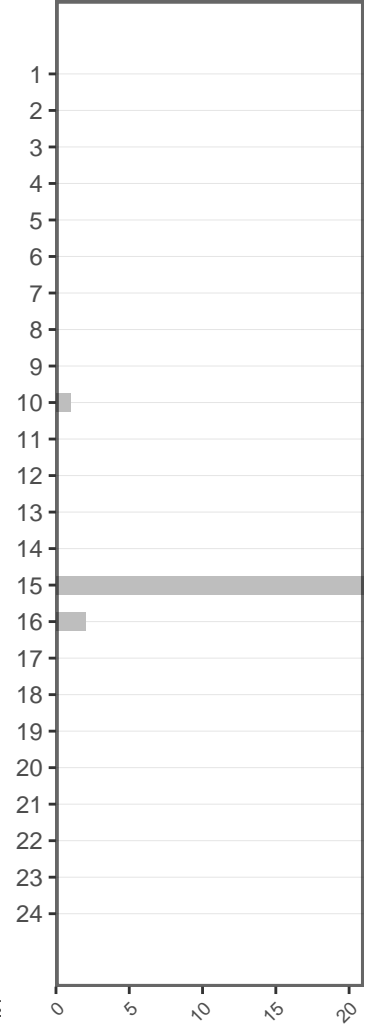
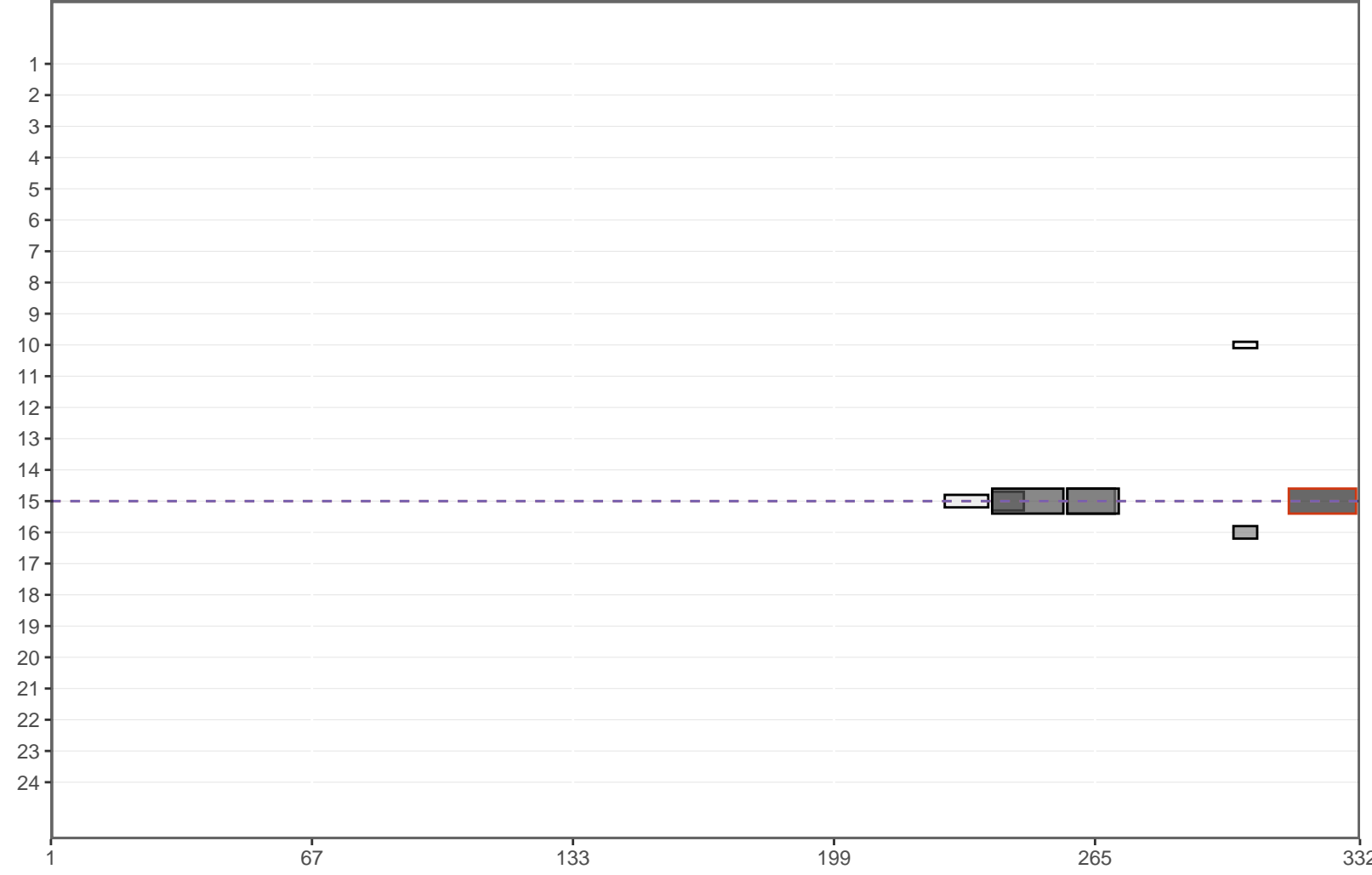
MW indication



Molecular weight



Gel Slice

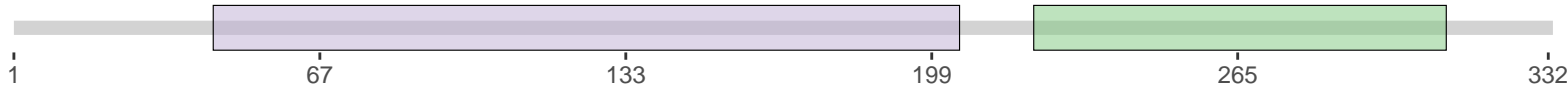


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VNGEDYVSEPAESRRFRALLDGLRITFTGNRFVFGALGKALDGGIDIPHSEKRFAGFKDQKQLEDAVNRKQVYGGHVSAYMKTLMEDPEKYGSHFSEYIKTGLEADDLEEMKKVKKHAARADPSSKSKDKPPFKGHRKRYLKKLTYDERKARUERLRLNLAAGNDDEEDDN

NbL12g01190.1 uncharacterized_LOC104090208 [MW = 22.02 kDa]

No. of times detected



log(intensity)



Values from



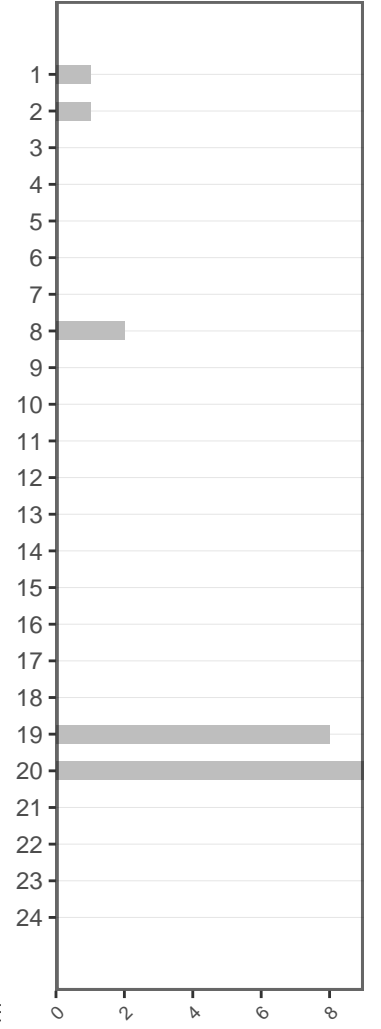
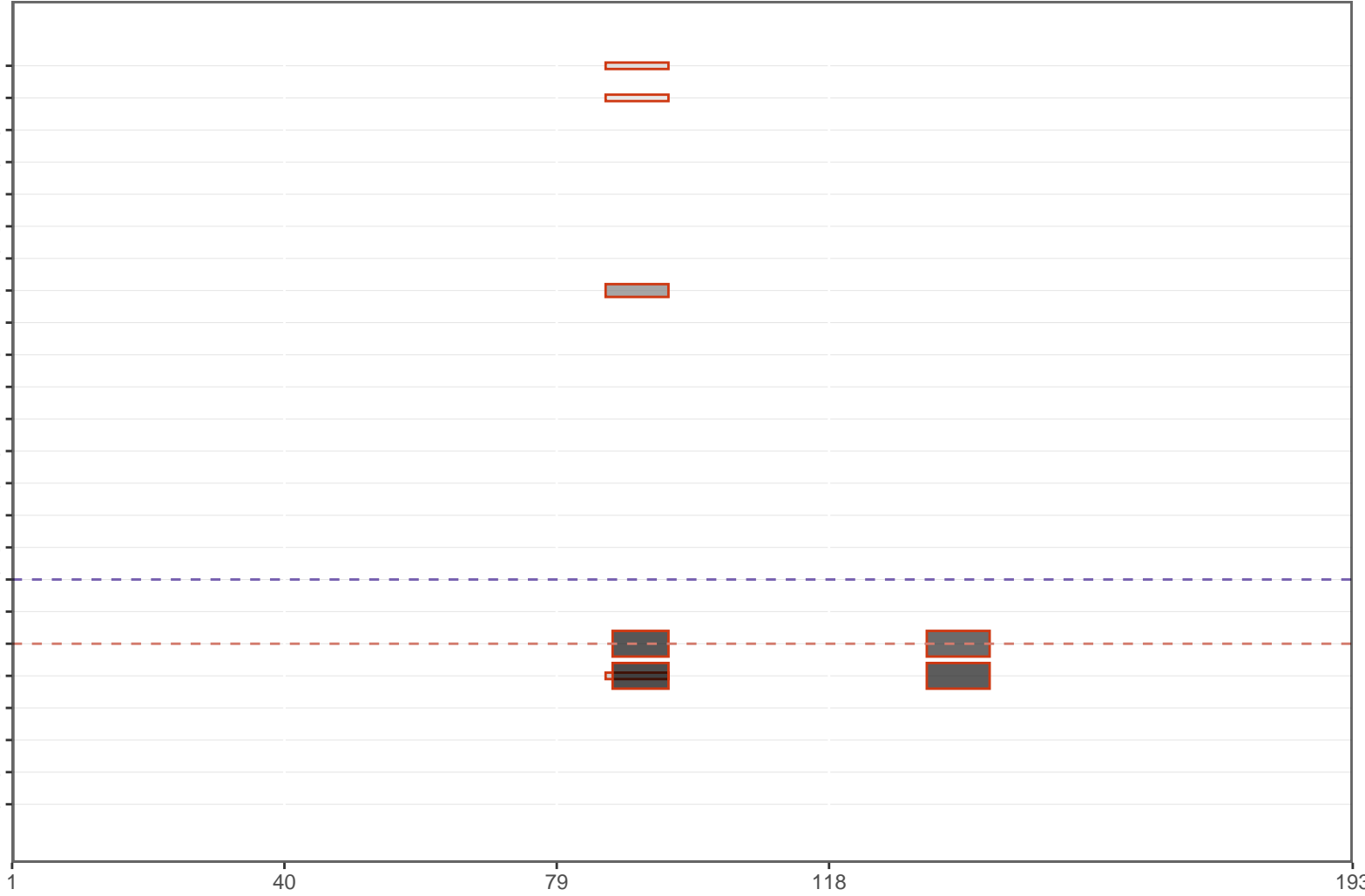
MW indication



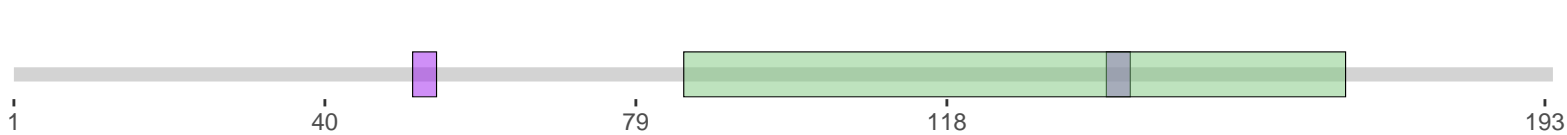
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

TERKKYYFLVAAKFMLEDEEHFQEGLFERLRLFGERDKGDFWLVKPEKFLDKFPNTRKLRPAWLVSTNGPWITVTFNRLGVLFFKPSKGGSLTVISIFKPSRR

NbL12g00990.1 uncharacterized_LOC104215819 [MW - SP = 11.14 kDa]

No. of times detected



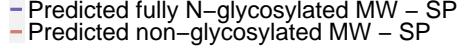
log(intensity)



Values from

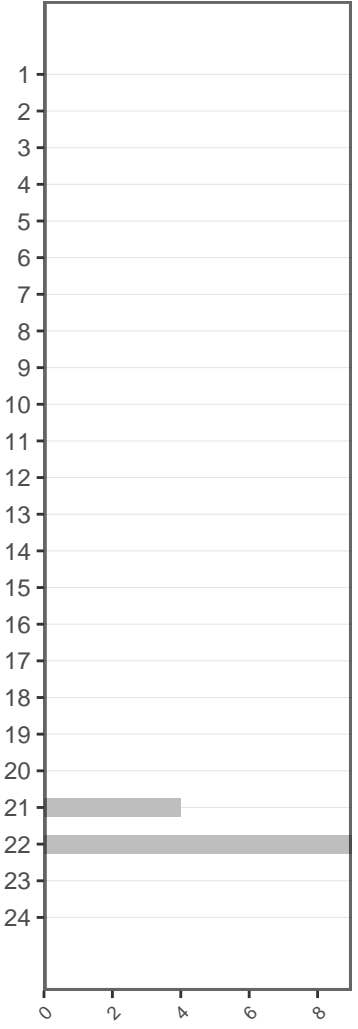
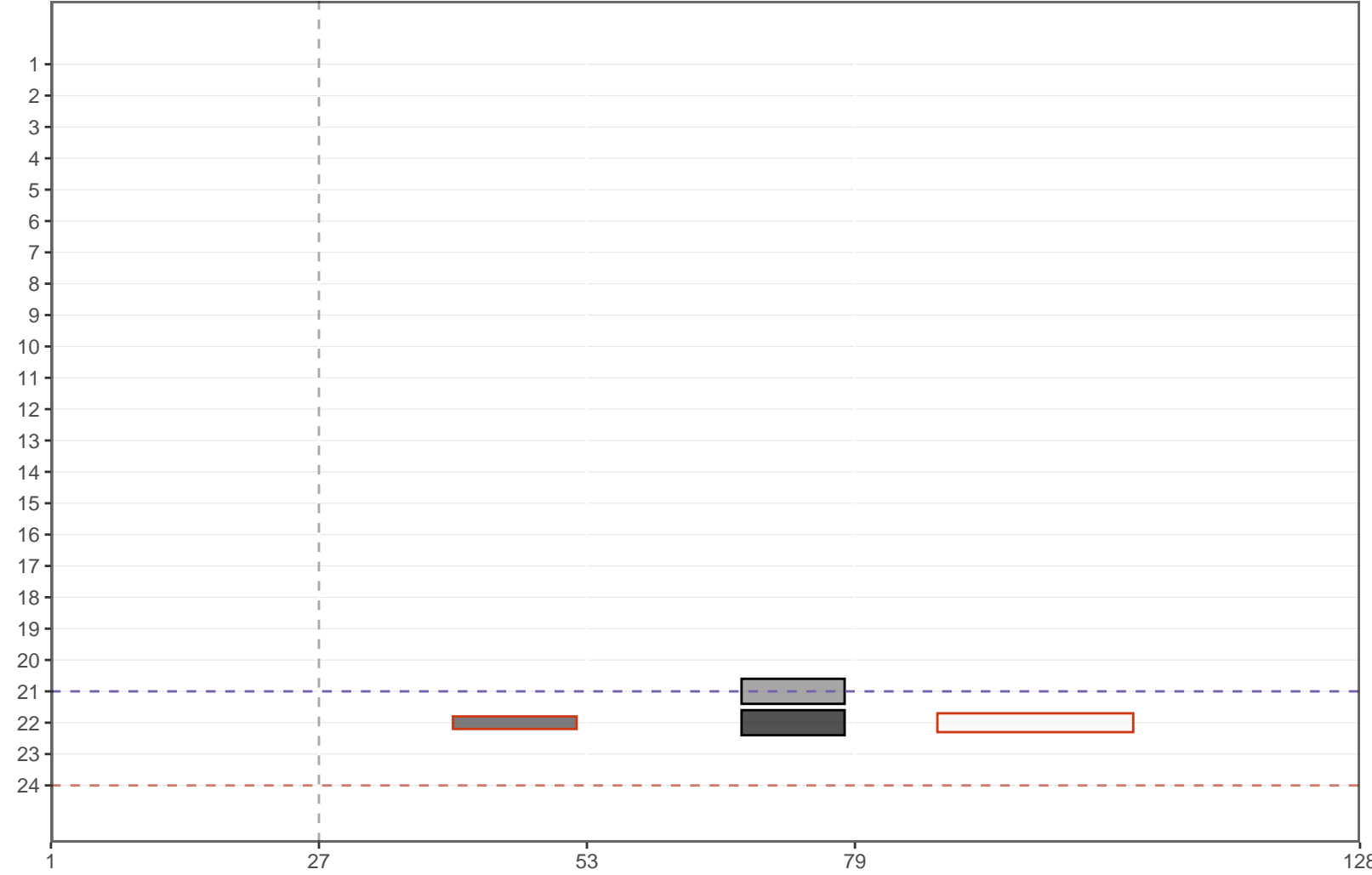


MW indication



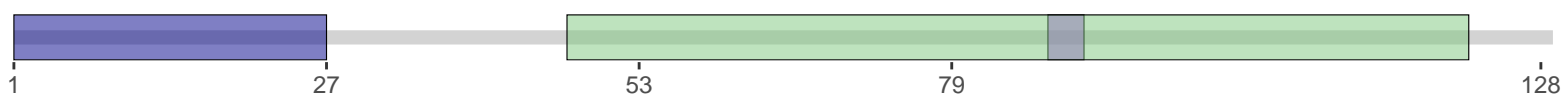
Molecular weight

Gel Slice



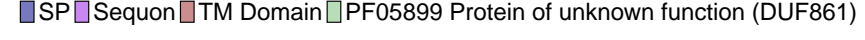
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SWPKWGCSPQKYQLKFDAAEETGVLRLGKVKVYKPKNNSGDEVEFGAGDLVIRKGLGECTWDVSVAVDKHKYKFDSE

NbL12g00980.1 WD_repeat-containing_protein_70 [MW = 71.56 kDa]

No. of times detected



log(intensity)



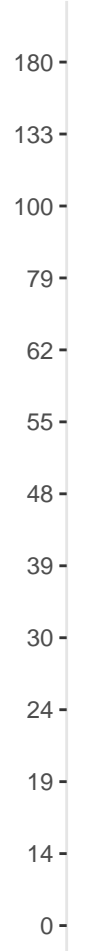
Values from



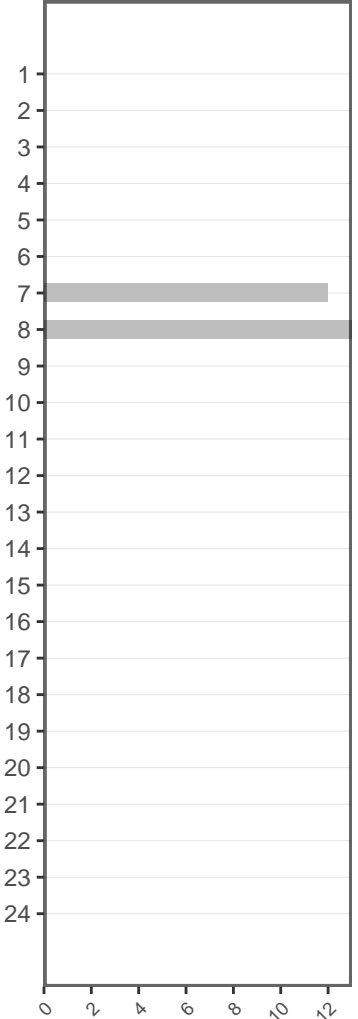
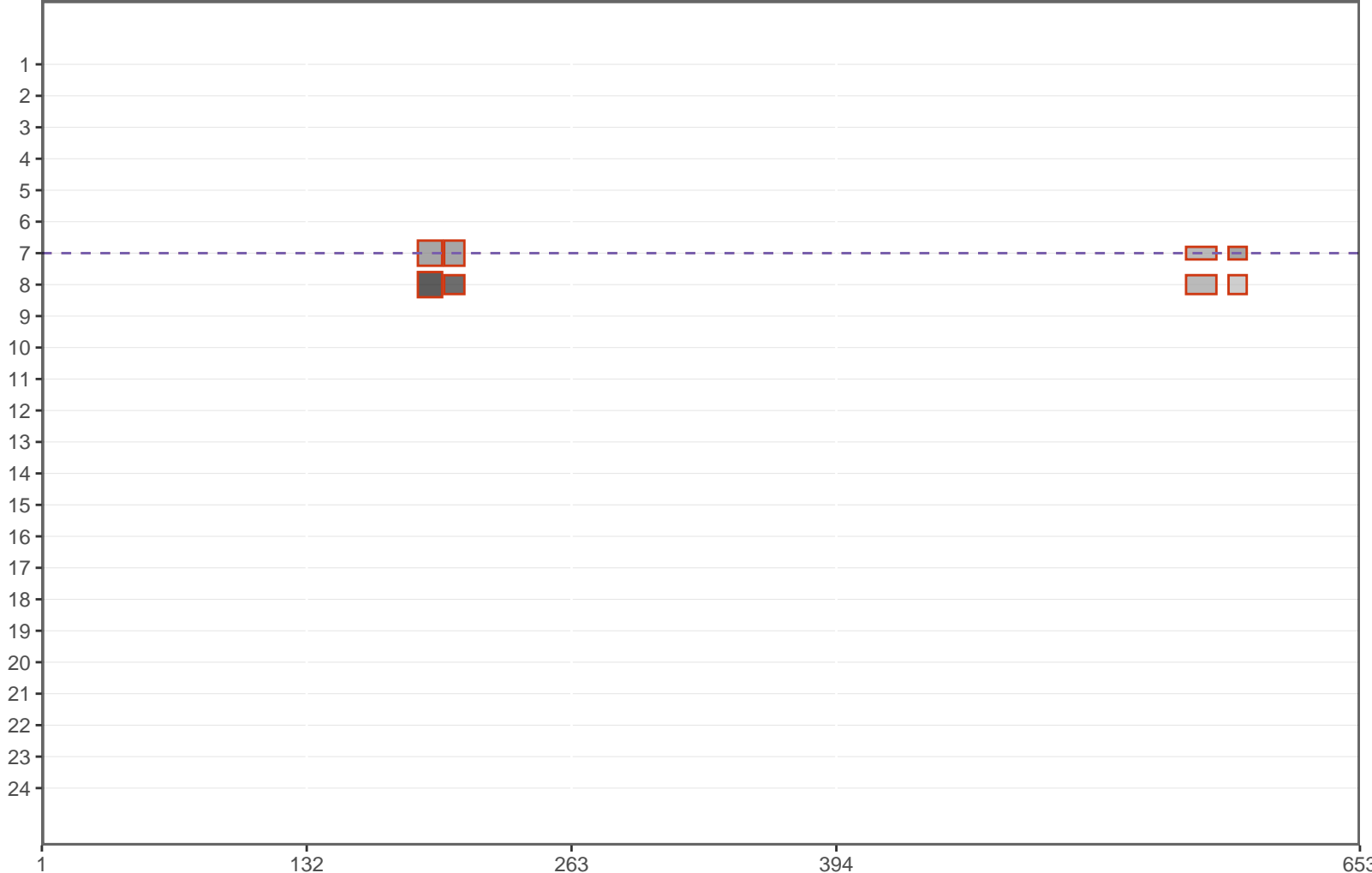
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

MDVNDPKSQKQVINKPKLARIGRVPVTTGAWDREGKRIAGGVGDGSGIWNLKPQWGSRPDTYVANAHSDDITGVKFSDDGRILLSRSSDGSGLKWDLRGMKEPLRVFDLPLNNAQTNAFSPDGLFTGTSVEKDGSGMLCFFDRGKLELVRVDSISPTYSVYVGGAWHFRLLNQTATVGDKREGGTHLYDPTLBERGALGVARAPRKKKSVDFDQAEFVHNPHALPLFRDQPSRKRQRREKALNDPLKSHKPEQPTGPGFGRVSGTSGELLYLLKQGGLIK

NbL12g00930.1 protein_FLUORESCENT_IN_BLUE_LIGHT_chloroplastic-like [MW = 31.99 kDa]

No. of times detected



log(intensity)



Values from



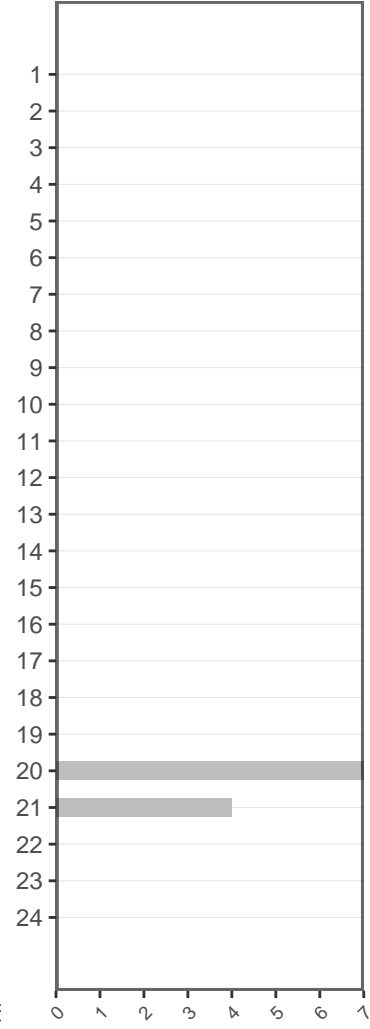
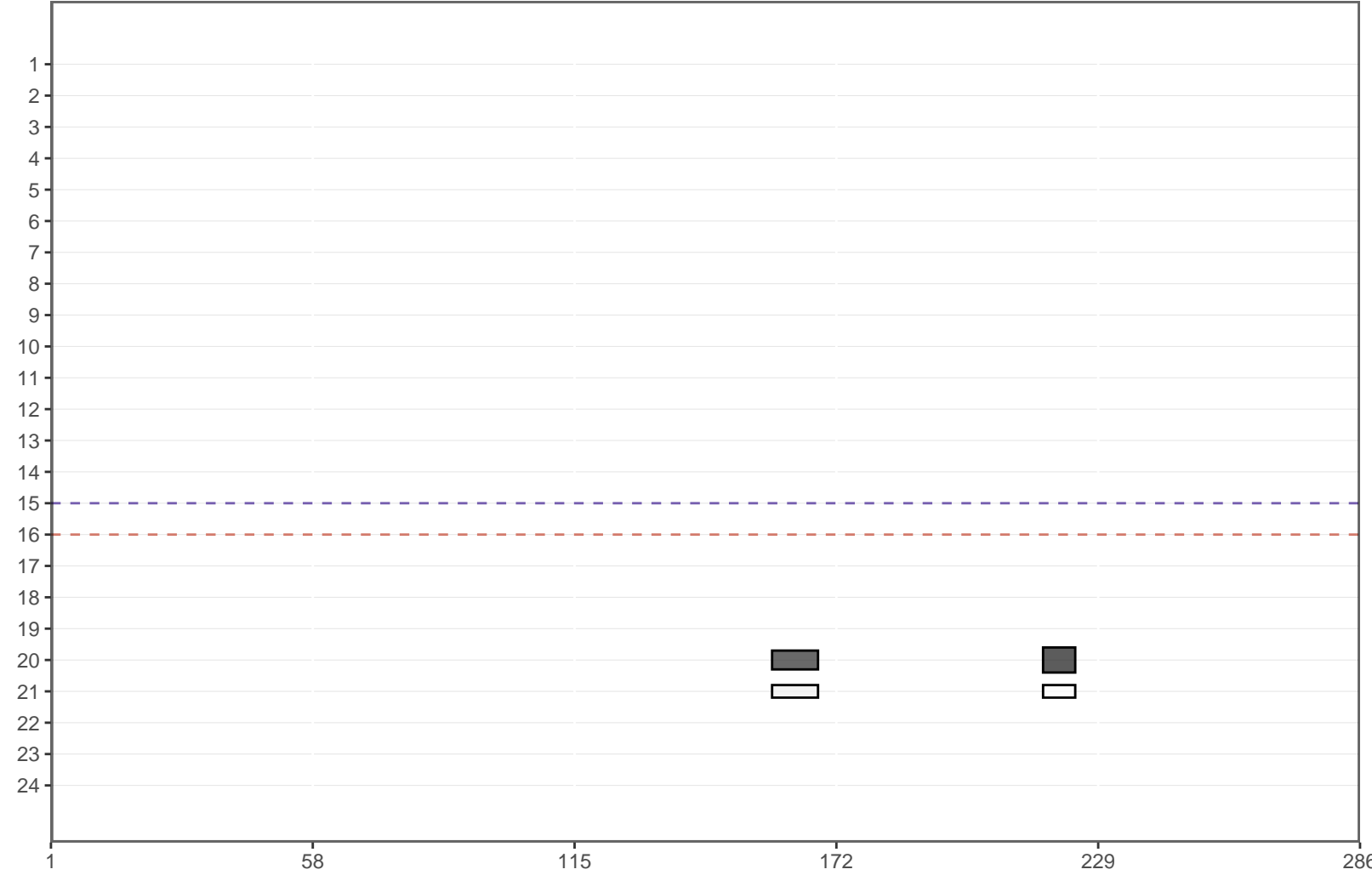
MW indication



Molecular weight

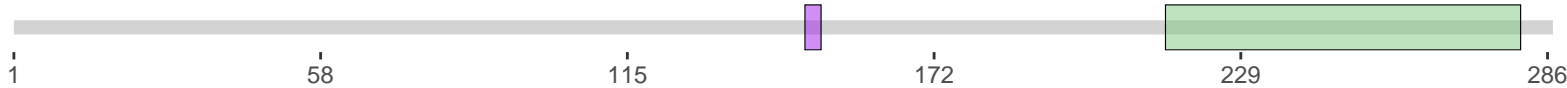


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IQINALRRQAKIESYAPNLSYAPVGERVAESEVVDPRKQELISGLIKNGKFLRNDAPEKADLEFKKALDLADGNLKEPLKENKAARGLGASLGRQGYREAIKRYHSMVLEISARHGEESGNTFAYGAAADCYTELGDLEGAAYKYNHARLETD

NbL12g00850.1 60S_ribosomal_protein_L14-1 [MW = 15.4 kDa]

No. of times detected



log(intensity)



Values from



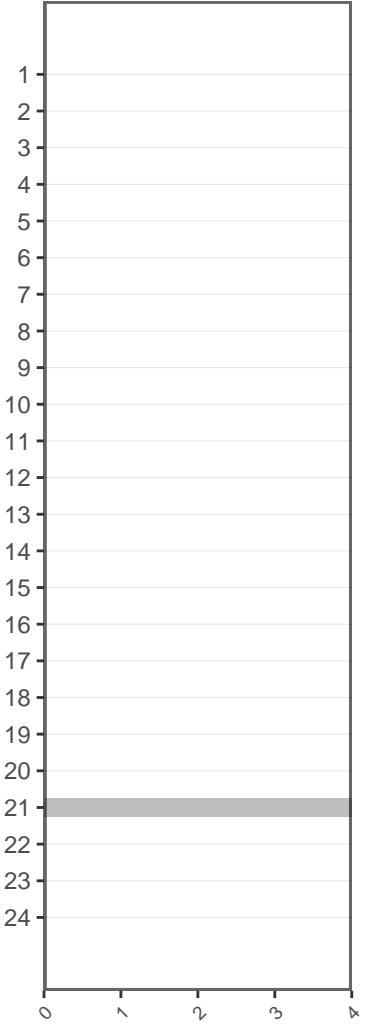
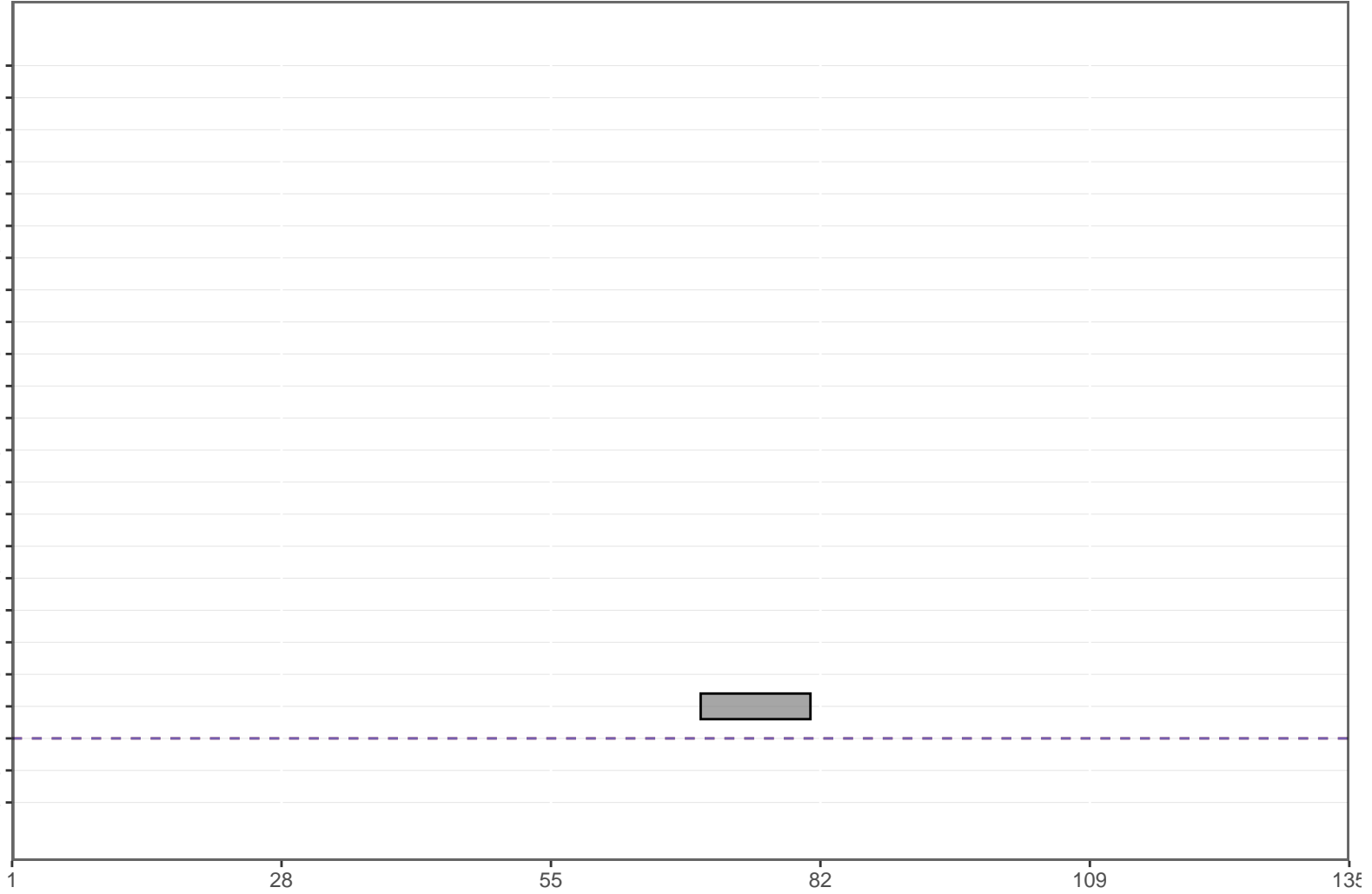
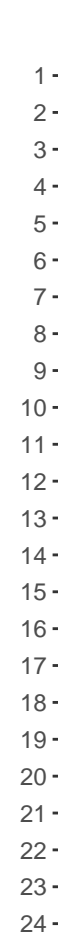
MW indication



Molecular weight

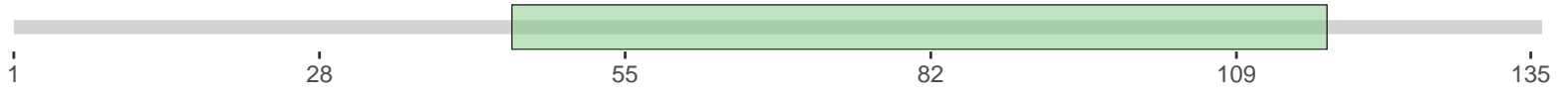


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILTDIKDKRIPKXKTLVAAMEAADVKNKWESSVGRKLVGKRRASLNDVDFRFLMLAKKRAGVVRGELANLKKETVA

NbL12g00680.1 F-box/kelch-repeat_protein_SKIP30-like [MW = 39.34 kDa]

No. of times detected



log(intensity)



Values from



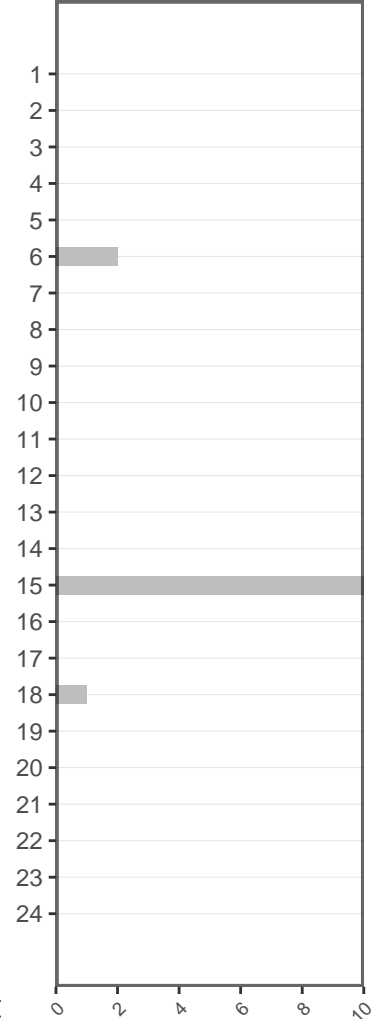
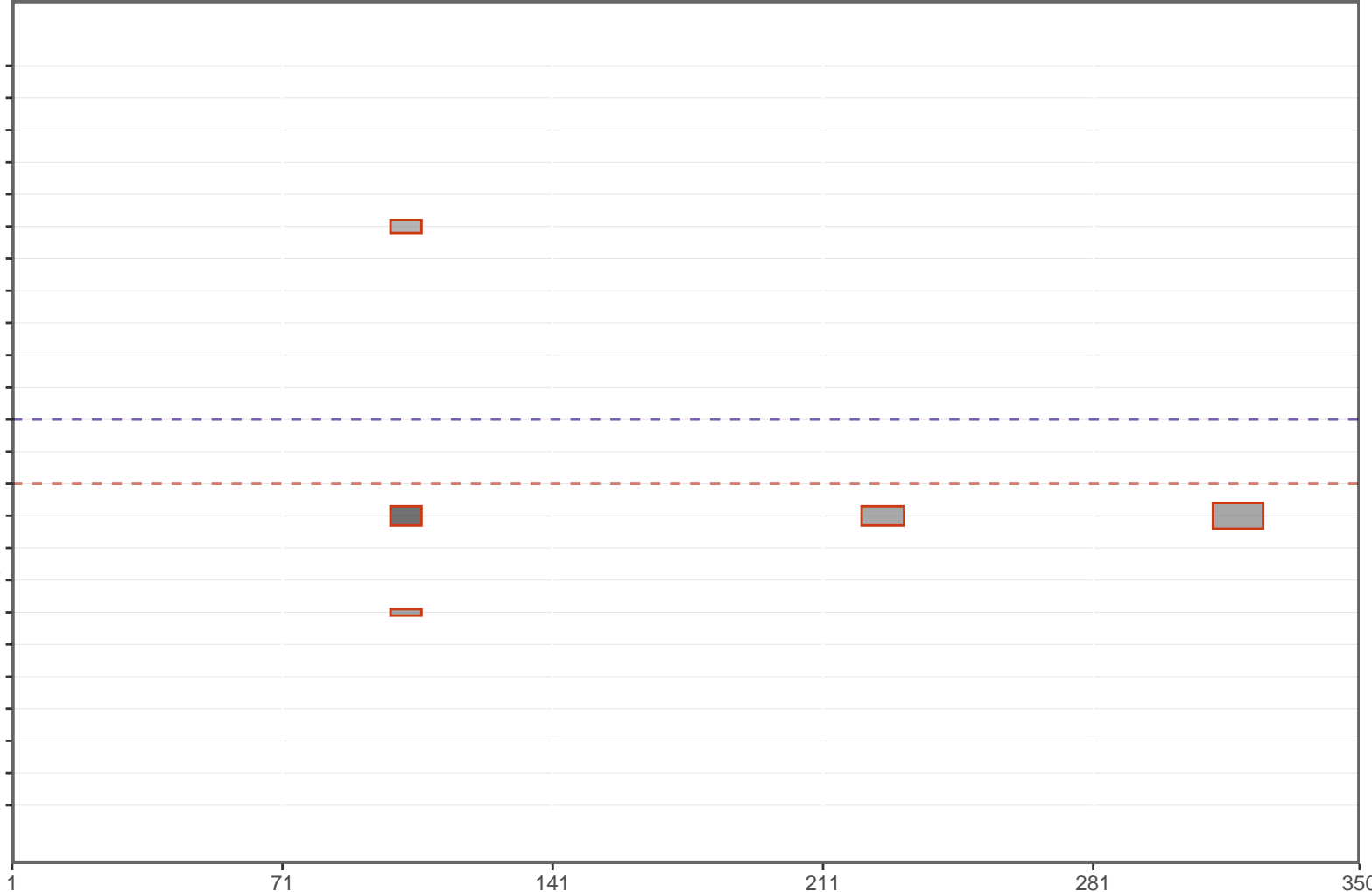
MW indication



Molecular weight

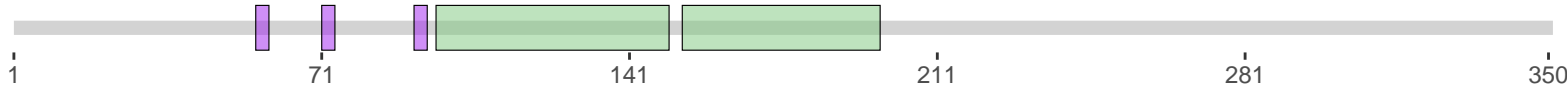


Gel Slice



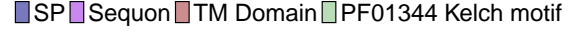
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

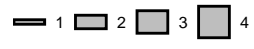


Protein sequence:

EGKIVAGGFTNYRKBIGNAEIYDFEKDWWQLPDLHHAHNSAGSGVVSGKVVHLKGLSTQVLEVKDQWTFVHEYSVLGQPMFTVREKLVVMMENWFIYKQEKVREMVSASEFRRRIGFAMGLGDDIYVGGVNGPEHWNGNKVLSQVDVLTGNERLWVRKVAFMTFRGRGTLACTQLRI

NbL12g00670.1 tRNA_(guanine-N(7)-)-methyltransferase_non-catalytic_subunit_WDR4 [MW = 47.11 kDa]

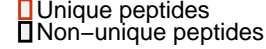
No. of times detected



log(intensity)



Values from



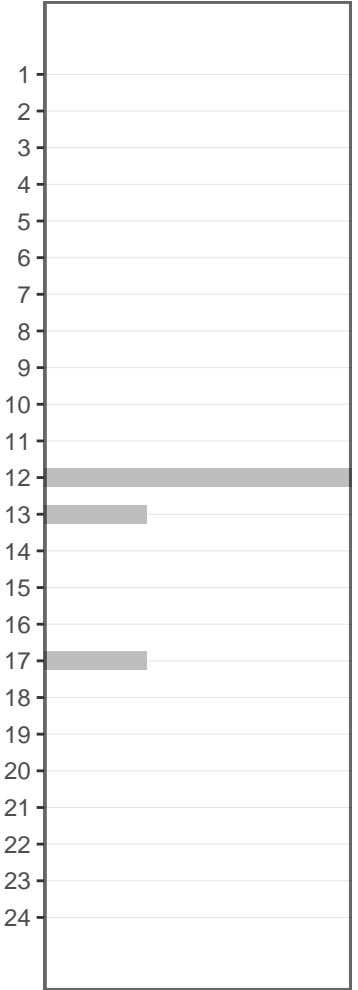
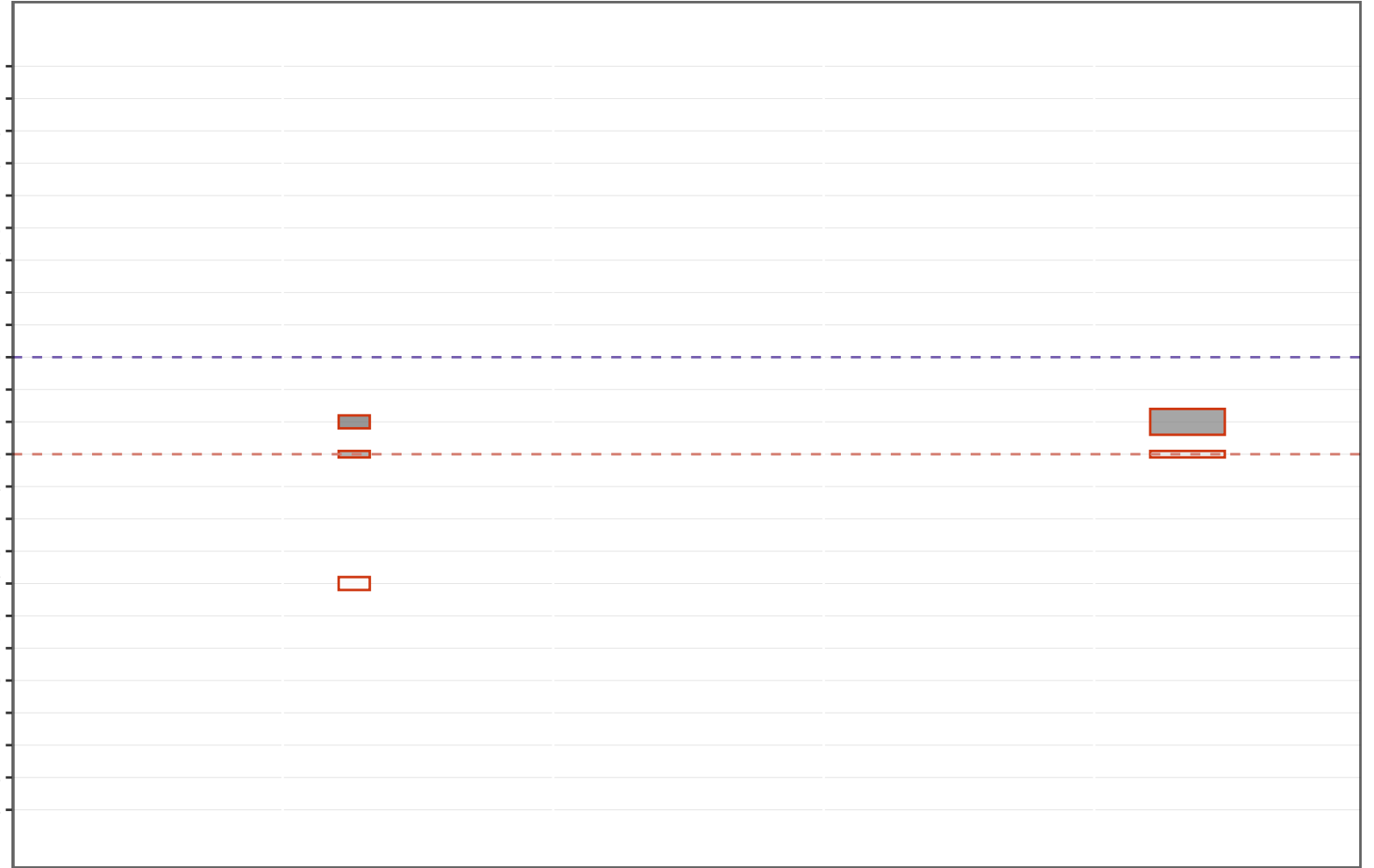
MW indication



Molecular weight



Gel Slice

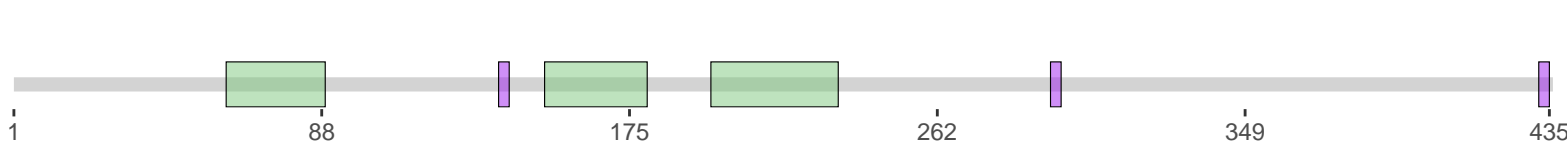


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description

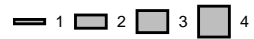


Protein sequence:

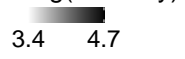
IQLAFICSKDSQORVLLGGGGSTVRLWDFDTGGSLDTGCHIGPETLGSQSKGVDDSLAVTDLCASTRGGSLMVAWQSLAGVLLSGNLRSRSLHFRARVPIRGETRIFRISIAVYSSNQLMVMVMASTLCAQDSAPLARVYVDFGFCESNDDSVHEHMRVLEDKDGGGEGLLGLTGLGQSSSEIKDALATAEAWKMTMGNLLKIKVYPSNDRFRKRGRNDKVKVNSP

NbL12g00550.1 elongation_factor_Tu_mitochondrial-like [MW = 49.06 kDa]

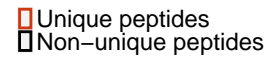
No. of times detected



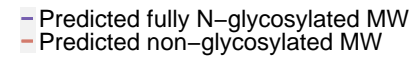
log(intensity)



Values from



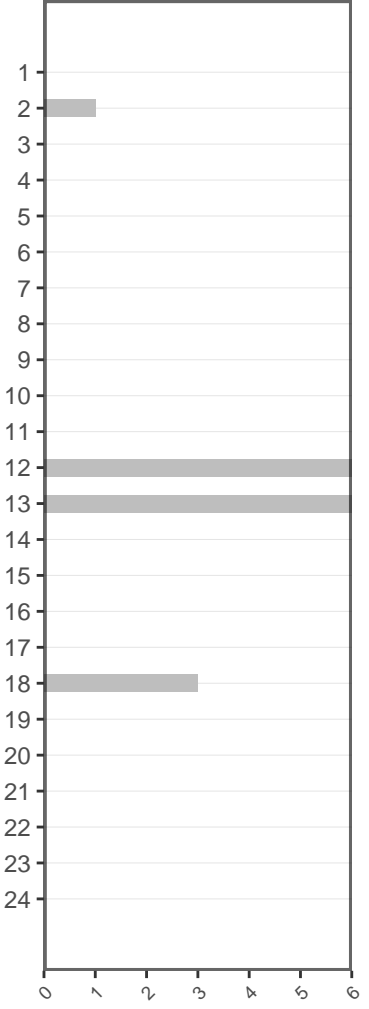
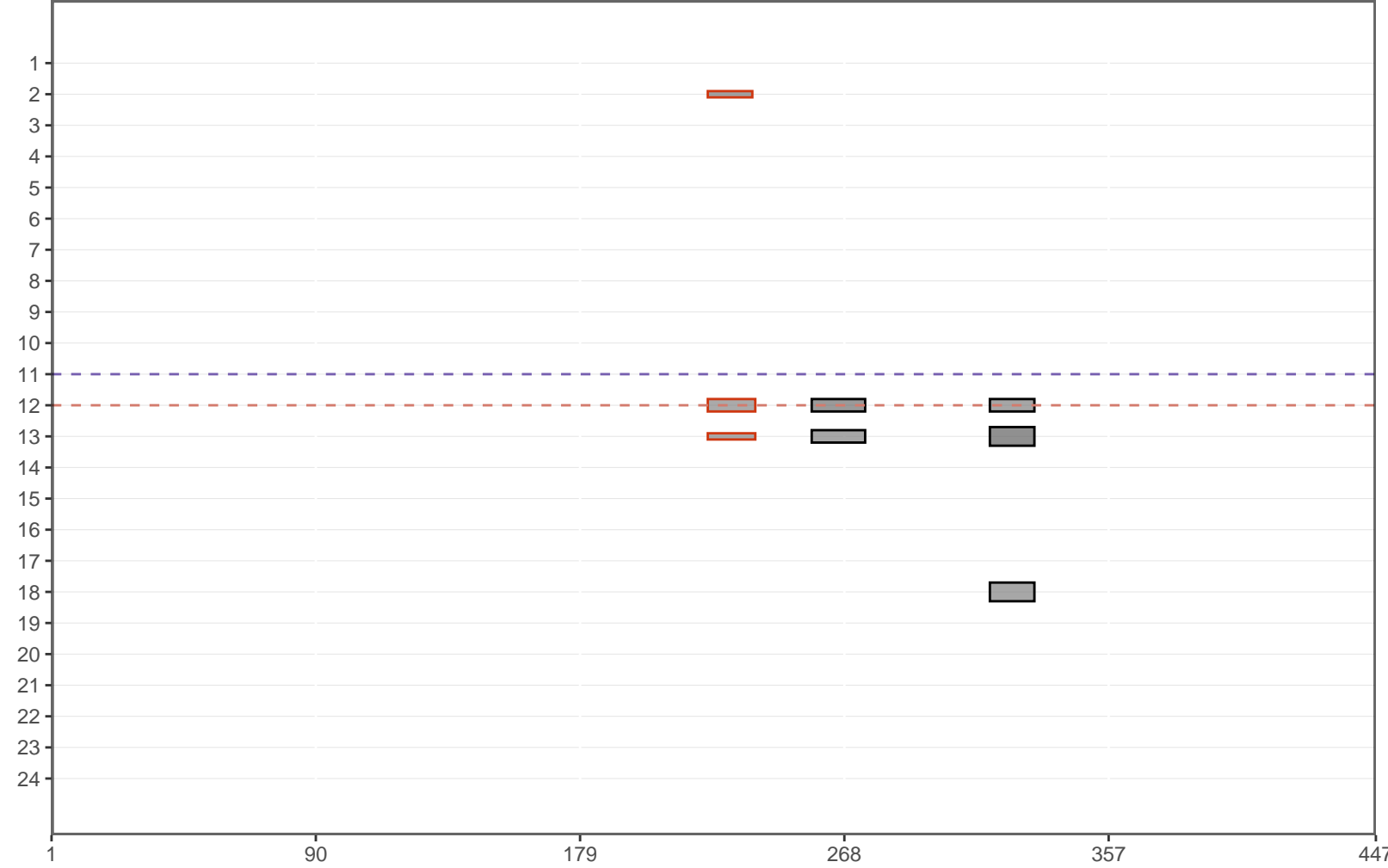
MW indication



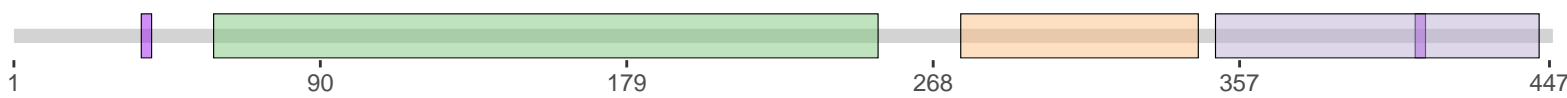
Molecular weight



Gel Slice

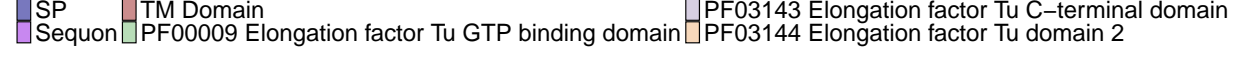


Protein length



Pfam domains

Pfam Description



Protein sequence:

IKFPGDEPIRGSALBALGISTNEIGKKAALKLMEAVDEVPDVRQLDKPFLMPEVDVFSQGRGRTVATGRVVEGDTIKVGEDEVIELGLMGGNKSTVTVGVEMFRKSLDYGAGADNVGLLRGLKRDMMIRGMVIAKPGQSVKTKYKFEAEYVLTQDEGGRTAFFSNYMPQFVIMRTADITGKVELPENKMMMPGDNVATFELMSPVPLDAGQRFLREGGRTVAGVYKWS*

NbL12g00450.1 glutathione_S-transferase [MW = 18.69 kDa]

No. of times detected



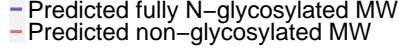
log(intensity)



Values from



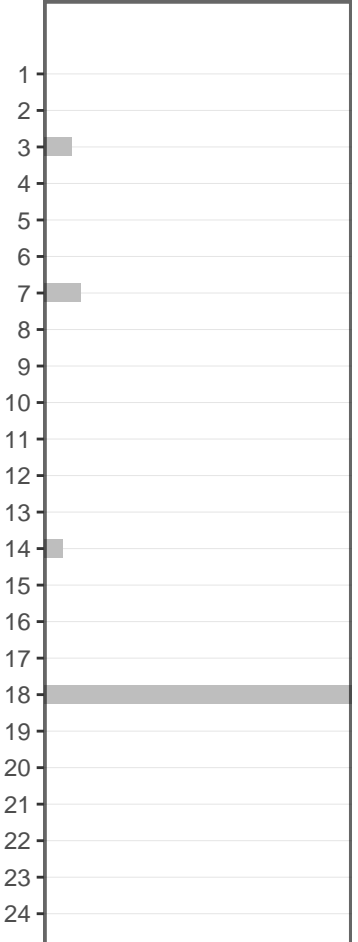
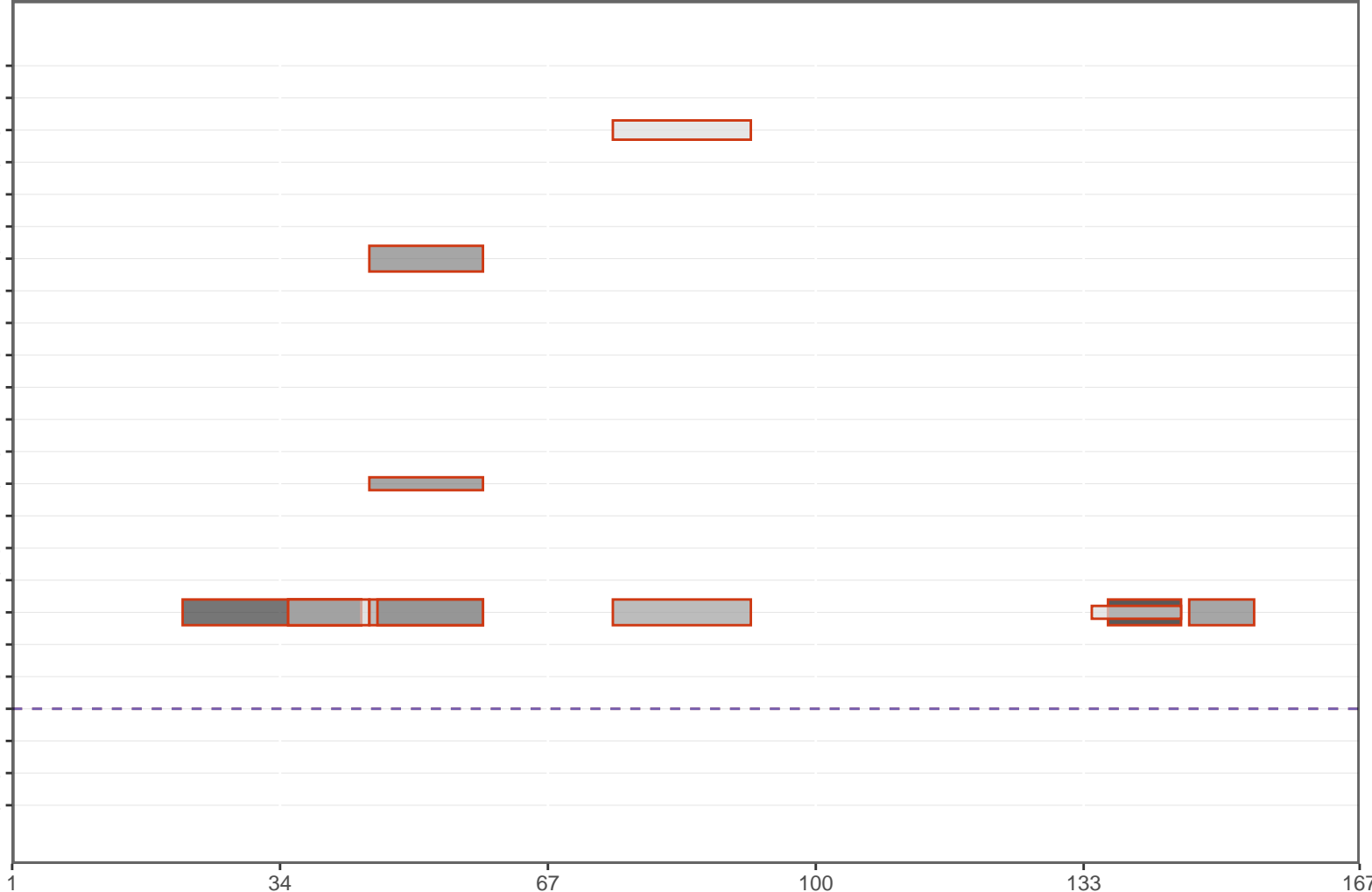
MW indication



Molecular weight

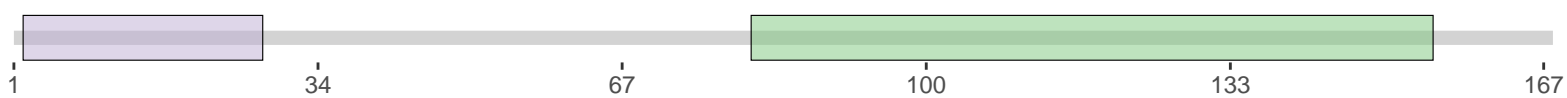


Gel Slice



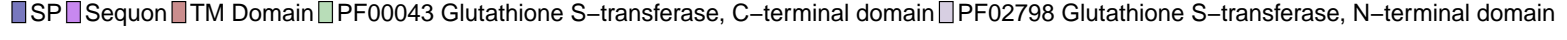
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

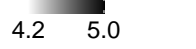
LVKPKMLGMVTDQVAWAENEKLGKLEIVESRLKESKYLGGSEFTLADLHAPVHYHLMGTRVKNLFDARPHKAWGADLARPWWSKALELHKQ

NbL12g00430.1 universal_stress_protein_A-like_protein [MW - SP = 19.55 kDa]

No. of times detected



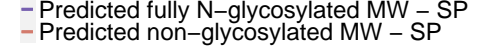
log(intensity)



Values from



MW indication



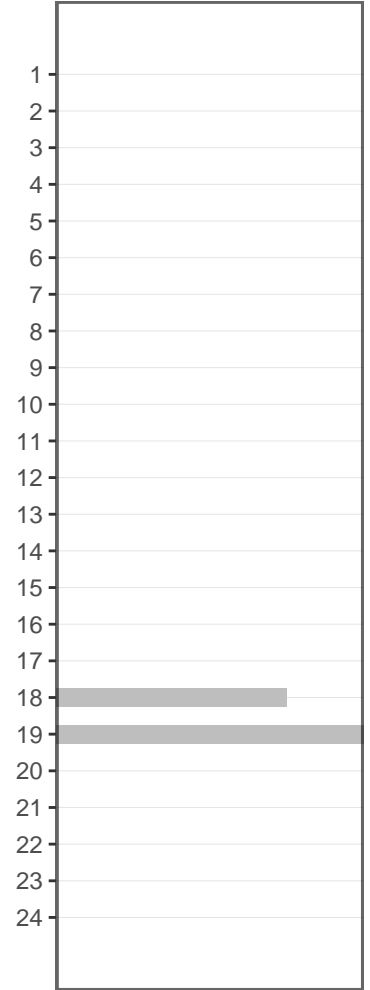
Molecular weight



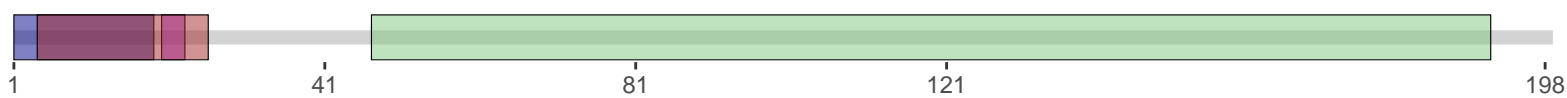
Gel Slice



Protein length

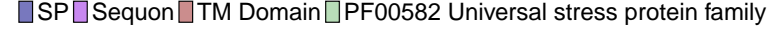


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PKSVGLTGLGSVEKLPSEIETDLKKAARVVEKAKEIGTAKGVNDVIVEVEEGDARNVLGEAVEKHHASILLVGSHTGYGLRRTVLGVSQYGAHHHGVMMVKKPKHKI

NbL12g00400.1 bifunctional_epoxide_hydrolase_2-like [MW = 36.42 kDa]

No. of times detected



log(intensity)



Values from



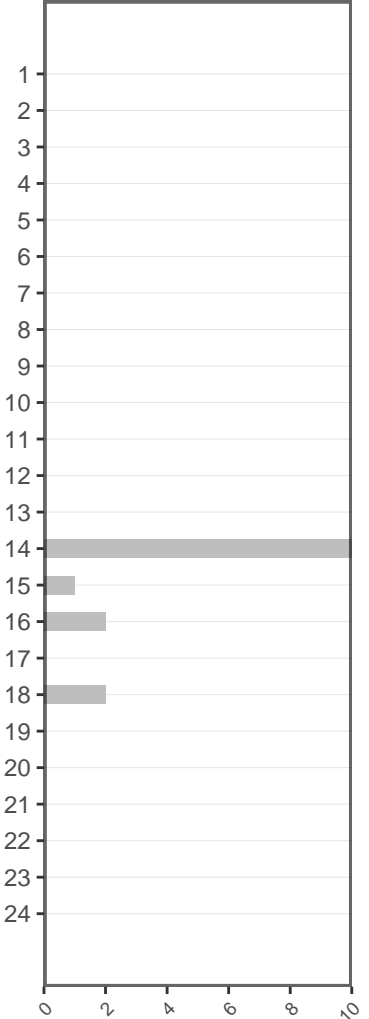
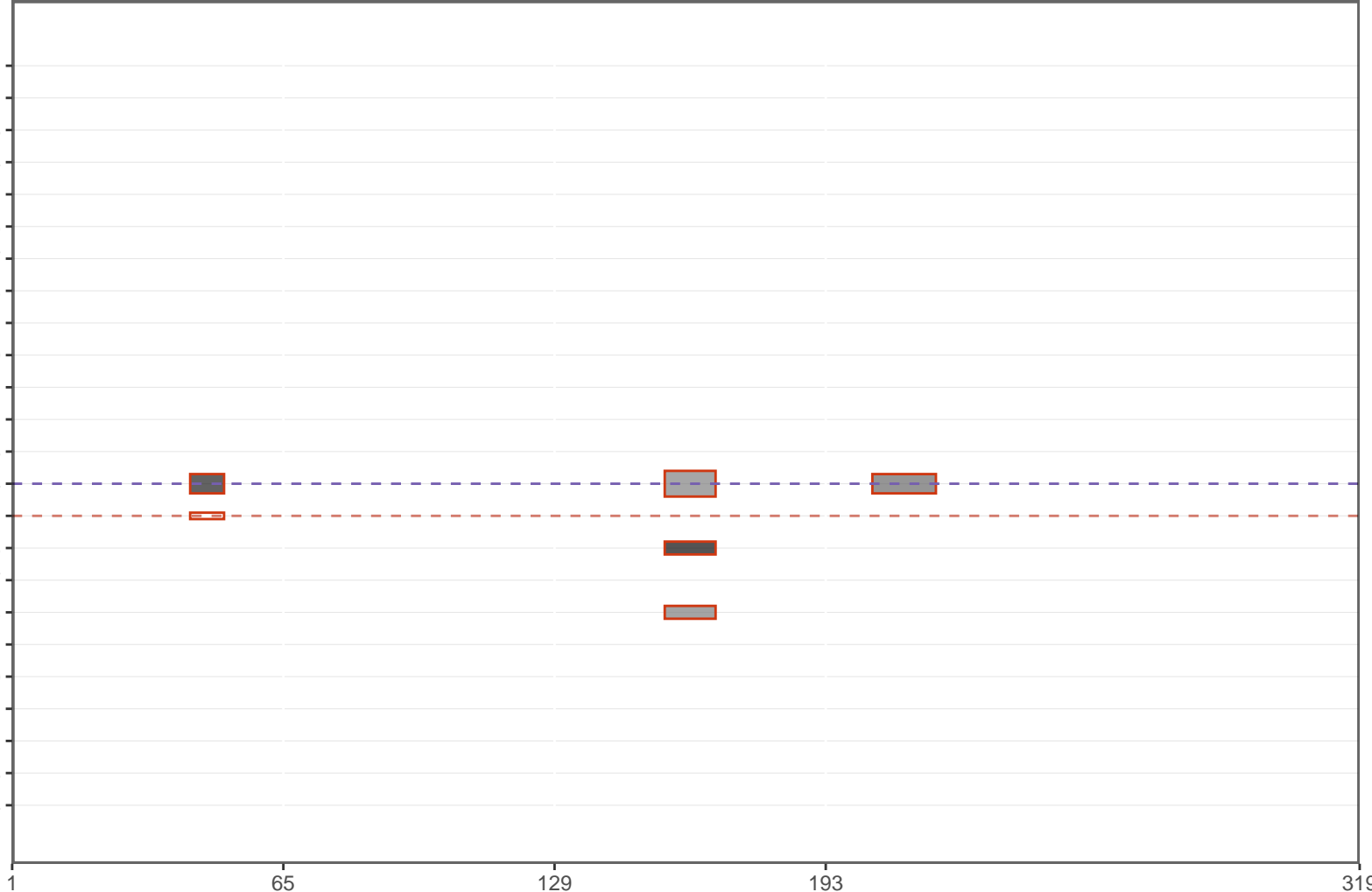
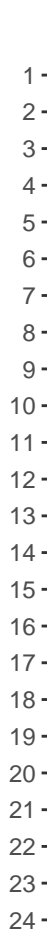
MW indication



Molecular weight

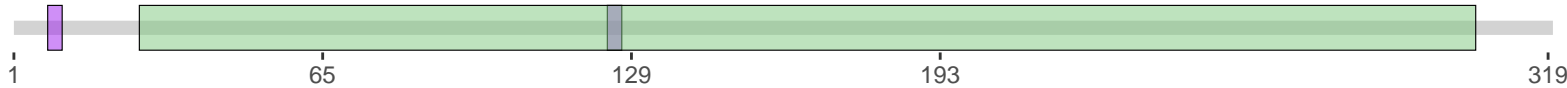


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

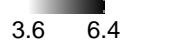
SDDYICRFQIEYGGVEEFARVDIARLAKFLISRNFAFLRIVSKKGFGGSSHTPKLPWLSSEEDNYANKFSGKGFGLNLYRAMDLNVELTAPWFGGQKVPKVFVGLDLFYNTFGVKEYSHKGGFGKMPFLQEVVIMEGVGHFNEKPEEINDHYDFQKPE

NbL12g00390.1 pectinesterase-like [MW = 64.09 kDa]

No. of times detected



log(intensity)



Values from



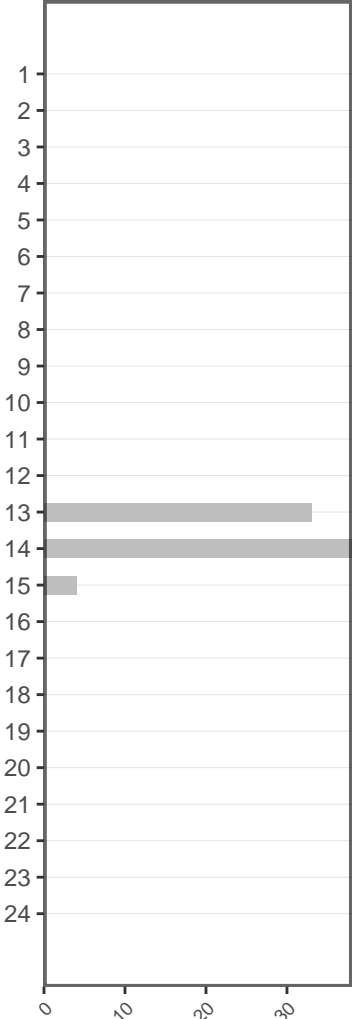
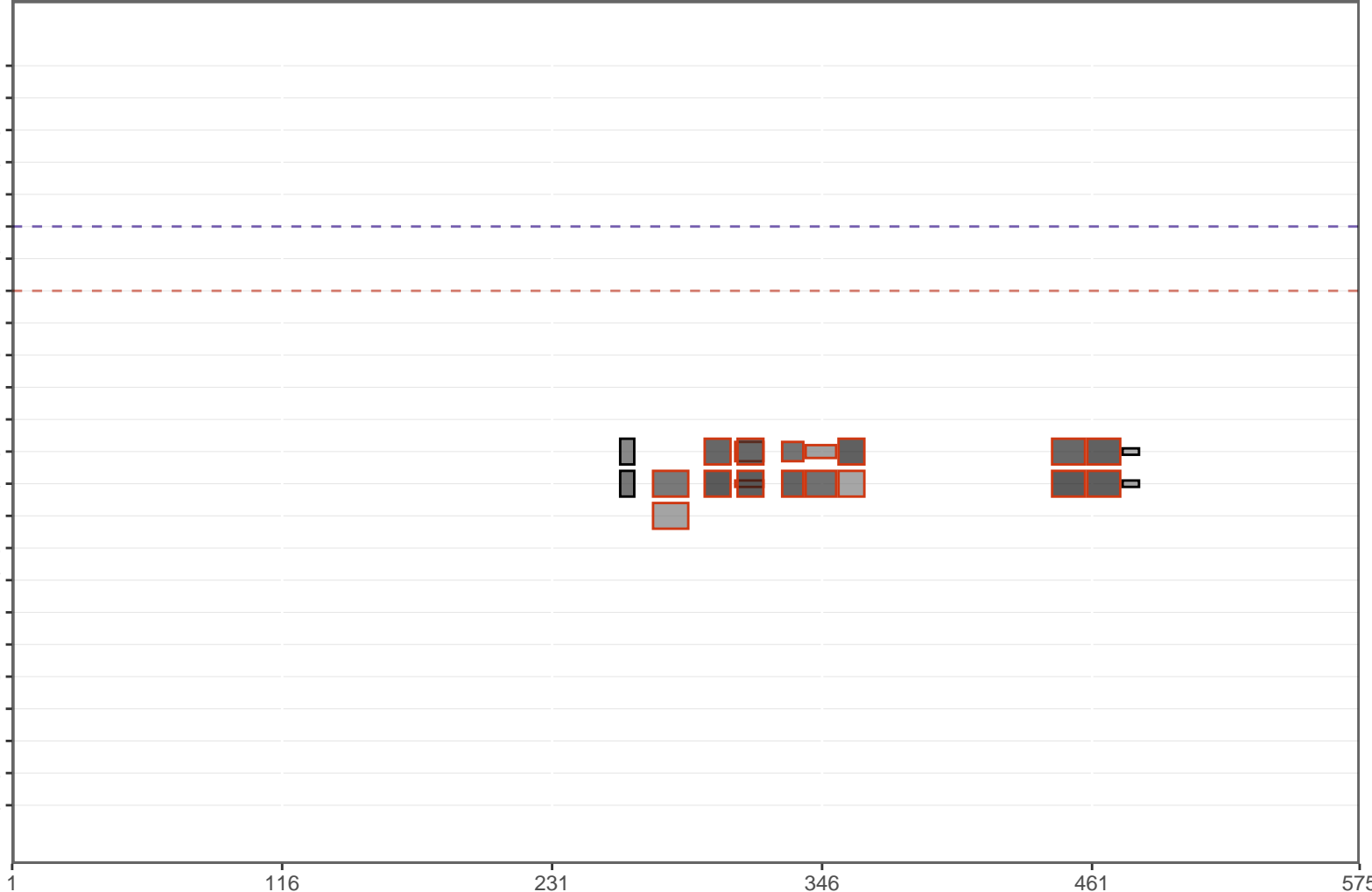
MW indication



Molecular weight

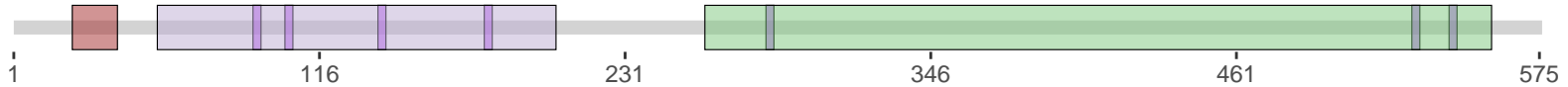


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ALSTAPNSSTRFVYIKAGHSEYHVERKKSMMIFVGGDGKTKQIKGNRNIVDGGWTFTRSATVAVGNGFARGITFENFAGPSKHGVALRSGSDLSAFYGGCFVYGDTLVHSLRQFYREGDNYGTVDFFGNAAVVFQGNLRYARKPNPNKNIPTAGRGREDPNQNTGISLNGKVAASDVLVPLSSFKNYLGRPWKGYRRTVFLLSYIGSLDPPGWLWDGDFALNTLYVGEYLNKPGPNTSARKKWPQYRVINSBAEASGFTVGNFQGSQVLPATGFPFFLGI

NbL12g00370.1 60S_ribosomal_protein_L19-3 [MW = 24.79 kDa]

No. of times detected



log(intensity)



Values from



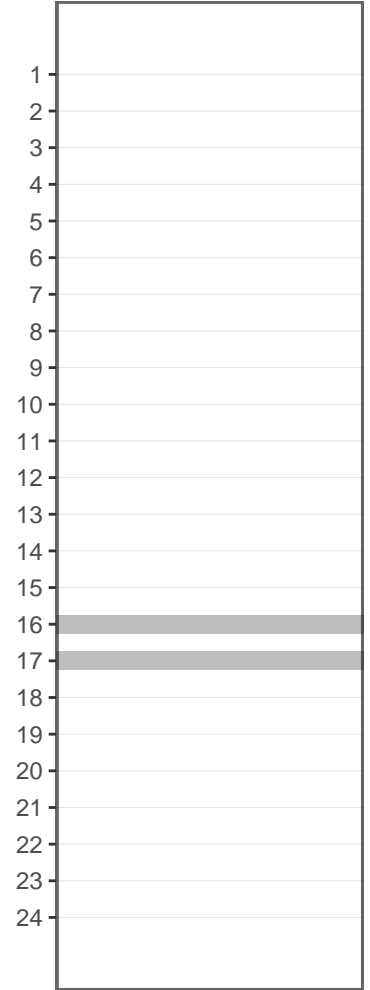
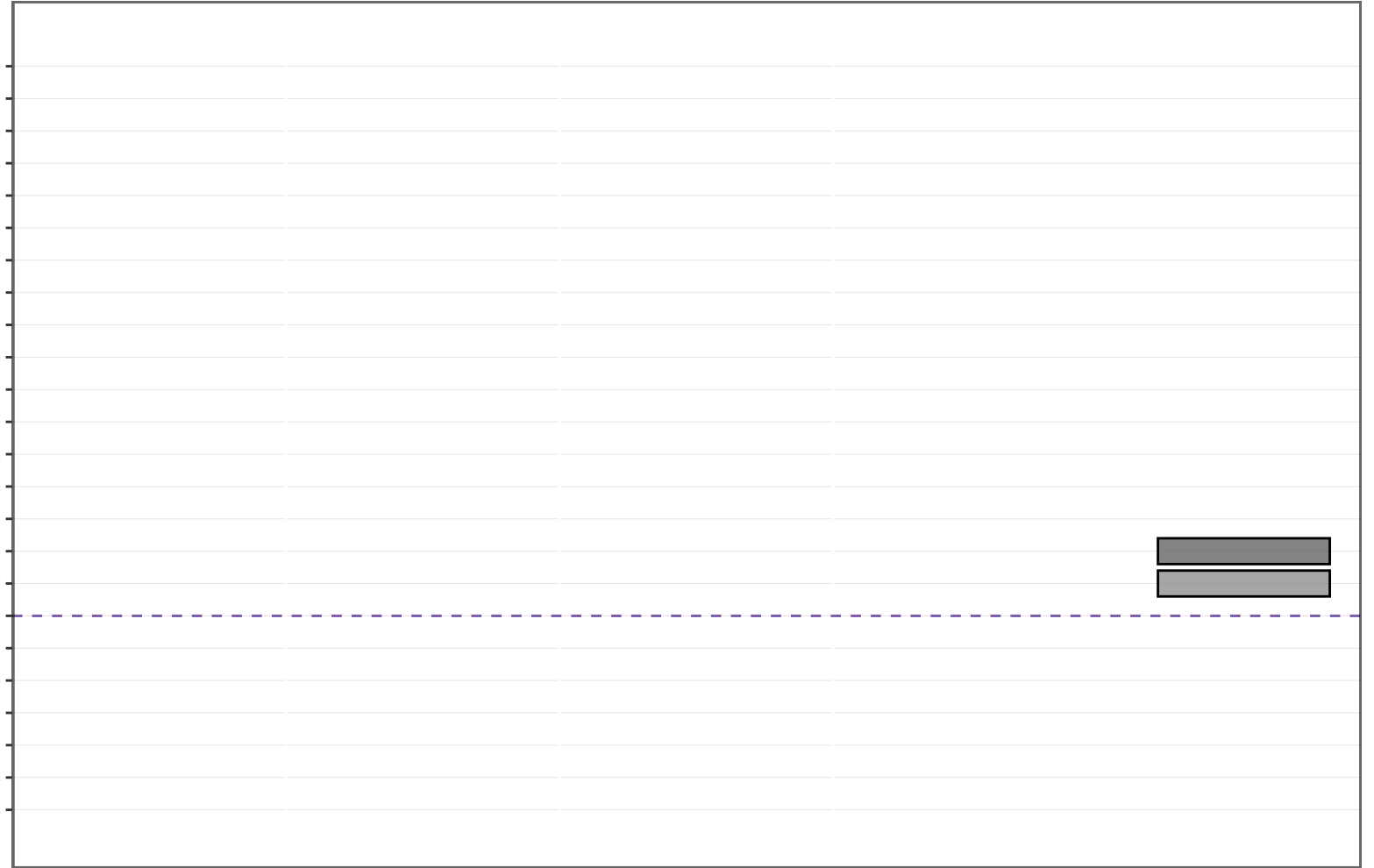
MW indication



Molecular weight



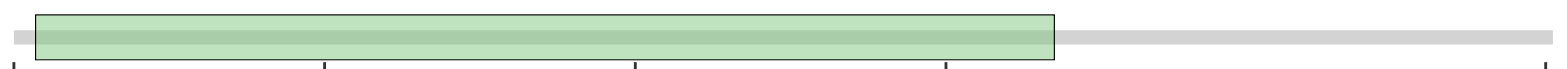
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

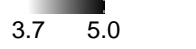
WMRRMVLRLRLSKYRESKKIDRHMHDMYMKVGNVFNKIKRVLMEHHTKAEKAREKTLDDGFARRANKASREKRFARRERLAGGPGERPVQPAAPAWAPTQPAQGGKSKK

NbL12g00350.1 probable_polygalacturonase [MW – SP = 46.36 kDa]

No. of times detected



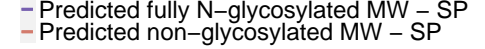
log(intensity)



Values from



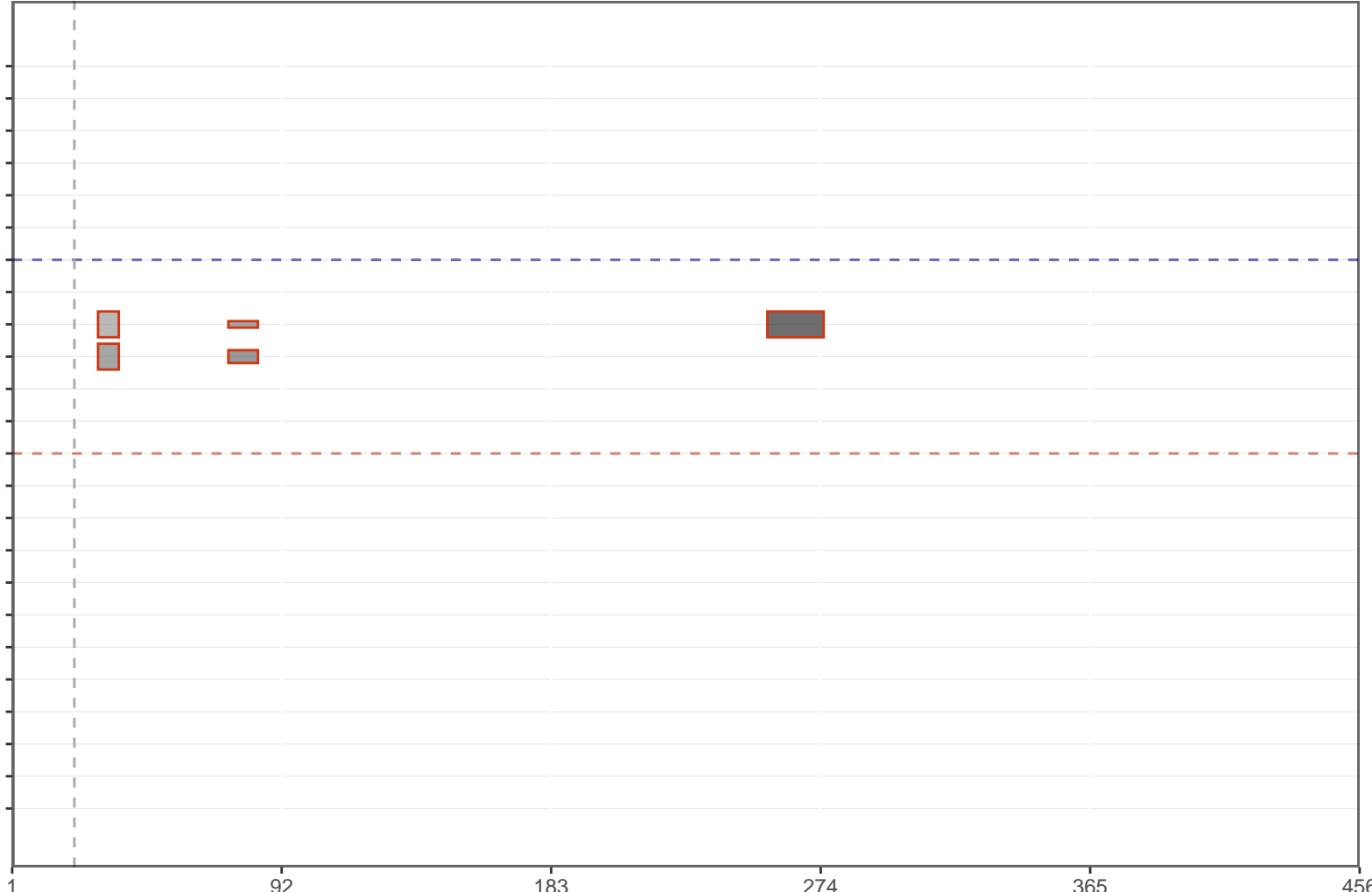
MW indication



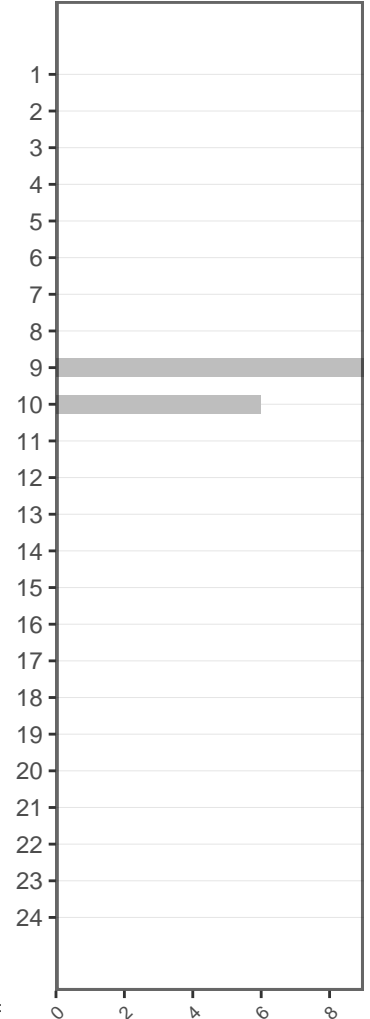
Molecular weight



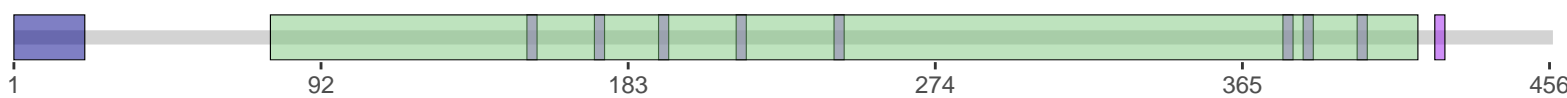
Gel Slice



Protein length

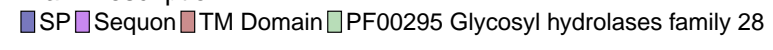


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ITVHSPANSPYTYGVPDSSEHVCIEINISMGHDAVVLKSGDWEYGEYGGKPTTNVHVRGVRLGSCAGAGLAFGSEMGGISNLAEHVYLDLFLGELKRTARGRGKDIIVTDVVMANLGVGIEATGHGDSHPDEKFDPSALPVVGGITTFEDIVGTNISTAGNFSGLAESPFTSGLENVTFEVSBNPTFWLGSIDIGSSGNVSPDPCPELQNSFGSTTSTCFALLHPVSGVAFSP

NbL12g00220.1 calvin_cycle_protein_CP12-1_chloroplastic-like [MW = 14.3 kDa]

No. of times detected



log(intensity)



Values from



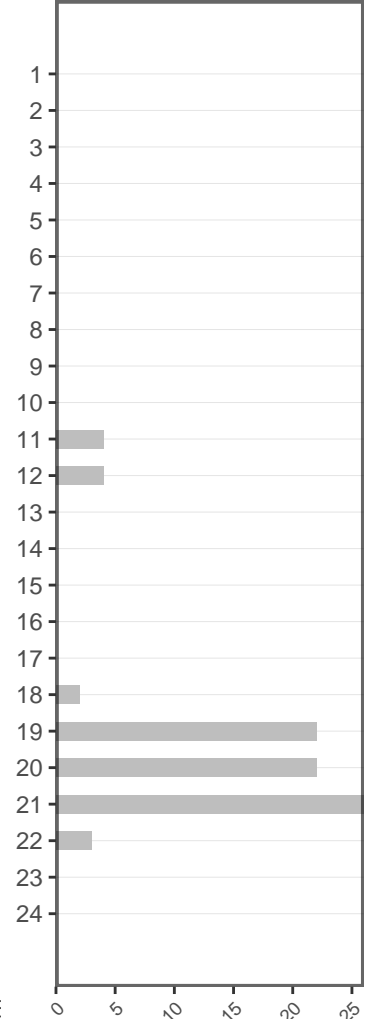
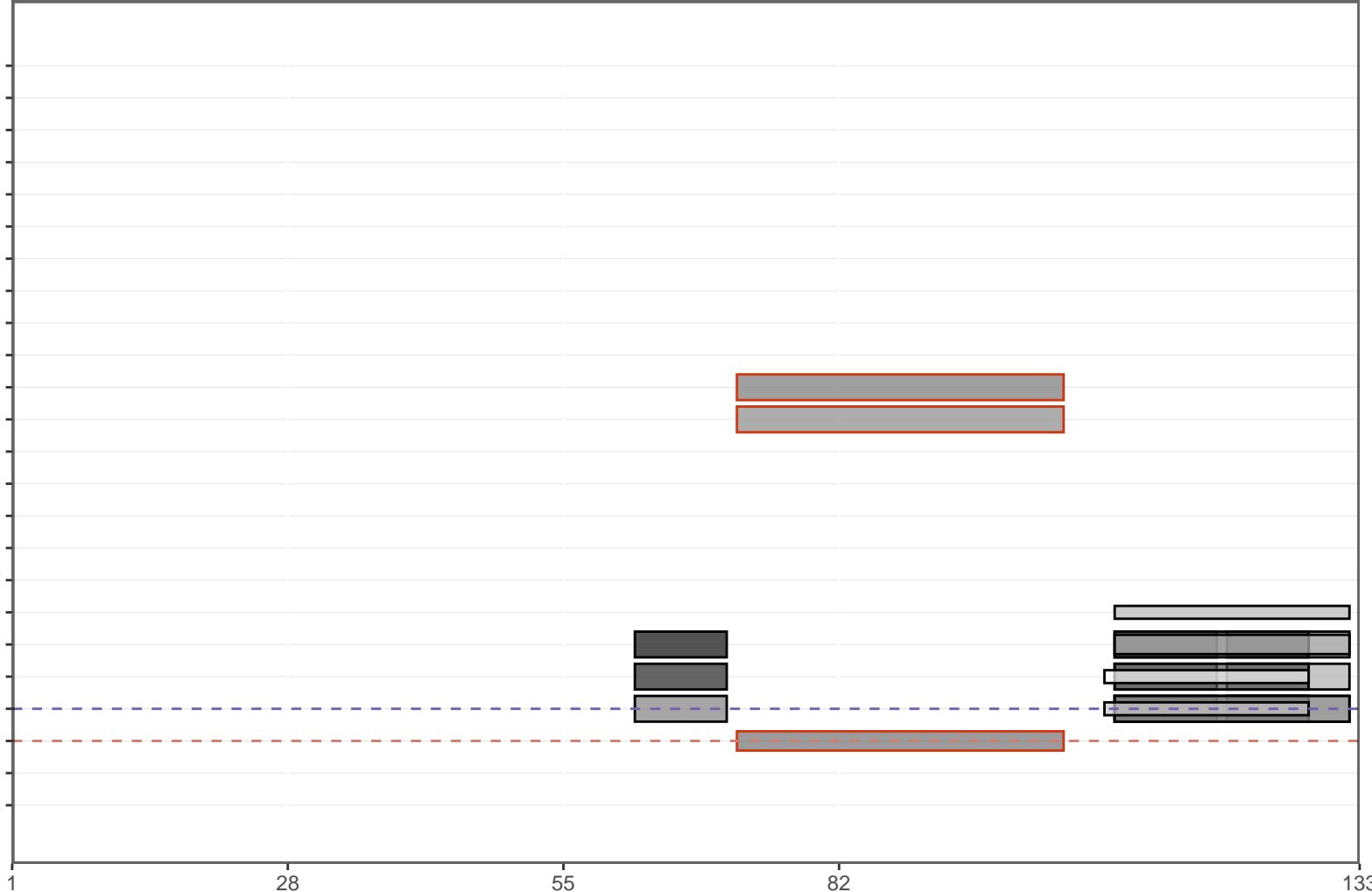
MW indication



Molecular weight



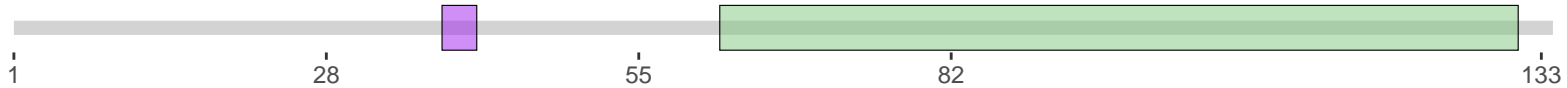
Gel Slice



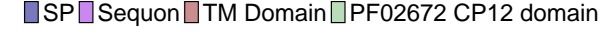
Protein length



Pfam domains



Pfam Description



Protein sequence:

SATPDNKLSDLVIAEIVKKEAEAGAEAFVSGEGAAAWDVVEASAAASHARDKKKESDFLENYKGNFETDECRITYGN

NbL12g00170.1 nodal_modulator_3 [MW – SP = 129.1 kDa]

No. of times detected



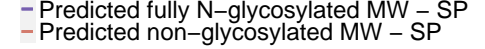
log(intensity)



Values from



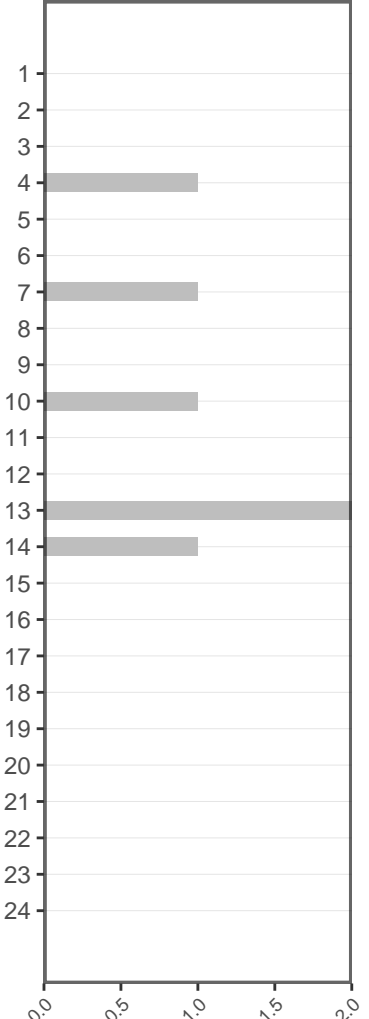
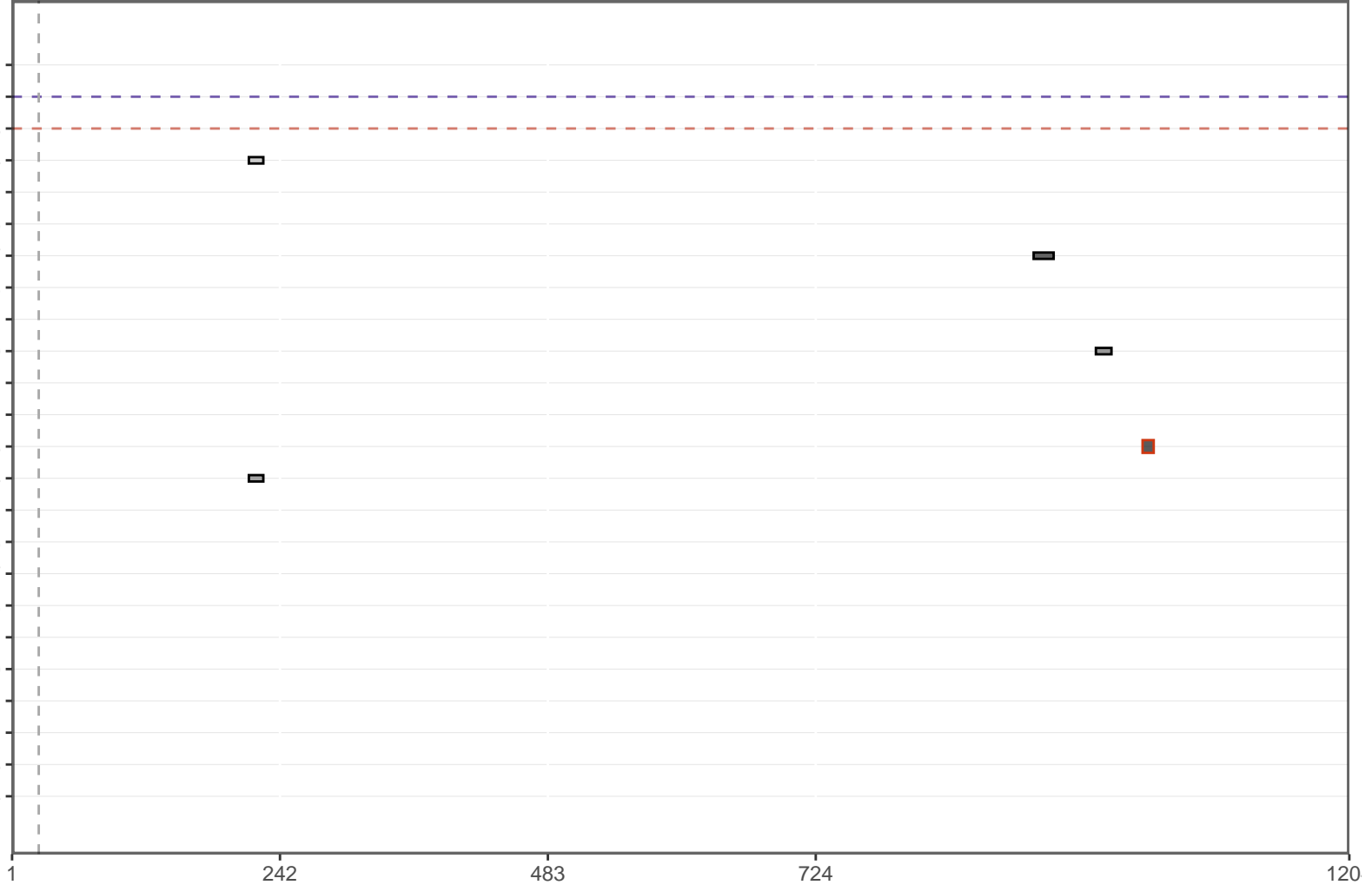
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

/DFVOKGRVTIISSHVDLSTQPDGSRMNLNKKGGQHVCVEYPGAHELSPFNSGIFGSSSVIHTSLSLFRYLKGESEYKKGHHVESSFSBIEGLPNIPLEVLDSSEGVVGGTFSKRVPDGVDSSAAVYEFEMWASAGGKFAFVPRDARDDDGGKILFYPROGHWAVTDDGGSSIPFFAGLGMHIEGVSPLNDVWVWIIAAGDGGSAFLKRDLELALETTTGTGDSFVAGLVDDBYSIEAKPGVHVKVYSPGSGFSGKLGQLVRYVSRDANEPFSLLSL

NbL12g00140.1 ABC_transporter_B_family_member_21-like [MW = 139.82 kDa]

No. of times detected



log(intensity)



Values from



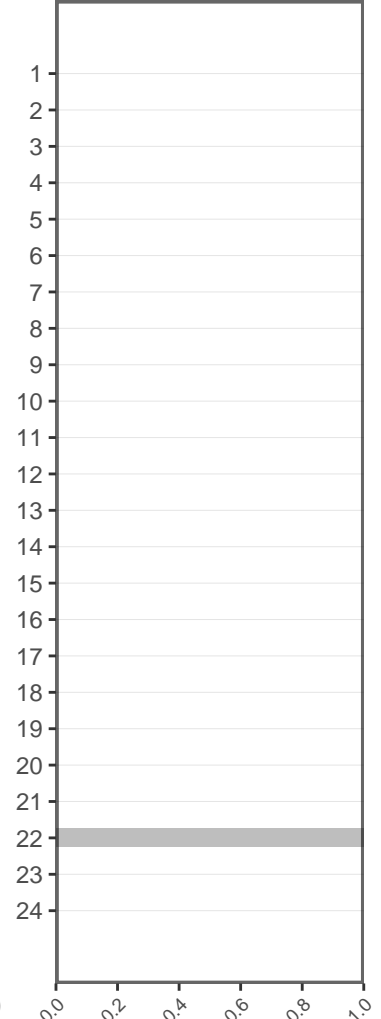
MW indication



Molecular weight



Gel Slice



Protein length



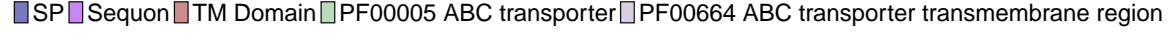
Peptide counts over 4 repeats



Pfam domains



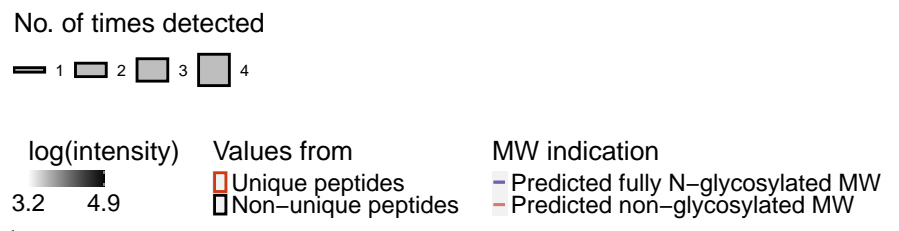
Pfam Description



Protein sequence:

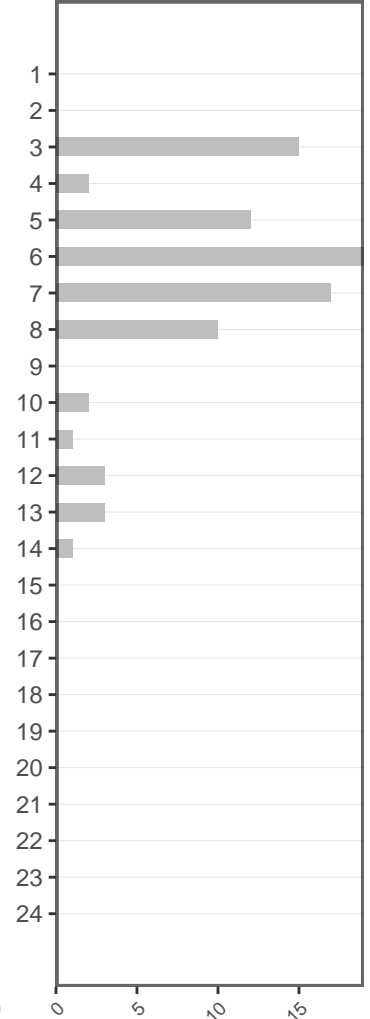
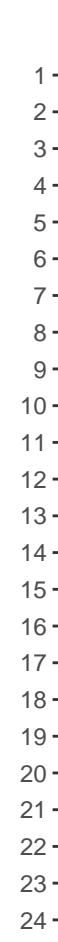
IQSGLNERERLDKSMGSGRGGSKTMBLLRISVRSRSGGNGNSRHSLSBISYGLFTGLVFPETANADTETGDEVSQKPLKVPPIRRLAVLNKPELPSVHGWAAHNGTLLPFGILGFSVVKTFYEPHQLRDKDFWALMFVVLGVVTLIAFPARTYLFSDAGKLIIRIRRMCFEKVVRMEVGVWFDESEHSSGIGARLSADASKVRALVGGDLAQMVDGSDATAAGLMAFEASWQLALILAMIPUGLNGYVQIKFMKFRSADAKMMVVEASQVANDAVGGIIRTVASFCAEEKYI

NbL11g24050.1 translocase_of_chloroplast_159_chloroplastic [MW = 158.33 kDa]



Molecular weight

Gel Slice

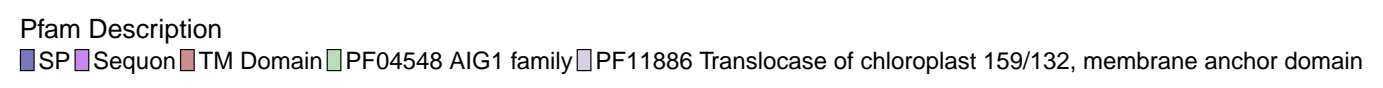


Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:

GLGSLRSLRPAIPGPNRPNLFTSSLSGNSGEGENNLSEENKLEKIQIRVKFLRLHRLGLSSDSIAQVLYRLALARRRNSPLFLEAAKMRARGLAEAGEGDDLDGFSYNIQVIGKSGVIGKSGATINSIFGEEKTPINAFGRPTTSVKEISGVYEGVWRVDFTPGLKSGVMEGGFNREVLSSANKFTKKRPPDFILYVDRLEDAQTRDLNLDLPMKLTITFCGLGSIWRSAVTLTHGASAPPDGPSSGSLPEYEVFVYRSHVYGGSGGAAGDLRMMSPFLMNPVSLVENHP!

NbL11g24030.1 WD_repeat-containing_protein_89_homolog [MW = 42.43 kDa]

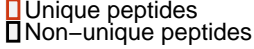
No. of times detected



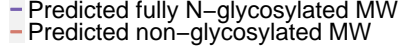
log(intensity)



Values from



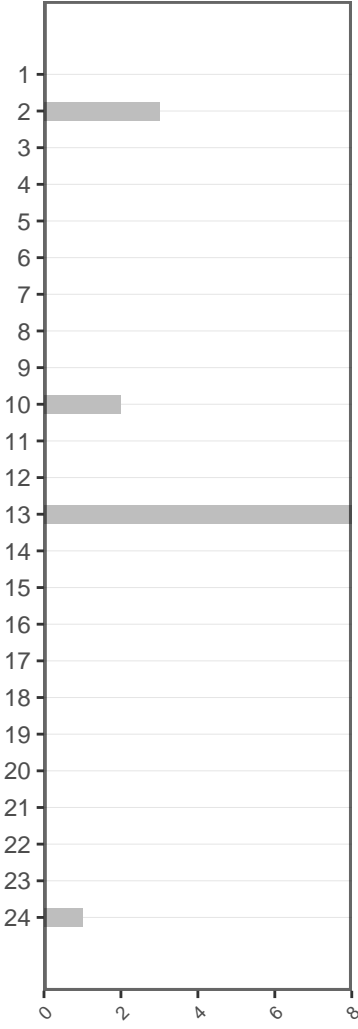
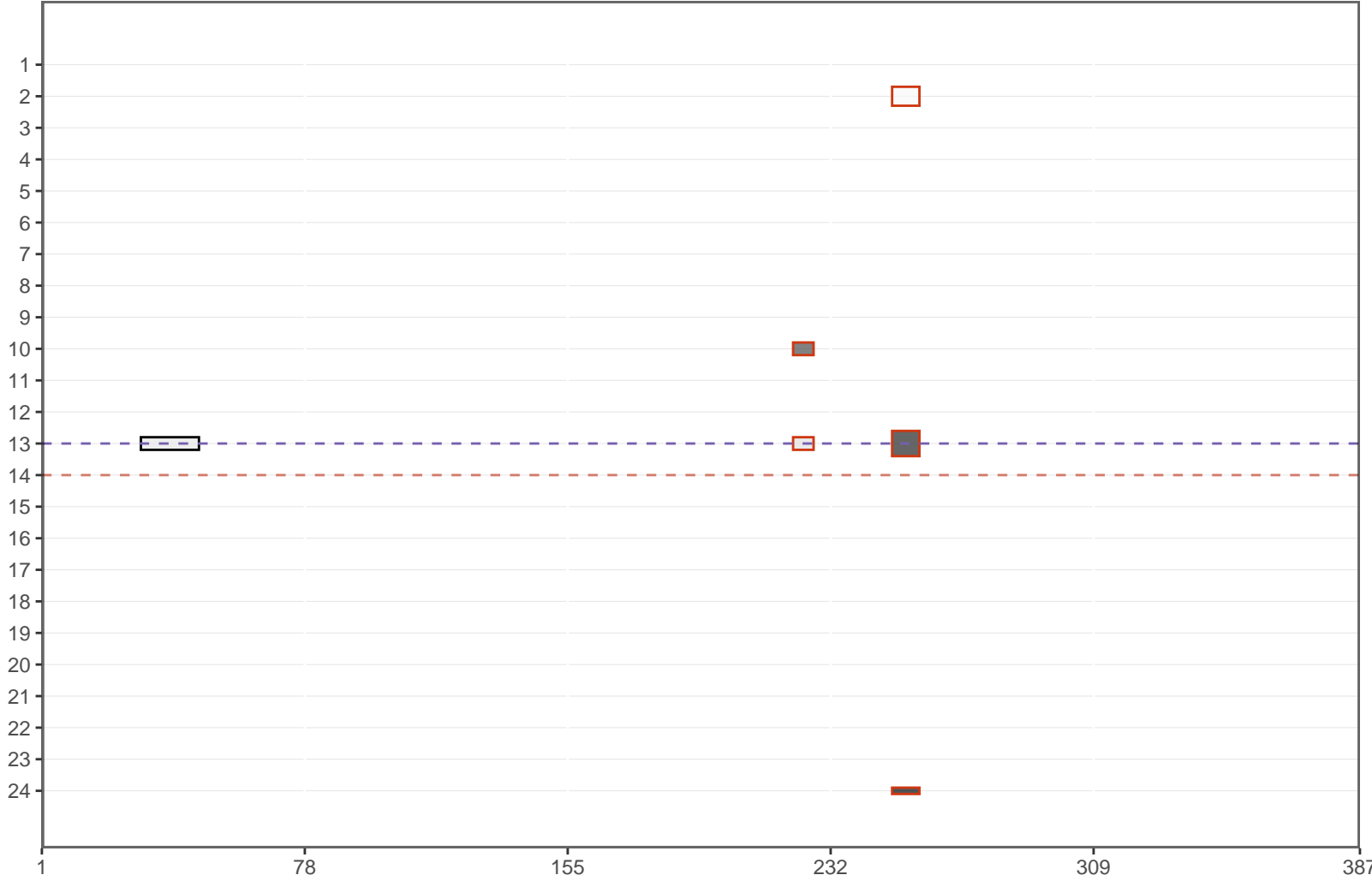
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DDRLISAASYDGLICLFDFTGGDNDQDHLVSLNVGTEVGVKVGFLGKNGKLVGLTHIETLSFVQWQKDERIEASFEDRALASKSWITNDVDFVFDCHYVSEEDRFWVIGGTNGGSLAVCPNYYGTRVIGVPEALGGGHEGIRSVLGGVPGIETMDNHGIFGWTGGDGRLLCQWLSGGSDNSQGWISTLAKSEKTRTKSRHSPIY

NbL11g24020.1 uncharacterized_protein_Osl_027940 [MW = 23.3 kDa]

No. of times detected



log(intensity)



Values from



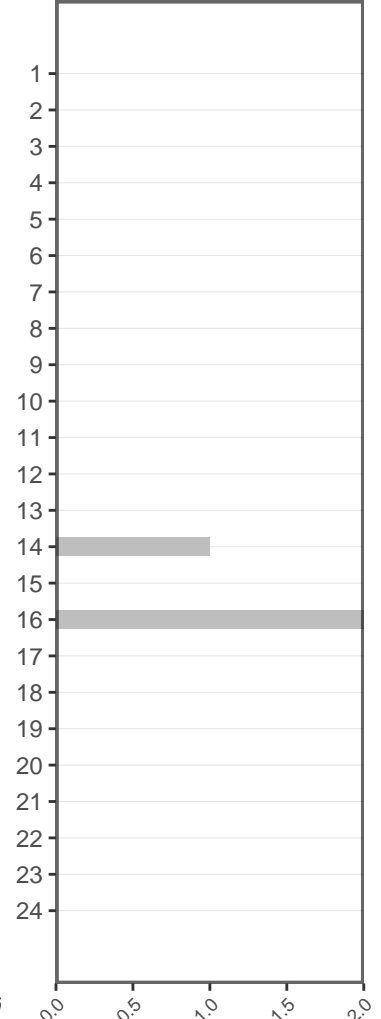
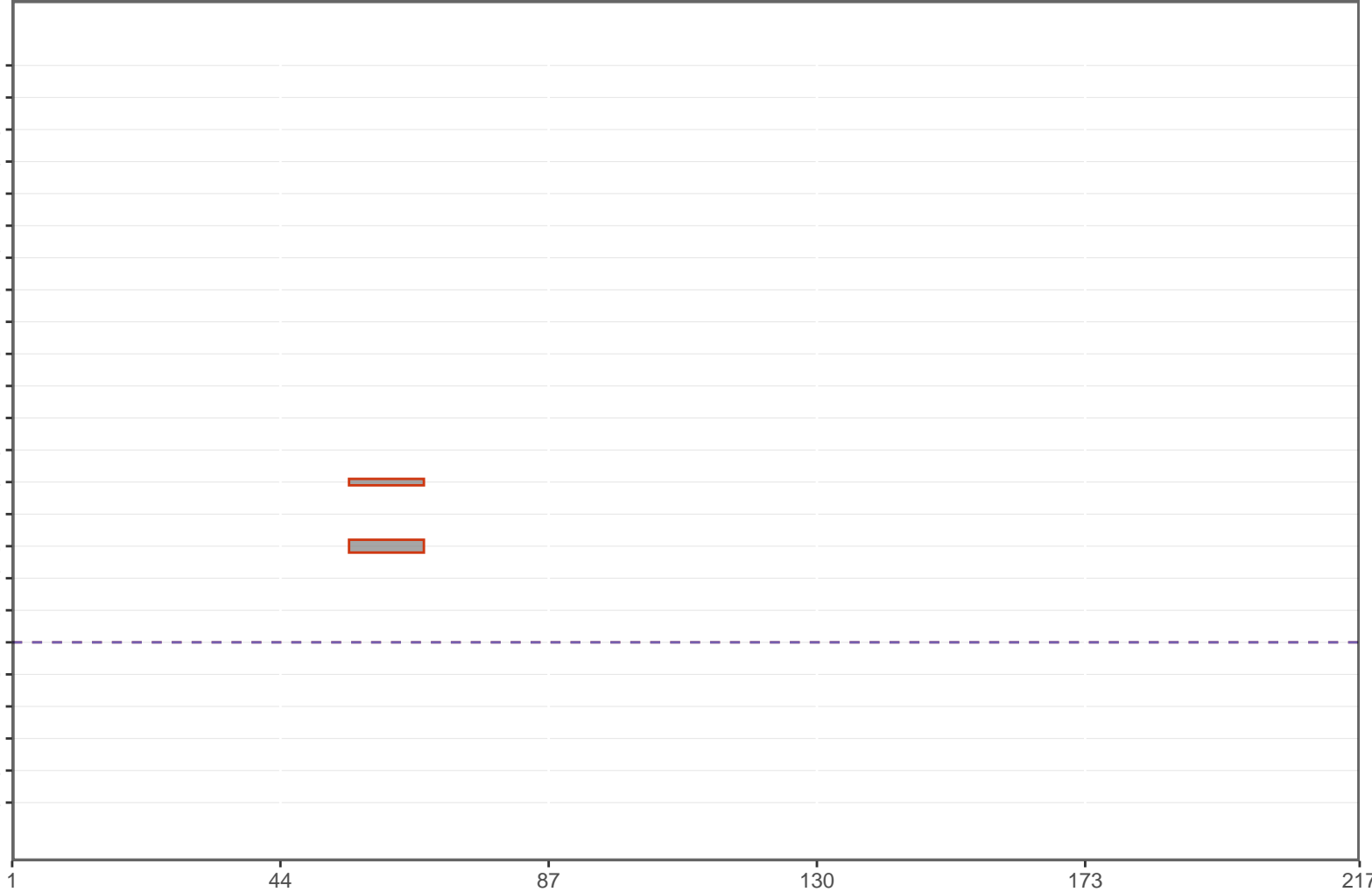
MW indication



Molecular weight



Gel Slice



Protein length

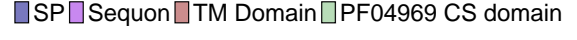


Peptide counts over 4 repeats

Pfam domains



Pfam Description

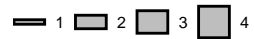


Protein sequence:

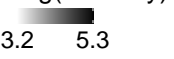
KYDWDKVVYDEDDADMGFGMDMMNMFSGFGDMGGMMGMMGGMDMAGMMGGMMGGMMGGMDMAGMMGGMDMGGDLDLDDSDDEEGEVKPSAKADEKVDGEPKEEGKVVDEAK*

NbL11g24010.1 ABC_transporter_C_family_member_14-like [MW = 168.99 kDa]

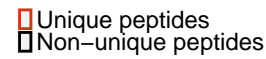
No. of times detected



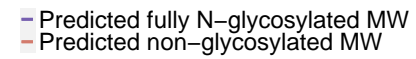
log(intensity)



Values from

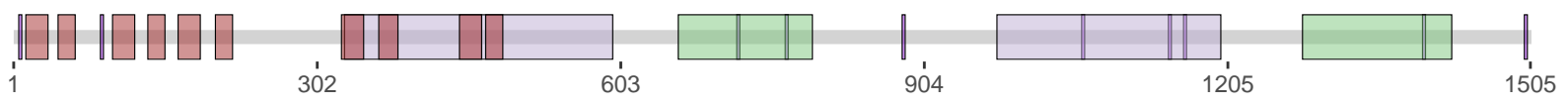
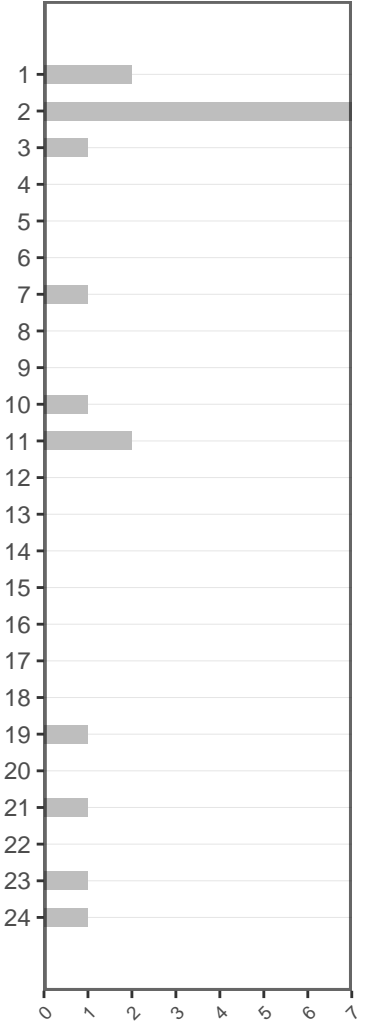
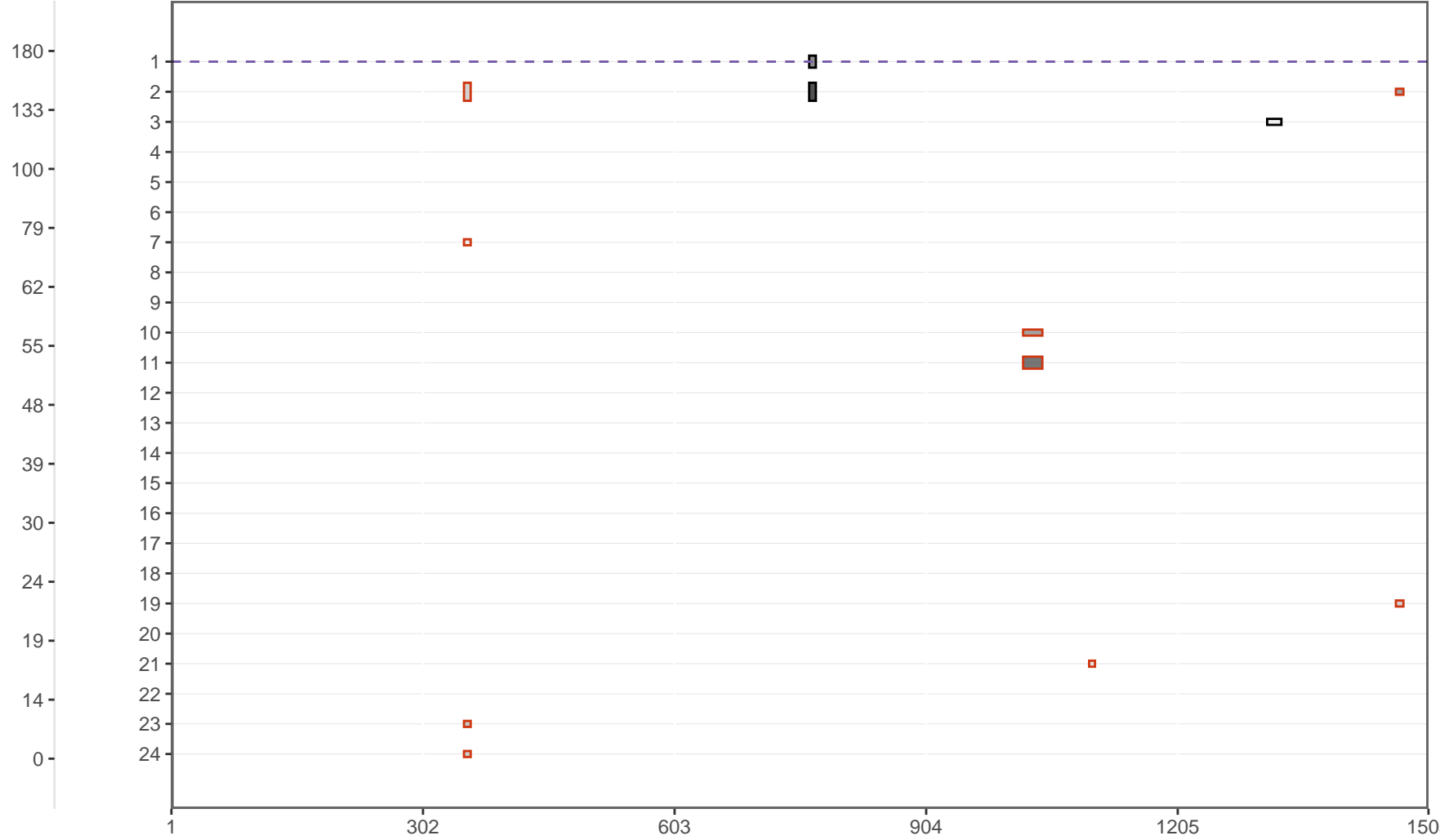


MW indication

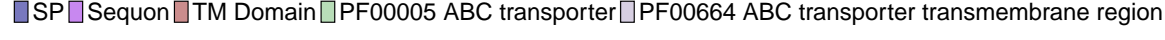


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

MRVCCLEKDLKLEMEFGDQTEGERGINSGGGKGRIGLARAVYQDDYLLDDVFAVDAHTGSEIFKQGVIRGILRDKTLVLTQVDFLHNVDLHVMRDGMVQSGKYSLEIAGMDFKELVAANHETSLELVDTKESNSVVEESKSRRLSKEENGEDEKSGQSTPERDQSKLKEEERETGKVSFRVYKLYTEAFGWVGVVLLVLFSLWQBSLMAAGDYVLAETSDRAMSENFSLFIEYGVIAVVSGLLIVRMVYVTFMGLKTSQIFFGKILGSLHAPMSFFDTPSI

NbL11g23970.1 mitochondrial_zinc_maintenance_protein_1_mitochondrial [MW = 11.85 kDa]

No. of times detected



log(intensity)



Values from



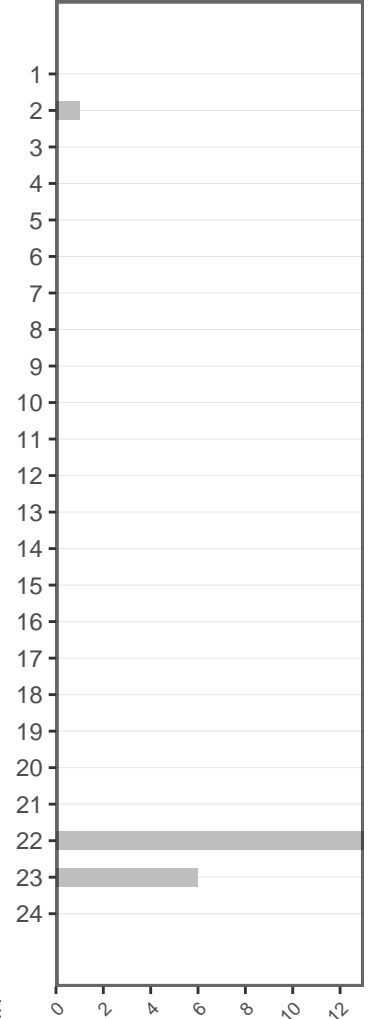
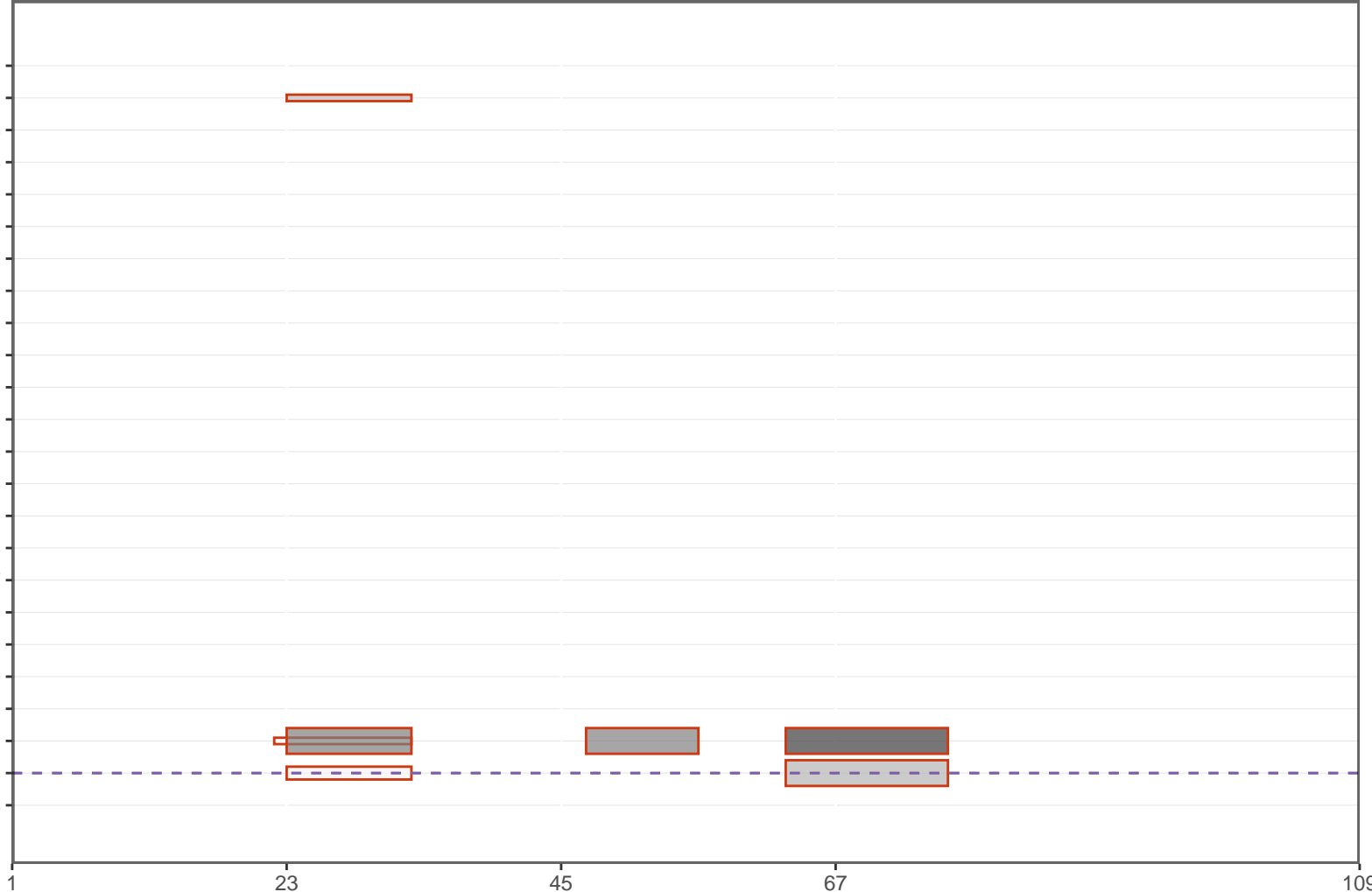
MW indication



Molecular weight



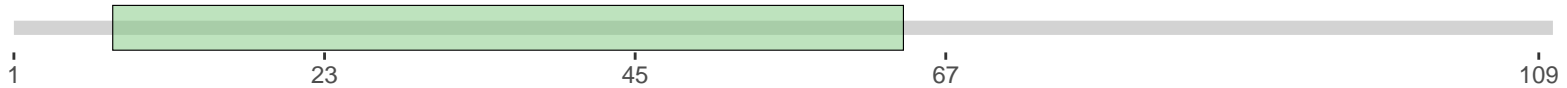
Gel Slice



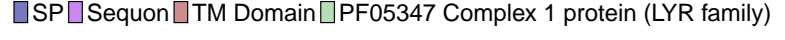
Protein length



Pfam domains



Pfam Description



Protein sequence:

IKFEENRHVTSEADQRLDDARDASEFISTMVAQKSPGAFVVKPEKEHGATLEIPSEELKKSIV

NbL11g23950.1 small_nuclear_ribonucleoprotein_Sm_D2-like [MW = 12.53 kDa]

No. of times detected



log(intensity)



Values from



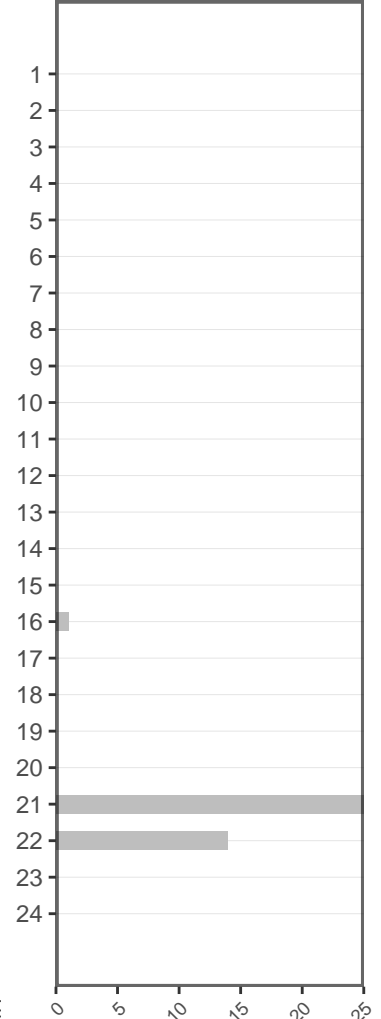
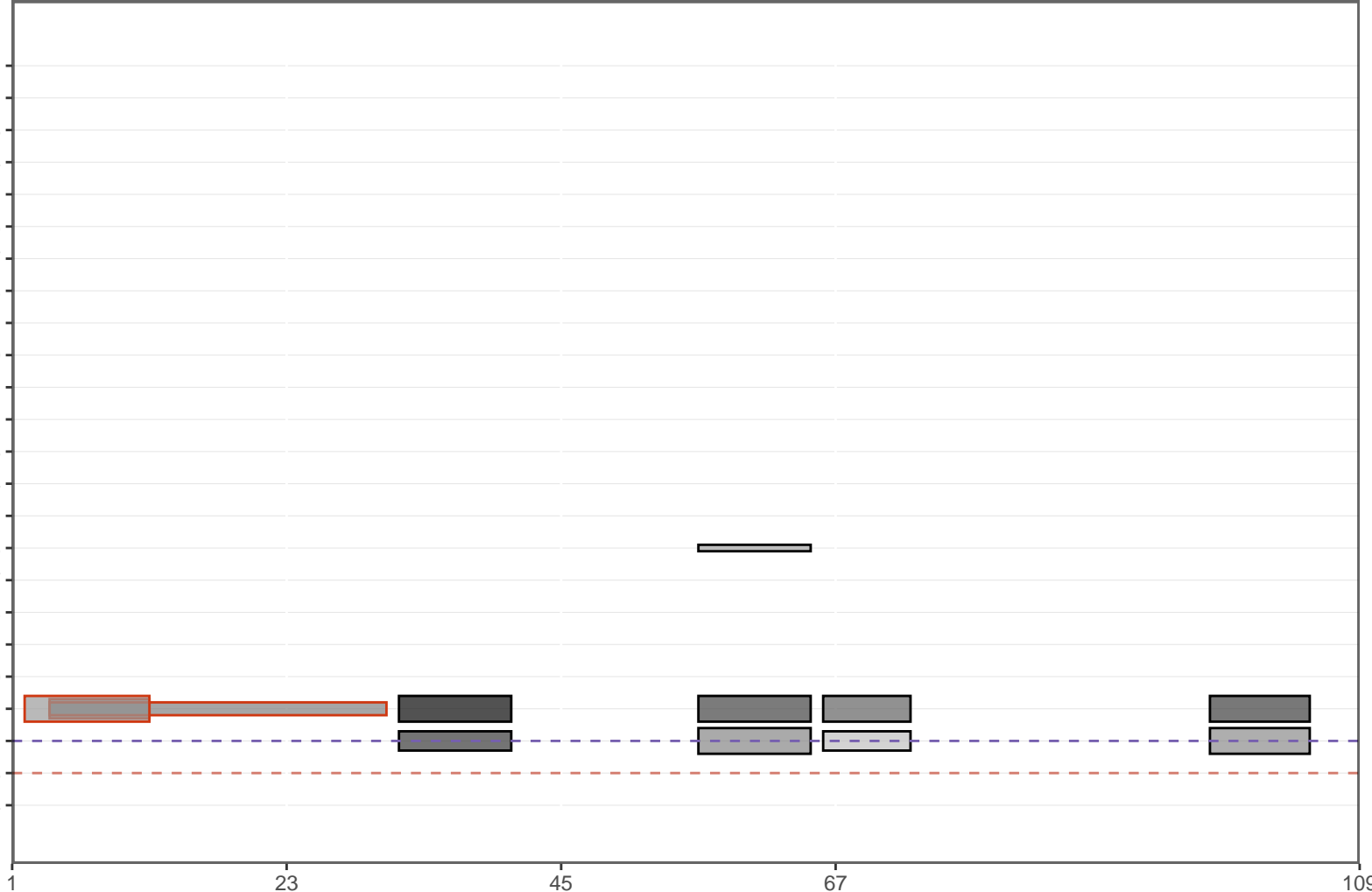
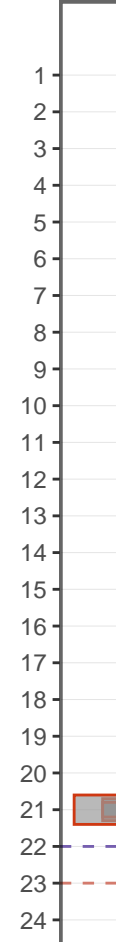
MW indication



Molecular weight

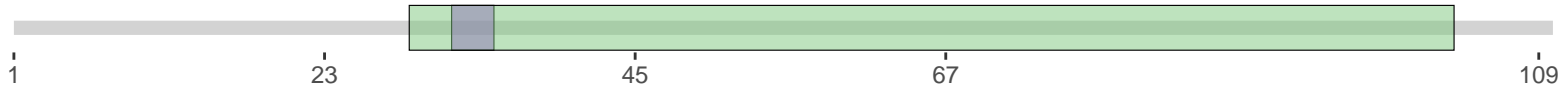


Gel Slice



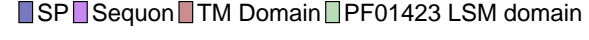
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

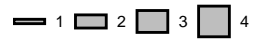


Protein sequence:

NNRKLLGRVRAFDRIHQNMVLENVREMVTEVPKTGKGGKKKAGPANKDRFRGKMFRLRGDSVIVLRNPK

NbL11g23890.1 26S_proteasome_non-ATPase_regulatory_subunit_1_homolog_A-like [MW = 107.94 kDa]

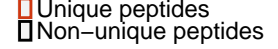
No. of times detected



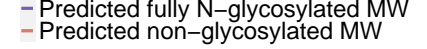
log(intensity)



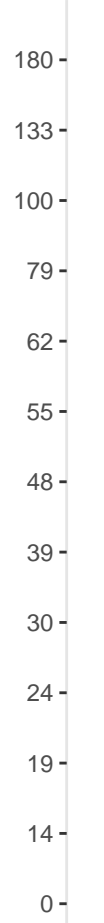
Values from



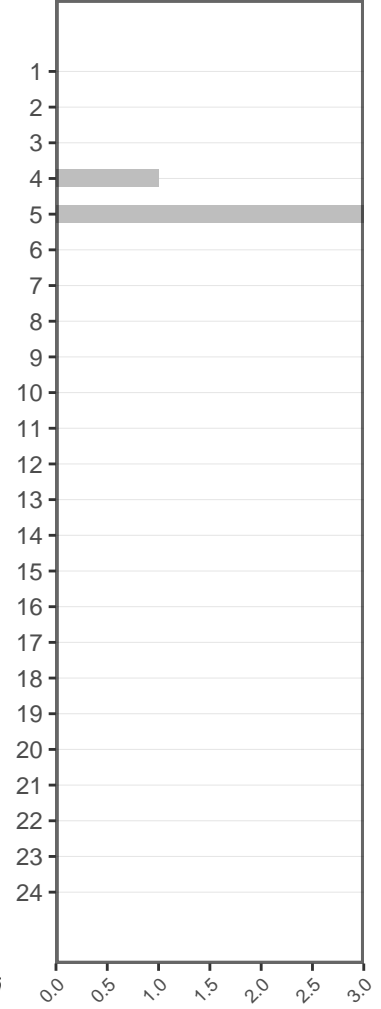
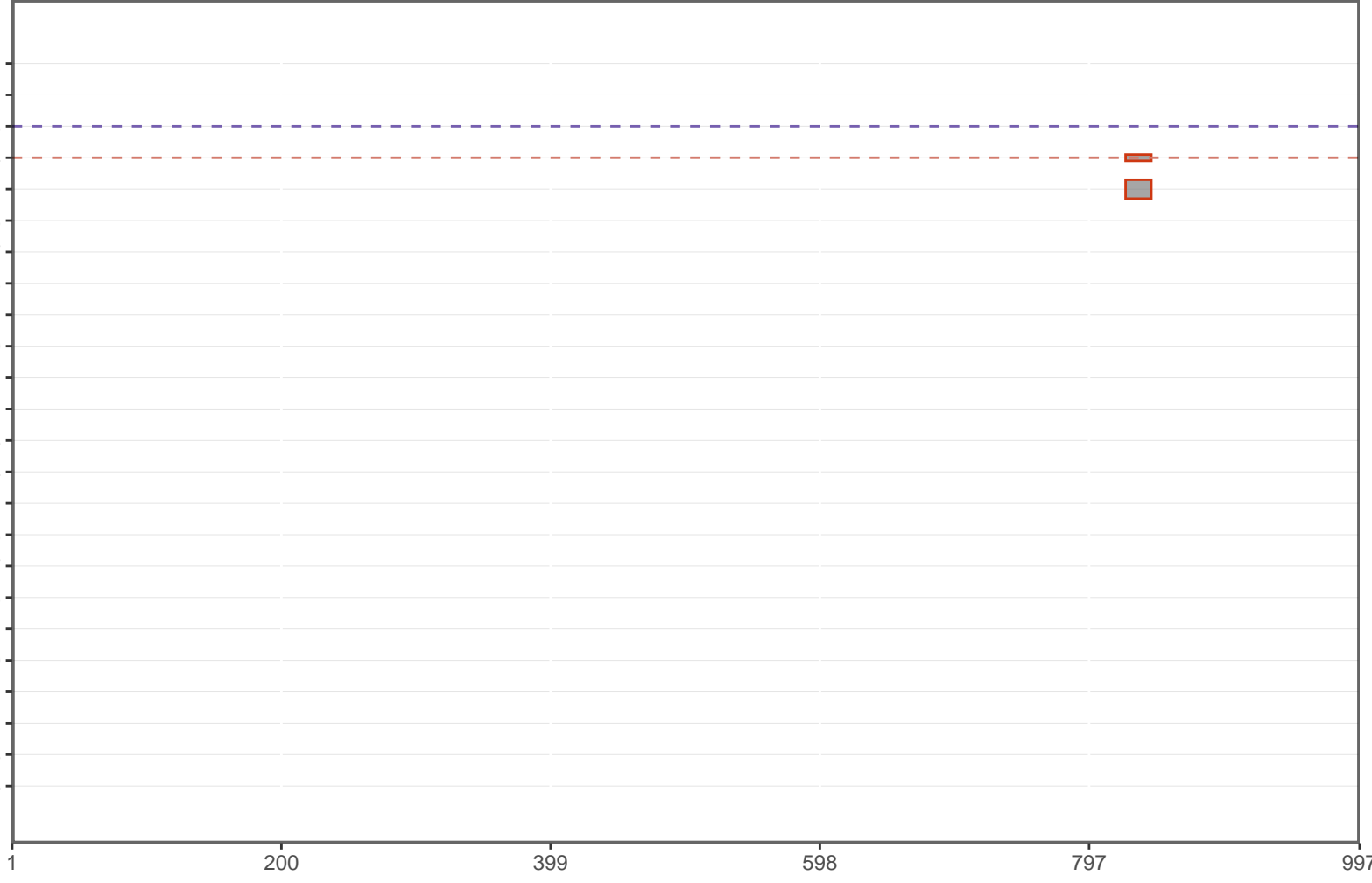
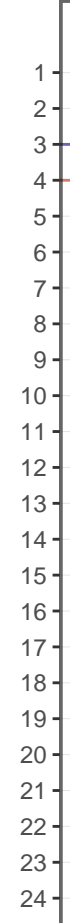
MW indication



Molecular weight

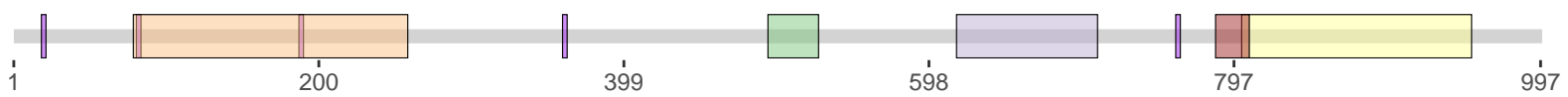


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01851 Proteasome/cyclosome repeat
- PF13646 HEAT repeats
- PF17781 RPN1/RPN2 N-terminal domain
- PF18004 26S proteasome regulatory subunit RPN2 C-terminal domain

Protein sequence:

STNVEVQHAGCLGLGLAALGTADEEDYDDKNNLYTDSAVAGEAANGIGMLLMVGTASEKAGEMLAYAHETQHEKIRGLGALTYVGREEEADTIEQMTRDDQDPLRYGGMVALALAYRGTANNKAIKQLLHFVSDVSDVRRRTAVLALGFVYKSEPEGMPIRVHLLSESYNPHVRYGAAMAVGISCAGTGLSEASISLEPLRTSDVYDFVRRGALLAMAMVAVQISEASDSRVGAFRRRLEKVLKDHEDTMSKMGALABQLDAGGRNVTIKLLSKTKIDKTTAVYGLAVF

NbL11g23870.1 60S_ribosomal_protein_L13a-4-like [MW = 23.48 kDa]

No. of times detected



log(intensity)



Values from



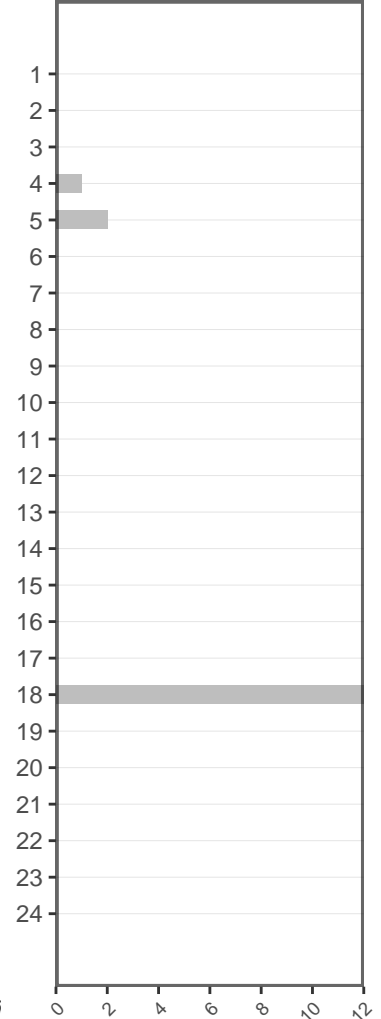
MW indication



Molecular weight

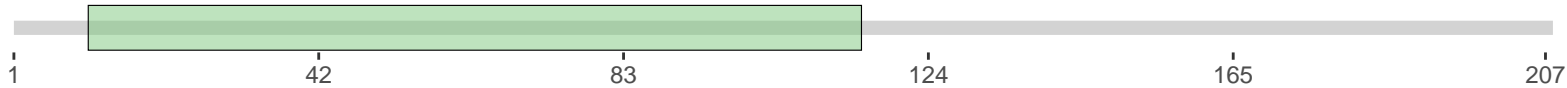


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGMIPKTKRGAALALRLKLVYEGVPPYDKIKRMVDPDLKVLRLQAGHKYDGLLGLSSEVGVWVYDTIKELNKRKERAGVAYERRKQLAKLRVKAKEKAAEEKLGPQLAIAIPKY*

NbL11g23830.1 epoxide_hydrolase_A-like [MW = 36.33 kDa]

No. of times detected



log(intensity)



Values from



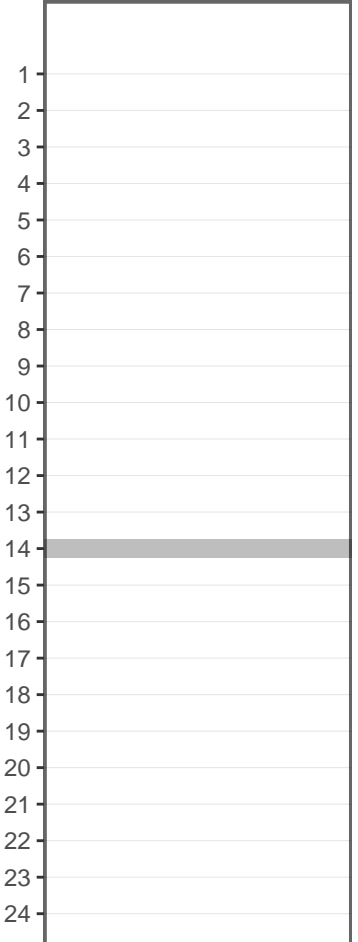
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

1 65 129 193 319

Protein length



Pfam domains

Pfam Description



Protein sequence:

SNDYIMCRFOKPGEEVEEFASVDATAVIKGFLSSRDPRPPGIPKIGDFHQAALAKSPATLPSWITEEDNHYAEKLUKTKGFTGGLNYYRNLDKNWELTAPFSGCKGIVPTKFAVGGDLATHYVPGTKKEYIHNDGRKKEVNIQEVVVMGEGVGHFINGEKPDENAHYDFIQRP

NbL11g23820.1 60S_ribosomal_protein_L18-2 [MW = 20.99 kDa]

No. of times detected



log(intensity)



Values from



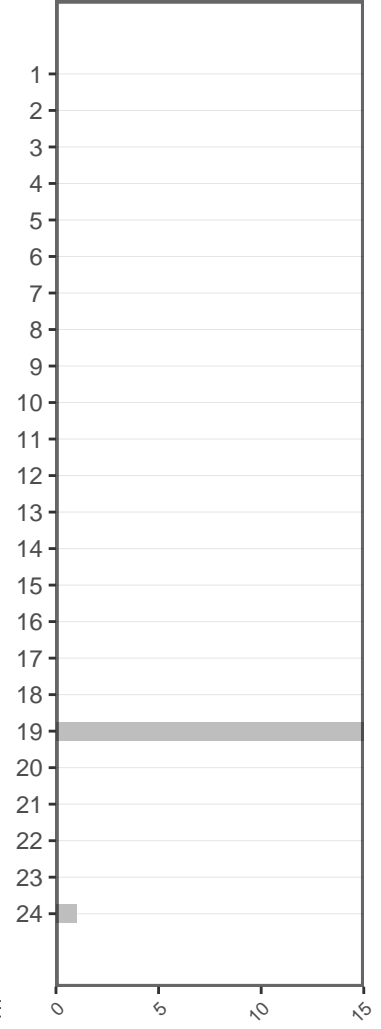
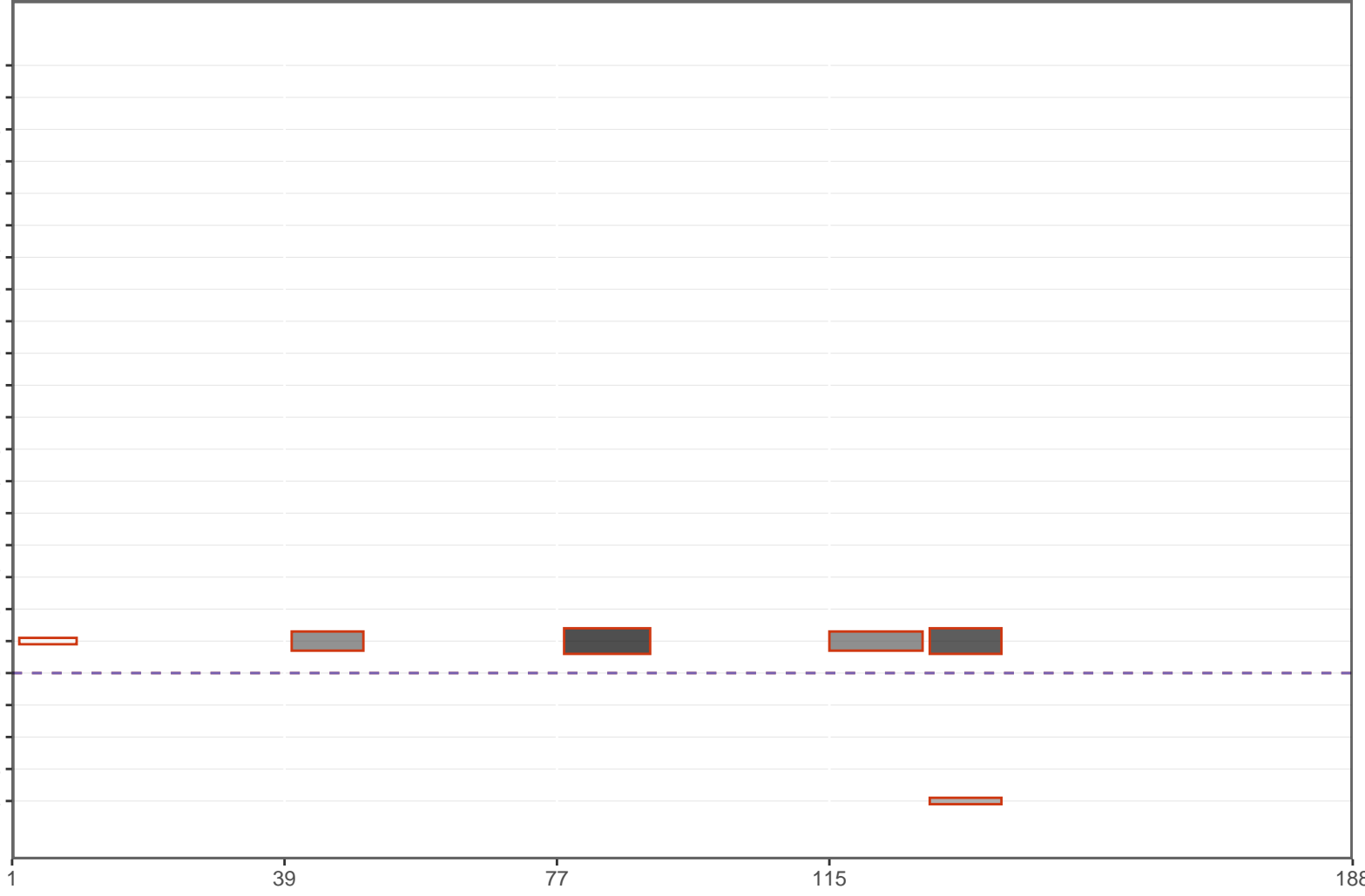
MW indication



Molecular weight



Gel Slice

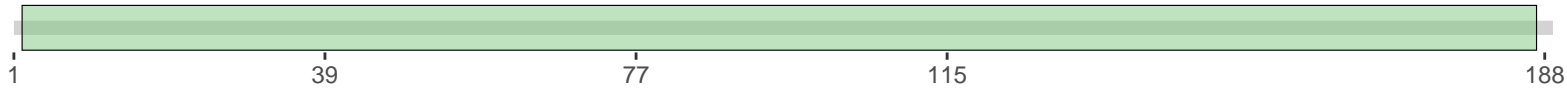


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

STVTDQRAYEYPSLKVTLRFETARARIEKAGGECFTFDQLRAPLGGNTVLLRGRNRREAVKHFGRAPGVPHSHTRKPVVRANKGRKFERARGKRKSRGFKV

NbL11g23770.1 U1_small_nuclear_ribonucleoprotein_A [MW = 28.35 kDa]

No. of times detected



log(intensity)



Values from



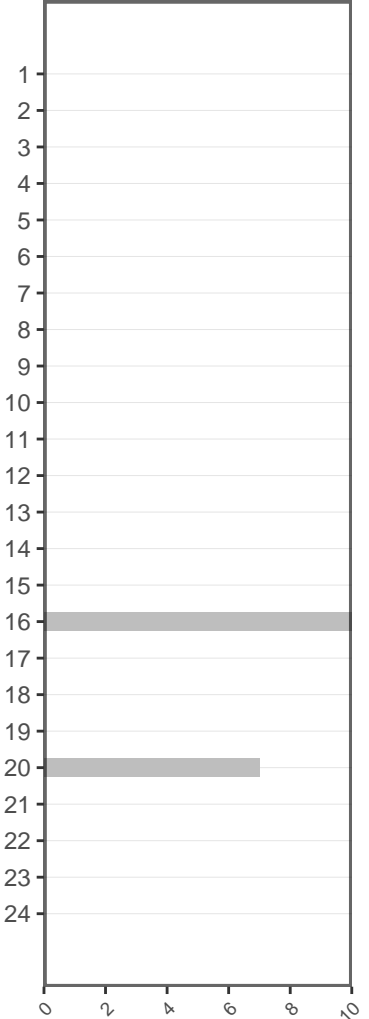
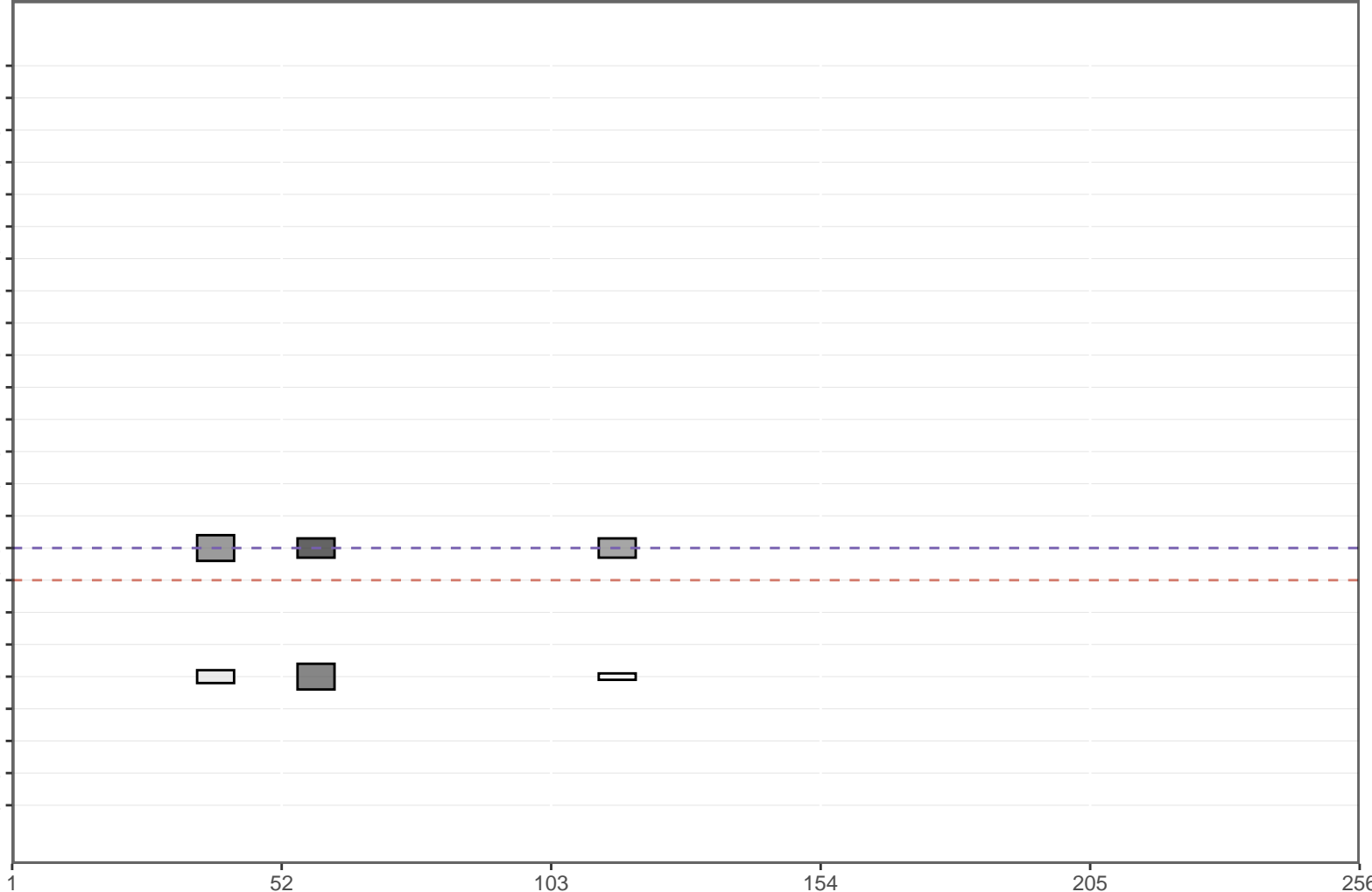
MW indication



Molecular weight



Gel Slice



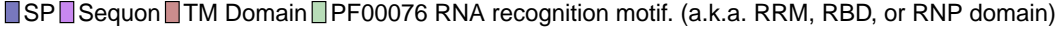
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TVPREKRRKHEDKGRKKKDDGGANGAMLNLAAGAYGAPRFSGIPYMGGAKAIVFAPAPPNSLFFVGNLPHGISTPMLQLMFFQYPGFKEVRMVDTKPGIAFVEYGDDEMGSTVAMQALQGFITPENPLMIFYAKK

NbL11g23700.1 glutathione_reductase_chloroplastic-like [MW = 57.73 kDa]

No. of times detected



log(intensity)



Values from



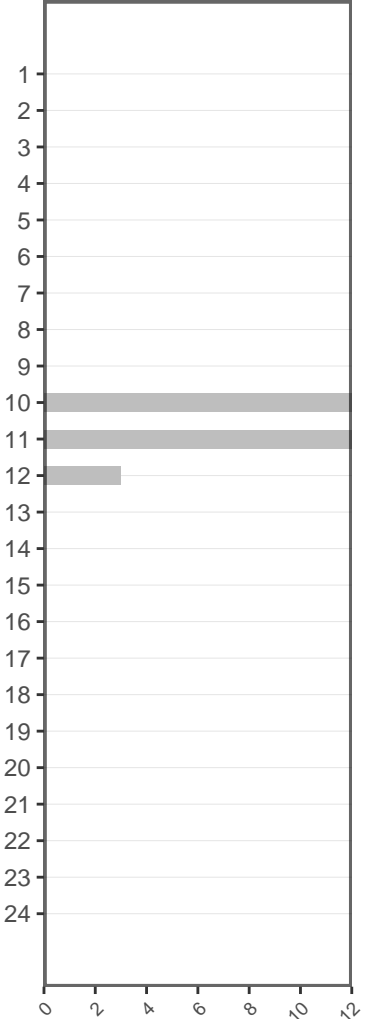
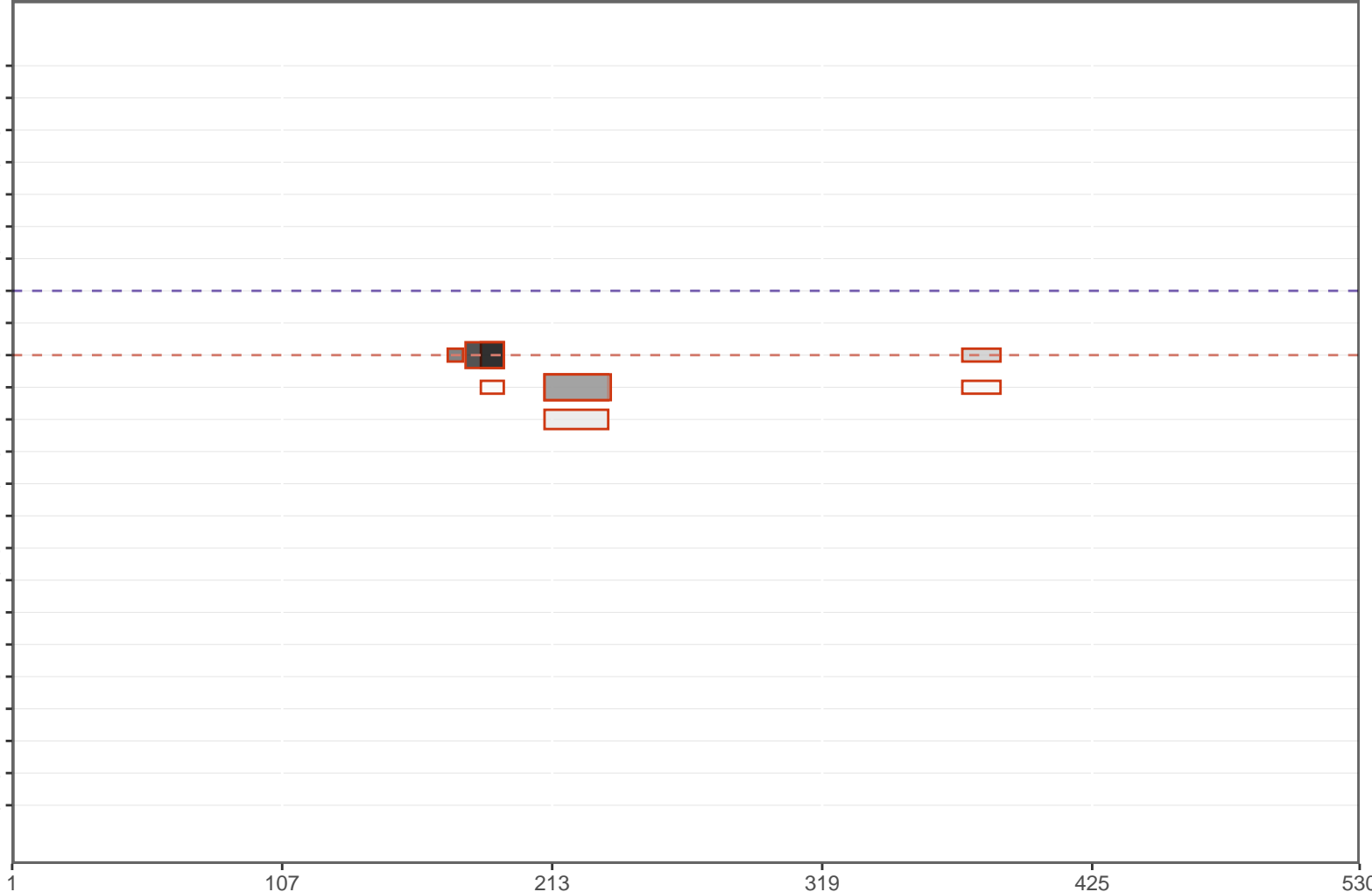
MW indication



Molecular weight



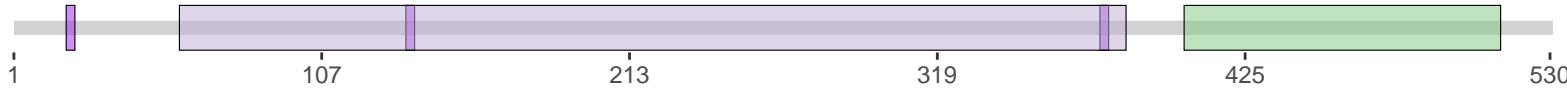
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF02852 Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain
- PF07992 Pyridine nucleotide-disulphide oxidoreductase

Protein sequence:

GMGATVLDLCFRKELPLRFGFDDMRRAVARNLEGRGTMHPCTFTLTKLEKTEDEGKIVHTDHESEVWADVLFATGRPRNTRKRLNLDVGVVELDKMGAAVKEVSRTNVPSIWAAGDVTNRINLTPVALMEGTGAKTVFGGKPTKPDVSHIPGAVFQIPLPLVVLGLGEEQAIEQVNGEVSVYVYTFSTFNPMAKNTISGRGKESVMKLLVEAETDKVVLGASMGCPDAPLEIMDGIWALKGATKEGFDETLYGHIPSAAEFVYVTRMSETRRVRSNKKPTNL

NbL11g23550.1 TBC1_domain_family_member_13-like [MW = 54.99 kDa]

No. of times detected



log(intensity)



Values from



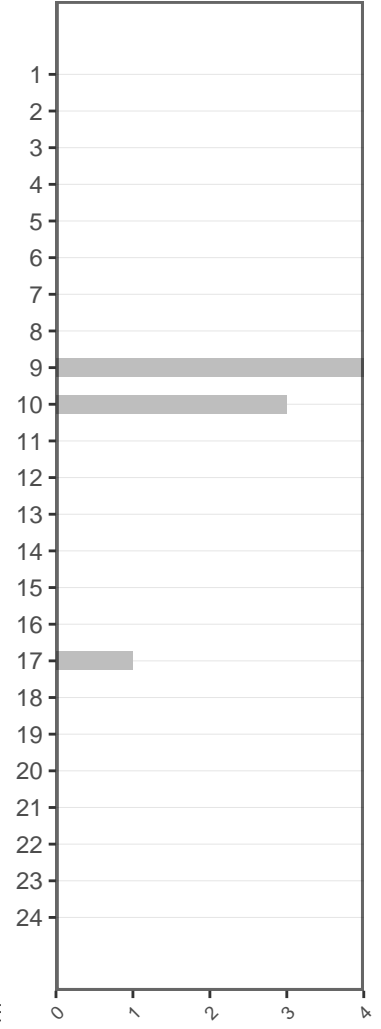
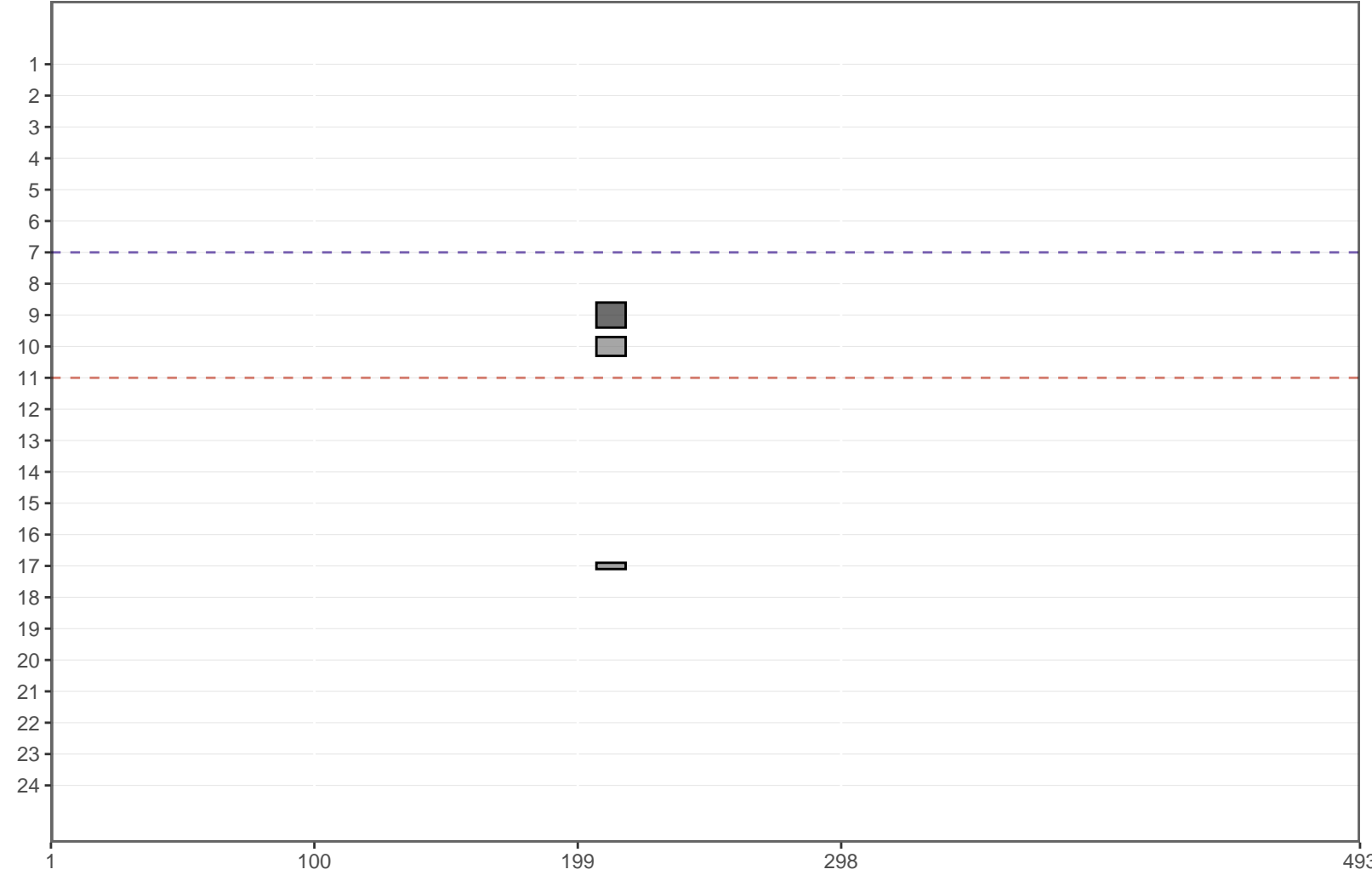
MW indication



Molecular weight



Gel Slice



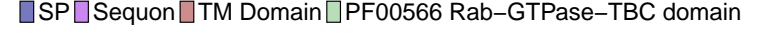
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VEDKGVLPKSEISHGEHPLSLGGNSIWNFFGDDTEIEGIDRDVWRTHPDLHFHFGDTPFAKSNQDALRNILVFANLNPQIRYVGGMELLAPLVYFRNDNPEENTASAEADTFGCVVELLGGFRDHFQDGLDINSVVGIRSTIKLGGLLKEHDEELWRHLEMTTKVNPQFYFRWITLLTQEFNFVDSLIIWDTLLSDPEGPGQETLFRVCGCAMLIVRRLLAGDFTSNLKLGNYPSSNISHLLYVANKLFRKSGAG

NbL11g23520.1 50S_ribosomal_protein_L13-like [MW = 23.63 kDa]

No. of times detected



log(intensity)



Values from



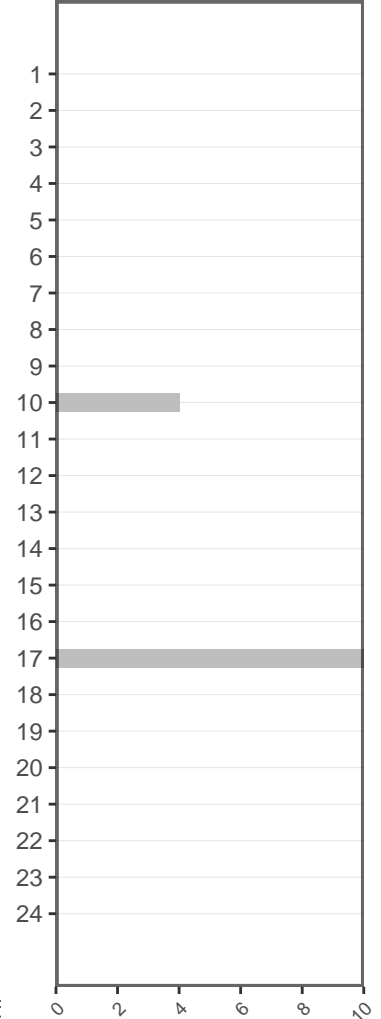
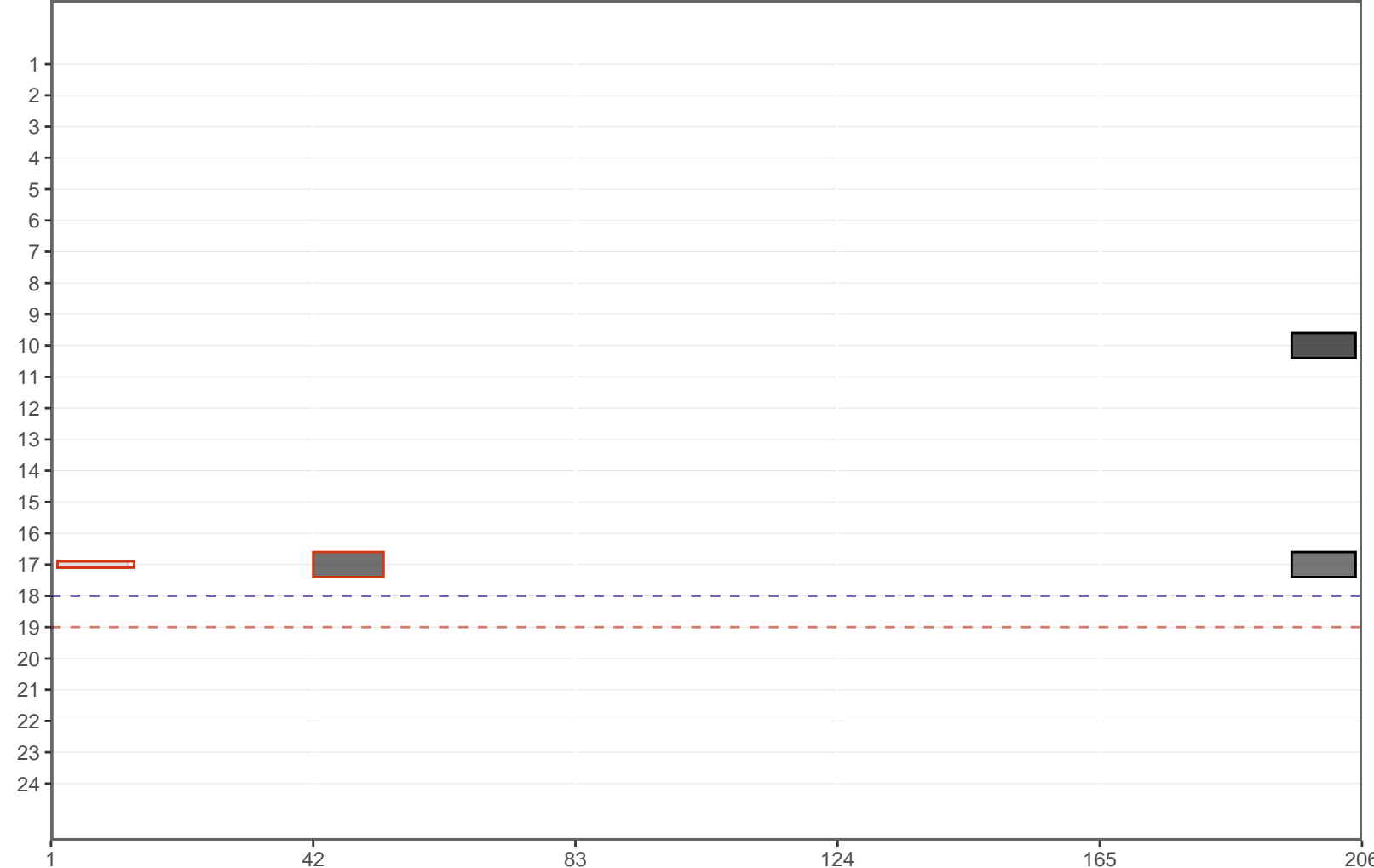
MW indication



Molecular weight

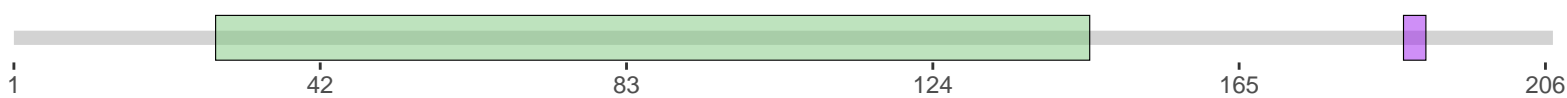


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

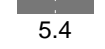
HTGYGHLEKERSLKDGMKDPTEVIRKAVLRMLRNKLRDDDRDRKLRIFAGDEHPFDORPLEPFLVMPDPRGVRELRPRTRRAMIRAGNKAEQGGGGTNTSKRKNKKEVEEVA5A

NbL11g23480.1 protein_BOBBER_1-like [MW = 29.77 kDa]

No. of times detected



log(intensity)



Values from



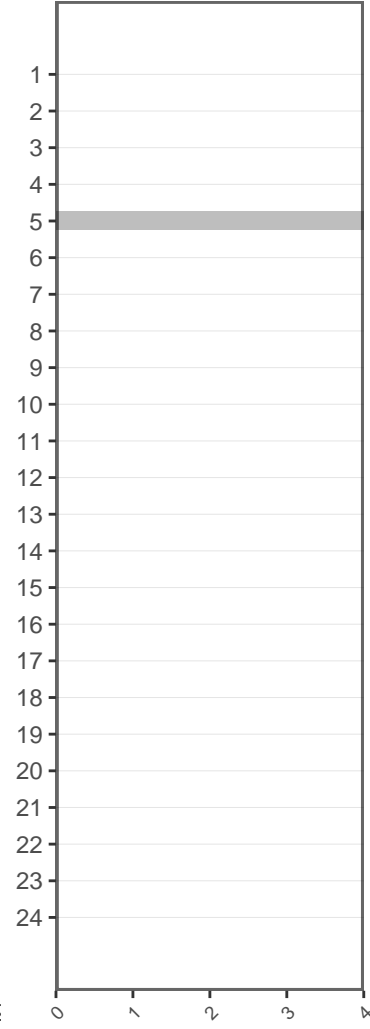
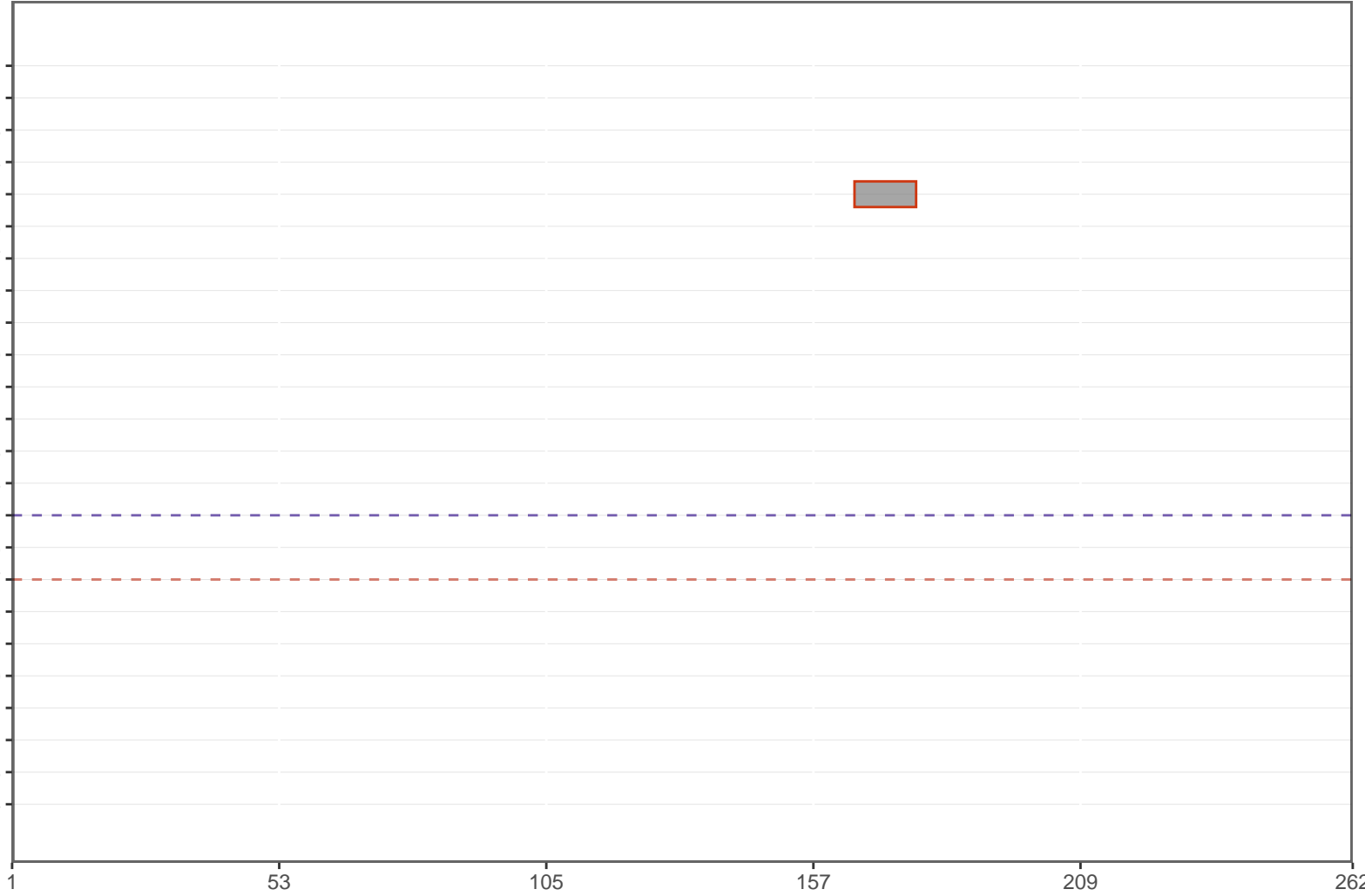
MW indication



Molecular weight

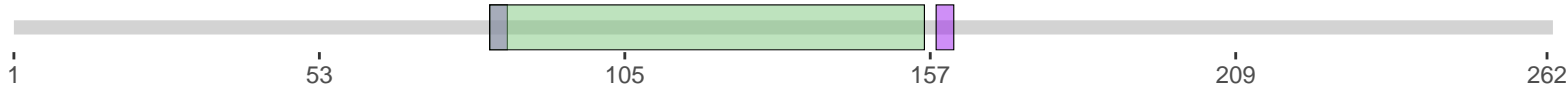


Gel Slice



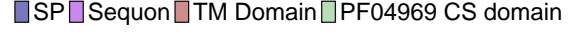
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KNDPPVIEGELLEPKADEGFWLEEDQKQVTLMTKRNGSDWVKSLFKGSPEDTQKAEPEPRRLSELETRBAVEKMMFDGKGLTKPTSDIENGDMVKKFMENPEIAKHFTNSPNAANGKGGKFNVRMMPSGGMP

NbL11g23400.1 adenosylhomocysteinase [MW = 60.9 kDa]

No. of times detected



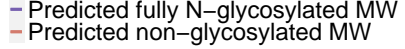
log(intensity)



Values from



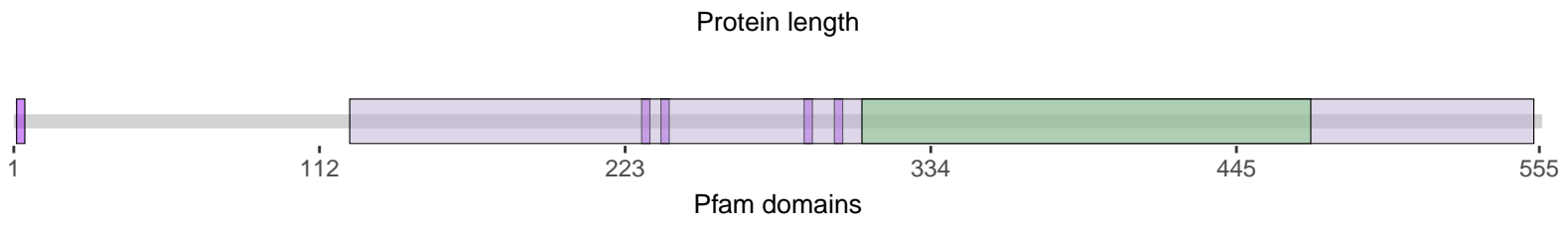
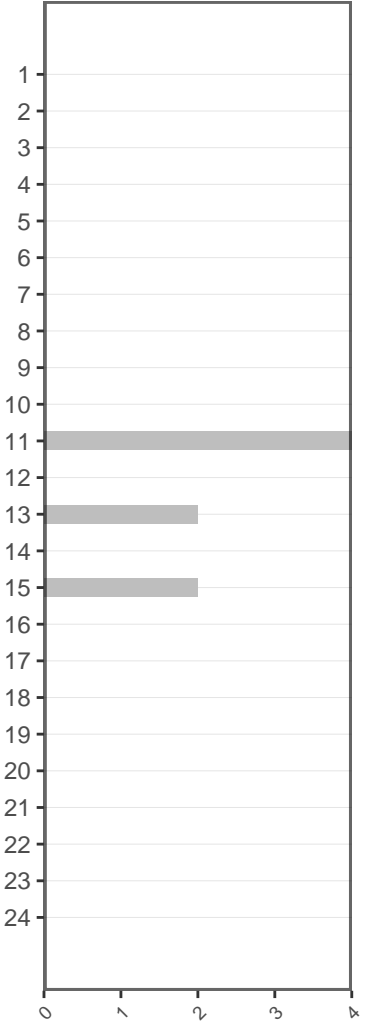
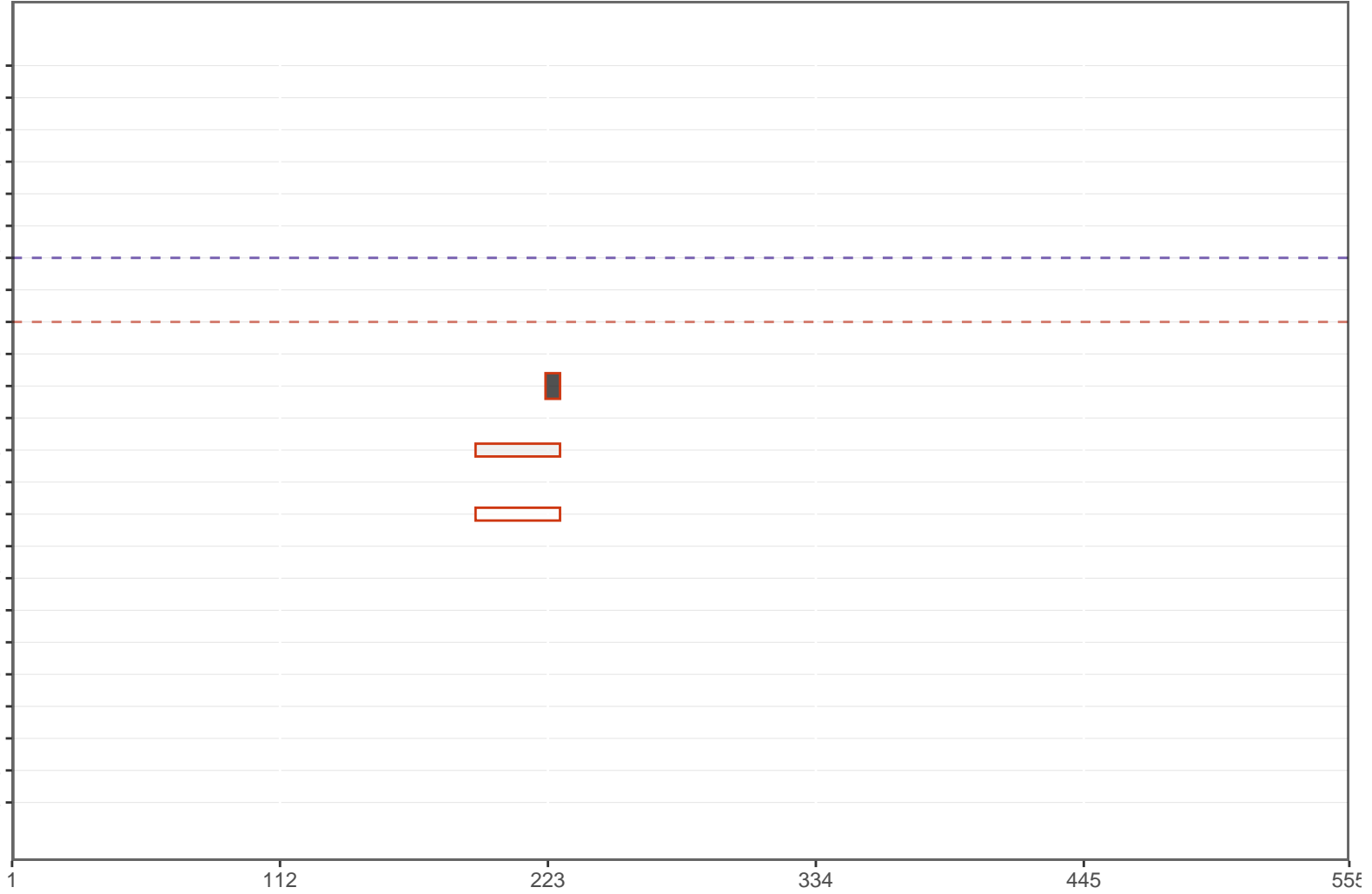
MW indication



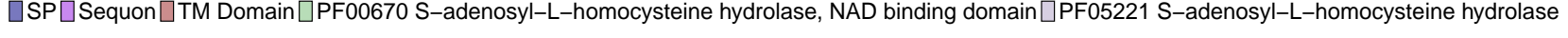
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

RLVGSEETTTGVKRLVGMQNGTLFPAINVDSVTKKFDNLYGCRHSPLDGLMRATDMAGKVALVAGYGVGKGAALKGAGARVITEIDPICALGATMGLVLTLEDVVSQVDFVTTGNDIMVDHMRMKNNNAICNIGHFDNEIDMLGLETYPGVKRTIKPQTRVWFFDFTNSGIVLAEGRLMNLGCATGHPSPVMSGSFTNQVIAQLELWNEKSSGKYEKKVYVLPKHLDEKVAALHLGKLGAKLTKLKGADGADHSIVPEGPKPNIYRI*

NbL11g23380.1 selenium-binding_protein_1-like [MW = 53.68 kDa]

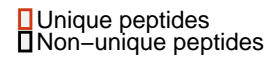
No. of times detected



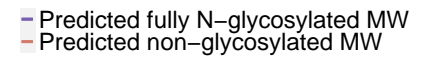
log(intensity)



Values from



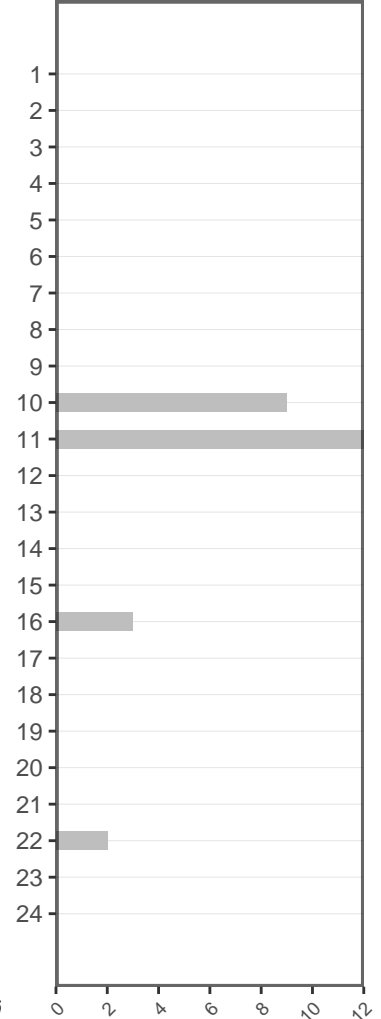
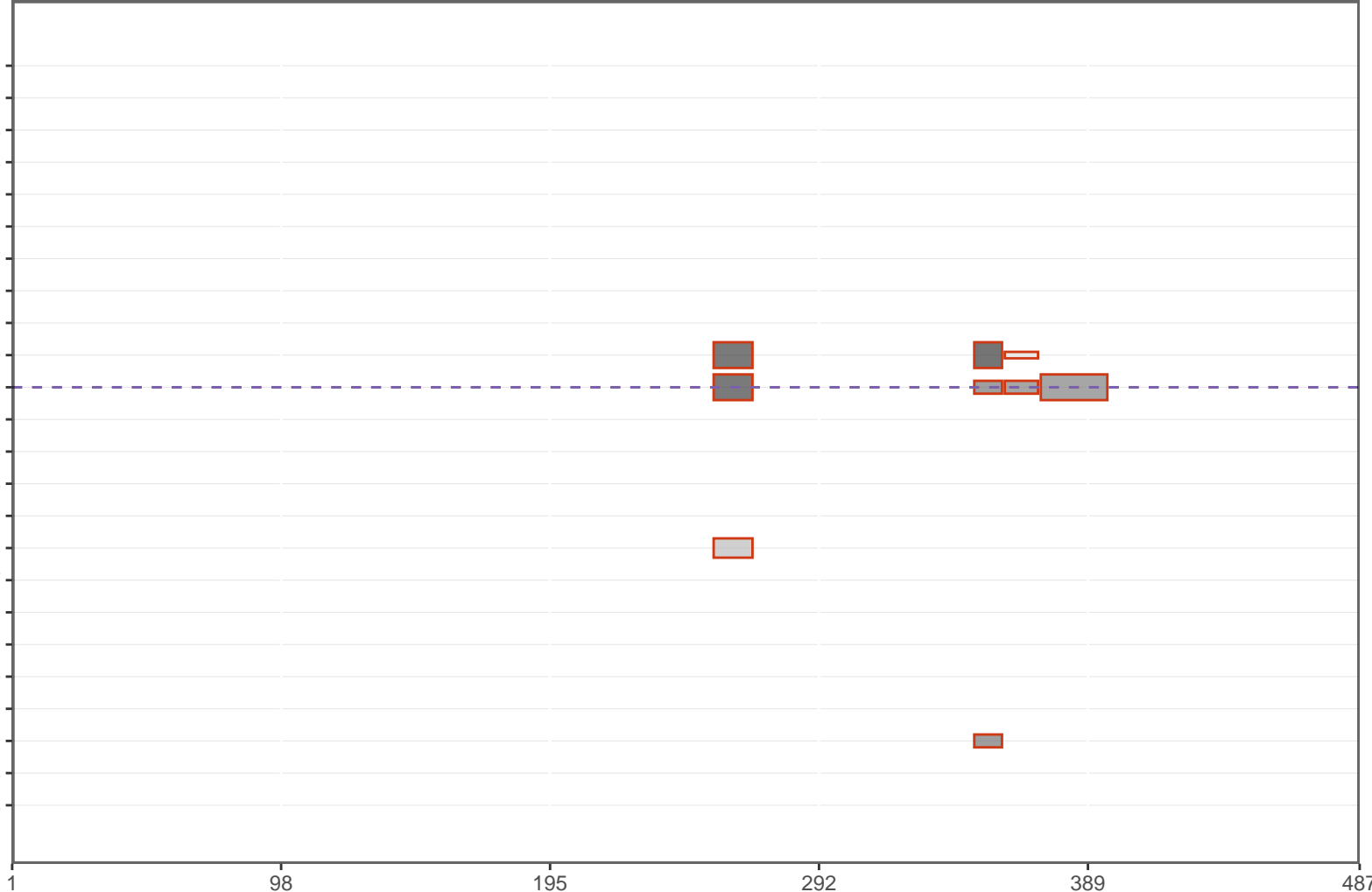
MW indication



Molecular weight

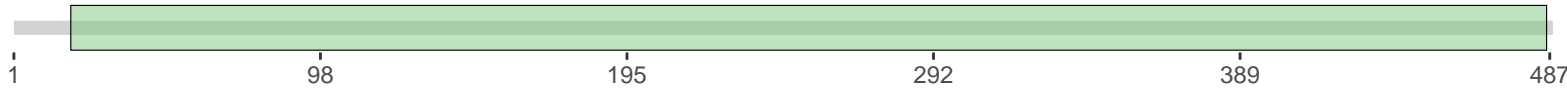


Gel Slice



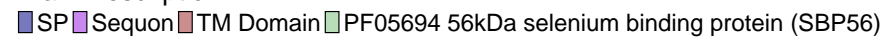
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

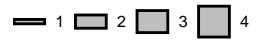


Protein sequence:

DHVTDLGLGRHLHYVTFWPGGELNKTLDLGNLGLFLEVRFLHNFSEANGVYSGALTEAMVRFKMPDGGWDEHEIAWPKVQNRILPEMPLGTFDLRSLDORFLYLANWHLGDRVQNEDFNPKLAGVYVGGVYFQKGNVLAEAEDGFTYGVDPVAVGHRLRGGPQMQLSDGKRLVATNSLFTWDRGFYPELLEKGGHILGIVDTEKGGGLVNPRTFVDFGAEPNGSLAHEMRYPGDGTSDIWI

NbL11g23360.1 receptor-like_kinase_TMK4 [MW - SP = 98.48 kDa]

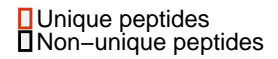
No. of times detected



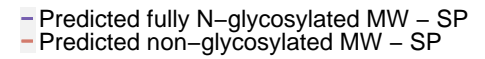
log(intensity)



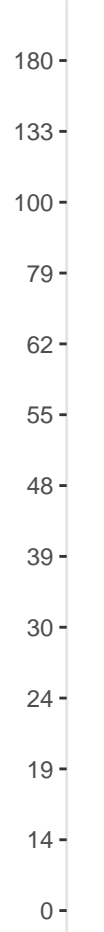
Values from



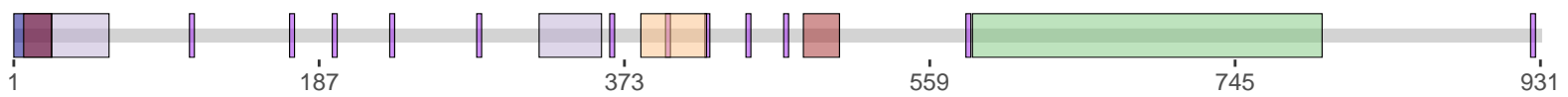
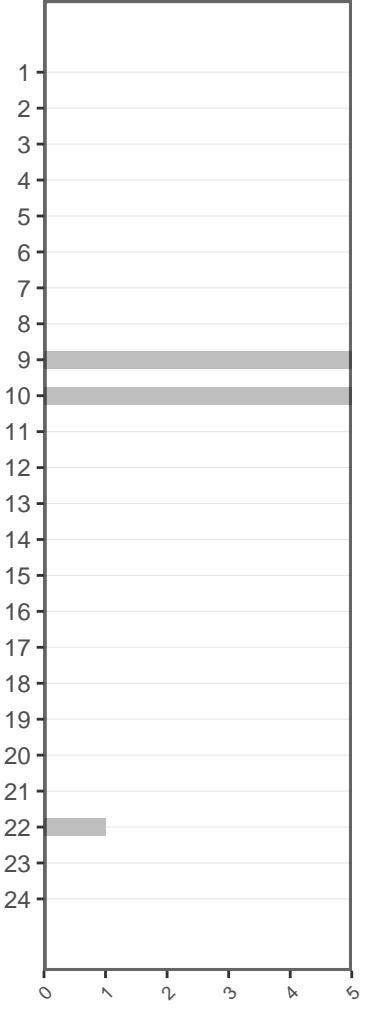
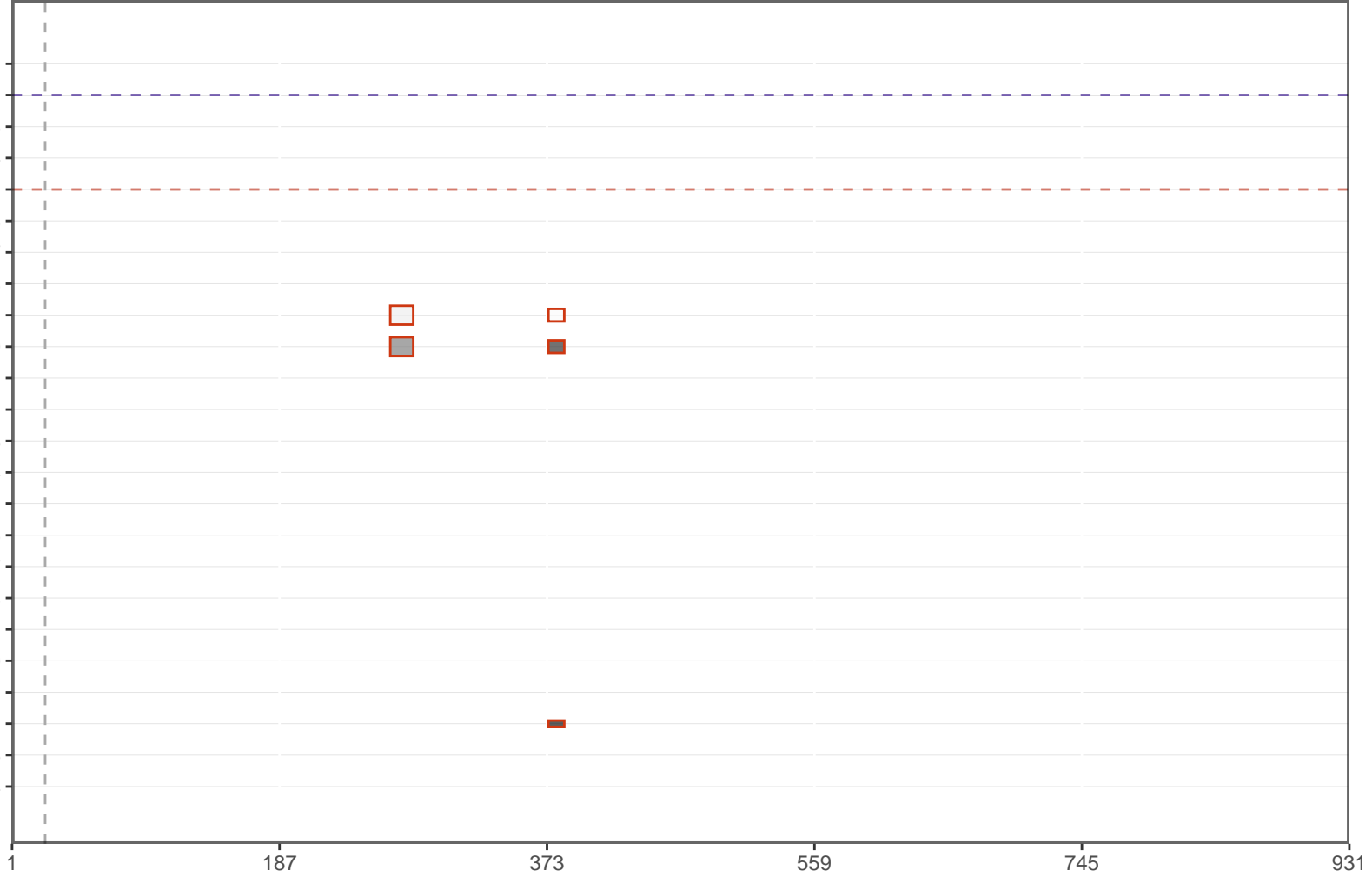
MW indication



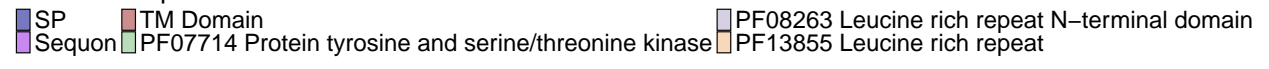
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

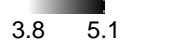
SGSGSNSSGSPGENSSGGKRPVSEAGMAGVVAWVFLVFLVSVKGLKRRQKRFGRVETPEKENEMVKSVPVSVGGNGVTDGPELGGSSGSDHSEIPFEGGNVAISQVLRQVITNFSSENLGRGGFGVYKGLHDGTAKVAKRMEGGAMGKGMNEFQAEIWLTKVRRHLVALLGGVNGNERLLVVEYMPQGLTSGHLFEWKELGKPLFTWKEKRVITALEVARGVEYLHLAGDSFIHRDLKPSNILGDDMRKAVDFGLVRNAPOGKYSET

NbL11g23220.1 cysteine_proteinase_inhibitor_B-like [MW = 19.34 kDa]

No. of times detected



log(intensity)



Values from



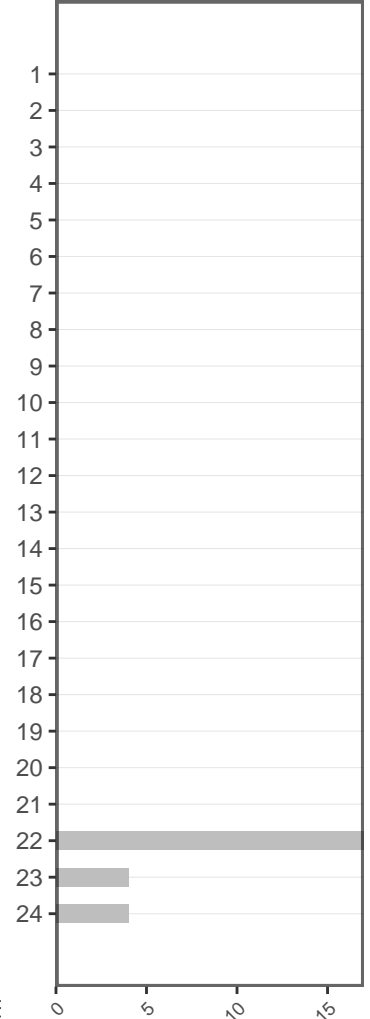
MW indication



Molecular weight

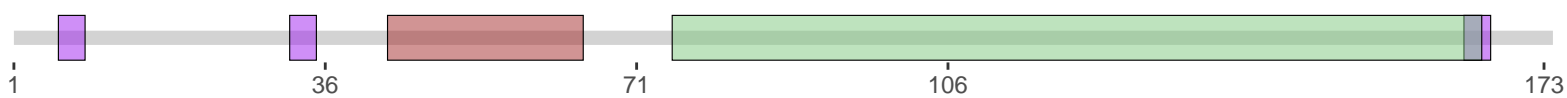


Gel Slice



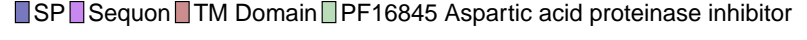
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SDVKTAKIQLDKFQVEEYNRNLQKQKQKVNNNNGLLSFSVEVEAEKGVVSGIKYLIKISATLSLSPKMFNVLVVKAWKKKELLNFSFSPATK

NbL11g23210.1 50S_ribosomal_protein_L24-like [MW = 17.6 kDa]

No. of times detected



log(intensity)



Values from



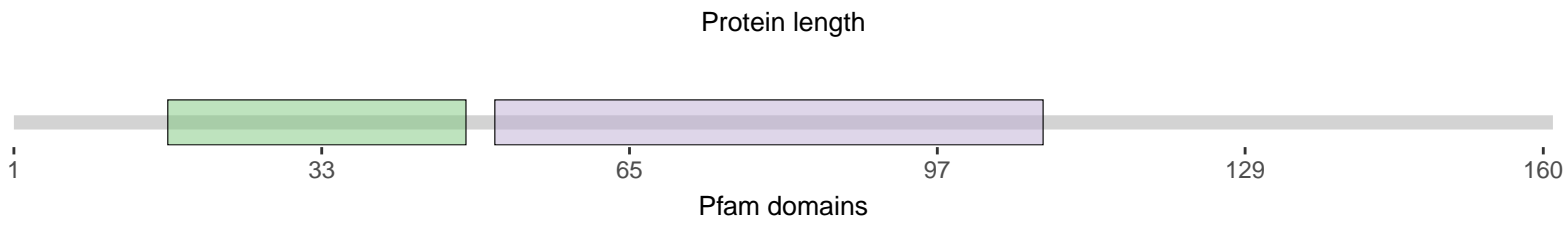
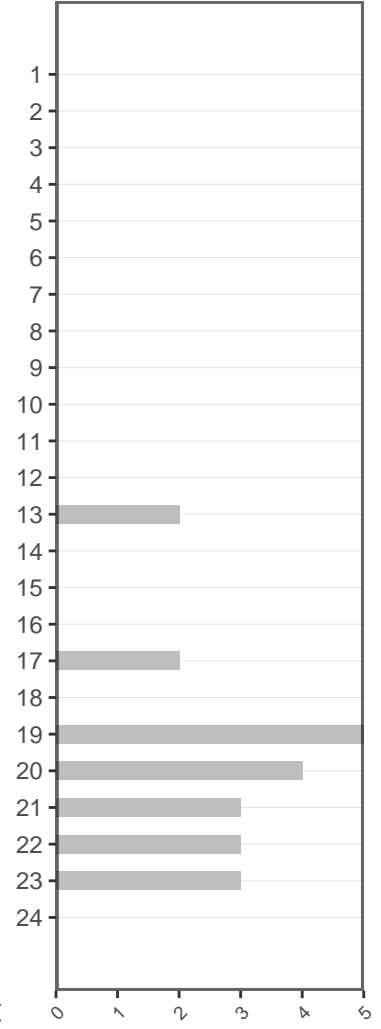
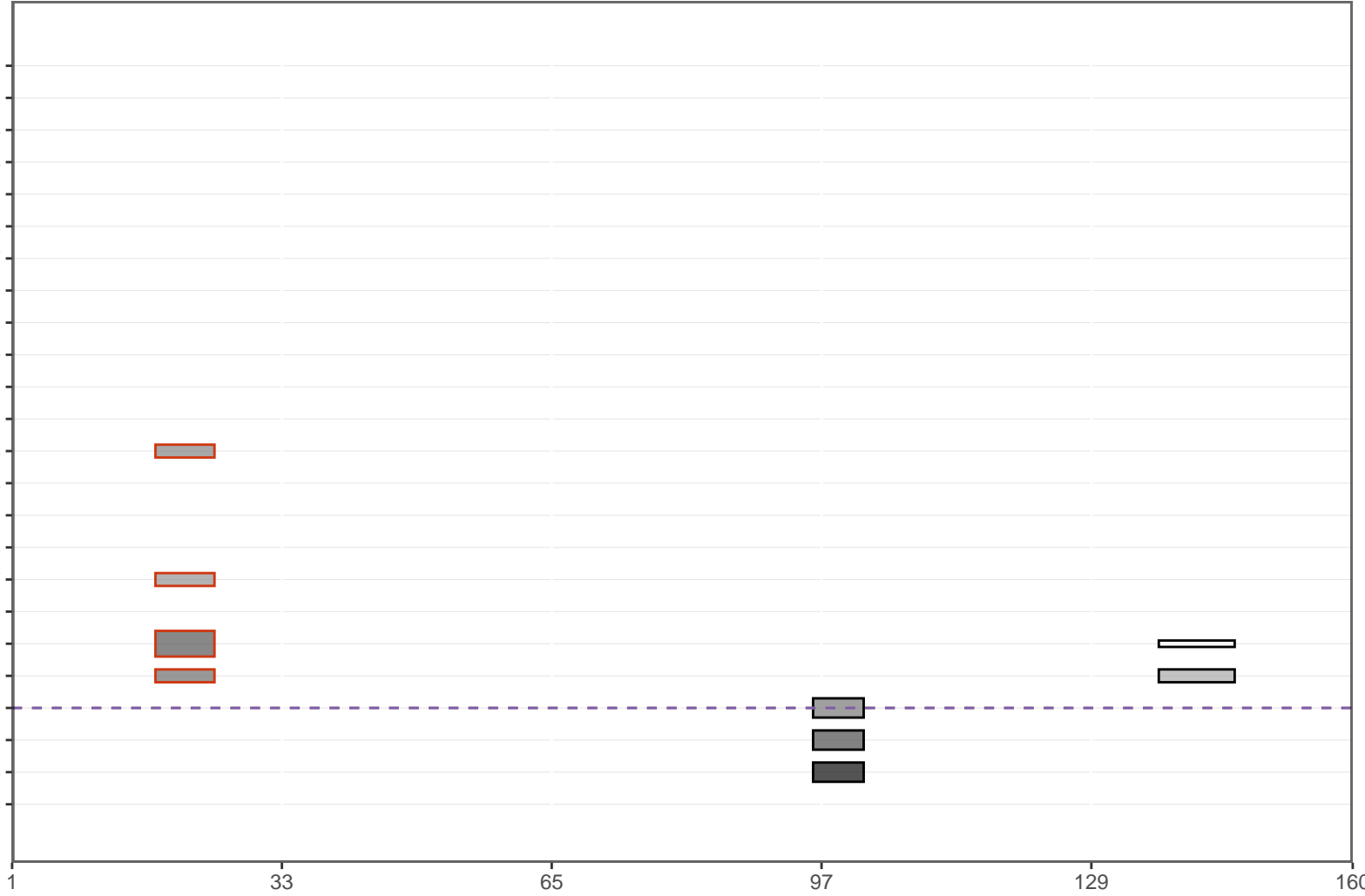
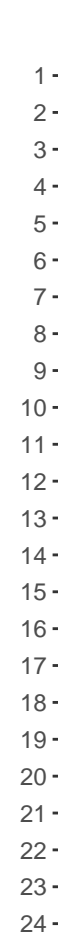
MW indication



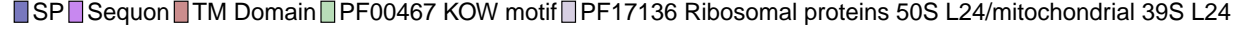
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

IFSVLEAPLHVSIVGVVDPVVGKPTKVGIRFLFEDGSGKVRVSRGIGAGSGIPRPEILKIRITPRPTVAGPKDTPMEVVMERTYDPKTKGMPDL

NbL11g23010.1 phosphoglucan_water_dikinase_chloroplastic [MW = 132.06 kDa]

No. of times detected



log(intensity)



Values from

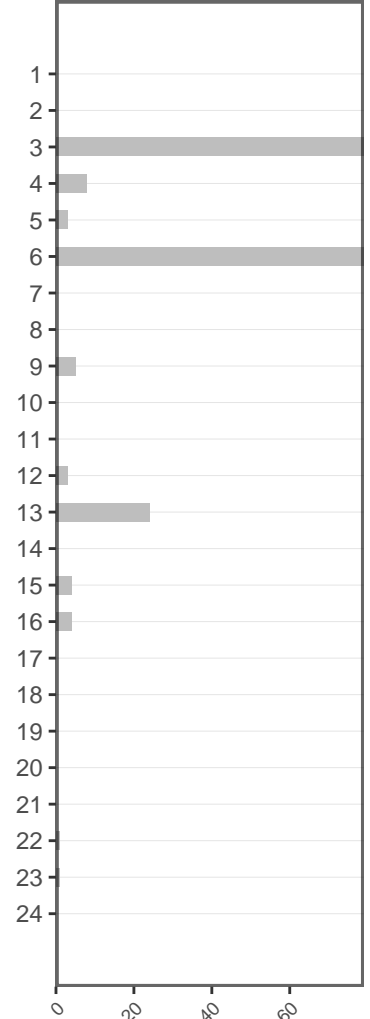
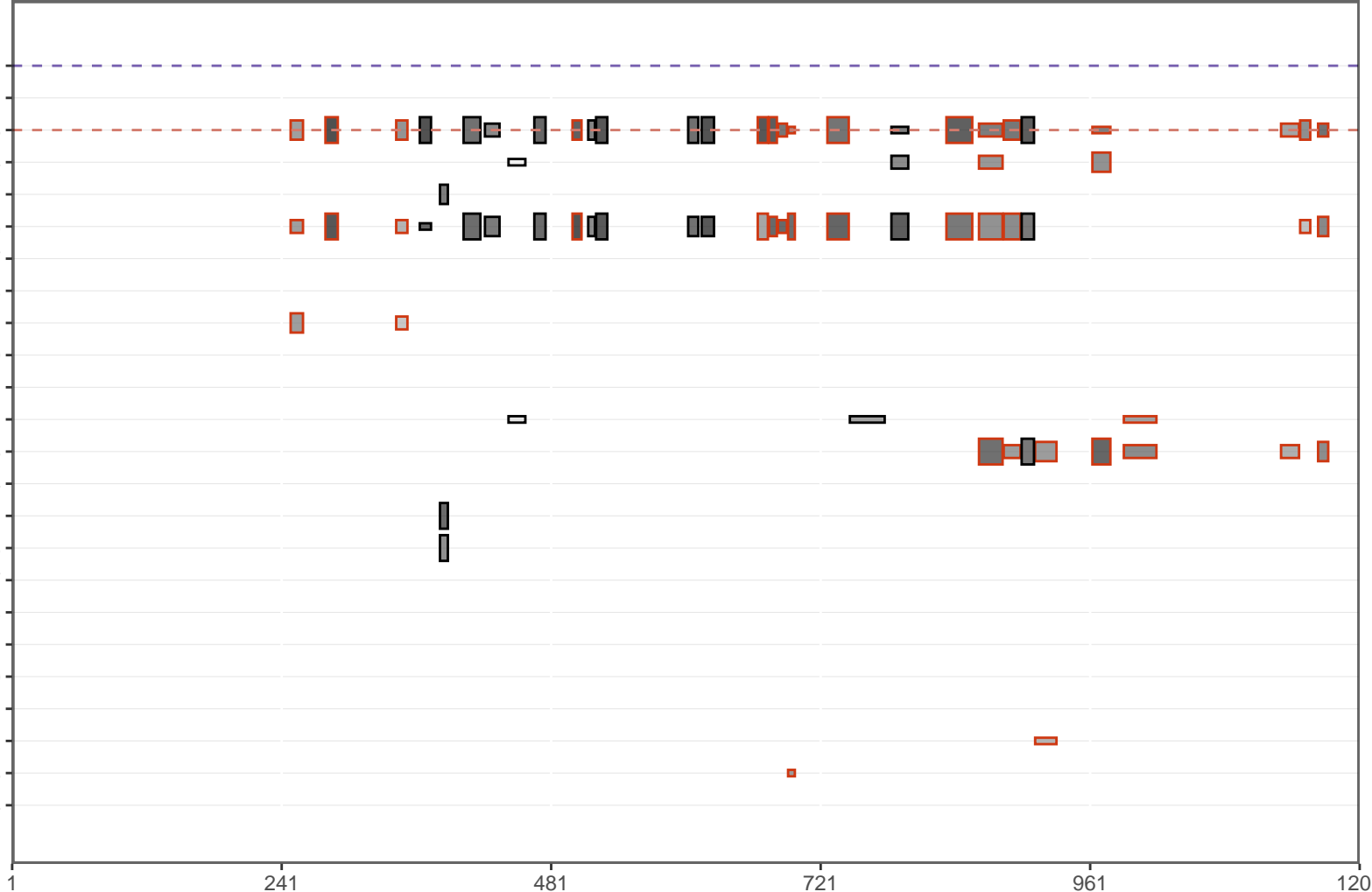


MW indication



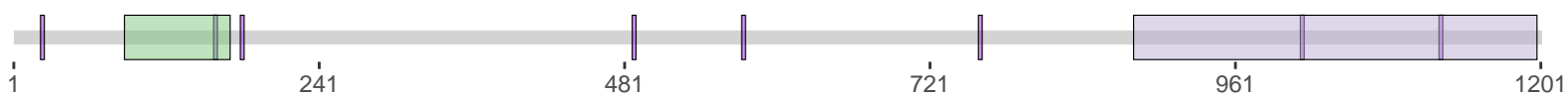
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

SP Sequon TM Domain PF00686 Starch binding domain PF01326 Pyruvate phosphate dikinase, AMP/ATP-binding domain

Protein sequence:

LNIVGIDQLGSLGWVPEEKAVGNELLSWKEKRLSETEGSEDKRIWALRLKATLDRGRRLTEEYSETLLQFFPEKVDLQKSLAIPENSVRTFTAEIRAGVVFQVQKLATLLKATRRITGSSGWDVLPDGFQGLQVNRIPGTLPSGATDPVILVVKADGDDEEYTAAGSNISGVLLQELPHLSHLGVVRRAGEKVVVFTGDDDDKVDIRELLGKYYRLEASDTGVKLTSSSEKGTVMQNKHLVVTAPSSAA6SDS6ASIAK6SHK6KEVPTGTGIPLADAEIQSSC

NbL11g22950.1 probable_aldo-keto_reductase_2 [MW = 38.58 kDa]

No. of times detected



log(intensity)



Values from



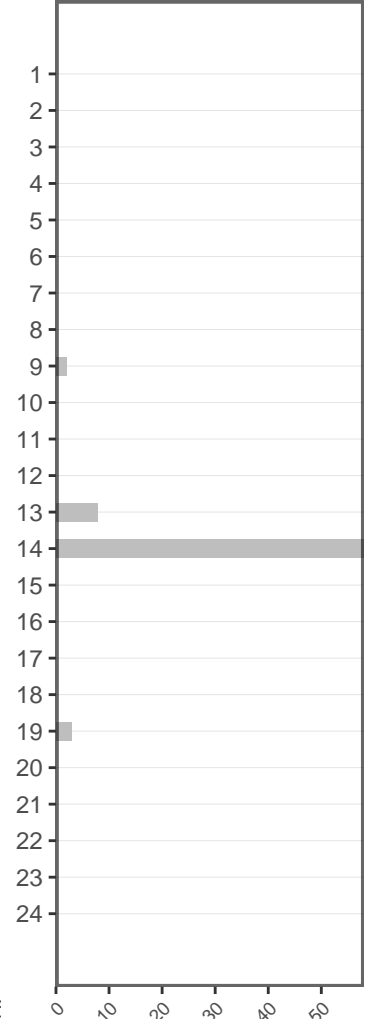
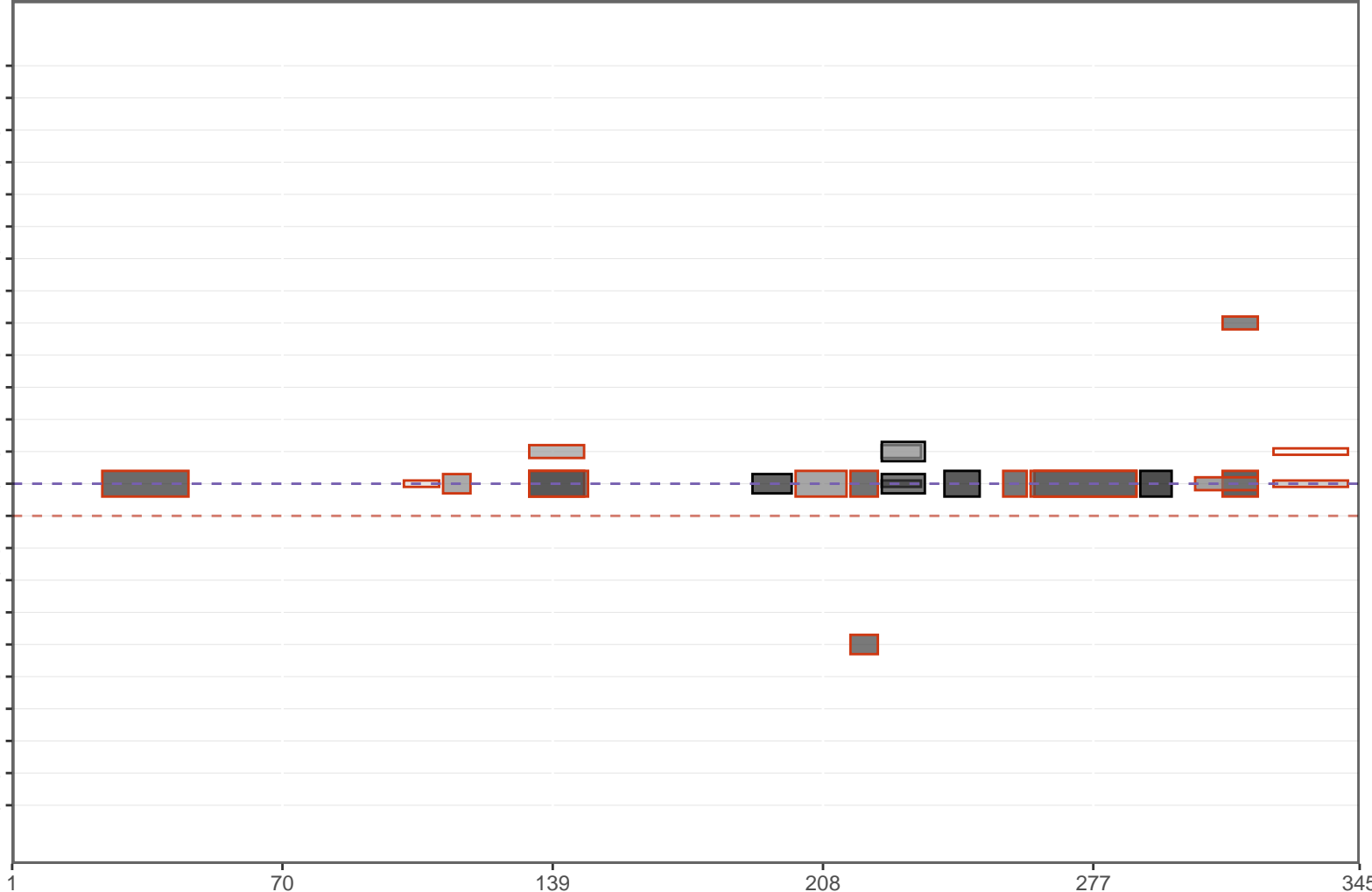
MW indication



Molecular weight

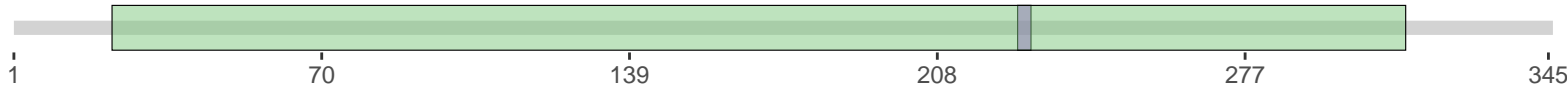


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ACASTIRRAHVAHPTAVQMEWSLITRDLEEEVPTGRELGGVVPYSPLRGFFSAGTKLIENLSEDDFRKQFRFRFPENFELNKGVFEKLVMAARKGCTPSGLALAWLHGGDDQCPPGTTNIENFNENVRALSVKLTTEDMKELESVASVVKGRHLVMSSTWINSETPPLSGWKTE

NbL11g22910.1 metacaspase-4-like [MW = 45.58 kDa]

No. of times detected



log(intensity)



Values from



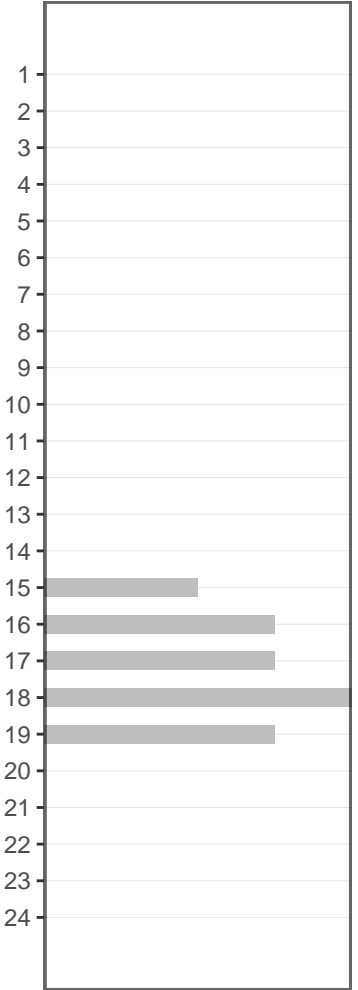
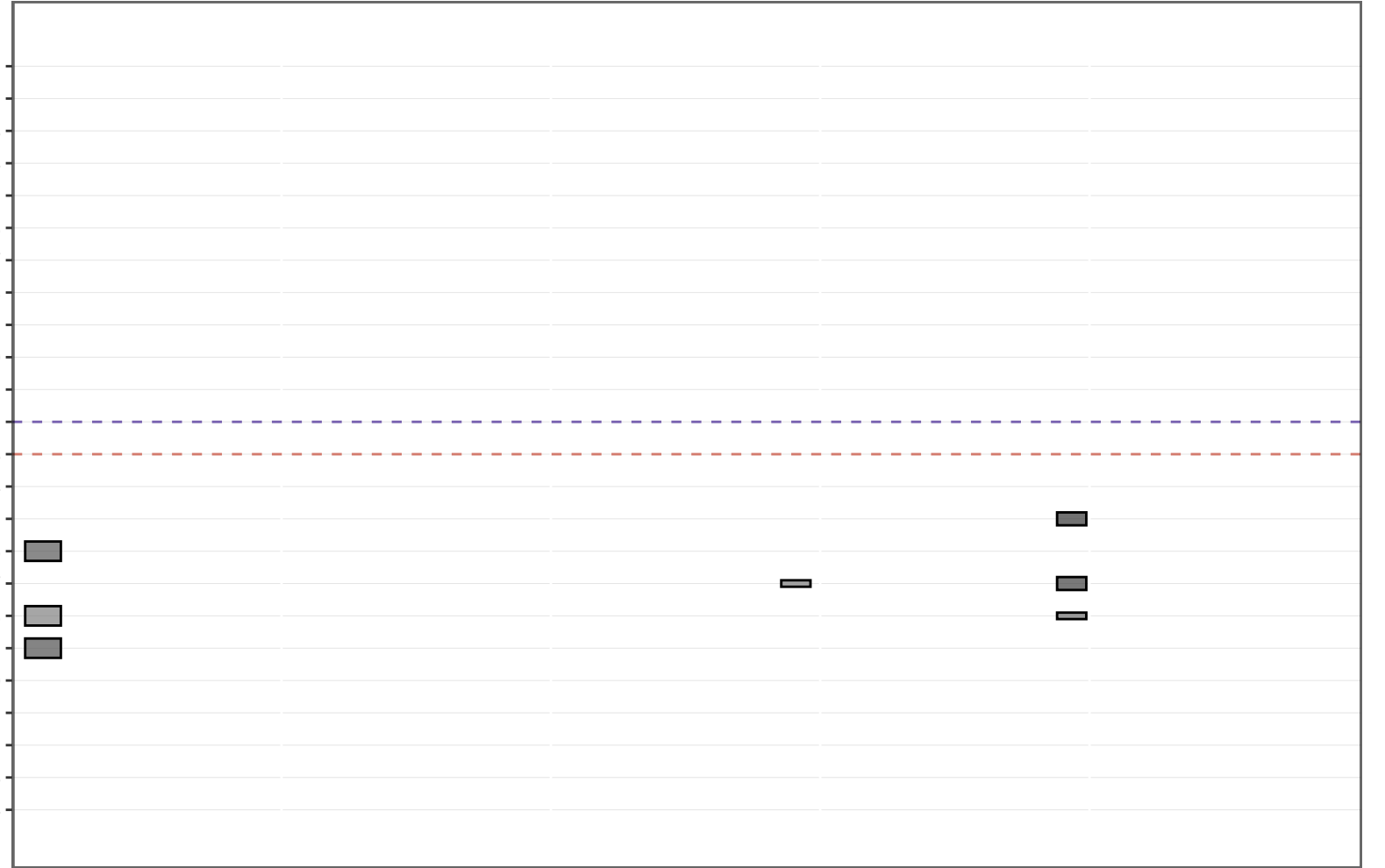
MW indication



Molecular weight



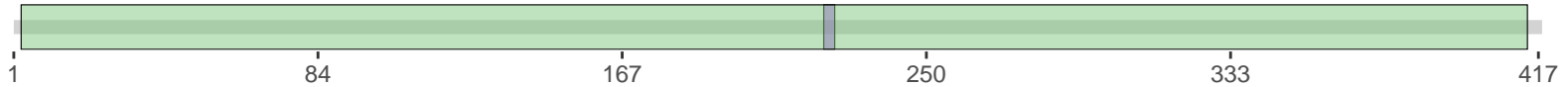
Gel Slice



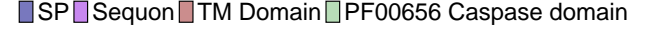
Protein length



Pfam domains



Pfam Description



Protein sequence:

RAEEEFSAESSVVEEDGGDQVHVNKSLPLSTLIEIKGKTKGDDIDVGLRPTLFDVFGEDASPKVKKFMKVFNLGHGNGEGEGSGLGMVGNLAGEFLKGLDENDESYAKPMETHVEGKQEVYAGSGSRGLPDSGLVSGGOTDQTSADATPAGGDSYGALENAIQELAESDGPITNEEVVWVKARKLKGKGGYQRPGLYGSDDHIVDAPFVQ

NbL11g22890.1 pirin-like_protein [MW = 36.81 kDa]

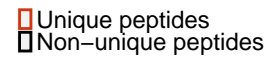
No. of times detected



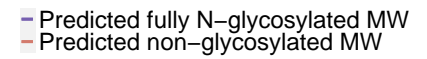
log(intensity)



Values from



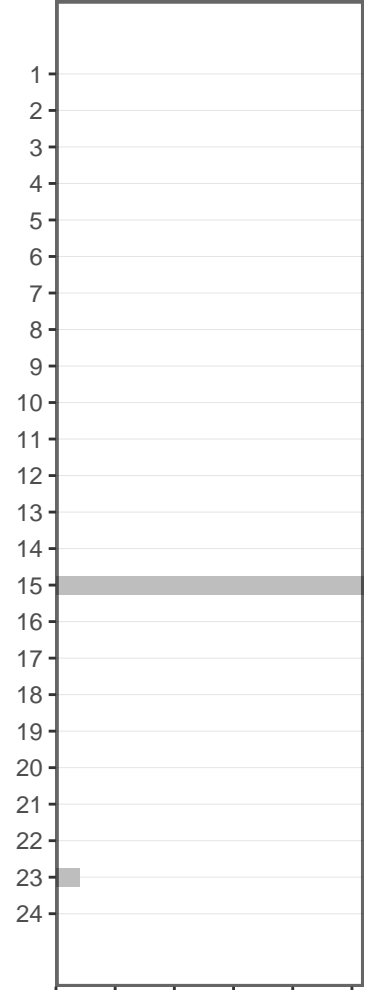
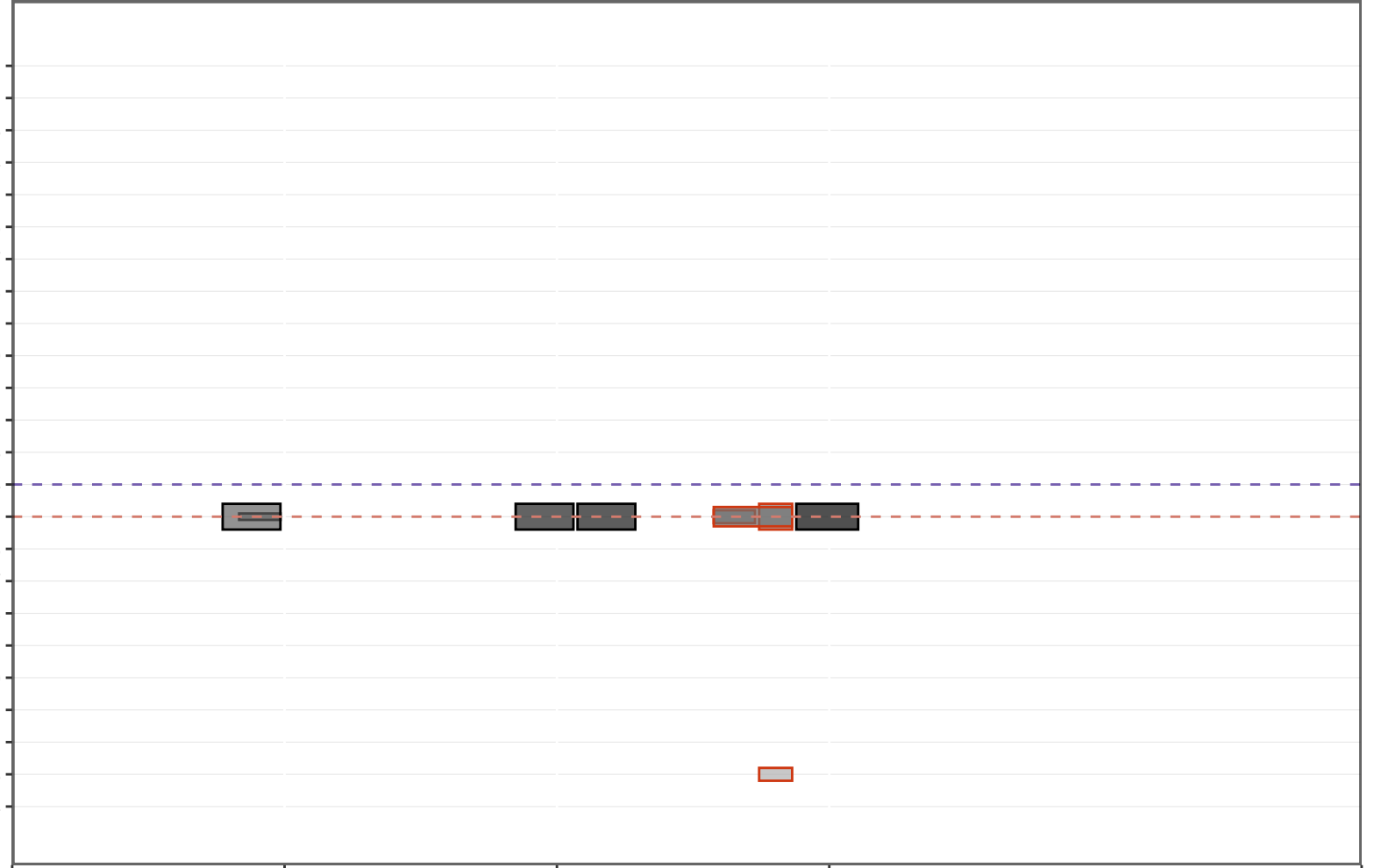
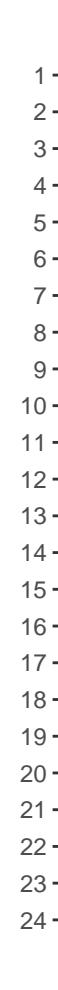
MW indication



Molecular weight



Gel Slice

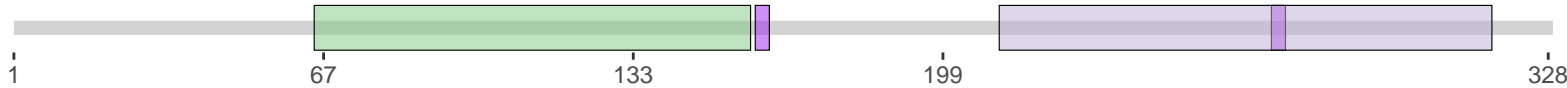


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description

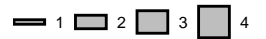


Protein sequence:

GLQLWNLSSKDKMEPRVYQELLNEDIPRAENEGVEVKIAGEAMGVQSPVYTRTPTMYLDFLQFTSYHHQATPESWNAFVYVEGEGVFGIPNSGVPVSAHLCVLPGEGLSVWVNSKPLRFVLLGGGPIKEPVAVGHGPFVMMNSGAIEDGTFEDVGVYKNGFENARYWRSGH

NbL11g22880.1 signal_peptide_peptidase-like_5 [MW - SP = 53.48 kDa]

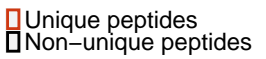
No. of times detected



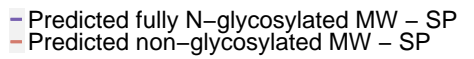
log(intensity)



Values from



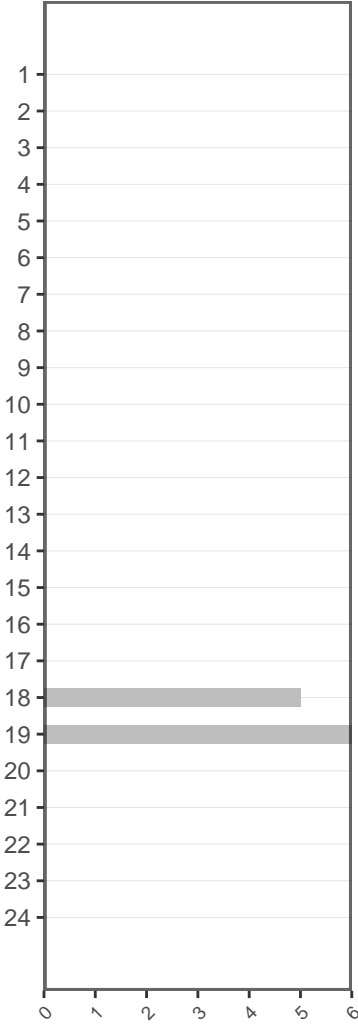
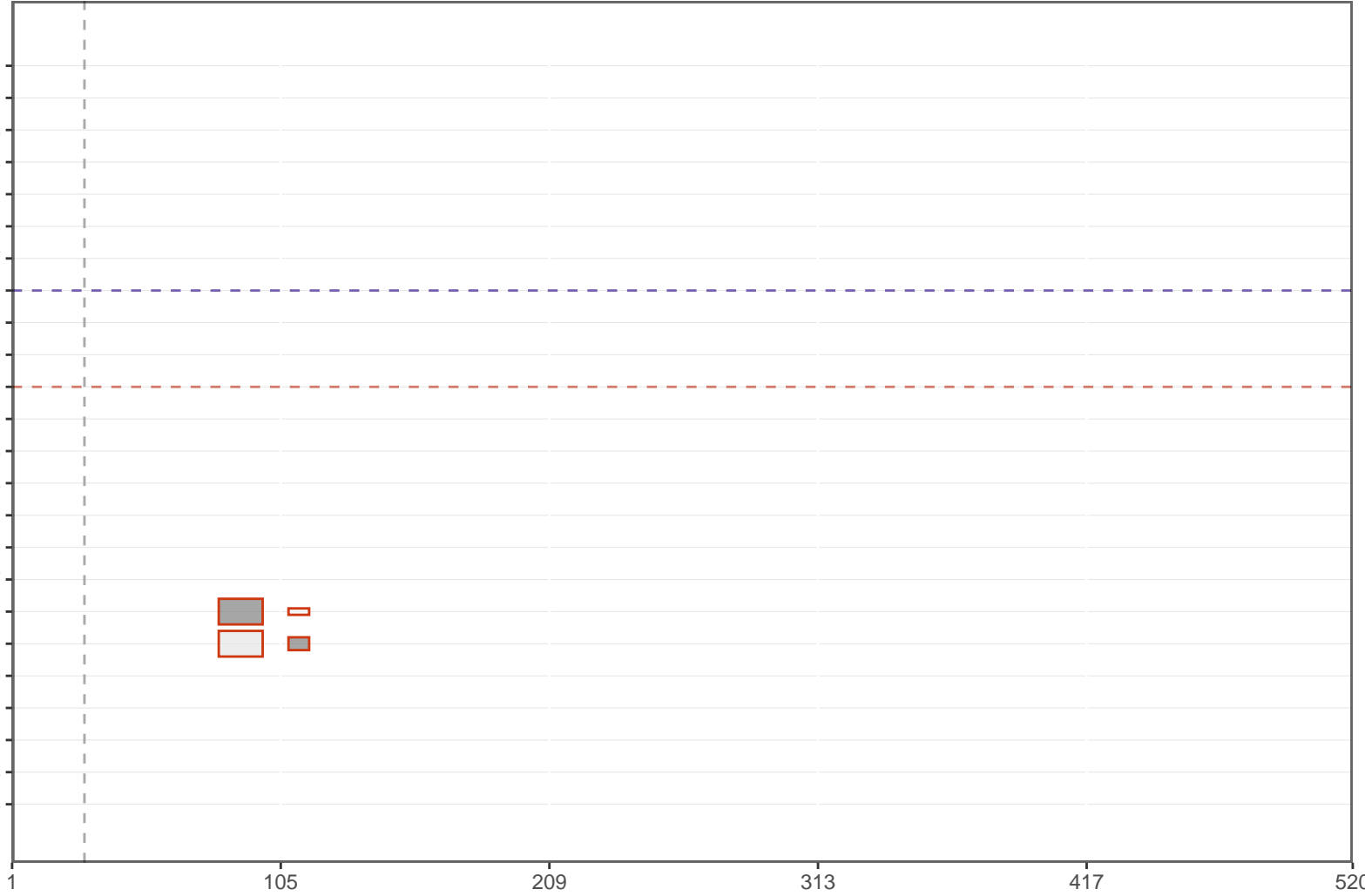
MW indication



Molecular weight

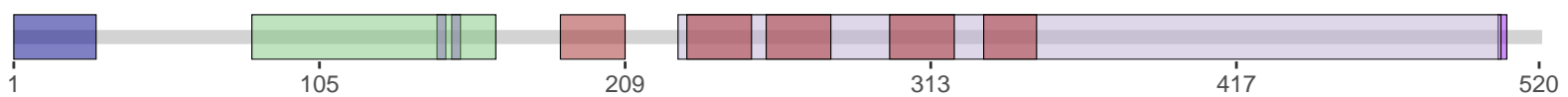


Gel Slice



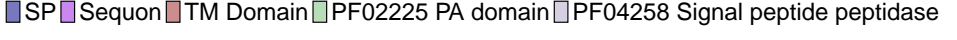
Protein length

Peptide counts over 4 repeats



Pfam domains

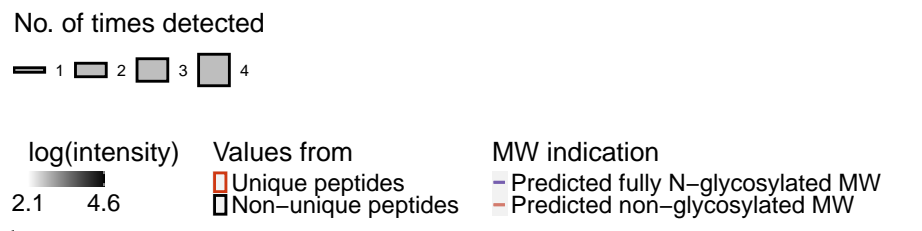
Pfam Description



Protein sequence:

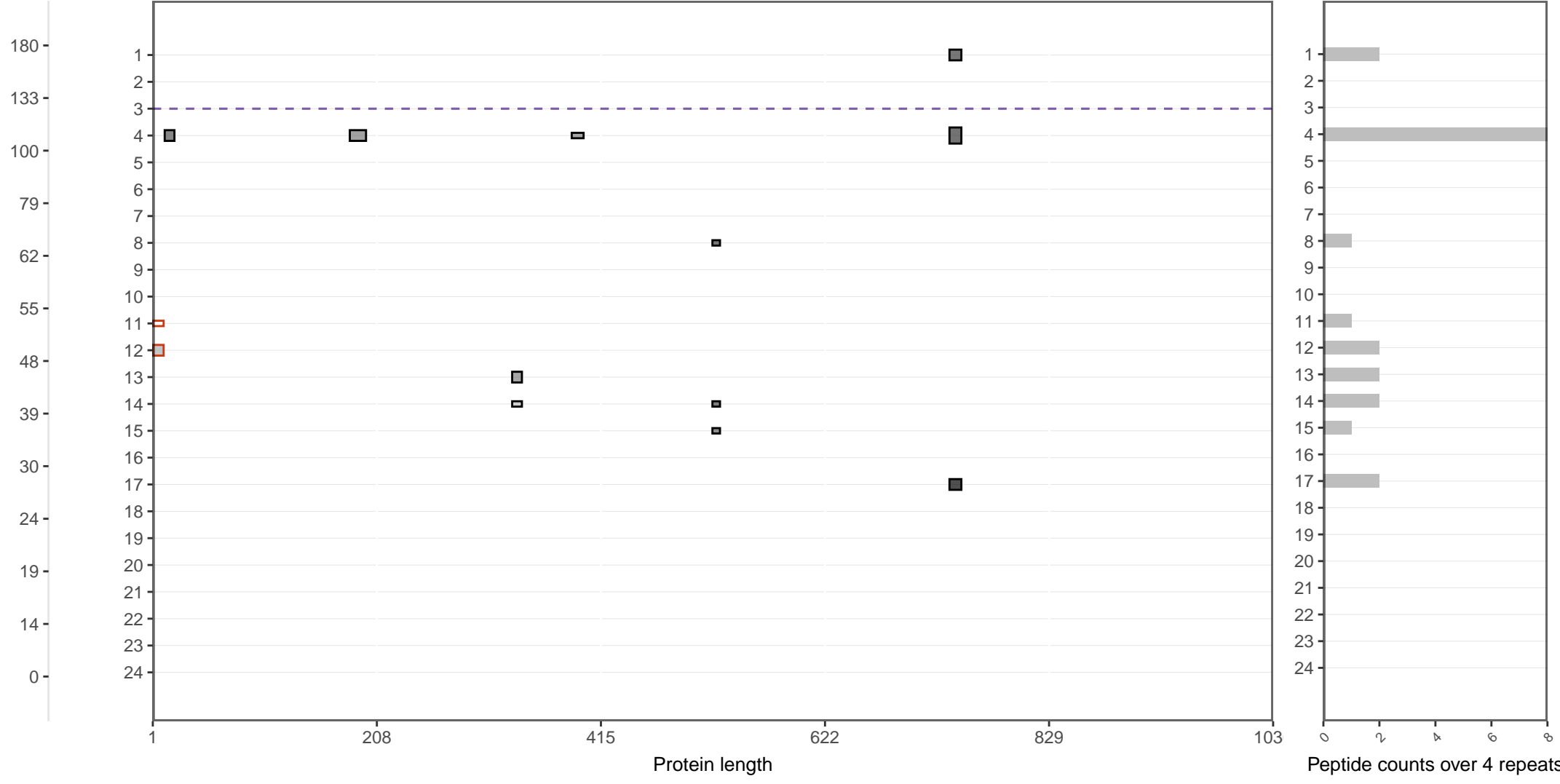
L L L Y F F M S T V F Y W L L L F G D G E G L H N G V S L S K Y R S C G K K T L N L P L L G E V T L S L A V L L L G V A F W A F W A N R K E S Y S W I G G D L G I A L M T V L Q L A Q L P N K W A T V L L G C A F Y V D F W F L S P T F H D S V M S V A K G A G G E S I P M L R V P K L T D P Y K G F D M L G F G D L F P L L G F T Y R F D E A R E K V L N G Y F L W L M I G V T G L G F T Y L G L Y M K H G O P A L L Y V P C T L G T C V L A L V R R E L K D L W Y R N E S R Q M A E E R L G S A

NbL11g22840.1 importin_beta-like_SAD2 [MW = 118.76 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF03810 Importin-beta N-terminal domain
- PF08506 Cse1

Protein sequence:

/AGMRDPLPVRVDEVFALRSFVEAGNDLDERPIPOLLDDEFFKLMNEVENEDVLTLETVDKFGSEEMAPVALGLDGNLAAAFWKGINMSEADEEGDDGALAAVGLRAGSTLSEVSRPLHFLFHEFLPLMRRMLTDDGGEVFEELVSVYMTFFSPTISMEMMSLWPLMKKALEDWADFFNLPVLDNYSRSTAHFLTKDQDYGQSLWNMISTVMGDKNLEGGDEPAPKLGQVVFQHKCKGQVDHWVEVYRITRIELRRAEKPKYKGLLMQVIADALY'NASTL'

NbL11g22640.1 chitinase-like_protein_1 [MW = 51.38 kDa]

No. of times detected



log(intensity)



Values from



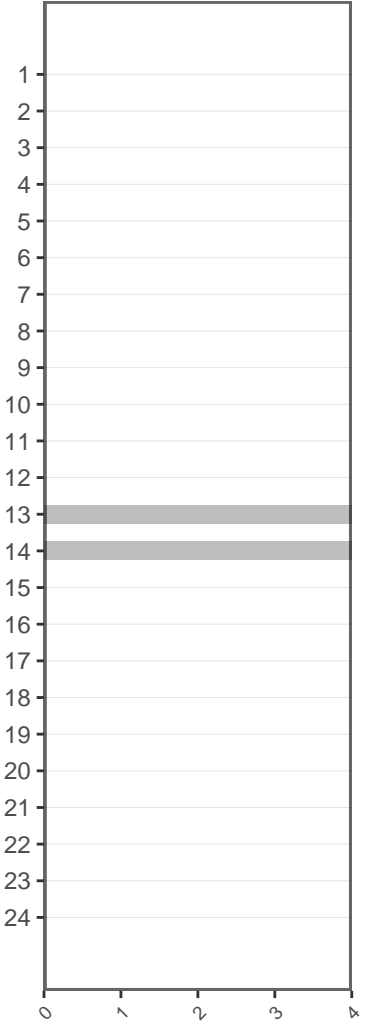
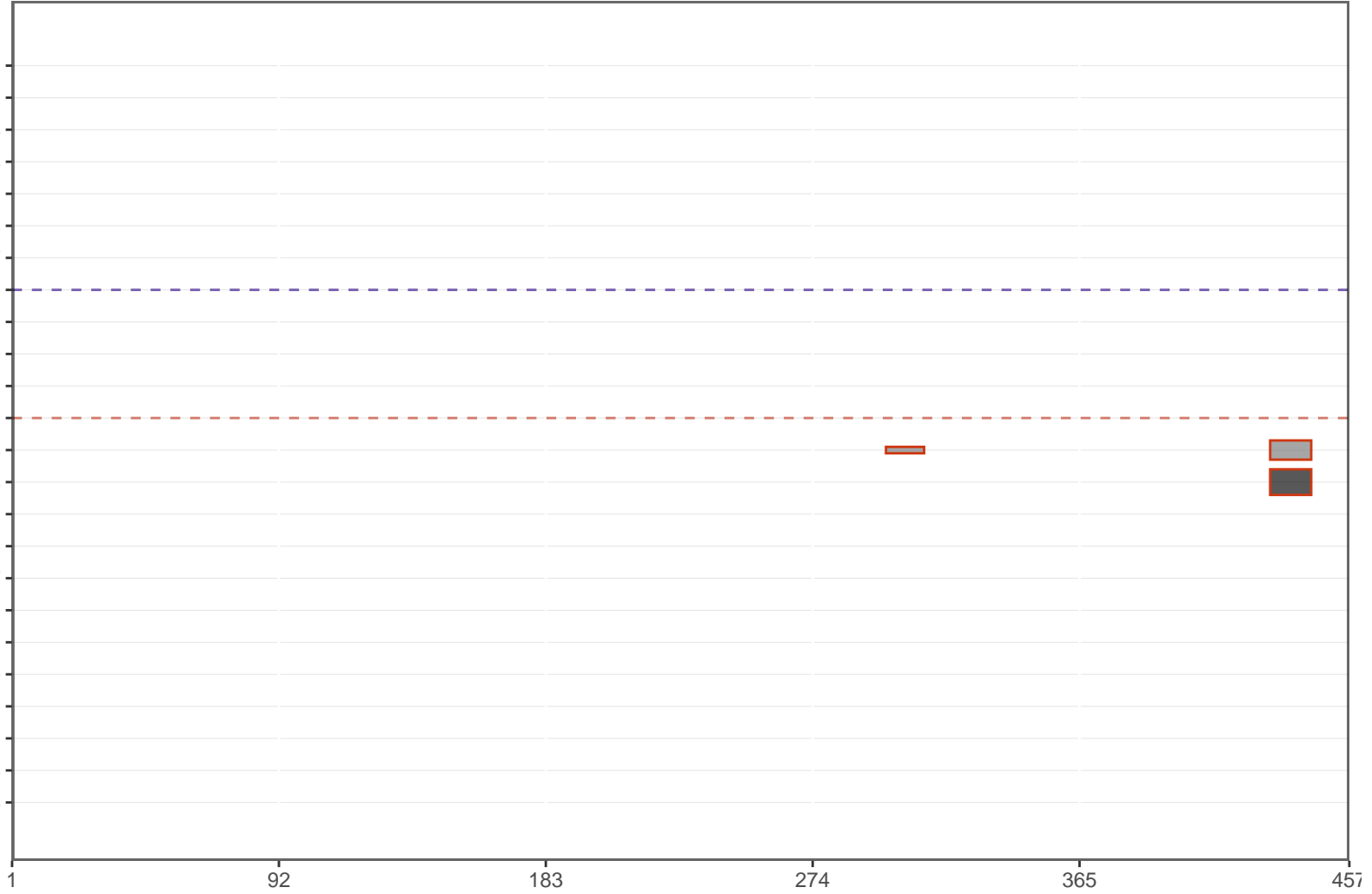
MW indication



Molecular weight



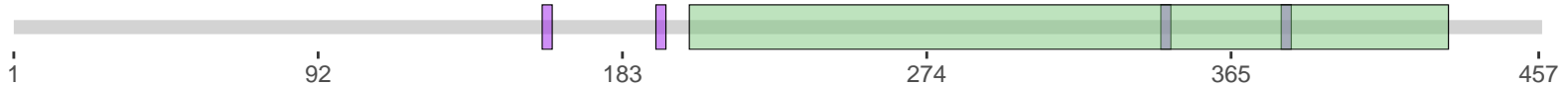
Gel Slice



Peptide counts over 4 repeats

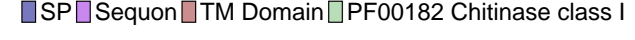
1 92 183 274 365 457

Protein length



Pfam domains

Pfam Description



Protein sequence:

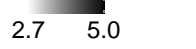
LDYSSSFNAAALYQPLGFTTGKRMQKEIAAFLGHVSGKTSQGVATGGLAWLGLGYNKEMSPSQYGGDFKLTYPCTPGAGYVGRGALPIWYNNYVGAAGEALKLNLLDHPVEYEQNATMAFDAAIWRWMMFMKKGGPSAHDVFGVGNWKPDKNDLTKRFFGFTTMNLYGDSVCGGGVDGMNNISHFGYYLDDMGVGREAGPHEVLTGEGKAFNPSTAPAA*

NbL11g22510.1 spermatogenesis-associated_protein_20-like [MW = 96.58 kDa]

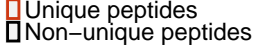
No. of times detected



log(intensity)



Values from



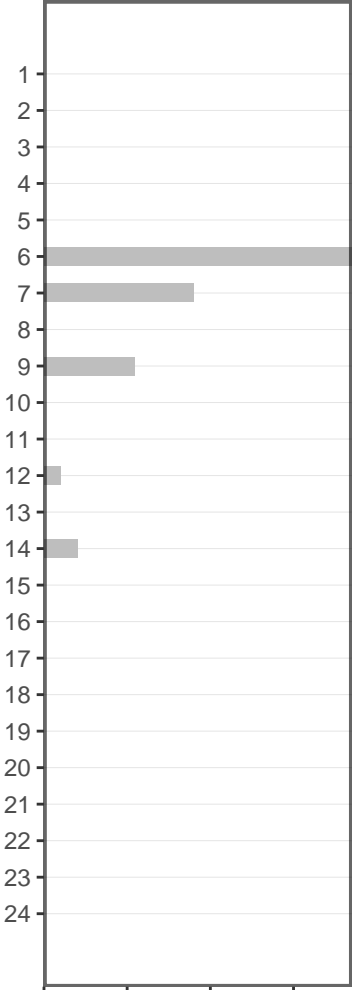
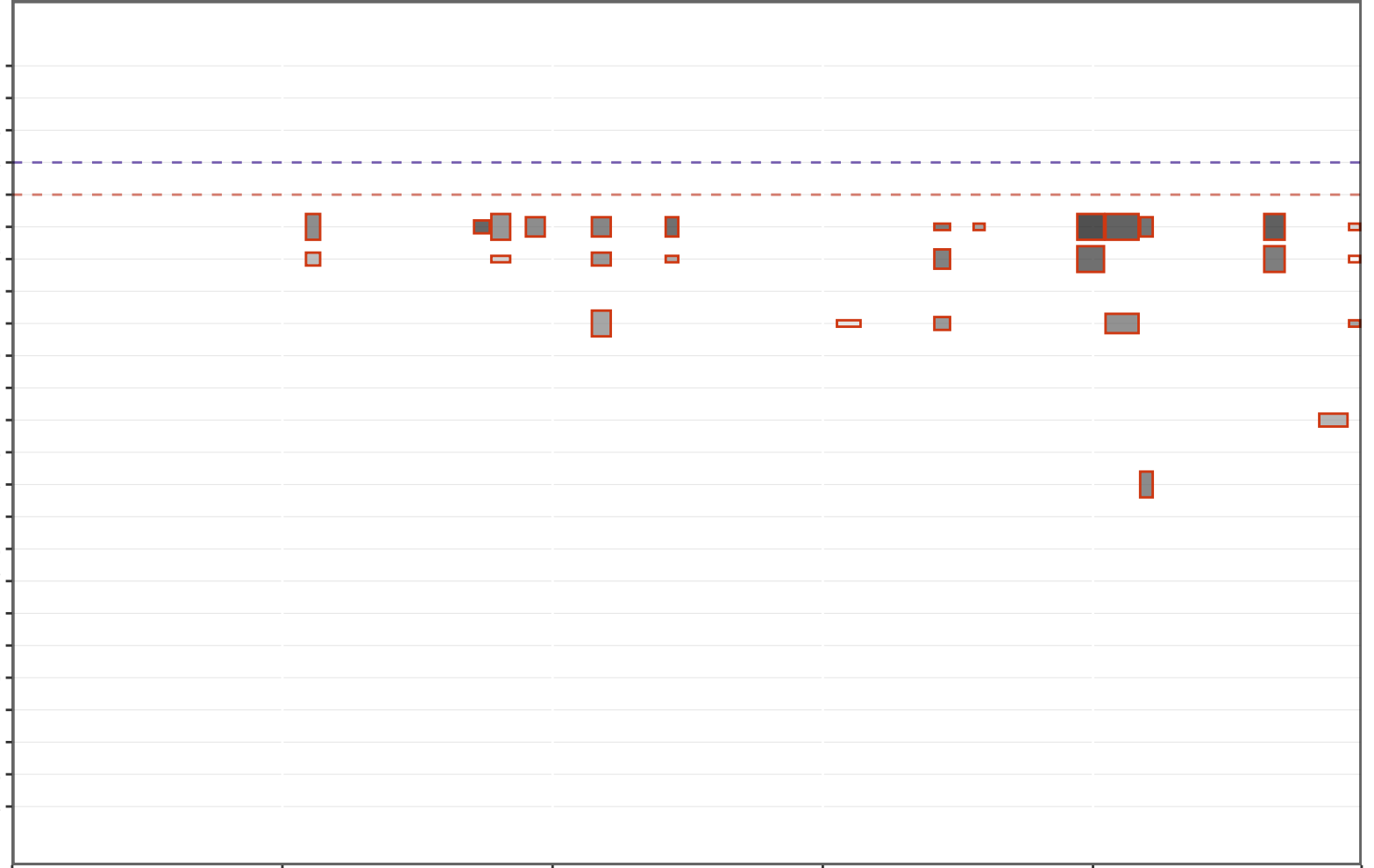
MW indication



Molecular weight



Gel Slice



Protein length

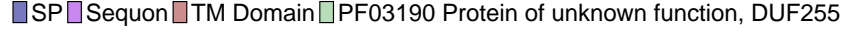
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

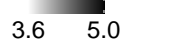
ITKDVFYSSLRDLQVLRDRMDGPNGEIFSAEDADGVEGEGASRRKKEGAFYVWDTDEVQNVGHEATLVKDHYYKPSGNGDLSRRSDPHNEFKGNVIERRSTVMSKSHALPVEQYLDLIGARQRLFDVRSERPRPHLEDKVVVSWNGLVVSGLAKASIKLKGPEGETRFYFVITGANPKYEMDAEKAAYFIRNLYNQDKRRLQHSFRNGPKAPGLDDVAFISGLLDDLYEFGGQVFWLGVWALELQETGDELFLDKAGGGYFSTTGEDPVLRLVKEIDHDGAEI

NbL11g22500.1 peptide_chain_release_factor_AP3_chloroplastic [MW = 47.12 kDa]

No. of times detected



log(intensity)



Values from



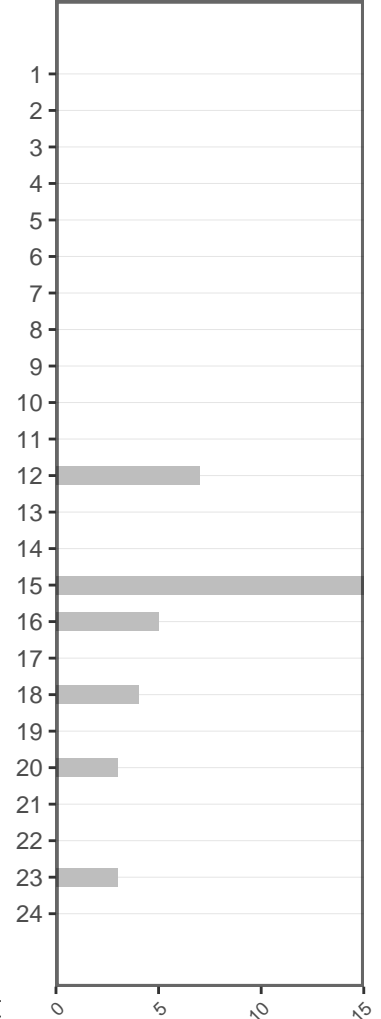
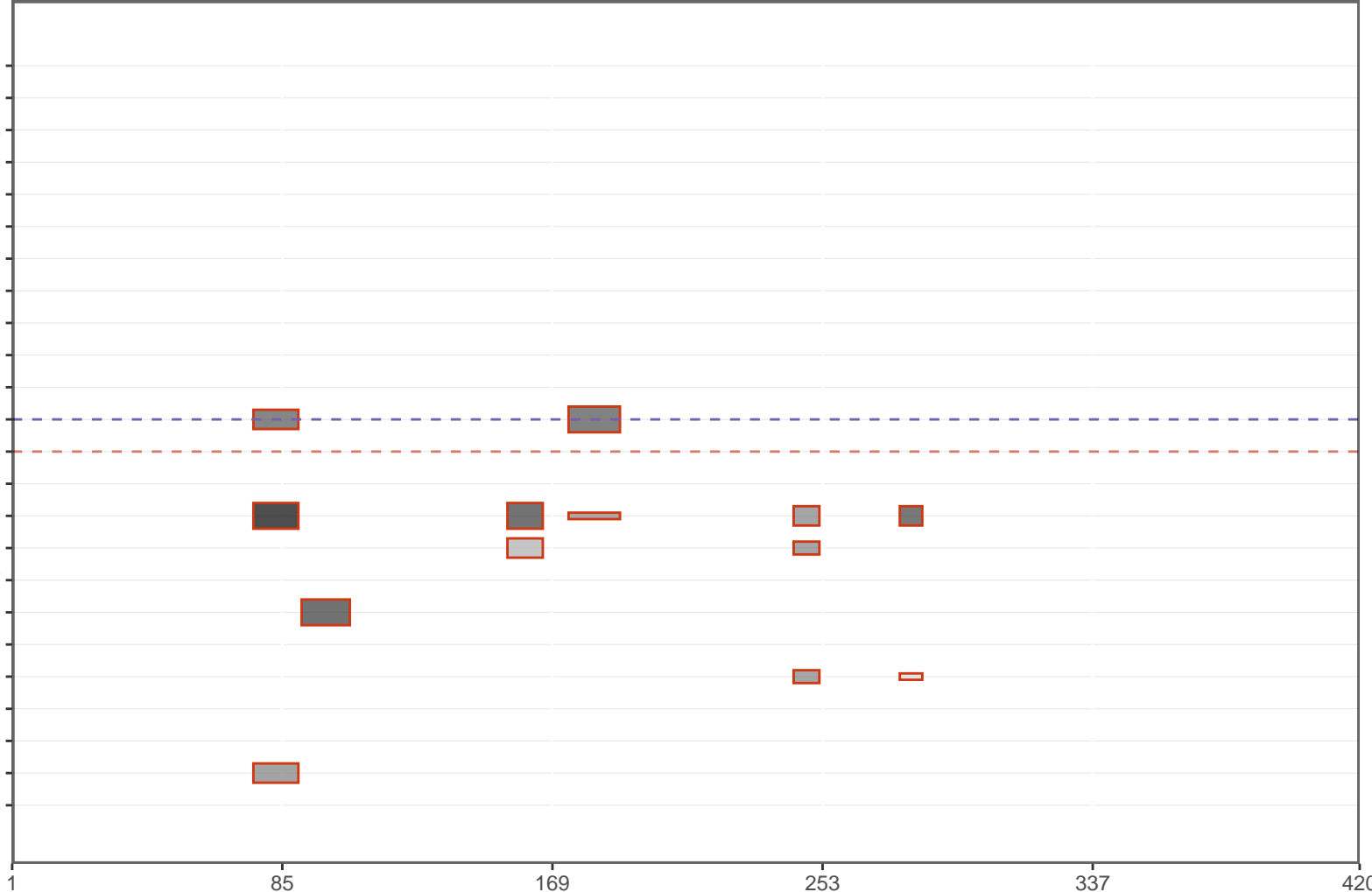
MW indication



Molecular weight

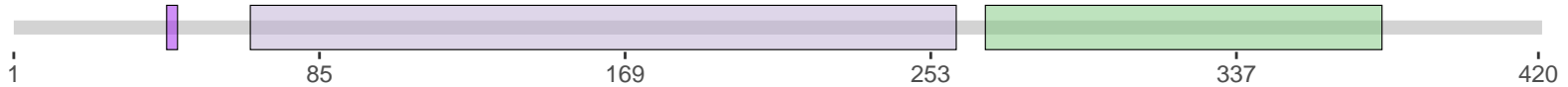


Gel Slice



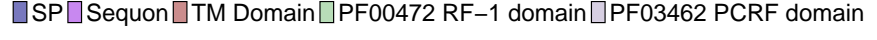
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IERNSWKFAPISCSSEAEKGGPKTYVMEIKGKRIVYSKLYEESGHRVGRVPTQETGGRVHTSTATWAMPEADEVDVEIDPKDIELTARSGGAGGQNNKVKETAVDLVHKPTGIRIFCTEERSQKNNKRAFQLLRKAKLYEIKLRGQGESIRNQRKLVGTGARGEKIRTYNYKDNFRVTDHRLKMMFELTSLFEGDIETAVGSGCSTMEQGELLOELAESAPV

NbL11g22410.1 protein_TRANSPORT_INHIBITOR_RESPONSE_1-like [MW = 65.19 kDa]

No. of times detected



log(intensity)



Values from



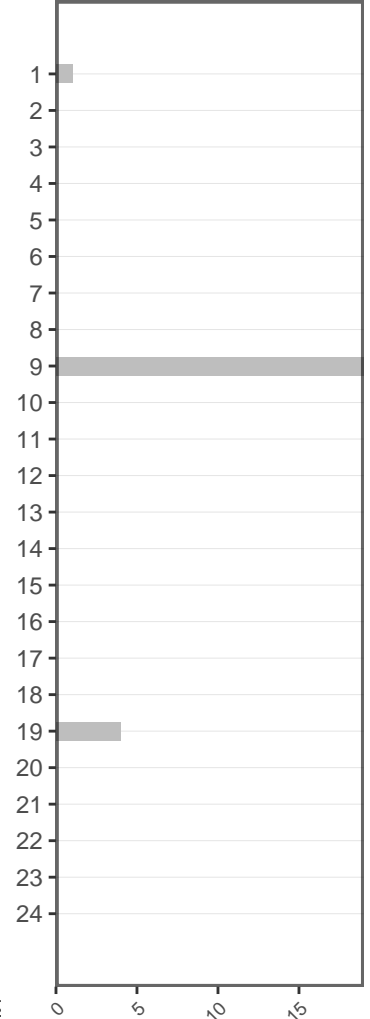
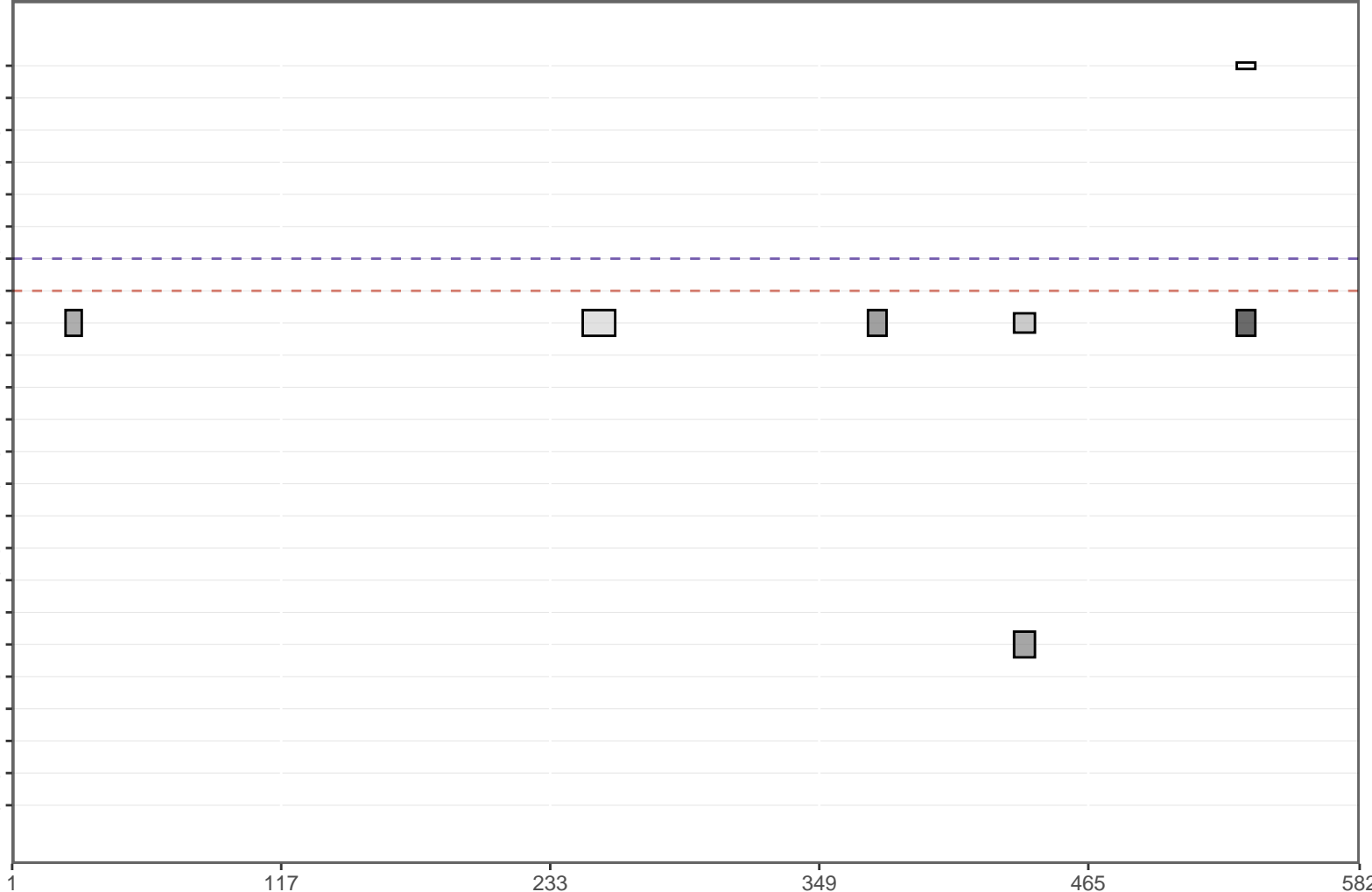
MW indication



Molecular weight

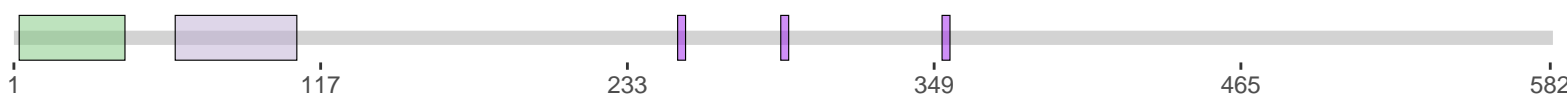


Gel Slice



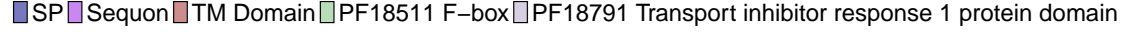
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PAIYPCSRILSLNLSVATSONPDLGKLSGCHNLGRLLWLDVIEDIGLEELAANKDKLDELRFVPSDFAPPEFNATLTEDGLIIVSDGPKLGSVLYFGROMTNAALYTKANRPNMIRFLRCHIEPSPDHLTLGLDAGFGAIVENCKELRRLSLGSLTDRVFEVIGTHAQKLEMSIAFAGDSDGLHHVLSGGESLRLKLEIRDCPFQDKALLANAAKLETRMSLWMSGGVYFSGACKLLAQKPRLLNVEVIDERGPDPTRPESGPKVEKLYHRTWAGPRFDTPGYVWTMDEI

NbL11g22370.1 protease_Do-like_2_chloroplastic [MW = 68.51 kDa]

No. of times detected



log(intensity)



Values from



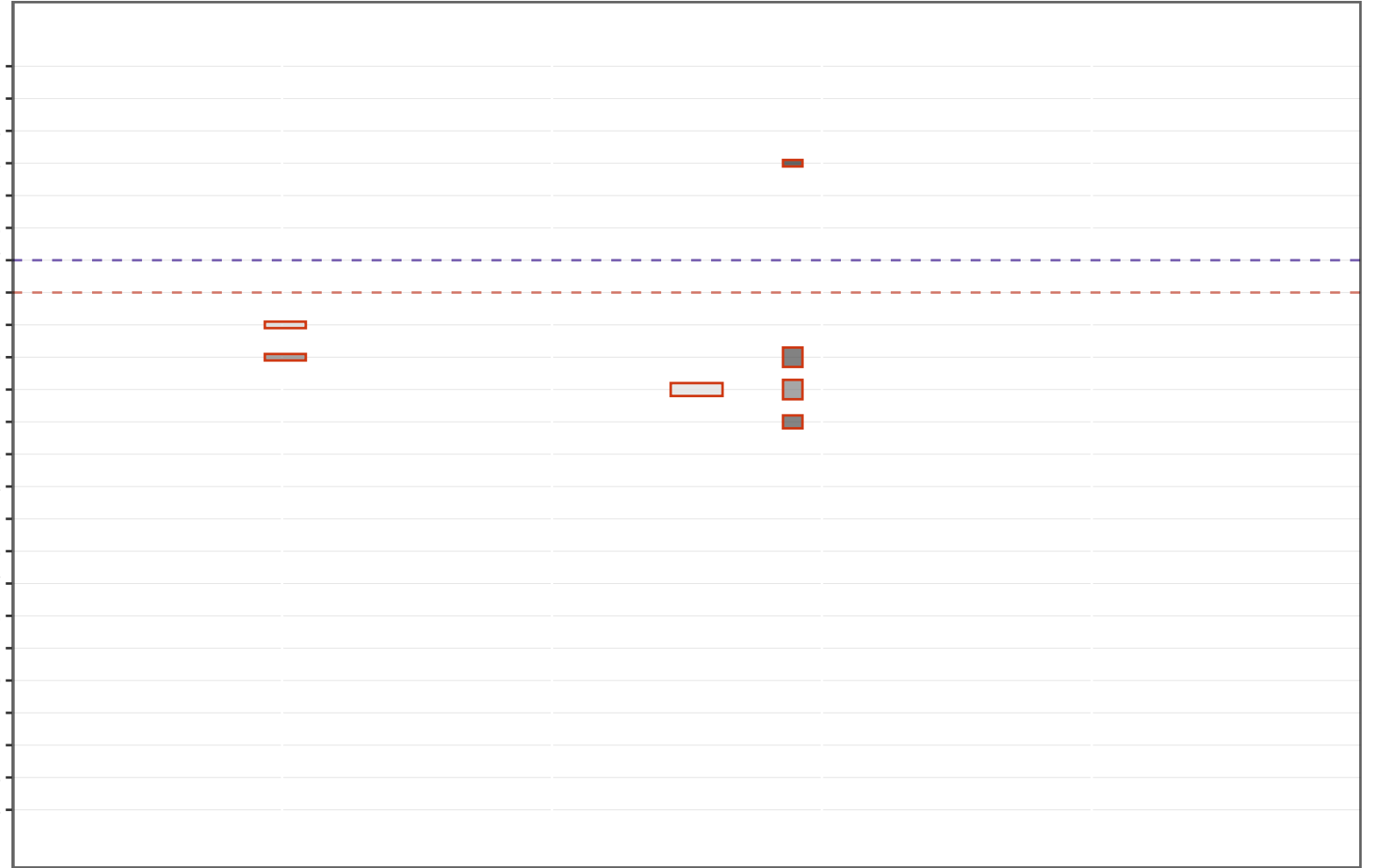
MW indication



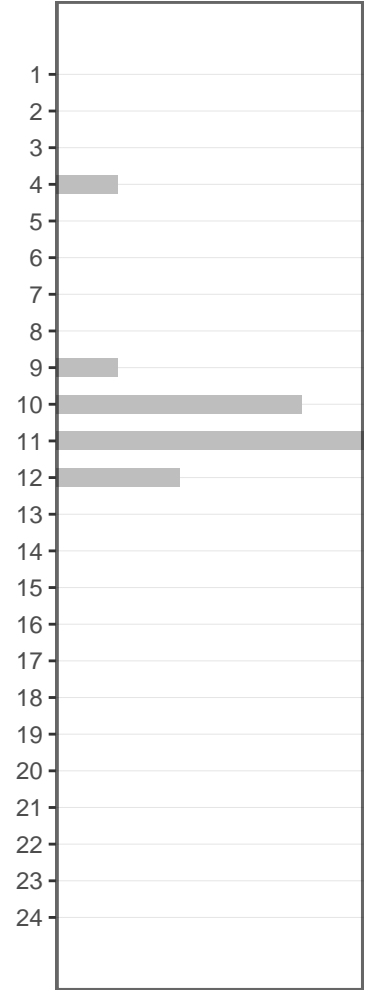
Molecular weight



Gel Slice



Protein length

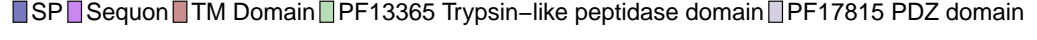


Peptide counts over 4 repeats



Pfam domains

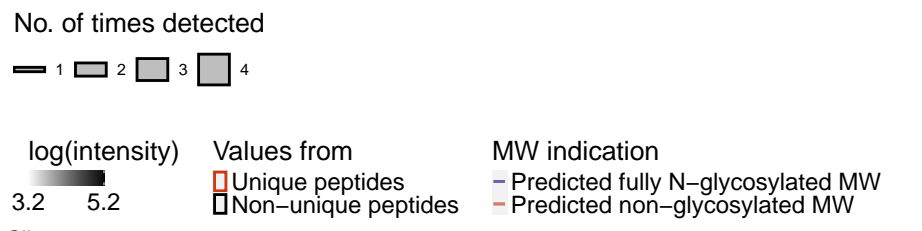
Pfam Description



Protein sequence:

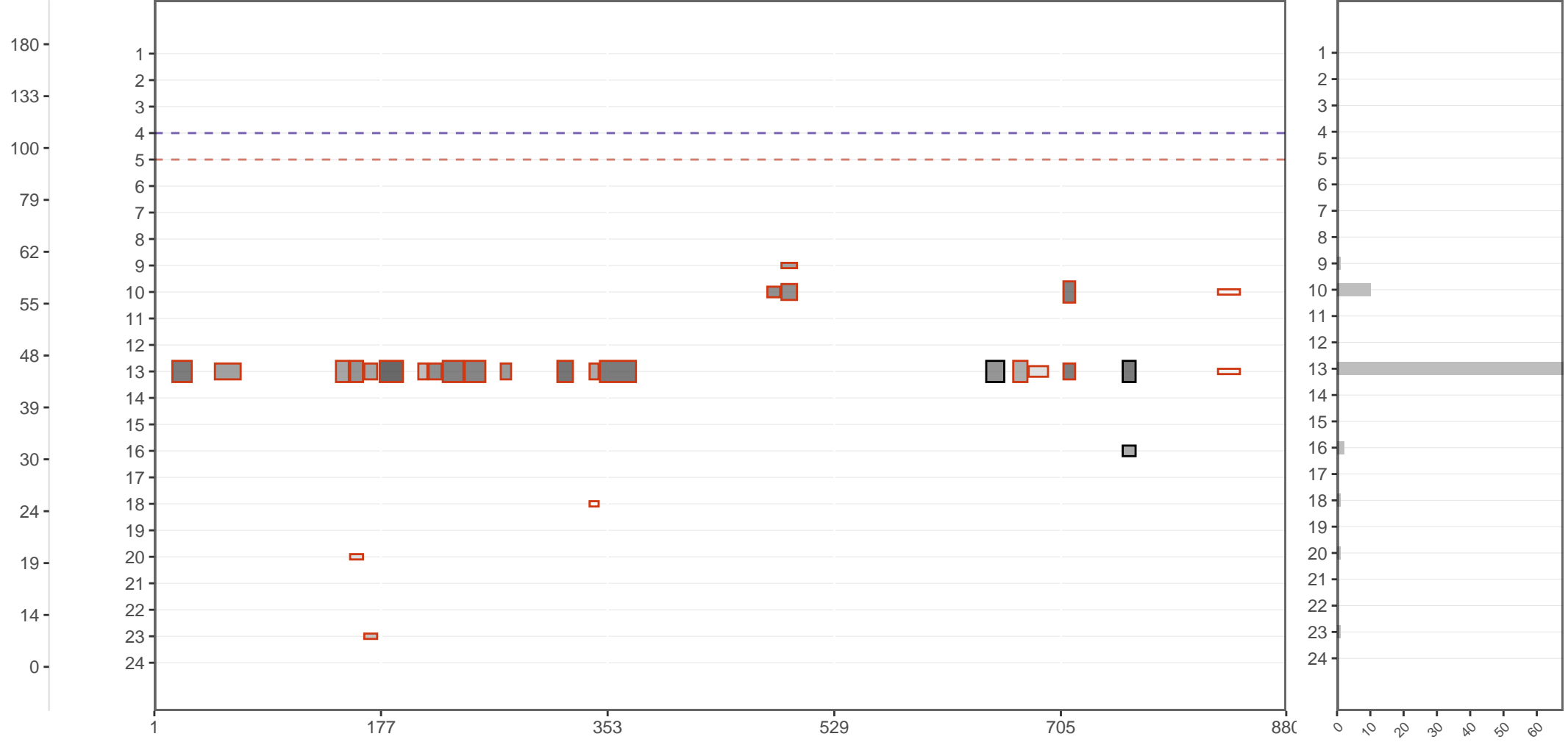
SEICIGVAFQVYRSDLETENGVYPTTVAHFLEDEVRNKGYSGGFDLGLVLLQKLESPMLRAQLKVPNSNEGILVRRKVEPTSDVSNVLAKEGDVWVFDGVRIGGEGTVPFRSRIARFRVLSGKFTGDVAELGHRAGEFMKVDVAVLPRVHLVPHYHIEGGDPSVLIWGLVFTFLSEPLGEECEGDSIGLKLTKARYSLAKFEGEQVLSQVLANEVNIGVYEDISNEGILKNGTRKNHHLAHLVDSGCKDKYLVLEFDNFWLVEREAAVSAASILKDKGIPMERSSDLLEPYDQR

NbL11g22260.1 serine/threonine-protein_phosphatase_BSL1 [MW = 96.04 kDa]



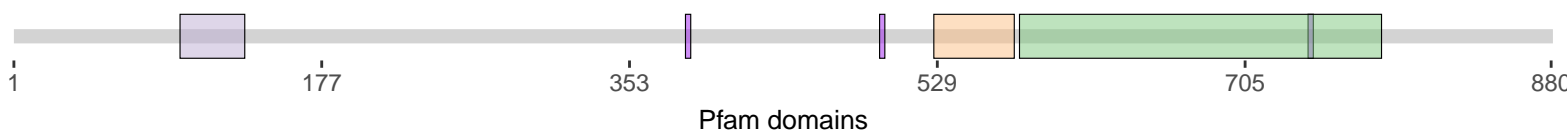
Molecular weight

Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP
- TM Domain
- PF13854 Kelch motif
- PF00149 Calcineurin-like phosphoesterase
- PF16891 Serine-threonine protein phosphatase N-terminal domain
- Sequon

Protein sequence:

AEAAAVVWLAQAASTTPETTSVSDSESSQVPTDGSDEDDSESARLHTRAAVVAKETVGNLGMVRRQLSLEDGFENESRRMLPQVNDISNPTKFKTRGKSPDGLHKKIISTLLRPNRWKAPVNRKFFLDSEYEVGELGVAEQIFMVEPTVLGKAPVYKFGDLHGGDFGLMLRFDVEYGFPTAGDITYDVLFLGDVDRGQHSLETTLLALLKIEYFENVHLRGNHEAADINALFGFRIEGIERMSESDGIWAWTRFNGLFNFLPLAALVENKIKMHHGGIGRSINSVYEQE*

NbL11g22100.1 exosome_complex_component_RRP4_homolog [MW = 36.53 kDa]

No. of times detected



log(intensity)



Values from



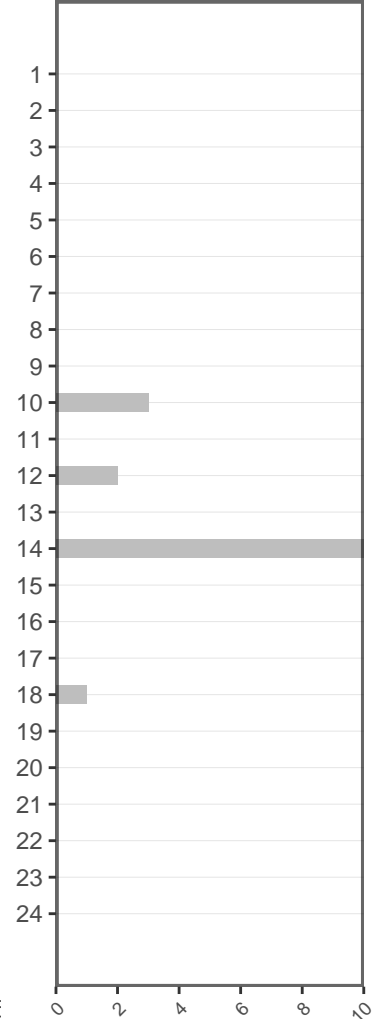
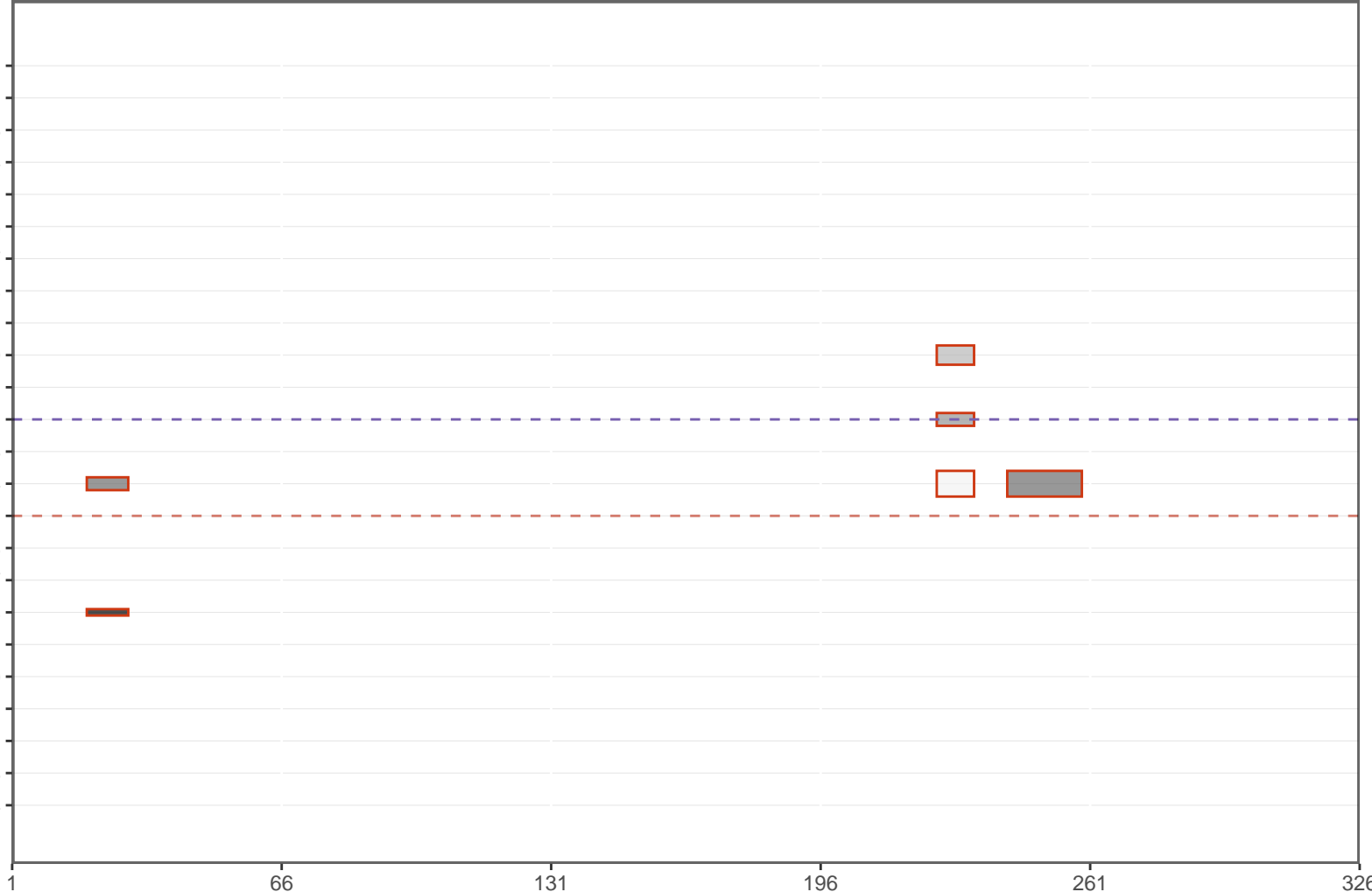
MW indication



Molecular weight



Gel Slice



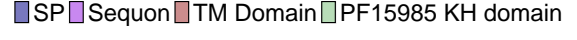
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

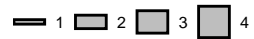


Protein sequence:

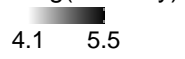
CAEYRFGQHGCSHLGARGSKYKLERGRLLTIPPLVWRKRGKHFHLLDQGVDLHSGNFIWGEHVEVDAMVEDQVKNKEDPQNRGSLGSSSEPTSTPTPETRYGICRIANATVFAALDFMVTLESVEMVNLGLSLNLGVDEMLKAEFHYQVQAEKEAERRSTLTKRR*

NbL11g22020.1 NA [MW = 25.99 kDa]

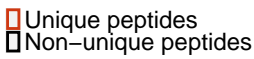
No. of times detected



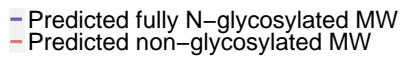
log(intensity)



Values from



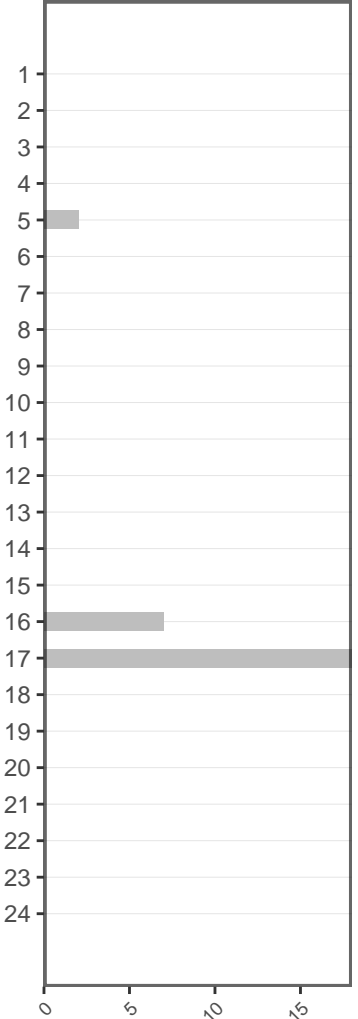
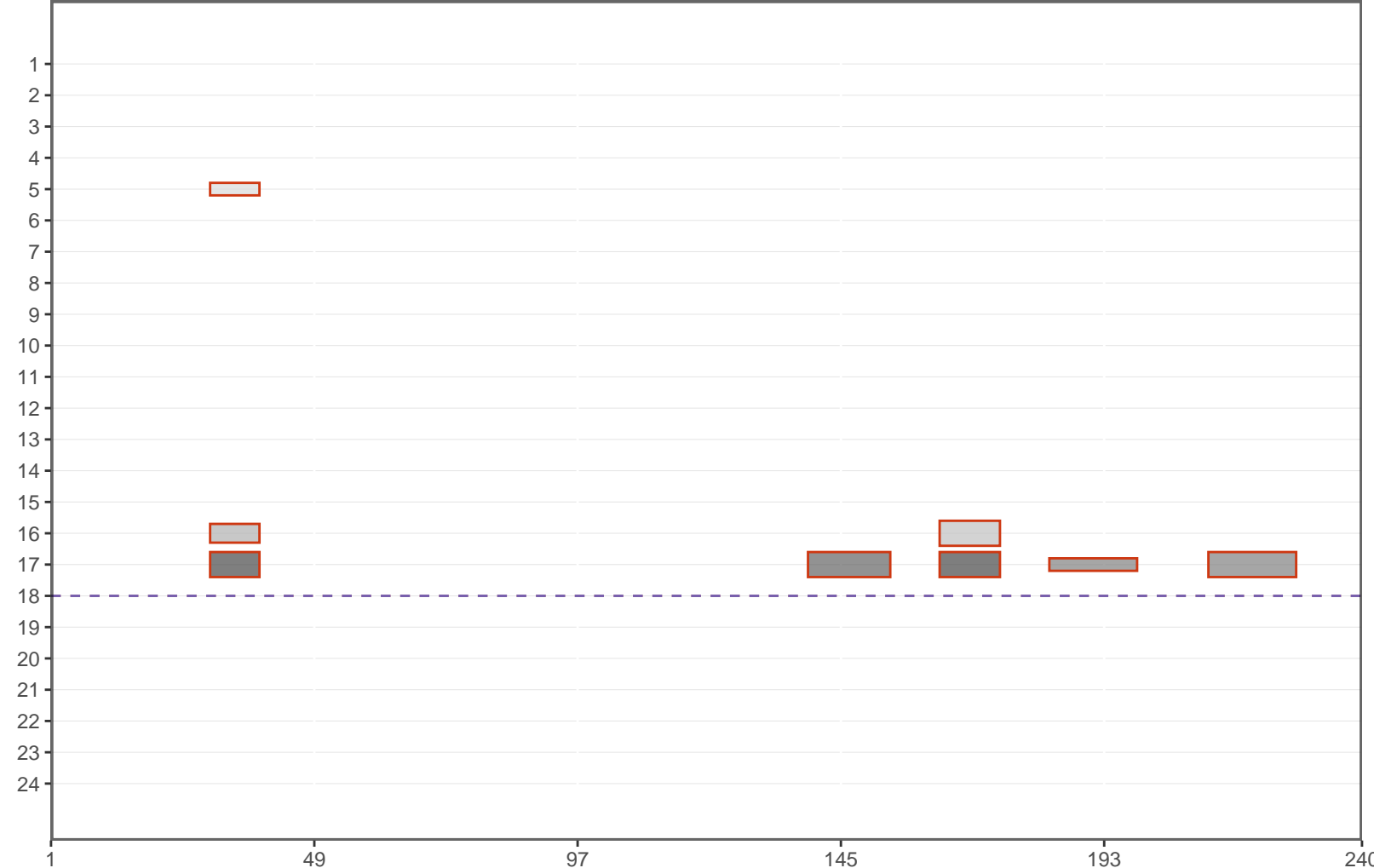
MW indication



Molecular weight

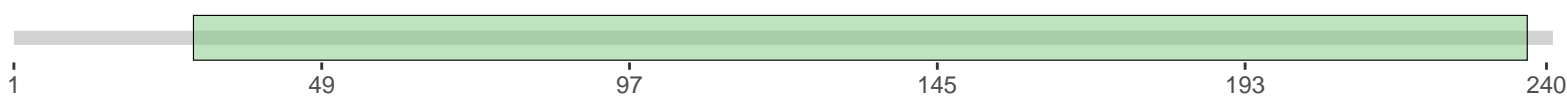


Gel Slice



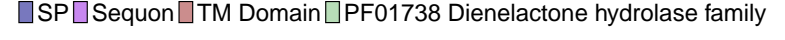
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

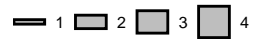


Protein sequence:

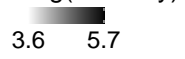
WKVVAALKDKIGISAGAGFGWGAKVVTDLAKSDYIGAAVGLHPSLVKVDKKEKAPIALAAEIDRISFPELKGFEELSSKPEVDSFVKVIFPSVKGHWTRVRYNDEKAVQSAEEAHRHMLDWFTKYVK

NbL11g22010.1 NA [MW = 26.03 kDa]

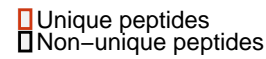
No. of times detected



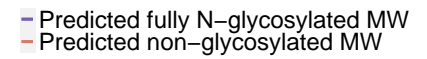
log(intensity)



Values from



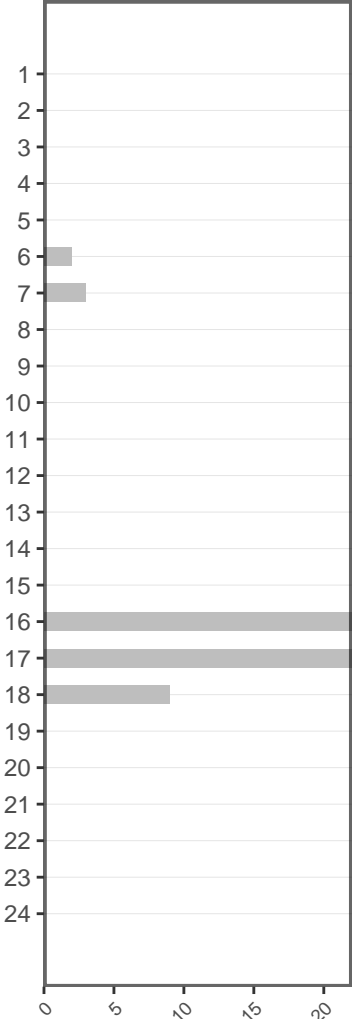
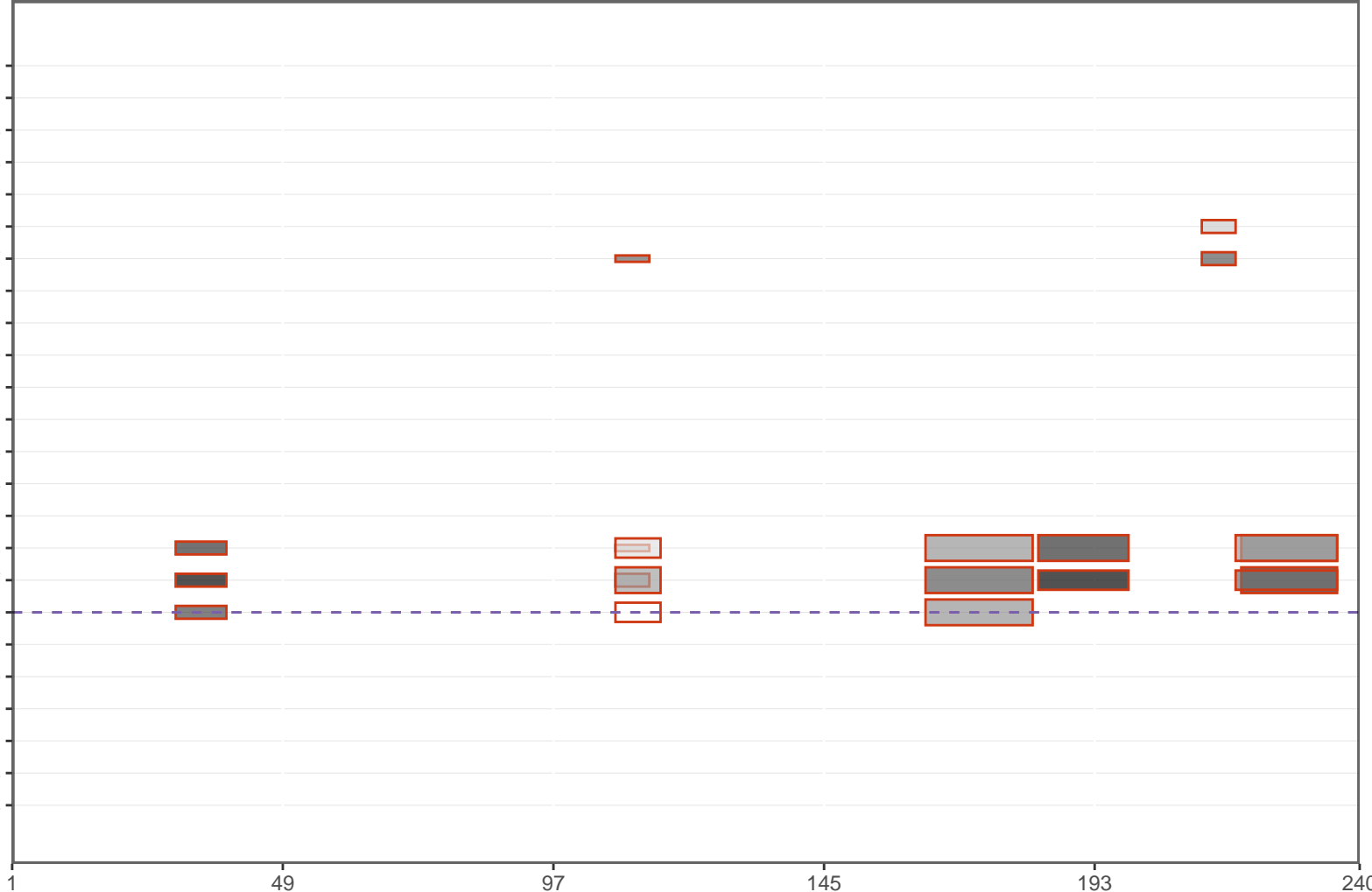
MW indication



Molecular weight

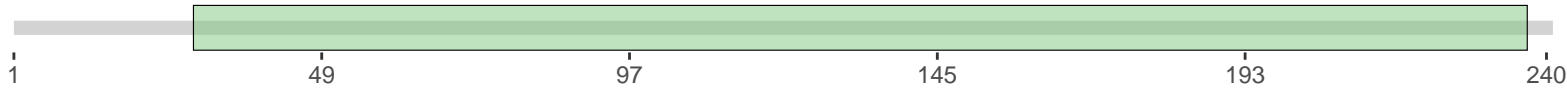


Gel Slice



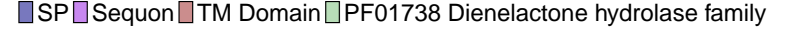
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL11g21960.1 isoamylase_2_chloroplastic [MW = 95.96 kDa]

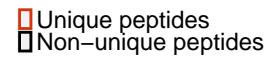
No. of times detected



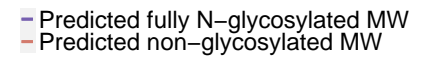
log(intensity)



Values from

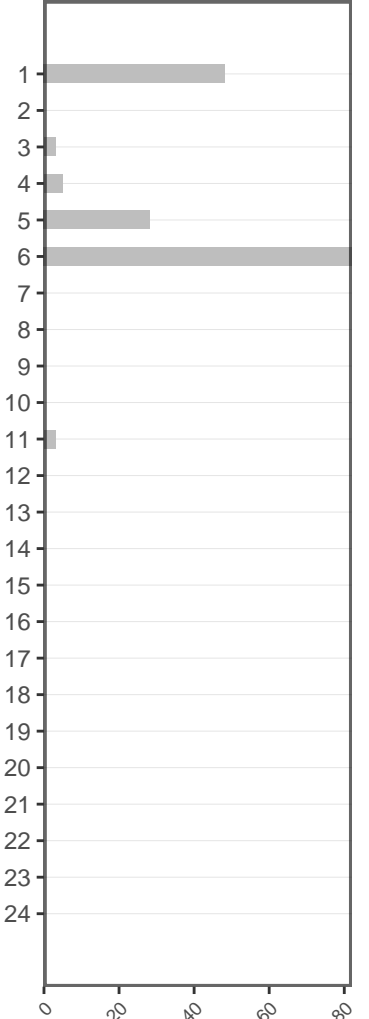
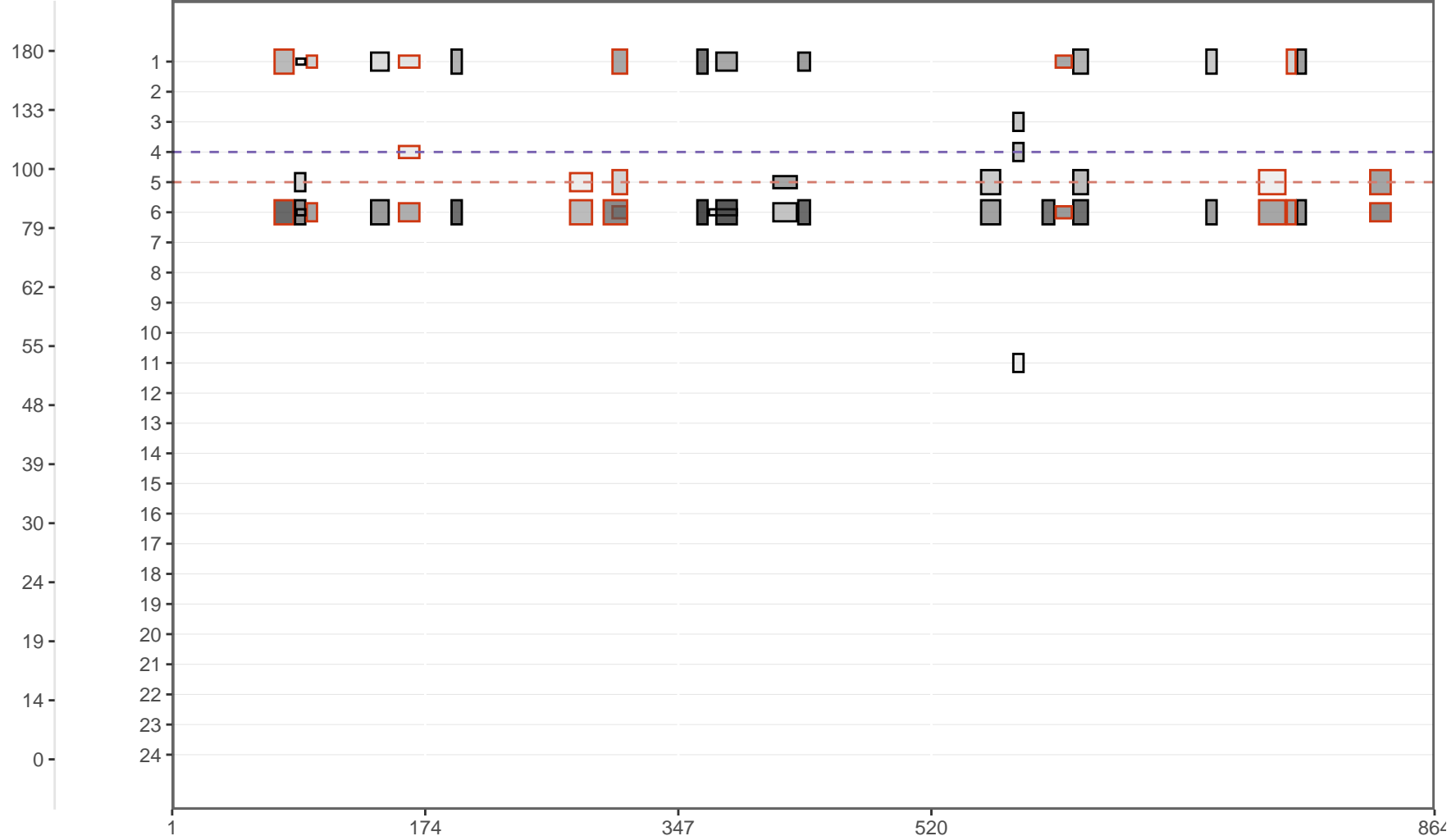


MW indication



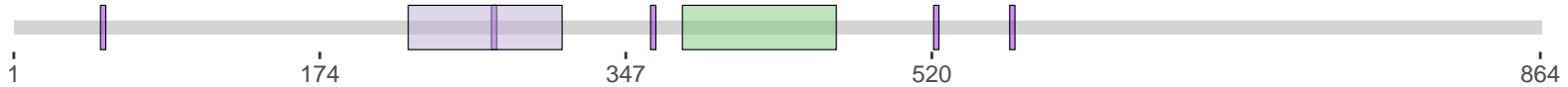
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

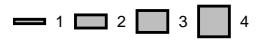
- SP
- Sequon
- TM Domain
- PF00128 Alpha amylase, catalytic domain
- PF02922 Carbohydrate-binding module 48 (Isoamylase N-terminal domain)

Protein sequence:

FSPGNMHRSSDFLEVIKSMKDMVKLHANGIEFLVWFTHAEDAPLMHIDNCGYVSIKGGDLNDFALNDFNDFVGGMLDGLRWVIEFHGDFVFNVAESLLKGFHGEILSRPLVEAIAFDPILEKVAIADYWDALANDSKEILFRHWKVAEINFRFGDDARDFLRGGKLLSATRLLOGGGDFSGGRGVPVDFNVAARNFGLTLDLVVFS6SEVAISELWVNDGEGPPTNNVLETRLQVKNFLFLFISLGVPLVNLNMGDEGLS66GSPVHQVRKSFQWSTLXTI

NbL11g21890.1 DEAD-box_ATP-dependent_RNA_helicase_24 [MW = 80.67 kDa]

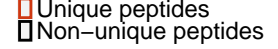
No. of times detected



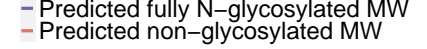
log(intensity)



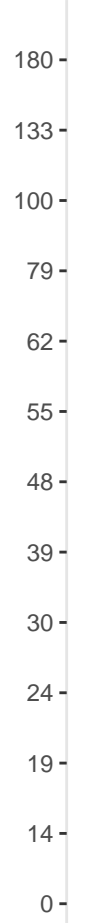
Values from



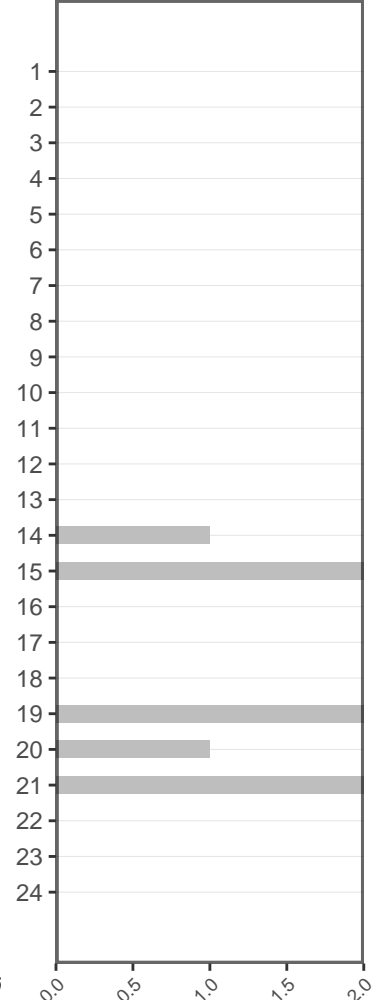
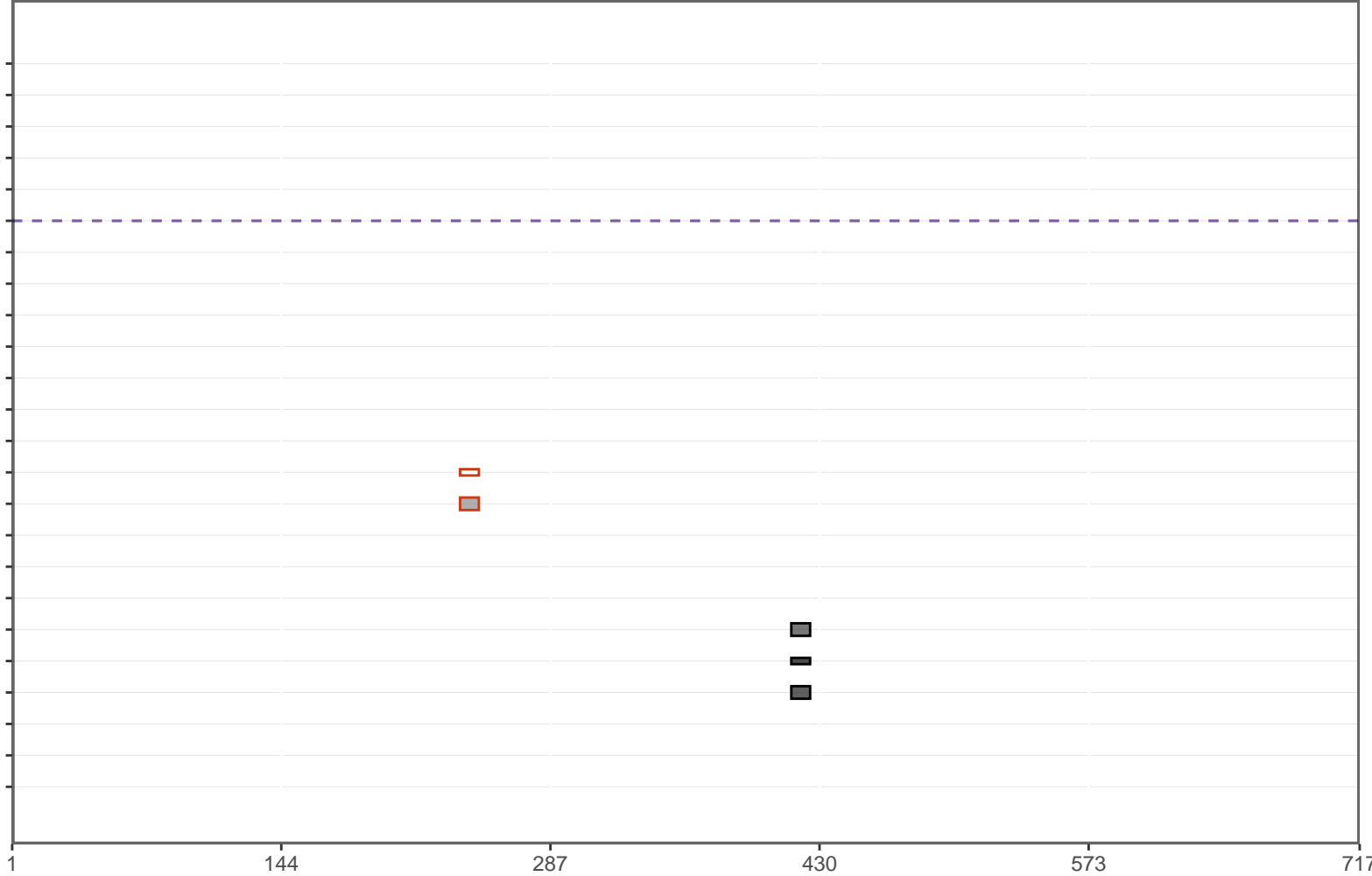
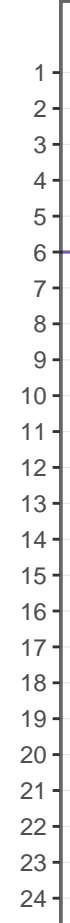
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

PTRELAHQIFVEAKKLEKSHGIRVSAVYGMKSLDQYKELKAGCEVWATPGRITMLRKKAFMLRATYLVLEADRMFDLGFEGAGRSVGGIRPDRGTLLFSATMPRKVVEKLARETELDPVIRVTVGEIGMANEDITQLVGVVPSNAENLPLWLEKLPVLDNGDYLVFASKATVDEIEGSLAQKGFVWALHSDKDKQVSRMETLQKFKSGISHVLIATDVAARGLDKSKSVVYNDIAKMDMMHVRIGRTGRAGSKDGTACTLITQKEACFAGELVNSLVAAGQTSIELMDL

NbL11g21760.1 chloroplast_stem-loop_binding_protein_of_41_kDa_a_chloroplastic-like [MW = 43.51 kDa]

No. of times detected



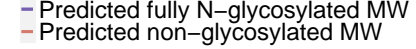
log(intensity)



Values from



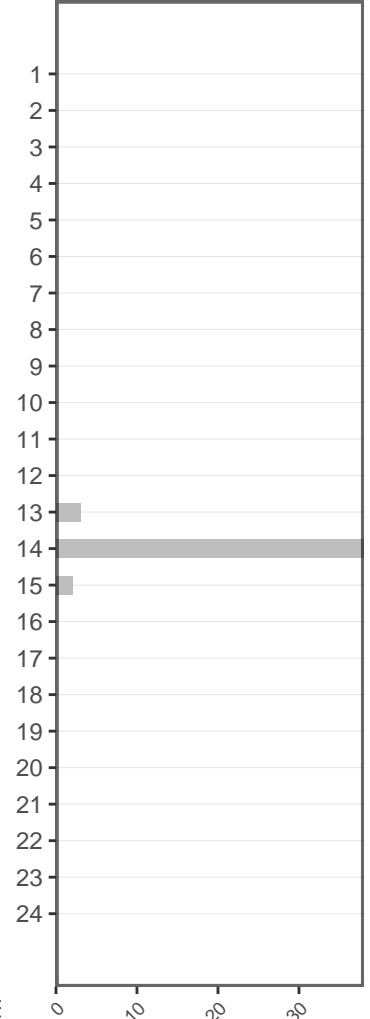
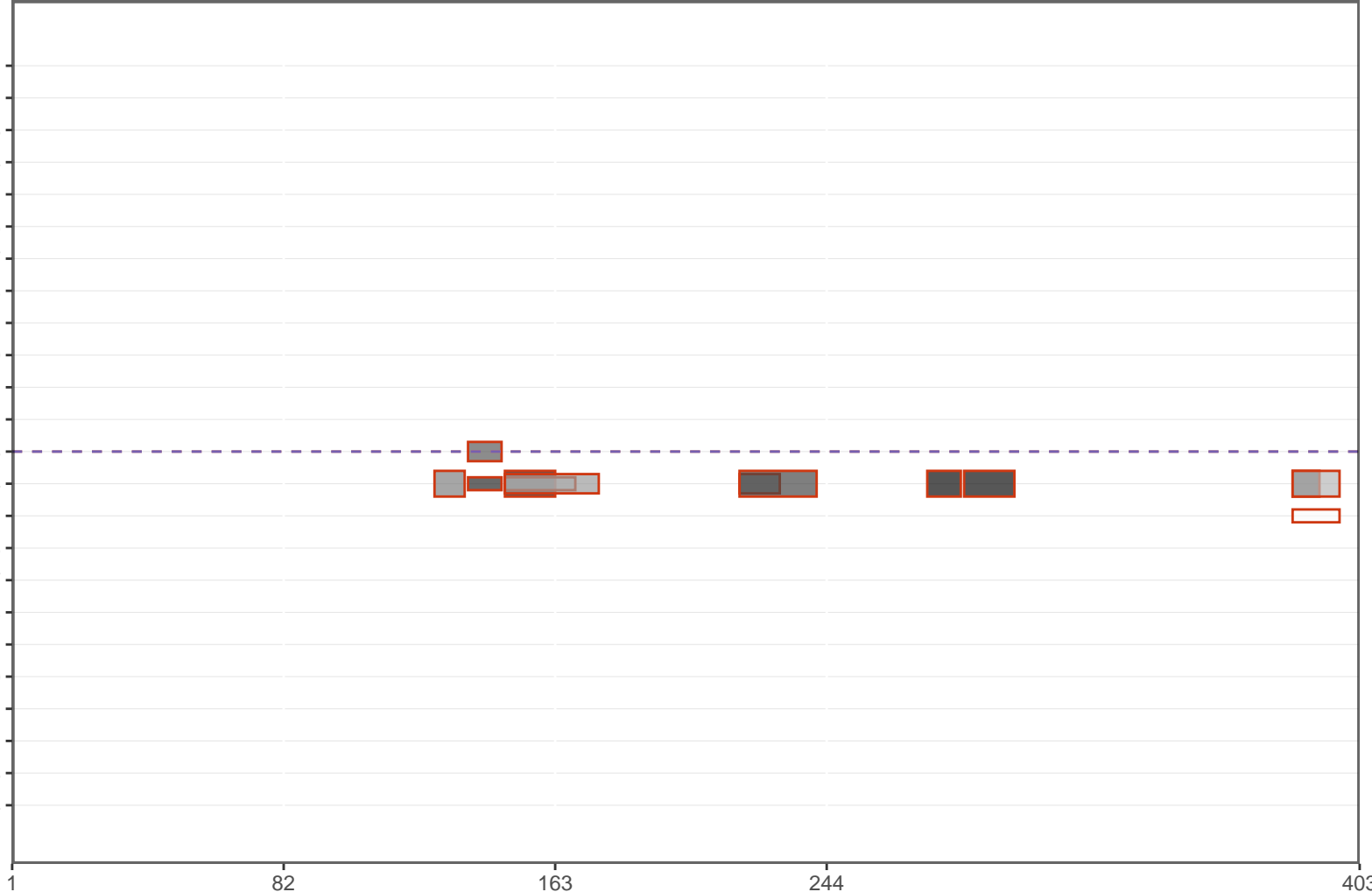
MW indication



Molecular weight



Gel Slice

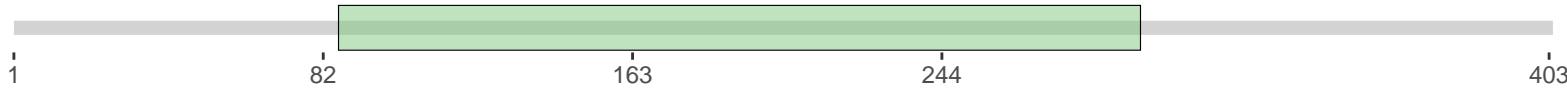


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

GTYKSTDEPHYVEGDAAKADAGHGVGEKYSEIFDWSBSFRPQVMIGSGNKKDCEEFDRIVRGRPVPIPGSGMQLTNAHVRLDSMLTAANKPAAGAHGFNCVSDRAVTLDSGMAKLGAKAAGLSEVNHVDPKAVGVDAKAKAFPRNMHFYSEPRAAKELGWSATTNLPEDLKERFDEVVWGRDKKEKIFELDDKILEALKVPAVAA

NbL11g21680.1 ribosome-recycling_factor_chloroplastic [MW = 35.41 kDa]

No. of times detected



log(intensity)



Values from



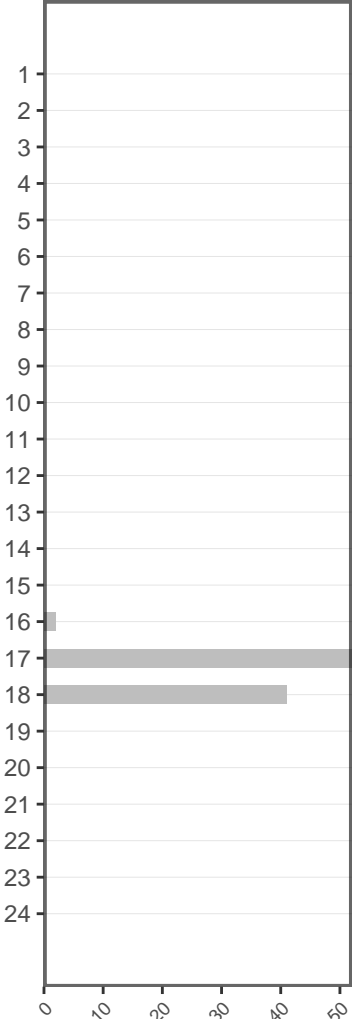
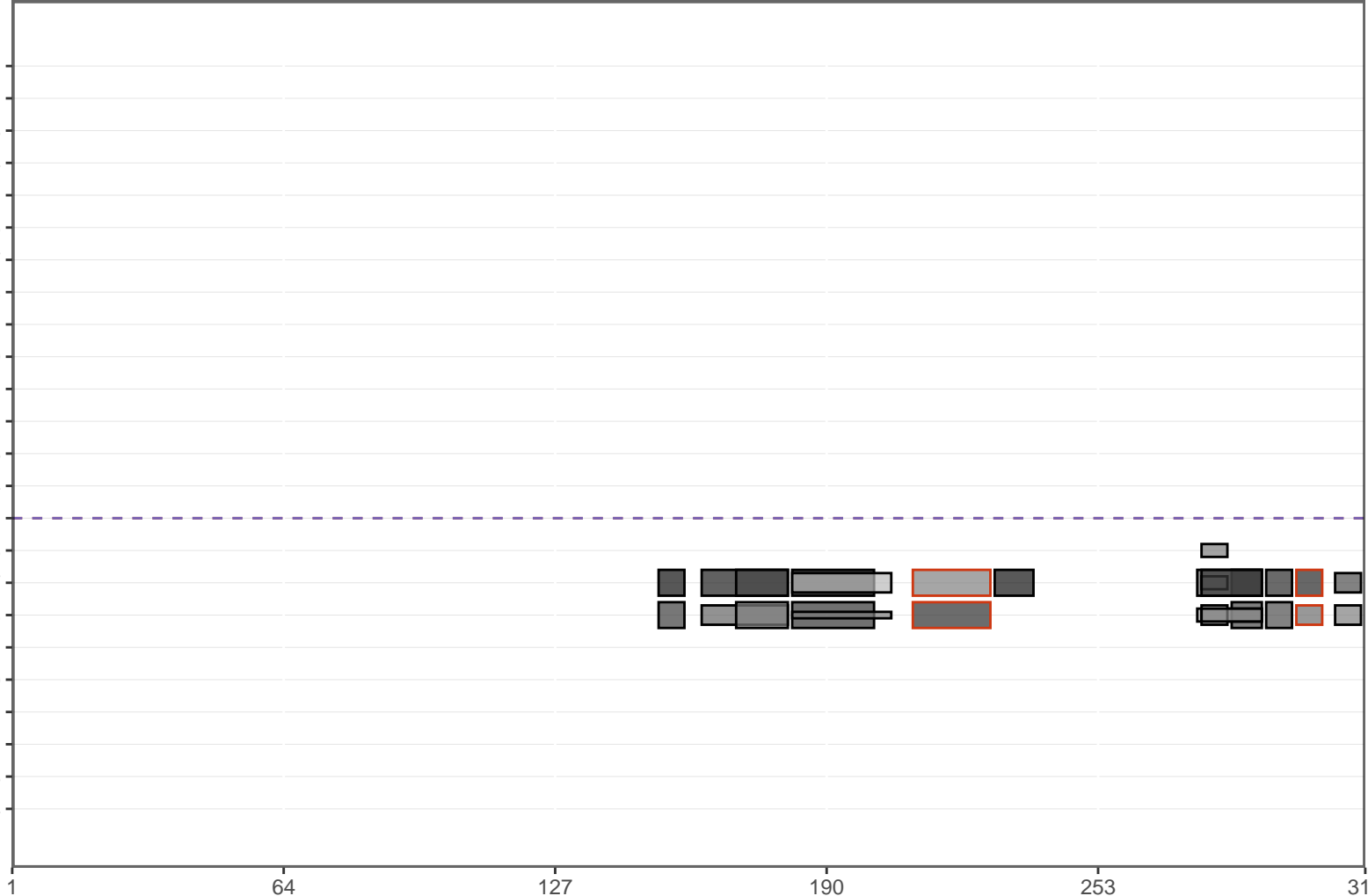
MW indication



Molecular weight



Gel Slice

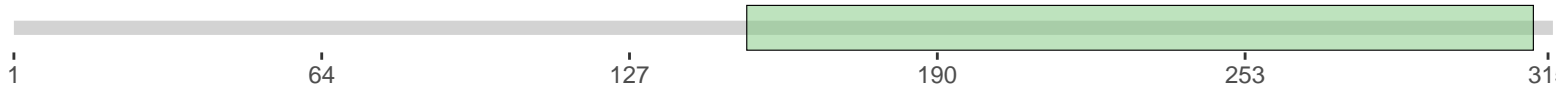


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description

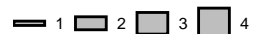


Protein sequence:

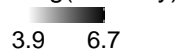
IEKTIENVRSNFTNSRITGRASPMALDKIEVDVYGTPTVSLKSAIQISTPDGSSILVQFPYDKSSLSKAIEKAAVSGDLGMTFNNDELIRMVLPOLTSDRRKLKSVKQAEEGKVALNRNRDLKAAVEKLEKEKLLSEDNVYKDLGGDLGKVTDEYMKKHIDTVFKQKEKELTY

NbL11g21530.1 dehydrogenase_(LOC107772922)_mRNA_AJ299256.1_Nicotiana_tabacum_mRNA_for_malate_dehydrogenase [MW = 39.85 kDa]

No. of times detected



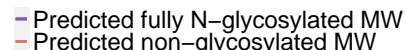
log(intensity)



Values from



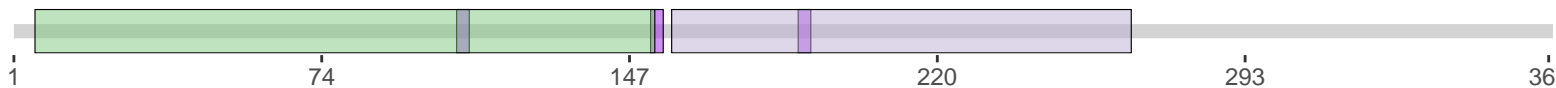
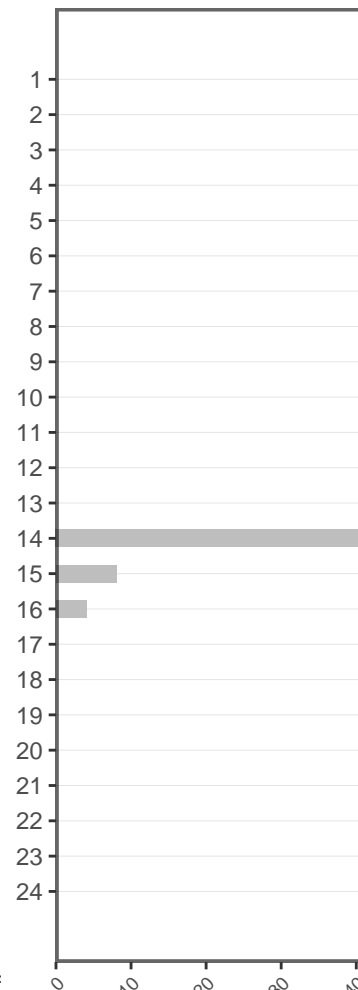
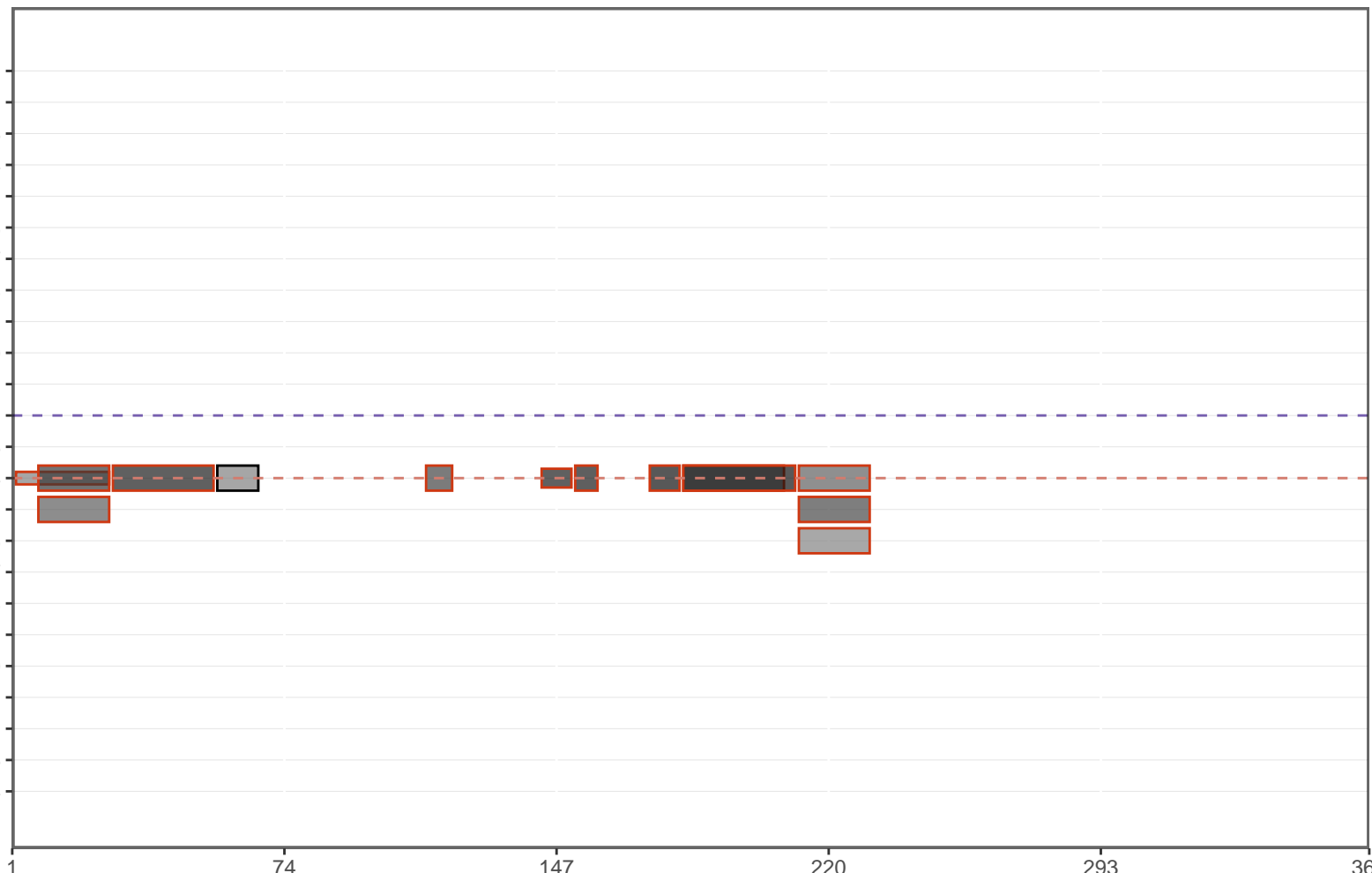
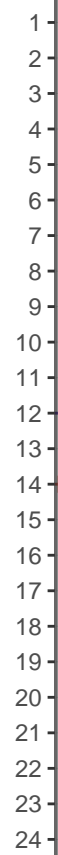
MW indication



Molecular weight



Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00056 lactate/malate dehydrogenase, NAD binding domain
- PF02866 lactate/malate dehydrogenase, alpha/beta C-terminal domain

Protein sequence:

IRLLNQQVSDVKNVHWGNHS66YPDVNHATVATPAGDKPVRLELVADDAWLNGEFISTVQGRGAARKKRLSALSAASSACDHRDWWLELQRELGLFWFTLMSGHTVSGLVLPISQLHAKMENGLFRVFDQLMSGGERBWTPLQRLNLYLRKKHWHPALPKLGHFLNGLFNWGVVILEVASVLNKAIVDSI

NbL11g21460.1 activating_signal_cointegrator_1-like [MW = 31.61 kDa]

No. of times detected



log(intensity)



Values from



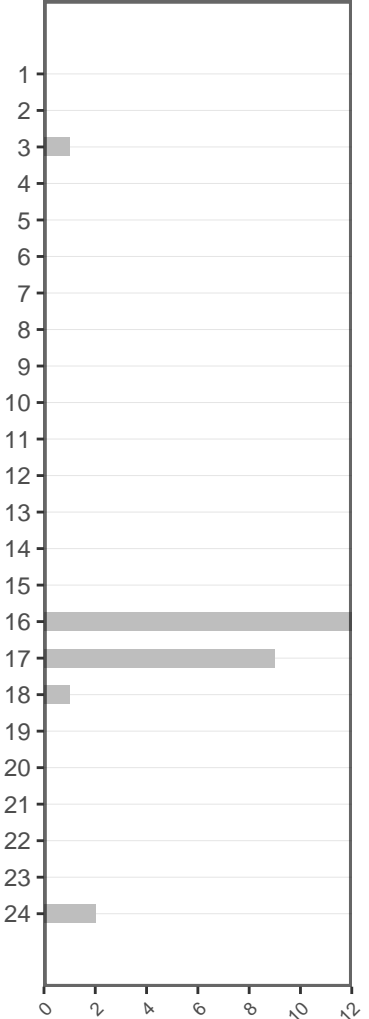
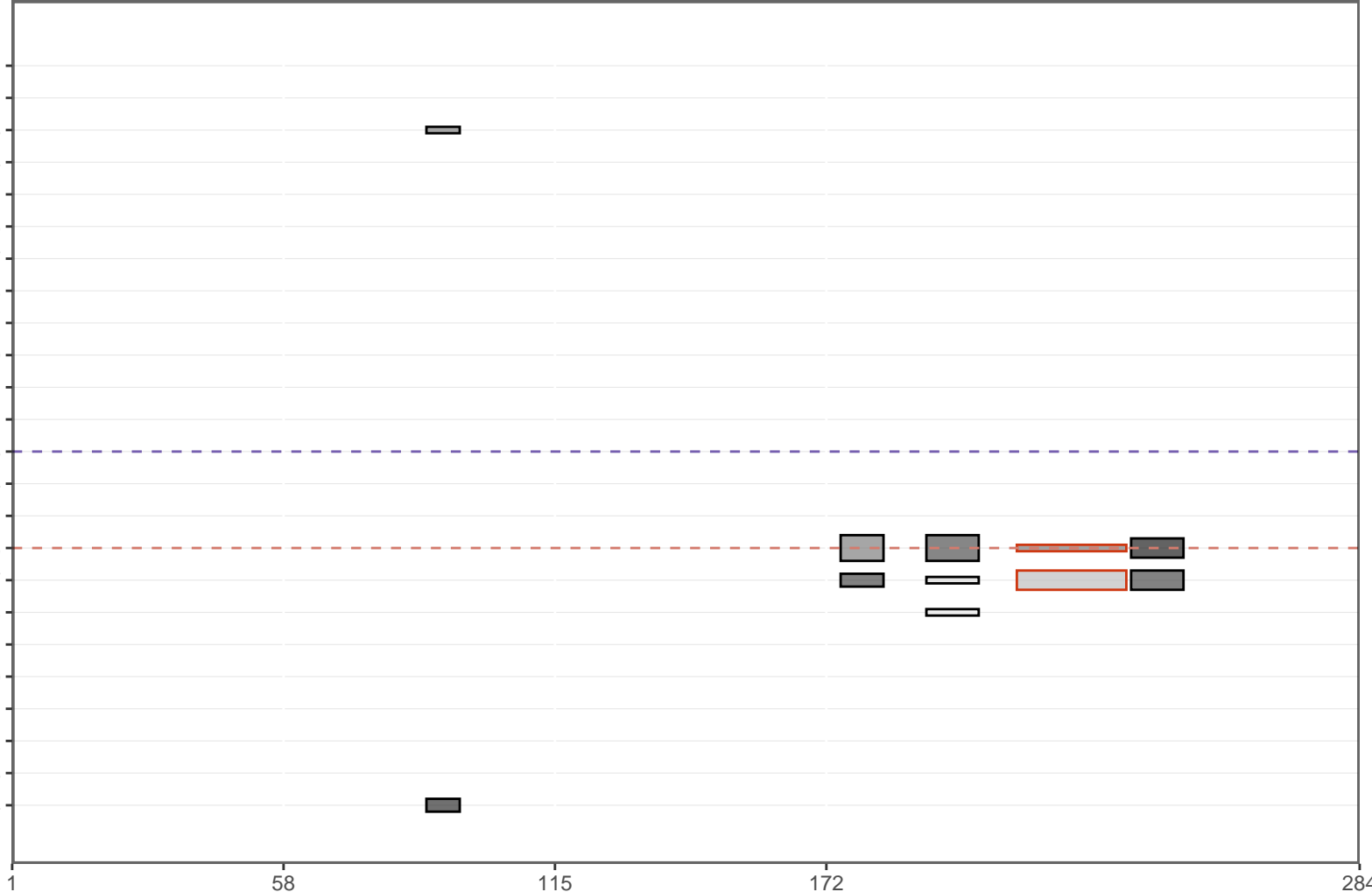
MW indication



Molecular weight



Gel Slice

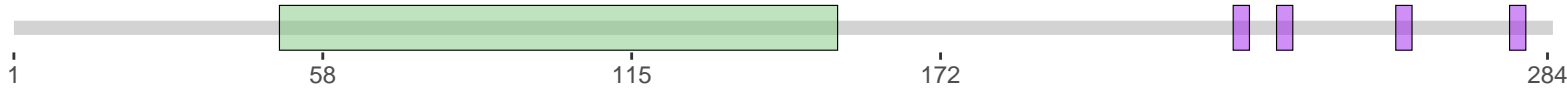


Protein length

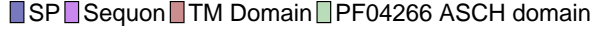


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VVGCYCEELVGVSDQIFEGVRLGGTKFGWLGEQPKLIVFFEMIRGSGVYVLERKRYEAIIRGISPVAPPLPVKFLPNPRDFPSKPSGLABLNSSSTSEVNRSENAAAGARAAATQFENKSSSGSSTVEVGDDEVSNTNRKRRIGV

NbL11g21410.1 probable_plastid-lipid-associated_protein_4_chloroplastic [MW = 28.63 kDa]

No. of times detected



log(intensity)



Values from



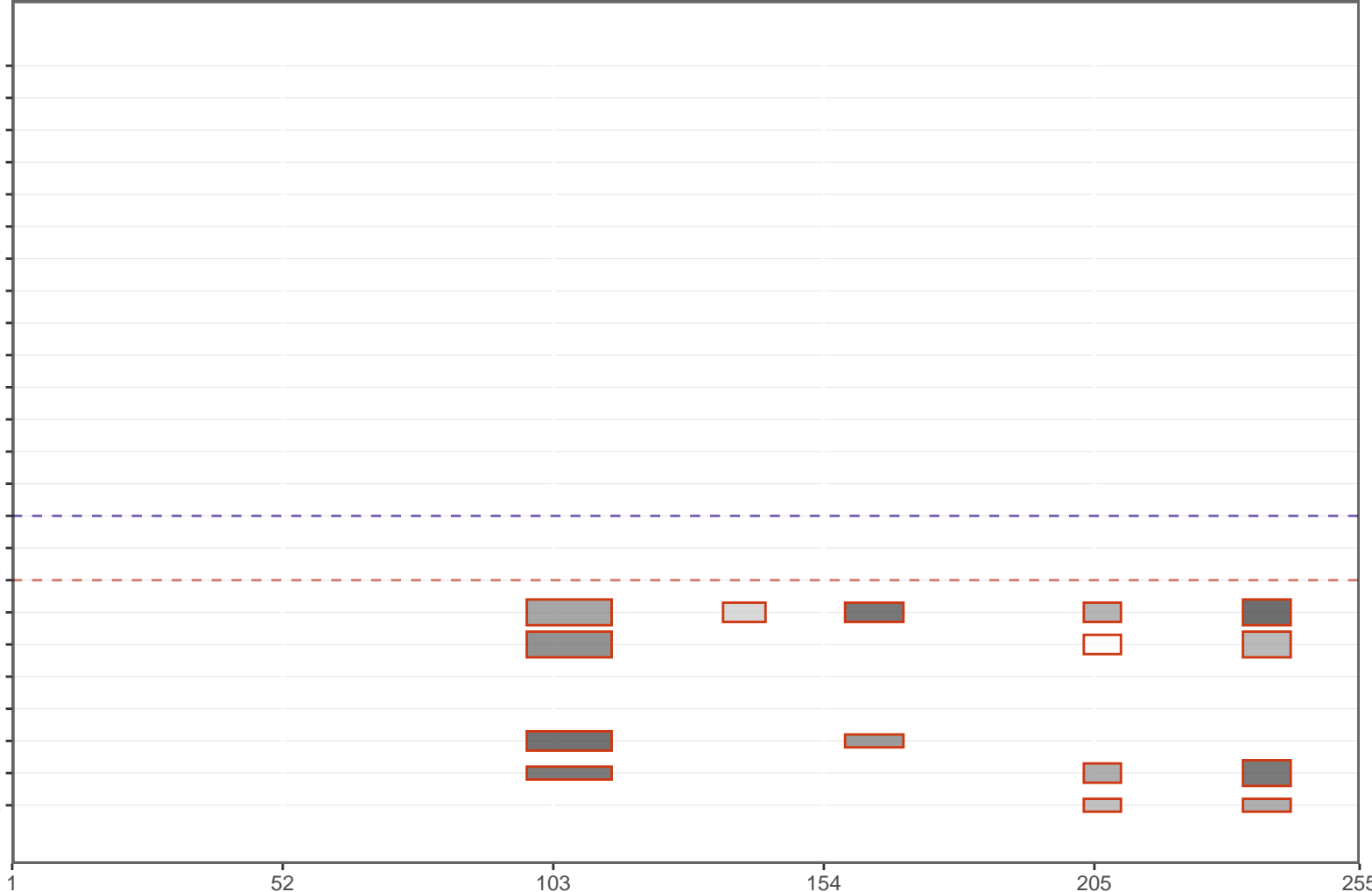
MW indication



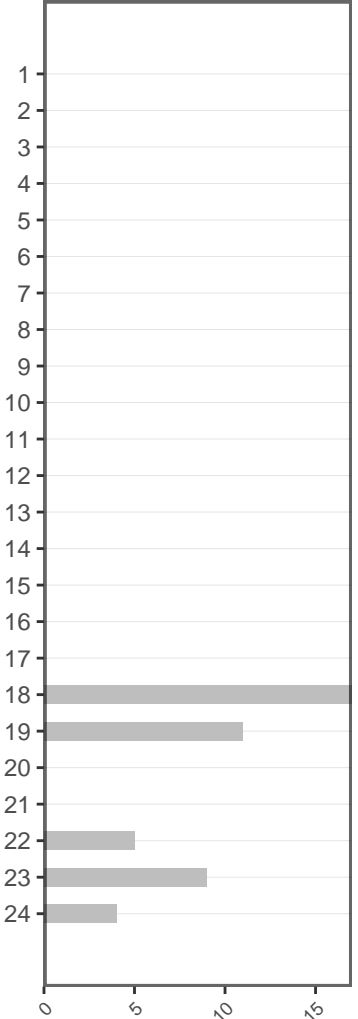
Molecular weight



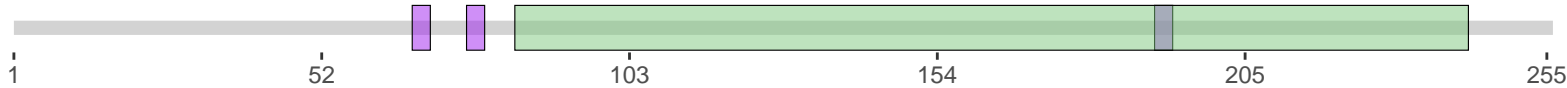
Gel Slice



Protein length

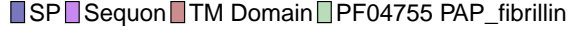


Peptide counts over 4 repeats



Pfam domains

Pfam Description

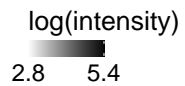
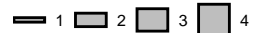


Protein sequence:

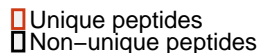
KLEACNPTEKFLKSNLLNGKWEIYFTTSKBIQTGRPKILRSRVNYGAINGDTLRAGNMEGLPFNFNQVTDLTPLNLSKVAWKFDFYKGGHPVWAPGRARGELEIFYLDEELRVSRRDGLNLFKMMVDPGRVPTPDI

NbL11g21400.1 uncharacterized_LOC109207172 [MW = 72 kDa]

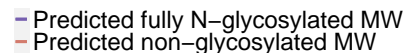
No. of times detected



Values from

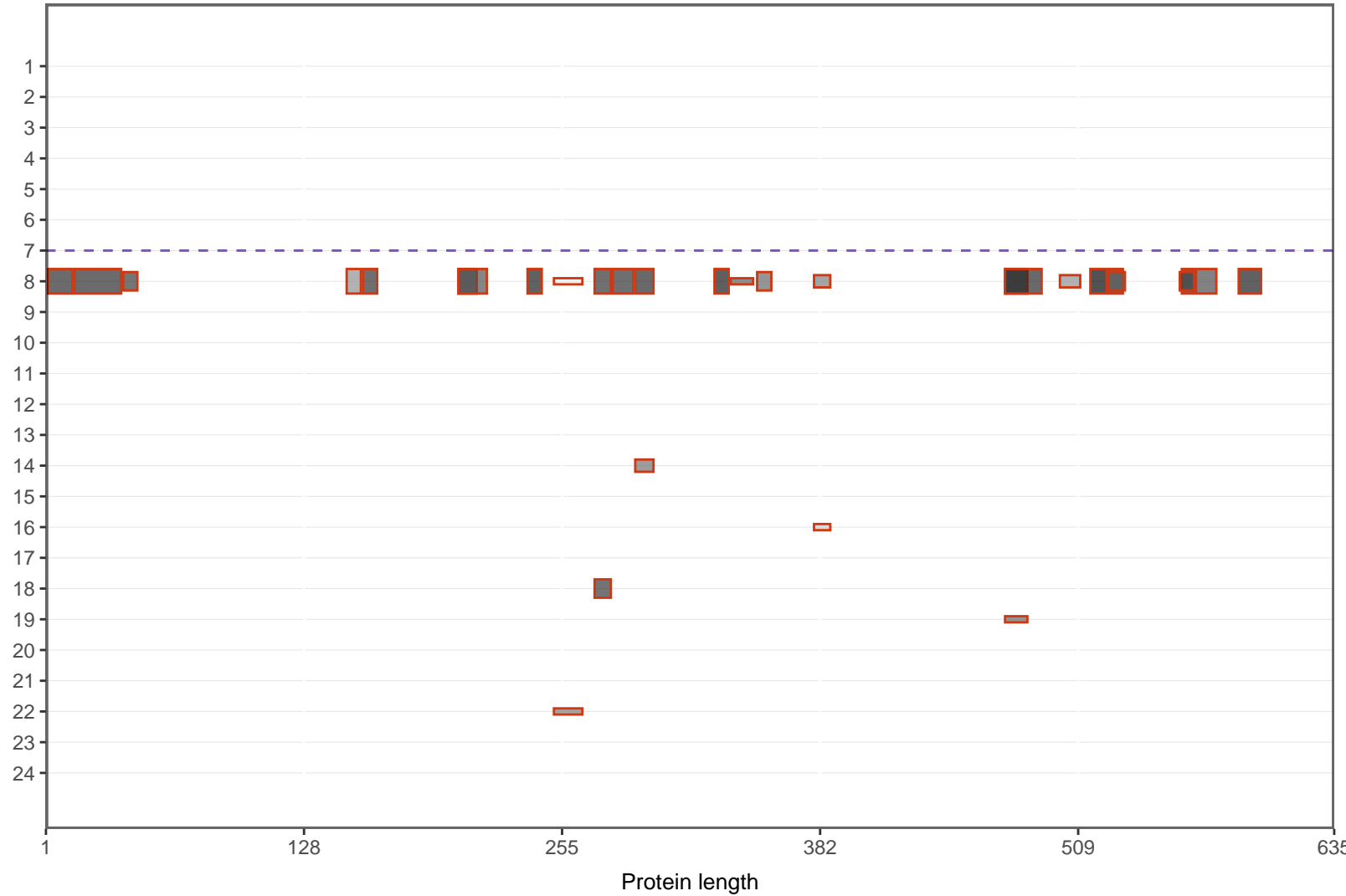
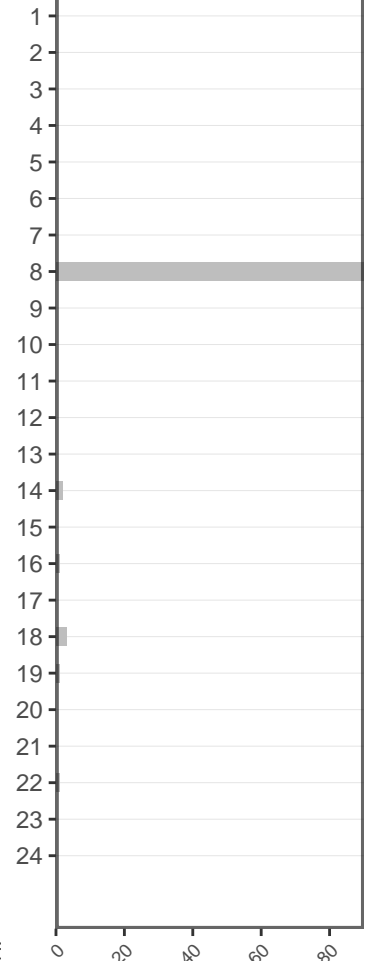


MW indication

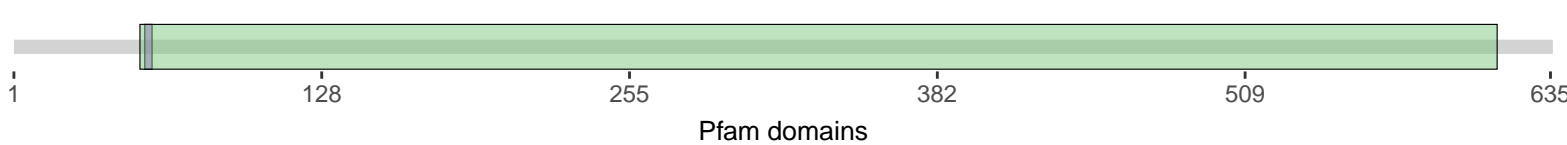


Molecular weight

Gel Slice

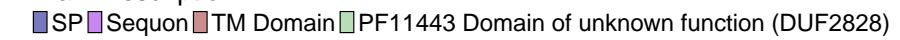


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YGEYNGVEEGHYAWRVRRDLKIDVLPYHKALELPEVYVMSAKKNSLPLYNRVASVAMKMYKELFLKHDKERFDKYLEDVKSGKAKAAGALLPHEIGALSDDGGDEVAELQWRMMVDLCKKGGALNGLNIAKAVDVGSGMSGIPMEVSVLGVLVSELSPEPWKGLTFSDPEMQRKVEGDTLKEKTEFRVRMDMGWNTDFQKVFYRILEVAVGGKLGEDQMKRIVFVSDMEFDGASENAWETDVAQQRKPFVETGKYNKPEVFWNLDRSRSTPYLEKSSGVALVSC

NbL11g21390.1 electron_transfer_flavoprotein_subunit_beta_mitochondrial-like [MW = 27.6 kDa]

No. of times detected



log(intensity)



Values from



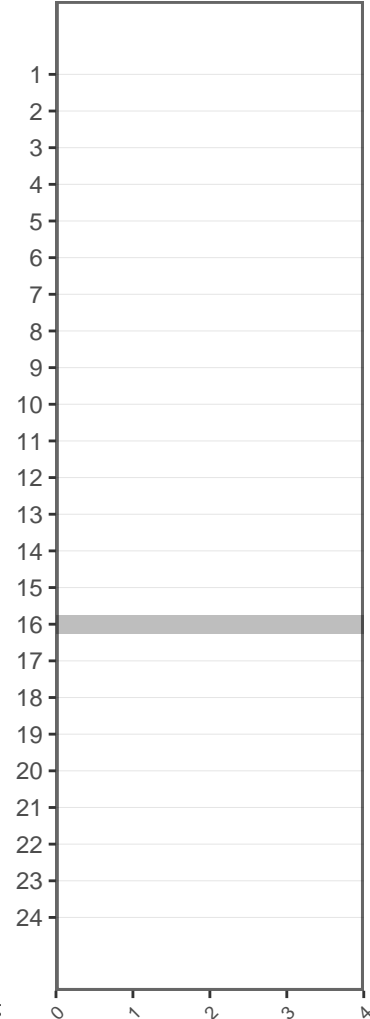
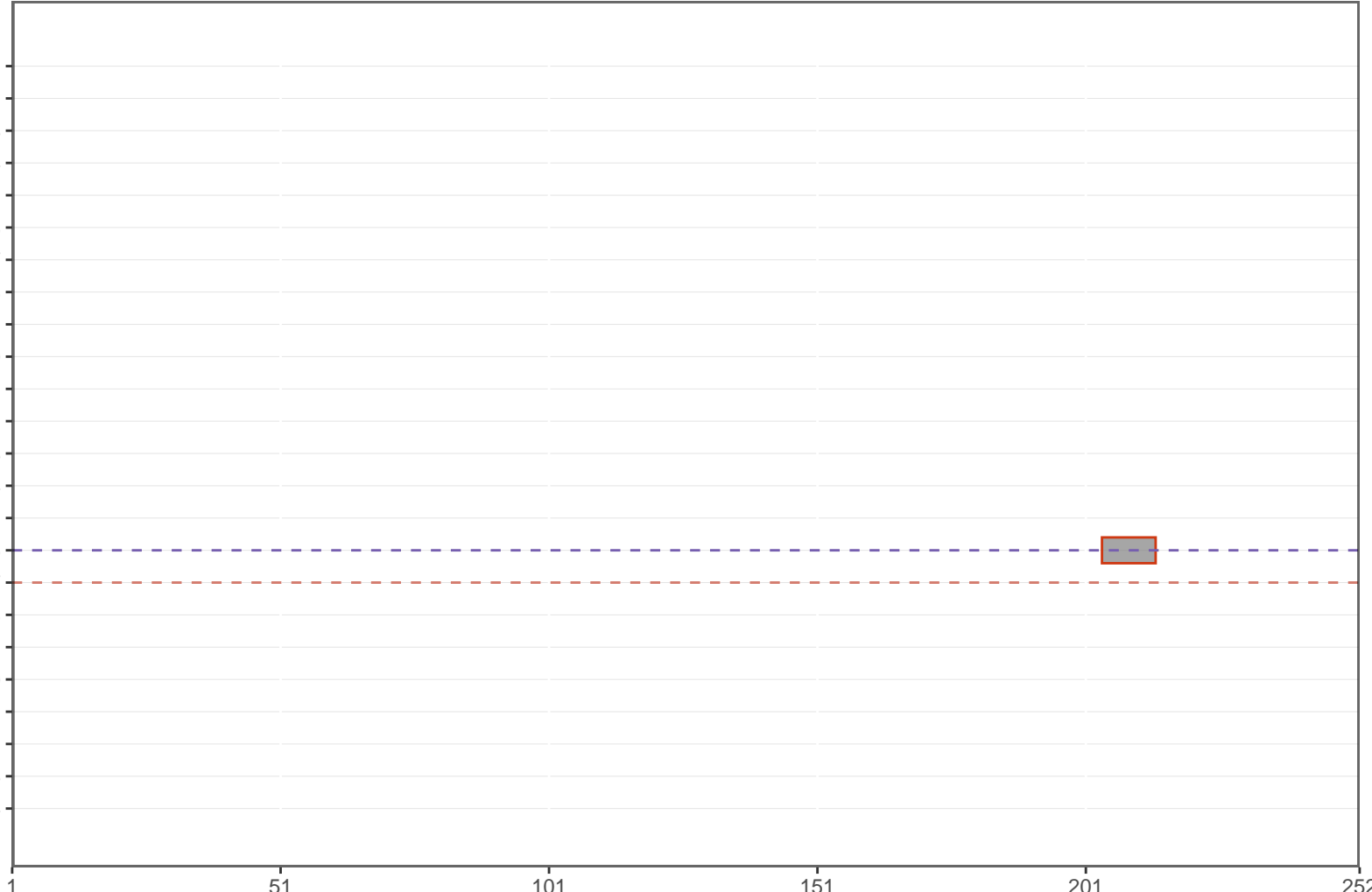
MW indication



Molecular weight

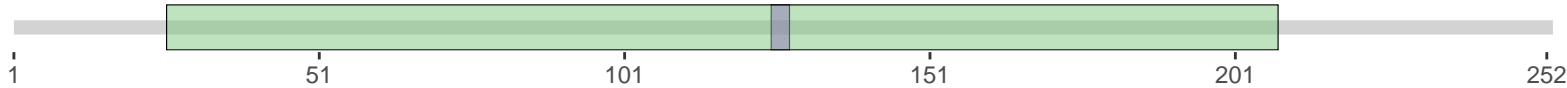


Gel Slice



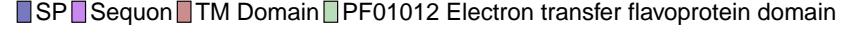
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LLGKAIIDNDQVCFQGMVAGLLKWPQGTFFASKVAVLKEKEKQVATVREVDGGIETLSLNDLPVITTDLRNLNGPRVATLPNMMKAKGPKPKKFTPDQLNMEIKGDFEVEVETEPFKRKAGLLISEVDELQKLNKEARV

NbL11g21240.1 proteinase_inhibitor_I-B-like [MW = 16.68 kDa]

No. of times detected



log(intensity)



Values from



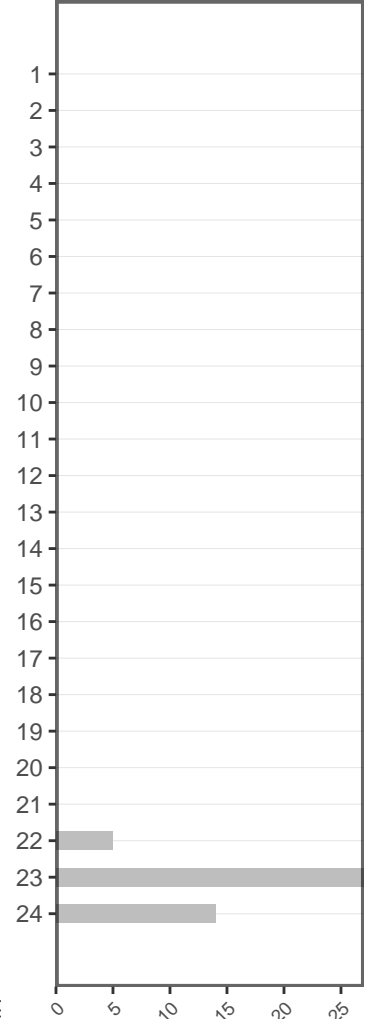
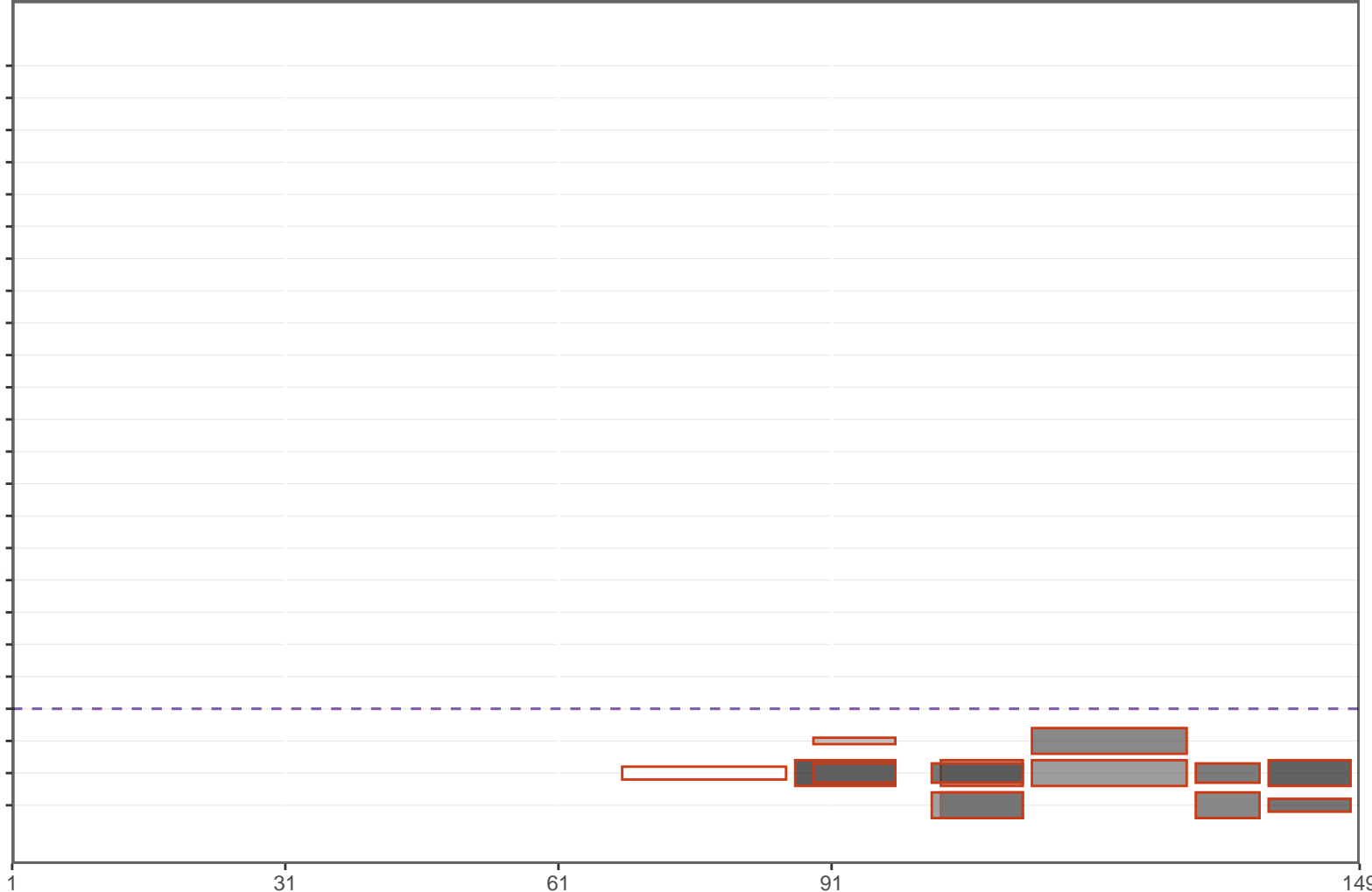
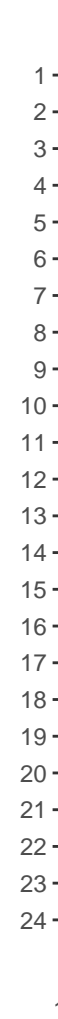
MW indication



Molecular weight



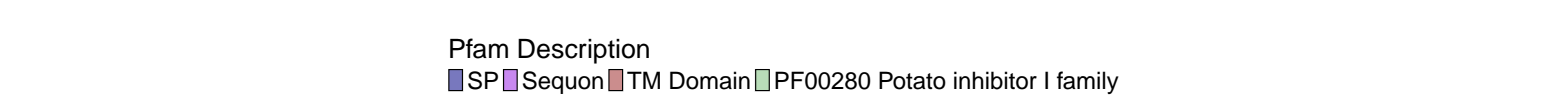
Gel Slice



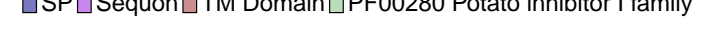
Protein length



Pfam domains



Pfam Description



Protein sequence:

CFPAAKENGVETLDDASLSLHGGKQKWFVEVGMGPRGRTAKKIEKENFLVWVHFLFRDMLQLDLDCSRVFLVWVWVWVQITPSVD

NbL11g21220.1 proteinase_inhibitor_I-B-like [MW = 16.65 kDa]

No. of times detected



log(intensity)



Values from



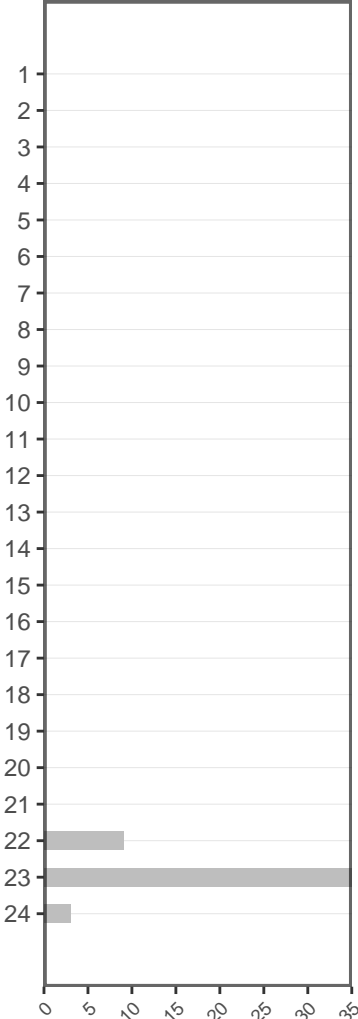
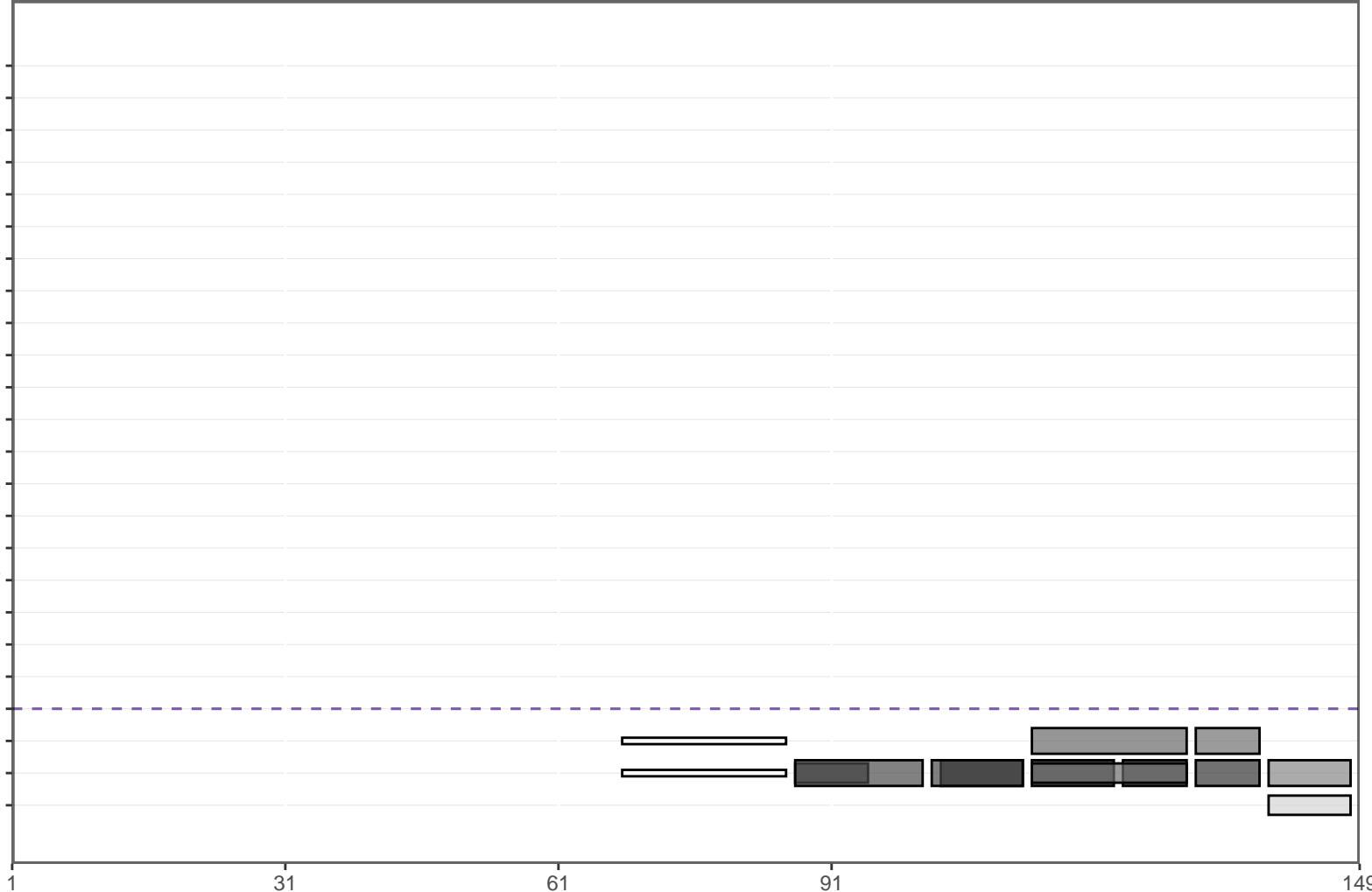
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

JFPMIAKENQVETLDQPELSIGKPGKGSWPELVGKPKWATAKRIEKENPKAVQVLFPGMWRPLNYYGGRVFWVWAKLVRDTPSMG

NbL11g21120.1 40S_ribosomal_protein_S15 [MW = 17.02 kDa]

No. of times detected



log(intensity)



Values from



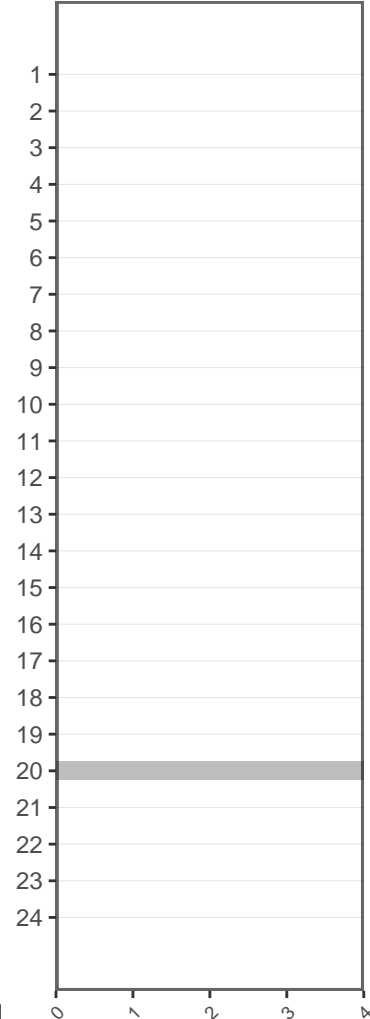
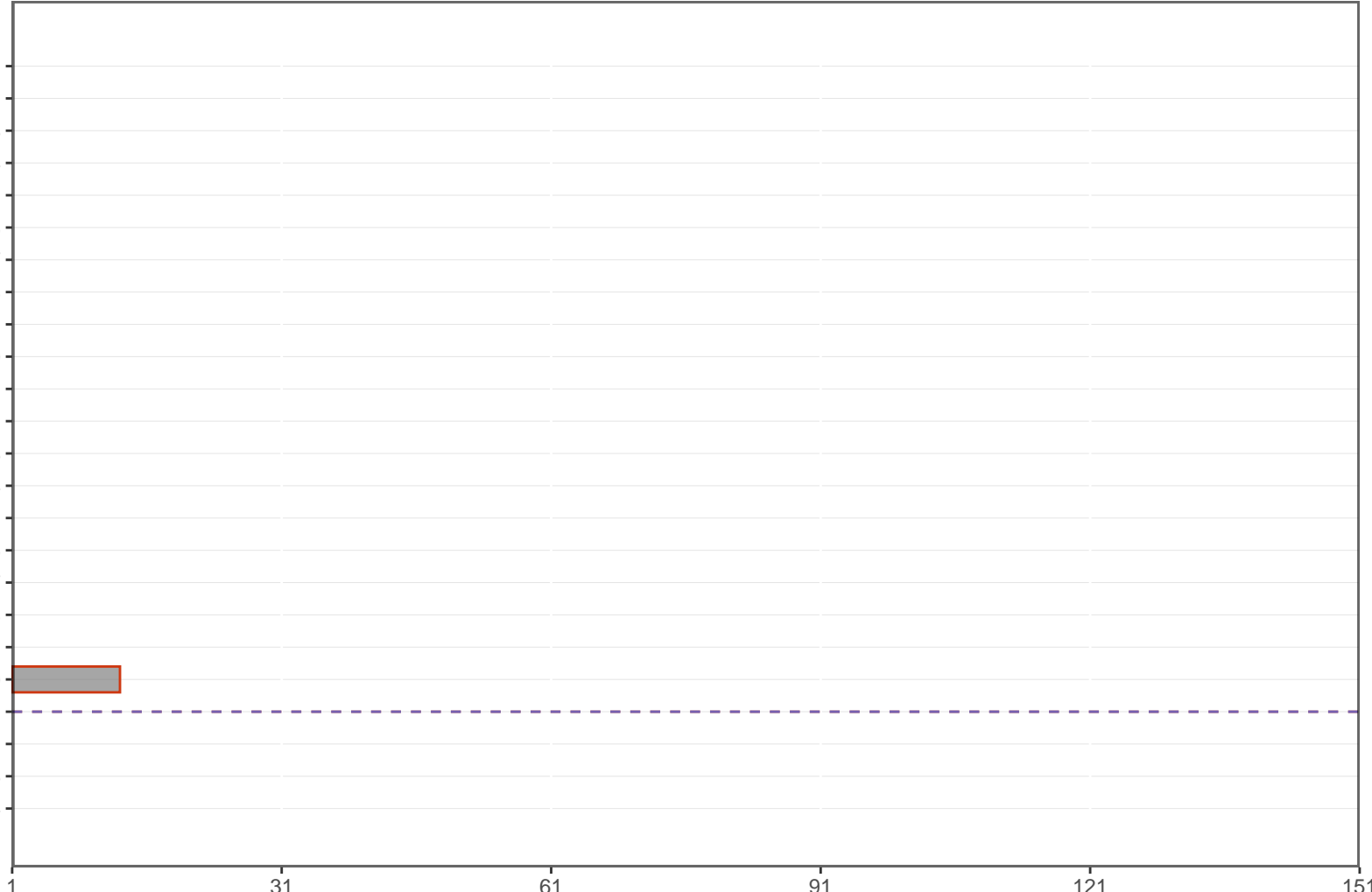
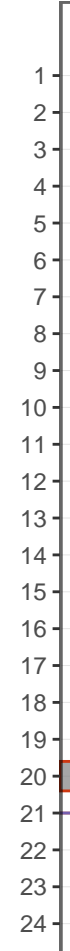
MW indication



Molecular weight



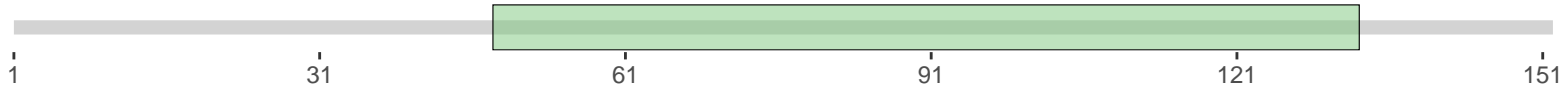
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

LIKILRKAAREAPPGEKPEPVKTHLRNMIIVPEMIGSVIGVNGKTFNGIEVKEPEMIGHYLAEFSDYKPVKHSRPGIGATHSRGSLK

NbL11g21000.1 protein_LYK5-like [MW - SP = 67.5 kDa]

No. of times detected



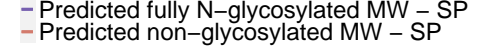
log(intensity)



Values from



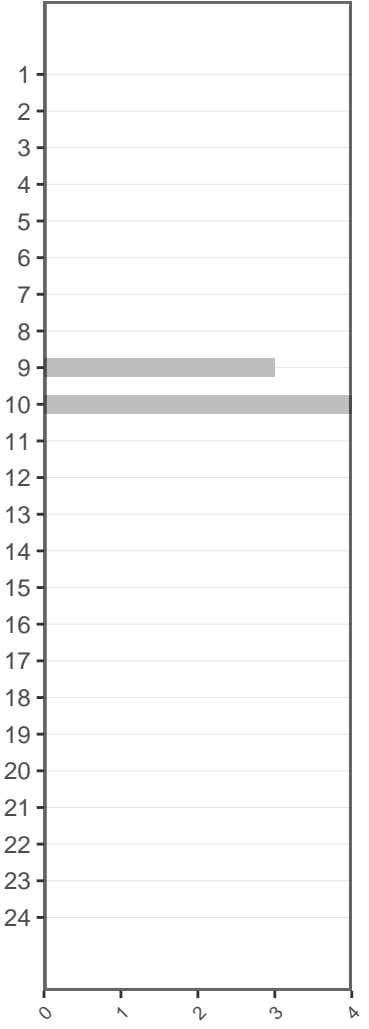
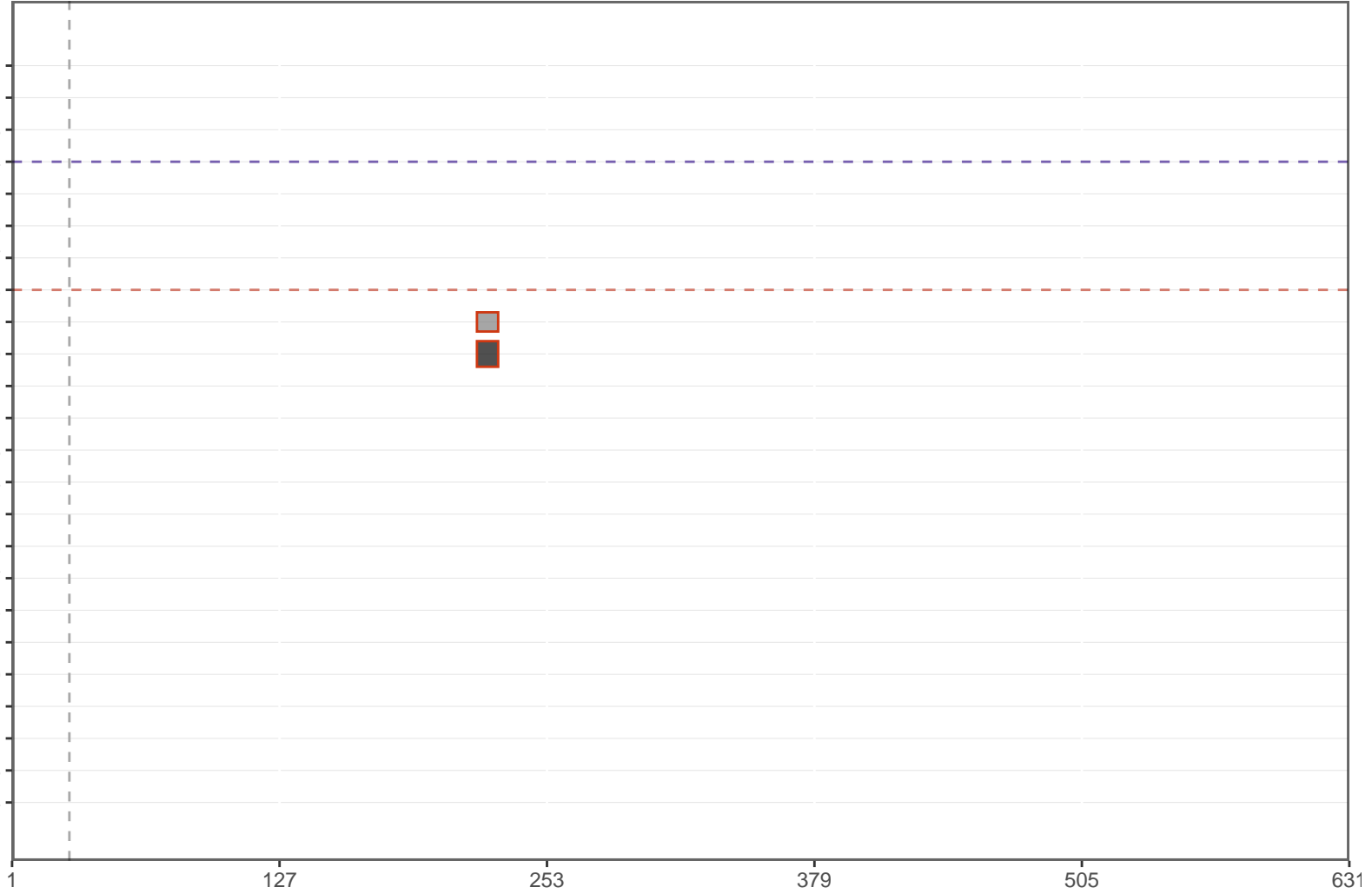
MW indication



Molecular weight



Gel Slice



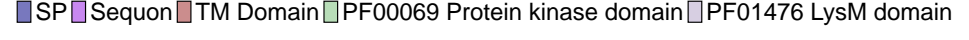
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LGSKIESLNKDVENVLMADVSDGLDKYKMYTFEGLWEATDFGDEGGLGGVYKGGHDEGFVFAIKKMKVWNAAREELKLGKWHGNIKLEGGFDIPKANDYLVVYEVENGSLHBIWLHEDKKENLSWKTRLKAIADVANGLLYHEHTRPRVYHKDKKSNILLDENMRAKVFANFLGAKSGGNATFMHVGTDGGVAPEVLTGIVGSTRKMDVFSFGVLLLELMGSGREAIIDNEGRVYAWVGELEGSEERKEKLGVEWMDDSLREECTHEGVMWMSVMSLSLNKDPSPKPSM

NbL11g20980.1 acylamino-acid-releasing_enzyme-like [MW = 91.1 kDa]

No. of times detected



log(intensity)



Values from



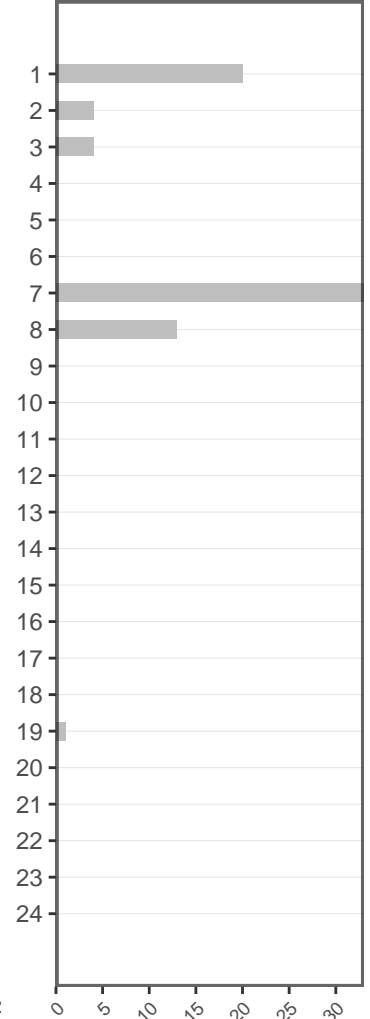
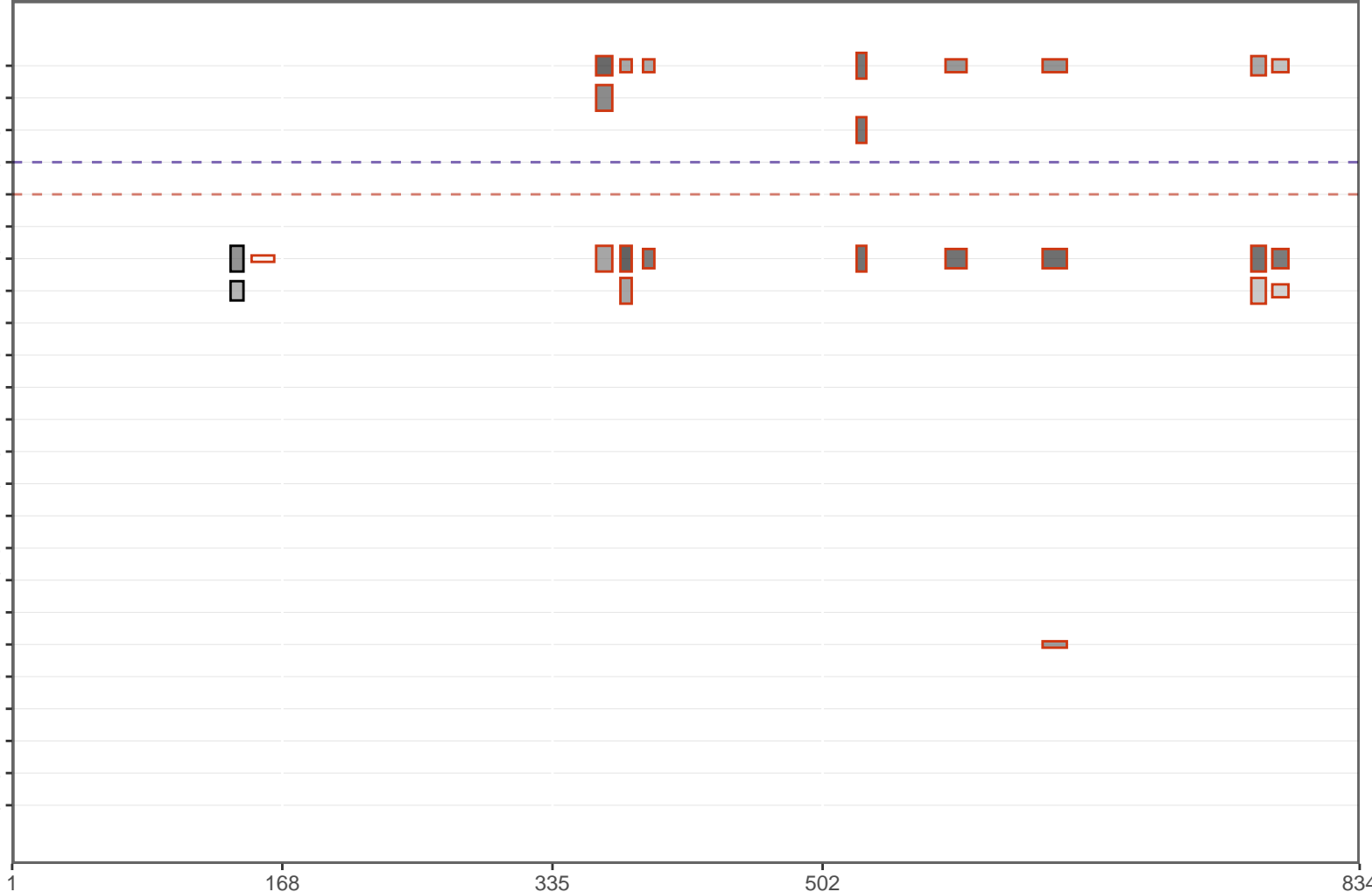
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SSVDSVWVHSATQSLHRIDWSPDKPEPDADIVVPPVMCPEDGGFPLGLVGNLLSKPWFSDGYTMLSSVVGSTEVLSVNLVSGKVRISPGNSGFSWLLADGNVNIWVGSFADVPEIKYGLVAKEVSDASWVLDISSPGRCSEKVMSSGDFEIKPVRDNYKNTGASNPYEIFVSSKSKRNLDPLVLLVHGGPHFISLSSFSKSLAFLSSIGYSLINNYRGSMDGFEEALOSLPKRGSDVDVLAIDHVNMLGLADPAKIVLGGSHGGFLTH

NbL11g20910.1 GDP-mannose_35-epimerase_1 [MW = 42.98 kDa]

No. of times detected



log(intensity)



Values from



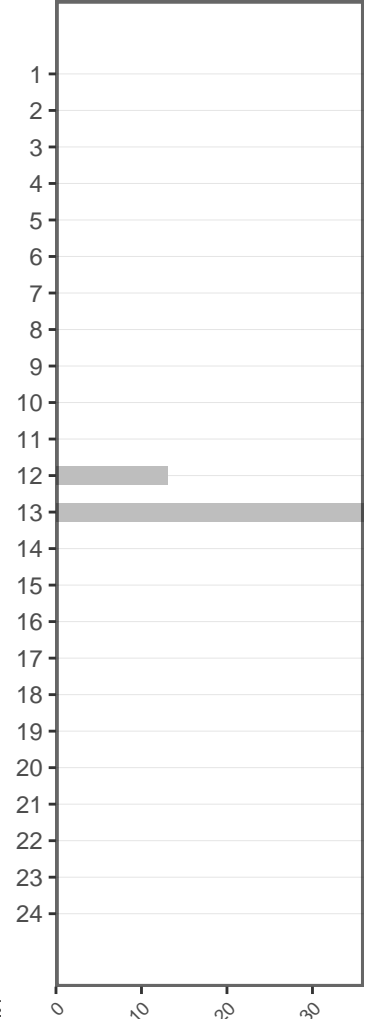
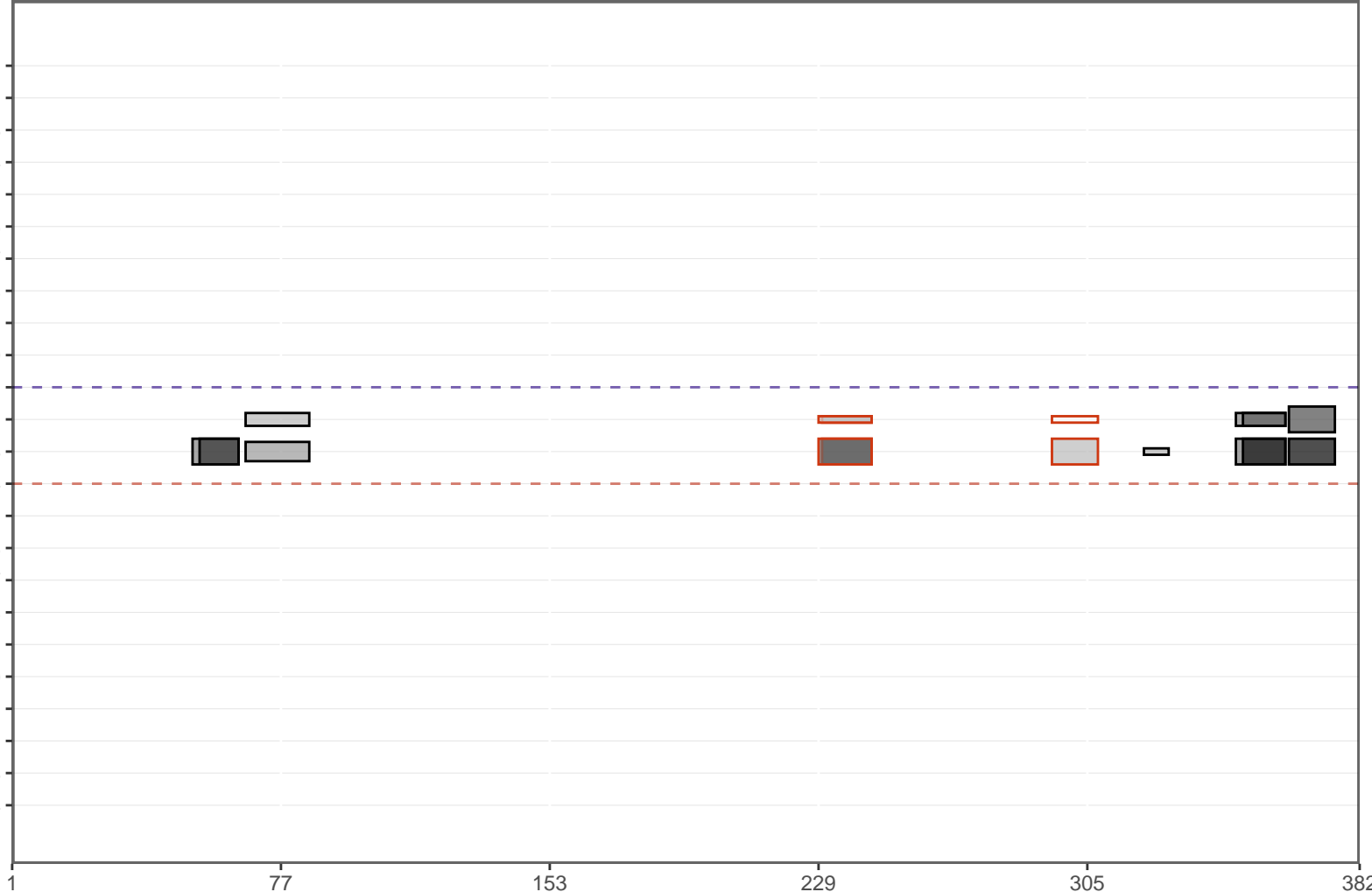
MW indication



Molecular weight



Gel Slice

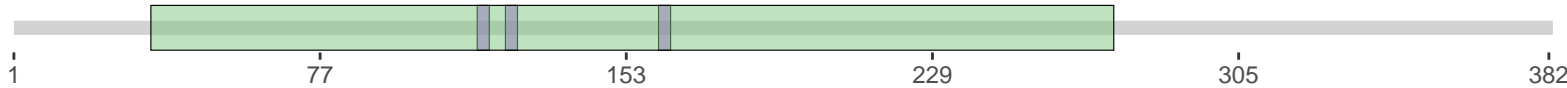


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

SLEKLAATEELCKHYNDKDFGIEGRIGRFRHNYGPFQGTWKGGRKAPAFGRKAGTSADKIFEMWGGDKGTRSFITFDECEVEGVRLTKSDFRPEVNVGSDVMGNMEMAMVLFEDKPLVYHHPGPEGVGRGRNSDNTLKEKLGWAPSMKLDGLRITFYFWIKKEQEKVKGGADVSVYGGSKVVGTDAPVQLGSLRAADGKEI

NbL11g20840.1 sucrose_synthase_2-like [MW = 92.72 kDa]

No. of times detected



log(intensity)



Values from

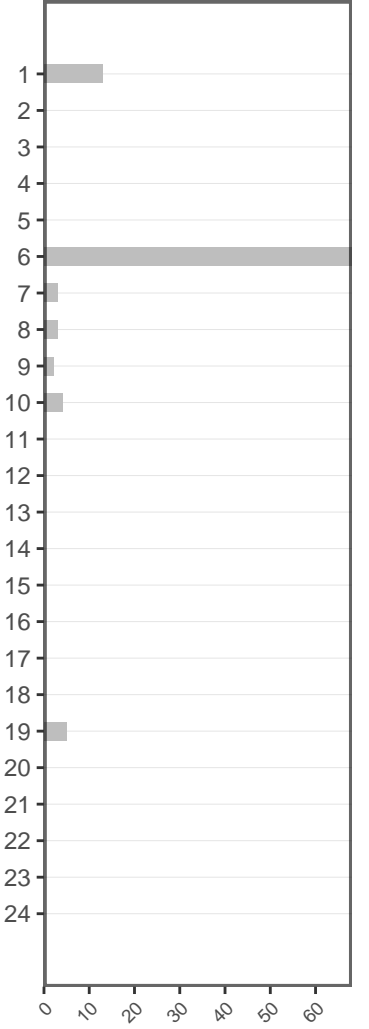
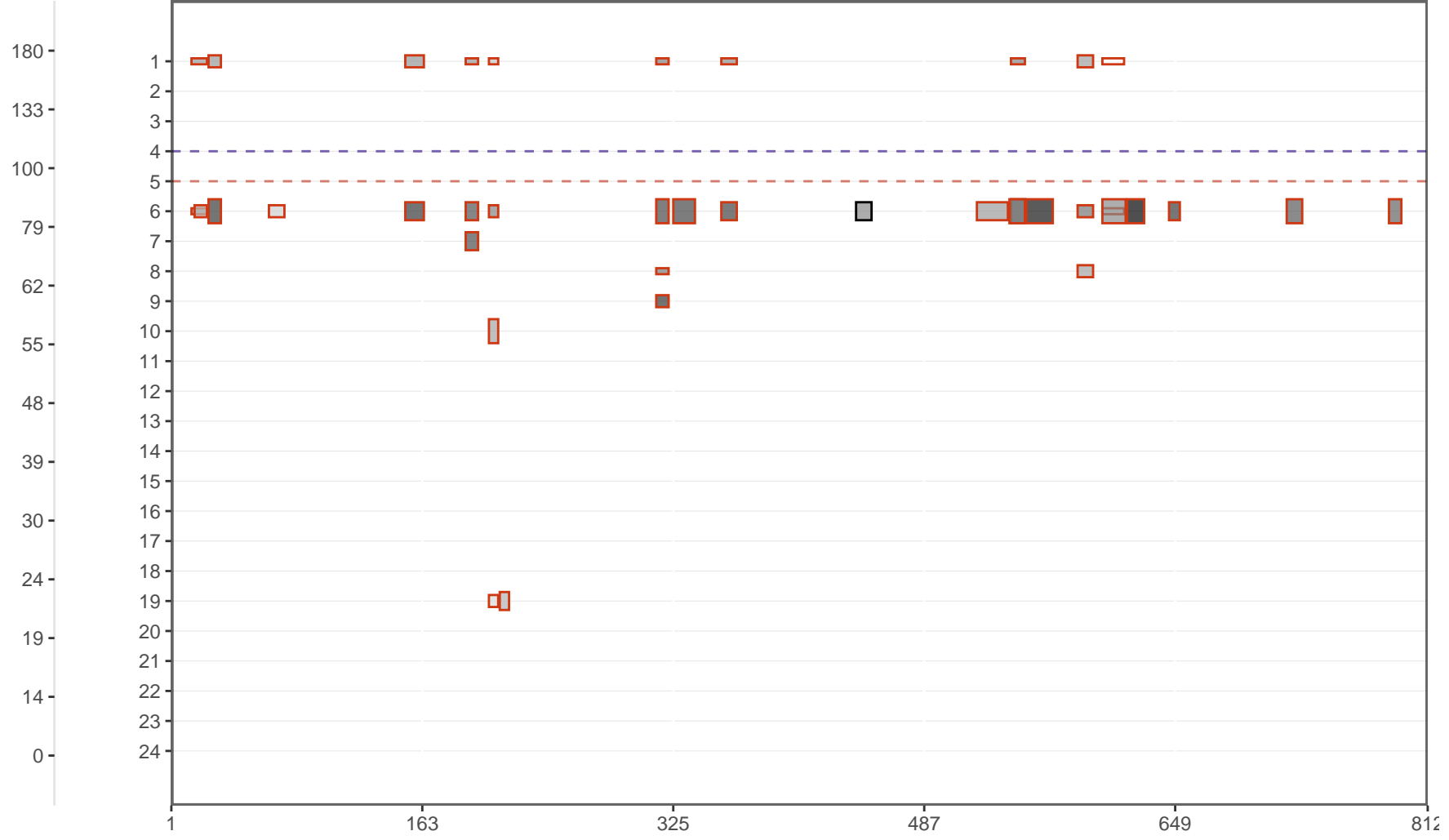


MW indication



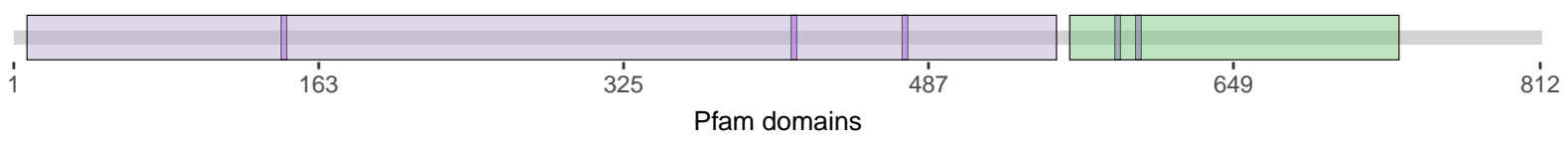
Molecular weight

Gel Slice



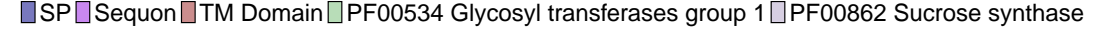
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EKPTEDVAASEMTASLGGKPLHIGVSDGNLVAFLAYKMGVYQGTAAHLEKTKYPSDHYWKKFEKYHFSGGFTADLLAMNSDFITSTYQEIAGTKNTYGVESHYHTAFLPLGLYRVYHGGIDVFDPKFNIVSPGADMAVFPYSDKTKRITSLHSGIEKLLFDPAQNEEHLGNLNDKSKPFSMARLDRWNTGLVGYAKNATRELTLNVAAGVNDVKKSDREITEIKMMALKEHKLDDGQFRWISAGTNRARNNGELRYVADKRGVDFQAFYEAFLGLTVVEMTCC

NbL11g20780.1 60S_ribosomal_protein_L19-1 [MW = 24.67 kDa]

No. of times detected



log(intensity)



Values from



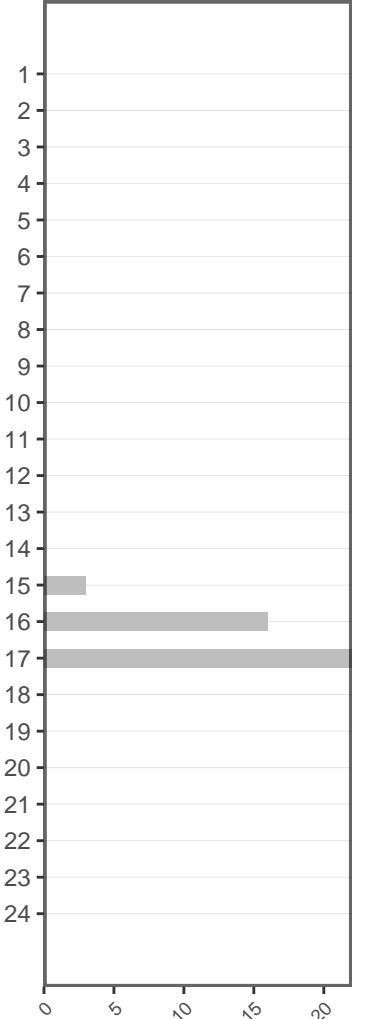
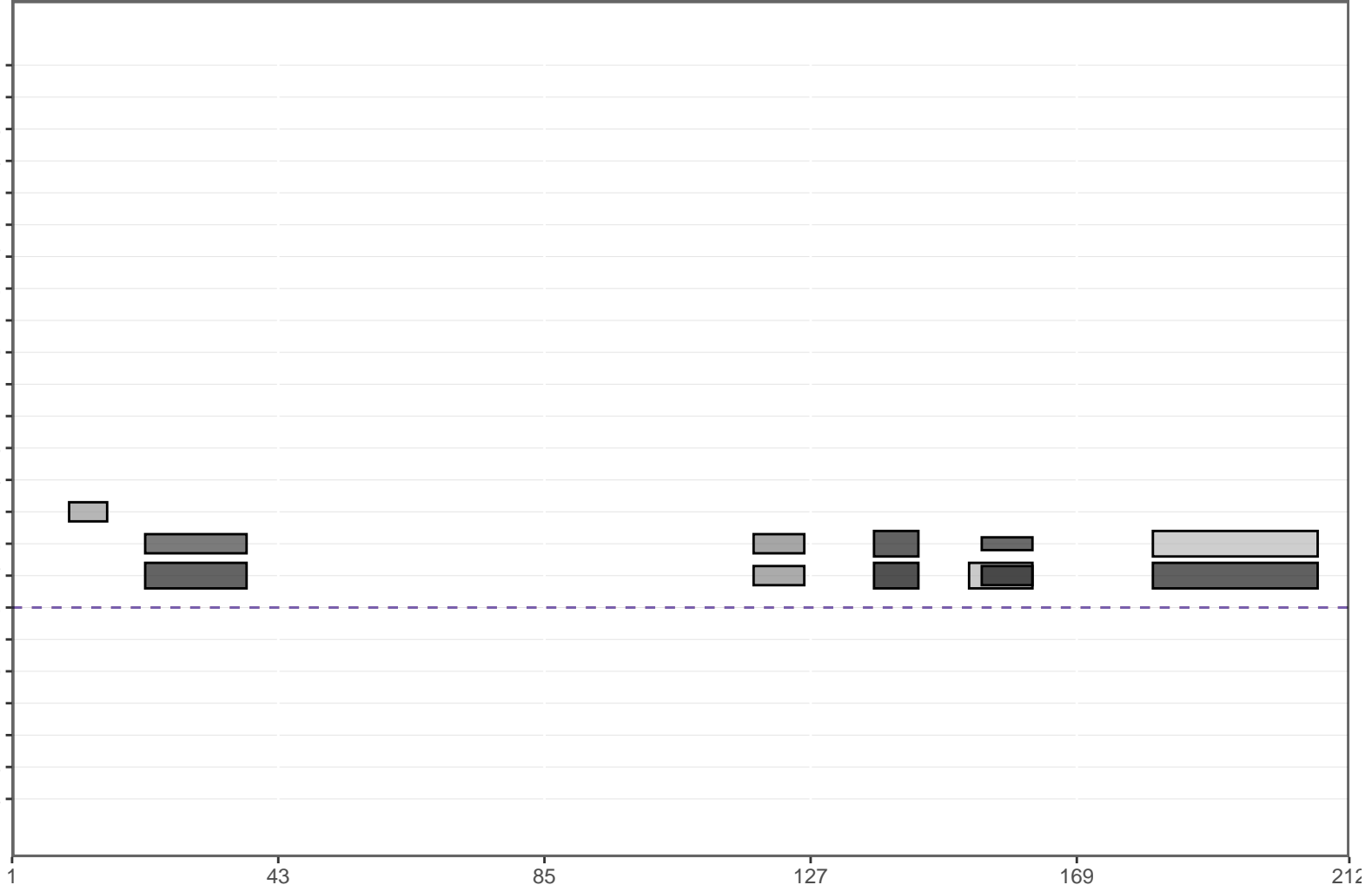
MW indication



Molecular weight

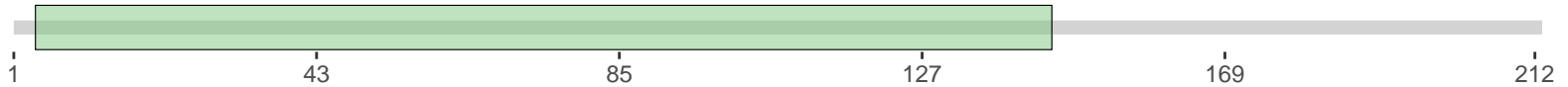


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

..WMRSMRVLRLRLAKYRESKIDRHMHVDMYMKVGNVFNKRVLMENHKTAKAEKREKLSDFEARRAKNKASRERKRFARREERLGGPGERPVQPAASATPQTAGGGKSKK

NbL11g20760.1 probable_polygalacturonase [MW - SP = 46.86 kDa]

No. of times detected



log(intensity)



Values from



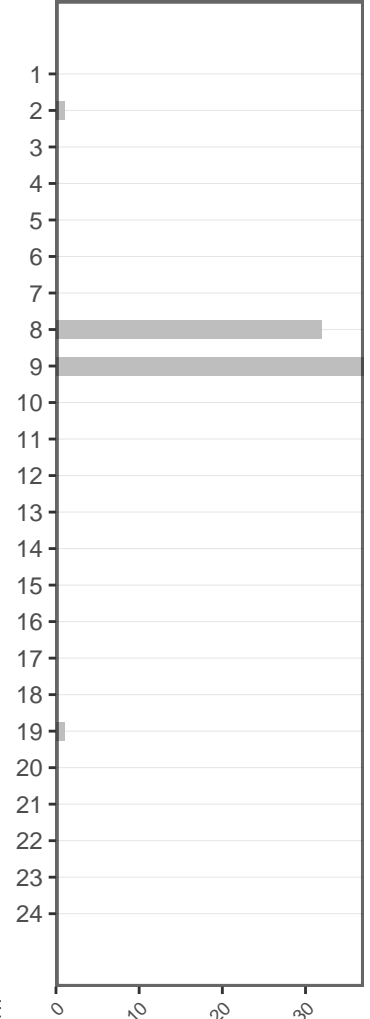
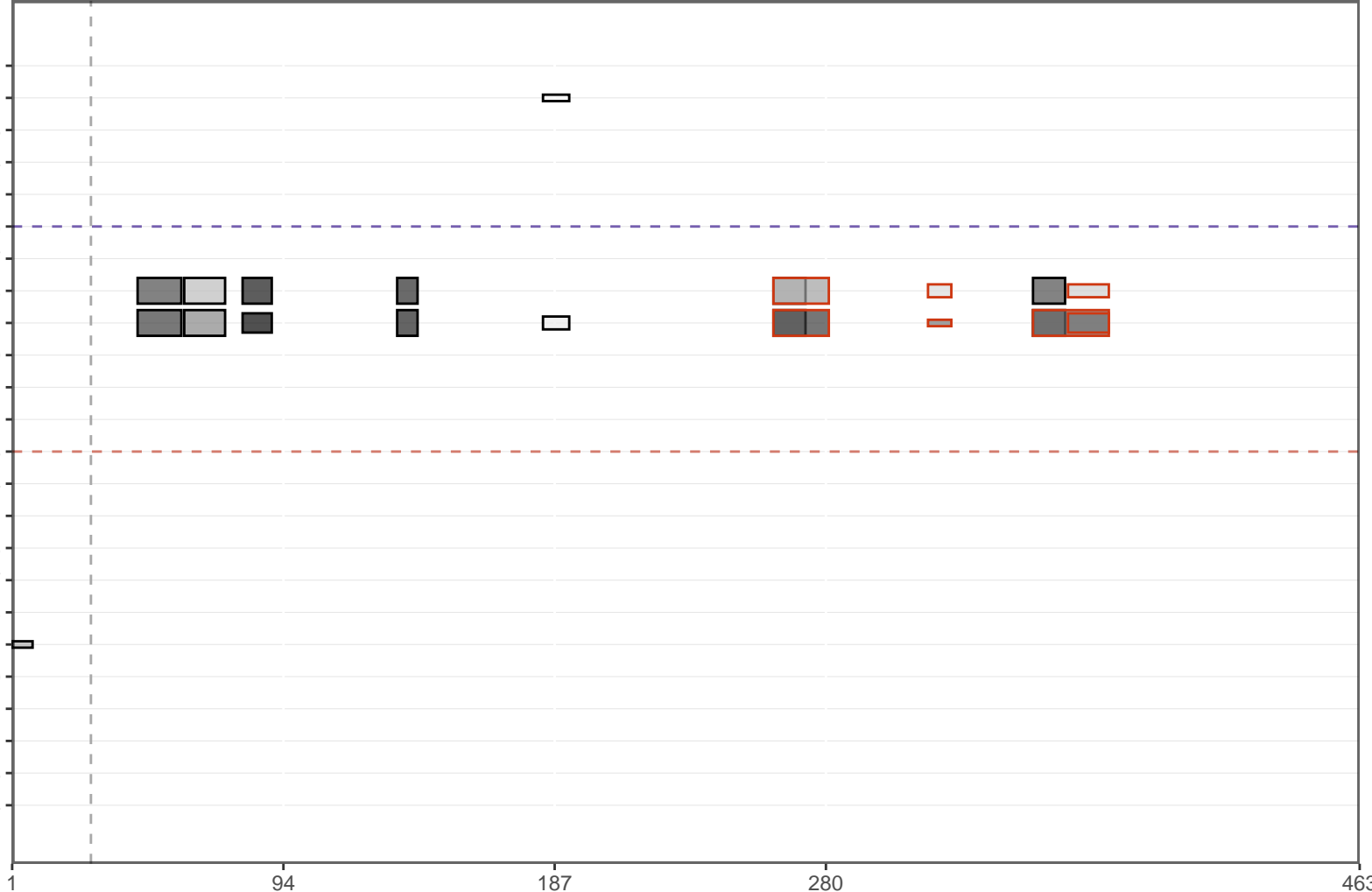
MW indication



Molecular weight

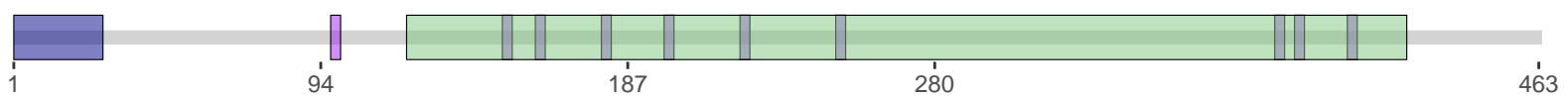


Gel Slice



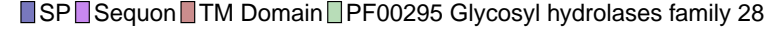
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

VQLNLTVHSPQCSPTNGIVFDSEEHVCIENSNTIGYDAVLLKSGWDEYGVGKPTSNVHVRGVRLLQSSAGSAVAFGSEMGGISAVLVEHBLRNSLFGELKTAGRGRGVKIDLFTNVVMENVGVGKATGYVDSHPDEKYDPSGLPIVSGITFKDVGVTNBSAGNFTGLSESPFTSLGLENSVFSIS6SDPTFWLQSDVSGSSENVPFPCPELQGLSLSVSSAGFALFNPVTEVAVL

NbL11g20620.1 CTP_synthase-like [MW = 61.81 kDa]

No. of times detected



log(intensity)



Values from



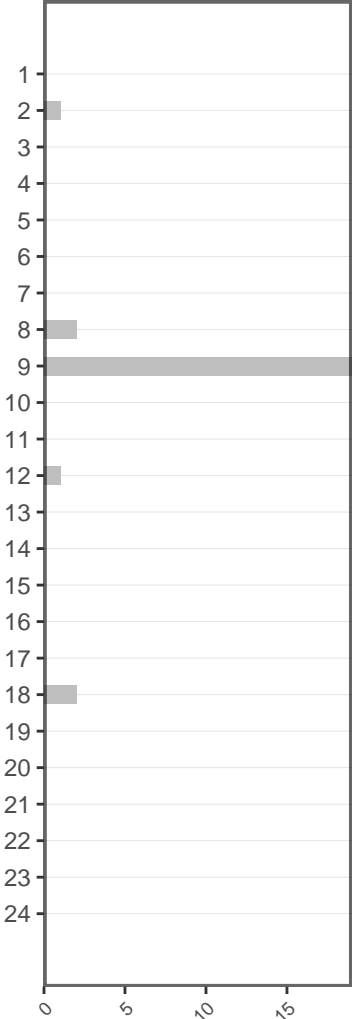
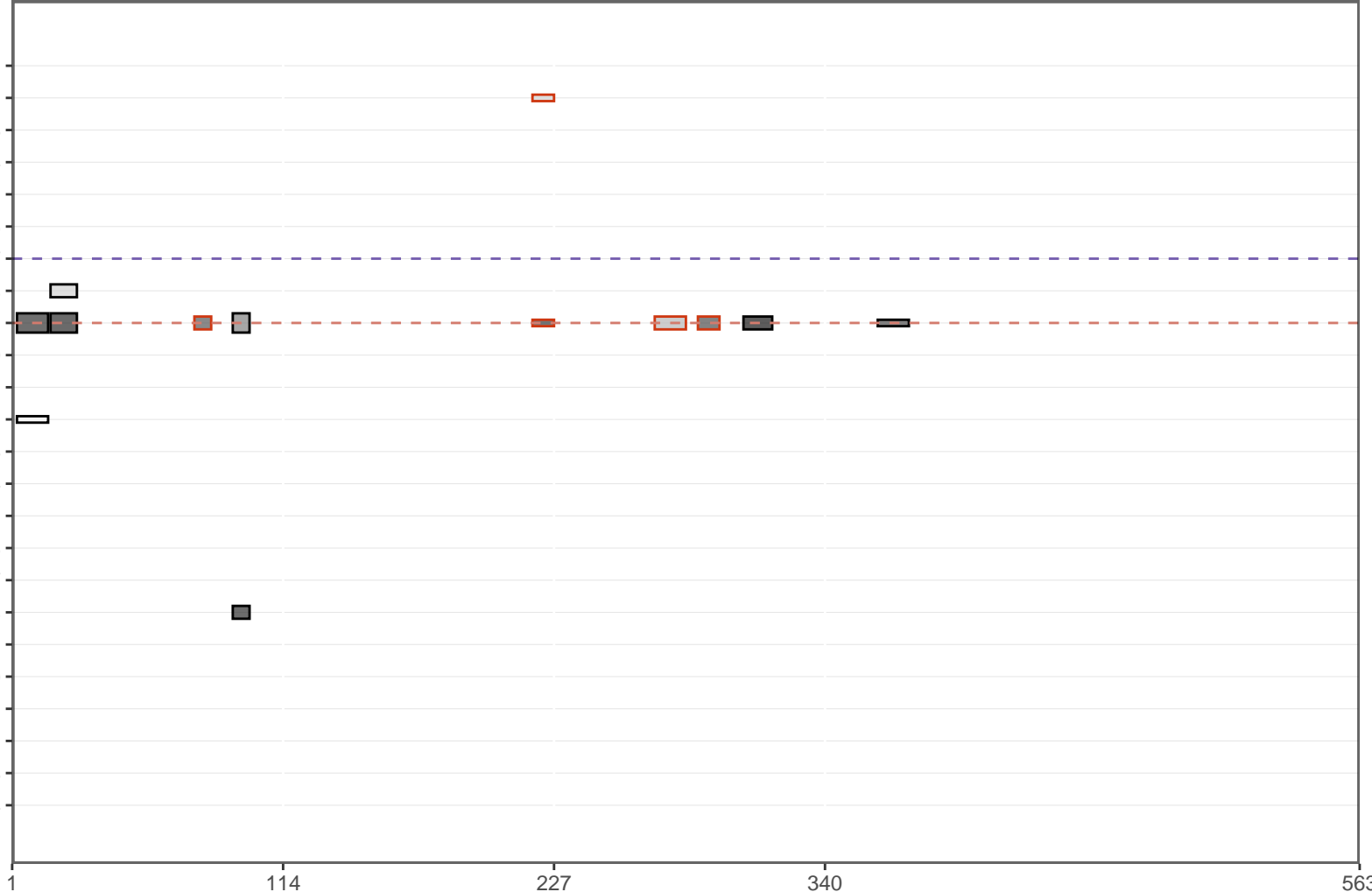
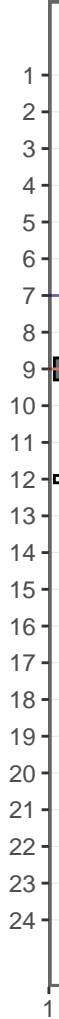
MW indication



Molecular weight

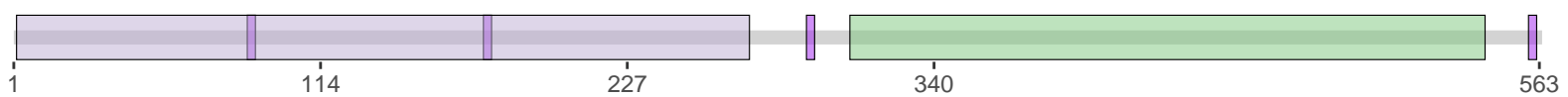


Gel Slice



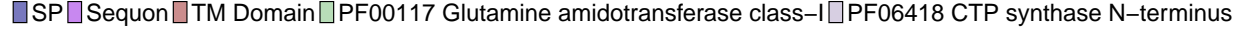
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DLLSVAKPYDLREWTRRAETFNLTKTVRIMAVGKIVGLTDSYLVKALLHAGIAGGKPKPSIDWAAASDLEDDGSAQSAPEAVATWETLRGAAGVLPGGFGDRGKGMILAAARYARENIPYLGDLGMDISVIEFARSLVHMKANSEEFDPQTPDLVVFMPGEGKTHMGSSTMRLGSRKTLFQTPDQITSKLYSNKIVYNERHRRHRYEVNPEVYGLTEEGMRVFGDESGKRMLELPGHRFYVGVQDFHPEYKSRPGRPSAPFLGLHMAATGLEAYVQTQNGSI

NbL11g20540.1 probable_beta-D-xylosidase_2 [MW = 87.92 kDa]

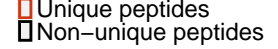
No. of times detected



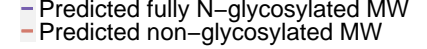
log(intensity)



Values from



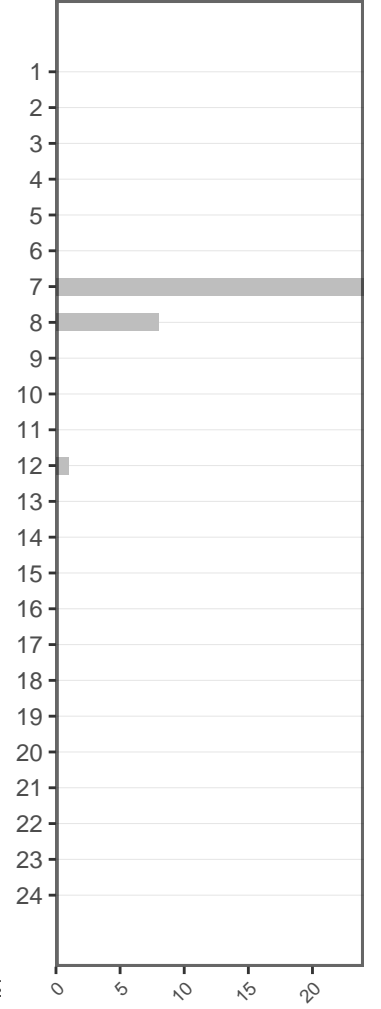
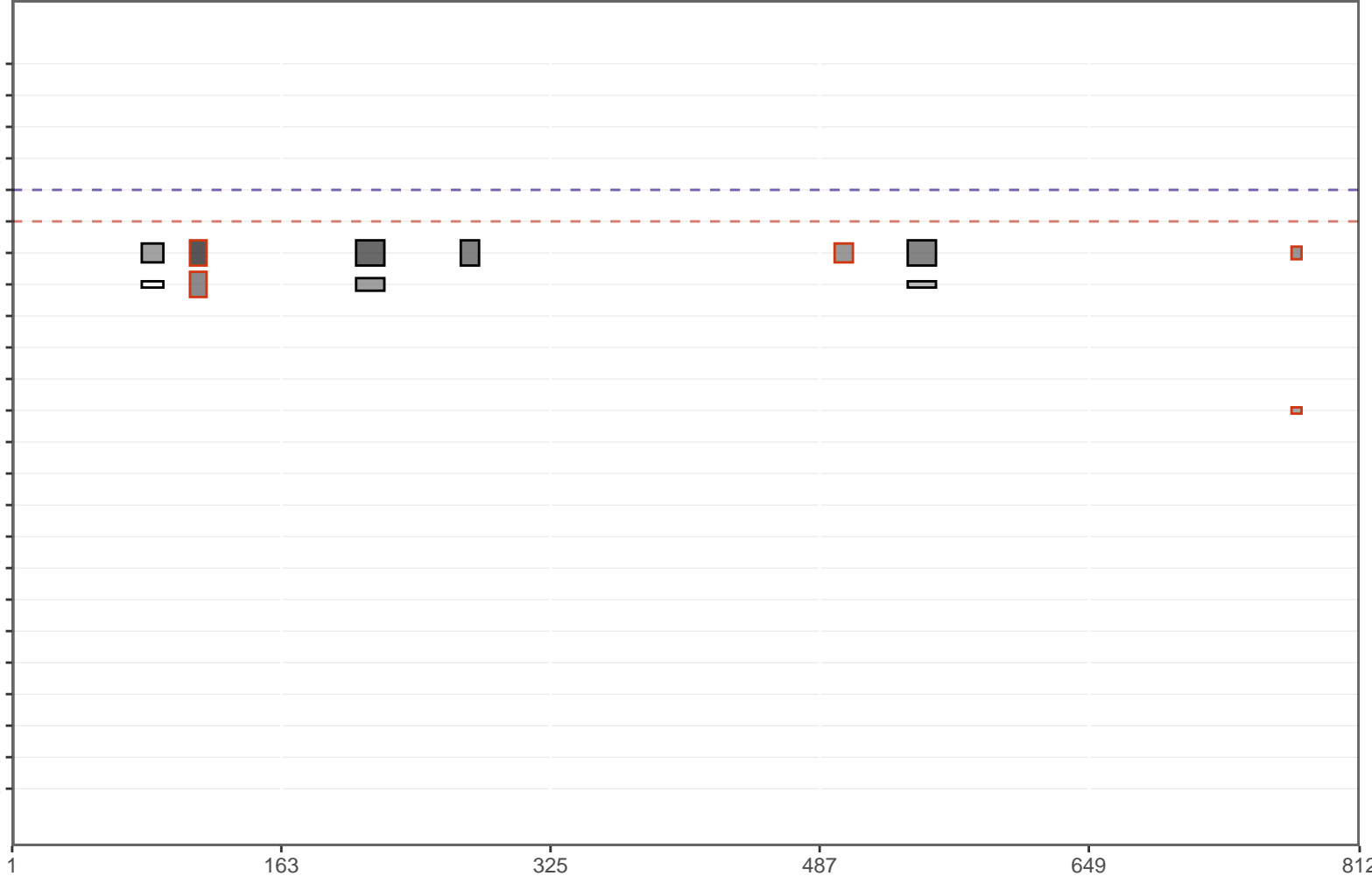
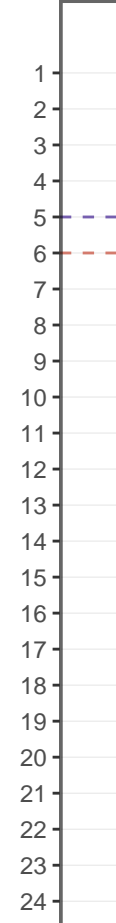
MW indication



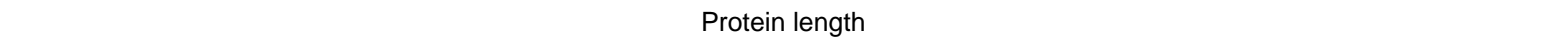
Molecular weight



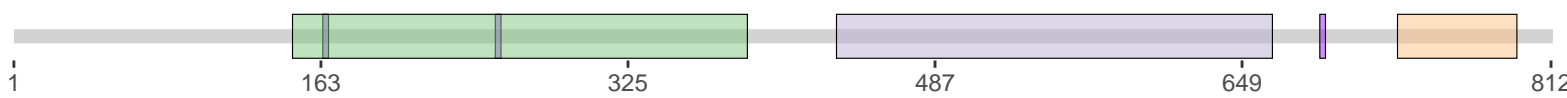
Gel Slice



Protein length

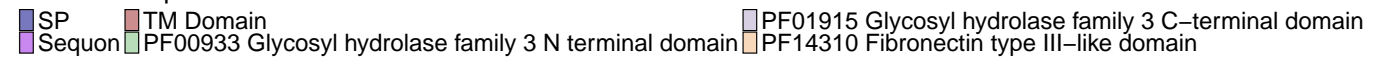


Peptide counts over 4 repeats



Pfam domains

Pfam Description

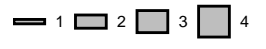


Protein sequence:

NTVAQMLRGMFDGEPGAPYGHGKPKVCGEPHDELAEARQGGVLLKKNHGPALPLSRPRHREVAWVGNSSVFLTMIGNVAGVAGVYTSPLGGIAKYAKTHRGGGSDVAGSDRDLFPGAVDAARGADMTLVMLGDDGSEAEFRDRTGLLLPGFQDHLSDVSKASRGPVILVMSGGPVDTFAEKDRIGGVVWGVYDQAGAAADLVFGAHPGKLPMTWVYDQEVYLNLLPMTTMDMRANLAKGVPRRTVRFYKGRPLVYVFGHGLSVTKFTINTAEAPMLAI

NbL11g20300.1 probable_pre-mRNA-splicing_factor_ATP-dependent_RNA_helicase_DEAH2 [MW = 82.14 kDa]

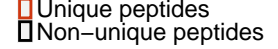
No. of times detected



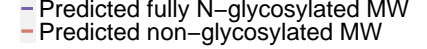
log(intensity)



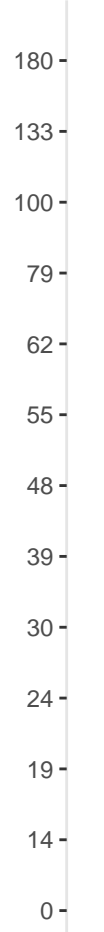
Values from



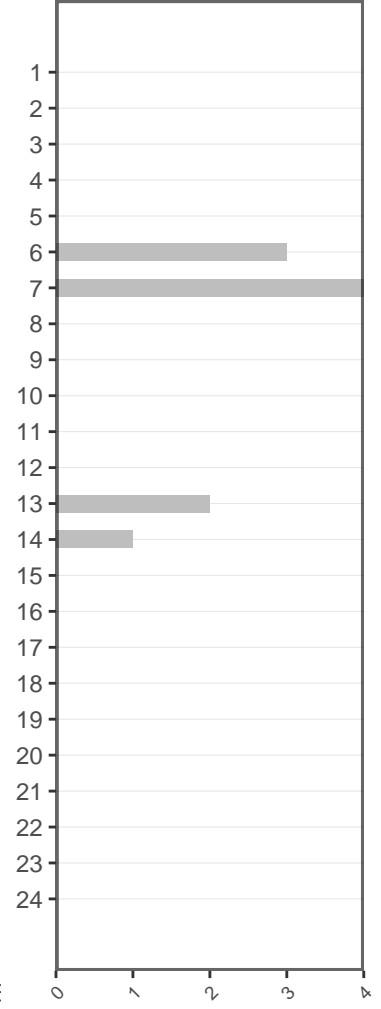
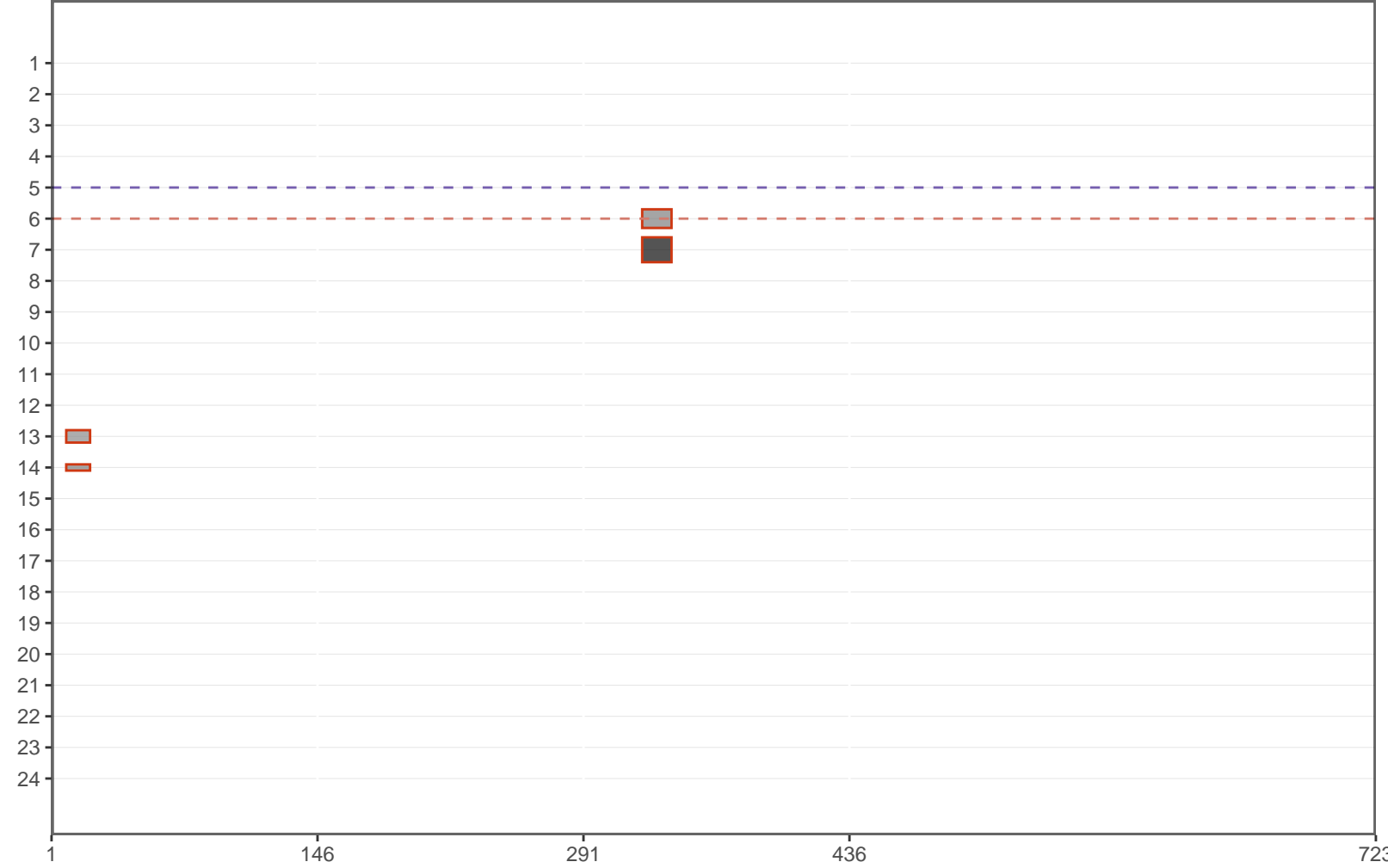
MW indication



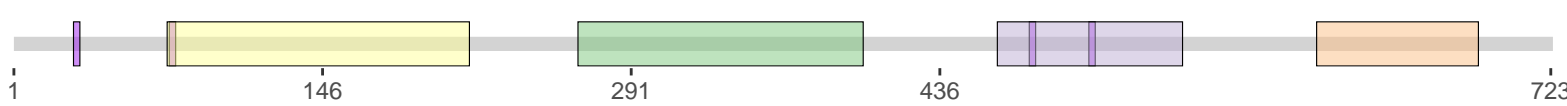
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00271 Helicase conserved C-terminal domain
- PF07717 Oligonucleotide/oligosaccharide-binding (OB)-fold
- PF04408 Helicase associated domain (HA2)
- PF13401 AAA domain

Protein sequence:

ISLTIDGIVYIDPFGAFKGVYVNRVREISLVSPISKASAHGRSGRAGRTPQKCFRLYTEKSFHNDLGPQTYPEILRSNLANTVLTLLKLGIDDLVHDFDDPPAPETLMRALEVLNHLGALDDEGNLTRLGEIMSEFPLDQMAKMLVVSSEFNGSNEILSISAMLSVFNCFVPRPEAQKAADEAKNRFHGHIDGHITMLNYYHAYKNTFEDPGWQVDFENFGRALKSADNVRQQLSRIMARFNKLGISTDFNERNYYNIRKAMLAGYFMQVAHLERTGHYLTVDKNOV

NbL11g20280.1 nifU-like_protein_1_chloroplastic [MW = 23.39 kDa]

No. of times detected



log(intensity)



Values from



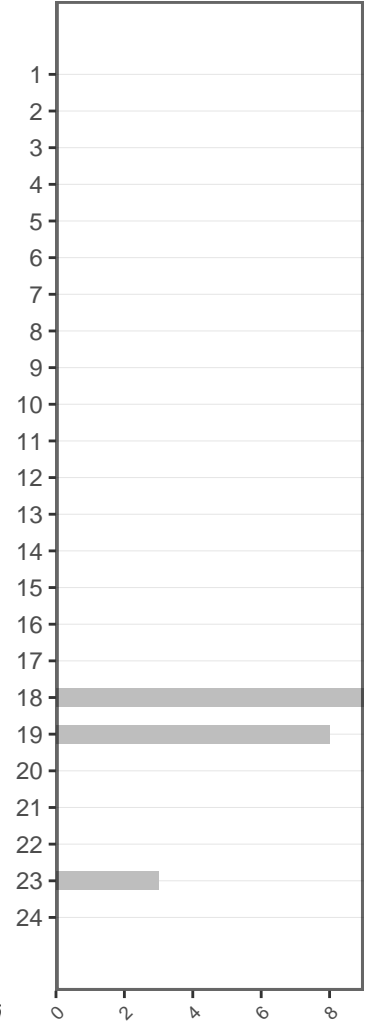
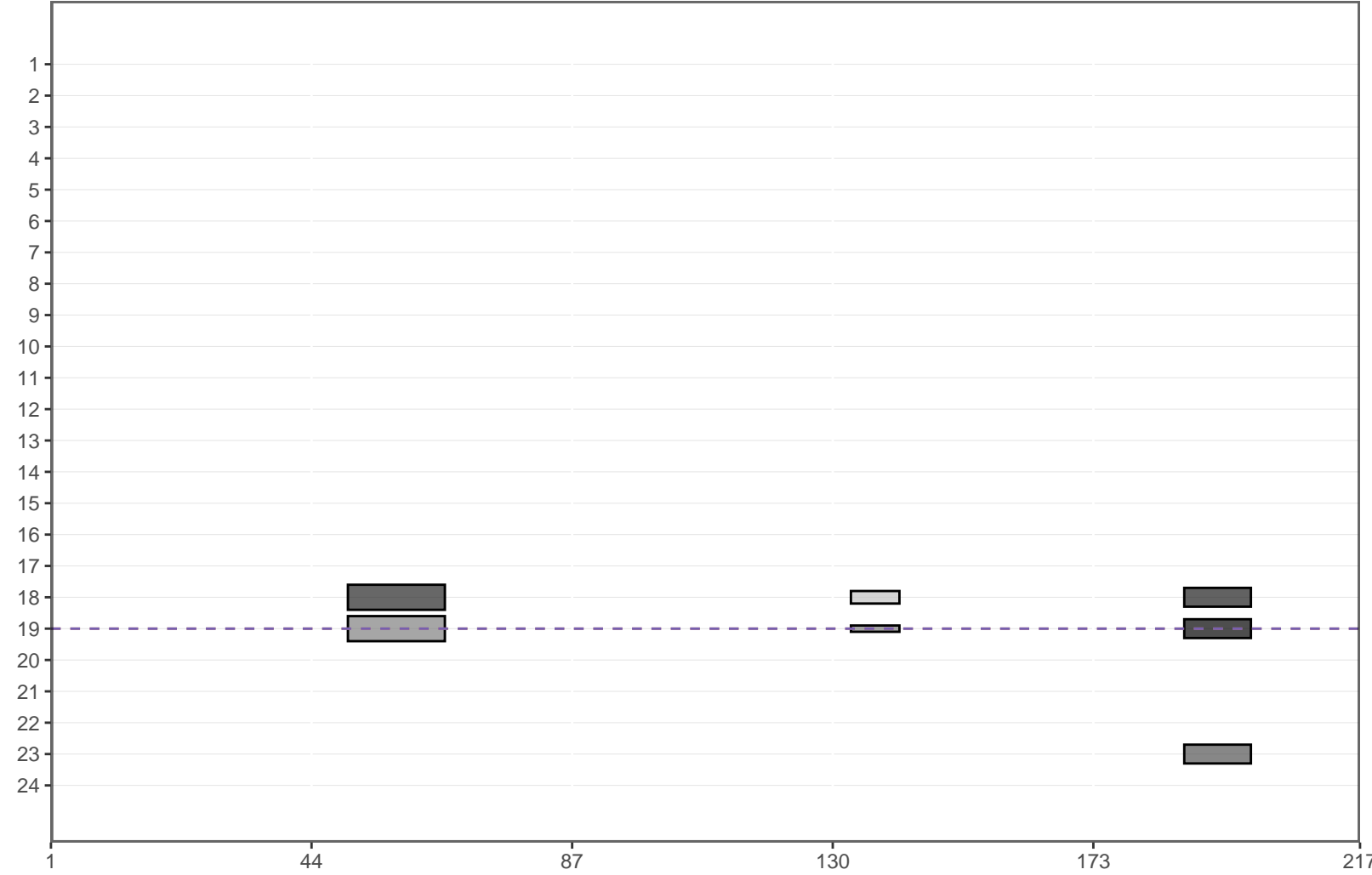
MW indication



Molecular weight

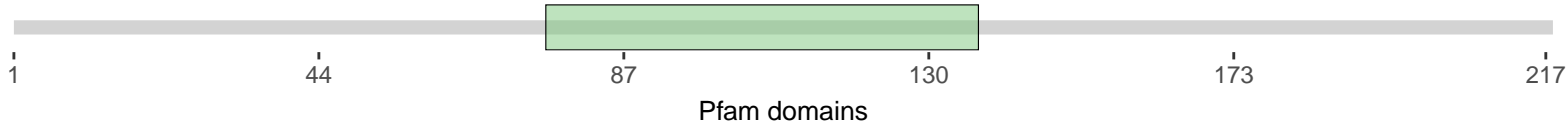


Gel Slice



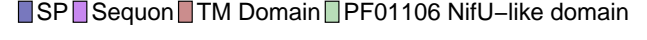
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VSVEDGVVSLQLOGAGECPSSFTTMMKMDIERVLUKEKFGAEAKDRGVYDEGVVETTVVEAANHLDLRPAINKFGGSEVLEVEEGNCKVYVPSDSIGSGKAAIKKFPDINNVVFTA*

NbL11g20170.1 uncharacterized_LOC104217660 [MW = 27.78 kDa]

No. of times detected



log(intensity)



Values from



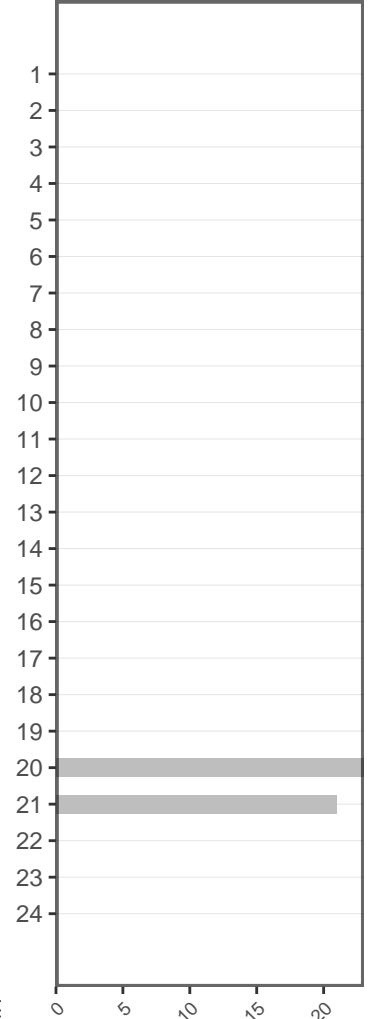
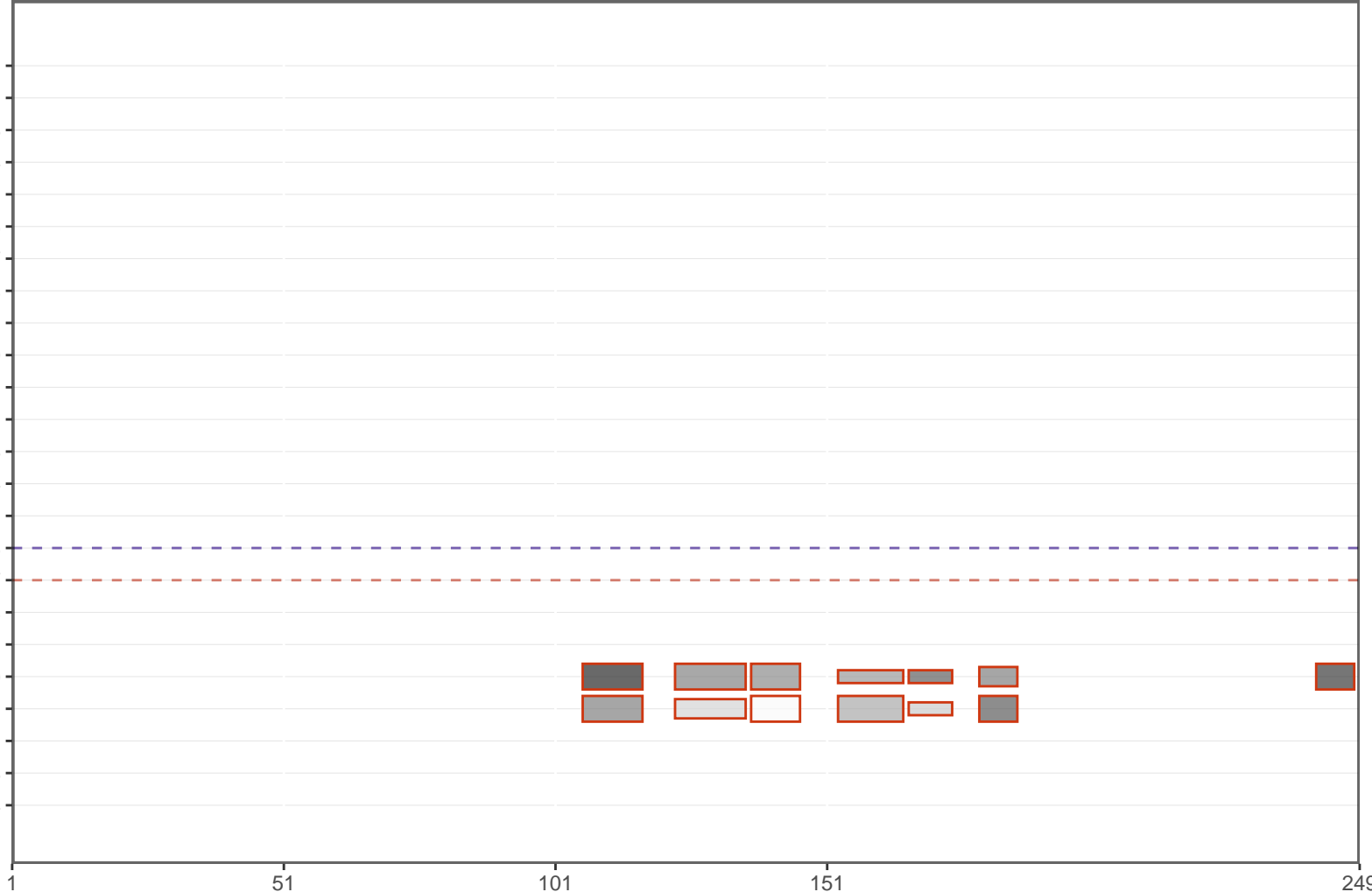
MW indication



Molecular weight

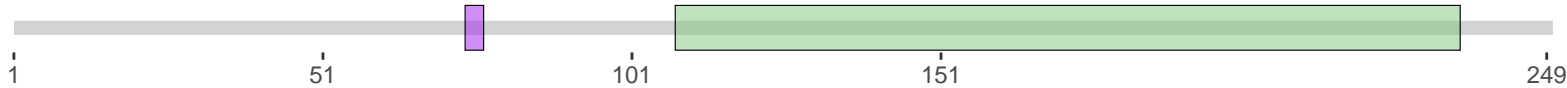


Gel Slice



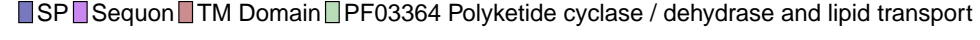
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SVAYKCYSDREAIQGMFFISWLEKPKLGRWBLKYKAFGGDIEVSWLARNMQPTTPNQHWRLEGLPNRGAVRFFPKGPSGDTIEFTVSEYVQPLLVPASALQPLENLLGRGLERFATFAKYSADTPK

NbL11g20090.1 uncharacterized_LOC109224790 [MW - SP = 50.26 kDa]

No. of times detected



log(intensity)



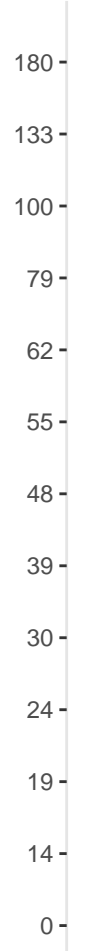
Values from



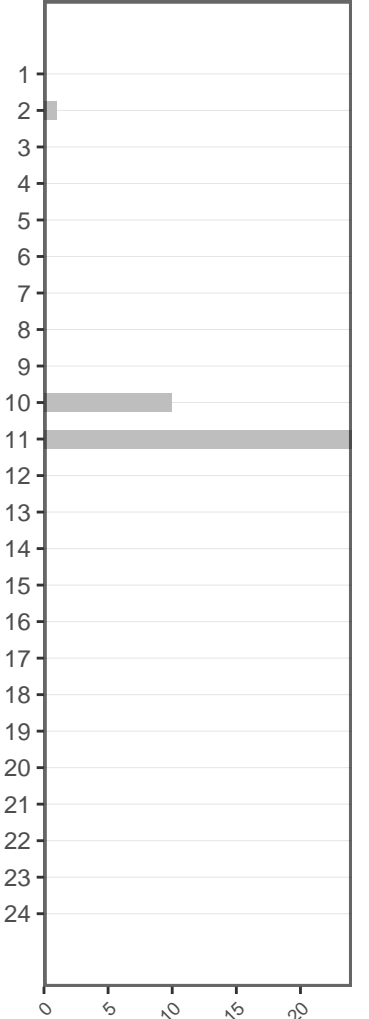
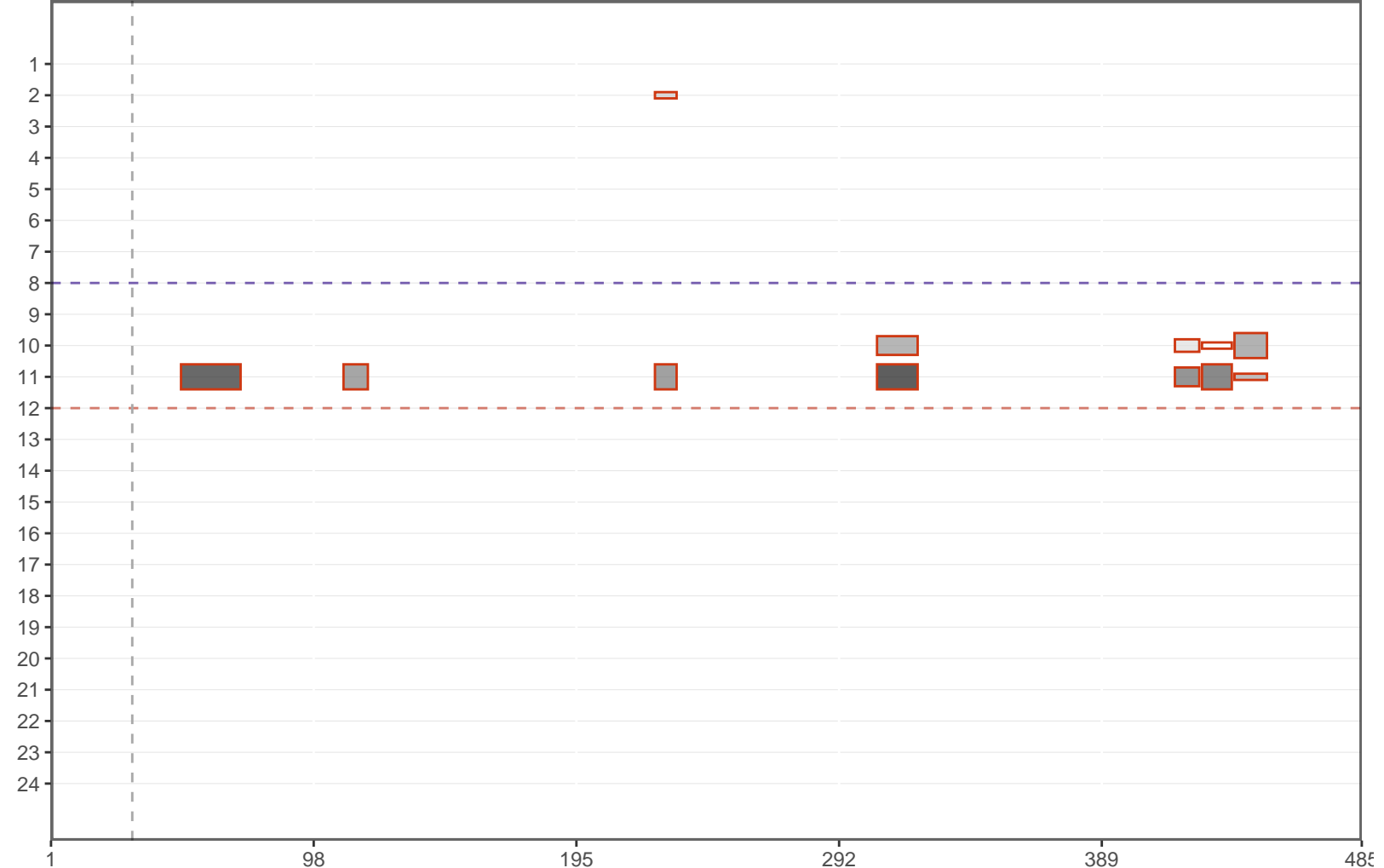
MW indication



Molecular weight



Gel Slice



Protein length

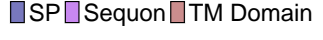


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

GWVFKIKLRTSKLPLVWMLMFRADATKGFSGGGVHYDTRGMKTLPEPNNFKVWLFLEWKGGGGPKSGDFYLHDGSCWKNNGAPGDGVDLTDTRVSEMINPETPAWGSFTNGNCPPHFHTPNNTKIYRNDTSHFPYSVHHYVAPGNAGHELEKPYGTGDPVSNPQAGELVQLLPHPIWADVGYPSKGGGGWVGDGRTWELDVGGLSSRLYFYGDPTPARRIWTSLELVGTEIFVSNKDEWAEWTLSDFDVLLTS

NbL11g20060.1 L-cysteine_desulphydrase [MW = 50.29 kDa]

No. of times detected



log(intensity)



Values from



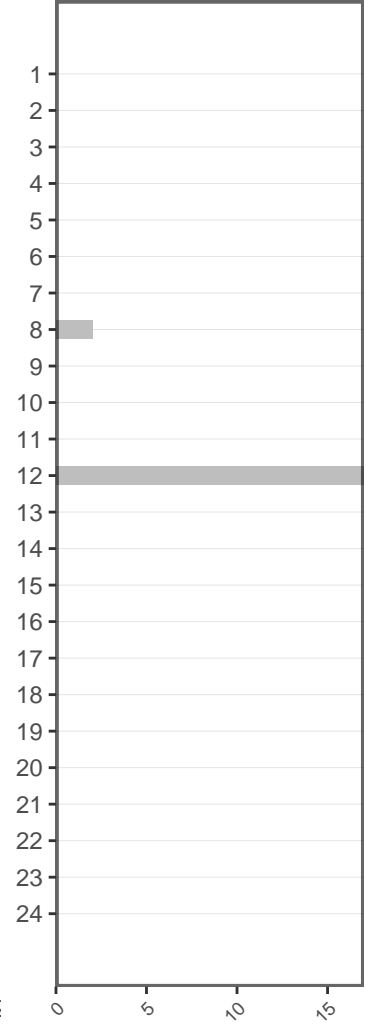
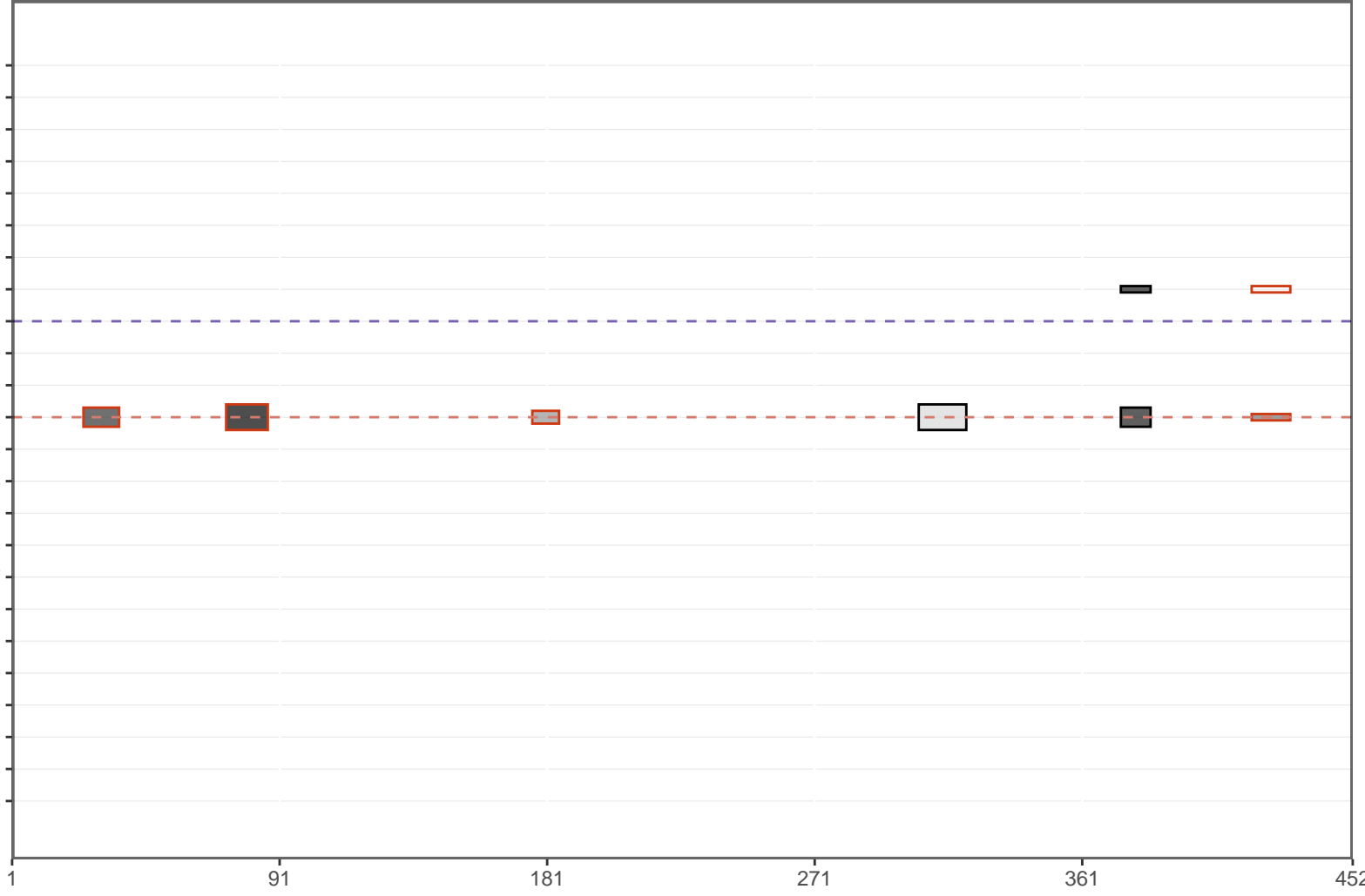
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IPVRLDKYKREEGVERVFDVAHAGNHHVDVEIEIGADEVYENLHKWFFGPPSVAFLYCRKSPVSPDLHPVVSHEYGNGLAIESAWGTRDYSGLVPELFINFEFGGEEIRMRNHNVAEMGGMLATAWGTLGGPPDMCPGMAMVGLPAGLRHLSNDALNLRTRLRGHLGIEVPHYQEKYFQGGDDGVTGVVRIHSGVYNTVDDYLLKLDALGLVHDGVTCKMLSP

NbL11g20050.1 protein_transport_protein_SEC23-like [MW = 95.02 kDa]

No. of times detected



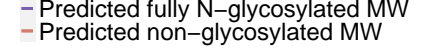
log(intensity)



Values from



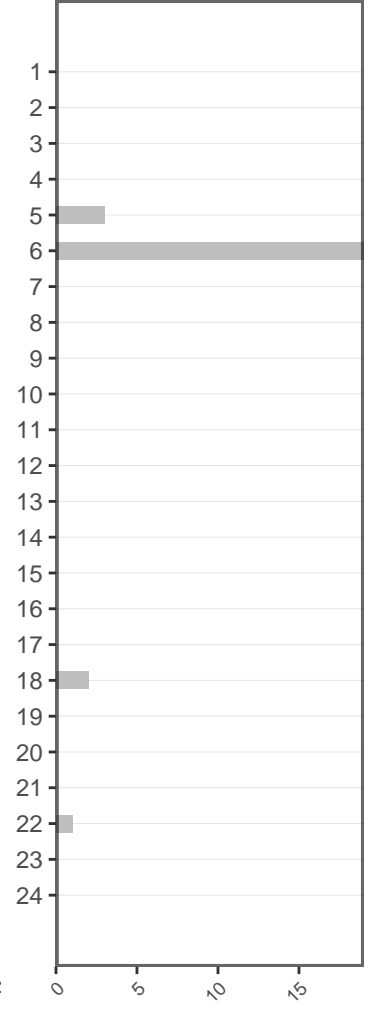
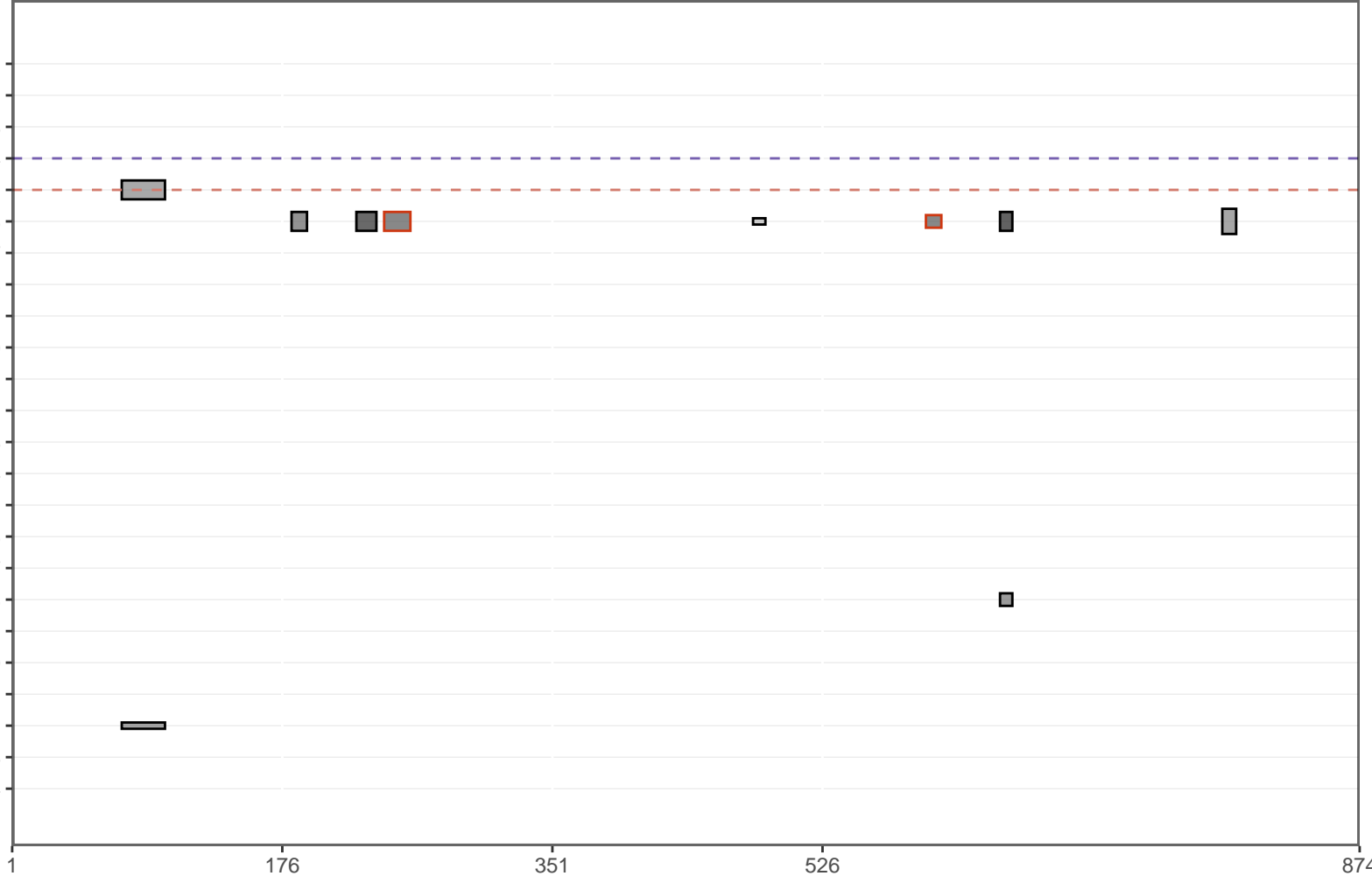
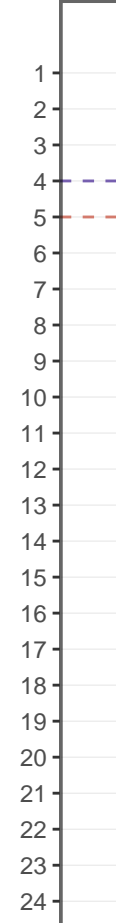
MW indication



Molecular weight

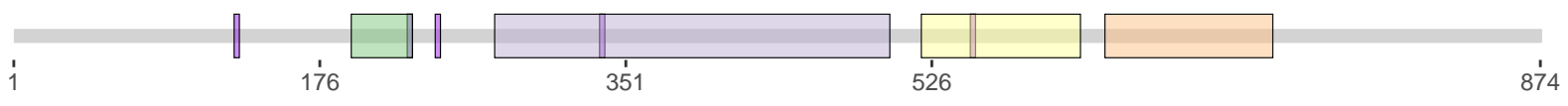


Gel Slice



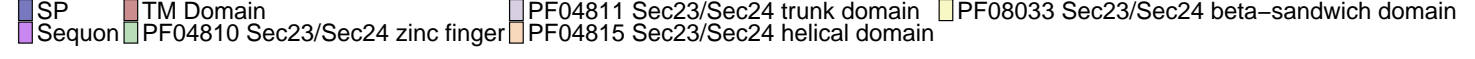
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGGPNTCGPGLVPSFSGHPNVAHMERALKWMTLGRFAFRKNTVDLGGTGPVWVPLGFLAKASGGVLLHDDFGEAFQVNLQRA6GRAAGSHLLLEVRGSEDFVSGVHGPGEEAAHVDSNETFRKNDLALVQMLSVETG9SFALSMETKRDIKRDFVYQFAFKFLDVFVQ6SDTRVTVRLPFTVDGVSGLLESVQDEVAWLLAKRTRLRAKYANDALDMRVTVDERKIDTSKFG6MPQ6KLYRFRPRELVLPELLFHLRGRPLG6LGHEDERSVLRNLFNAGFD

NbL11g19920.1 ADPATP_carrier_protein_1_mitochondrial-like [MW = 42.33 kDa]

No. of times detected



log(intensity)



Values from



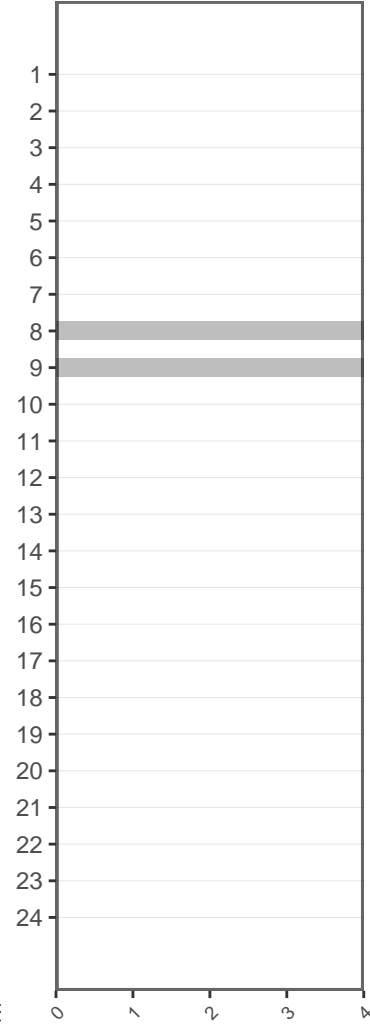
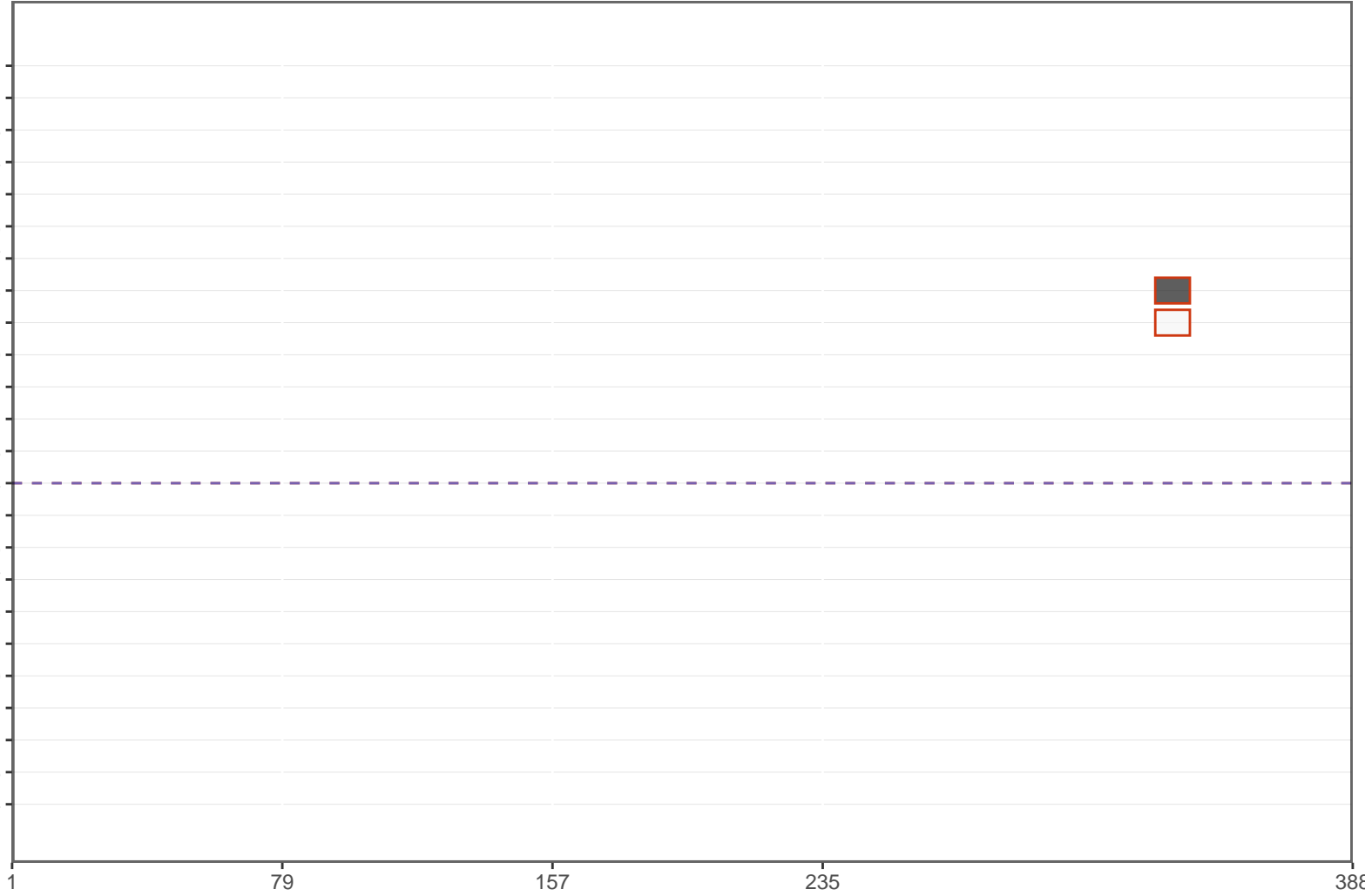
MW indication



Molecular weight

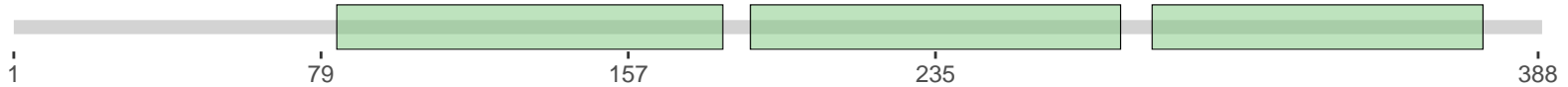


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ERDGYKWFACNLSGGAGASBLFLVYSLDVARTRRLANDAKAAKGGGERGFNGLPDIYRKTKEGDVGLYRGFTISGVGVYRGLVFGVYDGLKPVVIVGNLGDSPVAFSLGWSGITGAGLSVPIDTRRRMMMTSGEAVKYKGLDFAFSQIMRKEGAKSLFKGAGANLRAWAGADVLAGYDKLGLVYLGKRYGGGGG

NbL11g19860.1 uncharacterized_protein_At4g28440-like [MW = 16.17 kDa]

No. of times detected



log(intensity)



Values from



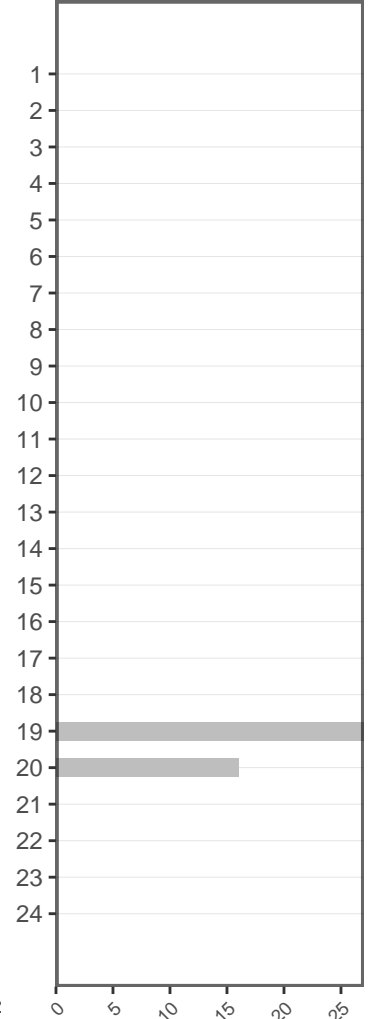
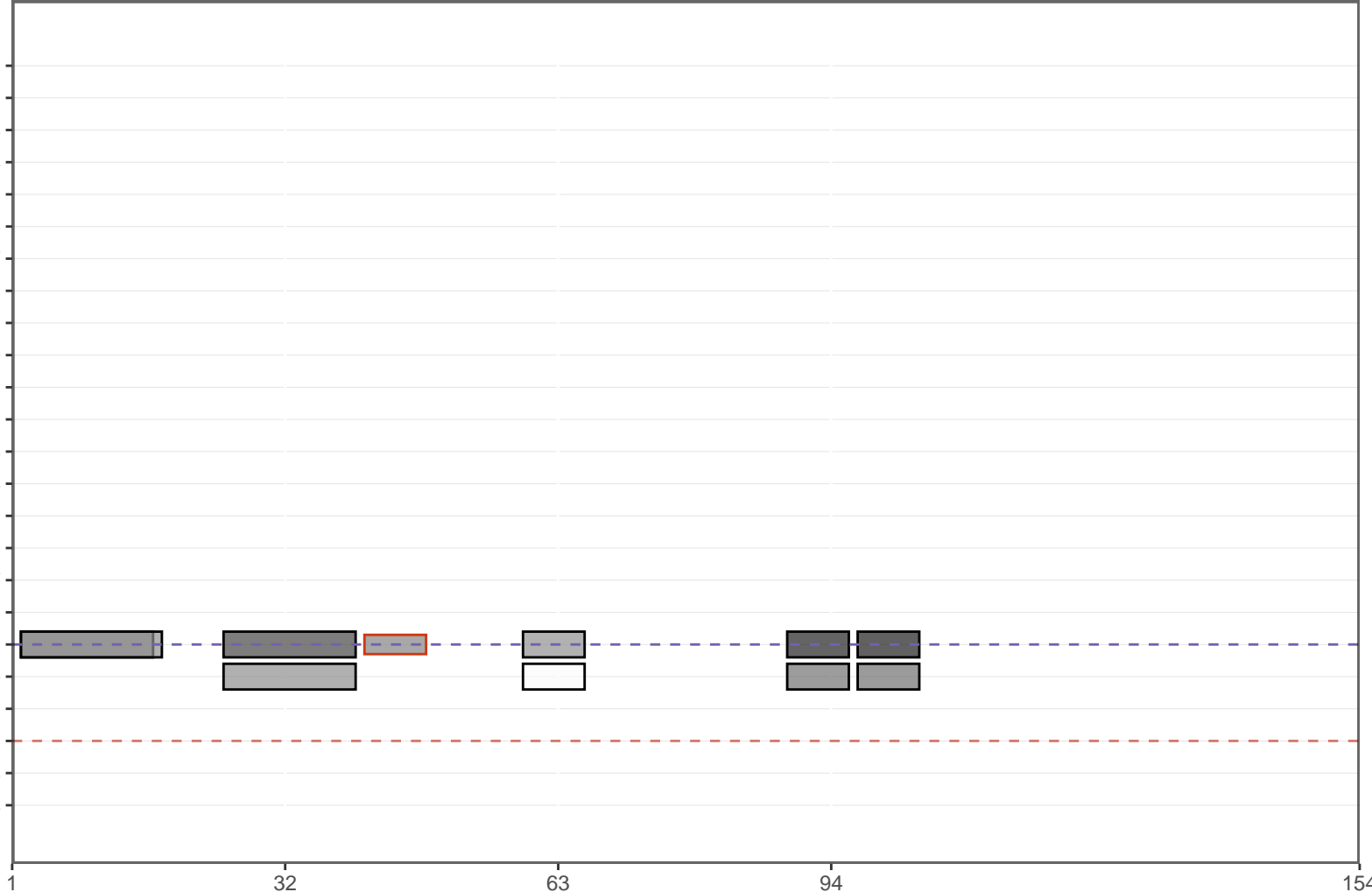
MW indication



Molecular weight



Gel Slice



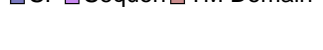
Protein length

Peptide counts over 4 repeats



Pfam domains

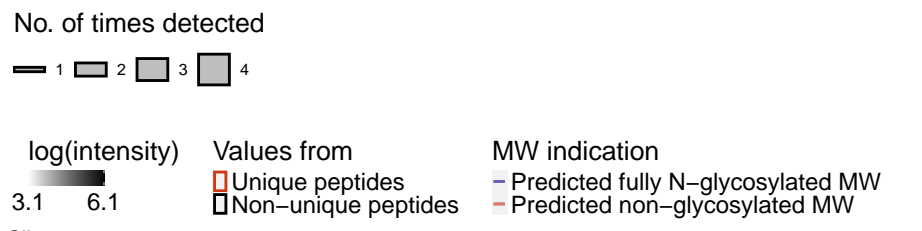
Pfam Description



Protein sequence:

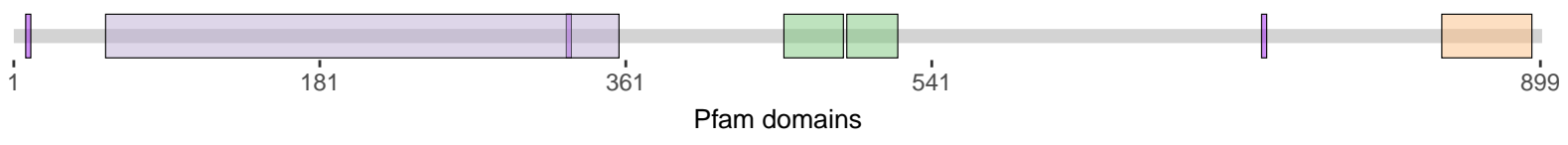
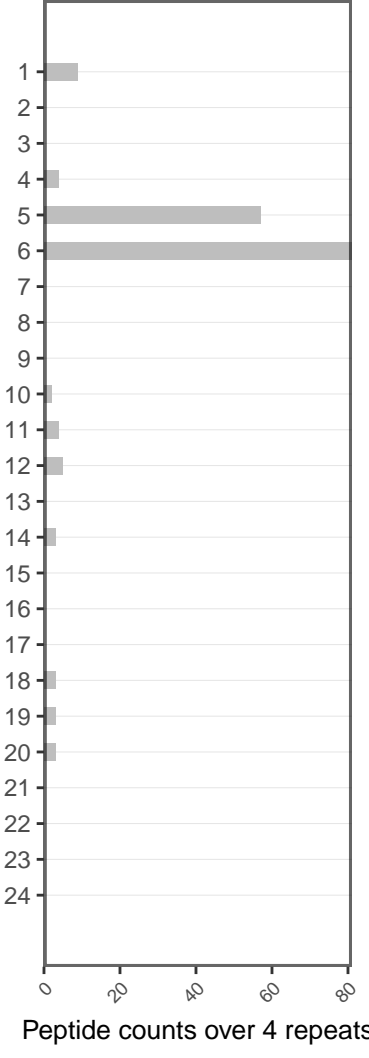
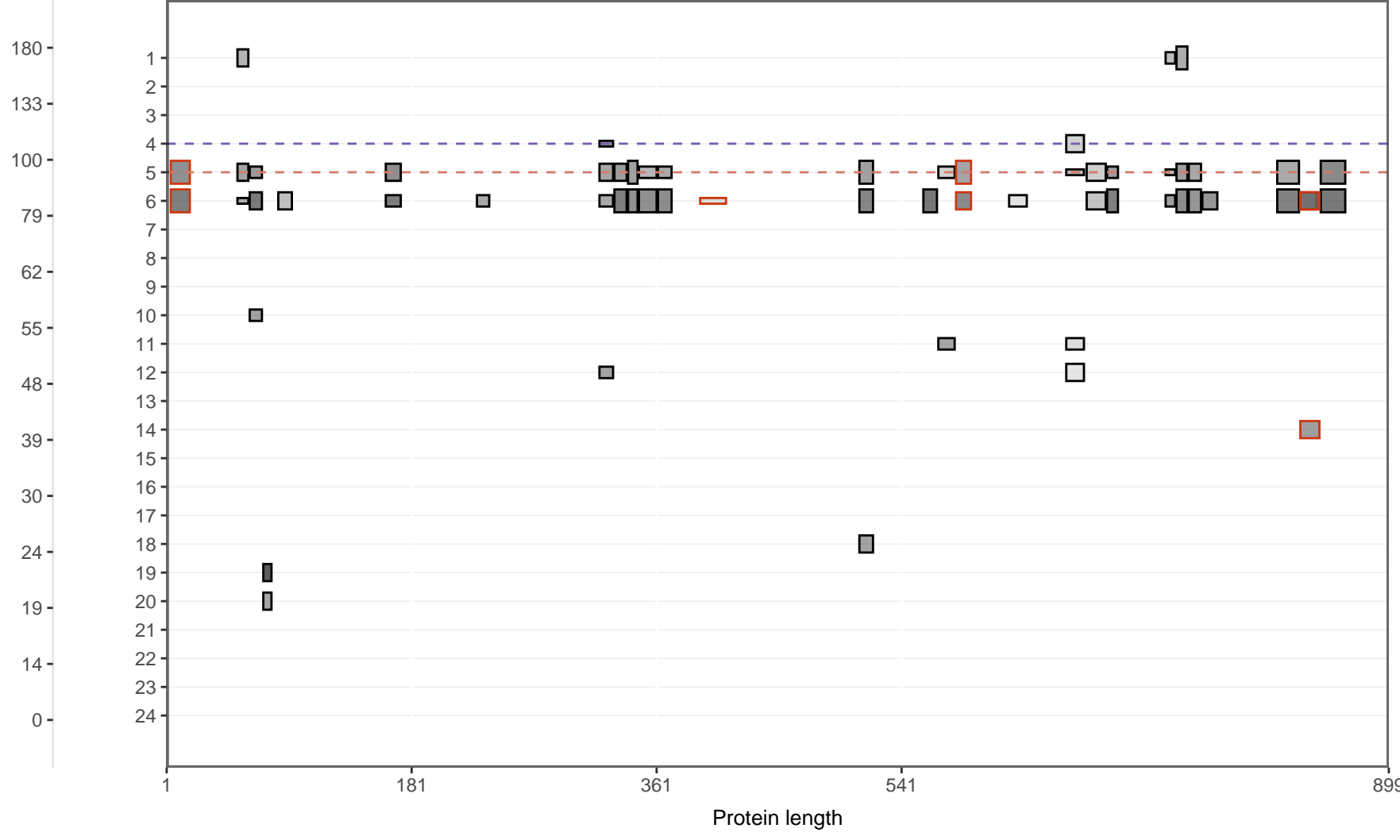
NPRAPRRISECLLGDDTGGSLFTARNEGVLLKAGATVILRNAKIDMFKGSMRLAVDKWGRVETEPADFVAIVEQNLGLVEVELVNEE*

NbL11g19850.1 26S_proteasome_non-ATPase_regulatory_subunit_2_homolog_A-like [MW = 98.35 kDa]



Molecular weight

Gel Slice



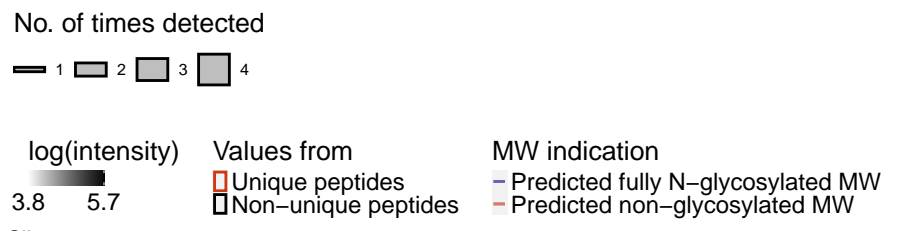
Pfam Description

- SP
- Sequon
- TM Domain
- PF01851 Proteasome/cyclosome repeat
- PF17781 RPN1/RPN2 N-terminal domain
- PF18051 26S proteasome non-ATPase regulatory subunit RPN1 C-terminal

Protein sequence:

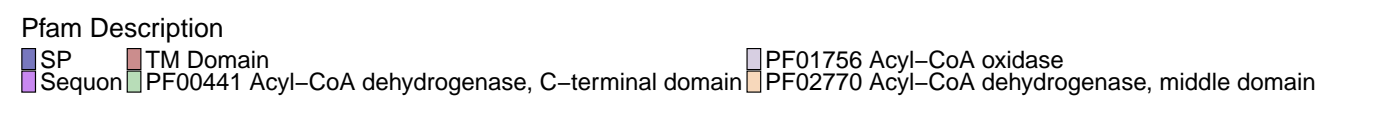
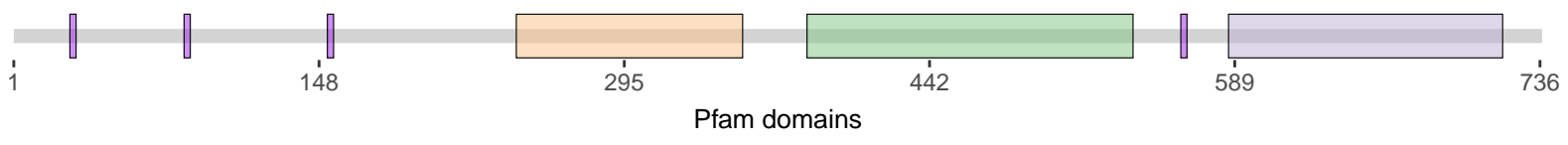
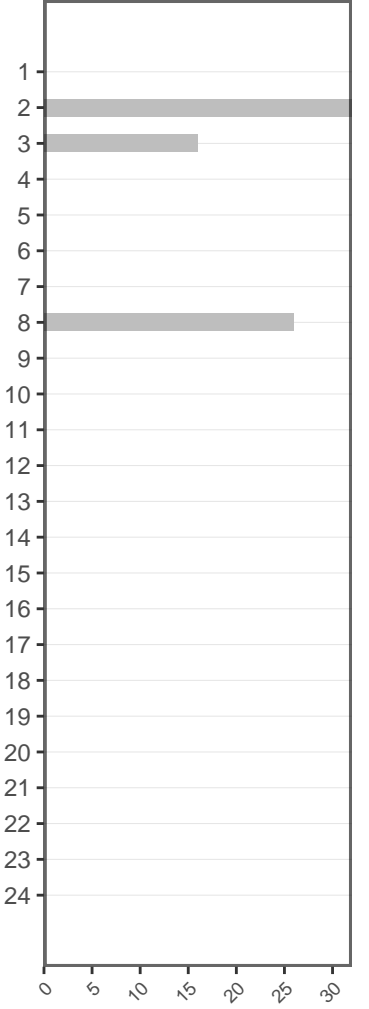
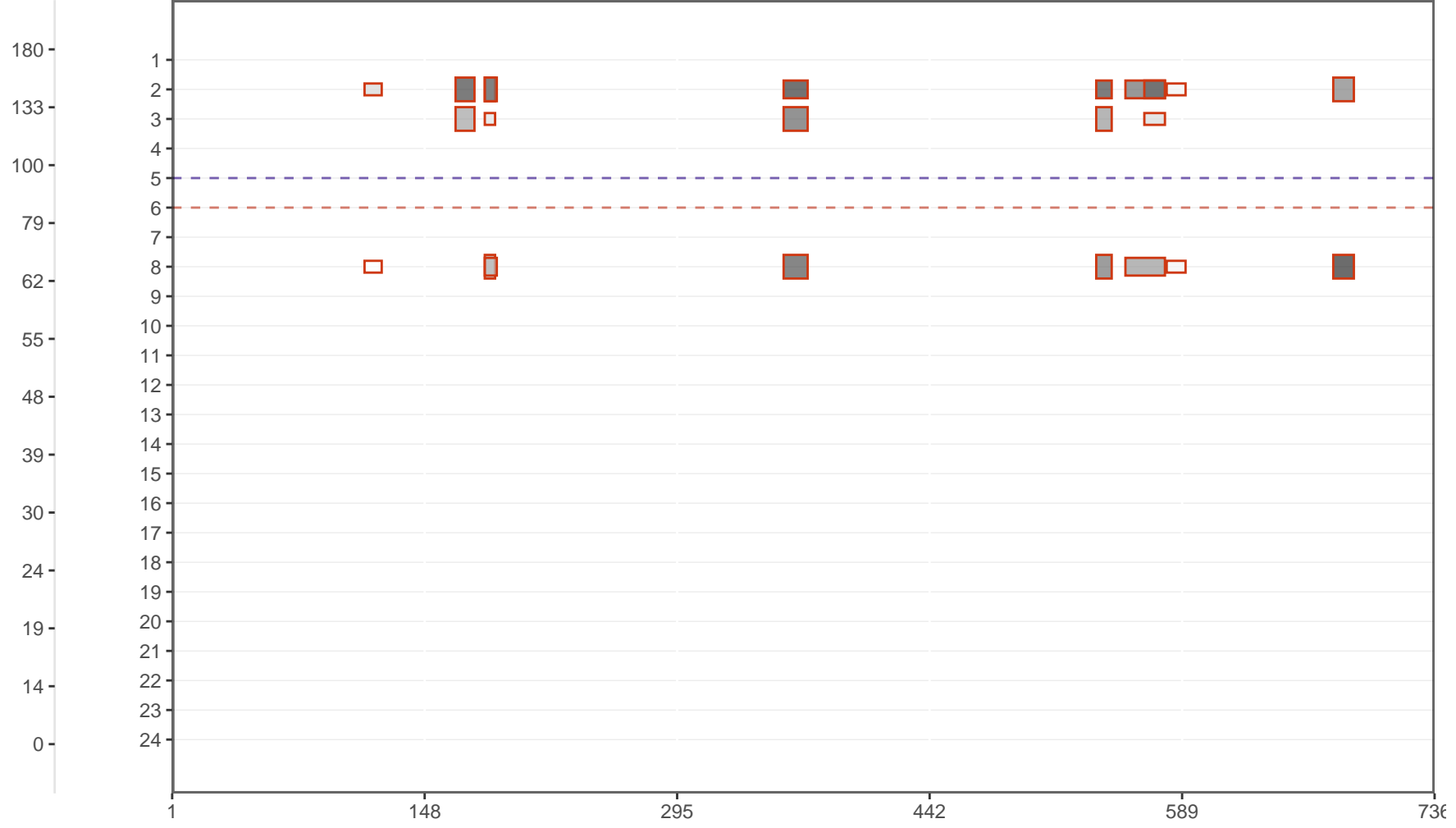
...VDVDSGLAQLDKYFHSTDTVIVAGALLGVGVIVNGIKNDGDPALLAEVYKDDPBRIGAIMGLGLAVAGAGNEQIRSLTPI.GDNKASLDFVAFANISGLVYVGSQNEEIMDAIVFALMERSESELGEPLARLLPLGLLVLGKQGESVEATTEVSKTFHEKIRKHGDMTLLSGAVAGTGNVKKVQHFVGGCAQHLKQGETYQGPVAVGIAMVAMSEELGEMTIRSLHLLQYGEQNRRAVPLALALLGKGNPKVNVMDTILSRLSHSDTEVMAAIRGLIGAGTNRARA

NbL11g19780.1 acyl-coenzyme_A_oxidase_3_peroxisomal-like [MW = 82.77 kDa]



Molecular weight

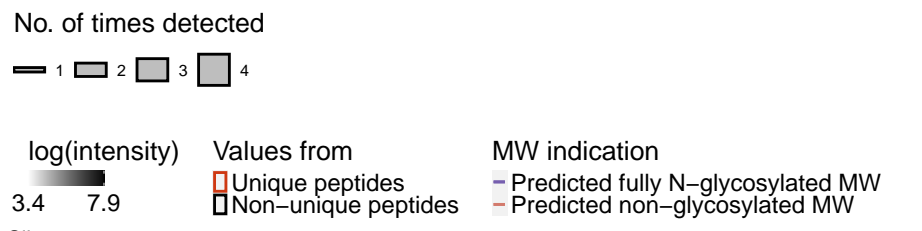
Gel Slice



Protein sequence:

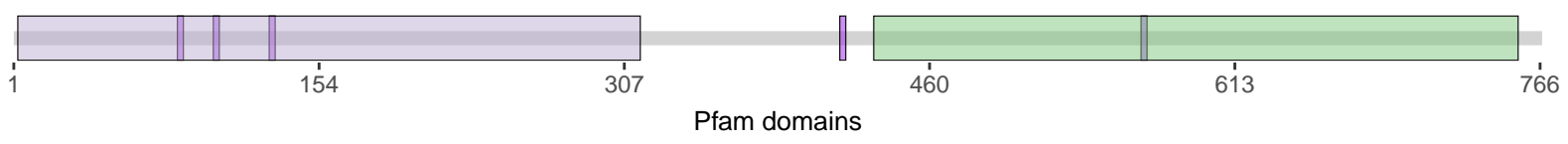
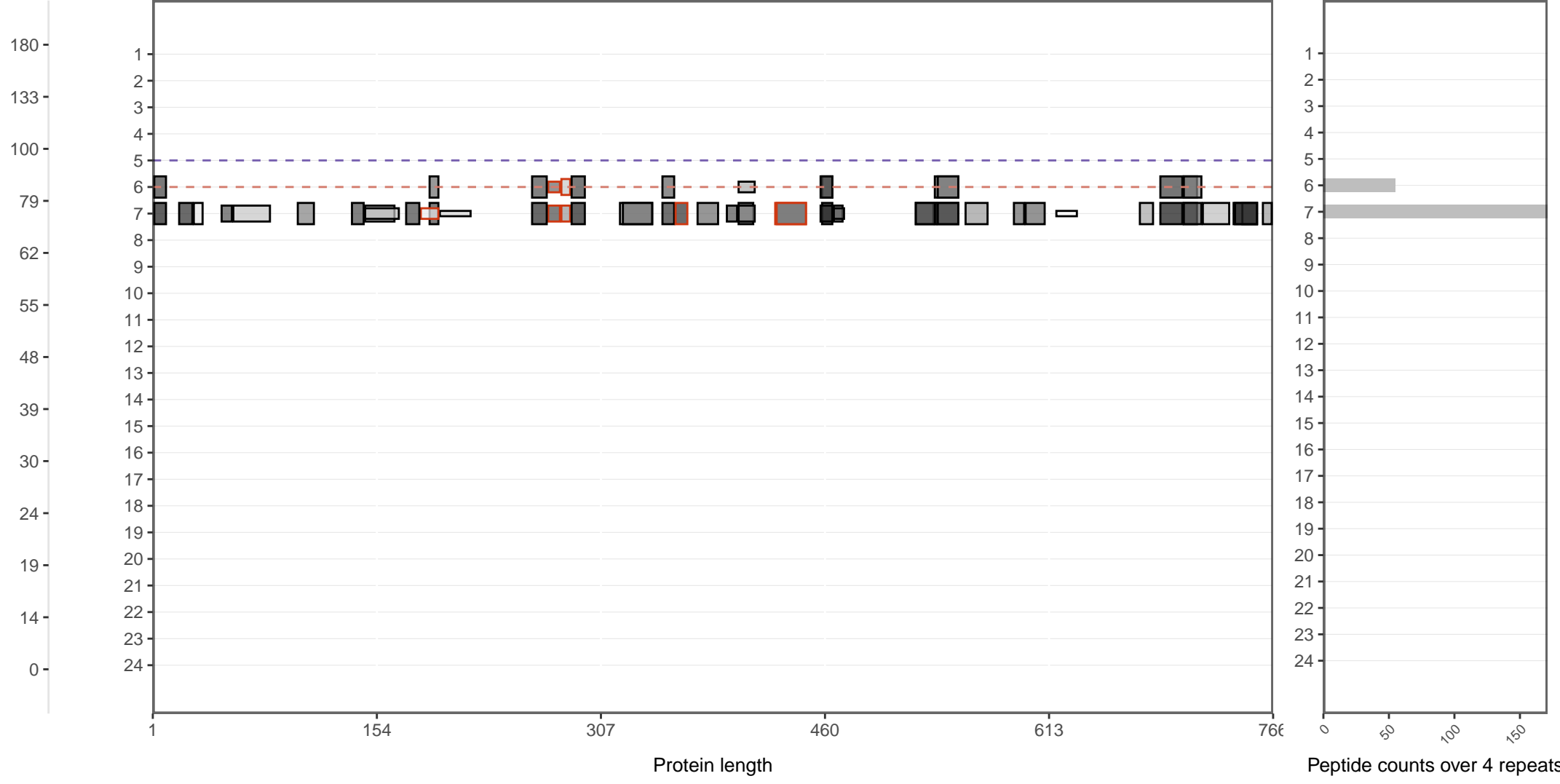
IPRENLLNSVADVSPFGKYLTAIKDPDQRFIAAFMPLTSGRVTIATVATYSANIGLATALRYSLTRAFSEVTPNGPEVULIDVPSHGRRLLPLLAKTYMFAFANLYKKYVKRTPMKNVHHVSSAFKATASWHNMRTLQEGREACGGGGLKTEHYRVLGKGFDFVGGTFEGDNNVLMQGVSKALLGEYMTAKRSKPKFKGLGLEHMMNNSRPVVPSSQLTSSAMRQSGFGNDIFGLRERDLLERFAAEVSLGDSGSKSEKEYAFTLNVLQLAEDLGRFSDRAVLHTLLEAEATV

NbL11g19670.1 5-methyltetrahydropteroyltriglutamate--homocysteine_methyltransferase-like [MW = 84.57 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF01717 Cobalamin-independent synthase, Catalytic domain PF08267 Cobalamin-independent synthase, N-terminal domain

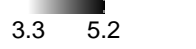
Protein sequence:
 SAKDEAFFSANAAGASRKSPRVTEAVQKASAAALGGSDHRRATNVSARLDAGQKKLNLPILPTFTTGGFPQTAELRRVRRREYKAKKISEEYVKAKEEKIKVVDLGEELDIDVIVHGEPERNDMVEYFGEQLSGFAFTANGWVGSYSGRCVKPPHYGDVSRPKPMTVFWSSAAGEMTKRPMKMLTGPVTLNWSFVRNDQPRFETGQALAKDEVELEKEGTVQIDEAALREGPLRKHAFYLNVAWHSFRITNVGGDITGQHTHMYSYFNFDIHSIDMDI

NbL11g19630.1 glyceraldehyde-3-phosphate_dehydrogenase_GAPCP2_chloroplastic-like [MW = 53.34 kDa]

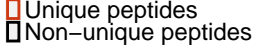
No. of times detected



log(intensity)



Values from

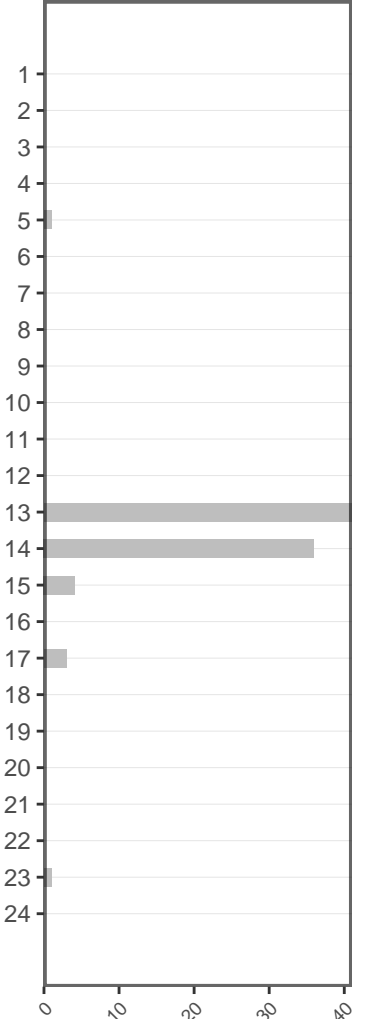
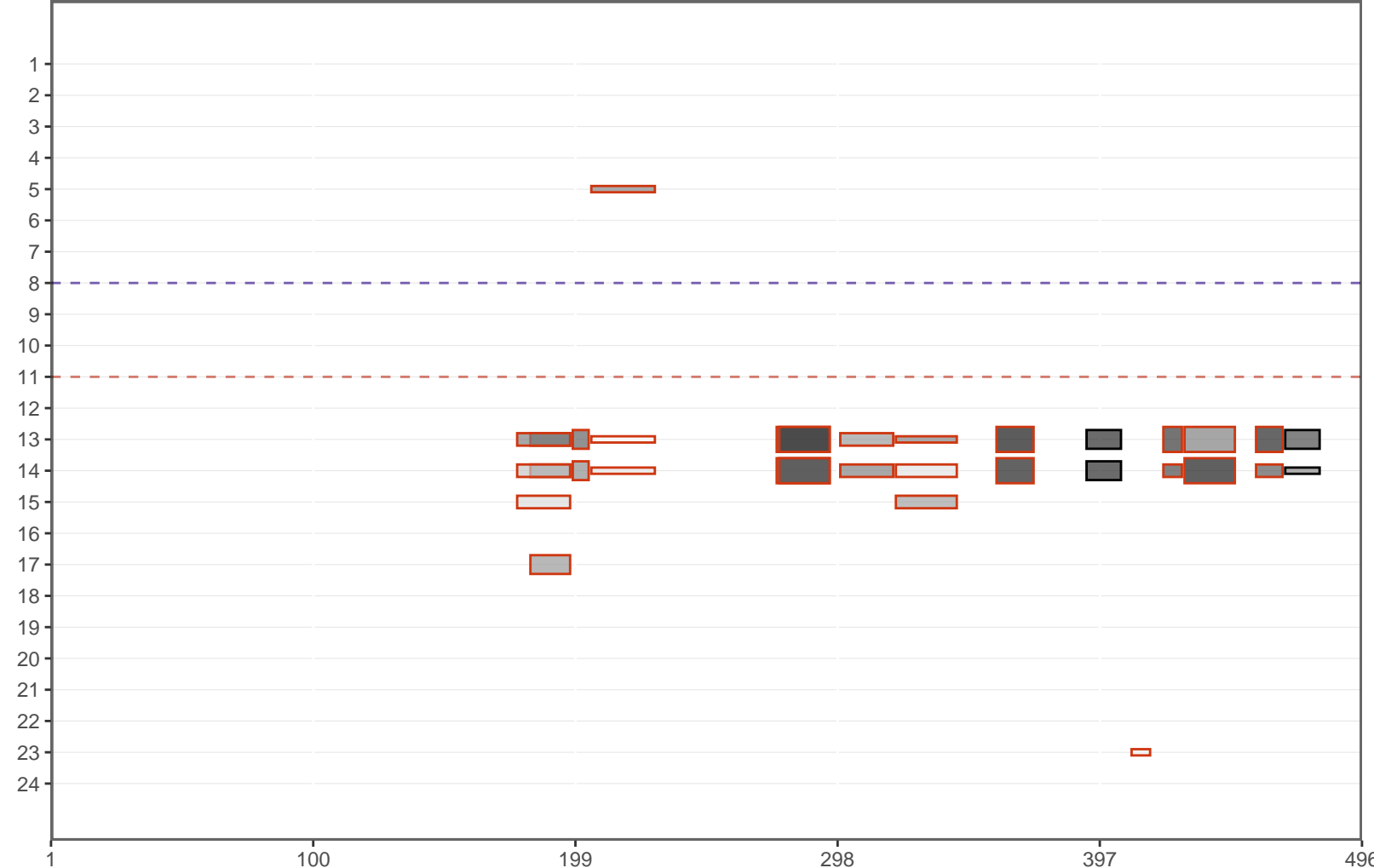
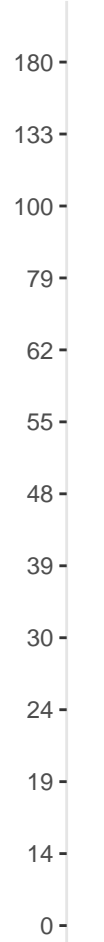


MW indication



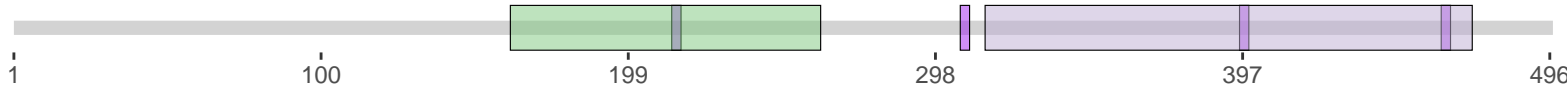
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00044 Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain
- PF02800 Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain

Protein sequence:

DDADIPVWGLGADYVVESSGVFTTVEKASAHKKGAKKVVISAPSDAPMFAVGVNERTYKTTMDVVSNASCTTNGLAPLAKVWHEEFGVEGLMTVHATATGKTVDGFSMKDWRGGRGAGGNIPSGTGAAKAVGKVLPELNGKLTGMARFRVPTPNVSVVLTCLREKSVSDVKKAAIKYASEGLKGLGYTDEAVSNDVGDGSRSSIFDAKAGIGLNSLMKLVSWYDNEWGYENRVLDEIHMALVAATN

NbL11g19610.1 nuclear_cap-binding_protein_subunit_1 [MW = 98.05 kDa]

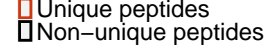
No. of times detected



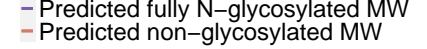
log(intensity)



Values from



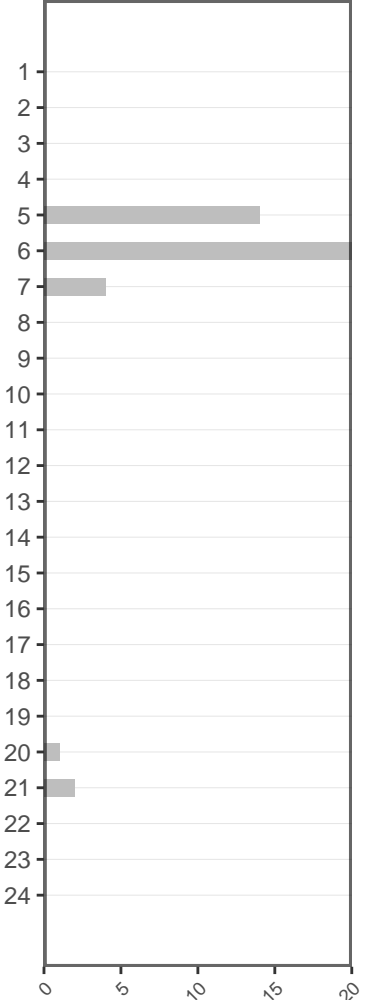
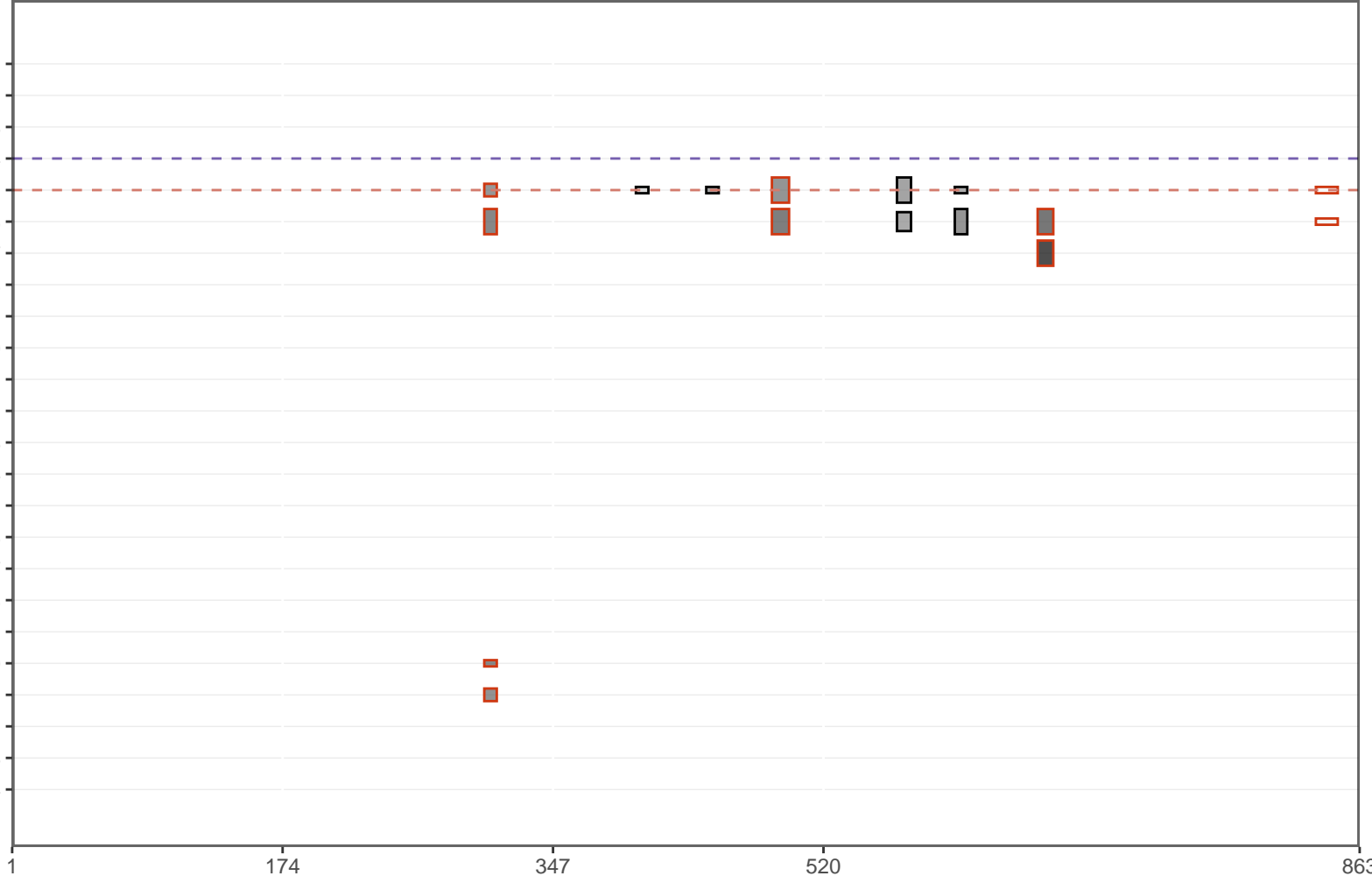
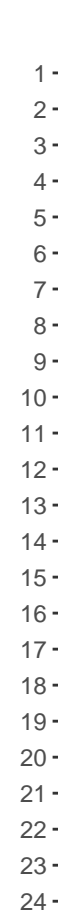
MW indication



Molecular weight



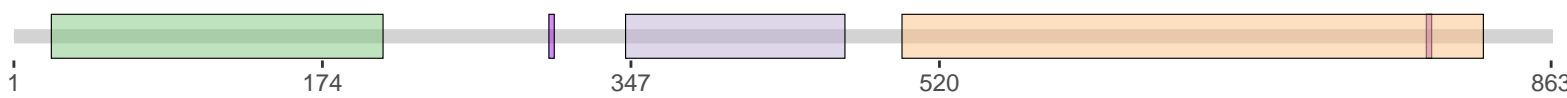
Gel Slice



Protein length

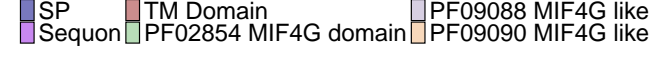


Peptide counts over 4 repeats



Pfam domains

Pfam Description

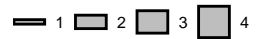


Protein sequence:

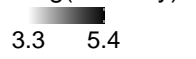
IFQFVWPVEEVAHLDLKPWAPQRFVQEVLEREVLSVWDKIKGSEHTPALEELLPPRGGPQFRYSAEQDTPTERALSVELKDMVNGRKSAREMSWEEENFFPAHGFDITLRVYVQTLIDGSKSFTHTLTVLERYGVGVIAKICTDDGQVQLSEVSGSYWQNSAQMTAISIDRMMEVRLSENLAVRWVFSSENLDRFHVSDGPWEILRNVAVKTYNRISDLRKEISLERGVVLAEEGASRARQQLDGAEEKLSIMDGPVLGENNVRKRLKSAEKAKXEEVSVRE

NbL11g19510.1 renalase [MW = 40.5 kDa]

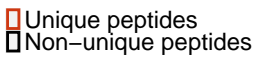
No. of times detected



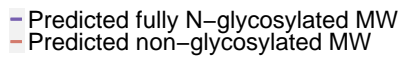
log(intensity)



Values from

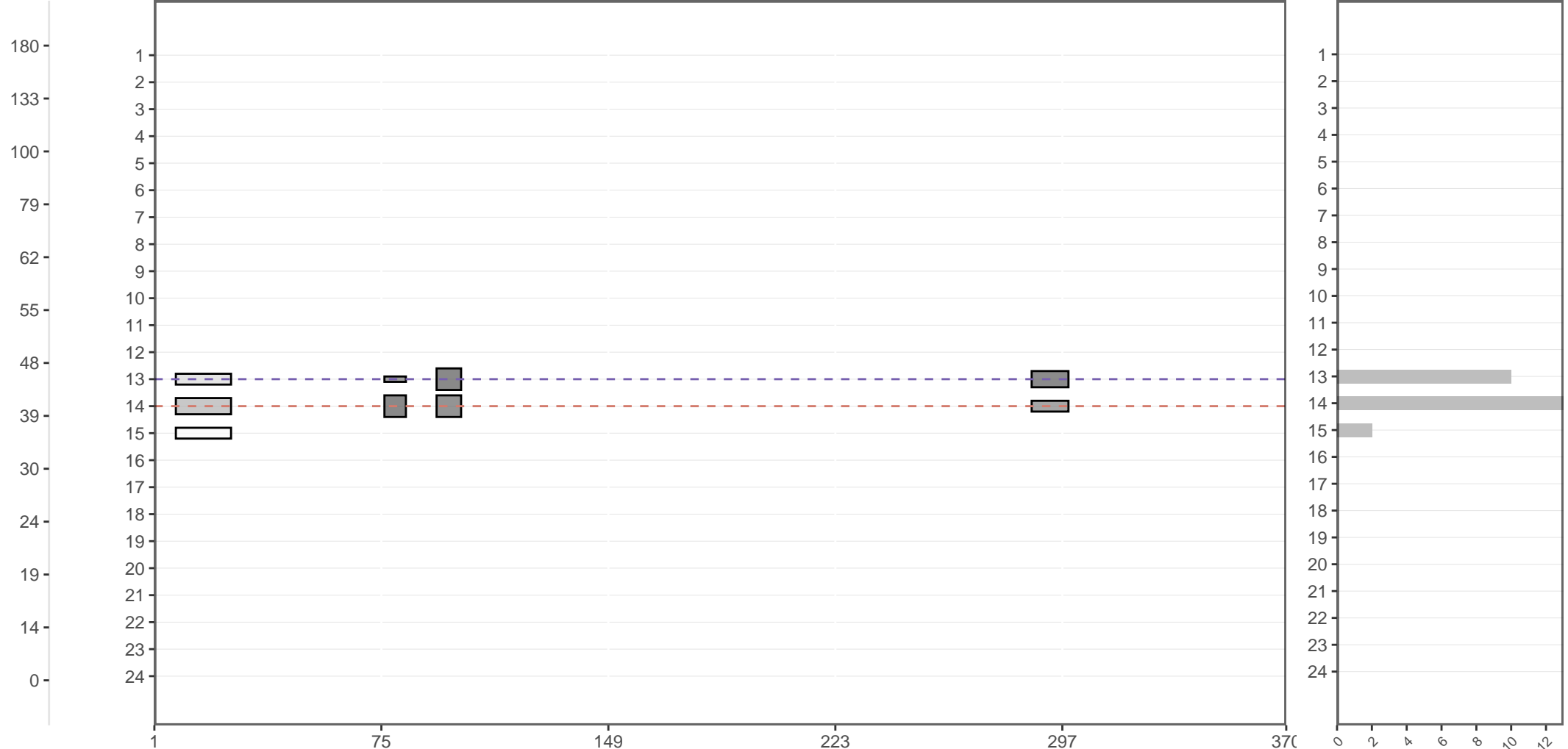


MW indication



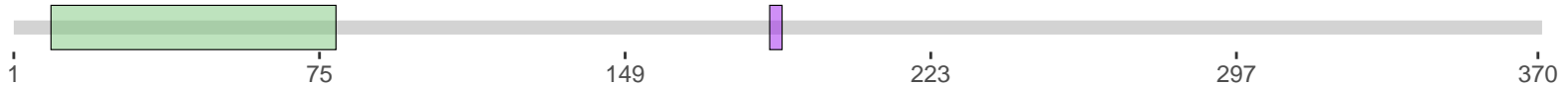
Molecular weight

Gel Slice



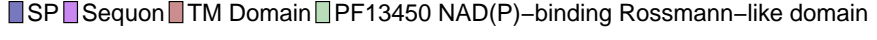
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

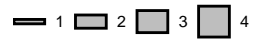


Protein sequence:

VVTSDKSTFSFKFTNVTGKMPIDMGKFFPEIPLKMTPEVPSRFALMAFEEELSEIPRIGFSFNSEVLRWAHCDSDSKPRRHNSGCVLHSTPEVARDVIAKTLGKPKSATLTKVAEELDFGFGSTKLNIPQAFNKAHRWGSAFPATSIAGDGEKGLWDKAKRIAGDGFVSPNVEGANSGLAAMAKGSEVFSRL

NbL11g19400.1 probable_calcium-binding_protein_CML21 [MW = 25.89 kDa]

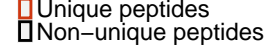
No. of times detected



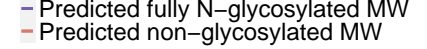
log(intensity)



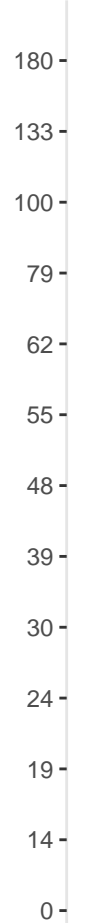
Values from



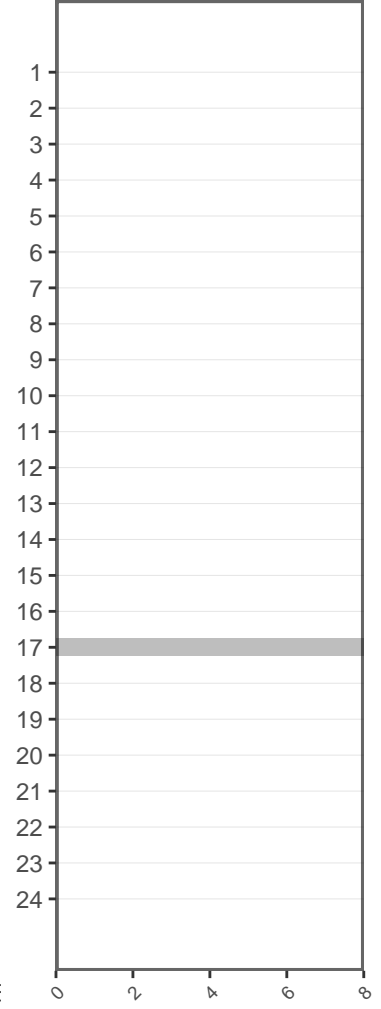
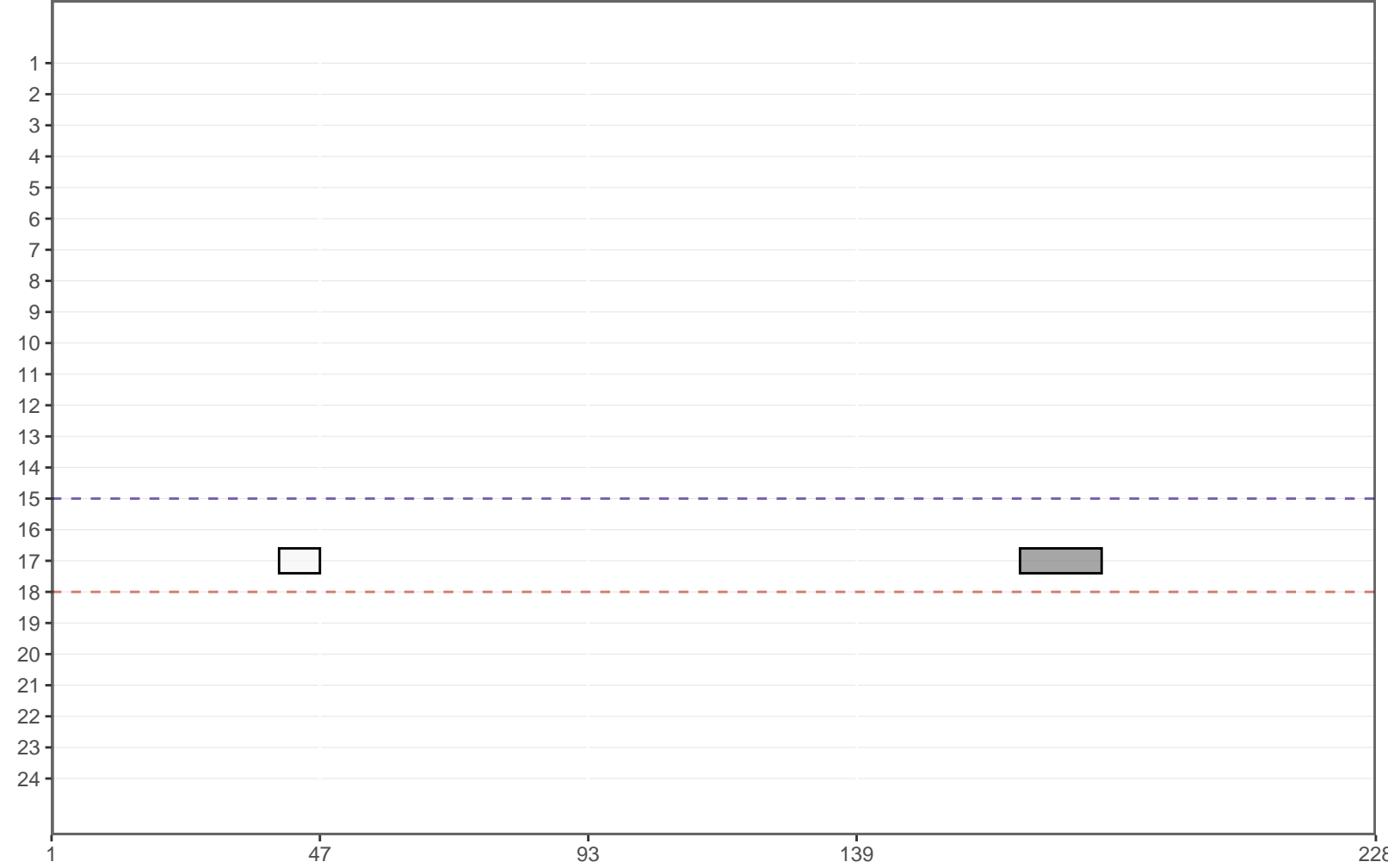
MW indication



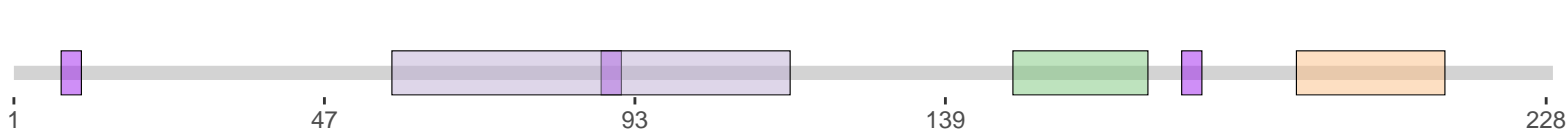
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

DNEDMGIEFSEFVALLGVVLLKDDPTALHAKSRMGLPLNLEWAFETLVDMFVFLDKNKDGYSRNEIMQAINETTSGERSSGRIGMRFRFEEMDWKNGMWNFKFELFAFTHHWVGIENDEDEEGEE

NbL11g19350.1 peptidyl-prolyl_cis-trans_isomerase_FKBP16-1_chloroplastic [MW = 27.94 kDa]

No. of times detected



log(intensity)



Values from



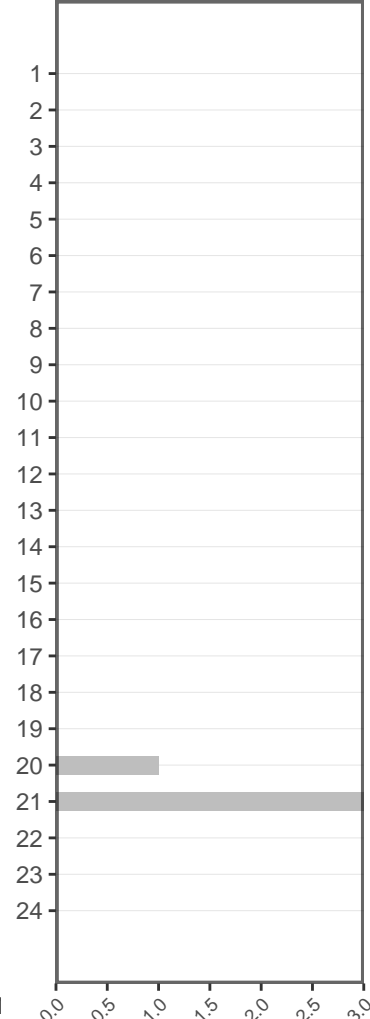
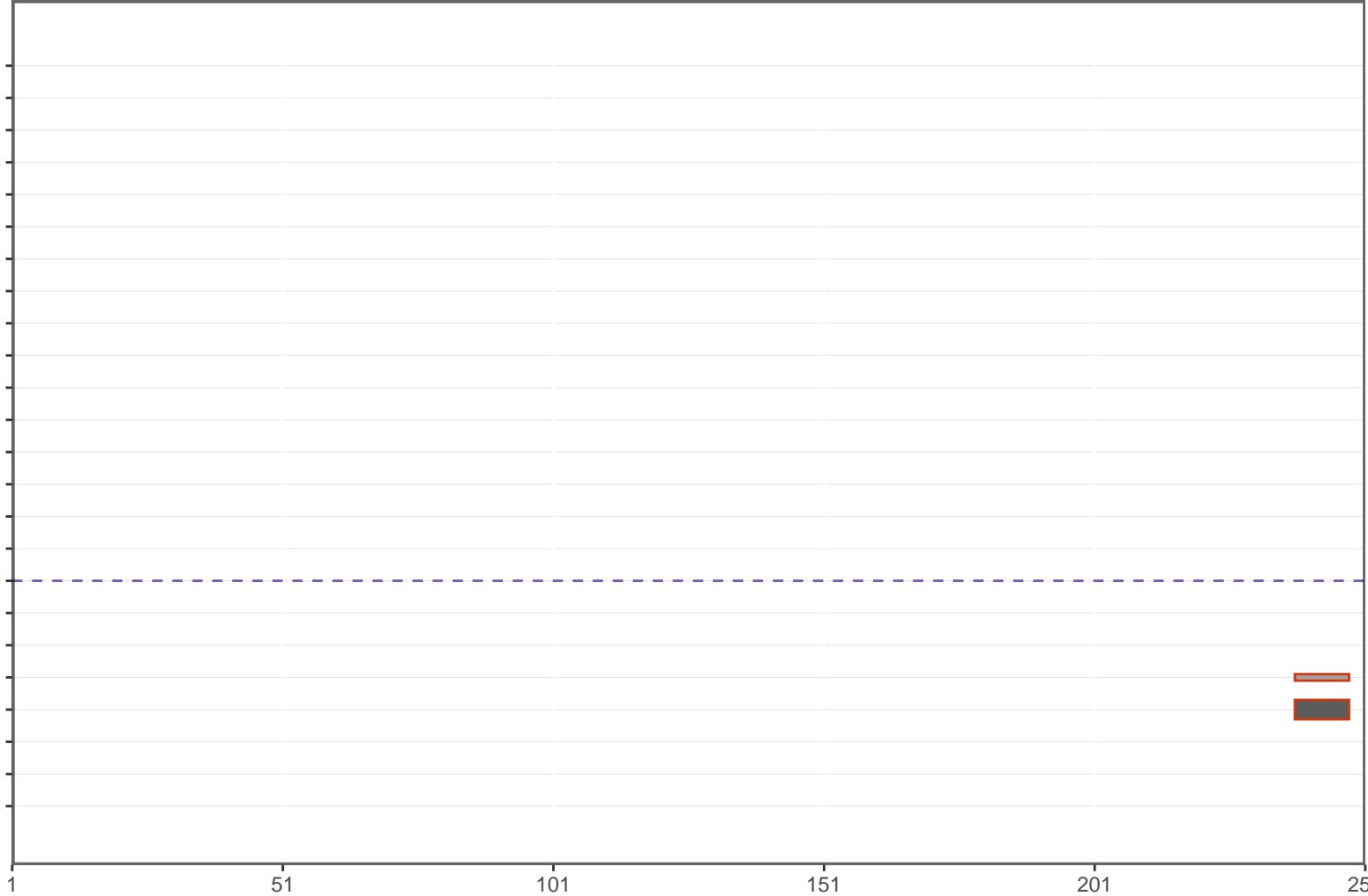
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

CEPDVIRFEAFRTLKLASGVRIQDVEEGEPAAHEGGDIVENVCRASNGYFVHSTVDQFSGESSPLVPLDDTQIEGLKEVLICAMKPGGKRRALIPPLGLGVINENLKPVEEFGRRRLSMHVKPELFI FEVQLLKLVI

NbL11g19340.1 heat_shock_cognate_protein_80-like [MW = 80.17 kDa]

No. of times detected



log(intensity)



Values from



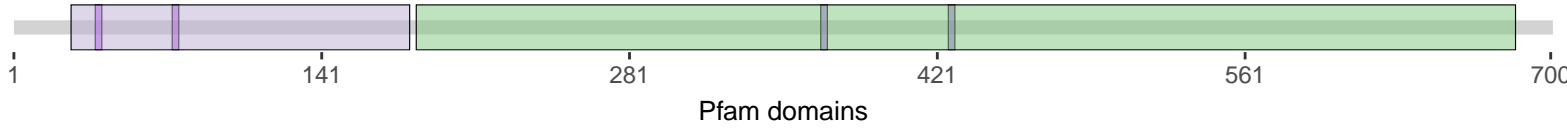
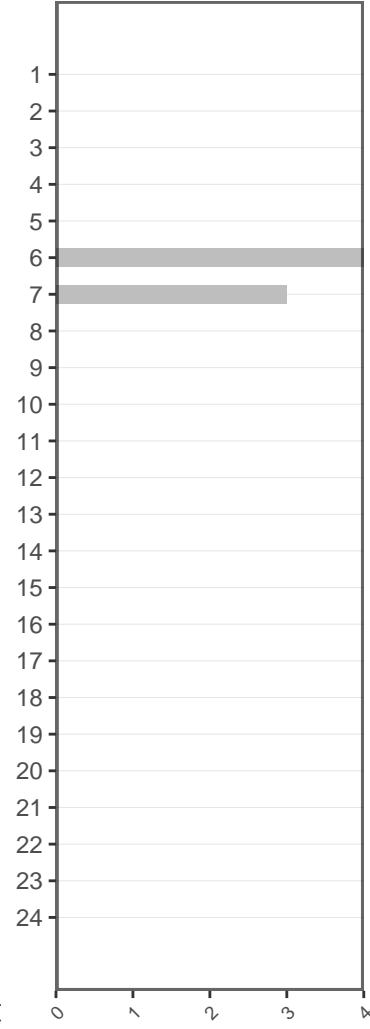
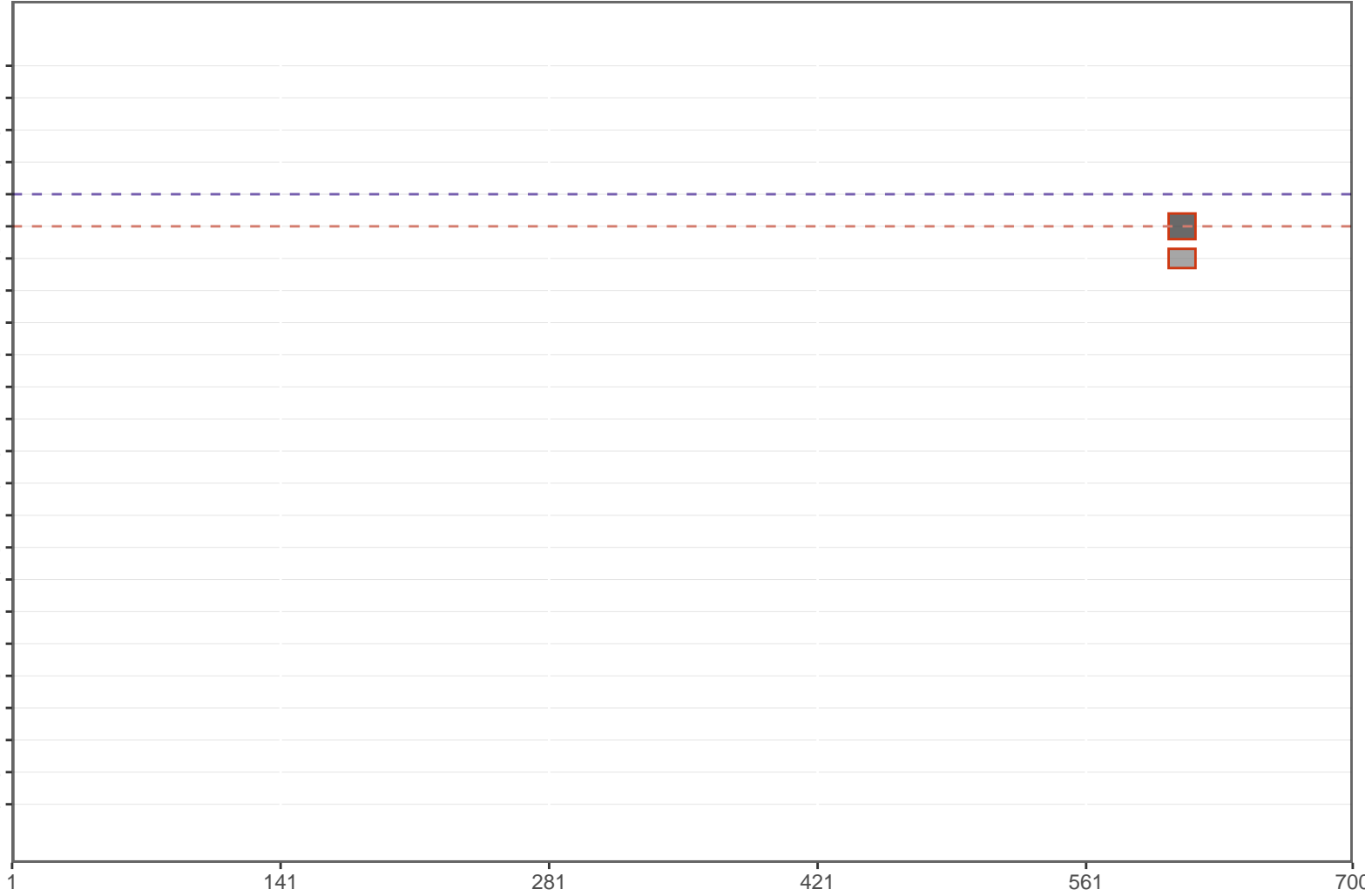
MW indication



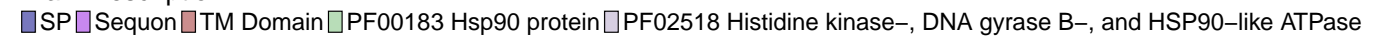
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

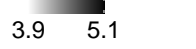
/FIMDNCCELPEYLSFVKGIVDSEDLPLNISRMLQQNKIKVIRKIKLVKKGIELFFFIENKEDFDKIFYEAFANIKLGIHEDSQNRFKFAELLRYHSTKSGDDMTSLKDYVTRMKEGQNDIYYVTGSEKKAIVNSPFLKIKKIKGYEVLVYVDAIDVEYGGQLKEFEFGKIKLSATKEGLKLDSEDEKDKKKEELKKEFGKGVKDKVLDGKVEKVVVSDRIVVDSPPGLVTGEYGVFTANMERIMKAGALRDSMAGVYMSKKTMEINPENIMDELKRRADAKNDKISKYLDVL

NbL11g19310.1 farnesyl_pyrophosphate_synthase_1-like [MW = 48.87 kDa]

No. of times detected



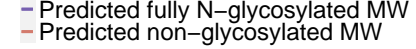
log(intensity)



Values from



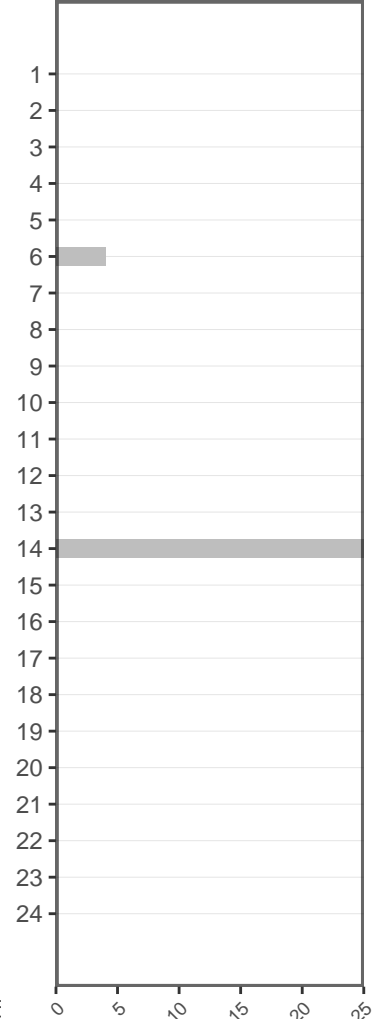
MW indication



Molecular weight

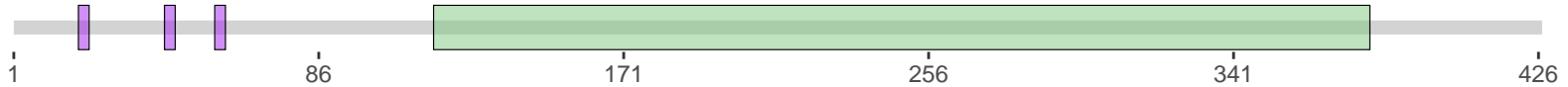


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGMIAANDGILLRNIPRIILNHFQKPKYYVDLLELFNEVEFGTASGGMIDLTLLVGENDEKLYLPHRRRVQYKTAYSFYLPWACALLMAGESLDHVAWKNILEMGYFQVGDHLDGCFADPEVLGKIGTDDQDFKGSWLVKALKHNGEKGKLLYENYKGDQDPKVAKVKALYNDKLEDDVLEYEKTTYEKLNSIEADPKAVQAVLKSFLAKYKROK

NbL11g19250.1 fasciclin-like_arabinogalactan_protein_1 [MW - SP = 41.12 kDa]

No. of times detected



log(intensity)



Values from



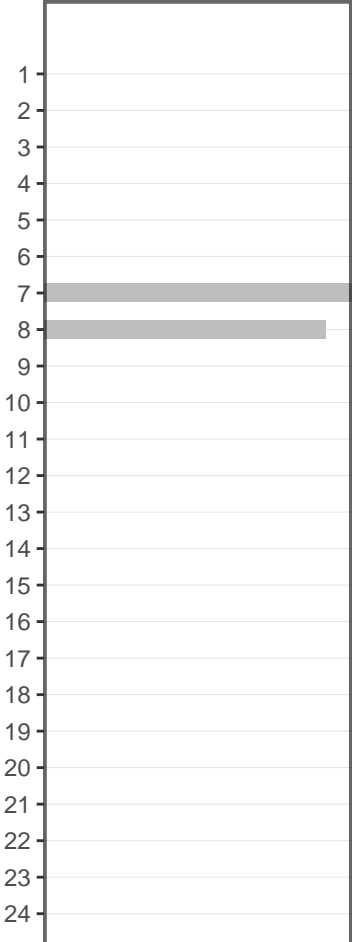
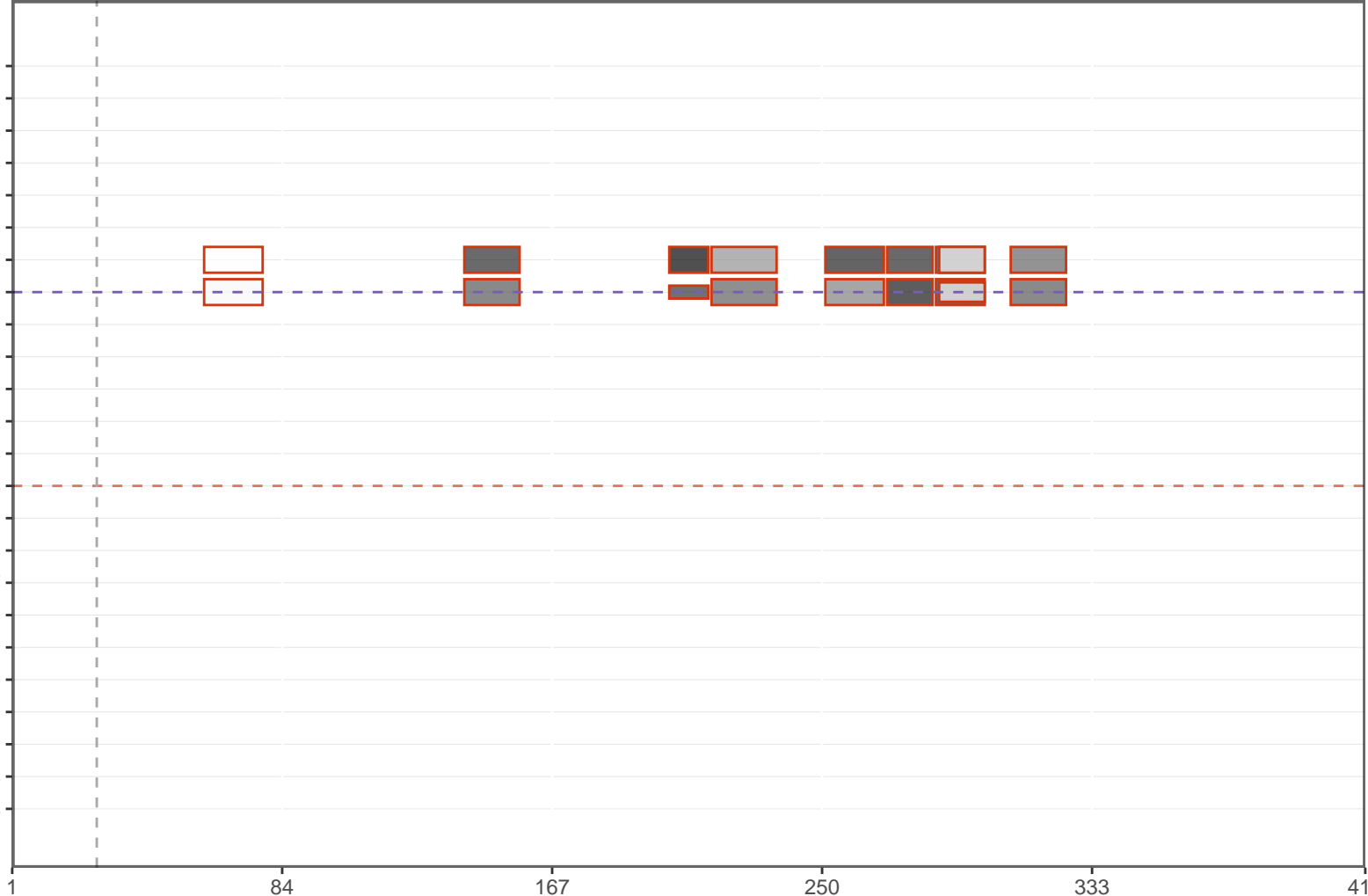
MW indication



Molecular weight



Gel Slice

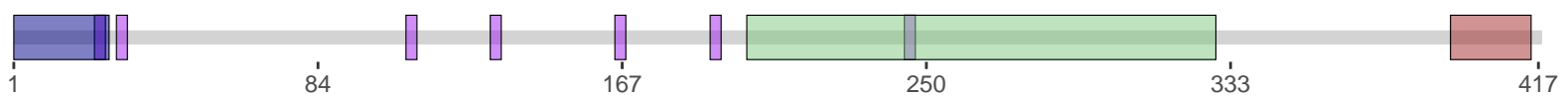


Peptide counts over 4 repeats

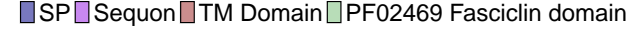
Protein length



Pfam domains



Pfam Description



Protein sequence:

IGCKVFAETLLSSPAEKTFDDNVDGGLTVFGPGDDMKMNFAPKFKNLTAAGKBSLLEYHGVPVYQEMDELKENGVMNLTADGSKKYDFVVGNDGNVFLTKIVTAKITGTLDEGPLAIFTNKVLMPKELFKTAPADTPMPPSPSEADAPSPKGGKHKHKAAPADTPADSPDGPSSDVAIDGNGSAFYVSGGPNVAGVLEMMVFFVLLI

NbL11g19180.1 30S_ribosomal_protein_S10_chloroplastic-like [MW = 20.71 kDa]

No. of times detected



log(intensity)



Values from



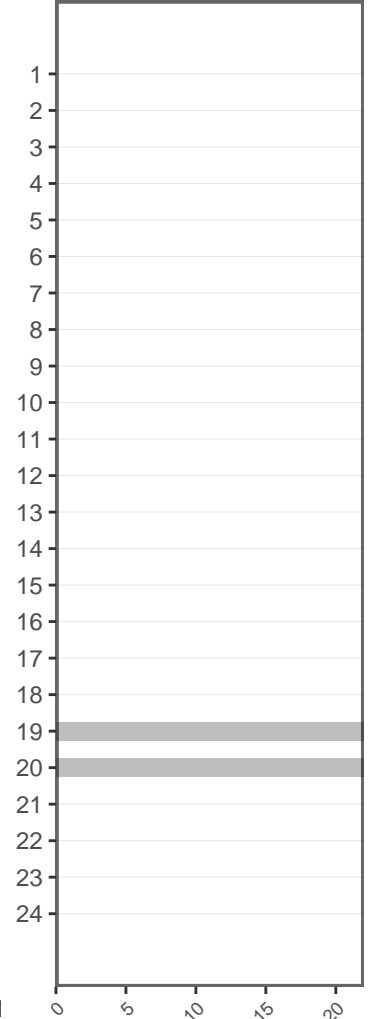
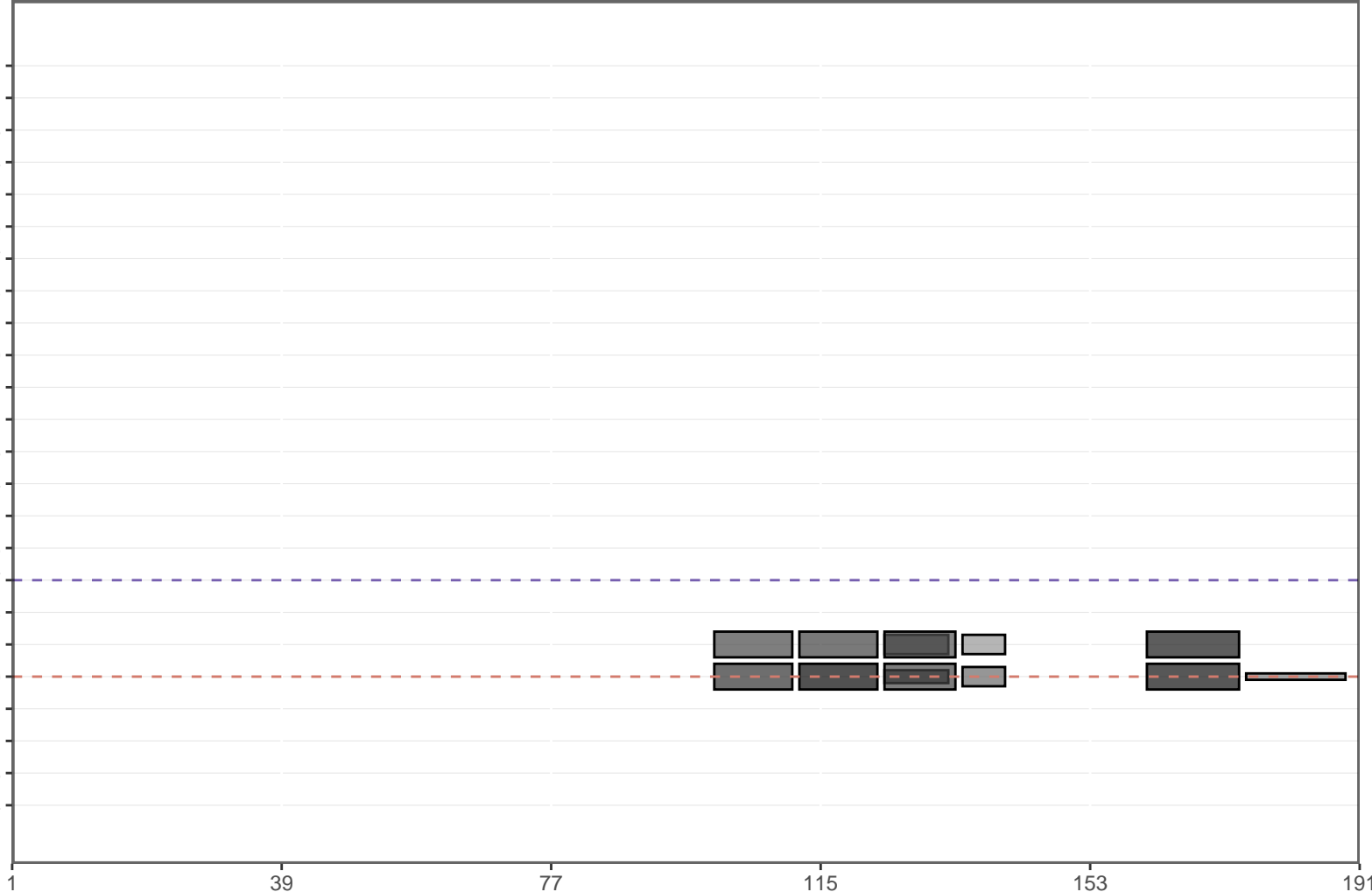
MW indication



Molecular weight



Gel Slice

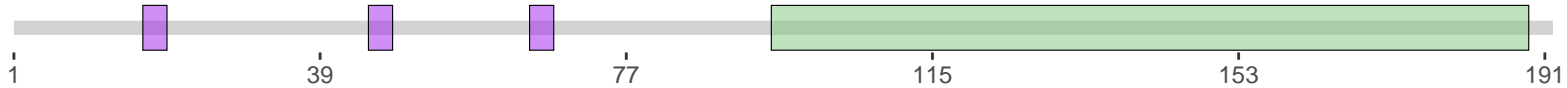


Peptide counts over 4 repeats

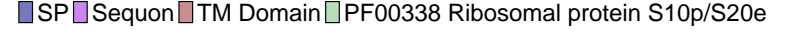
Protein length



Pfam domains



Pfam Description



Protein sequence:

GVDAADKAAAPKQKIRKLRBYWVPLIEDGCKQIMDAATTTNAAKTGVPVPLPTKRIYGVLSKSPHYHKDARFHFERTHQRLLDLYPTAGTIKMLLDLFRGVEVEVKL

NbL11g19150.1 40S_ribosomal_protein_S8-like [MW = 25 kDa]

No. of times detected



log(intensity)



Values from



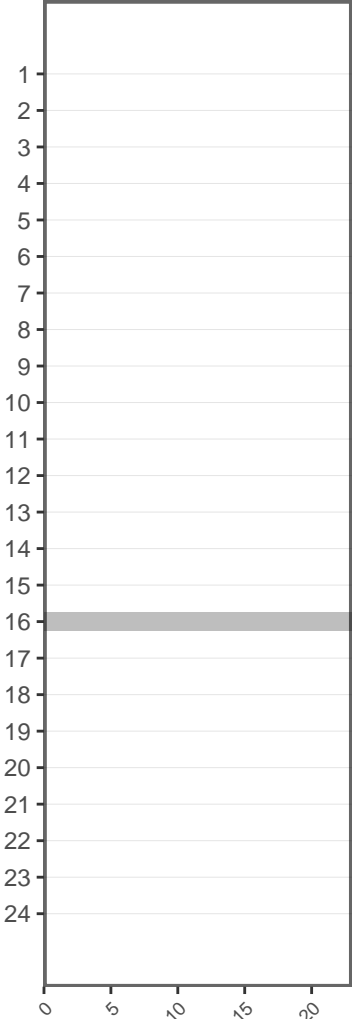
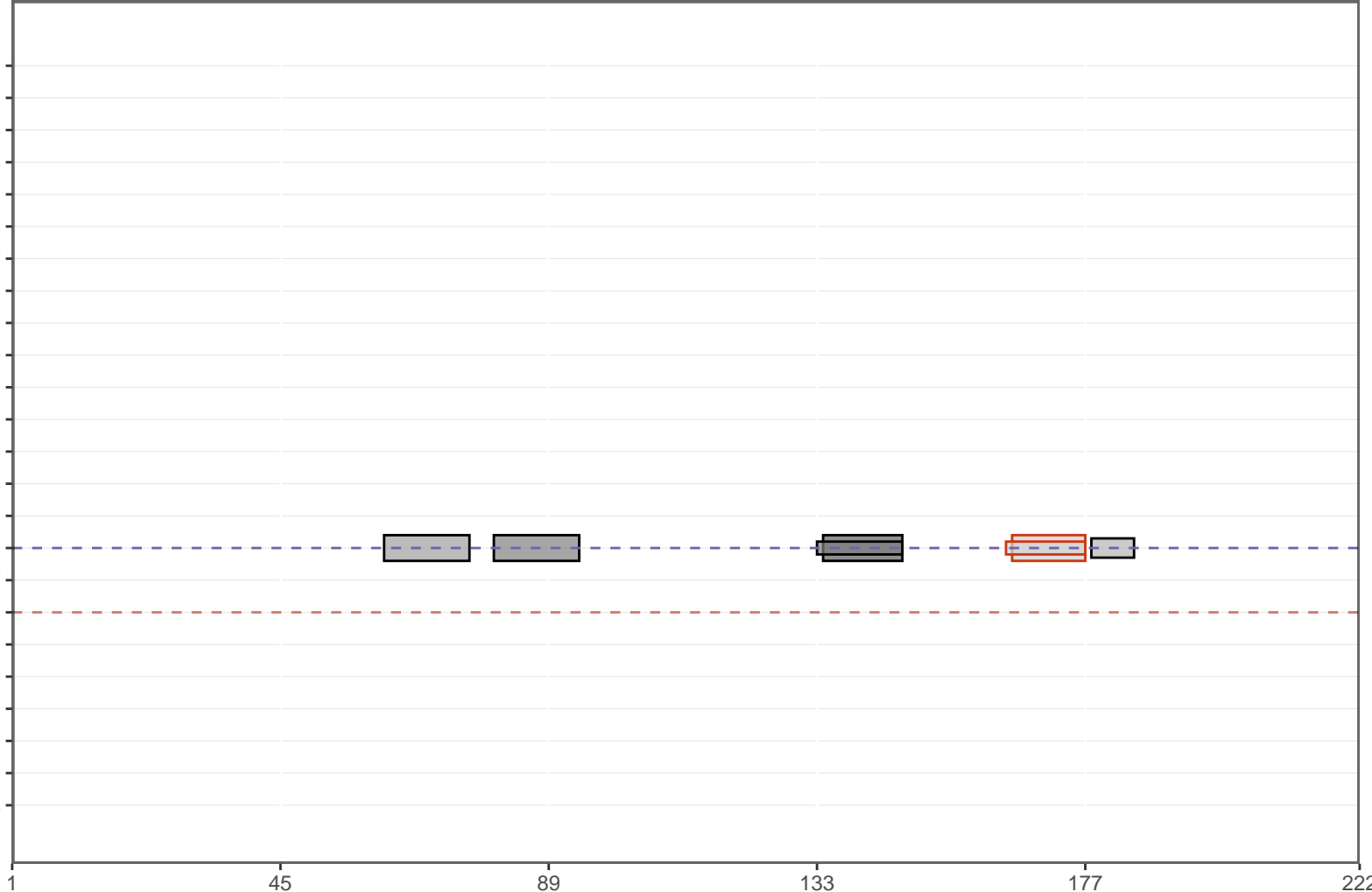
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LVKSAIVQVYDAIFPKWYLGHYGVDRKKKSAVKKEGEAEATAPAAEEKKNHVGRLKLRGGDRKIDPHVEEQFASGRLLAASBRPGGGGRADGVLEQKELEFYMKLQKQKKGKGAAGAA*

NbL11g19000.1 proline_synthase_co-transcribed_bacterial_homolog_protein-like [MW = 26.8 kDa]

No. of times detected



log(intensity)



Values from



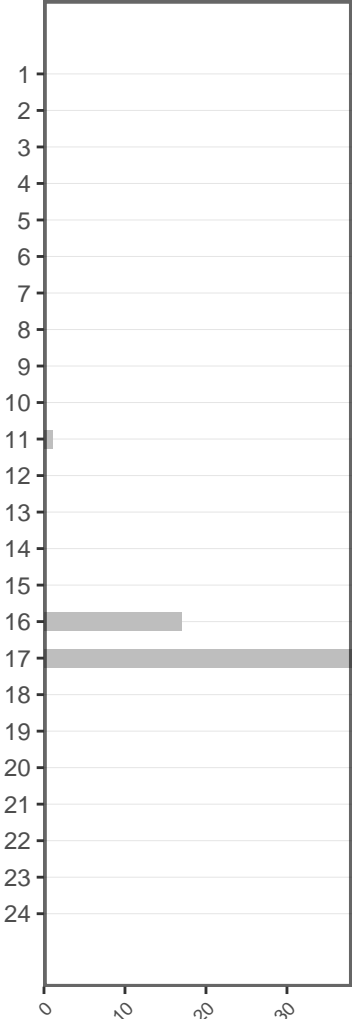
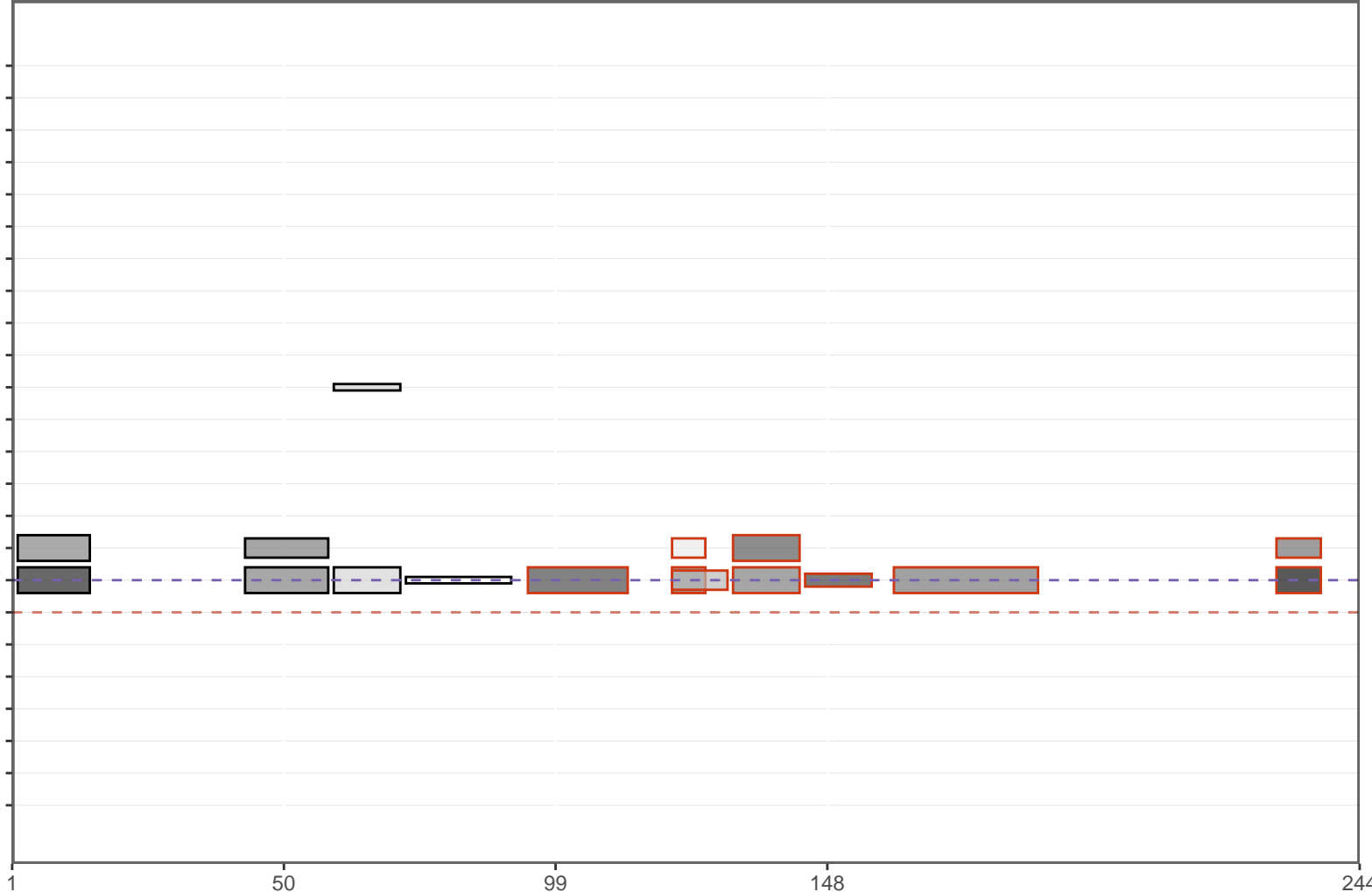
MW indication



Molecular weight

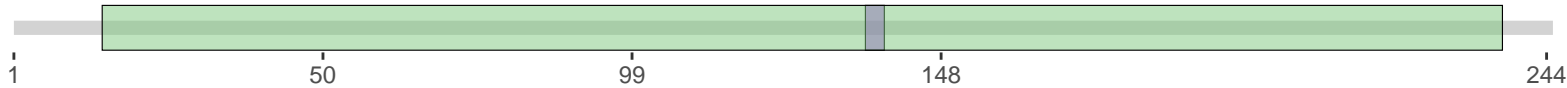


Gel Slice



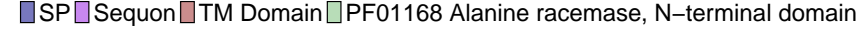
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NOKLANILDRMYSSIDRQPLKVLVQVNTSGEESKSGIDPNDVLAHVKLQDPNLEFSGLMTGRFDYVSTPENFKTLNCRTEVQKVLGMGEGSOGLMGMMSDFELAEIMGSTTVRIGSTIFGPREYKRGQ

NbL11g18960.1 reactive_Intermediate_Deaminase_A_chloroplastic-like [MW = 20.65 kDa]

No. of times detected



log(intensity)



Values from



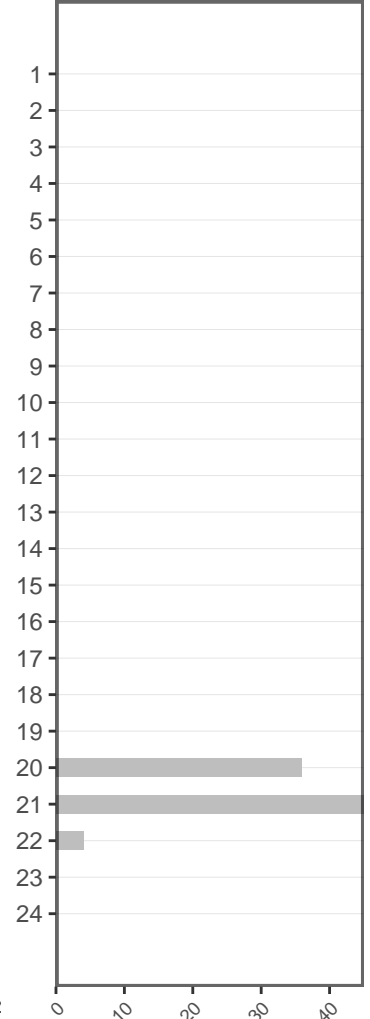
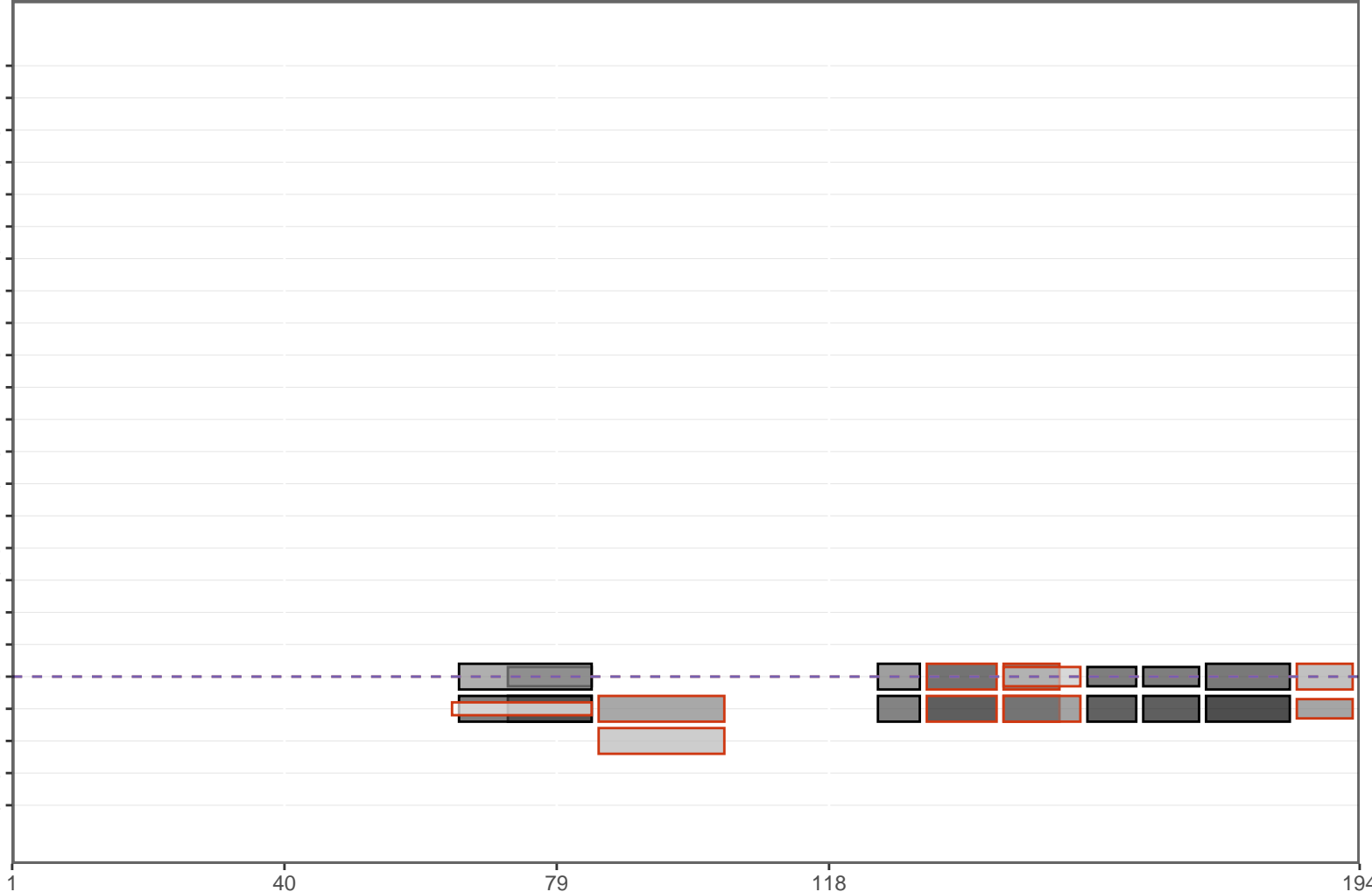
MW indication



Molecular weight

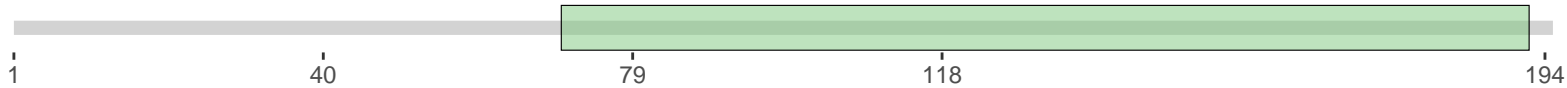


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IAIKANNFYVSGVLGLVLPETGKFKVSDSDVEDDTEGLNDFQVLYNMGSEIKASGVSYSAVYKTTLLADLKDFTVNEIYAKYFGSPAPARATYQVAALPMDARIEGIAAL

NbL11g18890.1 protein_LHCP_TRANSLOCATION_DEFECT [MW = 19.64 kDa]

No. of times detected



log(intensity)



Values from



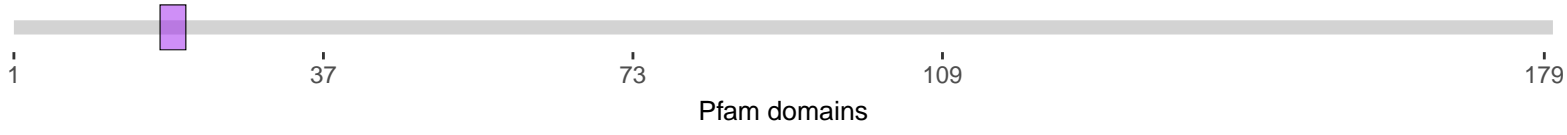
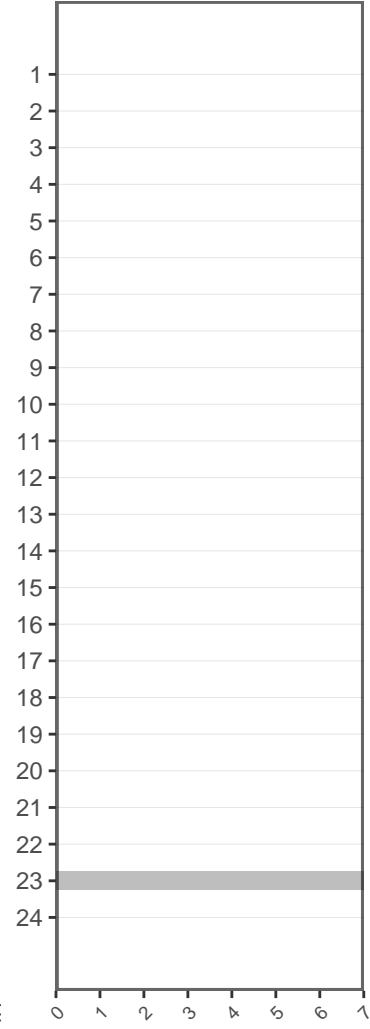
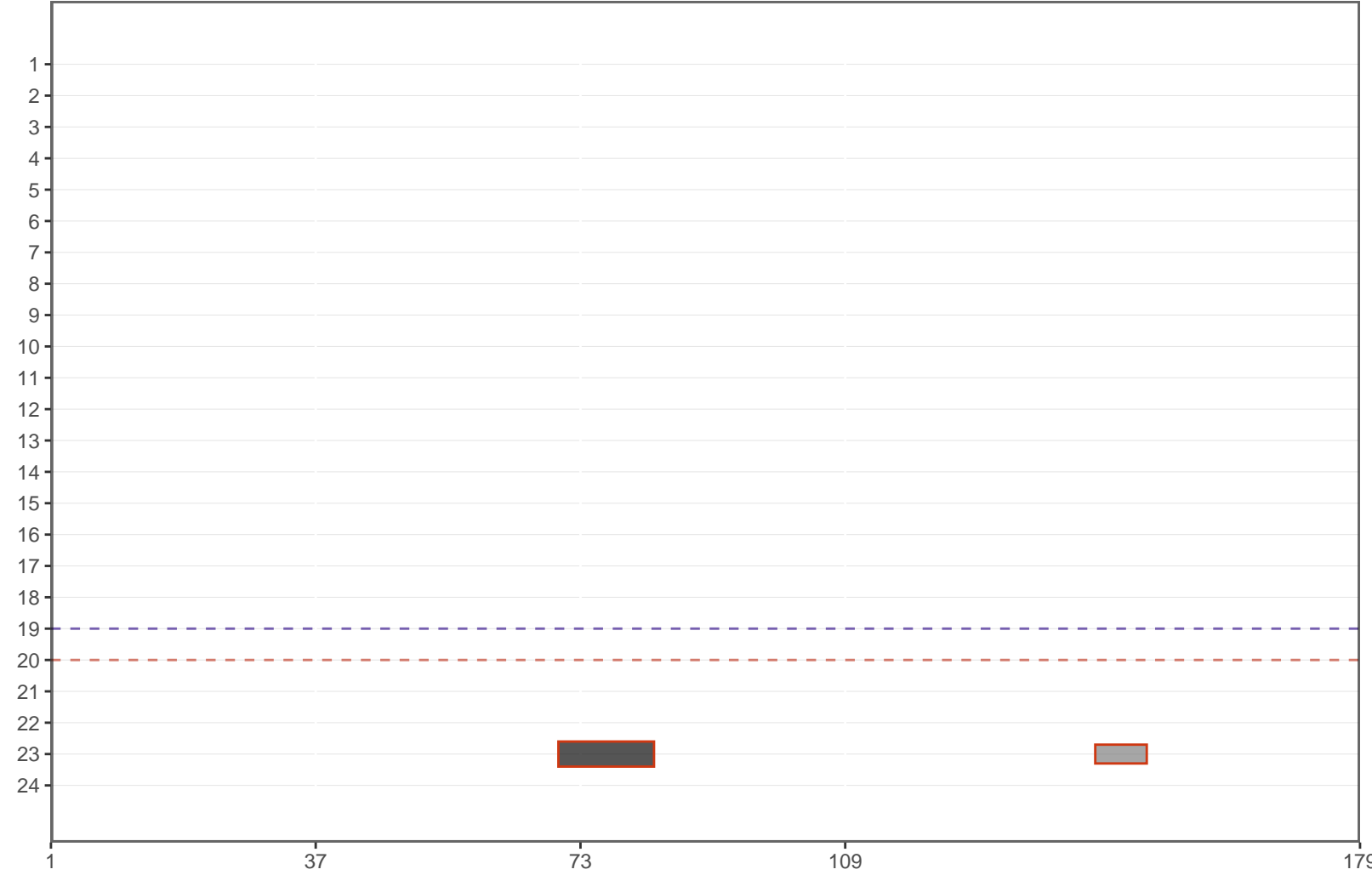
MW indication



Molecular weight



Gel Slice



Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

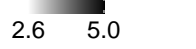
SVYGSQRDQDFDRDQVEQHFYFMGLAWEGTYDKMEALLGQNHHPVDILLMAETGDLPKIEELLRAGADYTVKIDADGRTALDRAAIDEKDFLNKYKQKA

NbL11g18850.1 tryptophan_synthase_beta_chain_1 [MW = 55.22 kDa]

No. of times detected



log(intensity)



Values from

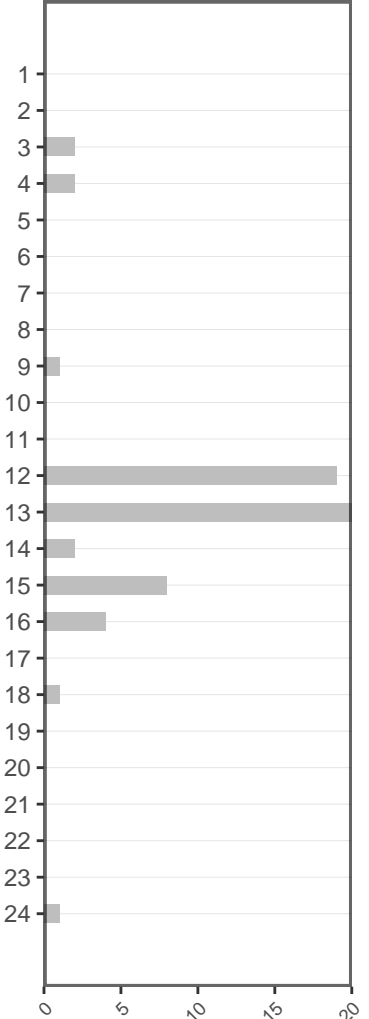
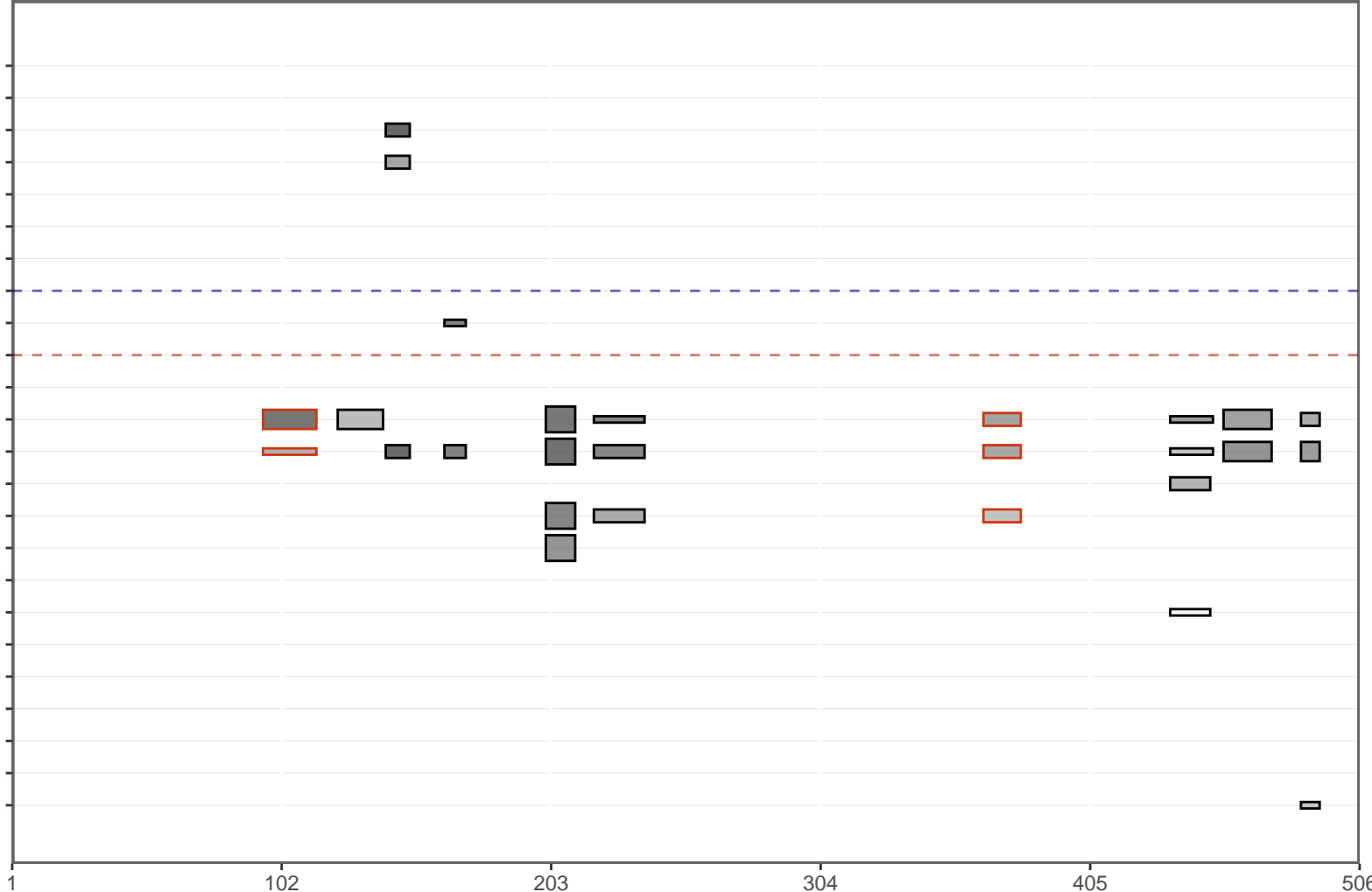
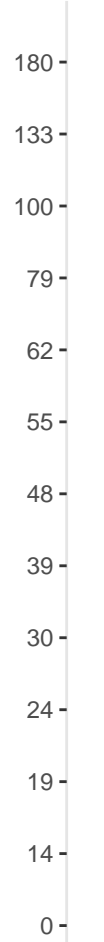


MW indication



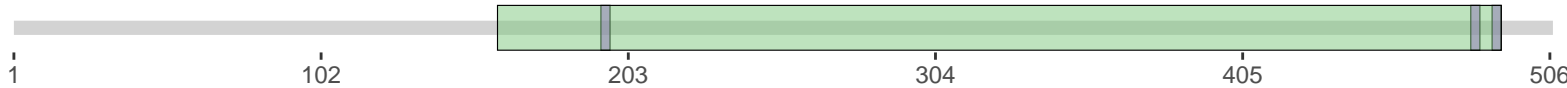
Molecular weight

Gel Slice



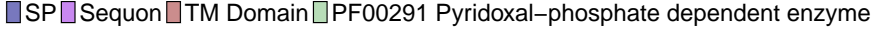
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

.ECICIMGADDERGALNIFRMRLLGAEVRGVHSGTATLKDATSEAIRDWTNVTETHYLSGVAGPHIPYPMVREFHVAIGKTRKQALEKWSGKPKDLVACVGGGSAAMGLFHEFVDDKDRVLRIGVEAAAGFDGDSGKHAATLTKGEVSVLHGAMSYLLGGEDGGIVPEPHISAGLEKPGVGPESHFLKDLGRAEYYSITDEEALAPKRLSRLGGIPALETSHALAYLEKLGKPLNGTKVAVLNSGSGKDKDVAHAKYLVK

NbL11g18750.1 trafficking_protein_particle_complex_subunit_3-like [MW = 20.83 kDa]

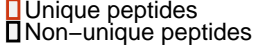
No. of times detected



log(intensity)



Values from



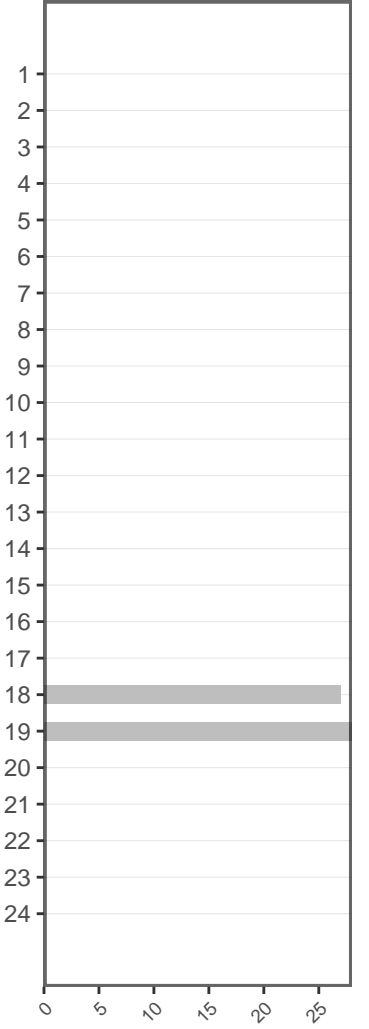
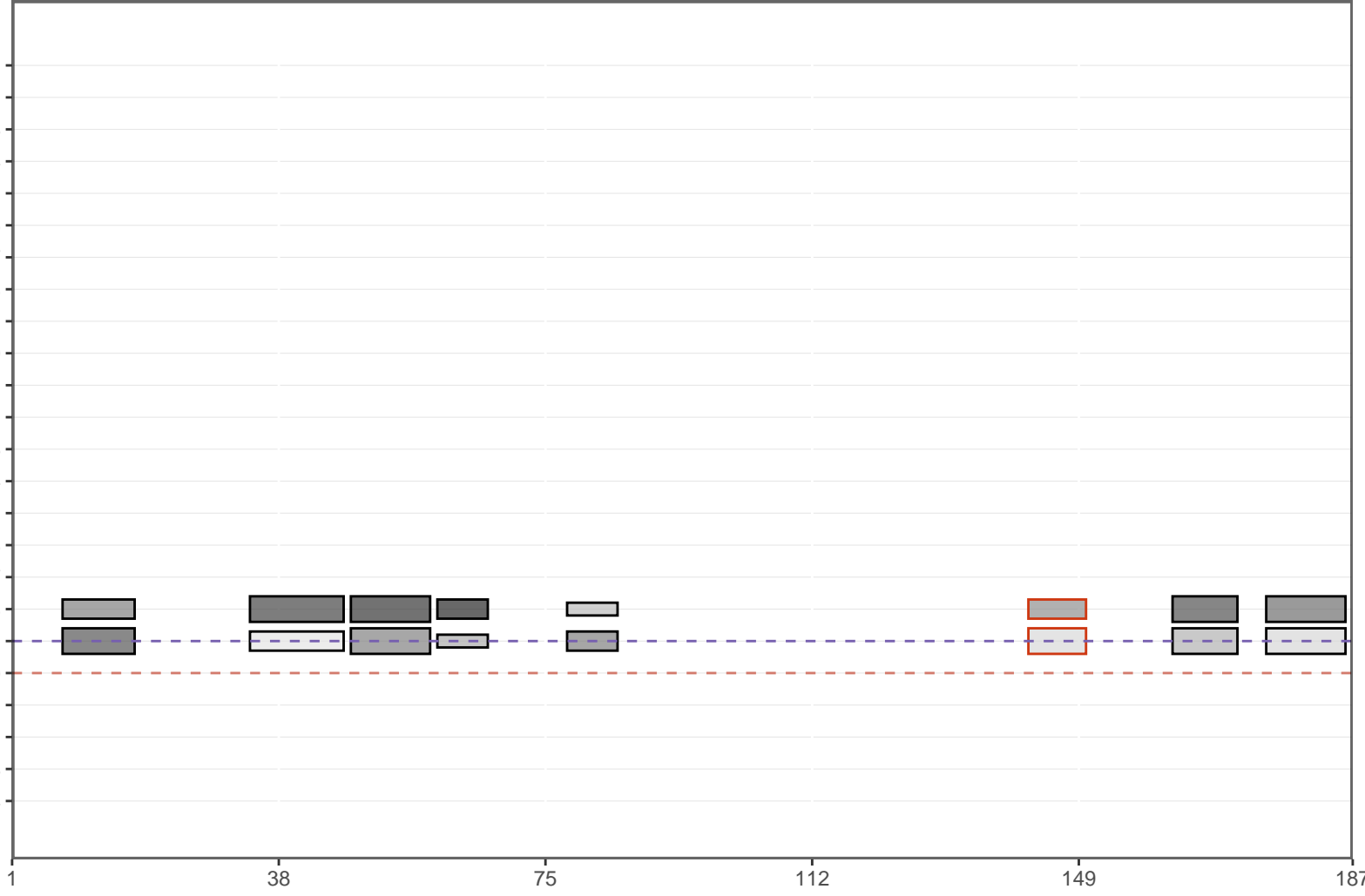
MW indication



Molecular weight

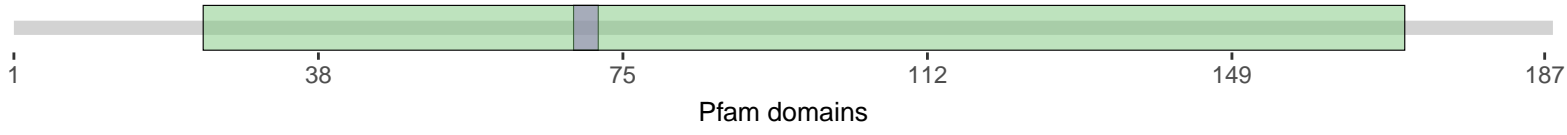


Gel Slice

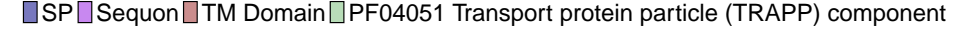


Peptide counts over 4 repeats

Protein length



Pfam Description



Protein sequence:

IVIAKGLKMFGLGVTAIVGNWDAEGTTGSLIEDNPLVDFVELPDTGGGLYYCNLGGVIRGALETYSMKTEVTWIRDMLRGDGFELQKLLKGVPEVYKDDK

NbL11g18680.1 60S_ribosomal_protein_L8 [MW = 28.21 kDa]

No. of times detected



log(intensity)



Values from



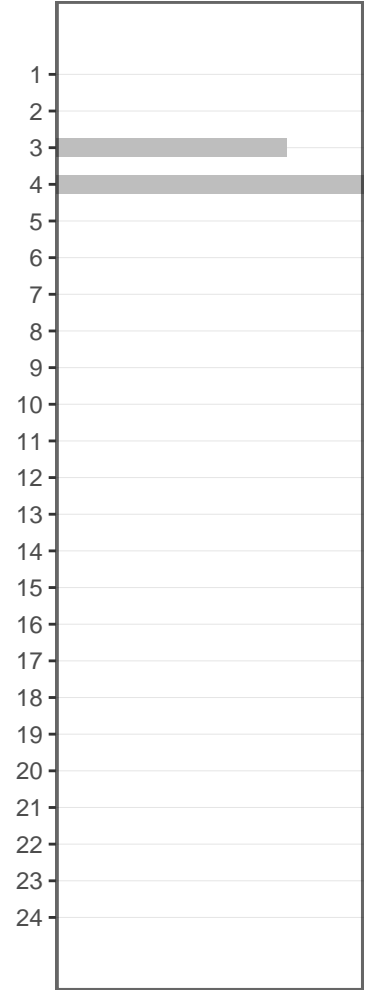
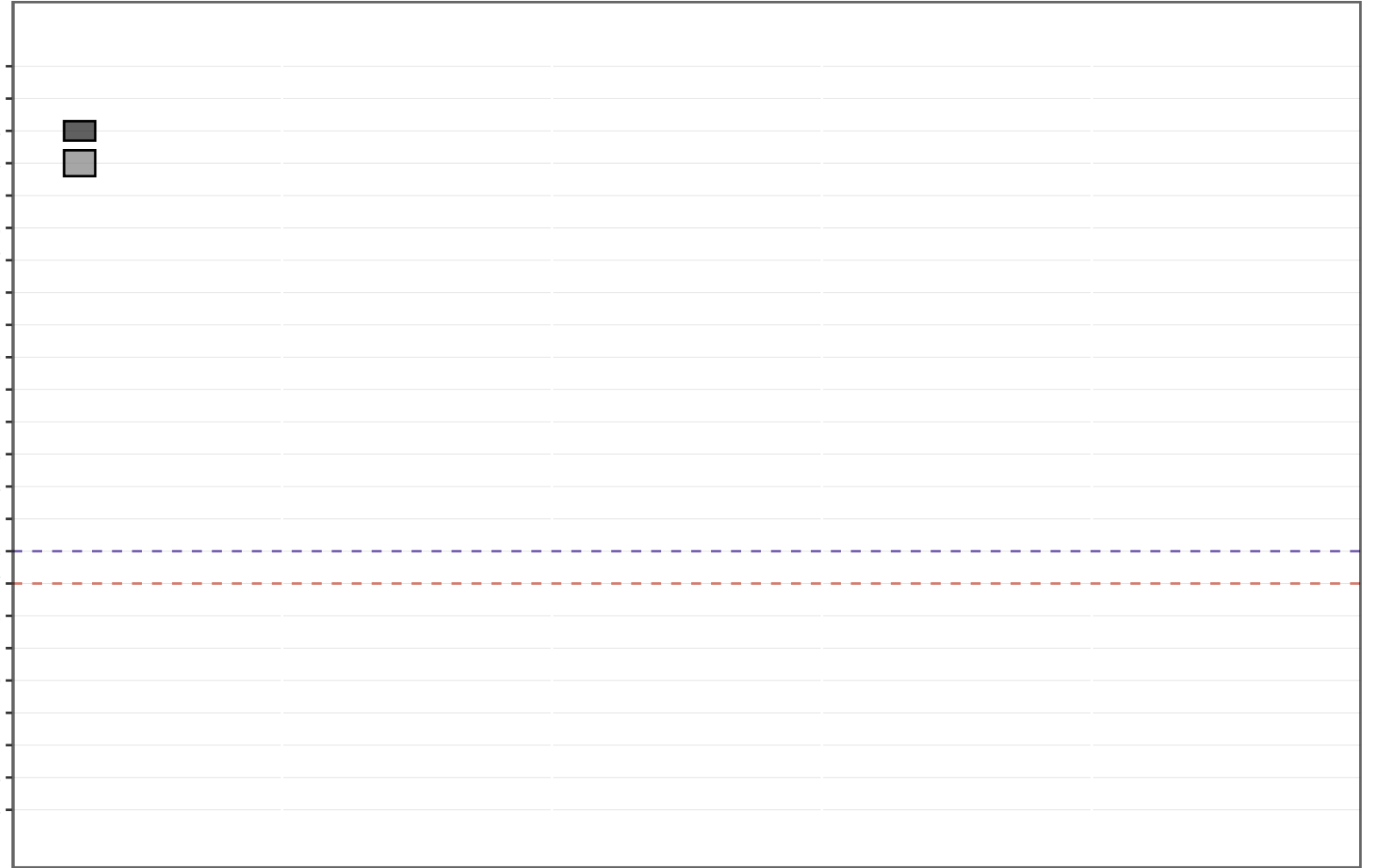
MW indication



Molecular weight



Gel Slice



Protein length

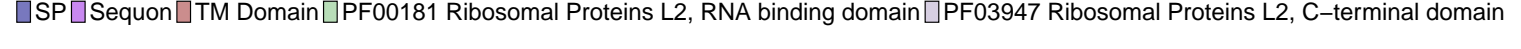


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKVGDGIVFARCSDGVAIVISHNPENGTTRVLPKLGAKKIVPFGCRAMGQVAGGGRTEKPKMLKAGNAYHKVYRKRNGWPKVIRGVAMNPFVEHPHGSGNHQHGHSASTVRRDAPPQKGLIAARRTGRLRGDAATAAKADKA

NbL11g18650.1 indole-3-acetic_acid-amido_synthetase_GH3.6-like [MW = 68.64 kDa]

No. of times detected



log(intensity)



Values from



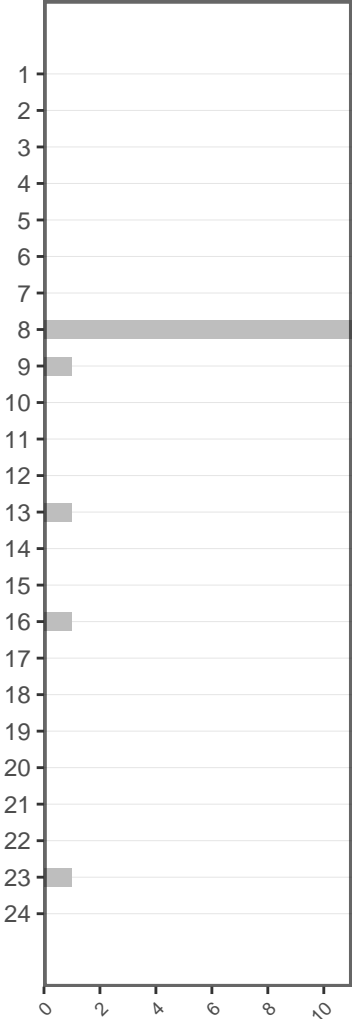
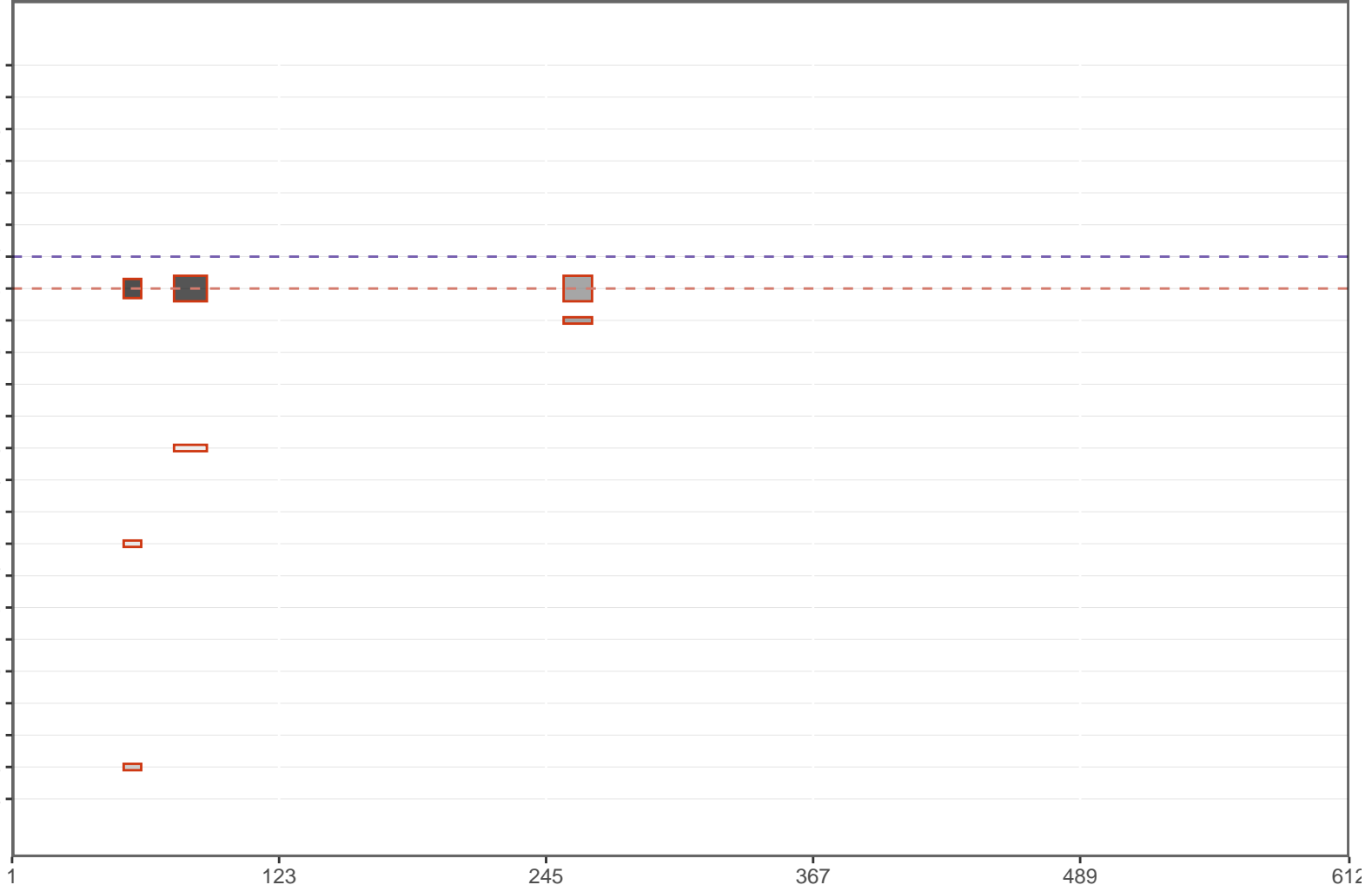
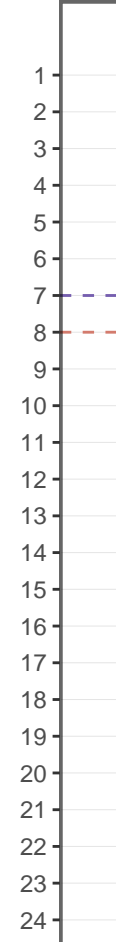
MW indication



Molecular weight

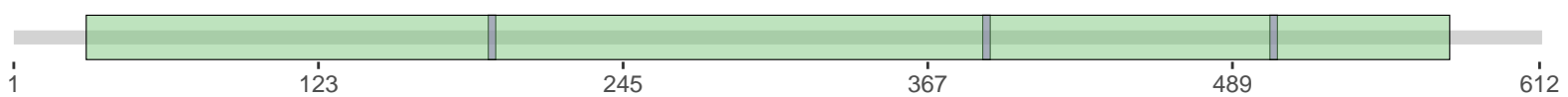


Gel Slice



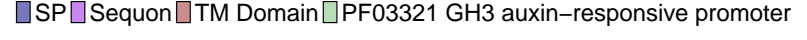
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

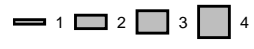


Protein sequence:

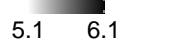
VOGIIVRLWPKTKYVDVAVTGTMSGQHPITLEYKSSSLLPLVSTTYASSEGGFGNINLPLKPESEVYFLPTMTGVEFLPGRINNEVKNISISALQNETEQGGLVDVLDVQIGGEYELVVTYSGLYRVRVGDLRVAGKKNAPQFTFRGNVLSIDSDKTDVEVLGNVAKNAASVLIPEFDMVTDKTSVADTSTIPGHYVFLFELSVNGSTPIPPVFENGLSIEESLNVYRGRASDKSIGPLERIVIGTDFDKLMDYGVSLGASINGYKTRQDKLPLLELLNSRVVSSH

NbL11g18630.1 probable_NAD(P)H_dehydrogenase_(quinone)_FQR1-like_1 [MW = 21.59 kDa]

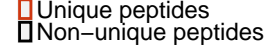
No. of times detected



log(intensity)



Values from



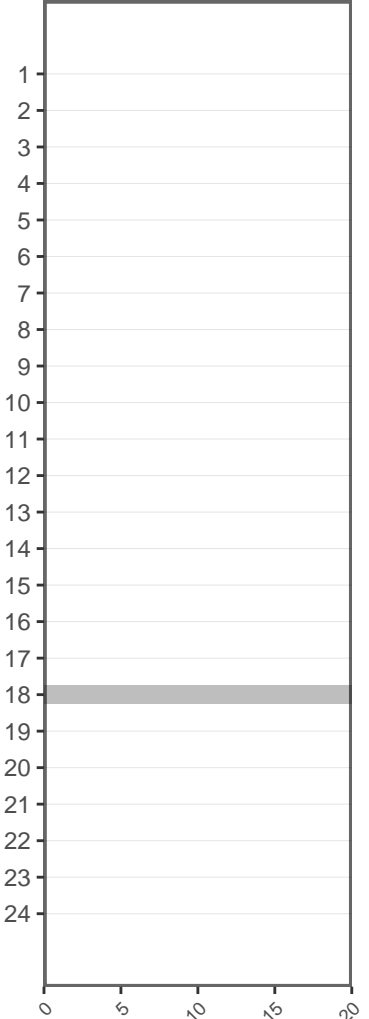
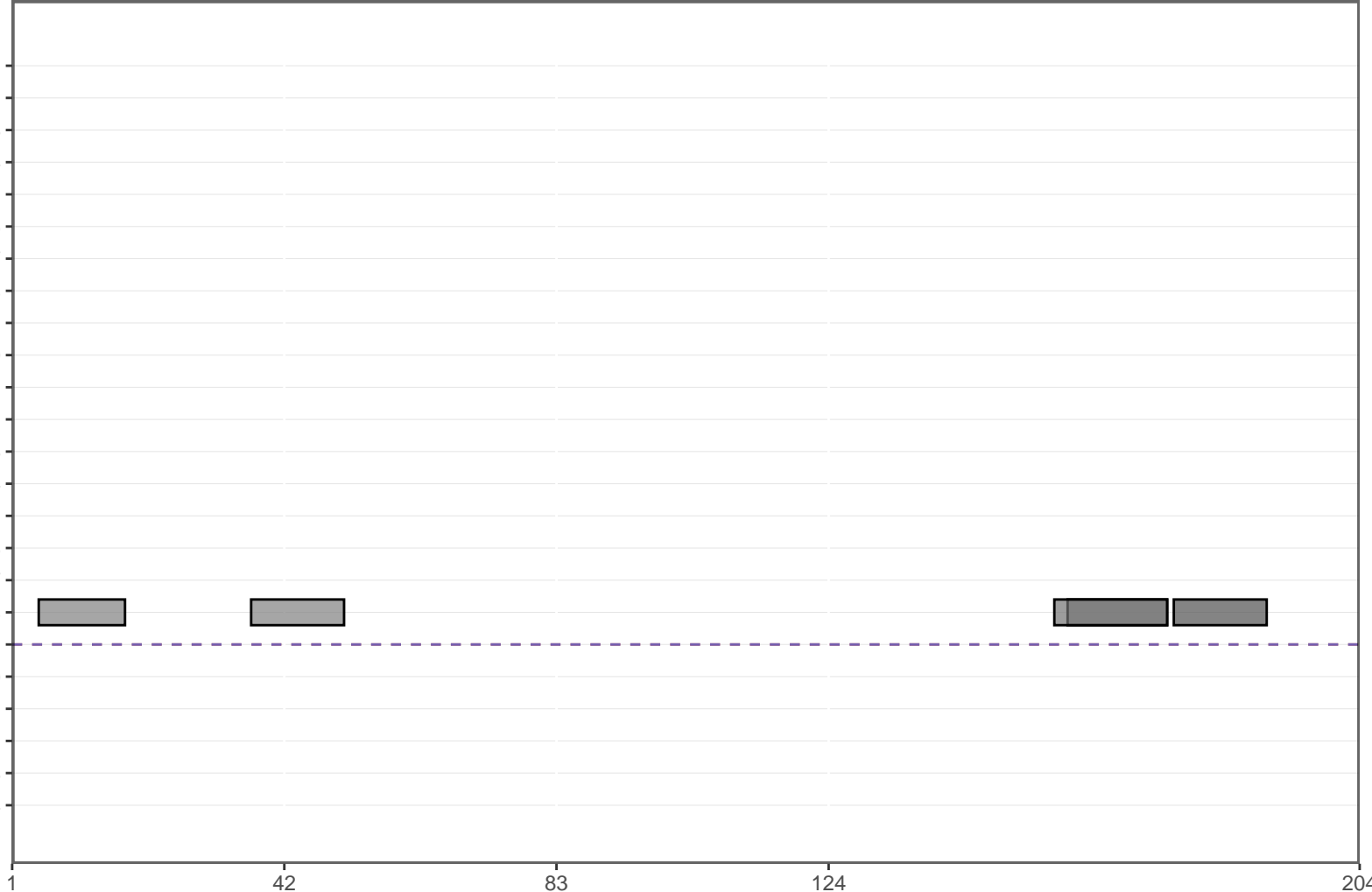
MW indication



Molecular weight

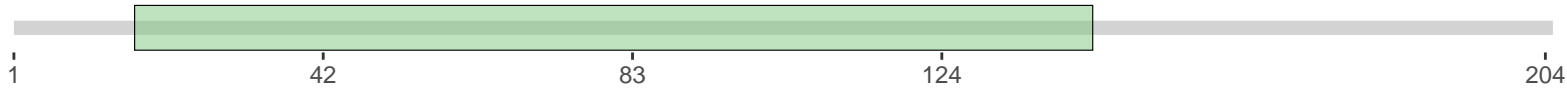


Gel Slice



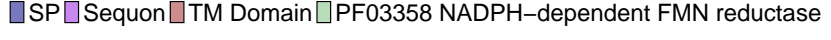
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KAFPLDATGGLVIRTGQLAGKRFVGFYSTGSGGGGQETPLTATQLVHHGMFVPHGYTFGAGMFMEMKVKWGGSPYAGTTFAGDGRSPDLELGGAFHQGKYIAGIANKLGAAT

NbL11g18610.1 bifunctional_L-3-cyanoalanine_synthase/cysteine_synthase_2_mitochondrial [MW = 39.33 kDa]

No. of times detected



log(intensity)



Values from



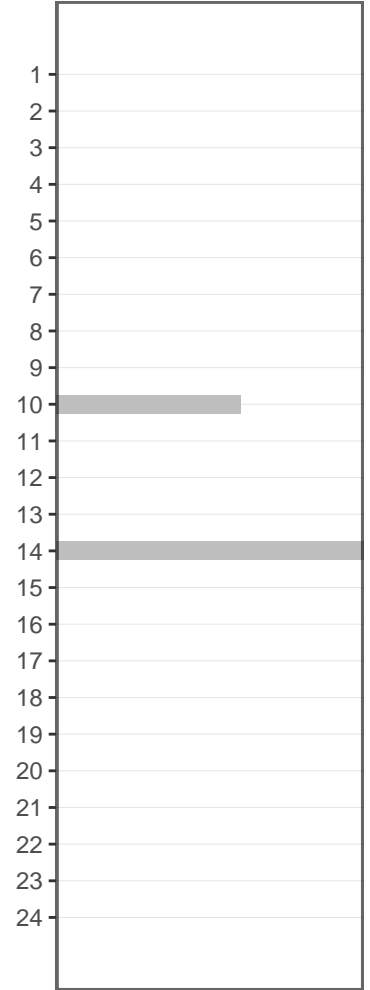
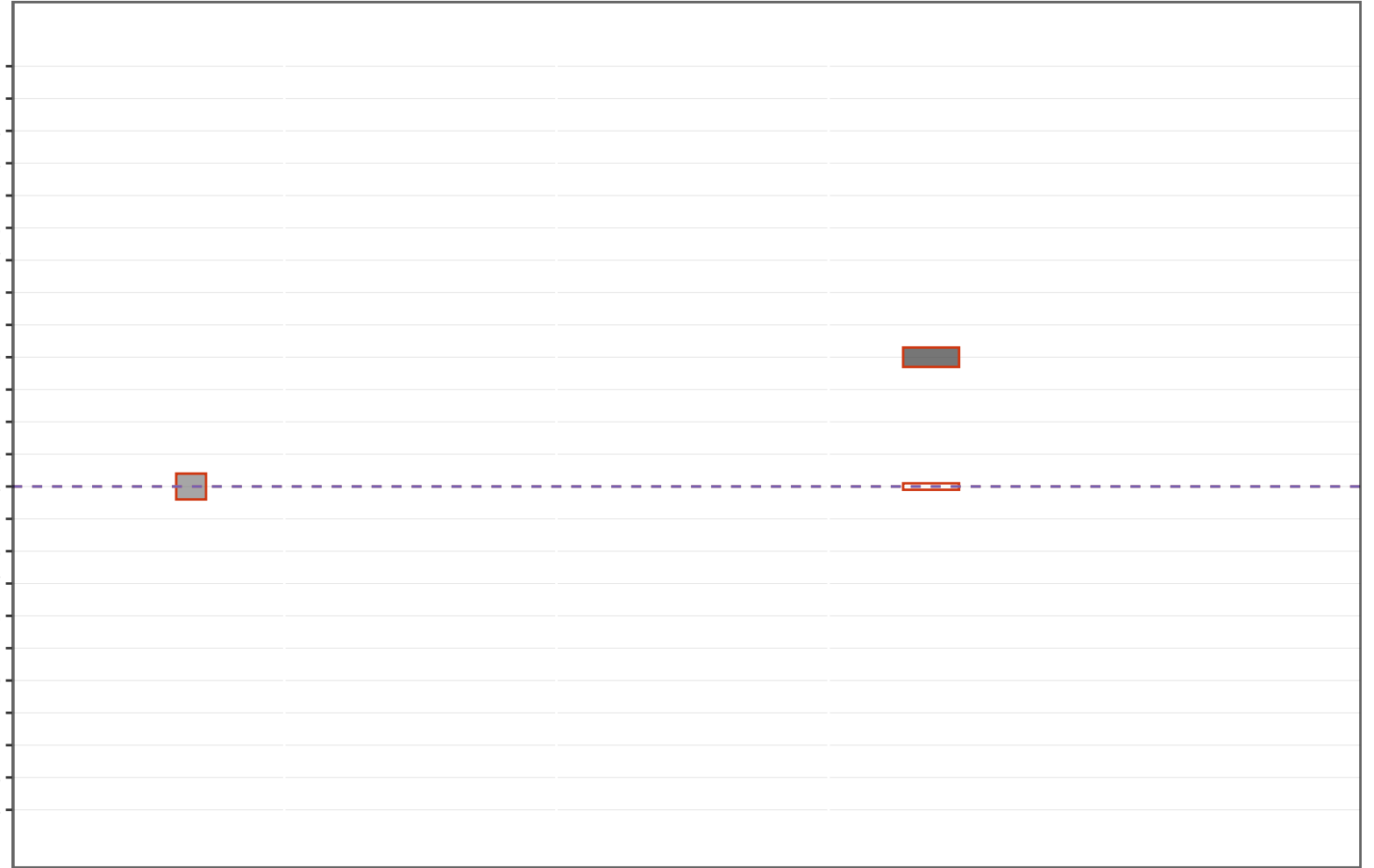
MW indication



Molecular weight



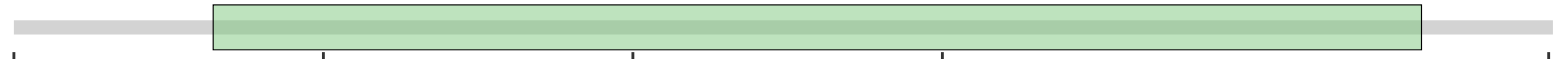
Gel Slice



Peptide counts over 4 repeats

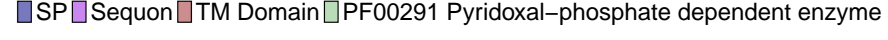


Protein length



Pfam domains

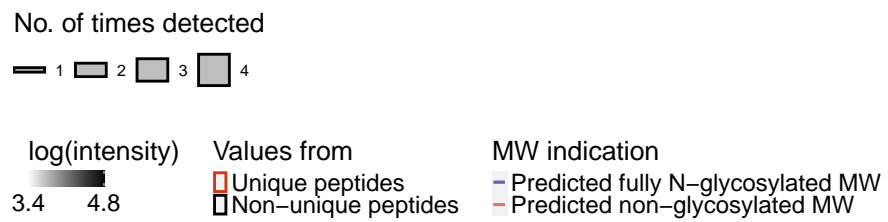
Pfam Description



Protein sequence:

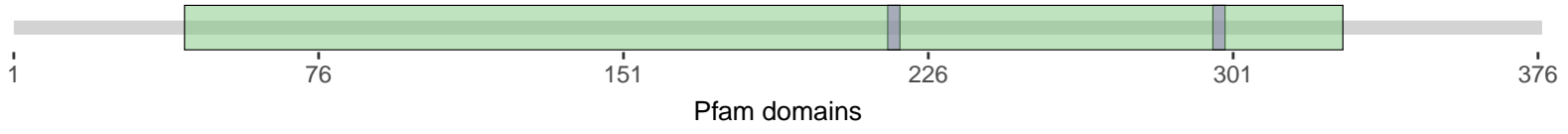
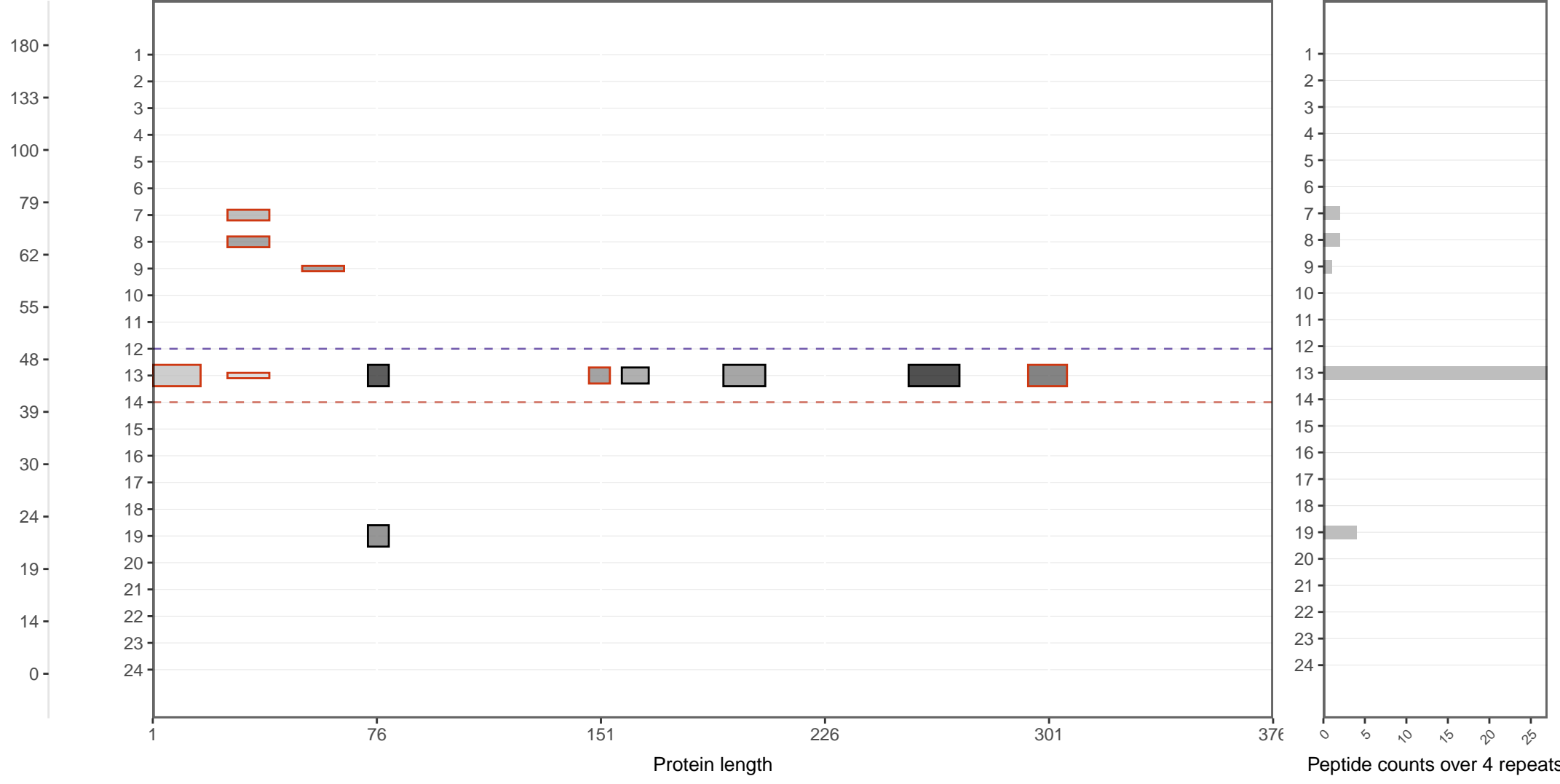
KAYDLESTPNFALGGFSPNANTQHFETTGFPEIWEETQGNVDFVMDIGSGGTVSGVGGYLYKSNPNVYVGVETESNILNGGKPGPHHTGNVGFKFDLMDIMEEVLVMSSEDAVNMARELAVKEGLMVGISGANTVAALQLAKPENKGLVTHASFGERYLSSVLYGDLRKEAENMQPVSVD

NbL11g18420.1 mitogen-activated_protein_kinase_homolog_MMK2 [MW = 43.13 kDa]



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain PF00069 Protein kinase domain

Protein sequence:

NANCDLKVGFGLARITSETDFMTEVYVTRWYRAPELLNNGSEYTAIDWVSGILGEMMTRQPLFGRDYVHQLRLITELIGSPDDASLGLRSDNARRYRGLPGYPRGFAARFFNNSPGAVDLLEKMLVDFPDRRTVDDALGHPVLAFLHDINEEPKPKPFSDFEGQPSFTEENKELWRSEVKFNPDPTH

NbL11g18370.1 desiccation_protectant_protein_Lea14_homolog [MW = 18.37 kDa]

No. of times detected



log(intensity)



Values from



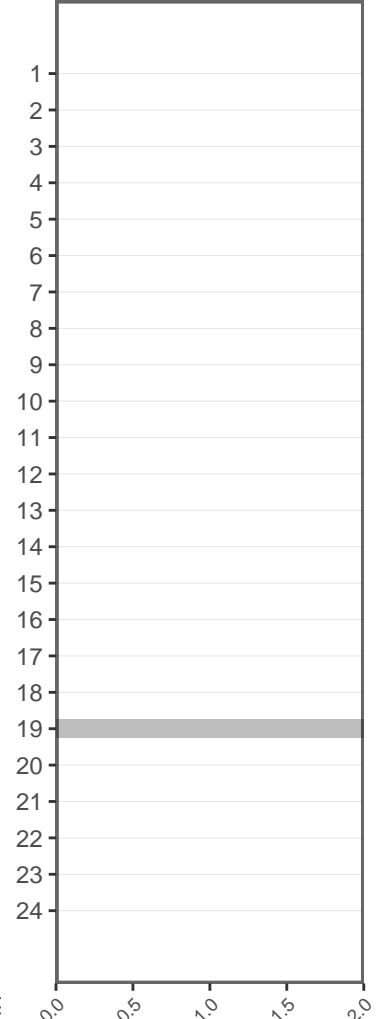
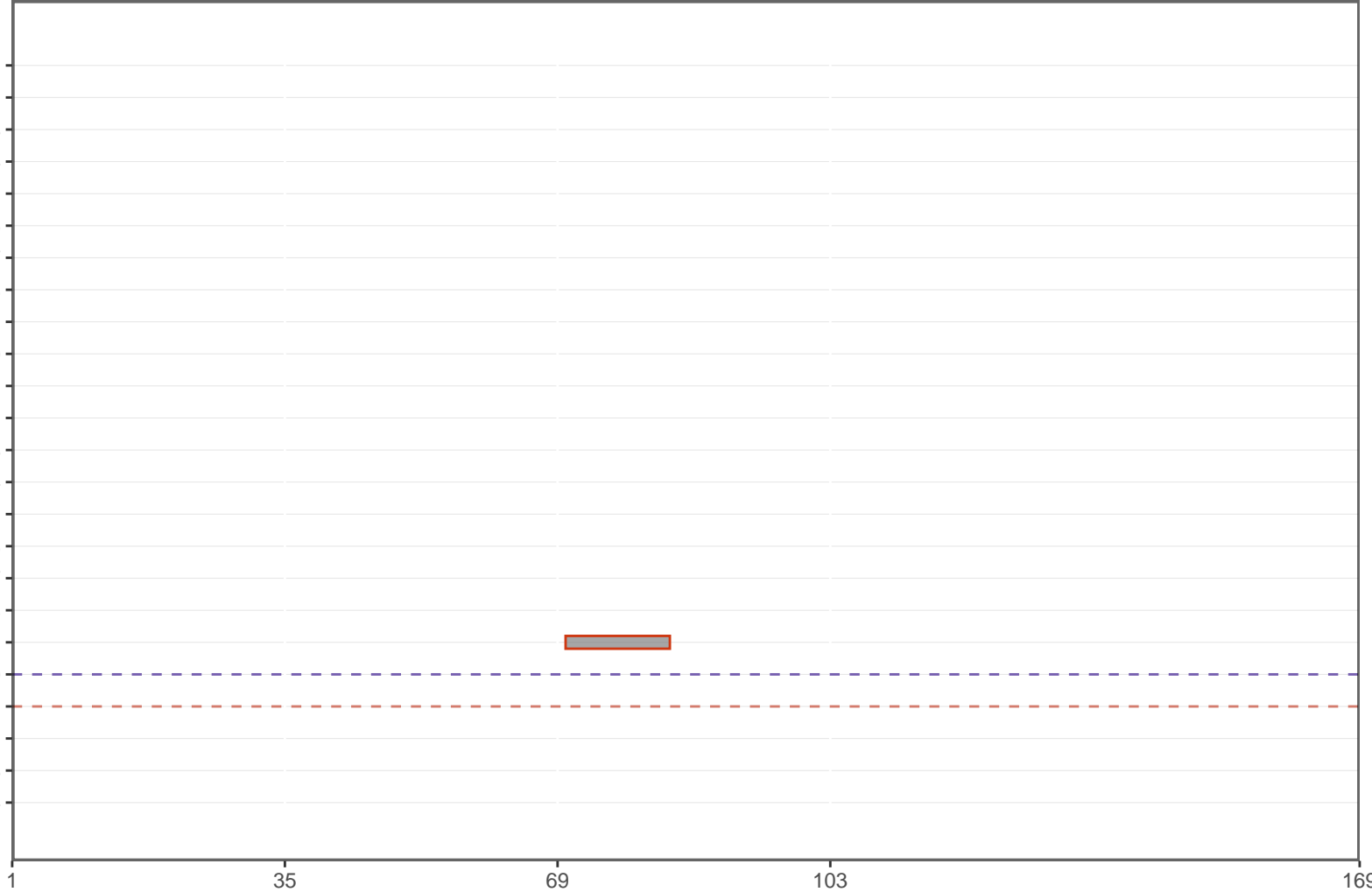
MW indication



Molecular weight



Gel Slice

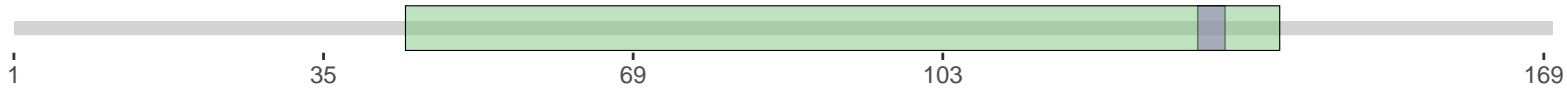


Protein length

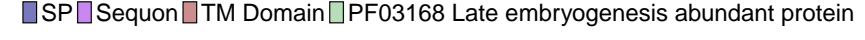


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VLSGTFDPGSSKADDTTMLGVFKVPHSVLVLAKDAGWDIDYTLLELGLTIDLPVIGNFTPLHSGEIKLPTLGLWKGEEEEKEDTEKVEI

NbL11g18190.1 eukaryotic_translation_initiation_factor_1A-like [MW = 16.35 kDa]

No. of times detected



log(intensity)



Values from



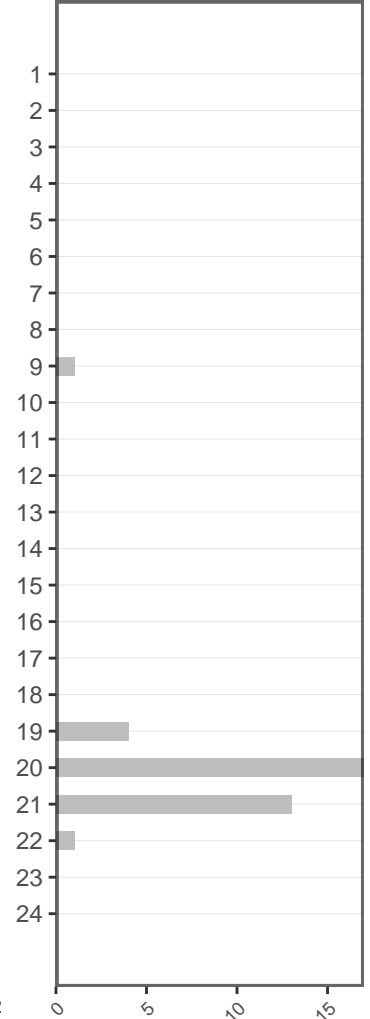
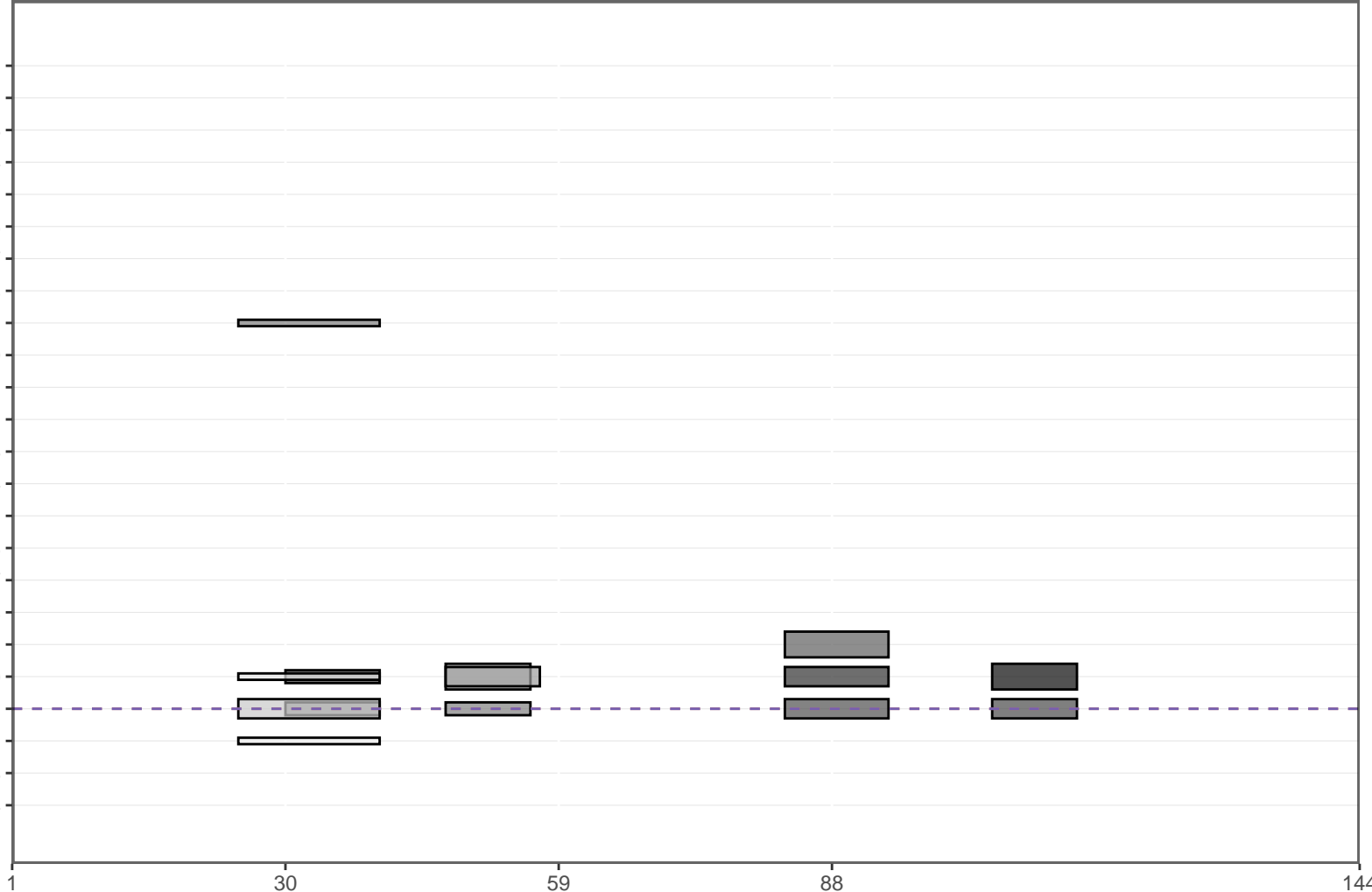
MW indication



Molecular weight

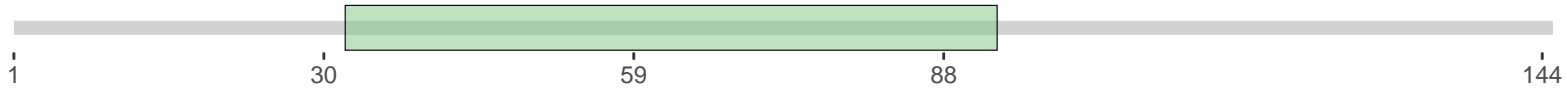


Gel Slice



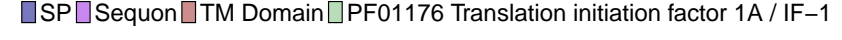
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RLCHRGKMKKKVVAAGDILVGLRDYGDQKADVILKMPDEARLLKAYGELPENTRLNEVNLDEEDDGGDDVIEFEDDEDIKI*

NbL11g18180.1 protein_CURVATURE_THYLAKOID_1A_chloroplastic [MW = 17.94 kDa]

No. of times detected



log(intensity)



Values from



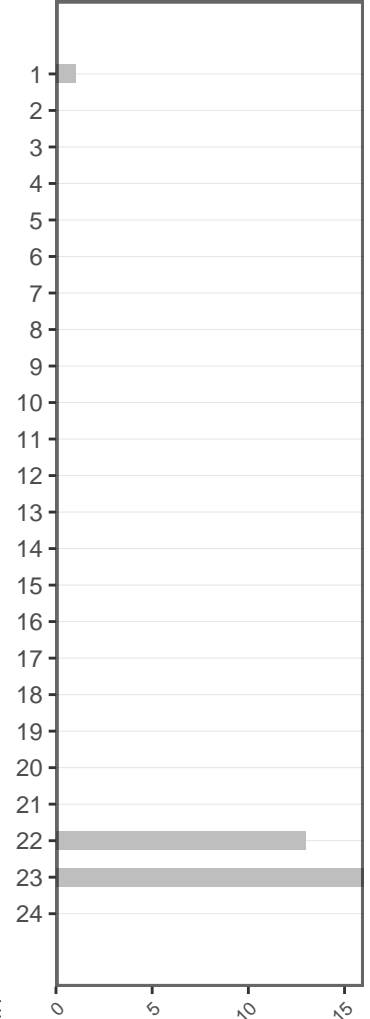
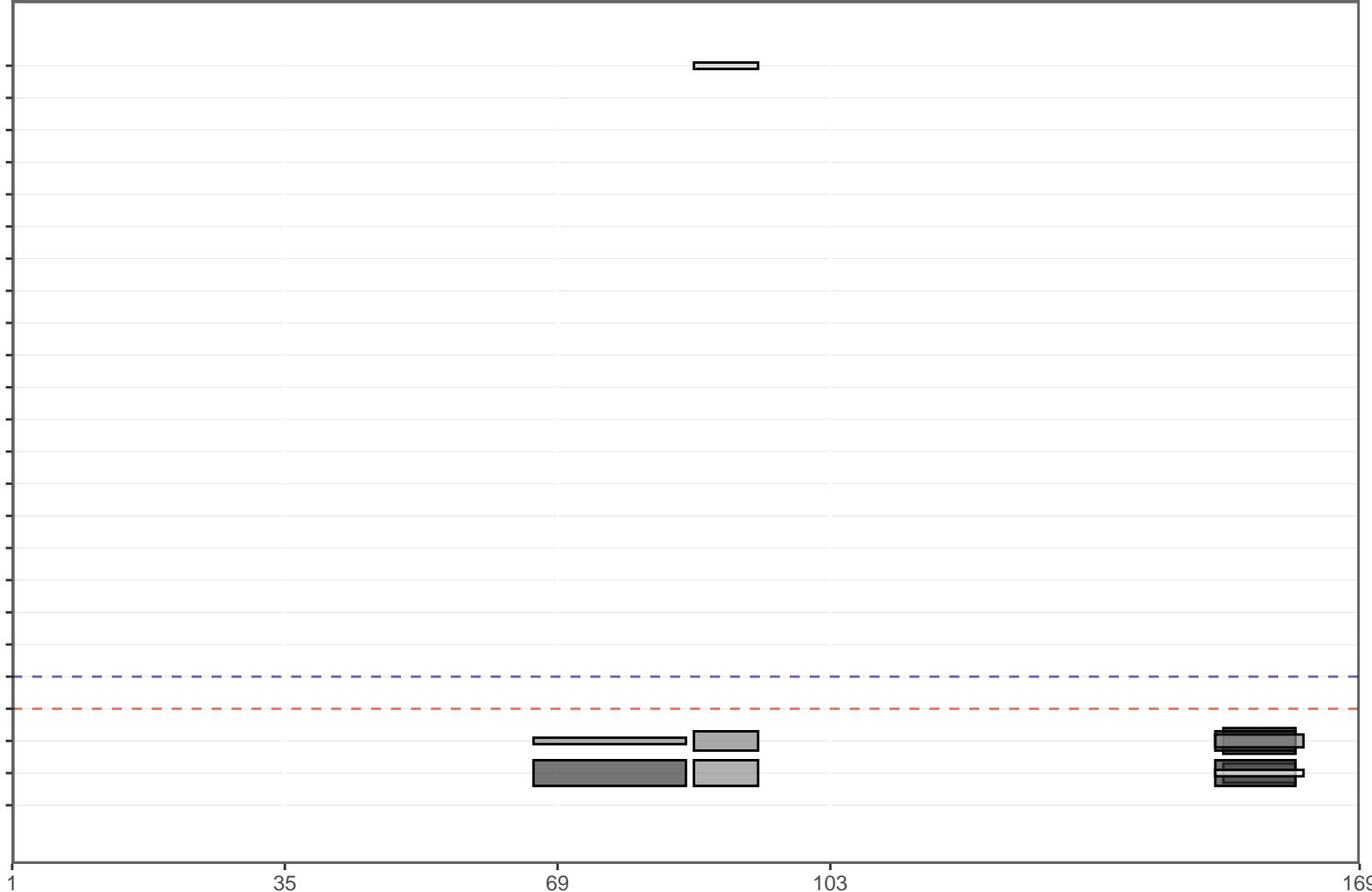
MW indication



Molecular weight



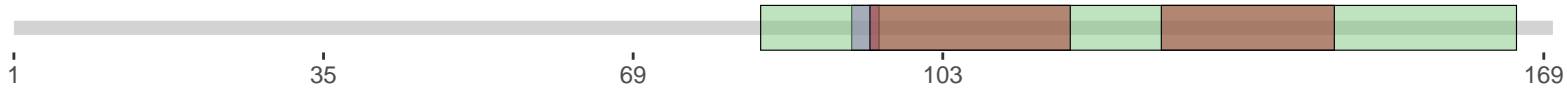
Gel Slice



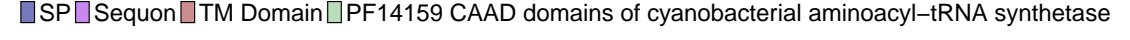
Protein length



Pfam domains



Pfam Description



Protein sequence:

ESGAVDTSELLTDLKEKWDVAENKSTVIVYGGGAMAVWLSSIVAGAINVFLPKMELVGLGYTGWFVYRLLFKSRKELAEIEQLKKKIAGTE*

NbL11g18160.1 GDSL_esterase/lipase_At4g01130-like [MW = 19.55 kDa]

No. of times detected



log(intensity)



Values from



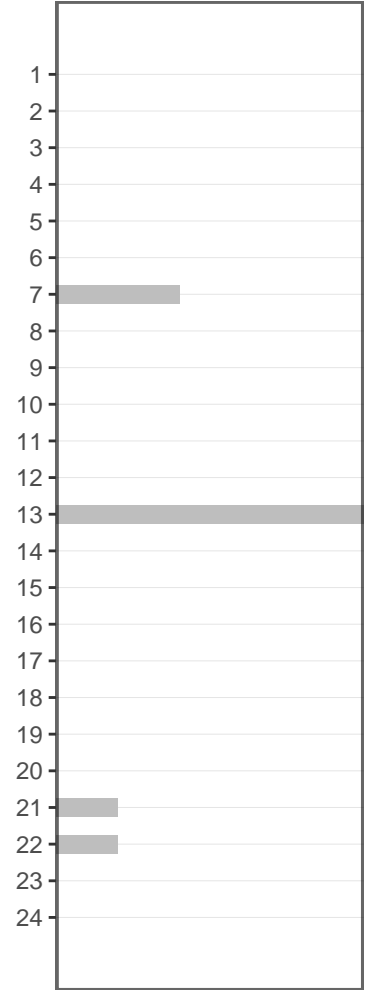
MW indication



Molecular weight



Gel Slice



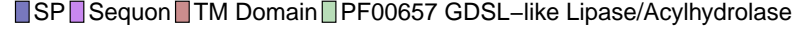
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VKYDFQHKGKTNLPSFDIFGKSLTFYFGNDFTGNLARIGISGVKEYLPQVVGQASTKEKVALGGRTFWVNLNLAIPGKNPFLVELPHNTSDIDQFGE

NbL11g18140.1 homoserine_kinase-like [MW = 17.33 kDa]

No. of times detected



log(intensity)



Values from



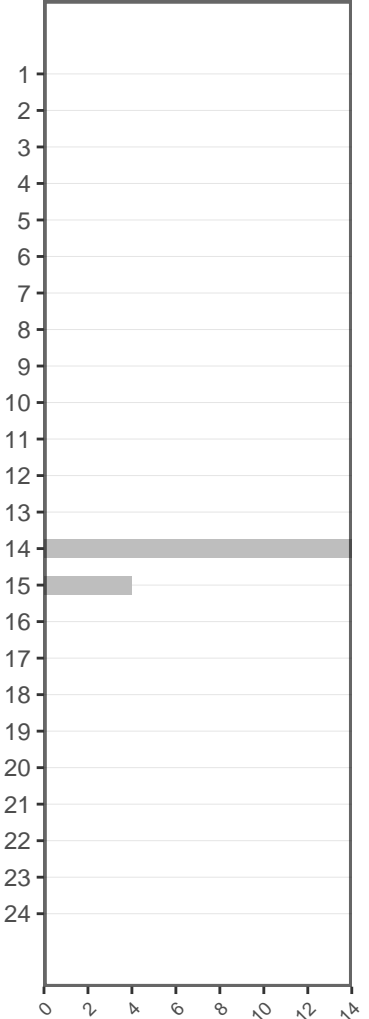
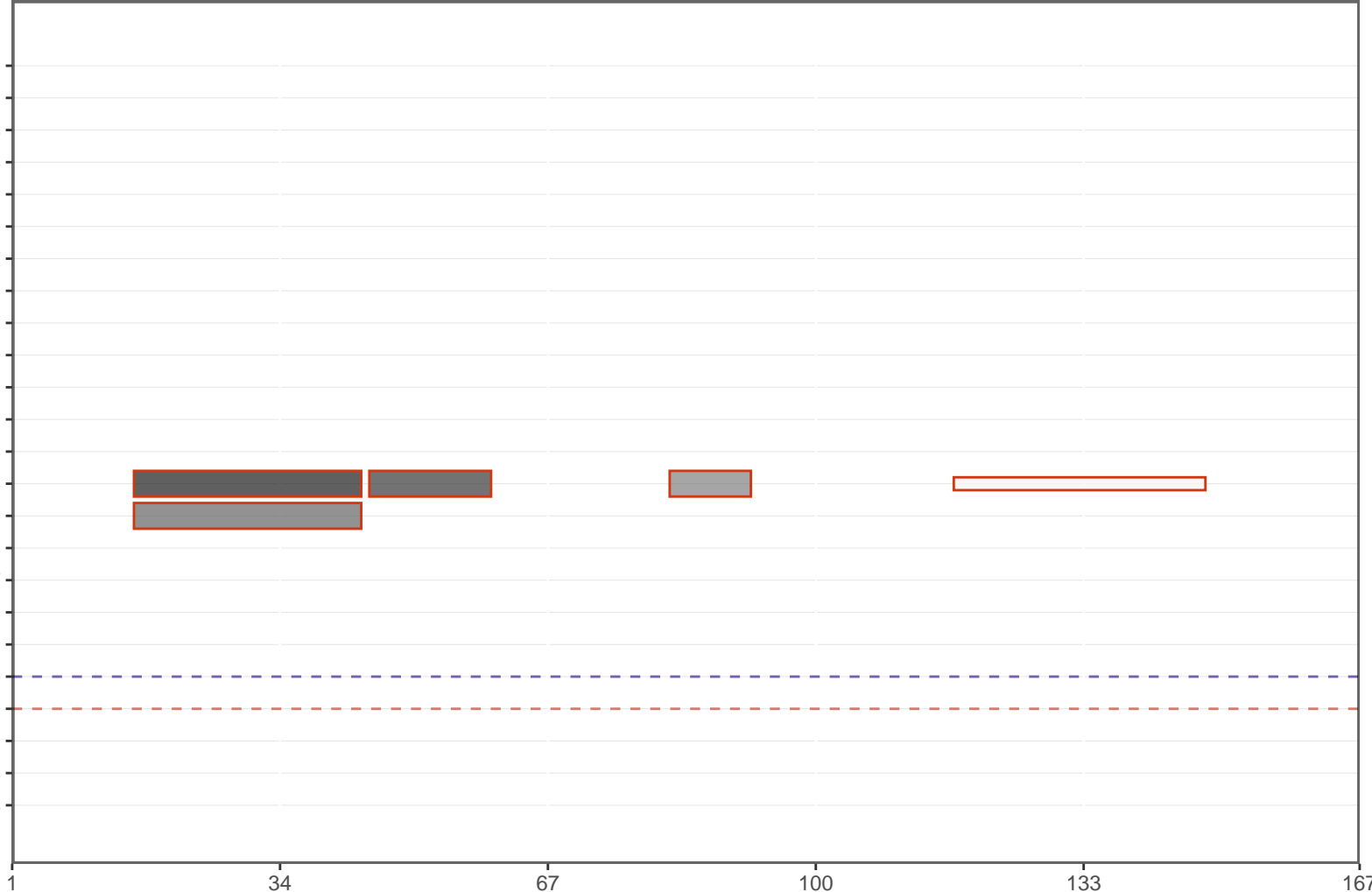
MW indication



Molecular weight

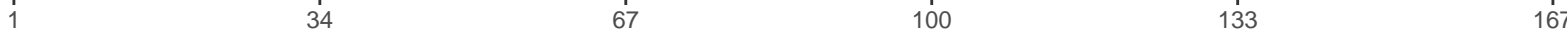


Gel Slice



Peptide counts over 4 repeats

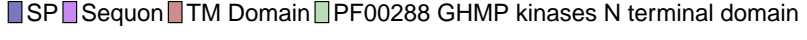
Protein length



Pfam domains



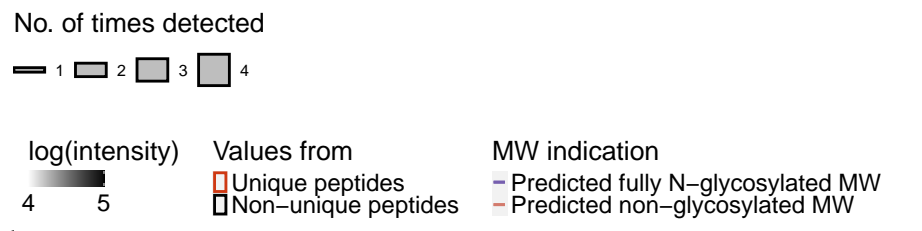
Pfam Description



Protein sequence:

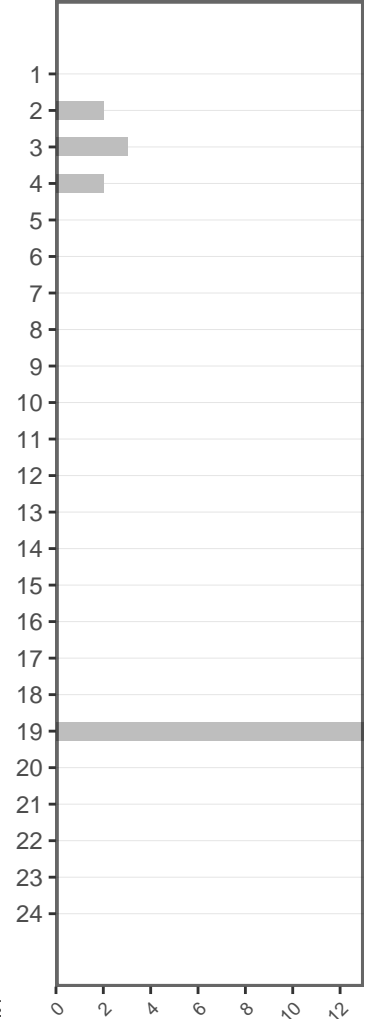
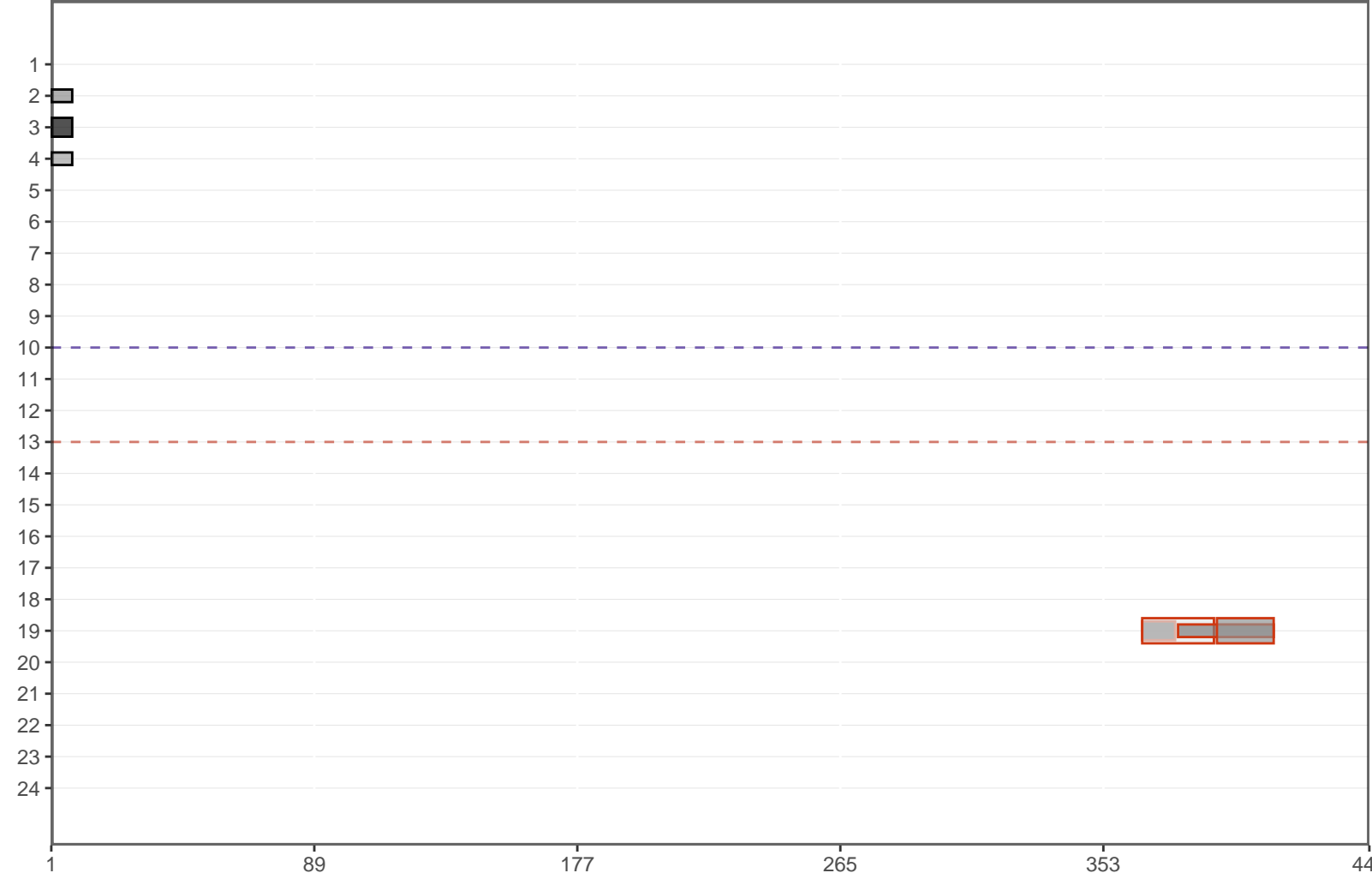
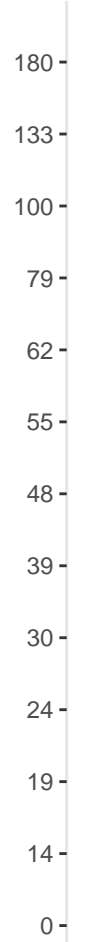
IPAMGGFYLRSYDPLELELEKPFLEKDLFVLVNPELEAPTKMRAALPNEVMTSHHHWNSGAGALVAALOGDGRGLGKVLSSDKIVFKGR

NbL11g17970.1 rhodanese-like_domain-containing_protein_4_chloroplastic [MW = 46.61 kDa]



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



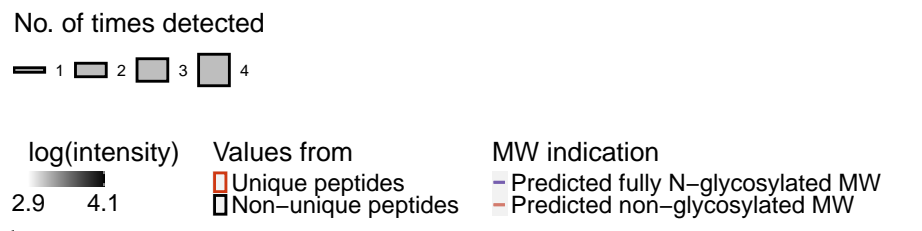
Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

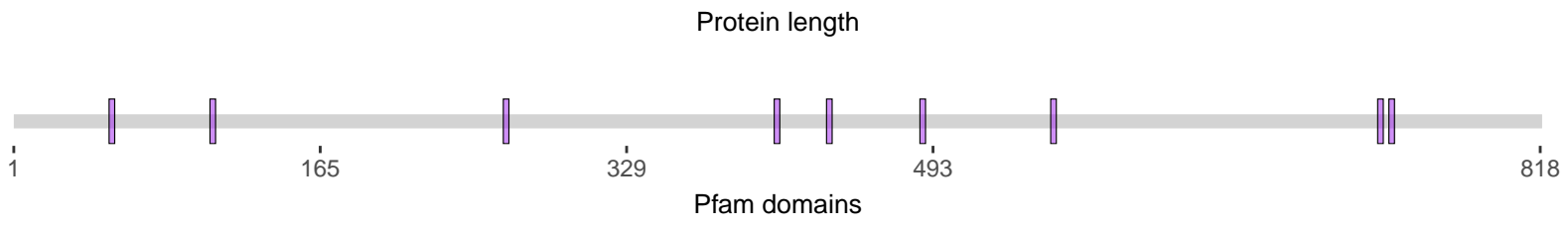
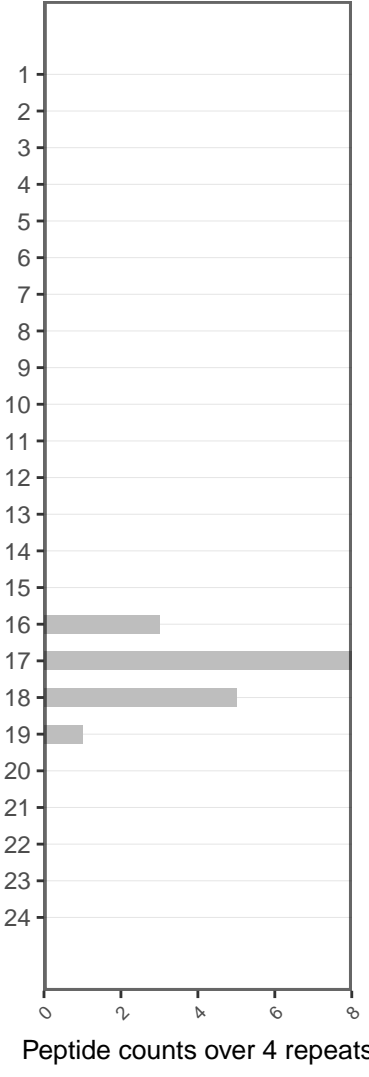
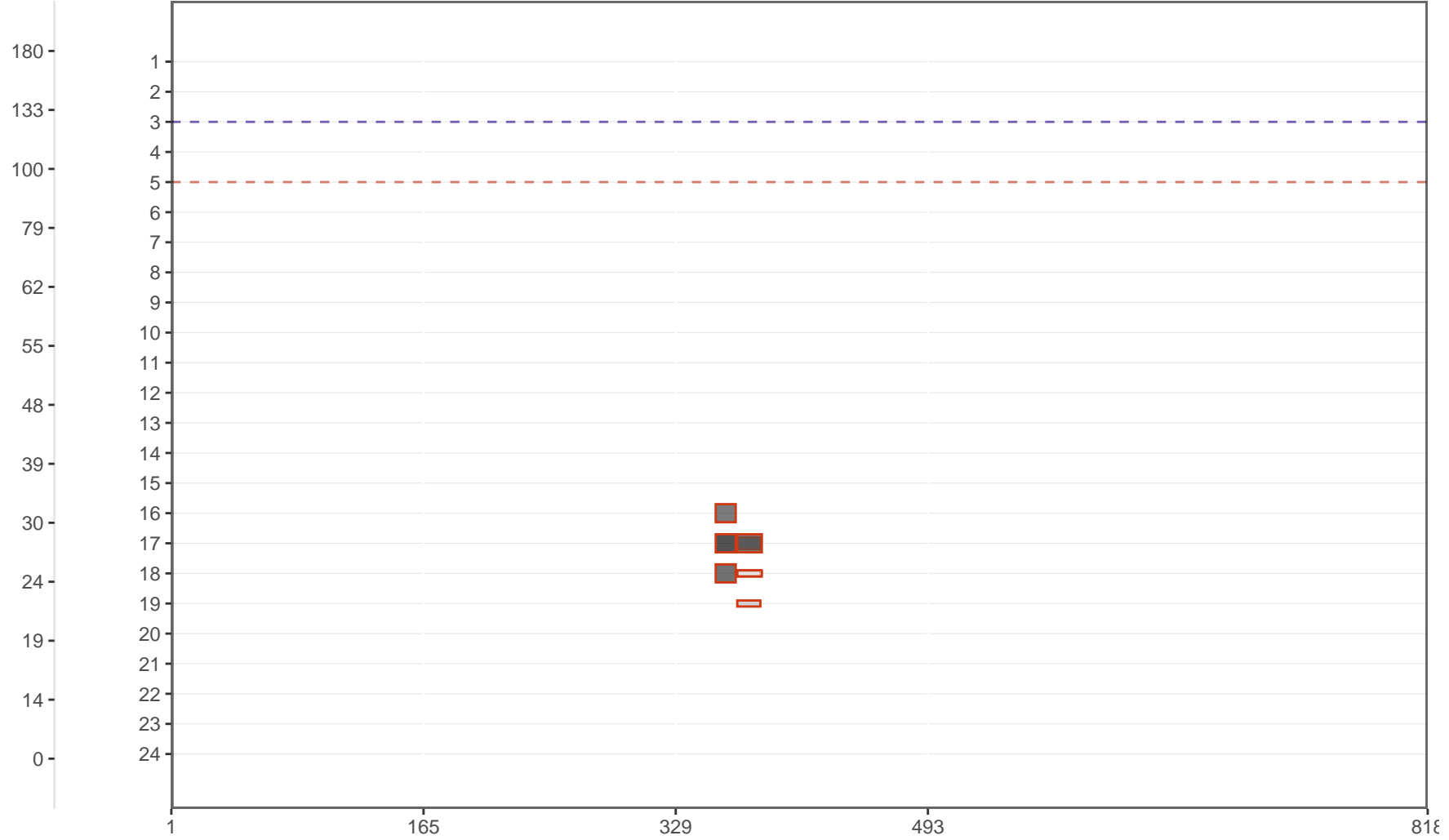
ISELVAEVLTSTNGFKAAAYAKDGAEGPRGWLNSGLFVWNAKPKTLELDLNSLDALDGLGEGSSDAVTIGLGAATAAGLGLAFSEVETLQLLGGAAALHQLKGLKLLFAEDRKLTLGGVDFELSTKIAPKELVDEIKGKIKALLPETVYSSNALLAPKKEGPAWVTDTEKTESVPOEDISPPKVEASSGPTPEVNSVANAIEKADALPNSRRLSPYVNPDFKPTSPMPMP

NbL11g17840.1 clustered_mitochondria_protein_homolog [MW = 89.68 kDa]



Molecular weight

Gel Slice



Pfam Description

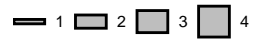
- SP
- Sequon
- TM Domain

Protein sequence:

NIDLYTDSADQVIGNETEDTNIKEEQLGDLKGGGEISDVISANASIKPGHVDVDFMEQGGVGAHVPTSDNPKVDLGEKDSRNLDPVYINLFLQMDHLKVKAAASLTGASRELSRKLASAAFFPSAGIARVAPLPMNINLPPPGTLPVVGPRVPMNMSLHGGPPTMLFNPIMSSPHLYLPPRHTPMNMMHPIRFMYPYVGGPQLFPPTFFRISSENFPHNHWAGCNAPTASEVVPKTVWPGGHVPEFVSPVPELPTDSEISAAKEPSEDESILATSLPVDL

NbL11g17710.1 exportin-2 [MW = 109.56 kDa]

No. of times detected



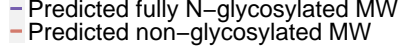
log(intensity)



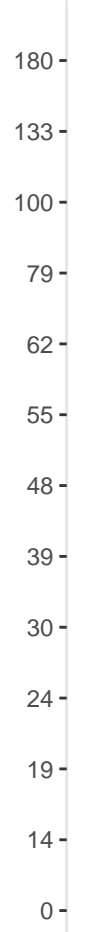
Values from



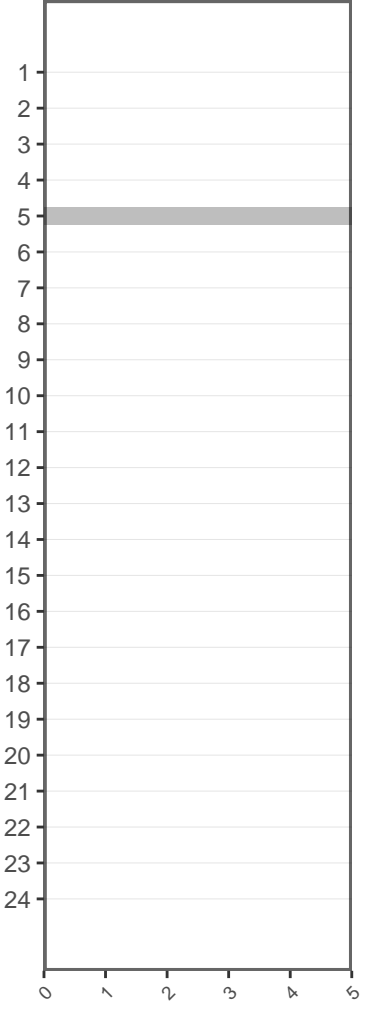
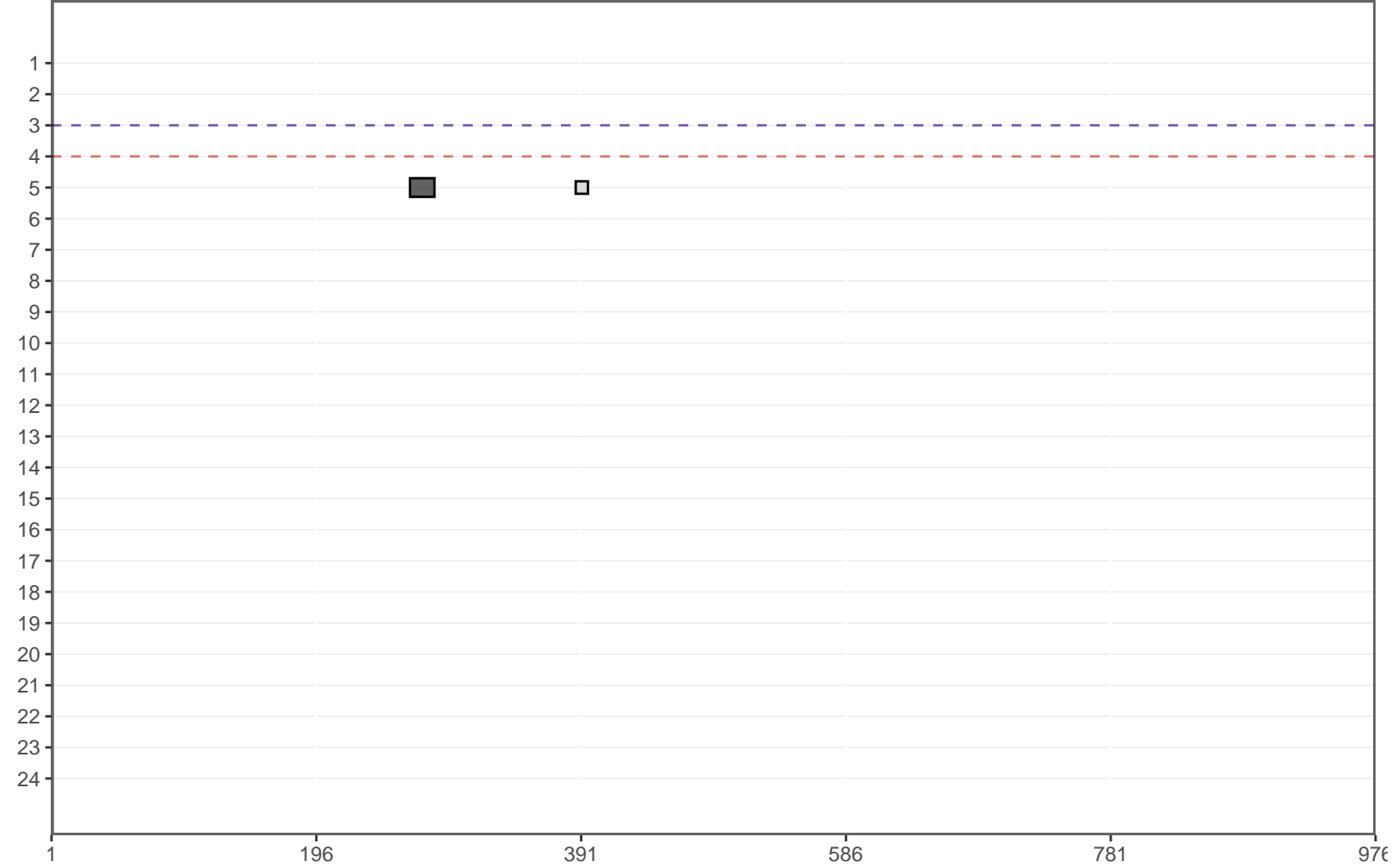
MW indication



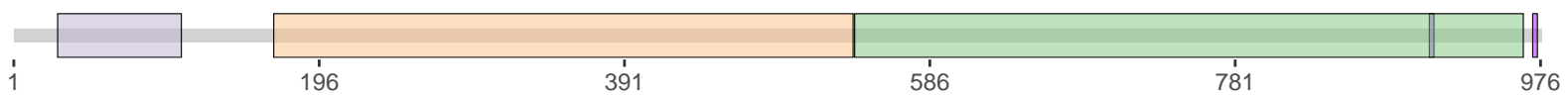
Molecular weight



Gel Slice

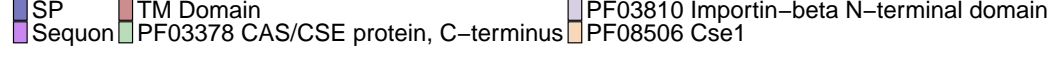


Protein length



Pfam domains

Pfam Description

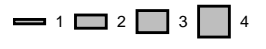


Protein sequence:

SVIVPELQSRDYNAPFMKAGALKFFTFMFRNGLPKAVAMALLADVRFLLAESNVVHSHVAASQIEKLLLVKDEGTRARYTATDISPFLVLMNLSFALEKPESEENGVNKGIMRVLGVAEISRWASAGITGLTNVLRVQGNPKNPFNHYLFESVWLRIRACEKNPTLSAFEGSLFELQMLANDVSEFFPYAFQQLSOLVELNRRPVPQHYVDFEILLPEGWKKSANVAVRLLGAFRLKAPHELNGGRLSNVIGIFNTLSGSPSTDEGGFVAVTNIENLGYDVSFP

NbL11g17620.1 bifunctional_fucokinase/fucose_pyrophosphorylase [MW = 118.2 kDa]

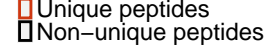
No. of times detected



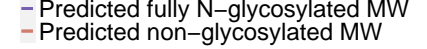
log(intensity)



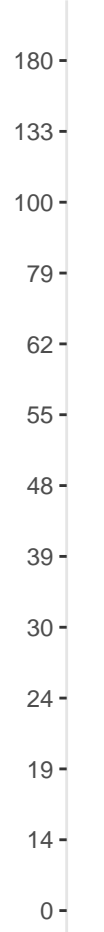
Values from



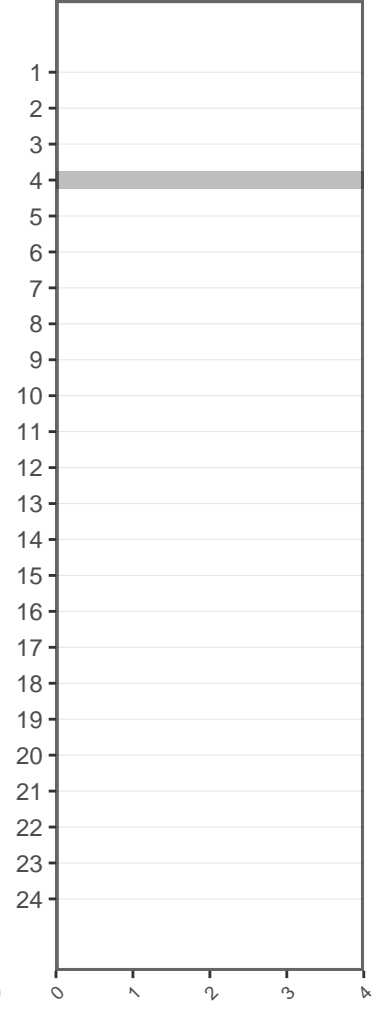
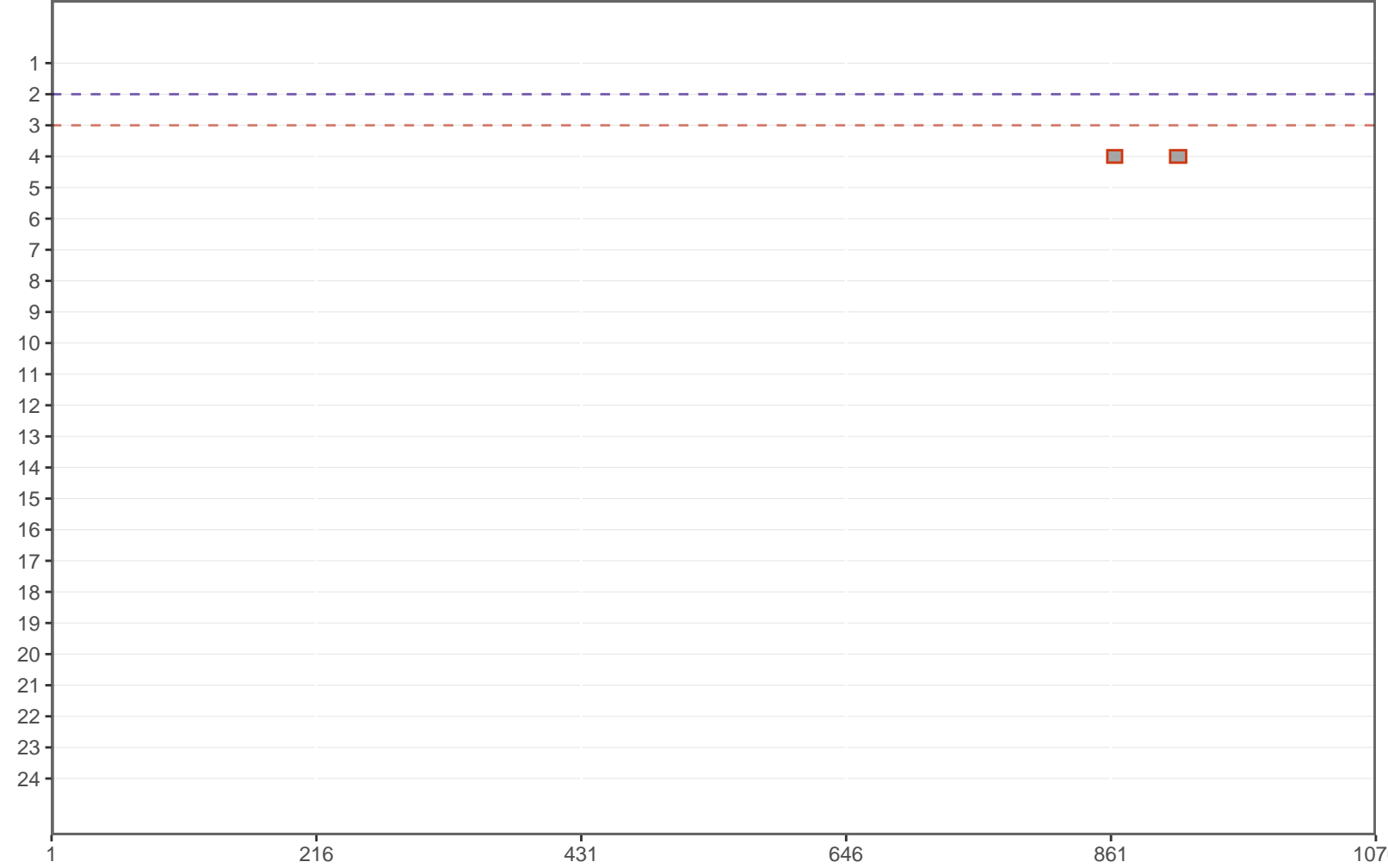
MW indication



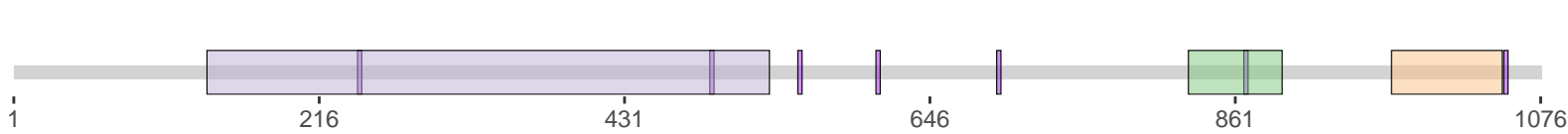
Molecular weight



Gel Slice

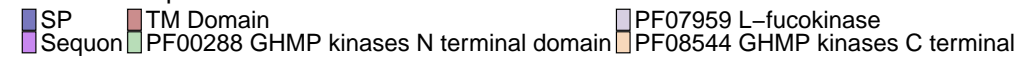


Protein length



Pfam domains

Pfam Description



Protein sequence:

NAKIFPLPYFEMLTALBWLMLGLDNGRNETLLSSWVQSKRIEELHKSIDFPHLGGSSSNHQADLASGIVNAQLNFDELGRNISQLGEEHAKESTGVCEVCKGFLSKCPNLGAGNSALPKRALGVHVDLFRACGNKEMALETERKVVAAVAETASAVRYGFKENLGGSSVSSAANPQNTNGCCVGGSHRRMVKIPLPVRVDFVGGVSDTPPWBLERAGGVLMMAITLEDLPLVGTIEREKGTGFIISDDHGNLSEIELSSVALPFESNDPFRLYKCALLTVNHK

NbL11g17570.1 ras-related_protein_RABA3-like [MW = 27.71 kDa]

No. of times detected



log(intensity)



Values from



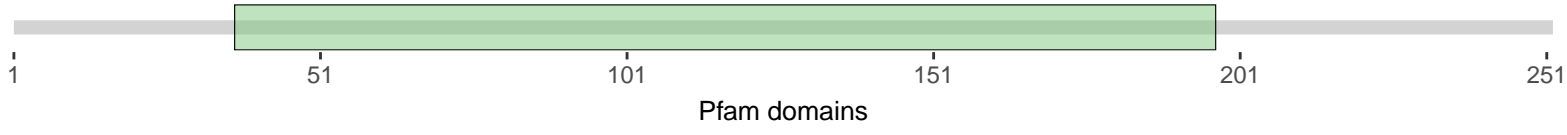
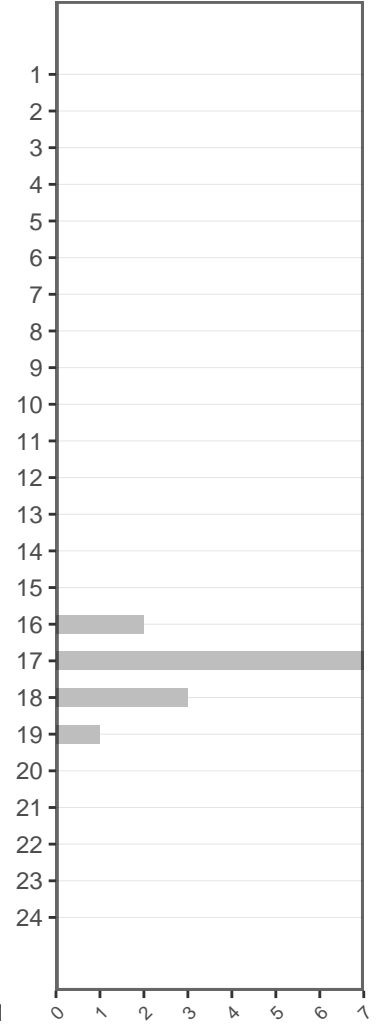
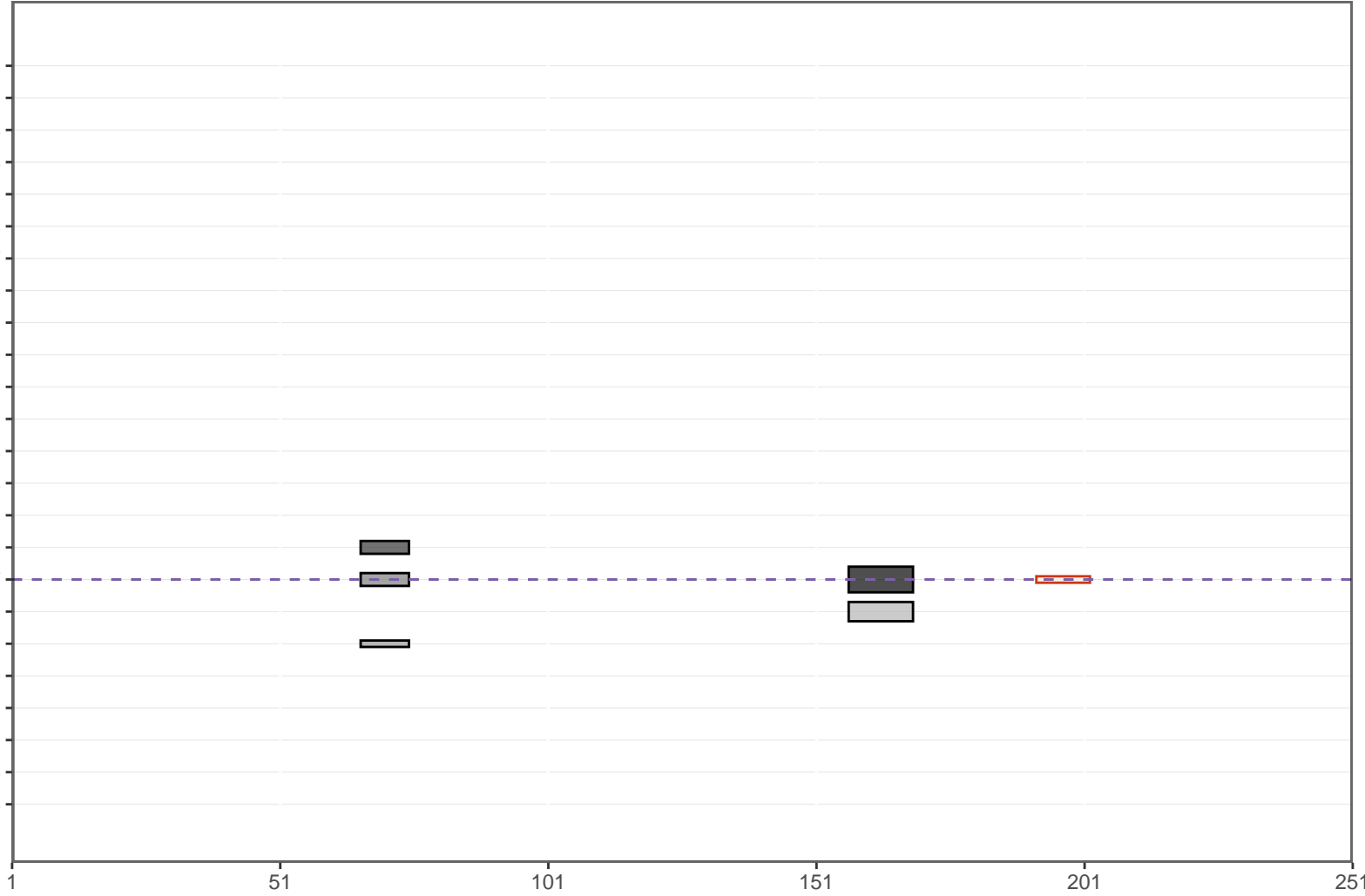
MW indication



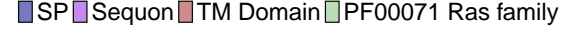
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

MLLYDITKRGSDFNARWVDELRLVHADSIVTLGKADIVDLRAVPTEDVFEFAERQGLFFSETGALSGHNVEGAFLLKLEIYVAVSRKTLHGSGANGNHKETNGLLGLNLDVHSGDFEVEEMKLLSGGSC

NbL11g17540.1 uncharacterized_LOC104241754 [MW = 29.54 kDa]

No. of times detected



log(intensity)



Values from



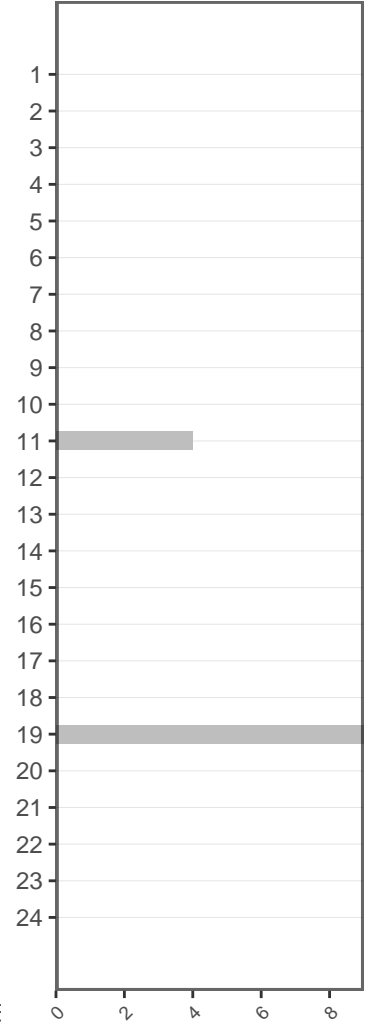
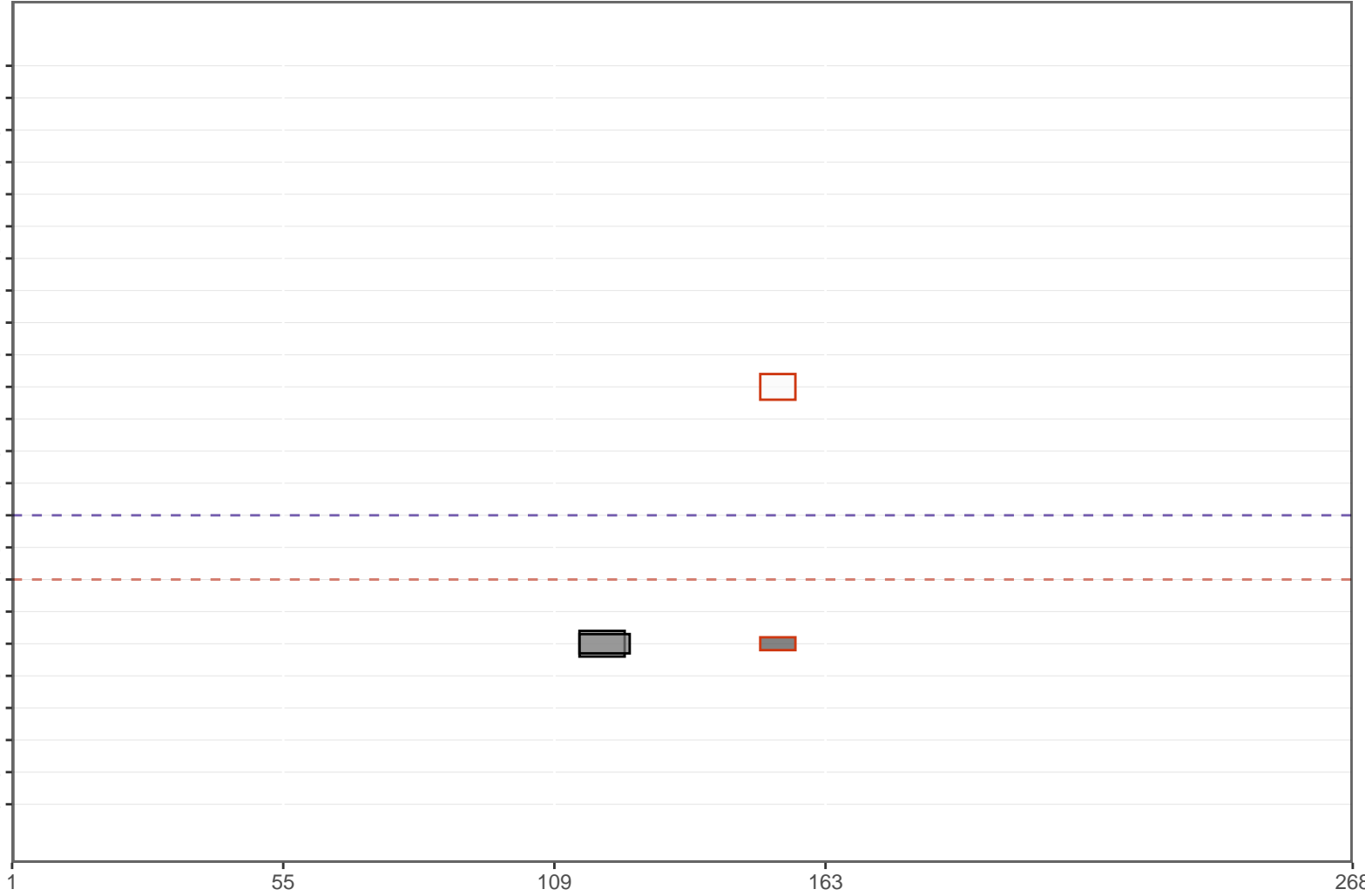
MW indication



Molecular weight



Gel Slice

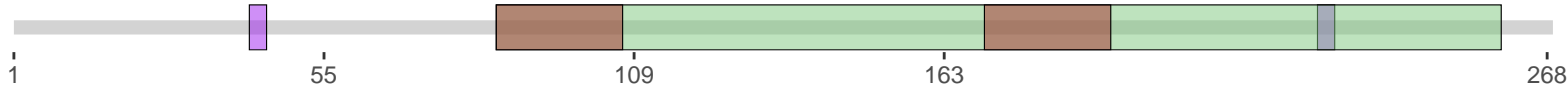


Protein length

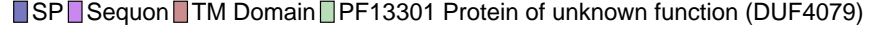


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ILKKQYKPLPYTPTEGTRPKPKPSVEARIGQLTEQRKELIKGSYKDKHFNAGSILLAWGVFESAGGVNTWFRTKLFGPHLFAAGITLWAAAAALVPMQRGNETARNLHIALNALNLVFWQIPTEGIDIVKVFEEFTSWP

NbL11g17480.1 homeobox-leucine_zipper_protein_ATHB-12-like [MW = 28.95 kDa]

No. of times detected



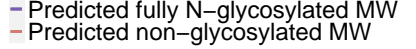
log(intensity)



Values from



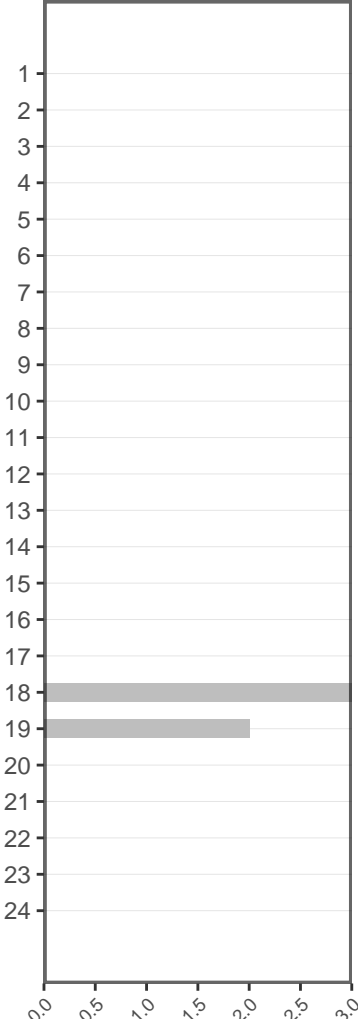
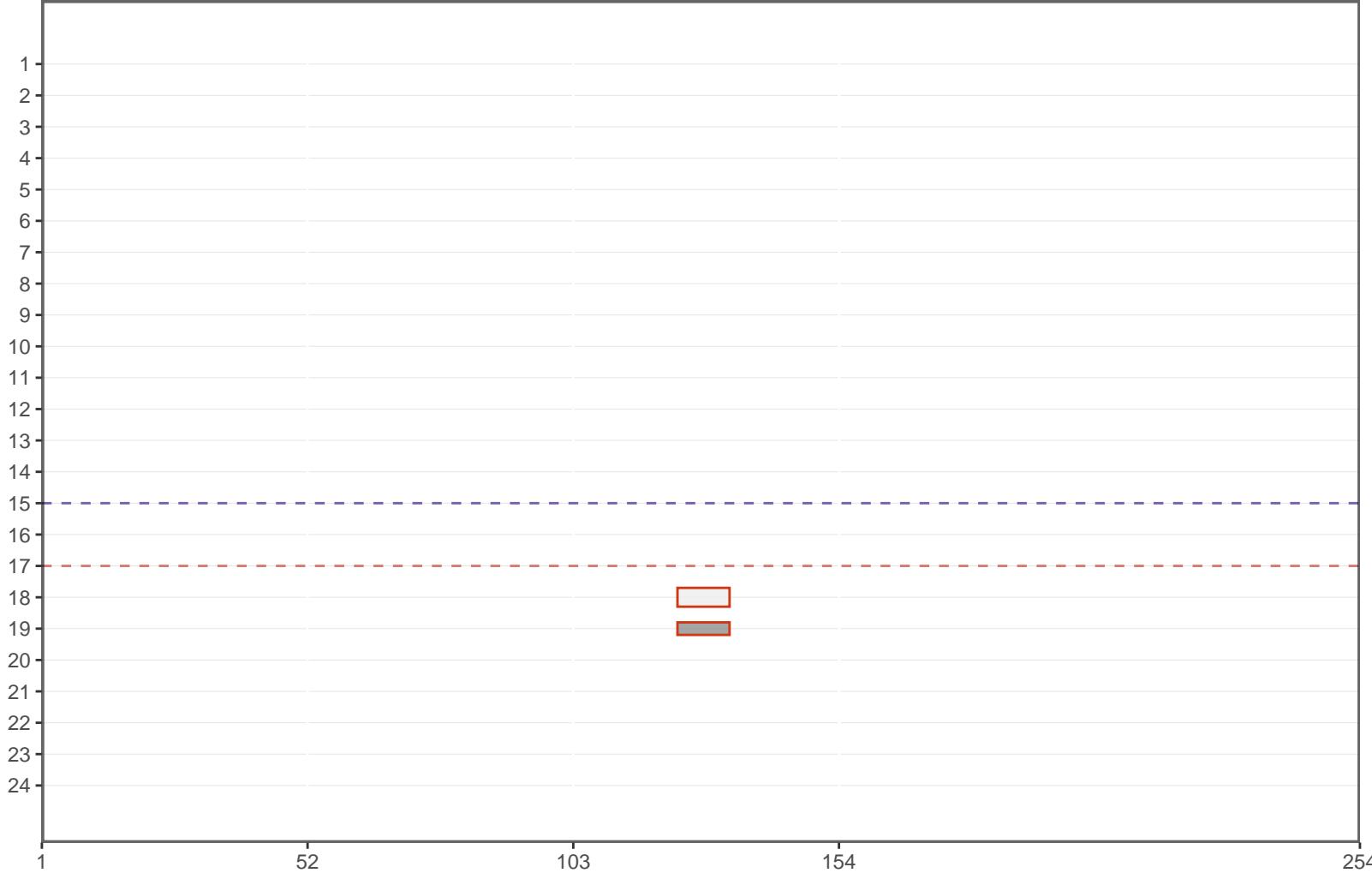
MW indication



Molecular weight



Gel Slice



Protein length

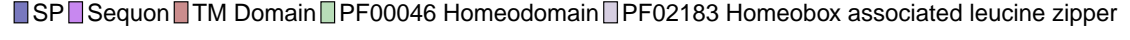


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

DYNSLKKENOSLLFQLGKLNLMKKEKEGGGQYGGVQGESVNRHNTIKSKEMDQKPLSEFDLSEHGIVNGVHGDDDSKIKADYFGLDEESDHLKMKVEAGDSILTSPENWGTLLEDGLDGGPNSCHYDQWVDFWS

NbL11g17270.1 aspartyl_protease_AED3-like [MW - SP = 44.78 kDa]

No. of times detected



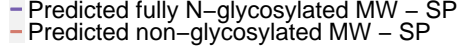
log(intensity)



Values from



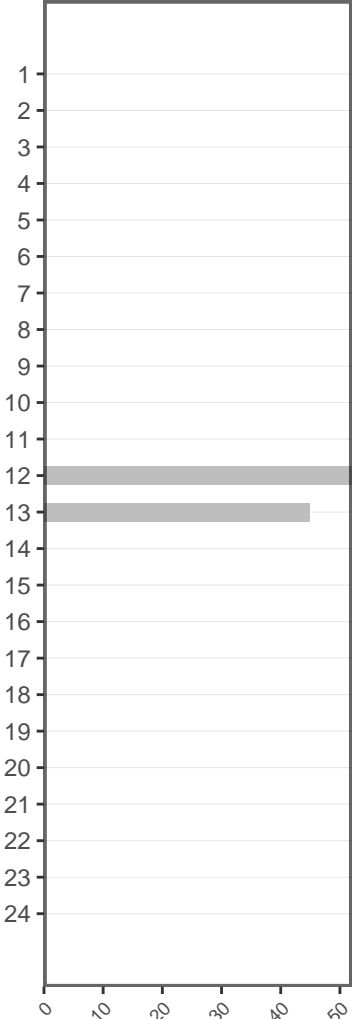
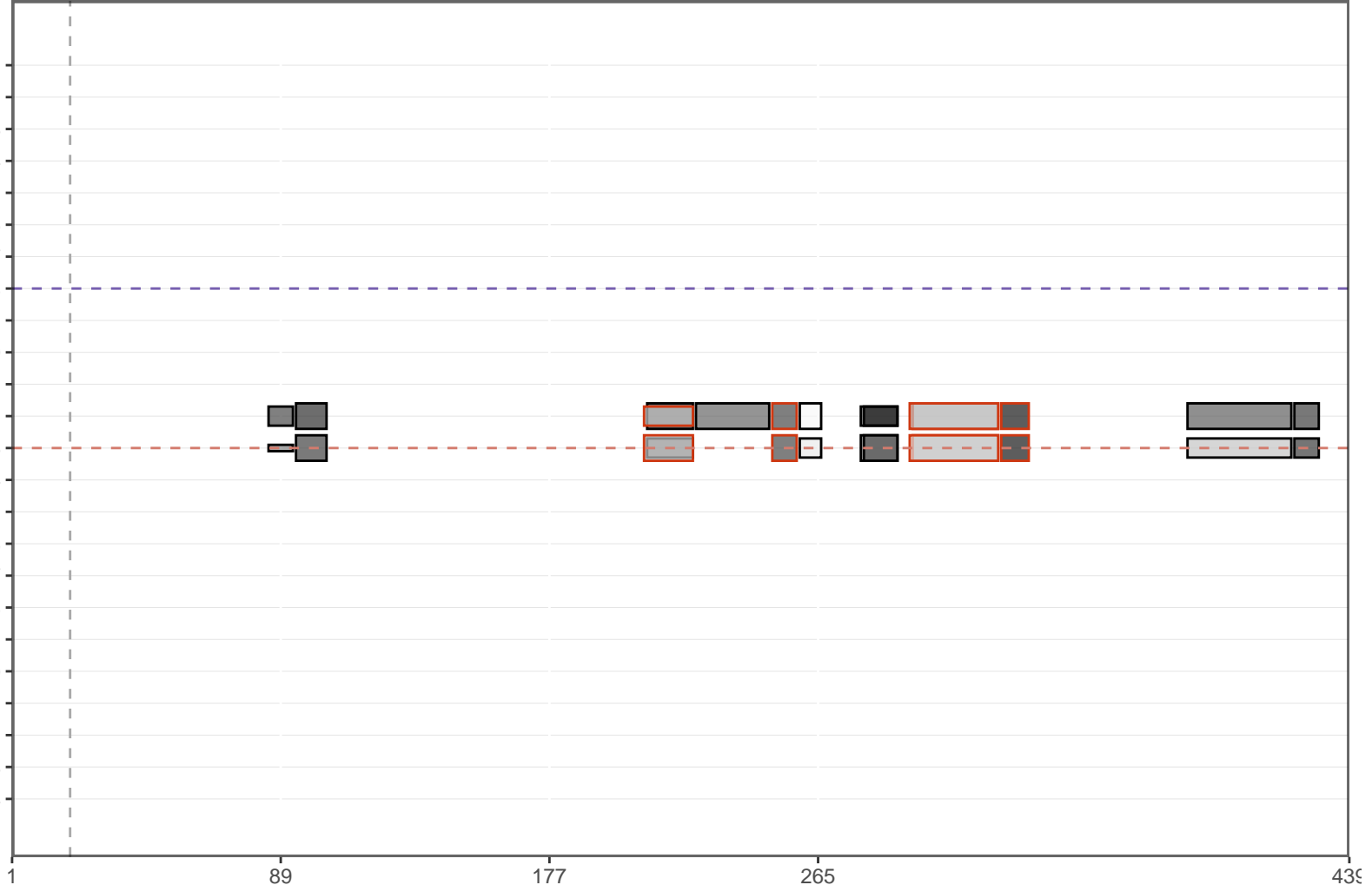
MW indication



Molecular weight

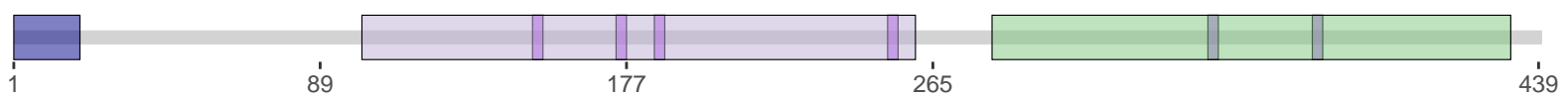


Gel Slice



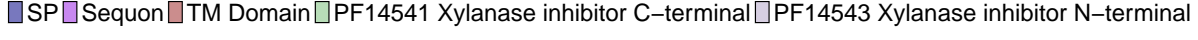
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VRKATGSSAPPGDGLLGLGRGLSFLSGTQGHVQGTFFVGLPQVYKSNFNFSGTLRLGPNQPKRIKTTQLLRNPRRSGFYVNLVGVKVGRRIVDIPPSALAFNPSTGAGTIDSGTVFTRLVQVYAVVWNEFRMRGRNTVTSLGGFDYTVPIPTITLTFMAGMNVTLQGNFLIRSSSSSTGLAMASPADPNVSLVIANWGGQNHRLFDVYNEKLGVAETCS

NbL11g17240.1 thioredoxin-like_protein_CITRX1_chloroplastic [MW = 20.56 kDa]

No. of times detected



log(intensity)



Values from



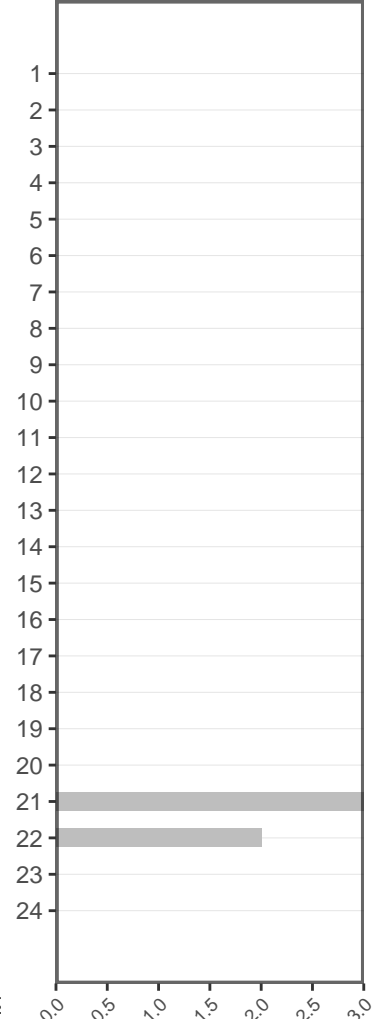
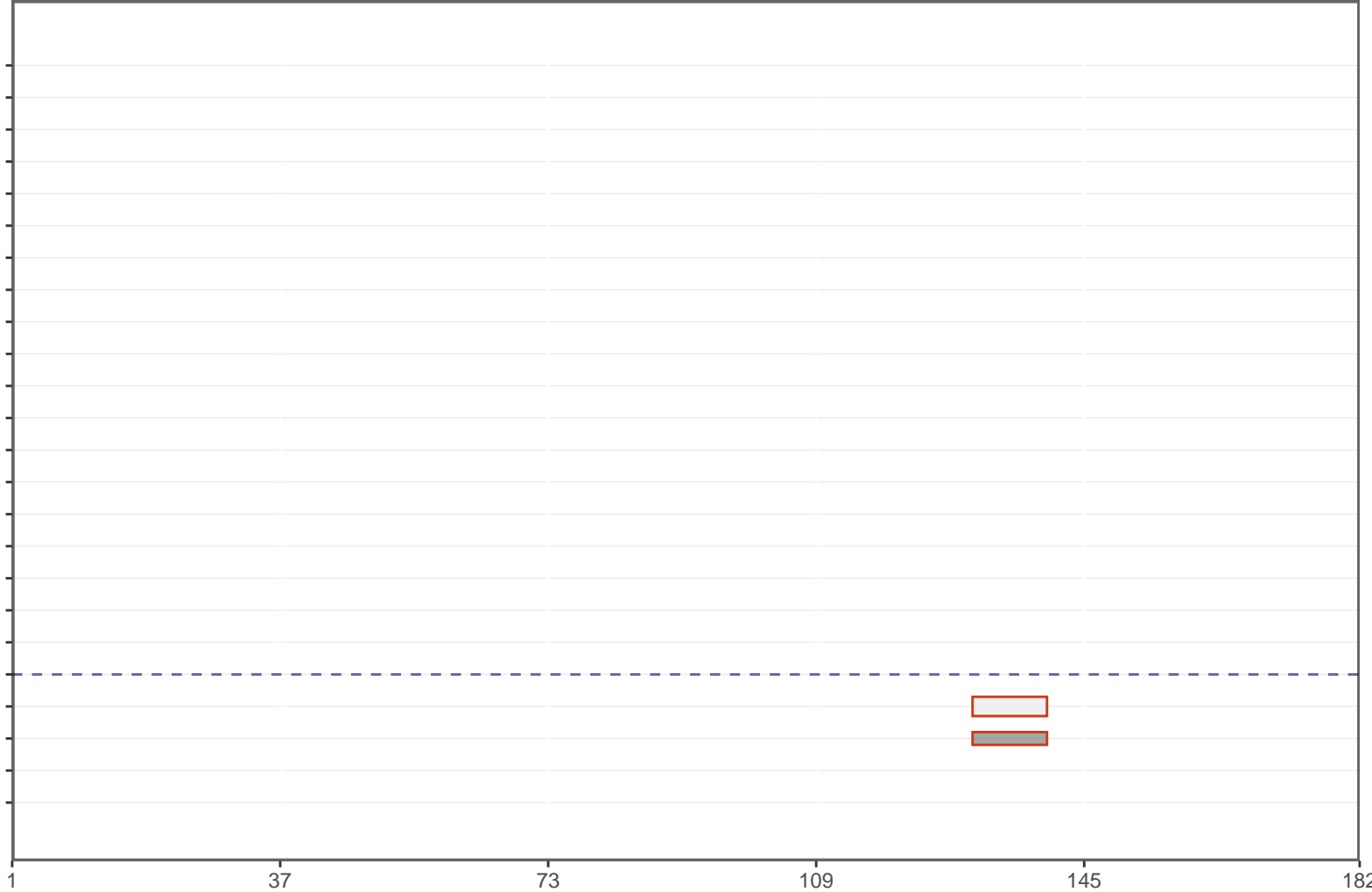
MW indication



Molecular weight



Gel Slice

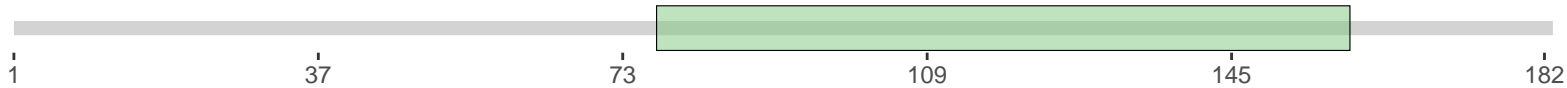


Protein length

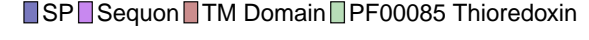


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KVSAKDIELKGERINVPIDFVATWGGPILMAGELEMLAVEYENALVVKVDTDDVEYFARMQVIRGLPFLYFISFPDPNKQAIRTEGLPIQGMRRHINDL

NbL11g17210.1 peptidyl-prolyl_cis-trans_isomerase_CYP22-like [MW = 20.61 kDa]

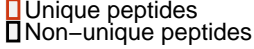
No. of times detected



log(intensity)



Values from



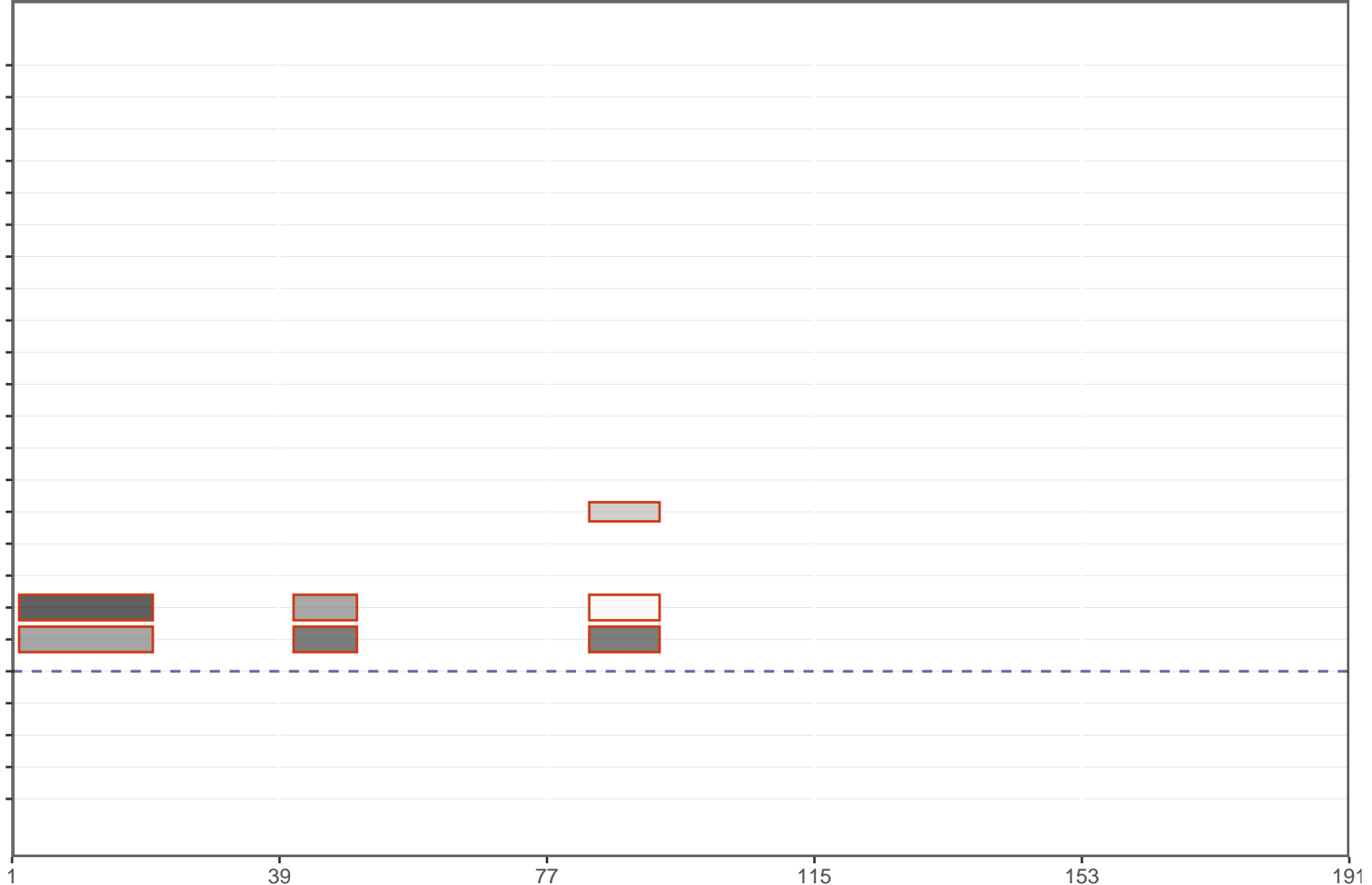
MW indication



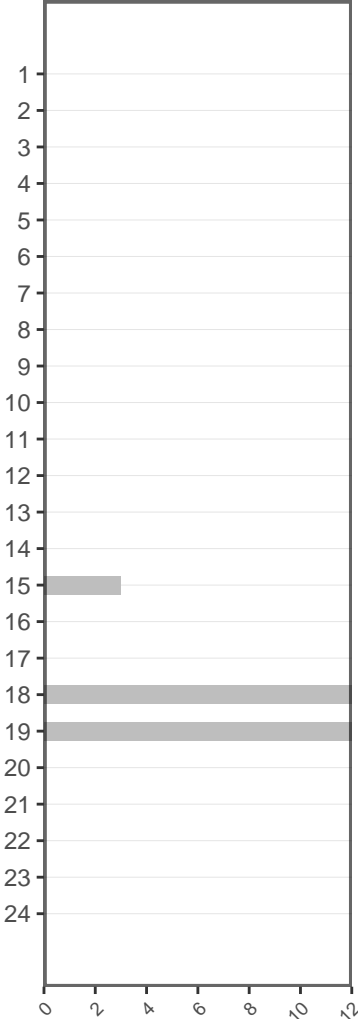
Molecular weight



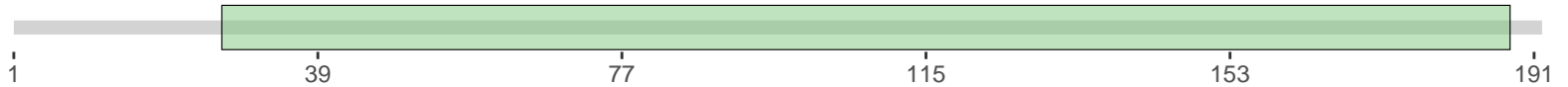
Gel Slice



Protein length

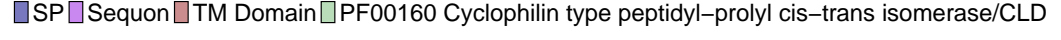


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FMVVOGDFLKGDSGGVSYGKFEDEFIAKHHTGPLLSSMANGFNPTNGQGFITCAKGDWLDNKHVYVLRVLDGGLLVRRKIENAVGANNKPKLADMAIEGSEM

NbL11g17200.1 uncharacterized_LOC109235373 [MW = 121.78 kDa]

No. of times detected



log(intensity)



Values from



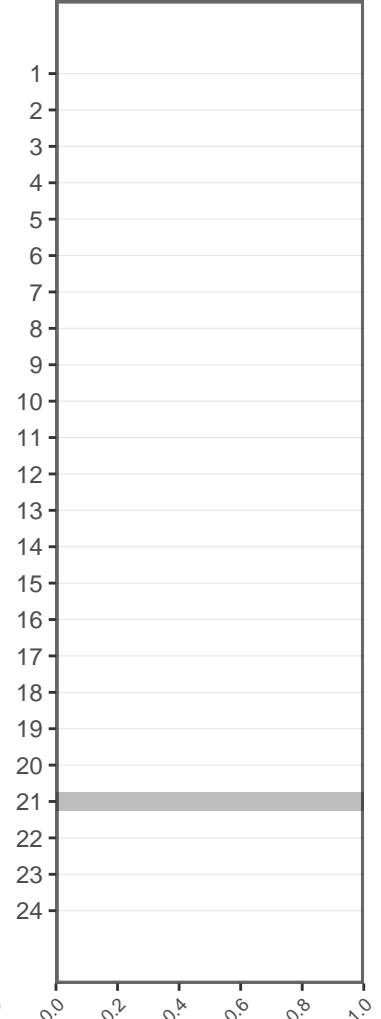
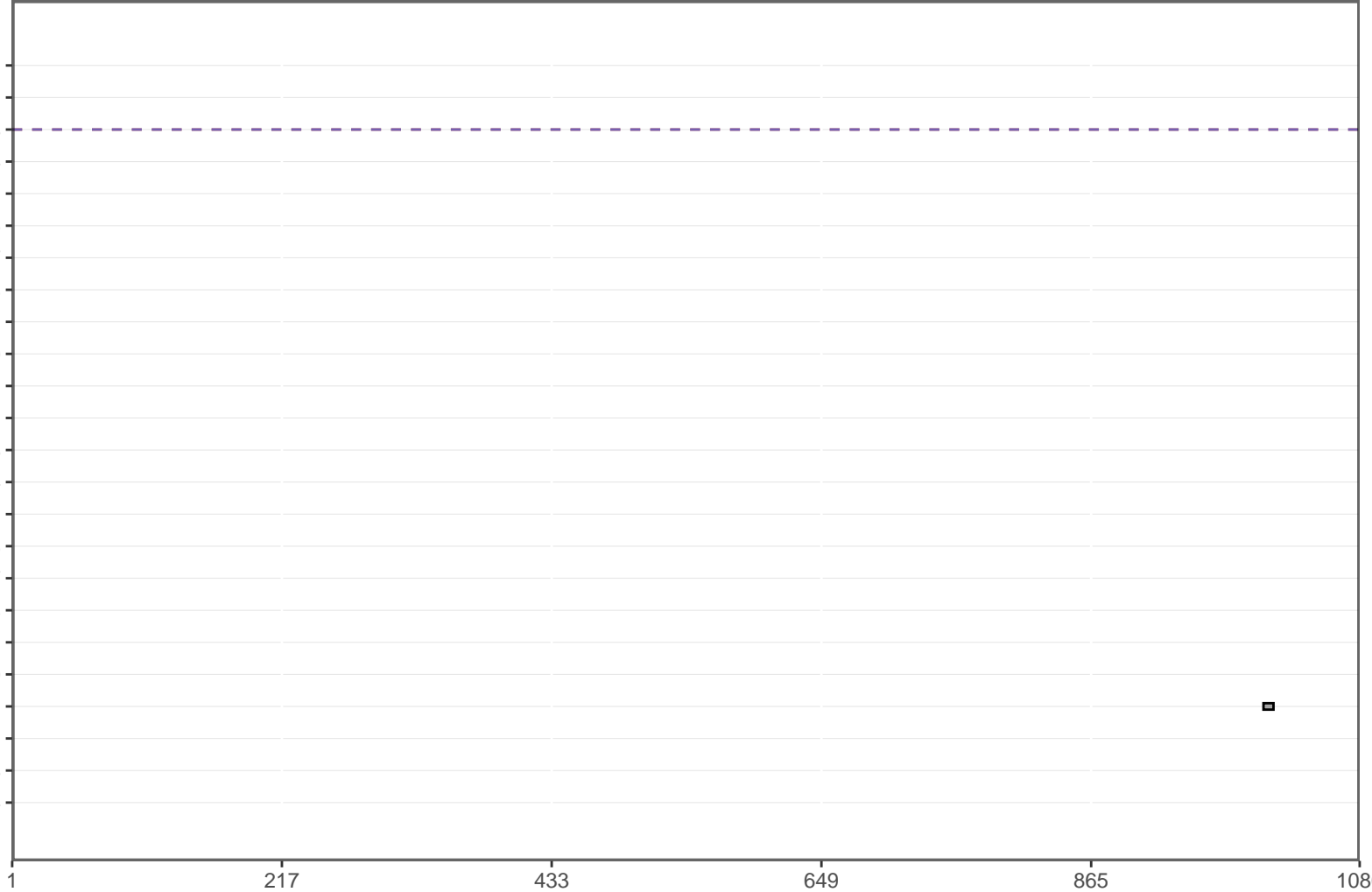
MW indication



Molecular weight

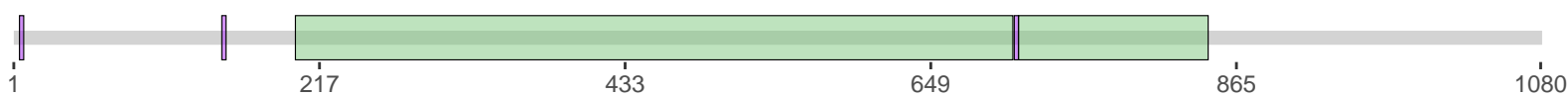


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

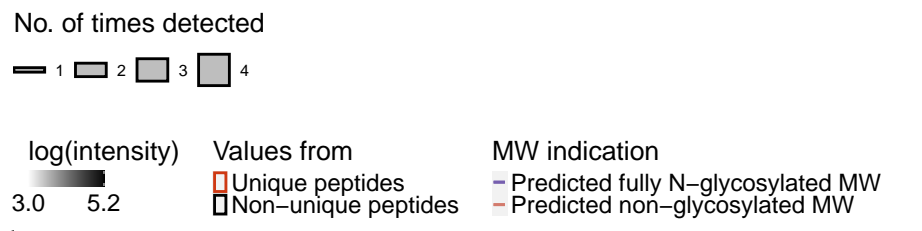
Pfam Description



Protein sequence:

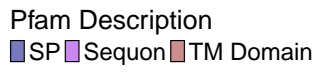
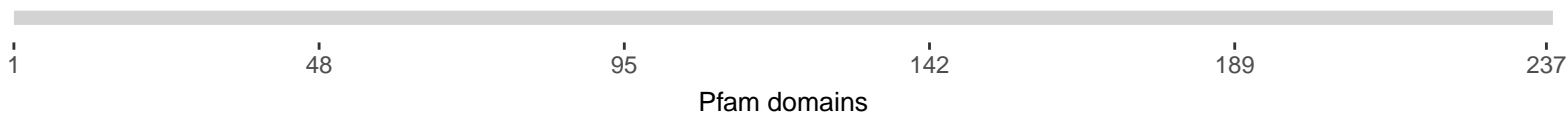
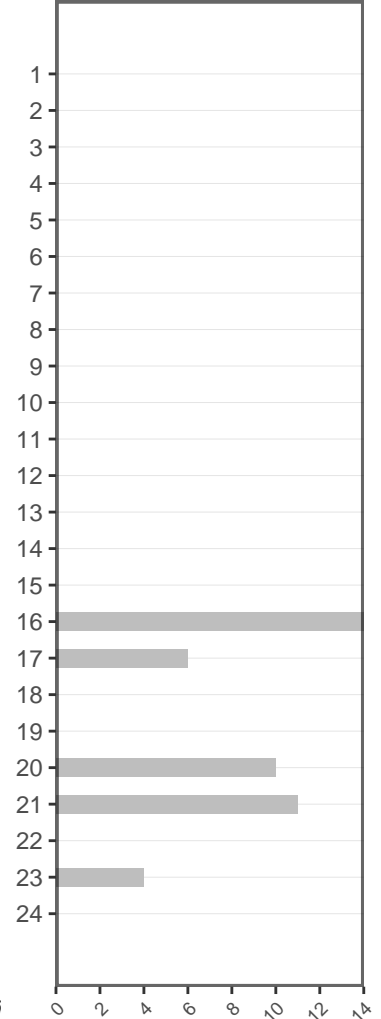
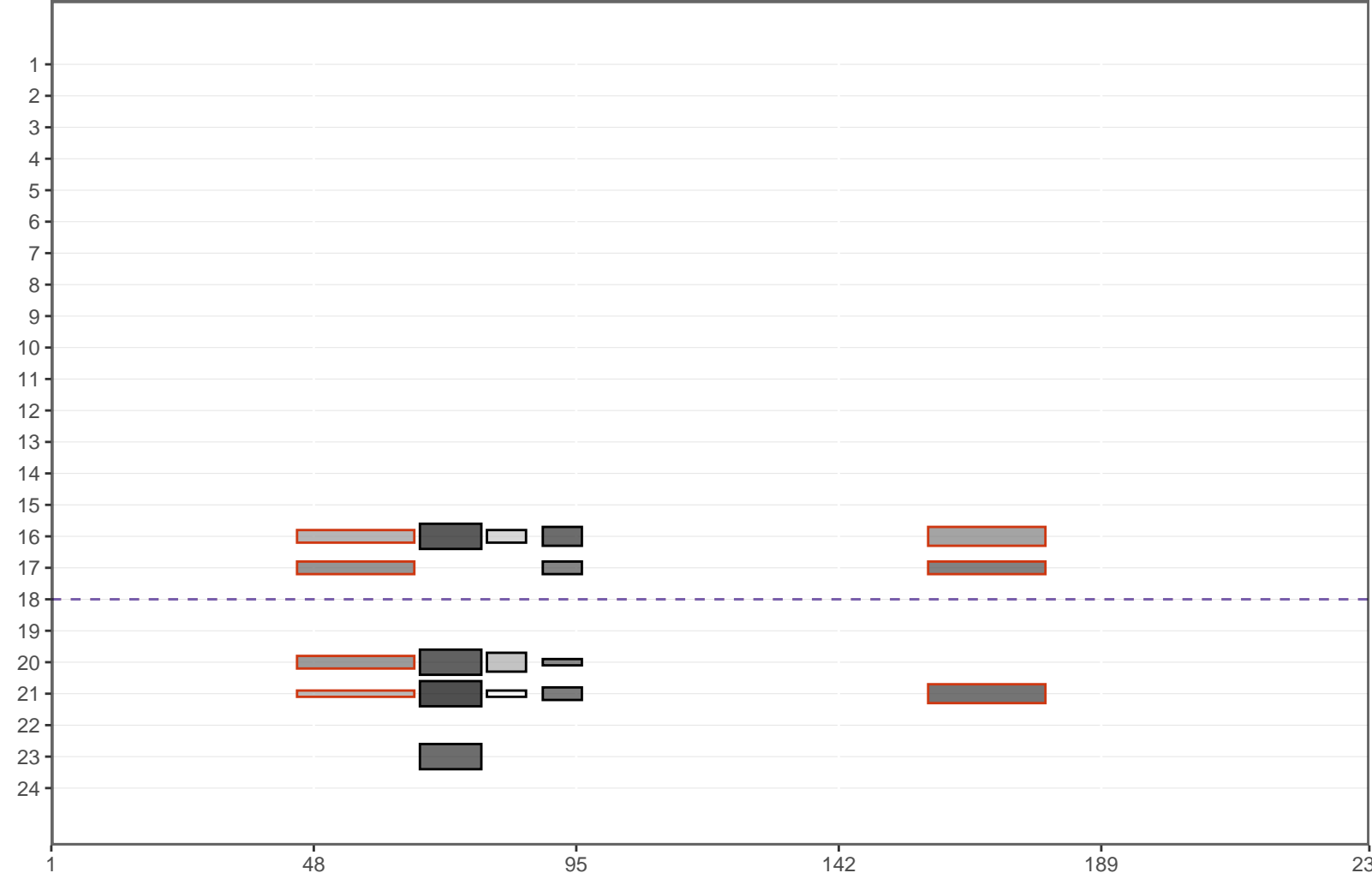
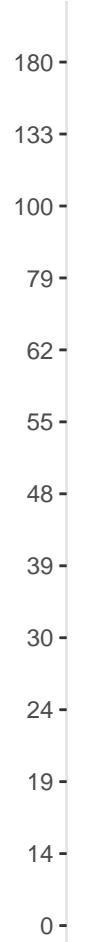
PISKVADKIQGLDYLHNVAEGSAMMENTWVAMLVRRLLLEPEPMAMQVAISDTEGIEFYVTSIKNAFTRIQDVEATHATNEHPLALLAEHTKELLHRDNTFVMPILSQRRHRAAAVVASILHKLKLVGKLRPFLENEVHETEDTIAVFPADSLGEGYMQVILSTGADGTSDDGYGRKLVNKRWTFVSPQGRHGGSSNEVYRVEETVDGFFALKVPMRPGELSSLFRGIDNAFGVYAKTLDKIANKEDVYPPVILTRYSREHGKAFVYKELKQTRIPDVKVSEIDVATSTLC

NbL11g17110.1 protein_MAINTENANCE_OF_PSII_UNDER_HIGH_LIGHT_1 [MW = 24.53 kDa]



Molecular weight

Gel Slice



Protein sequence:
 NYSVEPVIYVAESASISSGAGSTSDGAENTAAIAAGIALHIAAASBLLQVGNKSPFPVQTIEYEGPRLSYINKFKPMLQASVAETEAPTAPEVVGASVAPETEARNAPVEGSAFGVEGGEAPQDT

NbL11g17070.1 dnaJ_homolog_subfamily_C_member_2 [MW = 74.08 kDa]

No. of times detected



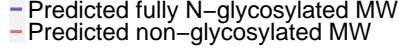
log(intensity)



Values from



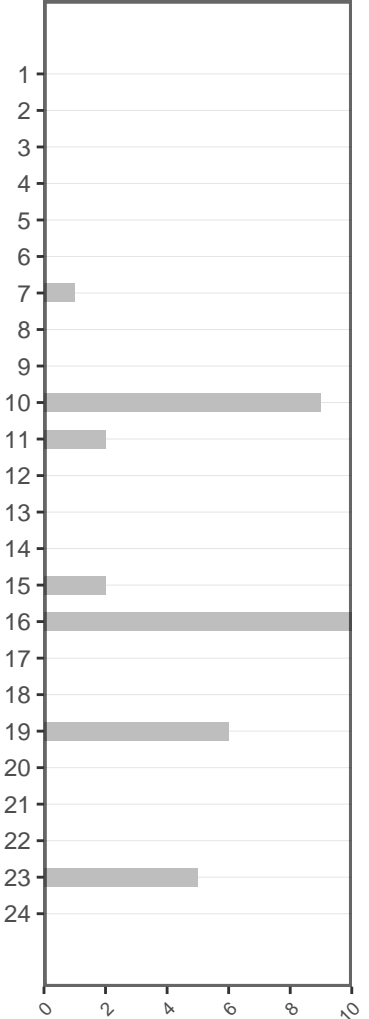
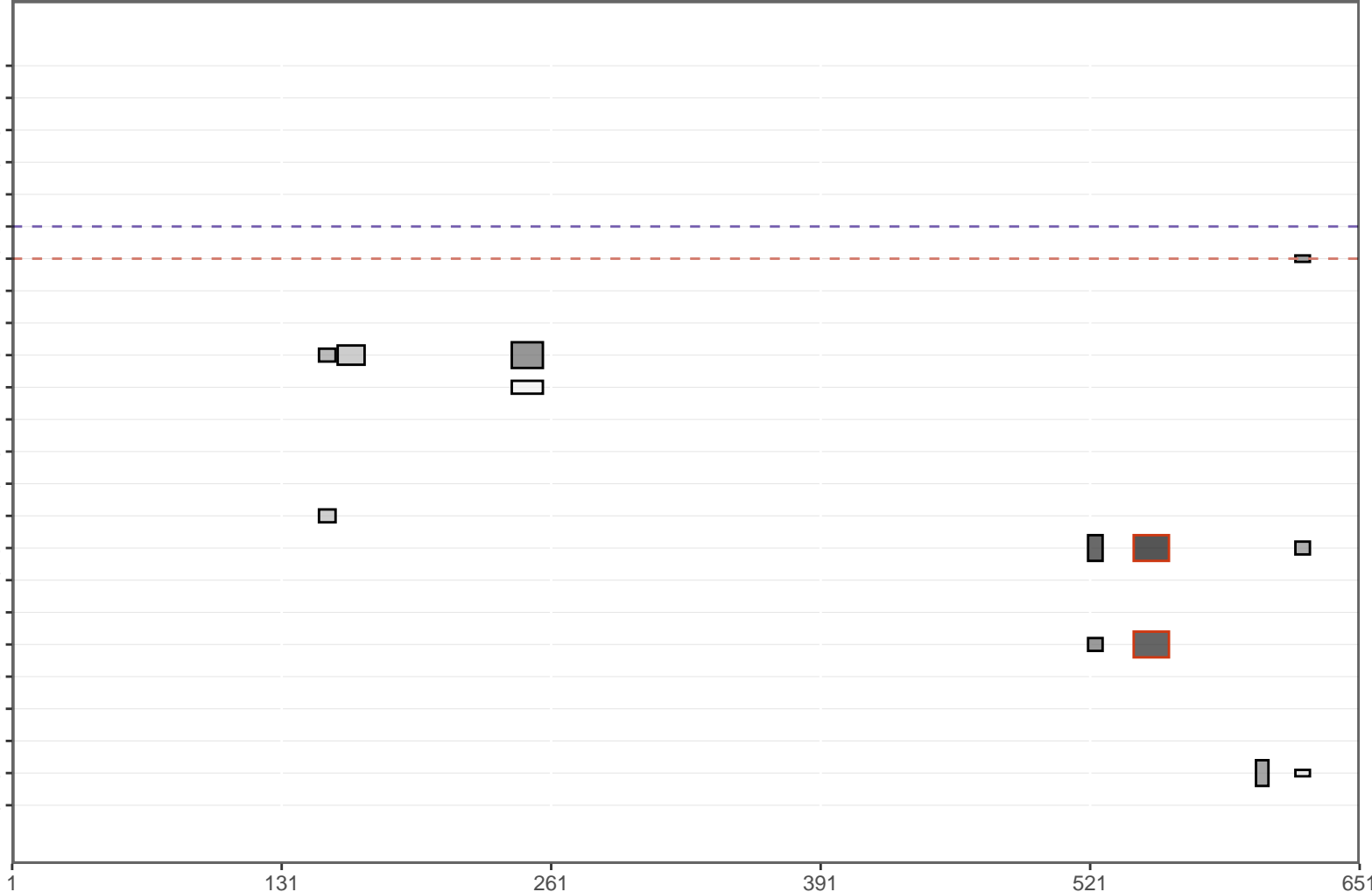
MW indication



Molecular weight



Gel Slice



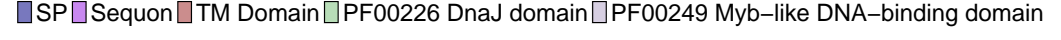
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LLAKLQEEAAARAAEEERKRRKEEGKRAAEVALGQKHLKEKELLRKERSRLRRLAAPVLSGRLLGLADDDIEGLGMSLDIEQLRNLDGKADGKDELMIAELLREALGHQHNLYKENKESKSHQNGSLEGGKRVPLMSSEKREKPKWSKEEIDLRLKGMKFKPKGTSTRRVEVMSEYIGTGRVVEELKATKTVLLQKPDGSAKAFDGFLEIKRKPAPTASPLSTRAEVEGVENSSKPEGGSAKLADGGESFPGNTNSGNTEDAPTANGVSSGSDSDWSVAIOEKALVQ

NbL11g17020.1 SUN_domain-containing_protein_3-like [MW = 50.55 kDa]

No. of times detected



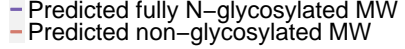
log(intensity)



Values from



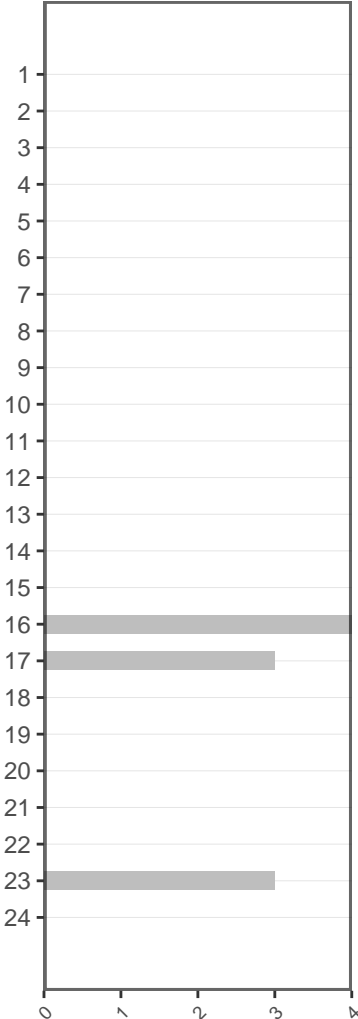
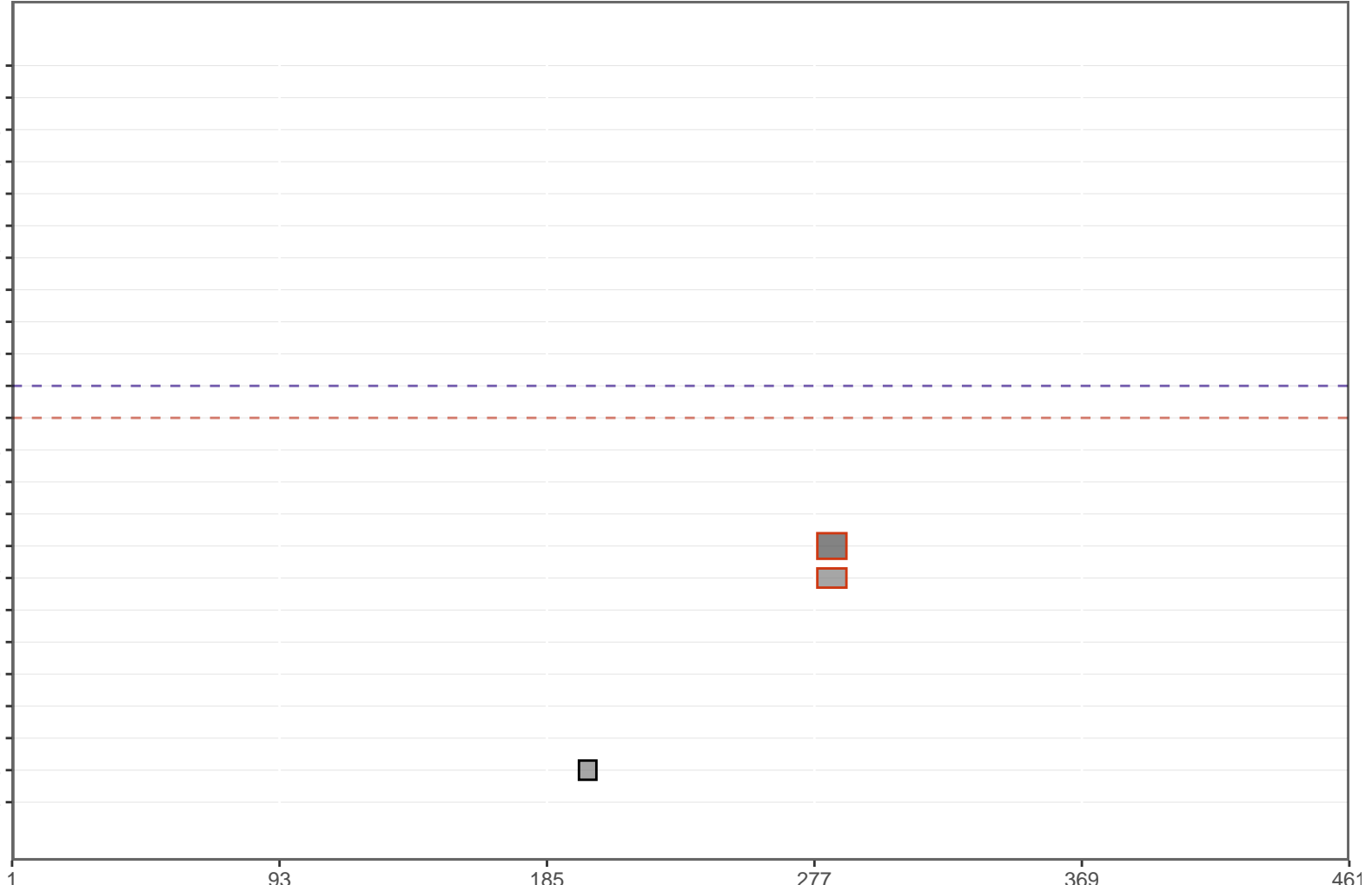
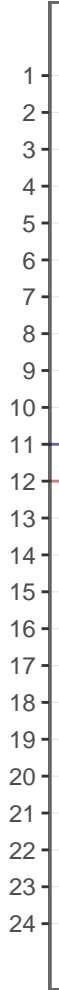
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISEFRKDYVSKDELTHFEFVYRNSKGGTEADDKSLDEFRAVAREVVEKEIEKHAADGLGRVDVALASGGGRVKNSEPFITKSGGGDVAWLLNKNVNSVDAKILTPSFGEGCGCFPLKGRDFVQIRLRTSIPFAVTLFHWAKVAVDRSAPKNGRISGWLHDKKETDLAADESEKMLTFEYFDLQKNAQTFFNLESAAGSSVIDTRFDFTSNHGMPTGIVRLRVHGREPNLSVMQSF

NbL11g16990.1 peter_Pan-like_protein [MW = 39.71 kDa]

No. of times detected



log(intensity)



Values from



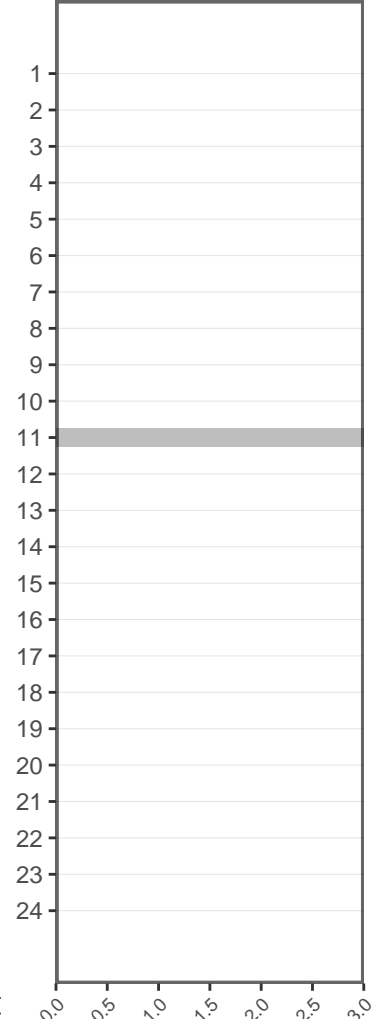
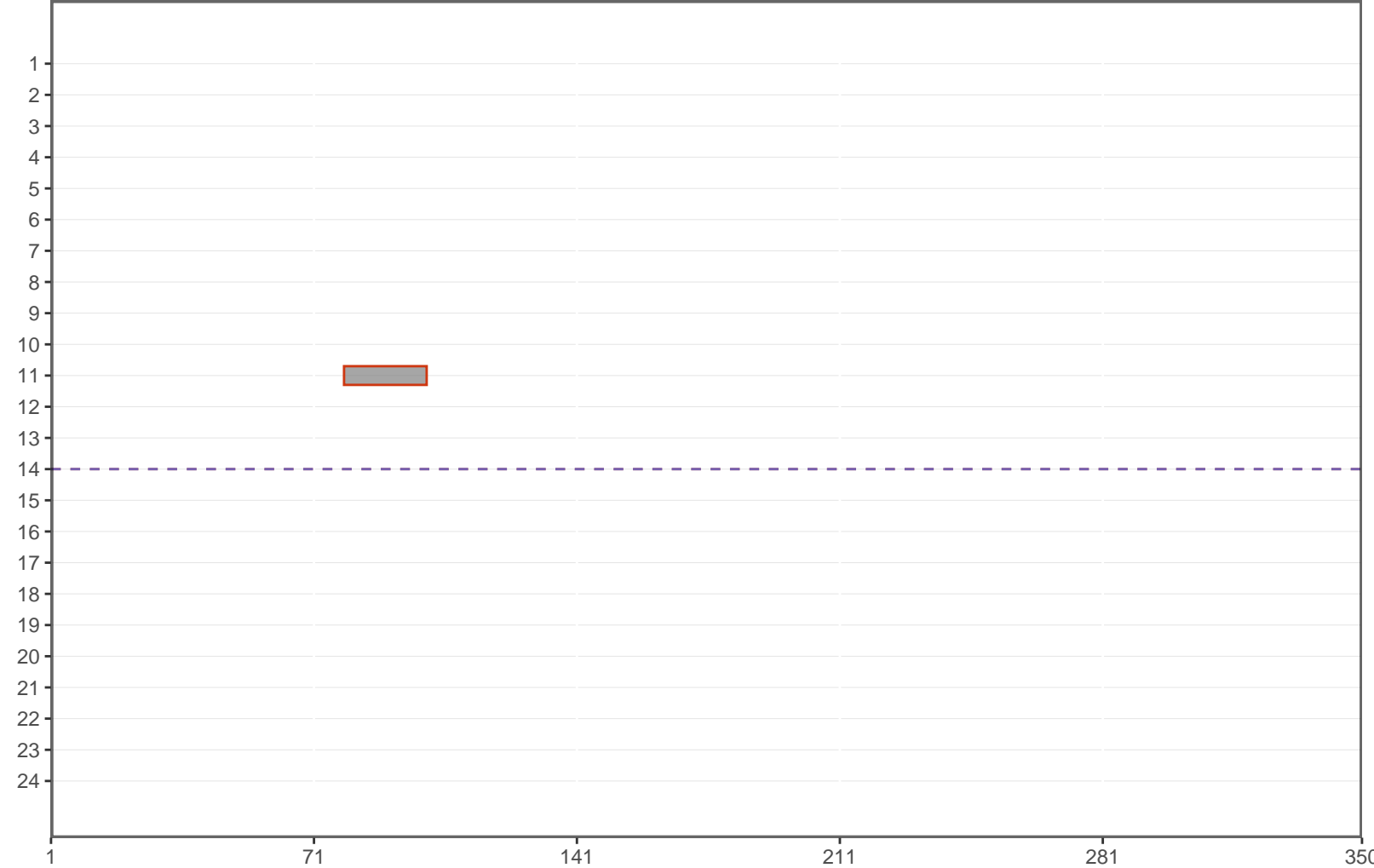
MW indication



Molecular weight

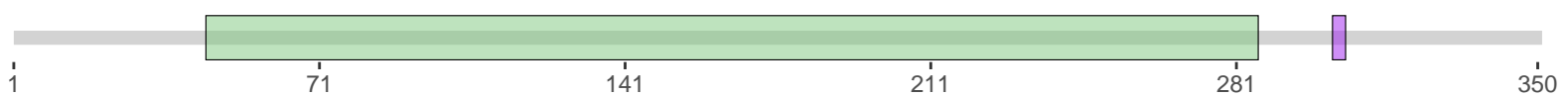


Gel Slice



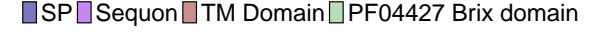
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MFQNFPAIDNTVNLPSGGRVLLNFKETKLDLRHYSIRLGPVGVSRIRKRVQNHQVPLRLSLGQVSDVTRKAGYGESEFPDDEAATVLSLSDGIRVNRASTKSAVKLGEIGPRMTLGLVKEEGLCTGRVIFSEYGNVSAKILGNEEEDGEGESEEEMDTDGGENADEEEEGEIEEGEIQD

NbL11g16900.1 proline--tRNA_ligase [MW = 61 kDa]

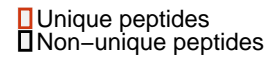
No. of times detected



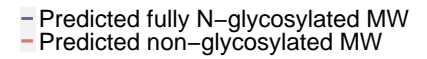
log(intensity)



Values from



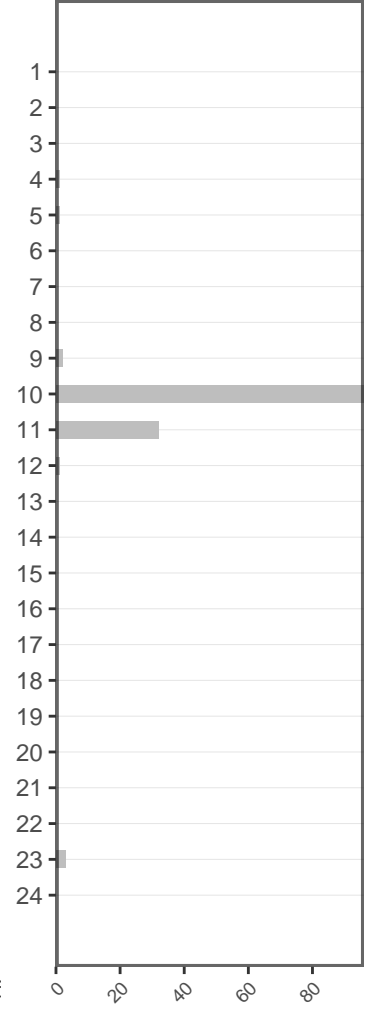
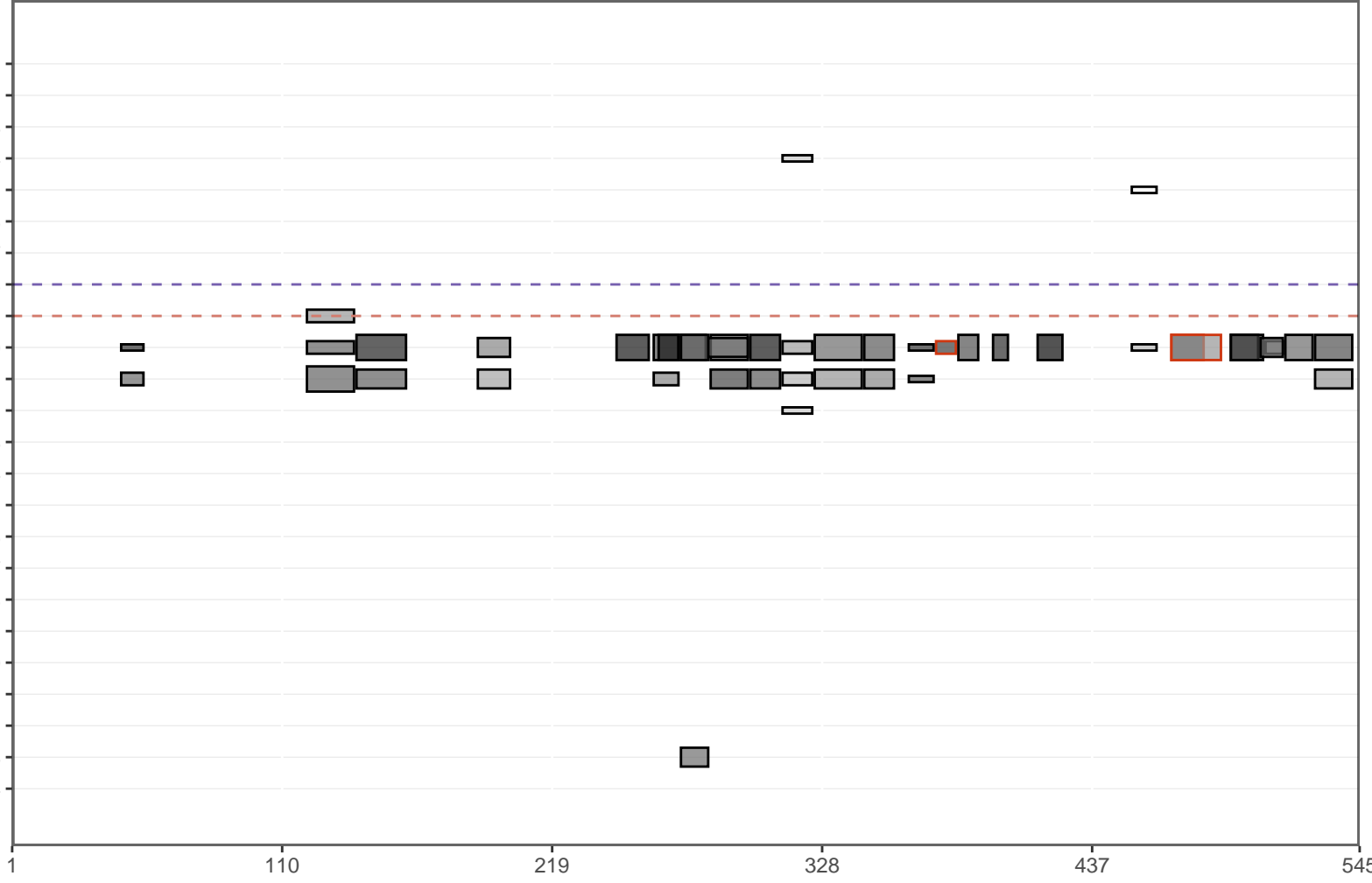
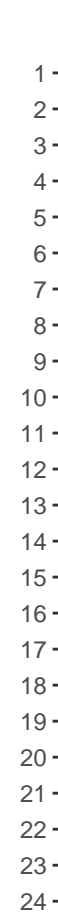
MW indication



Molecular weight

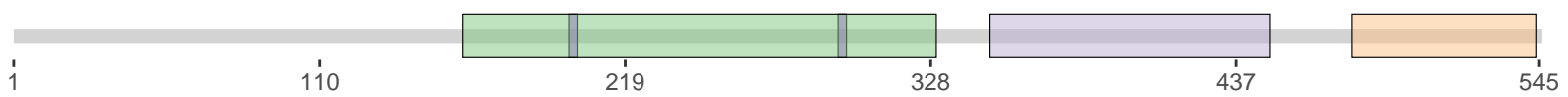


Gel Slice



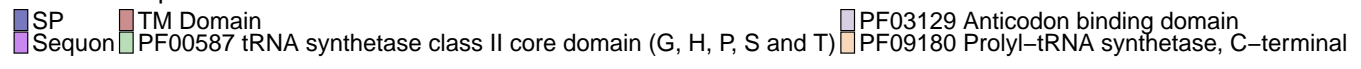
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VETTFAGASRTYITIEAMMGDRKALGAGTSHNLGGNFRANFTQFTDENGGRRGHVWGTSWAISTRFVGGIMTHGDDAGLLLPRLAPVGVVPIIWKNEKTKGVLTAASSSVKTELGAAGKVVDDTDGRTFGWVNFVEMKGVPLRIEIGPRDVSSTVVIERRDFPGKGVKFGIGMEPSSLVAVVIDKLNVEQBSLLERATAFRDGNIMDVSSYNELKEAIDGKWARGPVWASDEEELKVKWETGATRQFPFEPQEPKPKGLMTGNGADEVAIFAKSY*

NbL11g16880.1 DNA_gyrase_subunit_A_chloroplastic/mitochondrial [MW = 104.82 kDa]

No. of times detected



log(intensity)



Values from



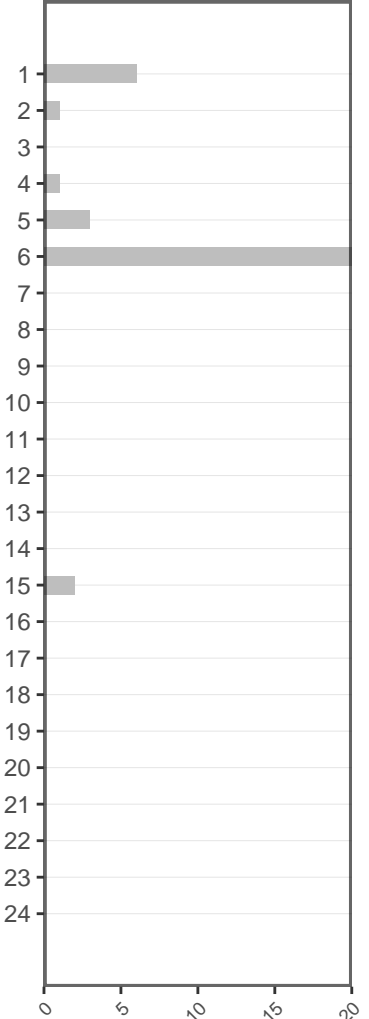
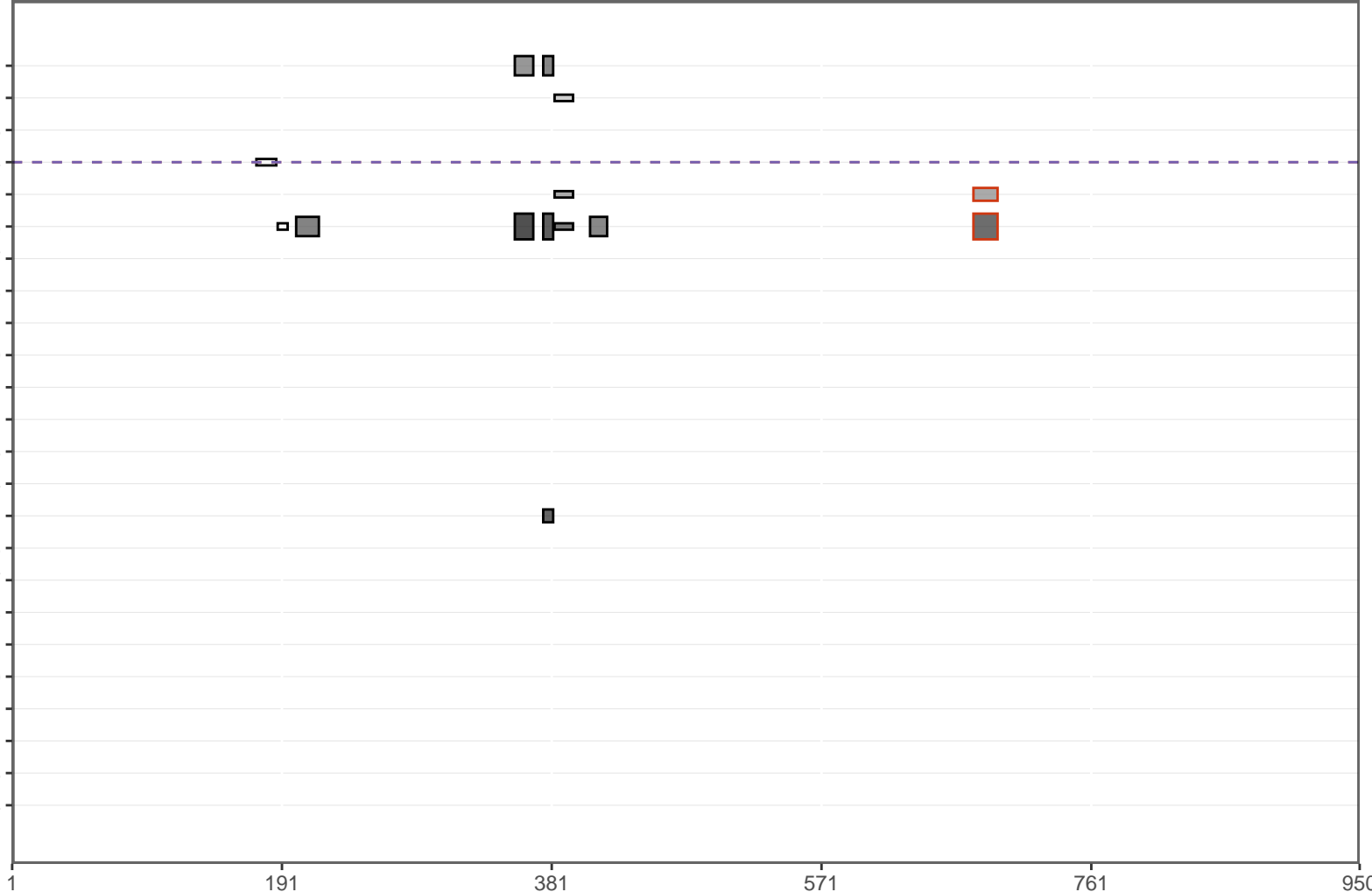
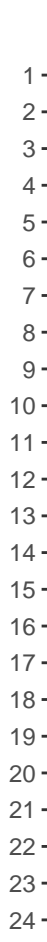
MW indication



Molecular weight

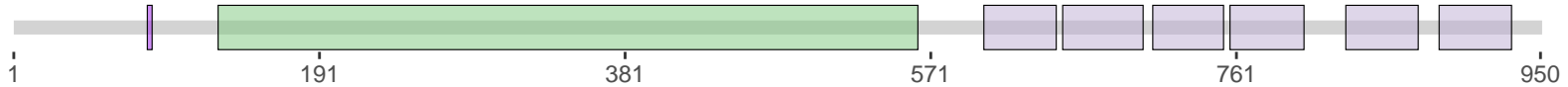


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

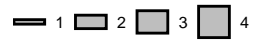
- SP Sequon
- TM Domain
- PF00521 DNA gyrase/topoisomerase IV, subunit A
- PF03989 DNA gyrase C-terminal domain, beta-propeller

Protein sequence:

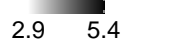
VERRAKFKLSQAEIRNHVEGIVGLDNLDEVINTIRKASGNLAAALRKEFELSEKQAEALDISLRRLTALERNKPFVEEGKSLRTQKLELLSKKQKQLHHEEAEIKKFFPRRSMLEDDTDSGEVEDIDVINEEMLAISEKGYVVRMKSDTFNLGNRGTGKSVGKLRVNDMMDSDFLVGRAHKVLYFSQDKGTVYSSPWIPEGSRRTAAGTFLVQLSLSDGERTSIFVSEFAGDQYVLMVTVNGYHKVSLAYFABIRGTGIAIGLVPGDELKWKVCCSSNDFVAM

NbL11g16800.1 beta-glucosidase_BoGH3B-like [MW - SP = 69.53 kDa]

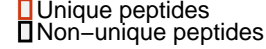
No. of times detected



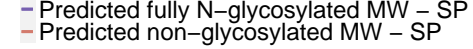
log(intensity)



Values from



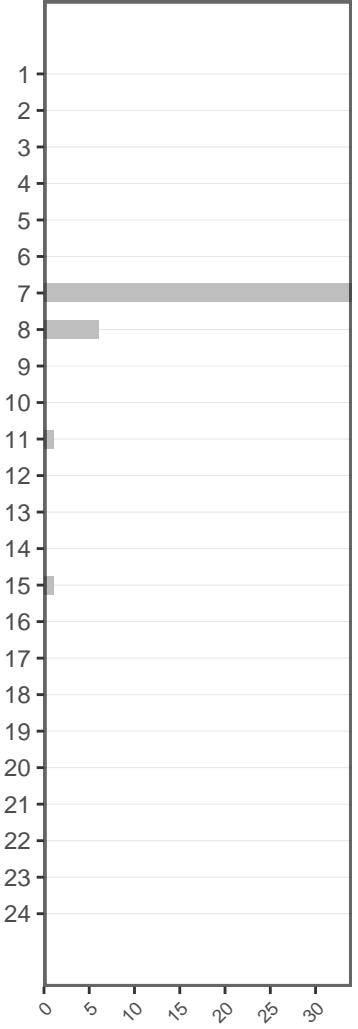
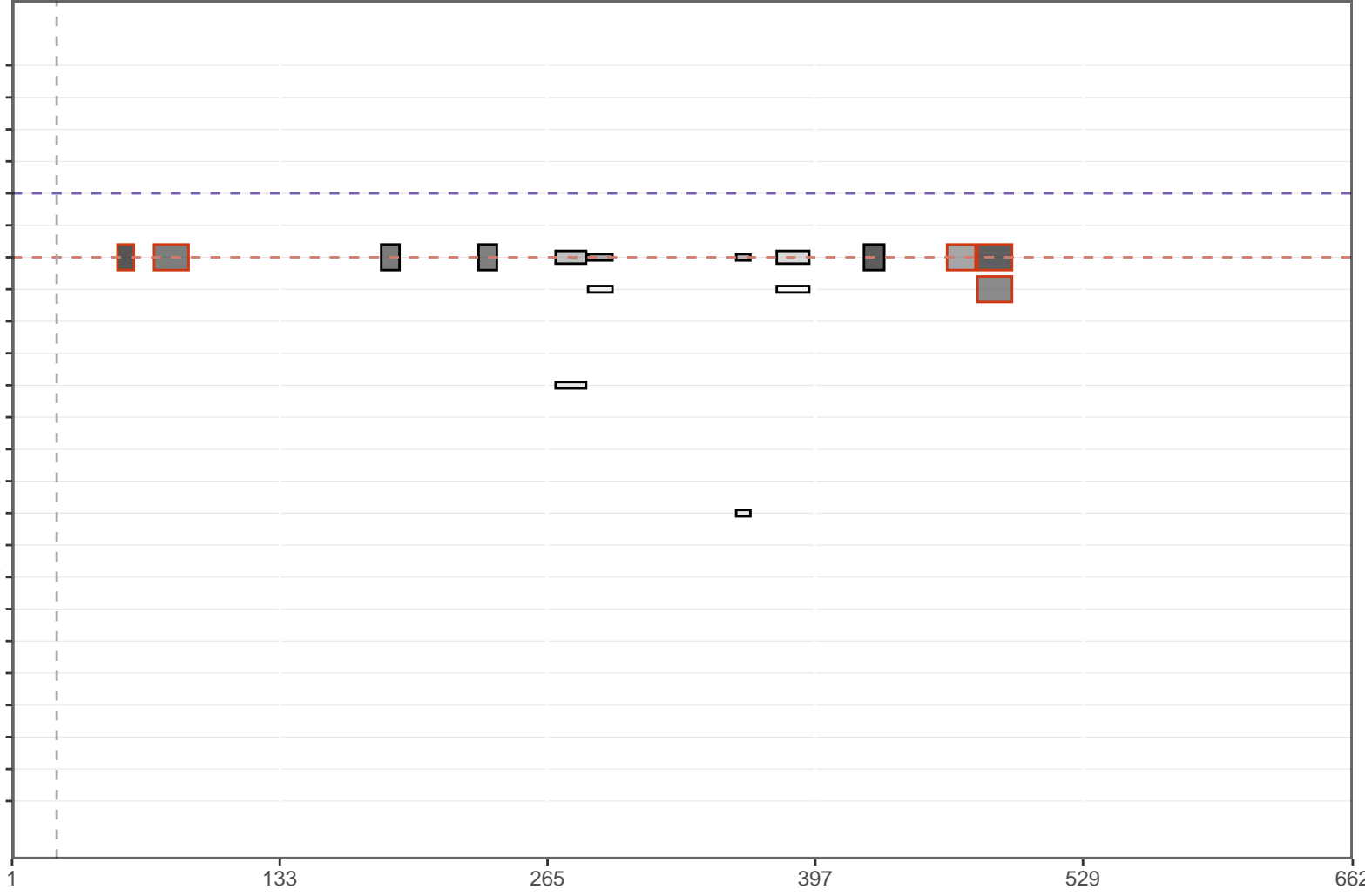
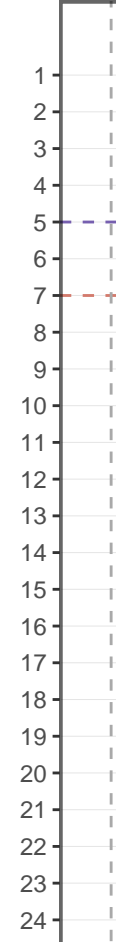
MW indication



Molecular weight

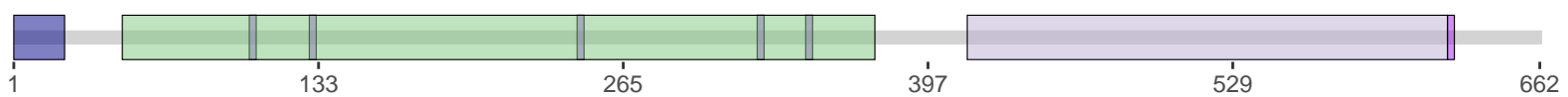


Gel Slice



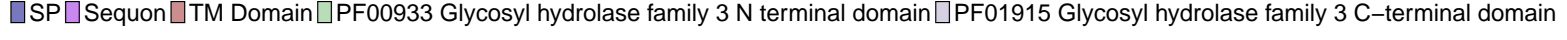
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ITSPHANYTYSVETSLAGIDAMVMVYNETEFNDLTYLVKNNFPMARIDDAVERILLVKFTMGLFENPYTDFSLKEVSGSEHRNAREAVRKGLVLLKNGKTDNDPLLPKAKKILVAGSHADNLFGQGGGWTIAWQFRGNDGTGGTLLGAKSAVDPGTEVTYLVLENFDSKVASRGRFDVAIVVGERPYAETAGDSPTLTADSGPDVNHVCPKVKGVYIIISGRPLVIEPLPSIDALWAWLPGSEGGGTDLFGDVGFTGKLPRTWKTVEGLPMNVGDPYDPLFI

NbL11g16470.1 PITH_domain-containing_protein_At3g04780-like [MW = 19.66 kDa]

No. of times detected



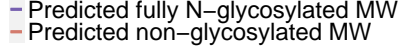
log(intensity)



Values from



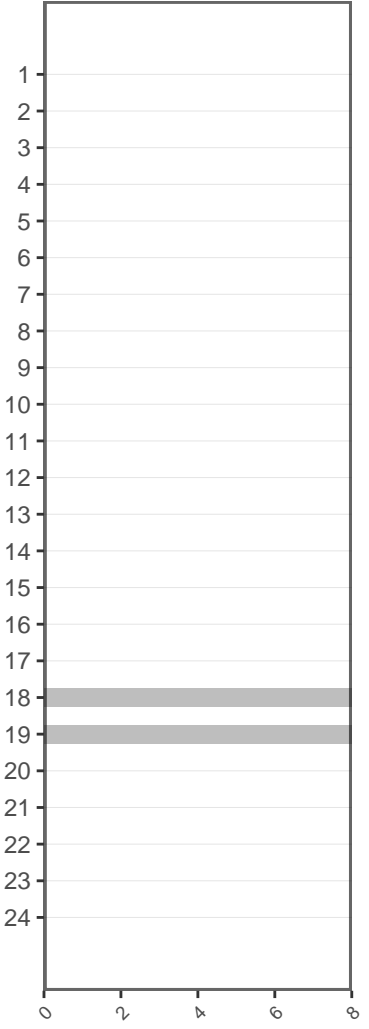
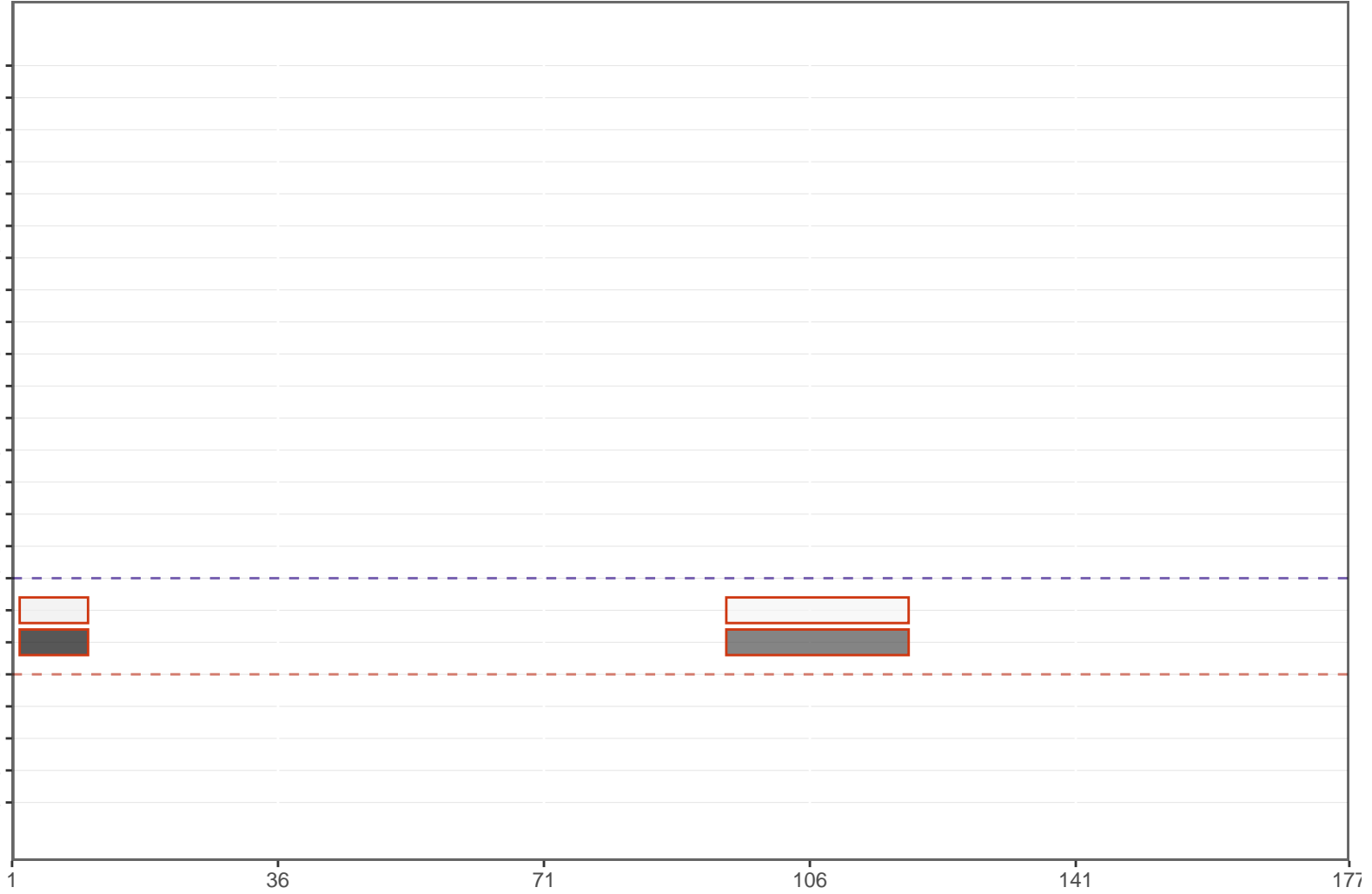
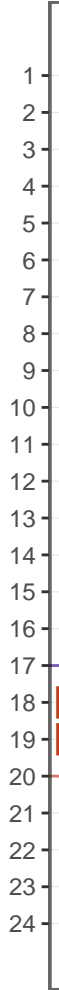
MW indication



Molecular weight



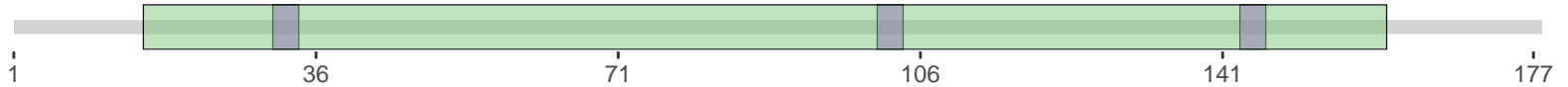
Gel Slice



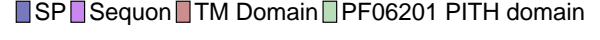
Protein length



Pfam domains



Pfam Description



Protein sequence:

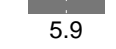
TVKGFEEEGPKTVLIFSNKDHMGFSNVSQPPSDTAVLSEDLNKGKPKVILKYKFNQVRSVTFIFEDNGSDSELTRVQKIVLYGTTVETDMKGLKKEIH

NbL11g16460.1 probable_ribose-5-phosphate_isomerase_3_chloroplastic [MW = 30.42 kDa]

No. of times detected



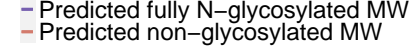
log(intensity)



Values from



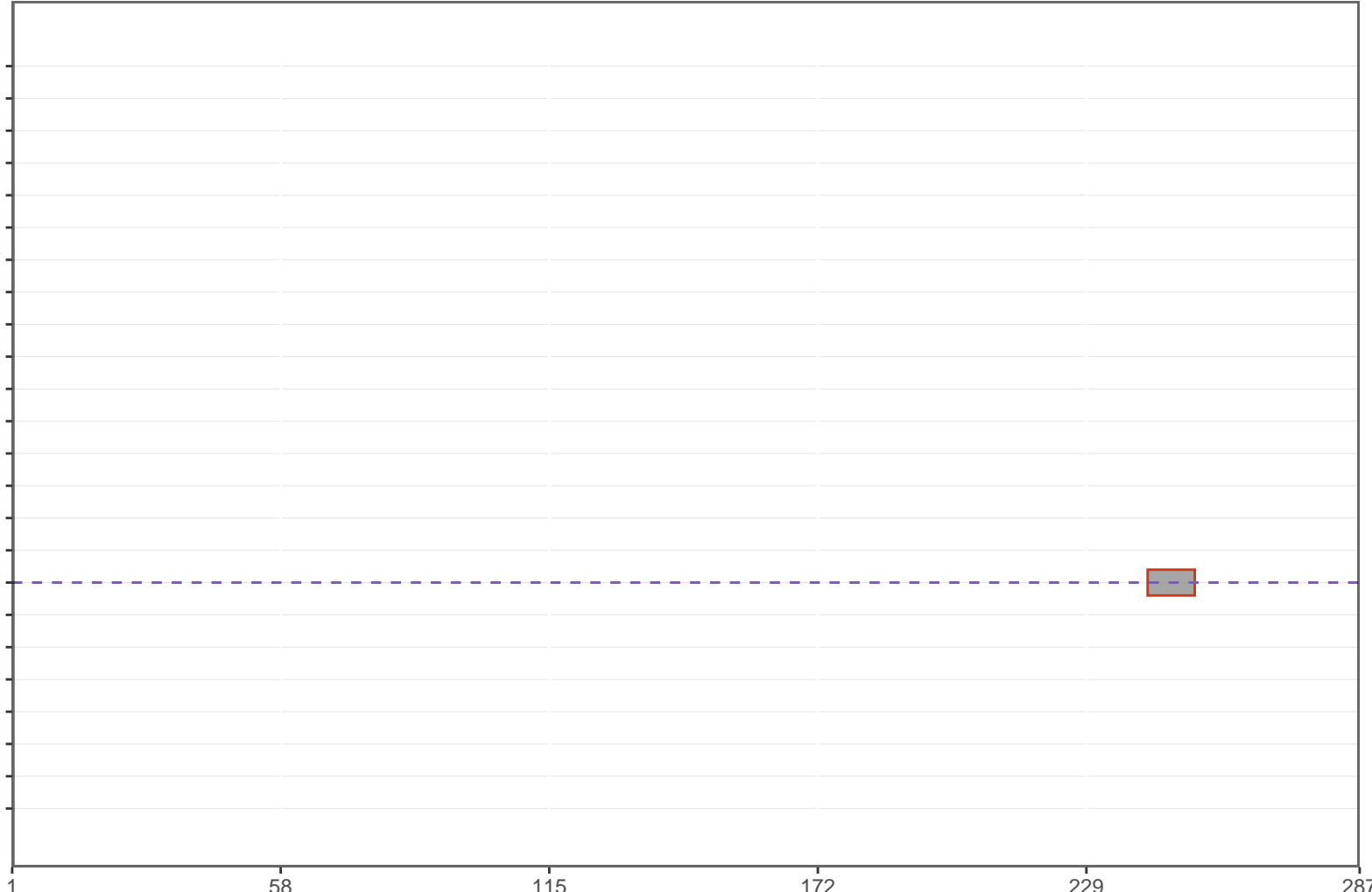
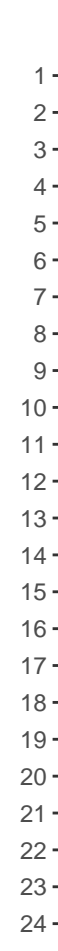
MW indication



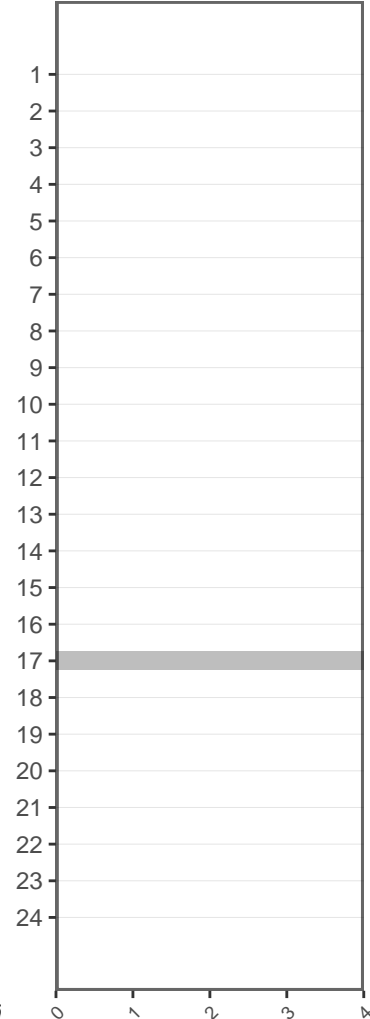
Molecular weight



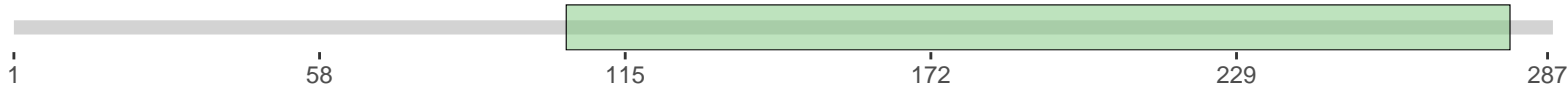
Gel Slice



Protein length

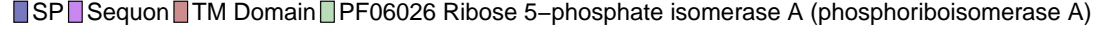


Peptide counts over 4 repeats



Pfam domains

Pfam Description

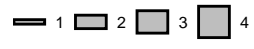


Protein sequence:

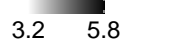
SLAIDGAEVDFNLELWGRGGALLREKMEVAASDKFVWVDDSKLVSLGSGSLAMPVEVDFGWKYNLVRIGLQELFKAEGVDKLRVDSGNGKPYVFDNSNYVDLYFKTPIRDSAVAGKEIAALEGVVEHGLFLDMTTAVIAGKEGVSIVGSKY

NbL11g16430.1 annexin_D4-like [MW = 40.12 kDa]

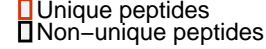
No. of times detected



log(intensity)



Values from



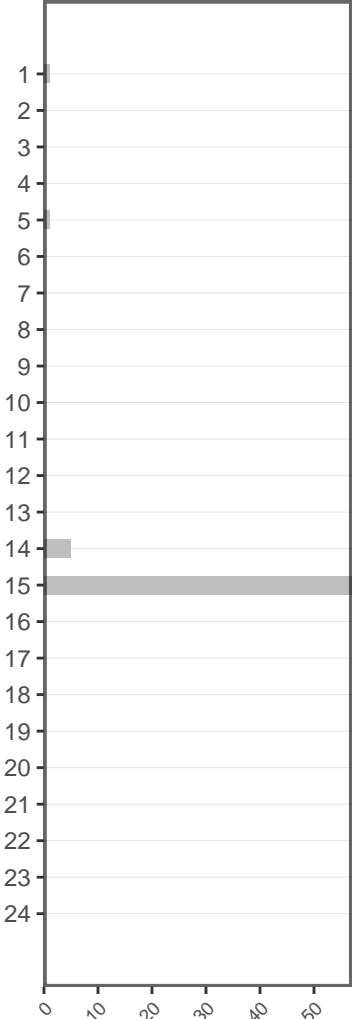
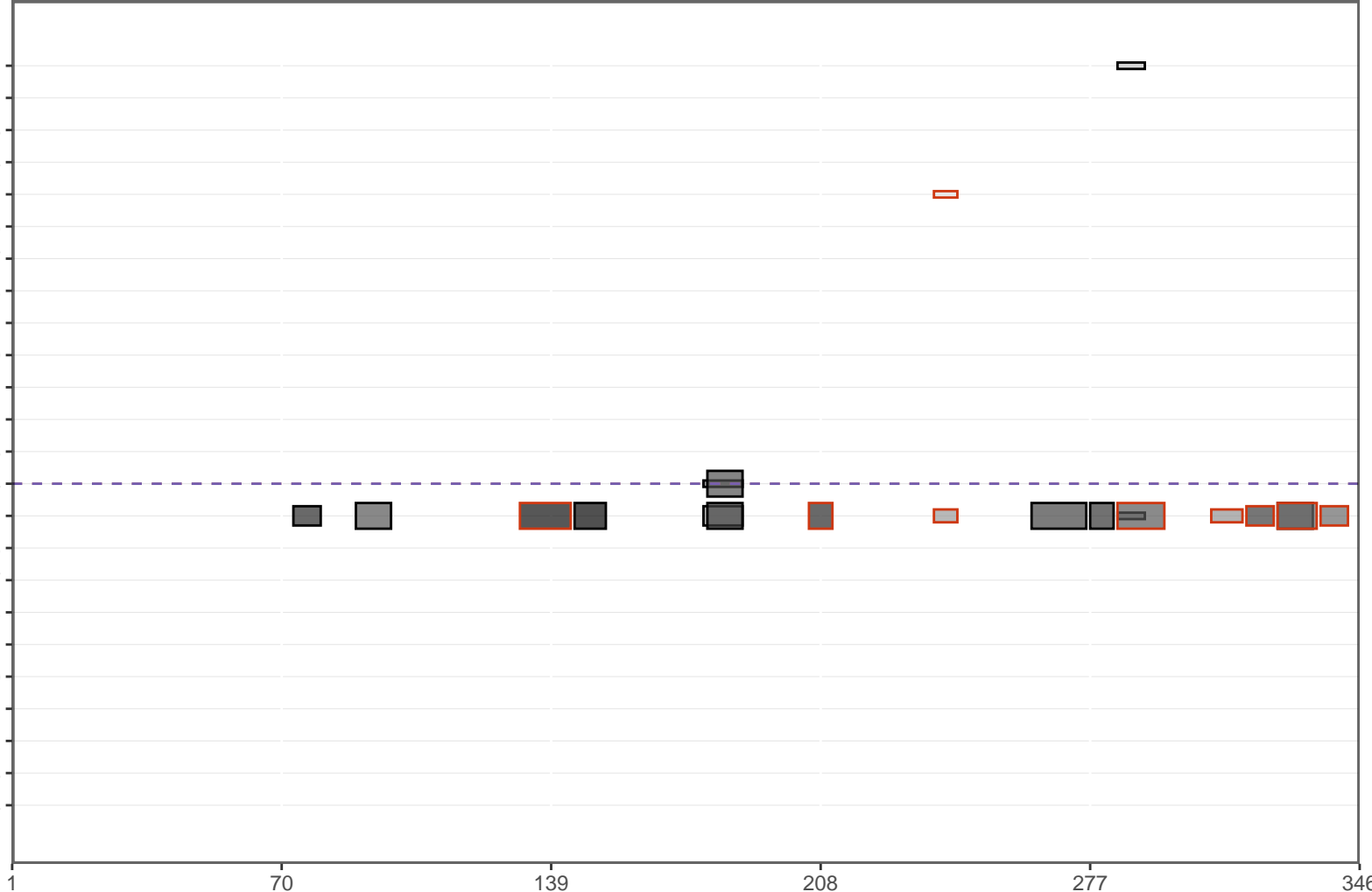
MW indication



Molecular weight



Gel Slice

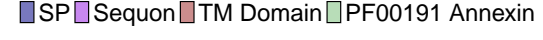


Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

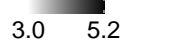
HSLFEHSEEDAFHQTFPERKLLVALVGSYRVEGPRVNDLAKSEAKIFVTLKDAKKLLEDEEHWLNSHRSKLHLKAVYSHYKEMTKGKYLDEDLGKYLKGGVQGLGSPQTYFSKILGSLRDLVDESAKDSVTRIVTRADDMMKQKEEFQKYGTTLSAKHEEVANGSYKXPLLTVAKEE*

NbL11g16310.1 phototropin-2-like [MW = 107.81 kDa]

No. of times detected



log(intensity)



Values from

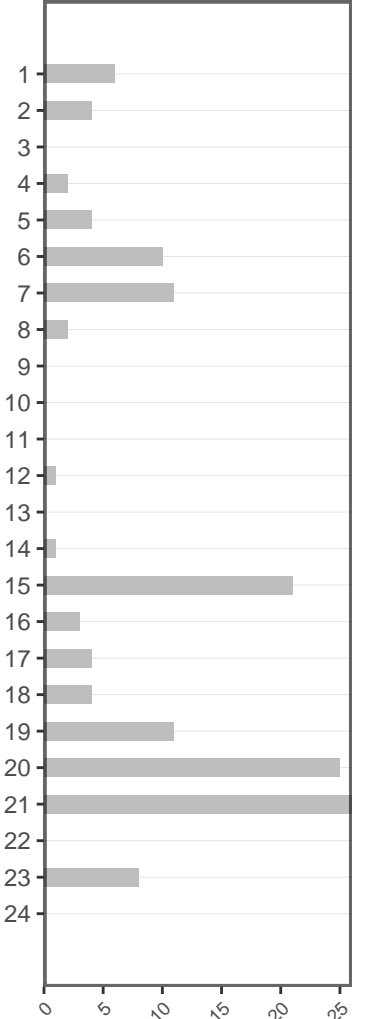
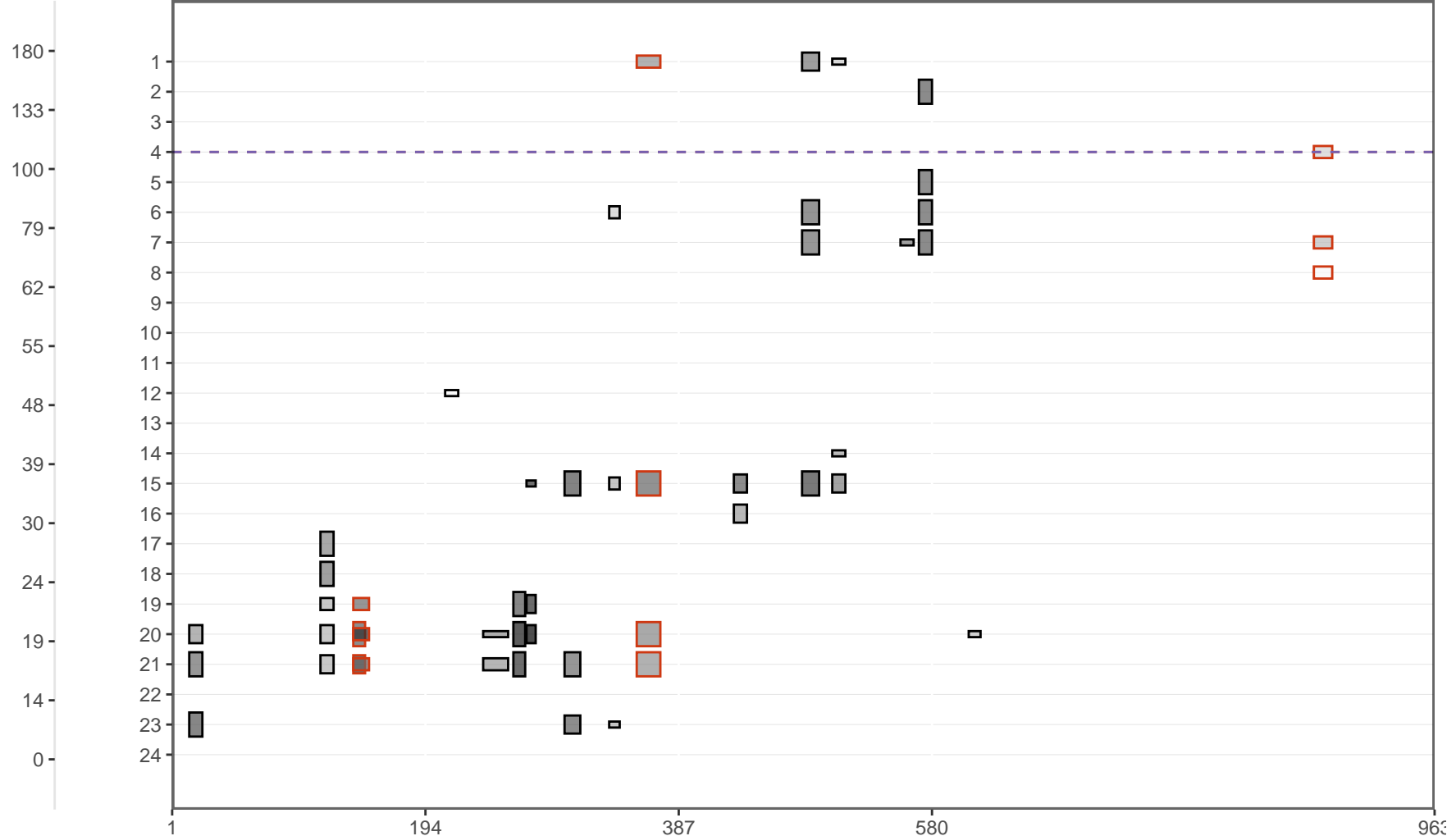


MW indication



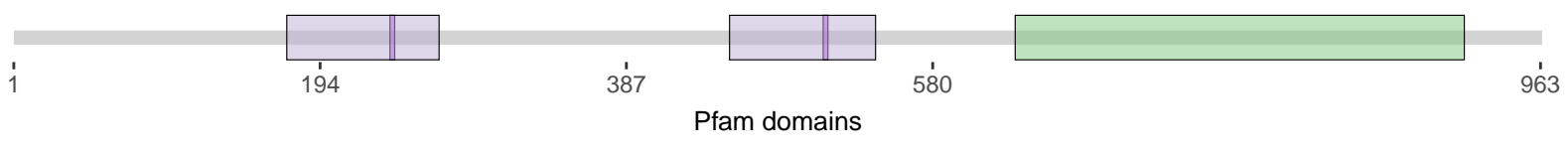
Molecular weight

Gel Slice



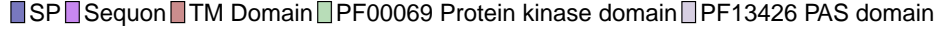
Protein length

Peptide counts over 4 repeats



Pfam domains

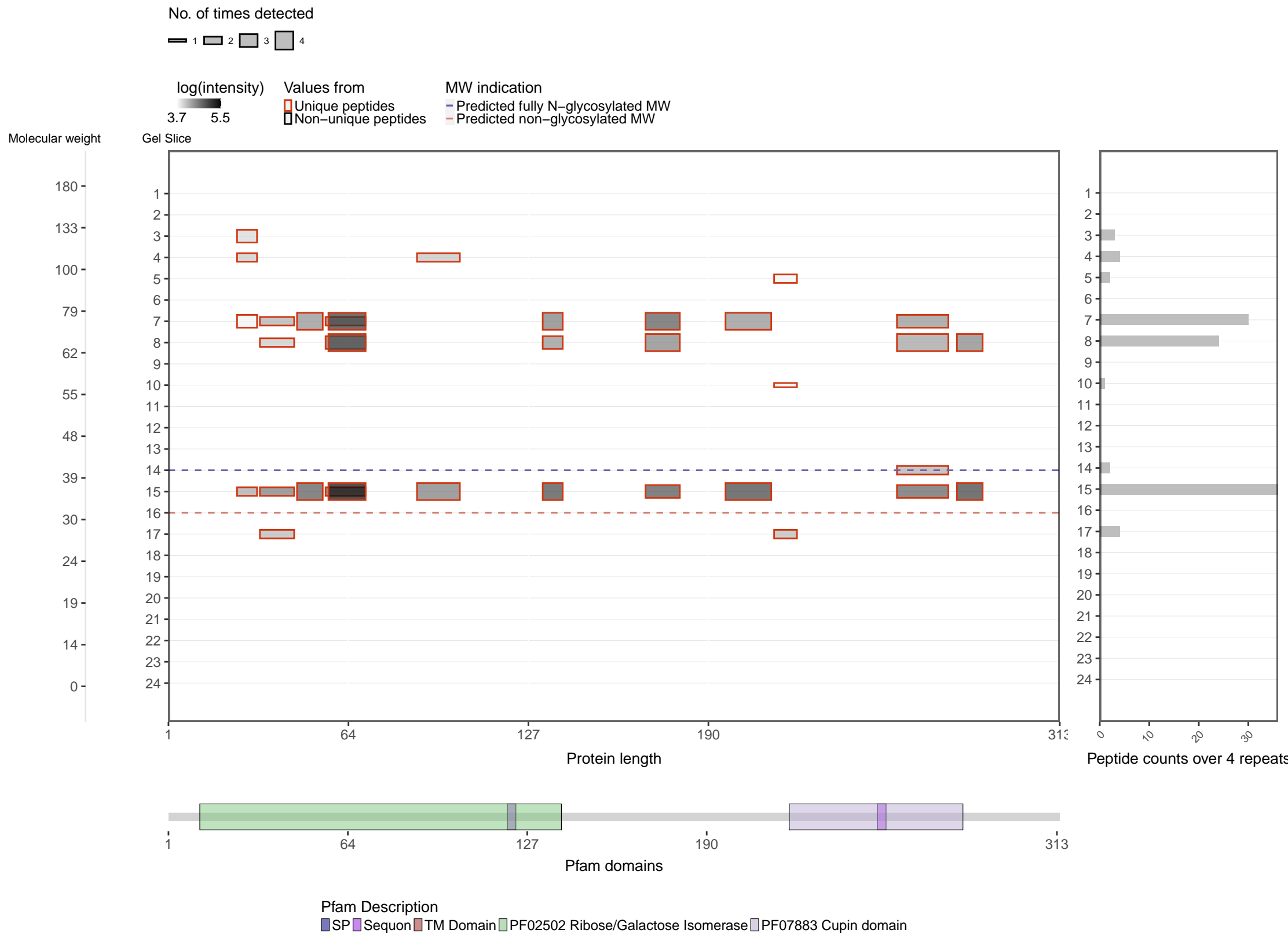
Pfam Description



Protein sequence:

LEUETREILGRNCRFLGQRPETDQATVQKIRDAIREGREITVQLINNTKSGKFWNLPHLQPMRDQKQELQYFVGVQVLDGSDHLEPLRNRLSEGQTEQSSAKLVKATENVDEAVRELDPANSKPELVAHLSKPVVPRPHKRDGSAWTAIGKTKANGERIGLNKFPVRLPLGGDGTGSHVLELVKSTGDLFAMKAMDKSIMLNRNKVKHRCVVEREIALLDHFPFLPALVSSFGTETHVGLTDFDPPGGELFALLDRGPMKFKESARFVAEVLGLEYLHCLGIYRDLKPEN

NbL11g16300.1 DNA_damage-repair/toleration_protein_DRT102 [MW = 33.8 kDa]

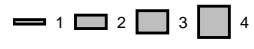


Protein sequence:

SGSNPWPDEIQDFLENSVTEMSKIGTGLTLLSEGEKGGAGNLSKVDREFKPIVEIPGGGSMITVRESPTSAFVKFTAGSVEPAAHHTFGHDLVLRKSKVYVNLKSGKKNYDLGVGDVLFTRPAGDVAHRVWYLEDTEFFLKWEGGQWDLVDFEDHAAAAAANDKEKES*

NbL11g16210.1 rubredoxin-like [MW = 22.73 kDa]

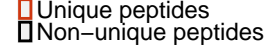
No. of times detected



log(intensity)



Values from



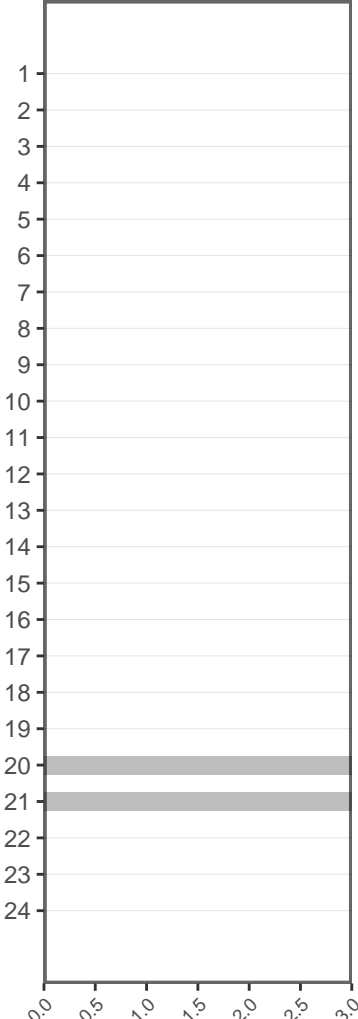
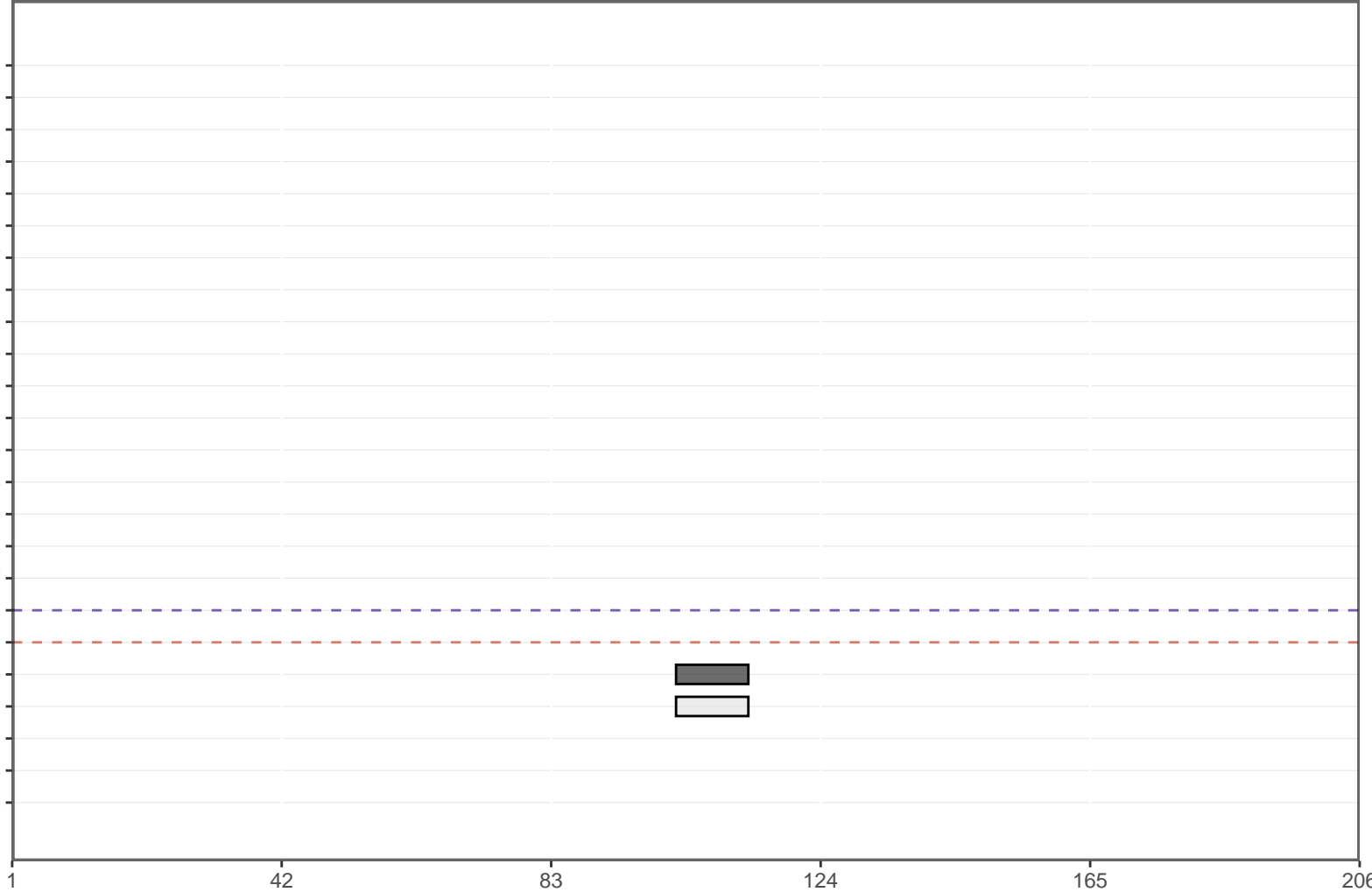
MW indication



Molecular weight



Gel Slice



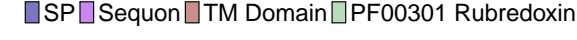
Protein length



Pfam domains



Pfam Description



Protein sequence:

INFDKRLEEKFAVLTGVEGRSGGFRKYEAAAGDPRVPIRPLGPFDDLPDWRPPTGGAAKSFFDNKGEVIAFGAQDQYGFQGNLTFGGKALLVYGGLLIGVFFLGGYFLQ

NbL11g16160.1 translation_initiation_factor_IF-2-like [MW = 52.65 kDa]

No. of times detected



log(intensity)



Values from



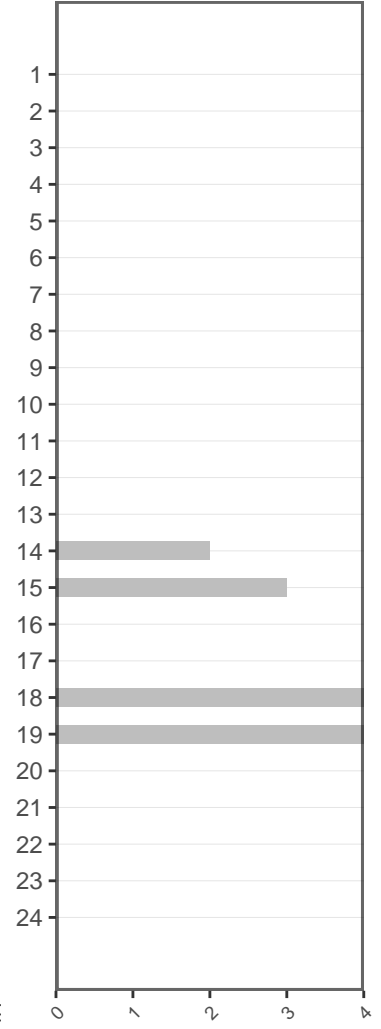
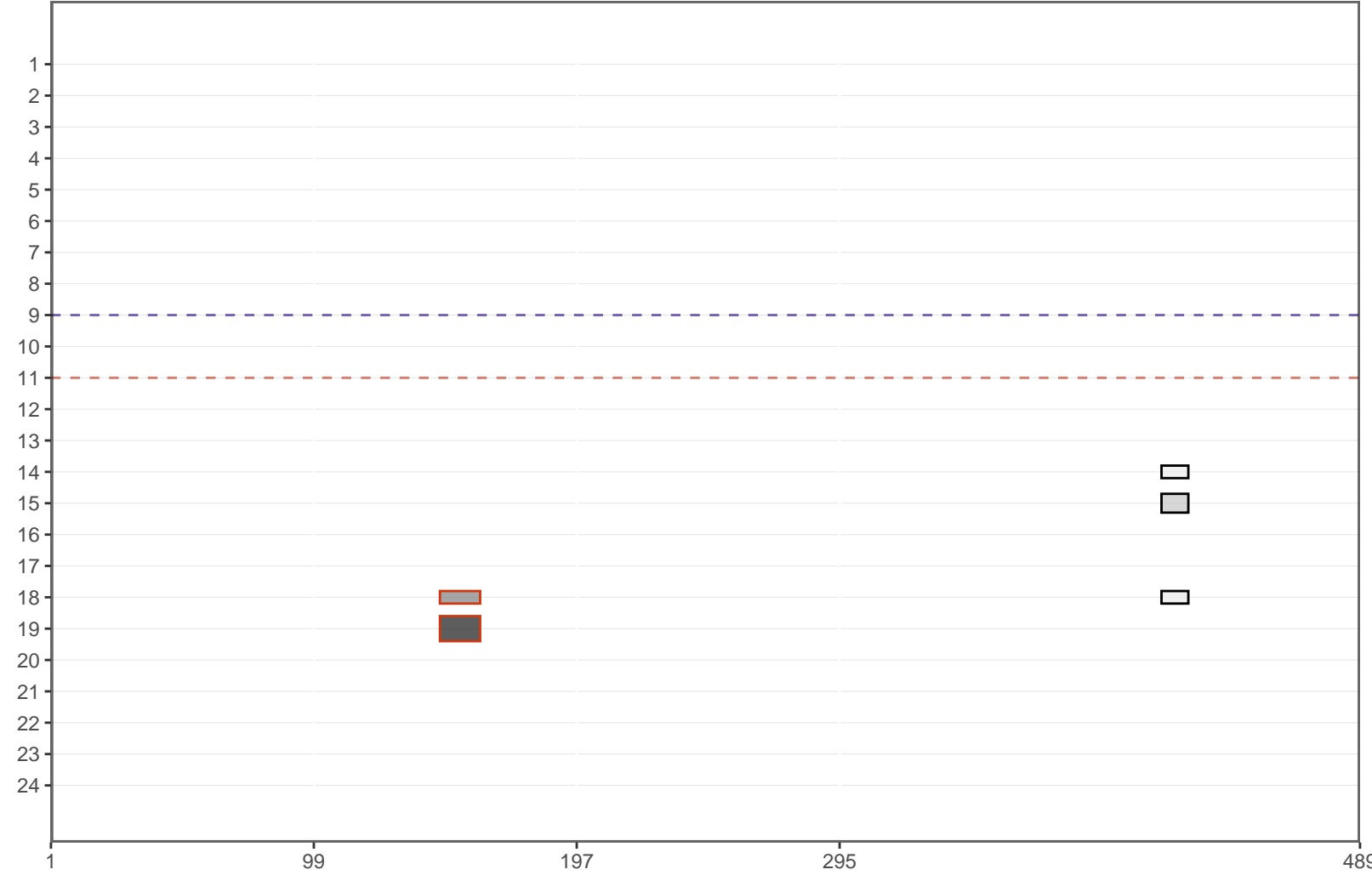
MW indication



Molecular weight



Gel Slice



Protein length

Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

VKKAVGILSRHSIDGGGGGGGGRGVGFGRGGRGMRGGRGGRGRRDENEDDLESGFYLGDNADGKLANLGPETMNTLAEAFEMSRVLPSPMDDAYVEALHTNMIECEPEYLMGDFEGNPDIDKPPISLGDALKMKPFLMAYEGIKDQEEWEKVIETMETVPLMKEVDYVSGPDRVATKAGGGQELERVAKTLPGSAPNSVKRTERAVLSLGSNPGWGFDDKGGDFMKKAVWEVSGHYK

NbL11g16030.1 4-hydroxy-tetrahydrodipicolinate_reductase_1_chloroplastic-like [MW = 36.54 kDa]

No. of times detected



log(intensity)



Values from



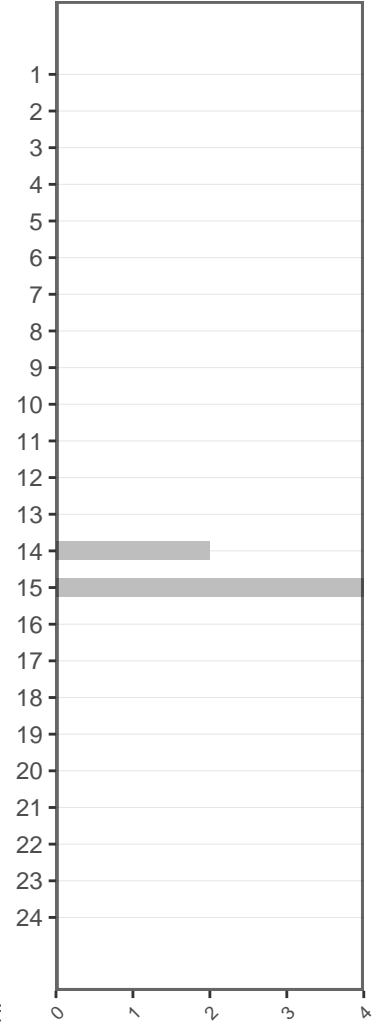
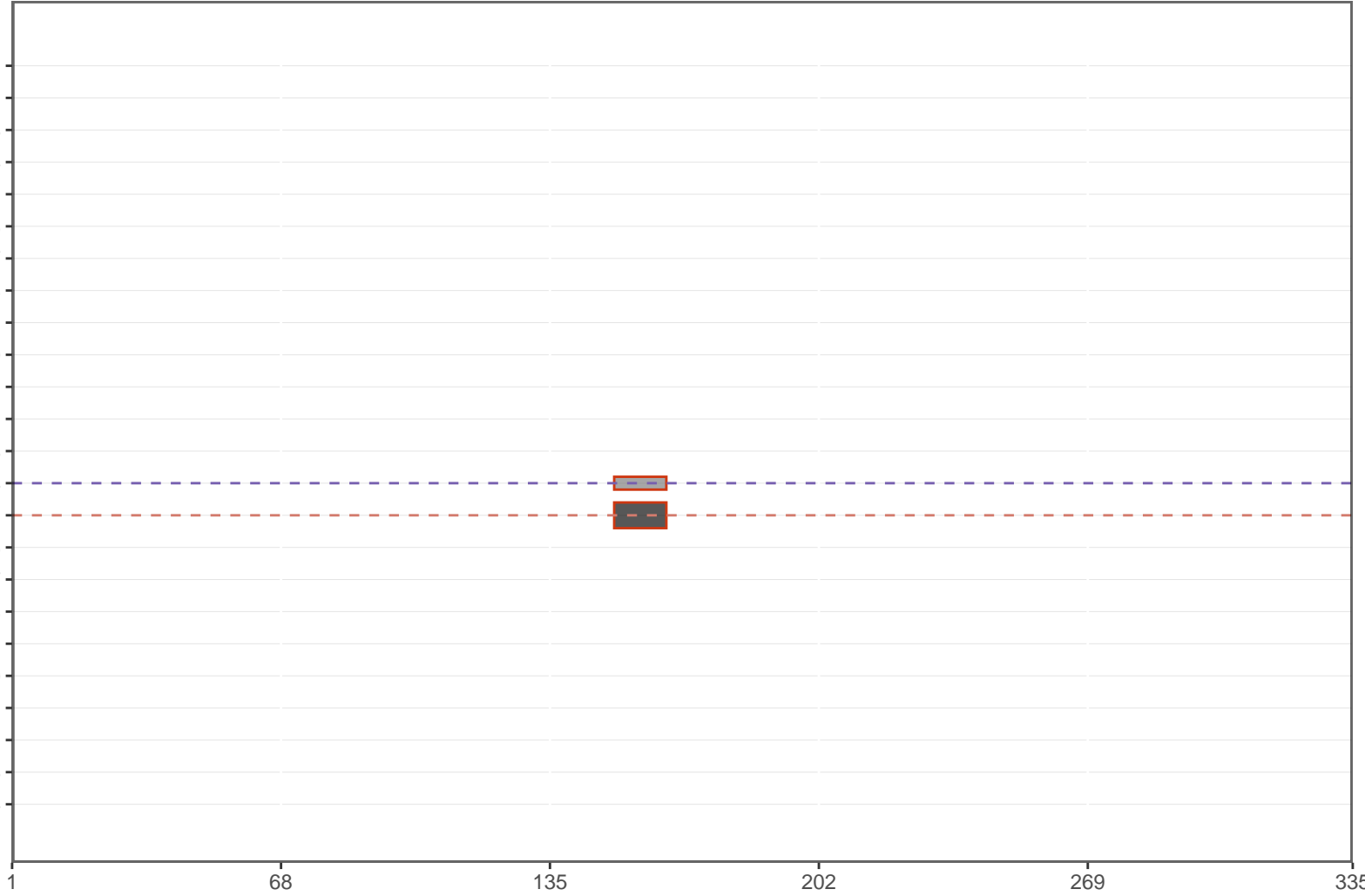
MW indication



Molecular weight



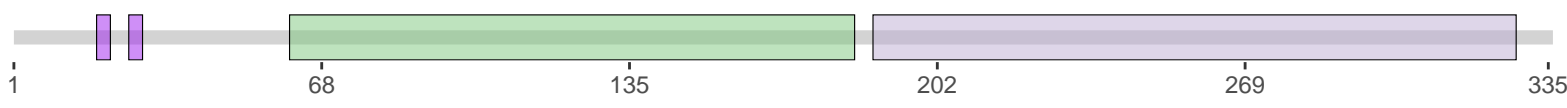
Gel Slice



Protein length

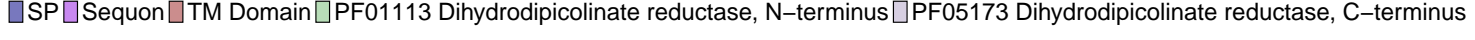


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YVLTGTTGGDRERLYKTVSDSKVYVVISPMGKGVVFLAAMEMAGDFPGAFSGVTLQVMESHGAEKLDTSGTAKAVISGFQKLGVSFDLDEVQLRDPKQGVEMVGVPEEHLHGHPHMYHLSFDQGVTFEFEGHNVGGRSVAEGTVDMLFLAKKVKLKEKRIYDMIDVLRGNMR

NbL11g15870.1 tryptophan_synthase_alpha_chain-like [MW = 33.81 kDa]

No. of times detected



log(intensity)



Values from



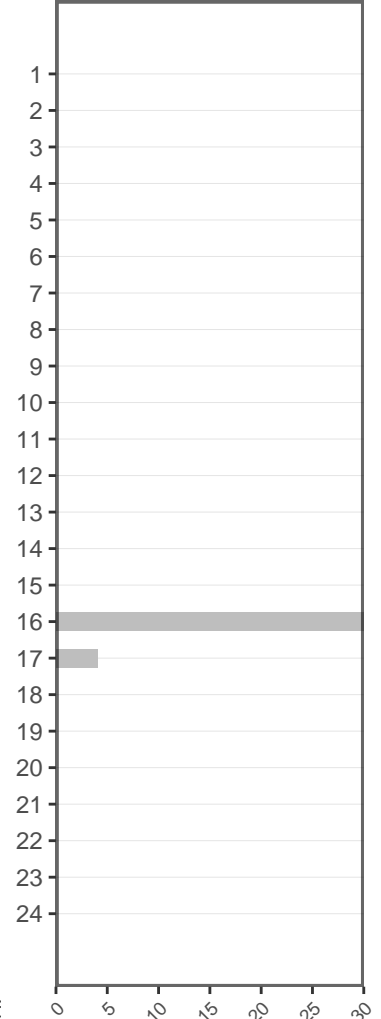
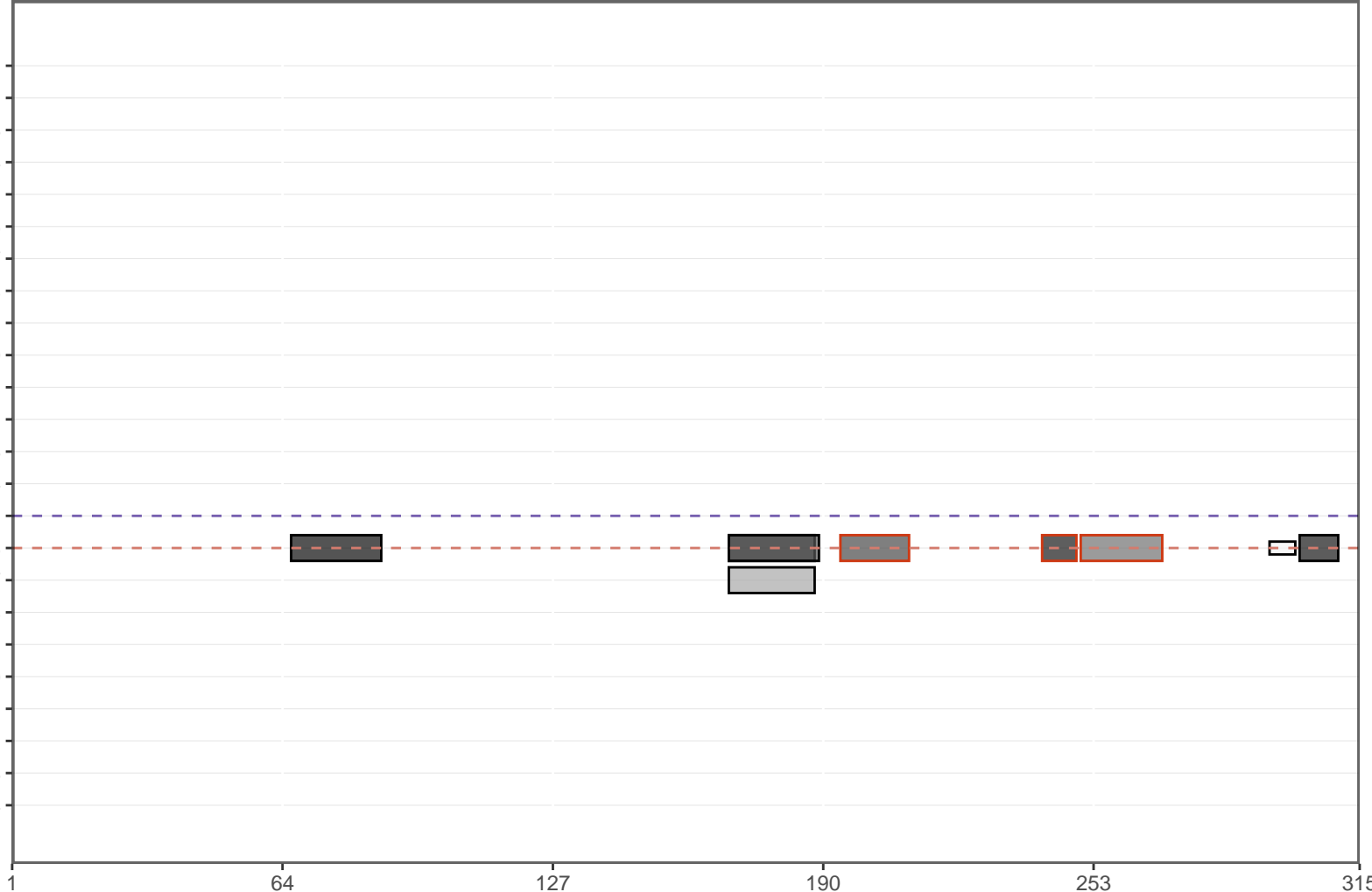
MW indication



Molecular weight

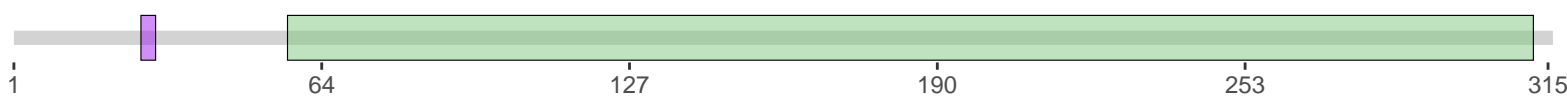


Gel Slice

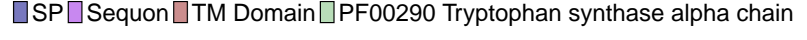


Protein length

Peptide counts over 4 repeats



Pfam Description



Protein sequence:

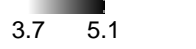
CPHALFTYYPNPLKRGTEKFMATVVRDAGVHGLVDPDVPLEETEILRKEARHNIELVLTPTPTVRMKATEASEGFVYLVBSGIVTGARESVSKVQSLIDIKKATEKPVAVGFGIKPEHVKVQVAGVGDVIGSAVRLGEAKSPPEGLKELEVFATSLKSALE*

NbL11g15800.1 glutathione_synthetase_chloroplastic [MW = 61.62 kDa]

No. of times detected



log(intensity)



Values from



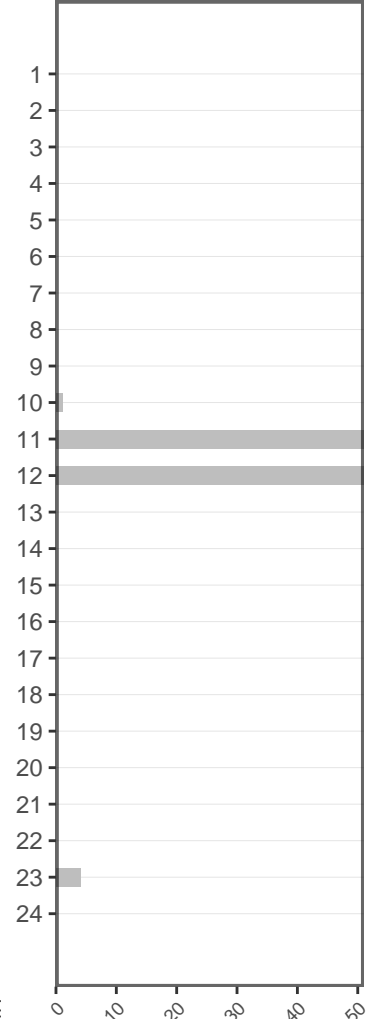
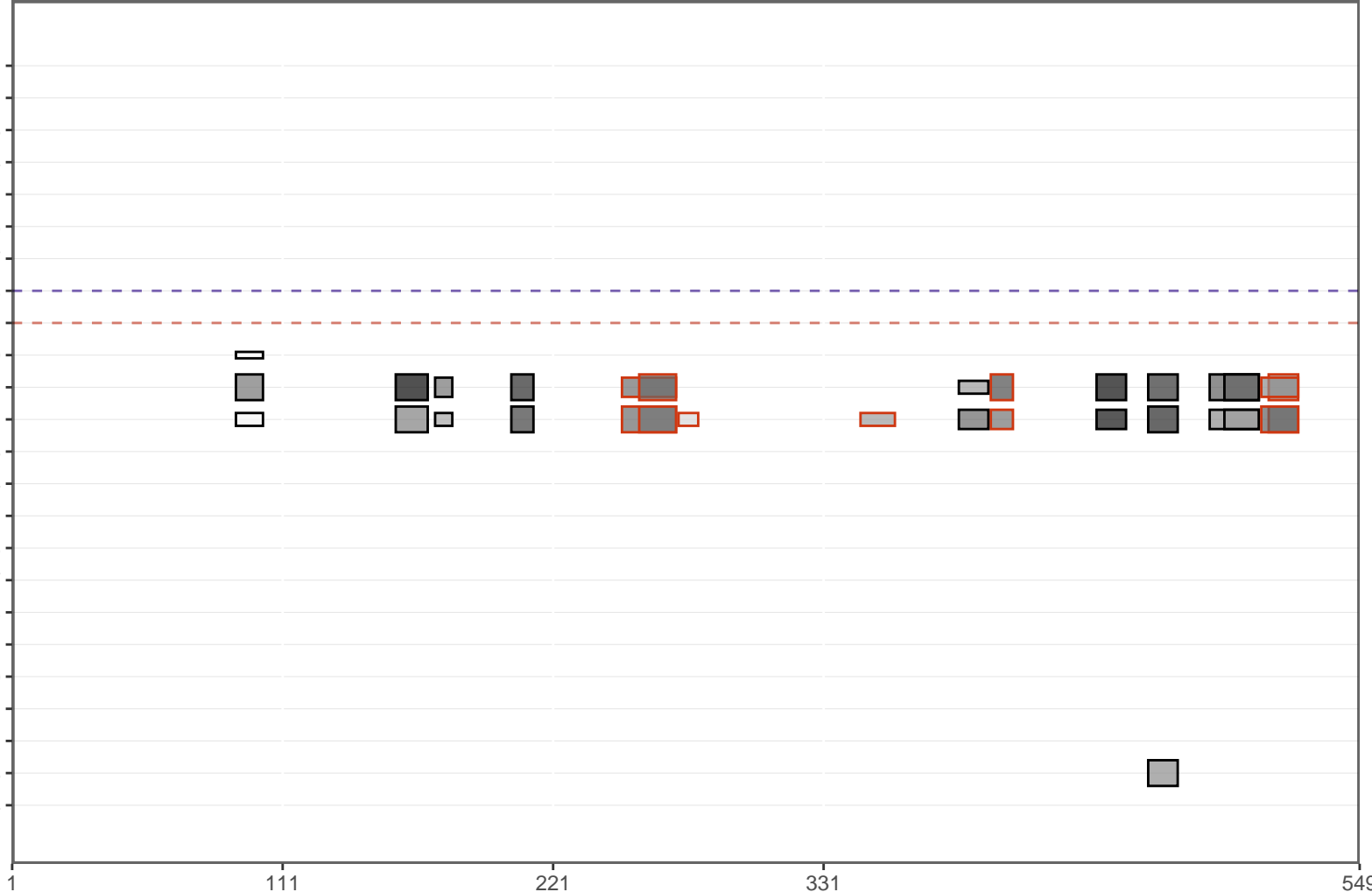
MW indication



Molecular weight



Gel Slice



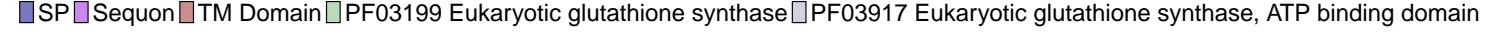
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

/NOFAEALAKAWNEYADPRAAVMEVVAEERNMVDQHWLGSALREKHKIVTRKTLAEIDAHGELLEEDGTLVVDGEPVAWYFRAGYTPSDYHSEGEWRARLLMEQSRVAKPESVYHLAGTKKIQDELAKPNVLERFLENKDDAKLRKGFAGLWBLDESNTVKDAIVRPGLYVMKPRGEGGNHYGEDVKEALLKIQEGTGSDDAFILMRNIFPTISHILMREGIPVKEQTISELGYGTYLKNEKELINQSGVLMRTKVSSSNEGQVAGFWLDSVLYV

NbL11g15780.1 UPF0603_protein_At1g54780_chloroplastic [MW = 31.99 kDa]

No. of times detected



log(intensity)



Values from



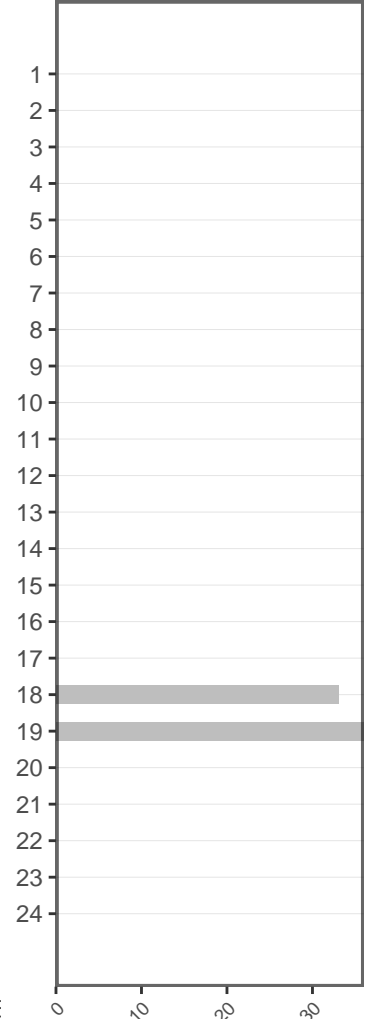
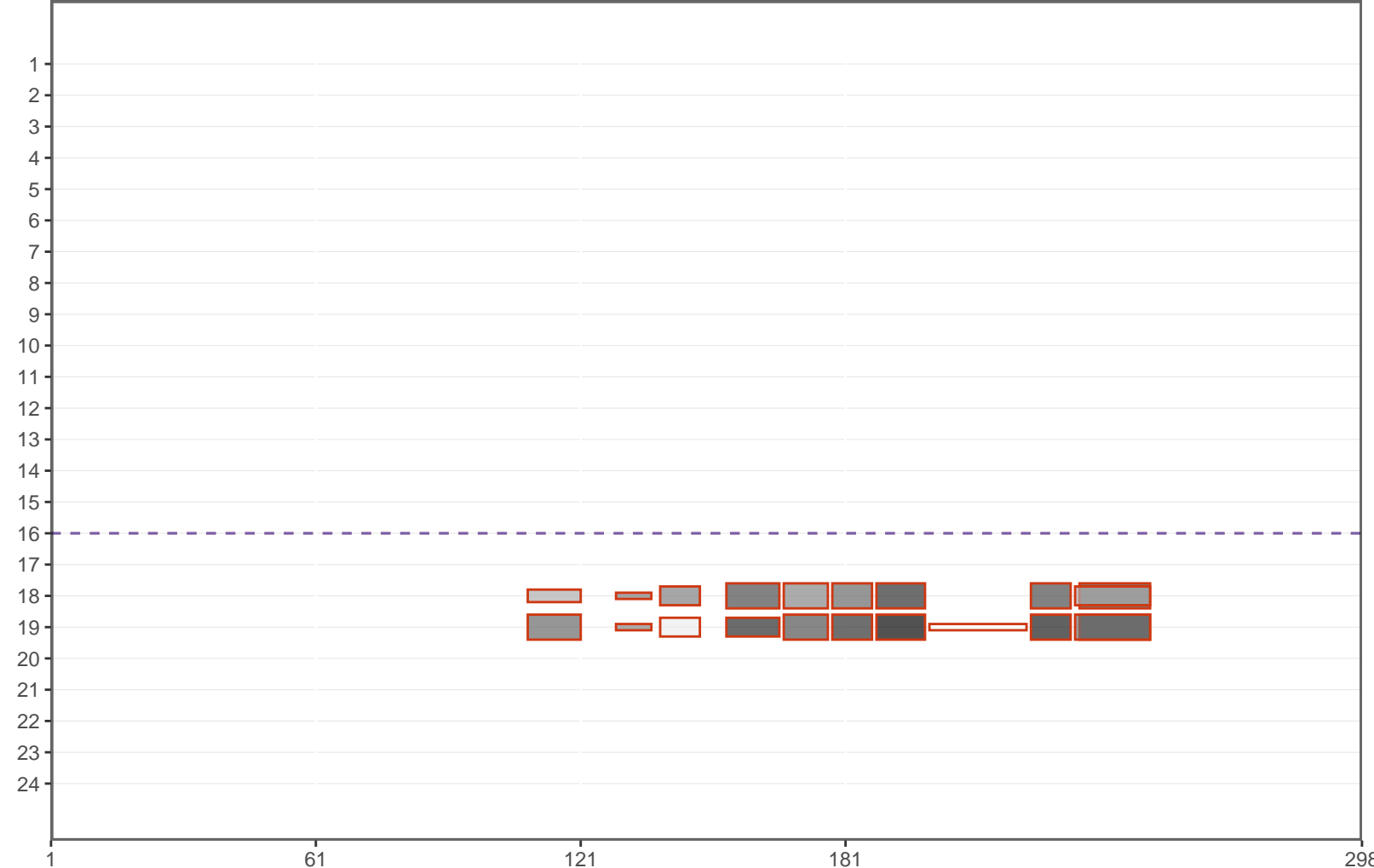
MW indication



Molecular weight



Gel Slice

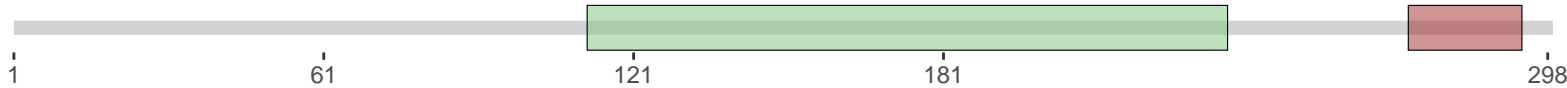


Protein length

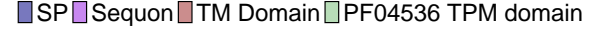


Peptide counts over 4 repeats

Pfam domains



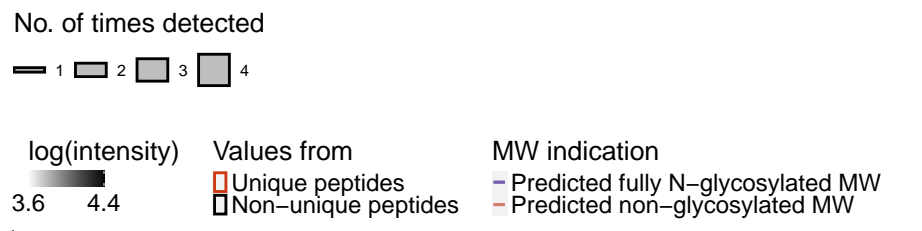
Pfam Description



Protein sequence:

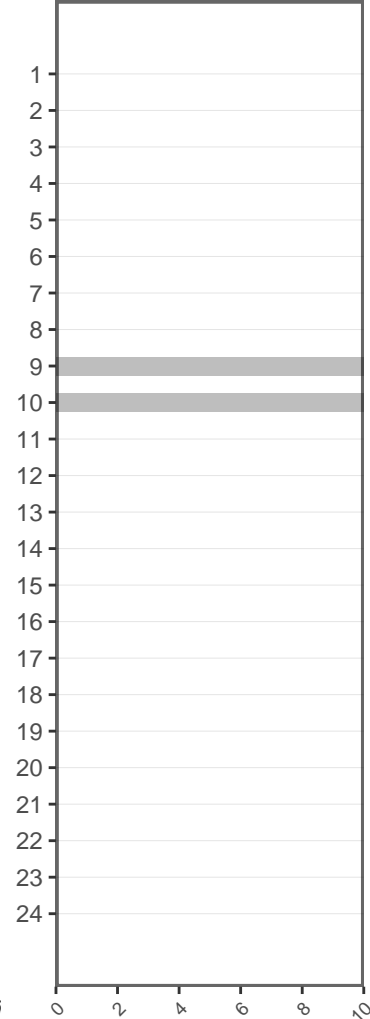
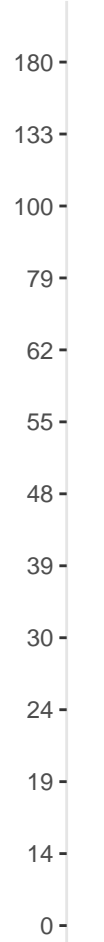
RKGFHINFTYRKLTSKADAFEVADTVLEKWPPEVEGGNDKGIIVLVTSQKEGATGGPDFVKAAGDVTLEDAVSENLVLAATEEKNEAVYSTAKRLVAIDGLPDPGGPQLKDKKRESFKSREETDEKRGGFTLVGGLLIAFVVPMAQYVAVSKK

NbL11g15760.1 branched-chain-amino-acid_aminotransferase-like_protein_1 [MW = 62.33 kDa]



Molecular weight

Gel Slice

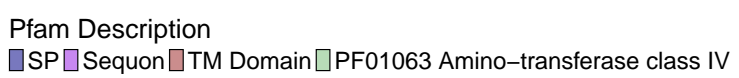


Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:

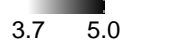
AVVGDIEVPRETAKYVDFDVAVGGDDAVWEGRLRVYSGKLFKLEEHLDRLFDSSAKALAFSNVPTREEVKEAFKTLTNGMYDNAHRLFLTRGKKVTSGMSPAFNGVGGTLVLAEWKPPVYDNEKGIILVATFTRRNSPNNLDGKHNNLNLLNLAKIEGNAAGADDAVMLDKDGYVSEETATNFIPLWKKGRVYTPHADYGLPGIFRATVMELVLEKENVLEERRISLSEFHTADEVWTTGTMGELSPVAKIDGRIGDGRVGPVYQRLGNAYKKLAEDSGVSPITYOKS*

NbL11g15610.1 mevalonate_kinase-like [MW = 40.83 kDa]

No. of times detected



log(intensity)



Values from



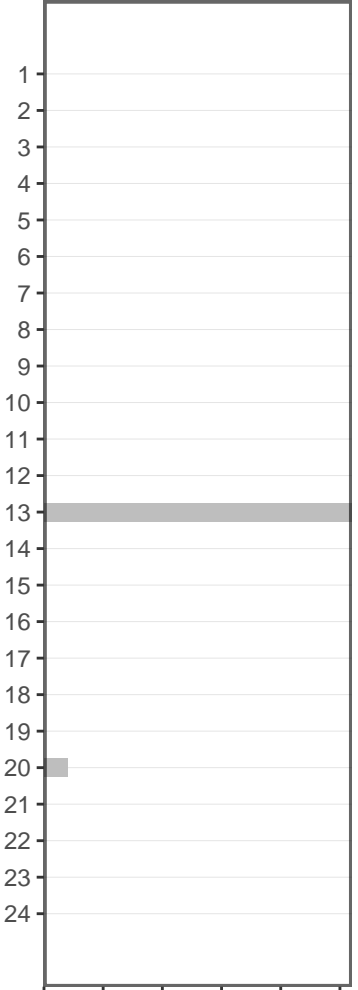
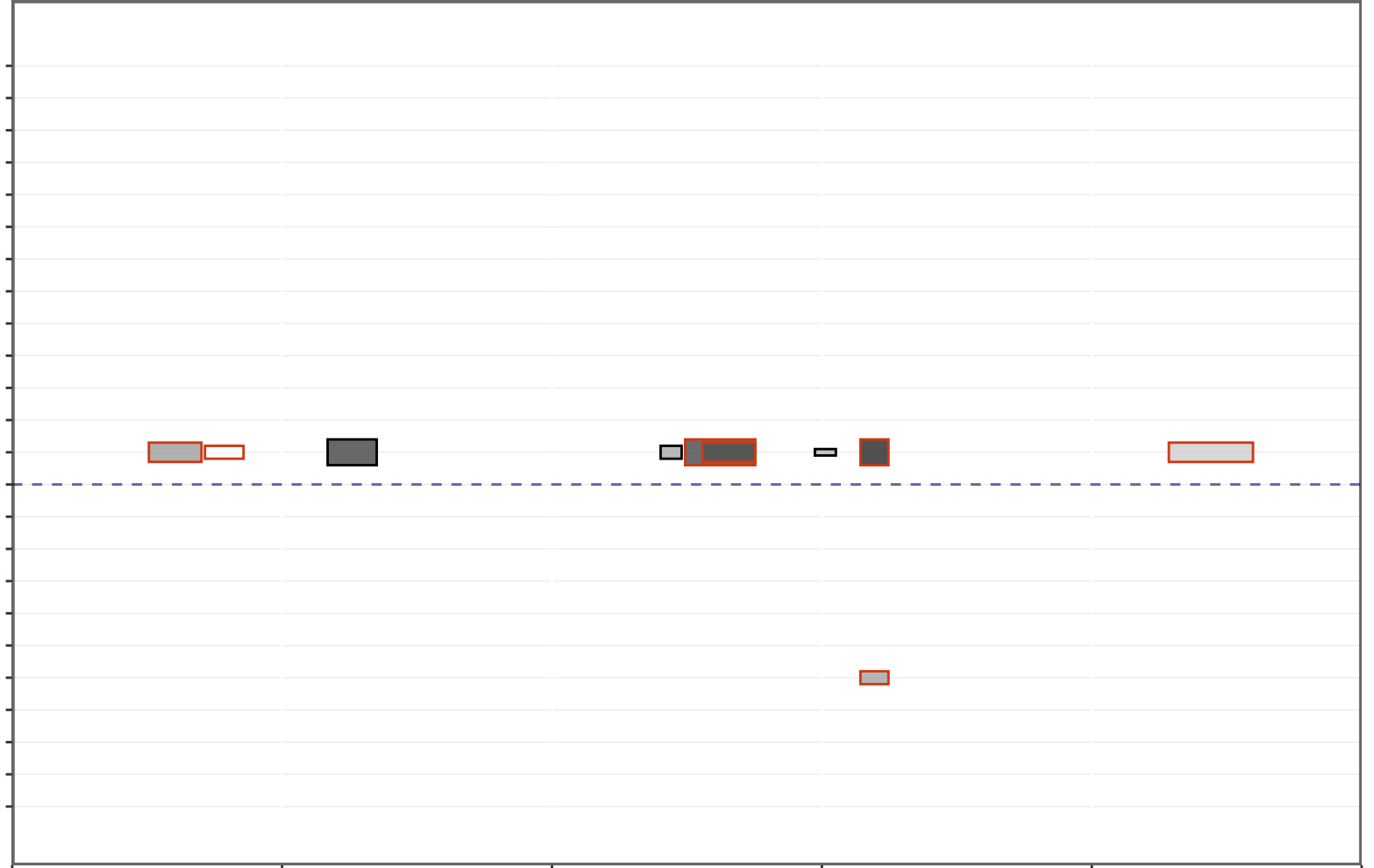
MW indication



Molecular weight



Gel Slice



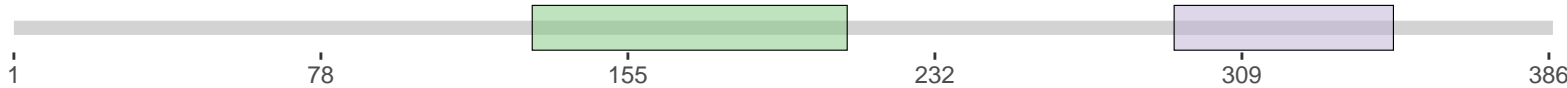
Protein length



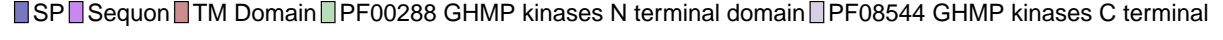
Peptide counts over 4 repeats



Pfam domains



Pfam Description

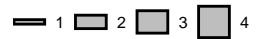


Protein sequence:

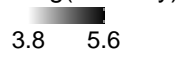
LELVNVAWFEQEKHDKPKSGDINTVSTYGNLHFKSGDTRUKTNMPLKMLINTKVGINTKALVASVSEKTLRHPTAMASVFTAVDSHSEVAAGSPVDDLAITEKEEKL EELMEMNNGLLGCMGVSHASIEVLRITLKYKLSKLTGAGGGGVLTLLPTLLSGTVADKVAELETGDFQCLLAGGGNGVEILFSGTQ

NbL11g15580.1 serine--tRNA_ligase [MW = 51.09 kDa]

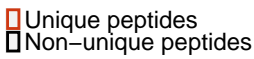
No. of times detected



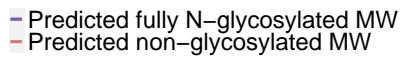
log(intensity)



Values from



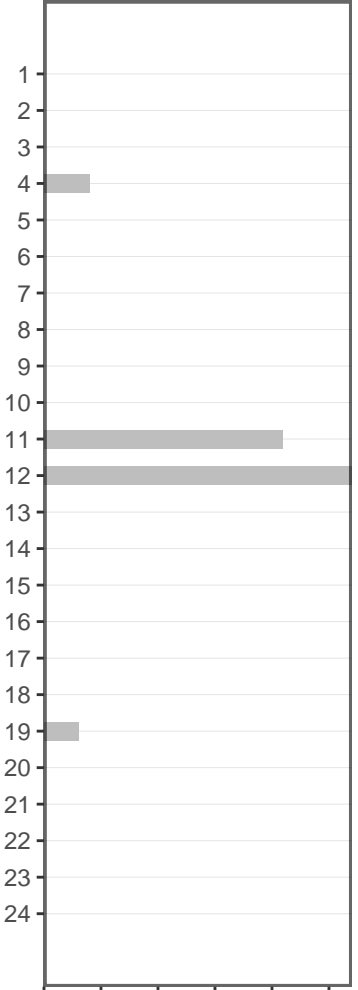
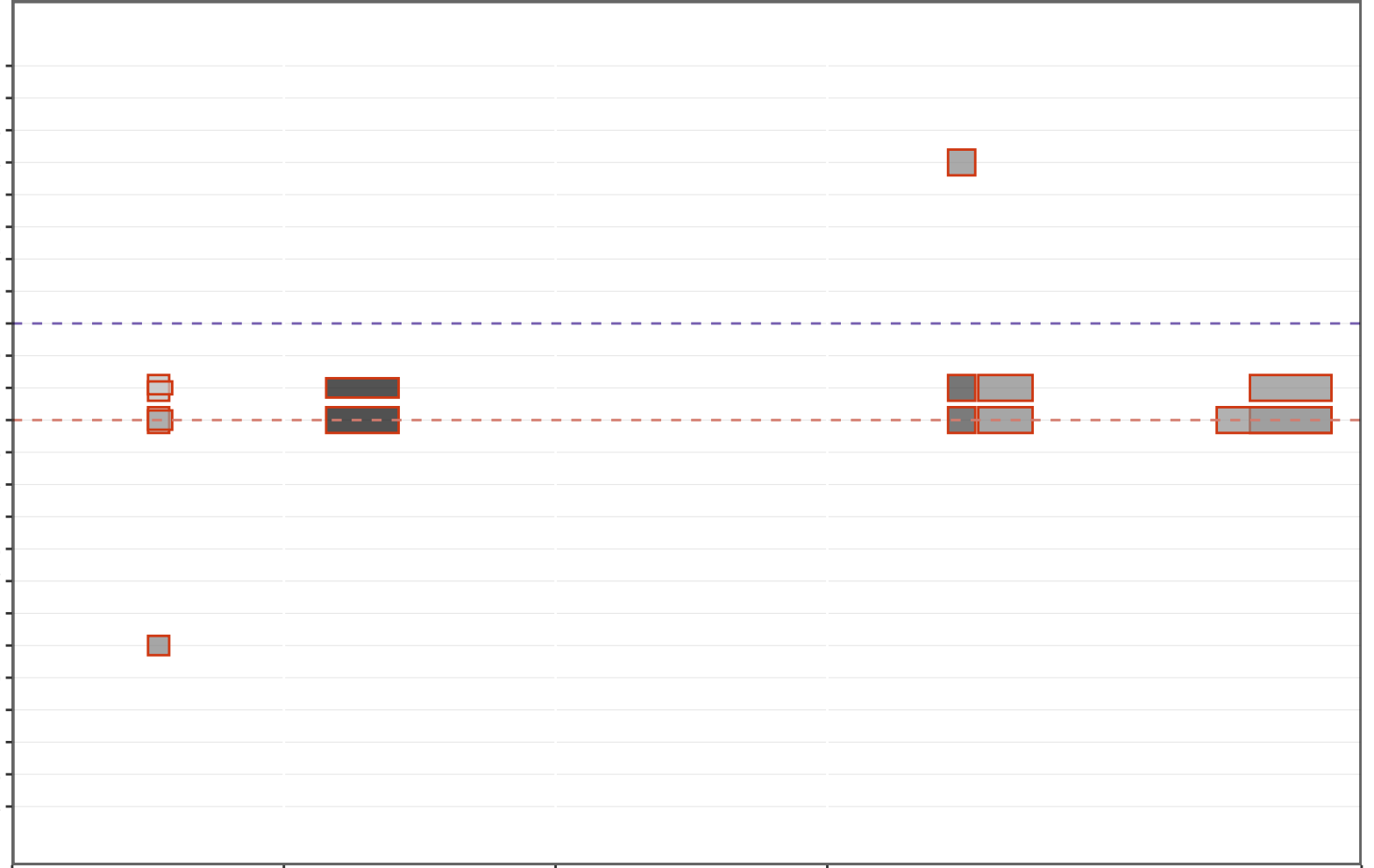
MW indication



Molecular weight

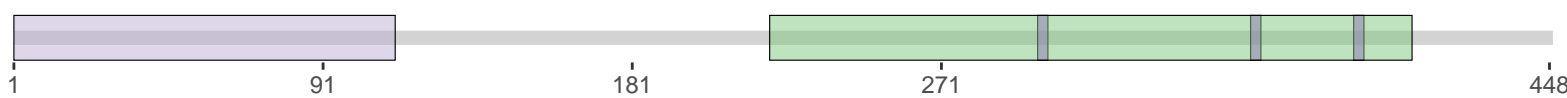


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00587 tRNA synthetase class II core domain (G, H, P, S and T)
- PF02403 Seryl-tRNA synthetase N-terminal domain

Protein sequence:

LAIQFDEELYKVTGEGDDKYLHATAEQLGAYHLDVHHPGQLPLRYAGYSSCFRKEAGSHGRDGLGFRVHQFEKVEGFLTSPNGNDGWDHHEEMKNSEFFQGLKIPYGVVSVGALNDAANKYDLEGVYASSTYRELVSNGCTDYGSRKLEIRFGGKKGNEGAKGVYHLLNSTLATERITGILENNQREDGVEIPEVLRPYMDGVTFMFGQTAPKAEAGKKKKA*

NbL11g15450.1 acetylajmalan_esterase-like [MW - SP = 39.6 kDa]

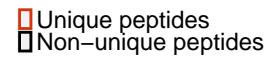
No. of times detected



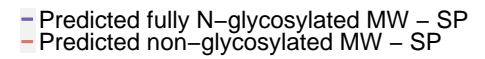
log(intensity)



Values from



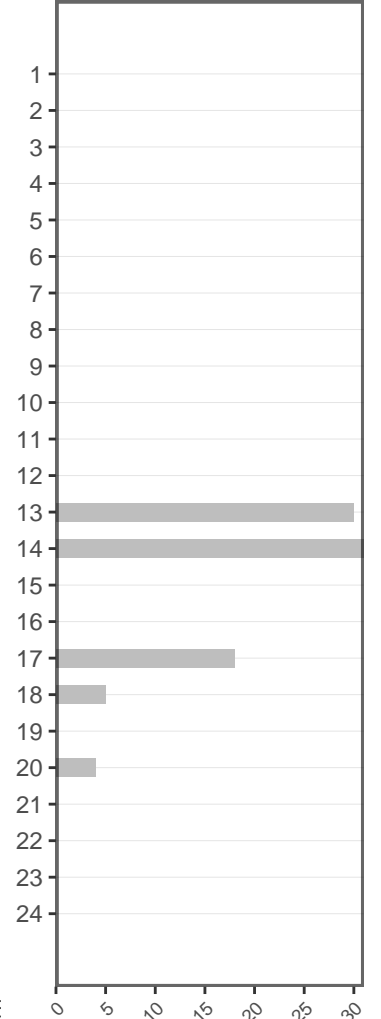
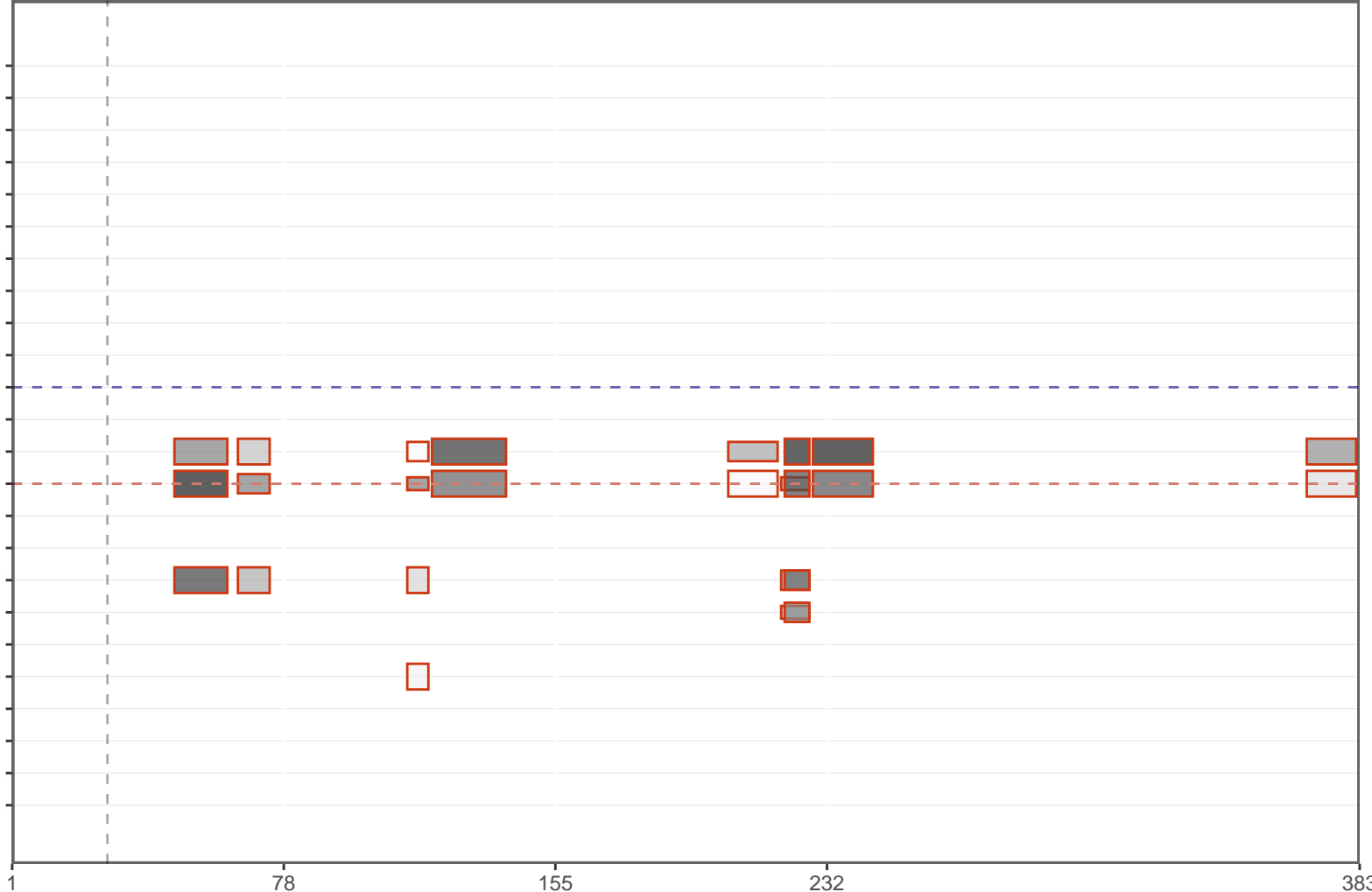
MW indication



Molecular weight



Gel Slice



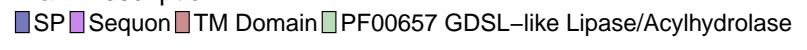
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ALFLVGGIGGNEFNALSGGKTLSESRIVPDVEAIHGVRRVIFGATRVVPCNPFPGGFPILTRFMTDENSEAVDEHCLKDFNSLHFFNDHLDGQALDKKEYPNTLYGQYNAWLLQNAVSLGFDKNSLHKACGGIGGDYNYNHNDGGTGVPCVCTDPTTYVSDGAAHTGEAYSWLARWLDNNLIPOLNQA

NbL11g15410.1 calcium-dependent_protein_kinase_5 [MW = 63.88 kDa]

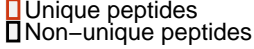
No. of times detected



log(intensity)



Values from



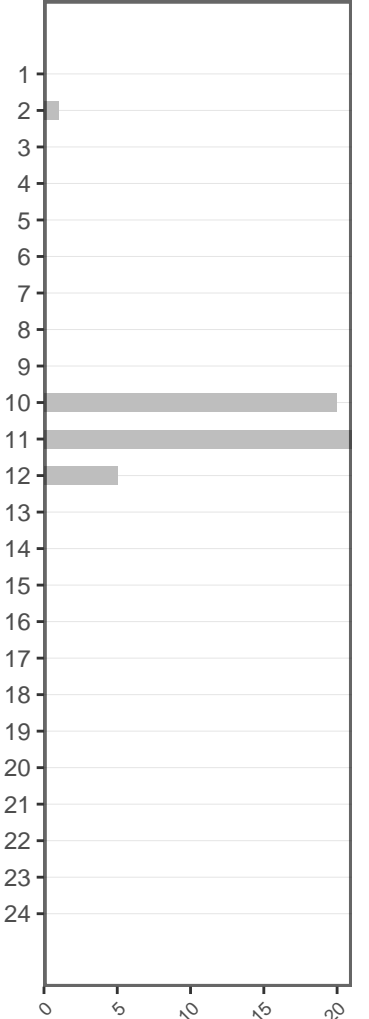
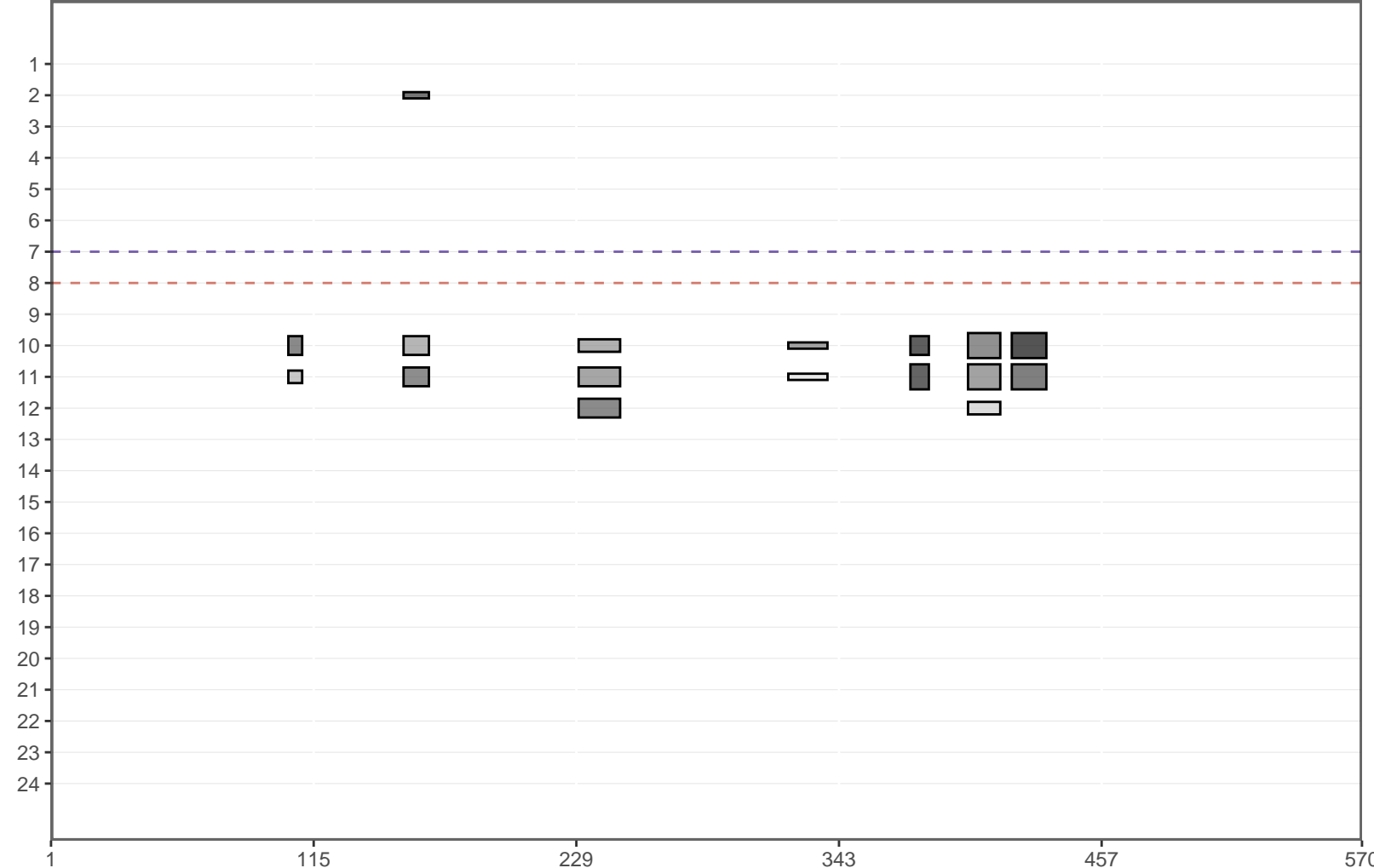
MW indication



Molecular weight



Gel Slice



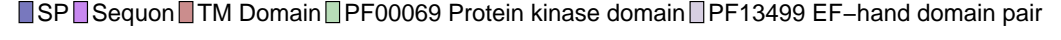
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PYYVAPEVLQIHYGSPEDAWWTAGVILYLLGGVPPFWAETGGGIFDAVLKGHIDFESDPVPLISESANDLRKMLCMRPSERLTAHEVLGHFWGCEGVAFPDRALDPAWLSRLKHFSAANRKYKMMALRVAAESLSEEEAGLKEMFKAMDTDNGSATTDELKAGLRKYSGTLKDIERELMDAAVDVNSGTFVGEFIAATHLKLDRHEHMAAFQYFDKDAAGYVTVDELGGACADHNTDVFDFEDIREVDGQNDGRIDVGEFVAMMGKGNPQIGRRTRMNSLNFMSRDAP

NbL11g15220.1 lysM_domain-containing_GPI-anchored_protein_2 [MW - SP = 35.25 kDa]

No. of times detected



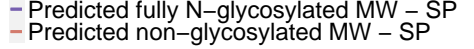
log(intensity)



Values from

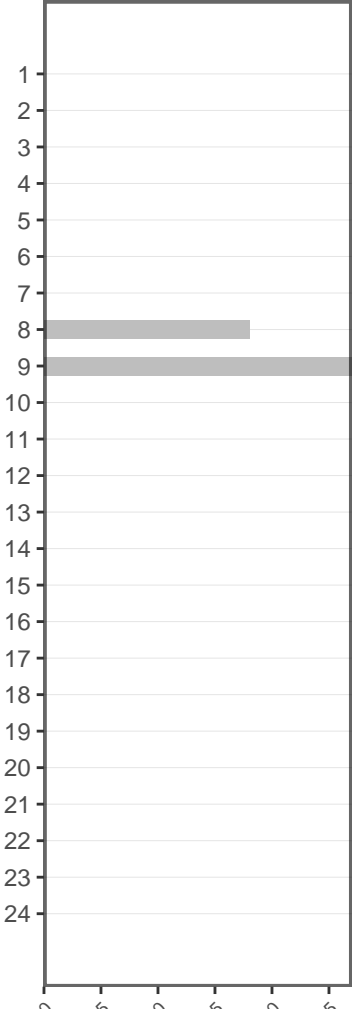
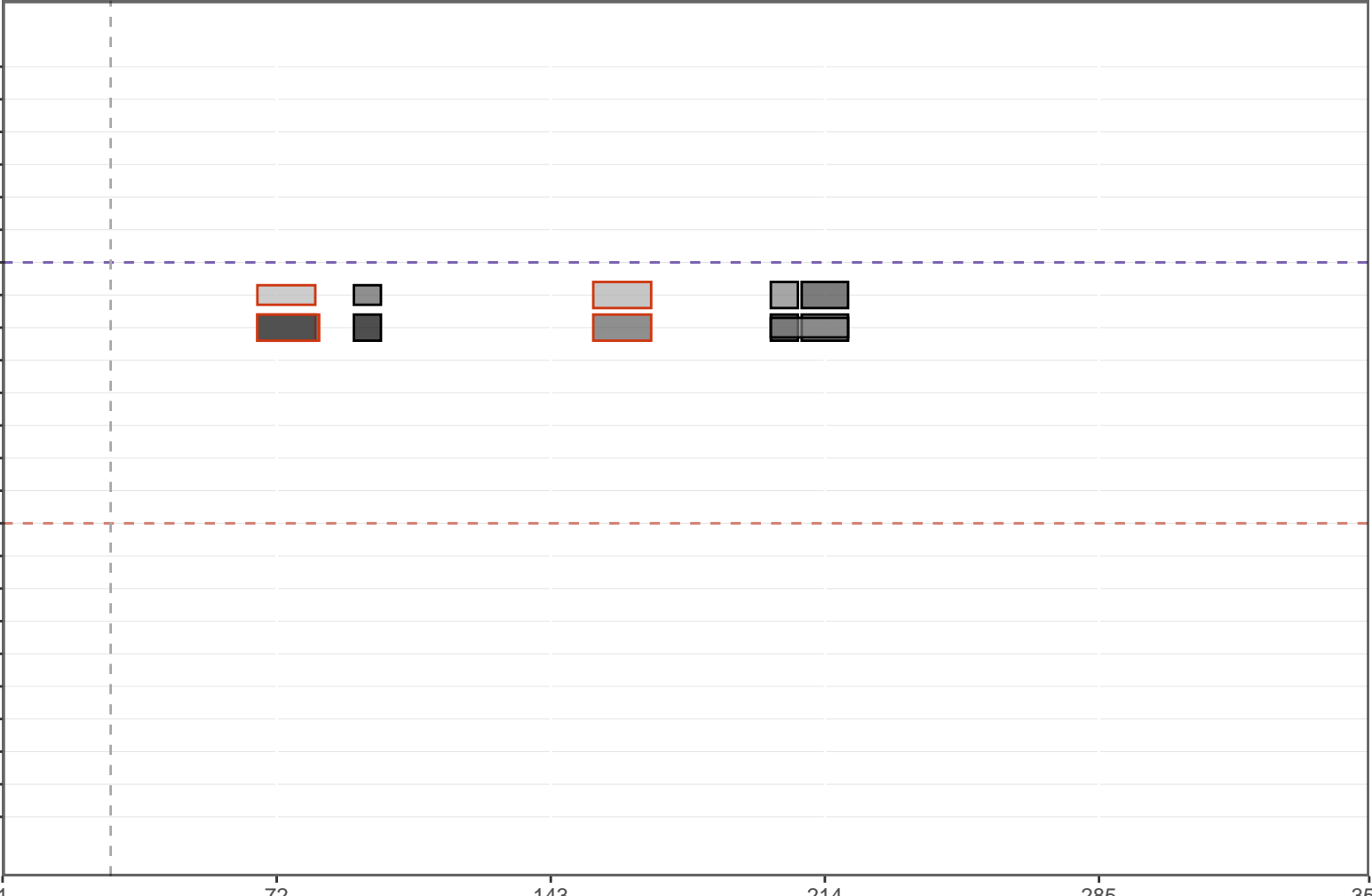
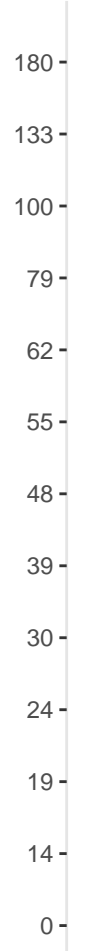


MW indication



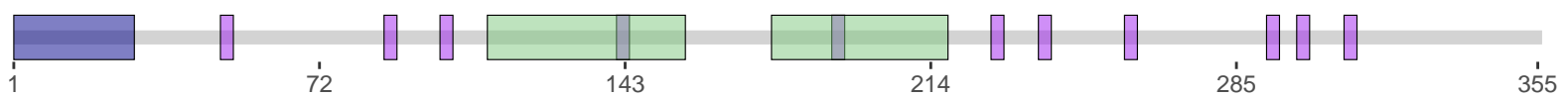
Molecular weight

Gel Slice



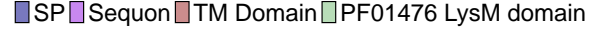
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SEKVVHYGR/LVAGNFTVDDIADGQVNVSGDITLKLINGLSDPKELIAGSVLDVPLKACGSMVNTSLDYLPLLPNDTVYFTANCVACKGDAKNWFLGCGPSPGKSKSLWKSQSPMDCCGLDFYHGMVTSDDCNSTAGAVAGYSNQTFFTSGLTQCPASTASEMTGTWRWNLVAHLALLEASVYMR

NbL11g15150.1 expansin-like_A2 [MW - SP = 26.47 kDa]

No. of times detected



log(intensity)



Values from



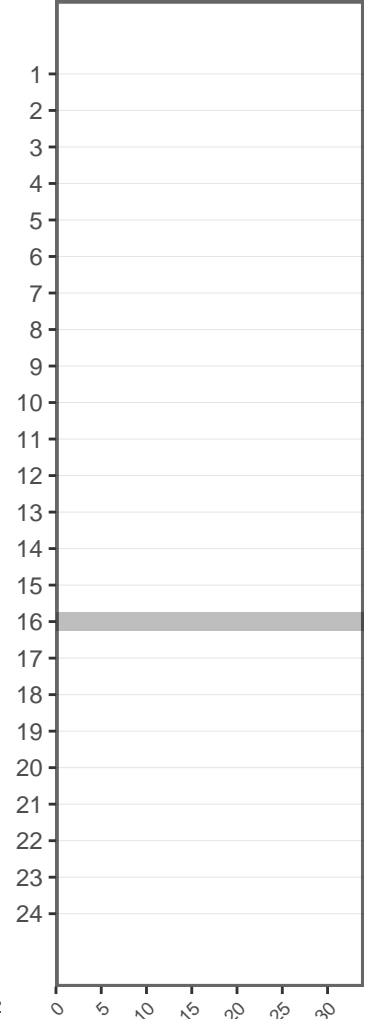
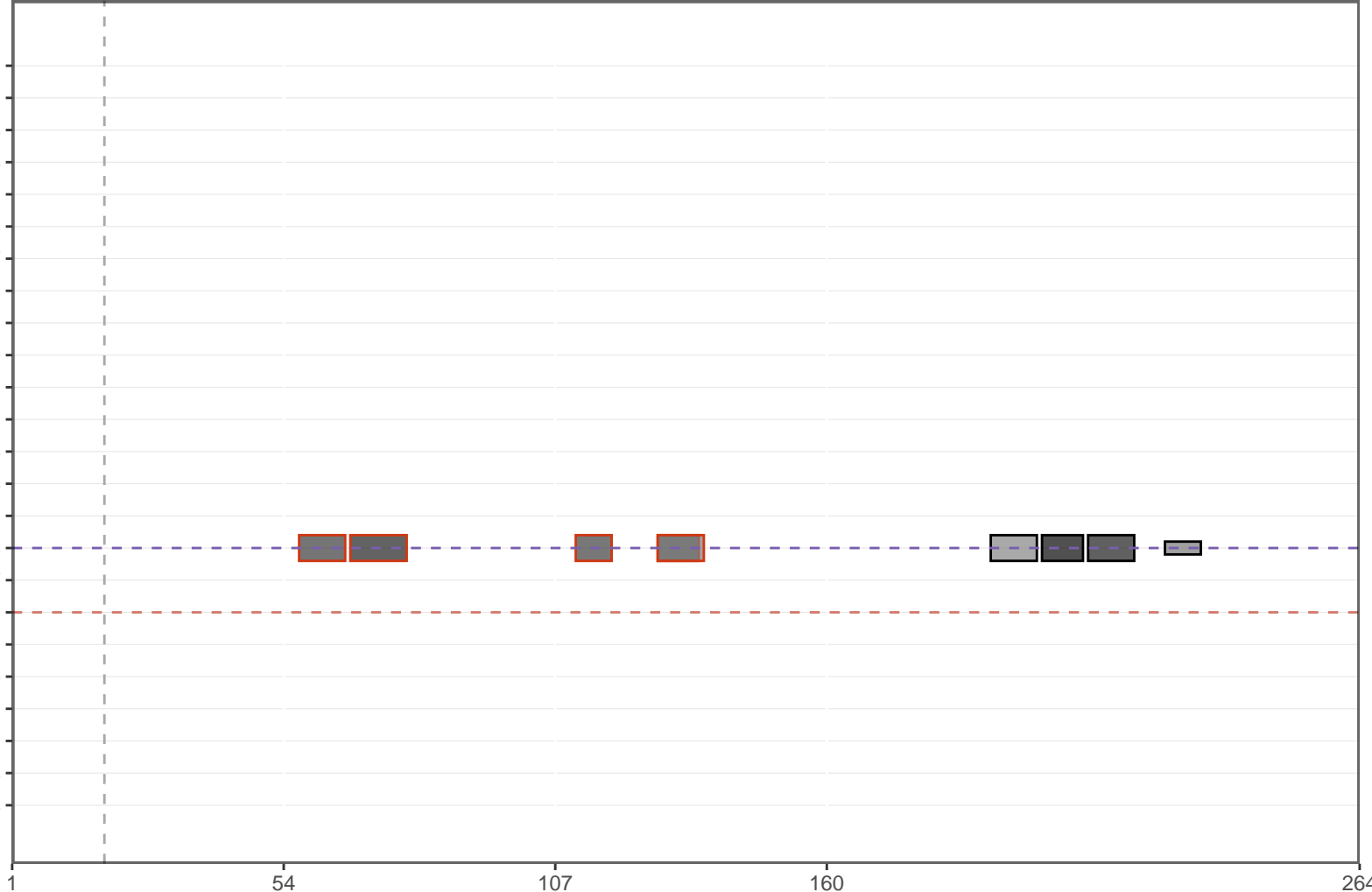
MW indication



Molecular weight



Gel Slice

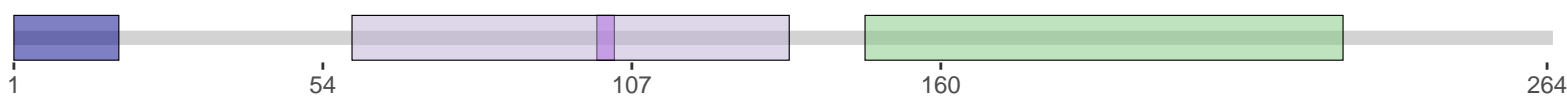


Protein length

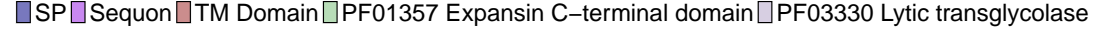


Peptide counts over 4 repeats

Pfam domains



Pfam Description

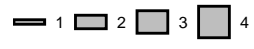


Protein sequence:

KAADVYKLGADVEYKRVPCDVKSKNLAIRVEE66GKPNLAISFLYGGGGTEIIVDVAQVGSSTWVFLSRNHGAWDTSRVPTGALQFRFVVTAGYDGGKWWAKSVLPADWKNQVHYDTGLGITDAQEGSPGDDGNWKLH

NbL11g14930.1 V-type_proton_ATPase_subunit_B2 [MW = 60.01 kDa]

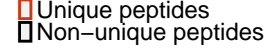
No. of times detected



log(intensity)



Values from



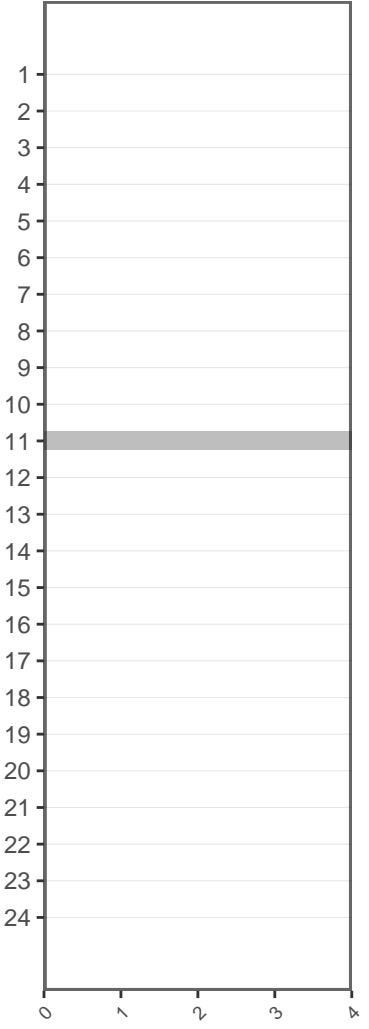
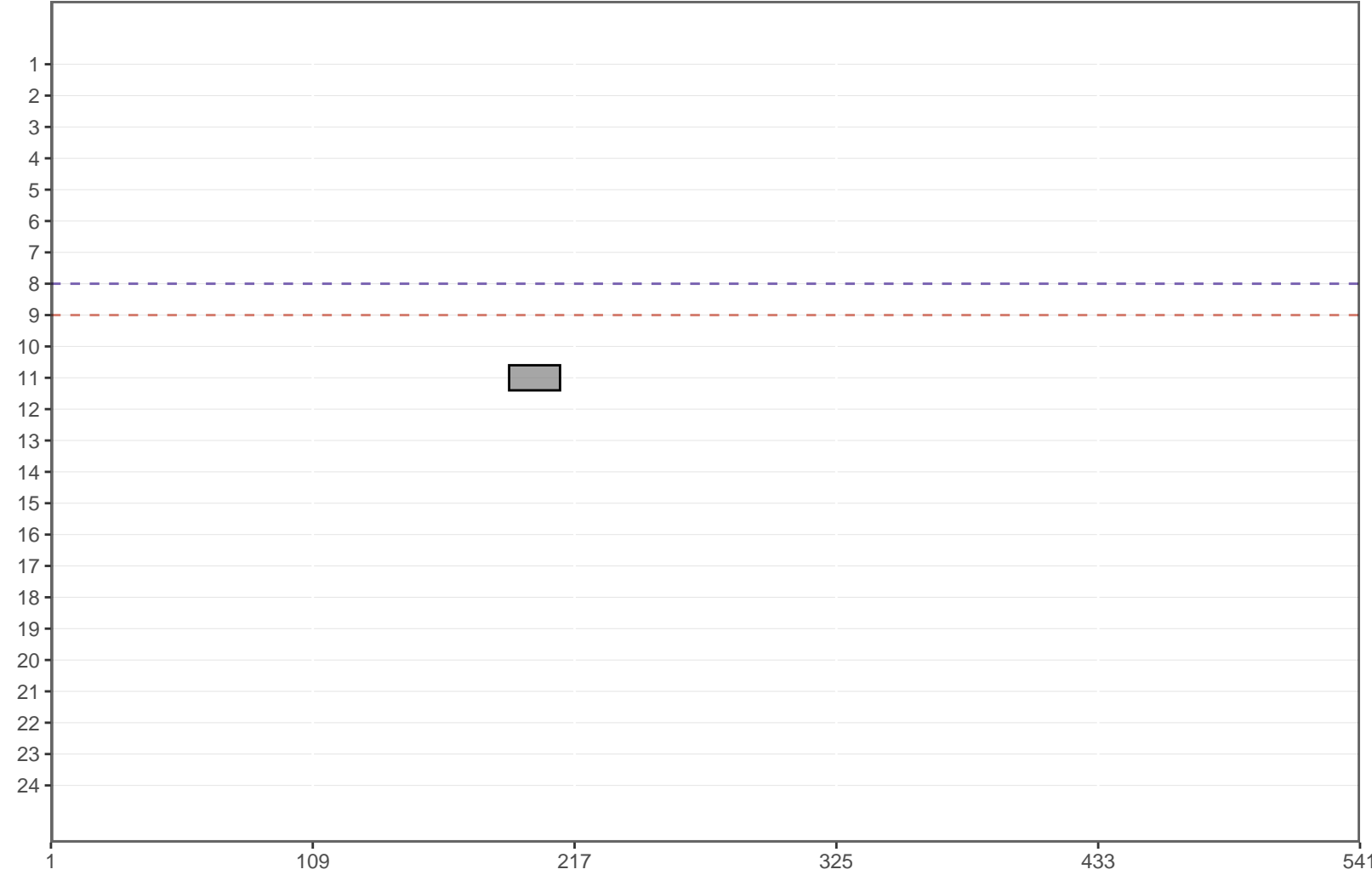
MW indication



Molecular weight

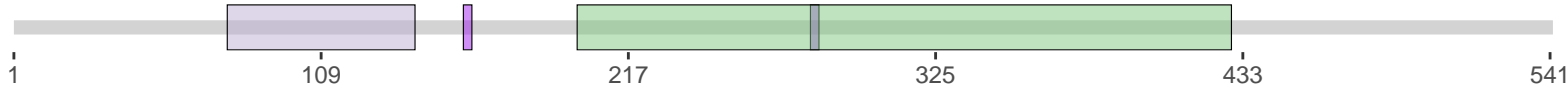


Gel Slice



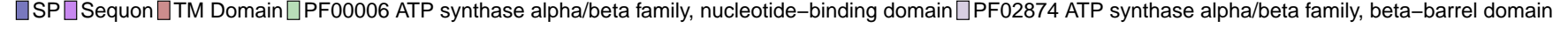
Protein length

Peptide counts over 4 repeats



Pfam domains

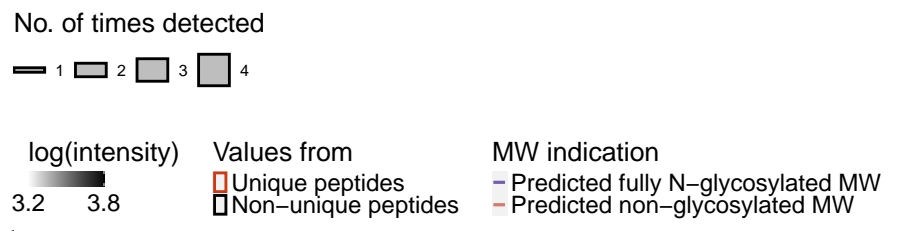
Pfam Description



Protein sequence:

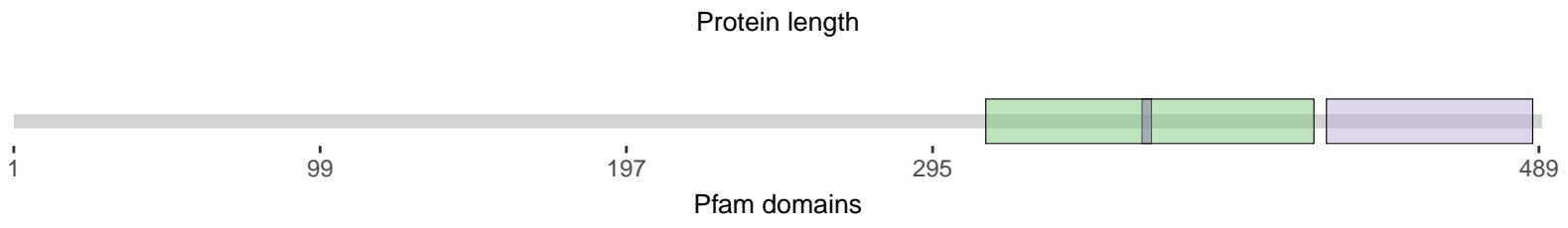
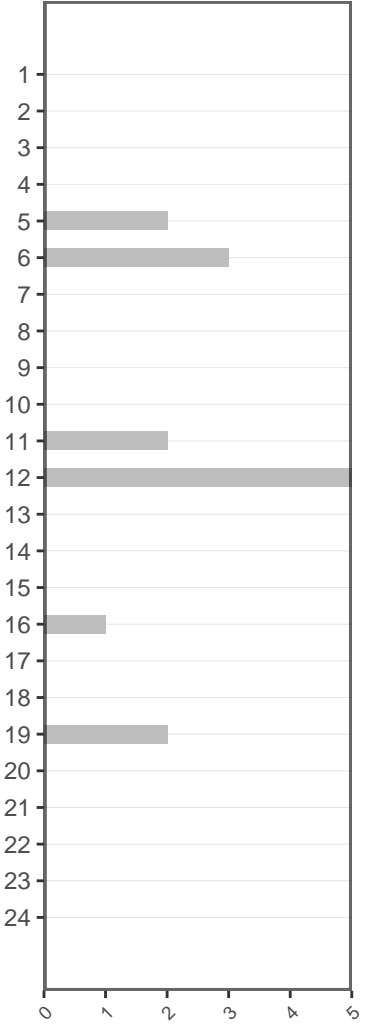
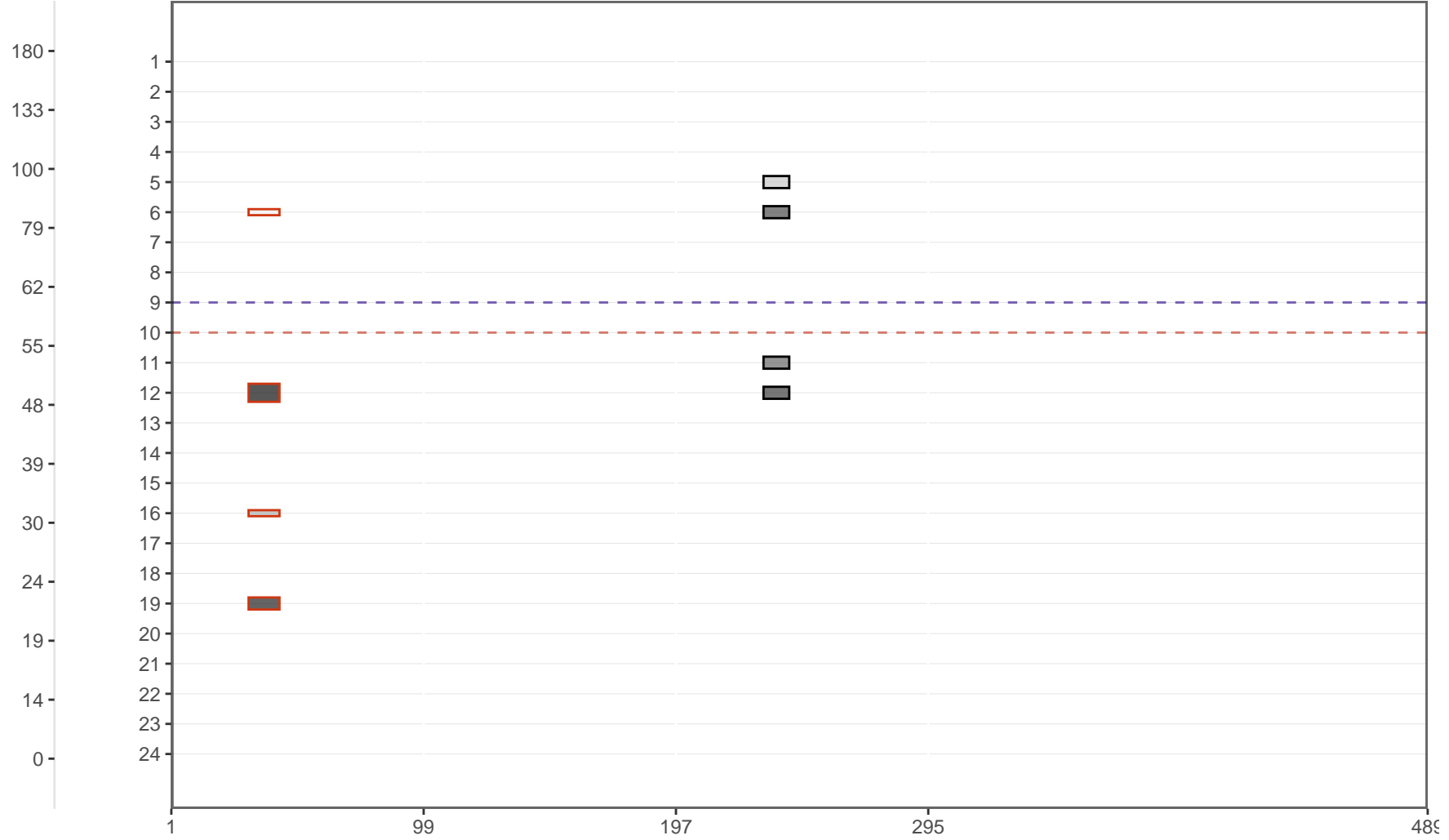
NFAIVFAMGVNMTAGDFKRFDEENGSMERVTFLNLANDPTIERIPRIALTAEYLVYEGGKHVLTDMSSYADALREVAAREEVPGRRGYFGVMTDLATYIERAGRIEGRITGSITQPIILTMPNDQTHPTPDLTGVTTEGGQYIDRQLNRRGYPPIVALPLSLRLMKGAIGEGMTRRHDSDVSNGLVANWAGIKDVGAMKAVVGEALSSDDLILYLEFLDKFERKFAVGGAYDTRNFQGLDLAWTLRIFPRELLHRIPAKTLDQVYRDASN

NbL11g14870.1 probable_26S_proteasome_non-ATPase_regulatory_subunit_3 [MW = 55.48 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF01399 PCI domain
- PF08375 Proteasome regulatory subunit C-terminal

Protein sequence:

IAHSNOQFSRYLYLKGKRTIQLEVDKESLLGAARKAPQAAVLFVQGNKVAIVRILLGEPERTVFMQKGMKALRPVYFELTNVIRIGDLELFRKVAEKFSSTFFSSDGTNLLVRLRHNVVIRTGLRNSISYRIGSLVDKAKKLRDLSFNPVADGESIVSKARDGADTLDHANGWMMVKETGDVSTNEPQAFNERRIAFLNMMHNEAVRALRFPFNSHKEKESAERKRERGGEGEELAKHAEEDDDDF

NbL11g14840.1 PIP2-7 [MW = 30.47 kDa]

No. of times detected



log(intensity)



Values from



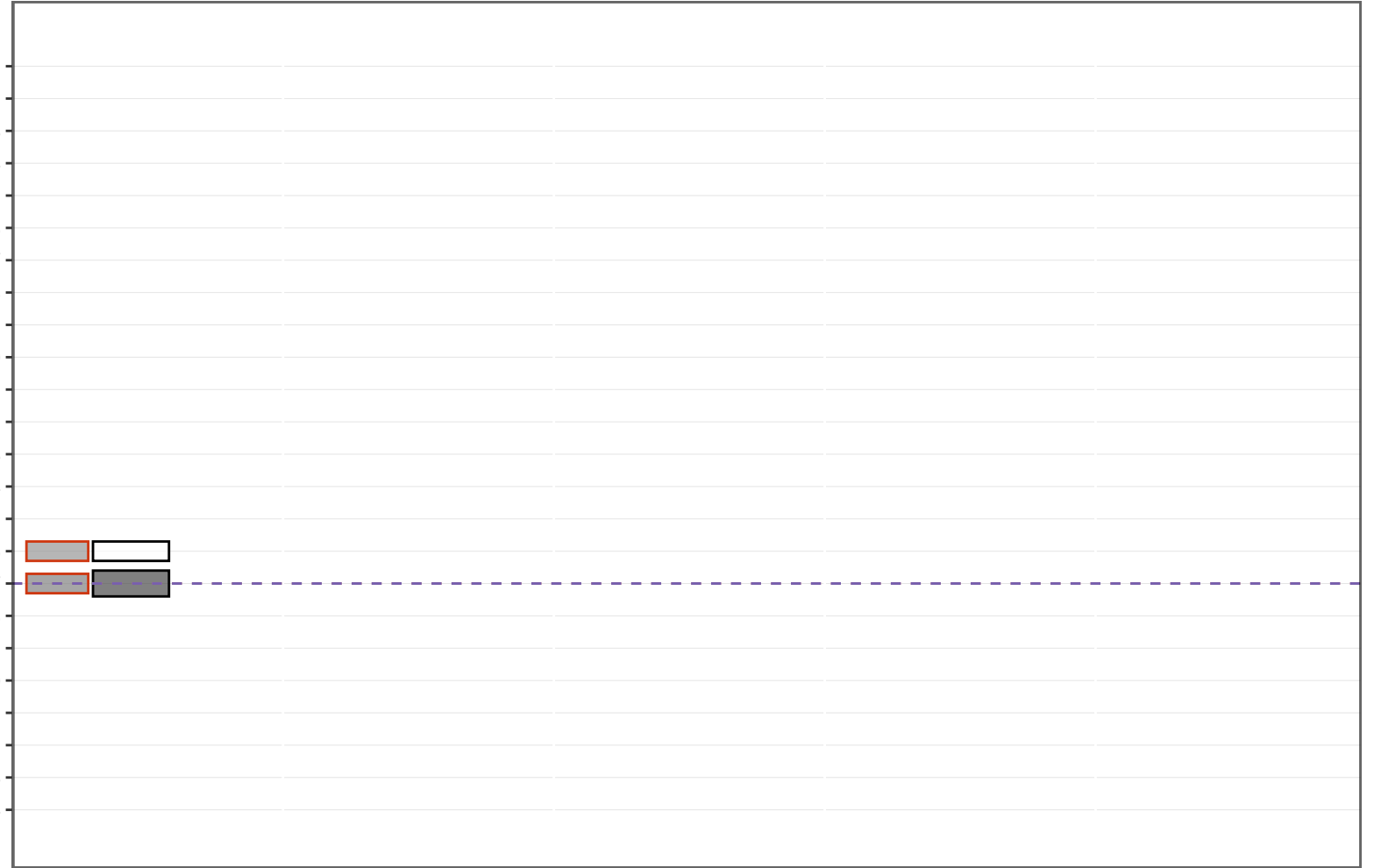
MW indication



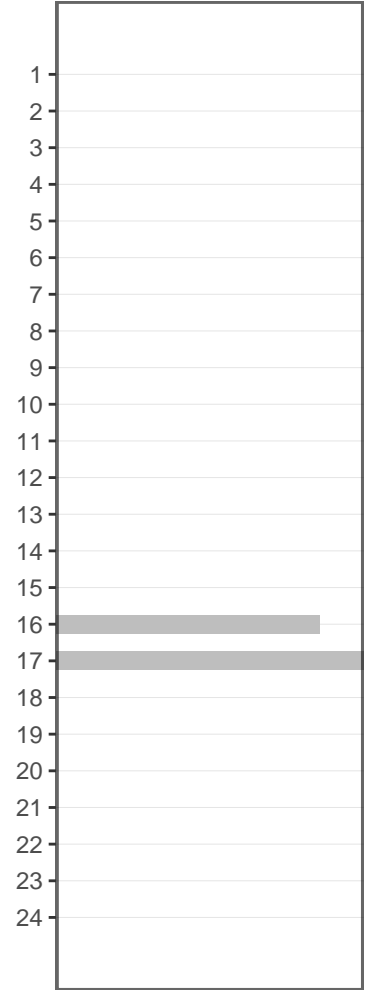
Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

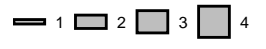


Protein sequence:

LGAIICGVLGKGFMRHYNTLGGGANFVQPCYKNGTALGAEIGTFVAVYVFSATDPKRSARDSHVPLAPLPIGFVFMVHLATPIPTGTGINFARFGGAIVVYNTDKVWDDGWFVWGFVGSALAAVYHQVLRGSAIKALGFRSNPTN

NbL11g14820.1 glycerate_dehydrogenase [MW = 42.31 kDa]

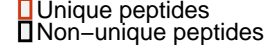
No. of times detected



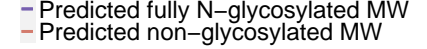
log(intensity)



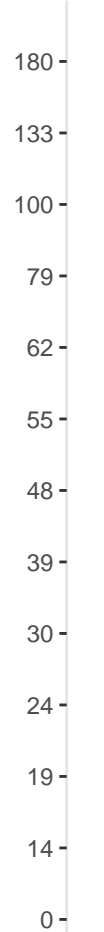
Values from



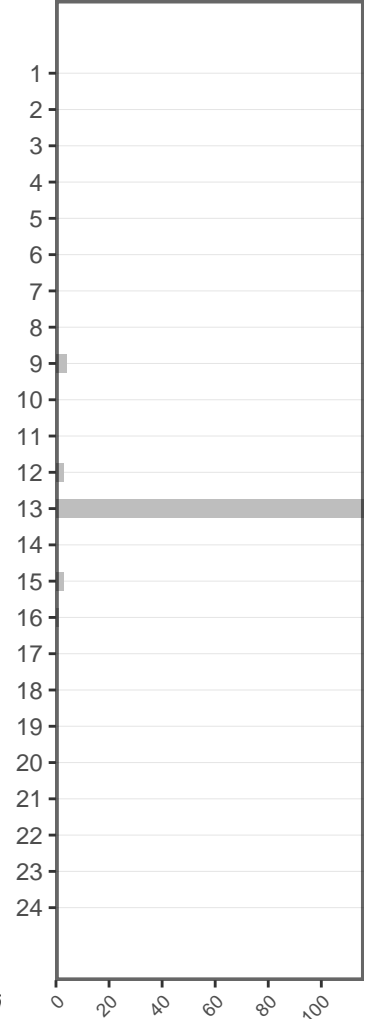
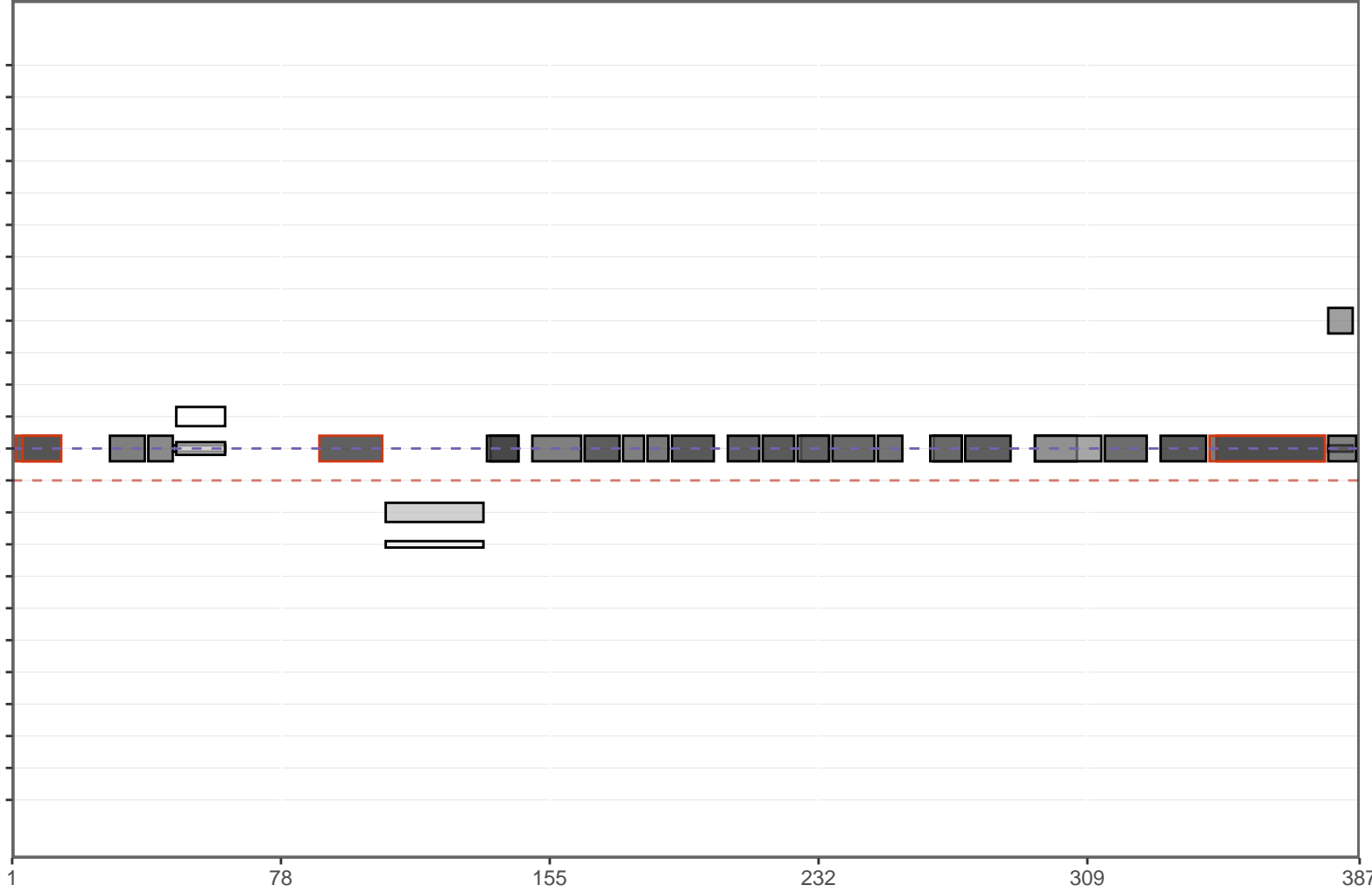
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF00389 D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain
- PF02826 D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain

Protein sequence:

ARMMEGFKMNLVYDLVQATRLEKFTVGGFLKASGEQPTVTKRAASMEEVLRADVSHLPILOKTTVHLVNERLAMMKKEALVNGSRGPIVDEVALVEHLRENPMFRVGLDFEDEPIYMKPGLADMKNVAVVPHIASASKWTREGMATLAAHLVGLKIKGYVWGNPNVSDAFLNENSGPPAAGPSVNSKTLGLPVSKL

NbL11g14690.1 L-ascorbate_peroxidase_3_peroxisomal [MW = 31.6 kDa]

No. of times detected



log(intensity)



Values from



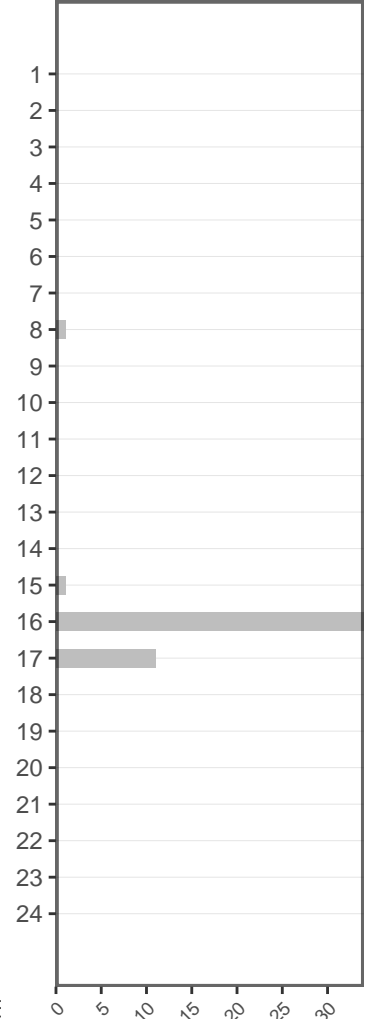
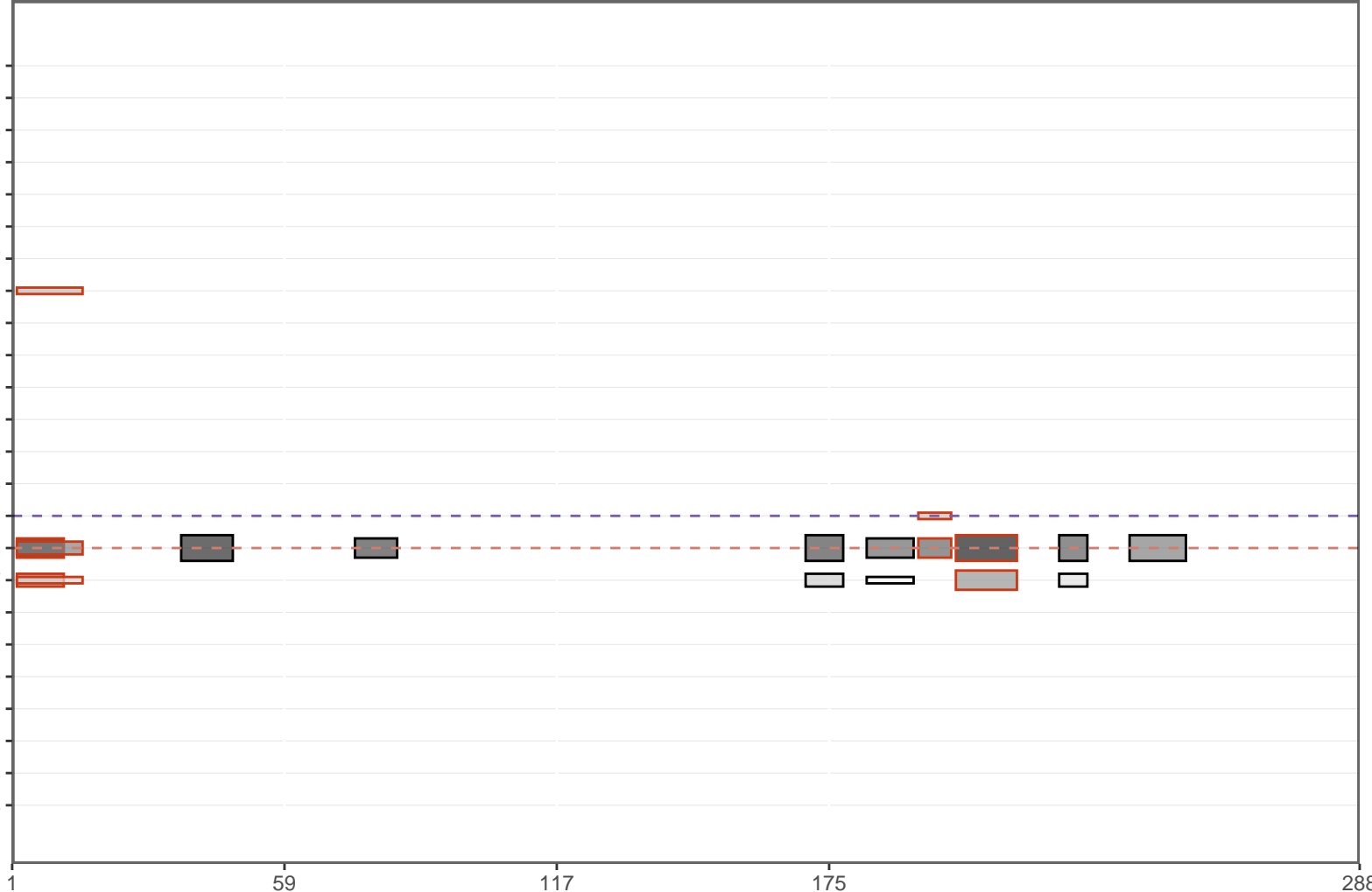
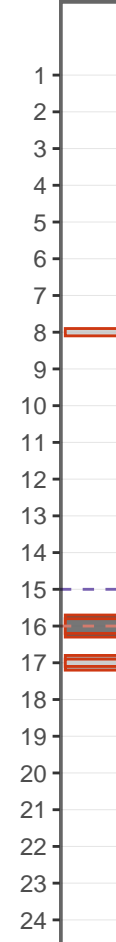
MW indication



Molecular weight

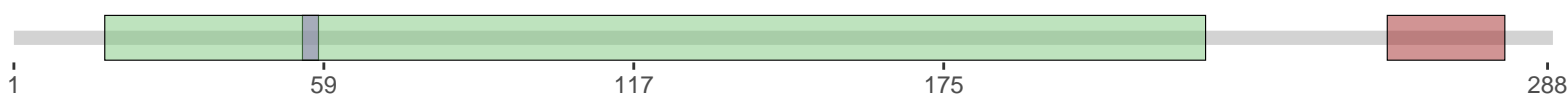


Gel Slice



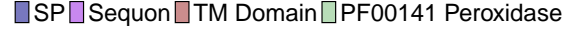
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

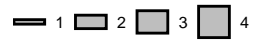


Protein sequence:

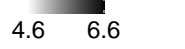
MAKQGVPHLKDVFYRMGLSDKDKDVALSGDHTLGRAHPDRSGFDGPPWTKPELKFQNSYFVELLKGETEGLLKLATDMLDDPEFREYVELVAKDEDAFFRDVAISHKLELSELGFTFSSGSKATLRDGTLAGSAVGVVAAVAALSLVWVEVRRKRMK

NbL11g14670.1 proteasome_subunit_alpha_type-7 [MW = 27.03 kDa]

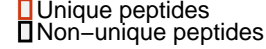
No. of times detected



log(intensity)



Values from



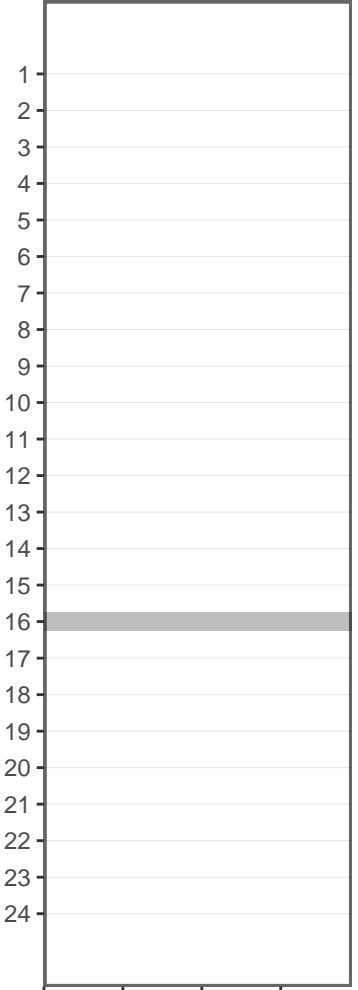
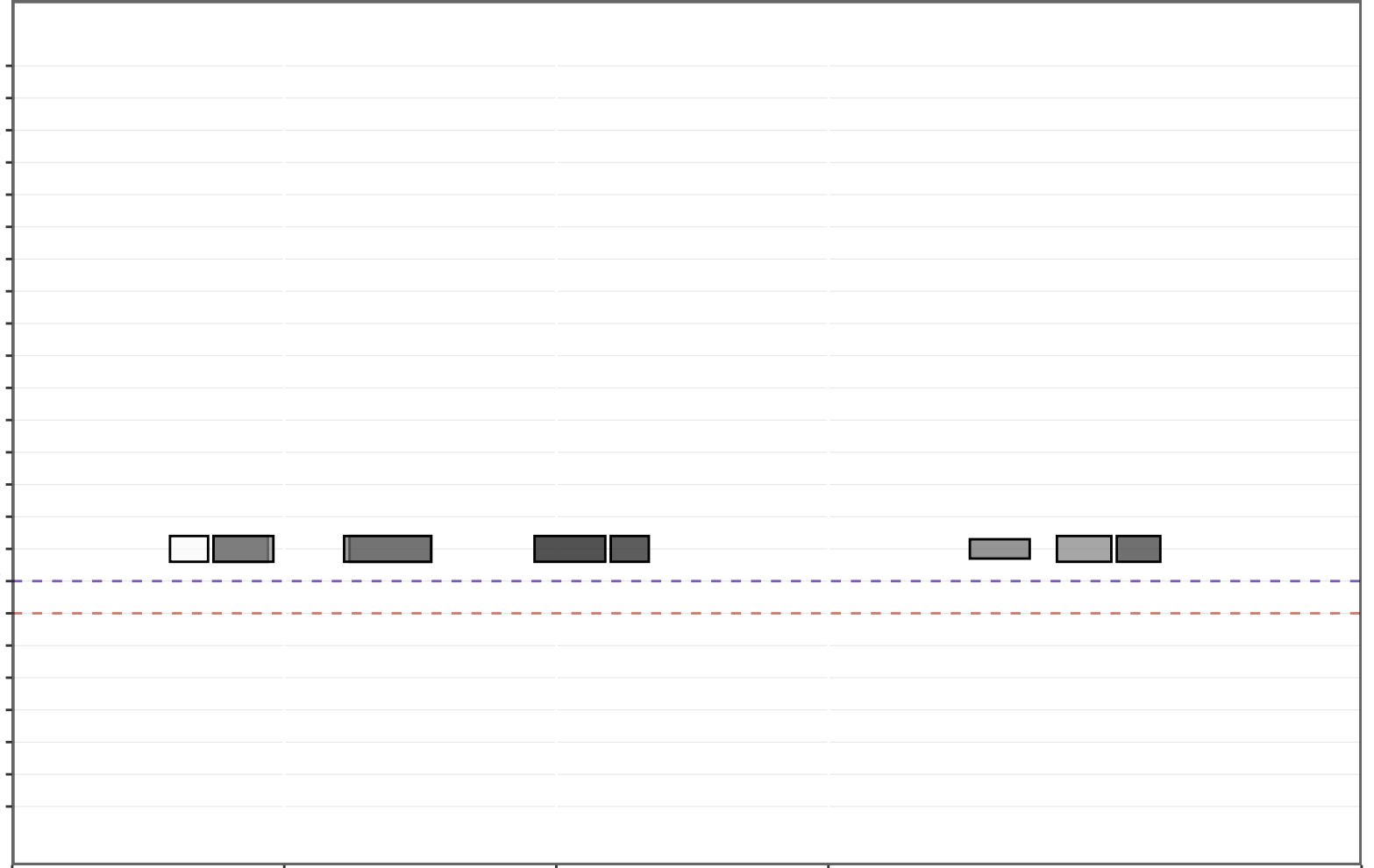
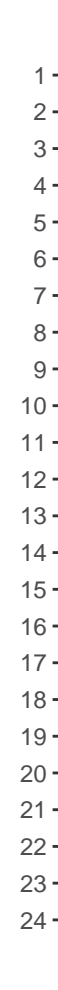
MW indication



Molecular weight

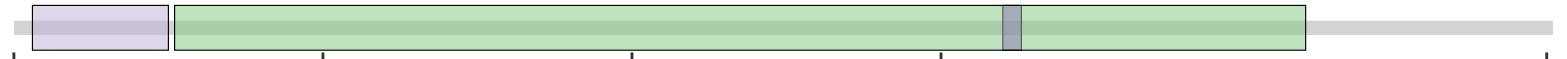


Gel Slice



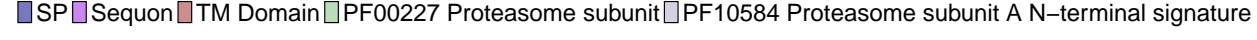
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

YIAGLOOKYTOSSGVRPFGLSTLHGFDPYTGVPALVOTDPSGTFSAWKANATGRNSNSLREFLEKNYKETSGGDETVKLARALLEVVEGGKNIEVWMTKEHSLKGLLEAEIDVAIEIEKAKAAEAANKAKPET

NbL11g14620.1 subtilisin-like_protease_SBT1.6 [MW - SP = 78.88 kDa]

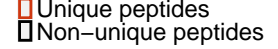
No. of times detected



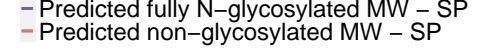
log(intensity)



Values from



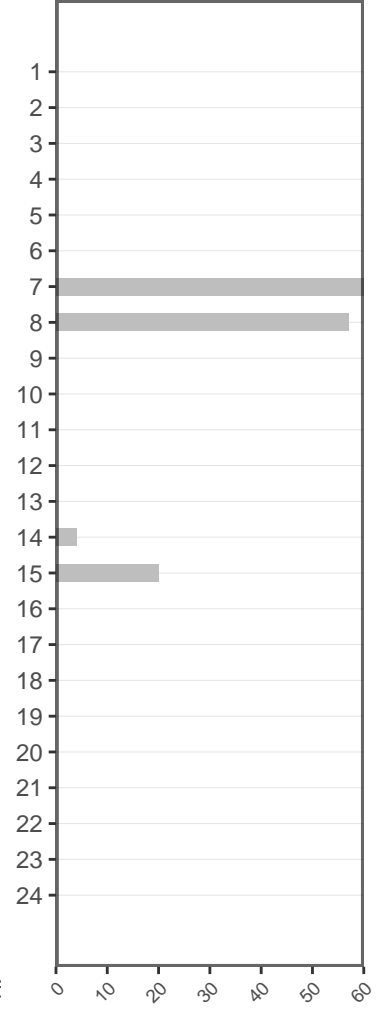
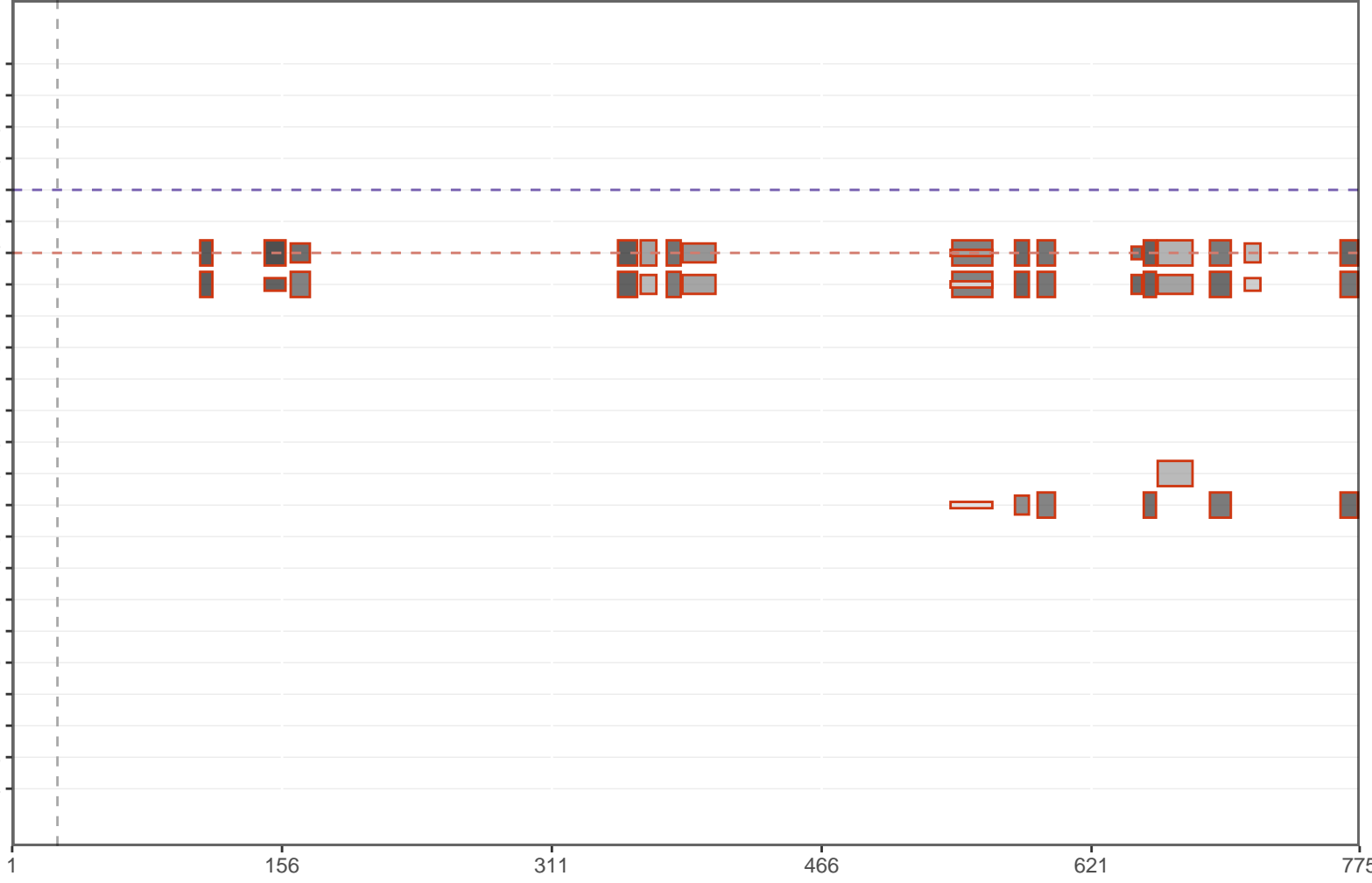
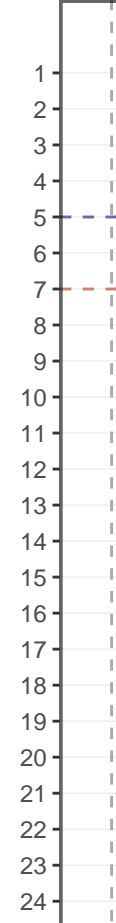
MW indication



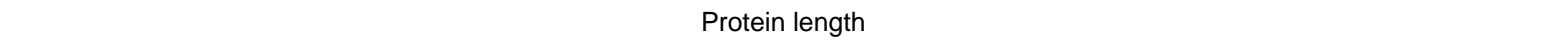
Molecular weight



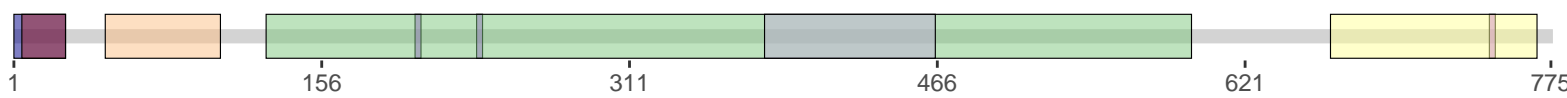
Gel Slice



Protein length

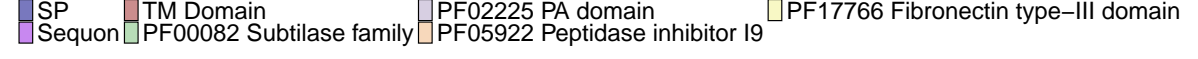


Peptide counts over 4 repeats



Pfam domains

Pfam Description

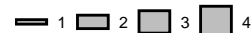


Protein sequence:

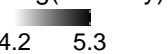
GKMYPVYYPGKSGVLSASLGMENSLDPHLVIRGKIVGDRGSRNPRVAKGMVYKAGVGMILANGVSNGEGLVGDHALIPTCAVGANEGDAKSYASHPTASATINFHGTIVGVKRPVVAASFSGRGPNGLNPEILKPKDIAIPGVNLAAWTDVAVGPTGLDLDLNRKAENLISGTSMAQPHVSGAAALKSAHSQVSPAIRSAMMTTANRVDNRLGPMTEATGKPRTPYDVGAGHNLDLALDPLGLVYDLANEDVYVFLGCAIEYDPKTIQVITKSPVDGPMKQKPLPENLYPSE

NbL11g14550.1 protein_2_(GRP-2)_mRNA_X60007.1_N.sylvestris_mRNA_for_glycine_rich_protein_2 [MW = 19.45 kDa]

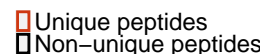
No. of times detected



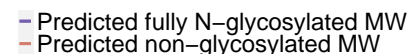
log(intensity)



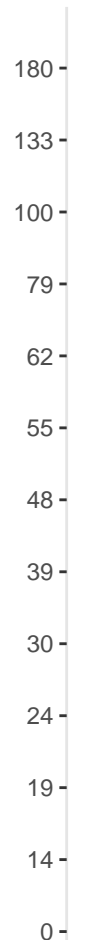
Values from



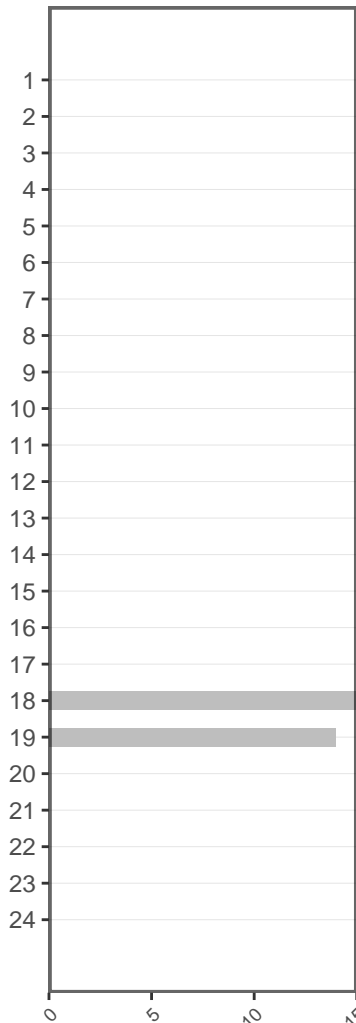
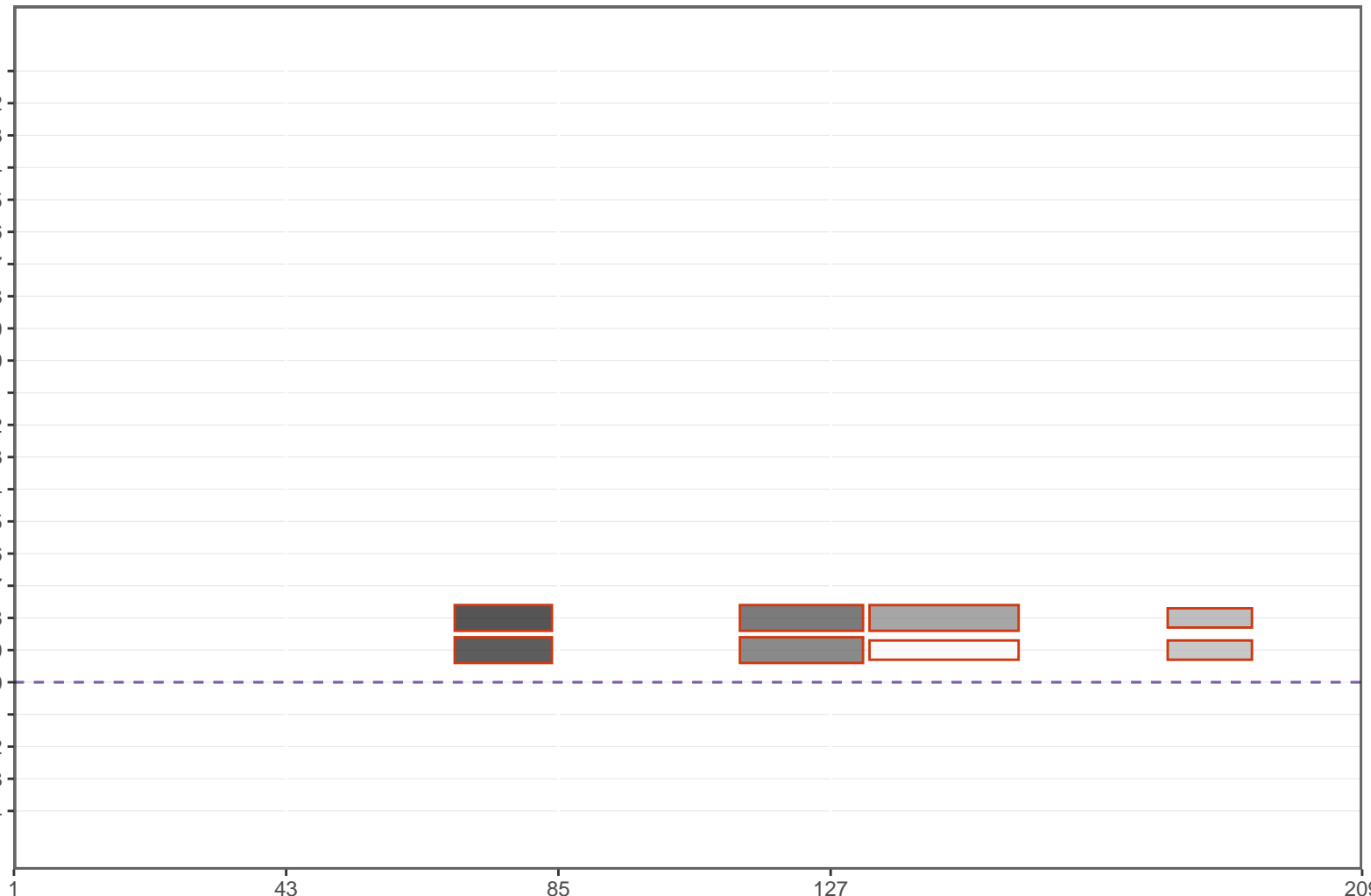
MW indication



Molecular weight

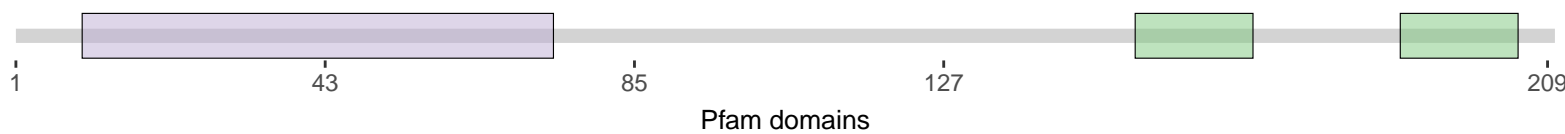


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

YGGGGGGYGGSGRGGRYSGDDGYSGGGGYGGSRVGGGGGGYGGGGGGGGGGGGSFGKGGEGHFAKDCGSGGGGGGRFSGGGGGGGGGGKCGEDGHFARECTSGR

NbL11g14520.1 PI-PLC_X-box_domain-containing_protein_DDB_G0293730-like [MW = 36.84 kDa]

No. of times detected



log(intensity)



Values from



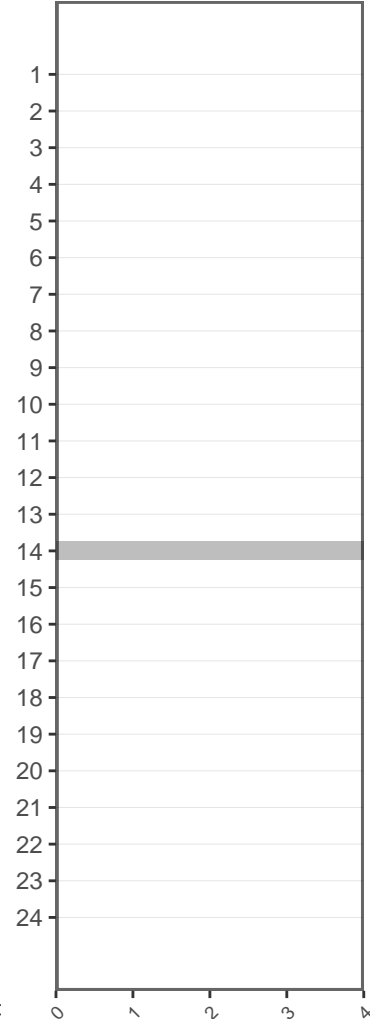
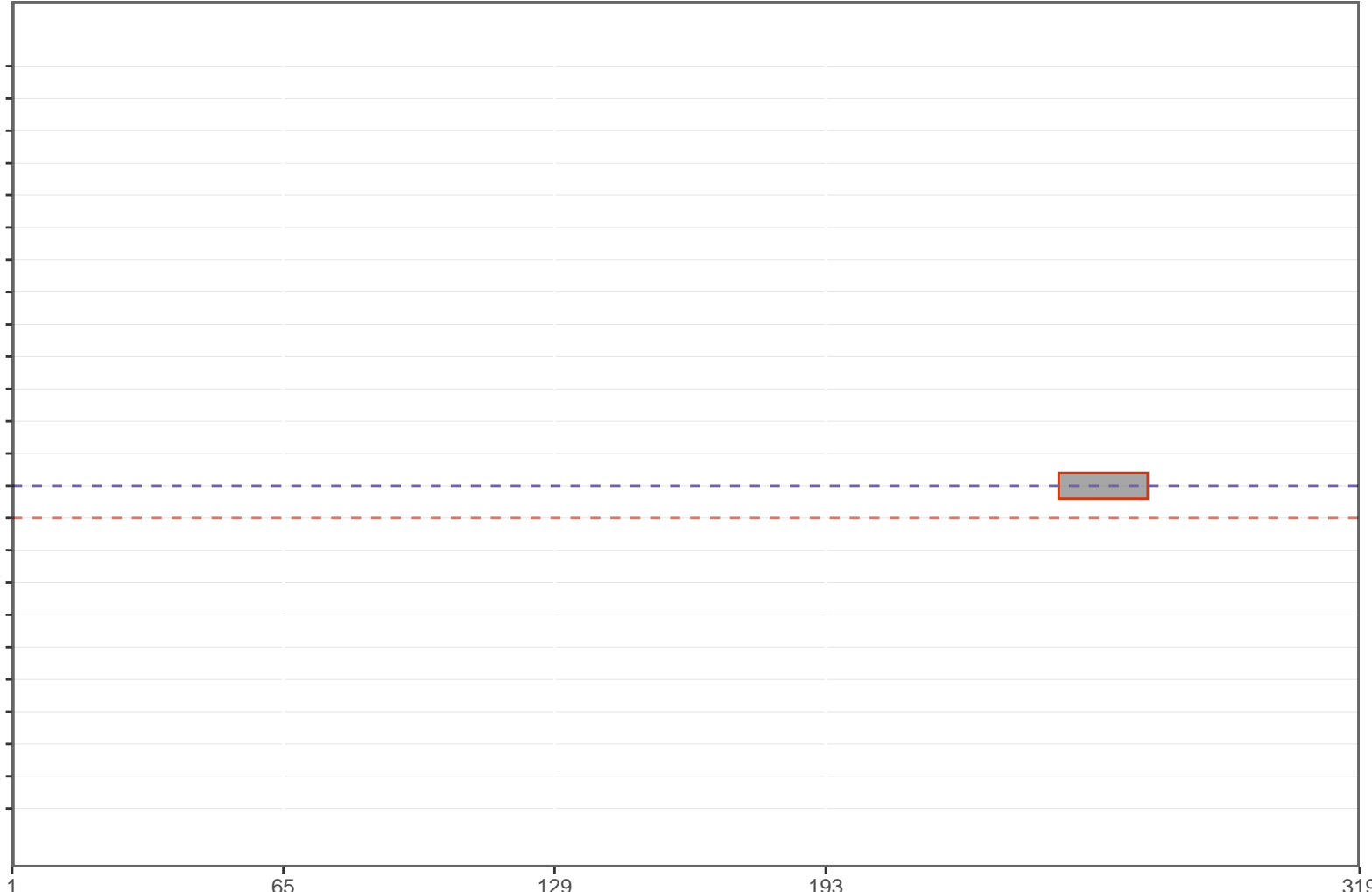
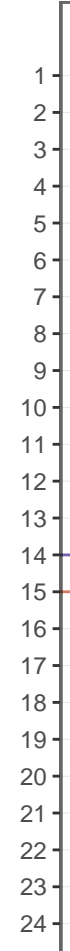
MW indication



Molecular weight



Gel Slice

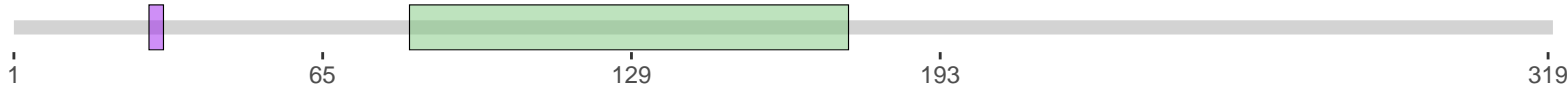


Peptide counts over 4 repeats

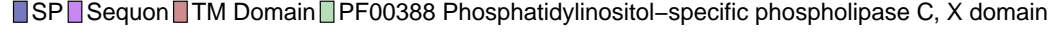
Protein length



Pfam domains



Pfam Description



Protein sequence:

GHEIDPEFDKYLELQDLGEYLHGDDSEVFKHTVAELLPKRIVGVWPKRKSQPKHGSLWSAGYLKDNWIDTLPETKFGSNMKHLEGGPVTSRKYFYRVENTVTPQADNPVGVKPVTRRHPVRLFTFESISRGVGDRLGYSDFDFEDFVDAQVGLTNARIEKVV

NbL11g14480.1 probable_amidase_At4g34880 [MW = 53.92 kDa]

No. of times detected



log(intensity)



Values from



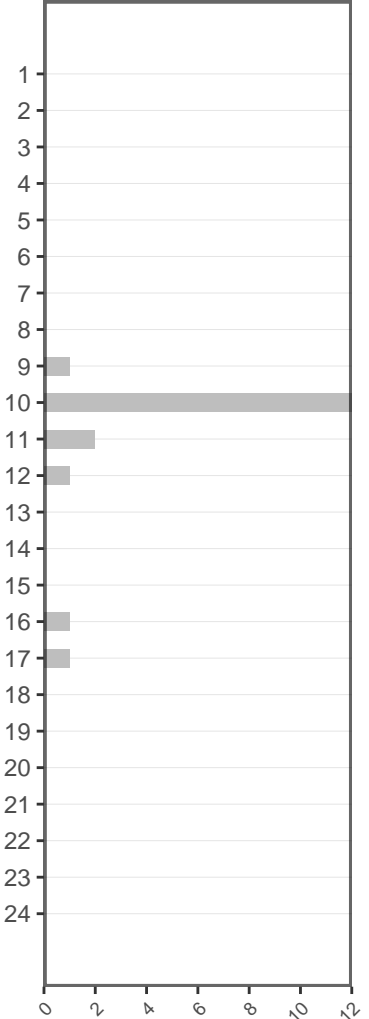
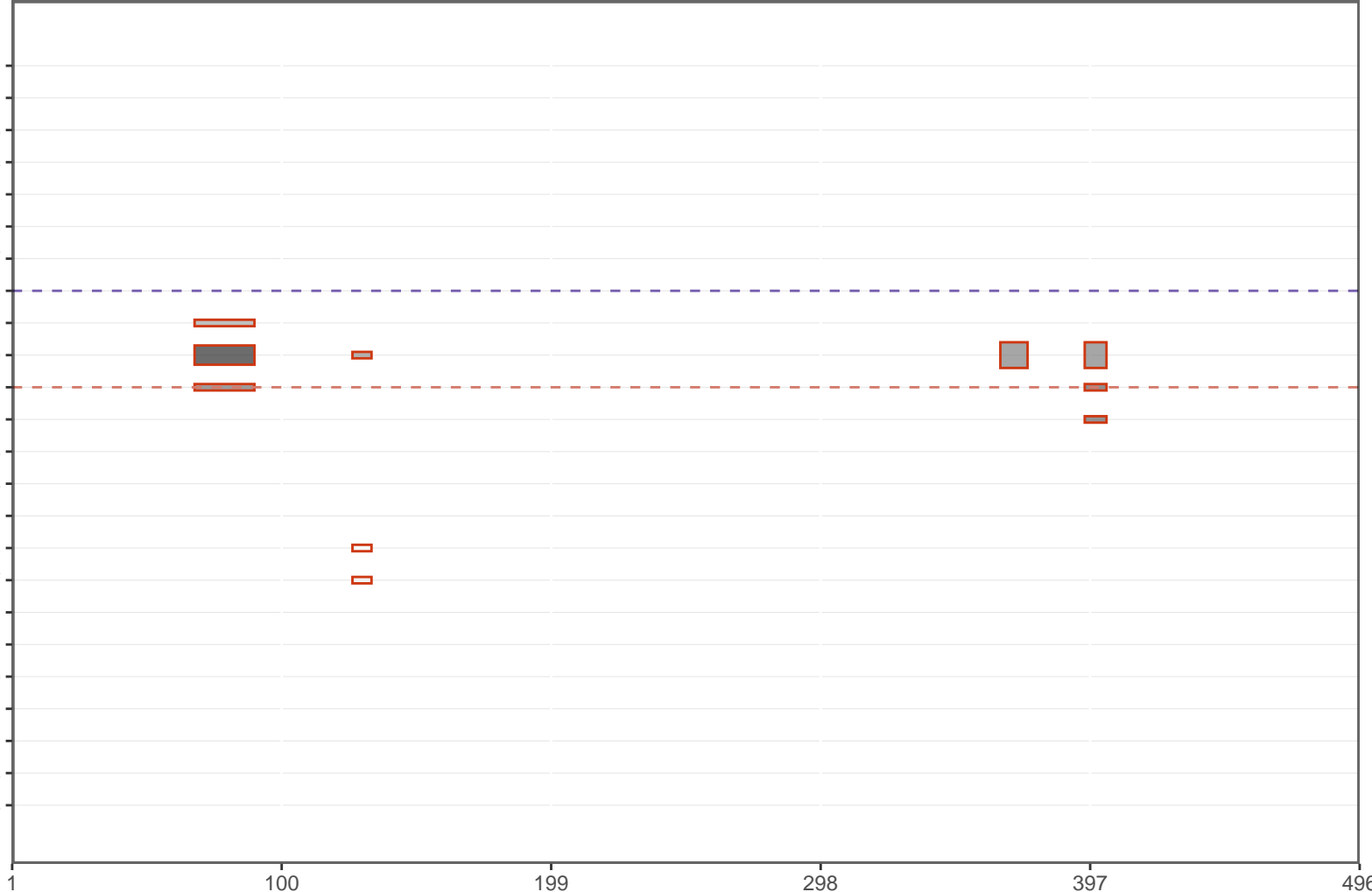
MW indication



Molecular weight

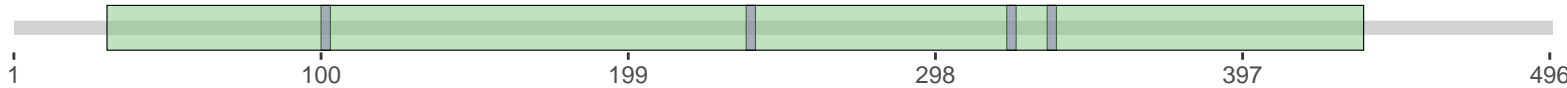


Gel Slice



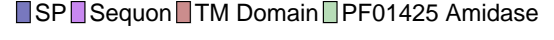
Protein length

Peptide counts over 4 repeats



Pfam domains

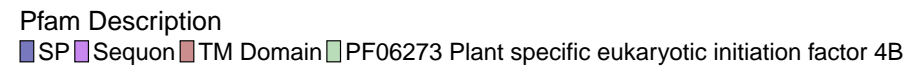
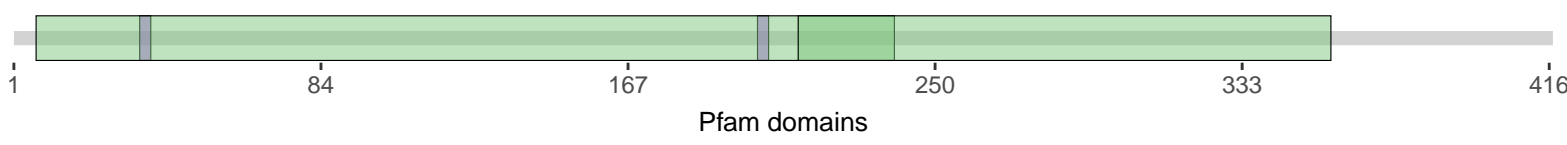
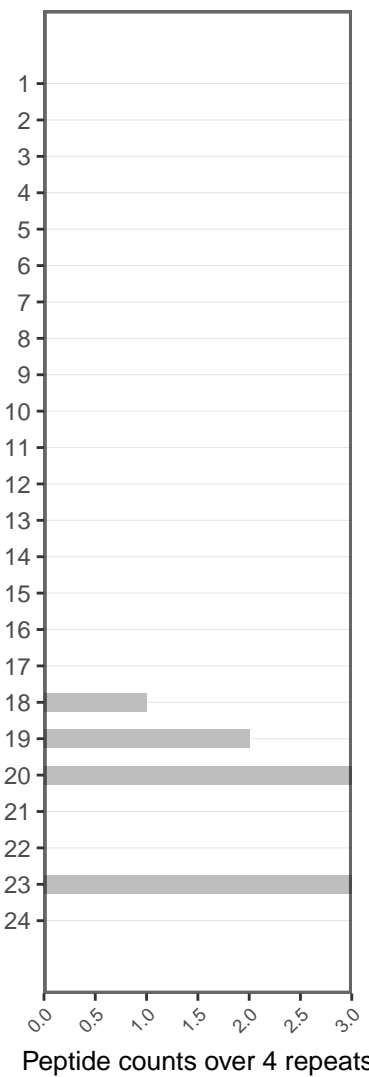
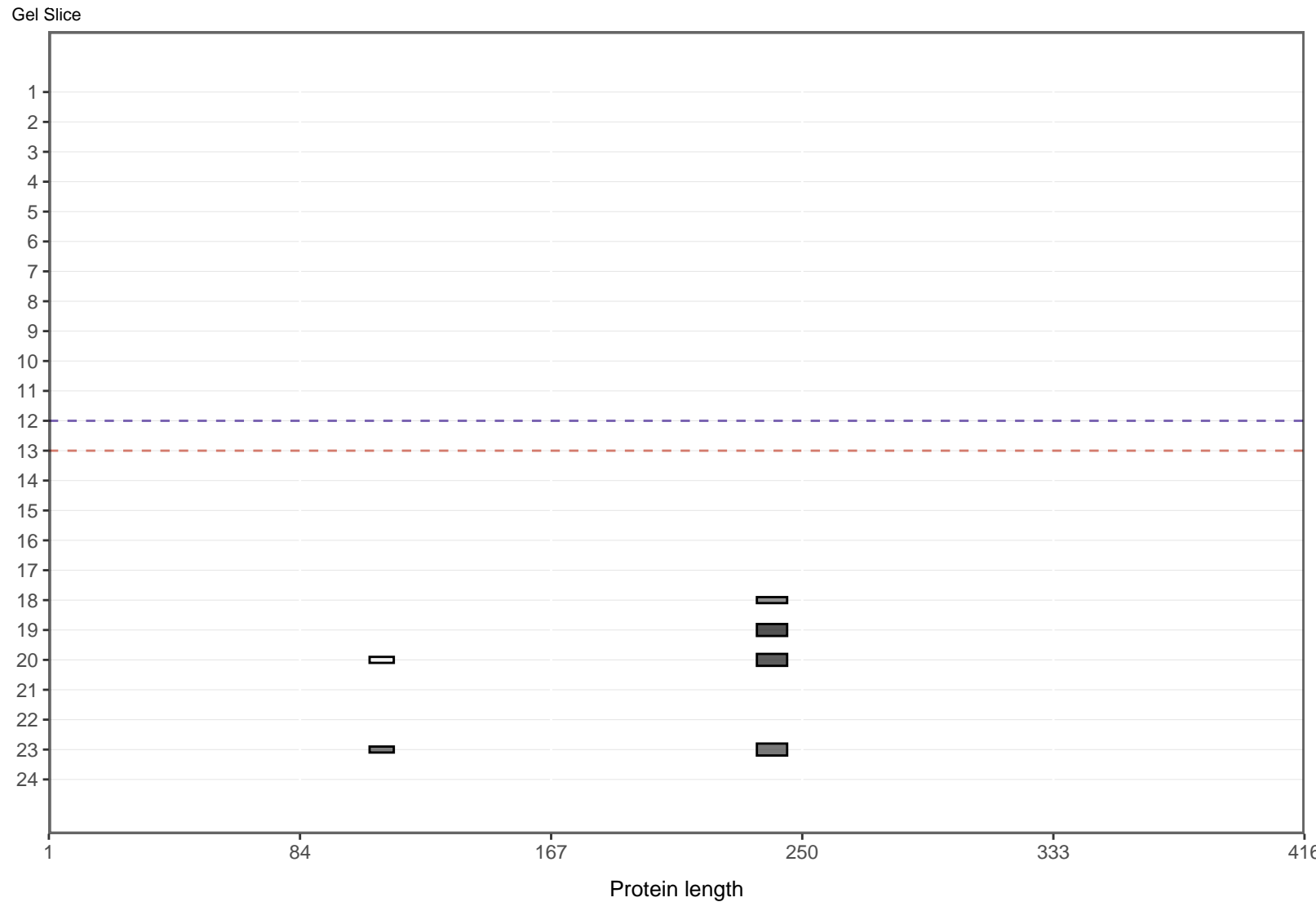
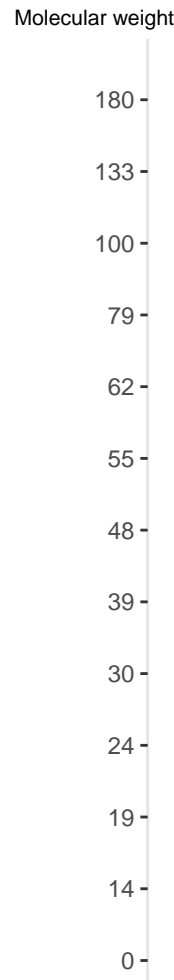
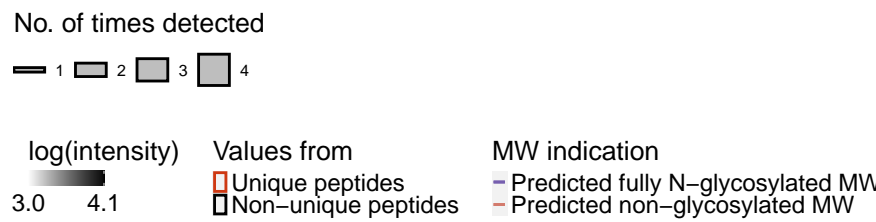
Pfam Description



Protein sequence:

ICRNVTDAVYMLDVIIVGVDPDEVTREAAKVIPEGGYKGLFREDLKGKGGIVRHPFVEMHGEIEKSAFHHLDLLRGGATLVNLSIPHIEEIMDPNHSGEALVMMVEKTAIVYVYKELTSPVRSGLADIAFNEIERNSELEKLTVEVDQHTFAAEKTDGVLGEEKVIEKLFHSRNGFEKMMKHHELDAMVTPGSRASPVFAIGGYPAITVWGVGESDGMFPGIGFGLKGTPEKLEIAVAFEGSSKVRPPPEW

NbL11g14460.1 eukaryotic_translation_initiation_factor_4B3 [MW = 44.75 kDa]



Protein sequence:

NIVGANKSFVPSGRFRDRGFGSGNGDSDSDKWKTRKGGGGAFDGLRERRGGGVEYSYNSGVDSSENWGRGKREELGGGGGGRPKLNLQPRFLPTEVGGNGGTTNEATVYVFKGSGNPFDAARRPREEVLEKKGDDWKEIDKLESLKVEVVSSESDKKAWGNKPFPMREEESTEKSWRKPQLNEVRLPLSAEVTVNGAVEETAQGAAKESGGSEPK

NbL11g14440.1 peptidyl-prolyl_cis-trans_isomerase-like [MW = 18.04 kDa]

No. of times detected



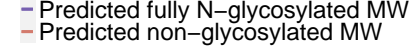
log(intensity)



Values from



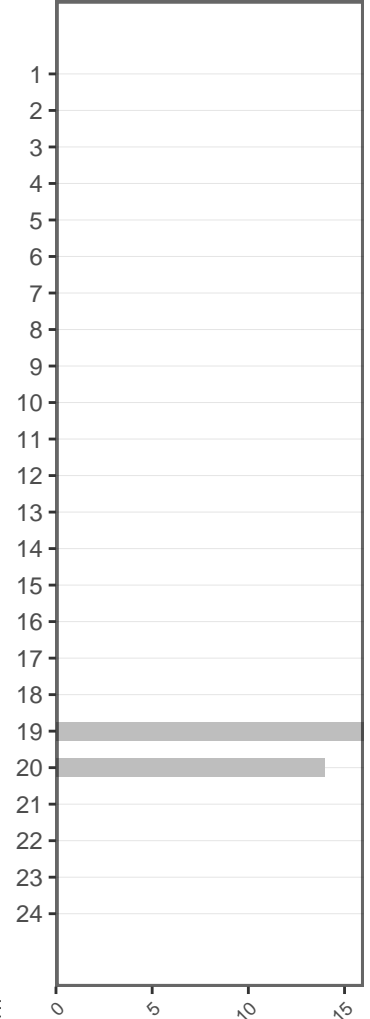
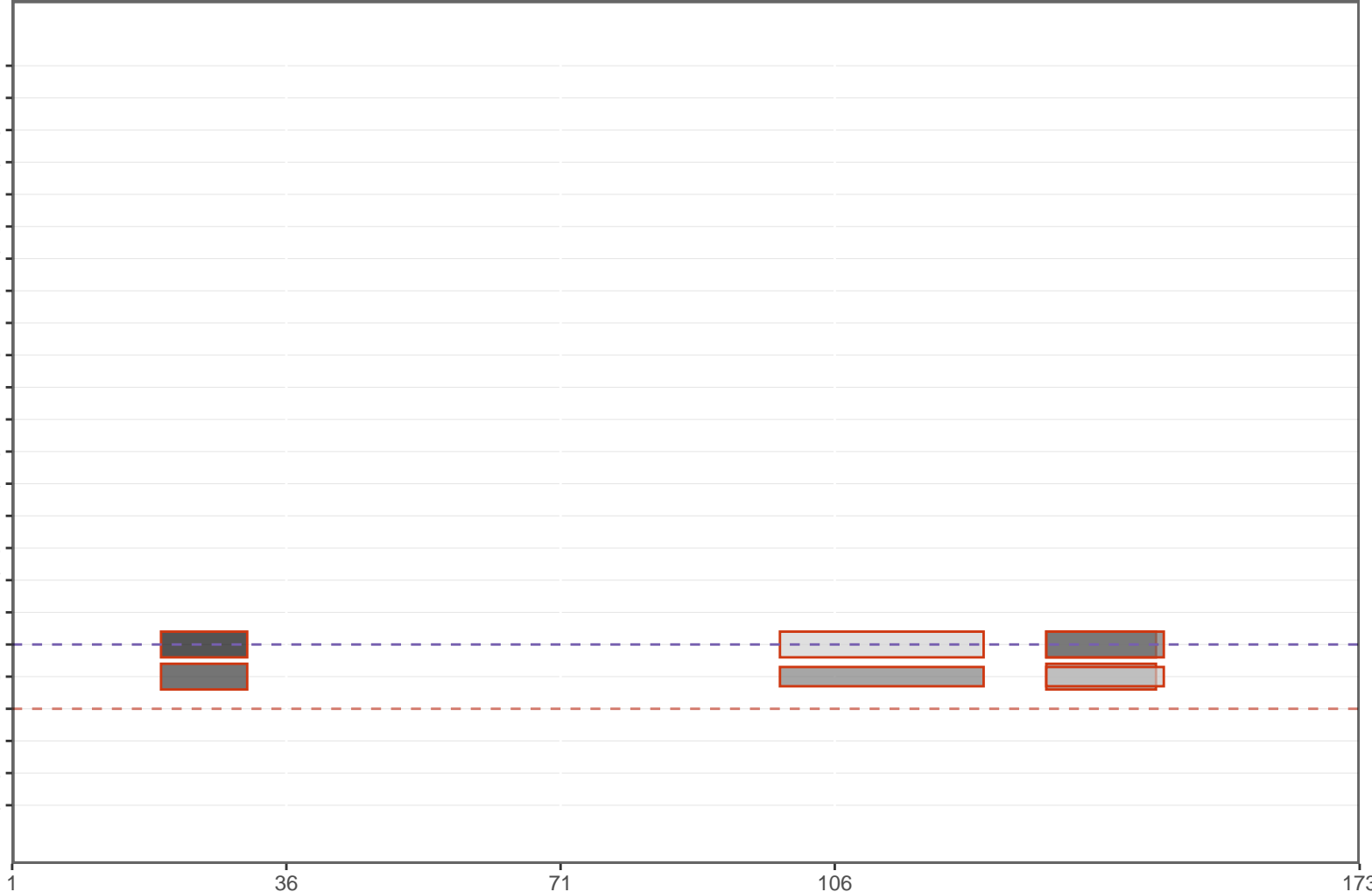
MW indication



Molecular weight

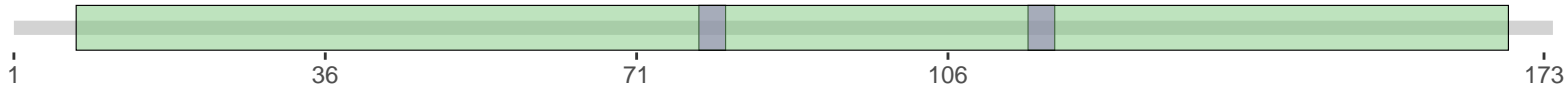


Gel Slice



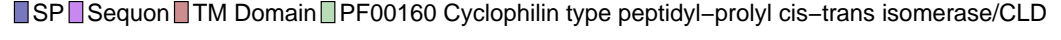
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FTAGNGTGGESISYGAKFADENFKRKHGTGPGVLSMANAGPQTNSGQFFICTAKTEWLDGKHVAFGGVVEGYDAIKKAQAVGSGGRGSKPVVADGGQLQ

NbL11g14390.1 triosephosphate_isomerase_chloroplastic-like [MW = 34.81 kDa]

No. of times detected



log(intensity)



Values from



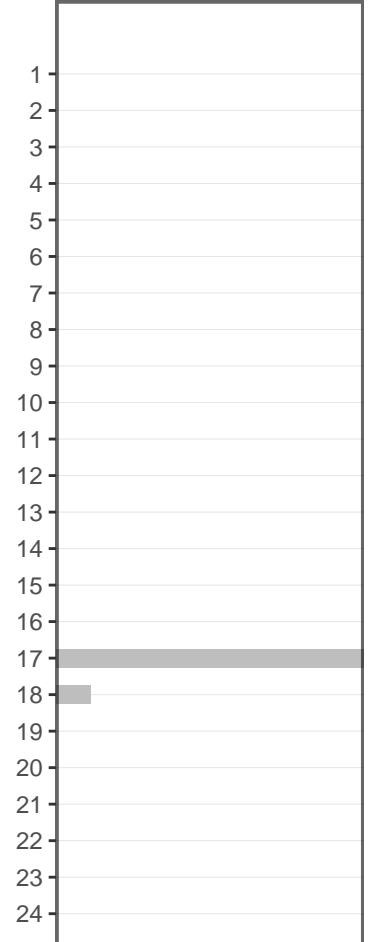
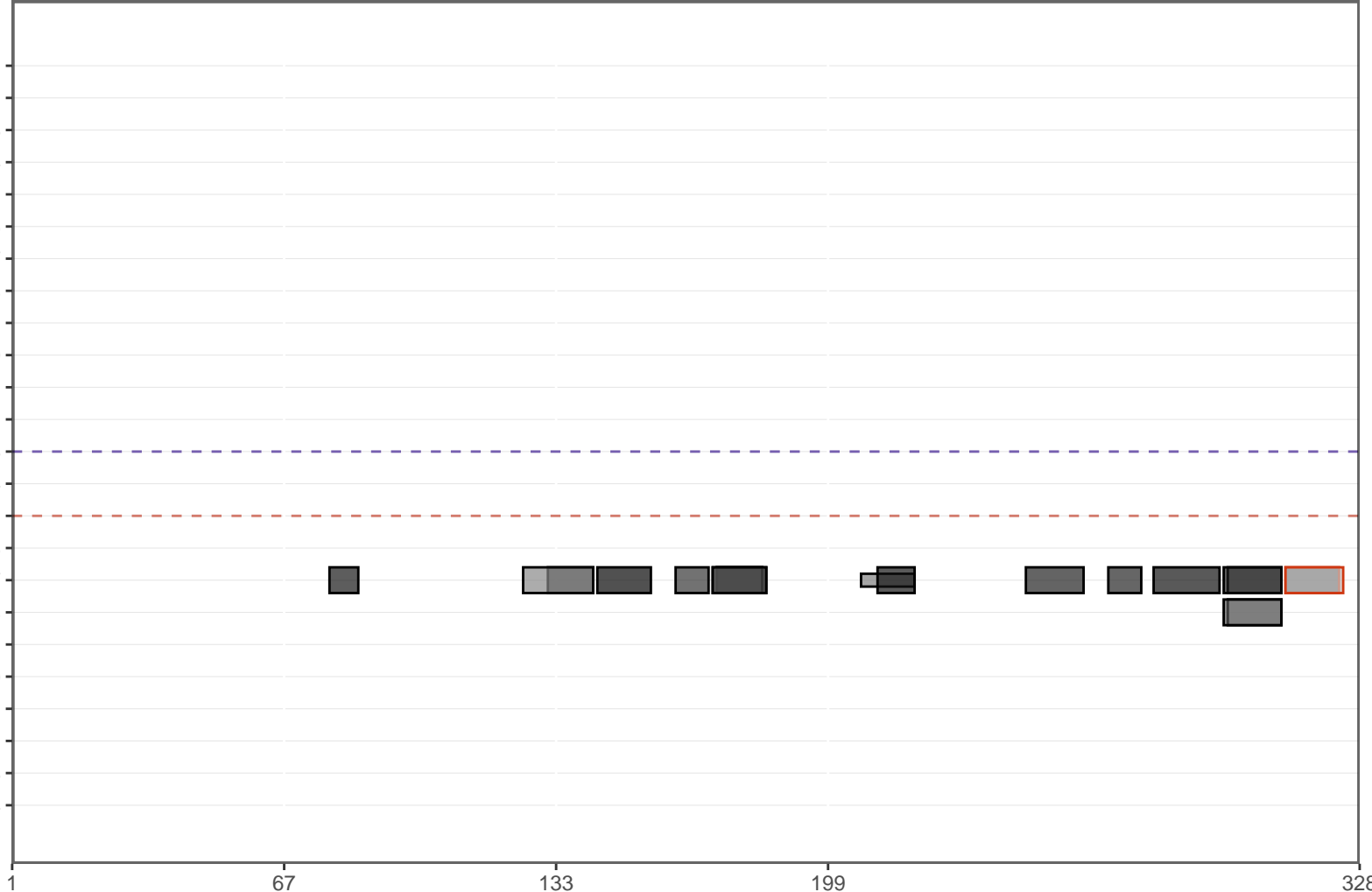
MW indication



Molecular weight

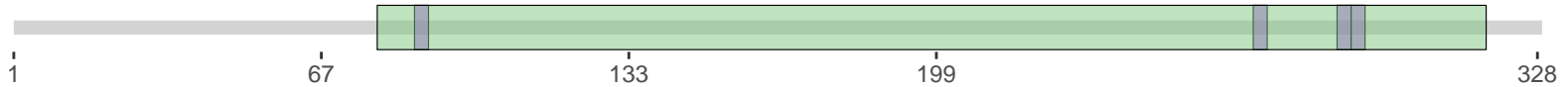


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam Description



Protein sequence:

EISVEQLKDLGCKWVILGHSEERRHVGGENDEFRIKKAAYALSGQGVGVIAIGELLQEREAGKTFDQVFGQLKAFADALPSWDNVAIYVEPVAWIGTGKVASPEQAGEVHAAVRDILTKVNSAEVASKTRIRHYGGSEVNGSNSSDLAKKEDIDGFLVGGASLKGPEFATIRIVSTKRWAA

NbL11g14370.1 5'-methylthioadenosine/S-adenosylhomocysteine_nucleosidase_2 [MW = 27.95 kDa]

No. of times detected



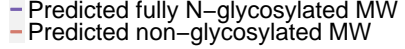
log(intensity)



Values from



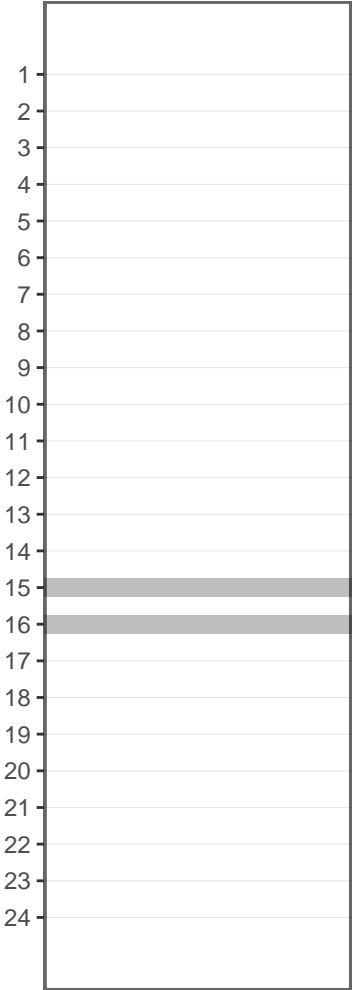
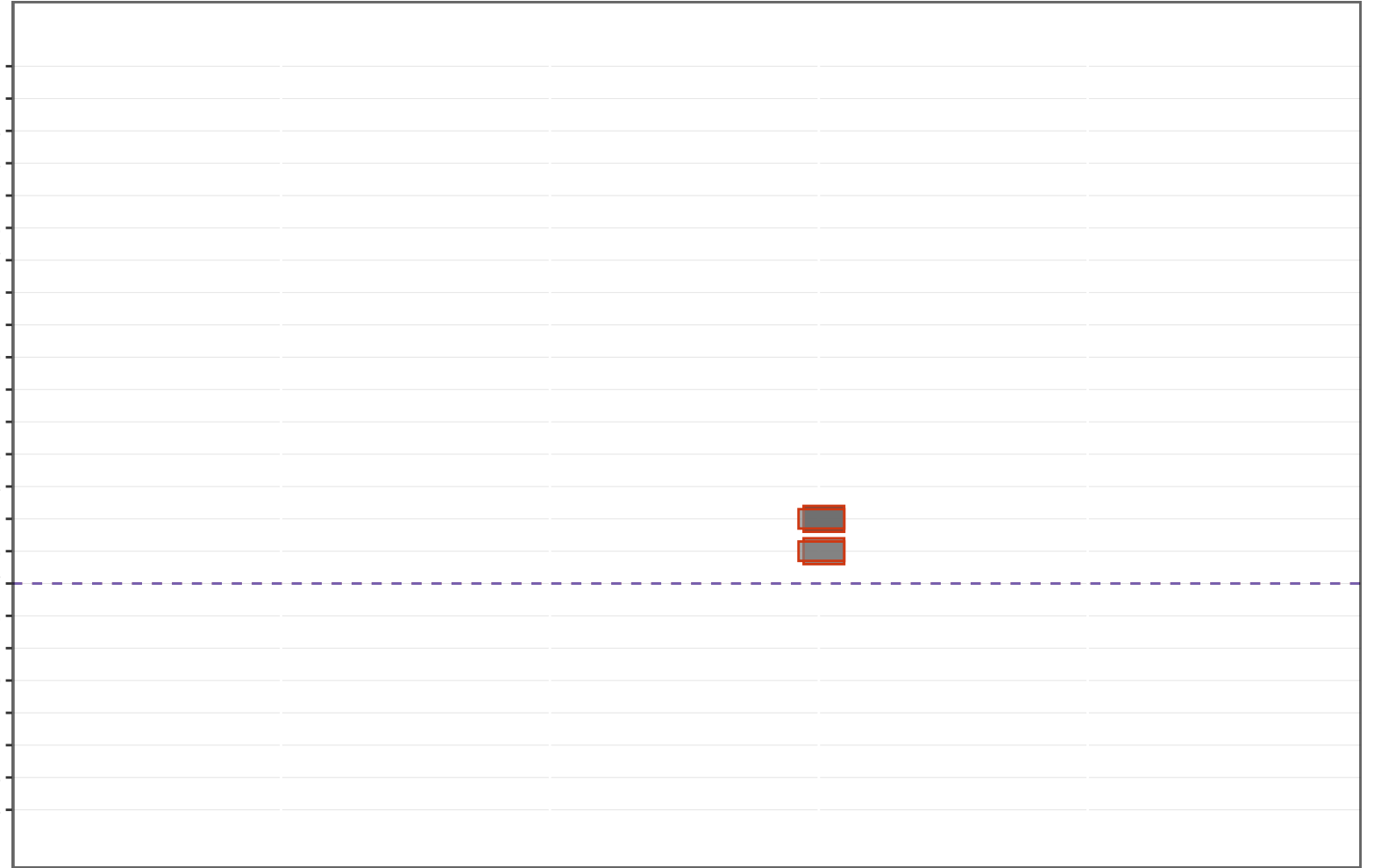
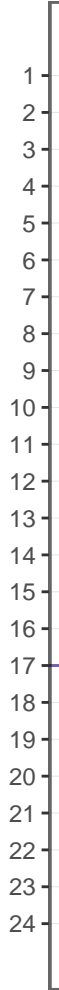
MW indication



Molecular weight



Gel Slice

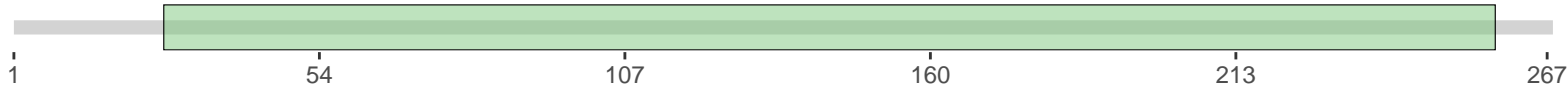


Protein length

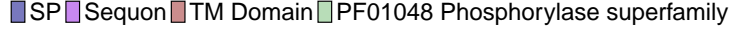


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

GAKGASIGDVFLLSEVAFHRRRPIPVFDYGVGRKAFATPYLLKELNLIKIGLSTGDLDMSPMDEASIVANDATVKDMEGAAVVYADLLKVPVIFLKAATDVIDGDKPTAEFFLLNLAAVTALDGTATLVVDCIGKGLSELV

NbL11g14320.1 uncharacterized_LOC104087214 [MW = 39.48 kDa]

No. of times detected



log(intensity)



Values from



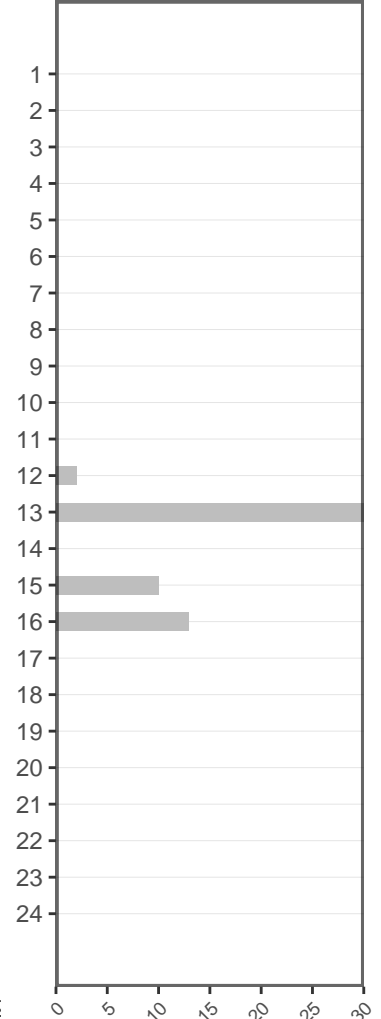
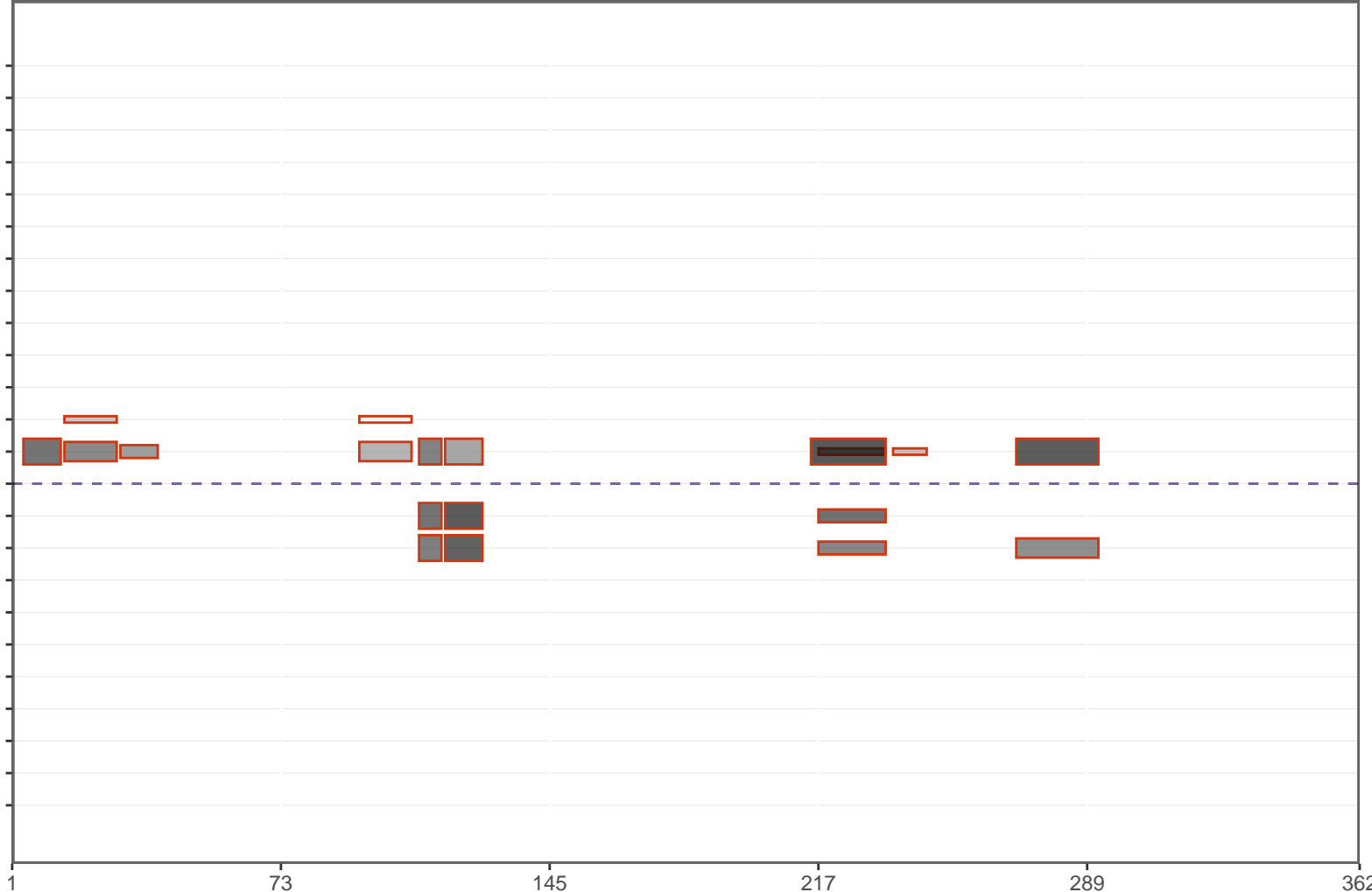
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

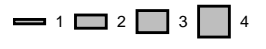


Protein sequence:

SDSWSMSNYYEPVADSDGASNEGQVSGETFLAEFKKVAESAAGRLEKQPVVAHSENTFDGSGRRLLSNKFELEKALDGAVKTVFKDRHGHMSKEYLRVALLDLAPAGLPPGAVDQMDKRIEACKMLDADDGKMKKEEFKLLTEVLGGMMLGLEGNPVSVSTNSVYVHEPLASASTLLOPPENSEM

NbL11g14290.1 26S_protease_regulatory_subunit_S10B_homolog_B [MW = 44.6 kDa]

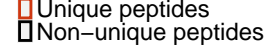
No. of times detected



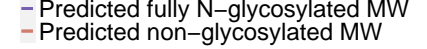
log(intensity)



Values from



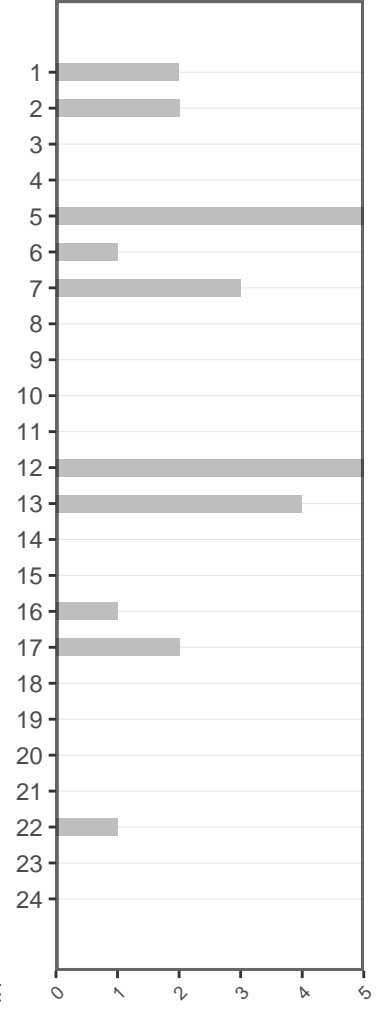
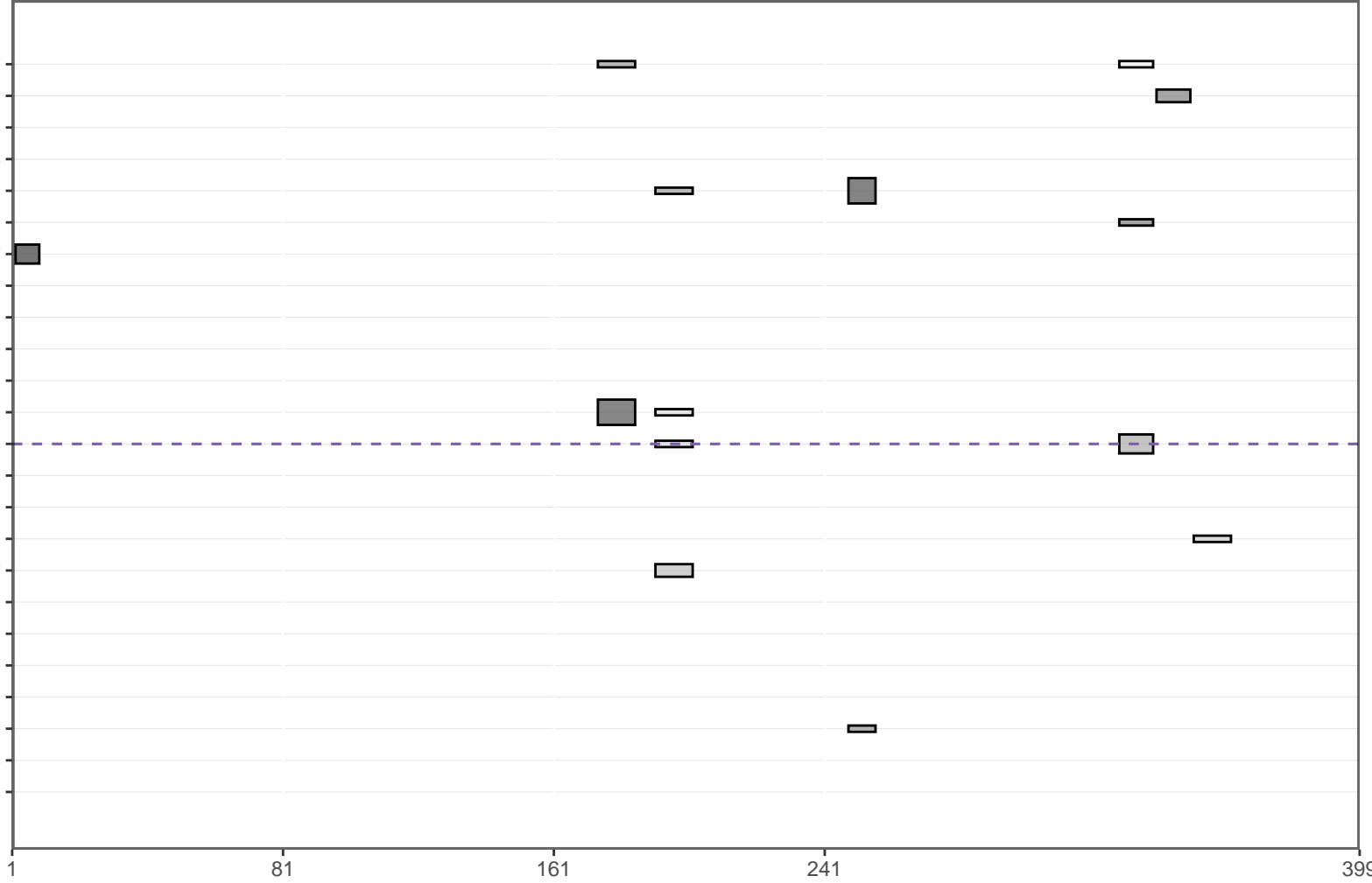
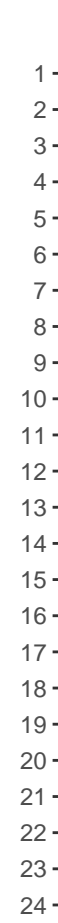
MW indication



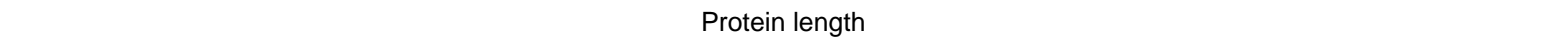
Molecular weight



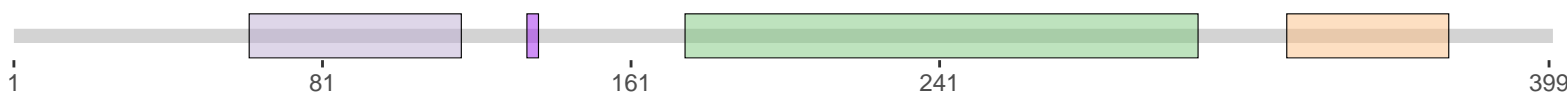
Gel Slice



Protein length

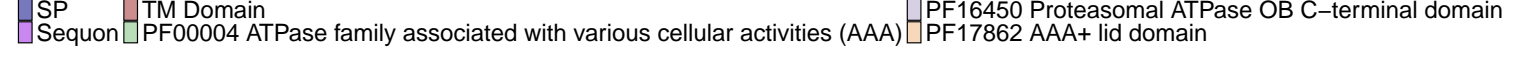


Peptide counts over 4 repeats



Pfam domains

Pfam Description

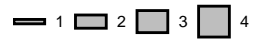


Protein sequence:

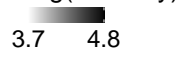
CTLLARAAASNDANFLKVVSSAIDKYGESARLIREMPFNWARIHQGPCHFMDEIDAIAGRRFSEGTSDREIQRITLMELLNQLDGFDDGLGKVKMMATNRPKVLDPALLRPGRLDRKIEIPLFNEGSRMEVLKIKHAGIAKHGEGIEAVVXLAEGFNAGDLRNVCTEAGMSAIRAERDVIHEDFMKAVRKLNDAKKLESSAHYSADFQKEL

NbL11g14220.1 receptor_protein_kinase_TMK1-like [MW - SP = 98.86 kDa]

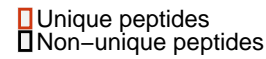
No. of times detected



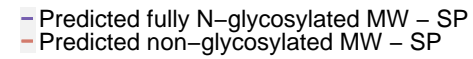
log(intensity)



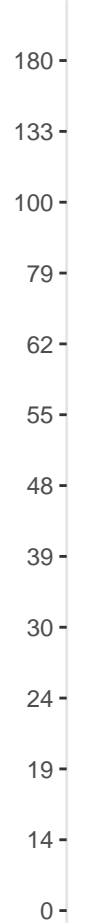
Values from



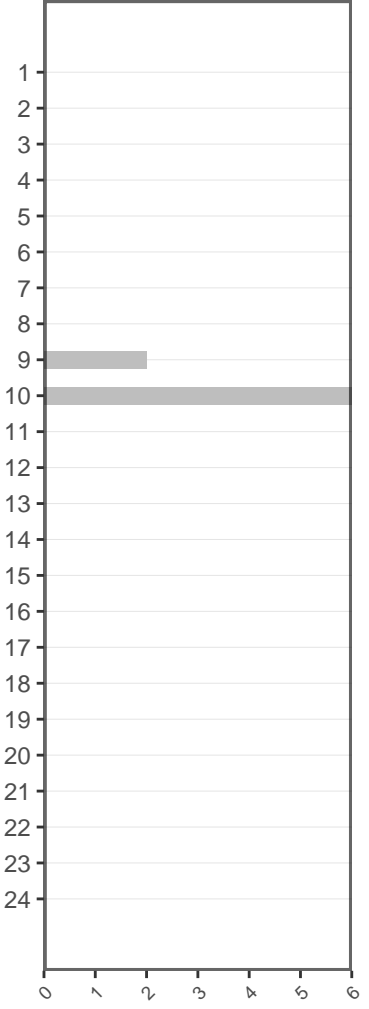
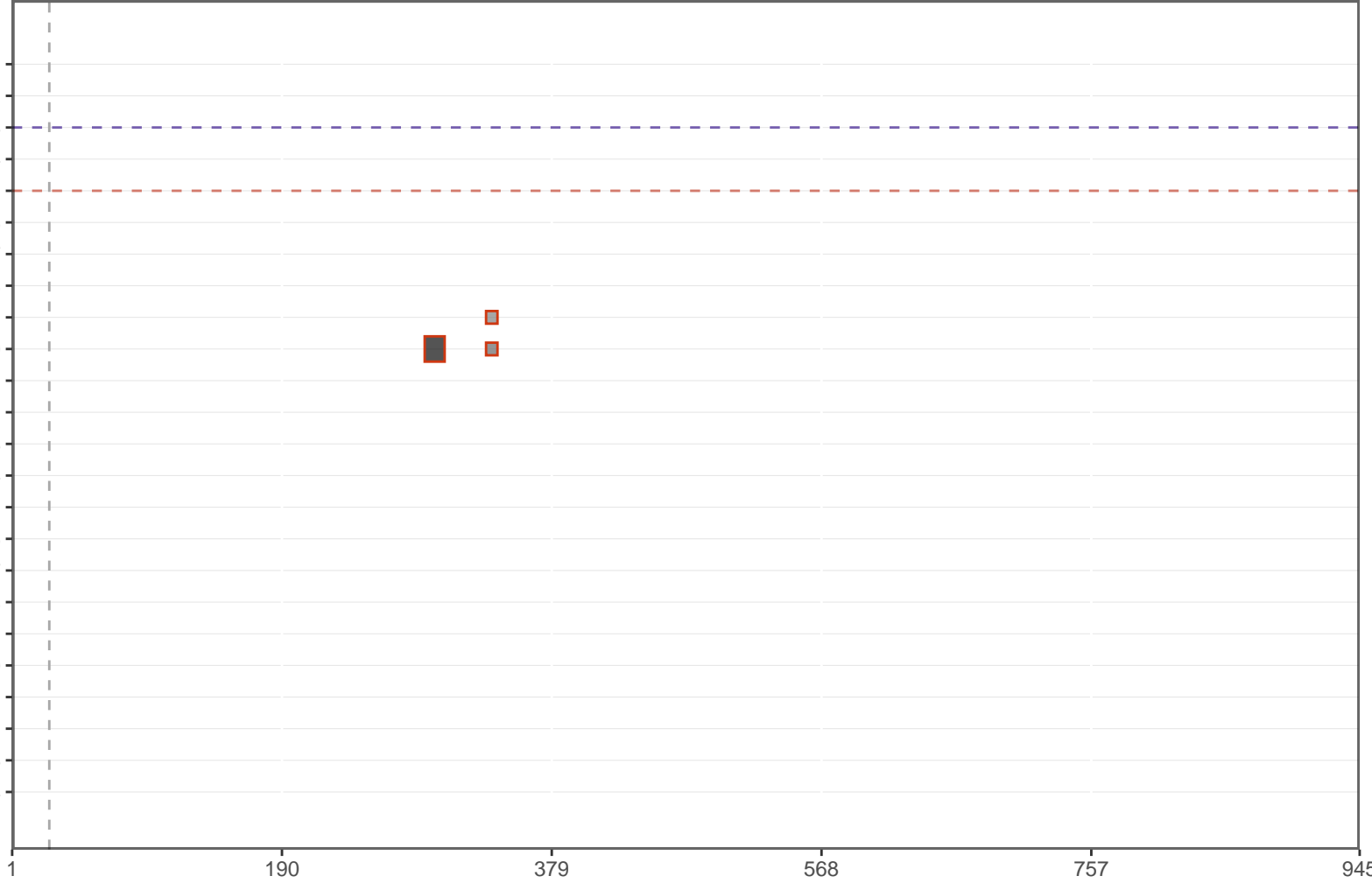
MW indication



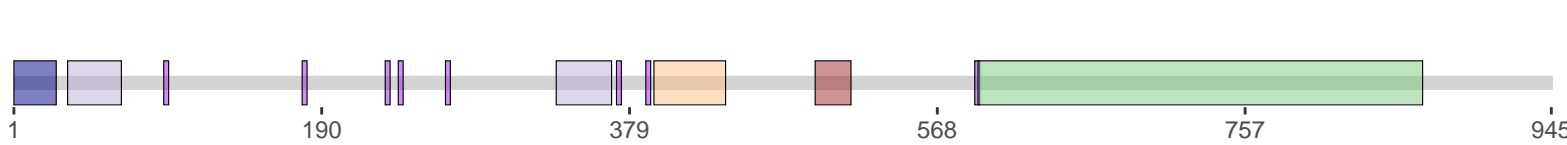
Molecular weight



Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

TPSGSTPGSSDGGGGGTHANGGKKSSTGVVGVSEVIGVCAAAVLAGLIVFGLVYRTHKRSRGRVQSPHTVWHPKHGGSDGDAVKITAGSSVNGGDSGSSAPGDLHVEAGNMVSGVLRDVTNPFSEVNLGRGGFQTVYKGLHDGTMMAVKRMESGVVMSSEKGLDFKSEIWAIVKWRHRLVTLVLLGYGLDGNERLLVVEYMPQGTLSRYLFLNWKKEGLKLEWTRRLTALDVARGVYHLGLAGGDFIHRDLKPSNLLGDDMRKAVADFGVLRAPDQKASL

NbL11g14190.1 purple_acid_phosphatase_2-like [MW - SP = 50.85 kDa]

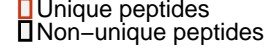
No. of times detected



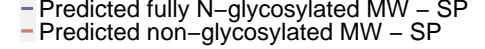
log(intensity)



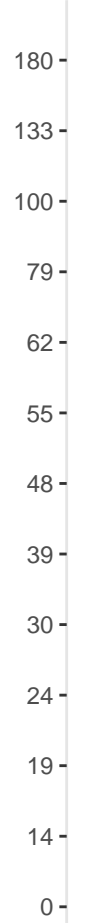
Values from



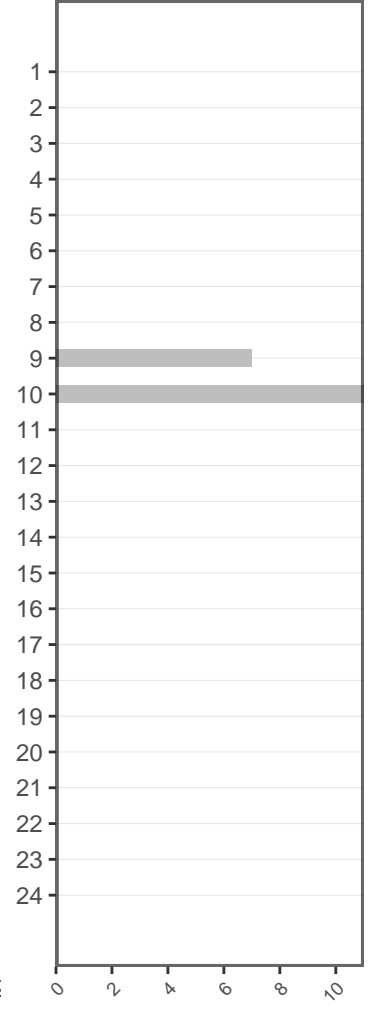
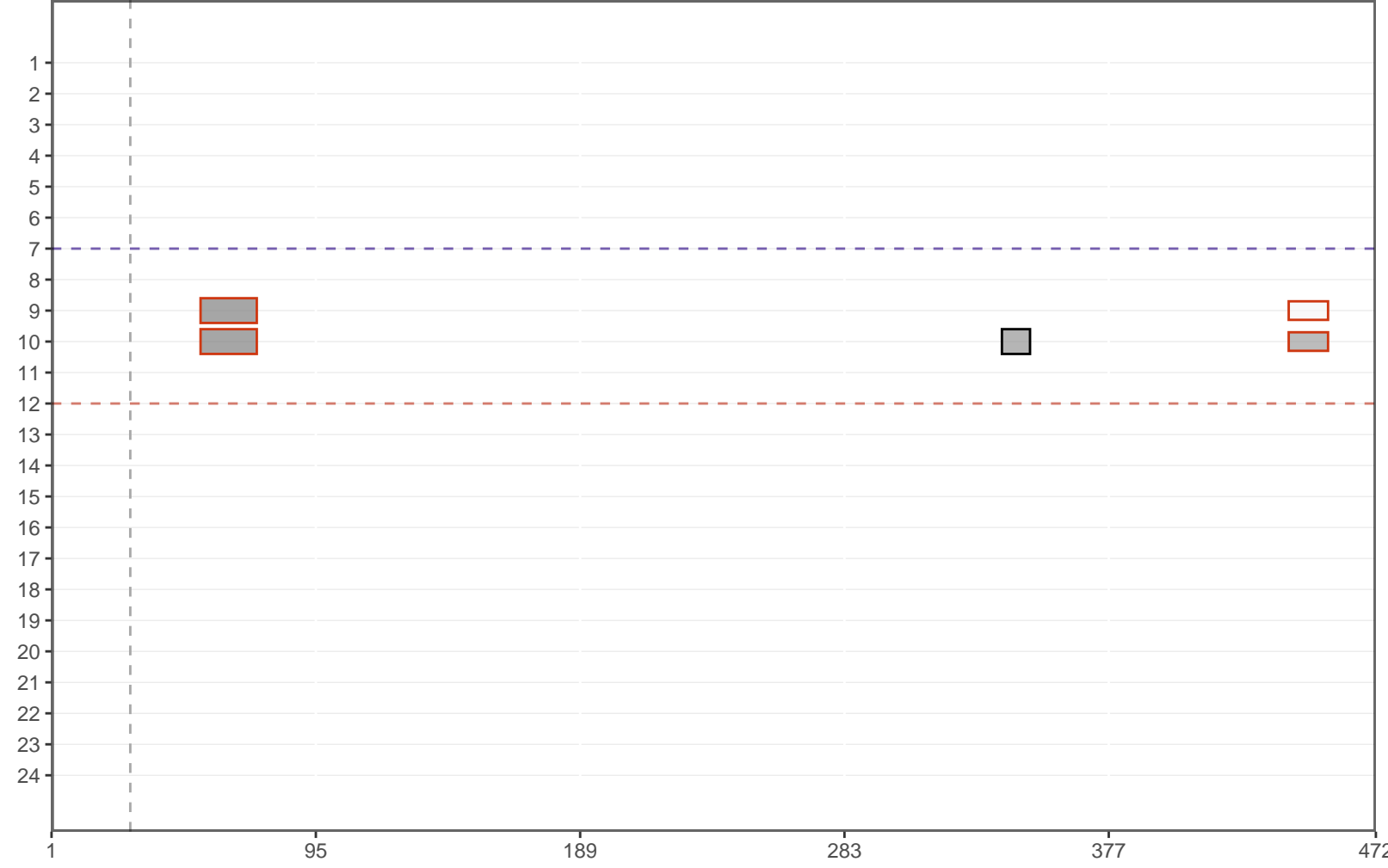
MW indication



Molecular weight

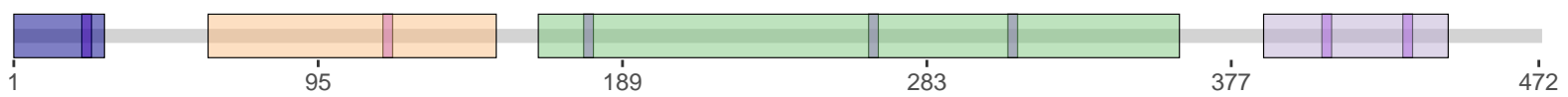


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TAYQPWVITAGNIEIDFAPEIGETKPKPKYTRHWVHPYRASNSTSPLWYSIKRASAGIVLSSVSAVGVKQYTPQYKWLLEELPKVNRITETPWLVLVHSPVNSVNYHYHMEGETMRVMVMEPVFVQYKVDVYFAGHVAHYERTERISNVAVNVNGECTPIRQGSAPVYVTDGGDLLEGLATNMTPEPQVSAFRAESFGHATLAKNRTHAVYVSWHRINGDGGVAEADKIVKNIWNPVDESMLAVS

NbL11g14110.1 cysteine_protease_RD19A-like [MW - SP = 38.04 kDa]

No. of times detected



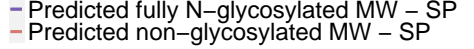
log(intensity)



Values from



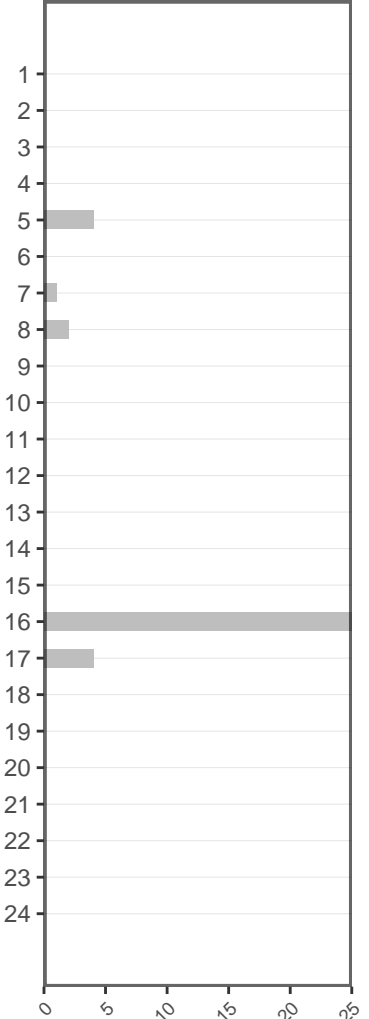
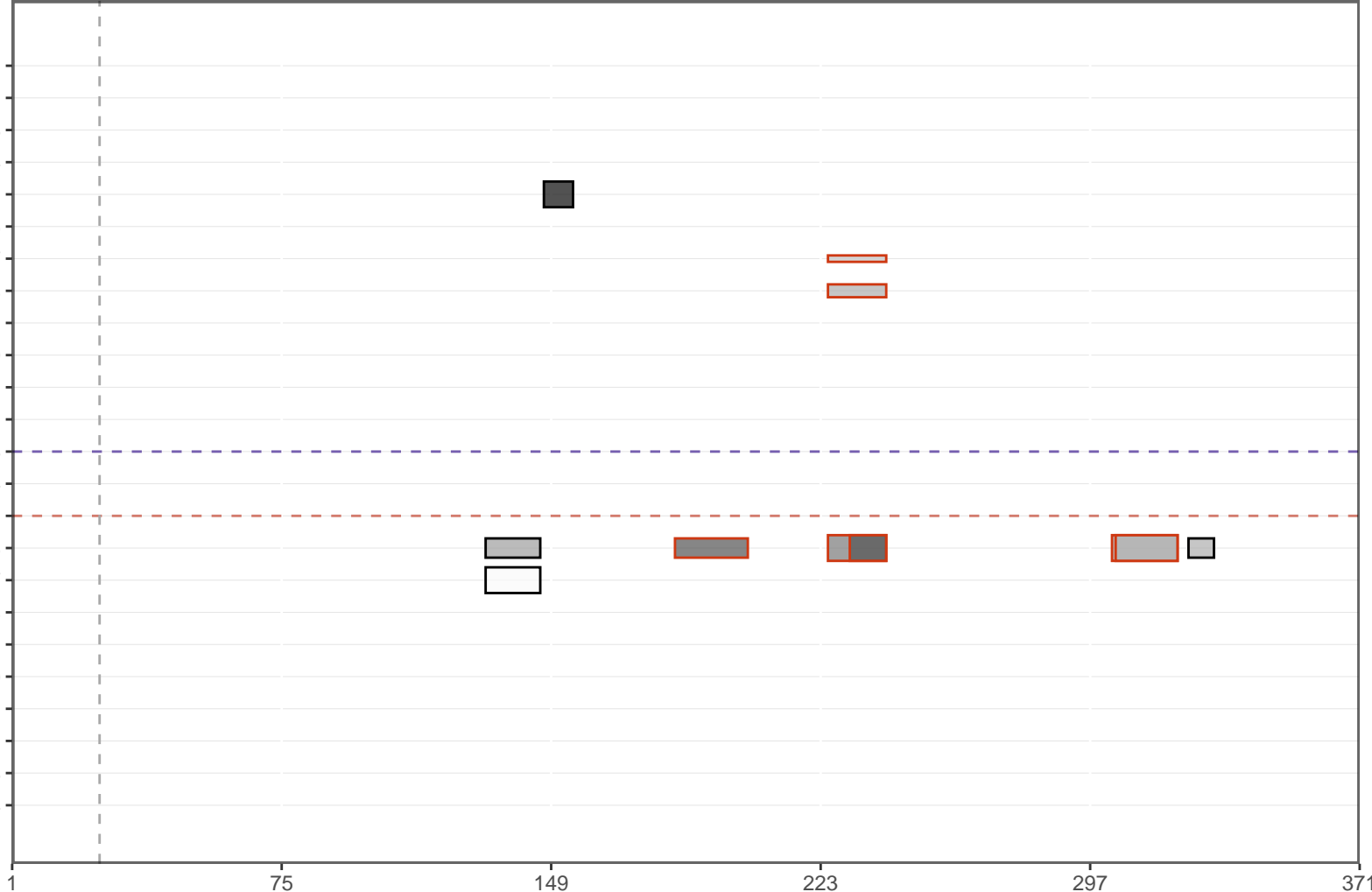
MW indication



Molecular weight



Gel Slice



Protein length

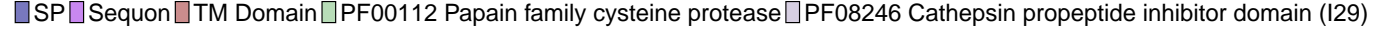


Peptide counts over 4 repeats



Pfam domains

Pfam Description

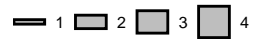


Protein sequence:

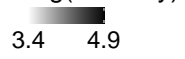
SANYLSTGKLVLSLSEGGVDDCHHEGDPPEKDSGDMDGNGGLMNSAFETLKAAGLMREEDPYTATDRGTGKFDNTKVAAKVNFVSLDEEQAANLVKNGPLAWINAVFMQITVYGGVSGPYSKSLDHDGVLVNGVGTGFSPIRMKEKPYWIKNWGEKVGENGYYKIGRGRNVGGVDSMVTAAVSTSHI

NbL11g14100.1 V-type_proton_ATPase_subunit_a2-like [MW = 92.44 kDa]

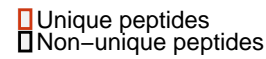
No. of times detected



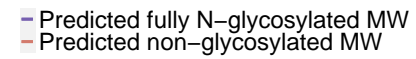
log(intensity)



Values from



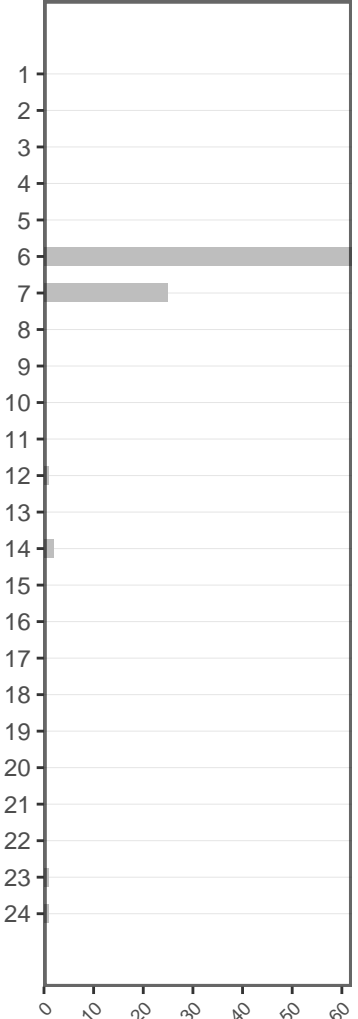
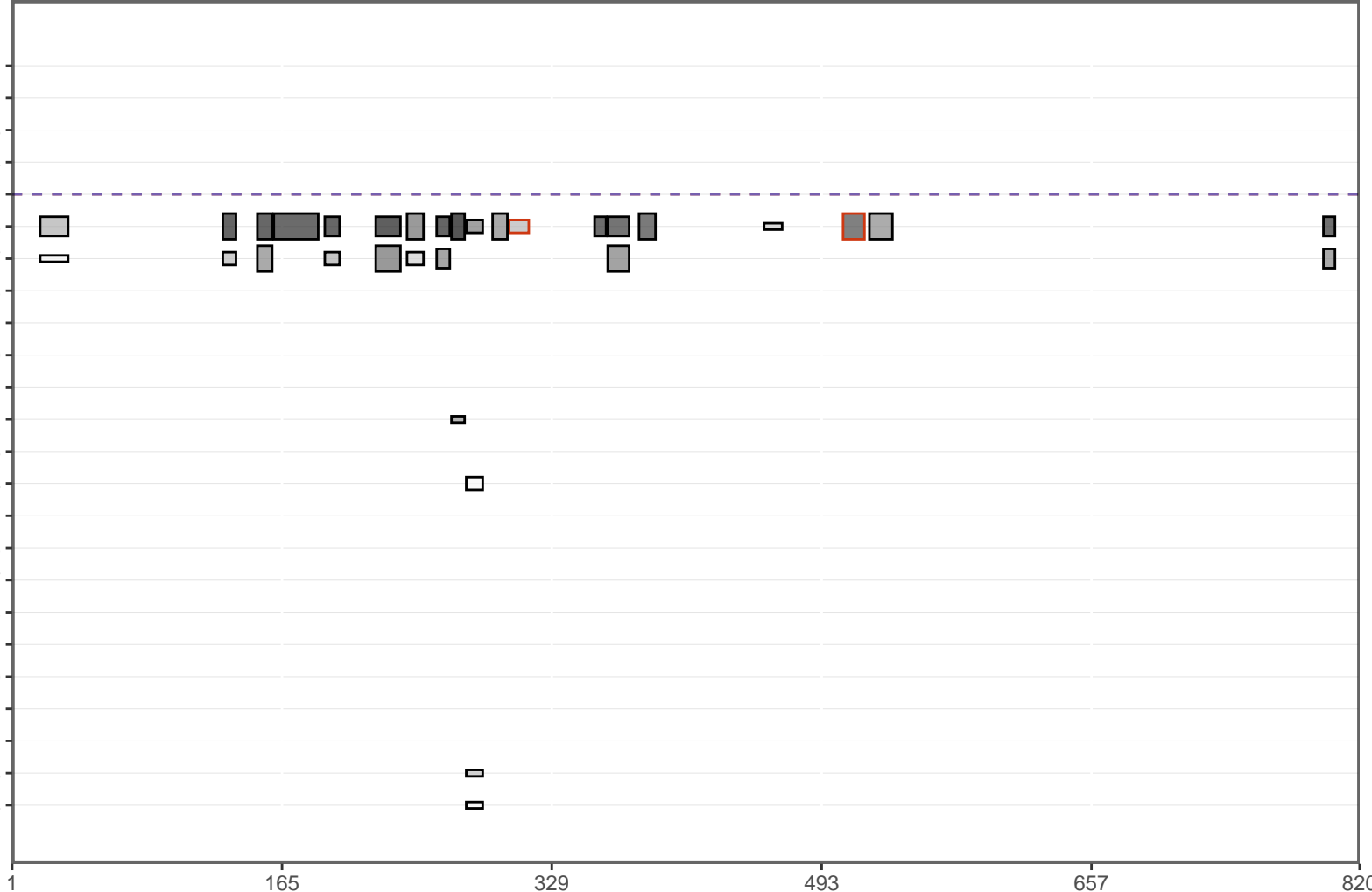
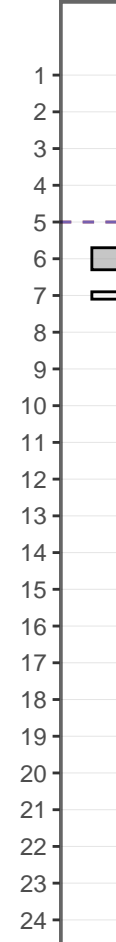
MW indication



Molecular weight

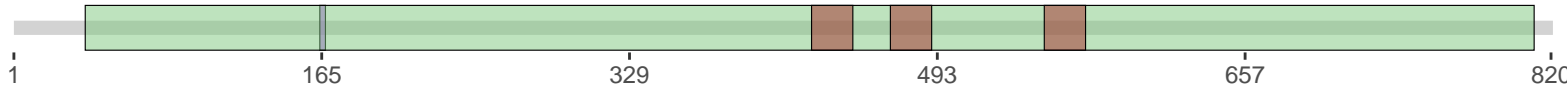


Gel Slice



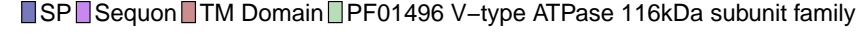
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SSFOEIVDAYGVAKYGEANPGVTVITFPFLFAVMFGDWHGIGCLLLATFLIREKKLSSQKLGDMEMTFGGRVIFMMSLFSYTGILYNEFFRVPFELGRSAYGCRDPGCGDSTAGLKVVRDTPYFGVDPWHGRSELPLYLNELKMKMSILLGVADMINIGFLSFFNALFFRSGINWQGFYQIFLNFALFGYLSLIVKRWGTGGADLVHMYVFLSPTDELGENLFGAGDKTTGLVLFSAIWAIVPVMILPKPPELLKQHERIHGGG6YALGEAEESLLVSSDOS

NbL11g14060.1 uncharacterized_LOC104113315 [MW = 43.25 kDa]

No. of times detected



log(intensity)



Values from



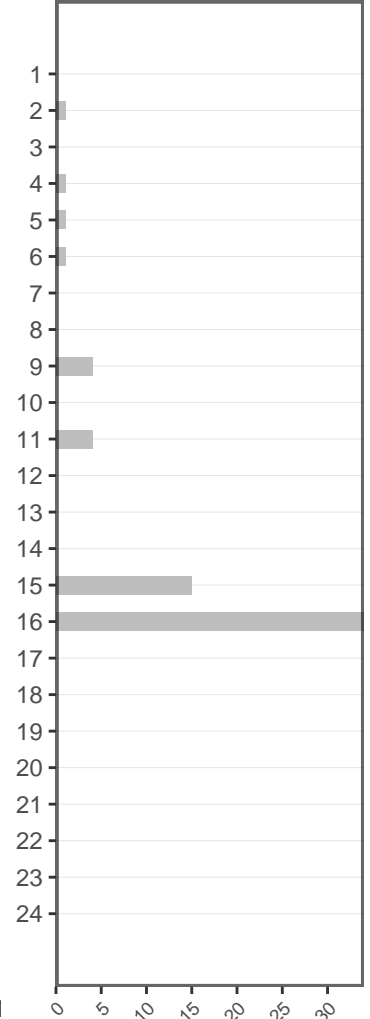
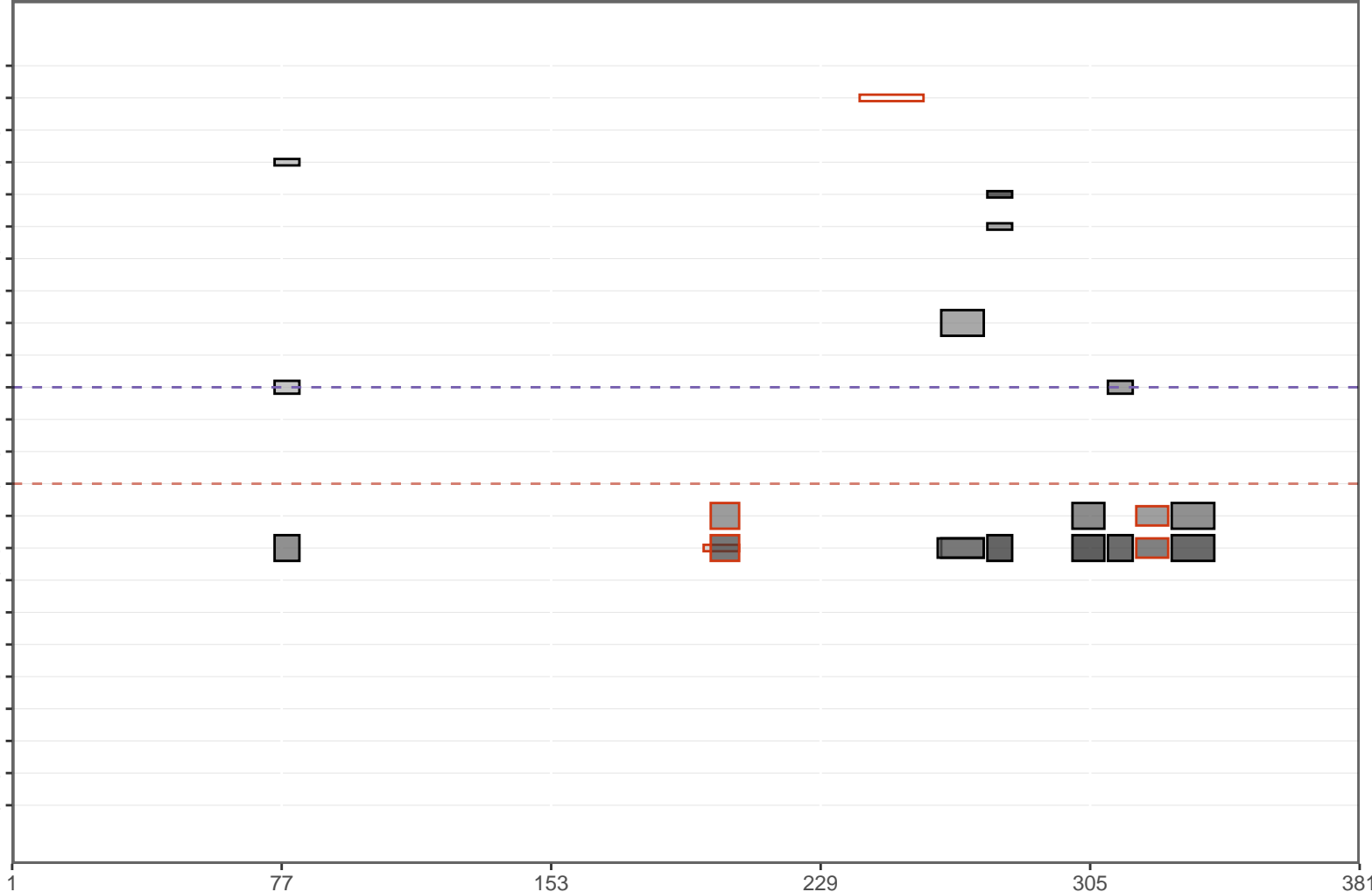
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

LALSVMNIVDRLVKTKKEDSSTGLKALEPILDEVEEISWPPVSDSEALSMEKENRREGDQGLDEGFLSEVNAQLRGAANKDQDKPGLLEAMLQKVLQYASRVLSKRSYAKKGNELVKAEGFLSEIKAPEEENKLLNGMTFVKGKDSPEELVAVKRRMERTLRITTEGGSYQRIIEVLYKGIARAGEIVKLVGG

NbL11g13940.1 fructose-bisphosphate_aldolase_1_chloroplastic-like [MW = 42.81 kDa]

No. of times detected



log(intensity)



Values from



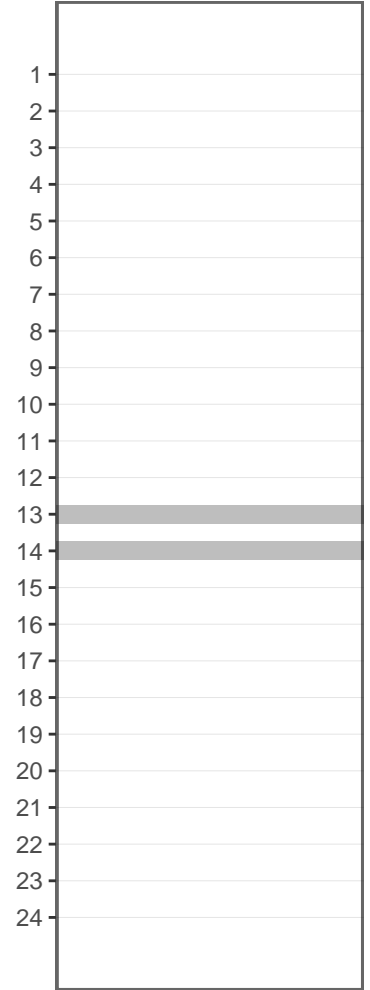
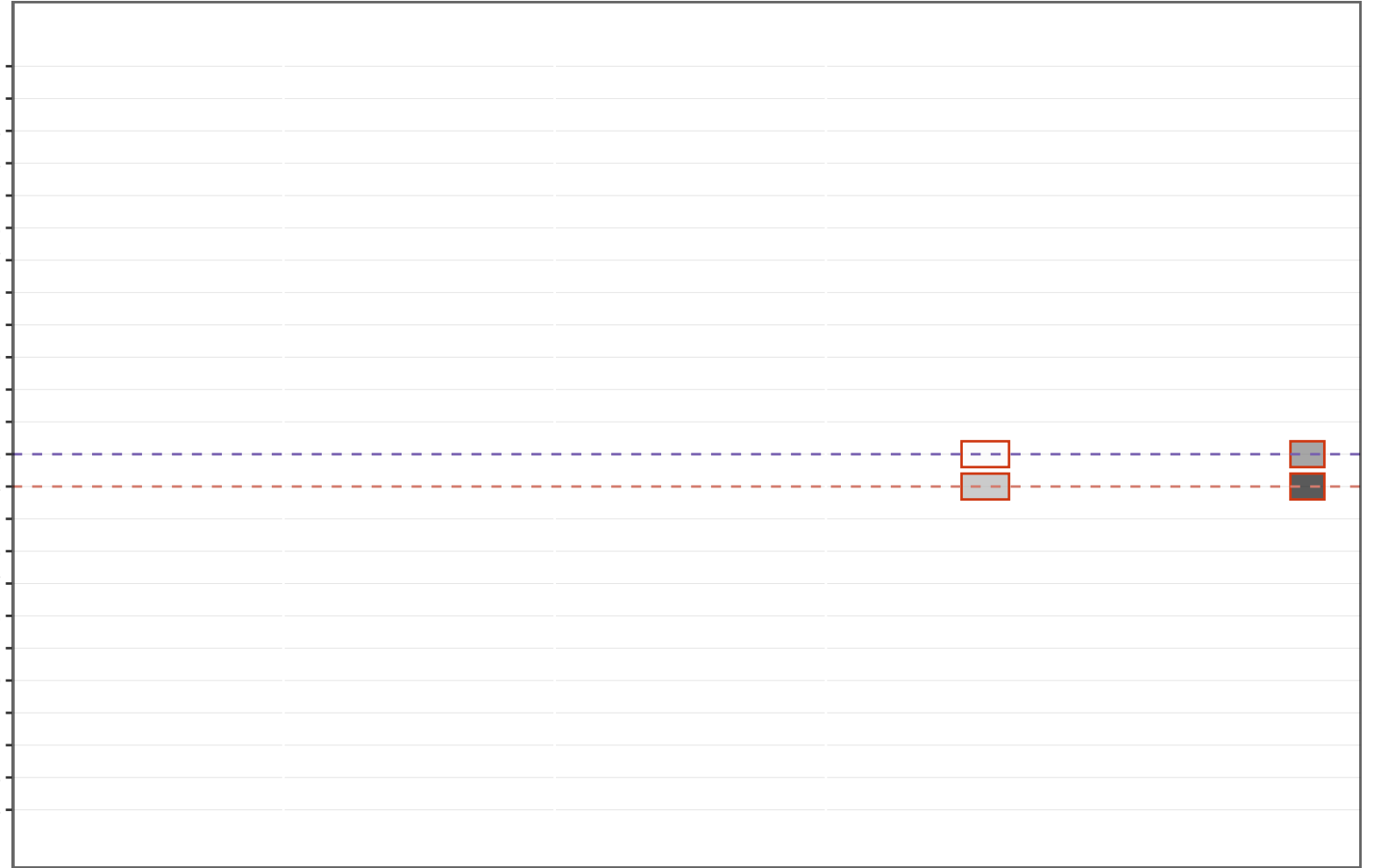
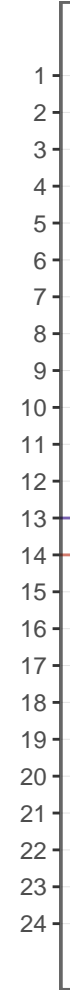
MW indication



Molecular weight



Gel Slice



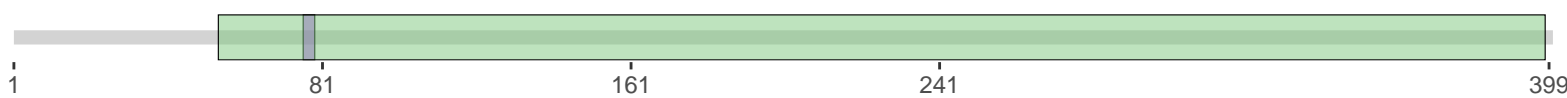
Protein length



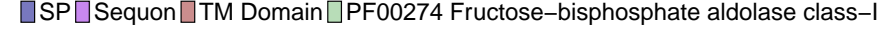
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

ITVSIPIKPSALIVNEAAWGLARYAASGDGGLVPIVEPEILLDGEHDIRTFEVAQKVAEVEFYLAENNVMEFEGILLKPSMVTTPGAECKDRAPQQVADYTLKLRRIIPVPGIMFLSGGGGSEVEATLNINAMNDAPNPWHVYFSYARALGNTGLKTVWGGPENKAAQGDALLTRAKANSLAQKRYTGEGESDEAKGGMFVKGVVY

NbL11g13910.1 NADH_dehydrogenase_[ubiquinone]_1_beta_subcomplex_subunit_9-like [MW = 14.65 kDa]

No. of times detected



log(intensity)



Values from



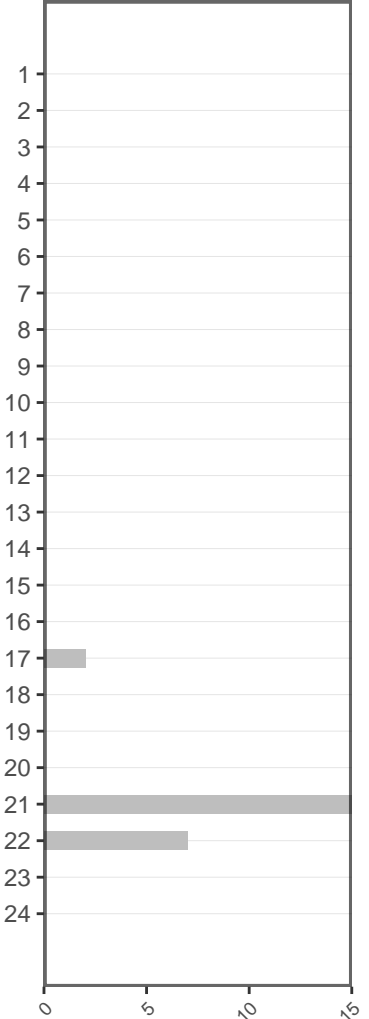
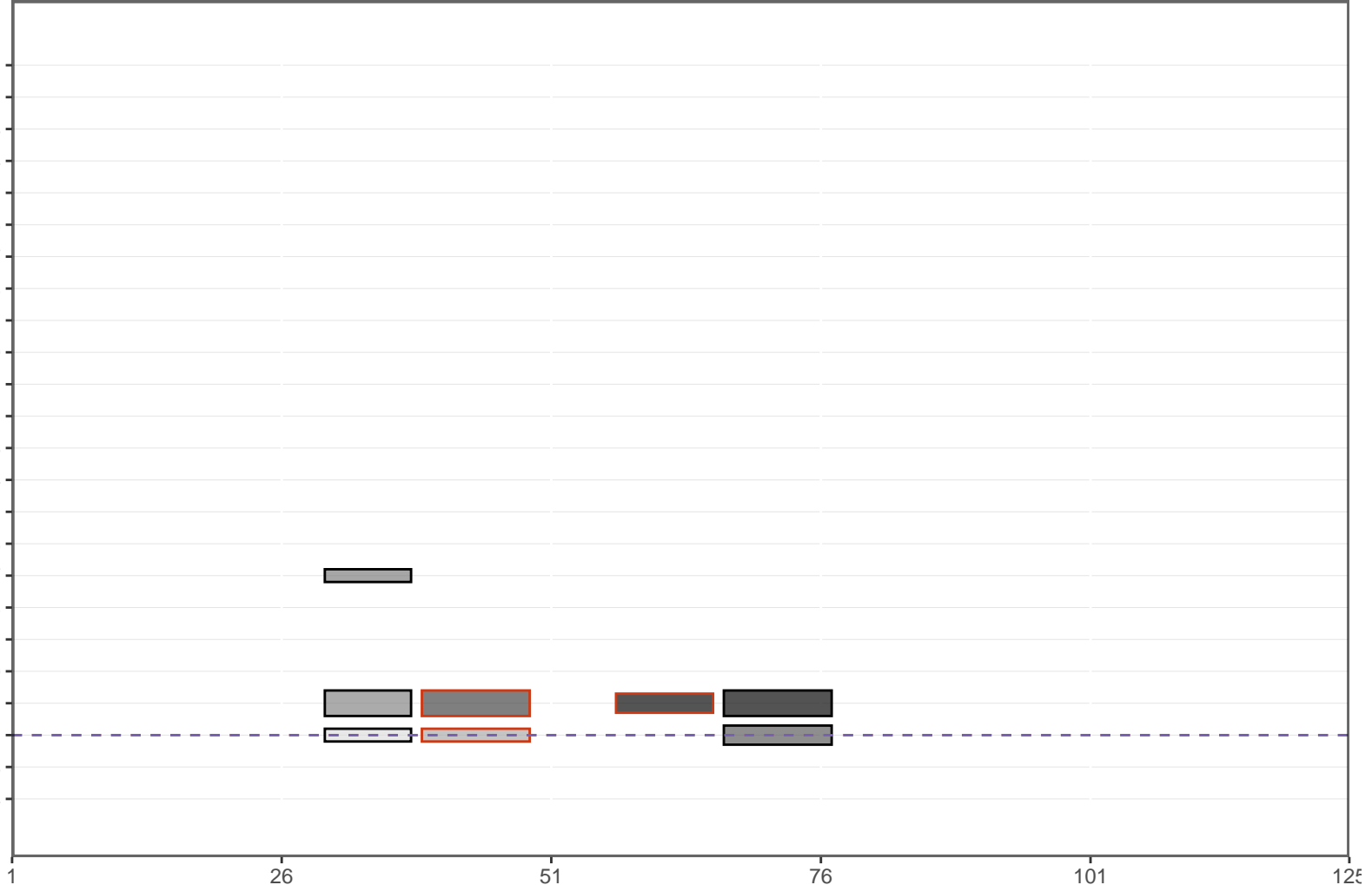
MW indication



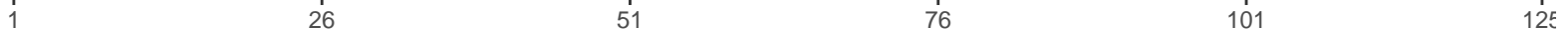
Molecular weight



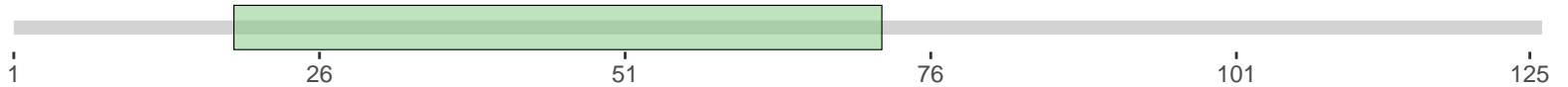
Gel Slice



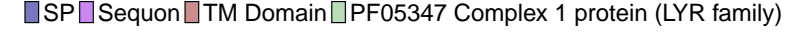
Protein length



Pfam domains



Pfam Description



Protein sequence:

^ERFEANRNVEDVETIDRLADGEAYNKWRHPDPYVGMFLYEFHNIQLGLNPKGVESAIRLIVHVFCEPAAQ^

NbL11g13850.1 NADP-dependent_D-sorbitol-6-phosphate_dehydrogenase-like [MW = 34.76 kDa]

No. of times detected



log(intensity)



Values from



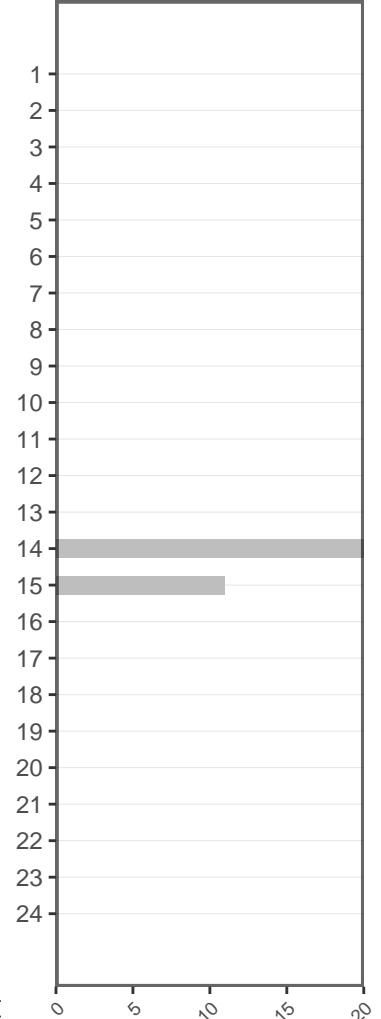
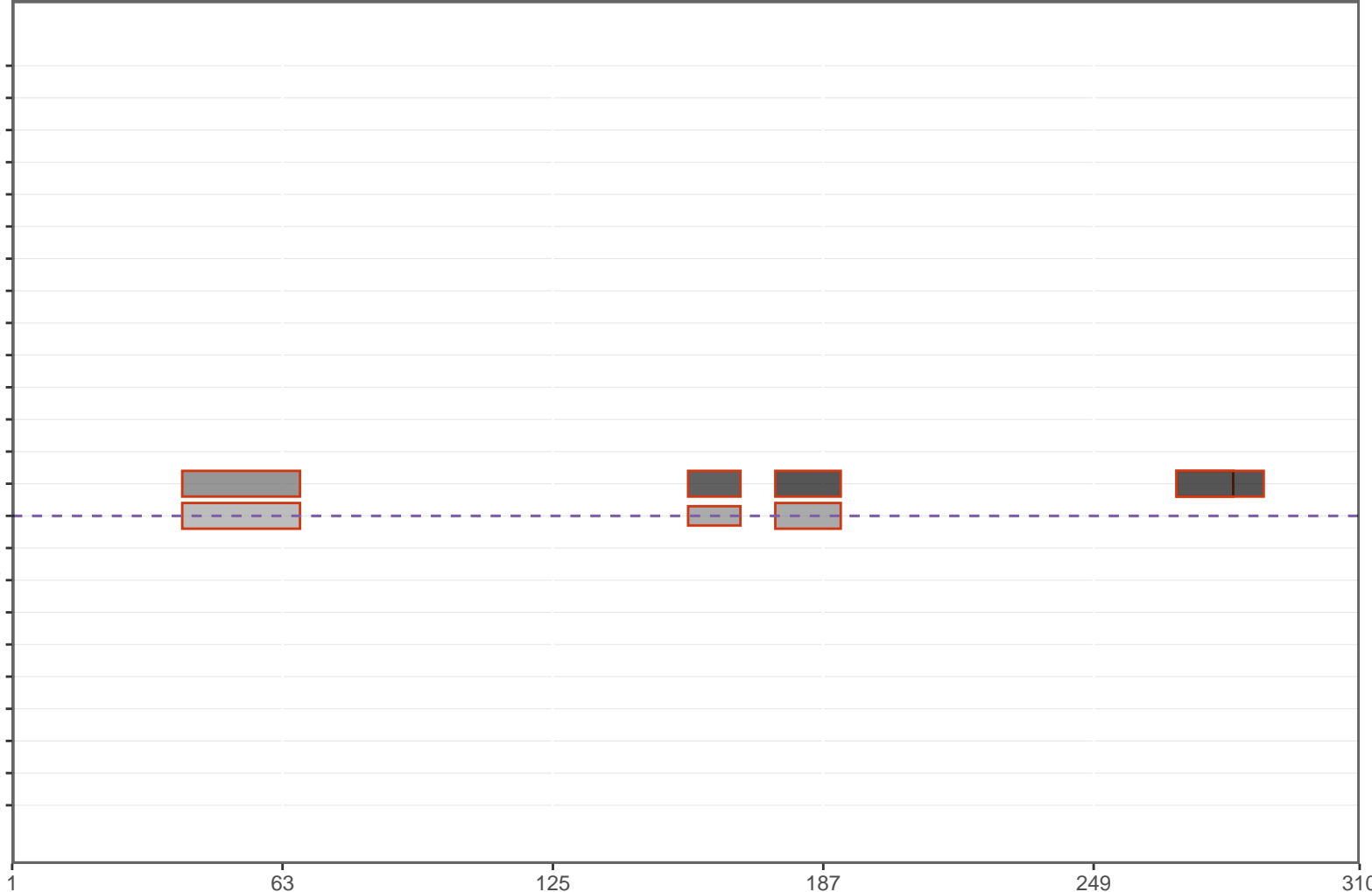
MW indication



Molecular weight

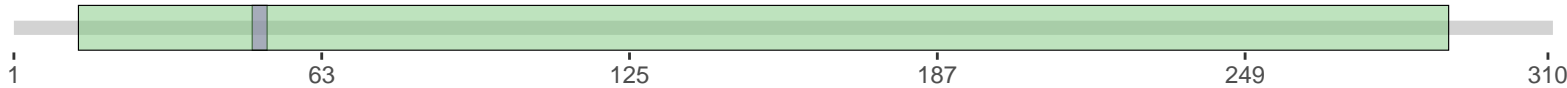


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

HAMENLVSLGLVRSIGISNYDIFLTRDGLAYKPKVYVNDIETHPIYFQRESLVKFGQKHGIGVTAHTPLGGAAANTEWFGTVSGLEDPAKGLAEYKKTAVGVVLRVWGIQRNTVWPKSSKLERLGENFNALDFELTKEDMDLVKBLDRKYRTRNGPKAFVGDIAW

NbL11g13790.1 dihydrolipoyl_dehydrogenase_2_chloroplastic-like [MW = 64.18 kDa]

No. of times detected



log(intensity)



Values from



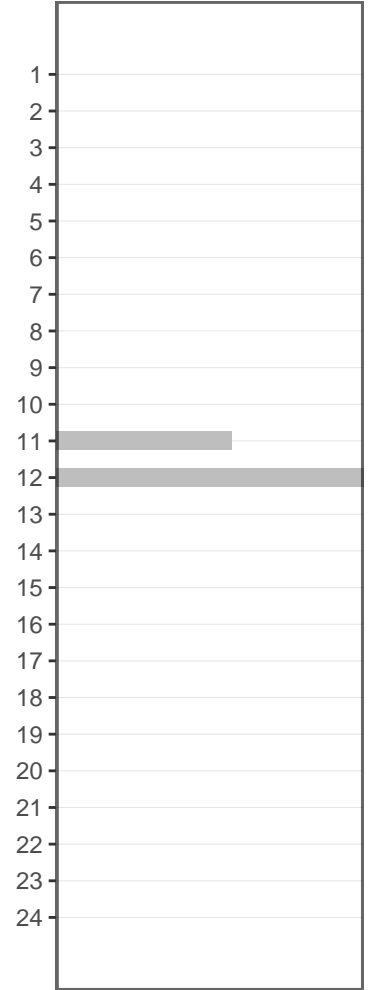
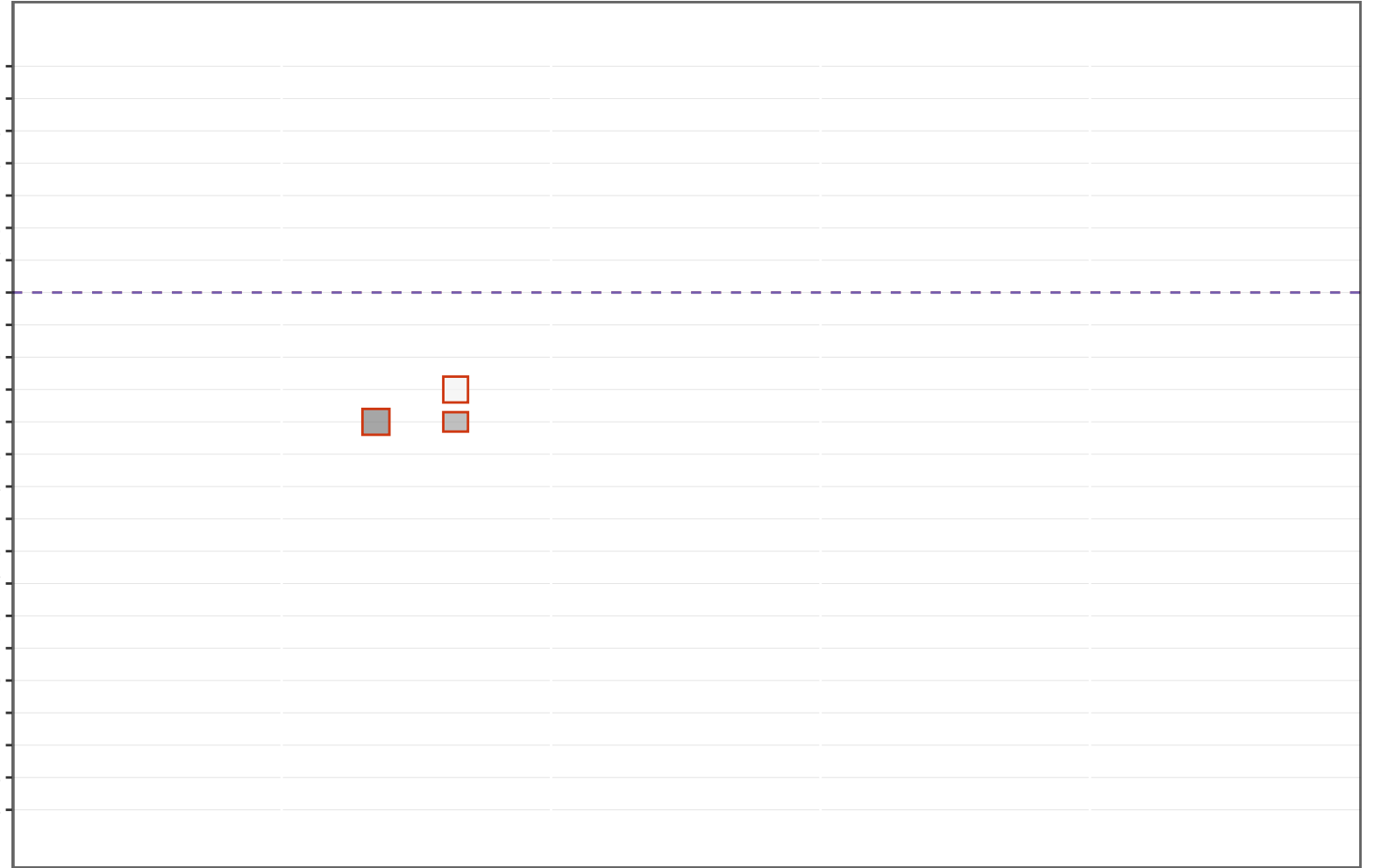
MW indication



Molecular weight



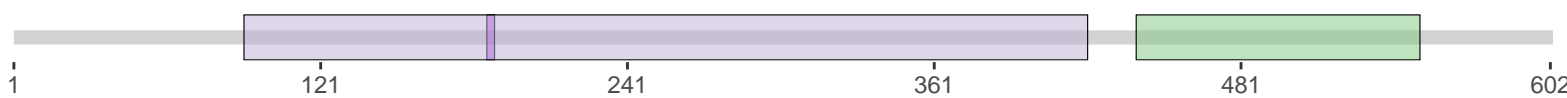
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

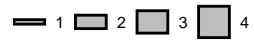
- SP
- Sequon
- TM Domain
- PF02852 Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain
- PF07992 Pyridine nucleotide-disulphide oxidoreductase

Protein sequence:

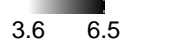
EALDQLMPGDFPEKGLAGRLVLRPKIDVHTGVFASKITPAKDGKPVTELVDAKTKELKDTLEVDAALATGRAPFTQGLGLENINVTGRGFPVDERMGEVDANGELVPHLYGIDGANGKMLAHASAGQISVVEGVYTKDHLNHLSPVAGFTHPVEISAVGLTEPQAREKAENEKGFEGIAKTSFKANTKALAEENEGEGIAKMYRFPDNGEILGVHFGMAHADLHEASNAIAMGTRIDKHFVAHHAFTLSEVIDELFKAQVGRKSLGGLRFLMFWLXLTLLVLLSI

NbL11g13750.1 calreticulin-like [MW - SP = 49.2 kDa]

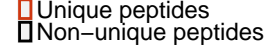
No. of times detected



log(intensity)



Values from



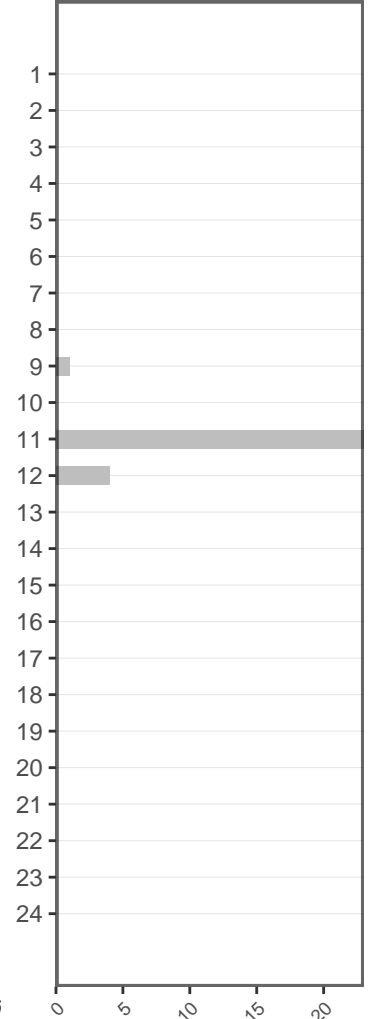
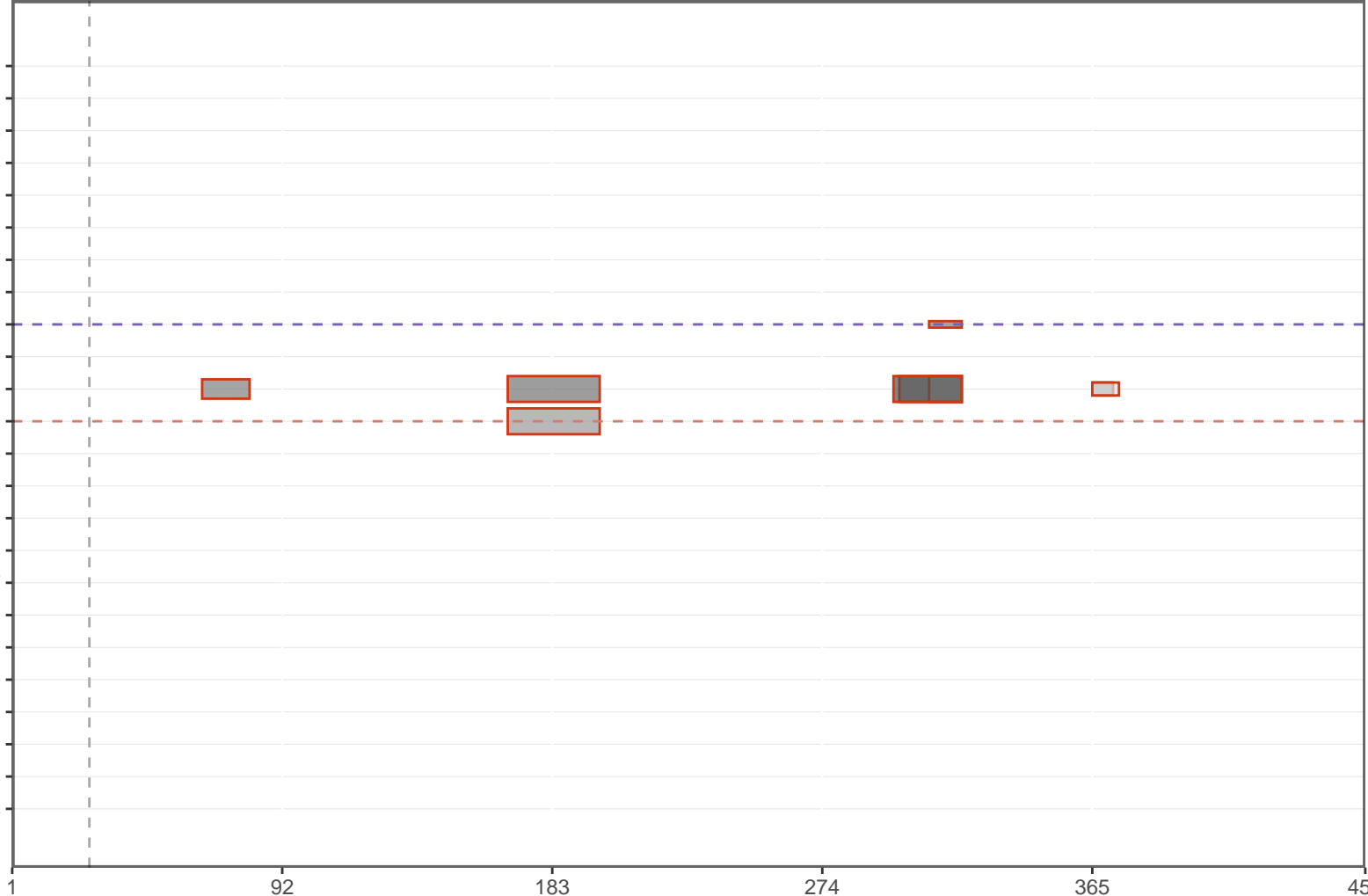
MW indication



Molecular weight

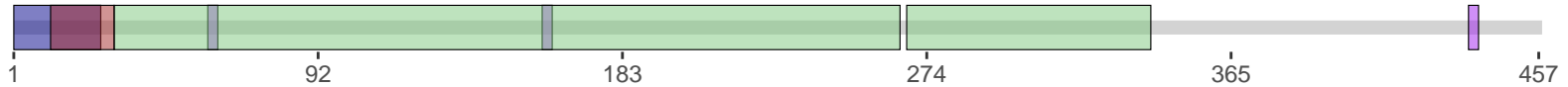


Gel Slice



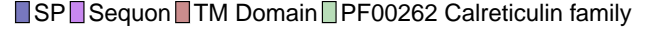
Peptide counts over 4 repeats

Protein length



Pfam domains

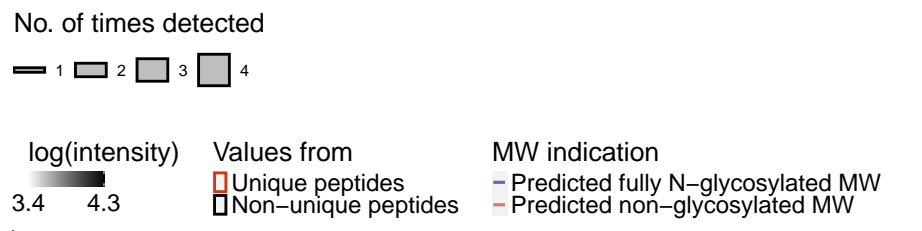
Pfam Description



Protein sequence:

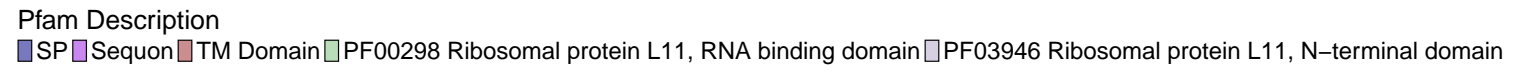
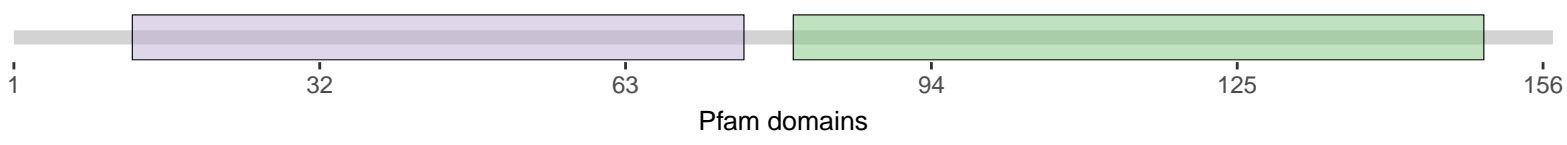
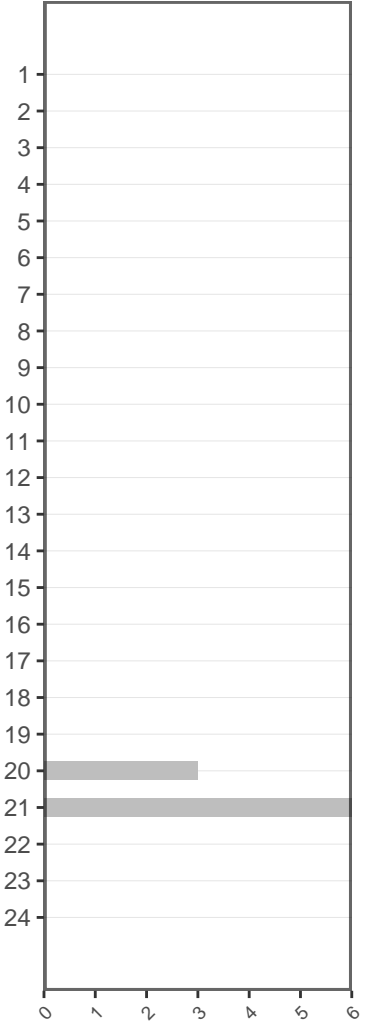
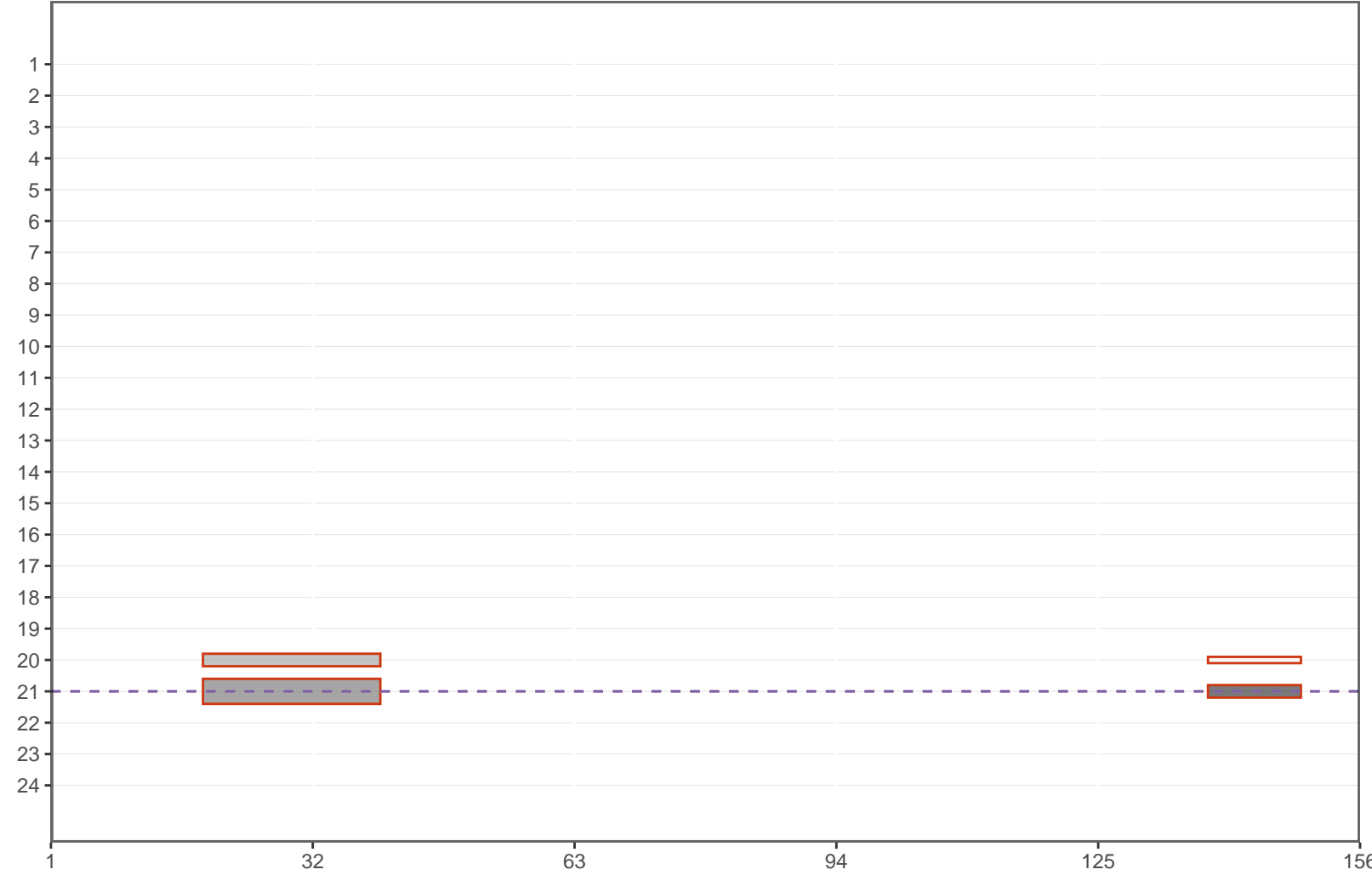
KQPSAKKPEIDWDEKEFIDDPEENKPEGVDDPEEFTPDPAKKPEDWDDDEEDGEWTAFTIPNPEYKGFVKPKKKNPNYKGGKWKAPLIDNPDFKDDPDLYVFPNLKYGVELWQVKGSTLFDNVIQDDPEVYKAAAEETWGGKDKDAEKAFDEEEKKREEEESKAAAPADSDAEEDDDDDDDSDADENSGESKDDAAHVRIYVSGLSFGKRGSGSRTFLVHNLTAVILLNLFQAMNCKDQGF

NbL11g13720.1 54S_ribosomal_protein_L19_mitochondrial-like [MW = 16.8 kDa]



Molecular weight

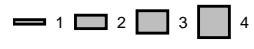
Gel Slice



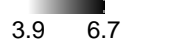
Protein sequence:
 VITIMAFKDGTFEFYKSPSVTWLKGAGIELGGSRPGHVASTLTLKHVYEAIKIKGSDFFDQVMPLEEKCKSIGTANSMGKVKQKELD

NbL11g13630.1 ATP-dependent_Clp_protease_proteolytic_subunit_5_chloroplastic-like [MW = 32.26 kDa]

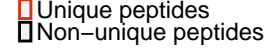
No. of times detected



log(intensity)



Values from



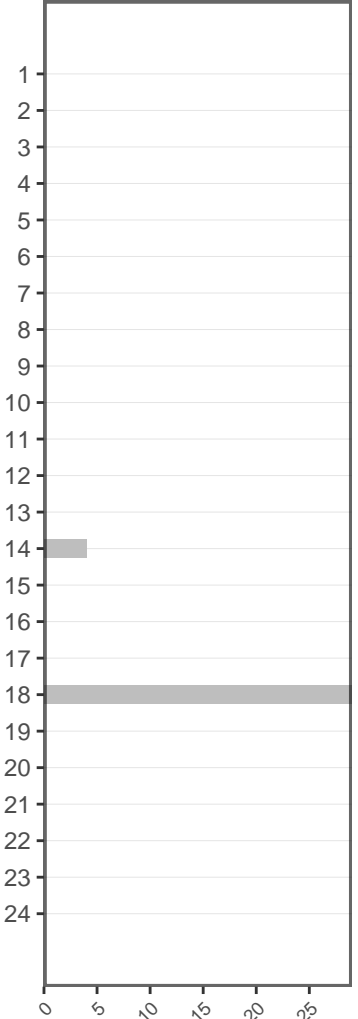
MW indication



Molecular weight



Gel Slice

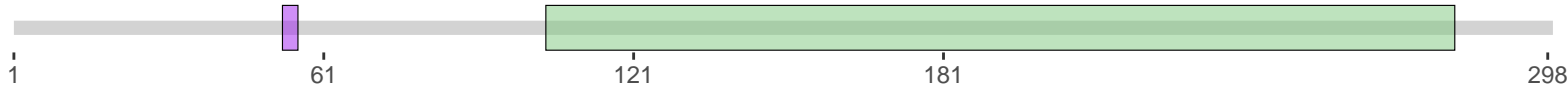


Peptide counts over 4 repeats

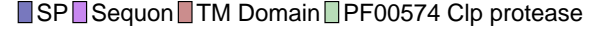
Protein length



Pfam domains



Pfam Description



Protein sequence:

IQLLYLDAVDPITKIDVIMFYVNSPPGGVITAGMAIFDITMRHHRPDVSTVGVLAASMGAFLLSAGTKRKYELPNSRIMHQPLGGAGGGQTDIQIANEMLHKKANLNGVLAHYHTGGSLEKINGDTRDFMFSAKEAKEYGLIDGVILNPMKALQPLAAAAEGR

NbL11g13560.1 uncharacterized_LOC107804171 [MW - SP = 38.31 kDa]

No. of times detected



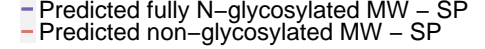
log(intensity)



Values from



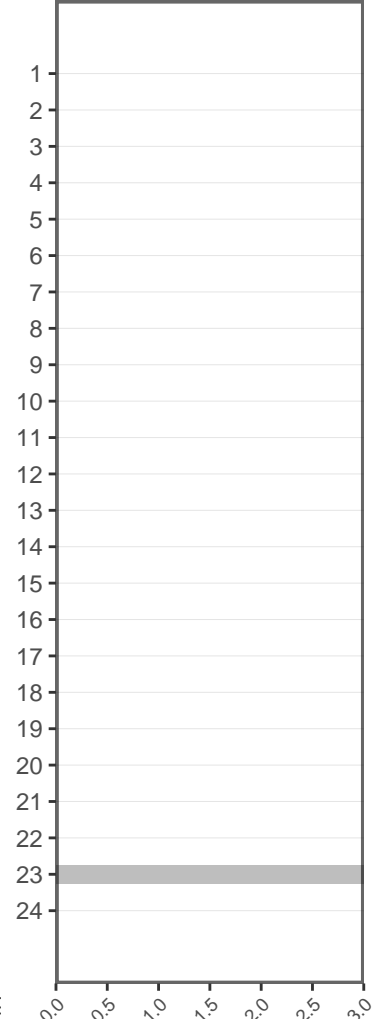
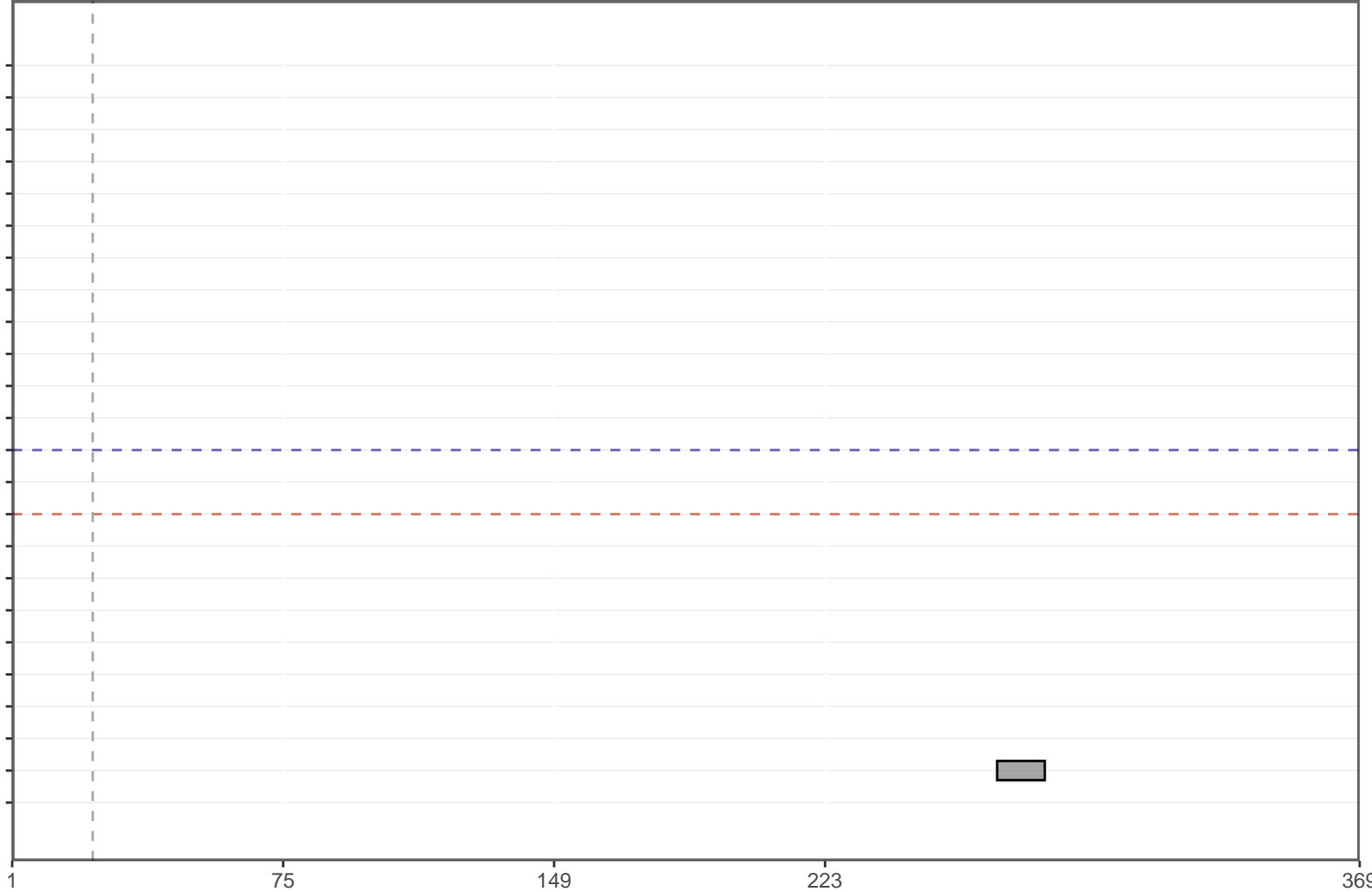
MW indication



Molecular weight



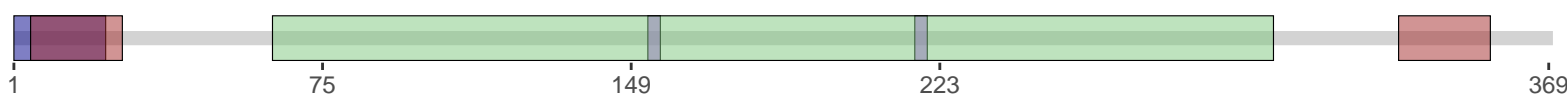
Gel Slice



Protein length

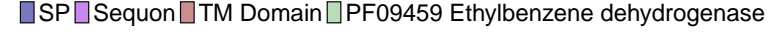


Peptide counts over 4 repeats



Pfam domains

Pfam Description

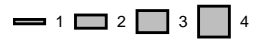


Protein sequence:

GRLYGGNPIIDNRDNGSGDRFGHVLVDLVAWNPICGNLGGVSPITGNDTAAQNDWRGAAWHSSFGTHSGYSDDESPYSTNGGKGTFFYFESRALRTMDRLGGDVGFTIGQTSKFAAFWYFEDGNPWHGSGHYTVSGDVAWPLDNPVPPGSSAGWVVRSSWDAAGDFALLEVVFVGFVGFVGLVHKKNAISFQRLD

NbL11g13530.1 NHL_repeat-containing_protein_2 [MW = 121.37 kDa]

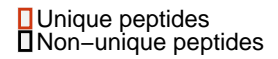
No. of times detected



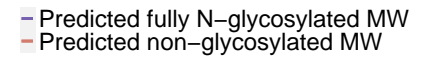
log(intensity)



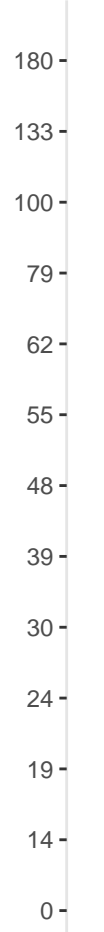
Values from



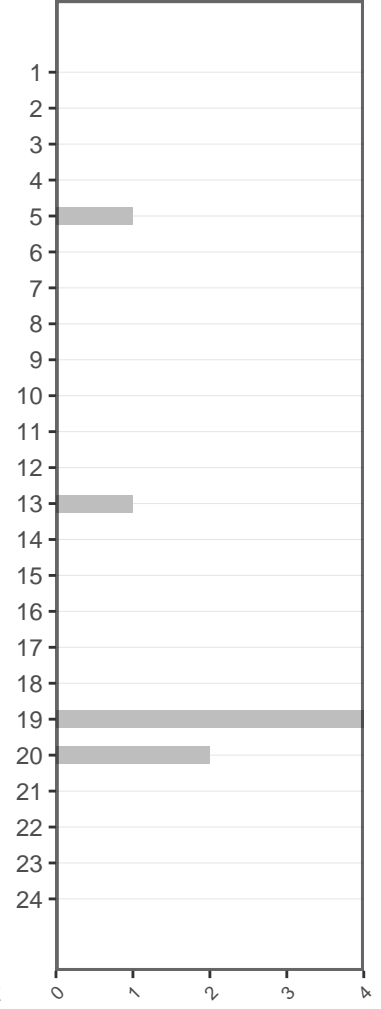
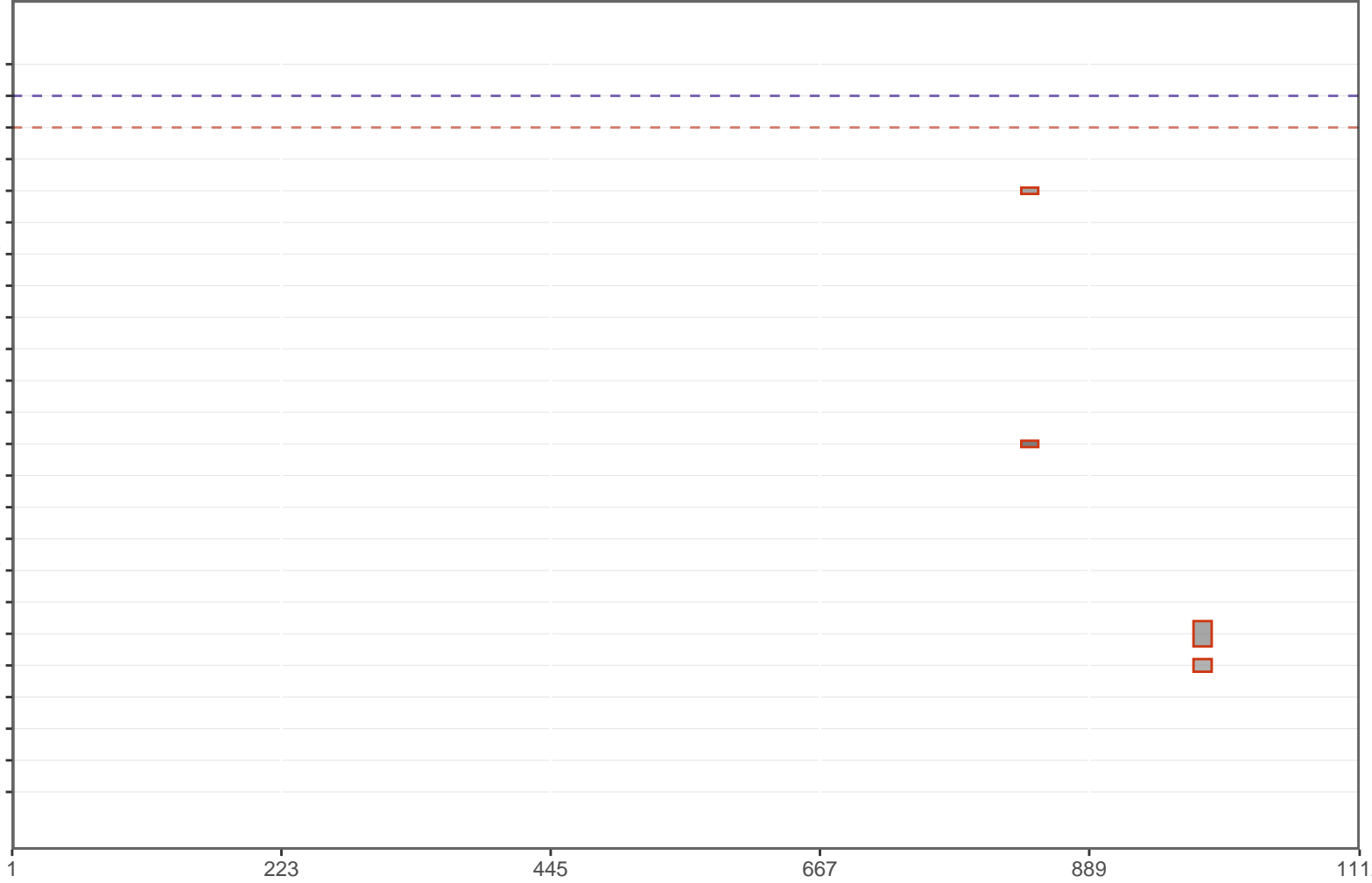
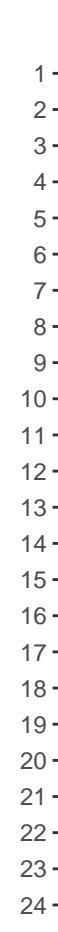
MW indication



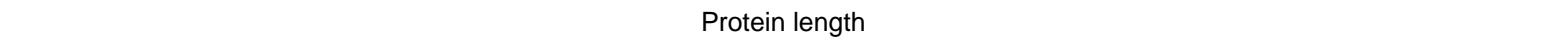
Molecular weight



Gel Slice

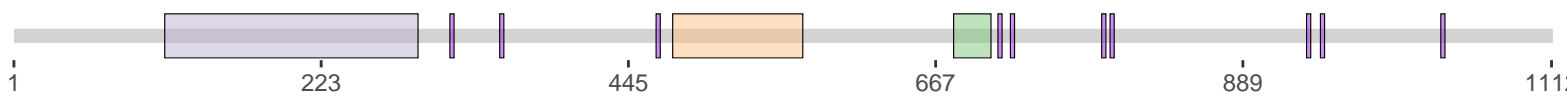


Protein length

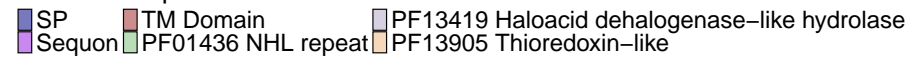


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VNDGEMNLVRELGVNSWTFVALVSPNGKLLAGIAGEGRKDKLPLVEALLFYGRKLLDSTPIPLRLEKNDPRLILTSPLKFPGLKLVADLNNRFLHSDENRNRIVVDTLEGNLFVQVGTGAELGRDGNFDDATFRNPOGLAYNAKKNLLVADTENHALRVDFVNETVRLTAGNKSGDVEGGGTGTAQLLNSPWWVCFEPENGIYVAMAGQHWVHETSDGVTRAFSGNGFERNKNNGSSSTNTSFAQPSGISLDRDLKEAYIADSESSIRAVDLRTGGSRLLAGI

NbL11g13450.1 probable_Xaa-Pro_aminopeptidase_3 [MW = 41.53 kDa]

No. of times detected



log(intensity)



Values from



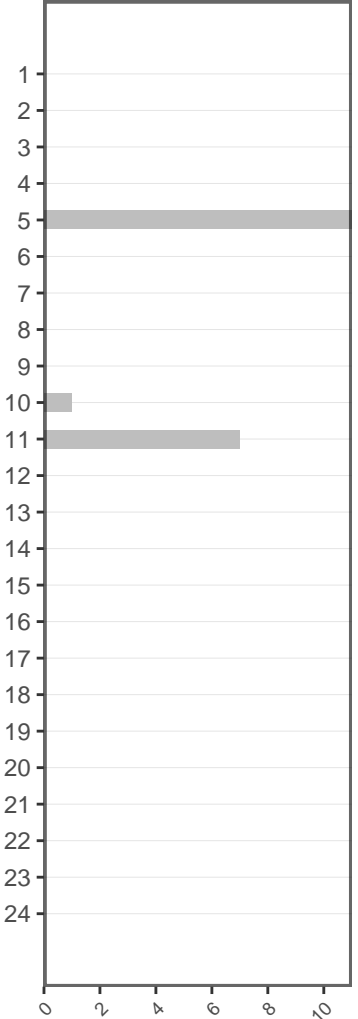
MW indication



Molecular weight

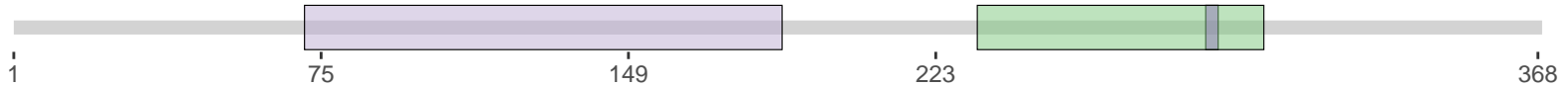


Gel Slice



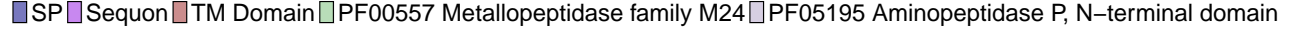
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LPQLSRMIESSSTVFNKTRTSGLYLEAVKAVSNVYKDFSVYTHEARFVKSFAELKLRDGSASADGALIGTMYSKLFPDEGMLGAKFEYEGRRVGAQRMAFNPLVGGGPNASVYHFFVMTKRLKMWTLGSSWLDASSTVMSVILLVGRPLENLFKRNFIILFWRQTRINAWSCAGLAGPSEKYITTRV

NbL11g13430.1 uncharacterized_LOC107799792 [MW = 23.01 kDa]

No. of times detected



log(intensity)



Values from



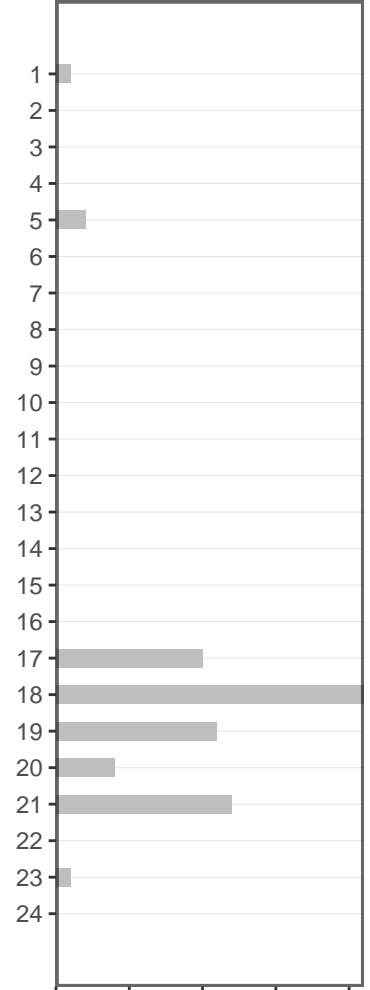
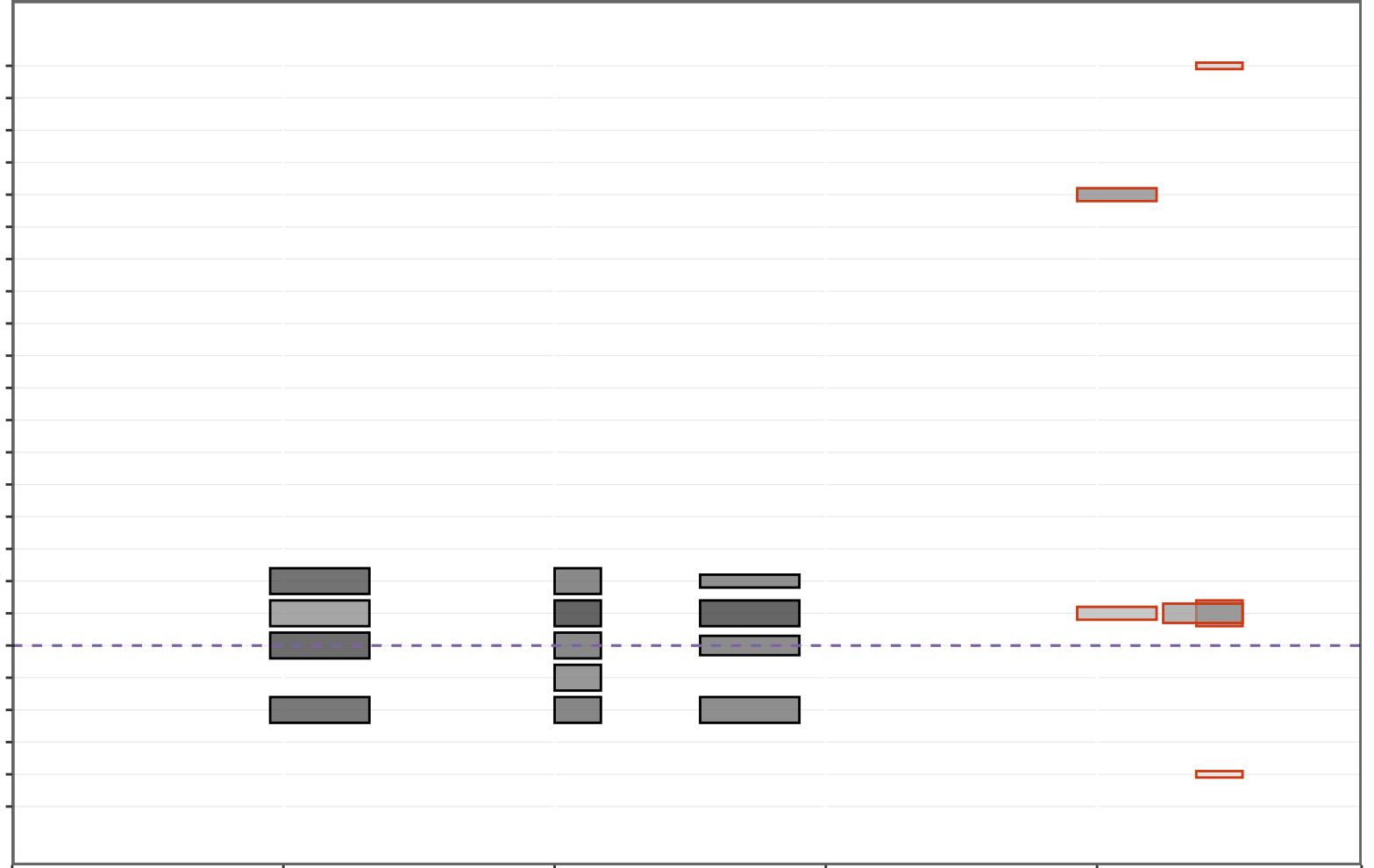
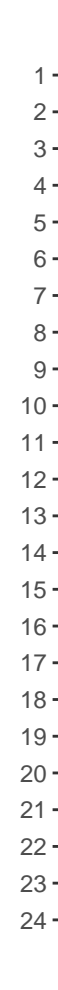
MW indication



Molecular weight



Gel Slice

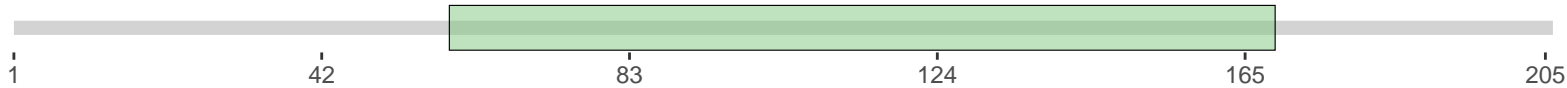


Protein length

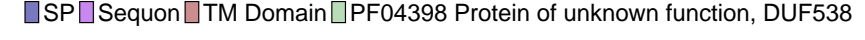


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

.KSKKXTEHKFEKIGRQVGHGTETVAIEQNKIKKLTGVAKKELLMWLTLETGVDVDPPTGKHKFKATSGLRFFVSAFEIDVPKKEEKVDNEVWKENKEVAAAALEKVEV

NbL11g13330.1 ABC_transporter_I_family_member_20-like [MW = 36.6 kDa]

No. of times detected



log(intensity)



Values from



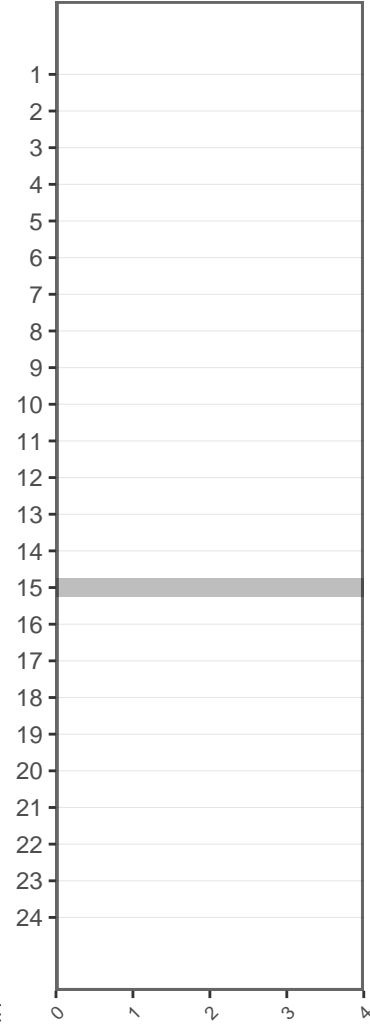
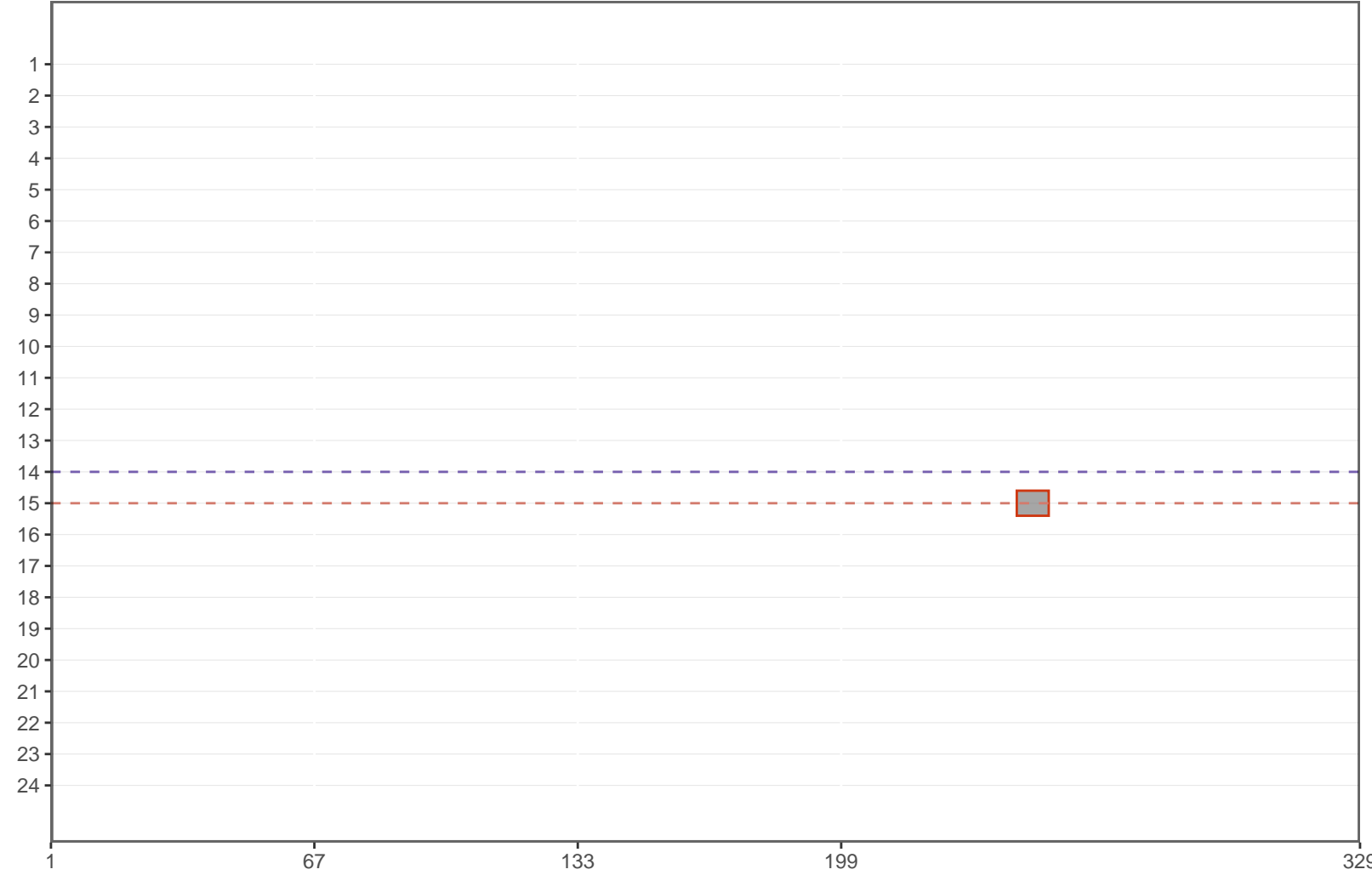
MW indication



Molecular weight



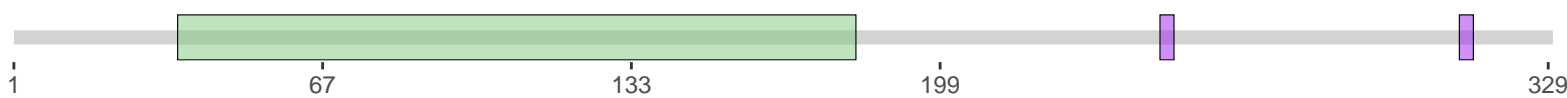
Gel Slice



Peptide counts over 4 repeats

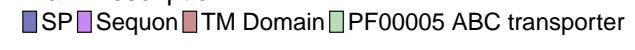
1 67 133 199 329

Protein length



Pfam domains

Pfam Description



Protein sequence:

KASDQRRRVQICAGSLKPKFKVLLDEITVDLGLARADLLKFLSKEGEEKGATIHATHFDGLENWPSHMLVYVHGKLGGLAMPMDKVKKEISLMLMRTVESWLRKERDEERKRRAERKAKGLPEYKGVGEGSRVYVGDPAARAARPLNNGWAGRLNETIAGEENFVLSNRVLR*

NbL11g13150.1 ATP-citrate_synthase_alpha_chain_protein_2 [MW = 46.45 kDa]

No. of times detected



log(intensity)



Values from

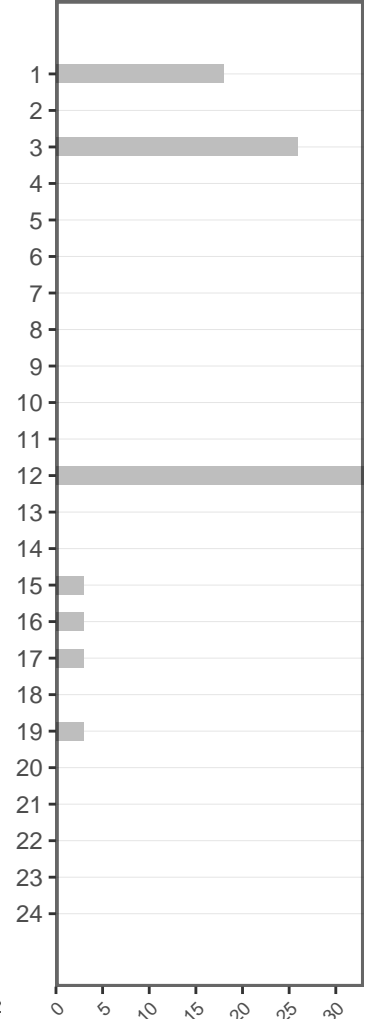
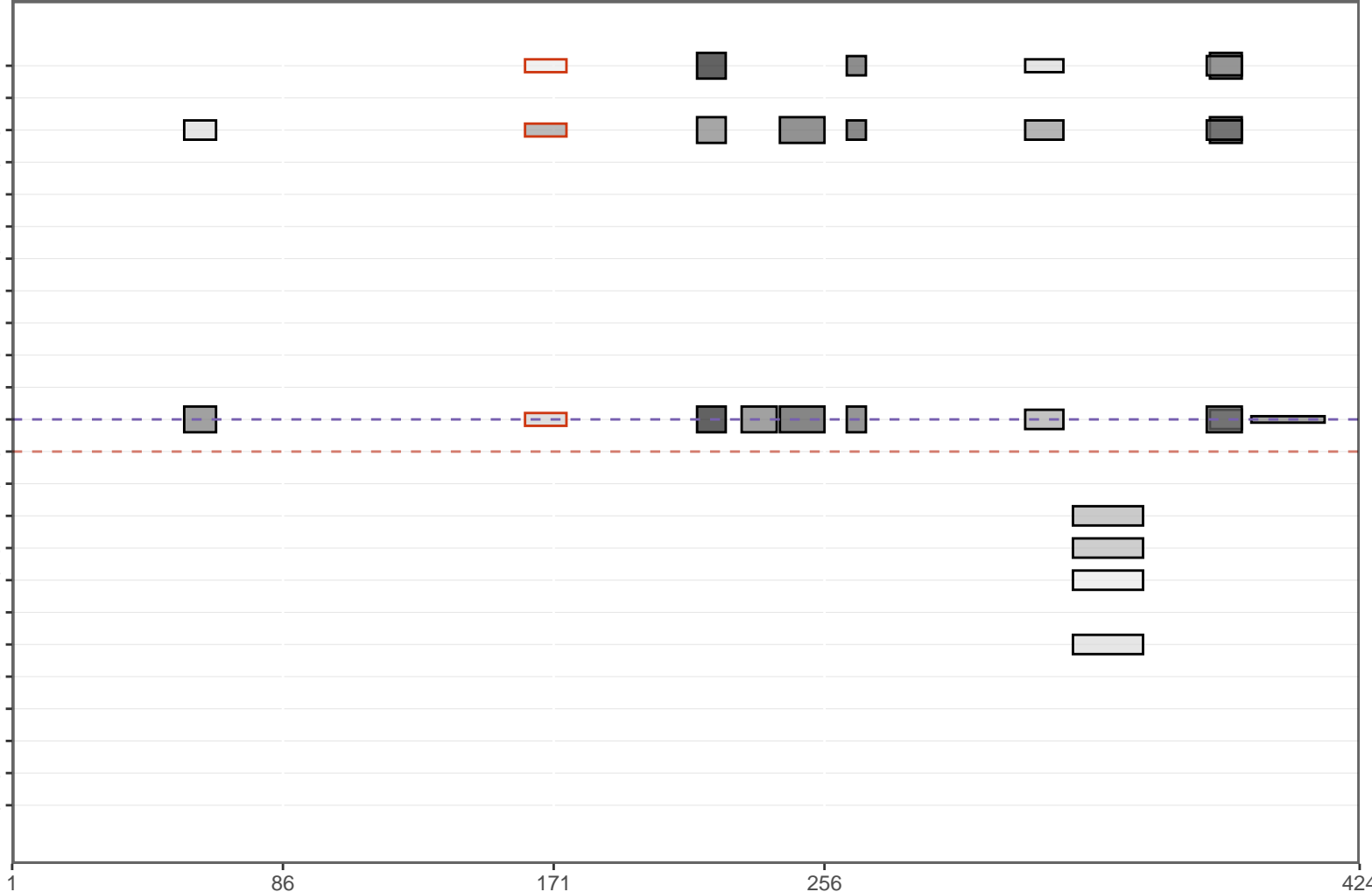
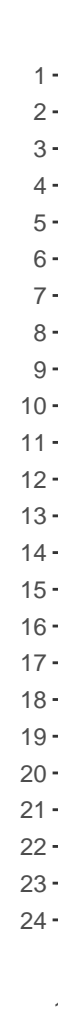
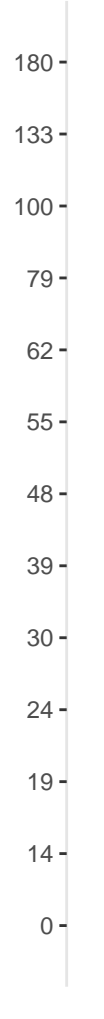


MW indication



Molecular weight

Gel Slice



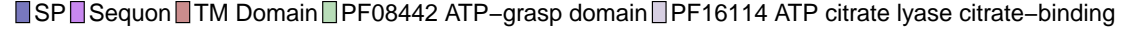
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

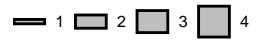


Protein sequence:

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NbL11g13130.1 S-adenosylmethionine_synthase_1 [MW = 43.22 kDa]

No. of times detected



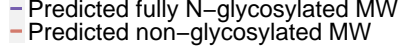
log(intensity)



Values from

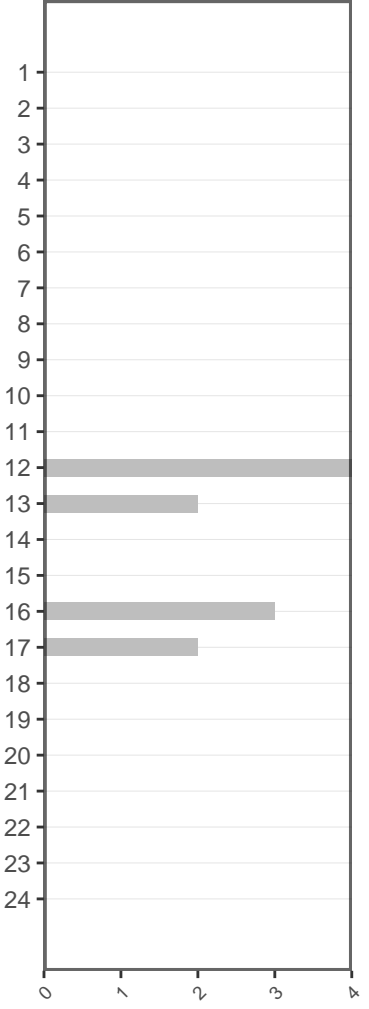
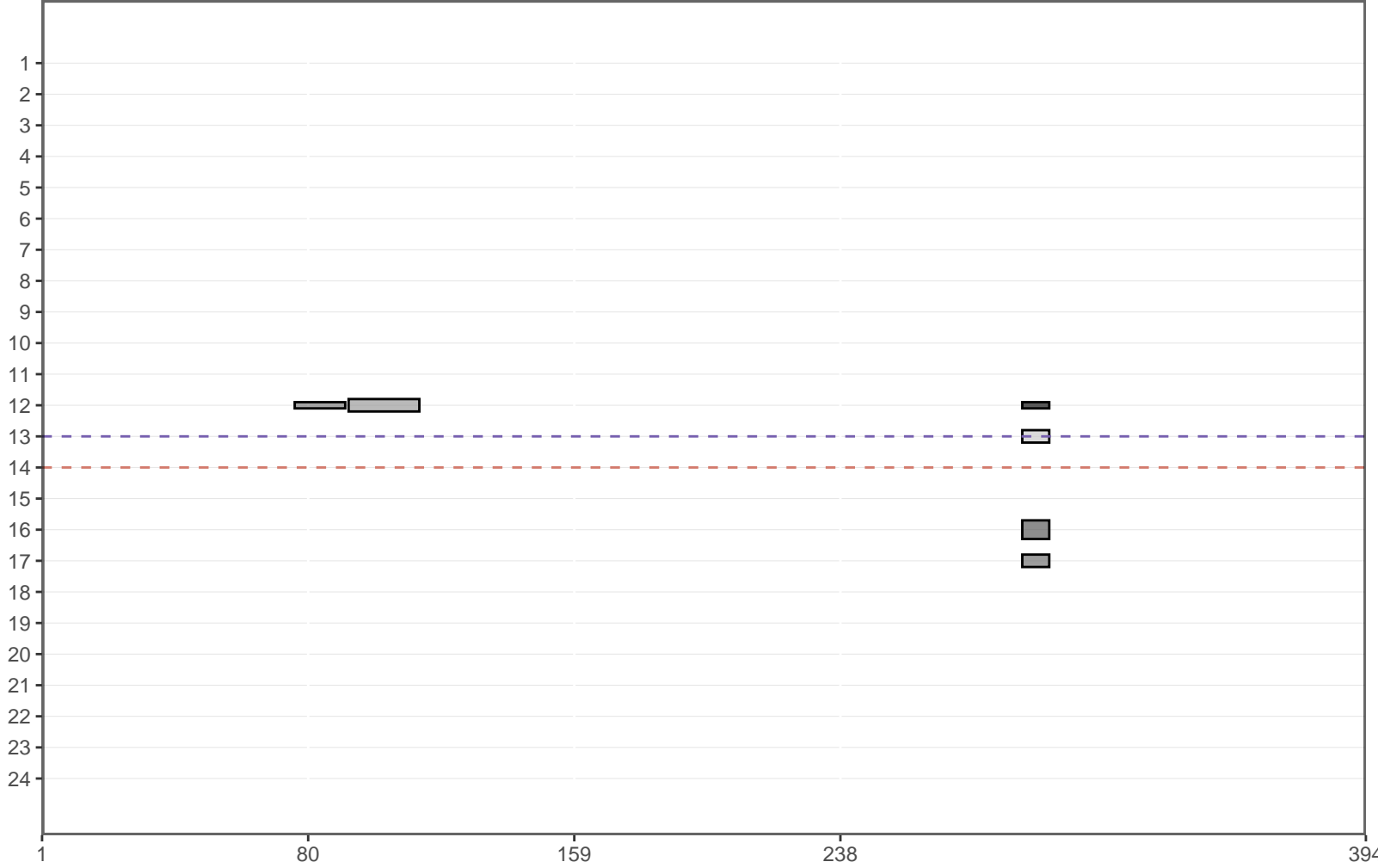
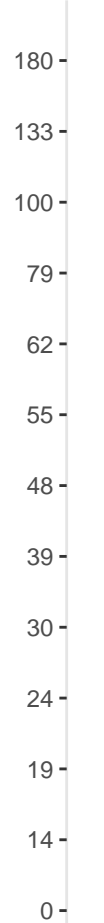


MW indication



Molecular weight

Gel Slice

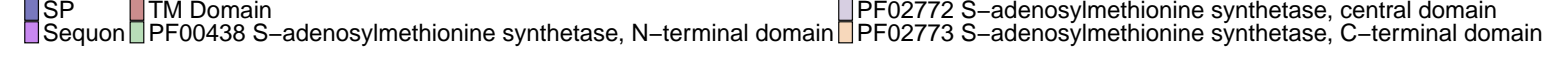


Protein length



Pfam domains

Pfam Description

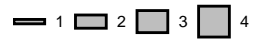


Protein sequence:

MVPPVRYHTVLISTGHDETVTNDEIARDLKEHKVPIPEKYLDEKTFIHLNPSGRFVIGSPHSDAGLTKRKHIDTYGGWGAHGGGAFSGKDPFTKVDKSGAYVIRQAQKSVASGLARRRQIVQSVYAVGVPEPLSVFVDTYGTGKIPQKEIKVVKENFDPRFGMISINLDLKRGGNGRFLKTAANGHFGRDDSDFTVEVVKPLKREKPGQ

NbL11g13000.1 cyprosin-like [MW - SP = 52.28 kDa]

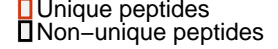
No. of times detected



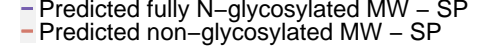
log(intensity)



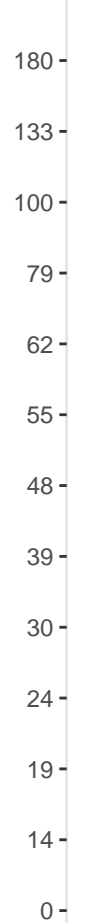
Values from



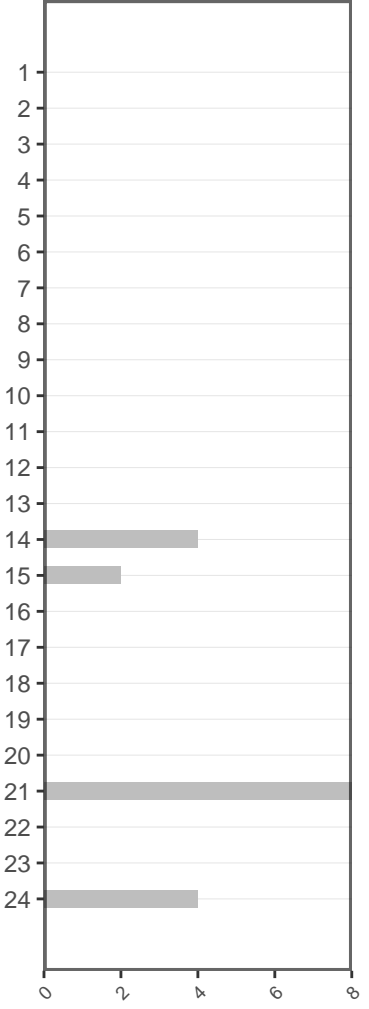
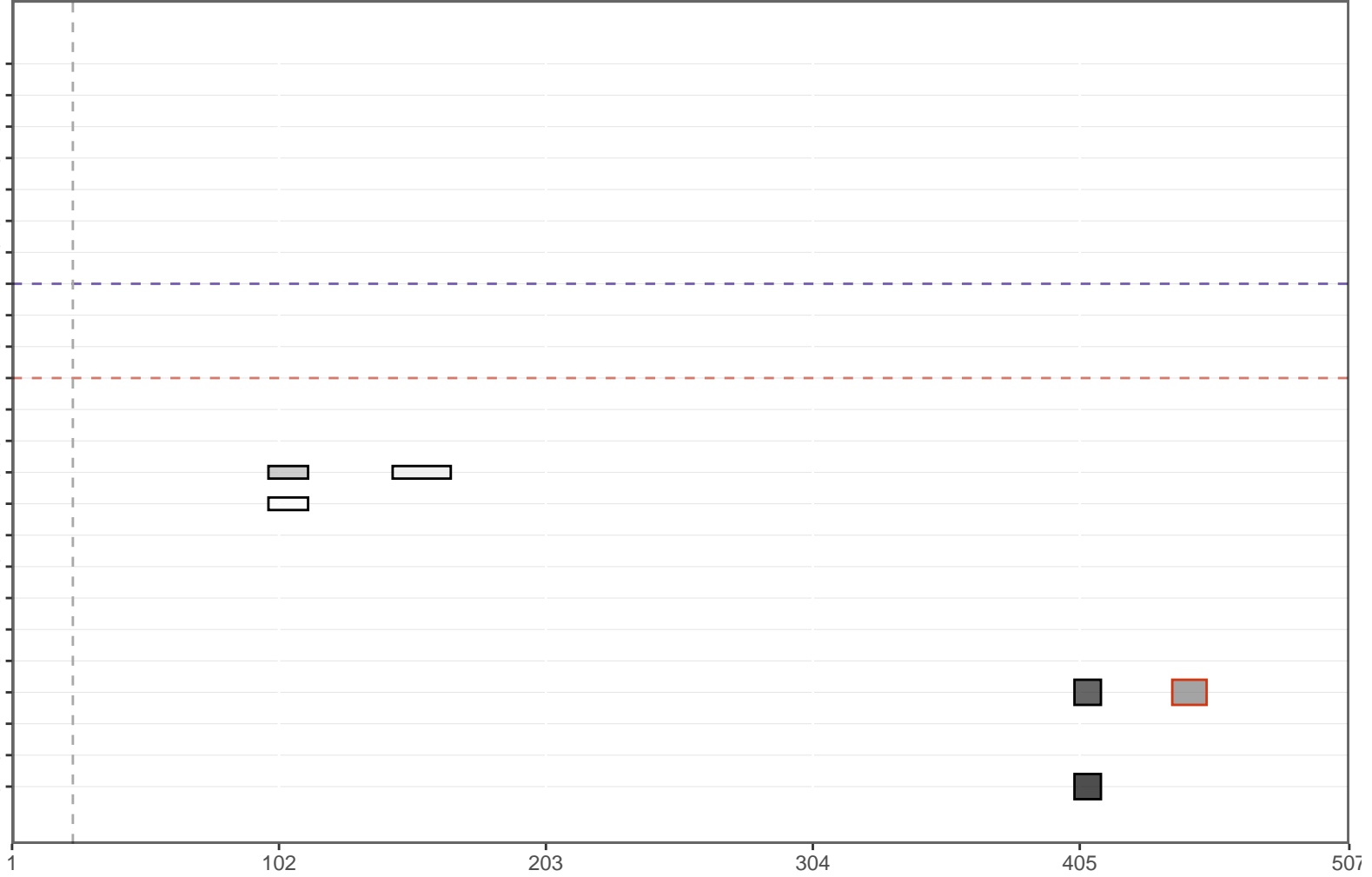
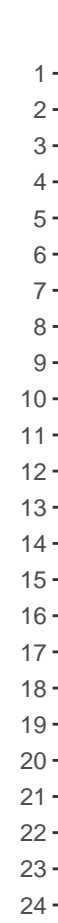
MW indication



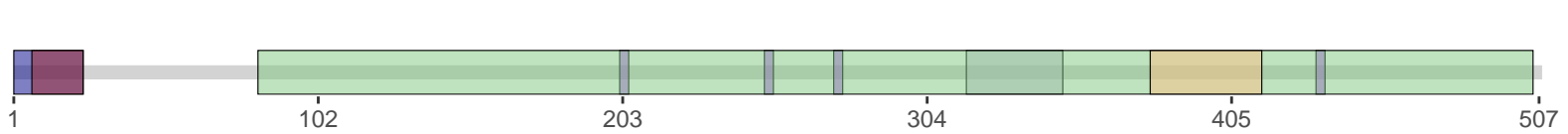
Molecular weight



Gel Slice

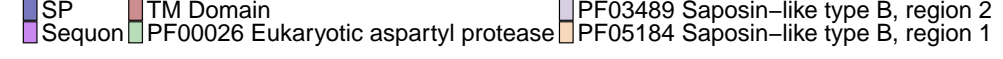


Protein length



Pfam domains

Pfam Description

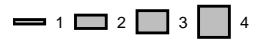


Protein sequence:

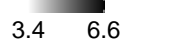
DSNIFKGNHTYVPLTQNGYWGDFNMGDFLGNASTGVGAGGGAADVSGTSLLAGPTTVVQINHAISGAEGVVSMECKTVSGYGVEMIVNLLVSGVRRPQVCGDAGLGFYNGAGHVSNNIRTVVEREAEGSSVGEAPLCTAGEMAVVMMQNLKQKQKTRVLEVVNLGCKLPSFMGESVDCMISAMPNIFETIKDQAVVLTPEGVYKLTGEGATRGISGFALNPPFPGLWLGDFVFMGVYHTVFDVGNRSLGFQEAIV

NbL11g12940.1 FK506-binding_protein_5-like [MW = 82.85 kDa]

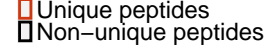
No. of times detected



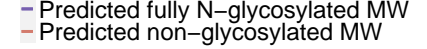
log(intensity)



Values from

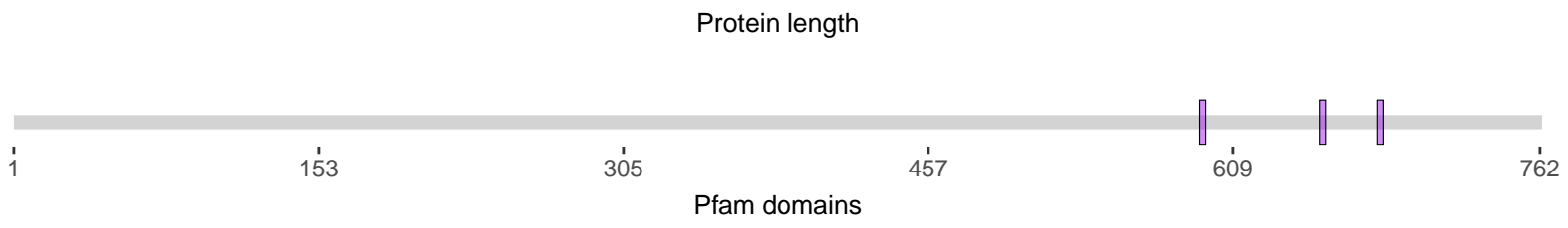
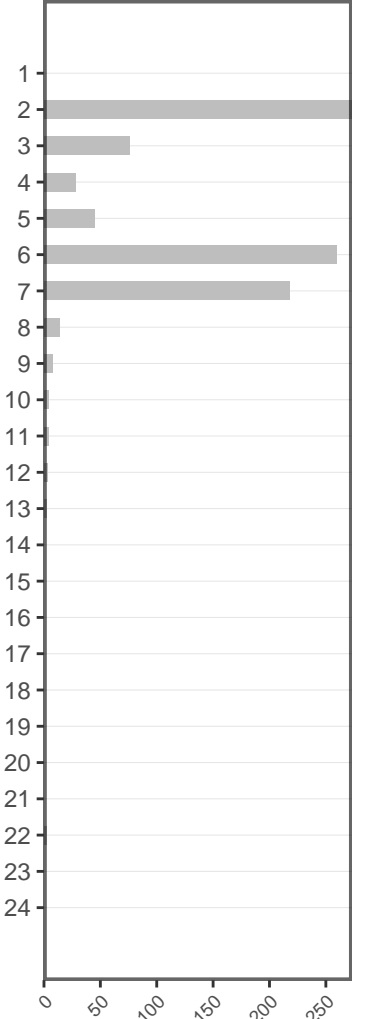
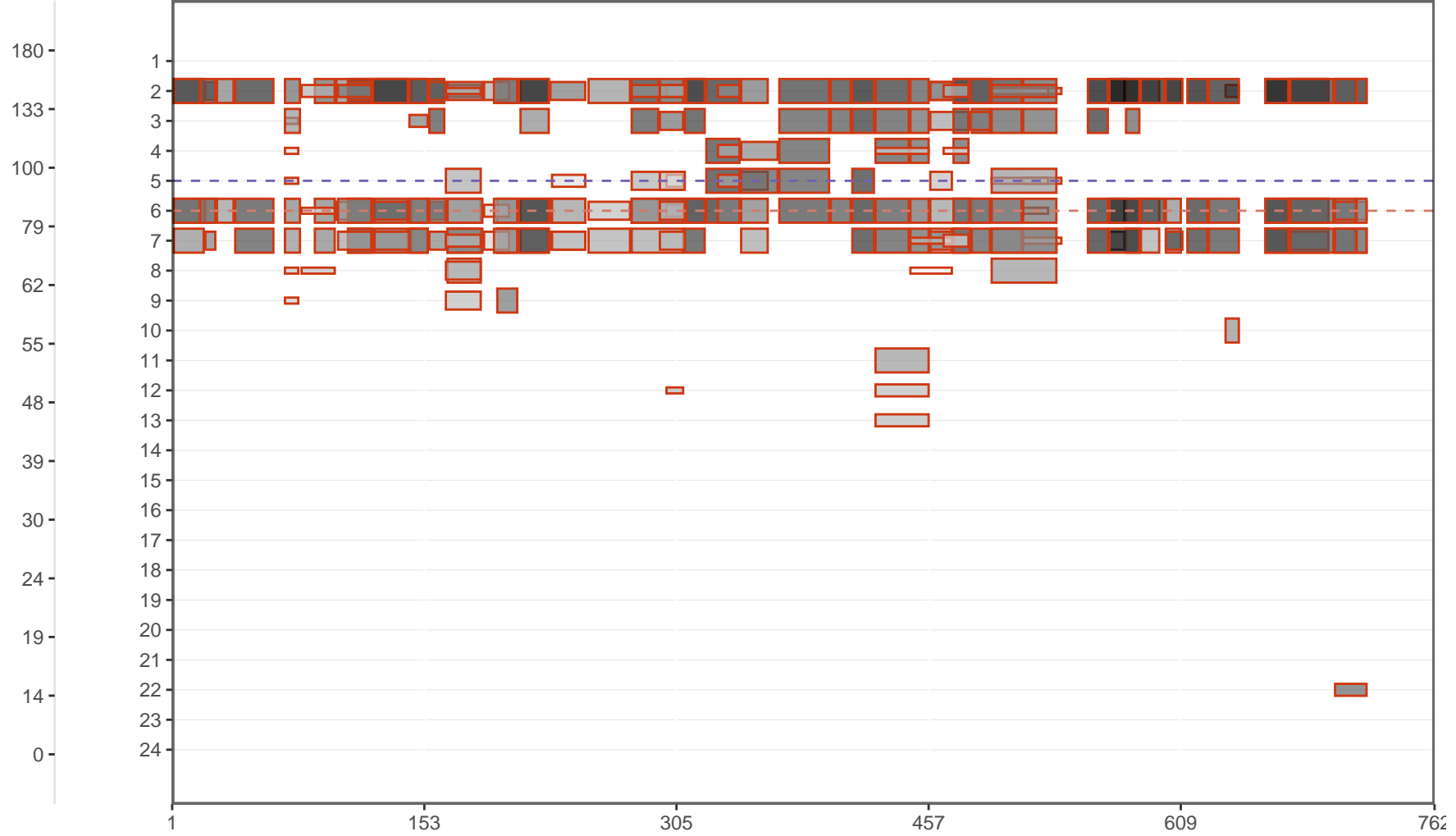


MW indication



Molecular weight

Gel Slice



Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

*YANKEPEEQPTTVDAVETPVGAVGNKNEGADLEAEPQKTVVTVSDVPAEPKEDISVAPSSEKPTATEKDFEVDGEAVTGKEAIPVDKVEAPKGGESLLAESGSKATSTFSLGMLMKTDEESPAEVDGNVAVVEEKEHESVPEATVAEAPKKEVEKVERETKDKYKTDQDQKGEKTVASEELAAPPDAKVVVETSEVAEKAPEVEISSRDMEPLAENESTKDKENIVTTNDQDEKREKVAEELAAPEAKVYETSEVAEKKVPELEIAGRDIENKNGSKQKDEKIAASEAN

NbL11g12930.1 probable_carbohydrate_esterase_At4g34215 [MW - SP = 27.28 kDa]

No. of times detected



log(intensity)



Values from



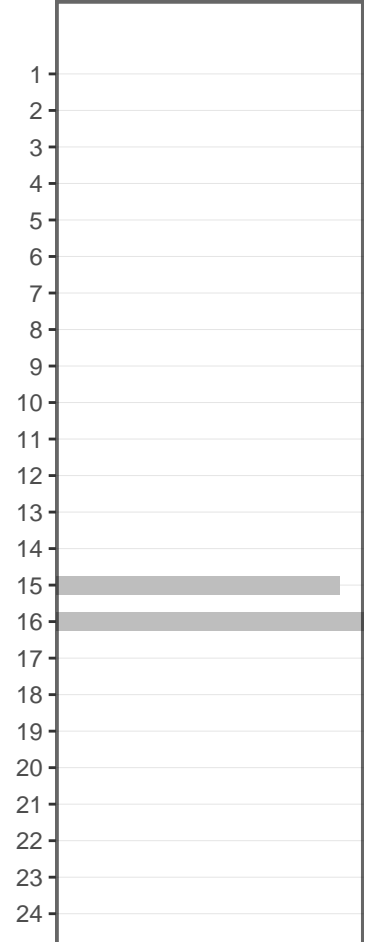
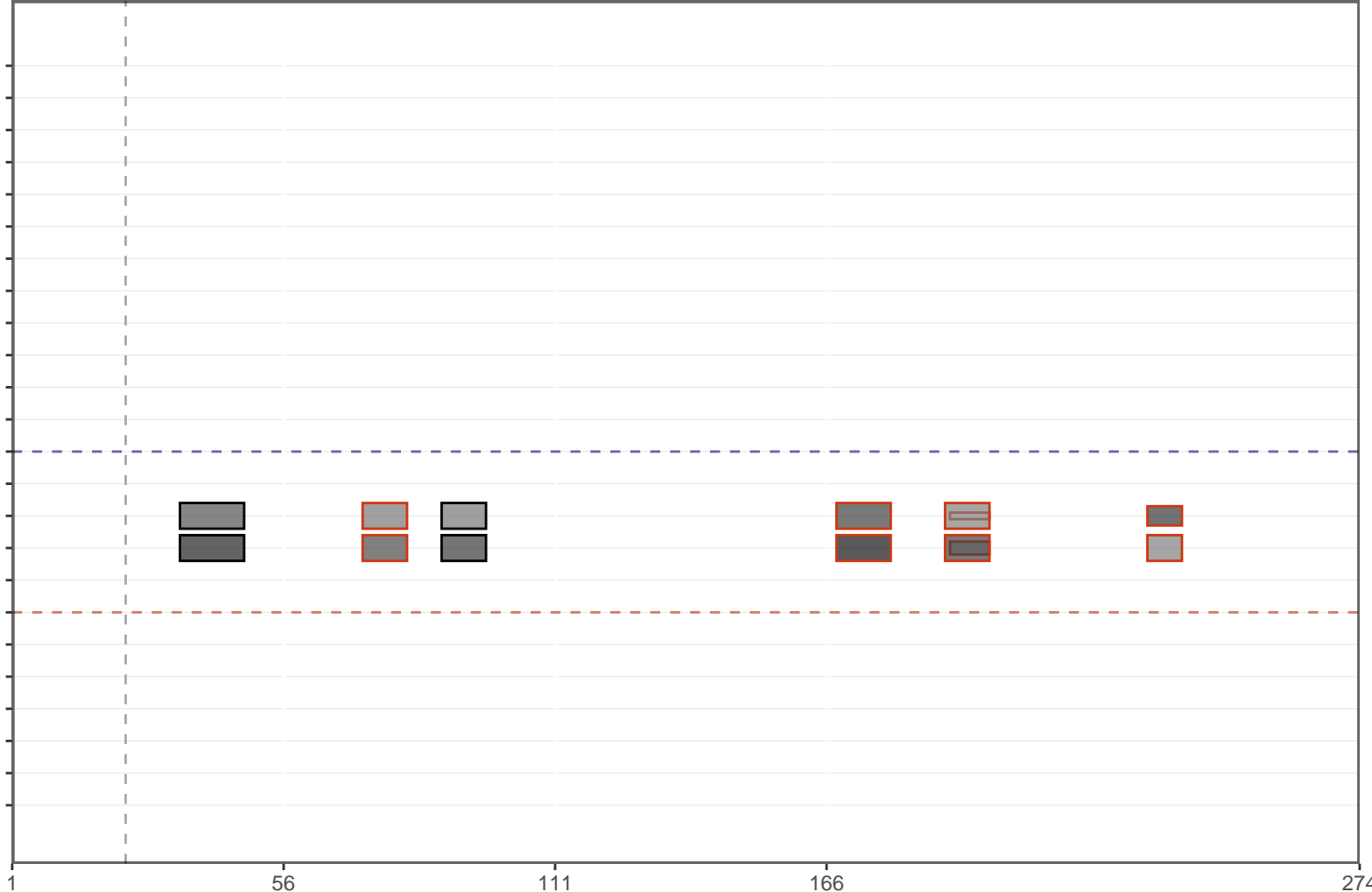
MW indication



Molecular weight

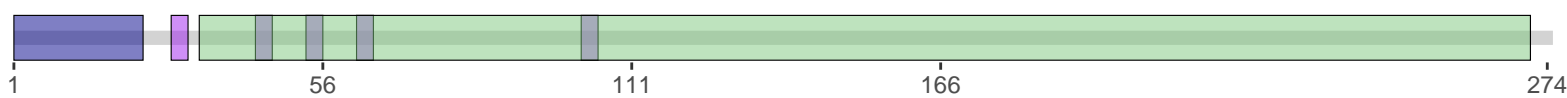
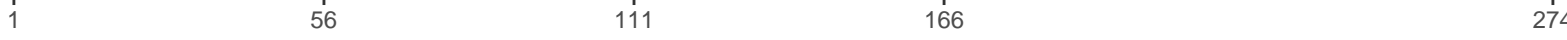


Gel Slice



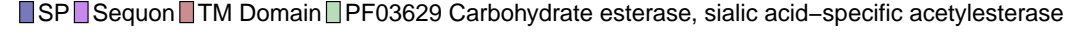
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IIVGIVGLYPCAVGGTSHIEWAFQDFLYKGMIRRTKATRFQGRVRRALLWYDGEESDKTLEDAKMKRKRLEFFNHRHDLGLPTLPVQVGLATALGFYMELVKRAKREINQVNRVYDAKGLQVGPDIYALTTAAGIQLGMLDAFLRI

NbL11g12900.1 pectin_acetyltransferase_12-like [MW - SP = 44.2 kDa]

No. of times detected



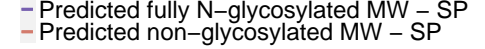
log(intensity)



Values from



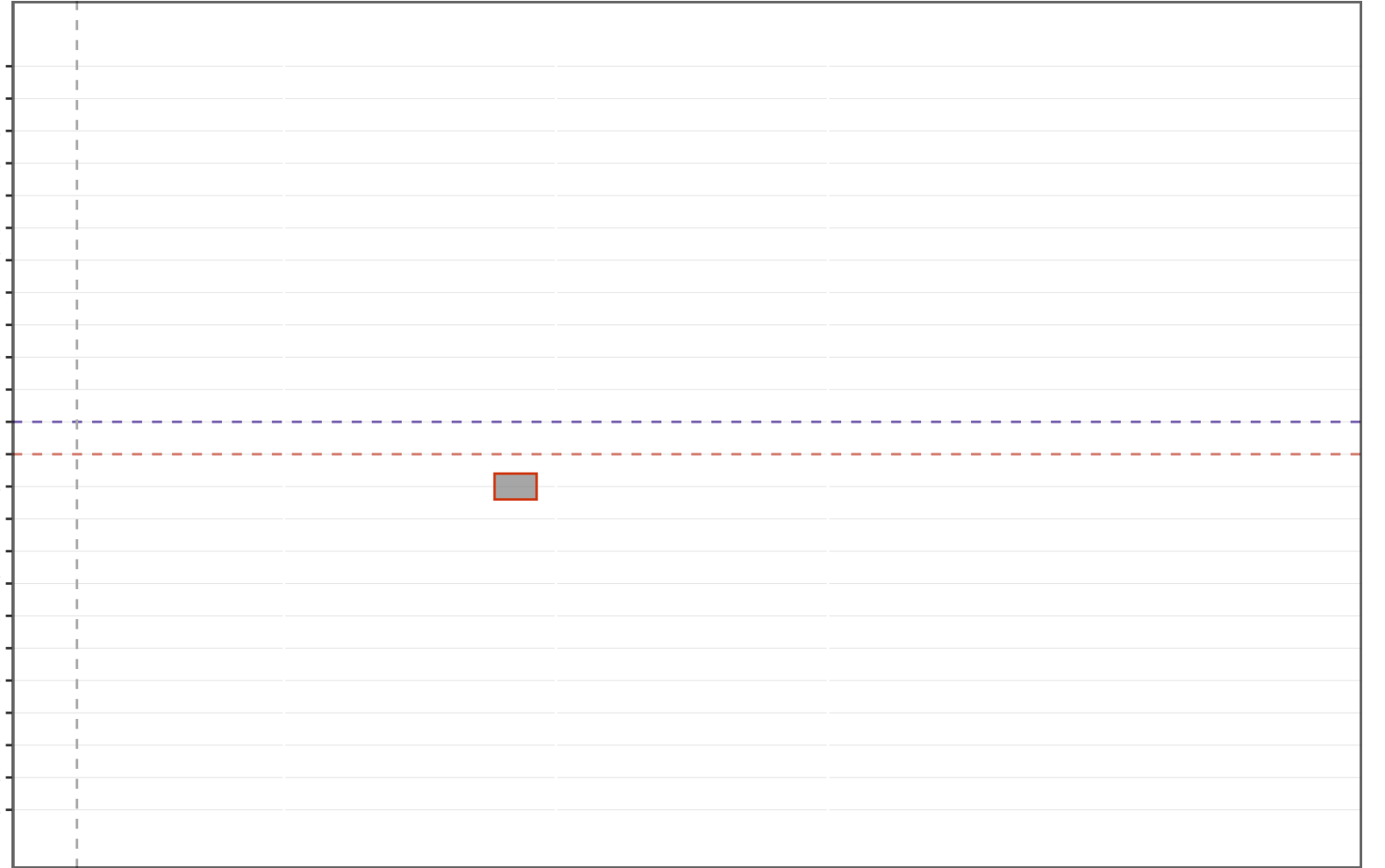
MW indication



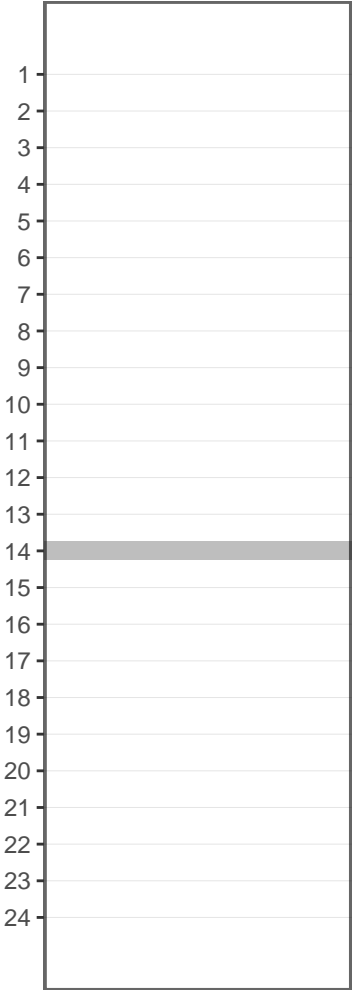
Molecular weight



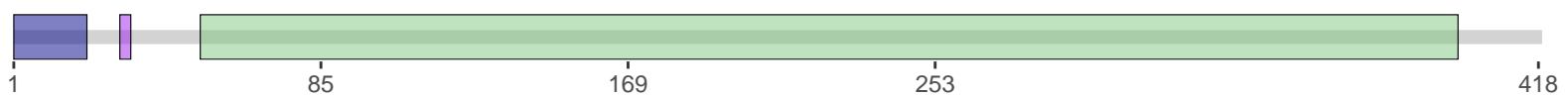
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LSGCSAGLASIMHDDFRNLPHSTKWKGLSDAGLFMDAVDVGGRRLRNFVGGVVKLGGHKTLPRCTNHLDTSGFFPENLNKIKTFLFLNAVDSWQLQESLAPRGADPHGWHDCITLNERGSPSQHFLQGFRIHMLNKKRFAAARGNGLFNSCFAHGQSERQDTWFDSDNSPMINKPALAVGDIWYFDRSGMKAIDGAYPCDRTCHNLIFR

NbL11g12890.1 flap_endonuclease_1 [MW = 45.89 kDa]

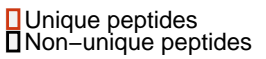
No. of times detected



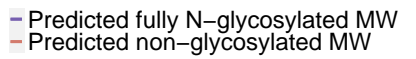
log(intensity)



Values from



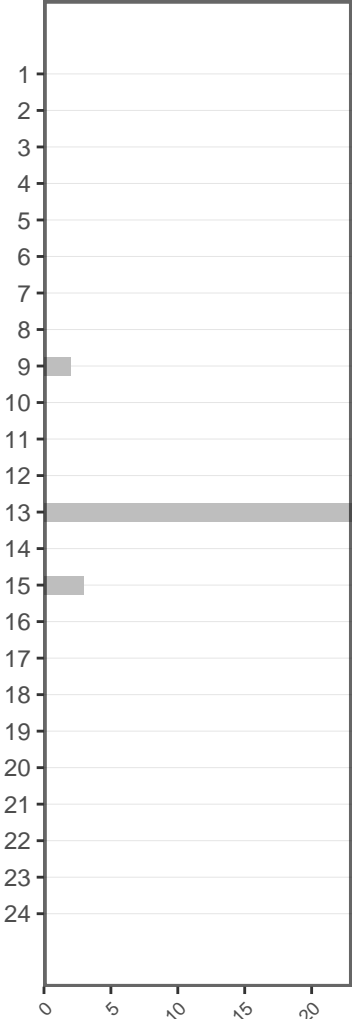
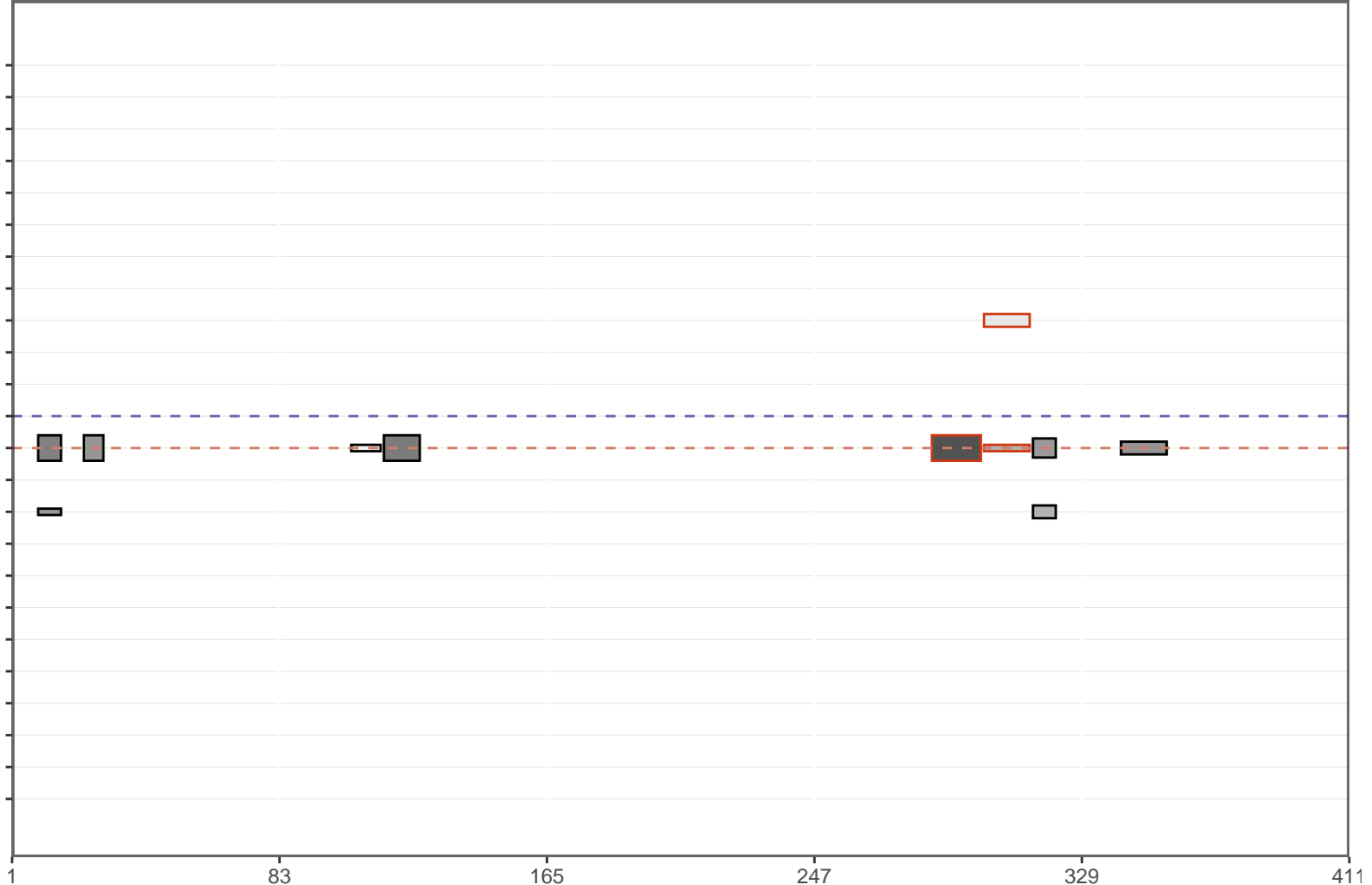
MW indication



Molecular weight

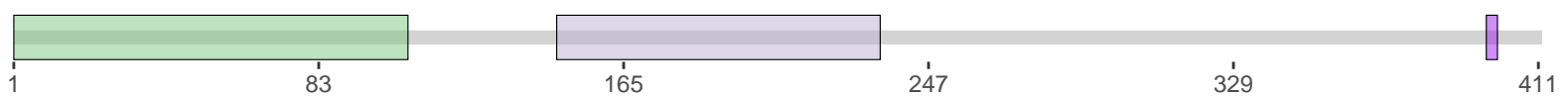


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

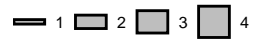


Protein sequence:

LRHLMDPSSKQIPVMEFDISQLELELEMDQFDLGLGGCDYDSDIRGIPOTALKLVRRHGSMEGLENNKERYQIPDDWPYEEARRLFKEFLVADDEGTLEKWAAPDEEGLNVLVYKENGFNDRIVTKVAEKIKTAKTKSBGGRLSFFKPIVSTAPVWRKGTGCVLVSFNPVTKFKTLGLGSRPMVLGGQIFPSLDLGSNYVPLSRHVFQGT

NbL11g12850.1 nectarin-1-like [MW = 26.36 kDa]

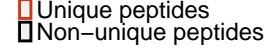
No. of times detected



log(intensity)



Values from



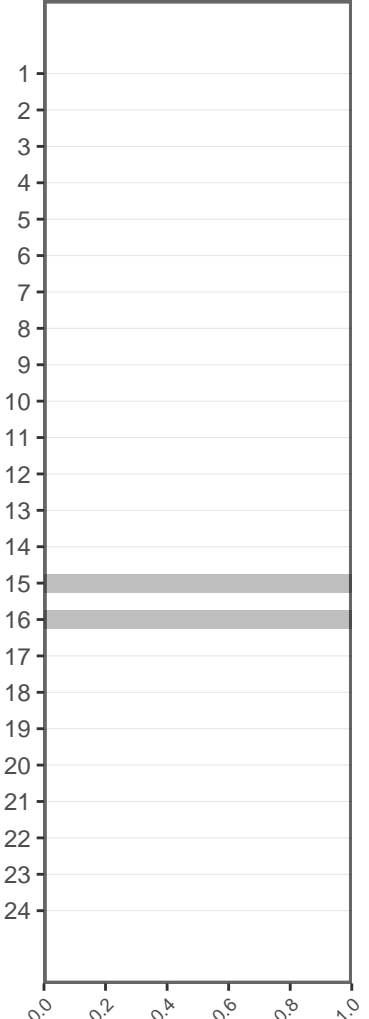
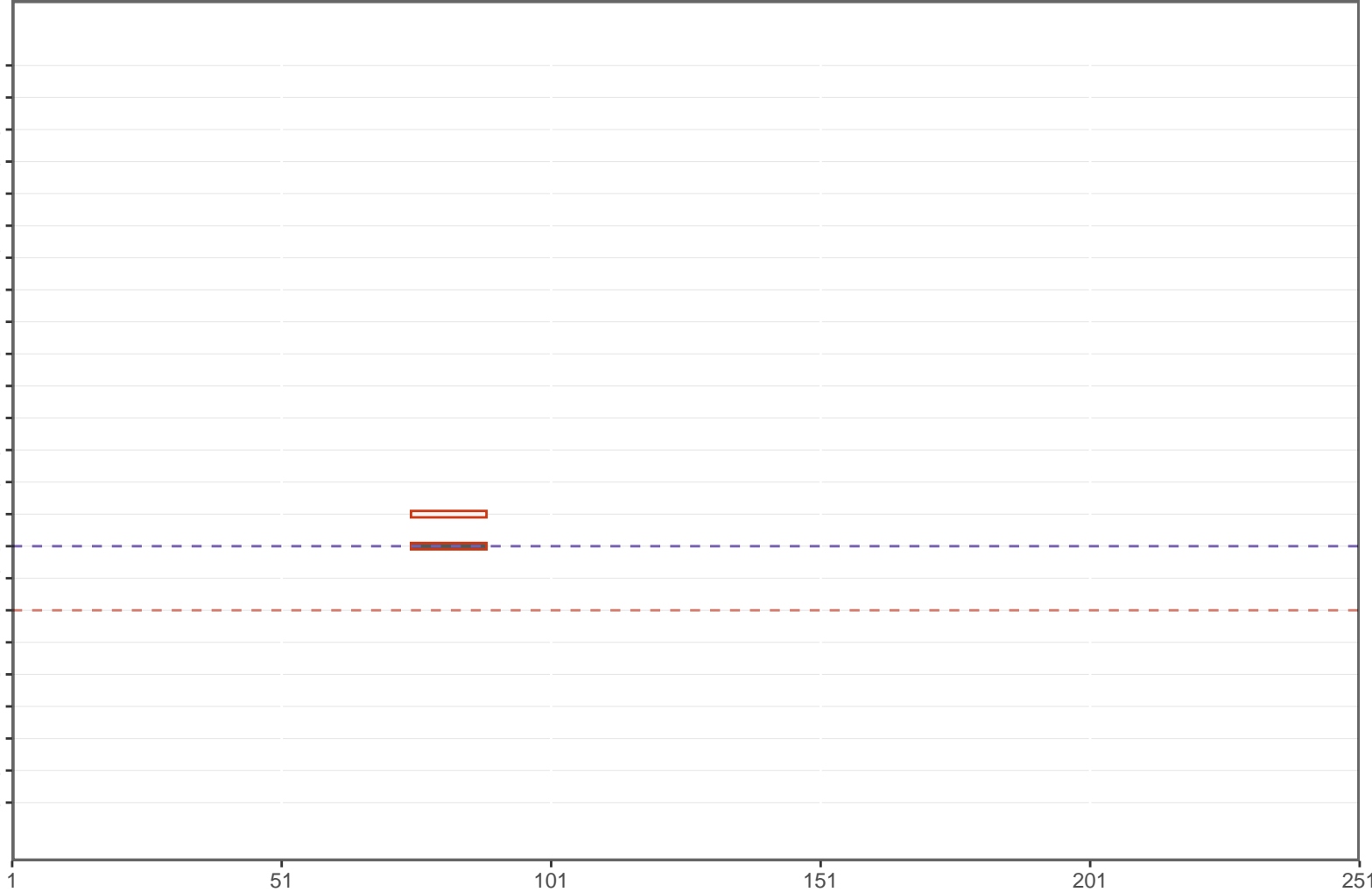
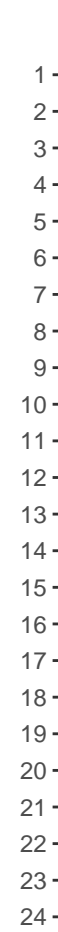
MW indication



Molecular weight

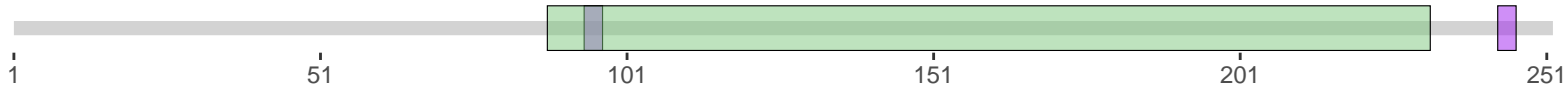


Gel Slice



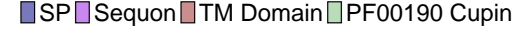
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

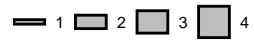


Protein sequence:

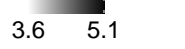
ITLGVSLARIDYAPGGINPRHPRATEMYYVLSGQLVGFITANLVKRVVGGVEVAFPRGLVHFGKNGKVPAAVAGFNSQLPGAQSMATLFAASFVFDVLDGQFQNTMVGQKIKRFAPGNRISFVY

NbL11g12840.1 nectarin-1-like [MW - SP = 20.65 kDa]

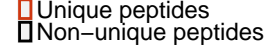
No. of times detected



log(intensity)



Values from



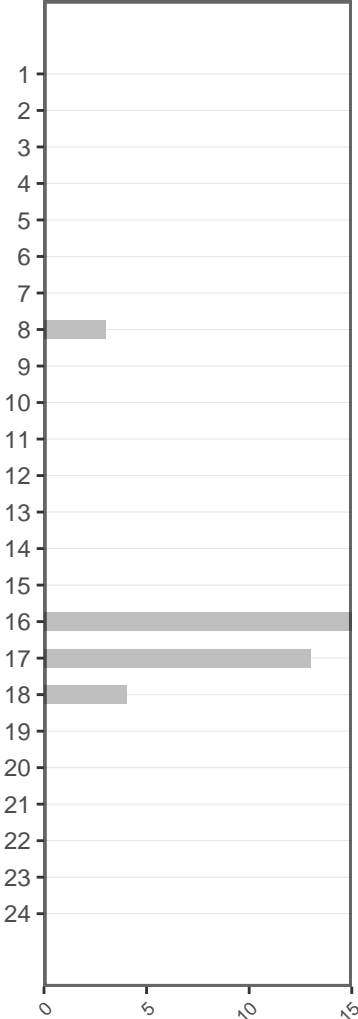
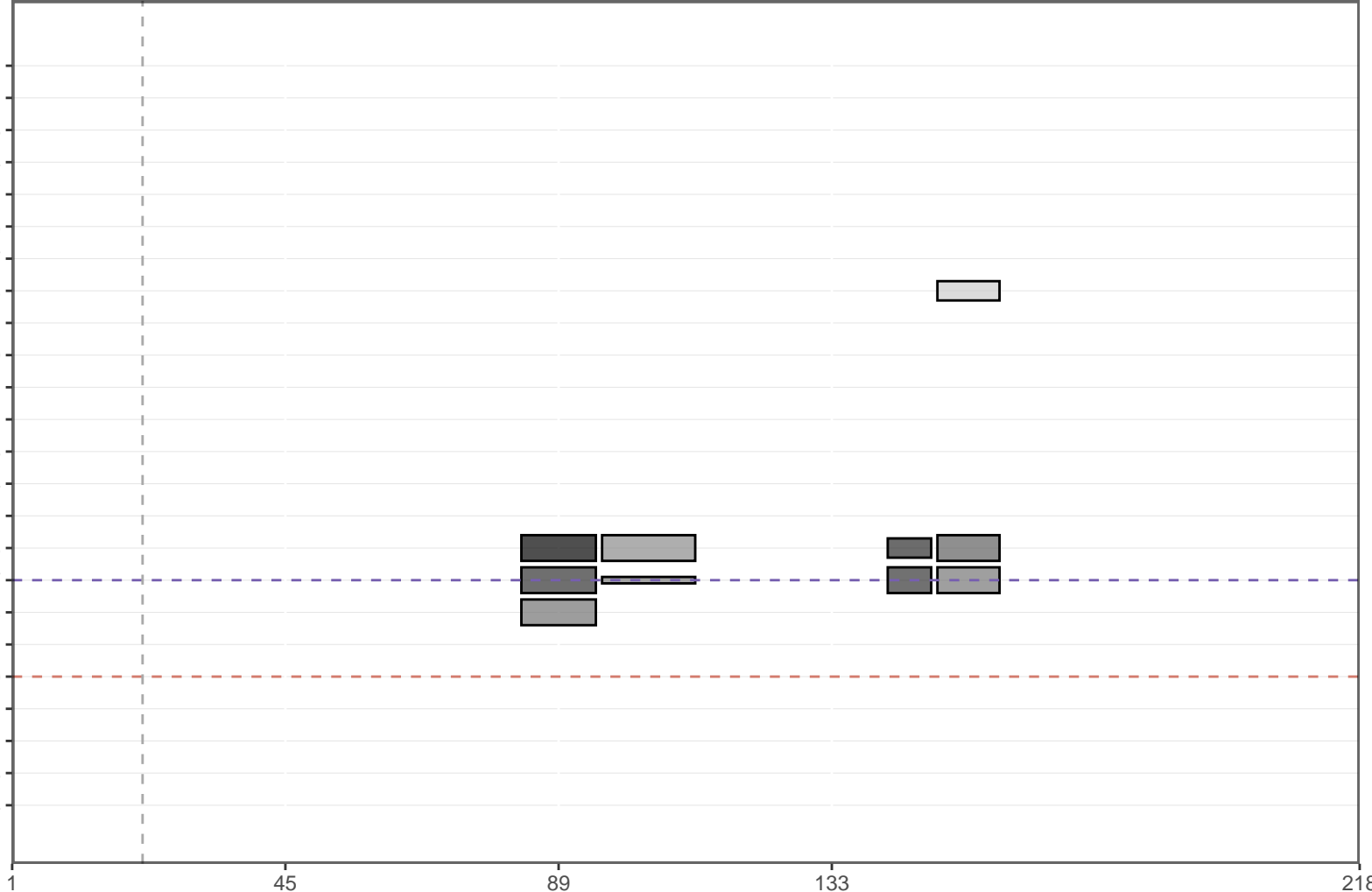
MW indication



Molecular weight



Gel Slice

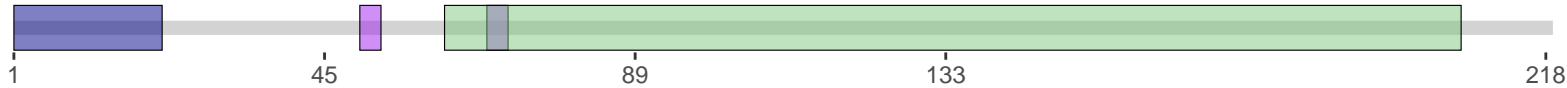


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

RIDYAPGGINPPIHTIPRAEMFVTEGELDVGRTTSNVLKSHIKVKEVVFVFKGLVHFQGNNGKVRVAWVAAFNSQLPGTGSIAITLFASTPTVDPHVLTKAFQIGTKGVKIKRRLAPKK

NbL11g12830.1 glutamate--tRNA_ligase_cytoplasmic [MW = 86.8 kDa]

No. of times detected



log(intensity)



Values from



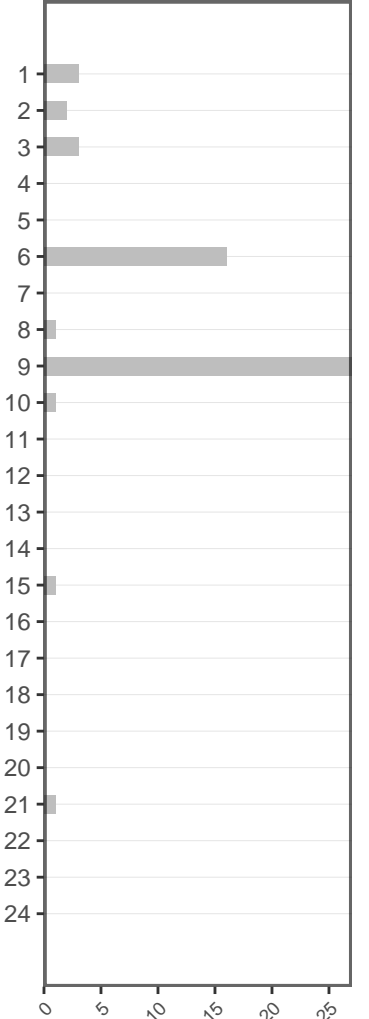
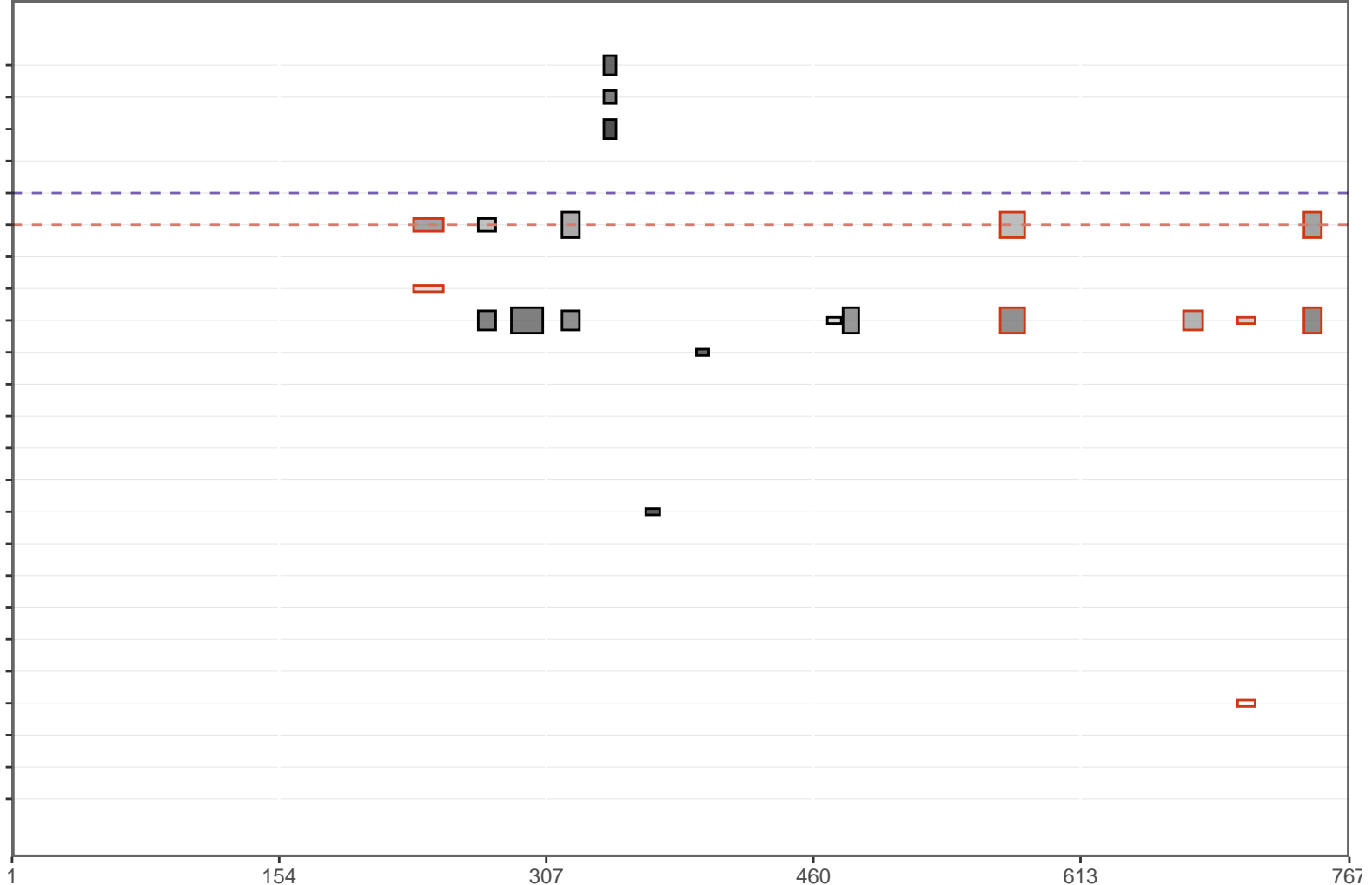
MW indication



Molecular weight

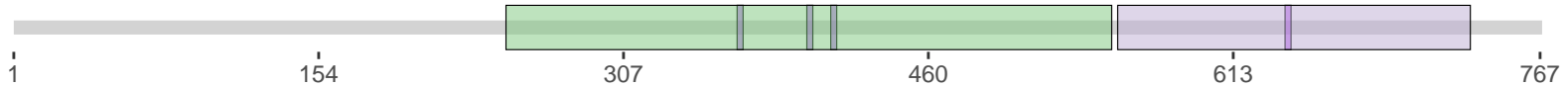


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00749 tRNA synthetases class I (E and Q), catalytic domain
- PF03950 tRNA synthetases class I (E and Q), anti-codon binding domain

Protein sequence:

LKLVKEMAGSERGTMGCVIRGKLMDDFNKVRDPVYYRGNKTPHRRIGAKYKVPYTFYDFACPFVDVAVEGITHALRSSEYHRRNDQYYRIGTDMGRFVHYEFSRLNLYVTLLEKRRKLWFFVGNLVEGWDDPRFPTVGGVIRRGLKIEALHFILEGGASKNLNMEWVKLWANKKLEDPVCRHTAVIEERRVLLTSLNGPDDPFVIRVPHKHKYAGAGEKATYYSKRWDVDDAVSISVNEEYTLMDVGNNAVKEIKDQEGNTHLEGLHLEGSYKTKLKLTLVLP

NbL11g12700.1 endoglucanase_25-like [MW = 68.69 kDa]

No. of times detected



log(intensity)



Values from



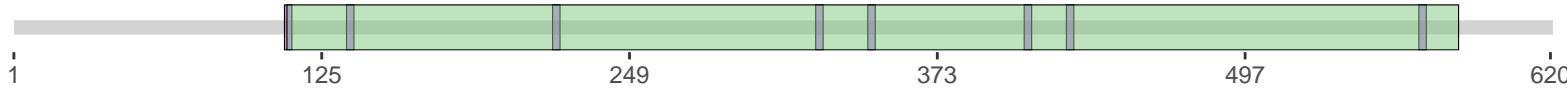
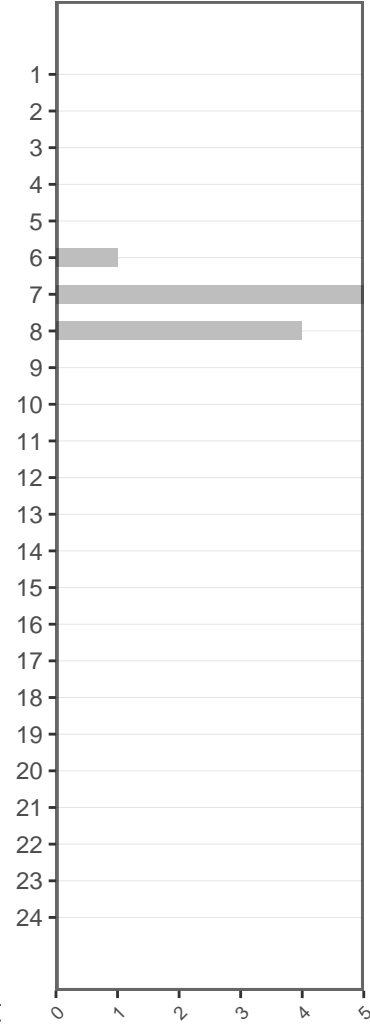
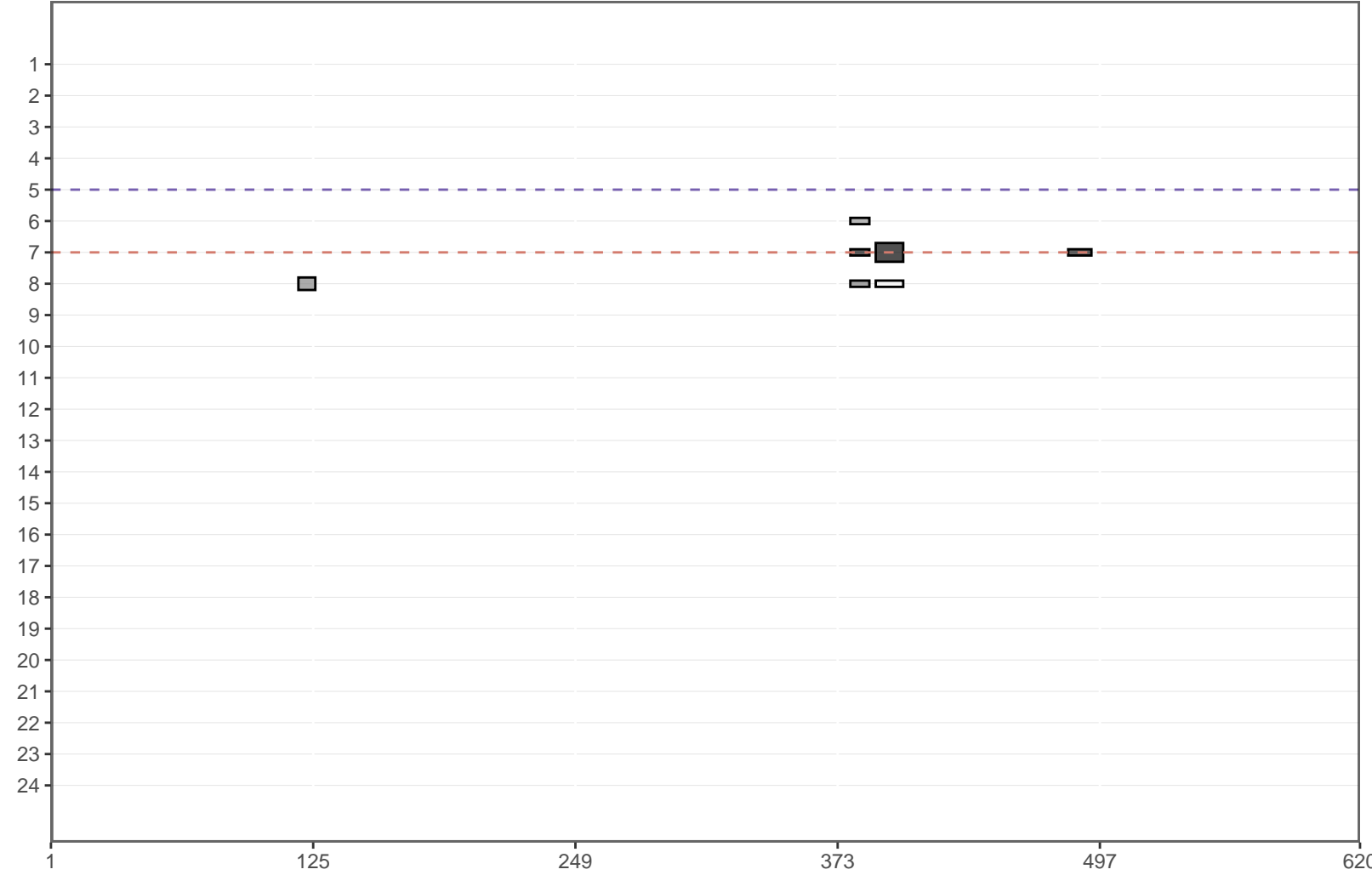
MW indication



Molecular weight



Gel Slice



Pfam Description
 ■ SP ■ Sequon ■ TM Domain ■ PF00759 Glycosyl hydrolase family 9

Protein sequence:

GAKTLFKSRDQRGRVYGVGNEAETFNSTGVWDEFIWAAMLYATGNSVYLQLATTPGLAKHAGAFWGGPDVGVLEWQNKLTGAQVLLSRMRLFLSPQVYVEELKTFHNGTSSIMCSYLPFTGSRNRTKGGGLQLNHGRPQLGVVNAAFPLATLFSQLEAADTPGVYCGFNFTYSTDVLRFAETGIDYLGKQNRKMBVAVGFGNHYPKRVHHRGASIPKPKVKKHCKGQKWRDSSKANFNINVGAMVAGPDKHDGFHVRISNKNYTEPLAGNAGLVAALVS

NbL11g12640.1 probable_leucine-rich_repeat_receptor-like_protein_kinase_At5g49770 [MW - SP = 101.86 kDa]

No. of times detected



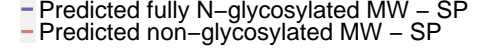
log(intensity)



Values from



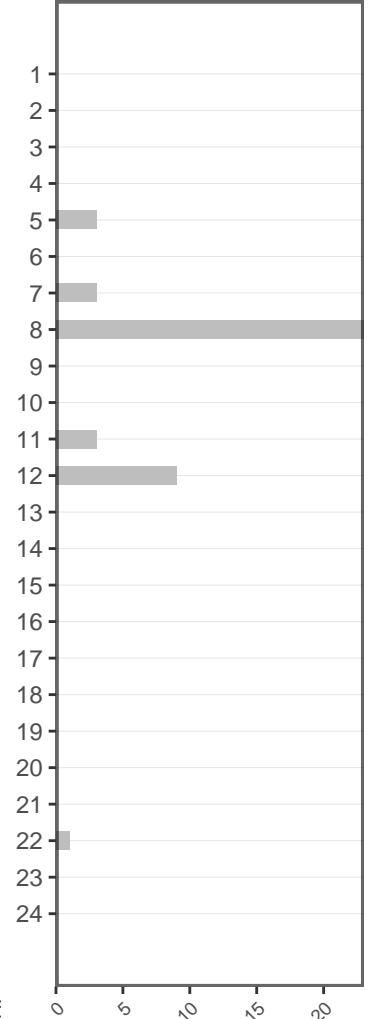
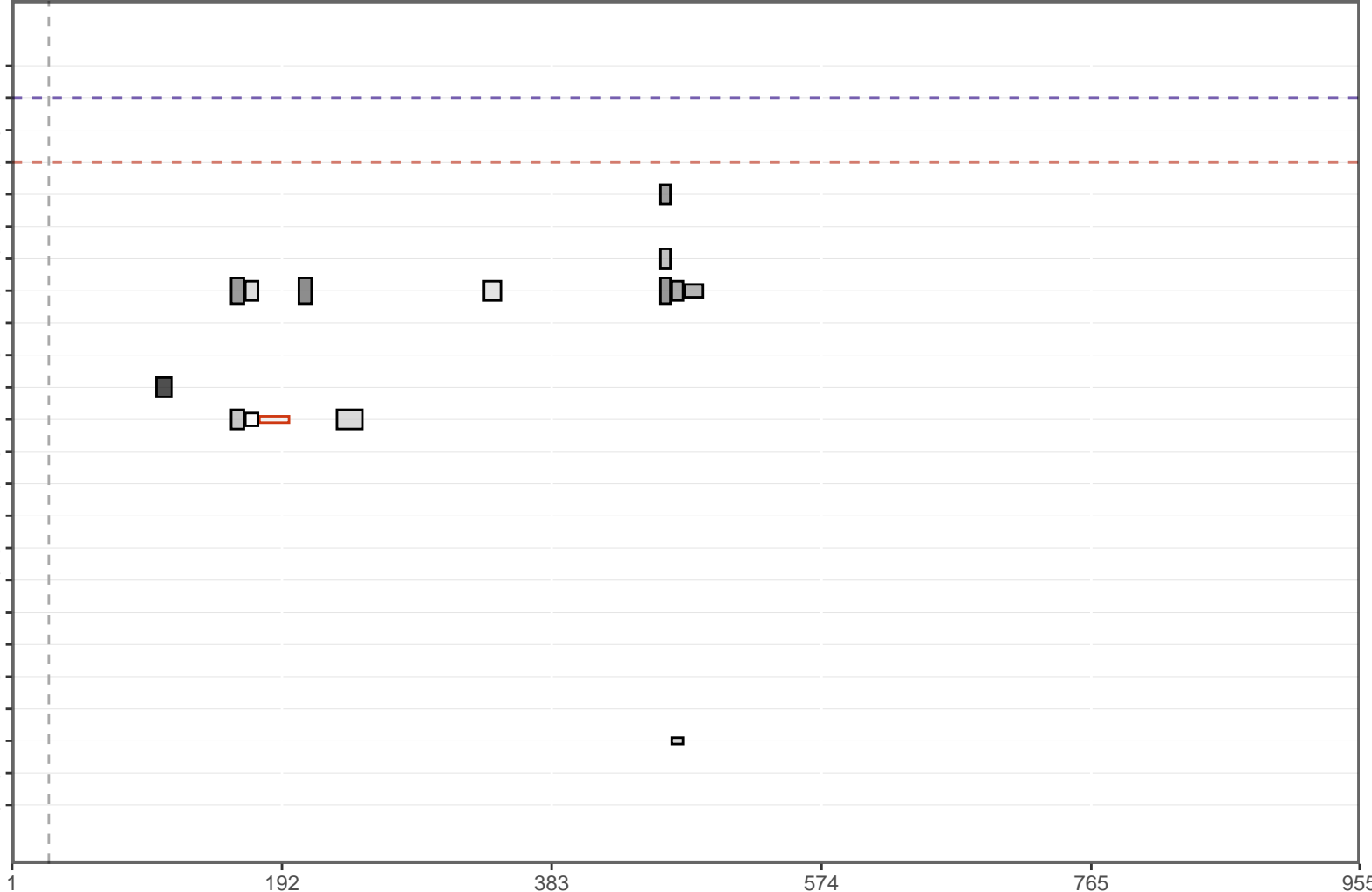
MW indication



Molecular weight

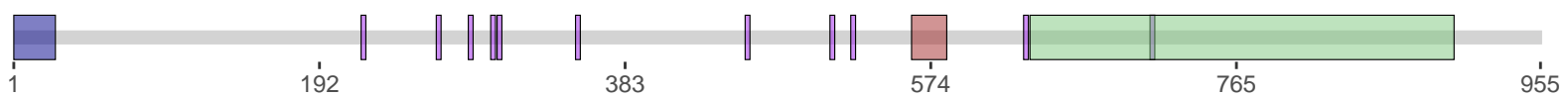


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

QKSLMLTQNRQLPFDVSLNFTKLDLHLVHVGFRS60DFNRRTGVS6GIGVLSNGTFRPSTGPFPPFGEYKVFDSAGTGHK66SSTGHGAAGVGSVLLVLAIVGIFRQKRAEDADRNDPFASWDSNKHSGAVPQLTGARFFSFEELKKMTNFFSETDNGSGGKQVYRGTLPNGQLVAVKRALGGSMGDALEFRTEIILSRVHKKVVQLVGFQDQAEQMLVVEYIPNGTLKNDLSGKTKGIRLDWMRRRLKALGAARGLQHLVDLNPPIHRDKS

NbL11g12600.1 cinnamoyl-CoA_reductase_1 [MW = 35.78 kDa]

No. of times detected



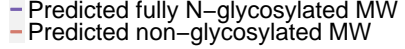
log(intensity)



Values from



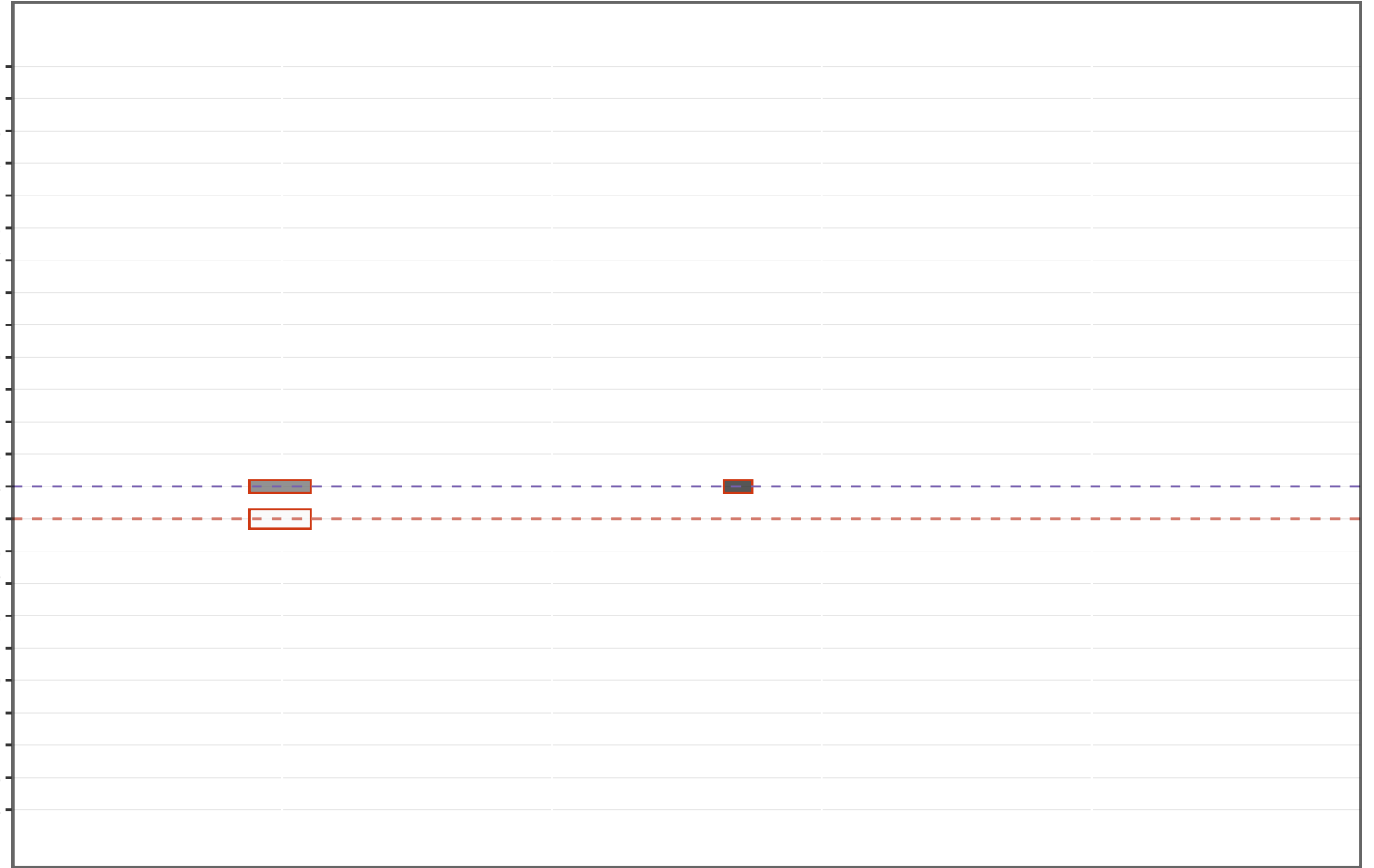
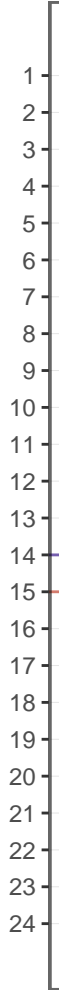
MW indication



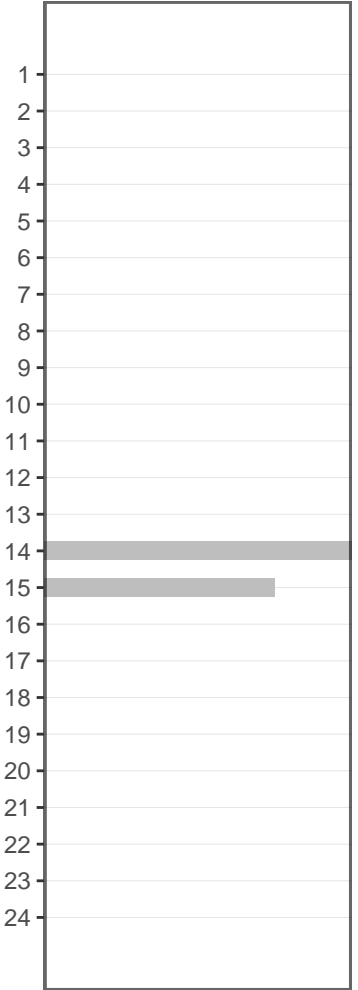
Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

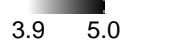
LDLDYCKSRQKQWYFVVKTLAEKTAWEFAEKNGLDVAWNPATDGLGQLLQPLGNASCAVLLGQLLGGSTDTQEYHWLGAHVHNDVAKAQLLFESPHASGRHLGTNGIYQFGDFAERVSKLYPEFFPHRIFETGETQPLVGGKDAKKLIDLGLVFTSVEGDAVRDTSLSKTKGFLKGGQGN

NbL11g12420.1 cullin-associated_NEDD8-dissociated_protein_1 [MW = 134.57 kDa]

No. of times detected



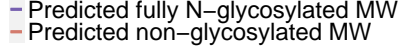
log(intensity)



Values from

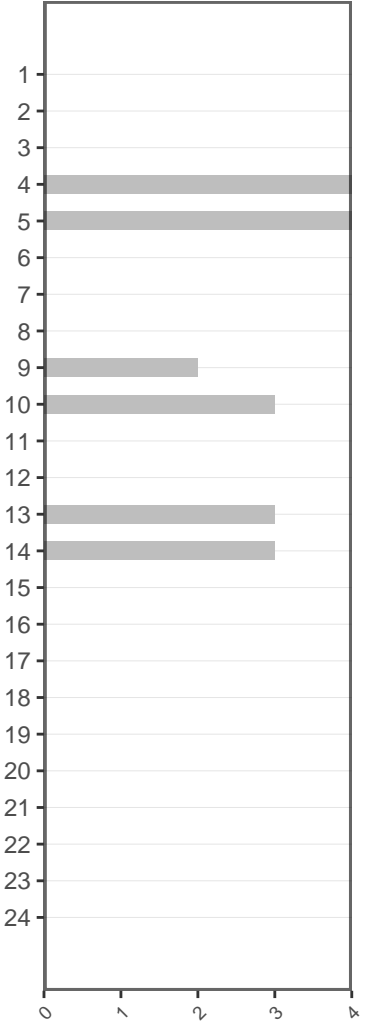
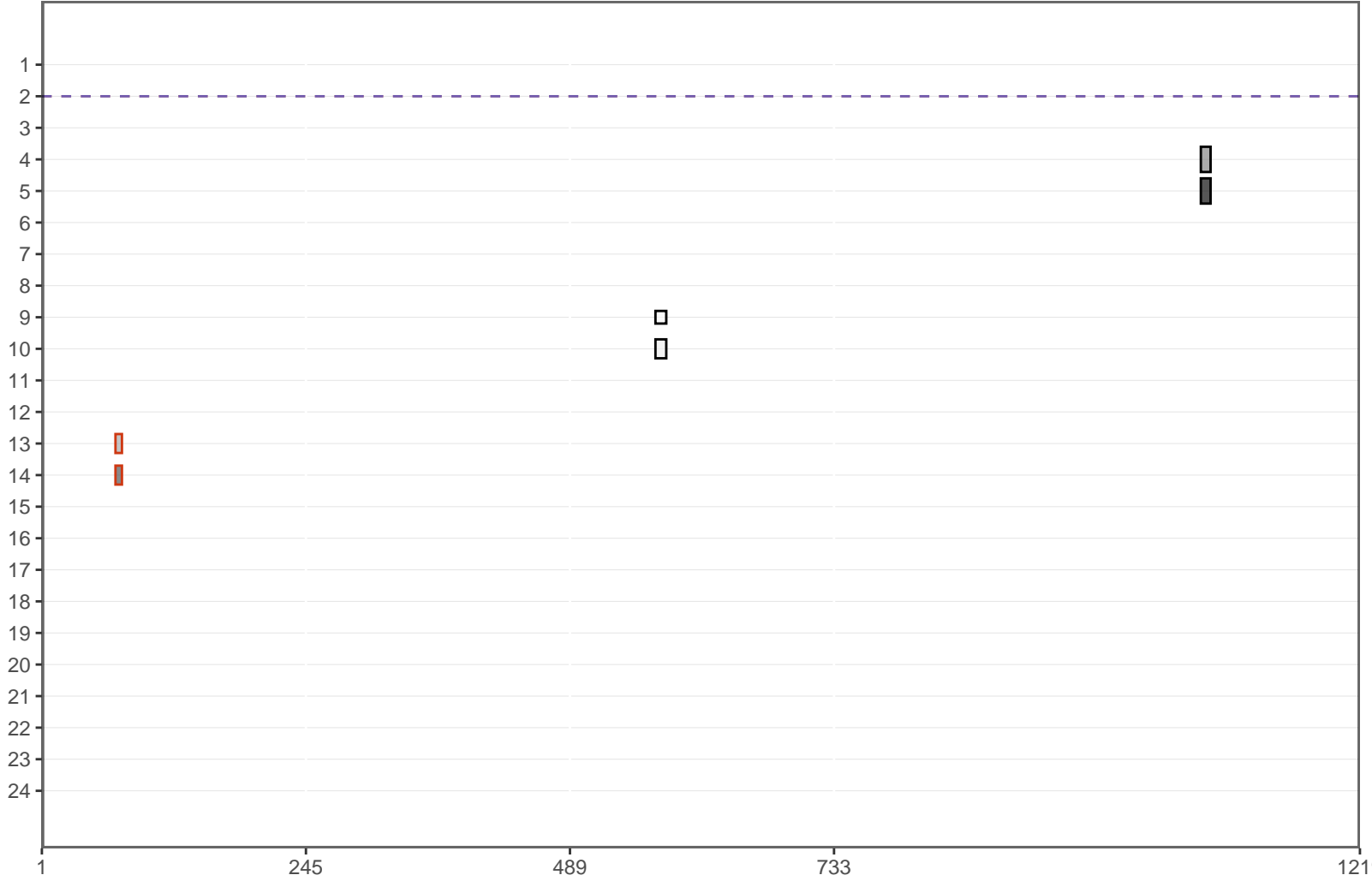


MW indication



Molecular weight

Gel Slice



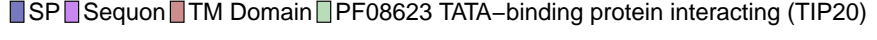
Protein length



Pfam domains



Pfam Description

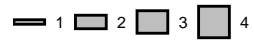


Protein sequence:

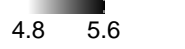
DHLQAEISACLPVIVDRMSNEITRLTAVKAFVAASPLHLDLSCVIEGVISELTAFLRKANRALRQATLGTLENTLVAWGDKIGSAAYEVVMELESLDSDLHMTALELGCETLMADRSSANVGLTVRNKVLPGALTIVRSSLGGGALMALGNFFAALVYSANTSFDTLLDGLLSTAKPSPQSGGVTKGALFSIAGGVAVLGLAAGDGKSGSTVNMLEDLKKDSSSTNSAKQHLALLGLGEGRKDLGSHAHIEINIVEFQSPFEEIKSAASVALGNVAWGNLPKYLFFLDKI

NbL11g12200.1 cytochrome_c [MW = 12.2 kDa]

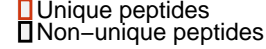
No. of times detected



log(intensity)



Values from



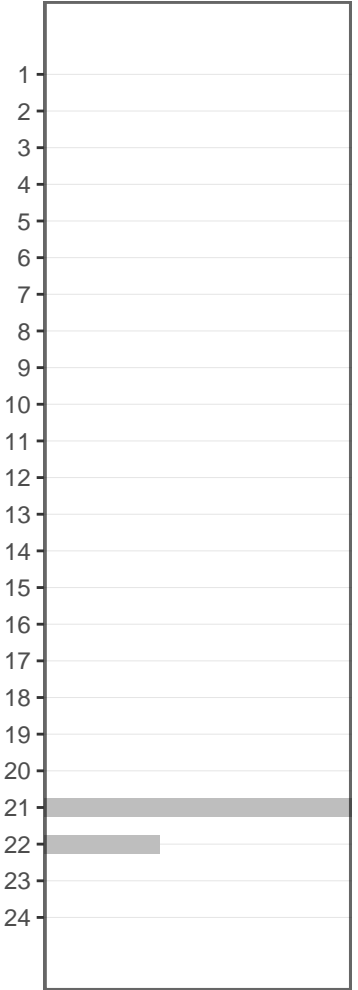
MW indication



Molecular weight



Gel Slice

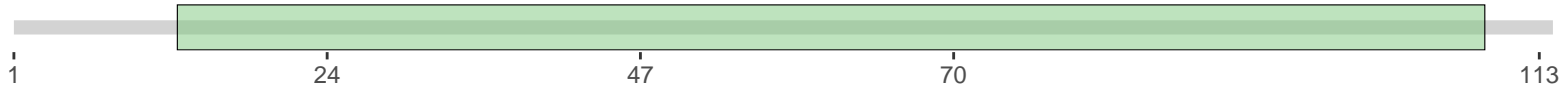


Protein length

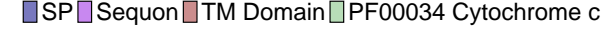


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

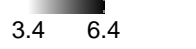
SLFGKSGSTTPGYSVSAANKNMVAWGGENTLVEYLLNPKKYPGDKMVFGLKPKQERADLWAKKETA*

NbL11g12120.1 ras-related_protein_RABD1 [MW = 22.43 kDa]

No. of times detected



log(intensity)



Values from



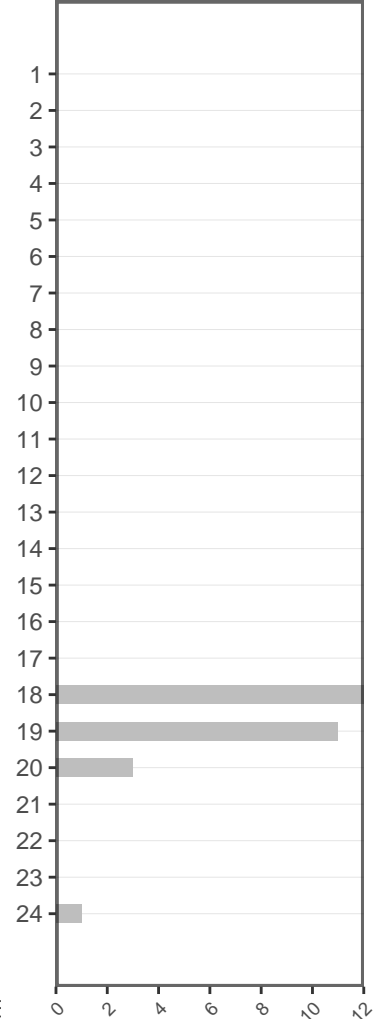
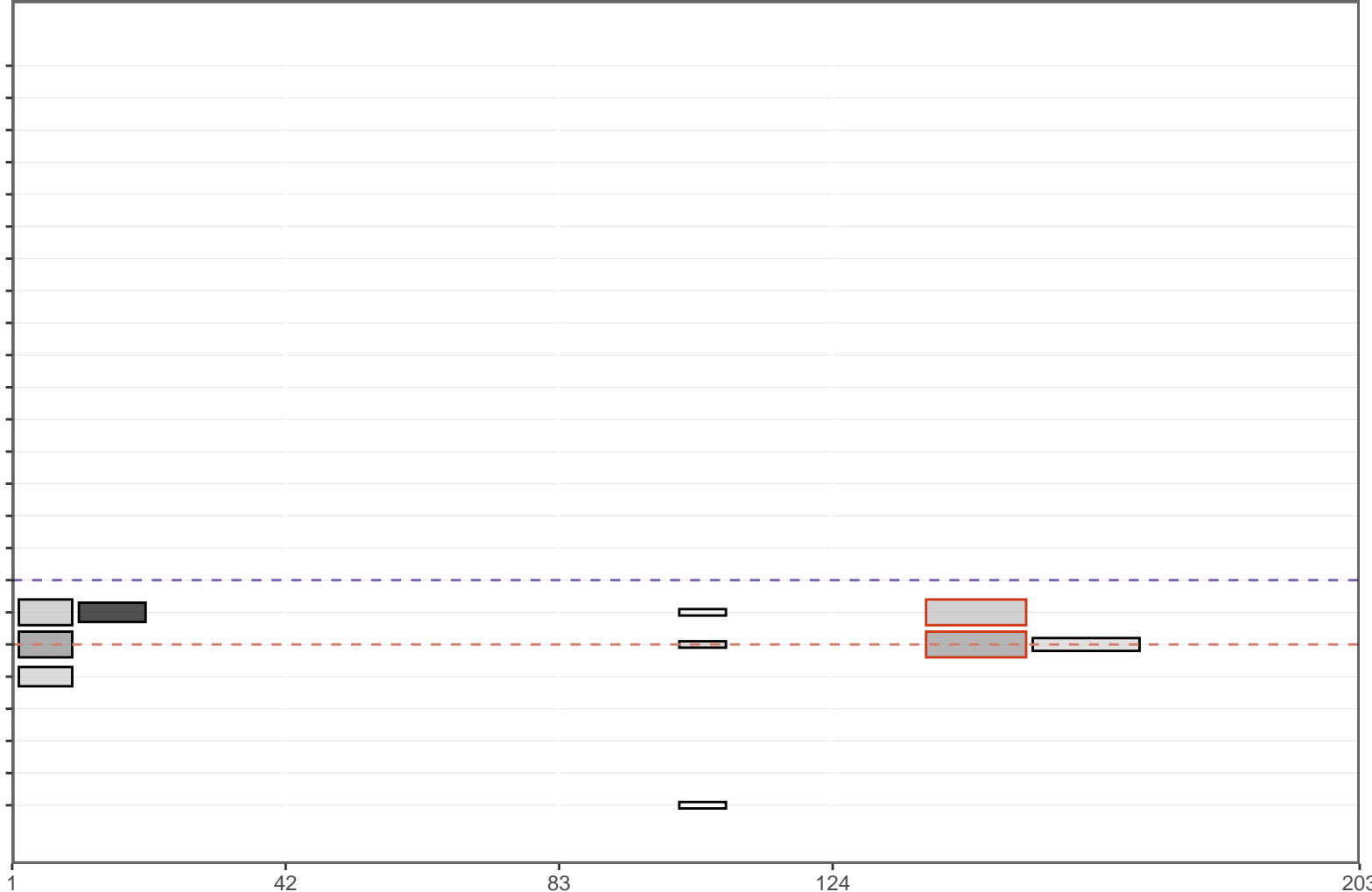
MW indication



Molecular weight



Gel Slice



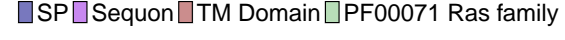
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TERESFNVKGWLNEDIRVNEGVKLLVGNKGDVENVKVVDTQTGKALADELGIPLFETSAKDSINVEQAFITMAGEIKKKMGNGSAGANKSGSTVQIKGQPIEGKSNCCG

NbL11g12110.1 acetolactate_synthase_1_chloroplastic [MW = 72.72 kDa]

No. of times detected



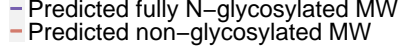
log(intensity)



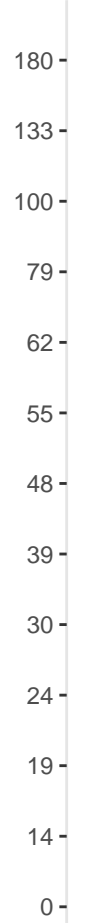
Values from



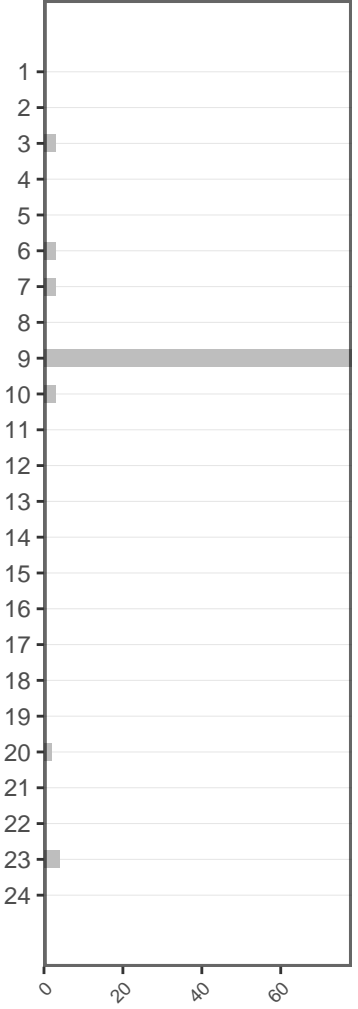
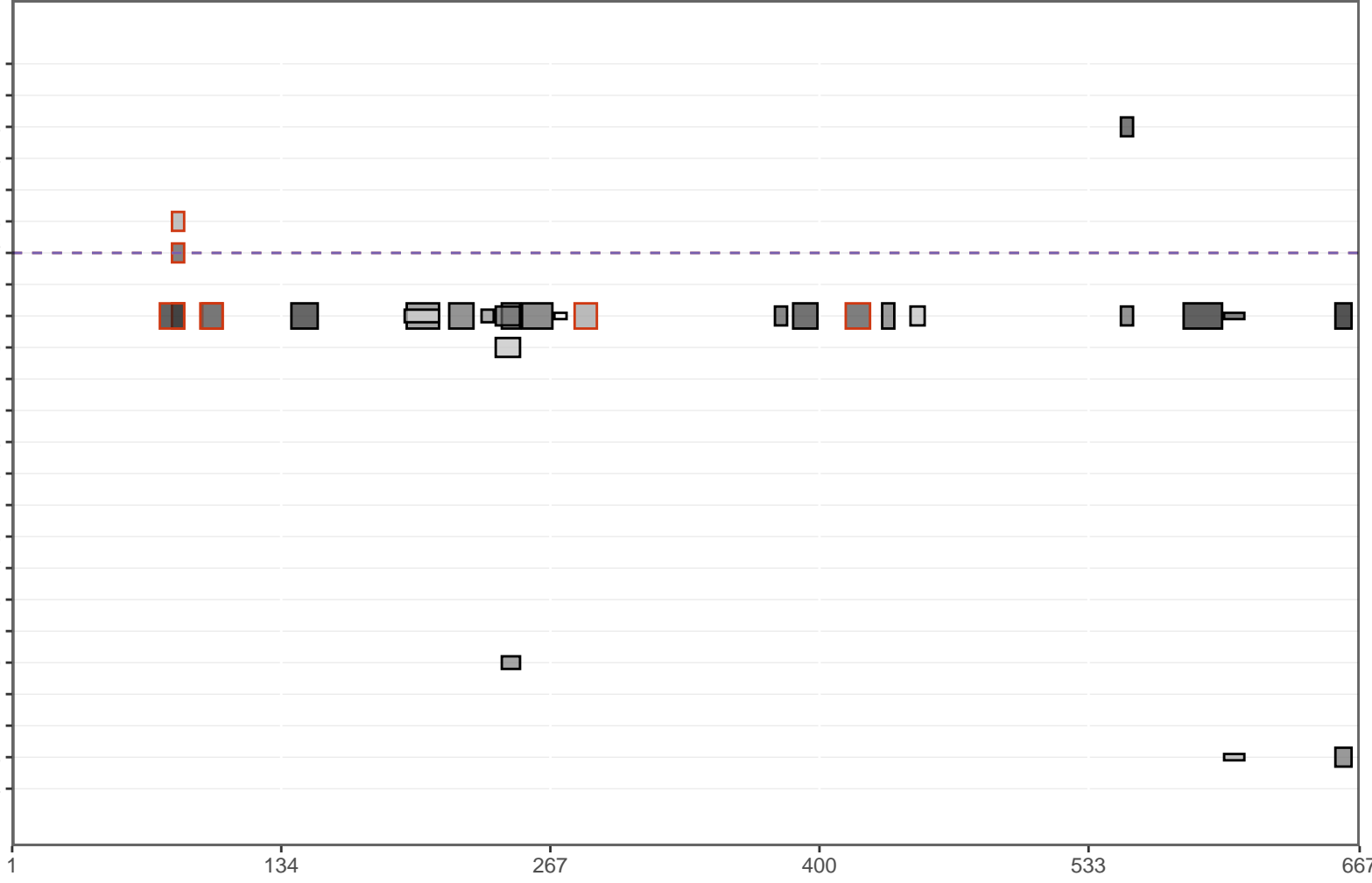
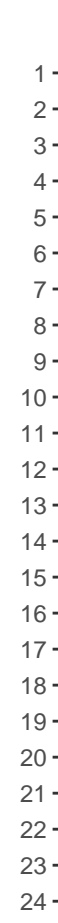
MW indication



Molecular weight

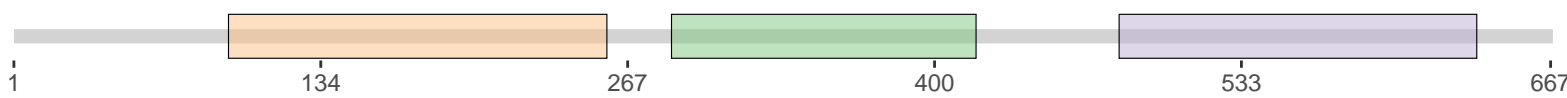


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00205 Thiamine pyrophosphate enzyme, central domain
- PF02775 Thiamine pyrophosphate enzyme, C-terminal TPP binding domain
- PF02776 Thiamine pyrophosphate enzyme, N-terminal TPP binding domain

Protein sequence:

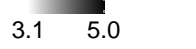
*VASTLMLGLGAFPTGGDELSEMLGMHGTVYANVAVDS6DLLLAFGVRFDDRTVTKLEAFARAKIVHIDISAEIGNKNGPHVSGADKLAAGLNLLESKEGKGLKLDFAVREGLTEGKHVHPLNFKTFGDAPPPYAGVLDDELNGNAHSTGVGGHGMWAQYKYKRPKRWLTSGGLGAMGFLPAAGAAVGRPDEVAVDIDGGDFIMNVGELATKVENLPAKMLLNHGLGMVVGWEDRFYKANRHTYVGNPSEAEIFPMLKFAEACGVPAARYTRDI

NbL11g12090.1 ras-related_protein_RABA2a [MW = 23.92 kDa]

No. of times detected



log(intensity)



Values from



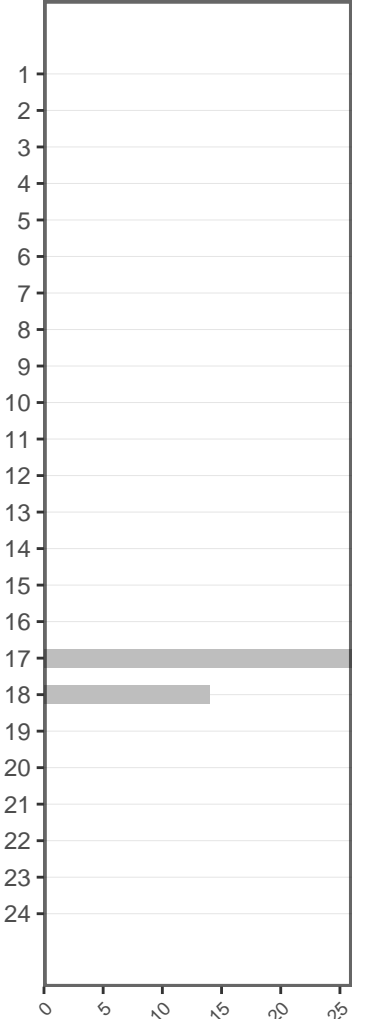
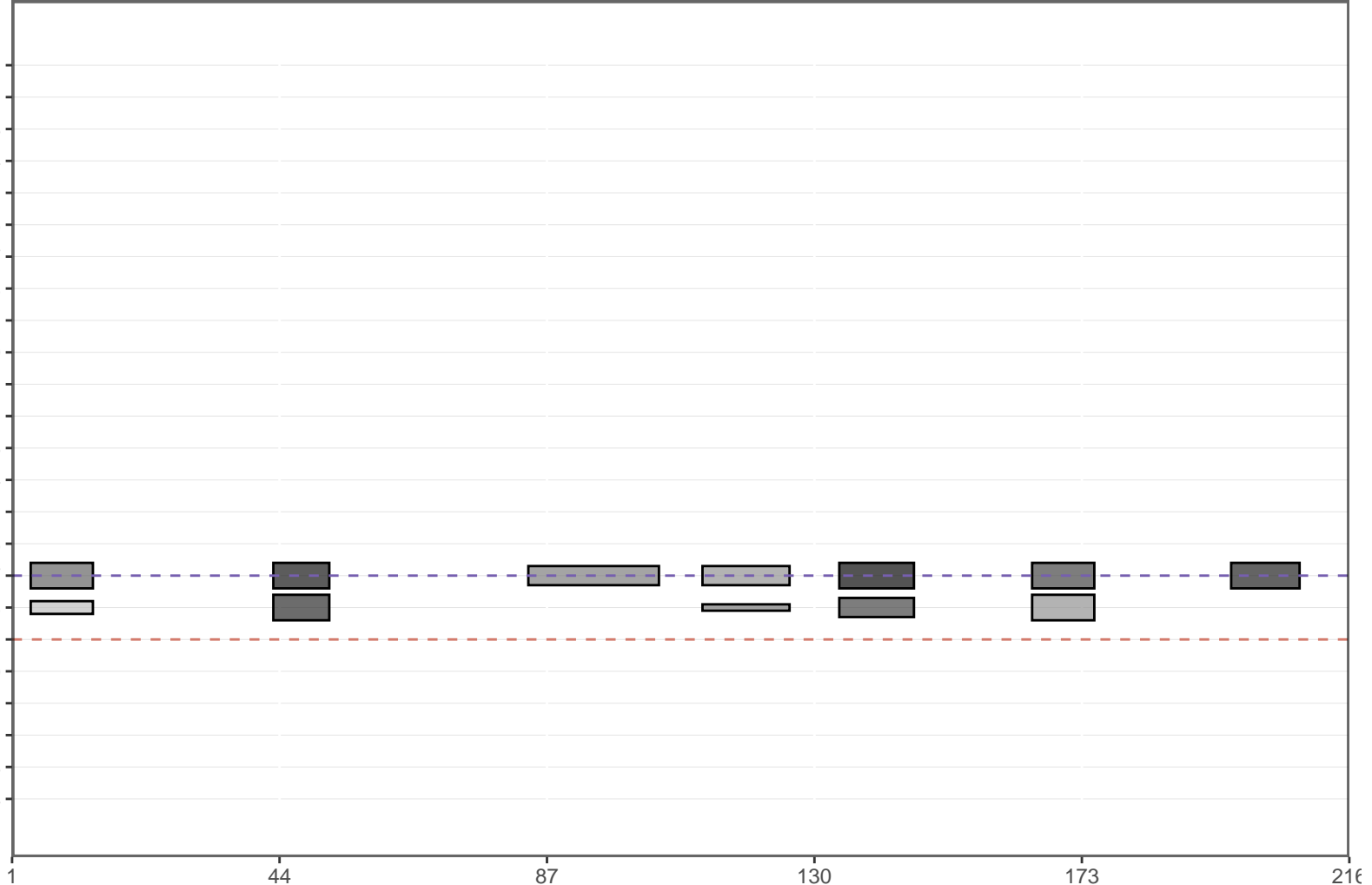
MW indication



Molecular weight

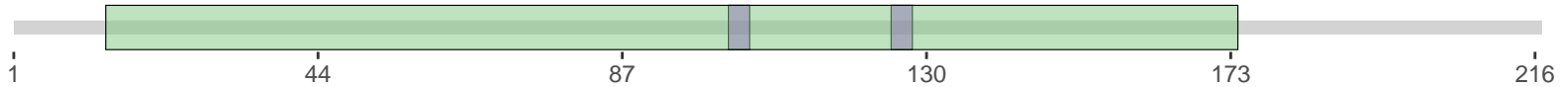


Gel Slice



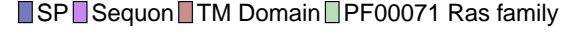
Protein length

Peptide counts over 4 repeats



Pfam domains

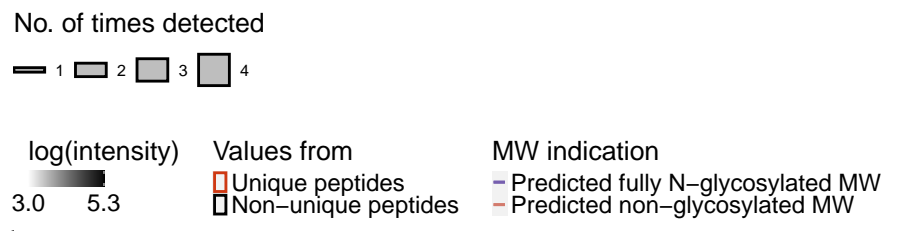
Pfam Description



Protein sequence:

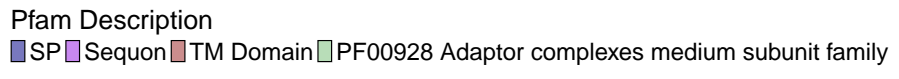
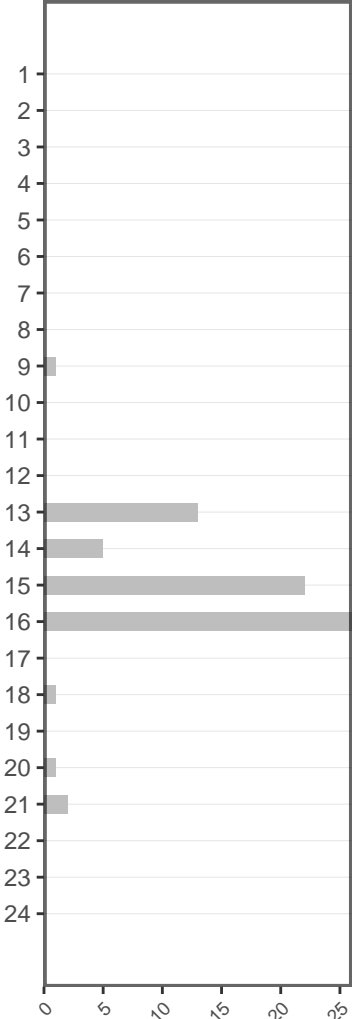
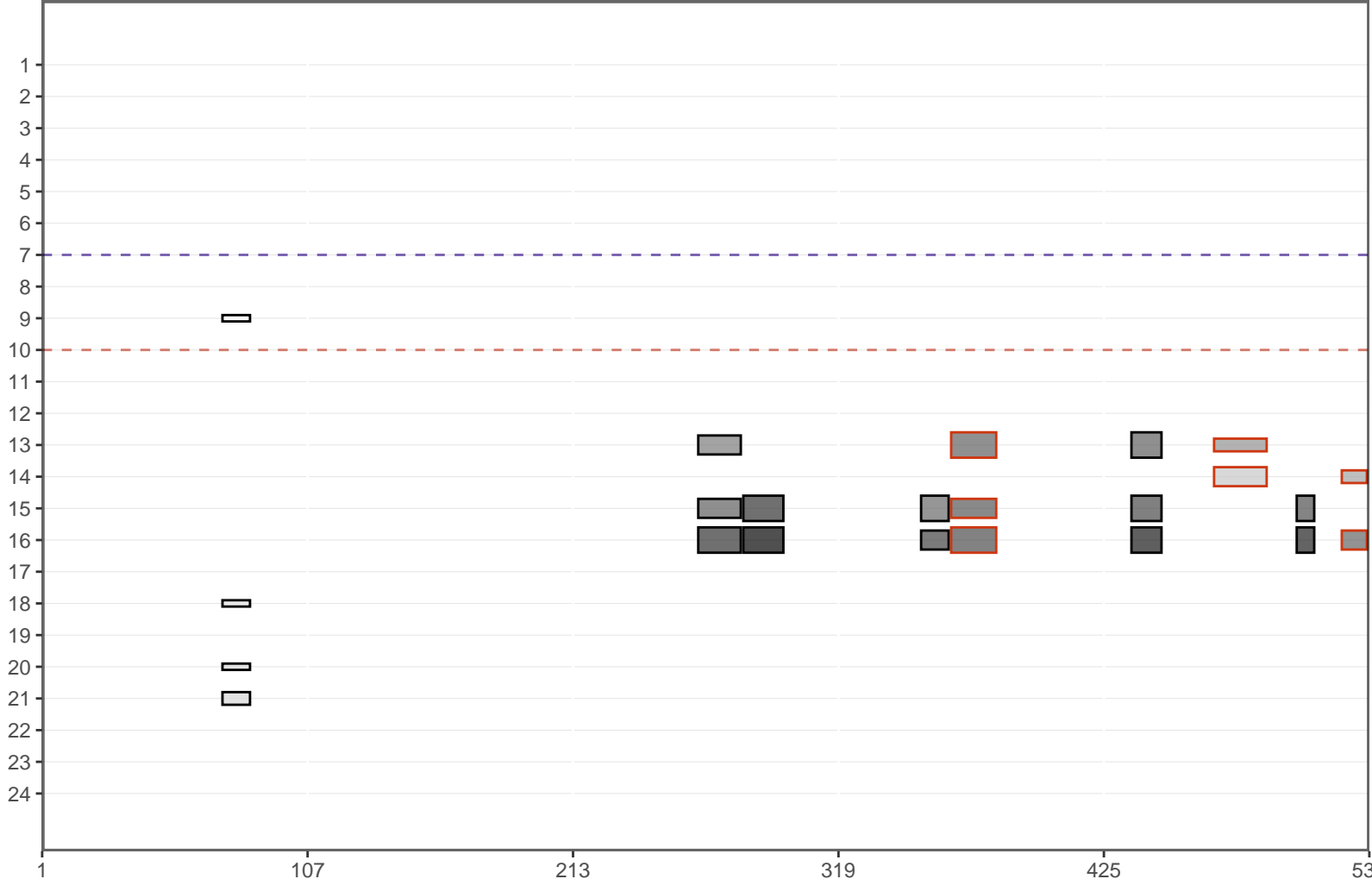
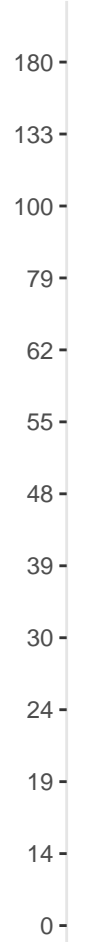
VTKPTTFENVSRVWIKELRDHADGNVIMUGNKTDKHLRAVDTEDAQSFAEKGLSFIETSALEATNVEKAFQTLSEIYRIISKPLSSSEEPATANKKGGKTLVVGAEFPKPKKACGSSS

NbL11g11990.1 coatomer_subunit_delta-like [MW = 58.07 kDa]



Molecular weight

Gel Slice



Protein sequence:

QKTDQFLKSLKAEGEVVEEDVRRPQGGAKRPAALPLDIPVTLFVEEKINVTLKRDDGVSNFQVGGTSLQLNGEDAFQVQIETSGNPTLTKTHPNNAKELFSMENLGLKDPNRPFTTGGGGDGVLLRWRMOTADESILPLTINQWPFVSGSETVWIEVETPQIDLGNVVISVPLPALREAPNVQDGEWRYDRPNVLEWLVLLHNSNRGGALEFVVPADPQVFFPQARETASRTFSDLKVVNLPKGGPTPKHSGRTQLATETVGVV

NbL11g11950.1 60S_ribosomal_protein_L3-2 [MW = 44.48 kDa]

No. of times detected



log(intensity)



Values from



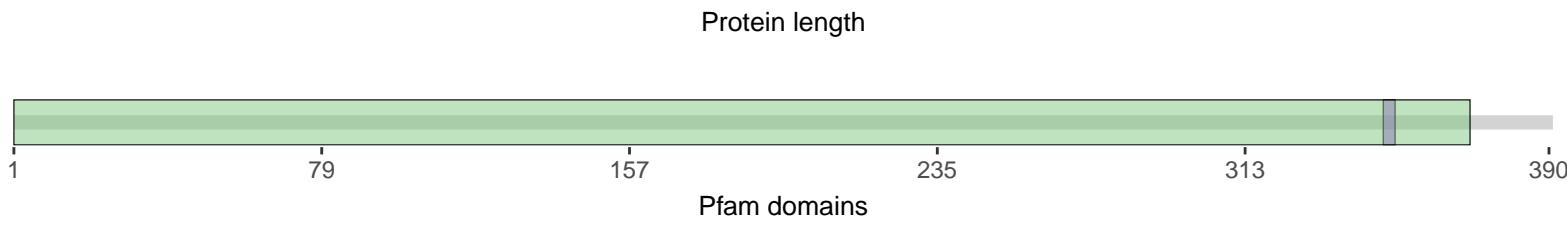
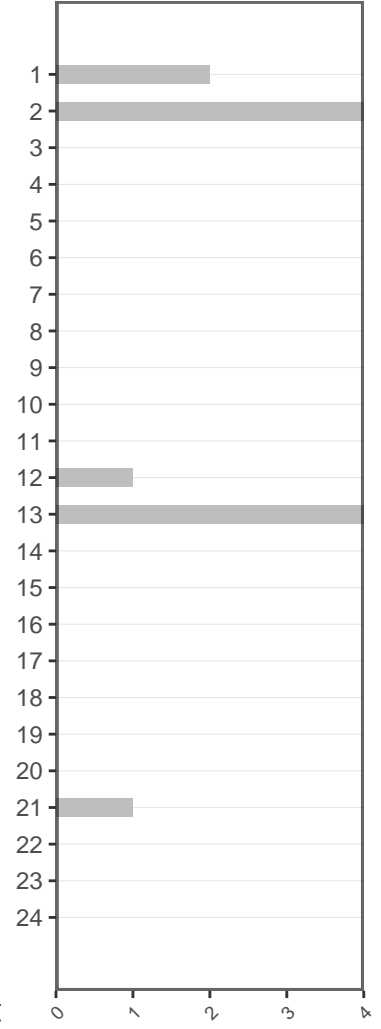
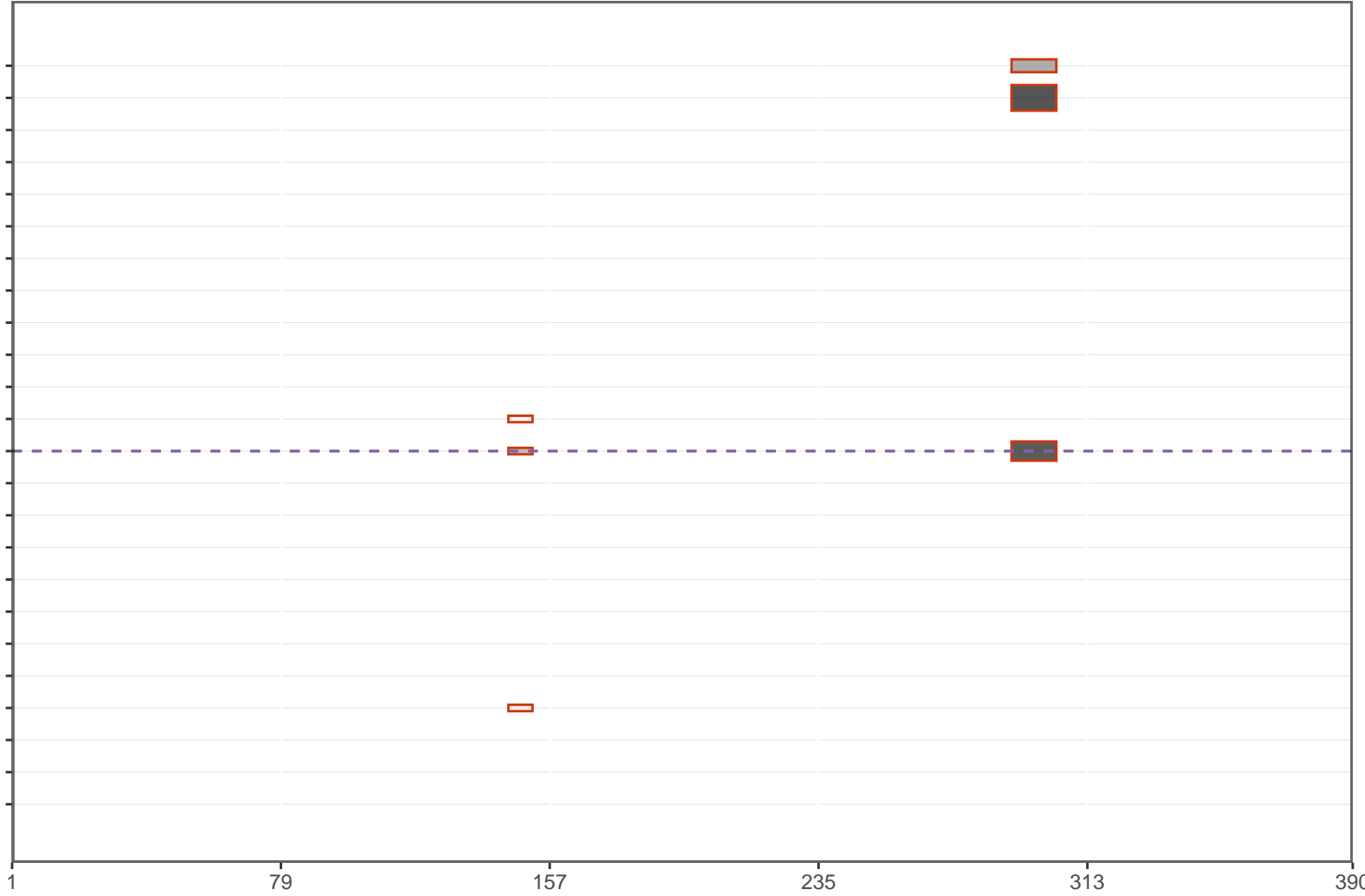
MW indication



Molecular weight



Gel Slice



Pfam Description
 SP Sequon TM Domain PF00297 Ribosomal protein L3

Protein sequence:

LMEIQVNGGDSQKVDKAWGFFENKIPVDLFDKQNDMDHGHVTKGKGFVTRWGVTRLRPRKTRHGLRKAQIGAWHPARVYTVARAGONGYHRIEELNKKVYRLGKAGDGHSAITEFDRTKNDITPMGGFFHYGVKEDFLIKGCGVPRKRVVTLRQGLLNGTRVALEEIKLKFDTSEKFGHGRFGTTGQEKAKFYGRLLKA*

NbL11g11690.1 40S_ribosomal_protein_S12-like [MW = 15.13 kDa]

No. of times detected



log(intensity)



Values from



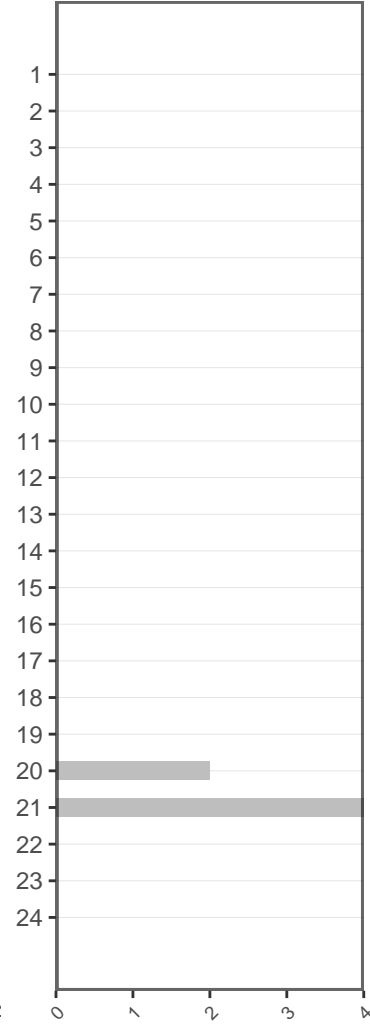
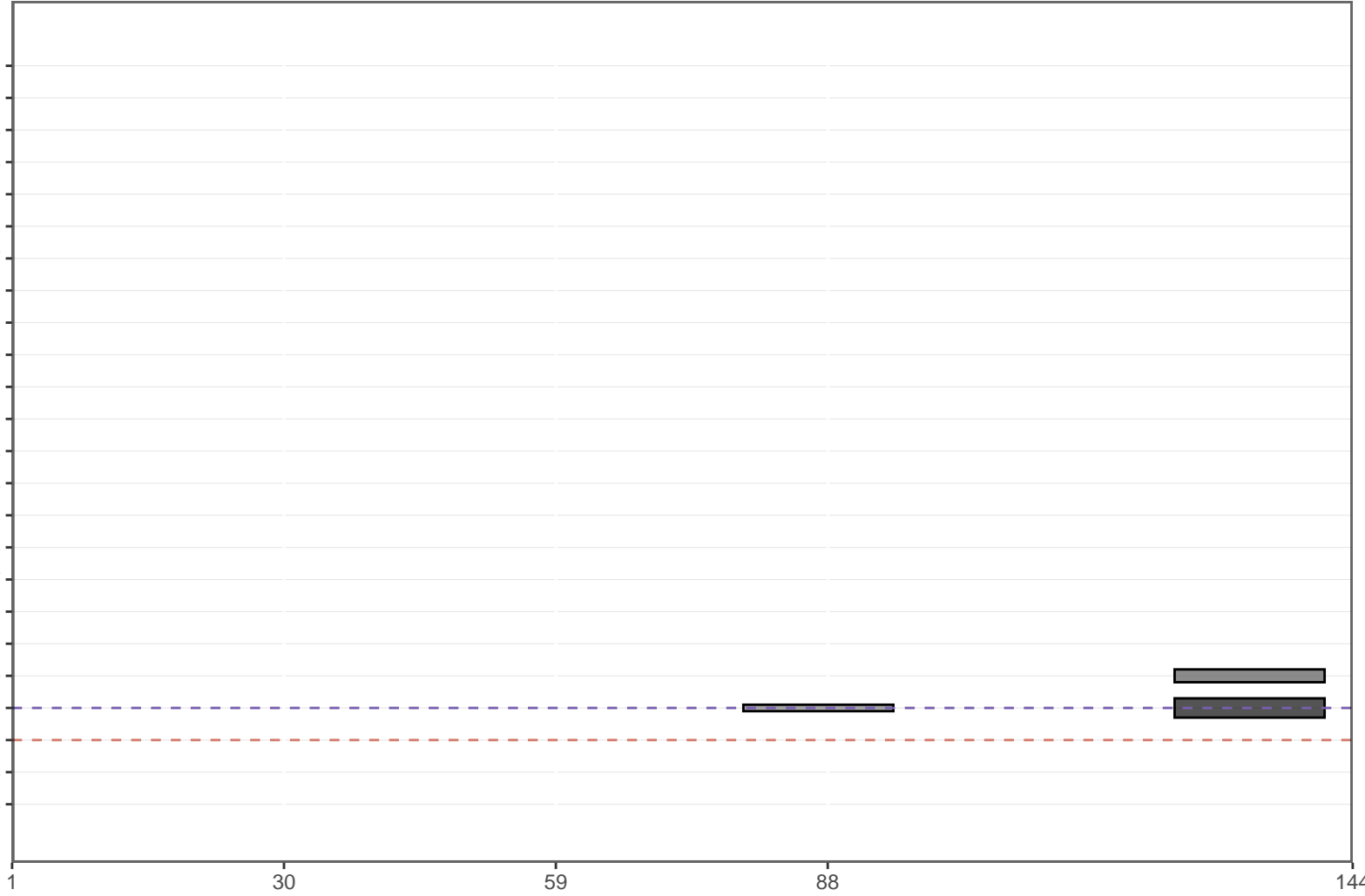
MW indication



Molecular weight

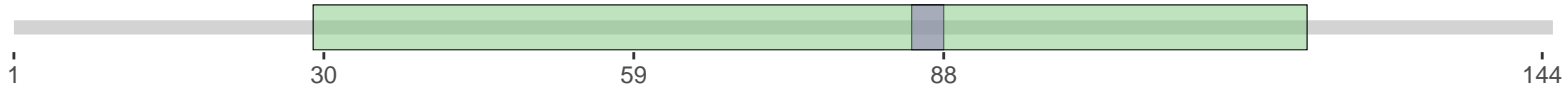


Gel Slice



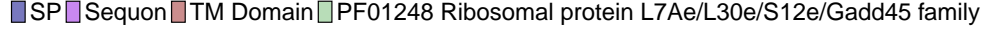
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

QLCLVLAEDCDQDPYKLVKALGADHNVSLITVPAKTLGEWAGLQKIDSEGKARKVVGGGGVVVKVYGEETEGLHIVGEYVKGH

NbL11g11640.1 ATP_phosphoribosyltransferase_2_chloroplastic-like [MW = 42.93 kDa]

No. of times detected



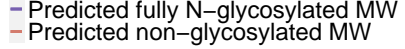
log(intensity)



Values from



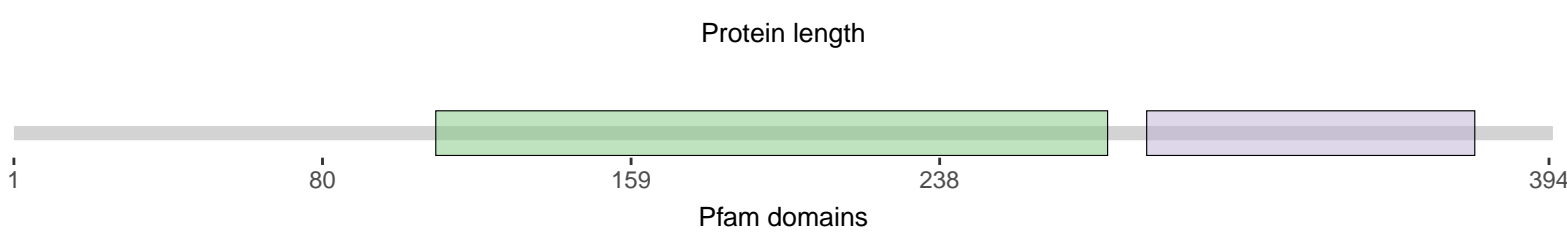
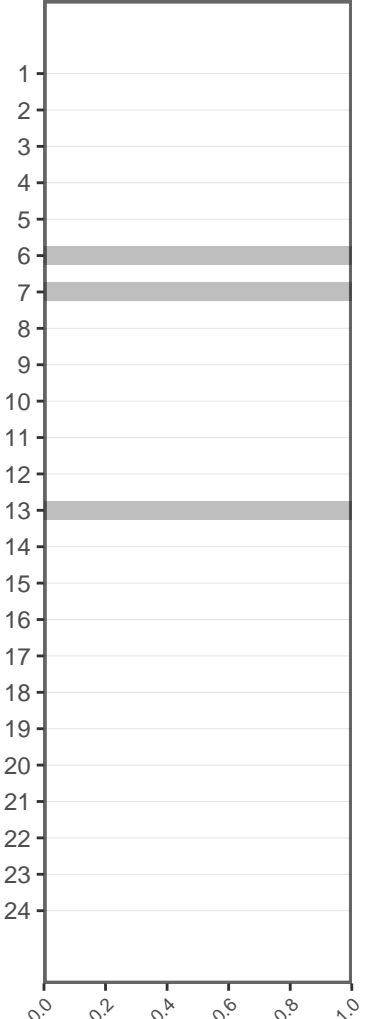
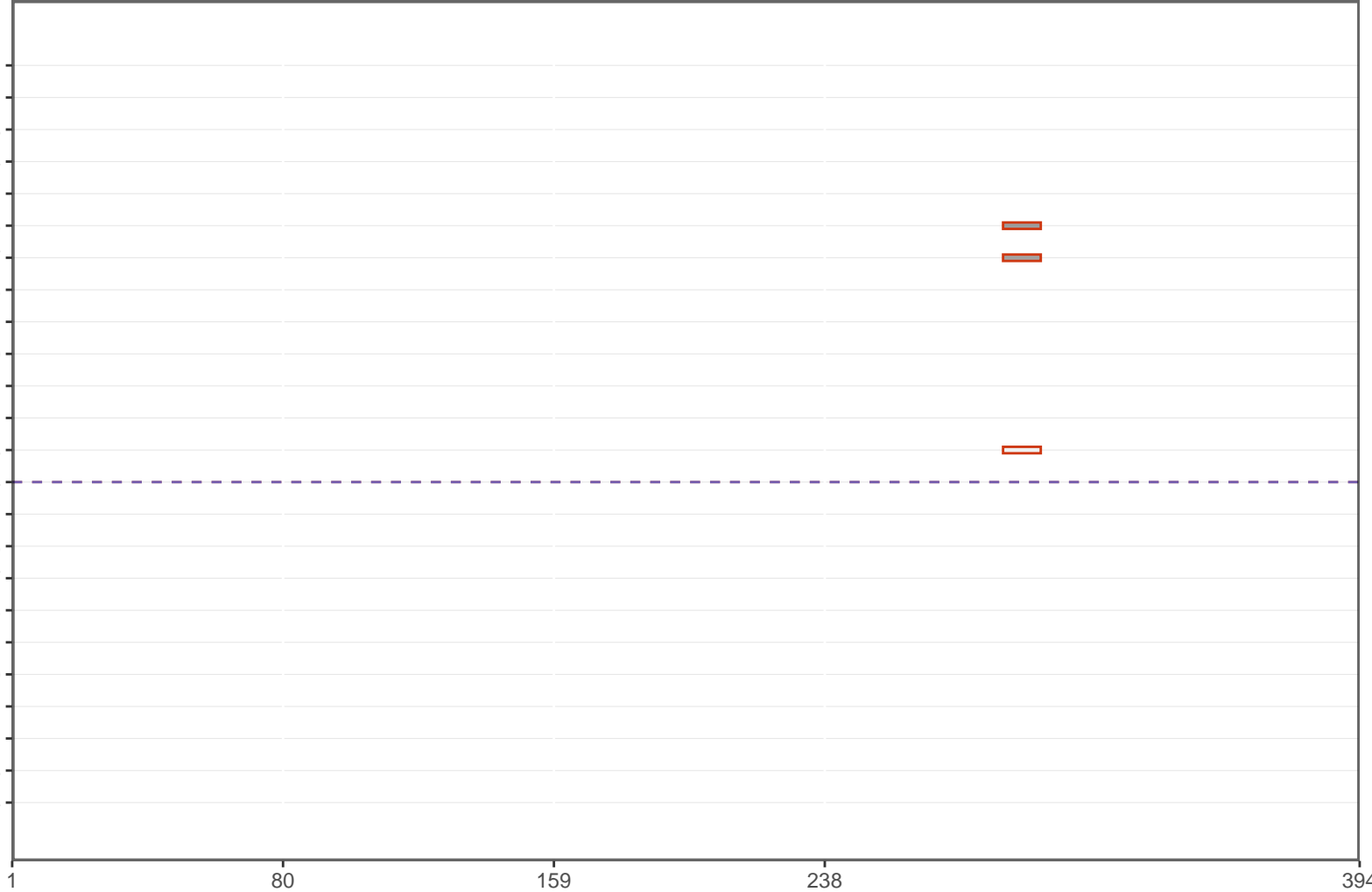
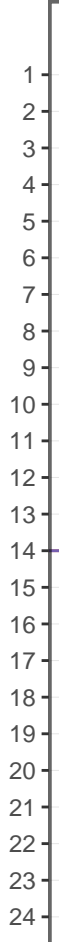
MW indication



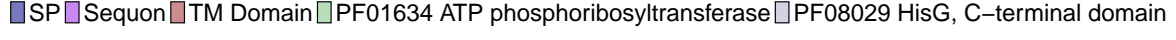
Molecular weight



Gel Slice



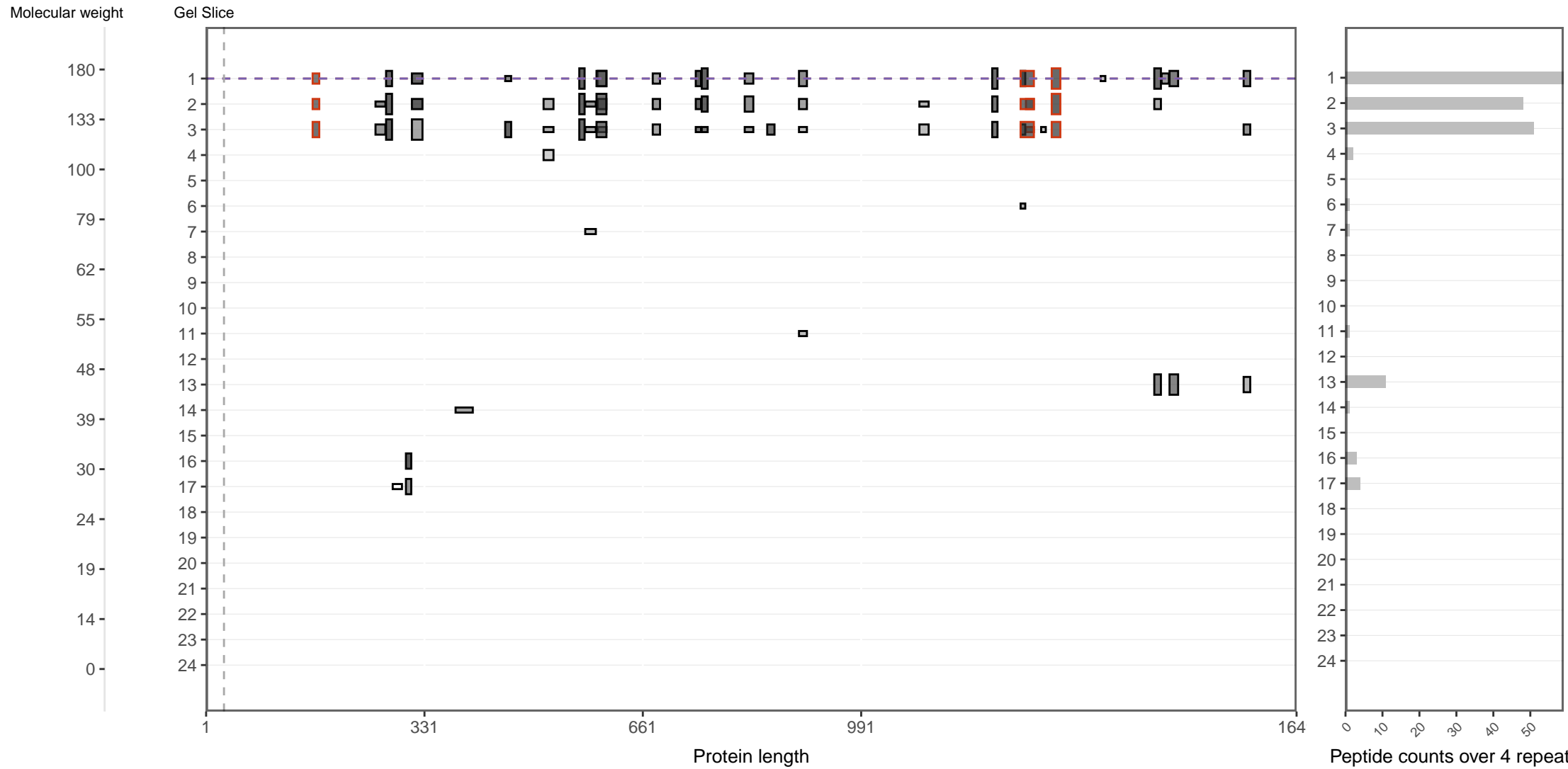
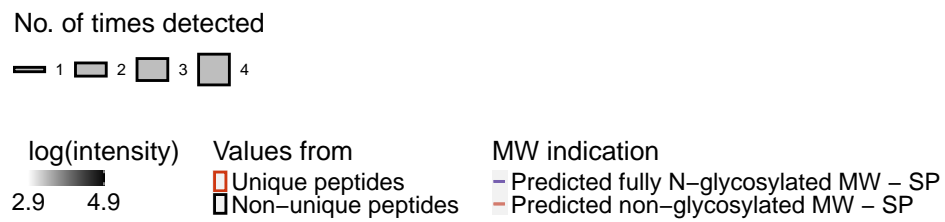
Pfam Description



Protein sequence:

SRPLRVAIGFTYLGPKFMKDKGLKHVTFSTADGALEAAPMGADAVDLVSSGFTLRNNLKEIEGGVILEGGAVLVGRKSLMGRKGVLDTHHEMLERLEAHLRAVGGFTVTANMRGSSAEAEVAERILSGTSLSGLOGPTVSPVFGKRDGRVTADYFAVIGVPKKALYKVVQQLRAIGGGVLIISPLTYFDEETPRWRLLMLGL

NbL11g11630.1 UDP-glucose:glycoprotein_glycosyltransferase [MW - SP = 183.1 kDa]

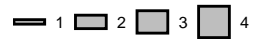


- Pfam Description
- SP
 - Sequon
 - TM Domain
 - PF06427 UDP-glucose:Glycoprotein Glucosyltransferase
 - PF18400 Thioredoxin-like domain
 - PF18401 Thioredoxin-like domain
 - PF18402 Thioredoxin-like domain
 - PF18403 Thioredoxin-like domain
 - PF18404 Glucosyltransferase 24

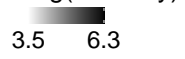
Protein sequence:
 LREGHYLMAGTTTGRRLGVLFNSVLDPHSLGSLFKVQFATSSVYSHKKGVLEFLDDGCSFYEHDPYHASSAGTSESSSESLDKVFLFELANSNGLSKKALKSALGSLSDKELRMHLNKVGTFLFGVGLVYGANAVTNRVIGLVDDTFLSHDLQLLESLFKGRKHVVEIEEYVWEEDPDMLTSEKFDVSDVMSVSSGSMRDRSSEGARFELLGAKYSAVLENESSSHDAVIDFLS65GGKLSLRLLEKSRPGRMLVLPMS6VLDLPLKNYRYVIFPTLDDFSSTDYT

NbL11g11530.1 ankyrin_repeat_domain-containing_protein_2B-like [MW = 37.3 kDa]

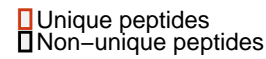
No. of times detected



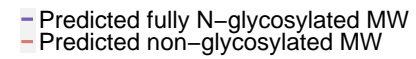
log(intensity)



Values from



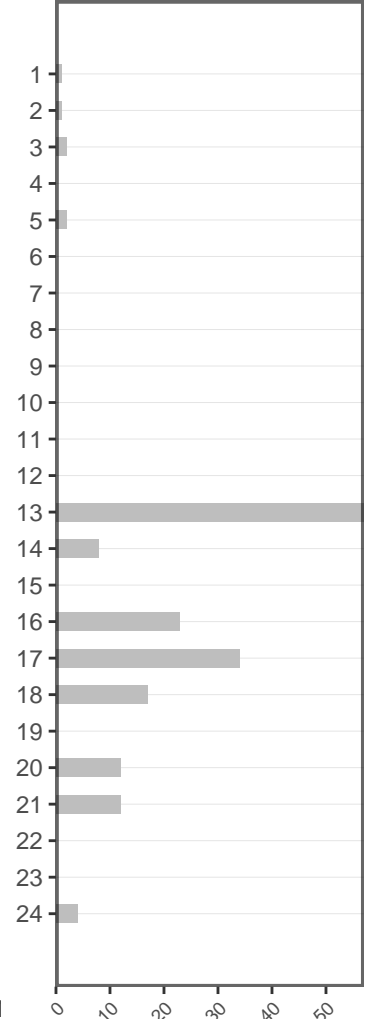
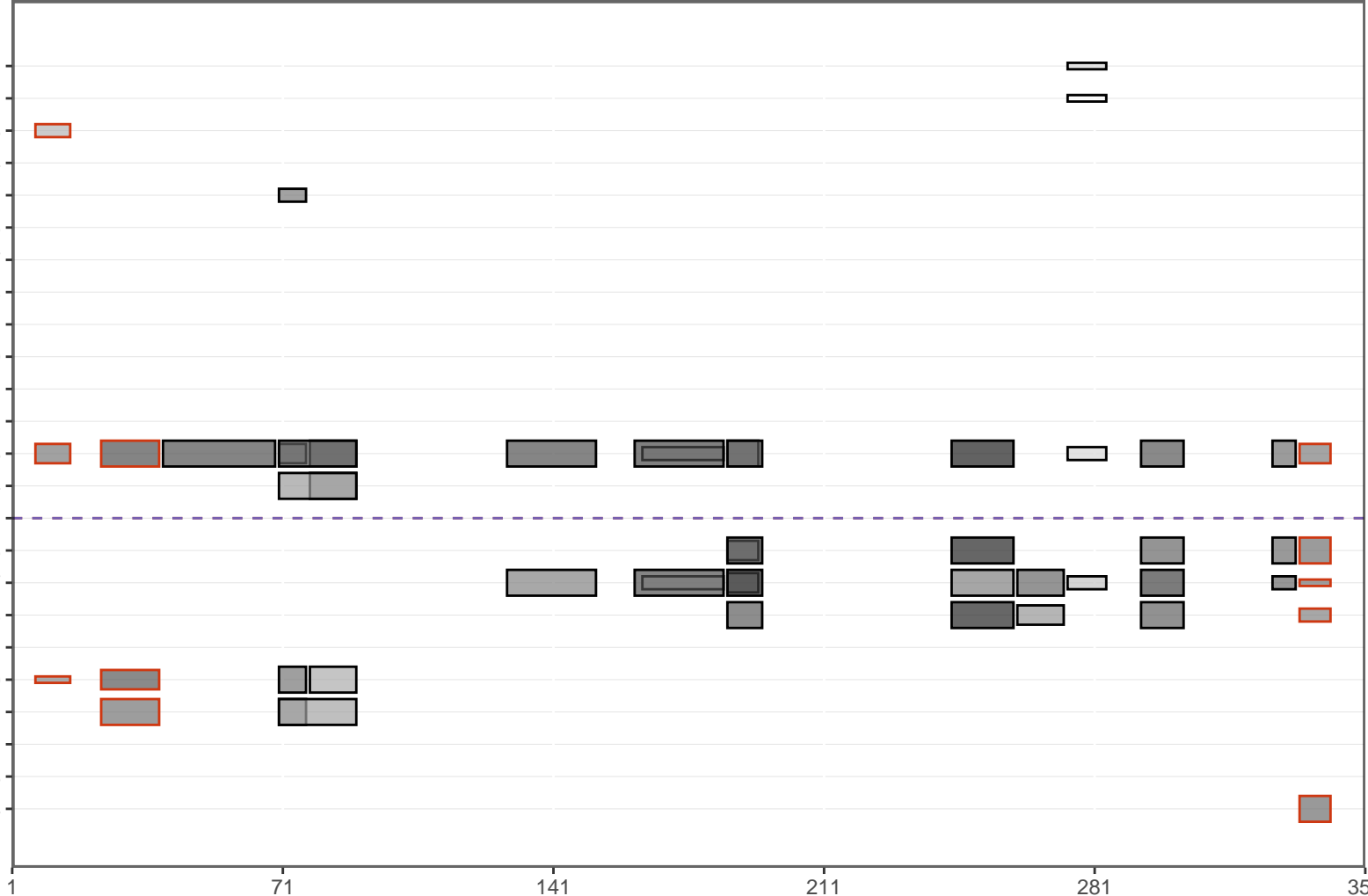
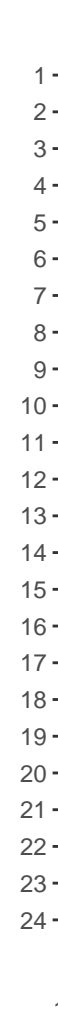
MW indication



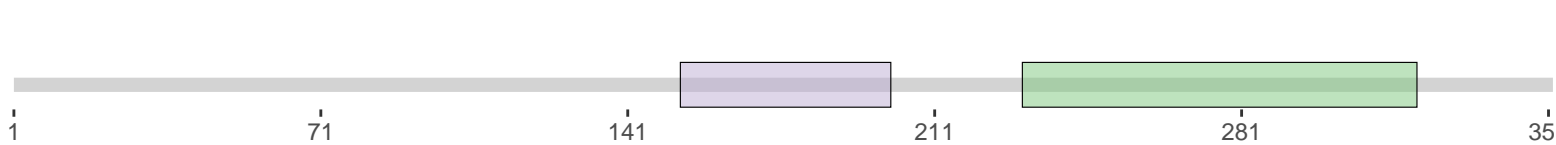
Molecular weight



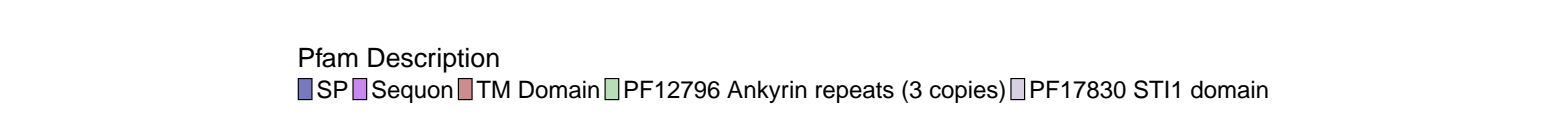
Gel Slice



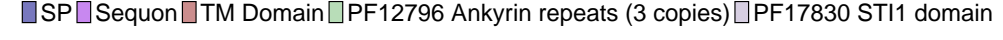
Protein length



Pfam domains



Pfam Description



Protein sequence:

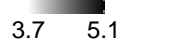
IRIKEDPSLKPLEEIEEGSGPAMMRVYWDGELTKKIGKEMGFAGGEGATSSAIPGCTDETEEANEDESVYHOGASVGDIEGLKAALTAGAKDKDEEDSEGRTALHFADGGVEVKDAGLLEAGAVDALKDKKNTALHYAAGYGRKEGAVALLENGAAVTLQNLGDKTPEVAKLNNNGGEVLLKLEKQVFL

NbL11g11420.1 60S_acidic_ribosomal_protein_P1-like [MW = 11.43 kDa]

No. of times detected



log(intensity)



Values from



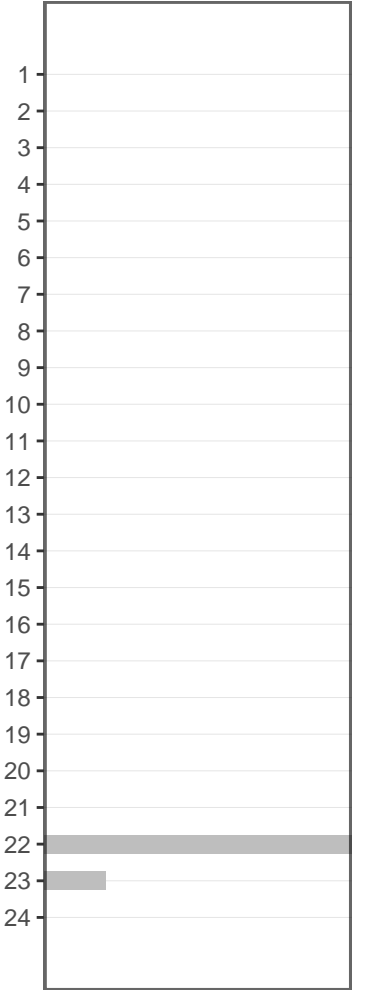
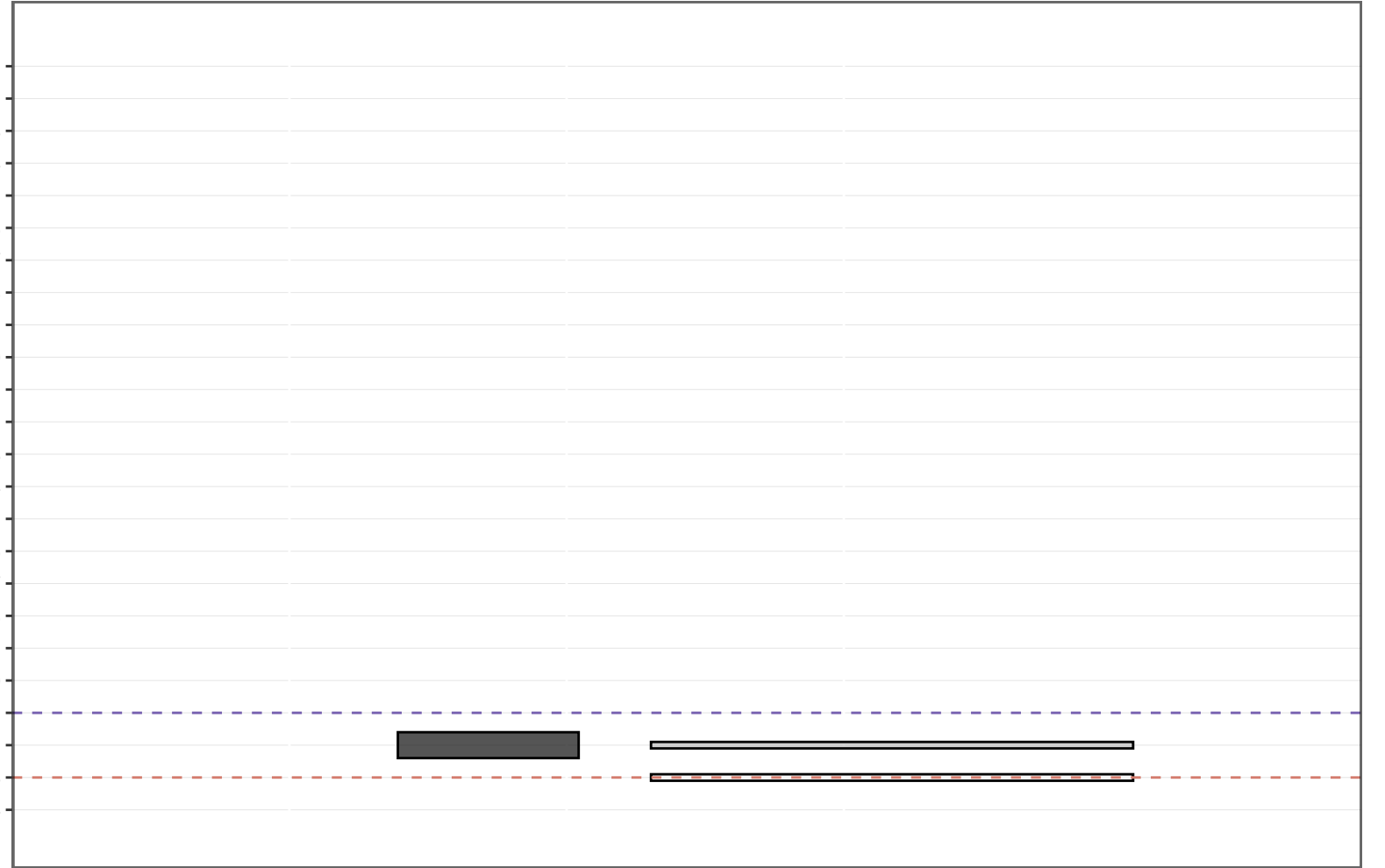
MW indication



Molecular weight



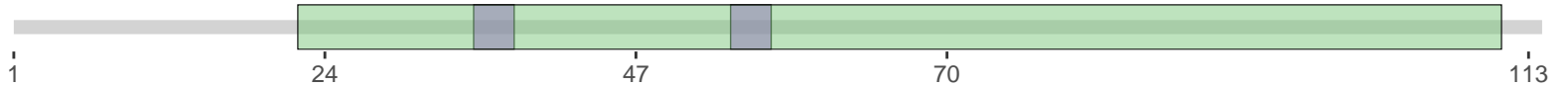
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

FAKLAEKRNLSQLIMNVGAGGGAAWVAAPTGGAAAGGAAAAAAAEKKEEKEEESDDMGFLFDI

NbL11g11400.1 basic_blue_protein [MW – SP = 10.41 kDa]

No. of times detected



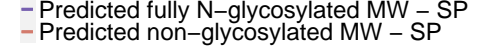
log(intensity)



Values from



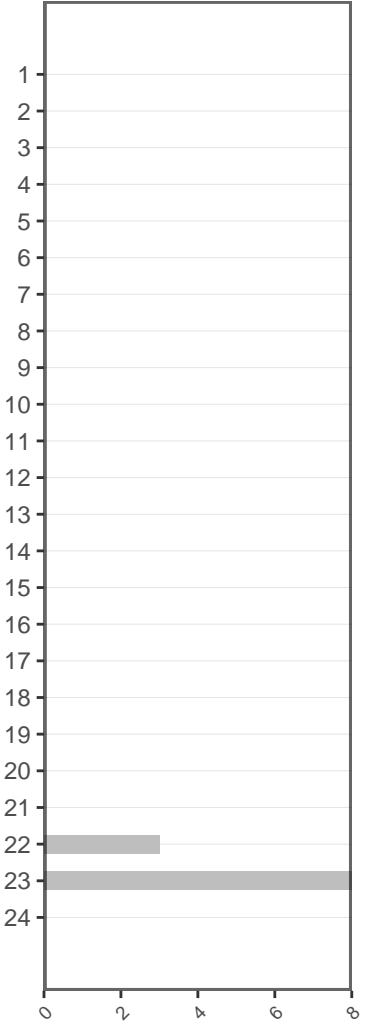
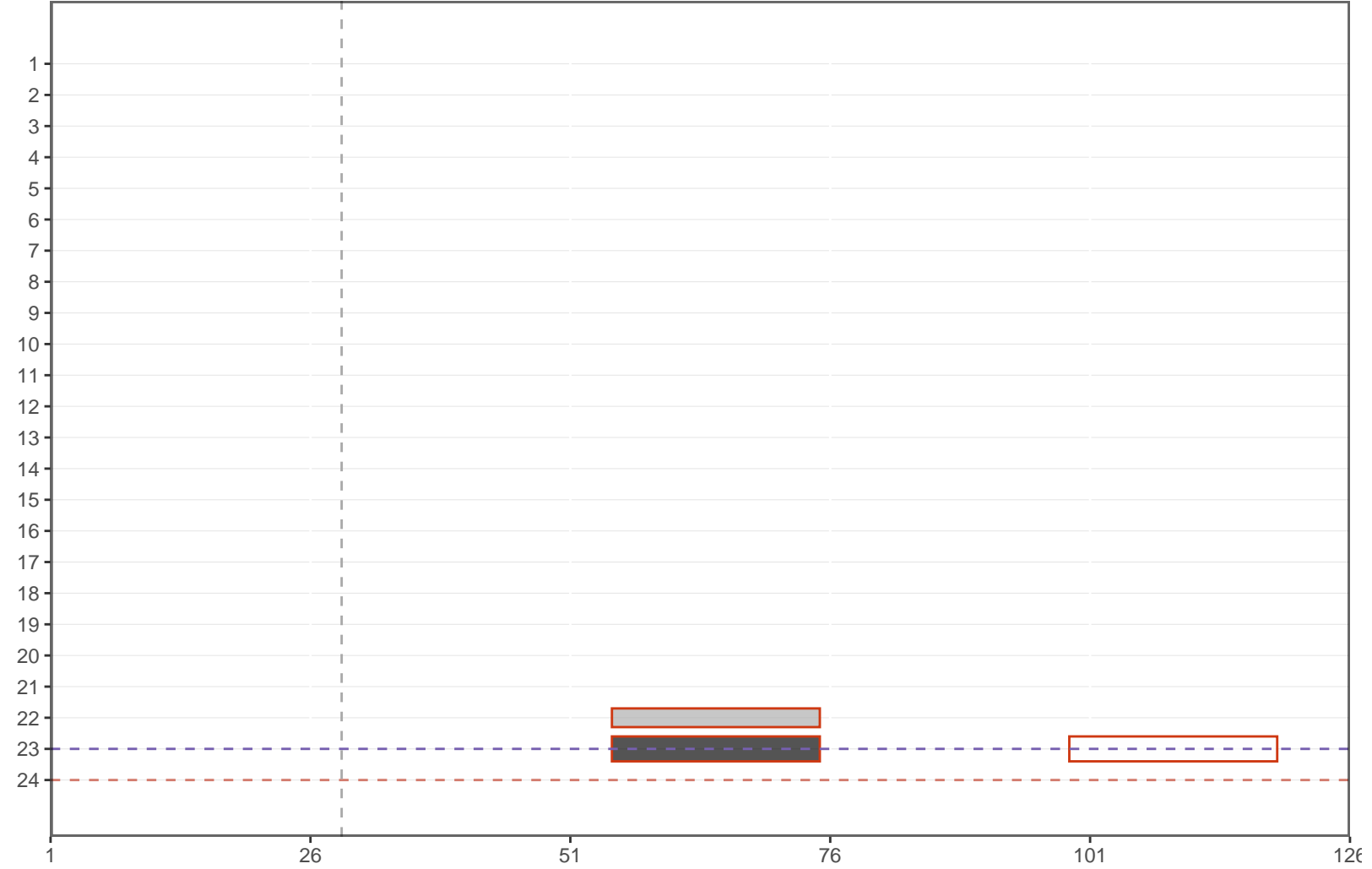
MW indication



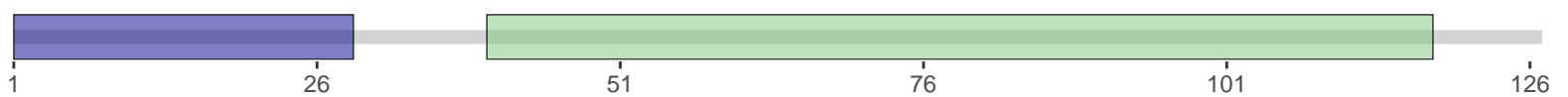
Molecular weight



Gel Slice

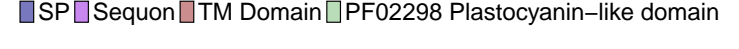


Protein length



Pfam domains

Pfam Description



Protein sequence:

IGKRFRAGDILAFNYPGGARHWVWDKAGYNGRTRPRGAKVYTKGGDKIKLVNGNYFIGNFPFHGGSGMKISVFAS*

NbL11g11370.1 partner_of_Y14_and_mago [MW = 24.98 kDa]

No. of times detected



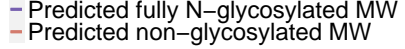
log(intensity)



Values from



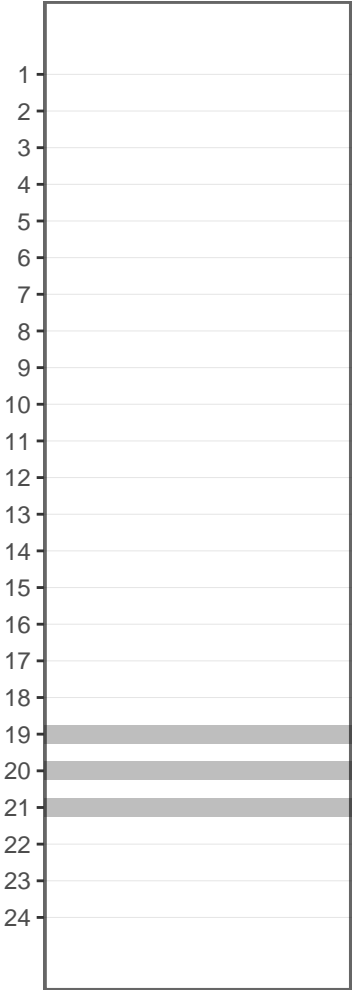
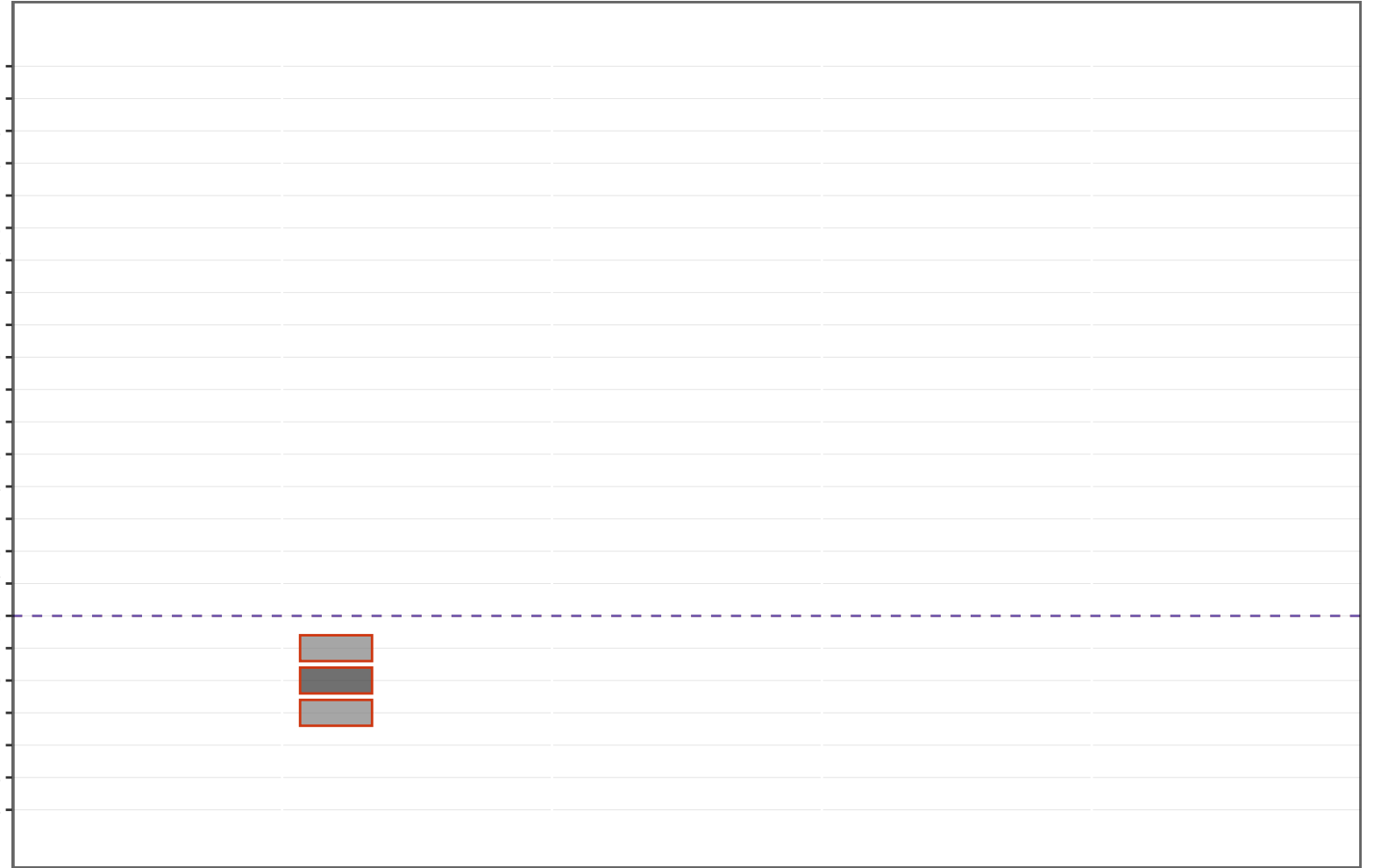
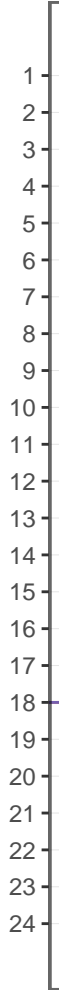
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

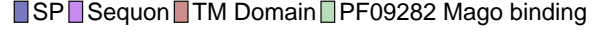


Protein length



Pfam domains

Pfam Description



Protein sequence:

RSKEKRCQAAVEKGTNPESSGSESSAENBVGVPQEVSMGQINLAISANPVVPLSNSESSAVGSDVDKIRIRALKKRRLTEAGGQKTEKDMKPEQLEKVALESWRKELKVLKEDKKAEEA

NbL11g11360.1 mRNA_turnover_protein_4_homolog [MW = 28.22 kDa]

No. of times detected



log(intensity)



Values from



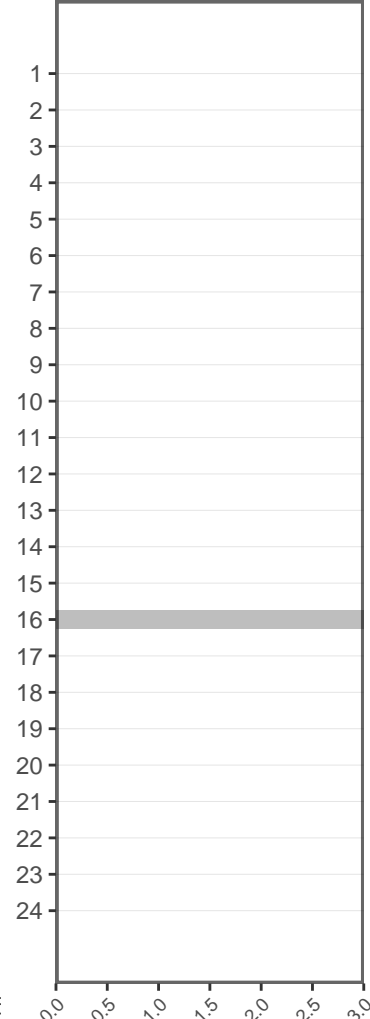
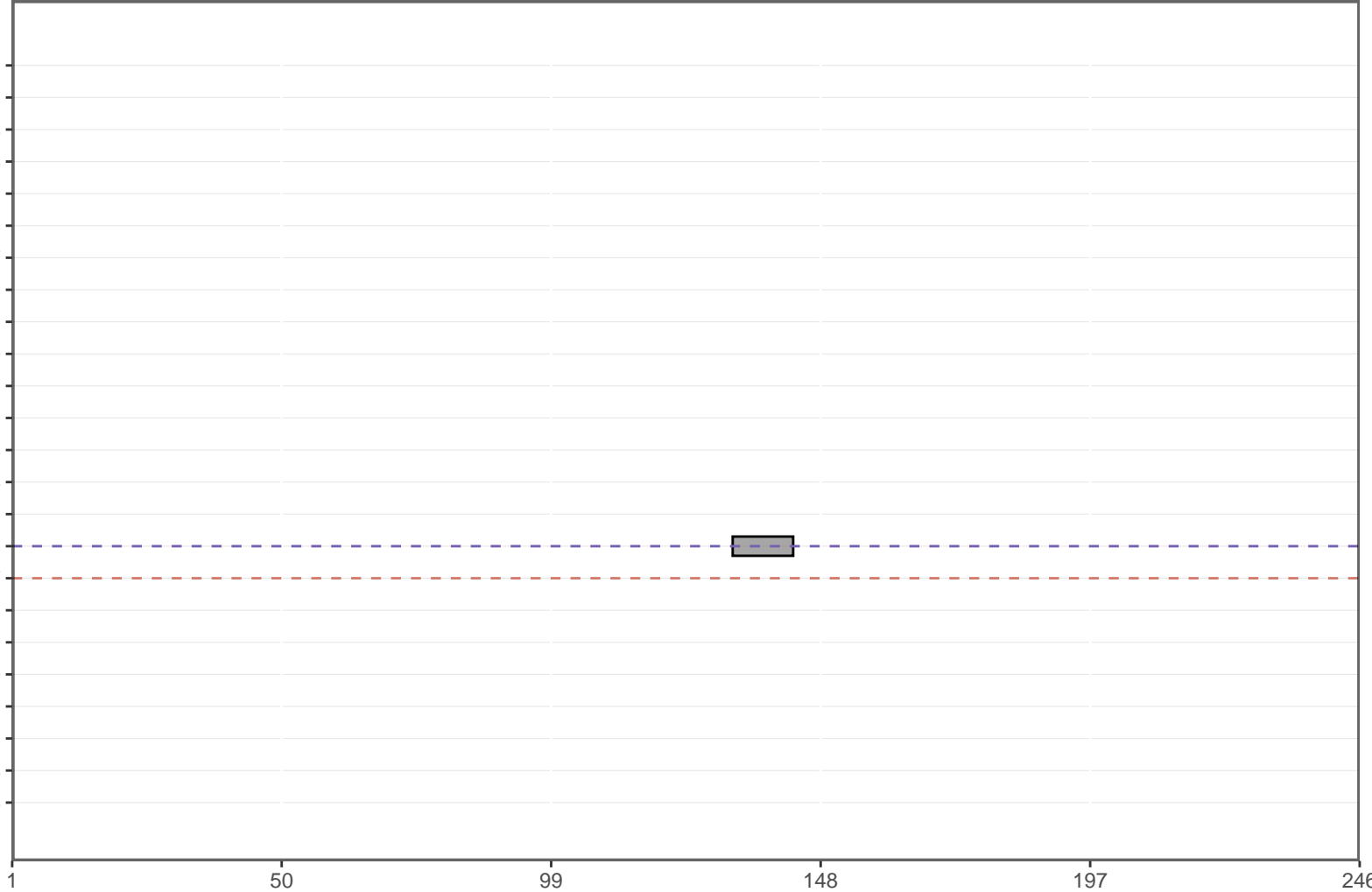
MW indication



Molecular weight

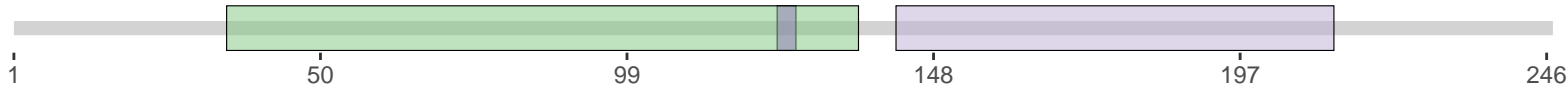


Gel Slice



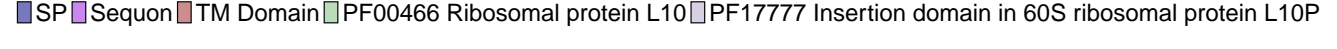
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SKLYRGDSGICFTNLKKEEVQRLFNFEFGYDFARTGSAATEKVELQEGPLDQFTHMEMEFLRNGRMPVRLNKGIVVELVSDFVVCCEEGKALSPFAARILRLGKMKMFRNLICRWTFDPEFEYREGLEESDESS

NbL11g11260.1 60S_ribosomal_protein_L3 [MW = 44.41 kDa]

No. of times detected



log(intensity)



Values from



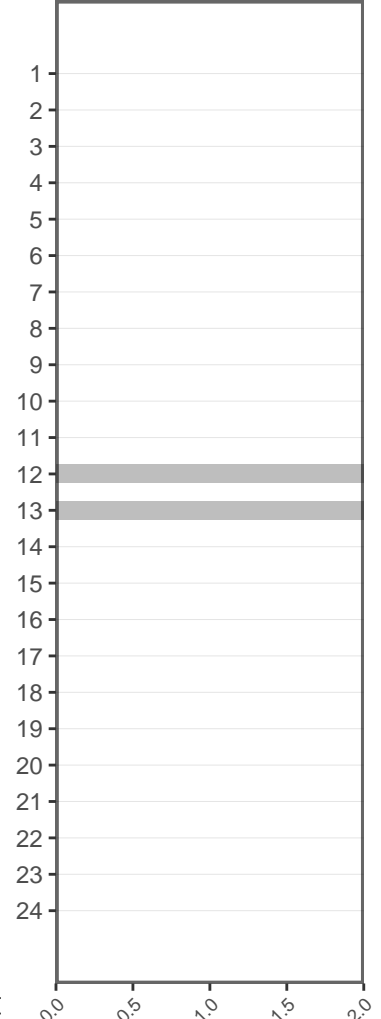
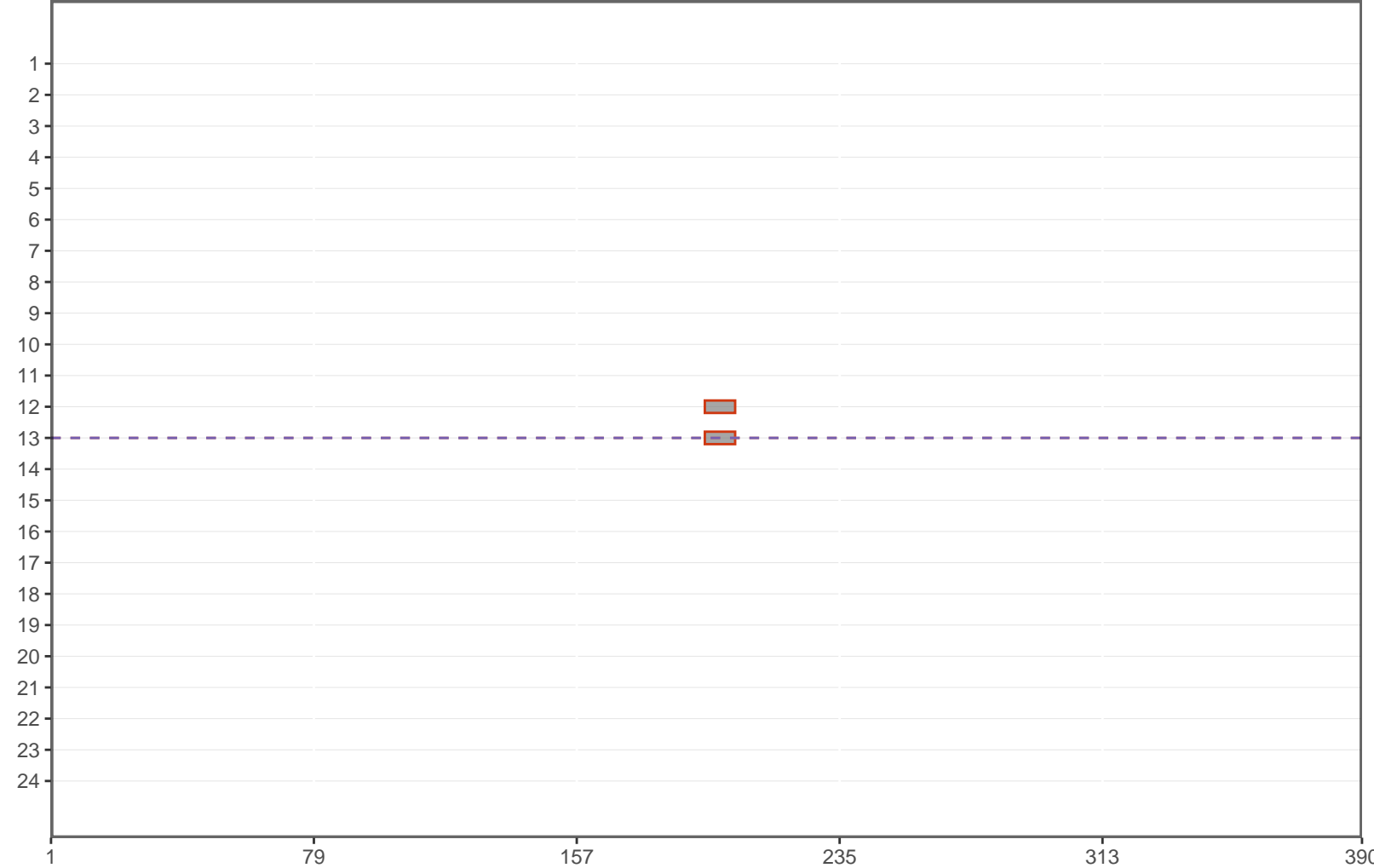
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

MEIQVNGGTIAQKVFAYGFFEKGVPIVAVFQKDEMIDIGVTKGKGYEGVTRWGVTRLPKTRHRLGRKAVGIGAWHPARVSYTVARAGGNGVYHRTEMNKKVYKLGKAGGESHAAITDFDRTEKIDITPMGGFFHYGVVNDWLLIKGGCVGPKRIVTLRGLSLLNGTSRVALEEKIKFDTSKFGHGRFQTQEKFKYGRKA

NbL11g11250.1 COP9_signalosome_complex_subunit_8 [MW = 22.59 kDa]

No. of times detected



log(intensity)



Values from



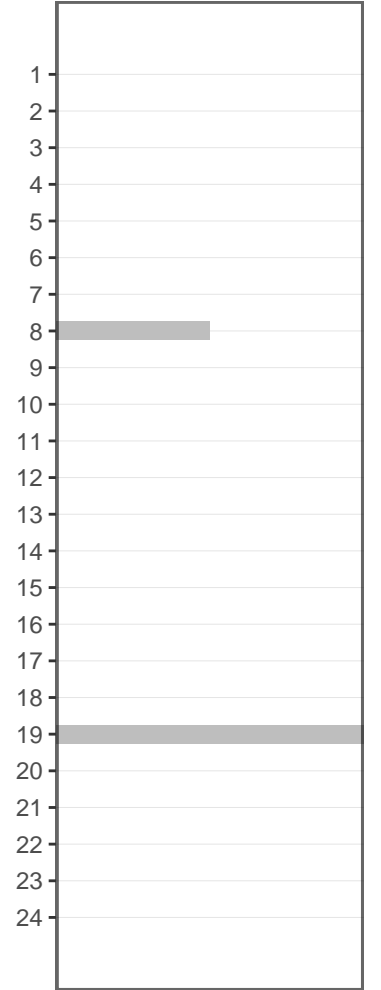
MW indication



Molecular weight

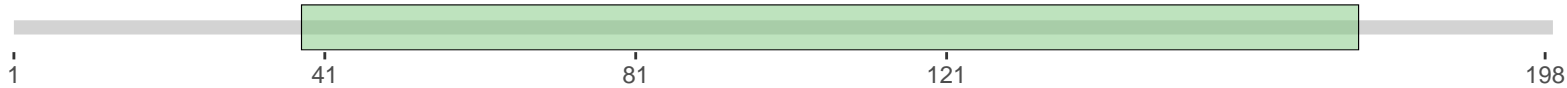


Gel Slice



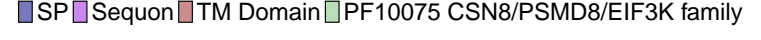
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

MTTRDYGVEIAREFSWTPDQPIVAFELRYRKRMFELLLSAVSTISTGDTAGFLGMNENDATNYVLOGGWLDPSQMLTKKGAIVTEQKLDPEKLRQITEYVPHLEH

NbL11g11160.1 actin-101 [MW = 41.64 kDa]

No. of times detected



log(intensity)



Values from



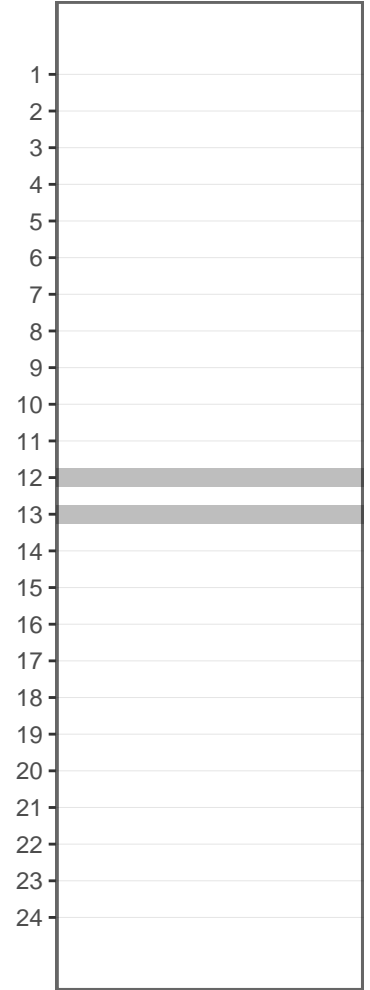
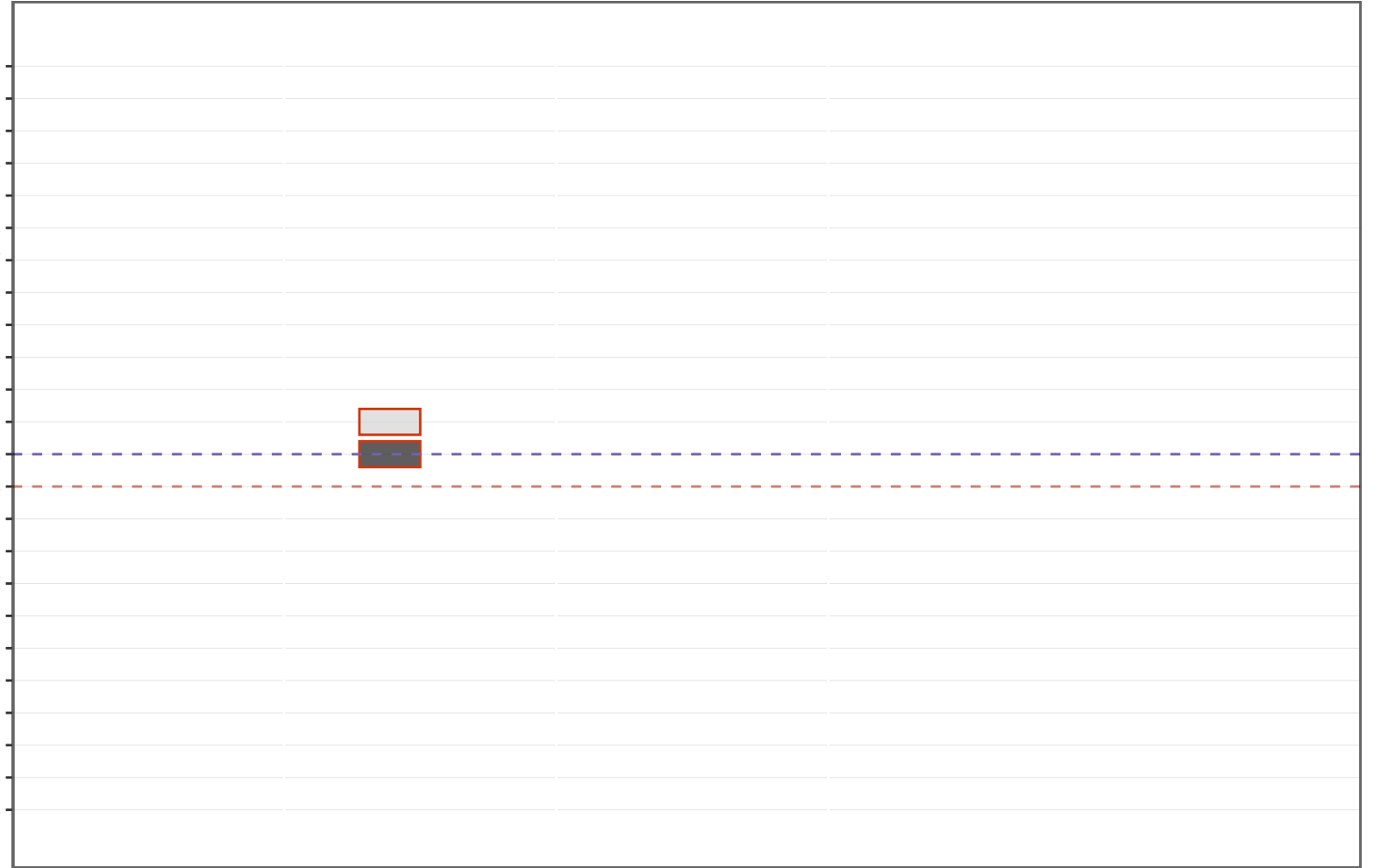
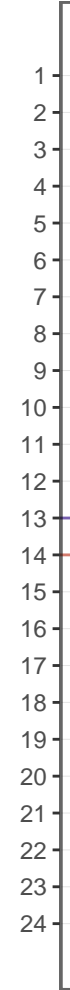
MW indication



Molecular weight

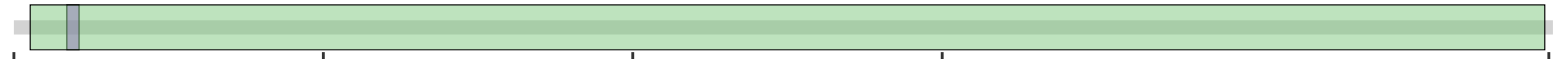


Gel Slice



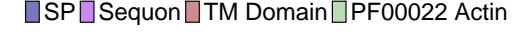
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PHAILRLDLAGRDLDLFDGLMILKLTFRGYSFTTSAERREIVRDRVKEKLAVALDYEQELETAKSSSSVEKSYELPDGGVITGGERFRCPFLVFGPRLVGMEEAGIHETTYNSIMKDDVDRKDLVGNVLSGGTTMFPDGIADRMKEITALAPSSMKIKVVAAPPERKYSVWIGGSILASLSTFGQMMVITKGEYDESGSPVHRKGF

NbL11g10980.1 beta-xyloridase/alpha-L-arabinofuranosidase_2-like [MW = 89.57 kDa]

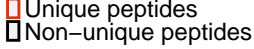
No. of times detected



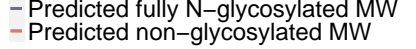
log(intensity)



Values from



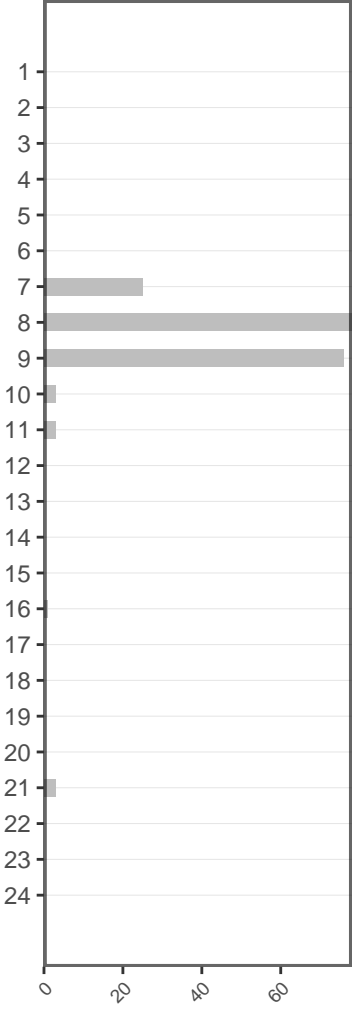
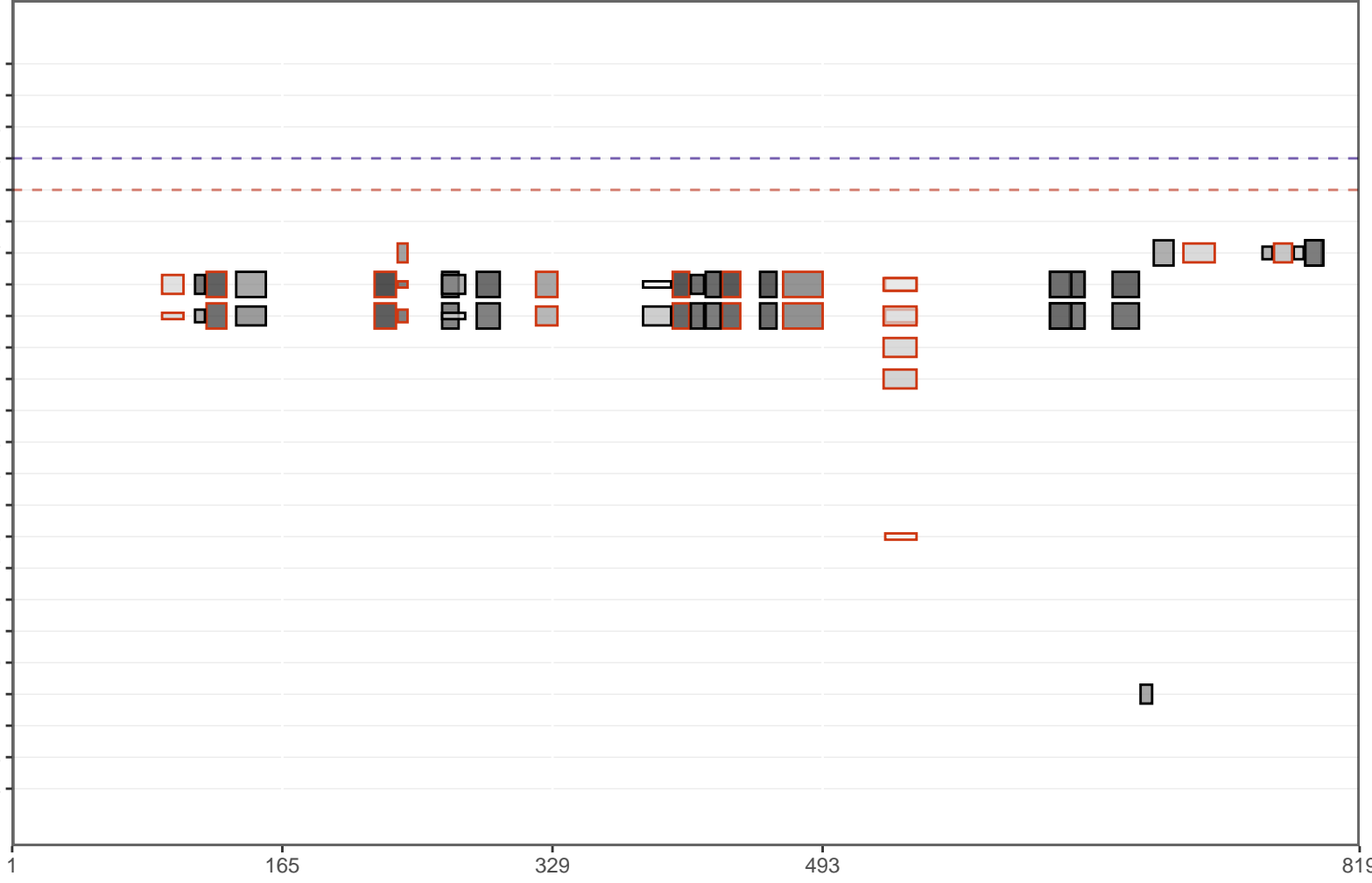
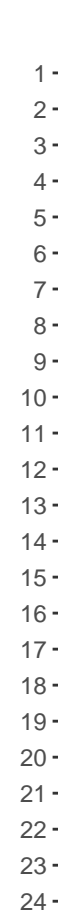
MW indication



Molecular weight

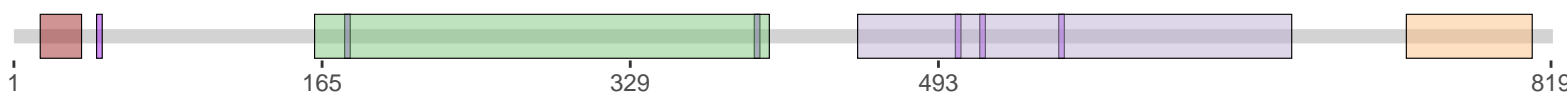


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00933 Glycosyl hydrolase family 3 N terminal domain
- PF01915 Glycosyl hydrolase family 3 C-terminal domain
- PF14310 Fibronectin type III-like domain

Protein sequence:

ESVDRVAVSNFNATLMLRLGFFDGGPKNHAYVGLGPKDVGSAEHGELAREAARGGIVLLKNSAGSLPLFPKSISLAVGPNANVGYTMIGSYEGTPEKLFITPLQGLNHSVTVYHPGGFNASVSCDPALEADAKKIAAADAVLVMGSDGQVERESKDRVNTLPGGGLLFEVAVSVEKGPVILVMGSGGDMVDFAVDNPKVTSIVHWGFFDGGGALADIFGYYNPSGRLPMTWYVQGVADKVDMTNMMMRADPKTGGPRGRVRFVWGPFTVFNFGDGLSYSNYKQ

NbL11g10930.1 non-specific_lipid-transfer_protein-like_protein_At2g13820 [MW - SP = 15.77 kDa]

No. of times detected



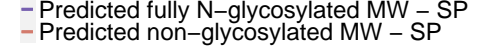
log(intensity)



Values from



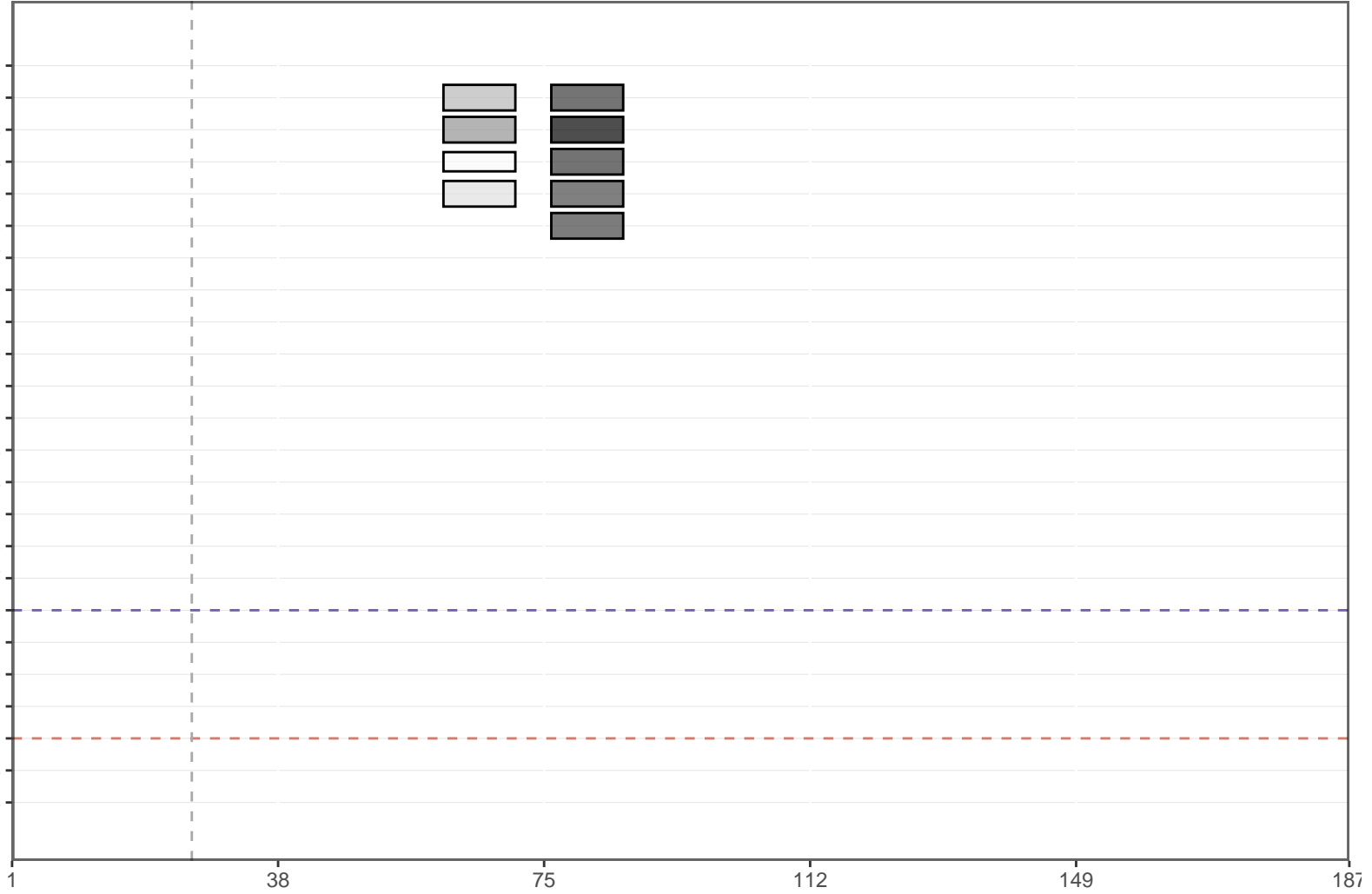
MW indication



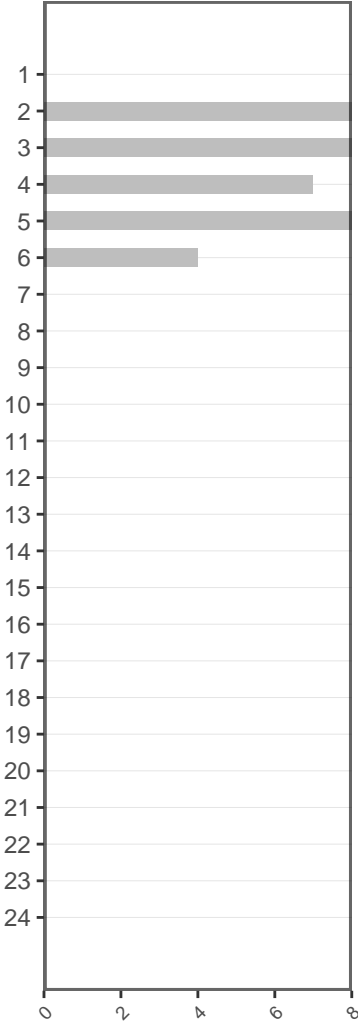
Molecular weight



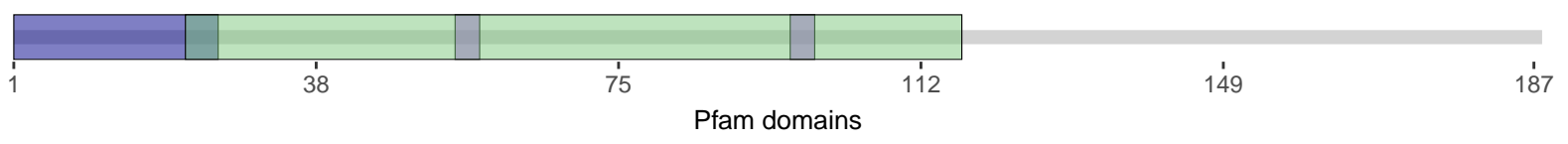
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

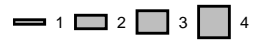


Protein sequence:

CLCEGFNLSAQLGVVLRITKAMALPMACHVSAPEVSSGGLSTDTGAAPLSPVAPPTMAGAWAPPTVEGASEVAPAPPGSSDNTLGLSISGLVLTAMAVAFQWF

NbL11g10920.1 probable_protein_phosphatase_2C_62 [MW = 86.78 kDa]

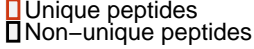
No. of times detected



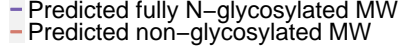
log(intensity)



Values from

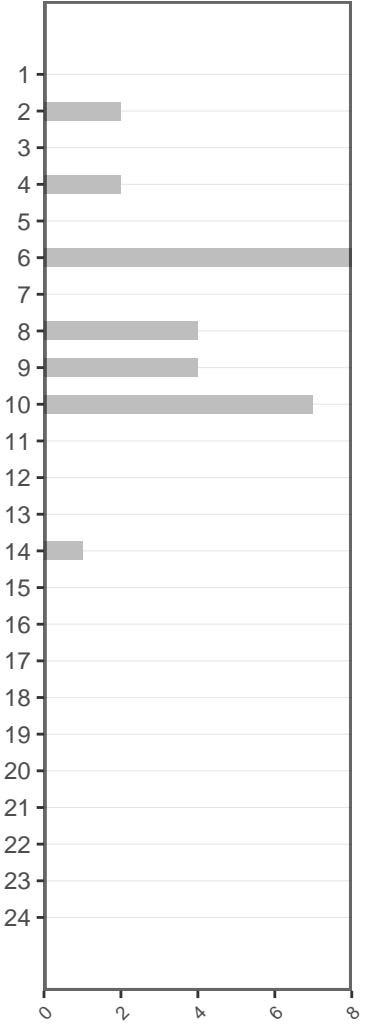
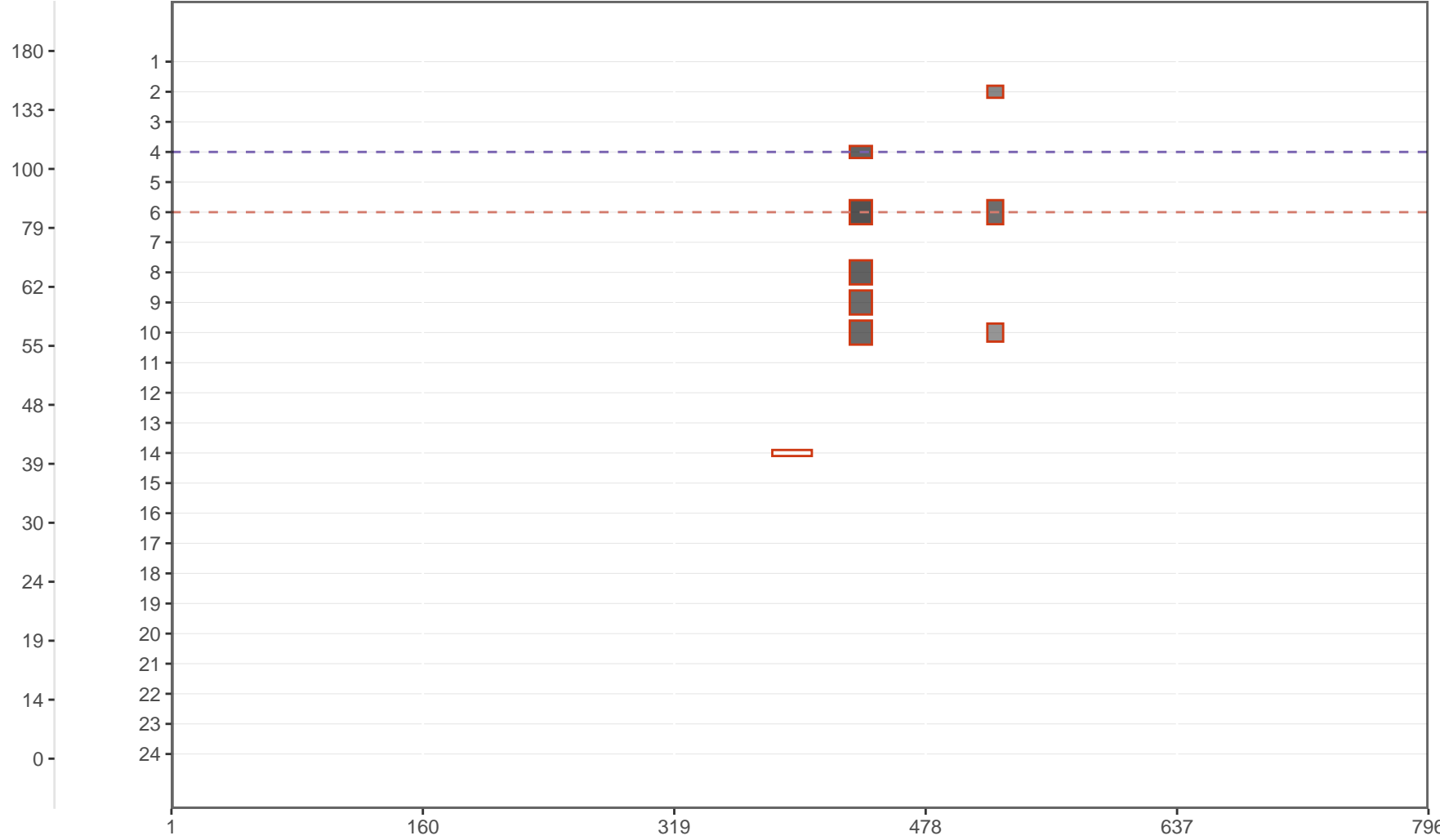


MW indication



Molecular weight

Gel Slice



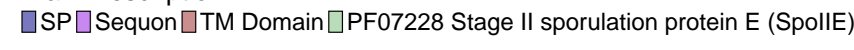
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EEENLENIETVYDEISPMADIRHFSIDAEELSTQVLSLELNDQTKLTFNSGDTEDGASQKGTFRDSDSEANVEVMPLSAMLEAEPLDEEVYDHLKLTSESNEEGESPLPREENLPNLSLEAEKEENAEENSEVREMSSGVEVYEDKSGEVLGSGSEKAPKELLSGGATLLEYPSKALTGQGHAEYFVAGGKWLGVADGGVGGWBLEGGSDPGVYAKELMQNSESVISGQGNMPPNDPKGVNLNLSVSKTDSFGSGSTALIAHFDGKDLHWASGGDSAFIRHNGSVYRKSPPMLHEFNLP

NbL11g10910.1 chlorophyll_a-b_binding_protein_CP24_10A_chloroplast-like [MW = 27.34 kDa]

No. of times detected



log(intensity)



Values from



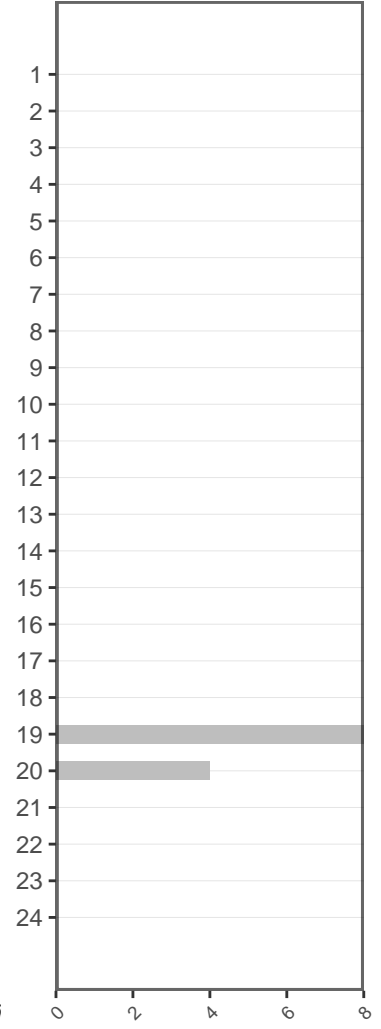
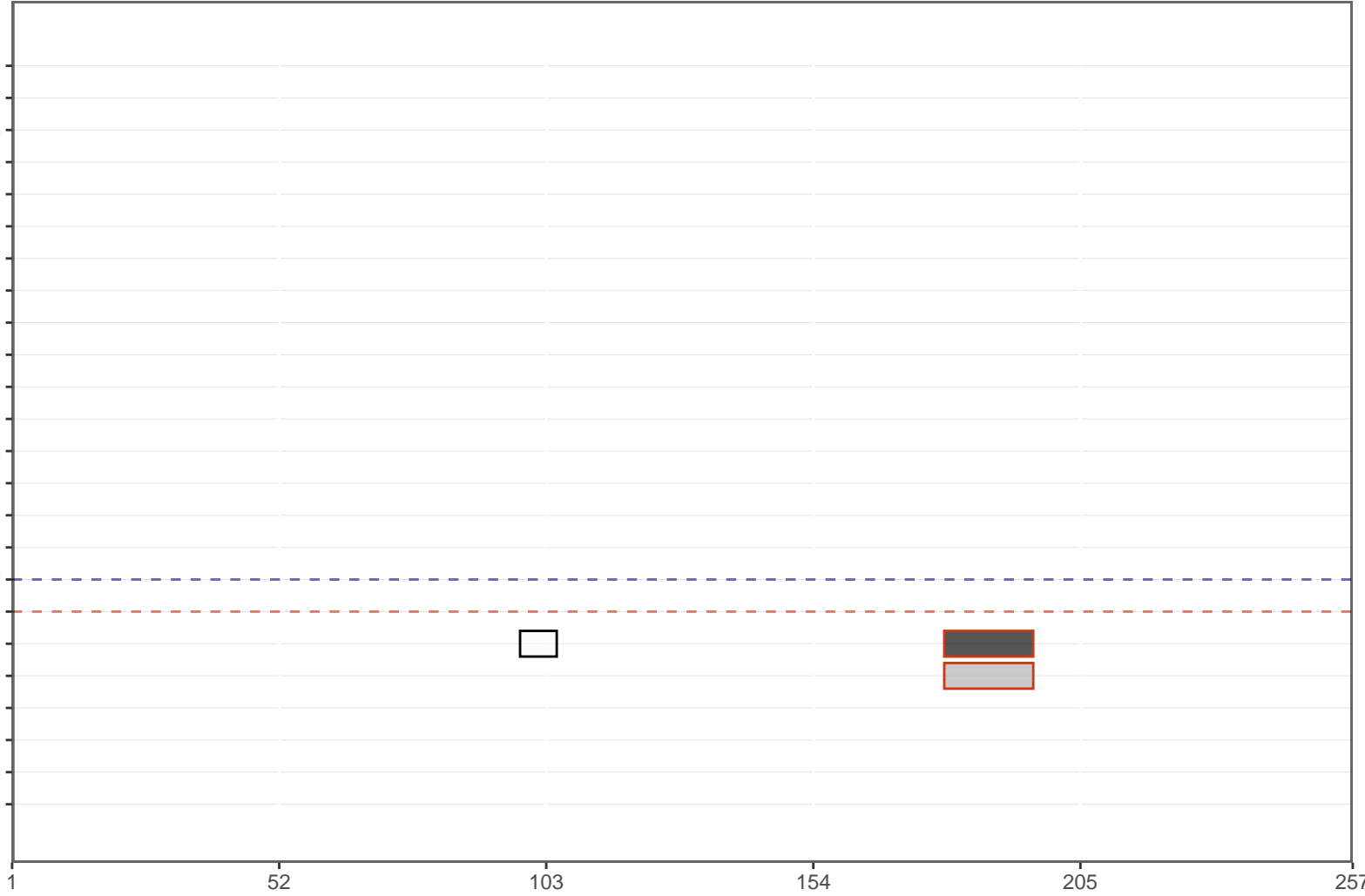
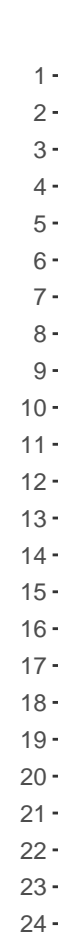
MW indication



Molecular weight

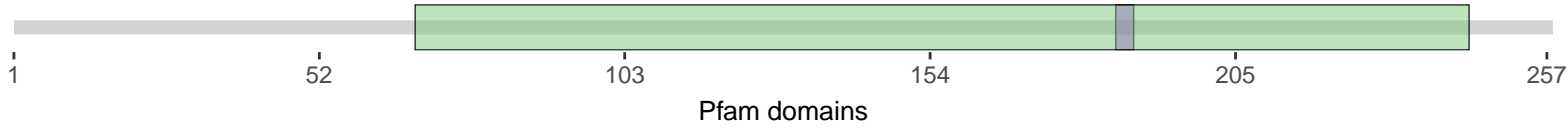


Gel Slice



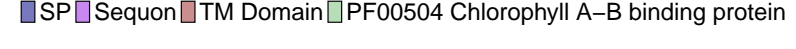
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

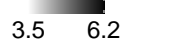
IGQAVSGIPWFEAGADPGAAAPFSGLLGTGLLLMGSWVEKRKRWDFNPEGSQVEWATPWKTAENFANFTGEGGYPGGKFFDPLSLAGTLGGGVYIPDTEKLERLKWAEKHARLAMLALIFFEAGGKTPLGALG

NbL11g10880.1 peroxidase_N1 [MW = 38.62 kDa]

No. of times detected



log(intensity)



Values from



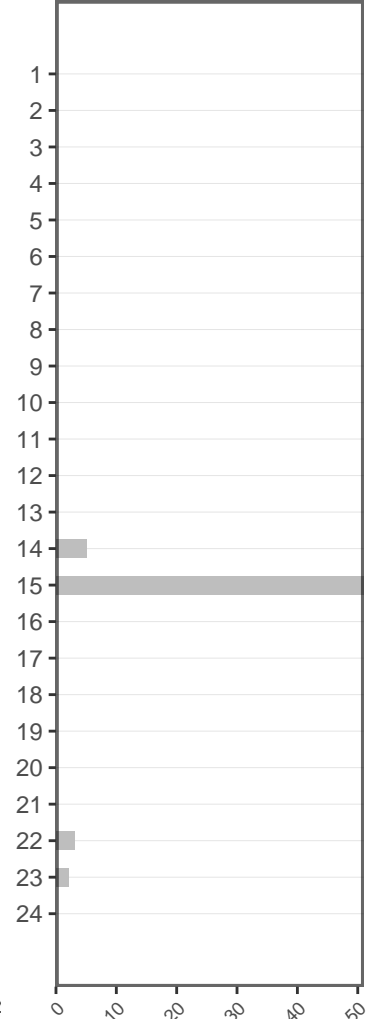
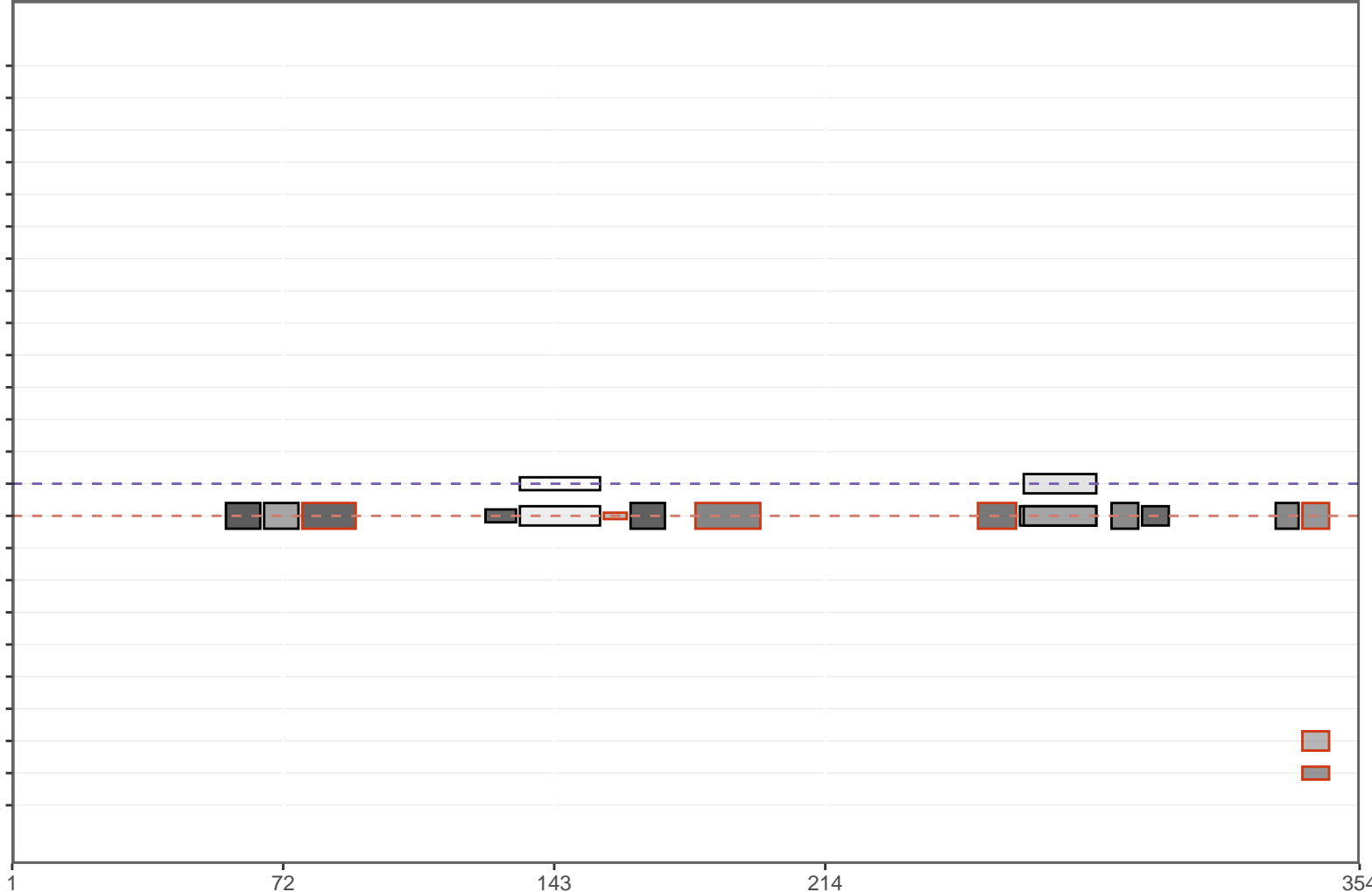
MW indication



Molecular weight

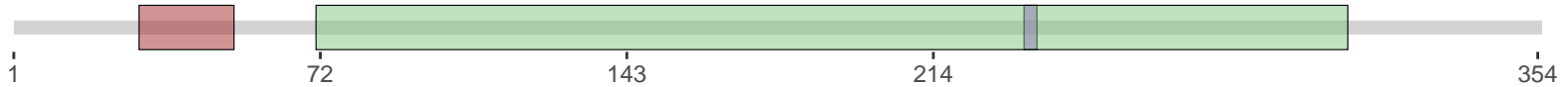


Gel Slice



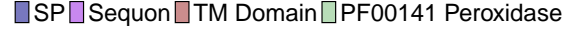
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SVPTGRDGRVSRADAGDLPAFFDEVDHGKFLRKLNFGDLVATGHTGTAGCAVHRDLFNFTSTGGPDSIDAFILPQLRALGPONGDAARRVLDTGVENNFDTYFNSLRNGRGLVESDQKLLWTDASTRFVYDFRFLGVRGLLGLTFQVEFRSMVMSNIEVKVETGPNGEIRKVCSEIN

NbL11g10690.1 nitronate_monooxygenase [MW = 36.12 kDa]

No. of times detected



log(intensity)



Values from



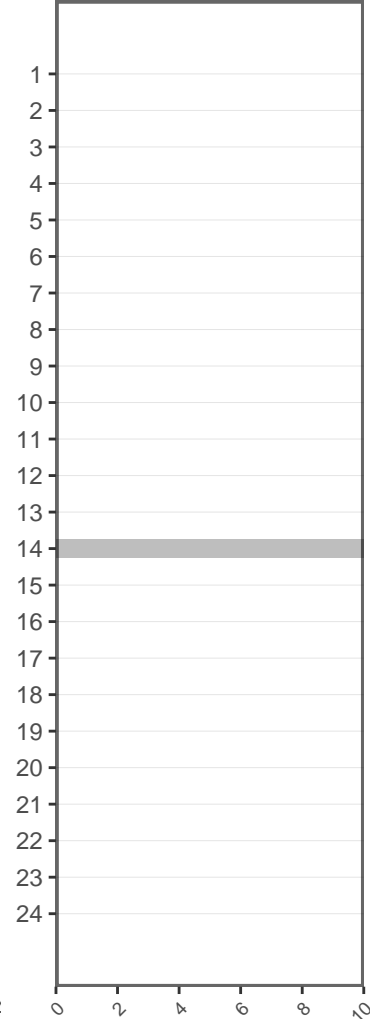
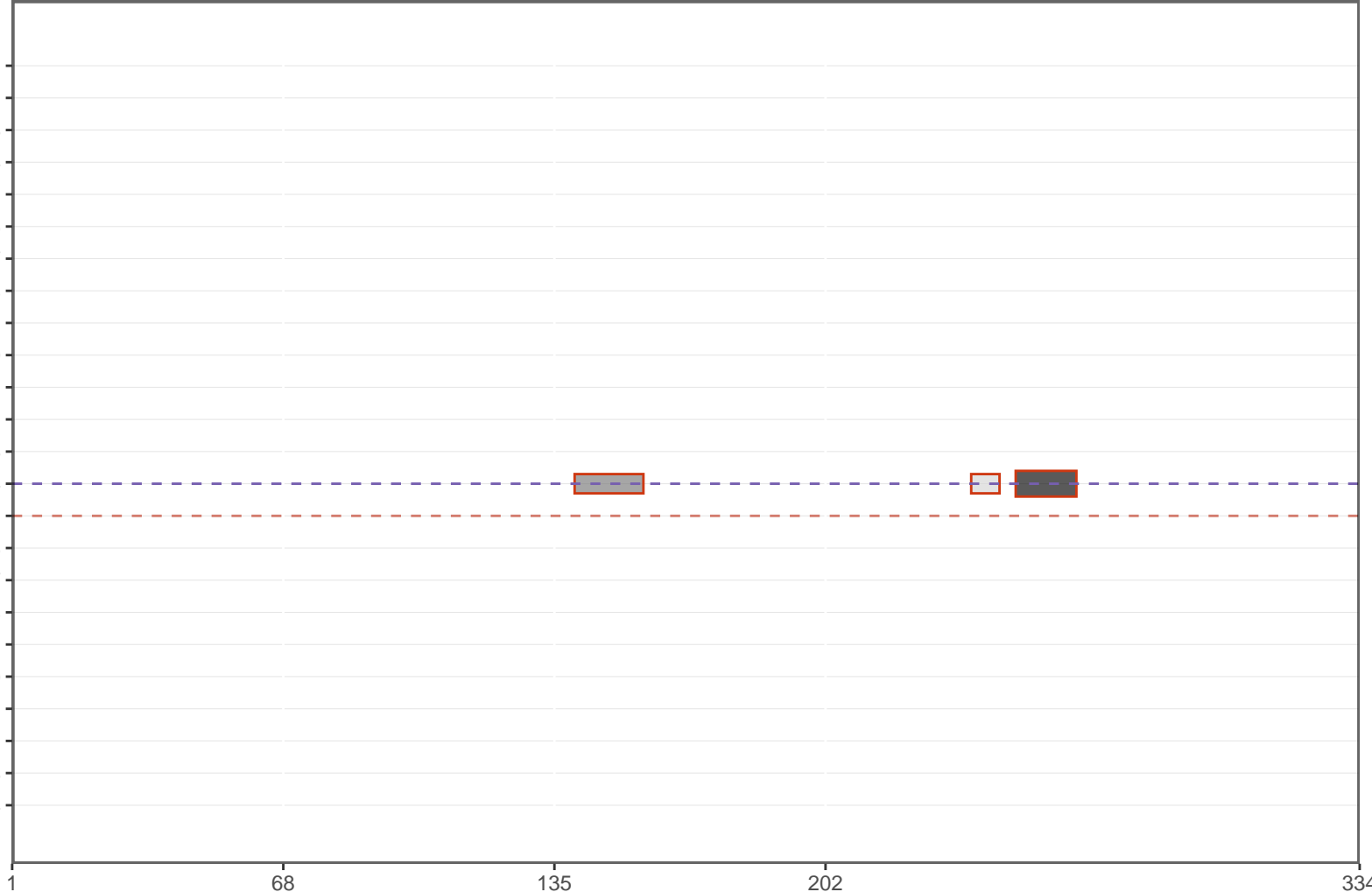
MW indication



Molecular weight

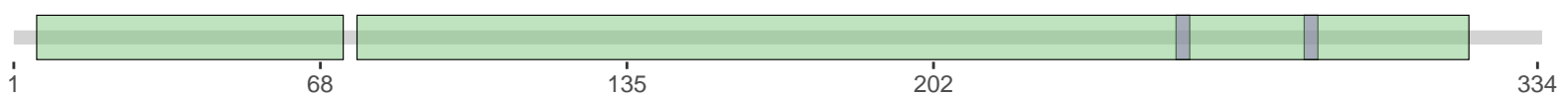


Gel Slice



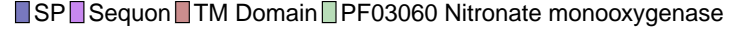
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

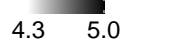
ILLPRVYDLYRGRDAVIAAGGVDAAGVAAALGAGQVSLGTRFLATEESVAHPTKRIKLEFEGETEYDIFGRARWPGAPHRVLAATPFKKEWALPSHENETNGPVGRTIHKGERVRRFAGTVPNASTTGDIESMMMYAGGSGIKLEIKELMGEVKGIVEGAGRUDOLFVPIW

NbL11g10680.1 protein_EXORDIUM-like_2 [MW - SP = 29.09 kDa]

No. of times detected



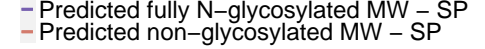
log(intensity)



Values from



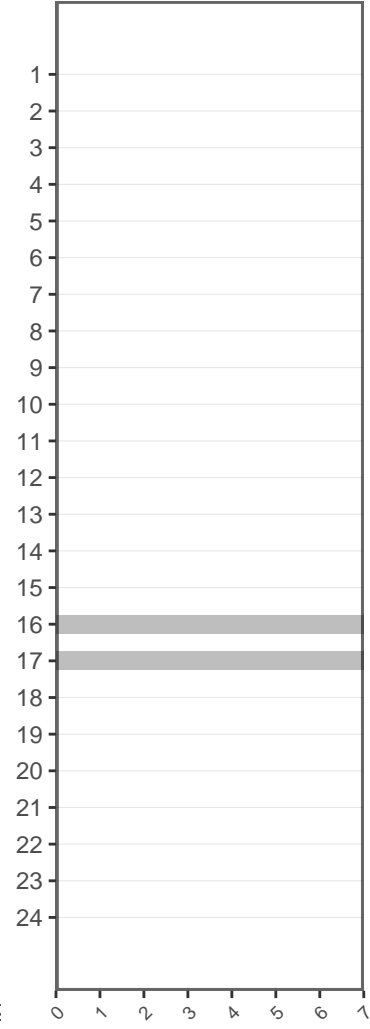
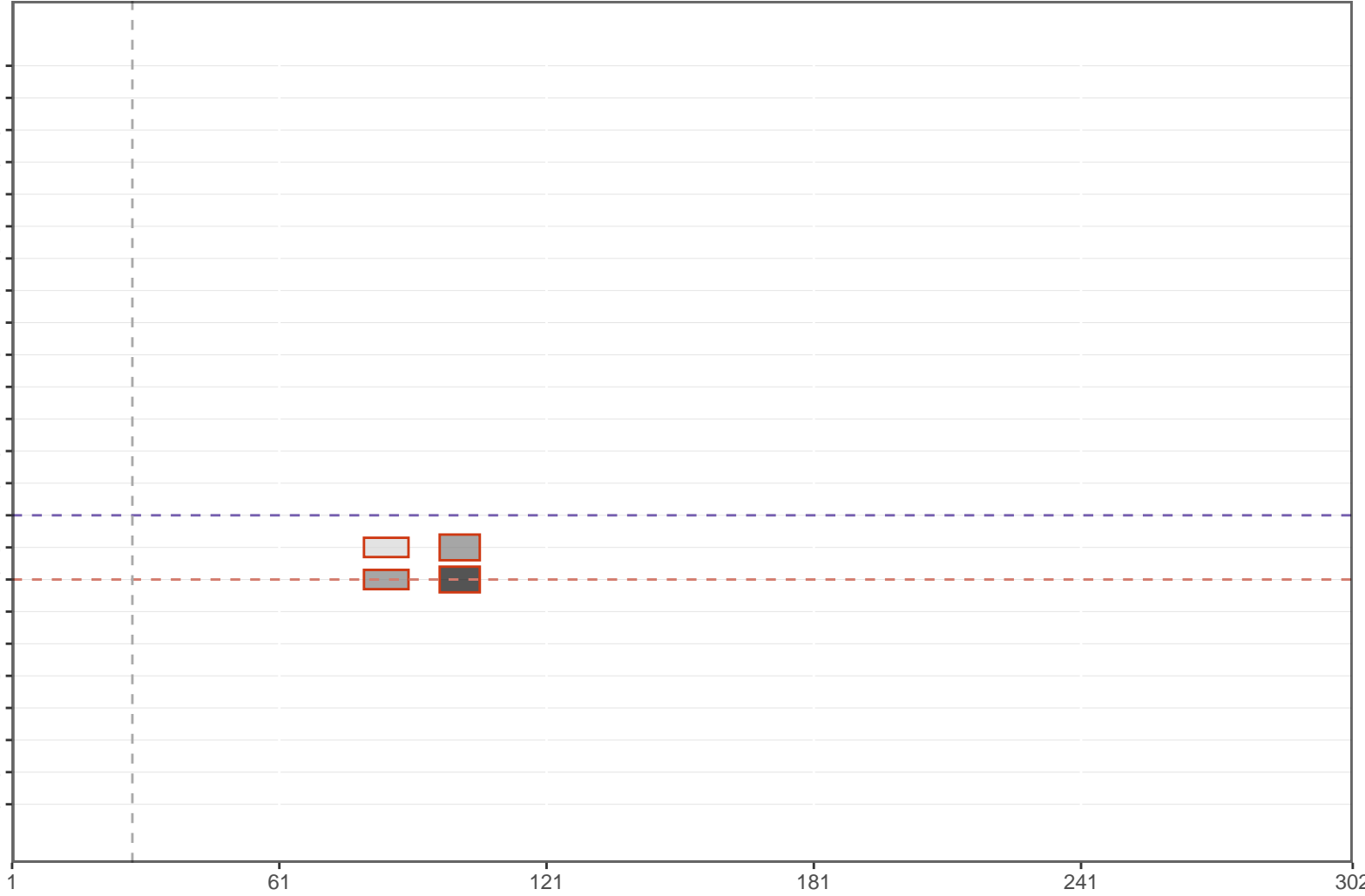
MW indication



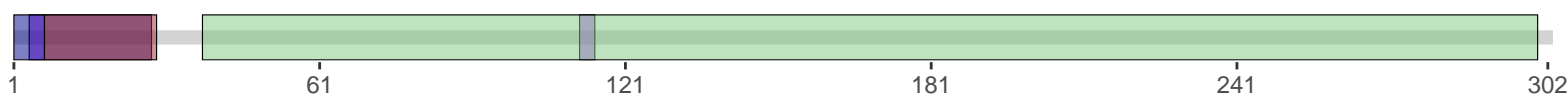
Molecular weight



Gel Slice

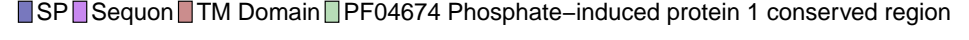


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

/LTKDVFVEGFCMSRDGTHGSTRGIRFAWVWVGNSETQAGGAGWPRFHQPIYGPOTFPLWAPNGVGVGDMINWATVLAGTVINPENNFGQGPAPLEAVSAGTGMVGGSYFGYGGQVLDKSTGASVNAHGVNRRFLPMMWDPKACSTLV

NbL11g10670.1 phospho-2-dehydro-3-deoxyheptonate_aldolase_2_chloroplastic-like [MW = 58.78 kDa]

No. of times detected



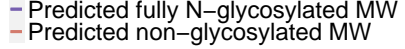
log(intensity)



Values from



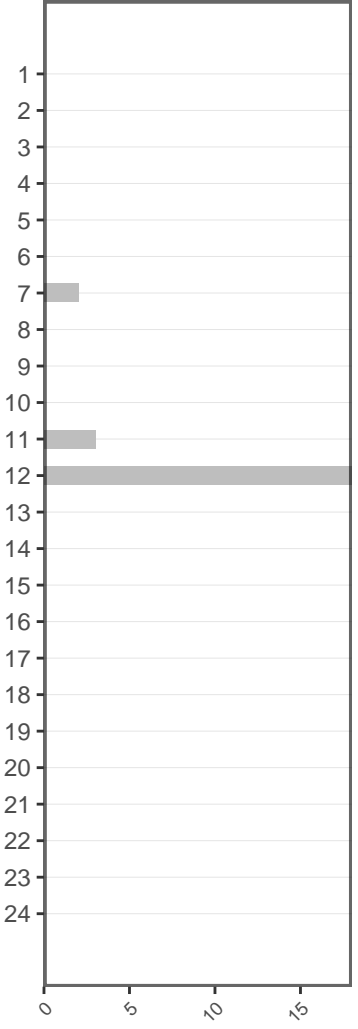
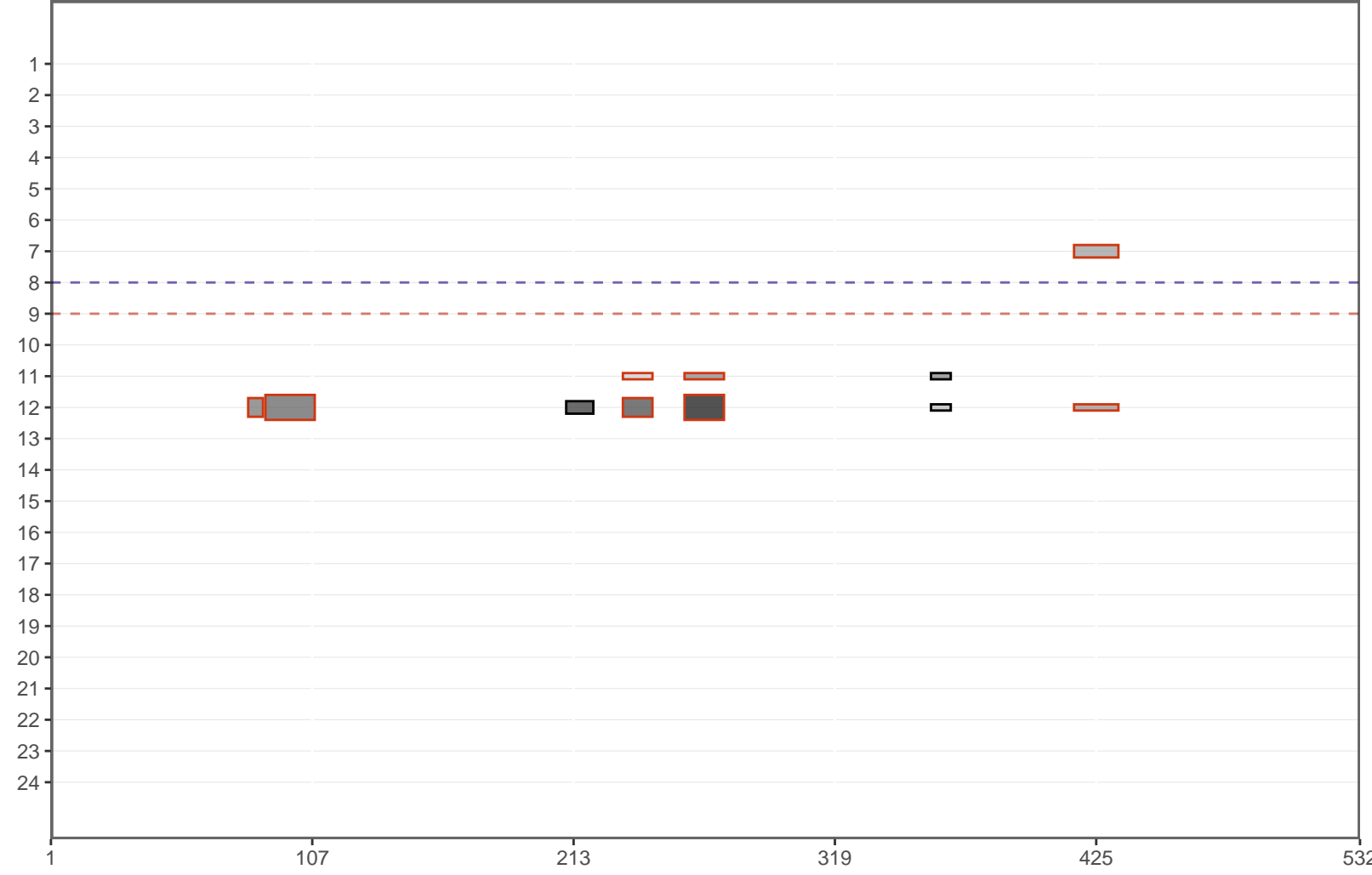
MW indication



Molecular weight

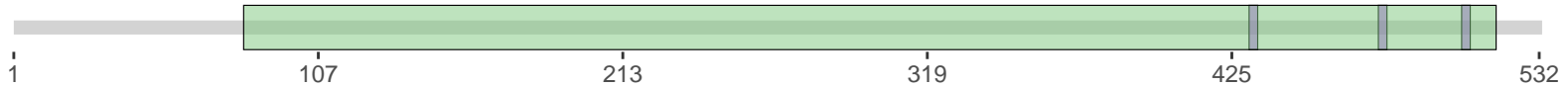


Gel Slice



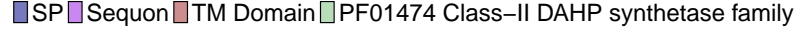
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

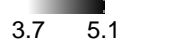
AGRINQWNLDFDTHSEGGDRVRELAHRVDEAMGFMSAAGITVDHPIMTTDFWTSHEGLLLPYEQALTRDSTGGLYVDCSAHMMWVGERTRQLDGAHVEFLRGIANPLKIKVSGKMDPDELKLIIDINPQNRPRITVIARMGADNMRVKLPHLRVIRGAGGIVTWVSDPMHGNTTKAPGLKTRFDSIRAEIRAFFDFVHDGEGGYPGGVHLEMTGQNVTECVGSGRITFYNLSSRYHTHGDPRLLNASGALELFLIAERLKRRLGPKFR*

NbL11g10520.1 bifunctional_riboflavin_biosynthesis_protein_RIBA_1_chloroplastic-like [MW = 60.16 kDa]

No. of times detected



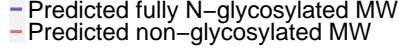
log(intensity)



Values from



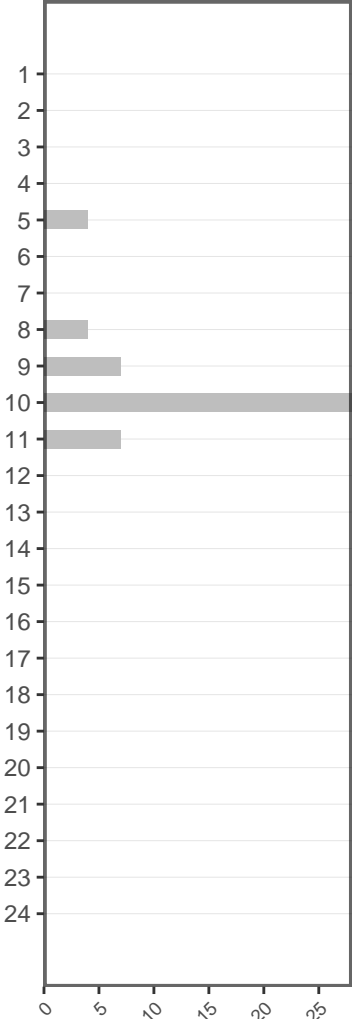
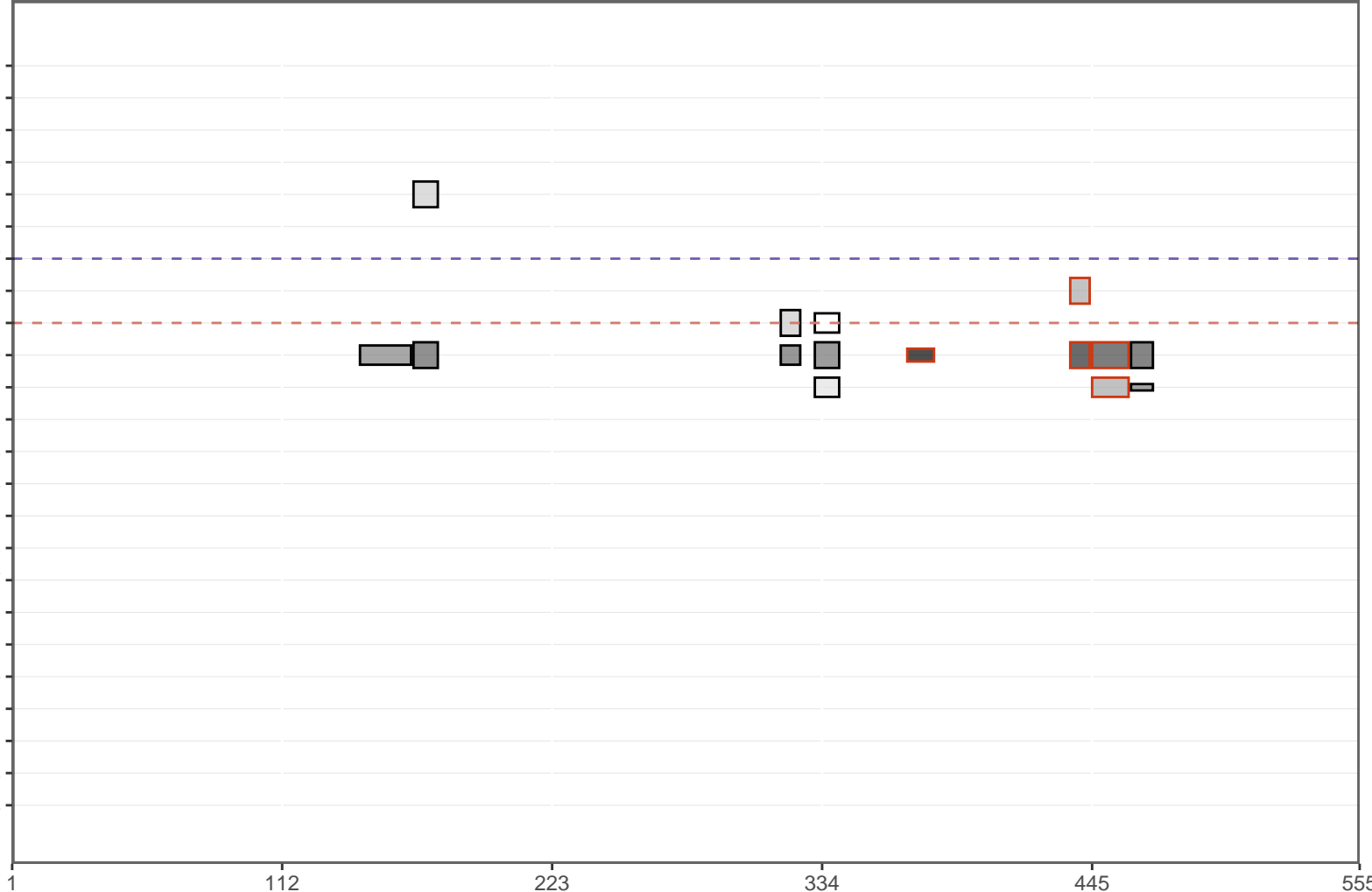
MW indication



Molecular weight

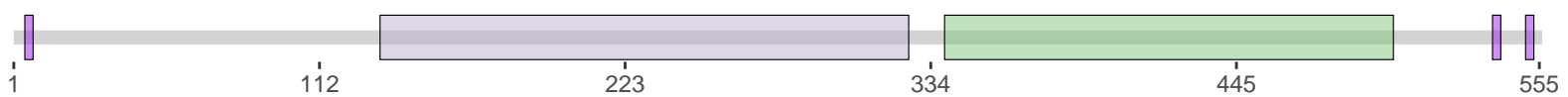


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SGVLKRAGHTEASVPLAMLAGLDPGVGVEDEEDGSMARLPKLPFOFAKEHNKHSVADLRVRRKRQDQLVEHSAARLPTMWGPFTHGFKGIDGIEHAMVKGDSGDDGLVRRVHSEGLTGFSGARDDGNGQLALAMQDGEAAGKGVLLVLRGHEGRGLGHKLRAYNLQDAGRTVEANEELGLPLVDSREYVGGAGMLRDLGVRTMLMTNPNPKYRGLKGVGLAISGRVPLLPPTIKENKKYLETKRKRMGHVYGLDURRATSENTSTTNGKPNVENSTI

NbL11g10290.1 guanosine_nucleotide_diphosphate_dissociation_inhibitor_At5g09550 [MW = 49.66 kDa]

No. of times detected



log(intensity)



Values from



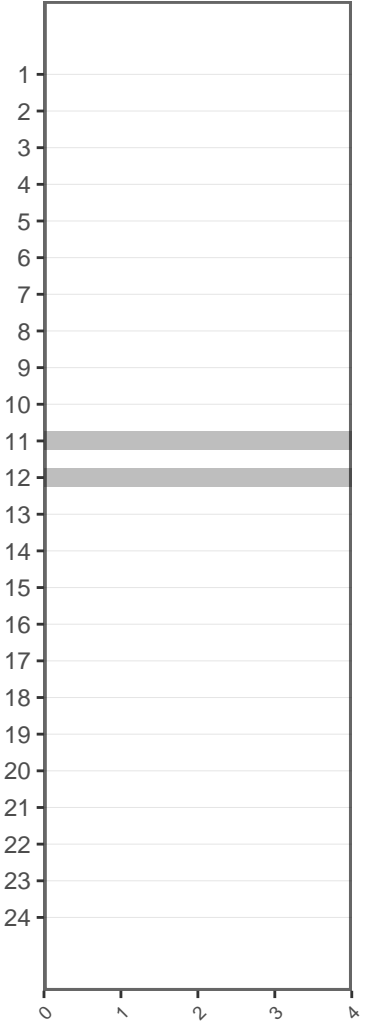
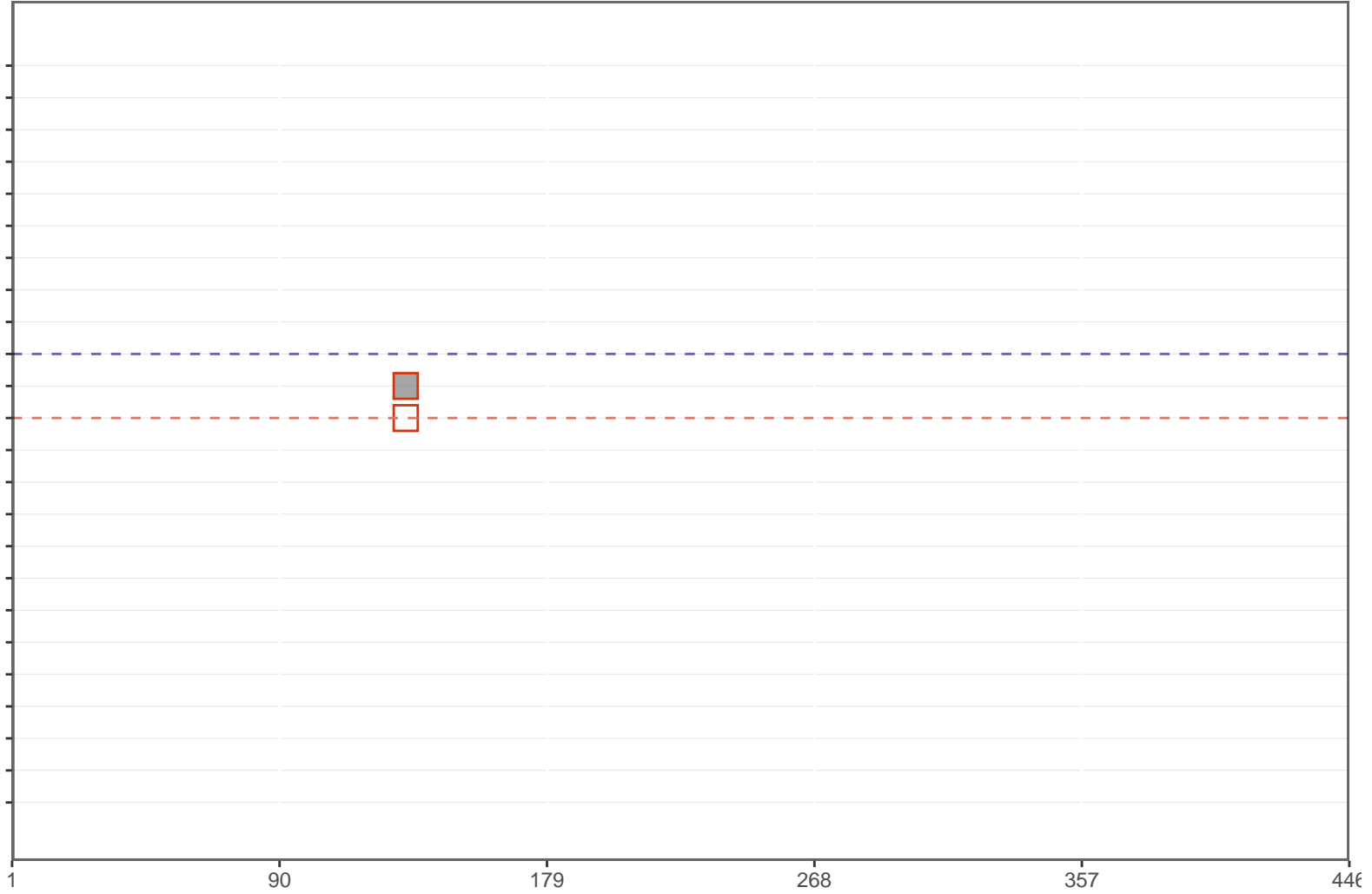
MW indication



Molecular weight

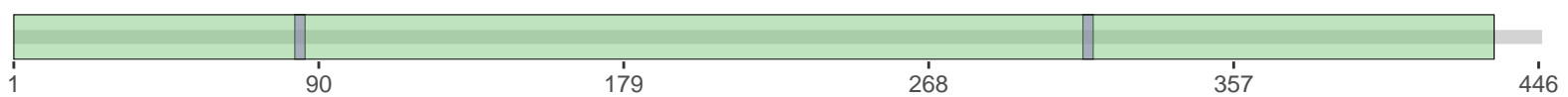


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AESLARFGAGSPYIWMYGLGELPQAFARLSAVYGGTYMLNKPQKVFEDENKIVGVITSEGTAKGKVVGDPSYLPDKVQKVKVARAIGMISHPIPDITNDSHSAQVILPQKLGKRSMDMYLFCGYSYSHVAPKGGKVFVSTEAETDDPETELKPGVGLGKPVDEIFYETYDRFAPSHSDAANDCFISKYDSTTHFESTVMVLDVMSKFTGKVVLDLSDLSAASATAEE

NbL11g10180.1 T-complex_protein_1_subunit_alpha [MW = 59.11 kDa]

No. of times detected



log(intensity)



Values from



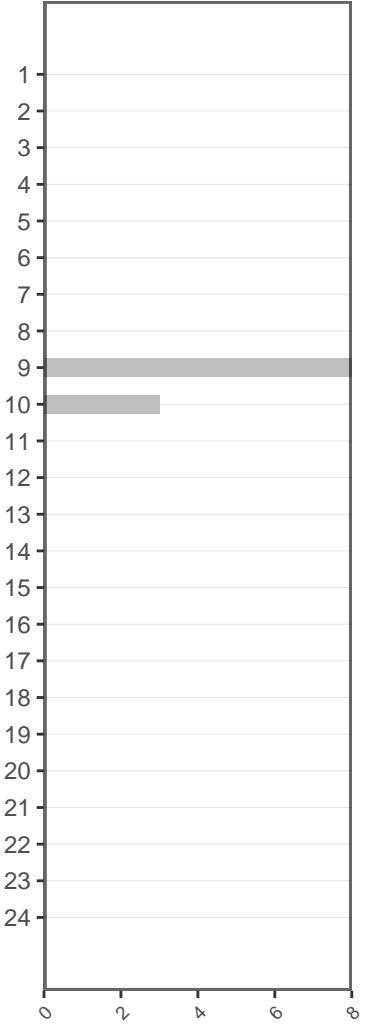
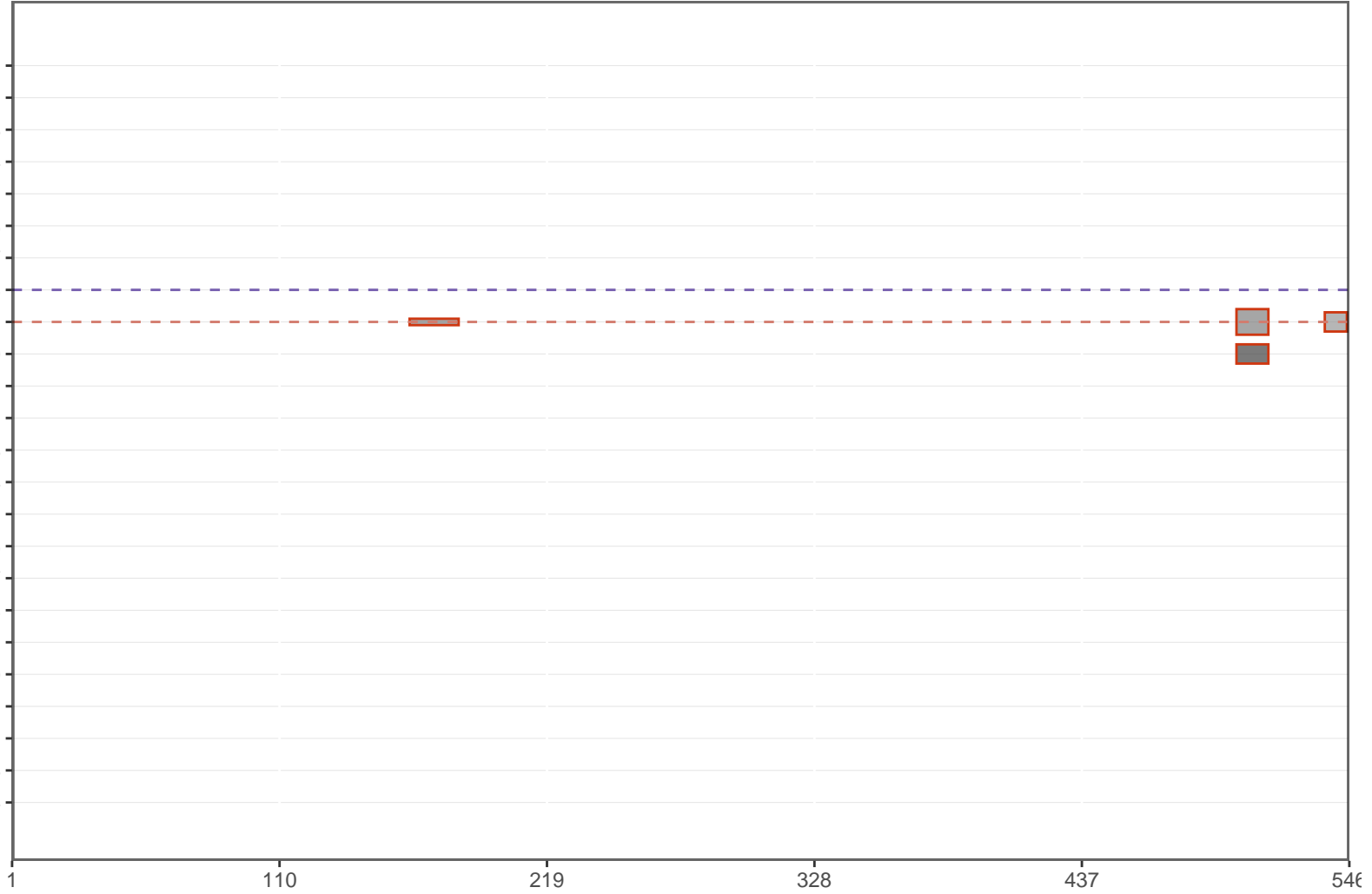
MW indication



Molecular weight

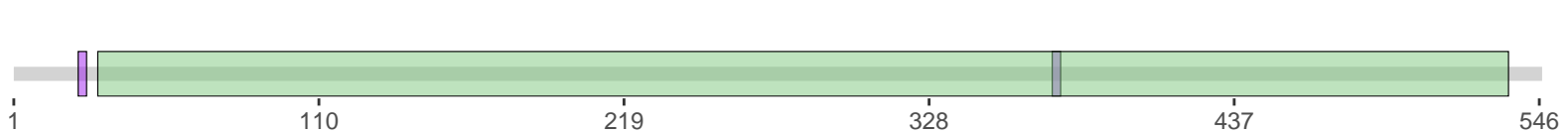


Gel Slice



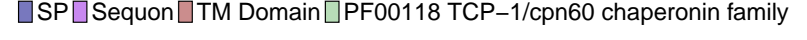
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DPRELEIRQREADMTKERIGKLLSAGANVYVLSKQIDDIMALKYFVEAGIAVRRVRKEDLRHWAKATGATVYVSTFADMECEETFEPELLGHAEVVEERIAADDVIMVWGTNRNSSVSLIRGANDFMLDEMERALHDALGVKRTLESTTVVAGGGVAEALGVYLEYLAFLTSGREGLAAPFAESLLVFPKVLNANAAKDSBLLVSKLRSGHYLAGTKADKKHLSSMGLDLAKGTVRNLLGAGVIEFAMGKVIKGFATSAATILRIDDMIRLVKDESGNDP

NbL11g10140.1 malate_dehydrogenase_cytoplasmic-like [MW = 39.49 kDa]

No. of times detected



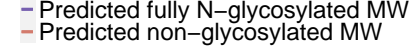
log(intensity)



Values from



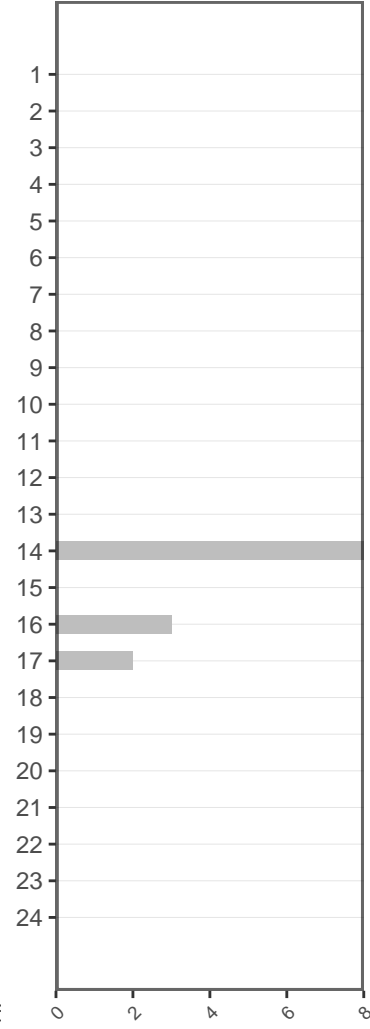
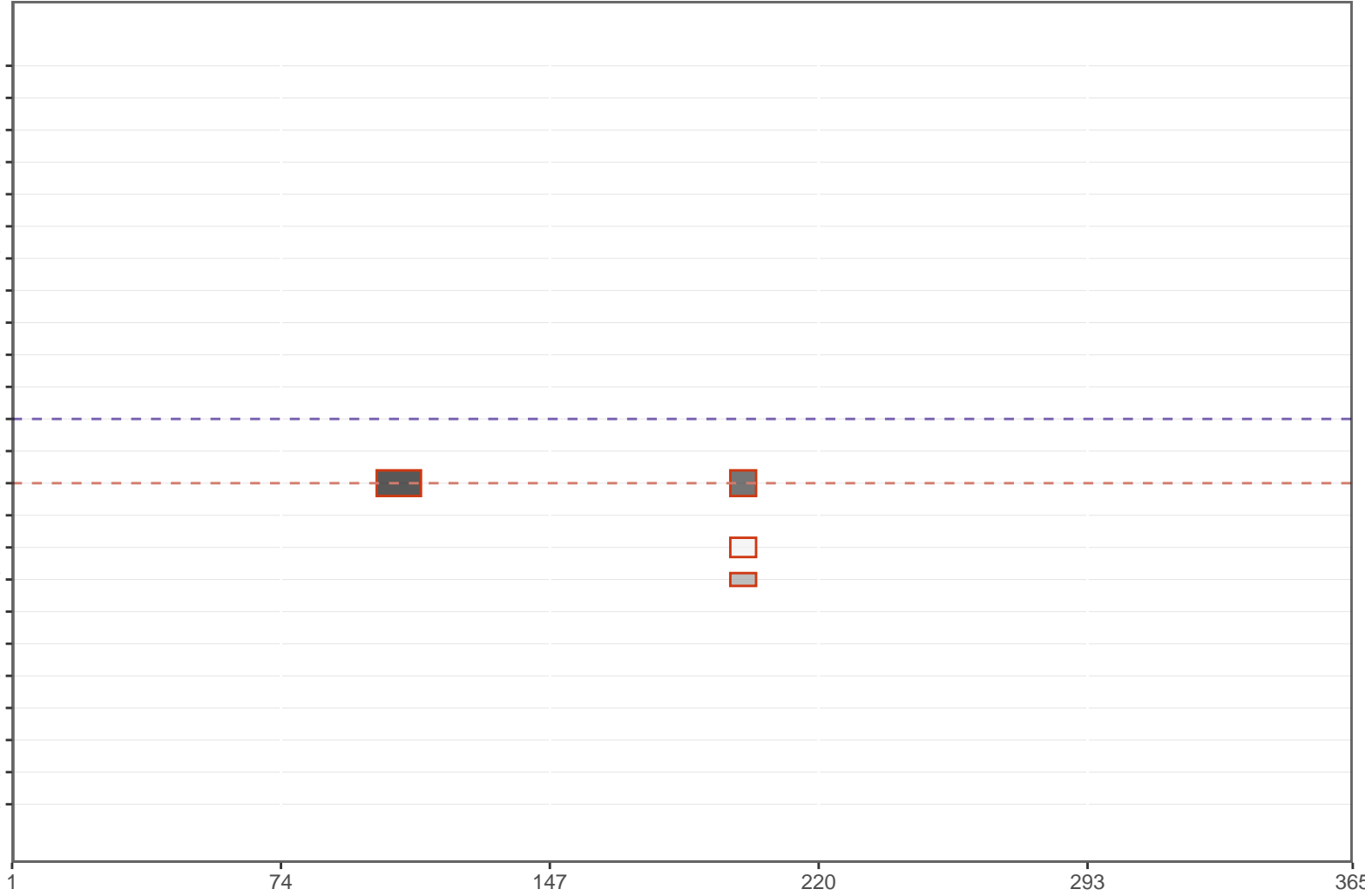
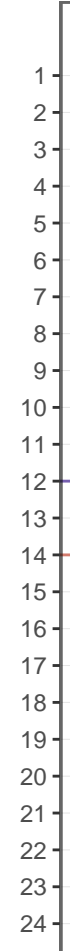
MW indication



Molecular weight

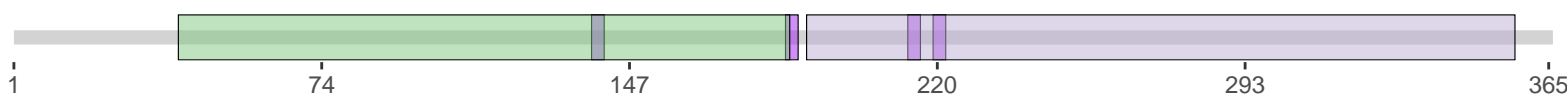


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF00056 lactate/malate dehydrogenase, NAD binding domain
- PF02866 lactate/malate dehydrogenase, alpha/beta C-terminal domain

Protein sequence:

LLLKEFAPSPFEKNTGLTRLDHNRALGQVSRERLNHHVGVKNNVTIWNHSTGQVDPVNHATVKTTSQGEKVRRELVANDQWLNTEFFTTVQGRGAANKARKLSSALSAASSAGDHRIRNIVVLTGTPKGTWWSMGVYSDGSGVPPGLIYSPFVTEGKEGWSIVGGLKIDFRFRKMDASAKELIDKSLAYGLN

NbL11g10110.1 elongation_factor_G-2_mitochondrial [MW = 84.29 kDa]

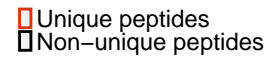
No. of times detected



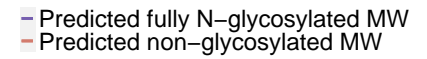
log(intensity)



Values from



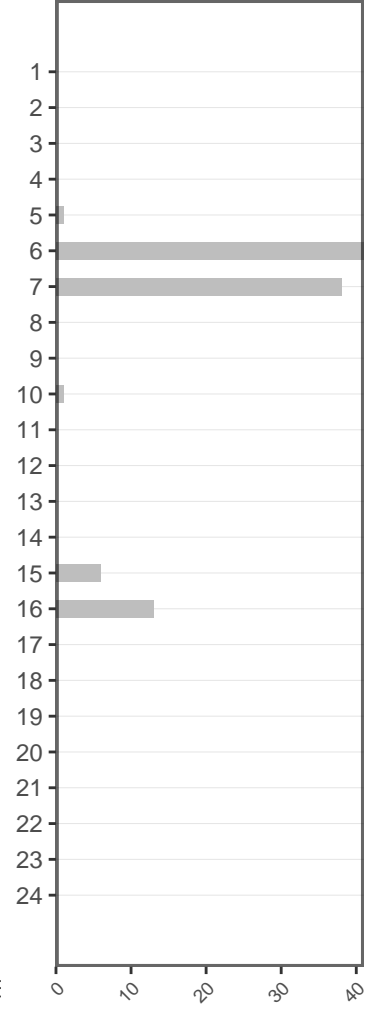
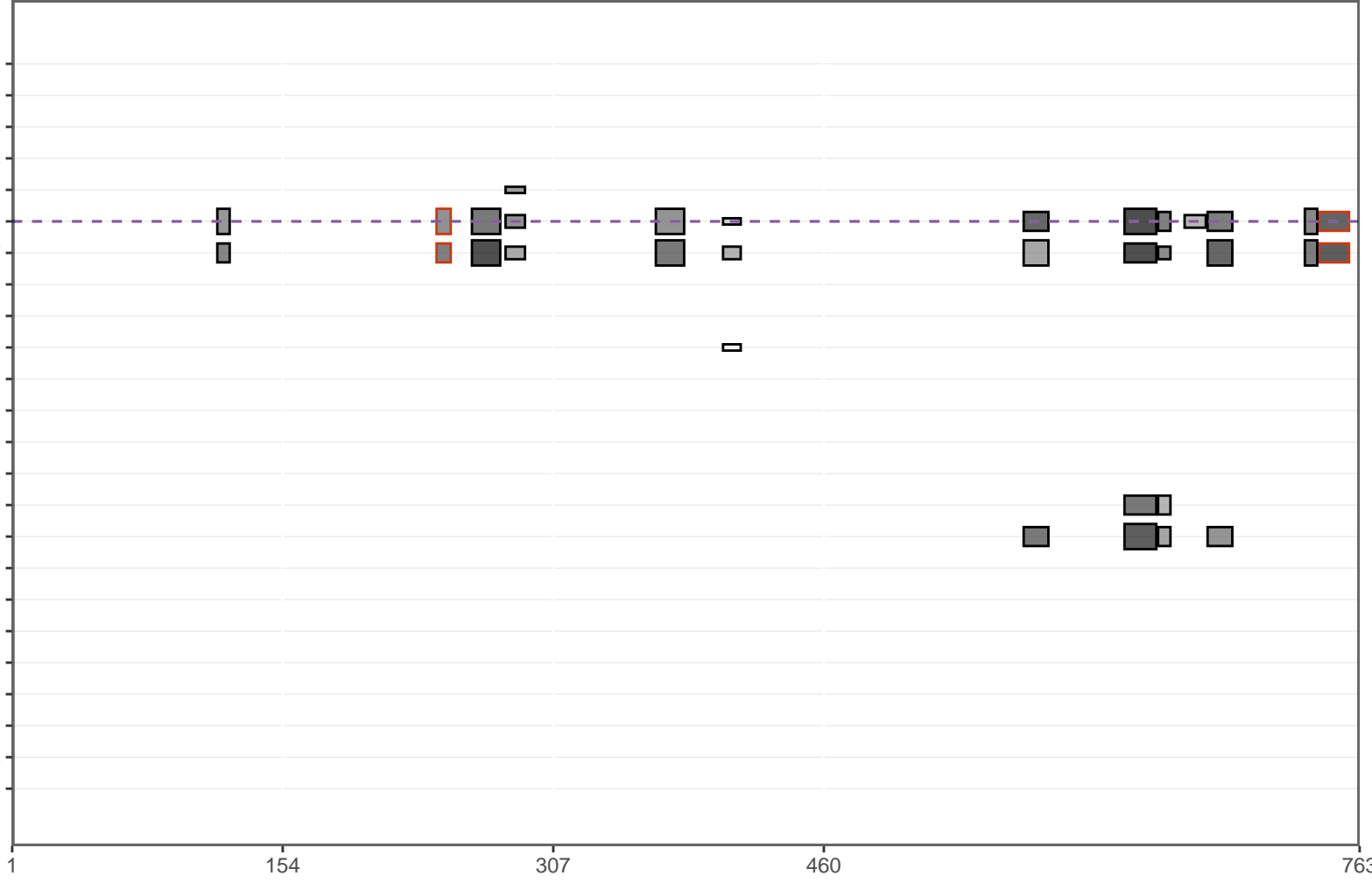
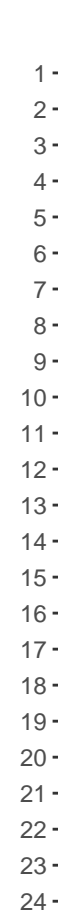
MW indication



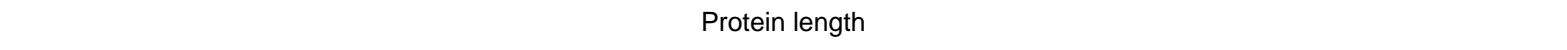
Molecular weight



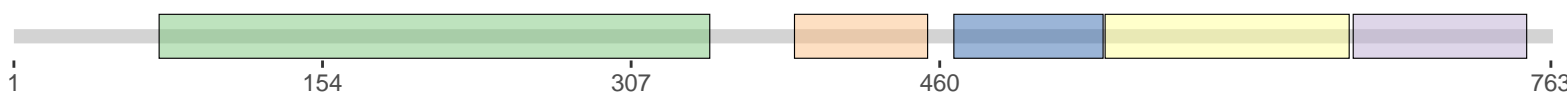
Gel Slice



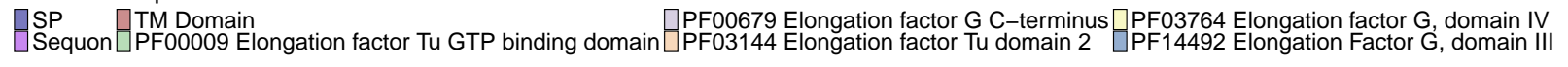
Protein length



Pfam domains



Pfam Description



Protein sequence:

IPTGRLVALFKLEEGFGLTFLRIVEGVIRKGDFFINNTGKRKIVRLRMHSNEMEDDGEAHAGQIVWFVGVDCASGDTFTDGSWYTMFGMNVPEFVMSLAVPVGKDGSGGQFSKALRFQREDPTFRVGLDAESGETHSIGMELHLDVYVERIRREYKVEAGVQKPRVNFRETITKRAFDFLHKKQSGGGQYGRVIGYVEPLEGGSSGKFEFDNMLVGGVAPNPFVMEKGFREAAANGSLGHIPVENIRVLTGDNHAWDSSELAKLASYAFRCQYAAKPF

NbL11g10000.1 phosphoribosylamine--glycine_ligase-like [MW = 54.82 kDa]

No. of times detected



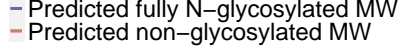
log(intensity)



Values from



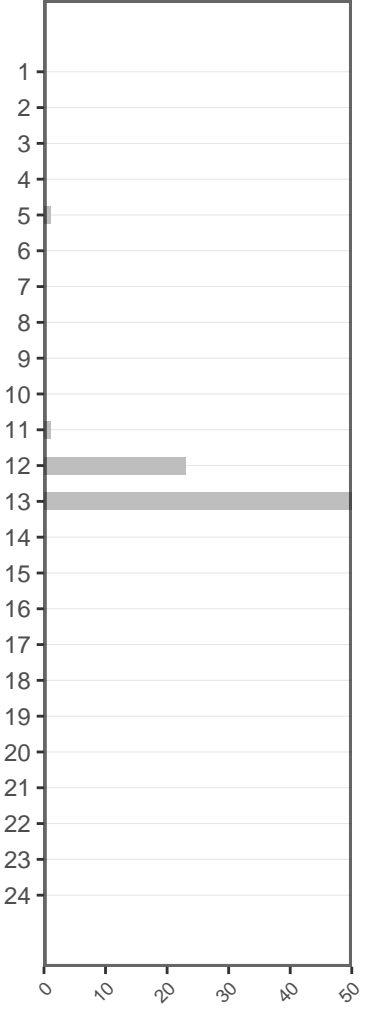
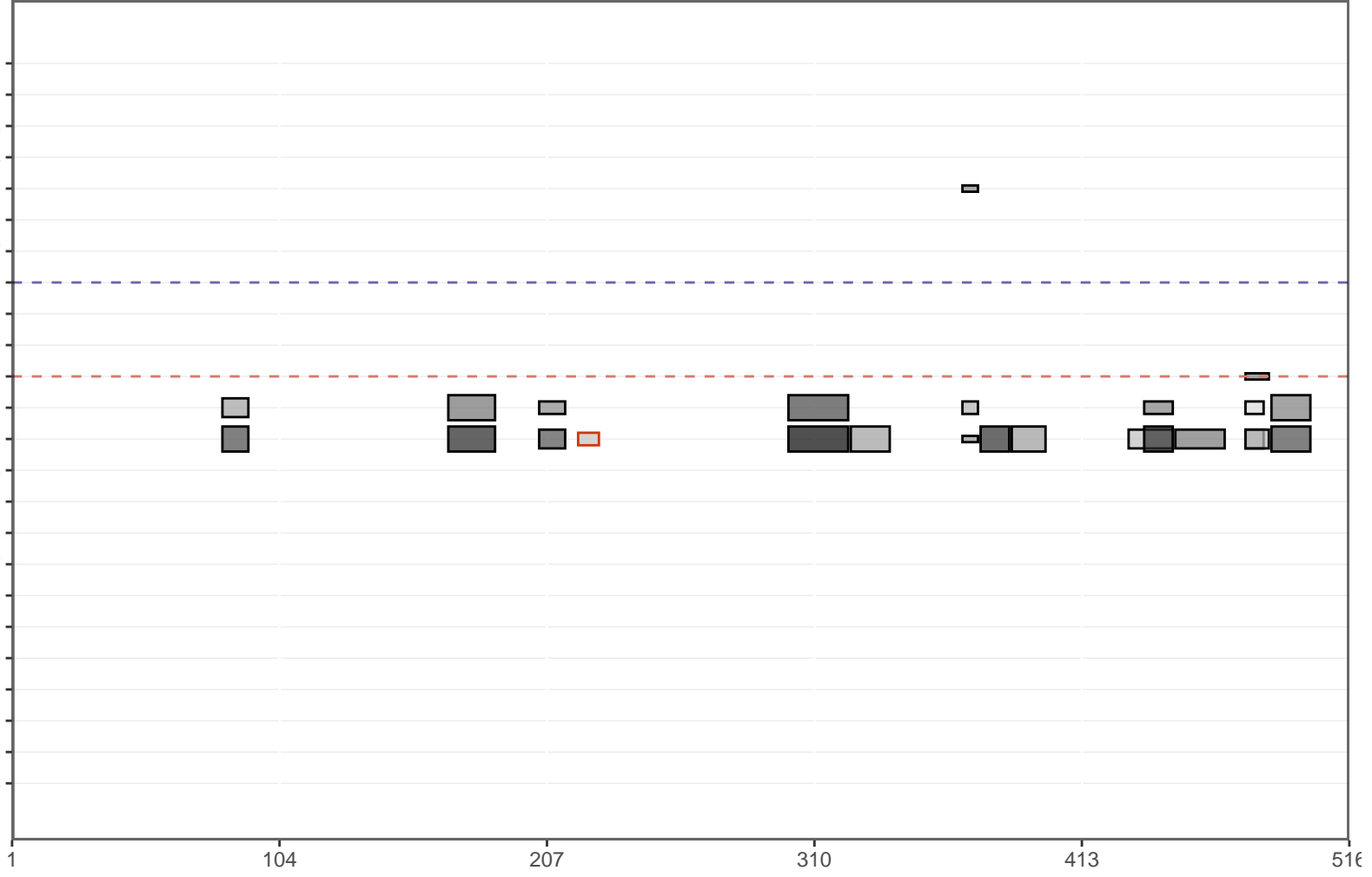
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01071 Phosphoribosylglycinamide synthetase, ATP-grasp (A) domain
- PF02843 Phosphoribosylglycinamide synthetase, C domain
- PF02844 Phosphoribosylglycinamide synthetase, N domain

Protein sequence:

EAVDSMLVENYFGAGSRVVEEYLEGEEAFALVDGEHAPLESAGDHKRVGGDGTGPTFGMGASNPAPVLTKELGSVVMESHFPTVKGMAEEGGKFGVGLVAGLMEKKTGFKLIEYNVRFQDFPDCQVLMVRLESQDVEVLLAAGRGLRGLVSLDWSFGSAMVVMASGKYPGSEYKGTVHKLEEEAQVAPSVKVFHAGTAFDADGFIATGRRVIGVTAKGEDLEEARDRAYQAVEQHGWPGGFVRRDGGWRALPQKQYS

NbL11g09790.1 peptidyl-prolyl_cis-trans_isomerase_CYP40 [MW = 40.32 kDa]

No. of times detected



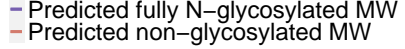
log(intensity)



Values from



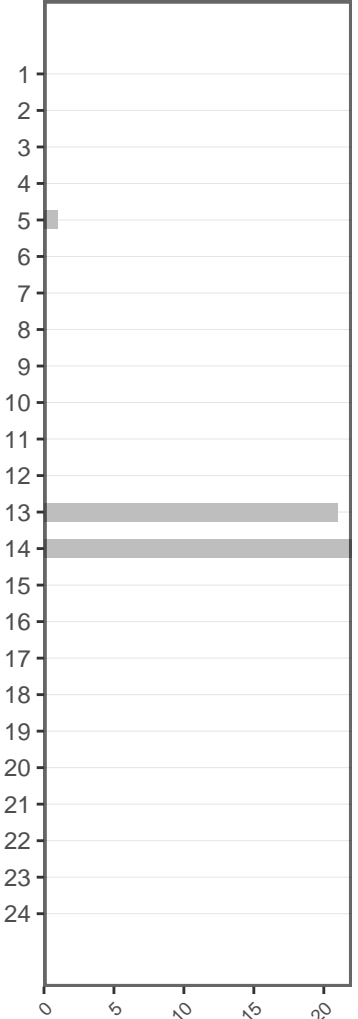
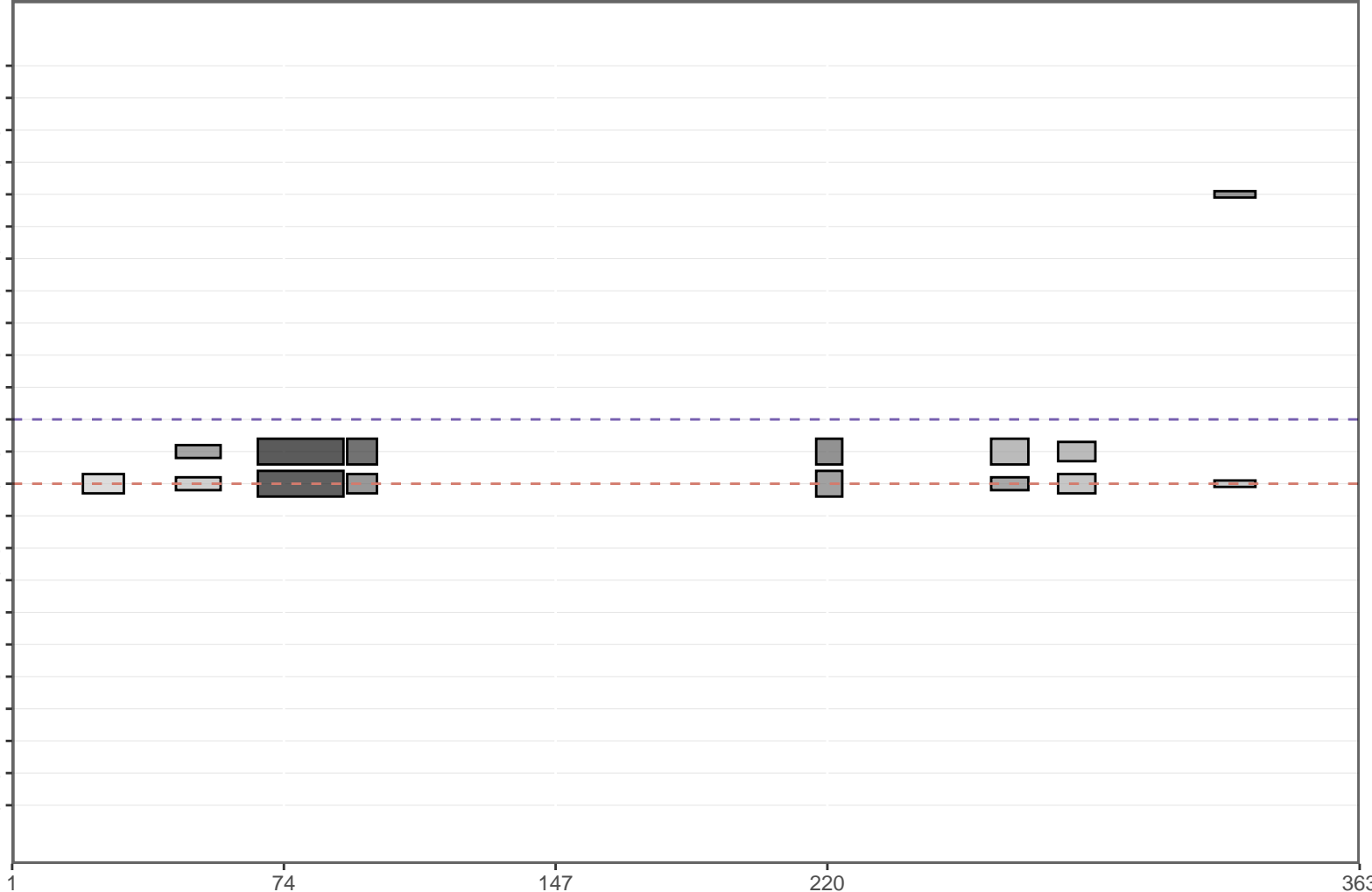
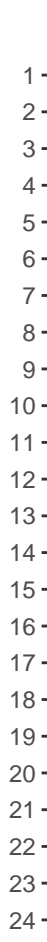
MW indication



Molecular weight



Gel Slice



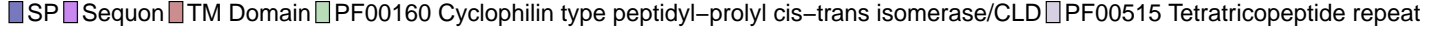
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DCGEIPEGADGGIANFFKDGDLVPPWADLDNNTDDISWVWVTALEAKAFGNENFRKGDYKMLARKYRKALRYLDICWEKEEIEDRSAYLRKMKSGQFTNSACKLKLGLDGLDADDFAMRDGENNAKALFRGGGAHMLNDIDAIVESYKALELEPNDDGGIKNGLAAAKKKIADRDRKEKKKWARMFQK

NbL11g09670.1 probable_N-acetyl-gamma-glutamyl-phosphate_reductase_chloroplastic [MW = 44.22 kDa]

No. of times detected



log(intensity)



Values from



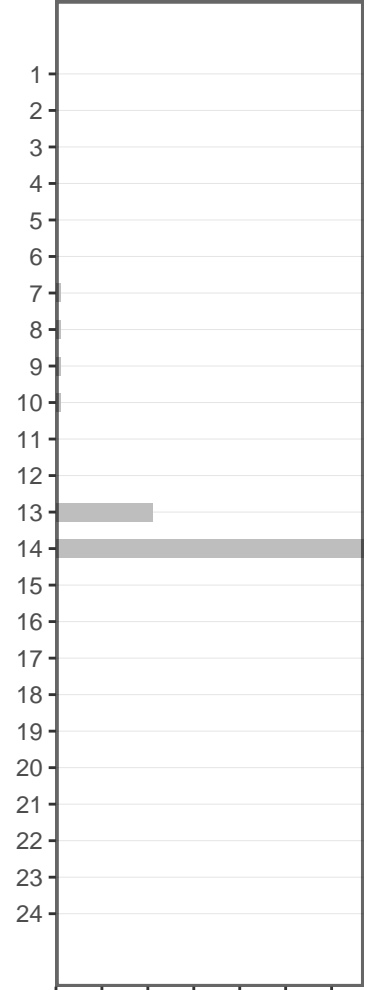
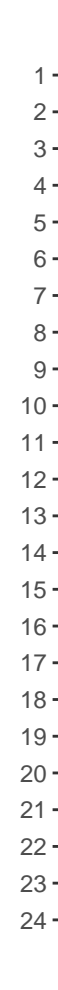
MW indication



Molecular weight



Gel Slice

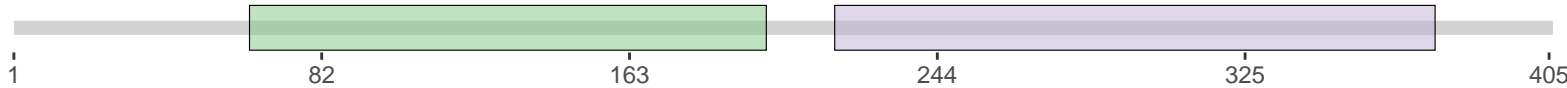


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF01118 Semialdehyde dehydrogenase, NAD binding domain
- PF02774 Semialdehyde dehydrogenase, dimerisation domain

Protein sequence:

.TETSRREIQSARLVANPGGYPTFEVQLFPLIKLNIEVRIIIDEKSGVSGAGRAAKEANLFTMEAGIRSYGTRHRHVPVEIEGQLBEAANSKVTVSTFTHLPMRMRGMOGTHYVEMAPGVTTGQDKDLHWYEHKEKFWLLKNEVPYTRHVTGSDNYGLMNVFDFRIPGRAIVSVDNLVKGASGGALGNLNLMLPENLGLGSLPLFP

NbL11g09490.1 2-hydroxyisoflavanone_dehydratase-like [MW = 35.05 kDa]

No. of times detected



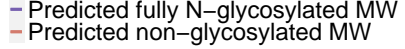
log(intensity)



Values from



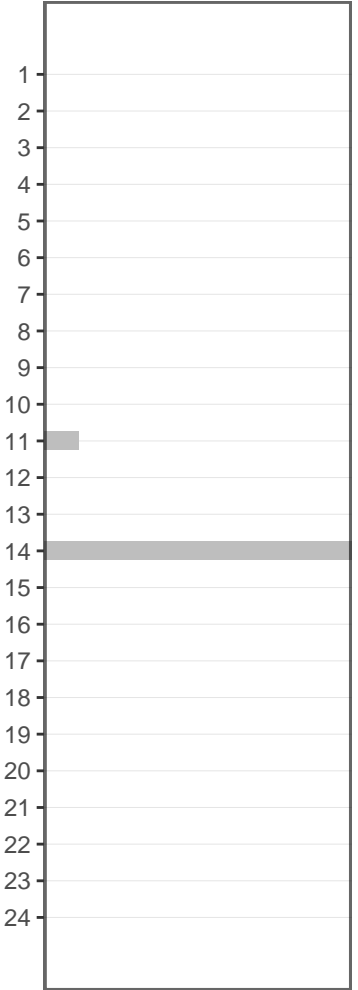
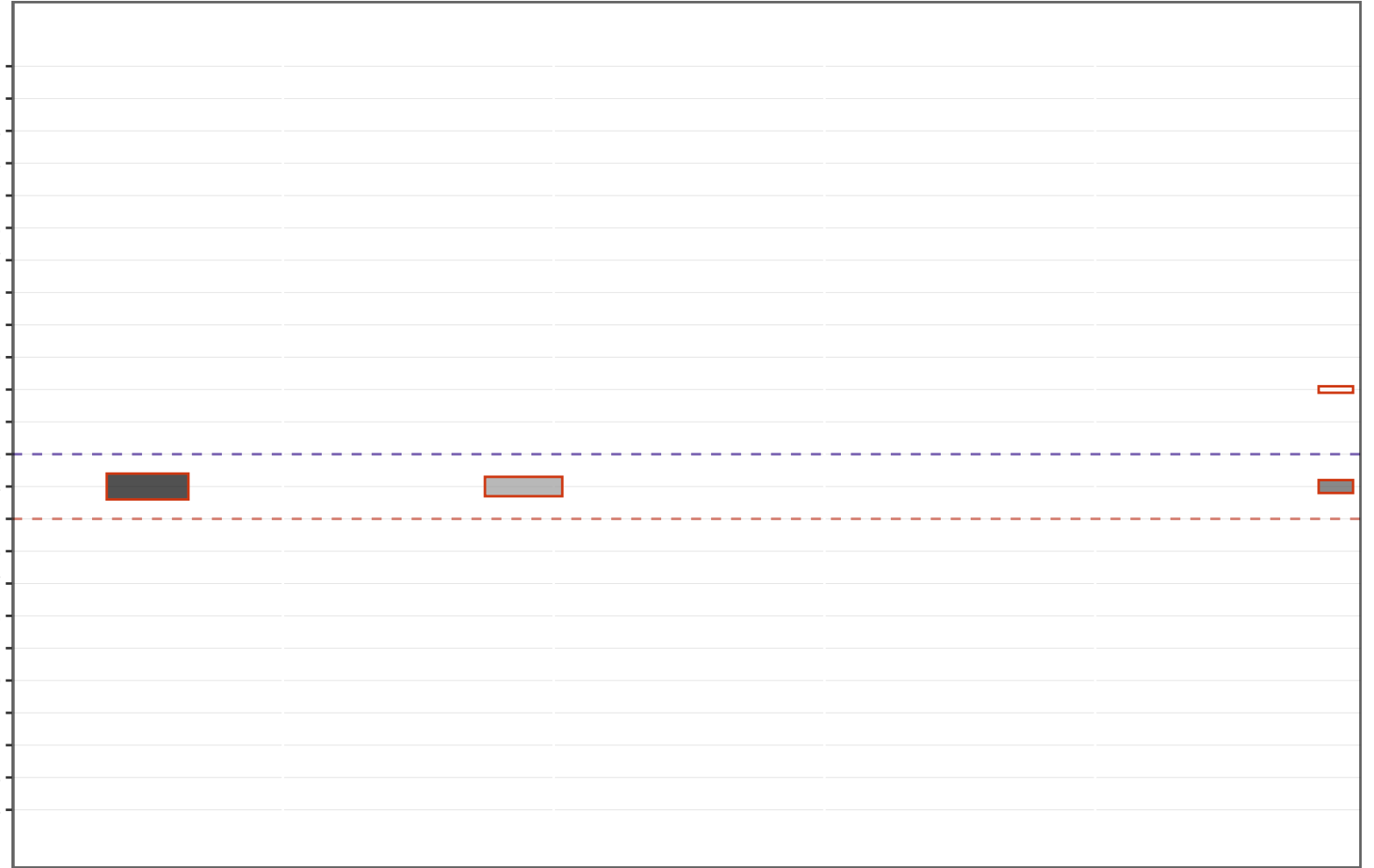
MW indication



Molecular weight



Gel Slice

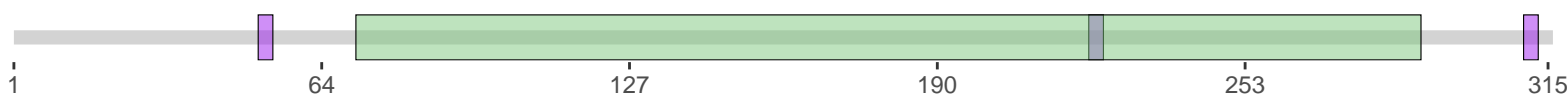


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

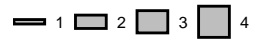


Protein sequence:

DHADLNRYFGDSEGANIAHNRVRLGKLDGKLDGFLGACPYFWGIDLDGEAENLDCKNYIEKLVWALAHFNSGLDPLMPEKDKLSLGGDKLVYVAAKDKLYRGLYKELLEKSGWQGTVEAIEKDEEHVPHLFAPTSENAMVLLKLVFLNGSKA*

NbL11g09420.1 ferredoxin--nitrite_reductase_chloroplastic-like [MW = 67.84 kDa]

No. of times detected



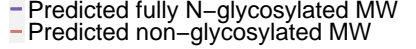
log(intensity)



Values from

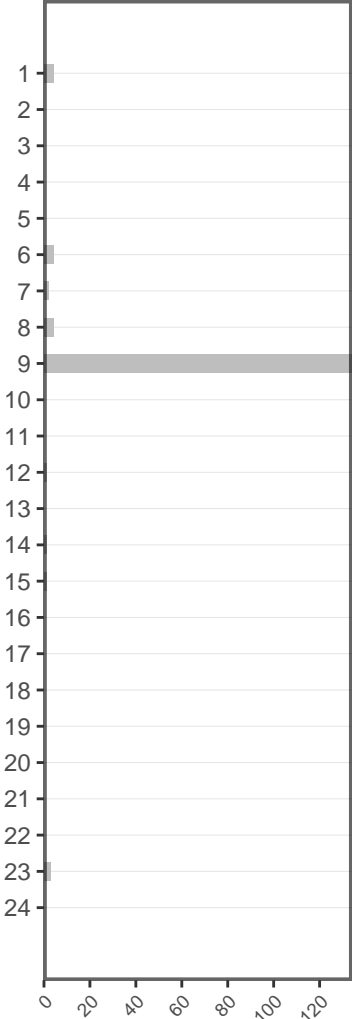
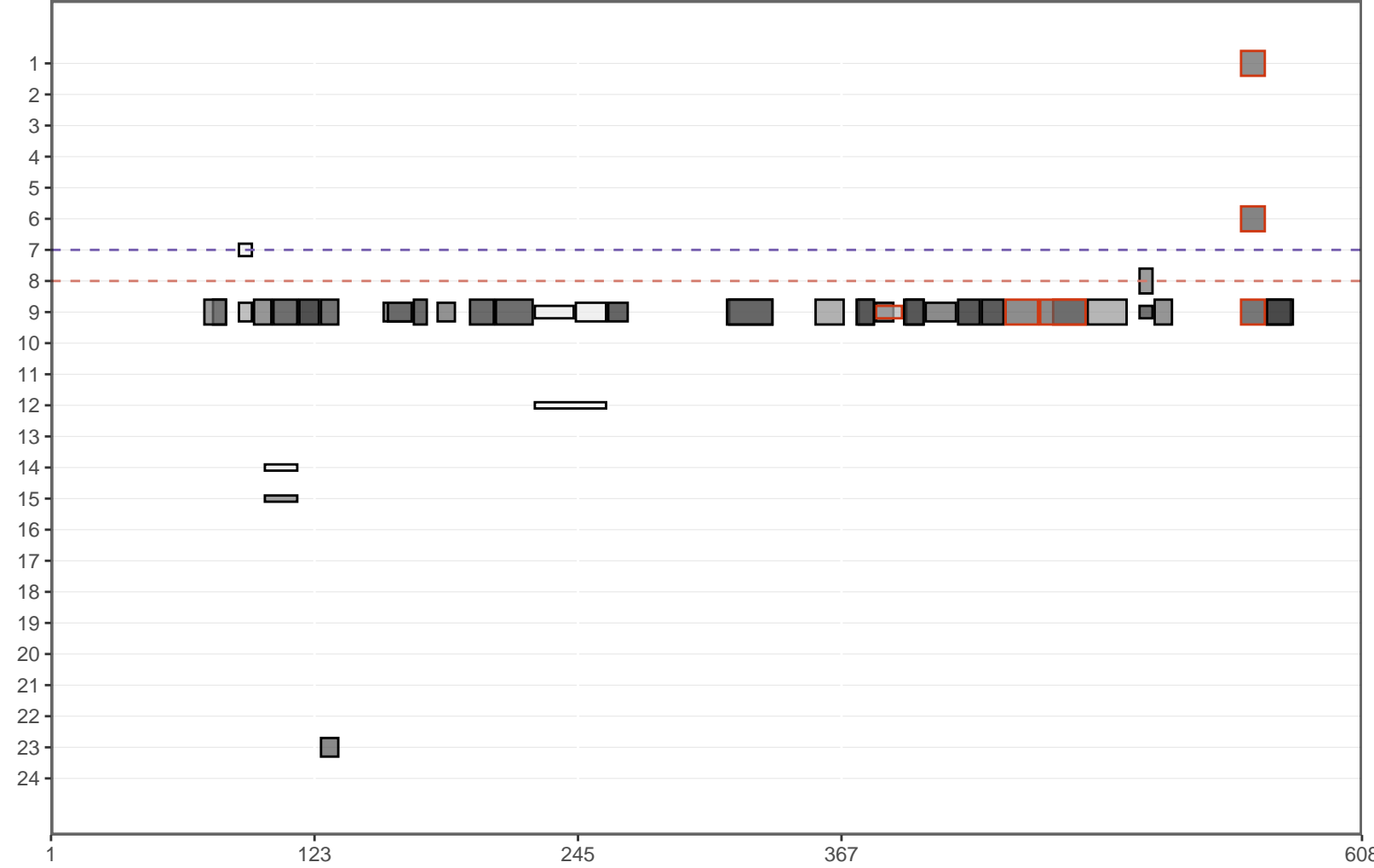
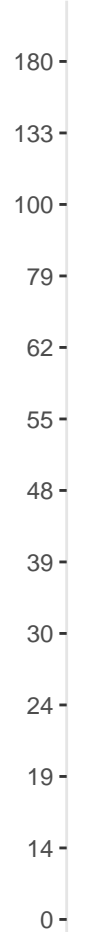


MW indication



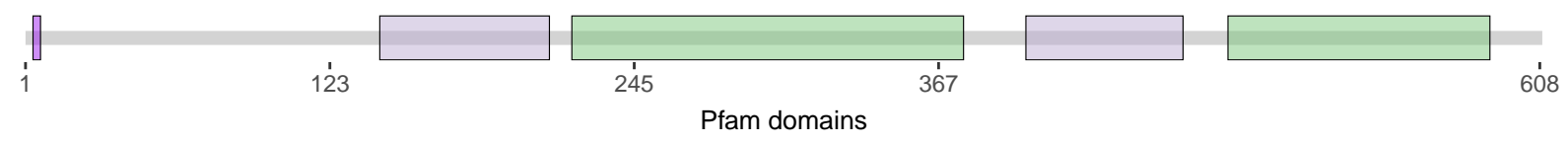
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01077 Nitrite and sulphite reductase 4Fe-4S domain
- PF03460 Nitrite/Sulfite reductase ferredoxin-like half domain

Protein sequence:

IPARKDGRFGFNLVGGFFSAKRQDEAIPLDWHPADDDVFPVCKAILEAFRLDFRGNRQKGRMMWLEDELGVGFRFAVEKRMPPQOQLERASPEDLVQKEWERRRDLGVHPQKQEGYVDFGLHPVGRVQADDMDELARLADEYVSGEIRLTVQGNIPNIENAKIEALLKEPVLSTFSPDPLMKGLMAGTGNQFGGQAIETKARLKITVEVGRVQVSLTKPVRMHWFGCPNTGGGVGVSDGFMGLTRDKNKTKVDGADVFLGGRIGSDSHLGEVYKVAVPCDGL

NbL11g09310.1 probable_quinone_oxidoreductase [MW = 68.32 kDa]

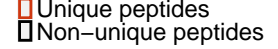
No. of times detected



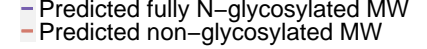
log(intensity)



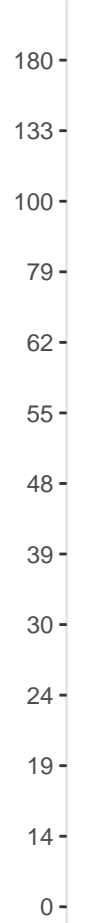
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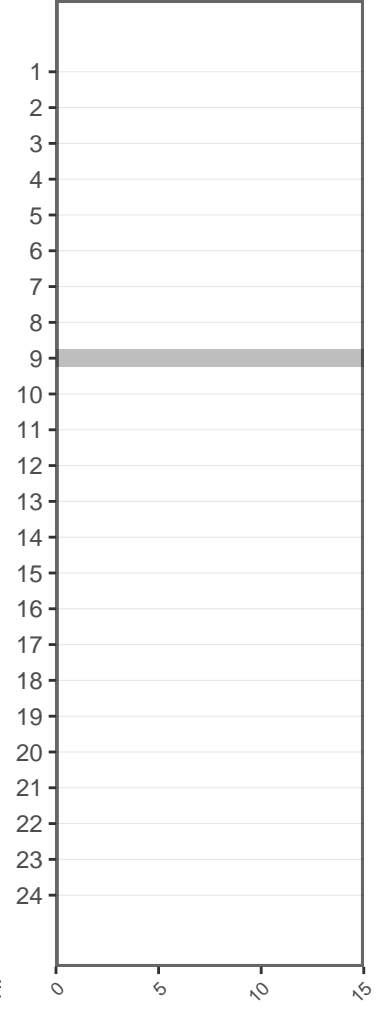
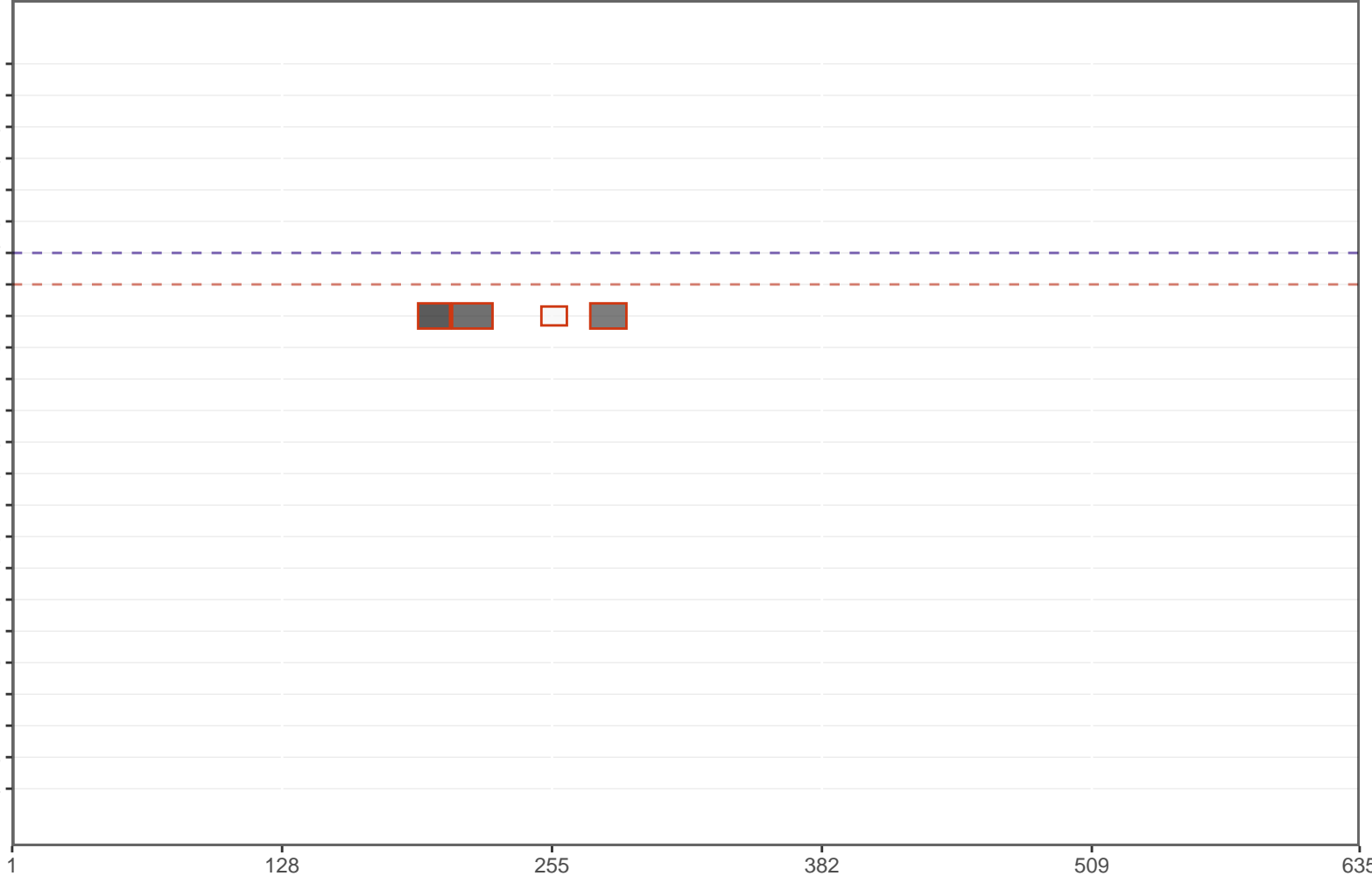
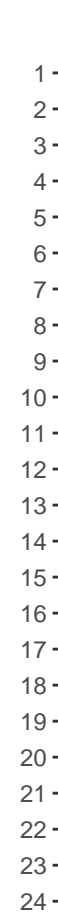
MW indication



Molecular weight



Gel Slice

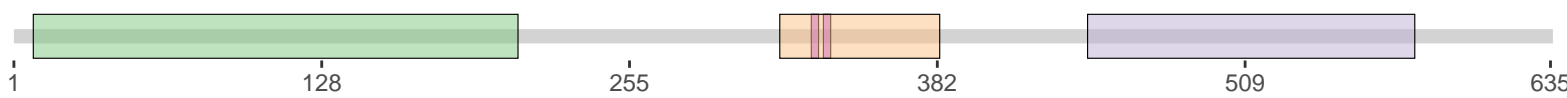


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

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NbL11g09070.1 adenylate_kinase_chloroplastic [MW = 33.98 kDa]

No. of times detected



log(intensity)



Values from



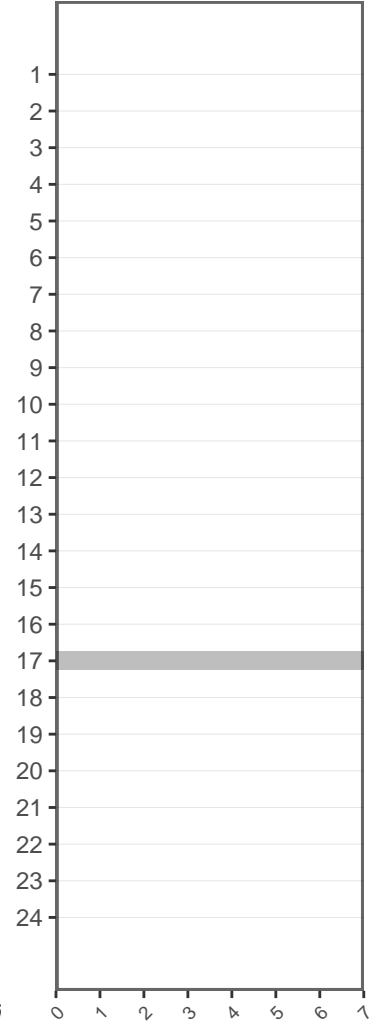
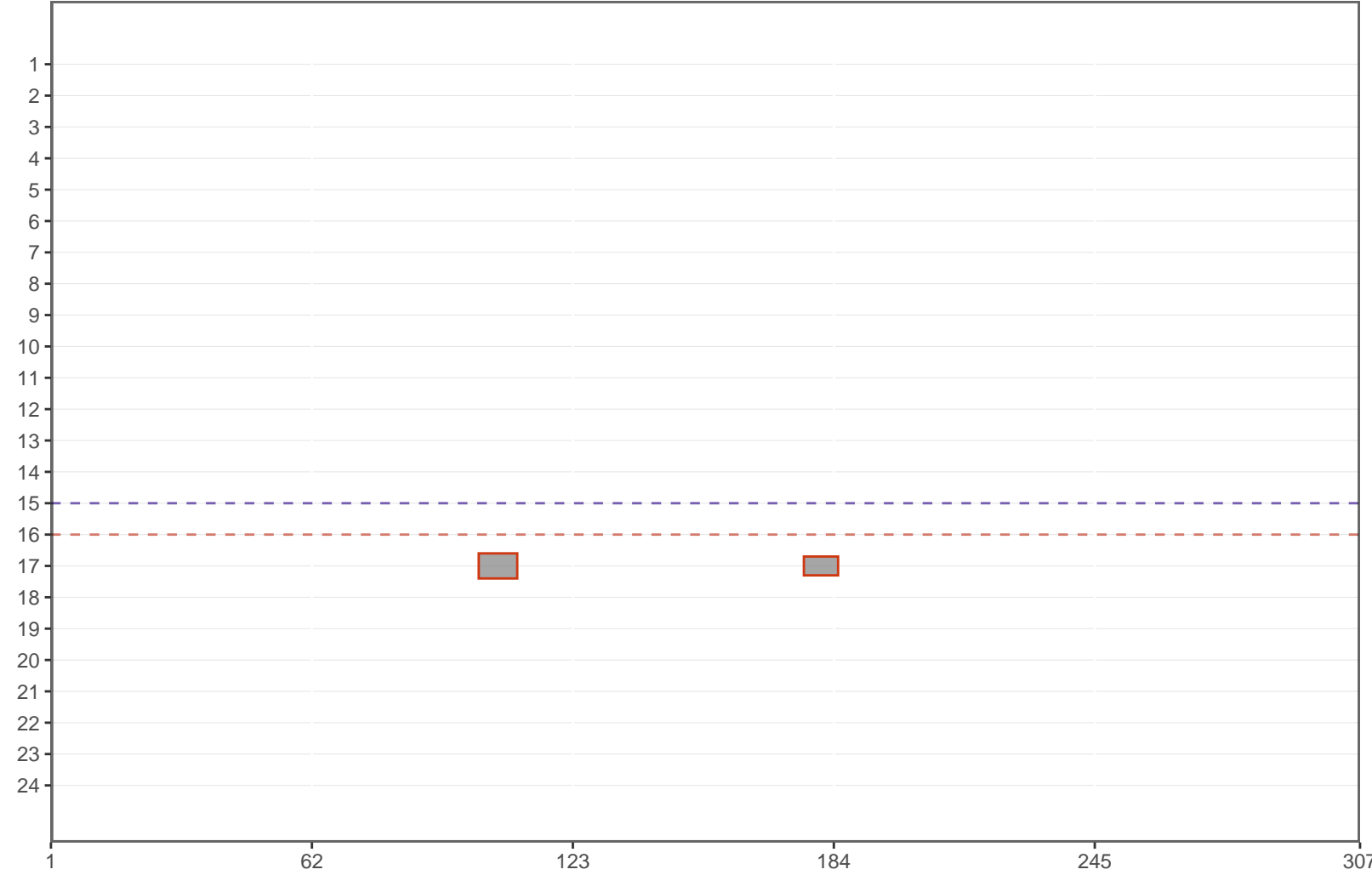
MW indication



Molecular weight

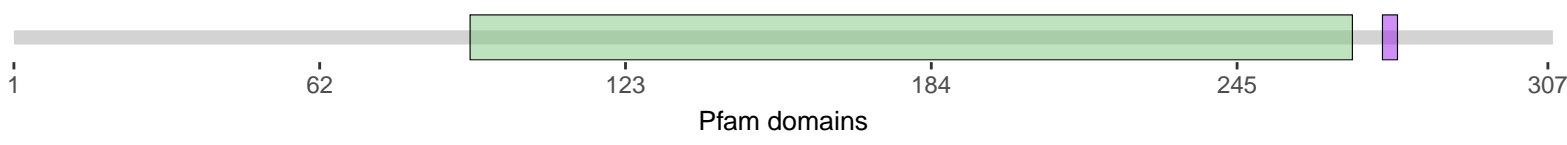


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

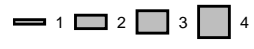


Protein sequence:

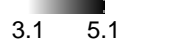
DKGKLVPEIVVTMAKERLNGPDRREKGLLDGVPKRS66GAALKEFGDFPDLFVPEEILVERVAGRRLLDPVTGNIHLYKSPPEETEEAARLQRFDDTEEKVKLRLLHTRHGNVEAVLSLYKDTLKVNGSASKGDVFAQIDDALTQLREKQKGLGTAAV

NbL11g09050.1 protein_TIC_40_chloroplastic [MW = 49.23 kDa]

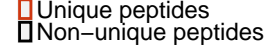
No. of times detected



log(intensity)



Values from



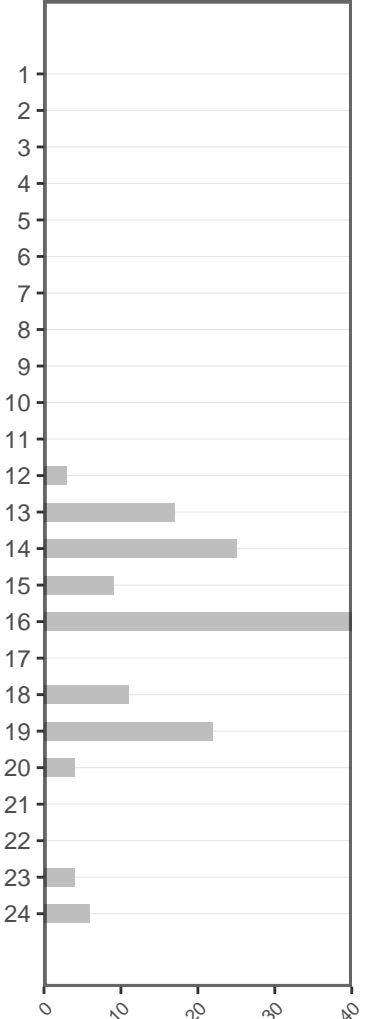
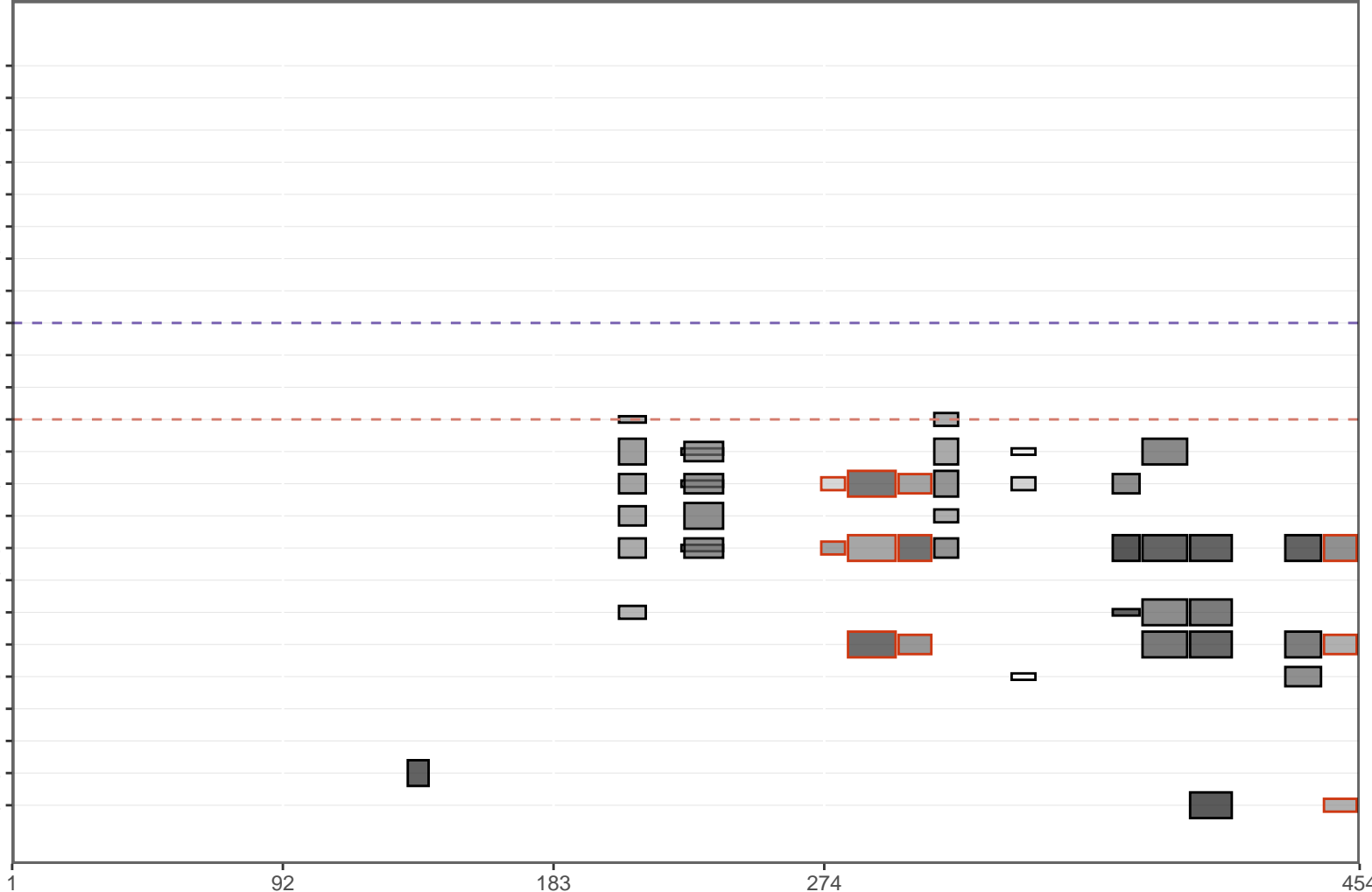
MW indication



Molecular weight



Gel Slice



Protein length

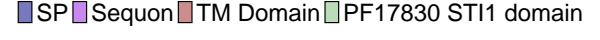


Peptide counts over 4 repeats

Pfam domains



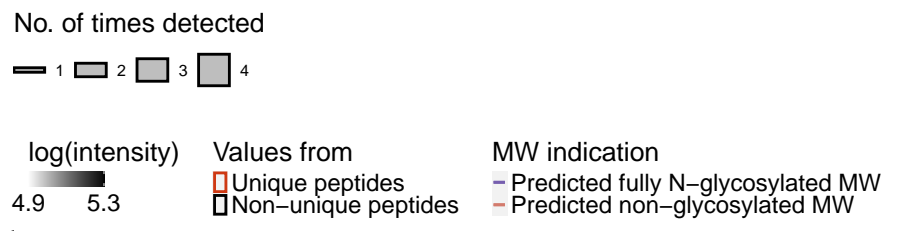
Pfam Description



Protein sequence:

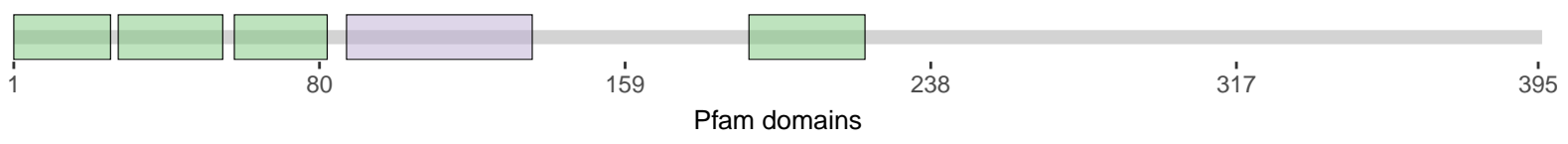
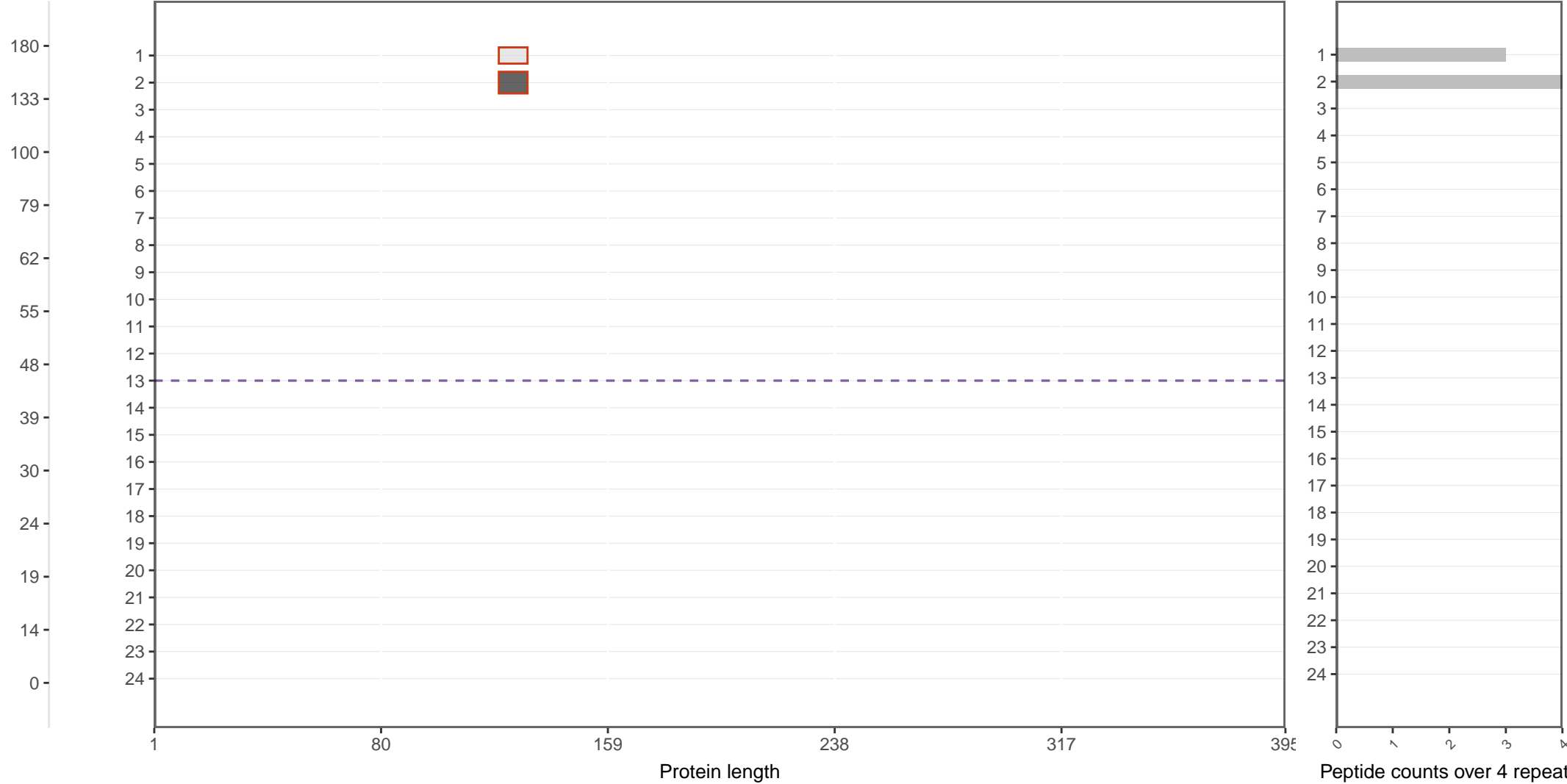
NDTEAERPPKQNAFVDSIDPDTFGKGFANFKKSTETASVTVDDVTVDDQVTQNGAASKSEFGANTSKSTGFGANTSDSTSTKSNFPMSEVAEIKMMDPTVQKMMVYPLPEEMRNPTFFKVMMLGNPQVRRGQLGDMLNMGDGNPVDNRMVDSLNKFDLSGFEIKGGFDQGLTPEEVISIKMANPQVMAFGNPRVGAAMDGSGNPLSIKYGNDKEVMDVFNKISELFPQVGGSL*

NbL11g08900.1 putative_pentatricopeptide_repeat-containing_protein_At5g37570 [MW = 44.07 kDa]



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain PF01535 PPR repeat PF13041 PPR repeat family

Protein sequence:

GTPKRDLYSCMIGLSEHGCGGAAVFFDRMLNEGIVPDEVSLKVMITACSRAGEEGRIFNLVINKYHKPSPDHVAVDLDLGRSGKLDAYEFIRSMAGHAGHAGAWGANLGAACKLHGDIEVGEVSHRLEFELEPQNTGNVYLLGNVYAAANRWLDVALLRQGMSEKGLKIPGCGSWYVVAIDGHSKLNKELGKEIKVDNLLHGW

NbL11g08740.1 elongation_factor_1-gamma_2-like [MW = 15.29 kDa]

No. of times detected



log(intensity)



Values from



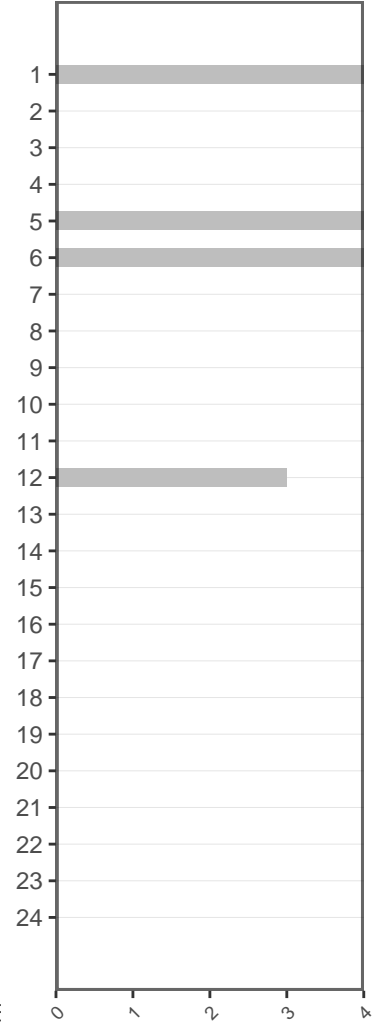
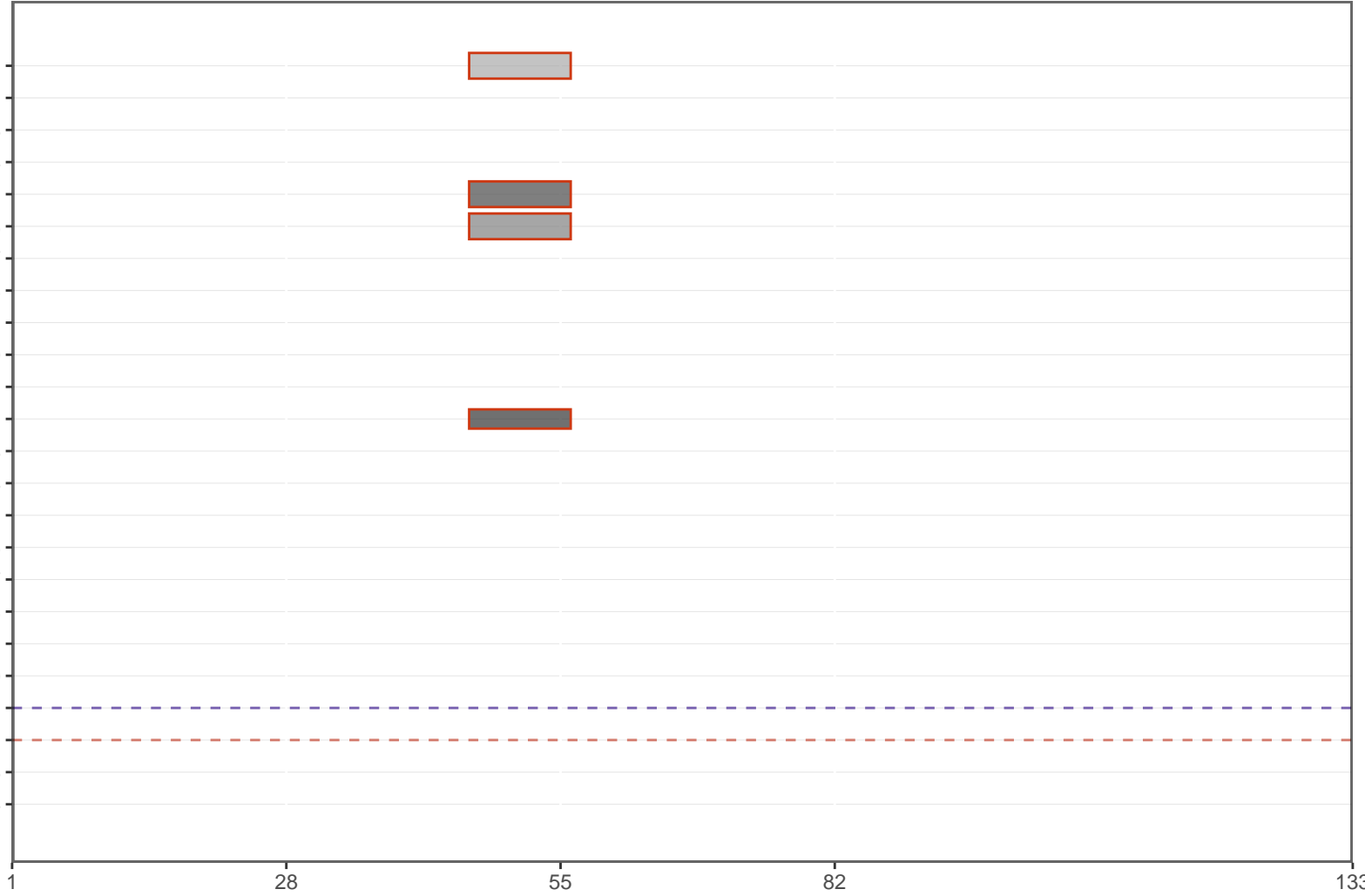
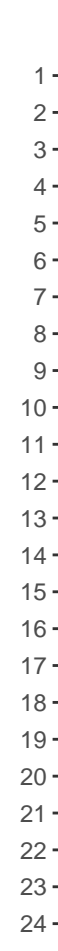
MW indication



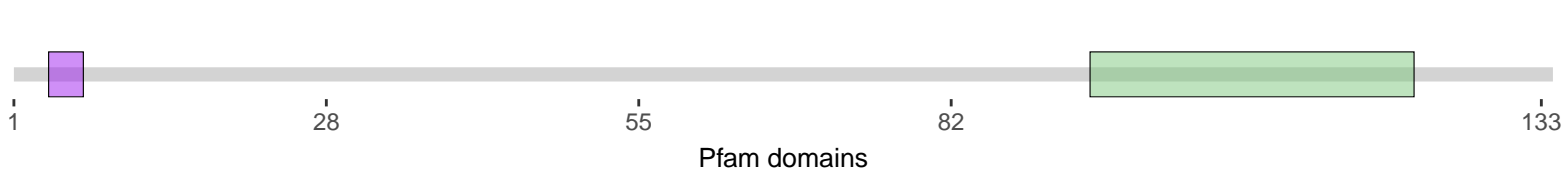
Molecular weight



Gel Slice

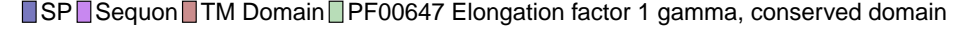


Protein length



Pfam domains

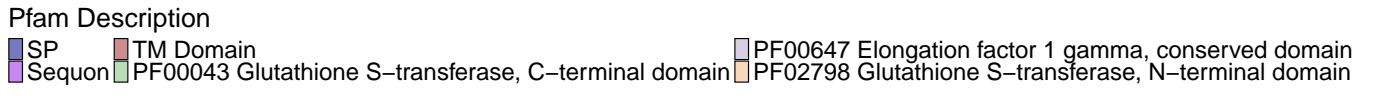
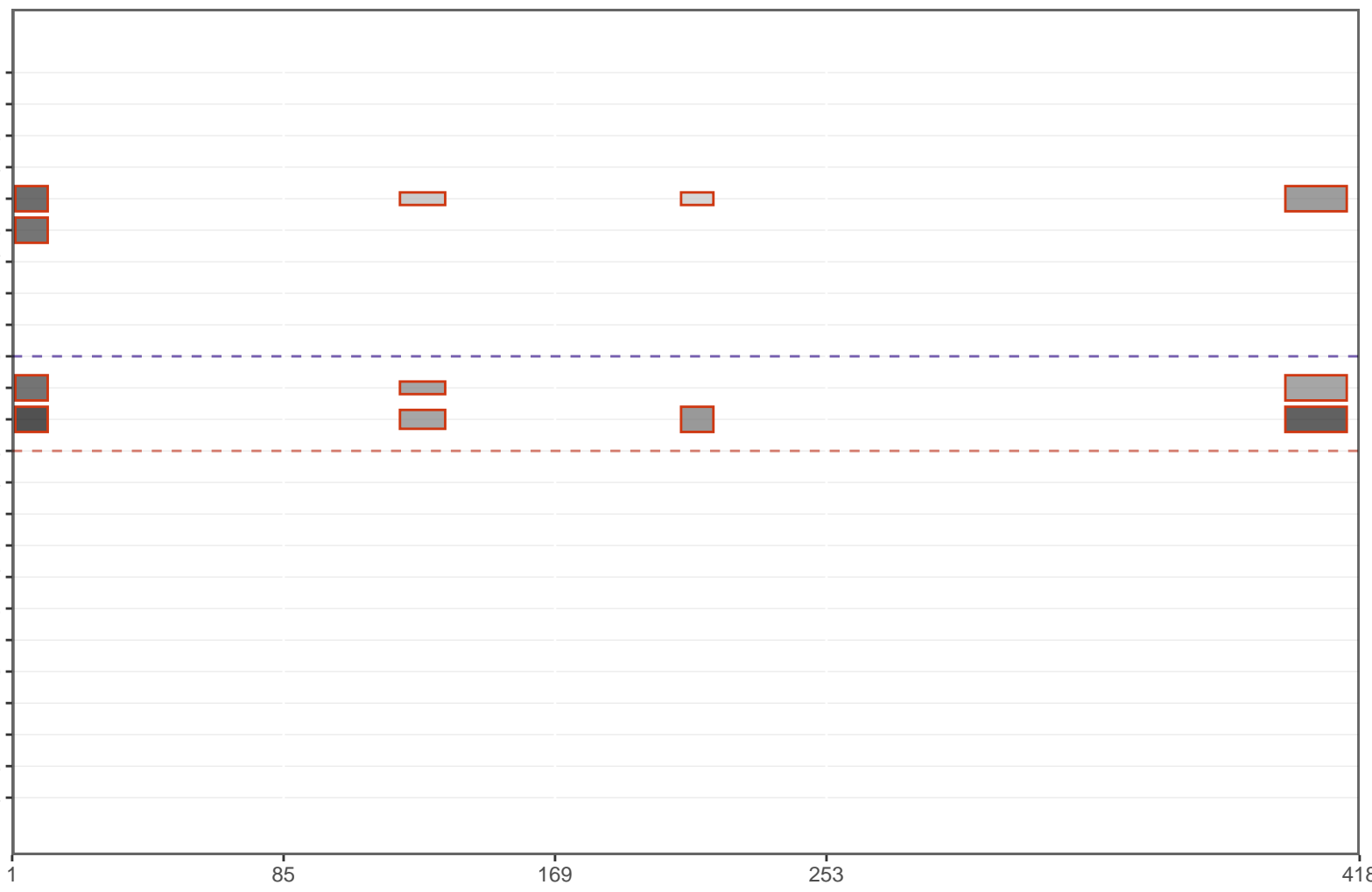
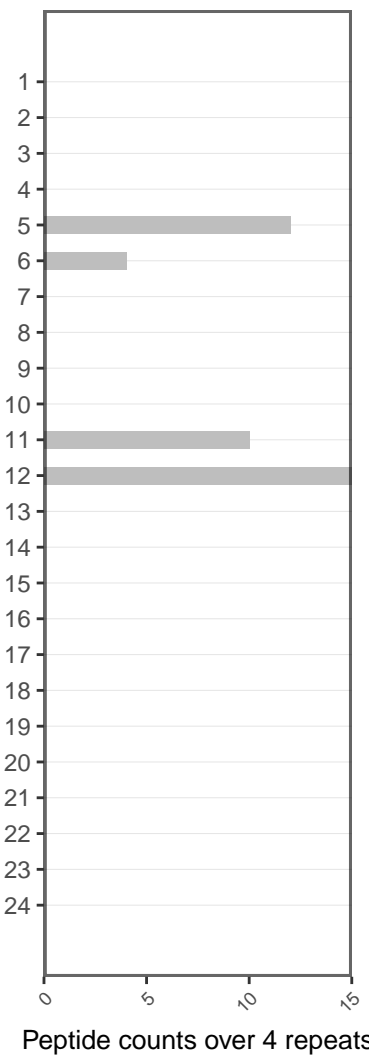
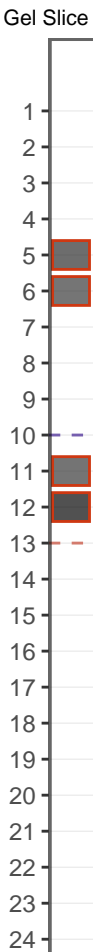
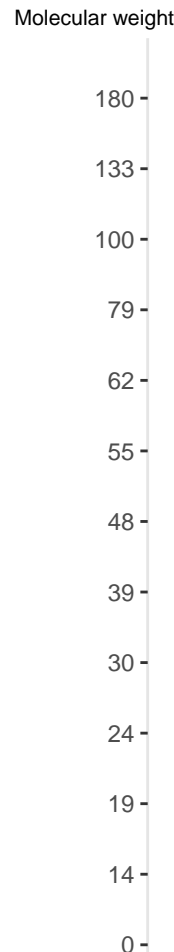
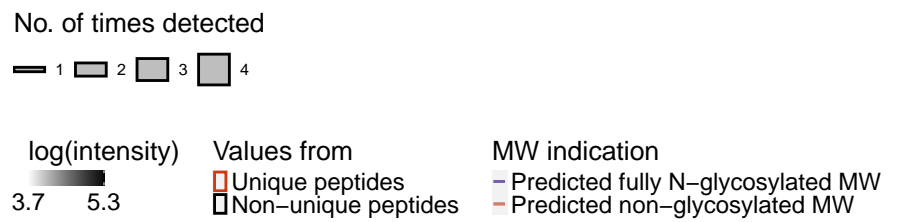
Pfam Description



Protein sequence:

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NbL11g08730.1 elongation_factor_1-gamma_2-like [MW = 47.67 kDa]



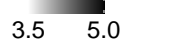
Protein sequence: FCKLGDVYQAEISPEPPSKKAPVKEPKKPKKKEEPKVEKKEEPKFEFEESAPKPKAKNPDLDFPPSKMLDEWKRLYSNXTKTFREVAIKGFWDMDYDEGYSLWFGDQYKGDENTVSEFTLNKVGGLQRMDLARKYAFGKMLVIGSEAPYKVKGLWVFRGKIEPKFMDECGVMELYEWKVEVDINDKAKQKERVNQMEDYEPFEGEALLDAKGRK

NbL11g08700.1 patellin-3 [MW = 59.34 kDa]

No. of times detected



log(intensity)



Values from



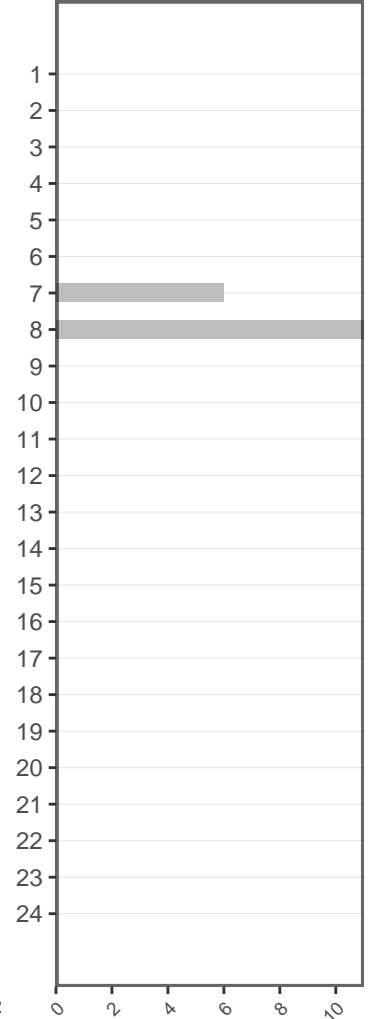
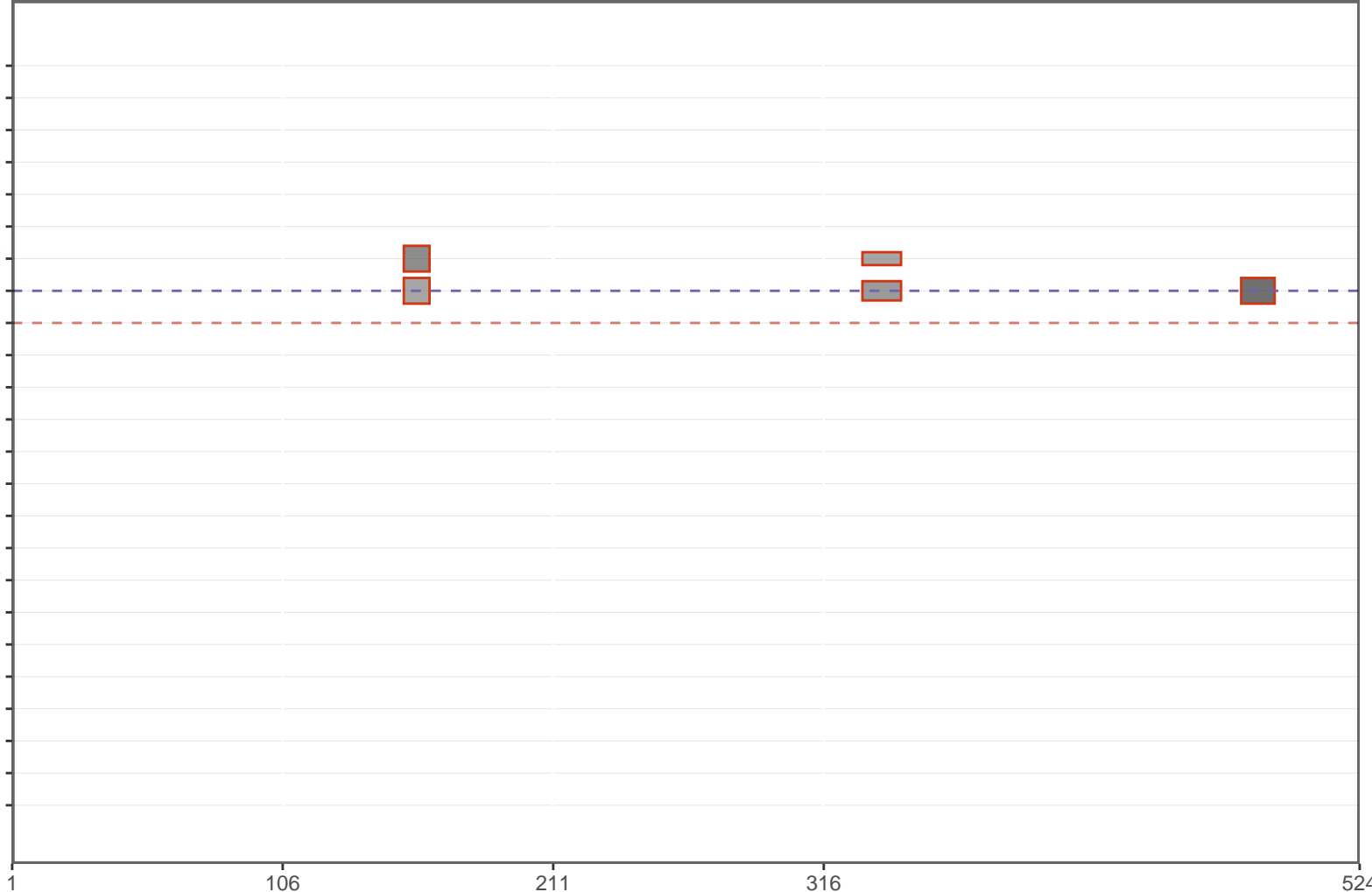
MW indication



Molecular weight



Gel Slice

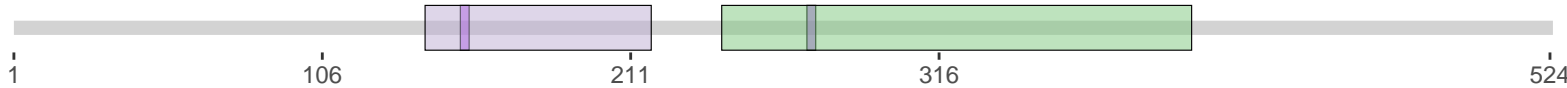


Protein length

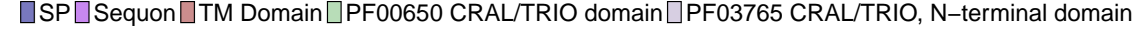


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IKKEGHPVCYNYVGEFGNKEVYKTFGDEEKRNKFLRWRIQGLERSIRKLDNPPGGINTFQVSDLKNSPGPKRELRLATRQALHLDQNYPEFVAKGVFNVPWVYAFYTMISPTMQRKSKFVAFGRKTAETLVKYYVSPGQVPPVGGVGLSDVGECPNPEFTVSDPYTEIHKRATKGTVEIIVNEKGIIVWELRVLGVWEVTVSAEYVFNPTDGGYTVNIQKPKRMAPTDEPVVSSSRVLELGGKILLIDNPTSKKKKLLVRYKDKPYST

NbL11g08690.1 uncharacterized_LOC104109700 [MW = 10.75 kDa]

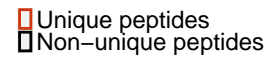
No. of times detected



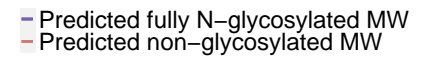
log(intensity)



Values from



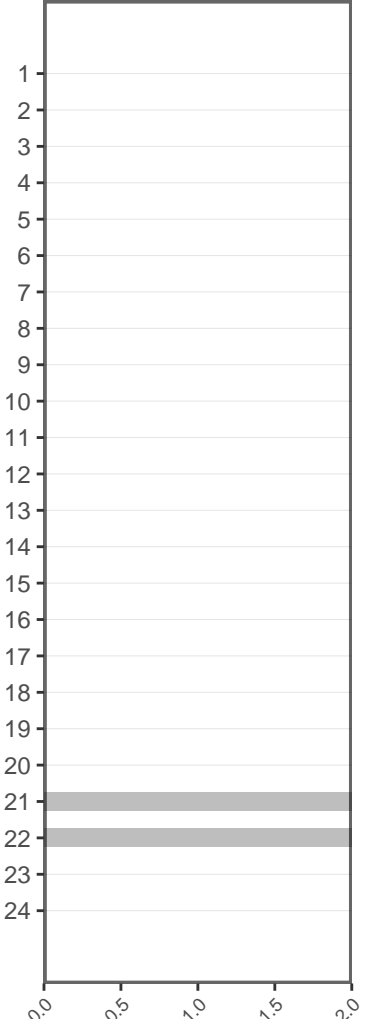
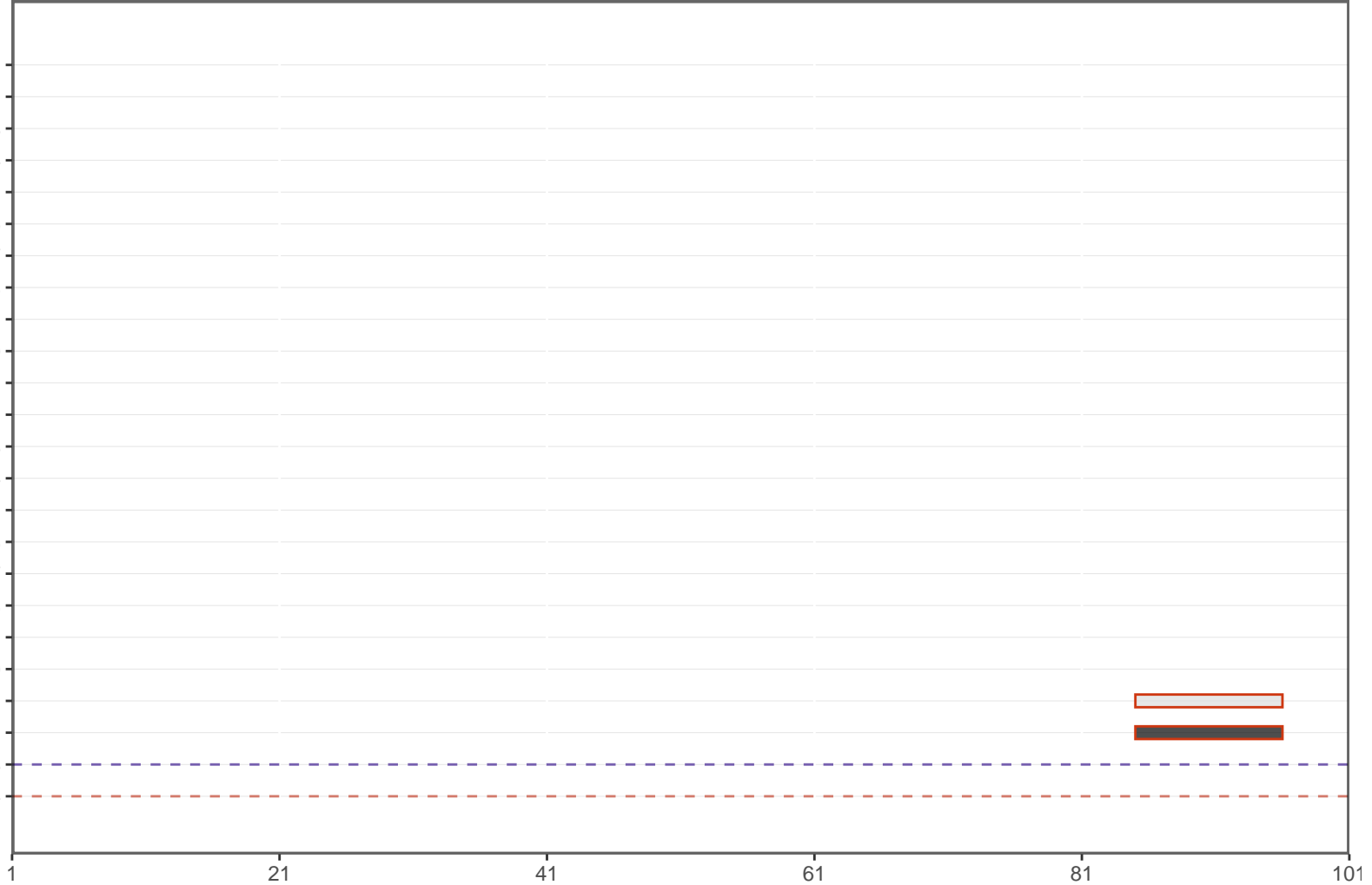
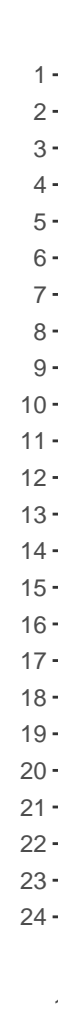
MW indication



Molecular weight



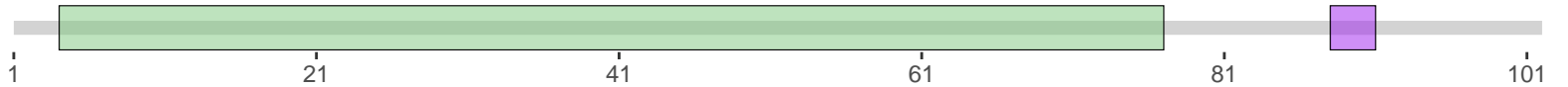
Gel Slice



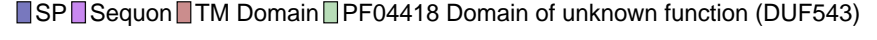
Protein length



Pfam domains



Pfam Description

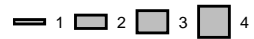


Protein sequence:

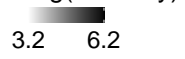
'SLUGFAGLLFRSPVTRWASTAFAGTGLGSAYTEGSQKLGYPKLTANVSEAPVTKDGEH'

NbL11g08640.1 patellin-3-like [MW = 69.43 kDa]

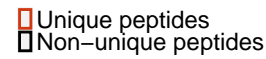
No. of times detected



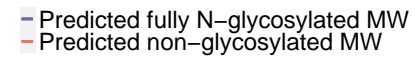
log(intensity)



Values from

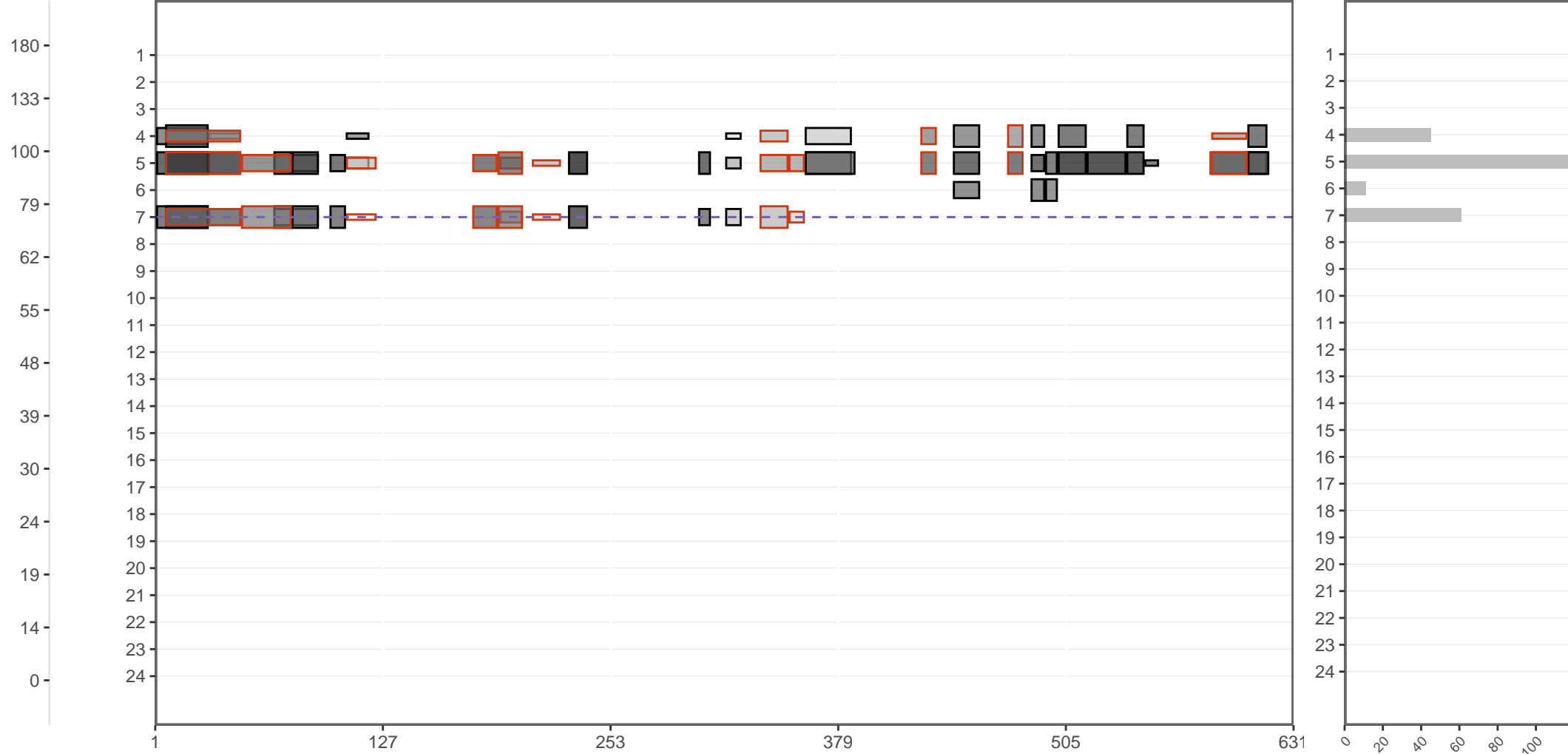


MW indication



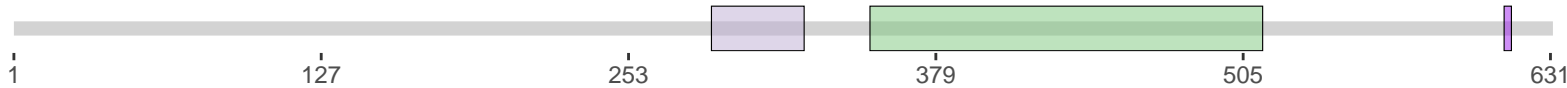
Molecular weight

Gel Slice



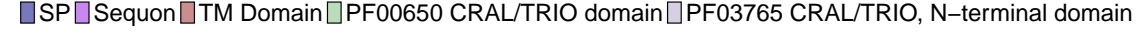
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

VLLKFLRARDPKWEAFAMKGVVWRKEFKIDELLEEDLSGLGLEKVVYVNGVKGKHPVGVNFAFGADQNELVGNFTADKEKMKVLRWRIGKMEKSRINLDFSPDGICTFVQVLDLKNNSPLVFFKELRQATNRALGLLDGNYPEFVAKGVFINVWVYVYVYRMINALFTRTKSKFVAGPSRBAETLKVYVPEGVPAQVGLSREGEGETTAEATEEDTKPTSKHTIEFFVTEKTSLVWEARVIGVWVYVGAEPVPSAEGGYTIVEKSRKVAADETVITNTY

NbL11g08520.1 probable_polygalacturonase_At3g15720 [MW – SP = 49.76 kDa]

No. of times detected



log(intensity)



Values from



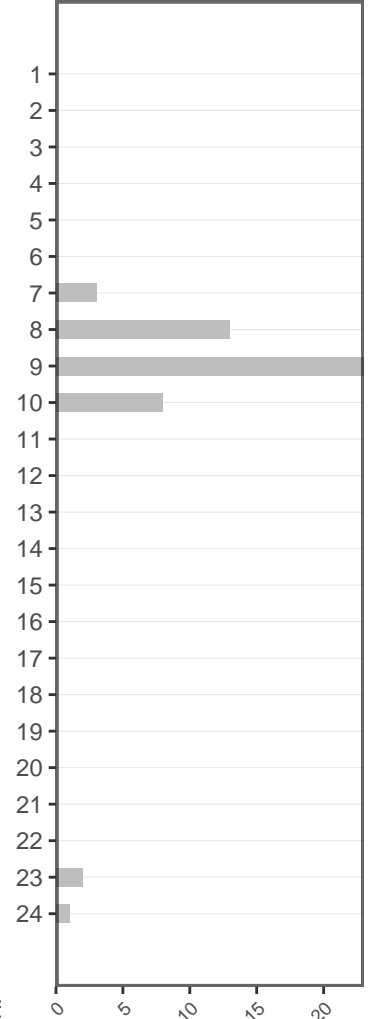
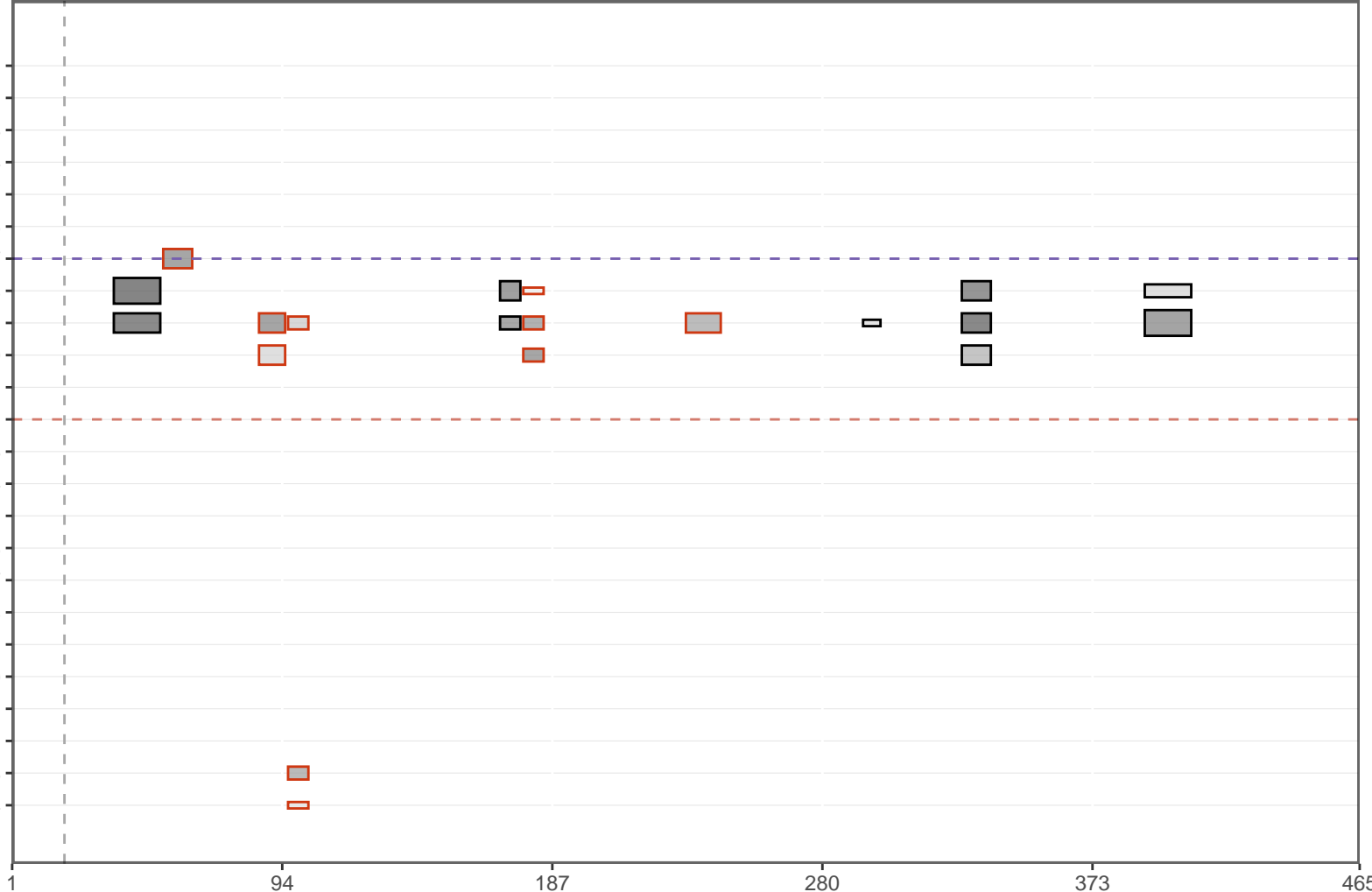
MW indication



Molecular weight



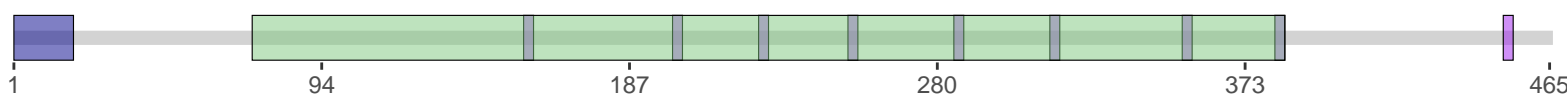
Gel Slice



Protein length

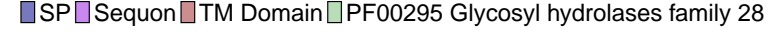


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DIEDSNNTVITRCYNTGDDAIPKSGTGPVHNLATNCWIRTKSSAKLGGASFYTFNNLFDNTFESHRLGLAQRDGGDSDITFSNINSTRYHPSPWAGRYAEPYVTCPRDTSKAGSISNLGFVNTSTSENGIFLGGGGVLSLNFNMLNLTYNRWTKYPPDGGWVQVIRPQGGDELVKHQTAGFMMEHDGLVFENYMKWNSDEMRWANNPLDFRPSTVWNSMLNIFYERSYQQ

NbL11g08390.1 60S_ribosomal_protein_L7a-1 [MW = 29.18 kDa]

No. of times detected



log(intensity)



Values from



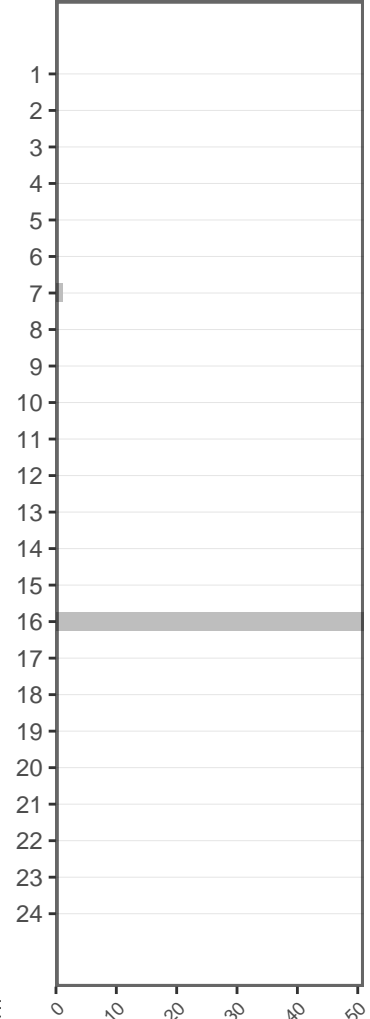
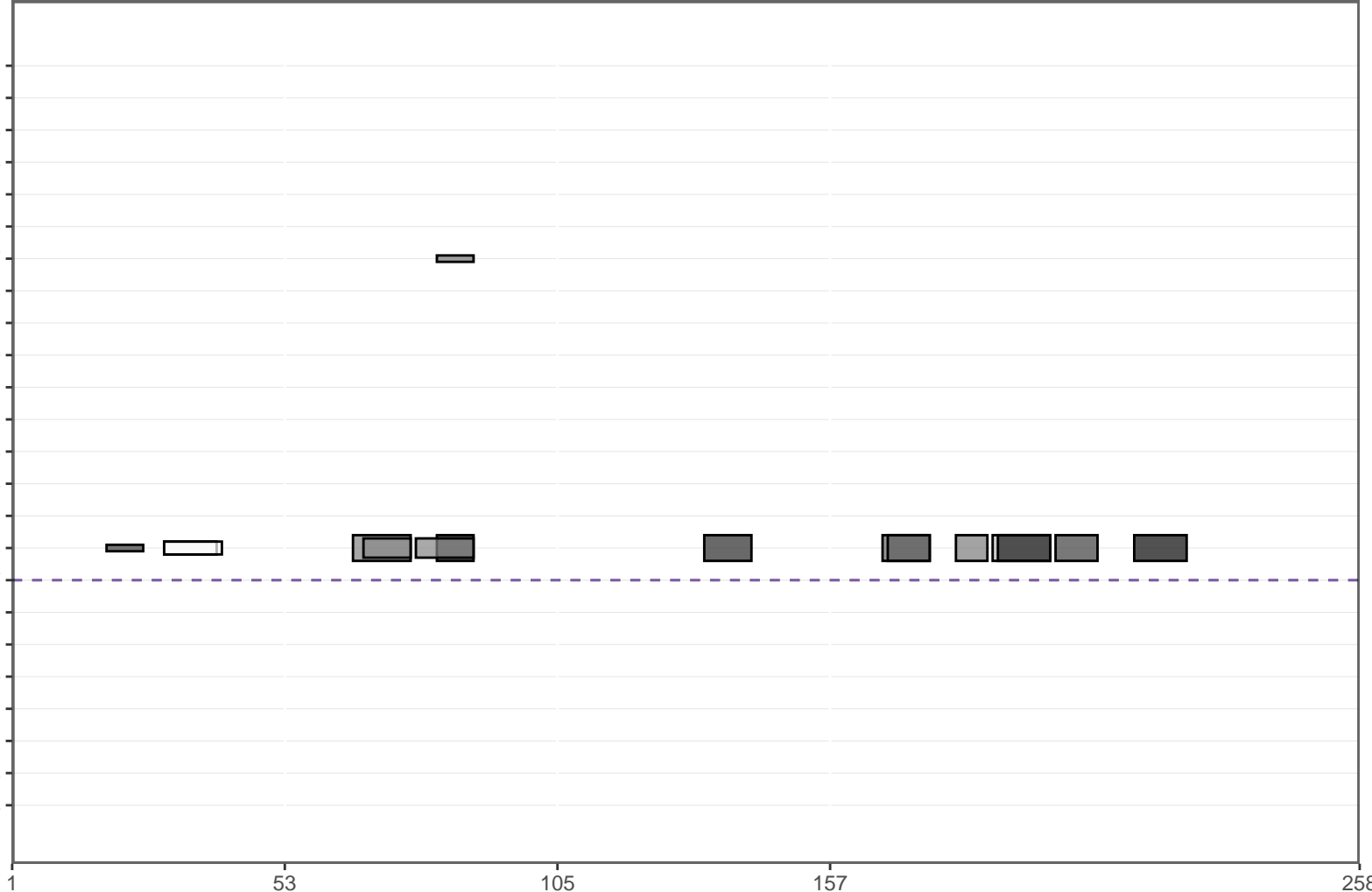
MW indication



Molecular weight



Gel Slice

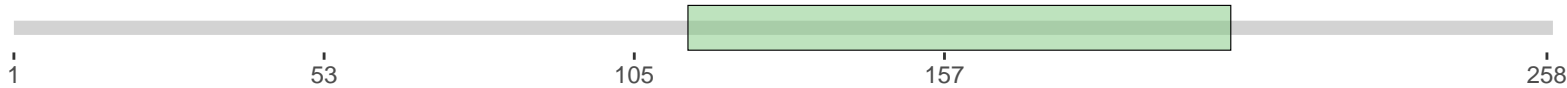


Peptide counts over 4 repeats

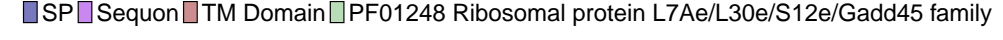
Protein length



Pfam domains



Pfam Description



Protein sequence:

EGKTPETKXPPIKYGLKHITVIEQNKAGLVIAHHDVDPHELWVLFALGRKMEIPYGVKGGKARLGSIVHKKTABALGLFTVKNEDKMEFRILEAIKANFNDKYEENRKKWGGVYMSGKSGARTKAKERVLAKAAQRNN

NbL11g08220.1 50S_ribosomal_protein_L13_chloroplastic [MW = 27.11 kDa]

No. of times detected



log(intensity)



Values from



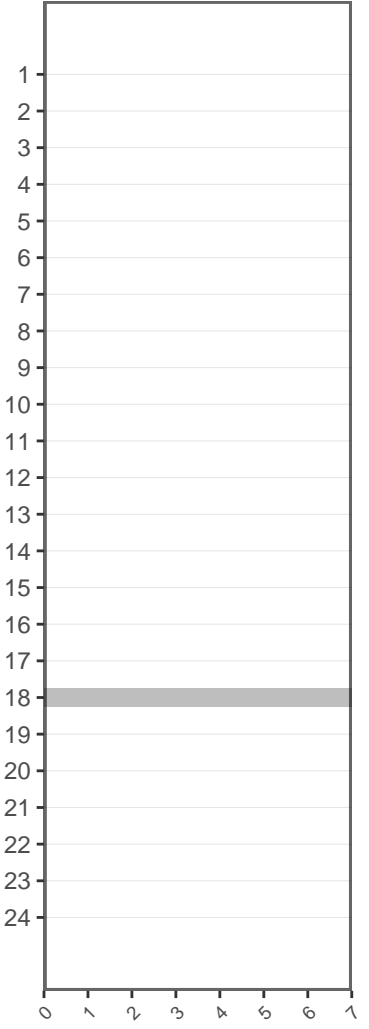
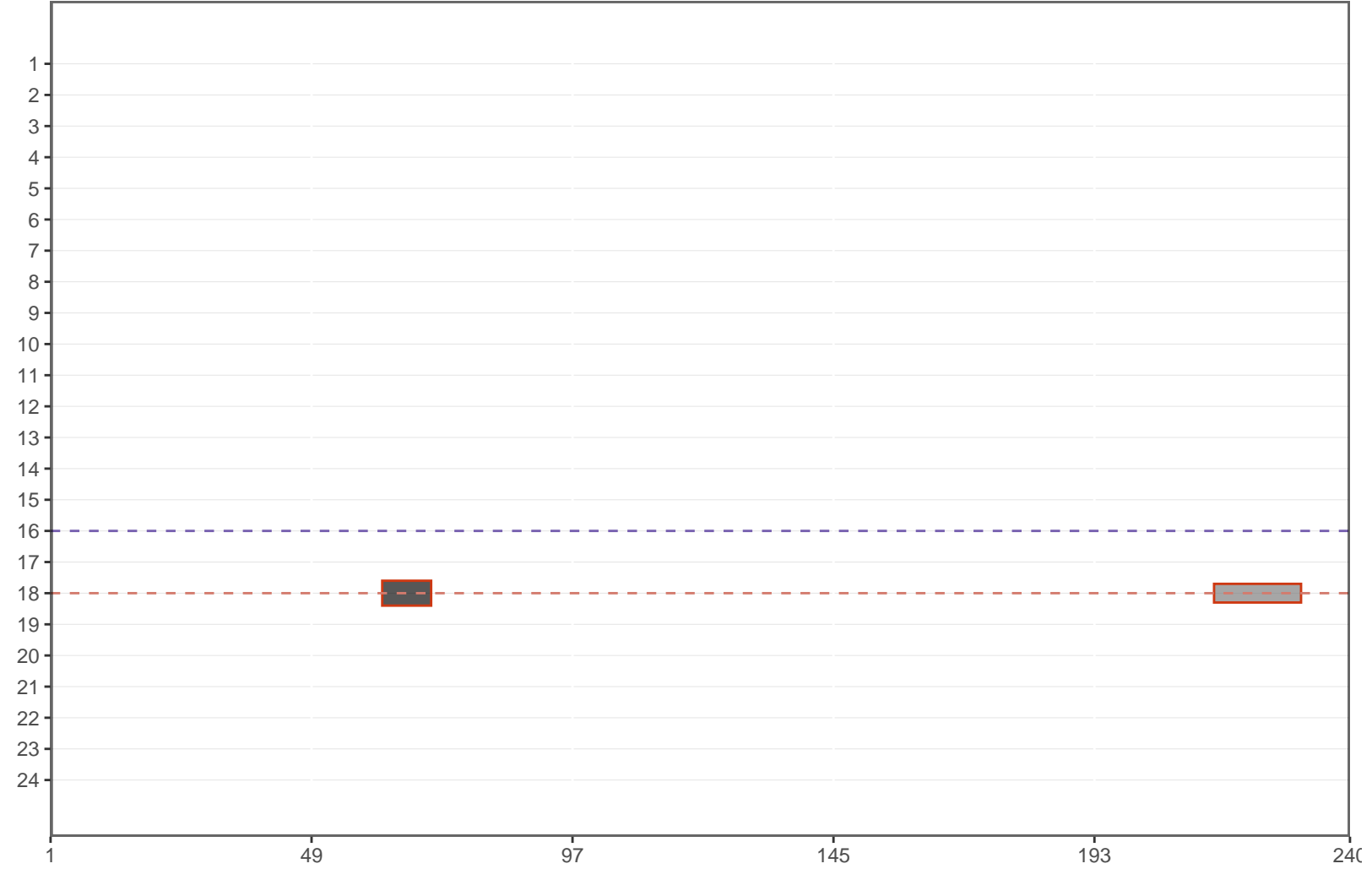
MW indication



Molecular weight

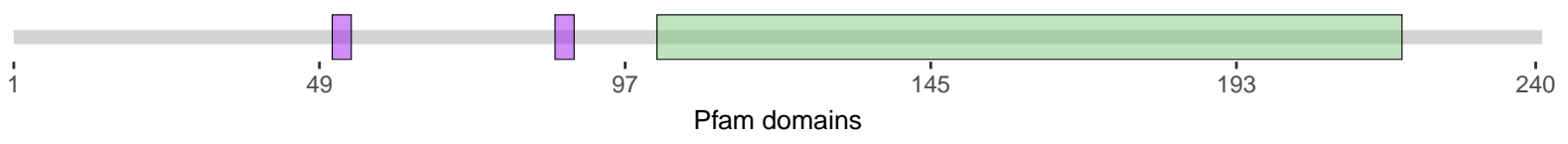


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DAASDLGRMASTAIHMRGNLATYTPVDMGAFVYVNAEKVAVSGKRTGKLRHRSRPGCMKVFDFDGLGRIPERIEHVAVRGMLPKRGLRGLFTHLKVYKGPENHEAGKPELPRDKRIKQR

NbL11g08130.1 ubiquitin_carboxyl-terminal_hydrolase_14-like [MW = 89.37 kDa]

No. of times detected



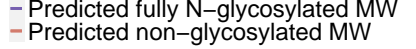
log(intensity)



Values from



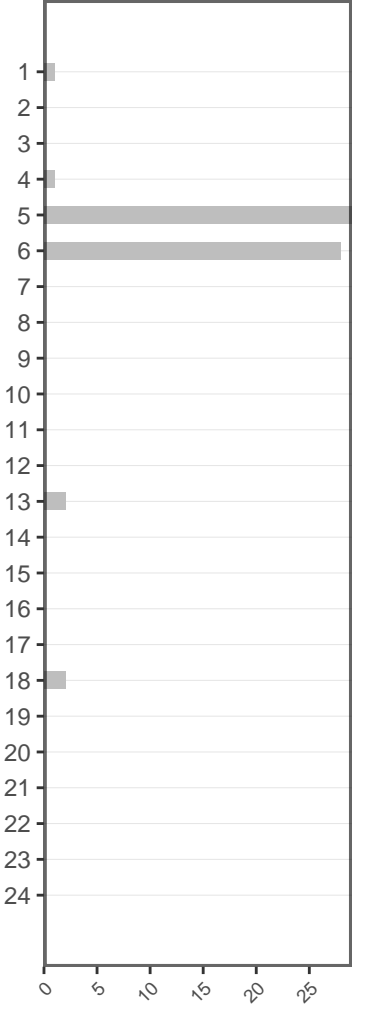
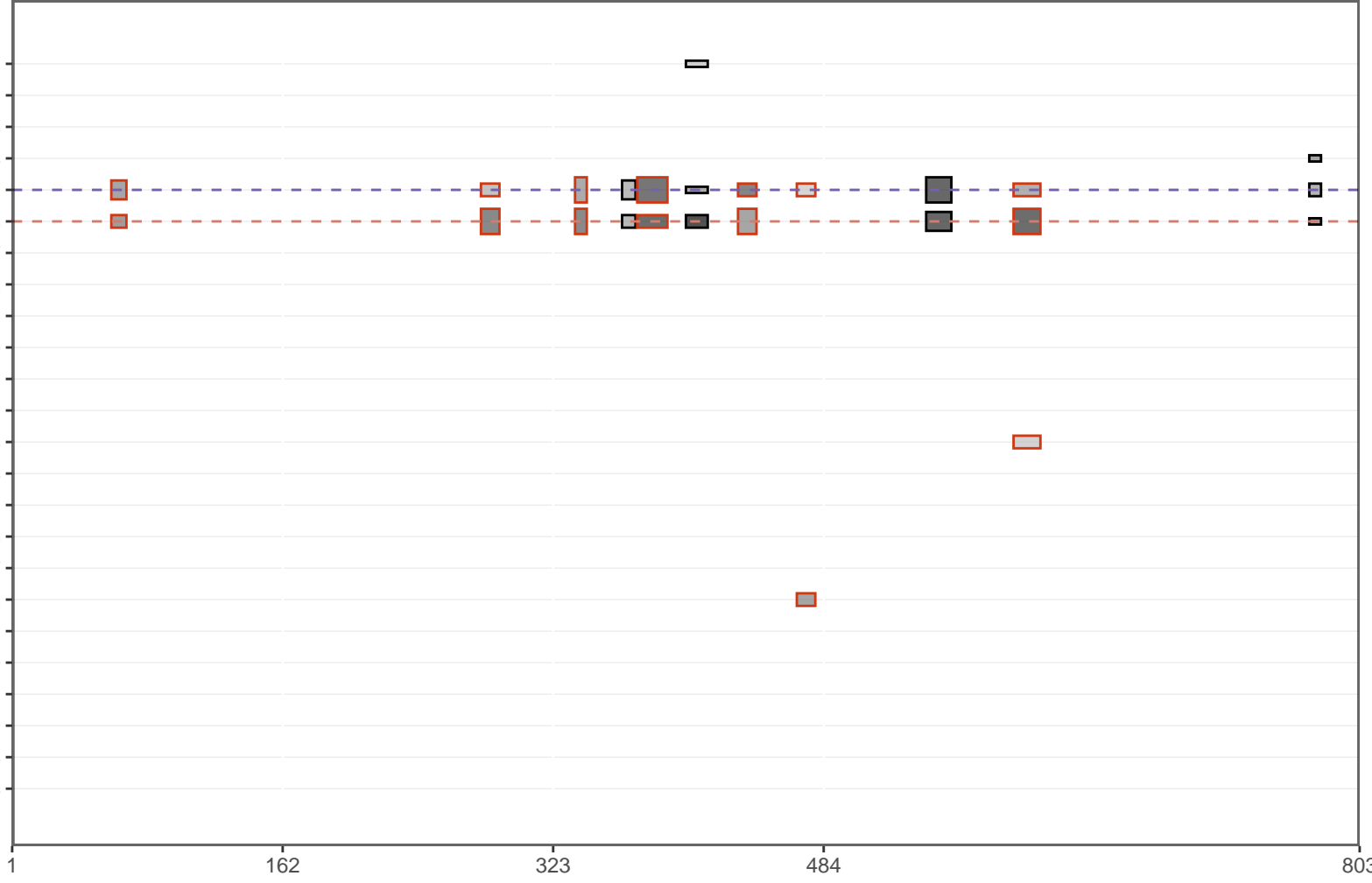
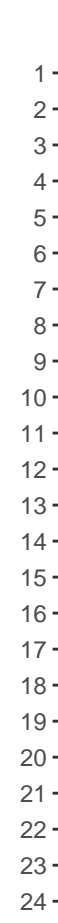
MW indication



Molecular weight

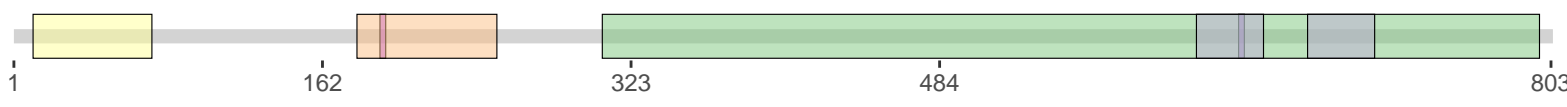


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- TM Domain
- PF00627 UBA/TS-N domain
- PF17807 Variant UBP zinc finger
- Sequon
- PF00443 Ubiquitin carboxyl-terminal hydrolase
- PF02148 Zn-finger in ubiquitin-hydrolases and other protein

Protein sequence:

IPSSLVQEGIRPRRMFKVIAAESHPEFSTMRGGDALEFLHFIDQVDMNIGNINFDPRSRKFGIEERLQCPGKVAWNGRKHLSLNPLEKAVNRELADHFKLKAAEAAGKGVSTDEIVRRVPLKDCGLDFSAPEEVHDFYETALKARTTAIKTAGLTSFDPHLLHMRKFMEEGWPKKLDVYVDVDPDIDGNMRSIGLQPREELLPETAAGDGEESPKLLADEVVAQLVSMGFNYLHDGKAAINTSNGGVVEEAMNWLAAHNDPDDSPISGQIQTPHIDRSKDTI

NbL11g08100.1 60S_ribosomal_protein_L8-like [MW = 28.16 kDa]

No. of times detected



log(intensity)



Values from



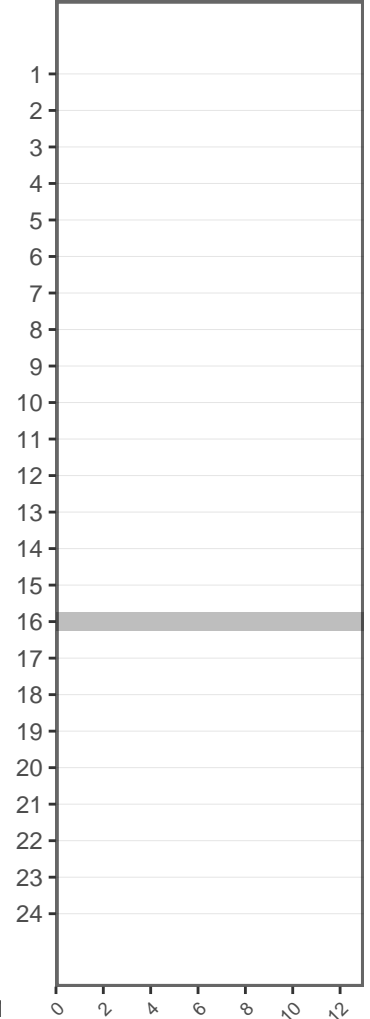
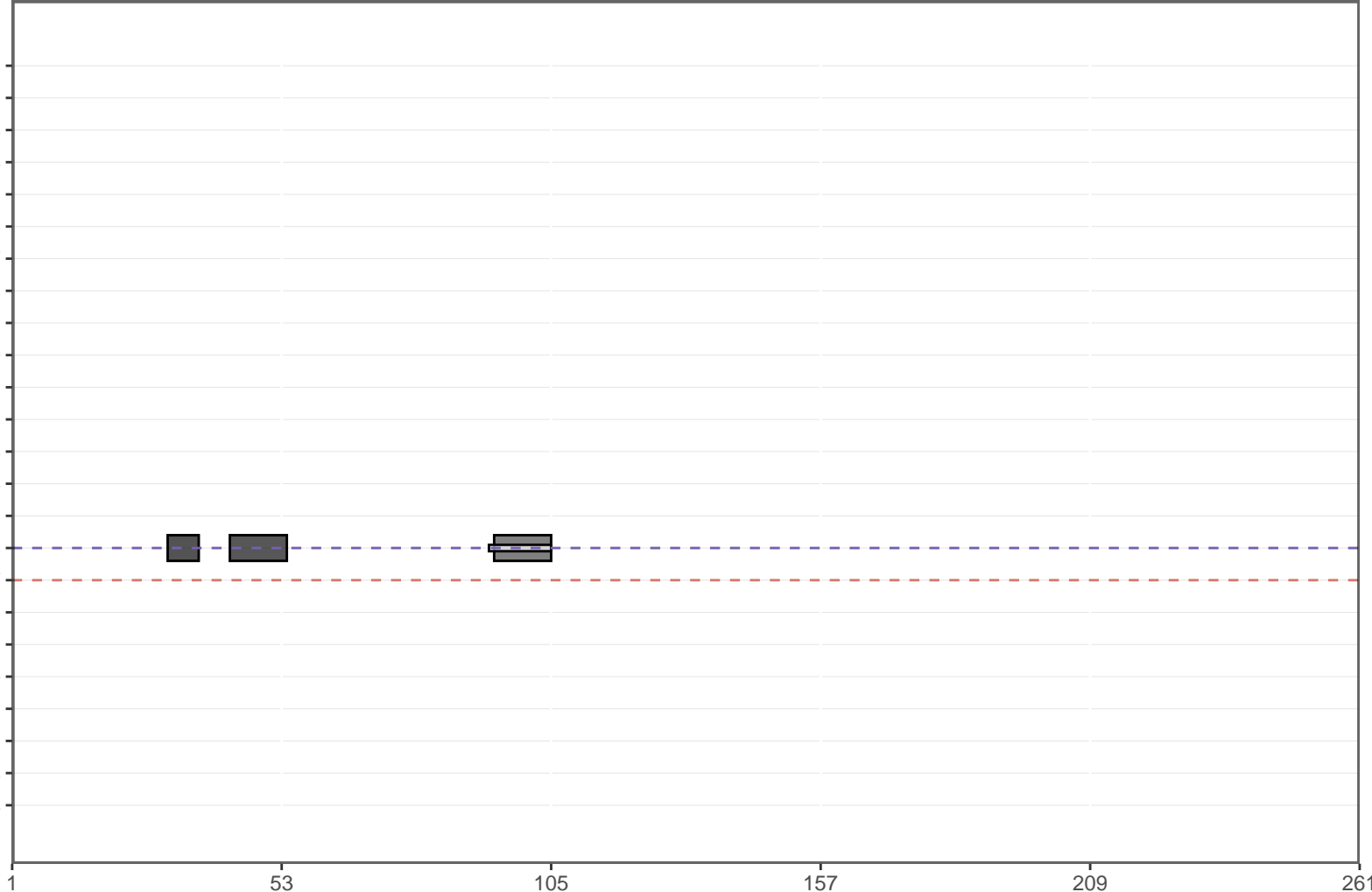
MW indication



Molecular weight

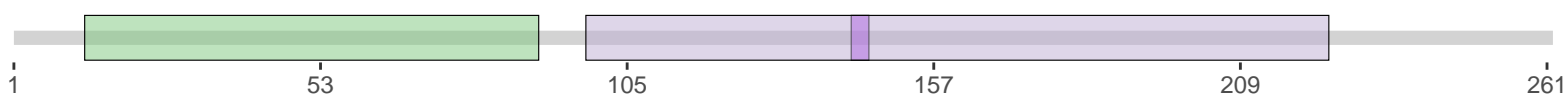


Gel Slice



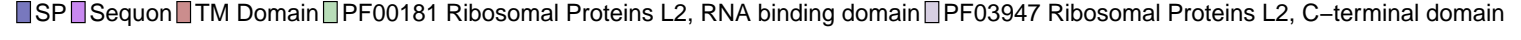
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

KVGDGRGVFARCSGDVAIVISHNPNQITTRIKLPSGAKKIVPSGCRAMIGVAGGGRTEKPKLKAGNAVYKVRVKNRNGWPKVRGVAMNPIVEHPHGGGNHGHGHASTVRRDAPPQGVKGLAARRTGRRLRGGAAATAKADKA

NbL11g08090.1 glycine-rich_RNA-binding_protein_3_mitochondrial-like [MW = 16.5 kDa]

No. of times detected



log(intensity)



Values from



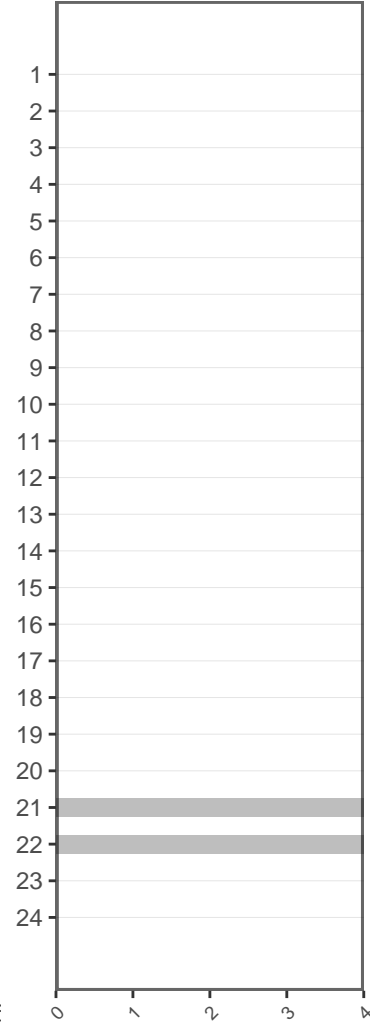
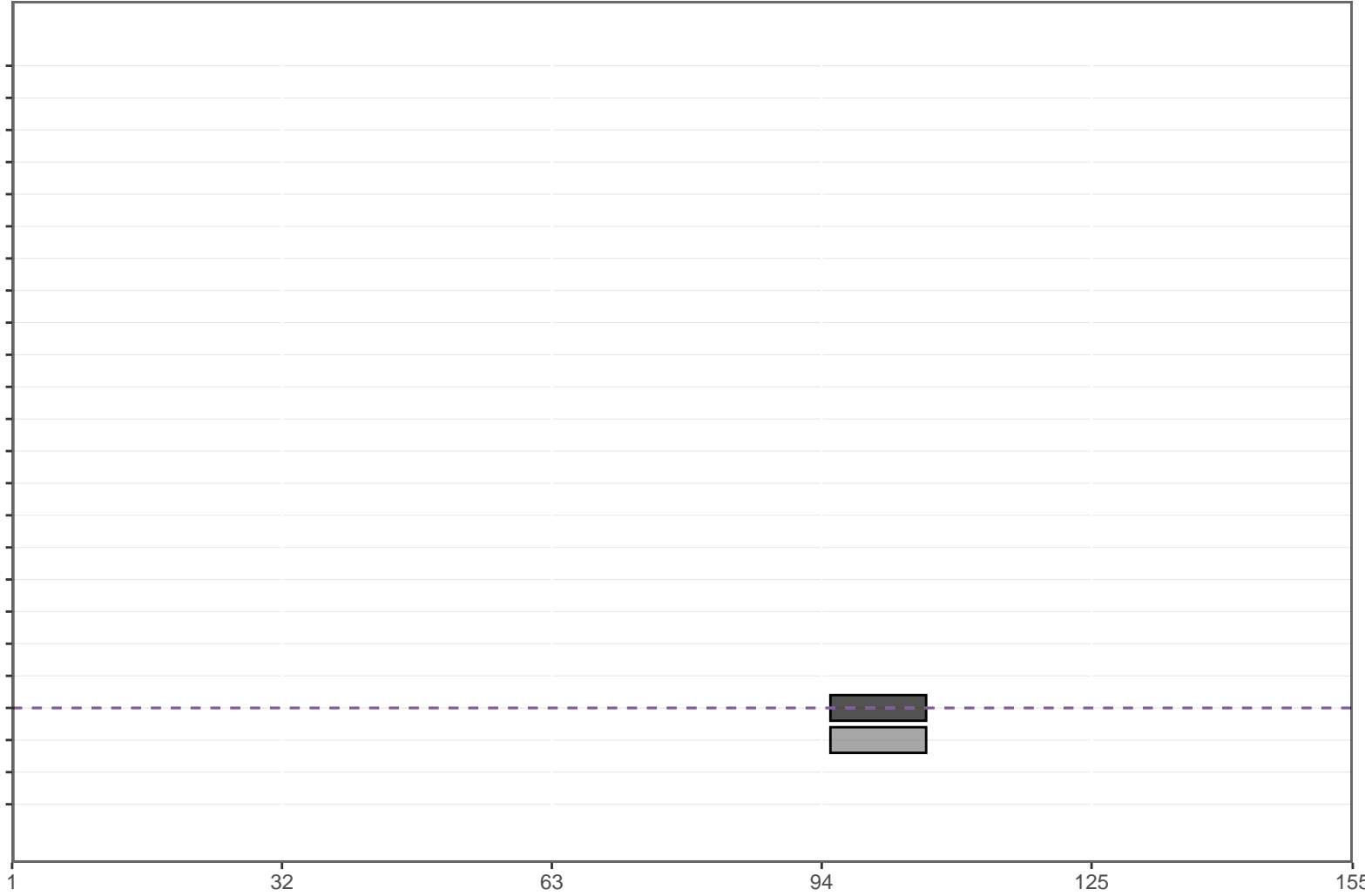
MW indication



Molecular weight

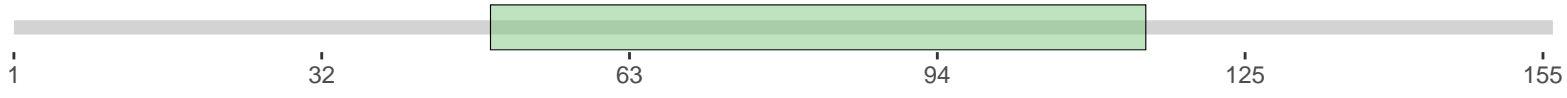


Gel Slice



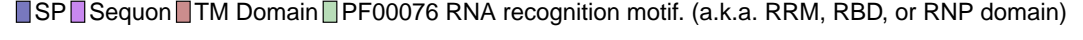
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AFAKHGEVYNAARVTDRIVSGYKSGFGFVRYATLEDAAGIKGLDGGFLDGWVFAEYARPRPPPELQNDNPPGGYGVNYPGVRNNM

NbL11g07960.1 electron_transfer_flavoprotein_subunit_alpha_mitochondrial-like [MW = 37.18 kDa]

No. of times detected



log(intensity)



Values from



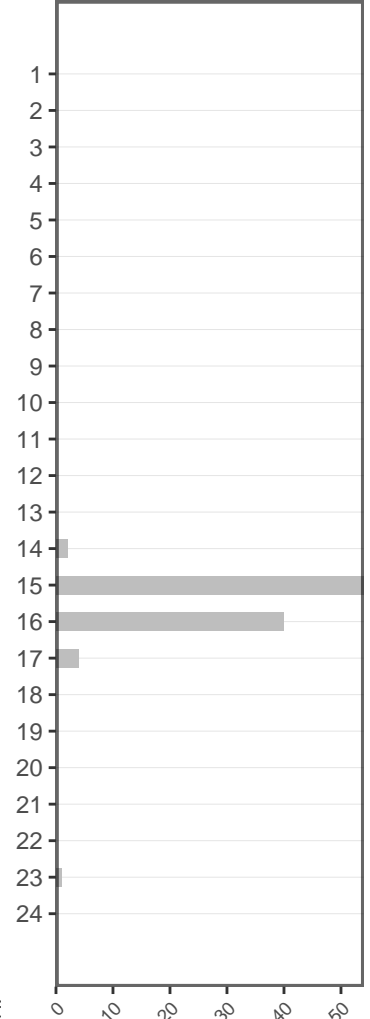
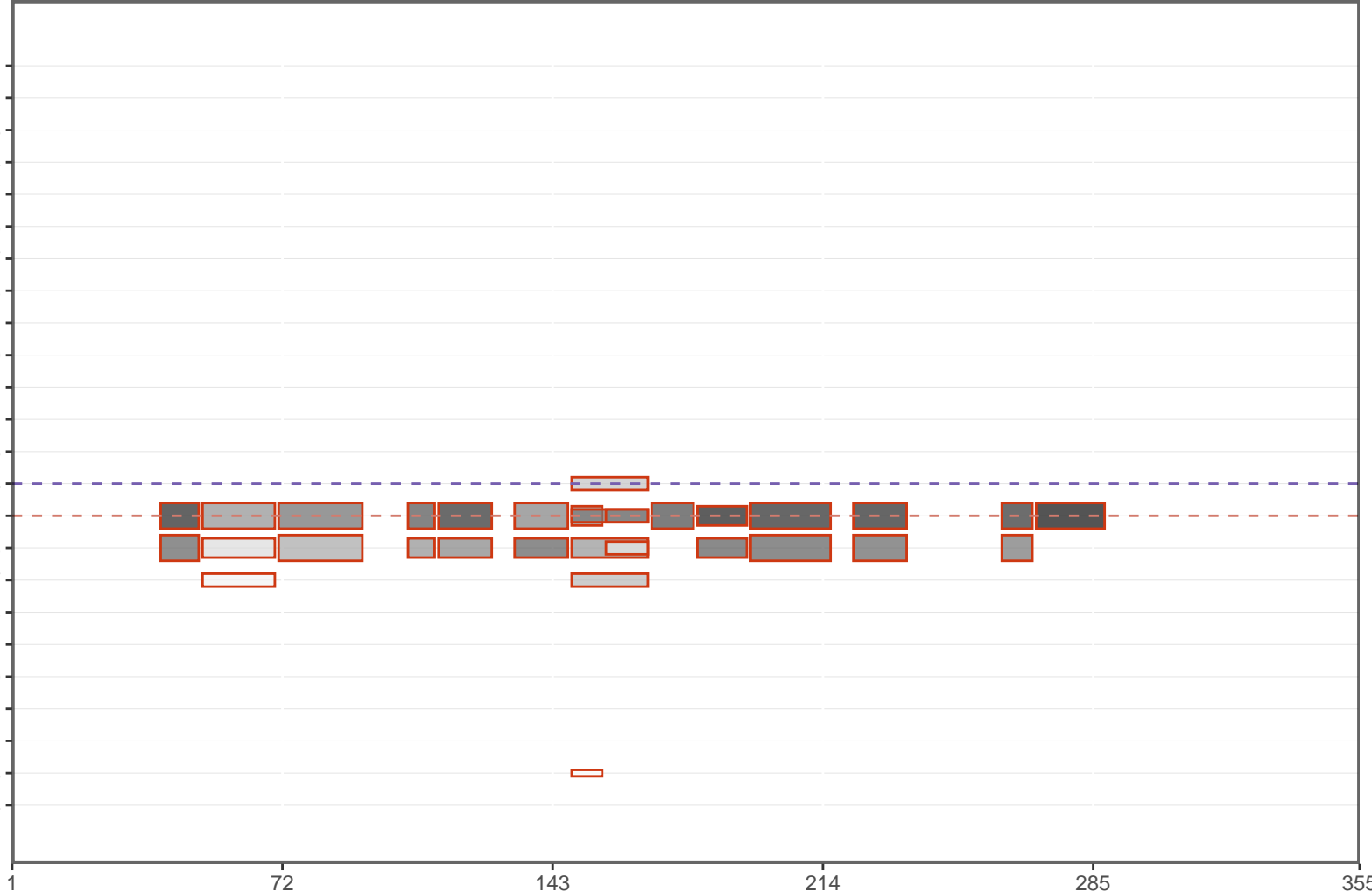
MW indication



Molecular weight

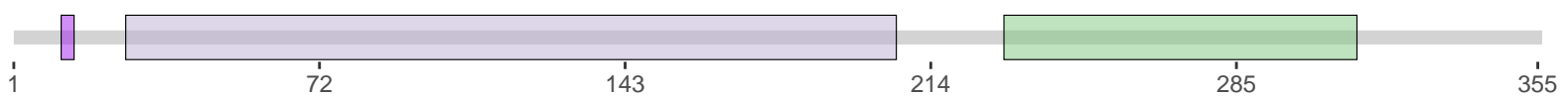


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00766 Electron transfer flavoprotein FAD-binding domain
- PF01012 Electron transfer flavoprotein domain

Protein sequence:

STVRYTGSSPCLSRATSPIASLPLADSKSDASIDQDL6TLDEDDVGVKSRVYKLSGQVVERPDLGNARIVTGGRGVKAENFRKMDKLAEKGAAGVATRAAVDAGFVFNLDLGVGGTQKVAPELYMAFDVSGAIGHMRDQKVVAVNKNKADAPFQIADYKGLVGLDFEIVPELLEKPEPK

NbL11g07940.1 chloroplastic_lipocalin-like [MW = 37.26 kDa]

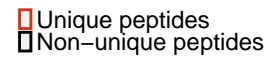
No. of times detected



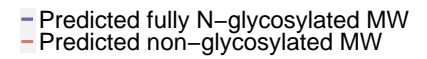
log(intensity)



Values from



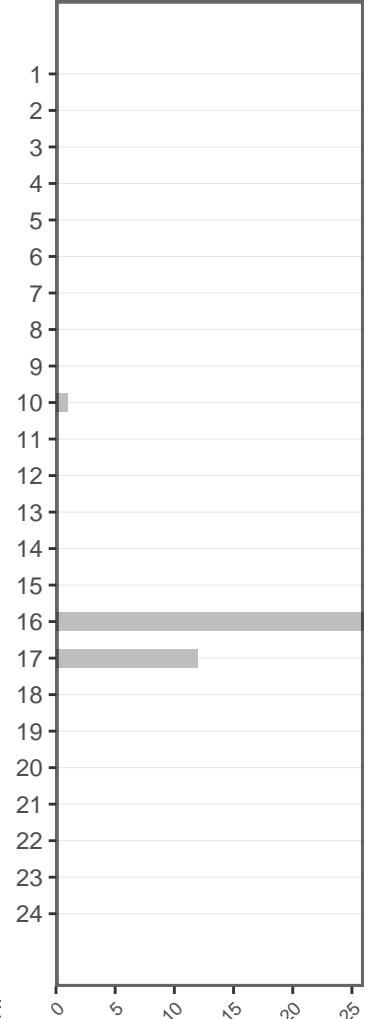
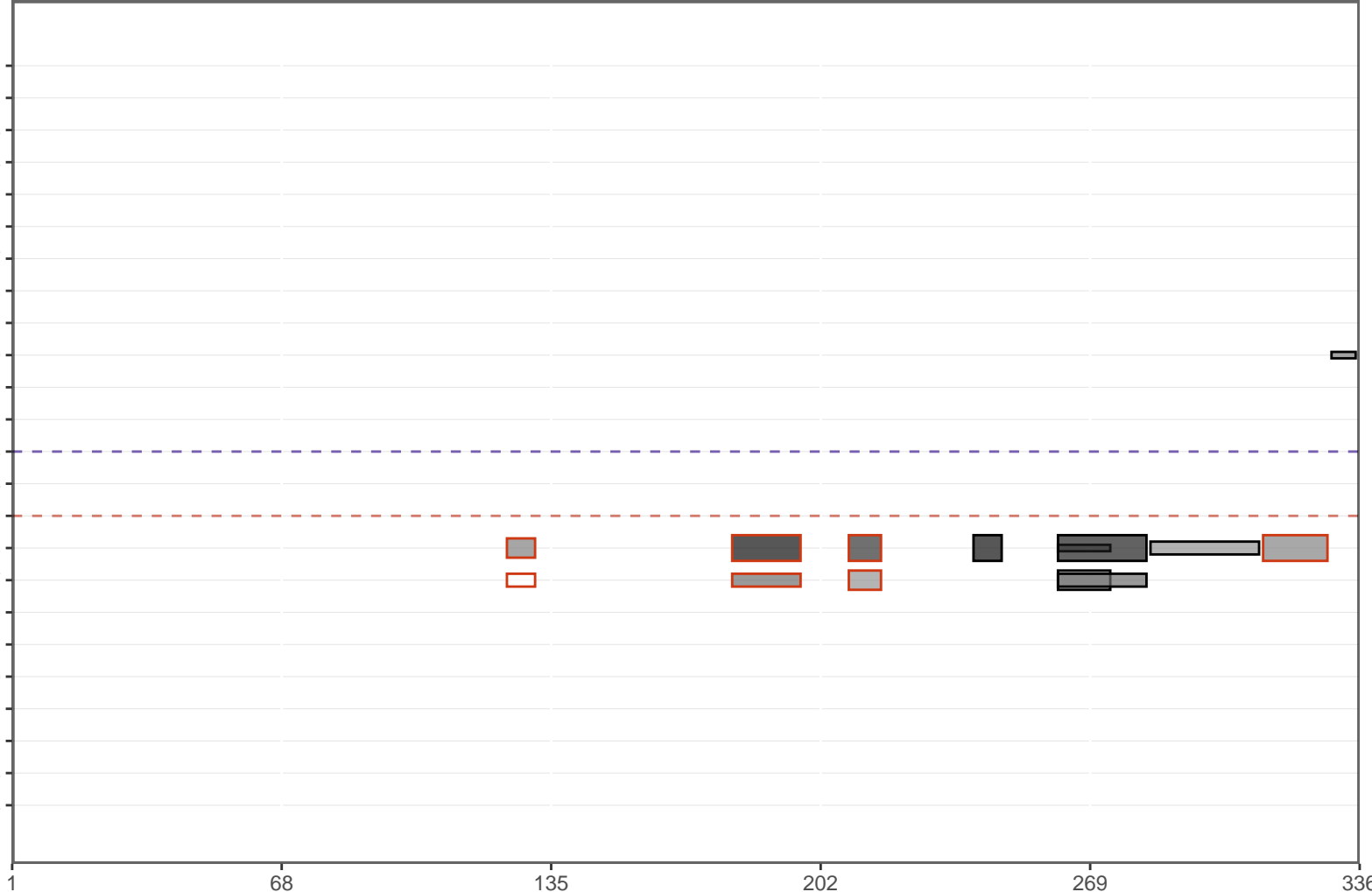
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

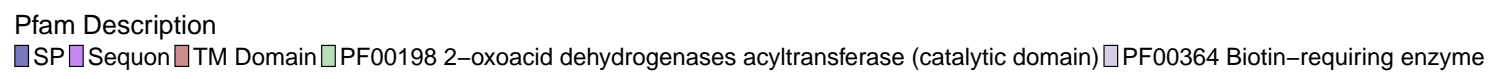
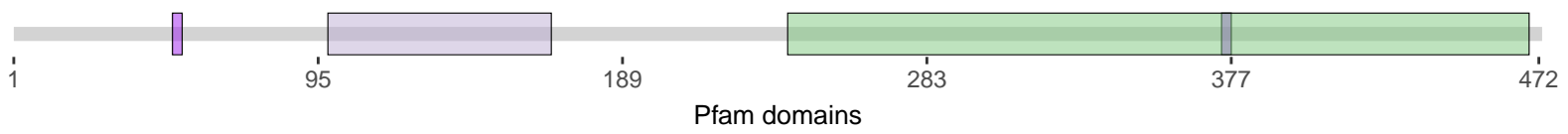
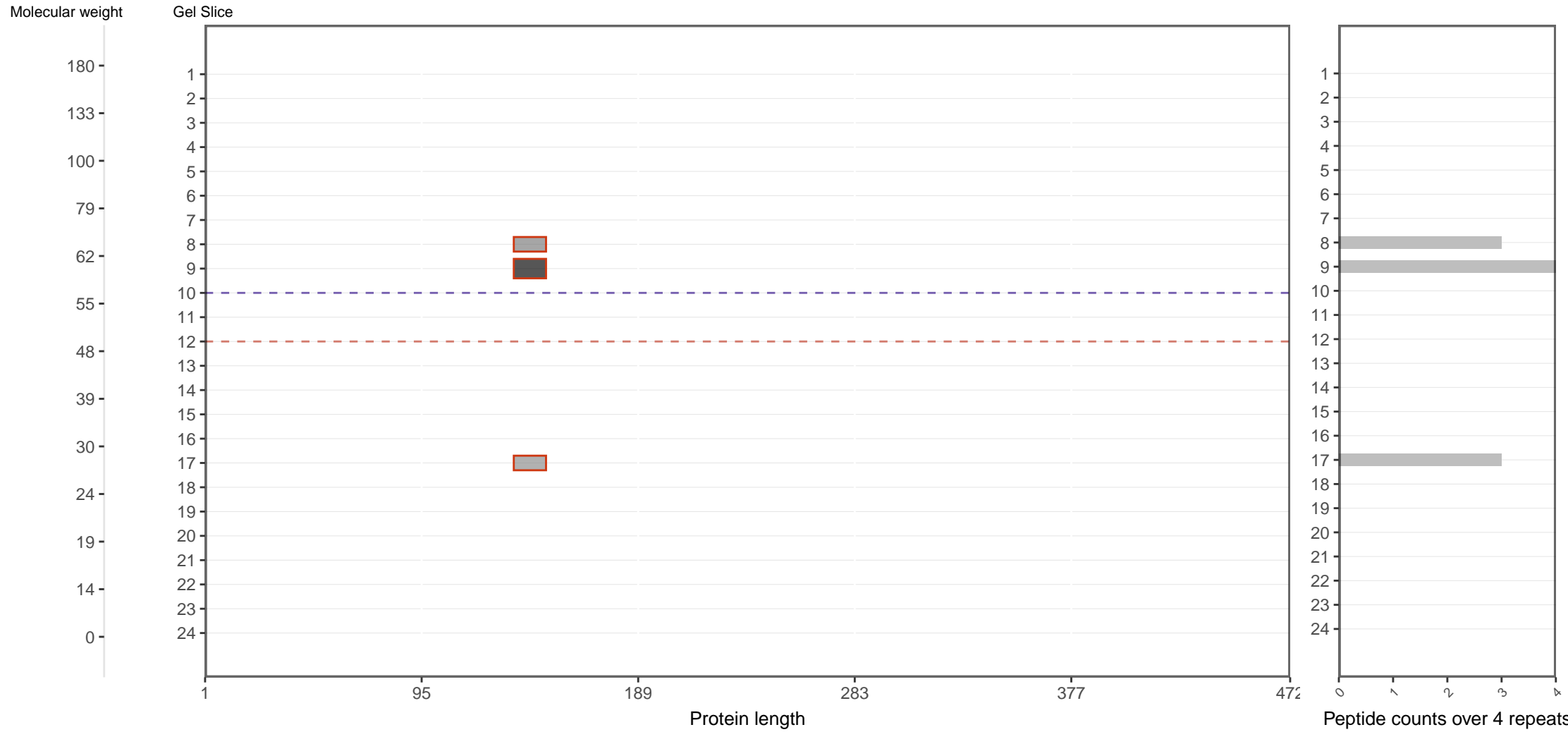
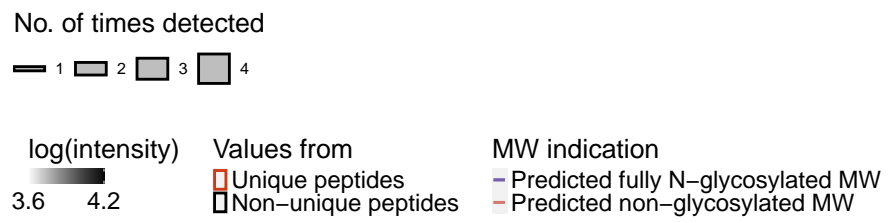
Pfam Description



Protein sequence:

MSAPAIQVDTFCVHGGPDGVTGIRGRVQGLTFEEDREKNETLERQEMIREKCYLRFPTLPPFKPEVDVATDIDNFALVSGAKDRSFQIVRTPDGRPKFIEKYKYLGSFGYDPSGQIKDTPDQCEVKTSGLAAMMSPGMGGALSNQFPDLELKAAVEFNFTSVFETLKKLVEVFKY

NbL11g07780.1
 dihydrolipoyllysine-residue_succinyltransferase_component_of_2-oxoglutarate_dehydrogenase_complex_1_mitochondrial-like
 [MW = 51.42 kDa]



Protein sequence:

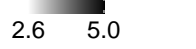
TSPPPPKRSATEPGLPPKERERRVPMTRLRKRKRVATRLKDSQNTFALLTFFNEVDMTLMKLRSDYDAFVEKHGVKLGMLSGFYKAAV/SALQNGPYNVAIDGGDDIIVRDYVDSIWAFTPKGLVYFVLRNAEKMFNFAIEKTINGLAKKATNGTISIDEMAGGDSFTISNGGVYSGSLSTPFPNPPQSALGMHGIYNRPMVYGGDDVYSRPMMYIALTYDHRLLIDGREAVYFLRRKIDVYEDPRRLLLDV

NbL11g07710.1 uncharacterized_LOC109235633 [MW = 45.54 kDa]

No. of times detected



log(intensity)



Values from



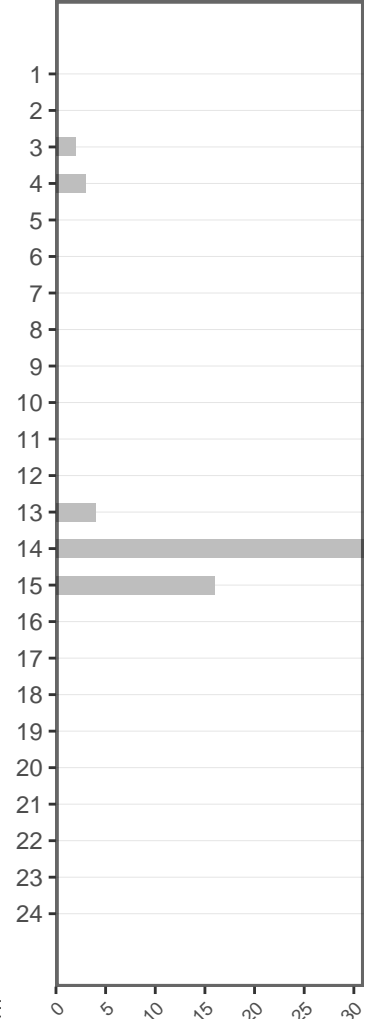
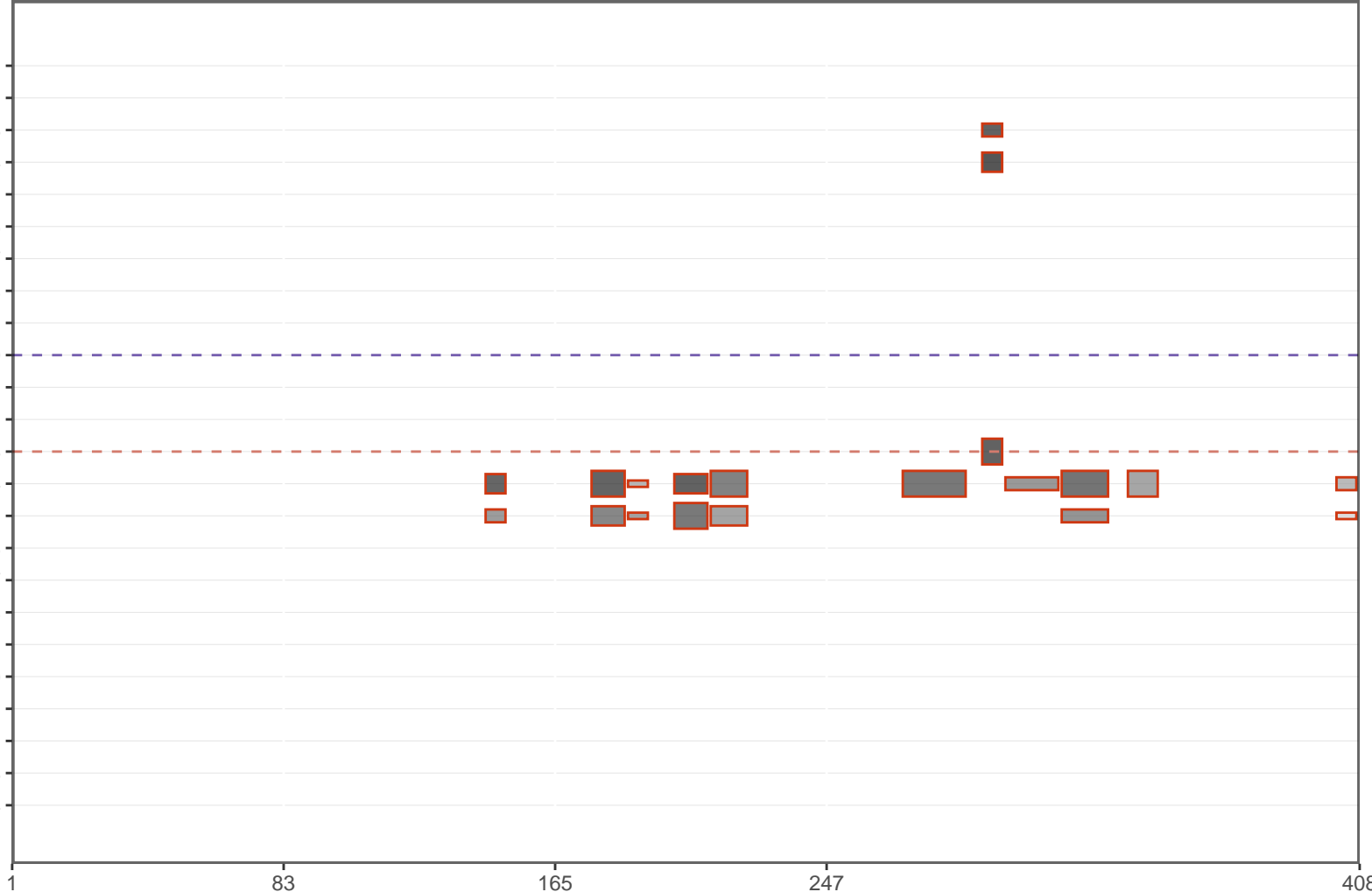
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

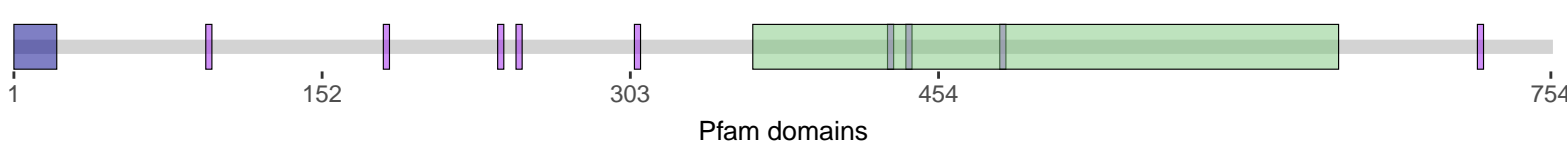
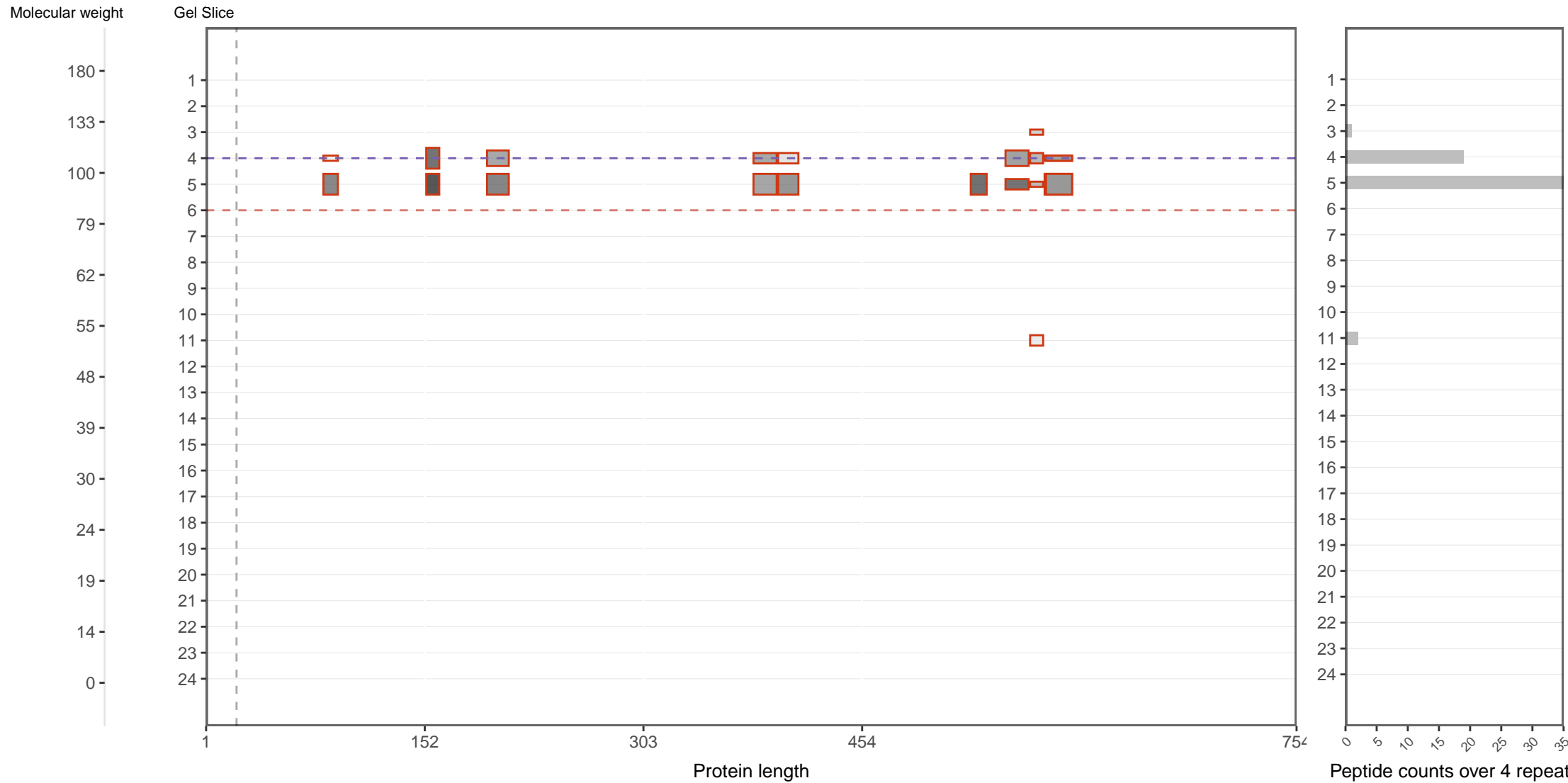
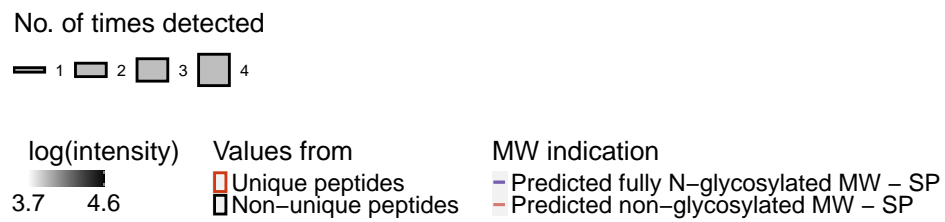
Pfam Description



Protein sequence:

WSSCLKRSYDGGVWTAREGLPPGILGPKNKPLLEGGSLCGSSVESWNSWGAEMEMTADSGRTWRKYGPVYKNDPLVQVQVYVYGTANGTLRVLRLRSFTGINKMSESHDGGVYVSWYAKPTFELNPNFNSGIDGTLKDGRLLLVYNTISRGVYKVALSGDDGDEWHDVYVTEETVGFESYPAVIGSSDGLVHITYTYNRTQIKHVVLPKPV

NbL11g07590.1 glycerophosphodiester_phosphodiesterase_GDPDL3-like [MW - SP = 80.1 kDa]



Pfam Description

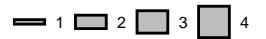
SP Sequon TM Domain PF03009 Glycerophosphoryl diester phosphodiesterase family

Protein sequence:

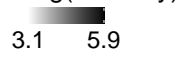
IGASGDYPGCTDLAKTKAAVDSADKLDGPRVGMKMDGIPKGLGRIKDKTTVAGSPFGNGSVAVPELNVITNGIFTNLTWDEKSLKPEISNPWSEFRILVNRNPKARNDDGDFVSLVDFTYAKNATTVSGVMISIEINAAVLAKHGFGVTAALAEISNTAVNGLAKKVMIGTDSVLAKEFRKSHYELVYRVADDSIDSDISEIKNFASVIVTKKVFPSSEEGFLGQGTQVYQKLGSSNLPVYVSLFNNEFVSGAWDFSDS66VEINNYHSGAGIDGVTFFPGTAARYRNRCLD

NbL11g07310.1 farnesyl_pyrophosphate_synthase_1-like [MW = 39.45 kDa]

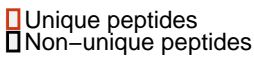
No. of times detected



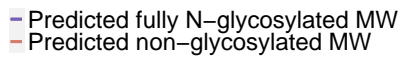
log(intensity)



Values from



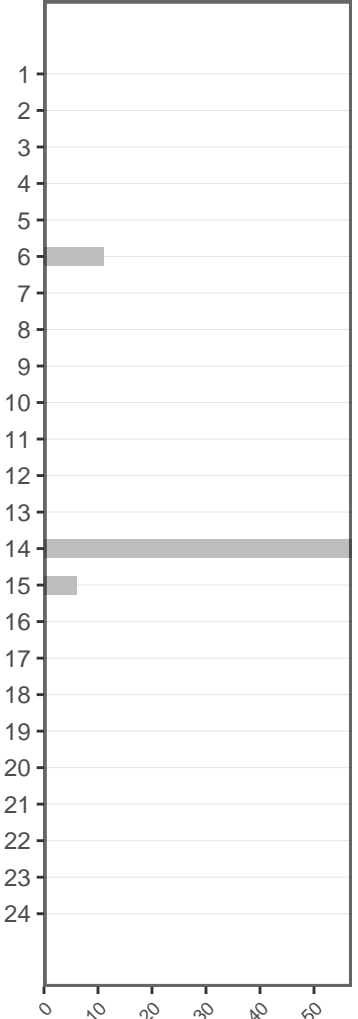
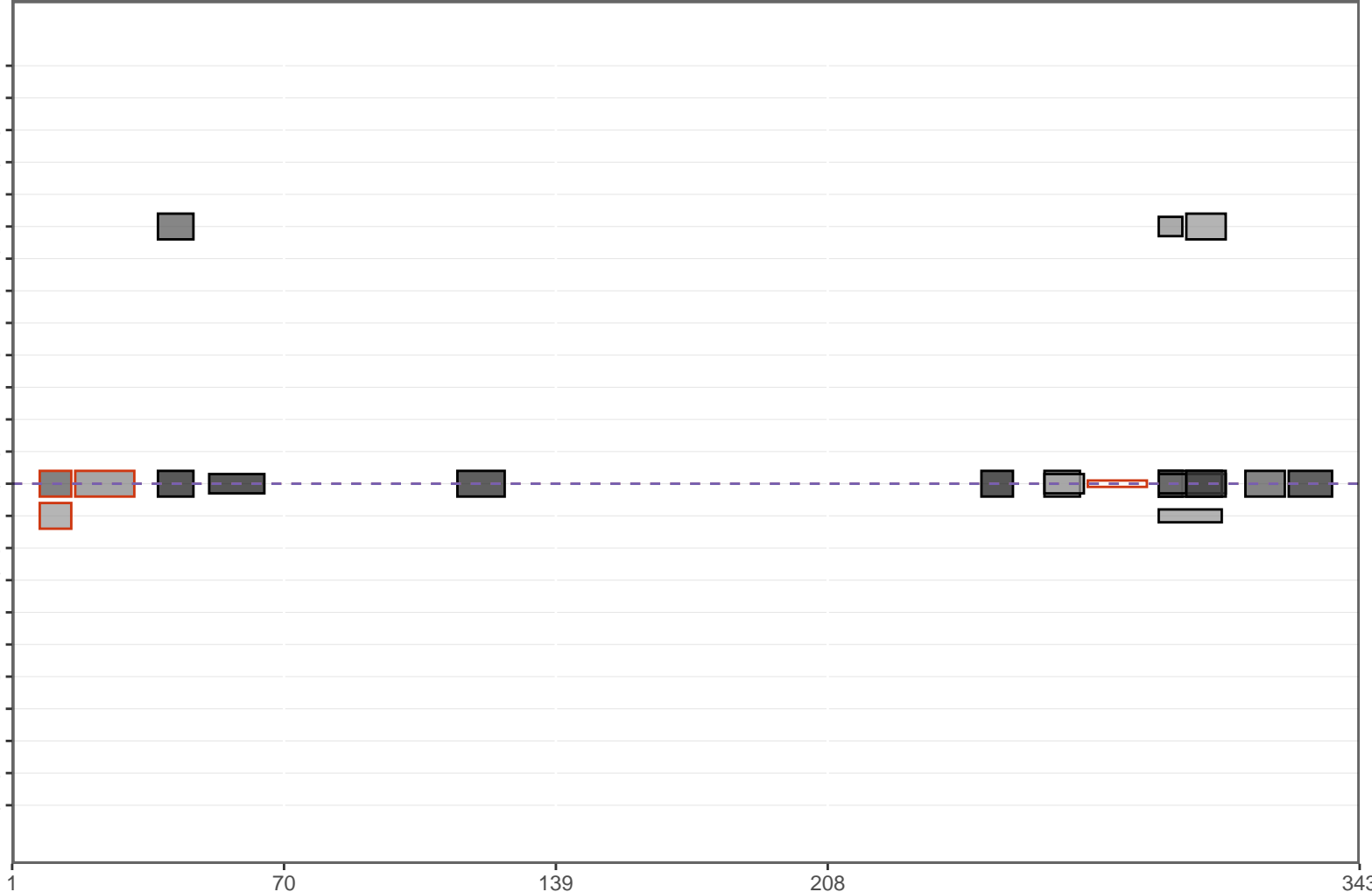
MW indication



Molecular weight



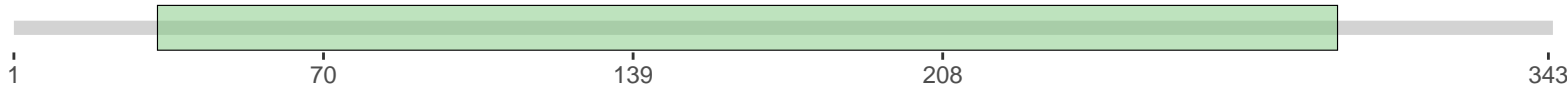
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

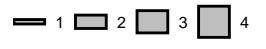


Protein sequence:

ITASGQMDLITLTVGEKDLKSKYSLPHRRIRVQYKTAAYSFYLPVAGALLMAGDNLKIHVDVWNLVEMGRYFQVGGDPLDFADPEVLGKIGTDIGDFKGSWLVVKALELNEEQKLLYENYKDKDDEEGIAKALYNDLKLLEEVLEVEKKSVEKLTSSIAAHPKSAVQAVLHFLGLGKIKRQK

NbL11g07290.1 heat_shock_cognate_protein_80-like [MW = 80.27 kDa]

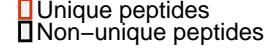
No. of times detected



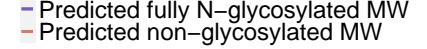
log(intensity)



Values from

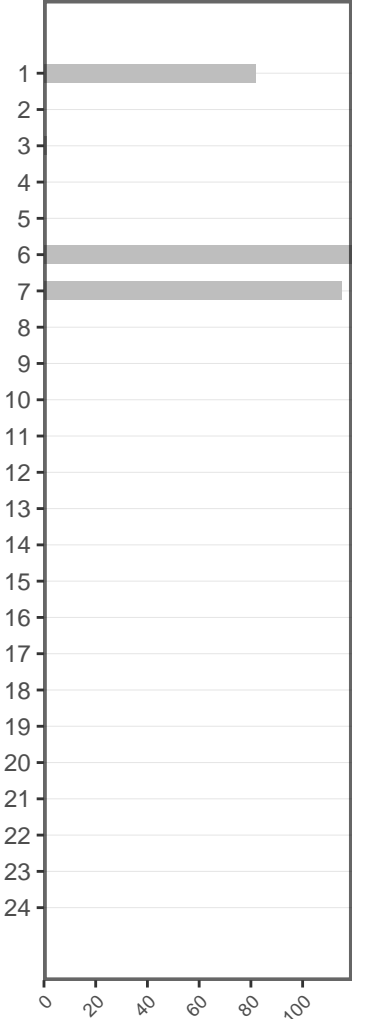
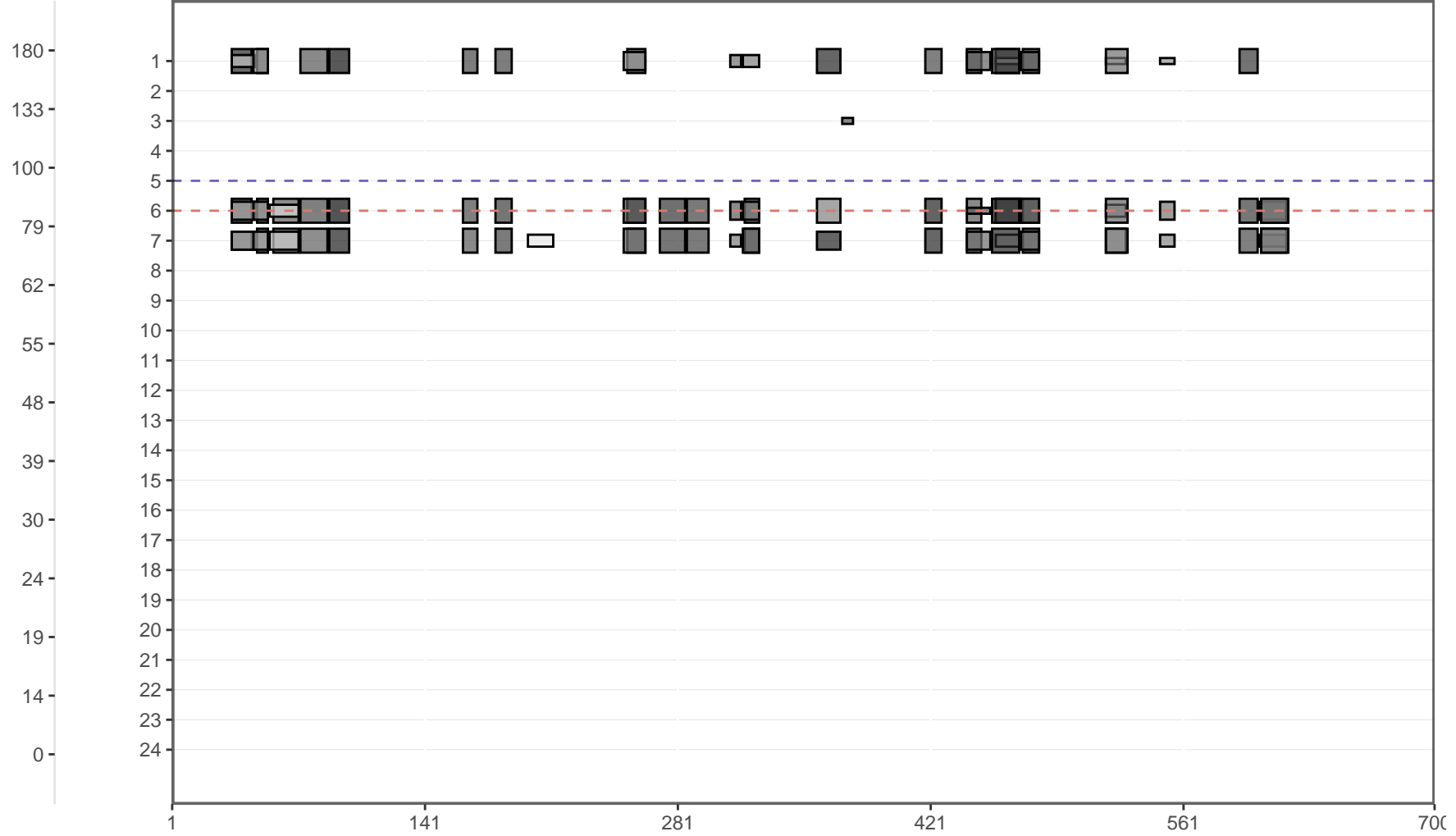


MW indication



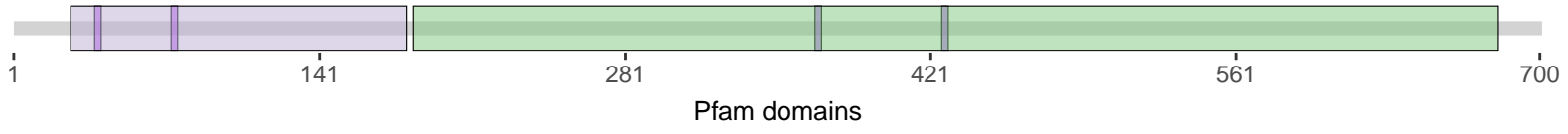
Molecular weight

Gel Slice



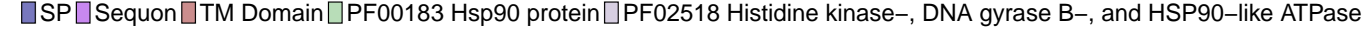
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FAMDNCEELPEYLSFVKGIVDSEDLPLNISREMLGQGNKLVKRNKLVKKGIEFFEAENKEDYKDFYFAFSKLNKLGHEDEGQNRKSKFELLRRVHSTKSGDEMTSLKDVVTRMKKEGQNDYVYTGESKAVENSPFLKELKKGKGYEVLYVMVAIDEVYVSGLKEFGKGLVSAIKEGKLGKLDSEDEKDKKHEELKEKFEGLKGVKDVLDGKVEKVVYSDRVVDFPCGLVTGEVGVWTANMERMKAGALRDSMAGYMSKTKMEINPENNAIMEELRKRADADKDKSKYKDLV

NbL11g07240.1 GPI-anchored_protein_LORELEI-like [MW - SP = 16 kDa]

No. of times detected



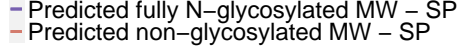
log(intensity)



Values from



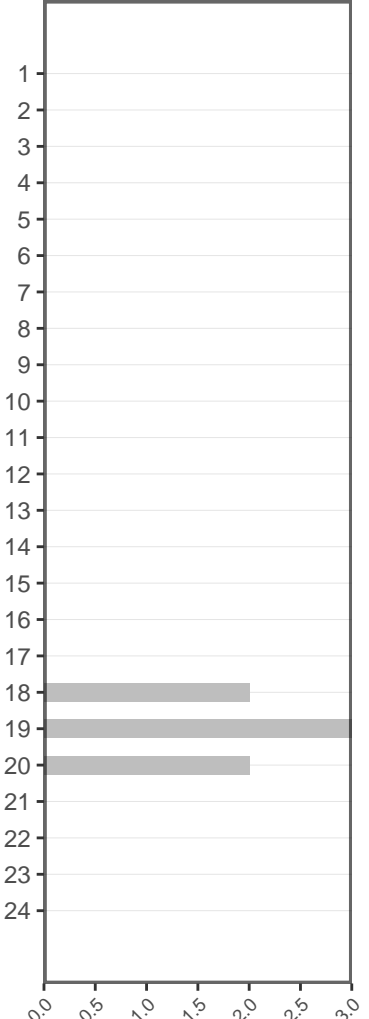
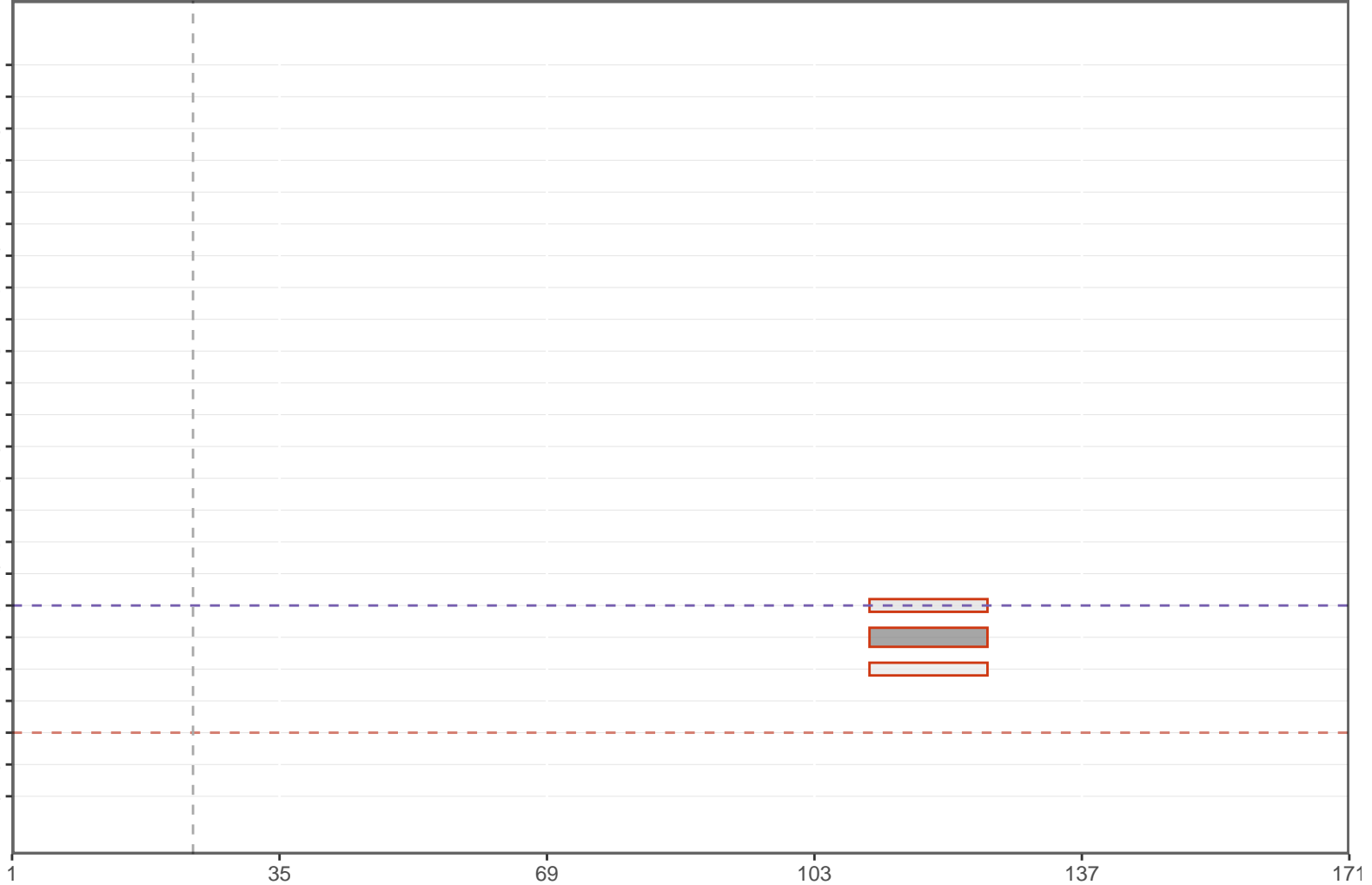
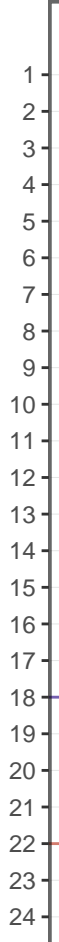
MW indication



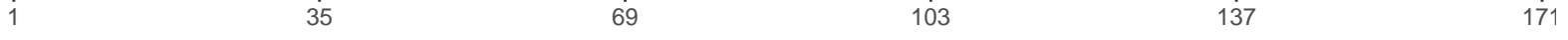
Molecular weight



Gel Slice



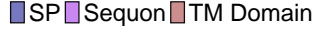
Protein length



Pfam domains



Pfam Description



Protein sequence:

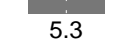
KQCCDAFYVQACFPADLLDNLNDGCGTTFMFSYINLRGKYRPLFGSMGTGTKEGLEPILAPGGGANDDANSSGNCKLSPVQIMATAFMVMFLFV

NbL11g07160.1 porphobilinogen_deaminase_chloroplastic-like [MW = 39.94 kDa]

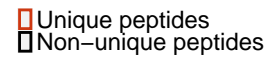
No. of times detected



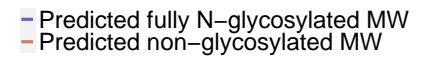
log(intensity)



Values from



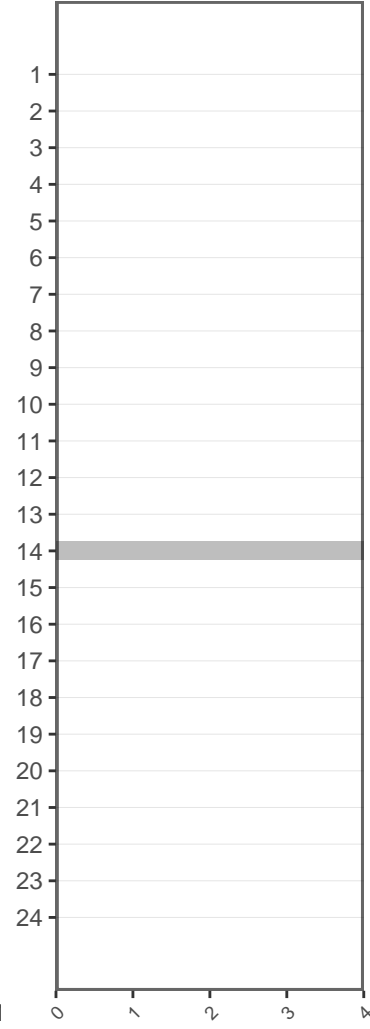
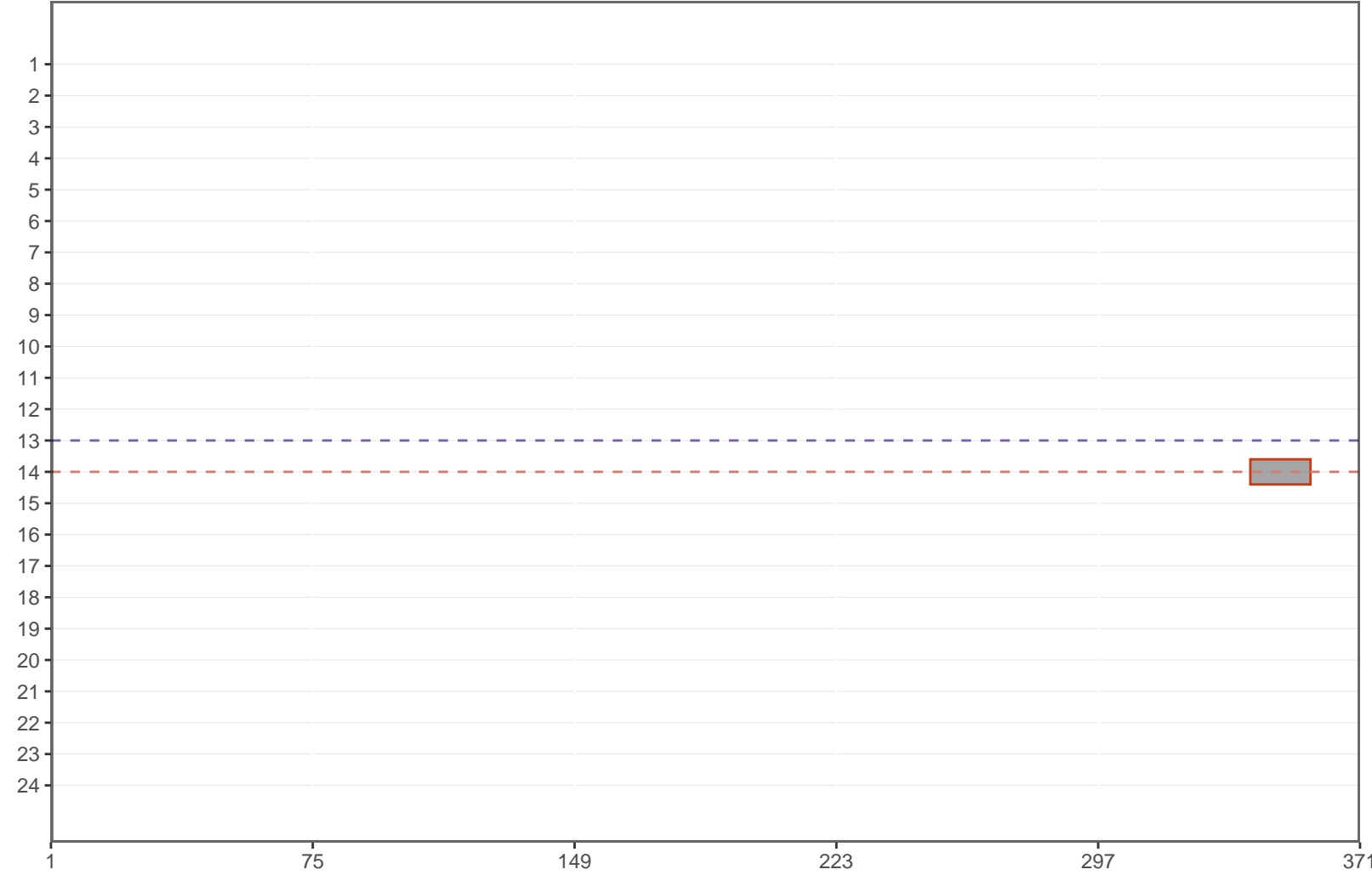
MW indication



Molecular weight

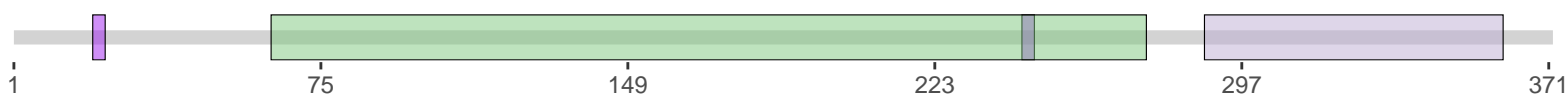


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01379 Porphobilinogen deaminase, dipyromethane cofactor binding domain
- PF03900 Porphobilinogen deaminase, C-terminal domain

Protein sequence:

ILALPSSGTVGTASLRKRSQILHRYPDLNLENFRCNVDGTRLRKLNIEGVGATLALAGLRKLDMTENVTSLPIEDMLPWAGGAGIACRSDDDETMANYALLNHEETRLAVAGERAFKTLDDGSCRTPNAGVACRGEODGDFKGLVASPDGTRVLETSRKGPVTFEDMTLMGEDAGKELLSRAGPQFFGN

NbL11g07140.1 thiosulfate/3-mercaptopyruvate_sulfurtransferase_1_mitochondrial-like [MW = 41.78 kDa]

No. of times detected



log(intensity)



Values from



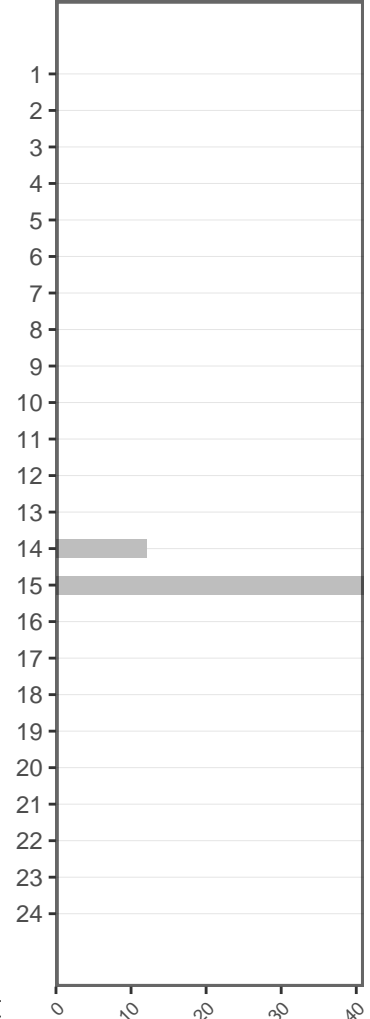
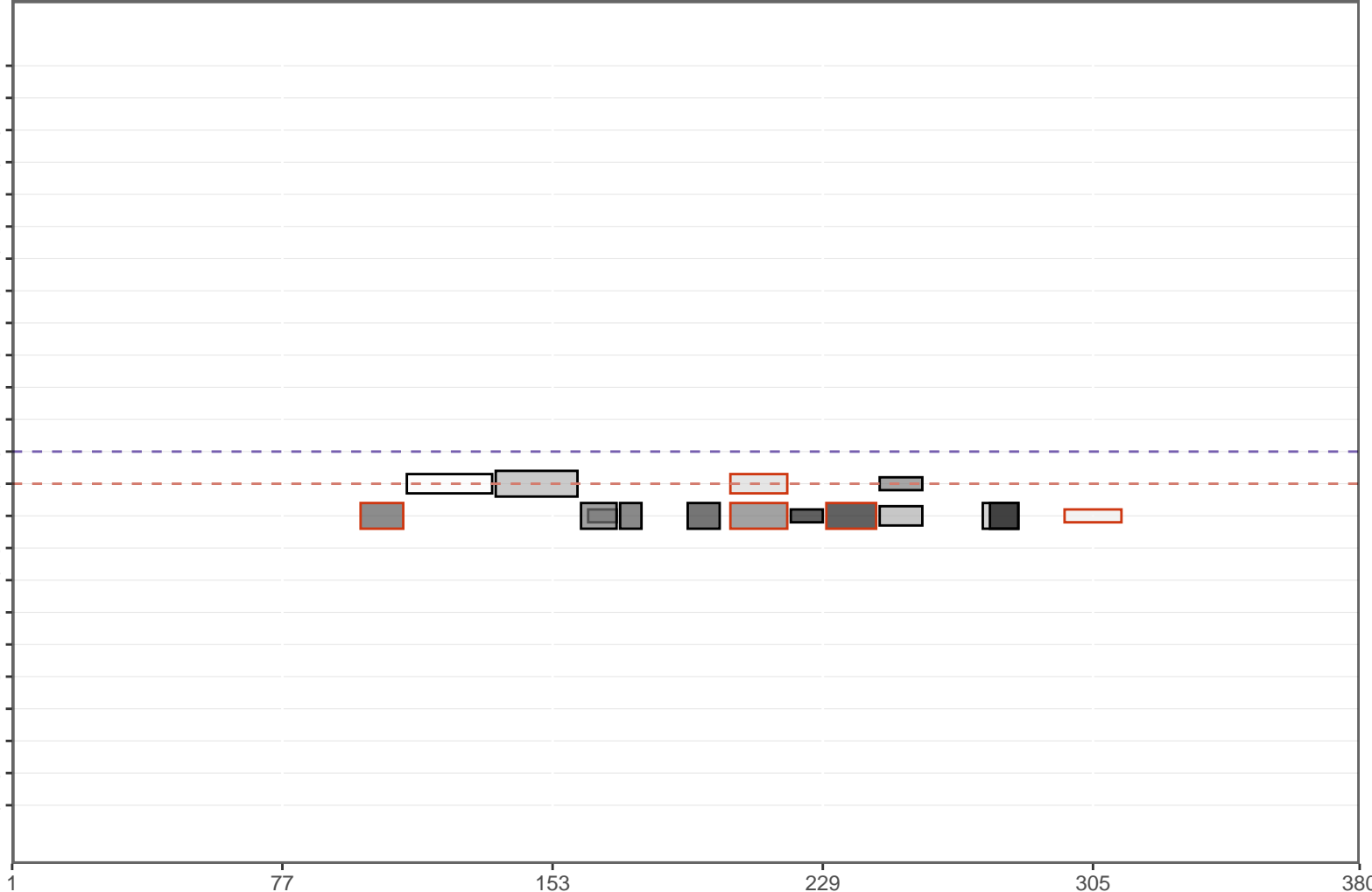
MW indication



Molecular weight

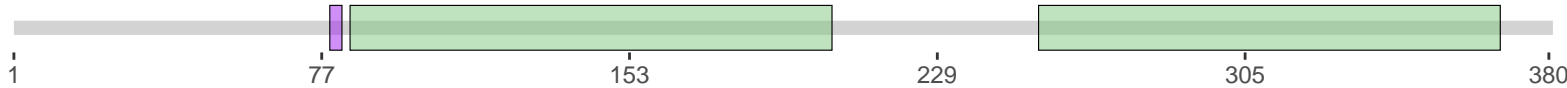


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

WWWVFRATGHDKVVWVLDGGLPRWRASEVDVESSASGDALKASAAEAEKVVGGGMVGFPTTFETKFGPHLVWNLDDVKNRNEDEKTYGHIDARSKARFDGVAPEPRKGRISGHVPSGKGFPPQMLDSSGTLREELNKKFDLEGISLQKPVGTSGGTGVTADIALGLHRLKTDIPVYDGSWTEWGANPDPVSTSETP

NbL11g07130.1 phosphoglycerate_kinase_cytosolic-like [MW = 42.49 kDa]

No. of times detected



log(intensity)



Values from



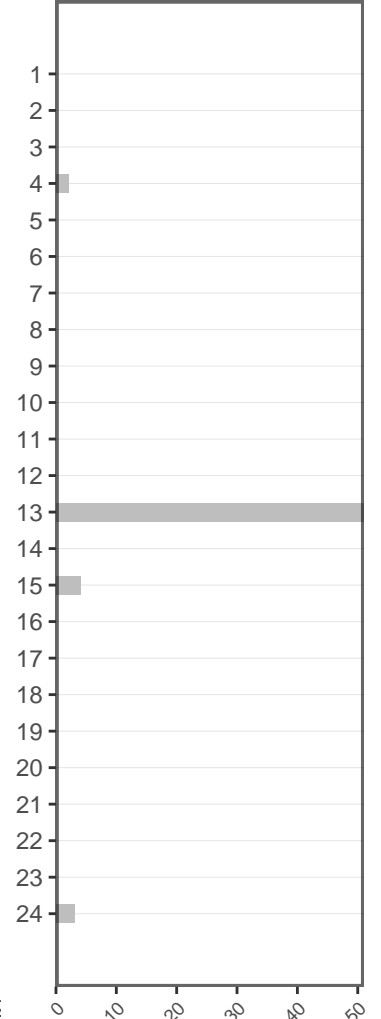
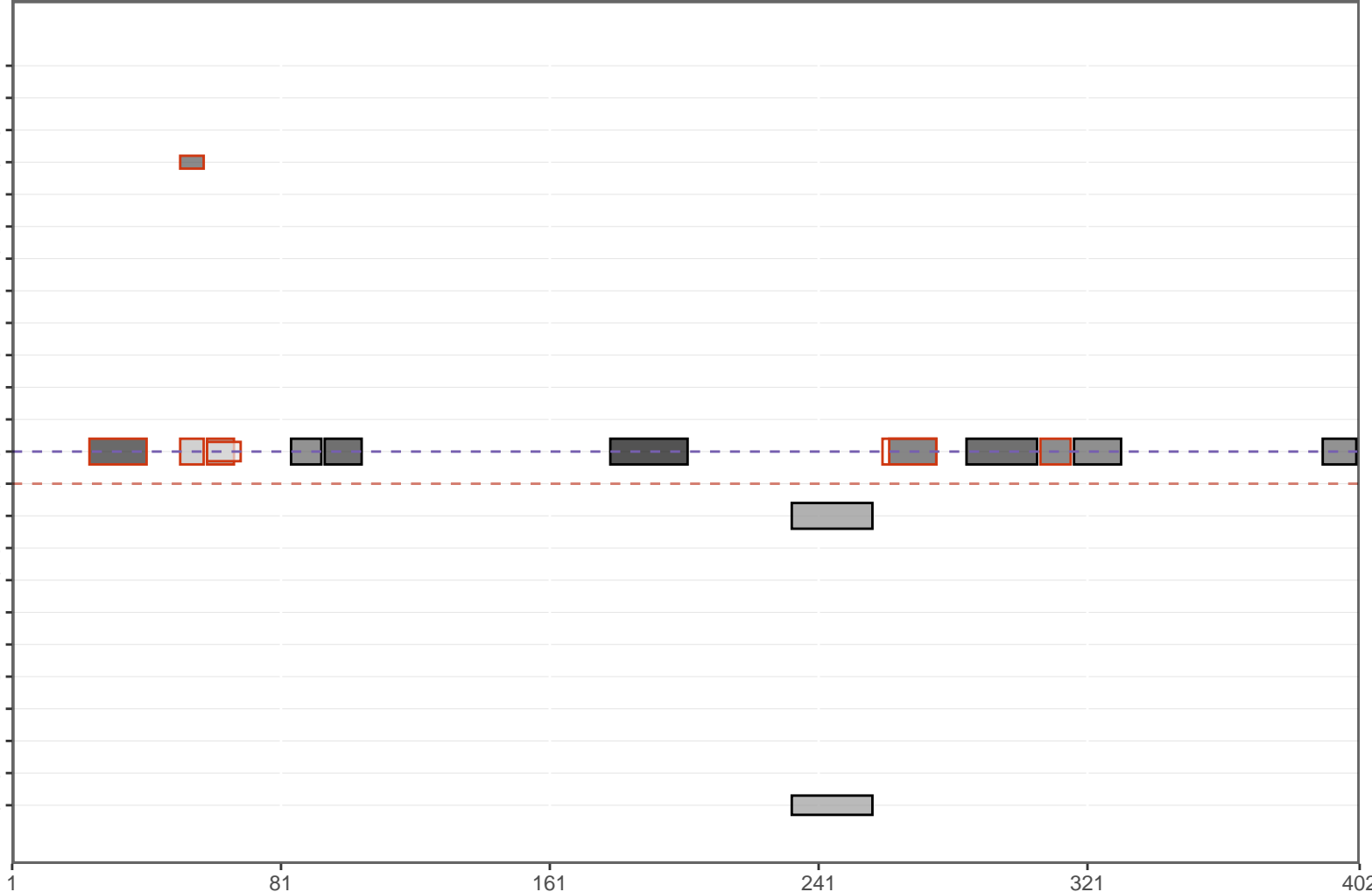
MW indication



Molecular weight

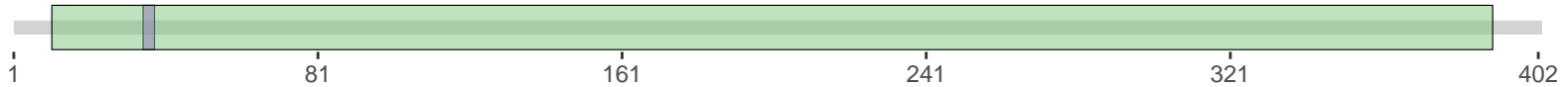


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

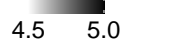
VSNPQKFAAIVGGKVSNGVSELEKVNLLGGGMIFTRYKAGQVSVGSSVLEEDKLDLATSLEKAKKAGVSLLLPADIVADKFAADANSKIVPASEIPDGMWGLDGPDAIKFGEALDTTKTIWNGPMGVFEFEKFAAGTEAIAKLAELSGKGVTTIGGGDEVAIVKVKGLADKMSHSTGGGASLELEGGKLPGLALDDA

NbL11g06990.1 40S_ribosomal_protein_S8-like [MW = 25.03 kDa]

No. of times detected



log(intensity)



Values from



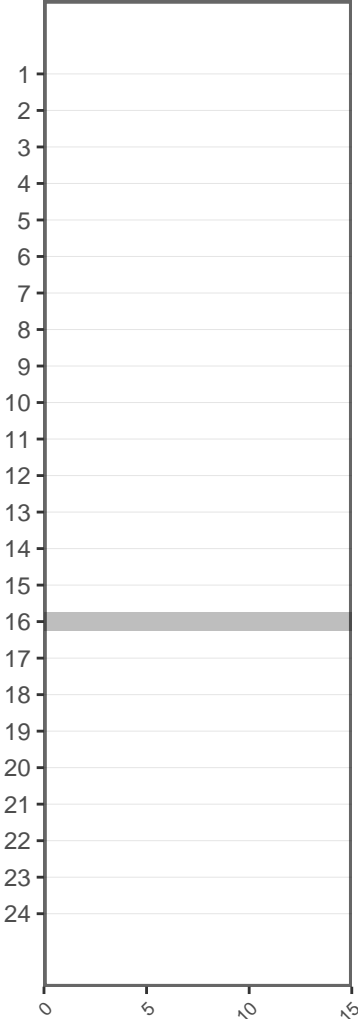
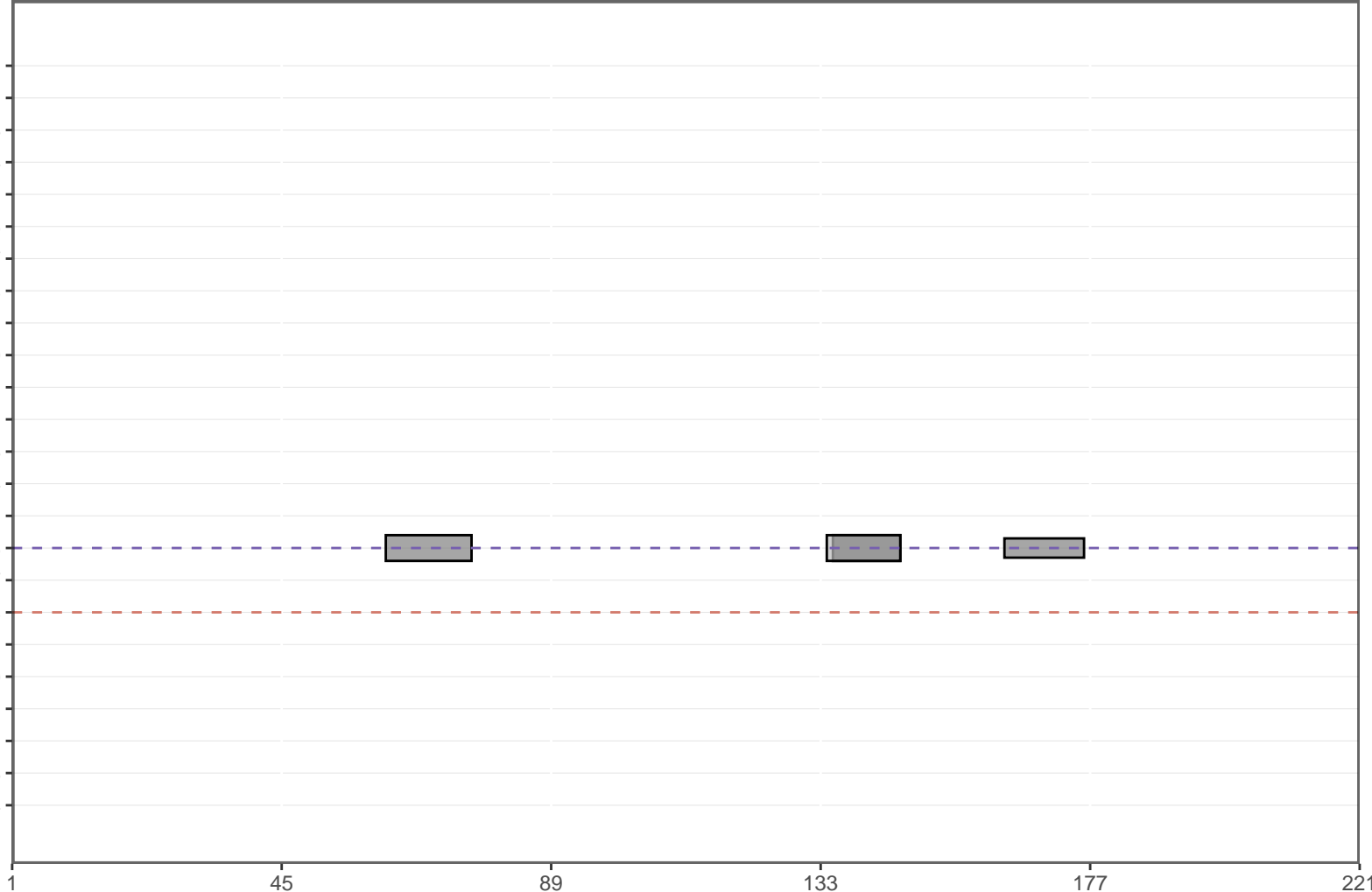
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

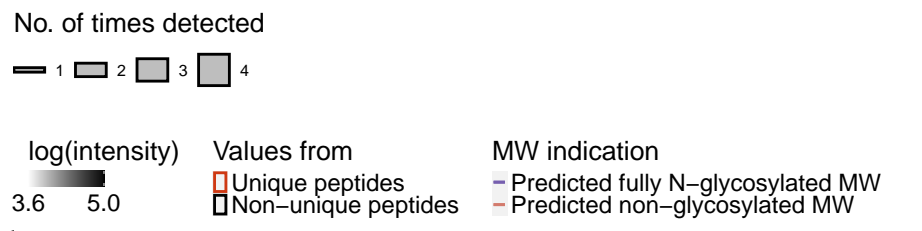
Pfam Description



Protein sequence:

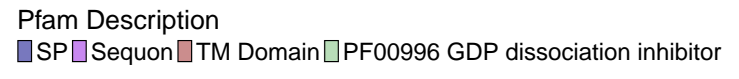
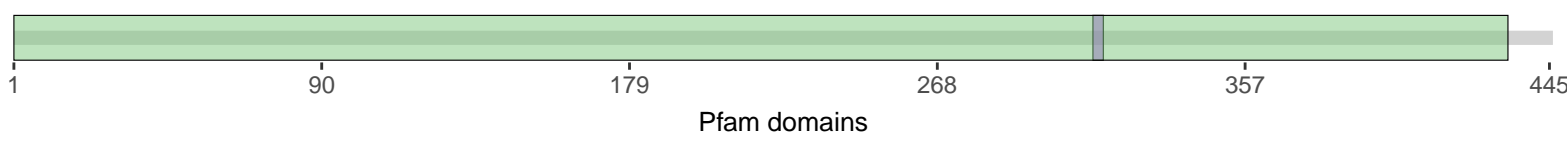
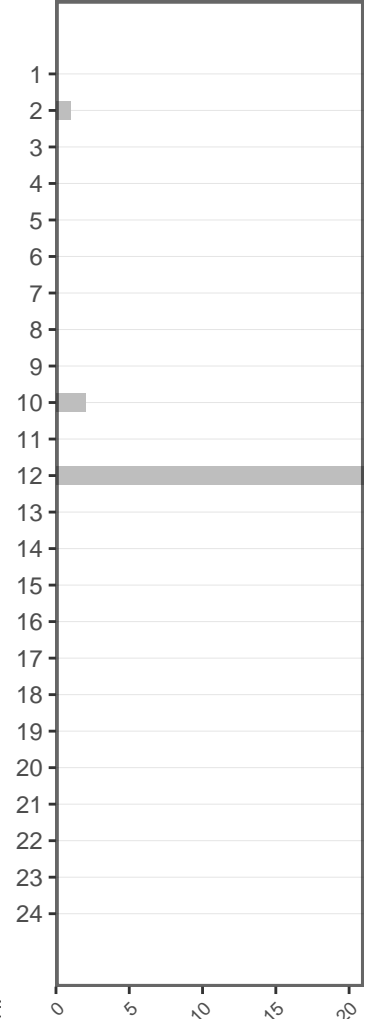
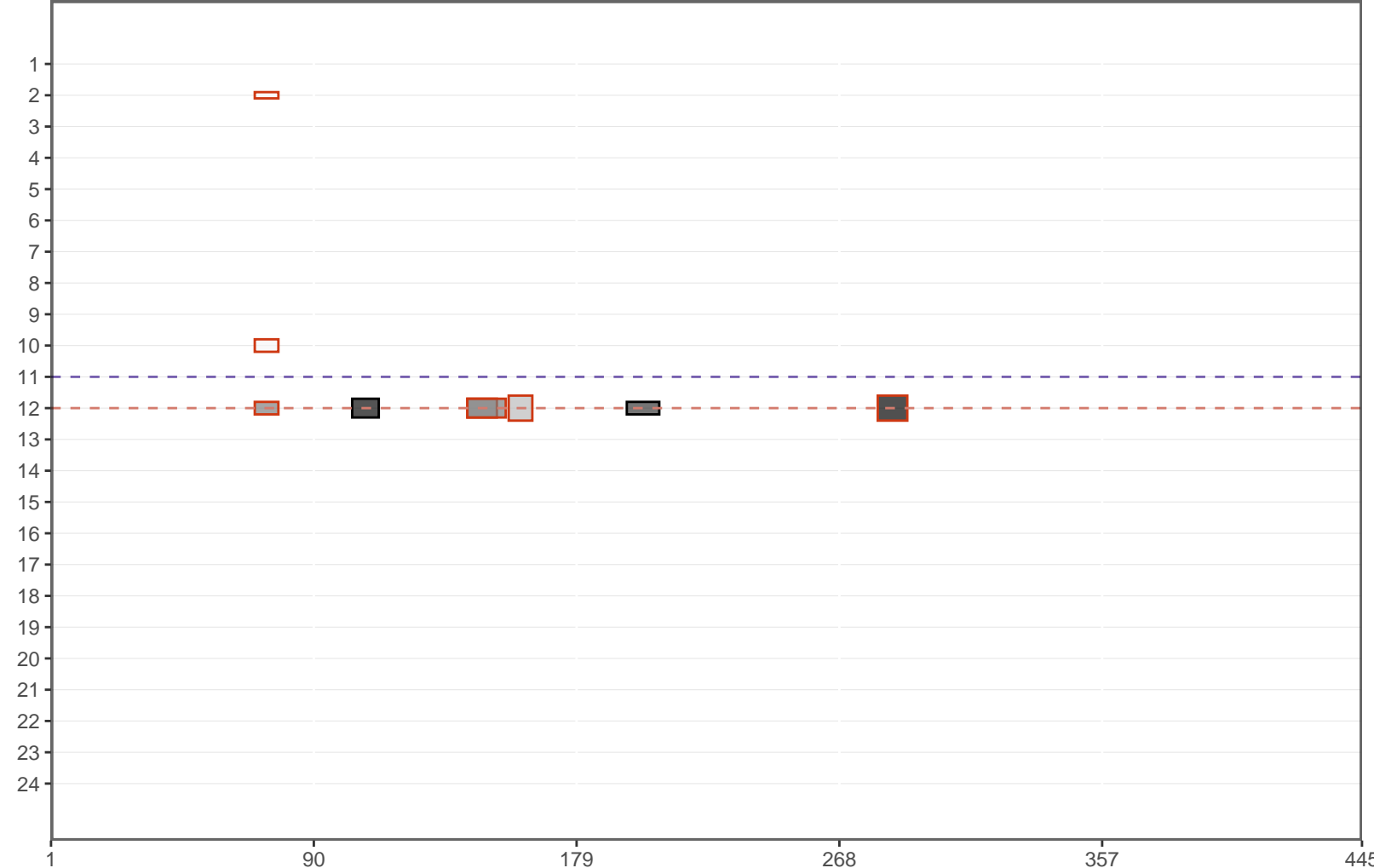
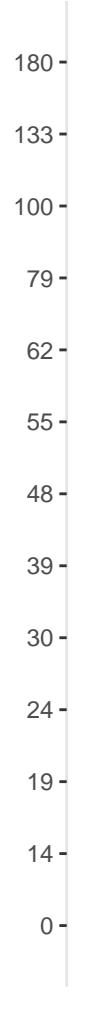
TLVKSALVQVDALPFKQWVFLGHYGVDRKKKTAASKKEGEEAEAVPEEKSNHVGRLKLRGGDRKIDPHHEEGFASGRLLAANSSRPGGCGRADGVHLEGKELEFYMKLGRKKKGKASGAT*

NbL11g06860.1 guanosine_nucleotide_diphosphate_dissociation_inhibitor_2 [MW = 49.85 kDa]



Molecular weight

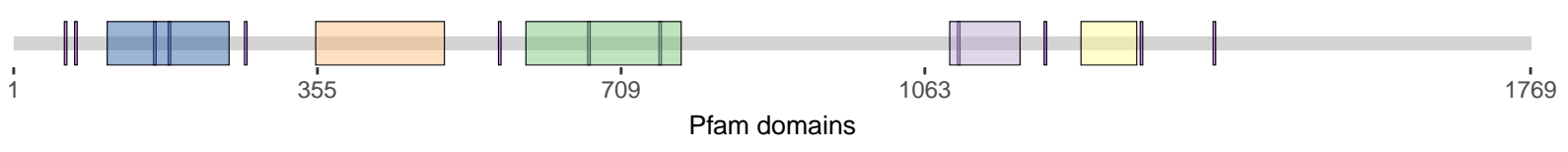
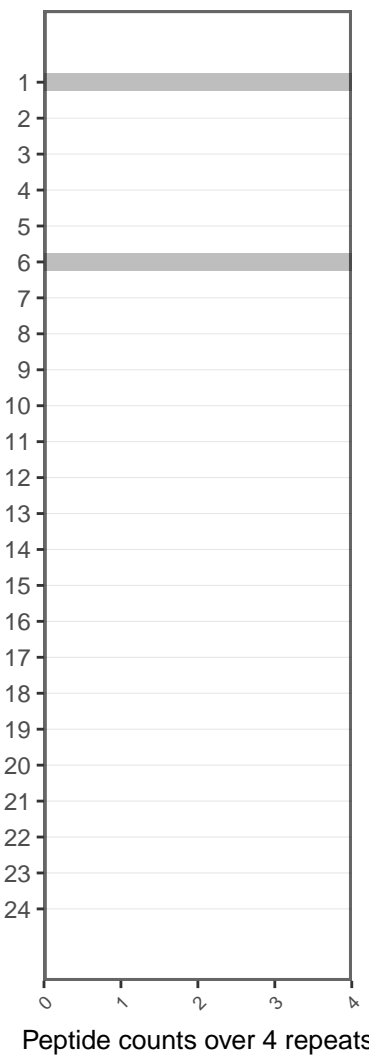
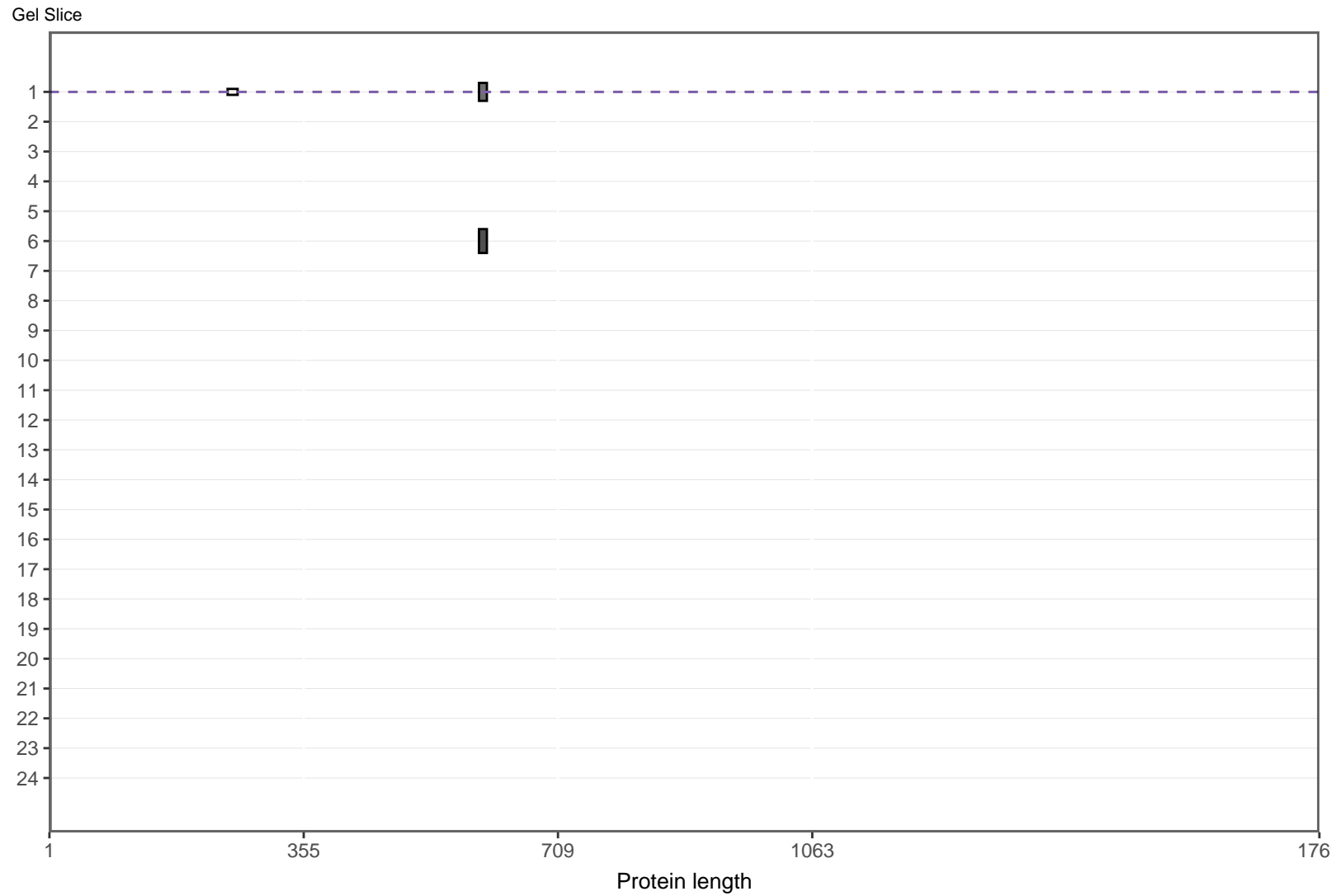
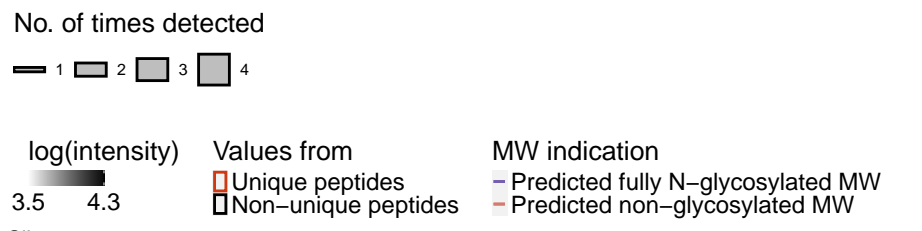
Gel Slice



Protein sequence:

KLYAESLARFGGSPYVFLVGLGELPQAFARLSAVYGGTVMLNKPEKVEFDEEGKVDGVTSEGETAKGKVVQDPVLTNKRKVKGRVRAIAIMSHPIPTNDGSHVQHLPGKLGKRSMDMLFCGGVYTHNVAKNGKFIQVSTEAETDNPSEKPGIDLLGGVDEFFAVDRFEPVNERSLDNGFISTVDPTTFHSESTVDDVNLNMYLTGTGKVLDLNVDLSAASAAEE

NbL11g06830.1 brefeldin_A-inhibited_guanine_nucleotide-exchange_protein_5 [MW = 196.42 kDa]



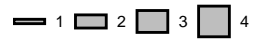
- Pfam Description
- SP
 - TM Domain
 - PF09324 Domain of unknown function (DUF1981)
 - PF16206 C-terminal region of Mon2 protein
 - Sequon
 - PF01369 Sec7 domain
 - PF12783 Guanine nucleotide exchange factor in Golgi transport N-terminal
 - PF16213 Dimerisation and cyclophilin-binding domain of Mon2

Protein sequence:

ILMEQDNKARYGVCMGFKAGHITHVLGMDTMRVAFLLTLRLNLHLPDMKSKNVEALRLLACDSDMEALQDTVAALVLEGISLRFIVTNPMAATVMDGNGISRDALLOSLRDLTKPTTEQVFNVSKLPSSEVVEFFSLGKVSAAEELRQVYRVSLSLGLKLVESVYNNMARIRMWVARIWVSLATHFIFAGSHPEEKVAMVAIDSLRGLGMKYLERAELANFTFONDILKPFVLMRSSRSRIRRLVDDGVGMKSKVGIKSGWRVFMFTAADDDLEPVESA

NbL11g06800.1 DExH-box_ATP-dependent_RNA_helicase_DExH10-like [MW = 111.5 kDa]

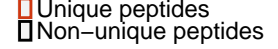
No. of times detected



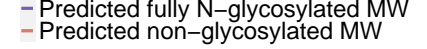
log(intensity)



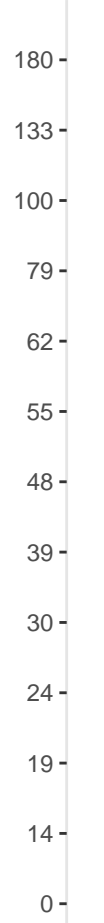
Values from



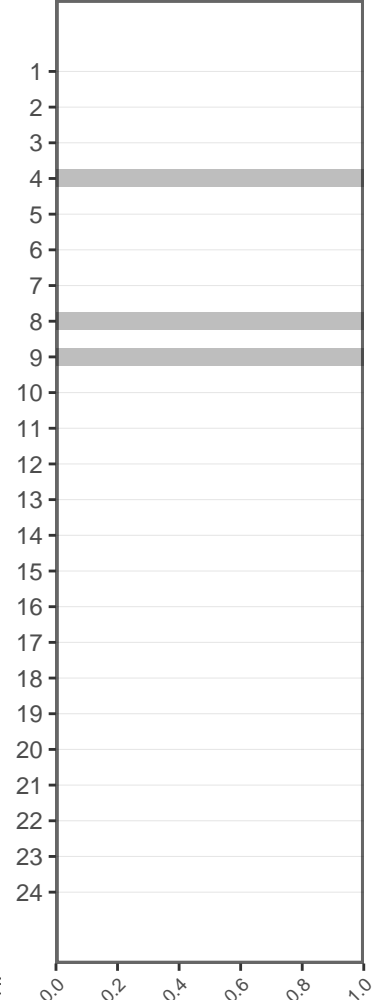
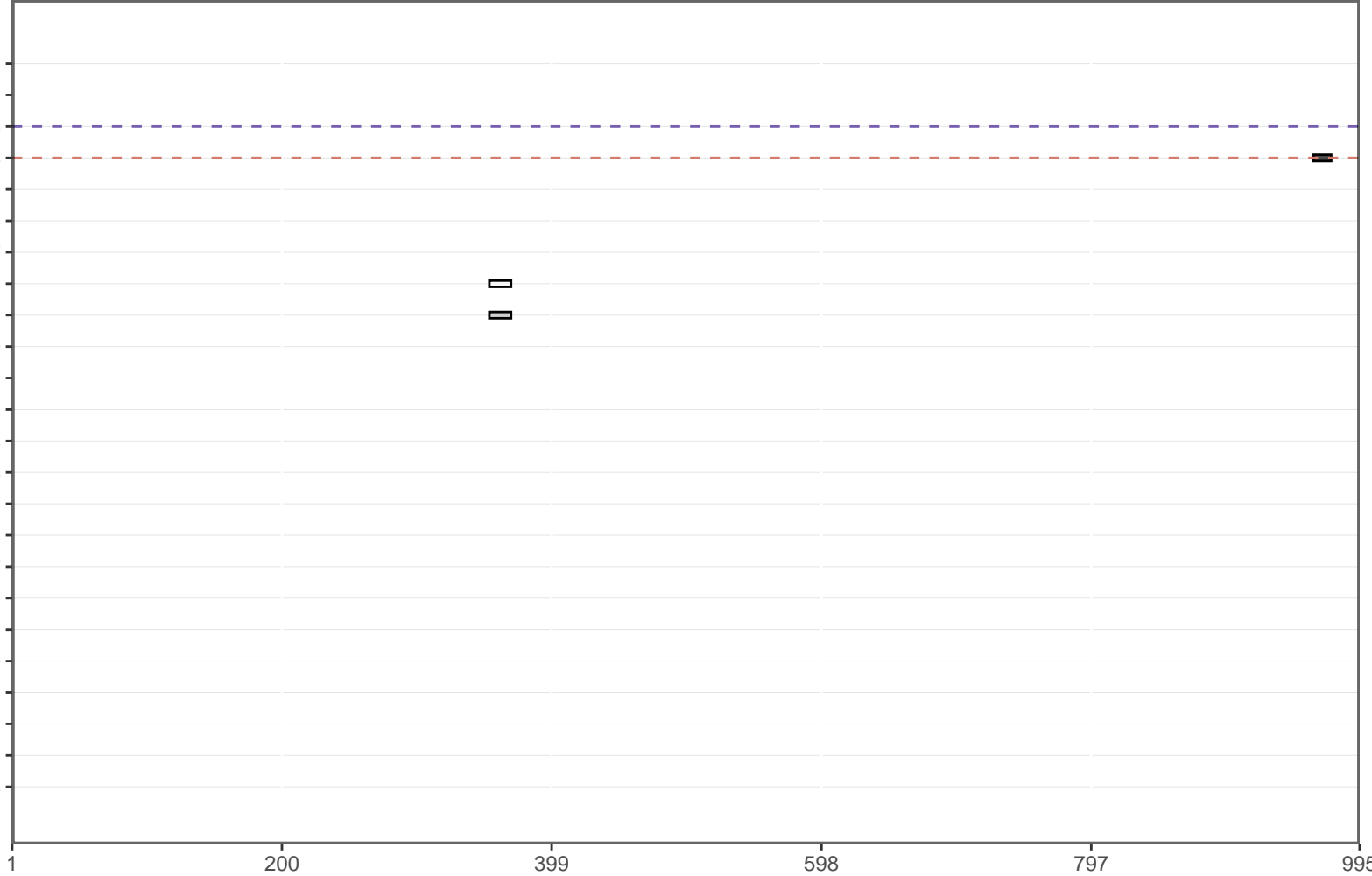
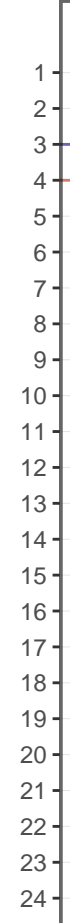
MW indication



Molecular weight



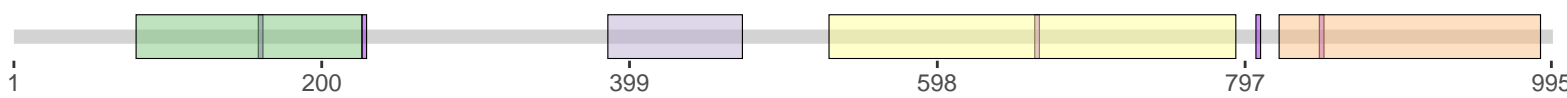
Gel Slice



Protein length

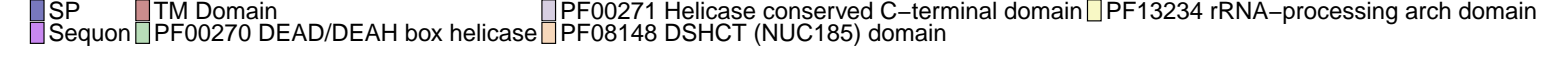


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEQMEIDNLKDMVLEGRKPLVSTFRRLGYSYFTLNLMRSREGGFTAEHVKNKNSFHFQYVEKALPDGKXKVKLEEEEAATLDA5GAEVAGYHKLKEIAGFEKLMMAEITRPERVYVFLPCRLVVKVREGGKDWGWDGYYVYVKKPPALGSLPALGASRGTGYVDTLLHGLGSSSENGSRPKPCPPRPDGEKAEHVVVPLPLISLSKLRISVPSDLRPLEARGSILLVLELEKRFPEGLPKLNPVKMDGIEDPEVYDMNWHHELEKLFSLPHKSGNEHQLKCFORKAE

NbL11g06740.1 probable_uridine_nucleosidase_2 [MW = 34.29 kDa]

No. of times detected



log(intensity)



Values from



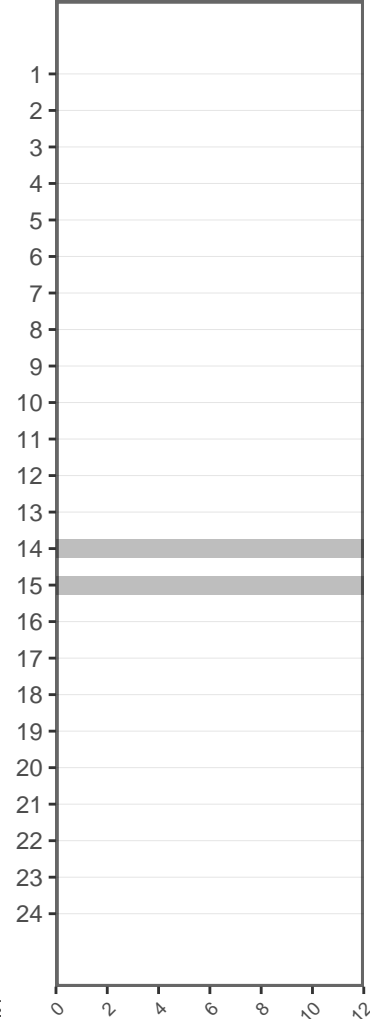
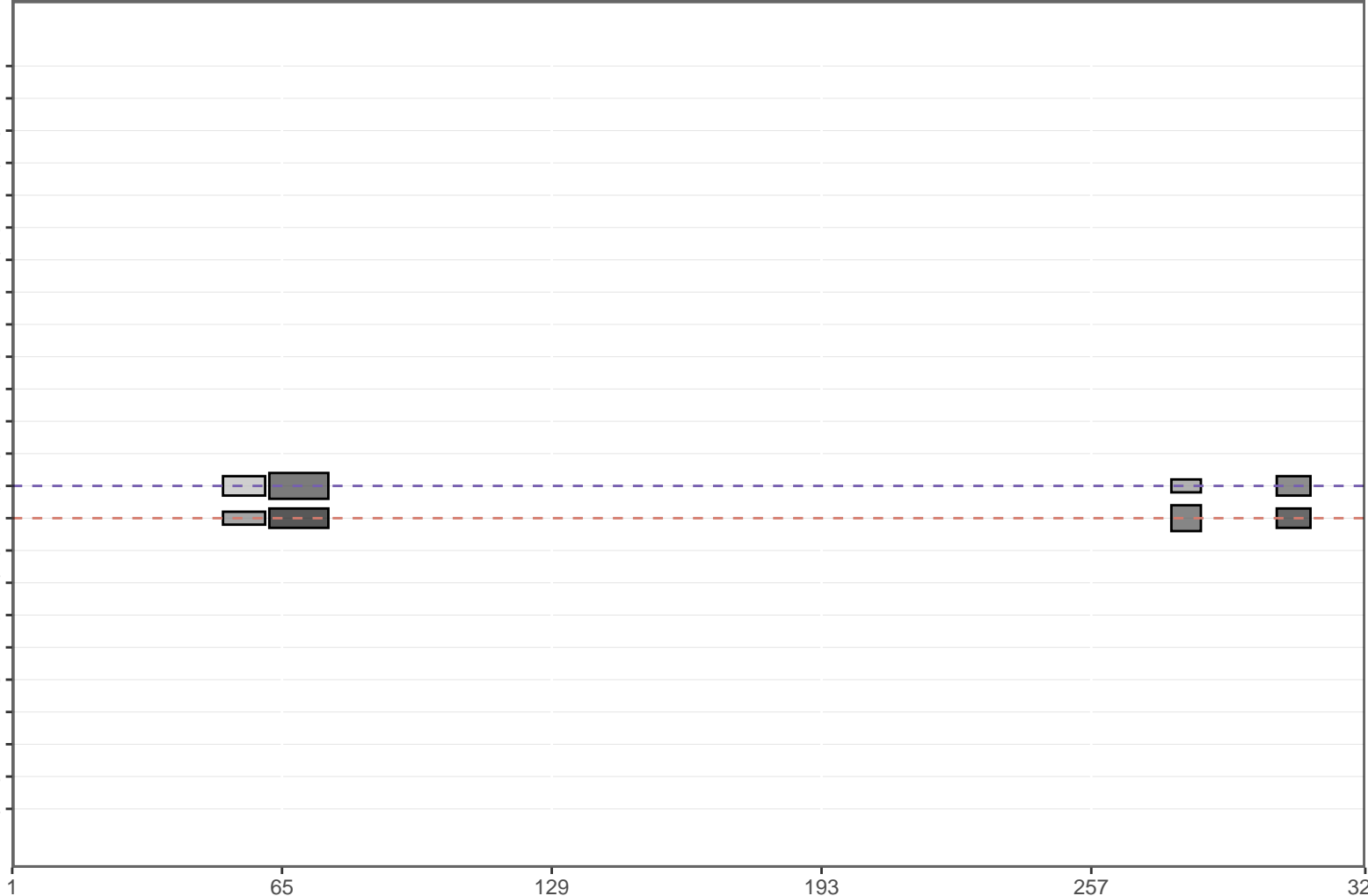
MW indication



Molecular weight



Gel Slice



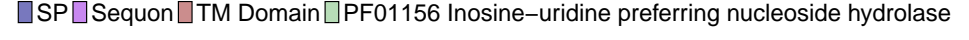
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

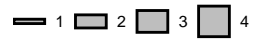


Protein sequence:

IQIVLVGGSFAVNGVNFMAEAFNFGDPAADIVFTSGADVLAVGIVVTHQVLTDSDRNELAKNGKFAKYLKILGVYFDYHHQAYSTKGVYVYLDPTALLAAVDPLFTYEGAVRVTGTRGLTFLYNNKQKRFGEVTEWGDKPKSVKVAWTVDAKPKLKLMLERLINS*

NbL11g06640.1 valine--tRNA_ligase_mitochondrial [MW = 109.55 kDa]

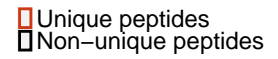
No. of times detected



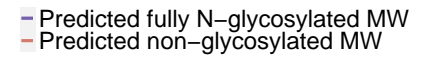
log(intensity)



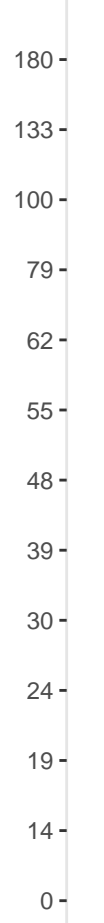
Values from



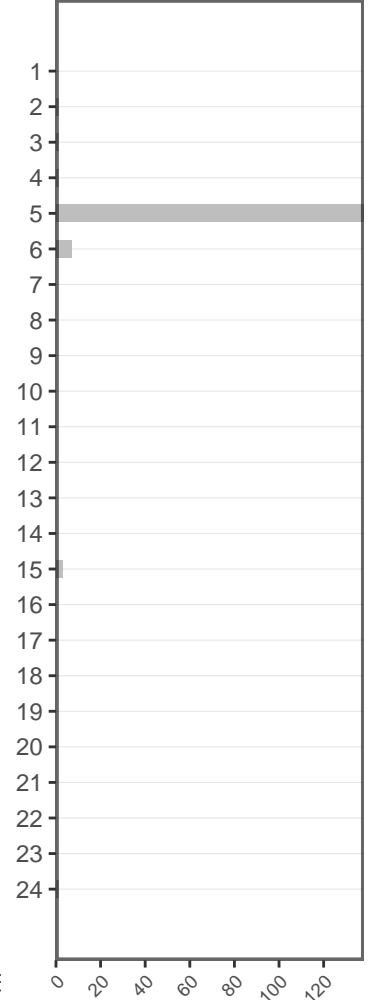
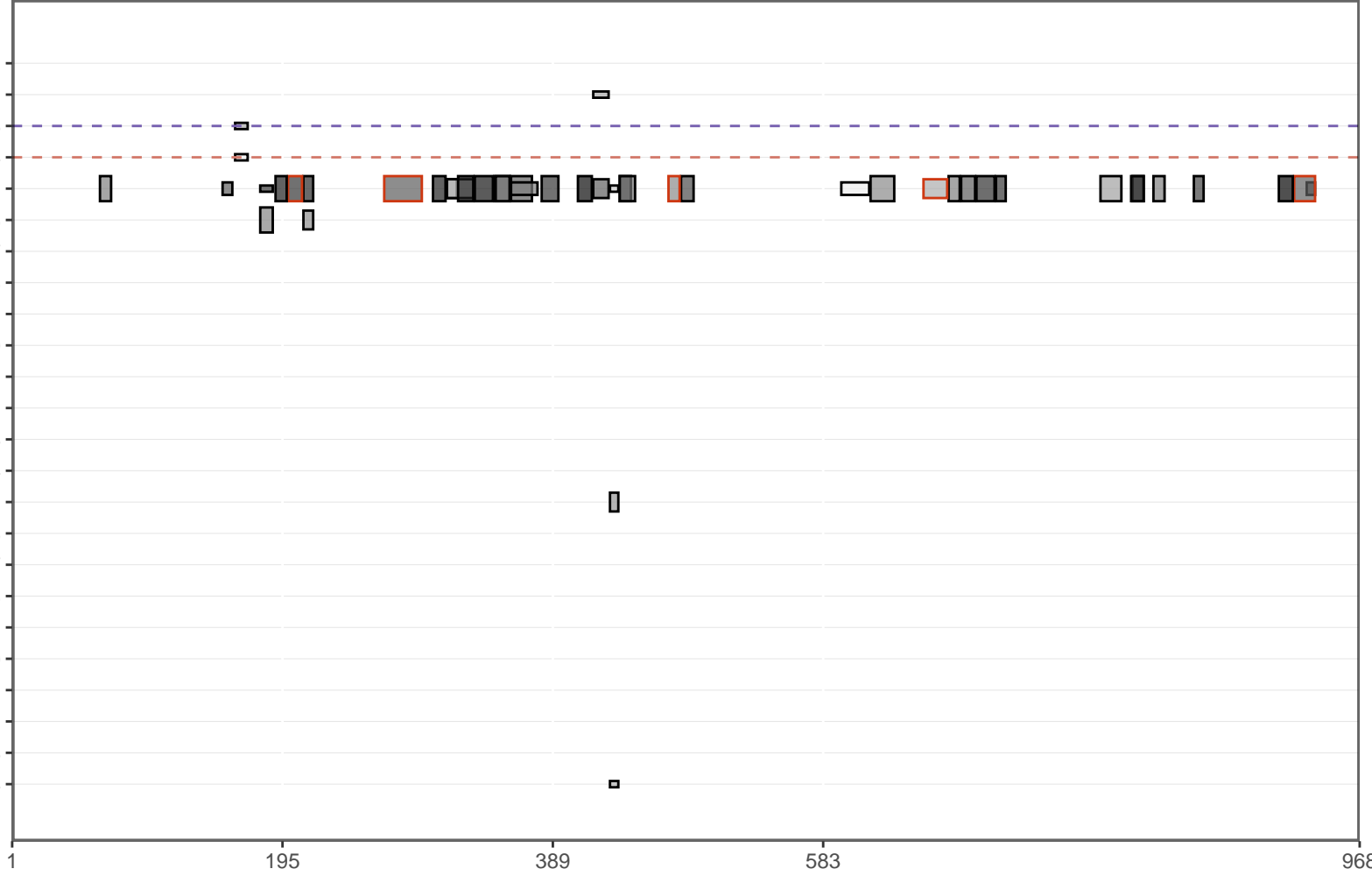
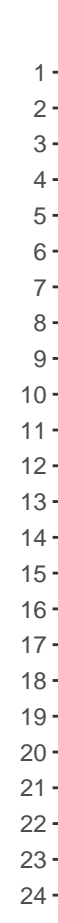
MW indication



Molecular weight

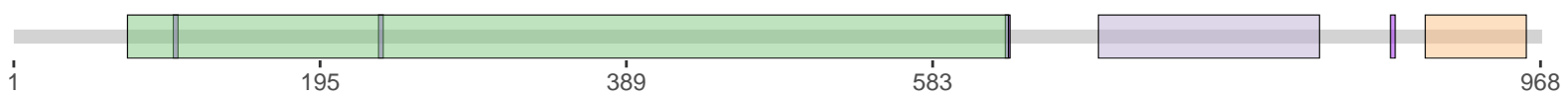


Gel Slice



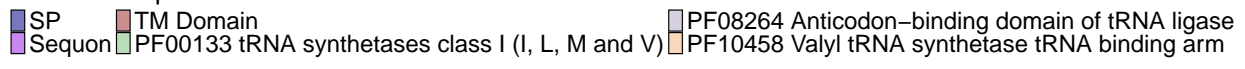
Protein length

Peptide counts over 4 repeats



Pfam domains

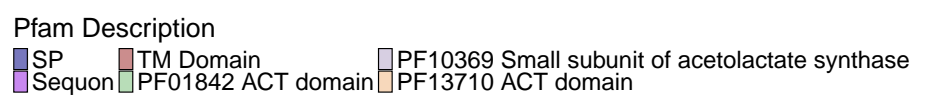
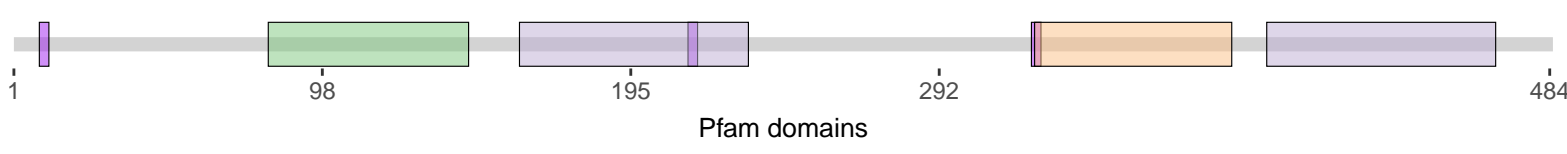
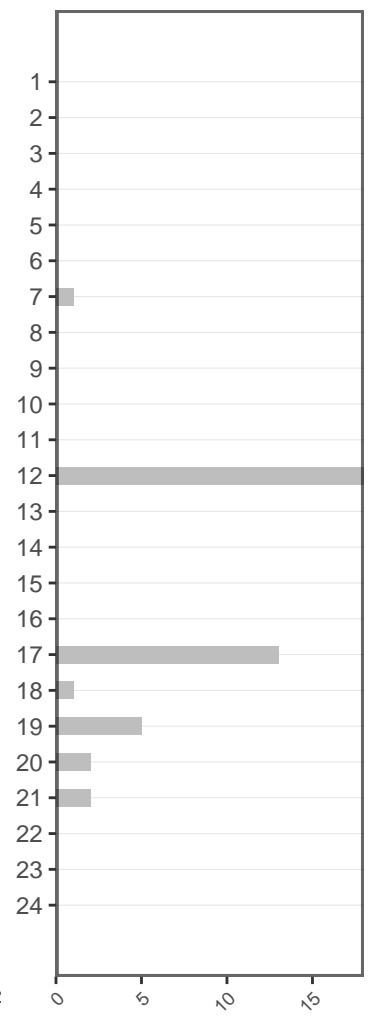
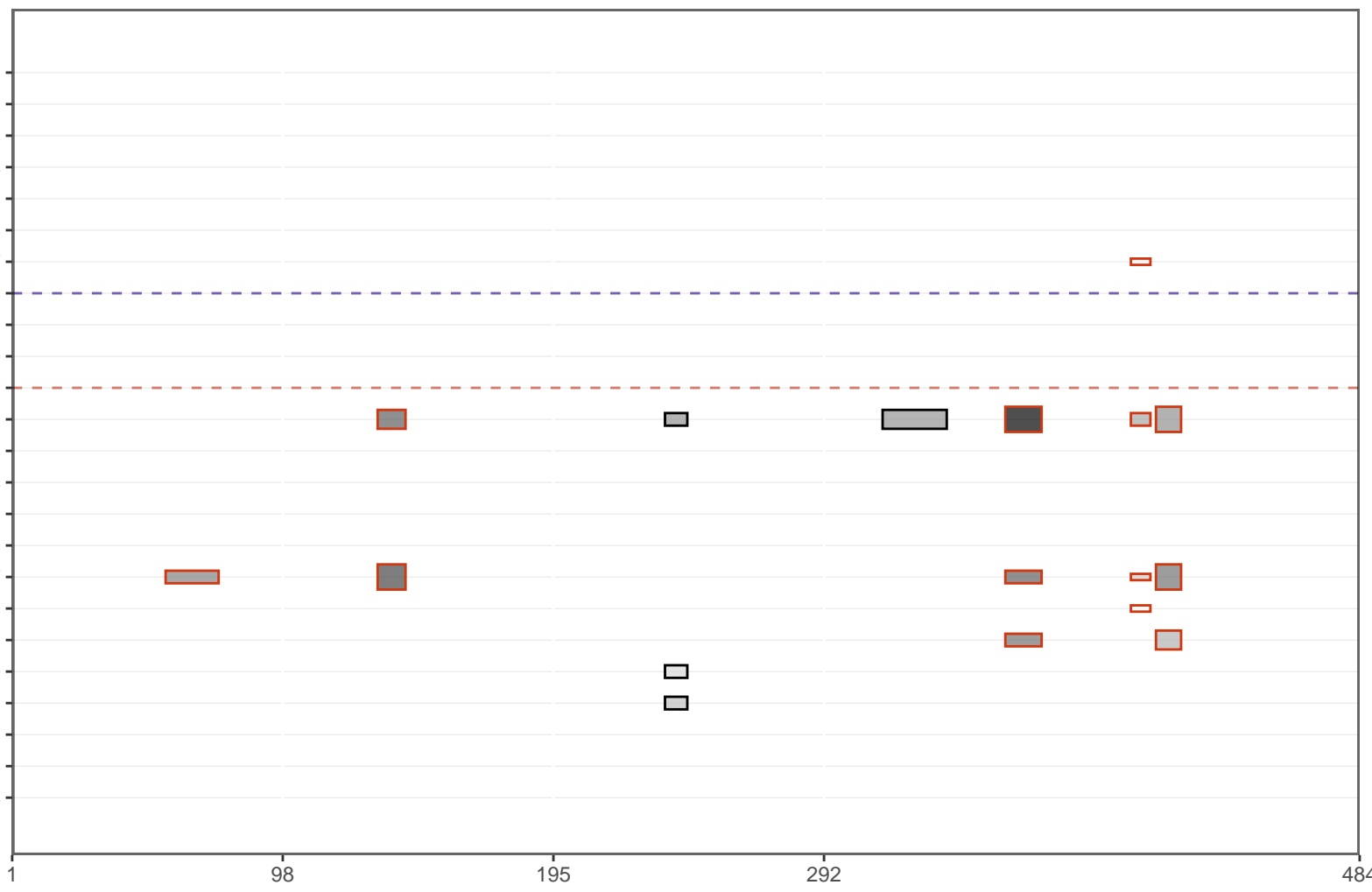
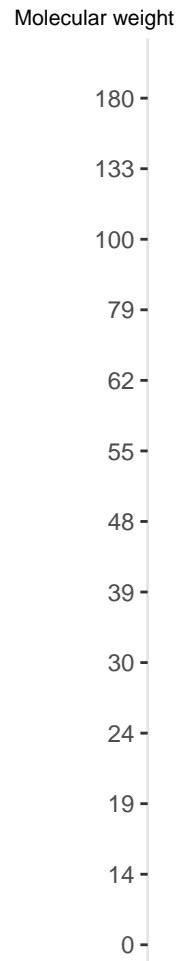
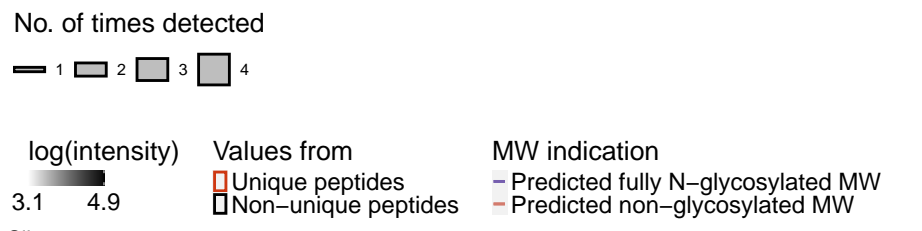
Pfam Description



Protein sequence:

SHRIPVYVYSGKDEEEVYARSHREALSKAGEKYGNKVEYGDQDVLDTWFSSSLWPFSTLWGPDESIEDFKRFVPTSVLETGHDLFFWARMVMGIEFTGTVPFSNVYHGLIRDGGGRKMKLTKGNVDPLDTAEYGTDLRFTLALGTAGGDLNLSMERLISKAFTNKLVNAGKFLRNLPHGGDTLAWAEALLAHKFDKVEGVKPLPEGVWVSKLHLVDEVTASVEKELFFGQVGREIVDFFWADFADWYEVSKARLYHSGDHSVAGVSAALLYFGSLKI

NbL11g06550.1 acetolactate_synthase_small_subunit_1_chloroplastic-like [MW = 53.34 kDa]



Protein sequence:
 REKMGESAPFYWRFSAAAYPDLGAMASGILRTIRNPNNGESMSMAEGGVYFETDDNNGVSGVLDAMHWGLNDEDTGRLRHSLMLVNDTPGLVNVITGVFARRGYNQSLAVGHAEVEGLERITTVPGTDESIVSKLVGQLYKLVVDHEVRDITHLPAERELMLKIAVNAARRNVLDSIFRAKAVDVSHTFTLELTGDLHKMVALGRLLPEYKICEVARTGRLALVRESGVDSKYLRYGVPL

NbL11g06520.1 2-alkenal_reductase_(NADP(+)-dependent) [MW = 38.07 kDa]

No. of times detected



log(intensity)



Values from



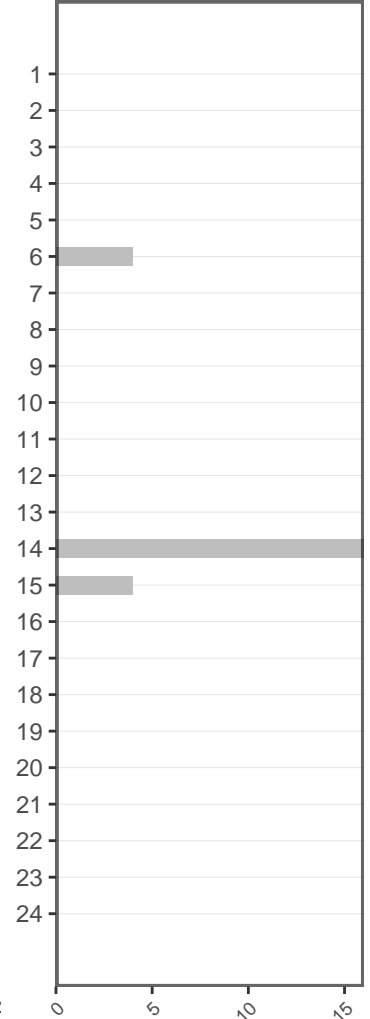
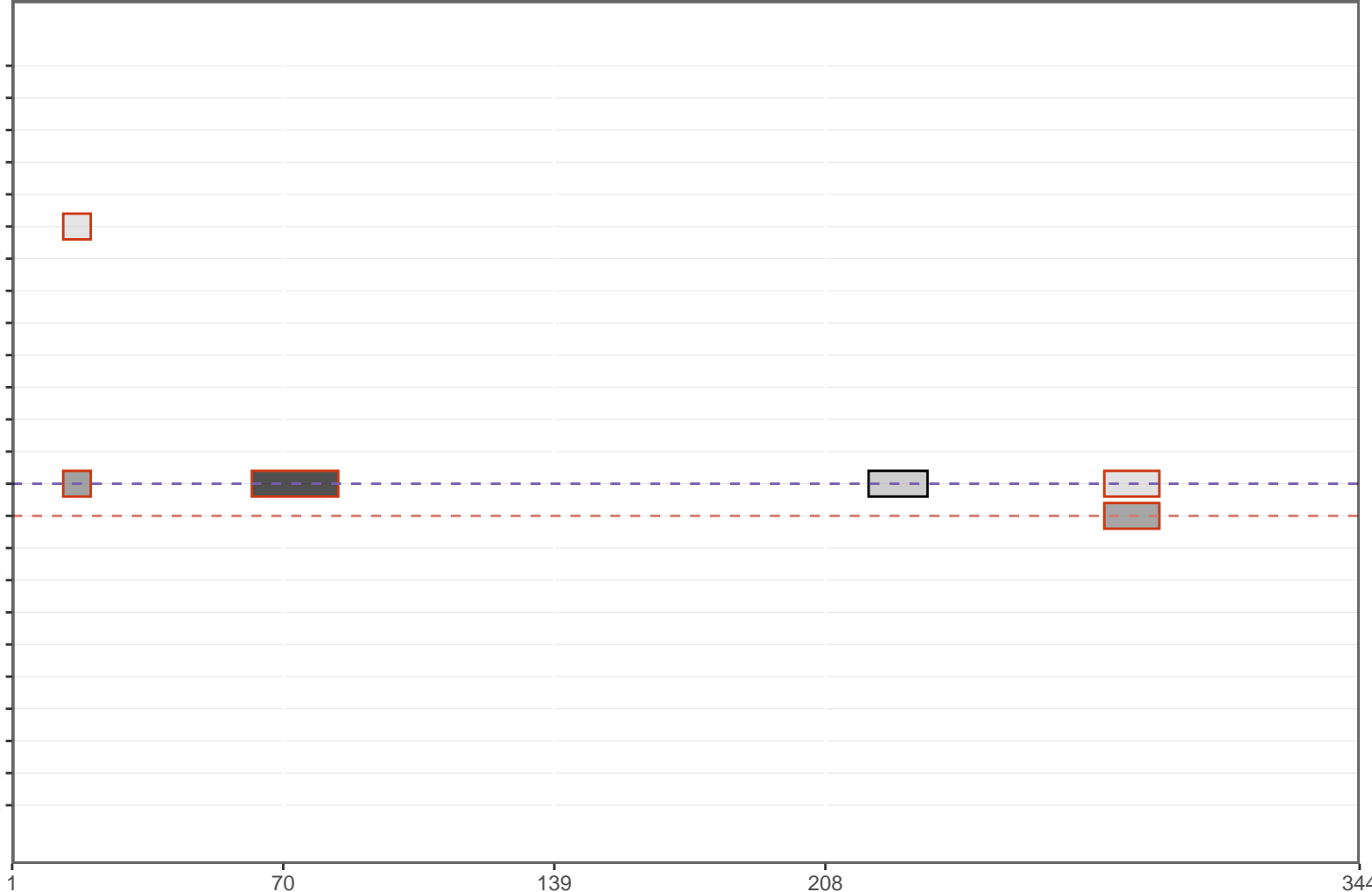
MW indication



Molecular weight

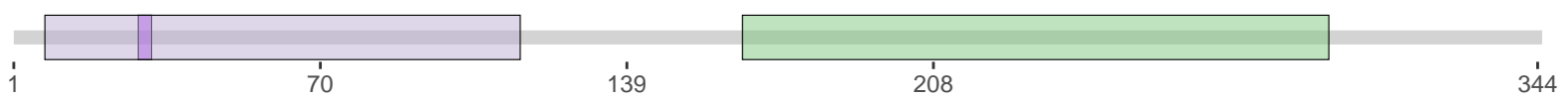


Gel Slice



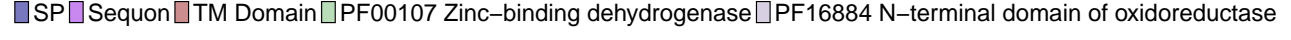
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

YSAASGAVGQLVGGFAMMLGDYYVSGAGSKEKVDLTKTFDFEAFNKEEGDLNAALKRYFDGIDYFENVSGKMLDAVLLNMLHGRIAVGGMISQVNYLEGTGVVNLFGLTRIRRMSEGLVDFDYHLYEKYLEMVPQIKAGKVVVYEDVVDGLEAPALVGLFSGRINSGKVVVYVREI

NbL11g06330.1 U5_small_nuclear_ribonucleoprotein_40_kDa_protein [MW = 41.32 kDa]

No. of times detected



log(intensity)



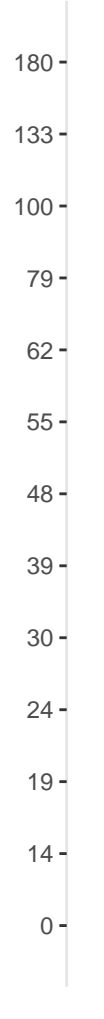
Values from



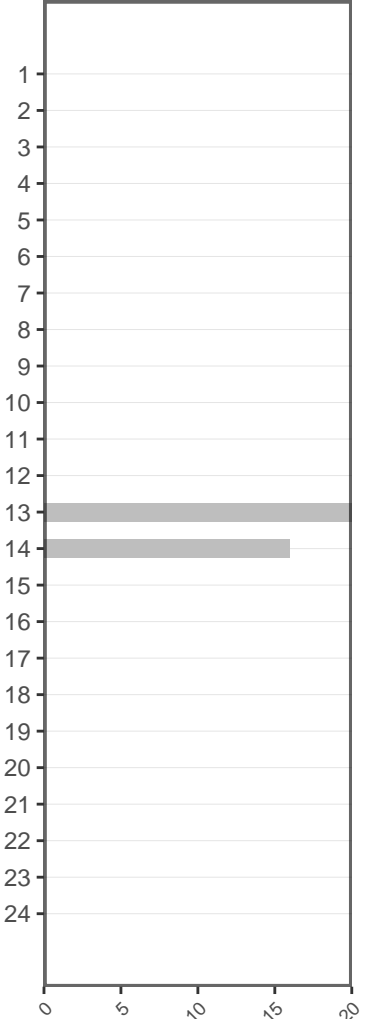
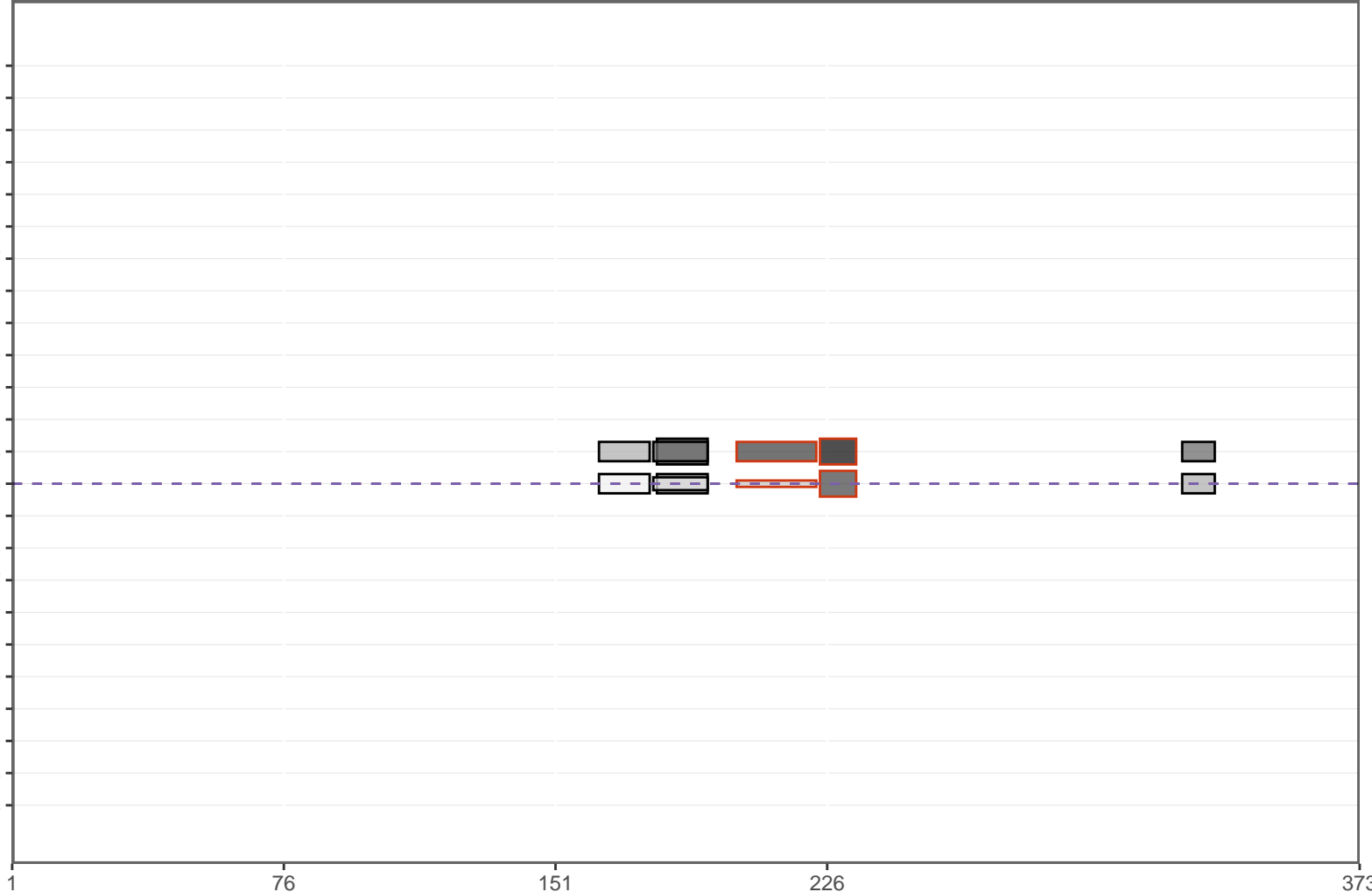
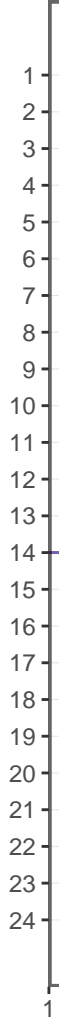
MW indication



Molecular weight

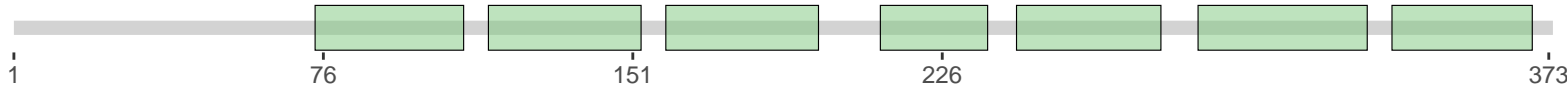


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DSARRGPLYVSGSDGTAKLWDMRGRGAGTFFPKFGITAVSFSDASDKYSGGIDNDKVVWDLRRCEVMTLGGHGDITFGMLSPDGSVLLTNAMDCTLRWDMRPVAPQNRGVKLEGHGHNFENLLKGSWSPDGSKVTAGSSDRMAYVWDTTSRRILYKLPQHTGSVNECVFHPNEPVGSGCSGDKQIYGEI

NbL11g06190.1 VHS_domain-containing_protein_At3g16270 [MW = 76.05 kDa]

No. of times detected



log(intensity)



Values from

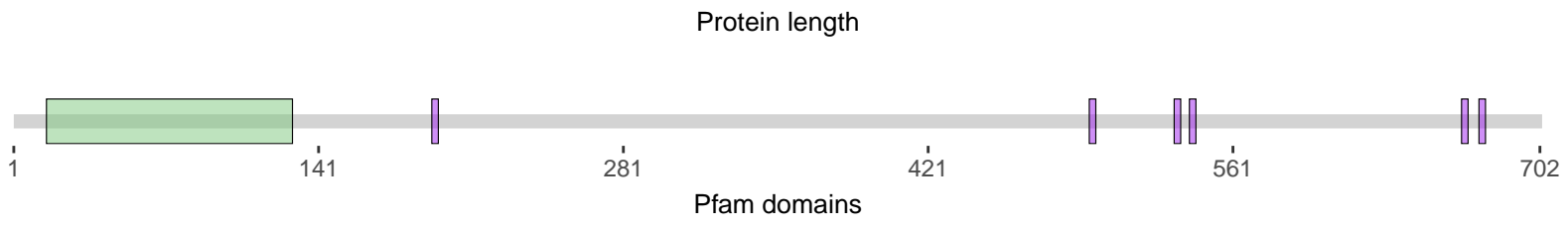
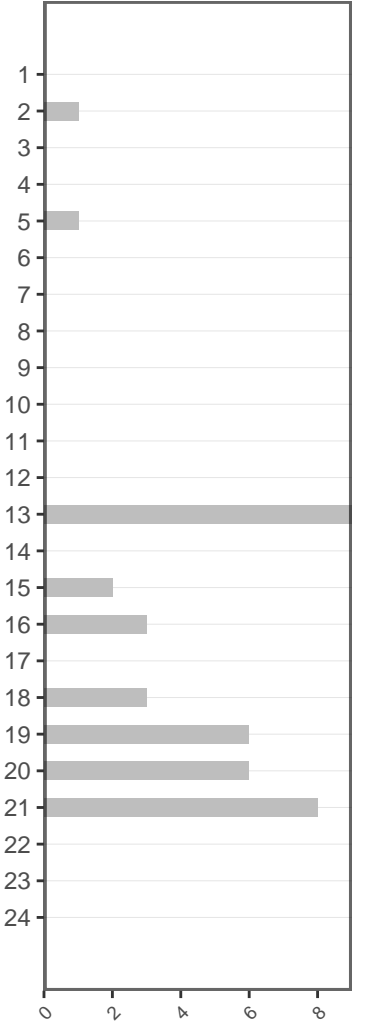
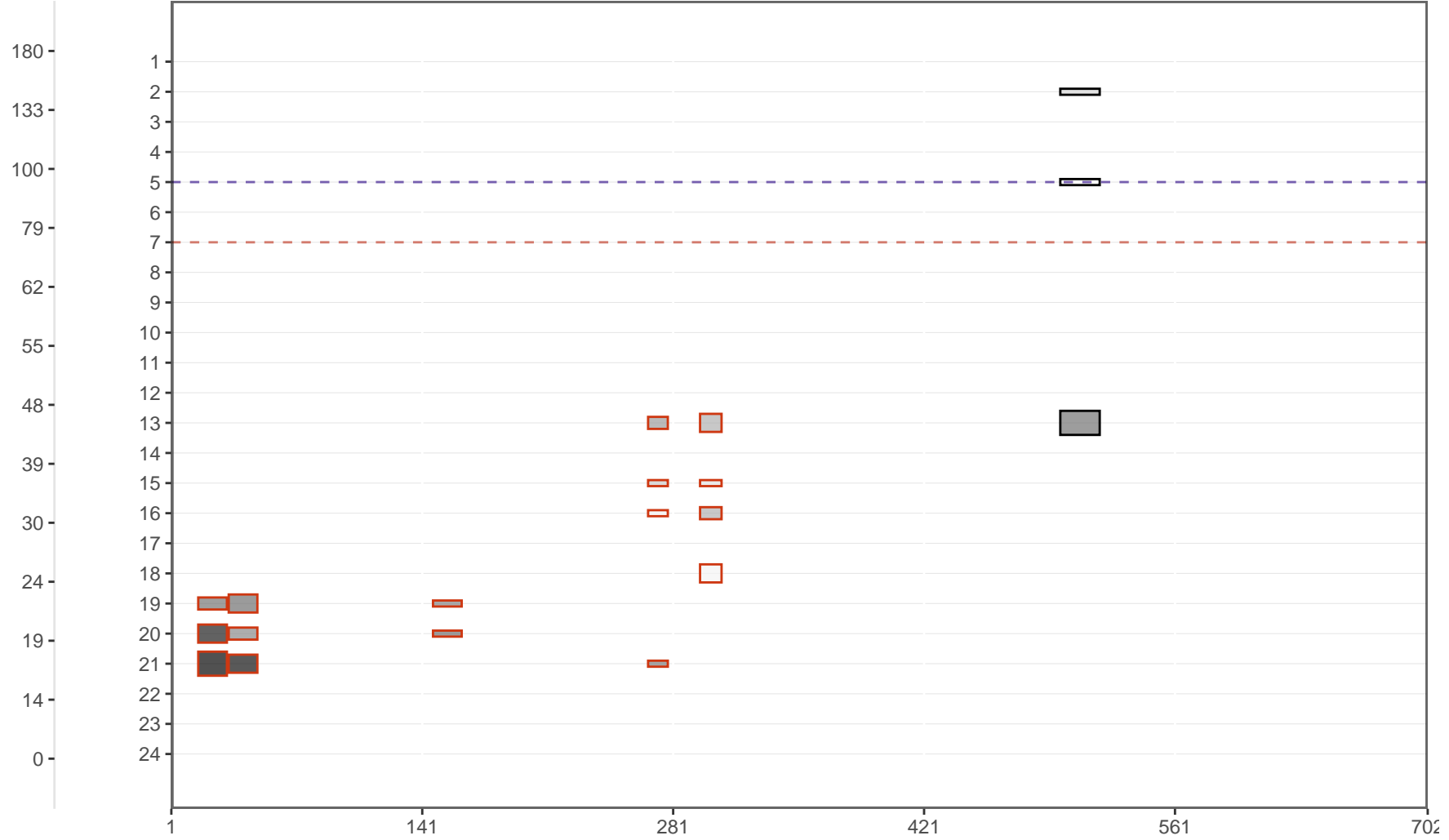


MW indication

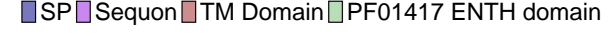


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

YFNEKDVVYKCSFQASLRKANKVLSLINDGGTADVSHVDRSARASTPWGMFDLDTGNSDDLFGADLLANMGGEGINASTSAAPLVLDLFGDNLGGVTSGGQKNDQDFADVFHFTSNEKALEADLFGGMFDKSDAAEVHSAVNRRTGPELFDIFGSPVEVTPQEPNPRKEHDLMNSFSLNDGDSKKGKNGSSRGTYGDMCGESTIDPHHGASNDALNSIFSSQAGGVNSNMFPLGAMQVNLPPGFVLPSPFAPQALNHNAMGNMFAOQQLFATLS

NbL11g05910.1 probable_pectinesterase/pectinesterase_inhibitor_34 [MW = 66.29 kDa]

No. of times detected



log(intensity)



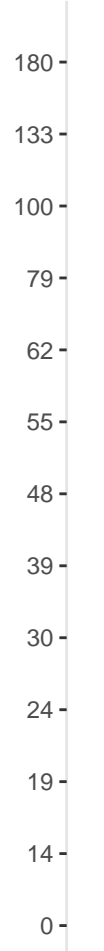
Values from



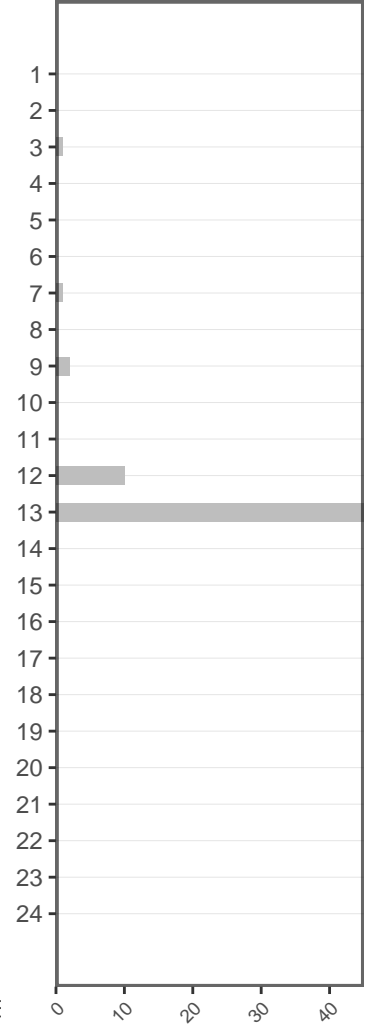
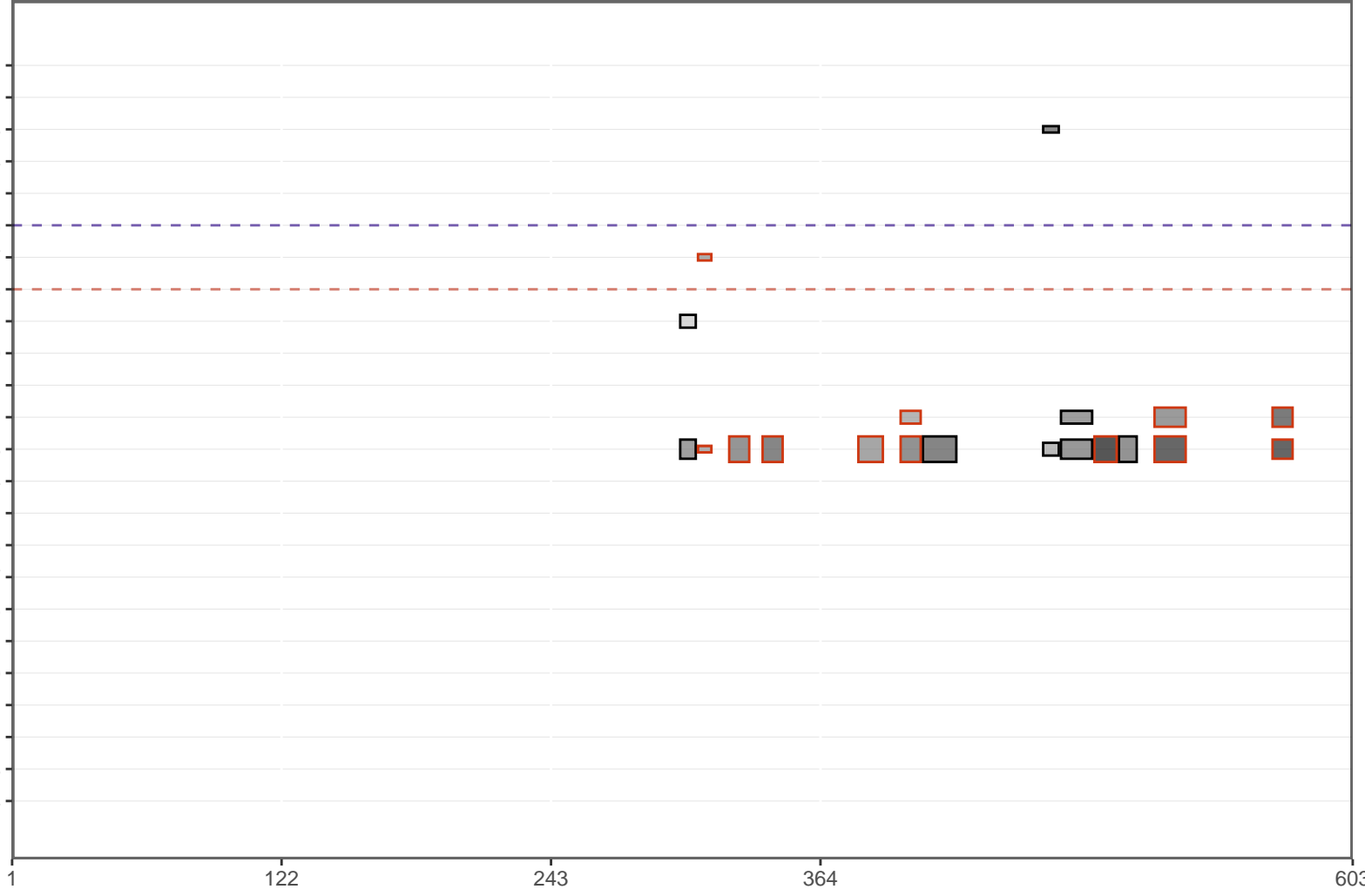
MW indication



Molecular weight

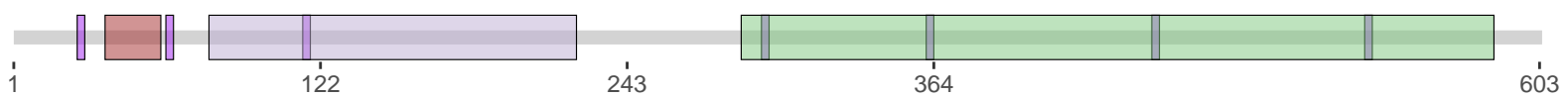


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DIVSKDNGTFRKTAEAANKVPGYENRRIWYKTRGYEEDNLKIGRKKENVMFIDGDKGKTVTGGKSVGNLTFHTASFAATGAGFVIRDTIFENYAGPKHQAWALRVGADHAAVYRGNIGYDGLVYVHSGRQFVREGAAYGVDFDFGNAAVLVGNDSYARKPMDFQKNTITAGNRKDPNGTGISHAGKIAATSDLEASKGSEFTYVLRPWLYRRTVAVLSNLGDHHPRGWLEWNAFALETLYVGEYMNYPGAAVGRVTVWPGYRIVTSVEEASKFTVAQDFC

NbL11g05840.1 binding_partner_of_ACD11_1-like [MW = 31.3 kDa]

No. of times detected



log(intensity)



Values from



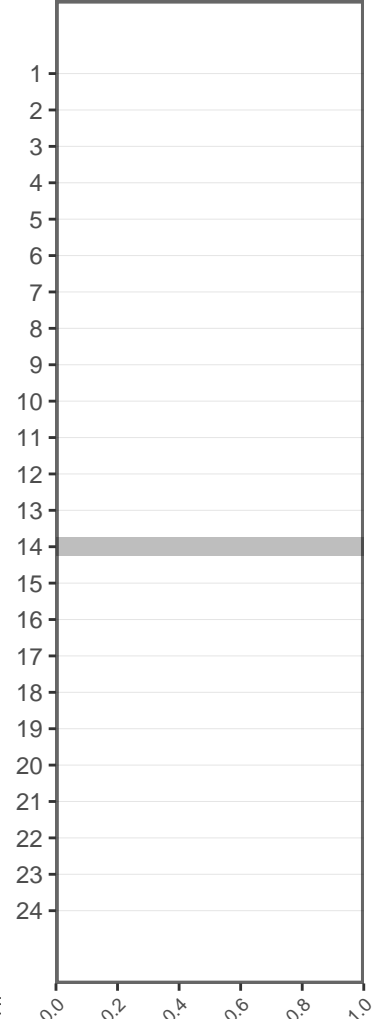
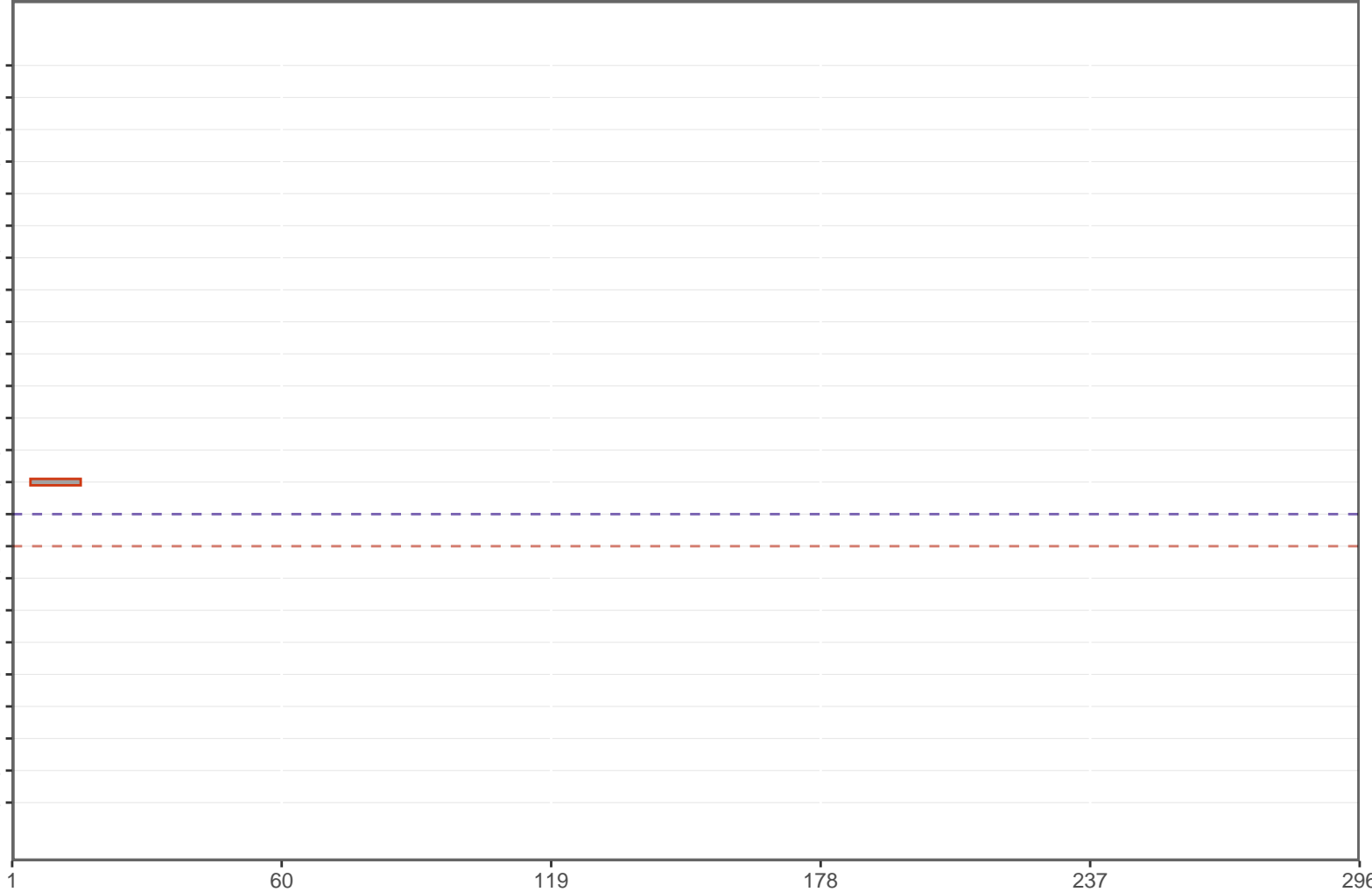
MW indication



Molecular weight



Gel Slice



Protein length

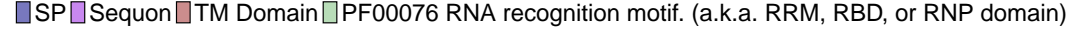


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KHKITSTTSARVLSLDGKYGLSEKIFFGATVNHVKEMDDQKQVSEKSKSAFAAAEQTVENAGSAAIKRNVYALTVGVTWAAGAFSRVTKAAGEVGGKTKELKLAEEEEKGRNSAKGHVQEHMETGTGKKEPTIESGOTGKEPANDSLGIGELTASSLPPKA

NbL11g05770.1 60S_ribosomal_protein_L13-1 [MW = 23.66 kDa]

No. of times detected



log(intensity)



Values from



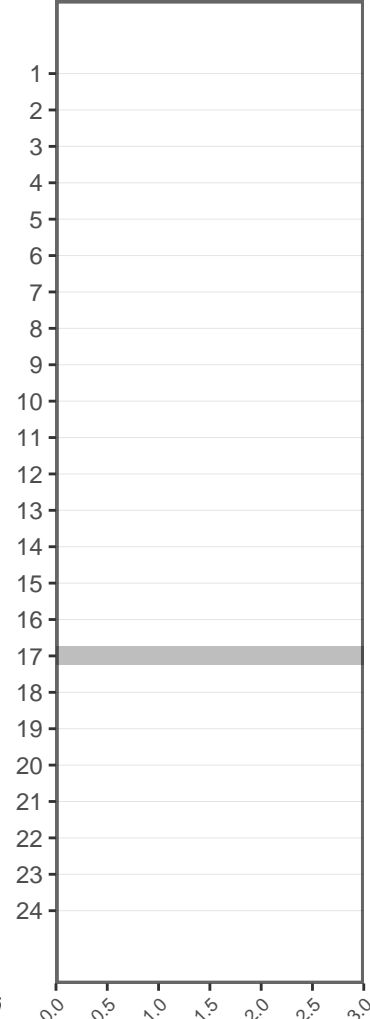
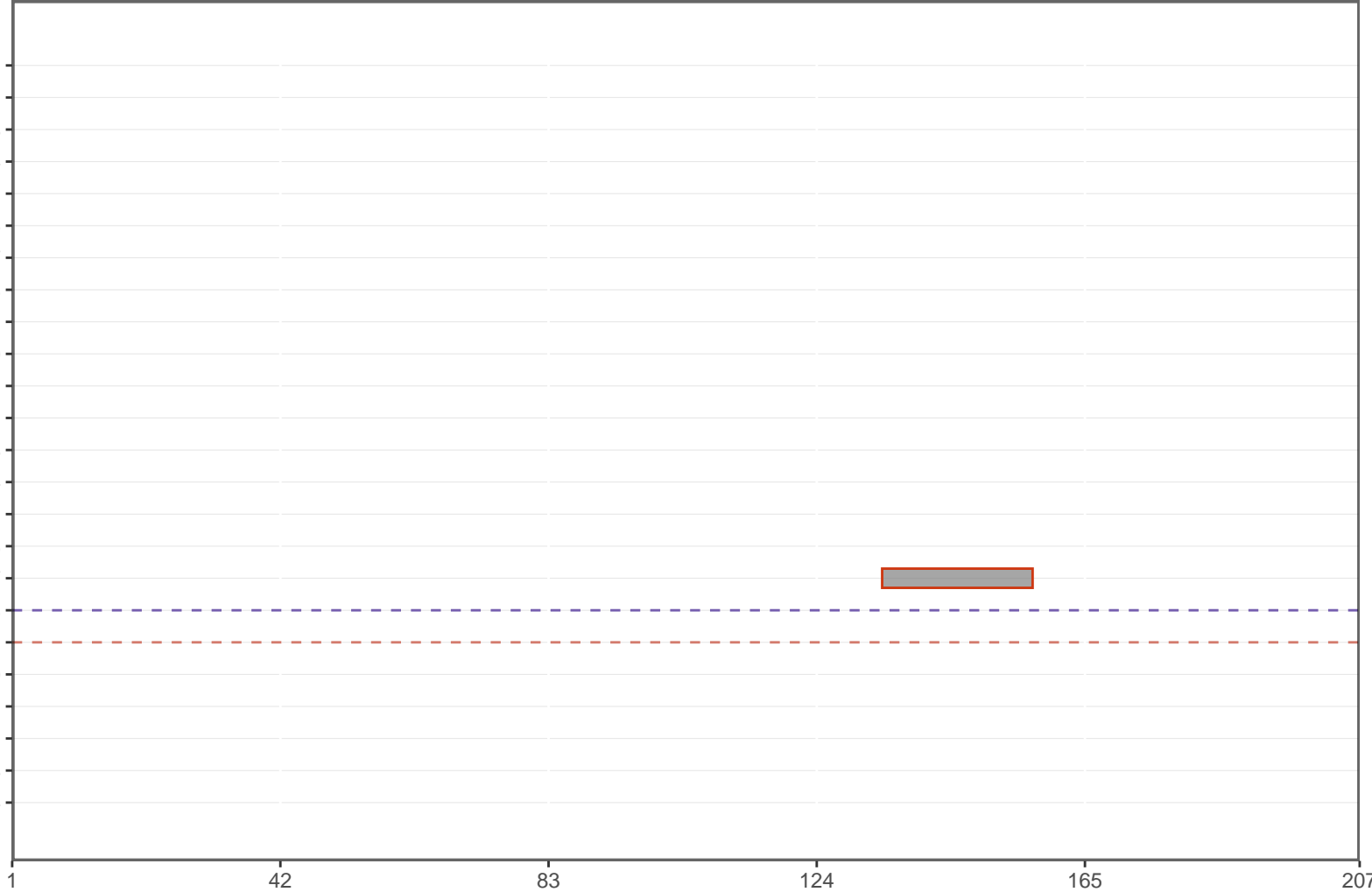
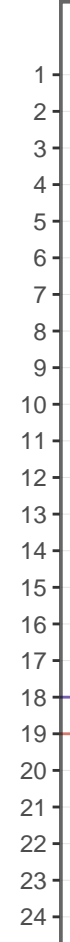
MW indication



Molecular weight

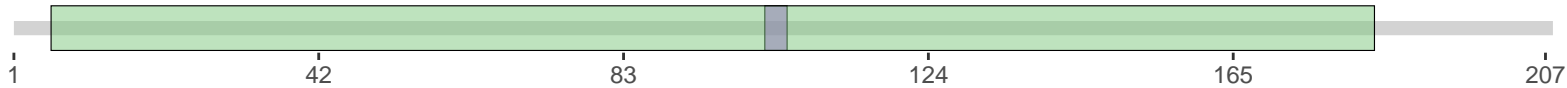


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

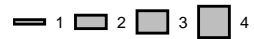


Protein sequence:

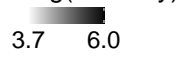
TIGIADHRRRNRSLSEGLGTNIGRLKTYKAKLVFPRRARKVKAGDSAPEELATATGVHGAYMPIAREKPEVDLWVTEEMKSFNAYGKLRVETNERHLGARMKRAAEAEKEEK

NbL11g05610.1 ribosome-binding_factor_PSRP1_chloroplastic-like [MW = 33.83 kDa]

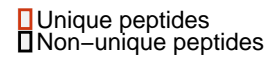
No. of times detected



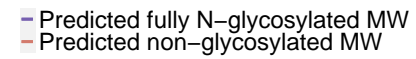
log(intensity)



Values from



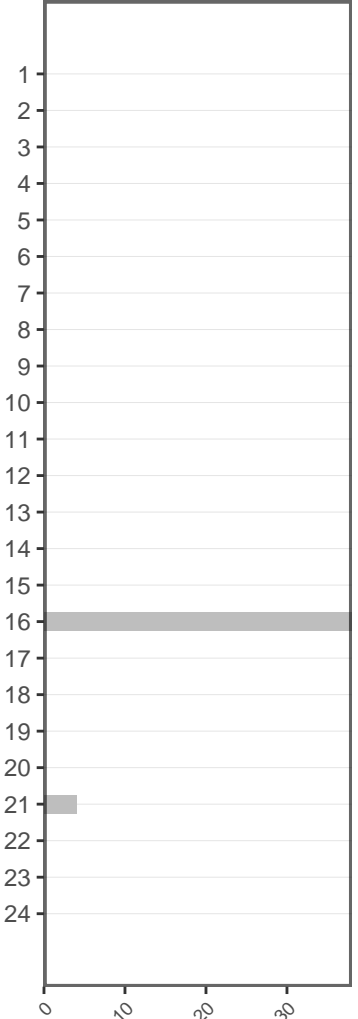
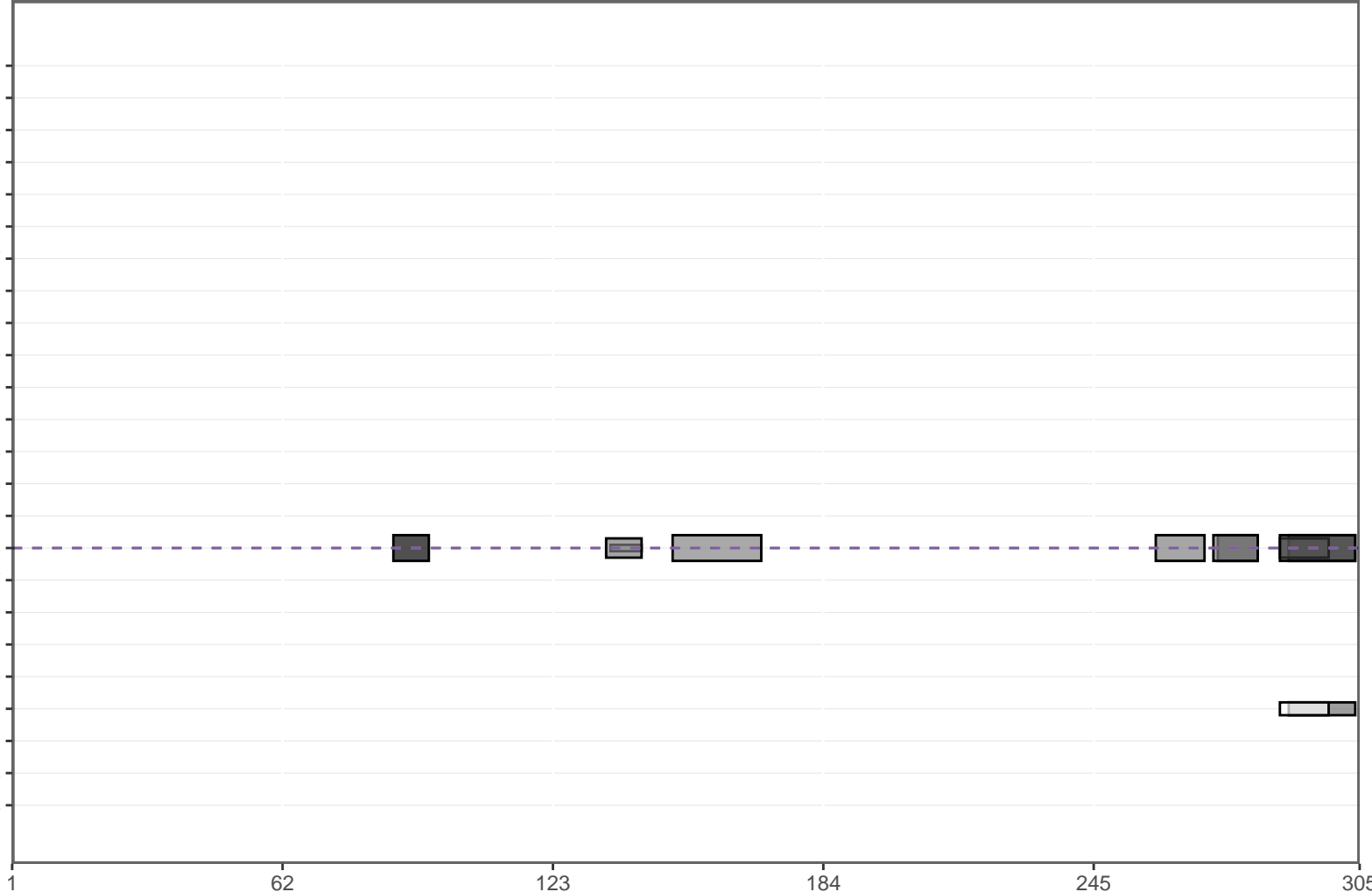
MW indication



Molecular weight



Gel Slice

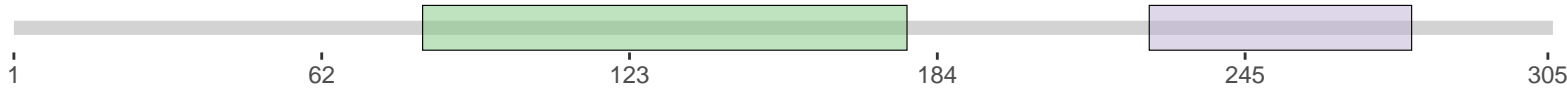


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

- SP Sequon
- TM Domain
- PF02482 Sigma 54 modulation protein / S30EA ribosomal protein
- PF16321 Sigma 54 modulation/S30EA ribosomal protein C terminus

Protein sequence:

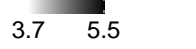
LFTXXIGVYRAEEDAEESVYGSIDMVSIGRKLRIKKEKSDHGRHMKGDFRLKVRDPELLAVQEDGLTLPQEEVEEDDESEGFVTEVREKLFDMPLPLVTEAIEQMESVHDYDFGRNNEETGEINVYRRKAGGVGLIPIKEDDKTLKLEPVEVELEKETSMAE

NbL11g05550.1 probable_6-phosphogluconolactonase_4_chloroplastic [MW = 28.58 kDa]

No. of times detected



log(intensity)



Values from



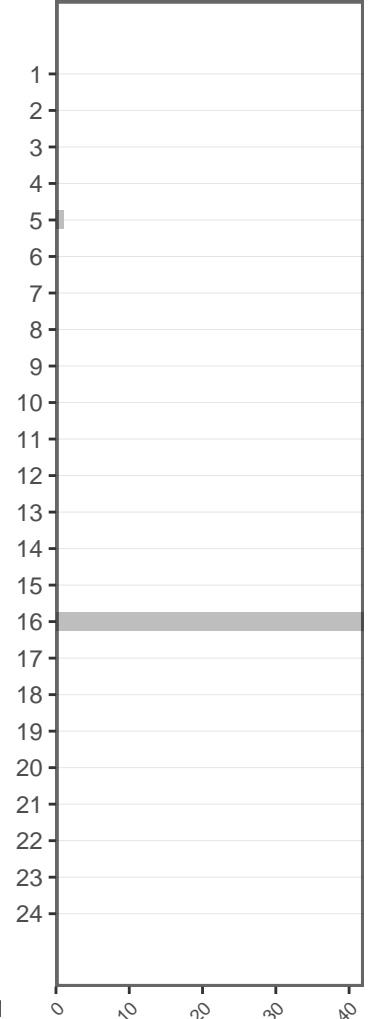
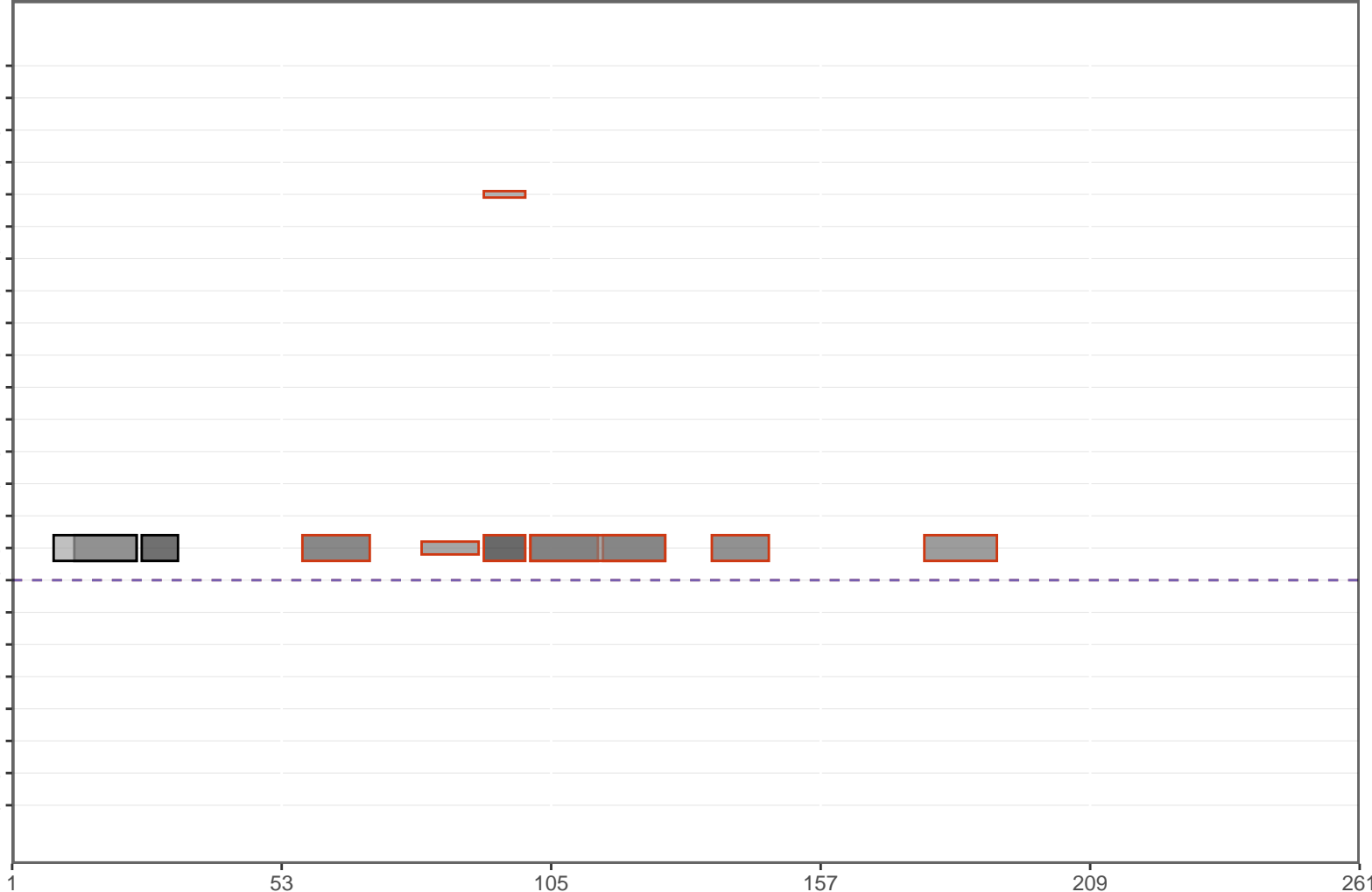
MW indication



Molecular weight

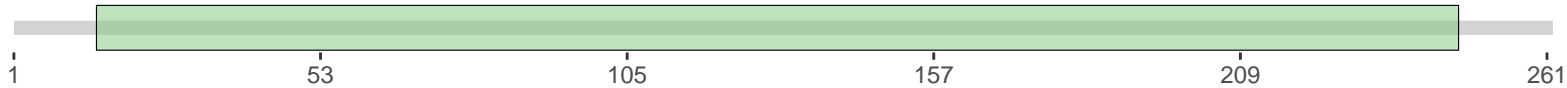


Gel Slice



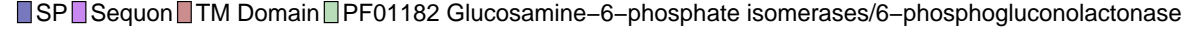
Peptide counts over 4 repeats

Protein length



Pfam domains

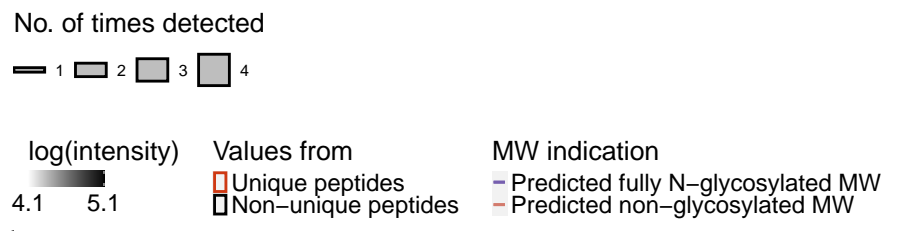
Pfam Description



Protein sequence:

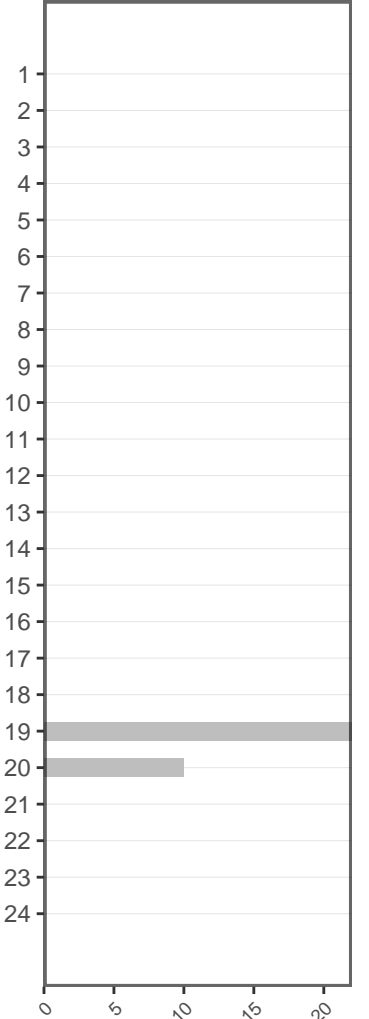
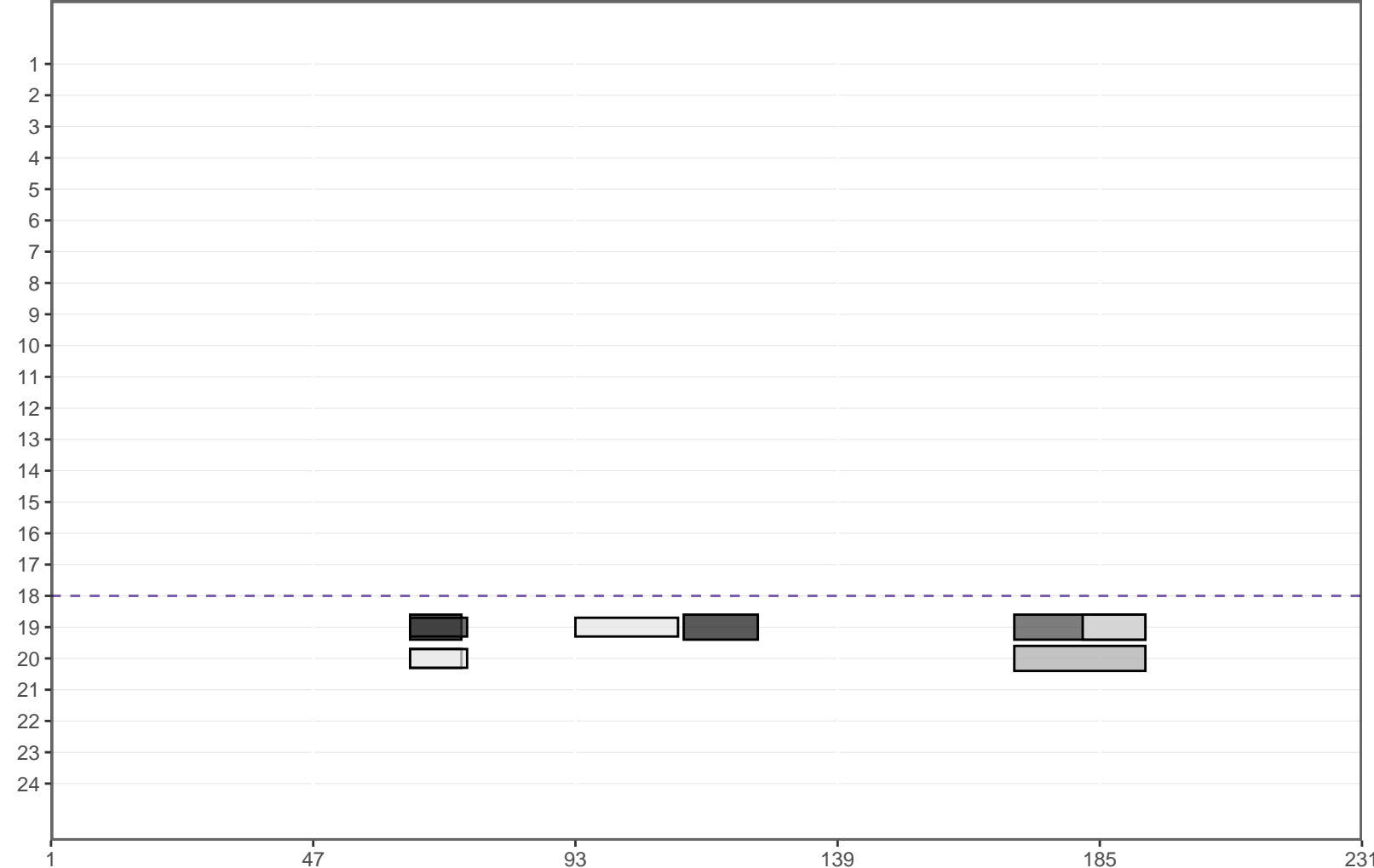
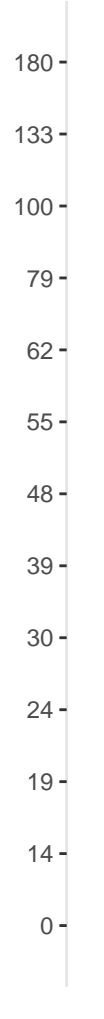
PEGAATDYEARVYKGLVEKVLPLSAVGGFPKFDMLLGMSPDGHVASLFFTRSGRHEKERLVTFITDSEKFKPPPPPIITFFPINSASEIAMVITGAELANMVDVLLGSGLTADGIPPPATEVSAEEELFWLFDKDAASKLQTSI

NbL11g05490.1 rhodanese-like_domain-containing_protein_14_chloroplastic [MW = 25.93 kDa]



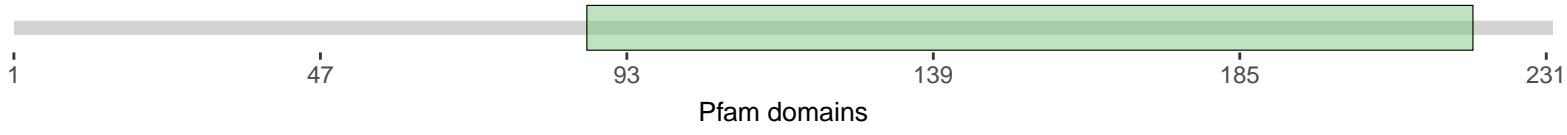
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00581 Rhodanese-like domain

Protein sequence:

LDVRFPEAFKFAHPEGANVGVYLIKETAWDQARRVAFVAFQIFSGTEENPEFQIMVESKINKDANIVAC55GDTMKPTQNLPEGGQGRSLIAAYLLILNGYTNVHLEGGILYWFKQGLPWSEE*

NbL11g05440.1 luminal-binding_protein_4 [MW - SP = 70.41 kDa]

No. of times detected



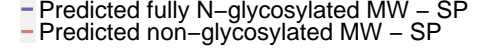
log(intensity)



Values from



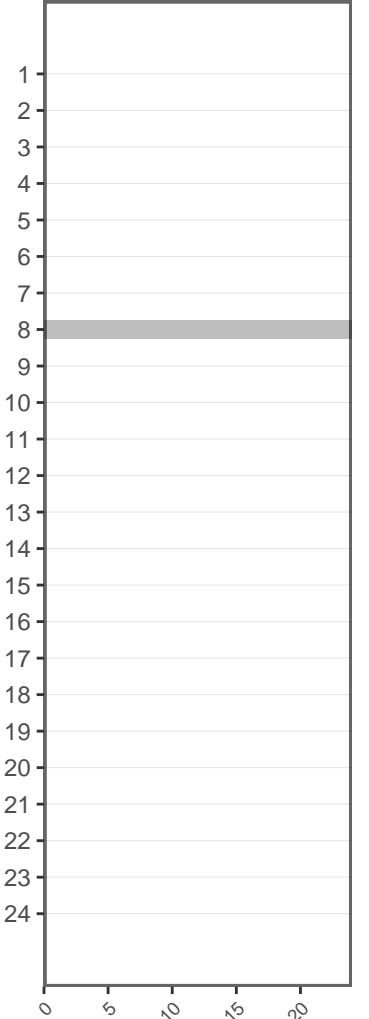
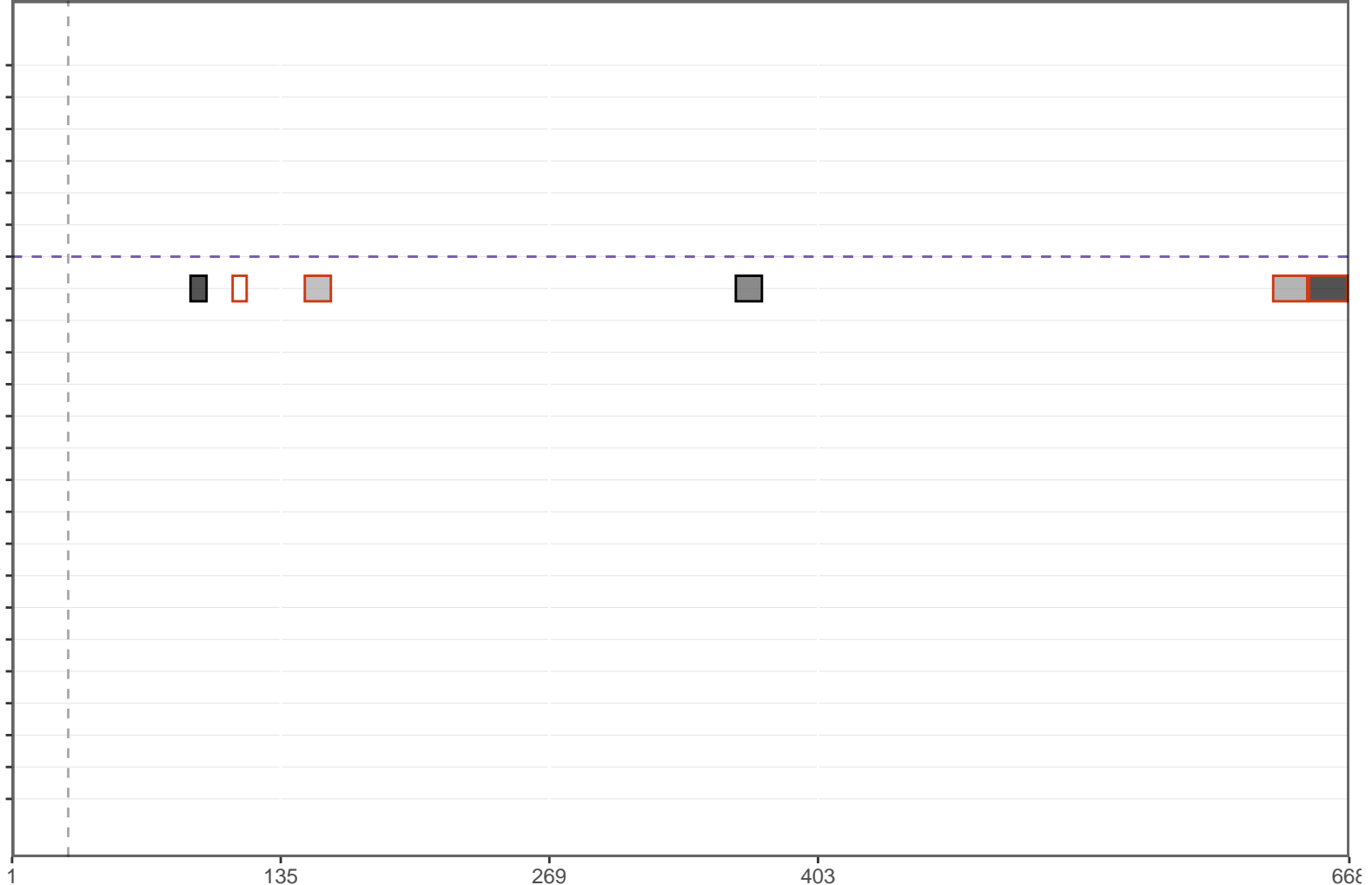
MW indication



Molecular weight



Gel Slice



Protein length

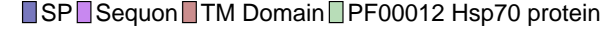


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

/D/SEPLTRARFEELNNDLFRKTKMPGKVKAMDDAGLEKTKGDEIVLVGGSTRIPKVGQLLNDYFDGKEPKNGVNPDEAVYGAAVGGGLSEGGDEKIDLLDAPLTLGIEYVGGVMTKLPKIPNTVPTKRSQVFTTYVDDGQFTVIGVFEGERSLTKDGRLLGKFDLGIAPFRGTPQIEVTFEVDANGILNVAEKDKASGKSEKITTNDKGRLSGEEIERMVKAEFEAEEDKKVKERIDARNBLETVYVMRNGINDKDKLADKLESDEKEKETATKEALEWLDGNGS

NbL11g05290.1 pyruvate_dehydrogenase_E1_component_subunit_beta-1_mitochondrial [MW = 39.53 kDa]

No. of times detected



log(intensity)



Values from



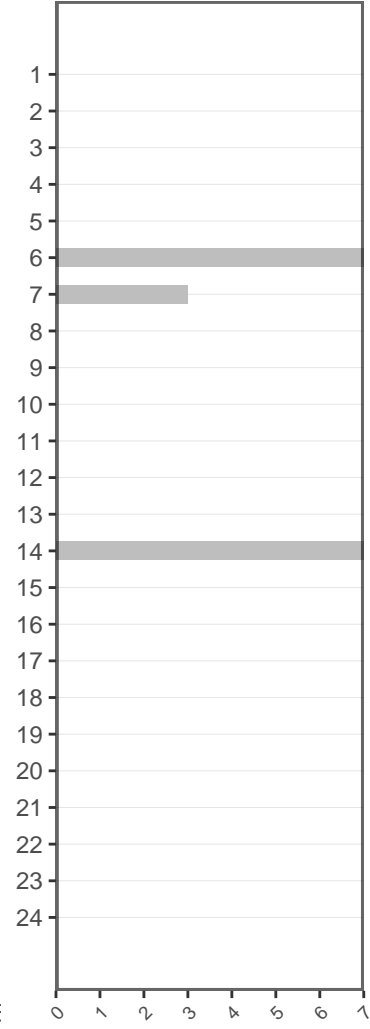
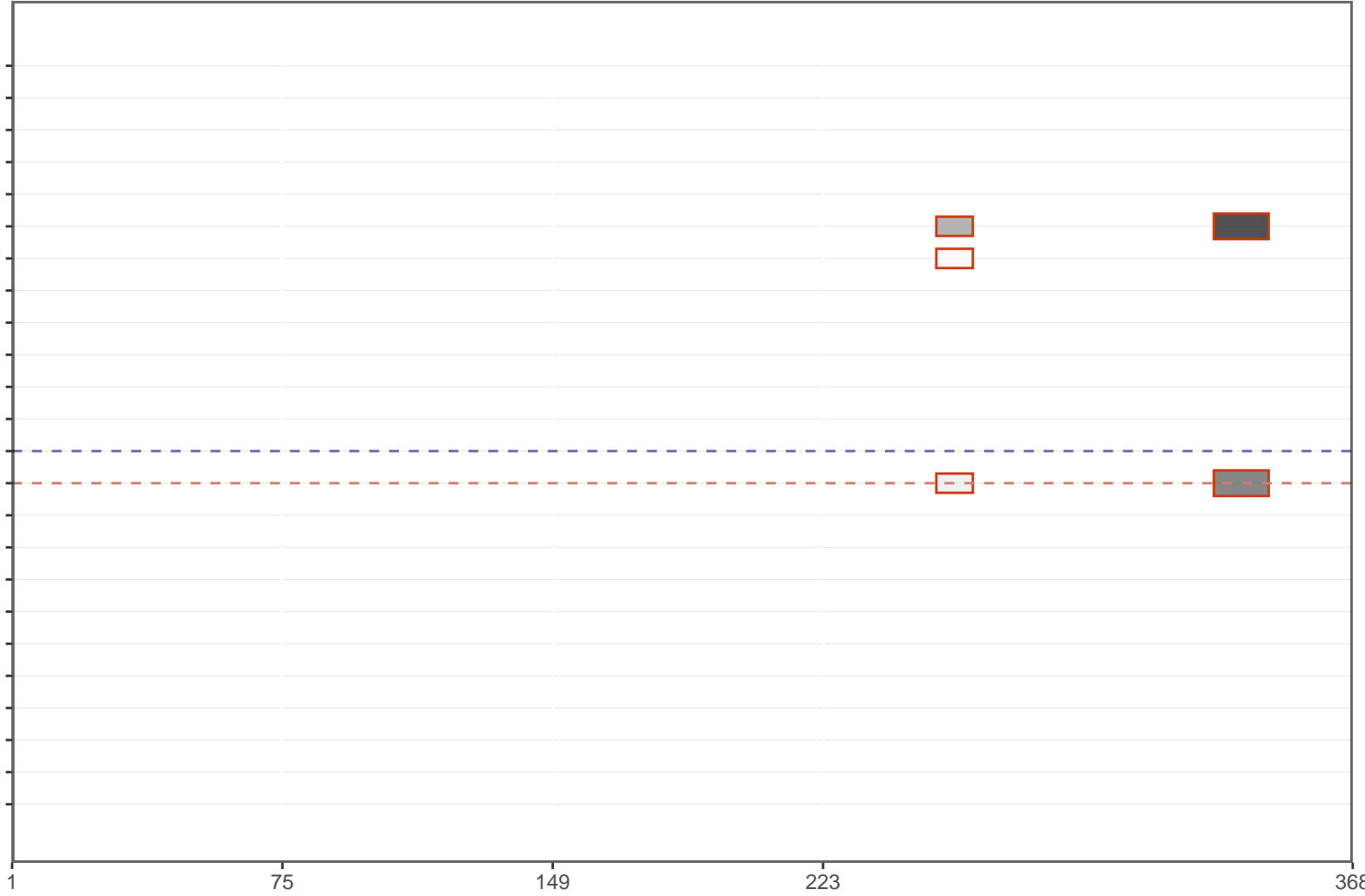
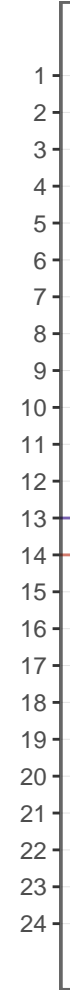
MW indication



Molecular weight



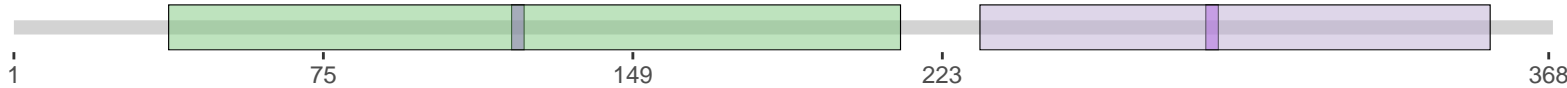
Gel Slice



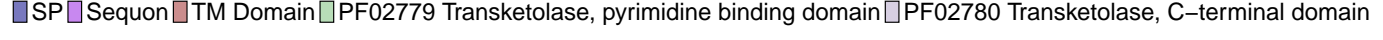
Protein length



Pfam domains



Pfam Description



Protein sequence:

AWFGSCPGLKYLAPVSSDARGLLKAIIRDPPVFLFENELLYGESFPISAEALDSSFLPIGKAKIEREGKDVITAFSGMVRICALGAAEILAKEGISAENVLRIRPLDRPANNASVVKTNLIVTVEEGFPQHGVAEGASVVEESFEYLDAPVERTIGADVPMPVYANLERMVAQVQEDVRAAKRACVRSST

NbL11g05280.1 ubiquitin-conjugating_enzyme_E2_27 [MW = 21.13 kDa]

No. of times detected



log(intensity)



Values from



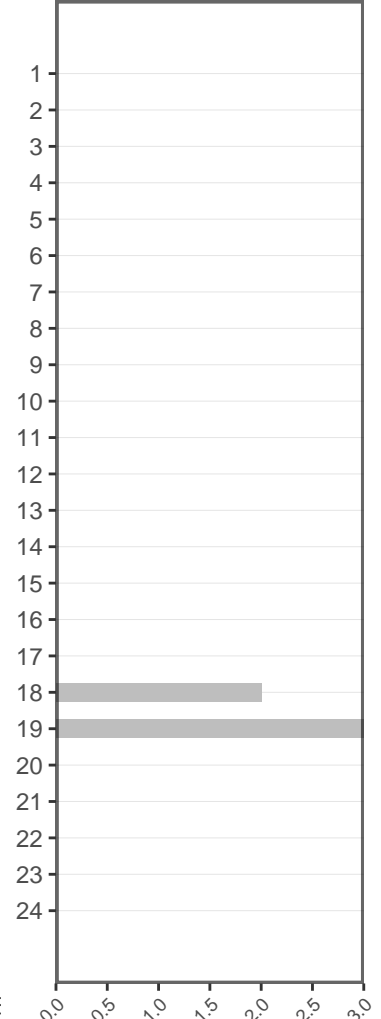
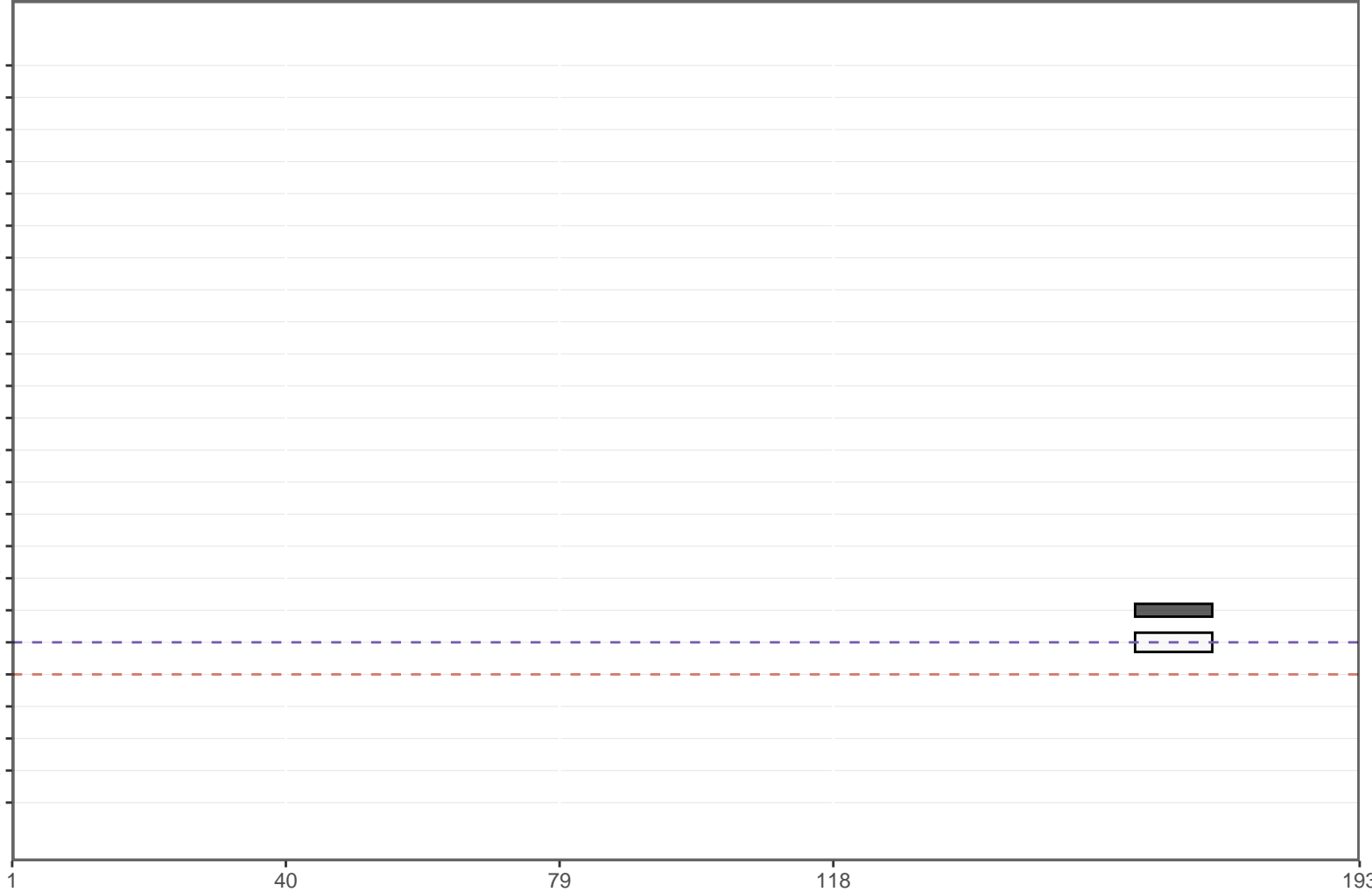
MW indication



Molecular weight



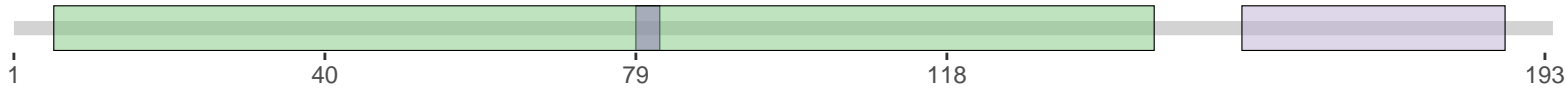
Gel Slice



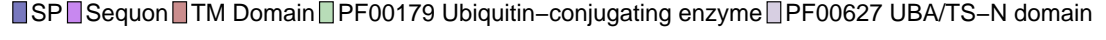
Protein length



Pfam domains



Pfam Description



Protein sequence:

SGAICLDLKDQWVSPALFKTKALLGIGALLFAPEPDDPDQDAVWQGYLRDQHTFVGTARYWTFETFAKLTGTTEENKQKLVEMGFPEADVRRTLEGTGWDENMALEKLGSG

NbL11g05250.1 40S_ribosomal_protein_S3a [MW = 29.73 kDa]

No. of times detected



log(intensity)



Values from



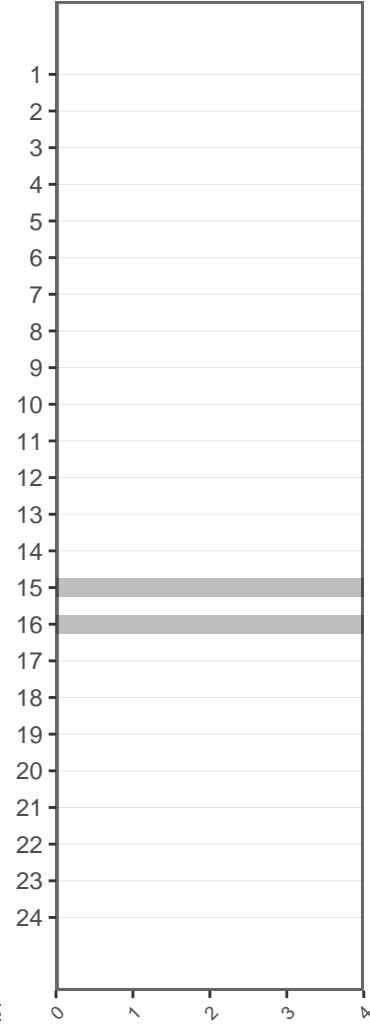
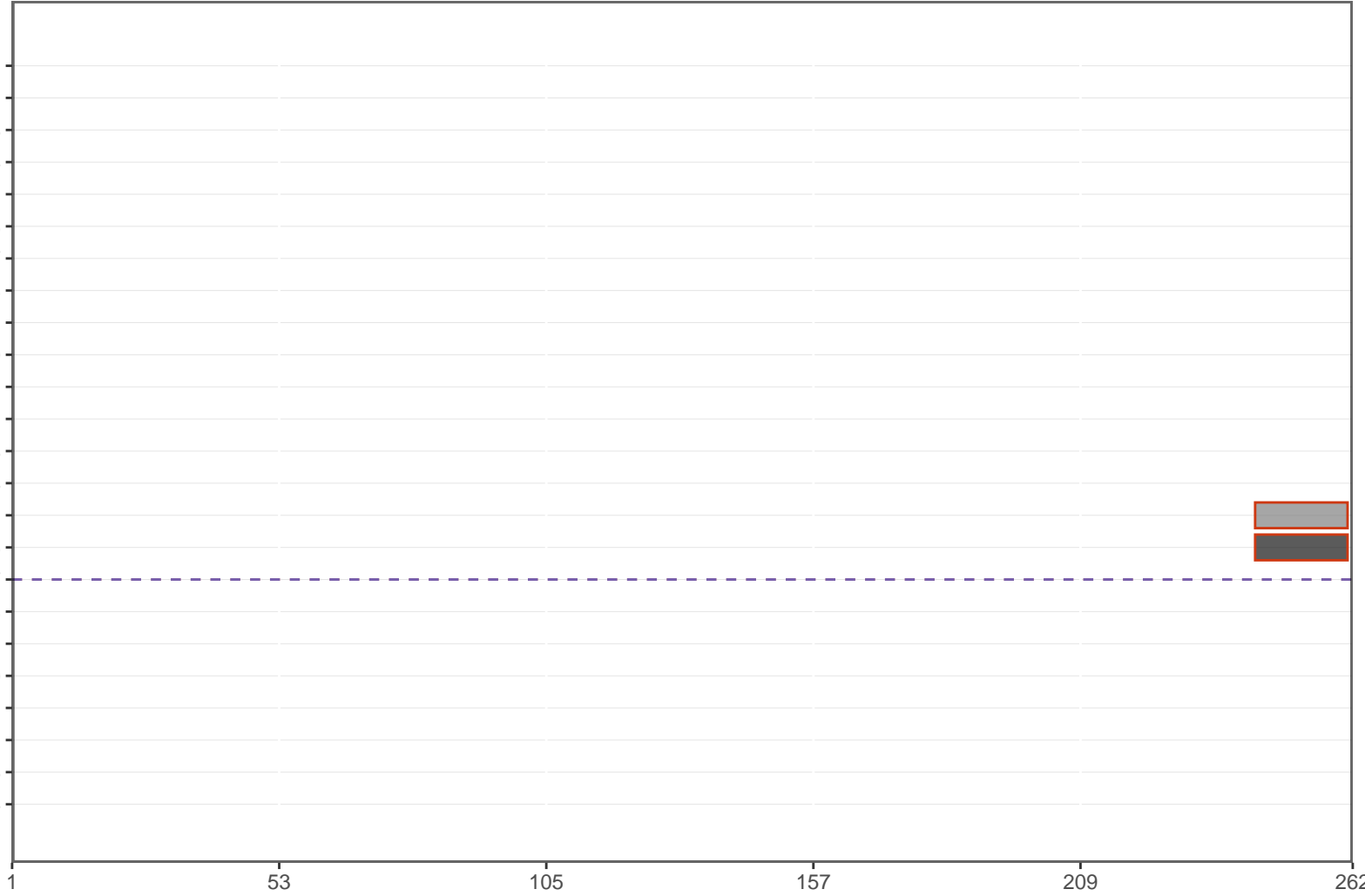
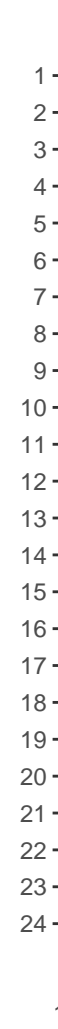
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

◀WOTLEAHYDVKTFDSYLRMFGIAFTKRRPNQKRTGVAQSSQIRGIRRMVEMRMNGASSCDLKELVAKFIPESIGREIEKATSSIFPLGNVYRHKVKKLAKPKFDIGKLMKMEVHGDSYEDGVKLRPADETVAEAEPEIPGA▶

NbL11g05210.1 50S_ribosomal_protein_L29_chloroplastic-like [MW = 19.07 kDa]

No. of times detected



log(intensity)



Values from



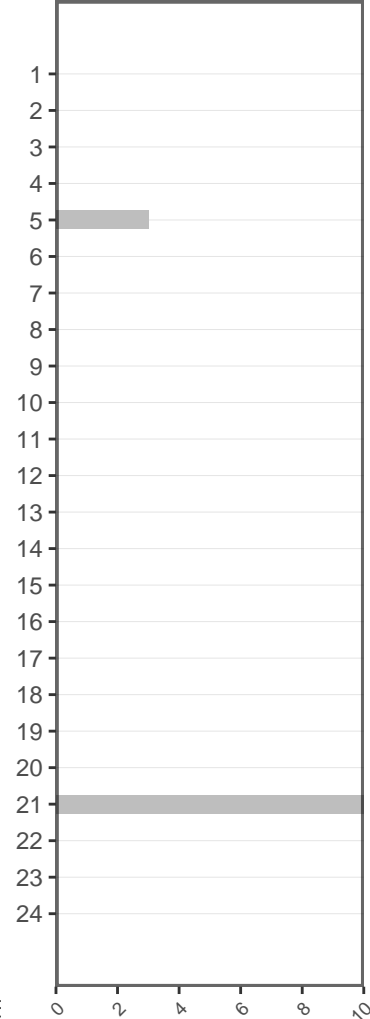
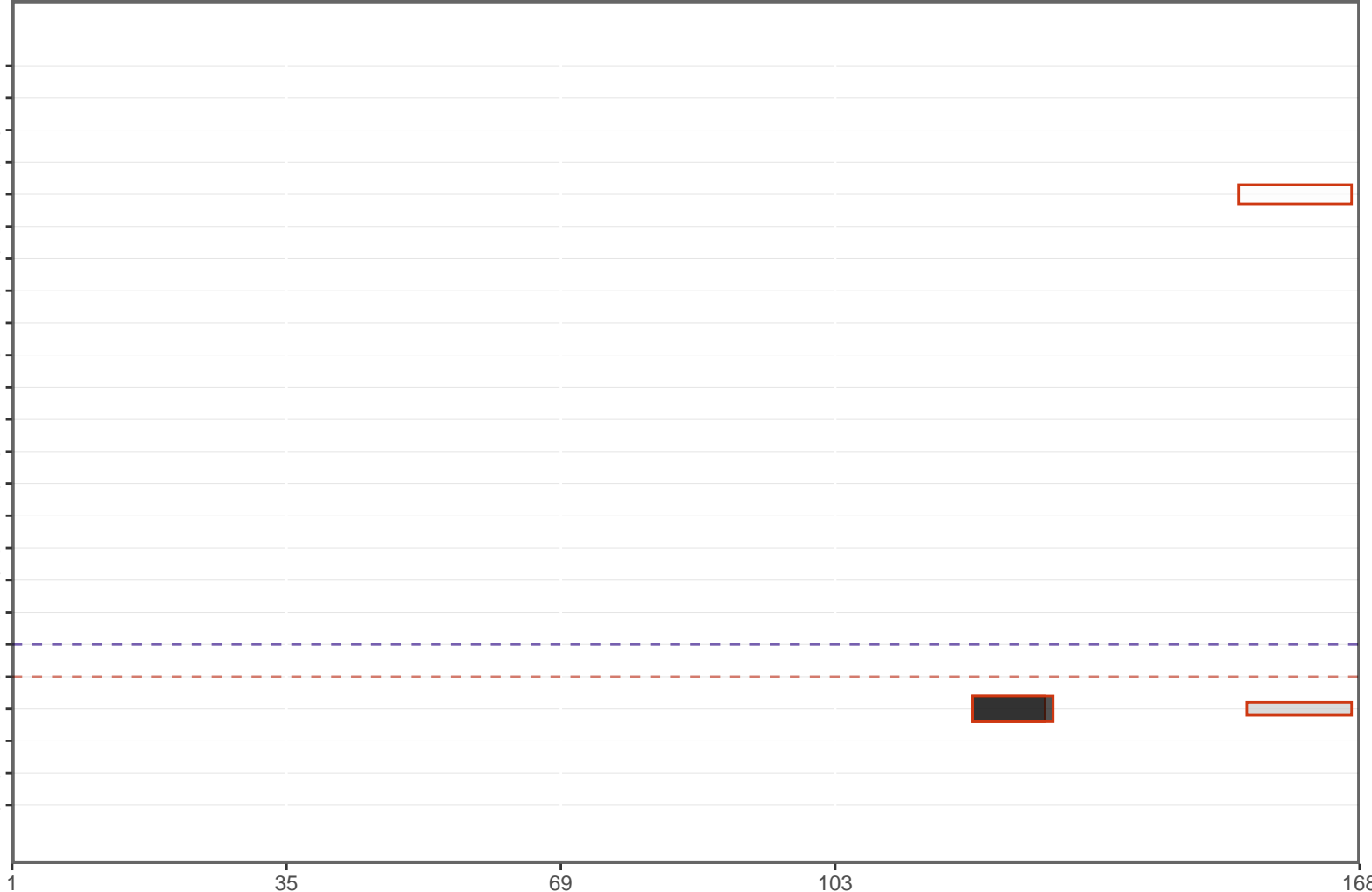
MW indication



Molecular weight

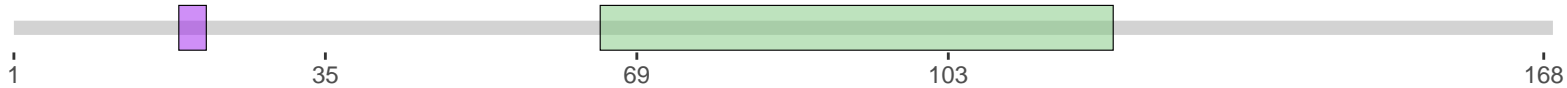


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

TEEIQEIVLQKGELEFMLRLGRSARNEFKSSEFLMRKRIRARMLTVKREIRELEEGNKRISRLDRKRWKNSVPRPPPSLKKLQEEEAAMAEKES*

NbL11g05150.1 putative_34-dihydroxy-2-butanone_kinase [MW = 61.85 kDa]

No. of times detected



log(intensity)



Values from



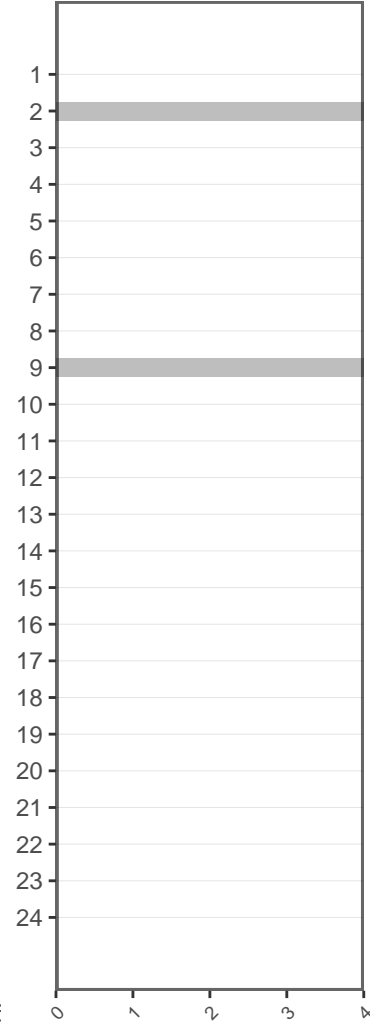
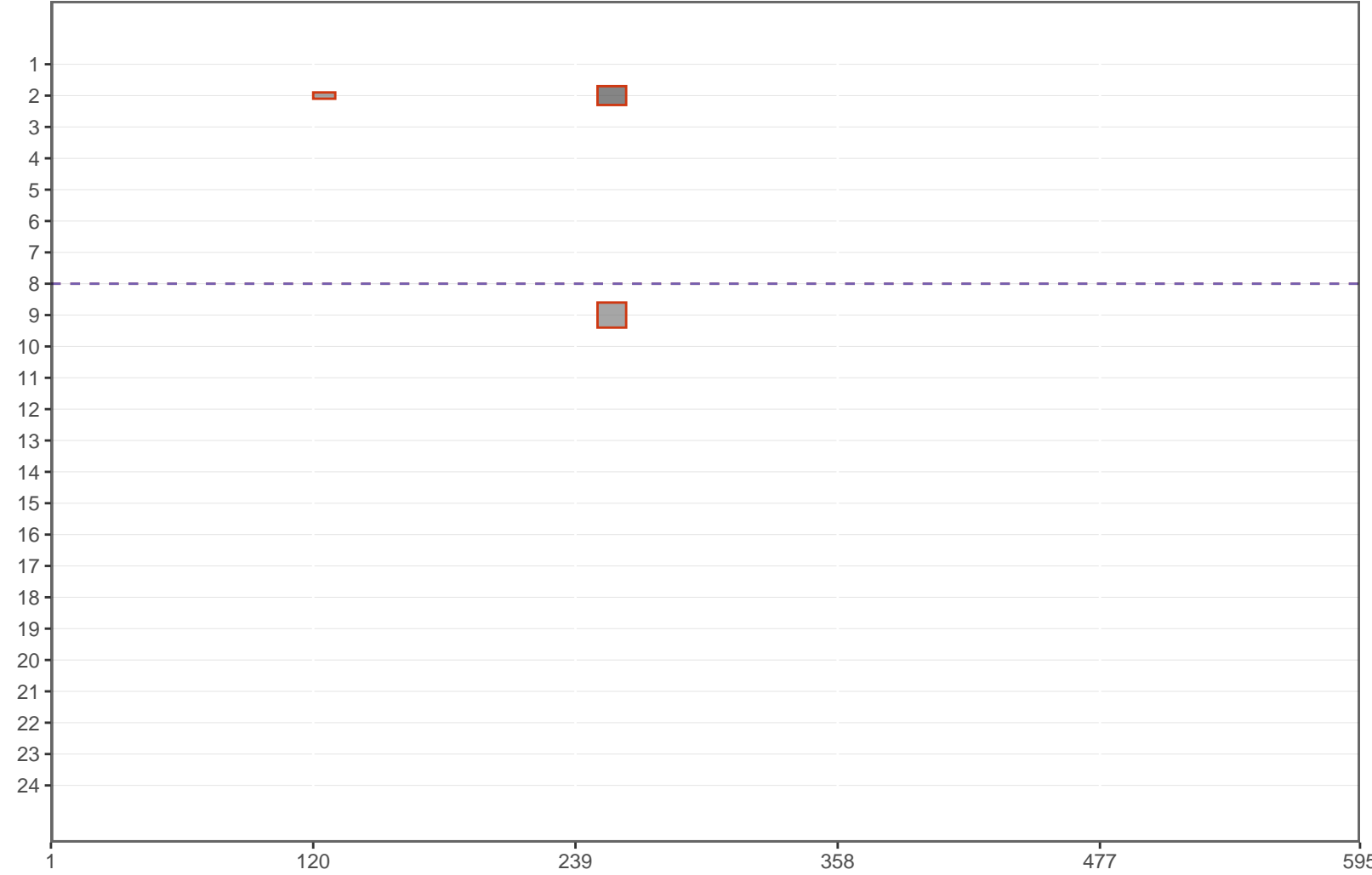
MW indication



Molecular weight



Gel Slice

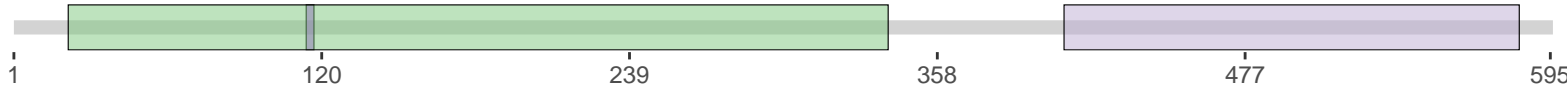


Protein length

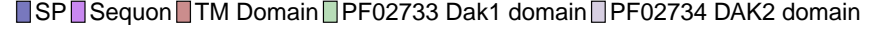


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

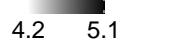
IAGKAVPLQLLEHGLAVDRVYTGSLMTSLMAGFSISVMKADGAILDRLDAPTKAPNWPVSGADGNRPKAFVPLPPPHISIGSDKTLRPEKLSLGHLEAAEAAMTELNLNRDNLNEWDSKVGDDGGDSTMFRGAWAILEDMKYVPLNDPAETVNEIGSSIRRVMSGTSGLYDFGKAAVAALKADSELVITLHWADLDAIAAVSKYGGARAGVYRTLLDALPALSALKERLEAGDNPVDAFVISEAAVAGAESTRKHMAGAGRSTYIPGDVLAIEIPDGMAMAAAV

NbL11g05110.1 CASP-like_protein_4D2 [MW - SP = 16.77 kDa]

No. of times detected



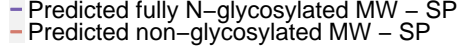
log(intensity)



Values from

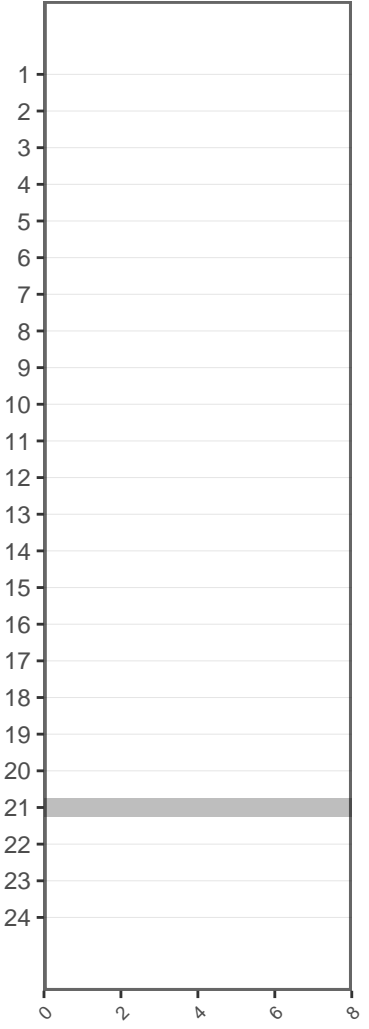
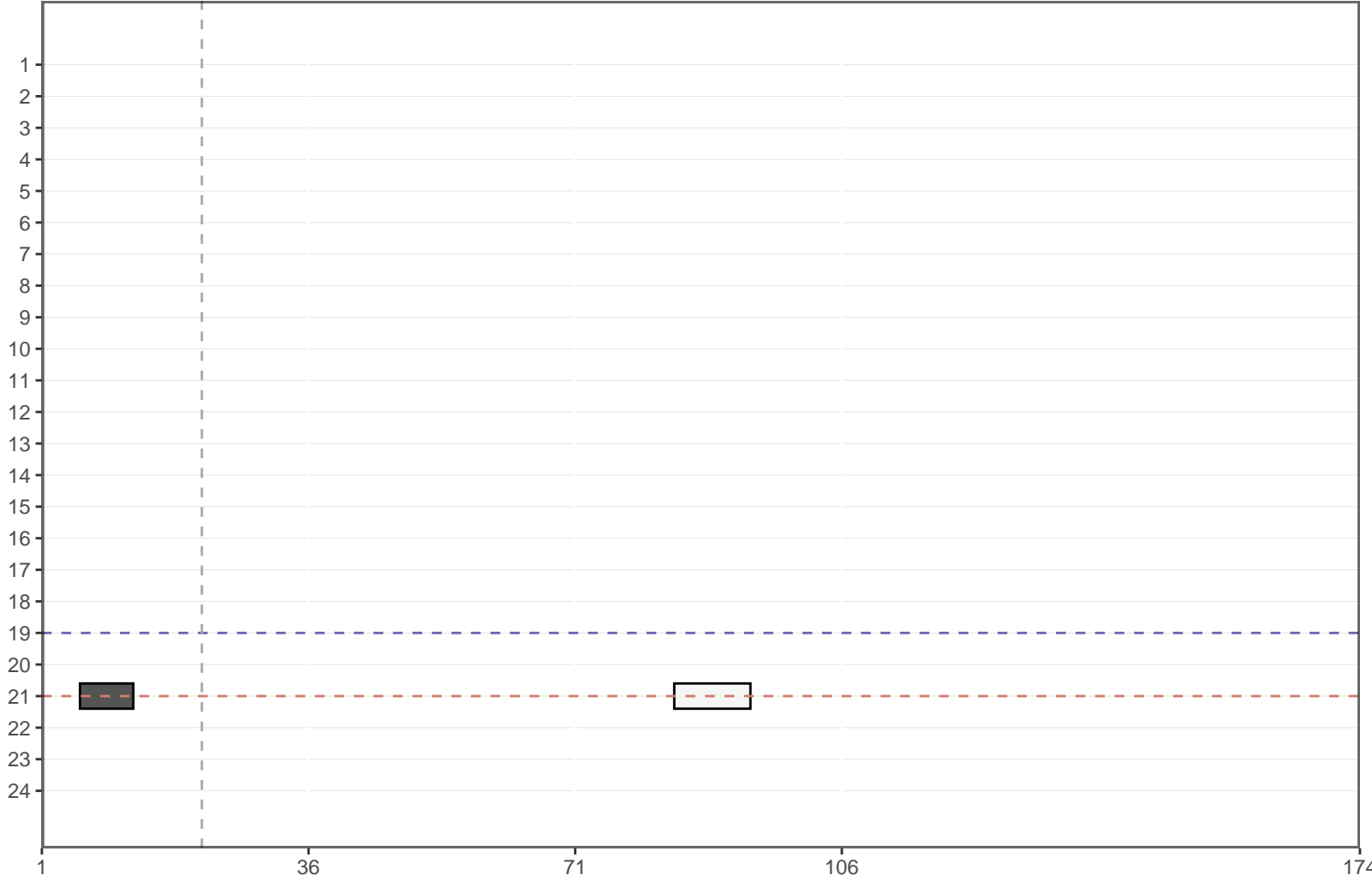


MW indication



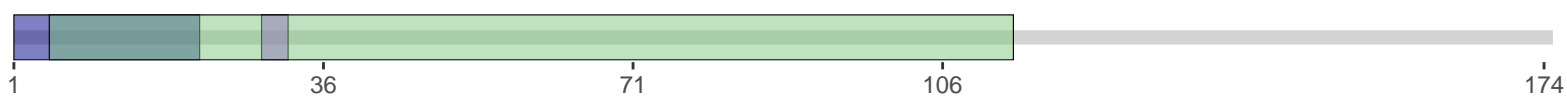
Molecular weight

Gel Slice



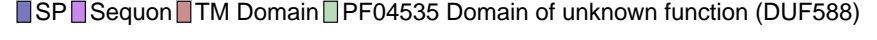
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AFTGEKVKGRFLGALDFYADKIFFFLAAGLVGFGVSBELKRYINGFVDIETSGDITFEELRTESKFFDRGLATPFLAGFTTMAVLTHTSFHRK

NbL11g05000.1 miraculin-like [MW - SP = 21.27 kDa]

No. of times detected



log(intensity)



Values from



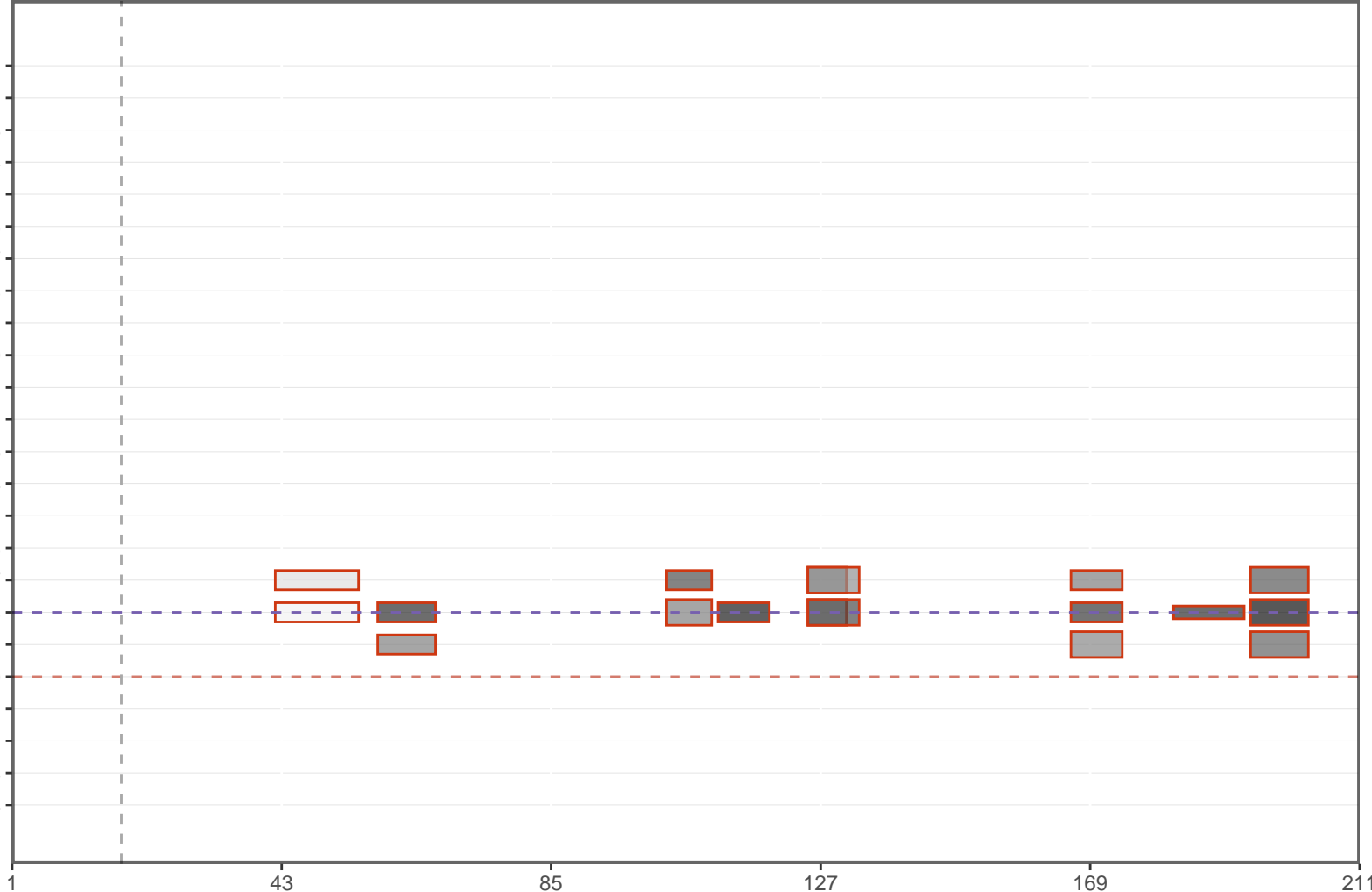
MW indication



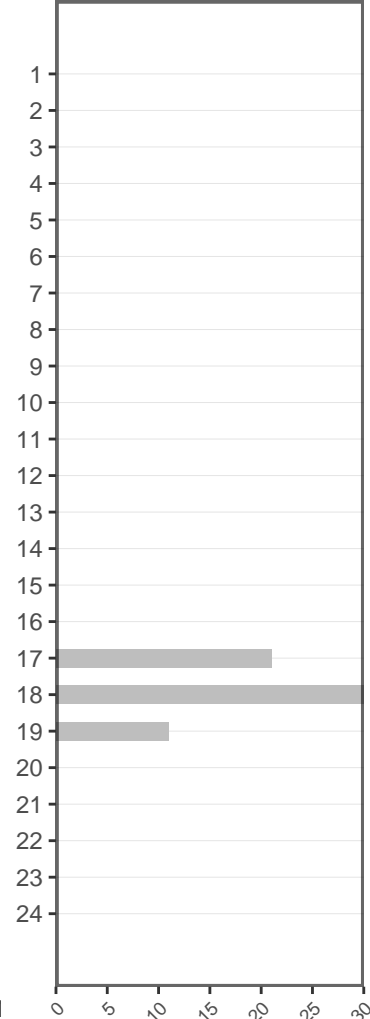
Molecular weight



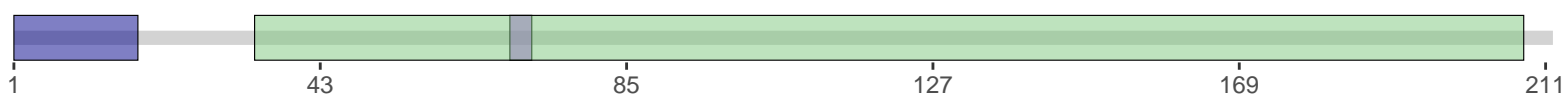
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

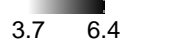
FDAAKGVVRLSTDLNVRFFPTTTCARETIWKLGTYYDDKLGKGYFVYTGVEGNPQTLSSWFKIEKLGTDKRFVFCPEVCKDKGKDKVGVYSGNDGVRFMALSDTFFRVMFKKTF

NbL11g04780.1 glyceraldehyde-3-phosphate_dehydrogenase_cytosolic [MW = 36.65 kDa]

No. of times detected



log(intensity)



Values from

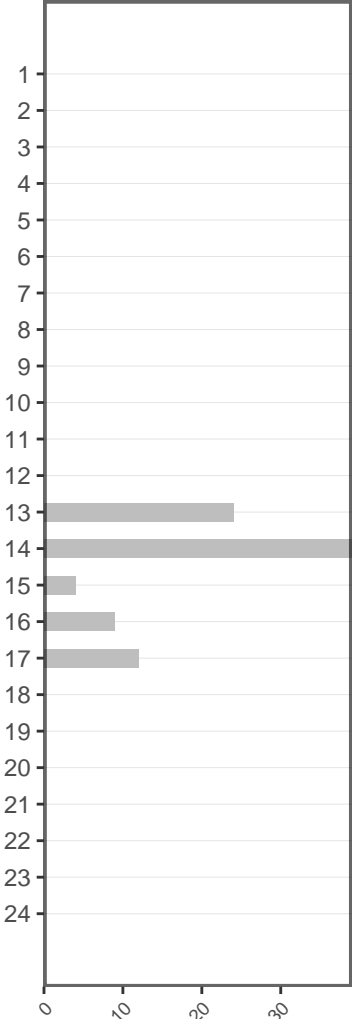
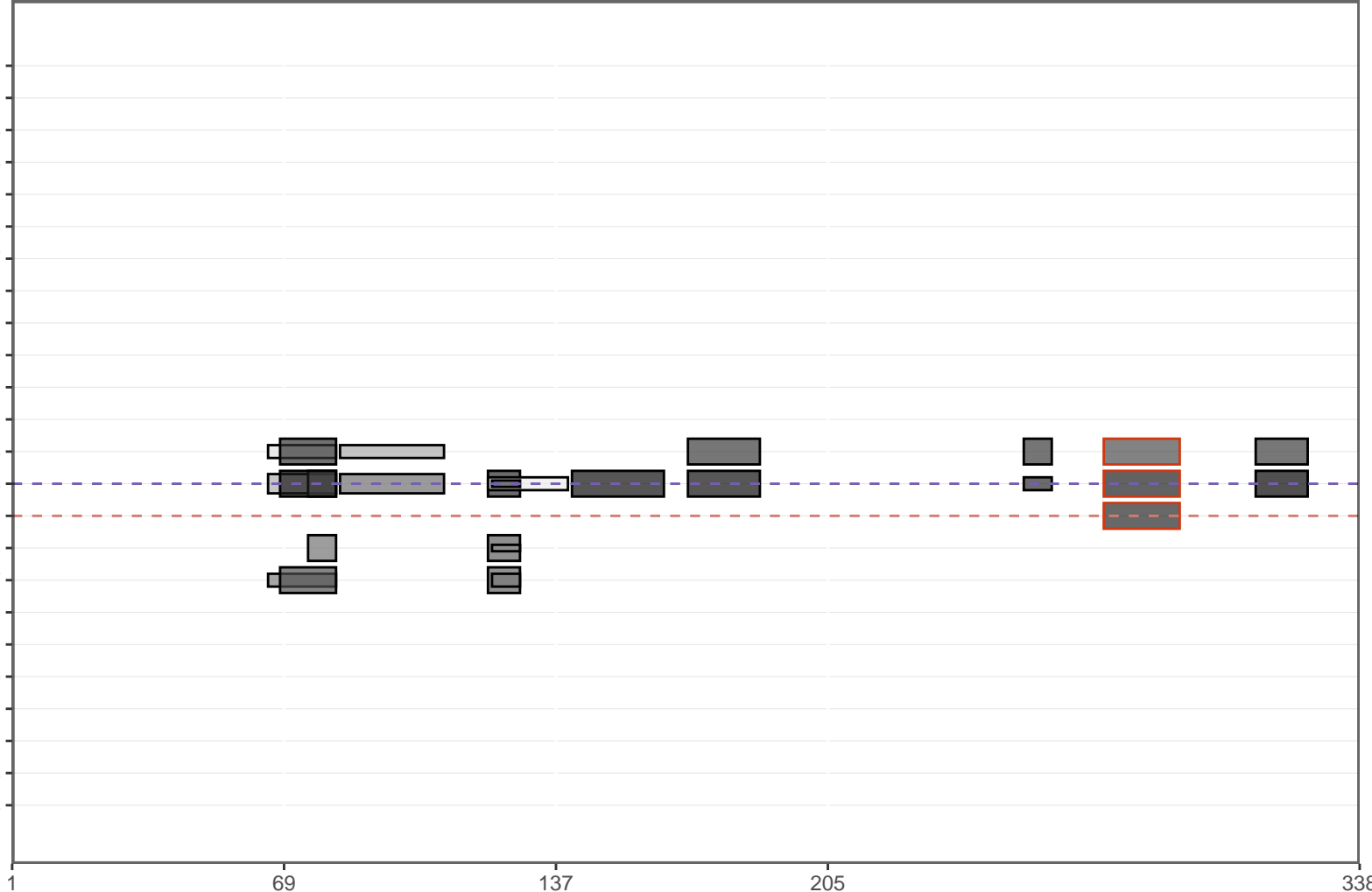
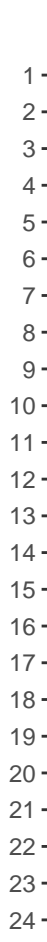
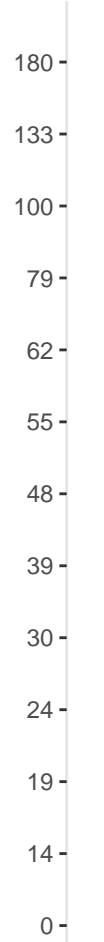


MW indication



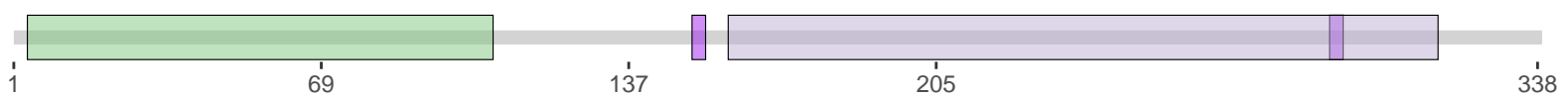
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00044 Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain
- PF02800 Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain

Protein sequence:

TTNCLAPLAKVYHDFGVEGLMTTVHGMTATQKTVDFGPAKQWFRGAAAGFNIPSETGAAKAVGKVLPSLNGKLTGMFRFPTVDVSVVDLTVRLKEKATVDEKAAKEESEGLKGLGYTEDDVTDFDIGNRSSFDAKAGIALSKNFVKLVSVDNEMGYSTRVVDLKHMAASVD*

NbL11g04680.1 elongation_factor_TuB_chloroplastic [MW = 52.65 kDa]

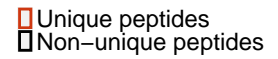
No. of times detected



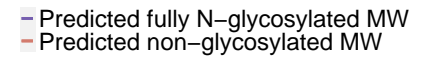
log(intensity)



Values from



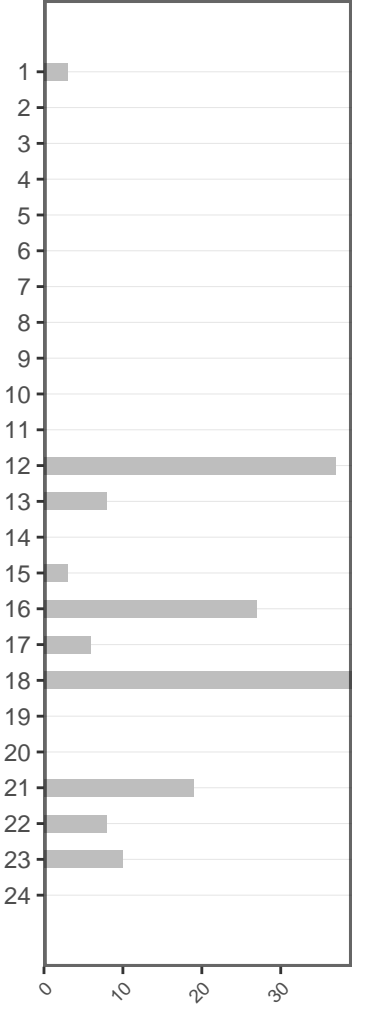
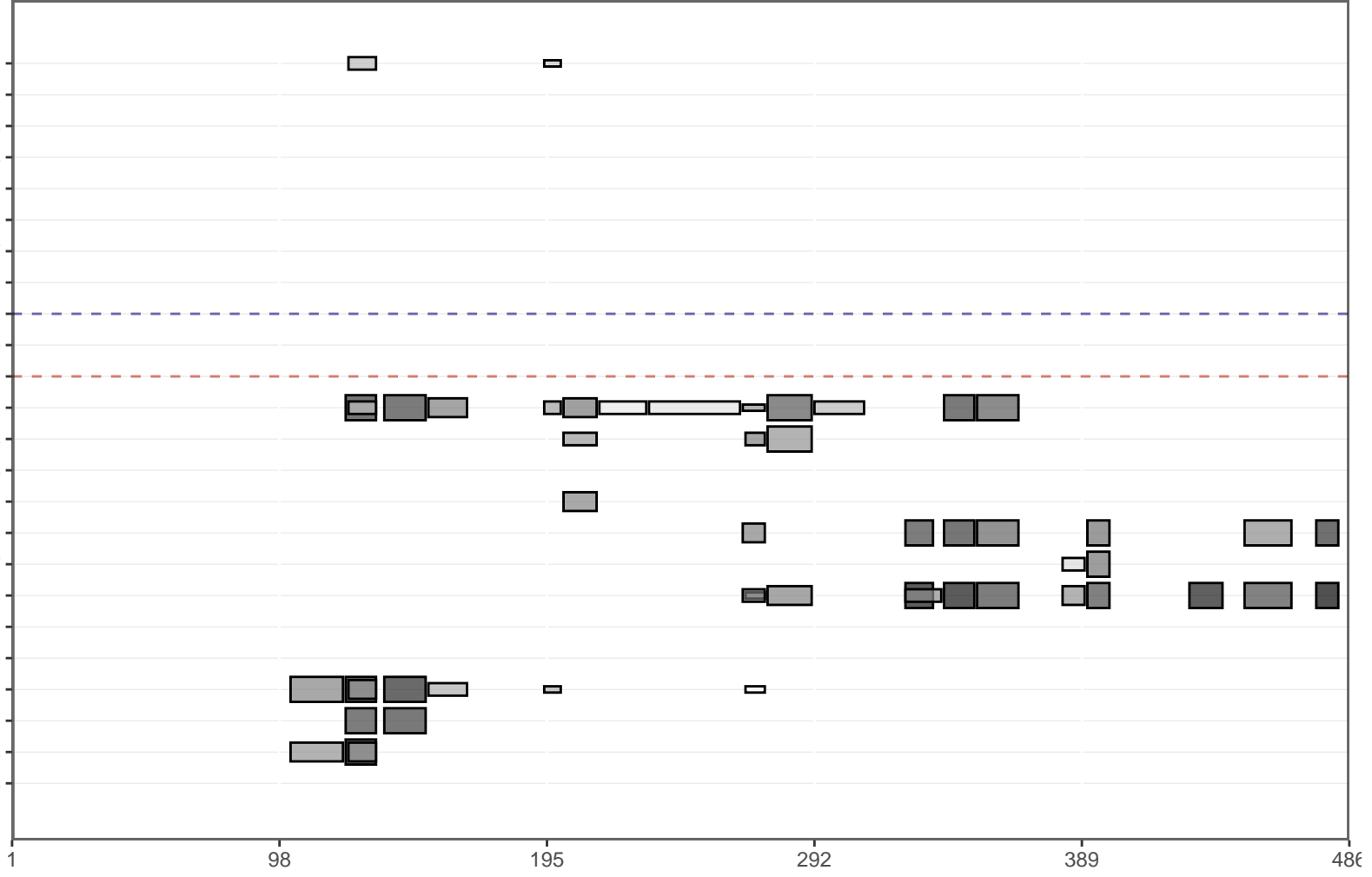
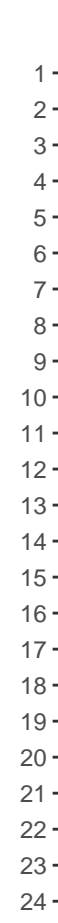
MW indication



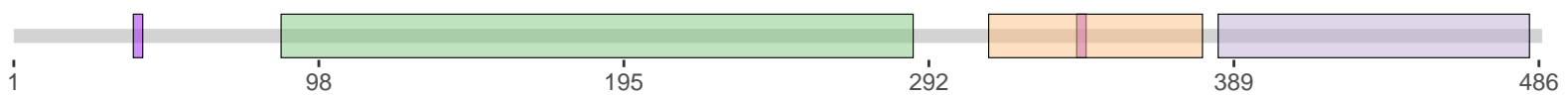
Molecular weight



Gel Slice

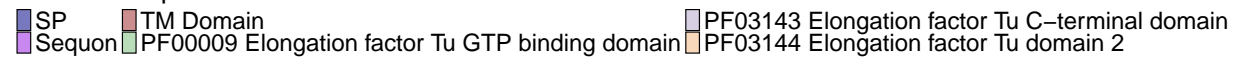


Protein length



Pfam domains

Pfam Description



Protein sequence:

/RELLSSYEFQDDEIPISGSALLALEALMANPSIKRGENQWVKIKYQLMDNVDYIPRQRTPELFMAIEDVFSITGRGTVATGRVERGTVKVGENDIVLGLKDRNTTFTVGVEMFQKILDEAMAGDNVGLLRGKIQKIDQRGMVLAKPGTITPHKFEALVYVKKEEGGRHSFFAGYRPFQYMRITDVTGKVTAIMSDKGEESKMMFPGDRVNMVVELIMPVAGEOGMFAIREGGKTVGAGVQIKLE

NbL11g04530.1 anthranilate_phosphoribosyltransferase_chloroplastic-like [MW = 42.38 kDa]

No. of times detected



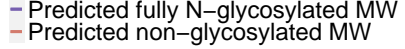
log(intensity)



Values from



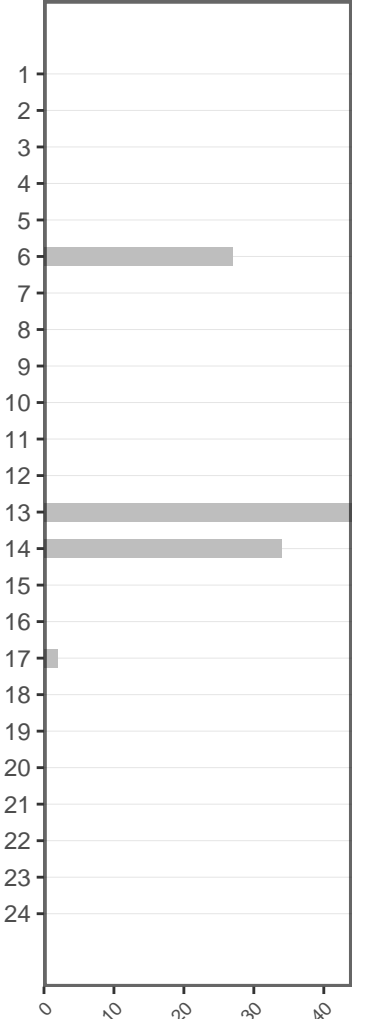
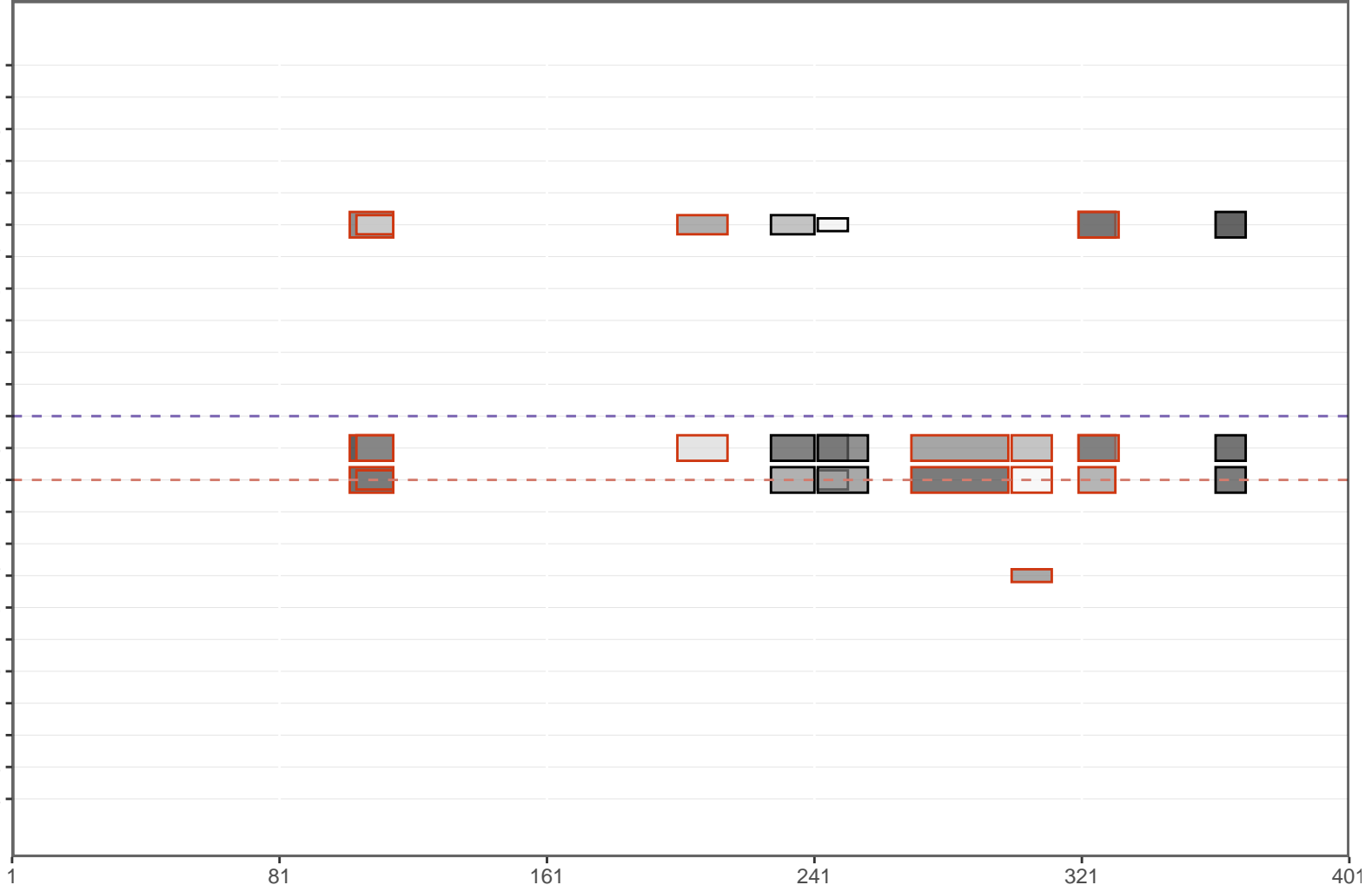
MW indication



Molecular weight

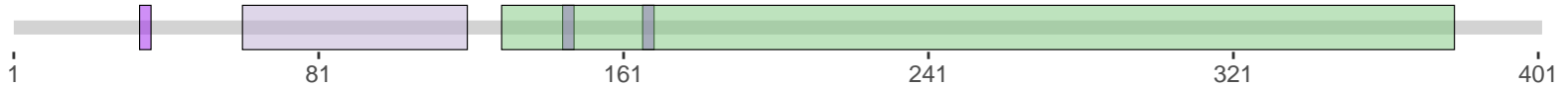


Gel Slice



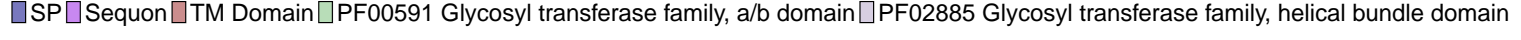
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PEGVKCYTRAGIGFMMAFVYHPAMKVRPIRKLKVKVTFNIGPMLNPARVFAVAGVYKEDLVHMKAKAVGRFGMKRALVHSEGLDEMPLGPGVLDVTFDNIKFKFDFPLVDFGIPRCTLKESLRGGGPDYVADMLKRVLSGEKGFADAFALNAAAALLVSGLVNLAEGVALARETVLGGKAKTLDLWVEVSEVKAAVSQVA

NbL11g04490.1 GDSL_esterase/lipase_At5g62930 [MW = 27.35 kDa]

No. of times detected



log(intensity)



Values from



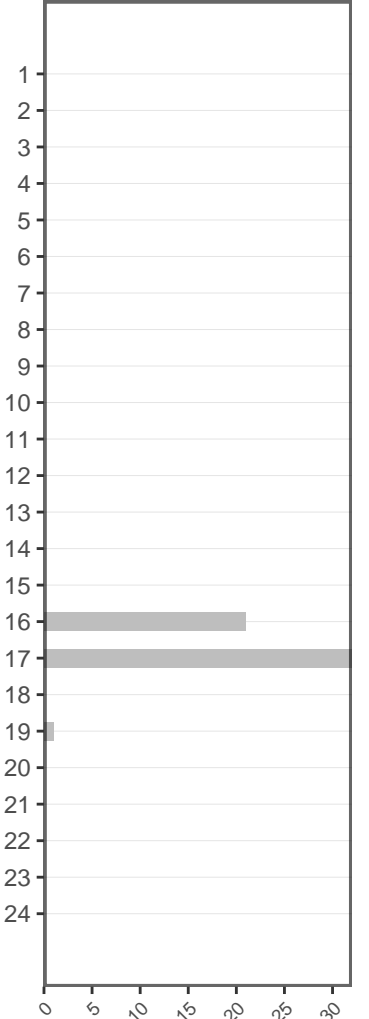
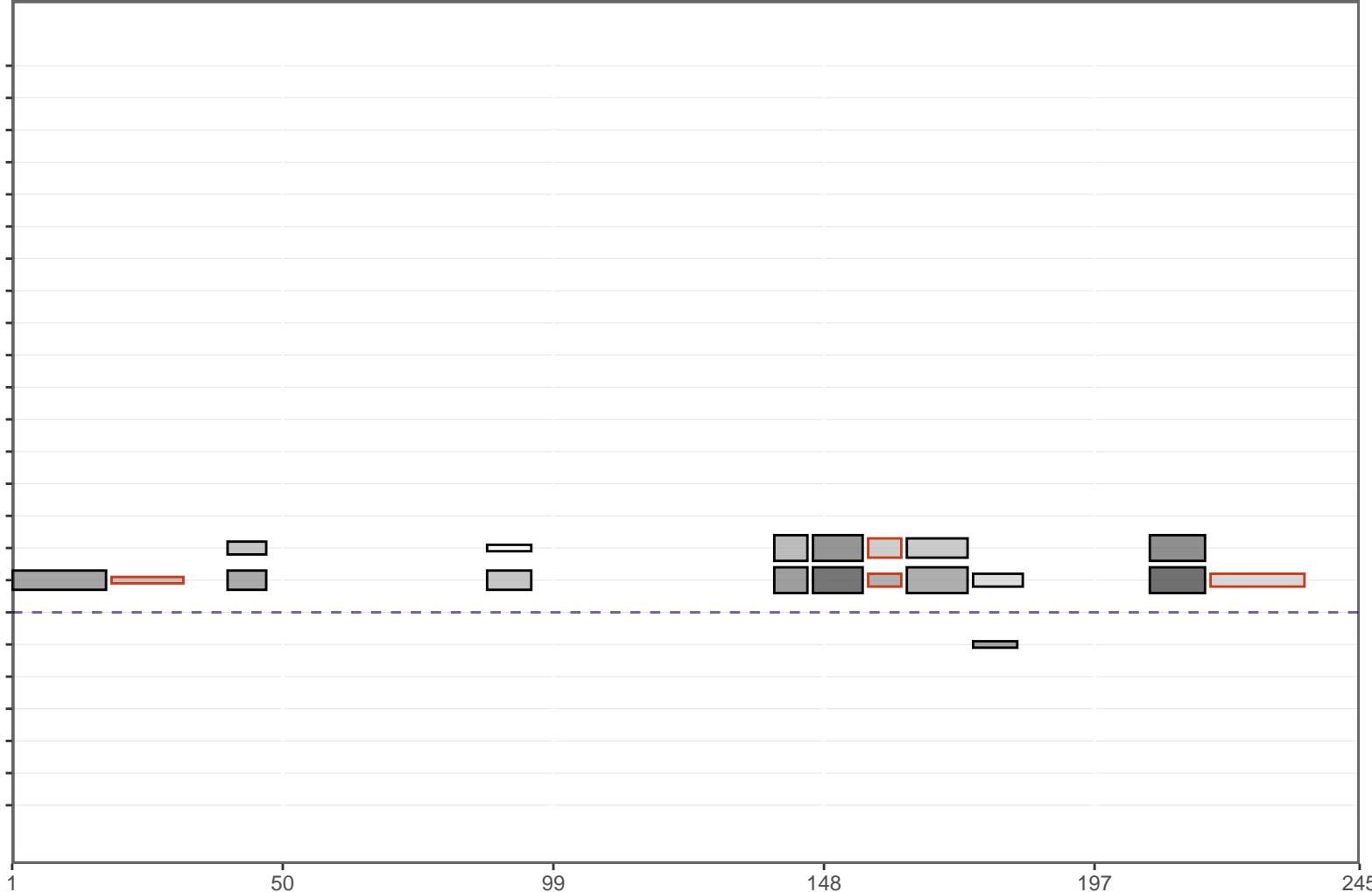
MW indication



Molecular weight

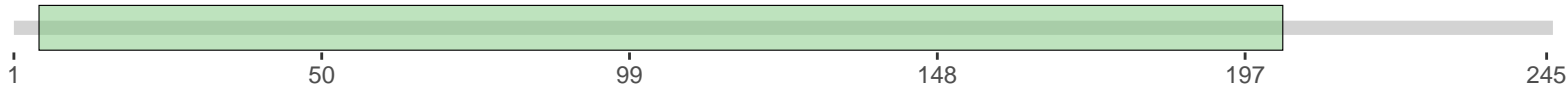


Gel Slice



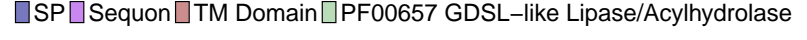
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SILVLYTTPPPVDEAGRFEGARSMYGDKAMELPERTNEVTGEYAKGGVQLARELGLPISNLWSKMOETEGWQKFLSDGLHLTAEGNAIHHQEVVWAFNAEAGFSAGKMPYVPHHSEINGNPKPTFQLGGRPVV

NbL11g04430.1 peroxisomal_membrane_protein_PEX14-like [MW = 56.97 kDa]

No. of times detected



log(intensity)



Values from



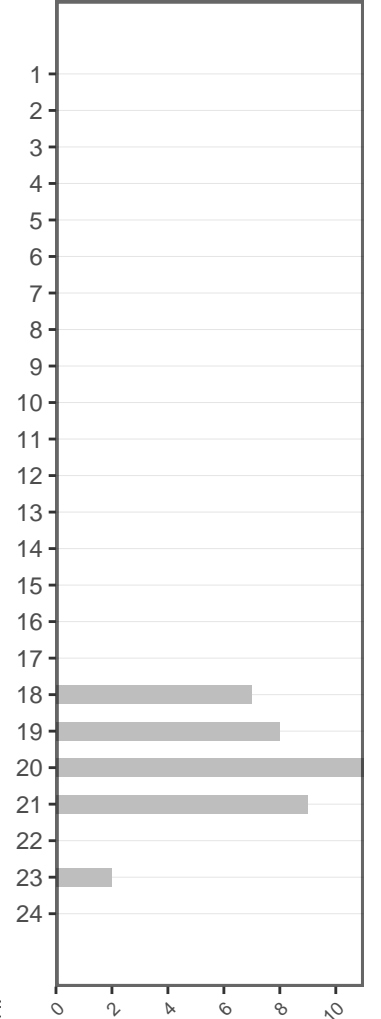
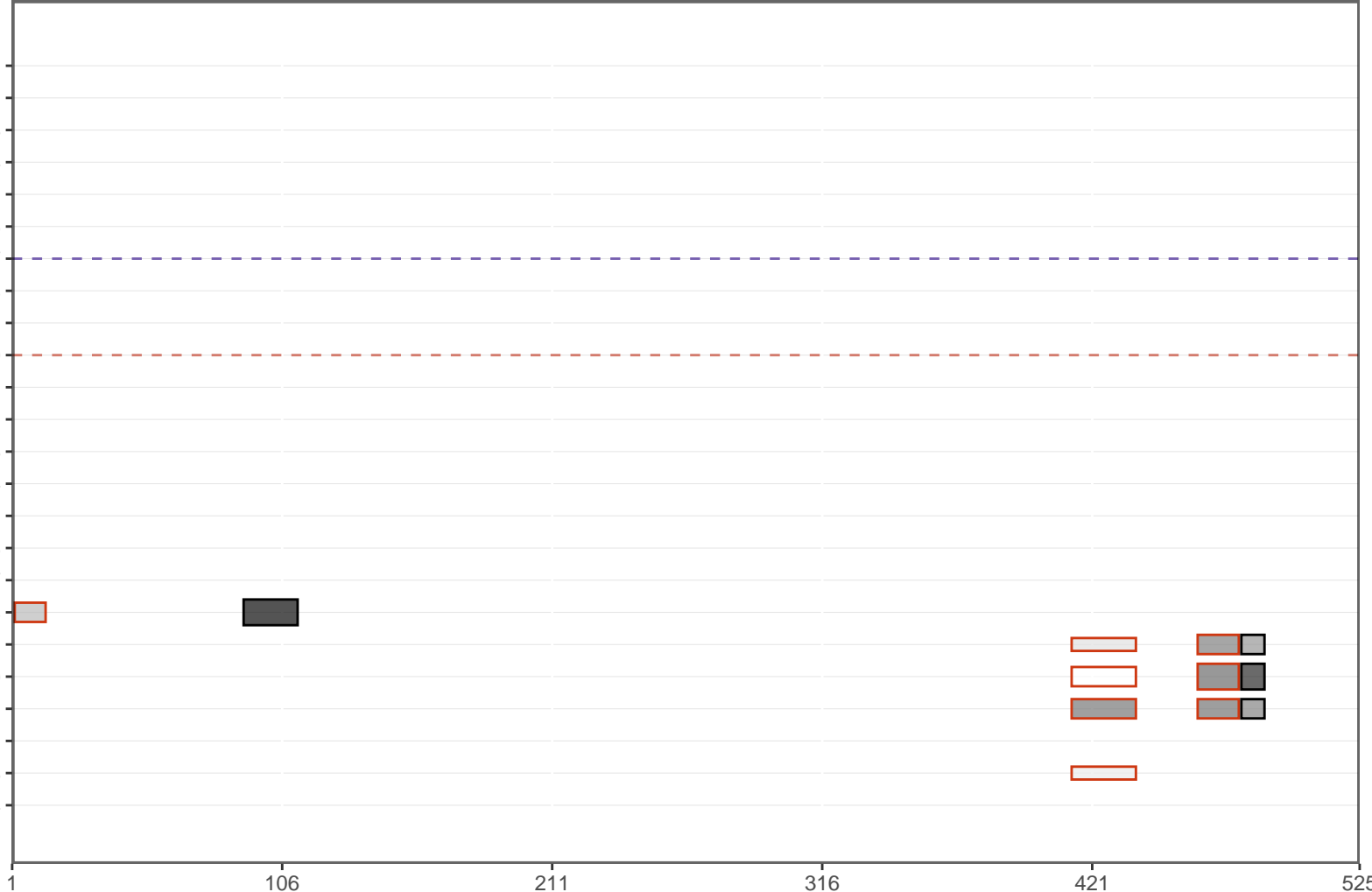
MW indication



Molecular weight

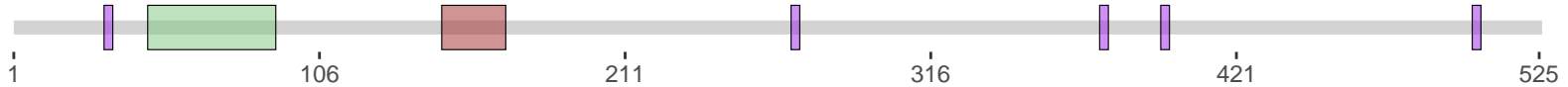


Gel Slice



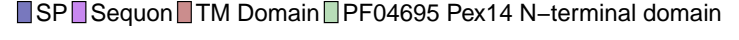
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

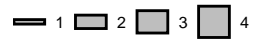


Protein sequence:

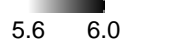
REMKMTSAIEKLEGGNTSGRIPTFLDDRRIEIVTGRSGYLNKIVDGDARSVRSLSPPAVVEFSPVAFPHKSYMEIMAMVORGEKPSNRIDNDGPPNPNPVPDRVAVPKPKPVEVGGIGENSTLLQSGSGDGLNYGYDNLNTGDSAAWVQRNRARTEIETEGETEGNGFSGFPAFVQERPIGRSVWVPPQPPVWMAEAAAIAIRPKPKVDFQNEQLTDDQLMARSSSEIDELQRIVTRISEGGAPFANGSSSALQISETPIGEGDQVLS-

NbL11g04370.1 E3_ubiquitin-protein_ligase_SIS3-like [MW = 42.28 kDa]

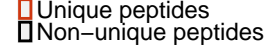
No. of times detected



log(intensity)



Values from



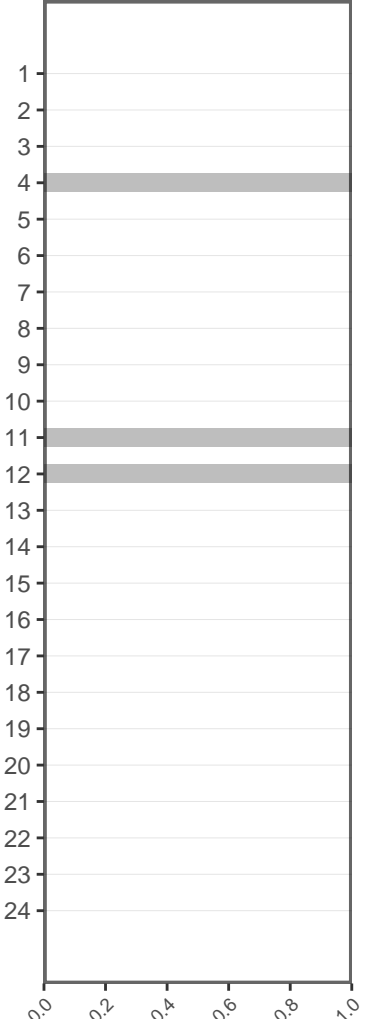
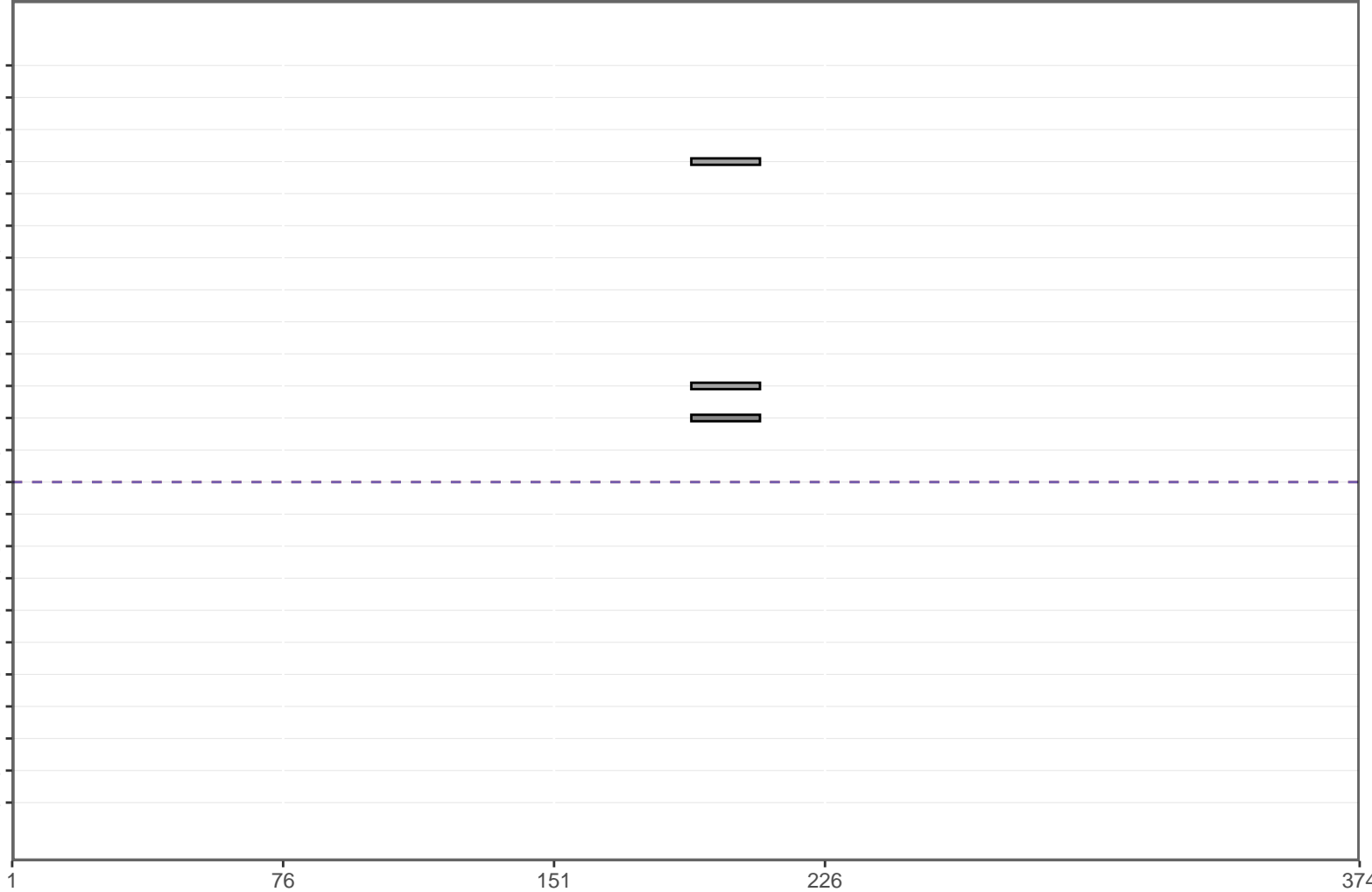
MW indication



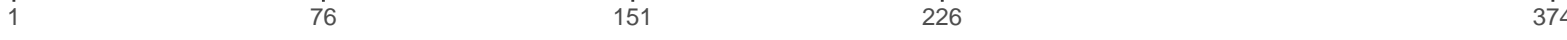
Molecular weight



Gel Slice



Protein length

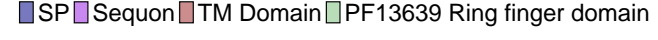


Peptide counts over 4 repeats

Pfam domains



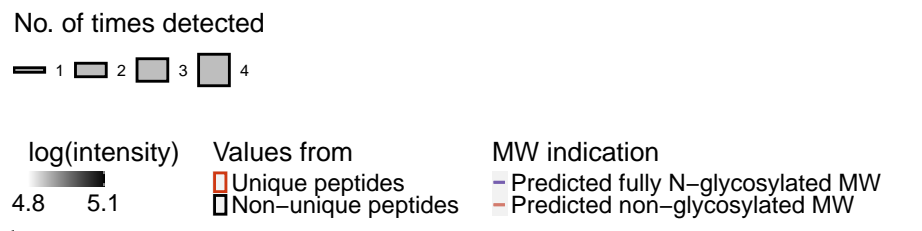
Pfam Description



Protein sequence:

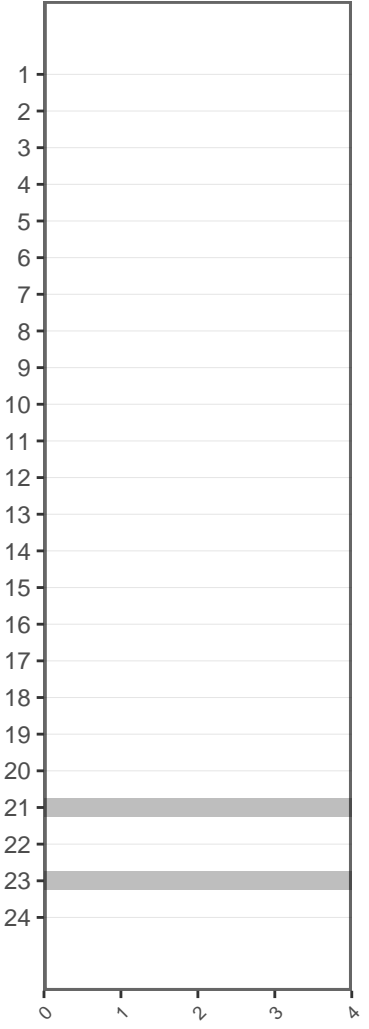
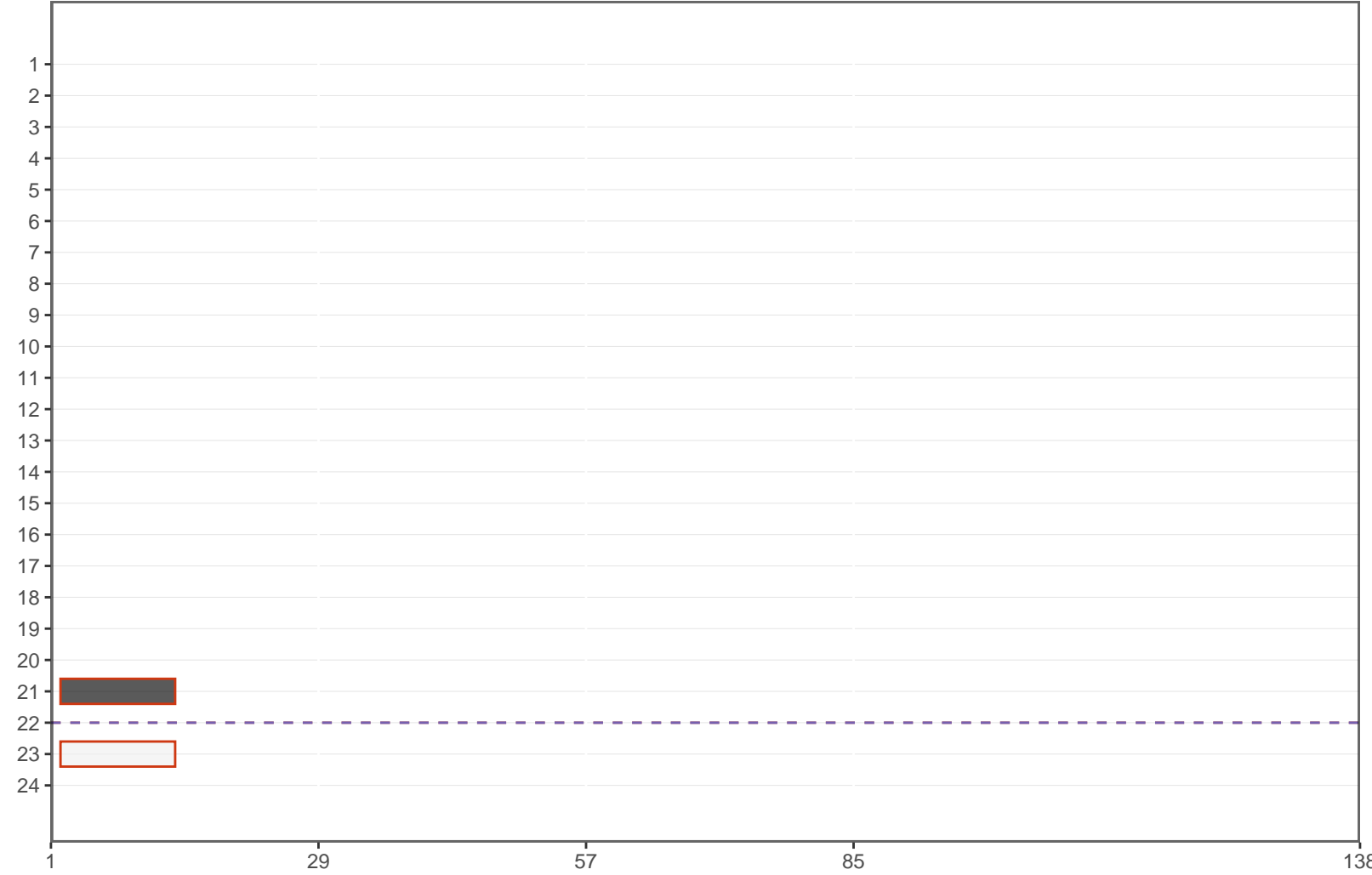
WTFVAAGQEMRGMGGDQATSHVPGVYLTQAGREAVEALIGELPKFMKAVPTDCSECPGLEEFRRVNEVRGLPCAHPHFVEGIDEWLRLLNWKPCRGRSSVFPNLDLSEALNIRADIESSTADVTEARYMRSGPSSGQVYLLRQGLLRPVRTQDTGMSGEVDATSGTAEGRNGALTPHHQGNMEPVQVVVEGSPREI

NbL11g04350.1 probable_26S_proteasome_complex_subunit_sem1-2 [MW = 15.87 kDa]



Molecular weight

Gel Slice



1 29 57 85 138

Protein length

Peptide counts over 4 repeats



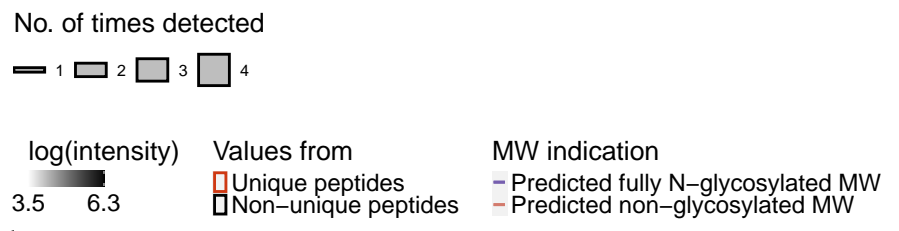
Pfam domains

Pfam Description

SP Sequon TM Domain

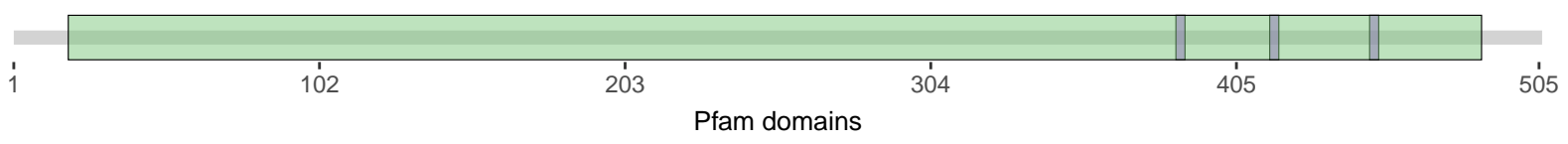
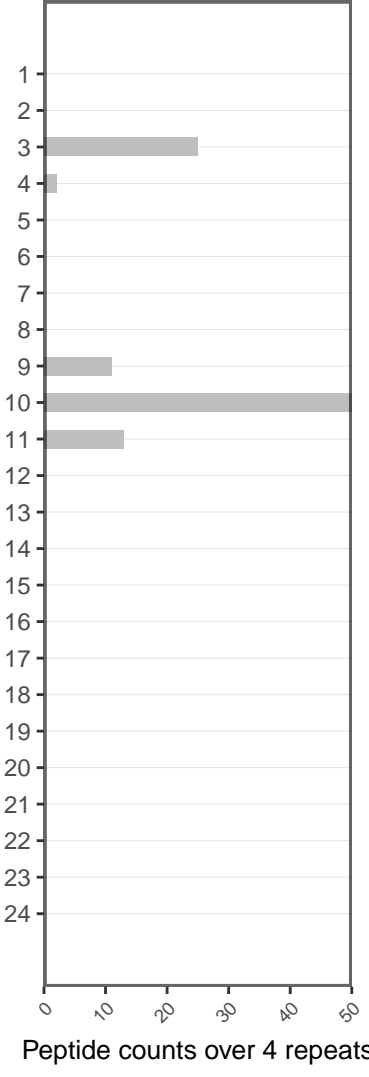
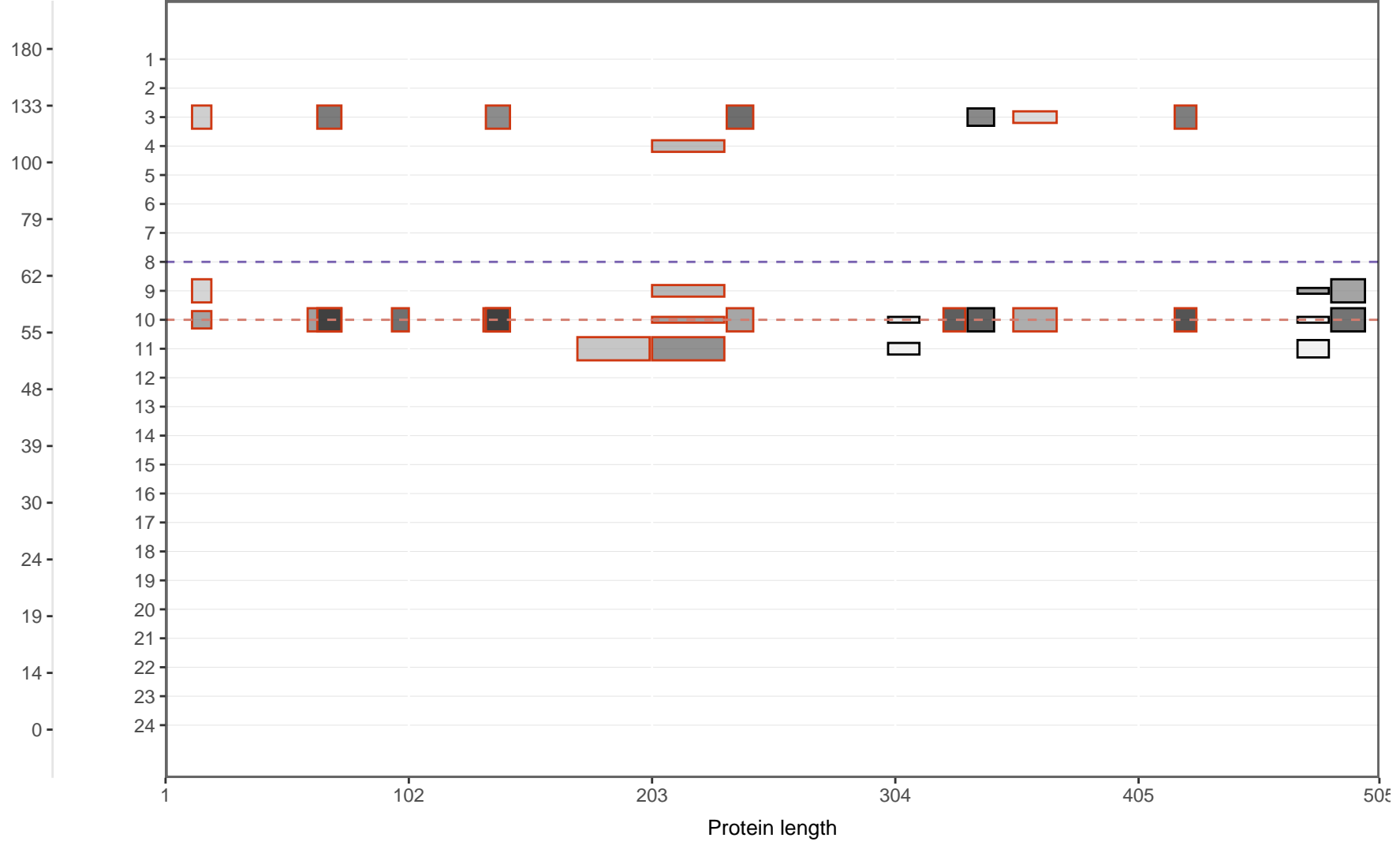
Protein sequence:
 WIIIVVVFENGRKRKKGKLPENGMGMMMMSMTSLFSKGNWKKATRRRNEPLKGLFFRNELGFCVGMFPFM*

NbL11g04250.1 betaine_aldehyde_dehydrogenase_chloroplastic-like [MW = 55.4 kDa]



Molecular weight

Gel Slice



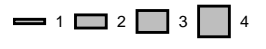
Pfam Description
 SP Sequon TM Domain PF00171 Aldehyde dehydrogenase family

Protein sequence:

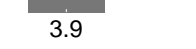
ITGVKMTAAAGLVNPFLELOGKSPVVFDDIDNLDLVAEVTFLGCFANAGQVGSATSRLLHGESIASEFLERLLWKNKLGDPLEEDCKLSPVSSGQYKVKLFISKANDGATILGGGERPQHMKKGYVYVQPTHTDVTNSMEIKWKEVFGPVLGVKTKFTEEEAELANDTKYGLASAVLKKDLERGERCFKAFGTGHIWLNQSGPPTFTQLPWGGRKRKSGFGKDLGEWGLENYLNKIQVYQYTSDEPWAFYKSPSKV

NbL11g04080.1 plasma_membrane_ATPase_2 [MW = 74 kDa]

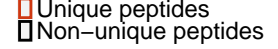
No. of times detected



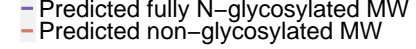
log(intensity)



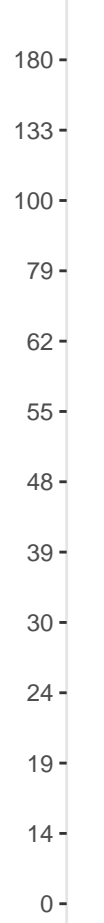
Values from



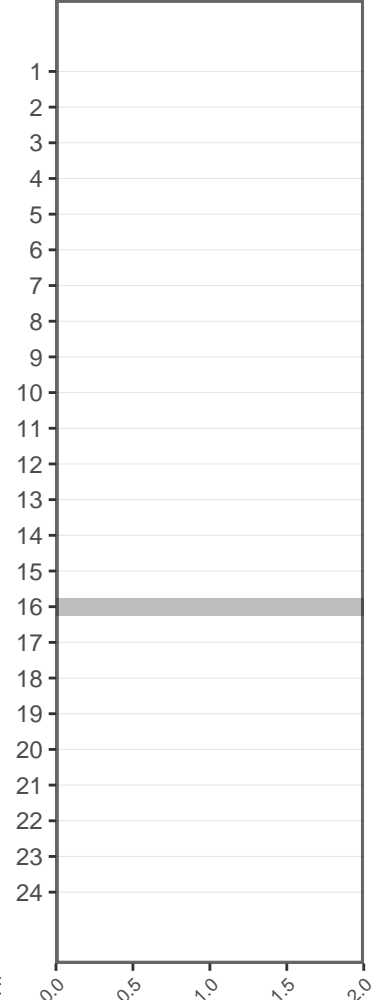
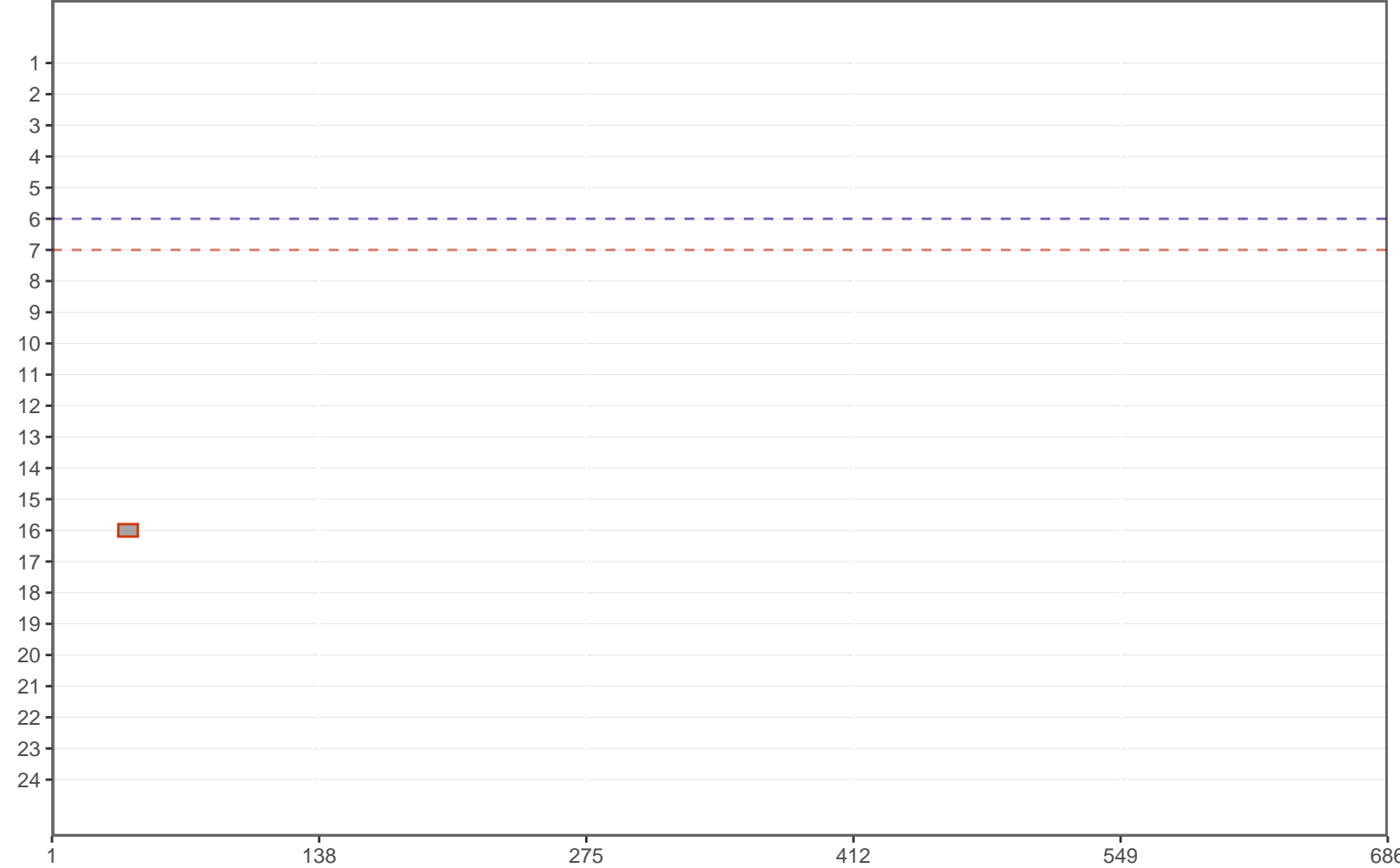
MW indication



Molecular weight

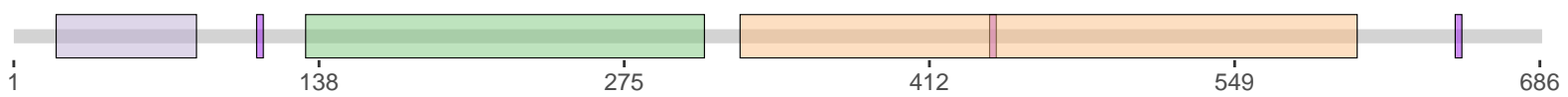


Gel Slice



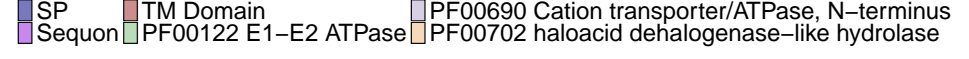
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

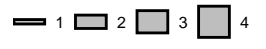


Protein sequence:

SSDKTGLTLNKLTVKNIIVEVFAKGVADFTVILMAARASRTENGDAIDTAIVMLSDPKEARAGIREHFLFPNPTDKRTALTYLDGEGKMHRVSKGAPFQILNLANHNSKSDERRVHVAIDKFAERGLRSLGVAYGEVPEGRKESTGGFVQFGLLPLFDPPRHDSAEFRALNLGVNYKMTGDQLAKGKTRRRLMGNTMYPSSALLGGTKDEGASLPIDELIEKADGFAGVPEHNYEIKRLQARKHLGGMTGGVNDAPALKKADGVADGDDATDAARSASDIYLF

NbL11g04000.1 delta-1-pyrroline-5-carboxylate_dehydrogenase_12A1_mitochondrial-like [MW = 60.75 kDa]

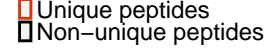
No. of times detected



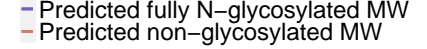
log(intensity)



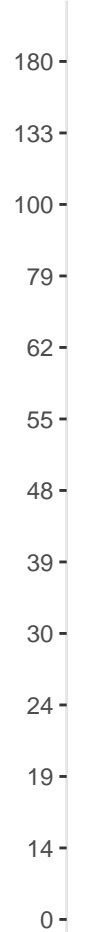
Values from



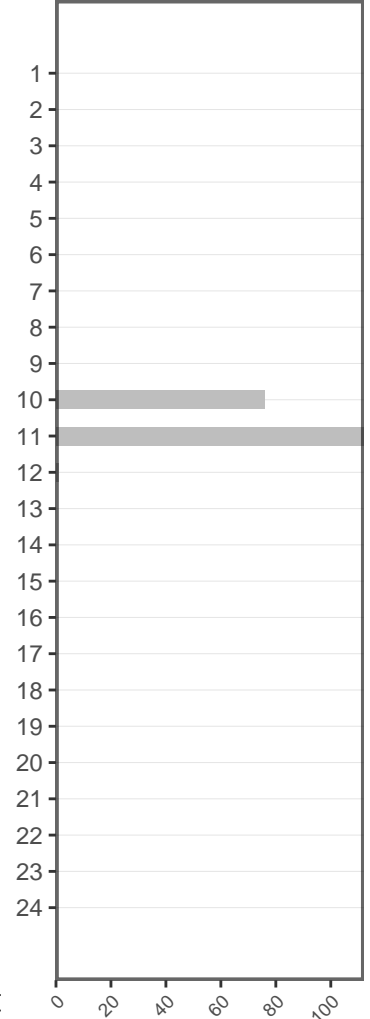
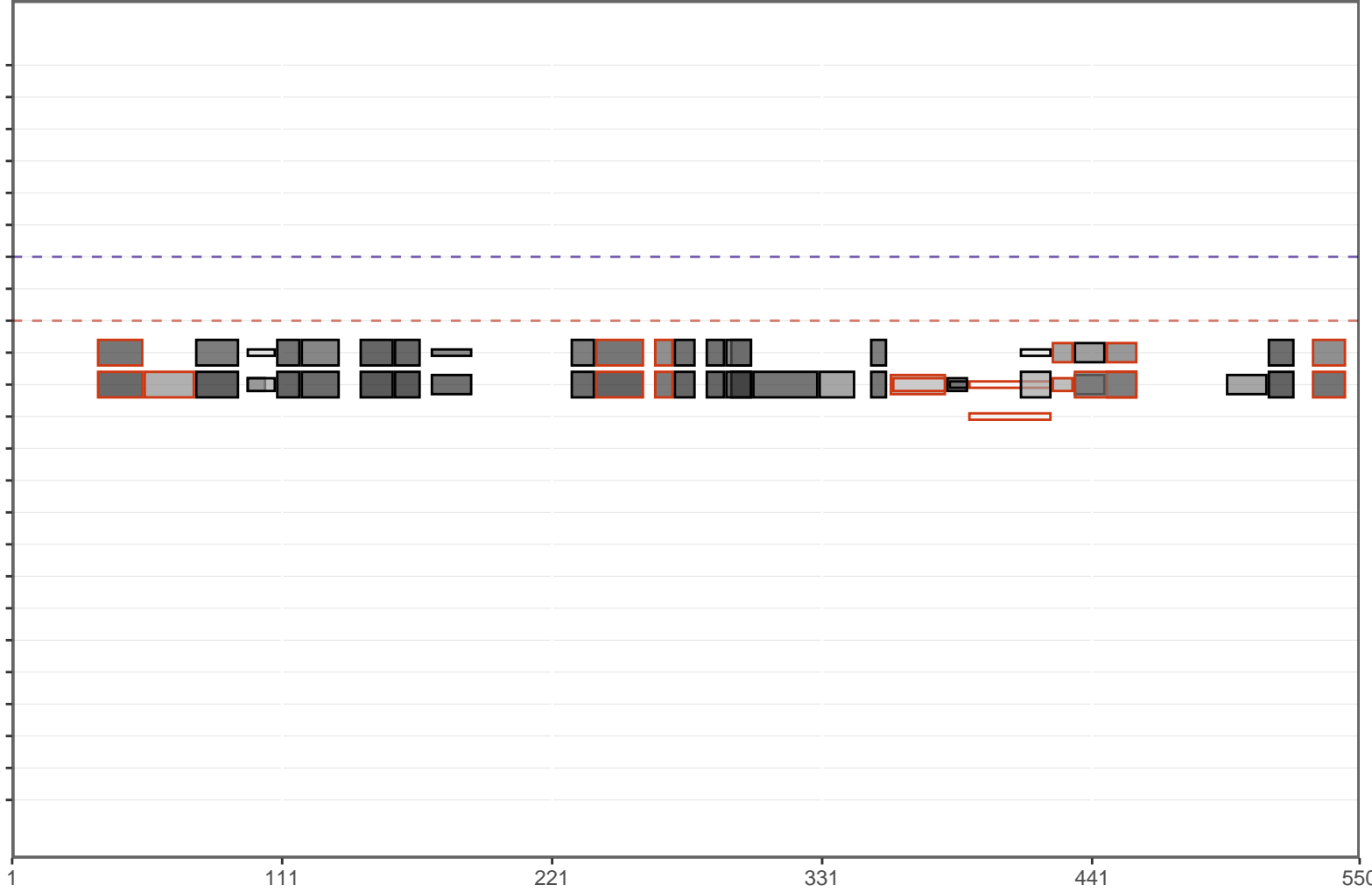
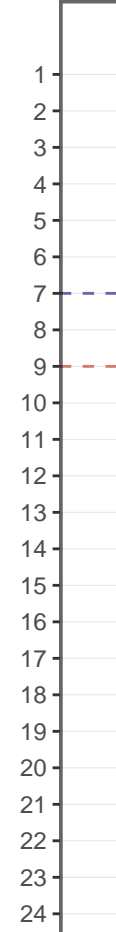
MW indication



Molecular weight

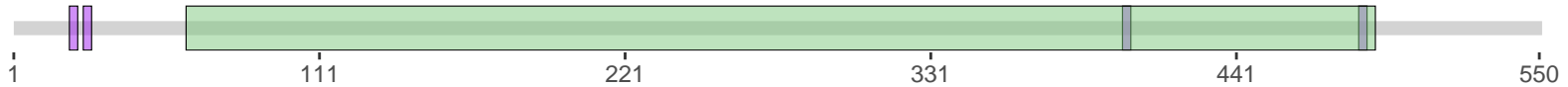


Gel Slice



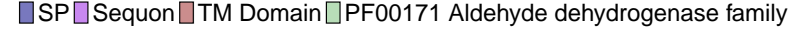
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TMNLLEGKPRMFLFTGSSRAEKLADLGRVKLEADGFDWKLGPVHEVDVVAWVGDQDAVAGSGKQKSAQSLFMHENWGRSSLLDKMTFLAARRKLDLITGPIVLTVEAMLDHAKKLLQIPGRLFFGGEPLQNSHPVYGAQKPTAFIFPLEELKGGHYHLVTKFPGFQVTEYKNDQLPLVLALEKRMHAHLTAAVVSNDFLGEVIGNSVNGTAYGLRARTTGAPQNHVFGAGDPRGAGIGTPEAKLWVSGHREVIVYDGVPLQWKTPTAST

NbL11g03820.1 ran-binding_protein_1_homolog_b-like [MW = 28.76 kDa]

No. of times detected



log(intensity)



Values from



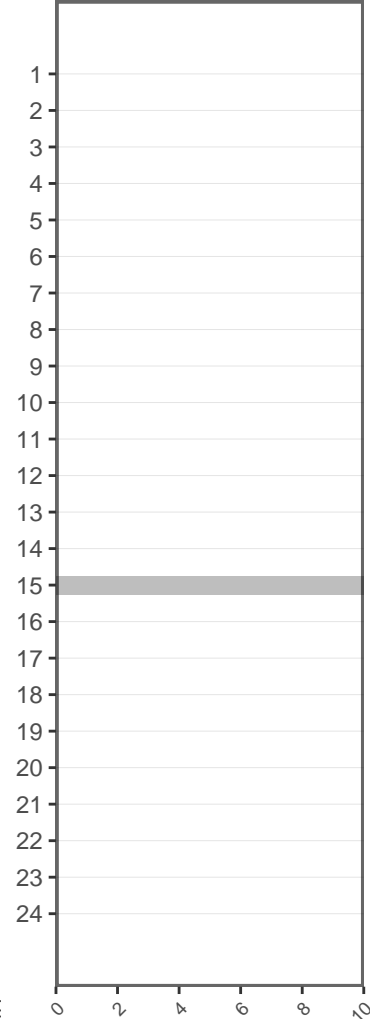
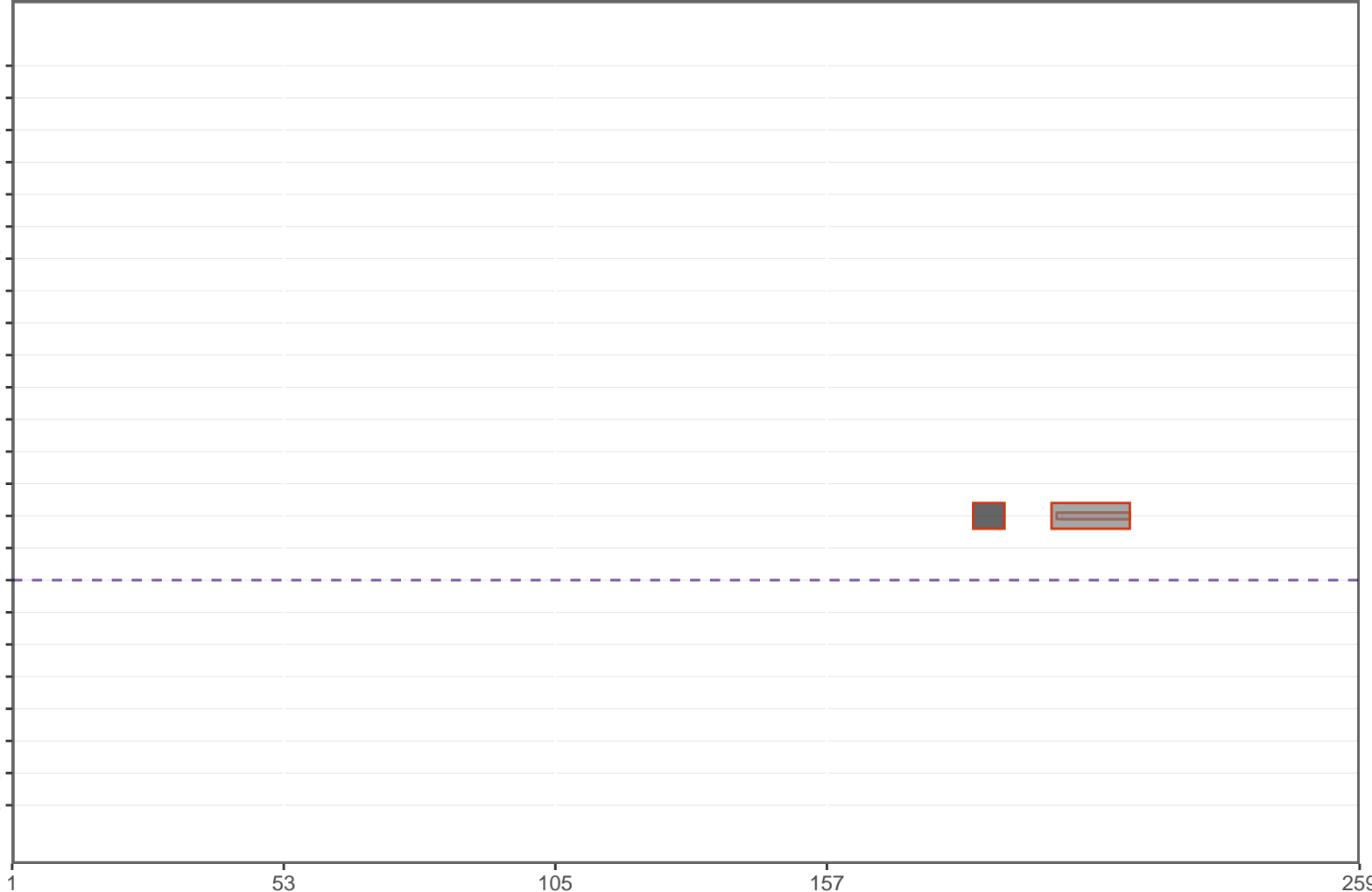
MW indication



Molecular weight



Gel Slice

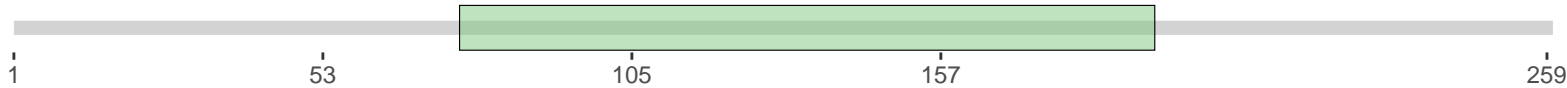


Protein length

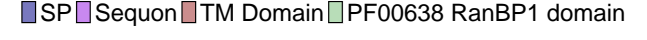


Peptide counts over 4 repeats

Pfam domains



Pfam Description

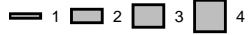


Protein sequence:

ETGKRLVMROSKRLKGVNHLVPTMTVQEHAGSEKSGVWHAADFAGELKDEFFRIRFASIEGKTFMETFRREVAESGKMKKKNEDASNAAGLLEKLSVEDKKSSEKVEKAEKTKEDDVKDAKPSDIAEKRDETASD

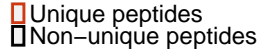
NbL11g03790.1 ERBB-3_BINDING_PROTEIN_1 [MW = 42.75 kDa]

No. of times detected

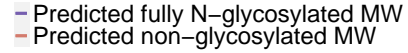


log(intensity)
3.1 5.4

Values from



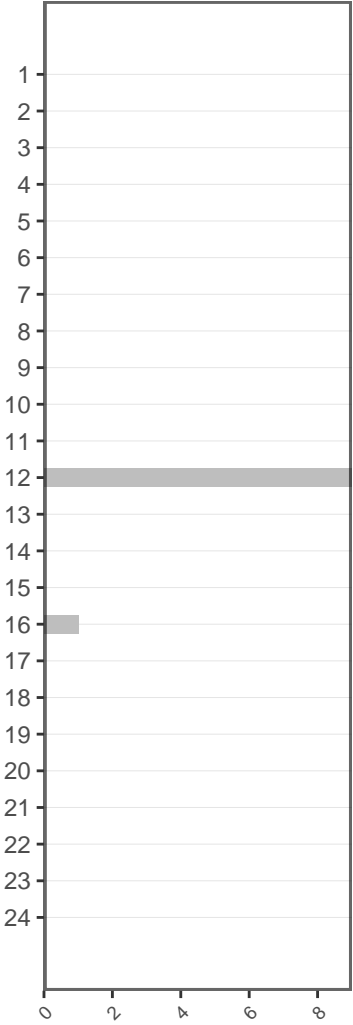
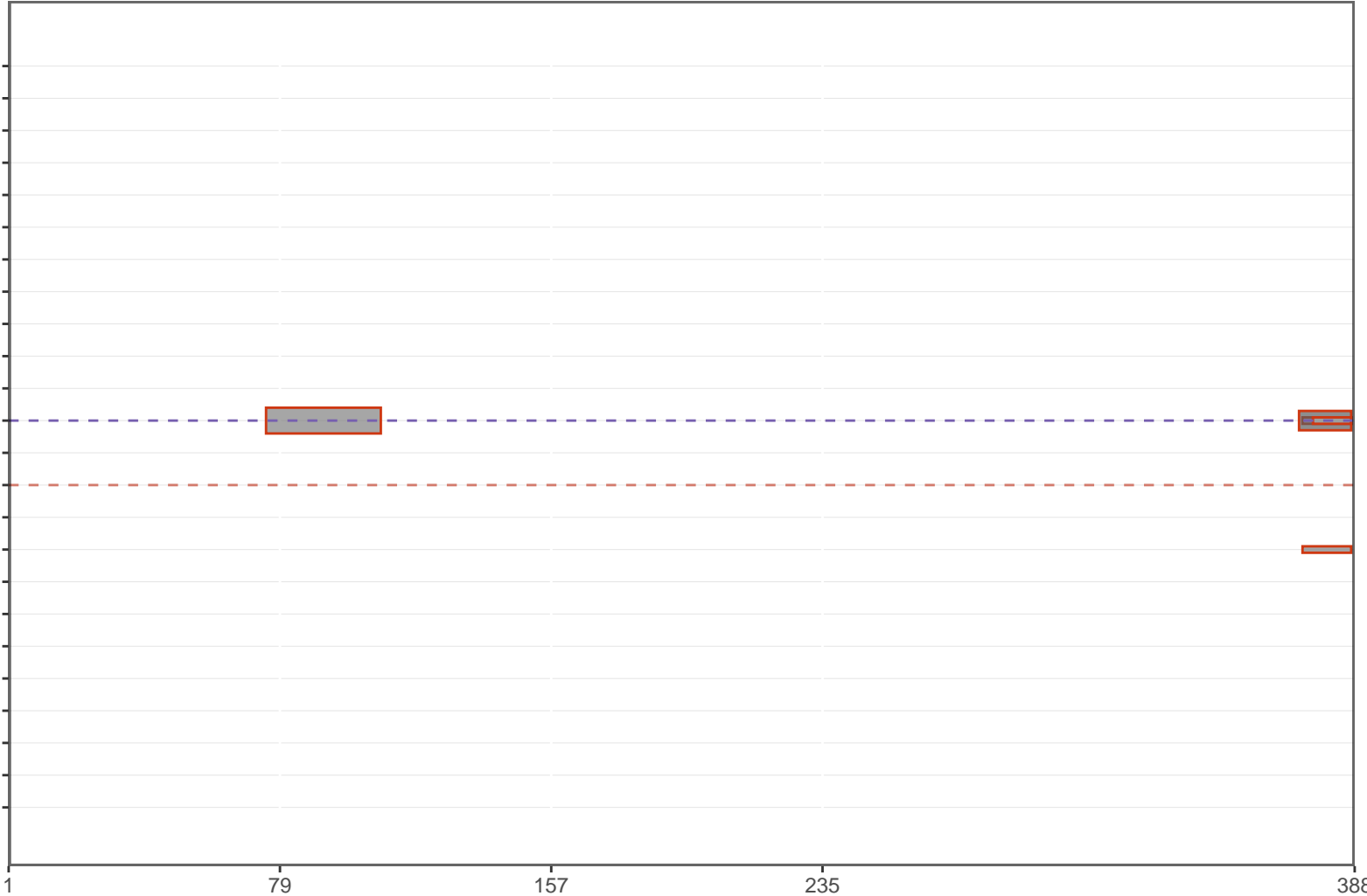
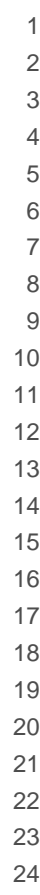
MW indication



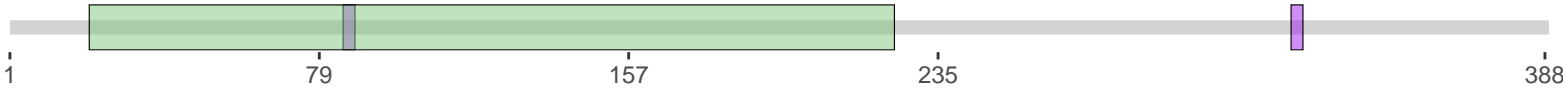
Molecular weight



Gel Slice



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SVLSHQMKQFYIDGNKVLVGVINPETRVDEAEFEENEYVSDIVTSTGEGKPKLIDKGTIYKRAVDKSYNLKMKASRIFSEIGKFPMPFTARDLEEKRAKRLGLVEGVNHELGPYVPLVHEKPGDLVAHKFTVLLMPNGSDRVTSHALQELKTKAKTIENEPEIKAWLALPKTKKKGGGGKGGKGGKDKTEDSSQAEPTEG

NbL11g03670.1 probable_pyridoxal_5'-phosphate_synthase_subunit_PDX1 [MW = 33.12 kDa]

No. of times detected



log(intensity)



Values from



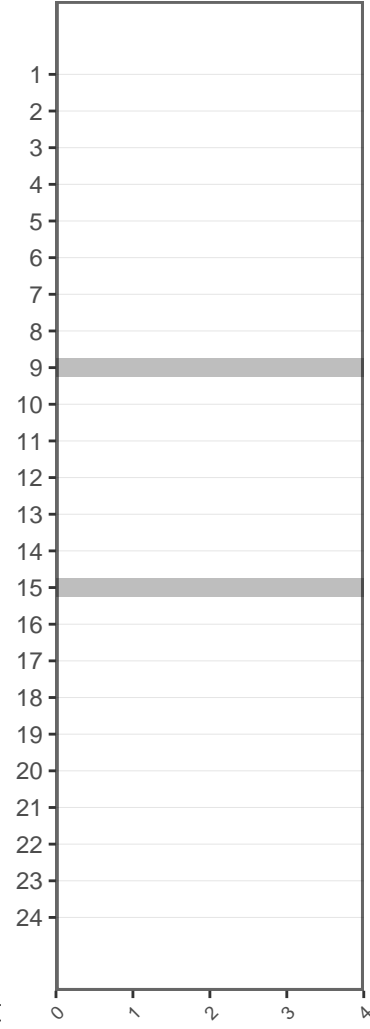
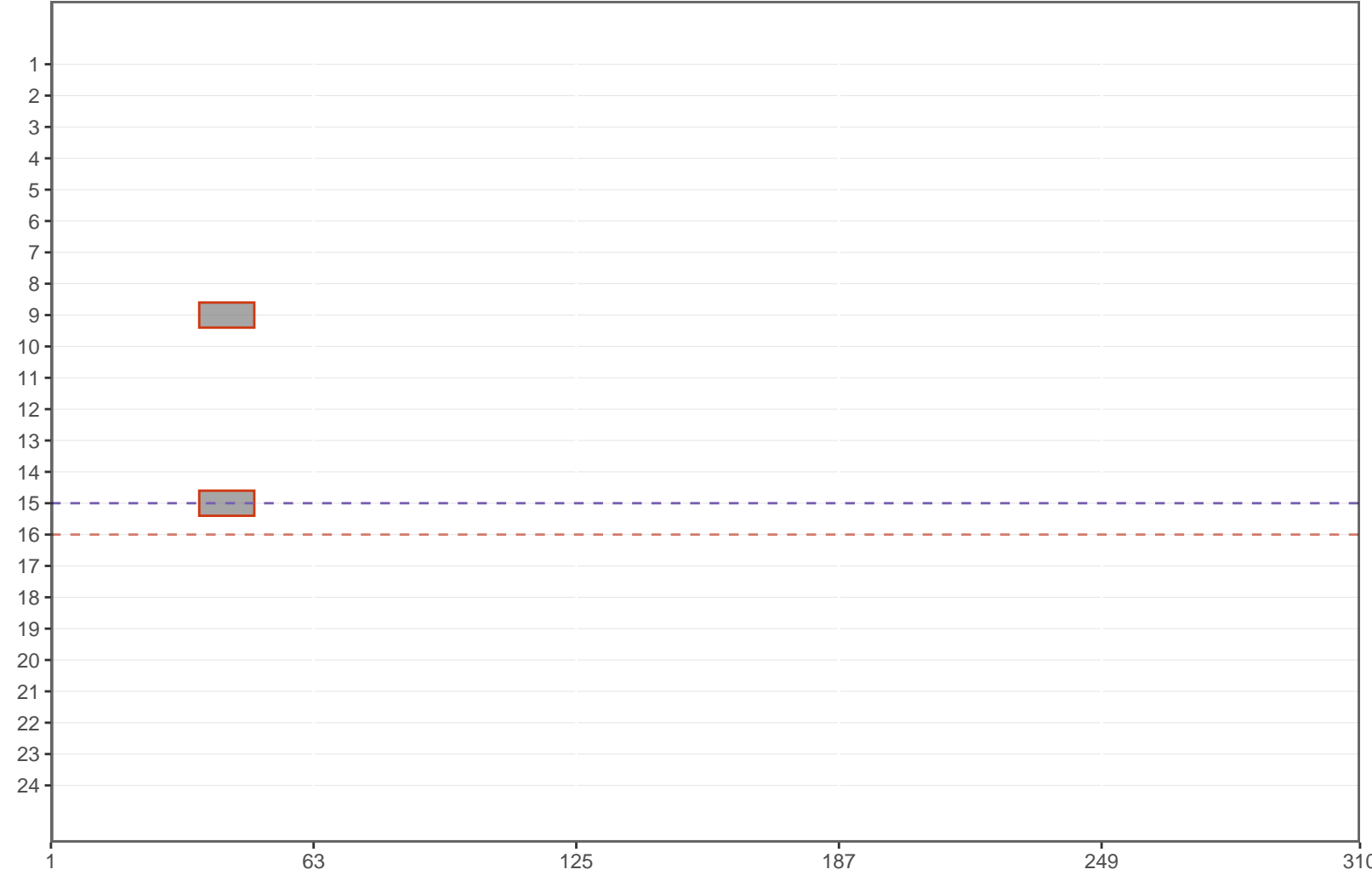
MW indication



Molecular weight

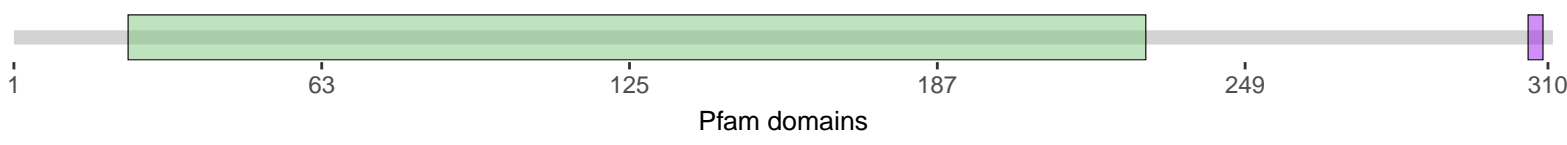


Gel Slice



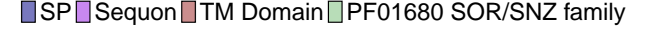
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CCCRNLGELRRIRREGAMIRTKGEAGTGNIEAVRHVRVMDGDRVLRNMDDEVEFFAKRLGAPFDVDMGTKQLGRLPVVFHFAAGGWATPDAALMMLQGGDGVFVSGGIFKSGDPAKRGRAIVQAVTHYSDPQLLAEISGGLGEAMVGINLDDKVERYANRSE

NbL11g03580.1 uncharacterized_LOC107793146 [MW = 12.17 kDa]

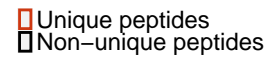
No. of times detected



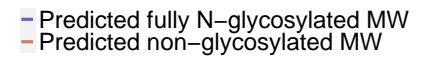
log(intensity)



Values from



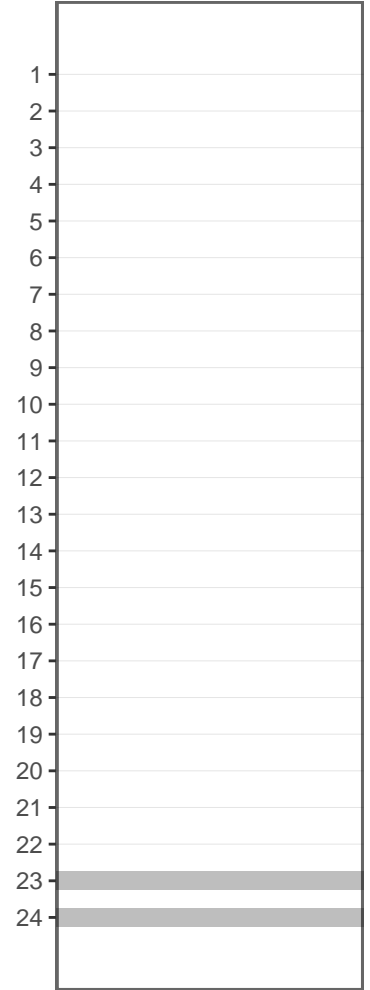
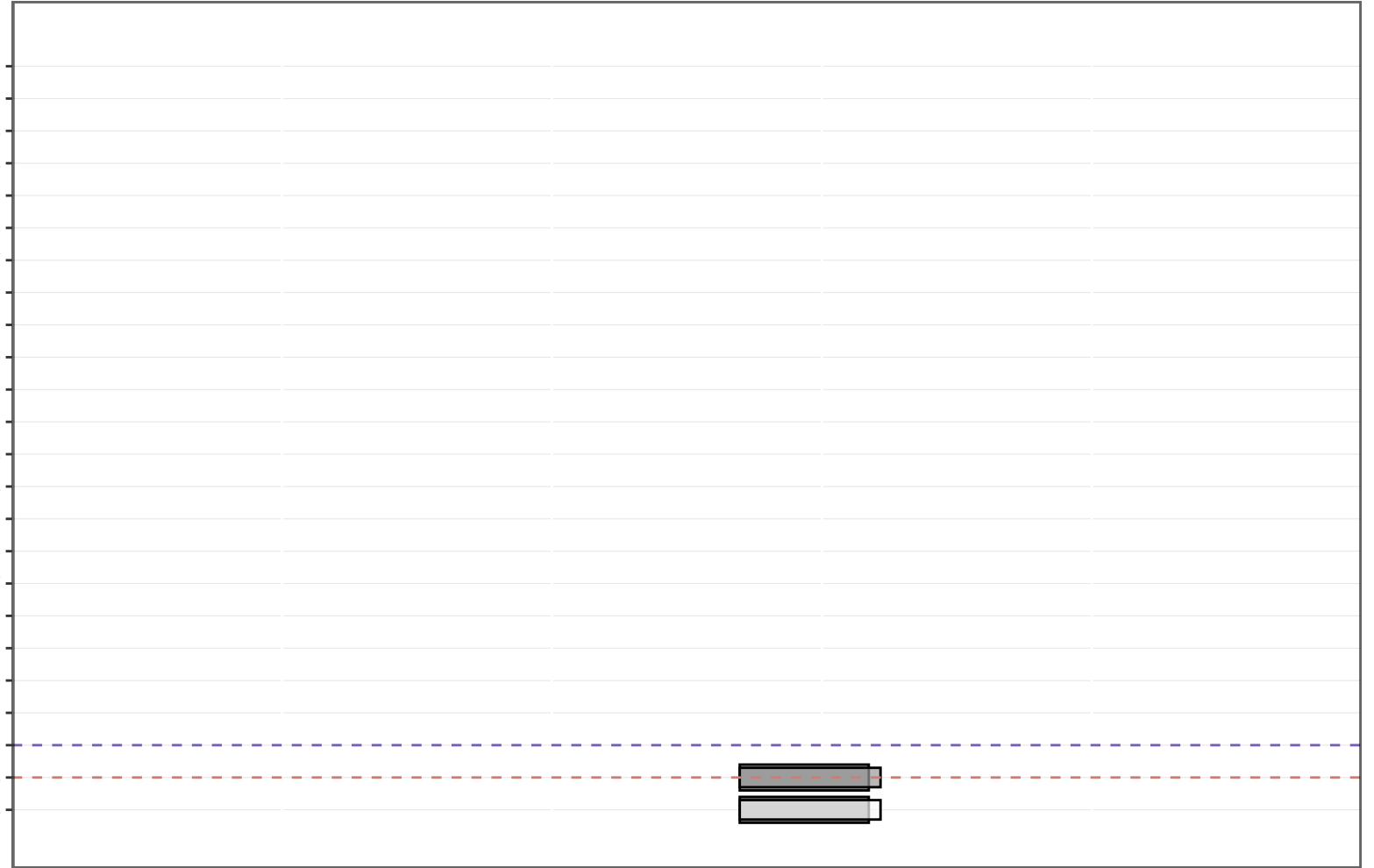
MW indication



Molecular weight



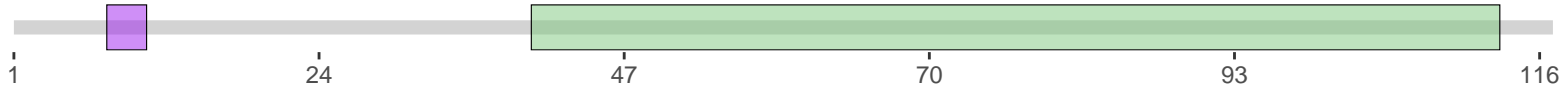
Gel Slice



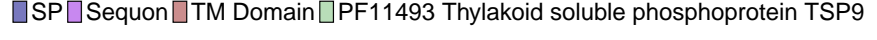
Protein length



Pfam domains



Pfam Description

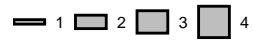


Protein sequence:

SSEKSLDLFILGSLQKEDGALLEVDPIKAKVEDKGVGTFSRGKNSVAVFPKKNNSGGGFGGGLFAKKD*

NbL11g03560.1 beta-glucosidase_BoGH3B-like [MW = 65.76 kDa]

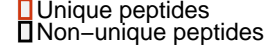
No. of times detected



log(intensity)



Values from



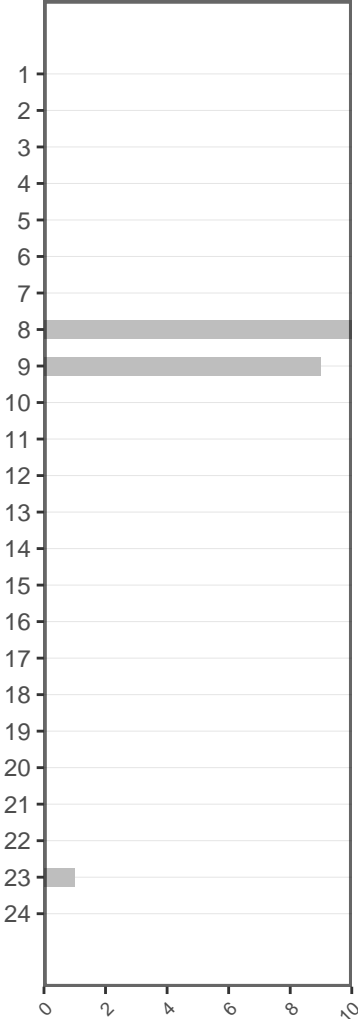
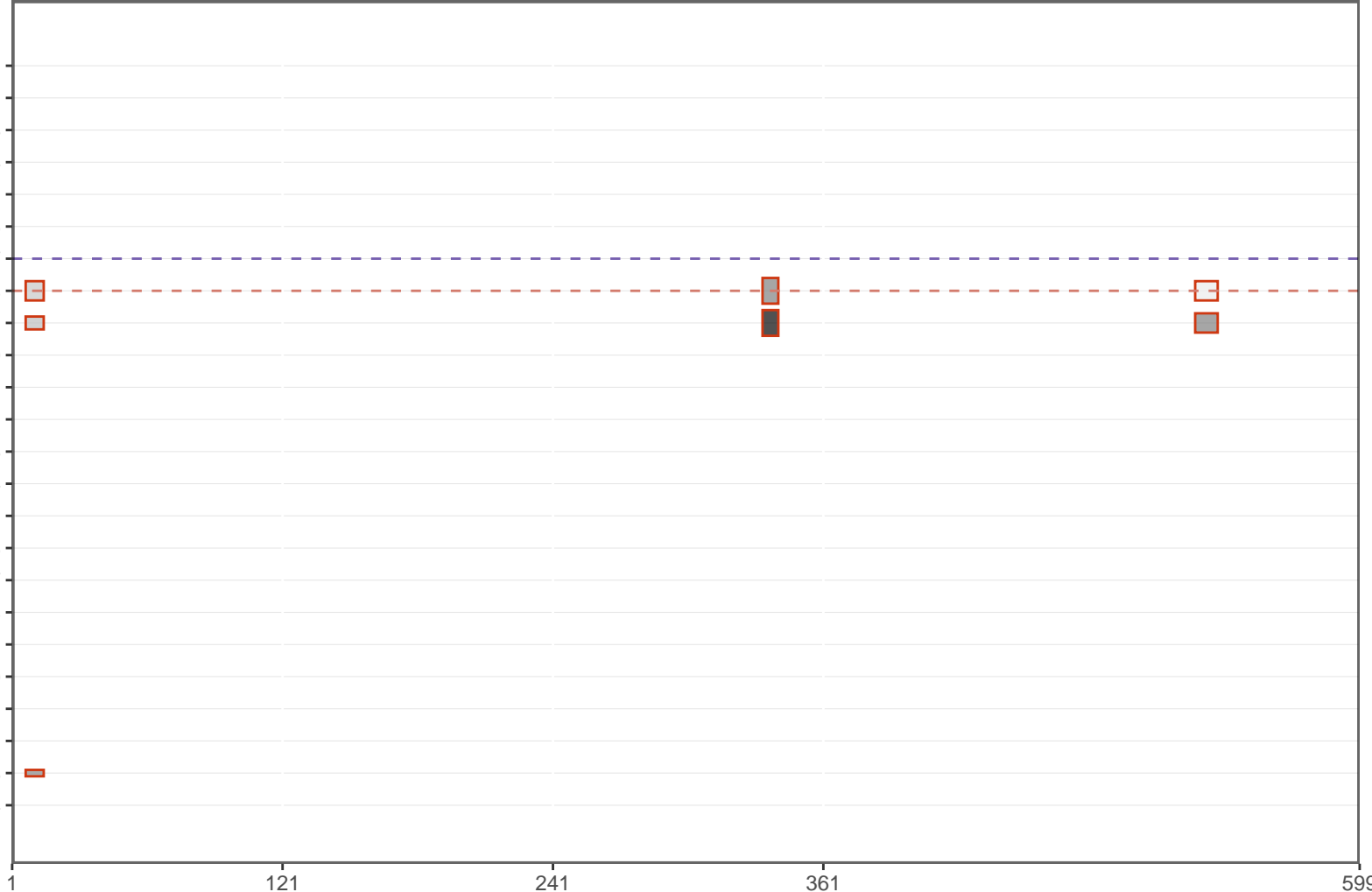
MW indication



Molecular weight

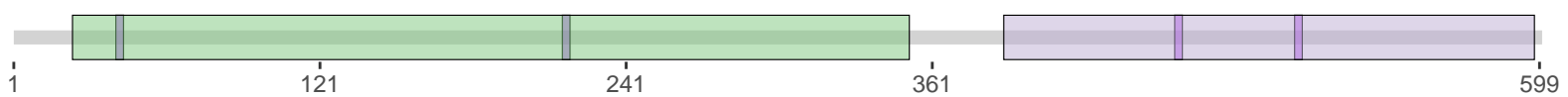


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

SP Sequon TM Domain PF00933 Glycosyl hydrolase family 3 N terminal domain PF01915 Glycosyl hydrolase family 3 C-terminal domain

Protein sequence:

ITWEALDRLTDPHGSDVRSKSTINAGIDMVMVFRYELFLEELLGLVKSQSEISMTRIDDAVERILRKFVAGLFEHPTDRSLLELVGCEAHRELAREAVRKKLVLLKNGKDPKPLFLDRNANKILVAGTHADDLGYGGGGWTATWTGSGRITVGTLLLEALRKLNGTEVFEFNPPTTETTFANQGEFSFAVAIGSEPGYGETGGDDPELKFNFNGTEATEFVADRVPPTVTLISGRFMAVLEPBLFEKVDFAVAWLPGETGTGTFDVLFGDPFPGKLPVTVFKTVVDLPMU

NbL11g03500.1 acyl-coenzyme_A_thioesterase_13-like [MW = 17.11 kDa]

No. of times detected



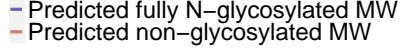
log(intensity)



Values from

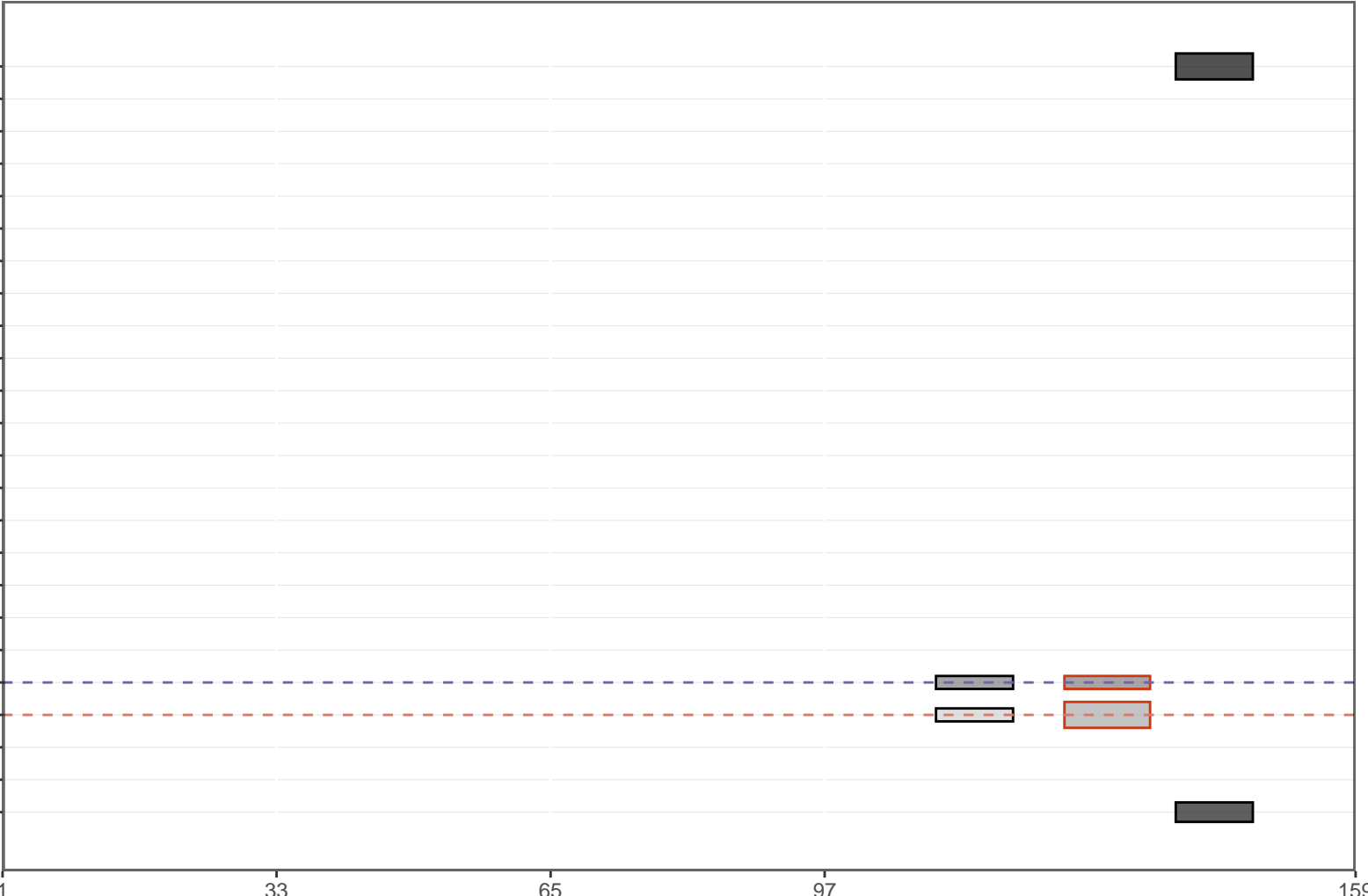
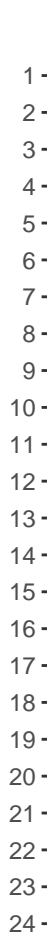
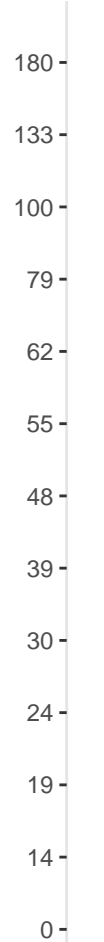


MW indication



Molecular weight

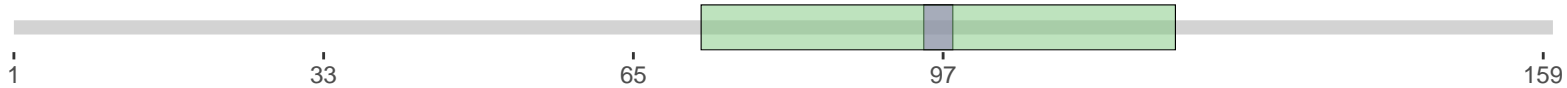
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

EQKLASGAIANLYDEVGGAVFVEGLPMNVVDMSIFLSAKADDELEHGRVLAGQKGGYSGTNVLMKMKATGELIAEGRHSLFGKHASKM

NbL11g03460.1 proliferating_cell_nuclear_antigen [MW = 29.23 kDa]

No. of times detected



log(intensity)



Values from



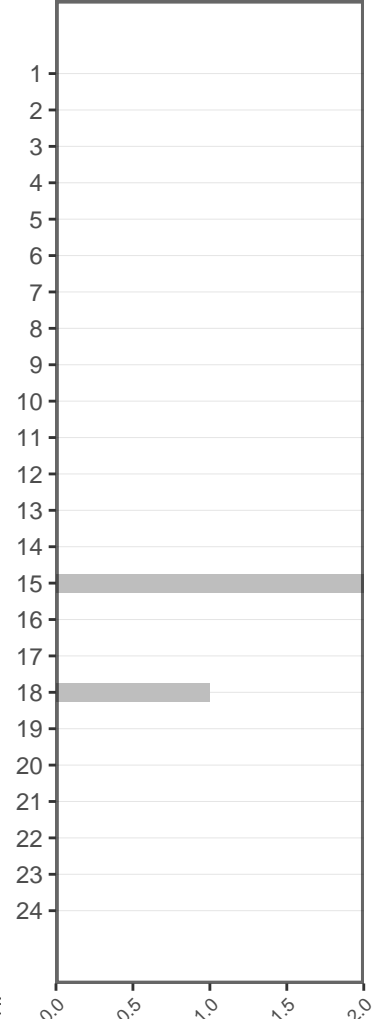
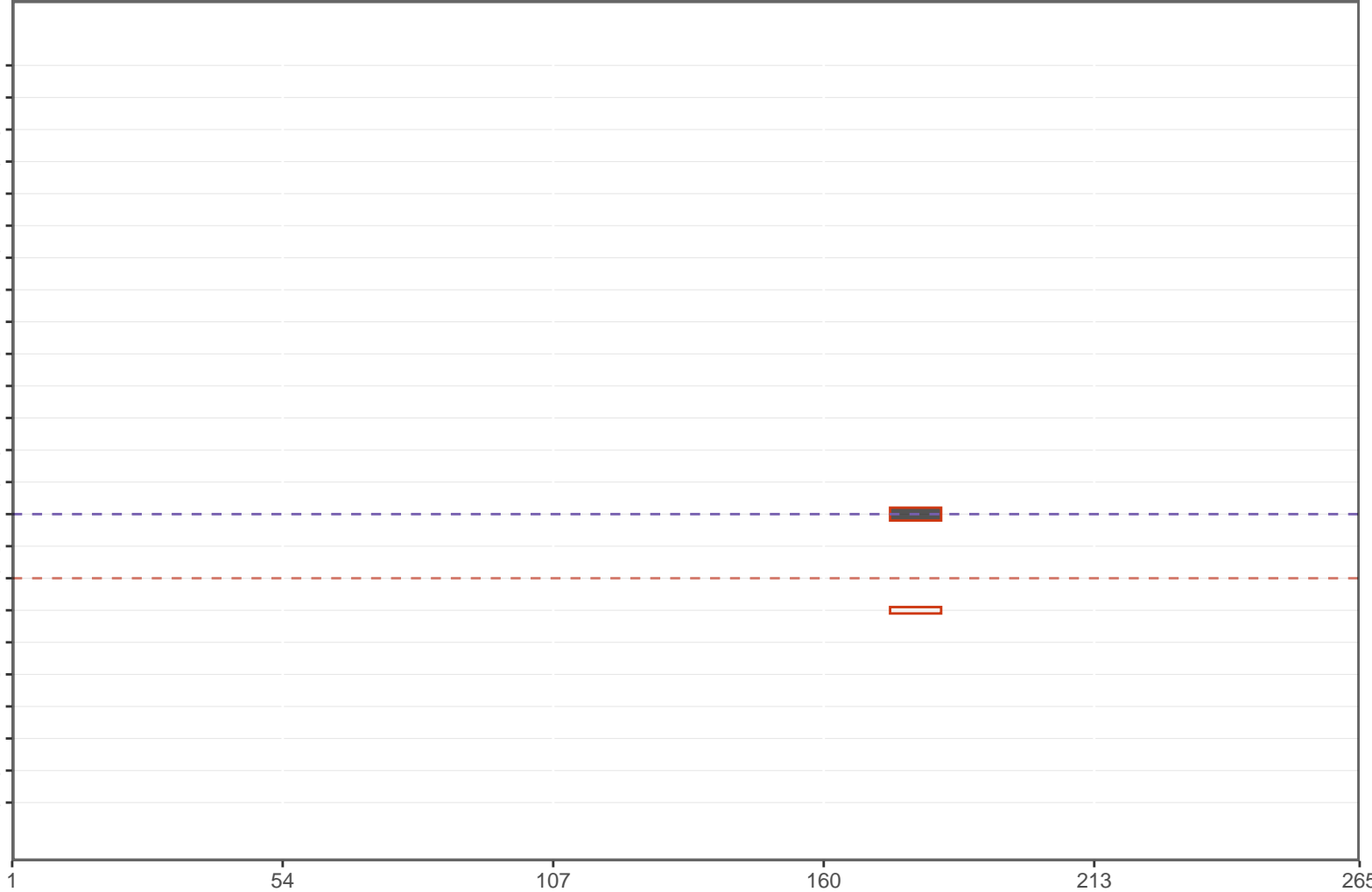
MW indication



Molecular weight



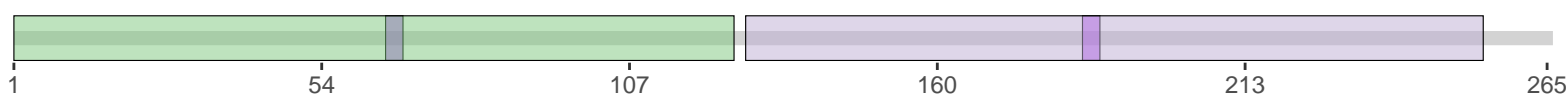
Gel Slice



Protein length

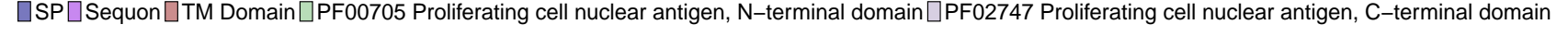


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KLMDIDSEHLGPEAEYHAIIVRMPAEAFARICKDLSSIGDQTVVIVTKEGVKFSTROGDGTANVVRGNITTVDKPEEATVIEMNEPVLSTFALRYLNSFTKATPLGNITVTSLSSELPLVVVEKKAEMGVIRFYLPKRIEEDDEETKP

NbL11g03450.1 cytosolic_enolase_3 [MW = 51.62 kDa]

No. of times detected



log(intensity)



Values from



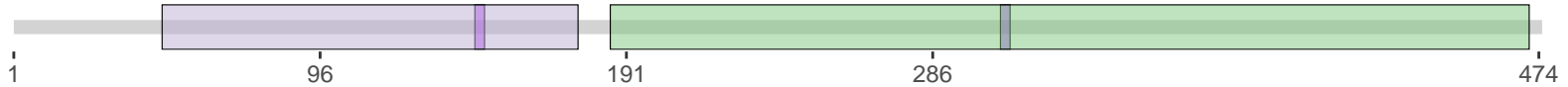
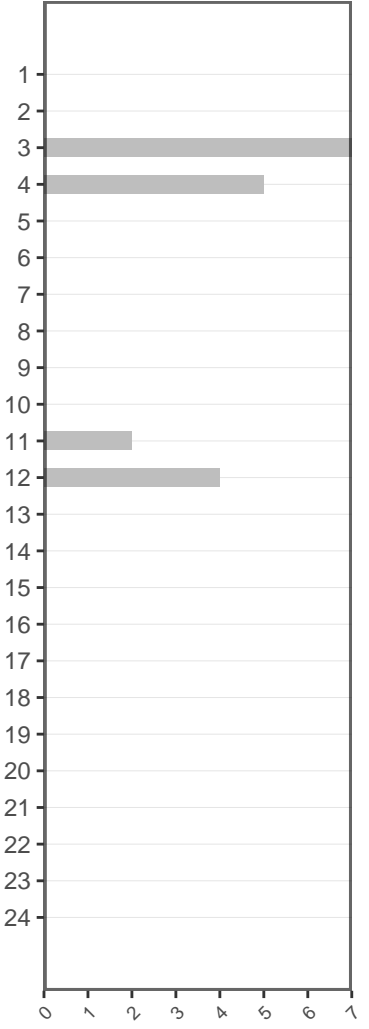
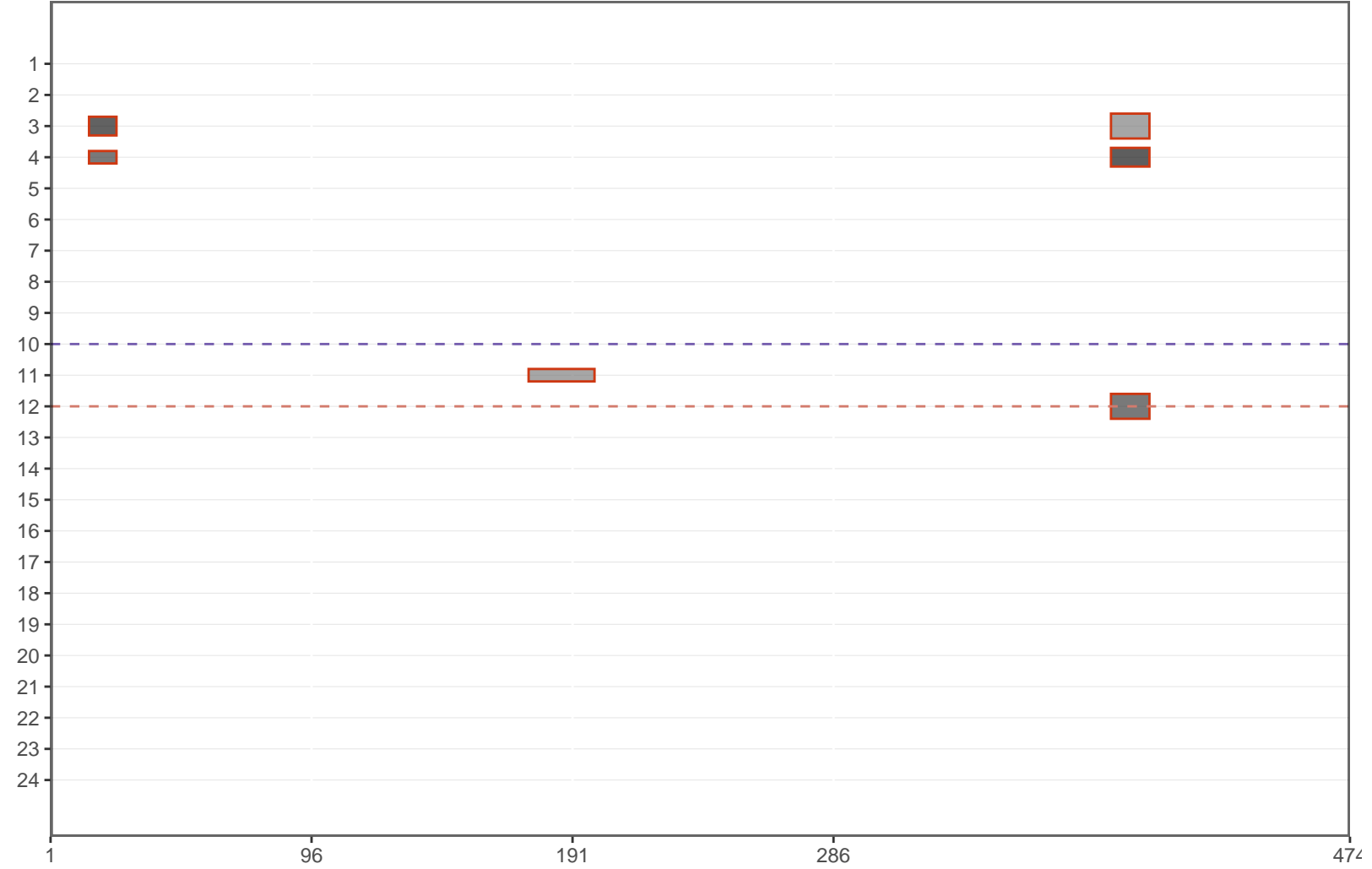
MW indication



Molecular weight

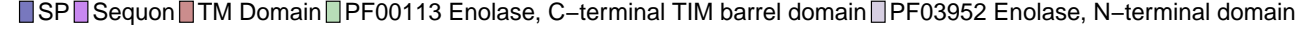


Gel Slice



Pfam domains

Pfam Description



Protein sequence:

IGSETYHHLKVVITEKYGARGNGVEDGGFAPDISLRDGLDLVAIGRTGYKEKIAIGVAATEFCIGTRVYDLDFKTPNKSGGNFKSGQDMDMYKELCADYVPVSIEDPFKEDWEHYYFSSLGMGVVDDLLMSNPKRIERAIGENAGNALLKVNQLGTVEAIEVYKMAKDAQWGVVVISQRSGETEDSFIADLSVGLATGGKAGAPRGRERLAKYINQLLRIEQELGDDQAFYIYGEKWRP

NbL11g03440.1 uncharacterized_LOC109226983 [MW = 17.6 kDa]

No. of times detected



log(intensity)



Values from



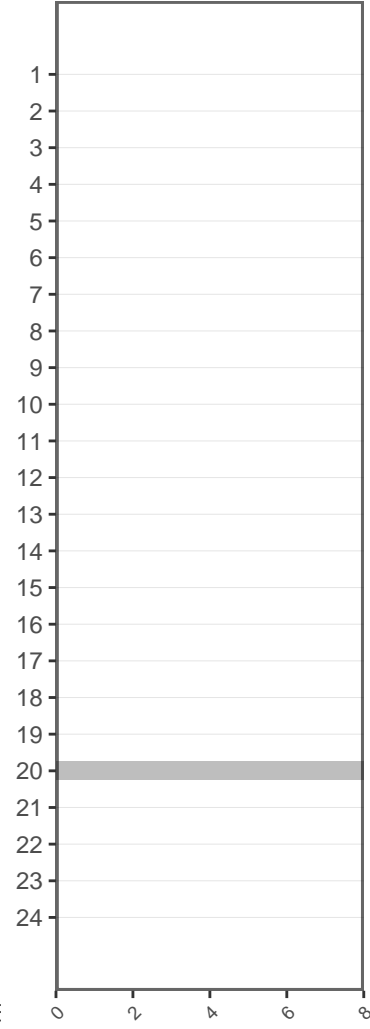
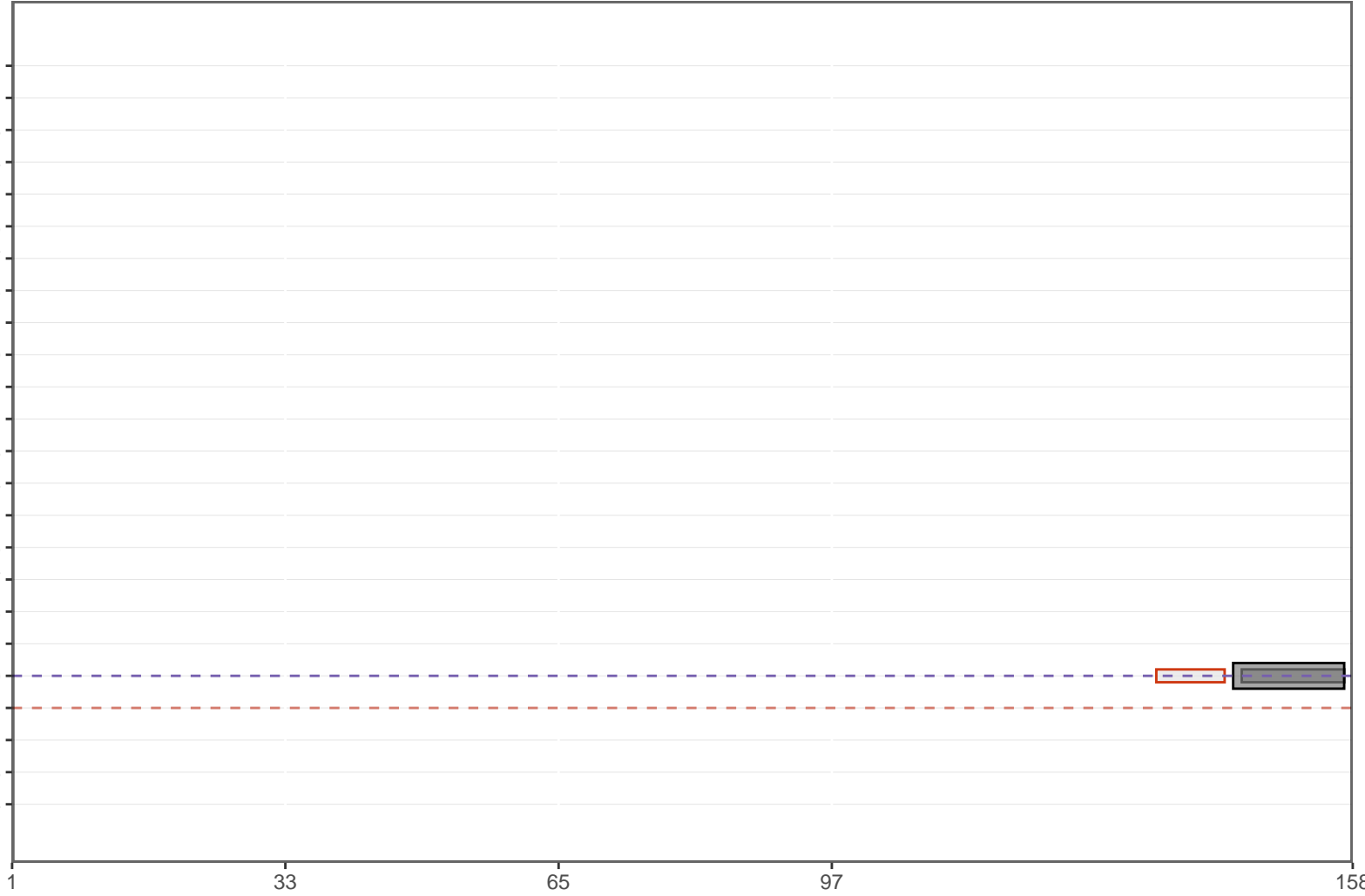
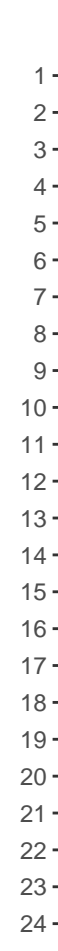
MW indication



Molecular weight



Gel Slice



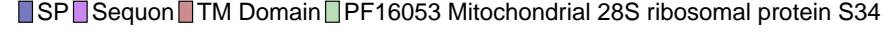
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

NWIGIGYHMAKTHWTFGIEYEIKRNLKNDGRHGKAWGLAYKDGLPADAPKMSGVHKKRWKYNFQKKAEGLDQKKAEESTPNSDVEAA*

NbL11g03380.1 phosphoserine_phosphatase_chloroplastic [MW = 31.94 kDa]

No. of times detected



log(intensity)



Values from



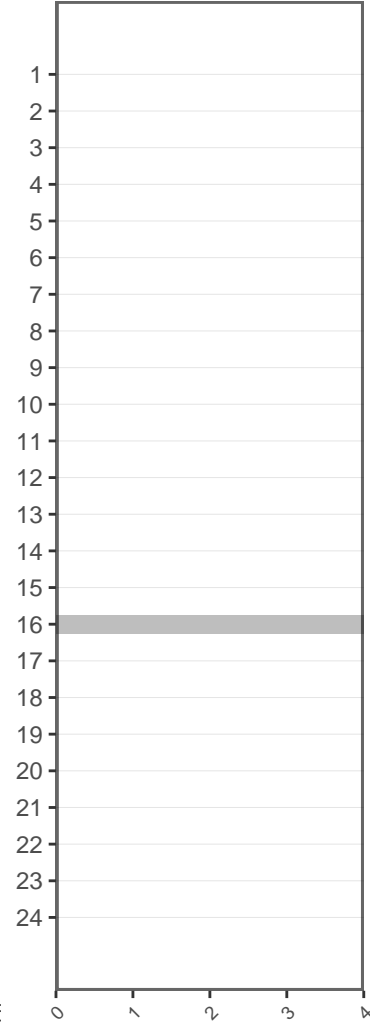
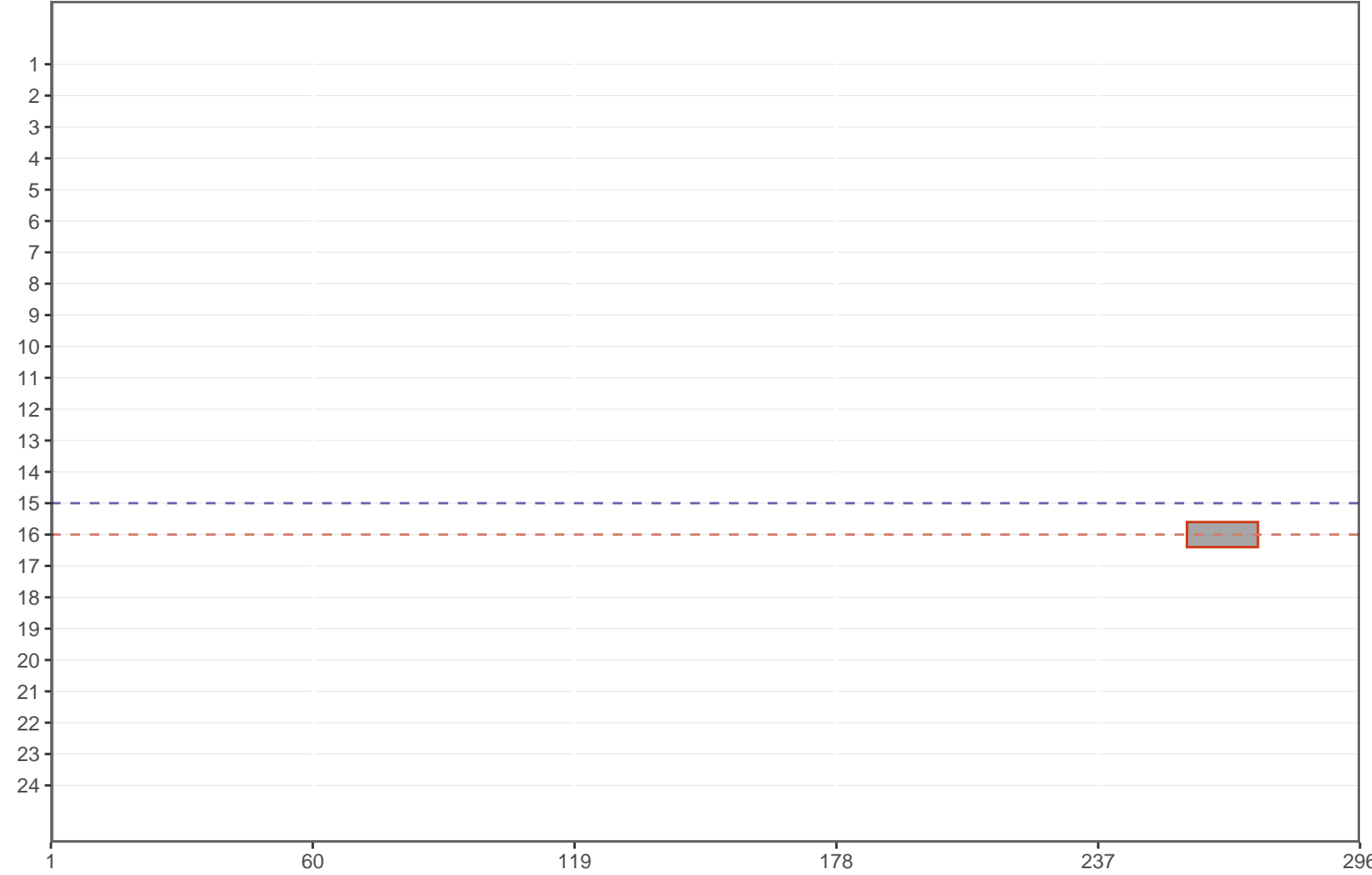
MW indication



Molecular weight



Gel Slice

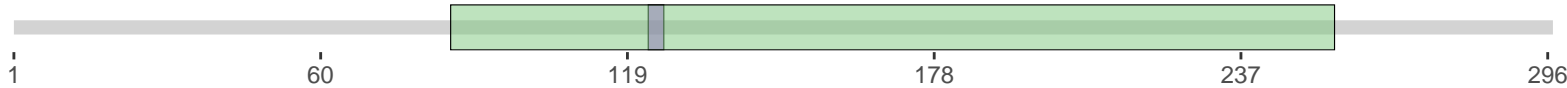


Protein length

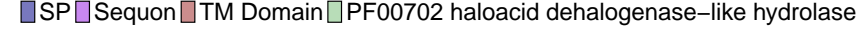


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ARLSLNPSLSQLODFLNRPRLSPGIDLKVKLKDKKKVVYLVGGFRMNPIASLIGLENFANDMLFGSDGEGAGFDKNEPTSRSGGKPTAVQGHKAGGYSVVMIGDGDATLEARMPGGADLFQYGVGGREPAWAKADWLVFNFKDLINLEI

NbL11g03300.1 DNA-directed_RNA_polymerase_II_subunit_RPB7 [MW = 19.55 kDa]

No. of times detected



log(intensity)



Values from



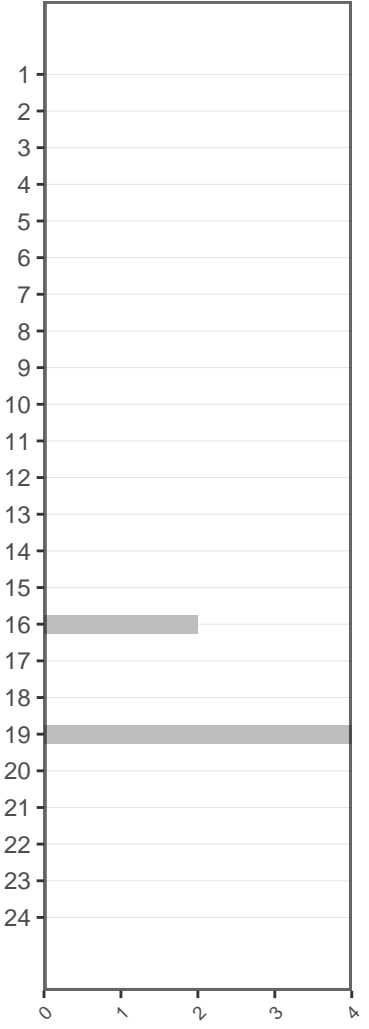
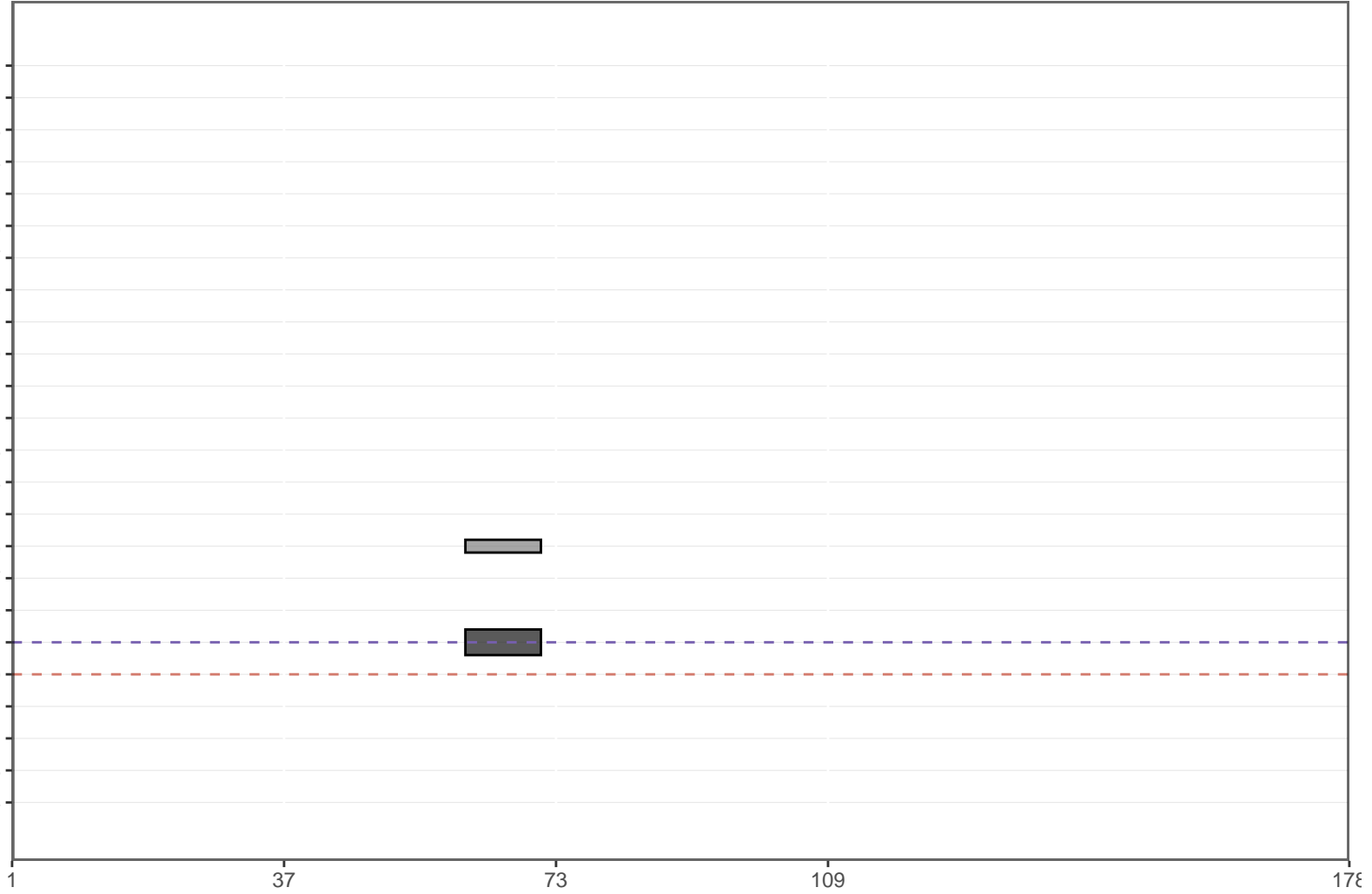
MW indication



Molecular weight



Gel Slice

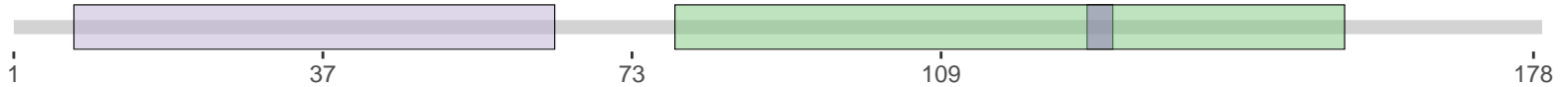


Protein length



Peptide counts over 4 repeats

Pfam domains



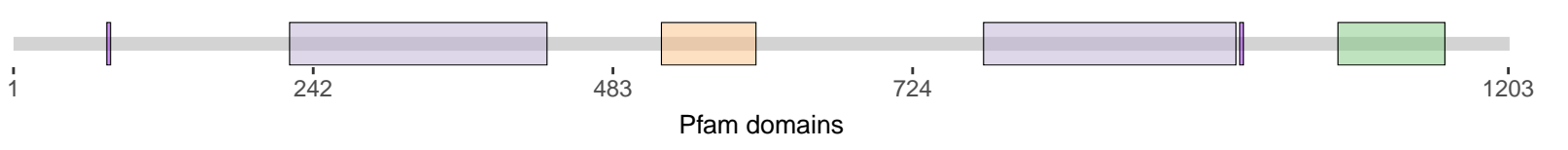
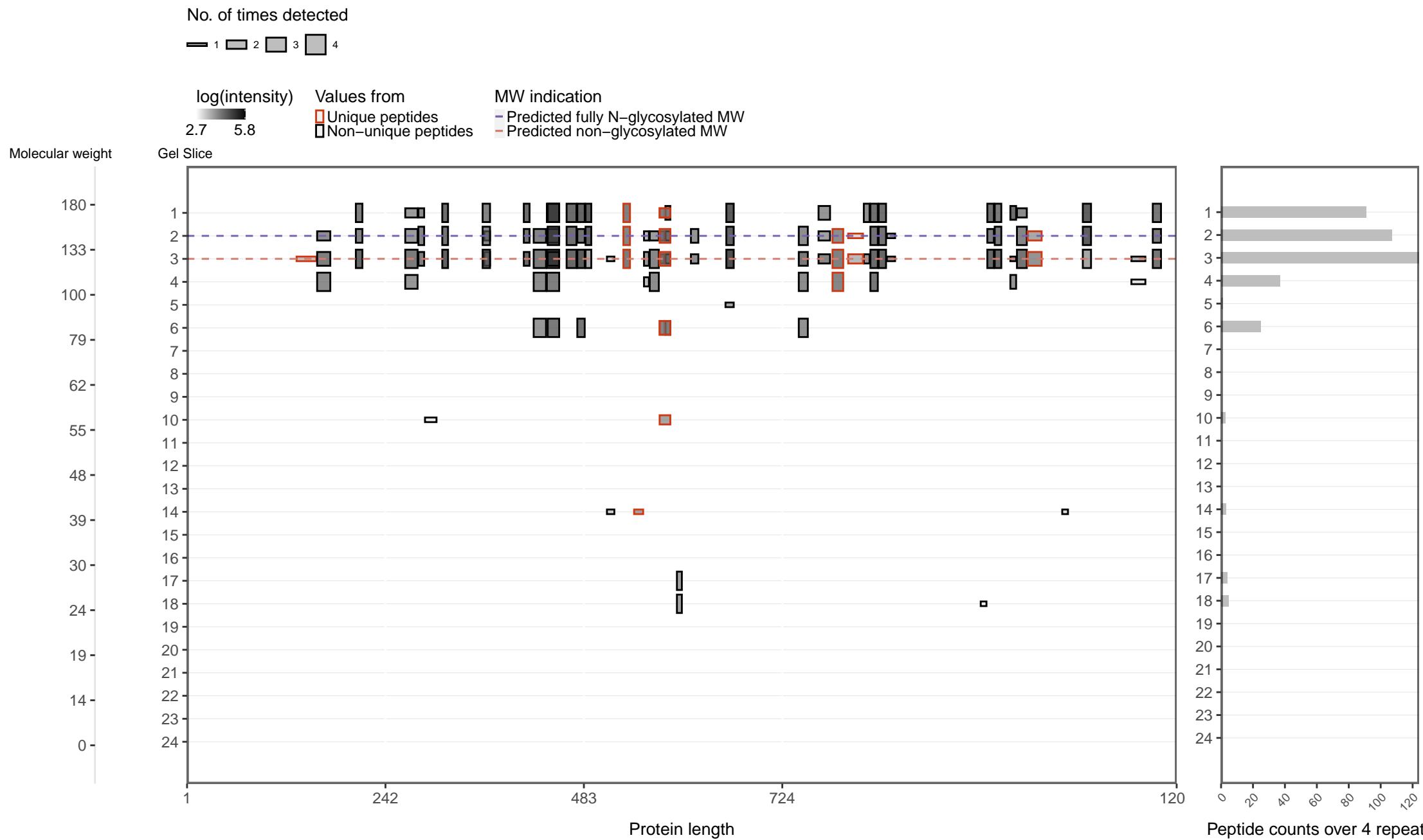
Pfam Description



Protein sequence:

FRFPKGEILEAVTAVNKNVGFFAEAGPVGQFVSNHLIPDDMEFGSGDVPNYTTSDDGSKIKKESVRLKIGTRVDATEIFDGIKDDFLGVISDPGANA

NbL11g03240.1 carbamoyl-phosphate_synthase_large_chain_chloroplast-like [MW = 131.8 kDa]



Pfam Description
 SP TM Domain PF02786 Carbamoyl-phosphate synthase L chain, ATP binding domain
 Sequon PF02142 MGS-like domain PF02787 Carbamoyl-phosphate synthetase large chain, oligomerisation domain

Protein sequence:
 MKRFGSDRQIAFATKSSSEEGVRSRRRLGLGKPKPKRVDTGAAEFEDATPVMYBSVDHECESAPTGNKKVLLGGGPNRIGGGIEFDYCGGHTSFALQDANGYETIMMNSNPETVSTQDTSRDLRYFEPLTVEDVLLNIDLEGDGGIIVFGGGTPLKALPQGNVLDERRPKTRSGAGVIRWGTSPDGGDAADRERFNTILNELGIVGPKGGIAKSENDAVAIEVGYFPAVVRPSYVLGGRAMEVYVNDKLVYLYLENAAKVKVPERPVLIDKYLTVDAVEIDBALDLHGNYVGGI

NbL11g03170.1 L-ascorbate_peroxidase_1_cytosolic-like [MW = 27.94 kDa]

No. of times detected



log(intensity)



Values from



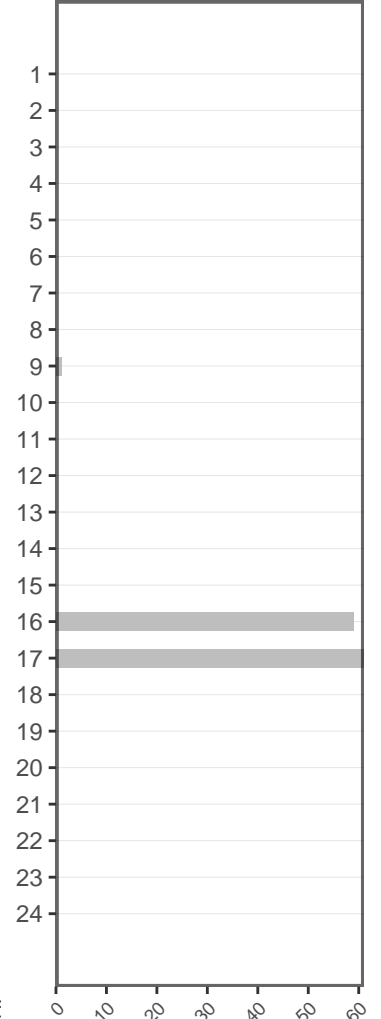
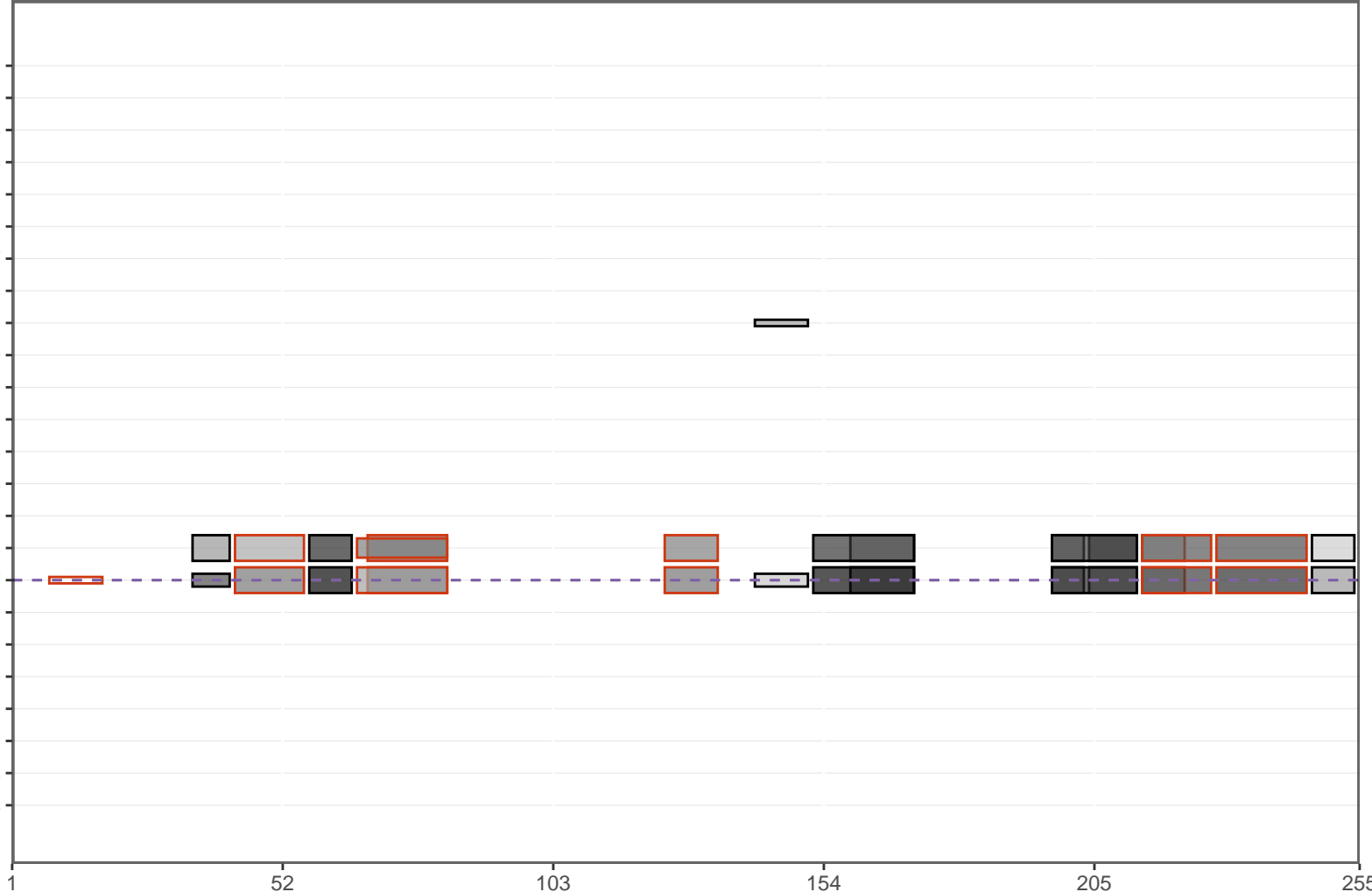
MW indication



Molecular weight

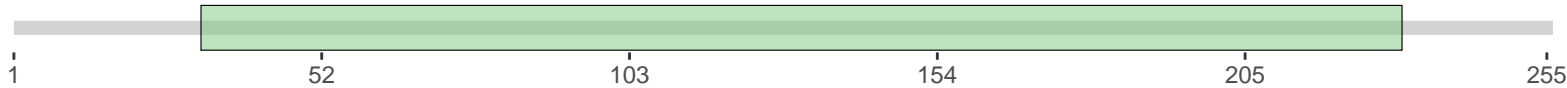


Gel Slice



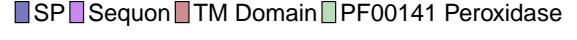
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PDVFFHFGREDKTEPPLLEGRLPQATKGGSDHLREDFVYKGMGLGSDKDIWLSGGHTLGRCHKERISGFGSPWTANPLIFDINSYFKELLSGEKEGLLQLPSKALLSDPVPFRPLVKEKWADEDFADVAEAMKLSLGLFAEA*

NbL11g03120.1 uncharacterized_protein_YKR070W [MW = 45.34 kDa]

No. of times detected



log(intensity)



Values from



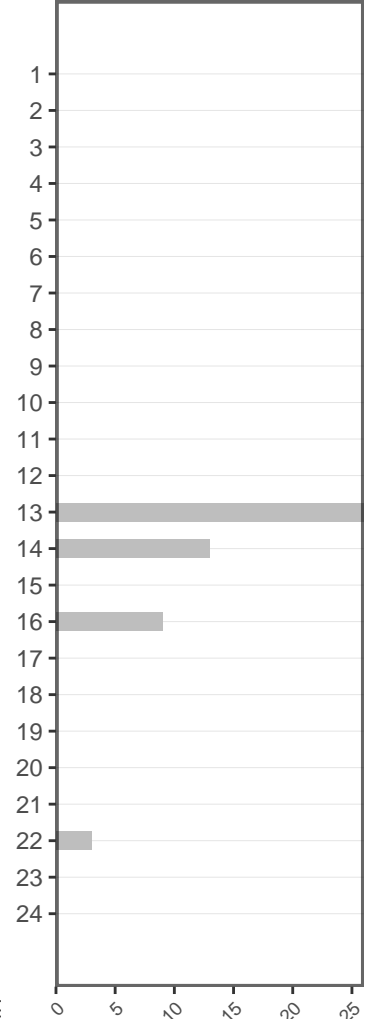
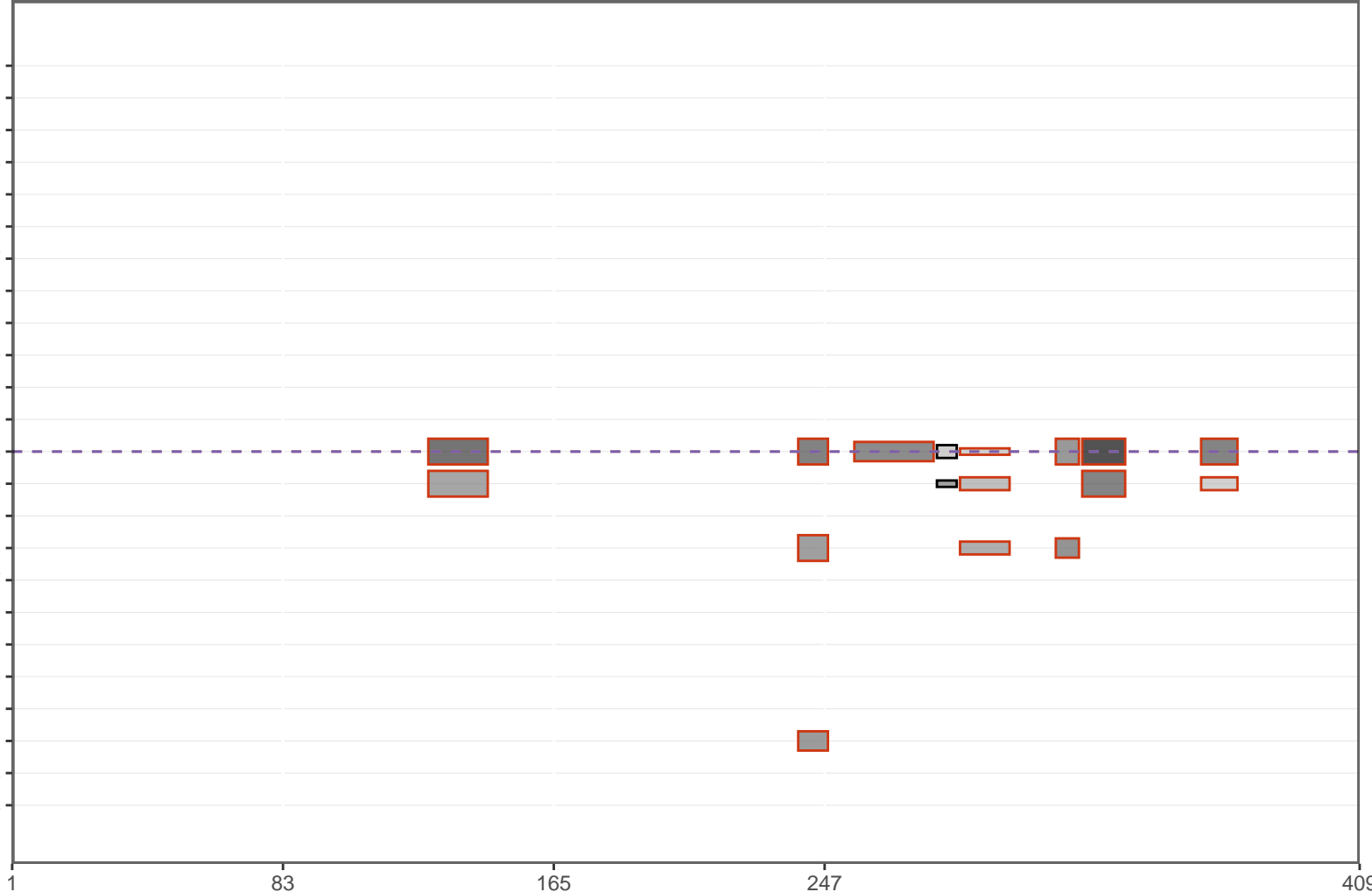
MW indication



Molecular weight



Gel Slice



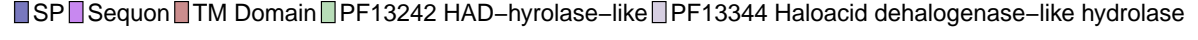
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

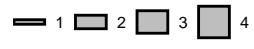


Protein sequence:

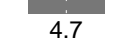
YKKVTTDKDDYVQNSKSKHFAISNDPSSGRVGVAVFVSSDSDWDRDQVLDLRTGGLPKGKIAHQPLFFANDDLAYGALFFSERLGMGAFRALAESVFNAAHPALKYTSYVGPSPFVFNKNAETVLTQVLSGSDGNDGREGQLPKTLVMIGDNPVADKIKGARGAGNPWFSLTRTGVTFKGKENHDDCPADLVDTVEEAVDYLSKEGDS

NbL11g02980.1 aquaporin_TIP1-3 [MW = 25.89 kDa]

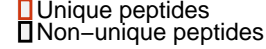
No. of times detected



log(intensity)



Values from



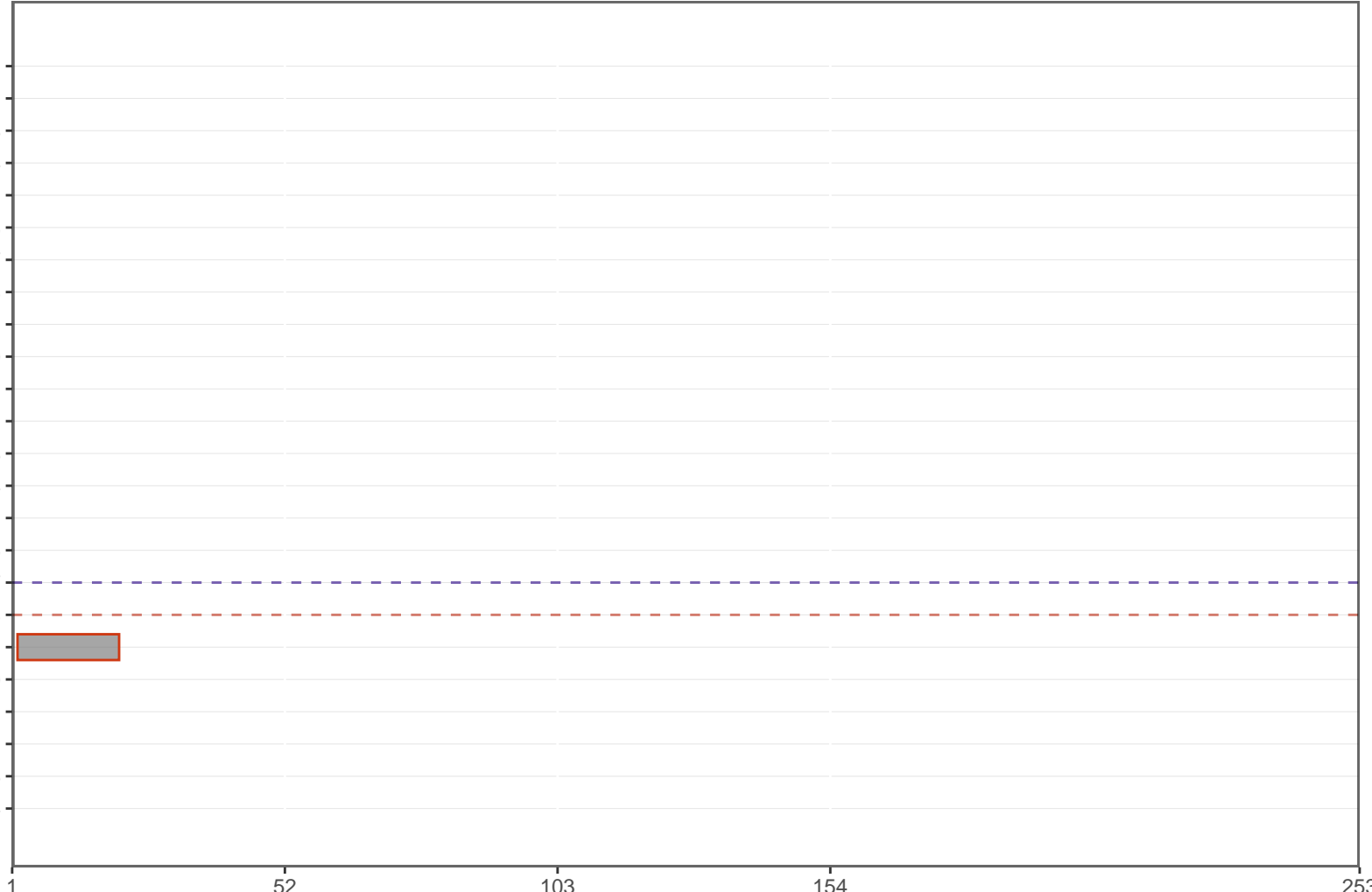
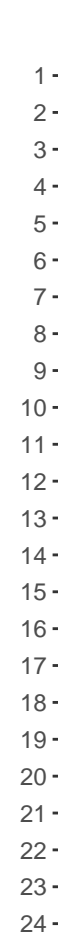
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ISVACVLLKFKATGGLETSFAFALSTGVTPWNAVFEIWMTFGLVYTYVATVDPKRGNGIAPAIQGFVGNLNLGGAFDGASMPKAVSFGPWVGVWTVNCHHWVWVWLGFPVGAIAALVVEIFIGDNTHEQLPTADK

NbL11g02900.1 uncharacterized_LOC104240093 [MW = 89.21 kDa]

No. of times detected



log(intensity)



Values from



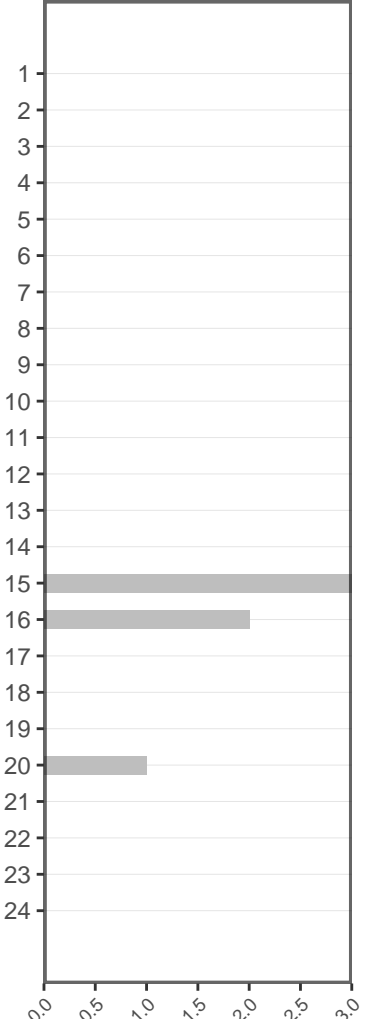
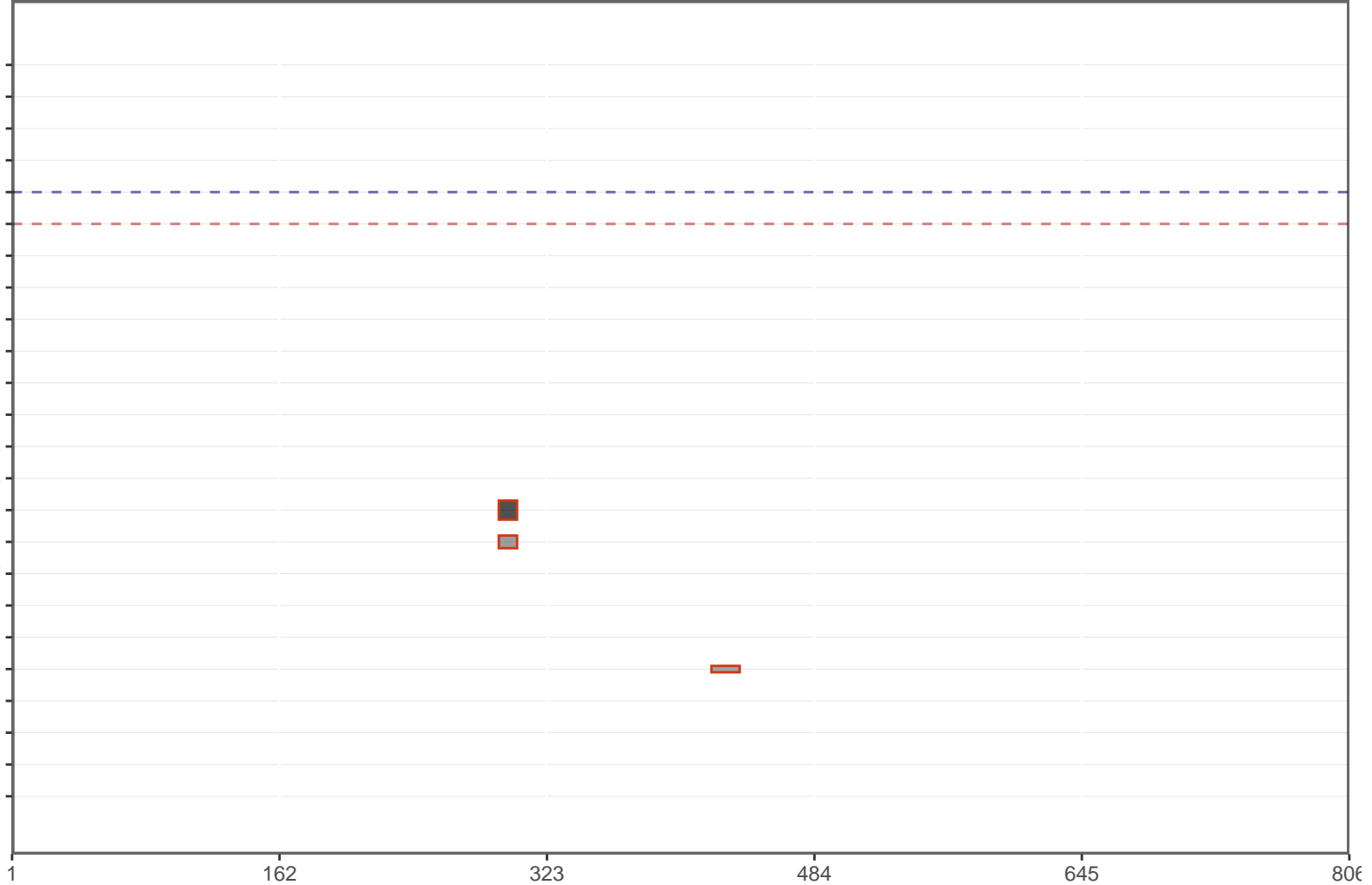
MW indication



Molecular weight



Gel Slice



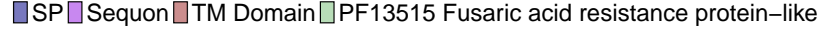
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SITINKRFMFAFKGSLGLGLALFGSHKENGFEWAGLFWAVSLAGAREASPKWVWYKADGTVALGSHYGLGGFVFEKYVQRFLGLLFWFVSSFLRQSKMYGQAGGSAVGVVILGRKGFQPPSEFAIARITETFTGLSGSIMEVILLQPTTRASTLKLQLSKFEILHEGIGSIFGSLGNLVETQNKLKFHNKMKKFGFGEAEAEPNVWFVFPNSAGYRKLMSGLSKMVDGLYFGDAILFDEEGGIDNFVWKTFLNKLDAQFMFKDFGSGFMKGFEEVSLVXSLAVLDKI

NbL11g02880.1 uncharacterized_protein_Mb0911c [MW = 15.36 kDa]

No. of times detected



log(intensity)



Values from



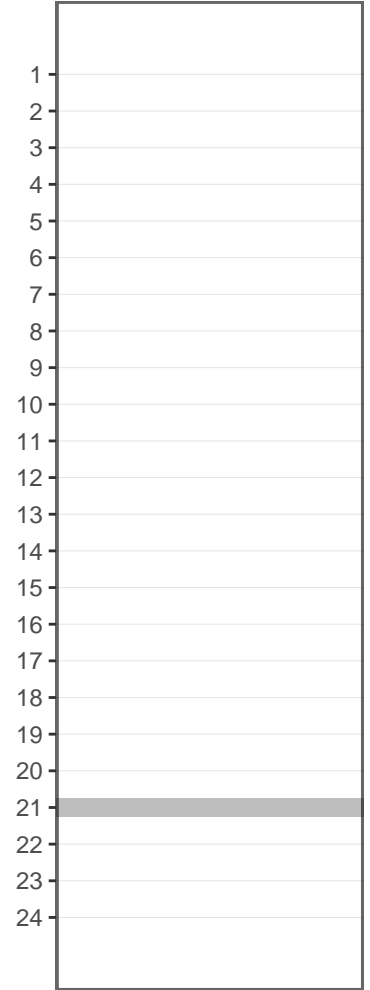
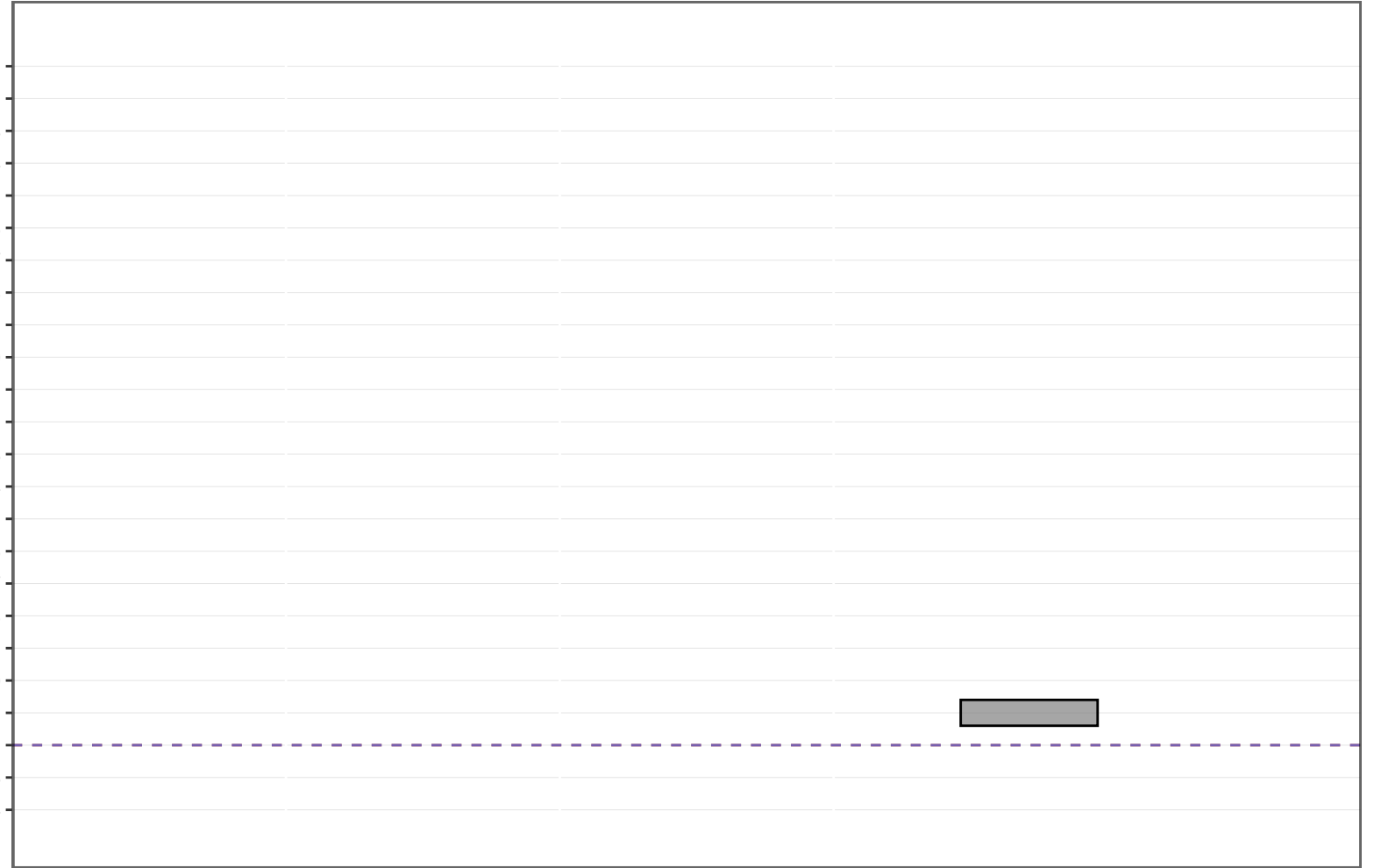
MW indication



Molecular weight



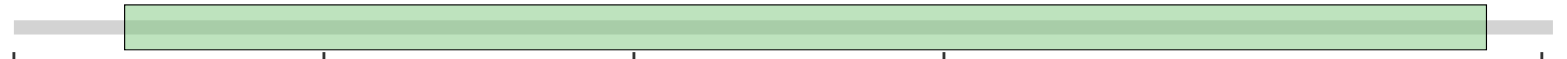
Gel Slice



Peptide counts over 4 repeats

1 29 57 85 139

Protein length



Pfam domains

Pfam Description



Protein sequence:

1HQHETDLDLTGQVDTFHRGRDRGPELGFDFVDDIAAYKRAVENGAWAVSQPEEKWGGKVGYYRDLGDNIVRLGSHVDPK*

NbL11g02850.1 heat_shock_cognate_70_kDa_protein_1-like [MW = 61.37 kDa]

No. of times detected



log(intensity)



Values from



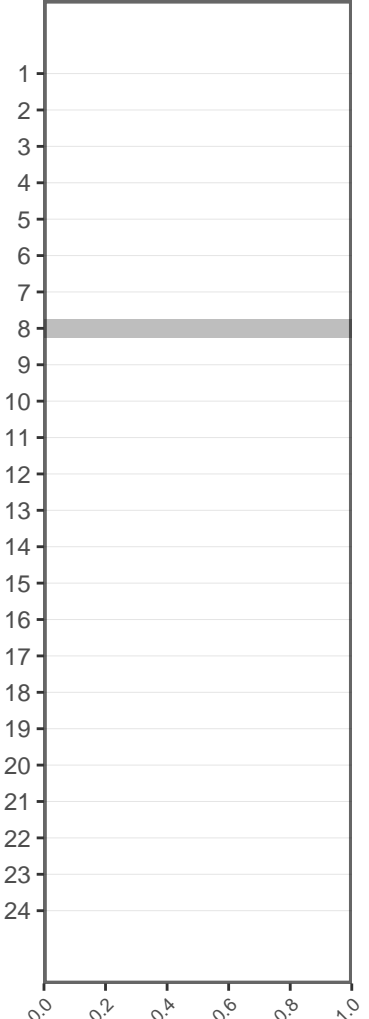
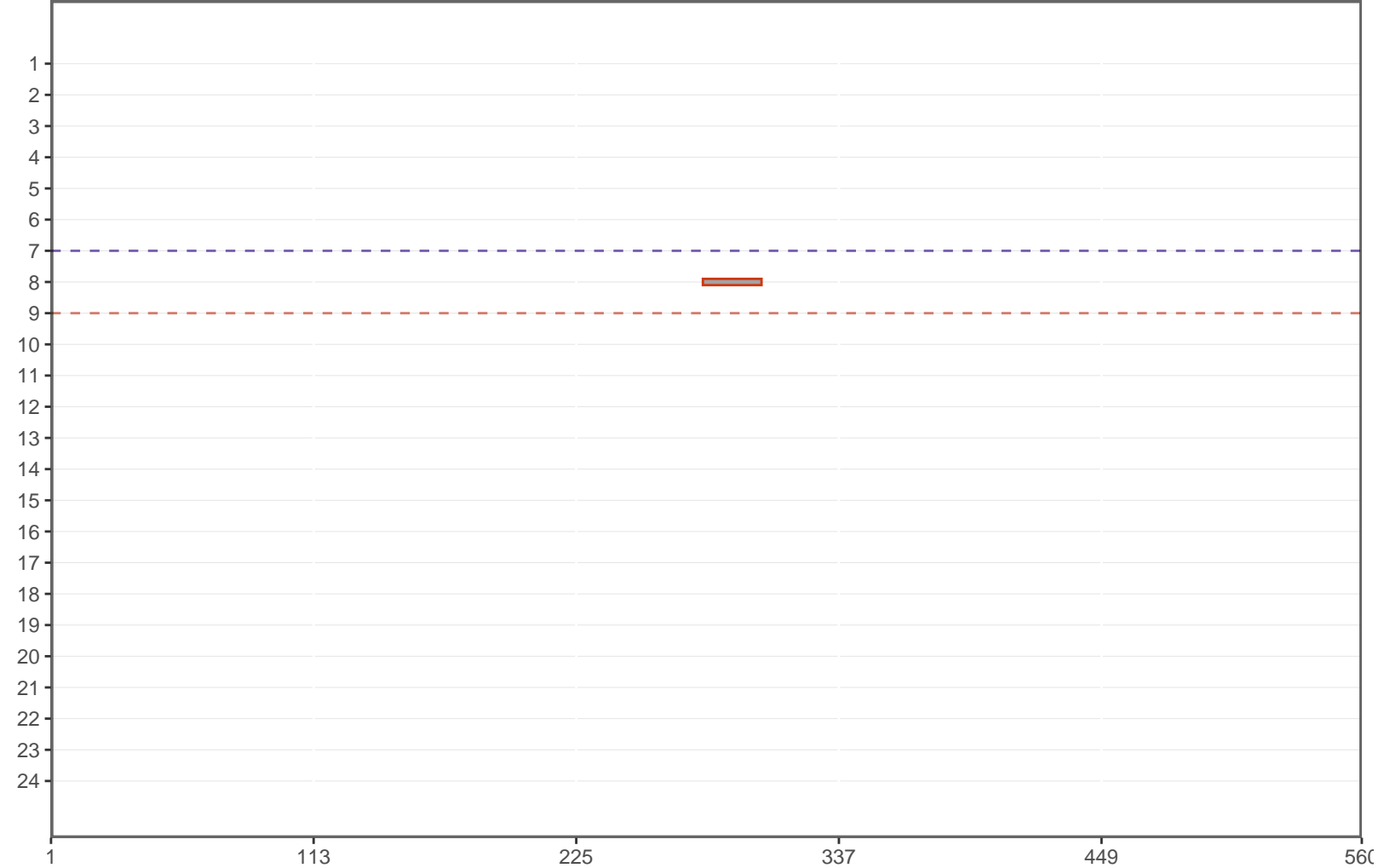
MW indication



Molecular weight



Gel Slice

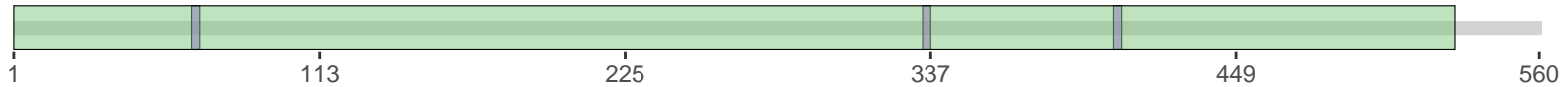


Protein length

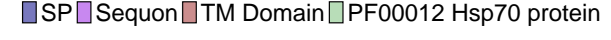


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

COFFNKGKELCKSNPDEAWAYGAAGAAISGEGDEKVDLLLLLVPLSLGLETAGGVMFLVLRNTTPTPKKEQVFSTVSDNGPGVLGVFEGERARTRDNNLLGKFLSGIPAPRQVPOITVCFDIDANGILNVAEDKTTGGKNTTNDKGRLSKEEIERMVAEAEKYKAEDEDHKKVVEAKNALENWYMRNTVKDEKIGSKLSTDDKKKIEAIDGAWLDSNGLAEAEDEFDKMKELEGINPIAAKMYGGAGGDGAGAMDDDDAPRAGASAGPKIEYD*

NbL11g02790.1 actin-like [MW = 41.73 kDa]

No. of times detected



log(intensity)



Values from



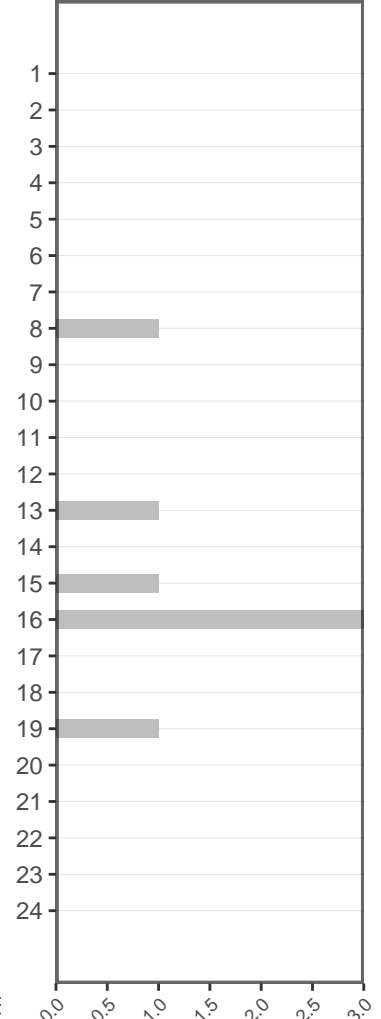
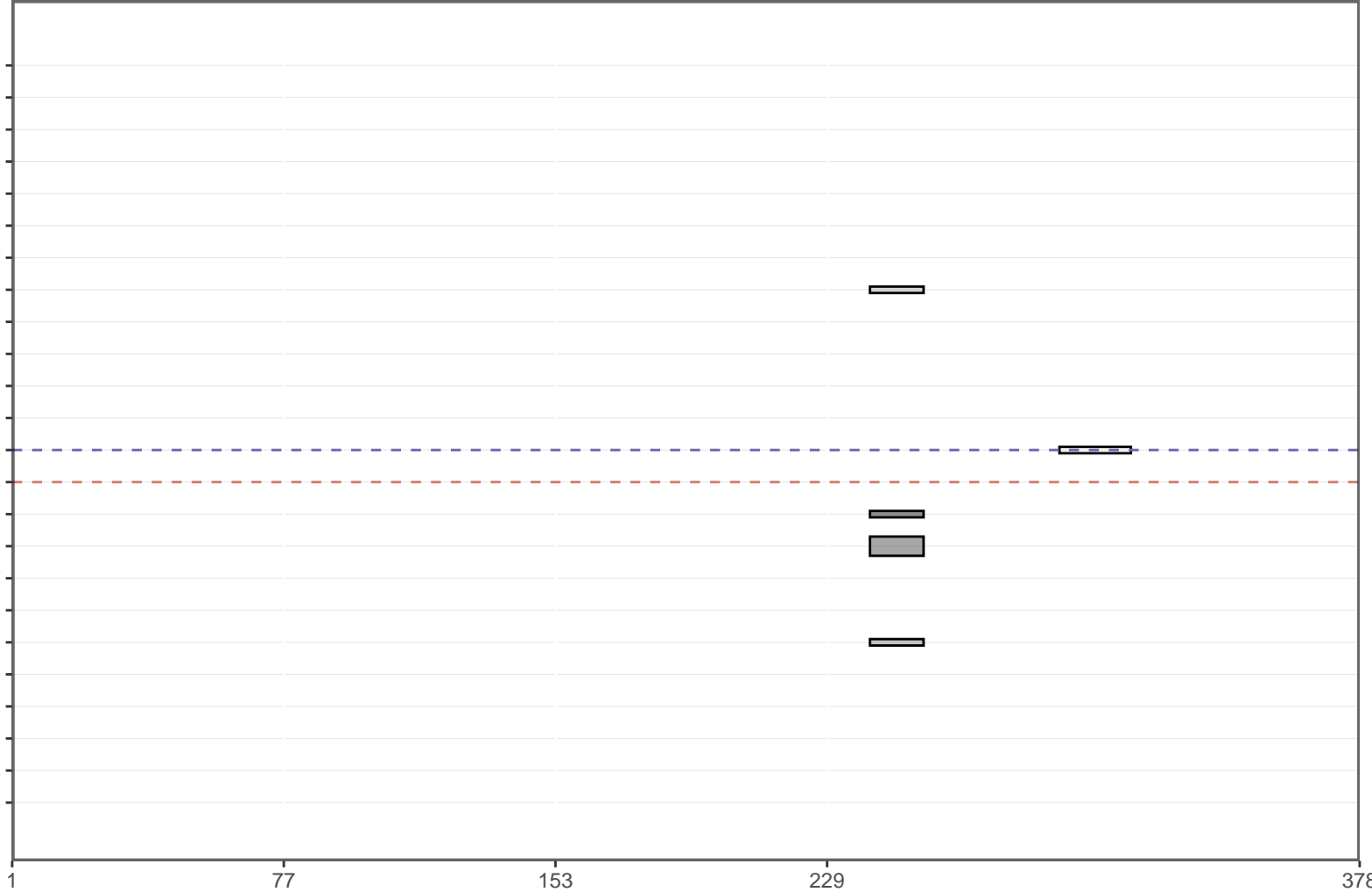
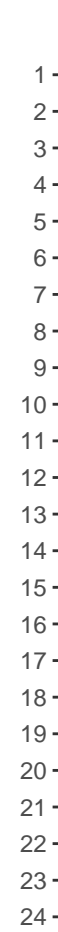
MW indication



Molecular weight

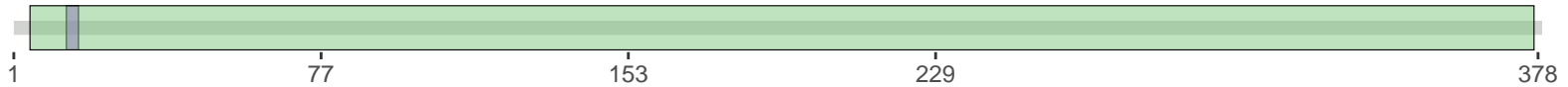


Gel Slice



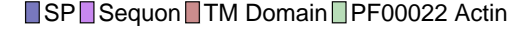
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

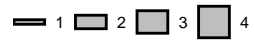


Protein sequence:

PHAILRLDLAGRDLDTDHLMKLTFRGYSFTTSAERREIVRDVKEKLSYALDFEQELETSTKTSSEVKEKSYELPDGGVITIGSERFRCPFLVDFQPMIGMEAAAGHETTYNSIMKCDVDRKDLGYNVLSGGSTMFNGLADRMKEKITALPSEMKIKVVAAPPERKYVYVWGGSLASLSTFQGMWAKAEYDESGPSVHRKCF

NbL11g02430.1 nudix_hydrolase_19_chloroplastic [MW = 48.48 kDa]

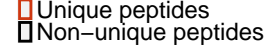
No. of times detected



log(intensity)



Values from



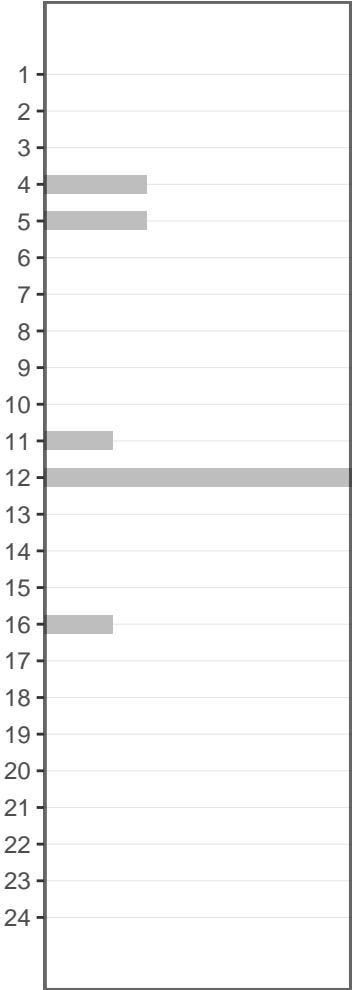
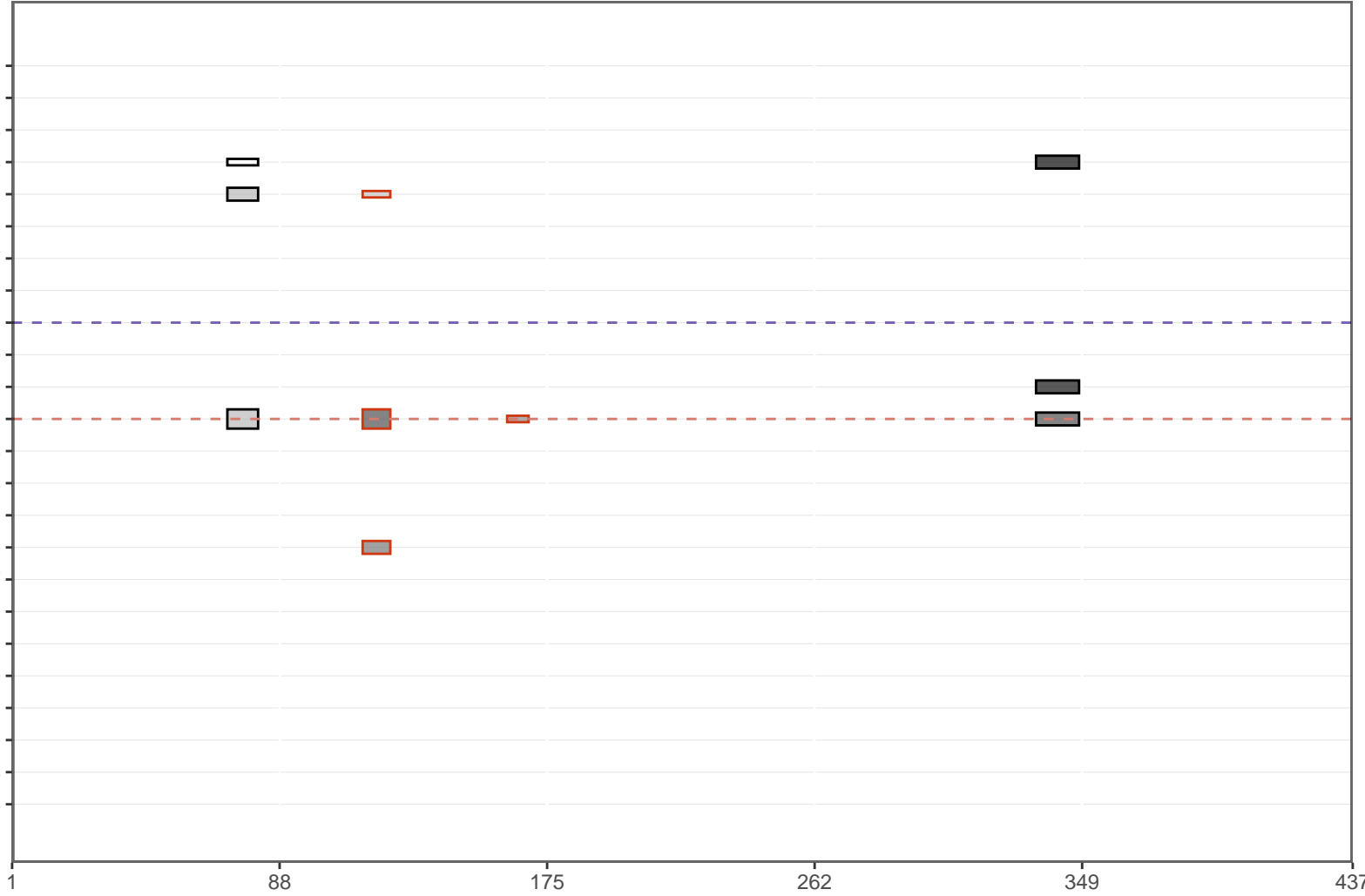
MW indication



Molecular weight

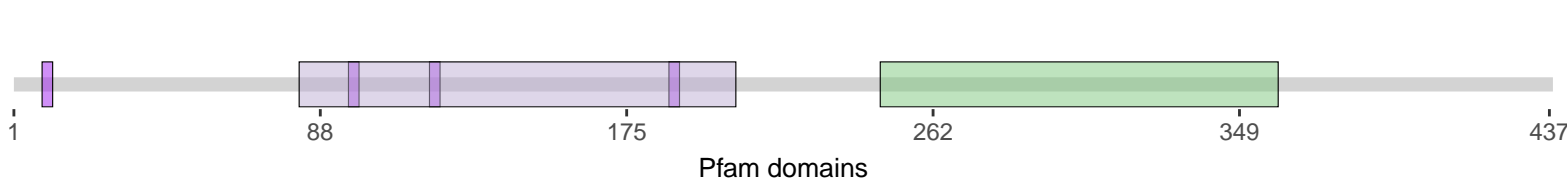


Gel Slice



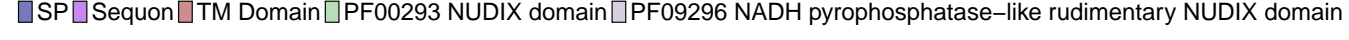
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ITVSRFCFCGCKNLLDAGRRKGGNELKPKKIKPRVDPVWMLVMDKENDRVLLSRGSRFVPRMWSQLAGMEPGESEEAARRETWEETGIEVGGVYHSSGQPPVPGPSEMPCQLMVGFFAVAKSLDINVDKVELEDAKWHGREDAKKAFTFEYKKAQRTAAGKVDQMKGVVERGGSLSEDFNVEGELAPMFRPGFPAIAHHLISWVNGEAQVWGLASSFNL

NbL11g02380.1 ruBisCO_large_subunit-binding_protein_subunit_alpha-like [MW = 62.37 kDa]

No. of times detected



log(intensity)



Values from



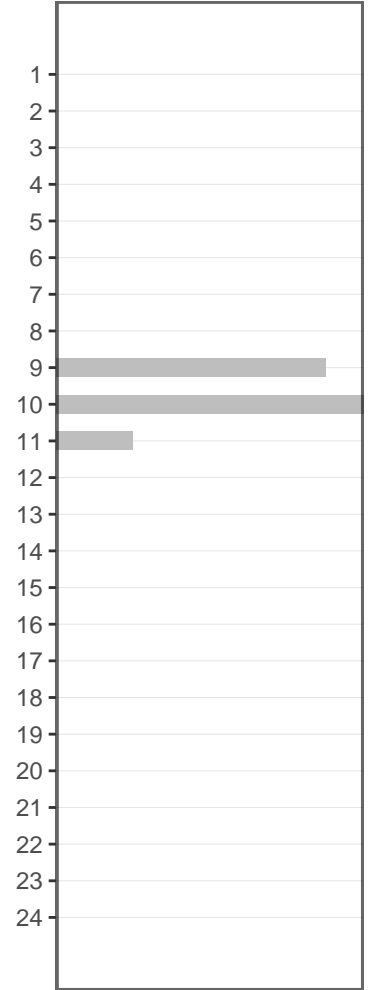
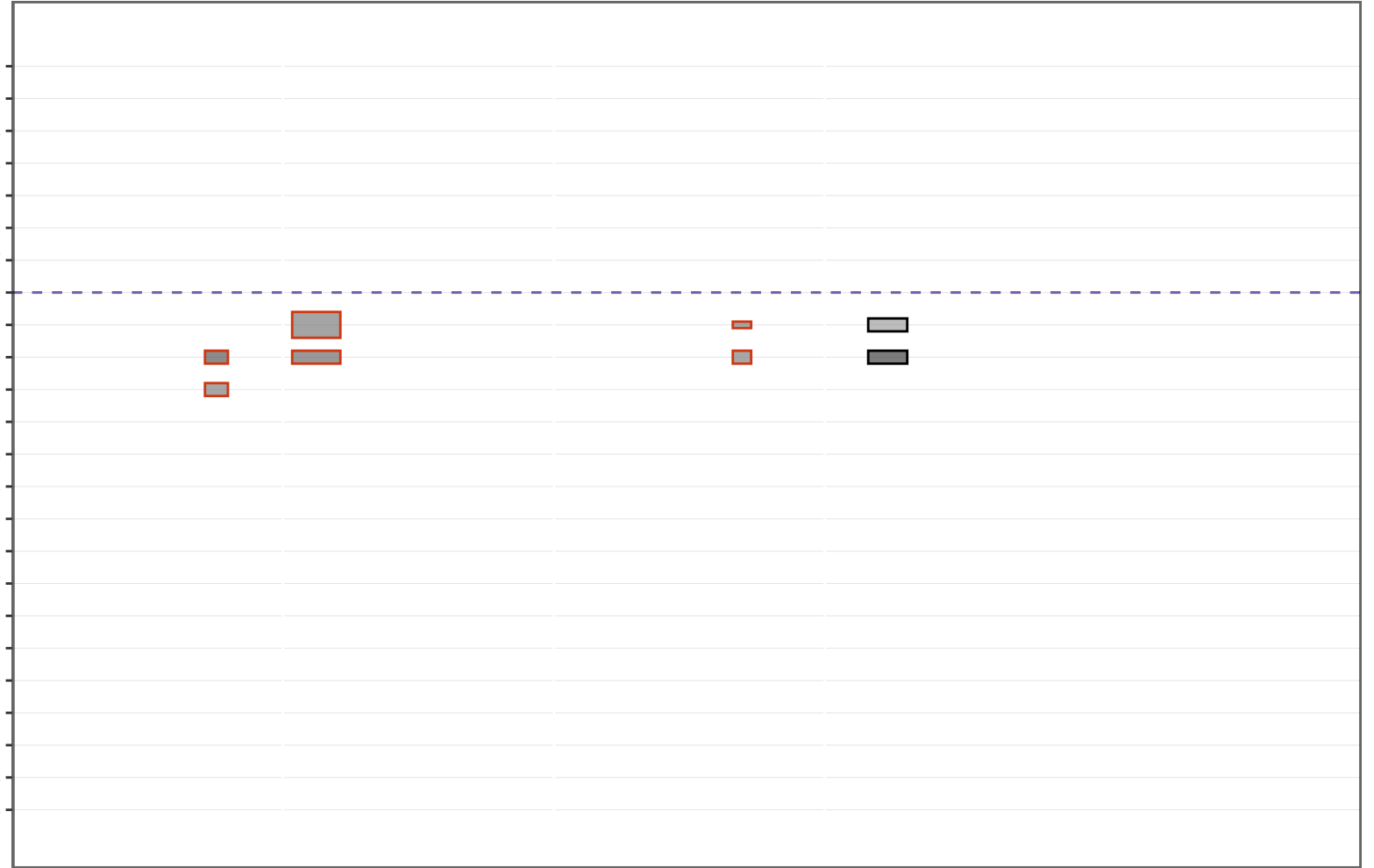
MW indication



Molecular weight



Gel Slice

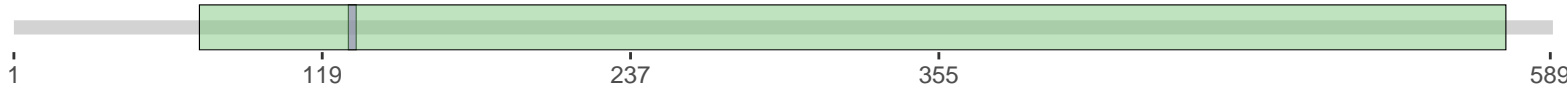


Protein length

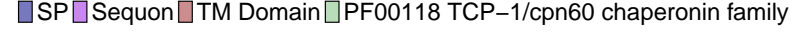


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

PLLEKSTELRAPLLNAGDVTGEALATLVNKLKRGVLSVAIRAPFGGRRKALLGDVAITGAEYQATELGMVENTPVEALGFARKVTSKDSSTHLSADDAQSKDEIGARISQLKELDMTDSISDSEKLAERIAKLOGGVAWVKGVAATEAELEDKRLIEDAKHATFAAIEEGVPGGGAALVHLSYVHAIKNLEEDPDKLGADIMQKALVAPSLIAGNAGVEGEVYVEKIKASKWKMGMGNAMTDKYNELVEAGVIDPAMVTRGALGNAASVAGVAVTTQAVVYDQHTPDVPAFA

NbL11g02370.1 (R)-specific_enoyl-CoA_hydratase-like [MW = 18.36 kDa]

No. of times detected



log(intensity)



Values from



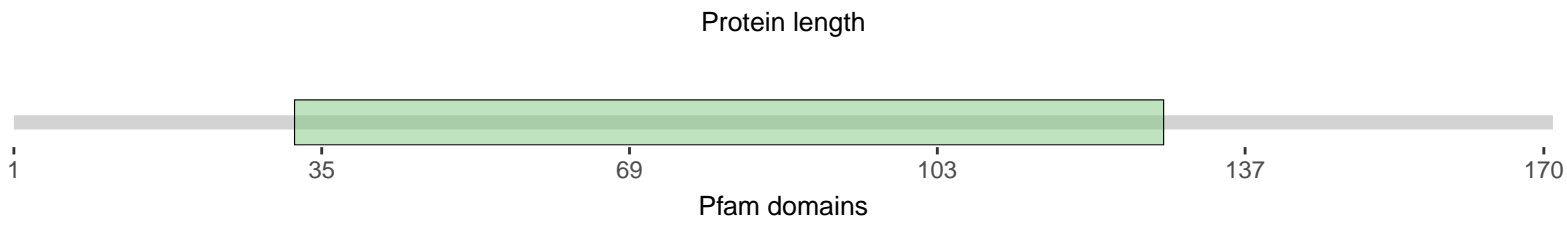
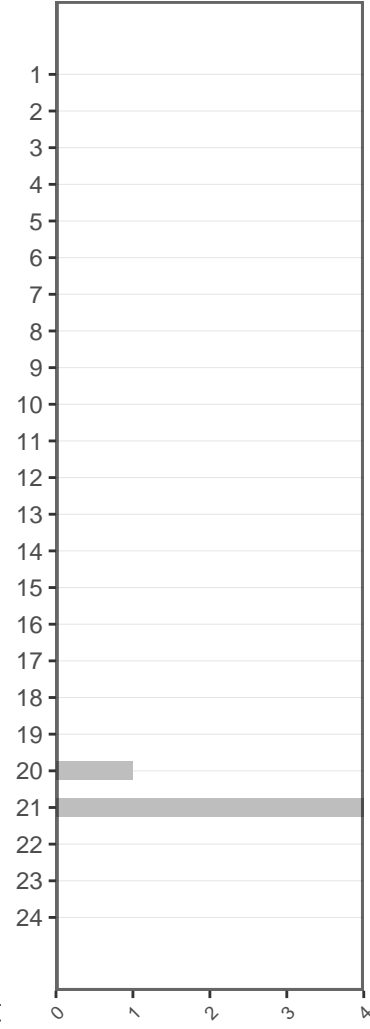
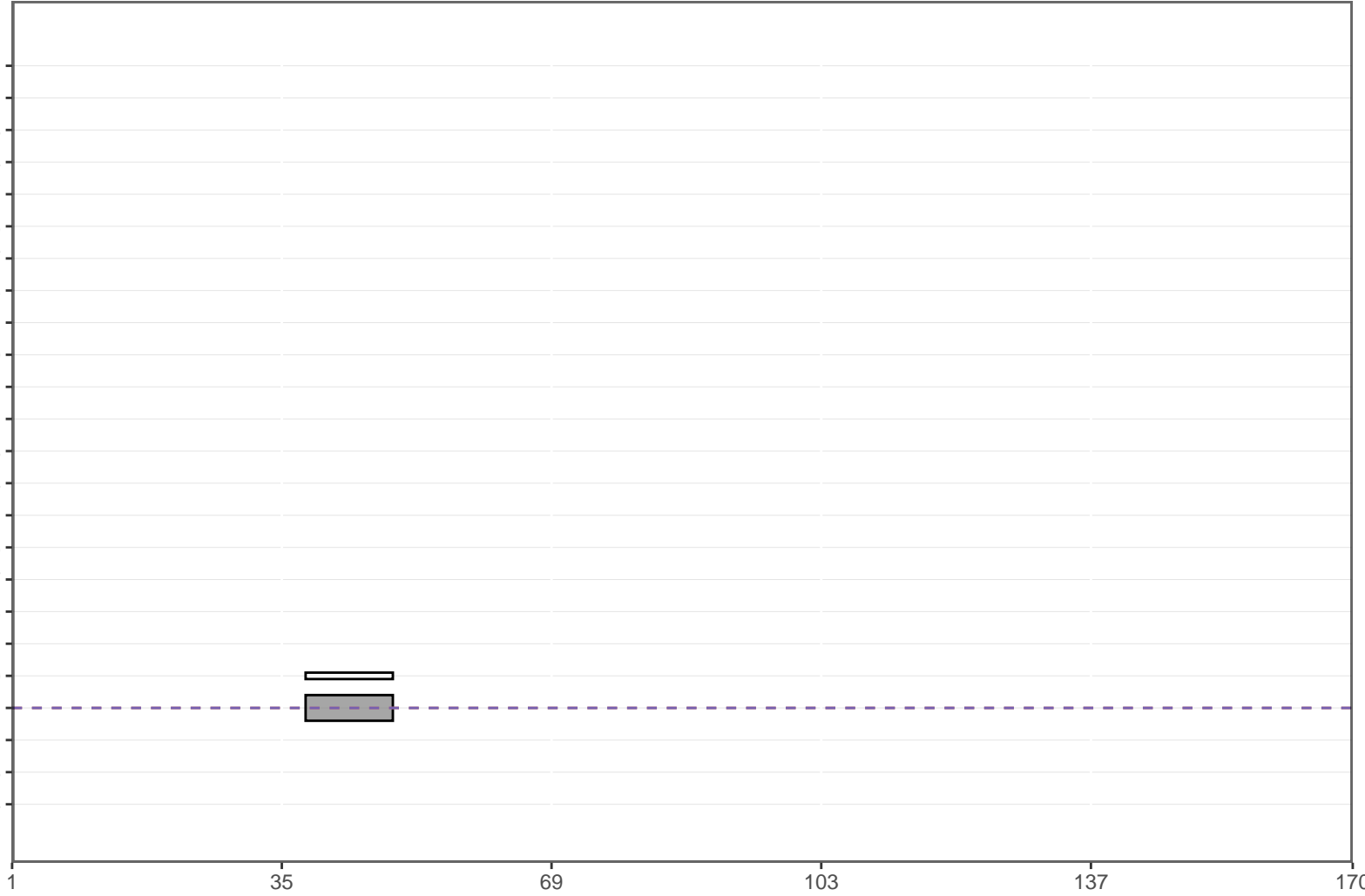
MW indication



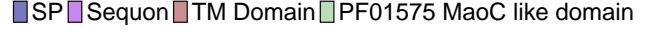
Molecular weight



Gel Slice



Pfam Description

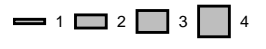


Protein sequence:

RLVPGMLVSLFPRHAAHFGALYVSGTLHFKLPIYIGDEIHAIEVQASIRGMKNKYAKLSTKGFKGDGPLVIDGEATALPSLMEPTLASTSS

NbL11g02310.1 cell_division_cycle_protein_48_homolog [MW = 89.37 kDa]

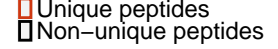
No. of times detected



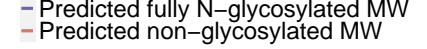
log(intensity)



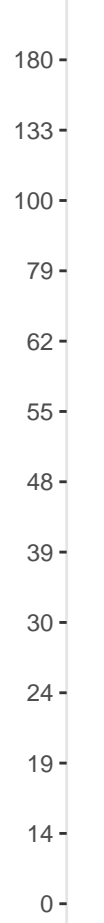
Values from



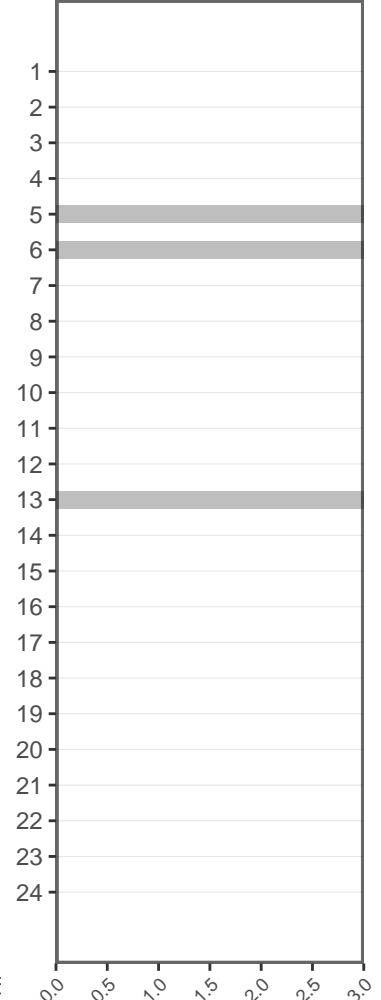
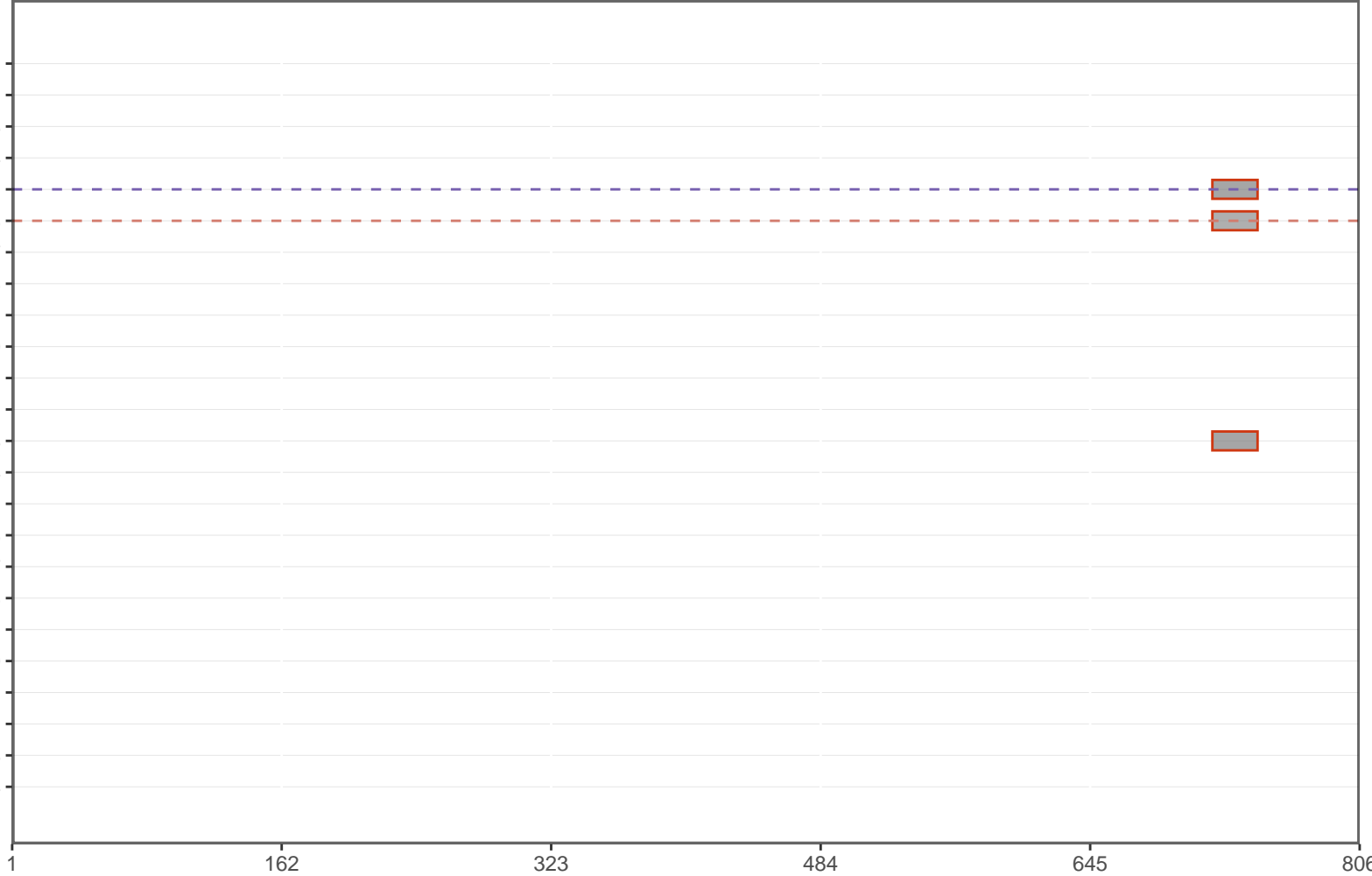
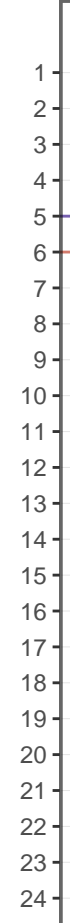
MW indication



Molecular weight



Gel Slice

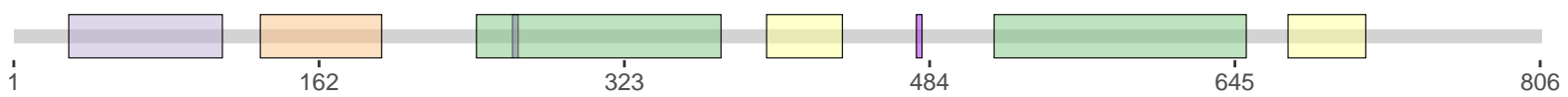


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF00004 ATPase family associated with various cellular activities (AAA)
- PF02359 Cell division protein 48 (CDC48), N-terminal domain
- PF02933 Cell division protein 48 (CDC48), domain 2
- PF17862 AAA+ lid domain

Protein sequence:

MKLAEEVDLERISKDTHGYGADLAALCTEAAAGQREKMDVLEDDSDSDEILNSMAVTFNEHFDALGTSNPSALRETVVEVPNVSWEIDGLENLKRLEGETVGVYVPEHPKFKFMSPKGLVLYGPPGGGKTLAKAIANEGGANFISVKGPELITMWFGESEANVREIFDKARQGAPOVLFFDELDSIATQRGSSVGDAGGAADRVLNGLLTEMDGMNAKTVFISGATNRPDIDPALLRPGRLDQLYIPLPDEDSDRHQHFKAQLRKSPLSKQVLDLRALAKYTOGF

NbL11g02170.1 probable_aquaporin_TIP1-1 [MW = 25.78 kDa]

No. of times detected



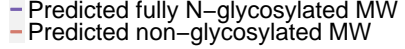
log(intensity)



Values from



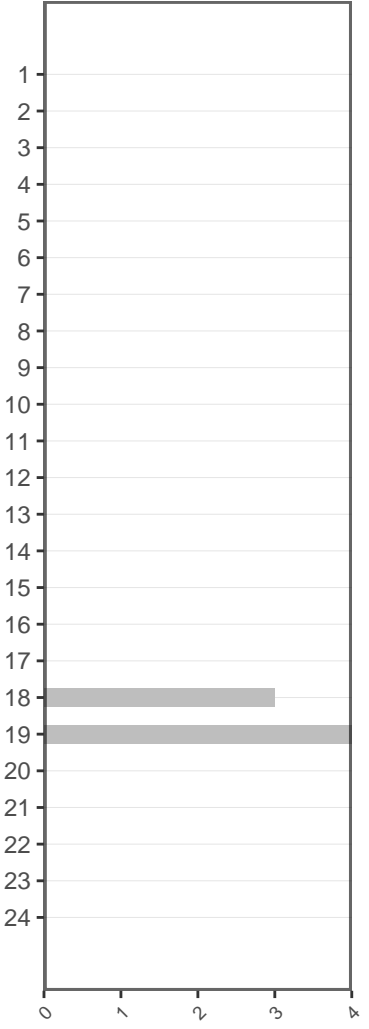
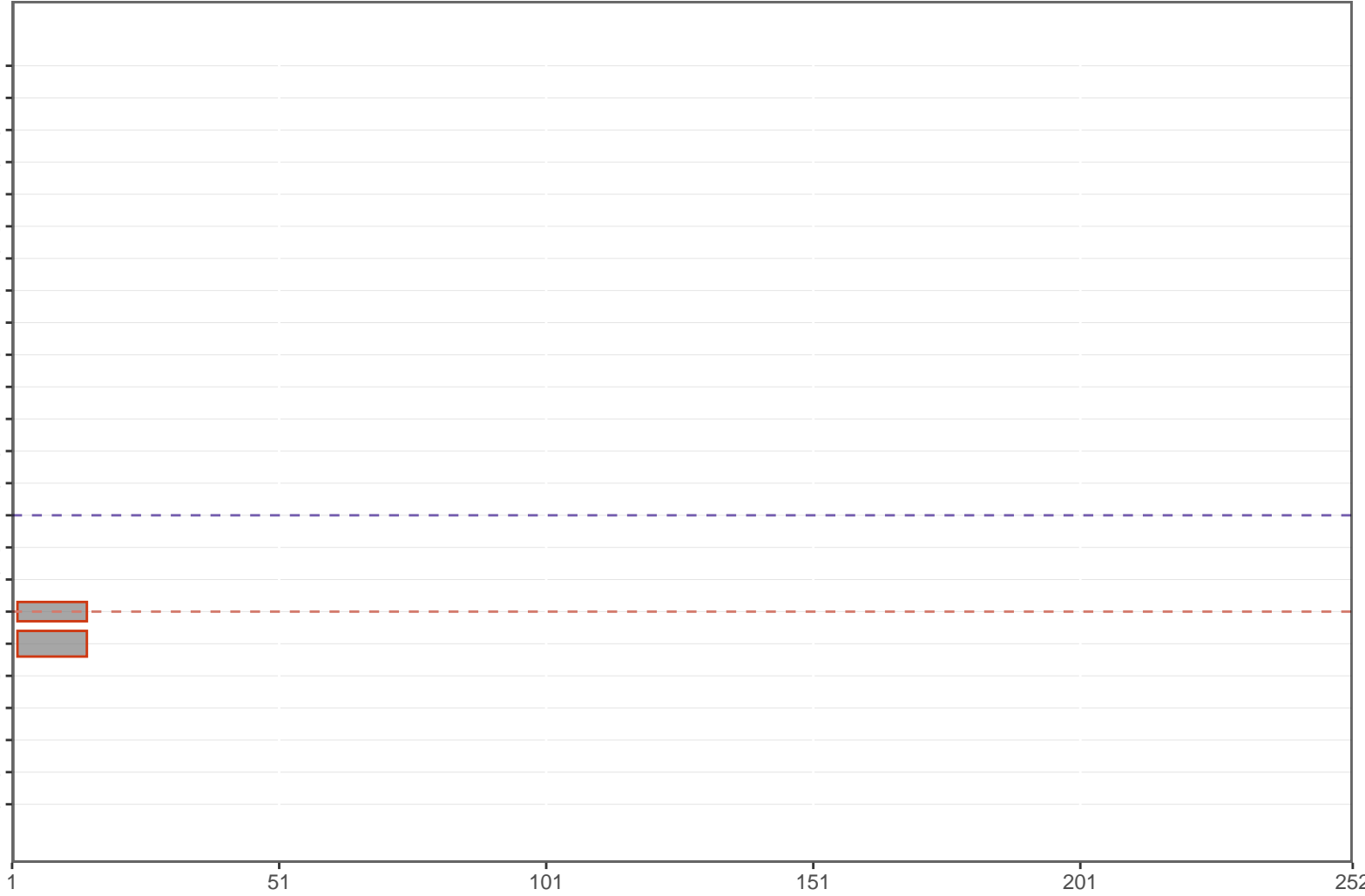
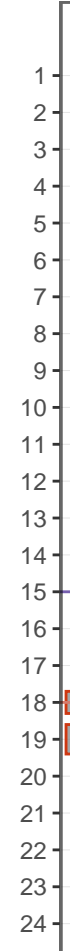
MW indication



Molecular weight



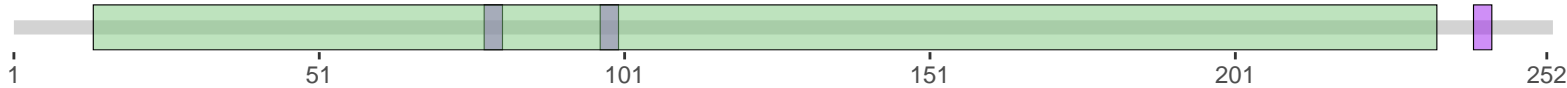
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

STVACFLLEFATGSMTGAFALSGVSVWNAFVFEVMTFGVYTVVATAVDPKKGLGVIAPLAFGVGANILAGGAFGASMNPAVSGPALVSWTWTQHWVWVWAGFLVGGGAGVYVELFNHSHLEPLSGDP

NbL11g01930.1 phospholipase_A-2-activating_protein [MW = 83.34 kDa]

No. of times detected



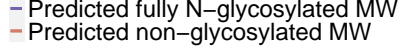
log(intensity)



Values from



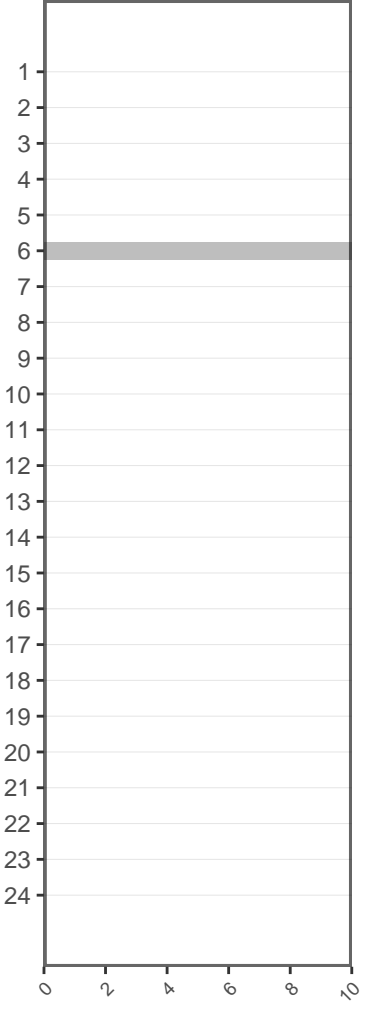
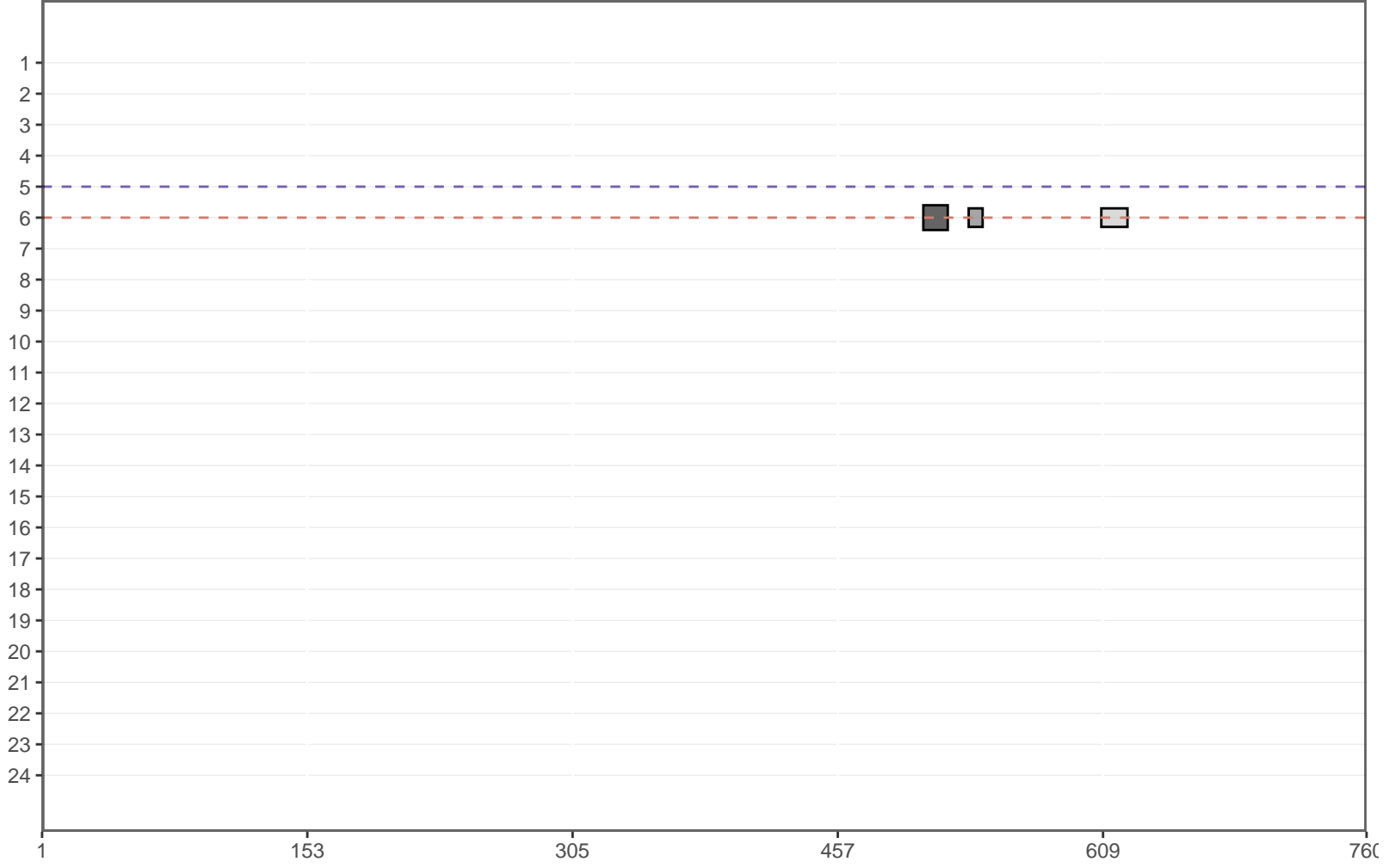
MW indication



Molecular weight

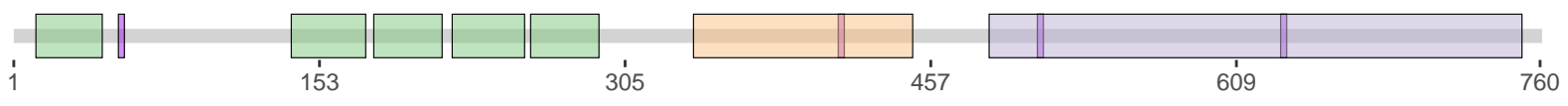


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

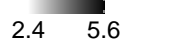
IEQKVDKIGEYVDPDQGMTHPHIDGIGYEVVFDVGDGDEPVRKLPYNRSDNPYDIADKWLKENLPLFRFQGVFEFLQNTGQRGFTFDPSPRDPYVGNLAVTPGGSPKPVATAANPTFKHHPKKGMLVFDALFDGILKRISFNSTLLGGSEKHMALTEAVMSRLASILNPKDTSYHSTKLSDDDVAVMLKLLKTPWLTMLFPVIEVLRMMLHADGAALFKHYENPNDVLMELIKKVTTSPLPLNLLTSVRAETLFLKNGSYHDWLLKHRGEVDAFSTCYLSSNK

NbL11g01880.1 4-hydroxy-3-methylbut-2-enyl_diphosphate_reductase_chloroplastic [MW = 56.05 kDa]

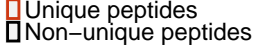
No. of times detected



log(intensity)



Values from



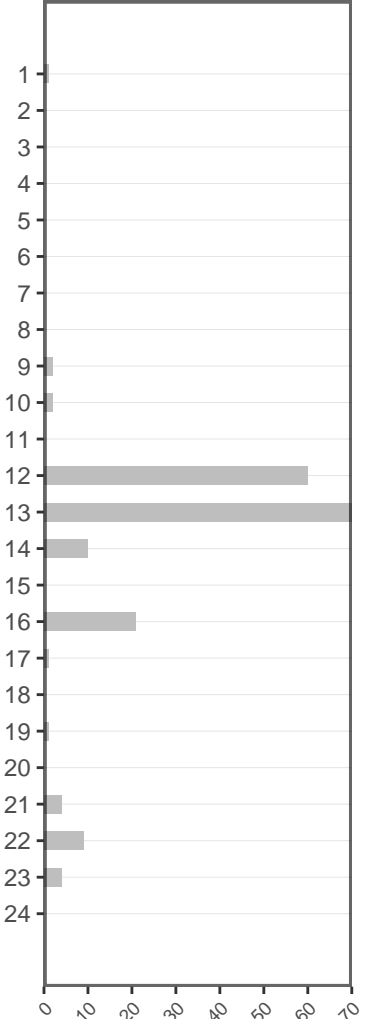
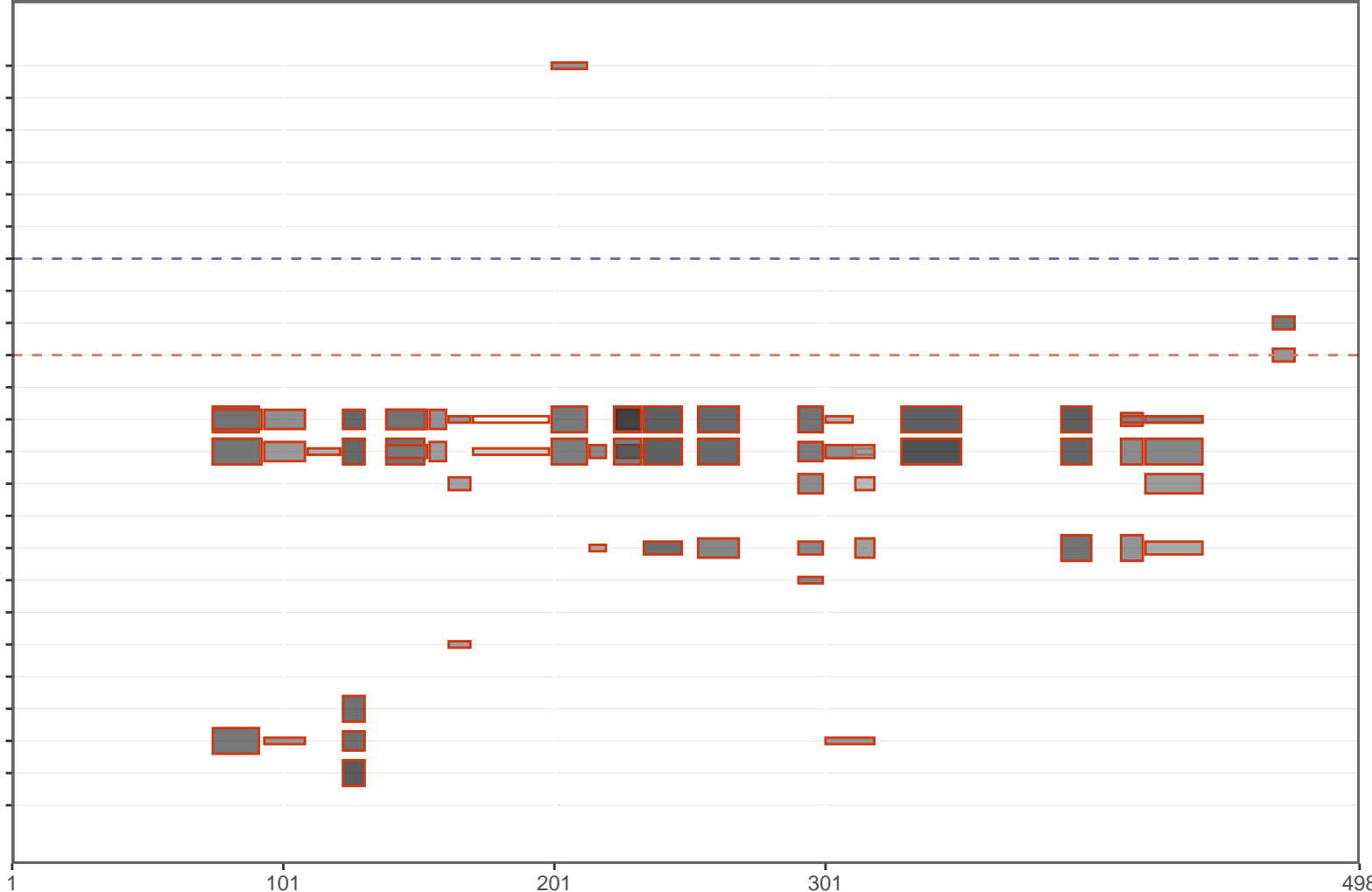
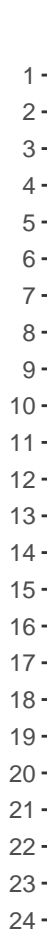
MW indication



Molecular weight

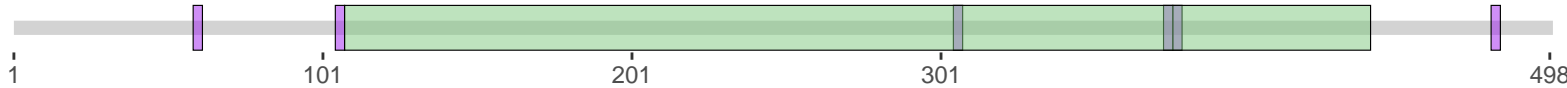


Gel Slice



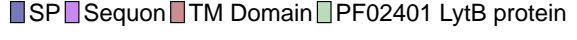
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

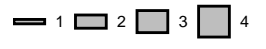


Protein sequence:

HEETVATASACKYIVKKNMAEATYVGDHLGGKLDGSSSEKFAFMKPKNAVSKGFNPDDLVKNGIANGDTMLUGETEIEGKLVERTMMGRYGVENINHHFISFNTIGDATERGDAMKLVLDGKLLMLVVGVGVNSNTSHLGEIAEERGPVYWDSEGRIGPGRIRI6YKLLHGEIVKENFLPEGPFTVGVTSGASTPDKNQMGRLGYRKLGLVLIAGIIOGQKVIDIYNEKVRGNFGRHRSFQHDQETEPVLL

NbL11g01680.1 coatomer_subunit_gamma [MW = 93.57 kDa]

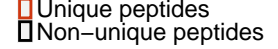
No. of times detected



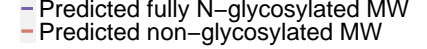
log(intensity)



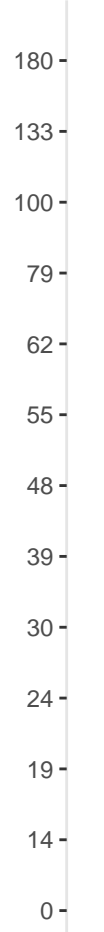
Values from



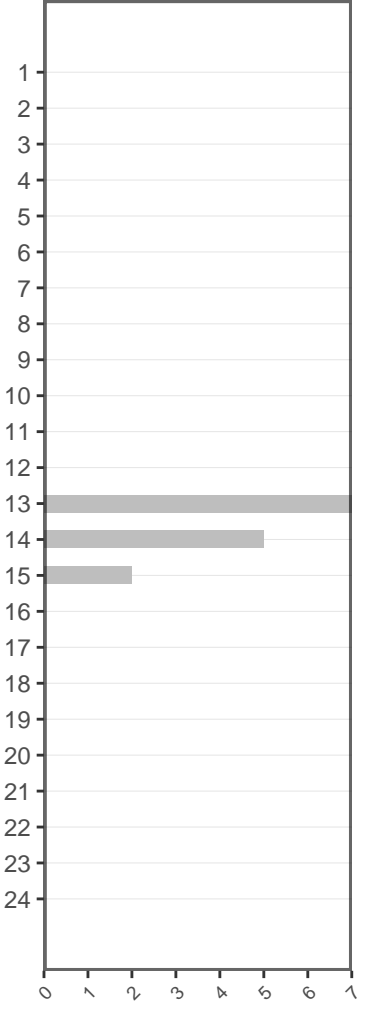
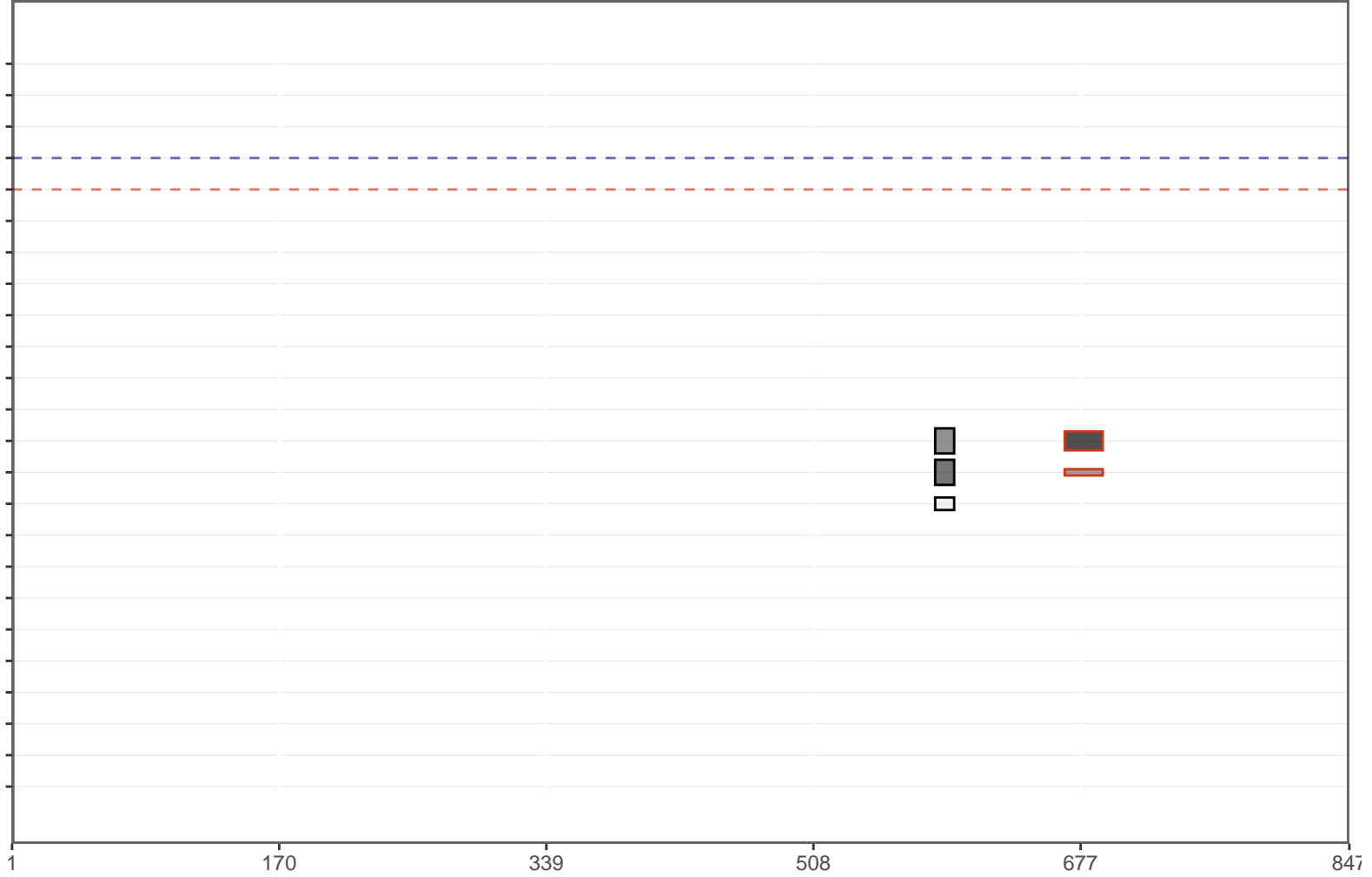
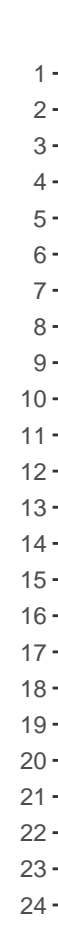
MW indication



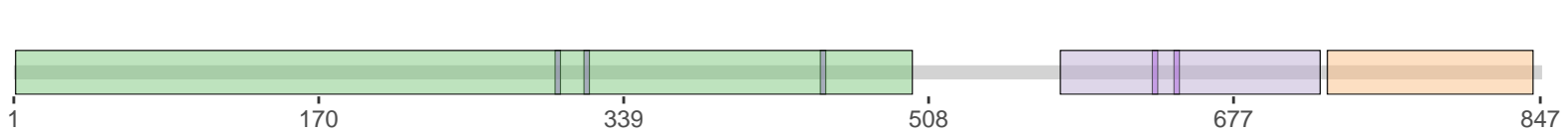
Molecular weight



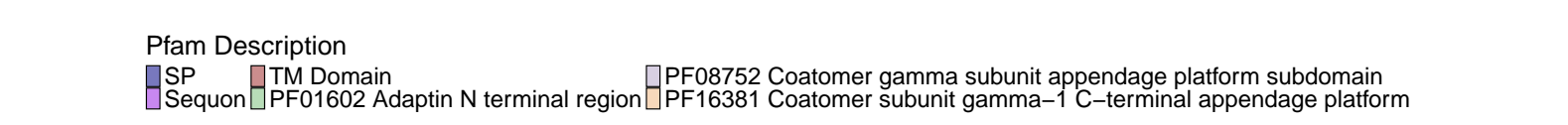
Gel Slice



Protein length



Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF01602 Adaptin N terminal region
- PF08752 Coatomer gamma subunit appendage platform subdomain
- PF16381 Coatomer subunit gamma-1 C-terminal appendage platform

Protein sequence:

STQLHFLQNEGPKTSDPSKIRWYNRVILENATVRASAVSTLAKFGALVDSLKRPRIFVLLKRGFLFDSDDDEVDRDRATLYLNTLGGDGAIVETDDEEKEFLFGSLGVFLTNLETSLKNYEPSEEFDDHSHVPEKVKSGPLSEKKAQKPKTGLAAPPVAFPTSTVDAYERLLSSPEFASYGKLFKSSAPVELTEAETEVAVNWKHFIDNHVFDQYNGDNTIPEQLLENVTIVVDASDAEEFSEVASKPLKLPVDTGQGTFTVFEKPEGVPAWGKFSNMLRFVWKEVDPSTGEAEDDC

NbL11g01550.1 glycine-rich_RNA-binding_protein_GRP1A-like [MW = 14.03 kDa]

No. of times detected



log(intensity)



Values from



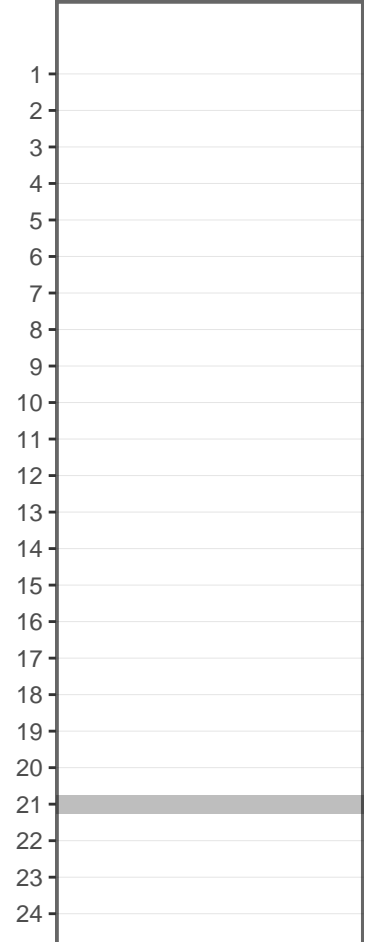
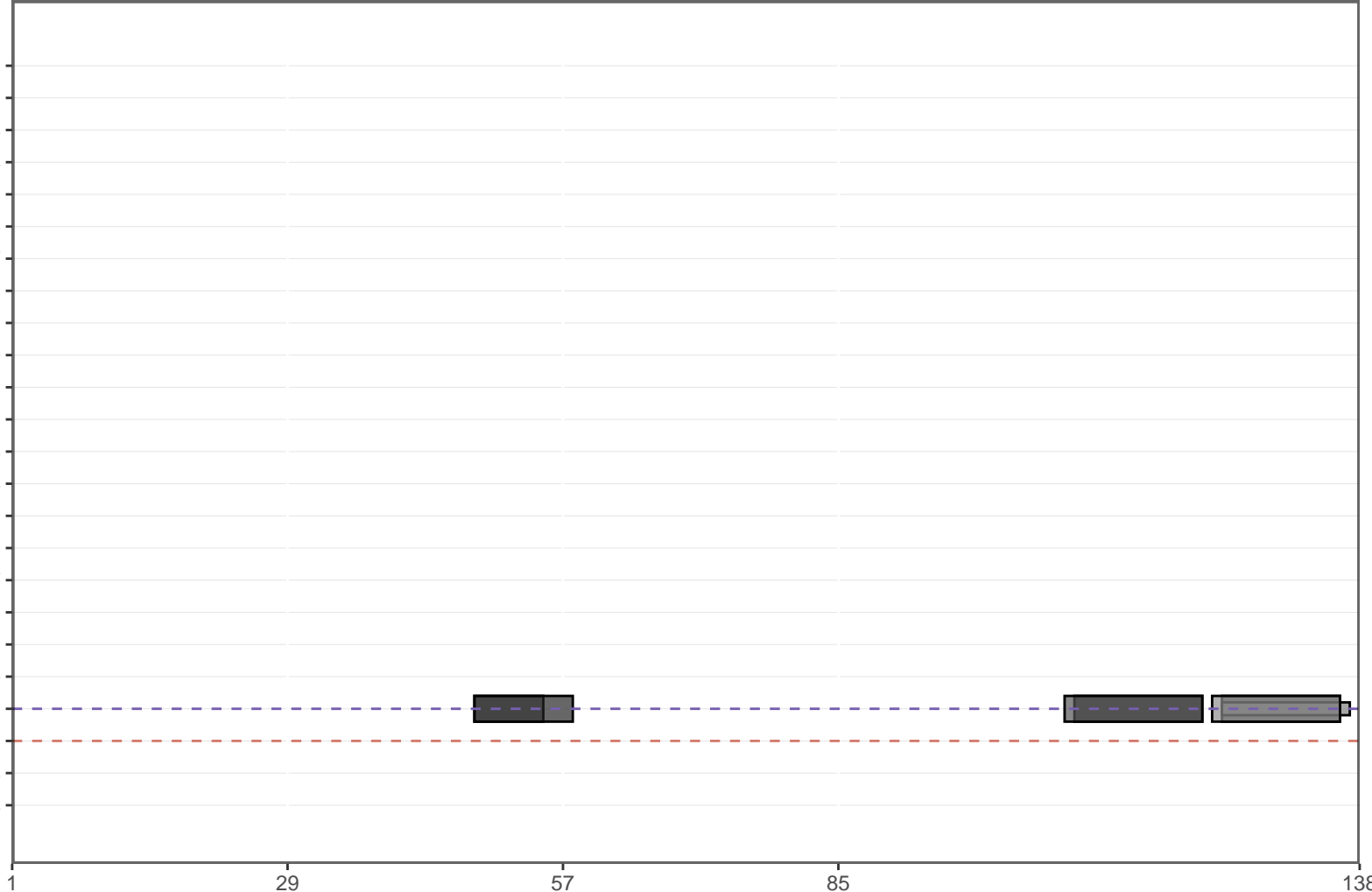
MW indication



Molecular weight



Gel Slice

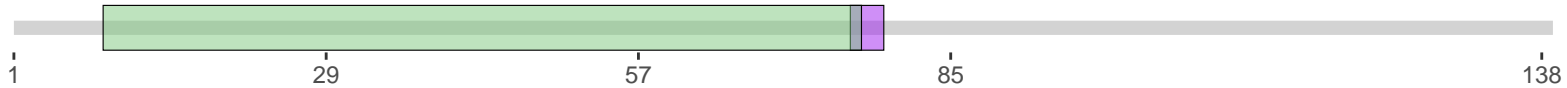


Peptide counts over 4 repeats

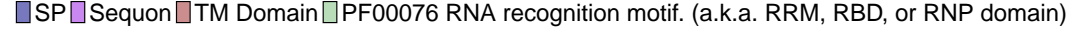
Protein length



Pfam domains



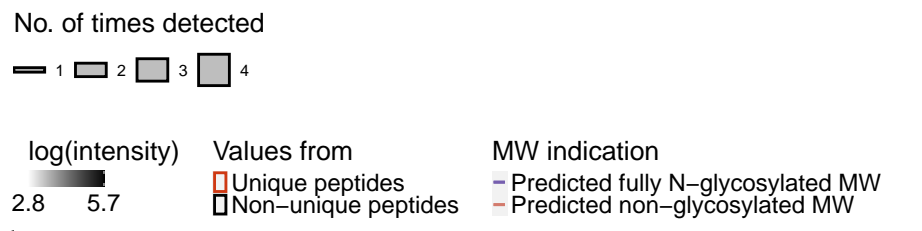
Pfam Description



Protein sequence:

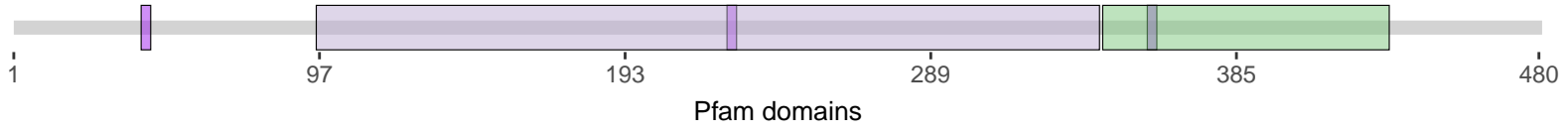
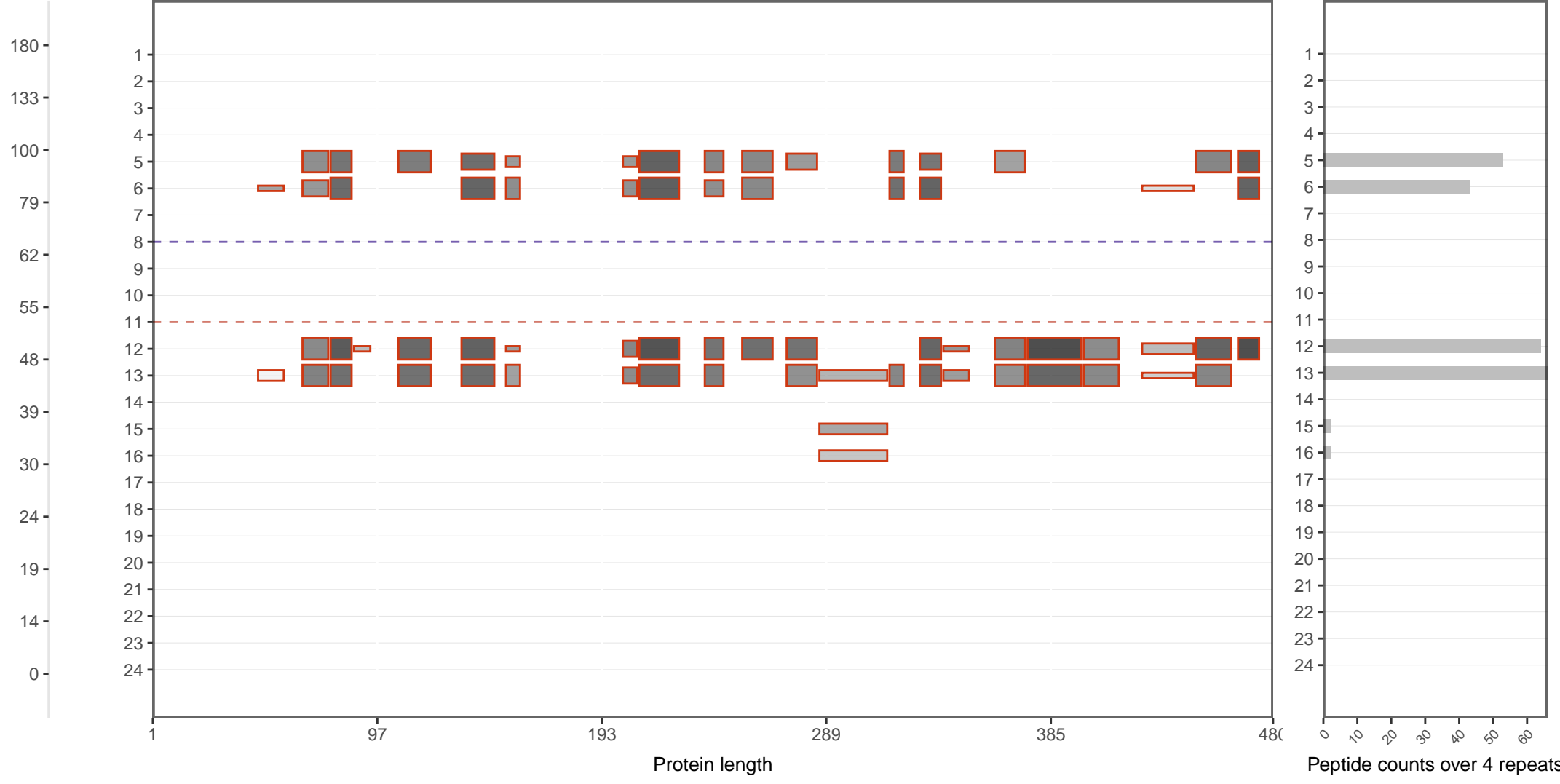
MRDAIEGMNSGQLDGRNITVNEAQRSGGGGGGGYRGGGGGGYGGGGRRGGYGGGGYGGGRREGYGGGGEGYGGGSEGNWRP

NbL11g01400.1 diaminopimelate_decarboxylase_1_chloroplastic-like [MW = 52.85 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00278 Pyridoxal-dependent decarboxylase, C-terminal sheet domain
- PF02784 Pyridoxal-dependent decarboxylase, pyridoxal binding domain

Protein sequence:

SSKFGIRNEKLOWFLDAWKAKHPQELKLVGAHCHLGGTTKVDIFRDAWLMVNYDEIRSGQFEIDYLNIGGGVGGIDVYHSGALPGRDLDTVRELVSRNLNIEPGRSIAHTGCLVRYVTGKTNKGNFVIDGSMELRPSLVDAVGHIELVSPPAEAVISRFDVYVGPVCGSADFLGKDRLELPAPSRGTGLVHDAGAYCMSMASTYLNLMKRPPEVWVEEDGSGIKRHGETTFEHLRFFEGL

NbL11g01340.1 chaperone_protein_dnaJ_10-like [MW = 18.28 kDa]

No. of times detected



log(intensity)



Values from



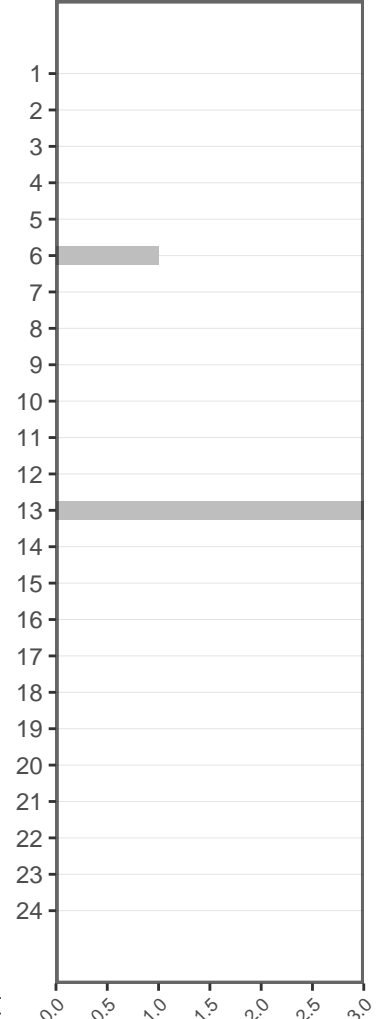
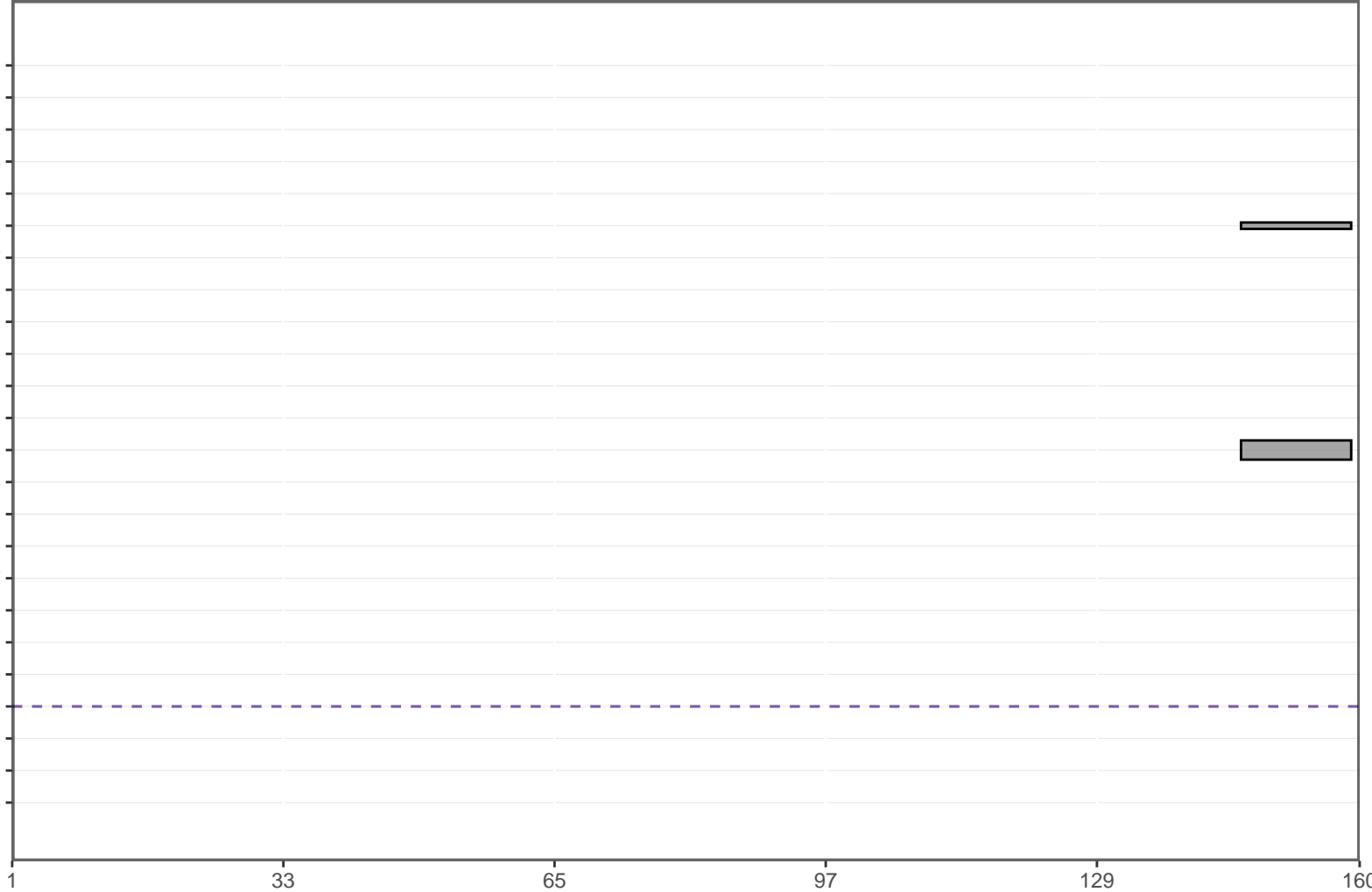
MW indication



Molecular weight



Gel Slice

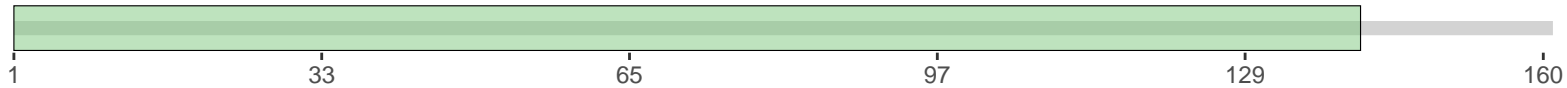


Protein length

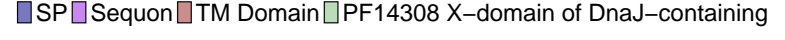


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IKVVEDAIKTMEEKKDKMKSLWGIVVDEIETLSRVGGVAVLKEFNPVPRDVLRLRLRARAMMKLGTIFDGAQPMVRRRESLRRENTDMVDGGTSEK

NbL11g01070.1 amidophosphoribosyltransferase_chloroplastic-like [MW = 62.02 kDa]

No. of times detected



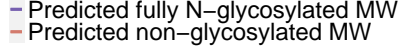
log(intensity)



Values from



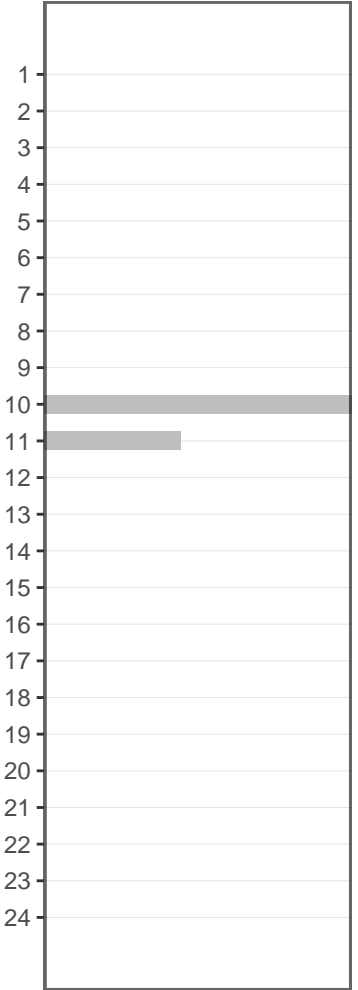
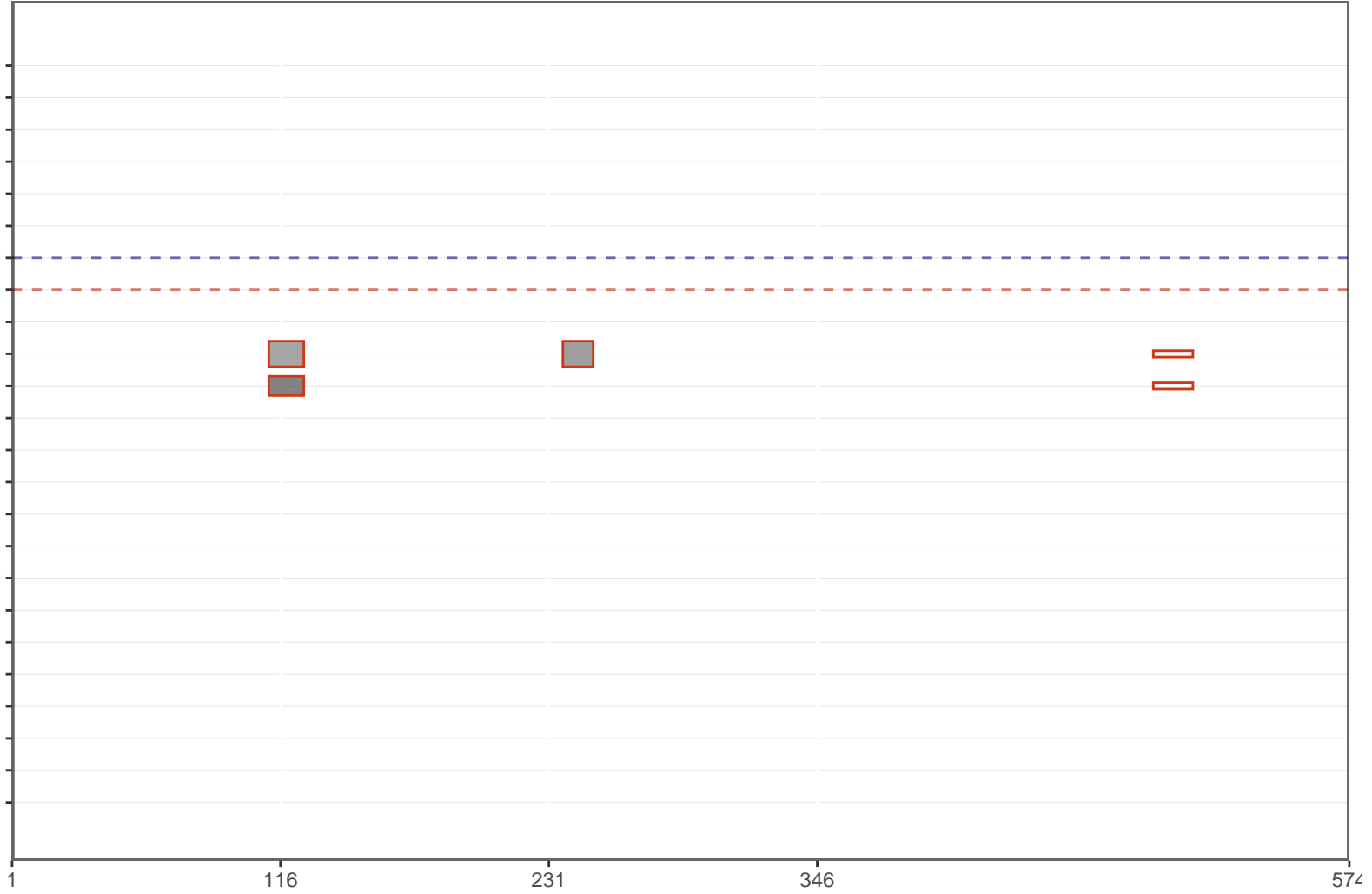
MW indication



Molecular weight

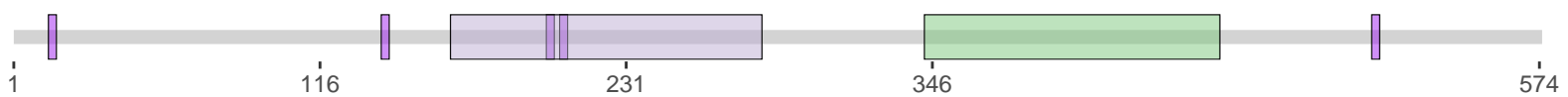


Gel Slice



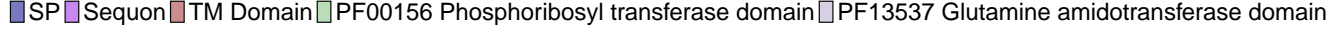
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

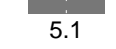
VTASETCALDLIEATYEREVNPGEVYVVDKDGVDGIGLMPHPERKSGIFEHYFALPNSVVFGRSVYESSRAFGELATEAPVEGDVIAVFDSDGVAALGAAGAAGVFFQDGLRSHYVGRTFEFPSSQKIRDFGKLLKLSPVRAVLEKGRVAVVDDSGVRRGTTSSKIVRLLEKAGAEVHMRIASPHIASDYYGVDTFSSDELINRMVSEKEFIFGSDSLAFLPMDSLNKLKLGANDSKFCVAGFCGNVYVPEPTGKVKRIGDFMDDGLSGDMRIDGGWLPSSSRVOKTLINE

NbL11g01060.1 peptidyl-prolyl_cis-trans_isomerase_Pin1 [MW = 12.97 kDa]

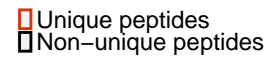
No. of times detected



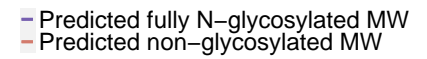
log(intensity)



Values from



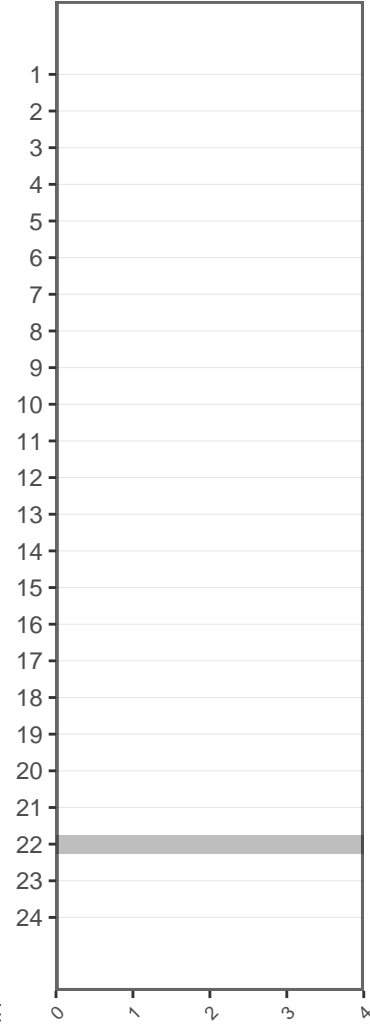
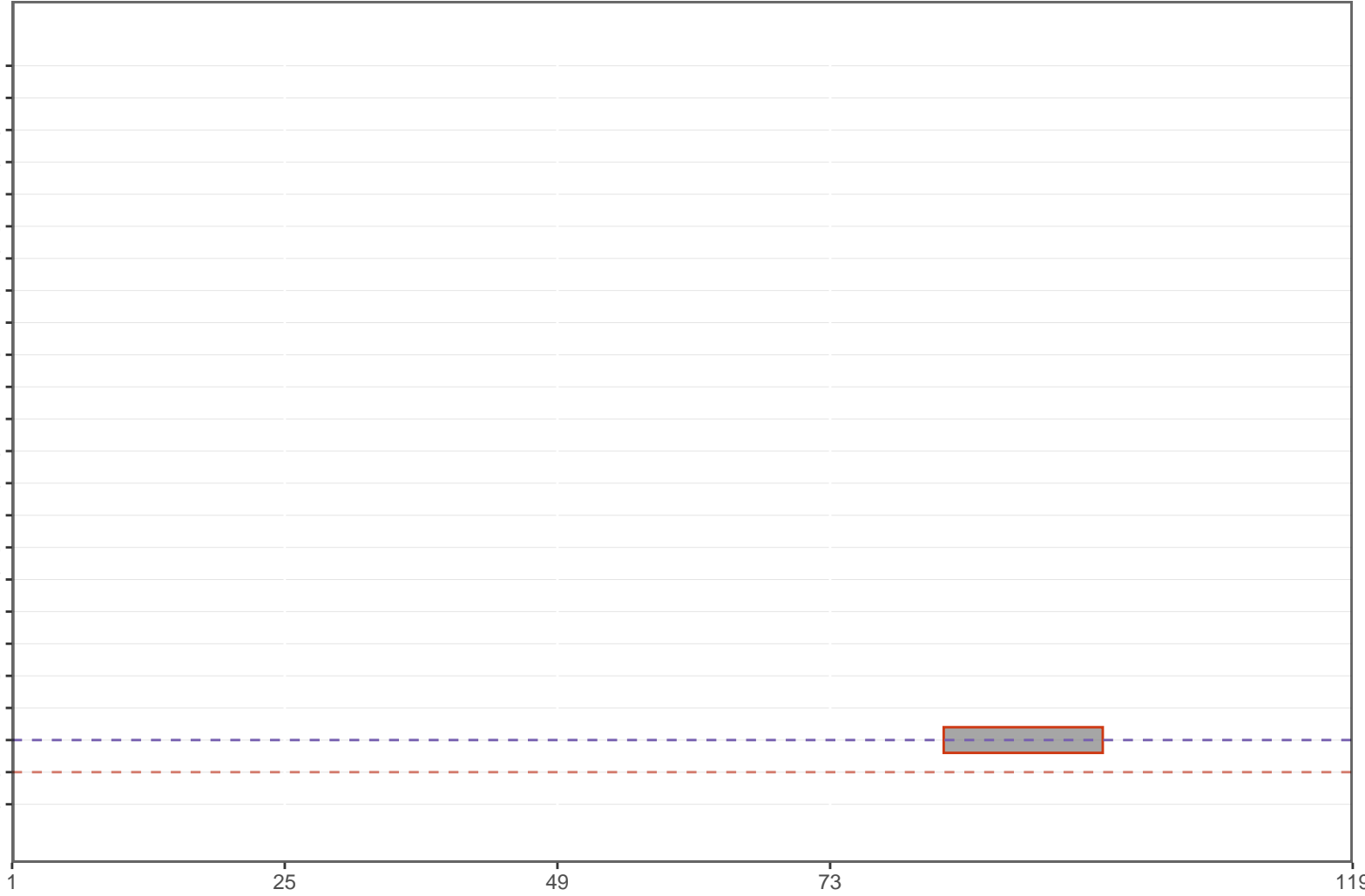
MW indication



Molecular weight



Gel Slice

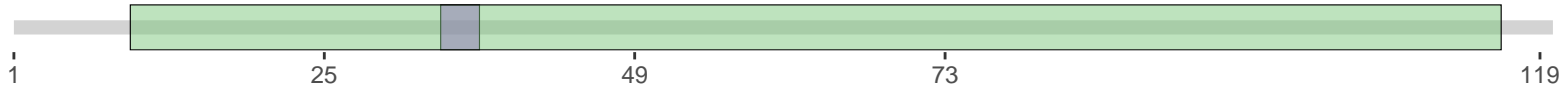


Protein length

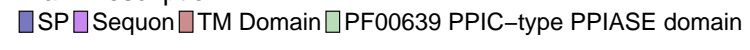


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

AFRDDIISQSKFEEVASRFSDGCEANRGGDLGFCRGGMKPFEDTFFALKVGEISDHDTDGGVHILRTG

NbL11g01030.1 probable_ribosome-binding_factor_A_chloroplastic [MW = 25.58 kDa]

No. of times detected



log(intensity)



Values from



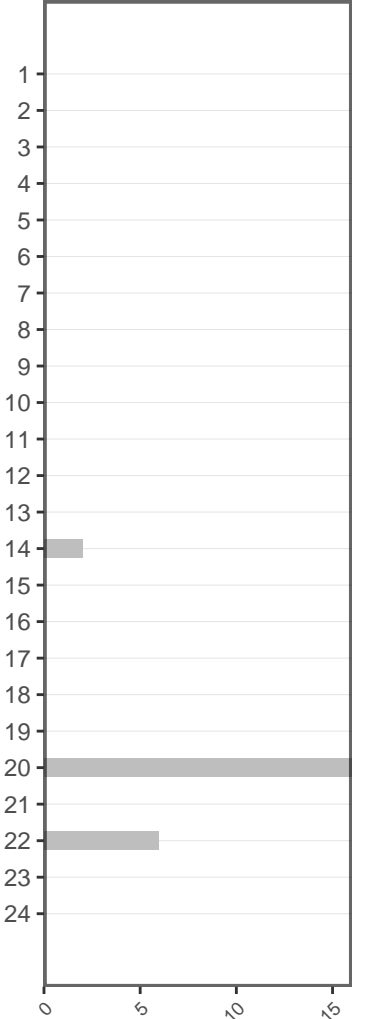
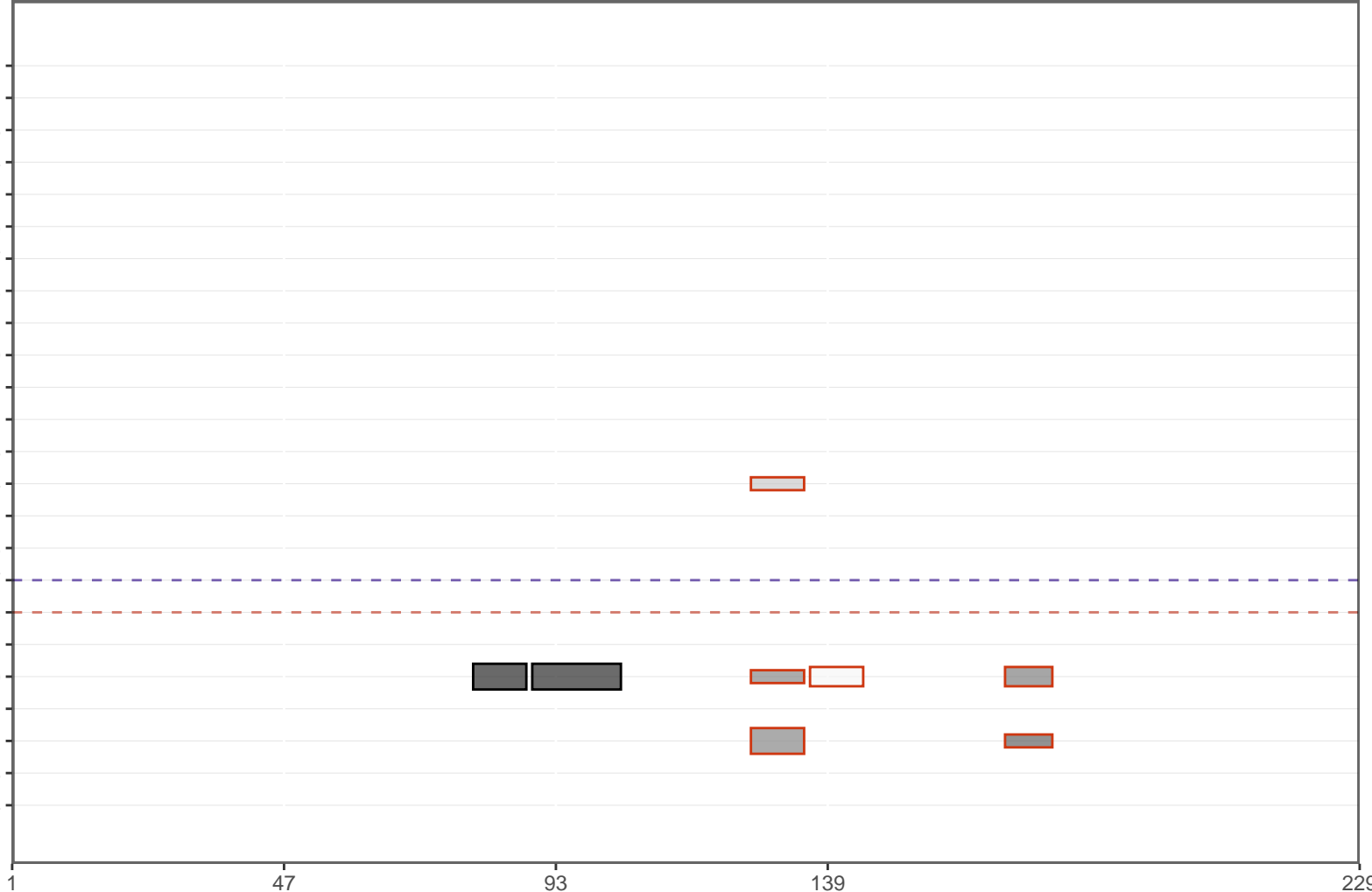
MW indication



Molecular weight

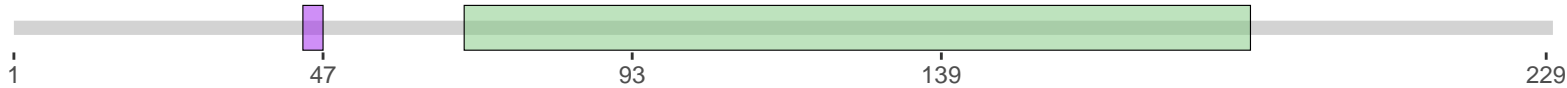


Gel Slice



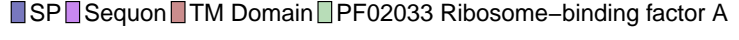
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IDRYLSLSTTSDVENVSTDLGVKVVVSVFVGDVGRGKEVALSGLKSKAKYVRSBELGRMRKLRLLTPERFIEDESIEGSRVLAALDRIKDENENKNAPSGASDNDGSDDDGDDGDDPDDGDIYVYK

NbL11g00880.1 single-stranded_DNA-binding_protein_mitochondrial [MW = 23.76 kDa]

No. of times detected



log(intensity)



Values from



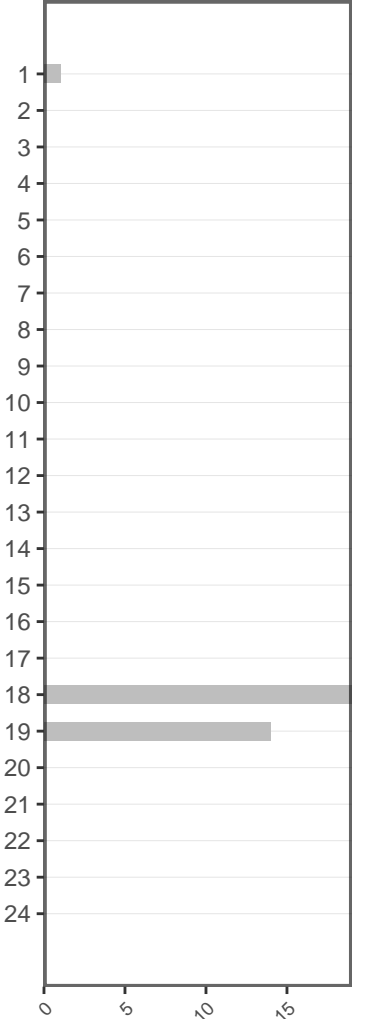
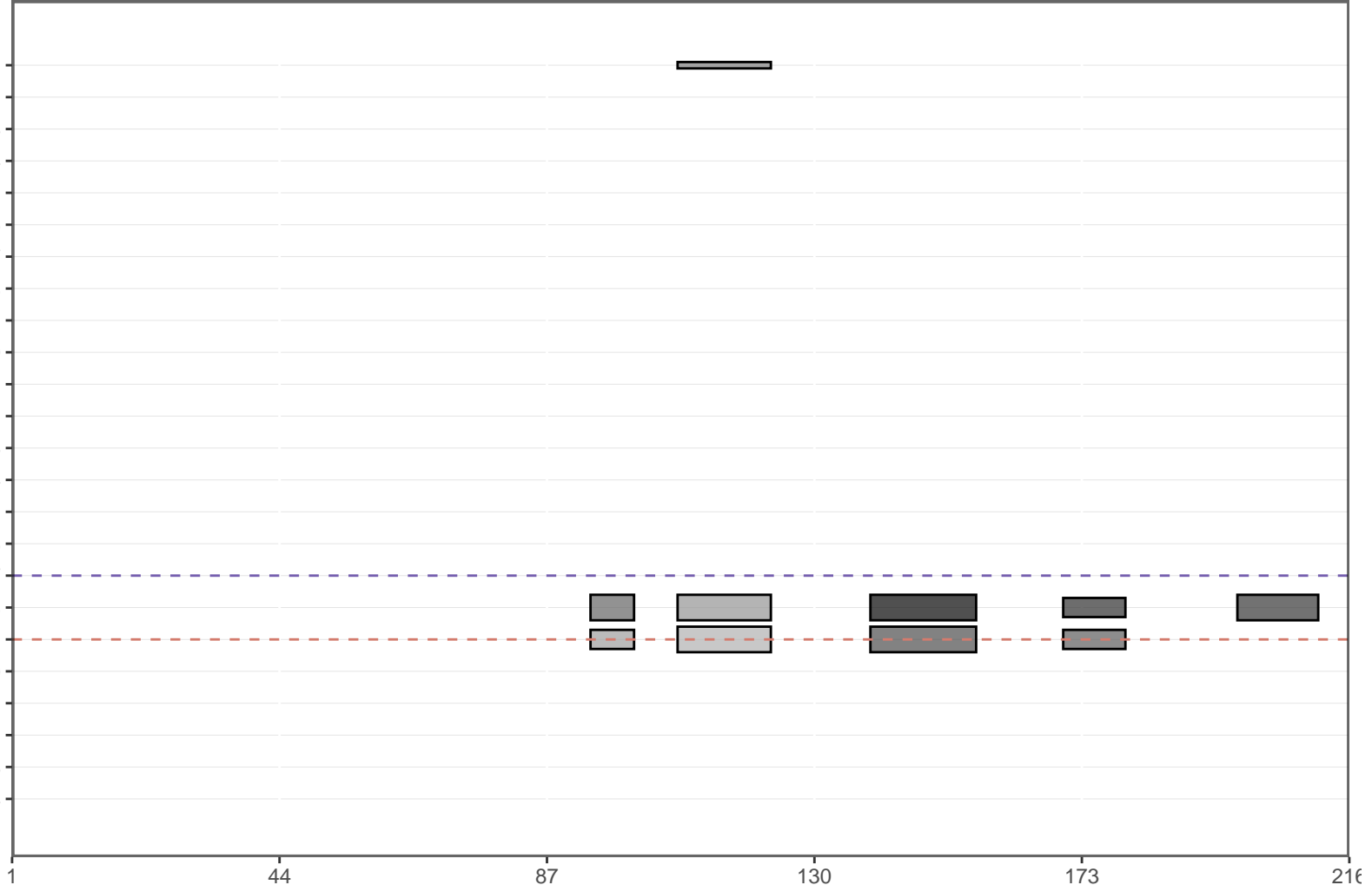
MW indication



Molecular weight

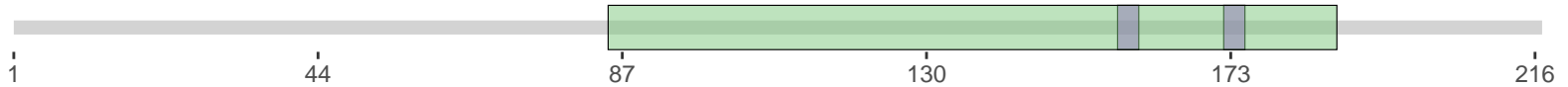


Gel Slice



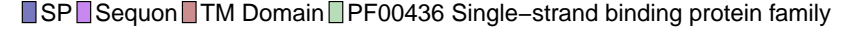
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGQSPVQKLRNGRITVITFTVGTGGMFDQRTGDRNLKPKGGQWHRVAVNDMLGGYSVQGLTKNSVYIEGDIETRYVNDLSEGVKSFICVRRDGRILKGGESVSSISIDELREGLL

NbL11g00760.1 deoxyuridine_5'-triphosphate_nucleotidohydrolase-like [MW = 18.17 kDa]

No. of times detected



log(intensity)



Values from



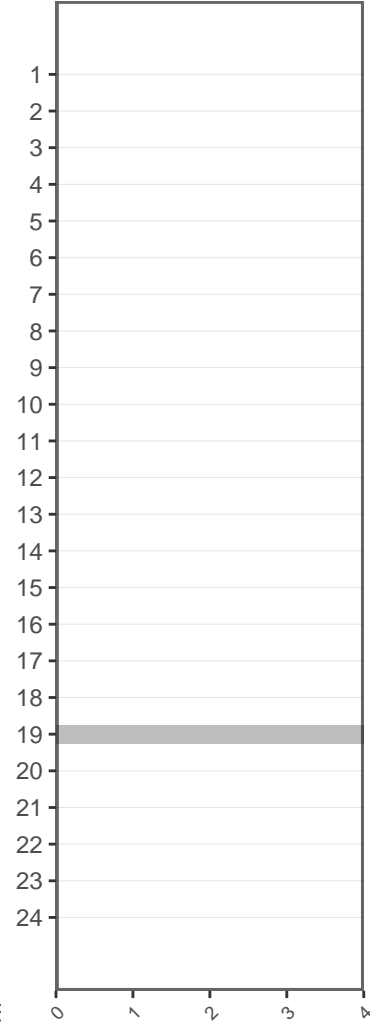
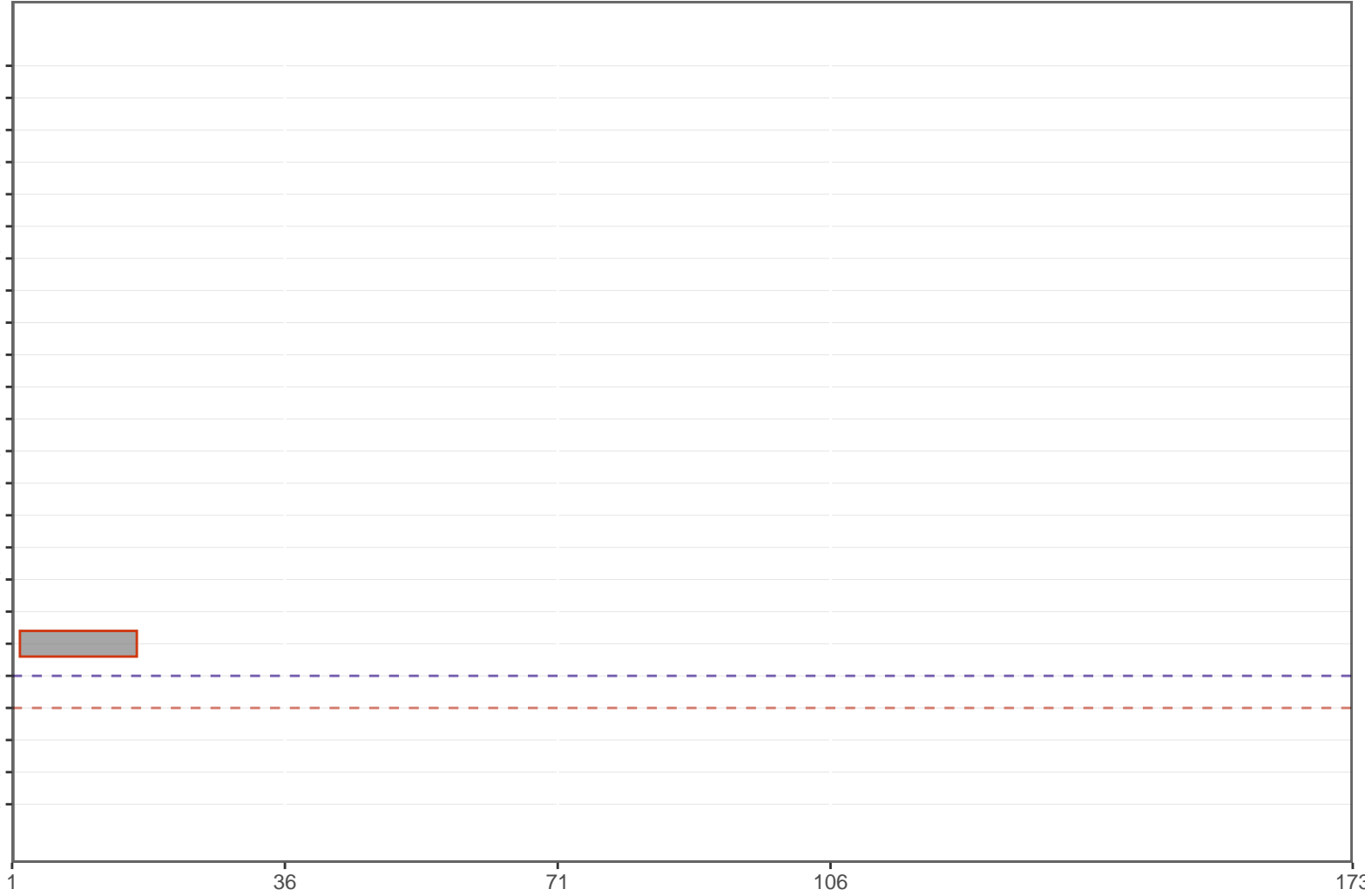
MW indication



Molecular weight



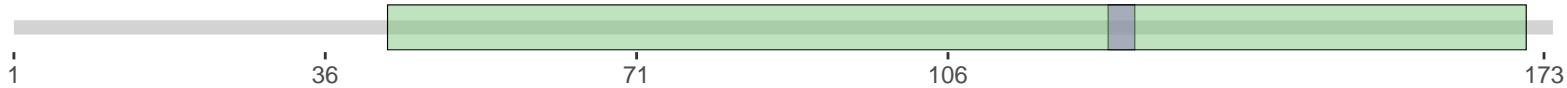
Gel Slice



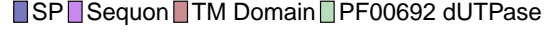
Protein length



Pfam domains



Pfam Description



Protein sequence:

LIPTDLSIAVPCGAWRMAPQSGLAWKHISIDVAGVHDADYRGRVGVVLFNHSIDVDFEKKAGDRAGLIGNVETPDVEEVDDLDSTVRGSGGFGSTGV

NbL11g00660.1 bifunctional_epoxide_hydrolase_2-like [MW = 38.02 kDa]

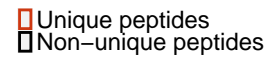
No. of times detected



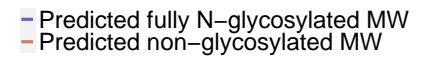
log(intensity)



Values from



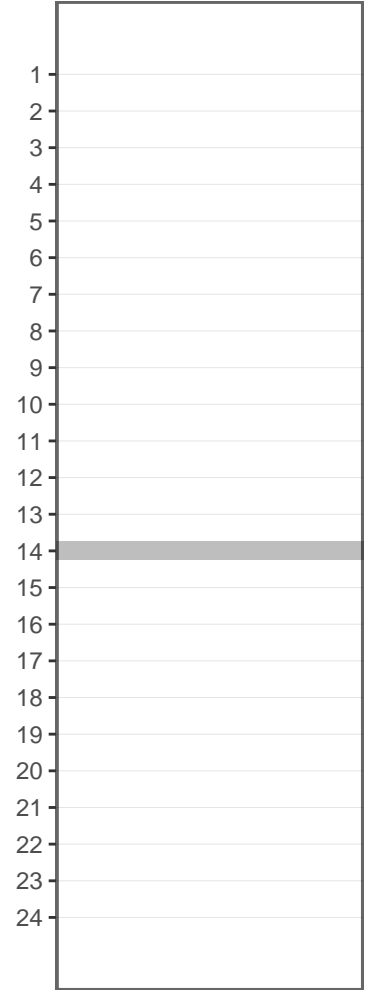
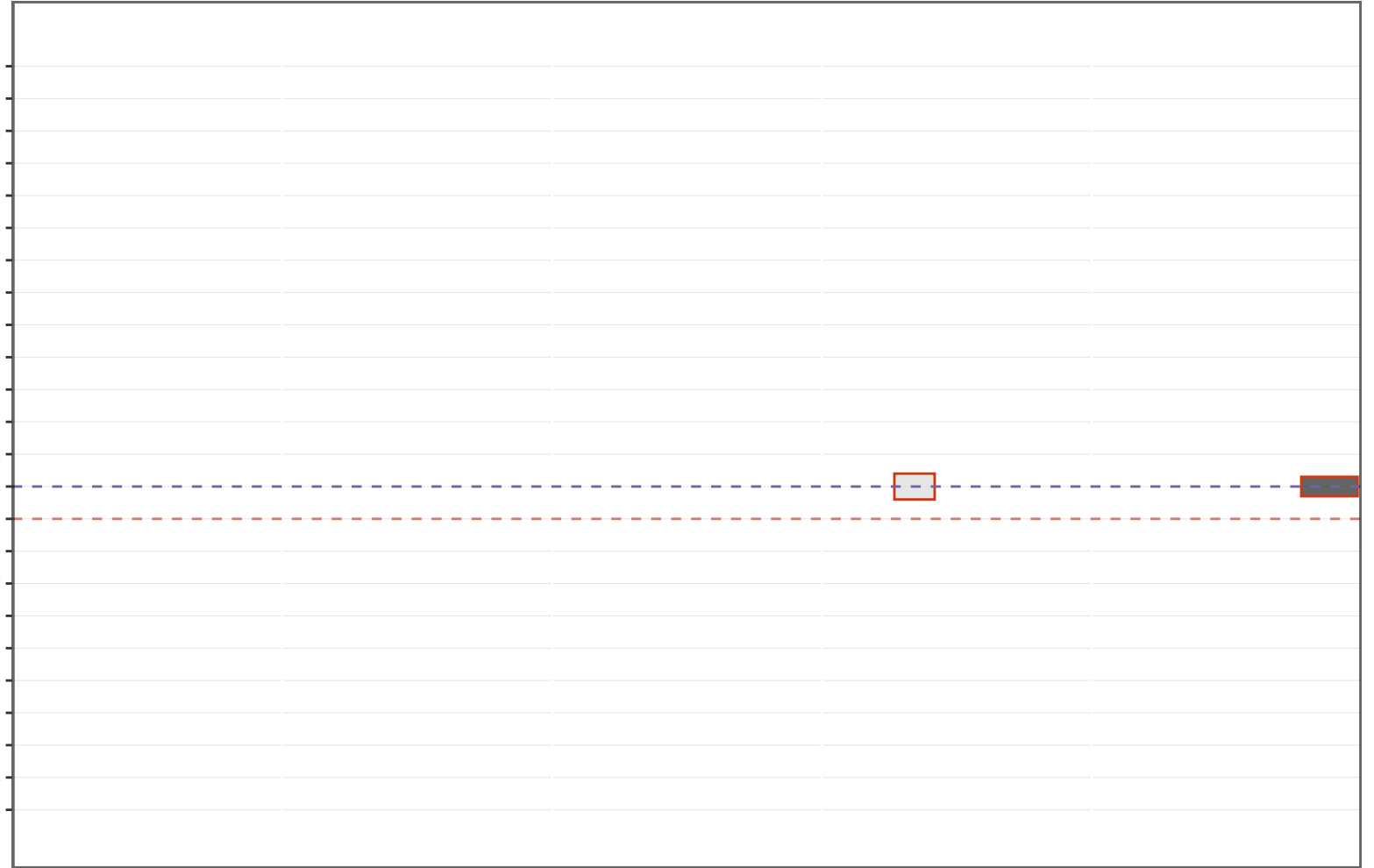
MW indication



Molecular weight

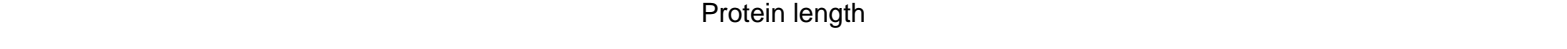


Gel Slice



Peptide counts over 4 repeats

Protein length



Protein length



Pfam domains

Pfam Description



Protein sequence:

KPIPTMRAFFGDDYHMCRFQDFRMEDEIANKGSEAVLKKILTRKCPFPCLPKENPFGISPDGKLPWVLSGDDLUKYYSTKFDQKFTGGLNYYRAIDLNWELTAAWTGAKAKVVPKFMVGEGLDLVYTFPGMKEYVHGGGFKKDVPMILDEDAVVMEGAHFINGERAGETNSHINFINKE

NbL11g00650.1 60S_ribosomal_protein_L18-2-like [MW = 20.83 kDa]

No. of times detected



log(intensity)



Values from



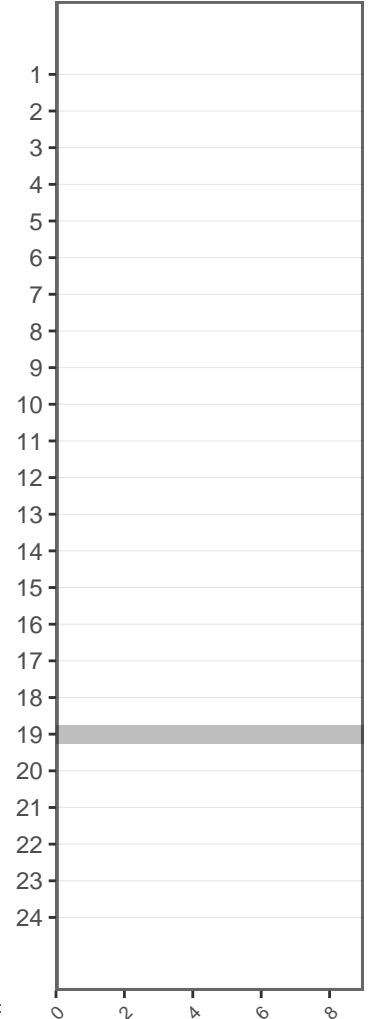
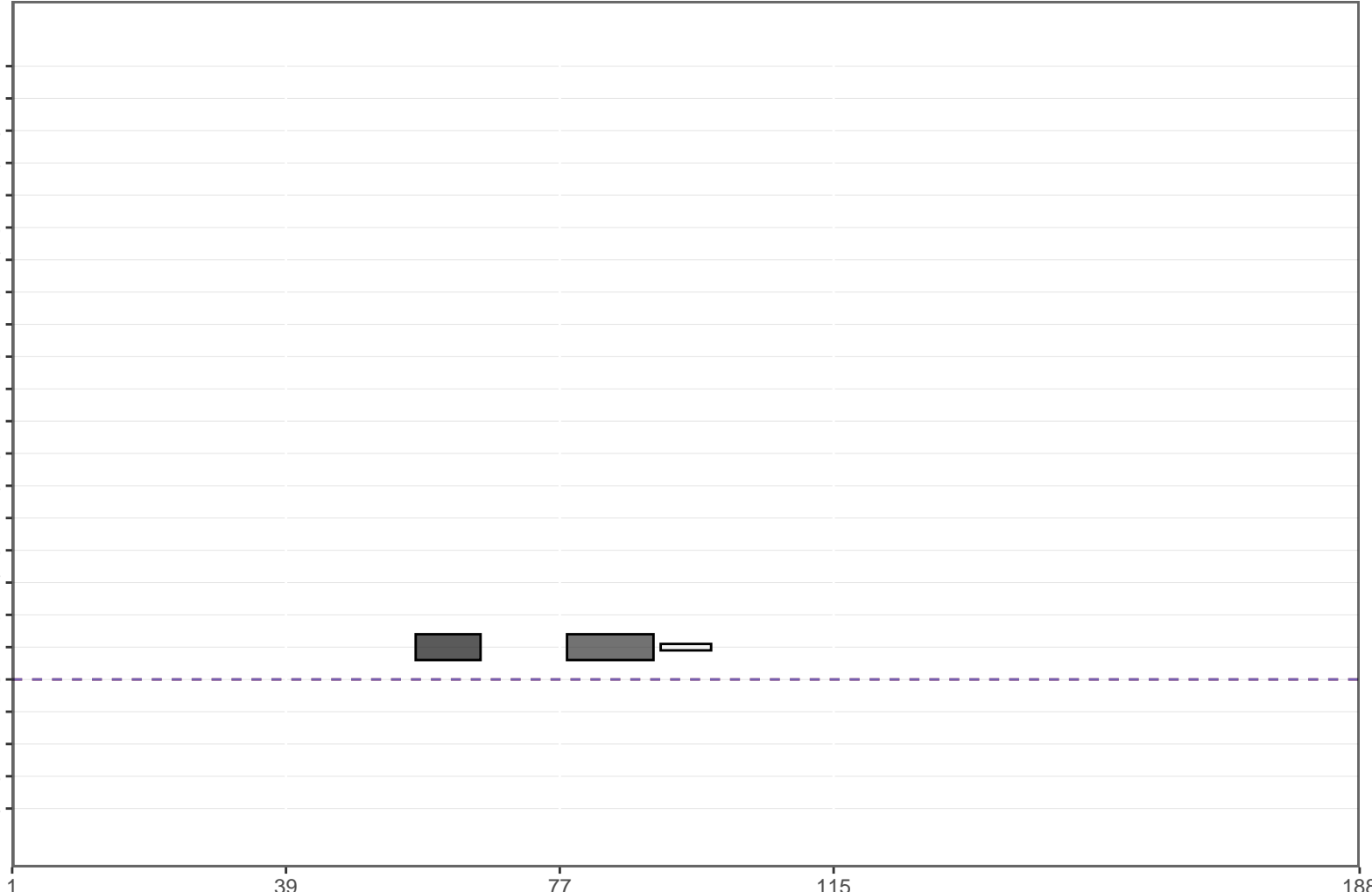
MW indication



Molecular weight

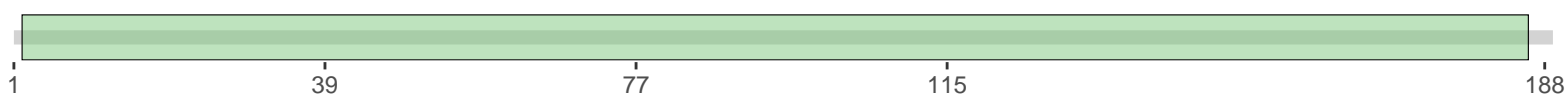


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

3TITDQVRAVEYPLAKVQALREFIKTARARIEKAGGEGELFDGLALRAPLQNTLLLRGPKNAREAVKQIFGAAPGVFHSHTKPFVRSKGRKFERARRRNSRGVKA

NbL11g00590.1 auxin-repressed_12.5_kDa_protein-like [MW = 15.95 kDa]

No. of times detected



log(intensity)



Values from



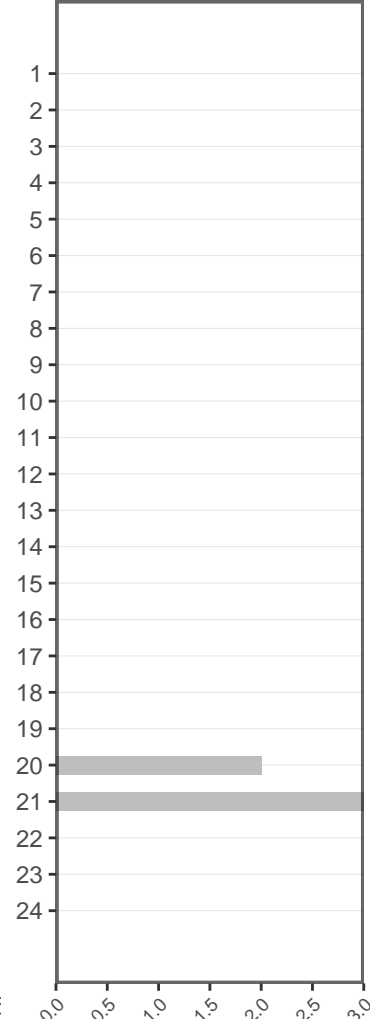
MW indication



Molecular weight



Gel Slice



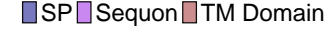
Protein length



Pfam domains



Pfam Description



Protein sequence:

IPRSFNEETSSGDAWRVTRISIMVWPPGSGNRD6FPVSPKGTTPPVFPFAGAGGREAYWERRRRFAVENASGVSPRSPRPVLDL

NbL11g00550.1 probable_Xaa-Pro_aminopeptidase_P [MW = 59.48 kDa]

No. of times detected



log(intensity)



Values from



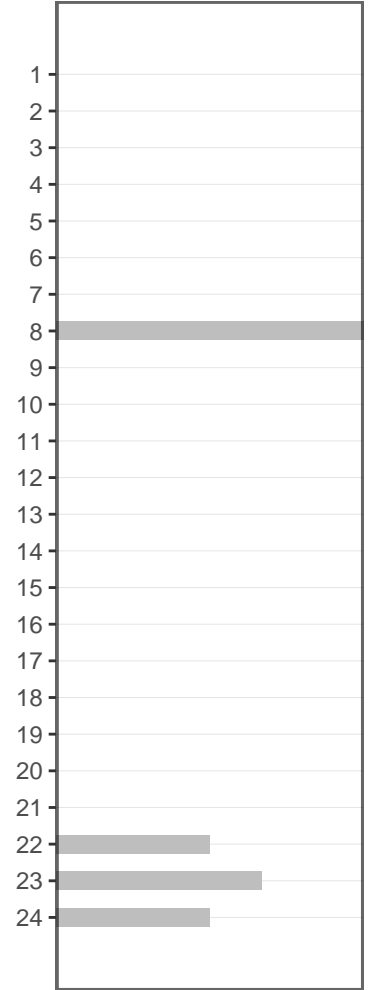
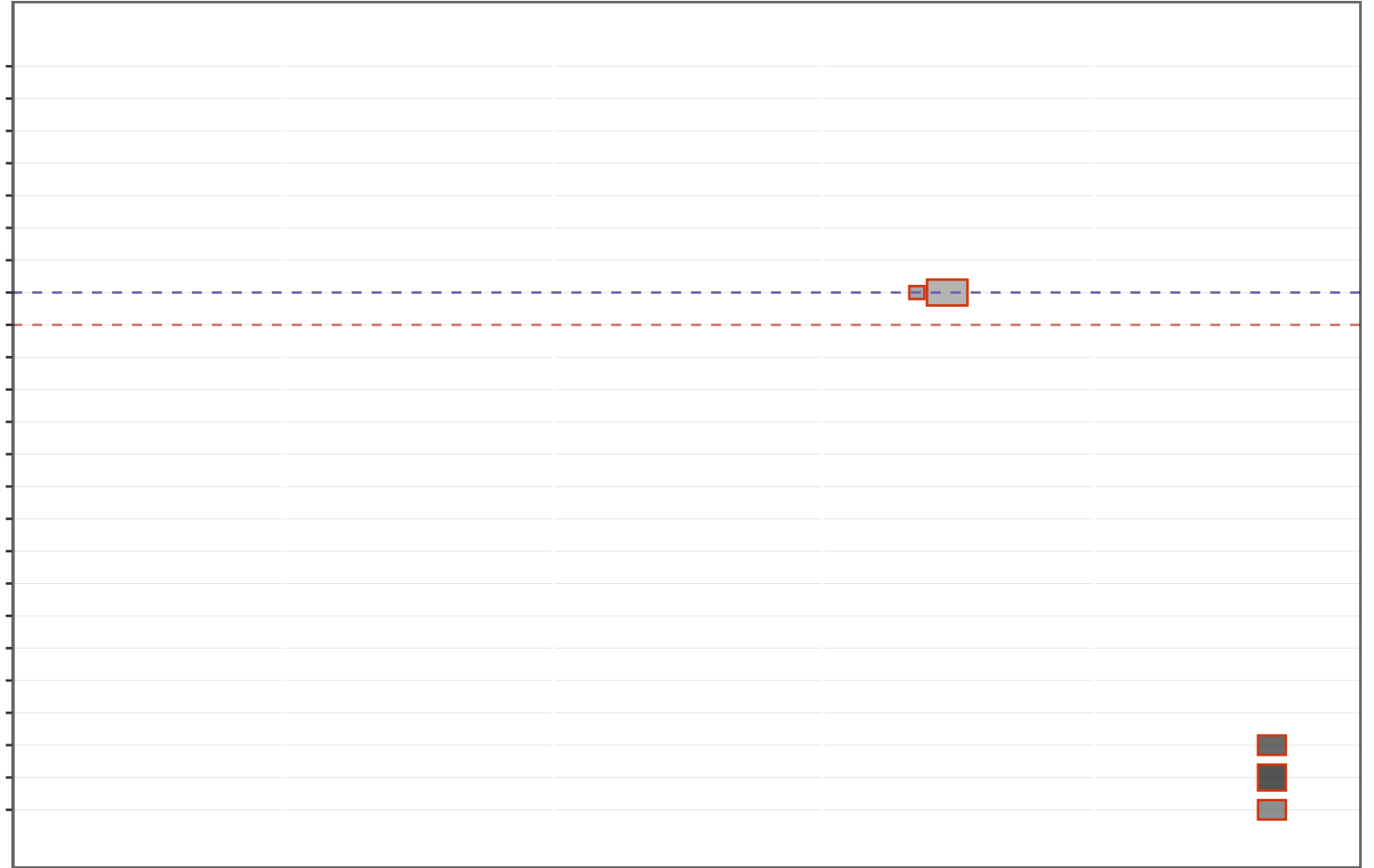
MW indication



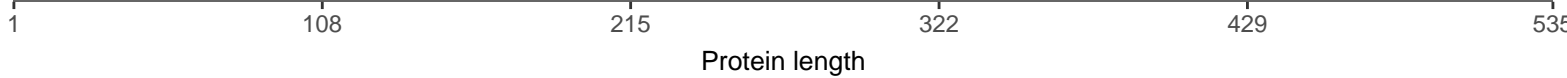
Molecular weight



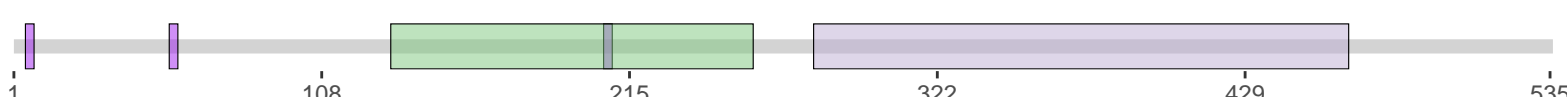
Gel Slice



Peptide counts over 4 repeats

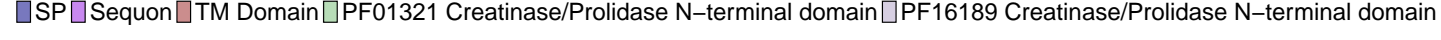


Protein length



Pfam domains

Pfam Description

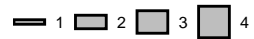


Protein sequence:

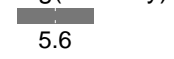
IDSKENHELLVLYDFNLVDENWKEGRPTPKERHLRHLKLVAGVDVSSKLSLRSELKHAGASAVISMALDEIWAALLNRGNDVPRSPVMAYLVLEIDGAKLFADDTKVTPEVMEHLTNAGIELRAYESILSEISLAAGANVLDTSVVAAILNAYESACVYKYPWNSATKSRRKKTANLDSNGSGGQPCAVYRSPSPVSLRKAANKDALEGMNRNCHLRDAAALAGFWAWLEDEIGRNVALTEVEVADKLEFRNGDGLDTSFDITGILVGIIMV

NbL11g00400.1 ATP-dependent_Clp_protease_proteolytic_subunit-related_protein_3_chloroplastic [MW = 35.73 kDa]

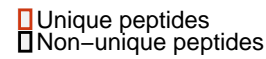
No. of times detected



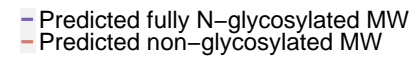
log(intensity)



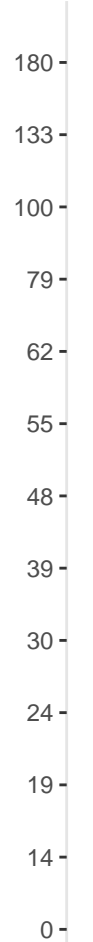
Values from



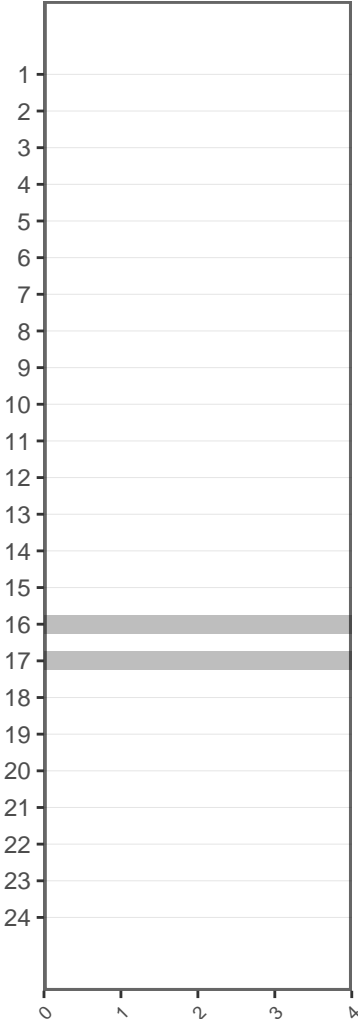
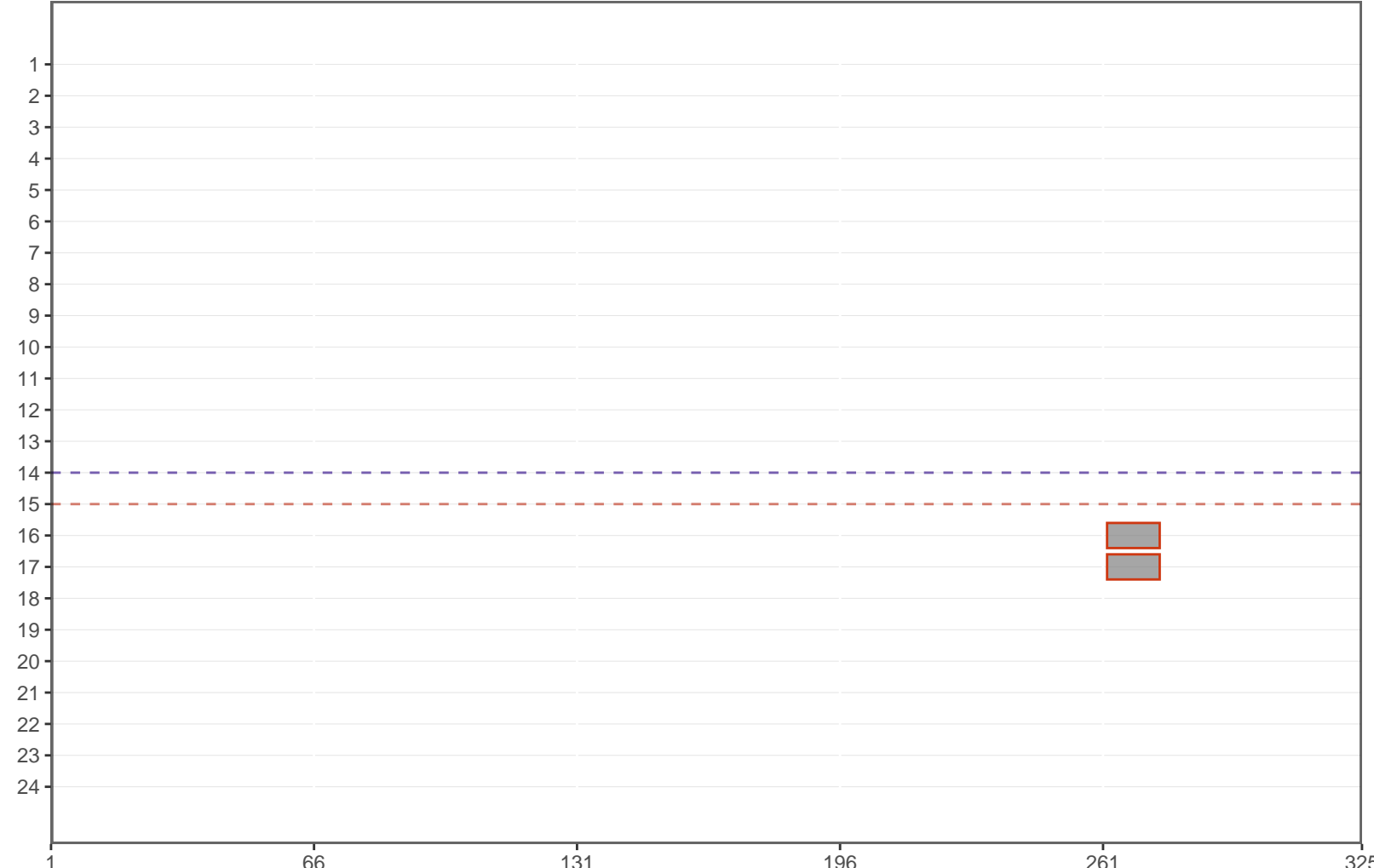
MW indication



Molecular weight

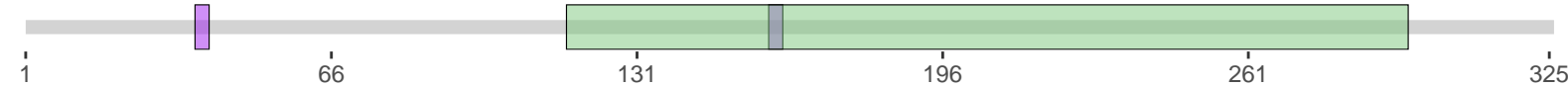


Gel Slice



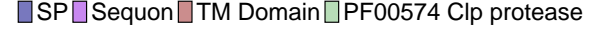
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DPKPEIYLYINSTGTRRDDGETVGMETEGFAIVDMMGLKNEHTVAVGAAGGACILLAAAGSKGRFMMPHAKAMGGPRVPSGLMPSGDFVIRAKEVINRDTLVKLLAKHTENSEETVANVMRRPFYMDATRAREFGVIDKILWRGDEQIMADVSAPEQWDMKAGKVDAP

NbL11g00320.1 xyloglucan_endotransglucosylase/hydrolase_protein [MW – SP = 31.66 kDa]

No. of times detected



log(intensity)



Values from



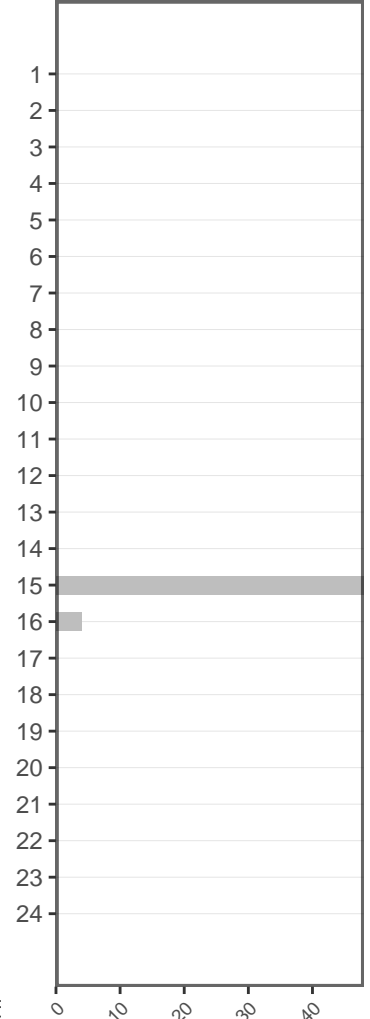
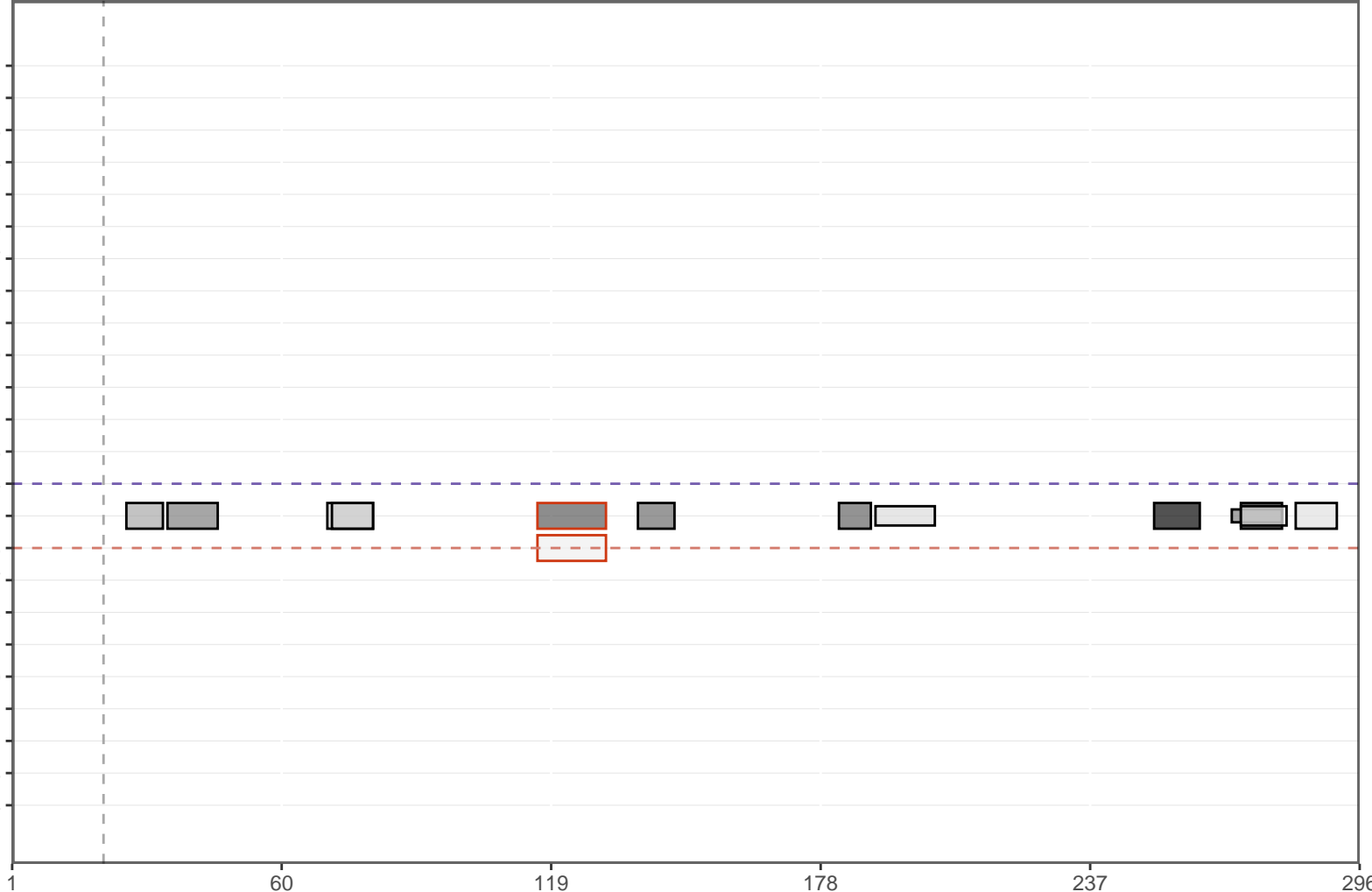
MW indication



Molecular weight

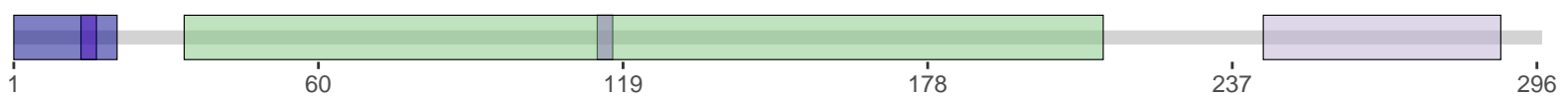


Gel Slice



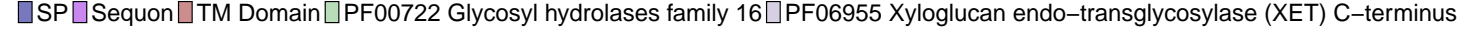
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

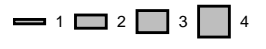


Protein sequence:

SRILYWFDPDKGYHSEYSLVWNTFGVDFVDDVPRIRAFKNSKDLGVKFFPFGPMKYSLWADDDWATRGGLEKTDWNAFFSASVTSFHYDGGCAATPLEVQIGNTKGMRRWDDQKAFQGLDALGVRRLLRWVRGKYTYVNYCTDRKRYPLPPECTKDRVY

NbL11g00170.1 acyl-CoA-binding_domain-containing_protein_4 [MW = 73.99 kDa]

No. of times detected



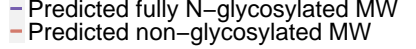
log(intensity)



Values from



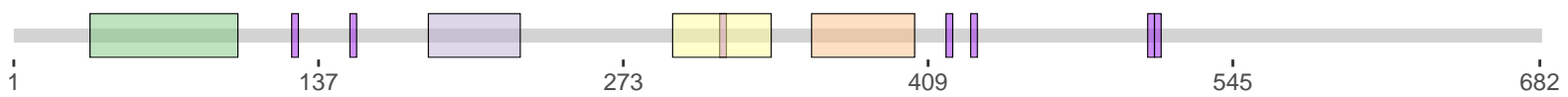
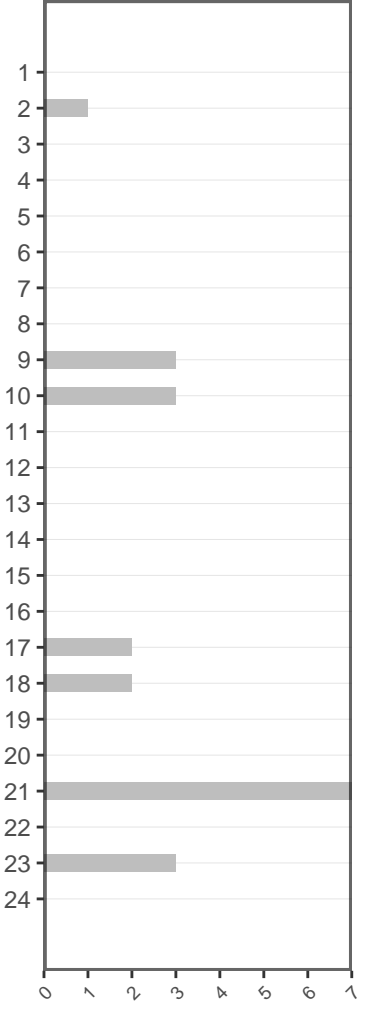
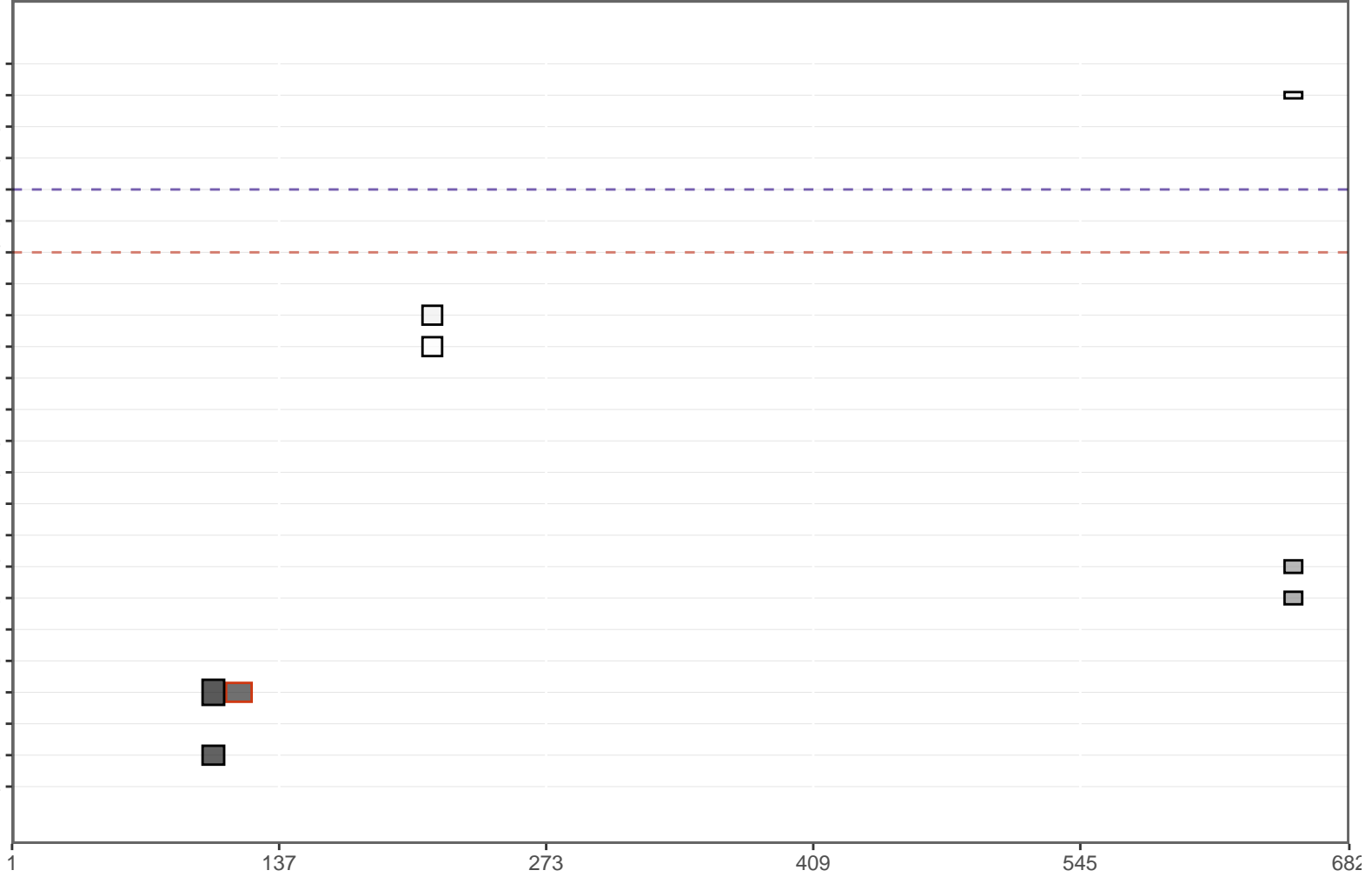
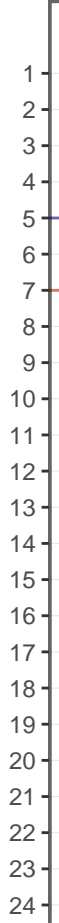
MW indication



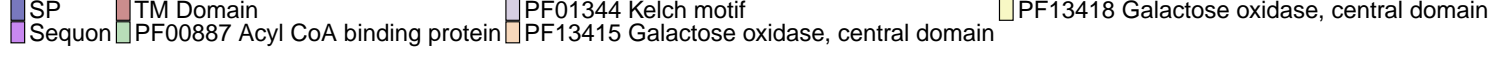
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

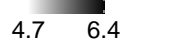
TMTVDKMTGLQVPPSPRSDHAAWAHRYLLVFGGSHATGNDLHVLDDLDTMEWNRPTQGGKPEIPRAGHAGVTVDENWFTGGNNKSGVSETVLANMSTLQWISVITVYDGRVPLASEGLSILVGGYNGEDILVDFGGYNGRYNEANVLPKPHKSTLQSKMMETVYDQVSAVGNATNRDLESETVYDGGKGFREIVDIEGEPVWVKVEETSERLLAALKAENELESSLKSKLQTLQKDDTDDEARNTGLYKKGDDAKLLELQYRQDLAADDSCIC

NbL11g00140.1 translationally-controlled_tumor_protein_homolog [MW = 18.91 kDa]

No. of times detected



log(intensity)



Values from



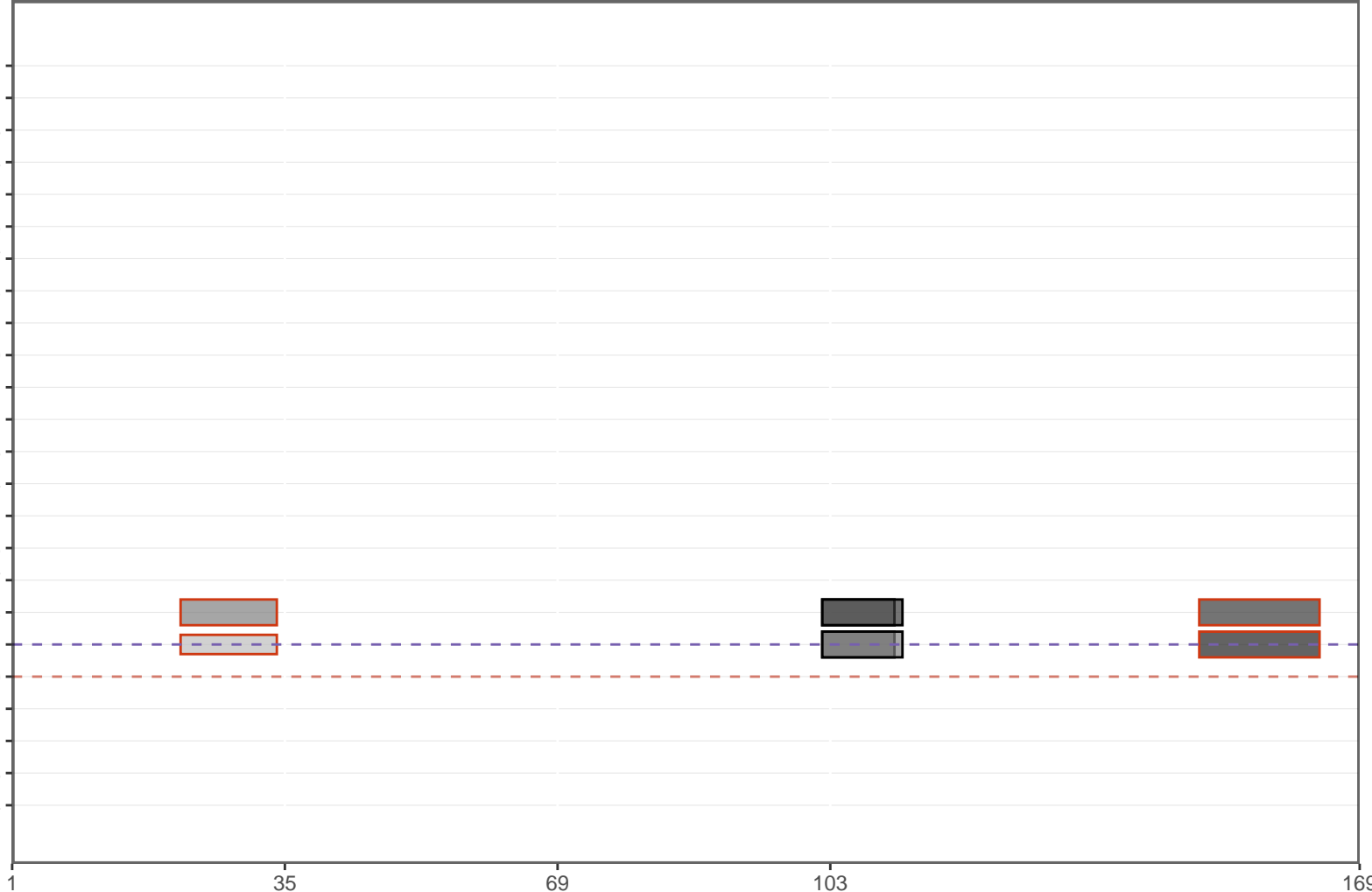
MW indication



Molecular weight

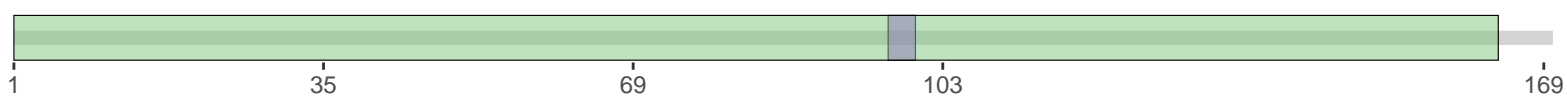


Gel Slice



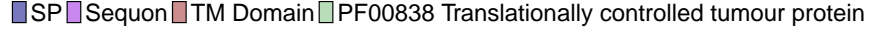
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VDTFRLEQPSFDKKGKGFVYMKRKYKLNTPKLEGEAGEAFKKNIESATKFLMSKLDLGFVGSMSHDDGALVFAYKDKGATDPTFLVAPQLKEVKG

NbL11g00110.1 60S_ribosomal_protein_L22-3-like [MW = 14.06 kDa]

No. of times detected



log(intensity)



Values from



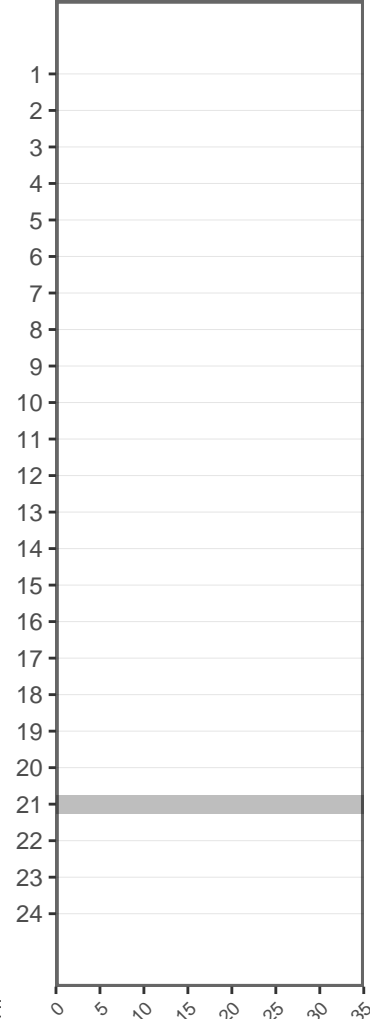
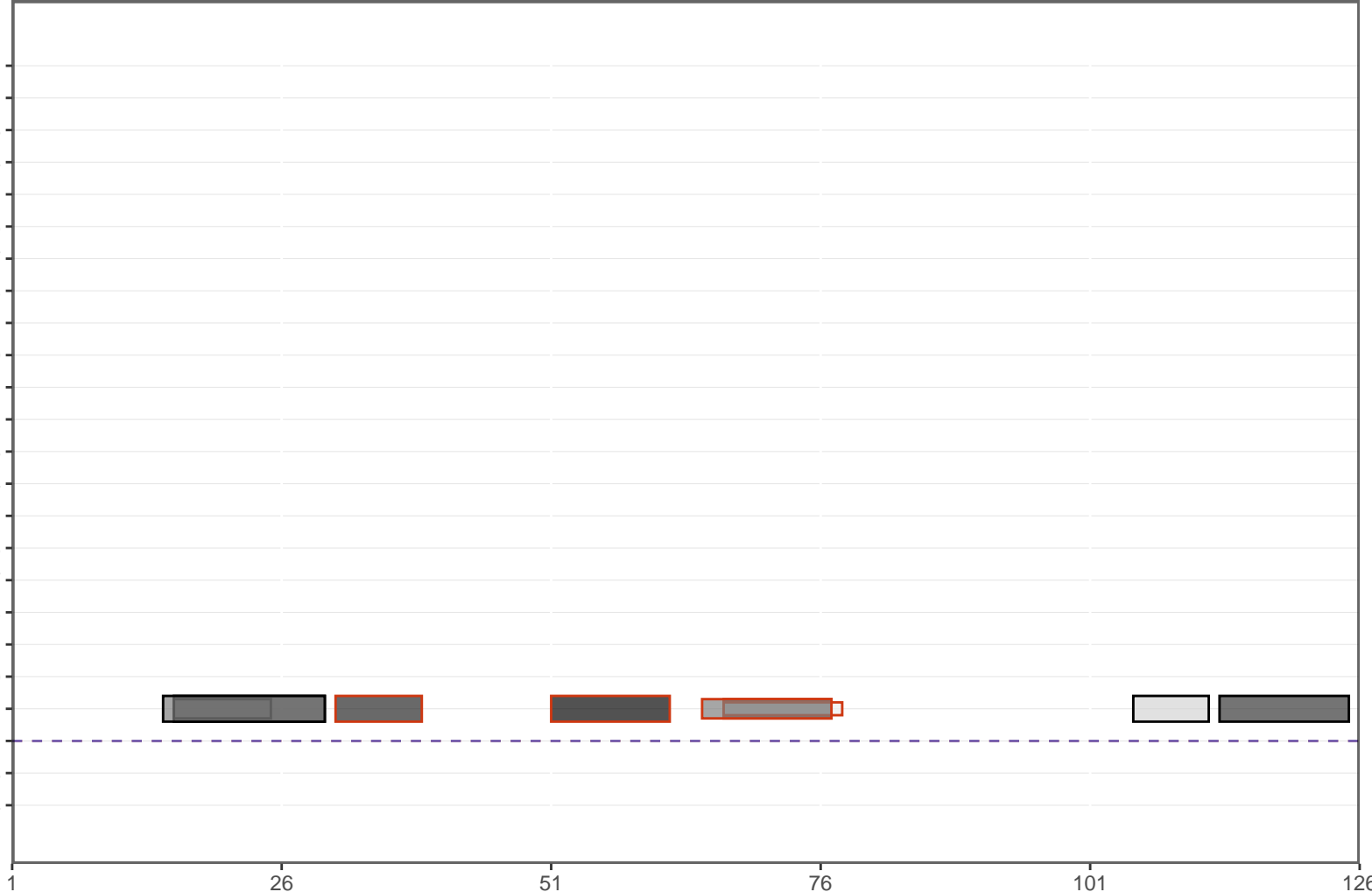
MW indication



Molecular weight



Gel Slice



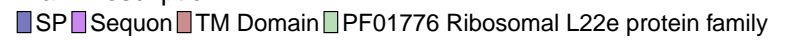
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

KAGALGDVLTITRDKTKITVTSSESTFSKRVLYKYLTKYLNKNNVROWLRVISAANDRNIVYELRVYFNAENEAEEDP

NbL11g00080.1 acetylajmalan_esterase-like [MW - SP = 39.73 kDa]

No. of times detected



log(intensity)



Values from



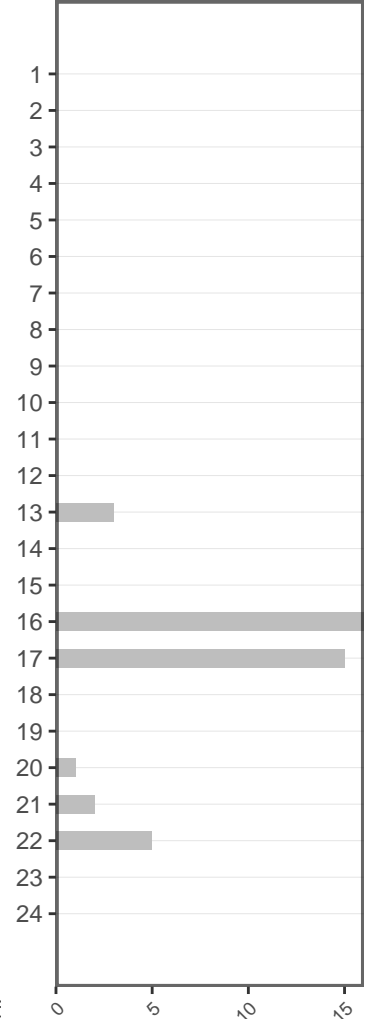
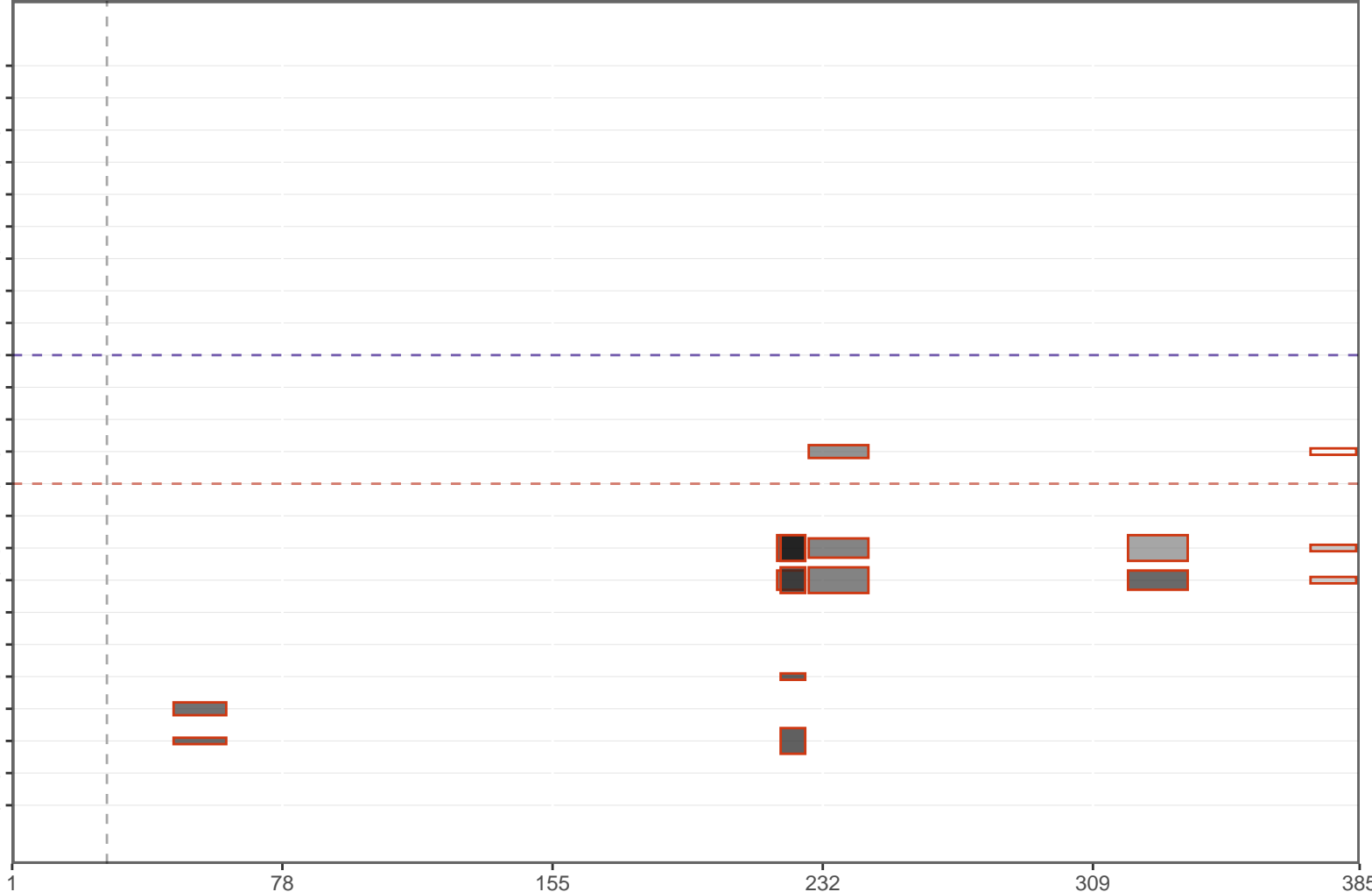
MW indication



Molecular weight



Gel Slice



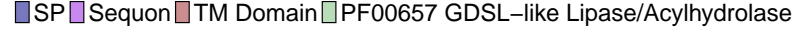
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

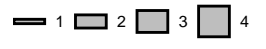


Protein sequence:

...FLVGEIGGNECTHLLLEGKTHEESRRVPEVEAIHQVRRVBLGATRIIVPQNFPSGGFFPLTKFMTNNSAYDEHNGKDFNLIFFNDHLGQAKGELKEYPNTLYGDYNAVYIWLGNVSLGDFDRINSLQKAKGGGGDYPFDIHNKNGGAPGVGVGVDPFTTYSWDGHLTQEAYSWLVRWLDNMLPQLNGQV...

NbL11g00010.1 brefeldin_A-inhibited_guanine_nucleotide-exchange_protein_1 [MW = 98.41 kDa]

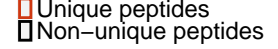
No. of times detected



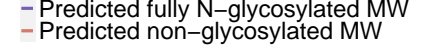
log(intensity)



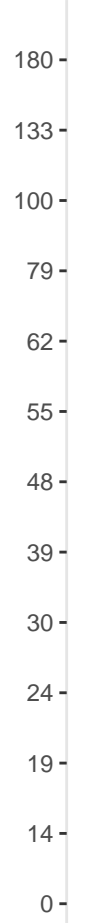
Values from



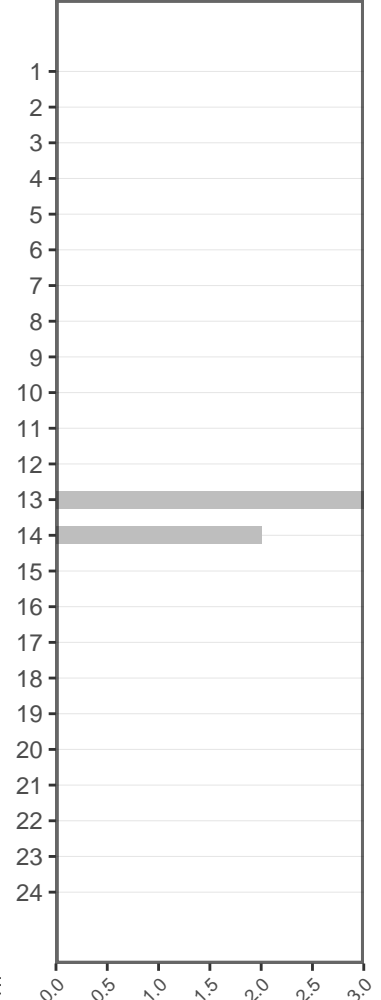
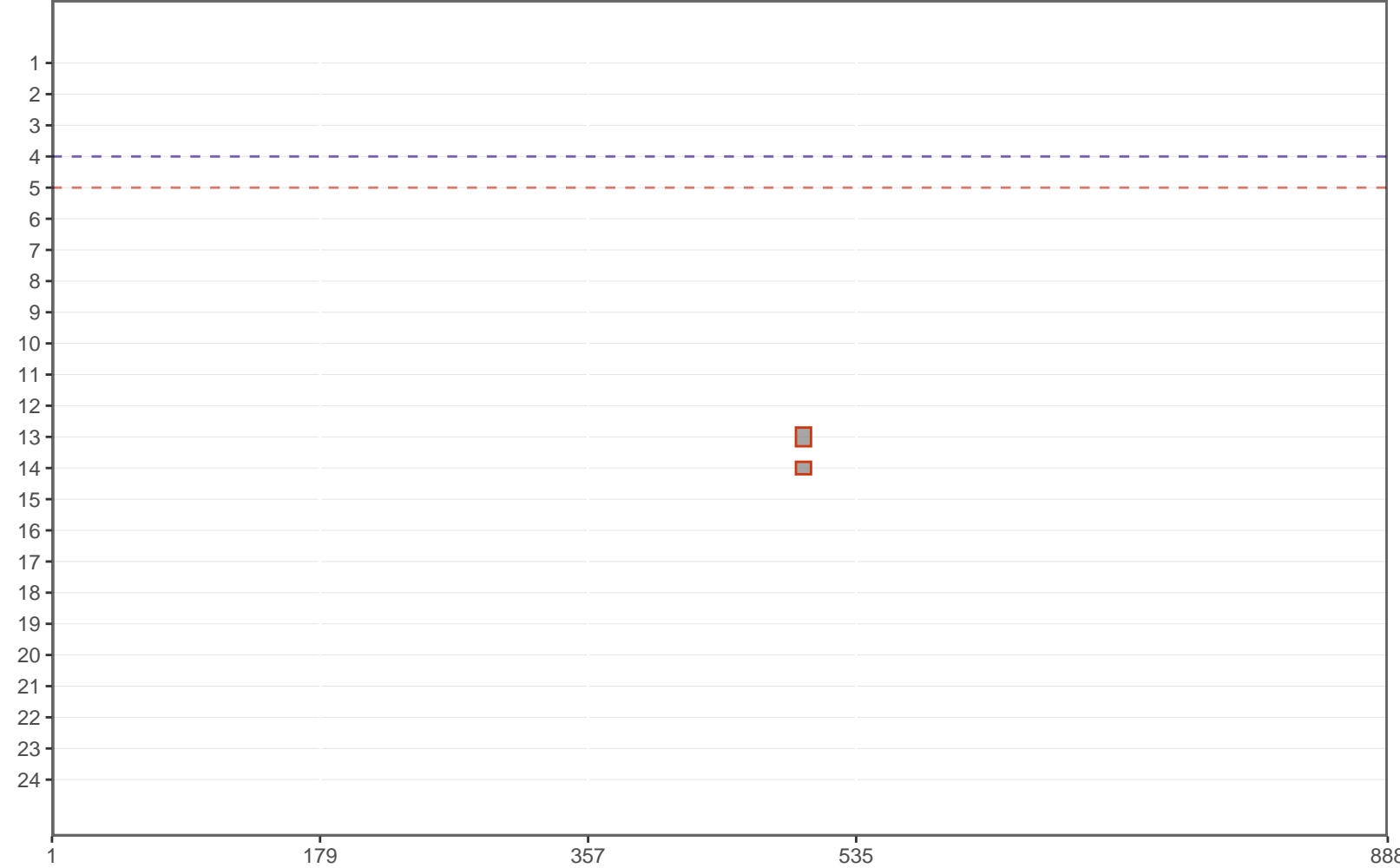
MW indication



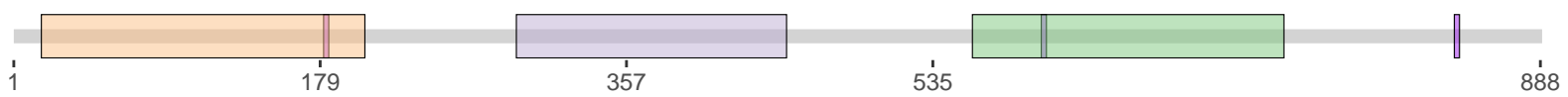
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

- SP
- TM Domain
- PF12783 Guanine nucleotide exchange factor in Golgi transport N-terminal
- Sequon
- PF01369 Sec7 domain
- PF16213 Dimerisation and cyclophilin-binding domain of Mon2

Protein sequence:

IIIDVFNYYDCCVDAPNFIFERTVNGLLKTKALGPPPGSTTTLSFVGDITFRSEGSVGLVTRIKSMGTWMDGQLKVGEPNLDKVSQDHEVPEAATSVSEEGNIQVLEHPEANSEFSGAAALEQRRAKYLEGKQGVSLFNRPKPSKGDIFLMTSKLGNSEPDVASFKNITGKLPSTIGDYLGEREEFPLKVMHAYVDFNFEGMDFGSESRVFLRGLRPLGEGAKIDRMEKFAERYGKGNENSFSAETAVLAYSVIMLNTDAHNSMVKDKMTKADIRRNNGIDGKLPENLYG.

NbL10g24670.1 probable_inactive_purple_acid_phosphatase_27 [MW – SP = 66.7 kDa]

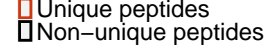
No. of times detected



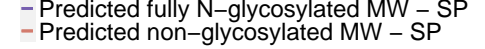
log(intensity)



Values from



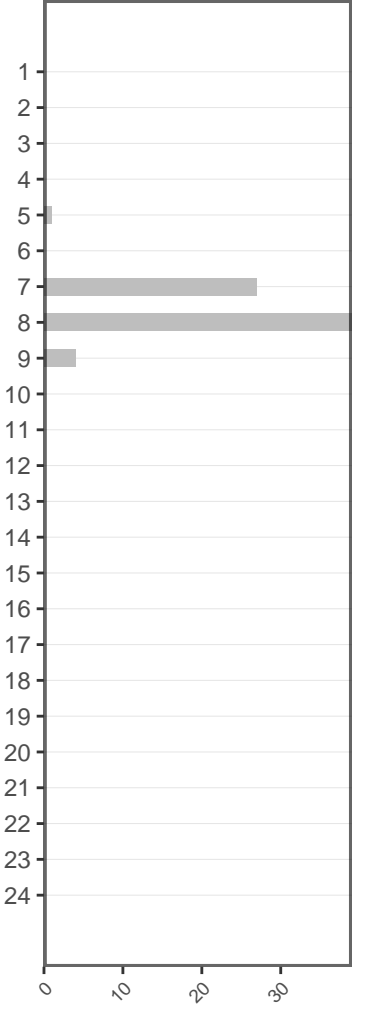
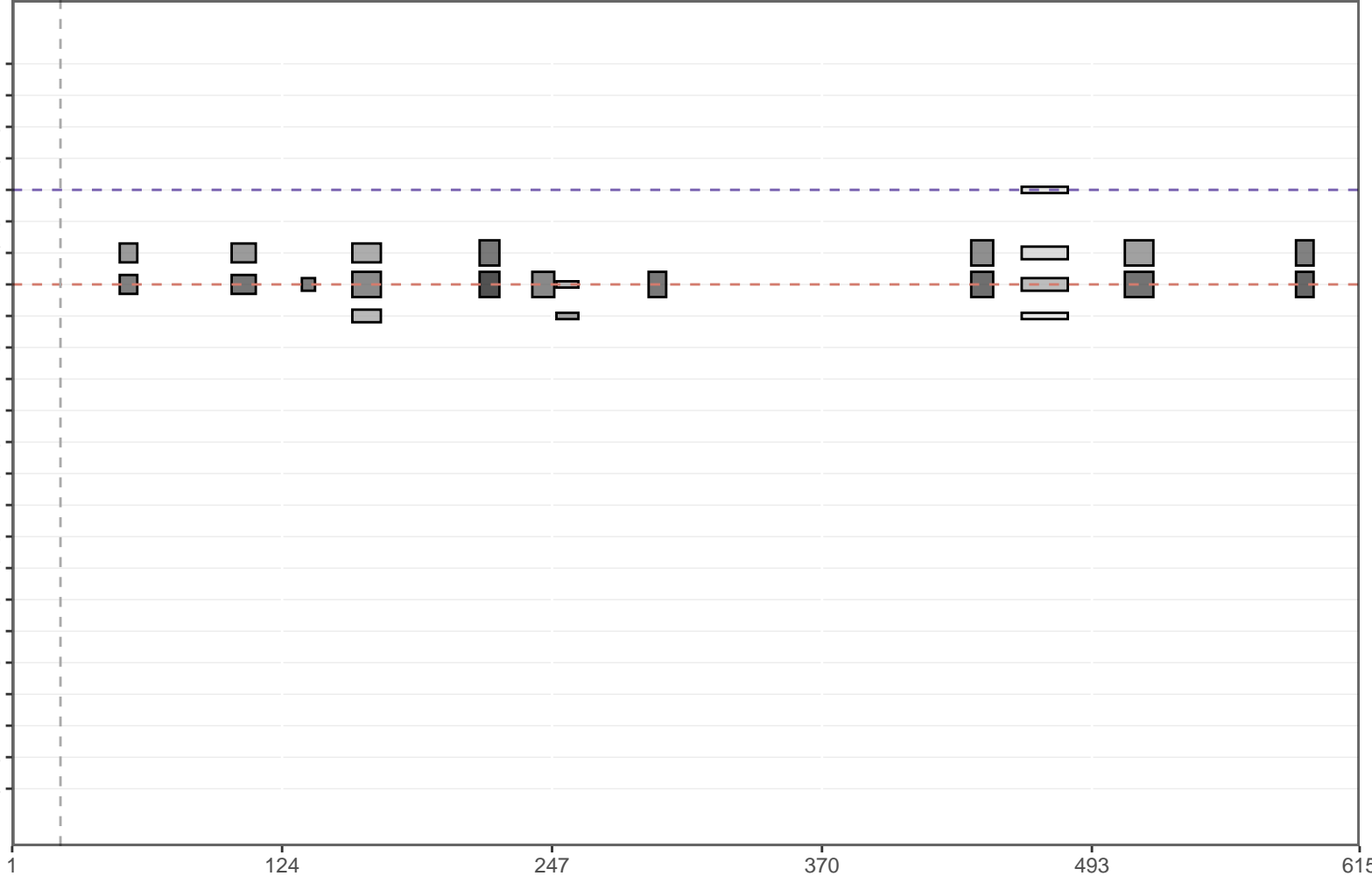
MW indication



Molecular weight

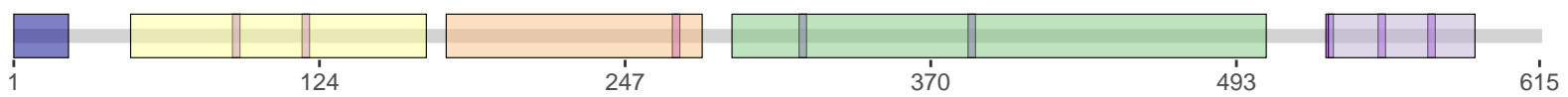


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00149 Calcineurin-like phosphoesterase
- PF14008 Iron/zinc purple acid phosphatase-like protein C
- PF16656 Purple acid Phosphatase, N-terminal domain
- PF17808 Fn3-like domain from Purple Acid Phosphatase

Protein sequence:

IGKAERDGSNEYSNYQPGSLNITFDGLIKLNDIVFHIGDITYANGVISQWDGFTAQVQPIASTVPIYMAISGNHERDCPTGTGSGFYEGNDSSGGEGGLAGTMEYVVDADRANKFVYSTDGGMFHFICADSEHDWRREGSEQHKFIEHCLASVDKRGKIPWLIFSARHVLGYSSDKWYGGGSEFEPAGREGLQKLGWQKYVVDYAFYGHVHNYVERTGPIYQKDCVNSERSHYGGVANGTHVYVGGGGHLSFSPVNTTWLWLYKDKVDWGFVLTAFNHSLLLFYKXSRDGI

NbL10g24660.1 snurportin-1-like [MW = 48.81 kDa]

No. of times detected



log(intensity)



Values from



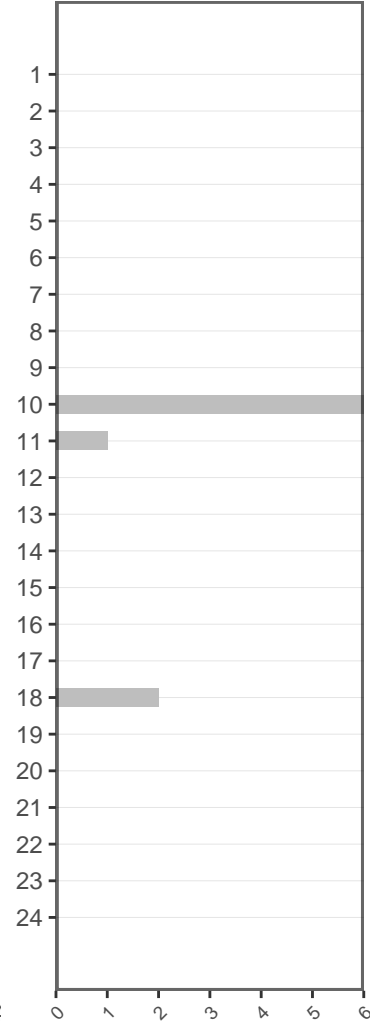
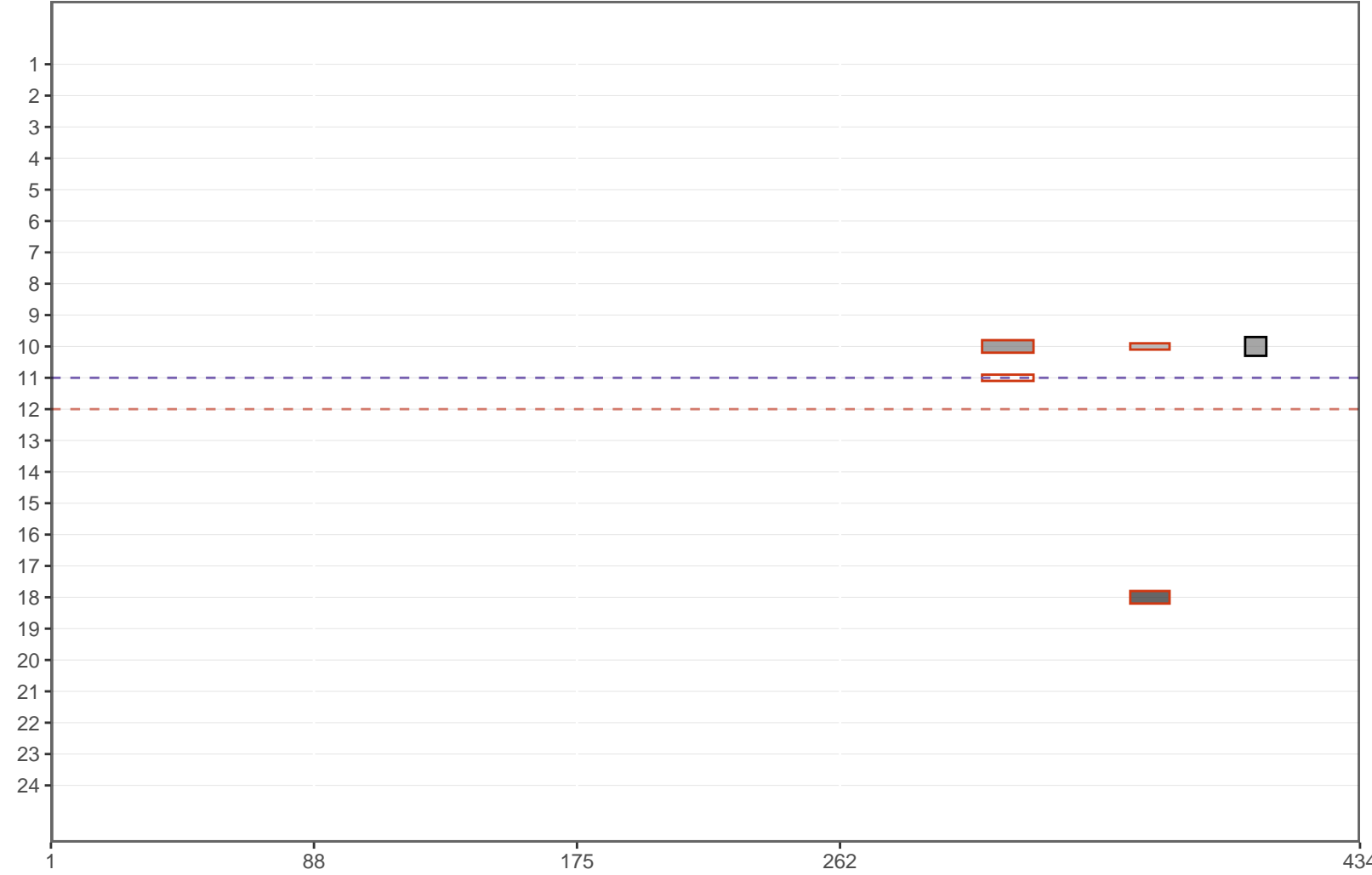
MW indication



Molecular weight



Gel Slice



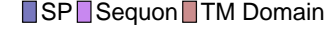
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GVCWAGLSLYECTAEFFRFVNLNSKLAETGAGDAPSTGCHRYKFTSLPVPYNGDKELHTAYAGGVPYKDGLLFYNKHAHYGTGNTPLVWKDENGSGVYIDTINKGQVPSGQGVVLELLDDGLRLATSDPPVVFQGLLGDPIQKTELHRGDLIKFAISEGGVLFQDSEKLEKADLVGLGKSNRRAFADGYSKVLFDQYARHSPLRIEHLFASISGGVEDGSRSTGDDAMAGP

NbL10g24550.1 photosynthetic_NDH_subunit_of_subcomplex_B_3_chloroplastic-like [MW = 21.64 kDa]

No. of times detected



log(intensity)



Values from



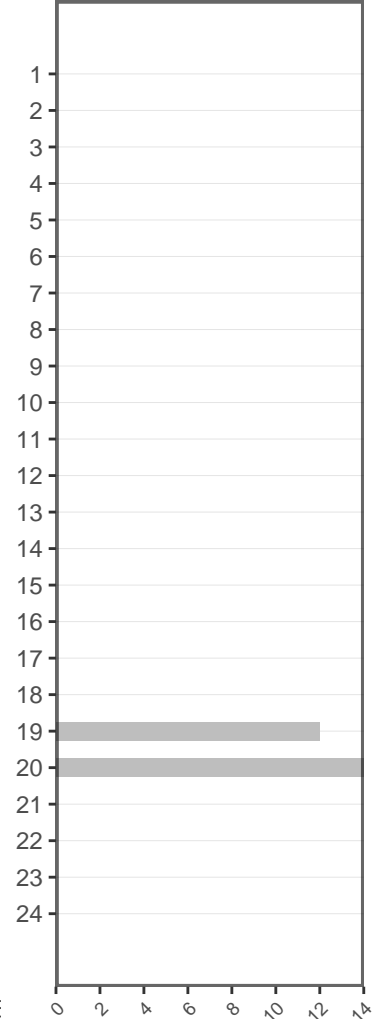
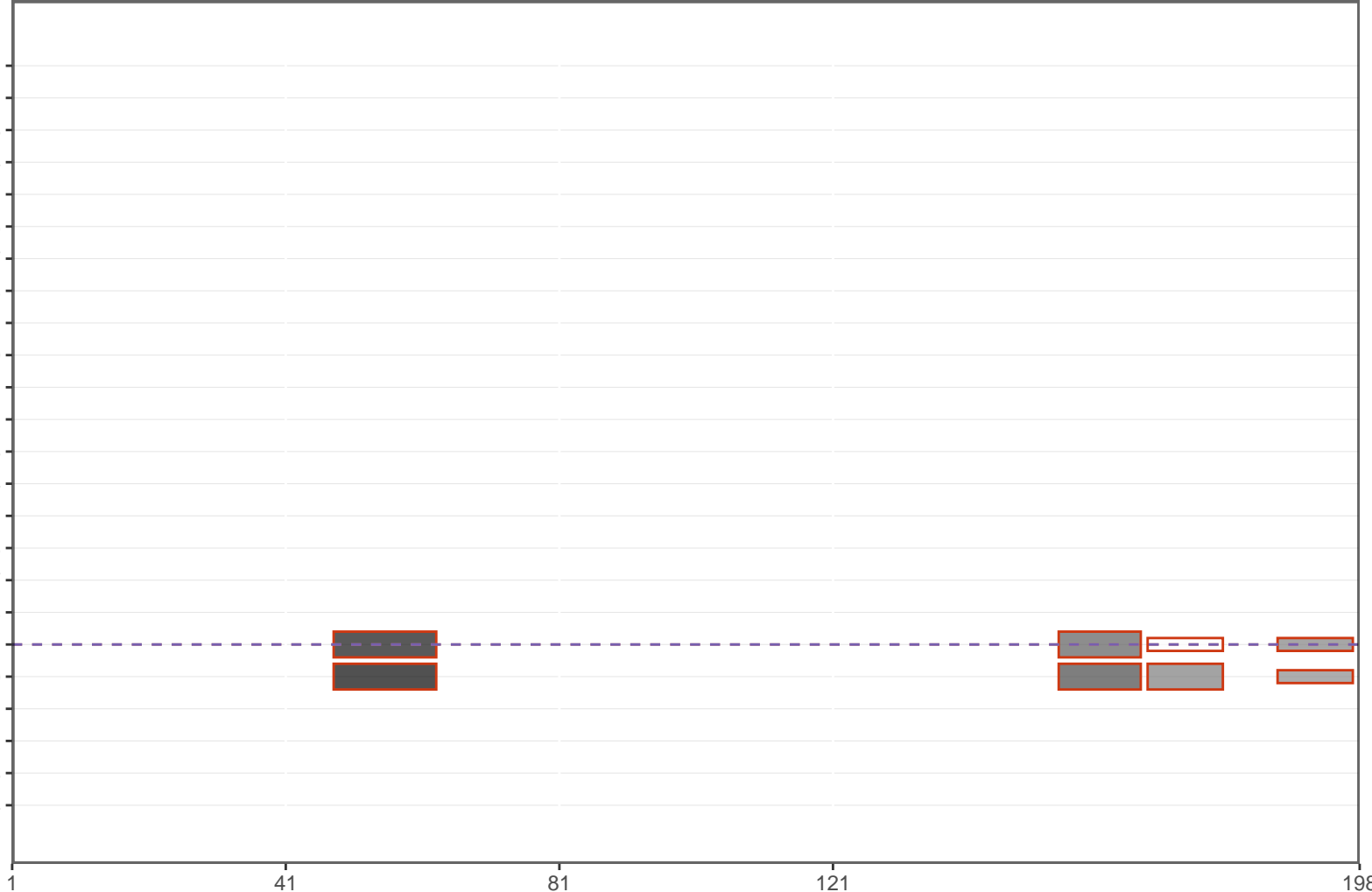
MW indication



Molecular weight



Gel Slice



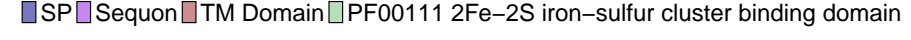
Protein length



Pfam domains



Pfam Description

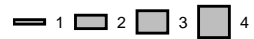


Protein sequence:

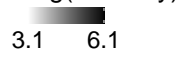
KLRLDMLDANVELYGPVRLNDGGGGTGTGLVEVEGKELLNPRDKENNHEDLKRHPKRWLADGANVGPDSRGMVIGQLPEWKAHEWNYRGLPPIQIEEKEK

NbL10g24540.1 50S_ribosomal_protein_L11_chloroplastic-like [MW = 23.12 kDa]

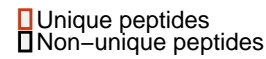
No. of times detected



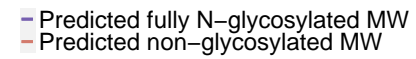
log(intensity)



Values from



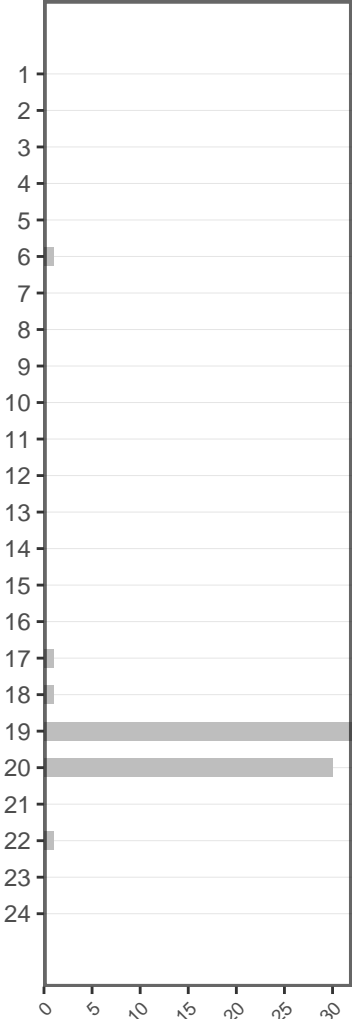
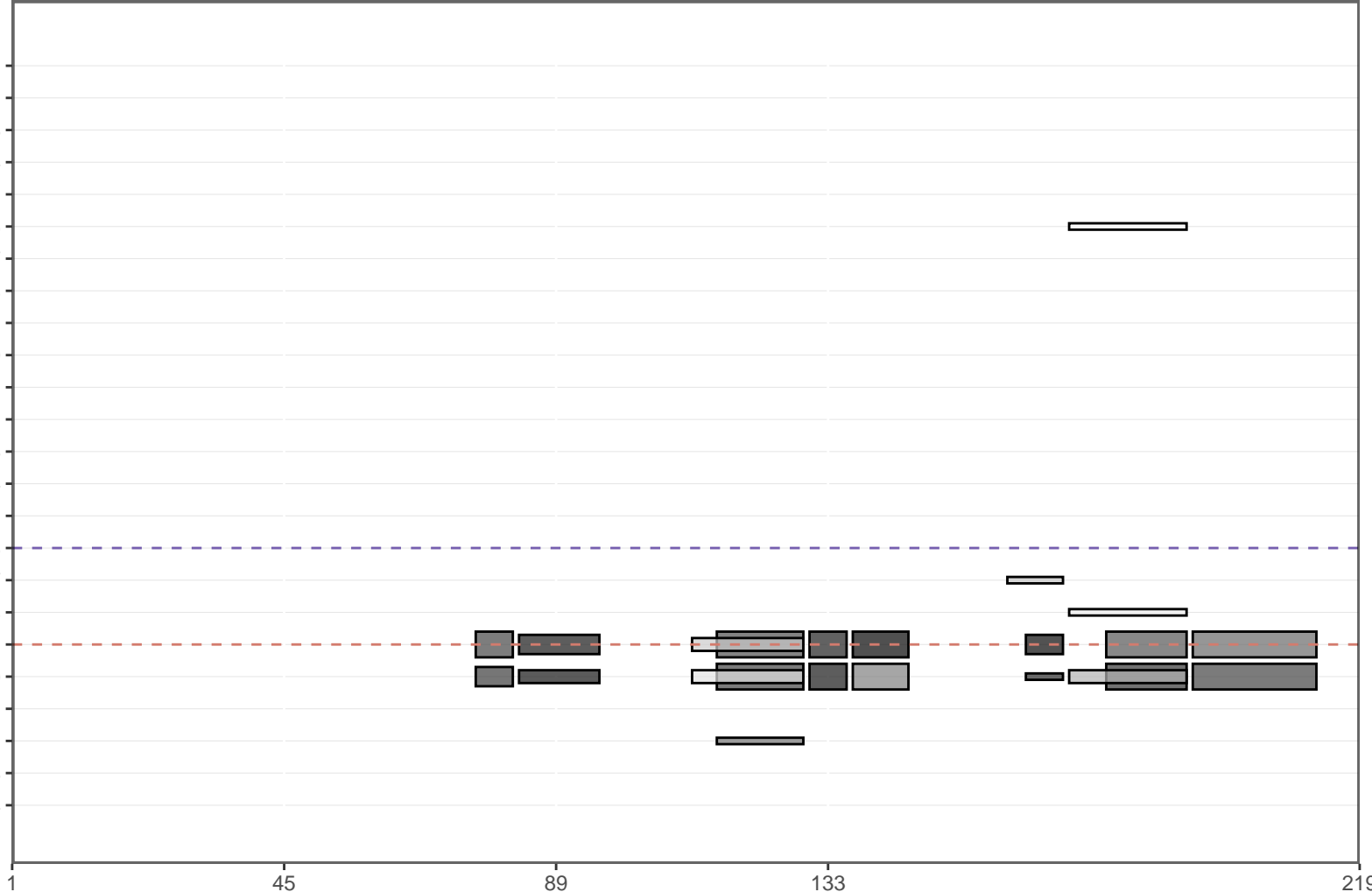
MW indication



Molecular weight

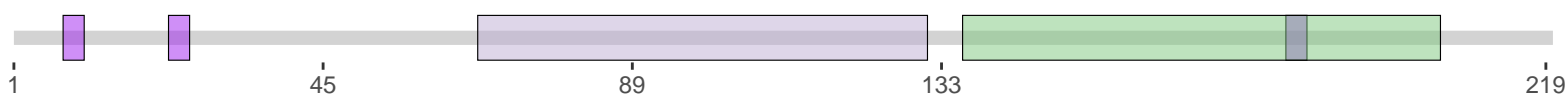


Gel Slice



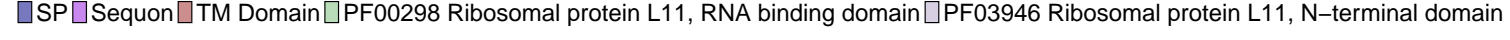
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISKGVNIIMFKIDYNARTADKAGVIVPEVTVVDDREFTFLKTPPAVLLKKAAGVEKSGKDPGRDKVIGITDQLKTAAGEKLPDLNGTTIESAMRIIAGTAAANGIDIDPPVLEPKKKELYV

NbL10g24530.1 soluble_inorganic_pyrophosphatase_PPA1-like [MW = 24.07 kDa]

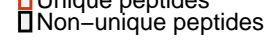
No. of times detected



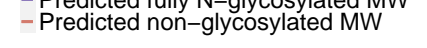
log(intensity)



Values from



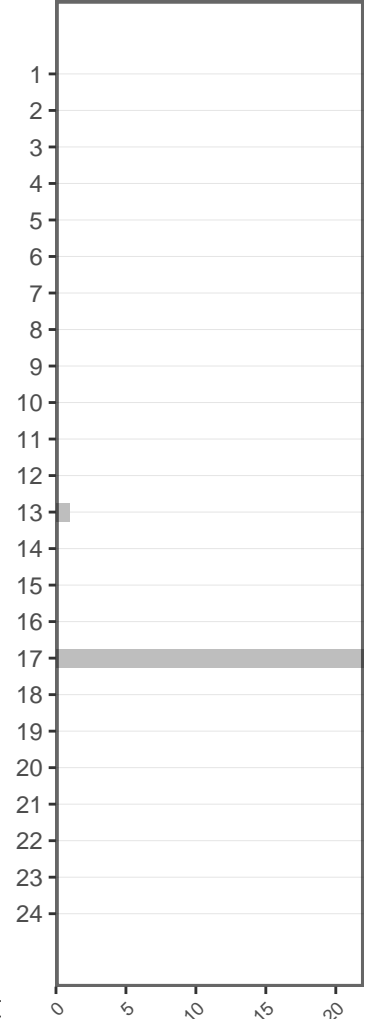
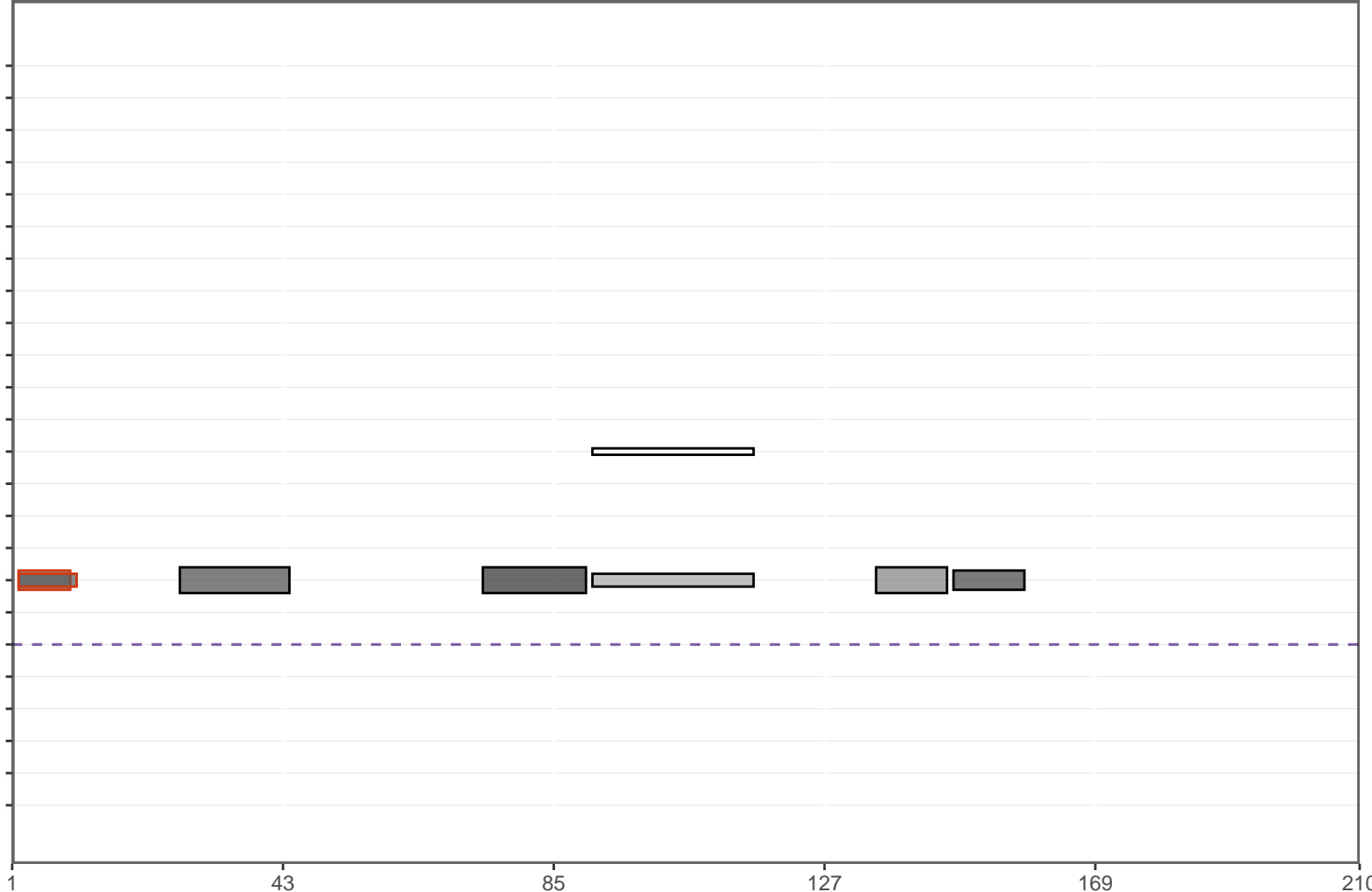
MW indication



Molecular weight

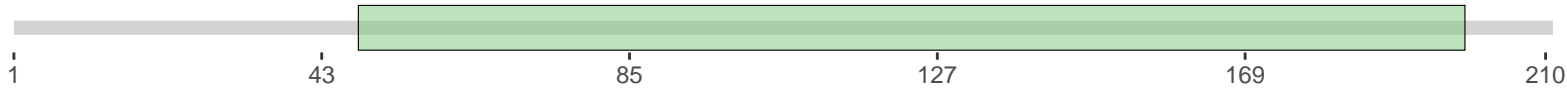


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LLCEDNDPMQVLLVLMGEPVLPQGLRARRAGLMPMDGGGKDDKIAGVGDDEPEYRHYTDINQLAPHLAEIRRRFFEDYKLEKEVAVNEFLPPNTAVDAIQYGMQLVAEYILETRK

NbL10g24410.1 uncharacterized_LOC104214638 [MW = 61.16 kDa]

No. of times detected



log(intensity)



Values from



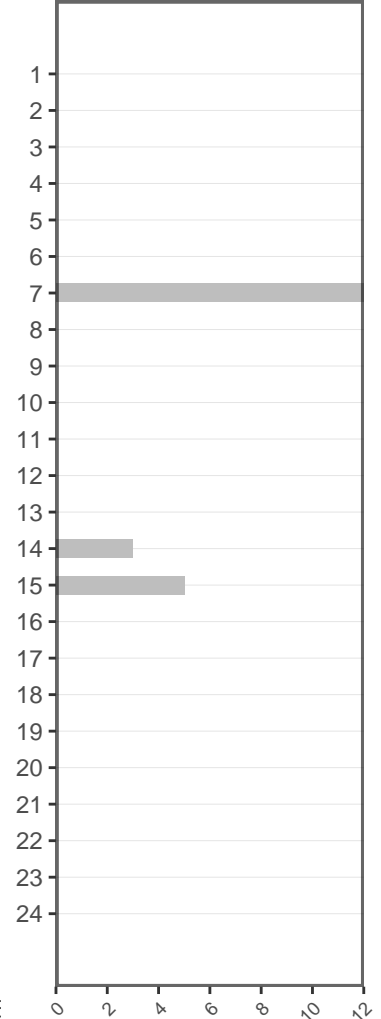
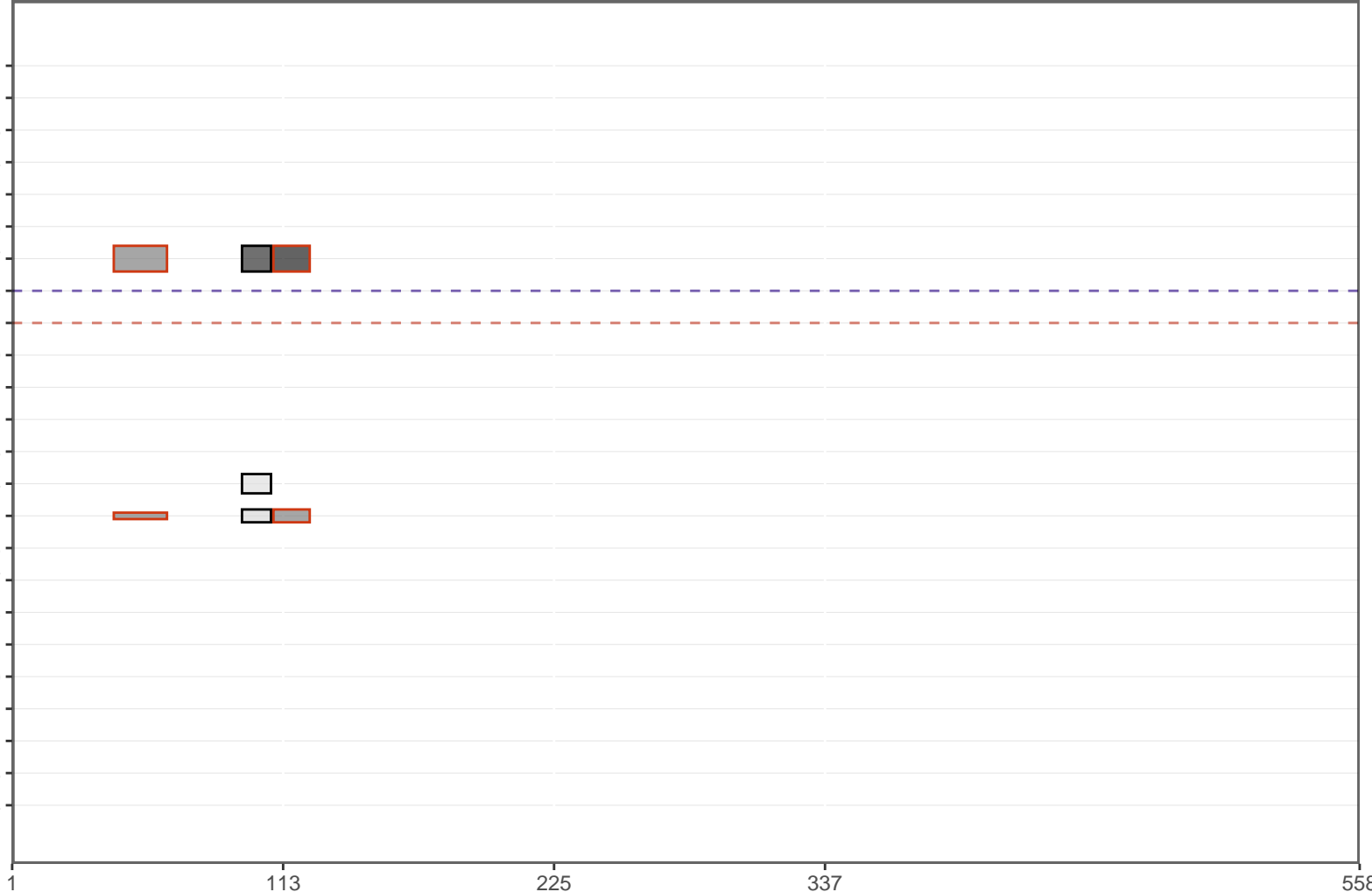
MW indication



Molecular weight

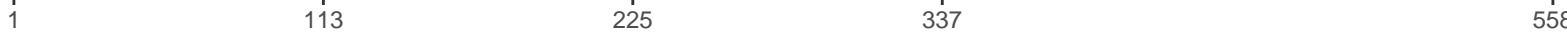


Gel Slice

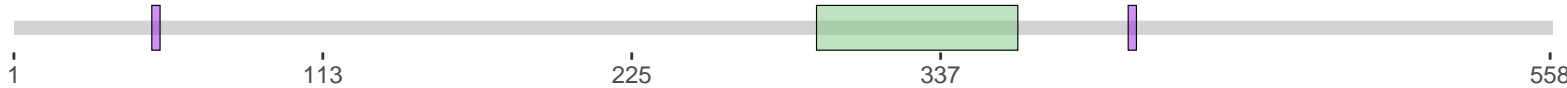


Peptide counts over 4 repeats

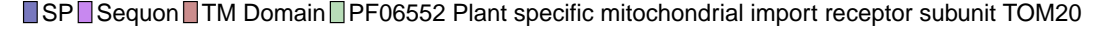
Protein length



Pfam domains



Pfam Description



Protein sequence:

TLNDYYNYWIAISDRANRGRTRAEELWKGATKNYEKAVGLNWNWSPQALNNWGLGELSAIVFIREKLTIVKMAISKFRRAAQLQDFHRAVINYLGTVLGLAEDMSRGTGGAVNAKDISPNELYSOSAVYAAHAAHKPNVSYVTSALKLVRSMLPLPLKVSYLETAPDGNPLAFHSDWKRSGFVLRHEGLQDISKVDGRGMSRSLSSNEADMSPNNGAKVDVPOIVVSVSAGSDLTLPDAGLIGDTHGPPVYMAADSWESLELWVLDLWLSLVTYTGARGKSDVLAGITS*

NbL10g24170.1 probable_trehalase [MW = 65.95 kDa]

No. of times detected



log(intensity)



Values from



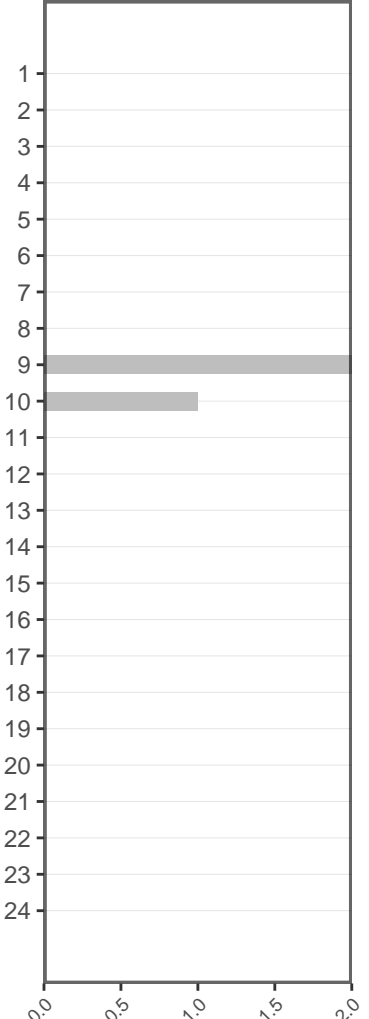
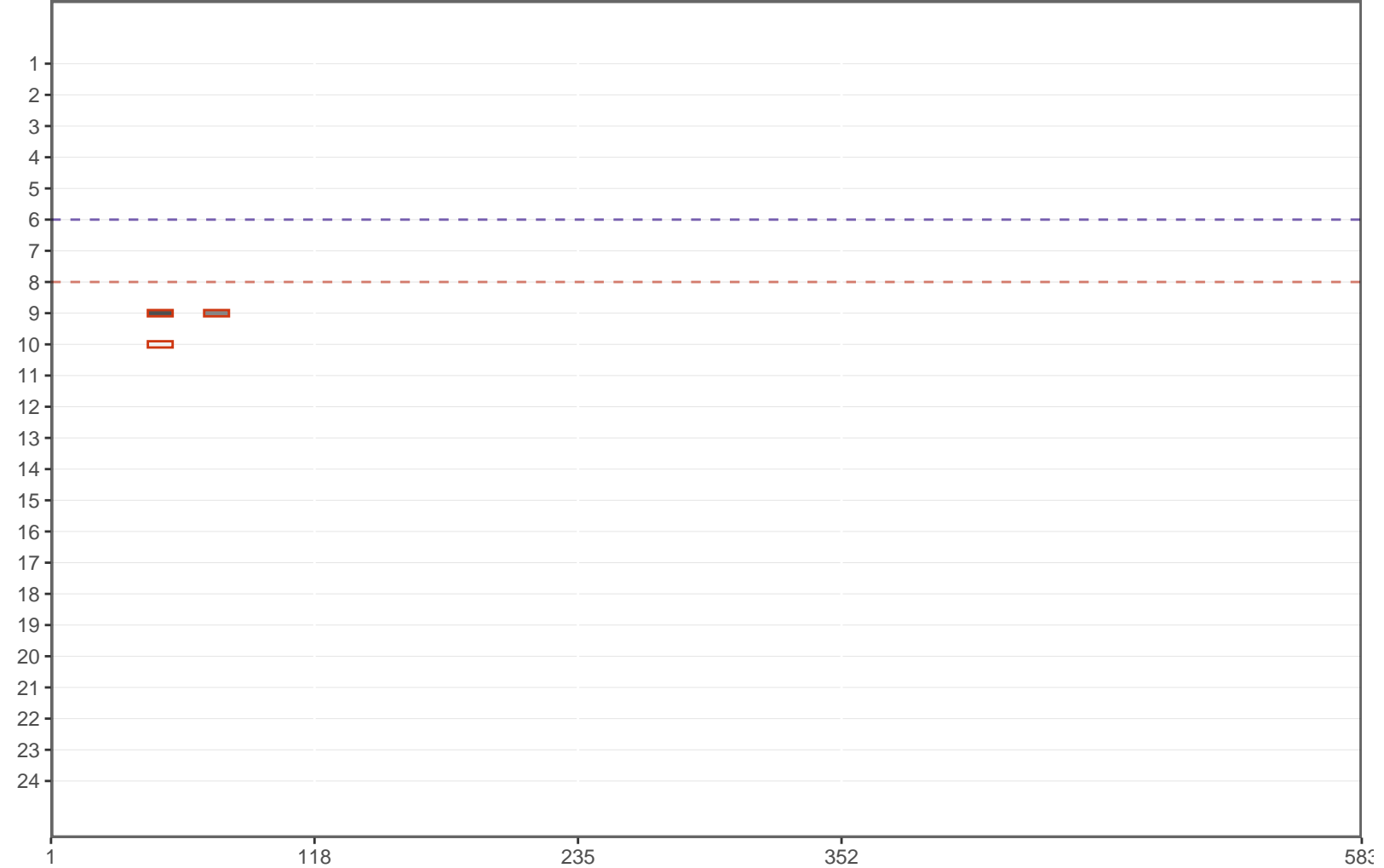
MW indication



Molecular weight

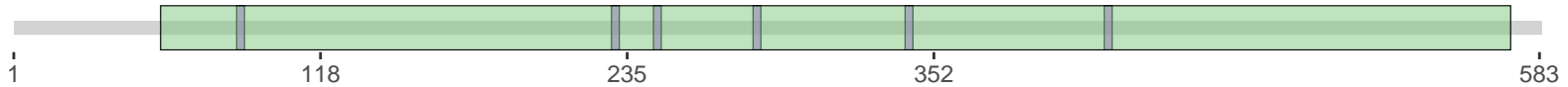


Gel Slice



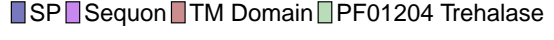
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

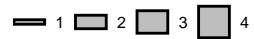


Protein sequence:

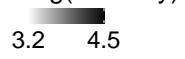
INHSLSRYAMWVKNKRPESSTIDKTKAKLPNNCKEHRQFYRDLASAAGSGWDFSRWRMRNEDLTTTSTSLPVDLNFLLKMEIDMVFLLANTIGESNVARFTEASGNRQRANGCFVNAEMQGWLDWVLDGENTGGDYYKWEHGHQNKKFAFNFLVWELFNSDDITRNVVQSLKSSGLLGPAGIASLNTFGQWDFPFGWPPVQVHMIEGLARSGLEEARALANDVIRWRFTNYAVYKKTGAMYEKVDVTKGAYGGGVYAAQTGFQWANGVYVLLALEFG

NbL10g24160.1 ABC_transporter_F_family_member_3-like [MW = 80.39 kDa]

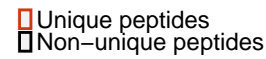
No. of times detected



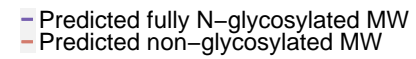
log(intensity)



Values from

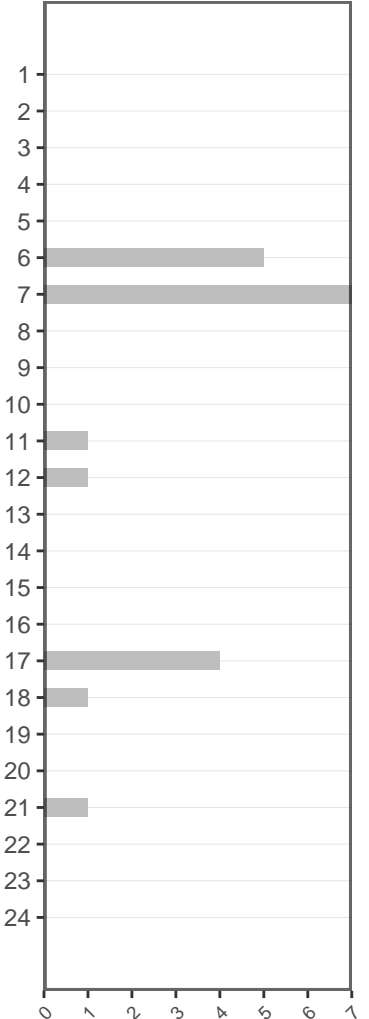
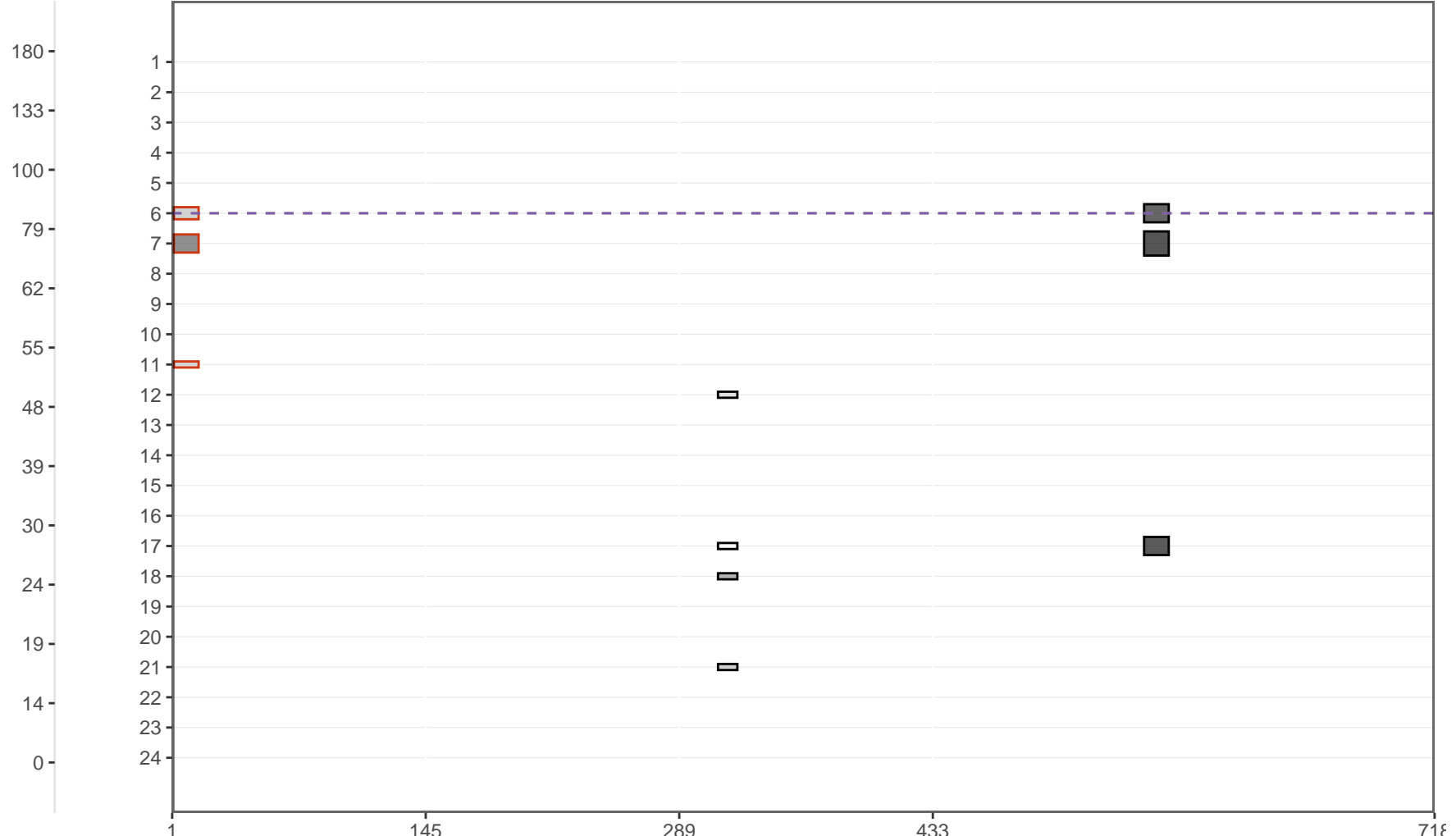


MW indication

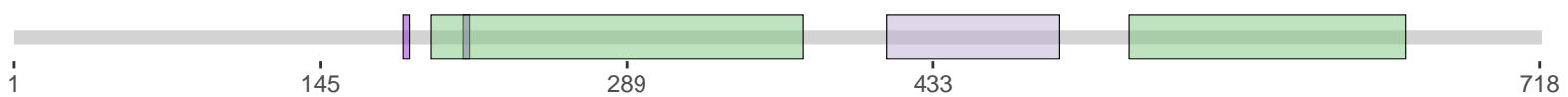


Molecular weight

Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

ISGGVRRMLRALRALFIEPDLKLLLDLDEPTNHLDLHVAVLLETYLKWKPKTFIVVSHAREFLNTVYTDHHLGNKQLSTYKGGDYTFERTRDEGVKNGKAFENERTRAHMGTFIDKFRYNARASLVGSRKALERIGRVDEVINDPKVYKFFPSPDDRPAGAPIISFSDASFGYGGGFLFKLNFGIDLDSRVAMVGPNGIGKSTILKUSGELQPTSGTYFRSAKVIKRVVFSQHHVDGLDLSNPLLYMMRQFPQVPEQKLRGHLGSGFTGNLALQPMYRLSGGOKSRVAFSK

NbL10g24150.1 glutamine-dependent_NAD(+)_synthetase [MW = 79.86 kDa]

No. of times detected



log(intensity)



Values from

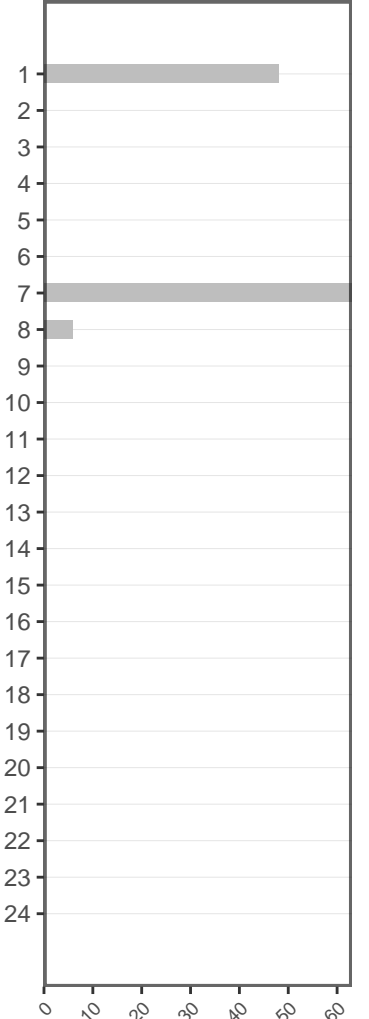
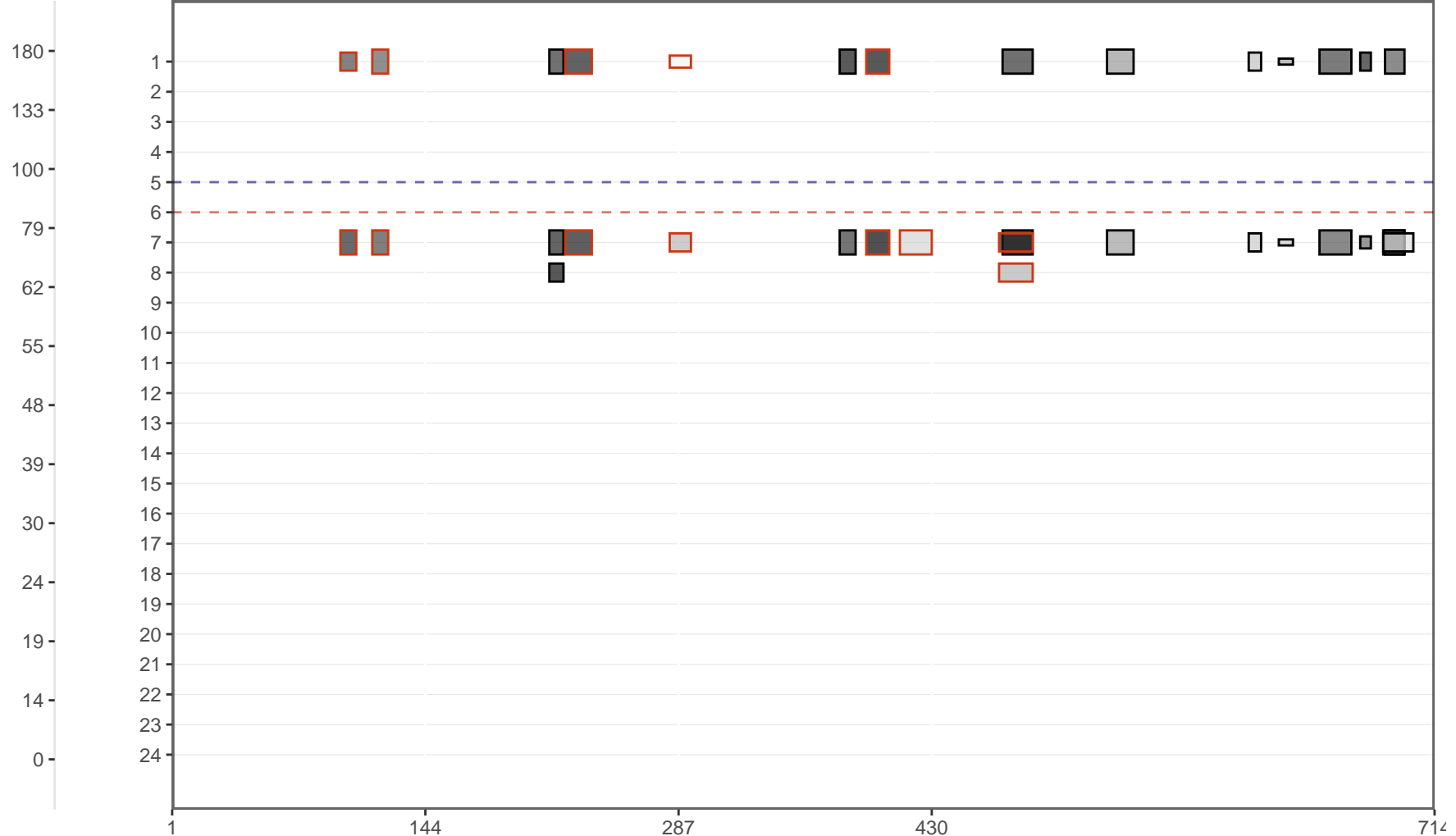


MW indication



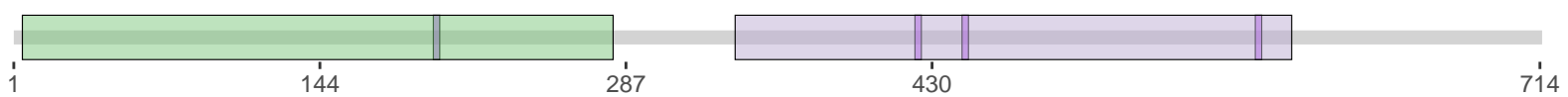
Molecular weight

Gel Slice



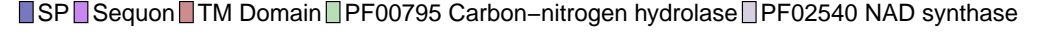
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RRSGASGFLPLSGADSSVAANGSMOQLVVKKEIANGDEQVKADAMRIGHVGGGFFPTDSEKFAKRFYTVFMSSENSEATTRAKVLADEIGSHLWNSIDGVVSSLSLFPQTLTGKRRPRKYVGGGSENENLGLNIGARVRMVLAFMLASLPLVWVHNKPGFVVLGSSNDEGLRGVLTQYDCSSADNPIGGSIGMDLRTFLKWAHILGVYSLAEIEAAPPTAELELRNSYGLDEVDMGMTYEELSVYGLRNRKFRGQFVSMRKNLGVYWGTKLTPAEVADKYK

NbL10g24140.1 luminal-binding_protein [MW - SP = 70.64 kDa]

No. of times detected



log(intensity)



Values from



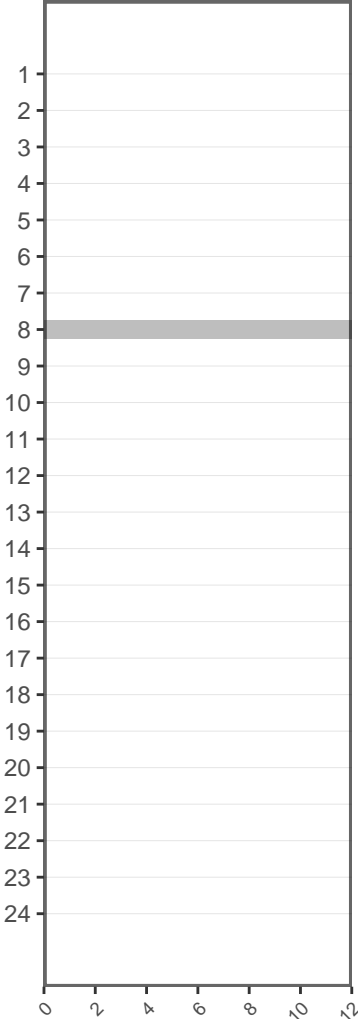
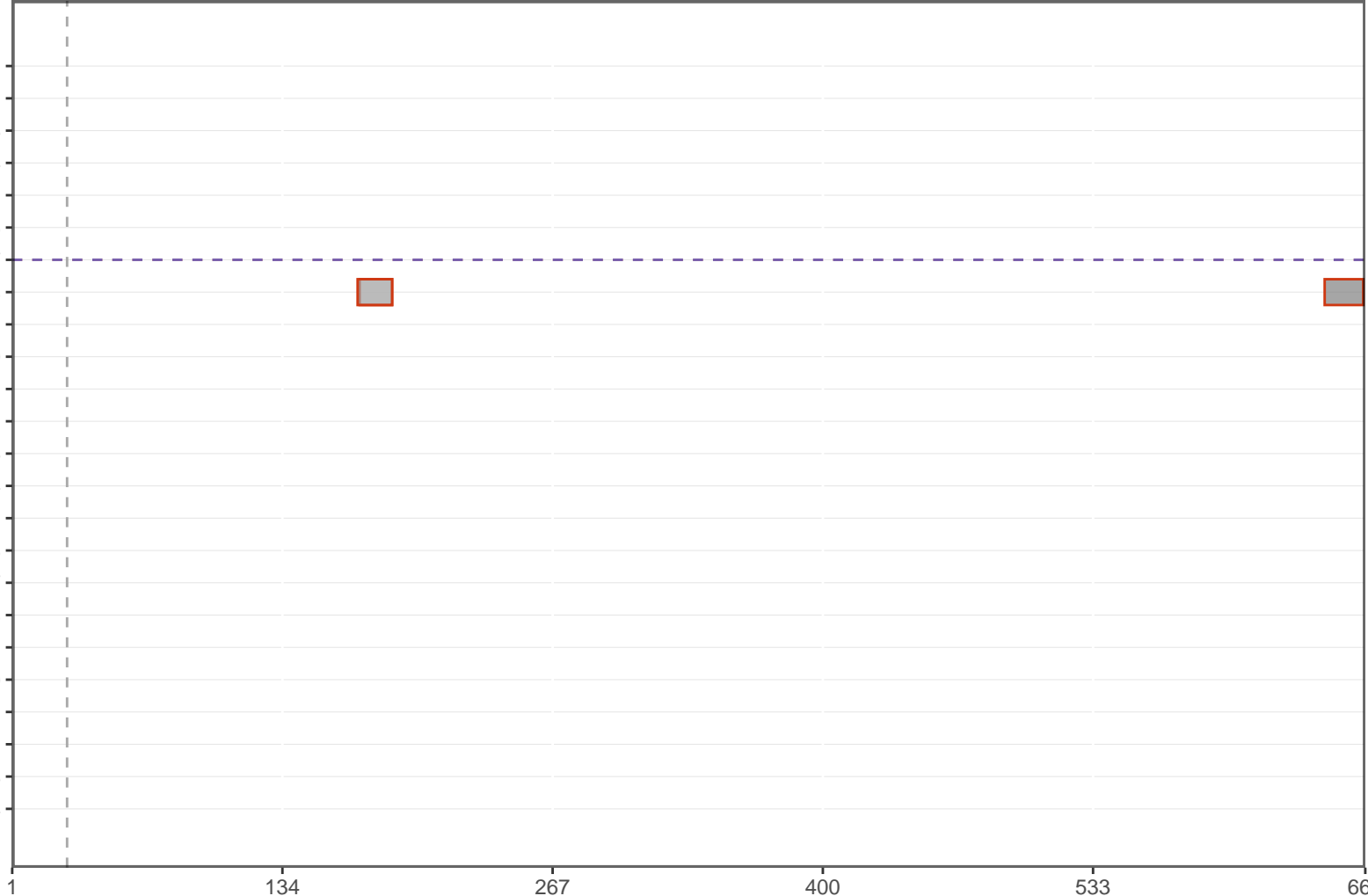
MW indication



Molecular weight



Gel Slice



Protein length

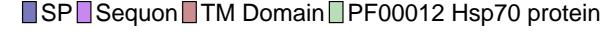


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

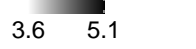
DFSEPLTRARFEELNDFRKTMGPKYKAMEDAGLEKNQDEIVLGGSTRIPKVGQLLKDYFDGKEPNKGVNPDFAVAVGAAVGGGLSGEGGDETKDLLLDVAPLTLGSETVGGVMTKLPKIPRNTVPTTKKSGVFTTYDQDQTTVSHGVFEGERSLYFDGRLLLKFDLGIAPAPRGTPTQIEVTFEVDANGILNKAEDKGTGKSEKITFTDNGKRLSGEEIERMVRREAEEFAEEDKVKKERIDARNLSELYVYNNMKNQINDKDLADKLESDEKEKETAMKEALEWLDQNGS

NbL10g24020.1 signal_recognition_particle_19_kDa_protein-like [MW = 18.44 kDa]

No. of times detected



log(intensity)



Values from



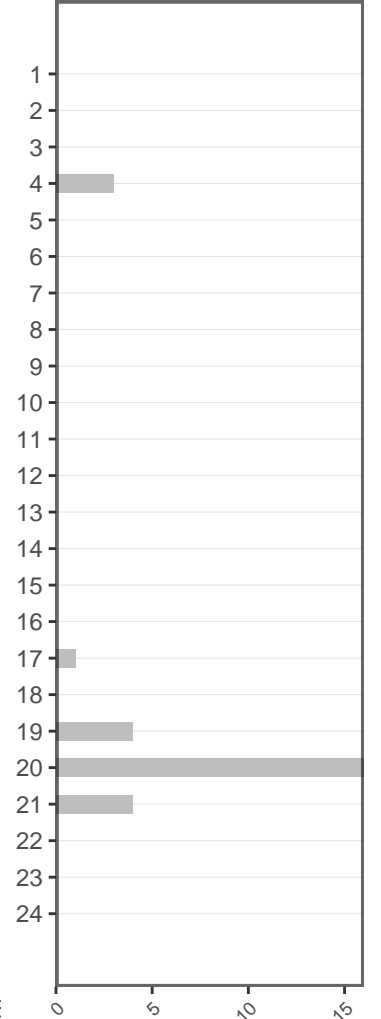
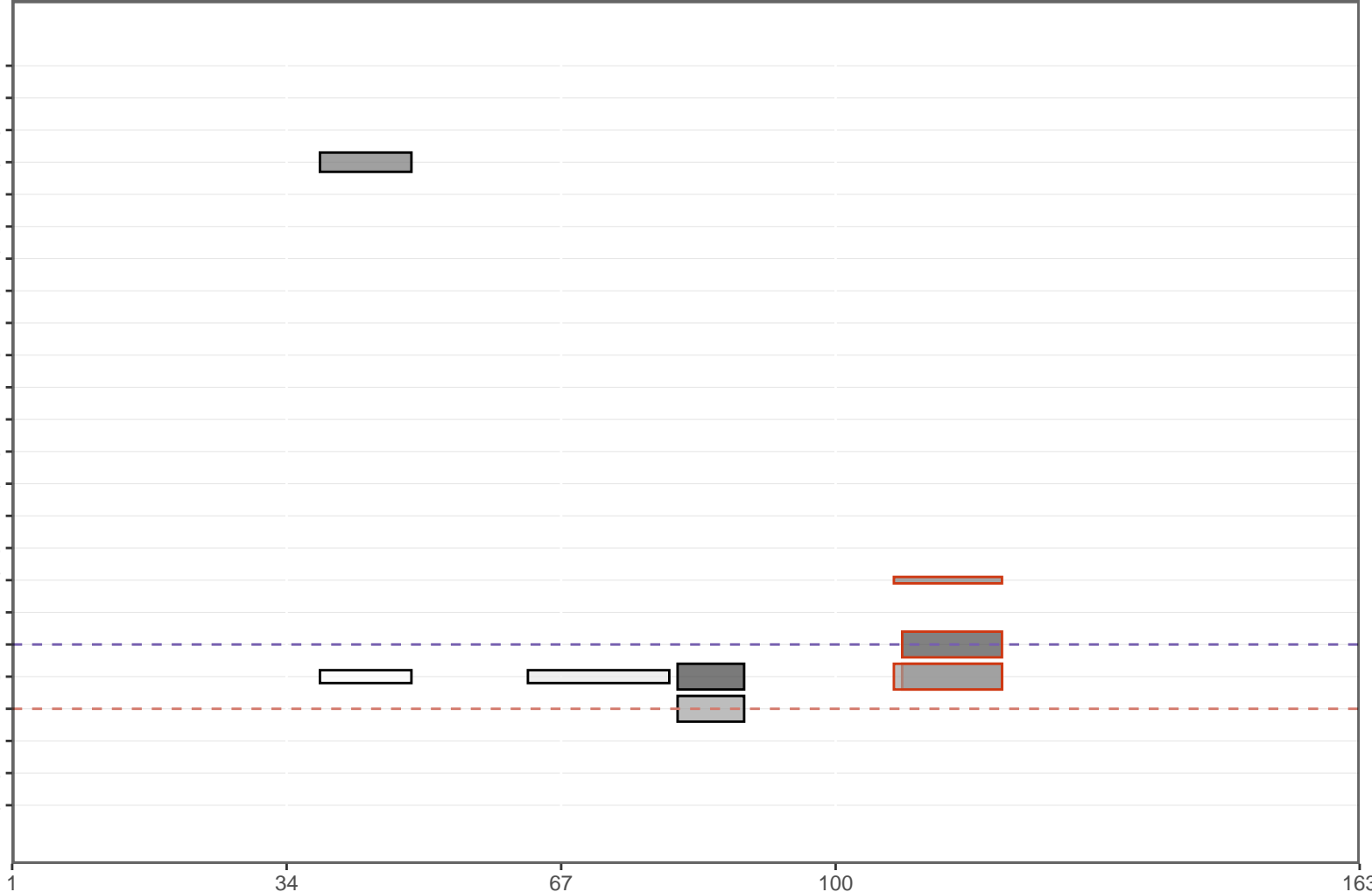
MW indication



Molecular weight

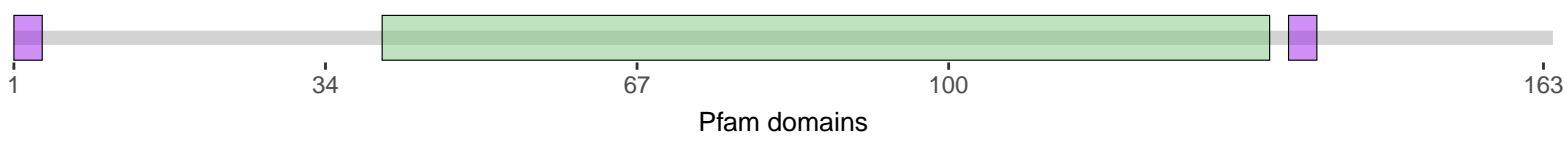


Gel Slice



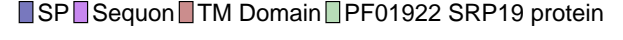
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TEISDCCNLYKIPCAEELDKAYPRDFMGRGRVRLVLLKEDDGTYPNPAISERKQLMIHVAELVRRHPNRTKKGEPASSAAGSEKSGKGGKKKR

NbL10g23990.1 26S_proteasome_non-ATPase_regulatory_subunit_8_homolog_A-like [MW = 30.86 kDa]

No. of times detected



log(intensity)



Values from



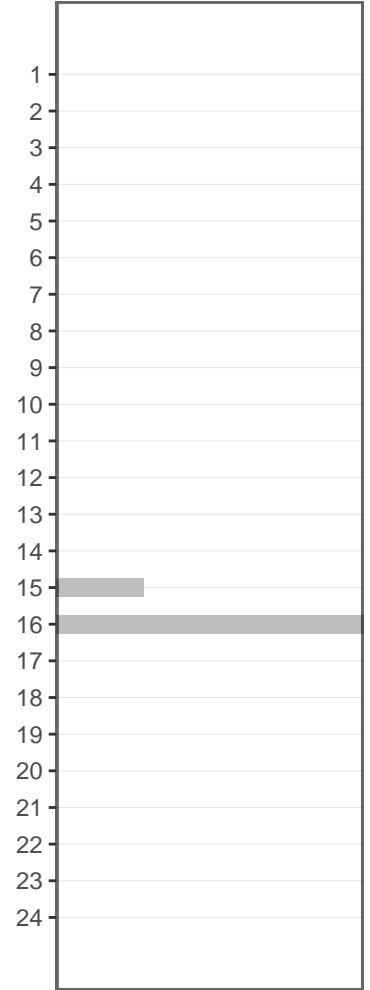
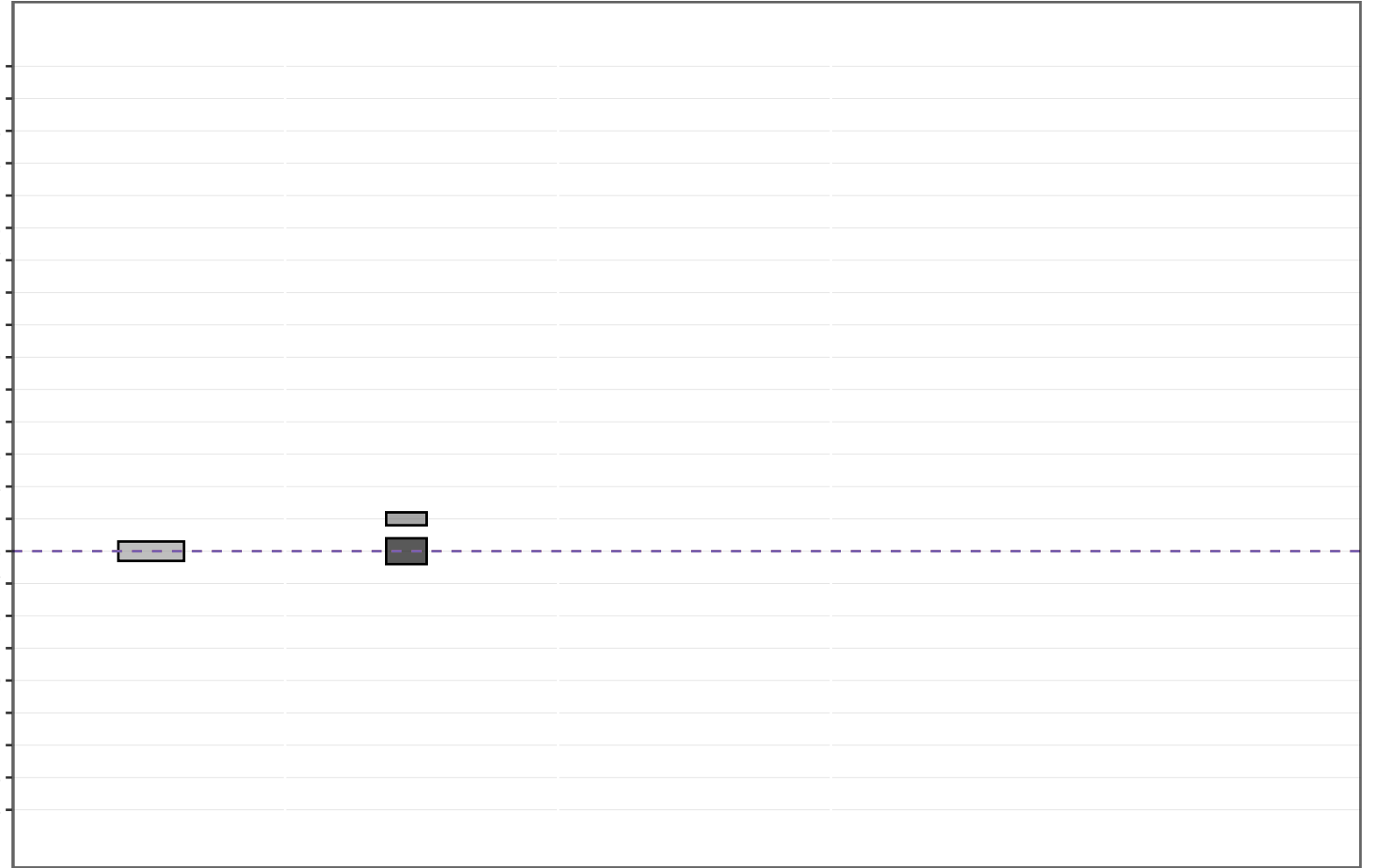
MW indication



Molecular weight



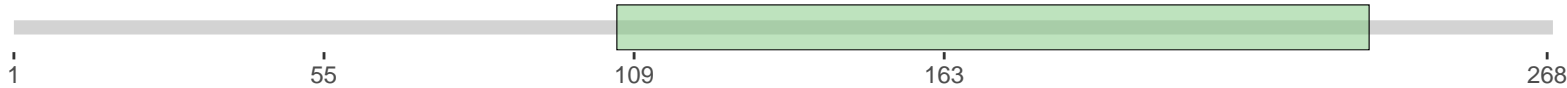
Gel Slice



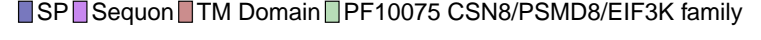
Protein length



Pfam domains



Pfam Description

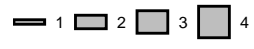


Protein sequence:

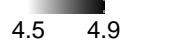
IRIAEFTHELLLSQALDNPGRHVALEQSMFEGAYHRVLSARGTVFDPATYVFMDLLAKTVRDEIMGSEKAYDRLETSDAHQMLLFSQDELFEVYRREEHPWEKDGTFVQKWDVSPKPEPQLQTGLSVAARELERIV

NbL10g23940.1 RNA_polymerase_II_transcriptional_coactivator_KELP [MW = 19.16 kDa]

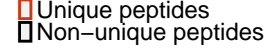
No. of times detected



log(intensity)



Values from



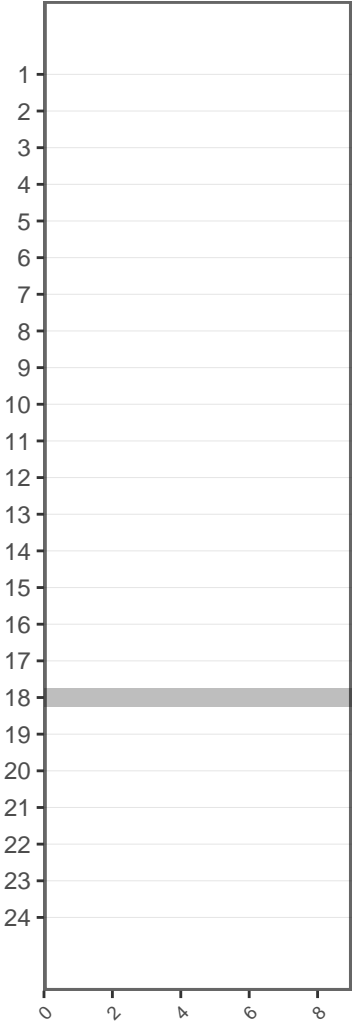
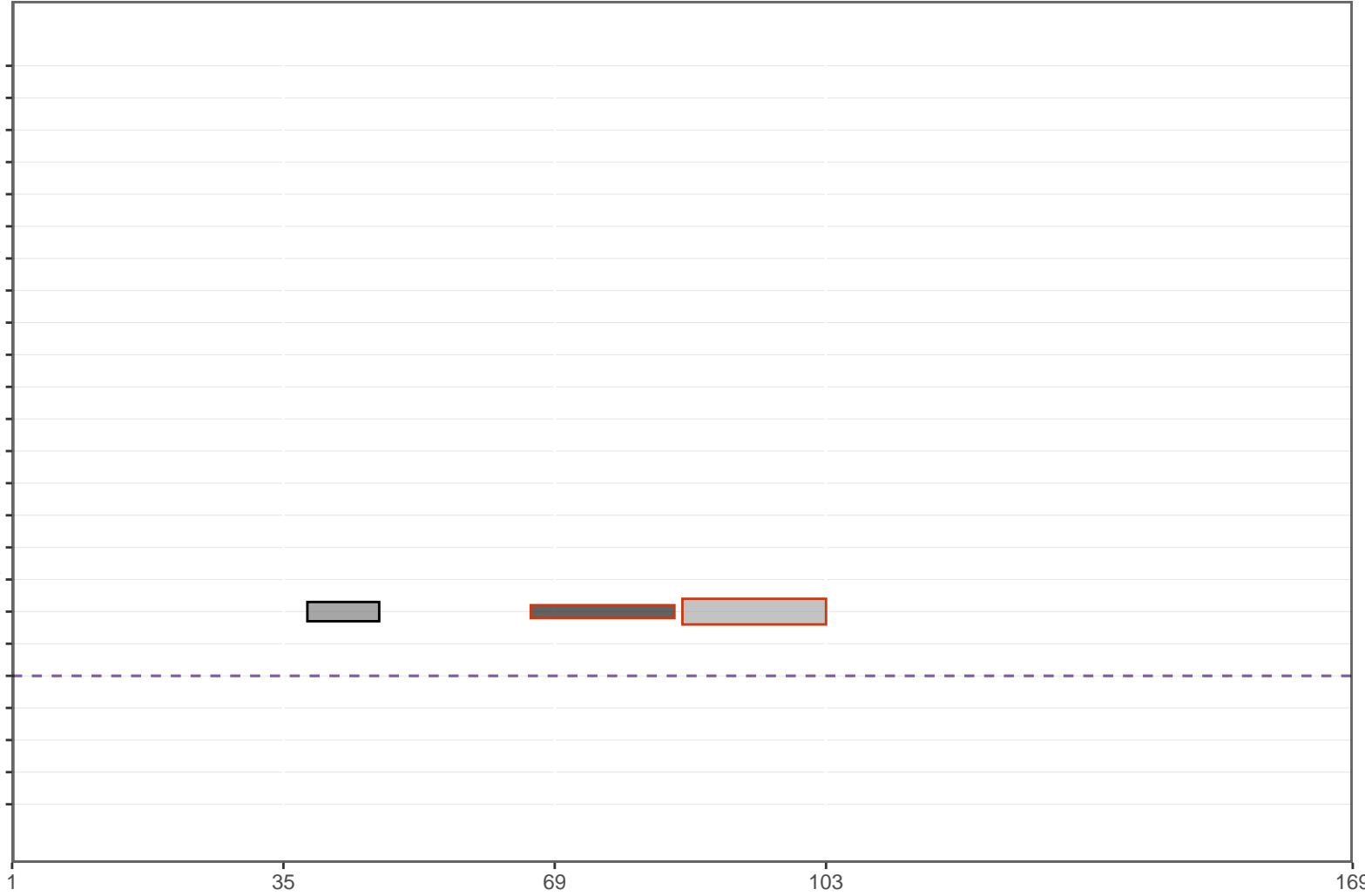
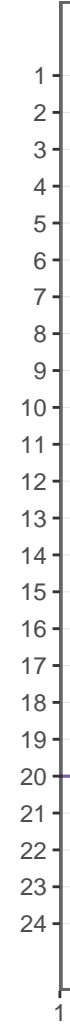
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

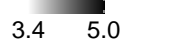
IEEEEEEDNKKKSSGAGDKEYDDGDLVGRLGHRKRVITTEFRGKTLVSIREYANKDGKELPTAKGILTAEQWATFNQNPWEKAIRKIMESRA

NbL10g23840.1 UDP-glucose_4-epimerase_GEPI48-like [MW = 38.68 kDa]

No. of times detected



log(intensity)



Values from



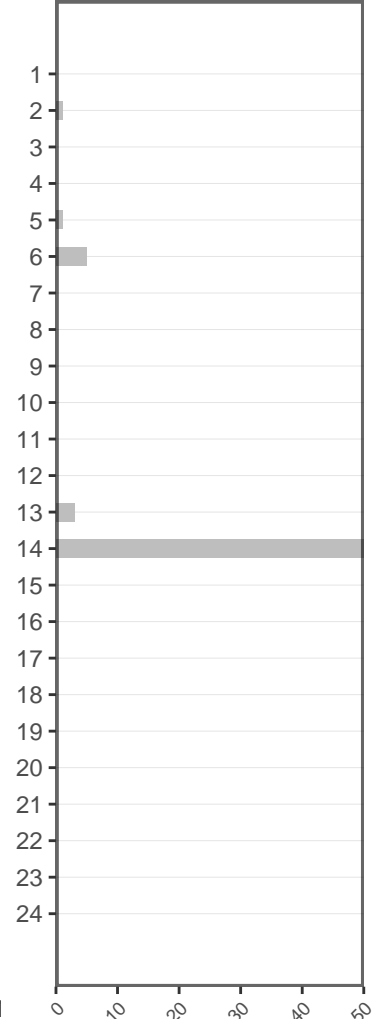
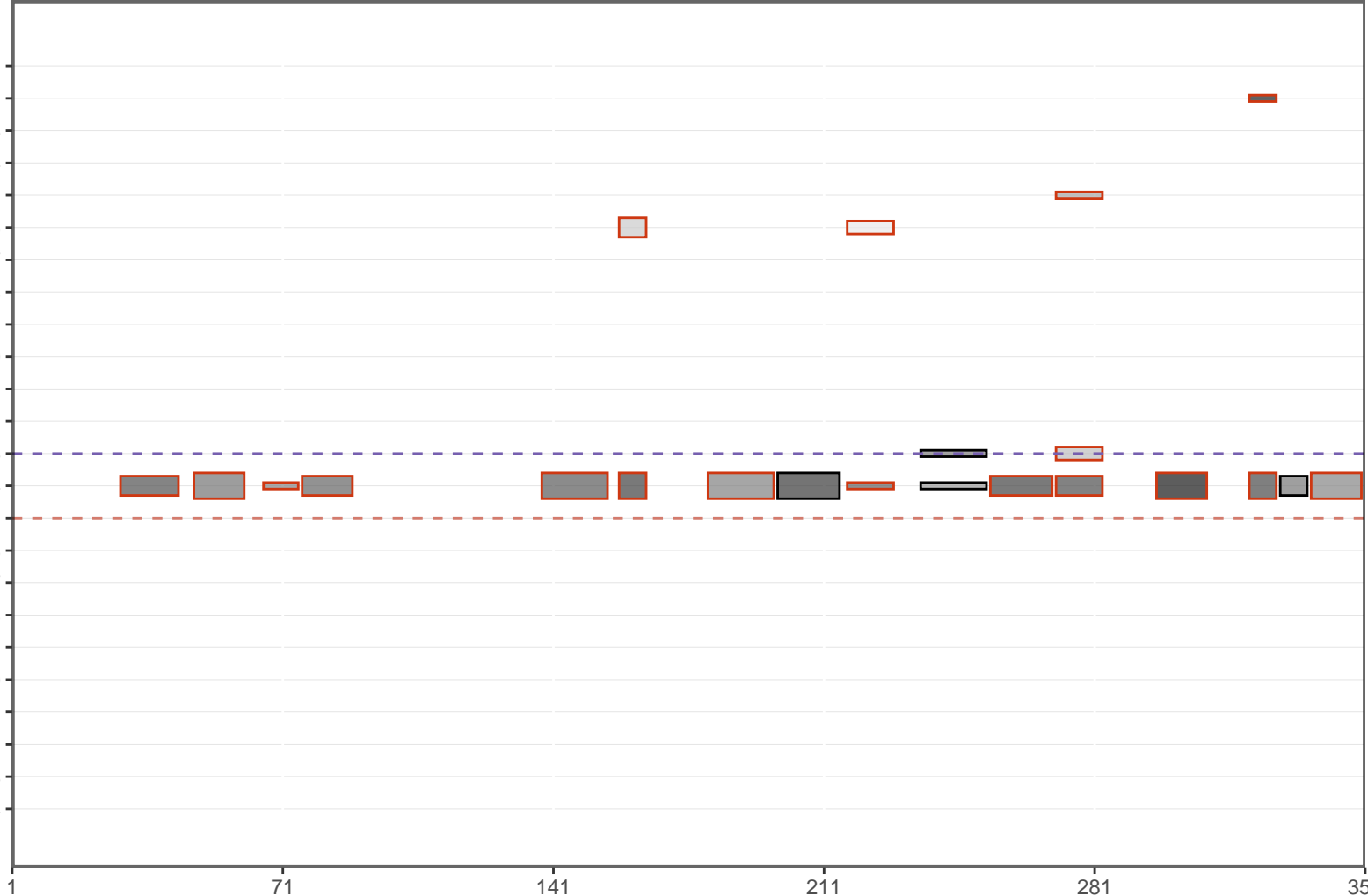
MW indication



Molecular weight



Gel Slice



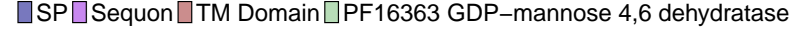
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IDVRSDSSEWILLRFRVYVGAHSSGYSYGEDPRGIPFNILMPFVQQAVGRRLALTYGTDTATKDGTVRDYKLVVLDLADGHAALQALGSDPSIGCEVNLGTGKGTSTVLEMWAAFEKASGKKPLVMSGRPRGDAEIVYATQKARELKWKAQYGEEMCRDQWVWASQNPVYGEIGESNCH

NbL10g23810.1 NAD(P)H-quinone_oxidoreductase_subunit_S_chloroplastic-like [MW = 27.22 kDa]

No. of times detected



log(intensity)



Values from



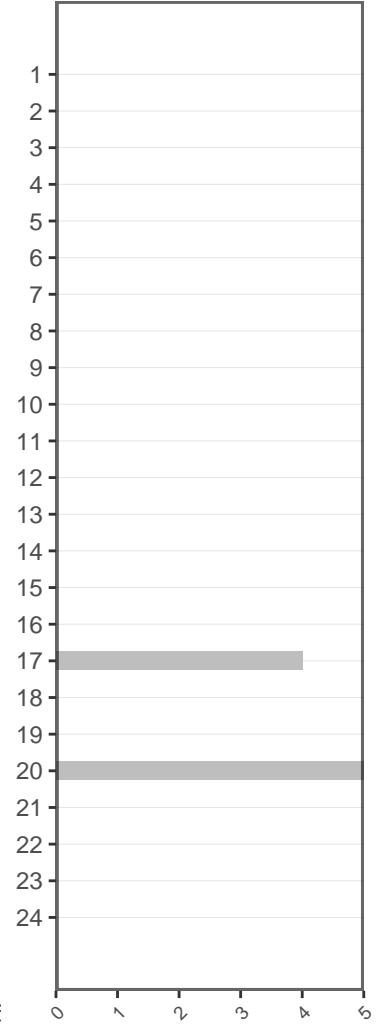
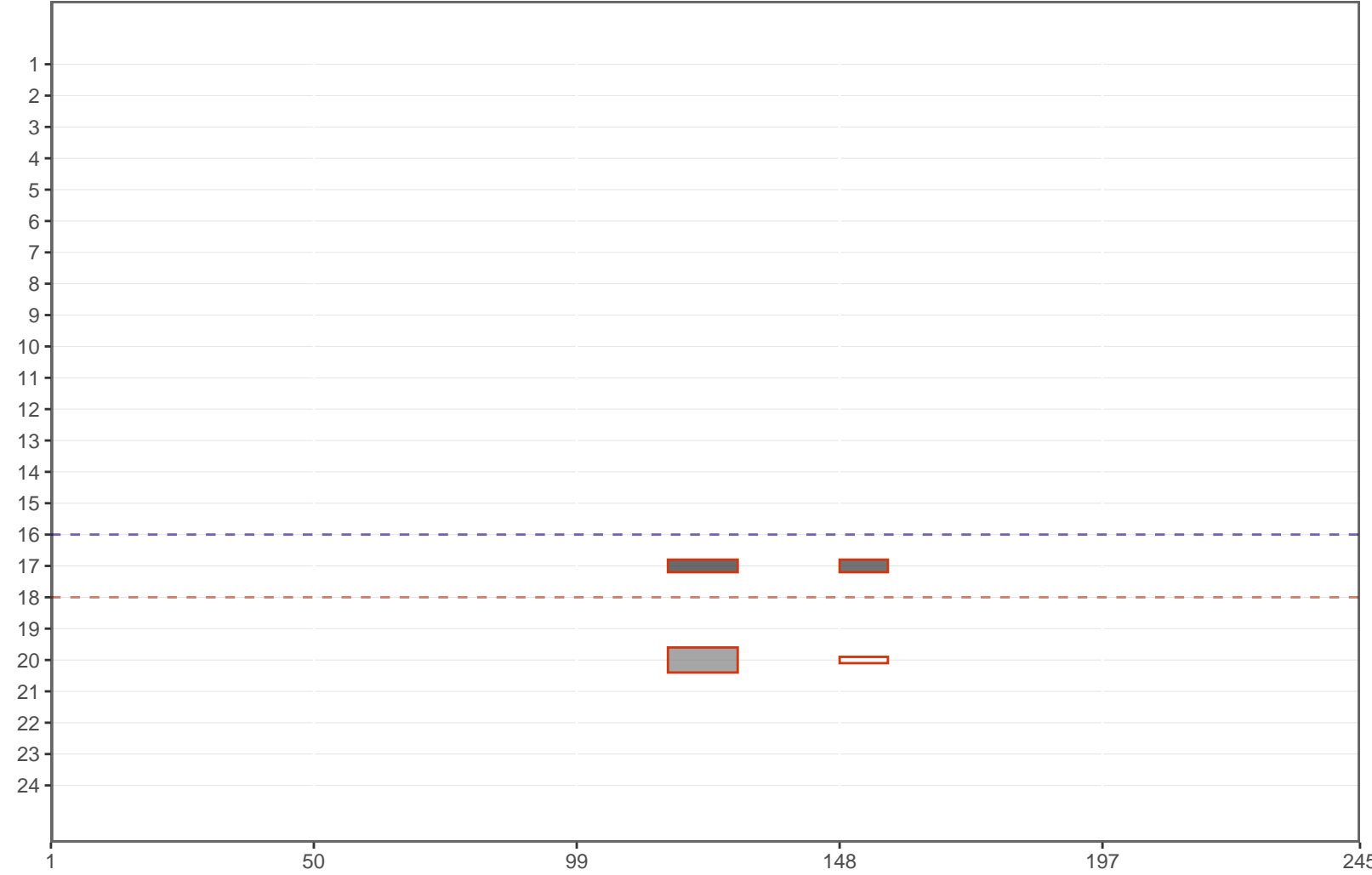
MW indication



Molecular weight



Gel Slice



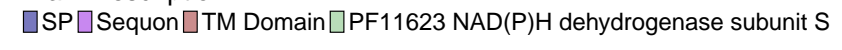
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EDGFEMMGLVGGFFGGEGKGLKFKFKENPPPKKESRIDGFLSLVKKPKPELPLLLPGMAVKNNSNPYYMYDGVQRITDGGKATVFEGGNWRURISFLLEELERERKGGPPMVPNRVLEITMLEKSSSE*

NbL10g23720.1 long_chain_acyl-CoA_synthetase_4-like [MW = 73.41 kDa]

No. of times detected



log(intensity)



Values from



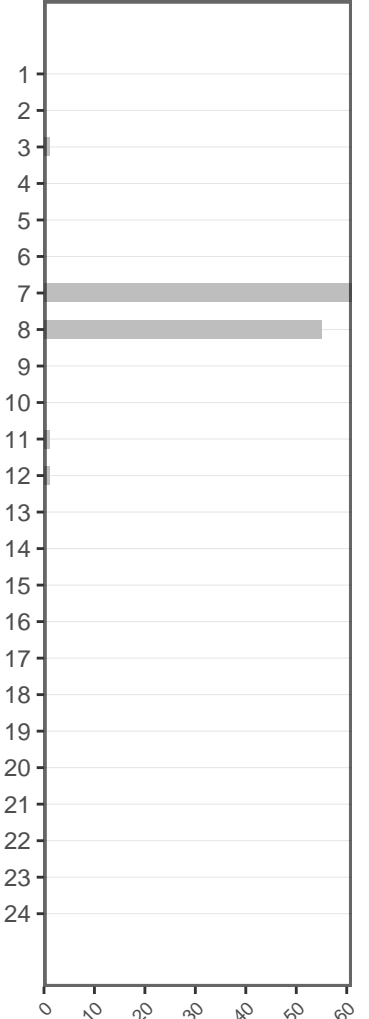
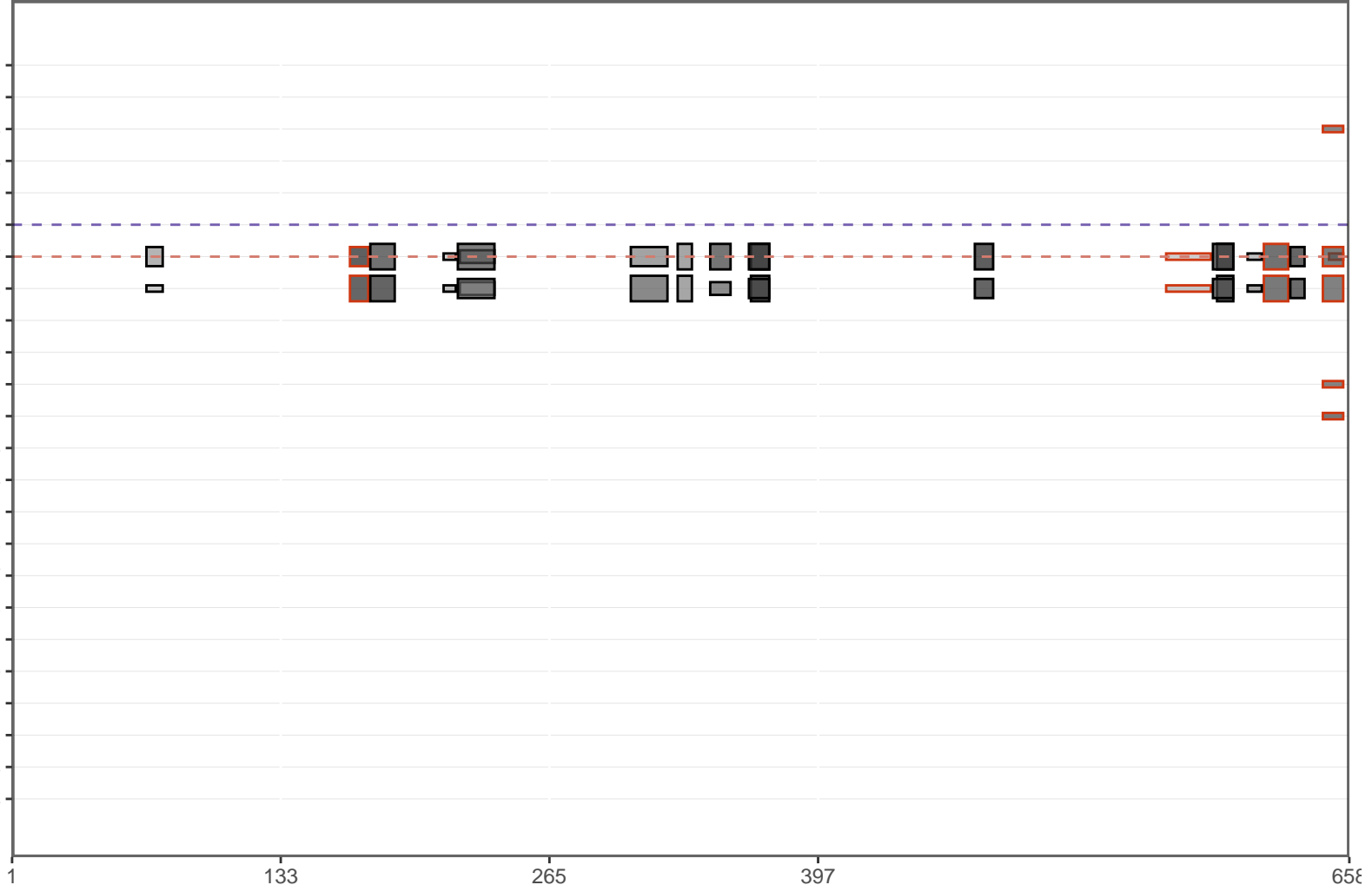
MW indication



Molecular weight

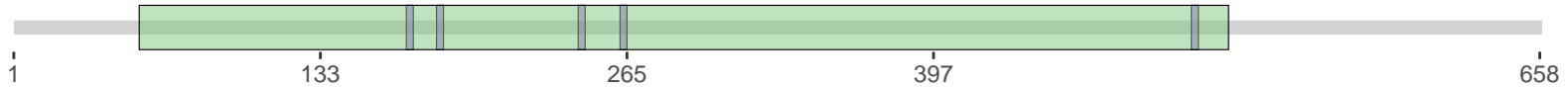


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FCAVPRVLDTRYSGLQKQKISSGGRLKSTLFLNLAWAYKHVYLNKKGRKHFEASPLSDKVWFSKYKEGLGGKVRLLGGAAPLAHVFAFLRVVACGHVLDGVLGTETAGTFVSLPNQYDMLGTVGPPVFNVDVLESVPEMAYDAL6STPRGEVGVVRRGDTLFGYKREDLTKVEMDGVFHTGDGEGWPNGLNIDRKKNFKL60GGEYVAVENLENIYGNPNFVDSWVYGNFSFESFLWALNPNQRAVEGWAGQNGLSGDFDLGENPKVKEYELGELTKAGKEKLLK

NbL10g23590.1 probable_polygalacturonase [MW – SP = 46.13 kDa]

No. of times detected



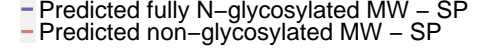
log(intensity)



Values from



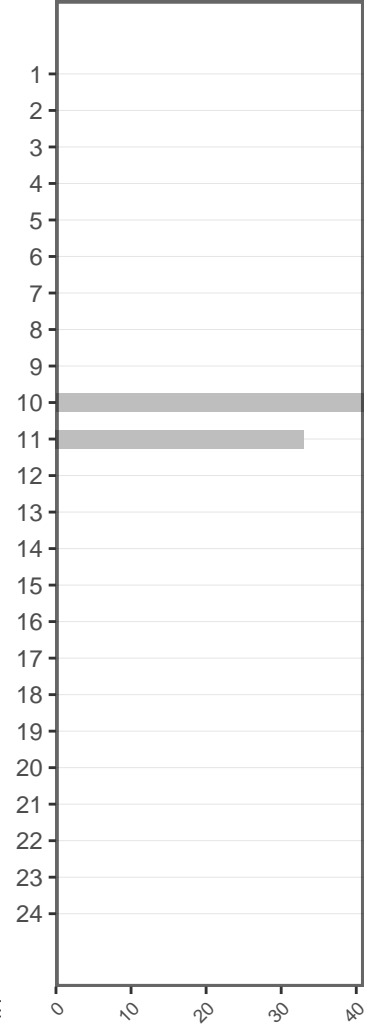
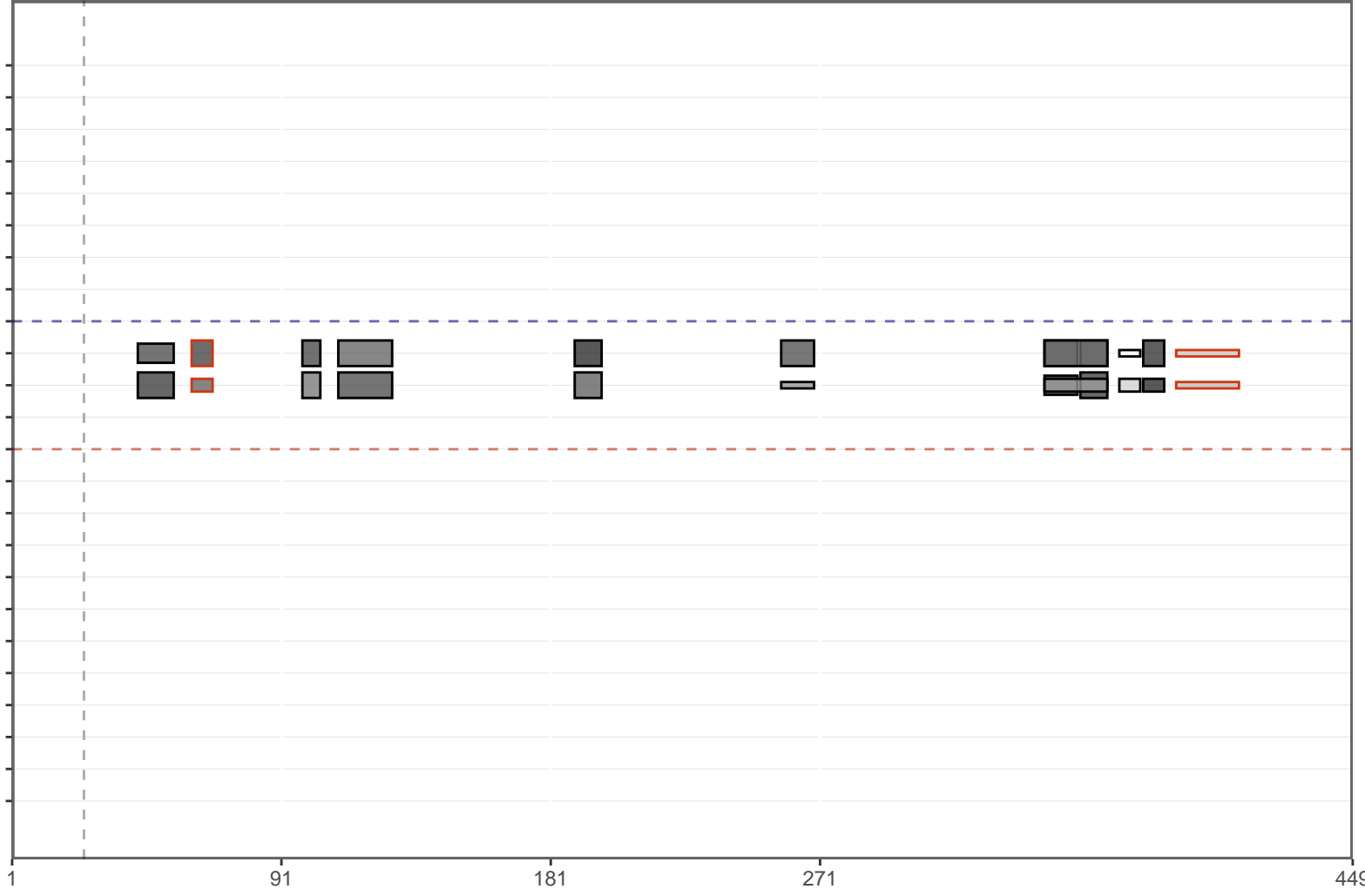
MW indication



Molecular weight



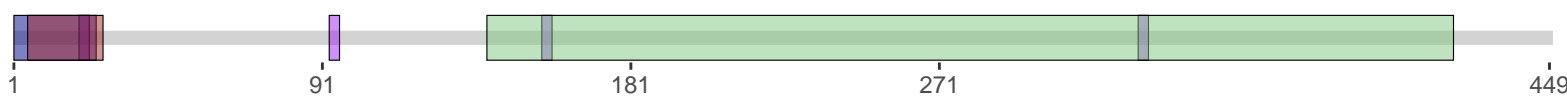
Gel Slice



Protein length

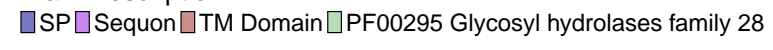


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CSNIVRYVYTLAPADFNTDGDIDP66SHVCEIDSY6VGDVAVKSGVDQYGIAYGRPSHGTRIRITGSSPFAGIAGVGETSGGAVDVAEHNLFNMGVGHKTKNIGRGGVIRNITVSNVYMENTRTGKIAGDGDVHPDEKFNPNALPIVKGKIKKDVWGEKVLQAGLIRGLKNSFFSGDLSNINLGNANPNPGRKSPWKGSDVSGAIGVSPWPGSELTSSQGTGEGSTYF

NbL10g23460.1 myosin-11-like [MW = 158.7 kDa]

No. of times detected



log(intensity)



Values from



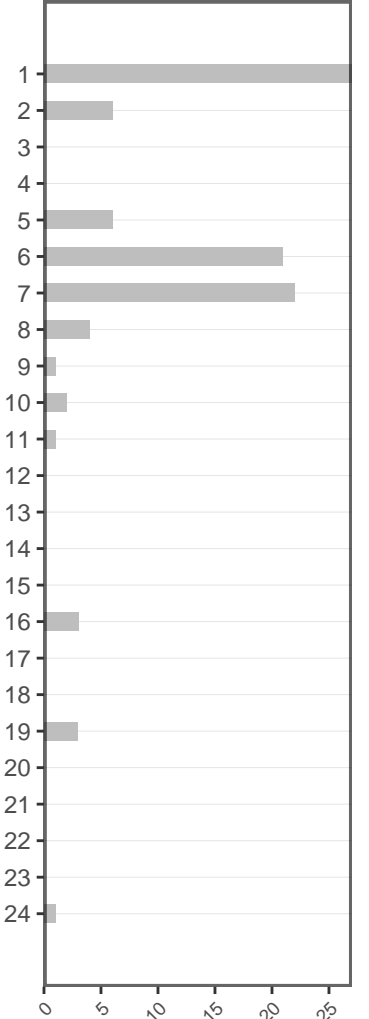
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

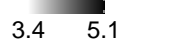
QKLELVQNEASTGVALTEEVNENLRQGIIEELQTEKNGLELVTERGKQESTESLAGAENQTKLSGKIVDLETKLNEKEEAHRKLVKEEKDGLVVQVNDLQAKVYKSLGKSTLEEKISSANNENNLTEEKGSFLSKLSELENTLVKVDHGHGAKKLEQVNEASTQALAEVNEELRKGIEELQTEKSGKLVTERGKQESTESLAGAENQTEKLSGKIVDLETKMKEQEEAGGKLVKEEKDGLVVQVNDLQAEVNSLSEGTSTLEENKRNENNLKKEEKESLLKISELK

NbL10g23400.1 putative_glucose-6-phosphate_1-epimerase [MW = 34.22 kDa]

No. of times detected



log(intensity)



Values from



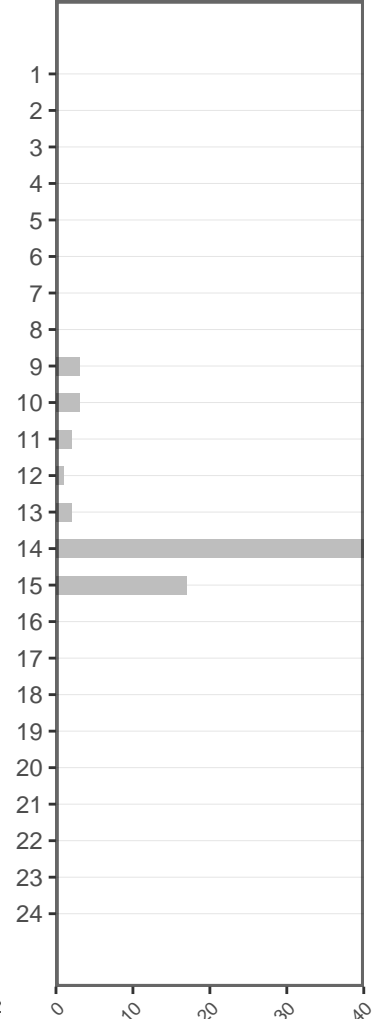
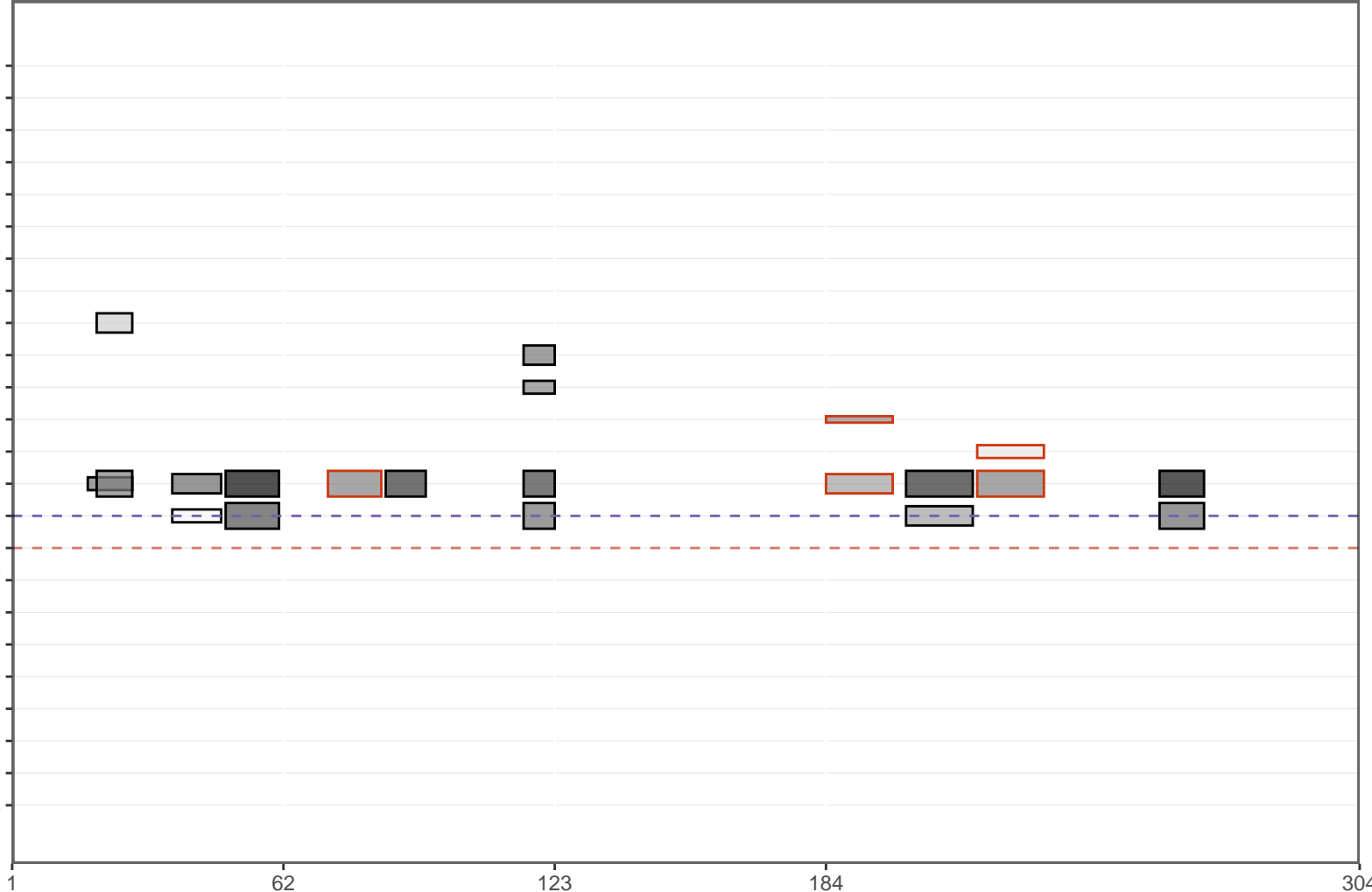
MW indication



Molecular weight

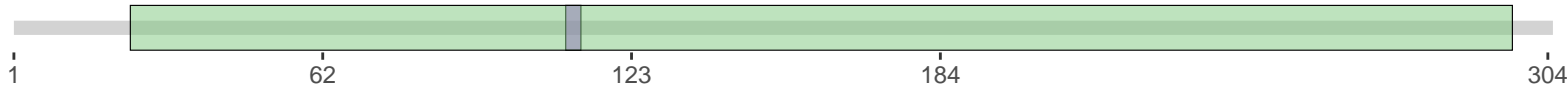


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

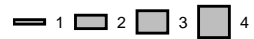


Protein sequence:

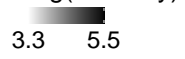
EFRLRVTLAFDGSLSFUSRIIRNVNKKPFGBIAYHTYFALSDISEVRYEGLETLDYLDNLGNRRERFTEGGDALTFTETVDRIYLS6SDVIAFDHEKRRTFVIRKREGLPDVAAVWNPWEKSKITADFGDDEYRHMALGVDAAEKPTLKGEEWTRGLEL6VMPSS

NbL10g23380.1 V-type_proton_ATPase_subunit_E-like [MW = 26.21 kDa]

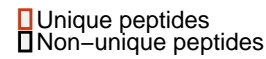
No. of times detected



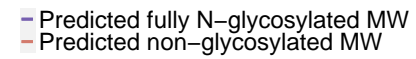
log(intensity)



Values from

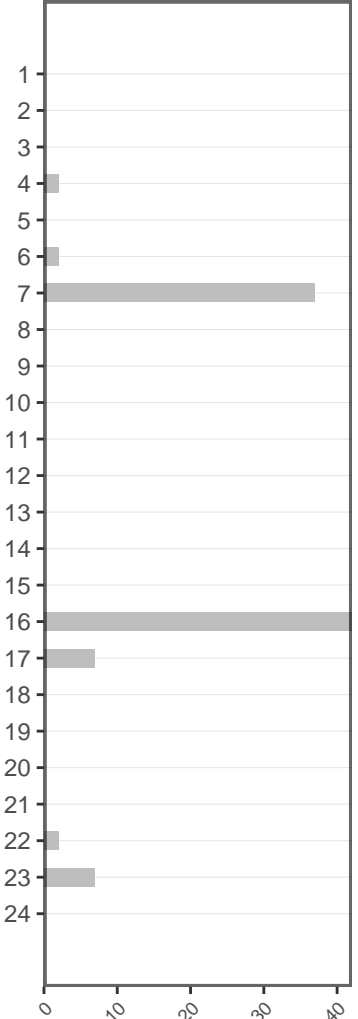
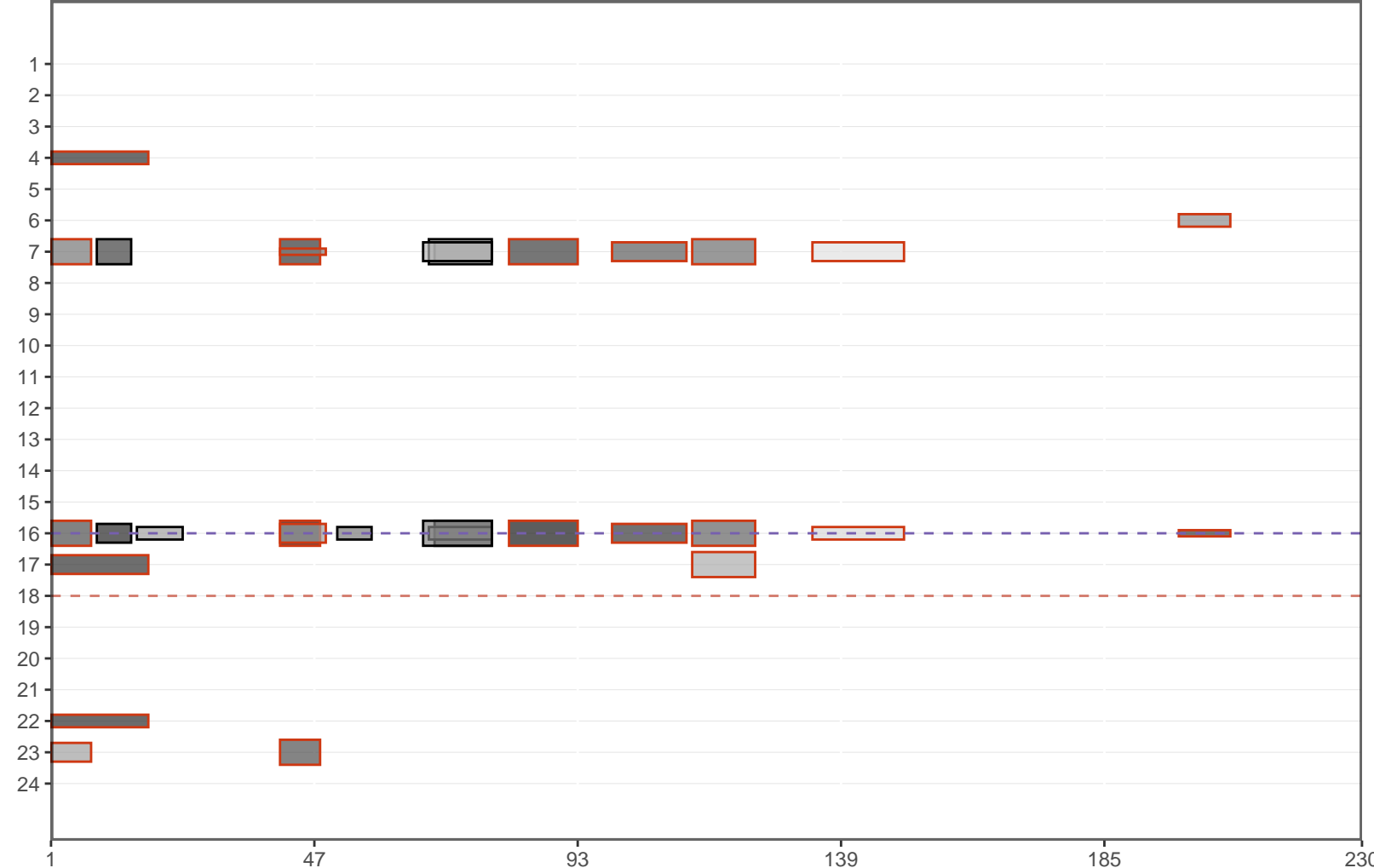
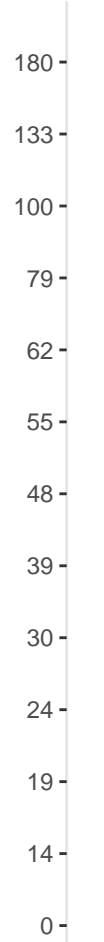


MW indication



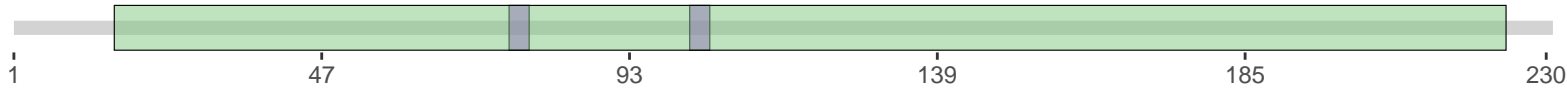
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NV/SQNH¹HYEKLLGDLN²QSLR³LKPE⁴VLLR⁵GR⁶ED⁷SL⁸VE⁹GL¹⁰DA¹¹AK¹²E¹³Y¹⁴AK¹⁵NS¹⁶Q¹⁷HS¹⁸PE¹⁹VID²⁰GV²¹LP²²SP²³SH²⁴NA²⁵H²⁶SS²⁷Y²⁸GV²⁹V³⁰LA³¹SR³²D³³GV³⁴ENT³⁵VD³⁶AR³⁷LE³⁸V³⁹FR⁴⁰N⁴¹KL⁴²PE⁴³R⁴⁴K⁴⁵CL⁴⁶FG⁴⁷Q⁴⁸AA⁴⁹

NbL10g23050.1 24-cyclodiphosphate_synthase_chloroplastic [MW = 24.3 kDa]

No. of times detected



log(intensity)



Values from



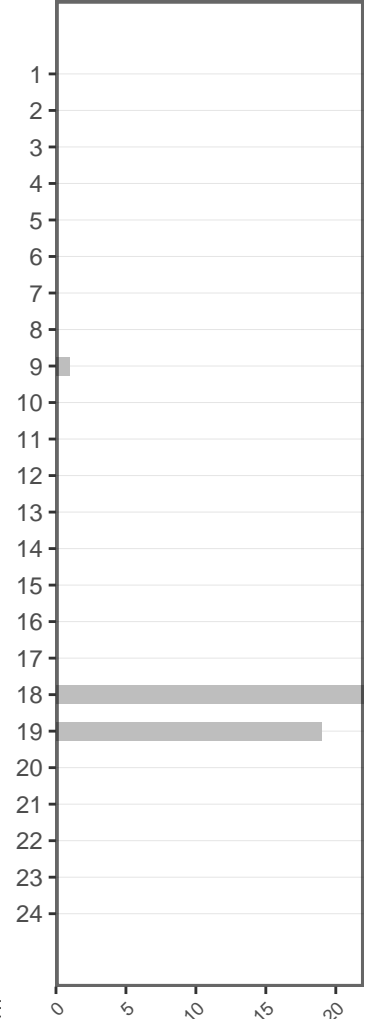
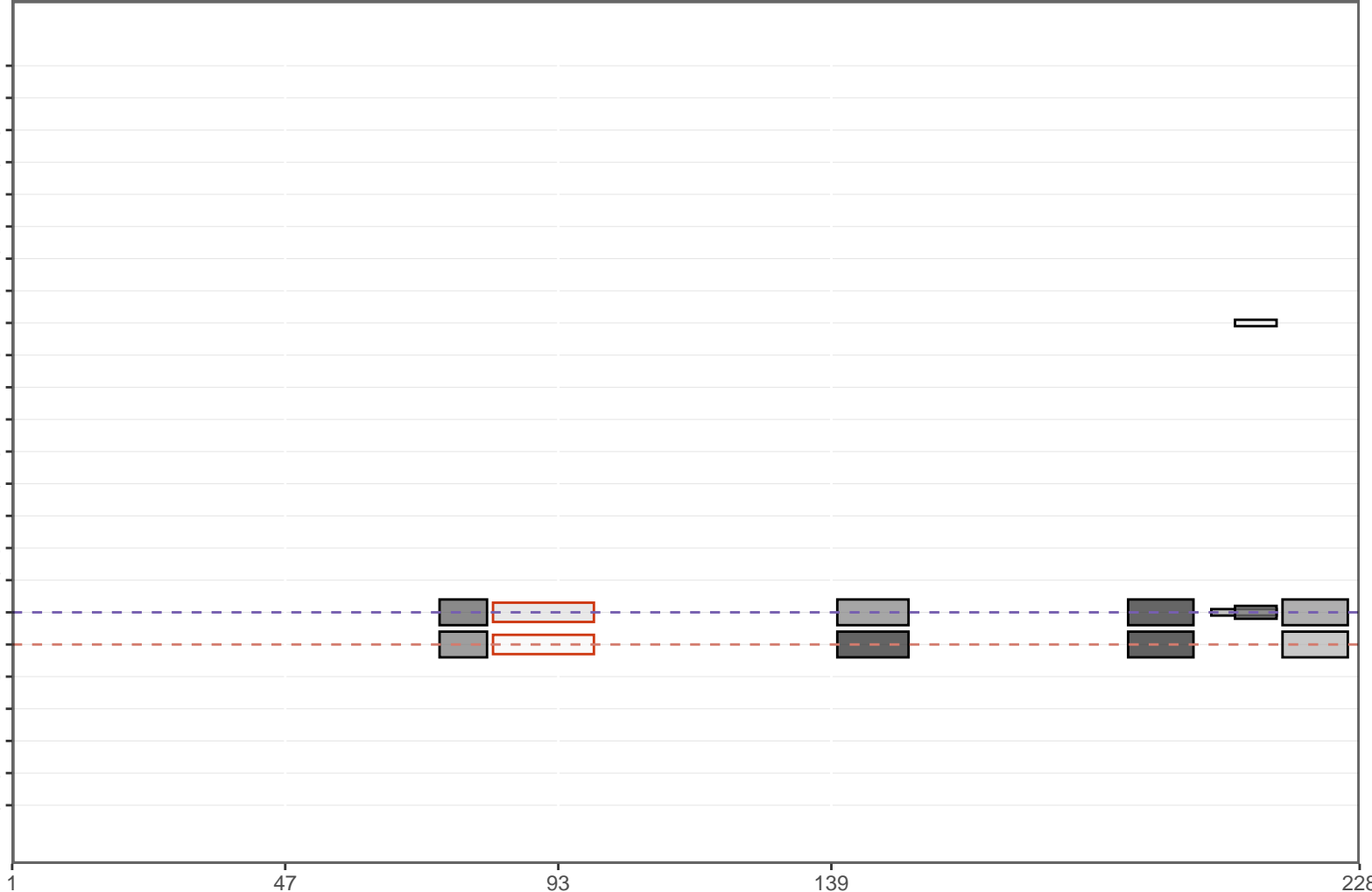
MW indication



Molecular weight

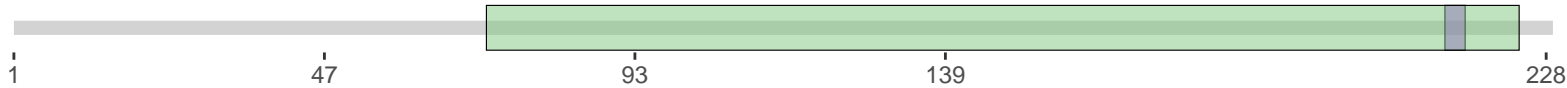


Gel Slice



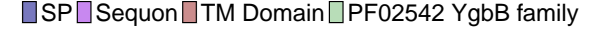
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AHSDGDVLLHICVQAILGALGLPDGQIFPDTPKWKGPSEVFMEEAVRLMHEAGYELGNLIDATLILGRPKVSPHKEAIRANLCKLLGADPSVNLNKAATHEKVDLGENRISAAHTVLLMKK

NbL10g22980.1 monodehydroascorbate_reductase_chloroplastic [MW = 53.34 kDa]

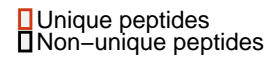
No. of times detected



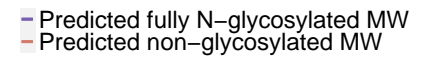
log(intensity)



Values from



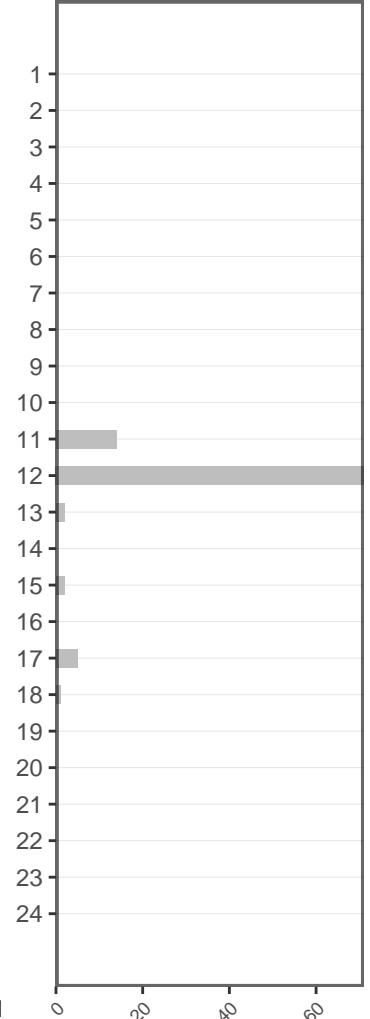
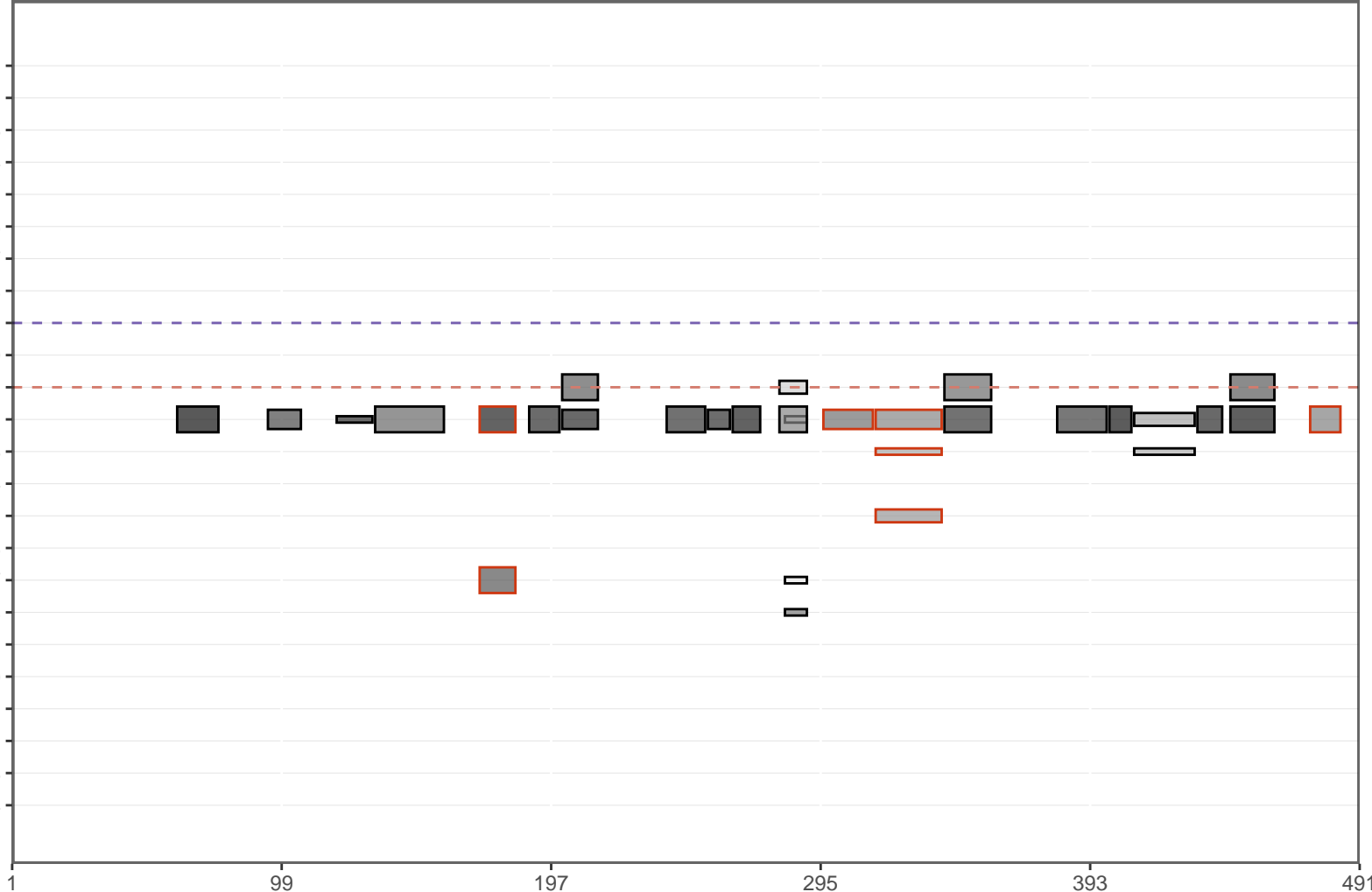
MW indication



Molecular weight

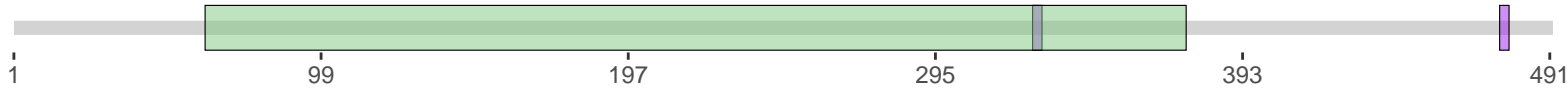


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MAA...WVLDLDTTFPEEHLPRLFTPLSLAGKYEQLYGQNGVYKFKGAKIKHLESGPDGRVWVWVLEEDGSSSETDTVVGIGAKPVPSPFDVYGLNSETVGGVADGGFRTSIPGIFAGVAAFLPKYKYNRIARVEHYDHRKAGQHKIKLLTAHTFTYDLYPFYSRVFEYEGSPRWVWVQFFGDSVGETVEVNGFDPKVATFVWIDSGKLGKYLESGSPPEEFOLLPKLARSGPQVQKELQNAASVVEALKIADASL

NbL10g22960.1 probable_polygalacturonase [MW – SP = 48.99 kDa]

No. of times detected



log(intensity)



Values from



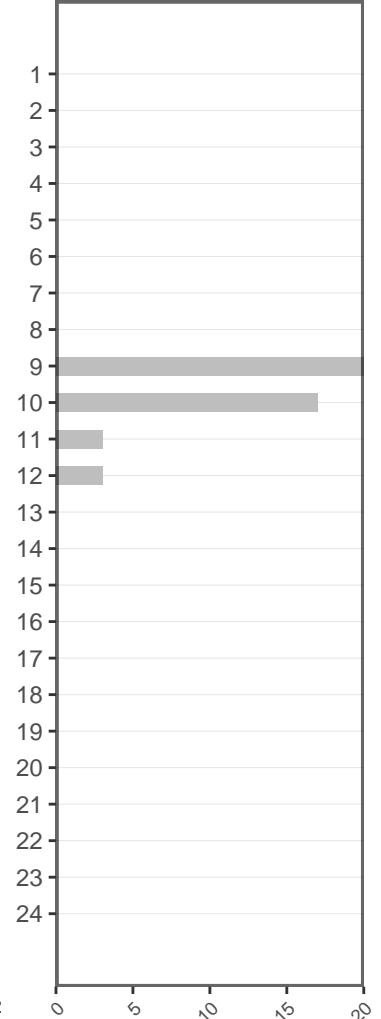
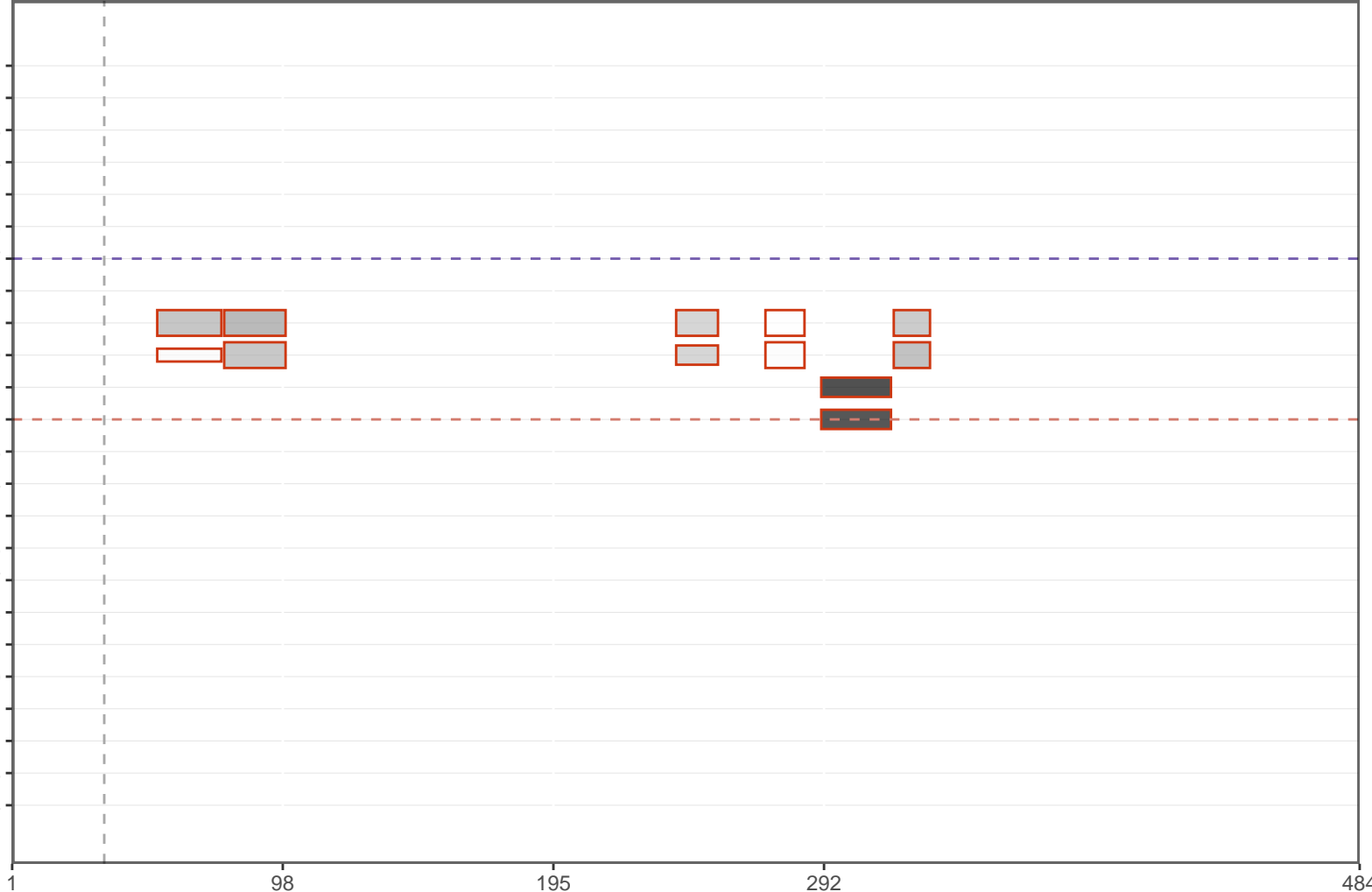
MW indication



Molecular weight



Gel Slice

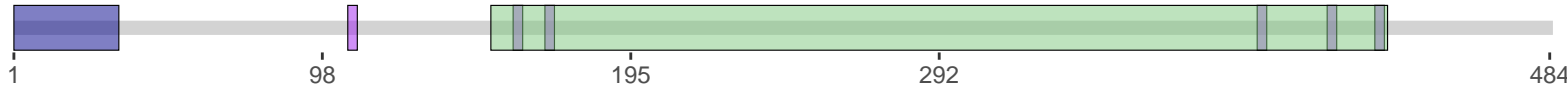


Protein length

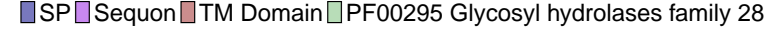


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

GITLAPVRSPTDGINPDSINRIEDCYWSDGDCIWKSGDWEYGVAFGMPFKGLAIRRITGISTATIALGSEMSSGGQDRAEDIVAINTEGSRVRIKTAGRGGVYKDYVYKGVTKMTKYVYFVMTGGVYGHSPDNNYDPNALPVDNNYRDMVAENVTAAKLAGISGDFFTGIGISNVTIELAPKAKKLTWNGTDSIGSISGVPQPCCELLPDGGTENAAPCNFPTENLPIDDMKVGTGSCRKLY

NbL10g22890.1 uncharacterized_LOC104246640 [MW = 39.62 kDa]

No. of times detected



log(intensity)



Values from



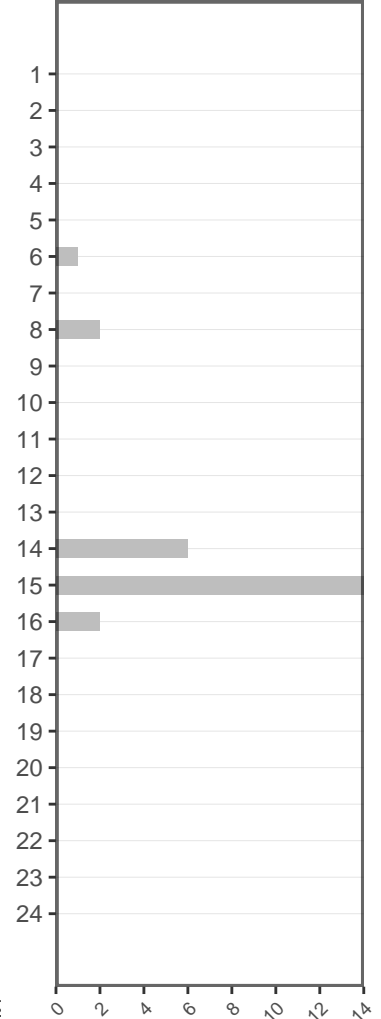
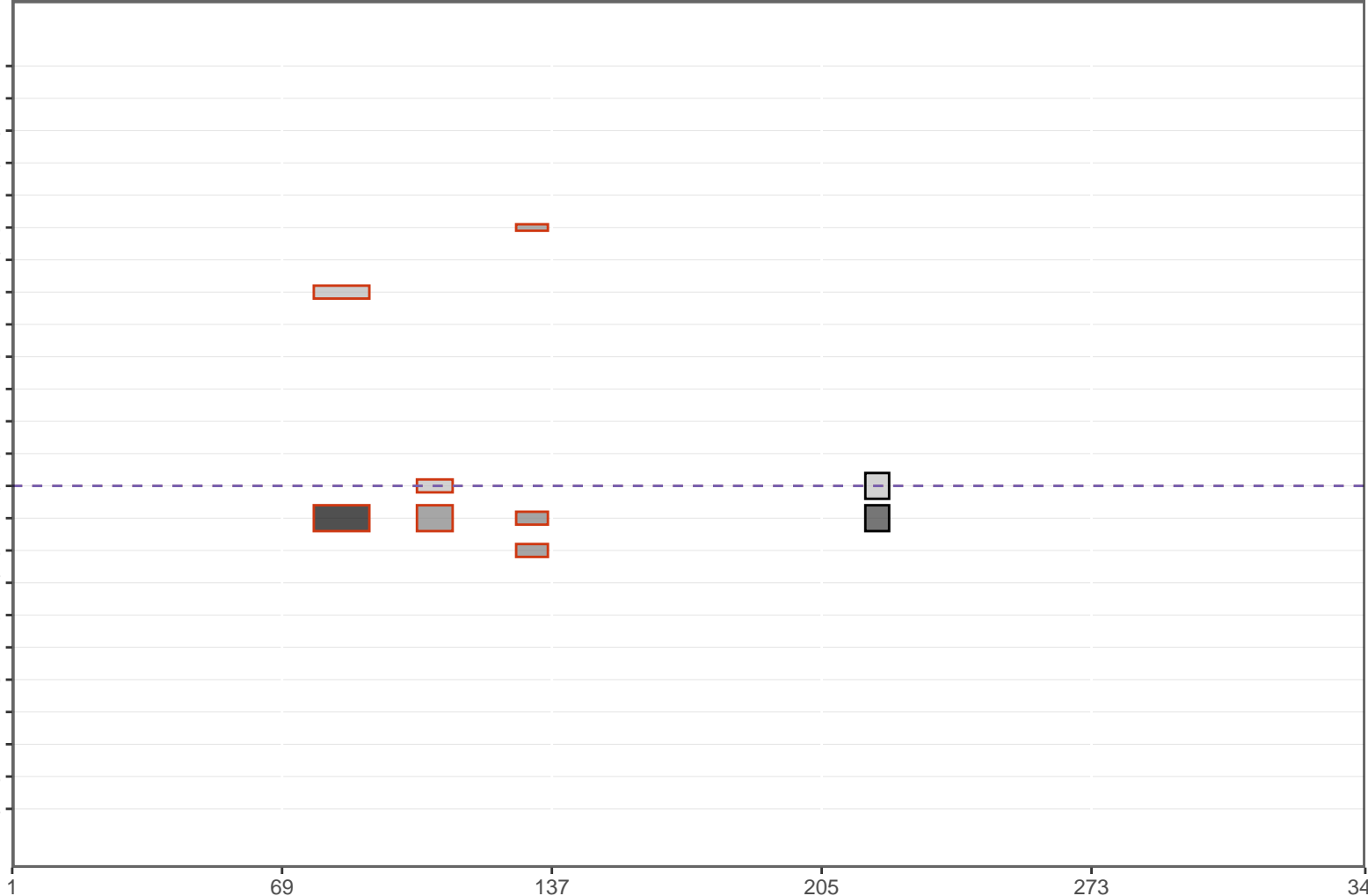
MW indication



Molecular weight

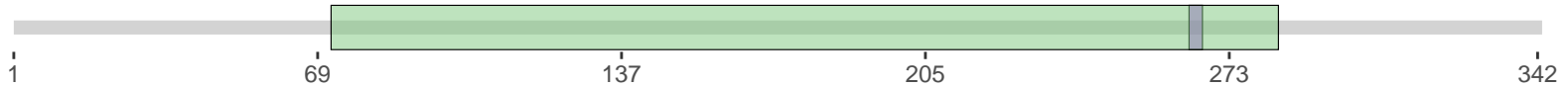


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IPRLREODFNFCQKEQMKIEKAVRARIYGRFFVRFNPGESAADYVDRITGFRRLRSDDIGRFQPPGQGGSPNMLVSHGLTLRVFLMRWVWVTEQFGLHNMBSGGMVMERGVGGRIYGLVHHTKEELQKFGMTDEMILDQEWQKIAKPGELNYDGLTGPSVYTFHFDQDDEEGNFEL*

NbL10g22730.1 vesicle-associated_protein_1-2-like [MW = 26.52 kDa]

No. of times detected



log(intensity)



Values from



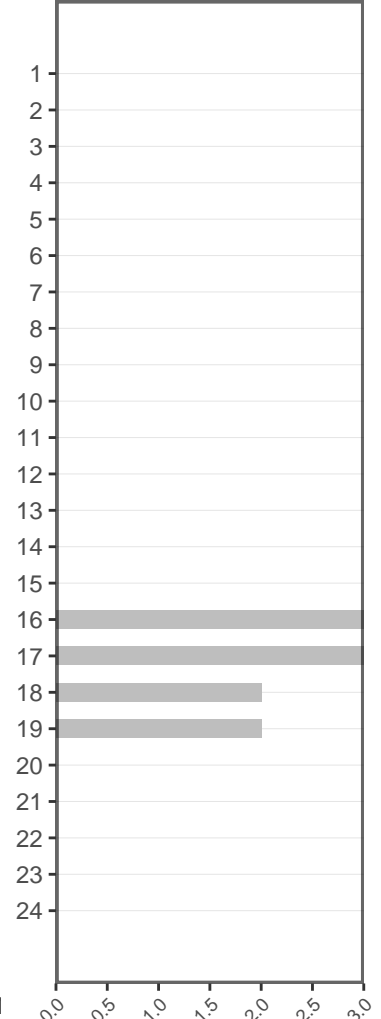
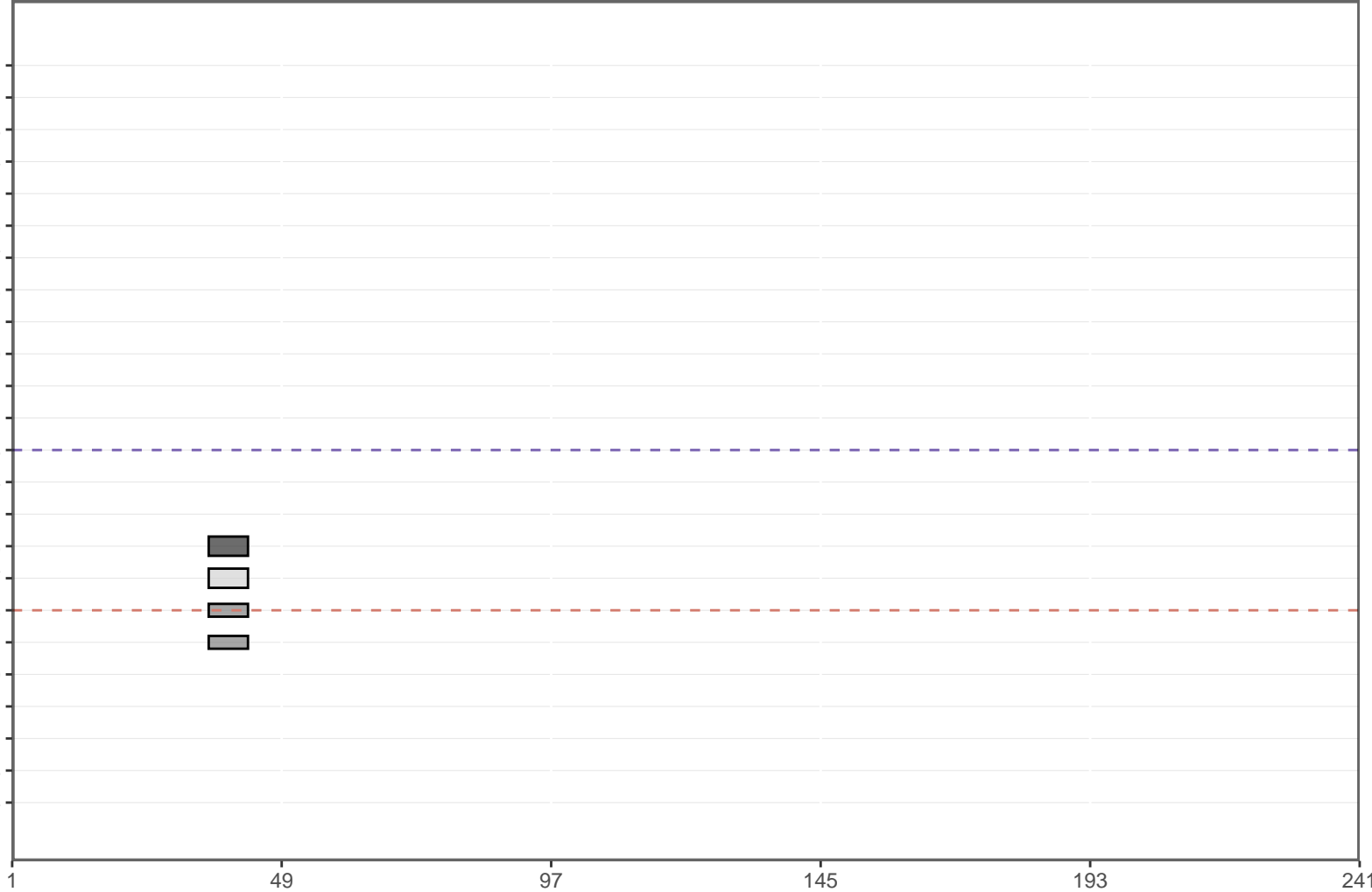
MW indication



Molecular weight



Gel Slice



Protein length

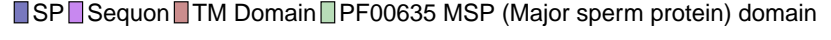


Peptide counts over 4 repeats

Pfam domains



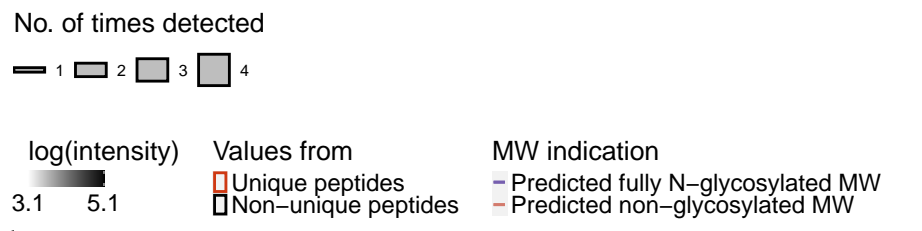
Pfam Description



Protein sequence:

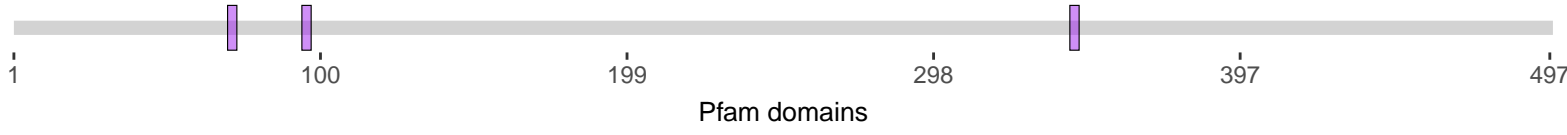
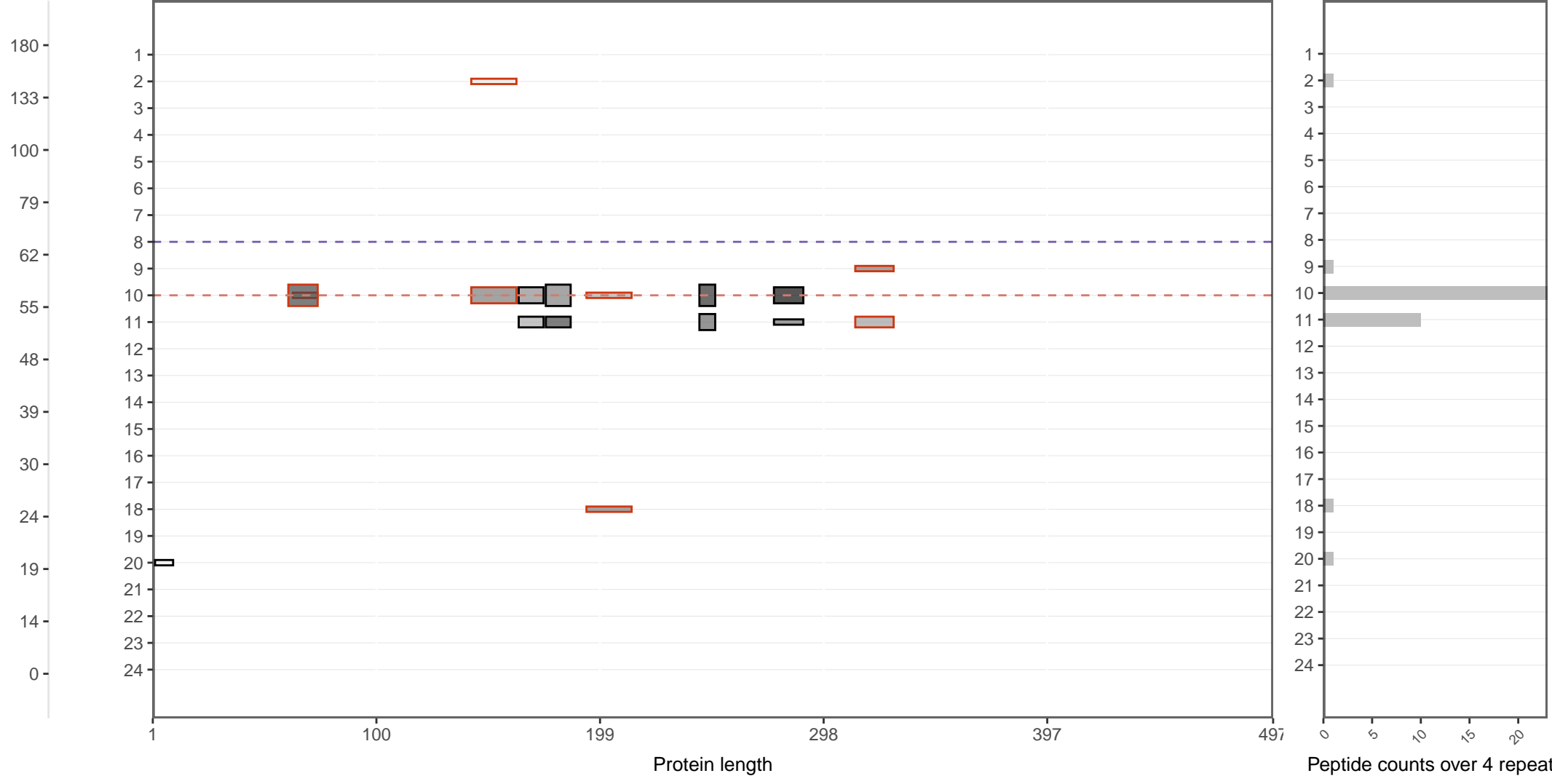
PEMFKKEEGNHYEDCKLRVYVPPGQPPFVQEGSEEGSSPRASVSENGTIVTSEFNNSIRAYNEQDSSSETKALISKLTKEKISVIQGNKLGQELALLRRNRSRGGIPITVYVJLGLGILGYLLKKT

NbL10g22420.1 uncharacterized_LOC107820933 [MW = 56.76 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain

Protein sequence:

KSRIHQKLPKFESEDFEKSDMEEDMGMPEGLVFFEDGSGYSRGPDVDPVIGELDESKYYISPTFKFEQCLVGGGHKRLRIVHTIEFNGGSDIQLRWVVEEQVWISPAFLSDSDTELDFKLGQRRLHPSELASGSKVWFEMSATPIYSEEGVTOETDQVYVYVLTENLKKRLLPENFVFGEEMLDMDDVTVLVLPGGFTSYVDVWVKDGLGIGVGVWYSDGVALVMERDVFEMDGKLEVRWVKSEMRRVITNPPLIWS

NbL10g22330.1 acyl-CoA-binding_protein [MW = 13.74 kDa]

No. of times detected



log(intensity)



Values from



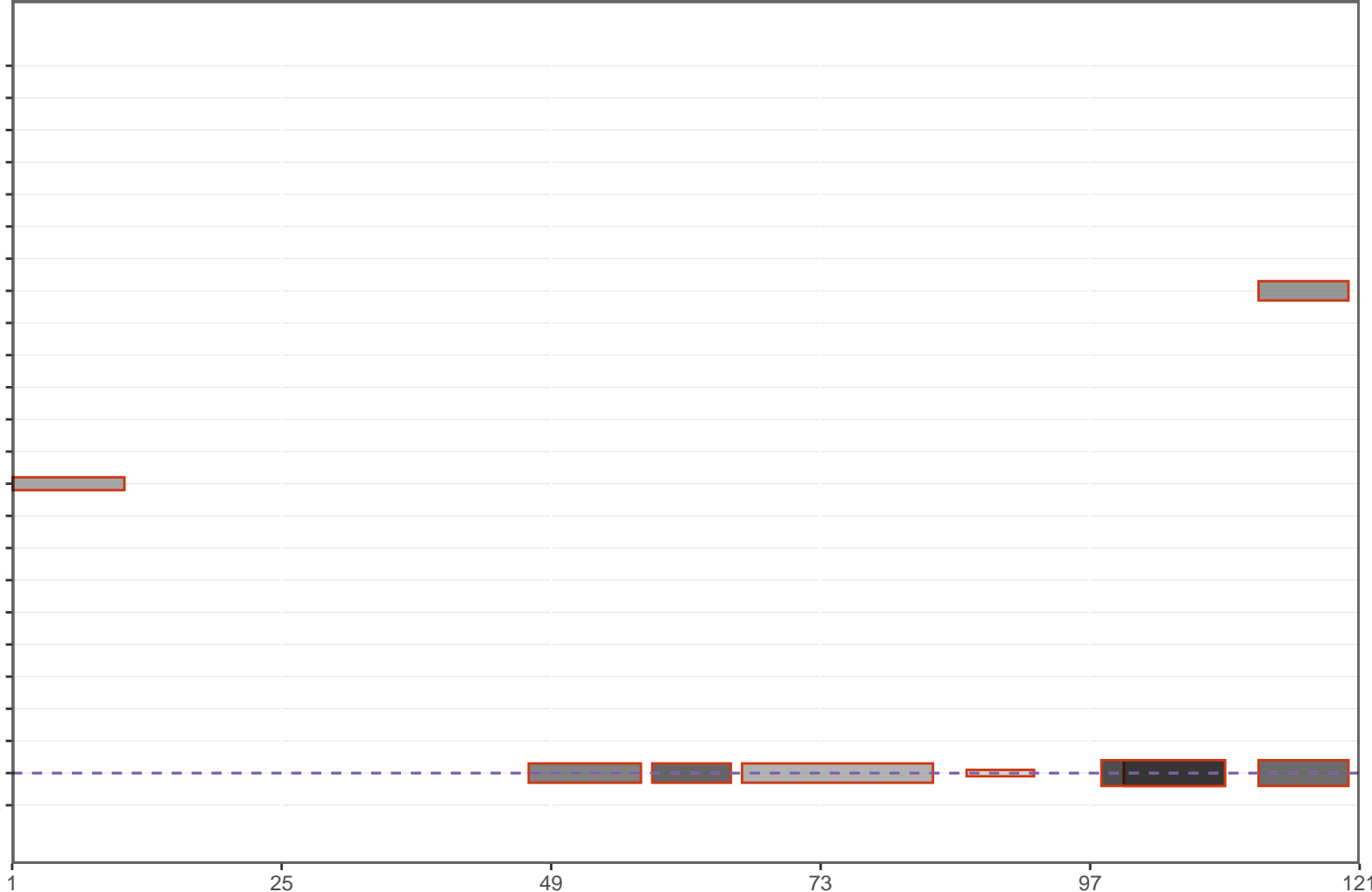
MW indication



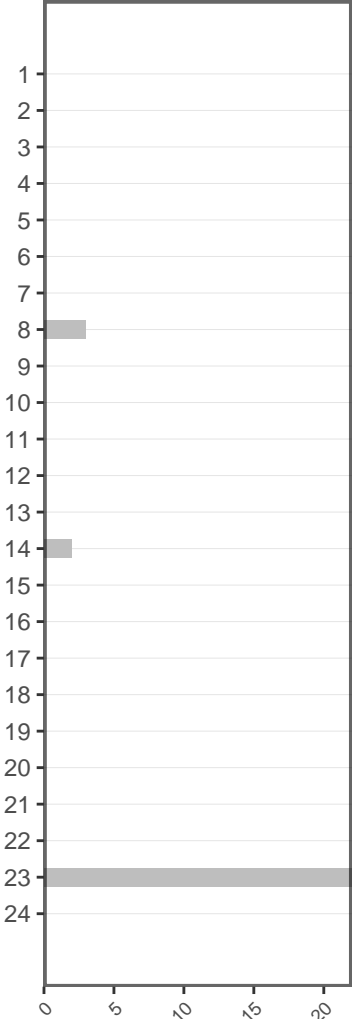
Molecular weight



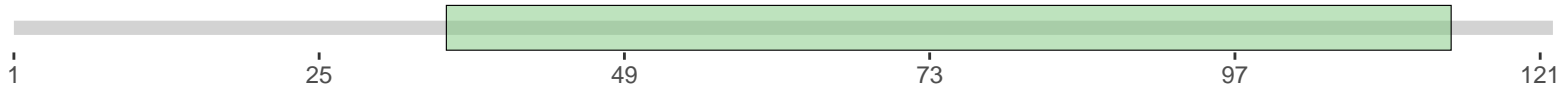
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

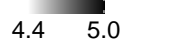
ESTSNENKLLYGLYKQATVGNVETGRPGIFNMRDRAKWDWAKAVEGKSKDEAMNDYTRKWLKEEAASA

NbL10g22320.1 60S_ribosomal_protein_L13-2 [MW = 23.58 kDa]

No. of times detected



log(intensity)



Values from



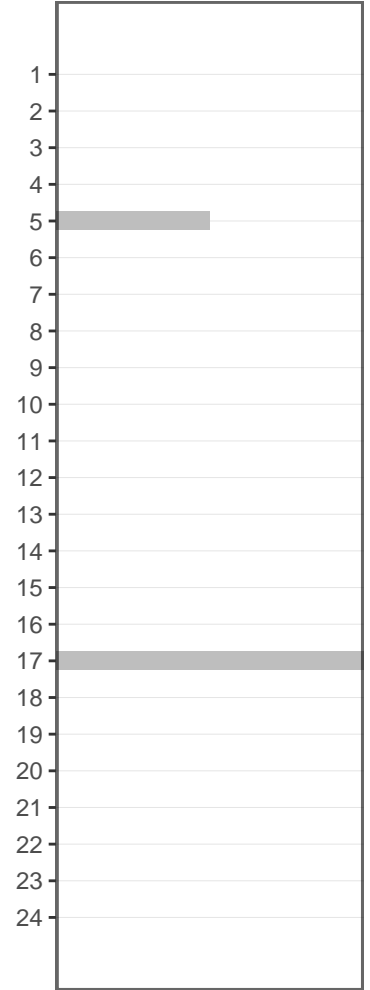
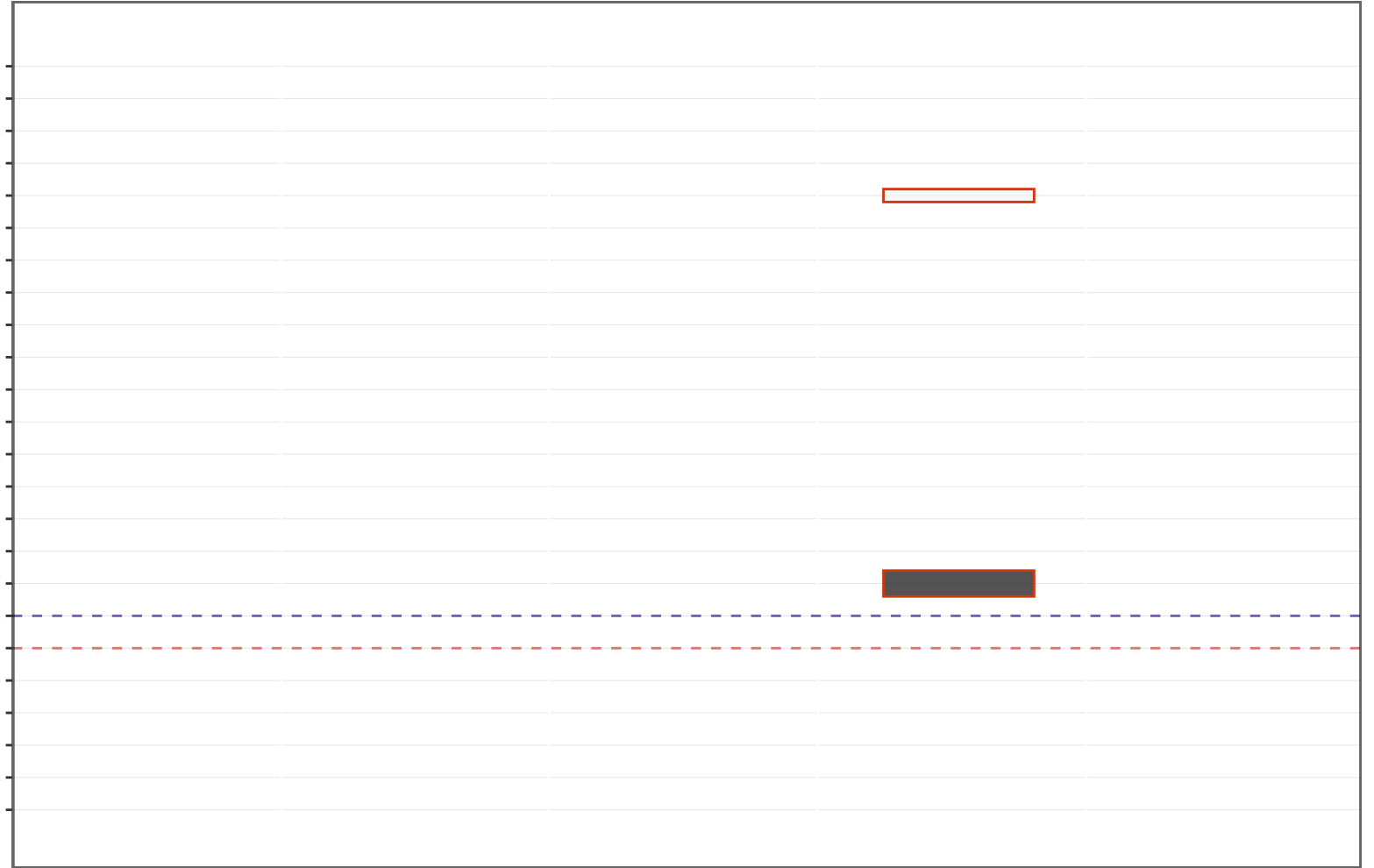
MW indication



Molecular weight



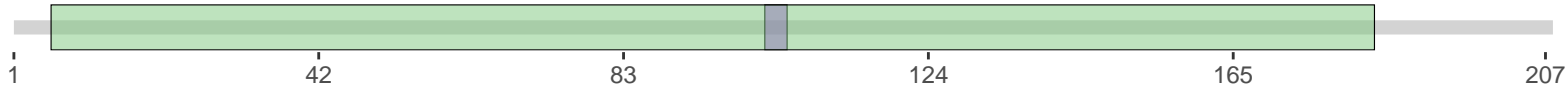
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

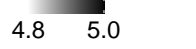
LPITGIAVDIRRRNRBLEGLGTVVORLTKYKALVFPFRRAKVKAGDSVVEELATATQVGGSYMPITREGPWEVLKVTDEMKSFNAYGKLIERTNARHIGARLKRAAEAEEKEEK*

NbL10g22210.1 phosphate/phosphate_translocator_chloroplastic-like [MW = 43.91 kDa]

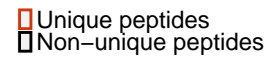
No. of times detected



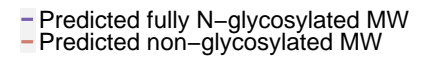
log(intensity)



Values from



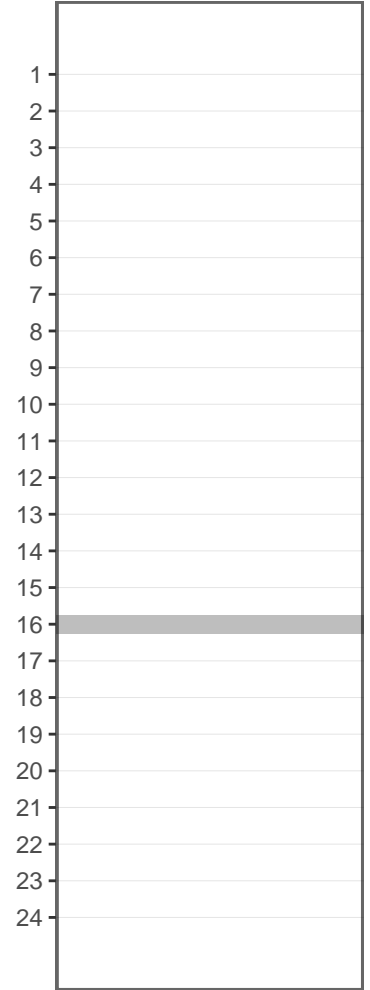
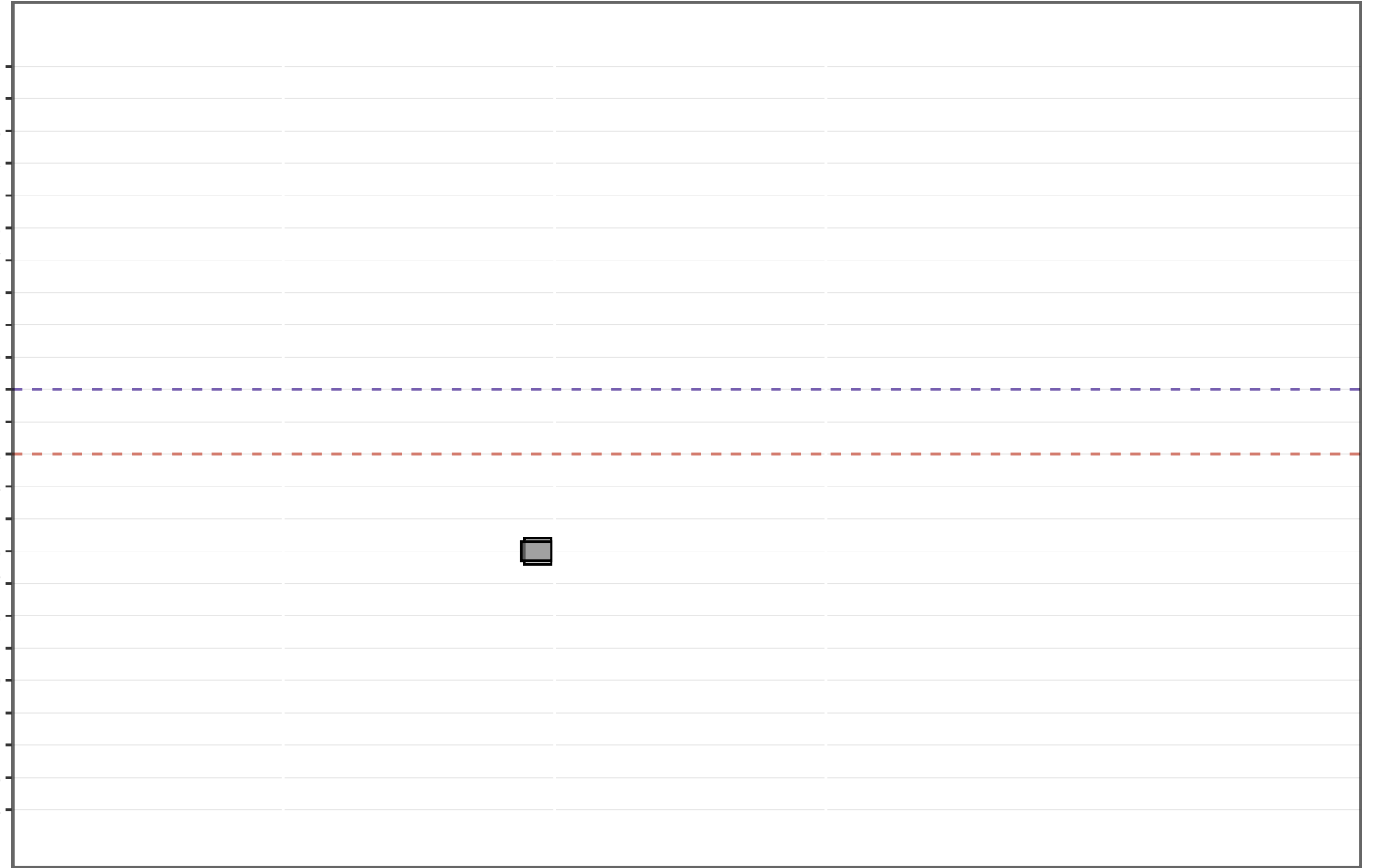
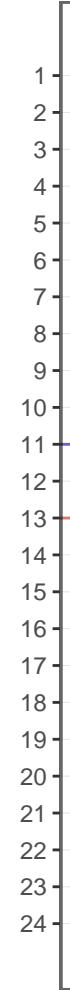
MW indication



Molecular weight

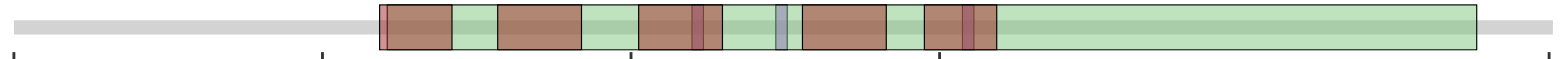


Gel Slice



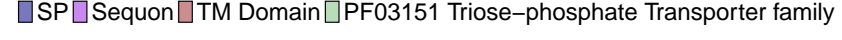
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

V/SFTHTKALEPFFNABSGFILGGQPLALWLSLAPVAVGVSMASLTSEFNWLGFBAMSNVVFYRSIVSKKAMTDMDSNVVYVHIALIFGIPPAIEGPGQLLGHGFADAIAKVGSLTKFVTDLFWVGMFHYLHNGVATNLERWAPLTHAVGNLKRKRVFVHGFBIIVFGNKNISTGTGIGTGVAVAGVALYFRIKAKMEEEKRVSPRTMGK

NbL10g22050.1 magnesium-chelatase_subunit_ChII_chloroplastic [MW = 46.37 kDa]

No. of times detected



log(intensity)



Values from



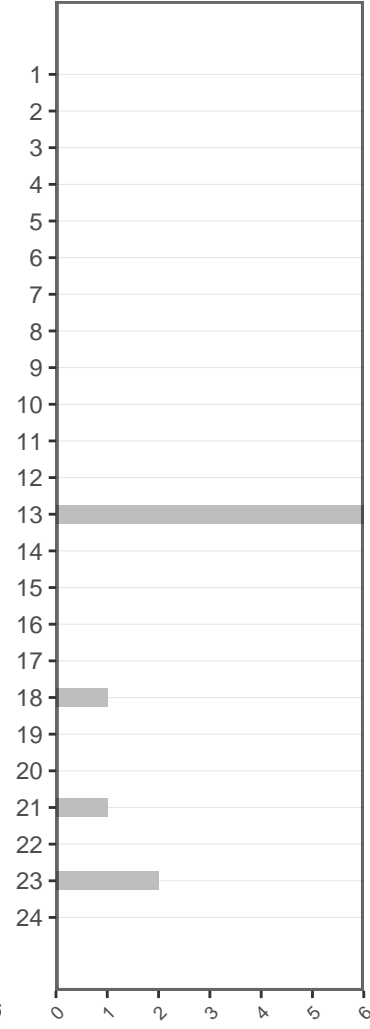
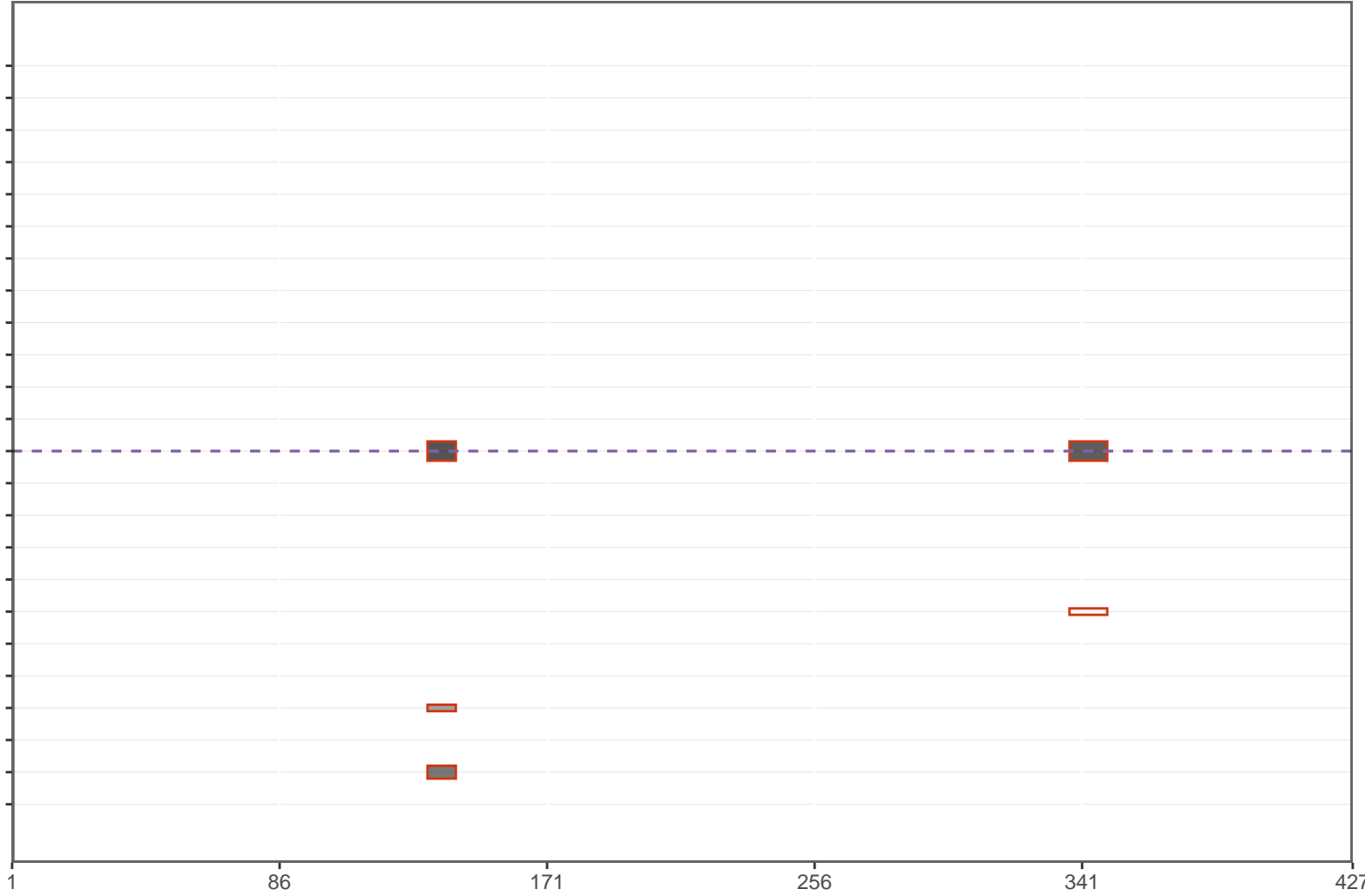
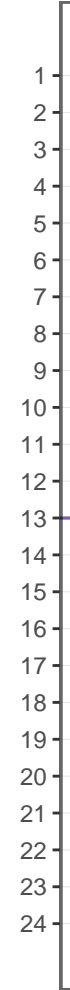
MW indication



Molecular weight

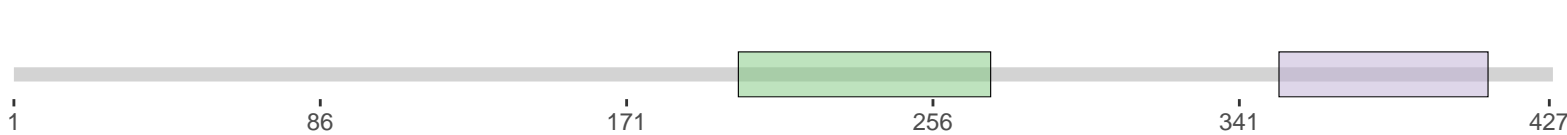


Gel Slice



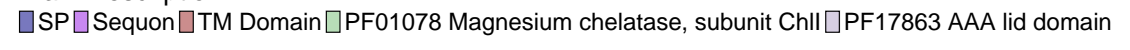
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IEKALTEGKAFEPGLLAKANRGLVYDEVNLLDDHLDVLLDSSAAGWNTVEREGISGHPARFLVGGNGNPEEGELRQQLDRFGMHAQVGTVRDAELRVKIVEERARFDKPKKEFRSEYKAEQEKLNQIDSRNALSVAITDHLRVKISKVCAELNVGLRGGDIVTNRARALAAALGKGMKVTPEDIATVFNGLRHRRLRDKPLSEISDGSVALVEKVEYFAI

NbL10g22030.1 anthocyanin_5–aromatic_acyltransferase–like [MW = 51.04 kDa]

No. of times detected



log(intensity)



Values from



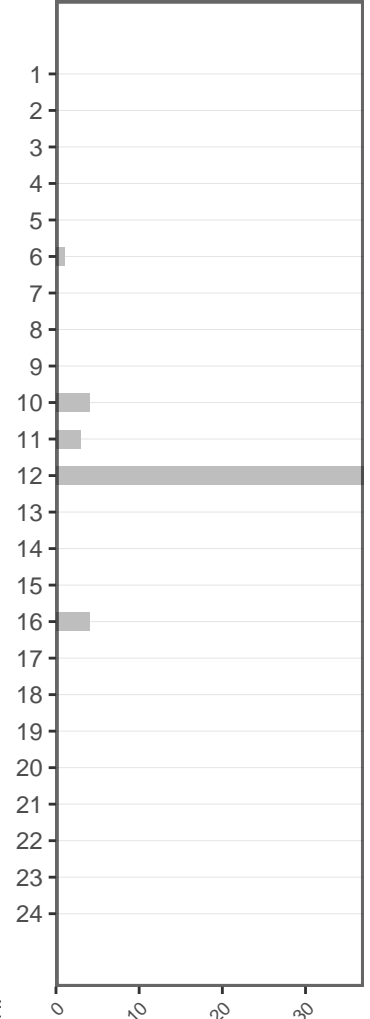
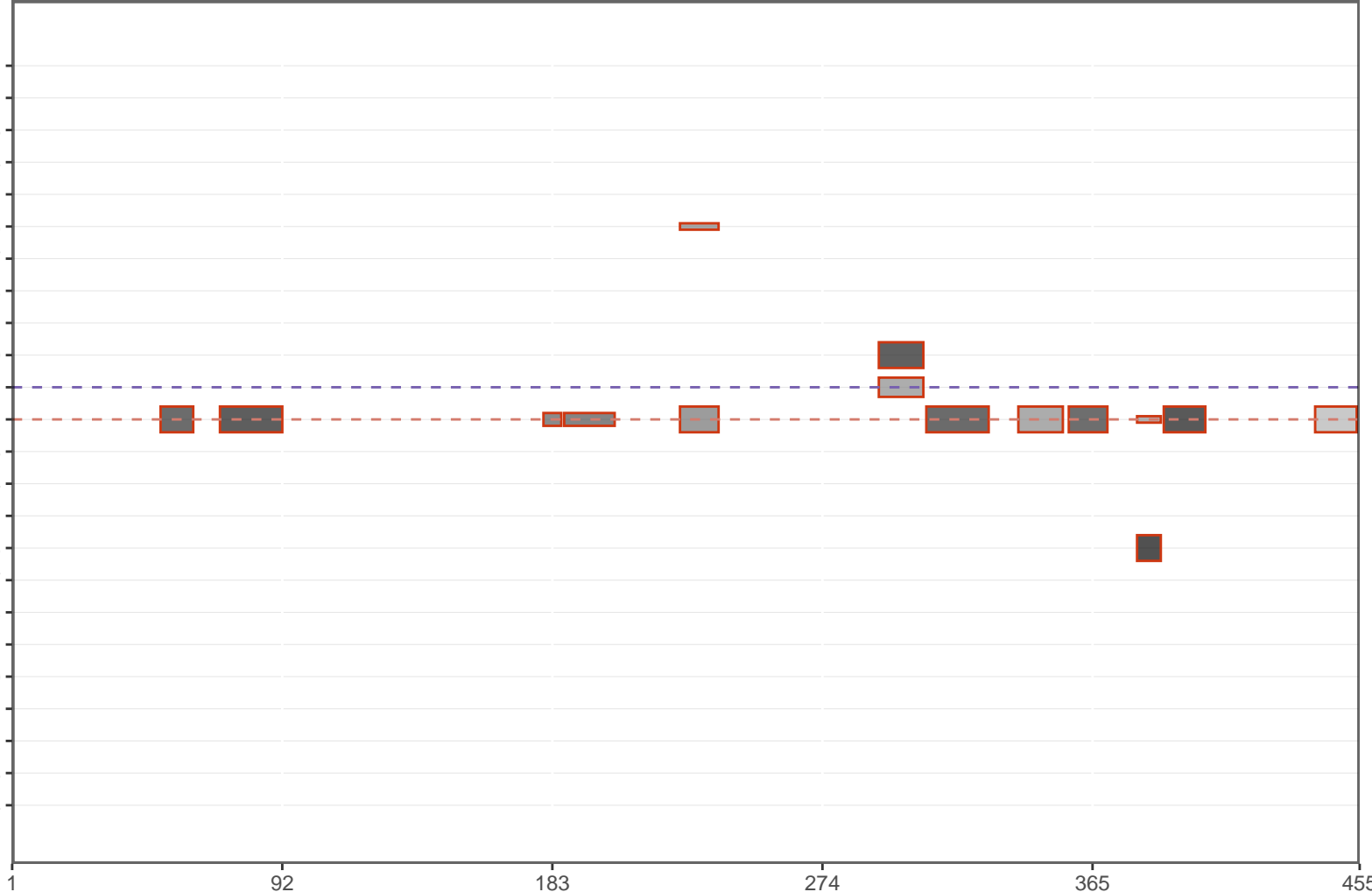
MW indication



Molecular weight

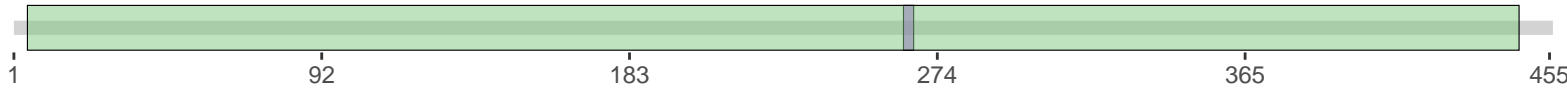


Gel Slice



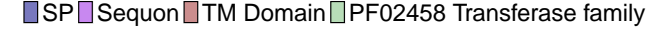
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LIVDEMKYKIMMTMSDIVTPPKVGRGTFVSRDILKFKNLISSRRPNLTHVTSFTYGVAVWGLKISEAATGKNDKNSVEFFGFAADGRAGNFPPLPPBYGKALVYVARTRHVDLAKGEGFTIAAELIGEAIQKRMKDEEVLGGVWFKEYDLDKRSVSVAGSPKLDLVAADFQWPKPEKLEFVSDIGDSDISMSLKYKDSDDGLEIGLSLSEKTRMNAFAMFTHGLSFLV

NbL10g21990.1 diacylglycerol_kinase_5-like [MW = 39.6 kDa]

No. of times detected



log(intensity)



Values from



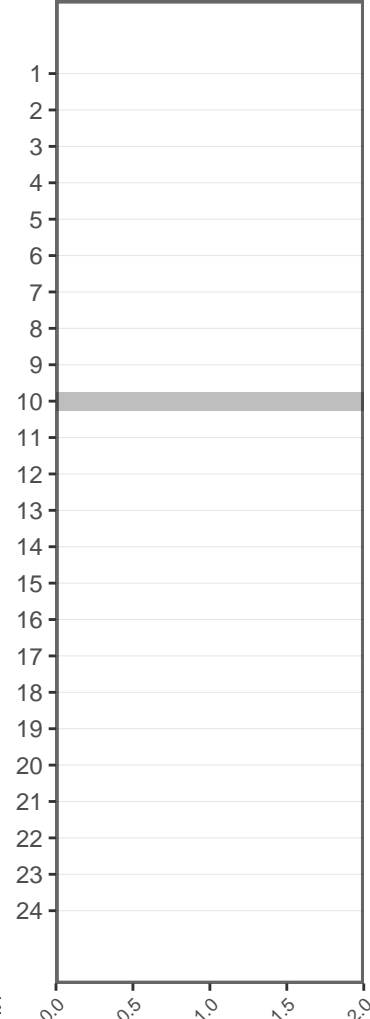
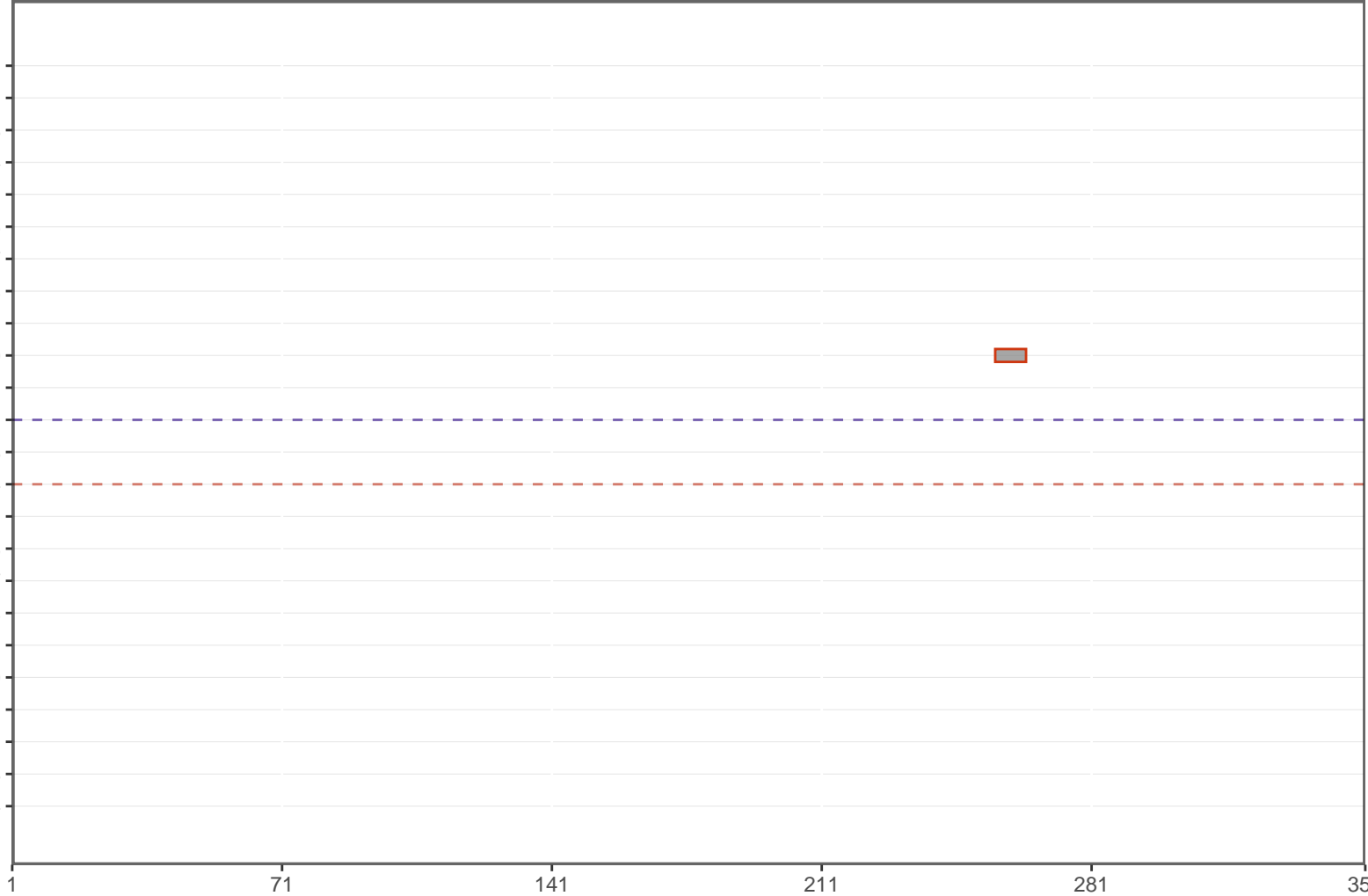
MW indication



Molecular weight

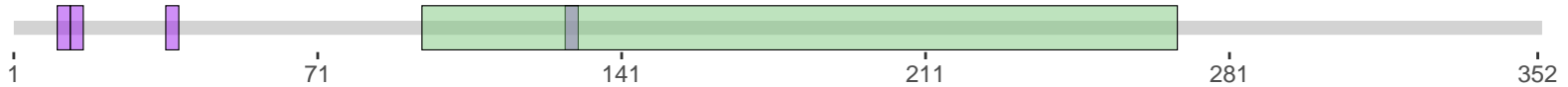


Gel Slice



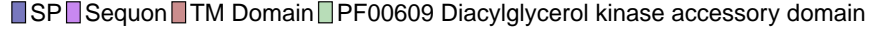
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IQGGVVDLHFPHSRGKGLNLPFGFGLNPGWTPNSNKRDRDLTPPFVDDGHLEVVGFQDAWHGSMALLAPNGHGTSLAGAHRRIFEFKGAADFTFMRIDGEPWKGPLVDDDTVAVEIHLGDVWMLATHGCRKEMHDPDSHWNHGGDDGDSGEEISVVEEQKFGAADTFKIPDEVDIHLG*

NbL10g21950.1 deoxyribodipyrimidine_photo-lyase [MW = 44.08 kDa]

No. of times detected



log(intensity)



Values from



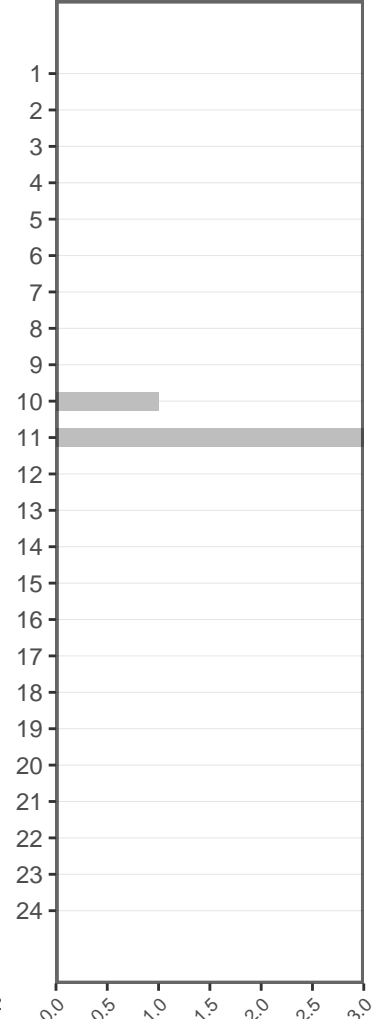
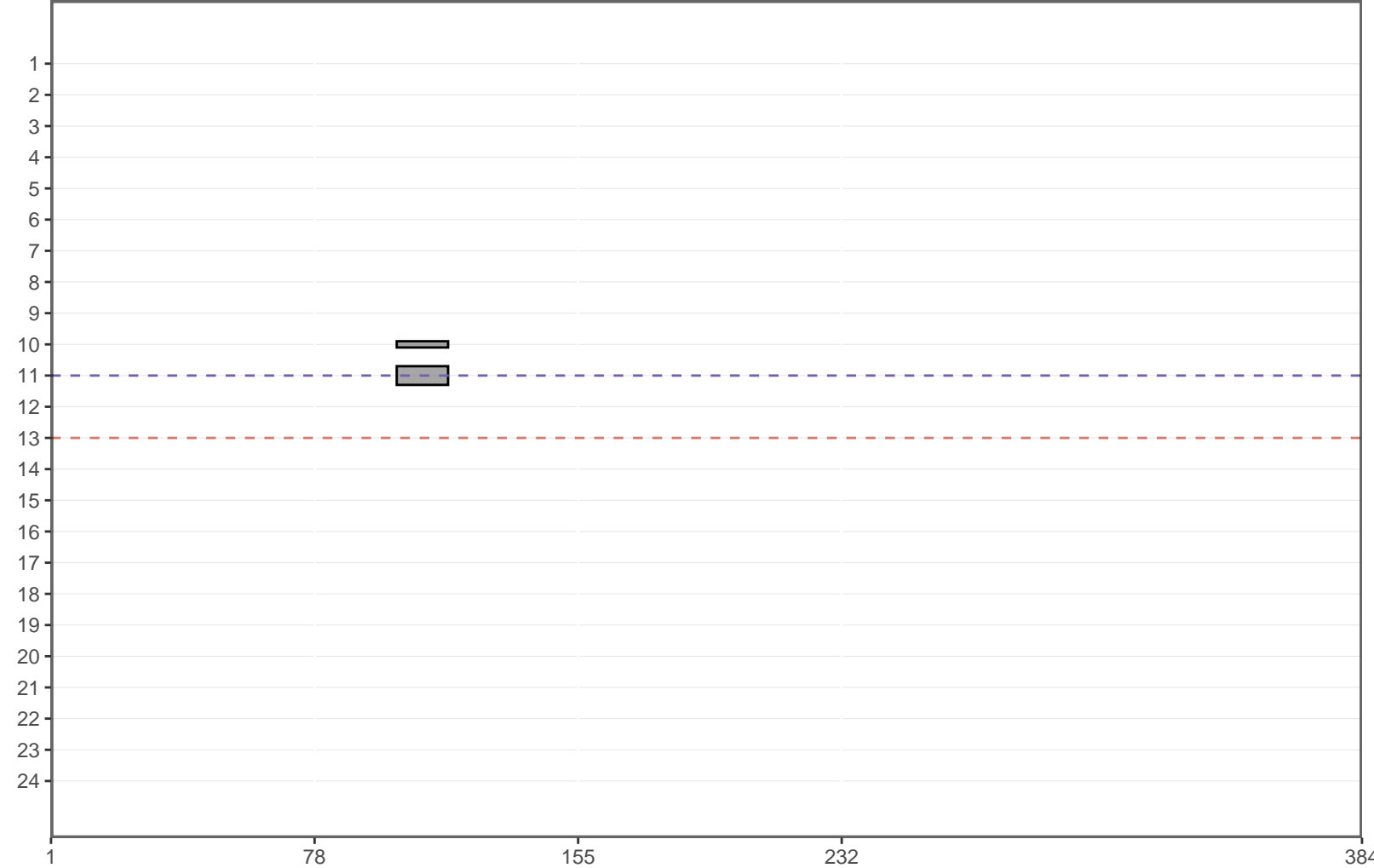
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

NPLKPOLSLGSLSPYLFHFGGSAQRCALEAKRVRKLYTQAVDAFLFELIVRRELADNFQYYQPRVDELLGAWEWARKTLMHASDKREHYMREGLKAGTADPLVNASGLEMHHYGMHGFMRMYWAKKLEWTSGPPEALATWYLNQKYHIDGRDPSGYVGCMMWSGGLHDGVLLHYAGSLGQRKLELFSLLFLLEK

NbL10g21940.1 uncharacterized_LOC109214416 [MW = 73.71 kDa]

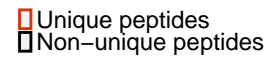
No. of times detected



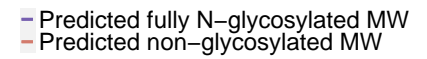
log(intensity)



Values from



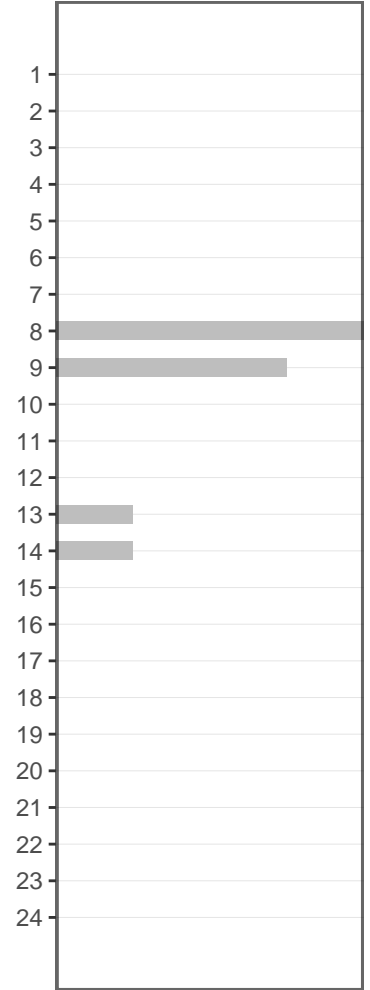
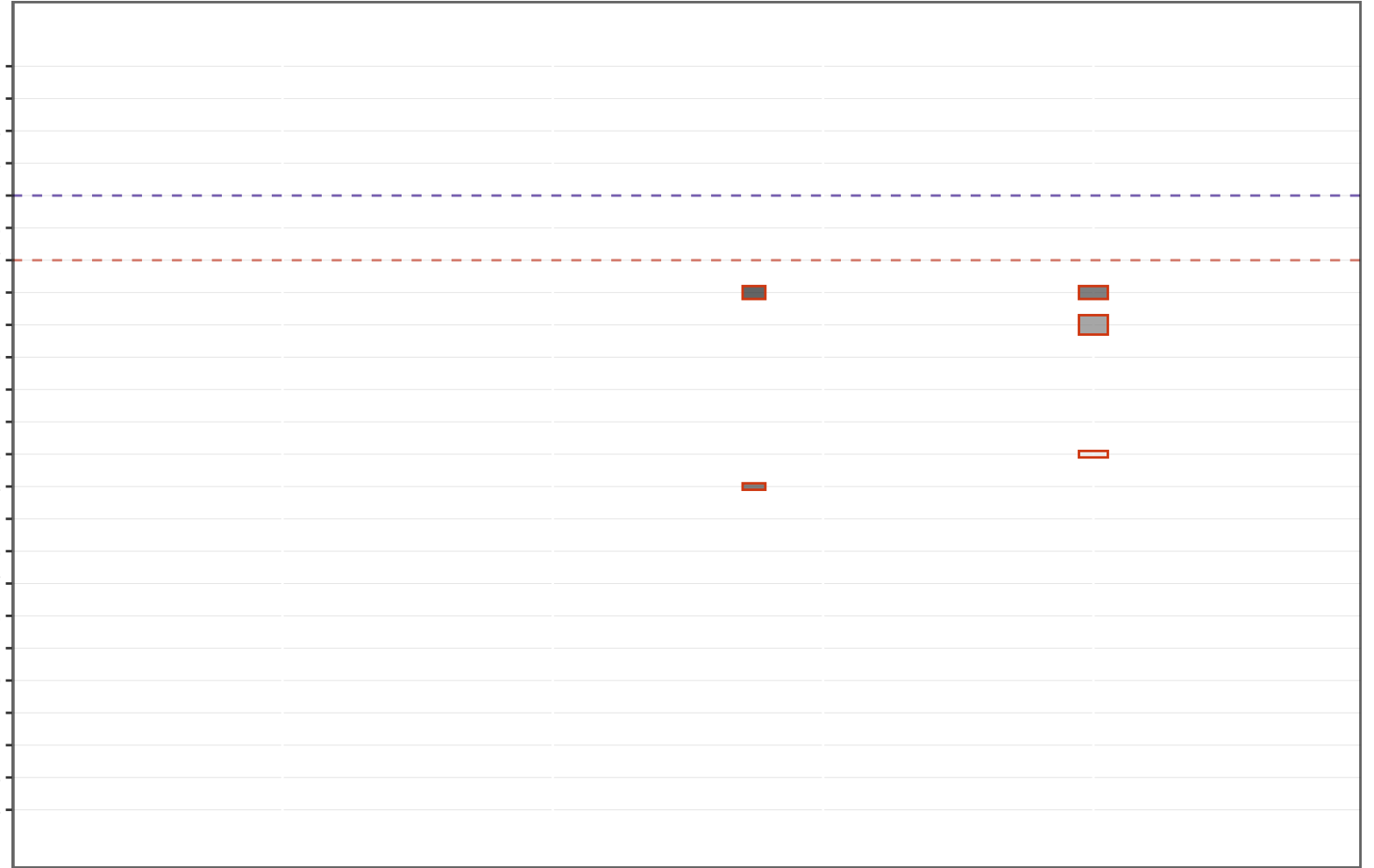
MW indication



Molecular weight



Gel Slice



Protein length

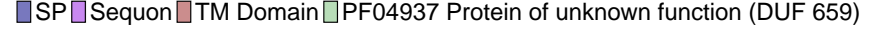


Peptide counts over 4 repeats

Pfam domains



Pfam Description

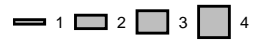


Protein sequence:

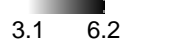
FHKYQLQEQYGHASLRVPLRBYERSDFEPVYTLVEDLSSARALGLVLLDEGKILSMEEGIARDIEEMRSPHFVNELEAVHSVLSKLIKTMAGDIDGTEKSRVGGCLPLWEELRVVVKDWGLKFKHVEGPKVIERRFNKNYHPWAAAFILDPVLRDNGSKYLPFKGLTFEGEKDVKLITRVSREEAHAALMELMKWRTEGLDPVYAGAVGLKGRDASSGKMIANPQSSRLVWETHLTFKSLGKVVRLIFLRASSGGYKKNWFLRWANAHHSRYGMQDKAQL

NbL10g21880.1 ATP-dependent_Clp_protease_proteolytic_subunit-related_protein_2_chloroplastic-like [MW = 35.66 kDa]

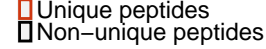
No. of times detected



log(intensity)



Values from



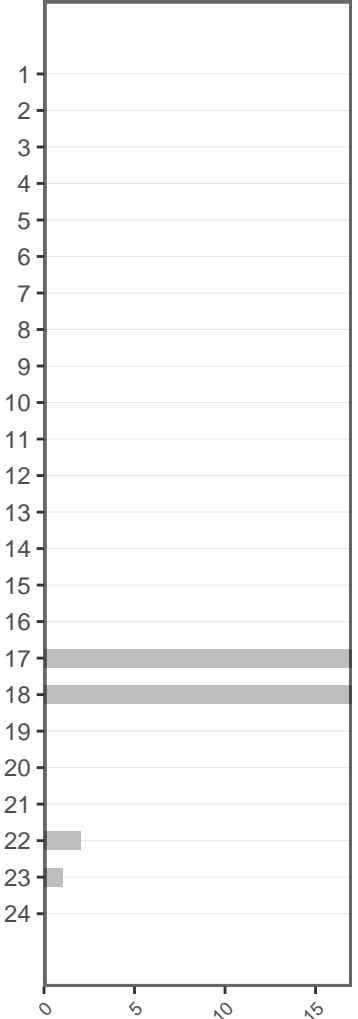
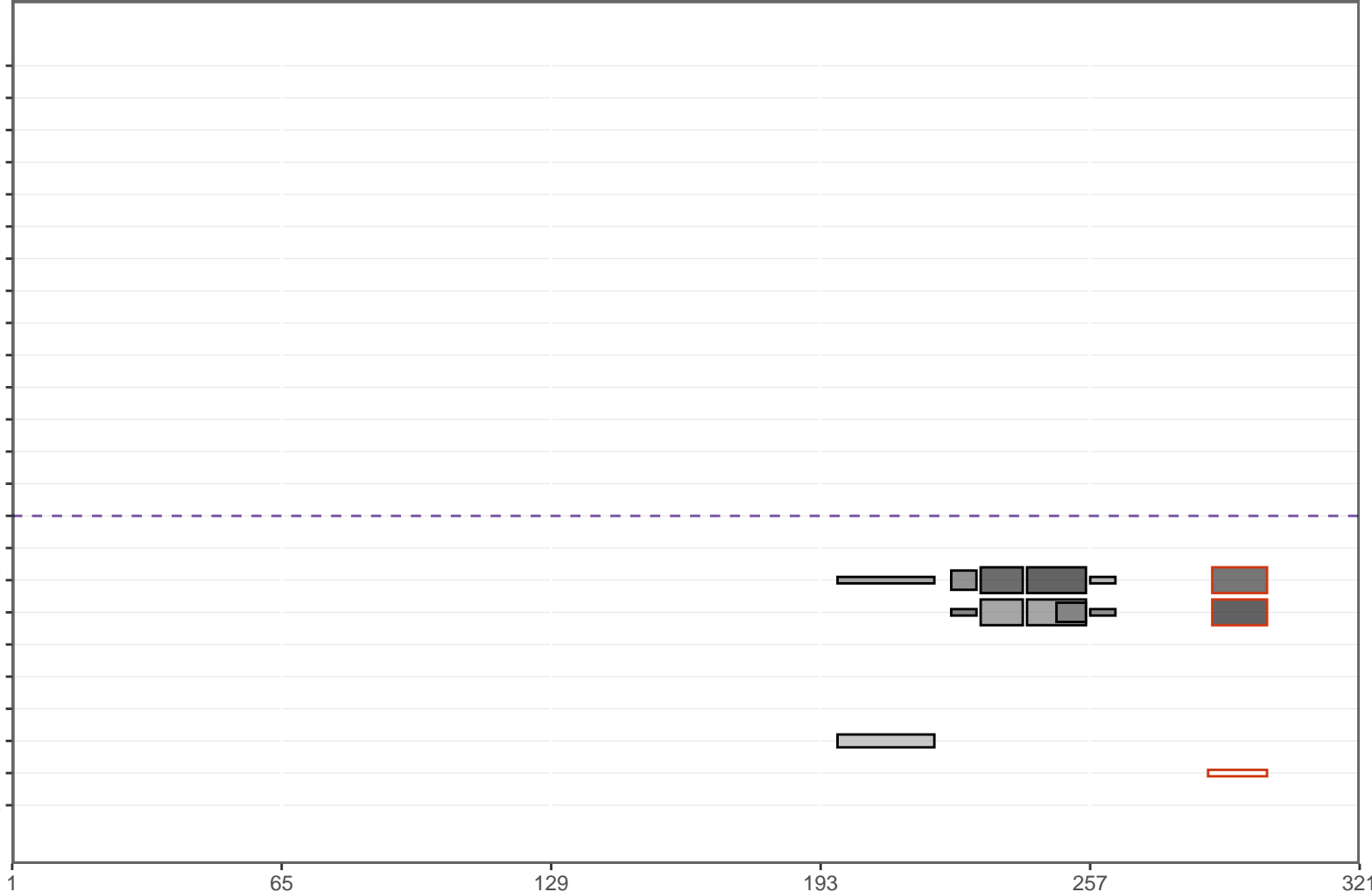
MW indication



Molecular weight



Gel Slice

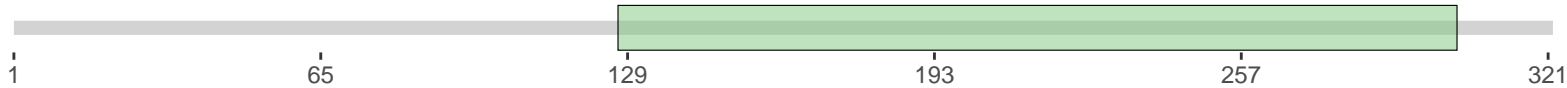


Protein length

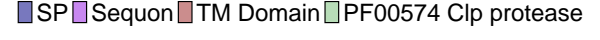


Peptide counts over 4 repeats

Pfam domains



Pfam Description

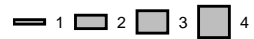


Protein sequence:

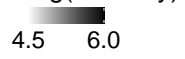
HIDEEF SNQLATMAYLDSIDGSKLYLVNGPGDLPSPMAIVDTMGSLSKSAVGTCHVGVYANLAGFLAAGEKNGRFAMPLERIALGSPAGAARGADDIRNEADELLRFRDYLFKELAEKGTGGPVEKVKHDLERMKRYNAGEALEYGLIDRIVRPPRIKADAPRKDTTAGLG

NbL10g21850.1 ATP-dependent_Clp_protease_ATP-binding_subunit_CLPT2_chloroplastic-like [MW = 25.8 kDa]

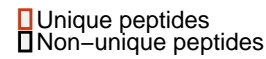
No. of times detected



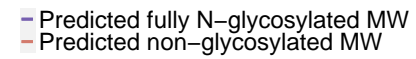
log(intensity)



Values from



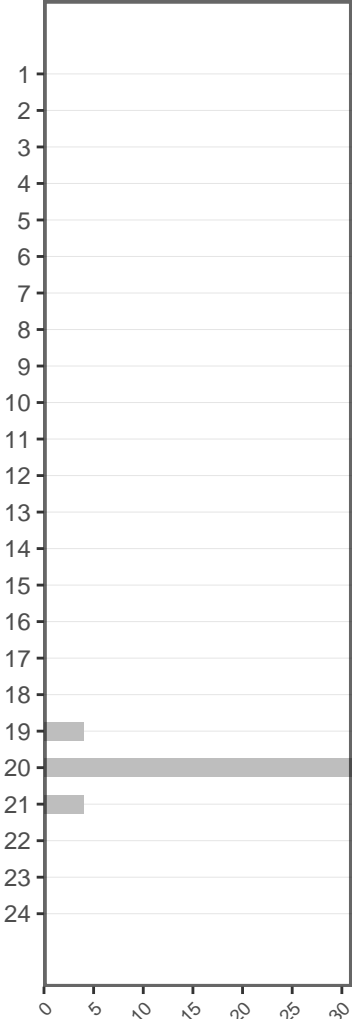
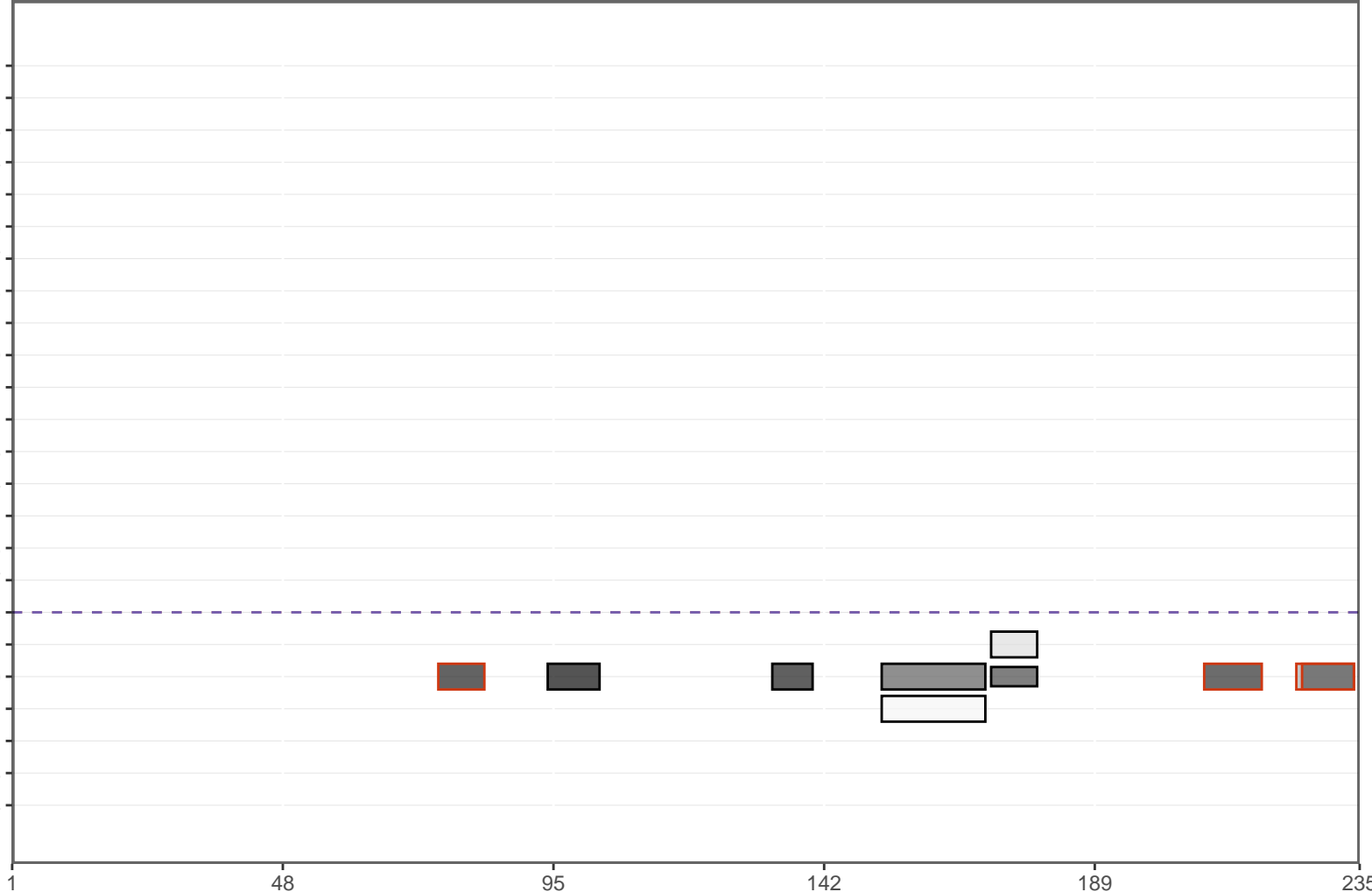
MW indication



Molecular weight



Gel Slice

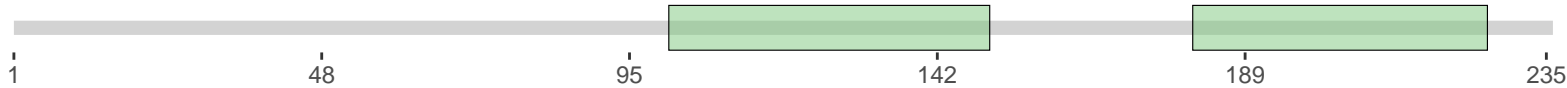


Protein length

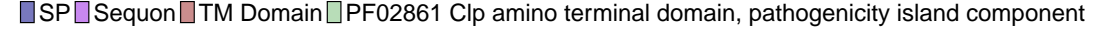


Peptide counts over 4 repeats

Pfam domains



Pfam Description

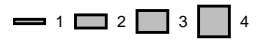


Protein sequence:

KYPTTGTTEALLMGIEGTFNFAKYLFRANBITLRFKVRREETVKILGKADMWFFSPEHPPLTDEAGKALDWALDEKLKSSSENGEITFTTHLLGVWSQVSPGPKLGGKLNDEKAGELKVKVISEPGFVDD

NbL10g21760.1 probable_LRR_receptor-like_serine/threonine-protein_kinase_At1g12460 [MW - SP = 92.56 kDa]

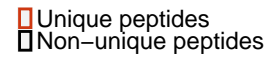
No. of times detected



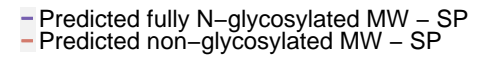
log(intensity)



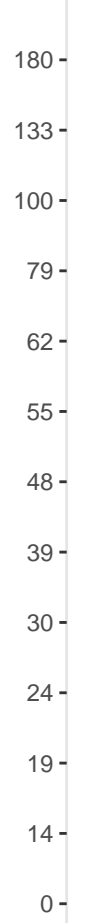
Values from



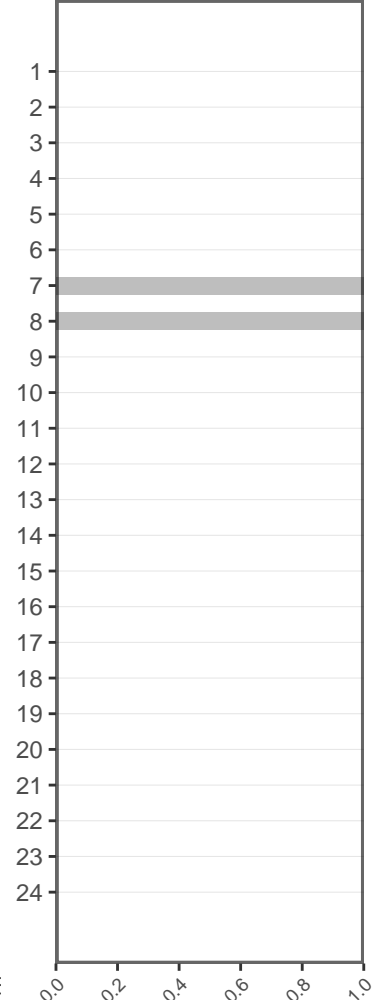
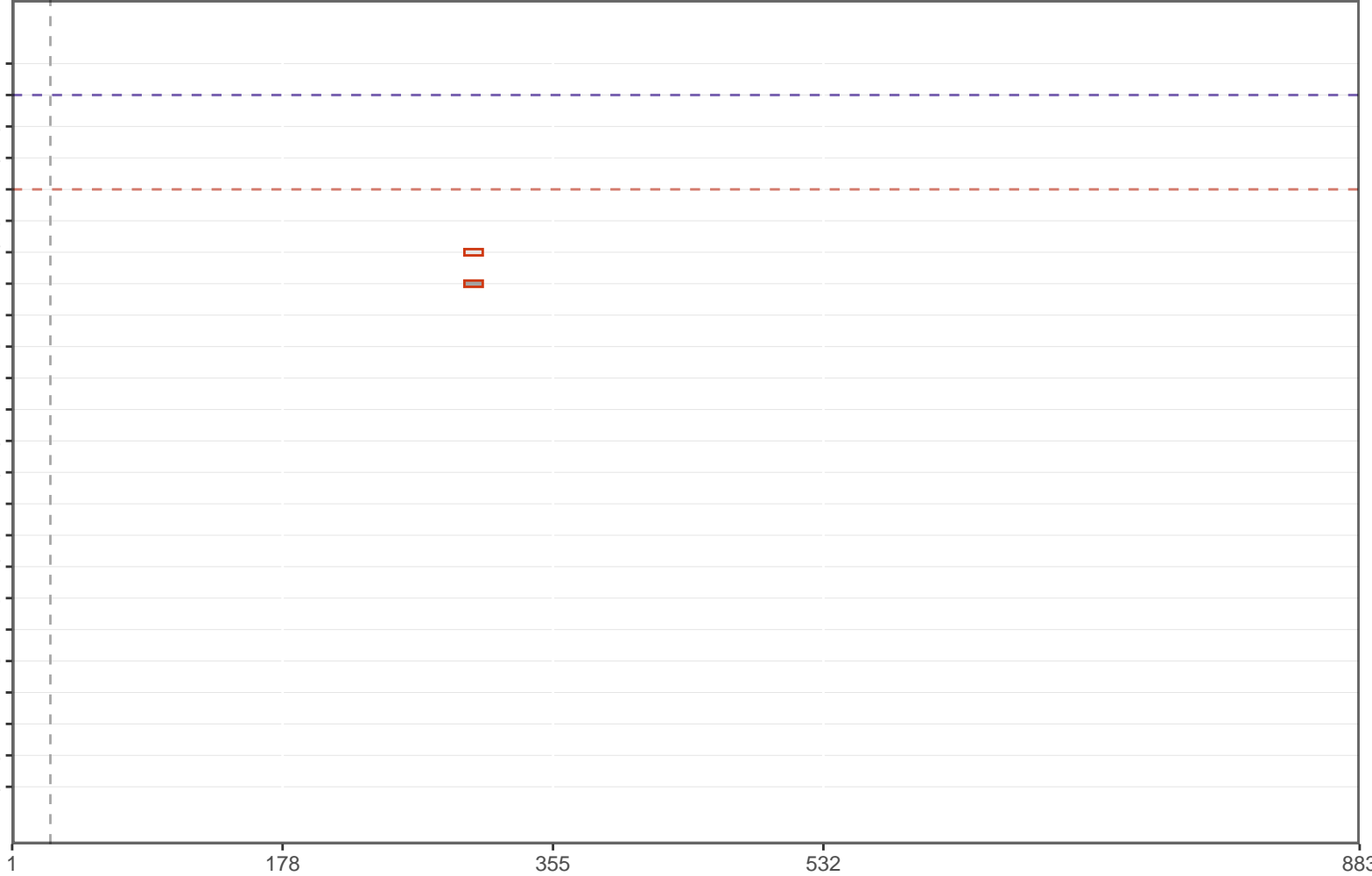
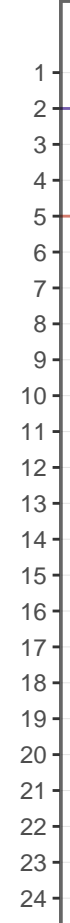
MW indication



Molecular weight



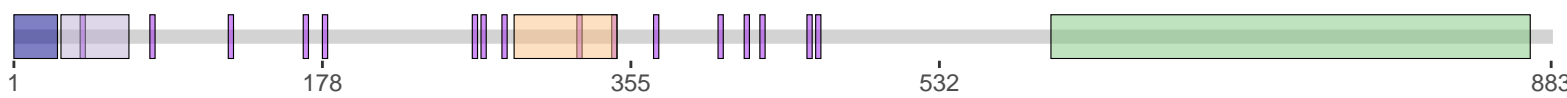
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SNLHFLDSENYLGGSPVALENMHLNTHFNQVYNLLSGAIPGTESEGGQFGRSAFFHNSGLGAPLEVSGSPGSIAPKGGKPRLSASAIWAIAVAALITGVQVITINMKARRRRRADETHVESTPLASTDENVIGKLVLFKTLPSKYEDWEAGTKALLKESLGGGTIGVYRTSFGEGVSLAWKLETLGRIRNQDDEFHEIGRLGTLQHPNLVALGGYYWSSSMQLLSEFVFNQGNLYDNLHGLGYPCGTSIGAAGTPELNWRRRFQIAGSTARALAKLHCKKPLILNV

NbL10g21690.1 enoyl-CoA_delta_isomerase_1_peroxisomal [MW = 26.84 kDa]

No. of times detected



log(intensity)



Values from



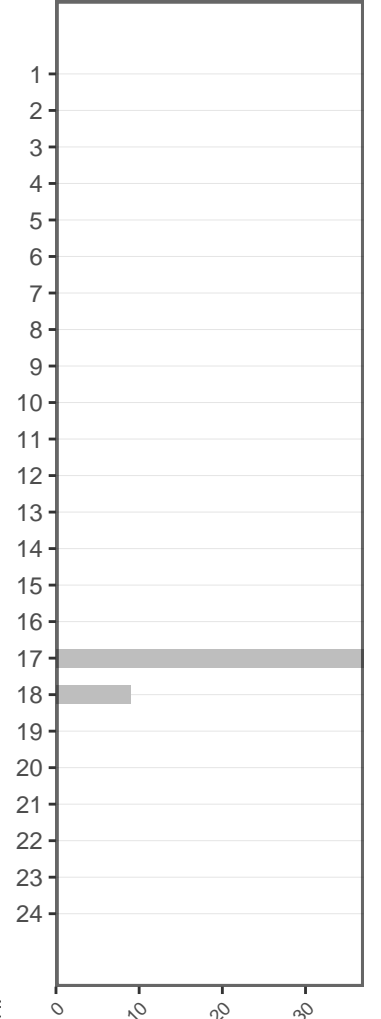
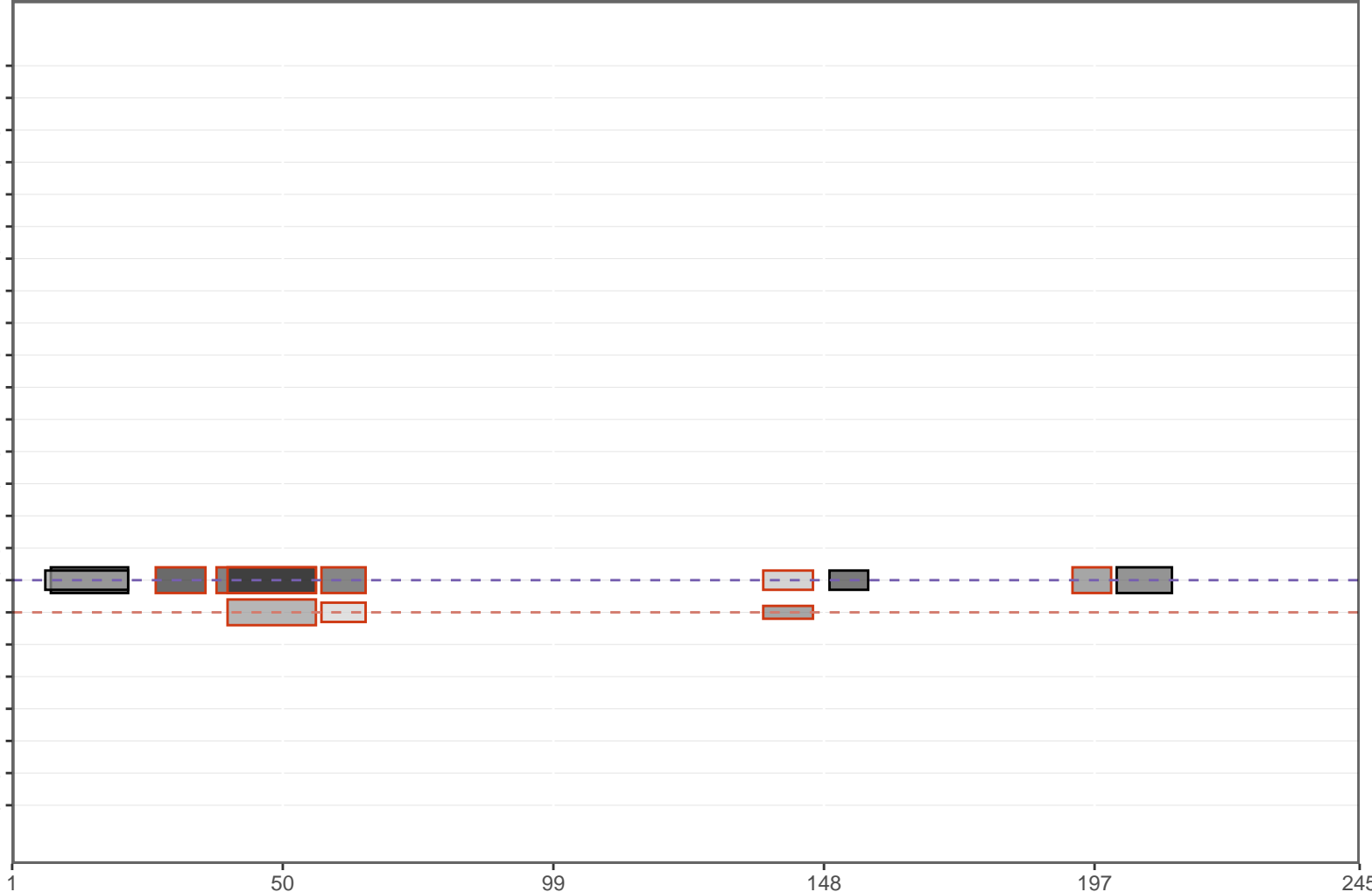
MW indication



Molecular weight



Gel Slice

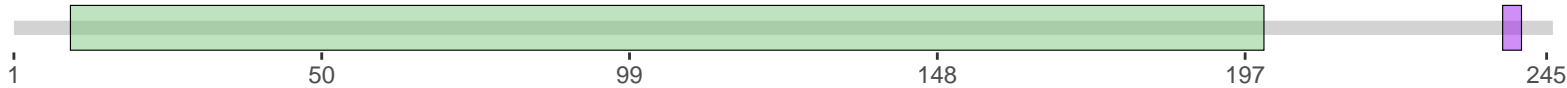


Peptide counts over 4 repeats

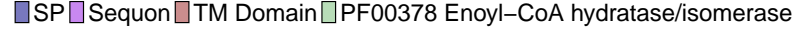
Protein length



Pfam domains



Pfam Description



Protein sequence:

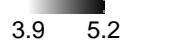
LSHDYILMRKDRGRFLMSELDLGLKVPWFSAALVKGKVGSPWVREVVLSKAKMTAEMGVEMGVDSAHSGAETVEAANVRLAEELVSRNWDGNVYADCRKFLGVLLNSLGSDETVDGVEEEKPNKTLGRLL

NbL10g21670.1 copper_chaperone_for_superoxide_dismutase_chloroplasmic/cytosolic [MW = 33.2 kDa]

No. of times detected



log(intensity)



Values from



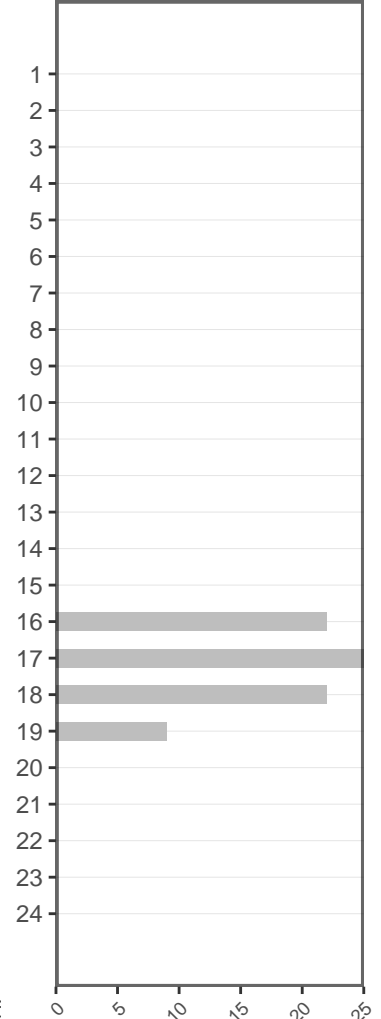
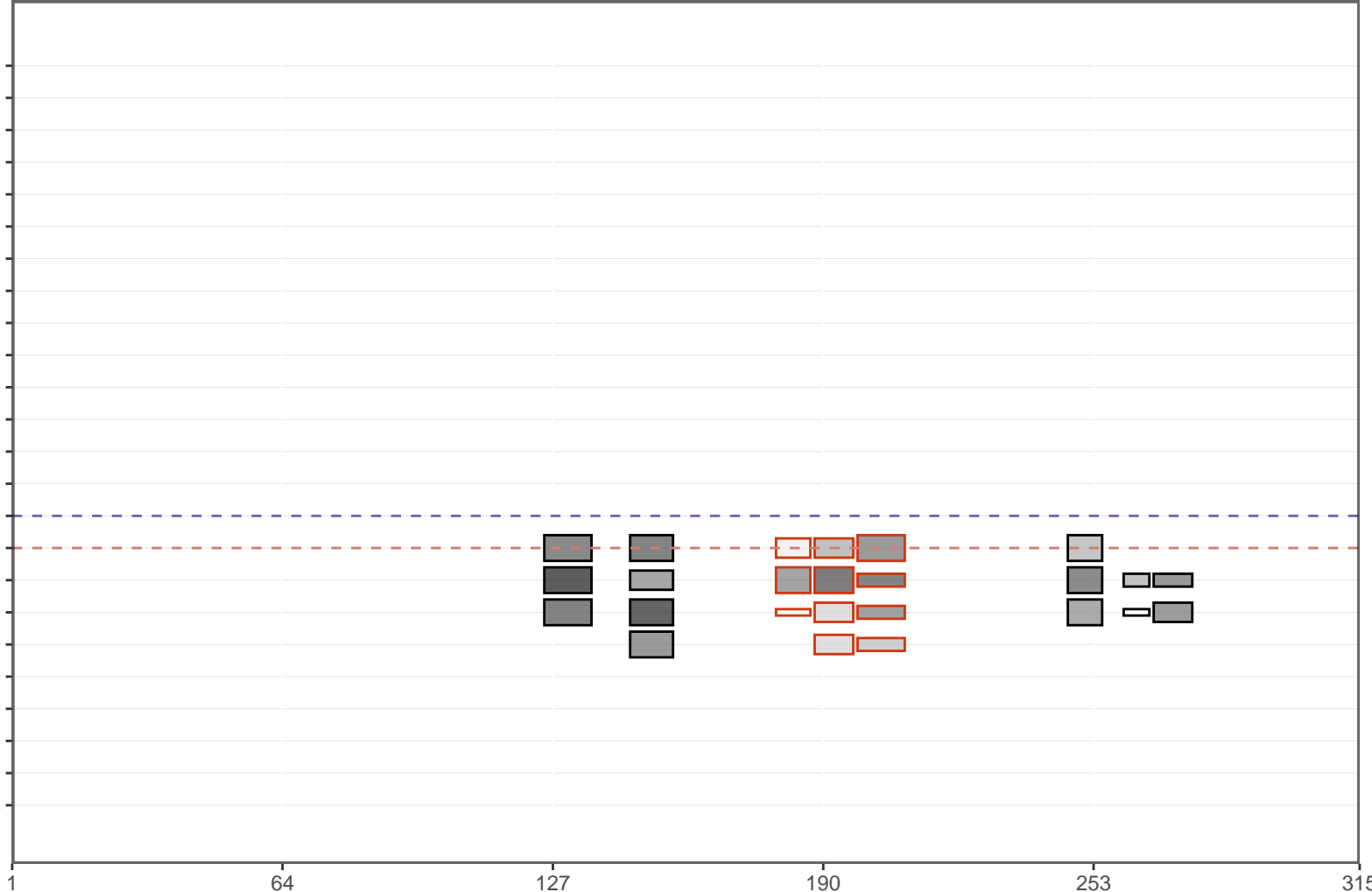
MW indication



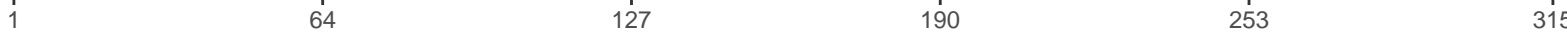
Molecular weight



Gel Slice



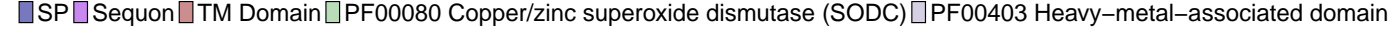
Protein length



Pfam domains



Pfam Description



Protein sequence:

KLITALELQTRKARLIGDGVPADEFLISAWEFKGPDIFGVVRLAGVNMELTRIEANFSLGSPGRHGWWSINEFGDLTRGAASTGRKLVSPPLDGLTLEVDVKGAEFYSGAKELRVLADLGRAMVYSTEDKSDPLKAAVARSAGVGENYKLLCTCDGTHIWEATNKL

NbL10g21650.1 subtilisin-like_protease_SBT1.2 [MW - SP = 77.03 kDa]

No. of times detected



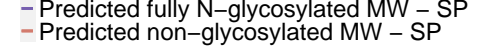
log(intensity)



Values from



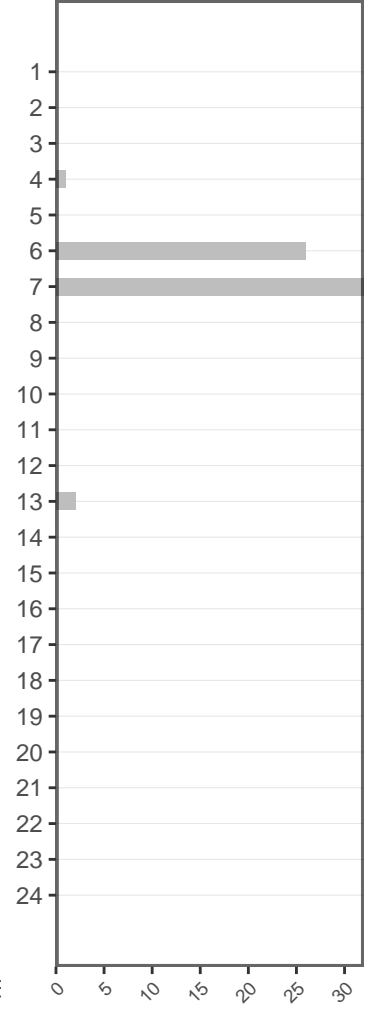
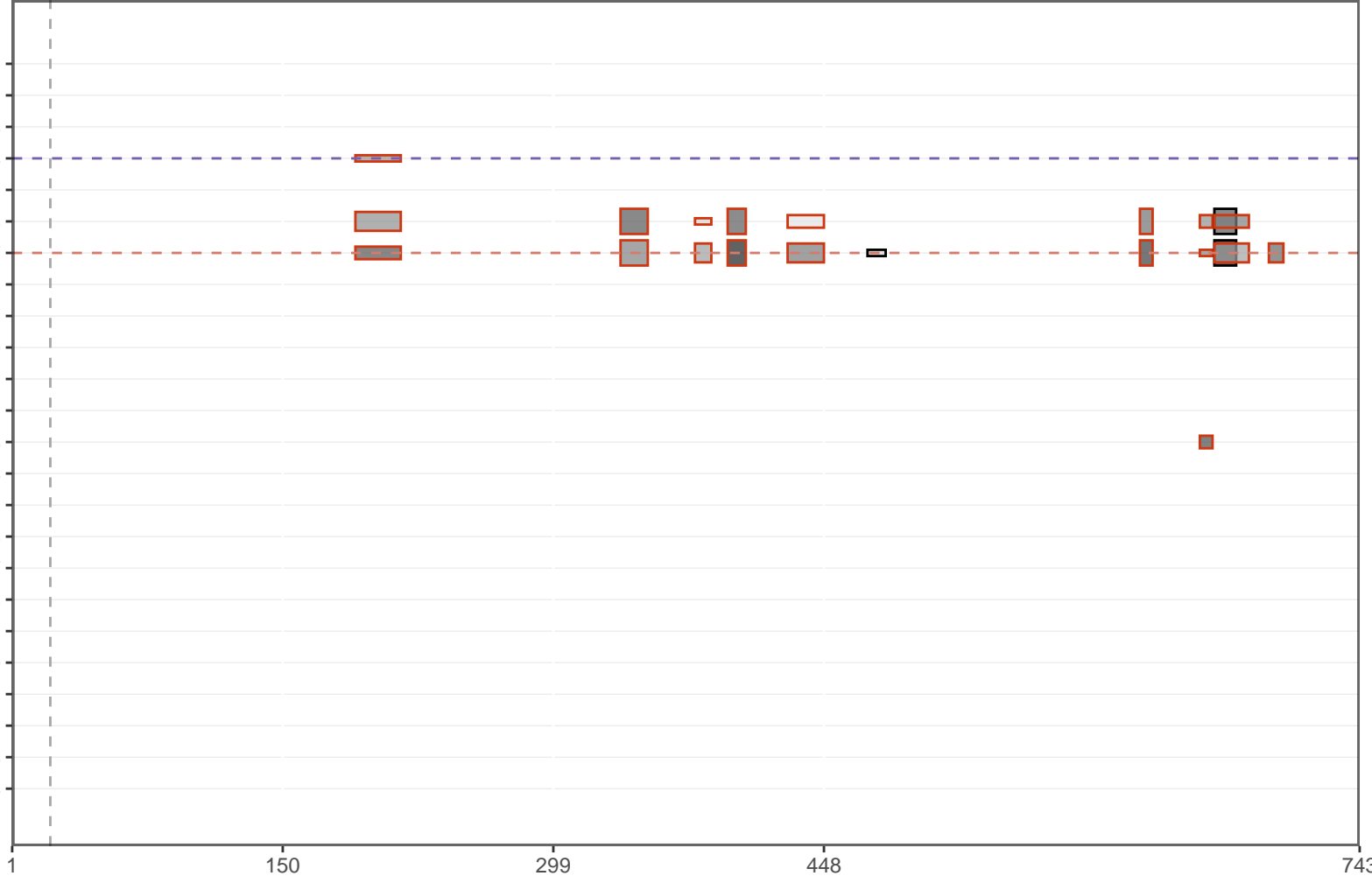
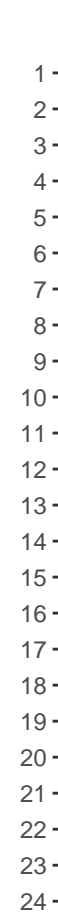
MW indication



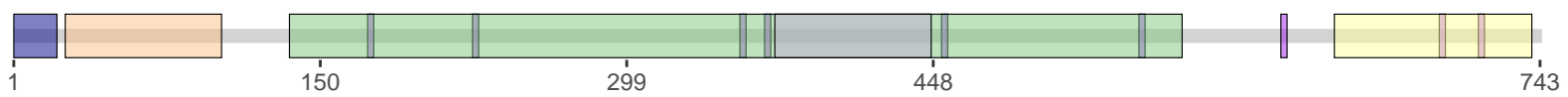
Molecular weight



Gel Slice

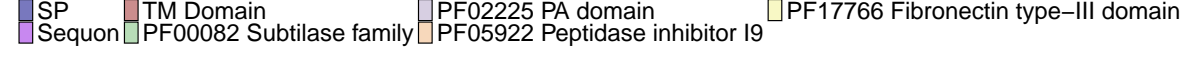


Protein length



Pfam domains

Pfam Description



Protein sequence:

FIALFDAGKASDQDAPFGREWAMTDPAKNGKIVLGGKDPSELTSGGGRNVKIDAGGVSMILNINPEFGVTKSATANVLPALVLSHEEGEKIKAVINSTNPAAMTFGGTVGDKNAPVAFSFGARPSRANPGLKPDHIGFQVNLAAWPTTIVNPKNNTNSGFINLGGTSMSCGHLTGIAALLKSAHPNWSGSAKSAAMTADTLNLANNPILDETLNPNIFATSAGHVNPSRANPDGLVYDTFPEDVLPVLLGGLNVTNREVGFLQRKVNGLGVKSIPEADLNYPSSFSIRLRSIT

NbL10g21630.1 coiled-coil_domain-containing_protein_18-like [MW = 76.04 kDa]

No. of times detected



log(intensity)



Values from



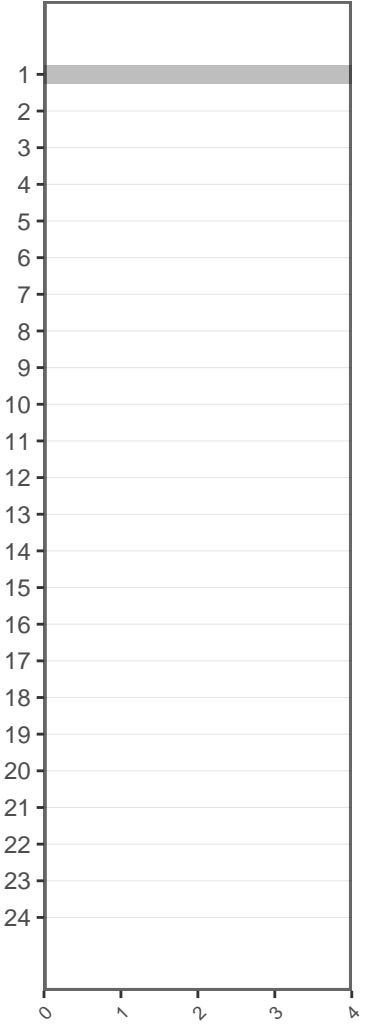
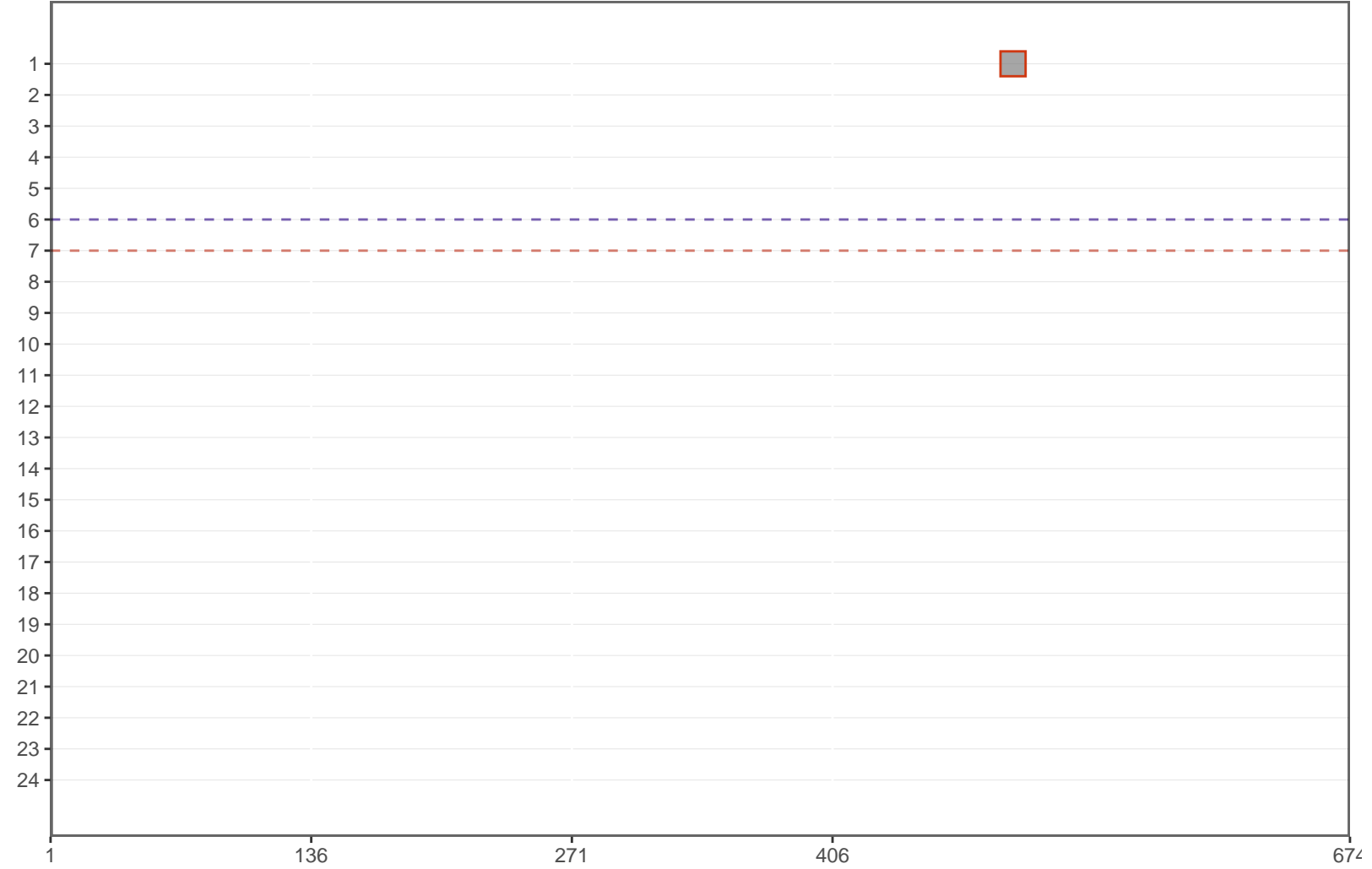
MW indication



Molecular weight



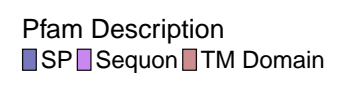
Gel Slice



Protein length



Pfam domains



Protein sequence:

MSDRIQKEEALKFRVTKTSEVGEIEKELATEVSALEKGRDEIEAGLKGVNSLAAANARLQNVREERDQFYEANDGVAHLKTRDELTKSIGSGKVEANLGTWNLFEDTWNLQSGSFTESKDKVEVLEKHEGVFVNLVQMLLSAYEKELRPSIDRISKFVENLKTLEGGAUVGGSVSKLSRPKSLEEEYLDYEAKITTFSEVDNMRQGFYGGQEKSRKDDPDMKQLFENIEKLRQEFESIERPALLEMEIPVQEGDDSSHETVDDNTGHPKQAVETAJAGESKQNEPP

NbL10g21580.1 glyoxylate/hydroxypyruvate_reductase_HPR3-like [MW = 37.76 kDa]

No. of times detected



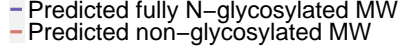
log(intensity)



Values from

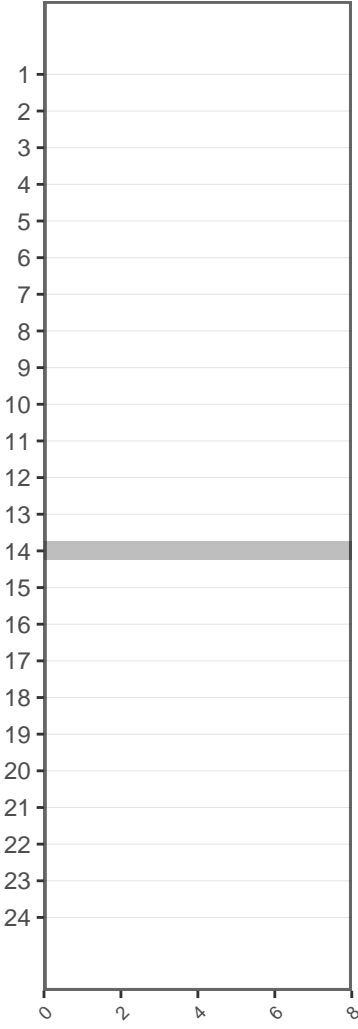
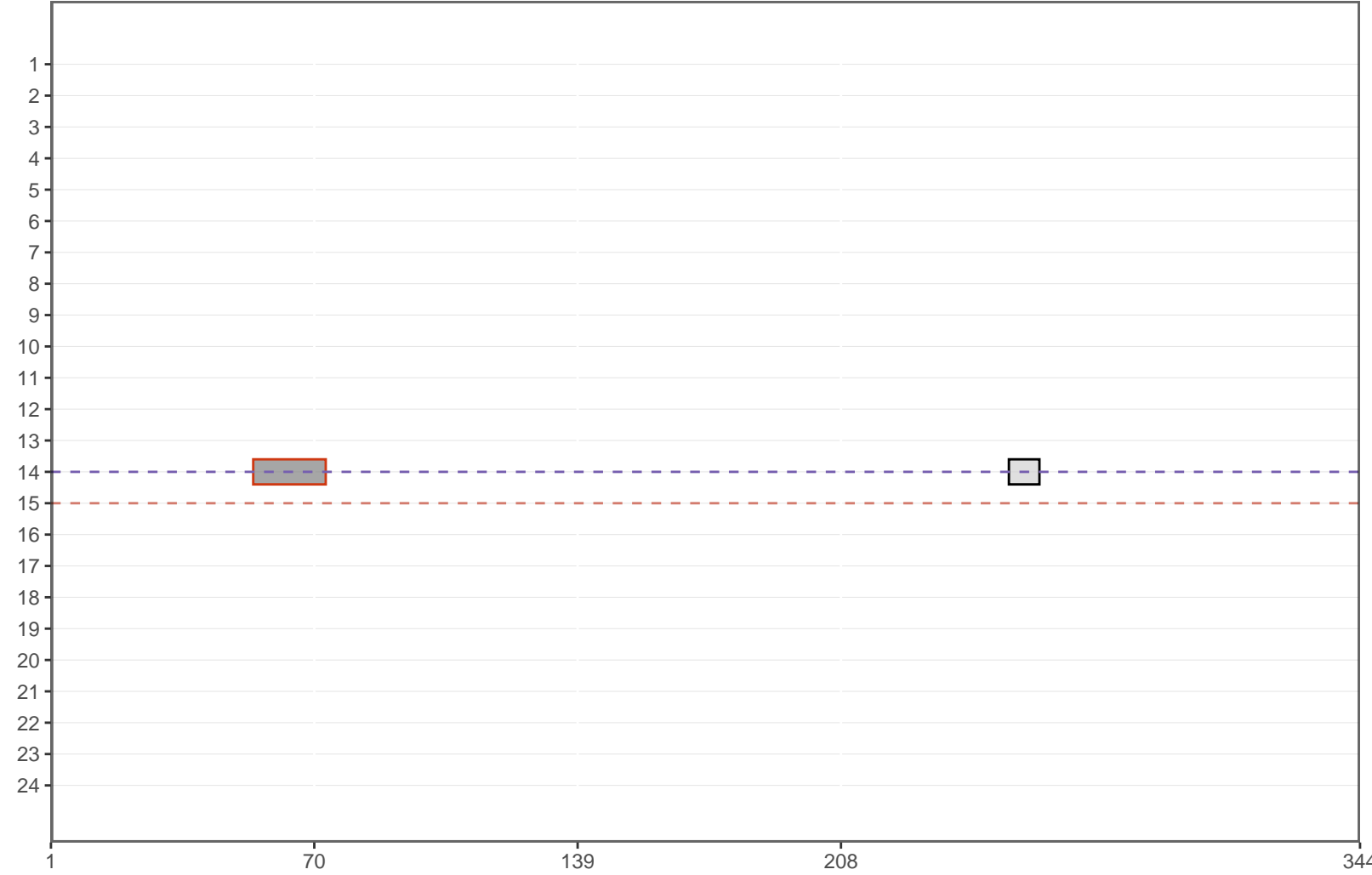


MW indication



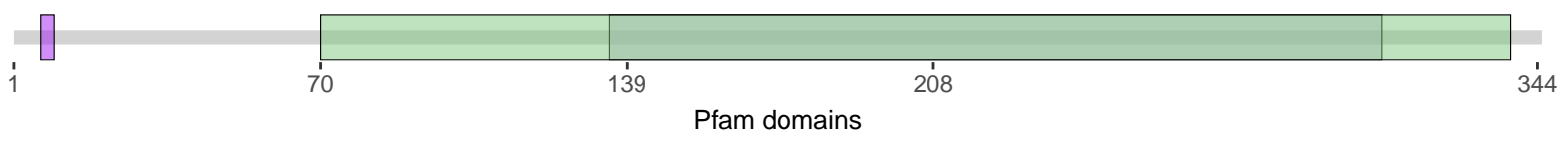
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF00389 D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain
- PF02826 D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain

Protein sequence:

VPIVIGELSPLYKIVGGKQGVIVLGGISGTRVGRLEAFGGISVATSRMRKPDVPPFPFHSNHIIDLATNDVILGGALTEETHHIDKEVLTALGKEGHNIVRGALVDEKEVLEFLKRGDGGAGLDVYENEPHVPPELFDLDNVALSPHLAVLTPESMEALEELFTYNLEAFFSNPLRAGIEYE

NbL10g21560.1 PGR5-like_protein_1A_chloroplastic [MW = 36.29 kDa]

No. of times detected



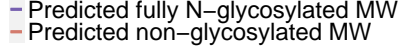
log(intensity)



Values from



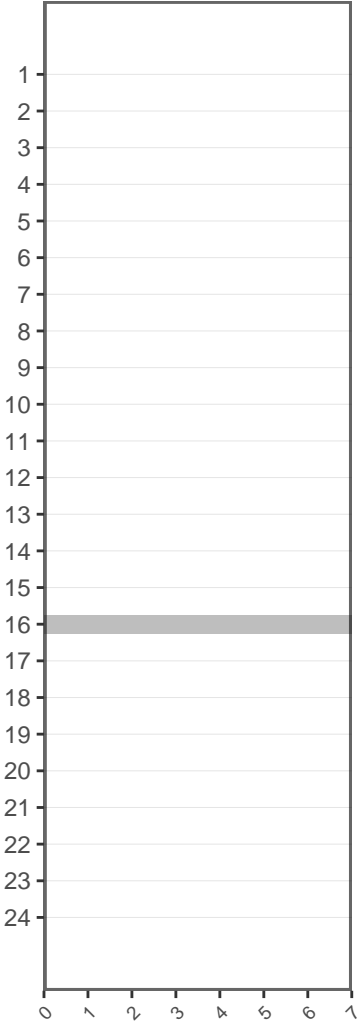
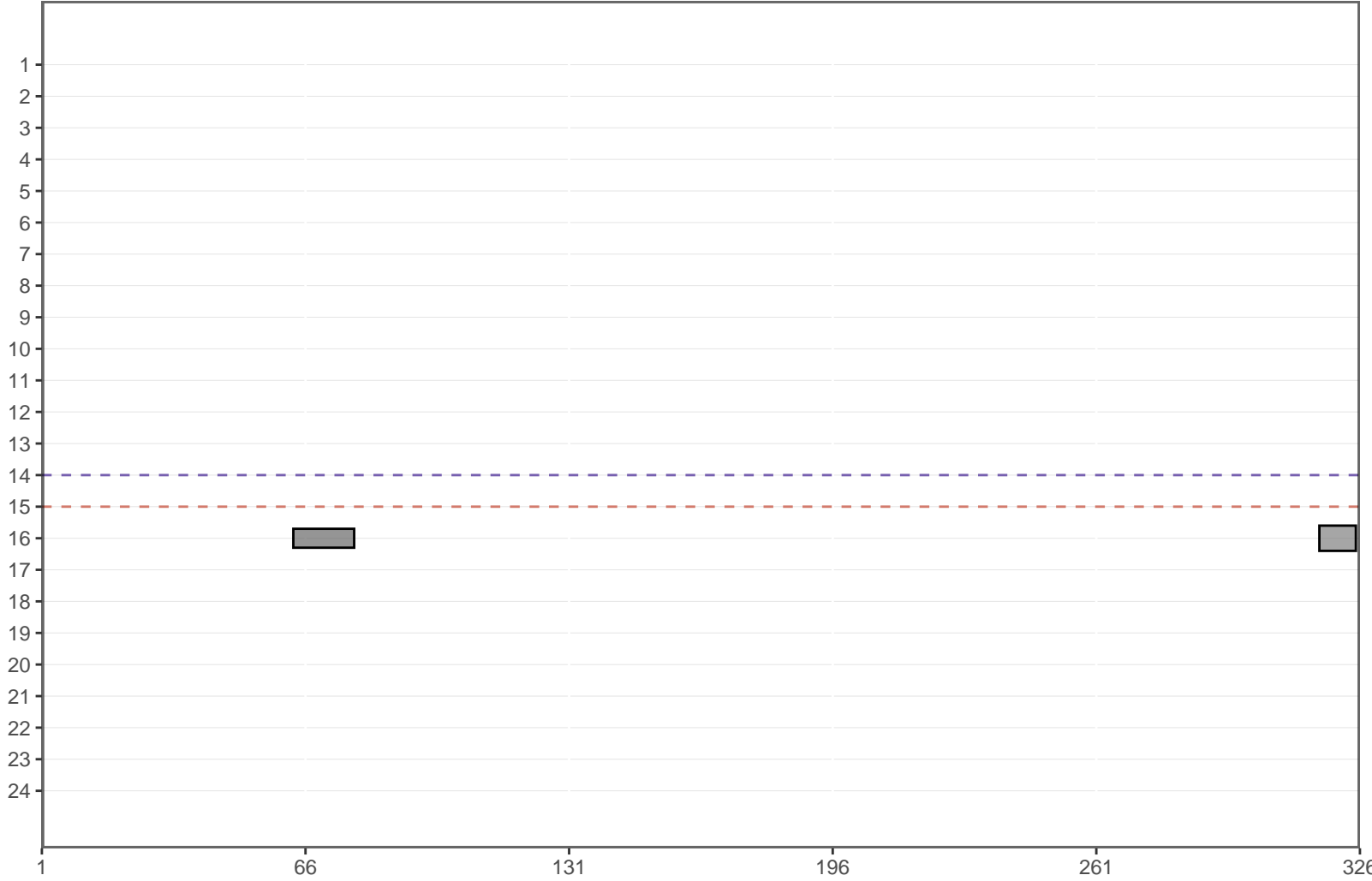
MW indication



Molecular weight



Gel Slice



Protein length

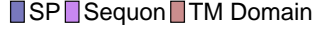


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ISMAYVSGNPIMTDKKFDKLLKLMKMGSDVVEGPRGELRRKRVYSDLVVYLRMFLNVPVAVLGLFFLDIDTGFETVYLLLEPEPFSRIFTFAALPFLWLSFTITNAIKDFLLKGPCCNGCTENTFFFGTILSVBGGGNTFNKVKGTNGCTDMVVDGTRLFLPEGSAV

NbL10g21450.1 hydroxymethylglutaryl-CoA_synthase-like [MW = 51.25 kDa]

No. of times detected



log(intensity)



Values from



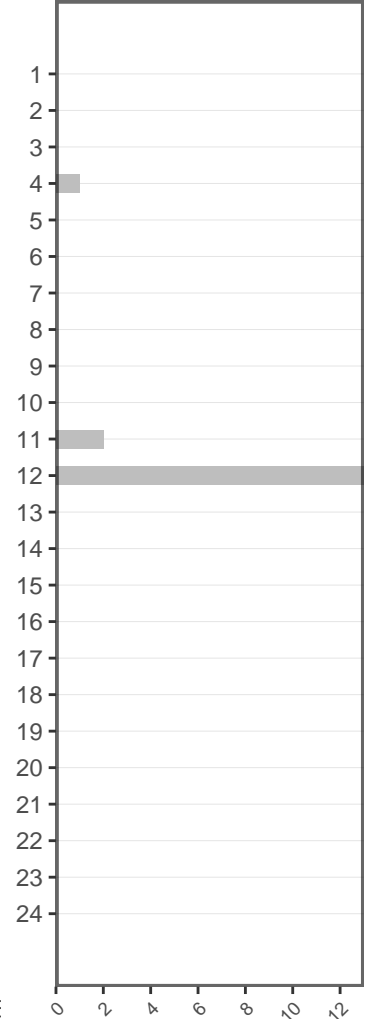
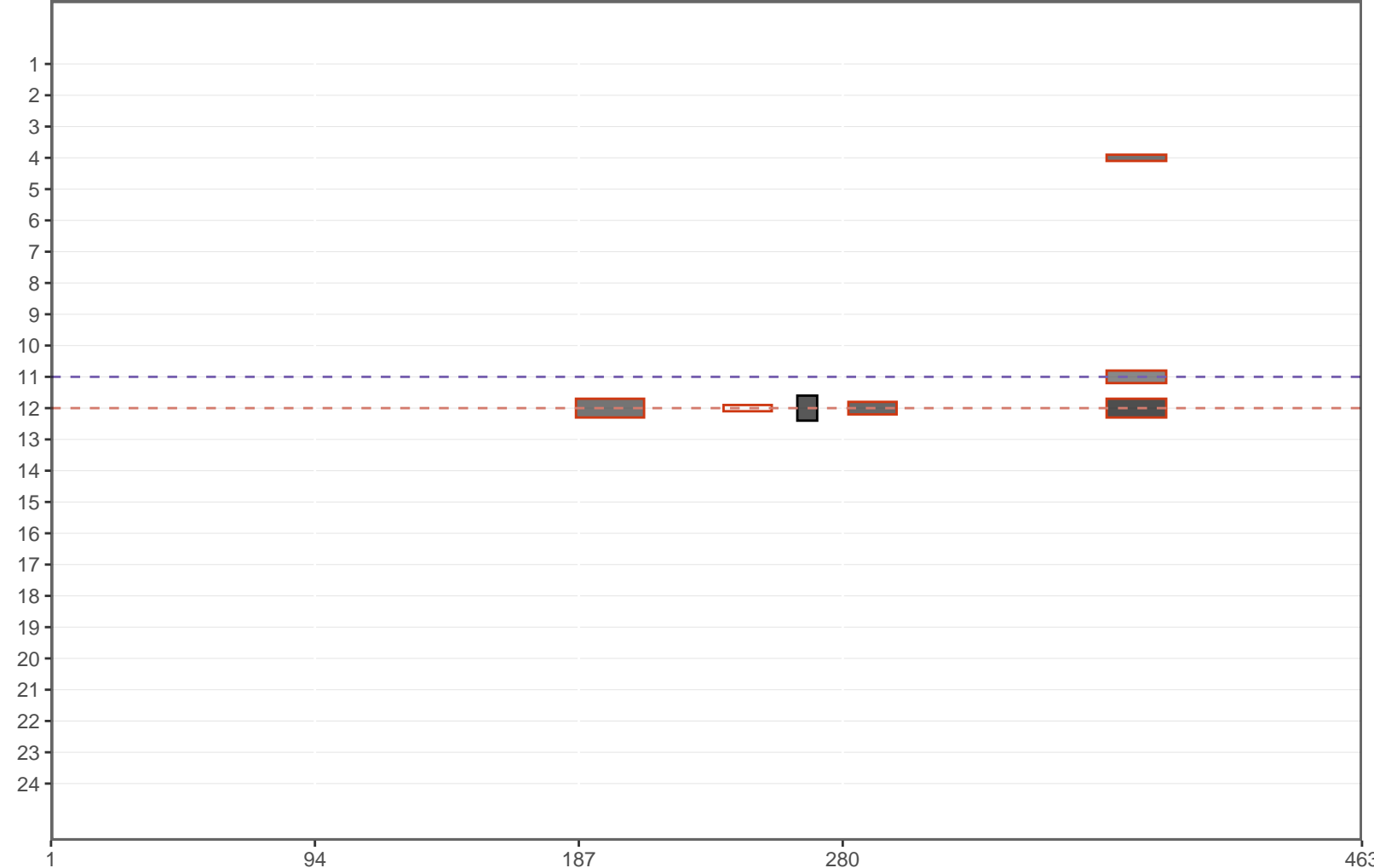
MW indication



Molecular weight

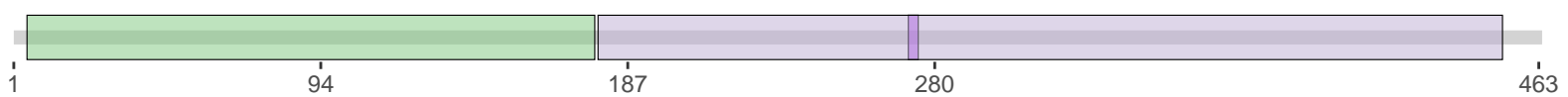


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF01154 Hydroxymethylglutaryl-coenzyme A synthase N terminal
- PF08540 Hydroxymethylglutaryl-coenzyme A synthase C terminal

Protein sequence:

ALDSCYKSLCNKYENLEGGFMSADAYVVFHSPYKIKVQKSGRLLFNDFLRNASSIDESTKQILAPFESLTDGDEYGRDLKASQGVAKPFYDEKVPPTLIPKQVGNMYTASLVAFAASLHKNKNTLAGORVIMFSGYSGGLTATMFLSKFNEGGHPFSLFNIAVMMVAEKLKSRHEFTPEKFEIMKLMHRHYGAKDFVTSKDGSLAPGTYLLEVDISKYRRFYAKAPEHGLNGH

NbL10g21430.1 protein_HOTHEAD [MW – SP = 60.11 kDa]

No. of times detected



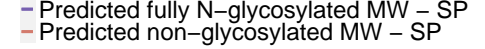
log(intensity)



Values from



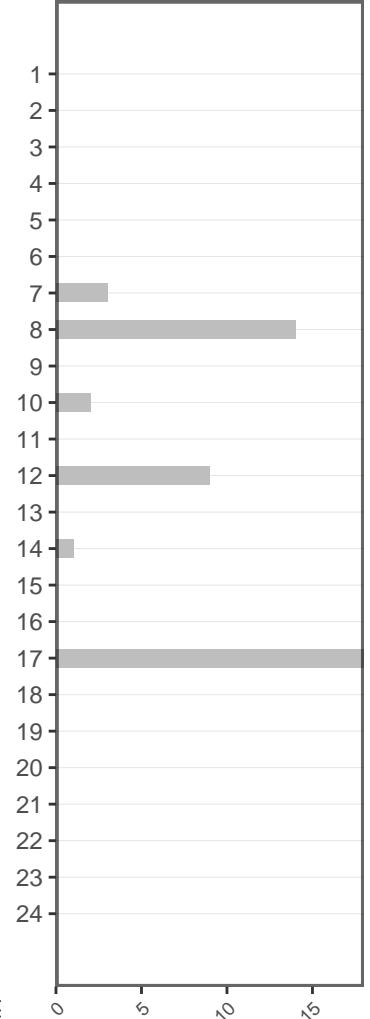
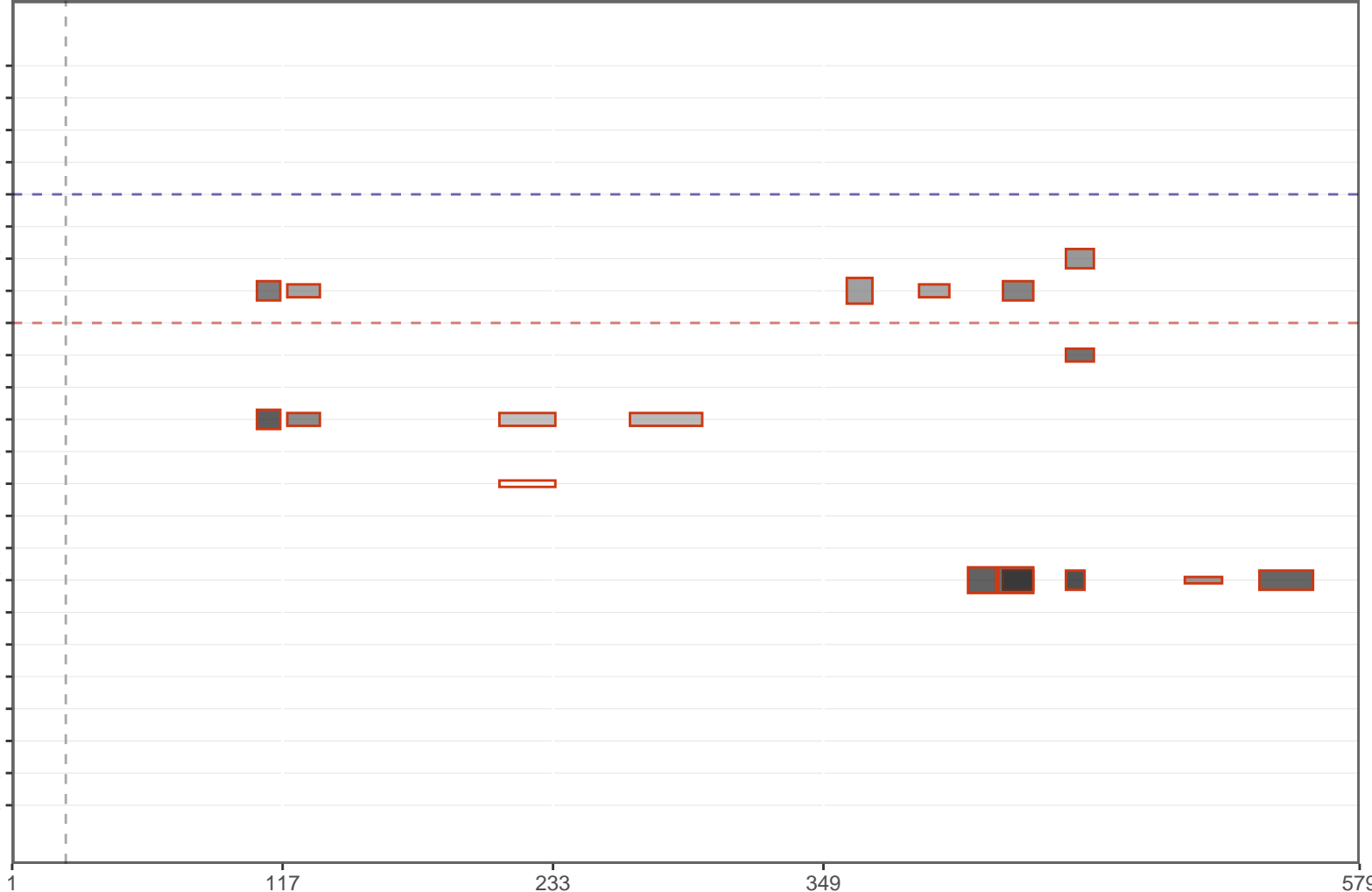
MW indication



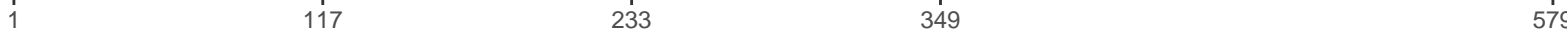
Molecular weight



Gel Slice



Protein length

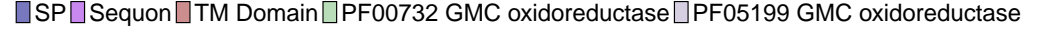


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

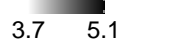
IGALGSPQMLMLSGVGPBAQLKHNHTVLDGPNVGGGMDNPMNAIFVSPRPVPEVSLQVIVGTHFGSYHEAASGENFAGRETQSDYGMFSFKDGLSTVPPKQRTPEALEKAINAMSELDDAAFRGDFIEKMGPNSTGHLELRTRSPNDPNSVTFNFKQGEDLQRCVNGLKVNIENESKFSKFRYDKGISRALLNFTASAPVNLPRHNDVSVLSLEQFGKDTMTIWHYHGGGQGVSRVVDGQVYKGIKLRVIDGSTFTYSPGTPQATVAMLGRYMOVRLNERL

NbL10g21380.1 NADH_dehydrogenase_[ubiquinone]_1_alpha_subcomplex_subunit_8-B-like [MW = 12 kDa]

No. of times detected



log(intensity)



Values from



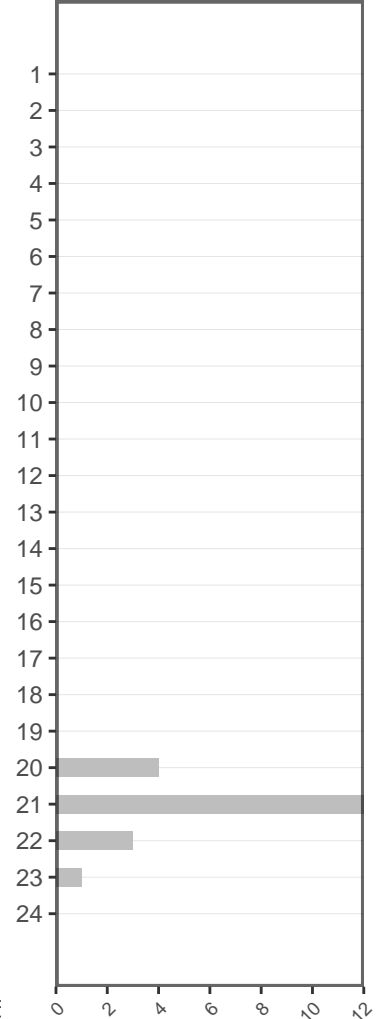
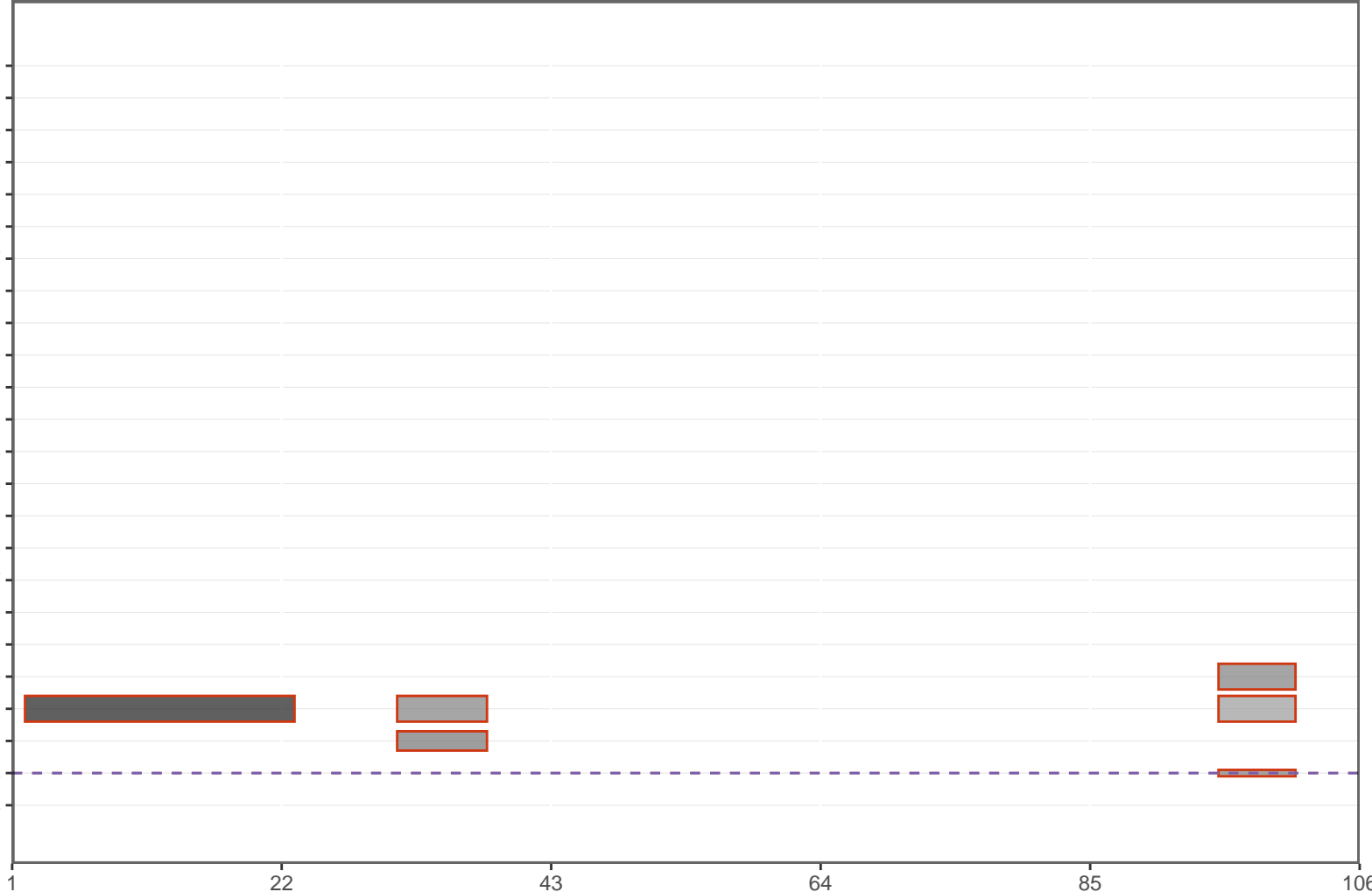
MW indication



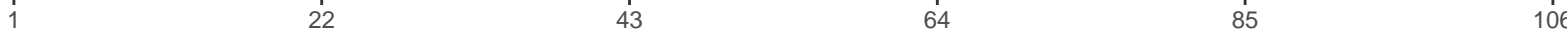
Molecular weight



Gel Slice



Protein length

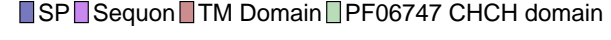


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

DDPNPEKCLIKGGQVTRDVLGLKLDLHGRNKNEMDVAAGGMVYNTNEFEMGRKEGGFEKAGPY*

NbL10g21360.1 uncharacterized_LOC109212508 [MW = 39.74 kDa]

No. of times detected



log(intensity)



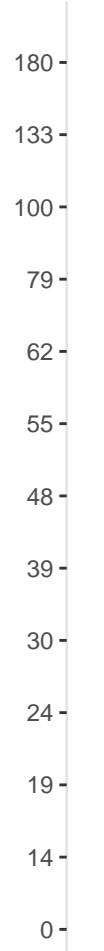
Values from



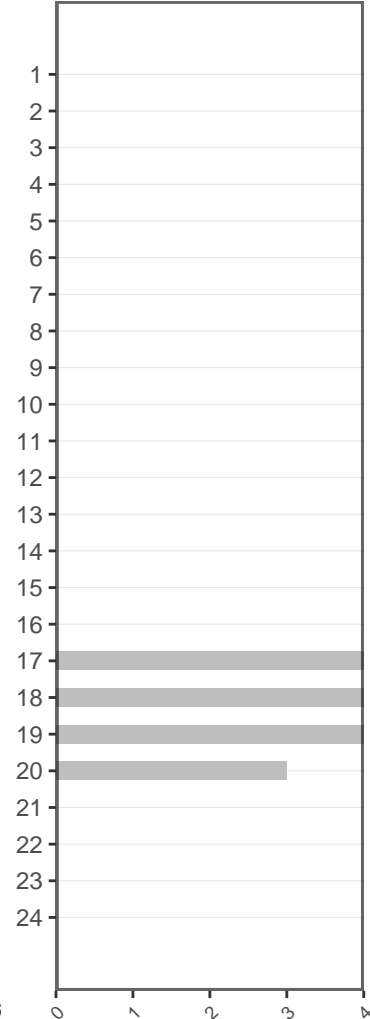
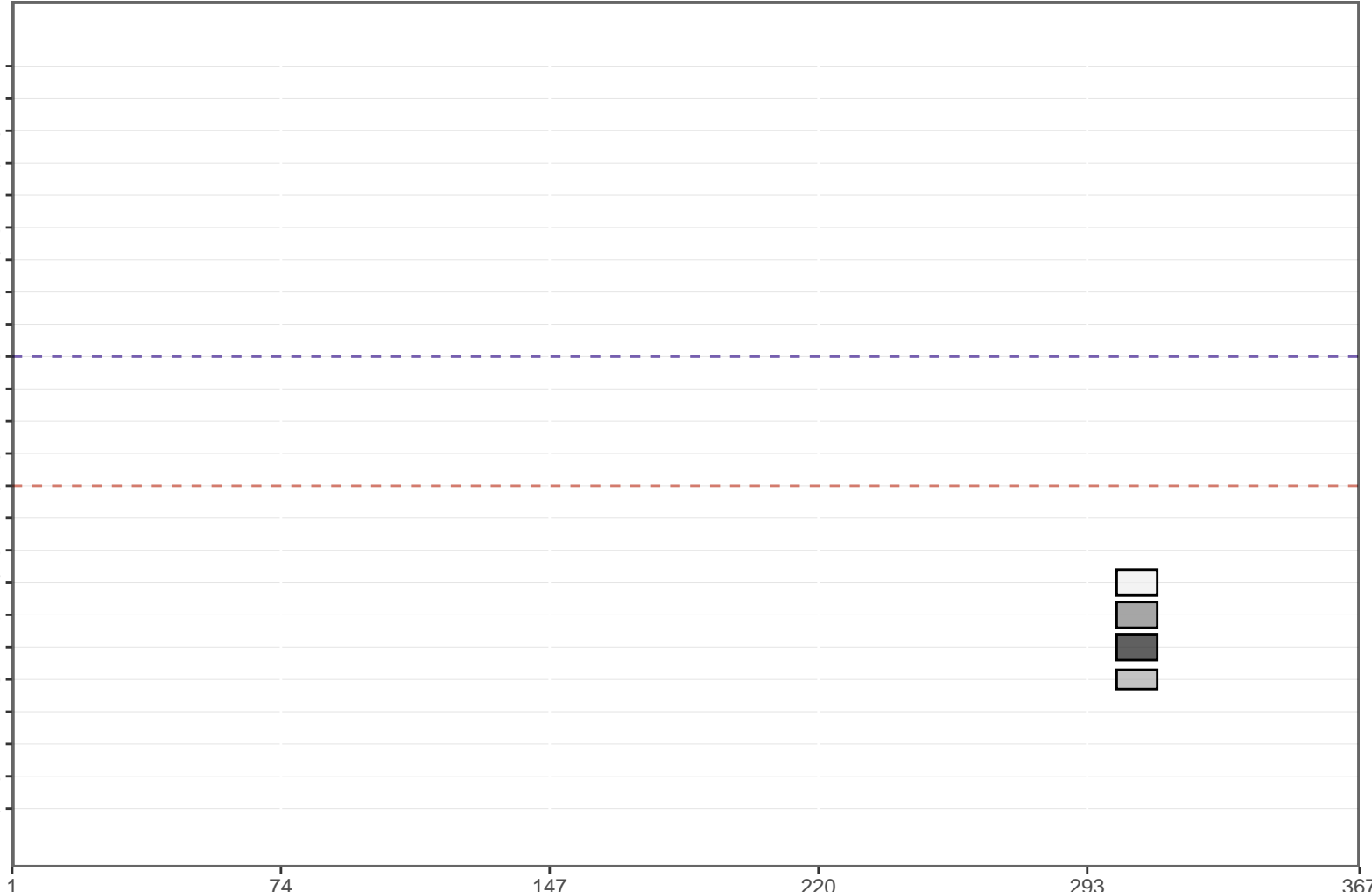
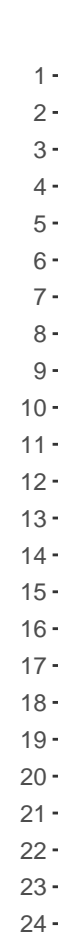
MW indication



Molecular weight



Gel Slice

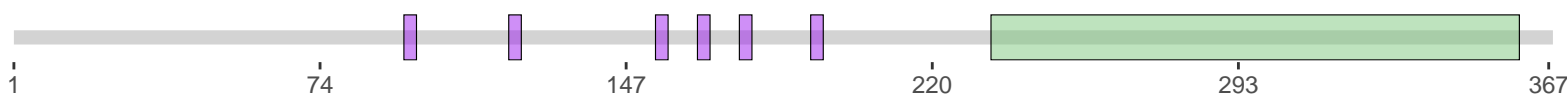


Protein length

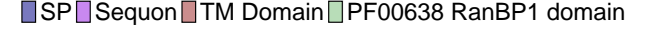


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

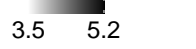
IFVGLANSSSFGLAIWSSGGLFNKSPFGLGSSVGTGSSVPVKYKSDAANDVQDTEDEVEQSPSPVWKTTEKGVTLHEVKGLVYKSTDPADKDAWKDRGTGQLSKKQEGVSKGTRESAPPTVMRNDVKGKLLNALLYPGIKTNMGNKNSVAIFHTSGDDDKDDAVARTFLIRTKTGEGRDLAAIQEYAPAA*

NbL10g21250.1 plant_UBX_domain-containing_protein_8-like [MW = 66.93 kDa]

No. of times detected



log(intensity)



Values from



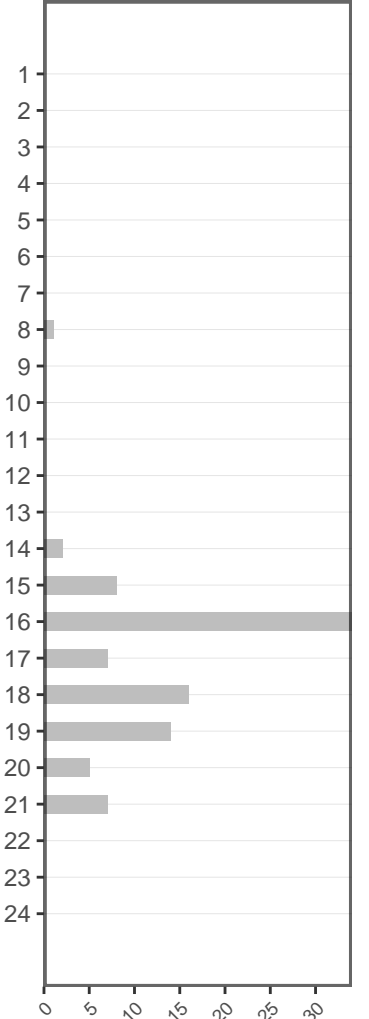
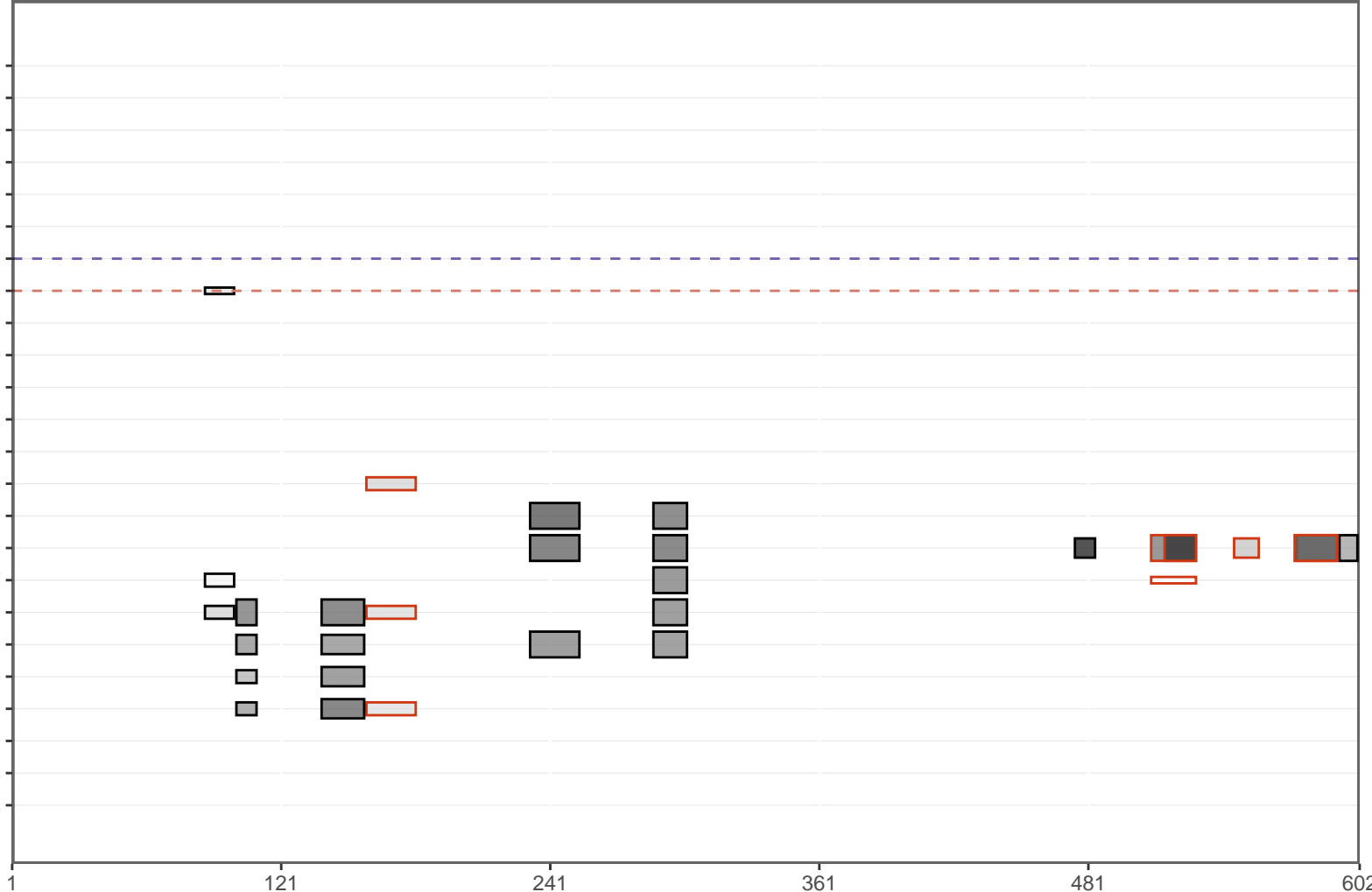
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EGYKPAEEDERDKGKFTSNGRDFRSEVGSFVPEAEDELLEERLWRRRKPKPISGSETAGDIEHVVYFLSSPRQHDNLNHSFRNGADFPDSEWGGISLSEHDEAVMLEAALFGGPFEGSGYRLFNPHQLMNGVEGPMSPYQWIRMPRRPSPSLWQRLRREGQDDHYHAALGADREKELKAKEEAALEEKQDEEESRRKAEKEEKEMERQLAAKESLPREPTTQENAVNLVWRMPDSSRRGRFLKSDRLGVLFQVHVGRAWKPGFYRLRYPYPRAFSI

NbL10g21180.1 protein_farnesyltransferase/geranylgeranyltransferase_type-1_subunit_alpha [MW = 40.27 kDa]

No. of times detected



log(intensity)



Values from



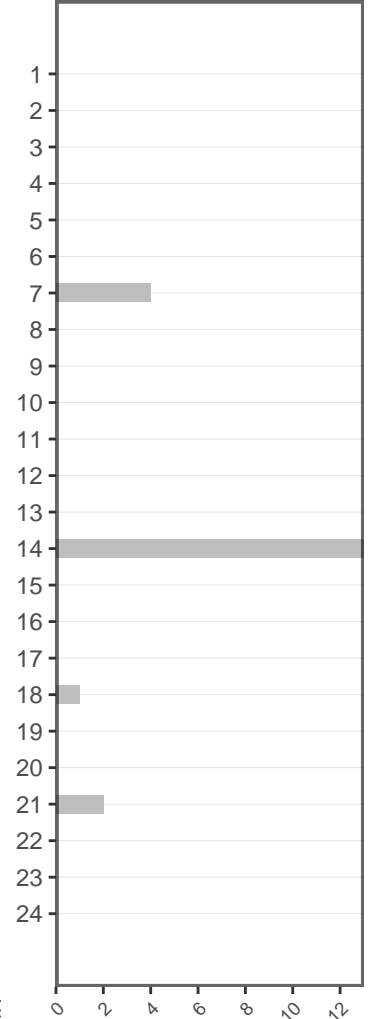
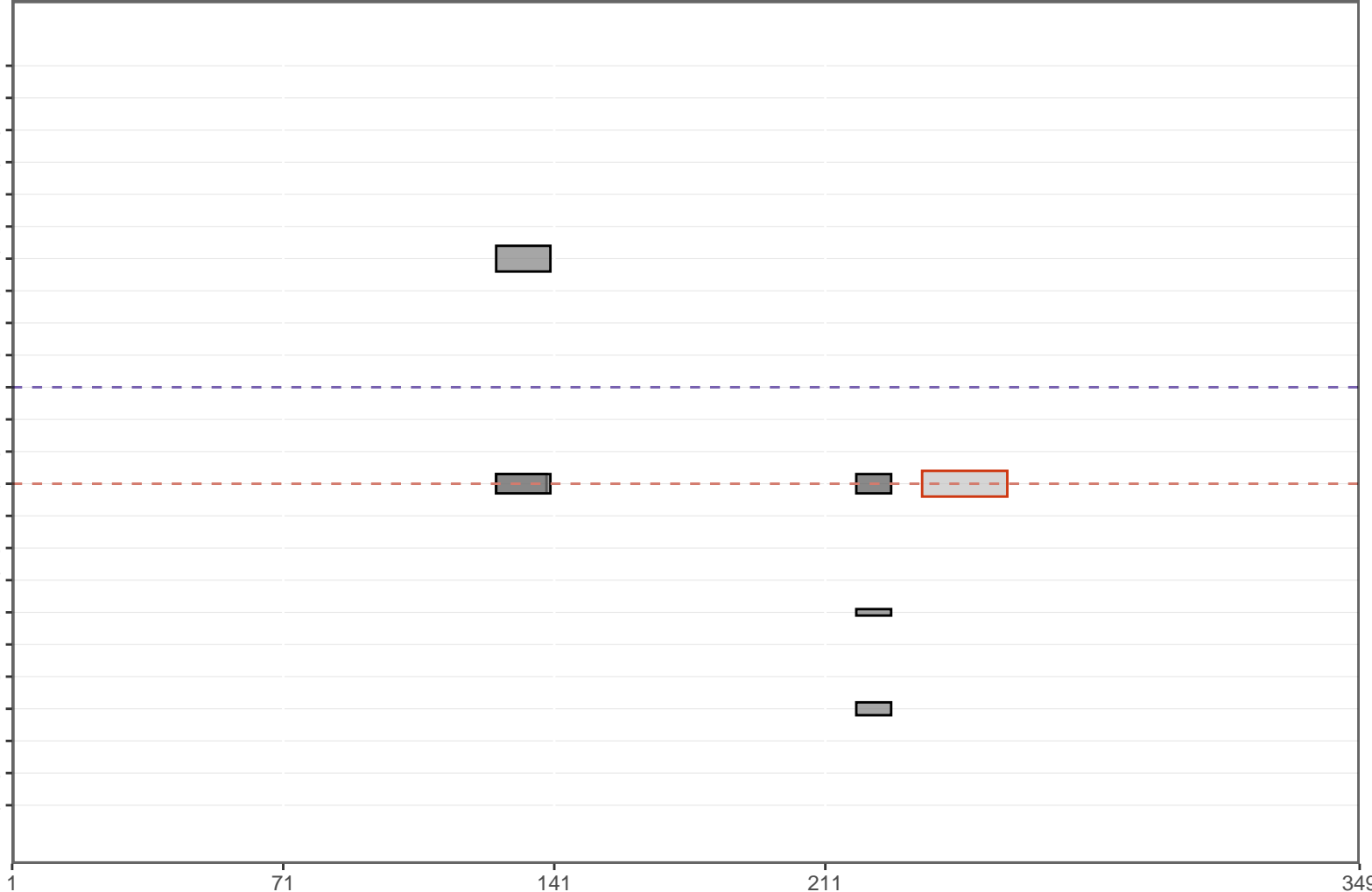
MW indication



Molecular weight



Gel Slice

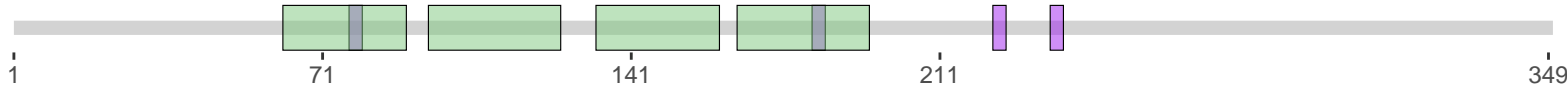


Protein length

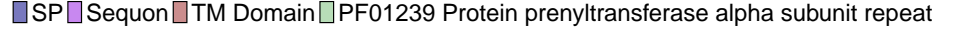


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LGQVENEIAYCOGLLEDDHYNSAWNGRIFVYTRRPLLGGLVAMRELEVSYTVQALRASPEWSPWRYLRGLYKNDTQSLGEDPQVAVLLELVTSKNNHVAHLSLLDLLCHGFPESEELKSAVDVITPESGSMDLPLAKRIGSILEHADPMRINYYWNRKSTLVQSAKQGNTRDLADLSMDQNL*

NbL10g21080.1 bifunctional_UDP-glucose_4-epimerase_and_UDP-xylose_4-epimerase_1 [MW = 48.11 kDa]

No. of times detected



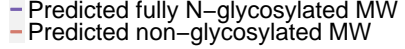
log(intensity)



Values from



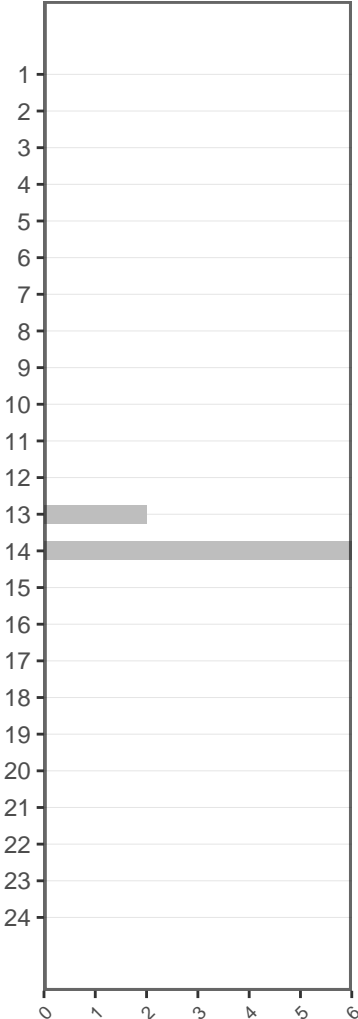
MW indication



Molecular weight



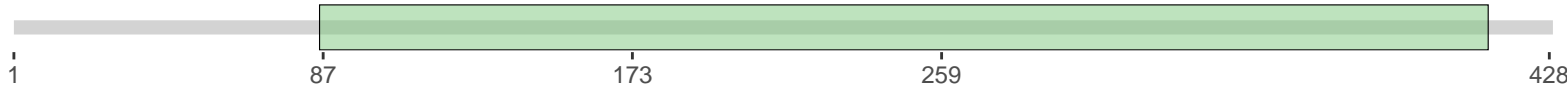
Gel Slice



Peptide counts over 4 repeats

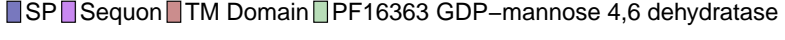


Protein length



Pfam domains

Pfam Description



Protein sequence:

LVFSSSATYGGOPENIPGVDFELKAMNPFVGRTKLFLEEIARDKQKADAEWNILLRYFNPVGAHESGKLGEDPRGIPNLMPIYGGVAVGRLELNFYGTDPYPTDGTARDYHVMDLADGHVVALGRLLKGNLGGVAVNLGTGKGVLEMAFAFEKASGKKIPLKMPRRPGDATAVYASTEKAKEKELGLKAKYVIGDEMGRDQWVWASGNPVGVDENP

NbL10g21060.1 riboflavin_biosynthesis_protein_PYRR_chloroplastic [MW = 66.11 kDa]

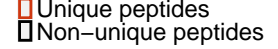
No. of times detected



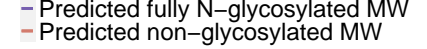
log(intensity)



Values from



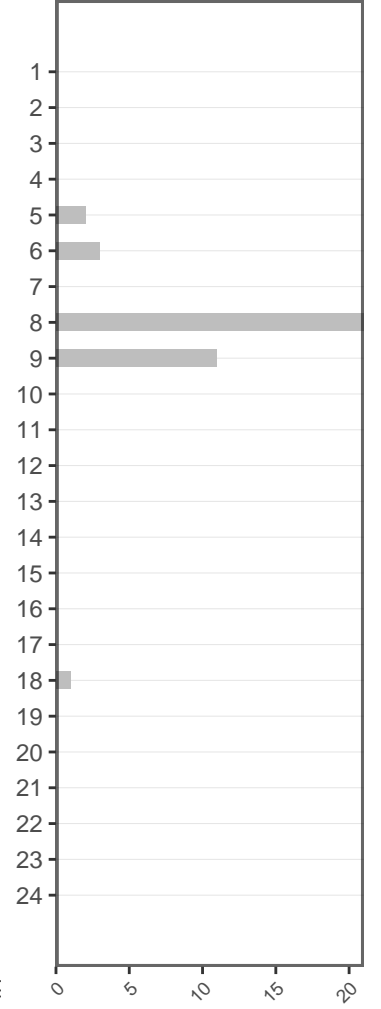
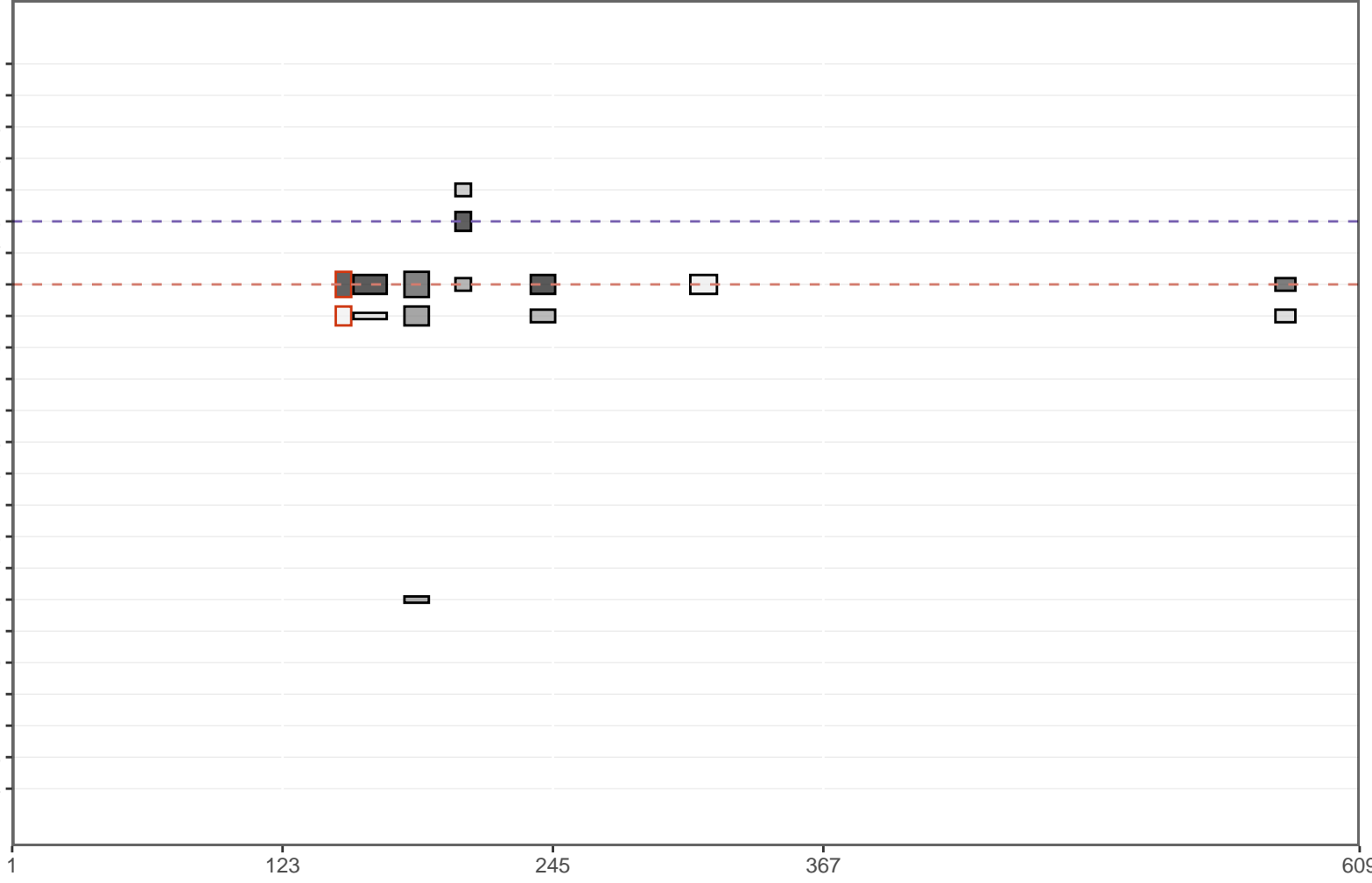
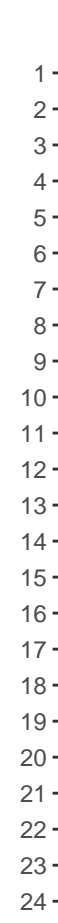
MW indication



Molecular weight

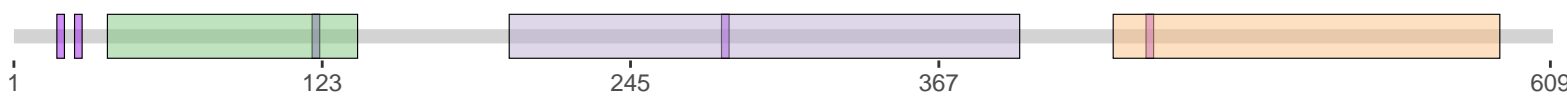


Gel Slice



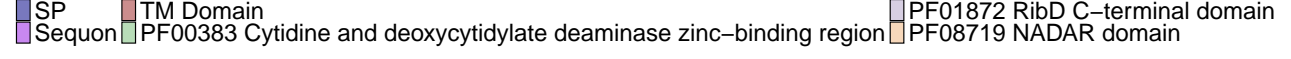
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

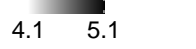
RGARRSFORLLASGVEVEFDLDRDVMGVLDYDRGVLGILVEGGGTLAASASGSHKVFAPKIKGKNAPSPVGEIGMIVEMTQALELIDVYCEIQGIDPLVSGFLGPVFDLTPPTPVEETSADIDTISPFESBIFFYKTKWDPYGGFSNFSLHPFQMPNENGEELVTVSSVEHYGAKQKFGASDLVAKGCVIEIGCAKSPFEAARIGRRRQRGGPNLVRPDVSESVKVDAMFYKAKGKFTFYPLKGLLSTAGBVLVEGSPHDLFWGGGRDGEGLNYLGRLLMKLR

NbL10g21040.1 osmotin [MW – SP = 24.21 kDa]

No. of times detected



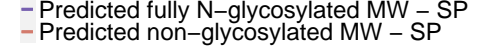
log(intensity)



Values from



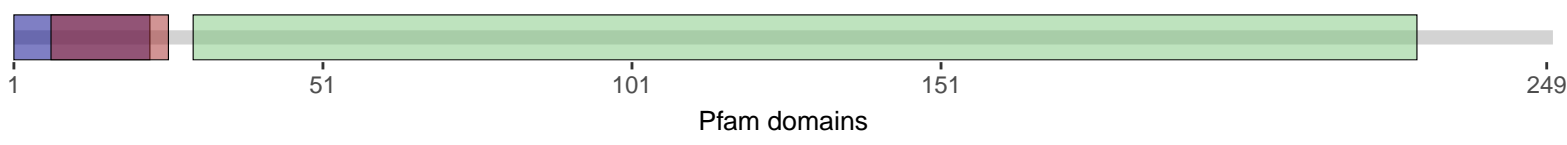
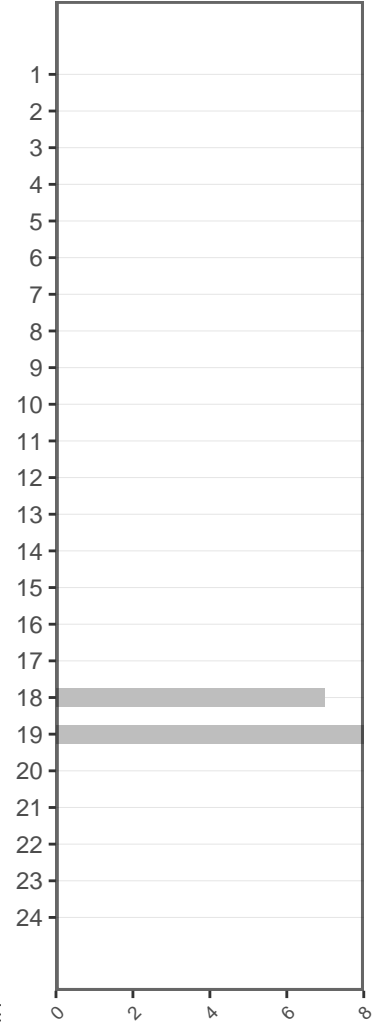
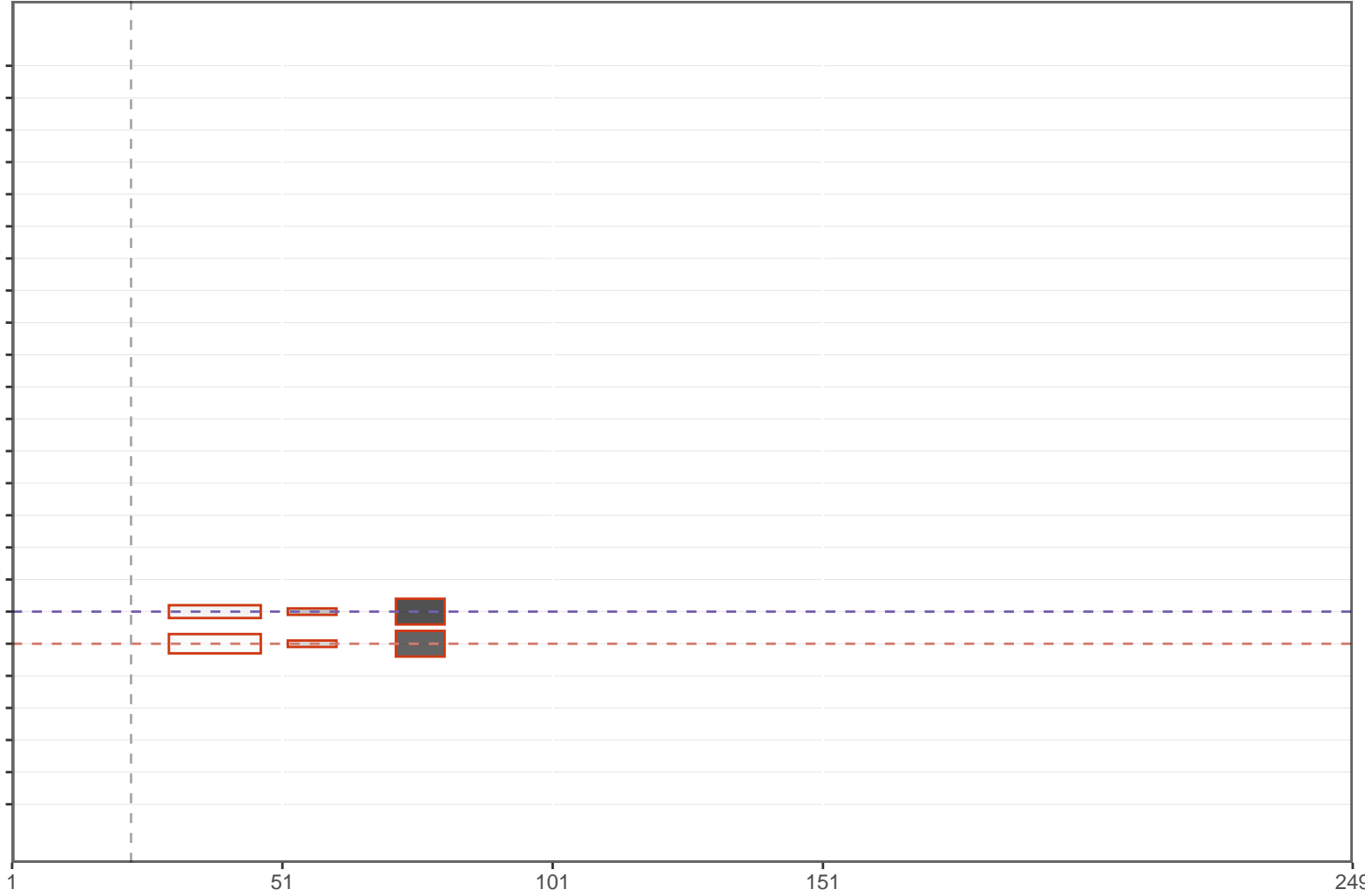
MW indication



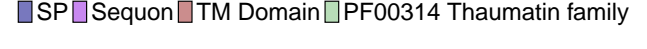
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

QFSGLDVWDSLVDFGNMFTFAPTNPGGKGAHHCNTANINGEPRRLRVPGGNNPCTTFGGGGYCGTQGPCGPTSFSEKFFKGRPDAYSYPQDDPTSTFTCPGGSTNVRVIFGPNGGGHPNFLEMPGSDVAK

NbL10g21030.1 osmotin-like_protein [MW - SP = 25.21 kDa]

No. of times detected



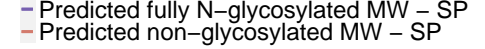
log(intensity)



Values from



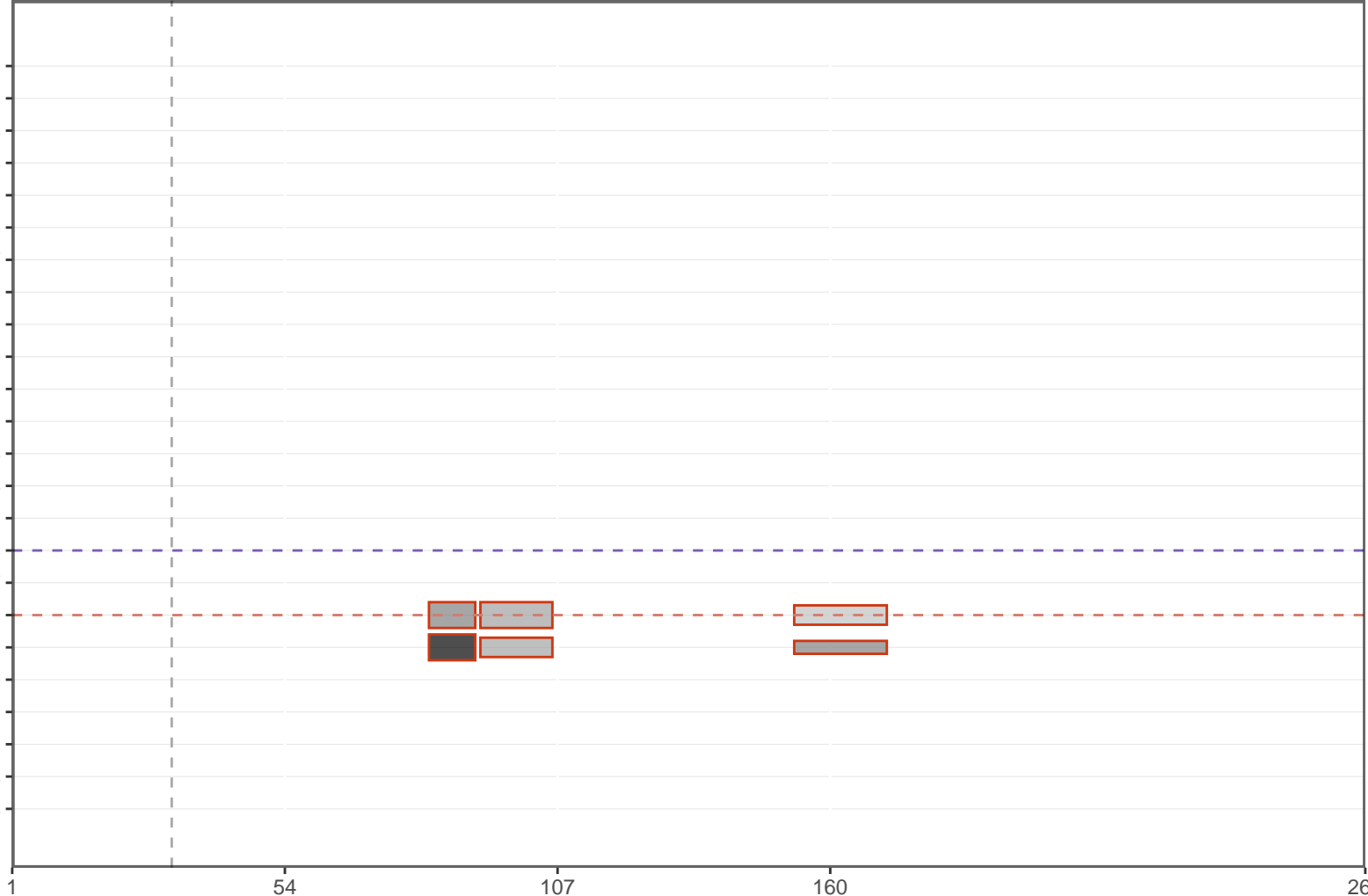
MW indication



Molecular weight

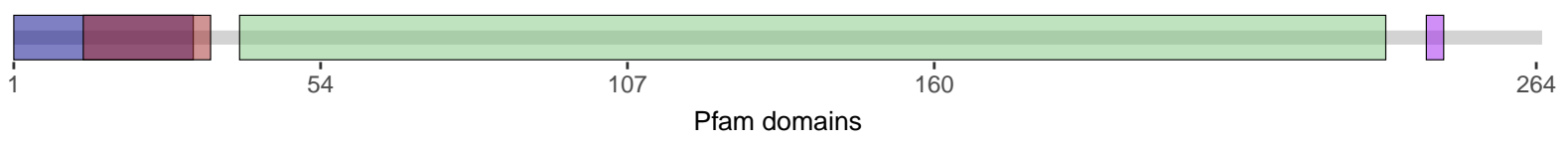


Gel Slice

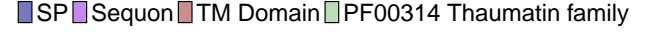


Protein length

Peptide counts over 4 repeats



Pfam Description



Protein sequence:

ALNQGSLNLDVDSVDFGNPMSFGFKPKPGKGHGIGGTANINGEGPGALRVPGGGNPCTTFGGGGYGGTGGPGPTELSRWFKGRCPDAYVYQDDPTSTFTTGTGWTTRKVMFGPGYGSANHNNTTFNPLEMPGSEHVAK

NbL10g20870.1 probable_phosphopantothenoylcysteine_decarboxylase [MW = 23.16 kDa]

No. of times detected



log(intensity)



Values from



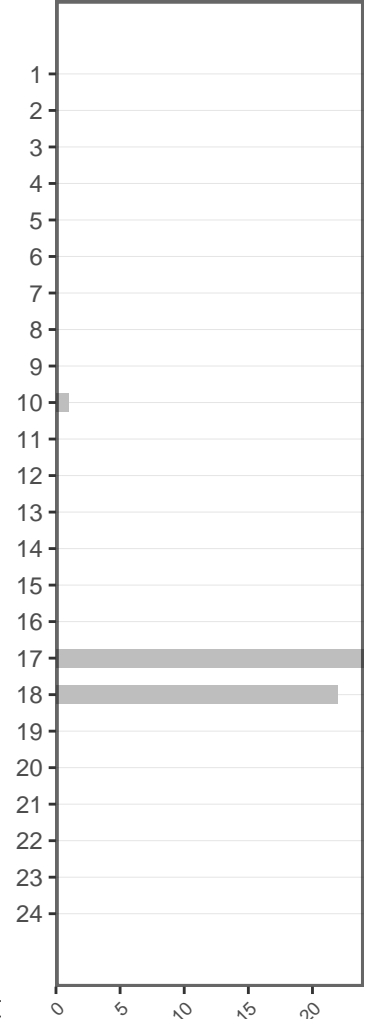
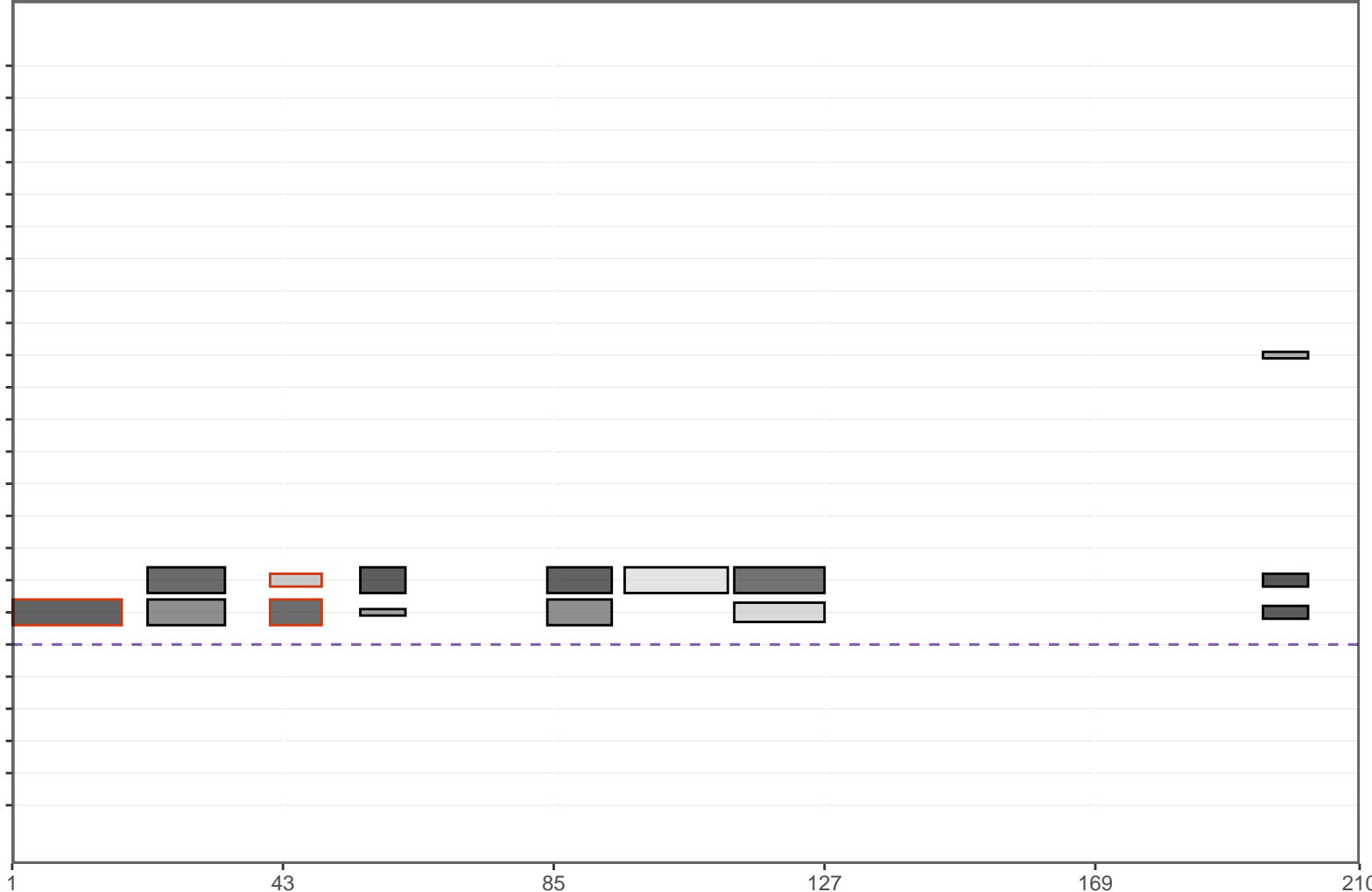
MW indication



Molecular weight

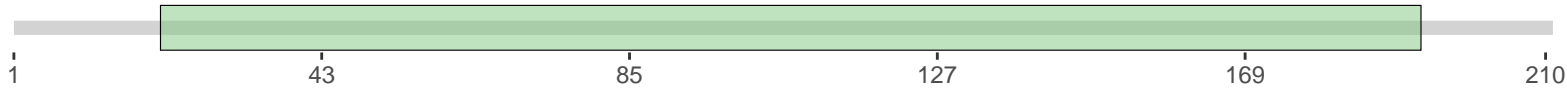


Gel Slice



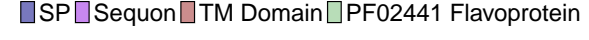
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

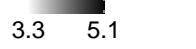
ELRRWADMIAPLSANTLKGKAGGLGDLNLTGIRAWDYKPLFWAPMNTLMWNNPFTEKHLMVIDELGSLIPPVKRLACGGYGGGAMAEPSLYGAVRIYYDQLREGGNNVA

NbL10g20860.1 glutathione_S-transferase_T1-like [MW = 28.62 kDa]

No. of times detected



log(intensity)



Values from



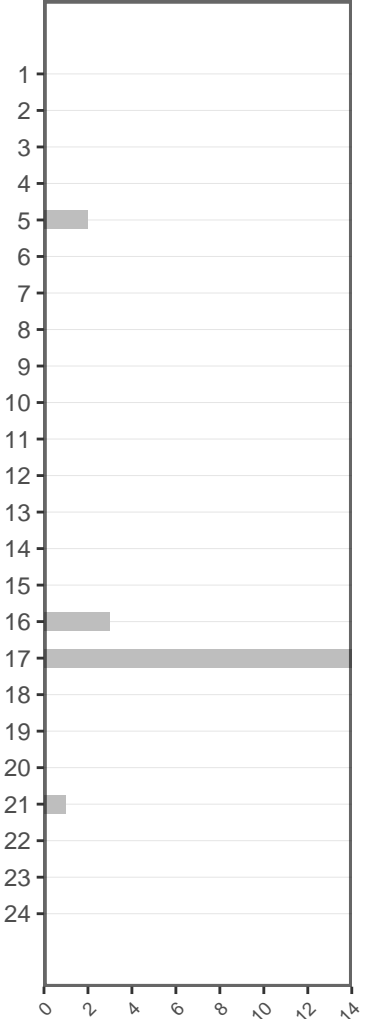
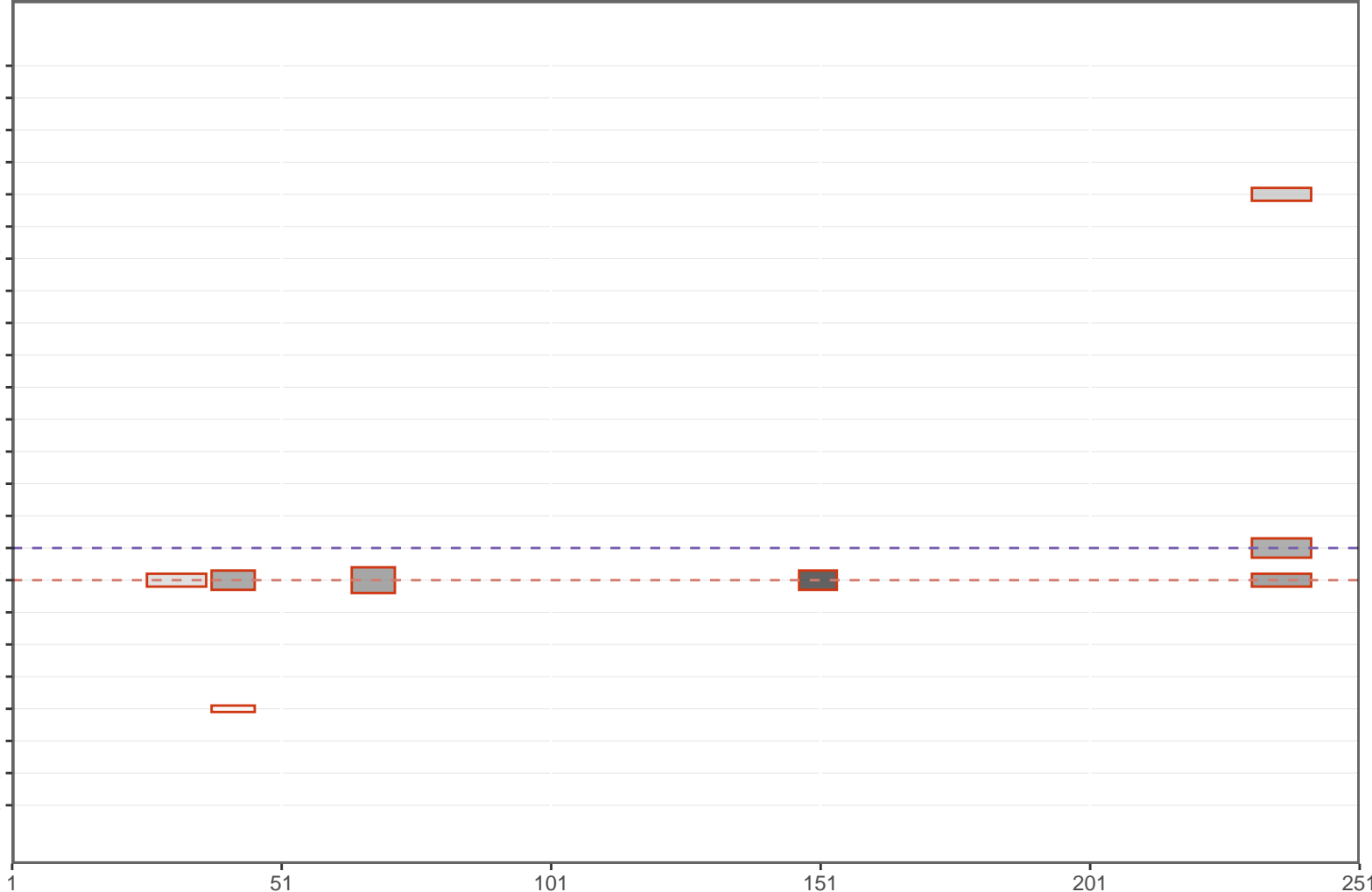
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

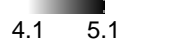
VYYFSTYLAAPFGLPLNGDAAAEAERVLLASLAKIESVWLQKGRFLGSGGQPSIADLSLVCEIMQLEVLDEKDRKRIGPYKRVLKWIDDTKNAMEPHFGEVHLIFKAKENFKQRDAVGSSSIPGSRKLDLHDKM

NbL10g20720.1 glutamate--cysteine_ligase_chloroplastic [MW = 58.93 kDa]

No. of times detected



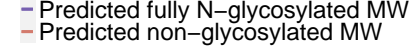
log(intensity)



Values from



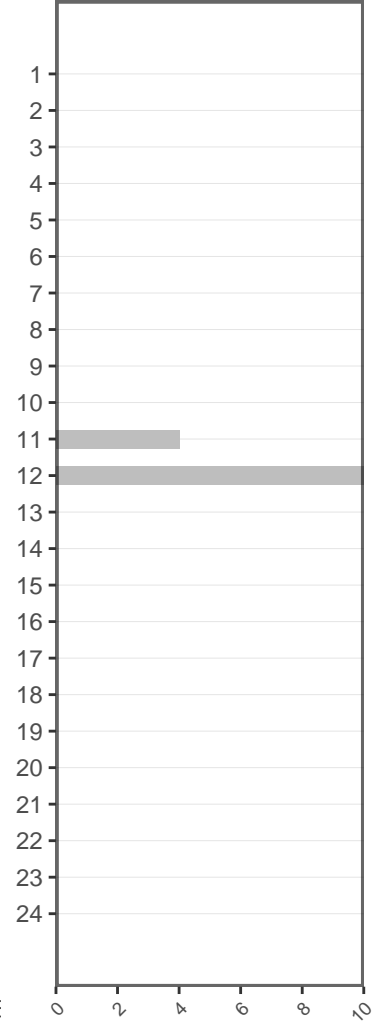
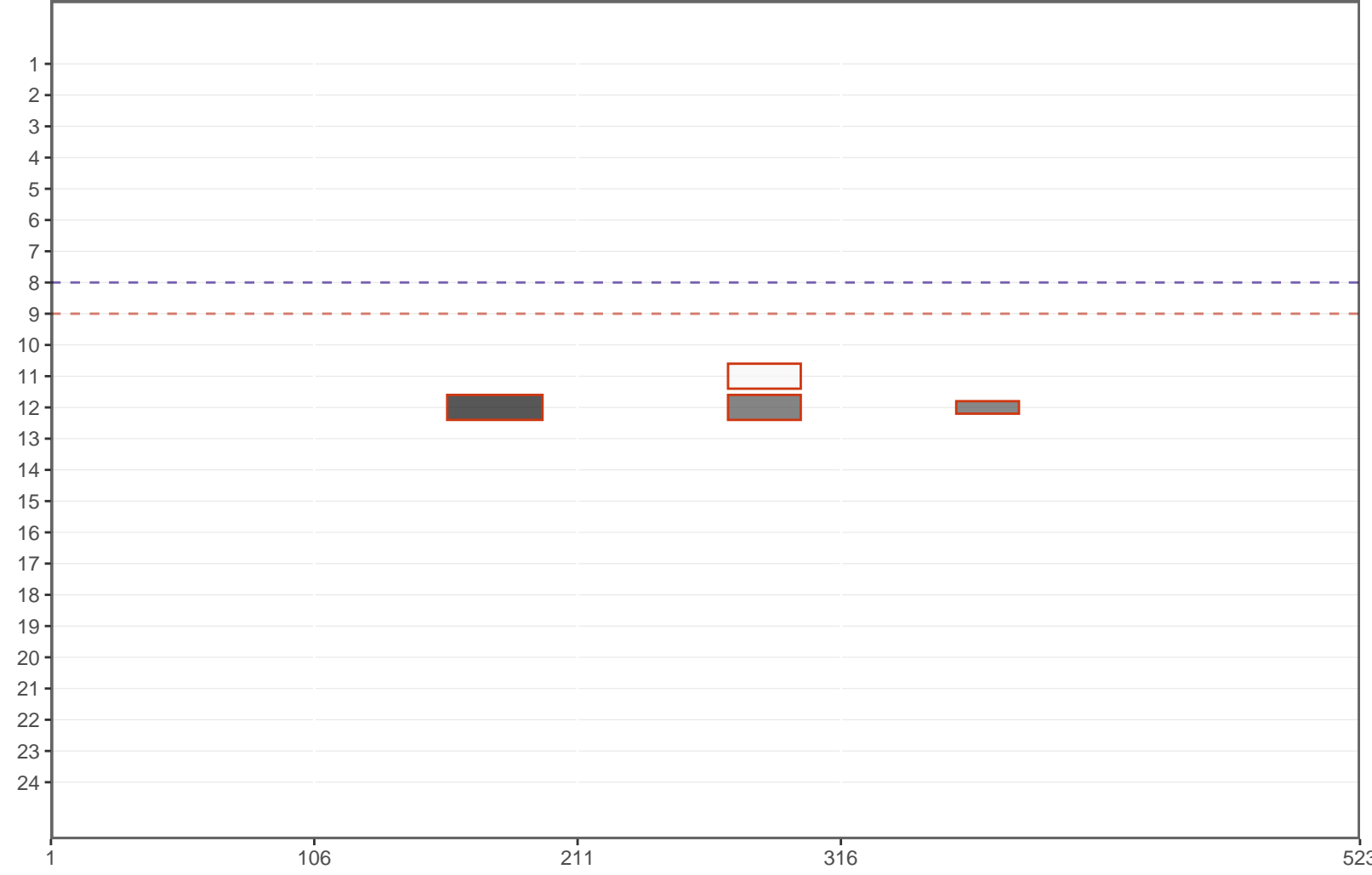
MW indication



Molecular weight

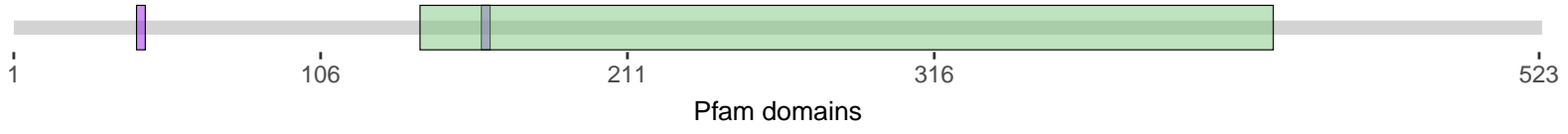


Gel Slice

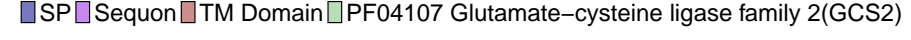


Protein length

Peptide counts over 4 repeats



Pfam Description



Protein sequence:

TCTCTQVNLDFSSSEVMIRKFRAGLAGLPATALFGNSPFTEGKPNQYLSMRSHWTDIDNNRAGMLPFVFDGDFGFEQYVDVAIDVPMYFVYRKKHYIDGAGMFRDFMNGKLLPFGDYPTLNDWENHLTTFIFEVIRKRYLEMIRGADGGPWRRRLGALPAFVAGILYDELGLQTVLDMTSDWTAEEEREMLRNKVPTSGLKTFRDGLLKHVAGDVAKLAKEGLELRIRGFKETGFLNEVTEVVRTGVTFAEKLELHWGKWRGSDVDFVEELY---

NbL10g20560.1 aquaporin_PIP-type_pTOM75 [MW = 30.77 kDa]

No. of times detected



log(intensity)



Values from



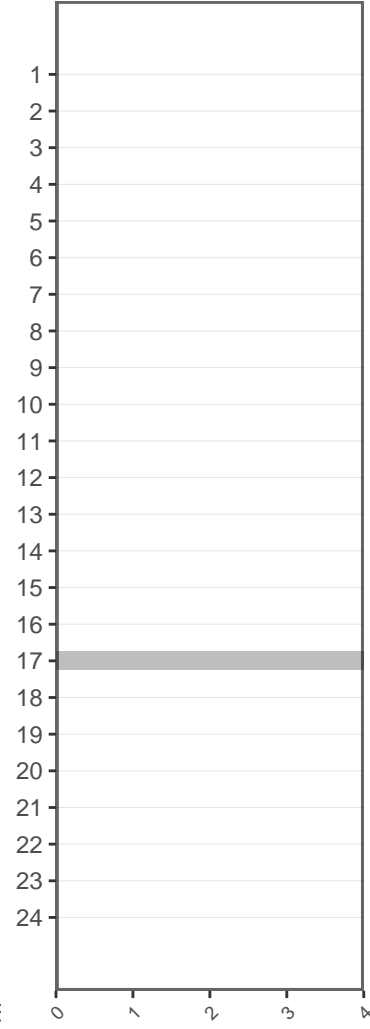
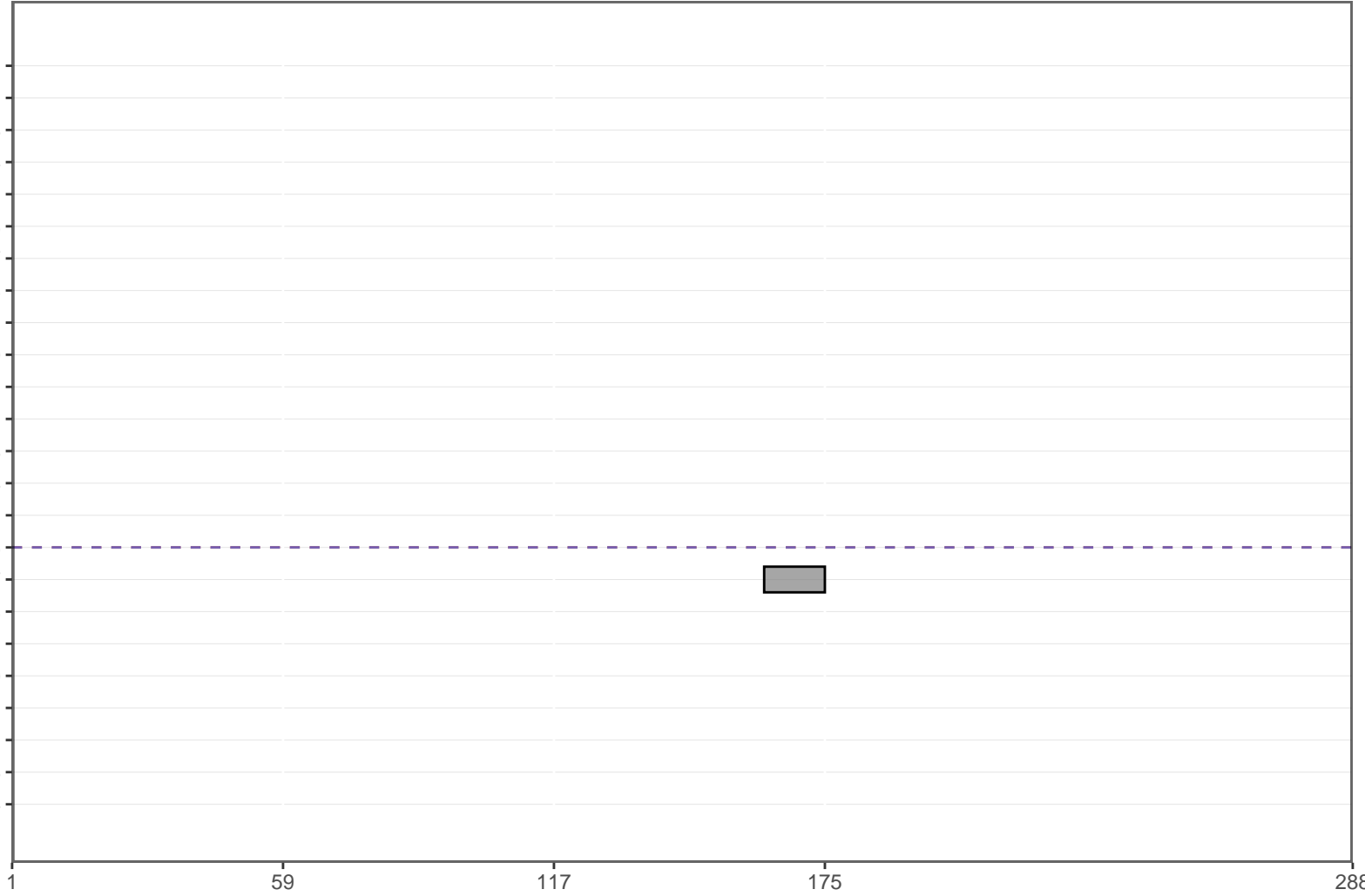
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

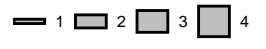


Protein sequence:

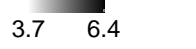
...TRAIFYIMVMOCLGAGGGVVKGFMGVYGRIGGGANVWPGYTKGDSLGAIEKGFVLYTVFSDAKRNARDSHVPLAPLPIGFVAVLHATIRITGTGNGPARSLGAIIHNDHWDDHWVWVGFPGAALAAVYHQIIRAIPEFKSP...

NbL10g20500.1 puromycin-sensitive_aminopeptidase-like [MW = 100.05 kDa]

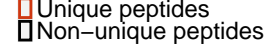
No. of times detected



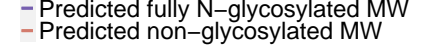
log(intensity)



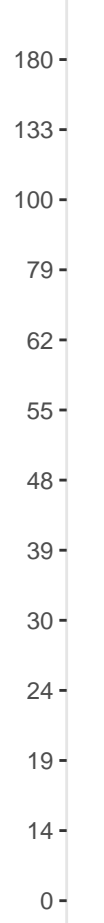
Values from



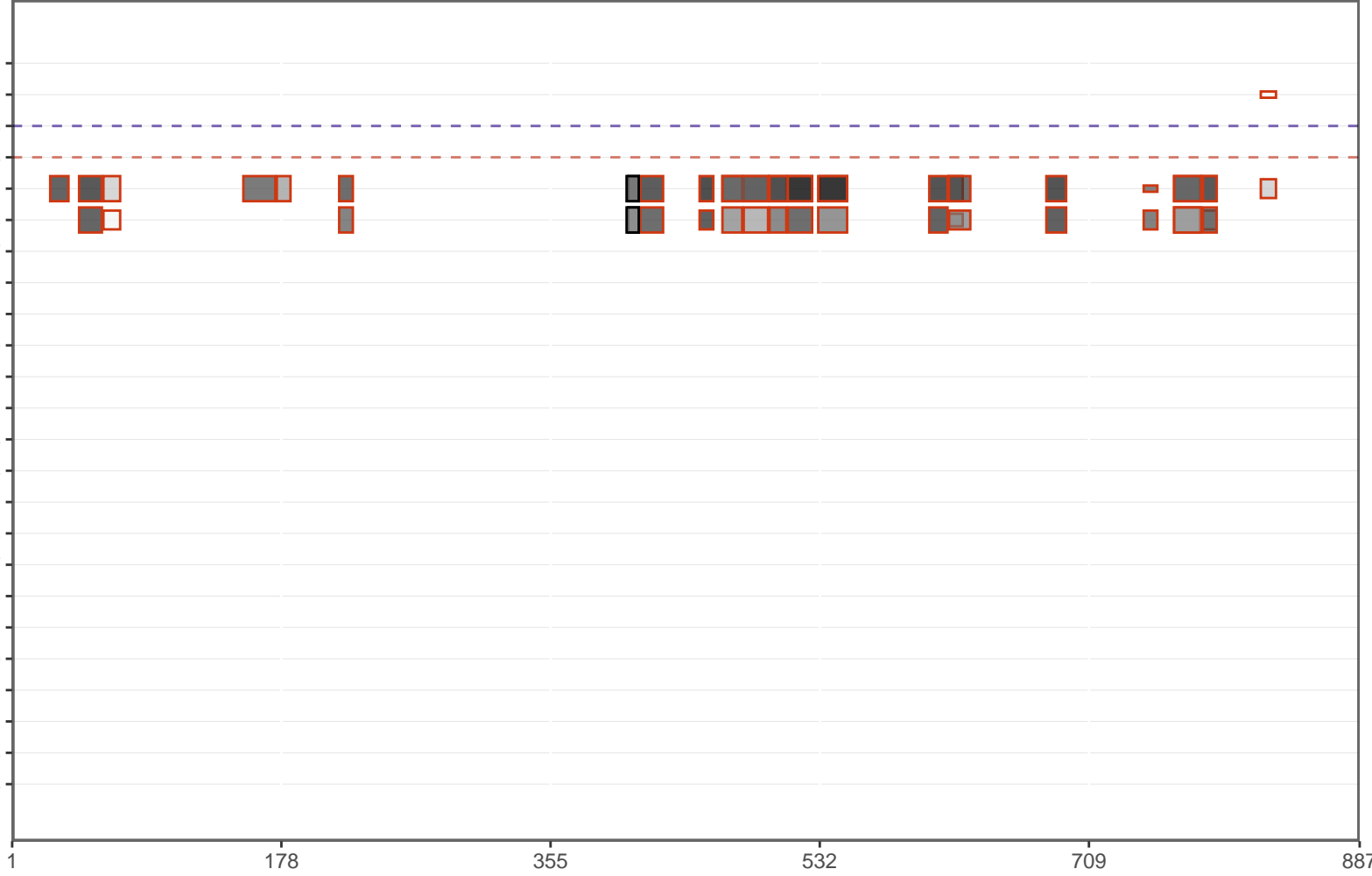
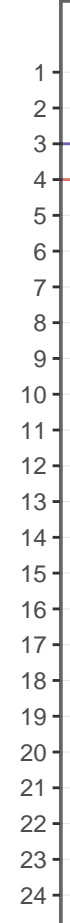
MW indication



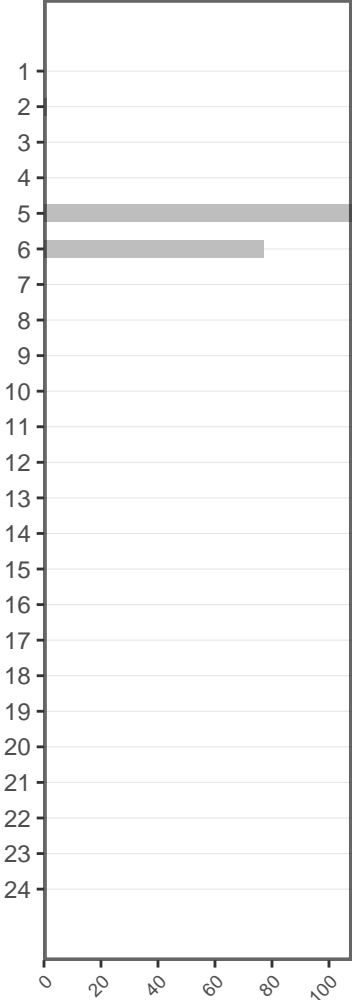
Molecular weight



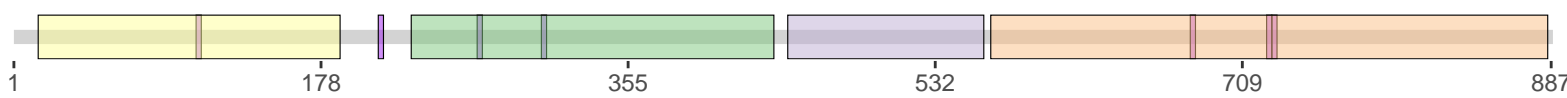
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01433 Peptidase family M1 domain
- PF11940 Domain of unknown function (DUF3458) Ig-like fold
- PF17432 Domain of unknown function (DUF3458_C) ARM repeats
- PF17900 Peptidase M1 N-terminal domain

Protein sequence:

RDANNADFANFLWYGGAGTPTVWVYETNYNAERSTFSKLFSGEIVRPTPGQPAKEMRIFVWGLDSSGKDMPLSSHYHDEKLEFSFANGGNVHTVLRITKKEEFVFNDESKPTFSILRGFSAPRLESRLTDSDLFLLAHDGDEFNRWEAGVLAARKMLSLVADFGQNKALVNPQFVGGIKSILDDSLDKERIAKATLPGVGEIMDMMTFVADPDAAHVAVRTFRKQLABELKEELLFVKNRSGSDVEYDFDHNMMARRAKNTALAYLGSLEGPEITELLLEYRNAT

NbL10g20150.1 uncharacterized_LOC109231095 [MW = 30.22 kDa]

No. of times detected



log(intensity)



Values from



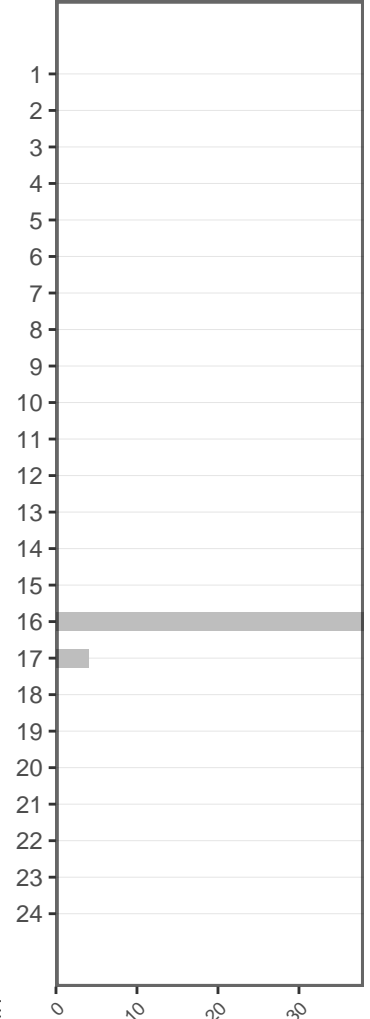
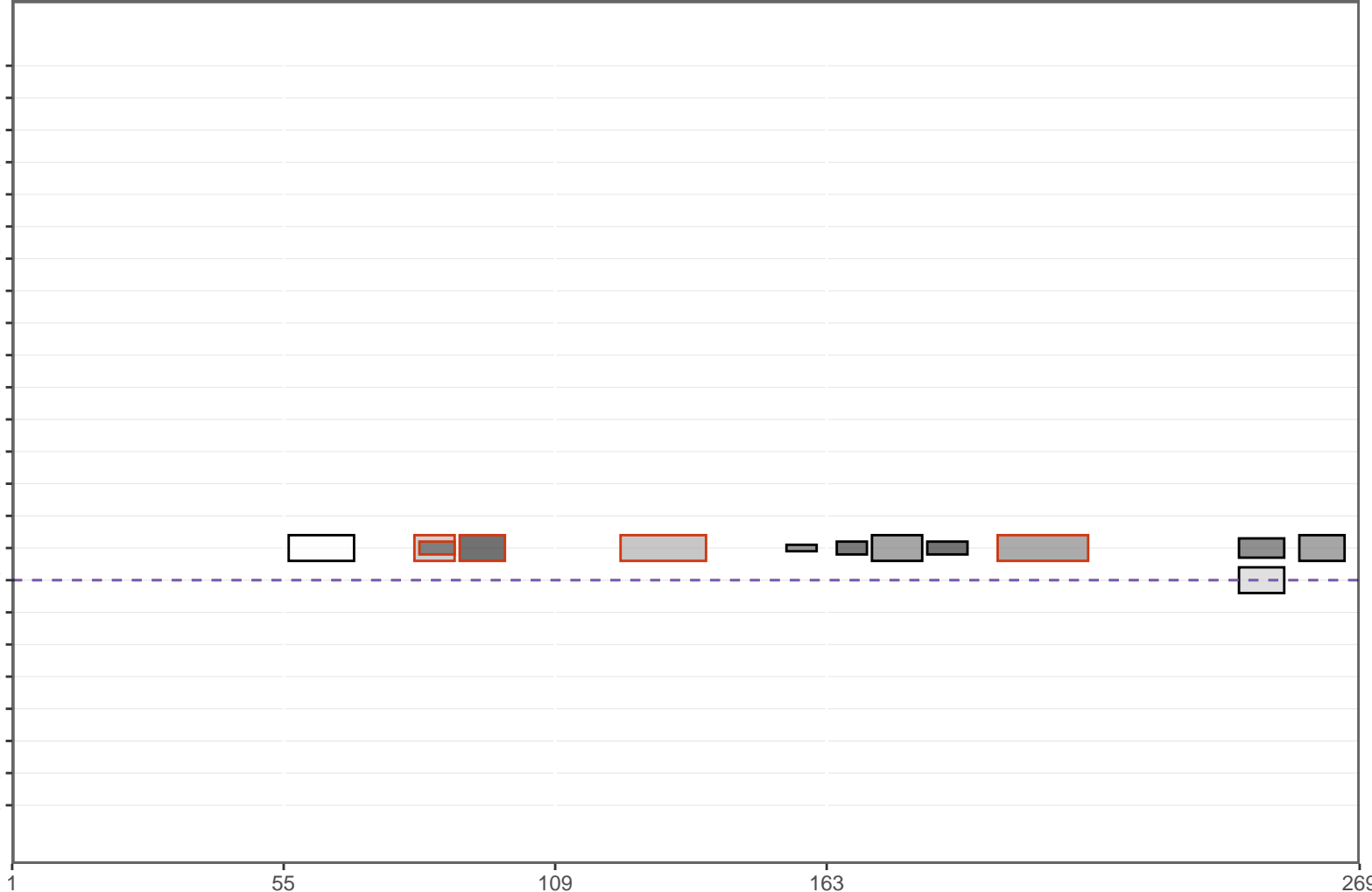
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

CVRDEWMSDSLATWIGANRFYGVDPALHFASAKLVVTTKGRFADALRELAGITPARIERYVGLGTGPKVYVYKLLQEMPEYDGLTHFVEDRLATLKNVKESELDGWNLYLGDWGVYNTQKEREEAASPIRILLGLSDFSNKLY

NbL10g20130.1 bifunctional_L-3-cyanoalanine_synthase/cysteine_synthase_1_mitochondrial [MW = 40.28 kDa]

No. of times detected



log(intensity)



Values from



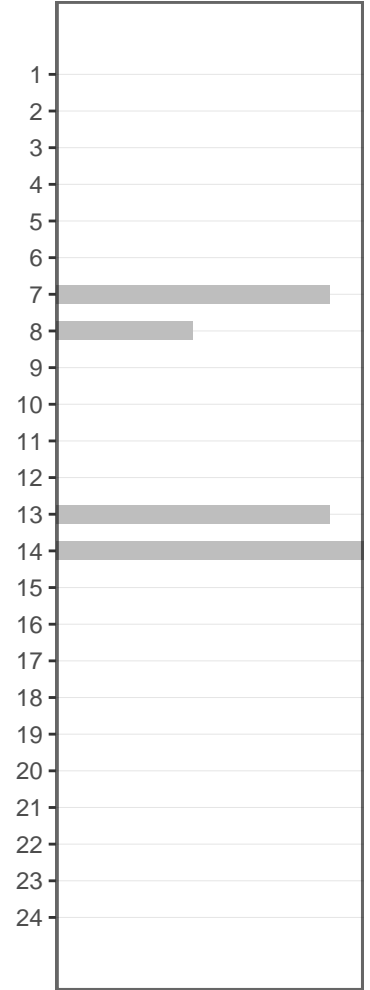
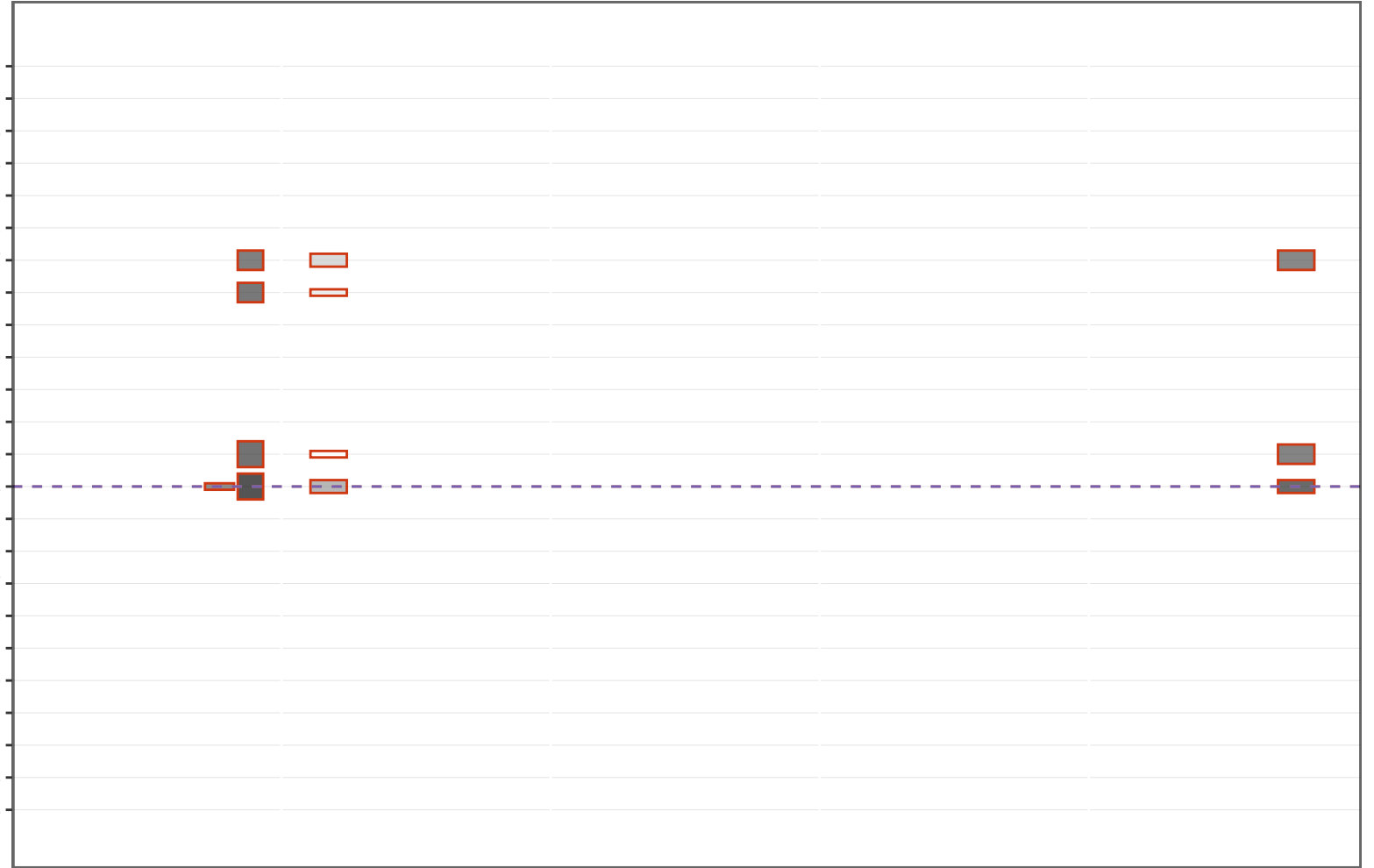
MW indication



Molecular weight

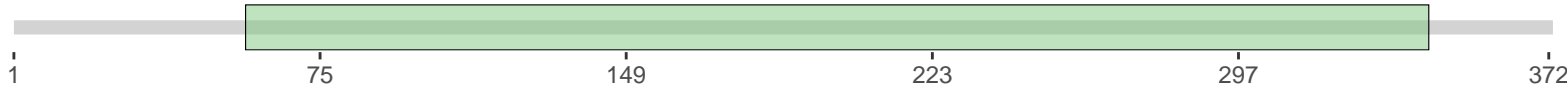


Gel Slice



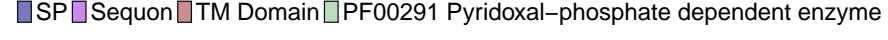
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GTVKKAYDLLESTPNFAMLGGFSNPANTGVHFETTSPPEIWEEDTGGNDFVFMGIGSSGGTVSGVGGVYLRKSNPNVYKIKGIEPTESNVLNGGKPKPSPHHITGNGVGFKPDILDMIEEVLVMSSEEAANNMARELALKEGLMVGISGANTVAALRLANKPENRGLNTHPSFGIERVLSVLYGELRKEAENMGPVFVDI

NbL10g20020.1 uncharacterized_LOC107784094 [MW = 12.39 kDa]

No. of times detected



log(intensity)



Values from



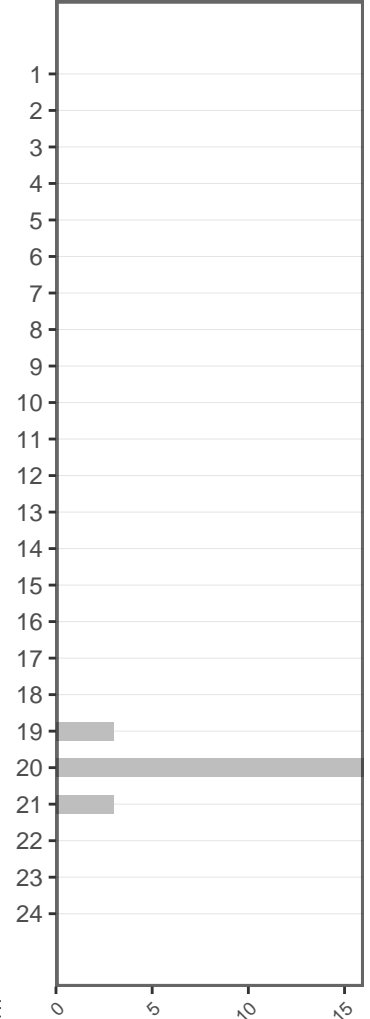
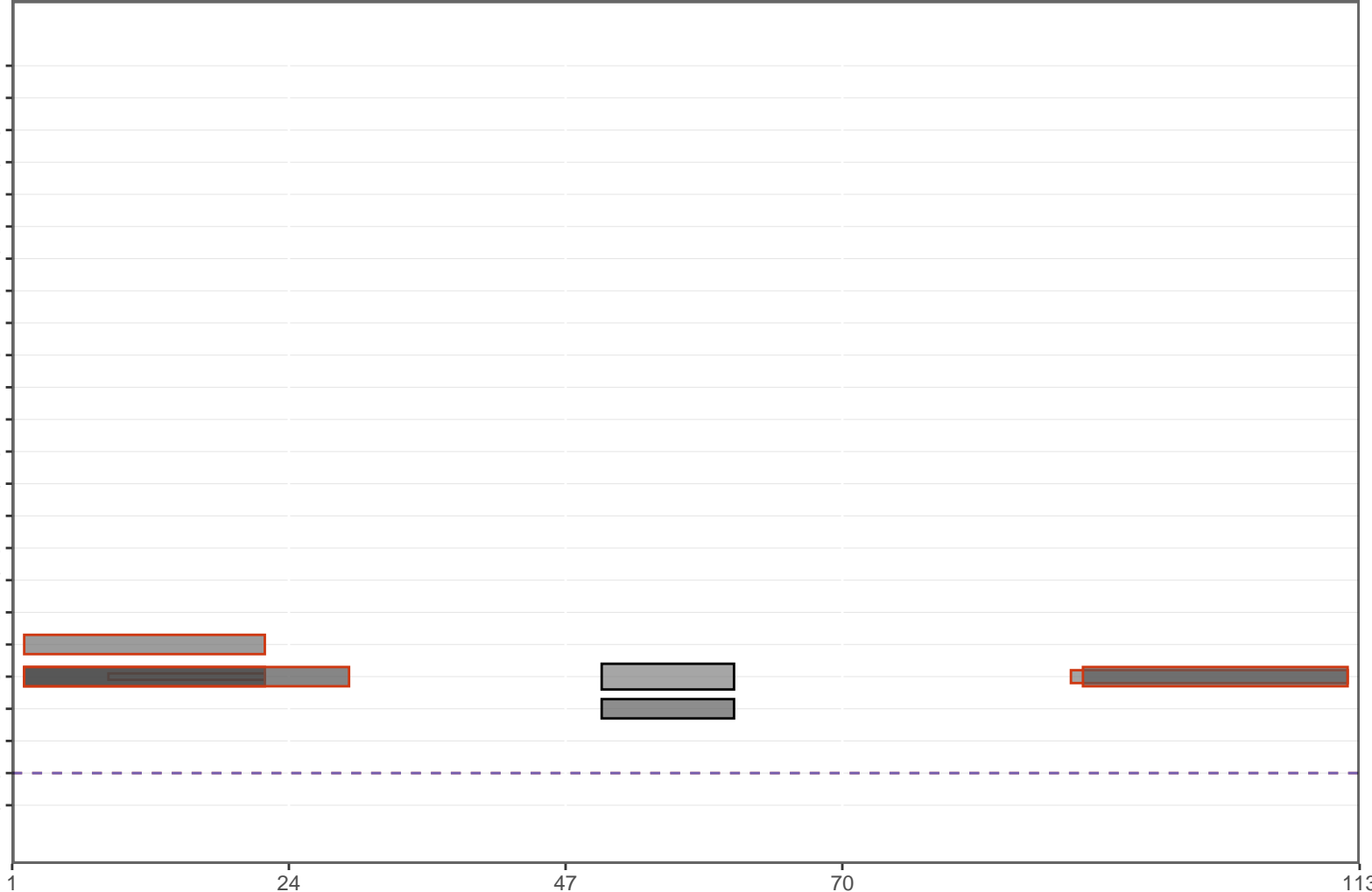
MW indication



Molecular weight



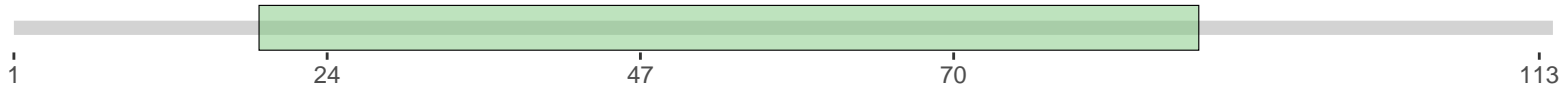
Gel Slice



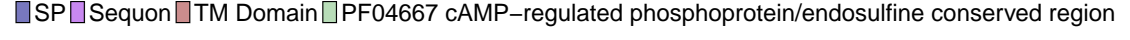
Protein length



Pfam domains



Pfam Description



Protein sequence:

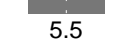
KDHERAYFDSADWALGKGGVANKPKGLEALRPKLGPTNGDTRVYKBPVAPSEGEDGSNMPPEQATANE*

NbL10g19910.1 ubiquitin-conjugating_enzyme_E2_28-like [MW = 15.44 kDa]

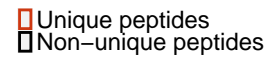
No. of times detected



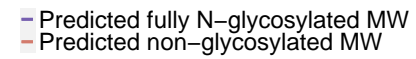
log(intensity)



Values from



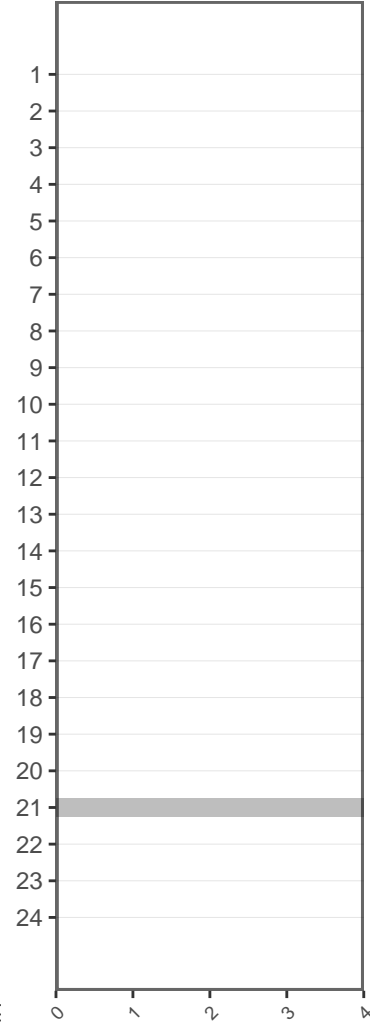
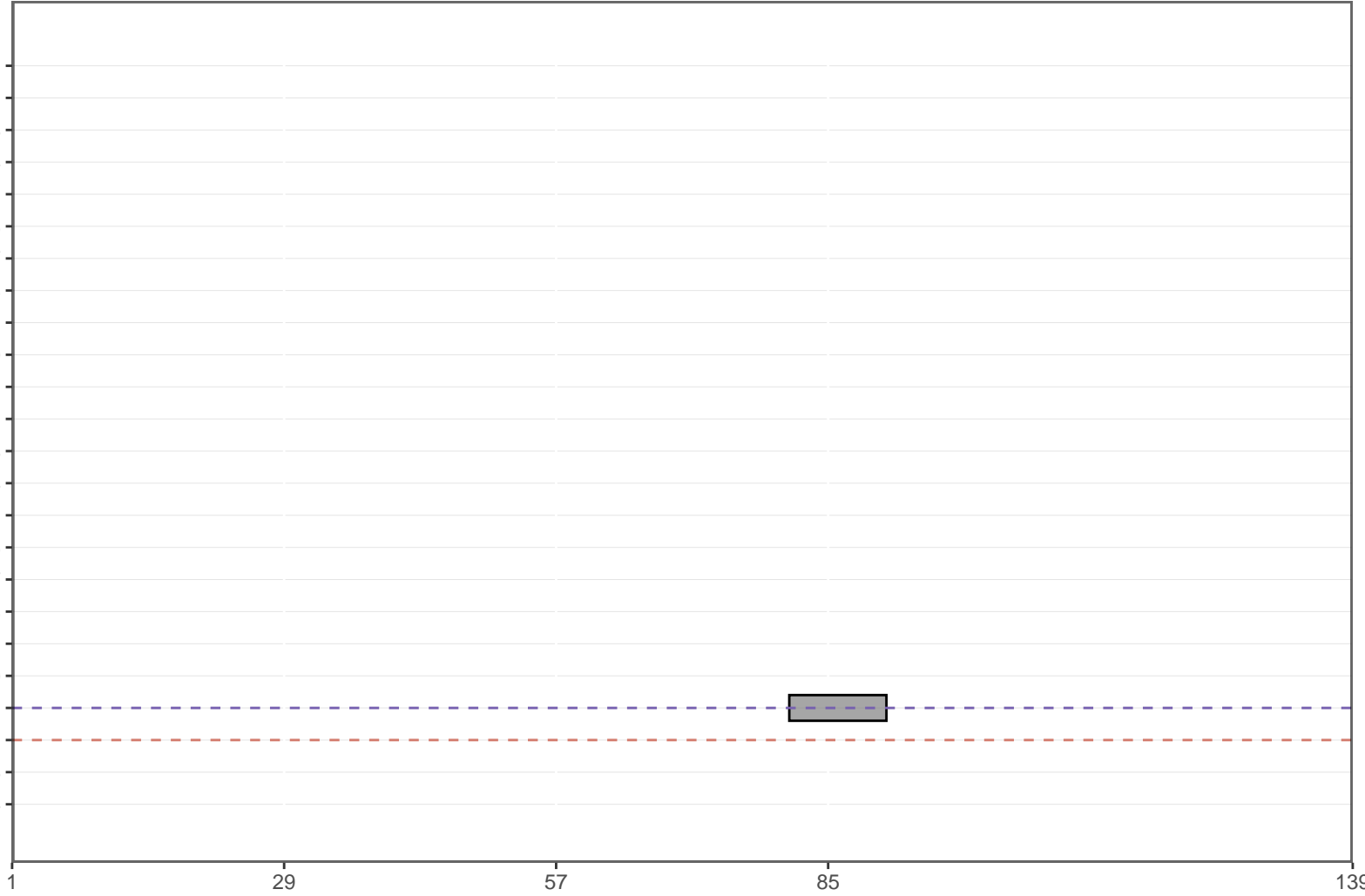
MW indication



Molecular weight

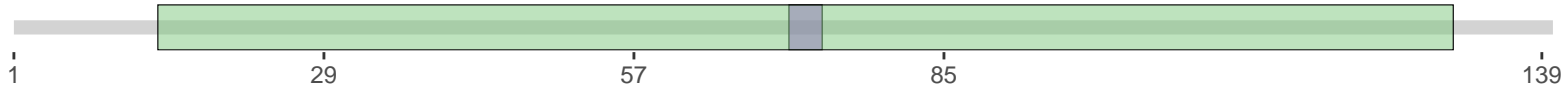


Gel Slice



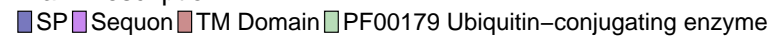
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

`*KVAFRTKYLHFNINENSGICLDLKEQWSPALTRKVLKLSGICLLTDPNDDPLVPEIAHMYKTRAKVETTRARISWTQKYAMG*`

NbL10g19820.1 anthocyanidin_reductase-like [MW = 38.84 kDa]

No. of times detected



log(intensity)



Values from



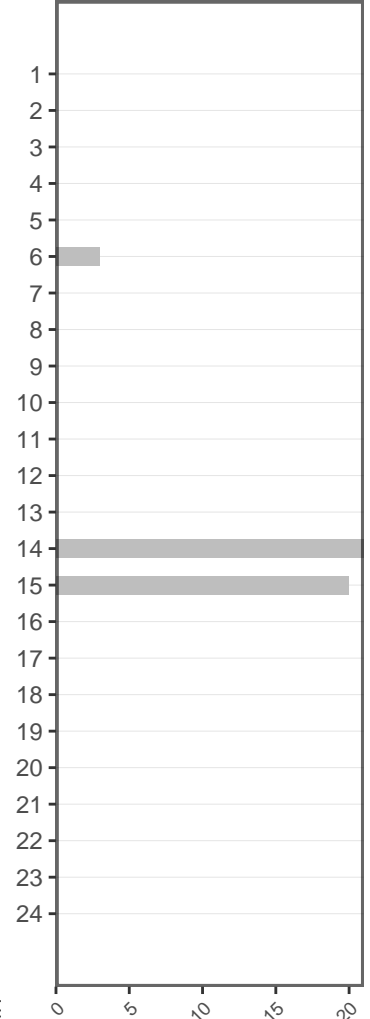
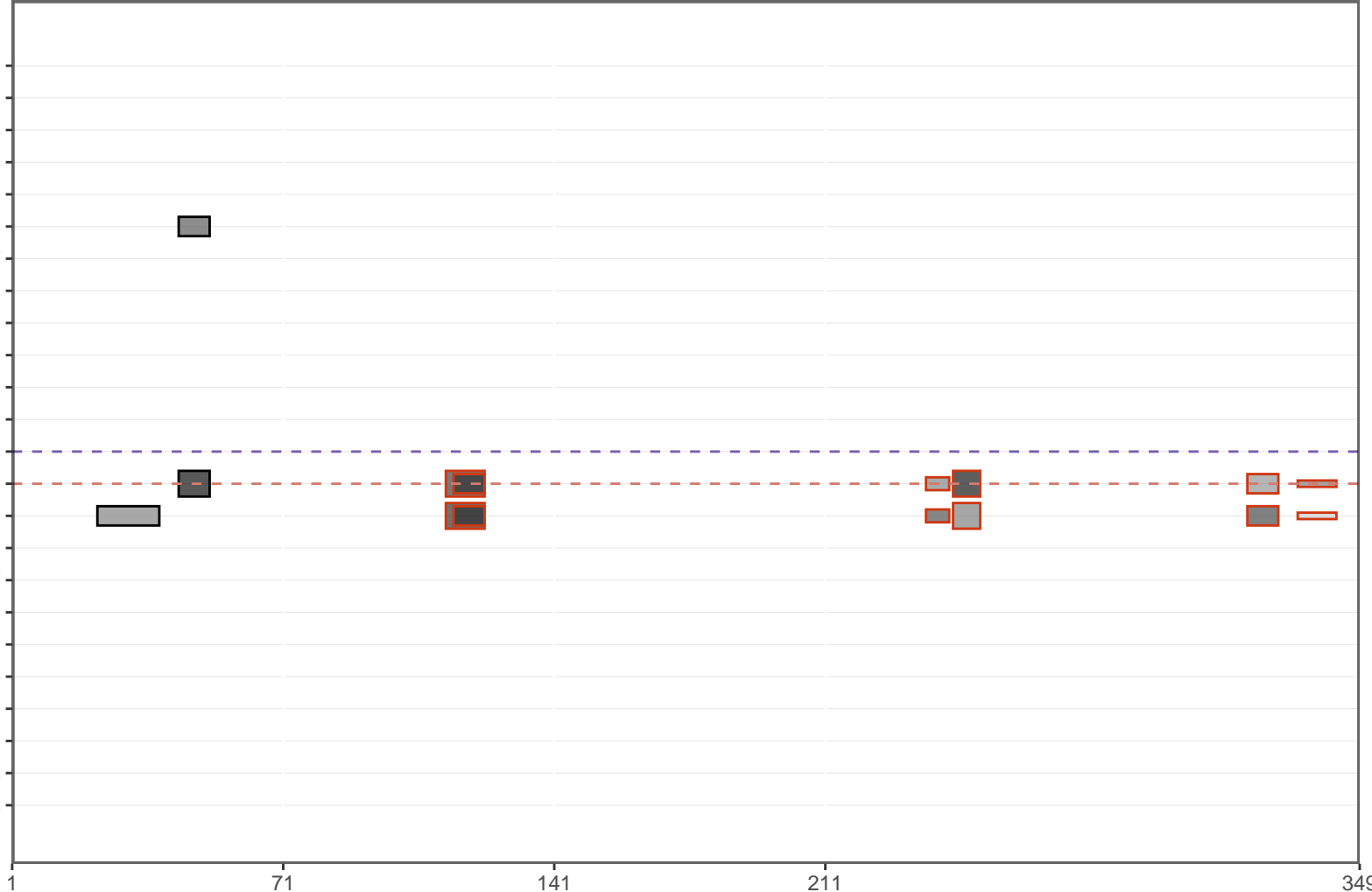
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ETCWPLNFSNPYANQGLKEYVESKMLAEKEMLNFGEGEGLEVFLGGGLVGGETFLPYPTFTSTALFLGLFTGDKSLYNSLKFLEELIGKVPVHVEDVGEAHLMSRAAWNGRFLCASSRISSAEIGGYYQQNYPEFNLNDEYLNDRNREIKRWGKIKLVDFVYKYGKMKELDDSVSGARKNGAF

NbL10g19630.1 heterogeneous_nuclear_ribonucleoprotein_Q [MW = 52.27 kDa]

No. of times detected



log(intensity)



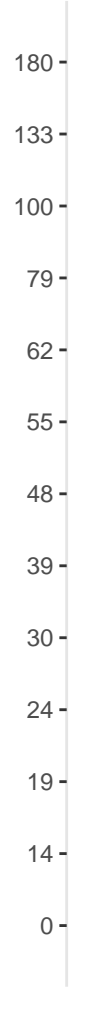
Values from



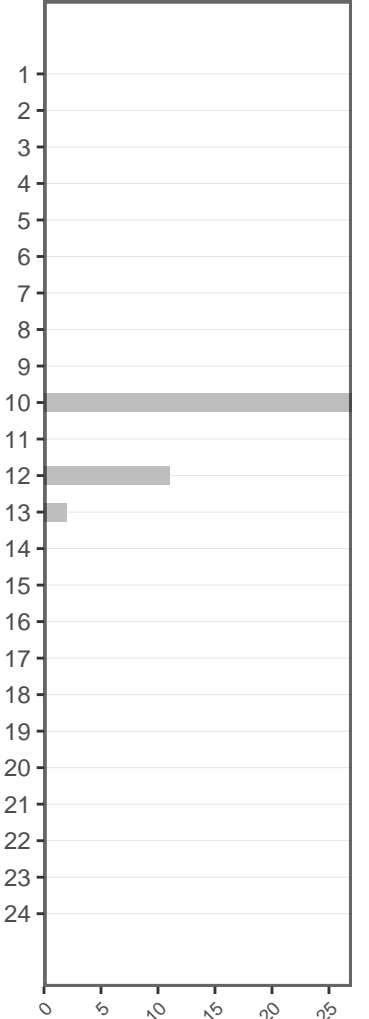
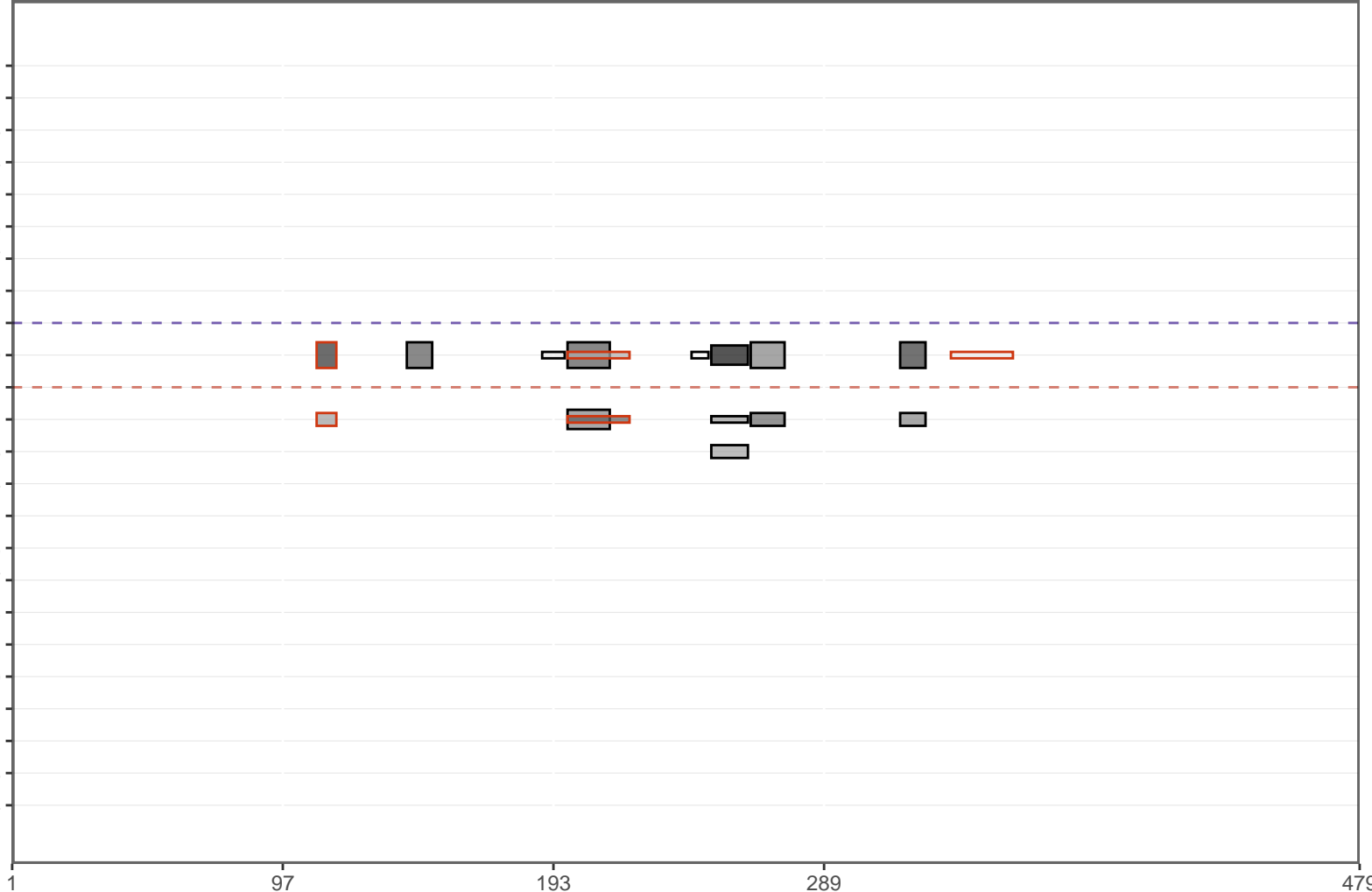
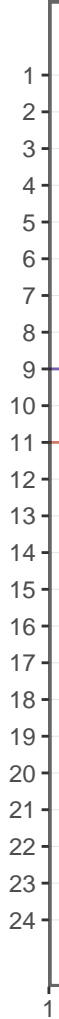
MW indication



Molecular weight

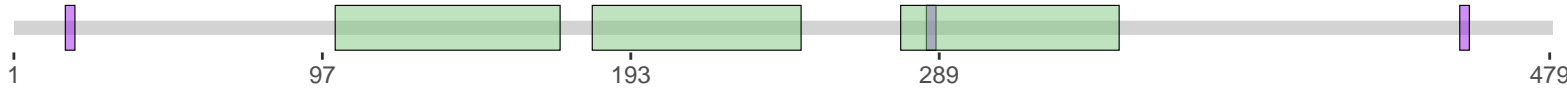


Gel Slice



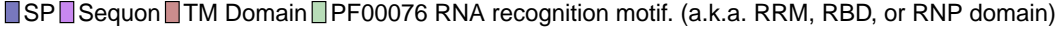
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NNACADYSRKKIMASANFKLEGNSTFTVWADNITPDHSAAGAAQKALVYKSPENTSTEQKKEIFGRHGDVTKVMPFPAKSGGKRDFGFVHYAERBSALKAWDGETYEVNSGVLEVLAKPQTEKFDAAAGPHNAMPINVYHPHFGAFPPVNPYGHLTGYSYAAAGFQGGPMYGRGPMFAGMGMMVPMVLPDGGIGYVLAQGPVGAFAVRRPRRDRNGSSGGPQGRGSSSGTGDSDNRGRVYRPV

NbL10g19560.1 protein_CURVATURE_THYLAKOID_1B_chloroplastic [MW = 19.22 kDa]

No. of times detected



log(intensity)



Values from



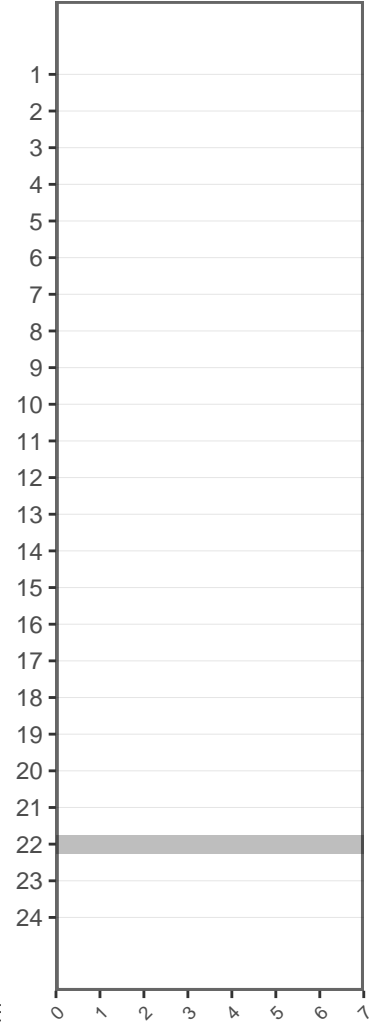
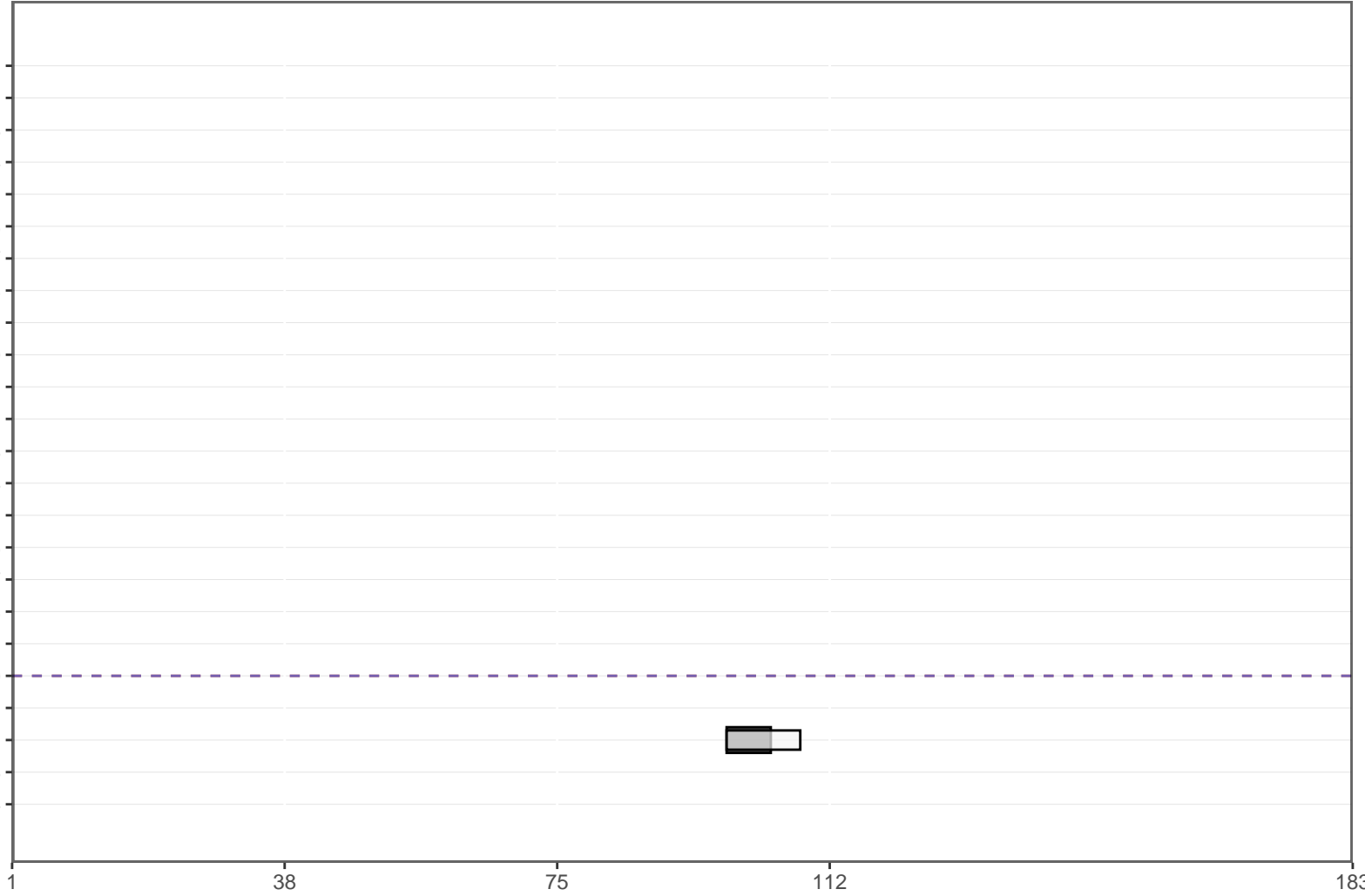
MW indication



Molecular weight



Gel Slice



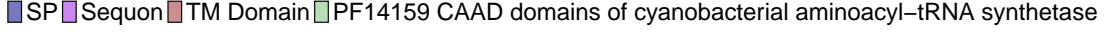
Protein length



Pfam domains



Pfam Description



Protein sequence:

TTAASSADMATTELPSELLGKNGDEAWKLDKRYAVSGLGVAALLLLWSSTGVSADRLLPLPGVLELVGIGVGTGWFAYKXVLFKPDREALISKIKDLNKEVIGSS*

NbL10g19550.1 caffeic_acid_3-O-methyltransferase-like [MW = 40.19 kDa]

No. of times detected



log(intensity)



Values from



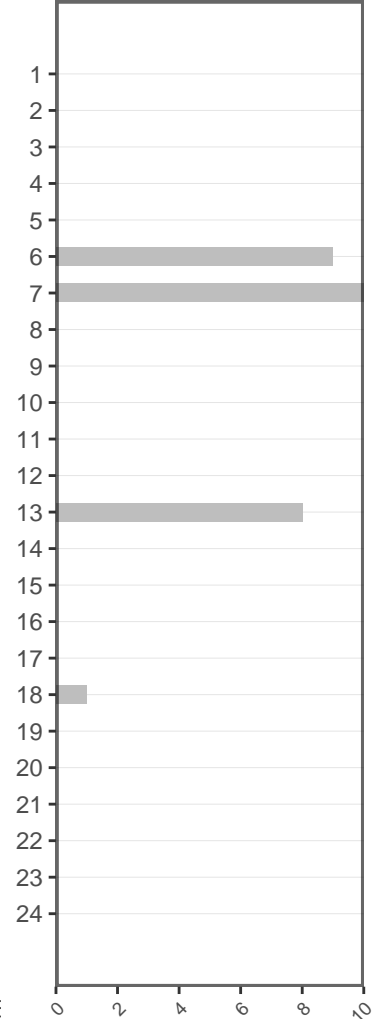
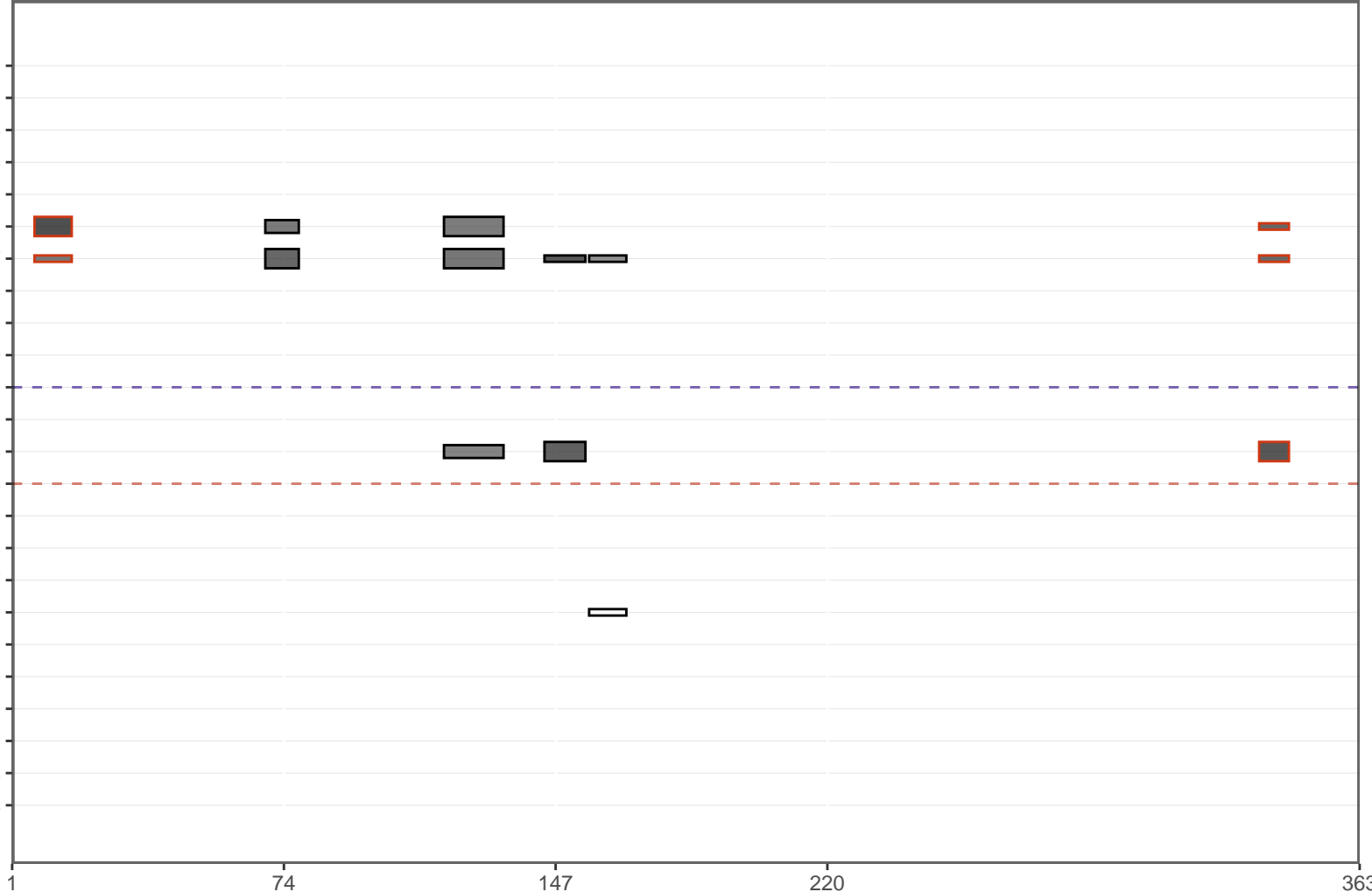
MW indication



Molecular weight

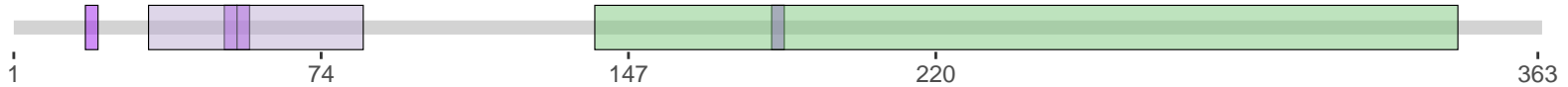


Gel Slice



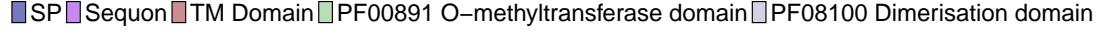
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PKFNDVFNAMLNHTTVMKKILENYGFENLKTLDVGGGLGVNLKMTAKYPTIKGTNFDLPHAVGHAPSYPGVVEHVGDMFESVDPDGDAMFMWLLHDWNSHNKLLKNGKYLKALGKGVVVEALPVKPDFTDITWIGVSGCDLMMAGNPNPQKGERSEEEFRFLATEAGFKGVNLGGVCFWVMEFFK

NbL10g19490.1 probable_2-oxoglutarate/Fe(II)-dependent_dioxygenase [MW = 38.84 kDa]

No. of times detected



log(intensity)



Values from



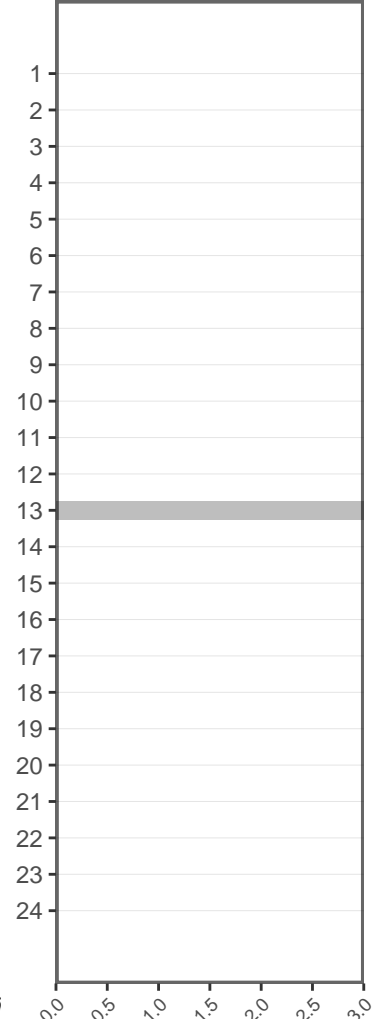
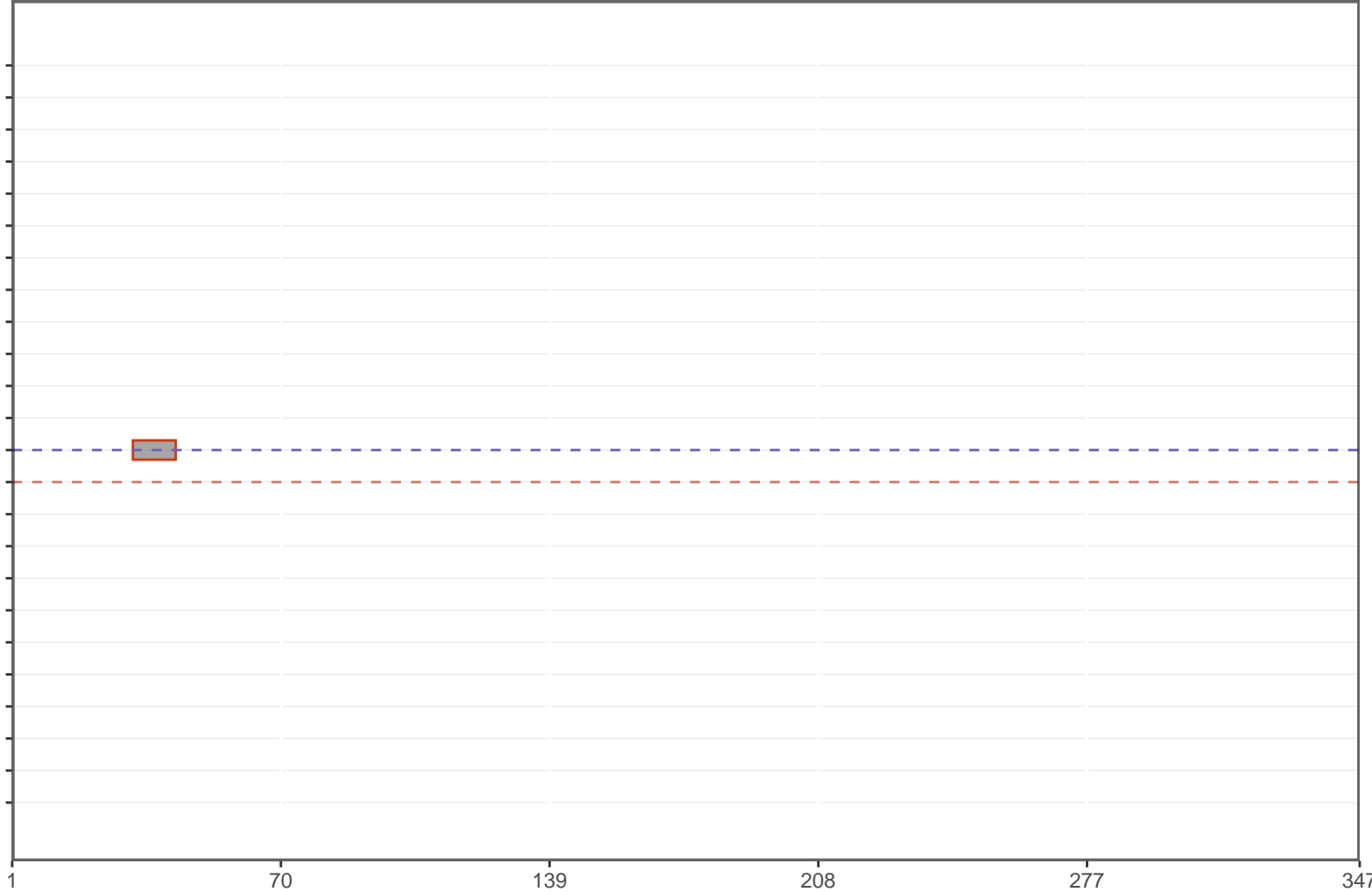
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

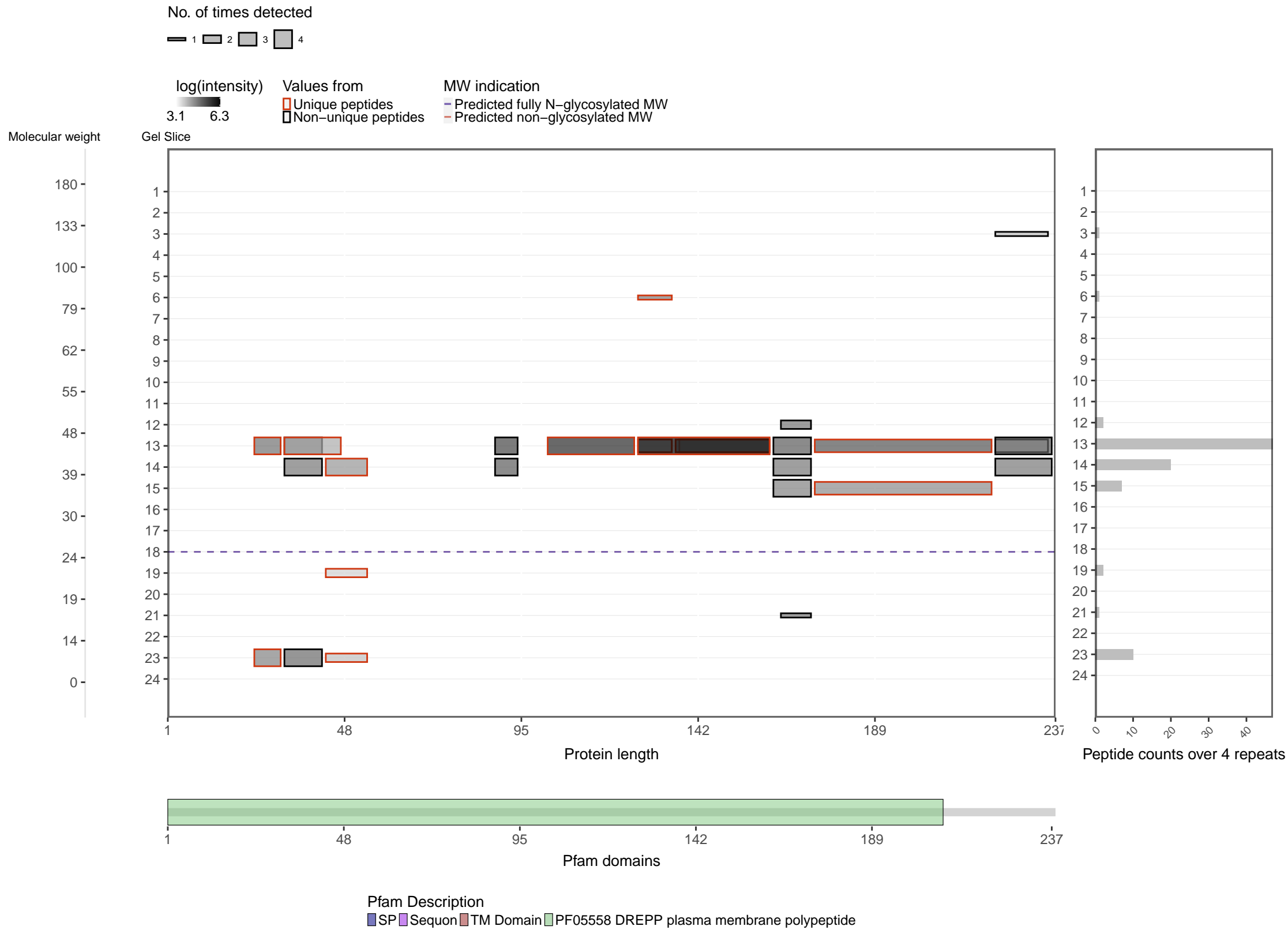
Pfam Description

- SP
- Sequon
- TM Domain
- PF03171 2OG-Fe(II) oxygenase superfamily
- PF14226 non-haem dioxygenase in morphine synthesis N-terminal

Protein sequence:

IRKVVYTAISDIHMKALADELLGLVSESLGDTGGSMENVVGEFYQNTISYVPPCPQPELTLGLGSHSDMGATLLIGDDVGGLEVFNGSEWVTVNPMEDAGDVLADGTEHSNGEYRBAQHRVATNARKARLSEVATFHDPKTRQIGSPSPAFHPPKRYRPIVYGDVYSSWYTKGPEGRNLDALLNGLN

NbL10g19480.1 plasma_membrane-associated_cation-binding_protein_1-like [MW = 24.77 kDa]

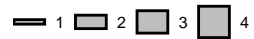


Protein sequence:

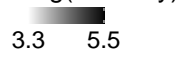
ISEASSNFGPSYYSGPVLFFVKVSTLTFTEDKKEEAAAPVAAGAEAEATTTAPVEVKEKEVVEAEAKKEEPAPAPAPAPAPAPAPAPAPAPAAAPAAAEVAPAEVAPADAPAKVVEEAPAAVAAPFPKAA

NbL10g19370.1 polyadenylate-binding_protein_RBP45-like [MW = 52.28 kDa]

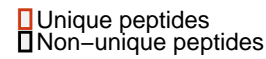
No. of times detected



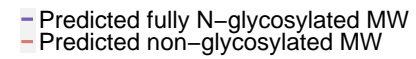
log(intensity)



Values from



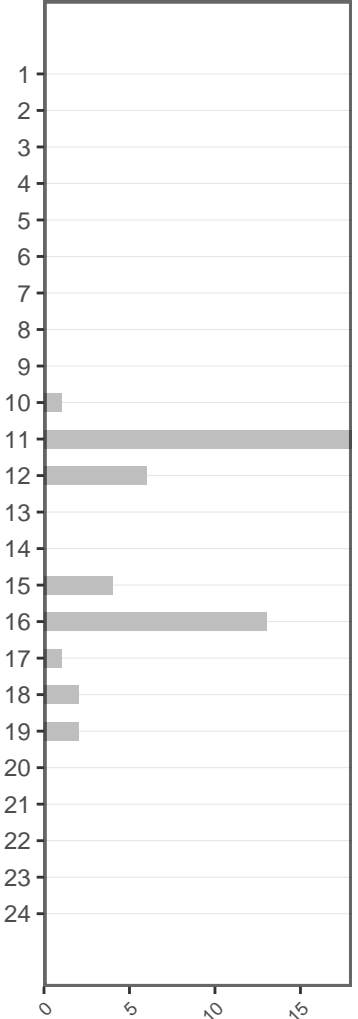
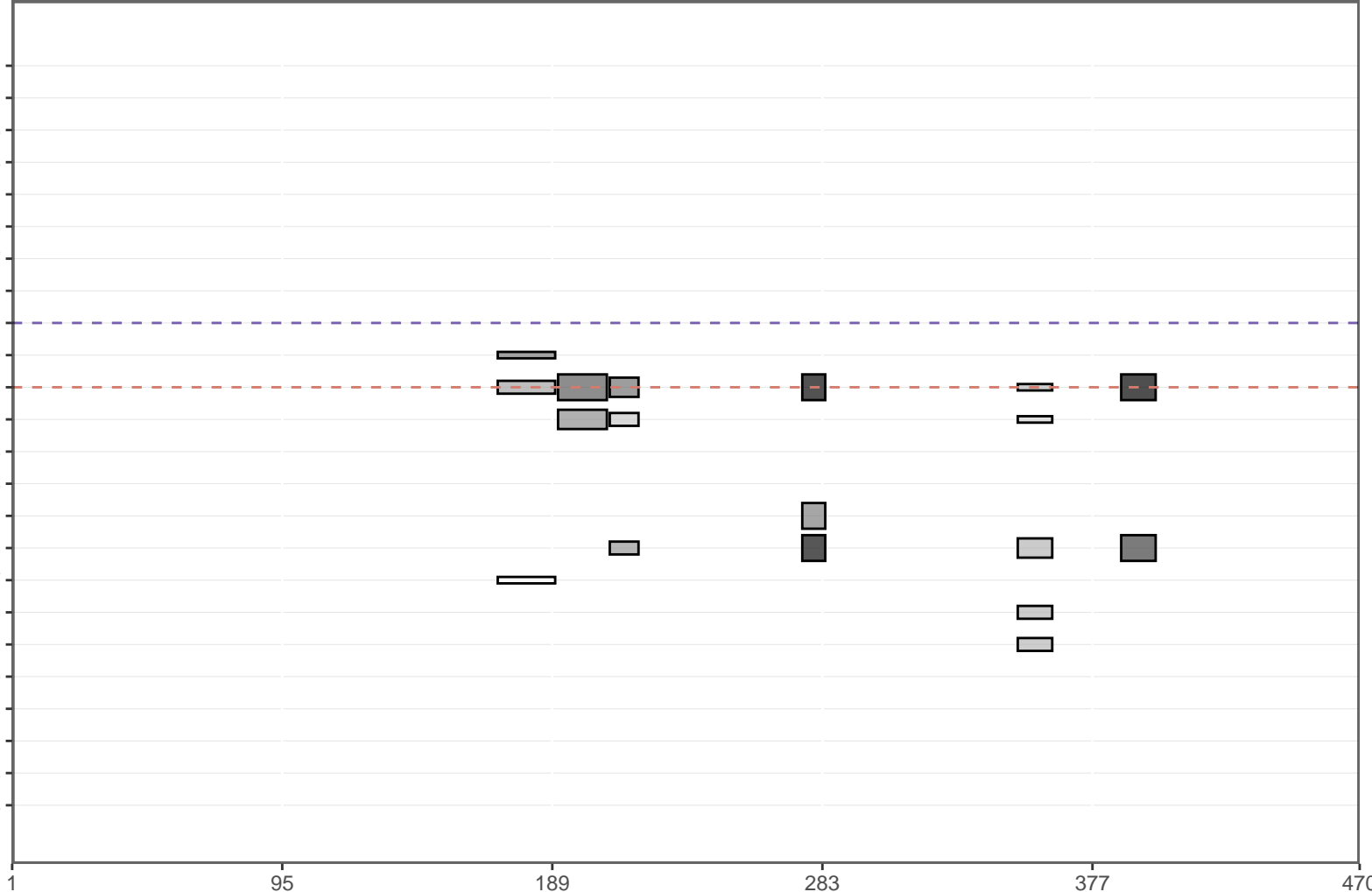
MW indication



Molecular weight

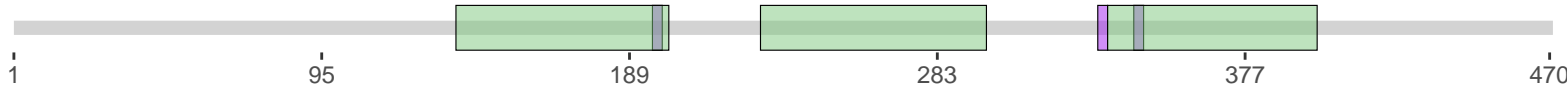


Gel Slice



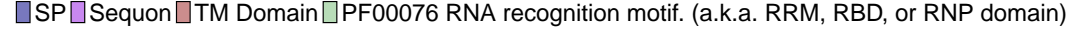
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IPETITFGQLAADVTDHMLGETFRANYPVSGAKIVTDETEGHTKGGVFRFGDESEGLRAMTEMNGKFGSTRPGRIPANPKSAGGOMQASVYQTLGTQINEDDPTNTTFVGNLDSNITDDHLRQVFGHYGDLHWPVVKRGGFVGFADRSCAEELRALSGTLGGOSRLSWGRSPSNKQDPQVDPNGYGGVYGYTFPGEVGVAFPAQDPNMFYAGYAGYGNVAPPQGGGGMGGQPQ

NbL10g19320.1 adenosine_deaminase-like_protein [MW = 40.93 kDa]

No. of times detected



log(intensity)



Values from



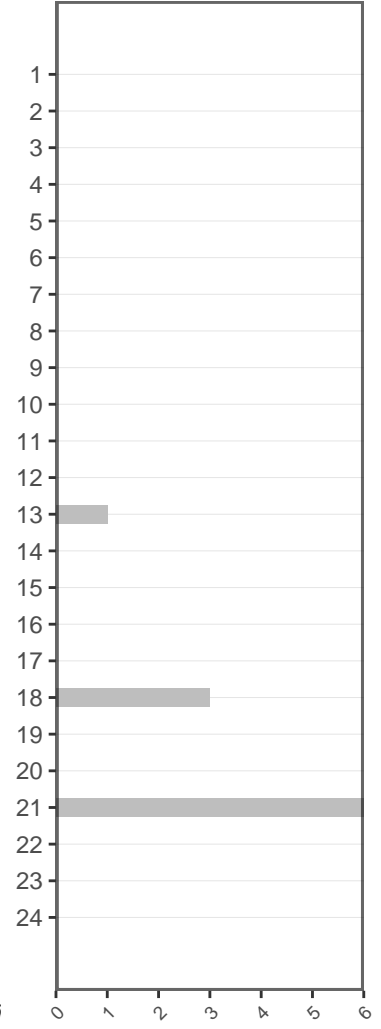
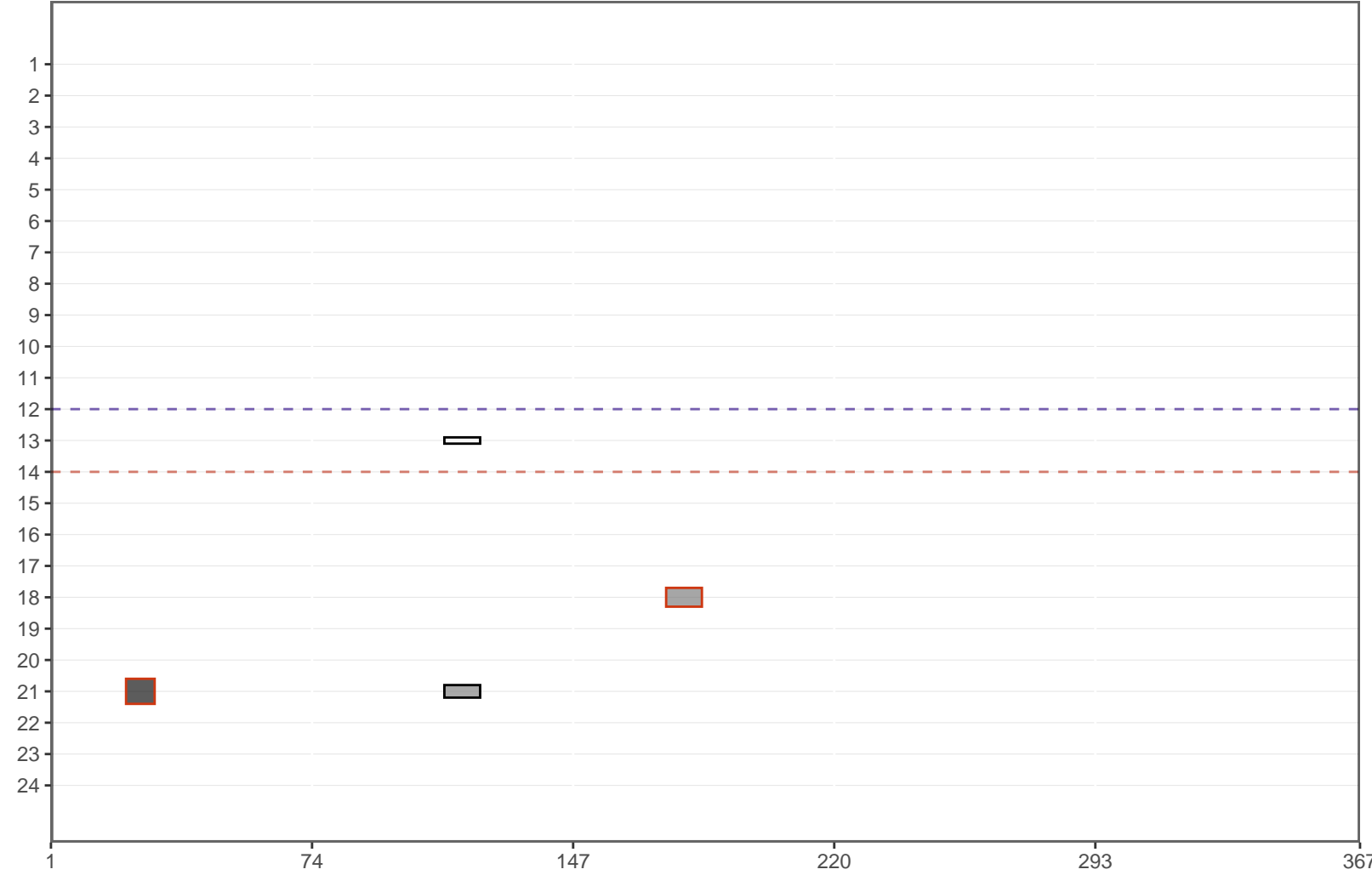
MW indication



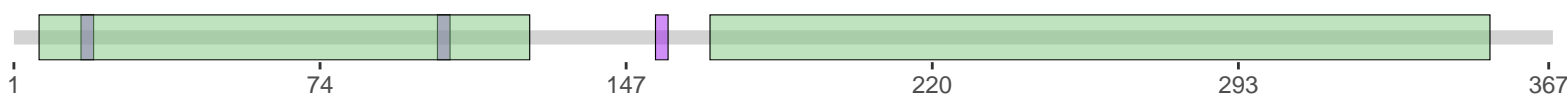
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

DRRESTEAAVETVYVLALEMRIHQGVVGDLSGNPIGEGWLFPLPALEFAKEQGLLITLHDSGEVNPVEIHAALDFLPRIGHAGCFEEEEWAKLKLKIPVEIKLTENIRFETISLSLDIHFADLYVSGHPVILCTDDSGVFTSTVSQGEYLAASAFGIQKREMFQLARSANKFIFAGDKVYKLELEQLFLAAKNLEF

NbL10g19110.1 keratin_type_II_cytoskeletal_1-like [MW - SP = 9.35 kDa]

No. of times detected



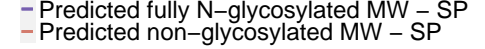
log(intensity)



Values from



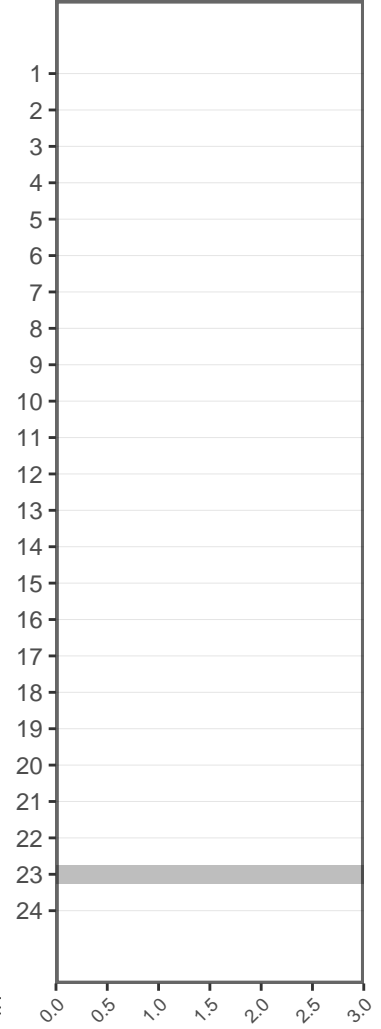
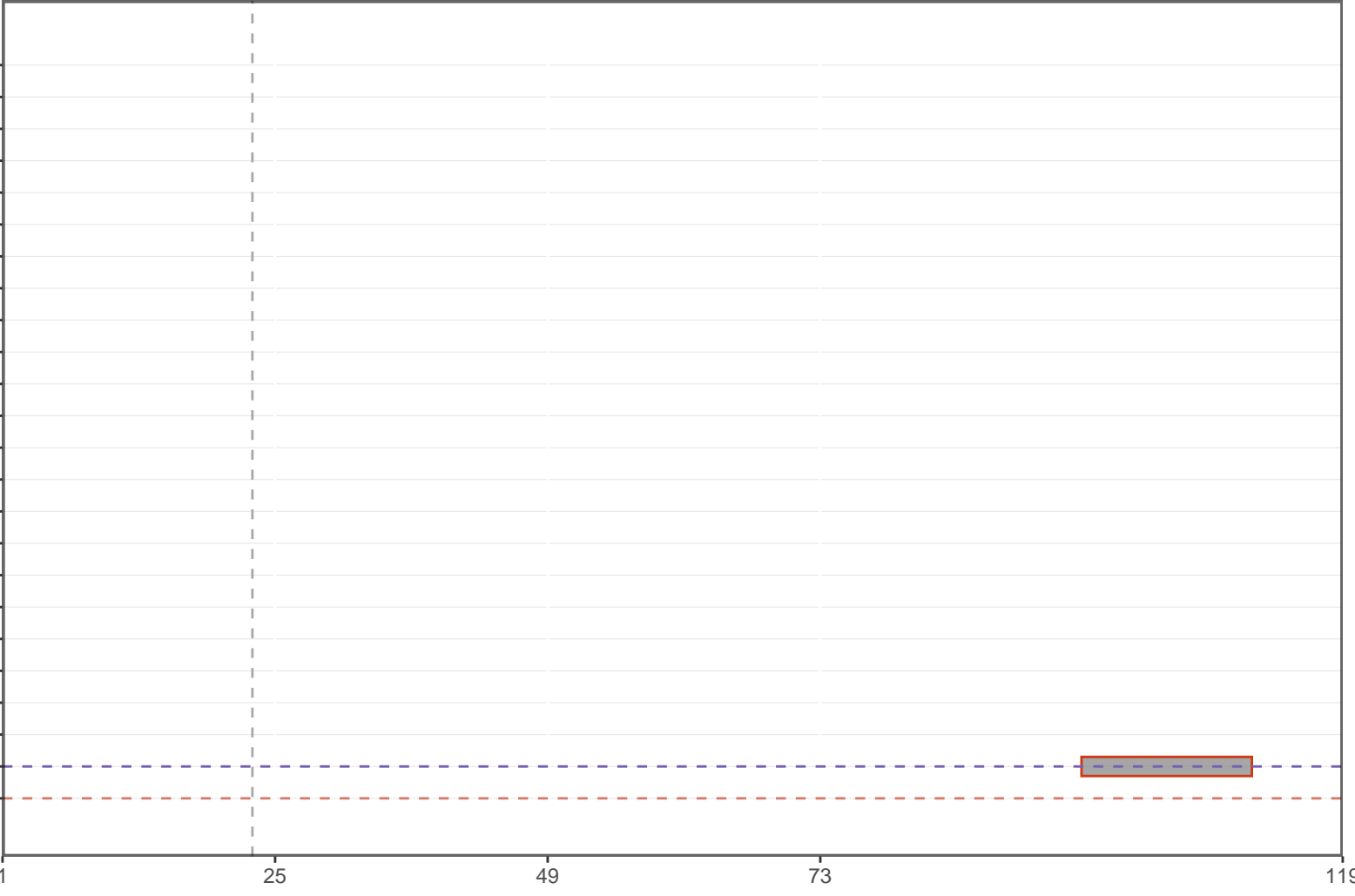
MW indication



Molecular weight



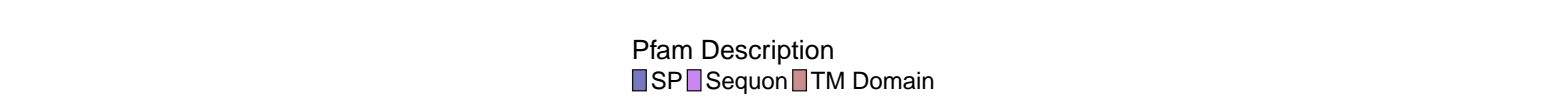
Gel Slice



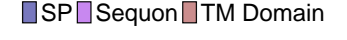
Protein length



Pfam domains



Pfam Description



Protein sequence:

IGFGPKGGYAKGGIRFTVVKDKGFLGKLLRCPAKGKFKFRAGKGYGYGGGGGGTMDCKKKGVYD

NbL10g19080.1 granule-bound_starch_synthase_1_chloroplastic/amyloplastic-like [MW = 11.9 kDa]

No. of times detected



log(intensity)



Values from



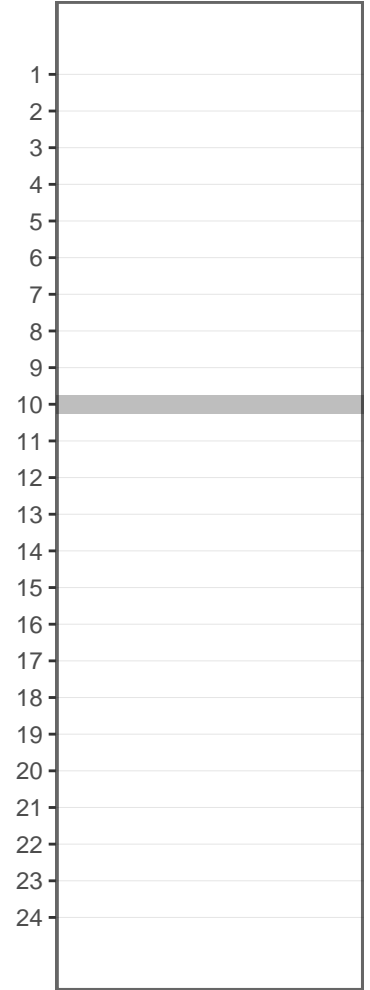
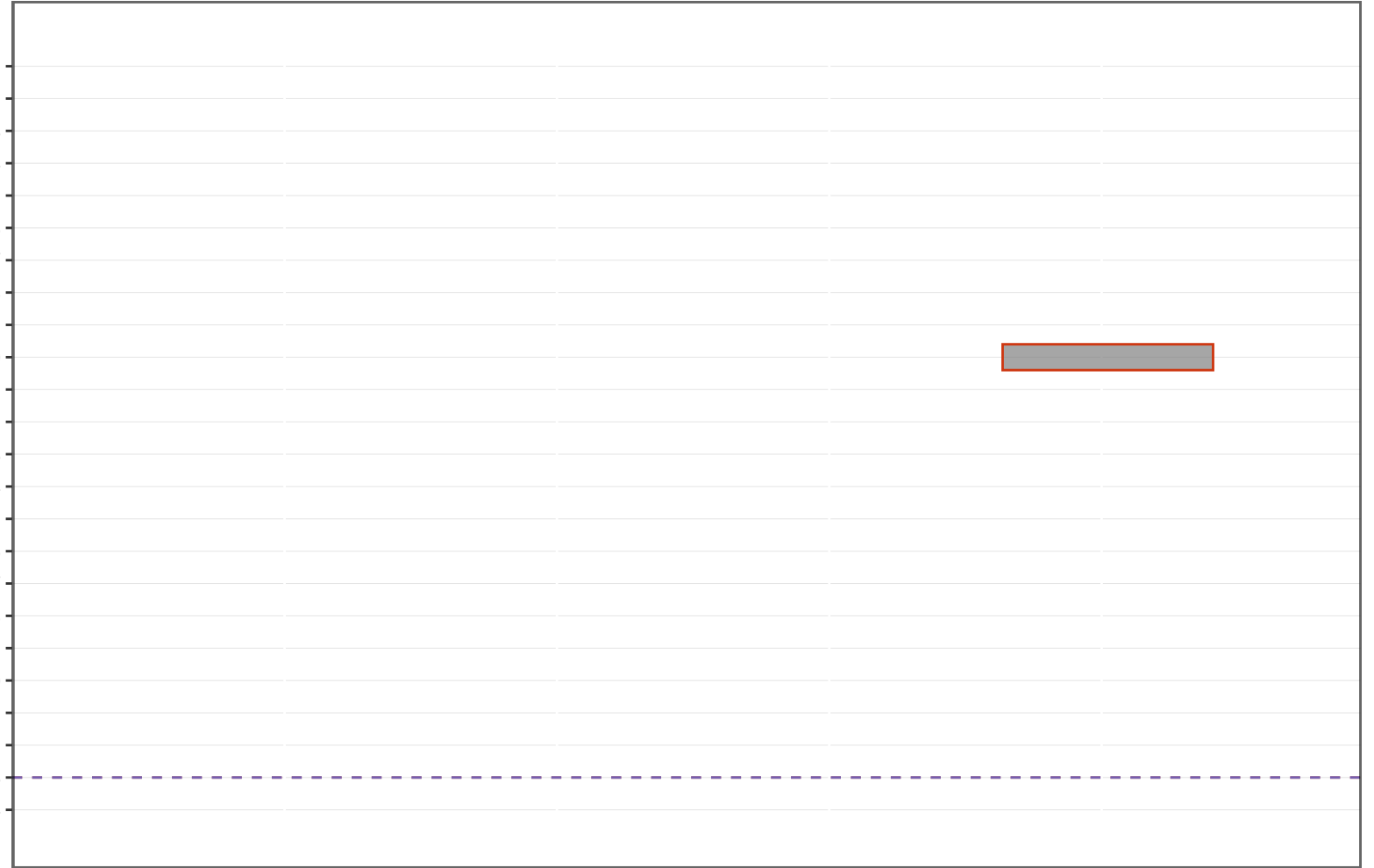
MW indication



Molecular weight



Gel Slice

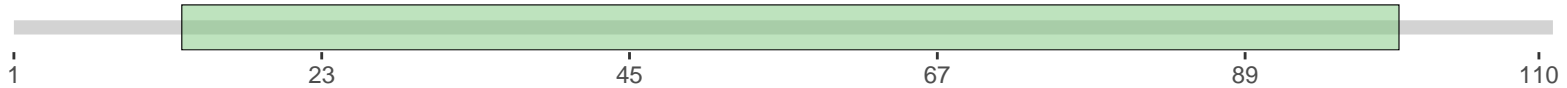


Protein length

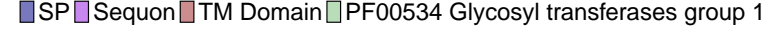


Peptide counts over 4 repeats

Pfam domains



Pfam Description

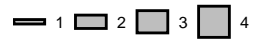


Protein sequence:

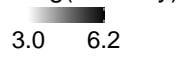
GVAKFNVPLAHMITAGADFMVPSRFEPFCGLGQLHAMRYGTVPICAGTGLVDTVKEGWIPYGSQR

NbL10g18840.1 nudix_hydrolase_3 [MW = 88.9 kDa]

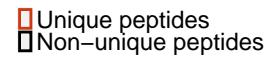
No. of times detected



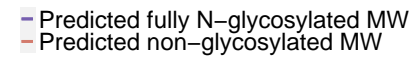
log(intensity)



Values from

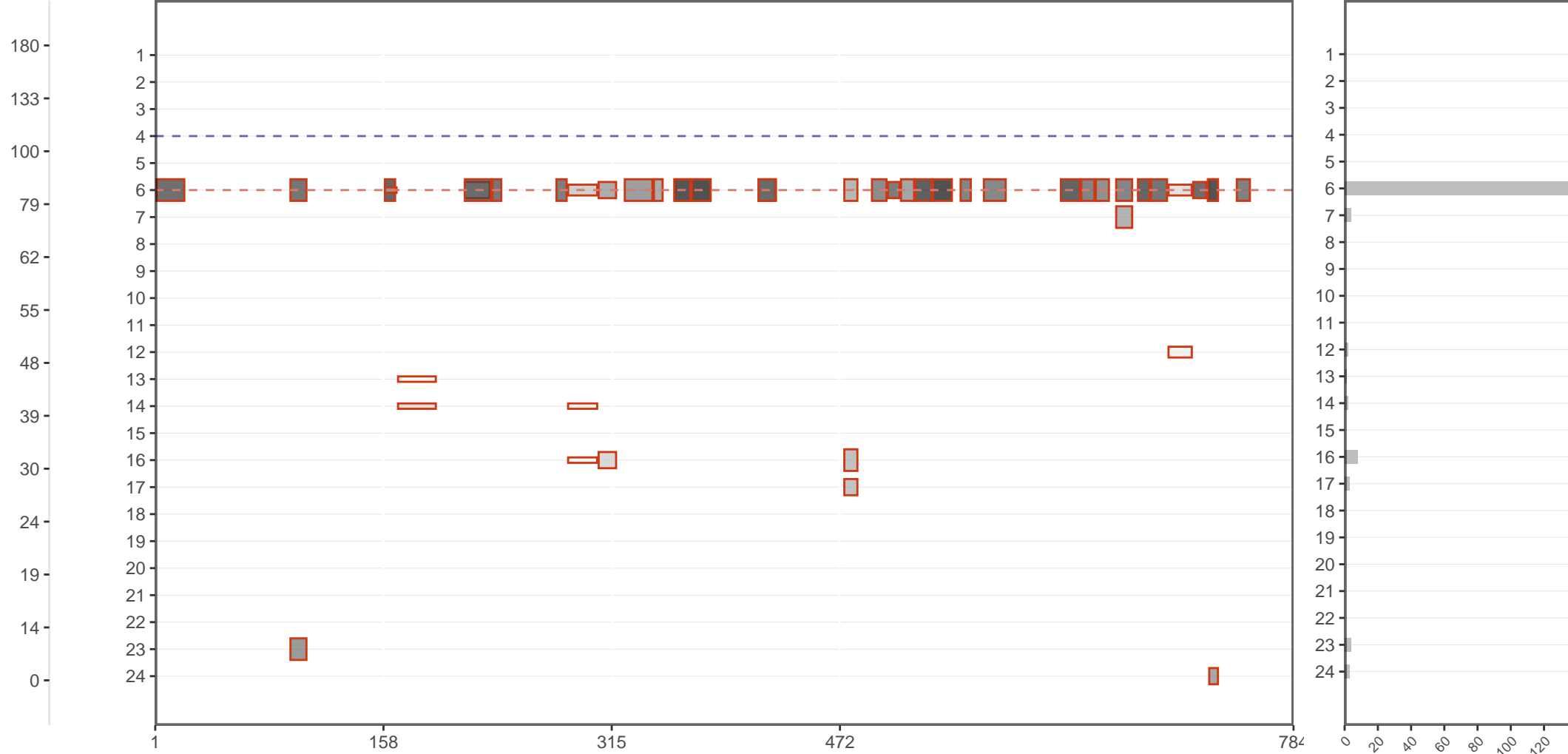


MW indication



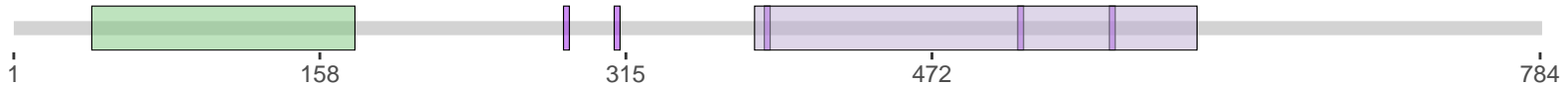
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

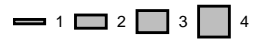


Protein sequence:

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NbL10g18810.1 ABC_transporter_E_family_member_2 [MW = 68.09 kDa]

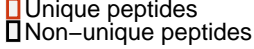
No. of times detected



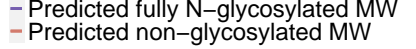
log(intensity)



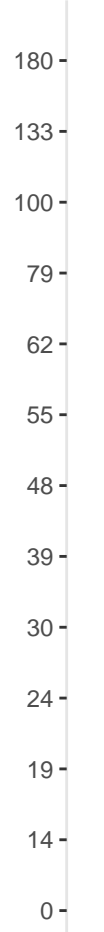
Values from



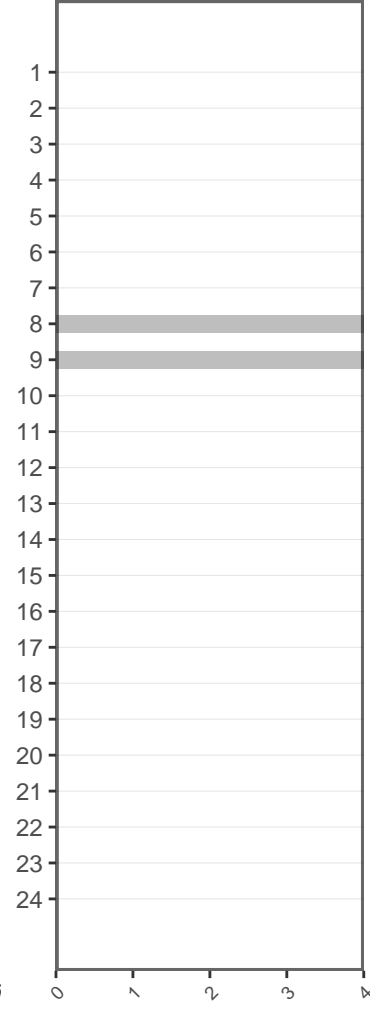
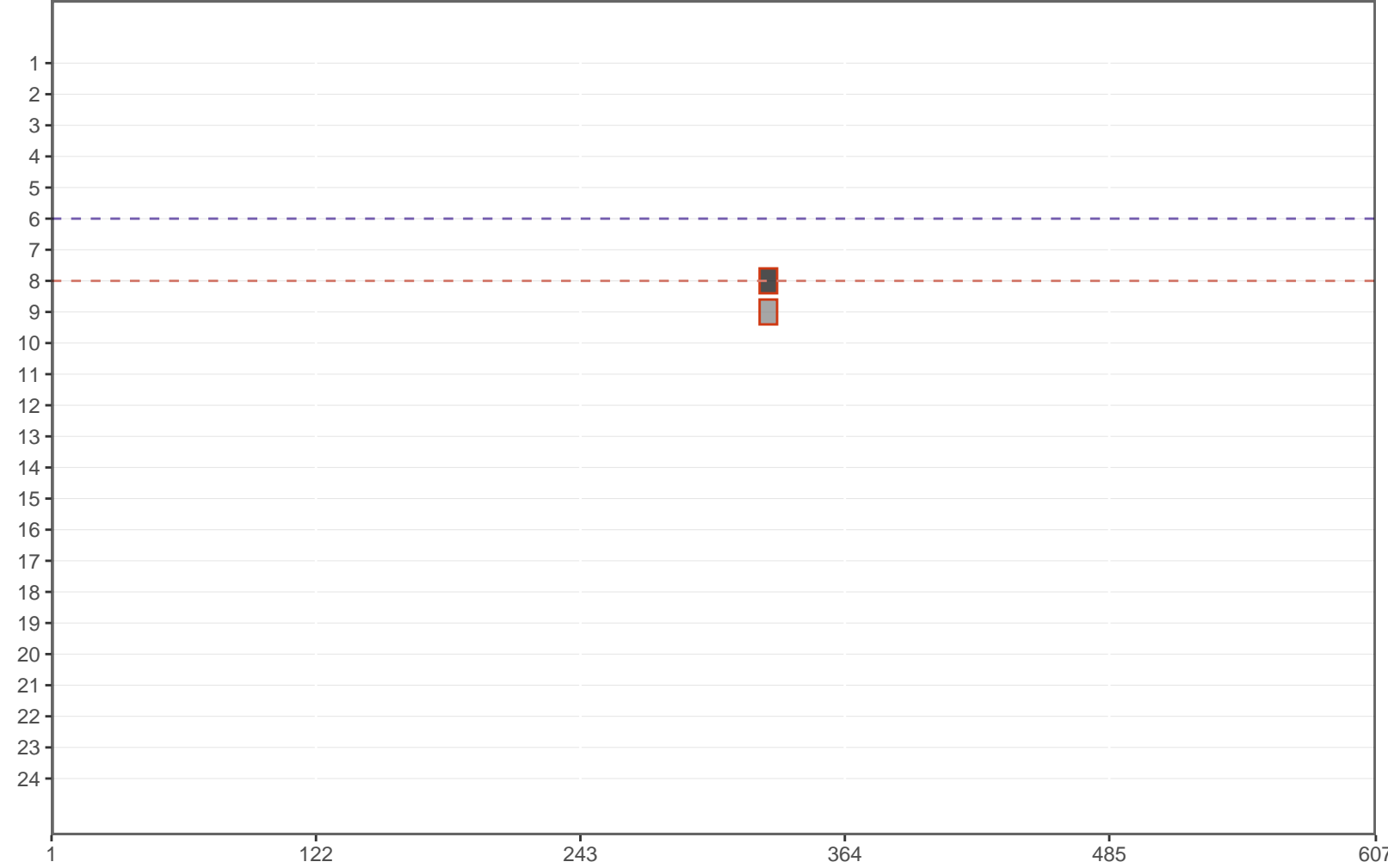
MW indication



Molecular weight



Gel Slice

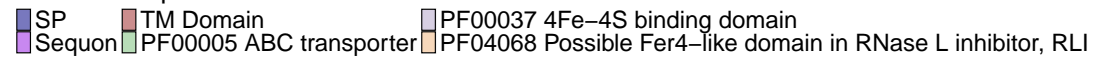


Protein length



Pfam domains

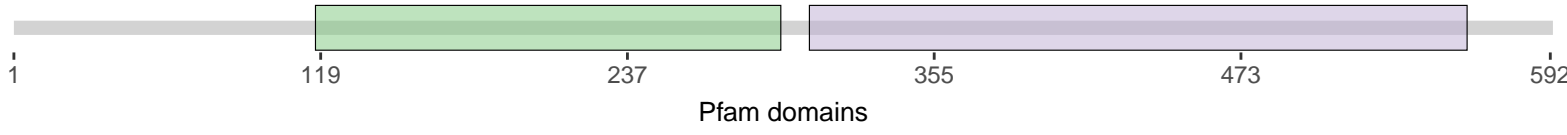
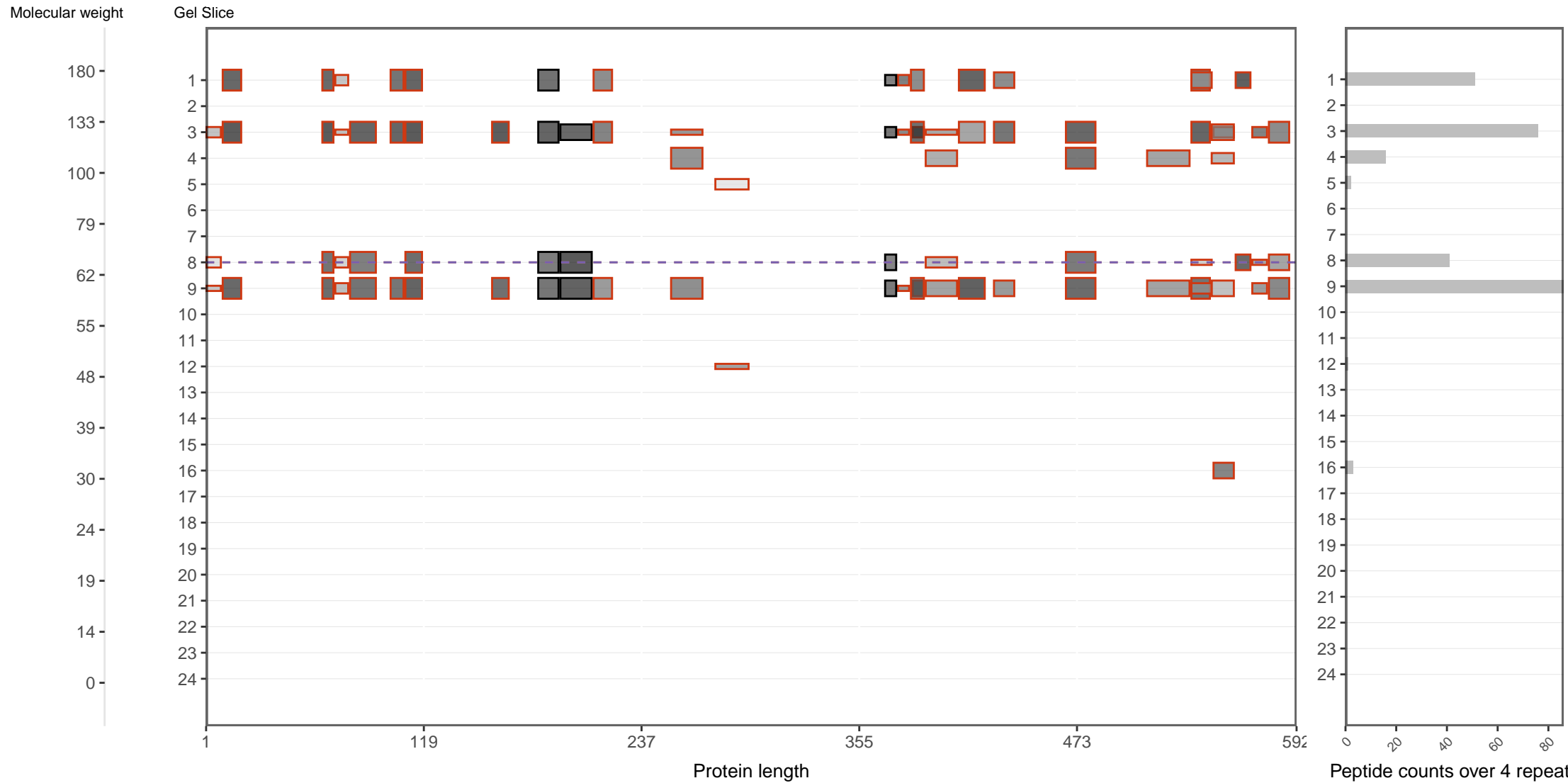
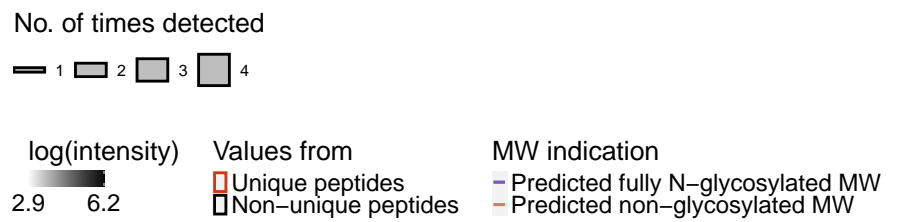
Pfam Description



Protein sequence:

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NbL10g18560.1 NADP-dependent_malic_enzyme-like [MW = 65.39 kDa]



Pfam Description

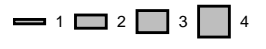
SP Sequon TM Domain PF00390 Malic enzyme, N-terminal domain PF03949 Malic enzyme, NAD binding domain

Protein sequence:

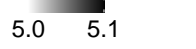
EDFANINAFELLAKYGTTHLVFNDDIGGTAVVLAGLIAGKLLGGSLADHTFLFLGAGEAGTGIAELIALEISIKTKGPEVETRRKHWLVDSKGLVSGRKEIIGSFKPKVAHEHPVNNLSDVAWIKGPTVLGTSVGVGRRTFTKEVIEAMASTNERPLMLALNPTSGAECTAEAAFTWSEGRAVFAAGSGPFPFSEYNGKLNIPGQANNNDYIFPFGFGLVMSGTRVHDDMLLAASEALAAQVTEEHFAKGMVYPPFADIRKISAHAAASWATKAVELGWATRLPRPENLVKYYAESI

NbL10g18390.1 polyphenol_oxidase_E_chloroplastic-like [MW = 67.64 kDa]

No. of times detected



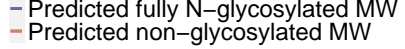
log(intensity)



Values from



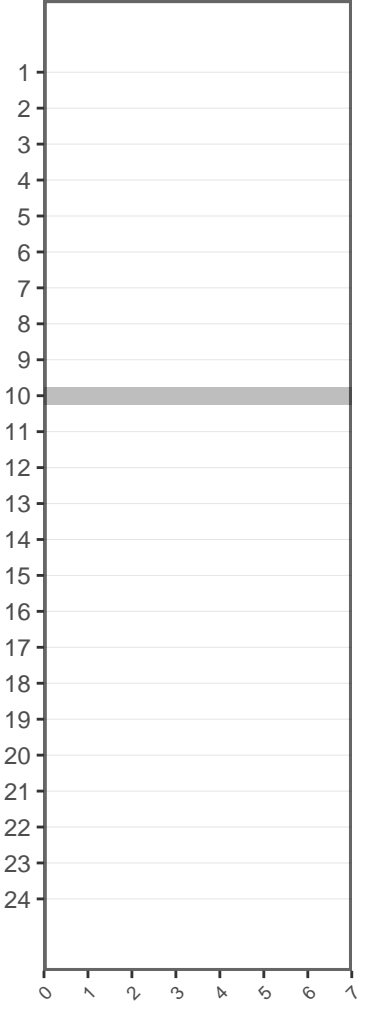
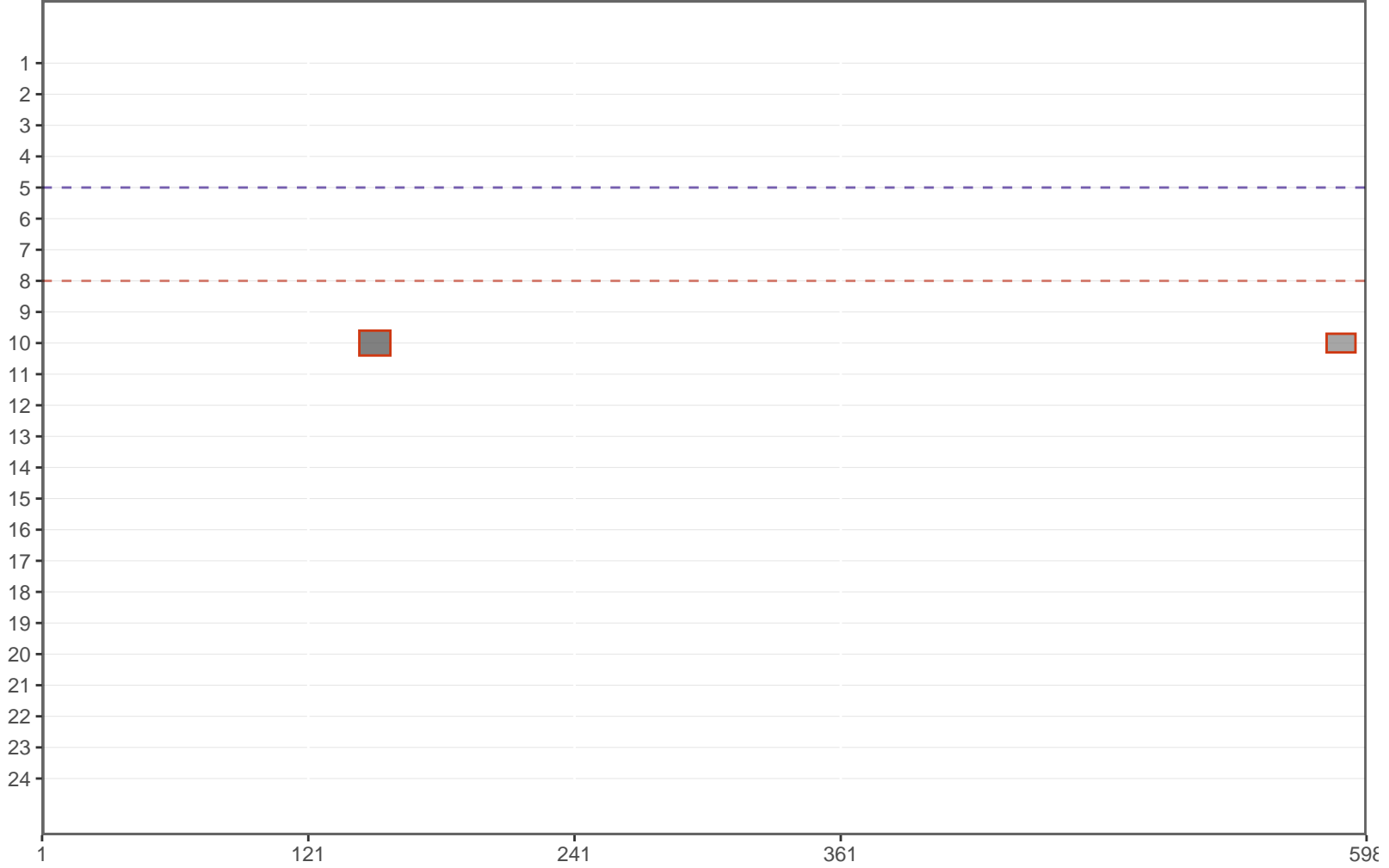
MW indication



Molecular weight

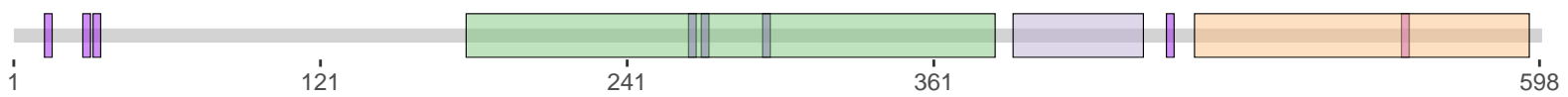


Gel Slice



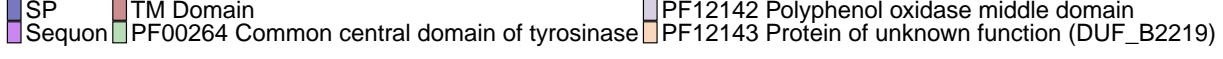
Protein length

Peptide counts over 4 repeats



Pfam domains

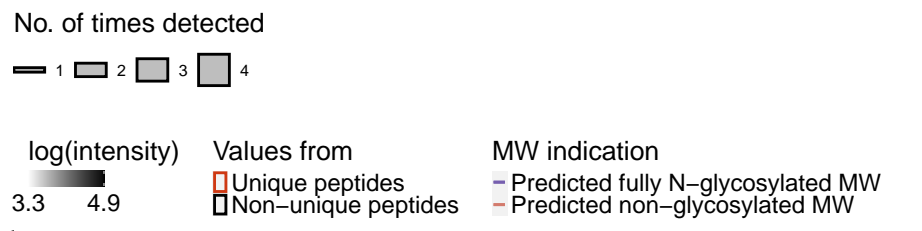
Pfam Description



Protein sequence:

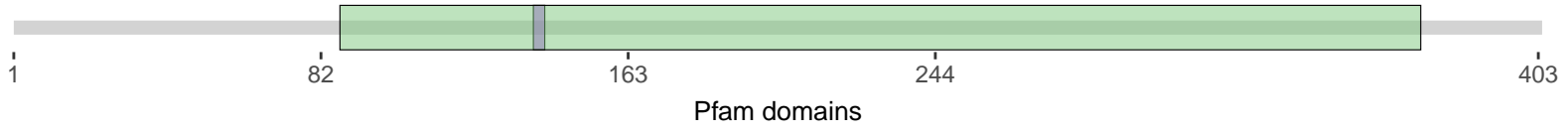
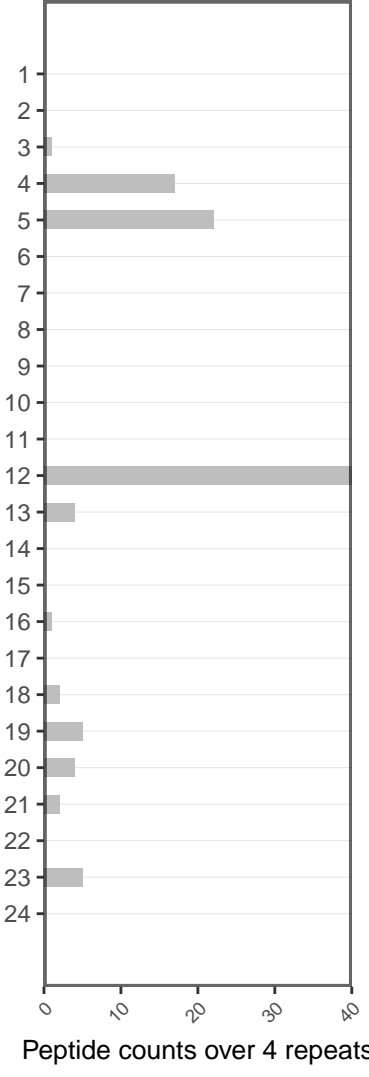
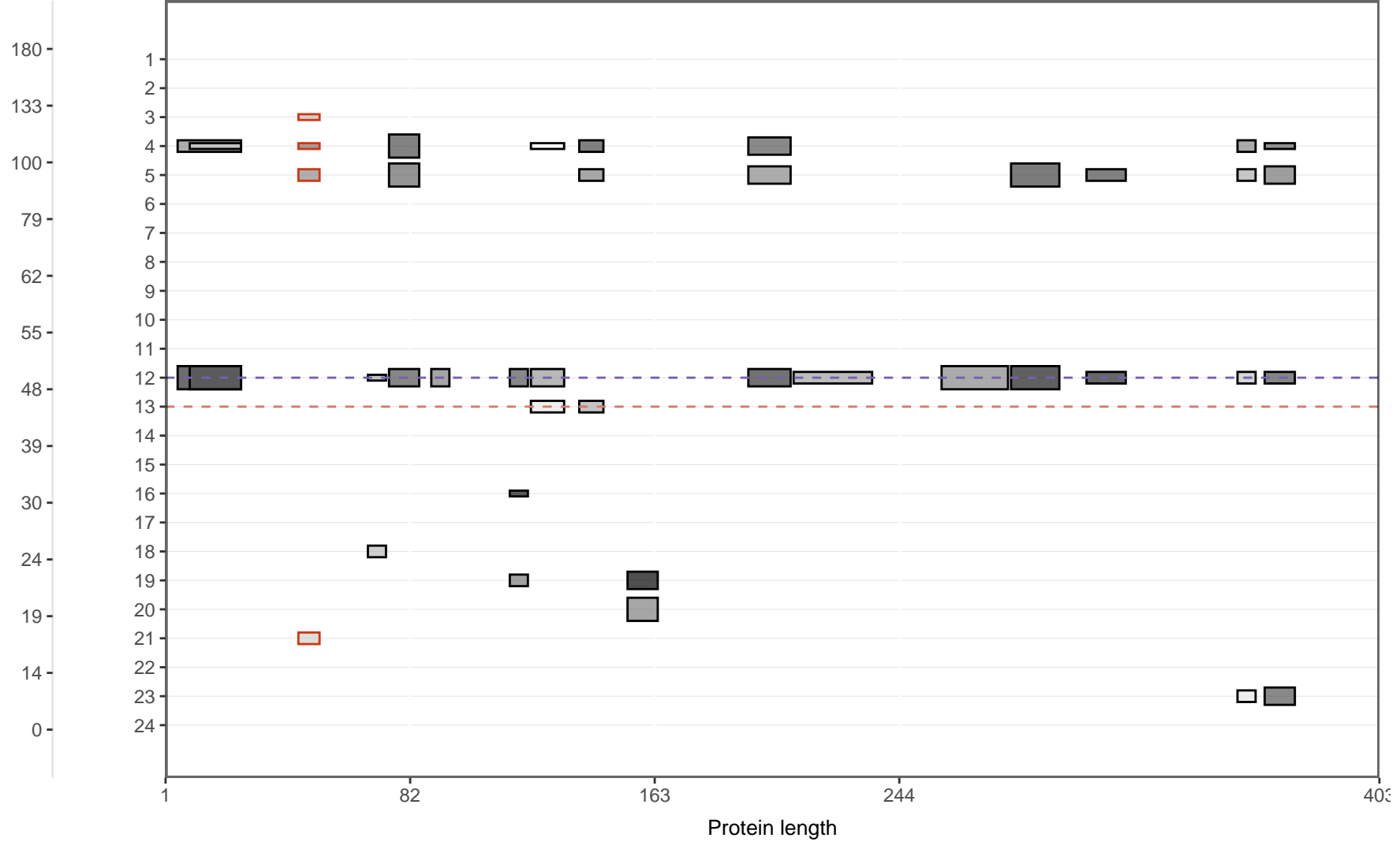
QLQDMNTNLTMYRDMITNAPCLLFFGGPVPVLTGTPSPGAGTENPHTPWHVVGSRPGENNWKHGEDMGNFYSAGLDPLFYSHHANVDRMWSSEWAKLGGKRRDLTKDWLNSSEFFFYDENRNPFRVVRDGLHSSKMGFDVAMPPTPWRNFKPTRKSNAGKYNLSSVPPAKVYFLSKLDRASFSDRPPSSGRTDGEKNEQEEMLTFNNKYDDGKYRFDFVFNVDKTVNADELDAEYAGVYTSPLPHVHGDNVSHVTSVTFQLATELLEDIGLEDEDTIATV

NbL10g18300.1 tryptophan--tRNA_ligase_cytoplasmic [MW = 45.92 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF00579 tRNA synthetases class I (W and Y)

Protein sequence:

ICVITYNKLYGIFGFGEDHGKVSFPPVQAVPSPSPFHLFSGNDNIRLIPCAIDQDPYFRMTRDVAFRIGYHKPALESFFPMLGGENGKMSAGDPSNAHYVDSAKEIKNKIRYAFSGGQDSLEHRKYGANLEVDIPKYLGFLLDDAELERIREEYGGRMALGTEVKKRLTEVLTDLVERHRRARALVDEMVDAFMVRPLPNMFM

NbL10g18290.1 glucan_endo-13-beta-glucosidase_5-like [MW - SP = 50.16 kDa]

No. of times detected



log(intensity)



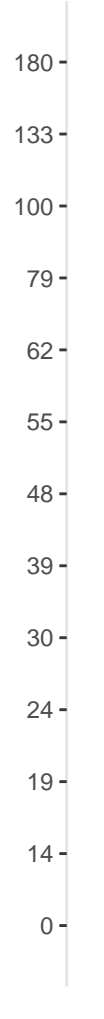
Values from



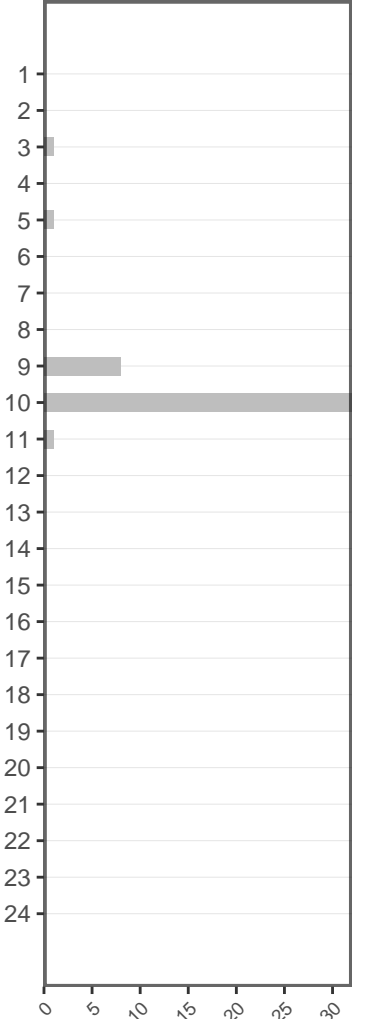
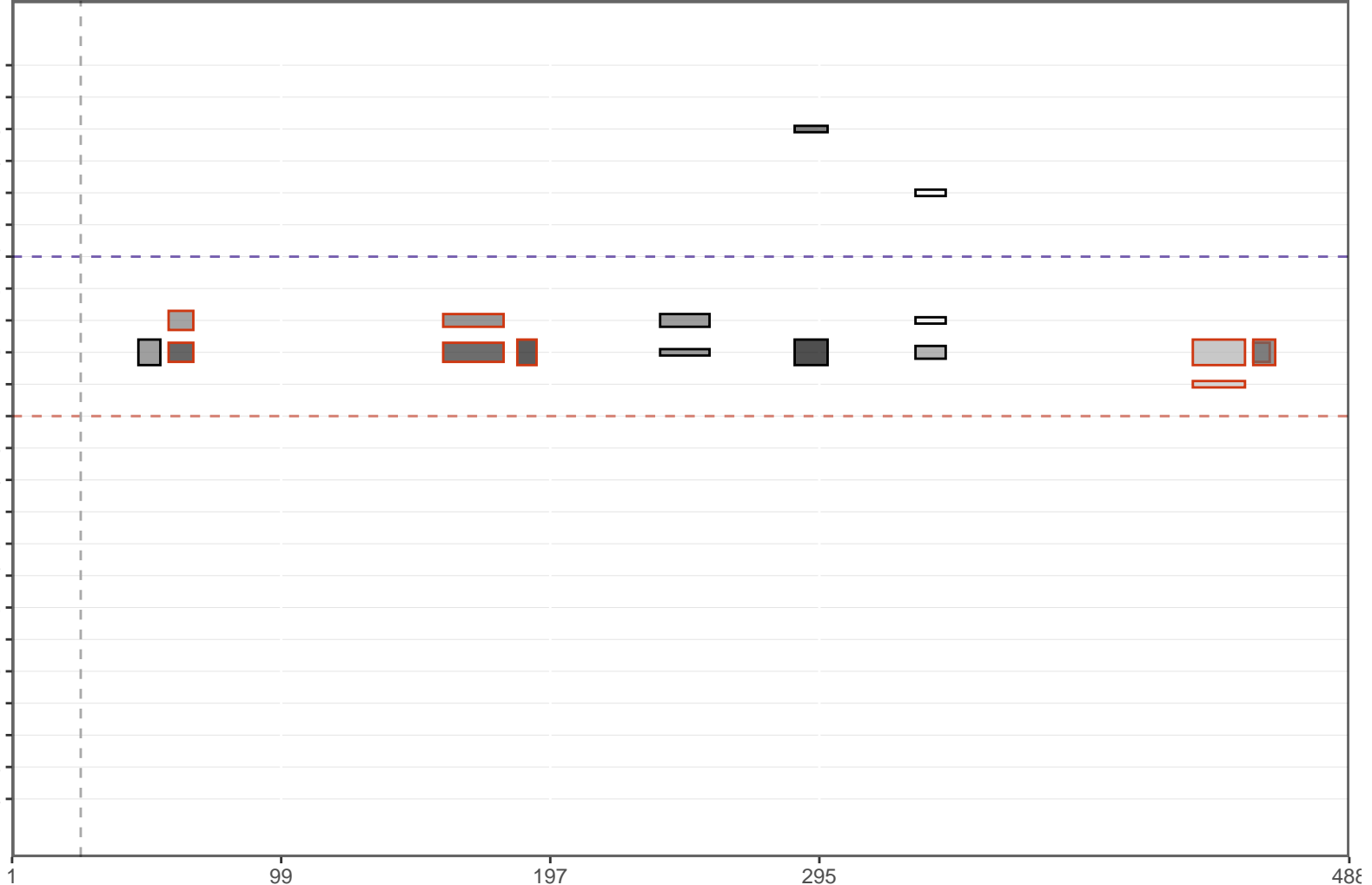
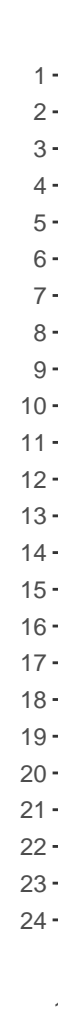
MW indication



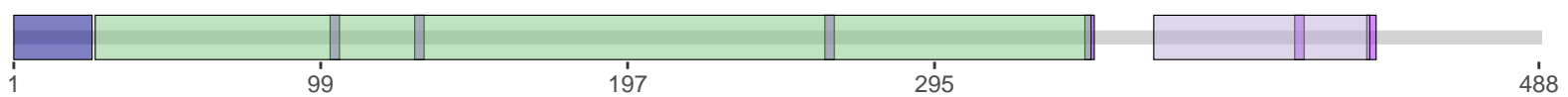
Molecular weight



Gel Slice

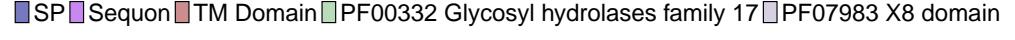


Protein length



Pfam domains

Pfam Description



Protein sequence:

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NbL10g17910.1 phospholipase_D_Z-like [MW - SP = 54.64 kDa]

No. of times detected



log(intensity)



Values from



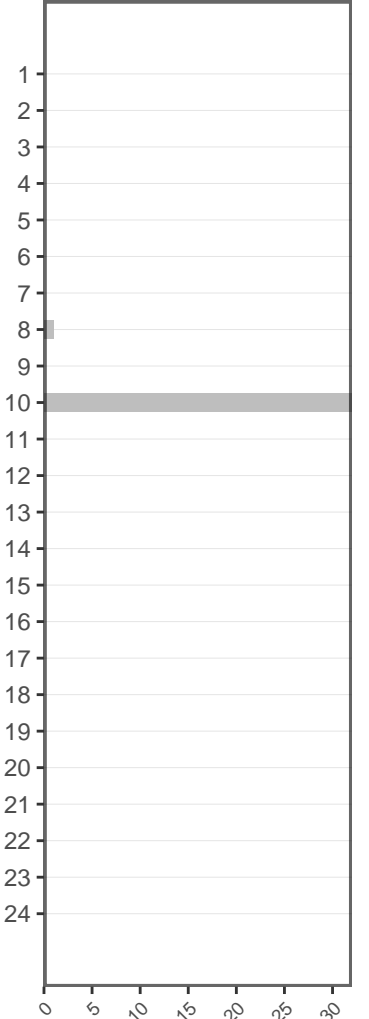
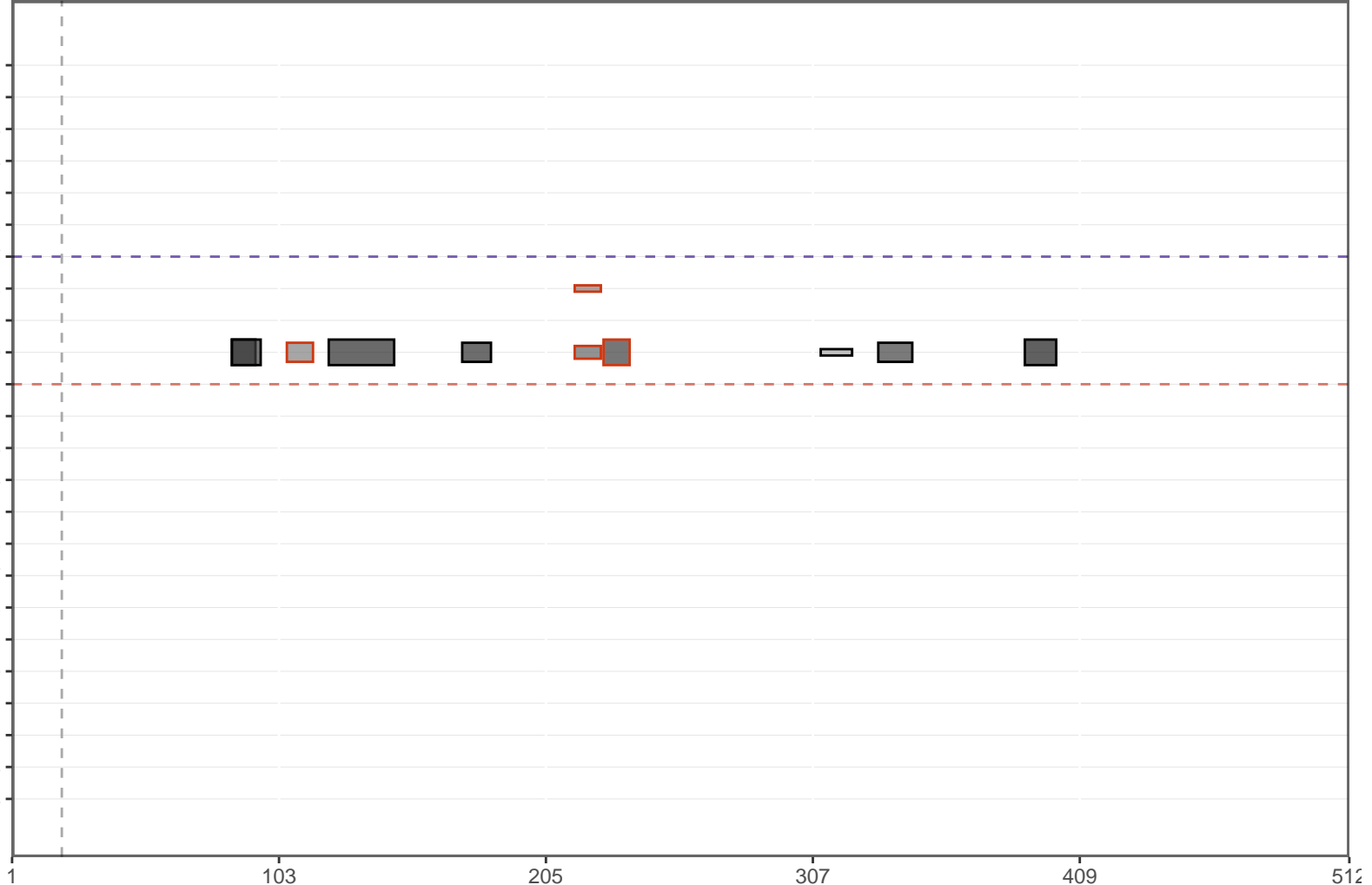
MW indication



Molecular weight



Gel Slice



Protein length

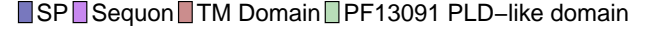


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

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NbL10g17900.1 tocopherol_cyclase_chloroplastic [MW = 58.96 kDa]

No. of times detected



log(intensity)



Values from



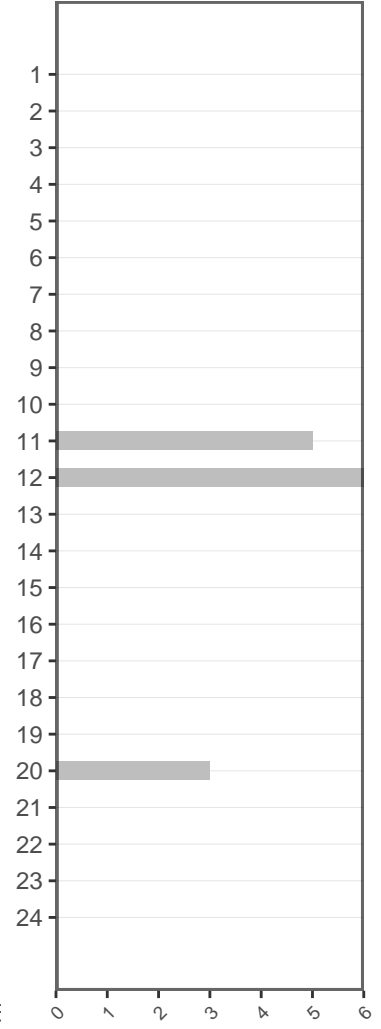
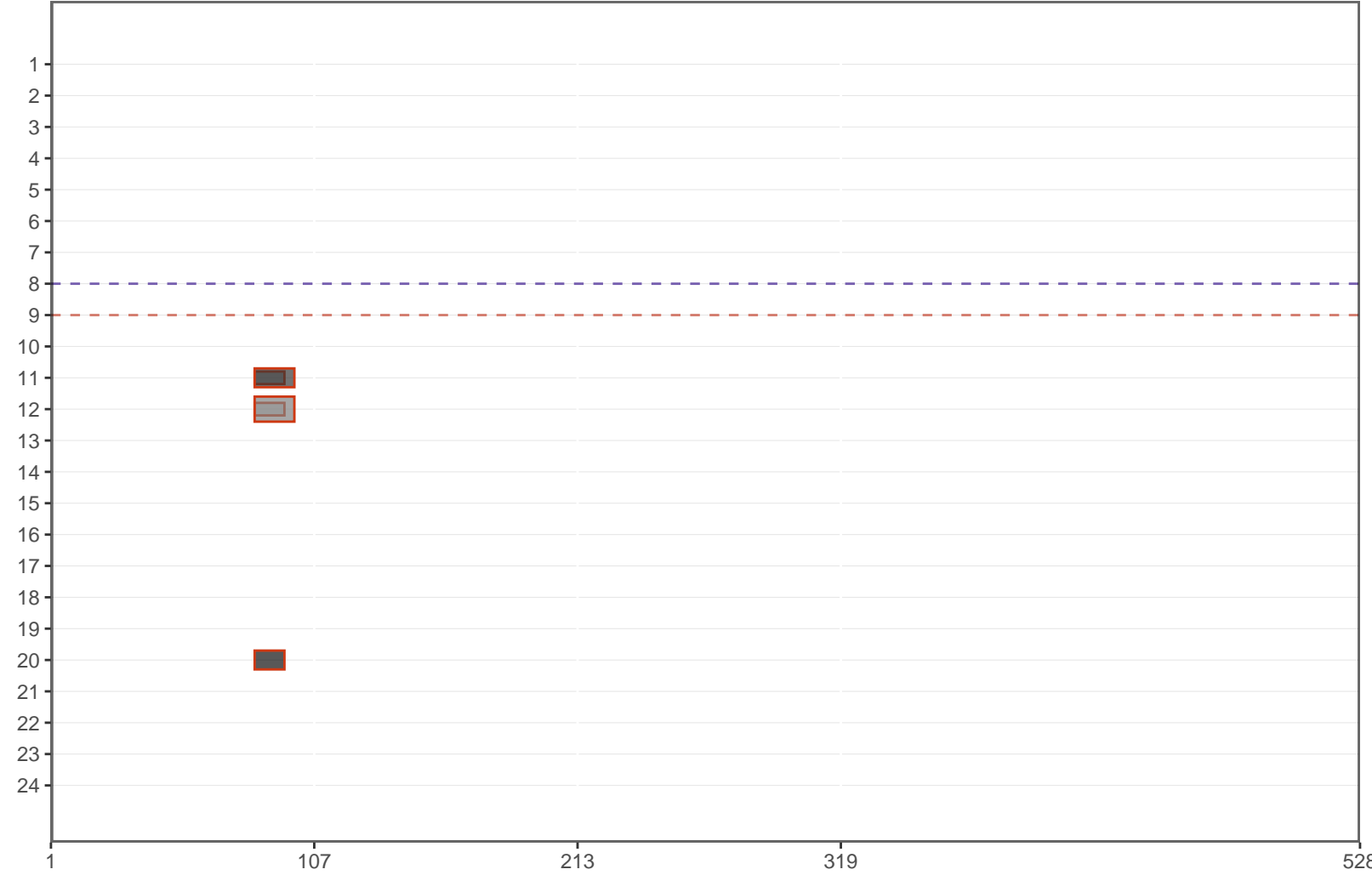
MW indication



Molecular weight



Gel Slice

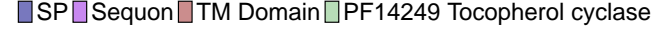


Protein length



Pfam domains

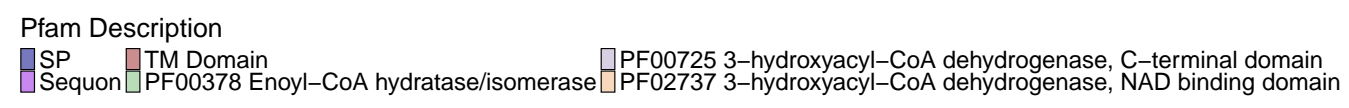
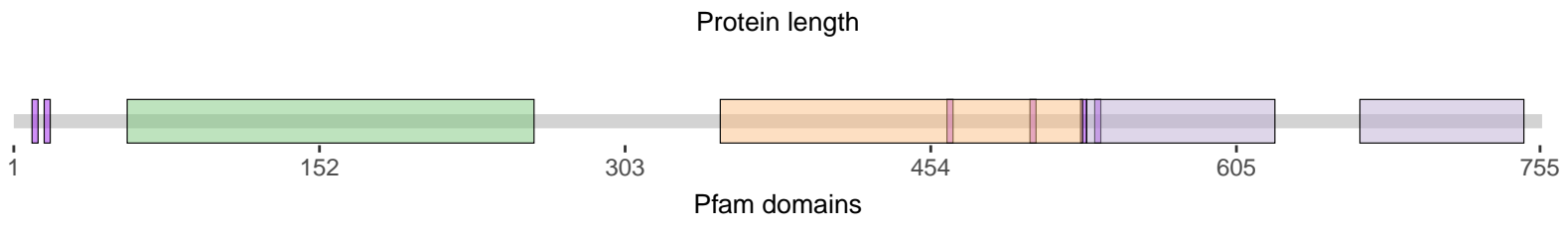
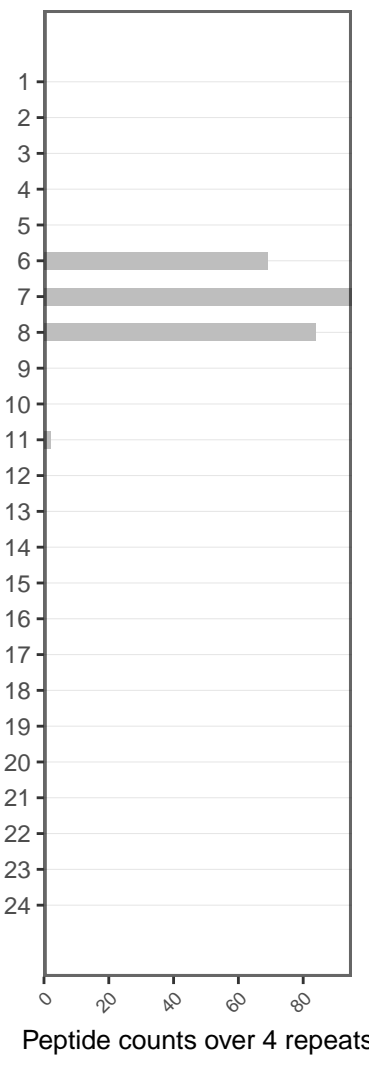
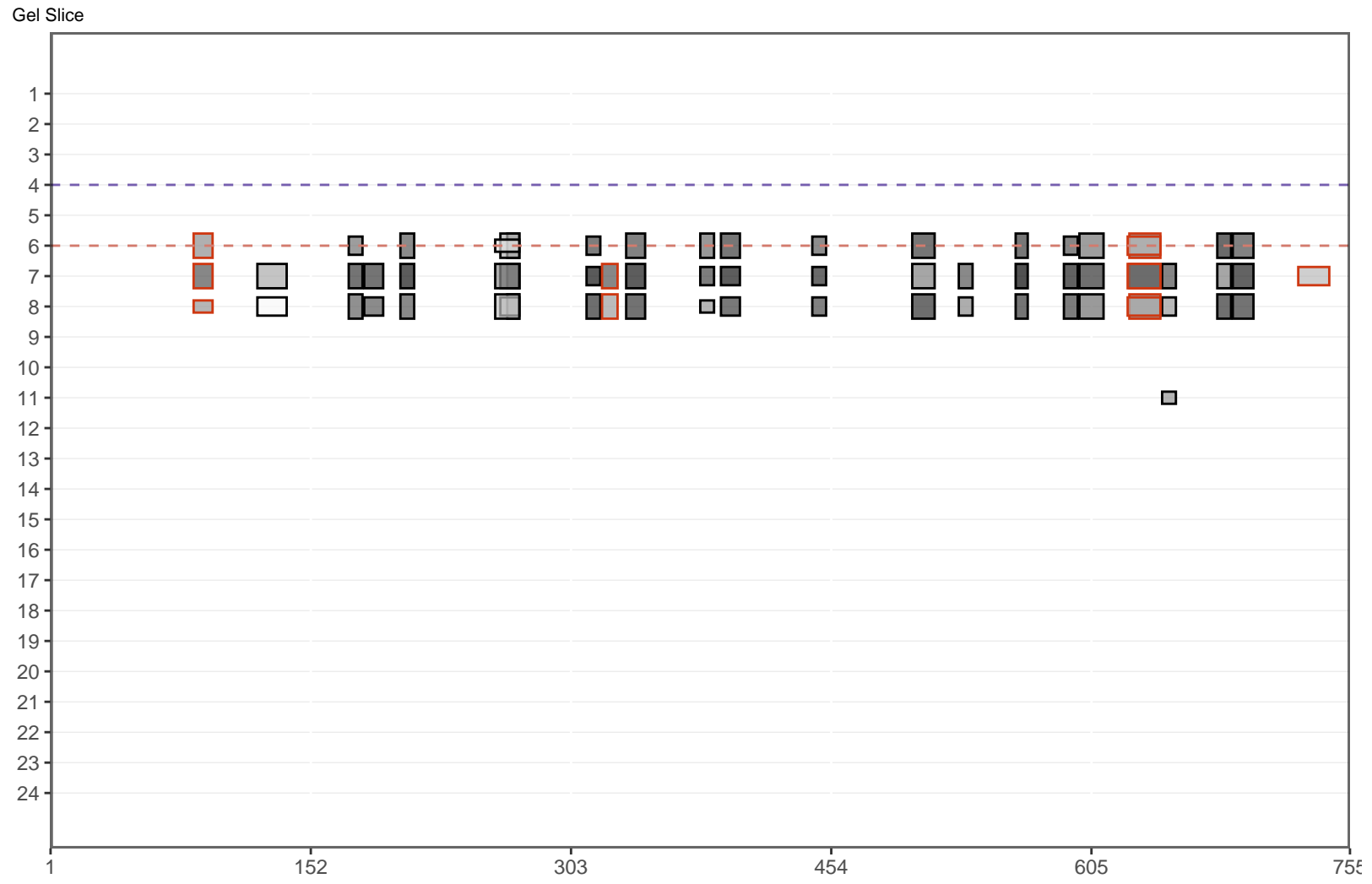
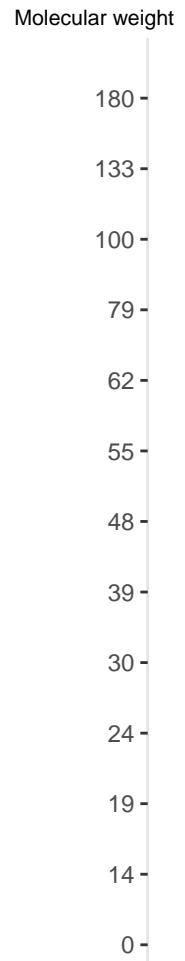
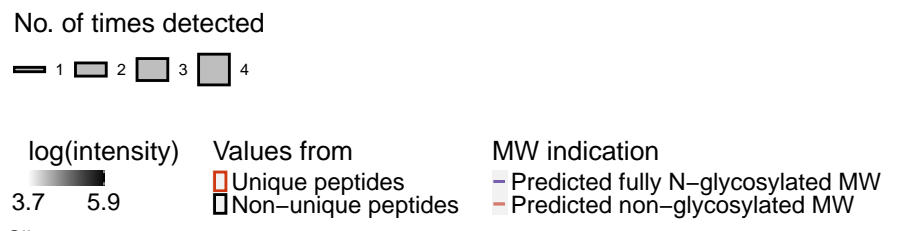
Pfam Description



Protein sequence:

SGRTDYTEIVETASWEYSMPRPVGGWGNKSGKSTAGWPAAPFVPEPHWQKMAAGLSTGWMEWDGQRVEFGNAPVSEKNWGGAFPRKRFWVGGSVFEGAIGDALTAGGRLQLPGLSGTFENALIGHYGGVFEFVFNWACVSWEIAQWGWKWHFGENETHVELEATAEDPGTTLRAPTDENGLAPAGRDTOFGDLRLRUIWERKSNKSGKGVLDVTSNMAAGLEVGGGPWFNTWVKGAQMPKWRANVPELDNAIFGLTFLKPPGL*

NbL10g17850.1 peroxisomal_fatty_acid_beta-oxidation_multifunctional_protein_AIM1-like [MW = 82.3 kDa]



Protein sequence:
 TALMSNMVYLLKENHEYLKAKVSEANLGGVITRQGLNGDKMKRTELSLKGTELDYEDLKDNDMVEANNEVSLKGSFEDIEKVGSSDDIFASNTSTLSLDVIGERTSSGDRLLGHLSFPAHMTLVEVNRTEENTSPQVIVDVRFTKTKMKKVPVWKNCTGFVANRSFFPMQGFOLLANLGVDFRVRVITEFGMLRGPFLQGLDLSGQIFLAGVKEFWAEPDRAFQSLVQLMVENGREGKKNKGYYTYKKGSKPEADHSVQVVEESMRFTNAPFGKPSVTDDE

NbL10g17840.1 peroxisomal_fatty_acid_beta-oxidation_multifunctional_protein-like [MW = 28.45 kDa]

No. of times detected



log(intensity)



Values from



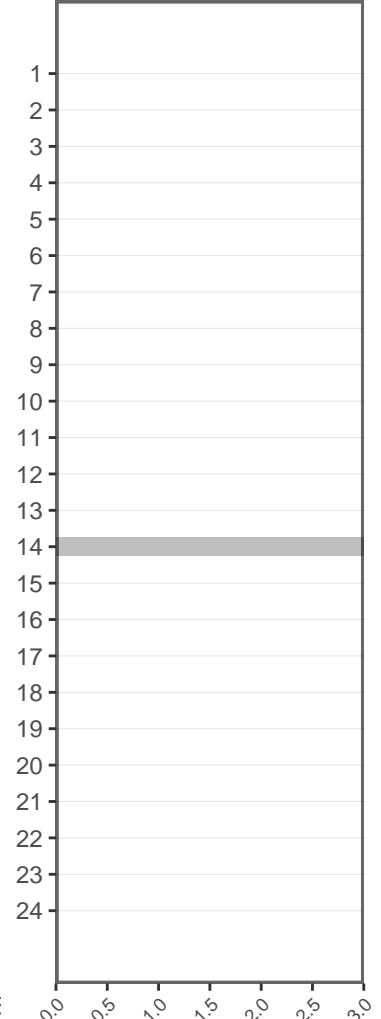
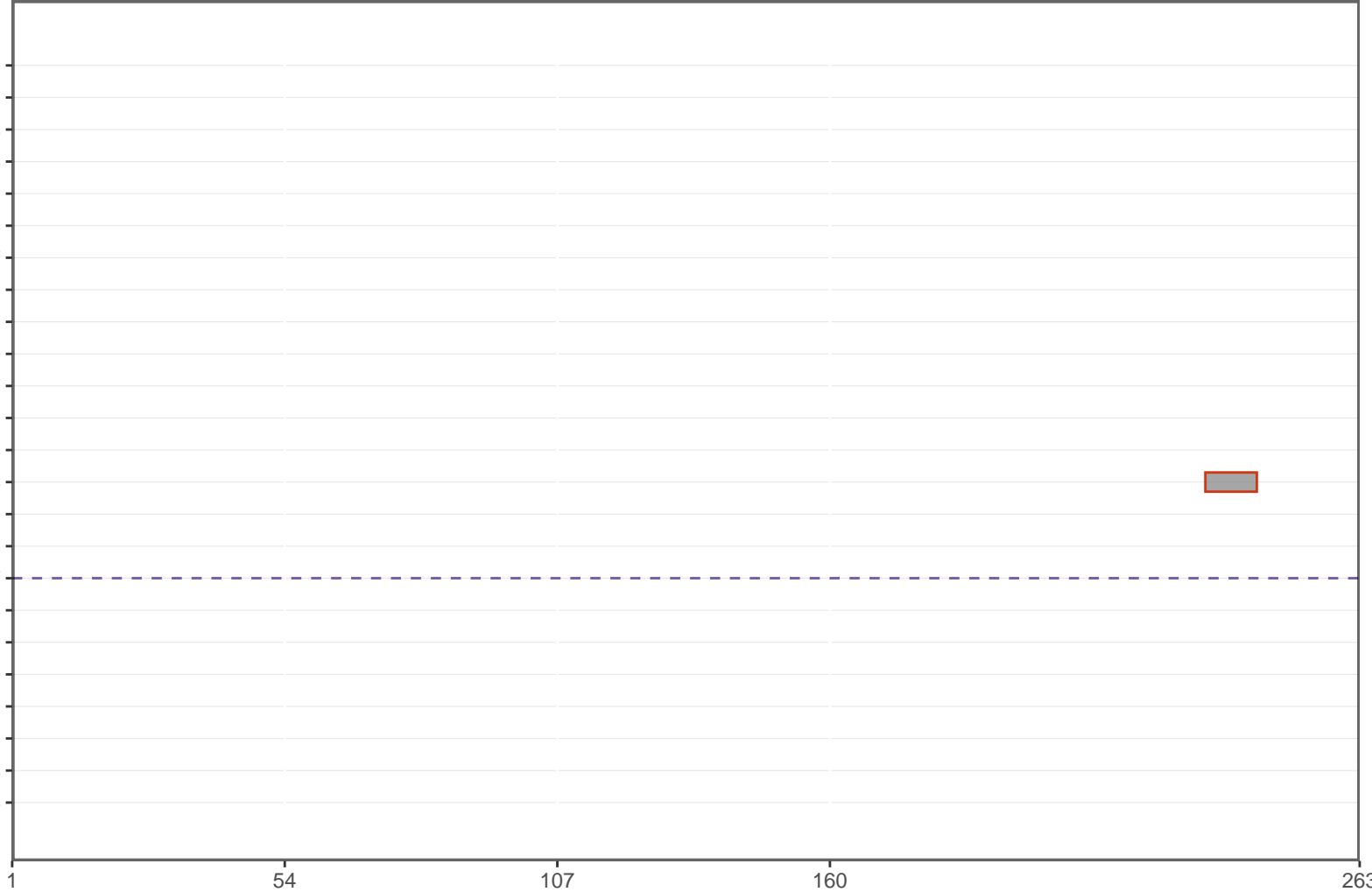
MW indication



Molecular weight



Gel Slice



Protein length

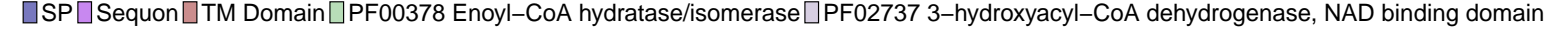


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KTSPSPHYKACLDWEVIGISGGVAGVLEKEDKVLRELVLKSKSRALLHYVFAERATSKVPGIFDQGLEHRKIEKVAWIGGGLMGGIATLHSFVHLVLEKIDYNGLQKLSKVEVNIQSLVKGSHLVEEKMKAFSEKVL

NbL10g17810.1 eukaryotic_translation_initiation_factor_3_subunit_L-like [MW = 65.69 kDa]

No. of times detected



log(intensity)



Values from



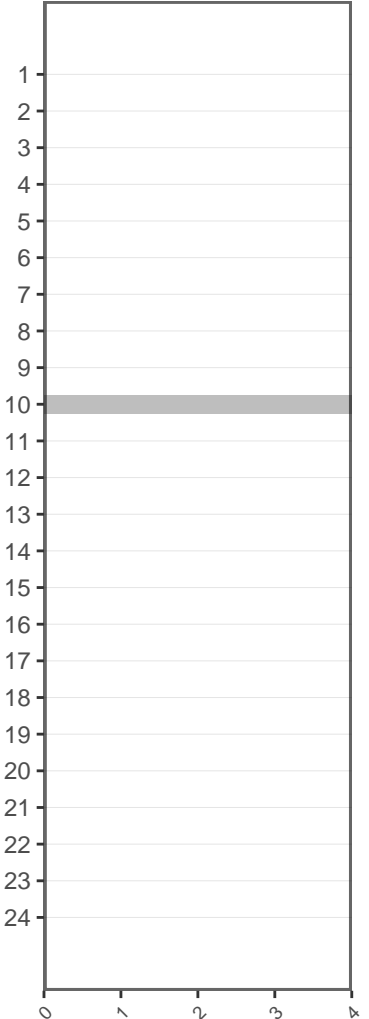
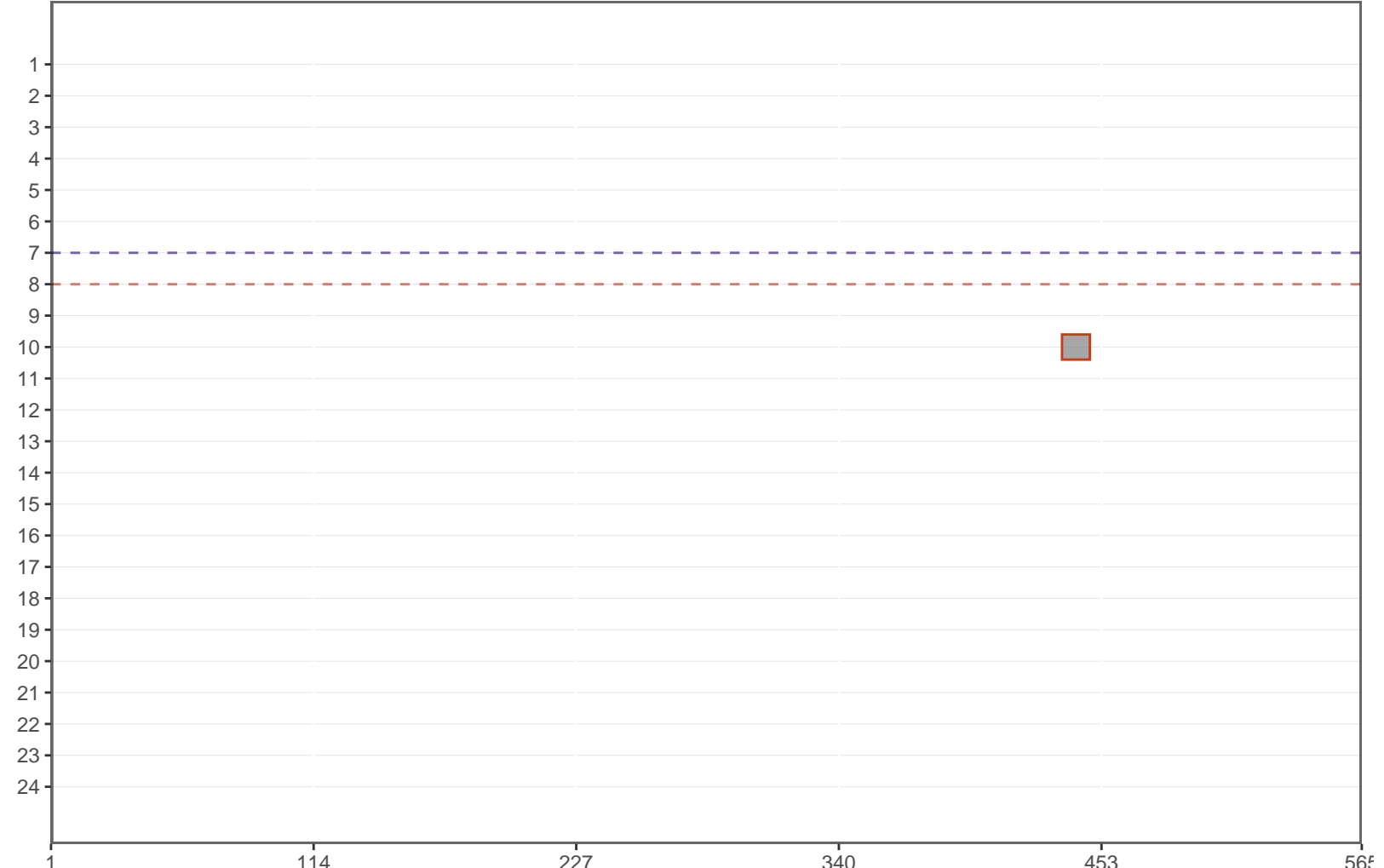
MW indication



Molecular weight



Gel Slice

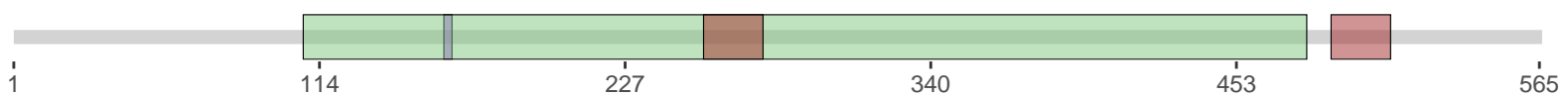


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

TSVIGSHITTYHYGFANLMLRRYVDAGEFNKLLVYKTKGYNHOKSPQYEQILKKNQGMVALLAISELCPQLKLVETVNSGLREKYGEMARMGRHYDDEAFALYDELFSYACPKFITSPAPFEEPLNYYNGDDVRLQKLFLEVKQDGLLAGVTRFLKVVSTISLGLKLANVMSVDEPTLRLTLTYGKTHAVDSDGKITNADVDFYDEIVRNTGTYVNIWFFVYLLLSLGNGLTTFKIKNLQDIVEVWVFLVGLGQDNFLBSIGVNRLLASMTFVQEQMAYVAFS*

NbL10g17780.1 la_protein_1 [MW = 51.53 kDa]

No. of times detected



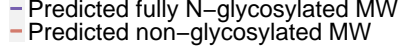
log(intensity)



Values from



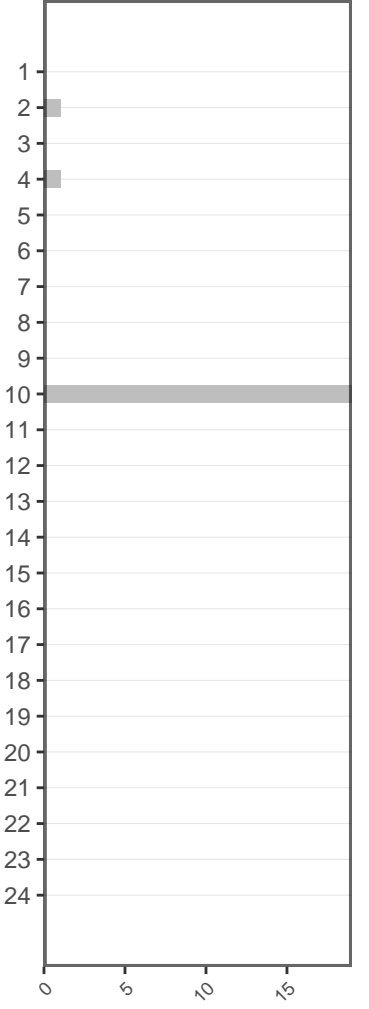
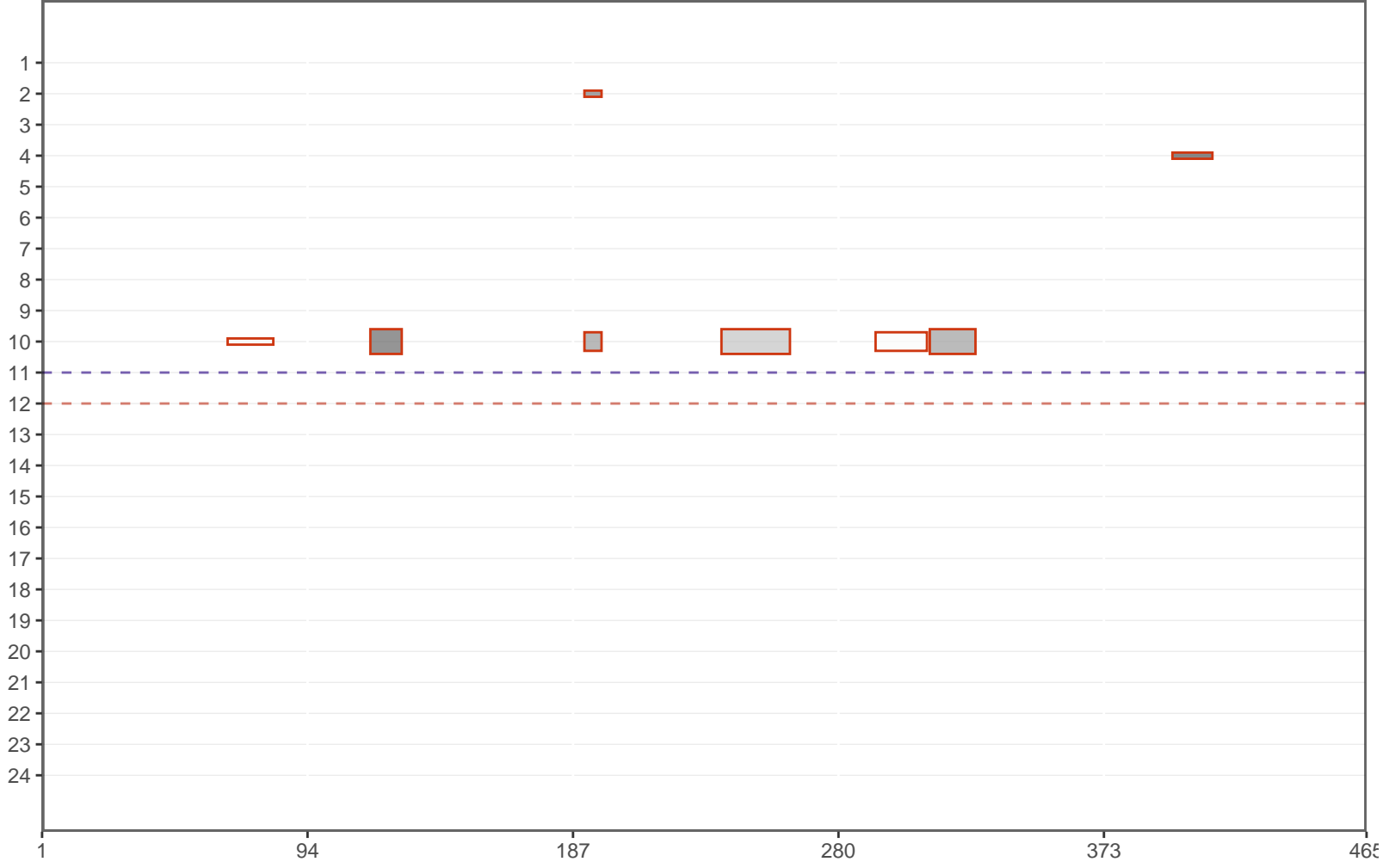
MW indication



Molecular weight



Gel Slice

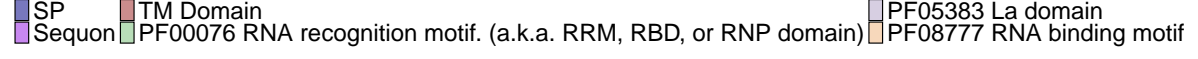


Protein length



Pfam domains

Pfam Description



Protein sequence:

DYPKGLIAFLMKKKKSTEGNGNHTAAEASAPETEGNKETTKDINVEVTEESVSEDKDEDDNNEKGDGKADNNGSGGETVYHNPEAVEKMGDSPTFEEDDGPAAEKLISAACKGNMDVVMREDLKGVFQKGTWVFDFTIGSESGYRIFENEGAAQKAAAGVLAEEGGITVQNYIAALDPVTGDMEKEVWEMFRNYQDKRRDFNKNKNGRGRYNRGGKHSRPRGNDLGGPRNFKQKVRT

NbL10g17770.1 coiled-coil_domain-containing_protein_25 [MW = 25.26 kDa]

No. of times detected



log(intensity)



Values from



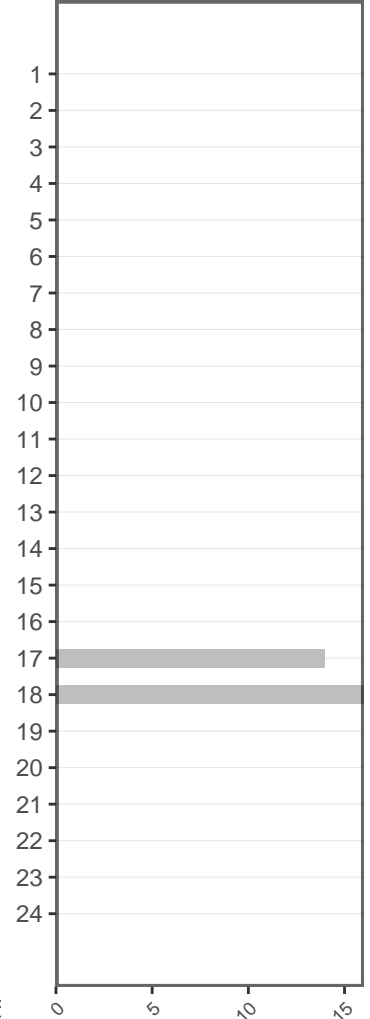
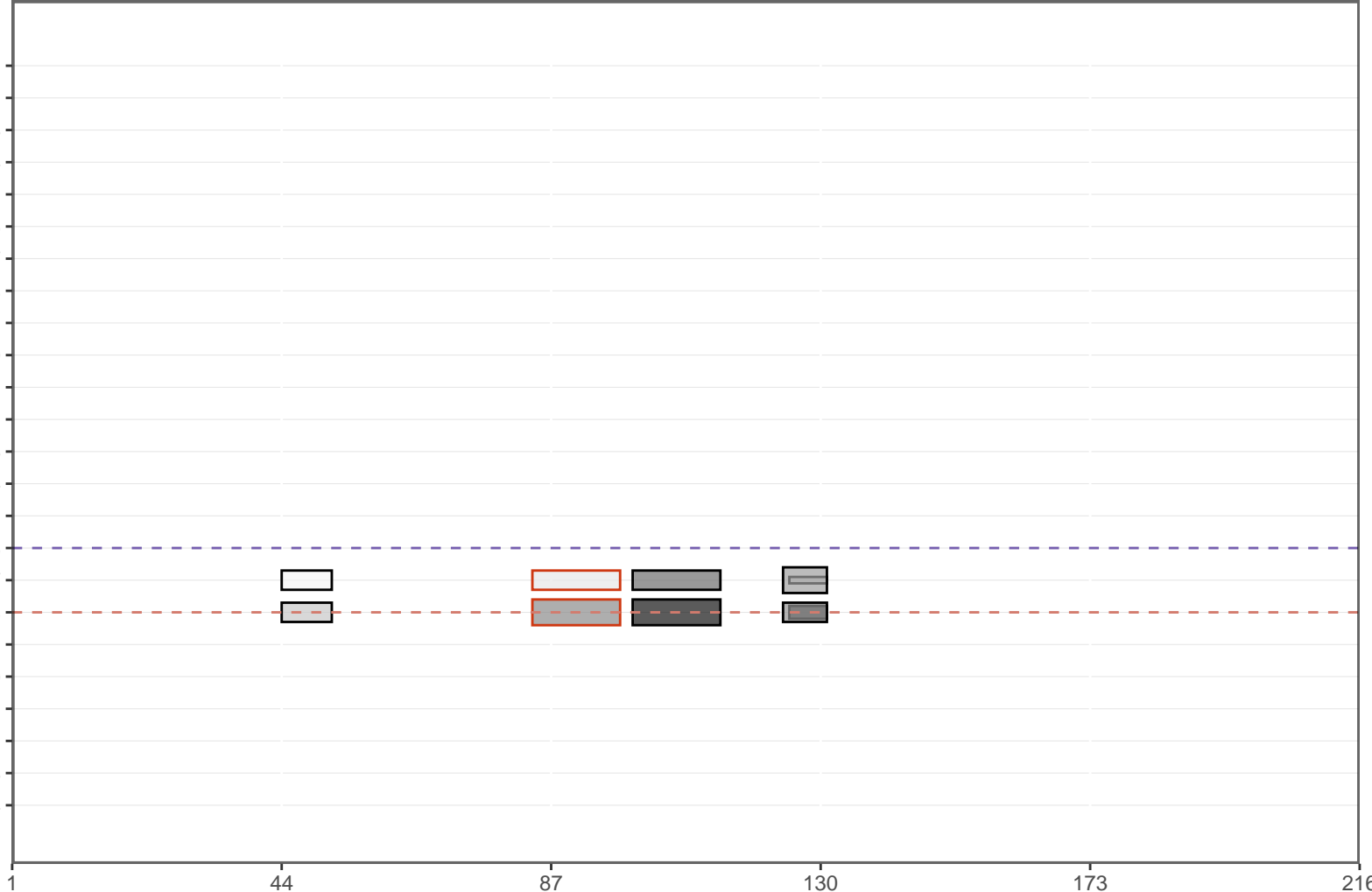
MW indication



Molecular weight

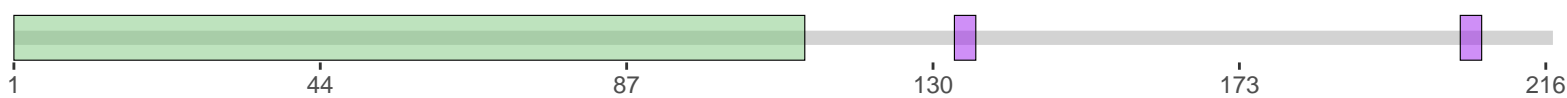


Gel Slice



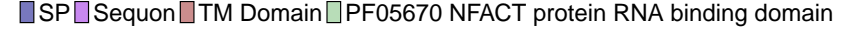
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LLKKTASMDVGVQVSPHNPKMVRTVYKVEKRINEIVNRLNRTYKPKDUAEREAANAAERARFKDQLREKKRREEMDRLEKERQAEIRGKYNLMVADKMTSNKDIASNTKSLGLEEDFM

NbL10g17660.1 uncharacterized_LOC109213855 [MW = 11.92 kDa]

No. of times detected



log(intensity)



Values from



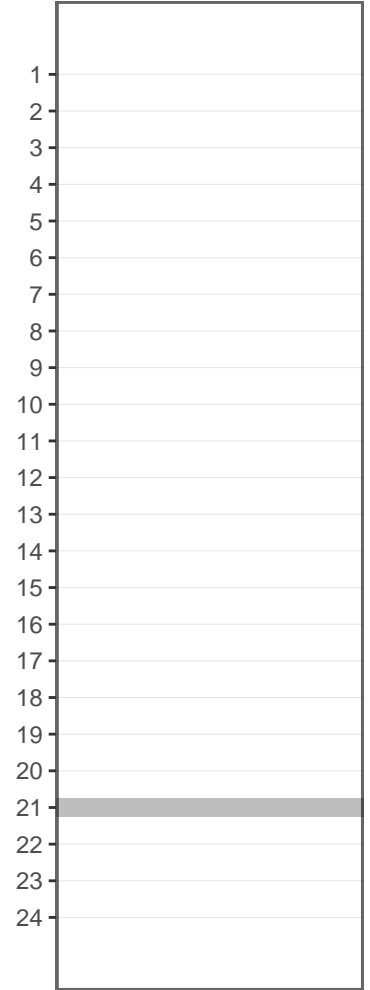
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MAVPAARLRKCMCGSLFGSPFFLIFAGWVWYRIFQGWKSMYLVQVSLVGFGLKGLSLFK

NbL10g17630.1 BURP_domain_protein_RD22 [MW – SP = 37.03 kDa]

No. of times detected



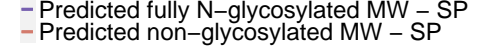
log(intensity)



Values from



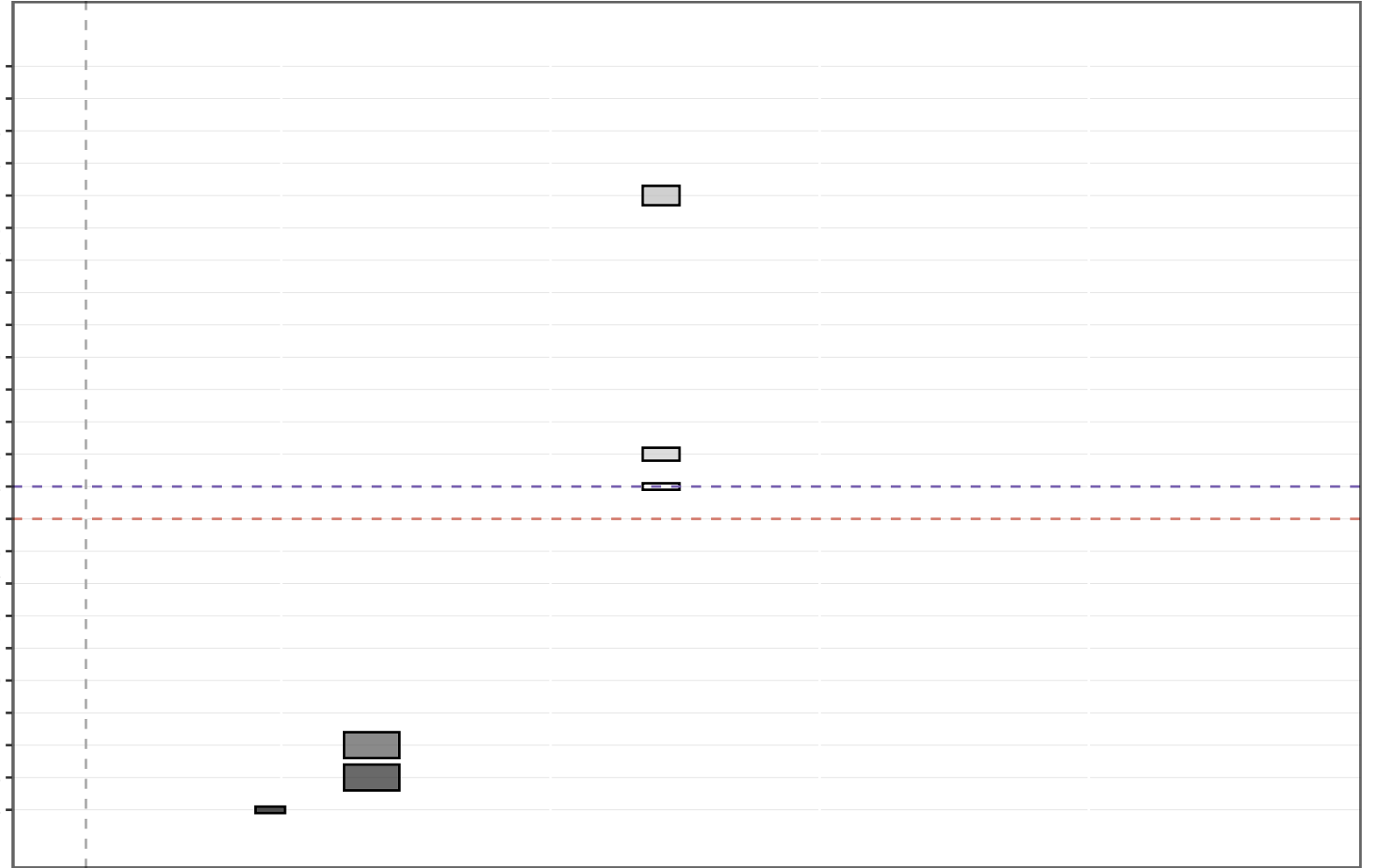
MW indication



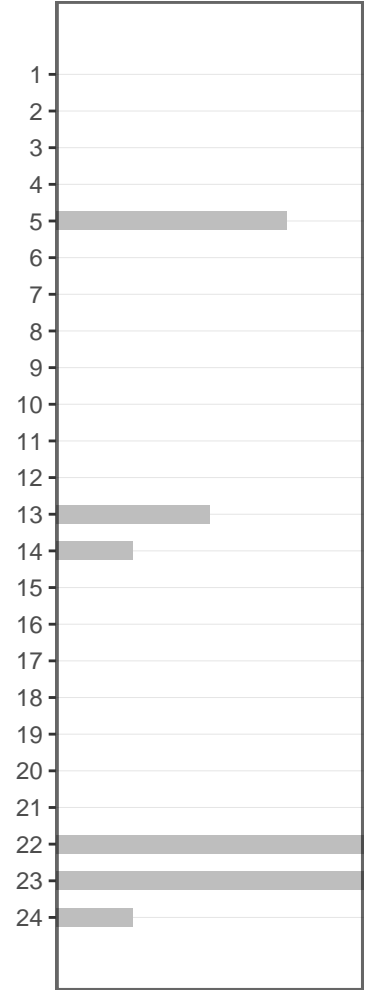
Molecular weight



Gel Slice



Protein length

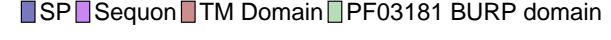


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LVKTTNNAATFLPRGVANSPFSSSEMPLELNGFVWPKPDEEAEILKGTVDGECEEPKIGKEKYCATSLSEMVDFSTKLGKVKVQPVSTETEKETGMQKYTLGTRKMGNGKSDAVVGHKGNVAVWFYGHKTETTDGVMVBLVGADGTKAKAVAGVGHKNTSAWNPKHAFKVLKVTGQVSPVGHFLPEDHIVWPKN

NbL10g17590.1 two-on-two_hemoglobin-3-like [MW = 15.3 kDa]

No. of times detected



log(intensity)



Values from



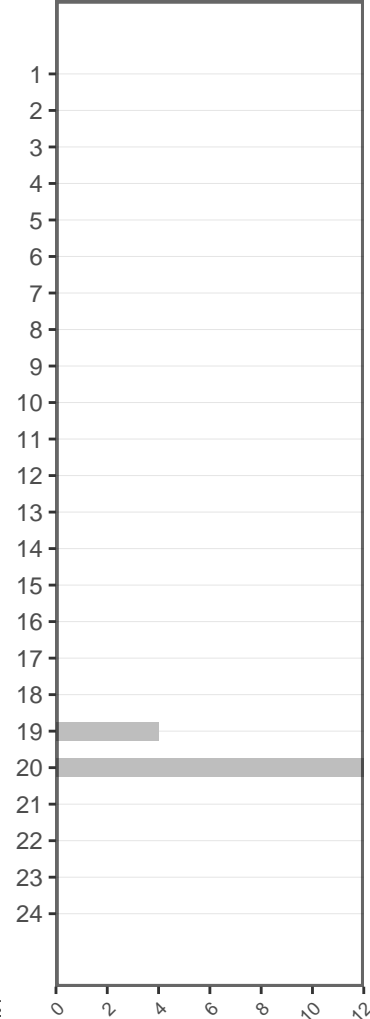
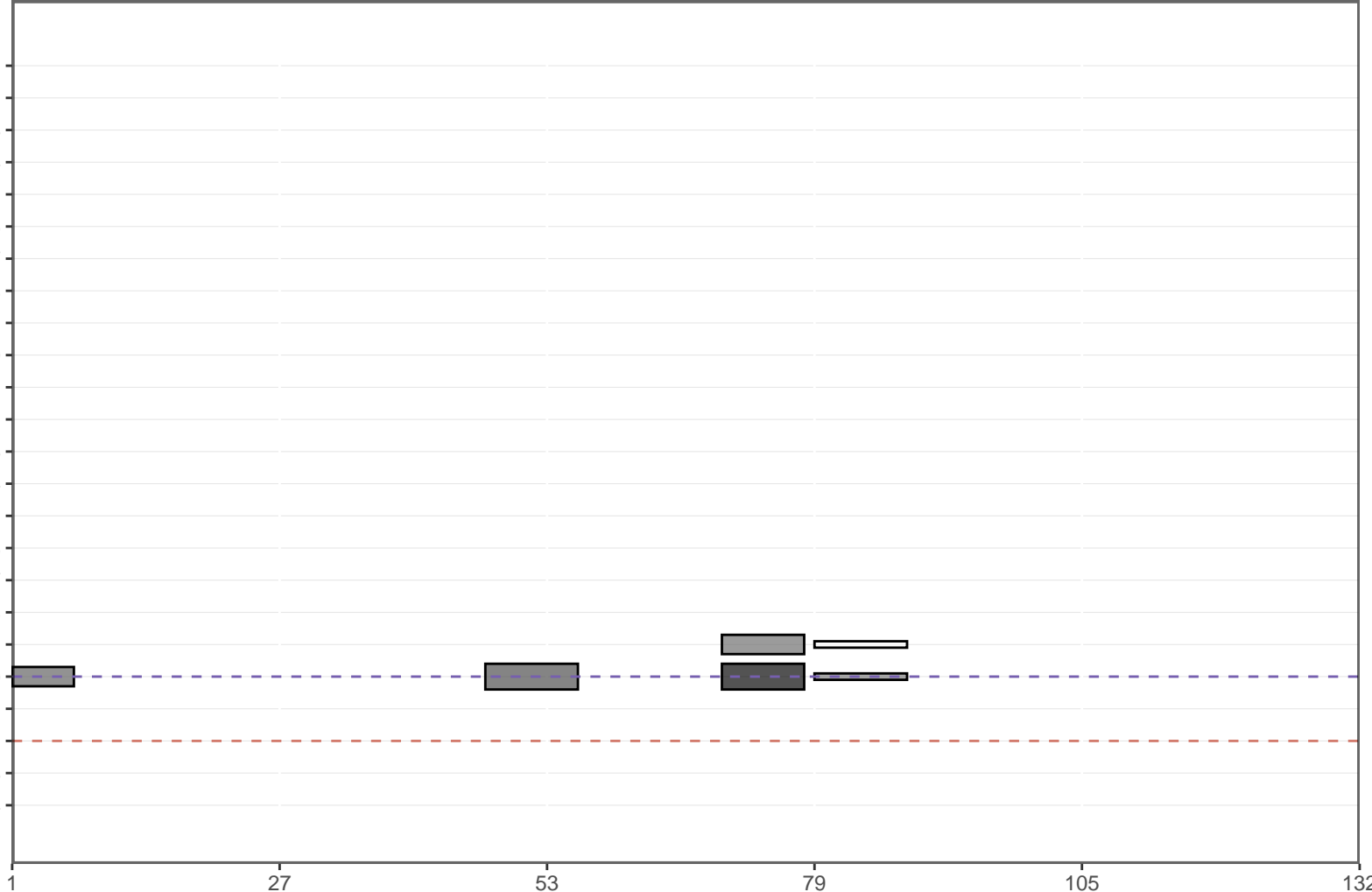
MW indication



Molecular weight



Gel Slice

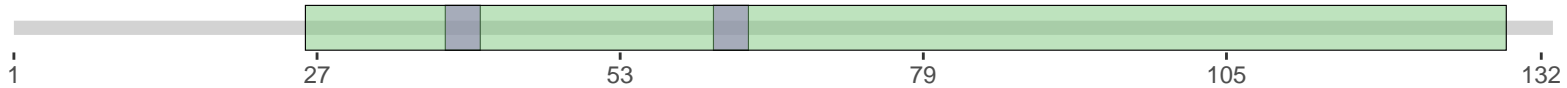


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

WFRSIFSNLSKEDAIRNQYEFFVQRMGGPPLYSGRKGRKHPALIGRHRFPVTHKAAERWLGQHMQLALDSEVTVIDEDGNN

NbL10g17500.1 50S_ribosomal_protein_L17-like [MW = 18.46 kDa]

No. of times detected



log(intensity)



Values from



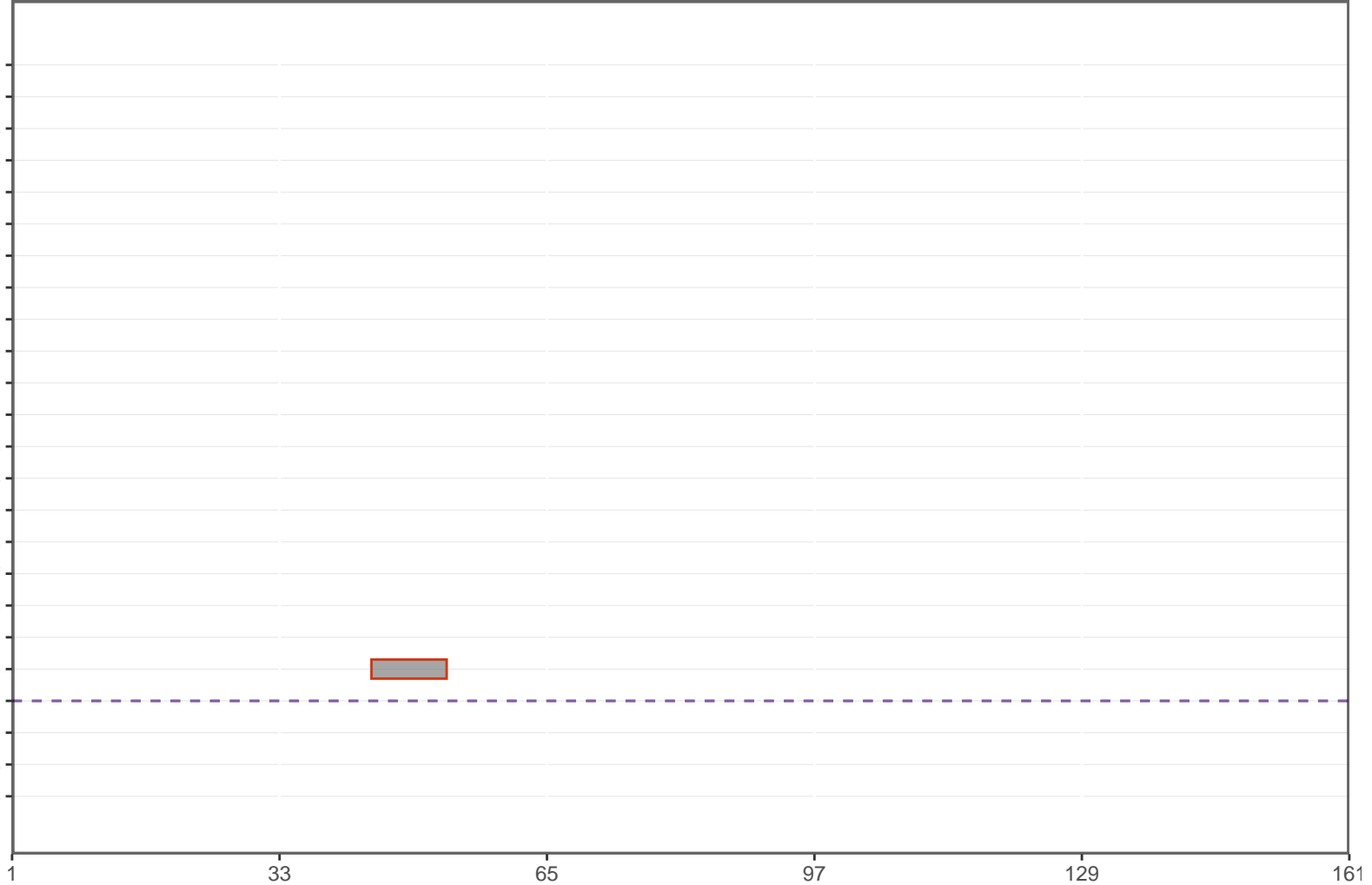
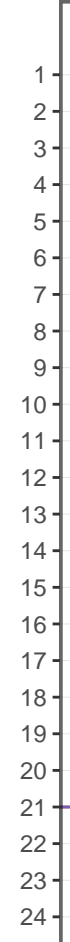
MW indication



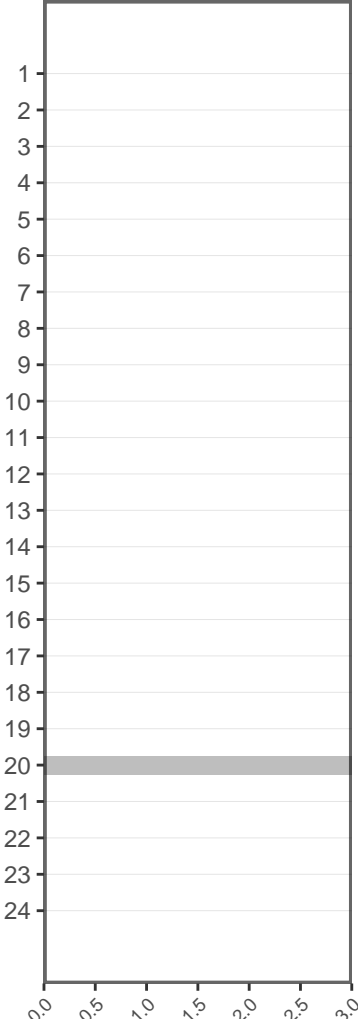
Molecular weight



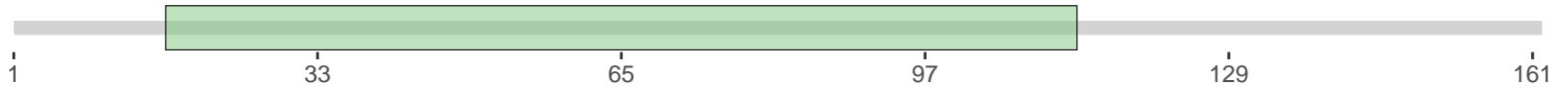
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VRGDDVHKLFTLAWRYKDRAGGQTRMLRTRIRRVGDAAPMAVIEFIDRENELRGKPPNPQPPQRPMDPWTRRLRGRQFAPPKEEKSSDSDF

NbL10g17410.1 psbP_domain-containing_protein_5_chloroplastic [MW = 33.49 kDa]

No. of times detected



log(intensity)



Values from



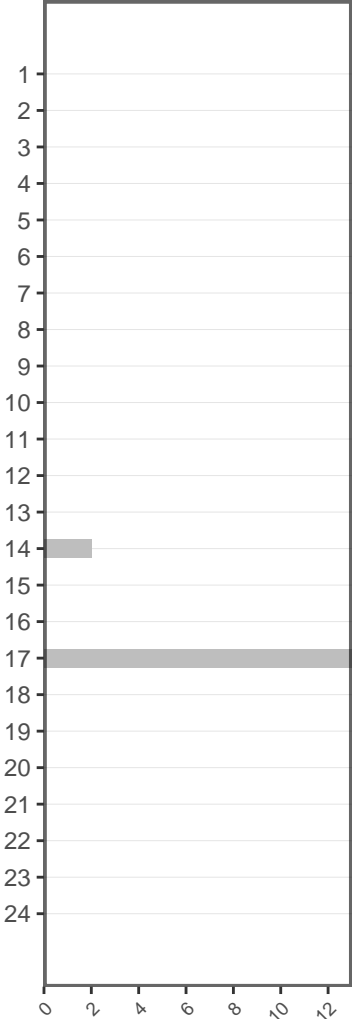
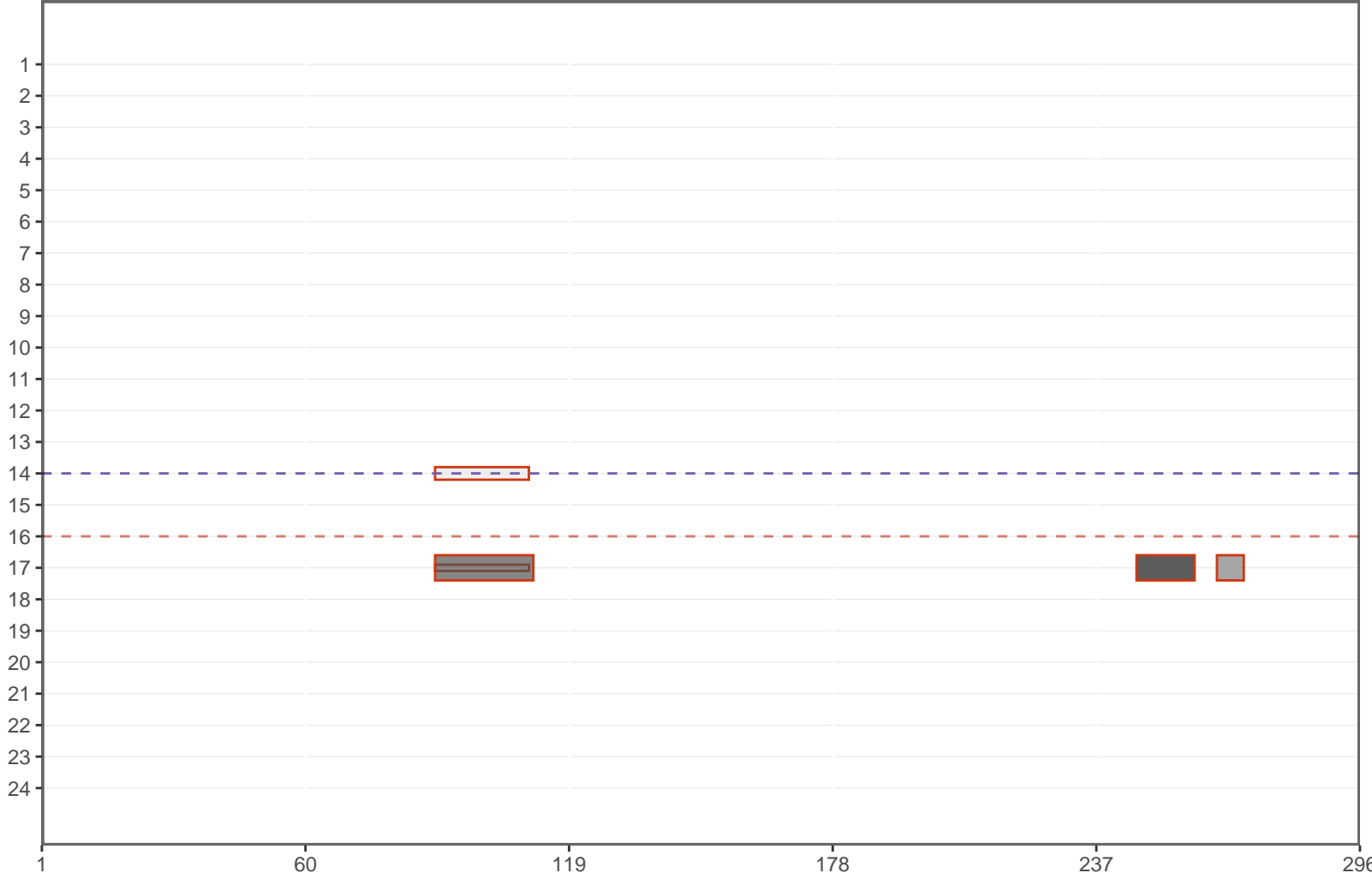
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RLRIVSERVYDIIDNLNLSVSGIPNPGFLKSEEEKSTWTAKDVAADVLSQKRALRVTSQRNLAESSLLDAHTSEIDGEPWYVEYLVKRSPTKTAQETLFRHYVAAGTAERDGLVYTFASLTKGQKQDRMGPFLLGKQKVASFRLLPPTESVVPYKDPWFV

NbL10g17260.1 non-specific_lipid-transfer_protein_1-like [MW - SP = 10.43 kDa]

No. of times detected



log(intensity)



Values from



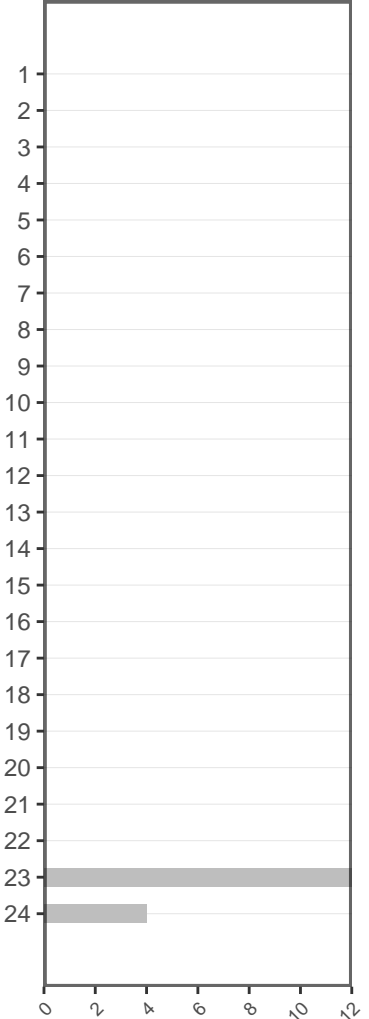
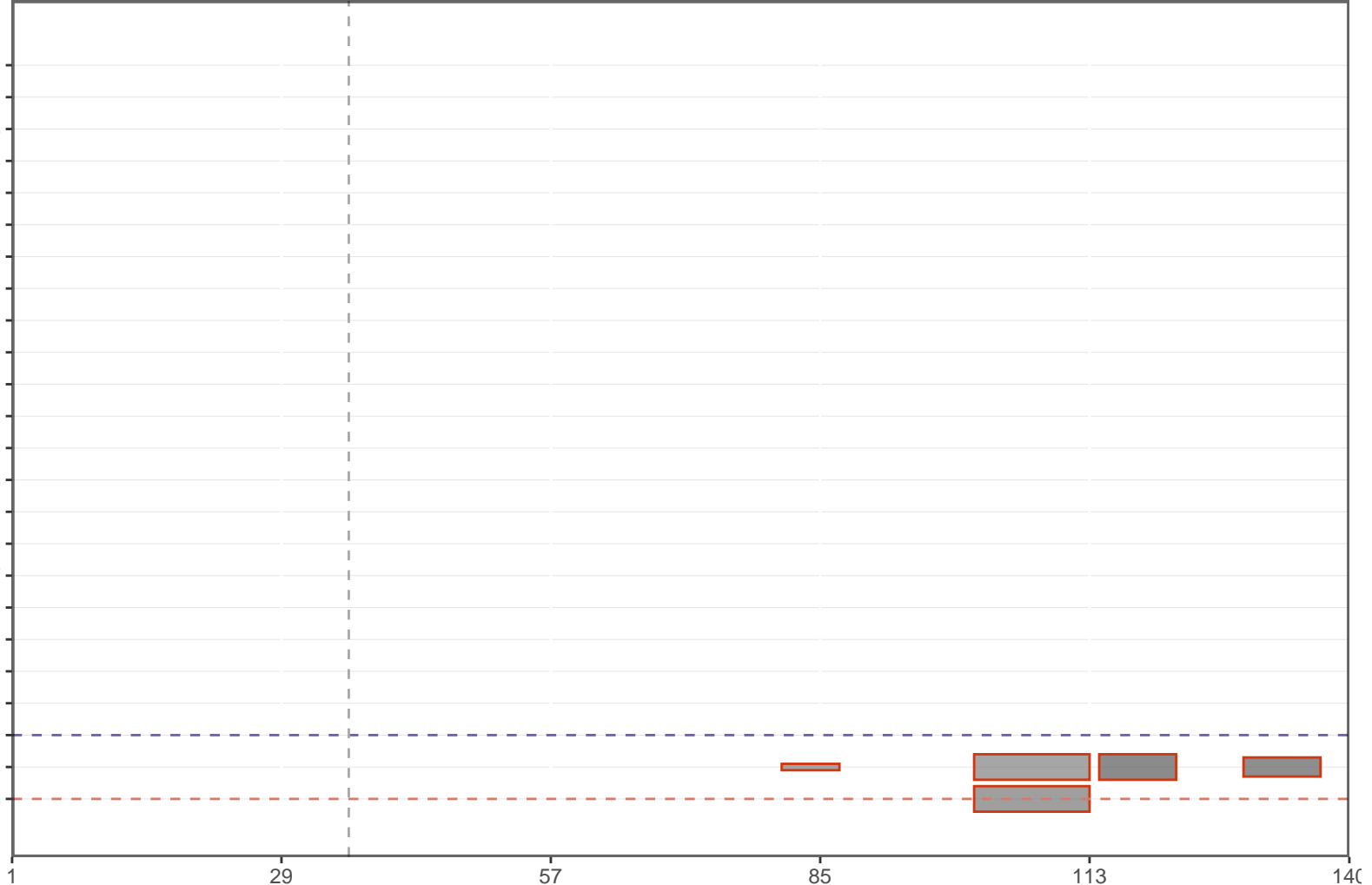
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IPCLGYLYLGASVPEEGCGGLKLLSAARTRTDRGAGGCVKSVASATGDGIERAASIPGIGKAKVFRKISANVDSKIK

NbL10g17250.1 non-specific_lipid-transfer_protein_1-like [MW - SP = 9.71 kDa]

No. of times detected



log(intensity)



Values from



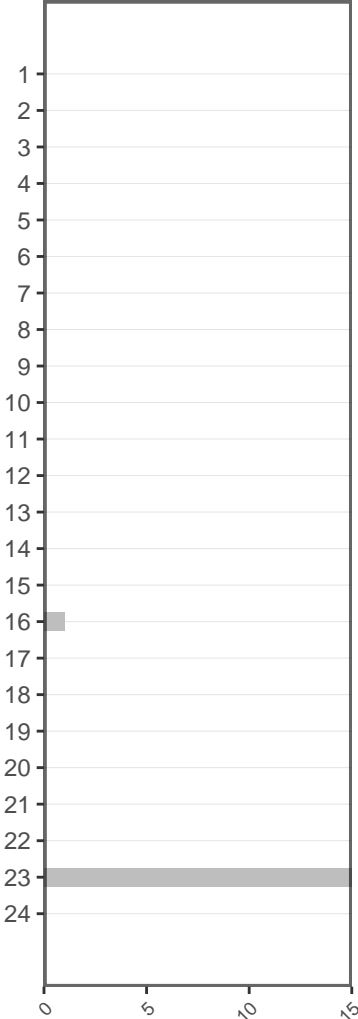
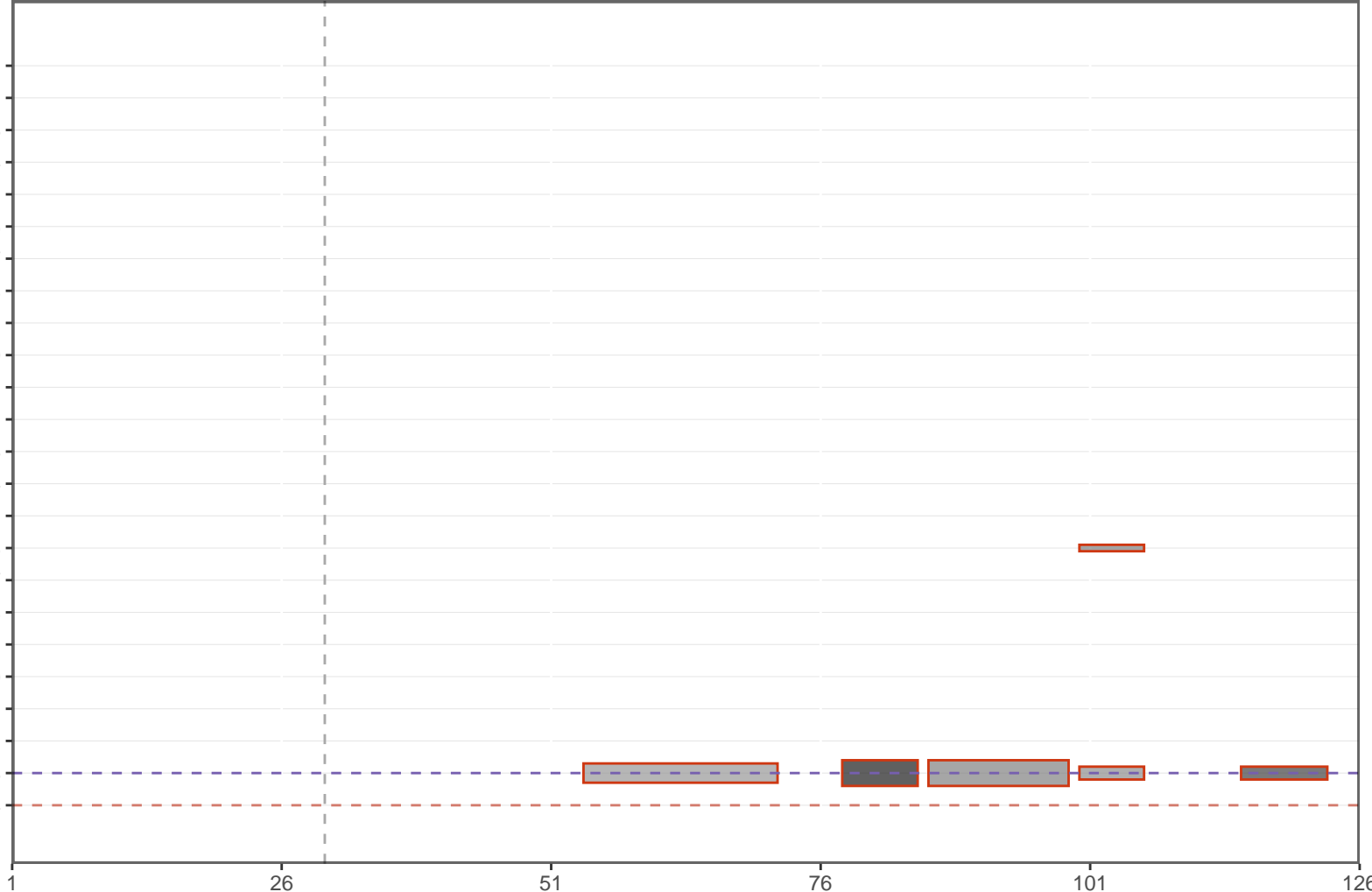
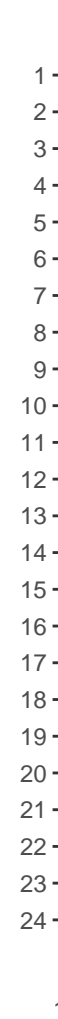
MW indication



Molecular weight



Gel Slice



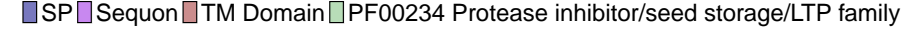
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ISSKQAAPSGCCCSGIGSLYTTARTFVDRGIVCGSLKAGAAISLGNBIDANKAAILLNKGGVTPVYKISPNDDSKVQ

NbL10g17230.1 6-hydroxynicotinate_3-monooxygenase [MW = 48.15 kDa]

No. of times detected



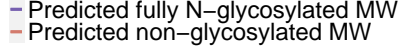
log(intensity)



Values from



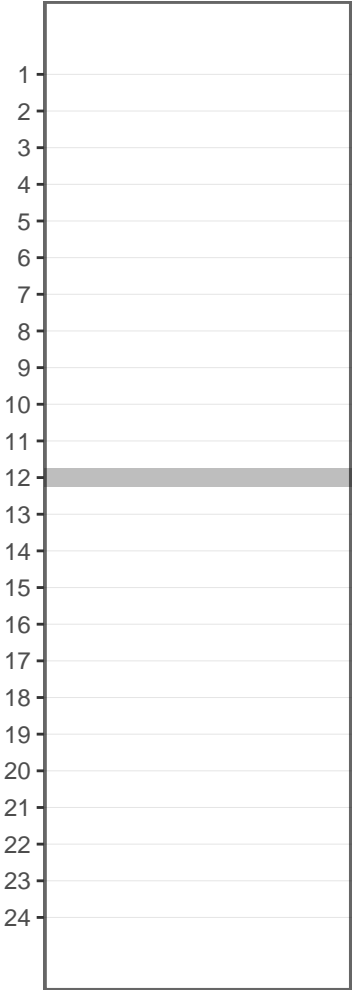
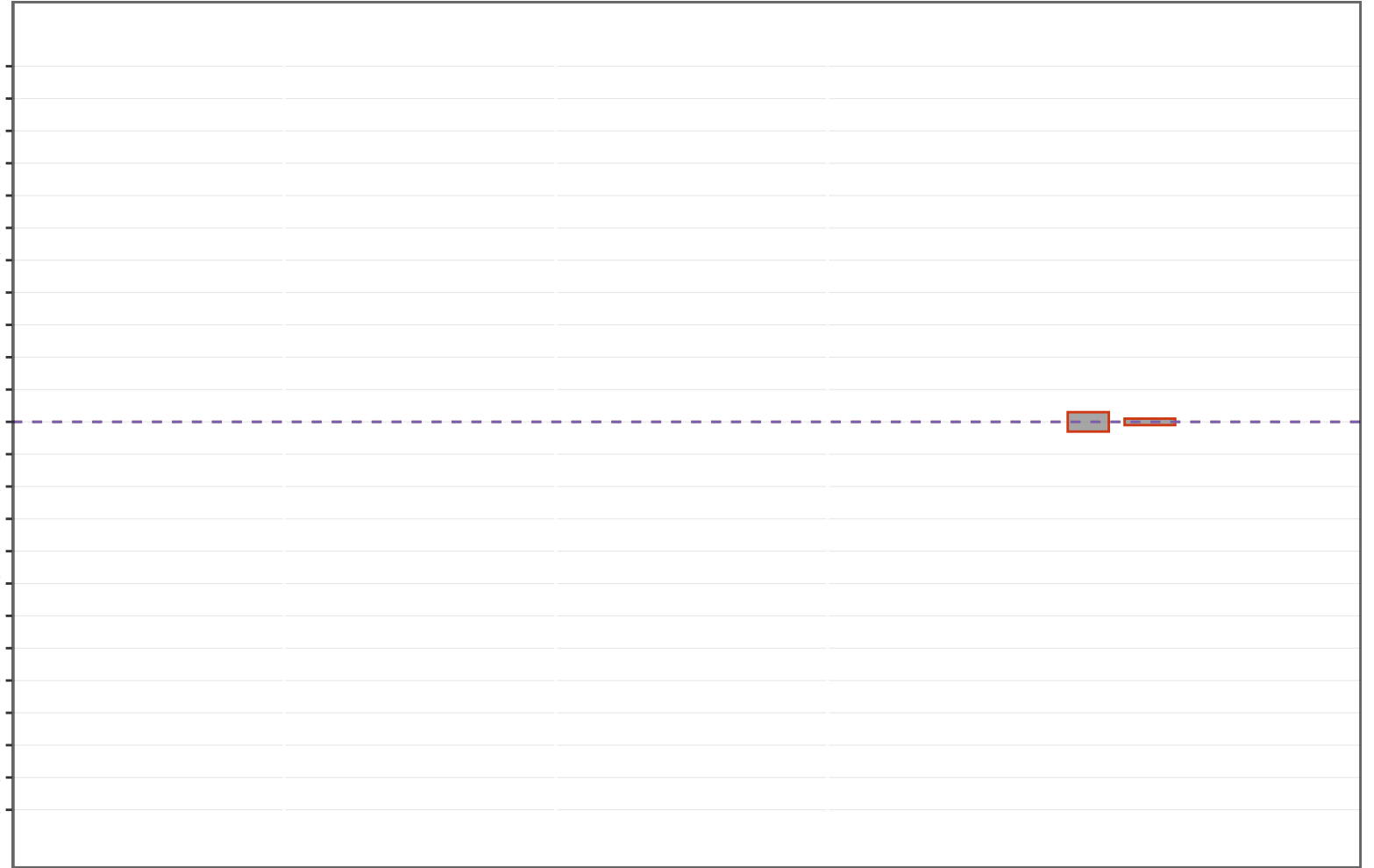
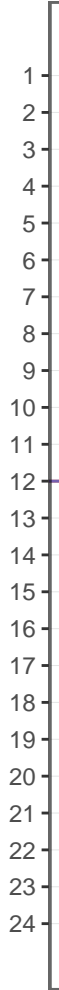
MW indication



Molecular weight



Gel Slice

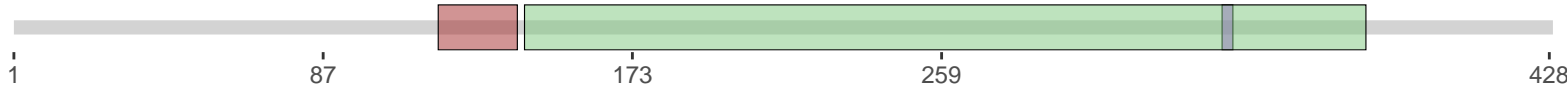


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VLDPSDKKXISEAISLSKLLYFDLGGKLYFDLSSGTHSEVYFELLNDRFNWVYINGPEPNLKGNSVTMKVNEISQNMHEEAEKTVAPLVLVRIKKEPFLLVYDQDPLGDFWQKYYLGGDAANPTTPHGLRSTNMSIVDAVLGKLEKWKGVENLNSALEEYQSRLPVASKQVLSHRRLGRKQGLSLSDRLSFDPKTAGSGEDGEEELQGNMPPYFYDPSLKI

NbL10g17200.1 EG45-like_domain_containing_protein [MW - SP = 12.03 kDa]

No. of times detected



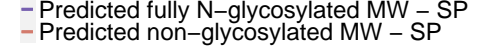
log(intensity)



Values from



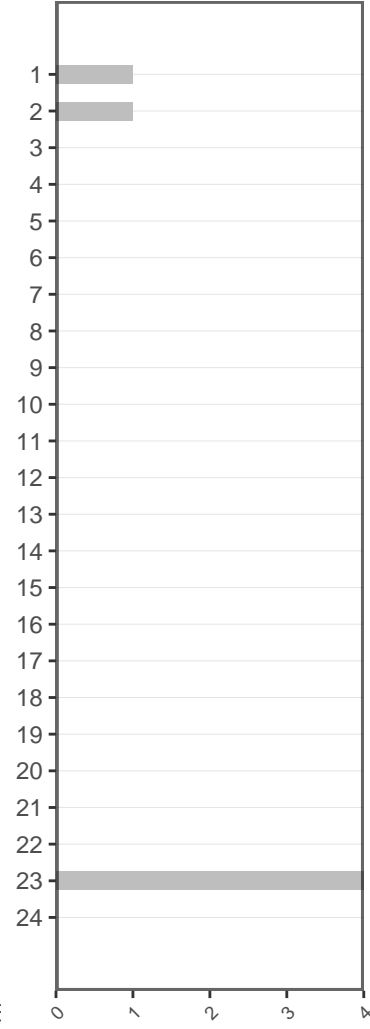
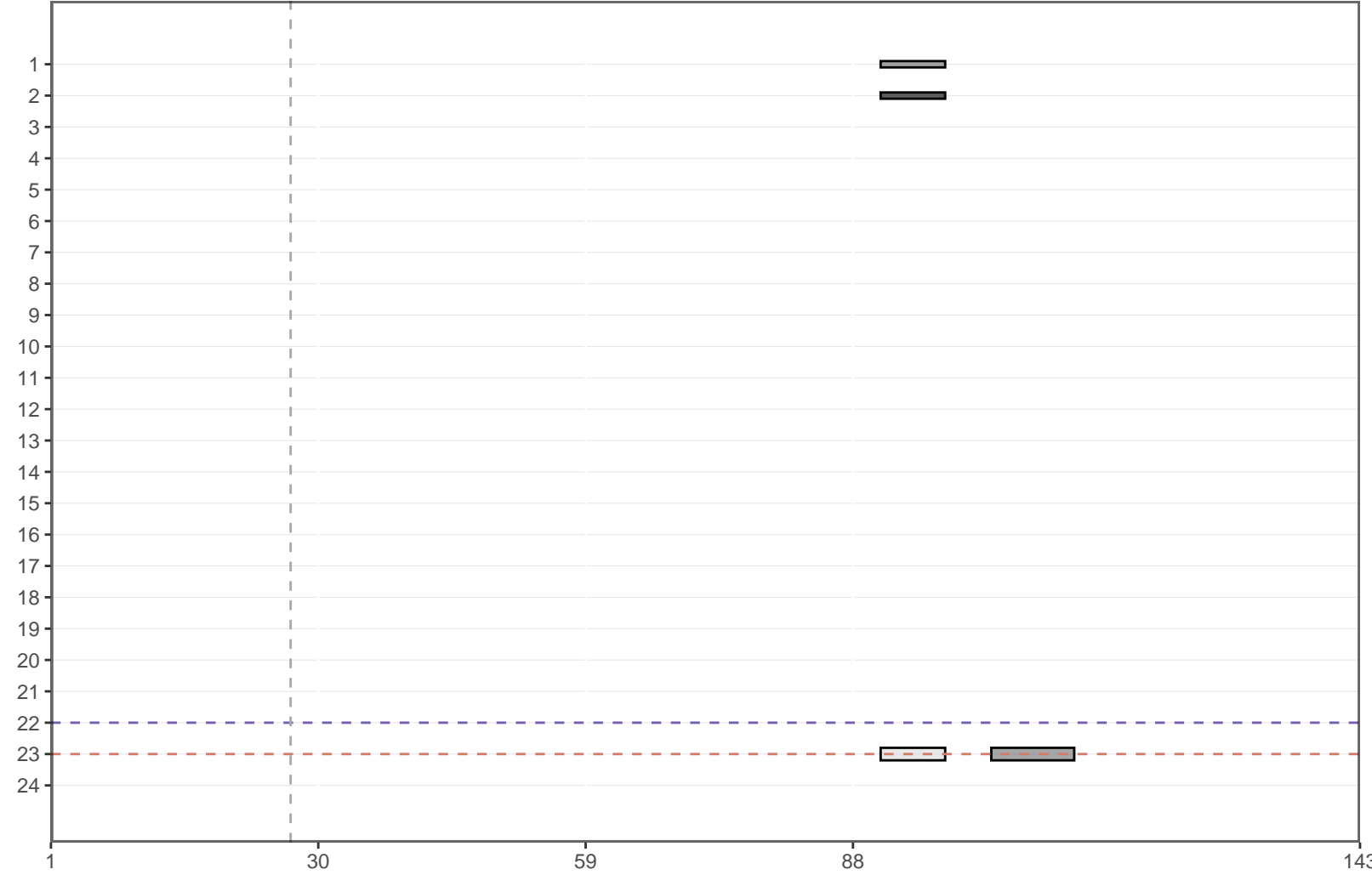
MW indication



Molecular weight



Gel Slice

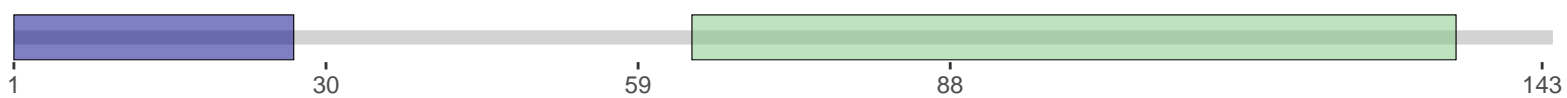


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

FAAAGEGIWDDGAGGRGVYUSGHSILPRACKSGETGIQIKIVDRAGTVAENPTROGTTIVLSNAFAAIDSNALSLNDFGGV

NbL10g17060.1 aspartyl_protease_family_protein_At5g10770-like [MW = 54.96 kDa]

No. of times detected



log(intensity)



Values from



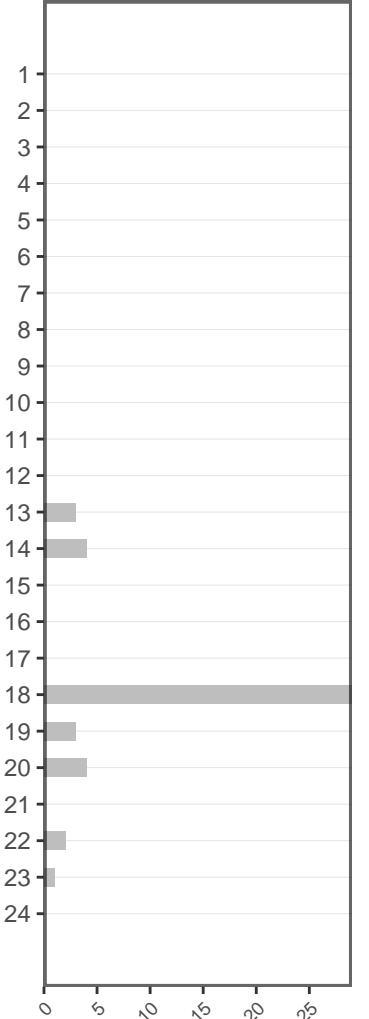
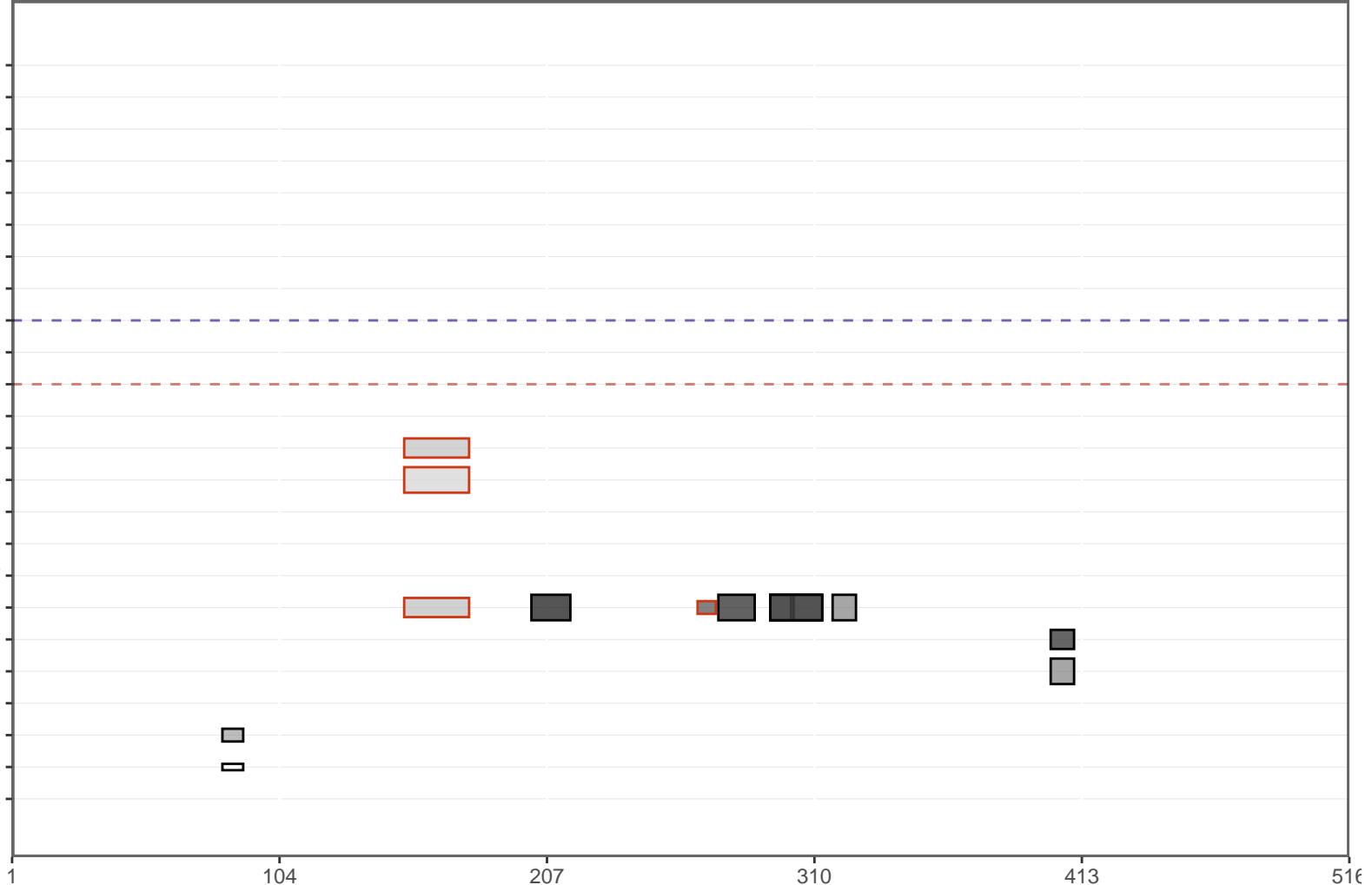
MW indication



Molecular weight

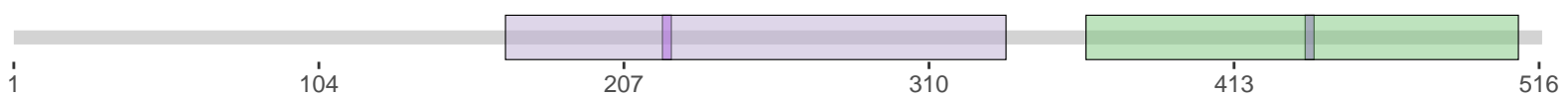


Gel Slice



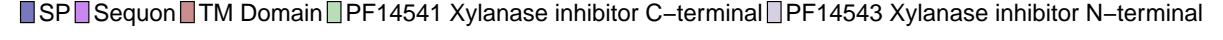
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

INCYYGVYGDSSFSVGVFFAKDITLTPKIVFDGFMFGCGGNNRGLFQKTAGLGLGRDPLSIVDGTAGKFGKVFYGLPFRGNGHLTFQNGNKIKTKAVNGITFTFPFASGGATFYFDVLGIVGVGKALSGFMFFQAGTHDGGTVITRLPSTAYSLKSTFKGFMSKYPTAPALSLLDTCYDLNYSITSPKISFNFNGNANVELDPNGLITNGASGVGLAFAGNADDDSGIFGNIQGGTLEVVYDAAGGLGFGYKGCSE

NbL10g16970.1 ATP_synthase_subunit_alpha_chloroplastic [MW = 32.94 kDa]

No. of times detected



log(intensity)



Values from



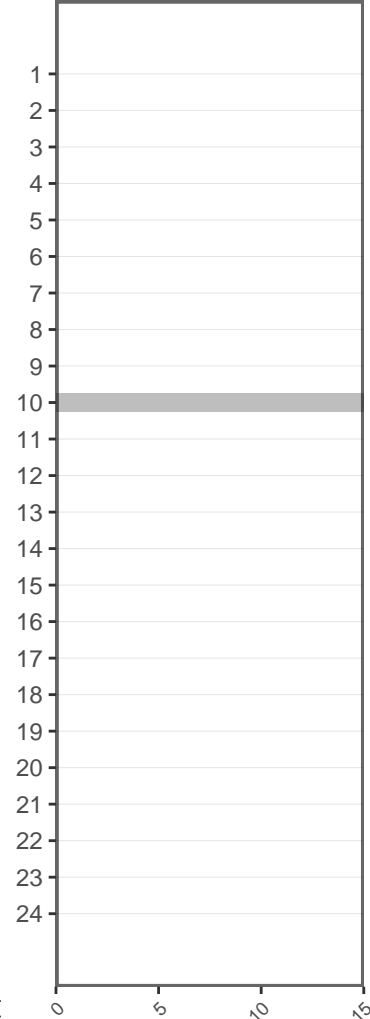
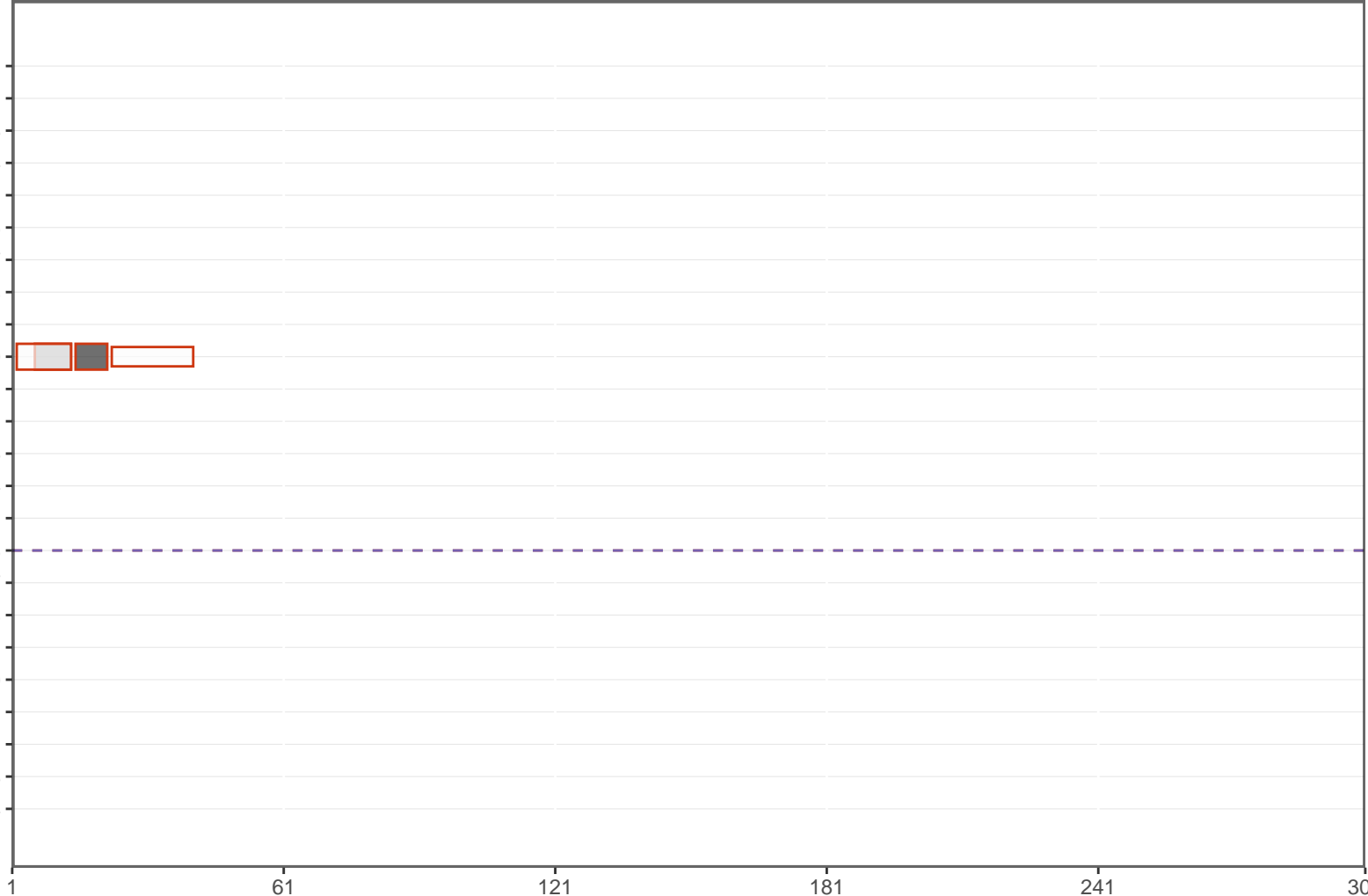
MW indication



Molecular weight



Gel Slice

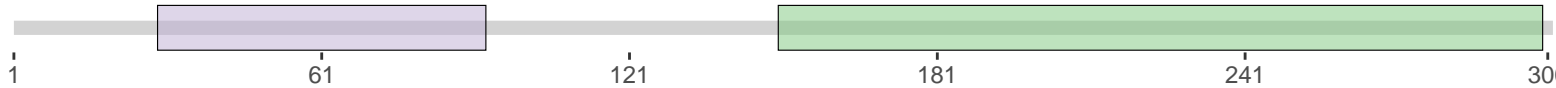


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF00006 ATP synthase alpha/beta family, nucleotide-binding domain
- PF02874 ATP synthase alpha/beta family, beta-barrel domain

Protein sequence:

SRRSYEPLQTGLAIDSMPIGRGOREIIGDRQTKTAVPTDILNQGSNVIYFYVAIGGKASSVAVVITLQERGAMEYTVAAETADSPATLQHLAPYTGALTEYFMVYRERHTLRYDDPSKQAQAVRQMSLLLRPPDRREAVPGDFYLH6SLI

NbL10g16940.1 uncharacterized_LOC109237937 [MW – SP = 38.26 kDa]

No. of times detected



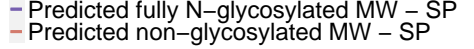
log(intensity)



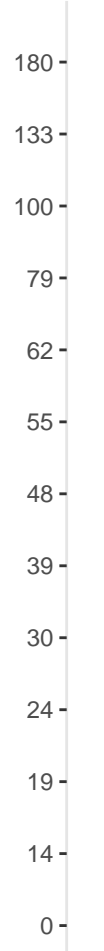
Values from



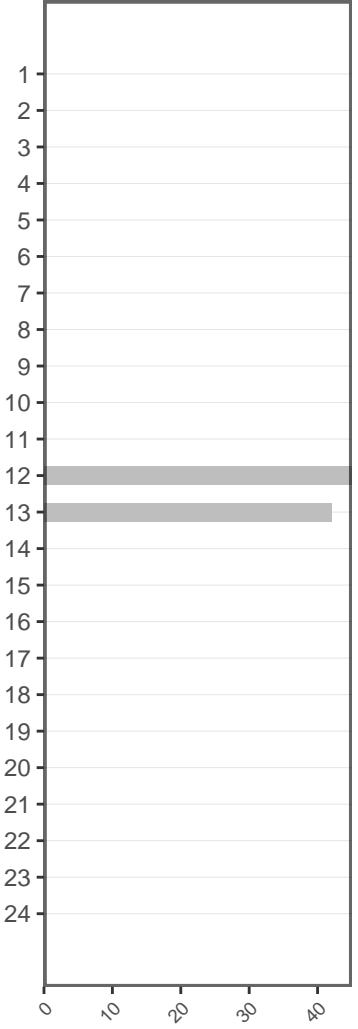
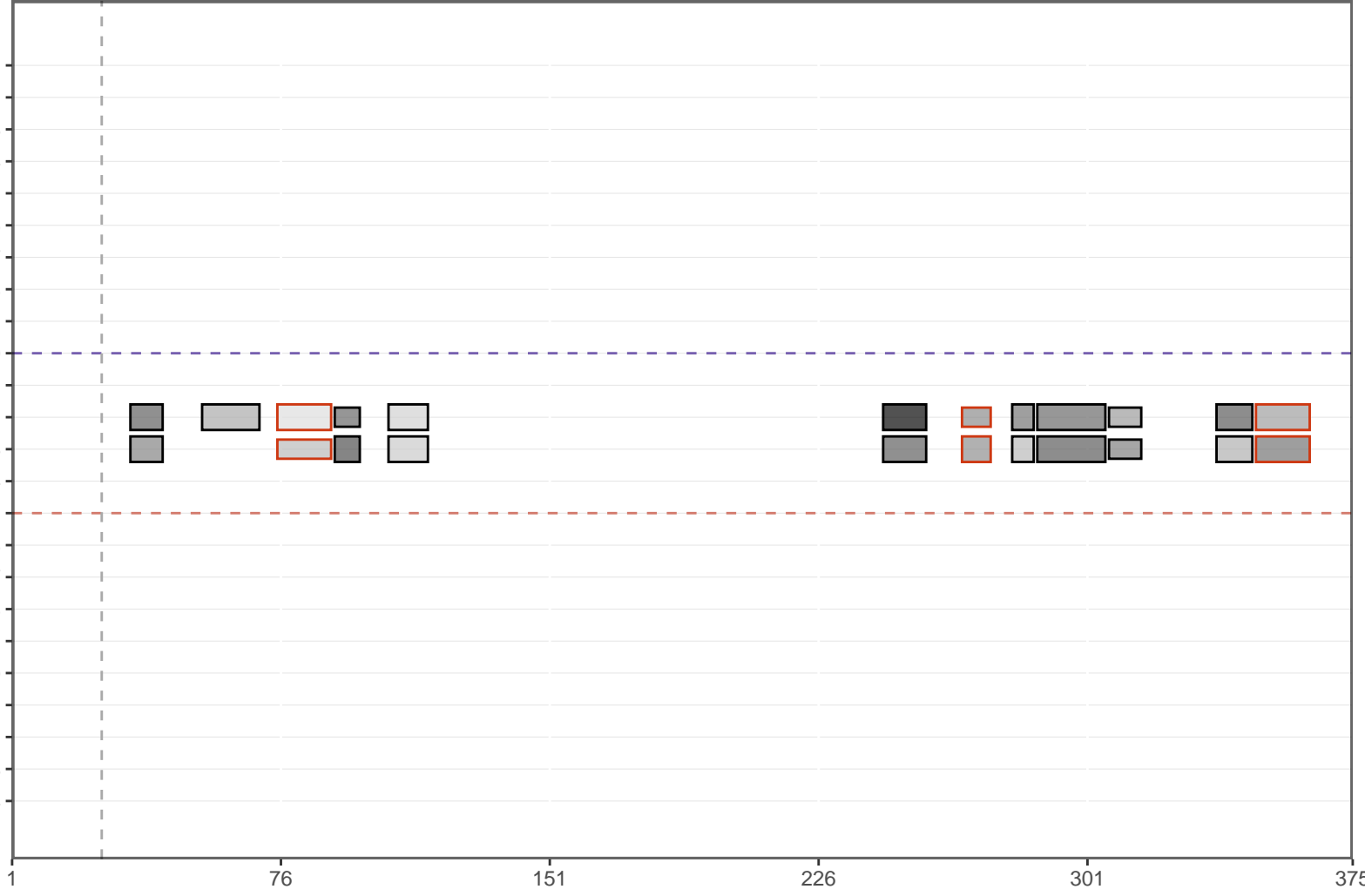
MW indication



Molecular weight



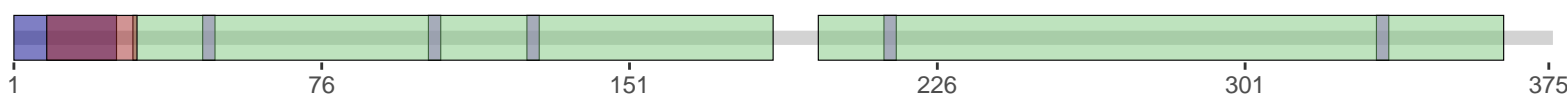
Gel Slice



Protein length

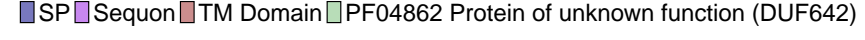


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ICGPLDISARSLYPPRATNLLKNGDFEEGPIYFNTBVGVLVPPNEDDHSFLPAAVVELKANKYLDSDHFVPOGKRAVELWAKESAWAGARTTRIGKMYELSKVGDANSCEGGMVEAFAGRDTLKVVPYESKGGKGYKRAVLRPKAAANRTRIMFLSTYYHTREDDFVSLGPPVDDVKKLLEVRNRRFL

NbL10g16820.1 early_nodulin-like_protein_1 [MW - SP = 18.51 kDa]

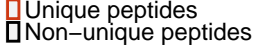
No. of times detected



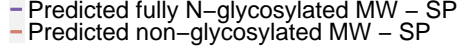
log(intensity)



Values from



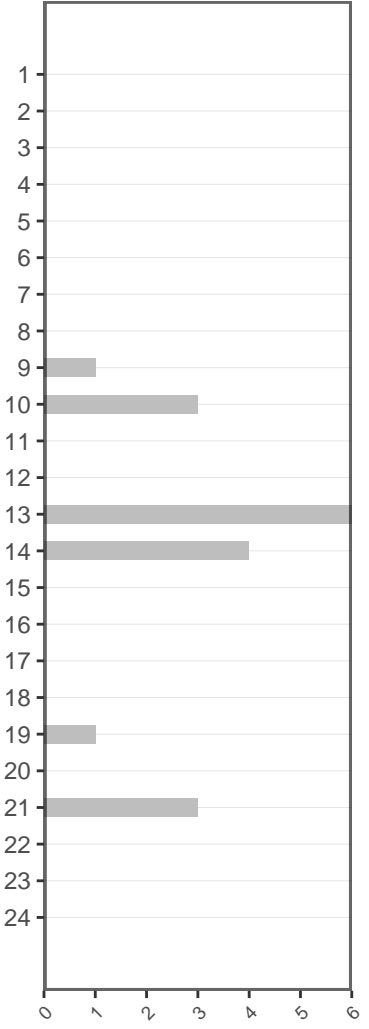
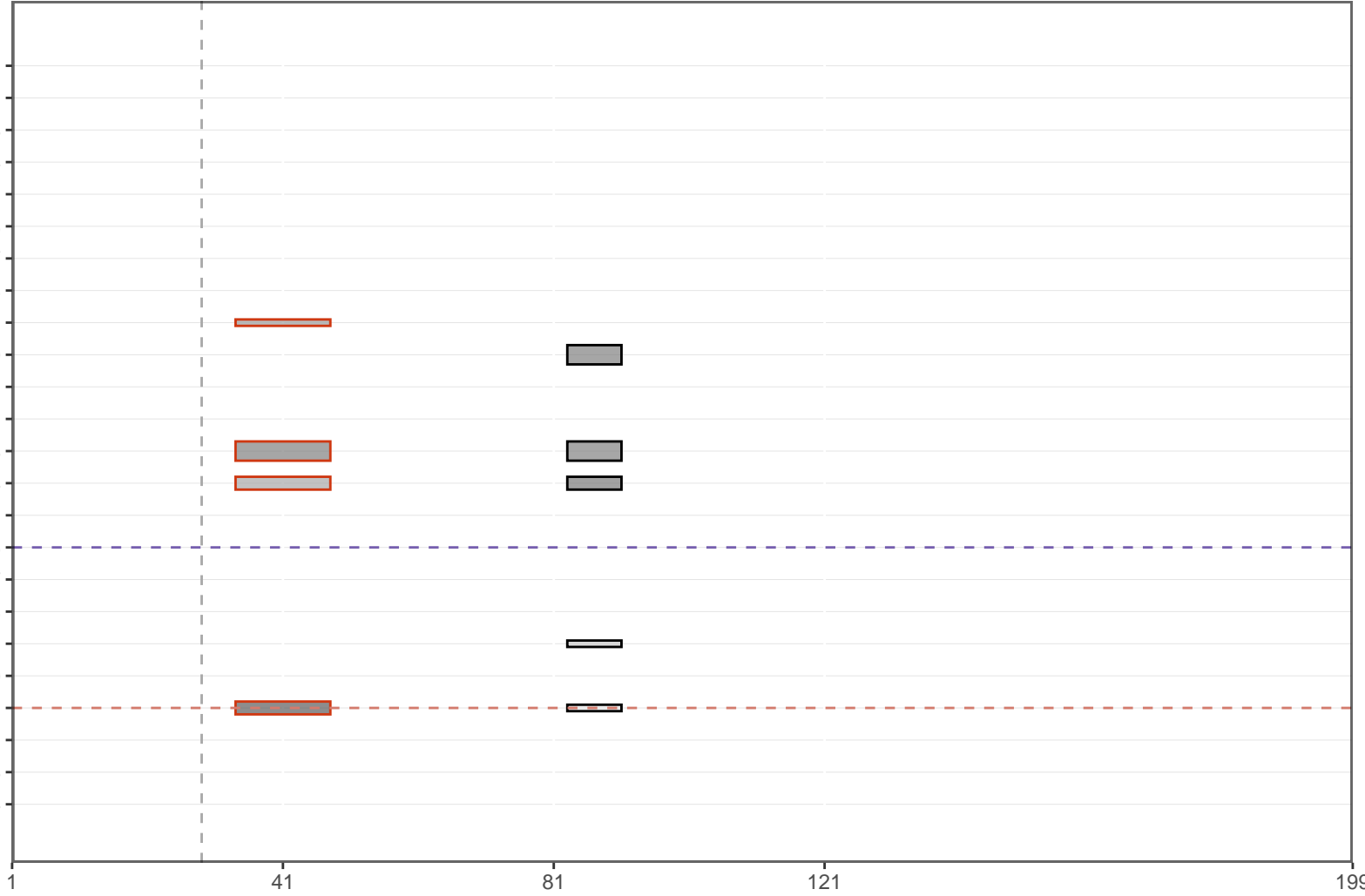
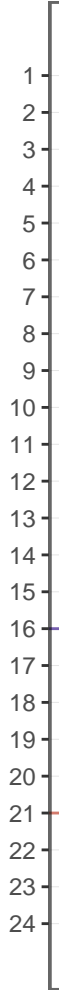
MW indication



Molecular weight

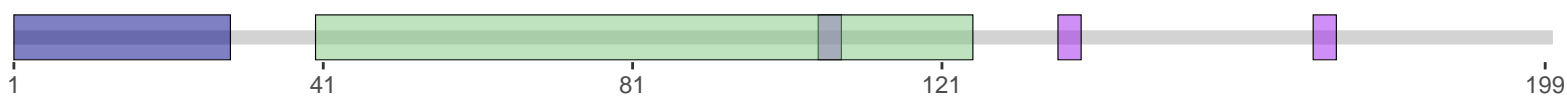


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

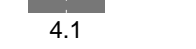
NSCNLKNPILYMNNGNSLNFNTKPGFEYFTSGAEGHCKEKSKLHPIPGNGTTVEEDSFAFAPSADSPWPTVFGSIPVDSANGS6SKLPIGIFAAGSLFFTLIR6TE*

NbL10g16800.1 exosome_complex_exonuclease_RRP46_homolog [MW = 26.47 kDa]

No. of times detected



log(intensity)



Values from



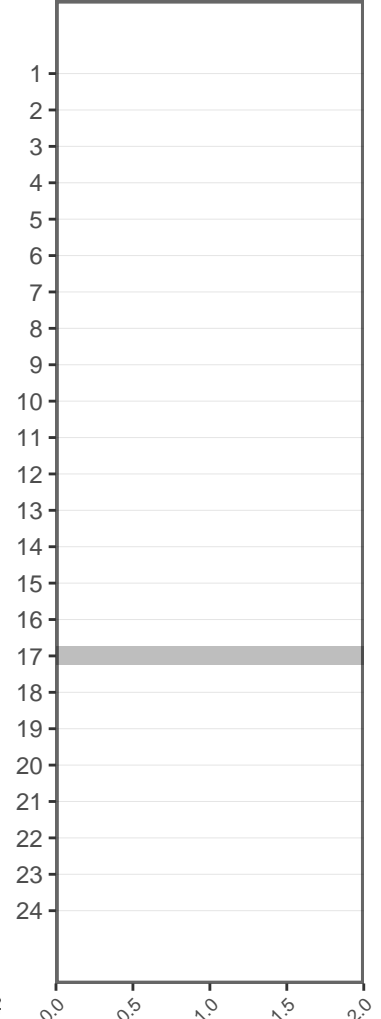
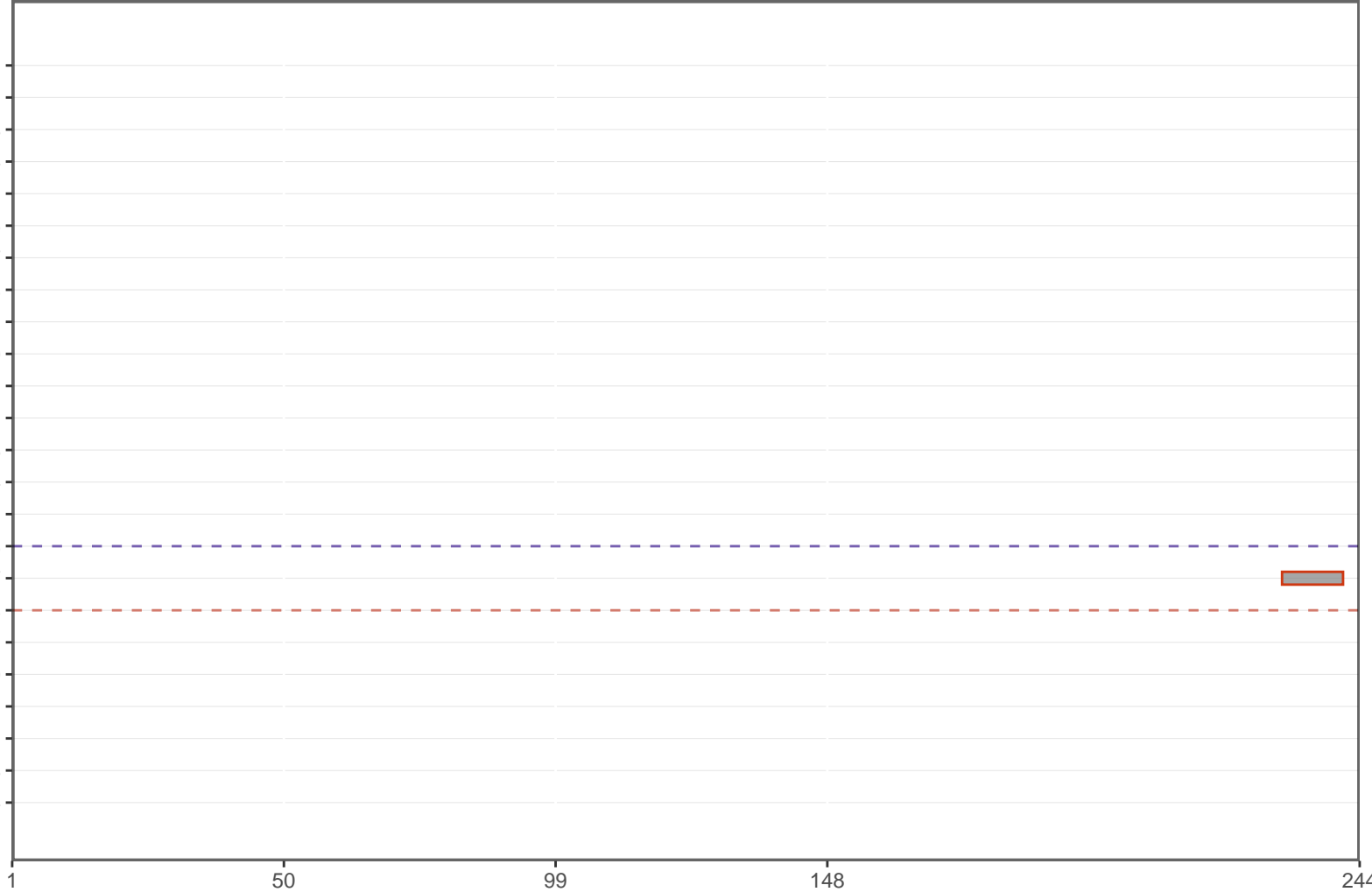
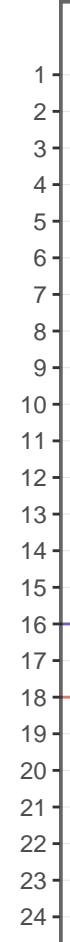
MW indication



Molecular weight



Gel Slice

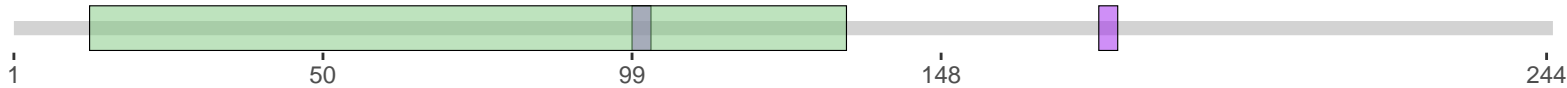


Peptide counts over 4 repeats

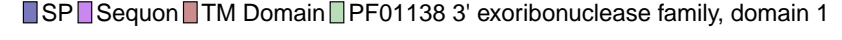
Protein length



Pfam domains



Pfam Description



Protein sequence:

LVNDGGALLPCAINAVGALVDAGIPLKHLEVAWAGDSLAESGHILLDPSKLEEQNMKAFVLYVFNSTLSVLPPEESLKVIRGEATEHGLTSTFTHGVMSEVDYHRLGLERGRAATGKLSDFLRFSFGSQVQSDSKLQ*

NbL10g16490.1 NADP-dependent_malic_enzyme-like [MW = 69.3 kDa]

No. of times detected



log(intensity)



Values from



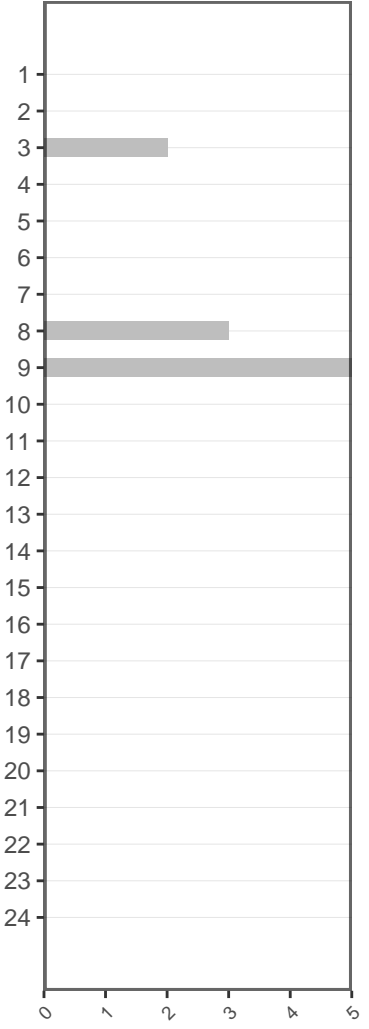
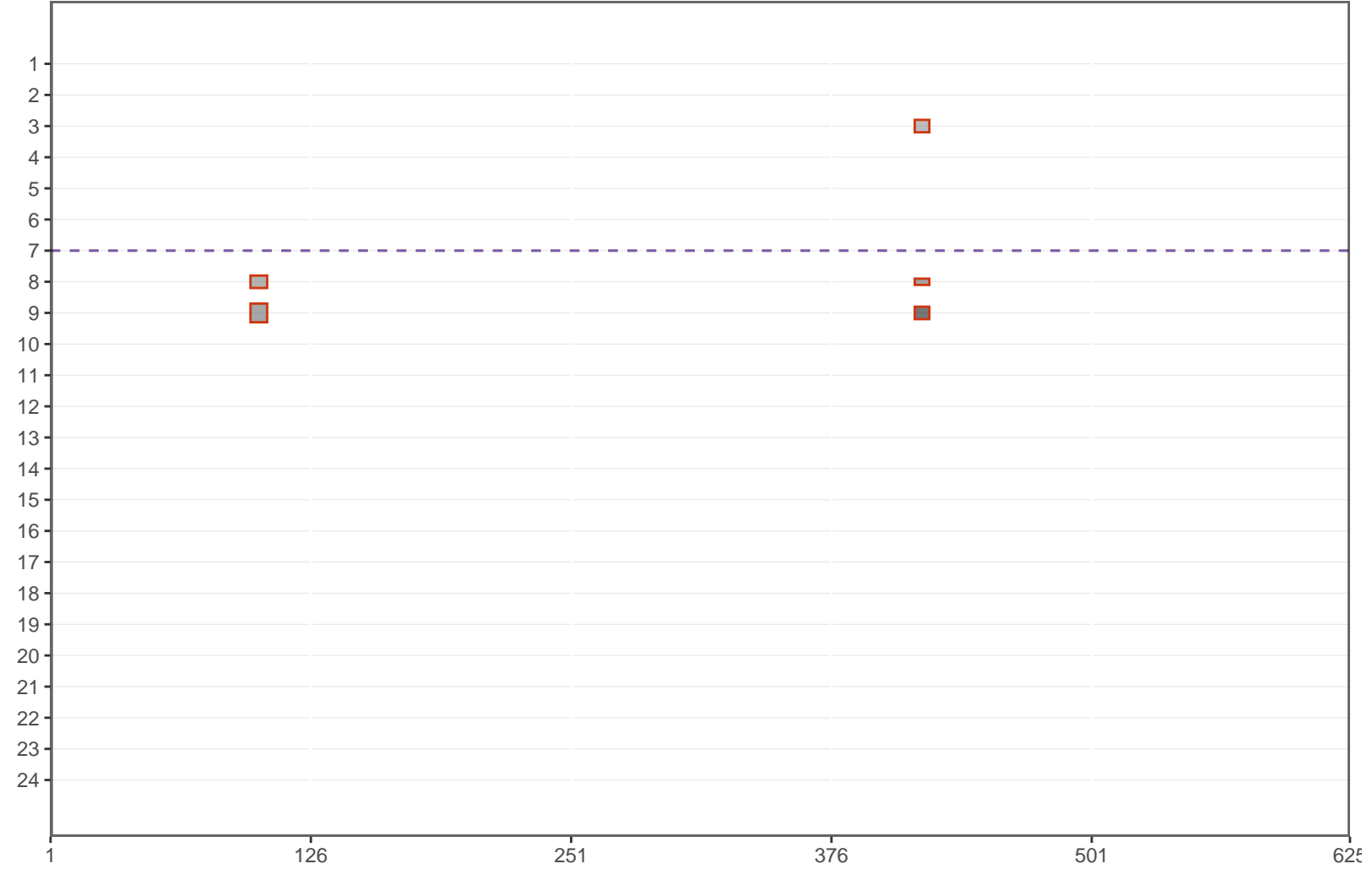
MW indication



Molecular weight

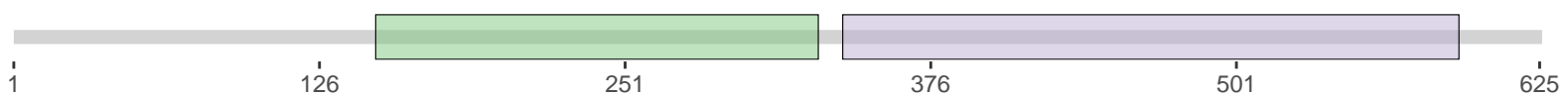


Gel Slice



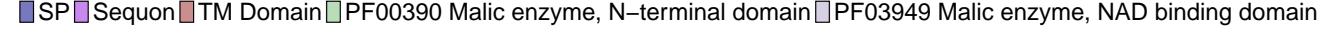
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EFMSAVKQNYGEKVLGDFEDFANNAFDLLAKYRTHLVFNDIDGIGTASVYLAGLIASLKLGGTLADHTFLFLGAGEAGTGAELMLETIKRRTSVPLEEARKKHVLDSKGLVSSRLLESGLGPKPKVAHGHGHEFVKELIDAKKAIKPTVLTGTSQVQKFTTKEVIETMAELNPKPLMALSNPFGAECTAEAEYTWKGHAFASGSPDFDFEYEGRTFVSGGANNVHFFPGFLGIMSGTRVHDDMLAAASELAAGVTEEDPLKGRVPPFTNRRISAHAAEVAKAYELGL

NbL10g16470.1 cell_division_control_protein_2_homolog_A [MW = 33.83 kDa]

No. of times detected



log(intensity)



Values from



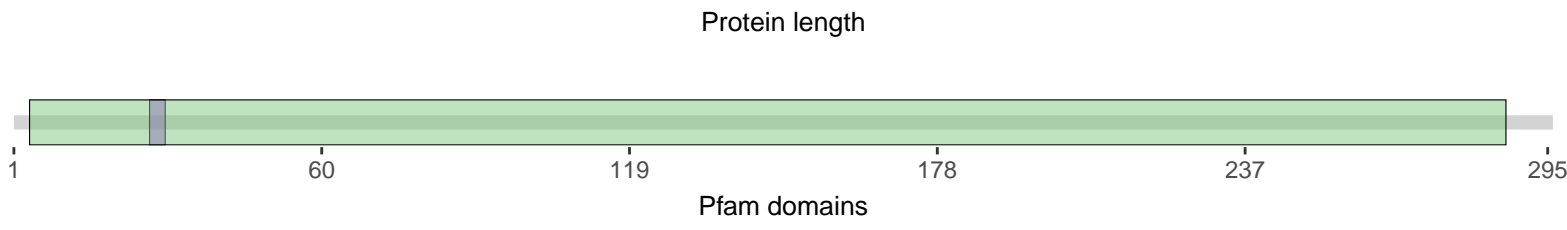
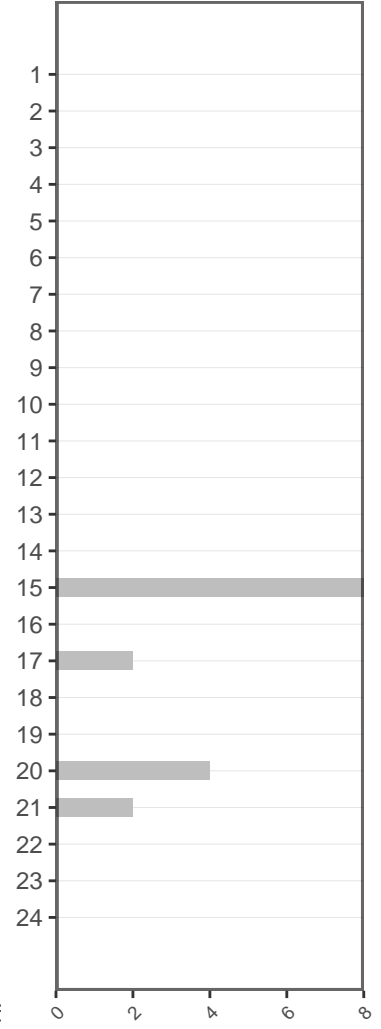
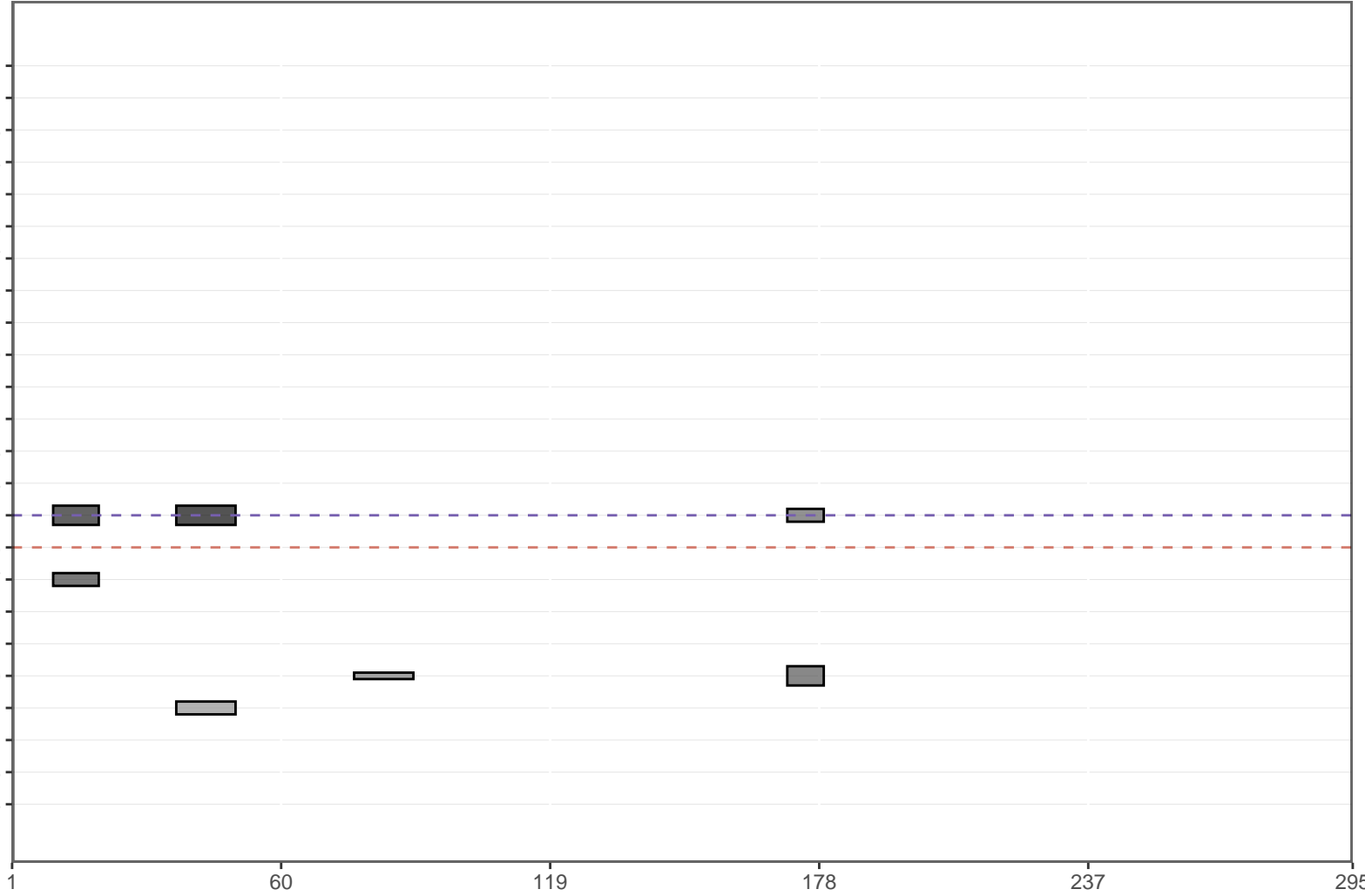
MW indication



Molecular weight



Gel Slice



Pfam Description



Protein sequence:

DDRRTNALKLAADFGLARAFGIPVPTTFHEVTLWVRAPPELLGSRHYSTPVDVWVWGGIFAEVMTQRLPFGDSEIDELFKFRVMTGTRFNEIDTWGVTTLFDPFKSAFQKWPQKDLAAVVPNLDGAGLGLLQKMLRLGPSKRITARNALEHEVFKGGVYP

NbL10g16320.1 uncharacterized_LOC109241480 [MW – SP = 151.69 kDa]

No. of times detected



log(intensity)



Values from



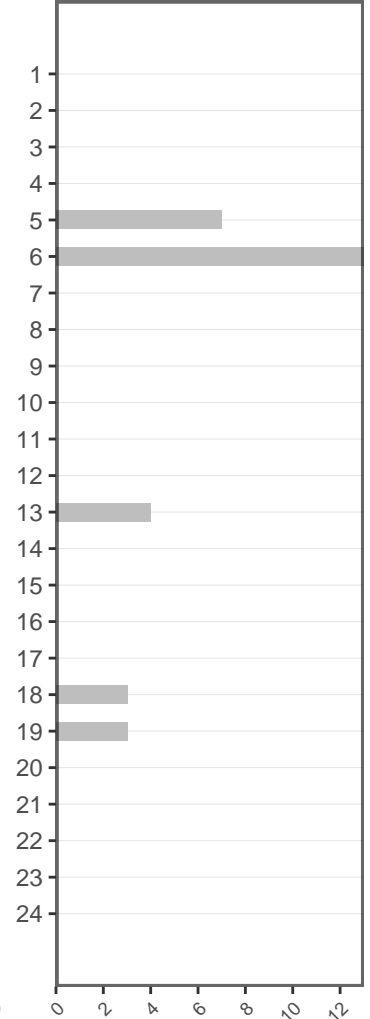
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

GGSGSILLFLKSLHGEGGTMSLGGSSSSGGGGGGGRHFHWSDPTGDVYLPATVNGEYTRGGLGGEGGGGGGTLGKPCPKGLVGFCECPGLGTFKNVTGSDRALGVSGLSDLPRAAVHVRGQVTERPCPKVGSERYHMPHCYTALEELVYFGGPAFLVLLGLLULLALVLSVARMKFGVDELPGVPTQGGQIDHSFPLESLNEVLETRVVEEGSHVRYLFFGPNTFSEPHLGHTRPPQKKEVVEGAFNTFDENTIAYQW

NbL10g16150.1 vacuolar-processing_enzyme-like [MW - SP = 50.88 kDa]

No. of times detected



log(intensity)



Values from



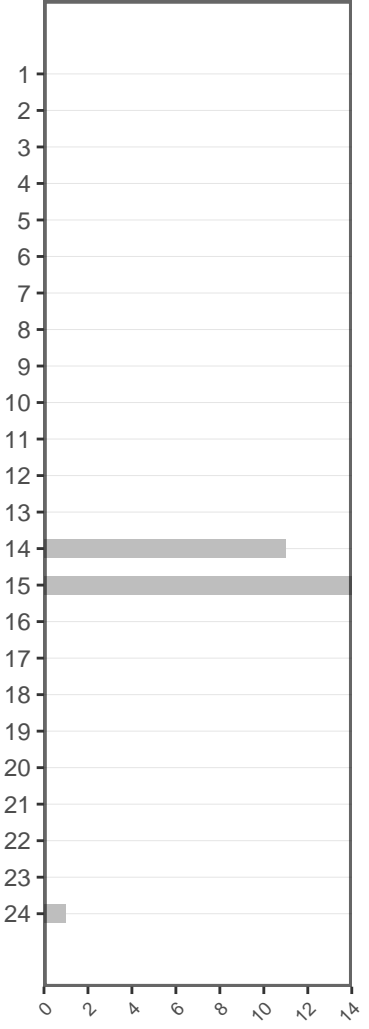
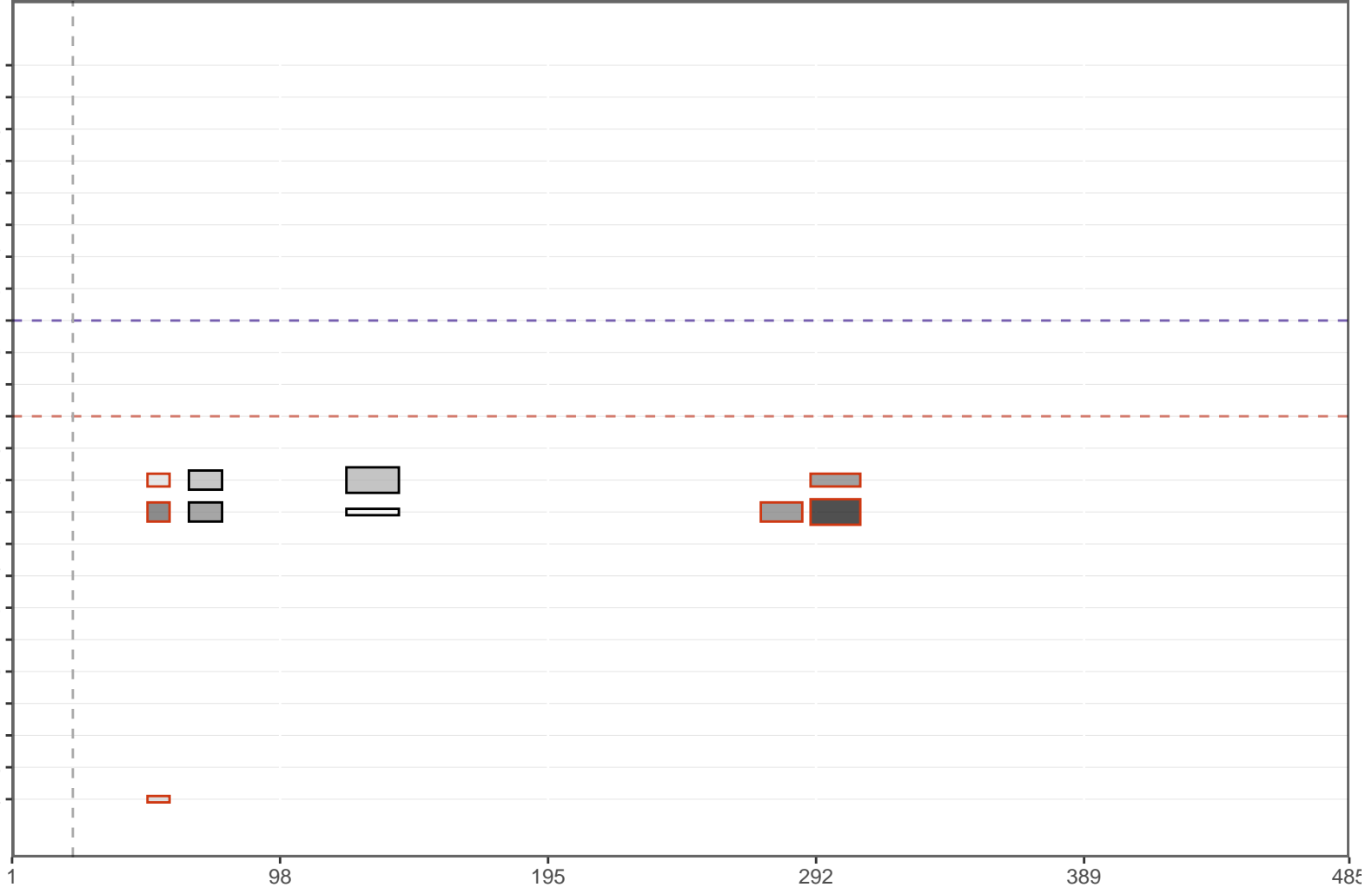
MW indication



Molecular weight

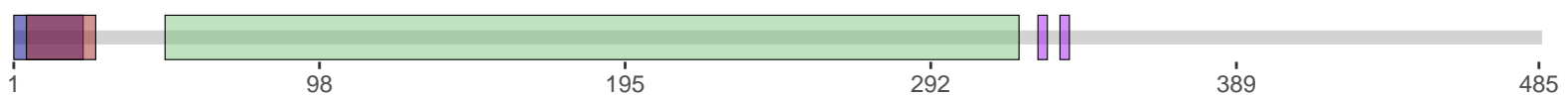


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

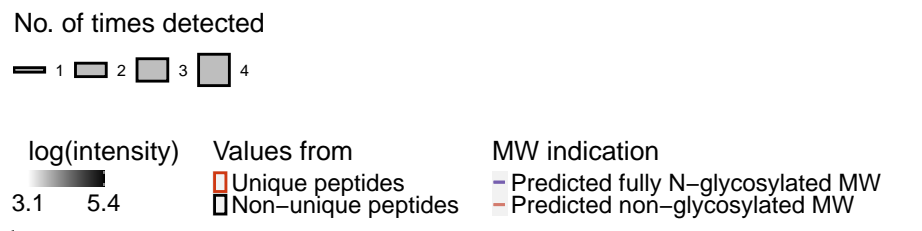
Pfam Description



Protein sequence:

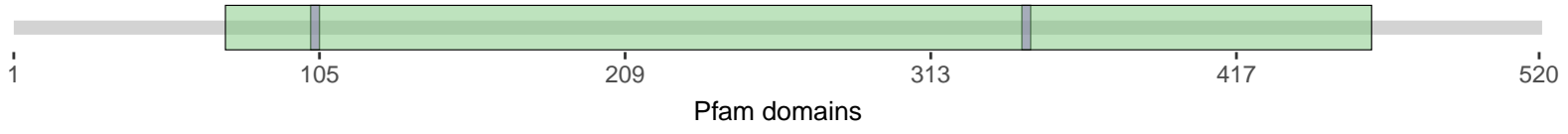
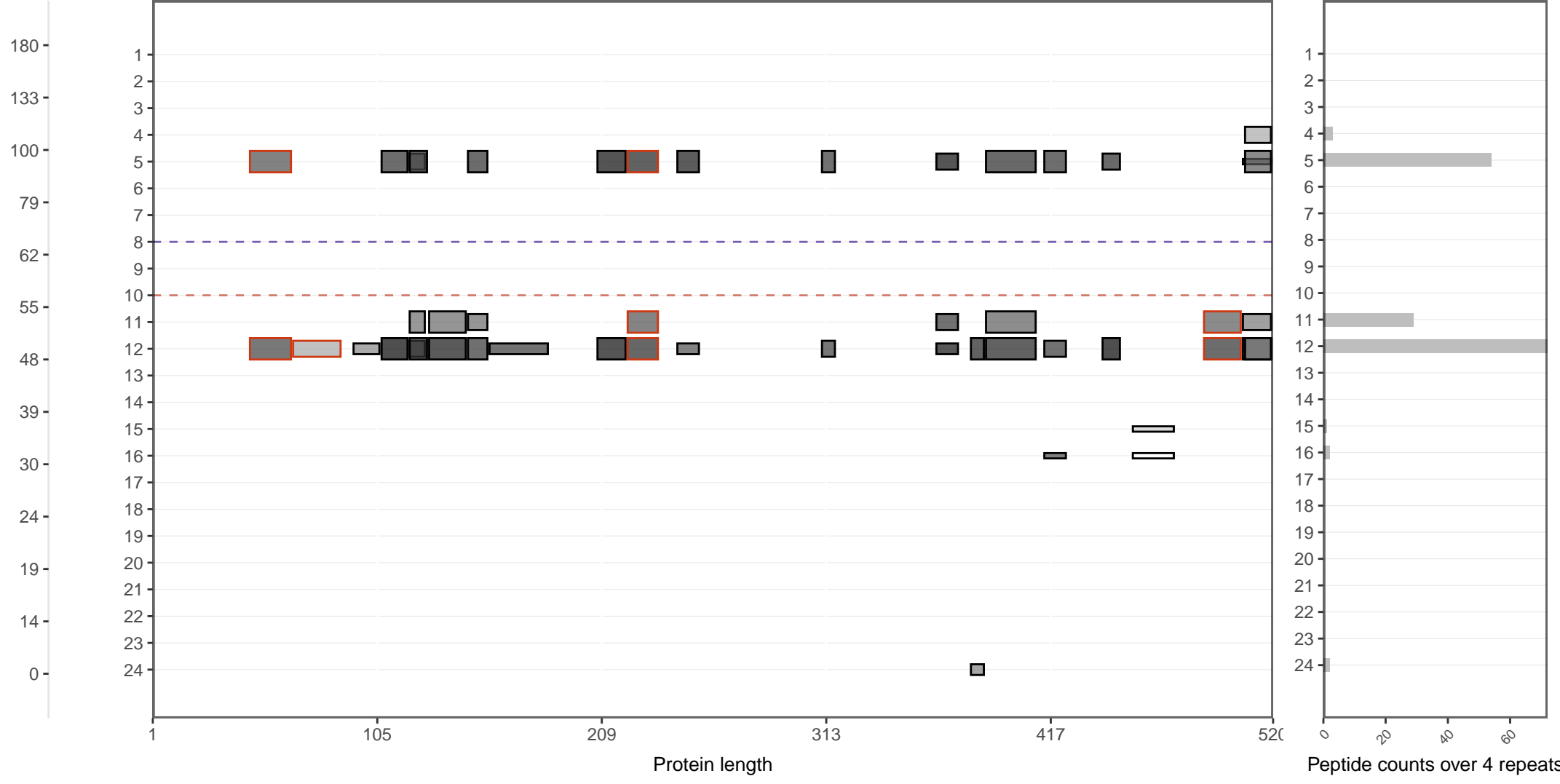
IEEDSWGTGYPGDPGPPPEVGTGLGLVAVSVMEDSEKHNLHTETLGMGYELVKRRRTANSEFPVASHVMQVGDGLKMDPLSLVMGTNPANDNYFLDENSSLGSAKPVNGHDAQLLHFWDKFLKAPQGGVRRKVEAGKQLTEAMSHRMHDDSLALVGLKLFQSEKSPVLRVVRPTGPELVDVDDWDGLKGFVRFETHGGSLGQVGMKIMRAVANIKNISGKMEQAKASAGAGLGLSLVYVWSSLDEAFSA

NbL10g16050.1 serine_hydroxymethyltransferase_3_chloroplastic-like [MW = 56.08 kDa]



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain PF00464 Serine hydroxymethyltransferase

Protein sequence:

IAGASAYPRDFYPRLRKADAVGALMMDDMAHISGLVAASVLANPFEYGDIVTTTHKSLRGRGGMIFKDPVLGVDESANNVFPGLGGGPHNHTIGGLAVLKHAKSAEFAKQGNQVSNCRALASRLTELGYKLVGGSDNHLVLDLRLPCTDGARVEKILDMASITLNKNSVPGDKSALVPGGRHRSRPMTRRGTFEKEFAVADFIHEGVGTFLEAKNSVSTNLGGFMKFTAPDFNLIDNLDLQKRVFAFTSGYPLGL*

NbL10g15970.1 abscisic_acid_receptor_PYL2-like [MW = 20.99 kDa]

No. of times detected



log(intensity)



Values from



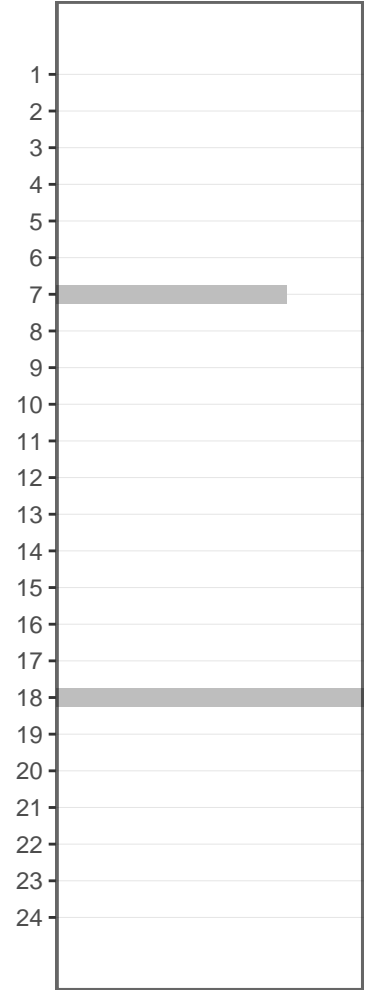
MW indication



Molecular weight



Gel Slice

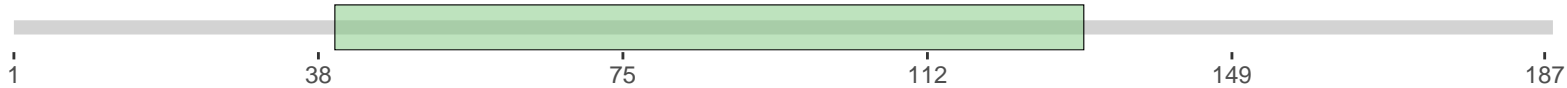


Protein length

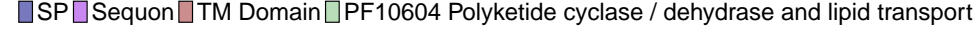
Peptide counts over 4 repeats



Pfam domains



Pfam Description

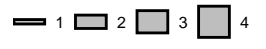


Protein sequence:

SMREIVSYVSGIPALTSFTEERLELDDDEKHLSPKVVGGHRLNLYRIVTSVNEFKNGKPYTIVLESYVDPEGNTGEDTKMFTDTVVKLNQLKLGVVMAALHGHE

NbL10g15890.1 glycine_dehydrogenase_(decarboxylating)_mitochondrial [MW = 113.89 kDa]

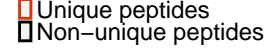
No. of times detected



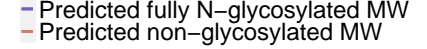
log(intensity)



Values from

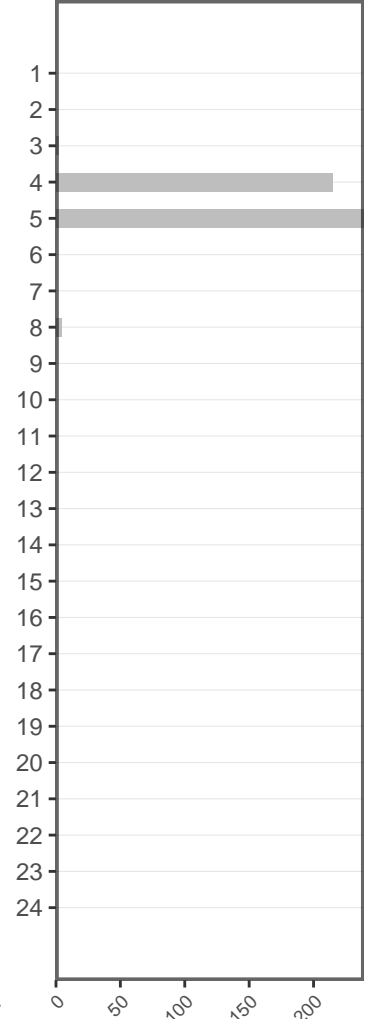
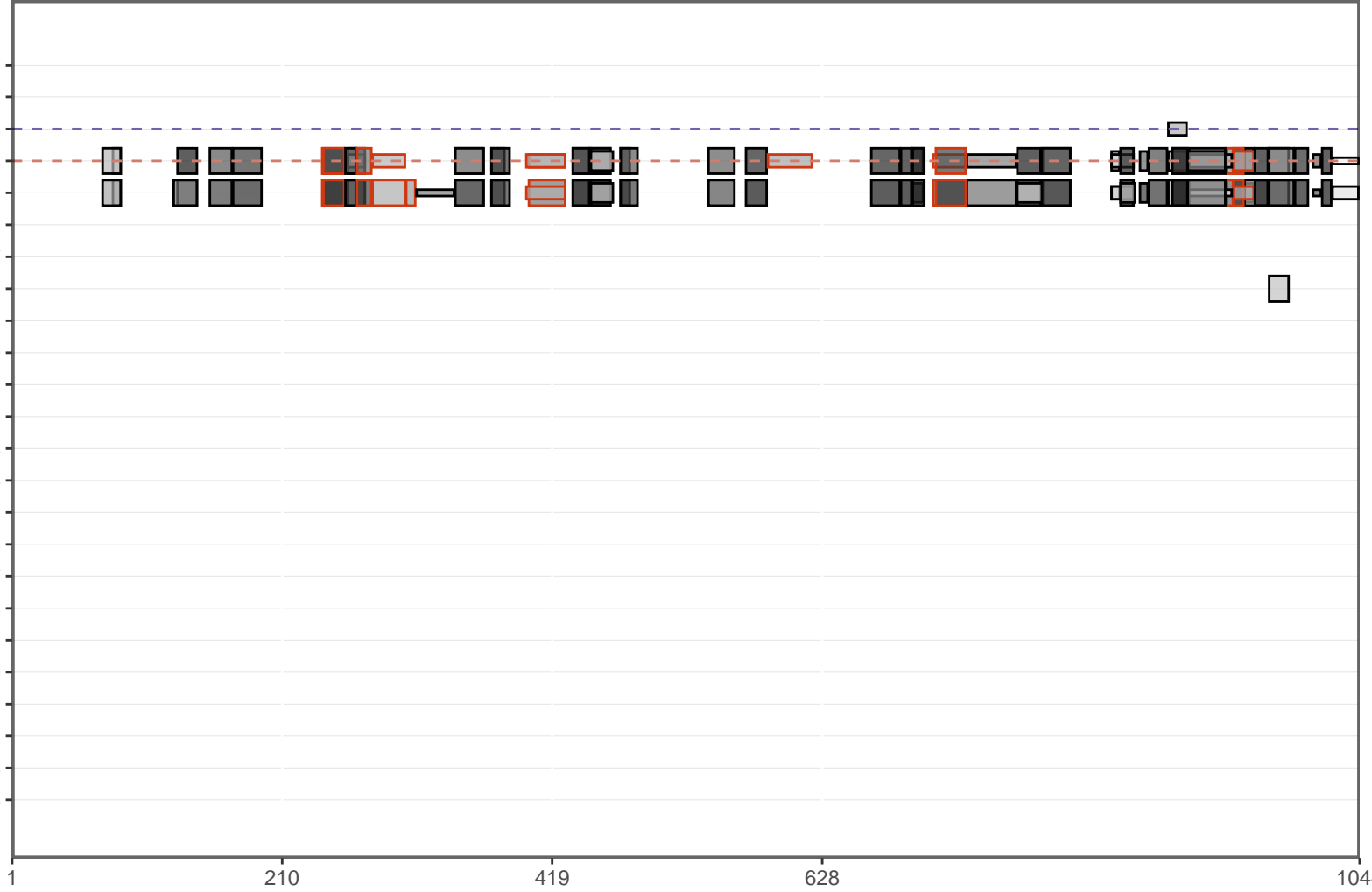
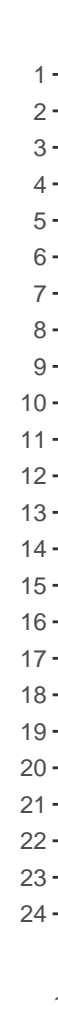


MW indication



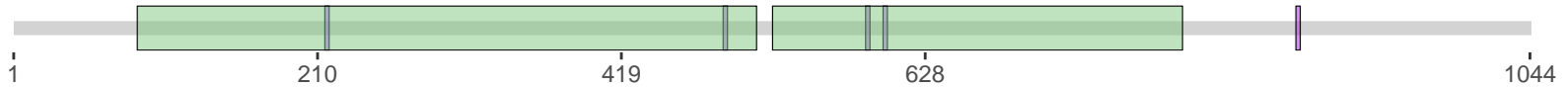
Molecular weight

Gel Slice



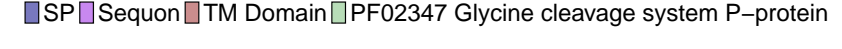
Peptide counts over 4 repeats

Protein length



Pfam domains

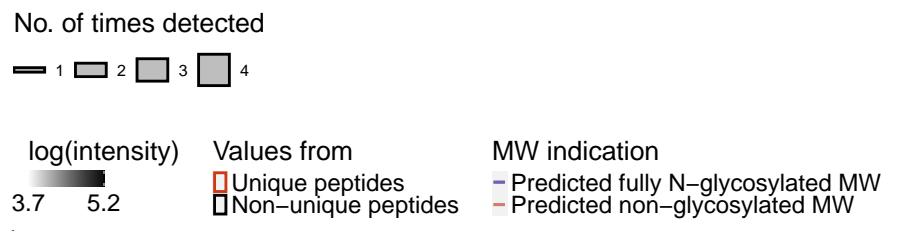
Pfam Description



Protein sequence:

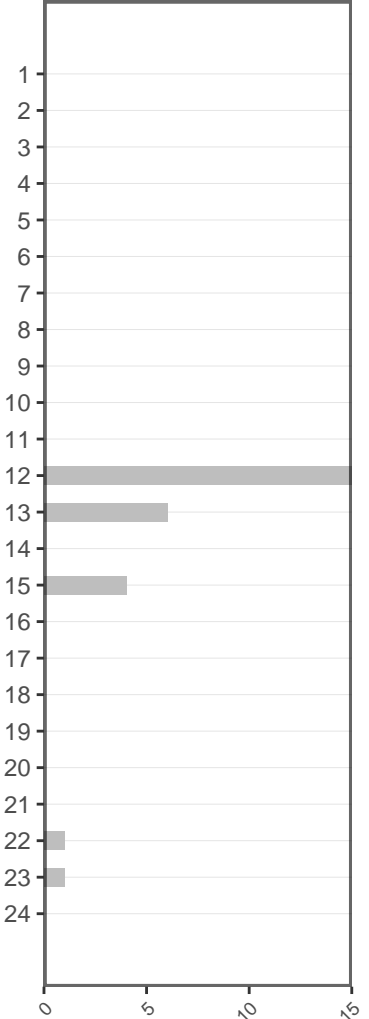
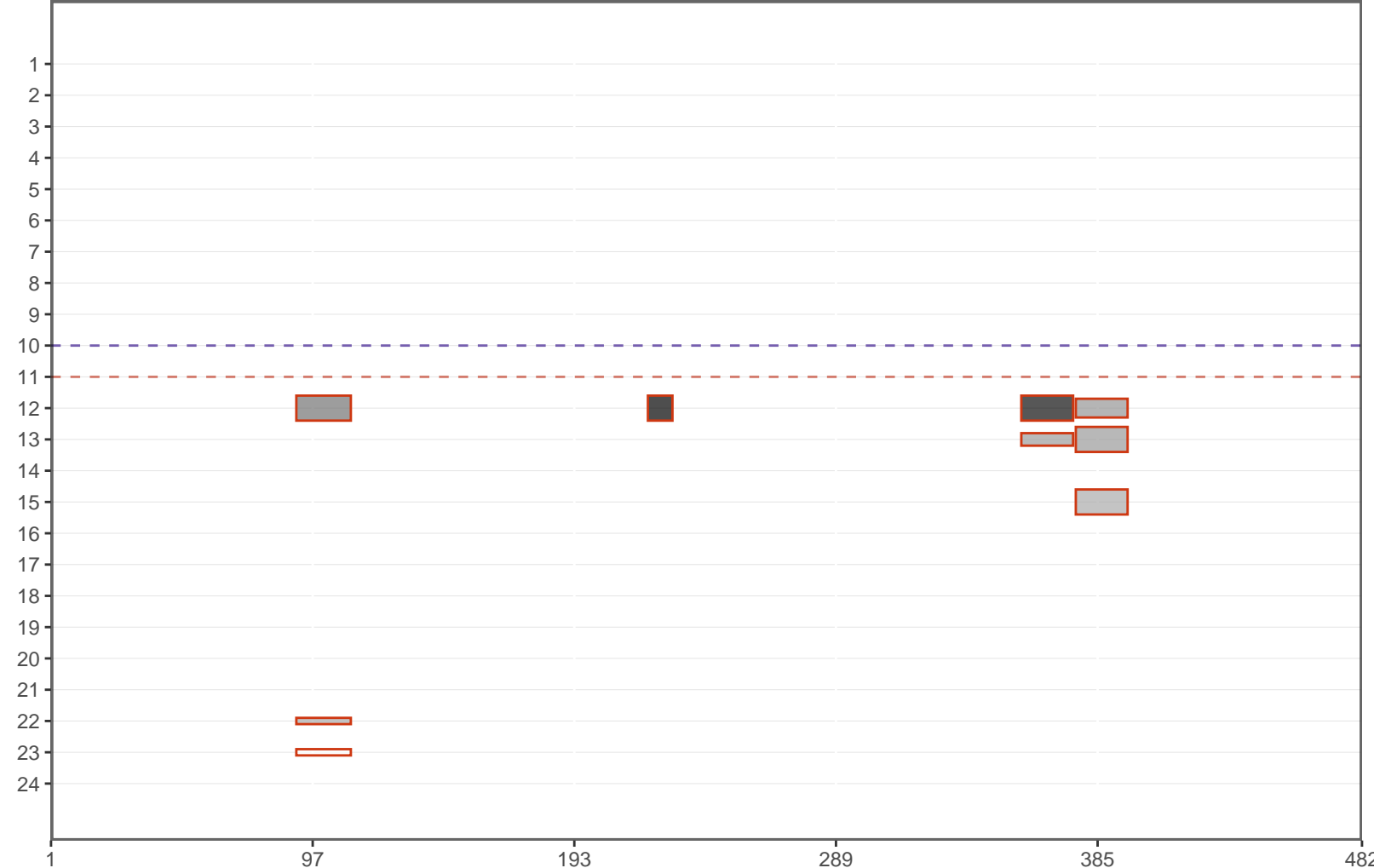
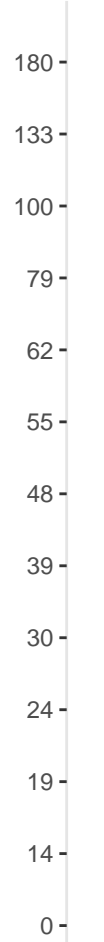
.FKYFALGKPVTTTADQSIAGEVENLIPSGILVRETPYLTHQIFNSYHTEHELLRVLHKLGEKDLSLCHSMPLFGSGTMLNATTEMMPVTVWPNFTNHPFATFEGAAQVQEMFKDLGDLCTITFDGDFSLQPNAGAAEYAGLMLVLAHWARGDHRNVCIPVSAHGTFNPSAAMOGAMKIVVGTDAKNINNEELRKAAEANKDKLAALMVTYPTTHGVVEEGDEICKIKIHDSGGVYMDGANMAGVGLTSPGFIGADVCHLNLHKTFQIPHGSGGPGMGPIGVXKILAP

NbL10g15840.1 UDP-sulfoquinovose_synthase_chloroplastic [MW = 53.35 kDa]

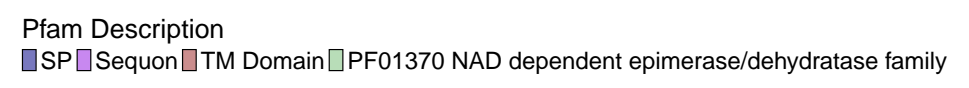
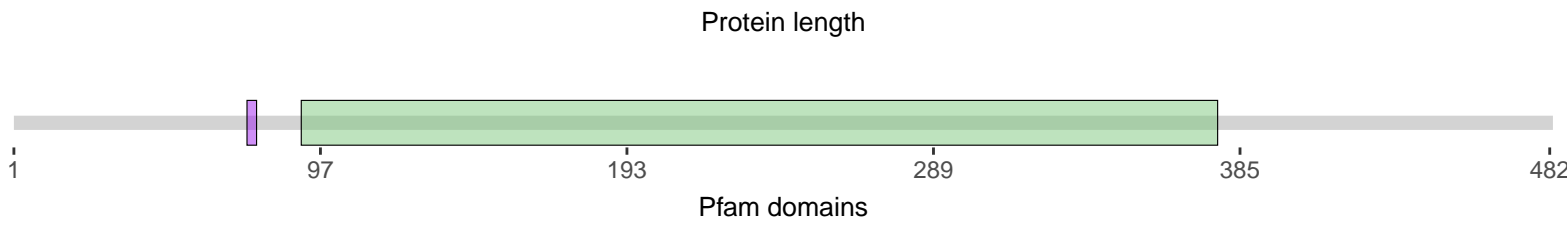


Molecular weight

Gel Slice



Peptide counts over 4 repeats



Protein sequence:

CLGTMGEGYGTPTNIDEEGFITTHNGRTDLPYPKGASFFVHLKVKHDSHINAFCTKAWGRATLNGGVYGVRTDETMMHEDLVNRLDYDAVGTALNRFQVGAAGHPLTVYGGKGGTRGYLDRDITVGGVEIAIANPAKPGEFRRVYNGFTQGFVNELAAVAKAGEKLGLEVKTSVFNPRVVEAEHYYNAKHTKLELGLQPHLLSDLSLNLFAVQYKDRVDTKQMPSEVWKKGAKPKTVAA

NbL10g15720.1 elongation_factor_2 [MW = 93.97 kDa]

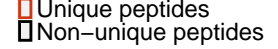
No. of times detected



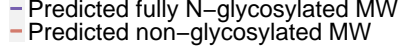
log(intensity)



Values from



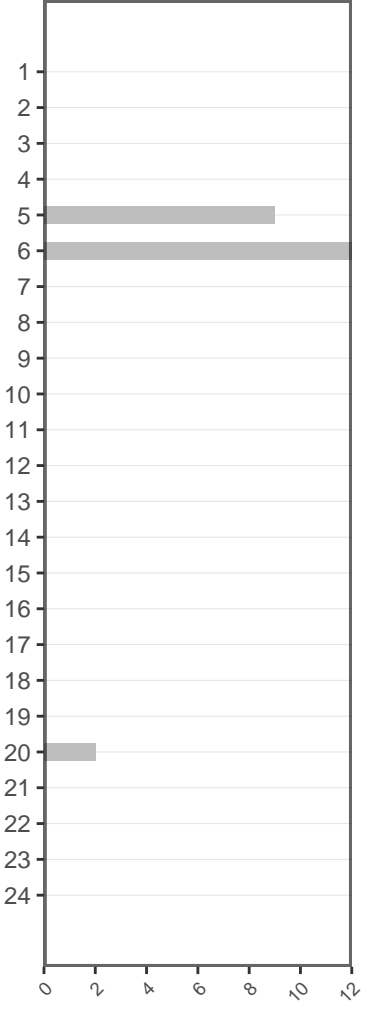
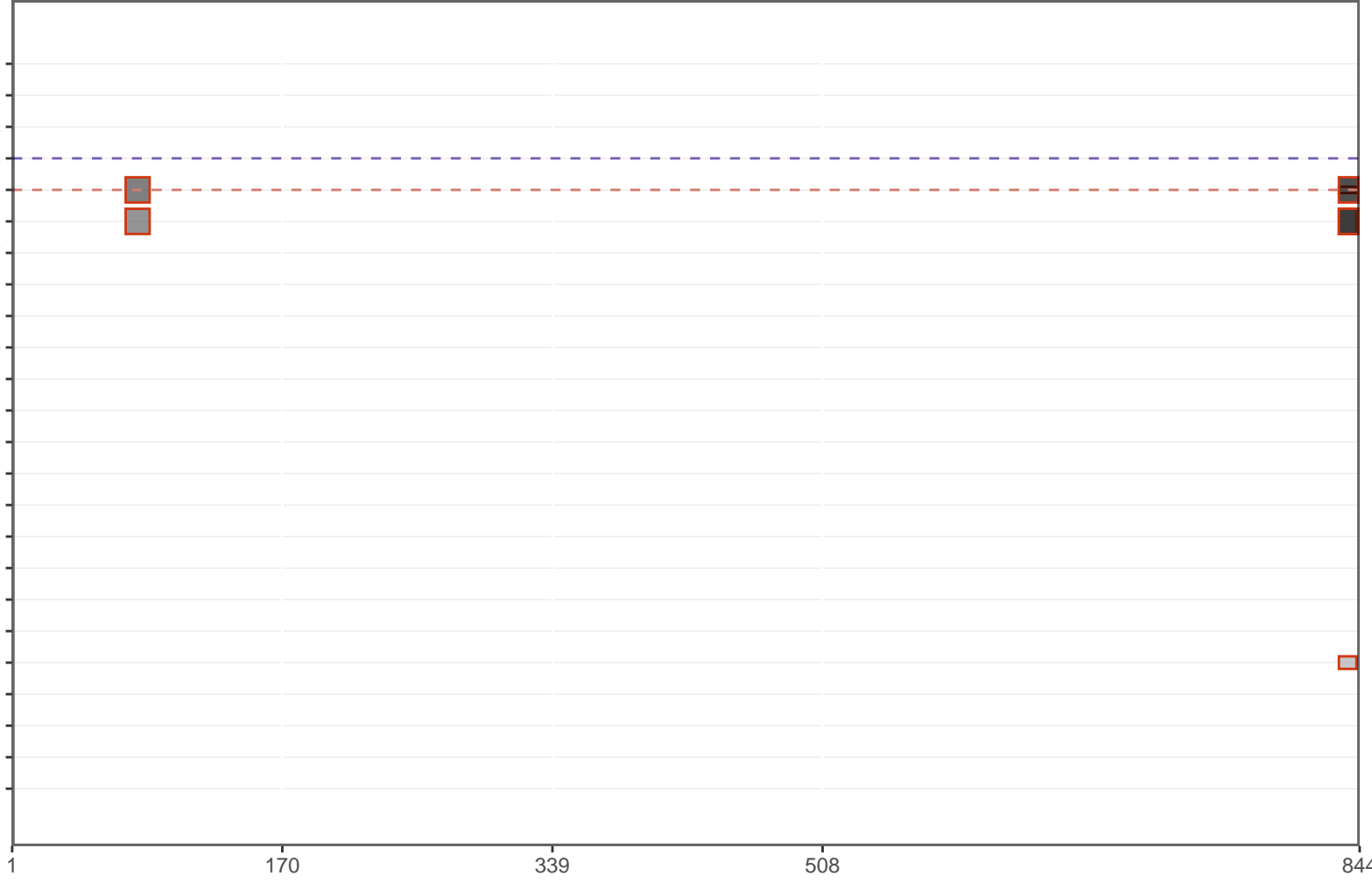
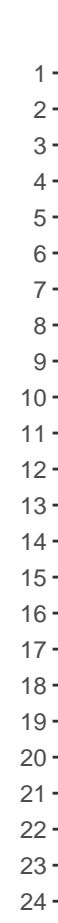
MW indication



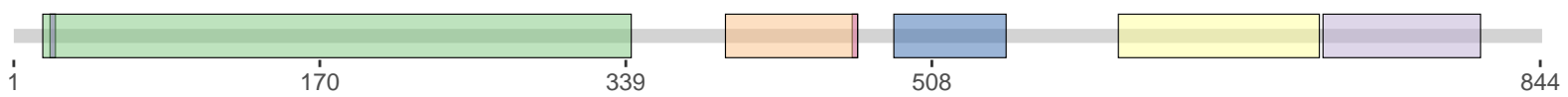
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

- SP
- TM Domain
- PF00679 Elongation factor G C-terminus
- PF03764 Elongation factor G, domain IV
- Sequon
- PF00009 Elongation factor Tu GTP binding domain
- PF03144 Elongation factor Tu domain 2
- PF14492 Elongation Factor G, domain III

Protein sequence:

/RIMGPNYYPGEKKDLYVKNVGRITVWVGKGETVEDVPCGNTVWVGLDQFTKNAFLTNEKEVEAHPIRAMKFBVSPVVRVWVGGKLASDLPKVEGLKRLAKEDPMVLCGSEEGEHAGADELHLEGLKLDQDFMGGAEIIVSDPVVVFRETVLEKSRITVMSKSPNKNRLVMEARPLEEGLAEIIDDGRIGPRDDPKVRSKILSEFGWDKDLAKKWKVCFGPETTGPNMVDVMCKGVQYVLEIKDQVWAGFQWASKEGALAEENMRGIGFEVCDVLIADAHF

NbL10g15690.1 cytokinin_ribose_5'-monophosphate_phosphoribohydrolase_LOG8-like [MW = 23.36 kDa]

No. of times detected



log(intensity)



Values from



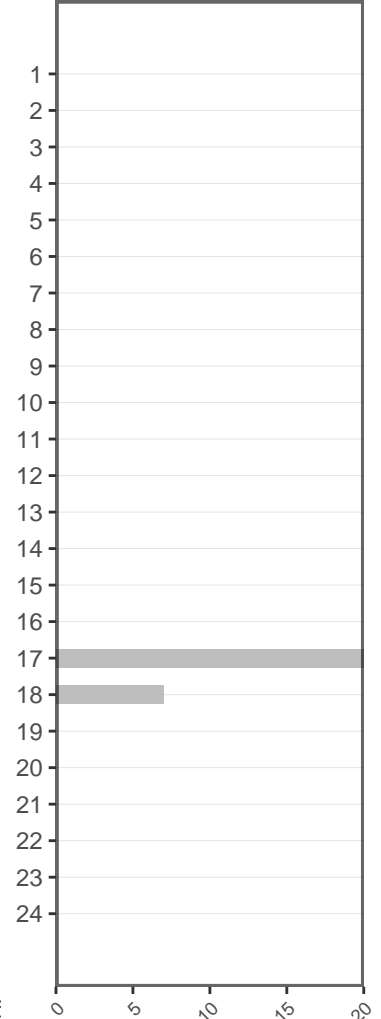
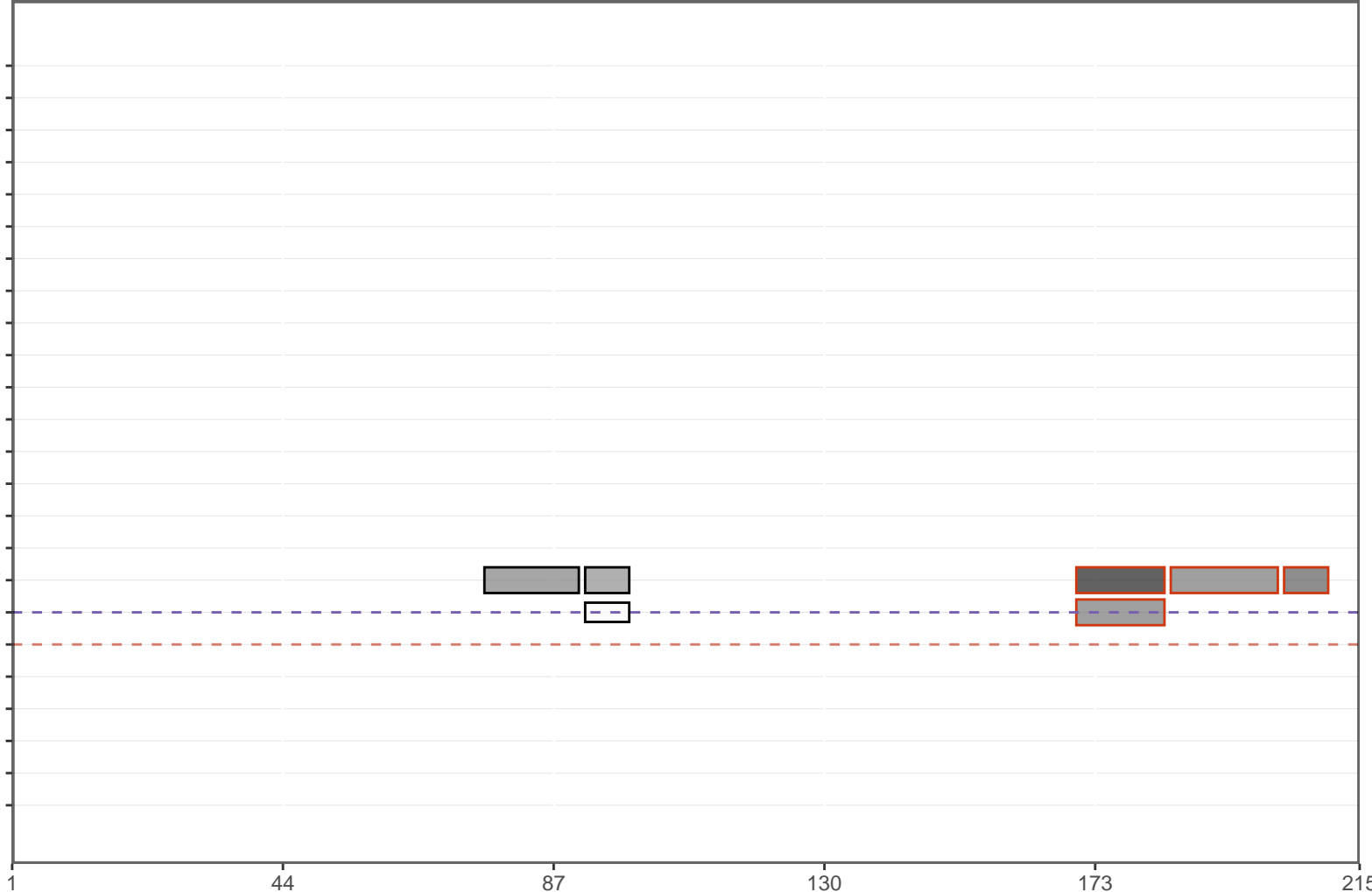
MW indication



Molecular weight

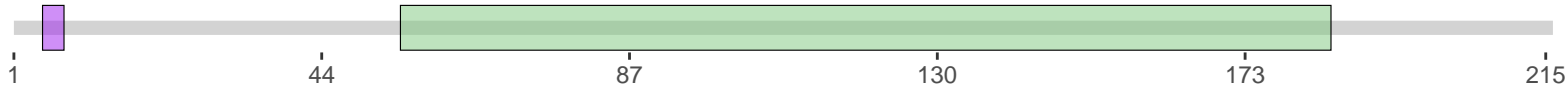


Gel Slice



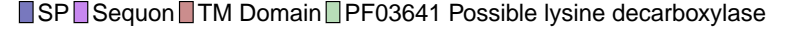
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL10g15540.1 ran-binding_protein_1_homolog_c-like [MW = 18.74 kDa]

No. of times detected



log(intensity)



Values from



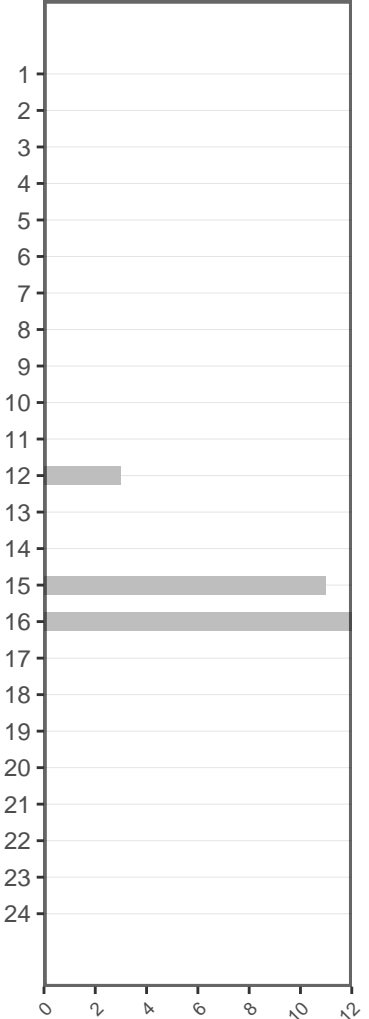
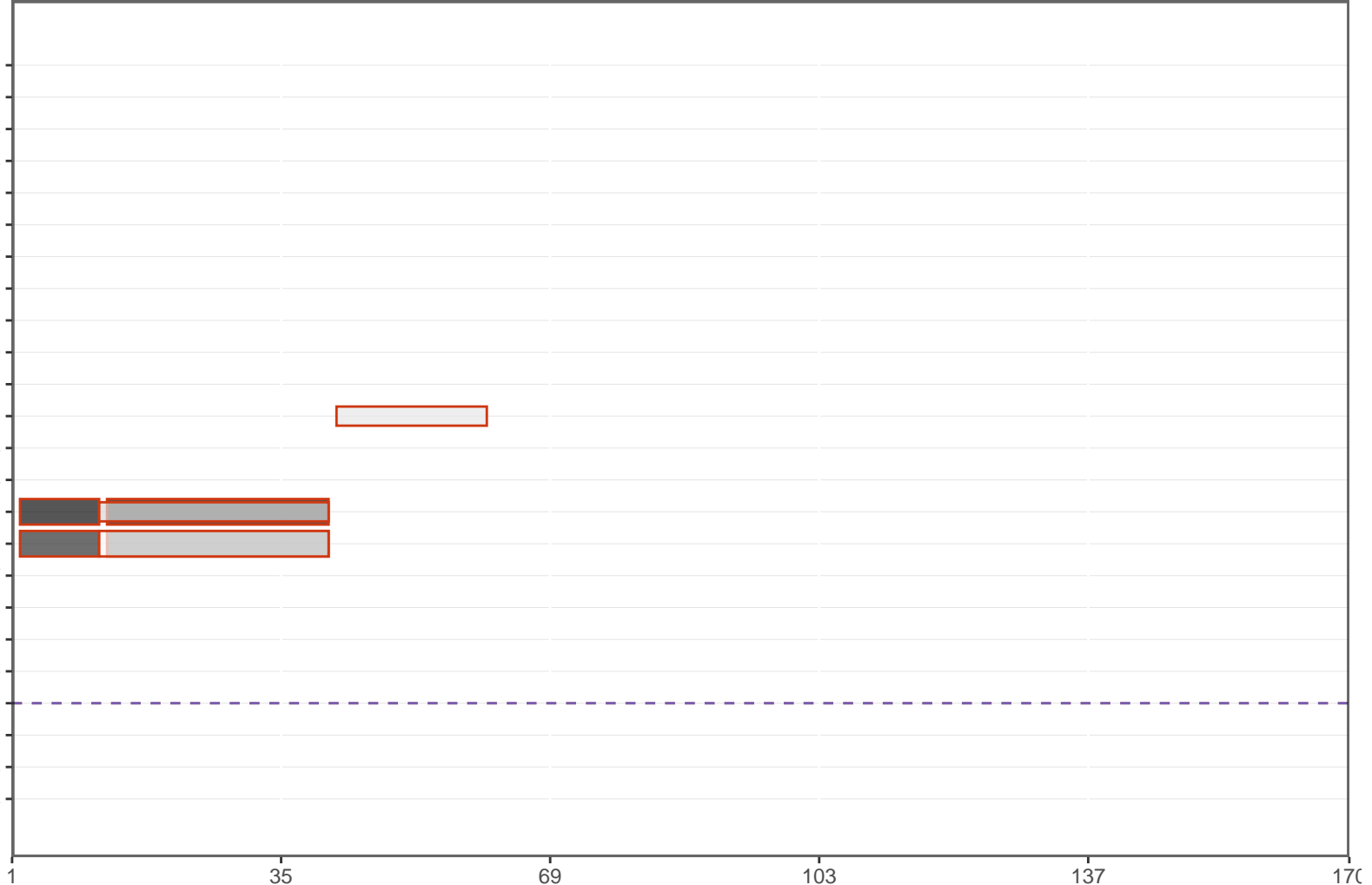
MW indication



Molecular weight



Gel Slice

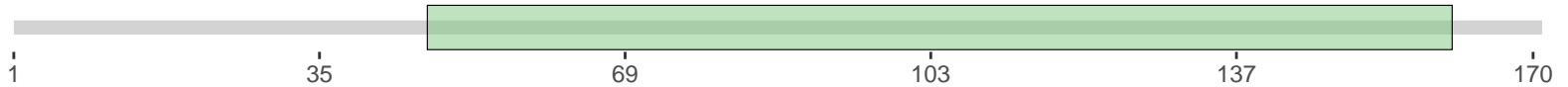


Protein length

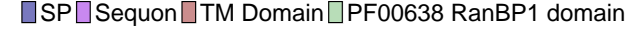


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

NAWKERGAGTVKLLKHMETGKRVLLVMRQSKTLKIGANHLVLPMTMBGIEHAGNEKSGVWHAADFADGELKEETFGIRFASIESEYVYVAFSGFGGCVFSP

NbL10g15520.1 SNARE-interacting_protein_KEULE [MW = 75.56 kDa]

No. of times detected



log(intensity)



Values from



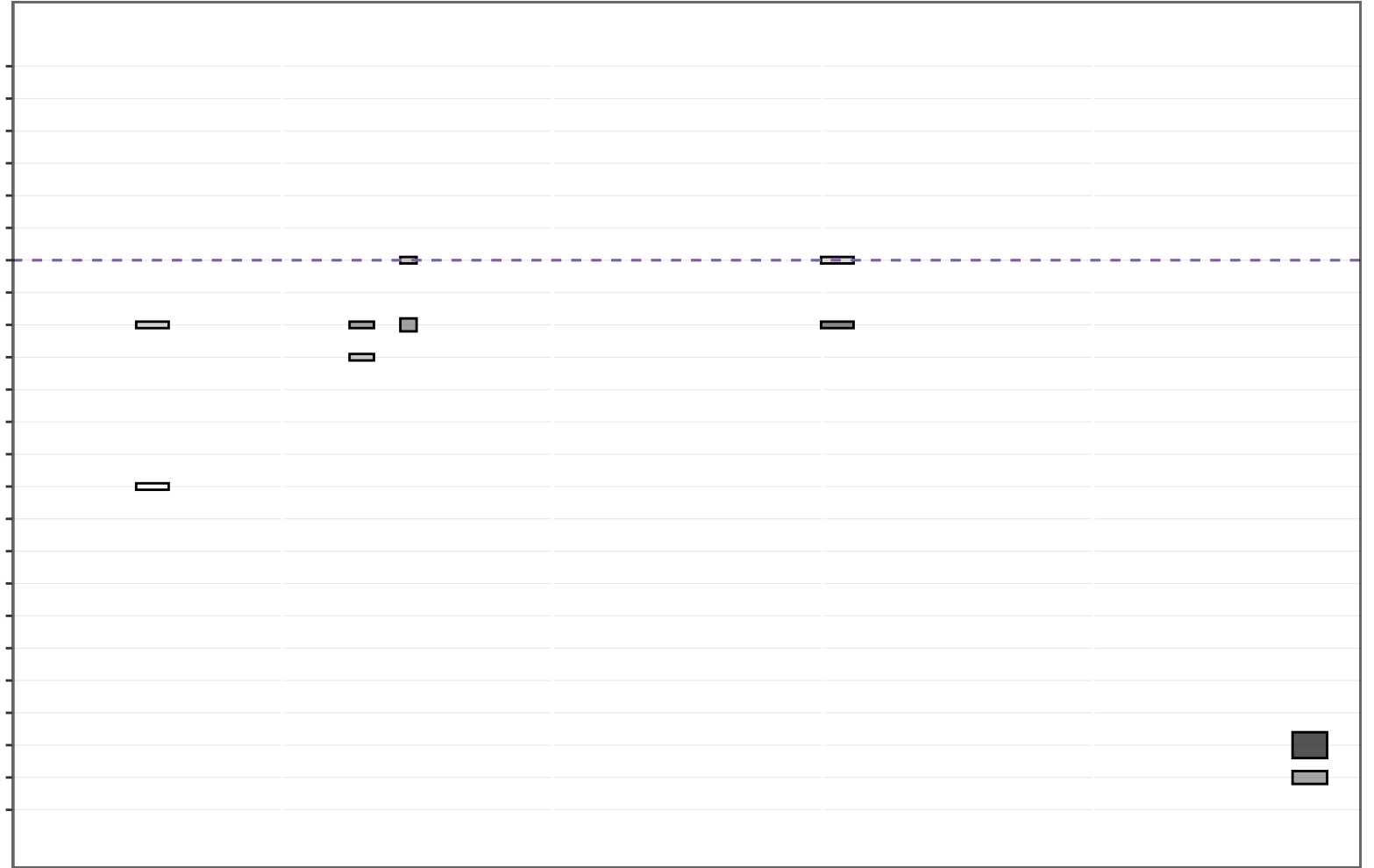
MW indication



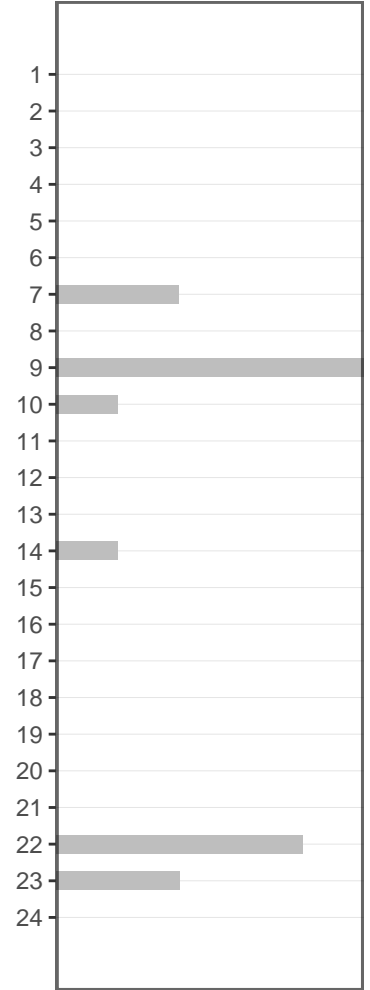
Molecular weight



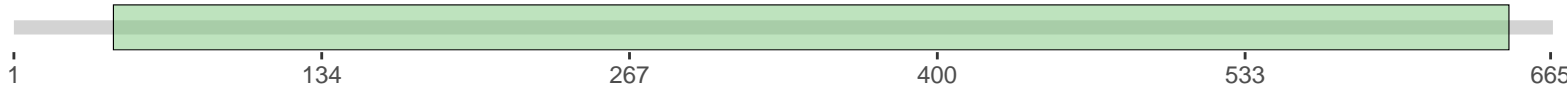
Gel Slice



Protein length

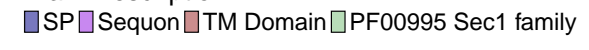


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL10g15500.1 thioredoxin_domain-containing_protein_9_homolog [MW = 24.26 kDa]

No. of times detected



log(intensity)



Values from



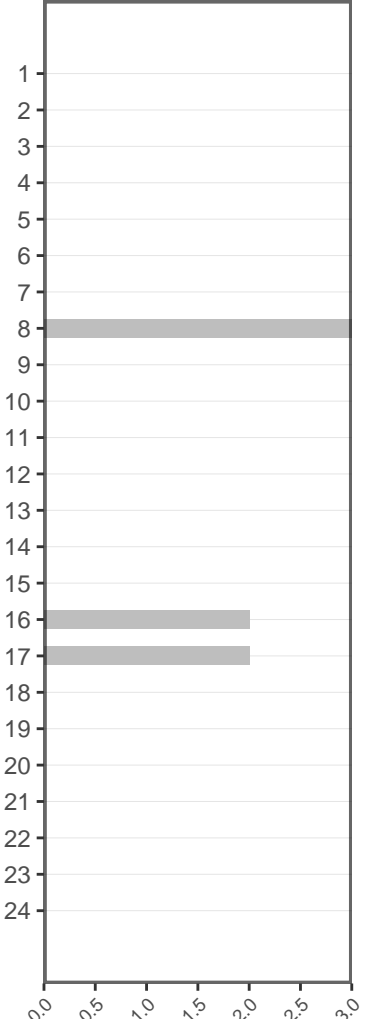
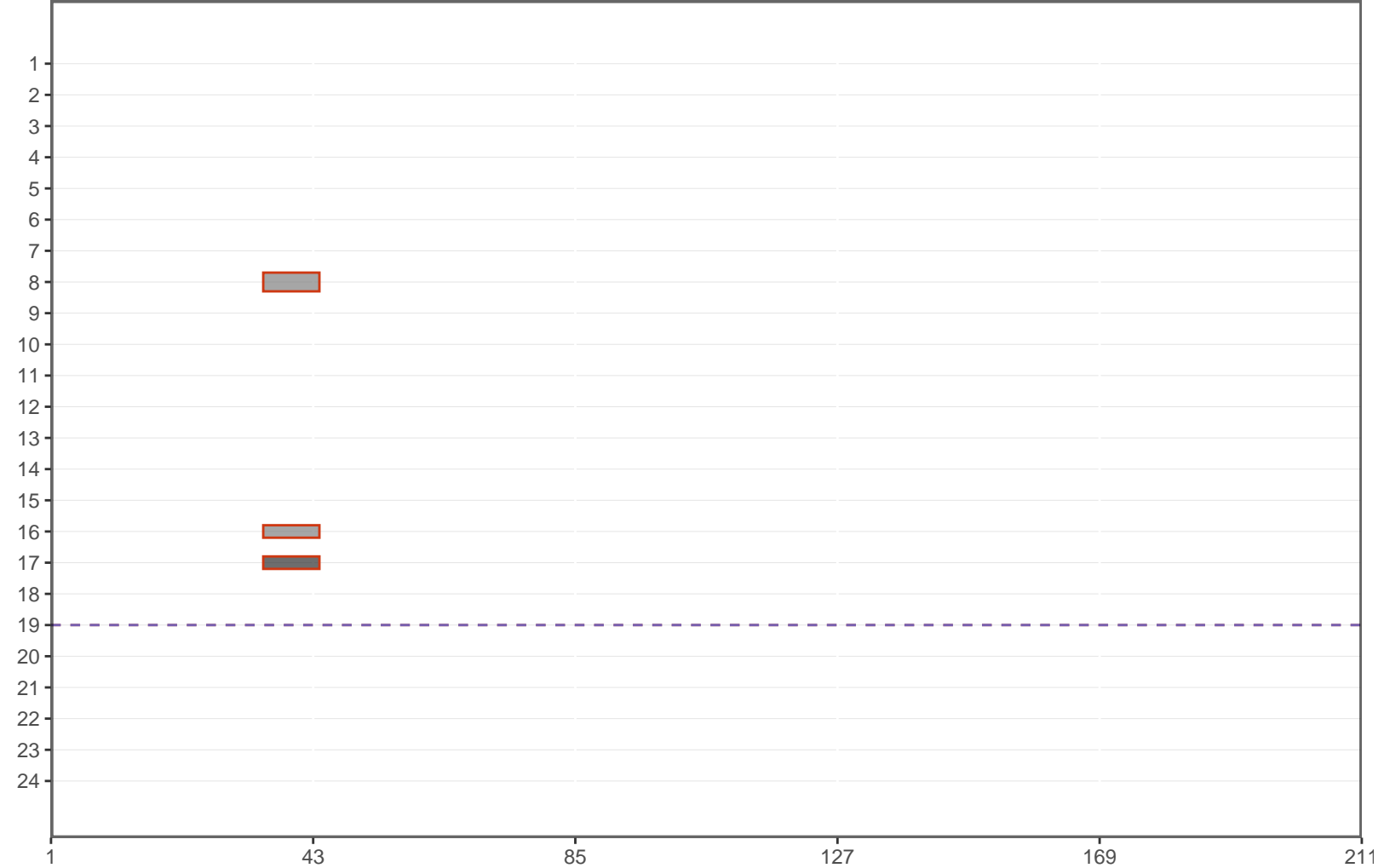
MW indication



Molecular weight



Gel Slice



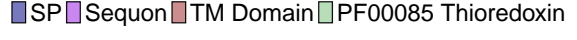
Protein length



Pfam domains



Pfam Description



Protein sequence:

IFYRDNIWPCVKMDKHLSLAKGHETRFVNIHAEKSPYLAEKLRIVLPTLALIVKHAKVEDYVVGDFELGHTDEFSTEELEERLAKAEVIFEGESGKLIKAPSKSVRGSANFDGSDSEI

NbL10g15460.1 putative_transferase_CAF17_homolog_mitochondrial [MW = 43.82 kDa]

No. of times detected



log(intensity)



Values from



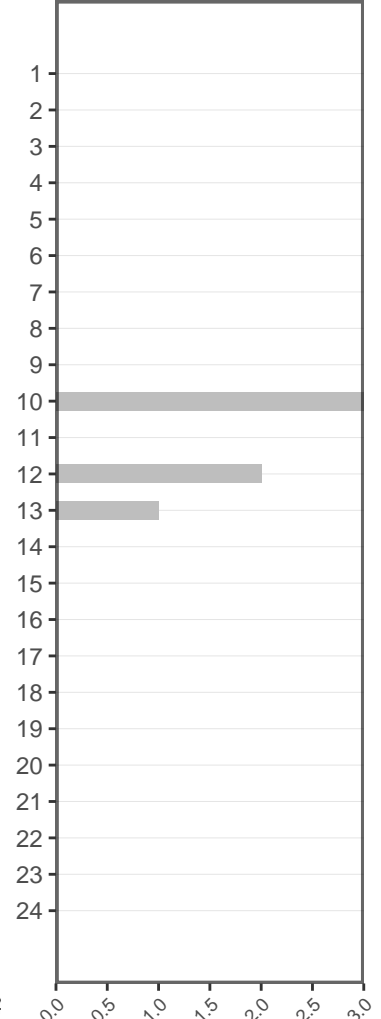
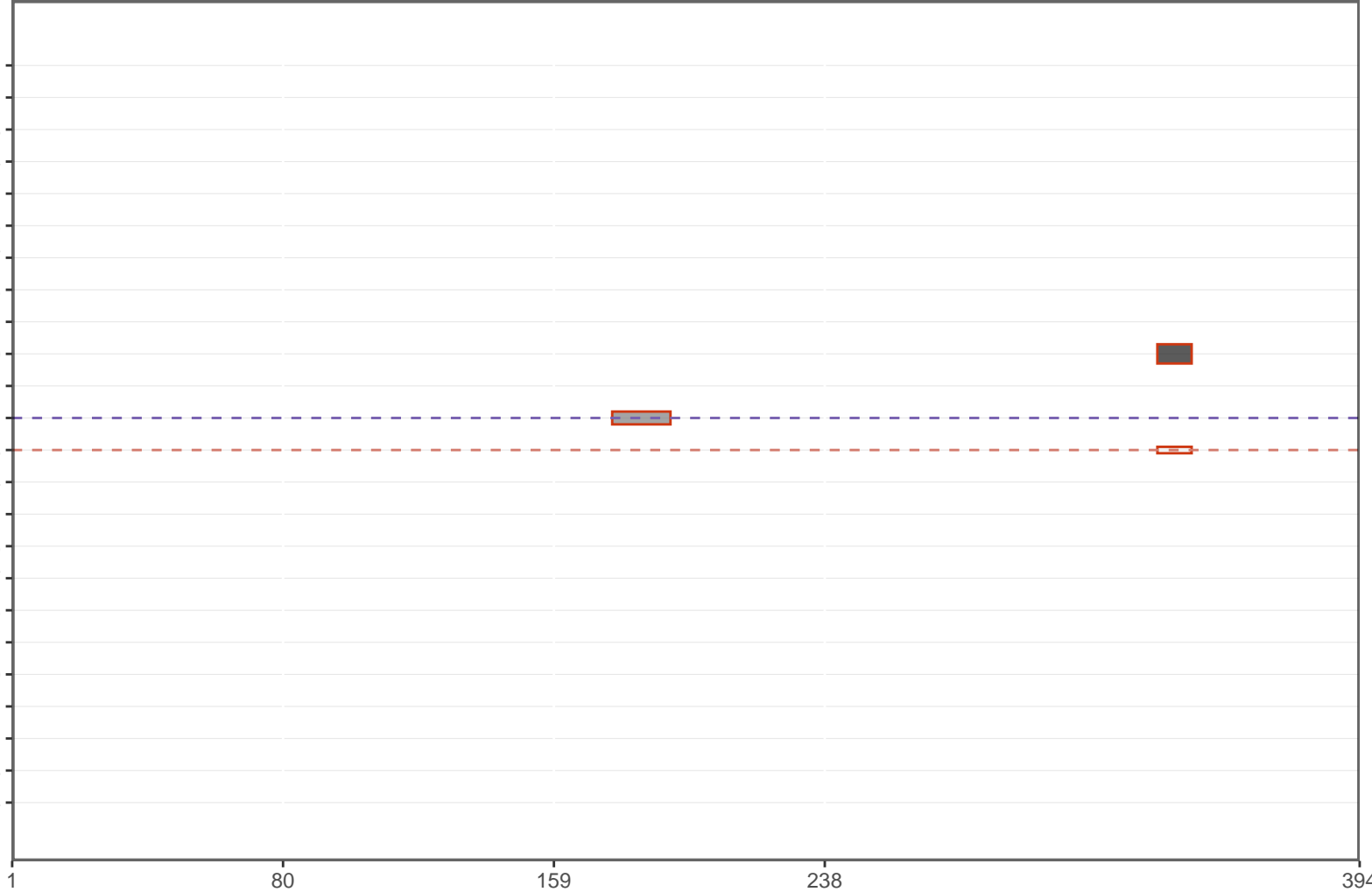
MW indication



Molecular weight



Gel Slice



Protein length

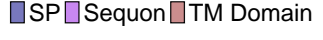


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

.GIWGGGFDRSQGSAGGNRIGWLWYRDRPLDCLGFRGIFPNITPLVLEADKETNEENLLWRLKGVAEQSAEIPKGEVPLEYVNLAGLNGISFDKGGYVGGELIARTHHRGVIRKRLPLKFNDSCKEVEQKVPRISEVVDASSGKAGVTITLGSRGLGLLRLEAFKGSLTRDLDDKVKVQAKPEWVRAEWLLDHQGGTAAV

NbL10g15330.1 uncharacterized_LOC107808286 [MW = 28.56 kDa]

No. of times detected



log(intensity)



Values from



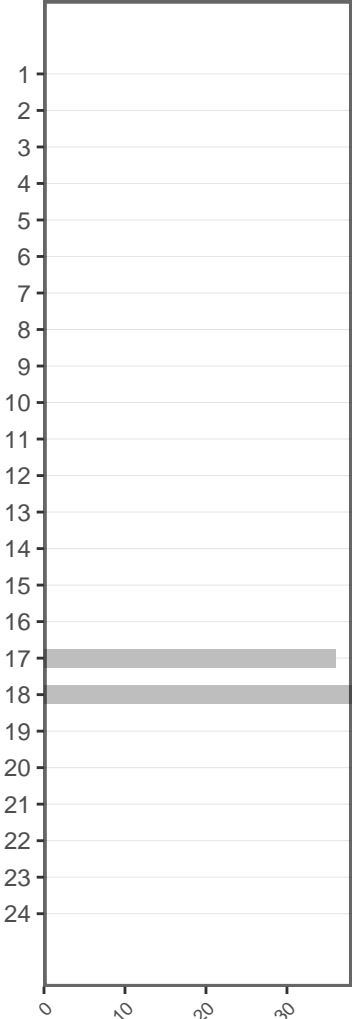
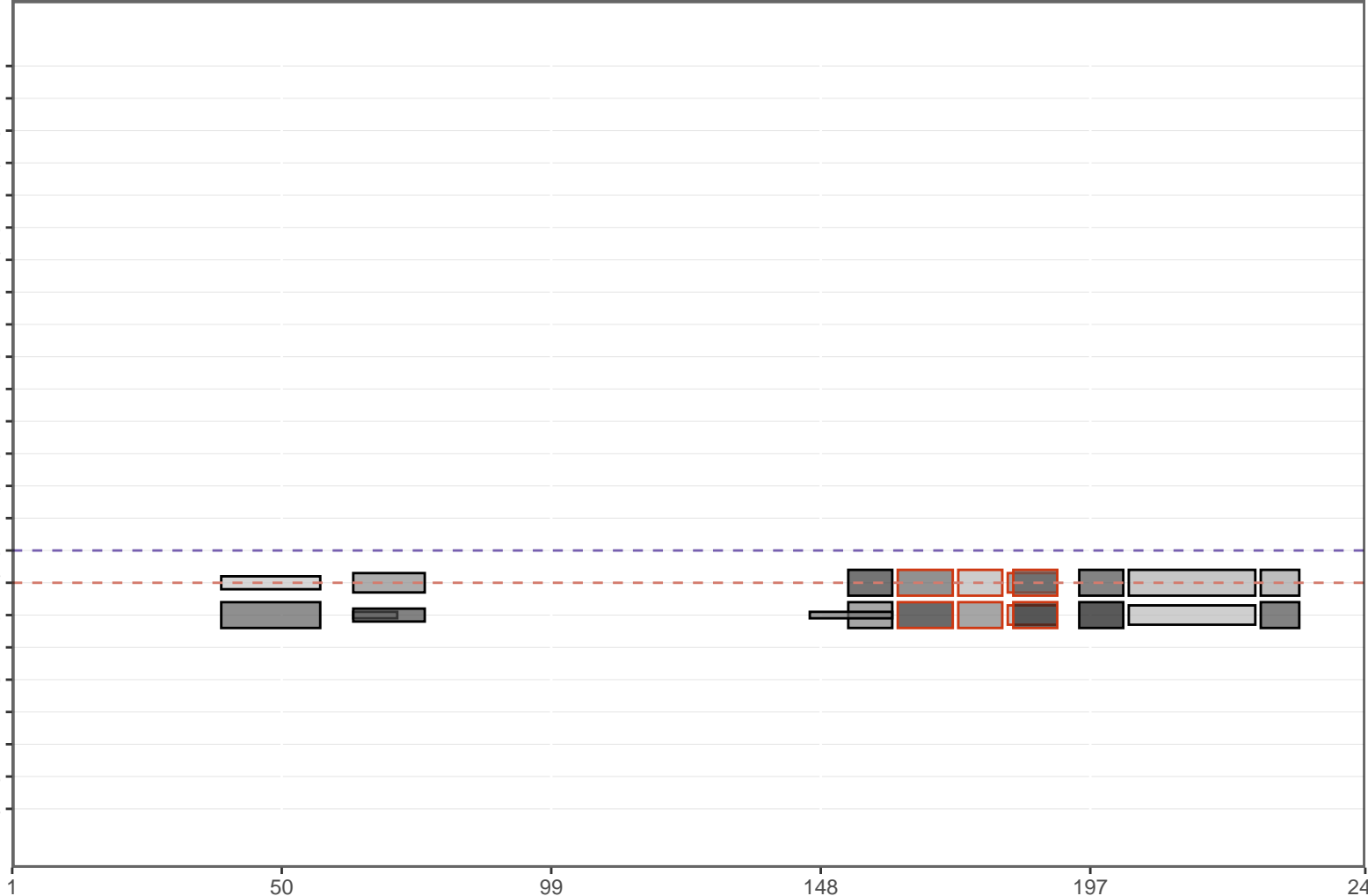
MW indication



Molecular weight



Gel Slice



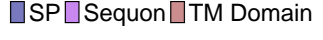
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

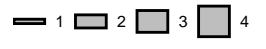


Protein sequence:

EAQIEIEFARLRPRPLAKKEFFDHLQVEVGNLRFSSMTKTQEVEDRUELELQKALHEATEAYDKMQADILATKKNLTDILTSKDKVATLDDLVERNELNRPLLTLDDENATAHVSNQKGAEMEKLRLGLVLRVLTV

NbL10g15310.1 elongation_factor_G-2_chloroplastic [MW = 86.07 kDa]

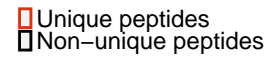
No. of times detected



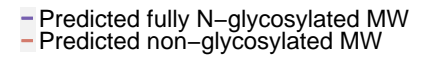
log(intensity)



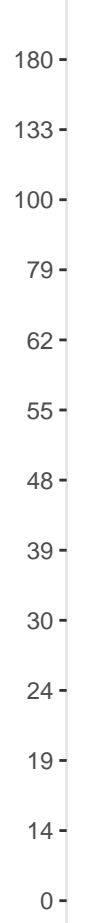
Values from



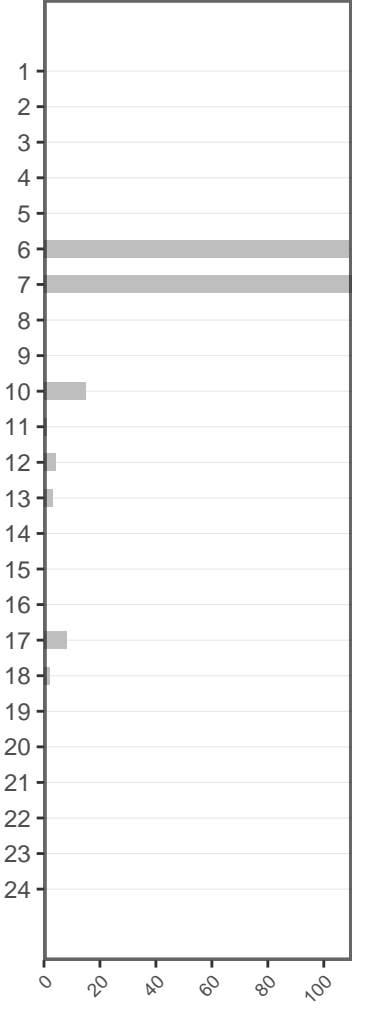
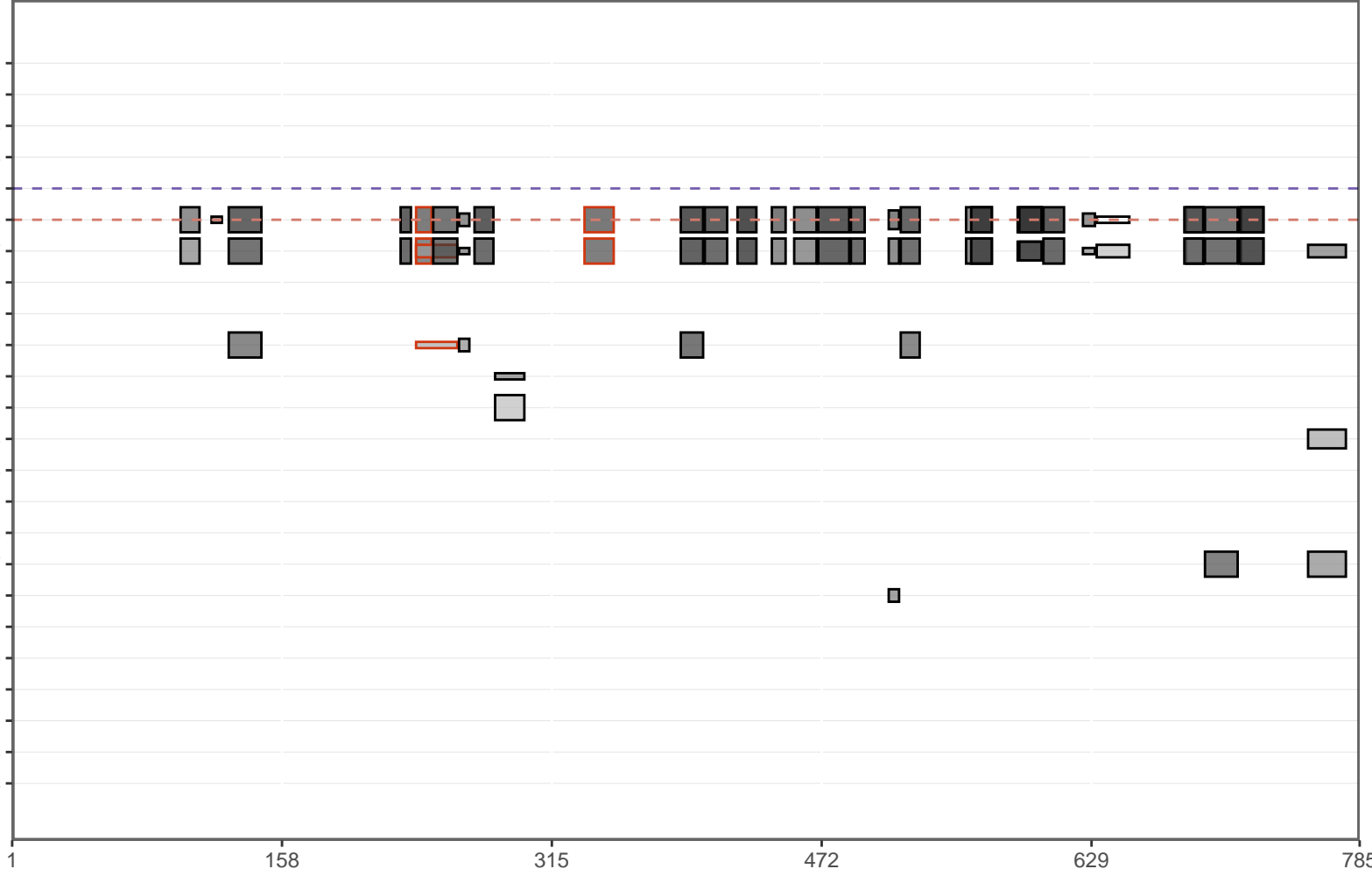
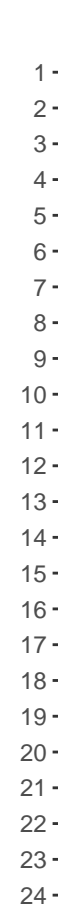
MW indication



Molecular weight

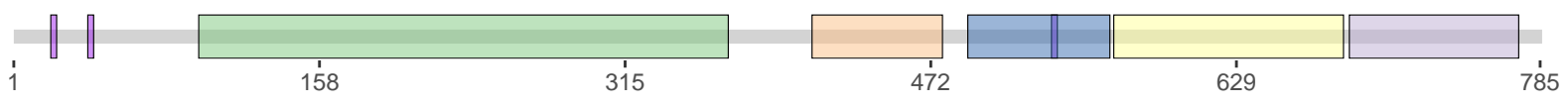


Gel Slice



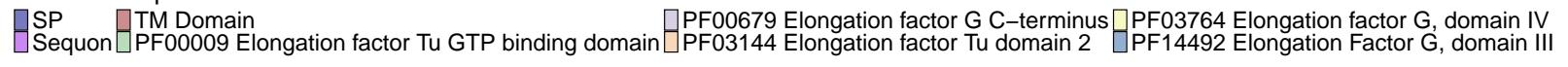
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

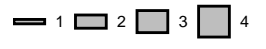


Protein sequence:

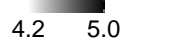
ENPEVTERAASDDEPFAGLAKIMNDPFVGLTFVRYVYSGKLSAGSYVWNNANKGRKRERIGRLLEMHANRREDIKTALTDGVALAGLKDTHITGETLADRPKPKVLERMDFDPDPVIVKAEPKTKADIDKMATGLKLAGEDPSFHSRDEINQTVIEGMSLELHEIVDRLLKRFKVEANVCAFDVWYRESISKNSEVYVYHKKQSGSGGQFADTVRFEPMETGGDYEFKSEIKGGAVPKVEYIPGVIMKLEEGMSNGLVAGFPVAVDVRALVVDGSHYHDVSSVLAFLQLAARG

NbL10g15300.1 hsp70-Hsp90_organizing_protein_2 [MW = 65.01 kDa]

No. of times detected



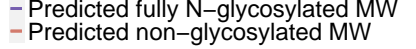
log(intensity)



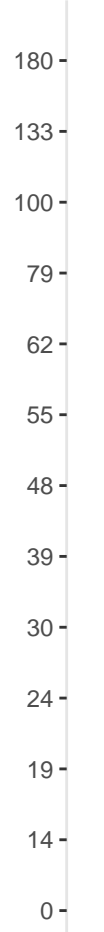
Values from



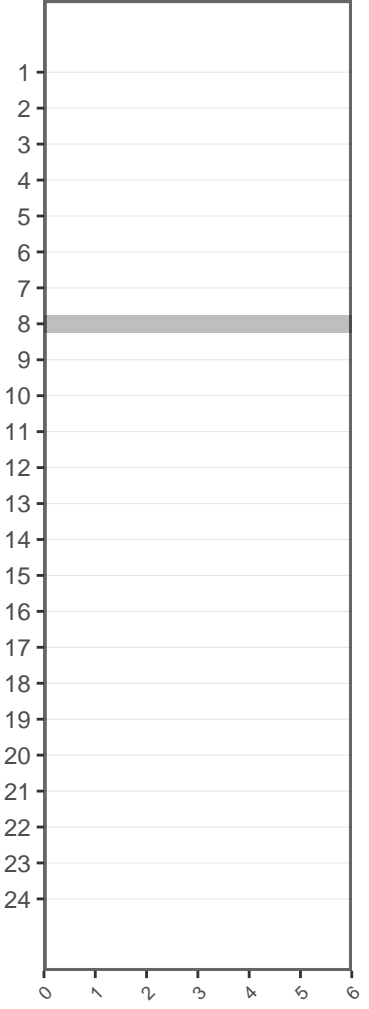
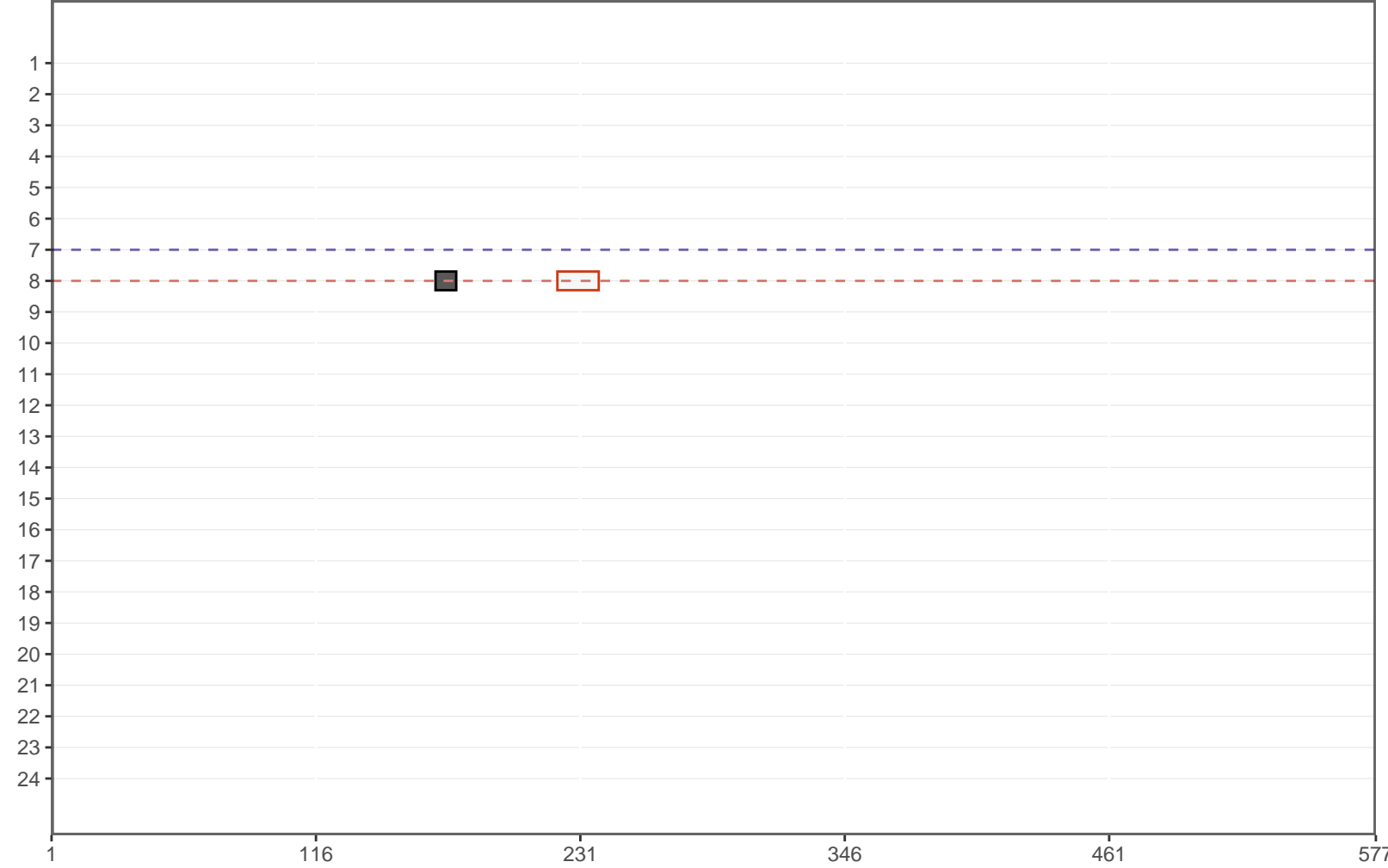
MW indication



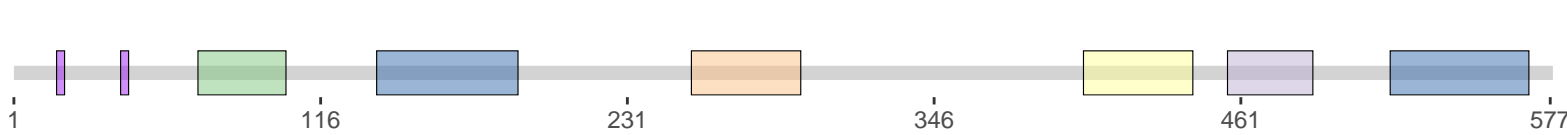
Molecular weight



Gel Slice

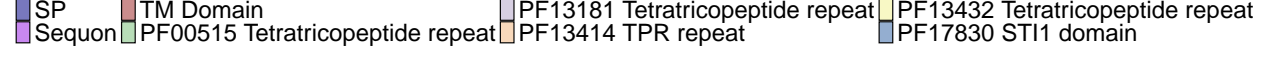


Protein length



Pfam domains

Pfam Description



Protein sequence:

ELDDDISFTINRAAVYLEMGKYEKGGKGGDAVERGRELRSDFKMIARALTRKGTALAKMAKSSKDFEAVIEVFGKALTEHRNFDTLKLNDAEKARKEGQEVFNQIADEEREKNGOFFKEMKYPEAVKHHTESIKRNPDPRAVSNRAAGYTKLAAALPEGLNDAEKIQLDPTFVKGYTRKGAIVGFFMKEVEKAMETYGQGLKHDPPNGIQLLDGVKRVQVQINRQSRGDLTPEELKERQAKGAGDPFQINLTPVMRQVLTDFQENPKAAGDHMKNPPLVINKQI

NbL10g15230.1 monocopper_oxidase-like_protein_SKU5 [MW – SP = 63.88 kDa]

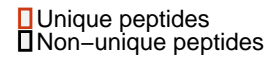
No. of times detected



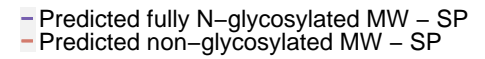
log(intensity)



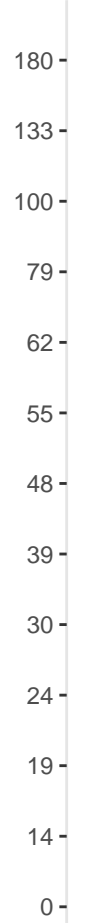
Values from



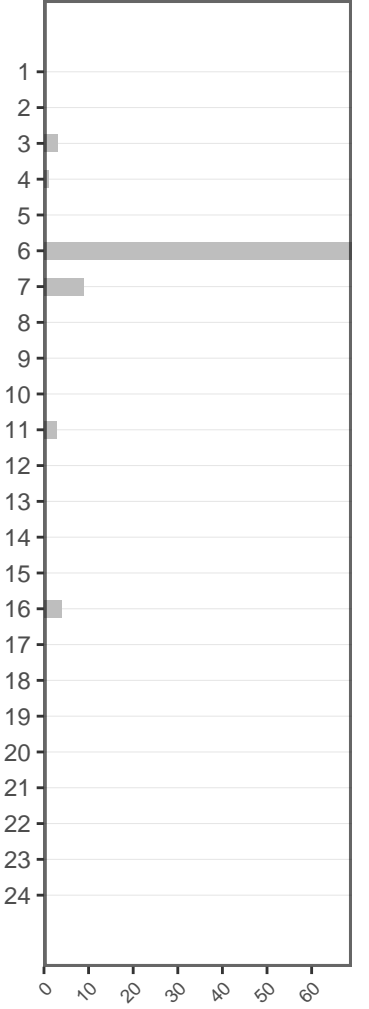
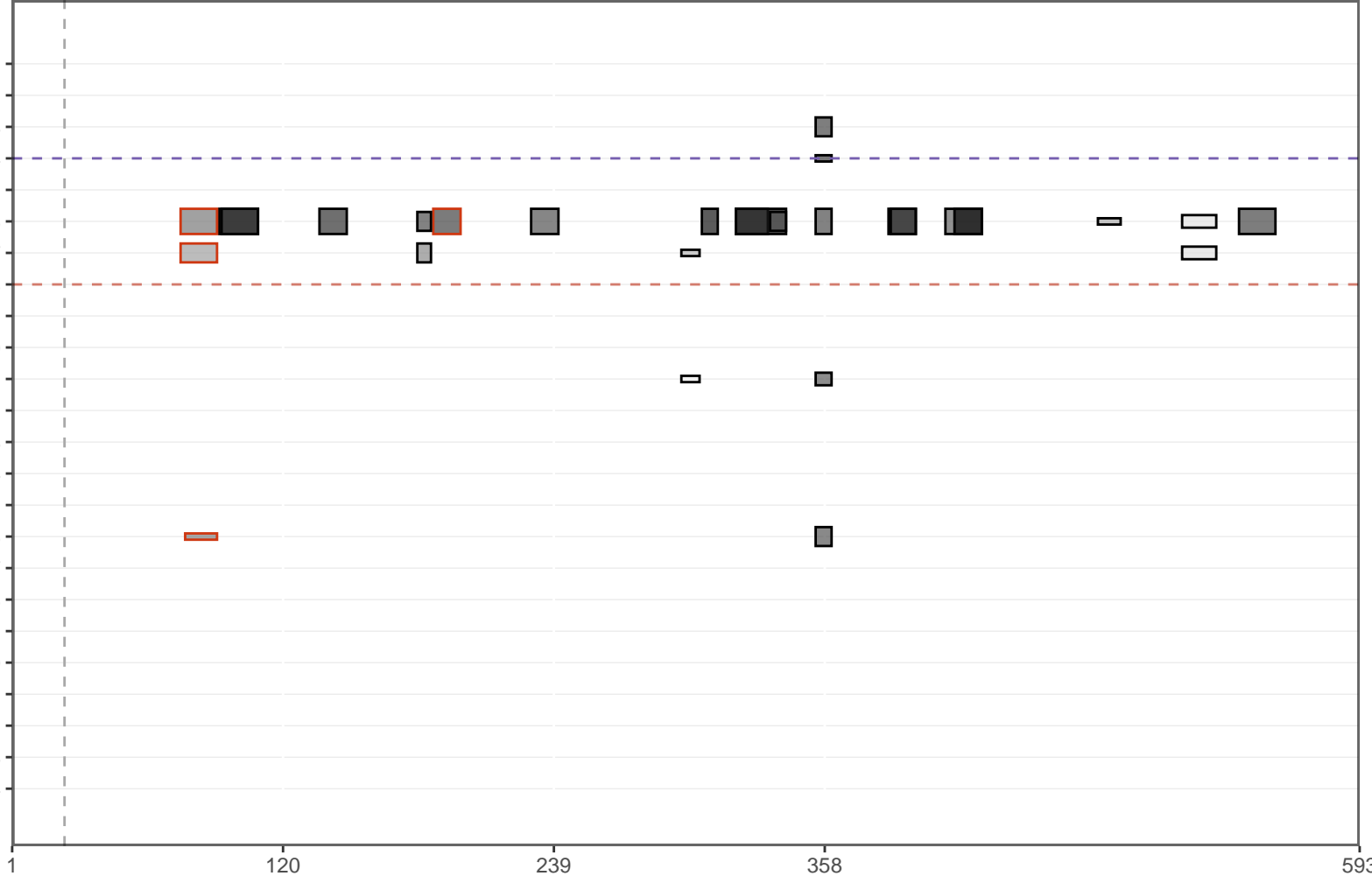
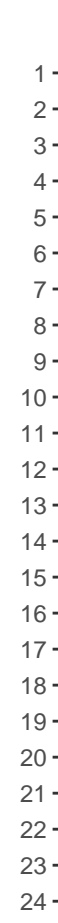
MW indication



Molecular weight

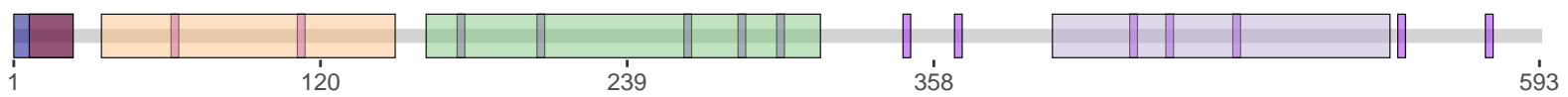


Gel Slice



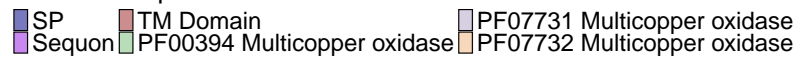
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SDYYVASARFYVQSGWQRVTVGLKLYTNSKGGKAHGFLEPPDQDFDKVTSVMDGARSIRWVVTASGARPNPQGGFRVYGSINVTETVWQNTPTMVDGKRRTLLNGISFVNPKTRPLRLADKYKLVKGVYKLFDFPTALTPGPPKMETSVINGTYRGMFIEIILGNNDTKVHTPHMSGVAFVYVGMDDYGVVWSNBSRGTYNKWDGIARTTTQVFPAGWATLVSLDNVGMVNLRTENLDSWFLGGQETVYRVVNPPEPSNKTETMPDPNLFQGLQKLPQDSSATSIRGNRSR

NbL10g15170.1 probable_xyloglucan_galactosyltransferase_GT19 [MW - SP = 48.29 kDa]

No. of times detected



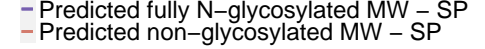
log(intensity)



Values from



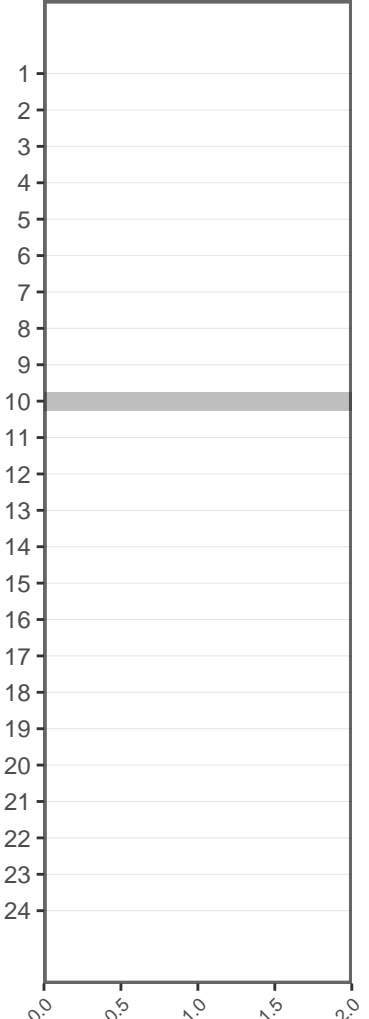
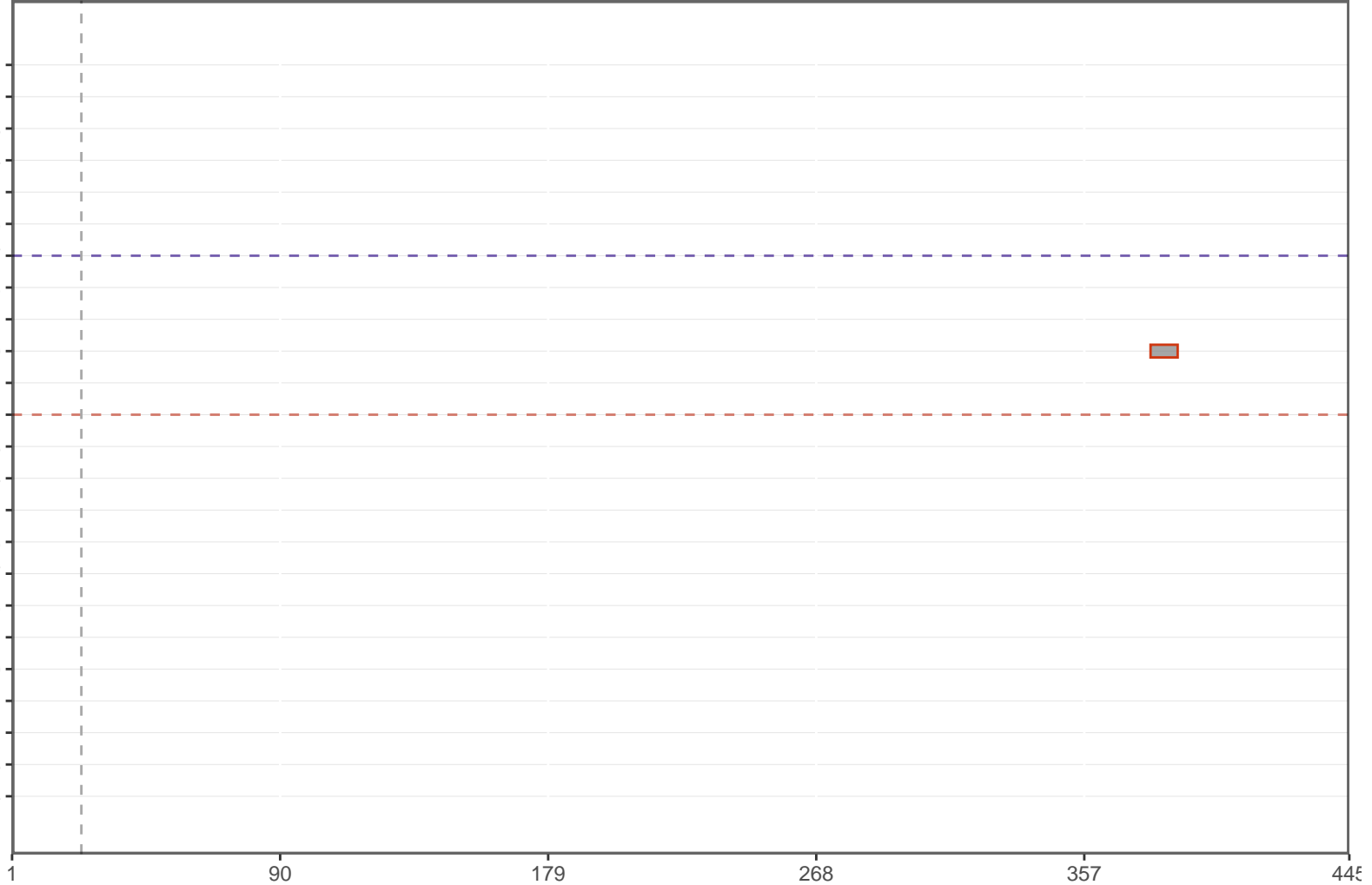
MW indication



Molecular weight

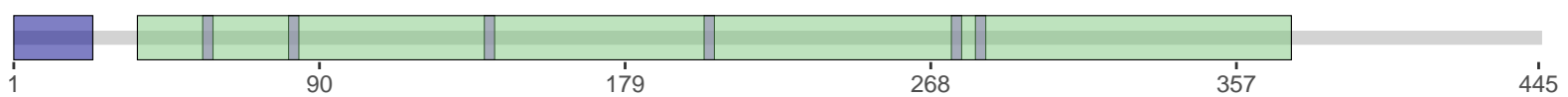


Gel Slice



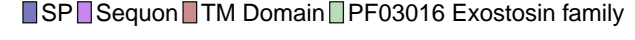
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

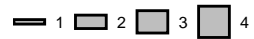


Protein sequence:

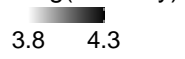
RAYPWQEQIIPYPTSFHPNLAFFGFWNRRVRSRINTLMLFAGGGGHSANPYRRSRILEGENVTSMANGTYQKLCFVDCSNGICEHPIREMKPMLGASFCLQPPGDISSRRSTFDGLAGGIPVFEDLSAKKQYGVWHLPAEKYEEFVTPKEDAVFKGLKVFDTLSPRAQVRRMRREKLEMMFRVMYRKHGSSGLGRKKDAFDIAEGTLERIKSALGEVAAG

NbL10g15150.1 adenine_phosphoribosyltransferase_3 [MW = 20.07 kDa]

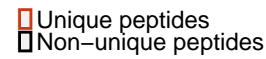
No. of times detected



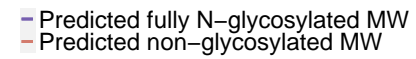
log(intensity)



Values from



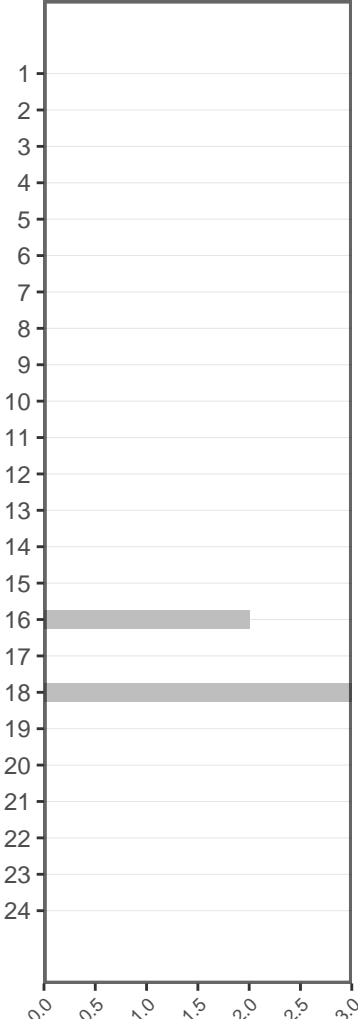
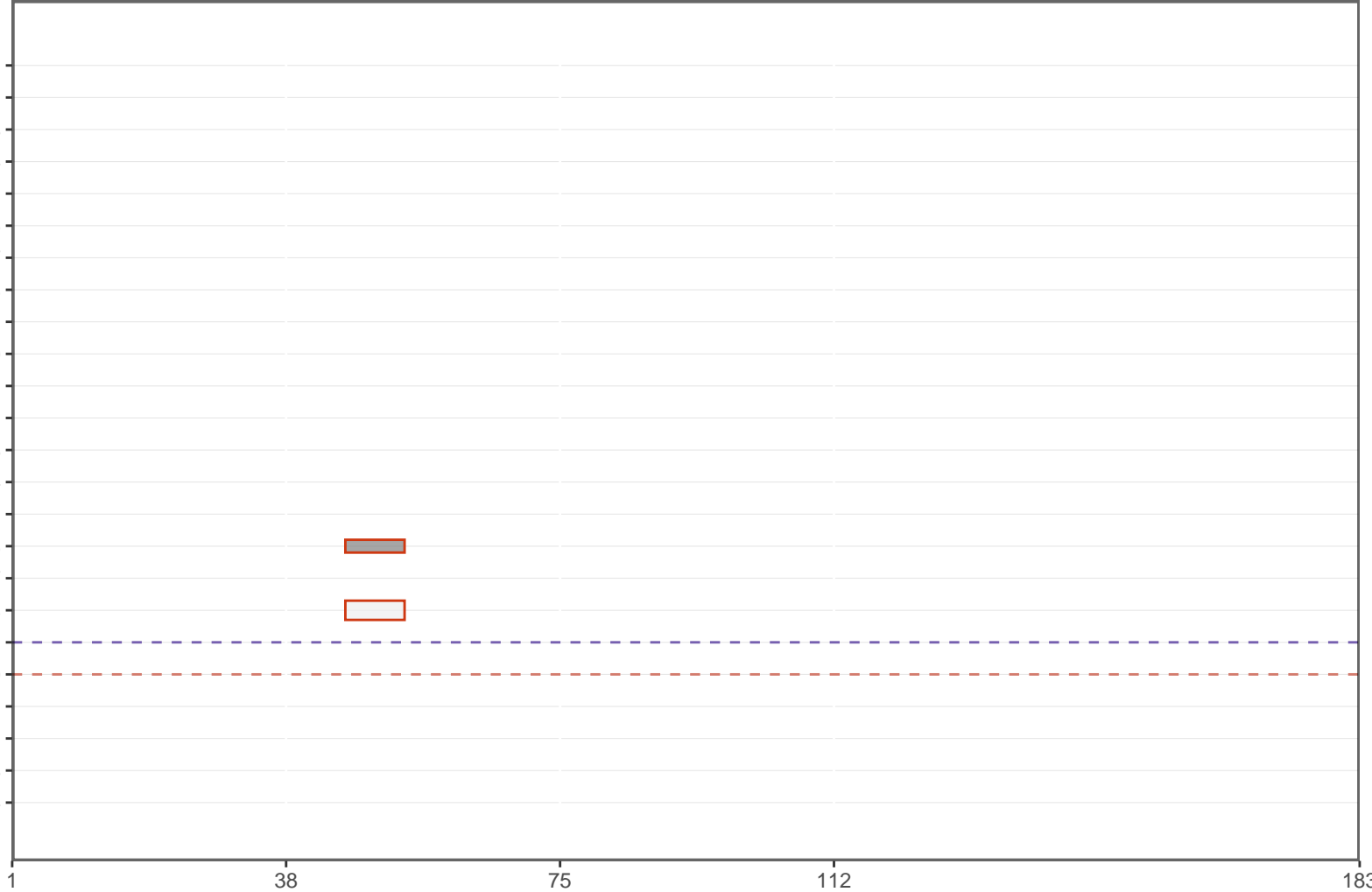
MW indication



Molecular weight



Gel Slice

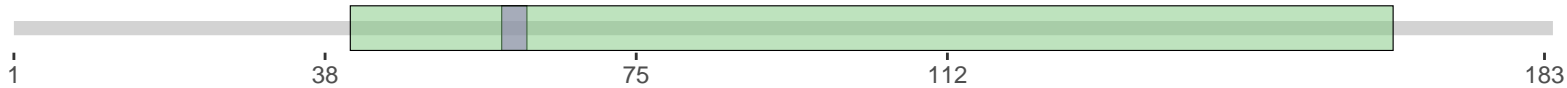


Protein length

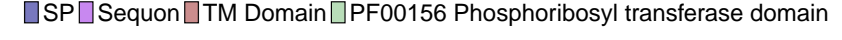


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

UGAKVPLRPNKLPGRVFKDQYDLEVGGDGLMHHGVAEAGERALVDDLIATGGTLRAMNLLERAGAEVVEGAGVIEIPDLKQKQGLNPKPLVLEGG

NbL10g15080.1 kDa_chaperonin_chloroplastic-like [MW = 26.41 kDa]

No. of times detected



log(intensity)



Values from



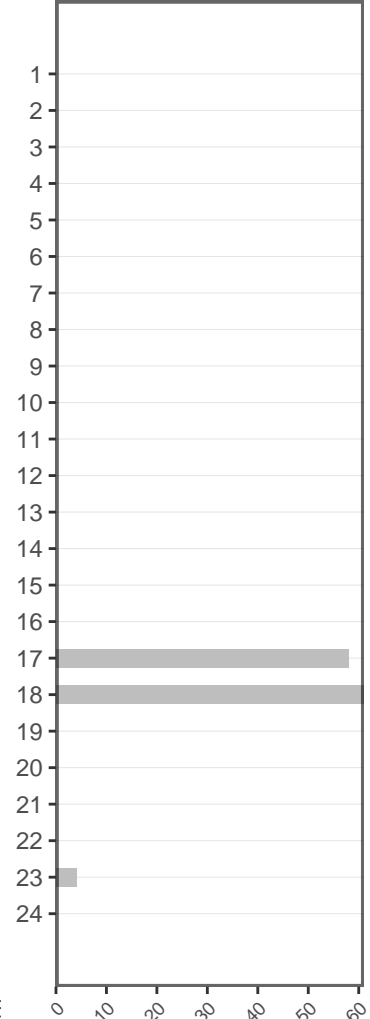
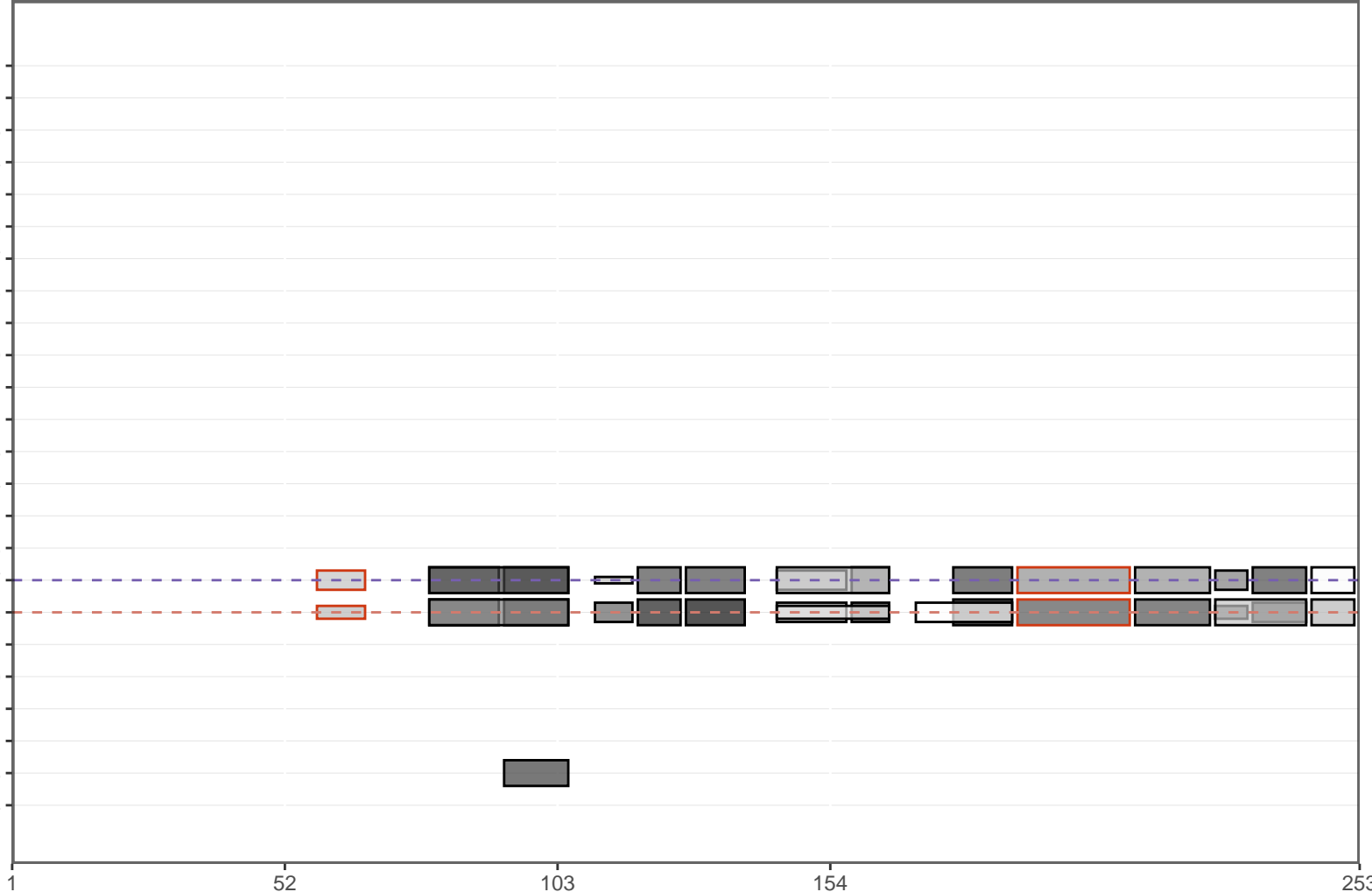
MW indication



Molecular weight



Gel Slice

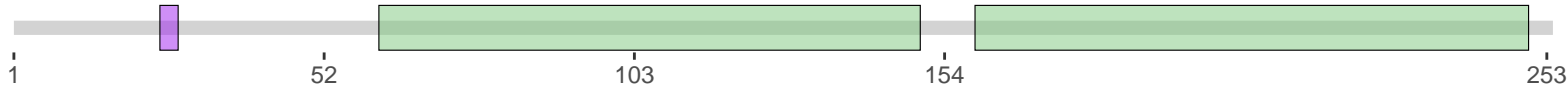


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

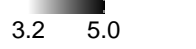
DISVYKTGAQVVYSKYAGTEVEFDGSKHLIKEDDVGVLVETDDKIDLQPLNDRVLKVAEAEKTAGGILLTEAAKERPSGTHVAGPGPLDEEDGNRKLPLVSPGNTVLYSKYAGSEFKGADGSDWTLRASDMMAVLS

NbL10g14910.1 peroxisome_biogenesis_protein_19-1-like [MW = 27.92 kDa]

No. of times detected



log(intensity)



Values from



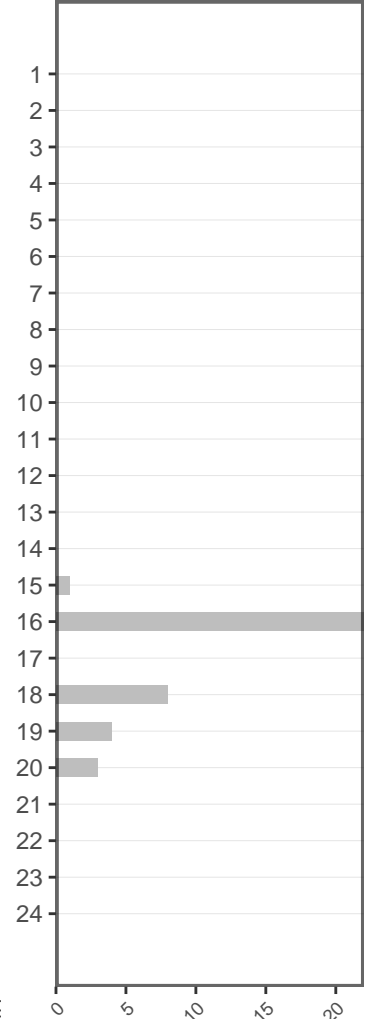
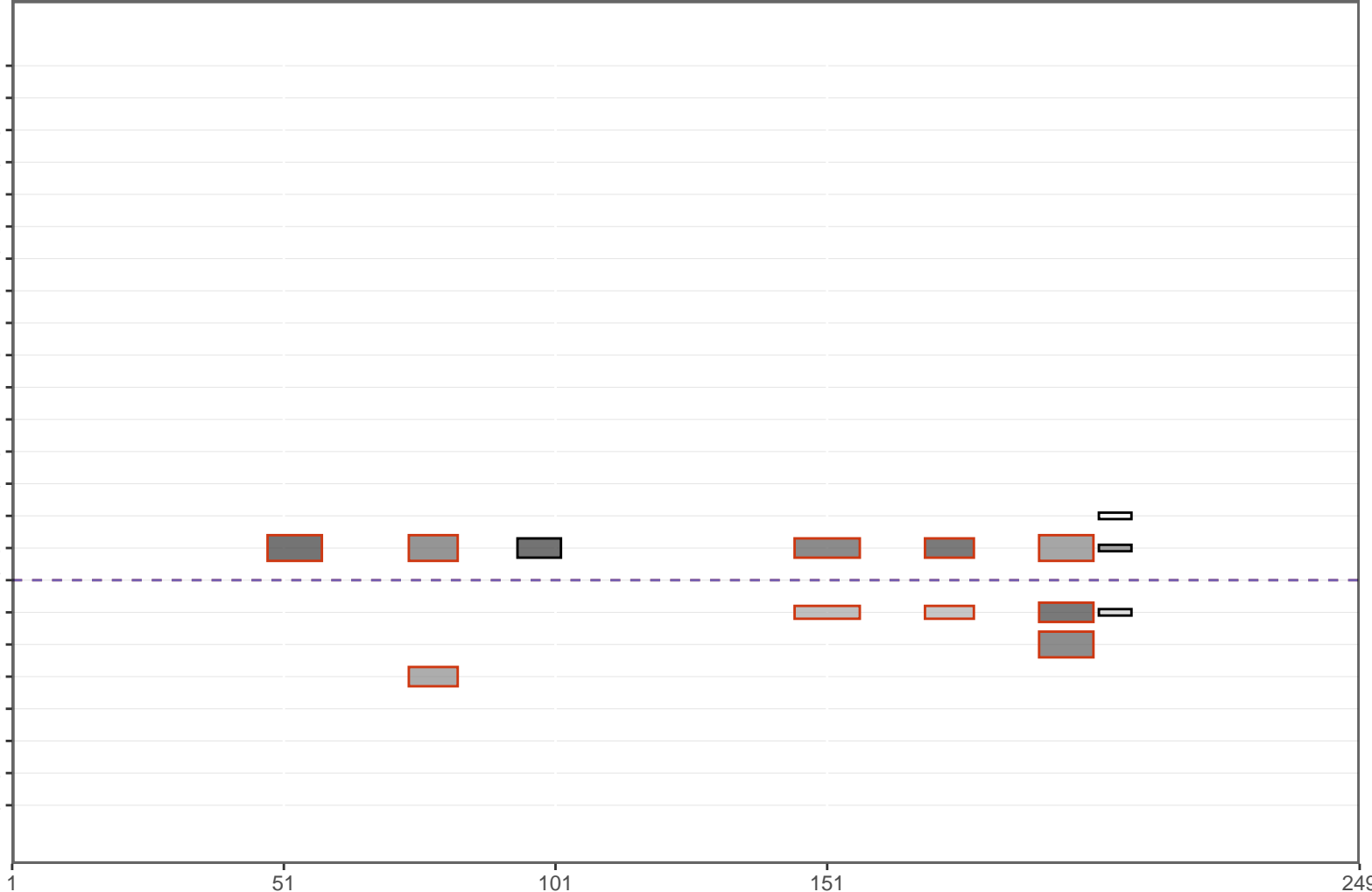
MW indication



Molecular weight

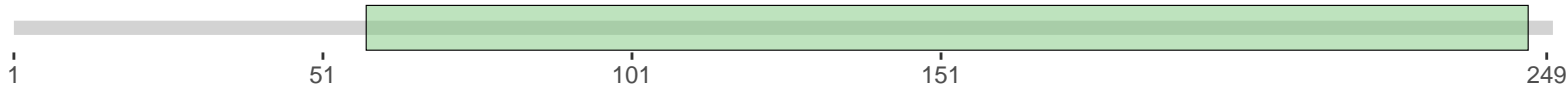


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DAMMEIYVQCFEELSGGGGMEIVETMMQQLLKEILHEPMKEIEERYPKWLEDNKAKLSTEDYGGYRHQYELIRDLNKVYETEPNFKIVELMQMKMKEGGPPNDVHVLAPDFDISLGLSPEMLEGGQNGCVM

NbL10g14800.1 uncharacterized_LOC107802887 [MW = 231 kDa]

No. of times detected



log(intensity)



Values from



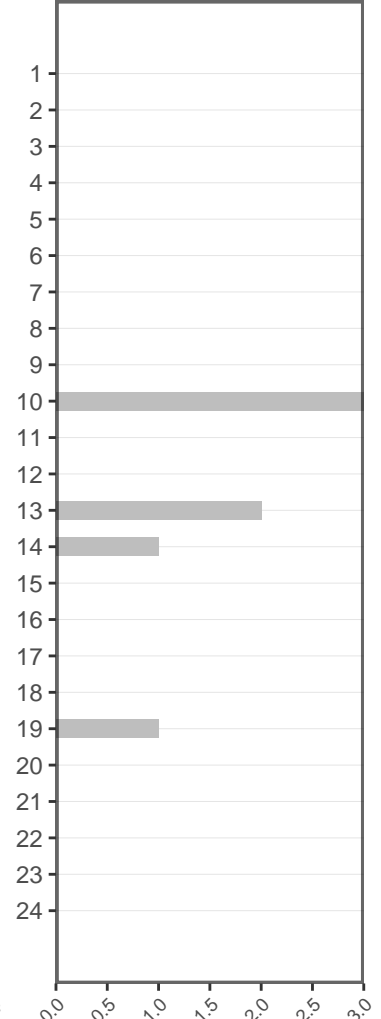
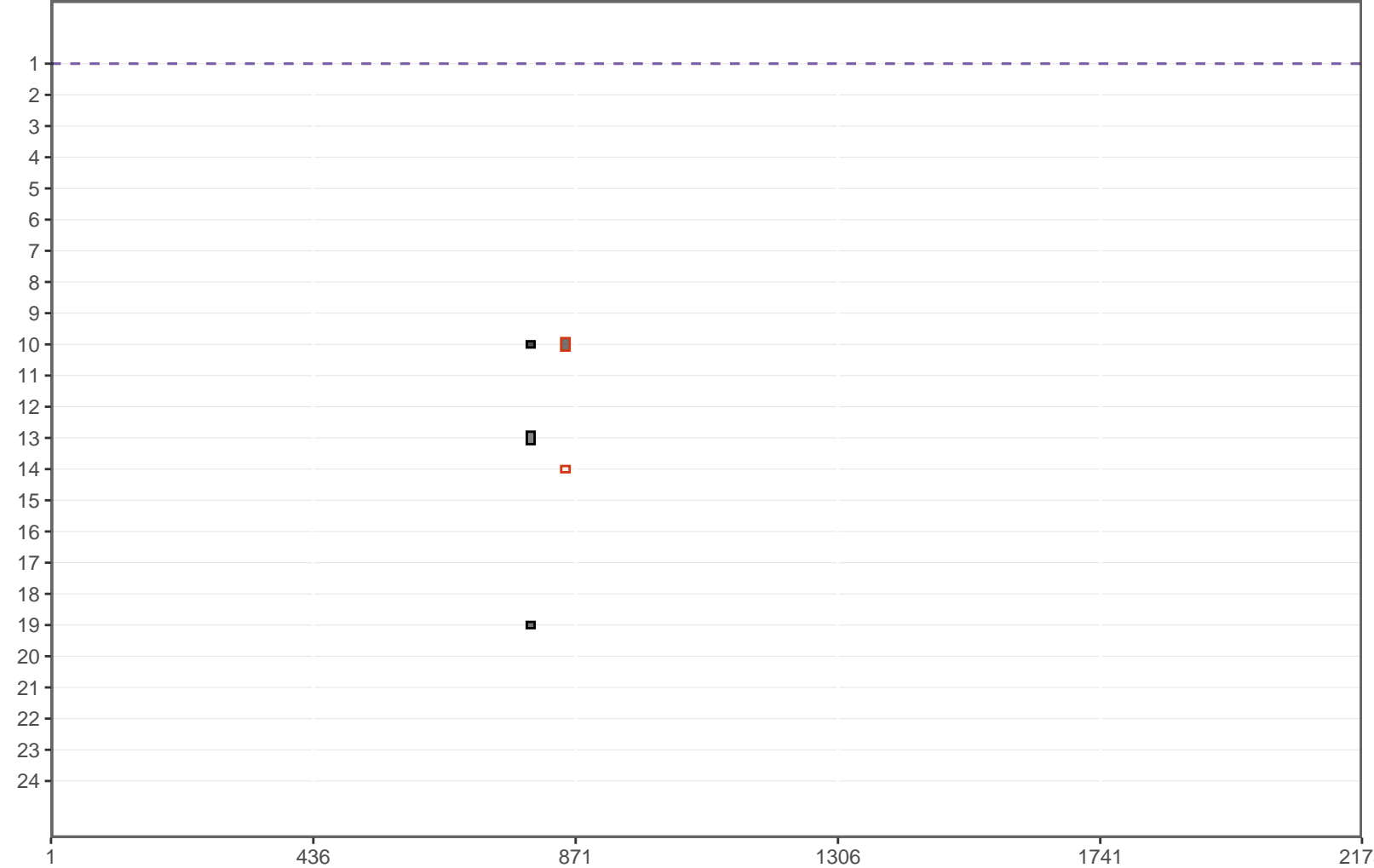
MW indication



Molecular weight



Gel Slice



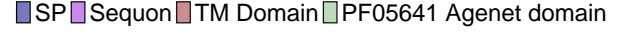
Protein length



Pfam domains



Pfam Description

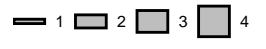


Protein sequence:

A C V D R I H G Q R S H I G N N E T F S H R S E M R N A G P R T P D G A T K G V M K N K V T T P A G R V S G K A N S H V V F N I P L S S P L W N M P T P S G E G L P S S G M A R G A V I D K K A L S P M F P V Q T P P R I N F V G H A A S V L P Q A P F F G S W A S P Q T S A F R L P V T E P V K L T P V K E S L S I S A G A K H G T P V S V A H G E S G L A G A S P R D E K N A S V L P A D Q K R R K R K K A S G T E N A H K L G G T S E S E V P A P A W C T Q L S E K A P A S D N F G S S E W A P L A V A I N G T G P A S A P I L G H F S T S V I A P L S S L A I P

NbL10g14700.1 peroxisomal_acyl-coenzyme_A_oxidase_1 [MW = 74.33 kDa]

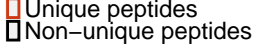
No. of times detected



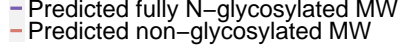
log(intensity)



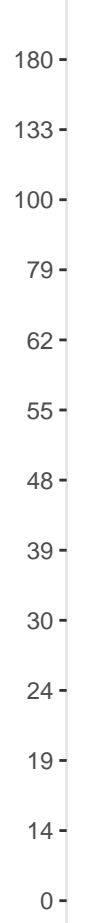
Values from



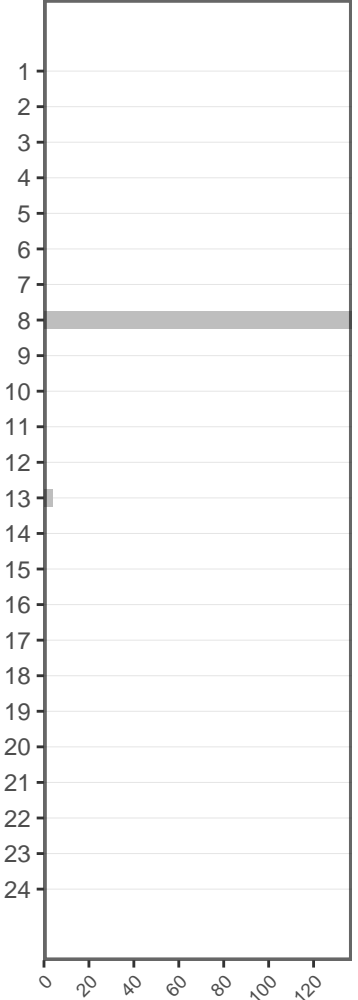
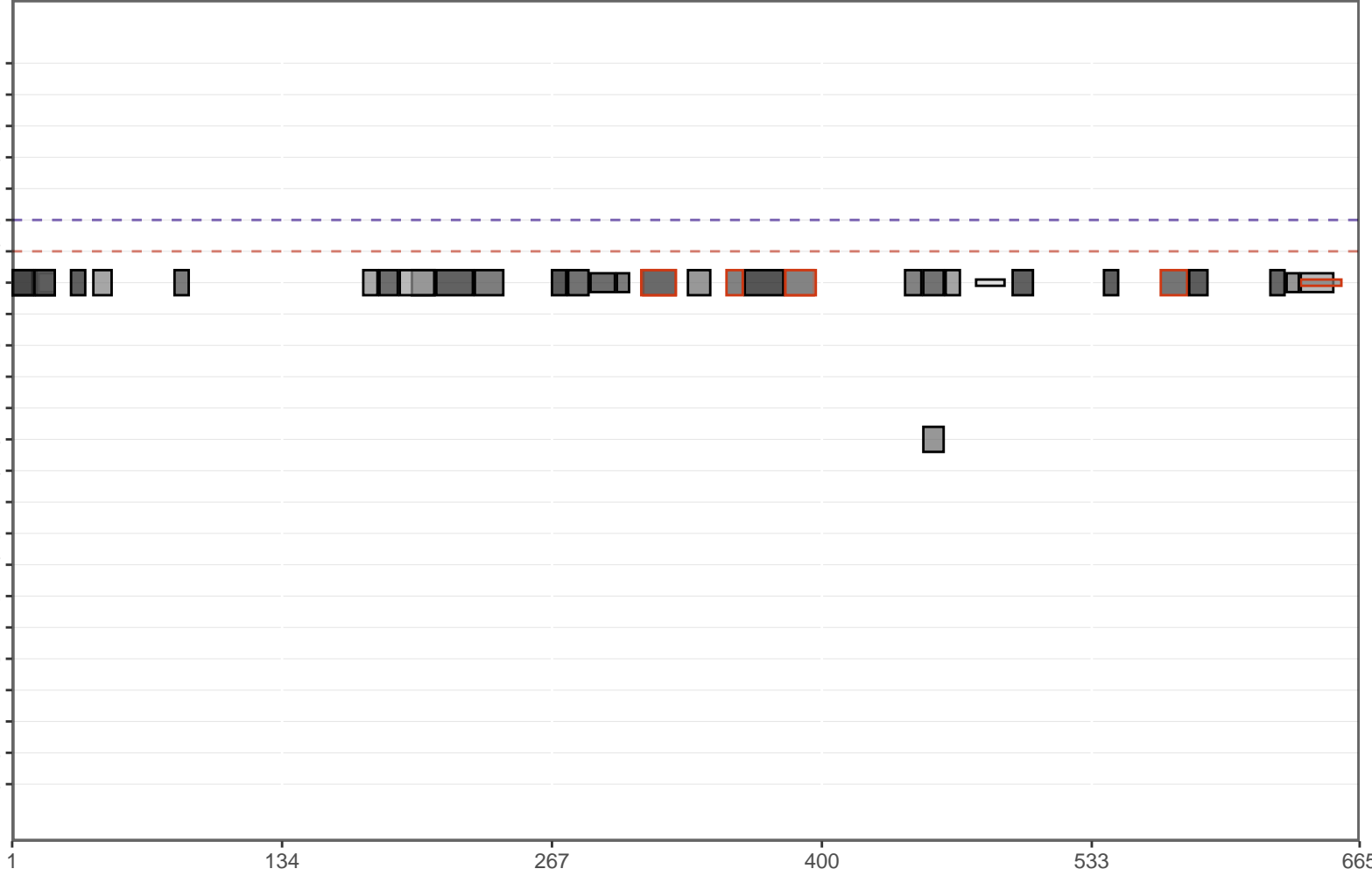
MW indication



Molecular weight



Gel Slice



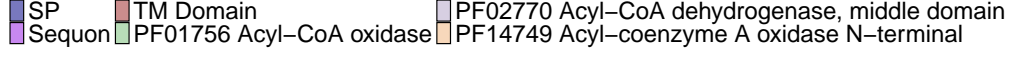
Peptide counts over 4 repeats

Protein length



Pfam domains

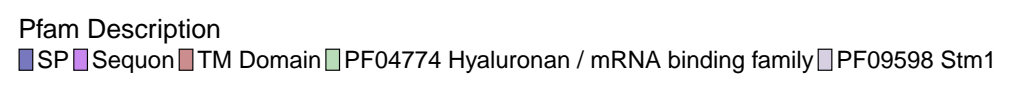
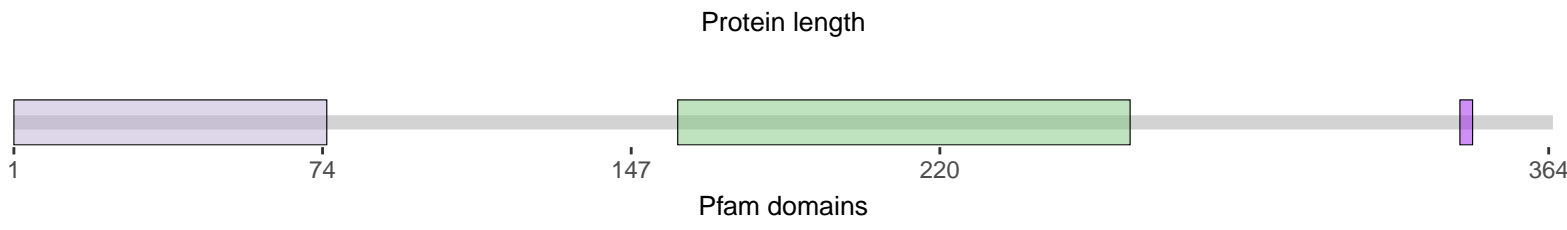
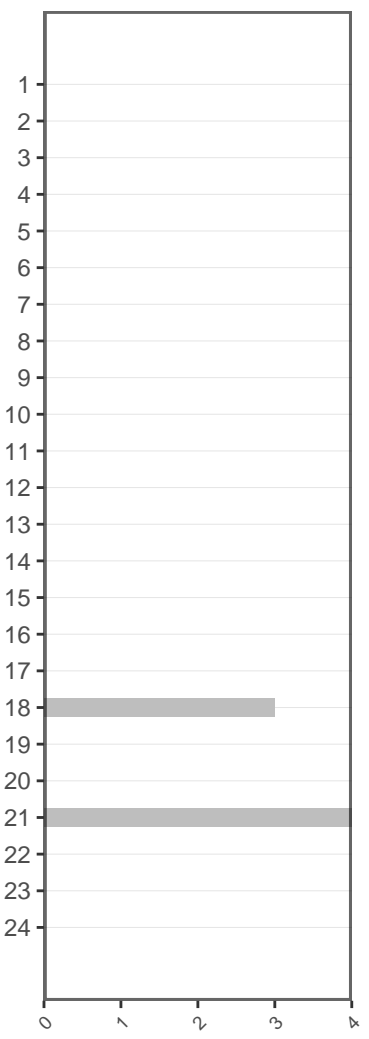
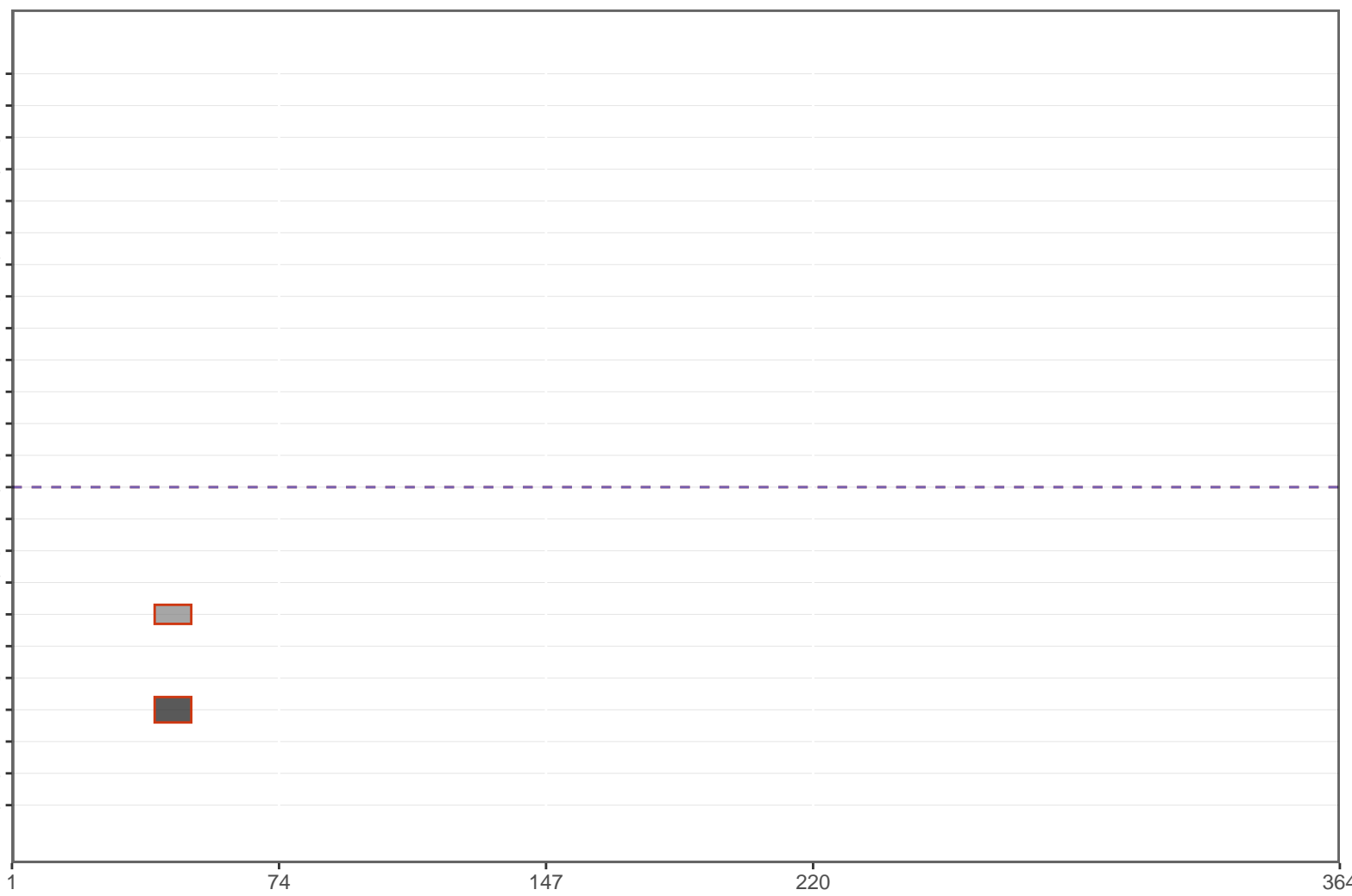
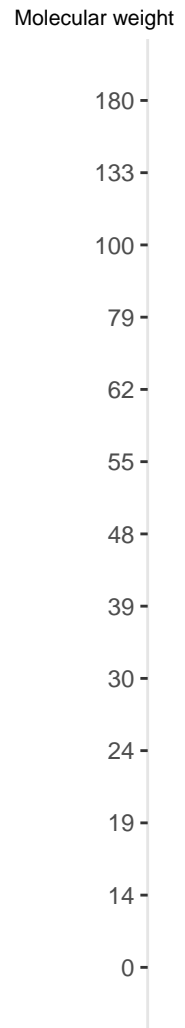
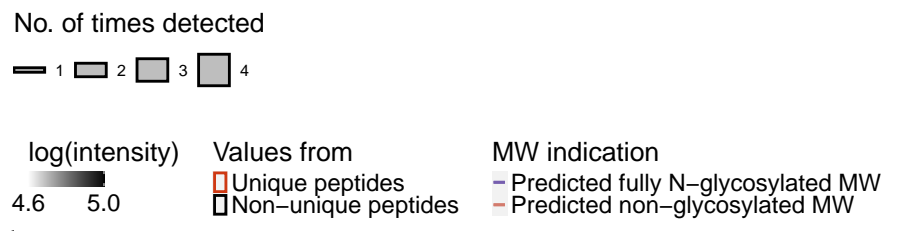
Pfam Description



Protein sequence:

IGGQEIQVVDYKTOGGRIPLFLLASAVAFRFGVEWLKVALYTDVYRRLGANDFSTLPEAHAGTAGLKVTTTATADGEECRKLGCGHGVLGSSGLPELFAVYVPACTYEGDNVLLLVGLQARFLMKTVDLGGGKPKVGTISYMGKIEHMGGRSDVWGAQKDKPISVLEAFEAARAARMSVAGAGNLKFDNPEEGFAELADLAEAAVAHQGLVAVKFRKELQDDPKGVKQGLEVLGGYSLFLLKHKHGGDFLGTGVTFSKQASLANDQLRALYGGQLRPNALSU/DAFYTD

NbL10g14380.1 plasminogen_activator_inhibitor_1_RNA-binding_protein-like [MW = 39.27 kDa]



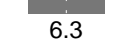
Protein sequence:
 GTGRNDYKREGAGRANWGTPDDEAPETEEPTVEGKIVPEKPAQGEEDAGDAKKDSAAEPEEKPEEKEMTLEEYKLLKRRKALLAGKPEERKVNLDKFEFSGMQLLSNKKKEDDFIKLGFPEKDKRKEAVEKAKKTQSNELFKPAEGENYVRGRGRGRGRGGYGGNGNNYSVEAPKIEDVGGFSLGAK

NbL10g14310.1 50S_ribosomal_protein_L19_chloroplastic-like [MW = 24.25 kDa]

No. of times detected



log(intensity)



Values from



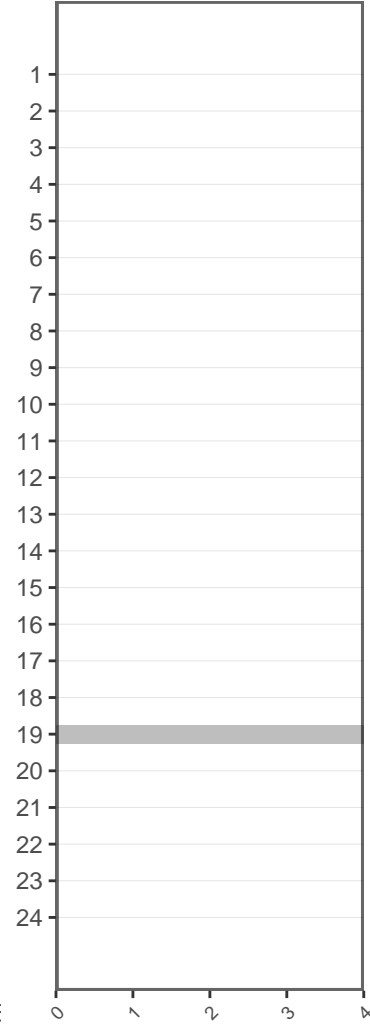
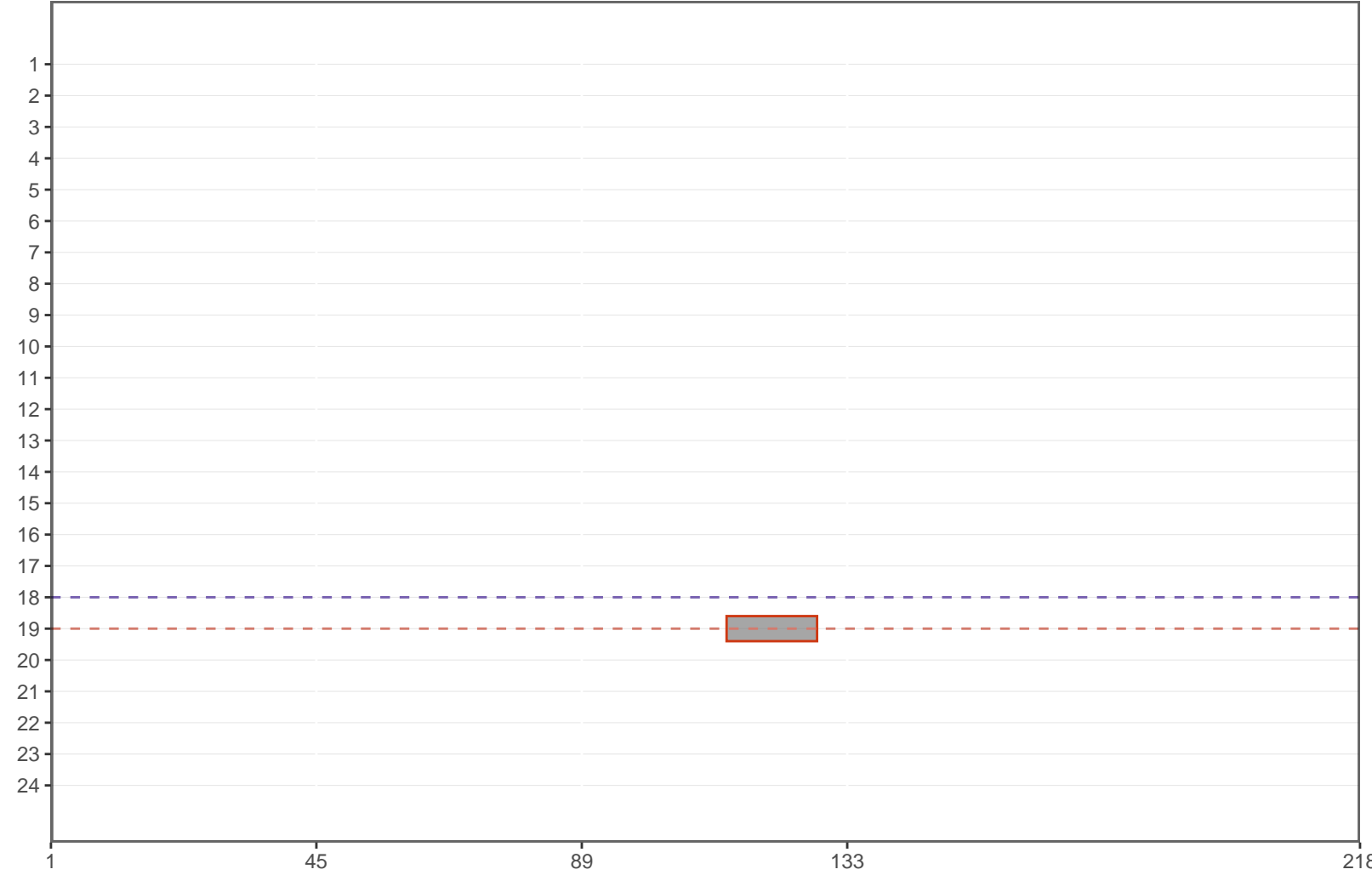
MW indication



Molecular weight



Gel Slice

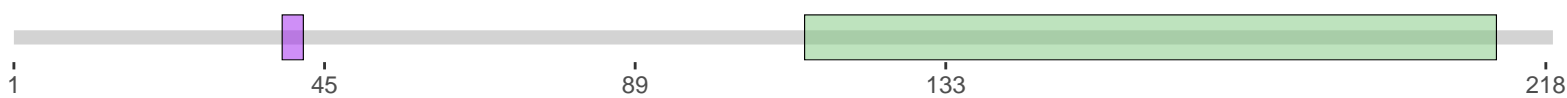


Protein length



Peptide counts over 4 repeats

Pfam domains



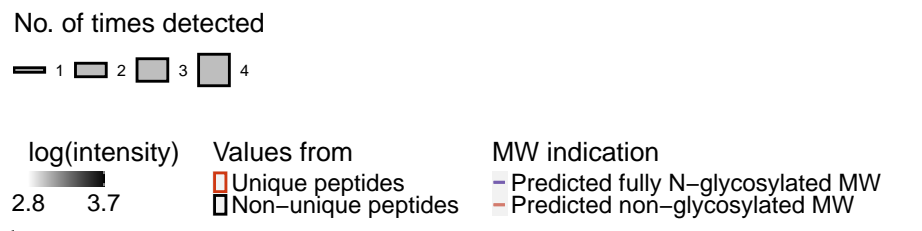
Pfam Description



Protein sequence:

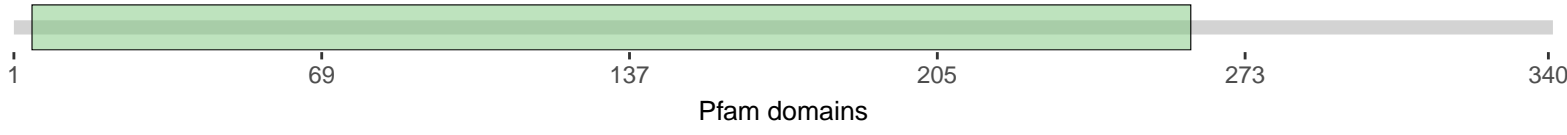
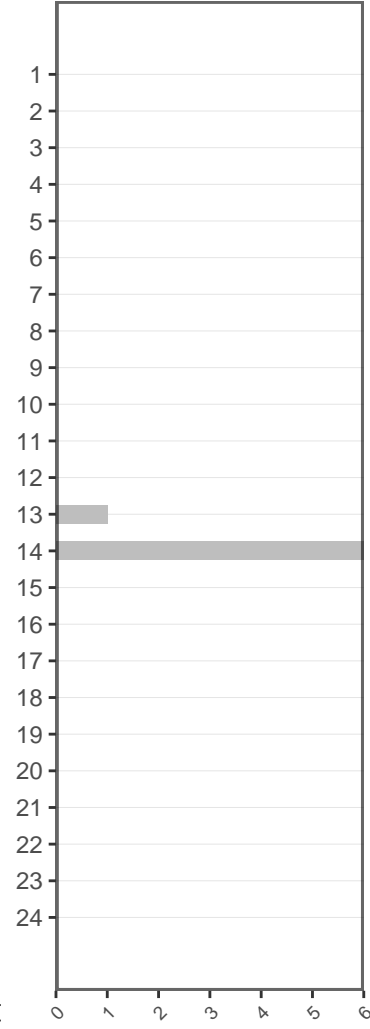
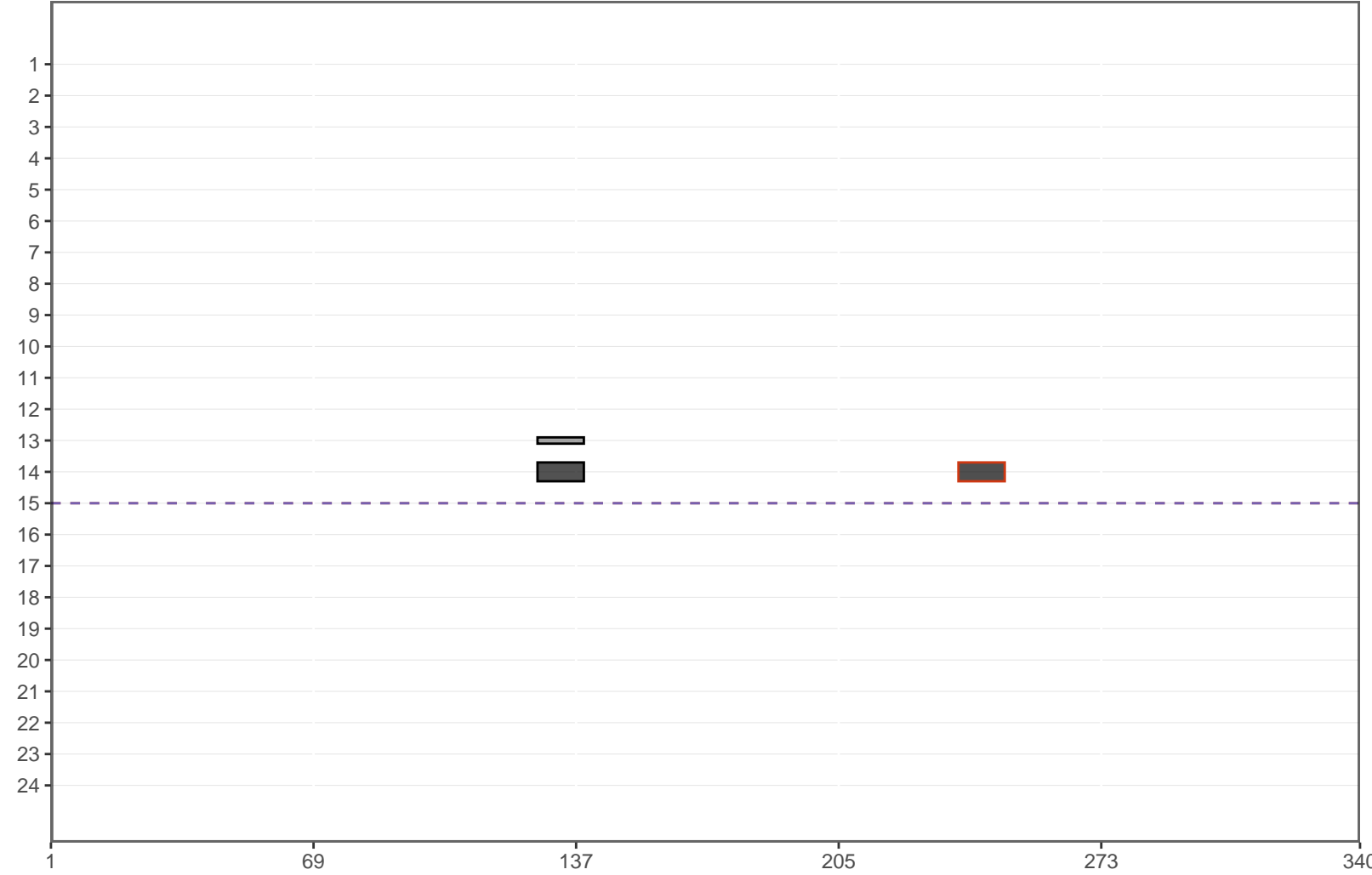
IERPPFPKRAKLGIMGLKGAESDAIRPDPRTGDVVEIKLEVPENRRRLSIVKGVISKGNAGHTTIRIRRIAGGVIEVFPVYSPNIKELVWVHRKVRRAALYLRDKLPLSTFK*

NbL10g14060.1 serine/threonine-protein_kinase_SAPK3-like [MW = 38.25 kDa]



Molecular weight

Gel Slice



Protein sequence:

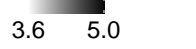
PKSTVGTAVIAPEVLSRKEVDGADWSSGGVTLVYMLVGGYFEPEDPNFRKTRGRMSAGYBIPDYVRISADCKNLLGQIFVNPKRITFPIKHPWFLKLNPKDLMGKRRKFEAESEGGQGVIEIMRIQGEAKIPGEVSKPEGQATAGTTEODDTEDESEIDSSNDFAVYV

NbL10g13930.1 poly(U)-specific_endoribonuclease-B [MW = 49.45 kDa]

No. of times detected



log(intensity)



Values from



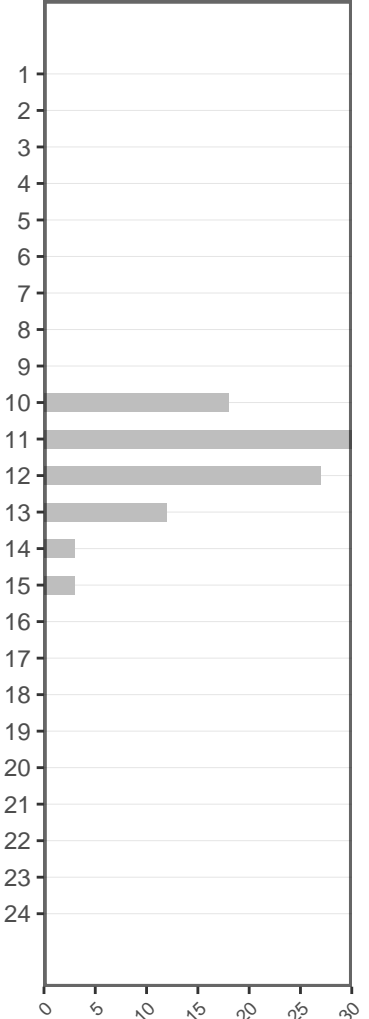
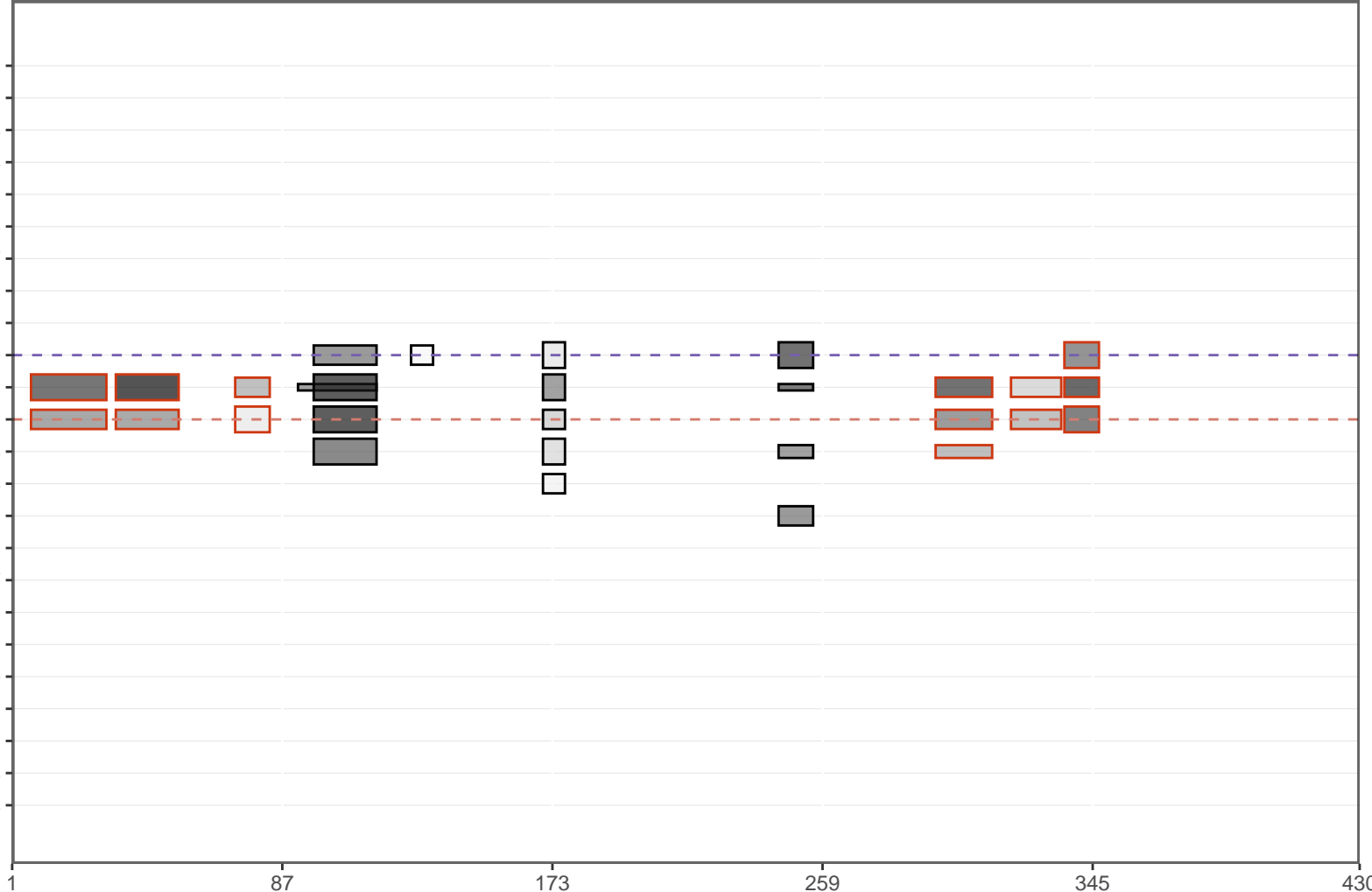
MW indication



Molecular weight

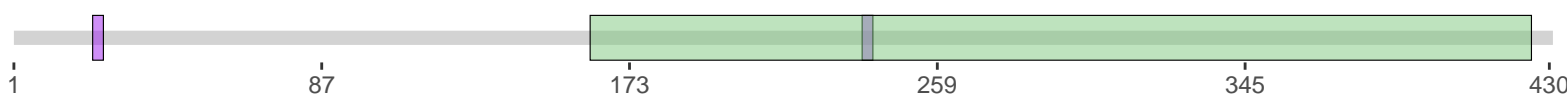


Gel Slice



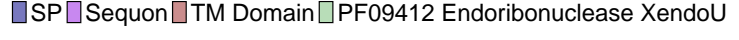
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KXEDMAEGCLFSVLSGDDVFNKPTVSRFCBLLDNVNPYHGGKKNVTSQEKQEGTAFEEISRTPIKYLYHKYLSLKRIVVGGDVEEFRKMMTHLWFDIYSRGTSAASGSAFHHVFDSEKEHGEKSVSGFHHWVLFQYLEEAKGSDVQGGYFRRRIRGEIPDSEITQLLTQFEWNGVLSKVSBSLIGVSPFEFEVAYTLGFFVGGEEHVEIGPYPNKKYRLGDNGSAPFVWEG

NbL10g13830.1 UMP-CMP_kinase_3-like [MW = 22.83 kDa]

No. of times detected



log(intensity)



Values from



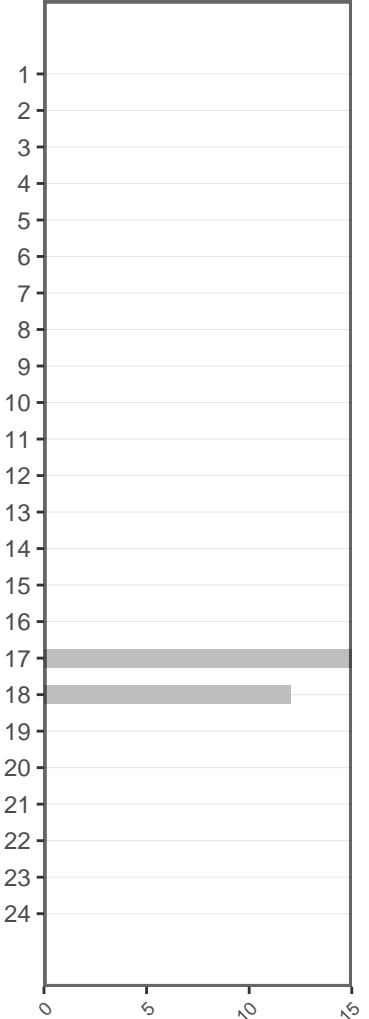
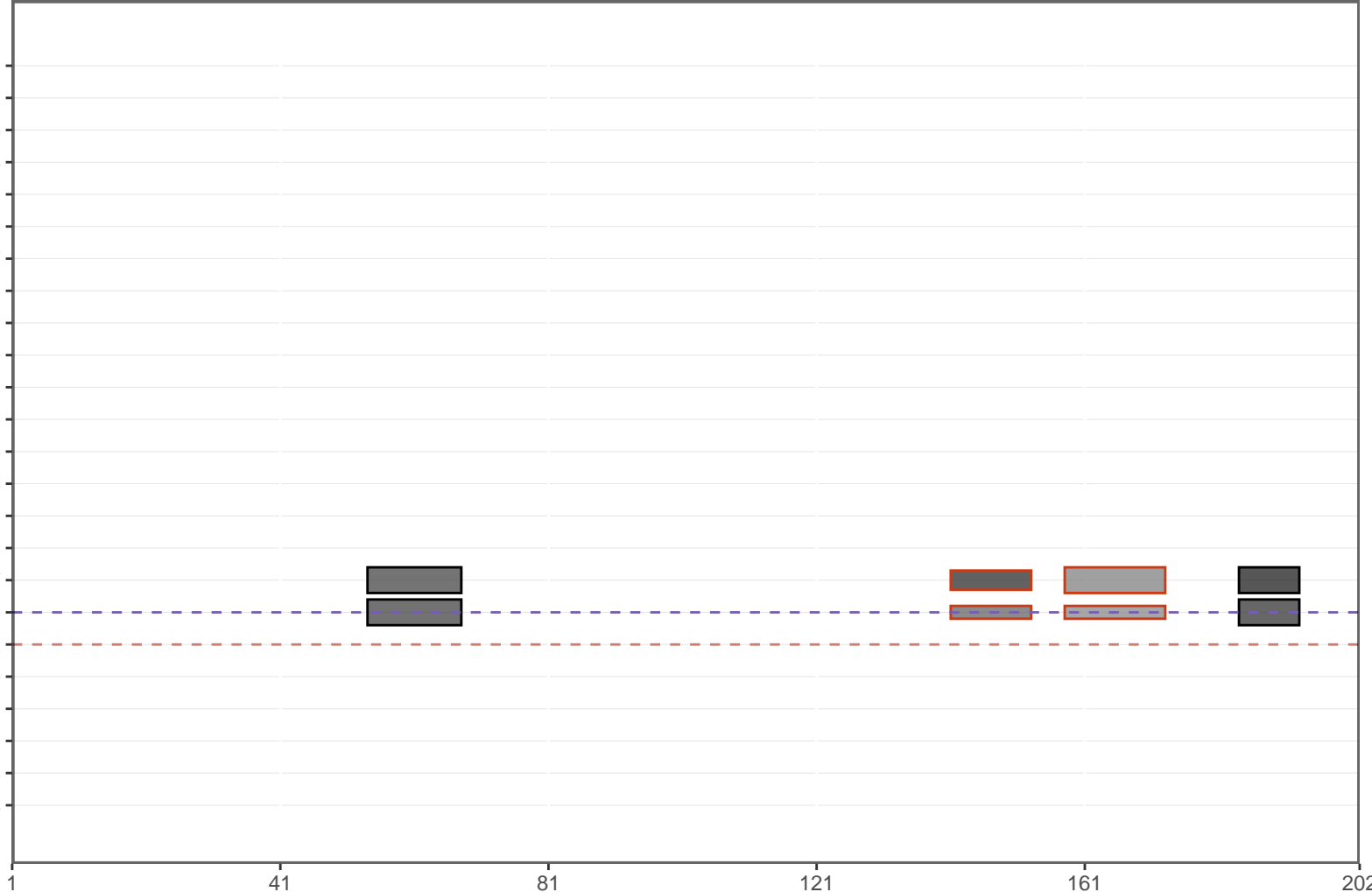
MW indication



Molecular weight

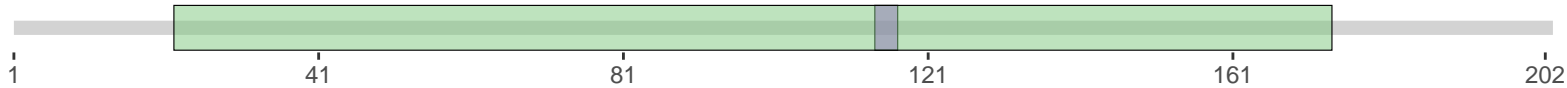


Gel Slice



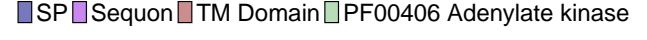
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AMQGMDSKFLIDGFRNEENWTFENLTKMEPEFVLYLDGPDDEMERLLLSRNEGREDNTETIRKRFVLESTLPVVEYEGKGVKWKVDAGKSDVEVFESGKSLGRKRG

NbL10g13800.1 haloacid_dehalogenase-like_hydrolase_domain-containing_protein_Sgpp [MW = 27.75 kDa]

No. of times detected



log(intensity)



Values from



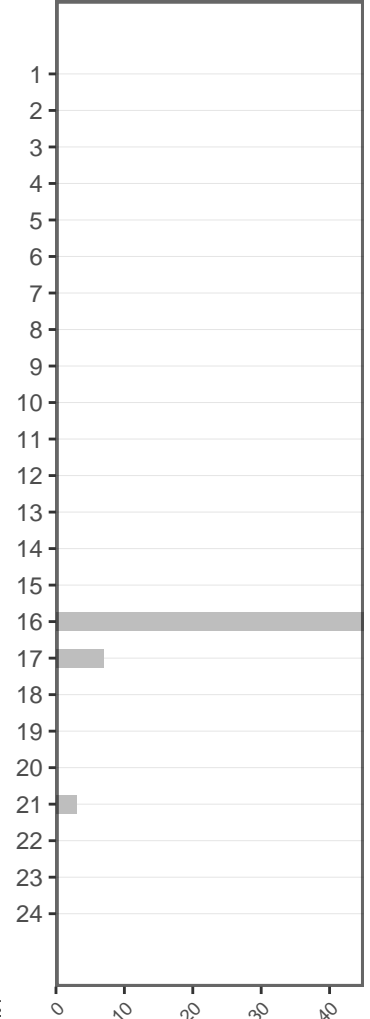
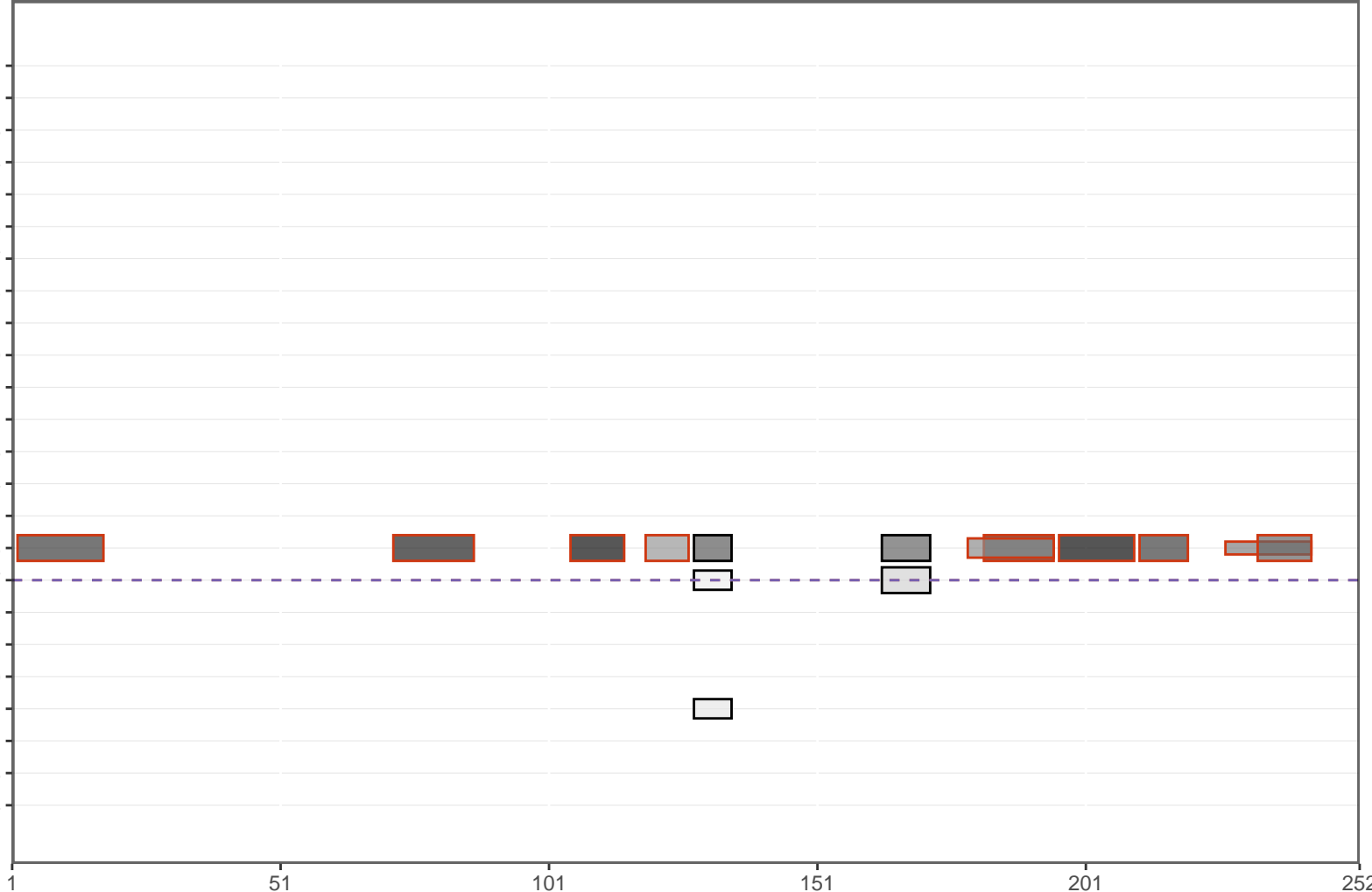
MW indication



Molecular weight

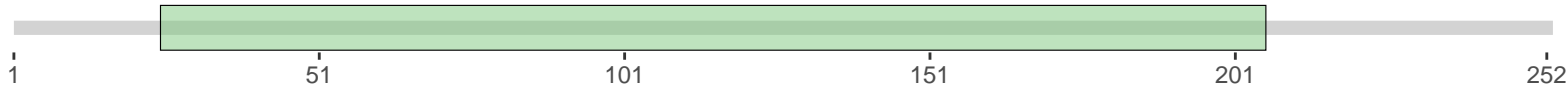


Gel Slice



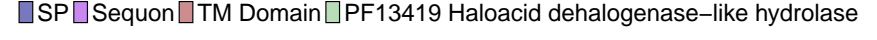
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGLYKYYKWIETHGLKRAVATNAPRLNGELIIEHGLKDFDFVVIIGEGECERAKPFDPYKALELLKVEKDHTRIFEDGVSGIKAGVAAGMVSVGLATRNPHLLMEAKPFLIKYKDYEDPKLWADLEEIDKXKSGAKATV

NbL10g13710.1 phosphoacetylglucosamine_mutase [MW = 65.93 kDa]

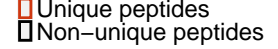
No. of times detected



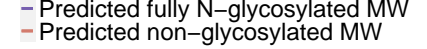
log(intensity)



Values from



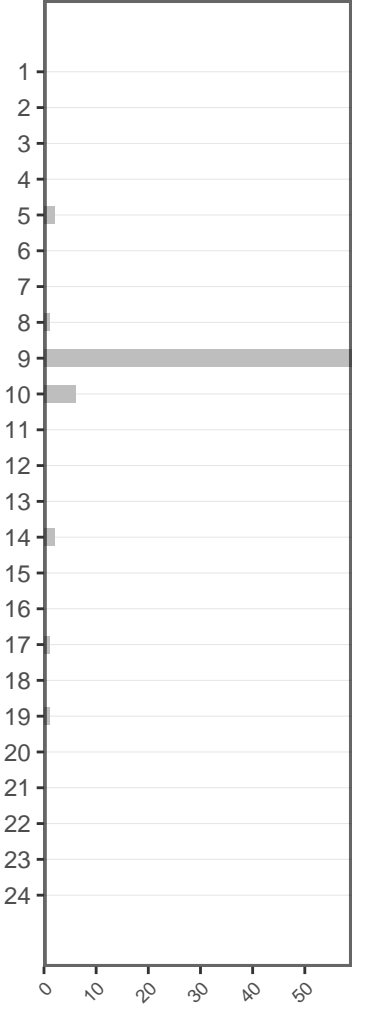
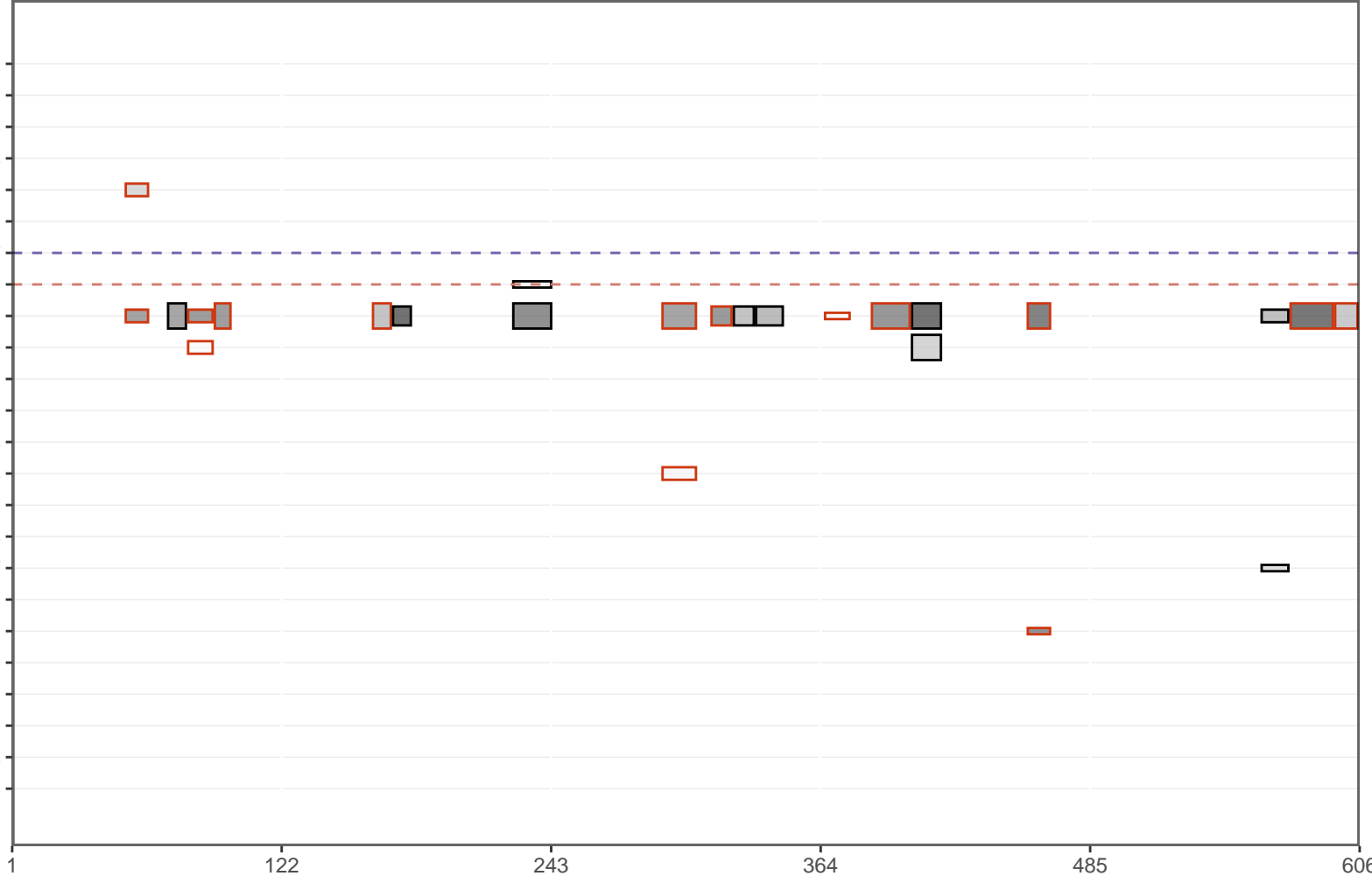
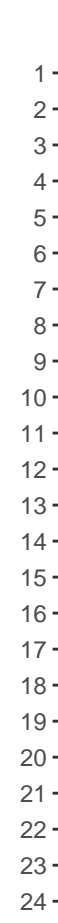
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00408 Phosphoglucomutase/phosphomannomutase, C-terminal domain
- PF02878 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain I
- PF02880 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain III

Protein sequence:

EVNRKGDQLNEGVGADIVQKEKVAFRSFGTAGLRCASLDGADRLVYFVLSNENNKIEIVDGGKLSLFLFKIQGLILNEGEDKNGDSYQVRLGVVQTAWNGPSTYKEMGLEVAITPTGKWLHEKAAEFDGIVFEANGHSTLFSQAFLOWLEVSHKTLSTSEGSAGKAAARLLAVSGLNVAVDGLSGLLLEVLKVMGWSHRWNEHLHDLPEKQLKVVYVDTAVVTANAETVAVGPIGQEAINEAKYRGRGFRPSPGTEQIRVYAEATSQDAAL

NbL10g13680.1 probable_methyltransferase_PMT14 [MW = 55.45 kDa]

No. of times detected



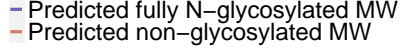
log(intensity)



Values from



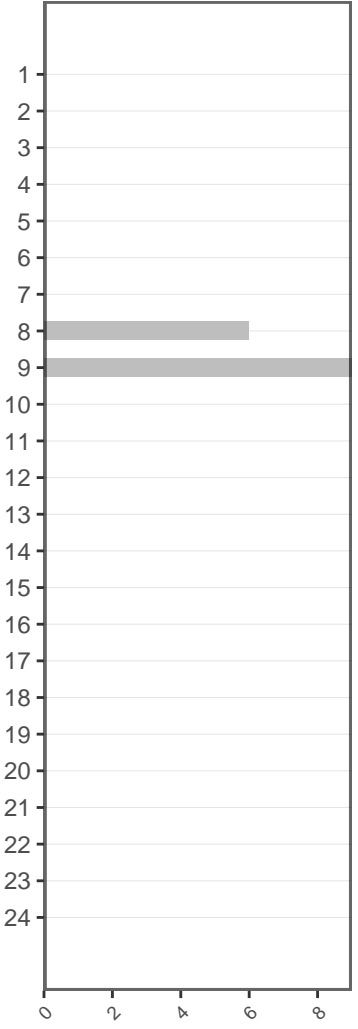
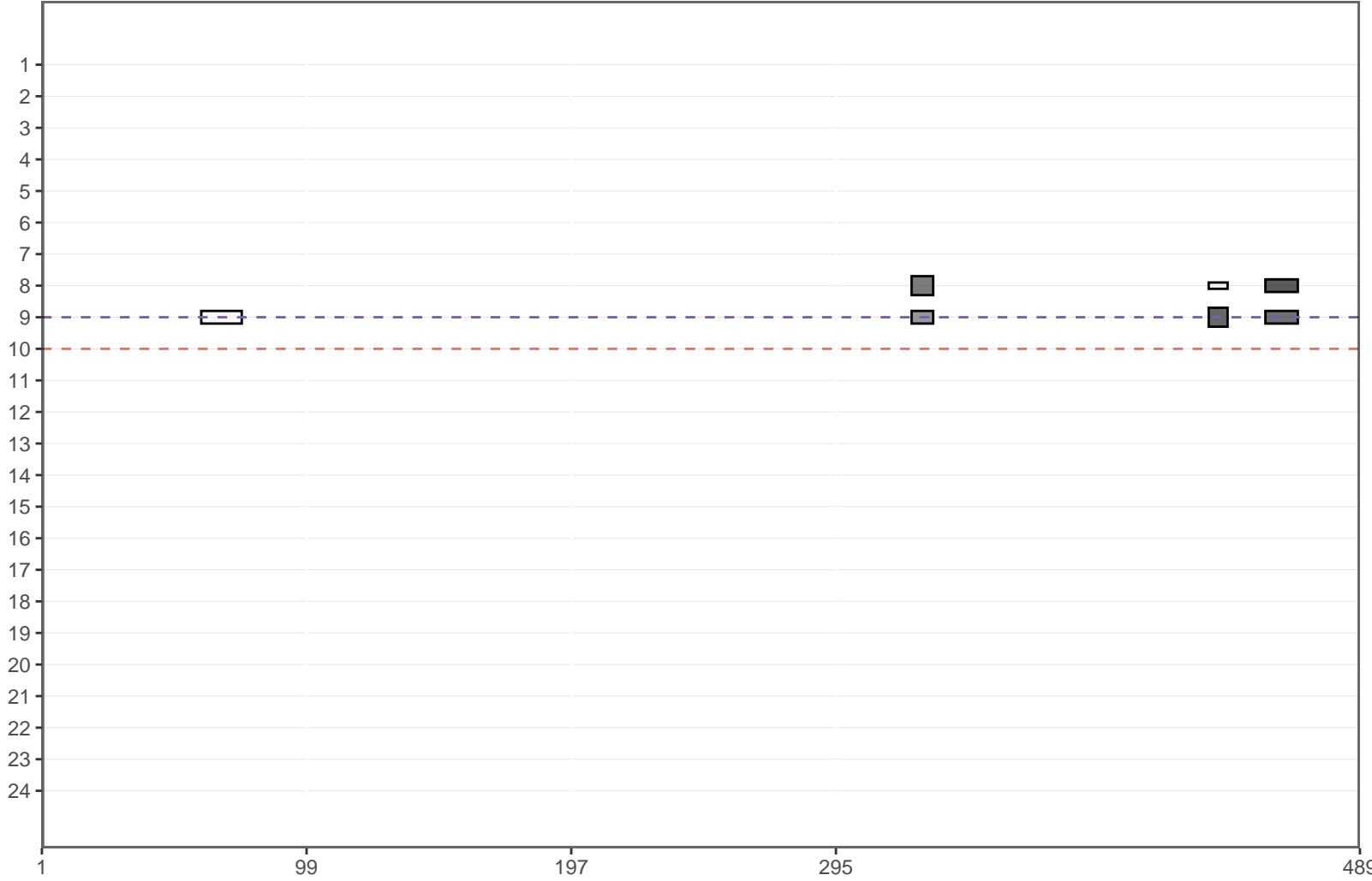
MW indication



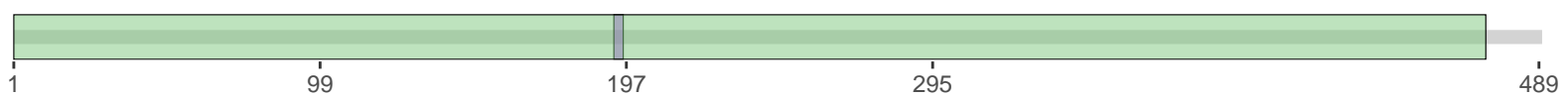
Molecular weight



Gel Slice

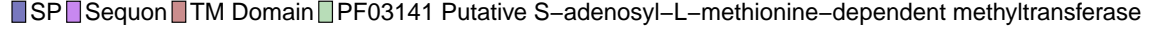


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL10g13550.1 probable_xyloglucan_endotransglucosylase/hydrolase_protein_8 [MW - SP = 32.06 kDa]

No. of times detected



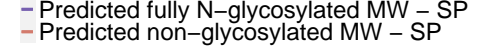
log(intensity)



Values from



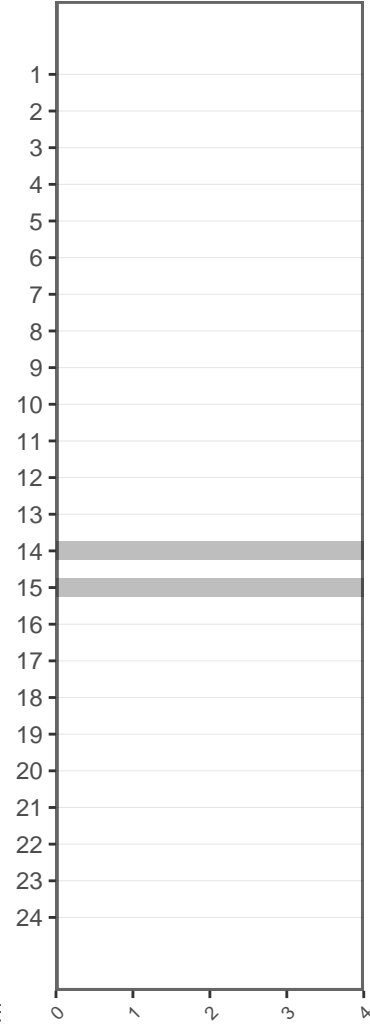
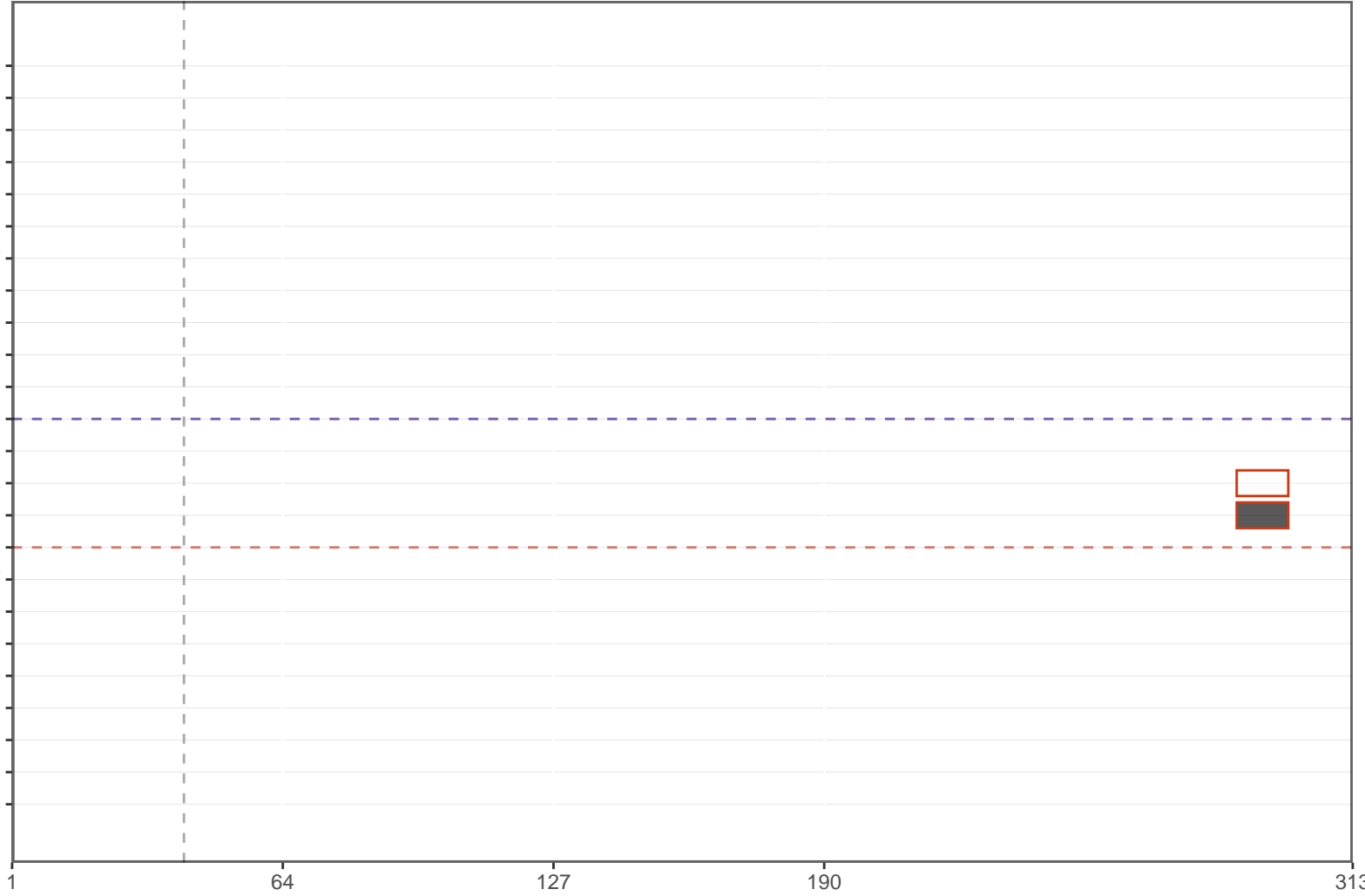
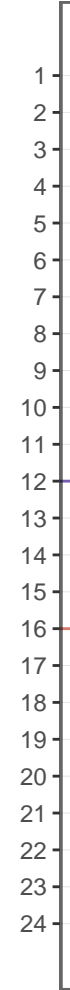
MW indication



Molecular weight

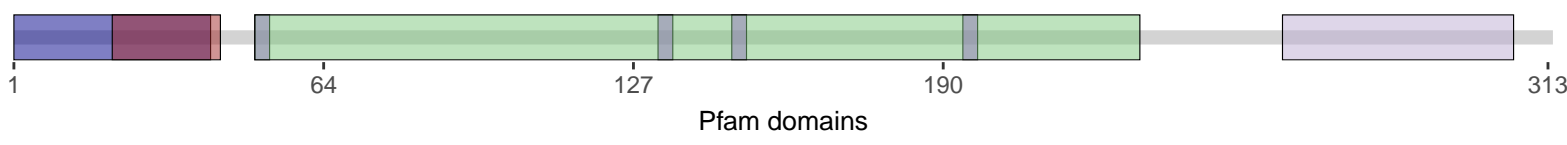


Gel Slice

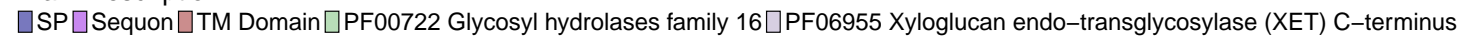


Protein length

Peptide counts over 4 repeats



Pfam Description

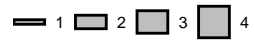


Protein sequence:

NGTGNREMRHILVFDPTEDHTYSILWNTHGIVFFVDRPIRVKKNANVTNFFPEKPMVLFSSHWNADDAWTRGLEKTNWNGPFVSVKDFSDVGGQWEDFPPTGCVSTTTKHWDDGDSWHLFNDQKMDKAWVGRNLVFDYDGGDTERFPKPKPECVLNPWEI

NbL10g13460.1 citrate_synthase_glyoxysomal-like [MW = 55.94 kDa]

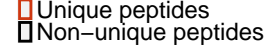
No. of times detected



log(intensity)



Values from



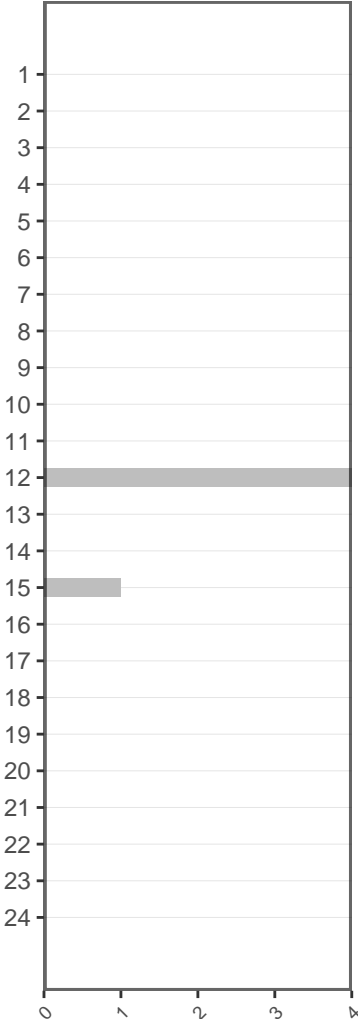
MW indication



Molecular weight

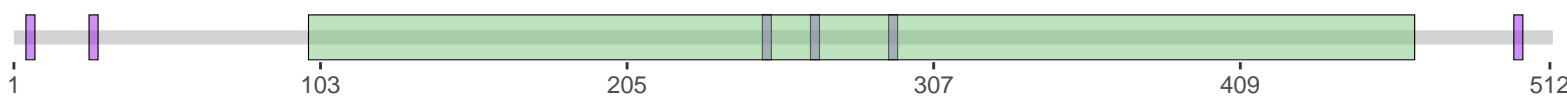


Gel Slice



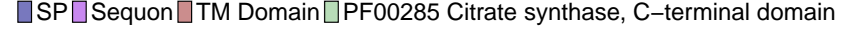
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LPSNLSYAENFWMLDLSGRVYKPNRRLARVLDLFLHAHEMNGSTAARHLASSGVVYTAAGAGVGLYGLPHGANEAVLKMISEIGSEVENPEFIEGVNKRKRKMSGFGHRVYKYNDRPAKVKKLADEVFSIVGRDPLIEVAIALEKAALSDEYFVKRKLKPNVDFYSGLYRAMGFTEFFPVLFAVRPMAGVLSHWRESLDDPDTRKMRPAQVYTGWVMRHYMLKERBPYTETDKLGGVSVSNATKRRLAG66A

NbL10g13430.1 ras-related_protein_RABD2a-like [MW = 22.54 kDa]

No. of times detected



log(intensity)



Values from



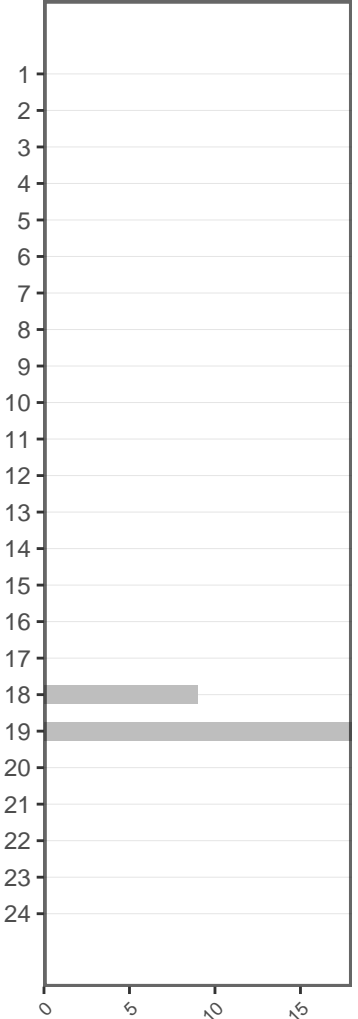
MW indication



Molecular weight



Gel Slice

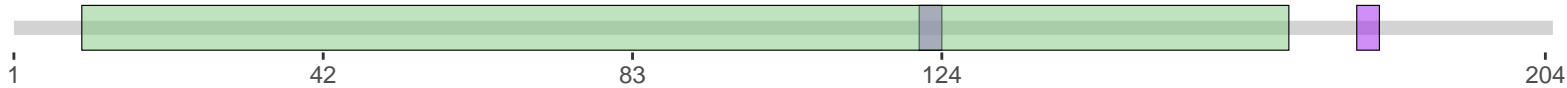


Protein length

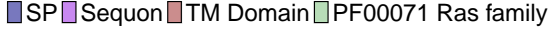


Peptide counts over 4 repeats

Pfam domains



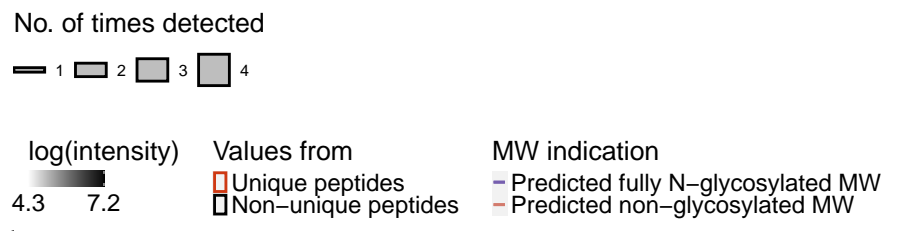
Pfam Description



Protein sequence:

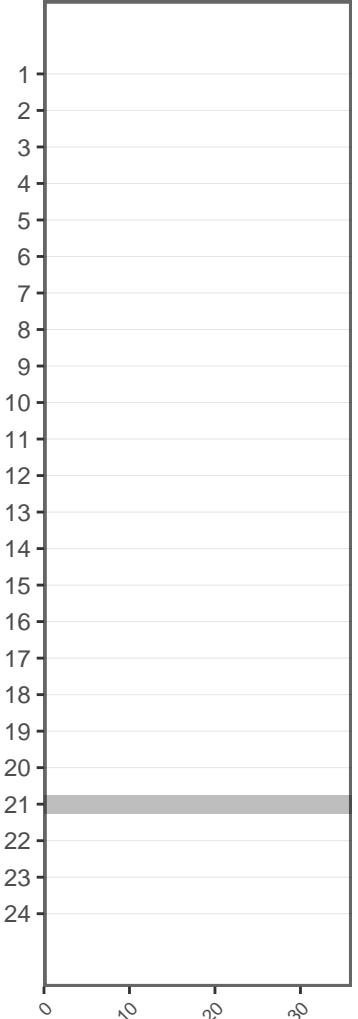
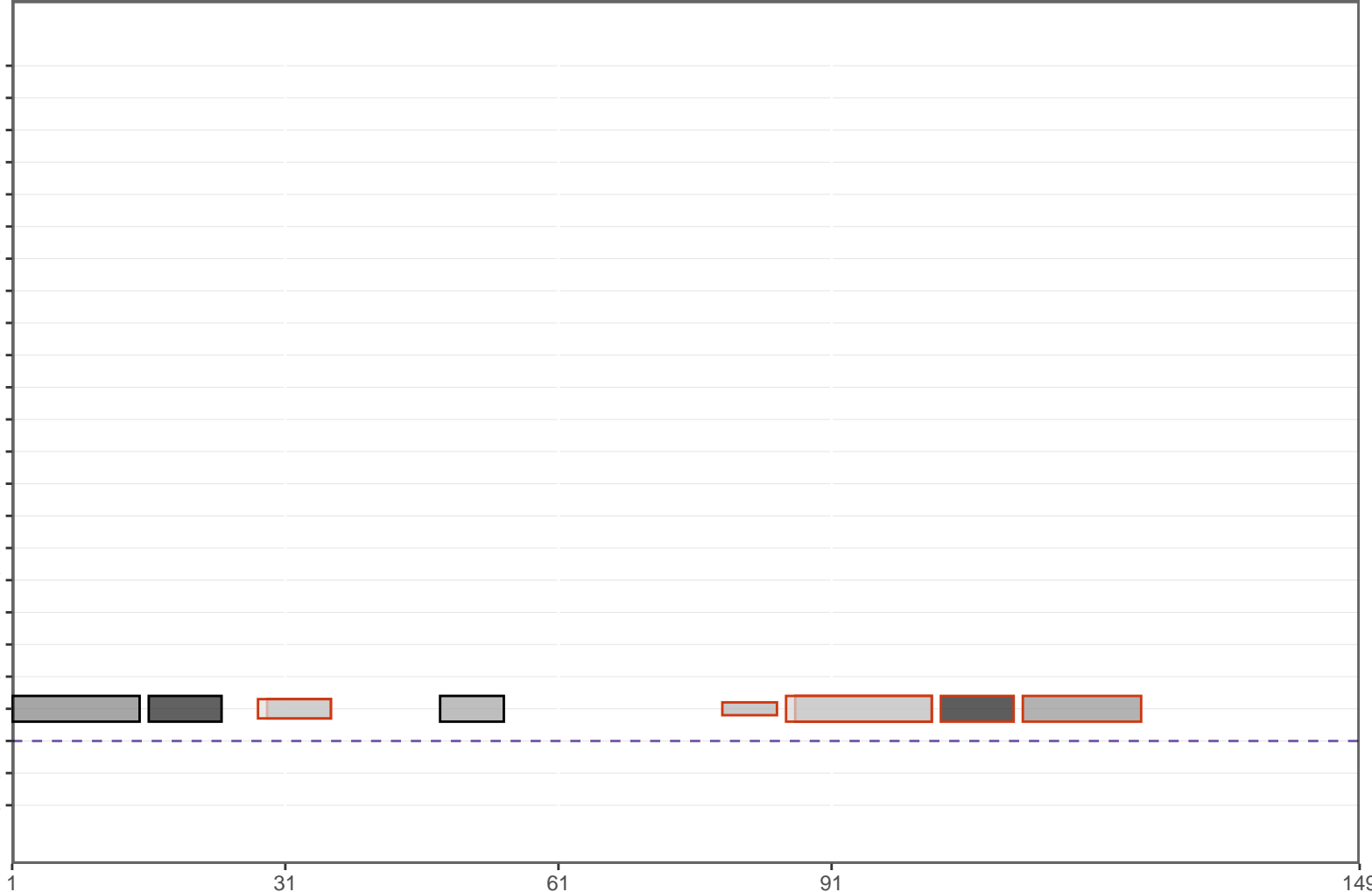
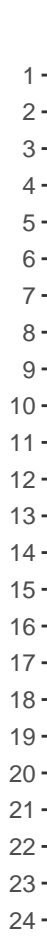
TQCESFNNKQVWSEIGRYASDNNKILVGNKSDLTNRVVEVETAKAFADIEGIPLETSAKDATNVEQAFMMATSAIKNRMASQPTNNSAKPFTVIRGGQPVTSGGGGCS*

NbL10g13420.1 nucleoside_diphosphate_kinase_1-like [MW = 16.16 kDa]



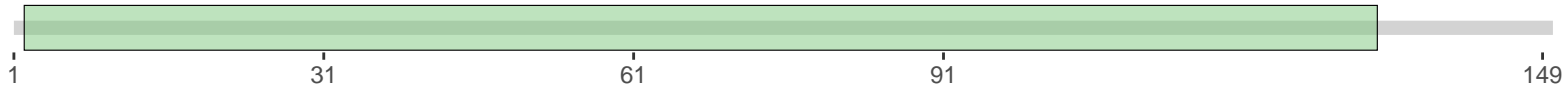
Molecular weight

Gel Slice

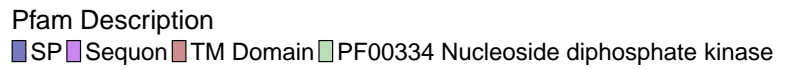


Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:
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NbL10g13330.1 ubiquitin-like_protein_5 [MW = 8.5 kDa]

No. of times detected



log(intensity)



Values from

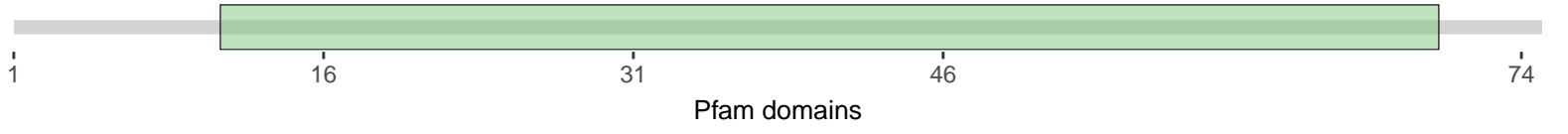
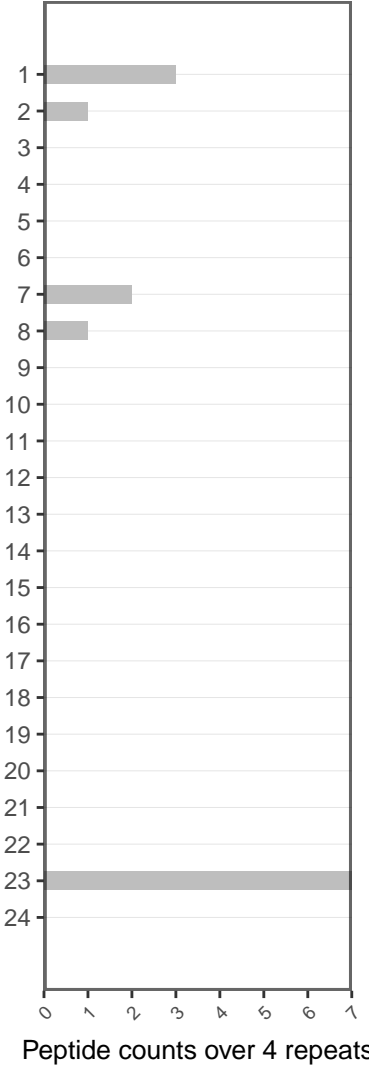
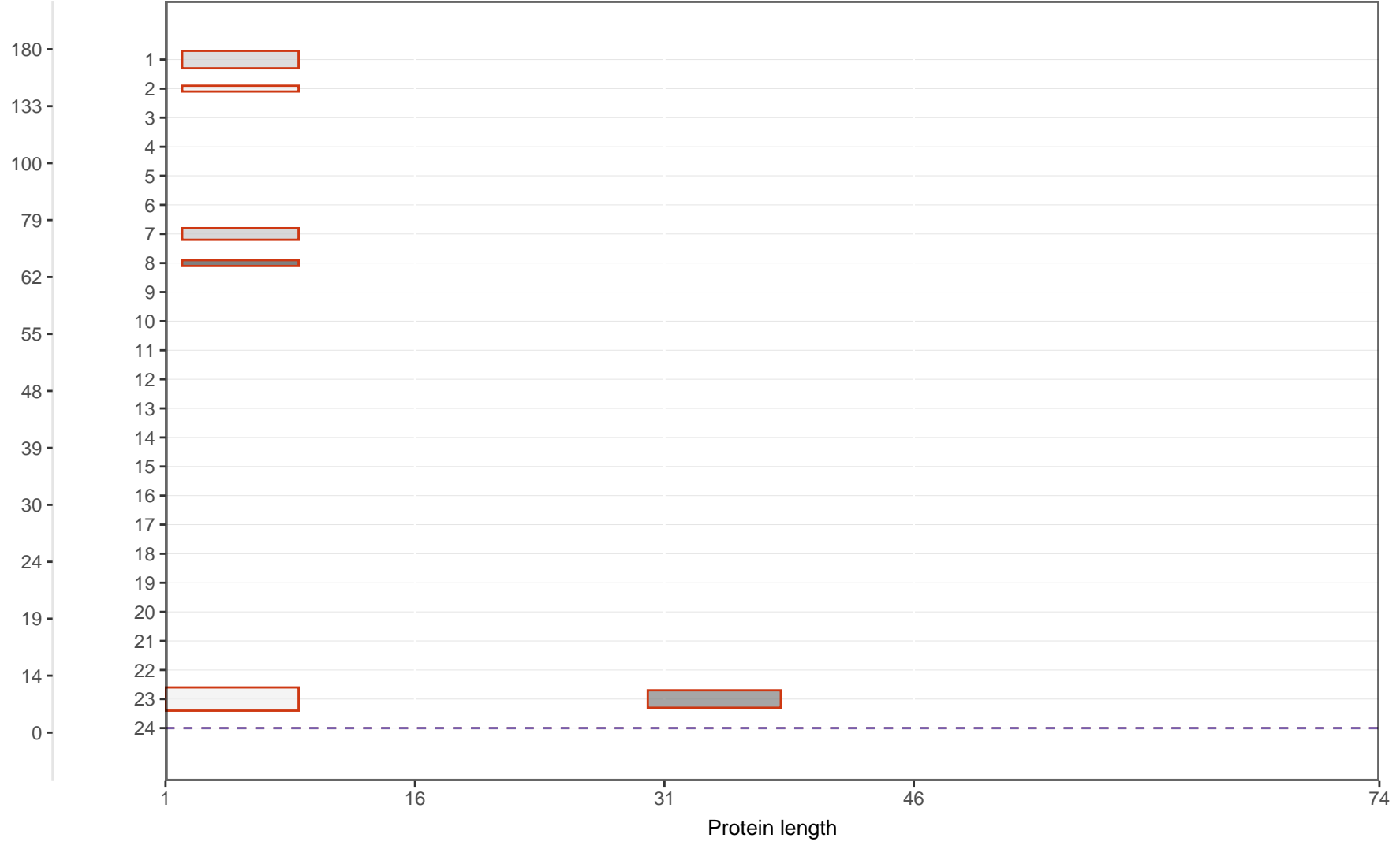


MW indication

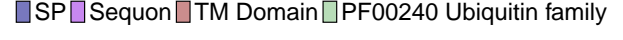


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

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NbL10g12800.1 protein_transport_protein_SEC23-like [MW = 85.22 kDa]

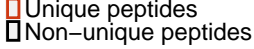
No. of times detected



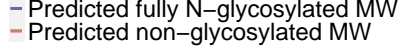
log(intensity)



Values from



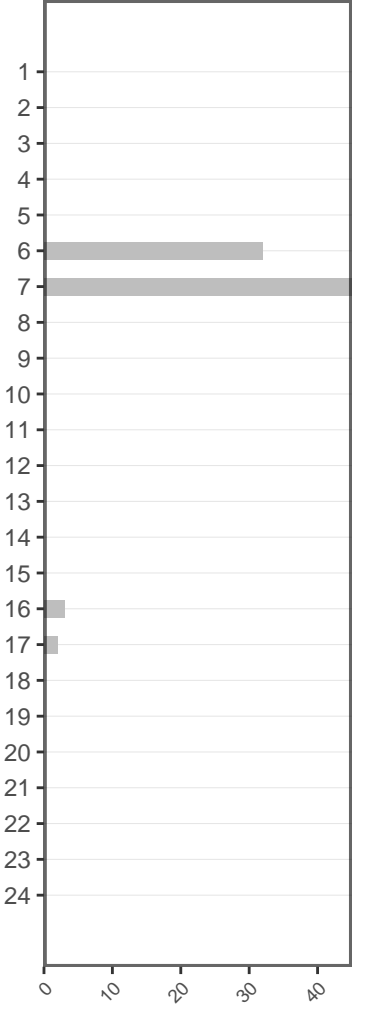
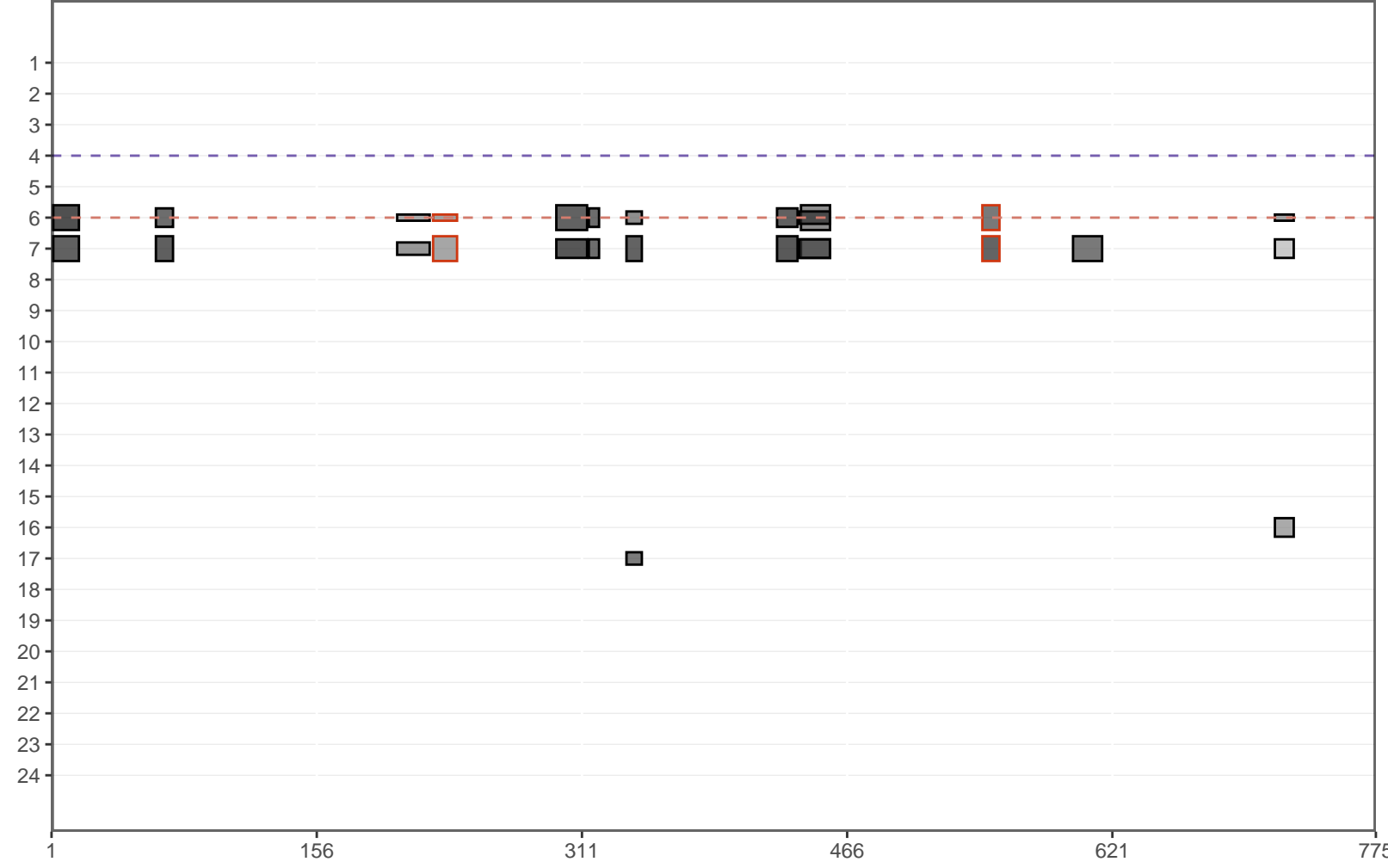
MW indication



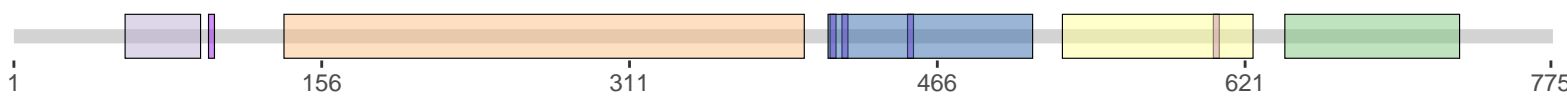
Molecular weight



Gel Slice

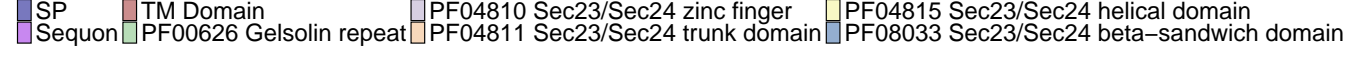


Protein length



Pfam domains

Pfam Description



Protein sequence:

MEKTTGGLVLAESFSGHVSFKDFKHFHFDGEGQGLGFSNGLFNGTLENGSKDKHGGHGPCTSELEKKGKRWVSTVIGEGNTTAWKLGGLDKNTGLTVFFDVSSEKSDPDSGNQNPQLVHFTSYGSHGGQTKLVRVTTITRRVWVDAVSTEELVGQFDGEEAAVAVMARLAVYKMEVEEDFATRWLDRNLRLGAKFGDYKDDPSGFTLNPSFSLFPQFMFHLRRSGQLQVFTNNSPDETAVFRMLNREGISNAAVMIGPFLTAQFQNSLPAFALLDVAIAADRILLDDAYFSVVF

NbL10g12780.1 adenosylhomocysteinase-like [MW = 53.14 kDa]

No. of times detected



log(intensity)



Values from



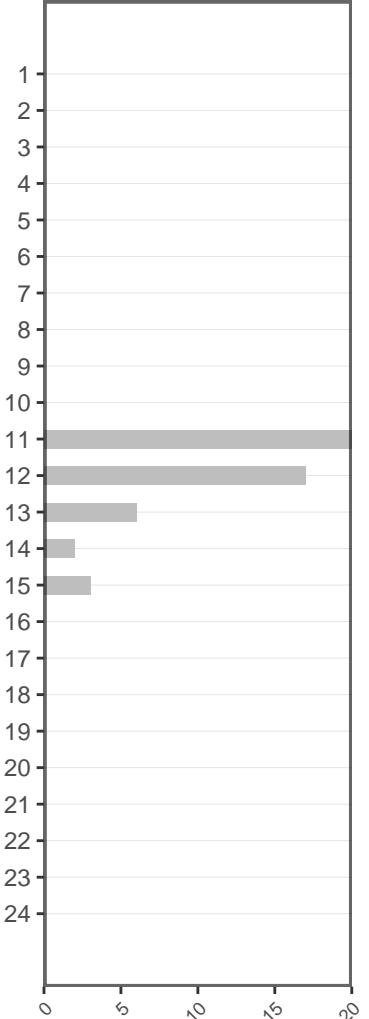
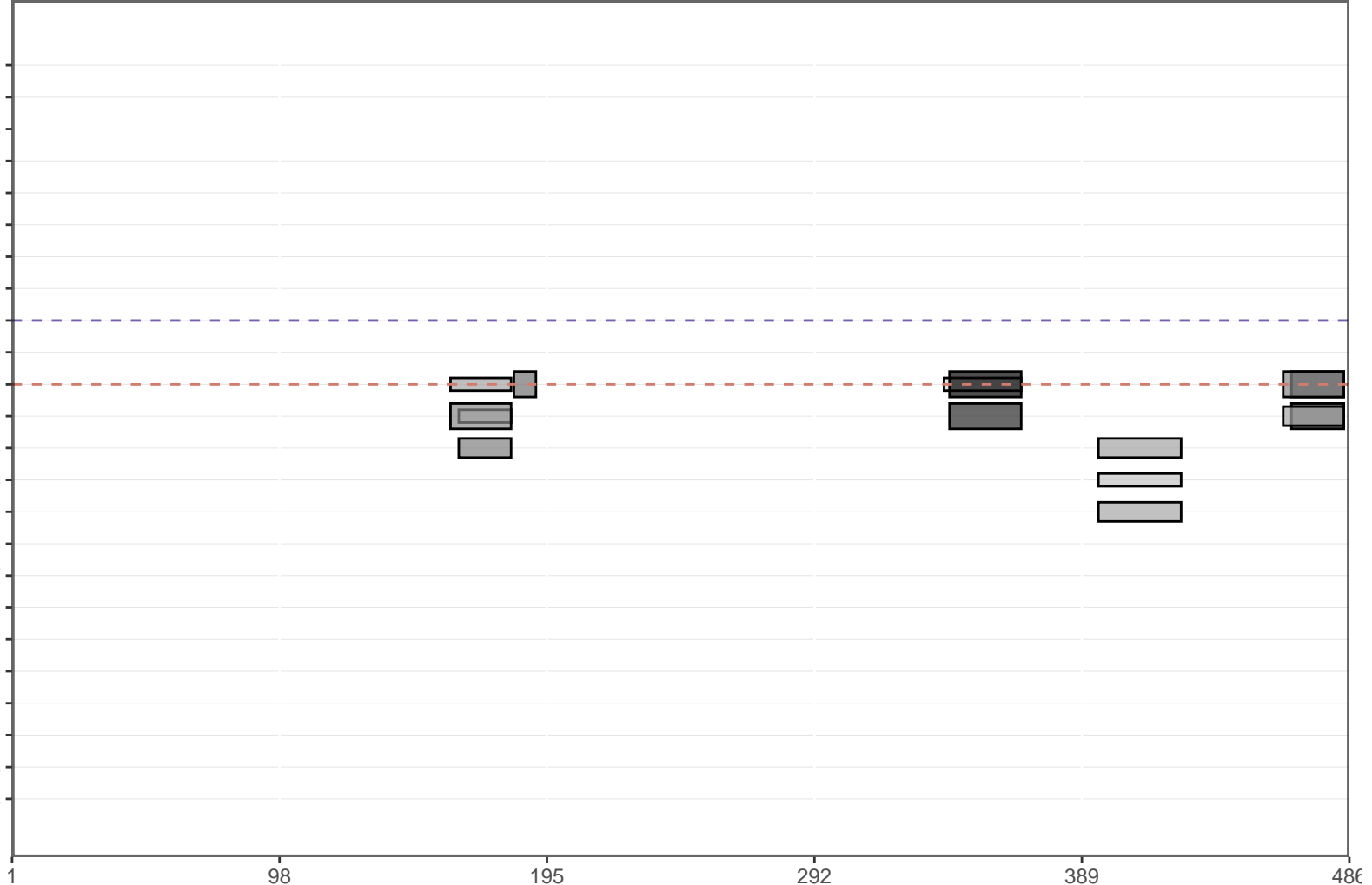
MW indication



Molecular weight

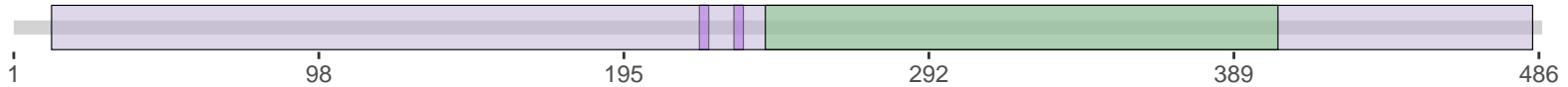


Gel Slice



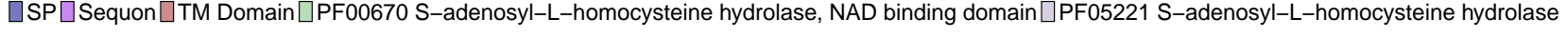
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NDSVTKSKFDNLYGGRHSLPDGLMRATDVMIAQKVALVAGYGDVKGKGAALKQAGARVIVTEIDPICALGATMEGLGVLTLEDVVSVDVDFVTTTGNKIMVDMHMRKMKNNANVNCNGHFDNEIDMLGETTFPGVKRTIKPQTRWVFPDITNSGIVLAEGRLMNLGGATGHPSEVMSCSFTNQVIAQLELVKWEKSTGKYERKVVYLPKHLDEKVAALHLGKLGARLTKLSKDGADHSEVPVEGPKYKPHRYV

NbL10g12770.1 serine_hydroxymethyltransferase_4-like [MW = 54.45 kDa]

No. of times detected



log(intensity)



Values from



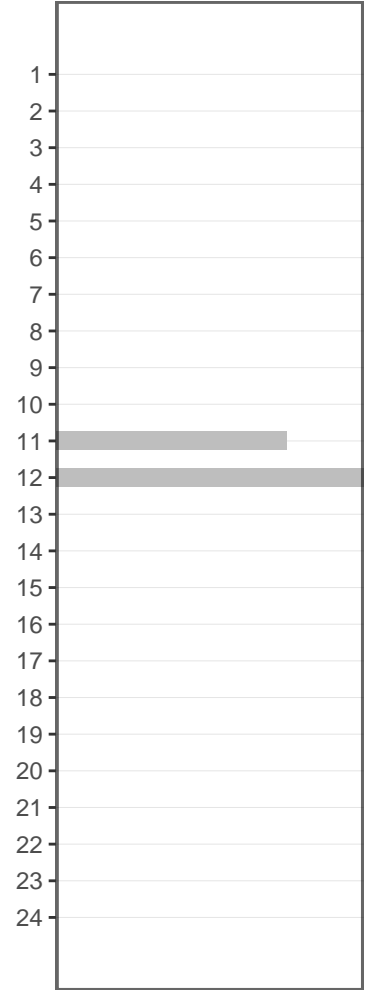
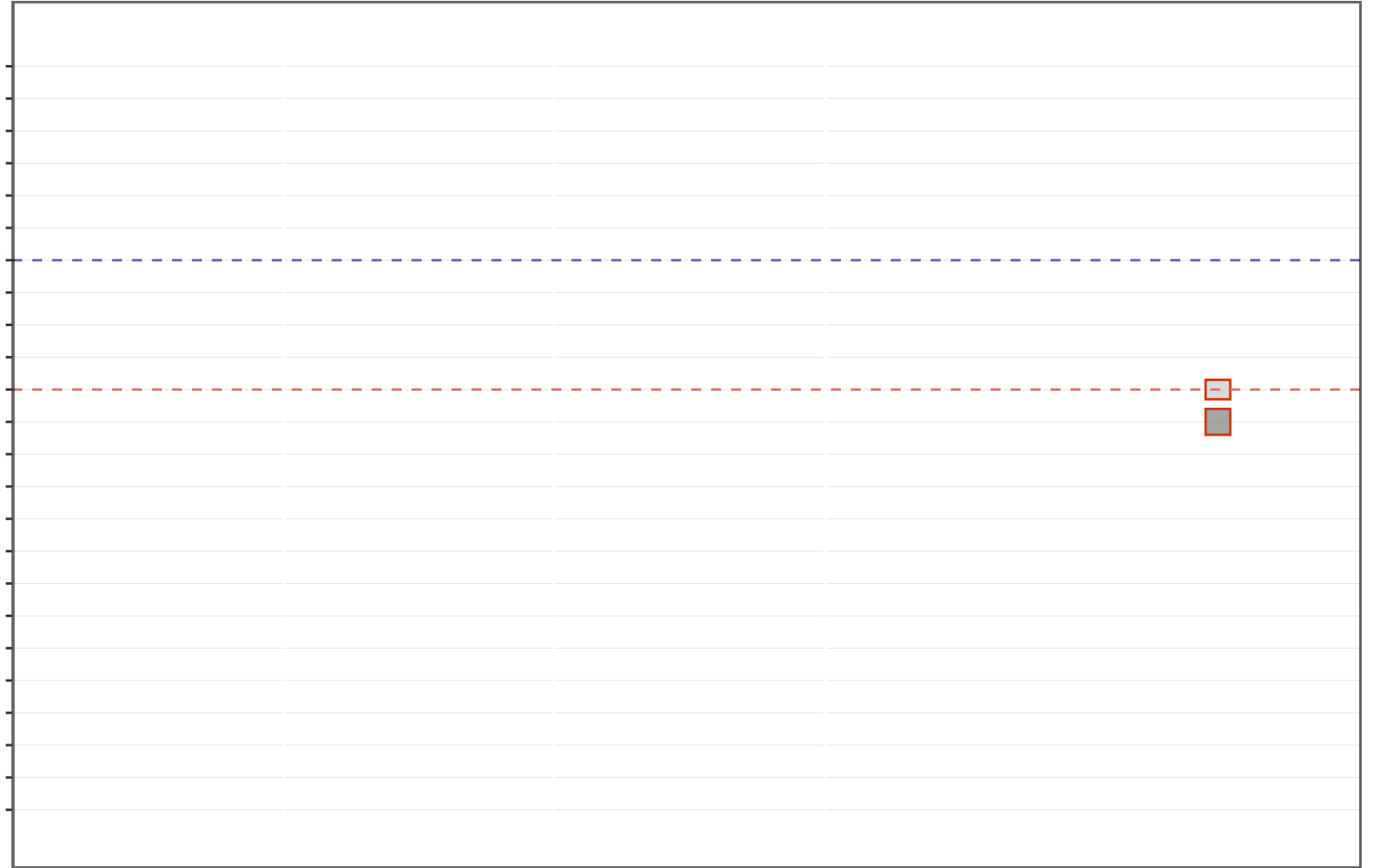
MW indication



Molecular weight



Gel Slice

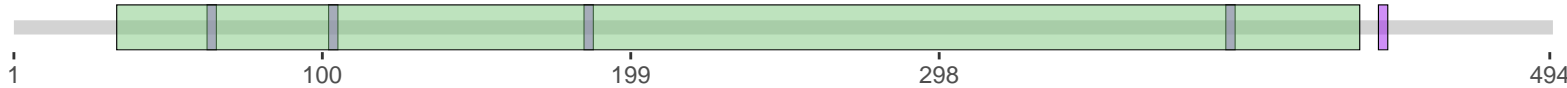


Protein length

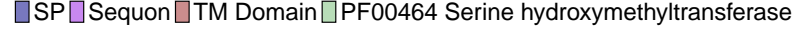


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

DMAHSGLVAAQEAADPFYGDVLTTHKSLRPRAGMIFVRKGGPKPKKGGPEDAVYDFEDKINFAVFPISLGGGPHNHQIGALAWALKGAATPGKAKQVKKANVALGNHLSKSGYKLVLTGGTENHLVLDLRLPLGLTGNKVEKLDLANITVKNKNAVFGDSSALAPGGVRIQTRMTSRGLVEKDFEQAEFLHRAVNTLNGKHEYKLLKDFNKGILNNKKEIEELKADVEKFSFSDMPGFKLSEMKYKDI

NbL10g12670.1 60S_ribosomal_protein_L13a-4-like [MW = 23.52 kDa]

No. of times detected



log(intensity)



Values from



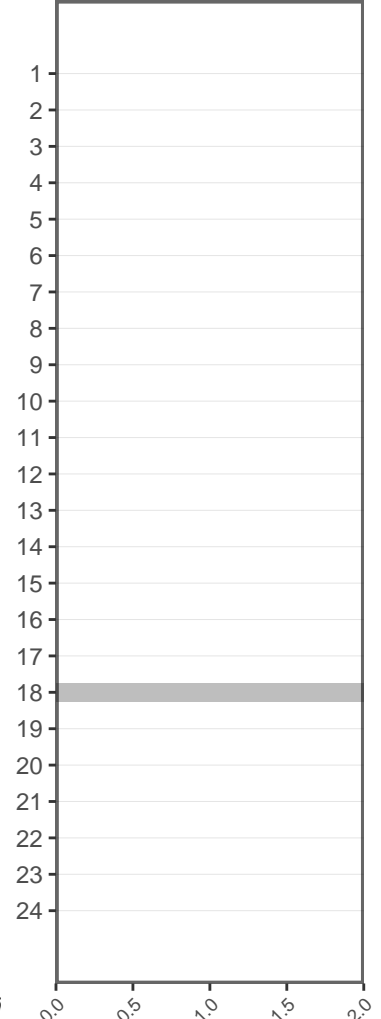
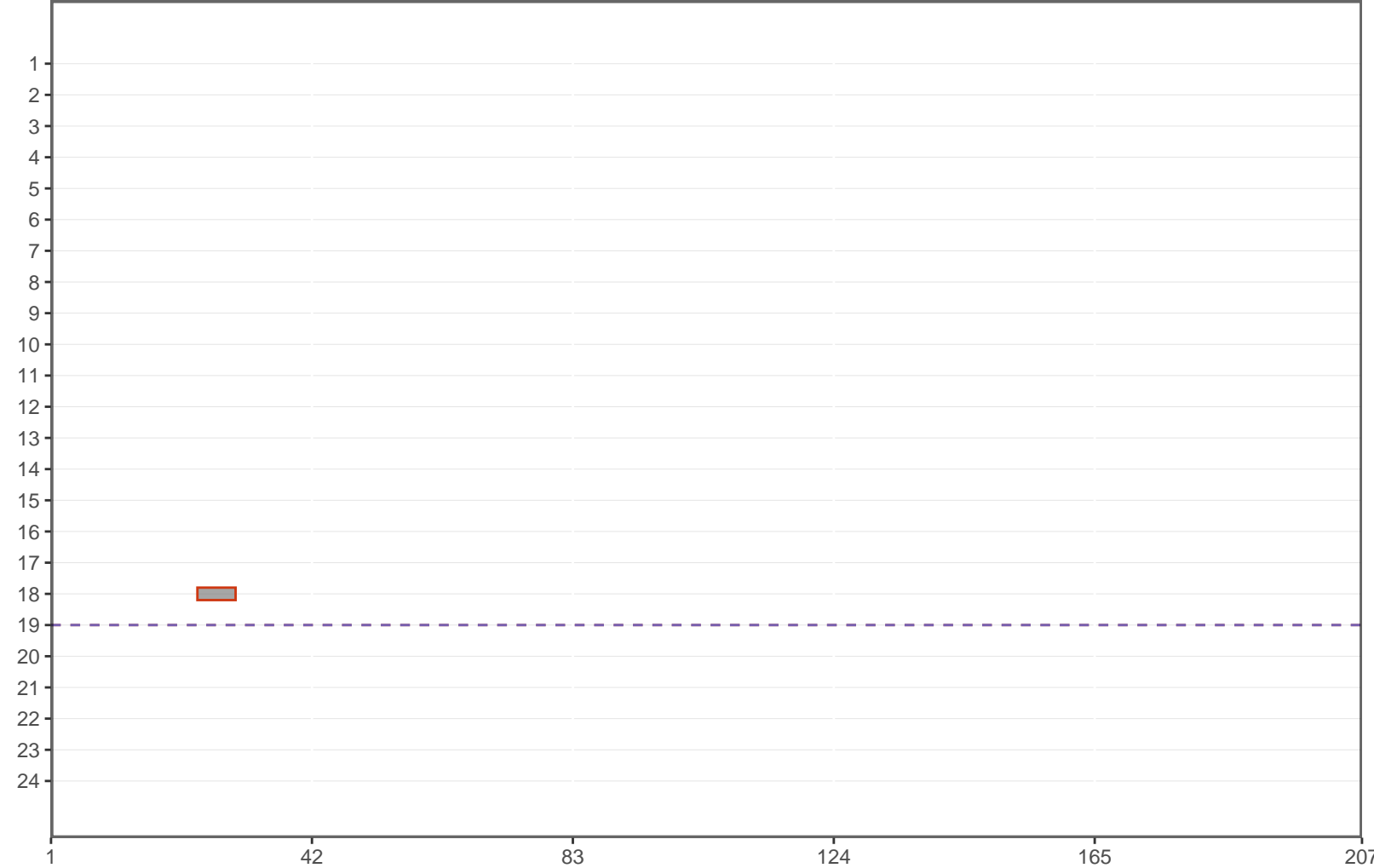
MW indication



Molecular weight

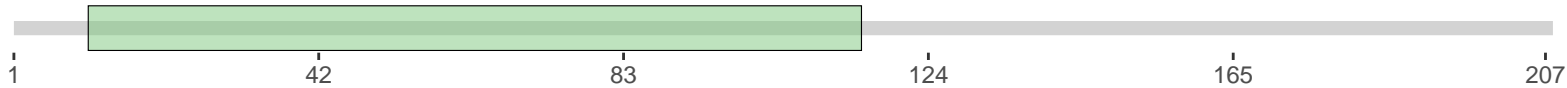


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGMIPKTKRGAALALRLKVVYEGVPPVQKVKRMVFDALKVLRLQAGHKYVLLGKLSSEVGVNHYDTIKELKPKERAGVAVERRKGLAKLRVAKKAEEKLGPLVAEPKY

NbL10g12620.1 probable_methionine--tRNA_ligase [MW = 90.66 kDa]

No. of times detected



log(intensity)



Values from



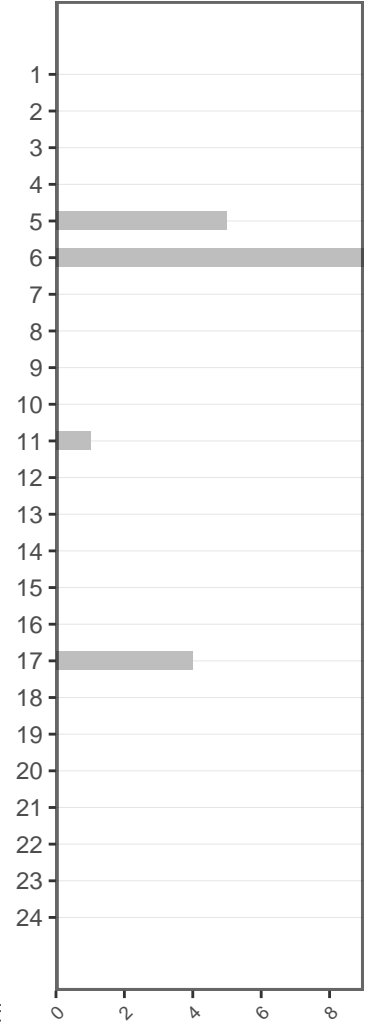
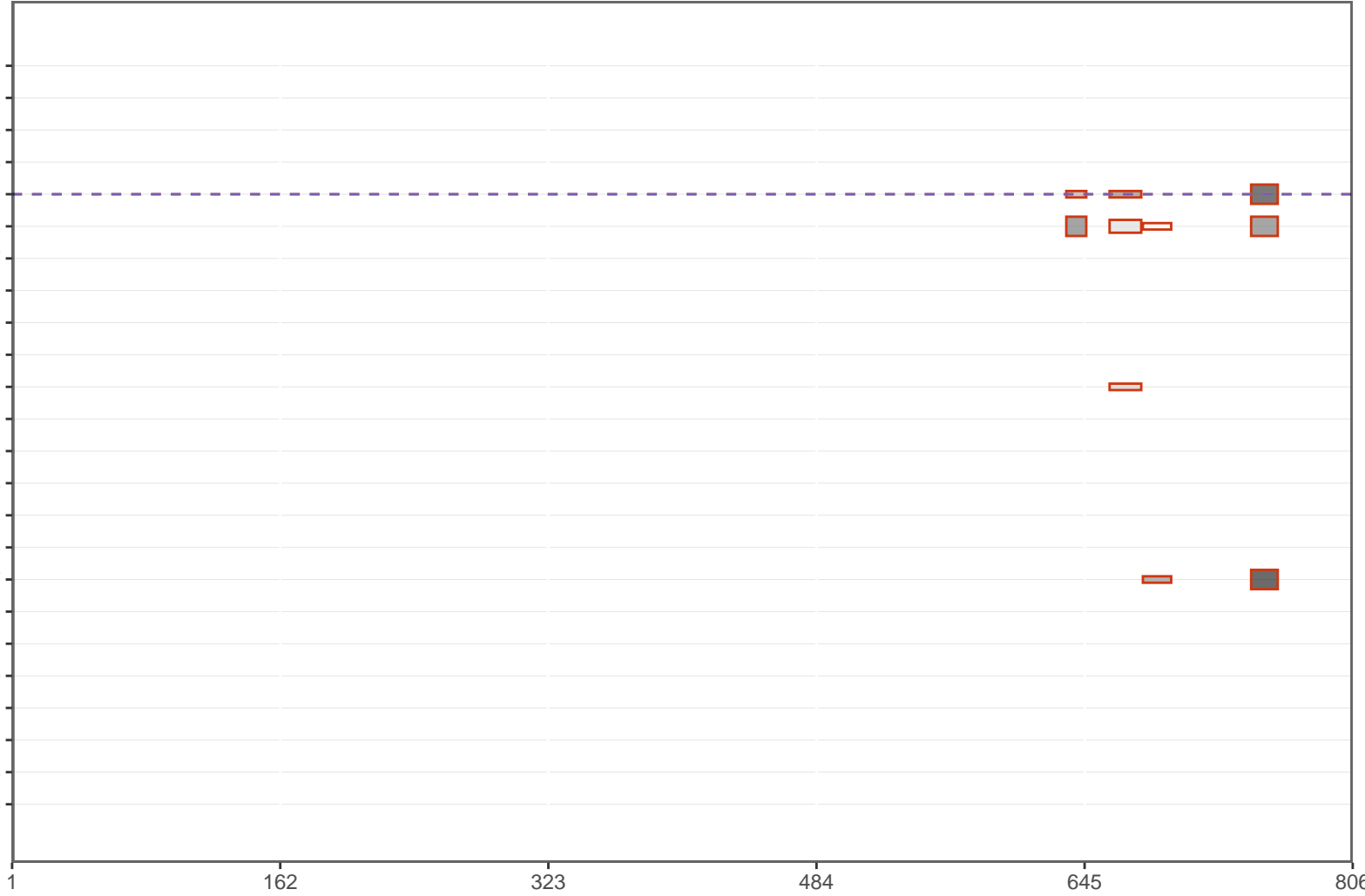
MW indication



Molecular weight

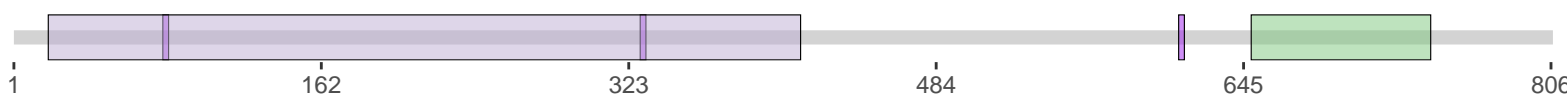


Gel Slice



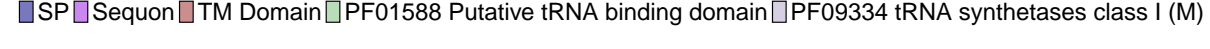
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LFTWDLQAKLNSELLSNLGNFVNRVLFSAIKDSASGGYGGIFPDVEGAESHPLTKALGEKVNHYVEQHYEAMKVKLGGKLVAMBVSGEGNGYLGESGFVWLYKEDRRRSGSIVMKTAGGLVYLLAGLLEPFMPSFRRLLKQLNLPETQLSLADEKGDVANSKRKPWNPMPGKHGTPFLFKELKDEEVEFYREKFNAGSGADRDRALKKAETDAKKMAEQLNKTWISDGNKERRAKKSSSEKSKAPDTVEGESISRLDIRVGLTFKAGKHFNADSLVVEEIDVGEALPRTV

NbL10g12550.1 dihydroxy-acid_dehydratase_chloroplastic [MW = 66.28 kDa]

No. of times detected



log(intensity)



Values from



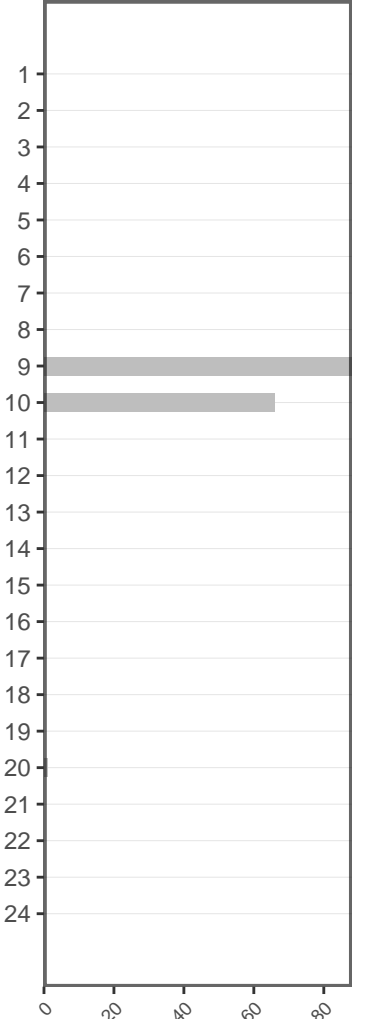
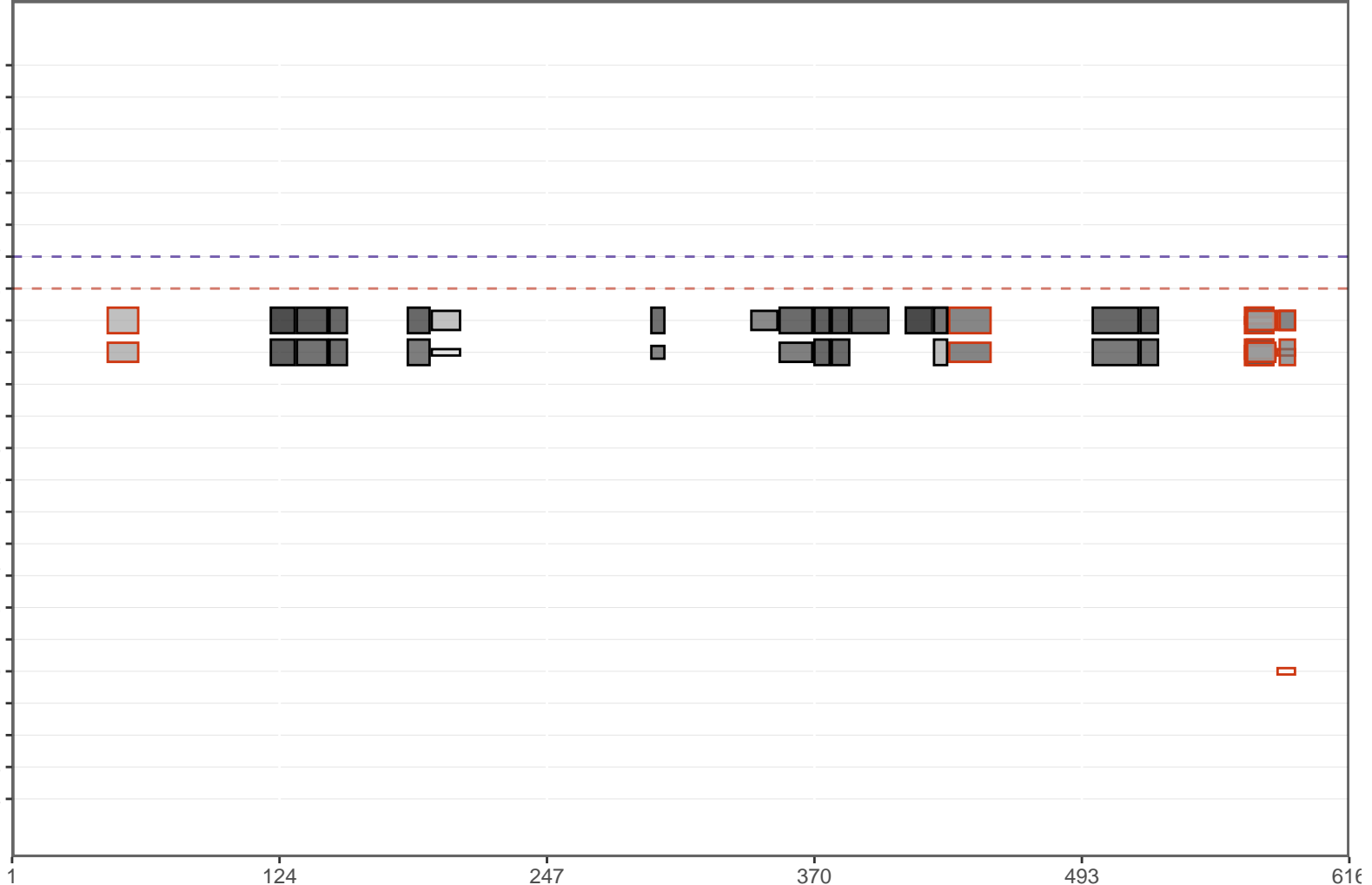
MW indication



Molecular weight

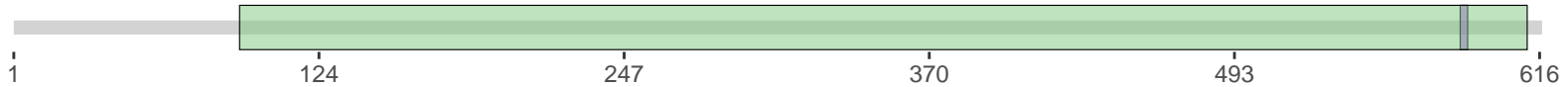


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GKYLLELLKMDLKRDRDITKXSLRNAMVMMALGGSTNAVHLIISRIVGLELTLDDFGKYSVAVPLADLKPSGKYVMEQVHKGGTVAIRHLLLEGLYLDGDCMTVTKKTLAENAKLFPBLAEGGQIRPLSNPKRETGHQILVGNLAPEGSVAKITGKEMVFGSPALVFEQEEAMIAISEDPLRFKGVVVRGEGPKGGPMPMLTPTSAIMGAGLGGKDCALLTDGRFSGGGHGVVGHQPEAGEGGPIGLVDDGDHTIDQKRKMDVQLSDSEEFQRKNTPTPI

NbL10g12480.1 chaperonin_CPN60-2_mitochondrial-like [MW = 61.05 kDa]

No. of times detected



log(intensity)



Values from



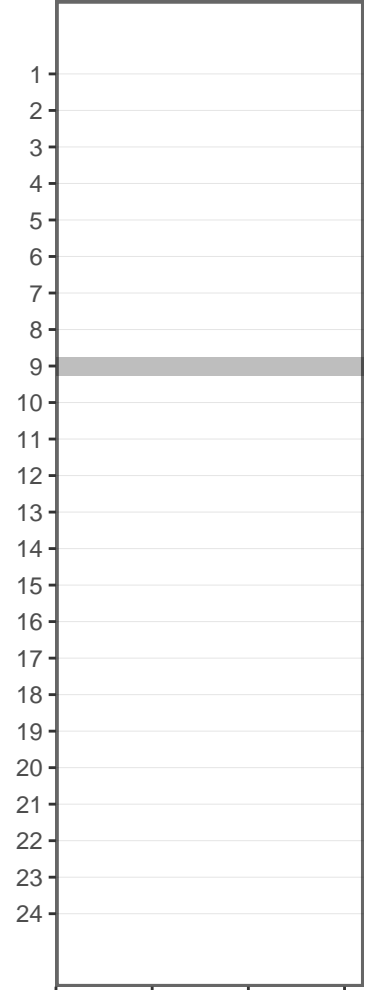
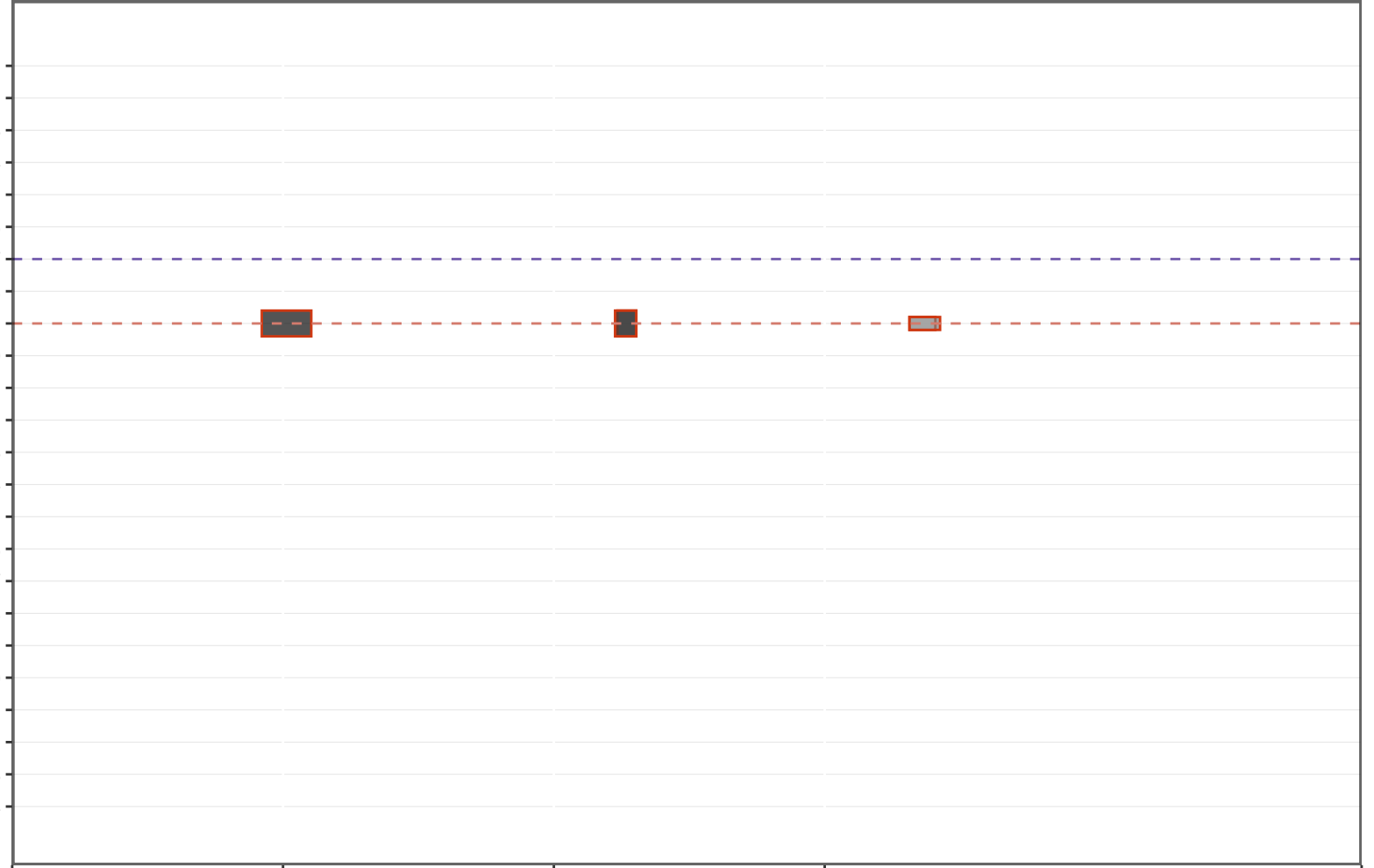
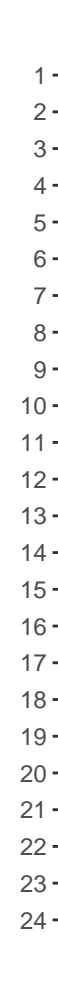
MW indication



Molecular weight

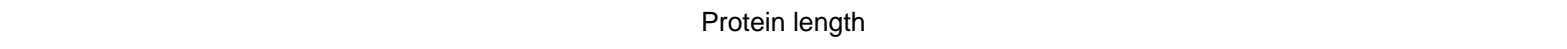


Gel Slice



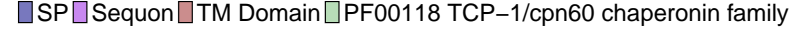
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

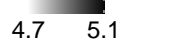
.KRRPLLYSEDEVSEELATLHLKLRAGIKVCAKAPFGFGENRKANLGDALATLTGGGVTEELGKLNLENVELDMLGKDKKVKYTKDKDPTVLDGAGEKKAIEERGEGRSAEIVSTSDYDKKELQERLAKLGGVWLVKVGGAASELVEGEKDKRVTDALNATKAAVEEGVPGGGVLLVYASKELDNLPTANFDQKIGVQIGNALKTPVHTAENAGVEGAVVYKGLLEGDDPDLGYDAAKGEVVDMMVKGSHDPLKVRTALVDAASVGSLLTTEAAVVELPKDTPSPPIPPGGGA

NbL10g12340.1 stress-response_A/B_barrel_domain-containing_protein_HS1 [MW = 12.15 kDa]

No. of times detected



log(intensity)



Values from



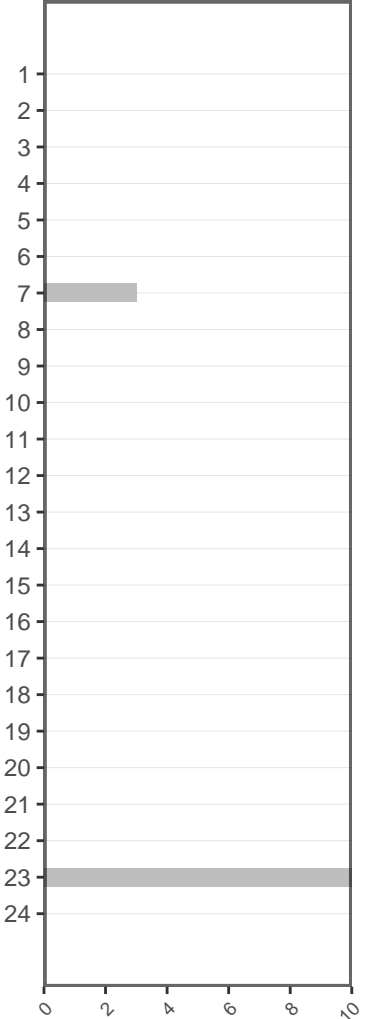
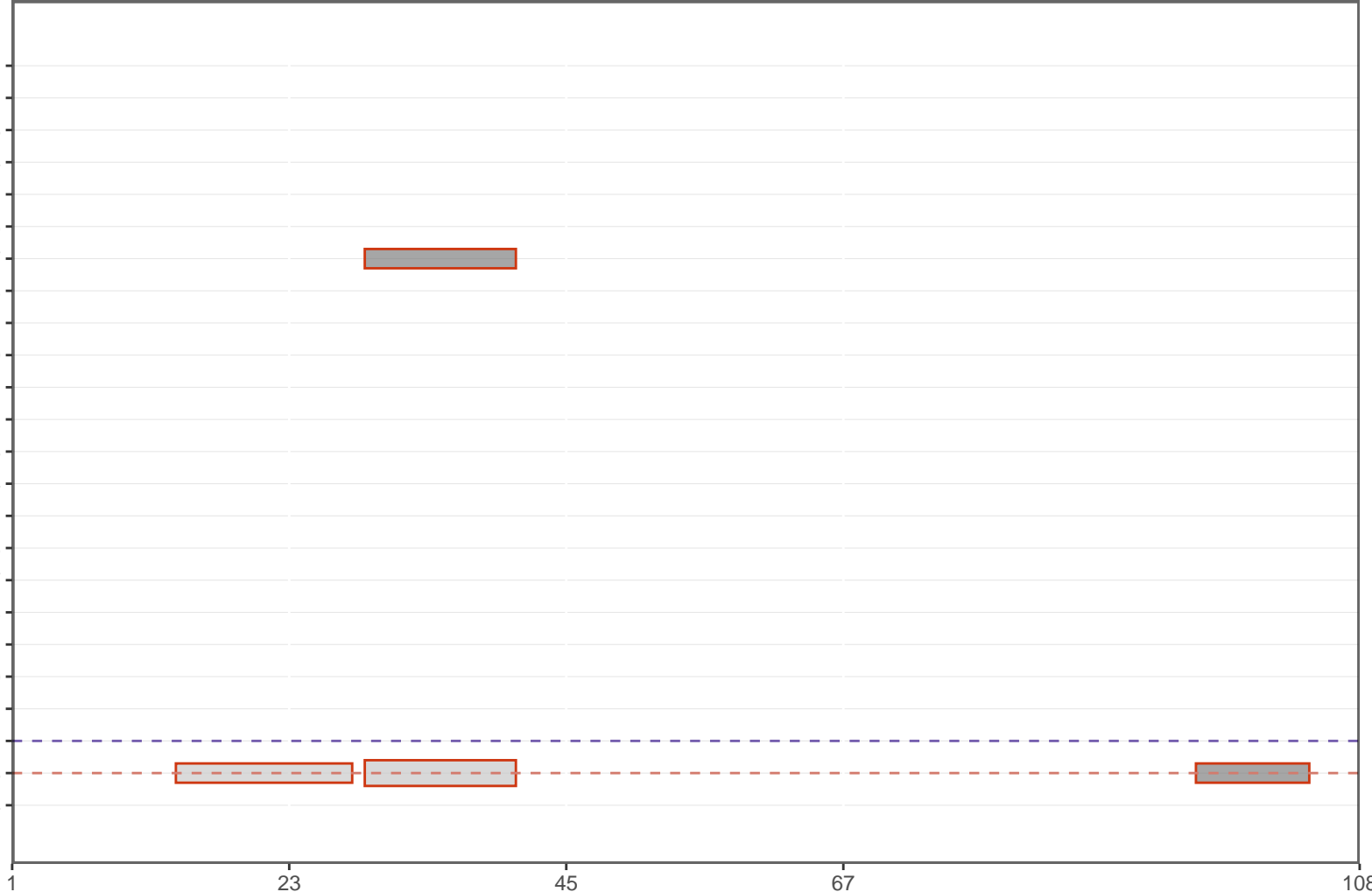
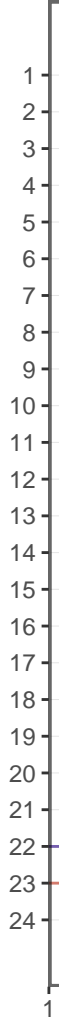
MW indication



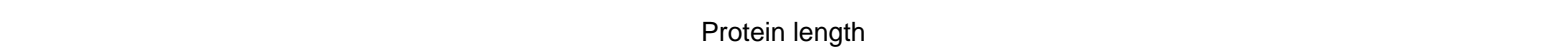
Molecular weight



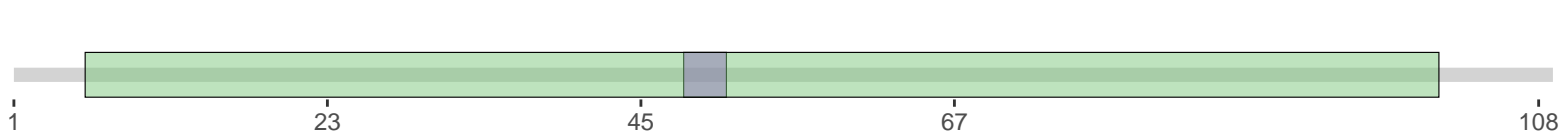
Gel Slice



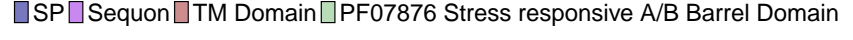
Protein length



Pfam domains



Pfam Description

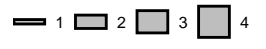


Protein sequence:

MAPHWGKNSIENFHGGFTHWVFESTFDSTEGIAEYDHPAHVEYANTLLPQLEKLVLDIKPKKVGPI

NbL10g12330.1 dihydrolipoyl_dehydrogenase_mitochondrial [MW = 53.4 kDa]

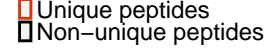
No. of times detected



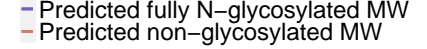
log(intensity)



Values from

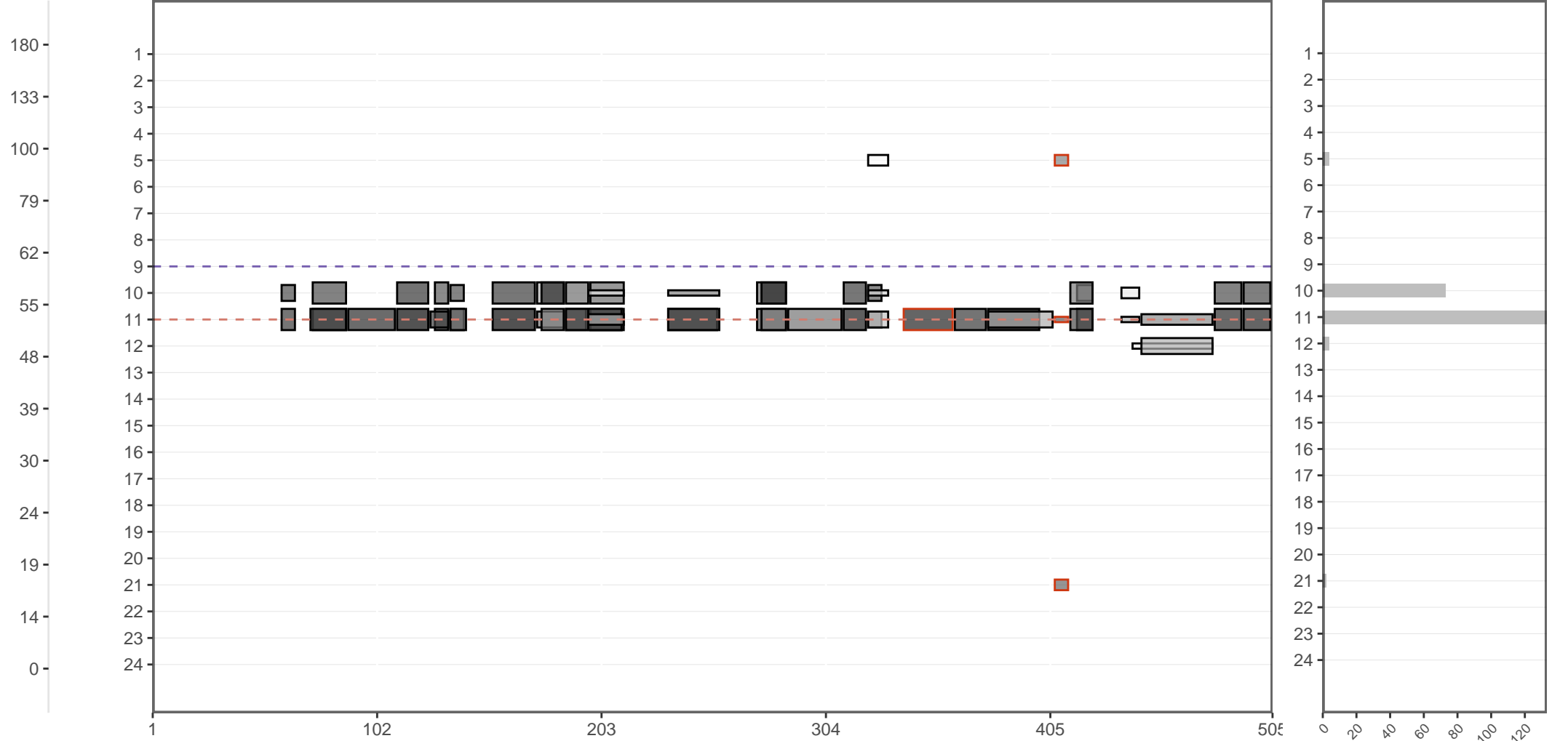


MW indication



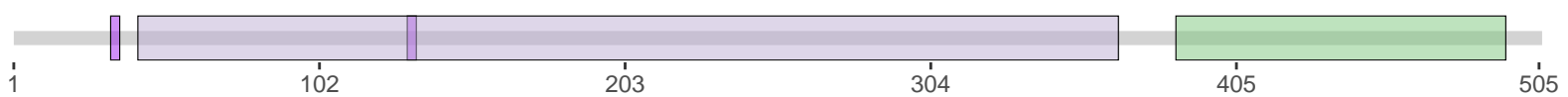
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

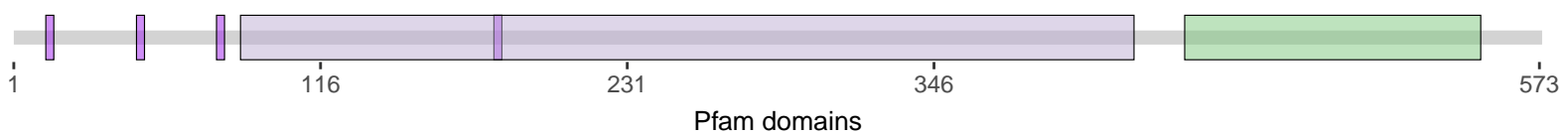
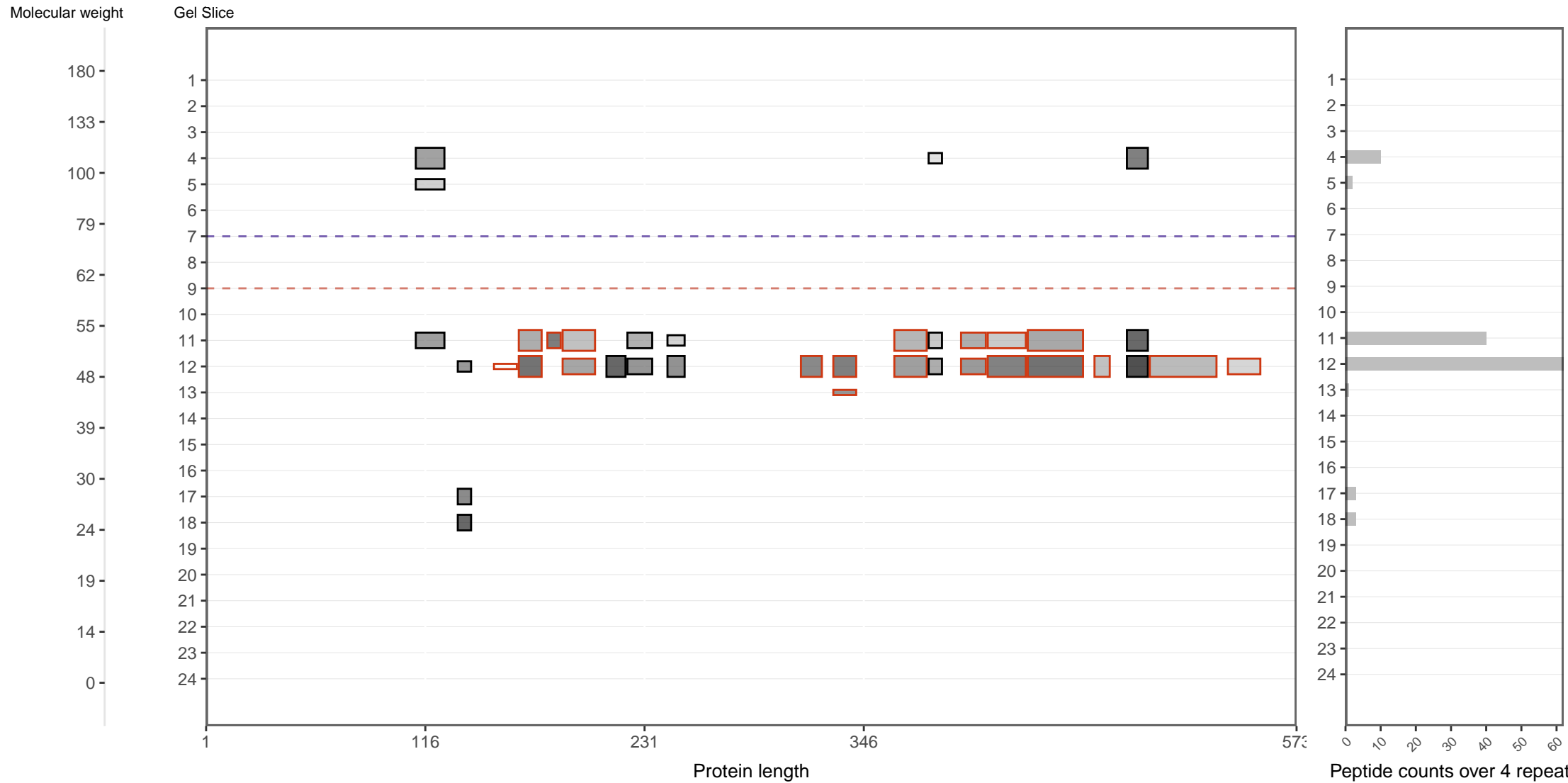
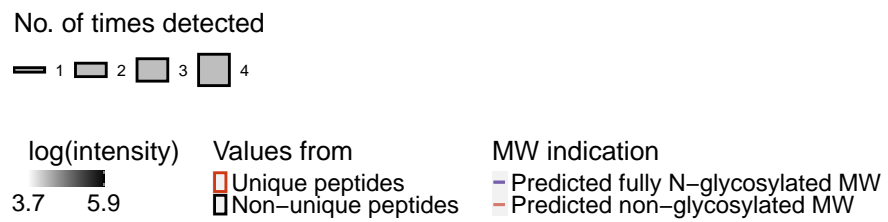
Pfam Description

- SP
- Sequon
- TM Domain
- PF02852 Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain
- PF07992 Pyridine nucleotide-disulphide oxidoreductase

Protein sequence:

VVEFGPDVPSMDGEVRKGFQRBLEKQKMKFLKTKVVSVEVTDGDKLLEPMAGDDQTLLEADVLLVLSAGRIPTSGGLDKQGVETDKAGRILLNERFATNPGVHAGDVGIPGMLAHKAEEEDGVAQVEFIAGKEGHVDYDLVPGVYYTHPEVAVGKTEEGKALGVDRYRQKFPFLANSRAKAIIDAEQIVKVAEKETDKILGVHIMSPNAGELIEAVLALHYGASSEDARTGHAPTMSEALKKAAATFYKPIHI

NbL10g12200.1 dihydrolipoyl_dehydrogenase_2_chloroplastic-like [MW = 61.6 kDa]



Pfam Description

- SP
- Sequon
- TM Domain
- PF02852 Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain
- PF07992 Pyridine nucleotide-disulphide oxidoreductase

Protein sequence:

IFSDVYTLGSEVTFIEALDQLMPGDFPEISKLGRVLVNPKRIDYHTGVFATKTRFKDKGRPVVIELTDKTKELKEILEVDALATGRAPYTNLGNLENNVLTGRGFIPVDERMRVIDADGKLVPLHYIGDANGKMLLAHAASADGIEVIEQVGRDHLVNLHLSVPAAGFTFPEISAVGLTFEPQAREKAENKNGFEISAKTGFKANTKALAENEGEGKLKLYRPDTGELGVHFGMAADLIEASNAALGTRIGDKFVAHHPFLSEVLDLFEKAKVNTDORSSVREPIA

NbL10g12180.1 5-methyltetrahydropteroyltriglutamate--homocysteine_methyltransferase-like [MW = 92.03 kDa]

No. of times detected



log(intensity)



Values from



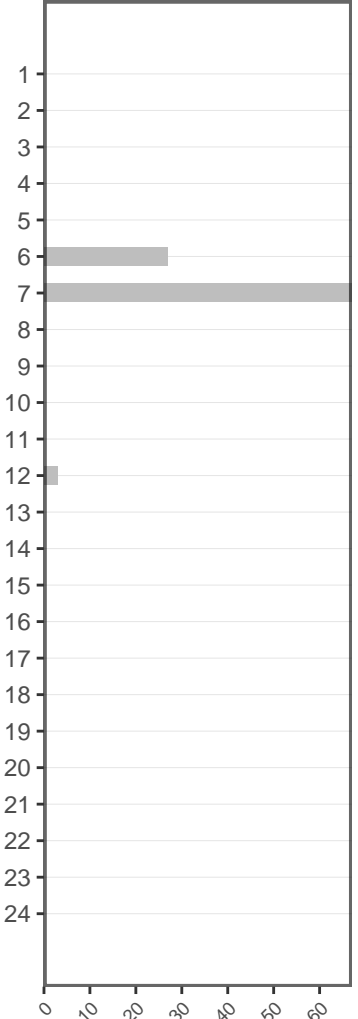
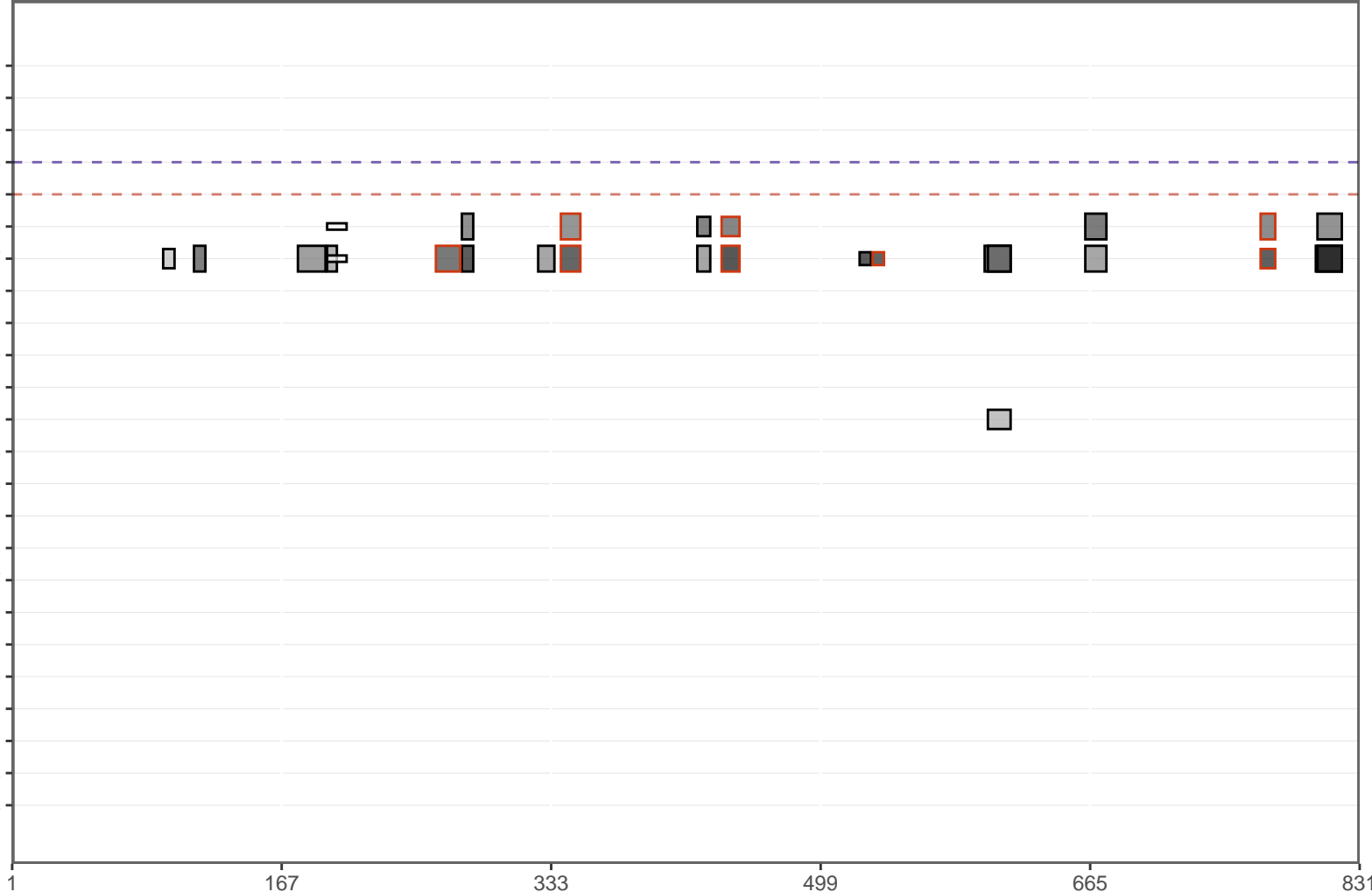
MW indication



Molecular weight

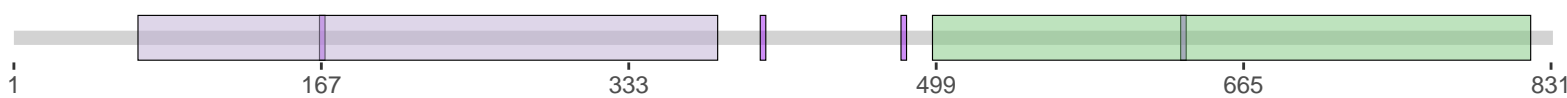


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01717 Cobalamin-independent synthase, Catalytic domain
- PF08267 Cobalamin-independent synthase, N-terminal domain

Protein sequence:

IETKLDDEIKSVLFAAAGKLVENALAKLAGRDEAFFSANAAGRTSRKSSPRVTEAVQKAAASLKGSDHRRATHVSRLEAQQKLNLPPTFTTGGFPOTLELRKVRREYKANKISGEGYVKYHSEIEISKVYVNLGEELDIDLHVHGEPEFRNDMVEYFGEQLSGFAFANGVWVGYGSRDVKPPIVYGVGRPKPMTYFVWVSLAGSMKRPKMGKMLTGPVITLNVSEFVRDDQPRFETGQIALKDEVEDELEKAGINVDIDEALREGLPKRKEEAFYLNWVWHSFF

NbL10g12050.1 folylpolyglutamate_synthase-like [MW = 68.15 kDa]

No. of times detected



log(intensity)



Values from



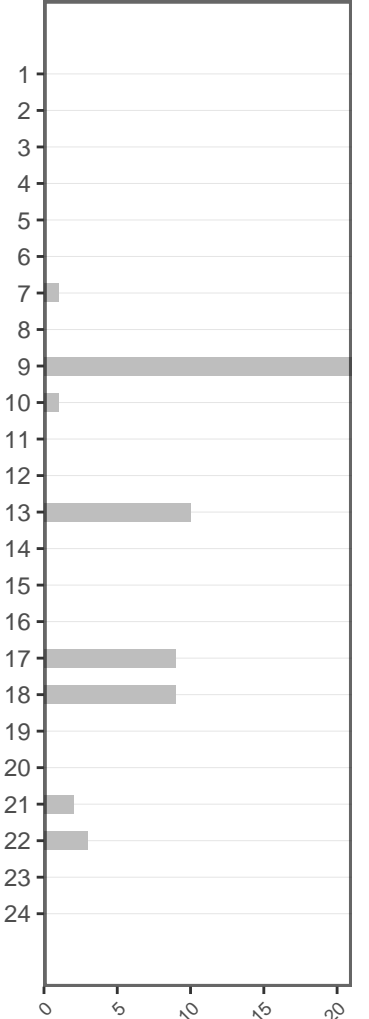
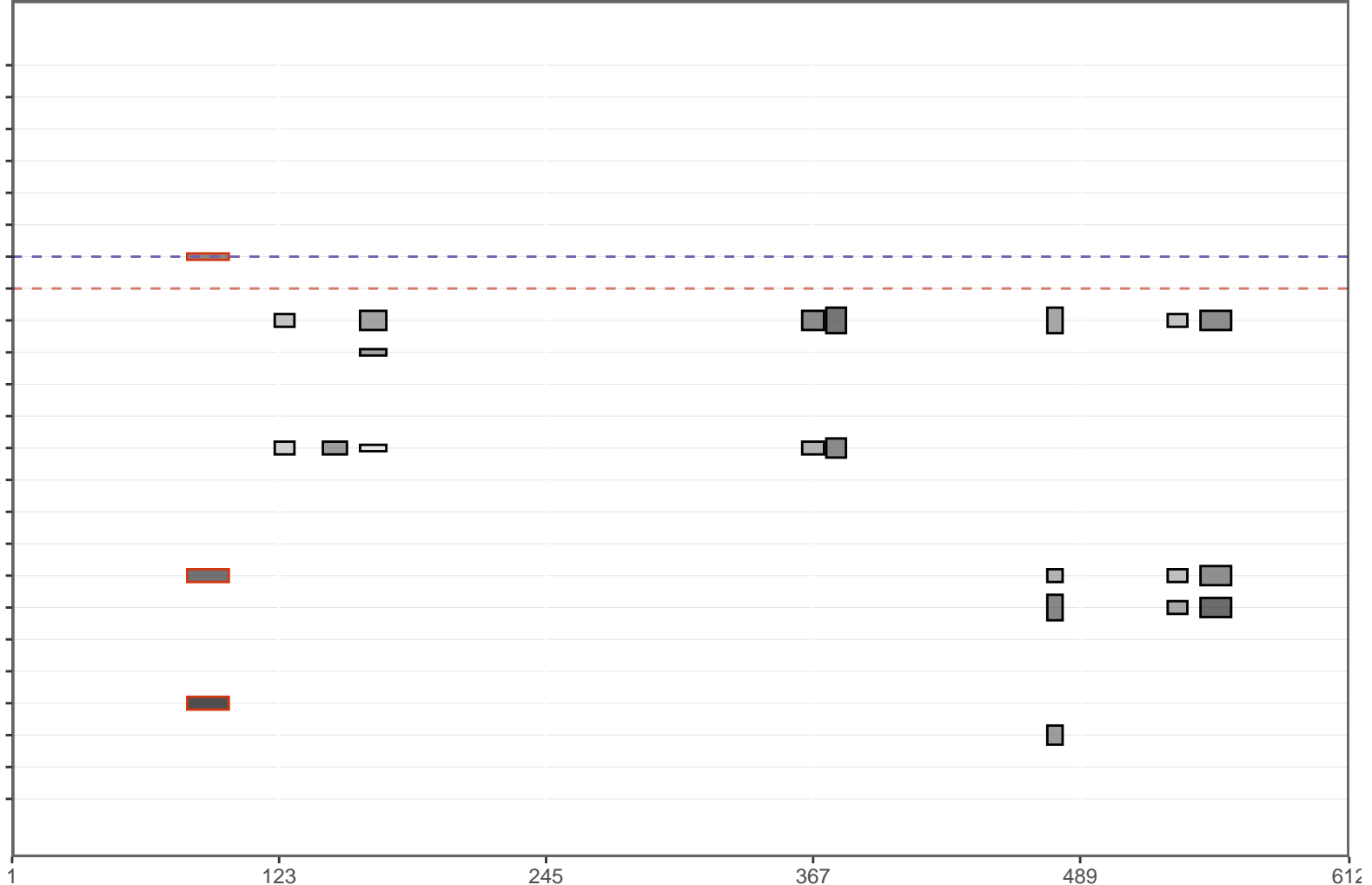
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

MLVLEKASELDVHLEVAAPLDANMLGHLGLEGEHGYNAGLAALG6STVLQRTHGVENHYKEMTNLPEQFVKGLATAALGGRAGIVPQGLIESE68SDVYFFDGAHSPESMDVCAKWFSLAHQGDGKQHSYVNRGRHNLGLVSHD5VEMGHHEASKK6STGFLFN6MSVDRDPOLLPRLMRACANHGIVFQKALFVFN6SVYKVGCTEMPTDGTQVDL6WGLTGRHWENLVHGEK6NDVKNKTDGQIYEEVTD6AEK6GARG6ENKVFPELPIANVLRDTRK

NbL10g11880.1 pleckstrin_homology_domain-containing_protein_1-like [MW = 16.66 kDa]

No. of times detected



log(intensity)



Values from



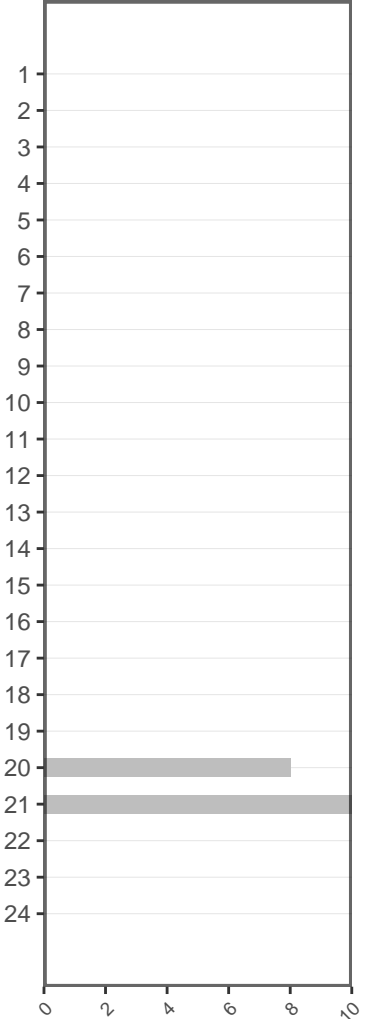
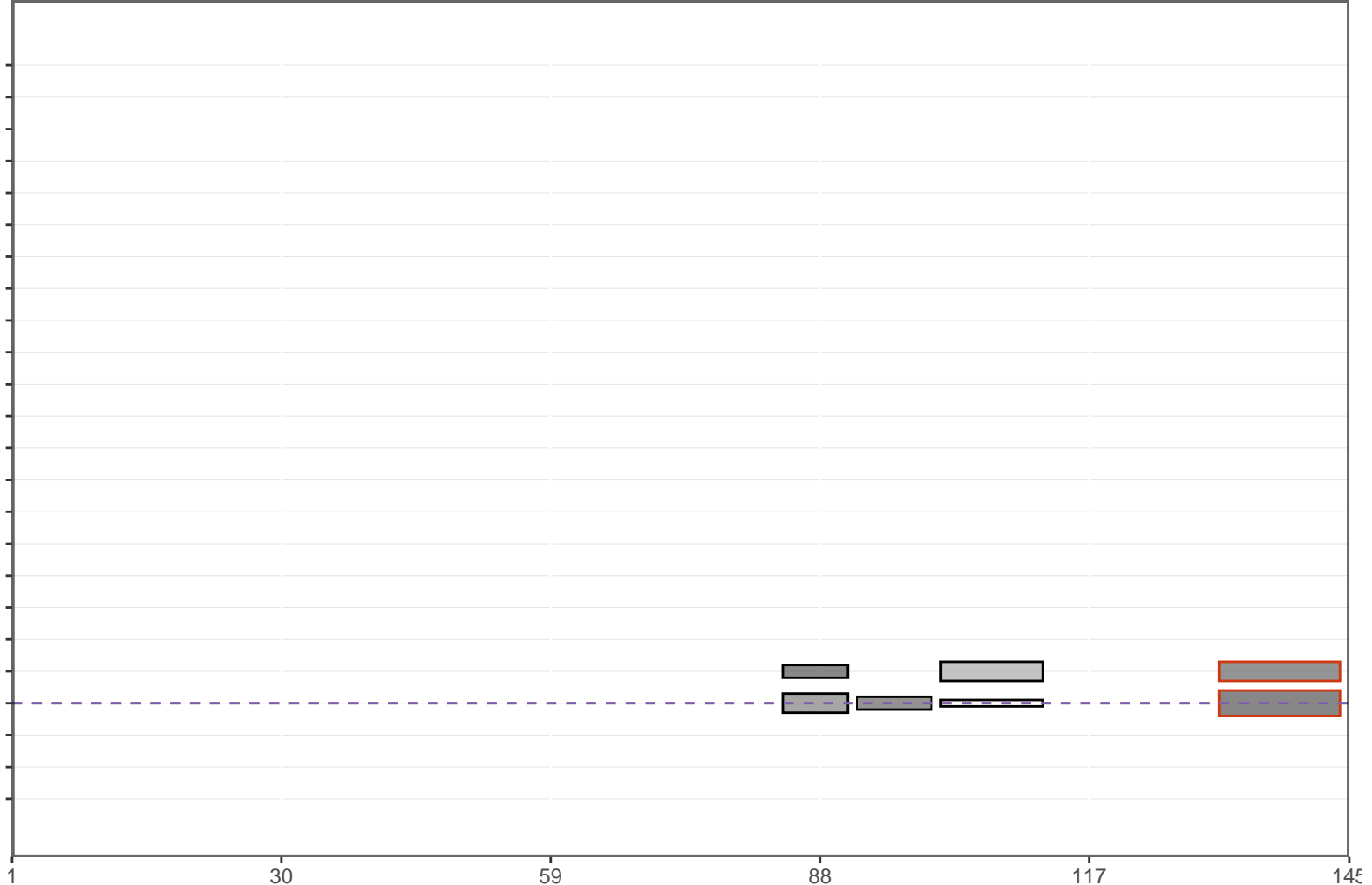
MW indication



Molecular weight



Gel Slice

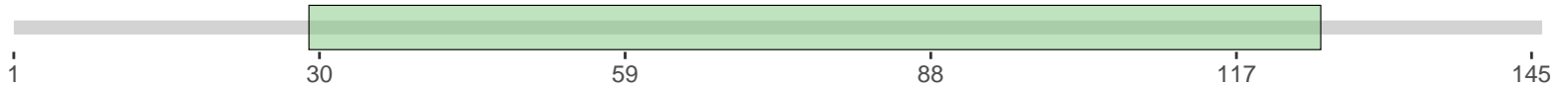


Peptide counts over 4 repeats

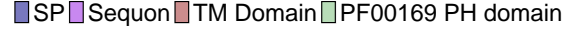
Protein length



Pfam domains



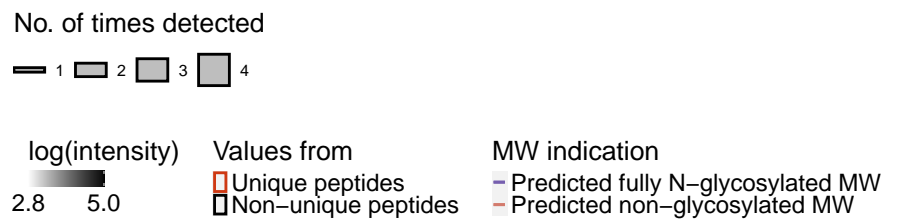
Pfam Description



Protein sequence:

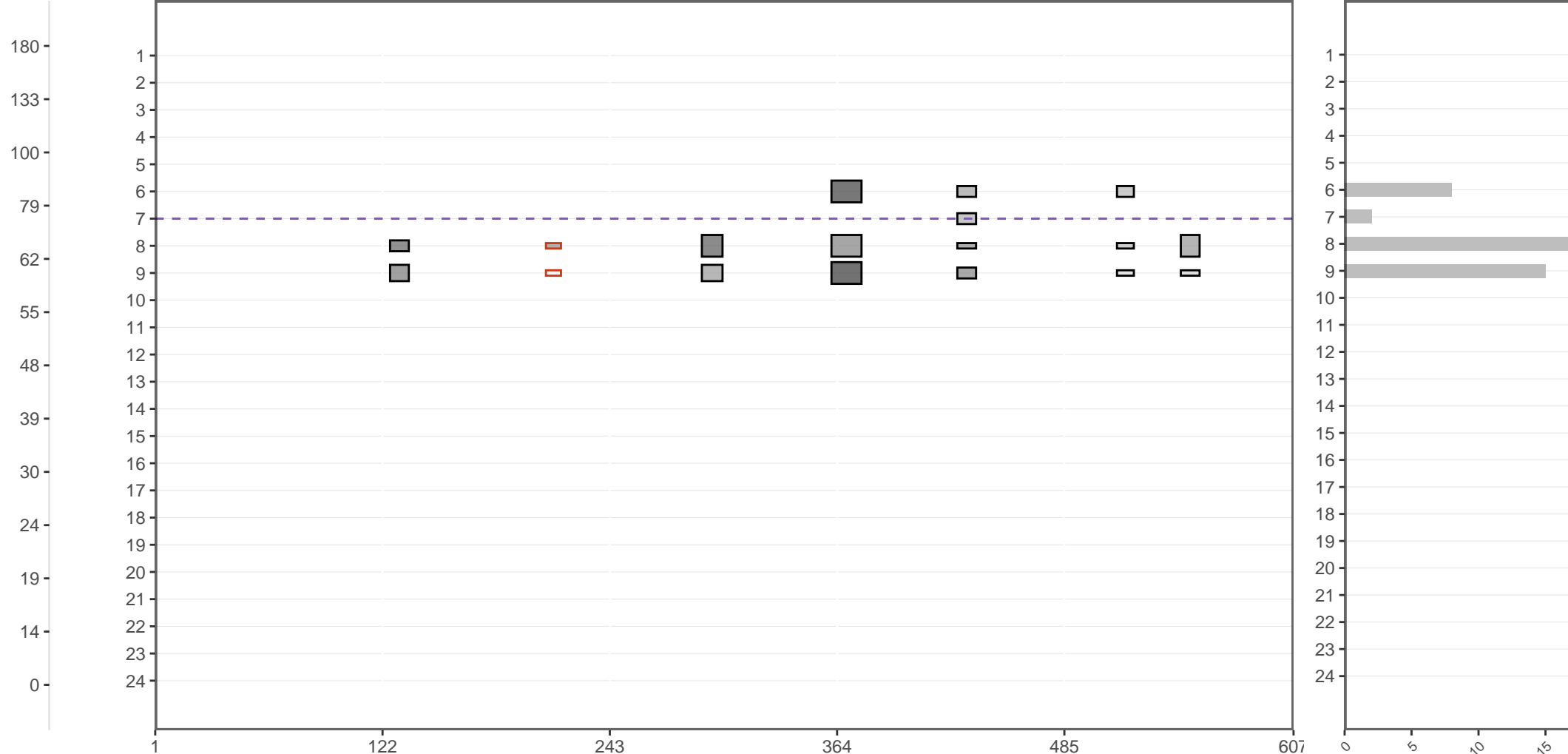
WFKEGSTGGSKPRGVIPVADCLTVKGAEDVLNKGFAPFLSTRADTMFYFADSEKEKEEDWNSIGRCVQHSRSVTHDELVDGSK*

NbL10g11810.1 coronatine-insensitive_protein_1-like [MW = 68.81 kDa]



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF18511 F-box
- PF18791 Transport inhibitor response 1 protein domain

Protein sequence:

SKYEMLPFASRLTKLDELMLDAAHCFLLGRCPNLEIEITRNVVGDRLGVLGGYCKRLKHLRIERGADDDGEMEDGGAVTHRGLTDLAKGLEYMVAWVSDTNEAFENGTVLRKNGDFRLVLDREERITDLPDNGVRRALLRGGYKLRFRFALVVRPGLTDVGLSVYGRVSPNVRWMLLGGVYGESEDEGLFESKGGCPNLQKLEVRGGCFSERALALAAQKLSRLVWVGGYRASSAGRDLLAMRPFWNLIPARRVATFEGNNGETVVAEHPAHLAYYSI

NbL10g11790.1 sedoheptulose-17-bisphosphatase_chloroplastic-like [MW = 45.65 kDa]

No. of times detected



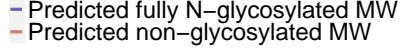
log(intensity)



Values from

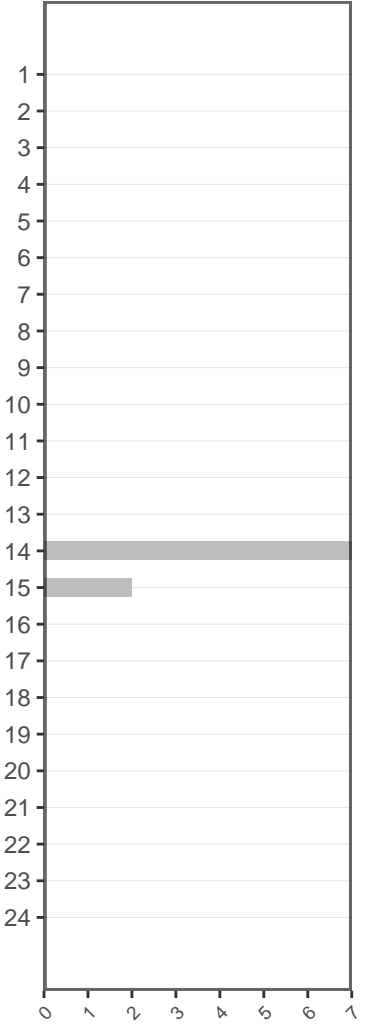
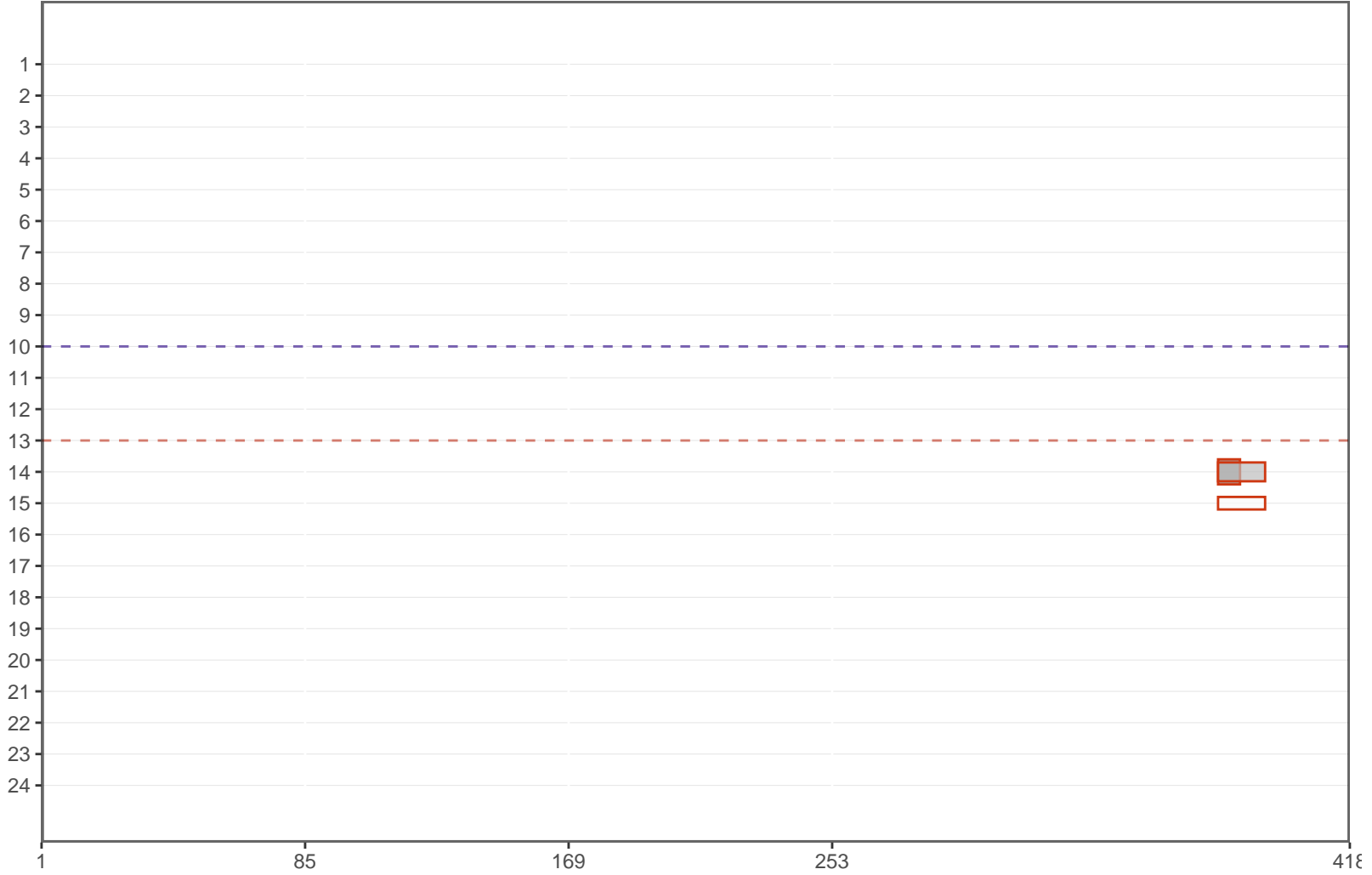


MW indication

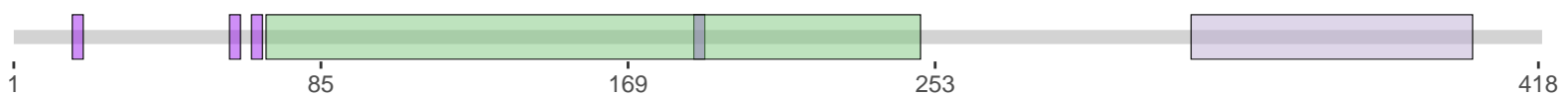


Molecular weight

Gel Slice

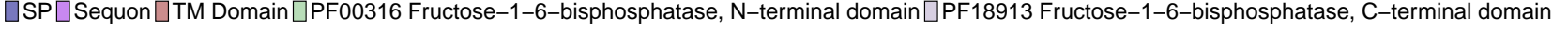


Protein length



Pfam domains

Pfam Description

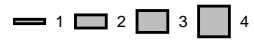


Protein sequence:

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NbL10g11700.1 clathrin_heavy_chain_1-like [MW = 198.65 kDa]

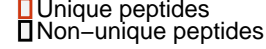
No. of times detected



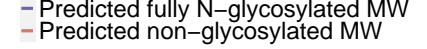
log(intensity)



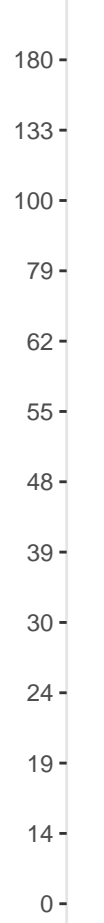
Values from



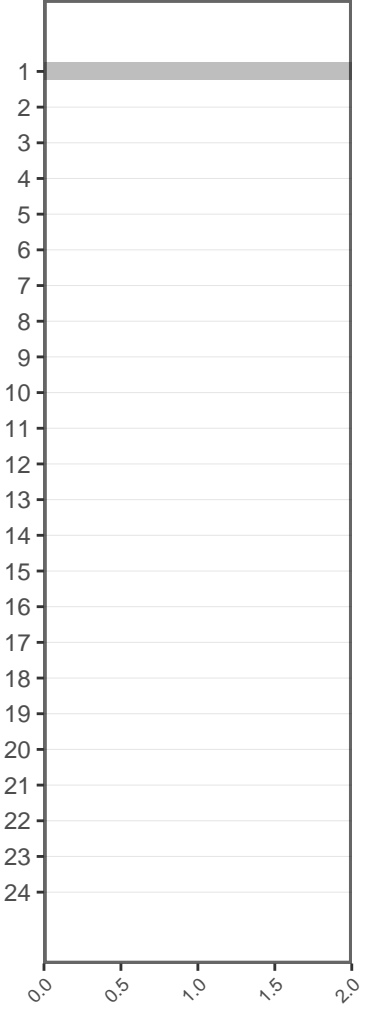
MW indication



Molecular weight

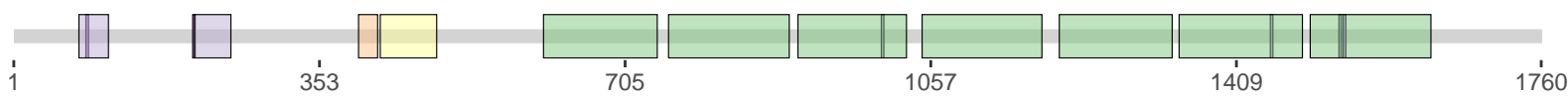


Gel Slice



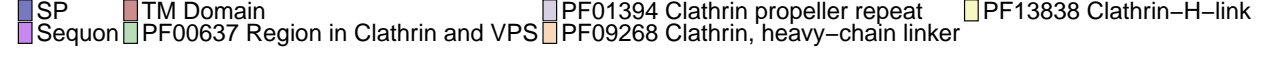
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YYQKYNPQNALVAGQLLDEDECPDFIKGLLIVRBLLPVDFLVAEGEKRNRLRLTGFLEHLVSEGSGDDVHYHNALGKIIDSNNPHEFLTNPYYDSRVVGGYKCKRDPFLAVWVRRGCGDEELINVTNKNLSEKLGARVYVERIMDGLWKEKVLTPENFRRLDQVYVSTALPEKSPFQVSAWAKAFMTADLPHELIELEKVLQNSAFSDFNGLNLLLTAKADPSRVAMDKINRLDNFDGPAWGEVAVEADLYEEAFKFKFNLVGAVNMLLENIRDNRAVEAFAR

NbL10g11680.1 probable_methyltransferase_PMT23 [MW = 68.84 kDa]

No. of times detected



log(intensity)



Values from



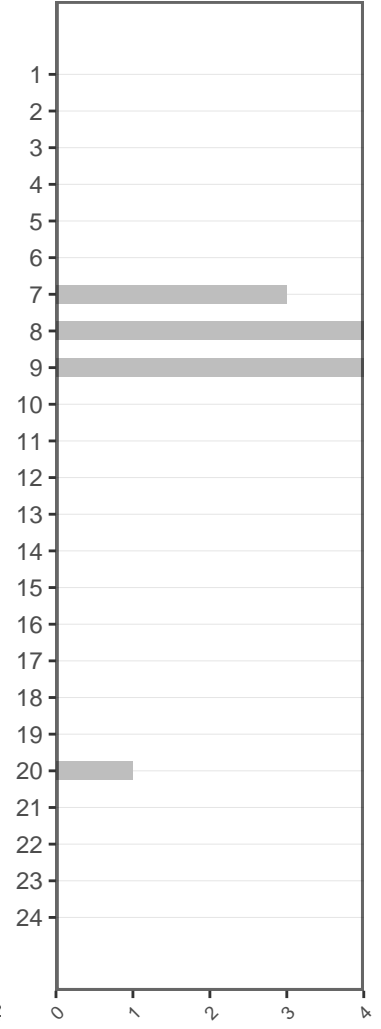
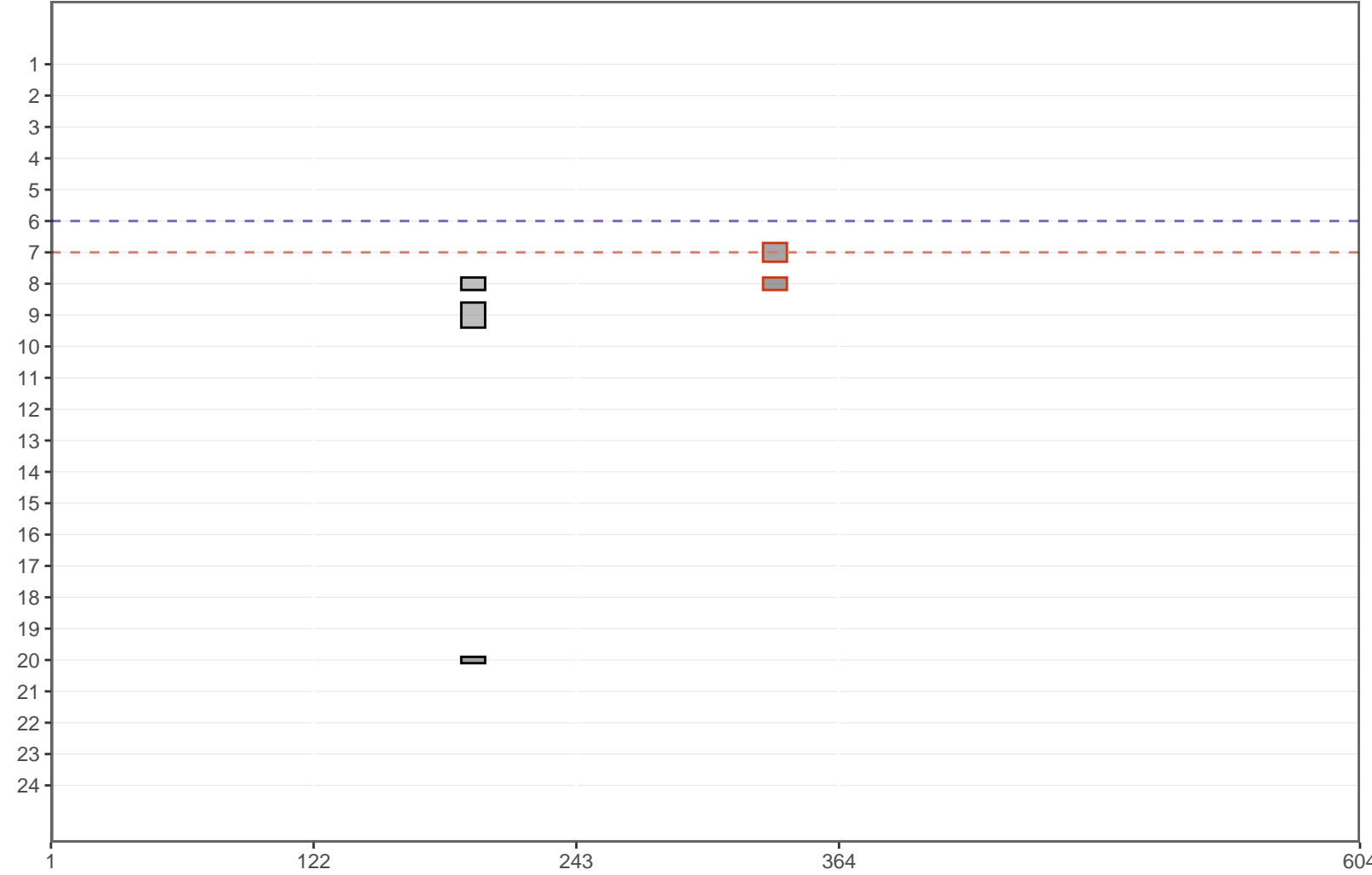
MW indication



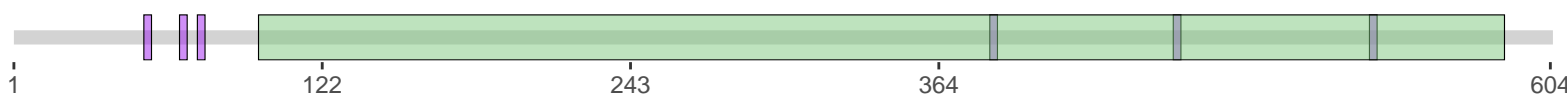
Molecular weight



Gel Slice

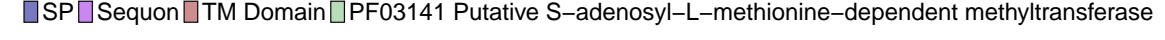


Protein length



Pfam domains

Pfam Description



Protein sequence:

IGKPLMELNRLRPGGFFVWATPVRDDEKDKVWKAMVLTGAICWVYKKTFFDSAGVGLVYKPKVTSSECYDNKKNPPLGDNIRPNSBWWAPLDNGLVPLPSTSEIGNAYEWPAPVDPQRLNKKPQRLGLKTDAAEEVFDEDKHWAALVSDVYVGLLAINWSEVRNMDMNAAGYGGFASAIIDPVAWMMNVIPITGPDTLGHFDRLGLGMVHDWQESFNTPRTYALLHSEFLFGLNLTQRCDLAEVAVEMDRILRPGGFLVGDITMQLMQLSSILRSLIHWSTL

NbL10g11470.1 peroxidase_52-like [MW - SP = 31.95 kDa]

No. of times detected



log(intensity)



Values from



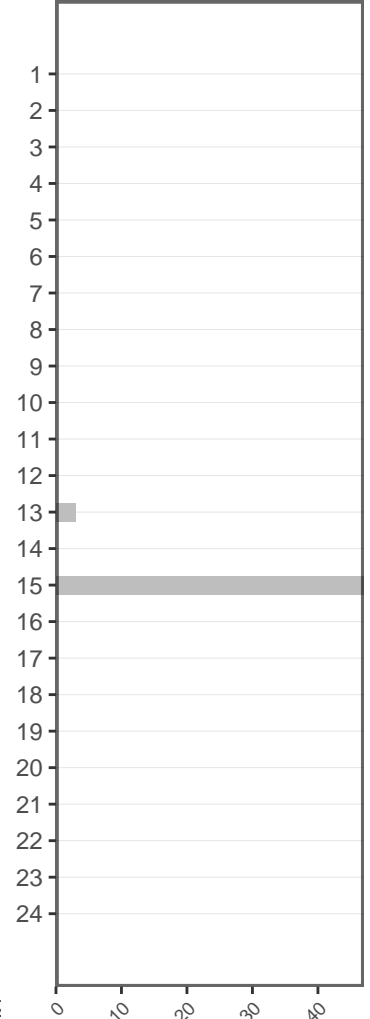
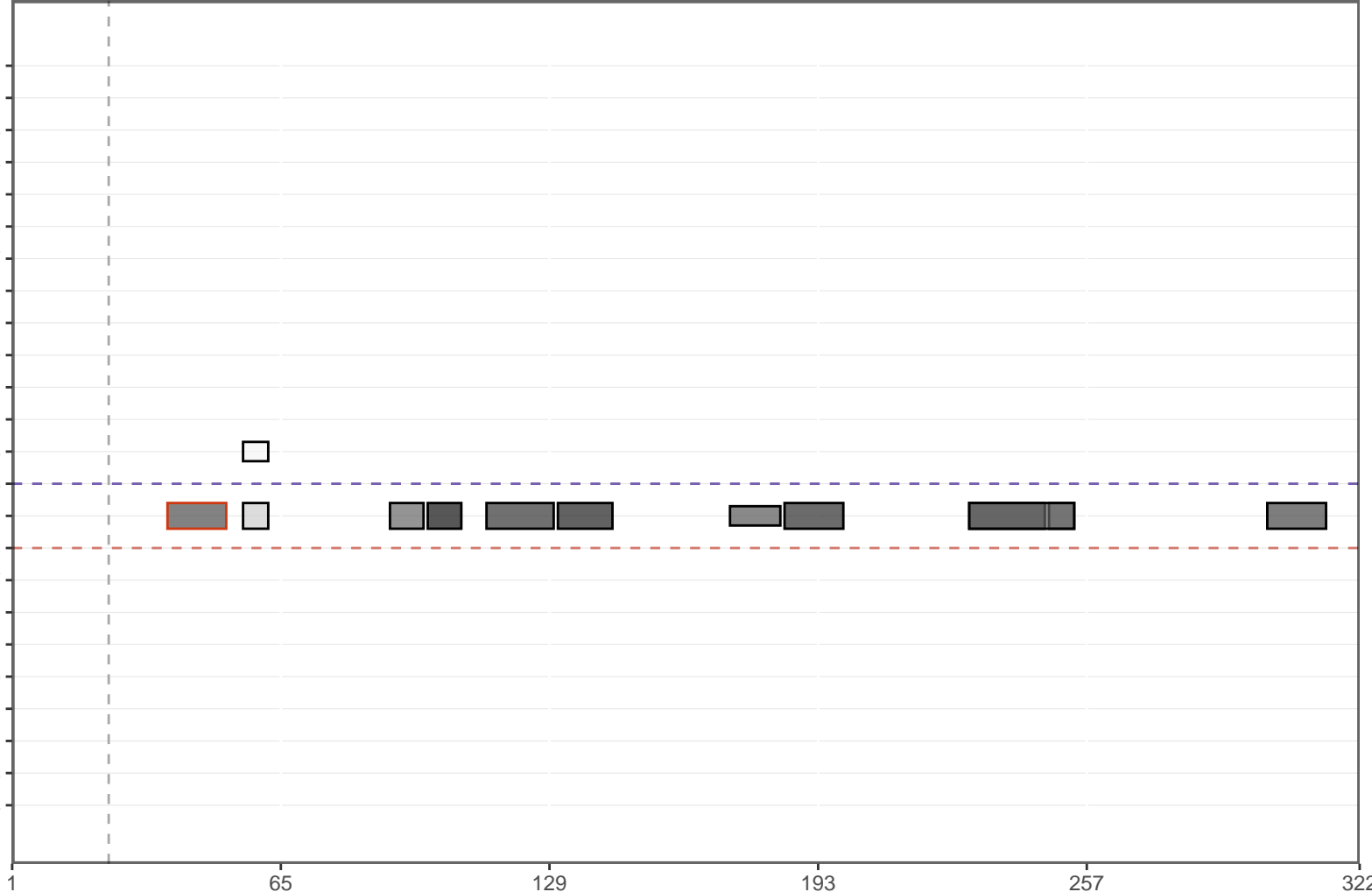
MW indication



Molecular weight



Gel Slice



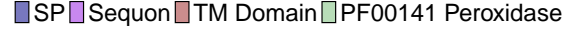
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ARTASQSAANSIPPAENLNRLHSEFVAWGLSTKDMVALSGAHTIGGARTCFRRARIYNETNLDASFARTROGNCPRSSGGSDNLAFLDLQTPNKFDDNYFKNLVKKGLLHSDGQLFNGGSDSVMSEYNNPSSFSDDFVTAMKMGDIRPLTGGNGEIRKNCRRIN

NbL10g11440.1 superoxide_dismutase_[Mn]_mitochondrial-like [MW = 25.51 kDa]

No. of times detected



log(intensity)



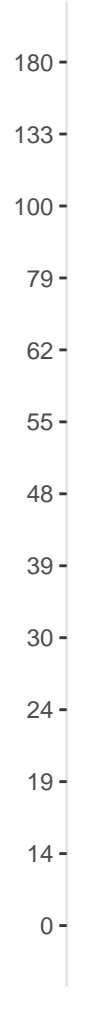
Values from



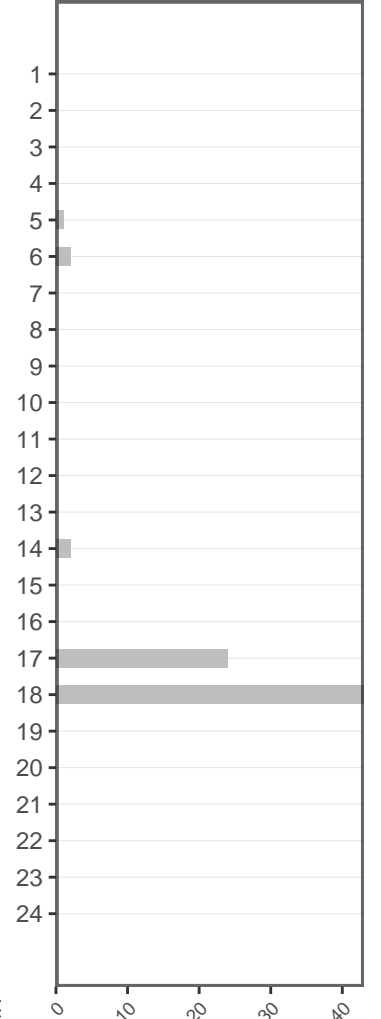
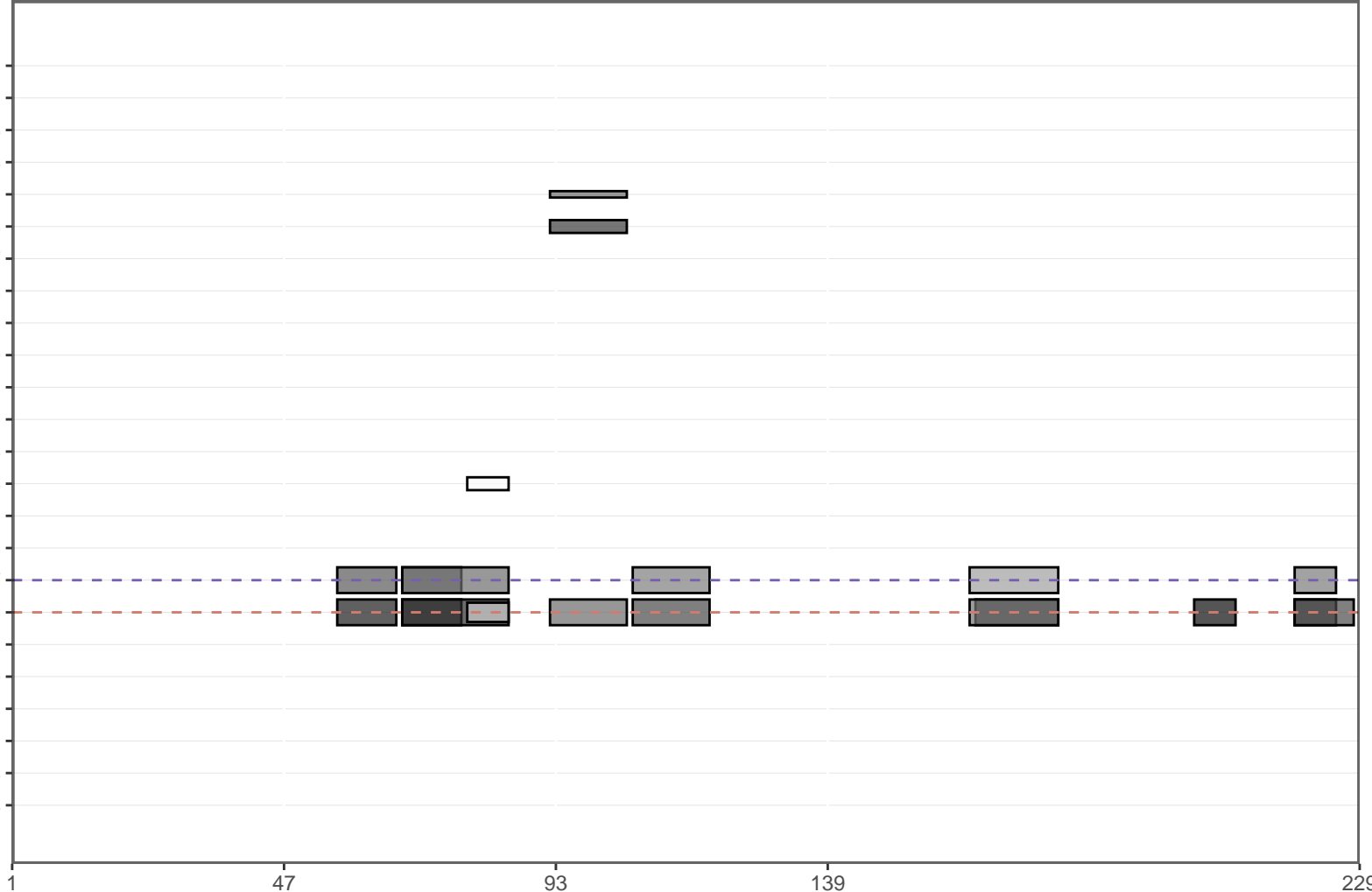
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF00081 Iron/manganese superoxide dismutases, alpha-hairpin domain
- PF02777 Iron/manganese superoxide dismutases, C-terminal domain

Protein sequence:

WNLAIQEGGGEPKGLGSAIDTFGSLALGKMNIEGAALGGSGWVWVLAIDKELKRLAVITTSNGDPLVTKGPNLPLFGIDVWEHAYVLQYKNVRPKLKNWVMMWNYAAEVYEKCP

NbL10g11330.1 ATP_synthase_subunit_delta'_mitochondrial [MW = 21.51 kDa]

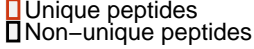
No. of times detected



log(intensity)



Values from



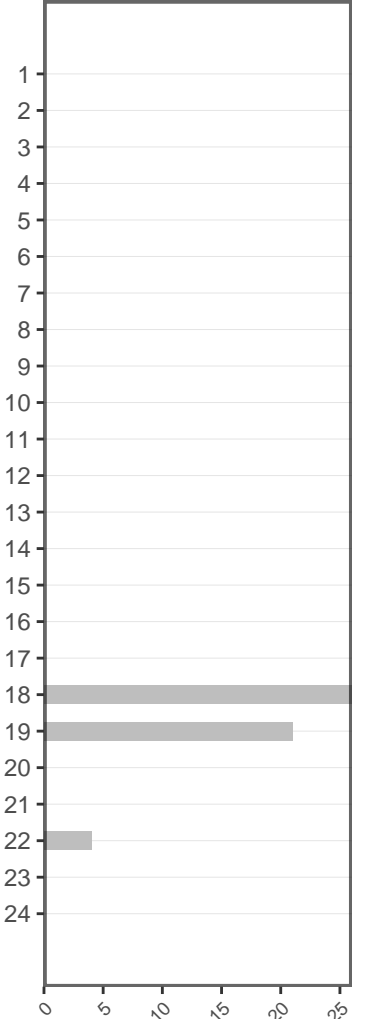
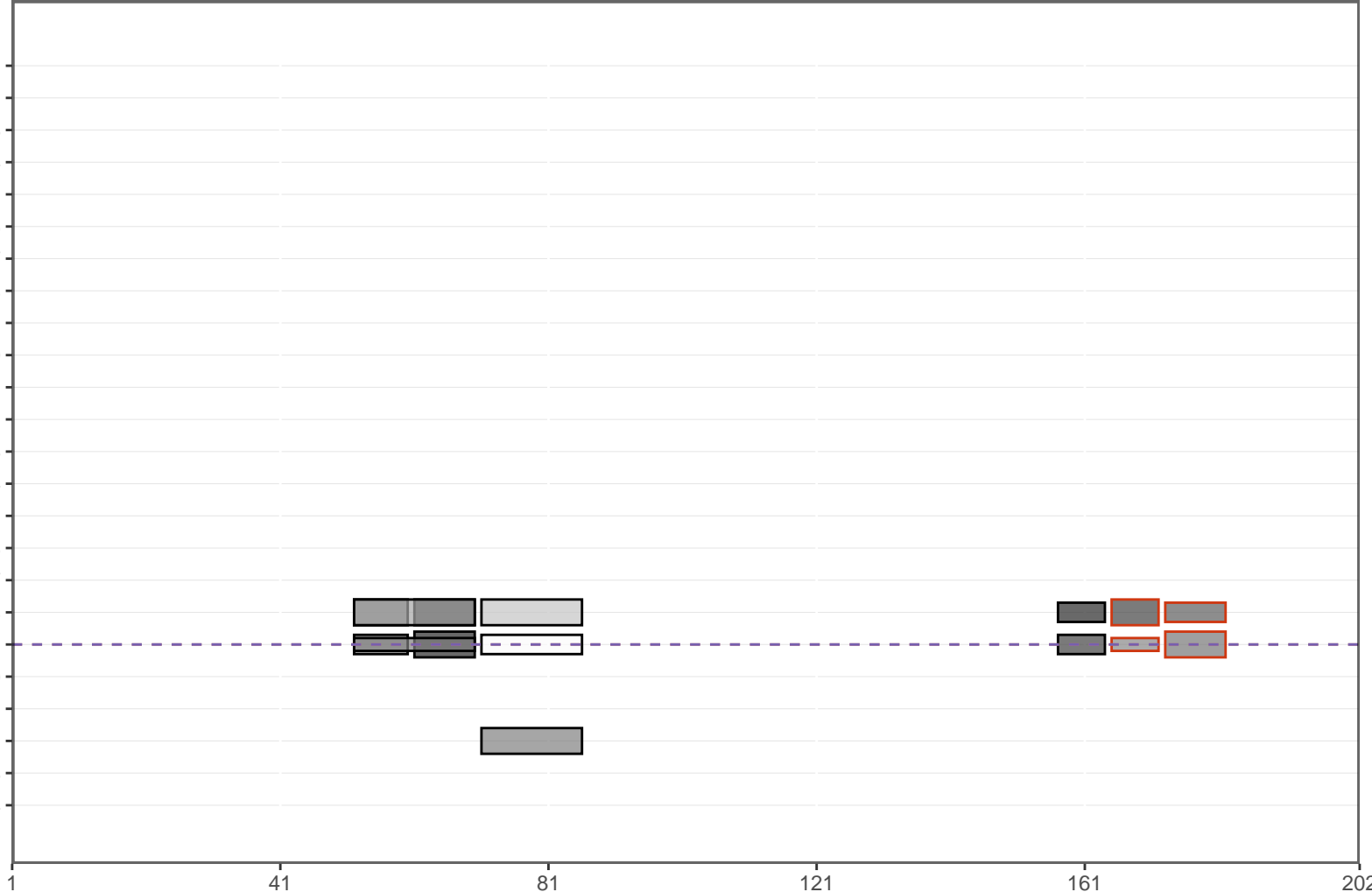
MW indication



Molecular weight

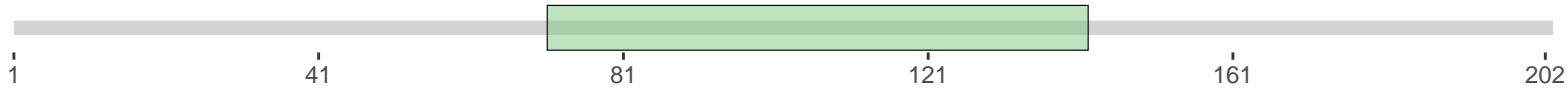


Gel Slice



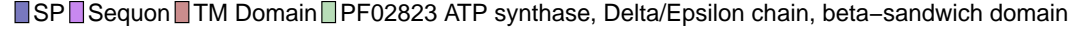
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EVDVYIPATTCQMGVLPQGHVATAEIKPGLVLSVHEGNDVTRKVFVGGGFAPVHANSFADIAVEAVPLDRIDPNLVKGLAEFTQKLGTAETVEKAEAGIKGVDSALNAALTC

NbL10g10970.1 inositol-3-phosphate_synthase-like [MW = 63.13 kDa]

No. of times detected



log(intensity)



Values from



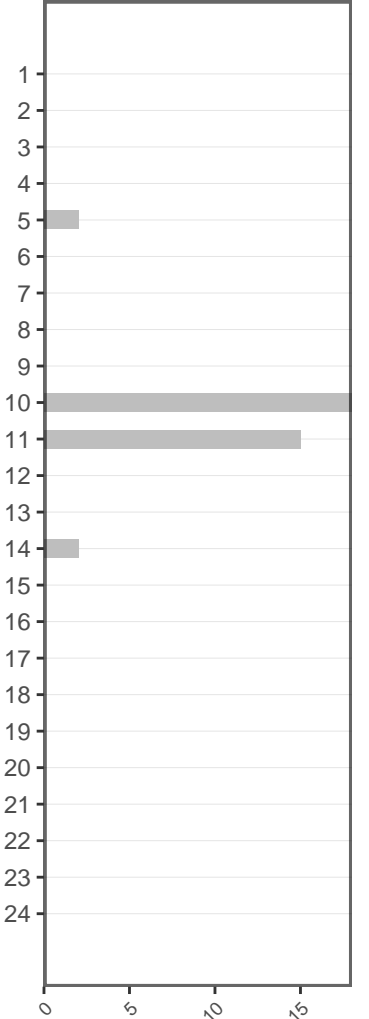
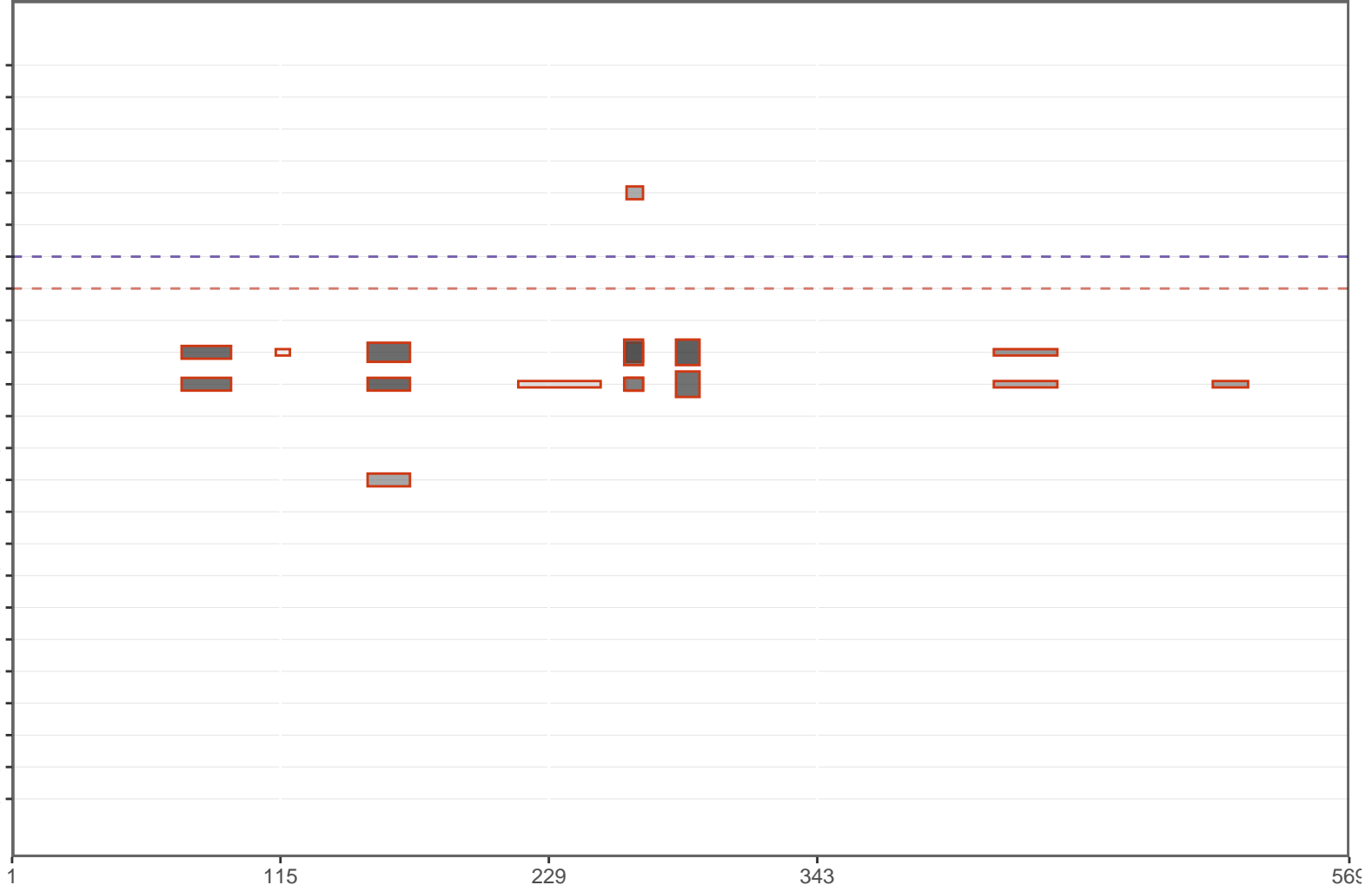
MW indication



Molecular weight

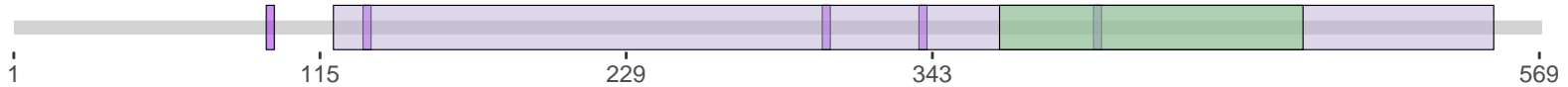


Gel Slice



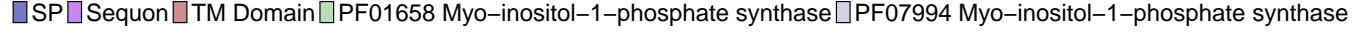
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

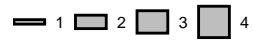


Protein sequence:

MDREFEKKKYDKVAVLWANTERYSNVGLNDTMDENLLAAVDRDEAEISPTLVAMADVLENVFFNGSPQNTFFVPLGLDLAKRNTLIGGGDFKSGGTTMKKVLVDFLVGAGIKPFTSIVYHHLGNDGMNLEAPQTRFRKEIKSNVDDMVGSNAILVEAGEHPDHVYIKYVFPVGDGSKRAMDEYTFSEIFMGKNTVLVHNTGEDLLAAPILDVLLAELSTRIGLKAEGEGKFKHSFHWATVLYLTKAPLVPPGTPVWNLISKGRAMLENLRAGVGLAPENMILEYK

NbL10g10830.1 polyadenylate-binding_protein_2-like [MW = 24.81 kDa]

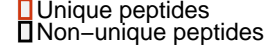
No. of times detected



log(intensity)



Values from



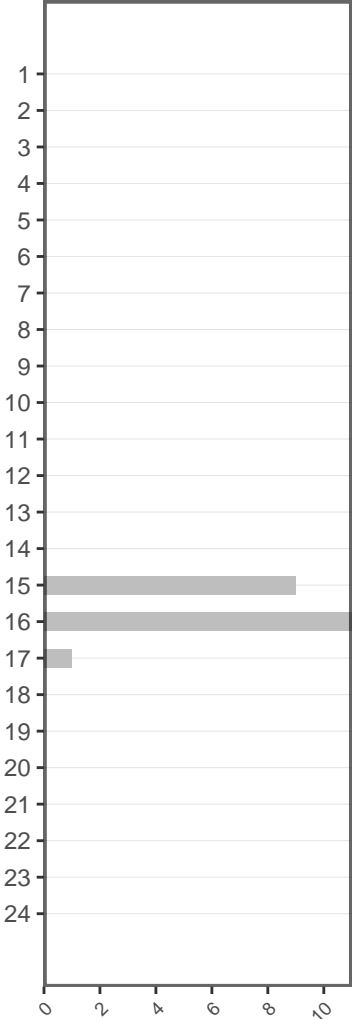
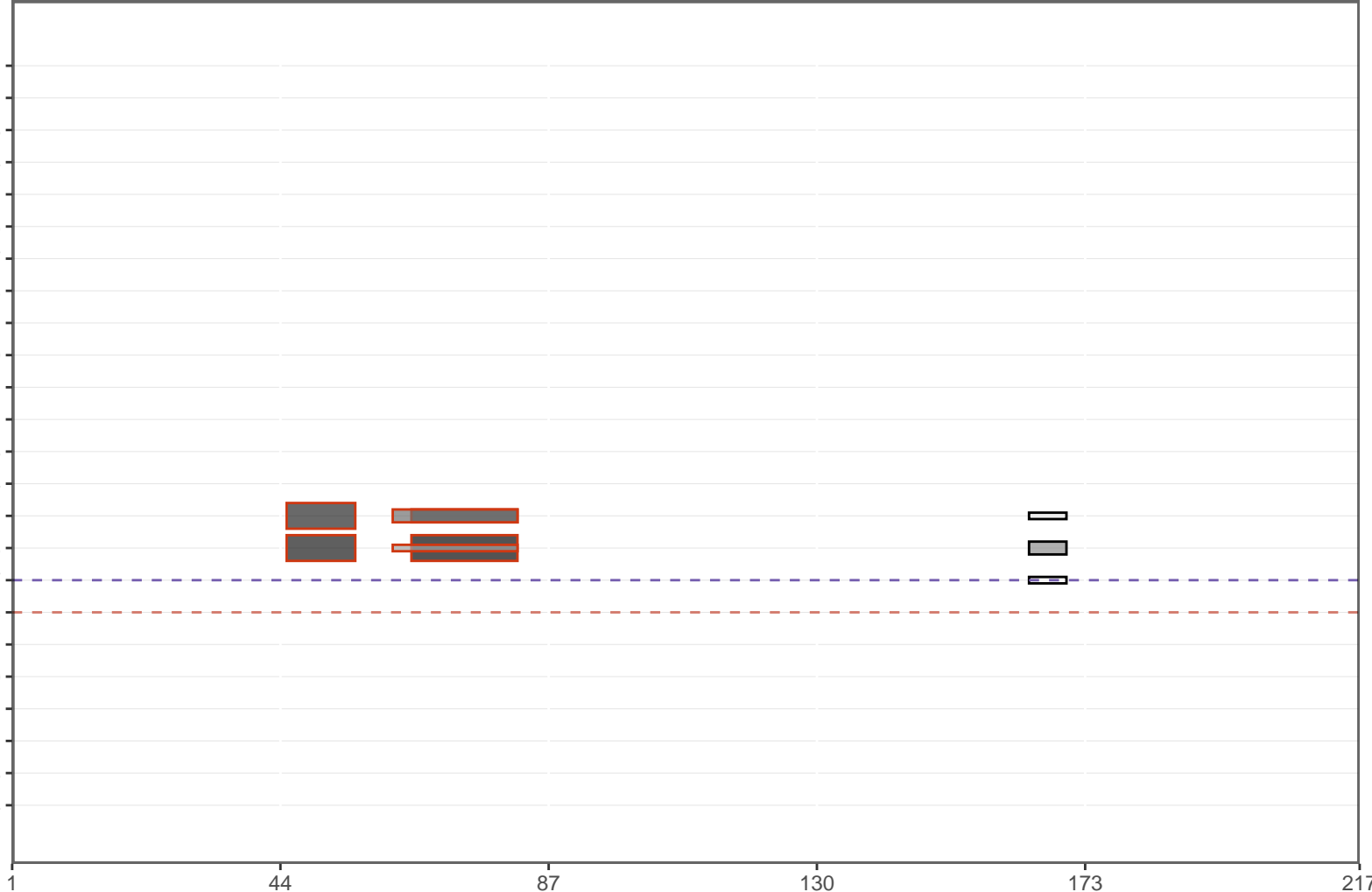
MW indication



Molecular weight



Gel Slice

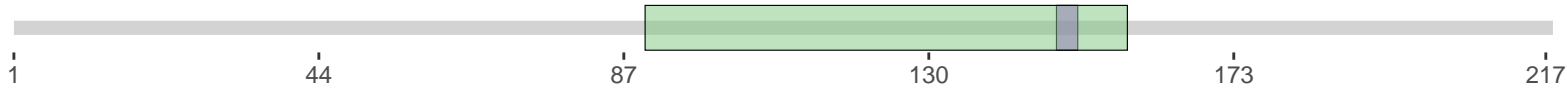


Protein length

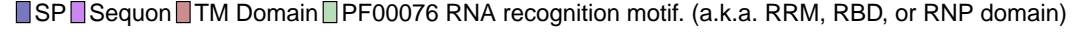


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VDVACTPEEVOQHIFGAGGTNVRVITLTKFGGPKGFAYVEFVEGEAIGVALQLNESELHGRGLKVMKRTNVPGMKQFRGRFRNPMVAVGFRPRPTPPEYFVSPYGFQKVPFRFRRTFRMPVY*

NbL10g10770.1 histone_H3.3 [MW = 15.41 kDa]

No. of times detected



log(intensity)



Values from



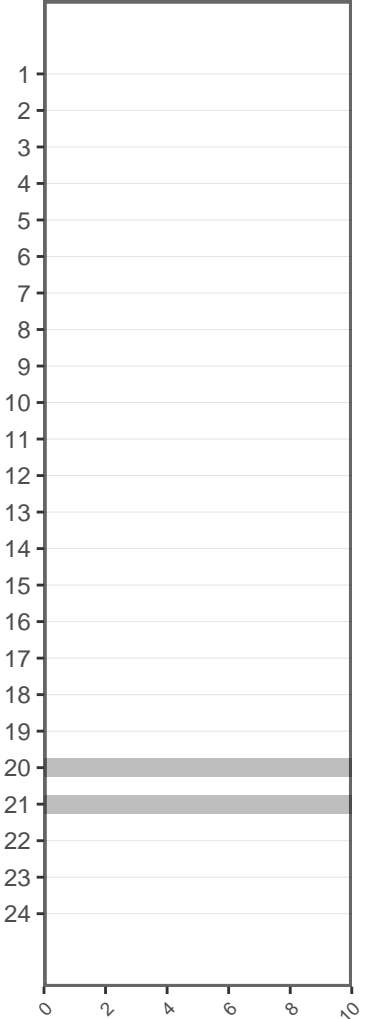
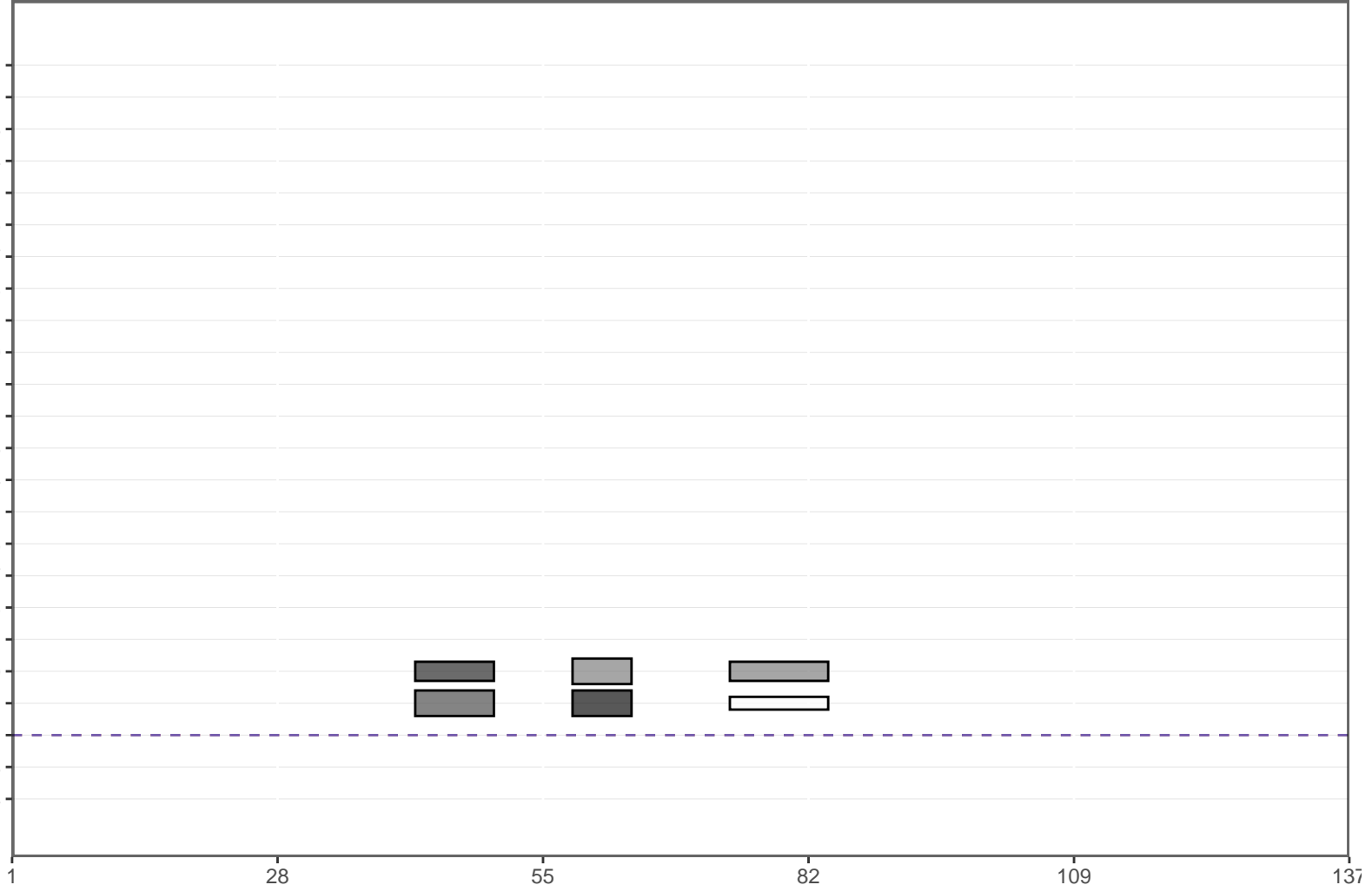
MW indication



Molecular weight

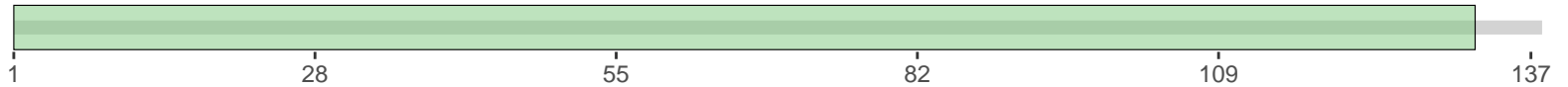


Gel Slice



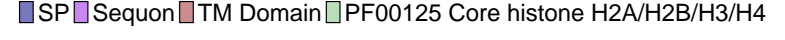
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KYQKSTELLRLKLPQRLVREIAGDFKTLRFQSHAVLALQEAEAALVGLFEDTNLGAHAKRYVTMPKDIQLARRRIGERA*

NbL10g10720.1 dihydrofolate_reductase-like [MW = 25.61 kDa]

No. of times detected



log(intensity)



Values from



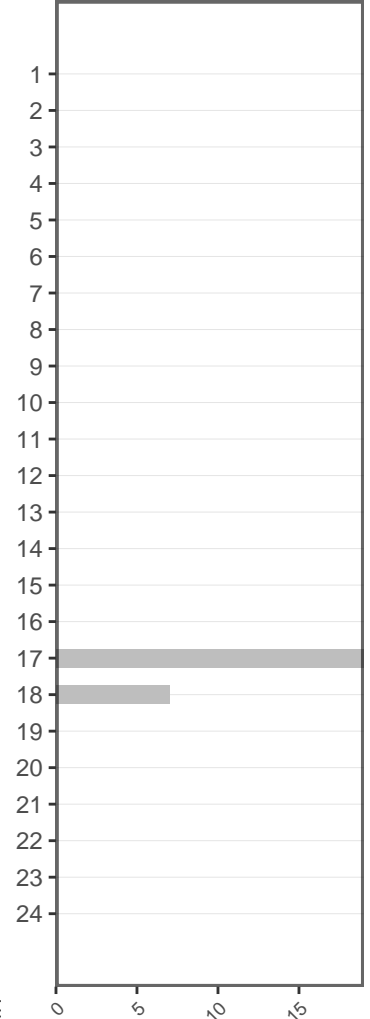
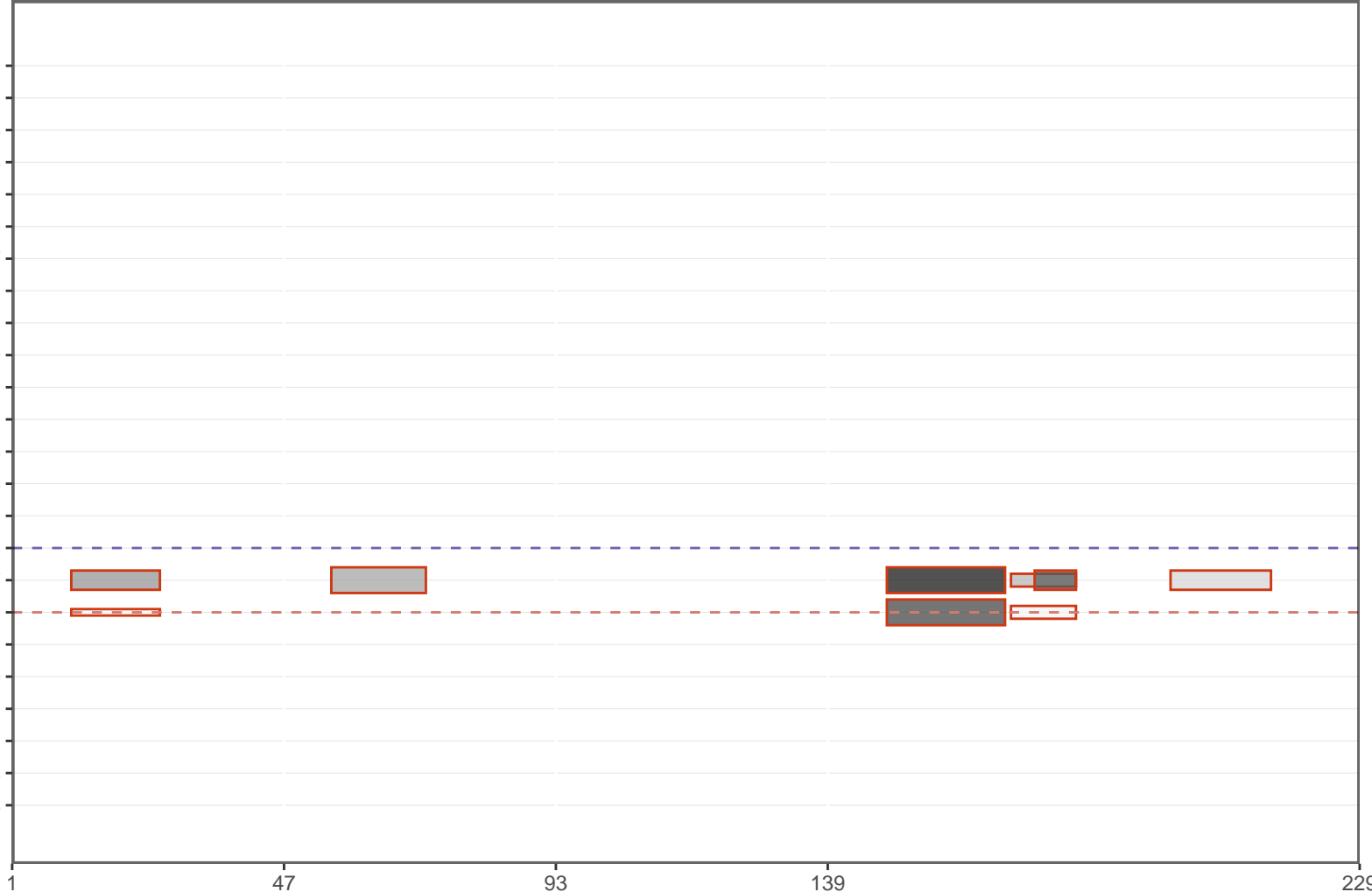
MW indication



Molecular weight

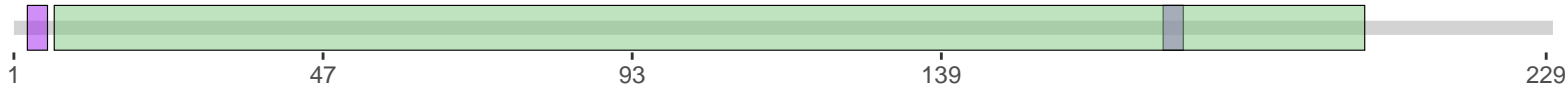


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

VLGFSDQATIVTATPMGMGWERVALTKVFNKFWIISGLMFGAPFGDPKLLANAVSSPIETPSLHFGEKEAKNTSEELVKGFPNPNVHHPEGHKVPNLDAESVETVTFINVKKKIMALGGDKM

NbL10g10650.1 O-fucosyltransferase_31-like [MW = 23.55 kDa]

No. of times detected



log(intensity)



Values from



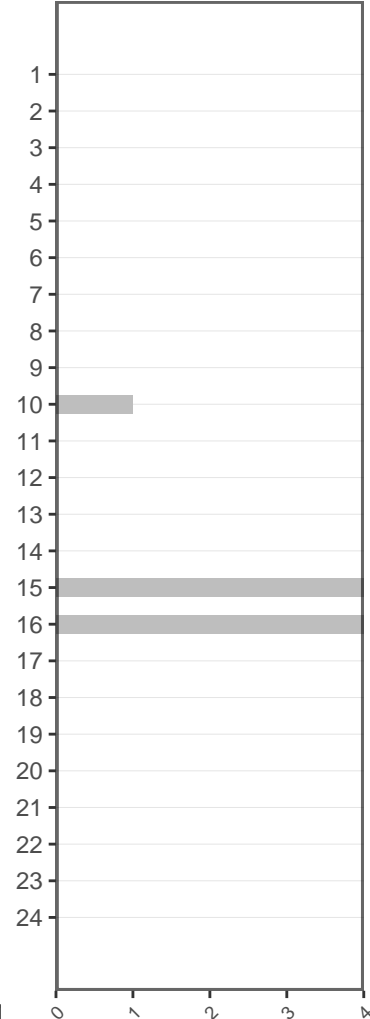
MW indication



Molecular weight

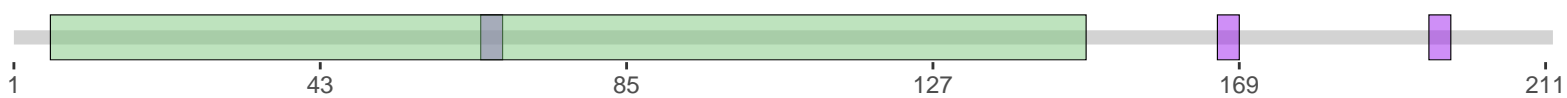


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEDKXSLASDERALKEKASLLAAVDYVVMHDFISAPGNMHNAMVGHRTYVNMKTRIPNALLGQLFNKTLSEWPEPEAVVEGHKNRQGGIRLRKNGELFTYPPNMGCDP

NbL10g10570.1 HMG-Y-related_protein_A-like [MW = 17.75 kDa]

No. of times detected



log(intensity)



Values from



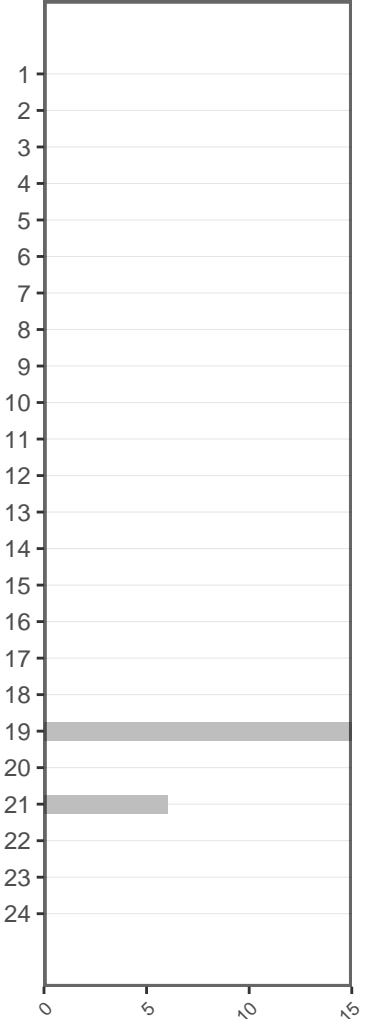
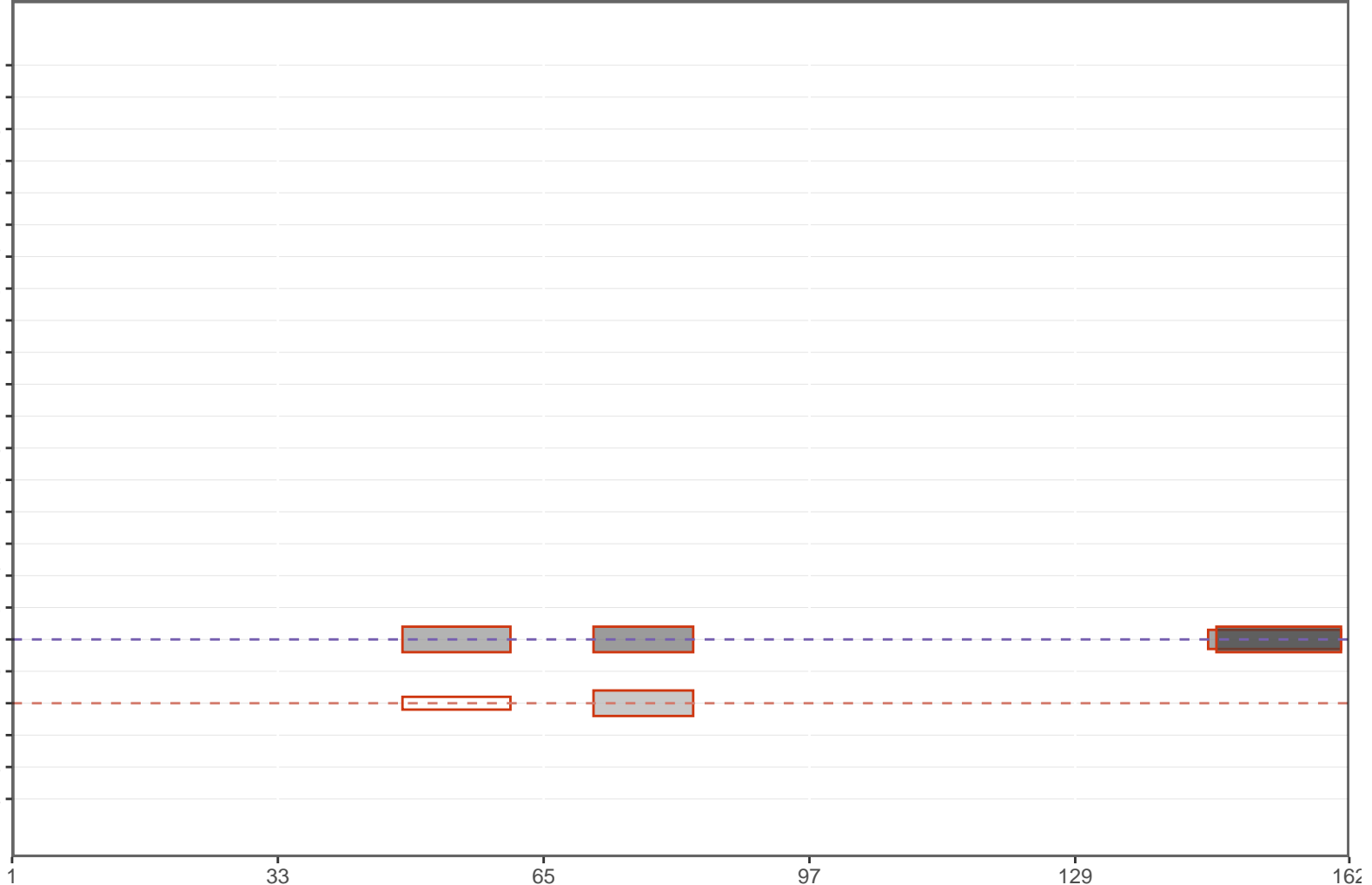
MW indication



Molecular weight



Gel Slice



Protein length

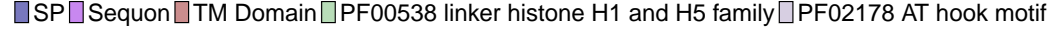


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

NYMKPTDIPQKHWGRGRPKPKVSLPPGAESGEIASRRRGRPRKNDNAPPTSGKPKPTAPNSSGKPRGRPKVRPQPMDDDDDDVEE*

NbL10g10340.1 major_latex_allergen_Hev_b_5-like [MW = 16.27 kDa]

No. of times detected



log(intensity)



Values from

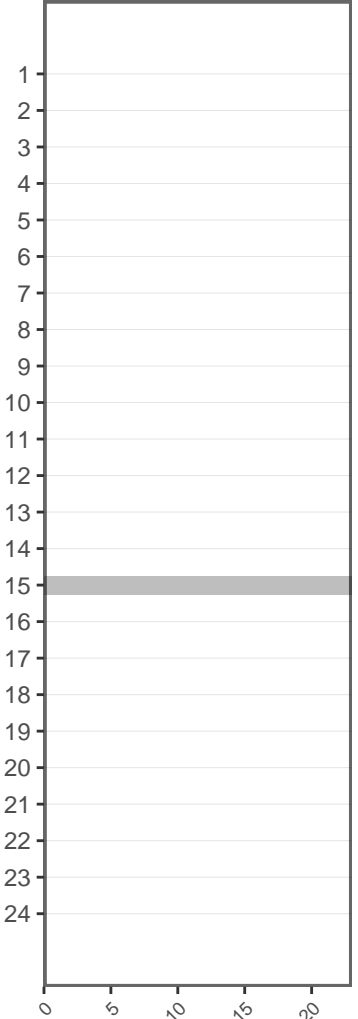
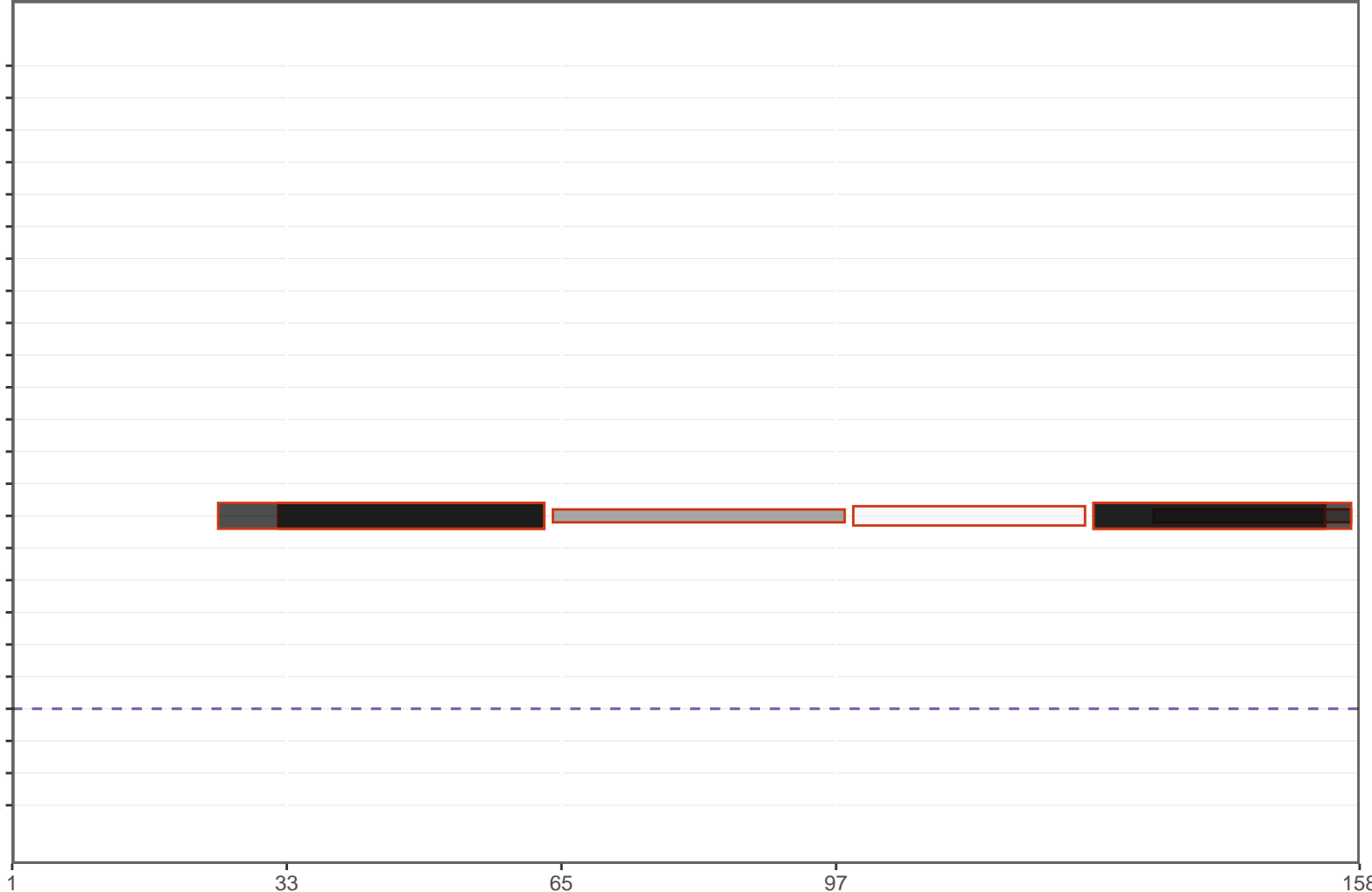
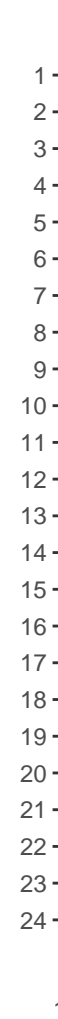


MW indication



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

LVWVEETPVAAEATTEAEETAPVAEETVAEEDTKAETETPVAEETVAAAEVETPWELAEVKTETEVEEGDKVETTEAPAAAATTEVPVKETEE

NbL10g10300.1 ras-related_protein_RABA5a-like [MW = 24.99 kDa]

No. of times detected



log(intensity)



Values from



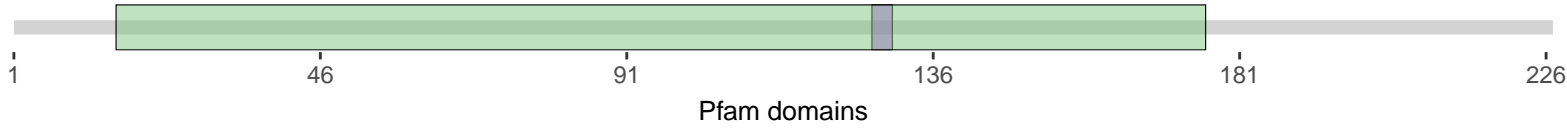
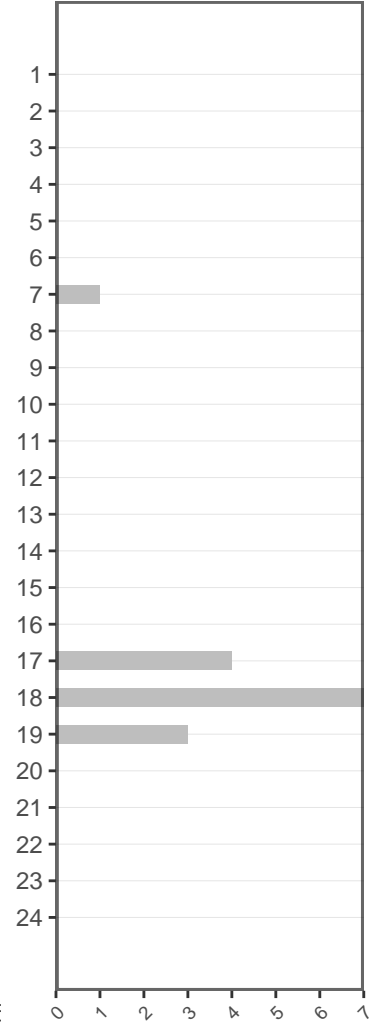
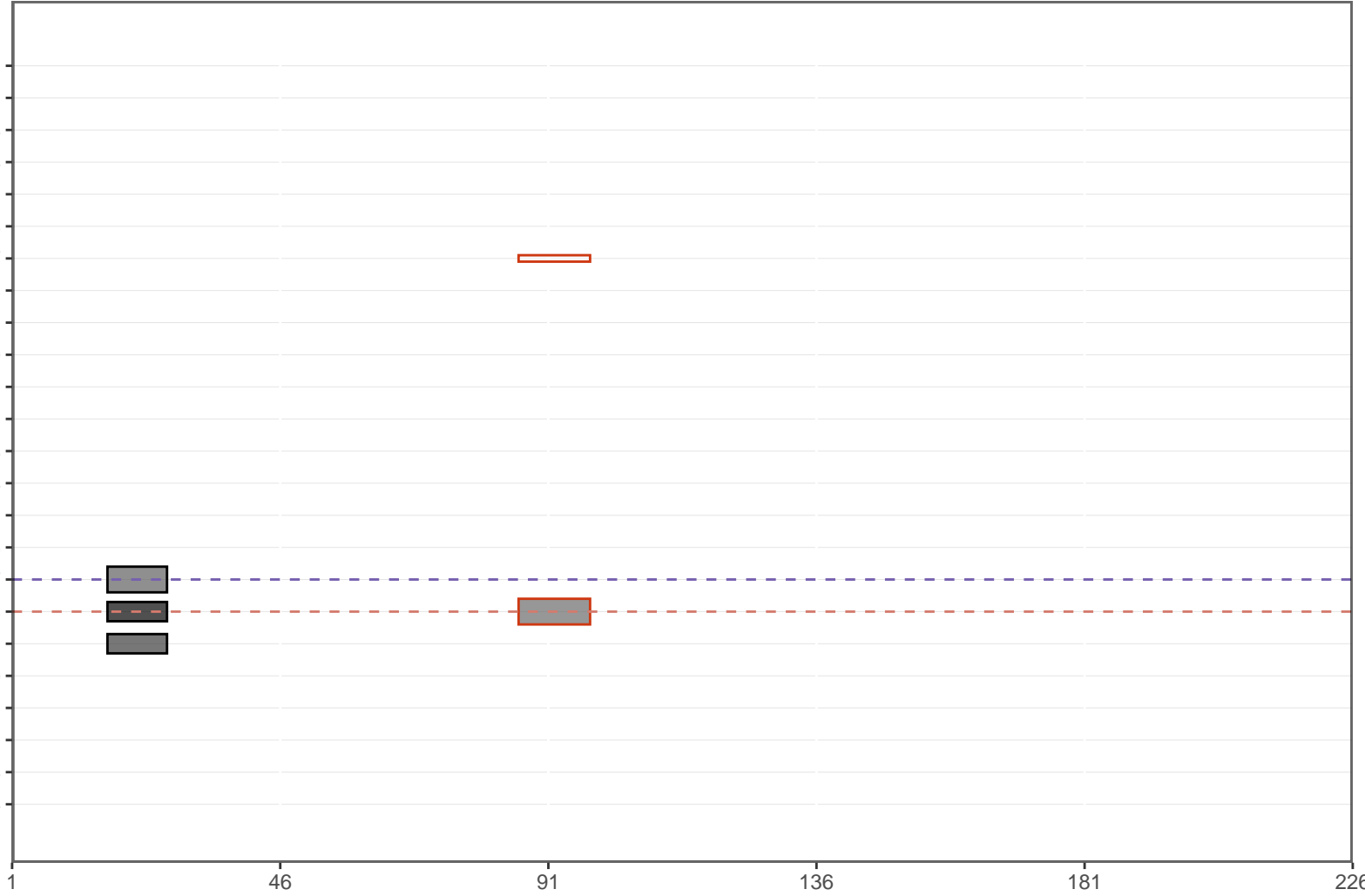
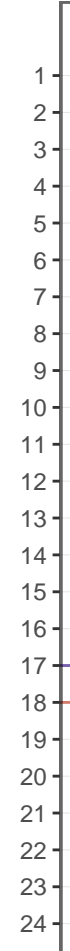
MW indication



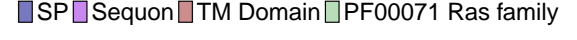
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

FTDSIGRWLNELQTHSDMNVVTLVGNKSDKDKAREVTTAEHGKMLAEAKGLFFIETSAIDSGNVAFAFQTVVREIYNLSRKHVDSGELQKDKSGRLANGKTVLVGADGNGSDTAETKGGCCGS

NbL10g10230.1 nudix_hydrolase_2-like [MW = 39.29 kDa]

No. of times detected



log(intensity)



Values from



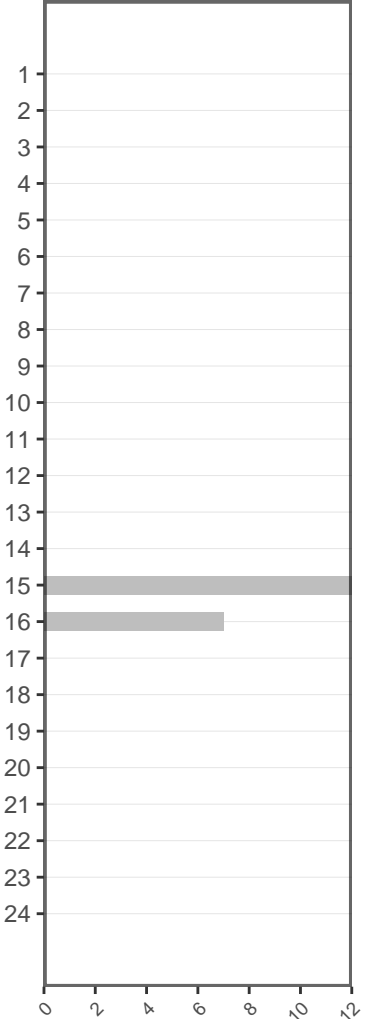
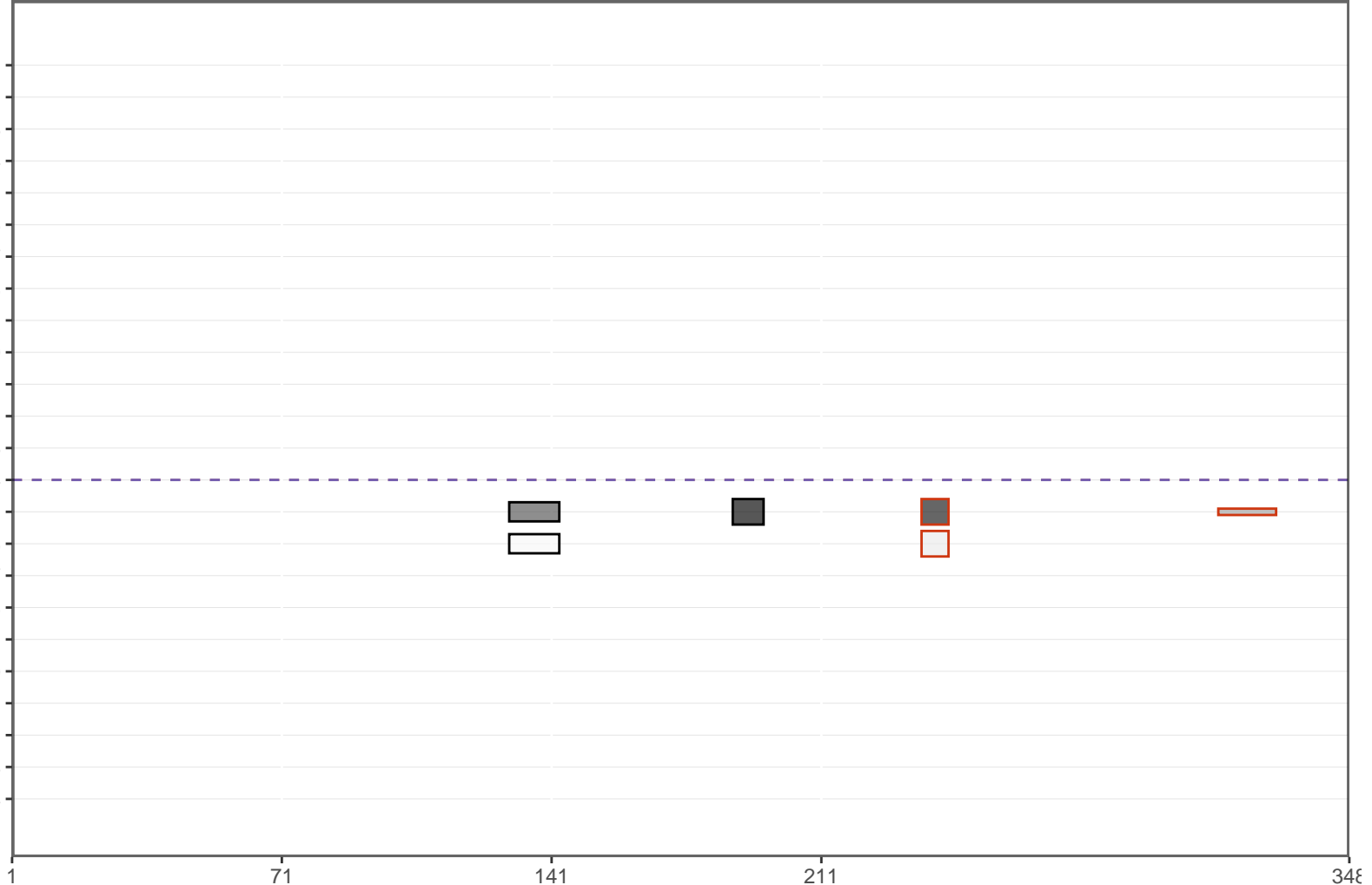
MW indication



Molecular weight

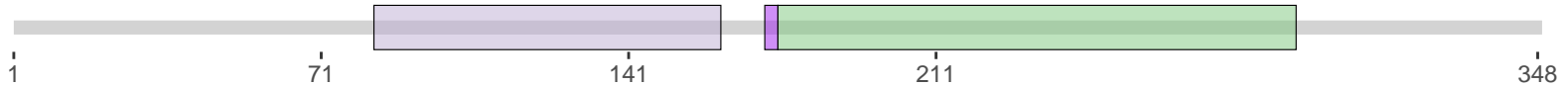


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

.PETANTIPNATHIRNGAGAFVNERNEVLVAQENKGRFRGTGVWKFPTGVVDEGEDDGDMAVREVKEETGVNNAKFVELAFRQSHKSFDFKSDLFFVGMQLPISFDQKQDAIEAAGWMPFEQVAAQPFVHGHHELLRWISDGSAKMEGRYTGFSVPTMTSFSQKNTFLVMNGNVRTGSNDP

NbL10g10000.1 actin-97 [MW = 41.69 kDa]

No. of times detected



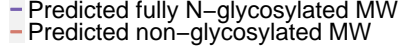
log(intensity)



Values from



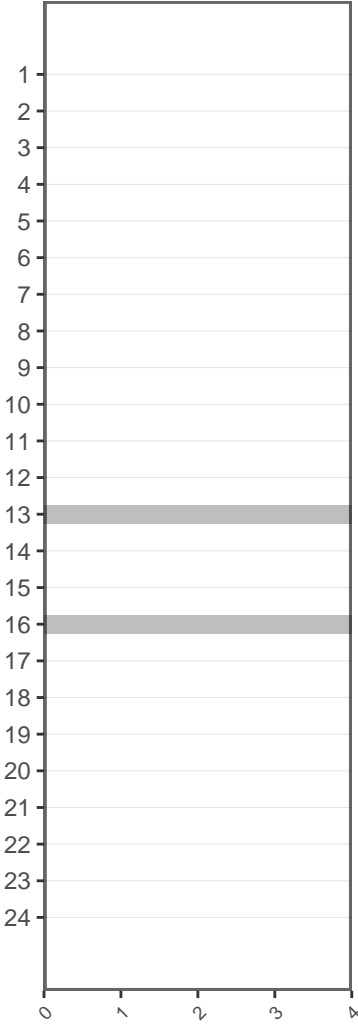
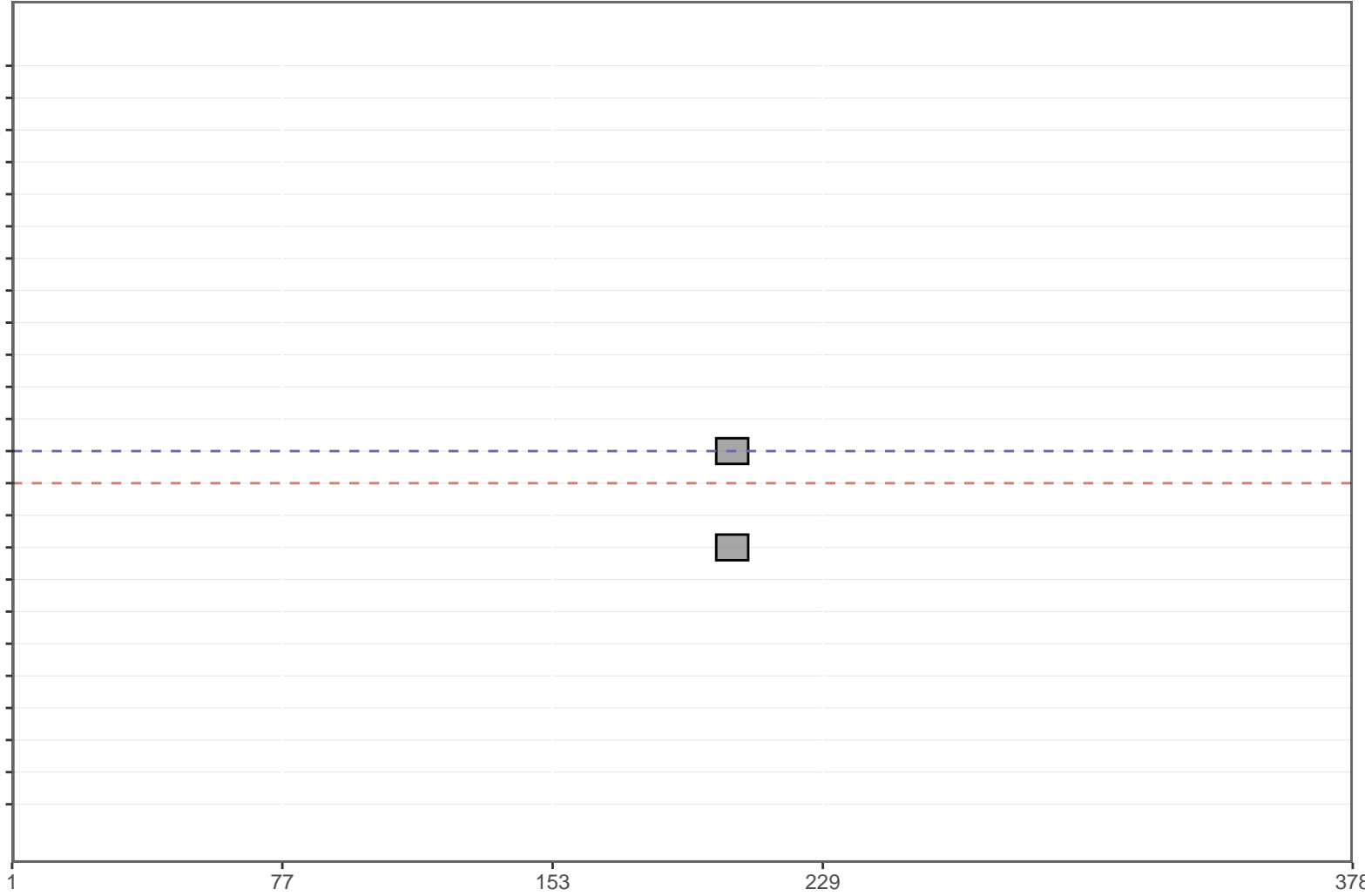
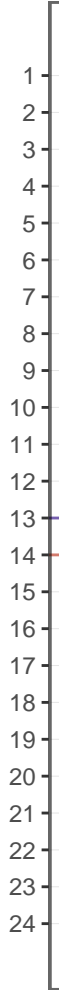
MW indication



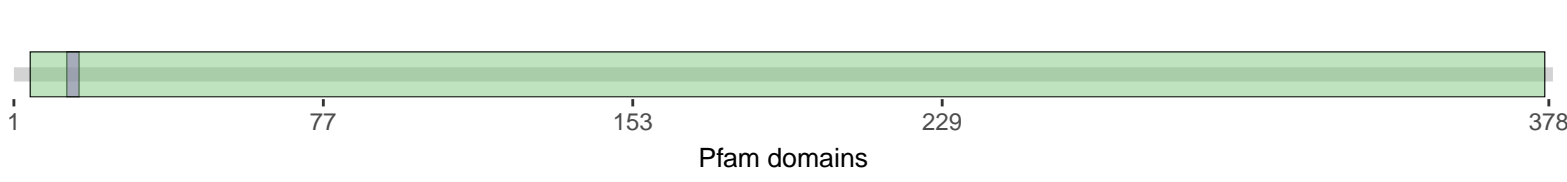
Molecular weight



Gel Slice

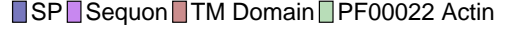


Protein length



Pfam domains

Pfam Description



Protein sequence:

PHAILRLDLAQRDLDLSDLMKILFERGVYFTTAAERIEVRDVKELAVYALDYEGELETSSKTSBSVVEKSYELFDGGVITGAERFRCPREVLFPQPMIGMAAGHETTYNSIMKGDVDRKDLVGNVLSGGSTMFPQIADRMSKERTALAPSEMKNVVAAPERKYSVWVGGGSLASLETFGQAMWIKAEYDESGSPVHRKGF

NbL10g09900.1 UDP-glucuronic_acid_decarboxylase_6-like [MW = 38.73 kDa]

No. of times detected



log(intensity)



Values from



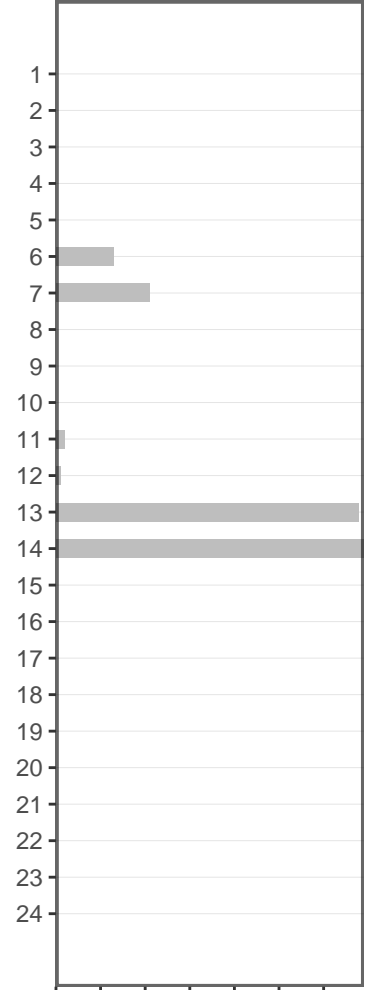
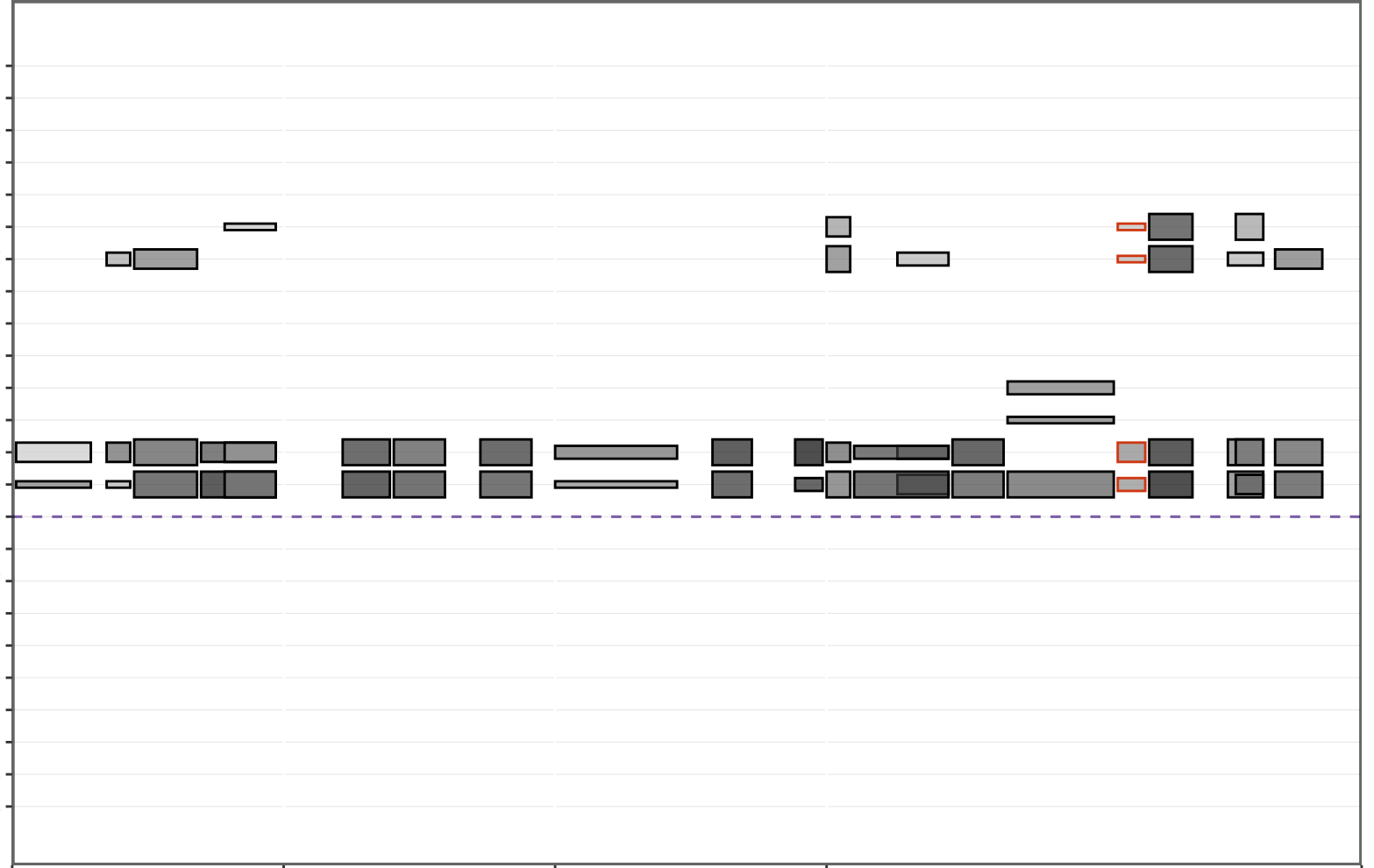
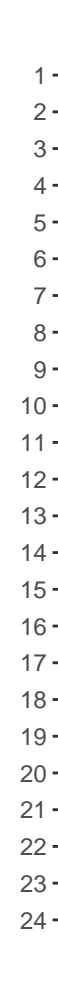
MW indication



Molecular weight

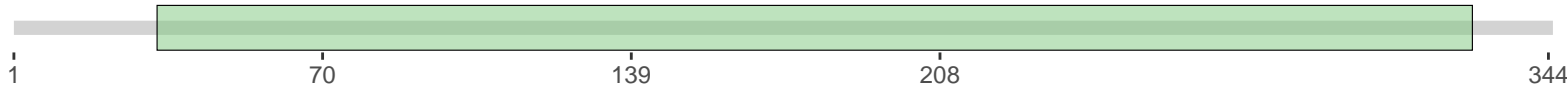


Gel Slice



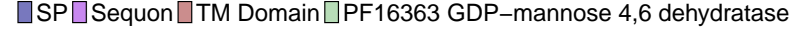
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ISYWGYNPIGVRSQYDEGRVAETLMFDYHRDHGIEIRIARINFTYGRPMNDGRRVSNFAGARDEALFVLPQTGRFQYVSDMVDGLRLMEGDNTPGPNPGEFTMELAEVNYKELNFEVNIITENTPDDPRGRKPPDKAKELLGWEPKIKLRDGLPMEEDFRGLGSRKK

NbL10g09890.1 methionine--tRNA_ligase_mitochondrial [MW = 68.46 kDa]

No. of times detected



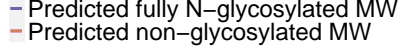
log(intensity)



Values from



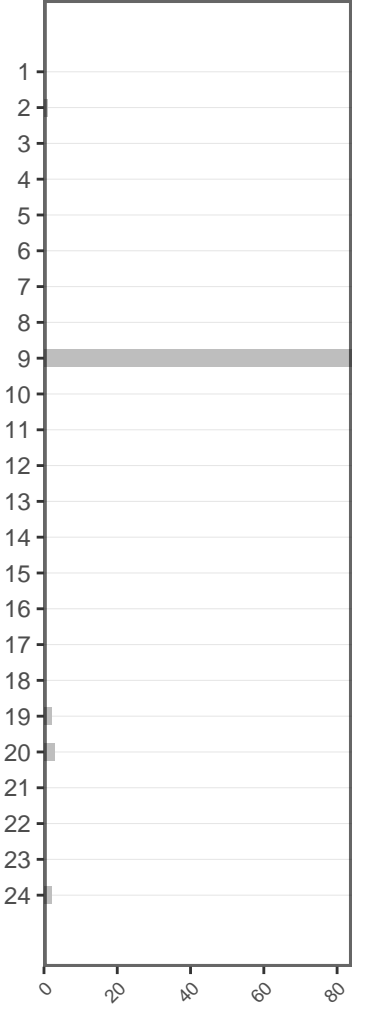
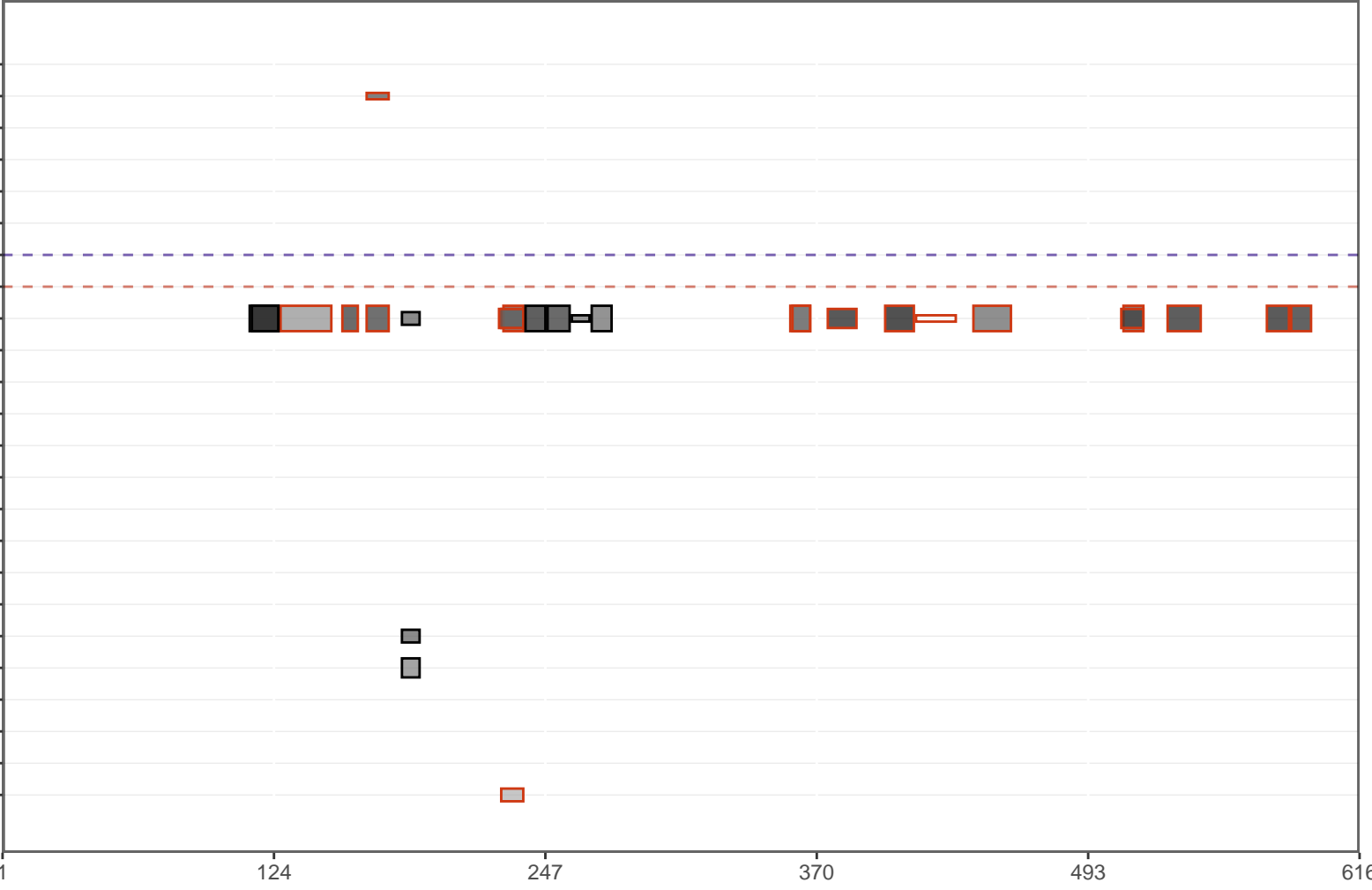
MW indication



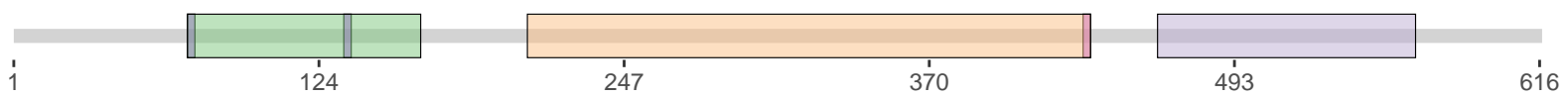
Molecular weight



Gel Slice

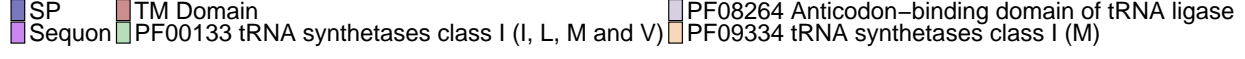


Protein length



Pfam domains

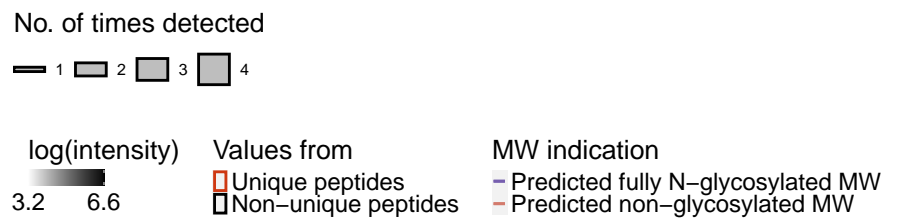
Pfam Description



Protein sequence:

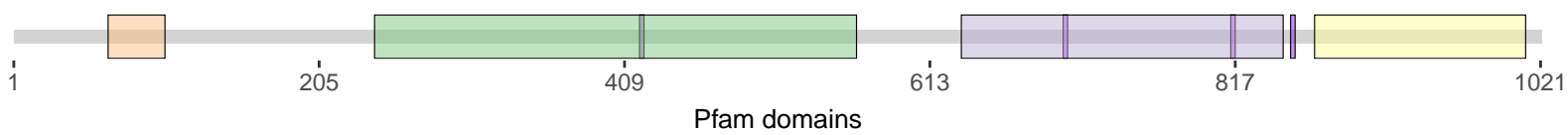
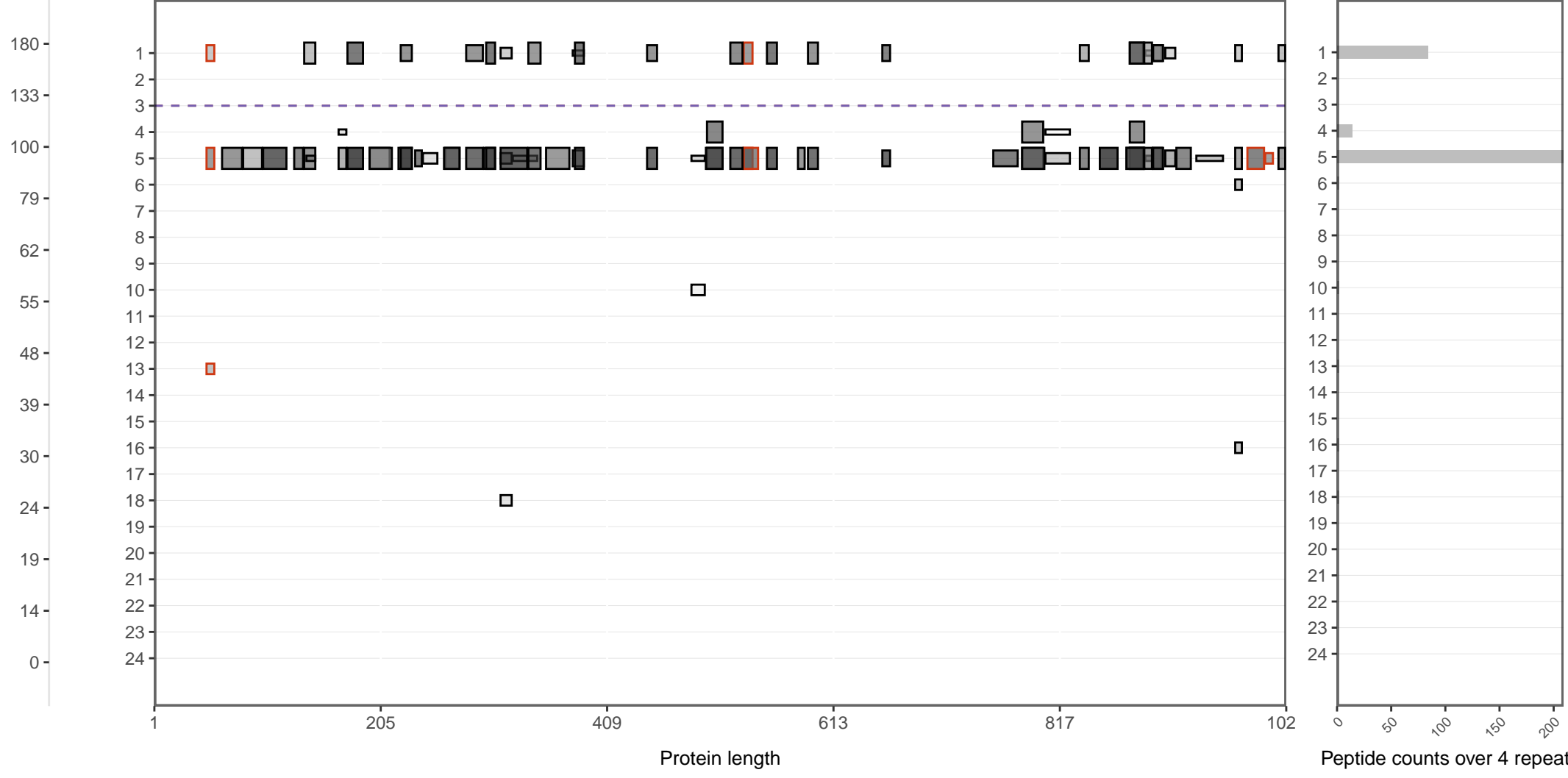
TIYVYFDALLGYVSALLEDELASLETAISGGWPAHLHGKDLRFHAWVWPMALLSAGIKLPRVFGHGLTNDGMMKMKLGNLEPTDLVGRFGPDARVYFFLREVEFGNDGQYSEERFININAHLANITGNLLNRTFLGLLKKNGSTLAVDSYVAAGDKPKFVEVKLVEKARVHYENLELSAAGETVLEIGNAGNSYVIDEQAPEWBLFKKGETAFETAAKDLVILEAMRIIAWALSPTPLGLSLKIVSGLGYTEDQFNHAWSDTKWGLKAGRMVAQPTPFARIEDQTEAI

NbL10g09850.1 2-oxoglutarate_dehydrogenase_mitochondrial-like [MW = 115.66 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00676 Dehydrogenase E1 component
- PF16078 2-oxoglutarate dehydrogenase N-terminus
- PF02779 Transketolase, pyrimidine binding domain
- PF16870 2-oxoglutarate dehydrogenase C-terminal

Protein sequence:

RFQHNEIDPSFTGPKMKIKRNPSELEINQMLLSGGVTKDDVKEKHKNRILNEEFVASKDVPQKRDVLSAFVAGFKPSGLSRVINTGKPELKNVKGKATLPLDQFKPHRAVKRIFDQRKMETGGVGDVWAGEALFATLIVEGNHVRLSGDQVVERGTFSHRHSHVLIHDGETGGQVYPLDHWMMNGNEMFTVNSLSSEFGVLGFELGYSMENPNSLVUWEAQFGDFANGAGVFDQGFVSSGEAKWLRQSGVLLPHGYDGGQPEHSSGRLEKFLQMS

NbL10g09770.1 beta-hexosaminidase_1-like [MW - SP = 58.98 kDa]

No. of times detected



log(intensity)



Values from



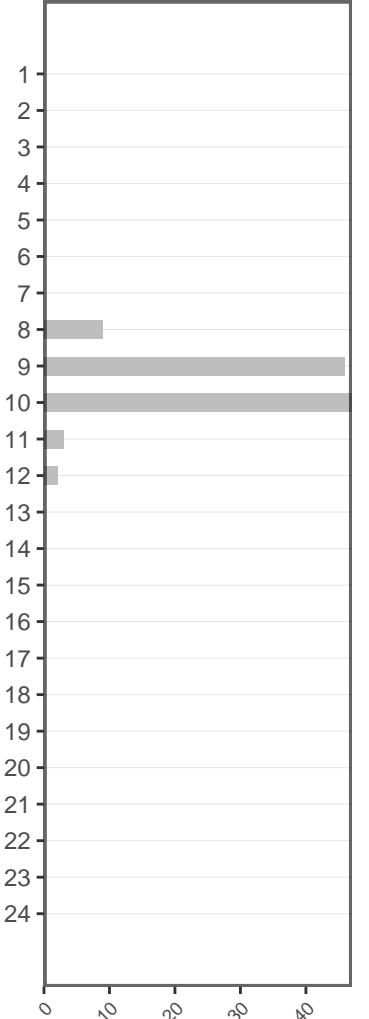
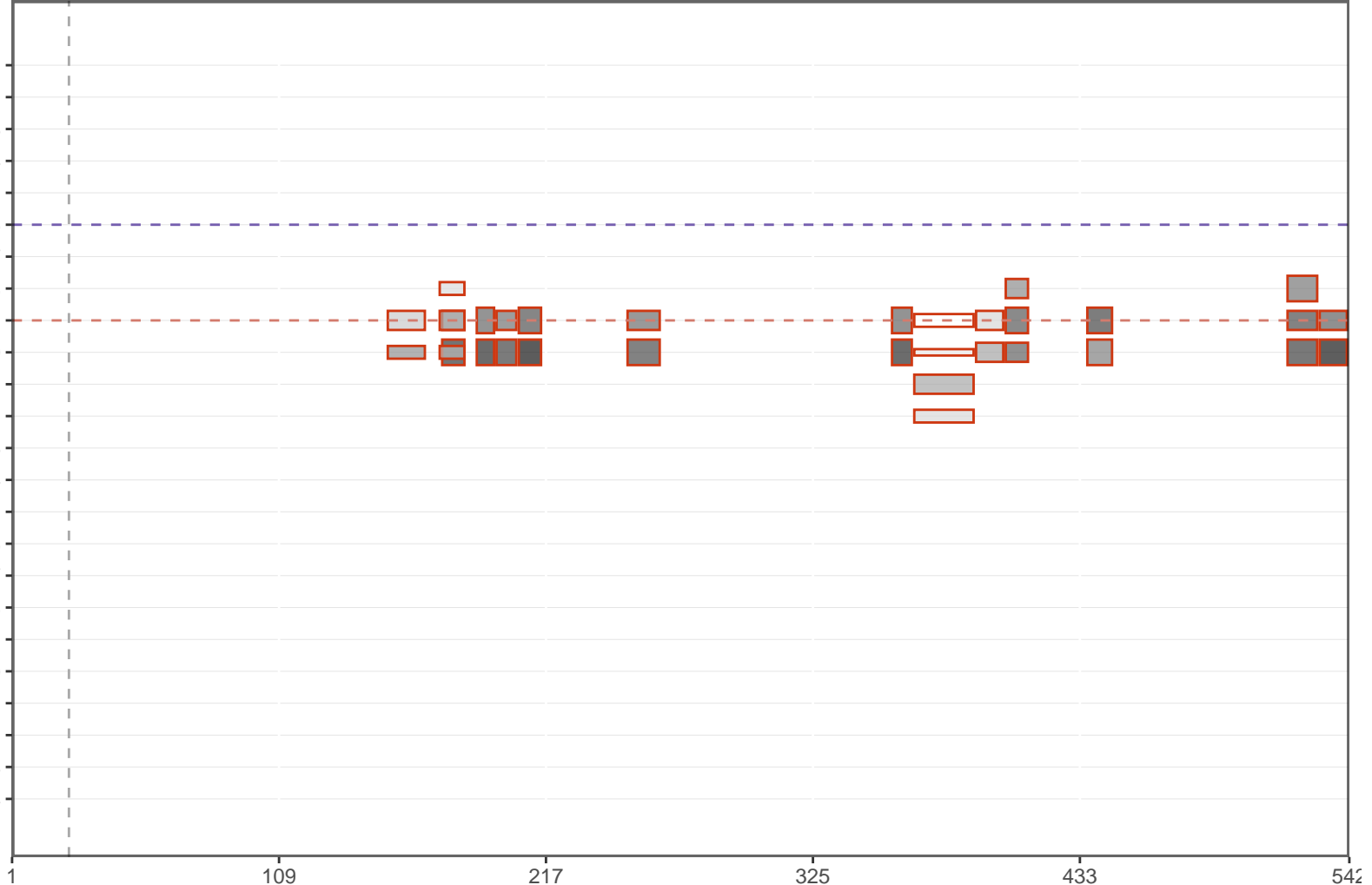
MW indication



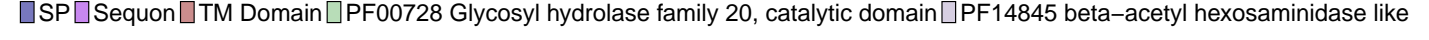
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

RGINVMAEVDYFGHAESGWGAGYFDLWPEPSGKEPLDVKNYTFRDVIAGLADMRIKFFPELFLHGGDEVNTGVTTPHKQWLDGHNMTSKDAYEYFVLRAGEIASHNMTPTNVEETNFTFPSKLNPGQTVHNNALRGVCGEAVAKGFRGYSNGDFWLDLQVFWDKVYKTEPLEGKNSISQKLLGGEGAMWGETADASGQGTWPRAAAARLWSDKEATSTNTSAAALORLEVFRGLLTRRGVPTAPVTFNFWRRPPLGPGSGYEQ

NbL10g09750.1 glutathione_S-transferase_DHAR2-like [MW = 23.62 kDa]

No. of times detected



log(intensity)



Values from



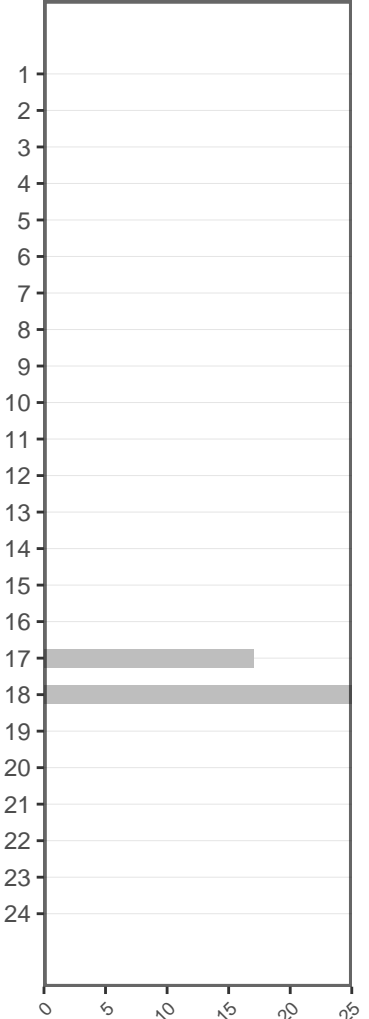
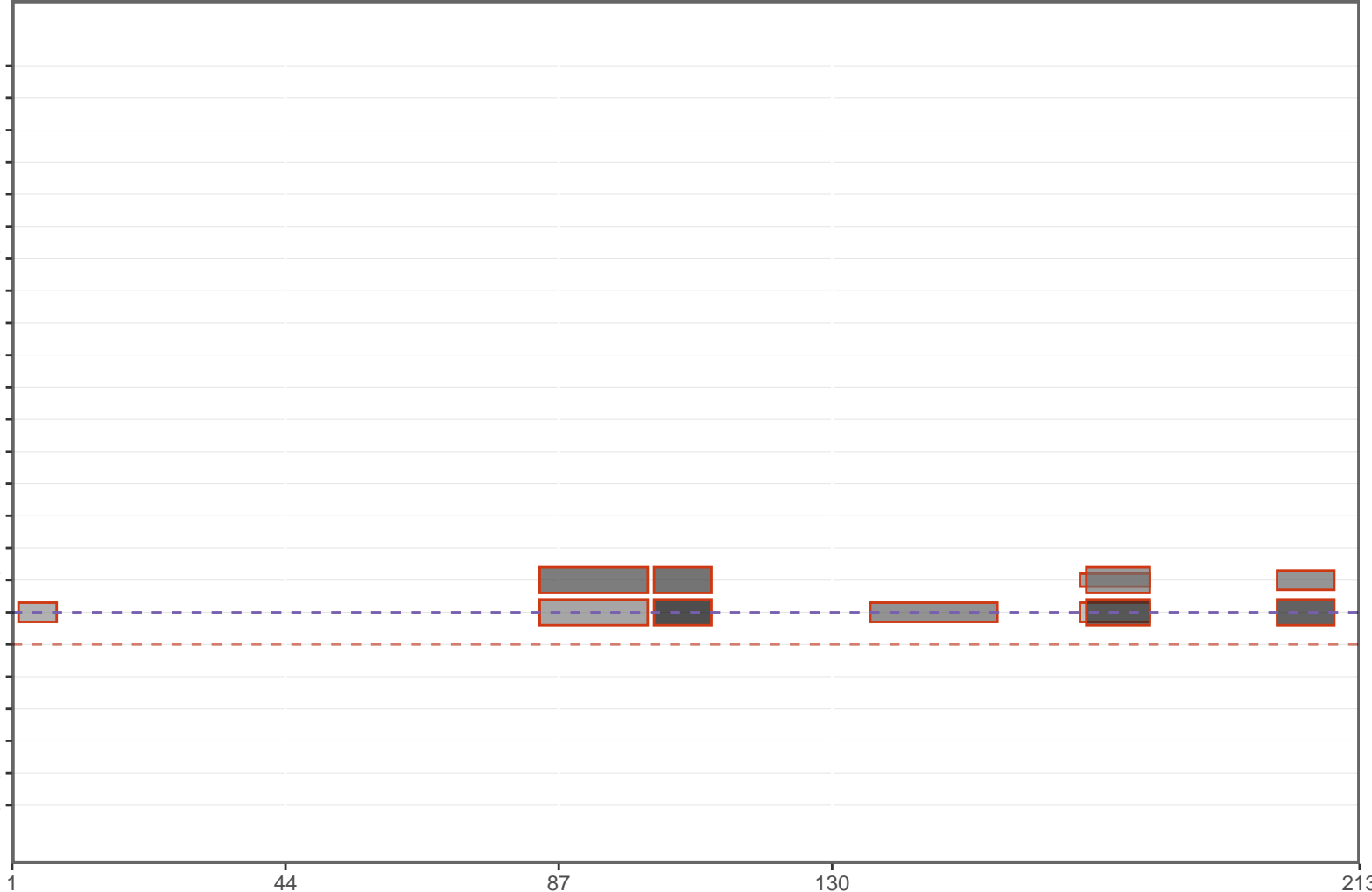
MW indication



Molecular weight



Gel Slice



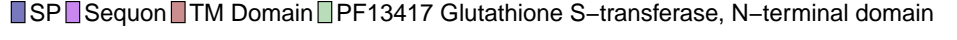
Protein length

Peptide counts over 4 repeats



Pfam domains

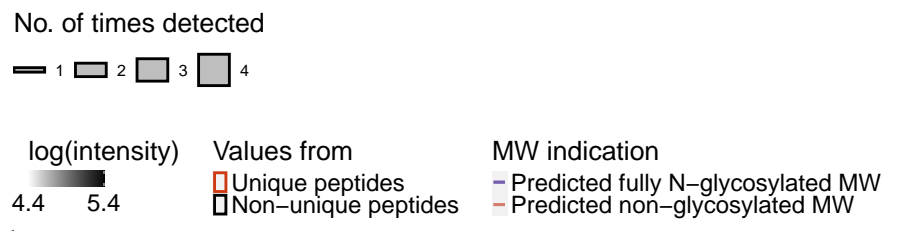
Pfam Description



Protein sequence:

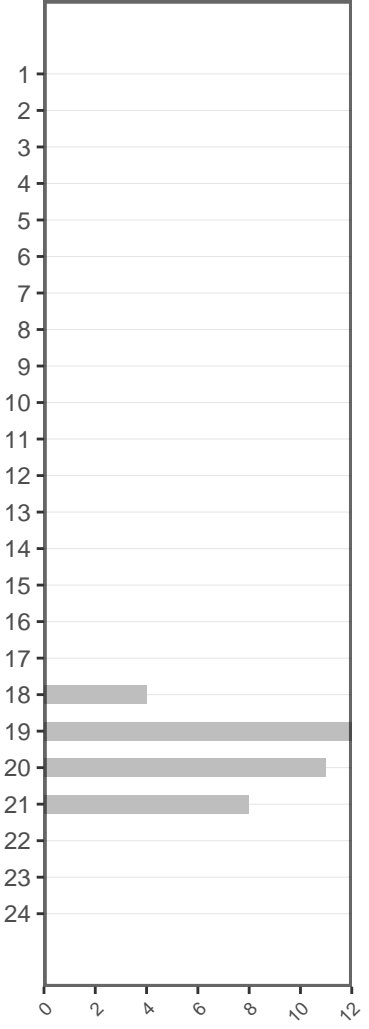
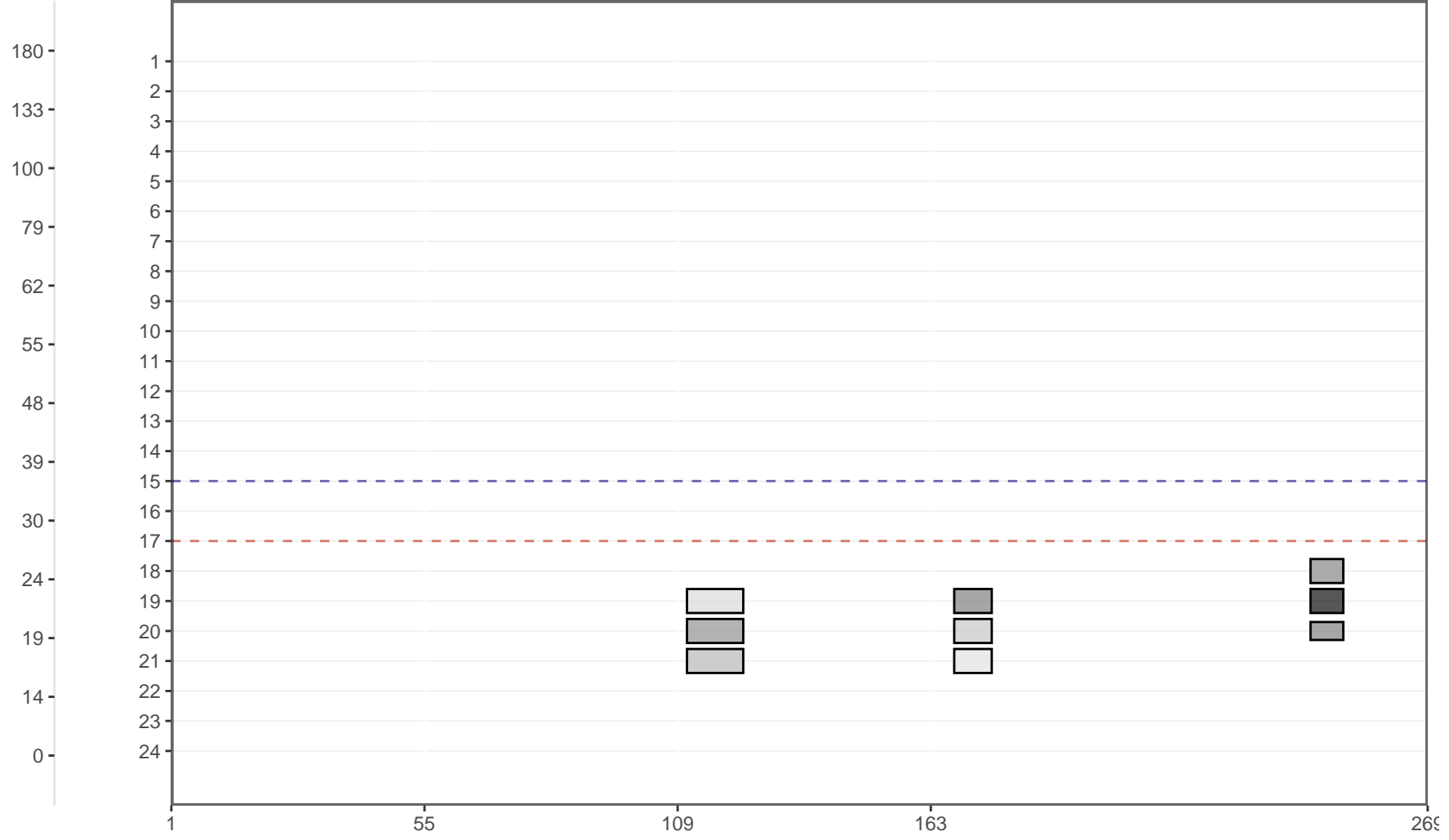
EFASVGSKIFPTTFVFLKSKDASDGTGEGALLDELKALEEHLKAKGPPVYNGANGCEVDLGLAPKLYHLEVALGHFKKQWVPEGLSHVRYNMYKLLFERESFGKTKAAKEYIAGWPKWNP

NbL10g09530.1 multiple_organelle_RNA_editing_factor_2_chloroplastic-like [MW = 30.32 kDa]



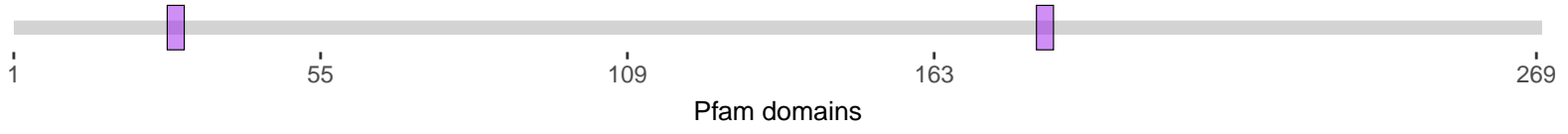
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:
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NbL10g09490.1 cysteine_desulfurase_1_chloroplastic-like [MW = 52.83 kDa]

No. of times detected



log(intensity)



Values from



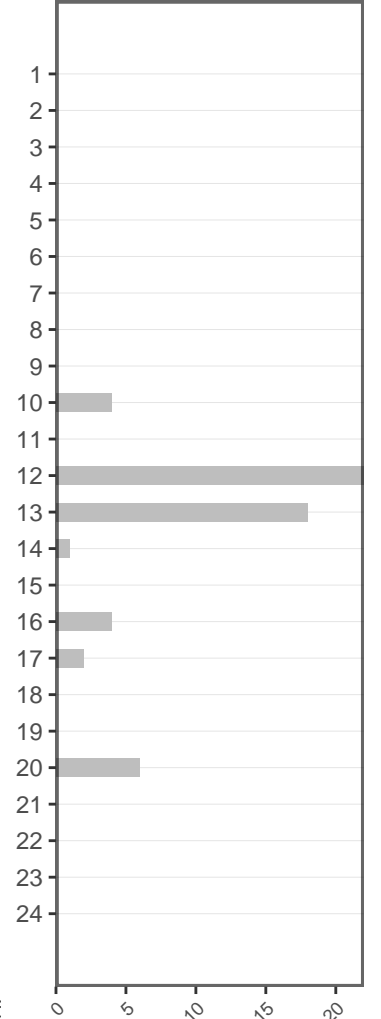
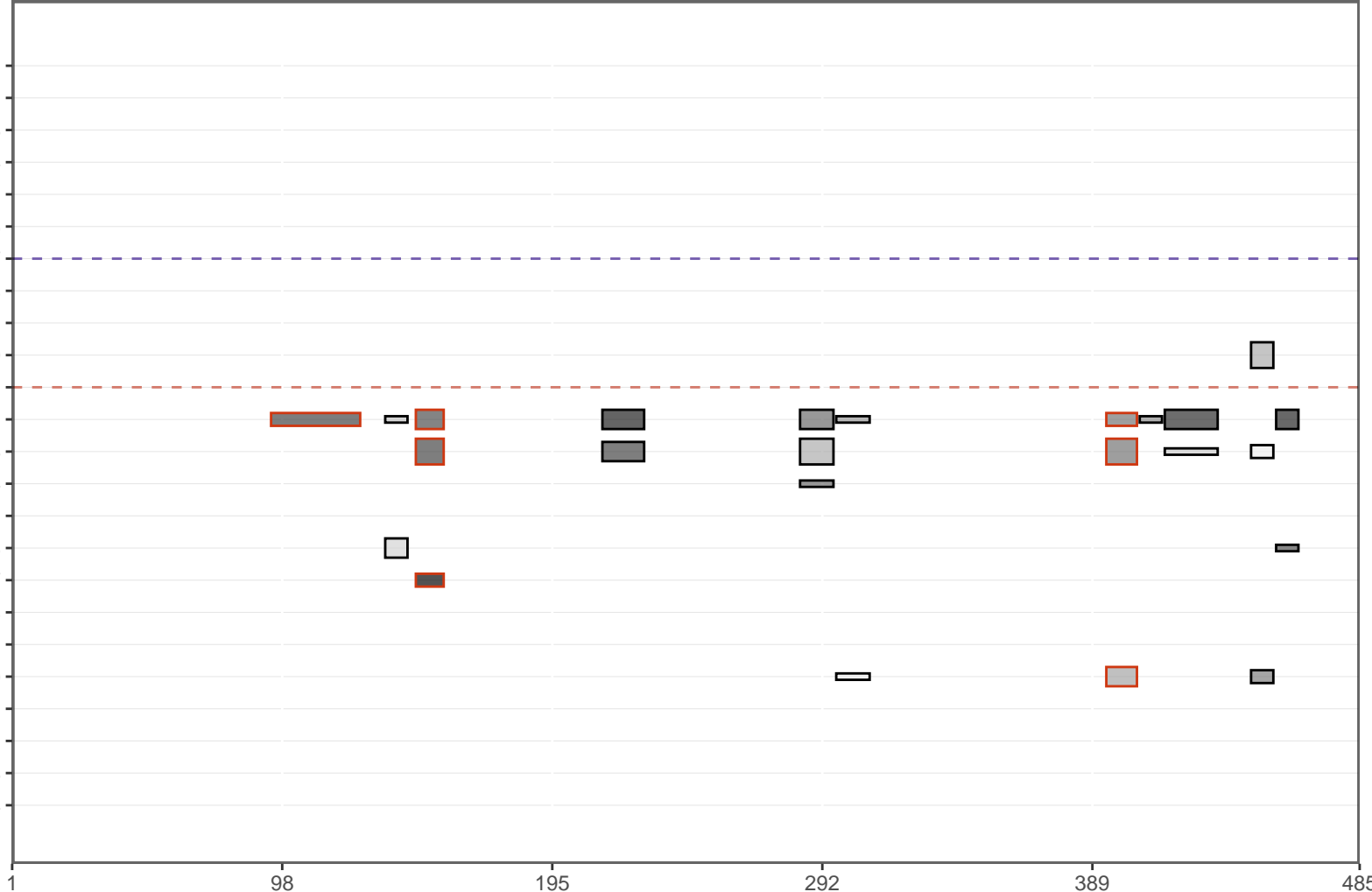
MW indication



Molecular weight

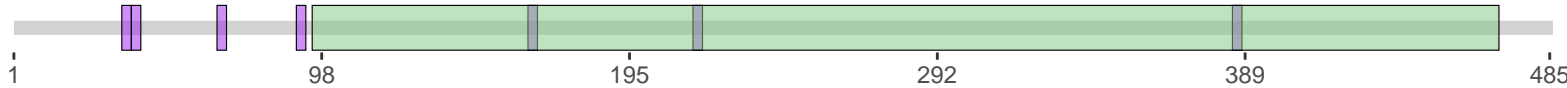


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SKTKLLVHIVSNMLASVLFMDEIVSVAHNDVGAQVLDVAGQGVPHMVVDVKTLDADFLVASSGKMGCPTEVGLVYKGGKLSAMPFLGGGEMADVLDHSTVAEPPSRFEAGTFRAGEAIGLGAIDVLEISGMOGHDIYEMELANLYDNLSSVSDVRYVGPAPSGTVMRAALGFSNVKDVHPTDQATFLDQGHGVAIRSGHKGAGPLHRLHGISSEARASLHFYNTKDDVDRFIEALKDTISFFTSFK

NbL10g09400.1 ubiquitin_carboxyl-terminal_hydrolase_12-like [MW = 130.62 kDa]

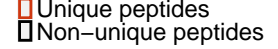
No. of times detected



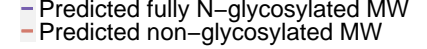
log(intensity)



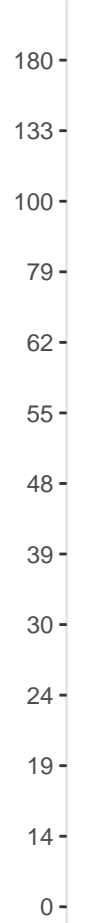
Values from



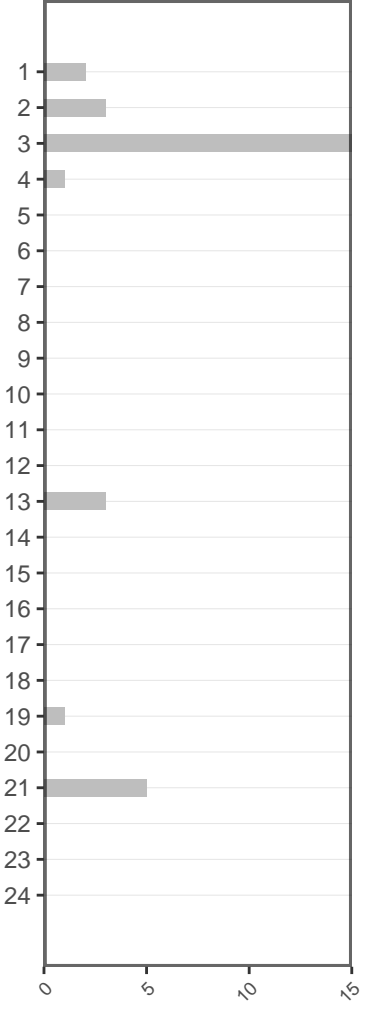
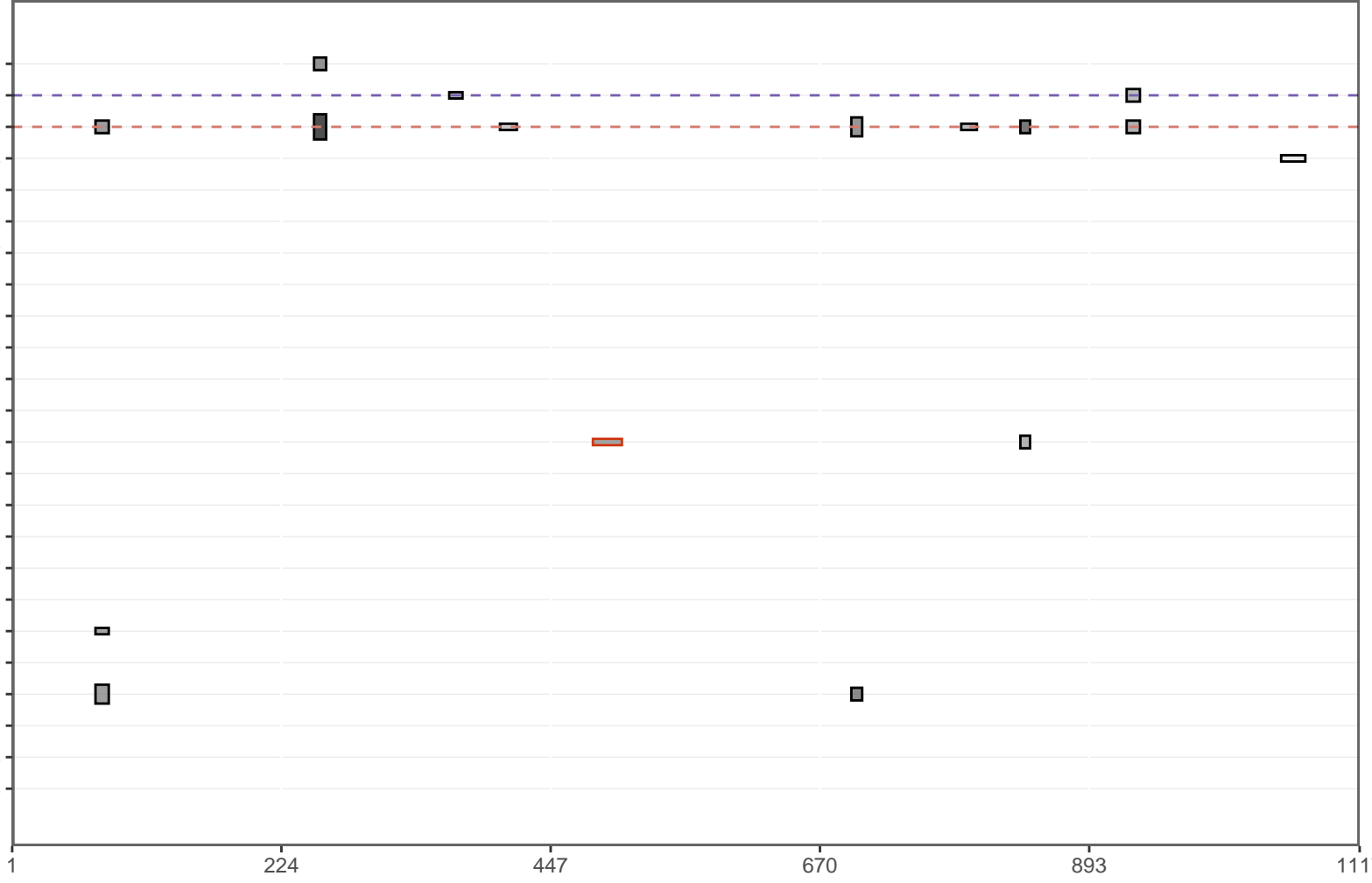
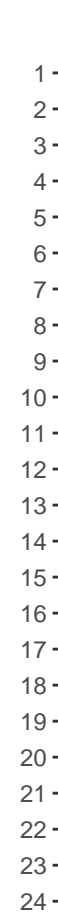
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00443 Ubiquitin carboxyl-terminal hydrolase
- PF00917 MATH domain
- PF12436 ICP0-binding domain of Ubiquitin-specific protease 7
- PF14533 Ubiquitin-specific protease C-terminal

Protein sequence:

IRLKKEQEEKQKRKEKAEALYTRIKVARDEDLGEGIGKEIFDLVDHDKVRFRIKQKMPFTQFKEEVAKELGIPVDFQRYLWAKRQNHTRYRNRPLTAGEEVDSVGLREVSNNANAELEKLFLEVEFGLDLQFPPEKTEKEDLLFKLYDPLKEIRYVGRLEFVWGGSKFLEIKLNLKELAGFFPDEEIELFEEIKFEPNVMGHEIDGKLSFRGSOLEDCDQKCFQKSLRNDQREGYRFEVPLFLEYVHNQRYVFRSLKPKEDFSLSKNNYDEVVHLARHL

NbL10g09300.1 40S_ribosomal_protein_S17 [MW = 16.22 kDa]

No. of times detected



log(intensity)



Values from



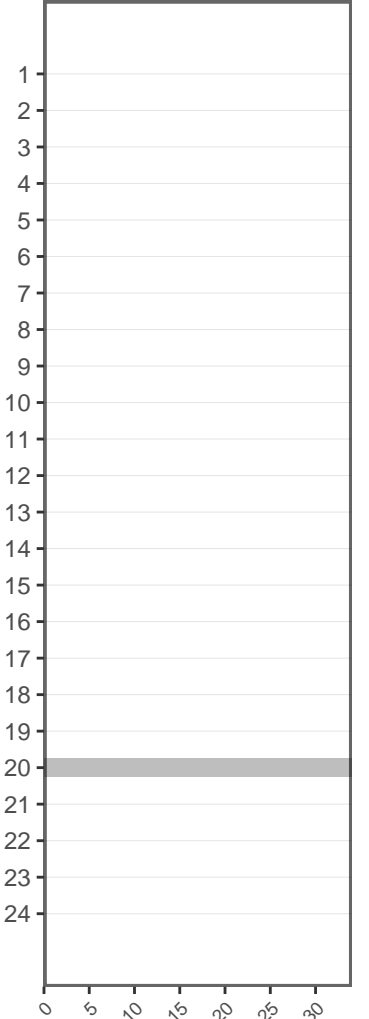
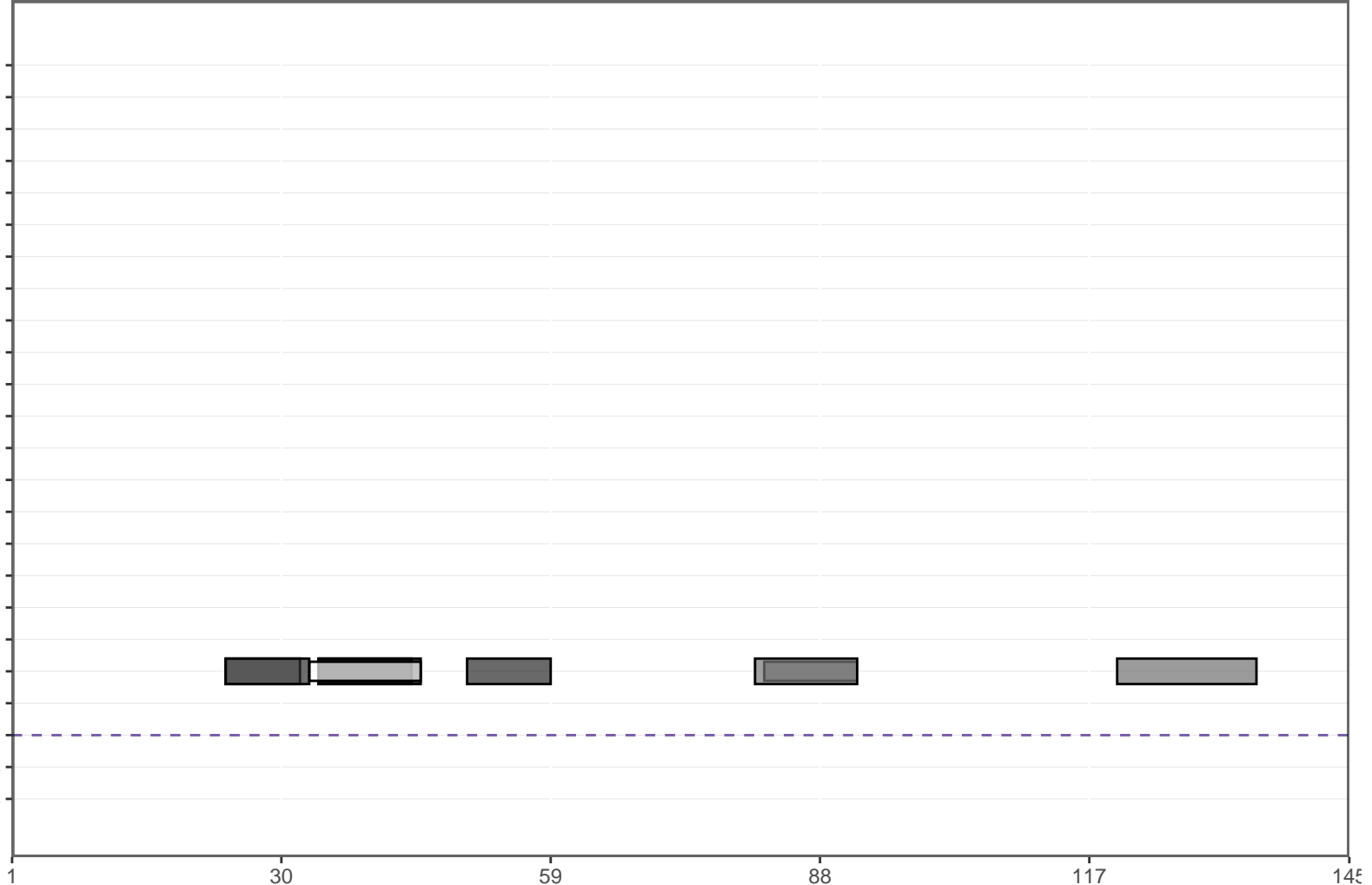
MW indication



Molecular weight



Gel Slice

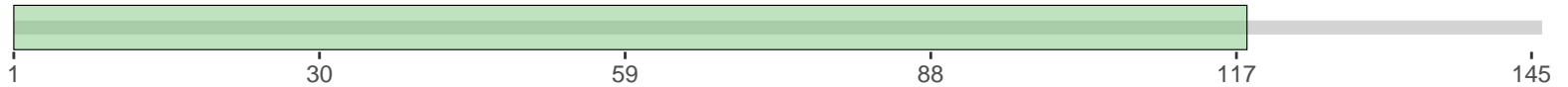


Protein length

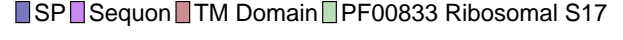


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IQKGPVIRGISLKLQEEERERRMDFVDEGAIKTDLIEVDKTELDMISALGMSDLPVWKGAAEPQAAALPTFYRGAGGFRKY*

NbL10g09250.1 copper_transport_protein_ATX1-like [MW = 13.63 kDa]

No. of times detected



log(intensity)



Values from



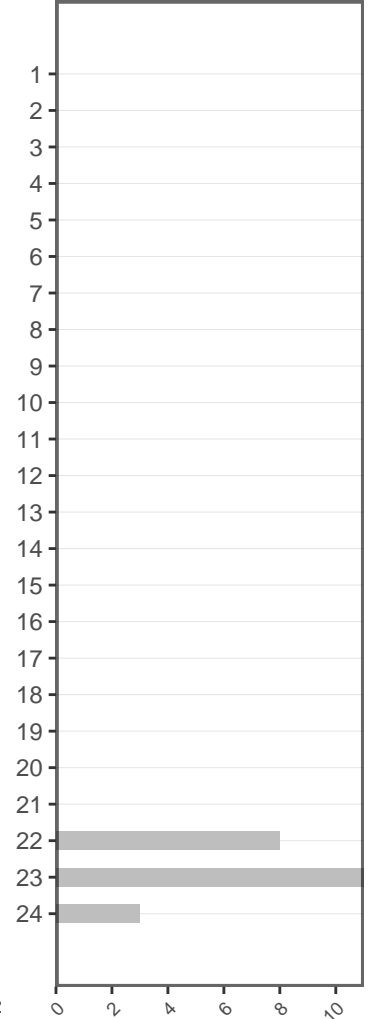
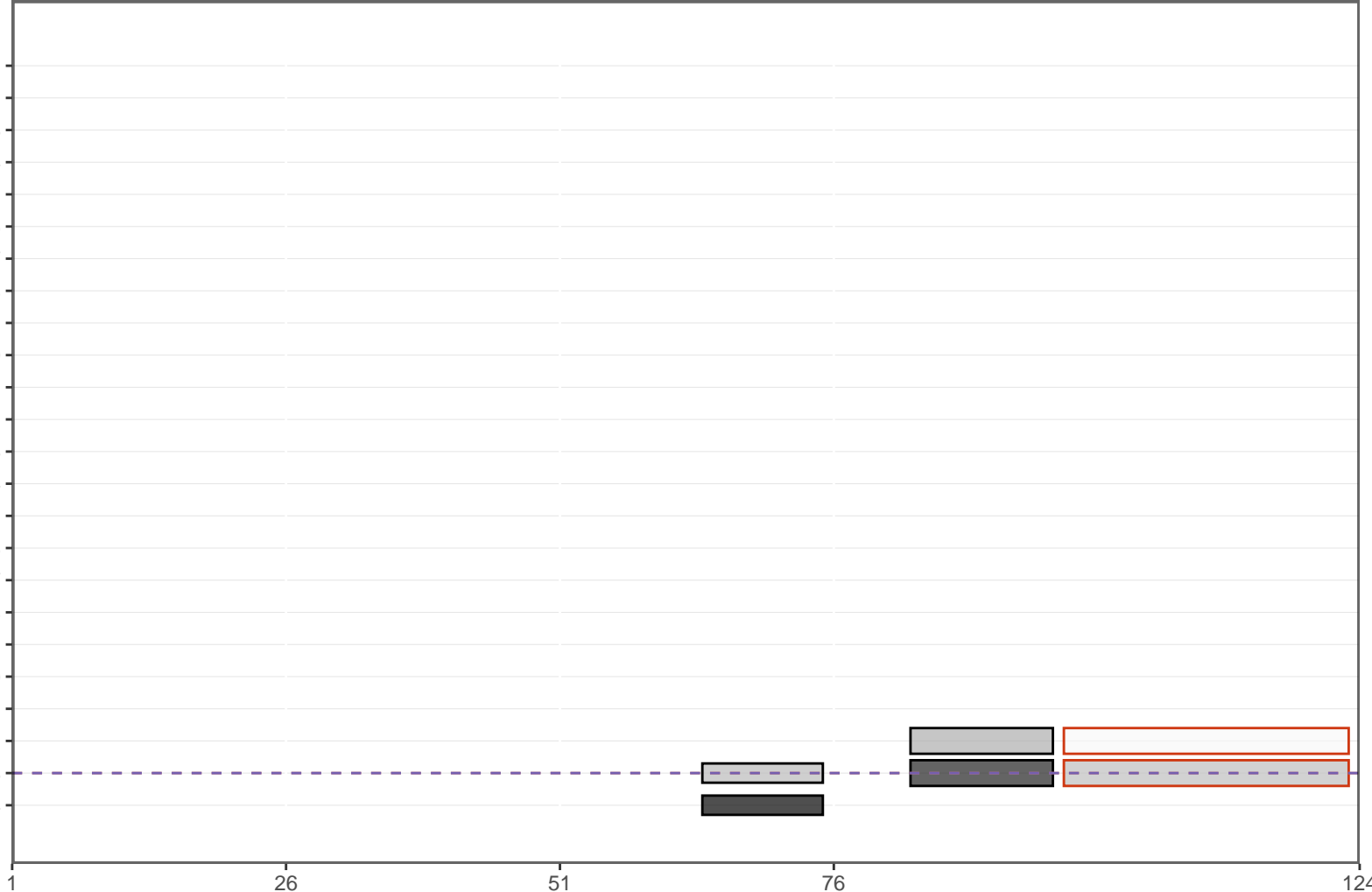
MW indication



Molecular weight



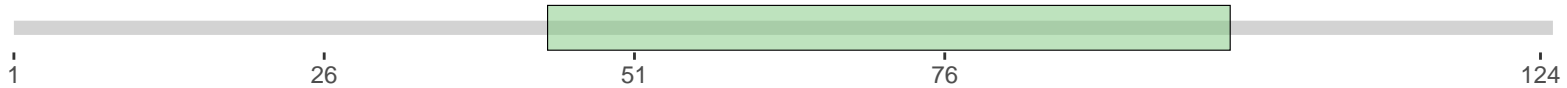
Gel Slice



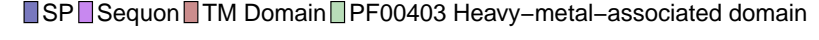
Protein length



Pfam domains



Pfam Description



Protein sequence:

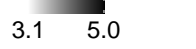
IGCYGAVKRVLQKMEGVENFDLKEQKVTYKGNVQPEAVLQTVKTKGKPTFSWEADEFMGTTEENPAEAVGTS*

NbL10g09110.1 protein_BTR1-like [MW = 35.7 kDa]

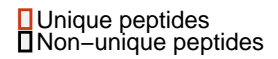
No. of times detected



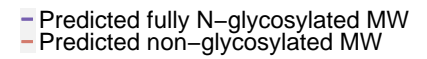
log(intensity)



Values from



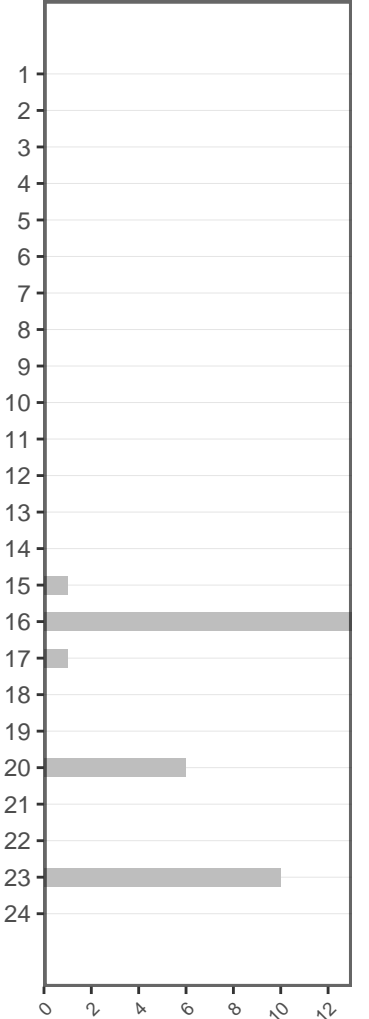
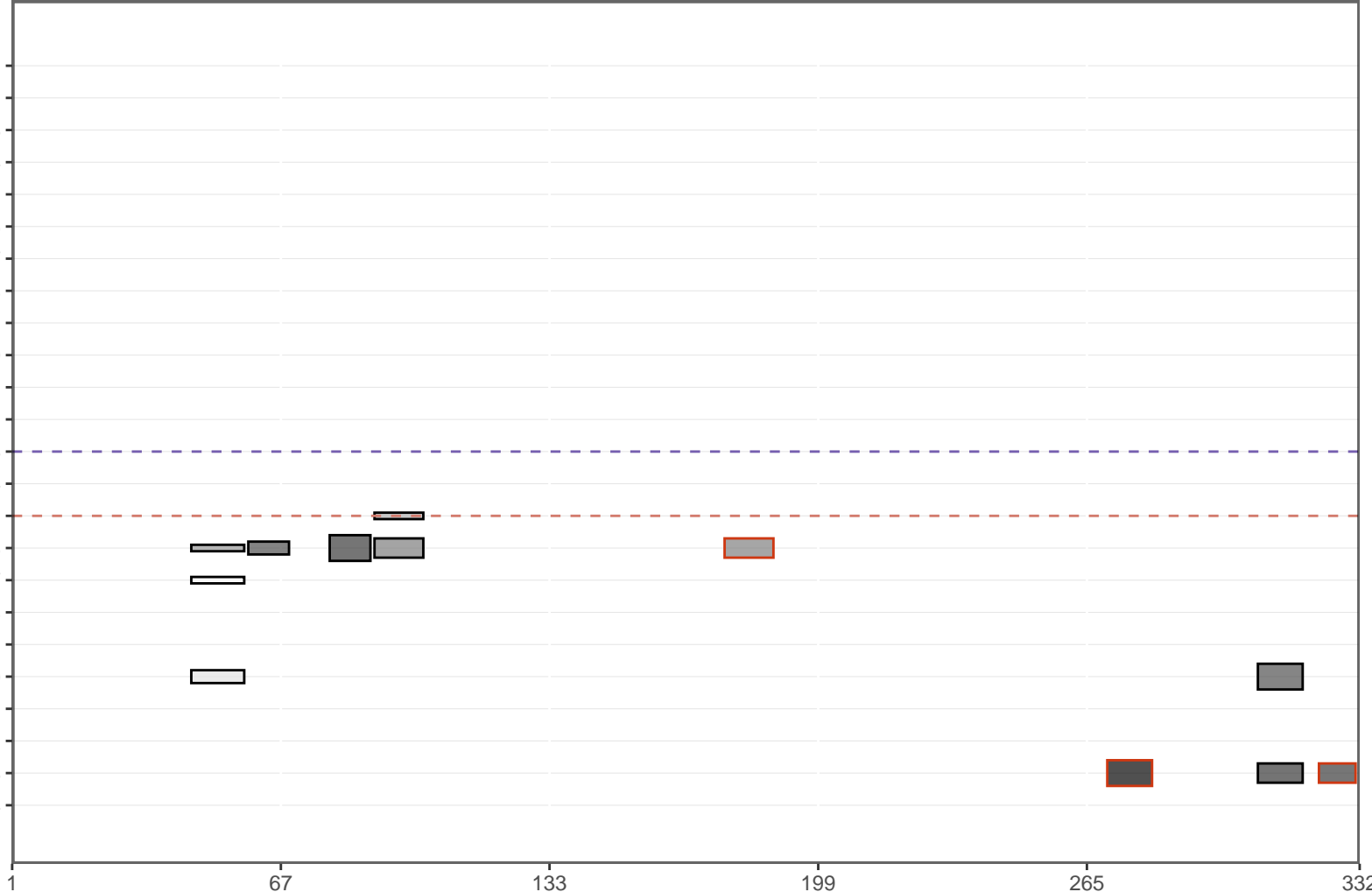
MW indication



Molecular weight

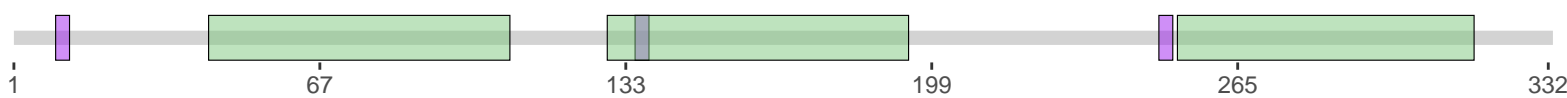


Gel Slice



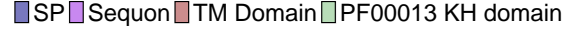
Peptide counts over 4 repeats

Protein length



Pfam domains

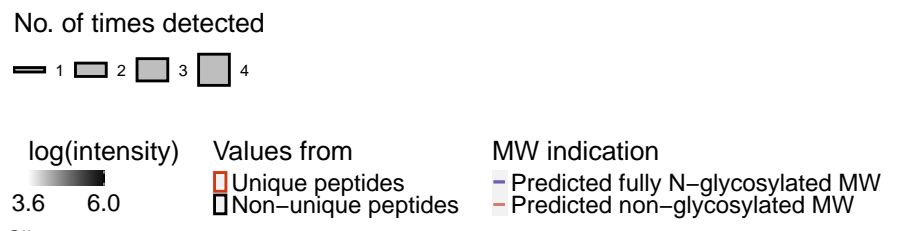
Pfam Description



Protein sequence:

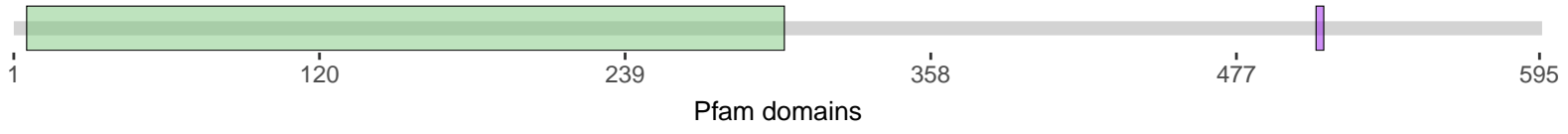
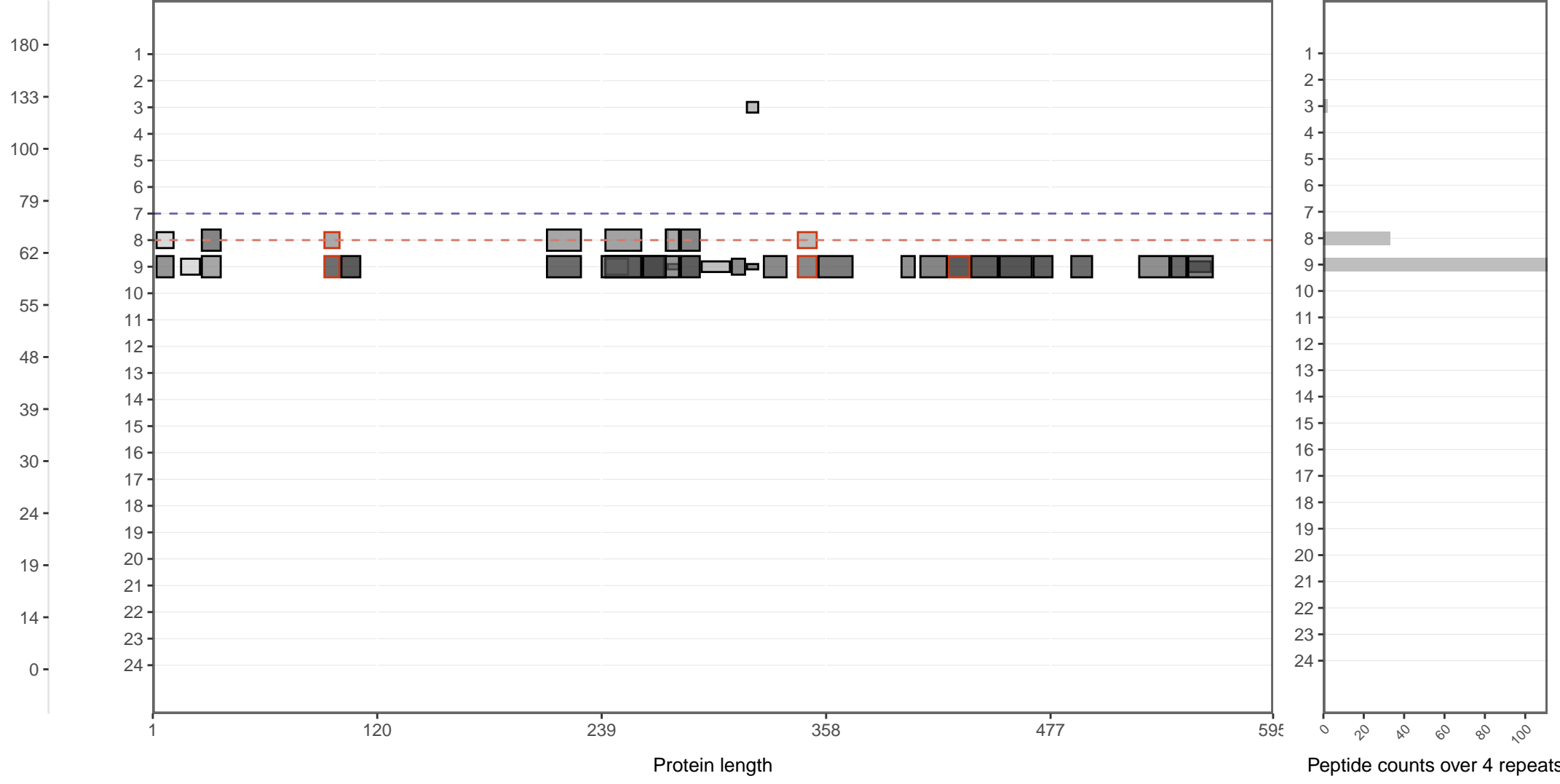
EDSHAGIKSSDQDNFPGPHDRLVITGTLGEGMRAIEILHKLAEEDSHYMQNNAFPFVAGVYGMNVGPRNGVGGFRFNRYGNVQNSIEDRNNISVTGVADEHGLVLRNGRSMIEISQSGARIKISDRGDFISGTSDRKVTITTGEDRAISMAESMISGQKVARVSEGDVFKVQ*

NbL10g08920.1 probable_methylenetetrahydrofolate_reductase [MW = 67.29 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF02219 Methylenetetrahydrofolate reductase

Protein sequence:

NMEKSAIALMLNLGHEESKERPLPWRPTNFRVKEEDWRPFWANRPKSYISRTDWDDEYPHGRWGNAGNPNPYGALSDYGFMRARSRDKKIQEEWAFALNSVEDYERFMNYLGLKLRSGPWSLELDGLGPETKIDHEHLSNINTKGLFTINSQPWVNGAKSDAPSGDGGVYVQKAVLEFFGSHKLNALVEKGGKAFPLTMAVANKEGNWIENANGTDINAVTWGVFPGKEVQPTVVDPAEFMVKDEAFENWSRGWALVQESDPRKLLGQVONSFTVLSLV

NbL10g08790.1 uncharacterized_LOC109225451 [MW = 29.71 kDa]

No. of times detected



log(intensity)



Values from



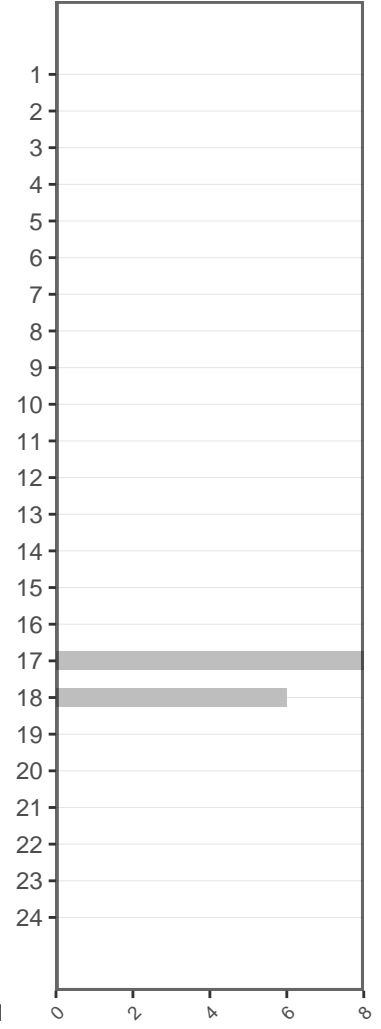
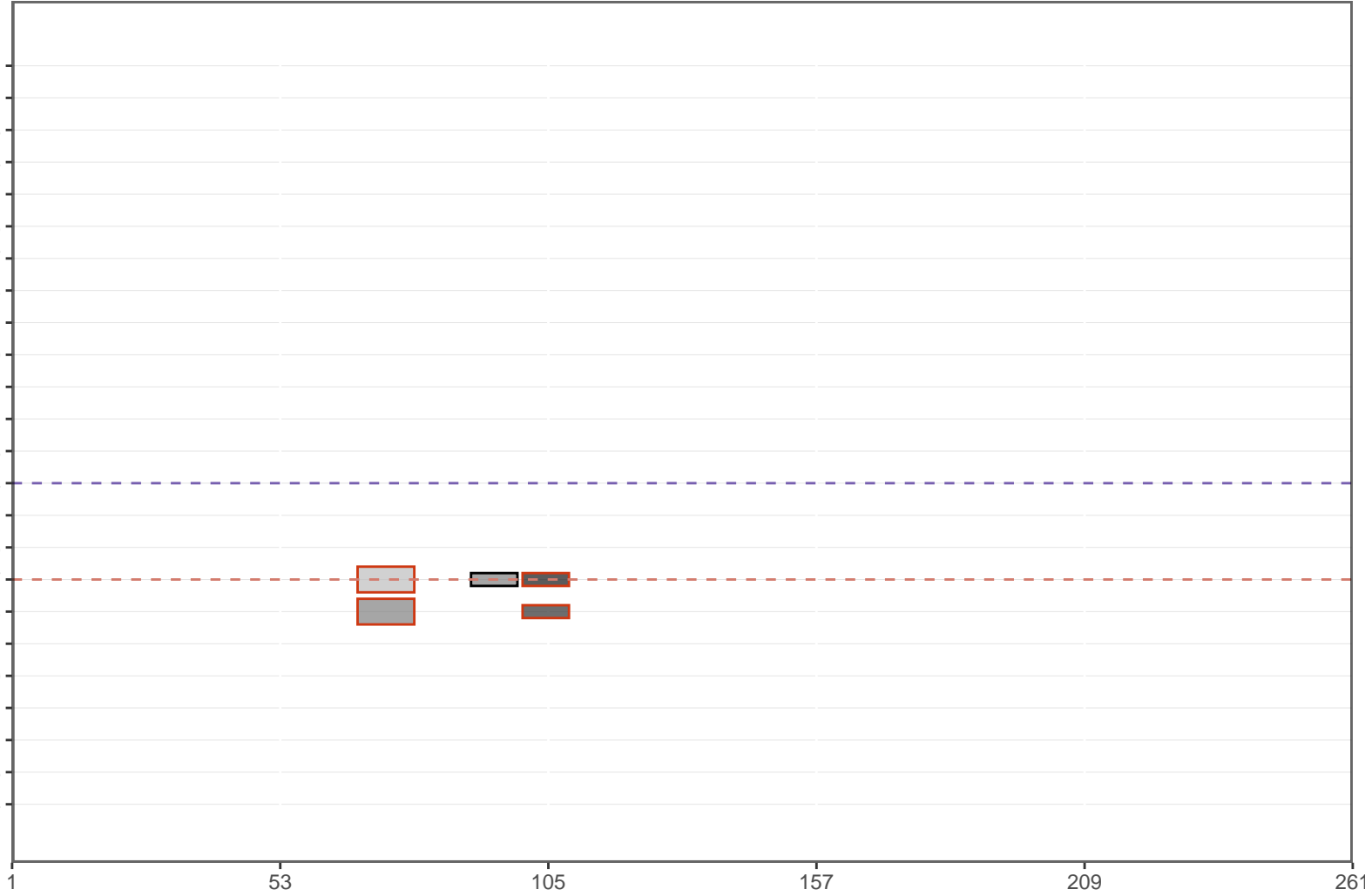
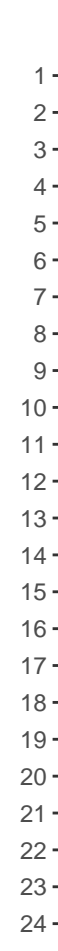
MW indication



Molecular weight

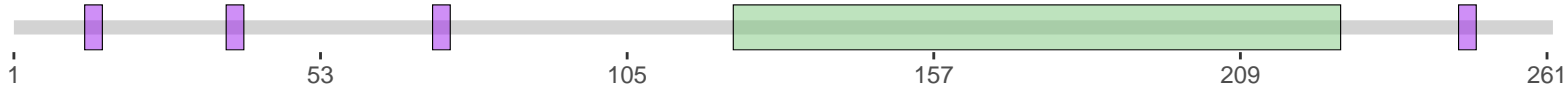


Gel Slice



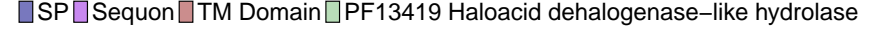
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DLEGLKNCMRRAVSYEGVEGLLNSLKENGYEHAFTNYPWQMIEDKHLNENLGVTFGSGFGKRRPDPDFYLEVWKHLNVEASSGIFVDDRRMRNVEAAVEVGLNGLGFQNAIDLLRKLDSLLGVNISENENPOLAEGSS

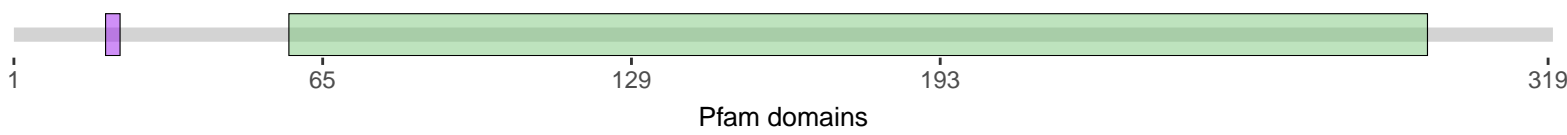
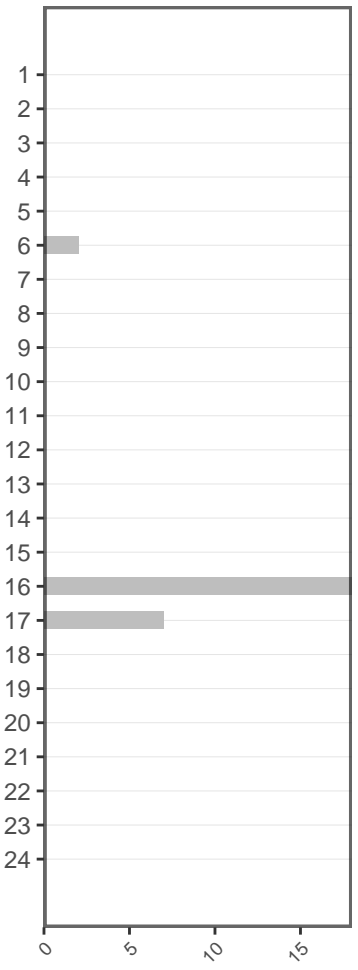
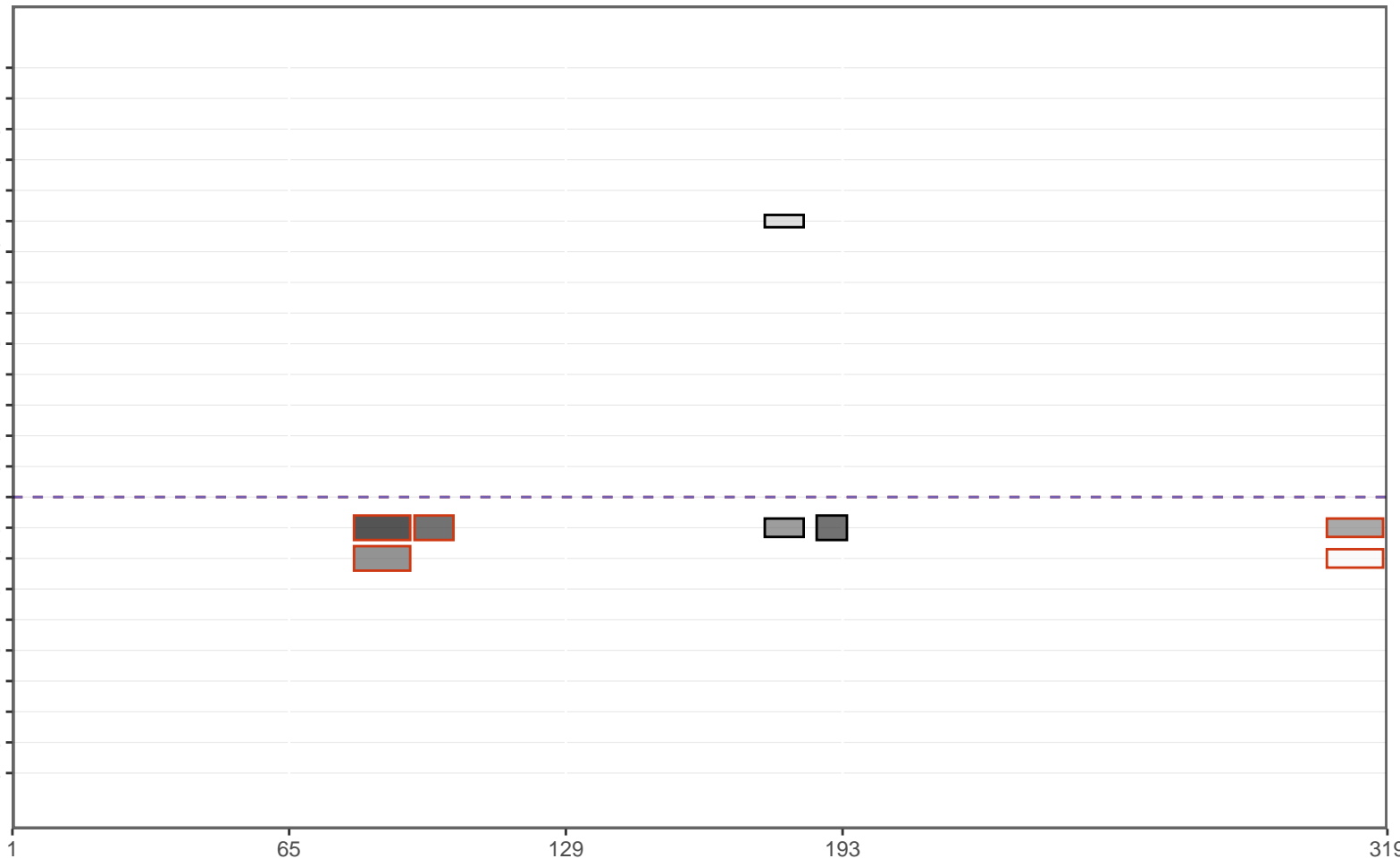
NbL10g08470.1
 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]_imidazole-4-carboxamide_isomerase_chloroplastic-like
 [MW = 34.73 kDa]

No. of times detected
 1 2 3 4

log(intensity) 3.7 5.6
 Values from Unique peptides Non-unique peptides
 MW indication Predicted fully N-glycosylated MW Predicted non-glycosylated MW

Molecular weight
 180
 133
 100
 79
 62
 55
 48
 39
 30
 24
 19
 19
 20
 21
 14
 23
 24

Gel Slice
 1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
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 19
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 21
 22
 23
 24



Pfam Description
 SP Sequon TM Domain PF00977 Histidine biosynthesis protein

Protein sequence:
 ALSYIDEGASHVIVTSYVFNNGDMLEKELKLSLVGRKRLVLDSCRKKNMDEGEYVIVDRYQKFTDRLENEKYLNFADVADEFLLHGVDEGKKKSIDLWLLSKYSPPIVTVGGVTVYMADELEKIKLAGMGRVDVTVGSALDFQGNLAKGVVWVHALGDPLEAM

NbL10g08440.1 ammonia-lyase [MW = 78.73 kDa]

No. of times detected



log(intensity)



Values from



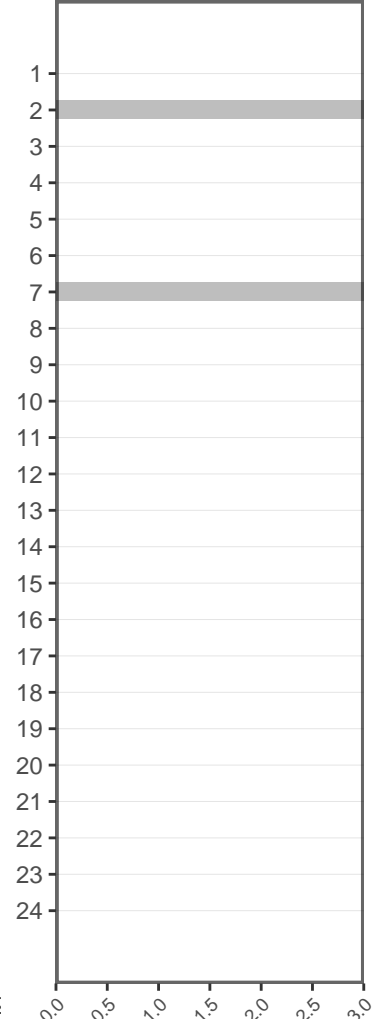
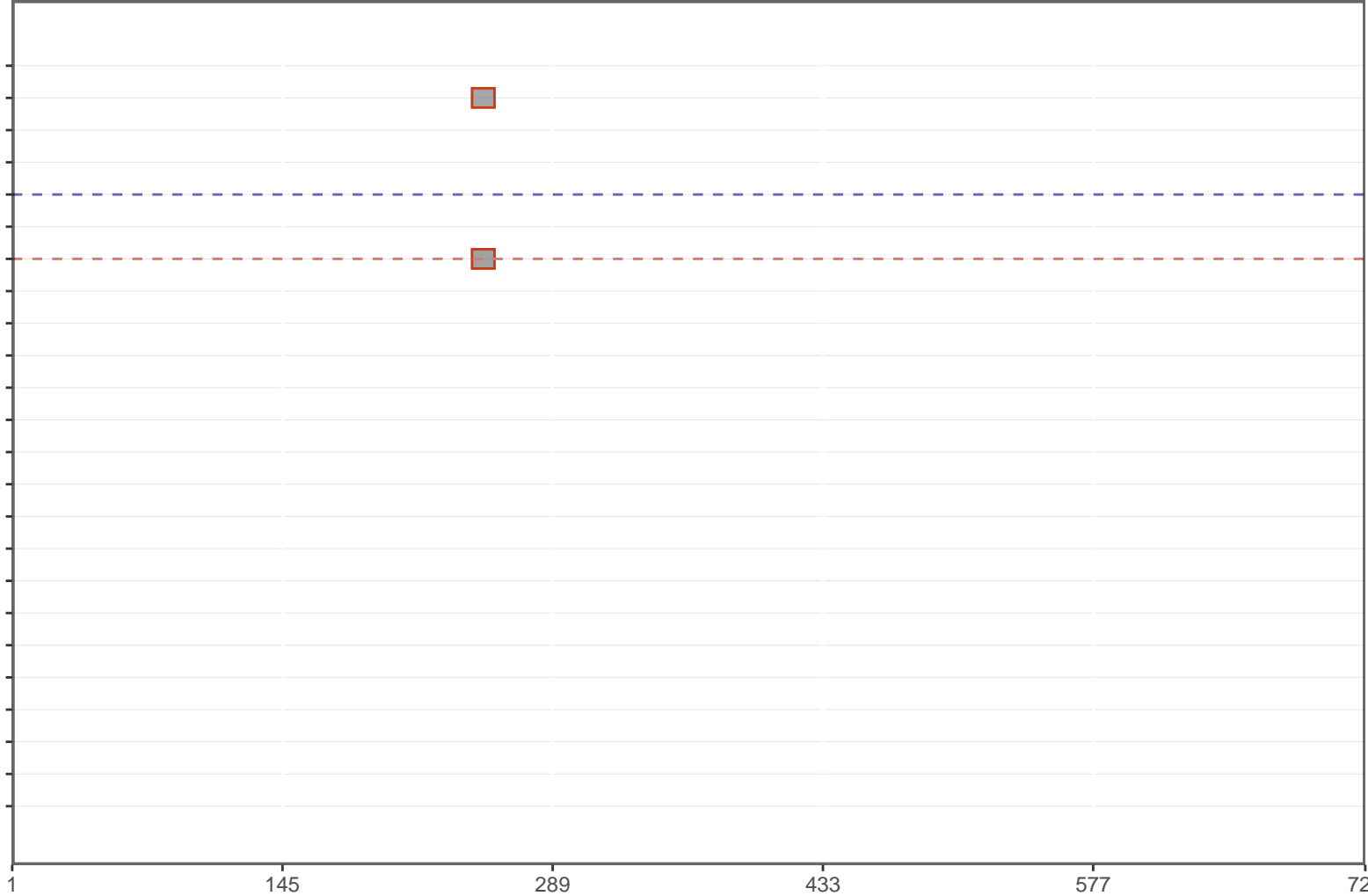
MW indication



Molecular weight



Gel Slice

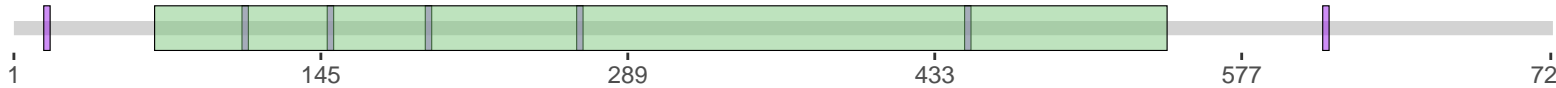


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

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NbL10g08410.1 calreticulin-3-like [MW = 51.1 kDa]

No. of times detected



log(intensity)



Values from



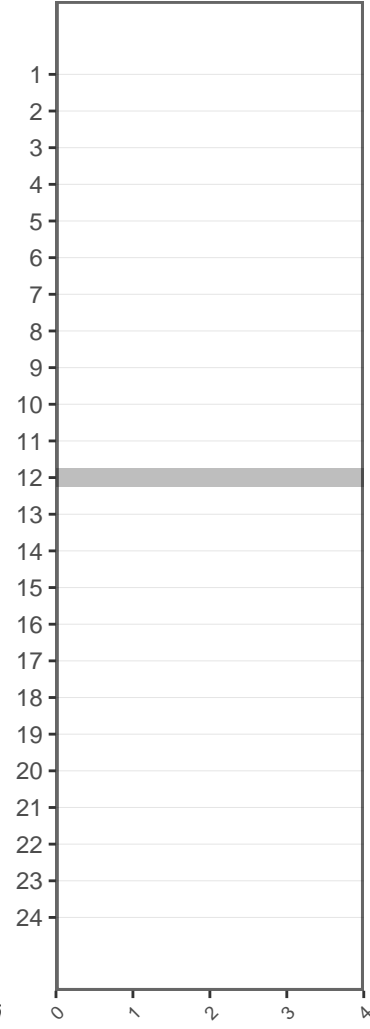
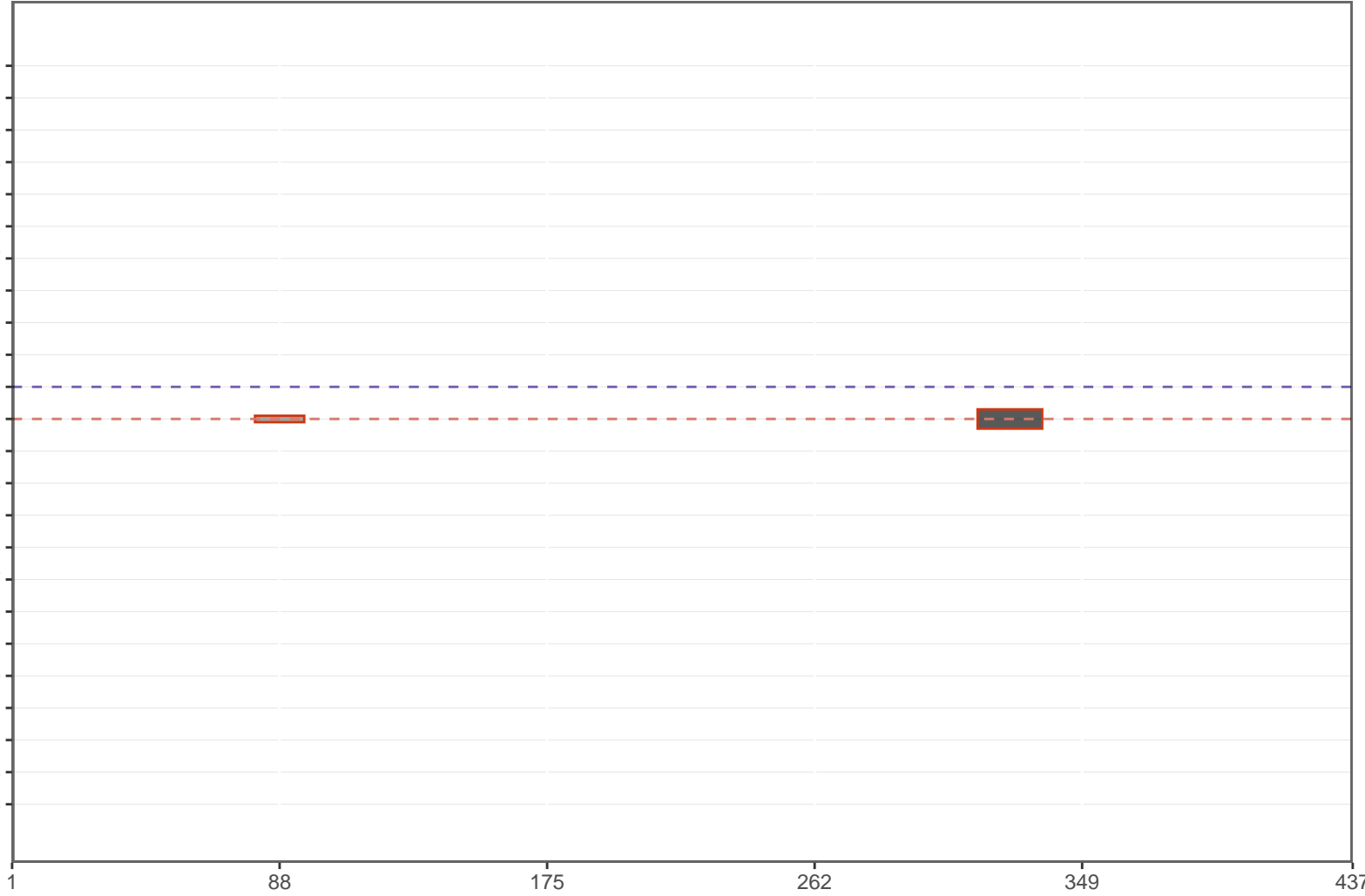
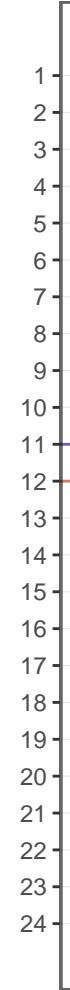
MW indication



Molecular weight



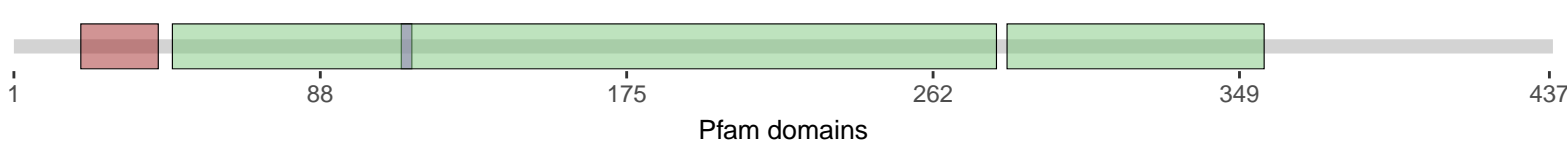
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

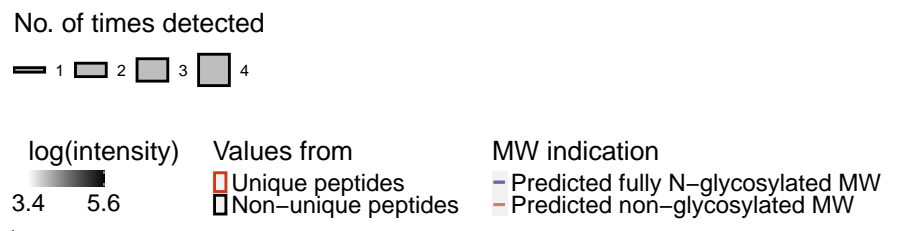
Pfam Description



Protein sequence:

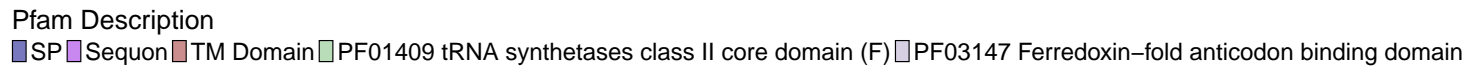
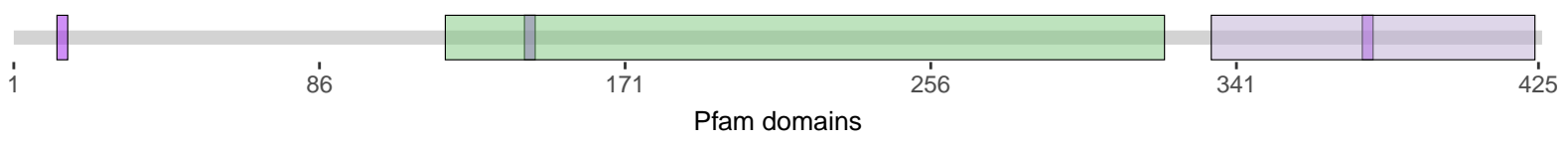
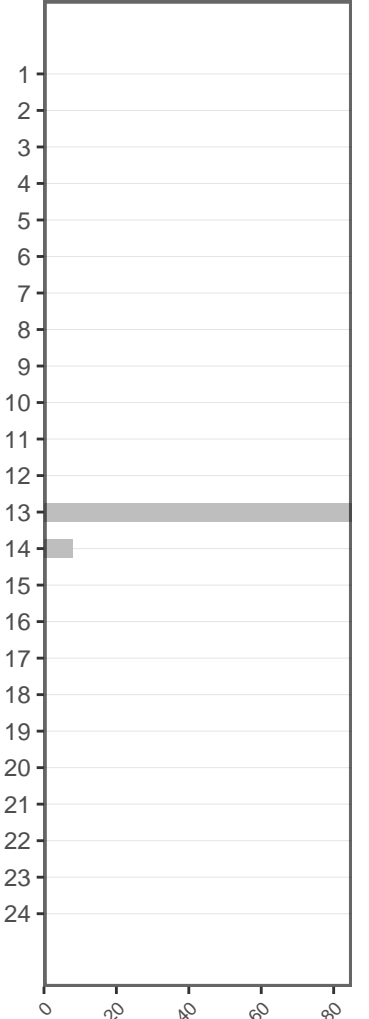
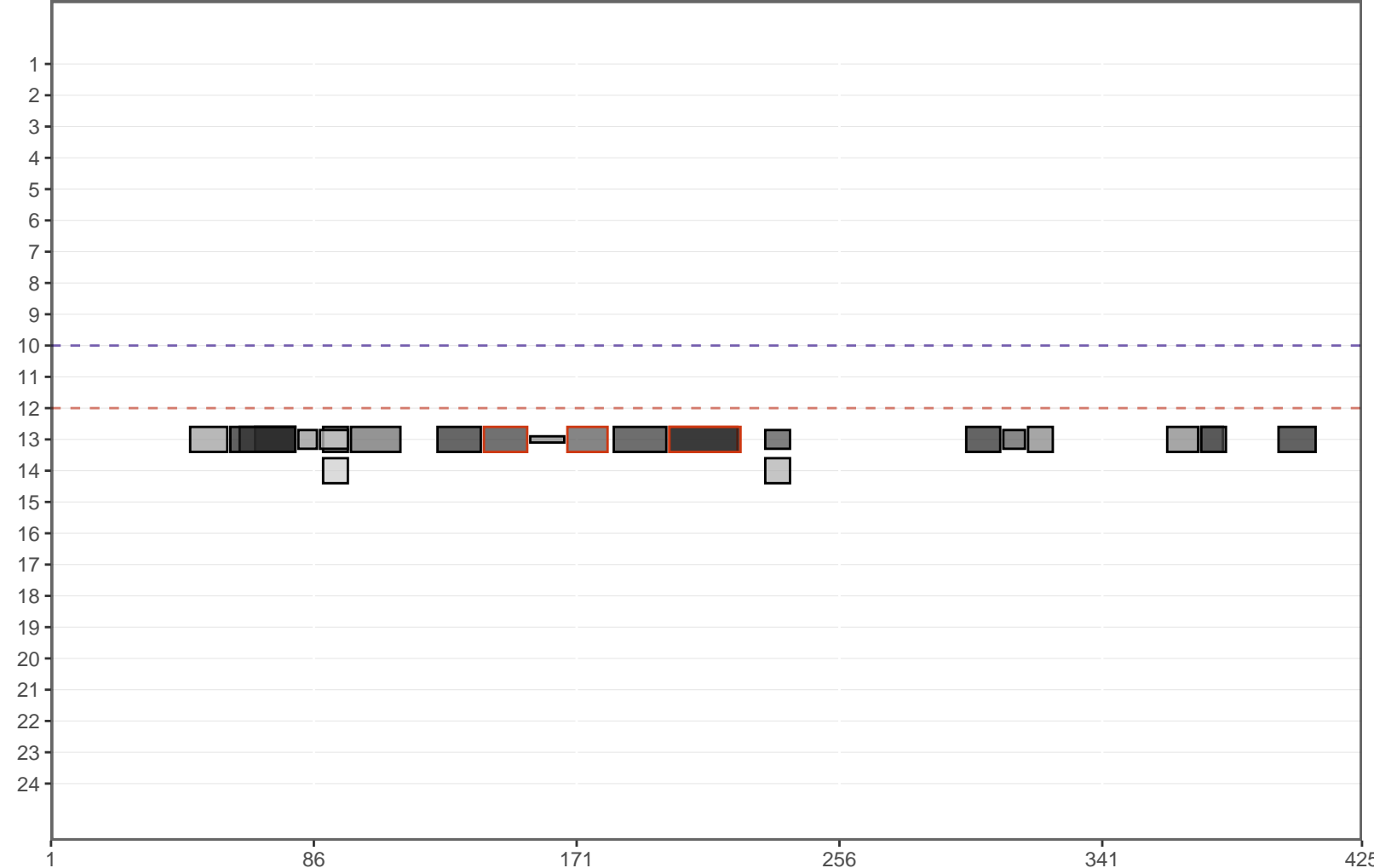
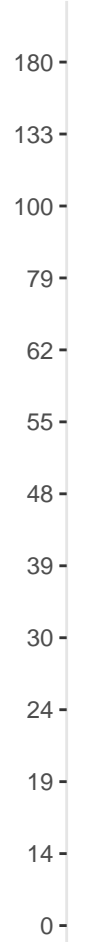
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NbL10g08380.1 phenylalanine--tRNA_ligase_chloroplastic/mitochondrial-like [MW = 48.59 kDa]



Molecular weight

Gel Slice



Protein sequence:
 FAPNDVEGSGADATSHAEDLKKGLEGLARHLFGGVEMRWVDYFFPTNPSFELEIFQNEWMEVLGGVTEGELKRSRGTNVAWAFGLGLERLMAVLDIPDRFLFWSTDERFTSGFSGRLLGLNFKFPSKYPPCYKDMSFWSDFETENLGEVVRGAGDLAEVVKLDNFTNKGKMTSHGVIYRVRSMERSLTDEEINDLGWKVRQGVESLKYVLR*

NbL10g08370.1 23-dimethylmalate_lyase [MW = 54.41 kDa]

No. of times detected



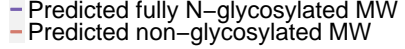
log(intensity)



Values from

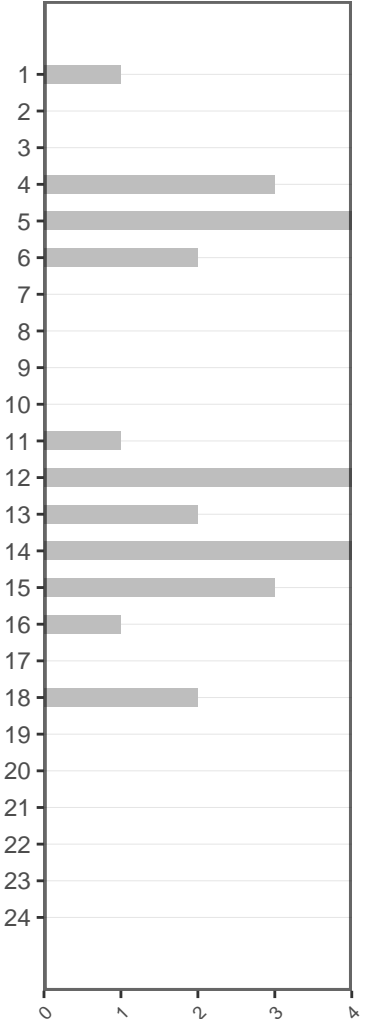
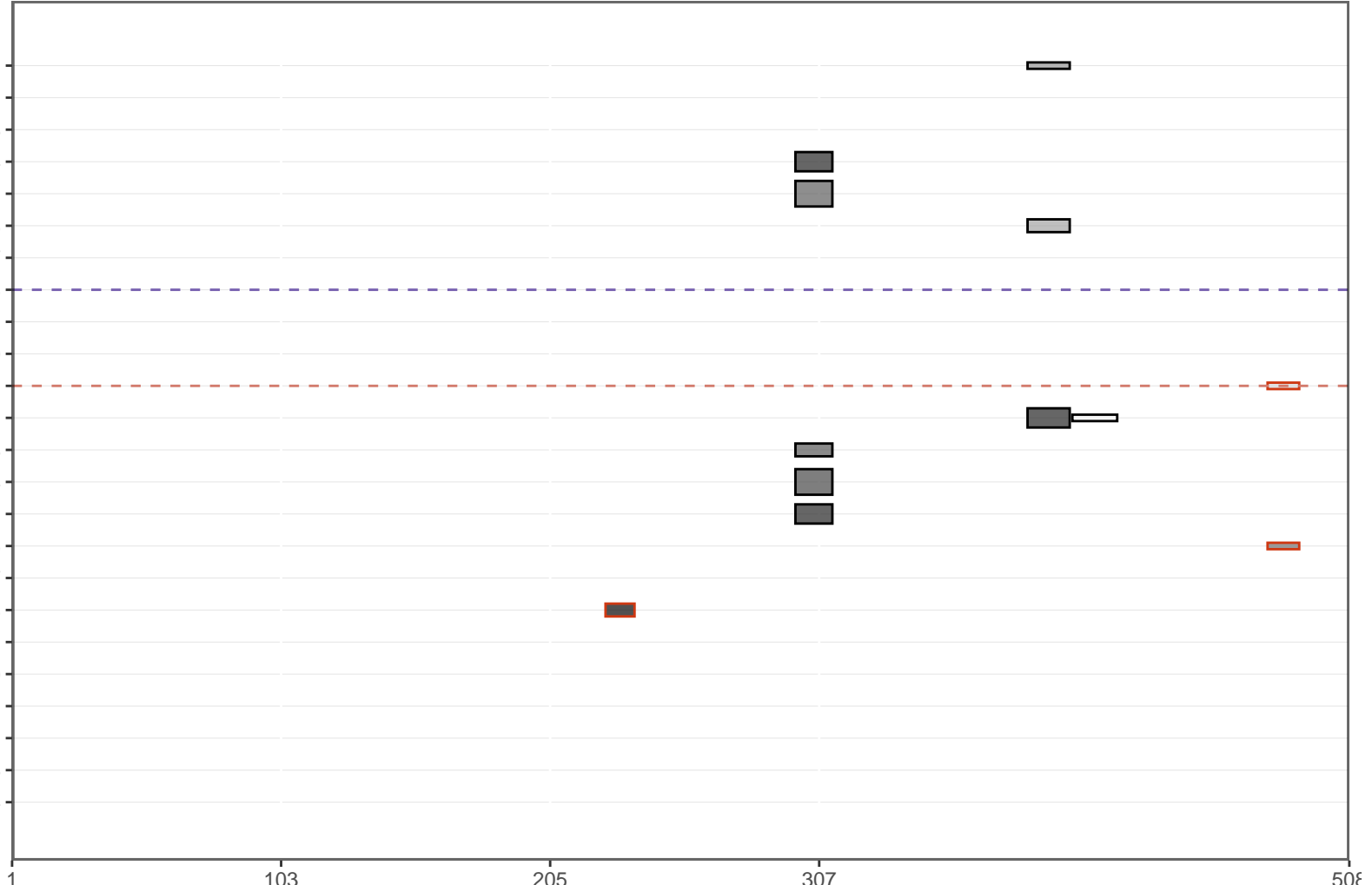
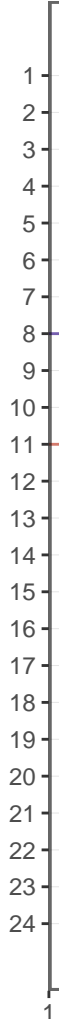


MW indication



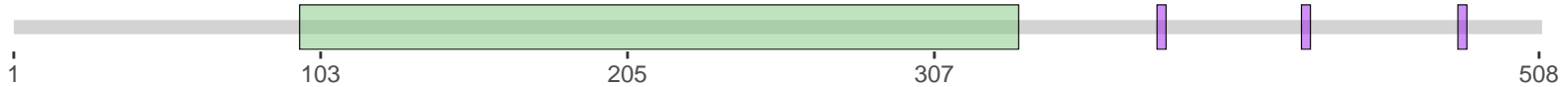
Molecular weight

Gel Slice



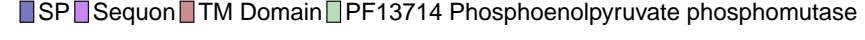
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MSRQAVSFEELVWRARALADAGADVLFIDALASIEENKAFQDYYVPLVPMANMLLEGGGKTPILPTELEELGGYKAVVPLBLMGVSHCAMQDALTAKGGRIIPSPGMPFEELEKILGFNTYYEEENLVYTTSSQLPBLKGNFSSRNEVGVQDQIPADTEQRGGQIPQNPVFLPEVYDKFSGEGAKGNFSGIWSRKLKVKITGRDGGVKKLDIRPAGFLEGITNIVPALVGVNKKALLDNATLEEGGKQLDFQDTMGDIHQVLE

NbL10g08350.1 biotin_carboxyl_carrier_protein_of_acetyl-CoA_carboxylase_chloroplastic-like [MW = 34.36 kDa]

No. of times detected



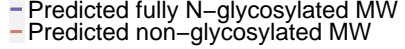
log(intensity)



Values from



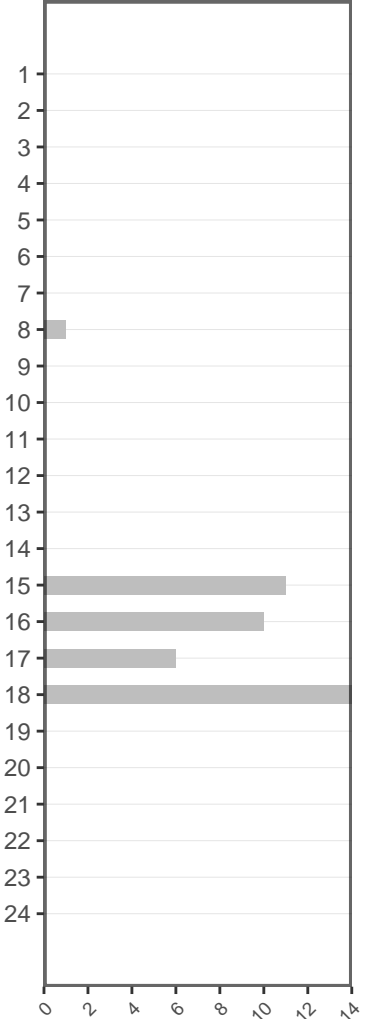
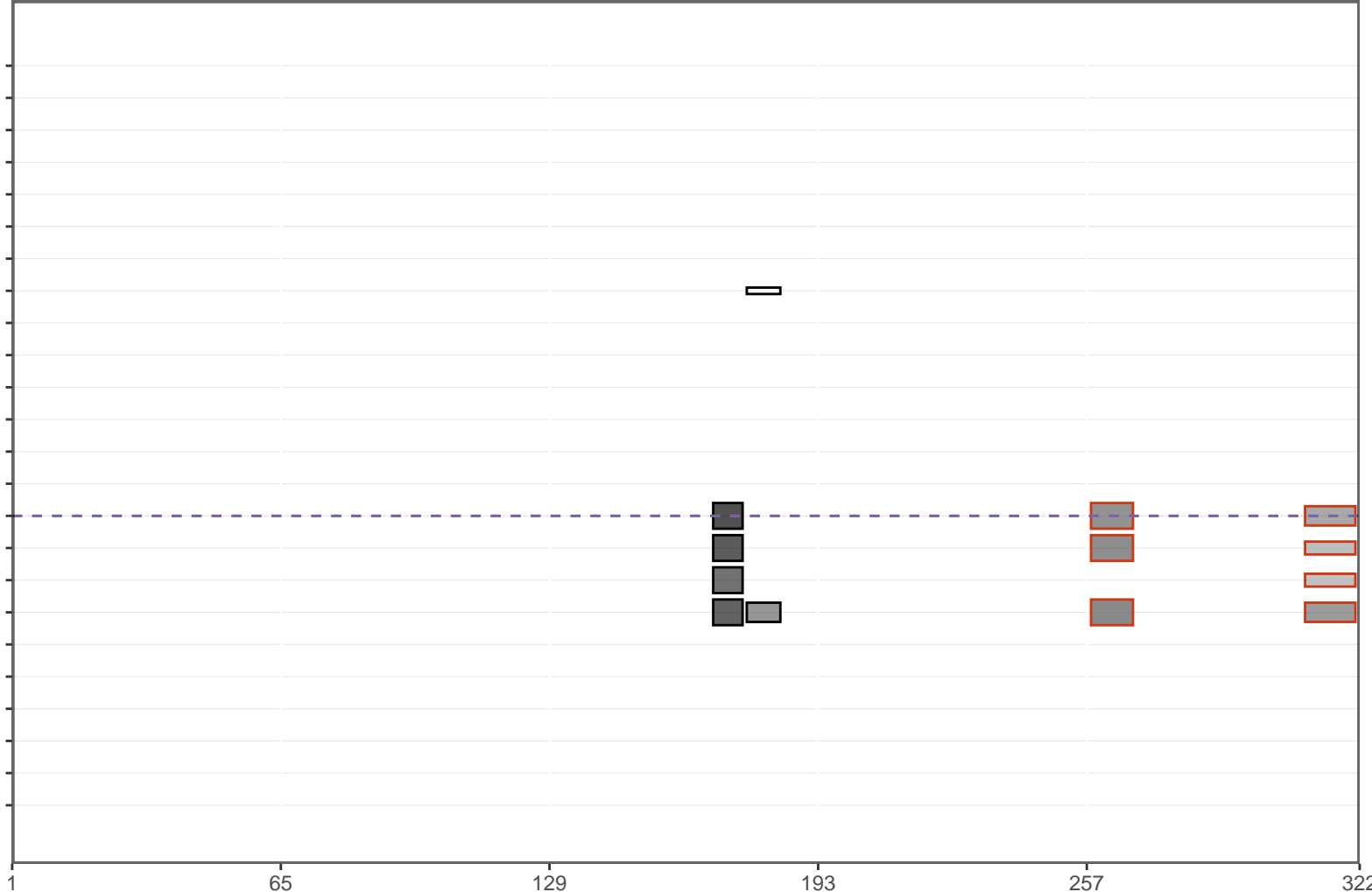
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

EEISNFTSQVSSLLWLVDRSDVVEHLKQLDCEILRRKKEALPQPPPPAHTPLLGGVYHPSVGFSPPPPPAAPPVQIPAPSPAANKPSDSVPLPKGMAGTFYRSPGCEPPIVKGDKVQKGGVLCHEAMKLNIEIEADQSGTIDIFAEEDGKSVSDMPLFVKNP

NbL10g08340.1 thioredoxin_F-type_chloroplastic-like [MW = 24.56 kDa]

No. of times detected



log(intensity)



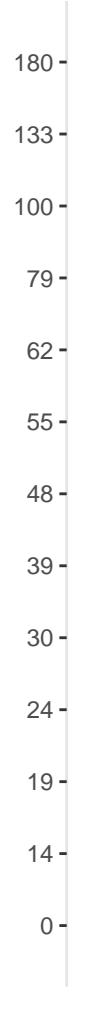
Values from



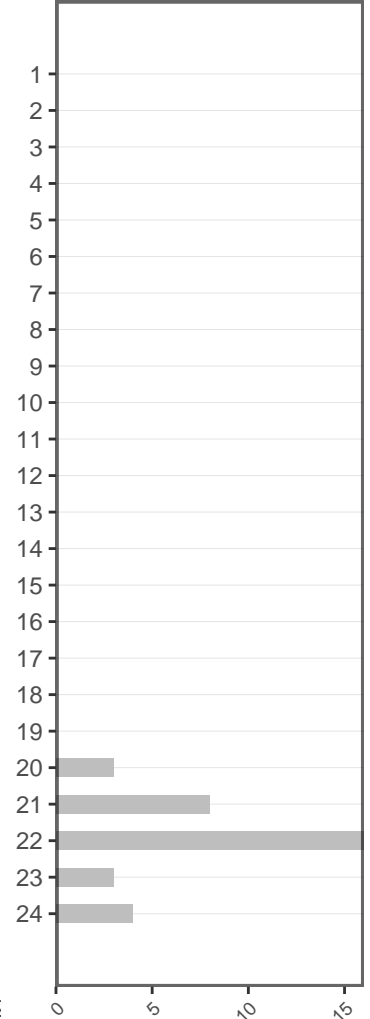
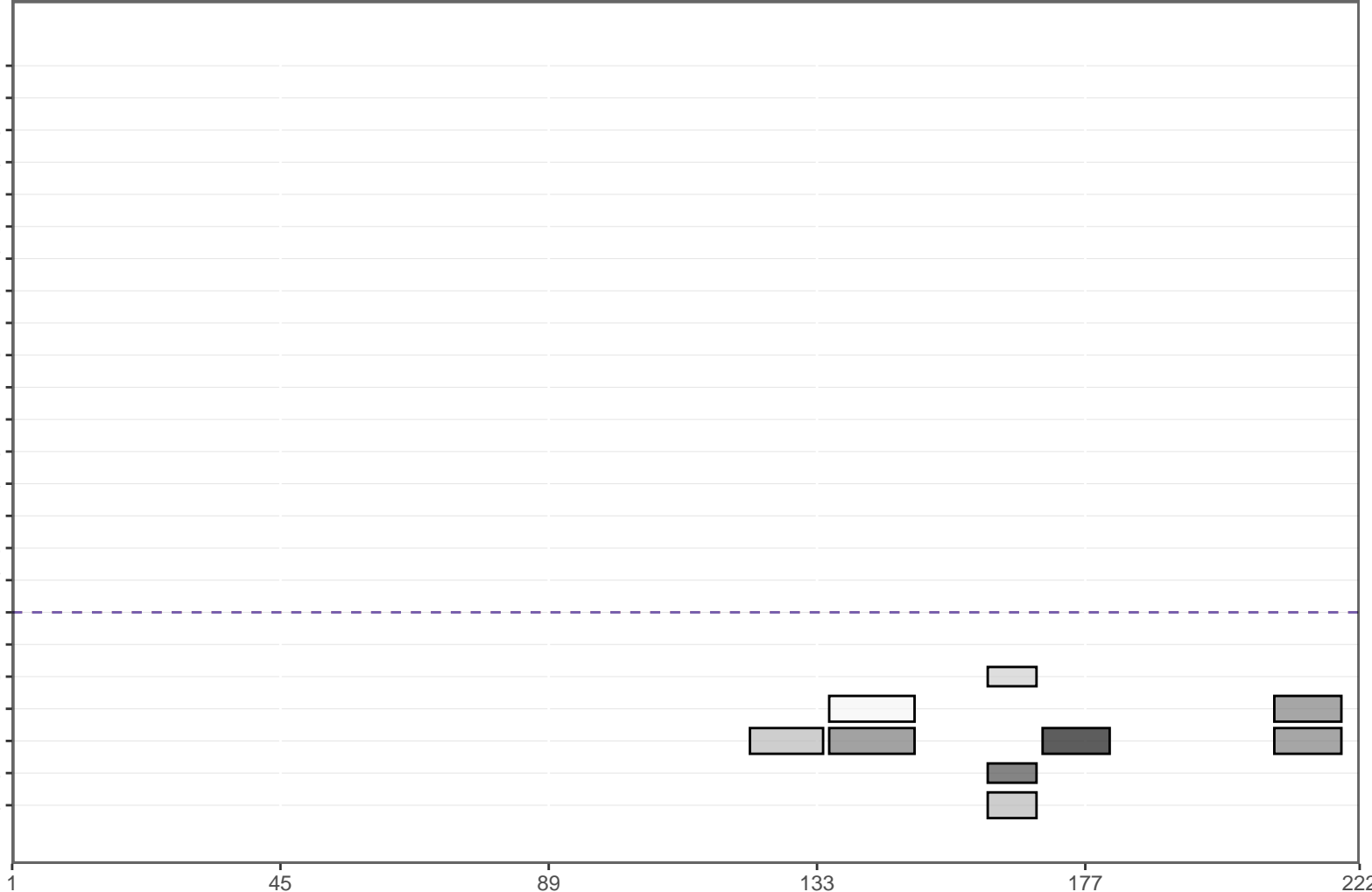
MW indication



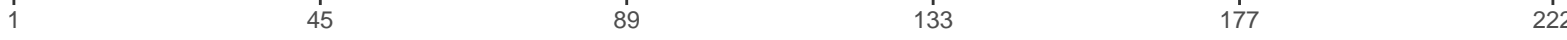
Molecular weight



Gel Slice



Protein length

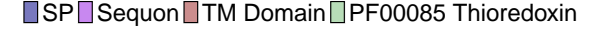


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

CVKCSDDATATTVTLGGVTEVQKDFWPIVEAAGDKTVVDMYIQWGGPKVIAPKFDLSKNYNDVVFLLDGNQDNRPLAKELGKIVPTFKLKNKVVKEVTGAKLNLAAIEDVRS*

NbL10g08330.1 T-complex_protein_1_subunit_gamma-like [MW = 63.27 kDa]

No. of times detected



log(intensity)



Values from



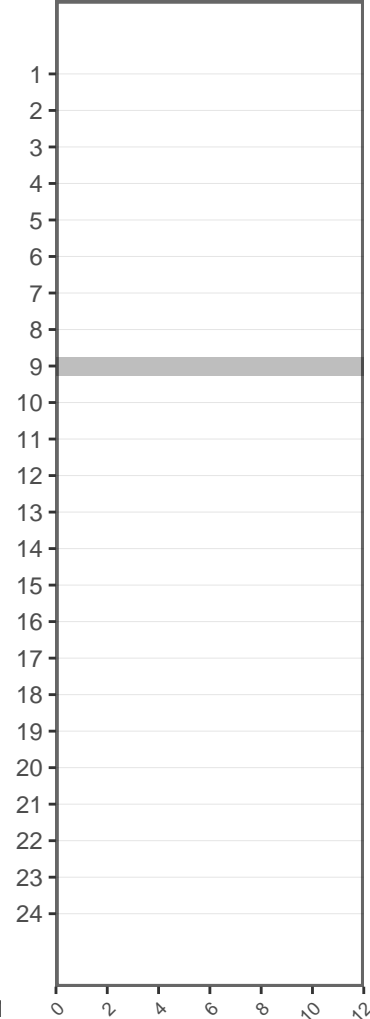
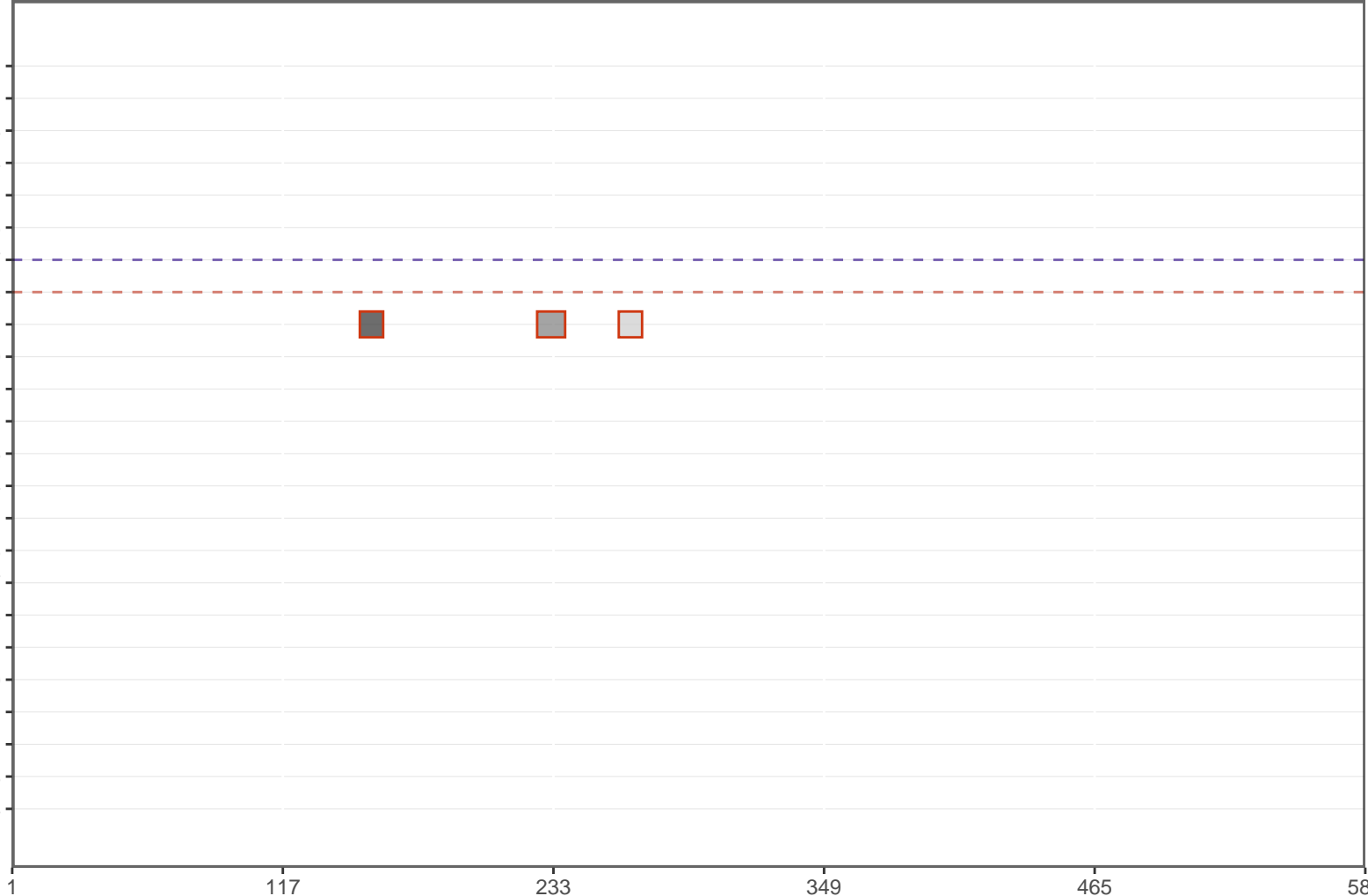
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

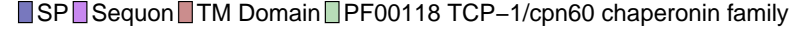
1 117 233 349 465 581

Protein length



Pfam domains

Pfam Description



Protein sequence:

IAELLREEDVTYLLKMEEEYHENMAGLRFKPKDVTTEKGLSPLASHYLSKAGVTAIRRLRKTDTNNRIAKAGGAVVNRPDLEQESDVTGAGLFEVKKIGDEFFTFVDDCKDPKACTLLRIGASKDLLNEVERNLDGAMSVARNIKHPLVPGGGATELTVSAMLKGKSSVEGIEKWPYEAAMAFAPRFTLAGNGGVNVRTMTALGGKHASGENAWIGDNGTGEADMKEHKWDSYEVKAGAFKTAEEAAGLLLRIDDDVSGIKKKGAPGAGRGGSKPKYIEEGDADND

NbL10g08270.1 10_kDa_chaperonin_mitochondrial-like [MW = 10.46 kDa]

No. of times detected



log(intensity)



Values from



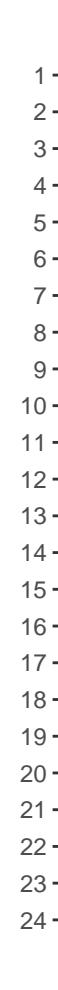
MW indication



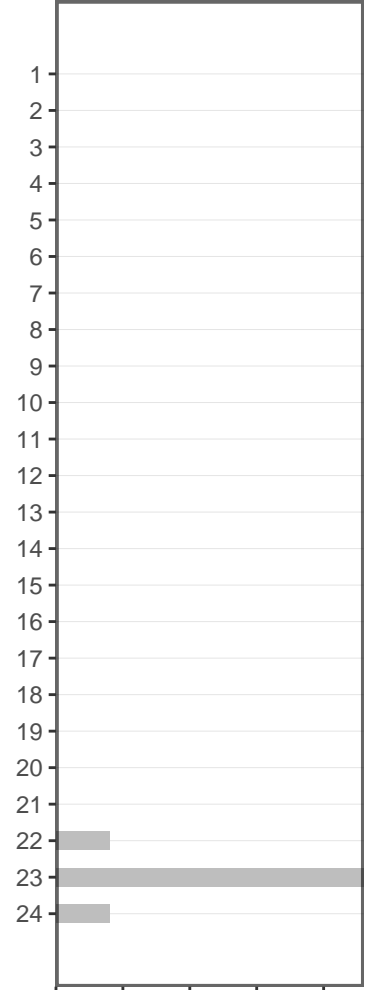
Molecular weight



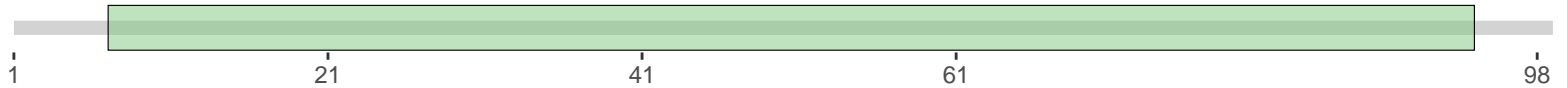
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISQKVAIVGPGLRBKSGNLPTAWKEGDTVLLPEYGGTGVKLGKEFHVYRDEDILGTLHD*

NbL10g08140.1 SAL1_phosphatase-like [MW = 15.48 kDa]

No. of times detected



log(intensity)



Values from



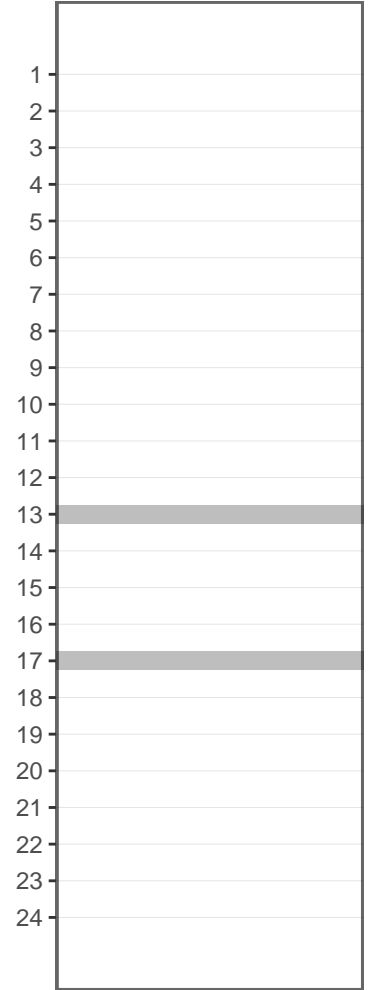
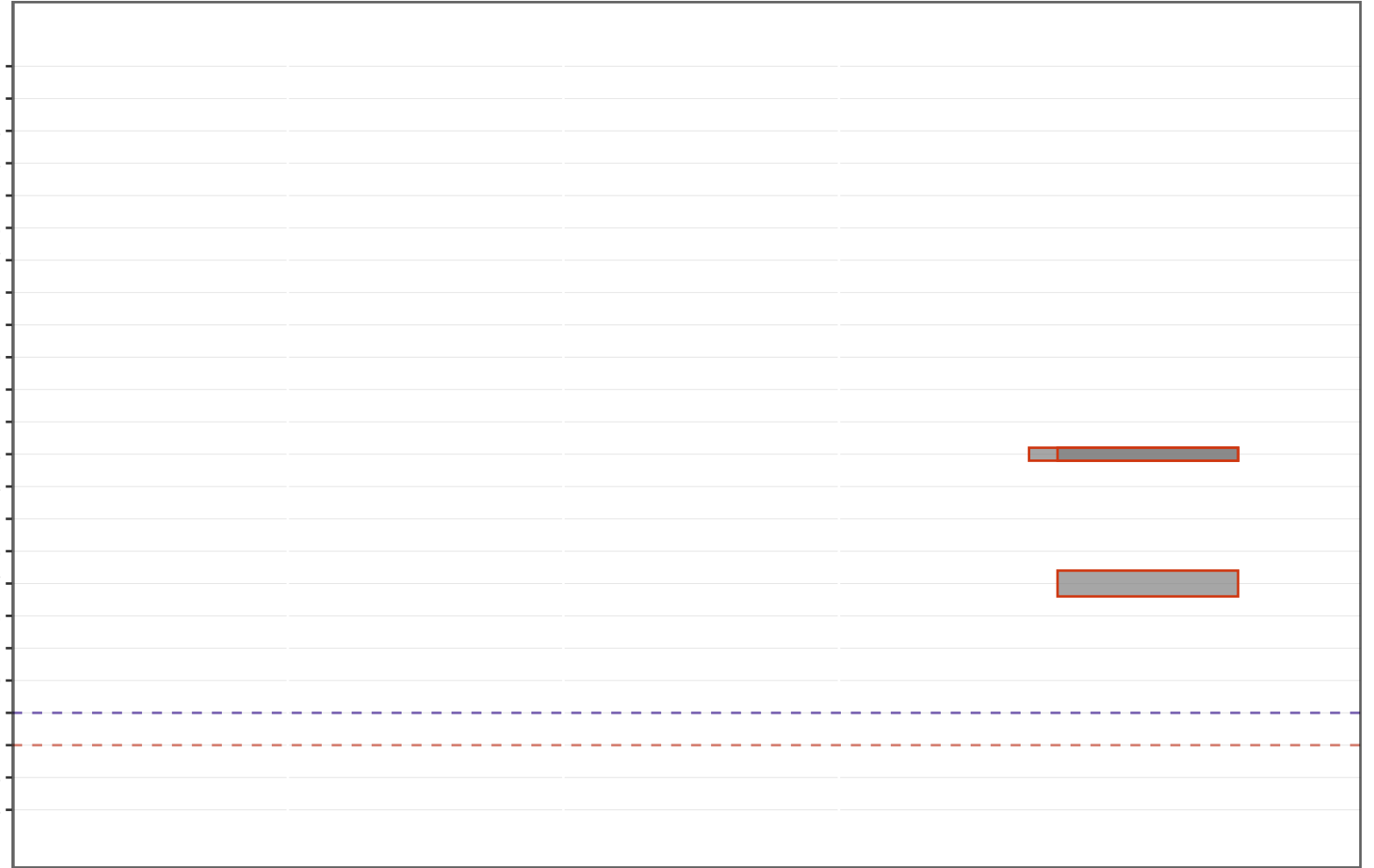
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length 1 30 59 88 143

Protein length



Pfam domains

Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

KASIKTLRTSSMSYDKGLAAAKKAASLAARLGGKVKQKALLGADVDQSKDKPVTVDYGGDAVVSVLQKELDSASSELVAEE

NbL10g08030.1 acyl-coenzyme_A_thioesterase_13 [MW = 16.45 kDa]

No. of times detected



log(intensity)



Values from



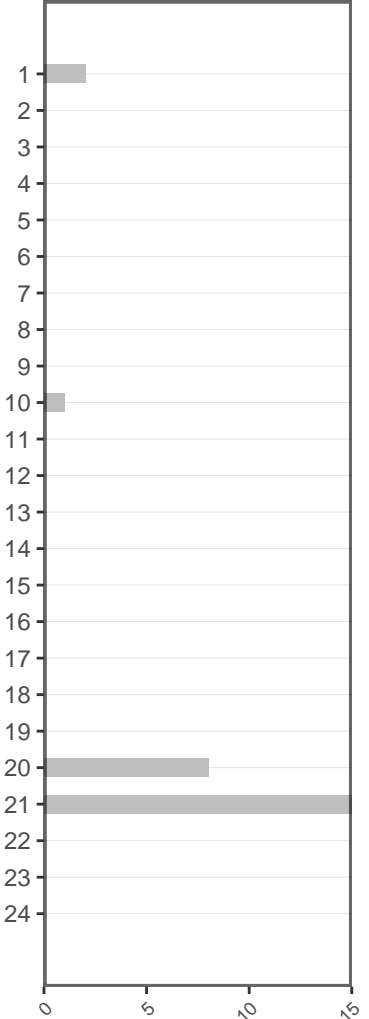
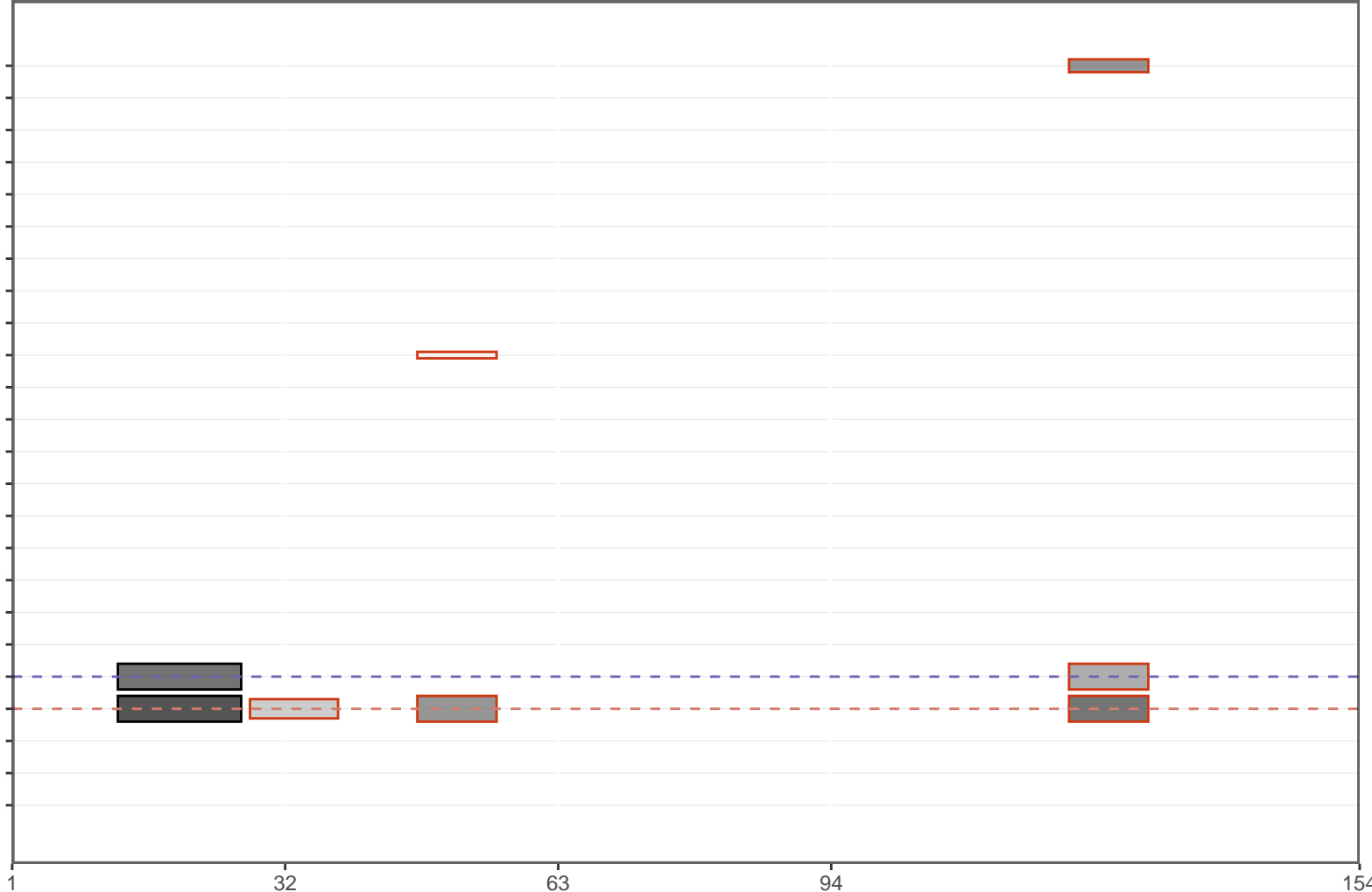
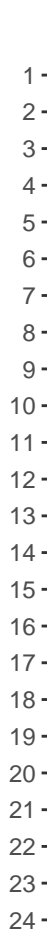
MW indication



Molecular weight

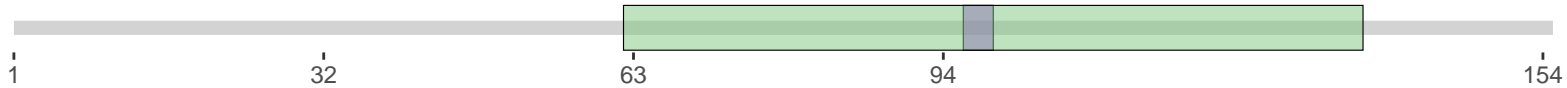


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FLHGGATASLVDLGSAWHTVGAFTGVSEINVSYLDAAPVGEIEVEATVLRVWKTGVVSEVLRKKEKQKIVRGRHTKYLVANSKLV

NbL10g07990.1 4-hydroxy-tetrahydrodipicolinate_synthase_chloroplastic [MW = 39.91 kDa]

No. of times detected



log(intensity)



Values from



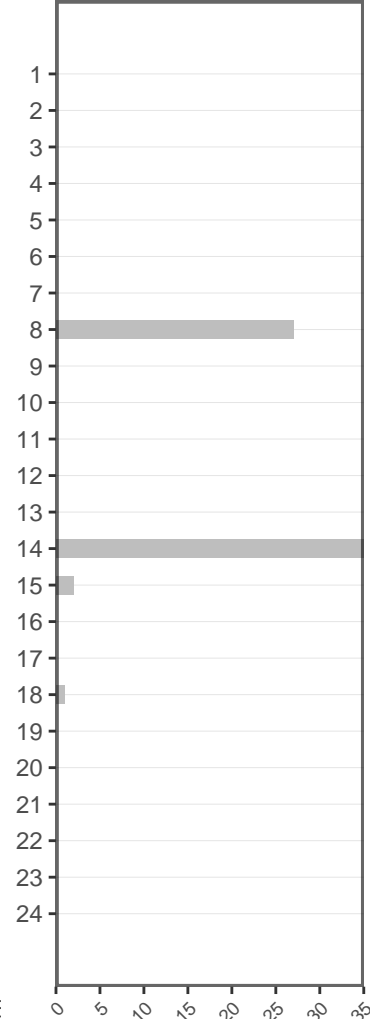
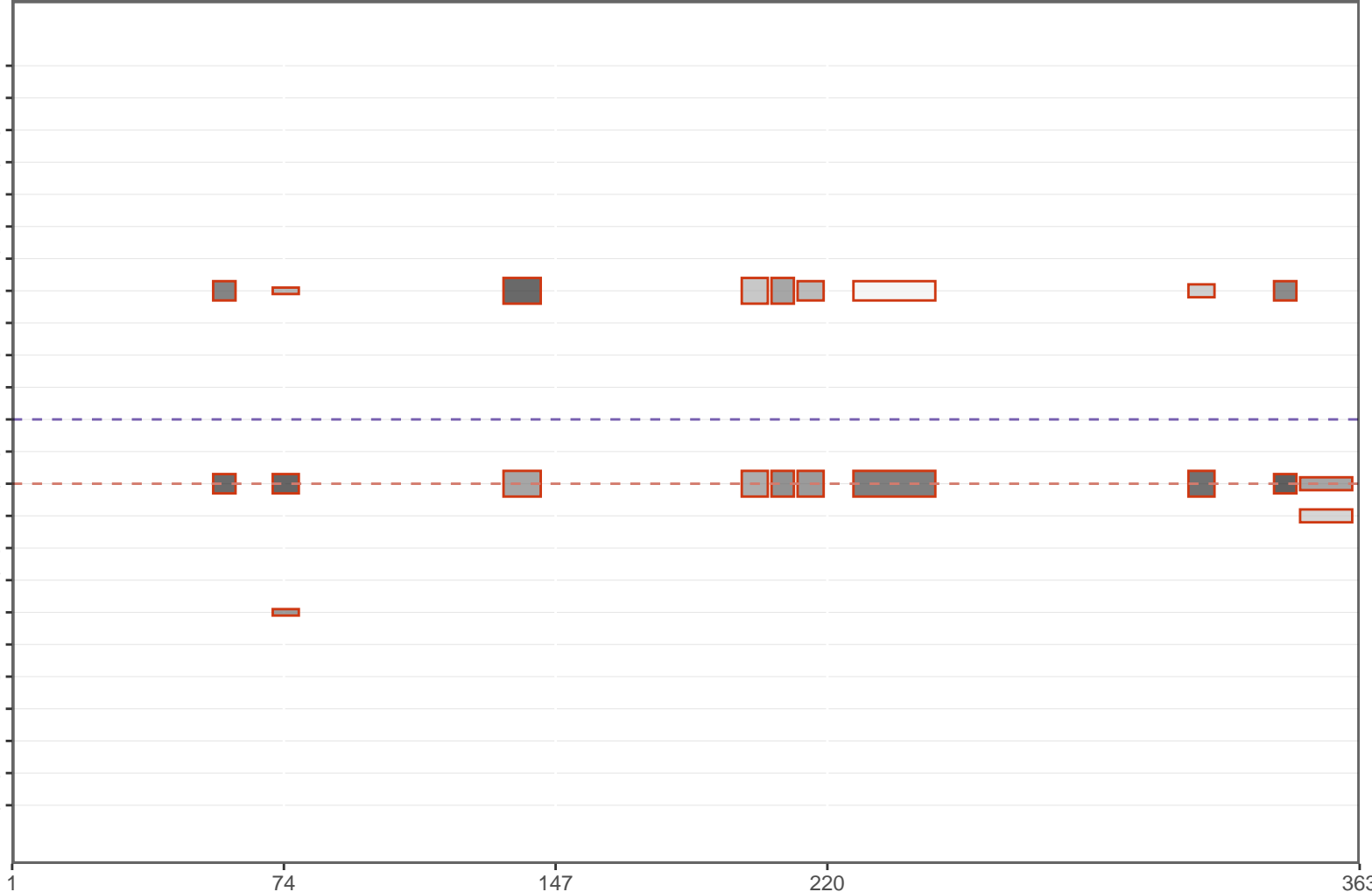
MW indication



Molecular weight

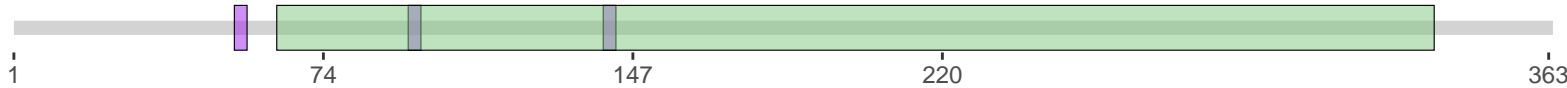


Gel Slice



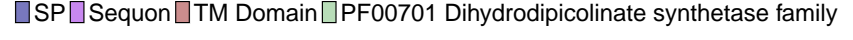
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CTSLLEGLSHFESVLPMPGPTIYNVPSRTGGDIPRRVIGTMAKNPILAGVKECVGNDRVEGQVTSNGIIVWGGNDDEGHVSRWDVYGATGVISVFNLPGLMRELMFGGKLNALNKLMPLEWLFHEFNPIALNTALQGLGVVRPFRPLPYVFLTKEREKRFVEIWEKIGRENFGERDVGVLDDNDFLARY*

NbL10g07980.1 probable_methyltransferase_PMT26 [MW = 89.25 kDa]

No. of times detected



log(intensity)



Values from

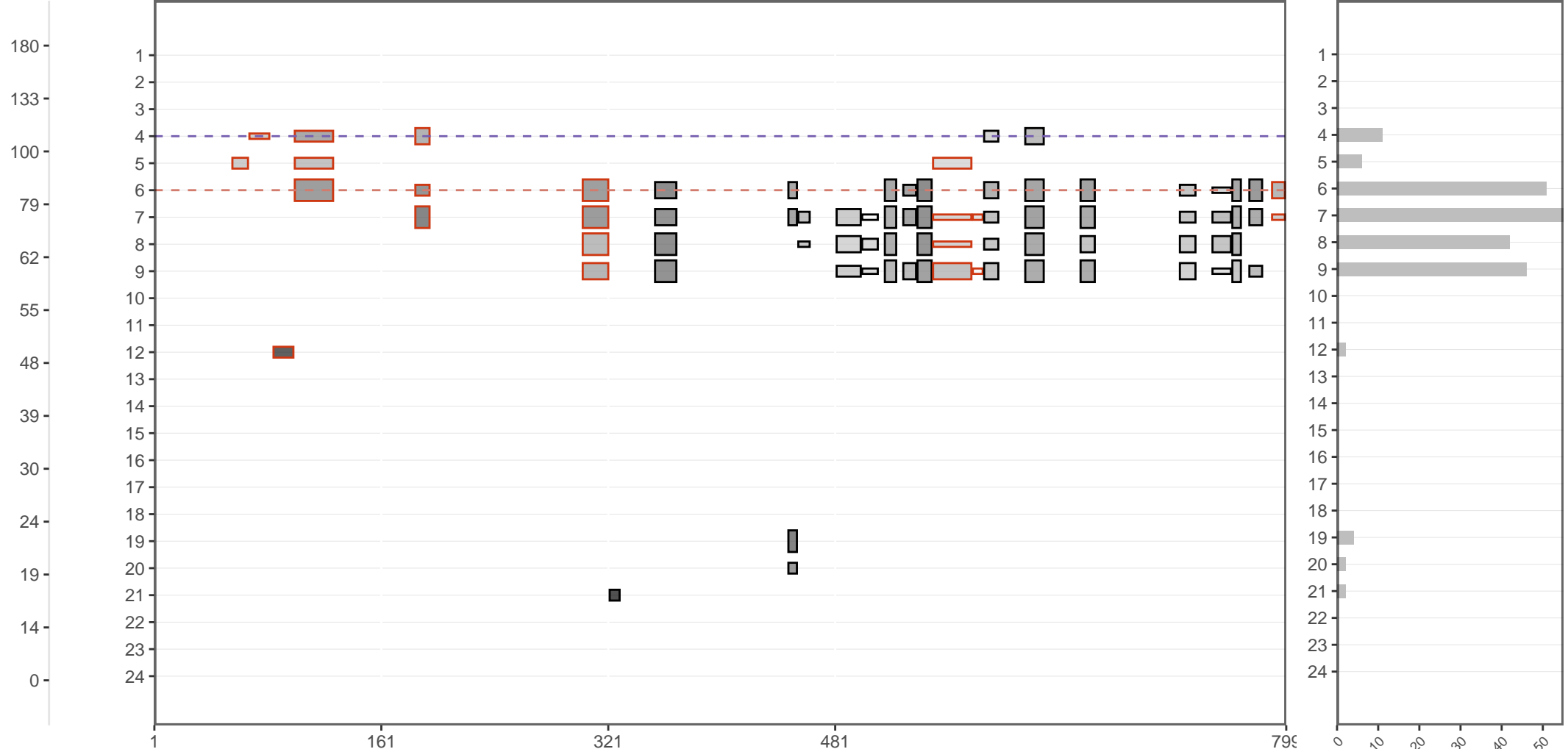


MW indication



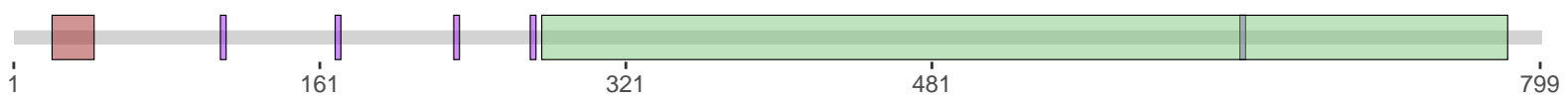
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

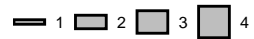
- SP
- Sequon
- TM Domain
- PF03141 Putative S-adenosyl-L-methionine-dependent methyltransferase

Protein sequence:

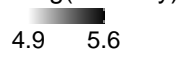
/PDAIWGKRTKRVLDVGGVASFQGGYLFDRDVLAMBLAFKDEHQAQVGFALERGIPMSAVMGTKRLRFFSRVFDVYHCAQRGRVFWHEGGKLLLELNRLRPGGLFVWSATPVYKGLPEQVDEWEAMKILTKAMGVELISKTKDRVNGVGVAYWRKPMQNECEQGRSEGAPPLQGESDDPNAAWYVPLGAQLHKAPWATERGSGQWPFESWPARLSKSPYWLSSQGVVYGGKPAPEDTADVEHWKHVYKNSVINGMGINWSTVRNMDMRAVGGFAALRDLVW

NbL10g07910.1 proteasome_subunit_beta_type-6-like [MW = 25.18 kDa]

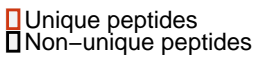
No. of times detected



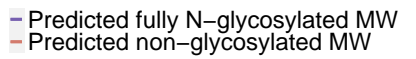
log(intensity)



Values from



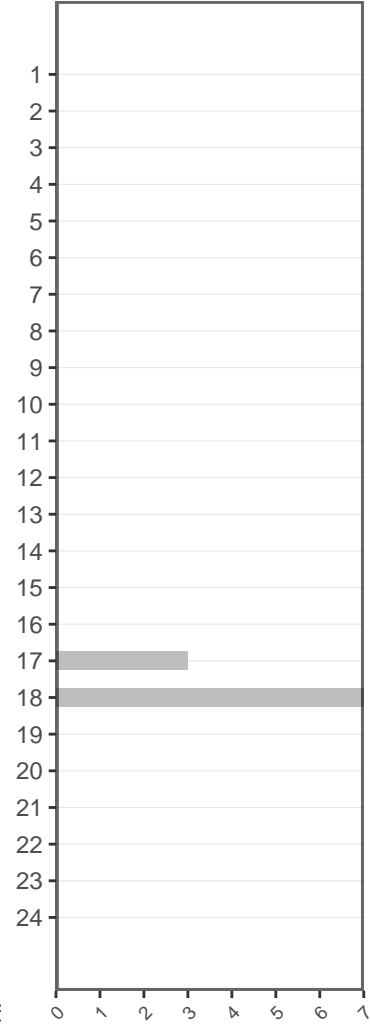
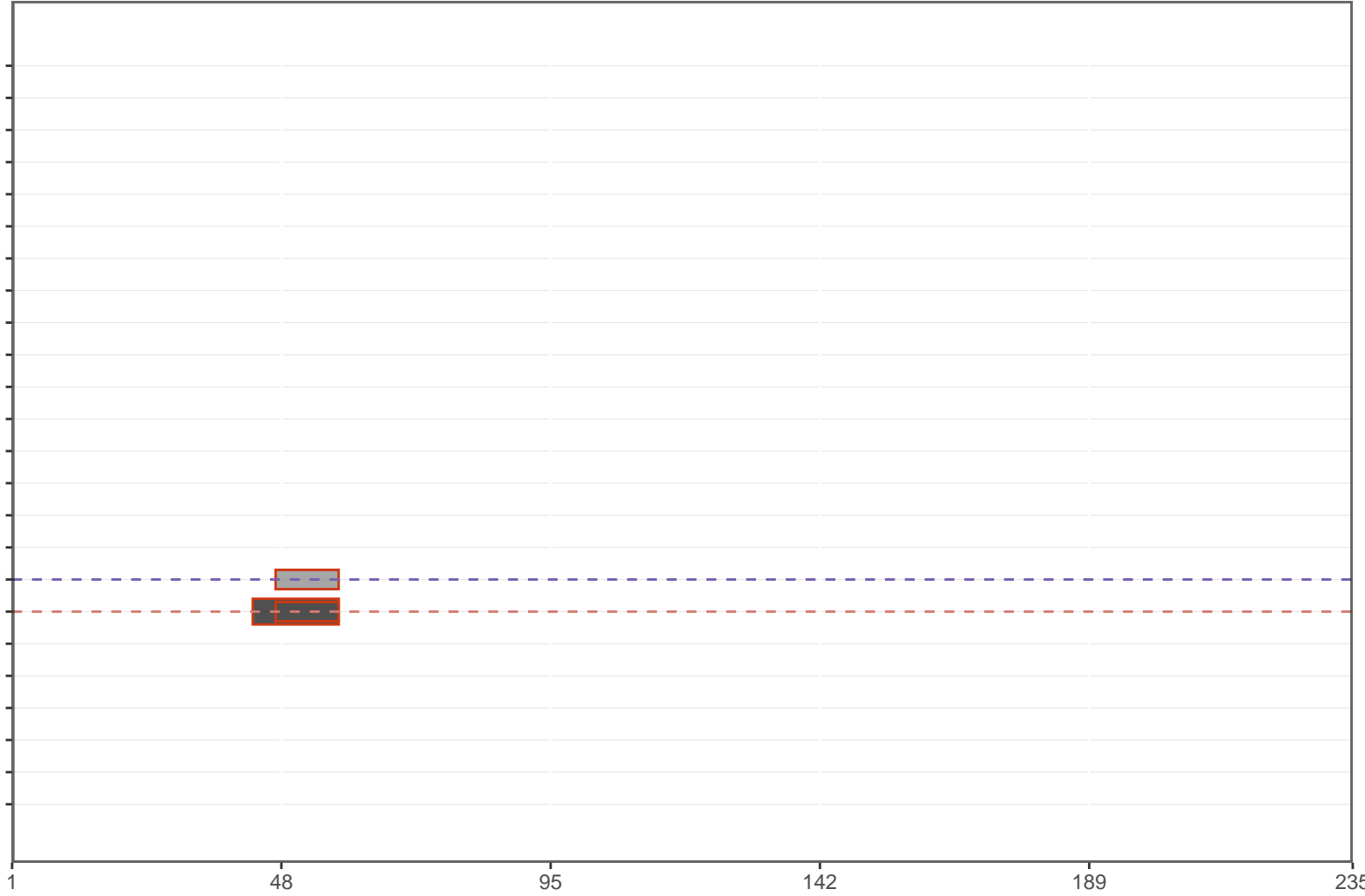
MW indication



Molecular weight

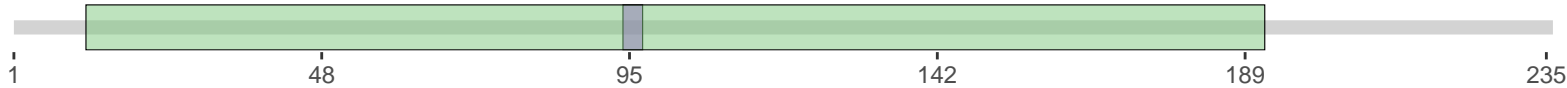


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

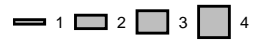


Protein sequence:

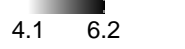
DRLOTGMIGGWYDKYEGGKHYGFLGGTVLEQPFANGSGGSSVLYGFFDQAWKEGMDGEEAEKLVITAVSLAIRDGSAGGVVRTVTINKDGATRIKEYPGDGLQLWHEELEPNLLELDVYVASESPDPMVY

NbL10g07690.1 protein_usf-like [MW = 26.45 kDa]

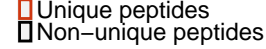
No. of times detected



log(intensity)



Values from



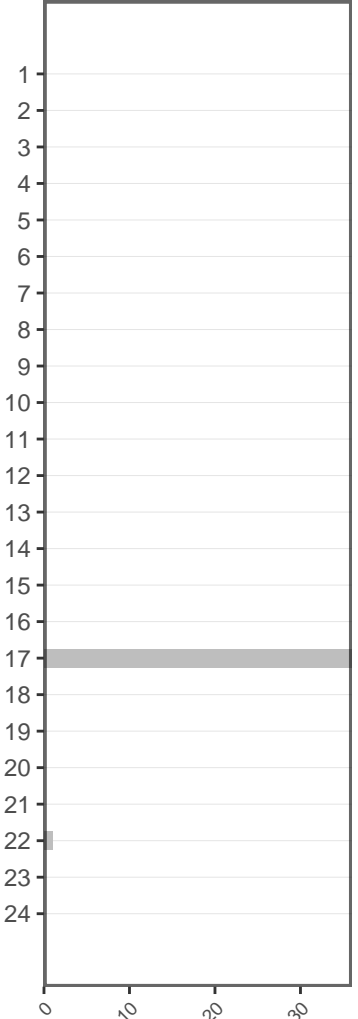
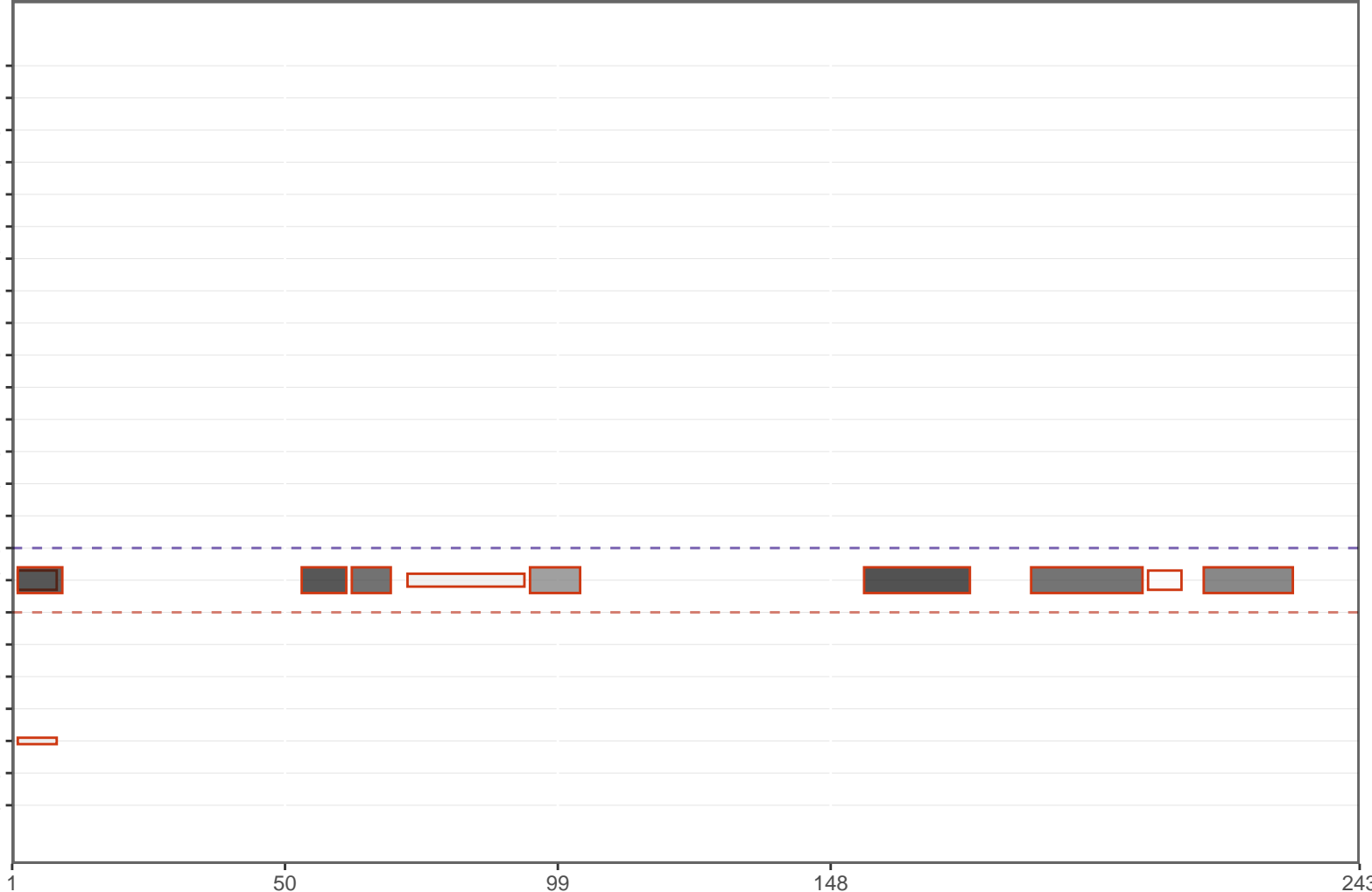
MW indication



Molecular weight



Gel Slice

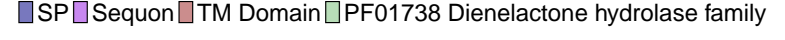


Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

GVYGYCMGGALAMSSVLVFGVDVAWFYGVFSPPELADPTAKAFVQAHFGEDDDGFVGFSDVKTGKALEEKLKTSQVPHVEVYFYPQTGHAFMKNKPEGVERRIKKMGMPQVEDAAVEQAWTRFRSWMRFLSAI

NbL10g07570.1 cytochrome_b561_and_DOMON_domain-containing_protein_At5g47530-like [MW - SP = 41.48 kDa]

No. of times detected



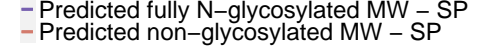
log(intensity)



Values from



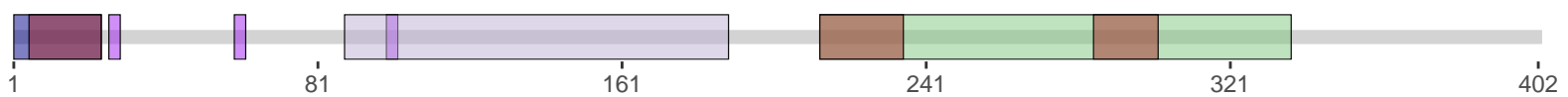
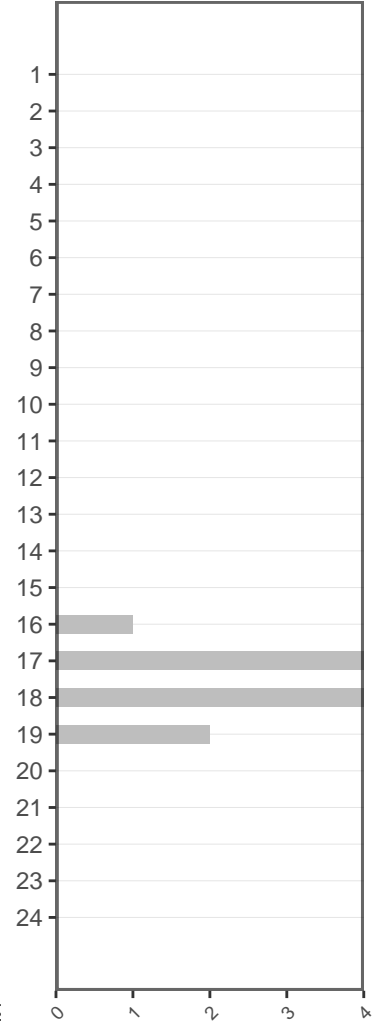
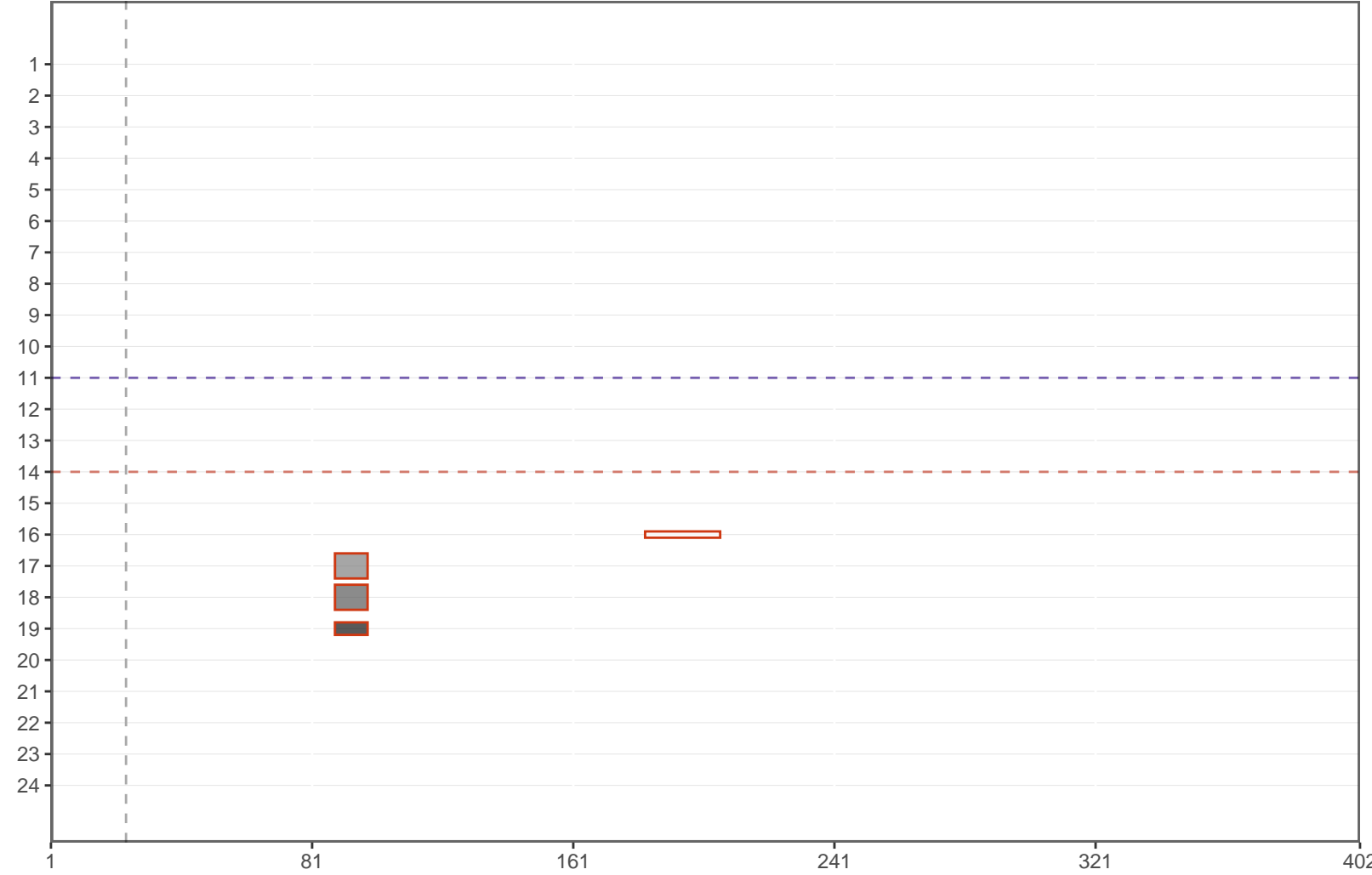
MW indication



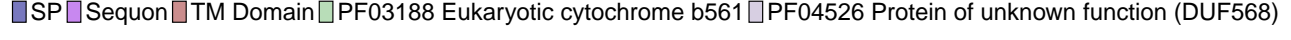
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

IDFASQTSAAAGGGSASSRRRRNTHGVLNNAISWGVMMFMGAVFARYLVKFKSANPWFYLVHAGDTSAYAVGVAGWGTLKLGSDVGVKFNTHRNIGTLFGLGLGVFALLLRPKFDHVKYRLVWNIYHHTIGVTVILSINVFEGFDALNGQKYVWRVYGVVIALGAAMMLEAFTWVIVKRIKTSVSDKYRPNNGANGVNAVANREV

NbL10g07550.1 thymidylate_kinase-like [MW = 28.98 kDa]

No. of times detected



log(intensity)



Values from



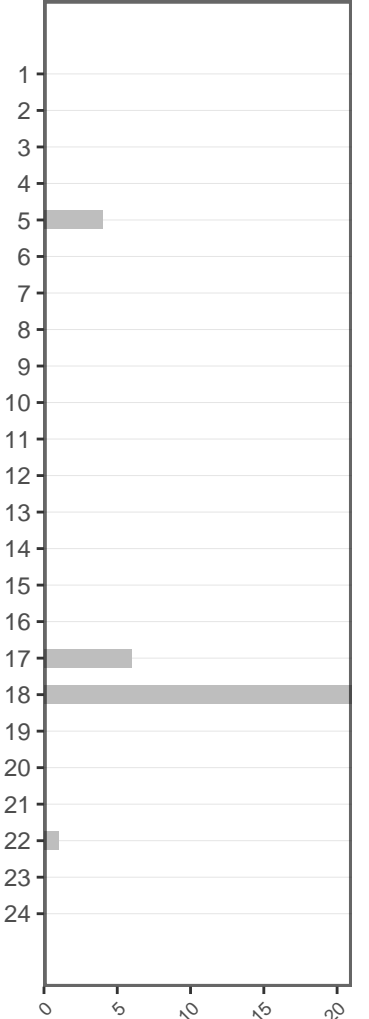
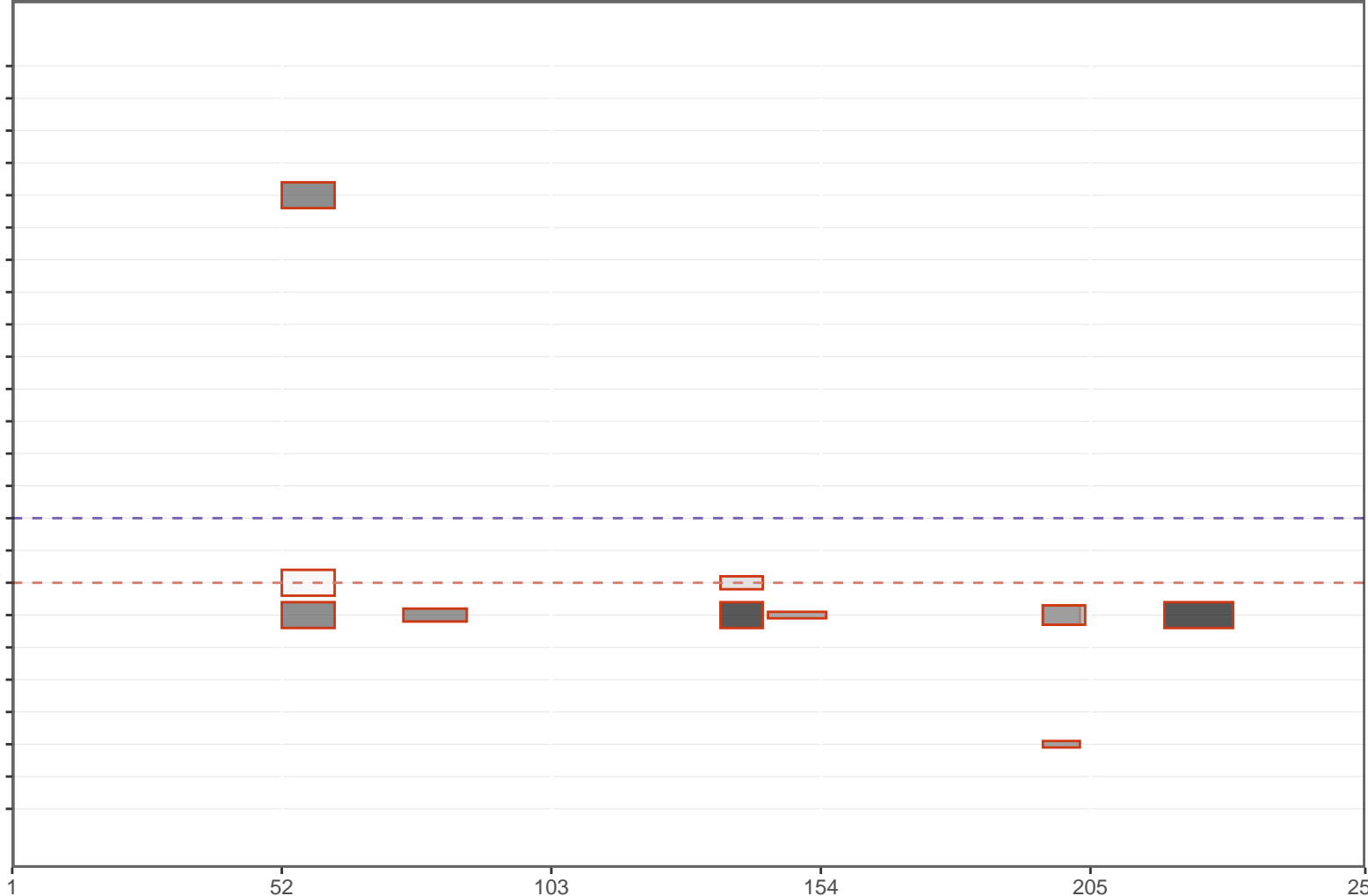
MW indication



Molecular weight

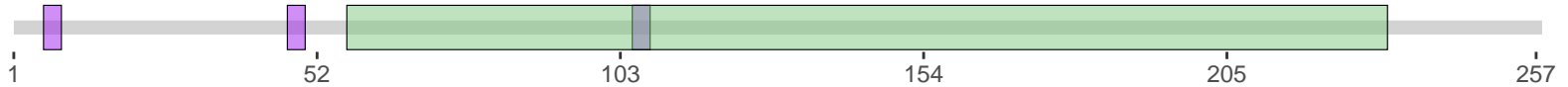


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

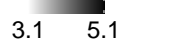
IHLFLSANRIVYKRMIMEDKLRSGTTLVDRIYVYSGVAFBSAKGLDIEWKAPKPEIGLLADLVYLDISPEKAAERGGYGGERYEQLFQKKVAKVYSLTHDSSKWKVWDATLPLVEDIEKLRREVLDSEMTQKQKPLSQWSP

NbL10g07470.1 uncharacterized_LOC109241615 [MW = 13.13 kDa]

No. of times detected



log(intensity)



Values from



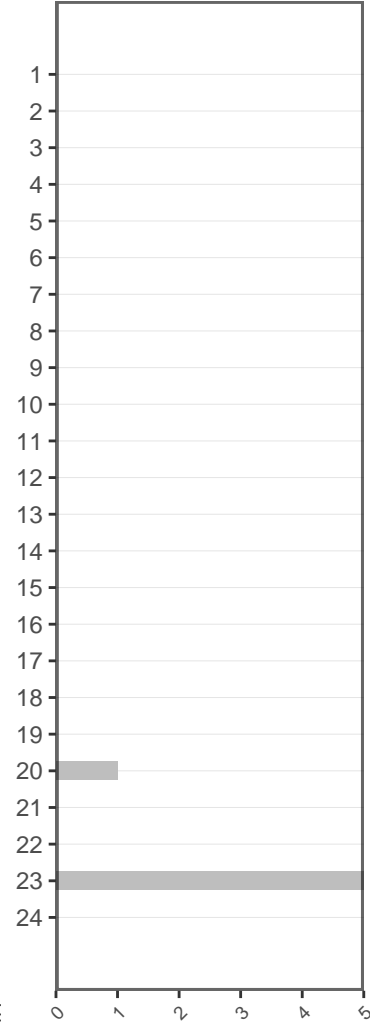
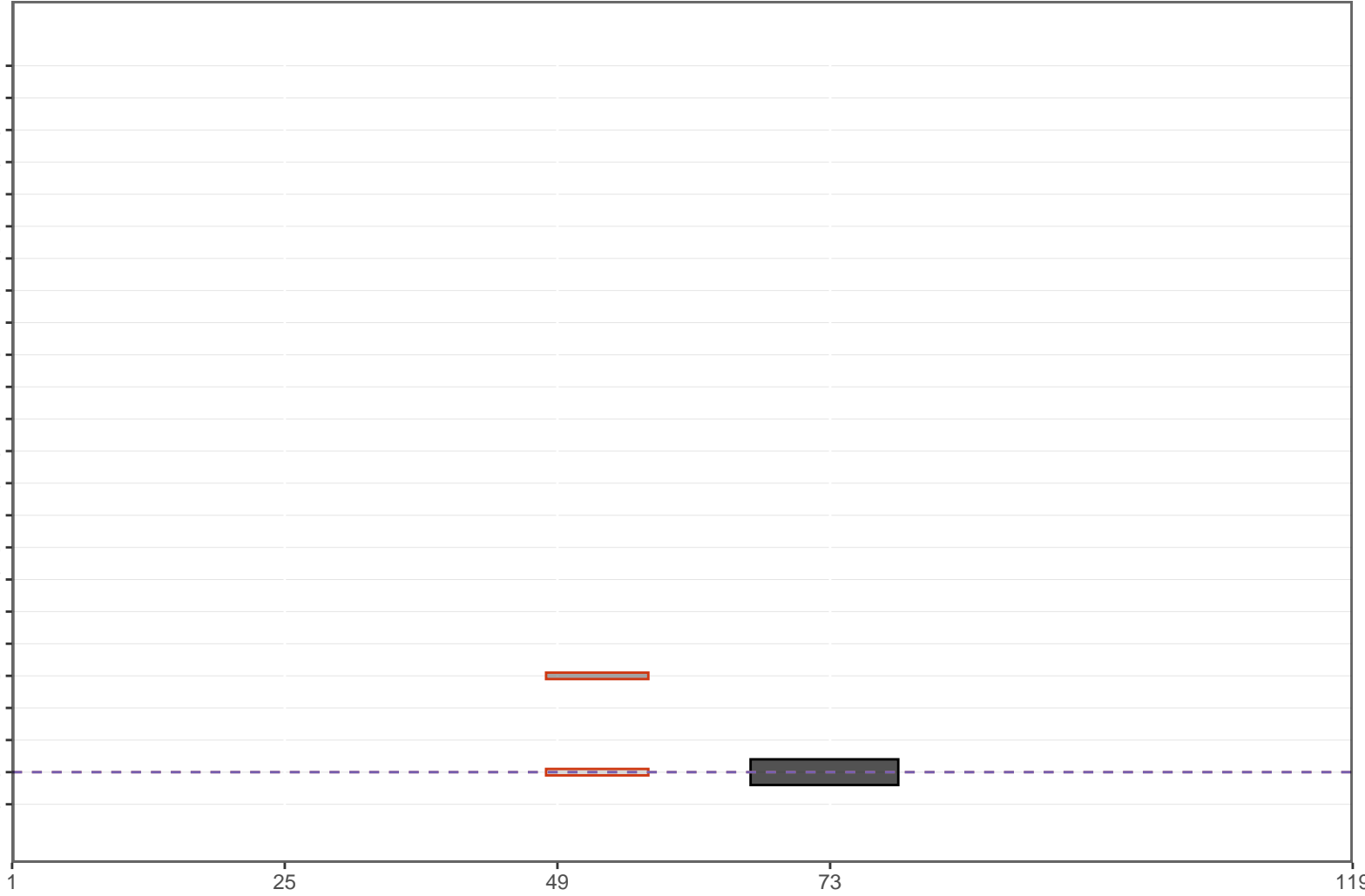
MW indication



Molecular weight



Gel Slice



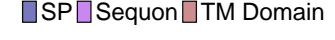
Protein length



Pfam domains



Pfam Description



Protein sequence:

AKLGGEEGDVKKDKKFFITKEGEPEGWQTAGERAGENPMMTFLPVIHFGMSTPFEVLAVAFANGWIKVPIR

NbL10g07460.1 nitrile-specifier_protein_5 [MW = 35.43 kDa]

No. of times detected



log(intensity)



Values from



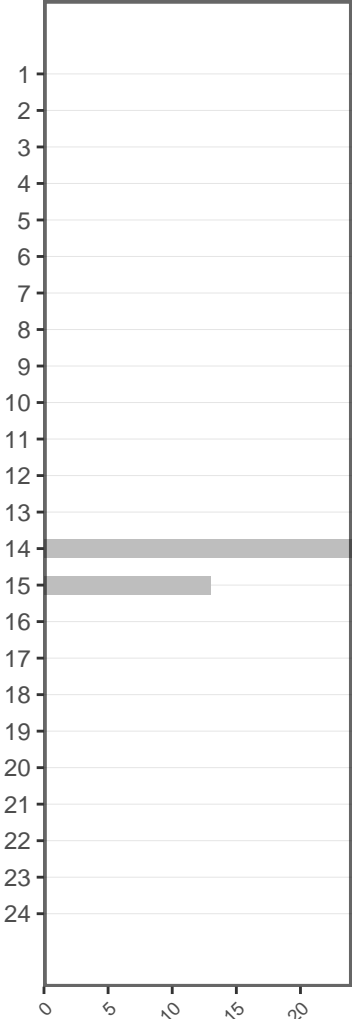
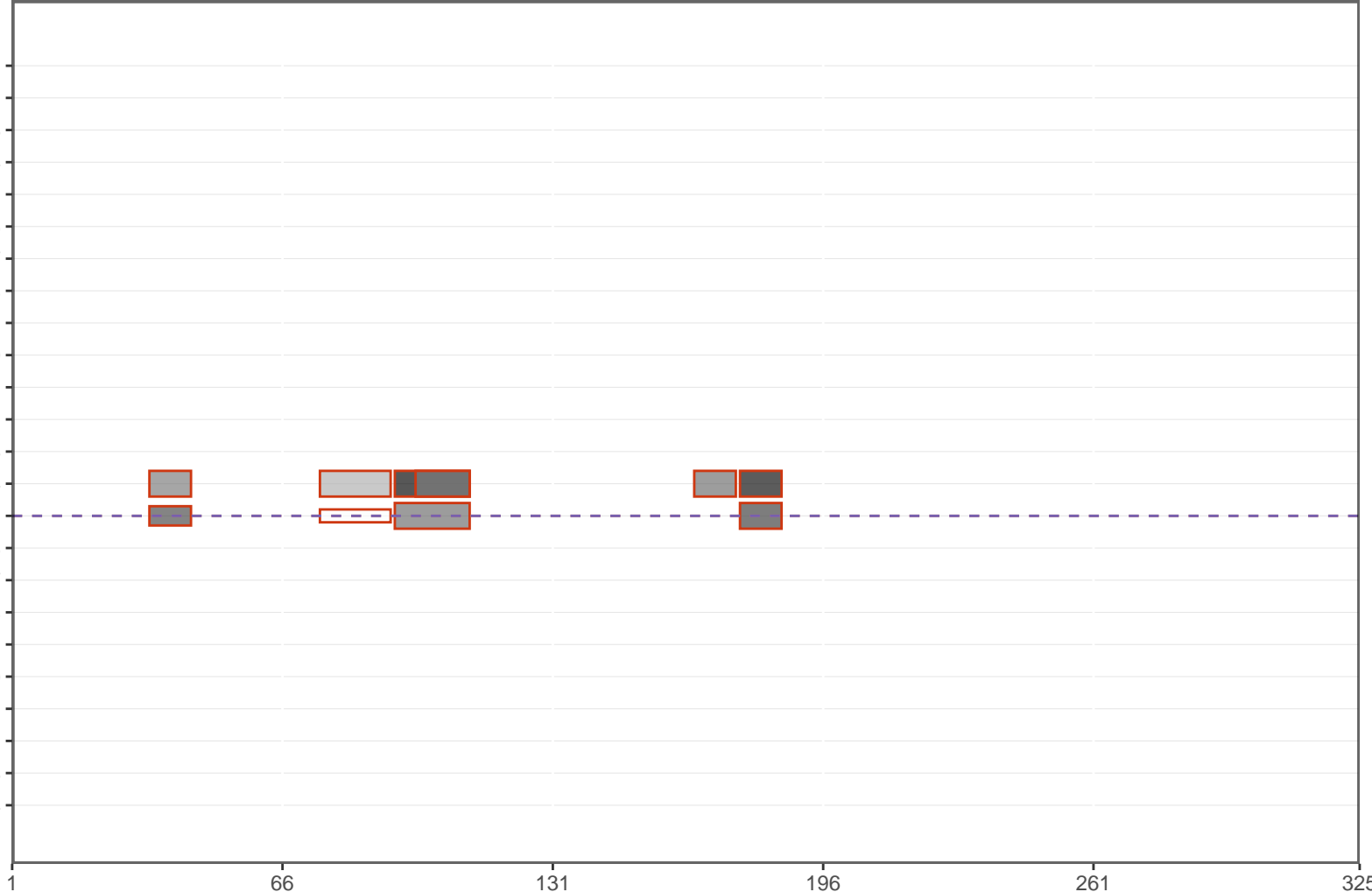
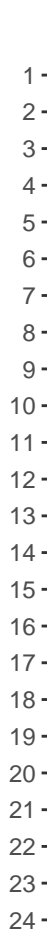
MW indication



Molecular weight

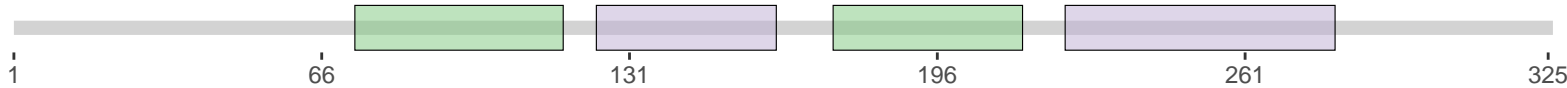


Gel Slice



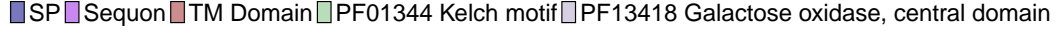
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SDLWAYDVIKXVWFFVPGENCKPRGGPLTILGKMWVYGFSGDELDDVHYFDAIEEKWVQVETNGEKPTARSVSTVGIQKIFVYGGEDIPDLGHLGAGKFGSDVYALDTETLVWKGWDSGDHPGPRGWGAFASGRRRDEEGLLVYGGNSPNDRLGGFFFTPLVET

NbL10g07330.1 nitrile-specifier_protein_5-like [MW = 38.52 kDa]

No. of times detected



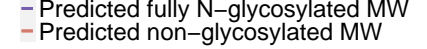
log(intensity)



Values from



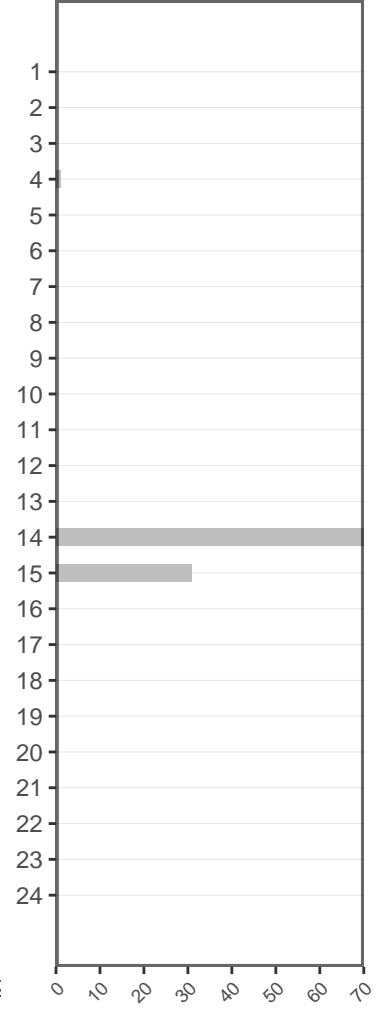
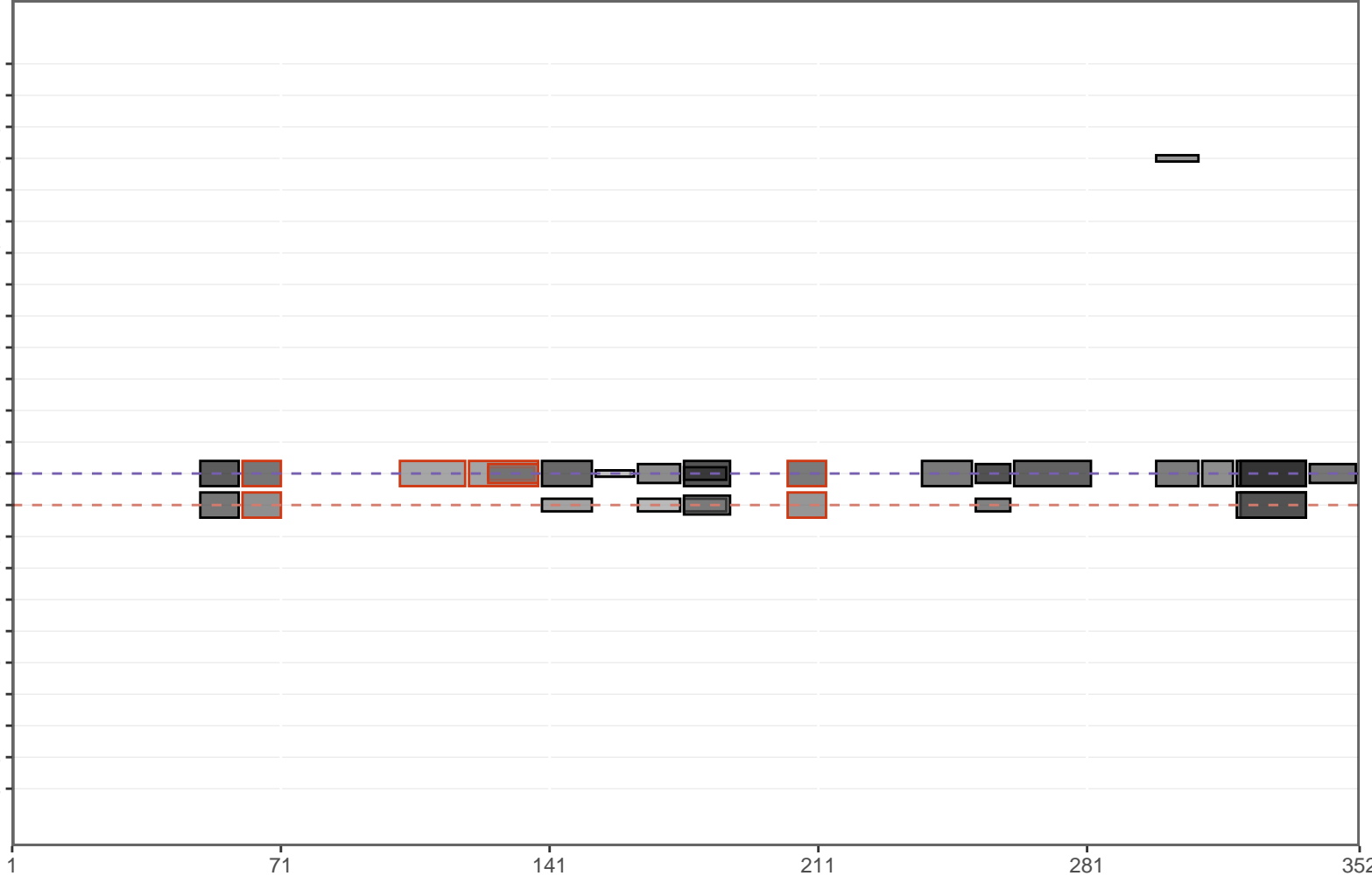
MW indication



Molecular weight

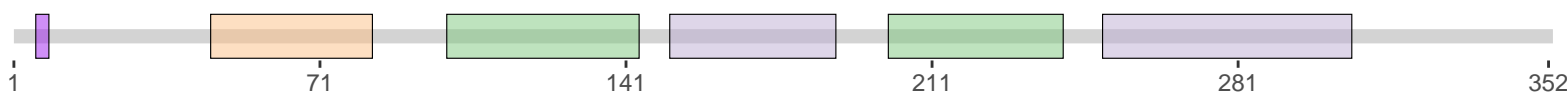


Gel Slice



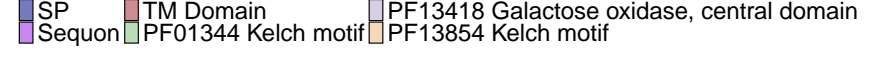
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

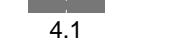
RIVYFGCGQAGRLSDLWAVDAVKKKWEFFVPGENCKPRGGPLAVLGGKIKWVYVFGSGDELDDVHYFDAEENKVVQVETNGEKPTRSVFSTVGGIKYIFVGGIDPDLGHLGACKFSGDVALDTETLWKGWIDSGDHPGPRGWAFAGRRDDEEGLLYGNGSPSNDRLGGIFFTFLVET*

NbL10g07320.1 4-hydroxyphenylpyruvate_dioxygenase [MW = 48.97 kDa]

No. of times detected



log(intensity)



Values from



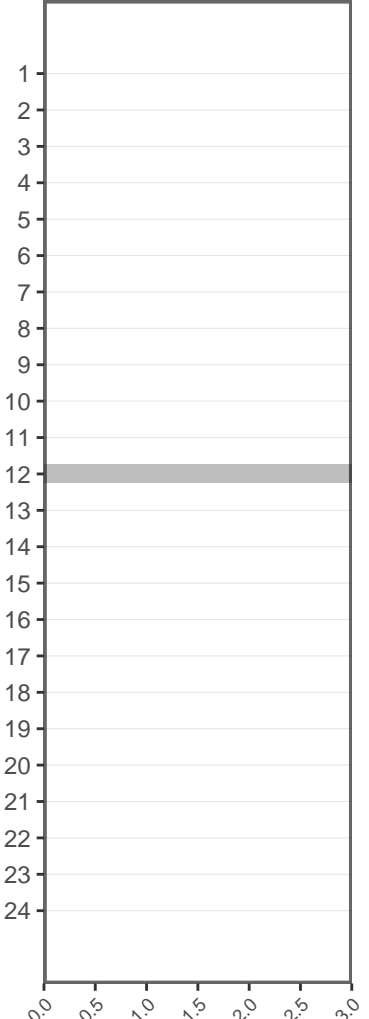
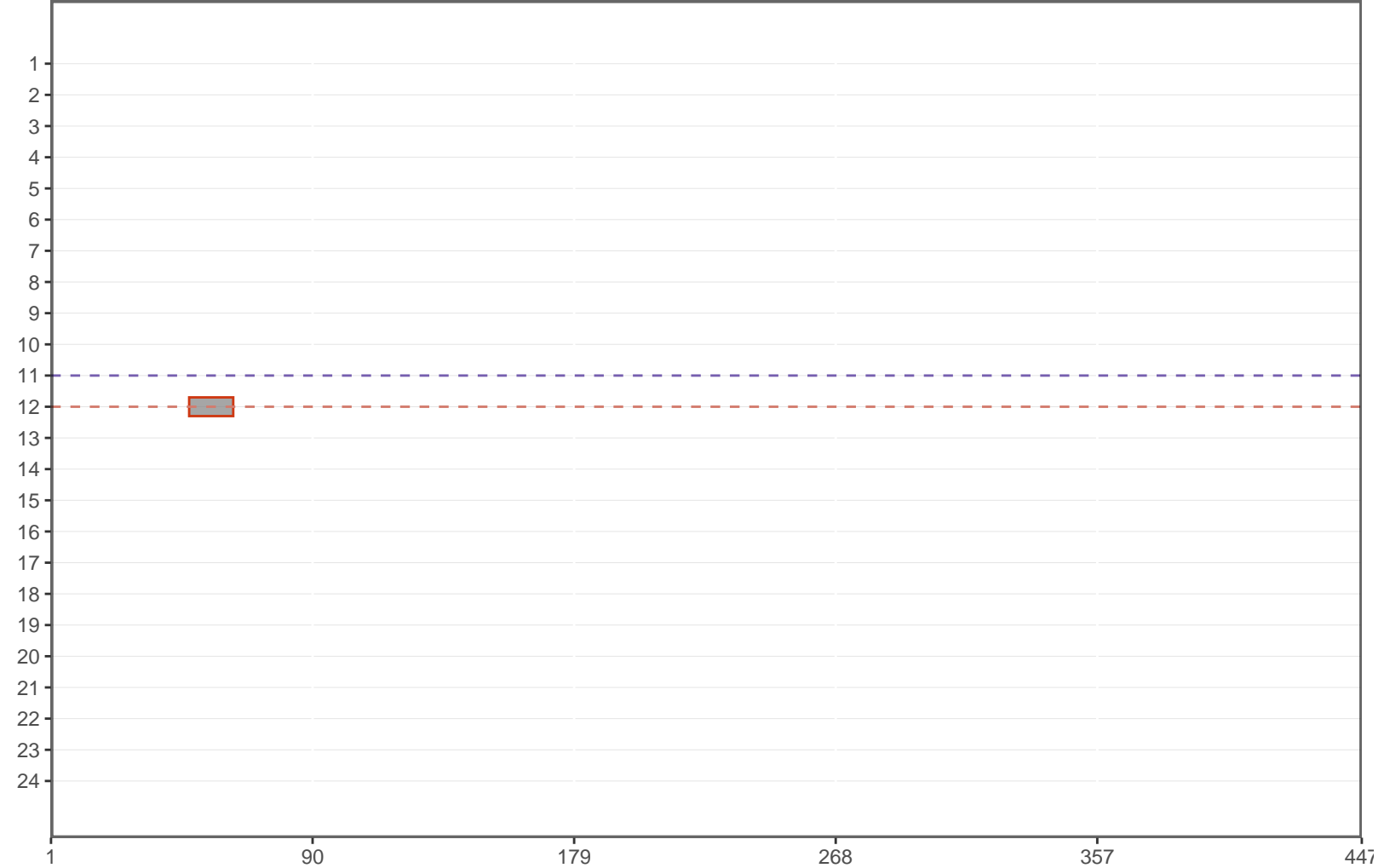
MW indication



Molecular weight

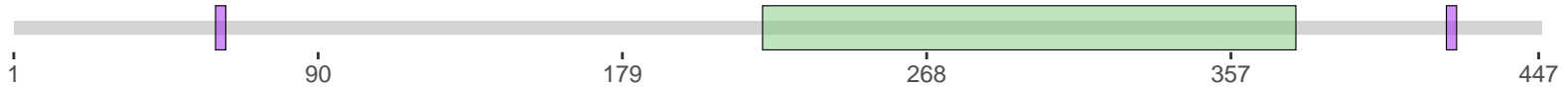


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YKELYGIRRLDIAVGNVPELGAWDYKRKFTGHEFAEFTSEDDVGTAEESGLNSMVLANNDETALFLPLNEFYVGTGRKSGIQTYLEHNEGAGVQHLALVTEDFKTKEMKRKSGVGGFEFMPSPPTTYKLNKIRAGDVLTEGGIAGEDIGLVDRDDOGLLQFTKPKVGRPTFIEIQRIGCMLEKDEKGGVYKGGGGGGKGNFSELSFSEIEVEKTEAKGNQAA*

NbL10g07270.1 oxygen-evolving_enhancer_protein_2-2_chloroplastic [MW = 28.72 kDa]

No. of times detected



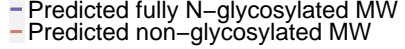
log(intensity)



Values from



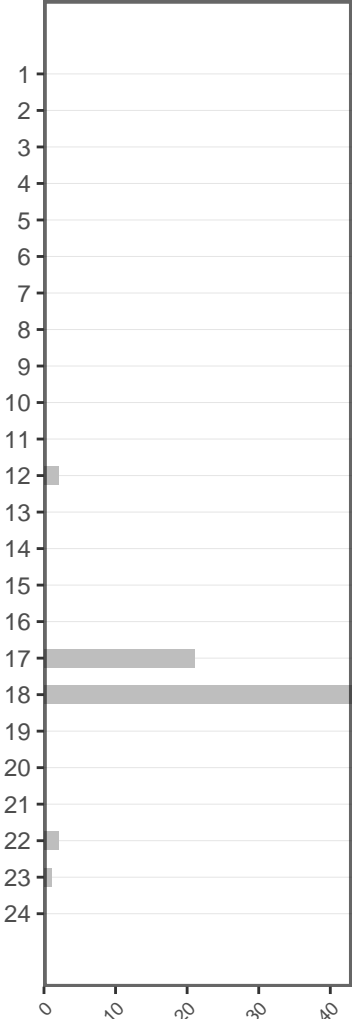
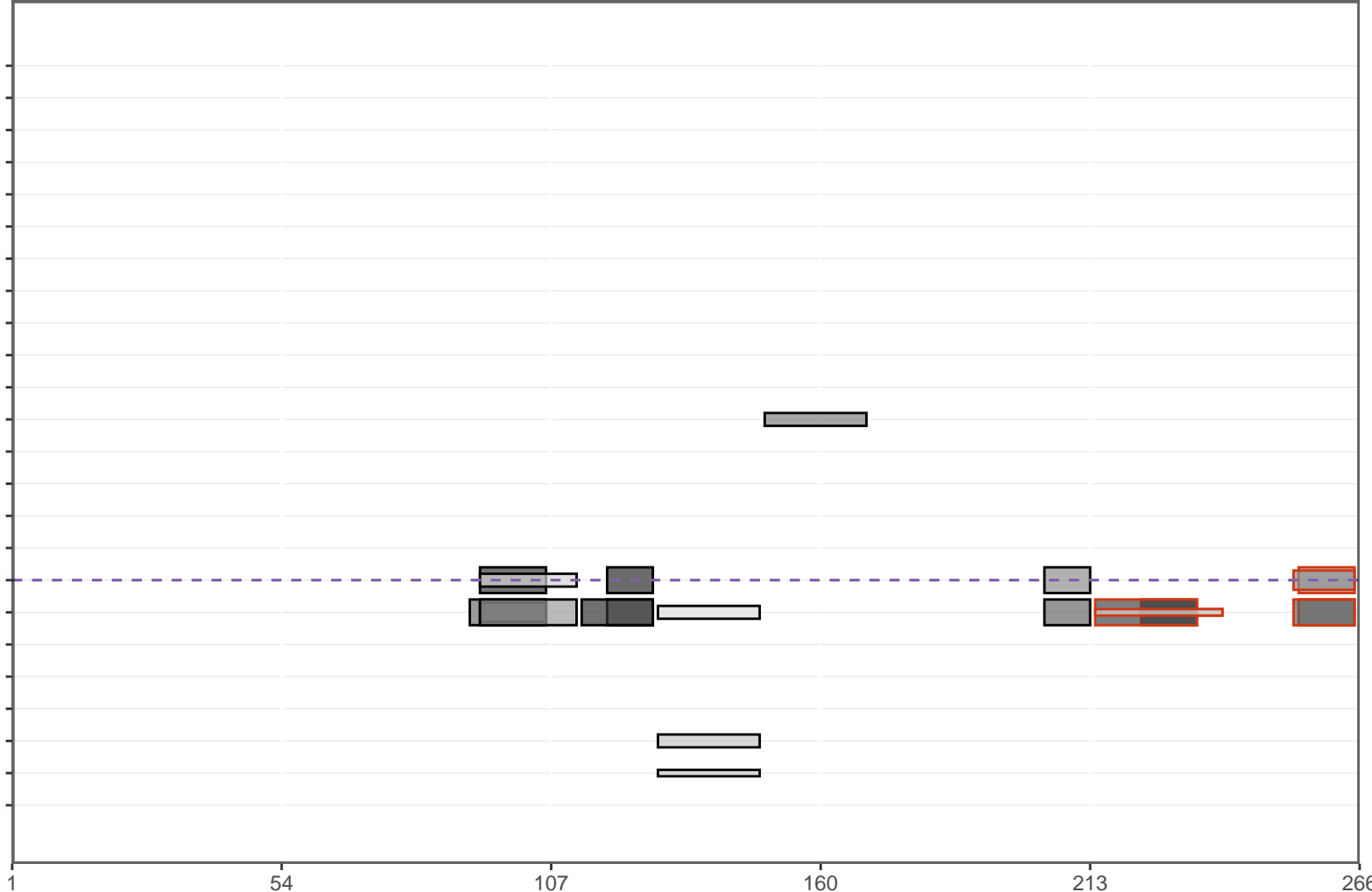
MW indication



Molecular weight

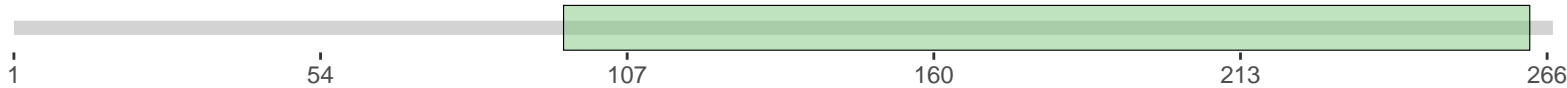


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEYPGQVLRFEEDNFDATSNVWATPTDKKBITDFGSPPEQFLSQVDVLLGRQAVSGKTDSEGGFEGSDWAMNVLSTSSAEVIGKPYVYLVLRTRADNDEGGKHQLTATVNDGKLYICKAGADKRWFGKGGKGFVENTVTSFLA

NbL10g07210.1 switch-associated_protein_70 [MW = 61.47 kDa]

No. of times detected



log(intensity)



Values from



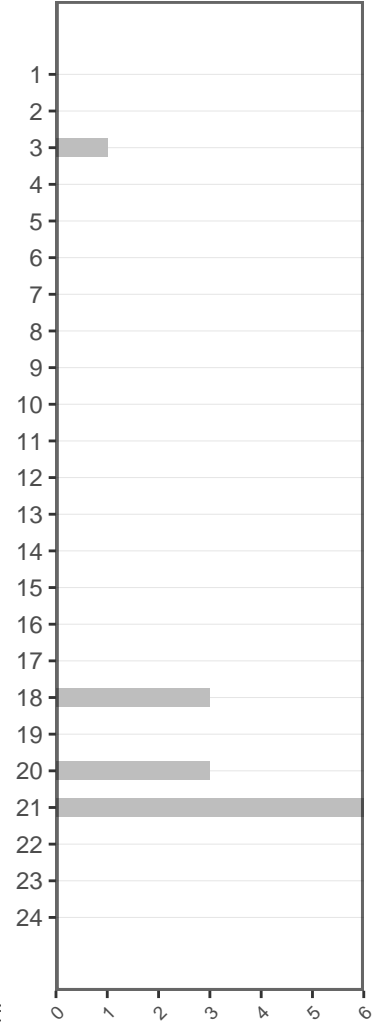
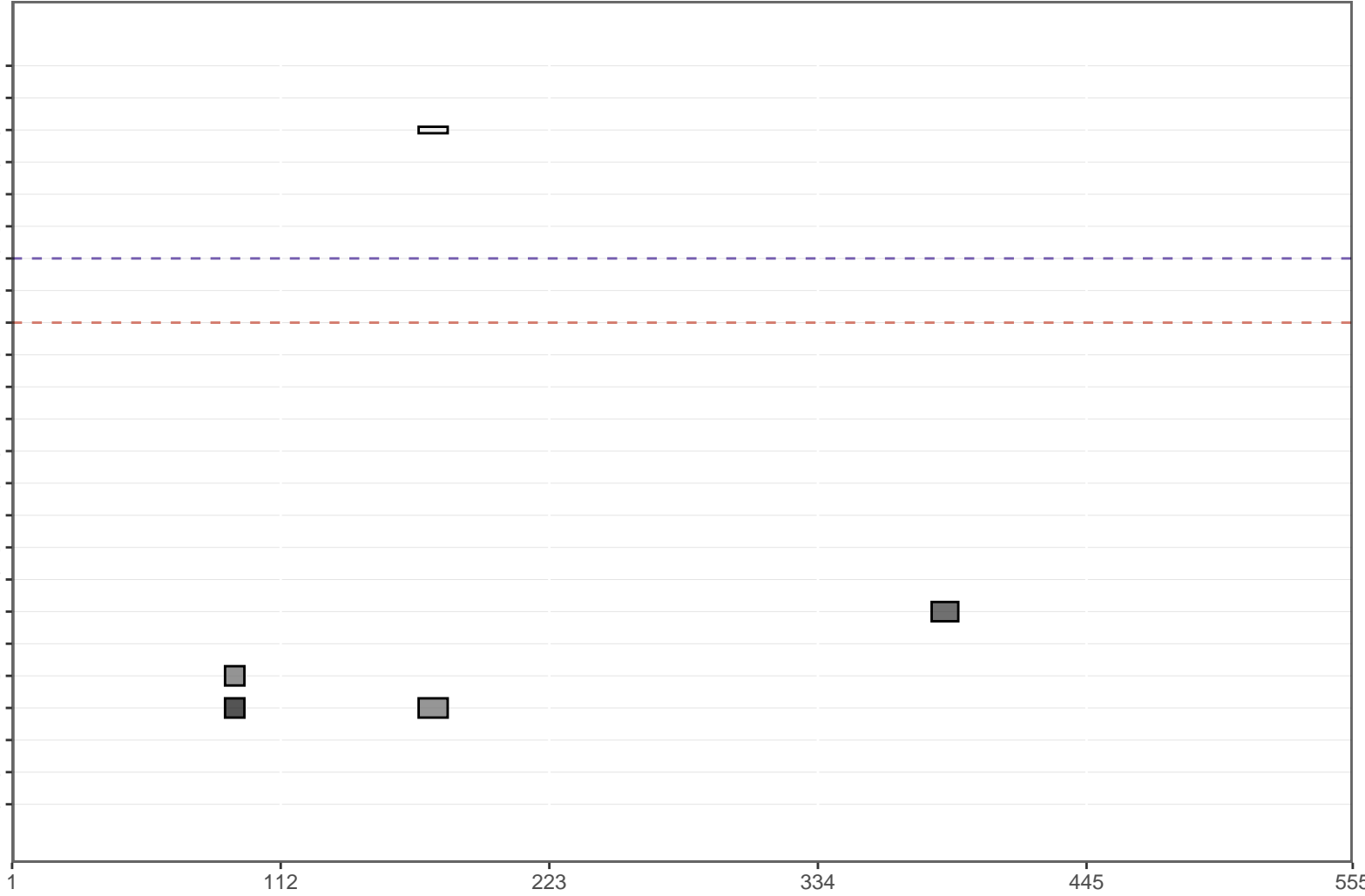
MW indication



Molecular weight



Gel Slice



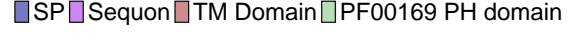
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TLRYKDDLELQNLAREVRRARDSTIKELVDKLSETAEAEAAASAAAGTMEGRKIKAGAEVERLKGDSKGLSESSKSLREFEENFMTLSKEMDQIKGRDSAGQEAHLVRSLELAKAREQAVILEGAVRAEERVRVTEADAEIRKEAAGTEAASAKKQGLLAVYVNLQAQLTRQGVDMNGVFKETESGSSINLPQTKHVDLSEENVDKAGLSVRAIDFENVVLDVADQTNHQSSGSGHEWSDKQPTESRIADREVASETERSELDPVVSFENPHQDHGINSILP*

NbL10g07170.1 cytochrome_P450_97B2_chloroplastic [MW = 64.65 kDa]

No. of times detected



log(intensity)



Values from



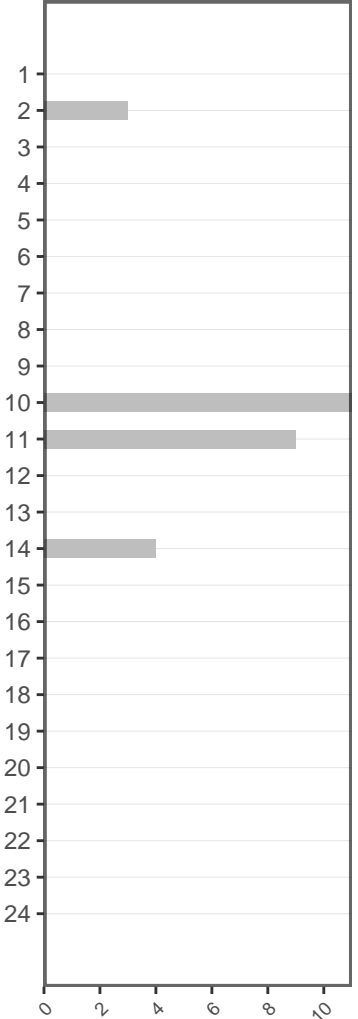
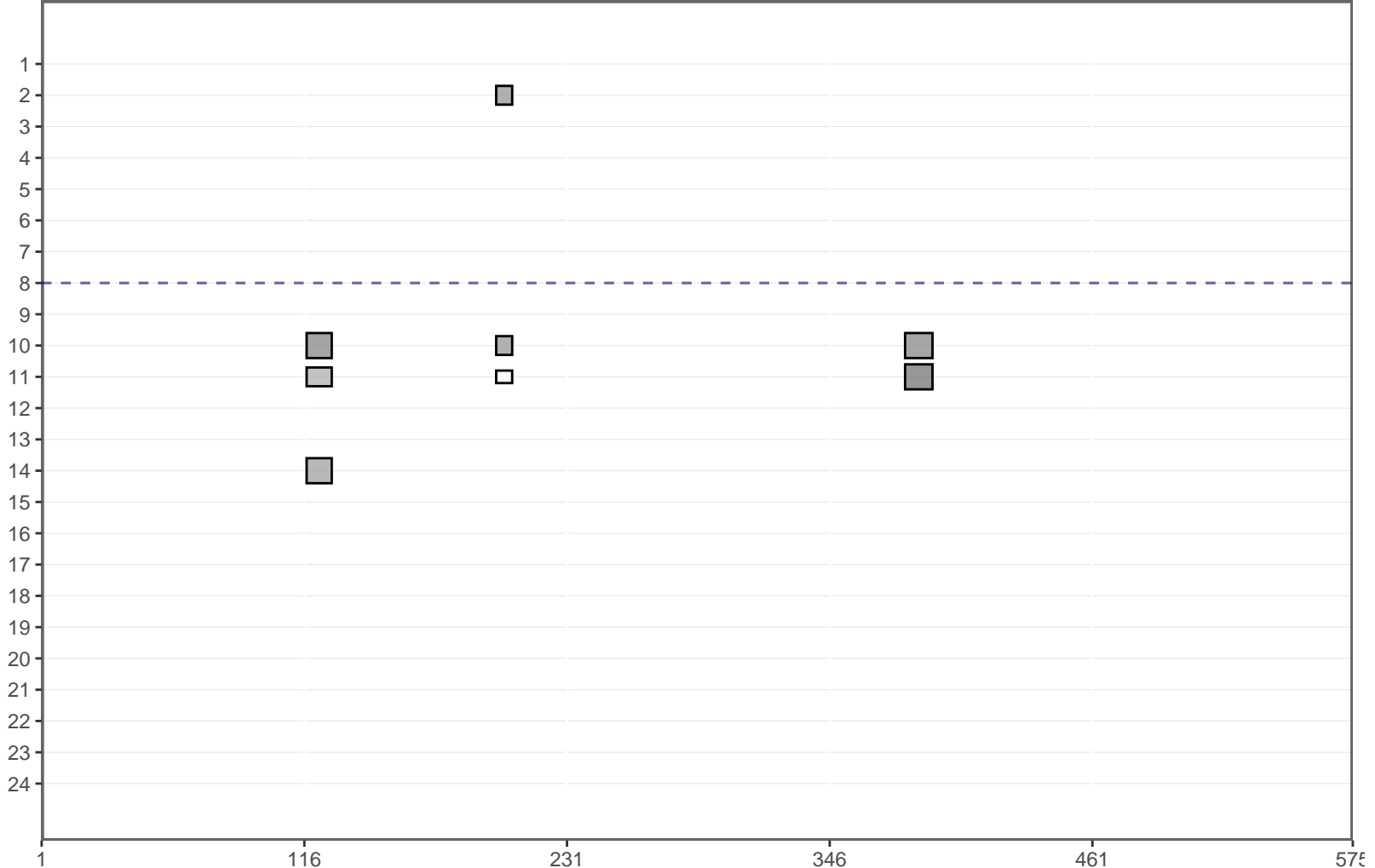
MW indication



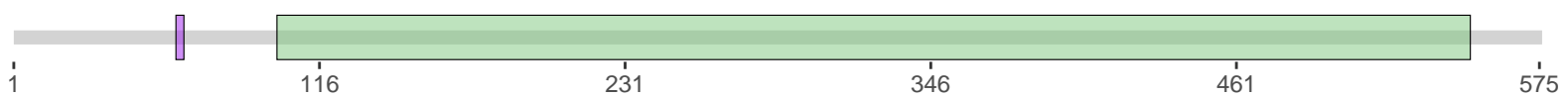
Molecular weight



Gel Slice

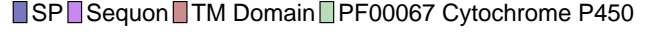


Protein length



Pfm domains

Pfam Description



Protein sequence:

YPRORKFQNDLKVINDGLDGLGNKAKETREEDAVKLGQRDYLNLKQASLLRFLVDMRGVDVDDRDLRDLMTLMLAGHETTAAVLTWVFLLAGHPVMMKKAGSEDAVLGGRRITTFESLKKLEYLRLLVVESLRLVPPQLLIRRLSKSDKLPGGVYNGDKDGYEIPAGTDVFLSVYNLHRSPIYFWDKPDFEPEPERFLVPKESSEVGGWAGFDFPERSPGALYVNEIISDFALPFGGGPRKVDGDFALMESTIALAMLLQKFDVIELRGRSEVVELTGATHITKTGLVCKLXK

NbL10g07150.1 probable_pectinesterase_8 [MW = 35.35 kDa]

No. of times detected



log(intensity)



Values from



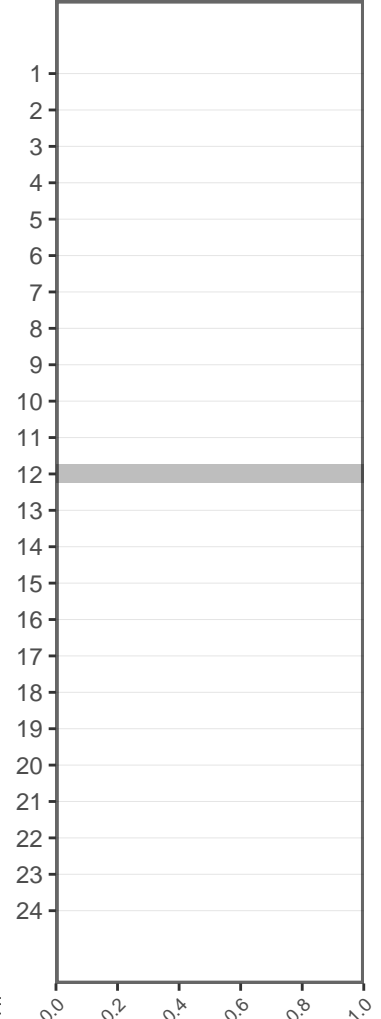
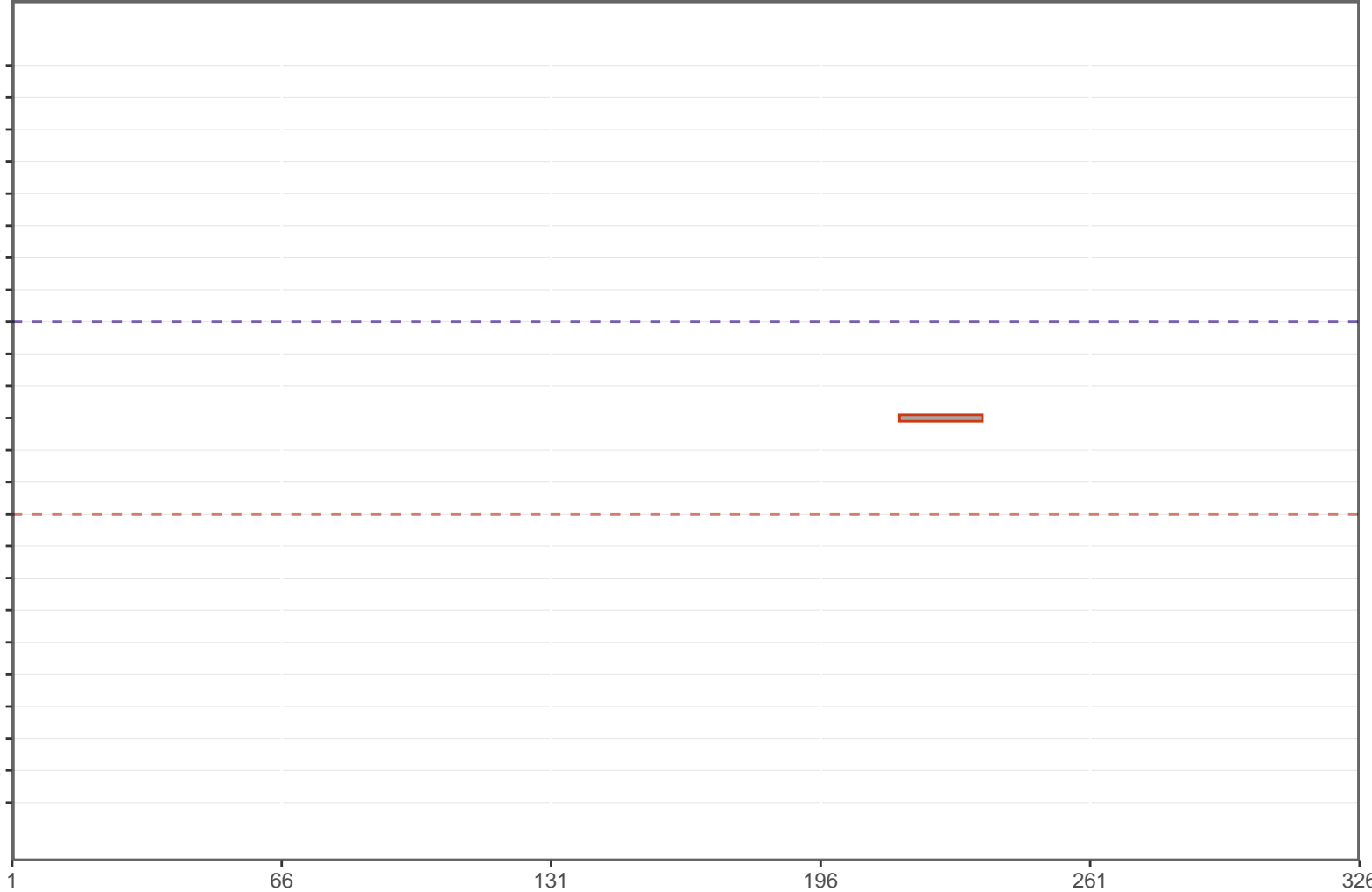
MW indication



Molecular weight

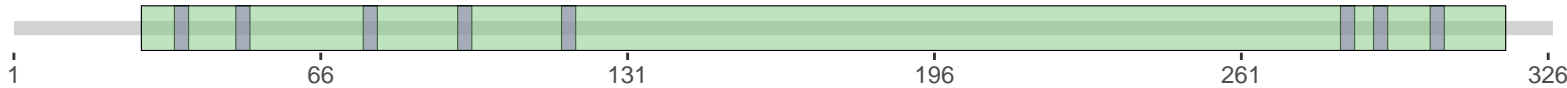


Gel Slice



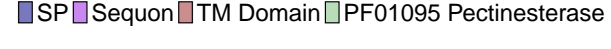
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FGAQQDTLHIDRGRHIFKKECHQGGSDIFVFGNGKSLVENGEUIMASPGWRBINGAVTAHGRASKEEDSGFAPVNCNNGVGGSRWLGRARWRFSTVVFANFSMTNIIISPDDGWNLDNDRSDGTIFYGEYNGTGAENMBSQRPVYVKLNLDGALPLFLSSFDADGWLGEFSN

NbL10g07080.1 glucan_endo-13-beta-glucosidase_6-like [MW - SP = 50.11 kDa]

No. of times detected



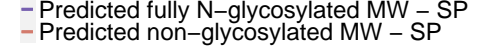
log(intensity)



Values from



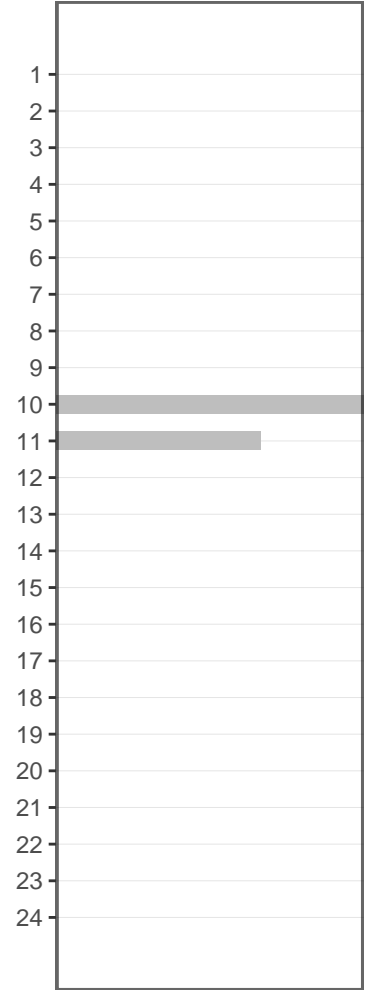
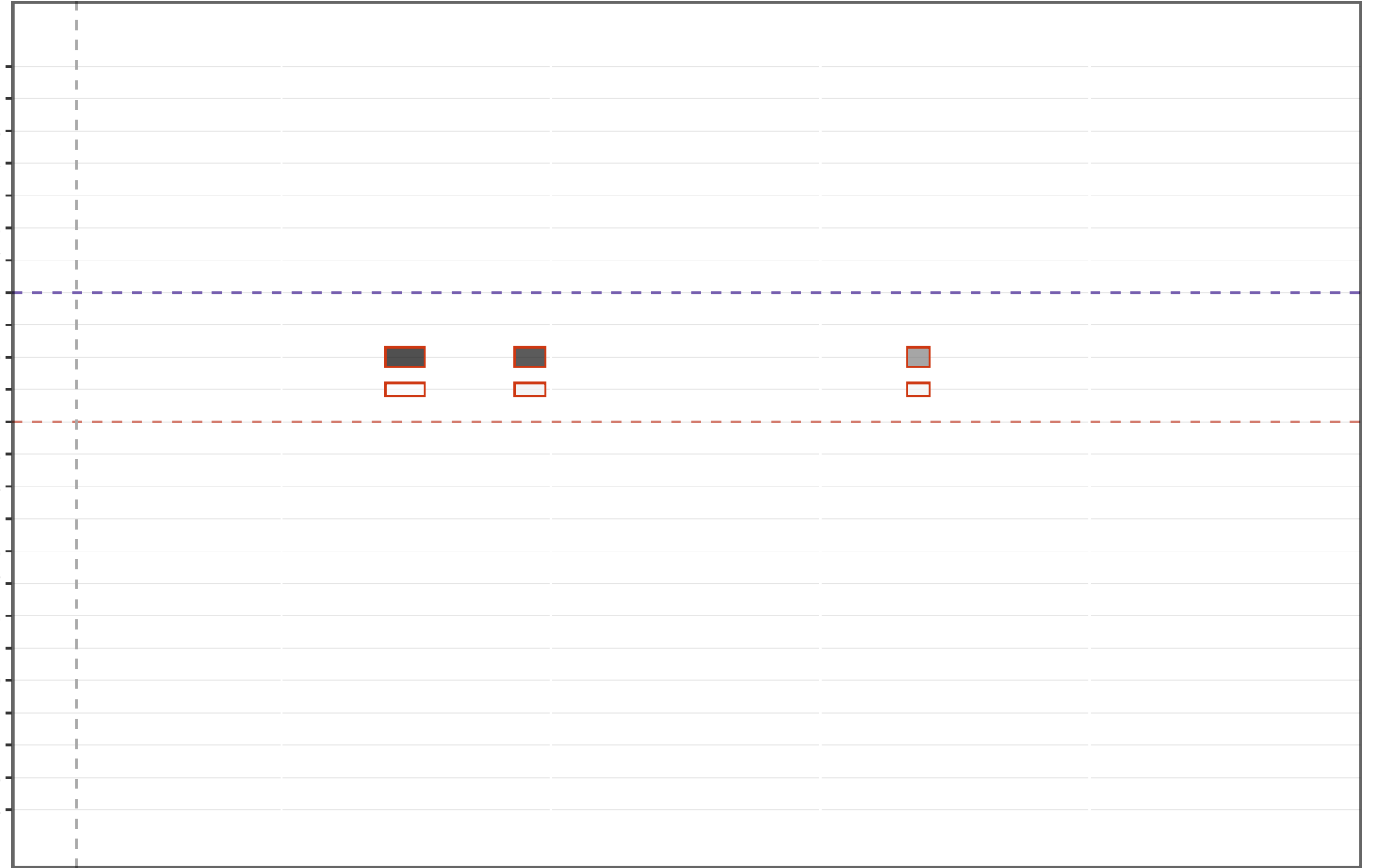
MW indication



Molecular weight

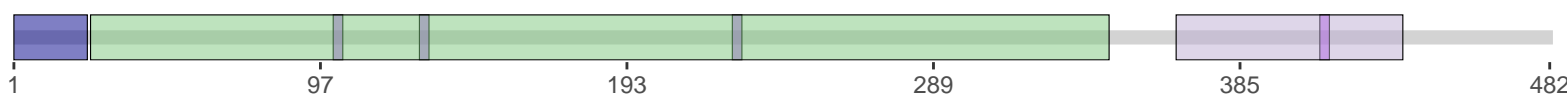


Gel Slice



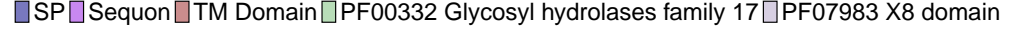
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NDGGTTYTNMFDANHDTLWALGKNGFGNPHIIEGIGWPTDSDRANAGLAGRFNGGFMGHISEGKGTPMRPGPIDAYLFLSUIDEAKSRIFQNFERHWGIFTYDGLPKYSLMLGTTNSGALVQAKNKKYLERHWGVFKPNAAVDDPGIAPEMSYACGLADCTSLGYGTCGGGLDARGNISYAFNSFYQINQLDDACKFQGLGTVTKSDPSTGTGRFLMIEQYYGAADRGLGYTRMALALLLVLTLL

NbL10g07050.1 uncharacterized_LOC104212881 [MW = 66.97 kDa]

No. of times detected



log(intensity)



Values from



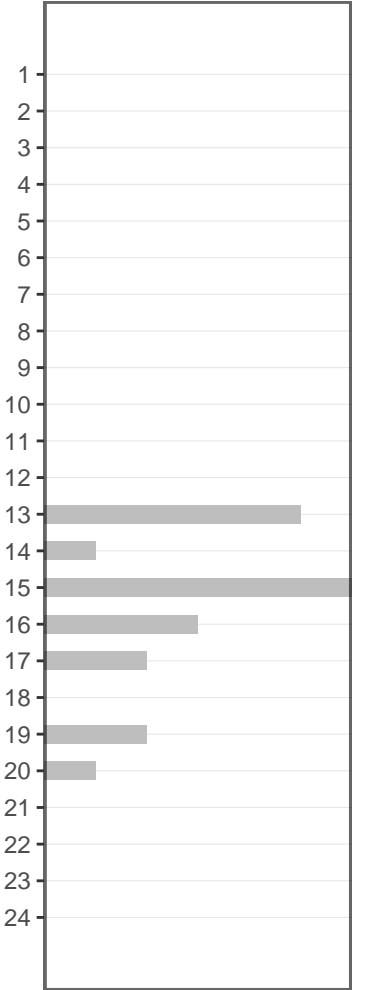
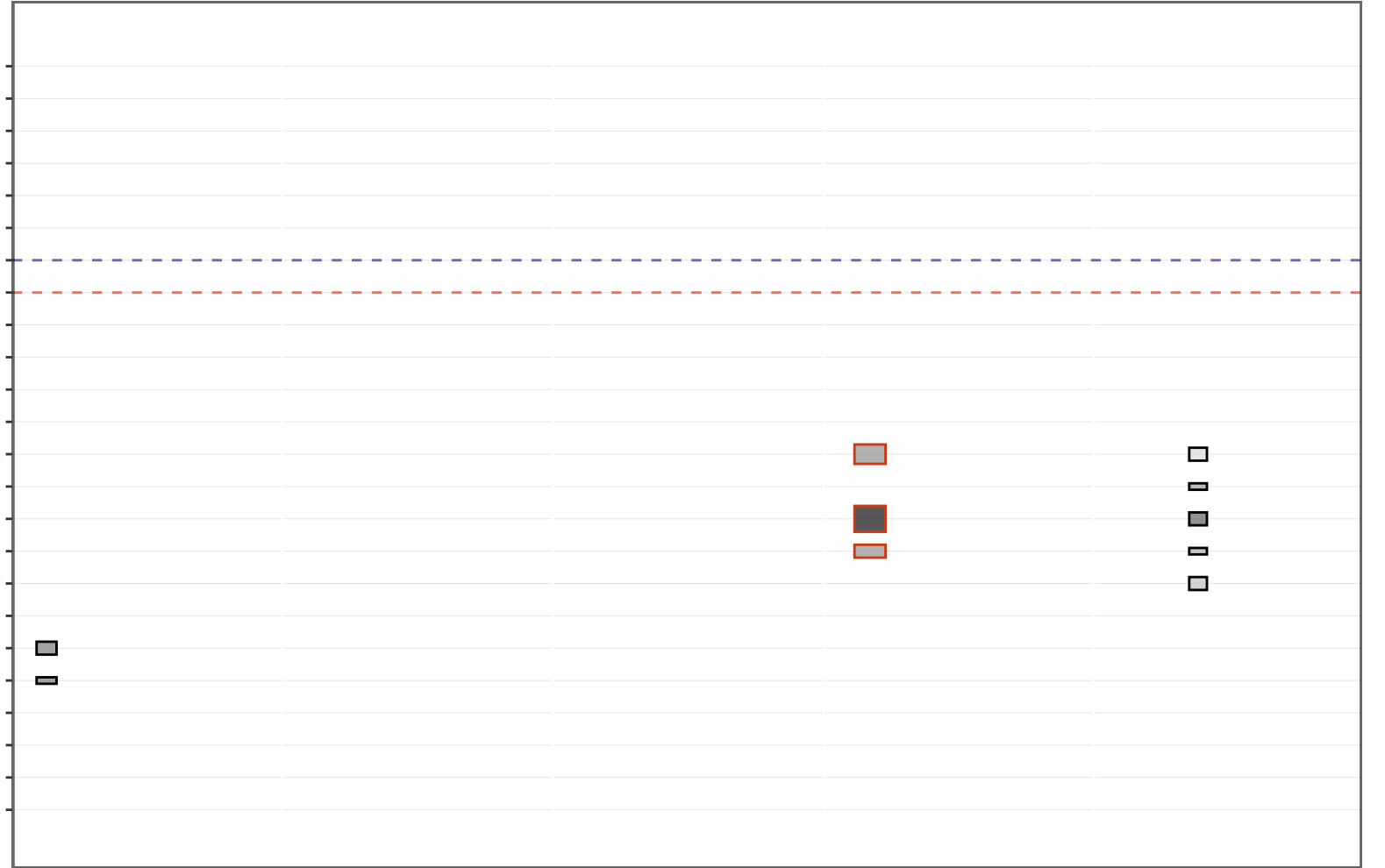
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

TPGSSTRHYSGNPPYPSANVYGTGSSSLWEPGRHWLTPDRGGRRERDRHSVGSISTEGLGMAEERNRGRPRALKPKBKGPIEDGSSSAHKEVESTNTPQPEQVNRREFVTDYEHAKFFVKSFSFSDNHHKSKYGVWASTPLGNRKLDAAYREAKERNADGPFVFFFSVNASGGFGVWEMGPFVDFENNAEHWGGDRWSSGQFPVWVHWKVPNSQLRHLLLEHNDNPKPVTHSRDSDGEVLPFEGLEMLKIFKNYEADTSLDDFFYYDEREKSLLEKSKORTLPG

NbL10g06950.1 20_kDa_chaperonin_chloroplastic-like [MW = 26.22 kDa]

No. of times detected



log(intensity)



Values from



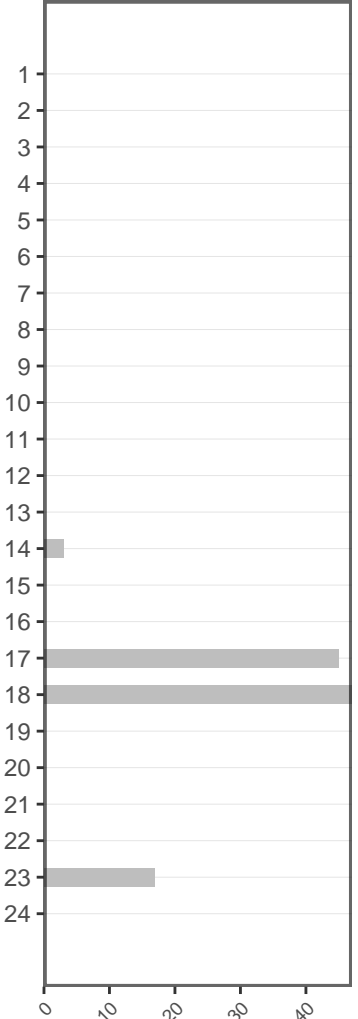
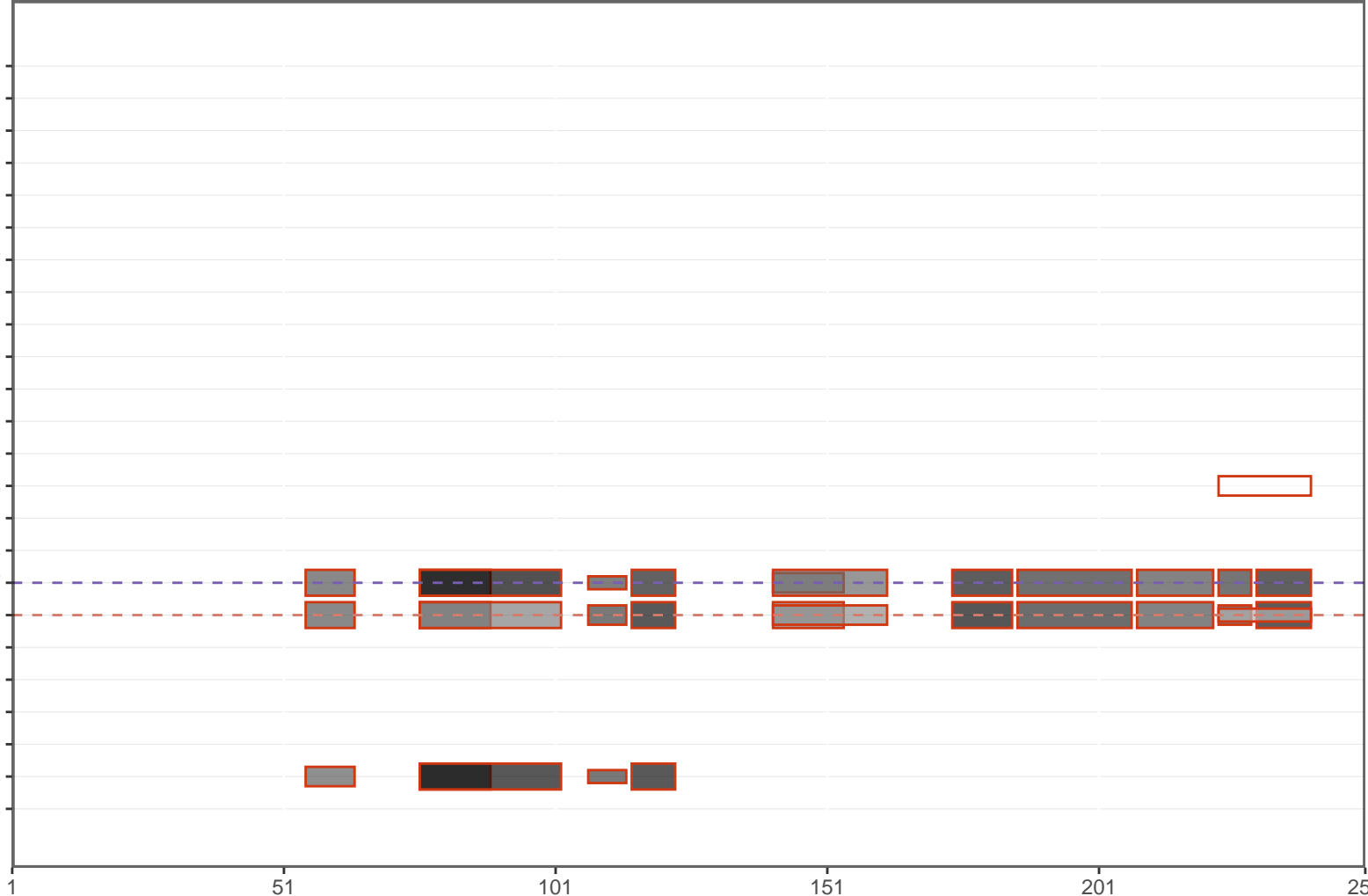
MW indication



Molecular weight

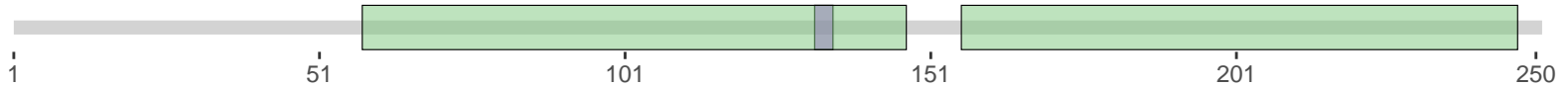


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

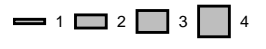


Protein sequence:

SVKTKAQVYISKYAGTEVEFGNSNHLIKEDDNGTLETDEIKDKLQPLNDNRVLKVAEAEKTAGQLLLEASKEKPSIGTVAWGPGLDEEGNRKPLVSTGNTVLYSKWGNFKGADGSEVIALRASDVMVLS*

NbL10g06900.1 pollen_receptor-like_kinase_3 [MW = 70.29 kDa]

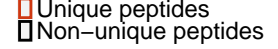
No. of times detected



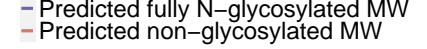
log(intensity)



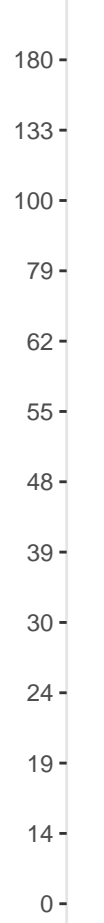
Values from



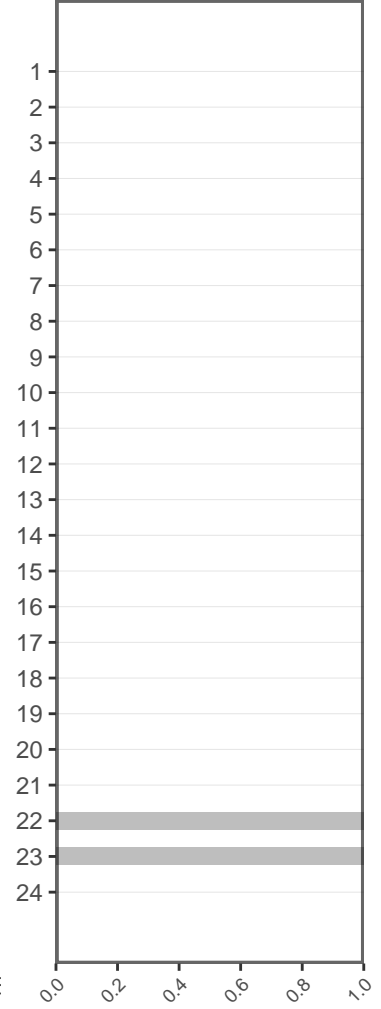
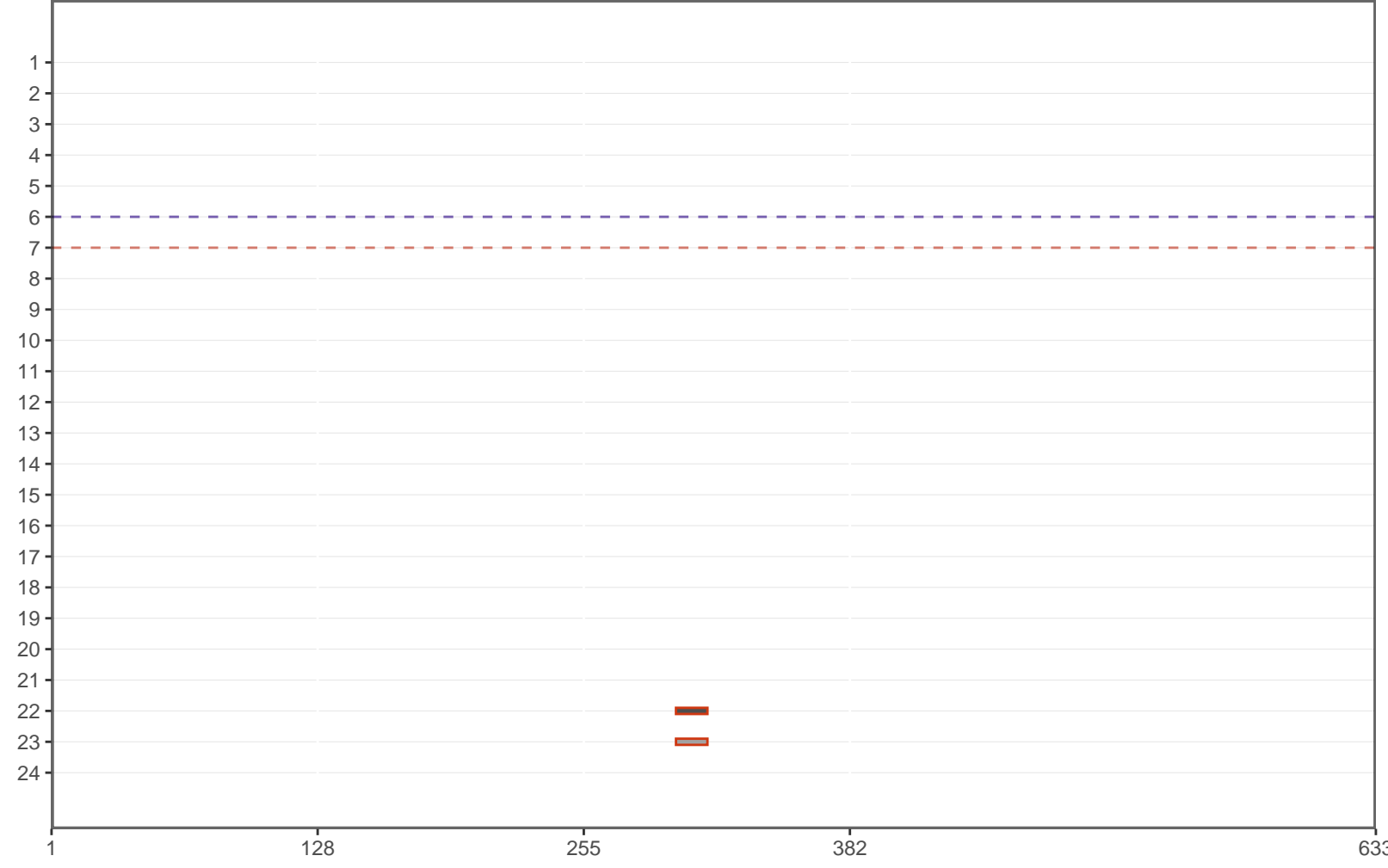
MW indication



Molecular weight



Gel Slice

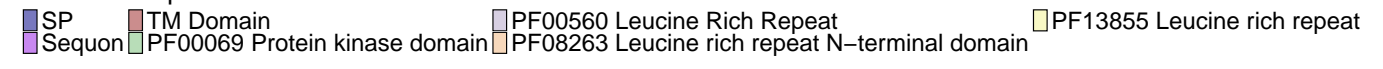


Protein length



Pfam domains

Pfam Description



Protein sequence:

ESVSYNPSSNKRSMELRNEMRBRRRGRGRSGSDMGDLVAVNEERGFGLPDLMKASAEVLGNGLGSAKAVLGNGLSVVKRLRKINKLKEFTDEIRKLAALRHRNLLGPLAVHYRKEEKLVVEVPEKGLLYLHGDGRGIAHAGLNWPTRLKIINGVANGMKFLHSEFASVDVPHGNLKSSNLLKTTNNEPLRTDVAFYPLNNSGAVDGLFAYKSPKSDVYGLGHILELTKGFPDGLNKGKCGTDVVGWVQSAEAKRVSLELDPOIATAKDSLEKME

NbL10g06850.1 cysteine_proteinase_3-like [MW - SP = 37.62 kDa]

No. of times detected



log(intensity)



Values from



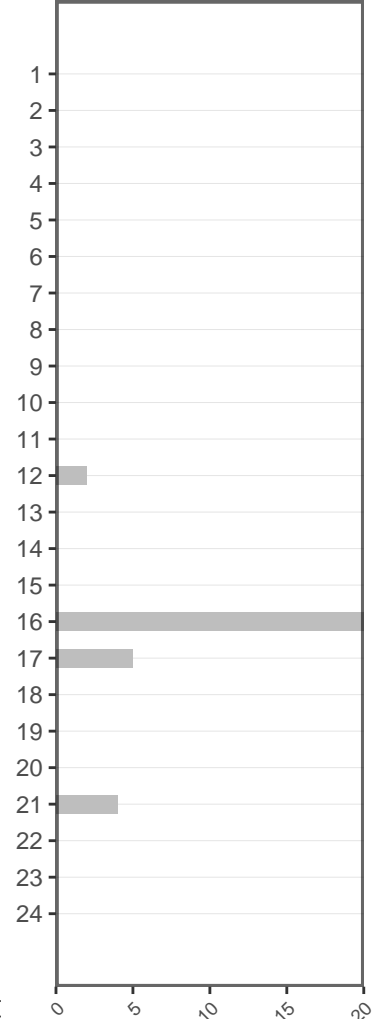
MW indication



Molecular weight



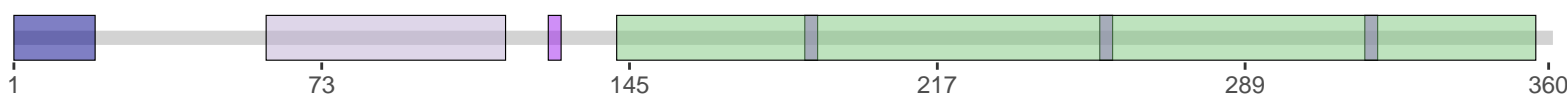
Gel Slice



Protein length

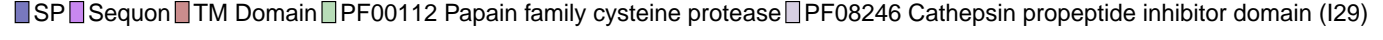


Peptide counts over 4 repeats



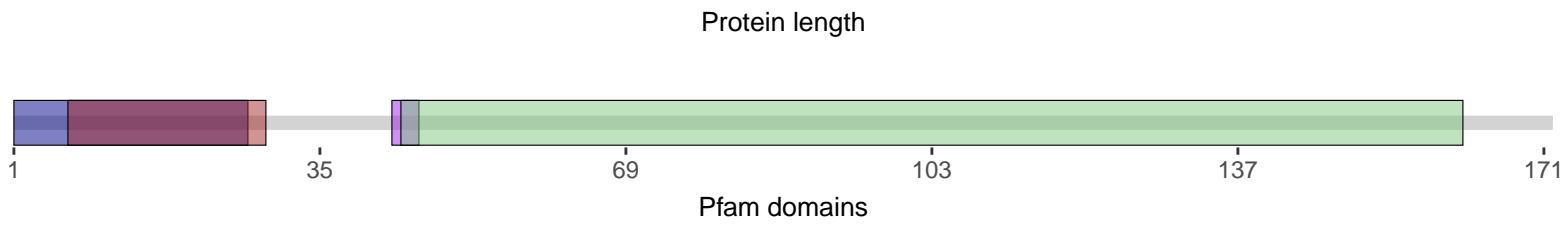
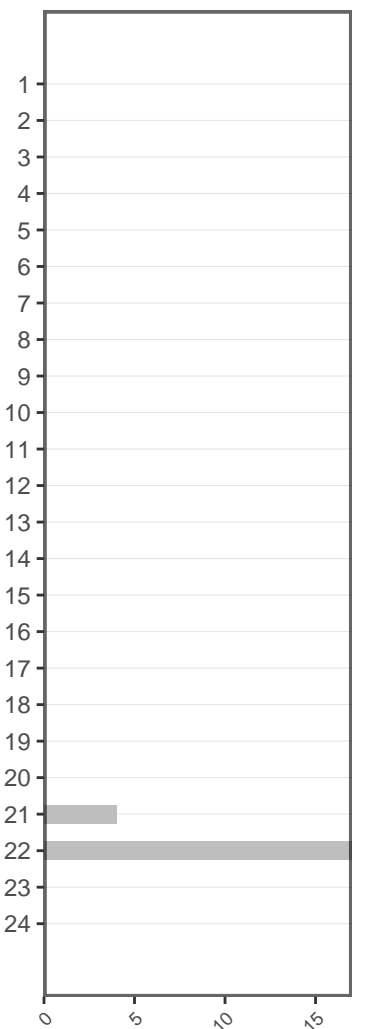
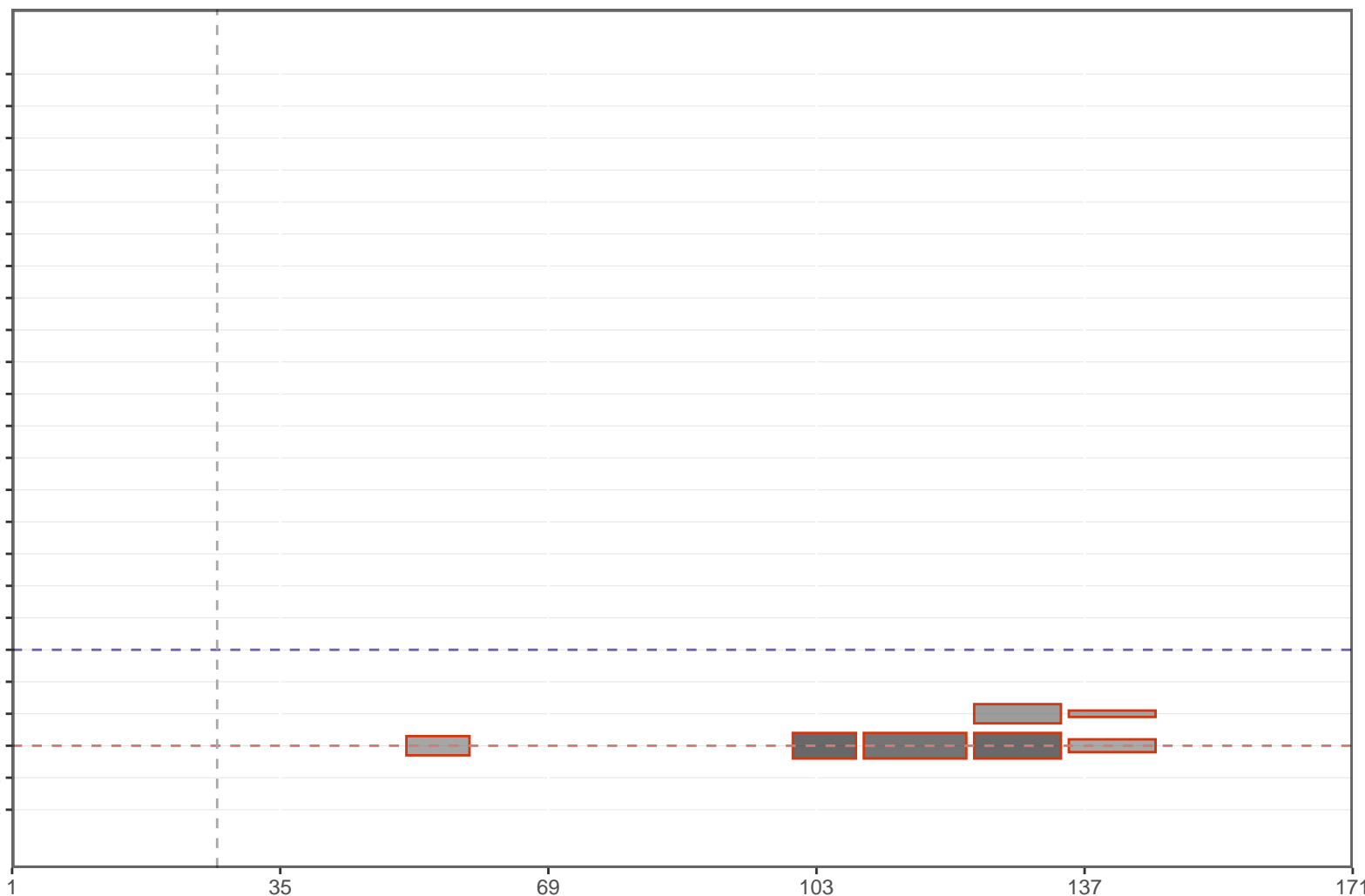
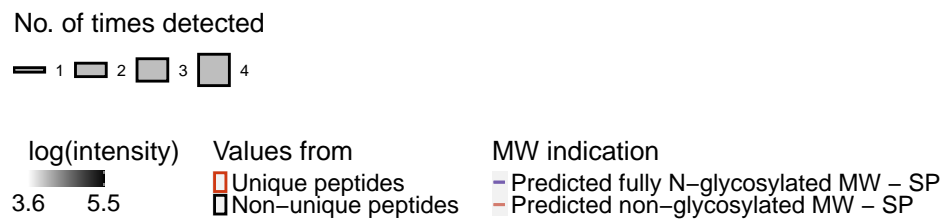
Pfam domains

Pfam Description



Protein sequence:

FSSTTGALAAVQAFGRNLSSEGGLLDAGAFNFGGHLGGLPQGAFAFEYKYSGLDTEEEYPIAGKAGVCKFSSENAVKYVGSVNTKDAEDELKAVAFIRPVSVAQVQVYKGRGKQYKGGYSSTVCGNTFGDNNHVALVAGYGVENGSTPYWLKNSWGAEWGQNGYFRMEMGRNMGATCASYPVAI

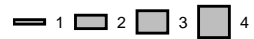


Pfam Description
 SP Sequon TM Domain PF06232 Embryo-specific protein 3, (ATS3)

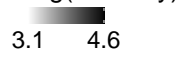
Protein sequence:
 IAFGDVYGFVYAPRLDNPSSRIFERGSTDTDFQIRGCPCTYEICVLLRLRVGSDGWKPEVWVYVGNRPVITFRYKFLFNGVWFGFNHCRKRVFGEV

NbL10g06740.1 casein_kinase_1-like_protein_2 [MW = 53.02 kDa]

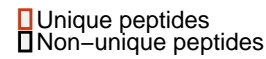
No. of times detected



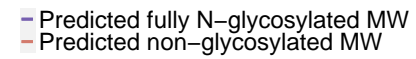
log(intensity)



Values from



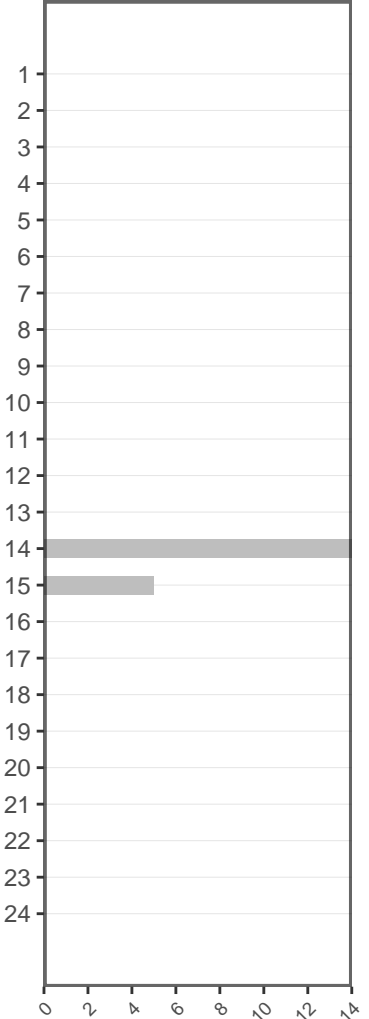
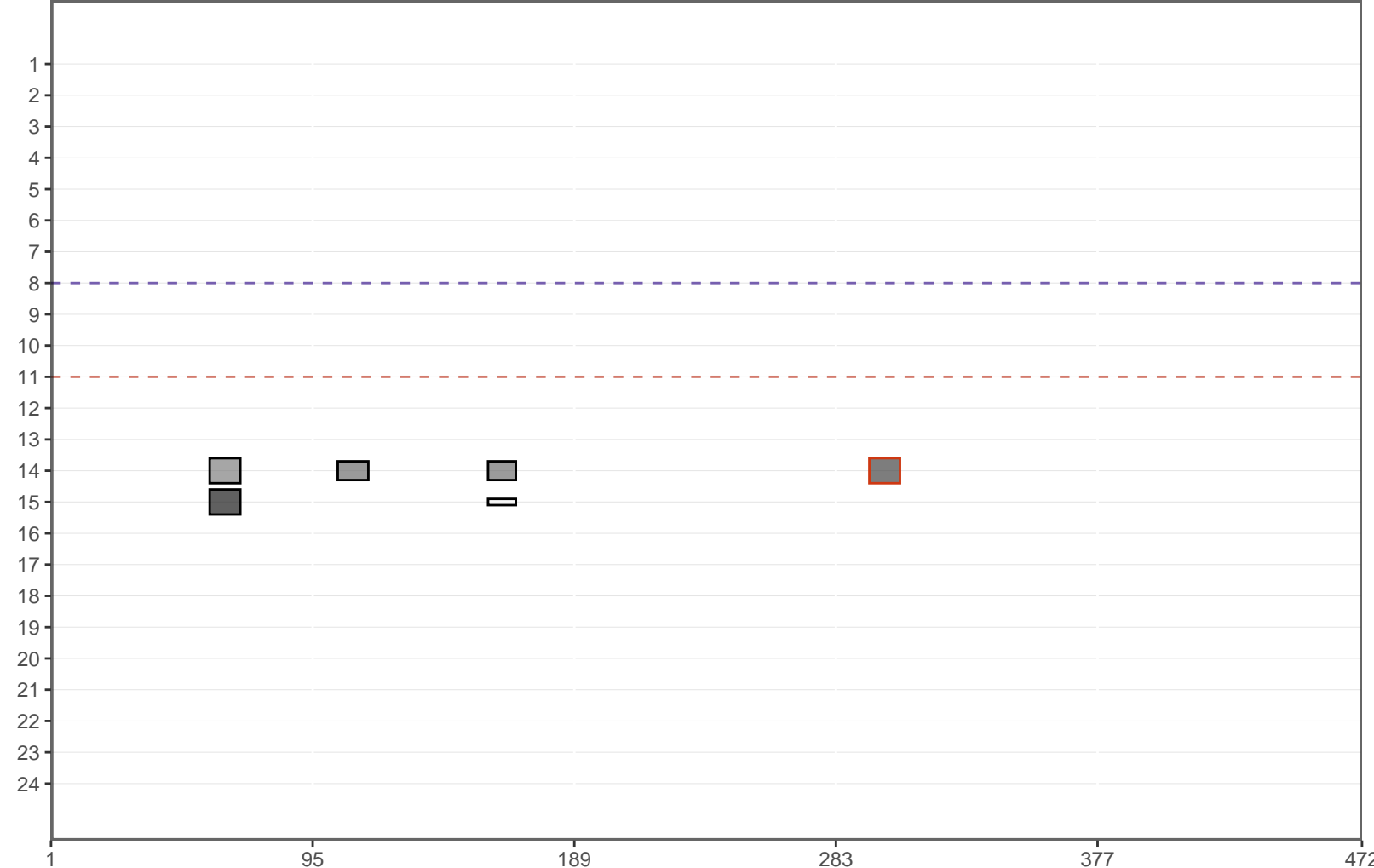
MW indication



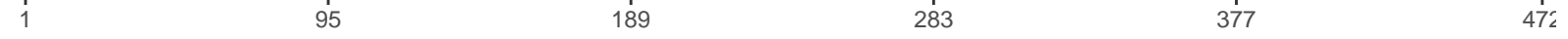
Molecular weight



Gel Slice

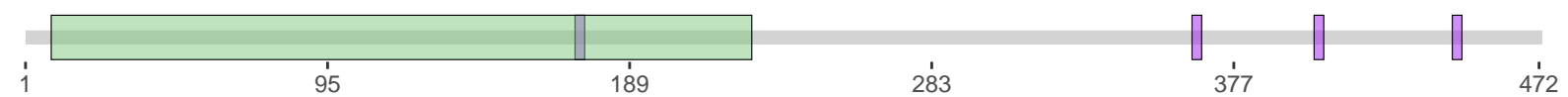


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

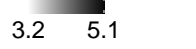
KYKIKSEKXVSTSIKALGRGYPTEFASVHYHCRLRFEDKPDWVYLRKFRDLRFIREGQFDVYVFWTLKYQGSGIAAFTSRPLGAGAGTSSGMPPIPAERNGSGEEEGSQPADPSRRRRNSGFLNAGSFGSKQKPLRINDGTSKDMILSSGTFVGRSSGSLRGLVSGSREFTFTMGNDSDPTRSRTPPEASPAFMHKI6SGQRSSPLVGS66DAKHASSGRNTSGINKYETFLKGERLHFDEEDRSH

NbL10g06610.1 probable_polyamine_oxidase_5 [MW = 58.1 kDa]

No. of times detected



log(intensity)



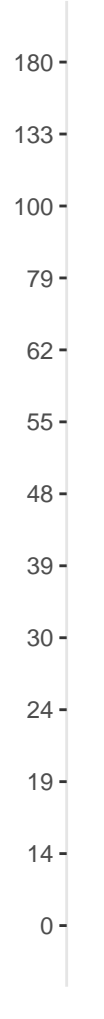
Values from



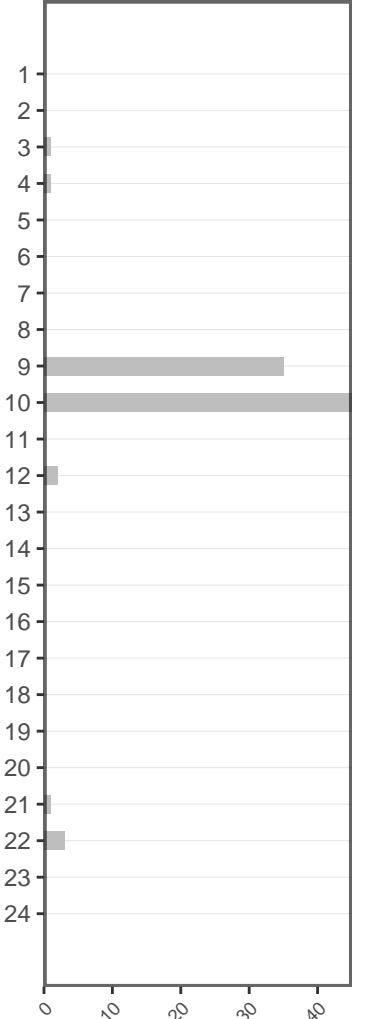
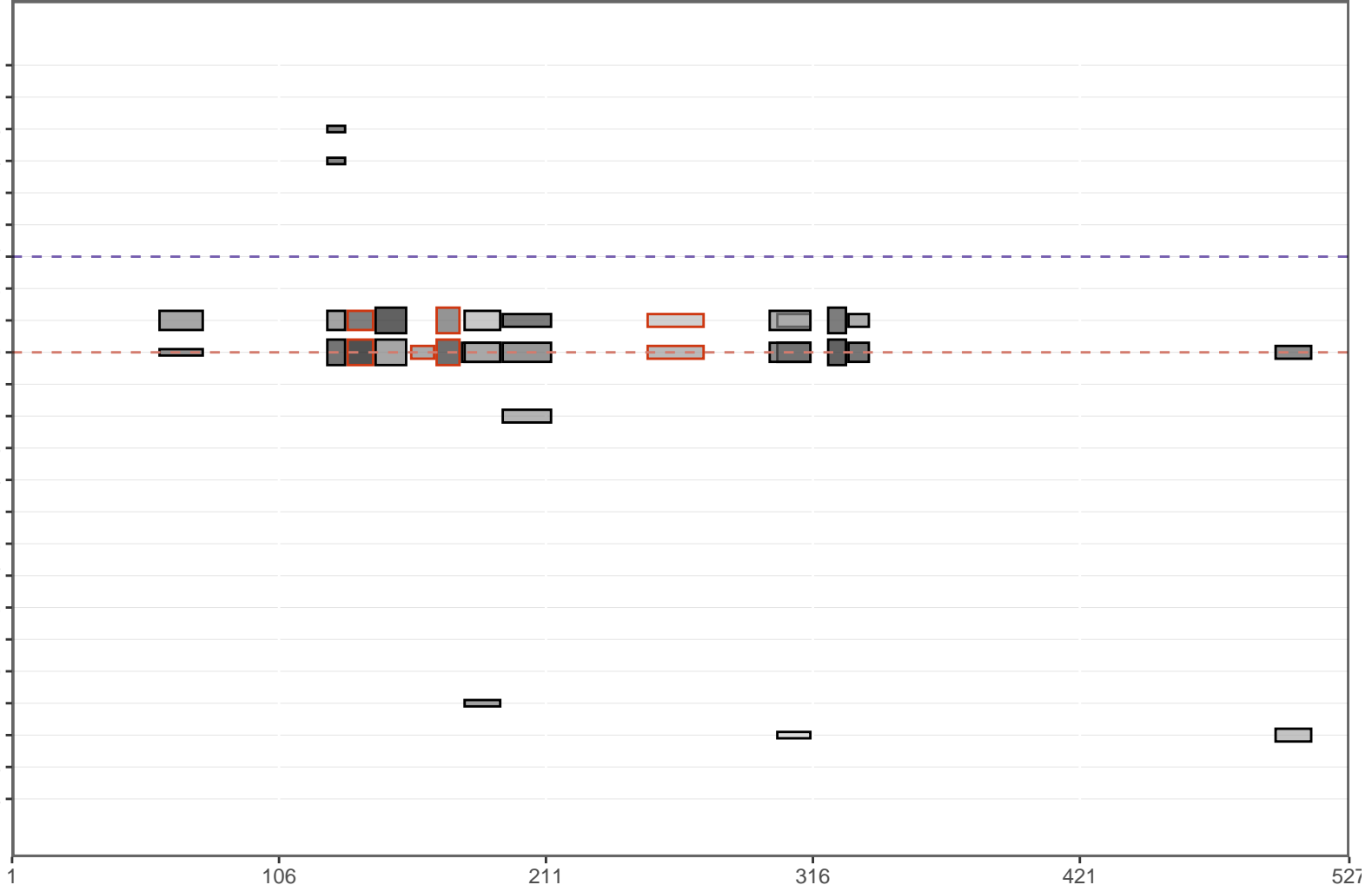
MW indication



Molecular weight

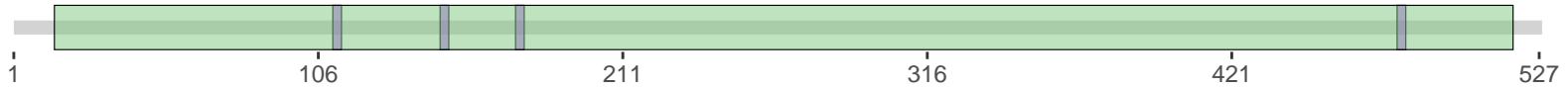


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

WQPDCCGLDVENGGDGTKPKKHFYDGMIMADHIVTVSLGLVKREIRDGSGMSPPLPFSKTAISKLGFGVWVKLFLQLSPTKDEDDGMKFPVGMVHFHSDSRRLRHFKIPWVWRRTASLCPHYSSNVLLSFWFAGAEALEGLGNEEIDGFSFTMSDFLANSKHVNKLSNGHAESSFKDKVKLKGWGTPLFLGSGSYVWVGSDDLDLTAELPTRSNVSGISPLQLFAGEATHRHVSTHGGAVFSGLEARNRLGHYHGDI

NbL10g06280.1 rRNA_methyltransferase_1_mitochondrial [MW = 57.66 kDa]

No. of times detected



log(intensity)



Values from



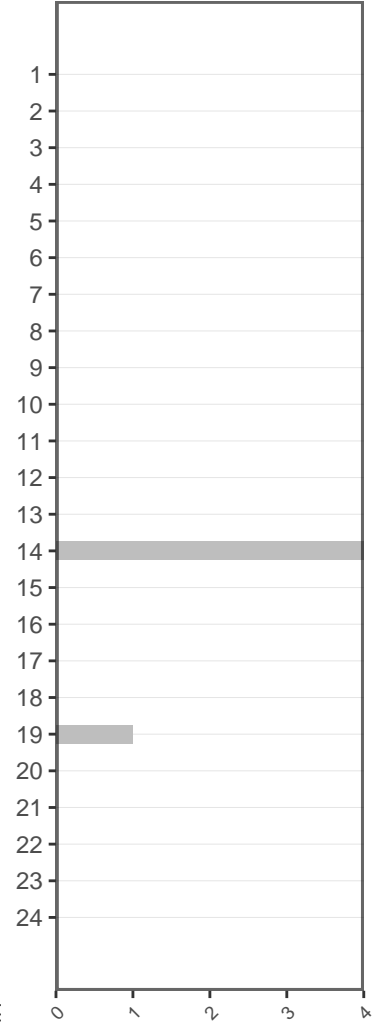
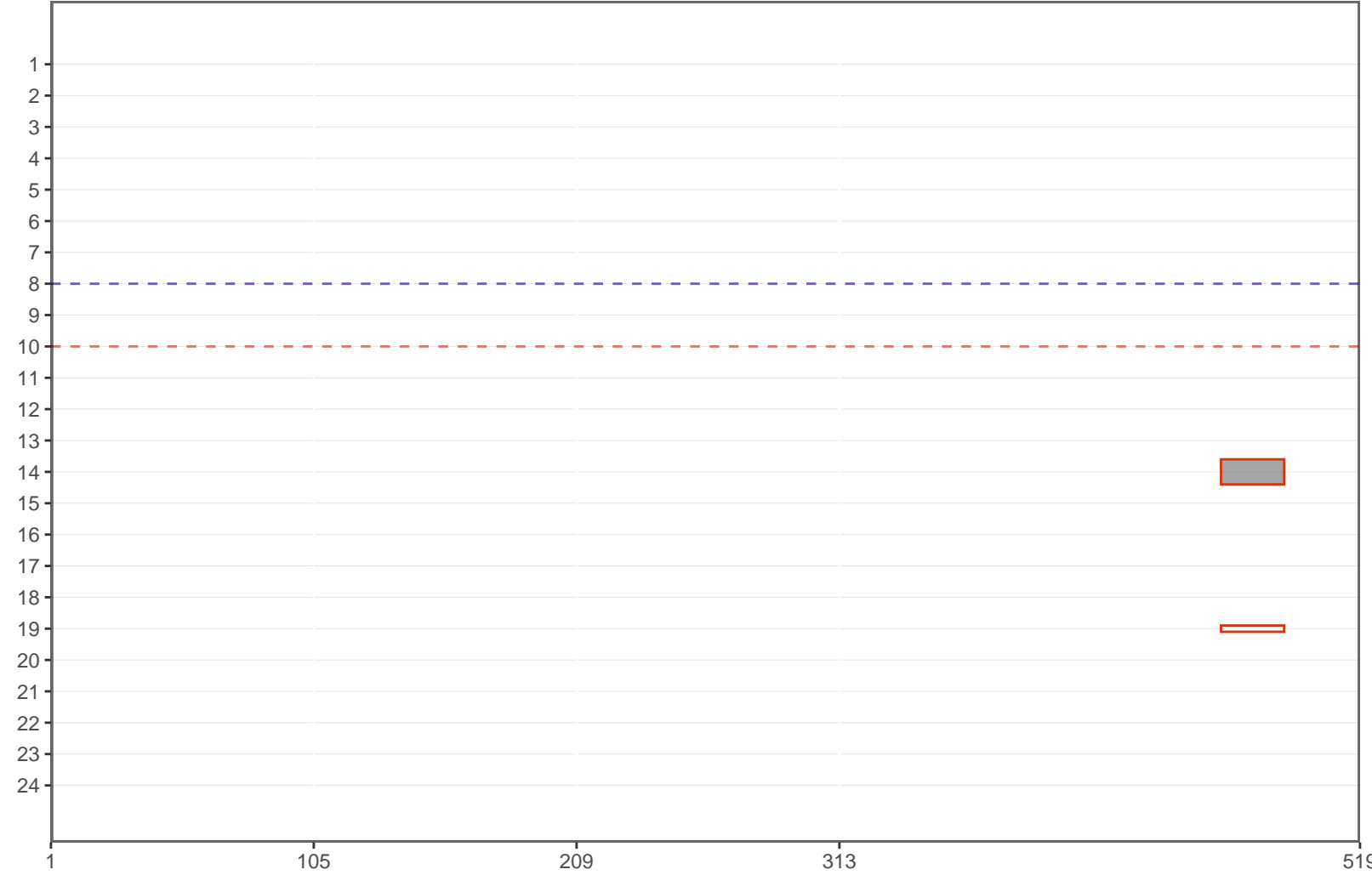
MW indication



Molecular weight

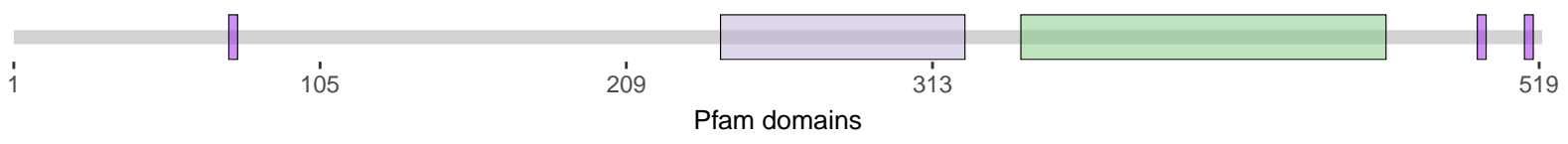


Gel Slice



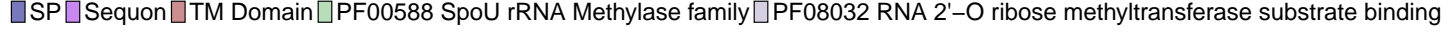
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GPVLAALSAGREFYSLYVQEGLDLSDGNRRKKDKKGFVRLVMAEKIGLSKVEVSKHDLNMFADNRPHDGLVLDASPLEMVGKELEPVSTEEESTPTLVVLDDEVTDQNLGAIRBAYFFGAGIVLGAANKSARLGGVVSASAGLELVELRSGKNMMQFLTSAAENGWRVHGGVSVSRAPLHEIVPGAPTLVLDGSEGTGLRPLVERSGTQLVWIPGNPVDIVHGEDEDDHSSSSGQNFBSFMAVESLNVVAAGVLLHLHLDGSGKN

NbL10g06190.1 probable_esterases_KAI2 [MW = 30.07 kDa]

No. of times detected



log(intensity)



Values from



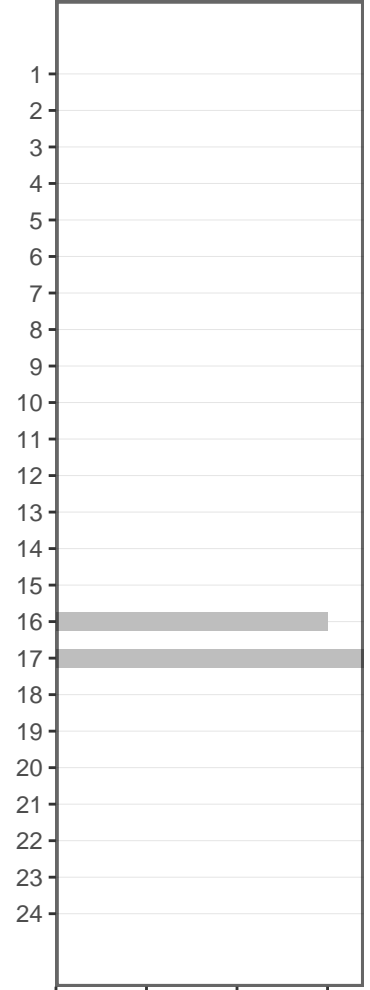
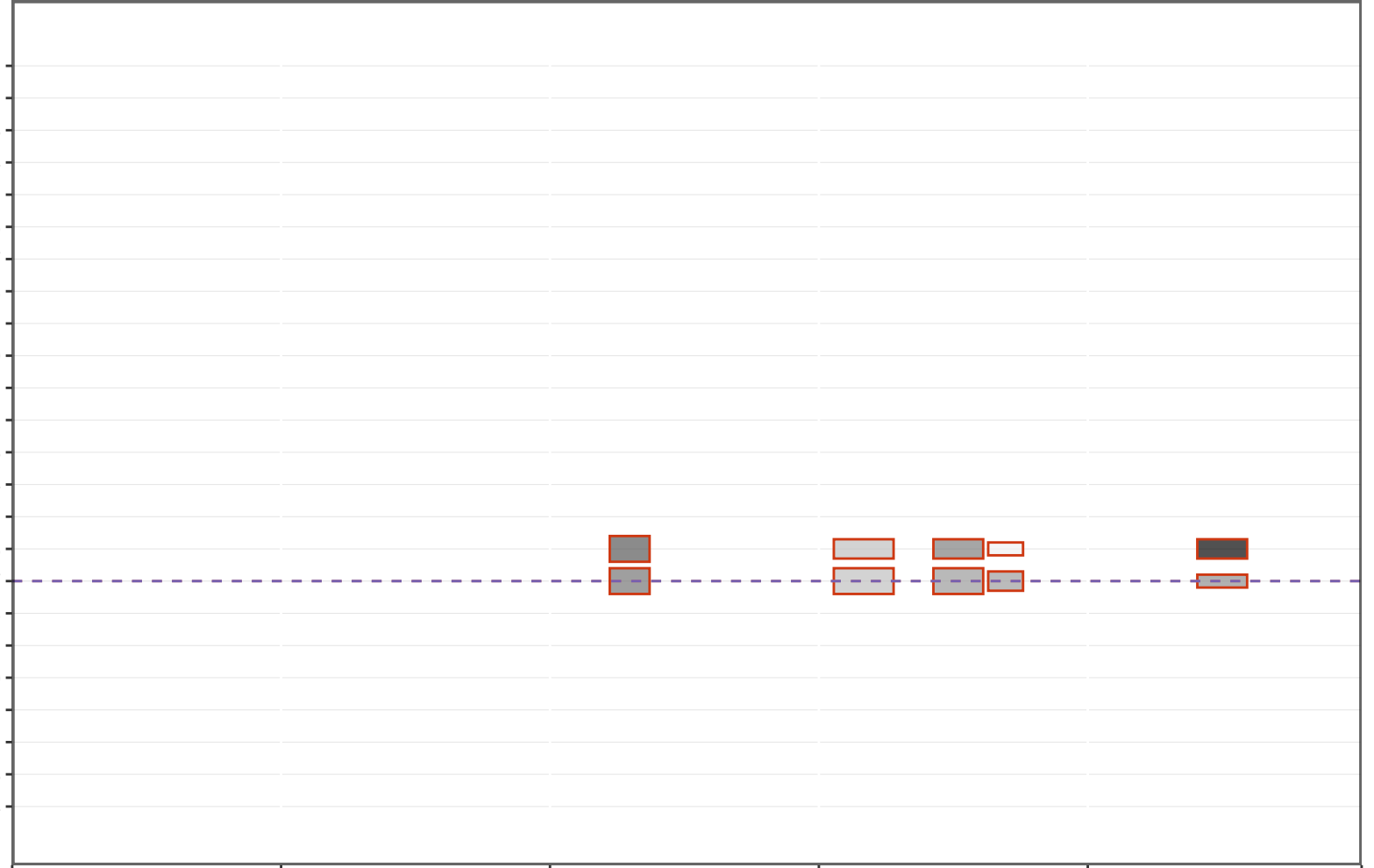
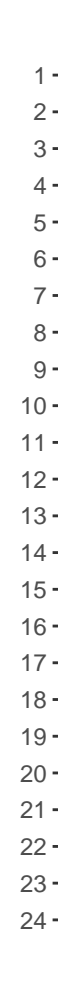
MW indication



Molecular weight



Gel Slice

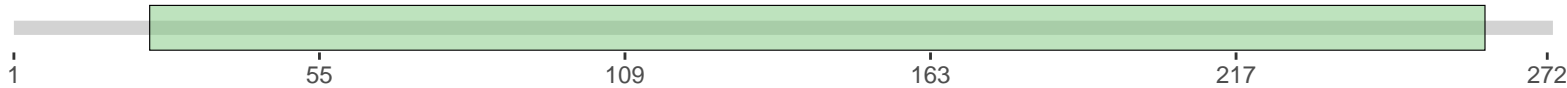


Peptide counts over 4 repeats

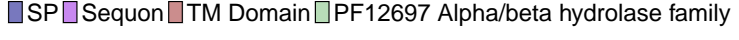
Protein length



Pfam domains



Pfam Description



Protein sequence:

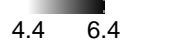
LLVASSPRFINLEDYVGGFEMTDIEGMFNIGENYGIWSSGFARIAVDPSDPPSVEKFEKLRMGVEVALPLAKTVFLSDYRGLKVVTPCTHQCKIDFVPSNVAIFMHTNKGASTVEINTRGHFPLQTAHEFLNIVHRVLTSP

NbL10g06040.1 thylakoid_luminal_15_kDa_protein_1_chloroplastic-like [MW = 23.32 kDa]

No. of times detected



log(intensity)



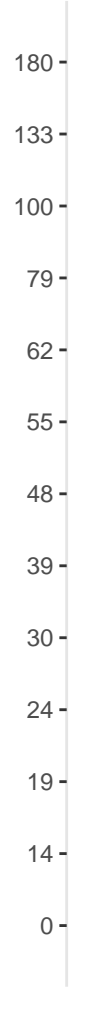
Values from



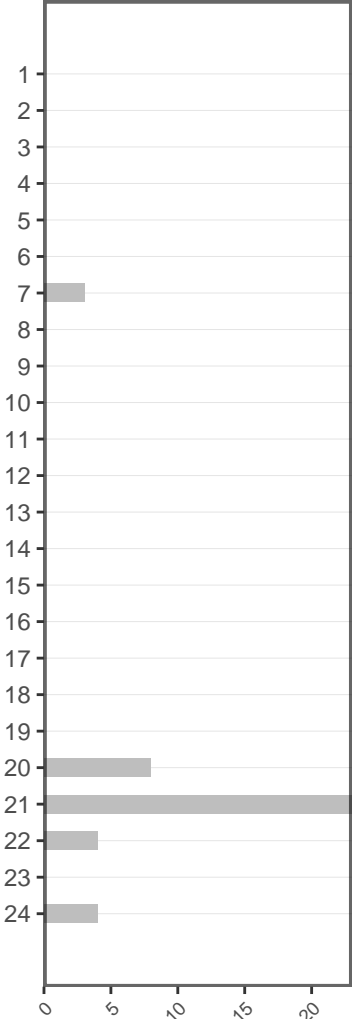
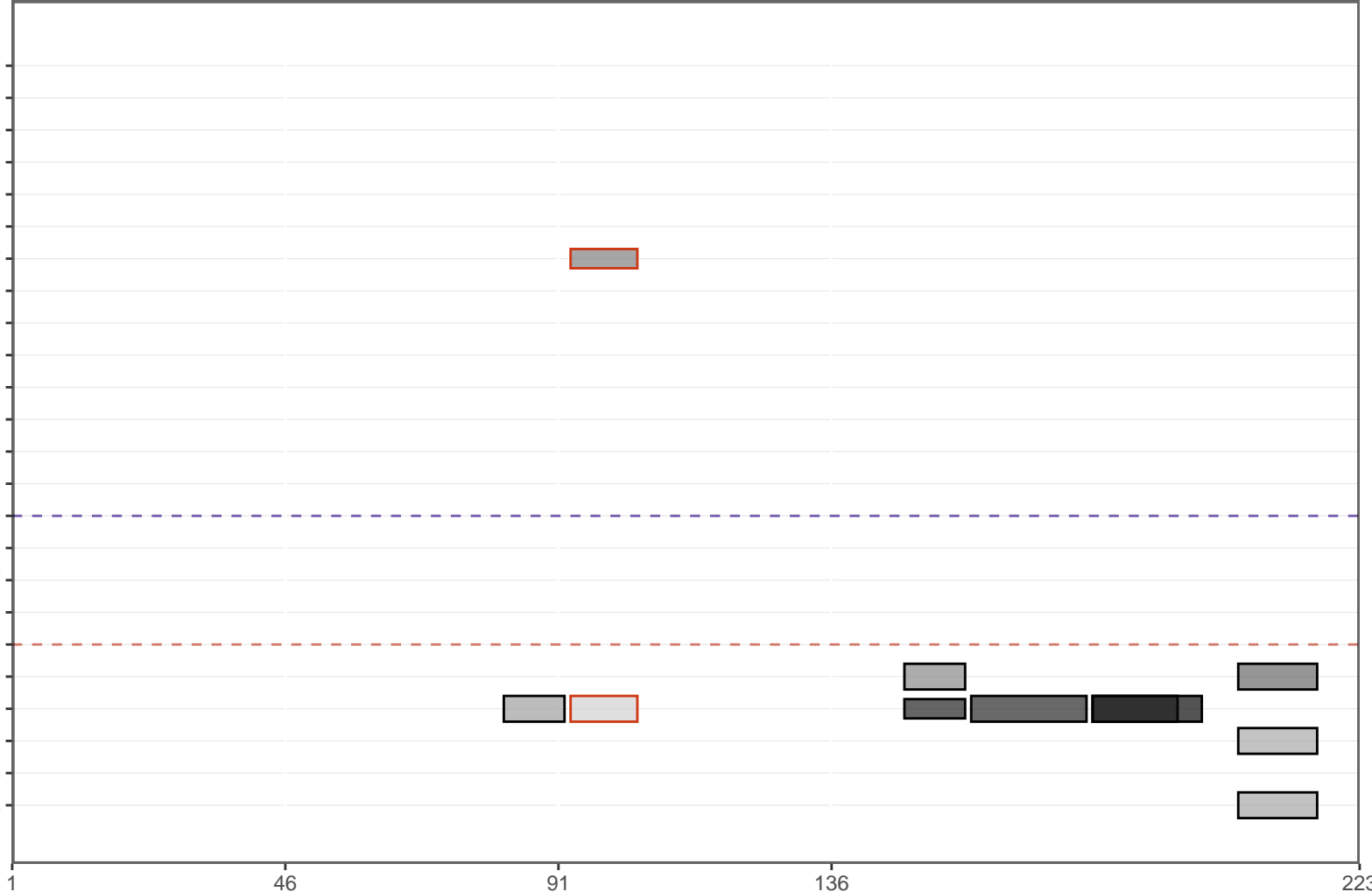
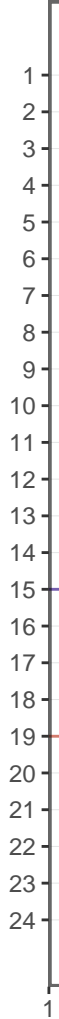
MW indication



Molecular weight



Gel Slice

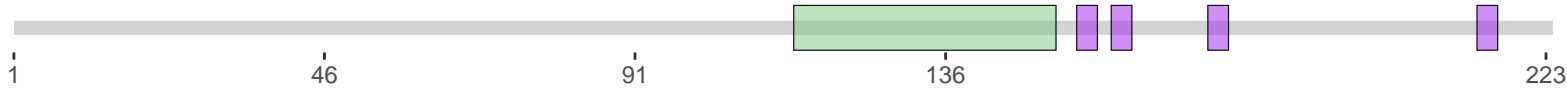


Protein length

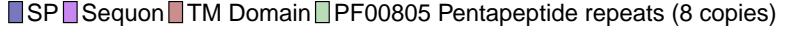


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IKDFSGKTLIKDQFKTSIRGAINFKGANLVGAFFDMLTGADLSADLRGADFSILANVTKVNLNANLEGALTTGNTSFKGSENEGADFTDPLRDDGIREYLCKIADGVNPFVTKGNATRDTLFCV

NbL10g05890.1 tropinone_reductase_homolog_At5g06060-like [MW = 31.64 kDa]

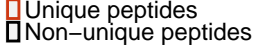
No. of times detected



log(intensity)



Values from



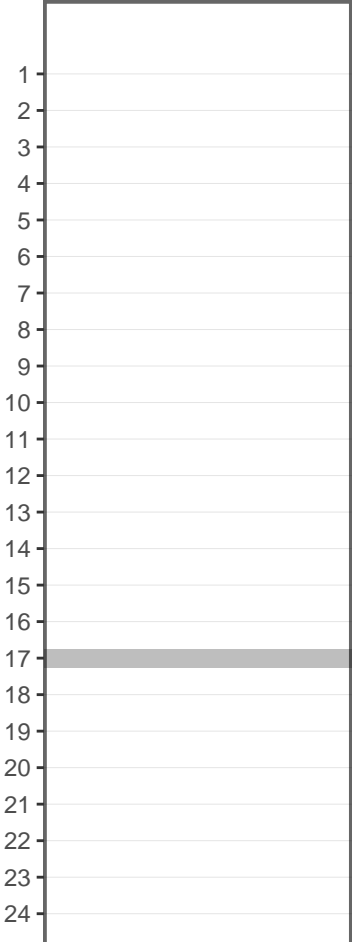
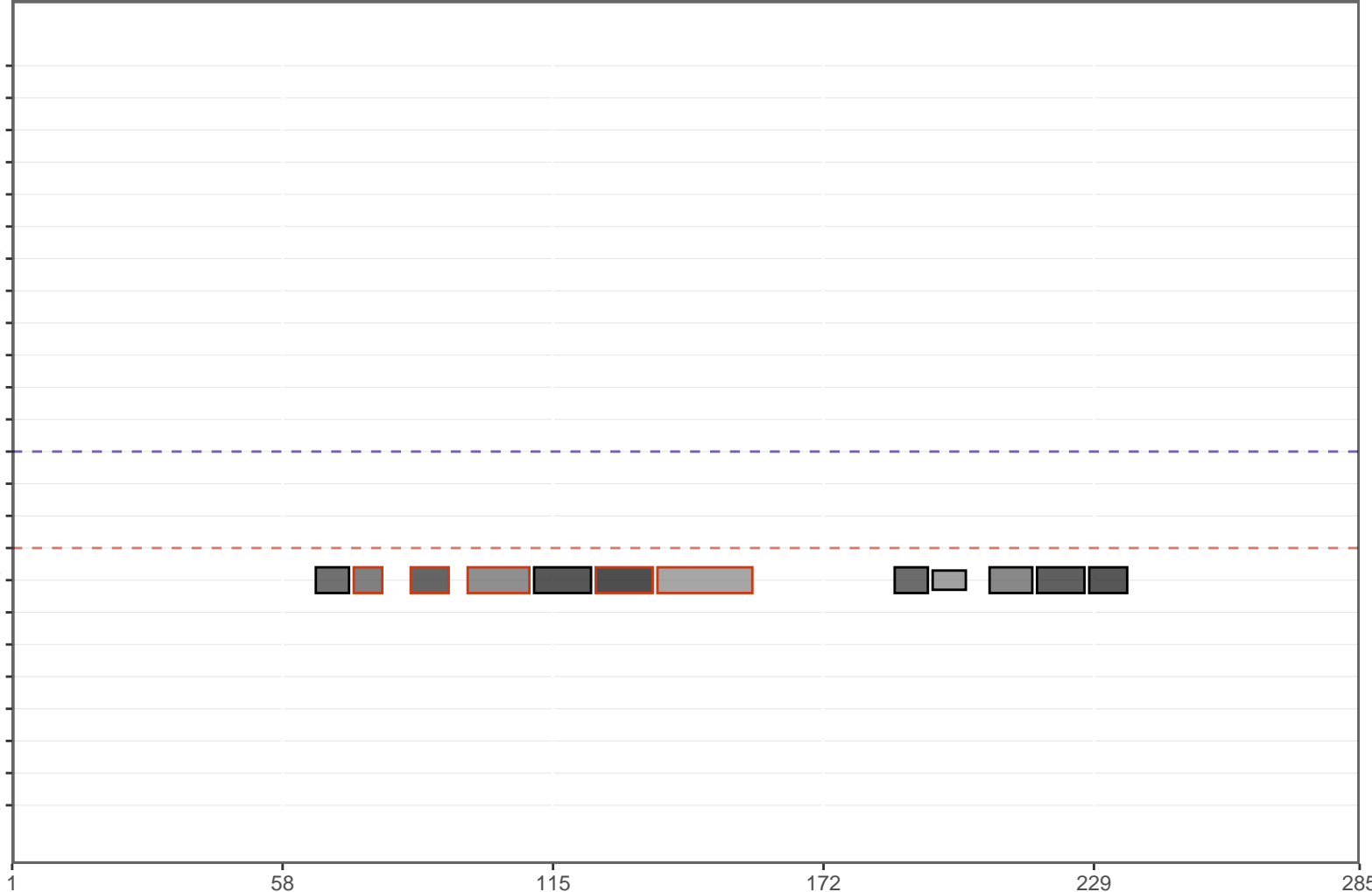
MW indication



Molecular weight

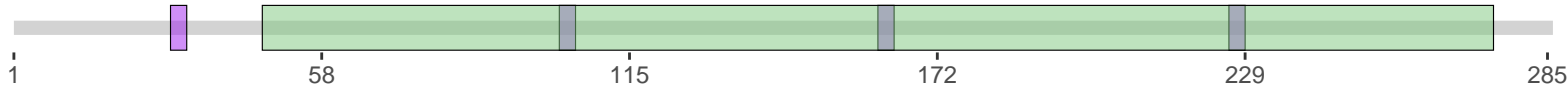


Gel Slice



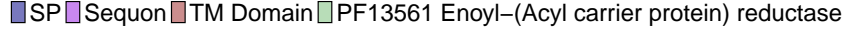
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DYTAEEYARLLSTNLESAHLOGLAHPLKASGNGSIVFISBSVAGLVHL66SGVYKATKGMNQLTRNLACEWAKDSIRVNGVAPVWVRTSLVEHLEKTKFLDGVIRTPLRAPGEE56QV6SLVWYLCPLGASVITGGVAVDVGDFVNGFEMTSVY

NbL10g05880.1 uncharacterized_LOC107798942 [MW = 23.31 kDa]

No. of times detected



log(intensity)



Values from



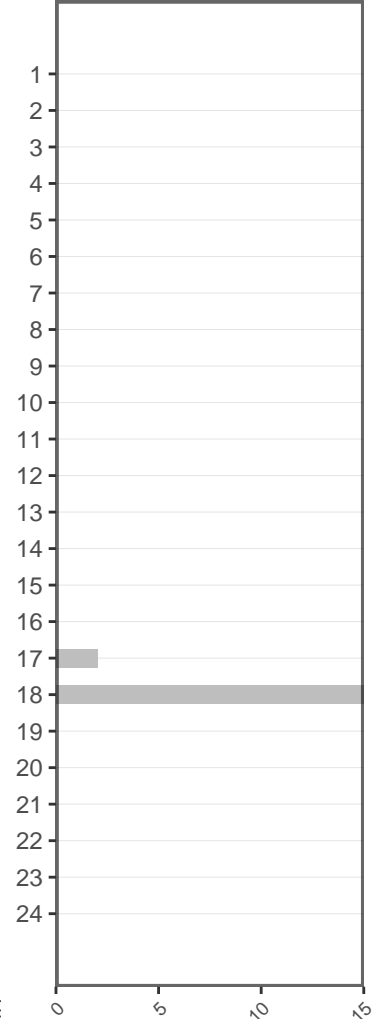
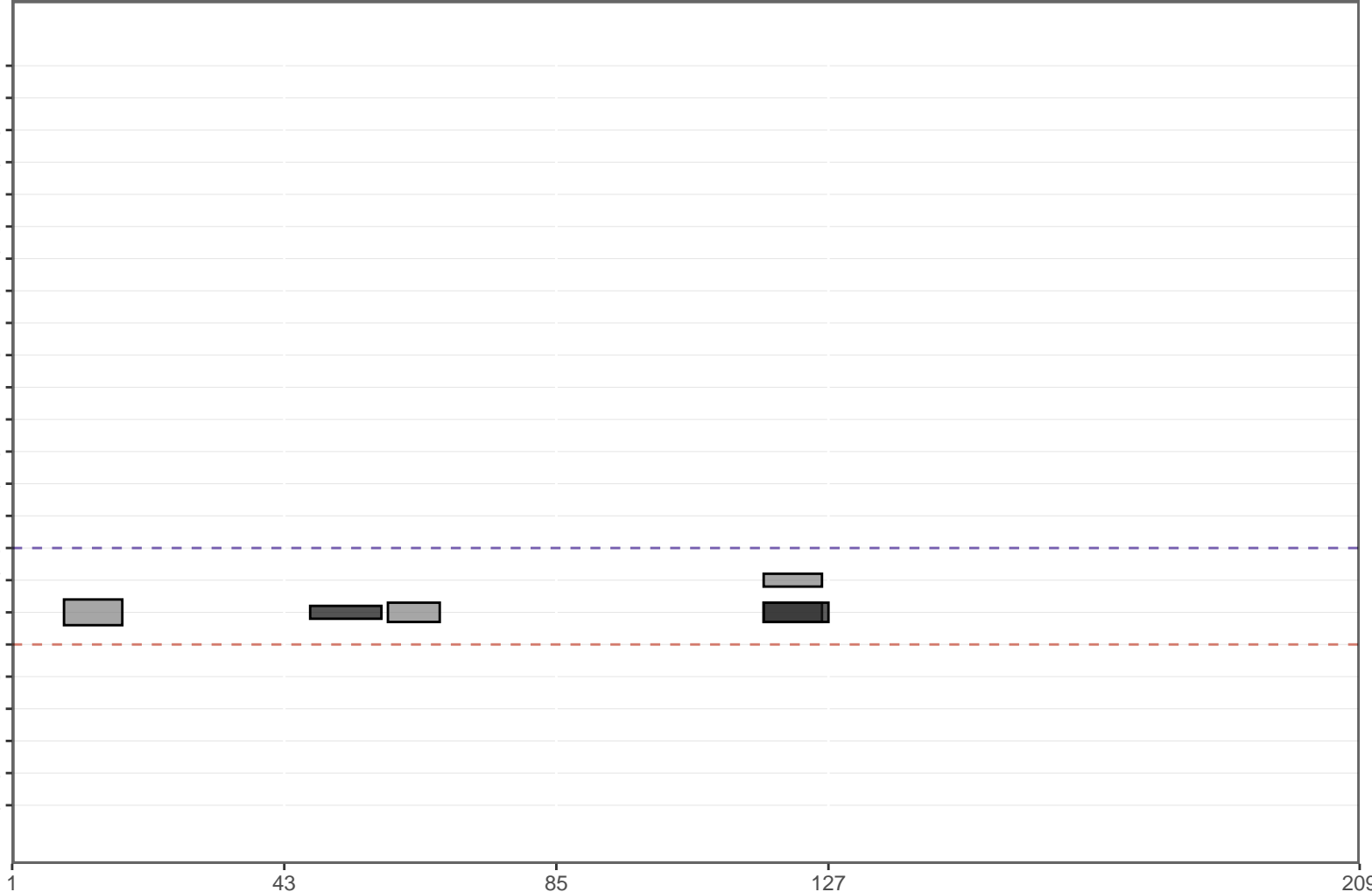
MW indication



Molecular weight



Gel Slice

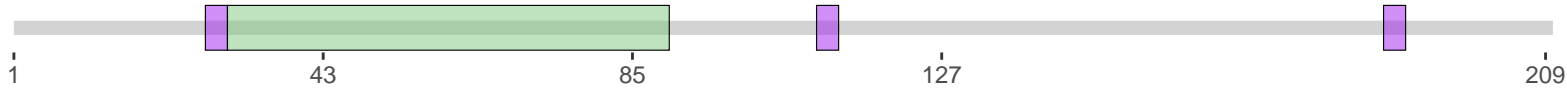


Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

SRDLYPRMEEEXKXMSKSKSSVDEDEPKKMHWLDEKRDTRSGSERRFRTRGRDREHGERSSEVAGAPAKFPVSSMRGYPAPRGVGGFLNSKIVGLLTVQVTAVGVGEC*

NbL10g05780.1 protein_DOWNSTREAM_OF_FLC-like [MW = 28.24 kDa]

No. of times detected



log(intensity)



Values from



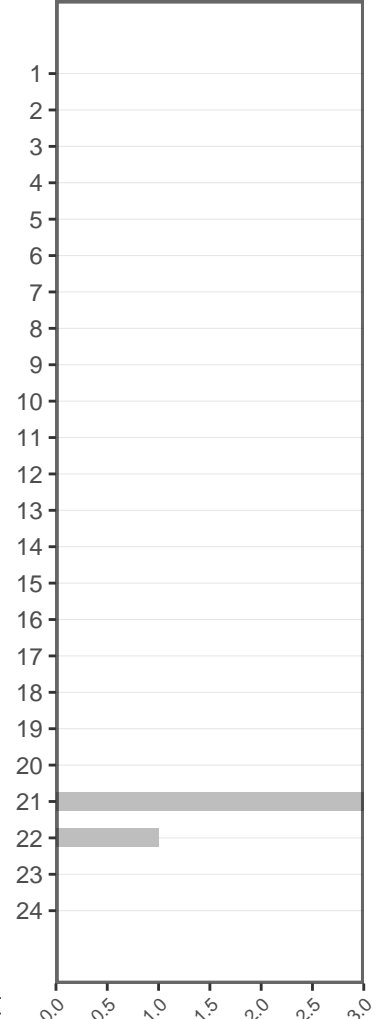
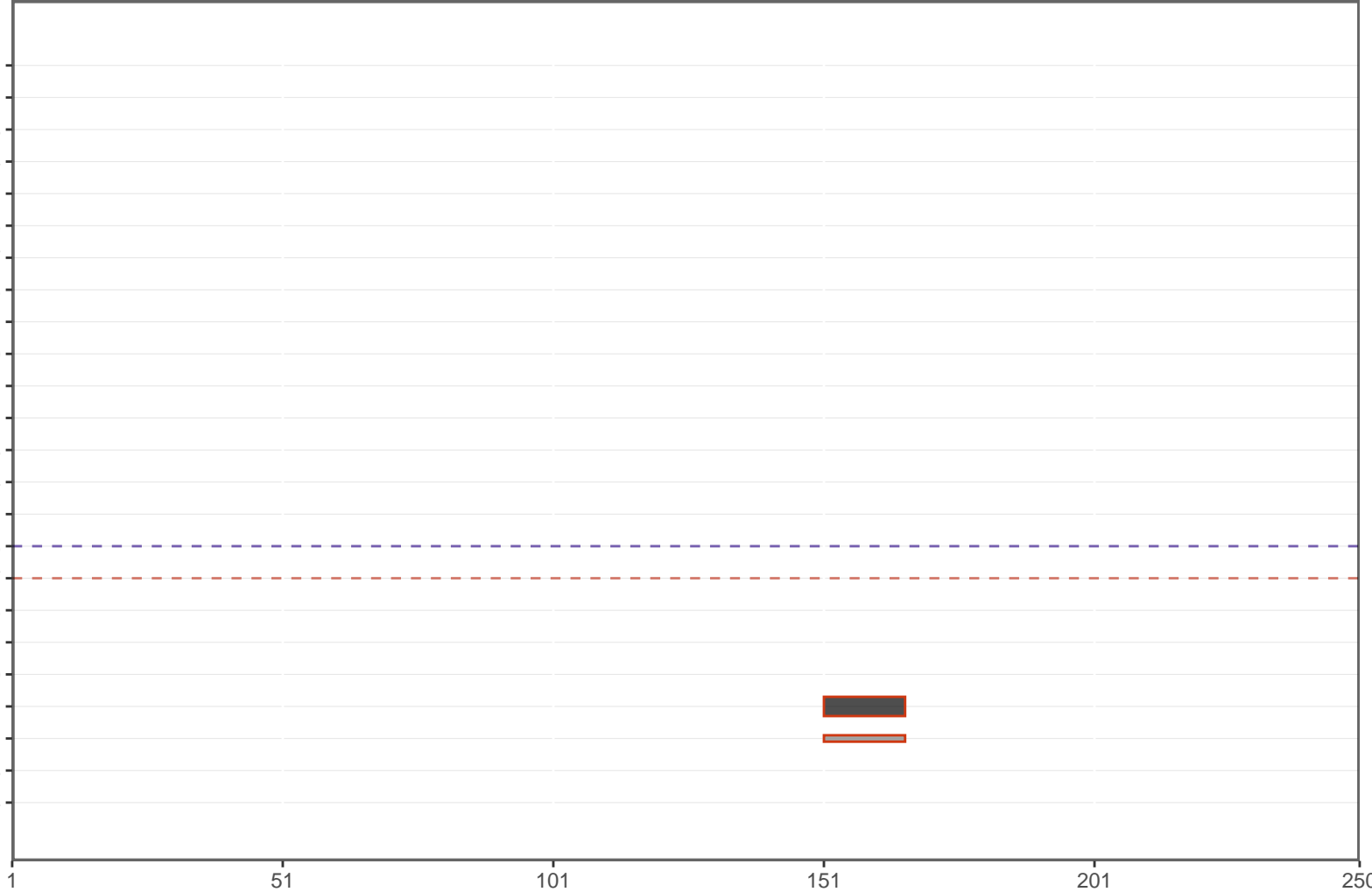
MW indication



Molecular weight

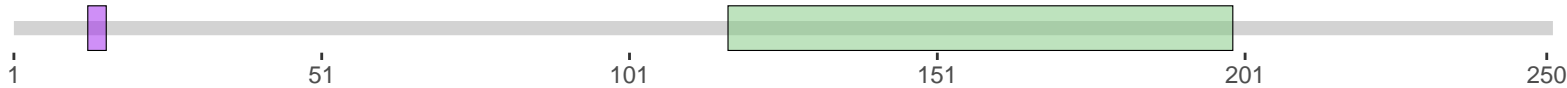


Gel Slice



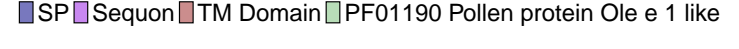
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

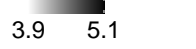
FLVKGKAYCDTCRGGFETPKYLAGAKVRIEGRHRVTEAPTFTVEGVTSKGEYNLVNSDRGGDDVCDLVKSPDTCAPNAGRDGRVILTRNMGMSNTRFANAMGFLRDEPLSSCTQLGGYQLTDDGV

NbL10g05540.1 peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase_A-like [MW - SP = 63.94 kDa]

No. of times detected



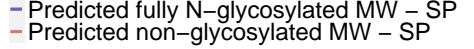
log(intensity)



Values from



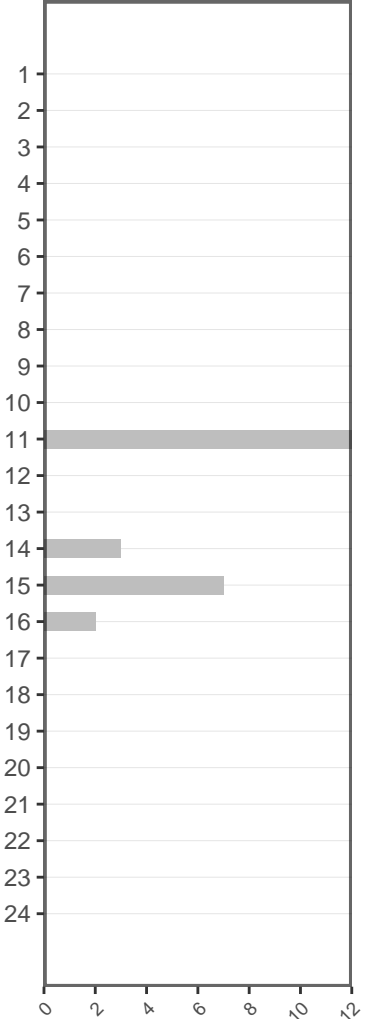
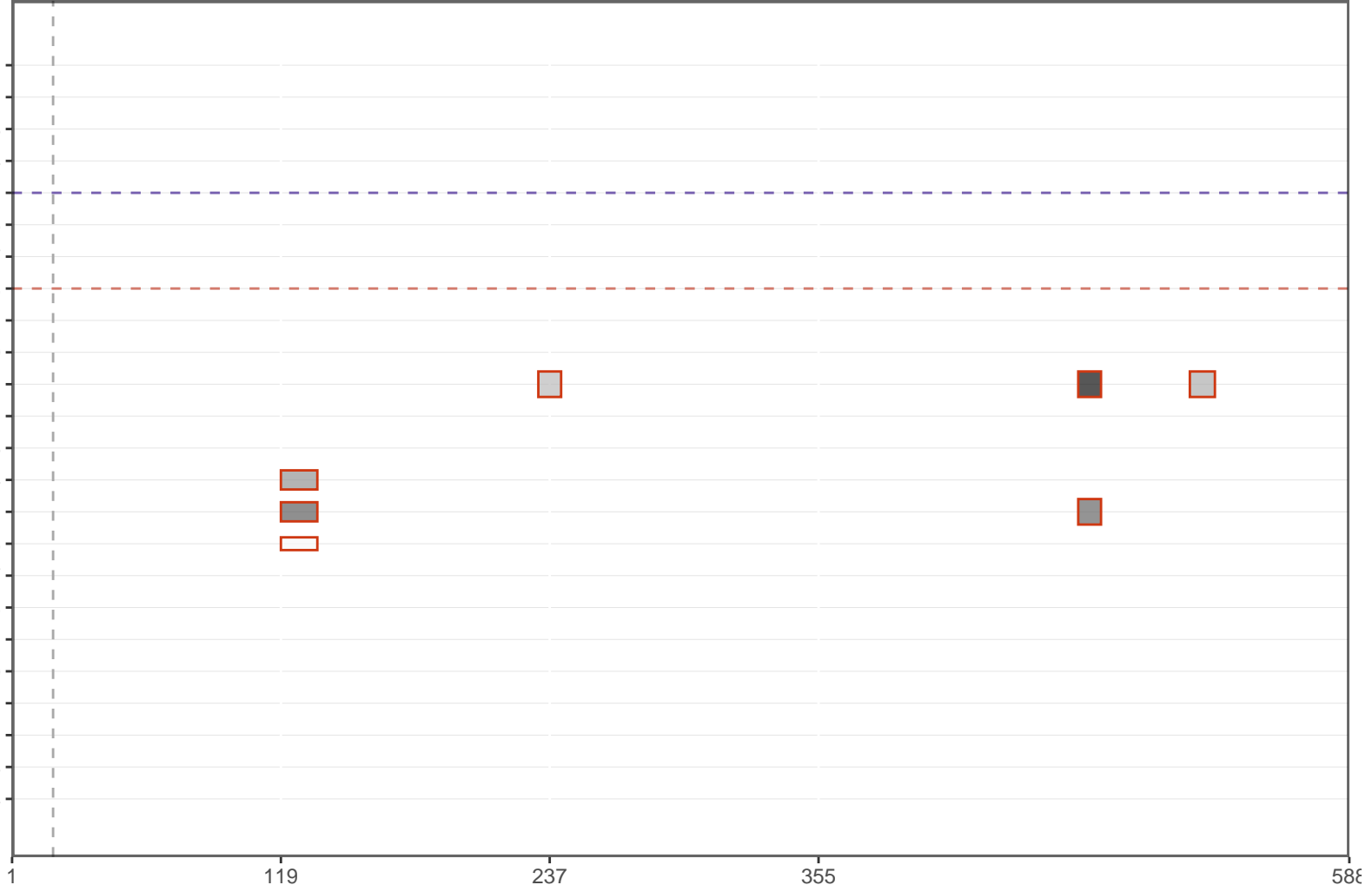
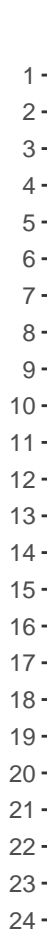
MW indication



Molecular weight

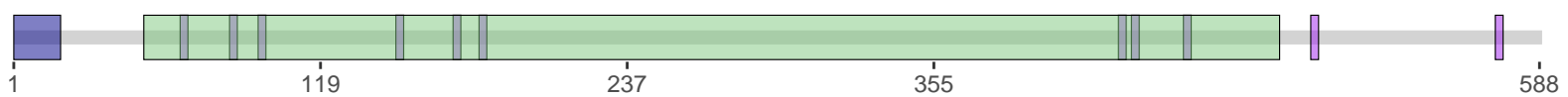


Gel Slice



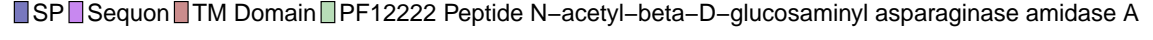
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

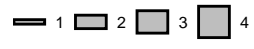


Protein sequence:

KRHHGAYREYLLMDKMLGSLVFPFVFTGRINPLFWEKRVKIGAFELPBYDIDTFLFAMLLDGGKDLGLGVAADGPFVLLDGNLHLVDDGDKPGEVGAIEVLVYGAQPKNLELSSSFHGLDGSFEIEMGRKRKFSGWVNSGSLTITVSRREVKLKNEIKFYHNGTEKRVKQNVREESVIRVVSDDTGITGRITVKKYKPLSMFTKRLPSTENDTSLMTOLDHEWRERKKSIGLSISLNRQKCGGMMVVDGHDVLSGGATGQGYVYRDNVDCYRSVSAANGTMSDI

NbL10g05530.1 eukaryotic_translation_initiation_factor_2_subunit_alpha_homolog [MW = 38.55 kDa]

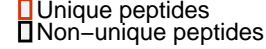
No. of times detected



log(intensity)



Values from



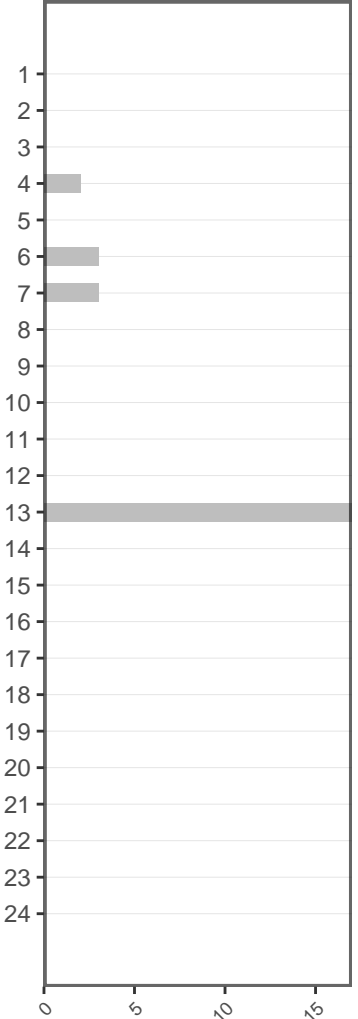
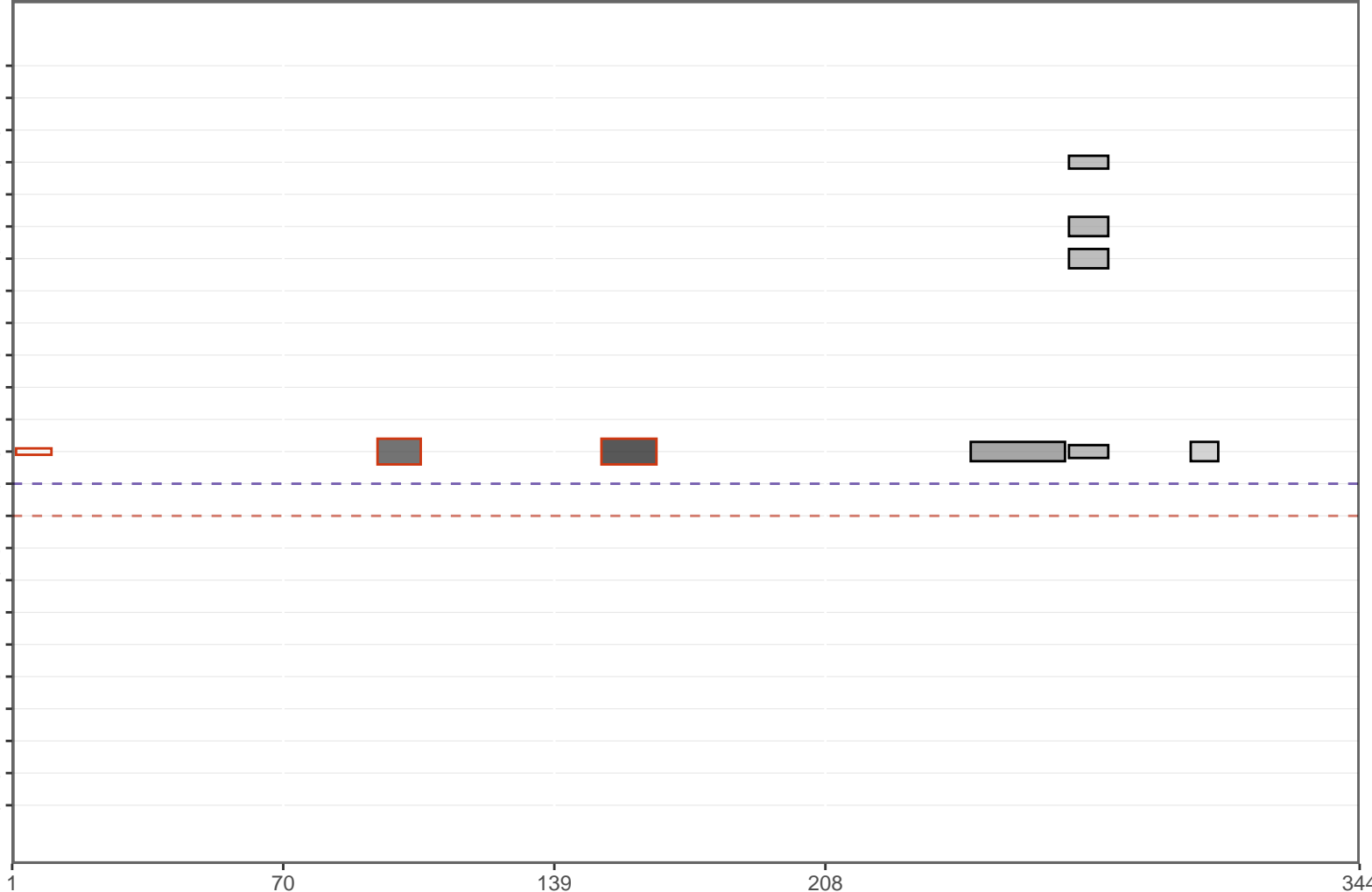
MW indication



Molecular weight

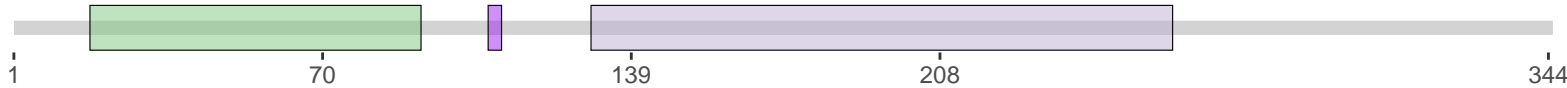


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00575 S1 RNA binding domain
- PF07541 Eukaryotic translation initiation factor 2 alpha subunit

Protein sequence:

ILNSLSTREYKENGPDGKEVTKVAPLSEEVKDALVKNRRRMTPLKIRADIEMKGFDFGLVHKEAMRKAEAAAGNDGCPVKKLWAPWVYLVNTGFLDKEGIALTKAAACTEEIERKGGKLVKKEAPRVAEREDKLLAEQMAKLGRENEEIGDGEDEEEEDTGMAEIDVDSGAGIRE

NbL10g05400.1 protein_HOTHEAD-like [MW - SP = 60.23 kDa]

No. of times detected



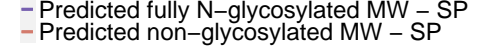
log(intensity)



Values from



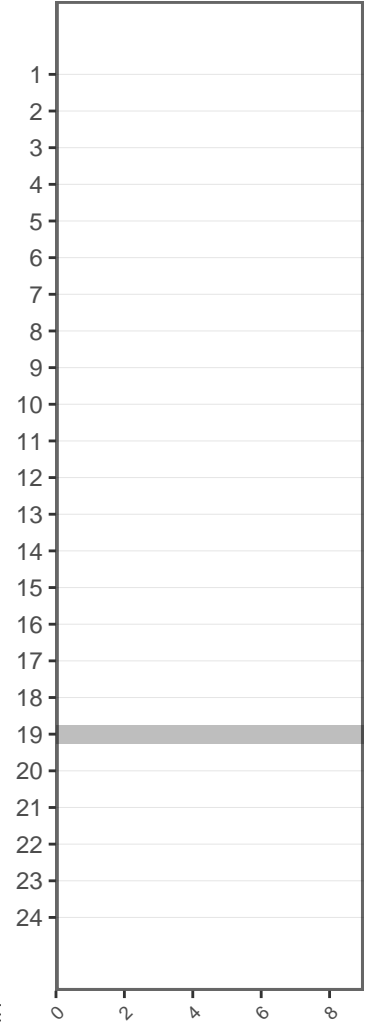
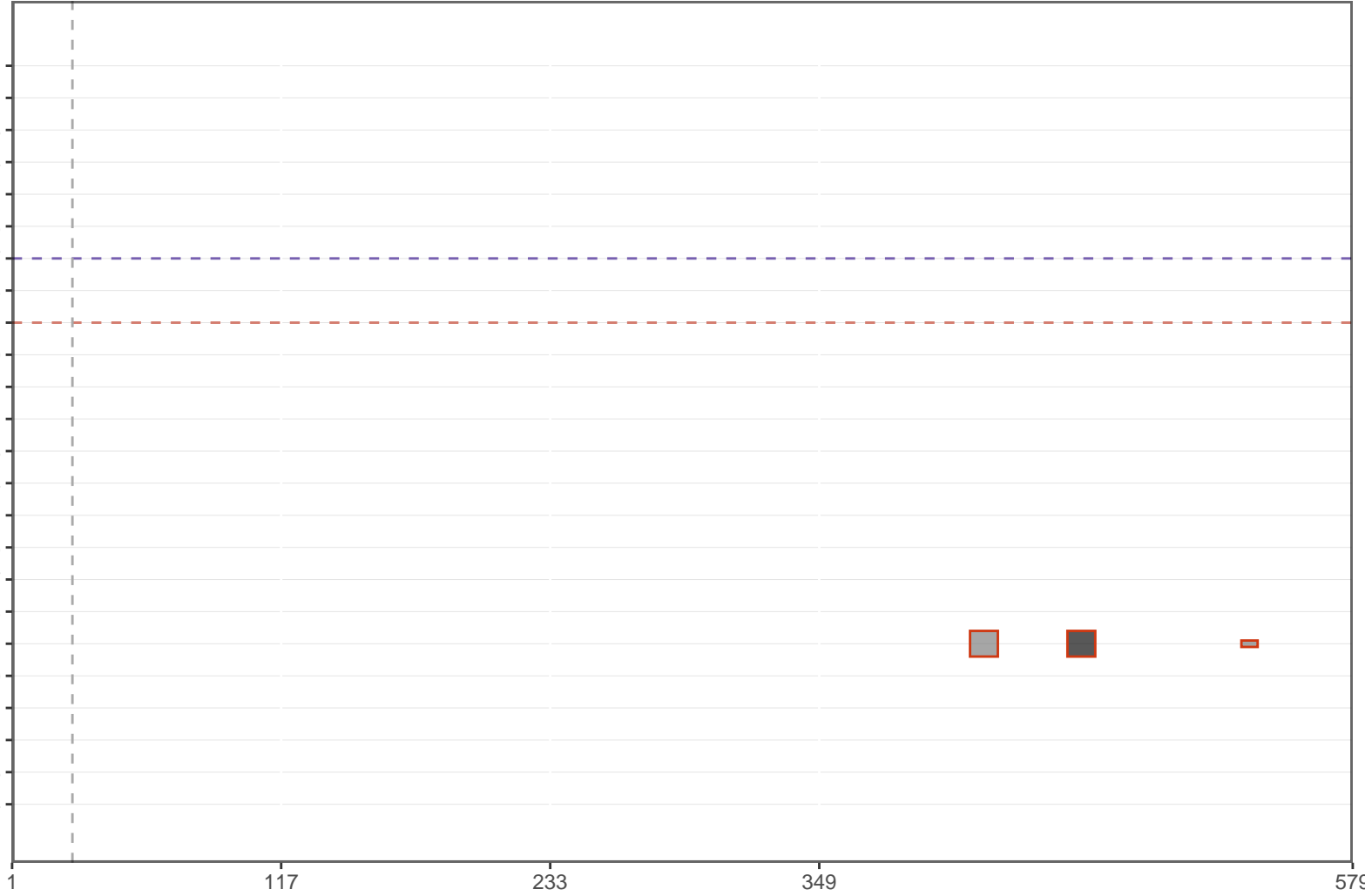
MW indication



Molecular weight

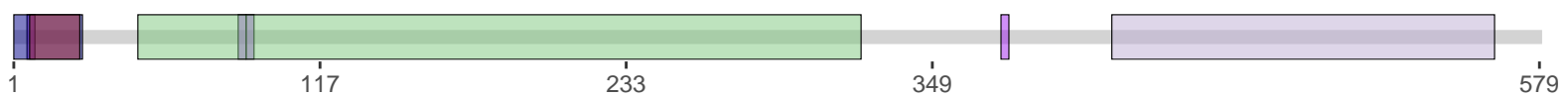


Gel Slice



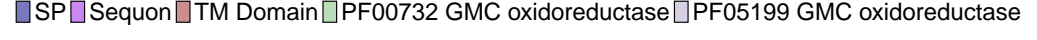
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LSAGALGSPQLMLGGIGPKAKLKAHGIYLVDPVAVGMMGSDNFMNAVFPSPFHPVEVSLKQVVGITGFKSEYEAASGPLELDWMRRHAHDFTTIANQNTMDPLKMPASAHFPGKPKPGLNHLHTPMAGLLEKWKVGYSTGFLLEKSKDPENENPKVTFYFKDPRDLGRGVGDMKTAIEVIESTGFSKFRVYPTFSAGLMDTMTLTFPLNLRPRHLSASVSLGEGFDITVMTWVHHGGGQGVKVDNRNRYVGVVGLRVIDGSTRFYSFGTNPQATVAMLGRYMGQKLLK

NbL10g05350.1 probable_calcium-binding_protein_CML13 [MW = 16.54 kDa]

No. of times detected



log(intensity)



Values from

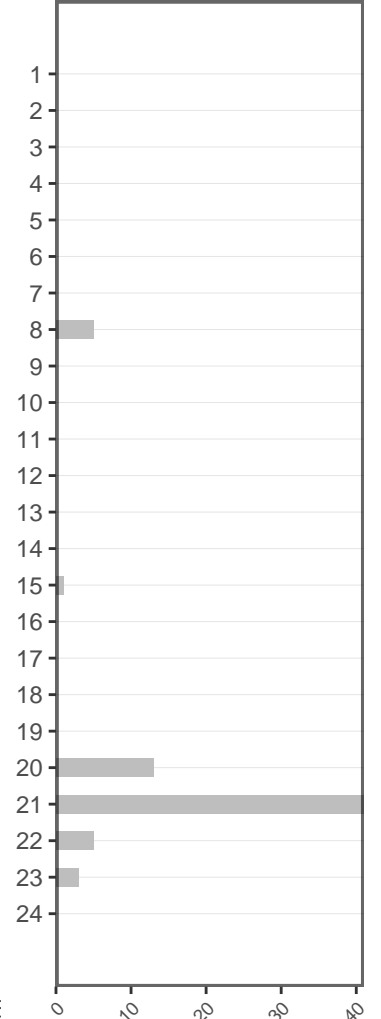
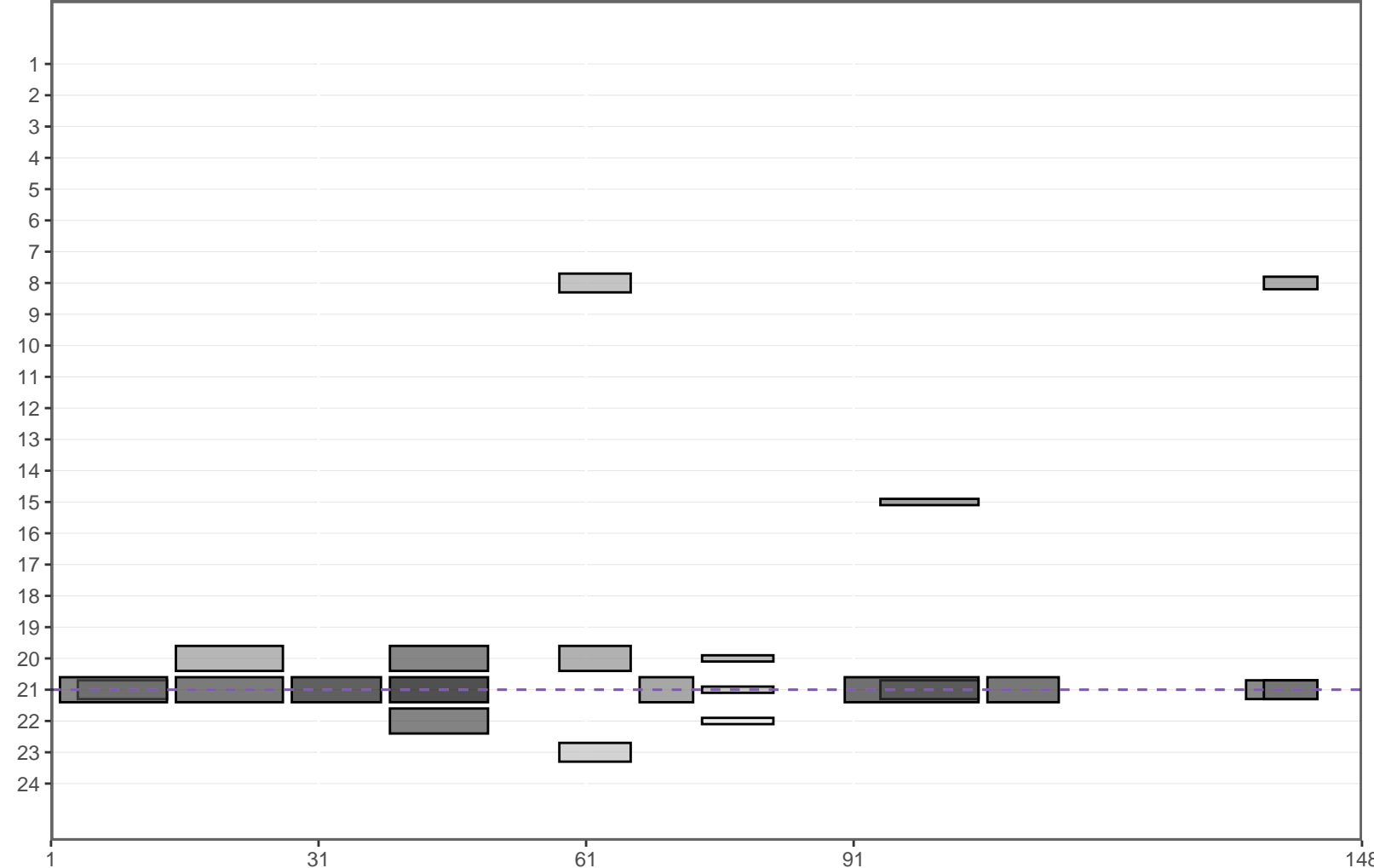
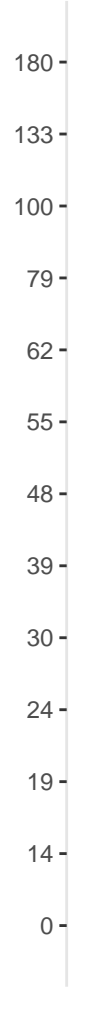


MW indication



Molecular weight

Gel Slice



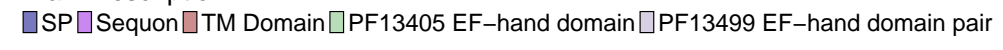
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PFDFNRFLLELMSQHLKPEPFDRGLRDAFKVLDKDGTFVWVSDLKHILTSIGEKLEAAEFDEWIREVAVGSDGKIRYEDFIARMCAGK

NbL10g05250.1 quinone_oxidoreductase-like [MW = 41.47 kDa]

No. of times detected



log(intensity)



Values from



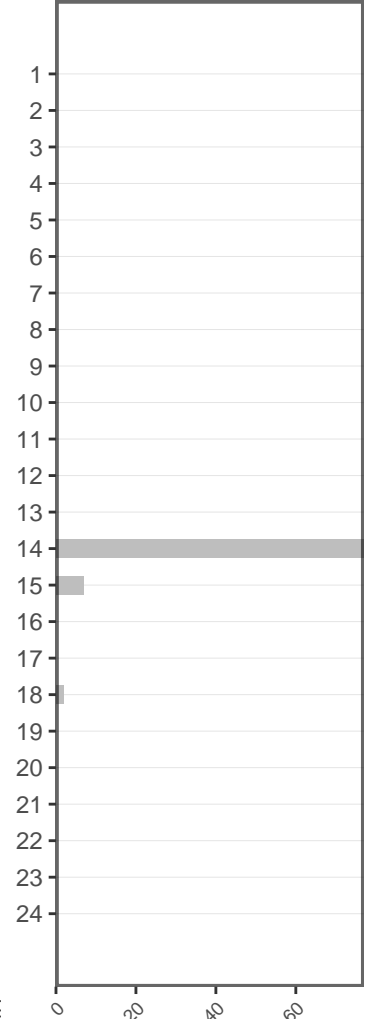
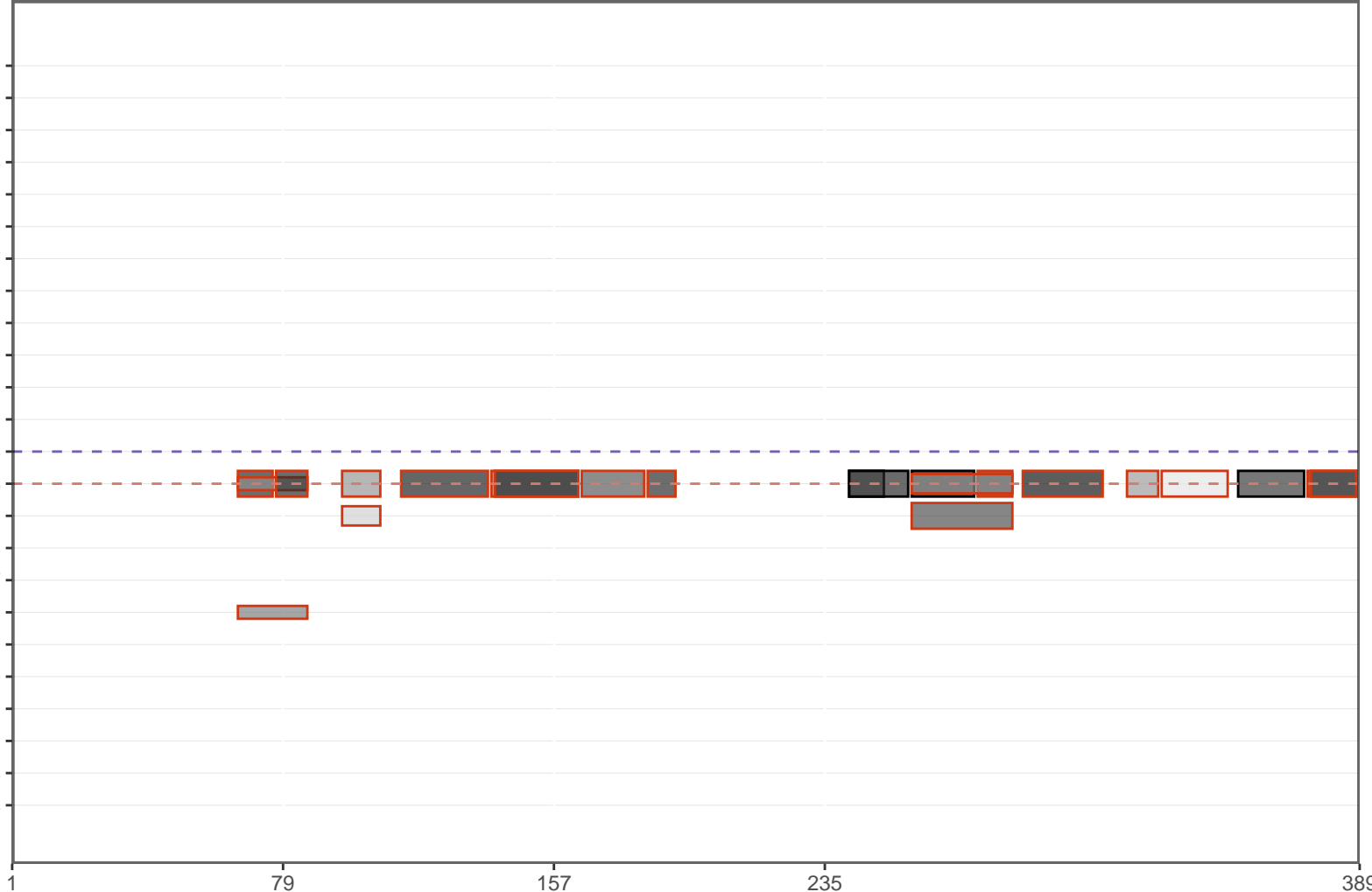
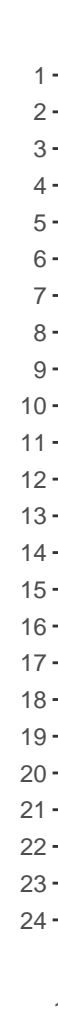
MW indication



Molecular weight



Gel Slice



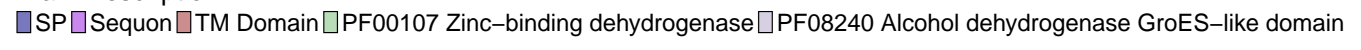
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IMTAQFLRRCFKVEHGHTVLMHAAGVGSLLGGWALGATVIGTGTETKEKAQAKDDGGHHVHYKEDFVTRVNEITSGGGVEVYVDSVKGKDTFGGSLDCLKTRGCMVDFGGASGLPDPVPLSALAVKSLFTRPMMHNYTTRDELLETAGEVFANAAGVLRVRYVNIHTYPLGQAQAHAHDLSEKRTGGSSVLLPDGQK

NbL10g05190.1 protein_mago_nashi_homolog [MW = 20.74 kDa]

No. of times detected



log(intensity)



Values from



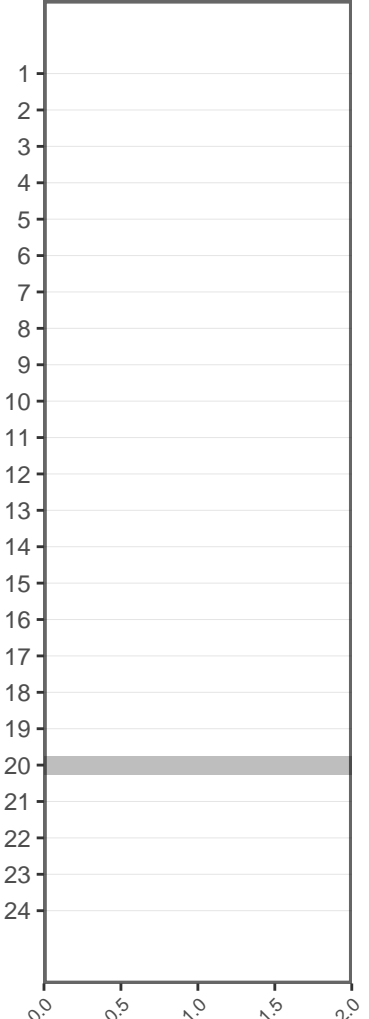
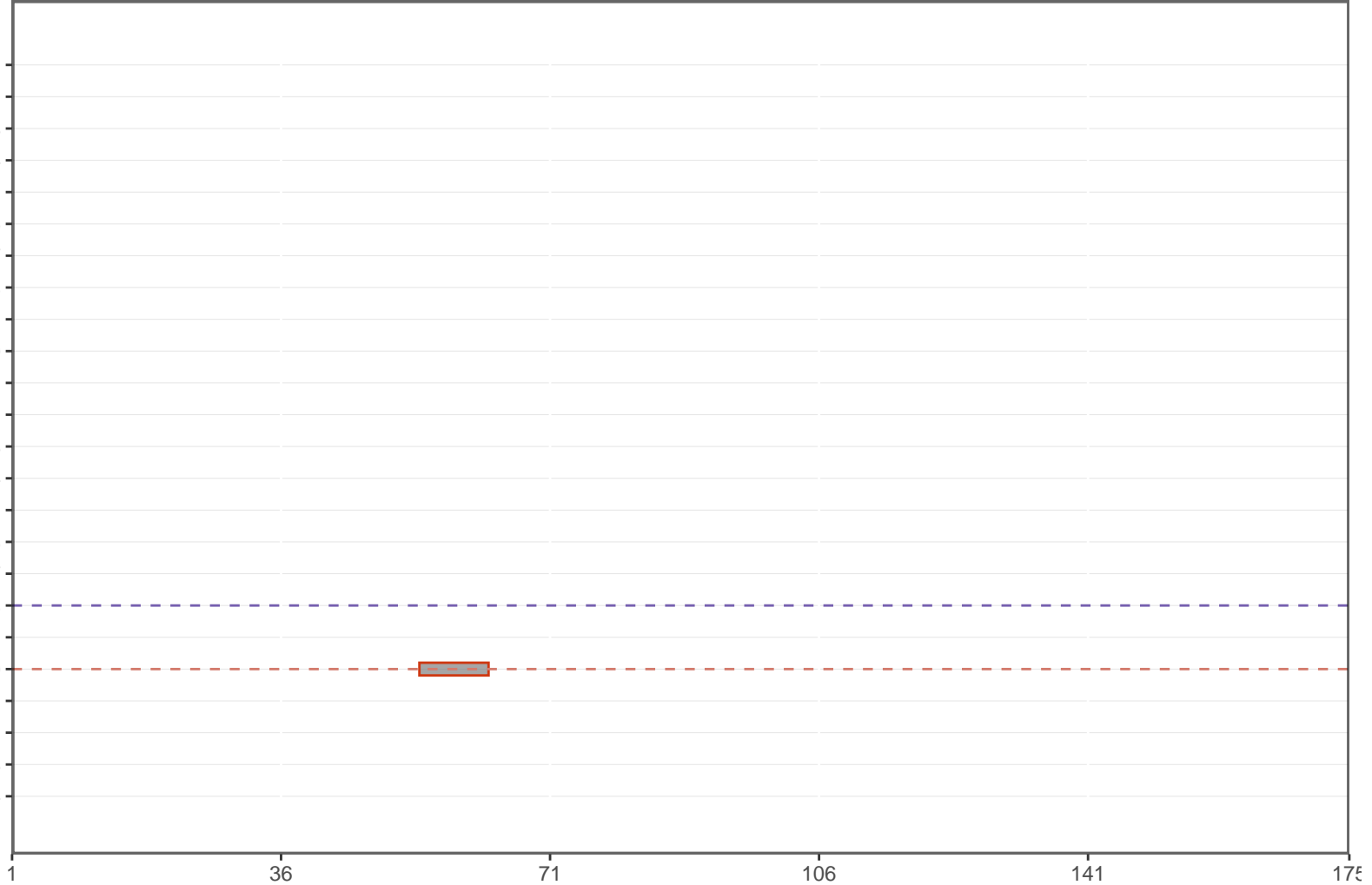
MW indication



Molecular weight

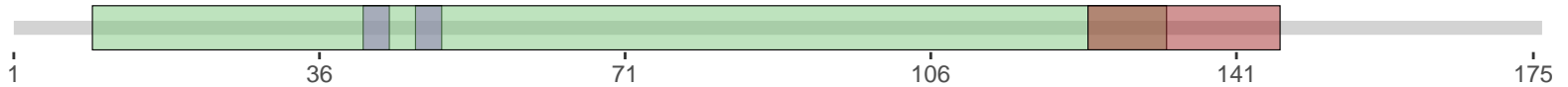


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IMKEDDNVPEPRDRVGRGELEVMGNEHGFSTSGKSLMDVDTKDPKPEGLRIFVYLVQVFIASFGIPYFMFMKFKLIRGIVLHQVWAKMWNLYTW

NbL10g05170.1 glutamate_dehydrogenase_A [MW = 44.87 kDa]

No. of times detected



log(intensity)



Values from



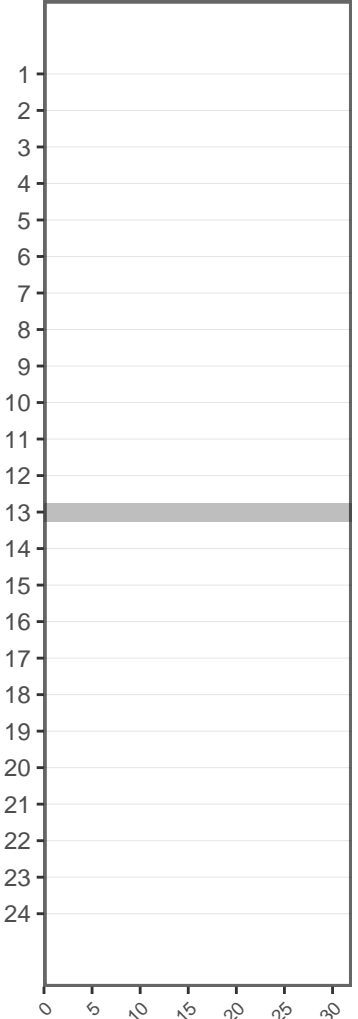
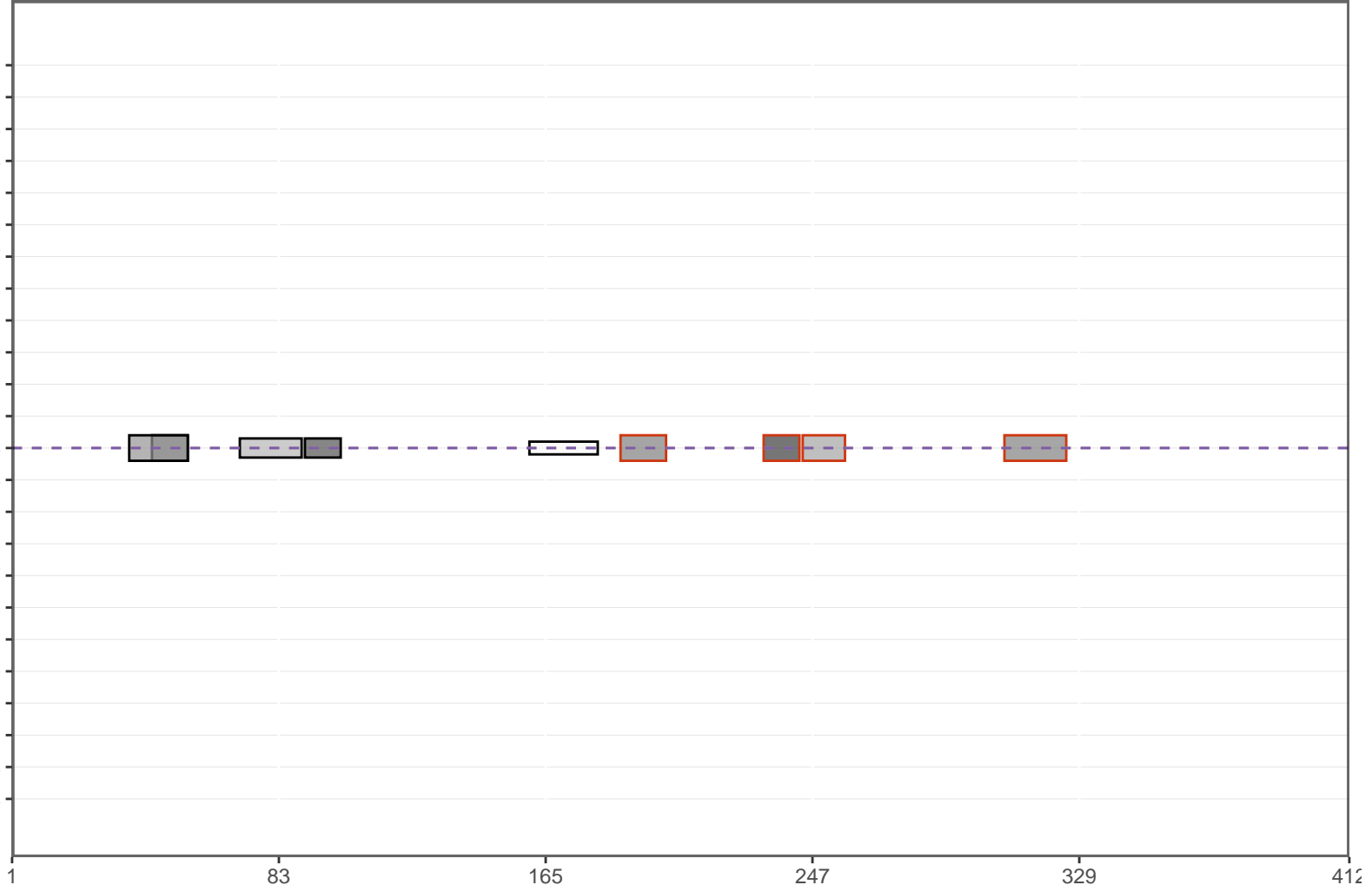
MW indication



Molecular weight



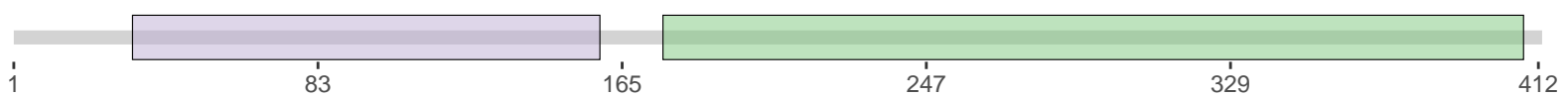
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00208 Glutamate/Leucine/Phenylalanine/Valine dehydrogenase
- PF02812 Glu/Leu/Phe/Val dehydrogenase, dimerisation domain

Protein sequence:

TEALLAEYGNKIDLFFANGFGNGAWAAKLHRRGGKVIIVSDITGAVKFPDGLDIPALLNHKEATGKLDPSGGGVAMNSDEVLTHEGDVLPALGGVLRRENSDNVRAKFRFEAANHTDPEADELRSKGGVILPDIYANAGGVTVSYFEWVQNGSGFMWDEEKVRELKKYMTKAFKLNKMGDGHDCNLRMGAFILGVNRVRAATFLRGEA*

NbL10g05160.1 superoxide_dismutase_[Fe]_chloroplastic [MW = 28.04 kDa]

No. of times detected



log(intensity)



Values from



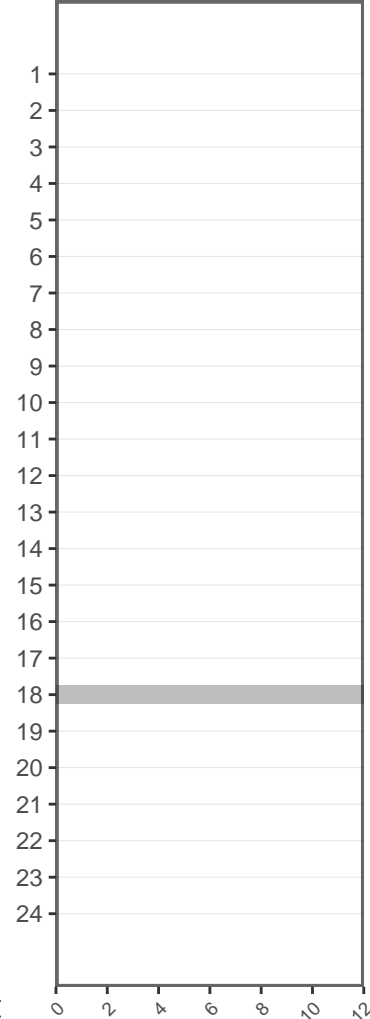
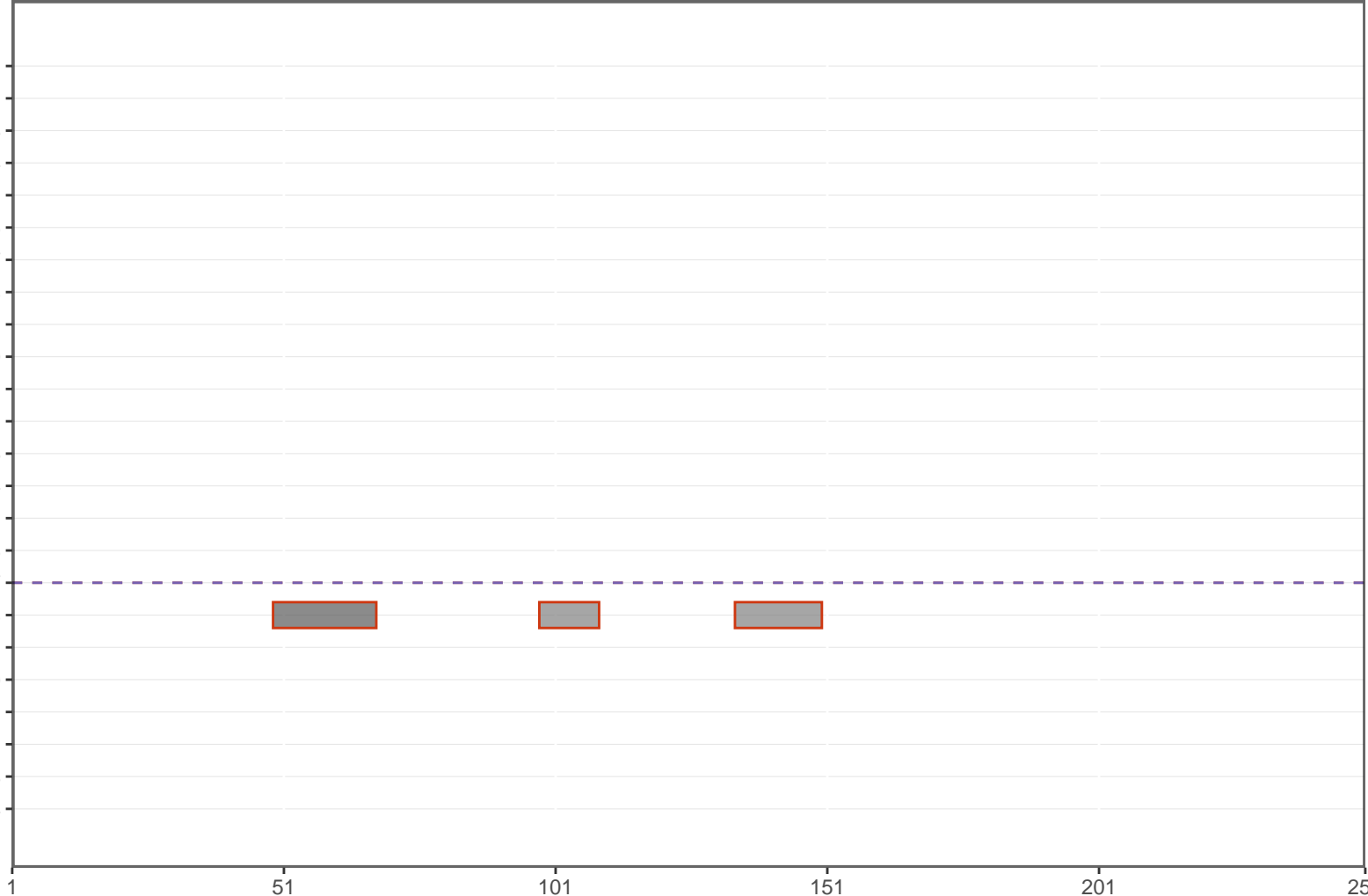
MW indication



Molecular weight

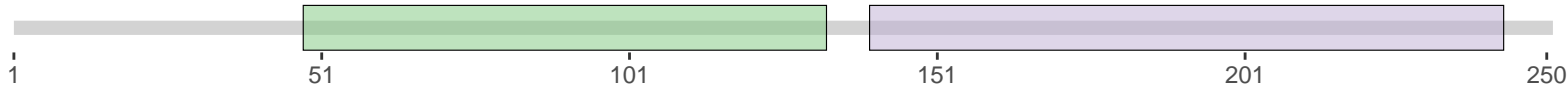


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00081 Iron/manganese superoxide dismutases, alpha-hairpin domain
- PF02777 Iron/manganese superoxide dismutases, C-terminal domain

Protein sequence:

PLPFAFNAAQAVNHNQFFWEEMKPNGGGEPSEGLLELINRDFGSDAFVKEFKAAATQFGSGWAWLAKPPEEKLLAVKTPNAENPLVGYTLLRDIWWEHAYVLDQGNRRPDVHSIFMEKLVSWEAVSSRLKAAAT

NbL10g05150.1 ATP_synthase_subunit_delta'-mitochondrial-like [MW = 21.42 kDa]

No. of times detected



log(intensity)



Values from



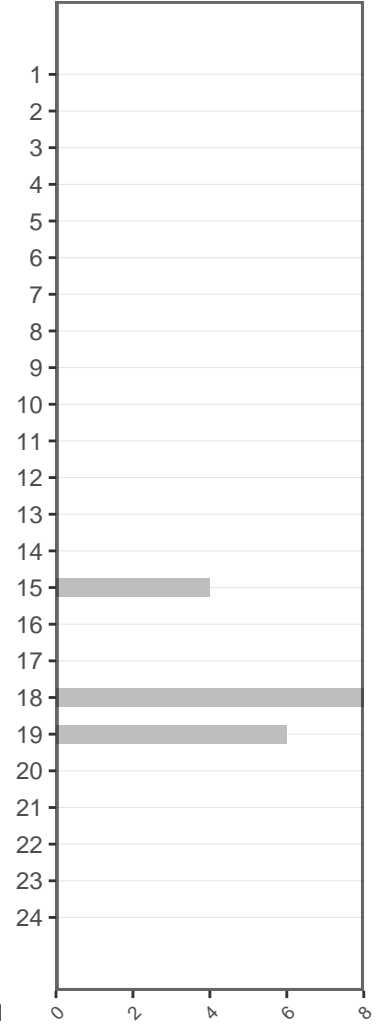
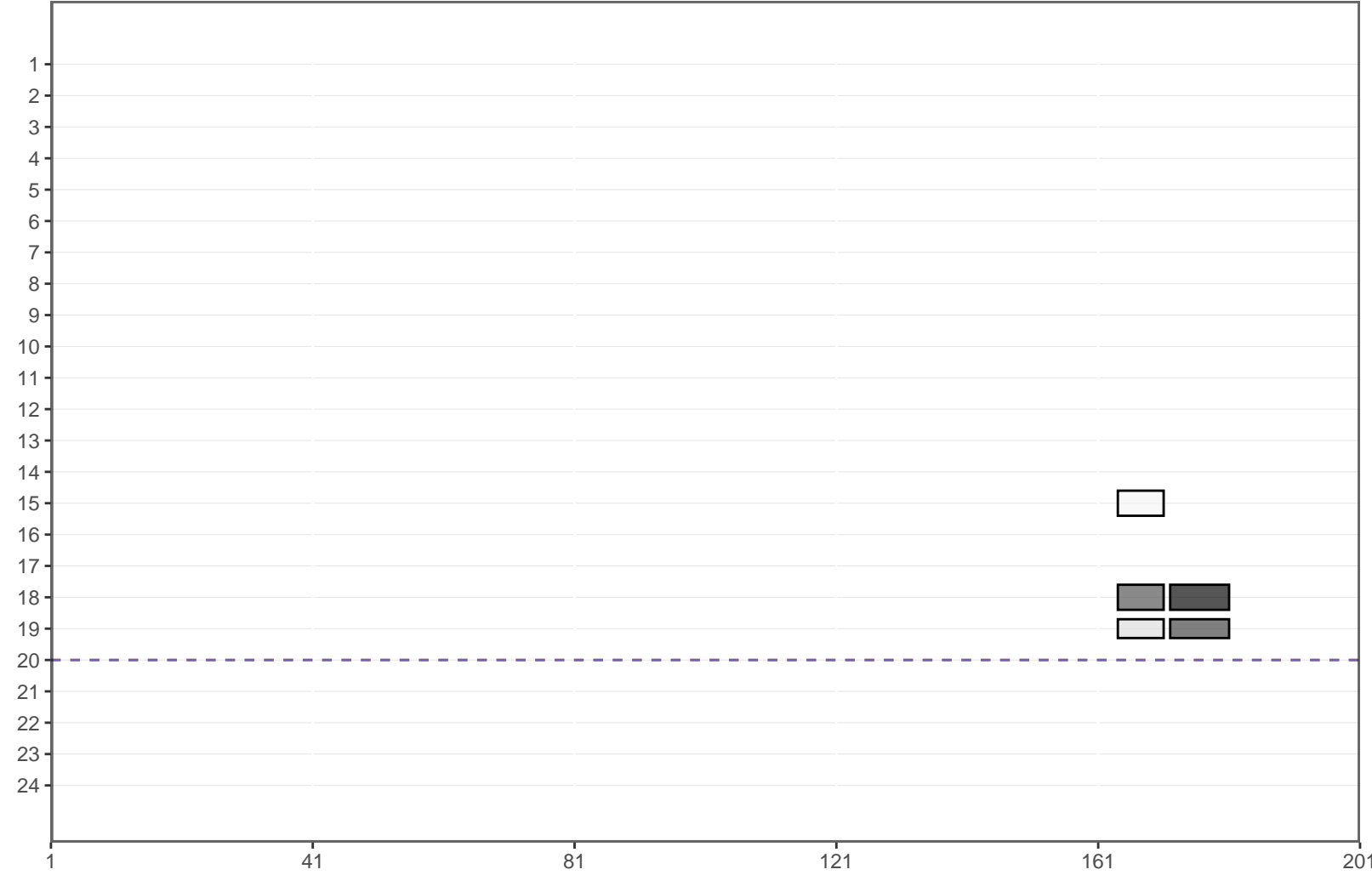
MW indication



Molecular weight

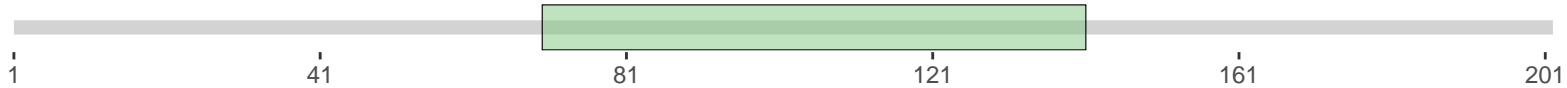


Gel Slice

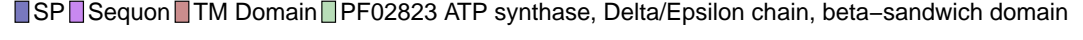


Protein length

Pfam domains



Pfam Description



Protein sequence:

IVDMVIRPTTGGMGLPGHWATIAELKPGVLSVHEGNDVSKYFVSGGFAFVHANSFADIAIEAIPLDKRDVDPNLVQKGLTEFTQKLESTASTDVEKAEAGIGVQVHSAALNAAITG

NbL10g05100.1 hydroxyacylglutathione_hydrolase_cytoplasmic [MW = 28.86 kDa]

No. of times detected



log(intensity)



Values from



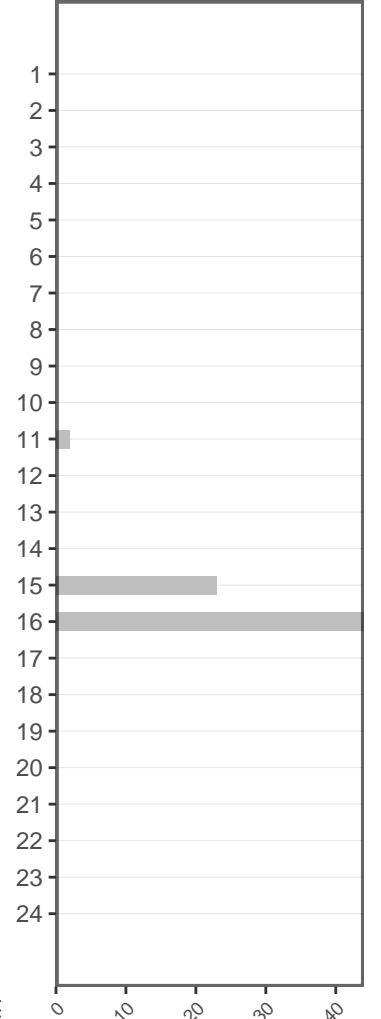
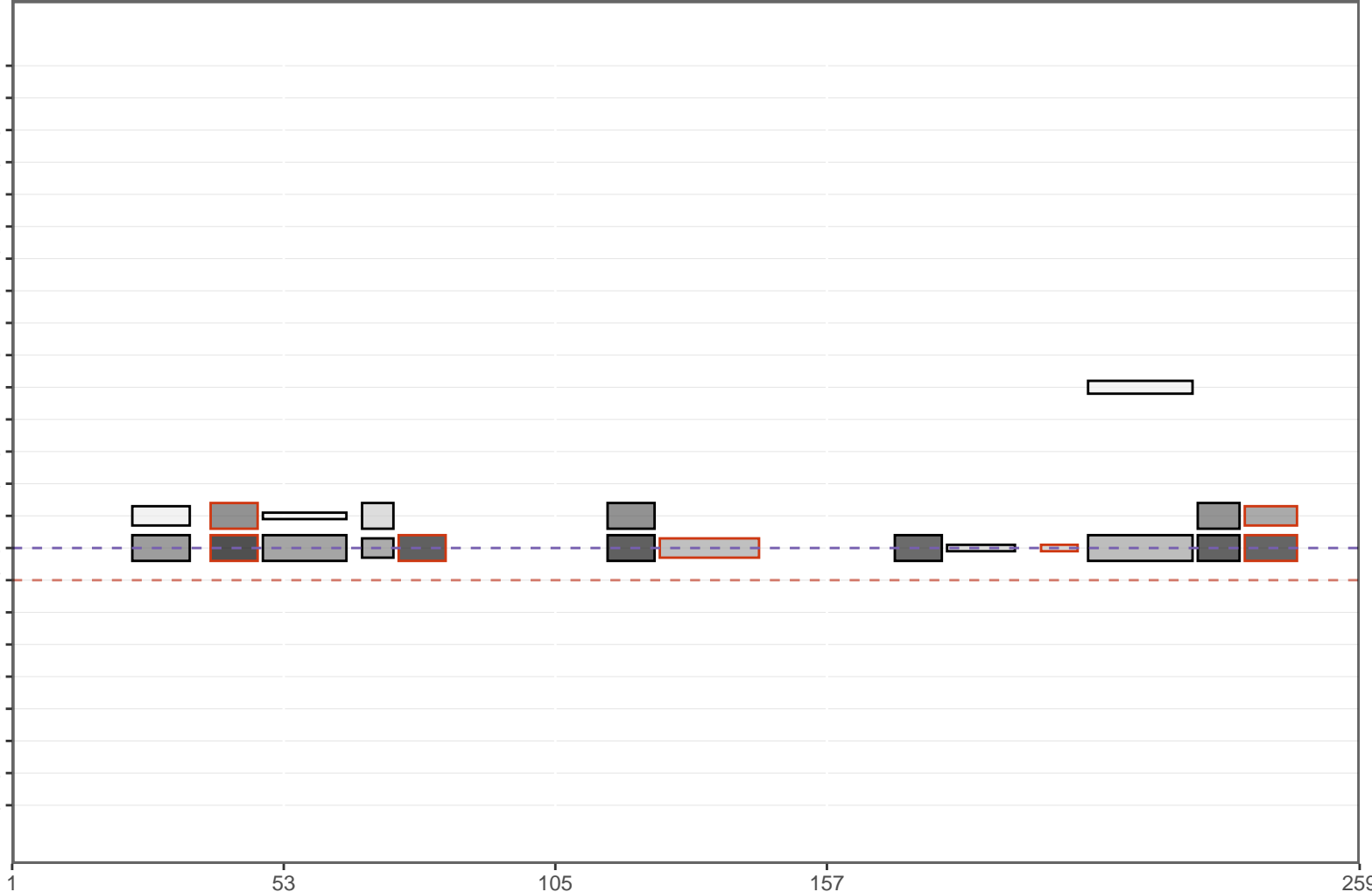
MW indication



Molecular weight



Gel Slice



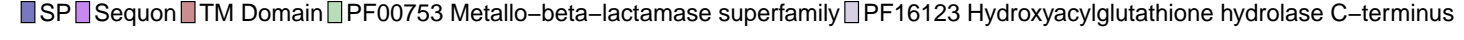
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SYVYTKGEGEDPWFVFTGDTLFIAGGCKFFEGTAEGMYGSLGVTLSGLPKPTRIVYVGHYEYTVKVLGFALTVFEDNKKIAKGLAWAHEHQRVRLPTIPSTRIEEMETNPFMRADLPEVGEKVGFTSFVEALREIRQRKDNWKS

NbL10g05090.1 ABC_transporter_I_family_member_6_chloroplastic-like [MW = 34.95 kDa]

No. of times detected



log(intensity)



Values from



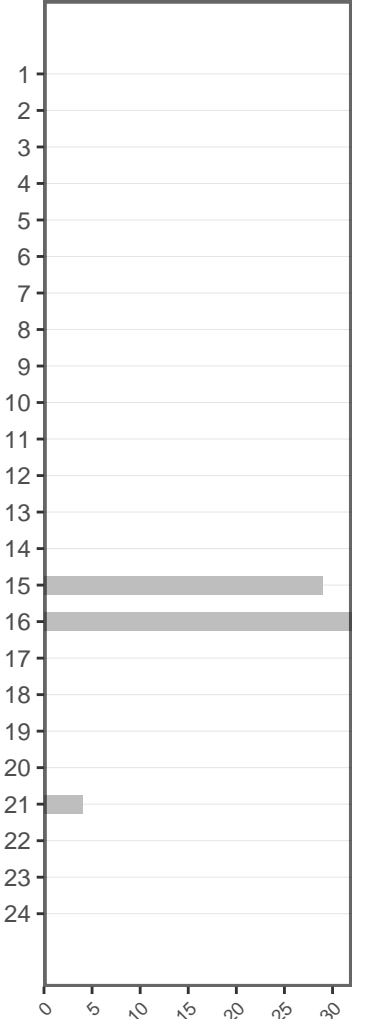
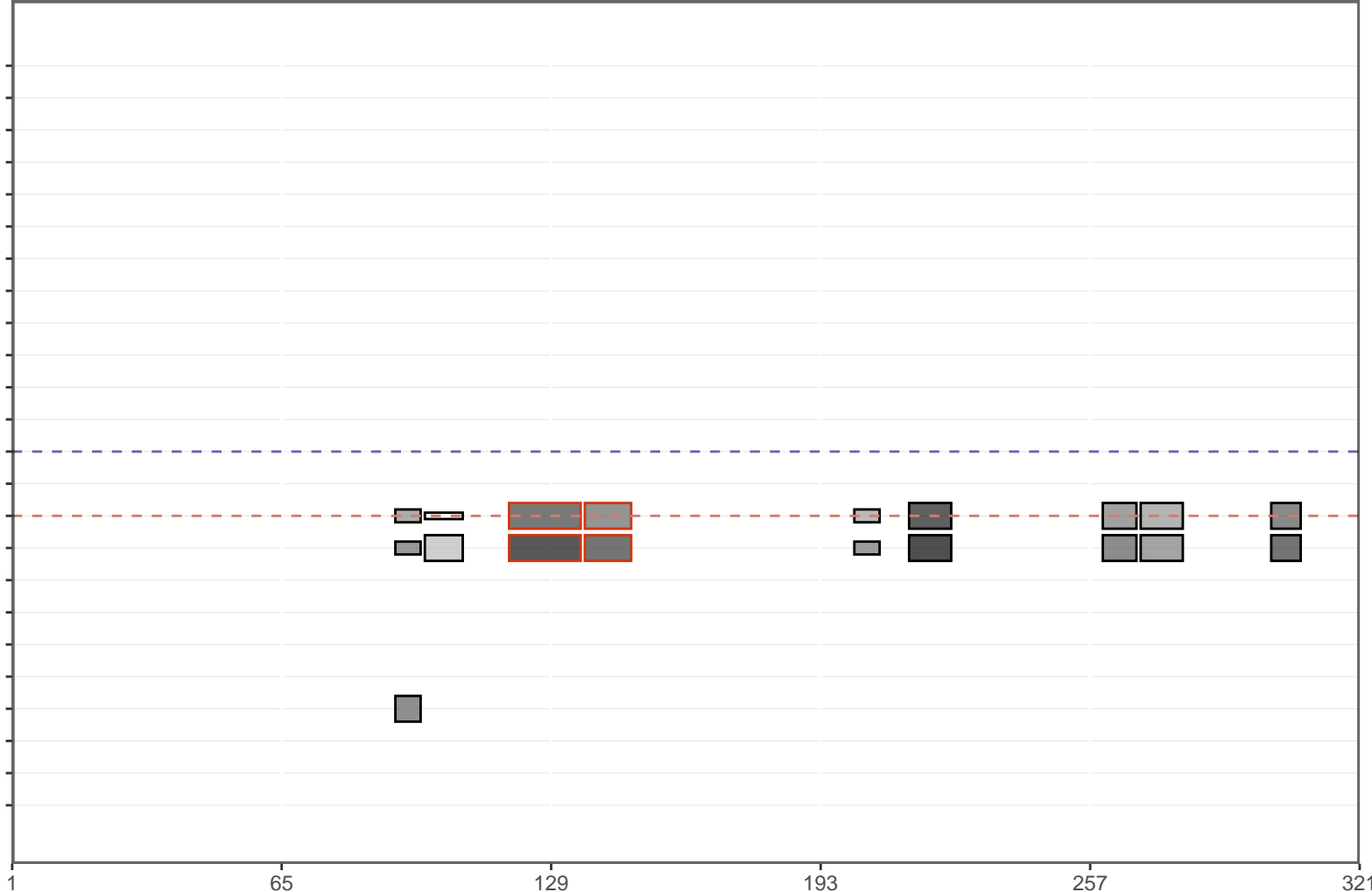
MW indication



Molecular weight



Gel Slice

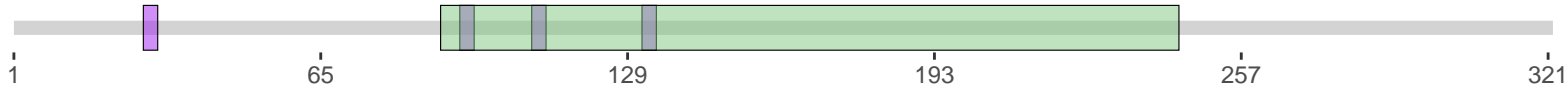


Peptide counts over 4 repeats

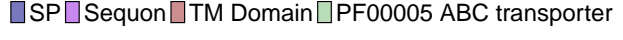
Protein length



Pfam domains



Pfam Description



Protein sequence:

PEERSLAGLFMSFGSPWIPGVSNDIFLMAYNAGRRKRLGLPELGPTEFYGFYAPKLELVNMIKDFLNRNINVEGFSGGGERKRNELQLAVLGLDALDEIDSGGLVDALRDVAKAVANGLLSPNLSMITHYLRLLLEFKFPTVIHMENGRIVKTDGDSIAKVLKEGKYKASGA

NbL10g05080.1 methylesterase_17-like [MW = 31.05 kDa]

No. of times detected



log(intensity)



Values from



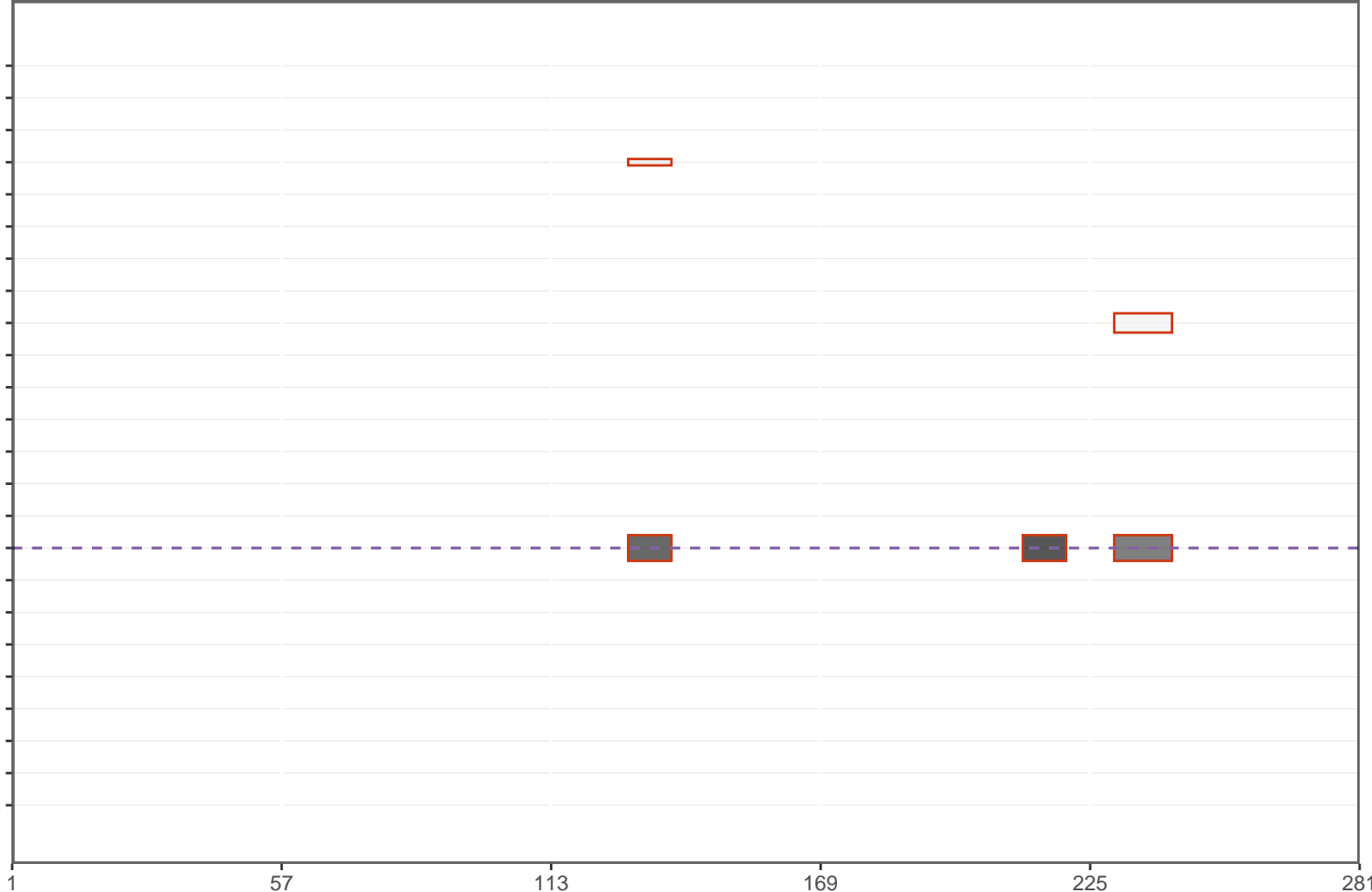
MW indication



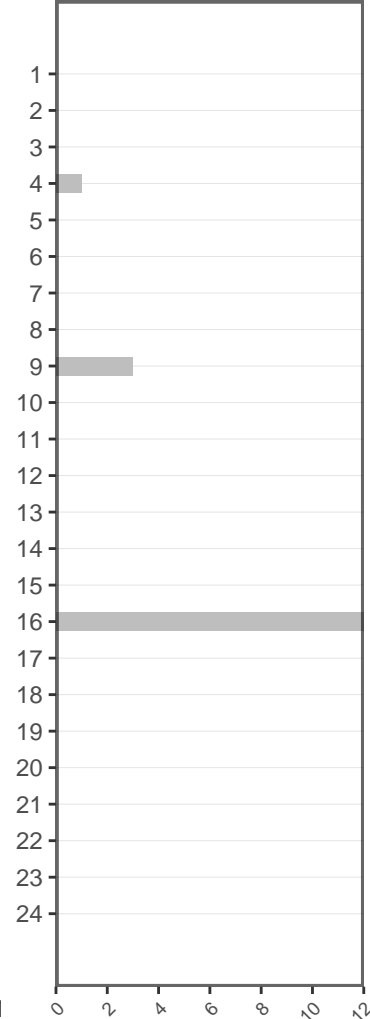
Molecular weight



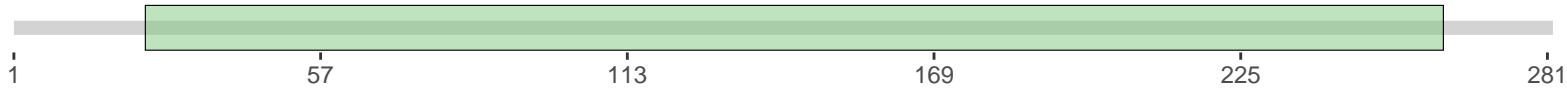
Gel Slice



Protein length

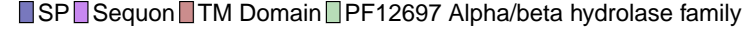


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RTGFVTEQDVKDGPDLSEFGEFNDVDMFGFLGPEQPPSSAVIKRSLQRKIHQTSPLDEDTLAAMLRLPQPIQALKSAGFRKEGEGAEVPRIVRTWYDRVVKPEQGDAMITRWPPGNVYTESDHSFFSAPFLFLGLINAAASLGGTDP

NbL10g05010.1 GDSL_esterase/lipase_EXL3-like [MW - SP = 37.3 kDa]

No. of times detected



log(intensity)



Values from



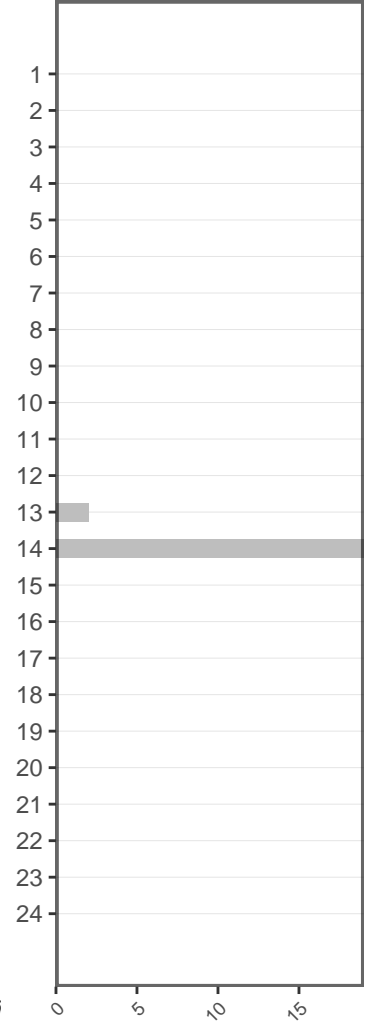
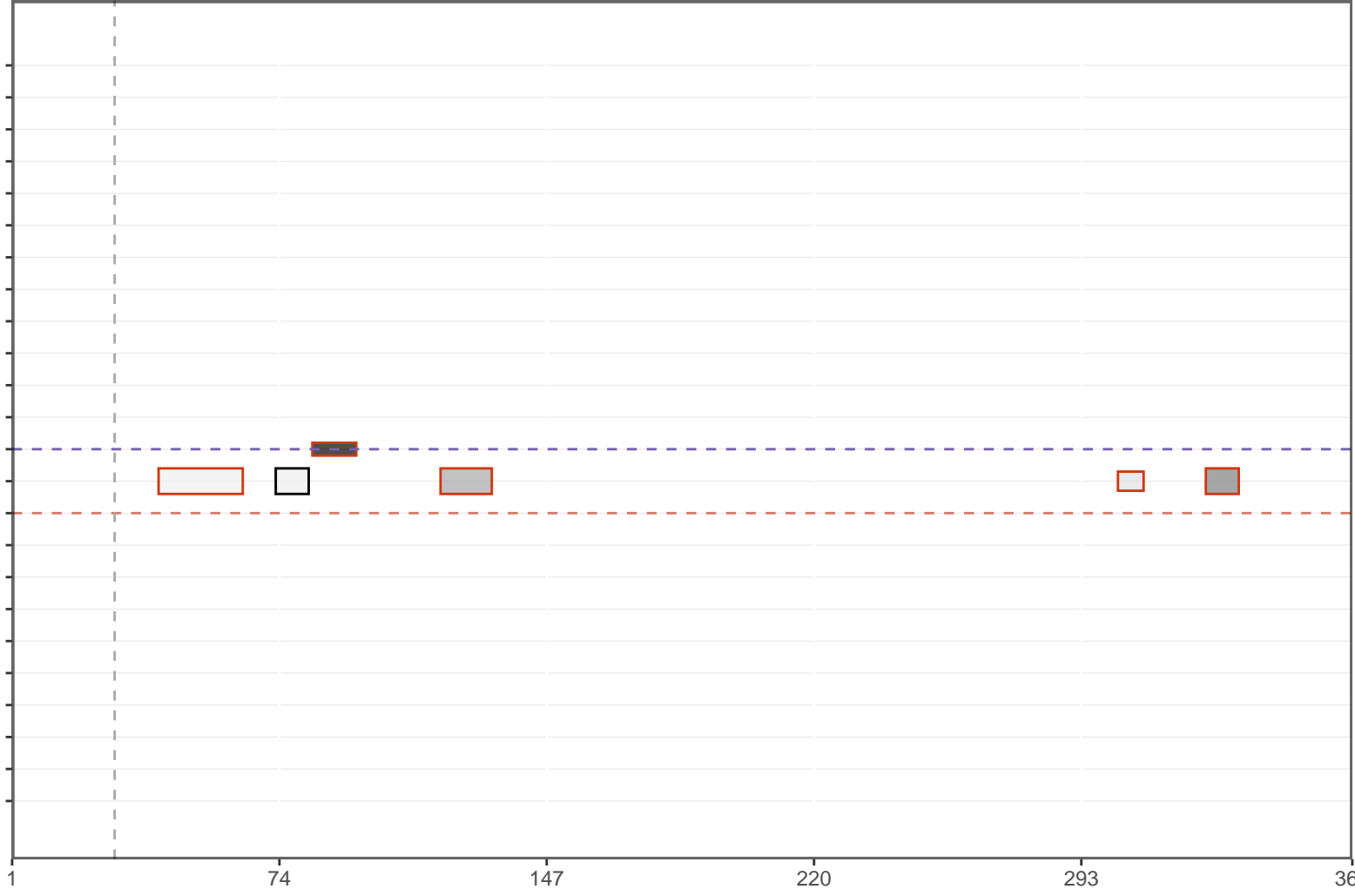
MW indication



Molecular weight

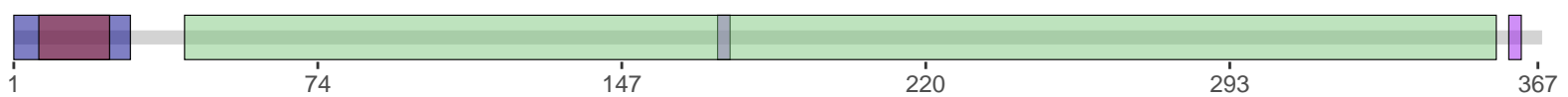


Gel Slice



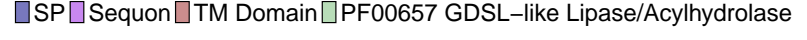
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LNSLFLVAGSYDAGLFGVYNDVIRGKLYDIDVYTNLLAAVWDFVGEVYELGARNIAFLGVPPLGGVYPAQRTLAGGPTRMCAEEVNDGASELANSKFSWIDSLHKKFPQKLVFDVANSLLDGVNPKYGFEEVKGKGGSSGNEVALGNKFSSETGEDDTRKFLFWDVSHLTKNGYRILVDRIKKNYTNLSFL

NbL10g04930.1 membrane_steroid-binding_protein_2-like [MW = 24.84 kDa]

No. of times detected



log(intensity)



Values from



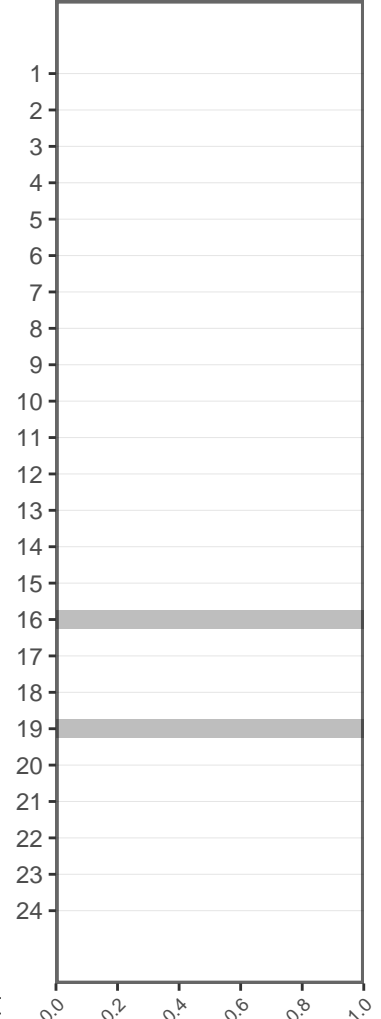
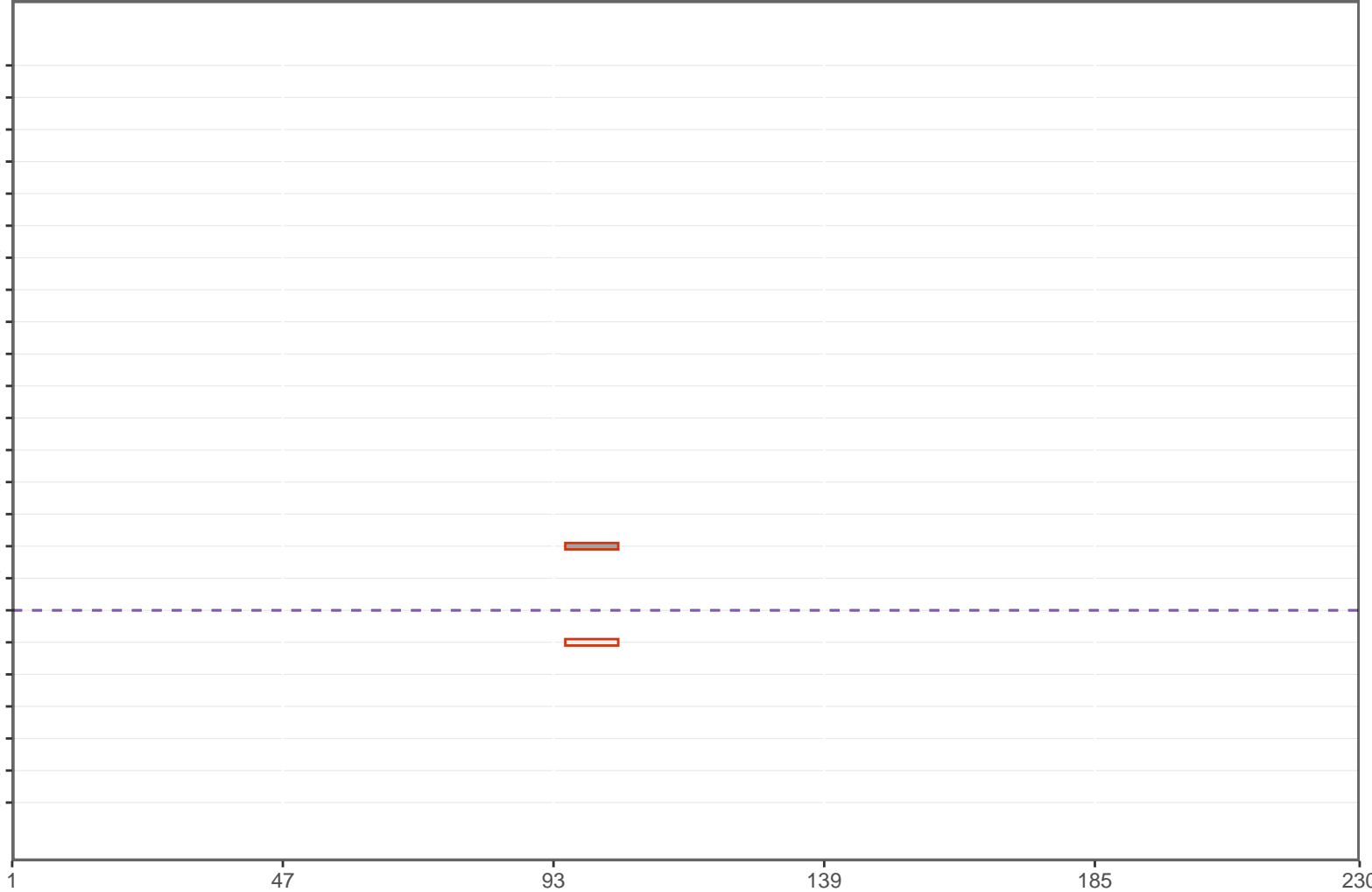
MW indication



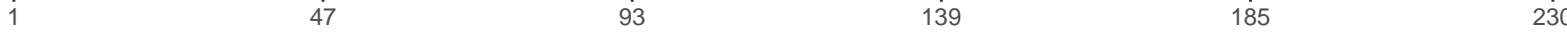
Molecular weight



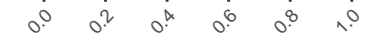
Gel Slice



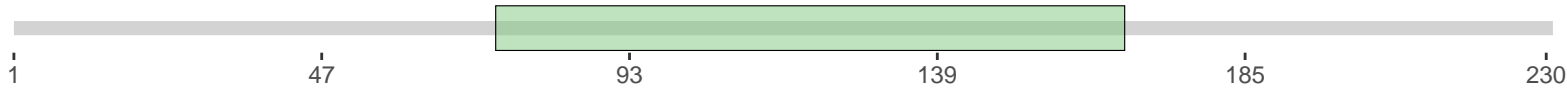
Protein length



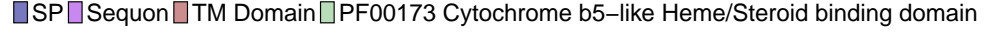
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

RMFYGGPGPYALFAGKQASRALAKMSFEKDLTGDISGLGPFELDALQDWEYKFMKYYVVGTRQAVPVTDGAANGSEVEATDREAKPAEDGASASBKPLEDDVPSAEVAETAETVEKSDVDVQKDP

NbL10g04920.1 tubulin_beta-1_chain [MW = 50.32 kDa]

No. of times detected



log(intensity)



Values from



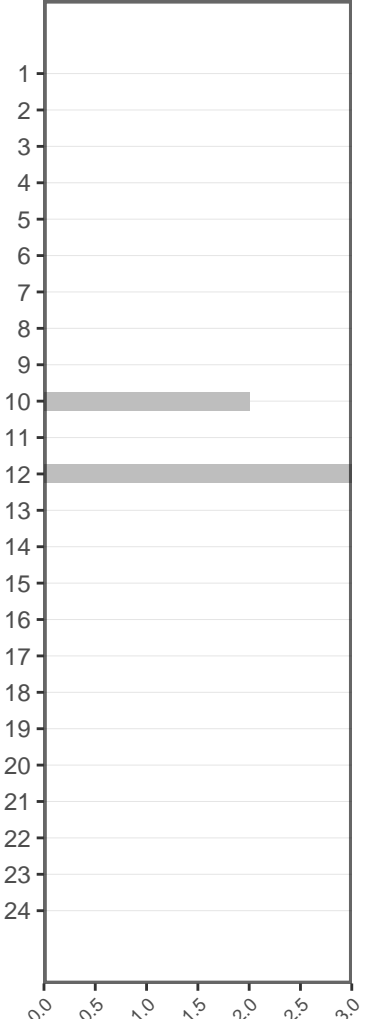
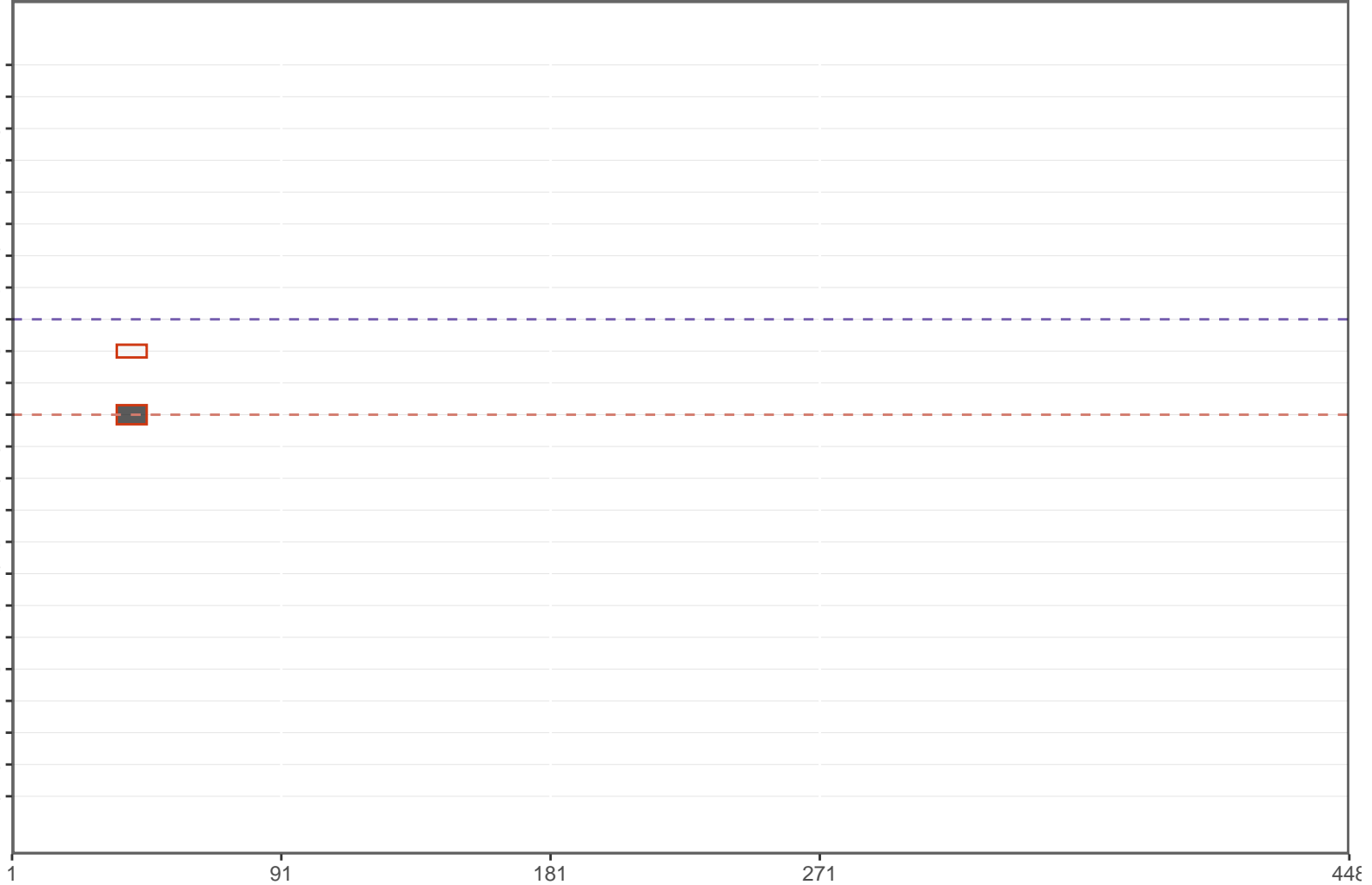
MW indication



Molecular weight



Gel Slice



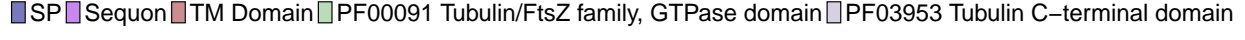
Protein length



Pfam domains



Pfam Description

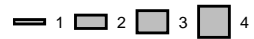


Protein sequence:

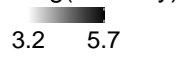
FRTLKLLTPSGDNLNHLISATMSEVGTGLRFPGLNSDLRKLAVNLIPFRLHFFMVGFAPLSRGGQYRALTVELTQGMWDKNNMGAADPRHGRVLTASAMFRGKMTKVEDEGMNNGNNSYFVLEWIPNNKSTVGDIPPTGLKMASTFRGNSTGIDEMFRVSEGFAMFRKAFLHWYTGEGMDEMFEETAEISNNDLVSEYGGVGDATDEEGYVDEDEEEHGEA

NbL10g04810.1 probable_glucan_13-alpha-glucosidase [MW - SP = 103.04 kDa]

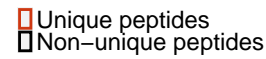
No. of times detected



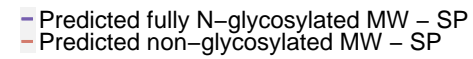
log(intensity)



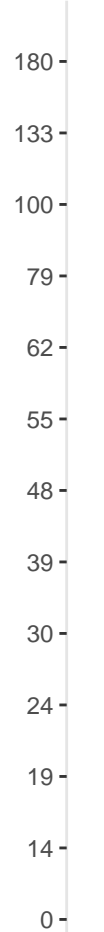
Values from



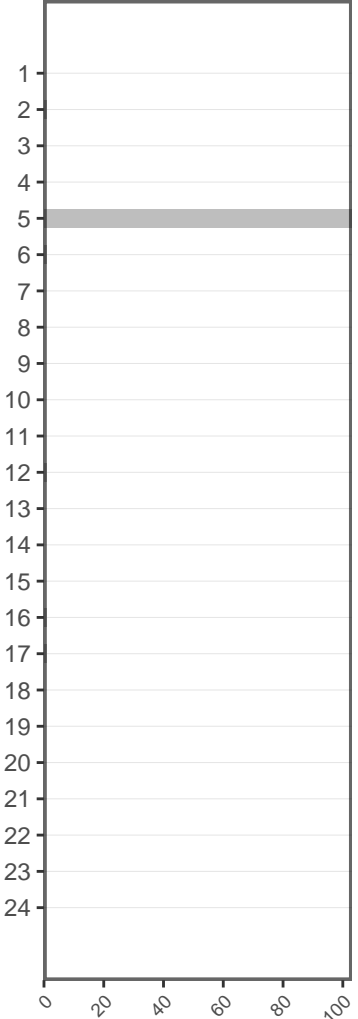
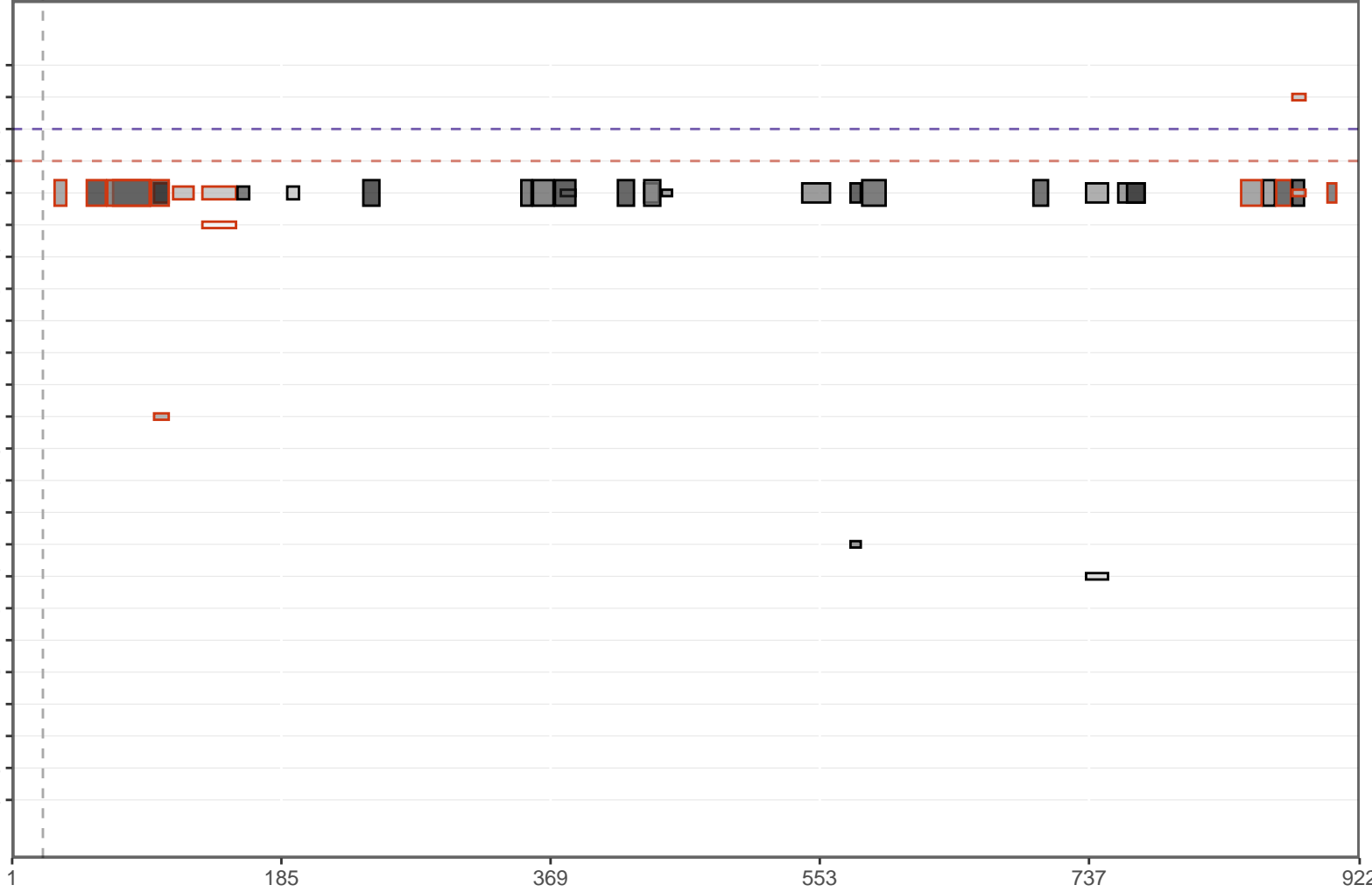
MW indication



Molecular weight

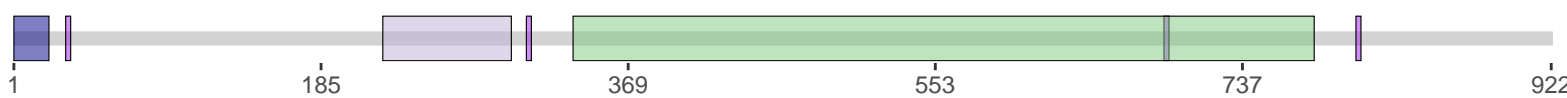


Gel Slice



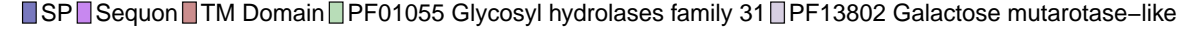
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

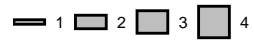


Protein sequence:

⋈K E A S E G Y Y K D A T G K D Y G W C W P G S S S Y V D L L N F E I R S W W G D K F S L D S Y T G S T G Y L H I W N D M N E P S V F N G P E V T M P R D A L H I G G V E H R E L H N A V G Y F Q M A T S N G L K R G D G K R P F V L G R A F F A G S Q R Y G A I W T G D N T A E W E H L R V S P M V L T L S I S G V F S G A D V G F F G N P E T E L L R W Y Q L G A Y Y P F R G H A H H D T K R R P W L F G E R N T Q L M R E A H I R Y M V L P Y F Y L F R E A N S S G T P V A R L W M E F F P G D E K F S N D E A F M V G N G L L V O G I Y T E R A P

NbL10g04760.1 aspartate--tRNA_ligase_2_cytoplasmic-like [MW = 60.57 kDa]

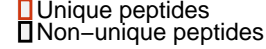
No. of times detected



log(intensity)



Values from



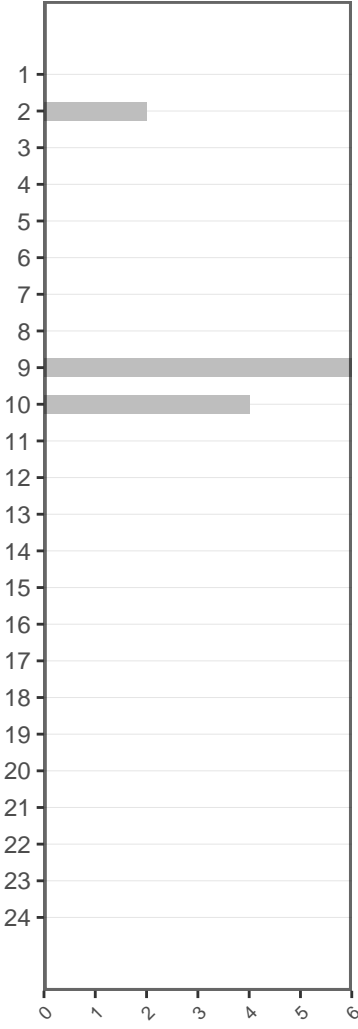
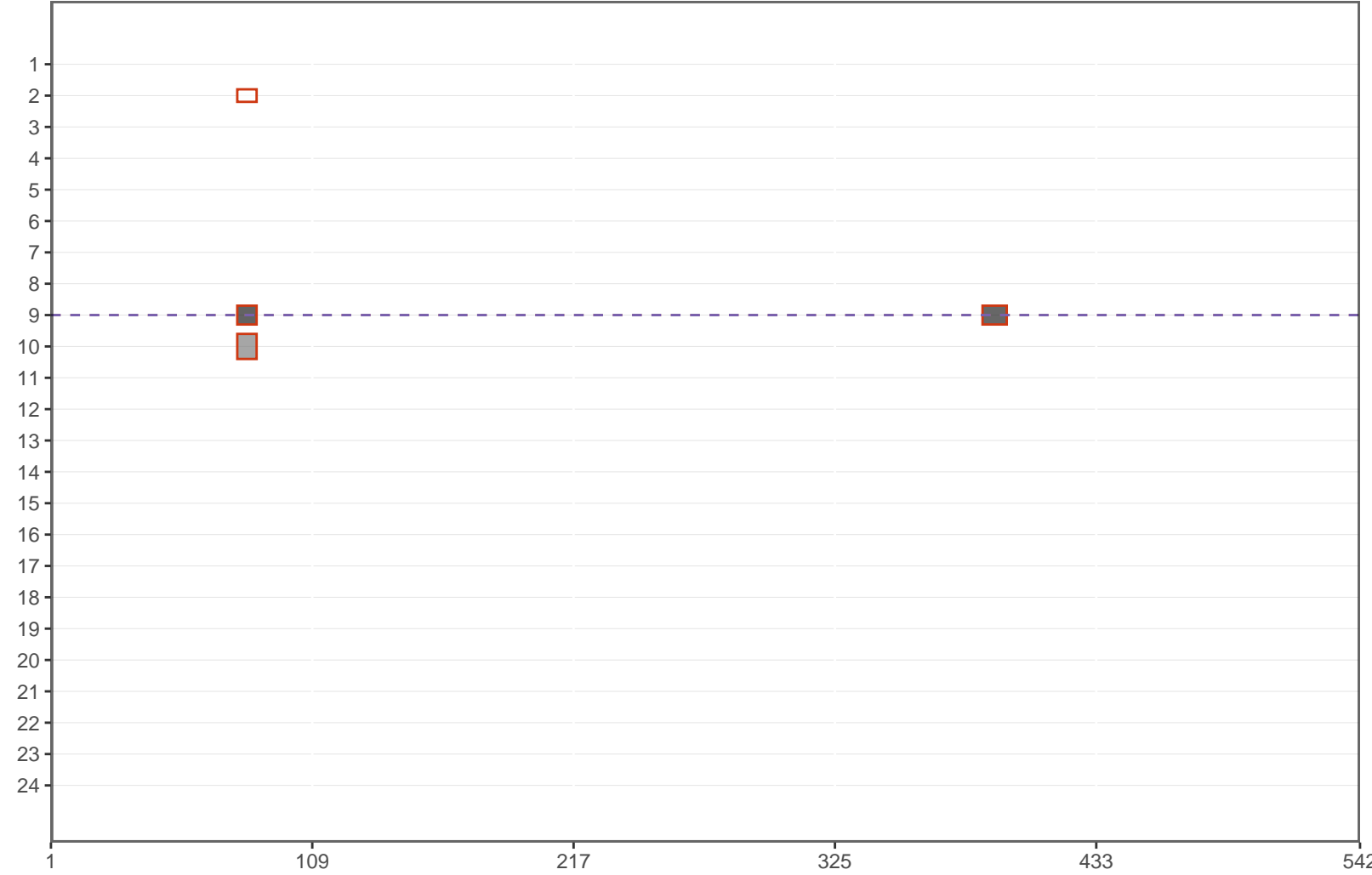
MW indication



Molecular weight

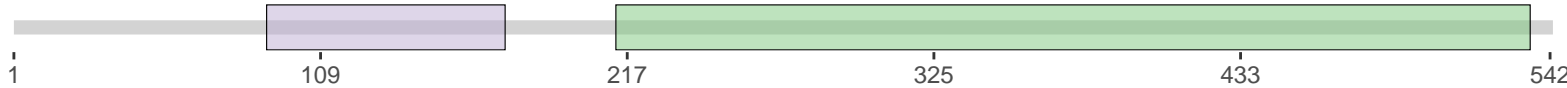


Gel Slice



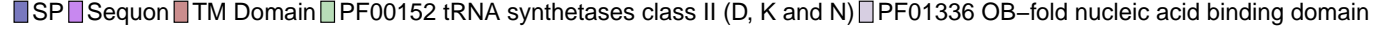
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IPKLGSSSEGGSAWFRLDKNGPCLAGSPQLHKQMAKMGDFGRVFEIGVFRFAEDSFTIRHLCEFTGLDVEKEHYSEVMIDVRLVFTFDLNDKNGKKELEAGRGVYFEFLKYFRGDKLTLTFEEGVQLKEAGIEVDVDFGDLNTESEGRHLGULVAKYGTDFYHLKYLPLAVRFFVTMPGVYDNPVNSNGFDVFRIRGEEHSGAQRVHYPEFLAKRAEEGGIDVKTISTYDSFRVYAPPNGGFGVGLERVYMLFDALNIRKTLFRRDQRIAP

NbL10g04740.1 acyl_carrier_protein_2_mitochondrial-like [MW = 18.69 kDa]

No. of times detected



log(intensity)



Values from



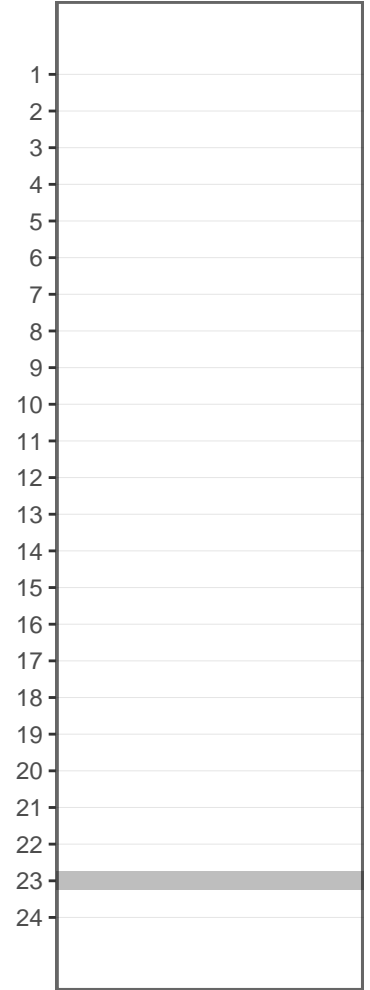
MW indication



Molecular weight



Gel Slice



Protein length

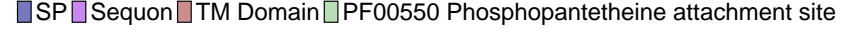


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

/FRRHFSSEVROGSLDKSEVTRRVINGVKNFKQKVDKVKVTPNAHFQNDLGLDSDTVEVWMALEEEFGFEPDNEADKINSINLAVDFIASHPQAK

NbL10g04730.1 calreticulin-3-like [MW - SP = 43.01 kDa]

No. of times detected



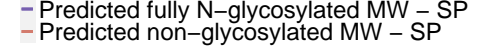
log(intensity)



Values from



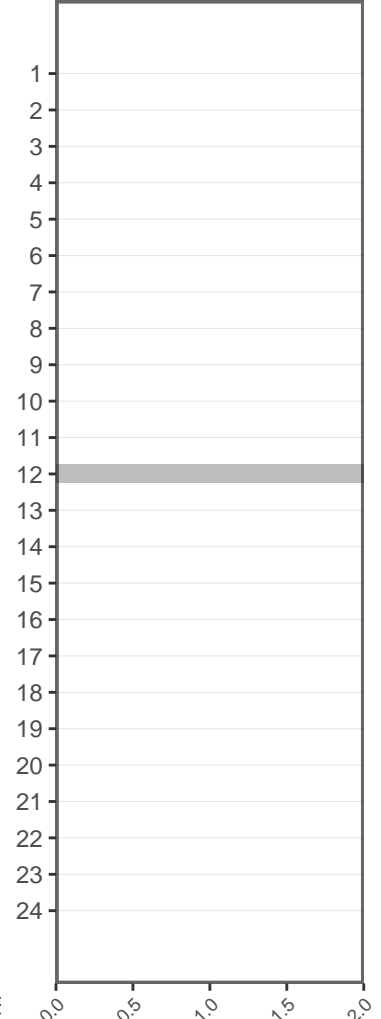
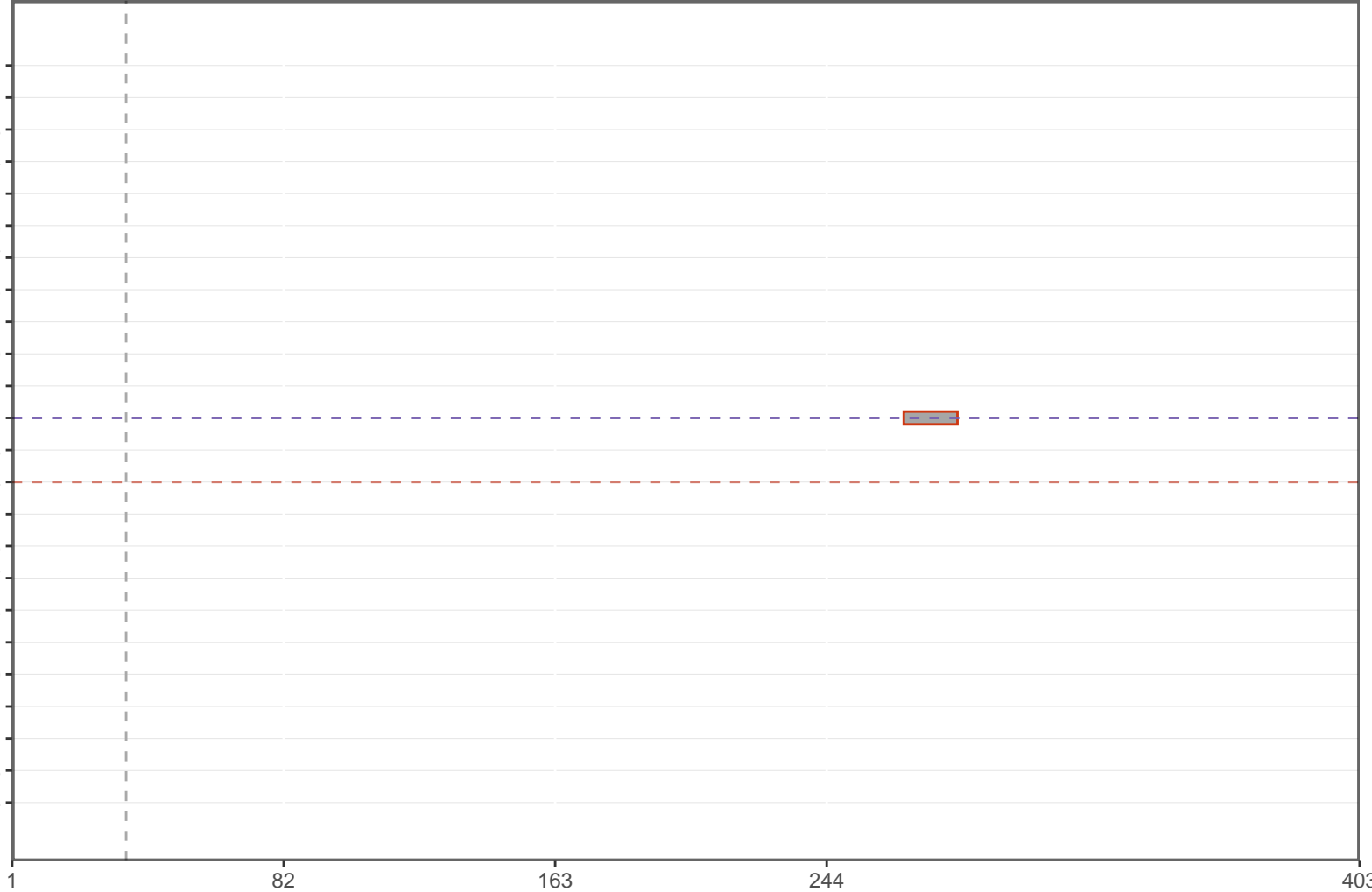
MW indication



Molecular weight

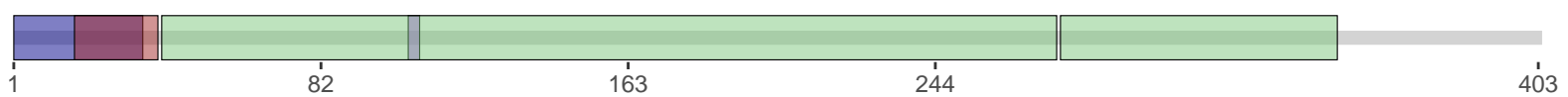


Gel Slice



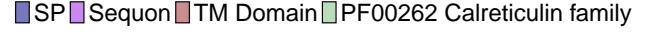
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TILRPSDASYSIWIDGREIRDGGMYTDWDLPPRRKKIDVNAKKNADWEDREVIEDPDDKPEGYDSIPREIPDRKAKKPNVDDDEEDGMWKPKNPNVPRGPKWRKKNPNVYKGVKIPWIDNPEFEDDPLVYKPKYVGVVWQVYKAGVDFDNLVGDPEFDYKQVGVGFANRREAEKEAFEEAEKVRKAKEERWHRDYMDDYHDEL

NbL10g04670.1 phenylalanine_ammonia-lyase-like [MW = 78.25 kDa]

No. of times detected



log(intensity)



Values from



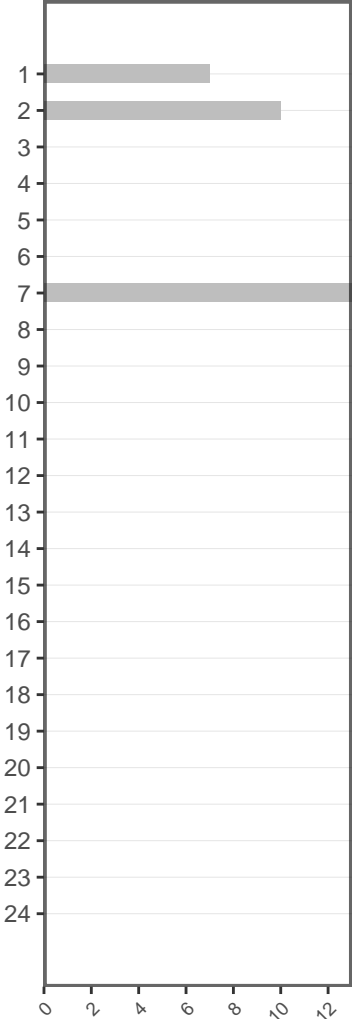
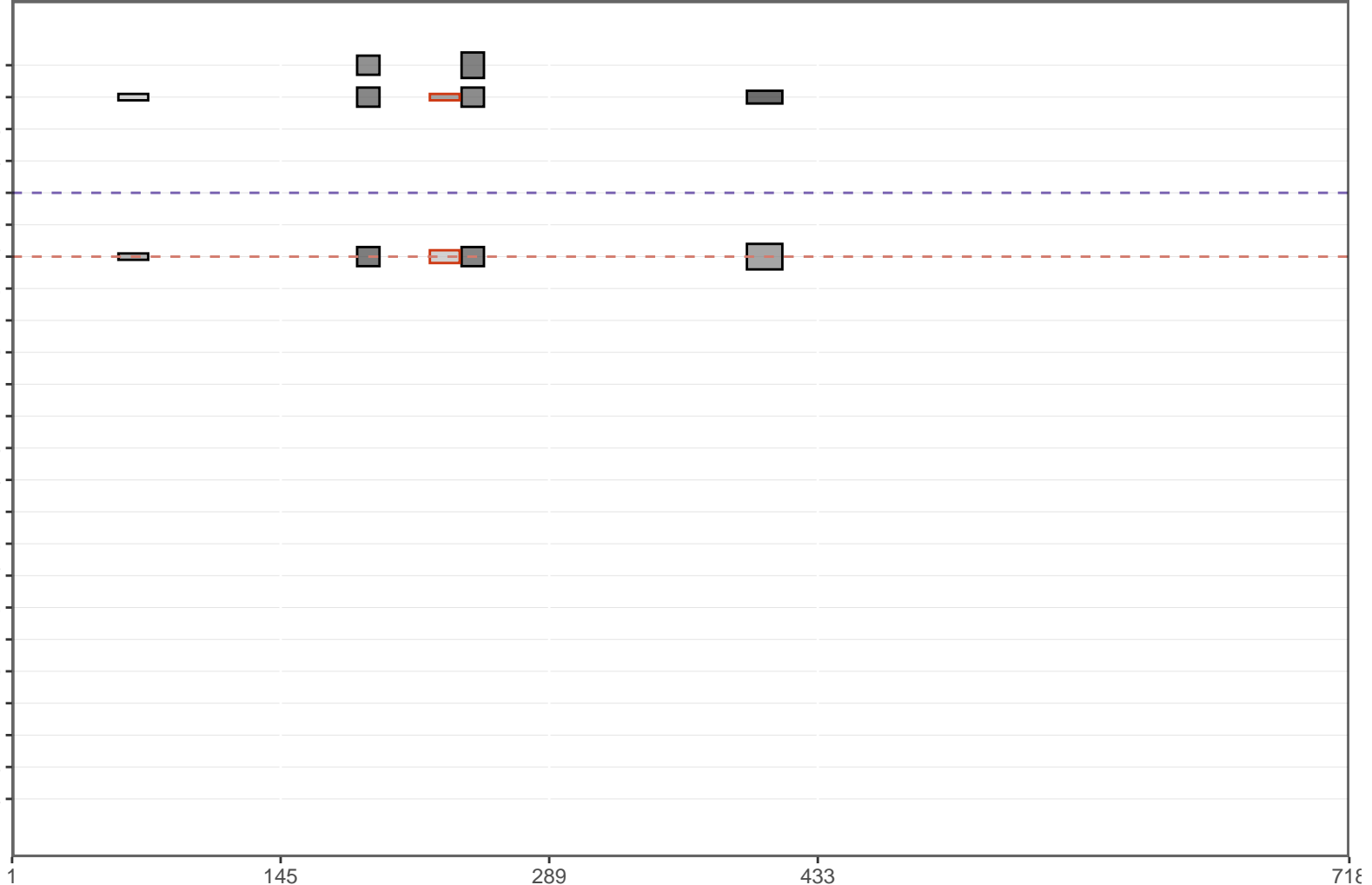
MW indication



Molecular weight

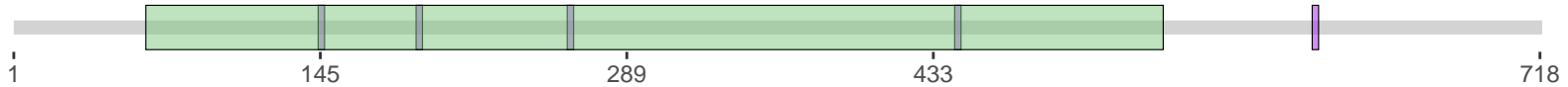


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

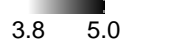
DKPKDQRYALRTSPQWLGPEIEVIRATKMERIENSVININPLIVSRNKALHGGNGFGTPTGVMDNTRILASIGKLMFAQFSELVNDYVNNKGLPNTGGKRNPLDYGFKGAEIMMA5YQSELGFSANPVTHNVDQSAEQHNGEVNLSGLISGRKTAEAVDLKLMSTYLVALGQAIDRLHLEENKAAEVKNVSLVAKVLTIGGNGELHPRRFQEKDLKVVDRVAFAYADDPCGSGNVPFLQKLRQVMVDHALLNNGEKENNYSTSFKEKGAFFEEELKALPKVESARCC

NbL10g04490.1 acetylornithine_aminotransferase_mitochondrial [MW = 54.01 kDa]

No. of times detected



log(intensity)



Values from



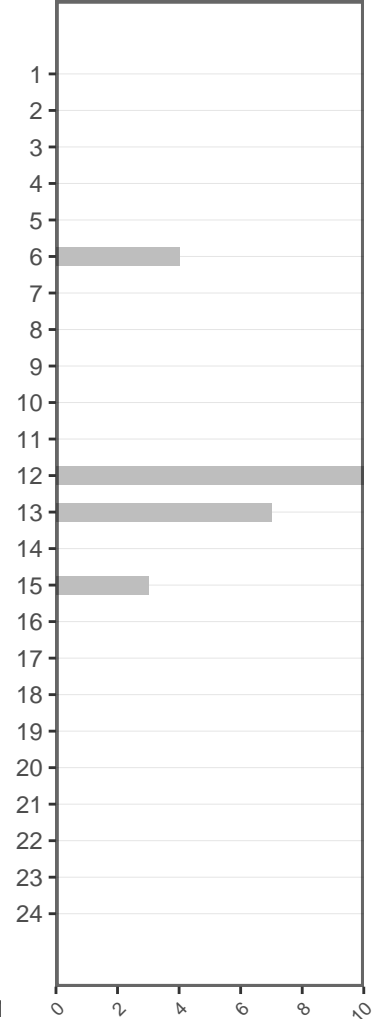
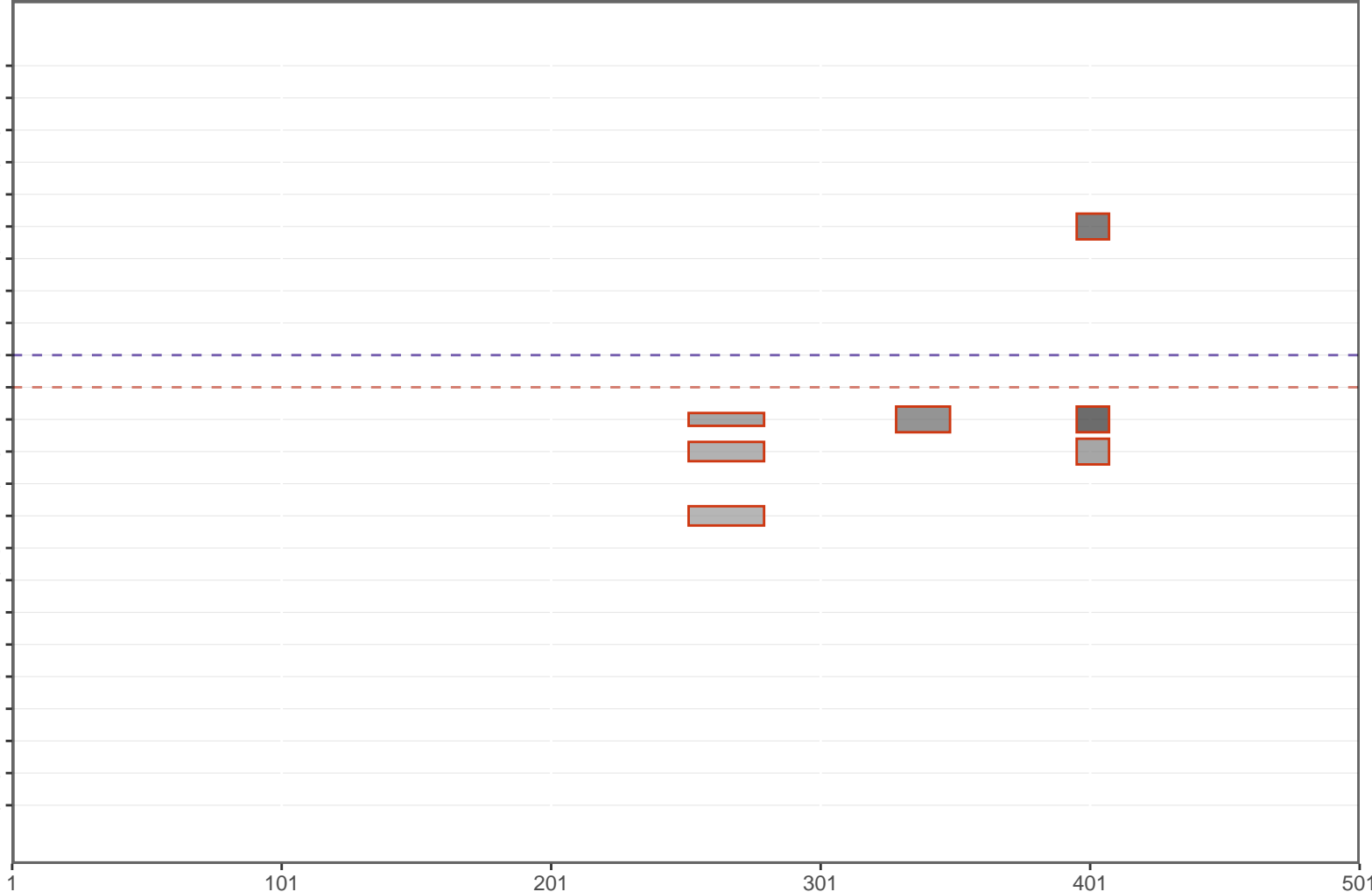
MW indication



Molecular weight

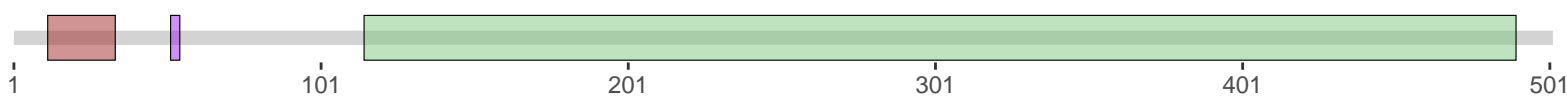


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL10g04410.1 uncharacterized_LOC109220890 [MW = 34.7 kDa]

No. of times detected



log(intensity)



Values from



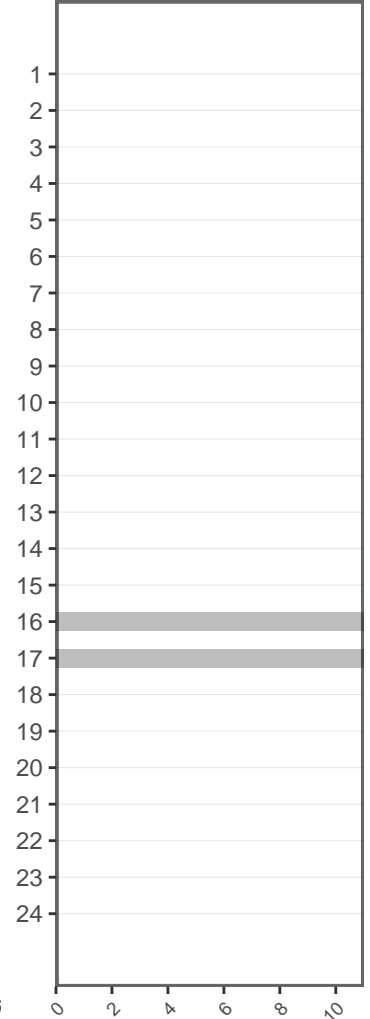
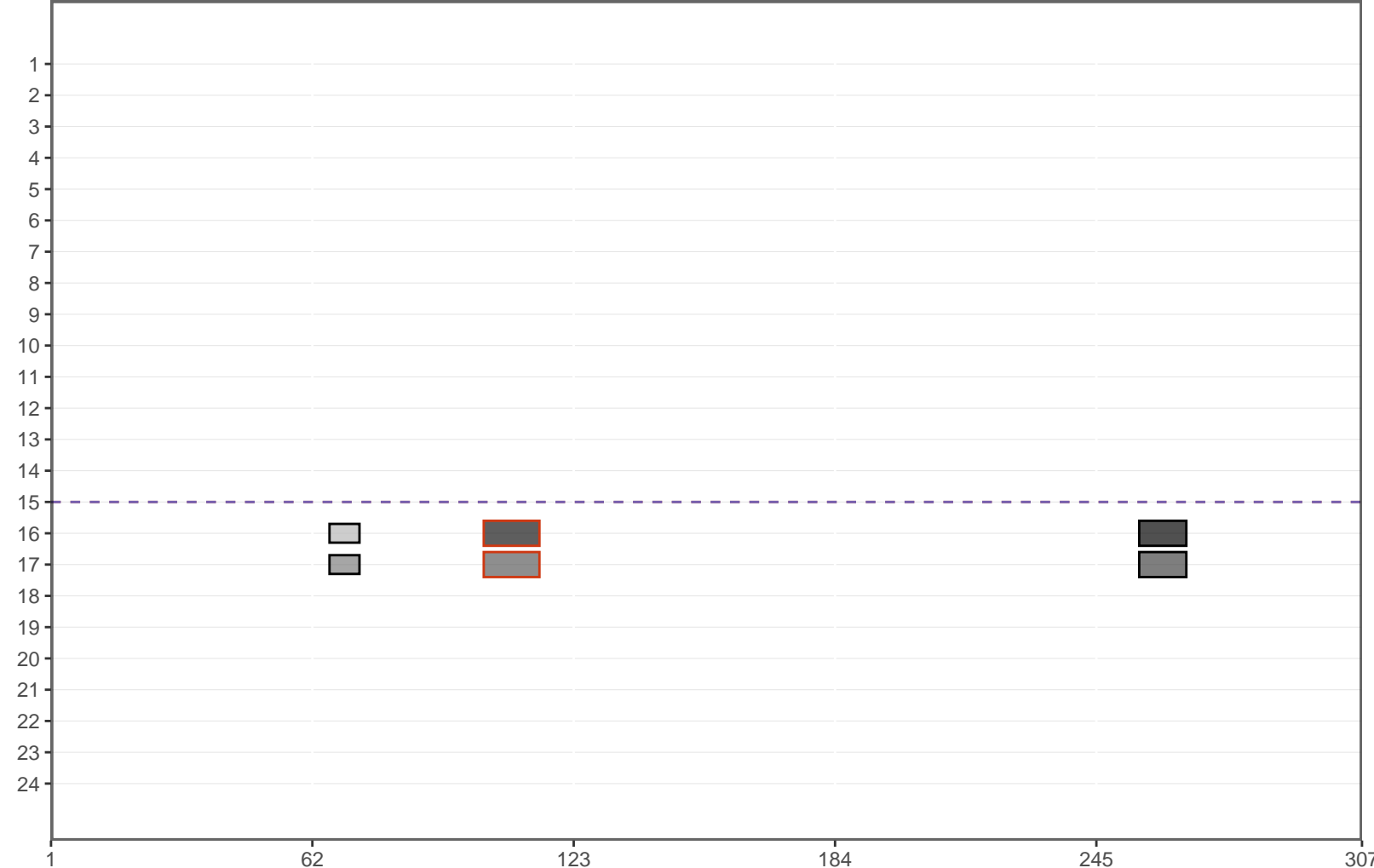
MW indication



Molecular weight

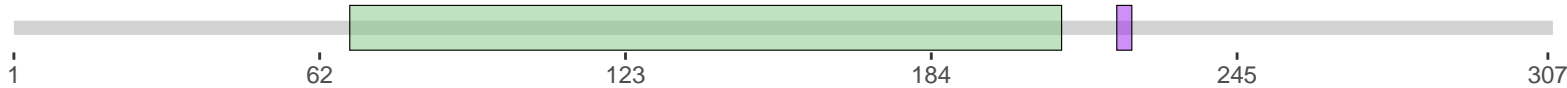


Gel Slice



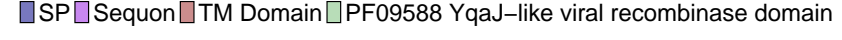
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GFAVHSDRLGIVGASPDGILLGCLPGGILEVKGPKYKNGKPEKGLPWNTMPEYVMPQVGGMEIMDRDWDVVYGVTPNGSTFRVYRERSGVYELMHELWFRWVWVNFVAREALSLGNEEDAKSYKPTPTTKTGLVIRSLKLAGAEAKMLGRDIAGHVEFFR

NbL10g04270.1 chorismate_synthase_1_chloroplastic [MW = 47.68 kDa]

No. of times detected



log(intensity)



Values from



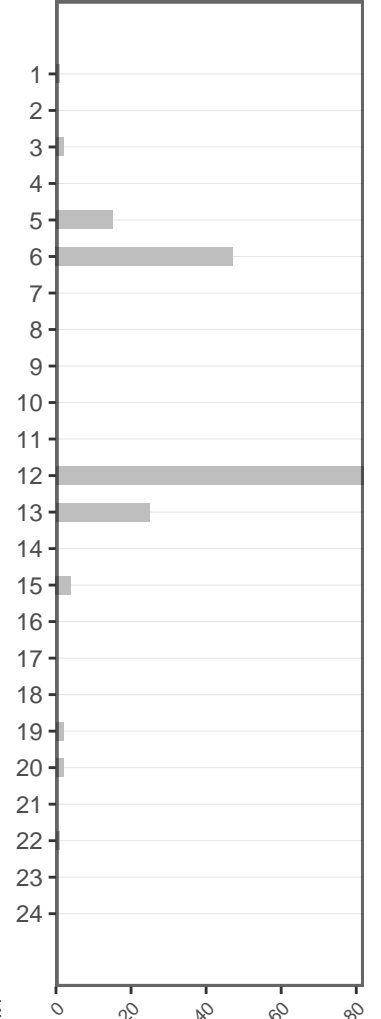
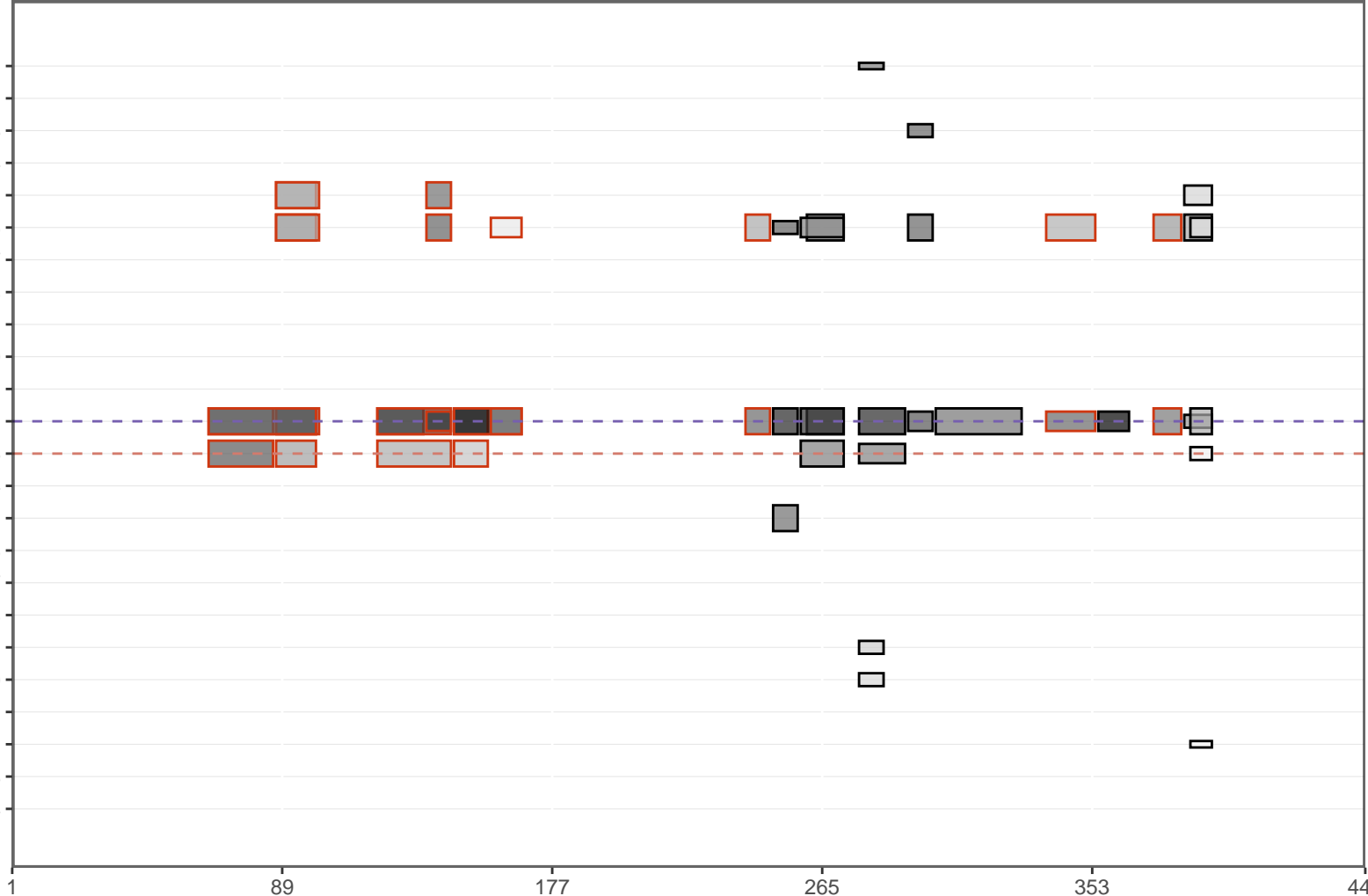
MW indication



Molecular weight

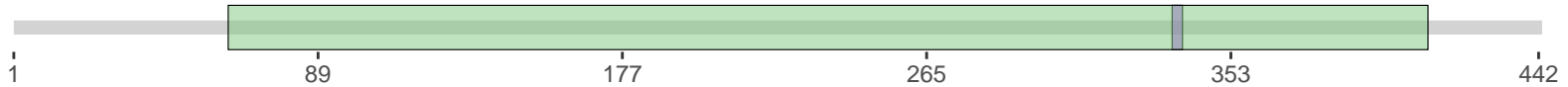


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

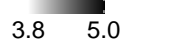
AYVSOVHQVYLLPEEWIDHQTMTLEQESNIVRCPDPEAEKMAAIDAVRVRGDEVGGVATGVRNVPRLGTPVFDKLEAEALAKAGMSLPATKGFEGFGSGFTMTGSEHNDFFYMDHGRIRTRTRNRSGGGGGGGISNGEVNIRMAFKPTSTIARKGGQTVTRDKHDDELIRGRHDFCVVRAVPMVEAMVALALVDQLMAHYAGCMFNPINPALGEPLOSSTPEGAETL

NbL10g04190.1 3-ketoacyl-CoA_thiolase_2_peroxisomal [MW = 48.95 kDa]

No. of times detected



log(intensity)



Values from



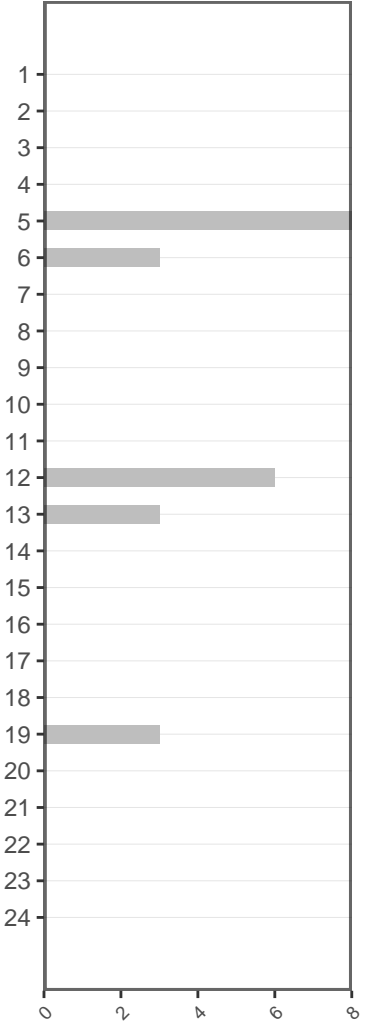
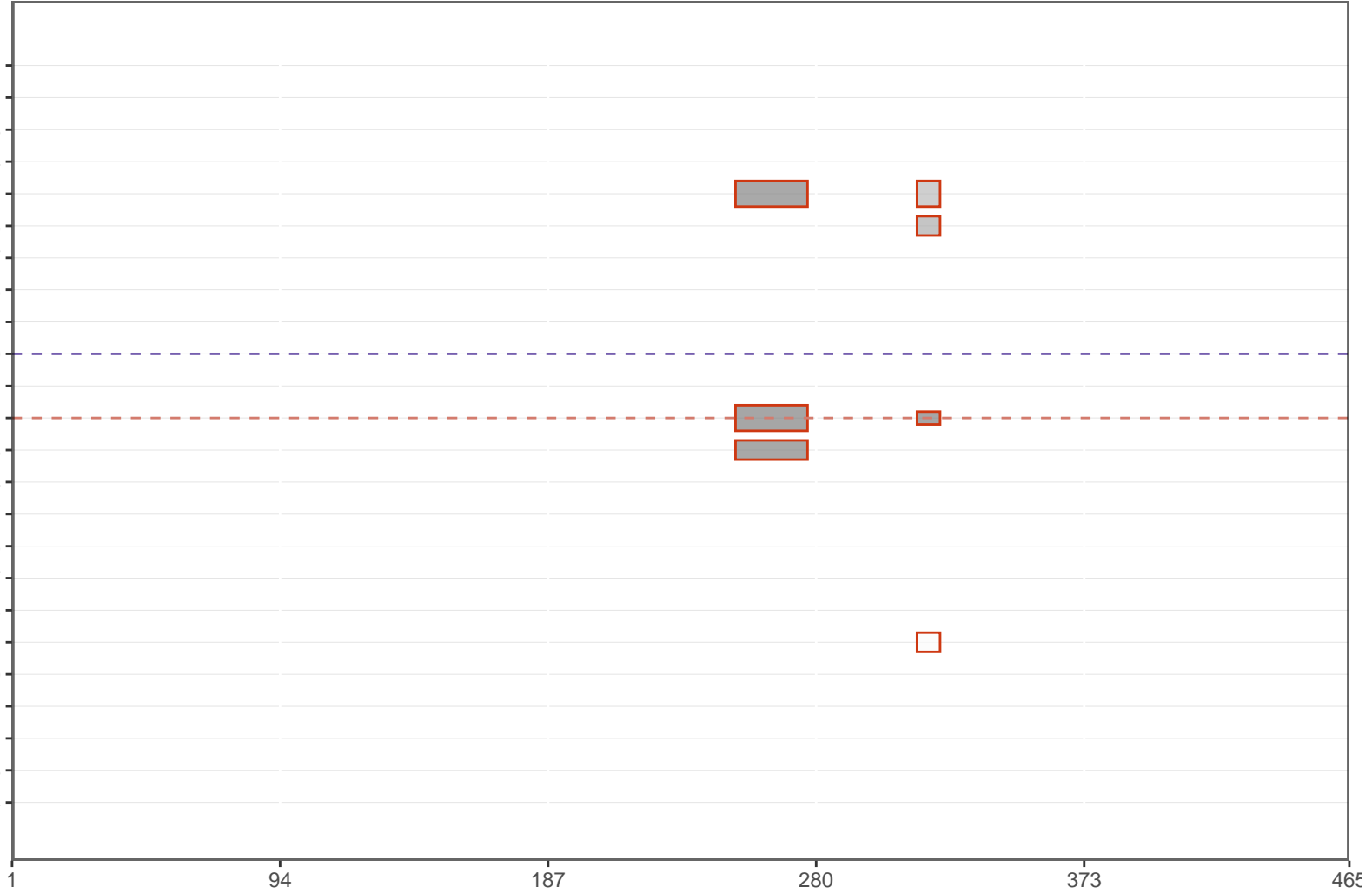
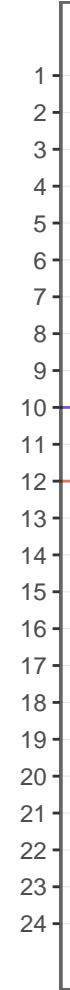
MW indication



Molecular weight

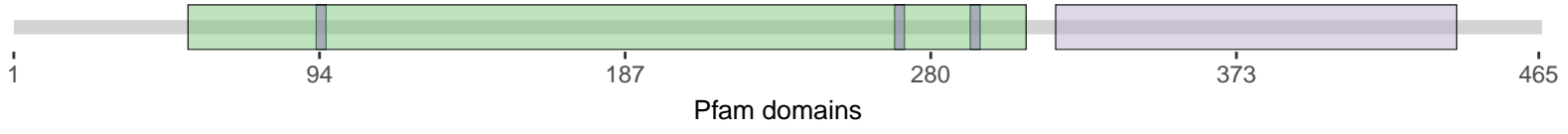


Gel Slice



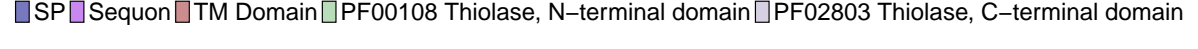
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

QAAVDSHRKAAALASAGKFKDEHPVPTKIVDPKTRDETPVTFHVDGGRPNASVSDLAKLPVFKKGGTTTAGNSGGVTDGAGAVLLMKRSLAMQKGLFVLGVFRFFAAGVDPNMGIGFVAIPAFAAKSGAGLEEDLFEINEAFASQVYGRKKLELDPEKINNGGAMALGHPFGATGARCVATLLHEMKRRGKDKRFGVSMCGTGMGAAAVFERGDGDELGNARKIGSHNLLSKDVL

NbL10g04140.1 probable_pectate_lyase_8 [MW = 53.83 kDa]

No. of times detected



log(intensity)



Values from



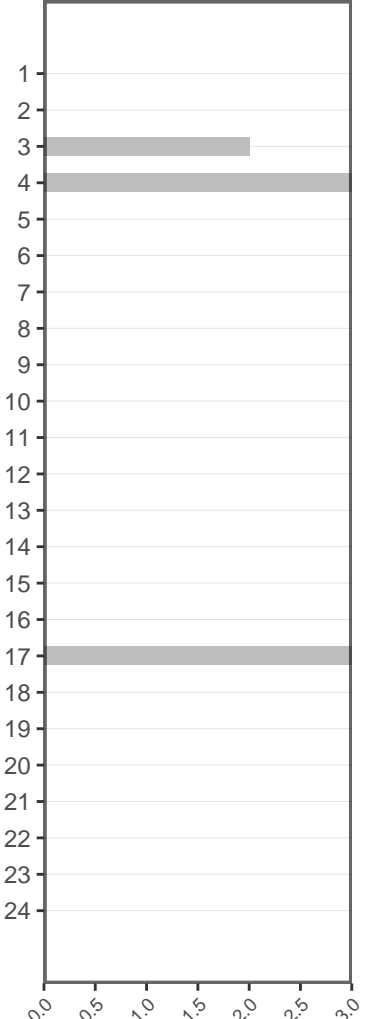
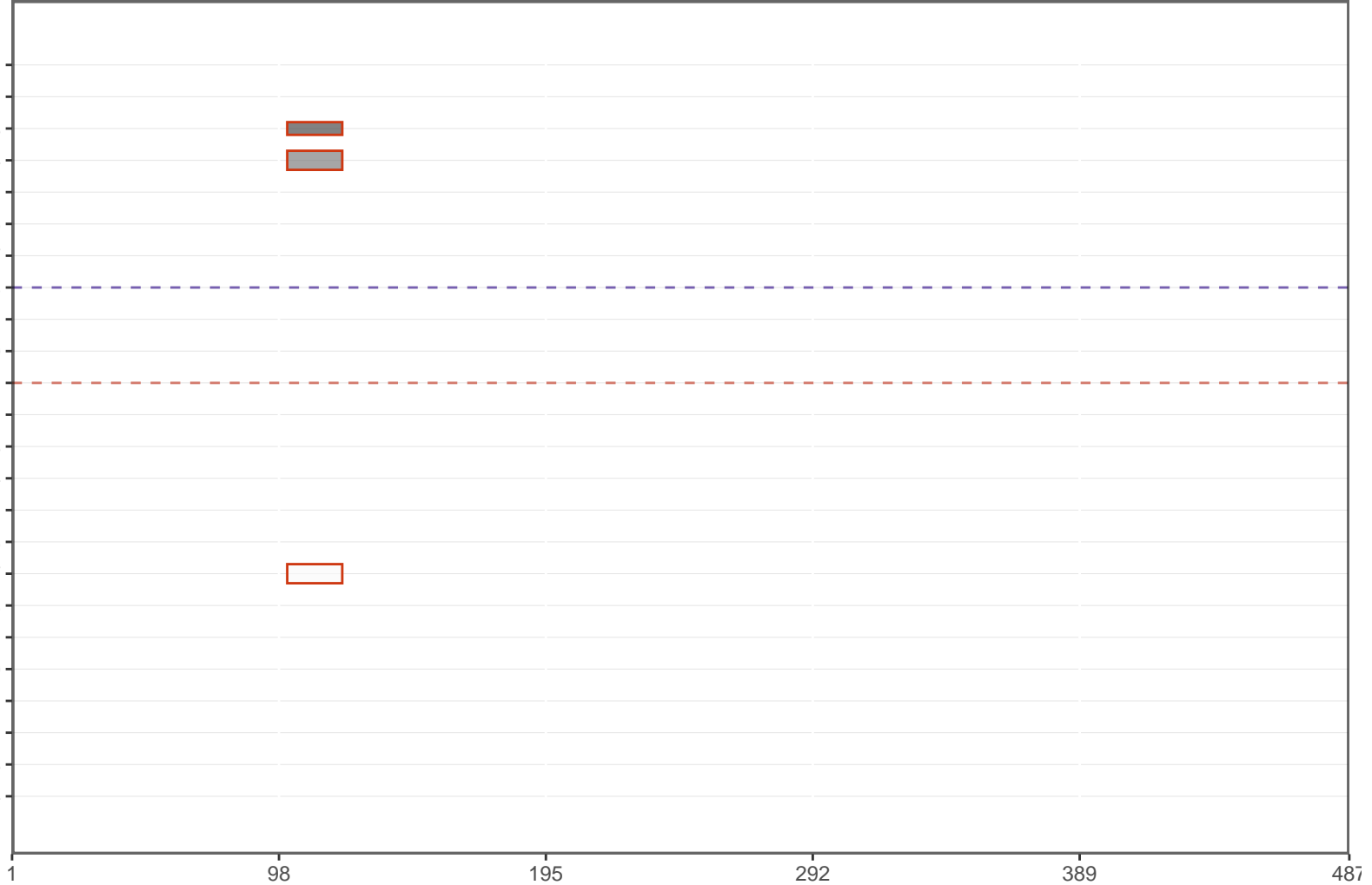
MW indication



Molecular weight



Gel Slice



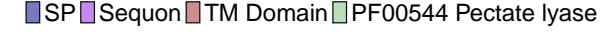
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IRGHNVHIANIGACITQGFVTNIIHGLHIDCKPTGNAMVRSPSPHFQWRMTADGDVAISIFGSSHIWIDHNLGHCADGLVDVAMGSTATISNHFHAFHNEVMALLGHSDEYTRKQMGVTVIYHIFGELGHRMPCRHGVFHVNNNDYTHVEMVYAGGSEANPTNSGGNRYLAPTFNPFAXEYTKRIVDTAAGQWKGWNRBEGDMLNGAVFTPSGAGASAVARASLGLAKSSSMVGAITSGAGPLACRRRSMQ

NbL10g03900.1 20_kDa_chaperonin_chloroplastic-like [MW = 26.37 kDa]

No. of times detected



log(intensity)



Values from



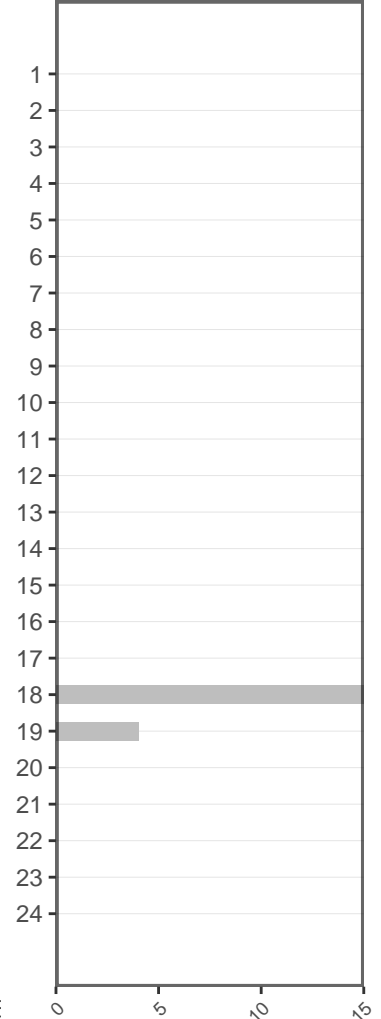
MW indication



Molecular weight

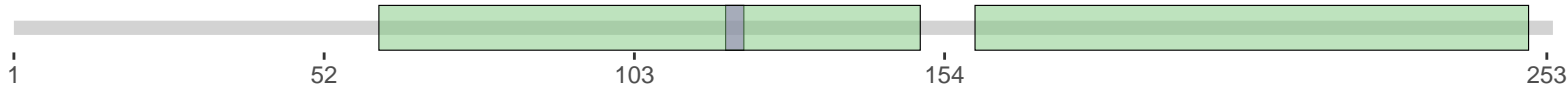


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EISVKNQTVLYSRKAGTEVLFDSGTHILKEDDVGILETDDKDLQPLNDRILKVAEVEEKTAGGLFLEEAAEKPSIGSVIAAGPQLDDEGNRKSLSVSPGNTVLYSKYAGNDFKAGDADVTLRASDVAVLS*

NbL10g03850.1 sucrose_synthase [MW = 92.47 kDa]

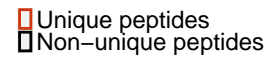
No. of times detected



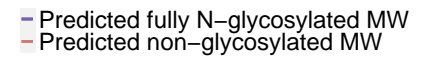
log(intensity)



Values from



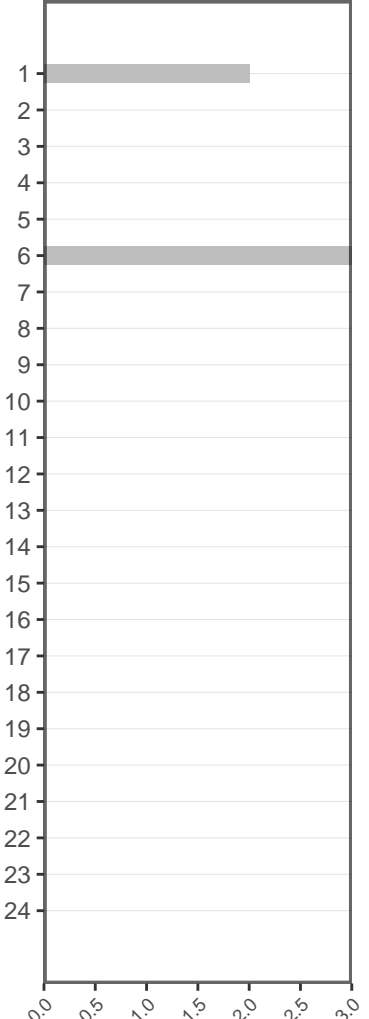
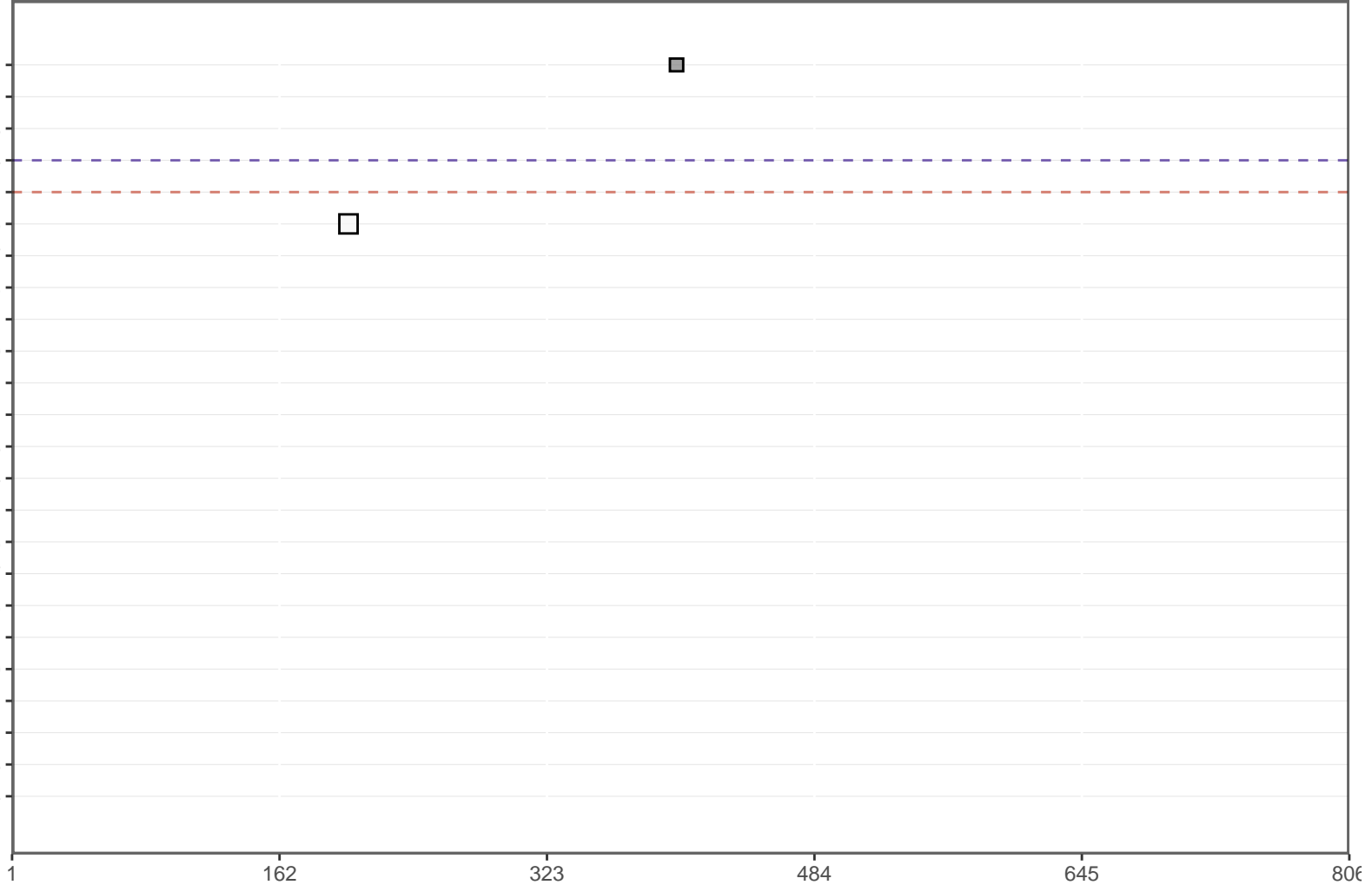
MW indication



Molecular weight



Gel Slice

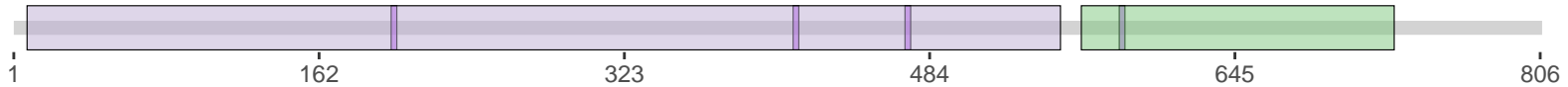


Protein length

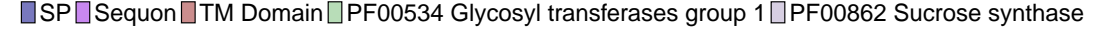


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

FTEDVAKLAEELGAKPDJLIGAYSEGNLWALLAHKLGVTGCTIAHAEKTKYPSDSVYWKFKDEKHYHFS66FTADLIMNHDTFITSTFQEIAGSKIVSGVYESHQAFITMPLGLYRVVHGIDVDPKFNIVSPGADINLYFPVSEKKRRLTALHPEIEELLYSDVENEHLGVLDKKNKPLFTMARLDRVANKLGLVYEWYAKNARLRELNLVYVGGDRRKEKDLLEGQAEMKMYELKTHNLNGDFRWISSGMINRVNSELRYVIADTRGAFVQPFYEAFLGTVVEALTCGLI

NbL10g03670.1 yrdC_domain-containing_protein_mitochondrial [MW = 30.4 kDa]

No. of times detected



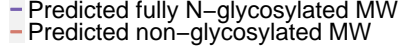
log(intensity)



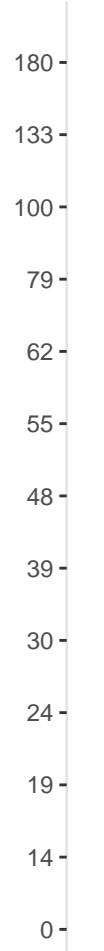
Values from



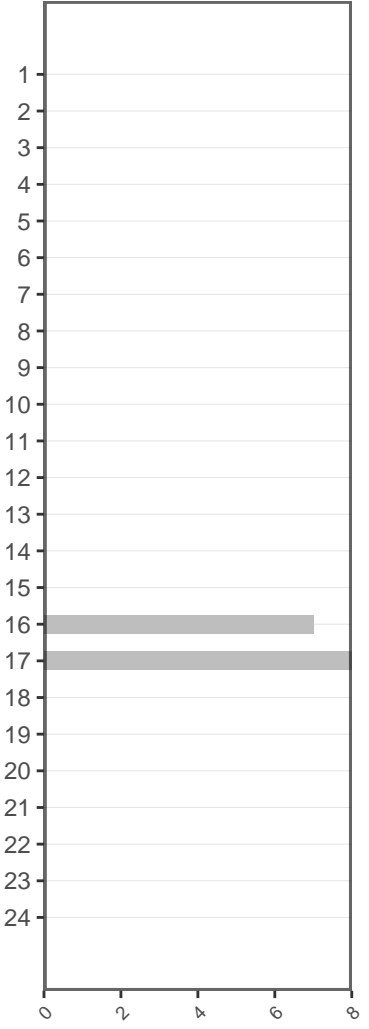
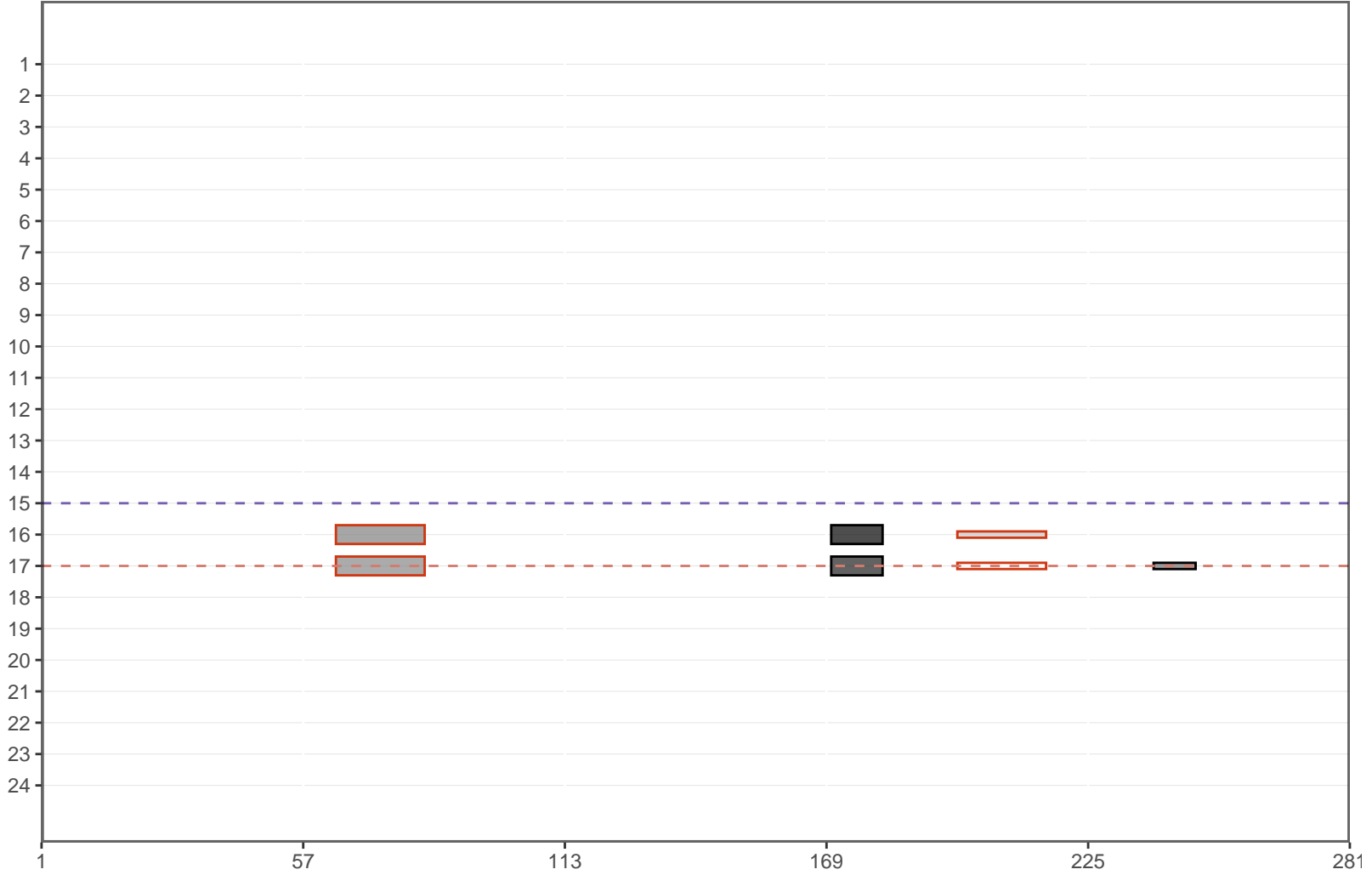
MW indication



Molecular weight

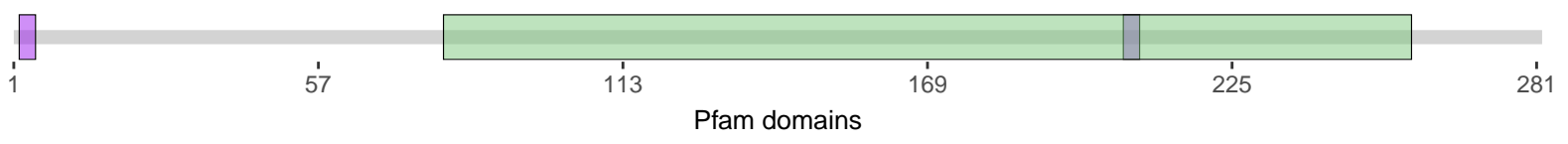


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SDVHIDQRYAVTDHLPHGLLDGLPCFVTVLRRGESSILEKLNPLGLESIGVRVDPYNFRIIARGSRSAIATSANLGGPSSINIKDFENLWEHCAYVDDGGVLDGDRAGSTVVDLTKLQYKILRPGSAKEETVALERHLLLEDGTGG

NbL10g03470.1 fasciclin-like_arabinogalactan_protein_2 [MW – SP = 40.47 kDa]

No. of times detected



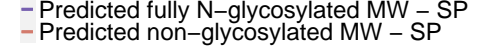
log(intensity)



Values from



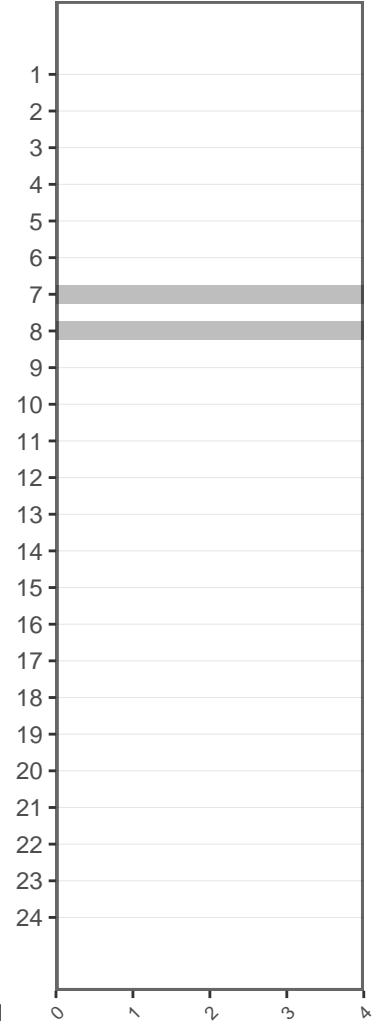
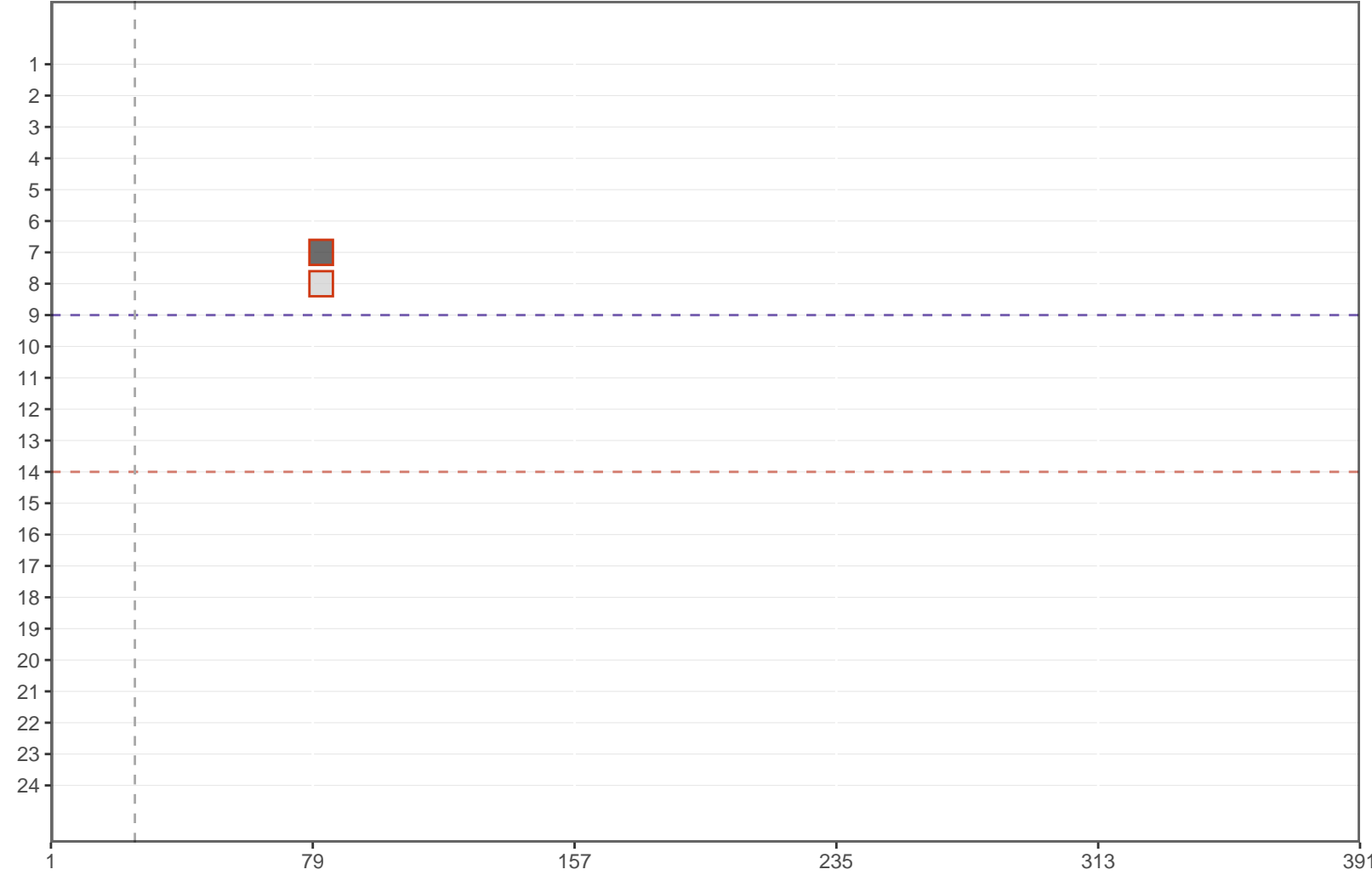
MW indication



Molecular weight



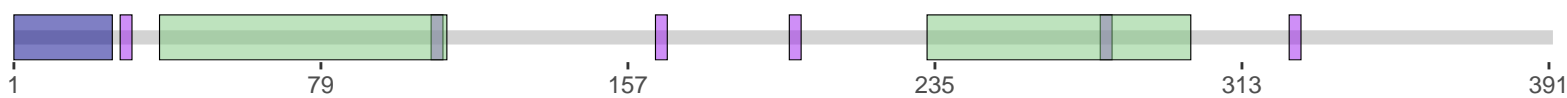
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

IGHF SASFYKSDIEIPNINSGIKGNIQSEAEAPVSAFAEIDHDLMTNKGCKEFALKLENSKTKTKTFDMENGLTVFQPIQKVVNSFLPKYKLNLTNGQTSLLLYHGIPDHSLEDEPLAVYKDKVLRQSELFKAQSHINSEDTVPEPNSGGDDGGVPAADATADNNGAMIMVNGWLMFTLIGWYLVEMNEVWVNLVAVET

NbL10g03250.1 NEDD8-activating_enzyme_E1_regulatory_subunit_AXR1-like [MW = 58.13 kDa]

No. of times detected



log(intensity)



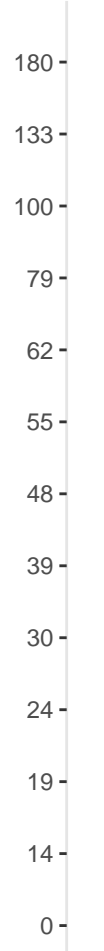
Values from



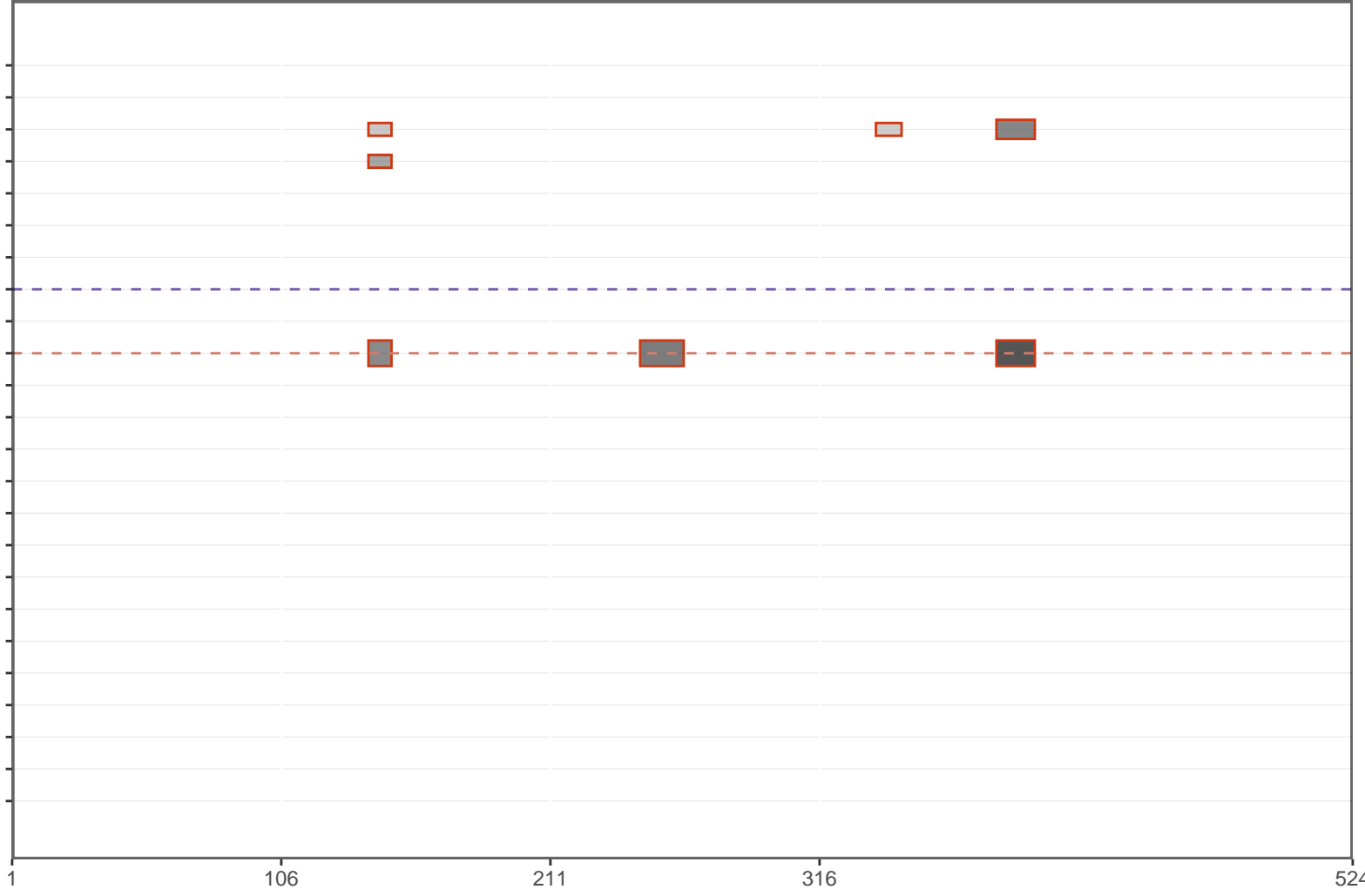
MW indication



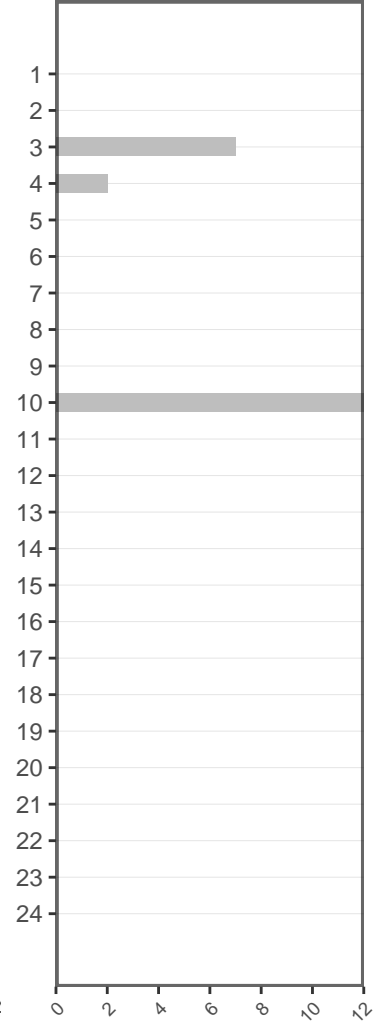
Molecular weight



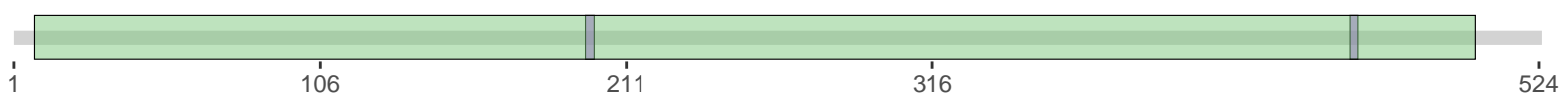
Gel Slice



Protein length

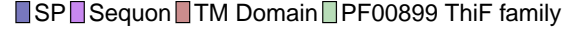


Peptide counts over 4 repeats



Pfam domains

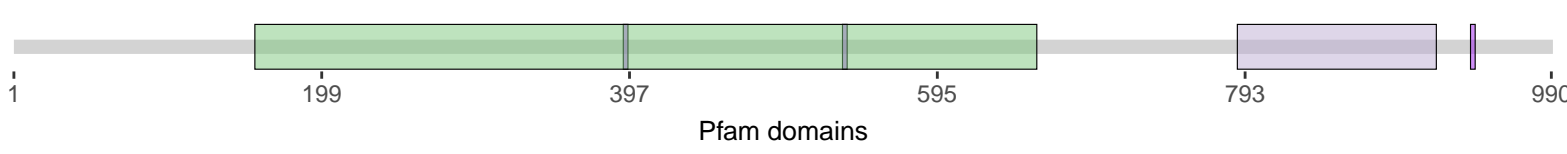
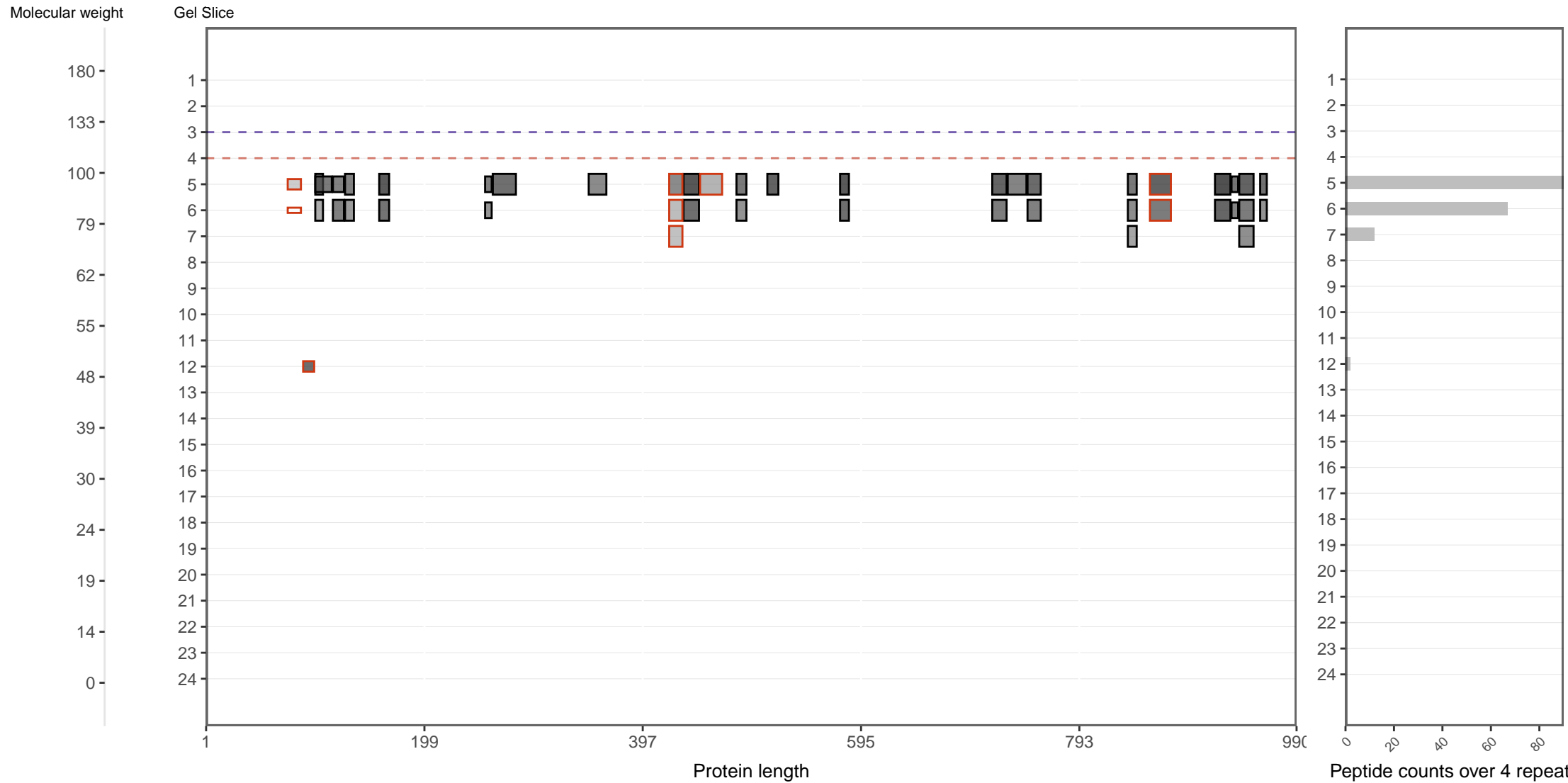
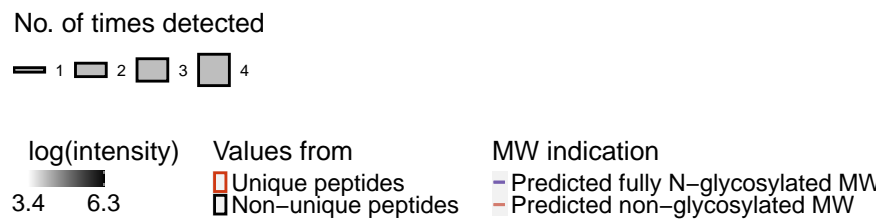
Pfam Description



Protein sequence:

SDEENYKEAVEASWKLFPDGGTGNLQKHDDGCTEVDSSSSDFWMMVAALKEFIANEGGEEPTLEGGSPDMFSSTELVNLQKTYGAKAEADVFMEQKVRNLKIKIGRDPASIAKHAHKSQGNARKLAVCRVRLIEDEFNSPVQPELQKYUIDEDYGTAVGLYLLRAADRFAANNKFTQGFQDGEDMEDIISRLKTTAVGLLNLDLGGNGSALSEDLINEGRVYGASELHAAVAFVGGVAGDEVKLLTRQFPMSTGTFIFNGIDHKSGLLL

NbL10g03240.1 aconitate_hydratase_cytoplasmic-like [MW = 108.25 kDa]



Pfam Description

SP Sequon TM Domain PF00330 Aconitase family (aconitate hydratase) PF00694 Aconitase C-terminal domain

Protein sequence:

IKSDVHISCLDNKVGFKGFVAPKDADEKVAKFSFHGGDAELKHGKVVAAFTSGTNTFNPQVMLGAALVAKKADLGLHKPKVWVKTSLAPGSGVTKVLLGSGLGKLVNQGDFHIVGGCTTCIGNSGDLDESVAISENDVIAAALVSGNRFEGVHPLFRANVYASPLLVAVWALAGTVDDIDFEKEPIGVNDGKNVYKQDWIPSTEEIAGVVG65VLDPMFKSTYEATKGNMVAWGLVPAKLYSWEPS65TIHEPPVYKDMTMDPFGPHGVNDVYCLLNFQDSITT

NbL10g03070.1 cytochrome_b6-f_complex_iron-sulfur_subunit_2_chloroplastic [MW - SP = 22.53 kDa]

No. of times detected



log(intensity)



Values from



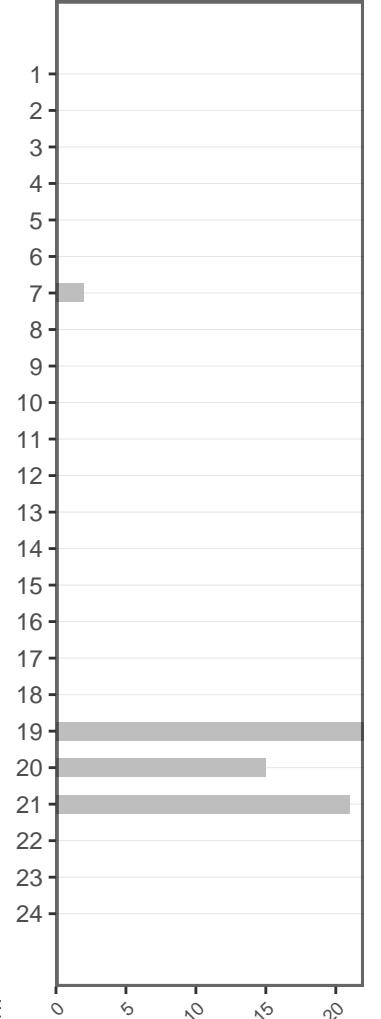
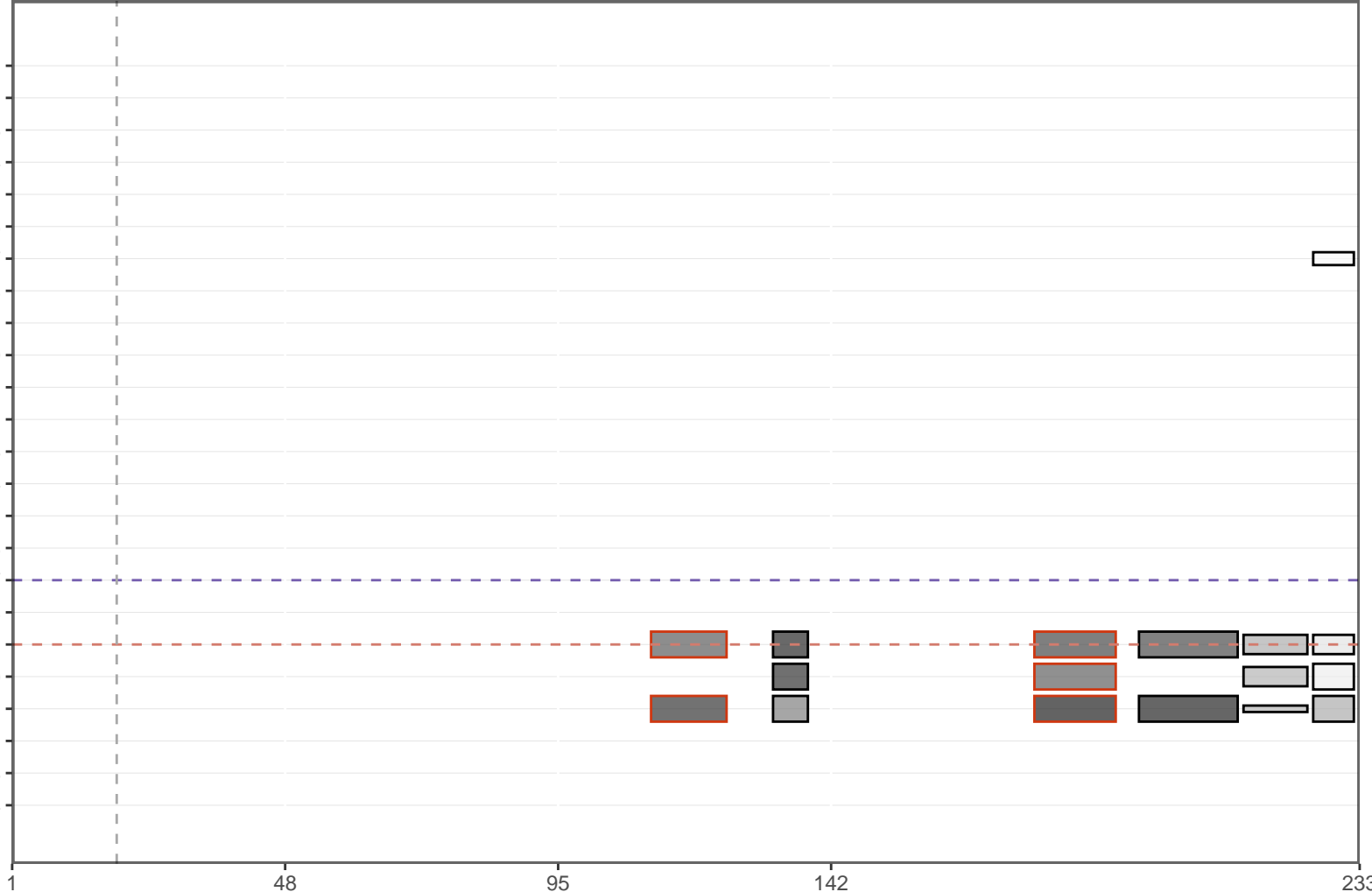
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

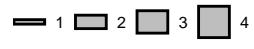


Protein sequence:

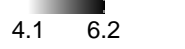
SGTPAKDALGNDVYASEWLKTHAPGNRTLFDGLKGDPTFLVVENDDTLATYGINAVGTHLGGVWPFNAENKFCFPHGSDYNNQGHVVRGPAFLGLALAHADDDGKVVFPVWVETDFRFTGEAPWVA

NbL10g02760.1 ketol-acid_reductoisomerase_chloroplastic-like [MW = 63.7 kDa]

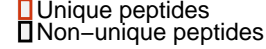
No. of times detected



log(intensity)



Values from



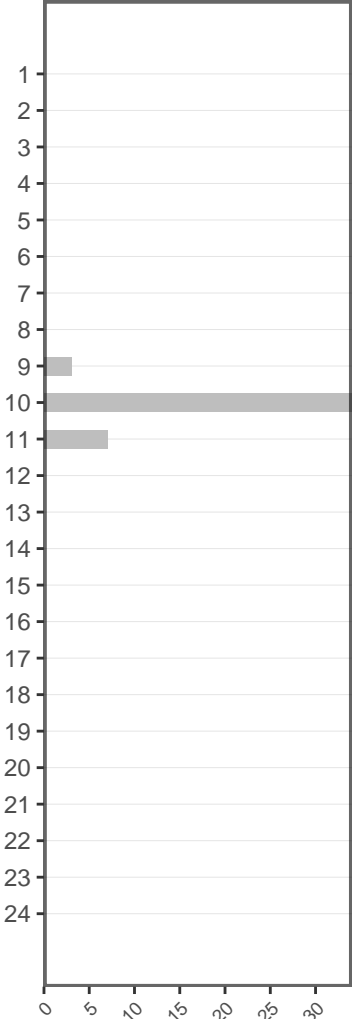
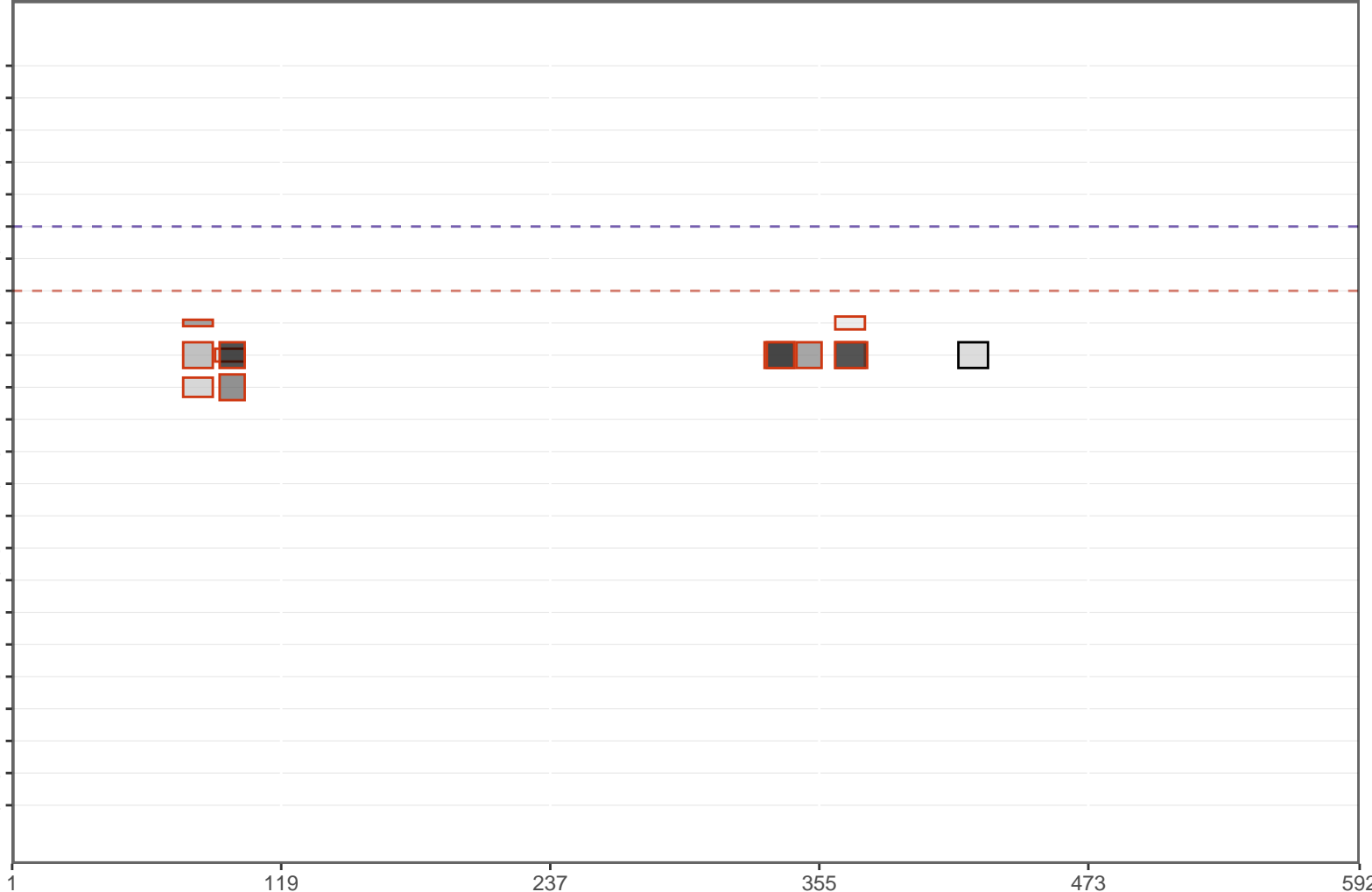
MW indication



Molecular weight

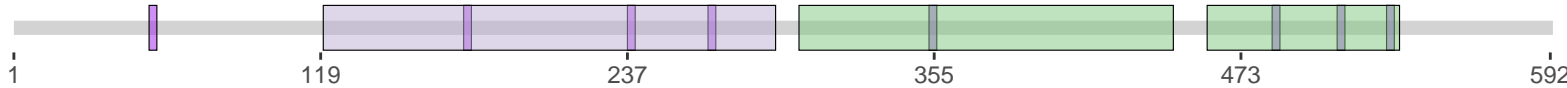


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01450 Acetohydroxy acid isomeroeductase, catalytic domain
- PF07991 Acetohydroxy acid isomeroeductase, NADPH-binding domain

Protein sequence:

YALGW5VALGSPFTTATLEGEYRSDIFGERGILLGAVHGVESLFRRTYENGMSSEELAYWNTVEGITGNISRTSTKGMALALVNSFTGDEKREFAIYASBAYPCIMELLYEGYEDVATGSEIRSVVLAGRRFSEKEGLPAPMFKIDQTRMVKYGERVNRTRPSGDLGLPLVFTAGVYVALMMAQIELRKKGHSHSYSEINIEGVESVDSLNPFMHARGVDFMVDNGSSTARLGSRWKAPRFQYKLTGGALVAVDNNPINMQLMTNPFVGDVPHHEAIEVCAQLRPTVDISVYKDAI

NbL10g02650.1 ras-related_protein_RABA1f-like [MW = 24.1 kDa]

No. of times detected



log(intensity)



Values from



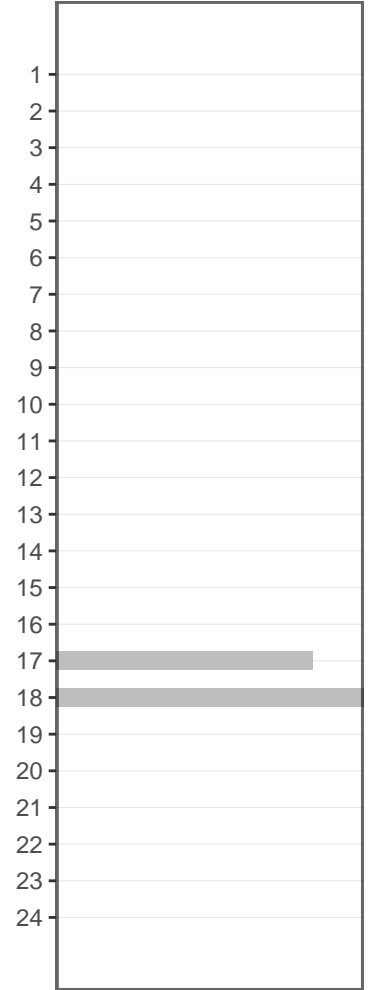
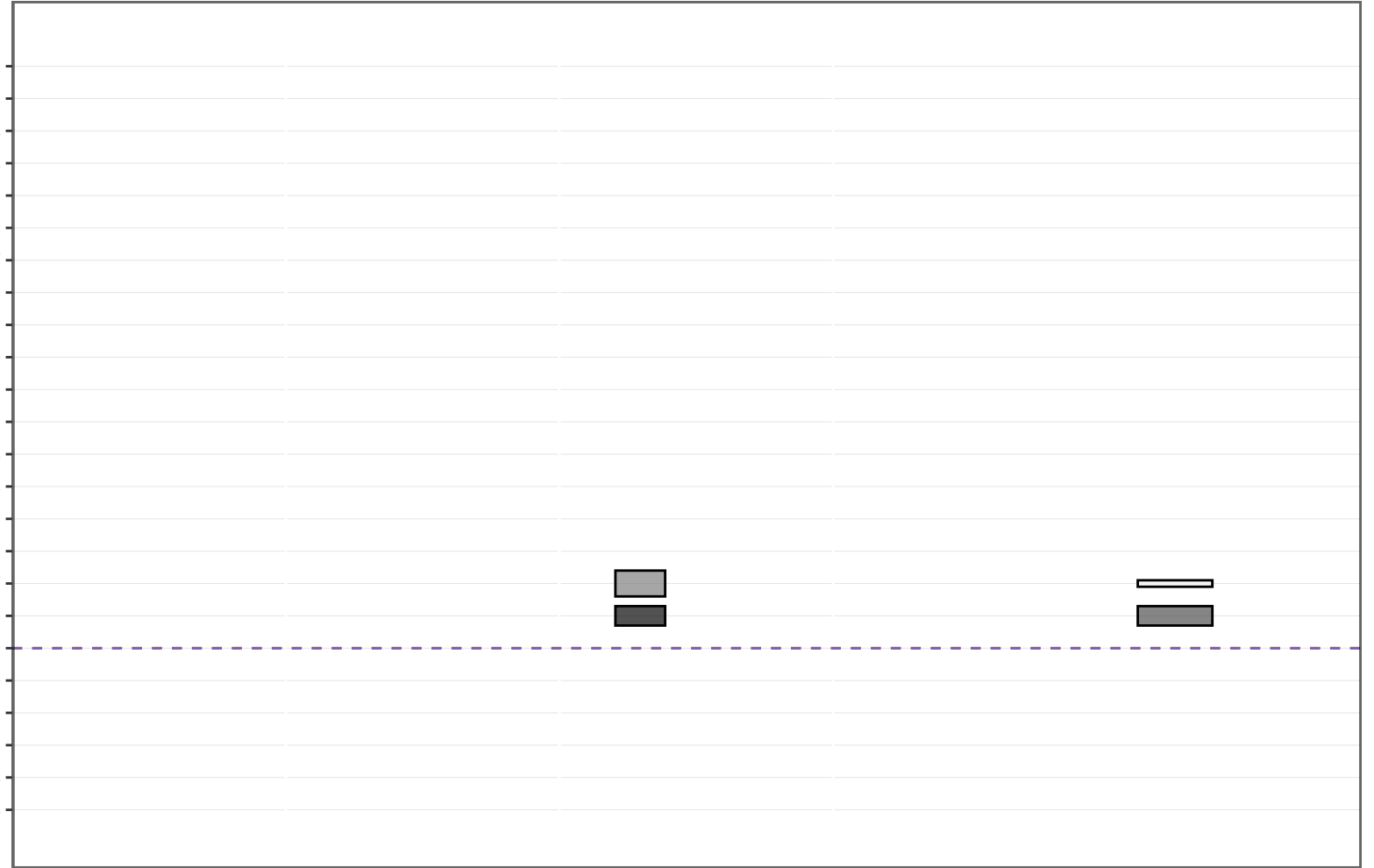
MW indication



Molecular weight

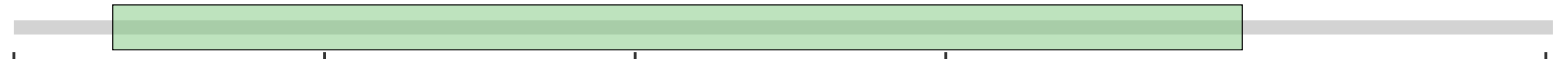


Gel Slice



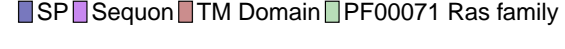
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RHVTENVERVYKELRDIHTDSSIVMLVGNKADLRHLRAVSTEDAKFAEKESTFFMETSALEGMNVDAFTEVLTQHRRVSRKALEVGGDDPMLPKGGTINVGKGDVSEVKKAGCGSS

NbL10g02440.1 vacuolar_protein_sorting-associated_protein_35A-like [MW = 89.47 kDa]

No. of times detected



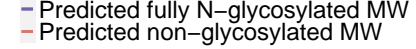
log(intensity)



Values from



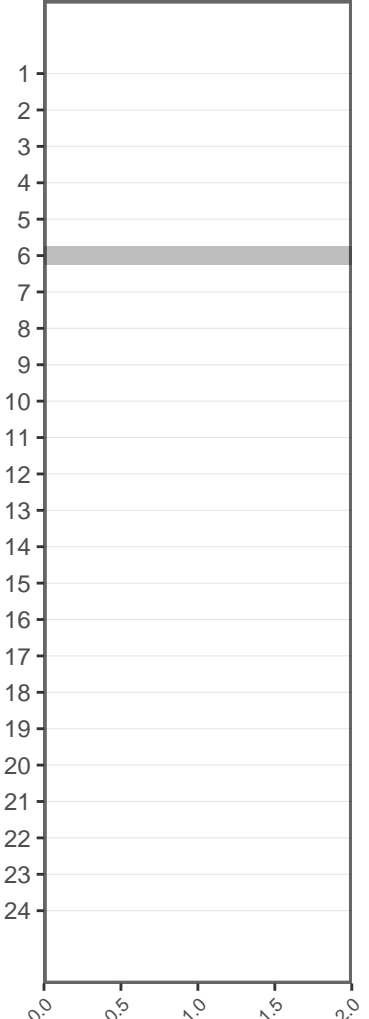
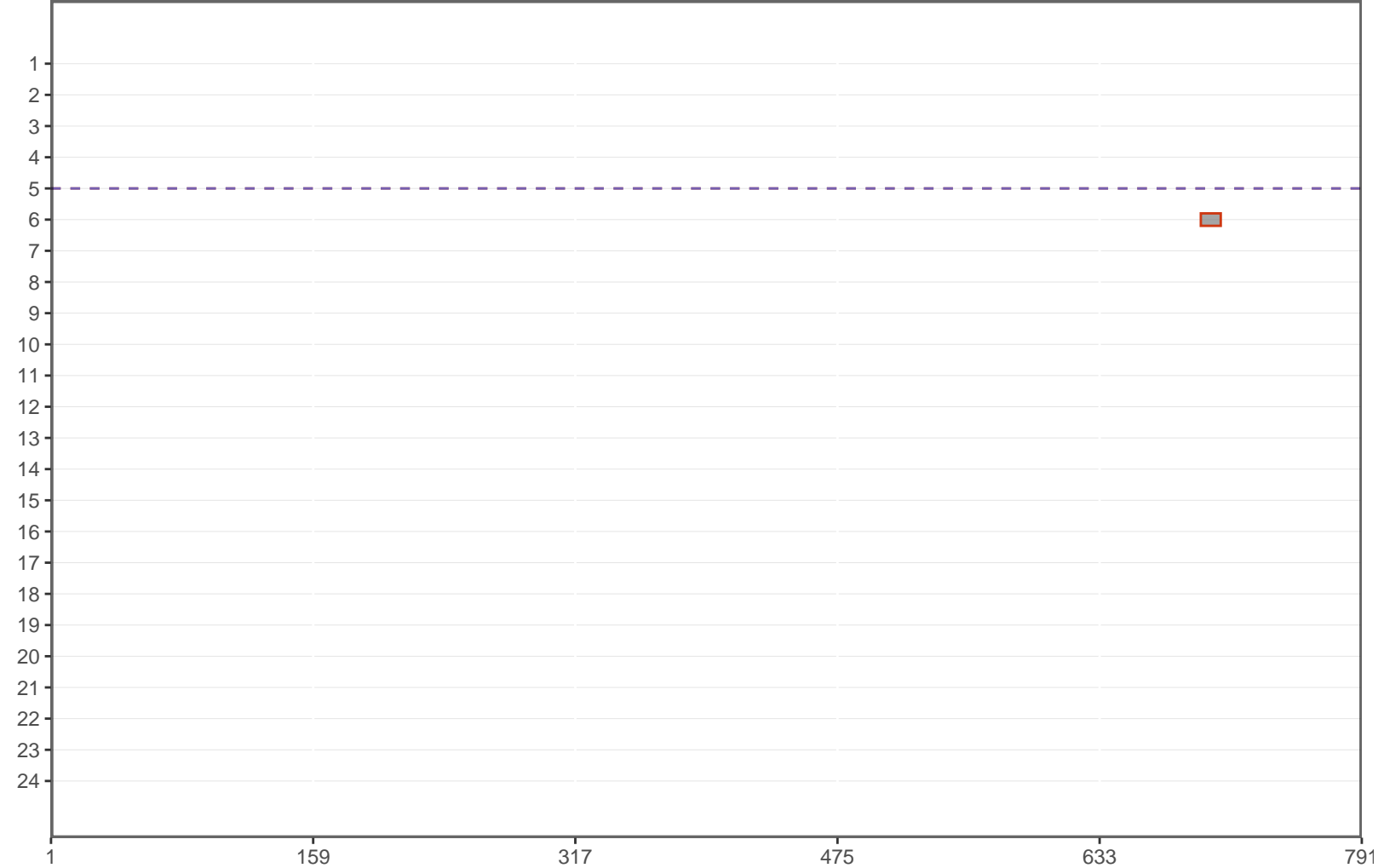
MW indication



Molecular weight



Gel Slice

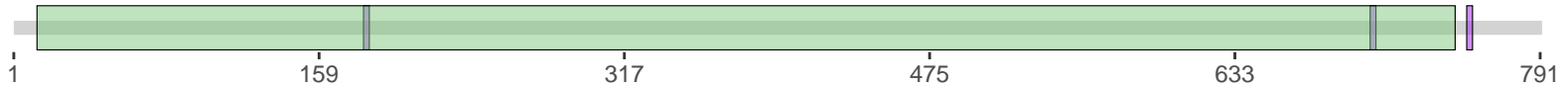


Protein length

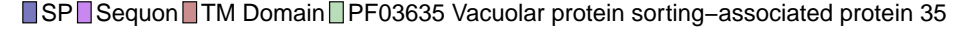


Peptide counts over 4 repeats

Pfam domains



Pfam Description

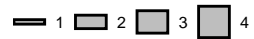


Protein sequence:

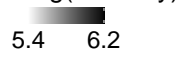
IGKGLKDKATKQKALLSAPLEKYKDDITALKLKNYPHMEHLDDATSKEMANLVGTLKSKTQISTAEKVEALFELMKGLRDLDDNLHDELDEEDFKEEQNSVARLQMLHNDPEEMLKIKISTVKKHILTGGKPKRLLPFTVPLPFLNLSKLVRRLLQNGDENAPEEASAMPKPKFQILNGHIESLSSVPPPELSLRVLEGAEEAANDALEPVAVEFFTQAVILVEEESDSKAGVTAHLLIGTLGRMNVFGVENRDLTKATGYSAKLKKPDGGKAVYSGSILFPVDDDSK

NbL10g02420.1 proteasome_subunit_alpha_type-6 [MW = 28.42 kDa]

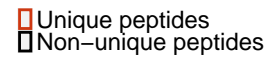
No. of times detected



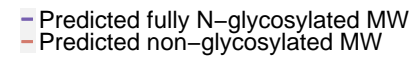
log(intensity)



Values from



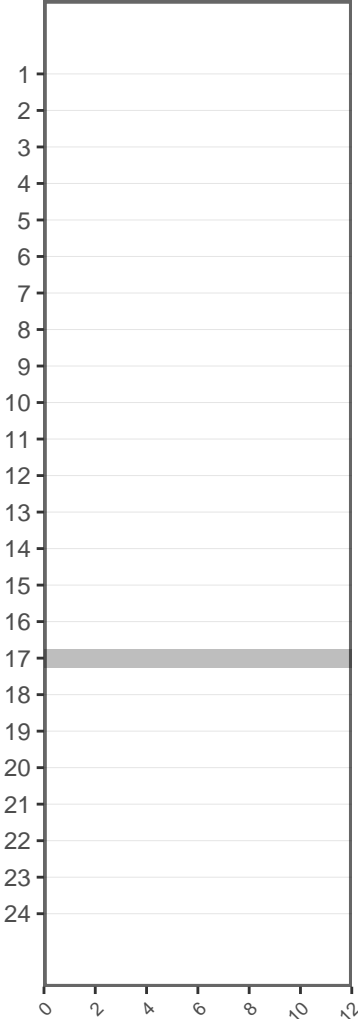
MW indication



Molecular weight

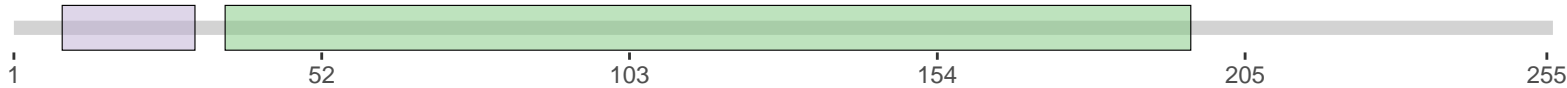


Gel Slice



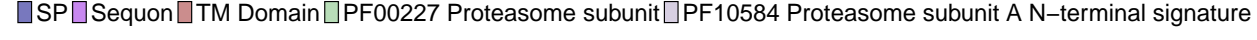
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

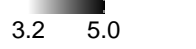
LSRWIADKSOVYTGHAMRPLGVVAMILGIDEEKGPQLFKGDPMGHFFGHKATSAGSKGEAEINFLKIKMKNDPMFSYEETVGVKGGKGVFRRLRLRPLFSLYPIFSSFTFLSLQVATAGIPVSRLLWYCYELKILWALN

NbL10g02260.1 probable_inactive_receptor_kinase_At2g26730 [MW – SP = 68.71 kDa]

No. of times detected



log(intensity)



Values from



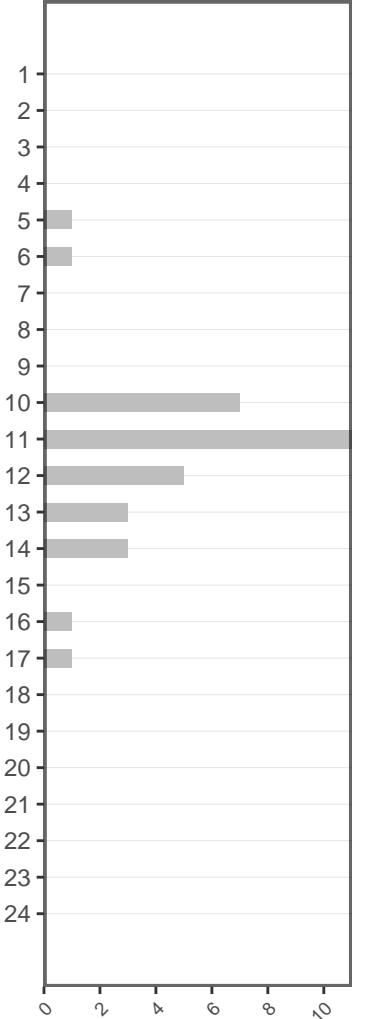
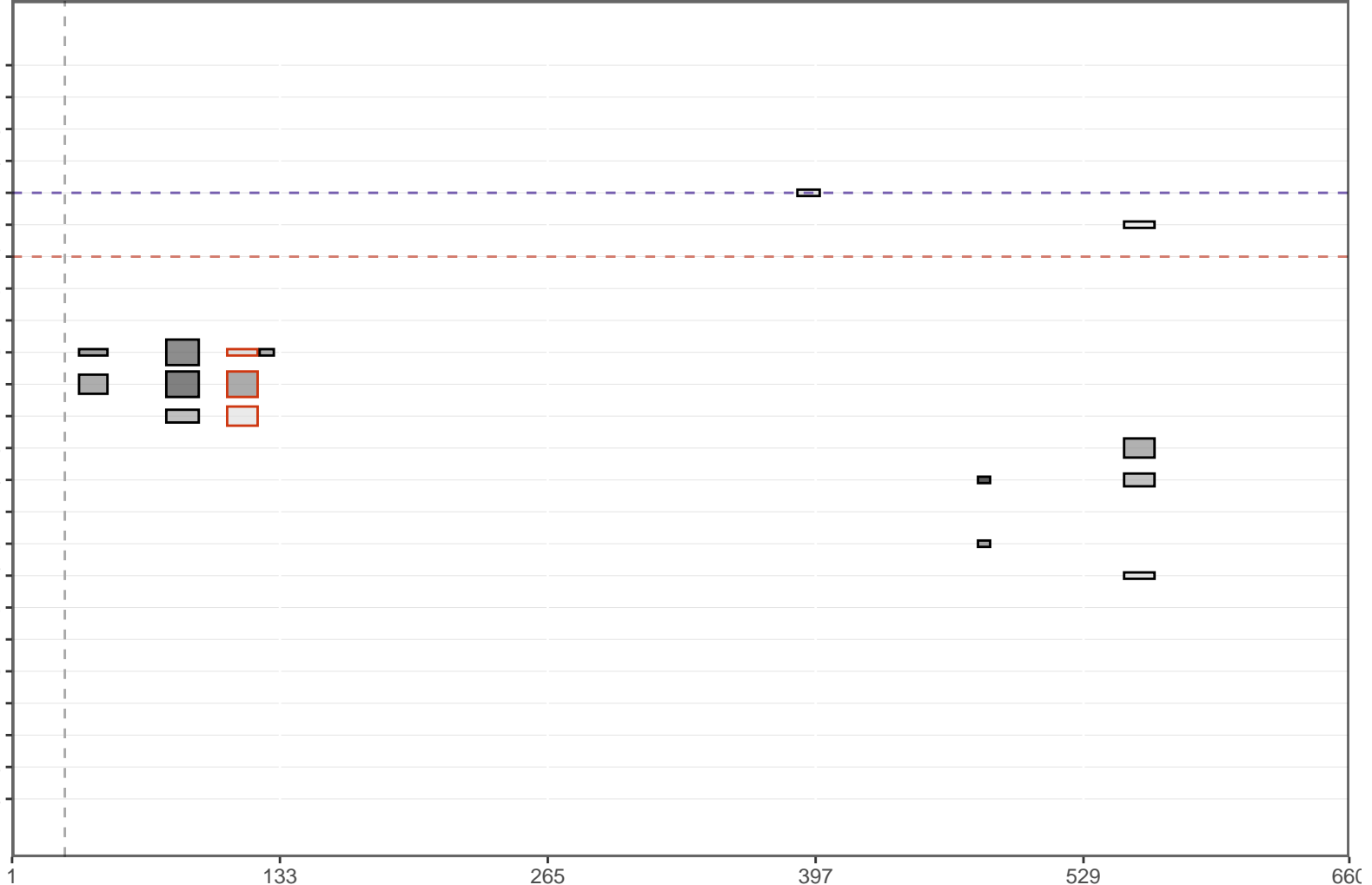
MW indication



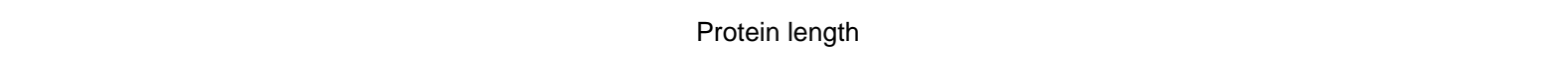
Molecular weight



Gel Slice



Protein length

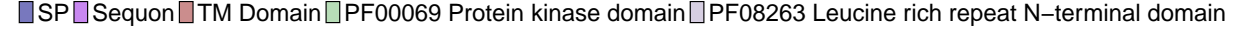


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DLTAEGERNKLVFNGGGGYSFDLEDLRASAELVKGKSVGTSYKAVLEEGTTVAKRLKDNVVTTRKEFEGQMDVLGKMKHENLPLRAFVFSKDEKLVSDVYPAGLSLHLSGRGSGRTPLDWDSMRIRVLSAARSISVLIHISGKIVHNSNKAENVLLKGNNGDQVGVSDVGLNPLFTTATPNNHRWAGLYRAPEVLETRKVTFKSDVYGFQVLELLTGKAPNGASLGEEDLPRWVQSVNREEWTAIEVFDVLELMRHYHVEEEMVQLLQGMACVAIVPQORPTI

NbL10g02160.1 carbamoyl-phosphate_synthase_small_chain_chloroplastic [MW = 47.22 kDa]

No. of times detected



log(intensity)



Values from



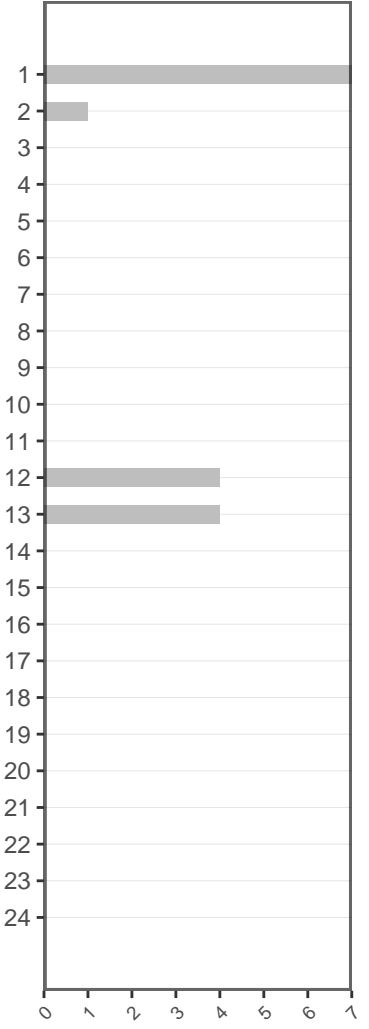
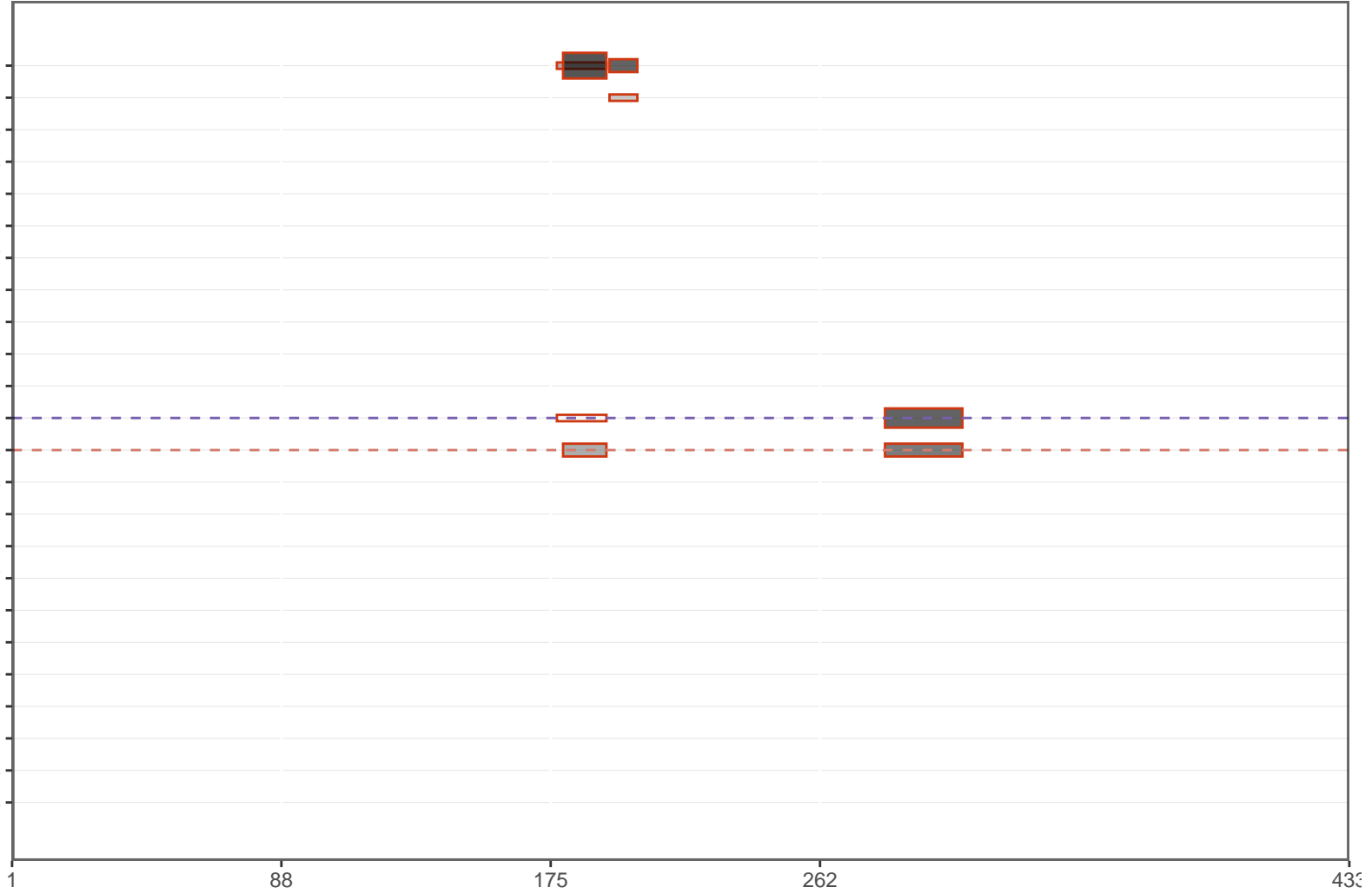
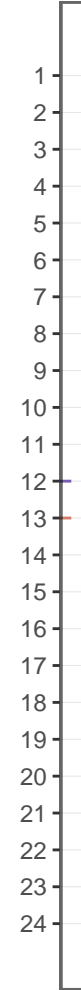
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00117 Glutamine amidotransferase class-I
- PF00988 Carbamoyl-phosphate synthase small chain, CPSase domain

Protein sequence:

DIVGVLTGVSCKSPYEVWVDTASDWDVFNDRNGRNETFTNVAVYDFGIKHILRRIRIAGYGGKTVVPTWPASETLAKMKPDGVLFSNGPGDRSAPVAVAEVAKLGIKIPFVFGIGMHLLGDALGGKTFKMKFGHHGGNHFVRNLRNGGVEIAGQNHNYAVDPESLPEGEVETHVNLNDGSCAGLASSKMKMLSLGYHPEASFGPHSDSPVFGFQIMKQEKVKA

NbL10g02120.1 probable_protein_arginine_N-methyltransferase_1.2 [MW = 45.1 kDa]

No. of times detected



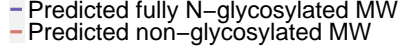
log(intensity)



Values from



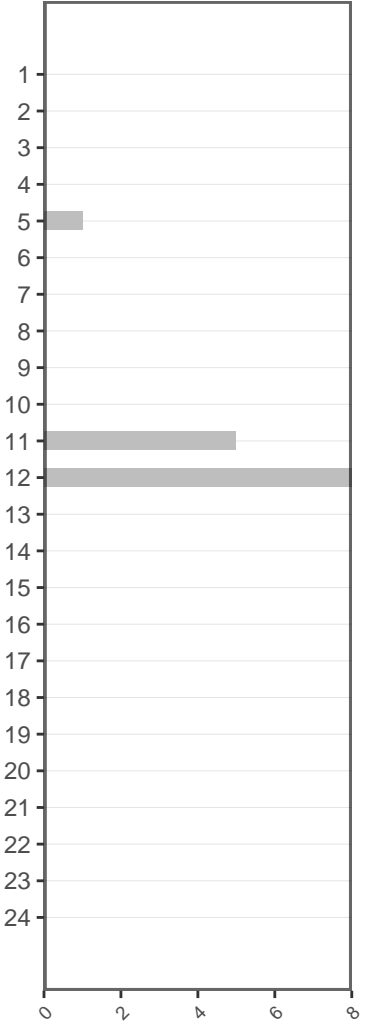
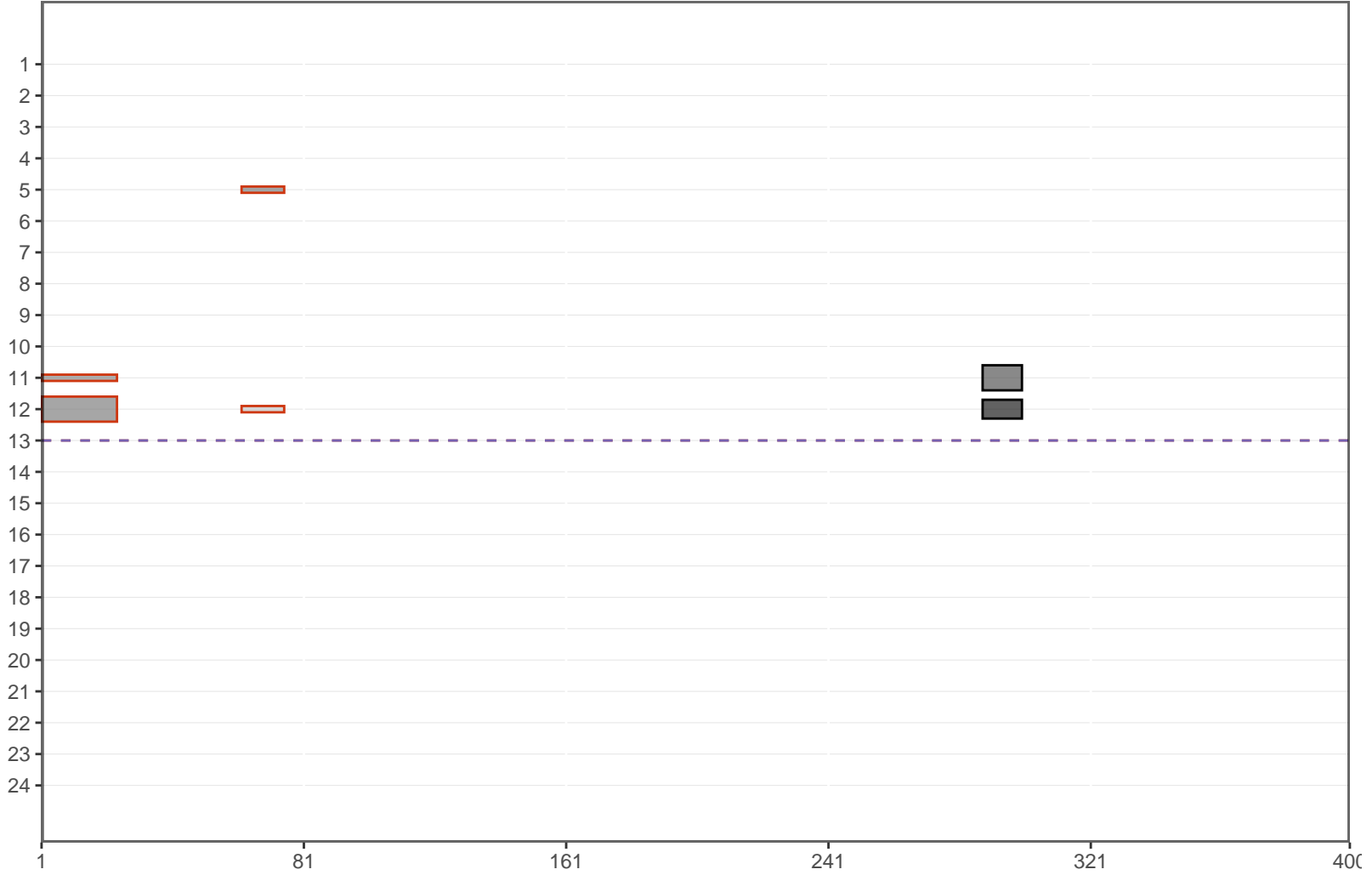
MW indication



Molecular weight



Gel Slice



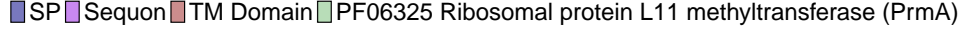
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISSEVIMGYFLLYENMLDFTVMARDKVAWKDGLVLPDKASGLVLAIEDGADYKTKIEFVNEVYGFDMSCRRKGMMEPLVDTVDQNGIVTNDQLLTKMDSIKMTSGDASFAPFKLAERDDYHALVAVFDVDFTKGKHLKMGFSTGPKSRGTHHWKGTVLVLEDVTRDGGAEAVVGSFTVAPNKNKPRDGDMLKYSVNGRHCRAVSRGTQYHRMR

NbL10g01940.1 gamma-glutamyltranspeptidase_3 [MW = 69.4 kDa]

No. of times detected



log(intensity)



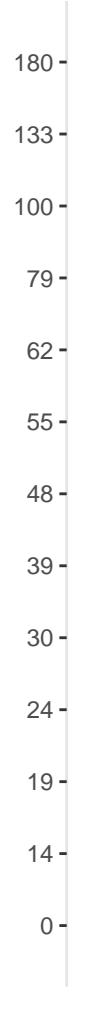
Values from



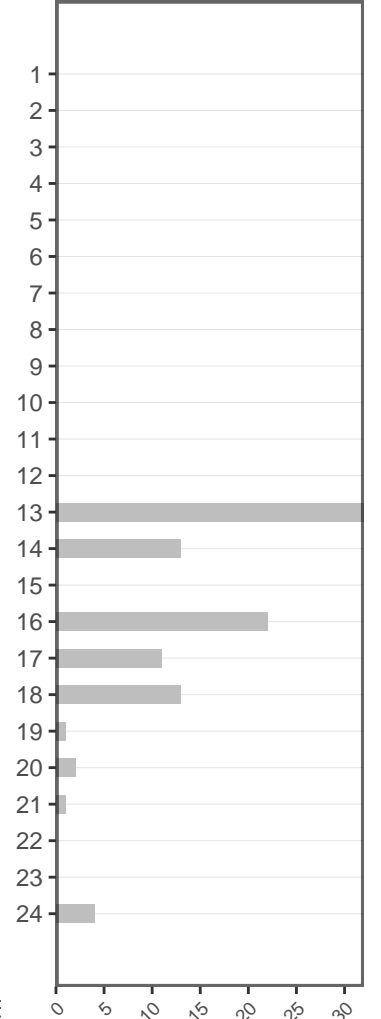
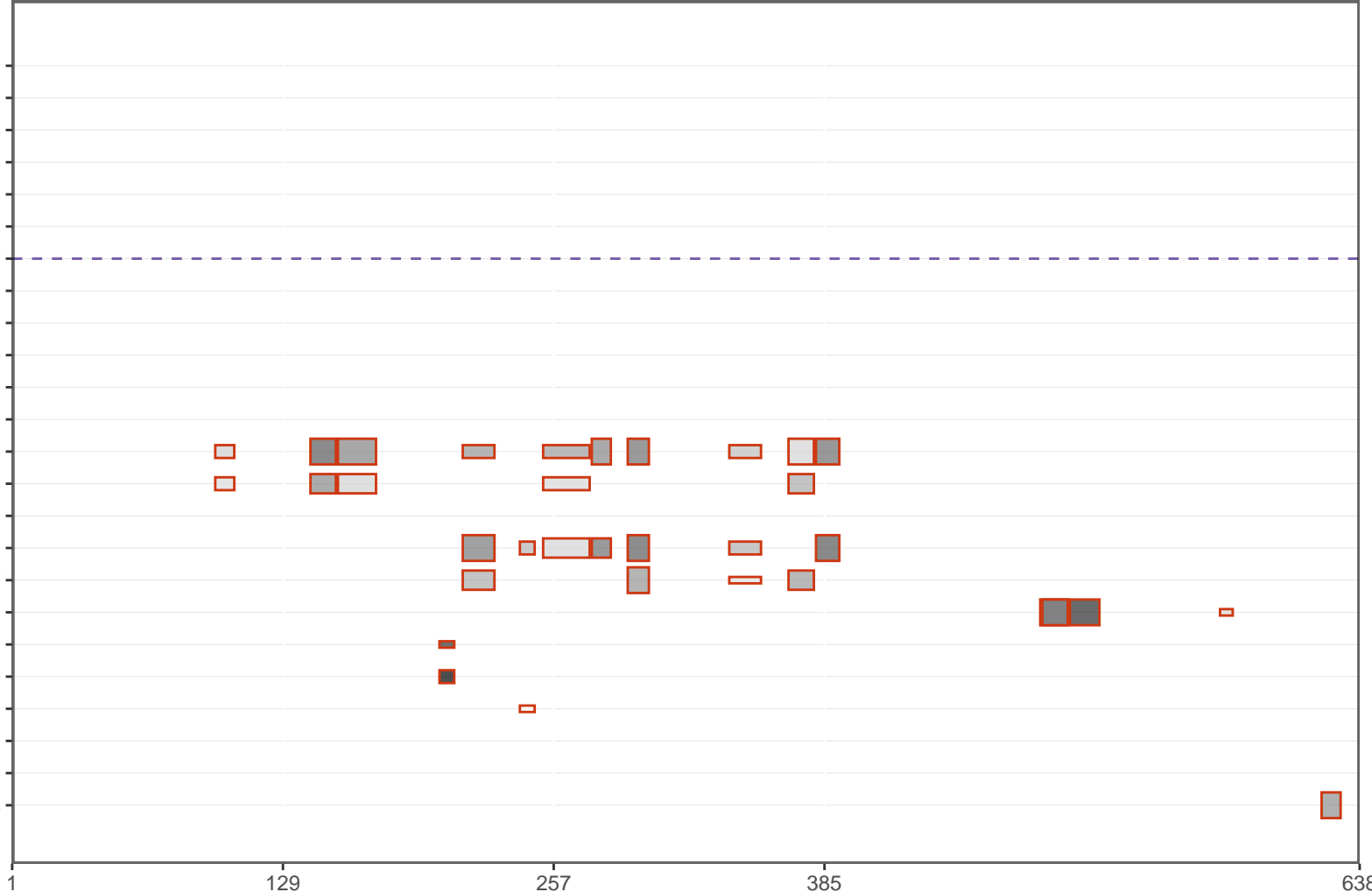
MW indication



Molecular weight

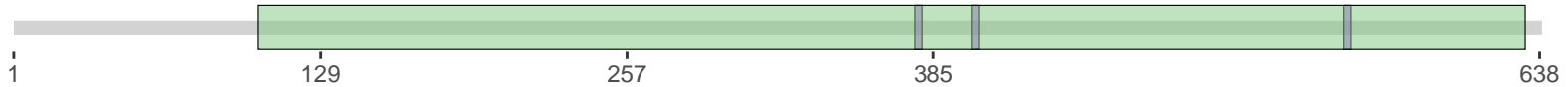


Gel Slice



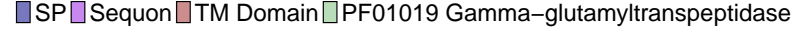
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

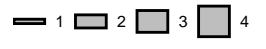


Protein sequence:

YKVEIPEAVTFNANMGYTVIGMALPPSSGTLGISLKLKLESYNTAEGLVGLHRIEAMKHMFVARMLDGPDFVNSKTVSDMLSPGFAKEIGRKFIDFTTFPSEYVMPRWGQLRDRHTGSHFGVDSDRNAVIVTITVNYAFAGVLSRSTGIIVNDEMGSDFSTNDISPDLELPPSNAFQPKRRLFSMAPIIVLKNQGLAGVIGSGGKIPWVQGVFINHFLGMDPLAAVQSPRYVHELIPVWLYENWTCIGDSHIELSDEKKHFLLEERGHGLEAHHNGGAICOLVQLPNS

NbL10g01890.1 arginine--tRNA_ligase_chloroplastic/mitochondrial-like [MW = 73.4 kDa]

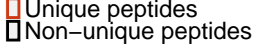
No. of times detected



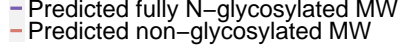
log(intensity)



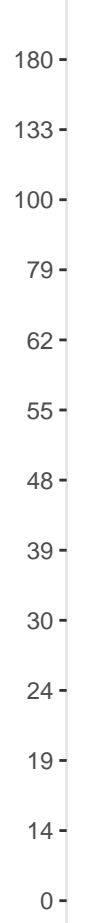
Values from



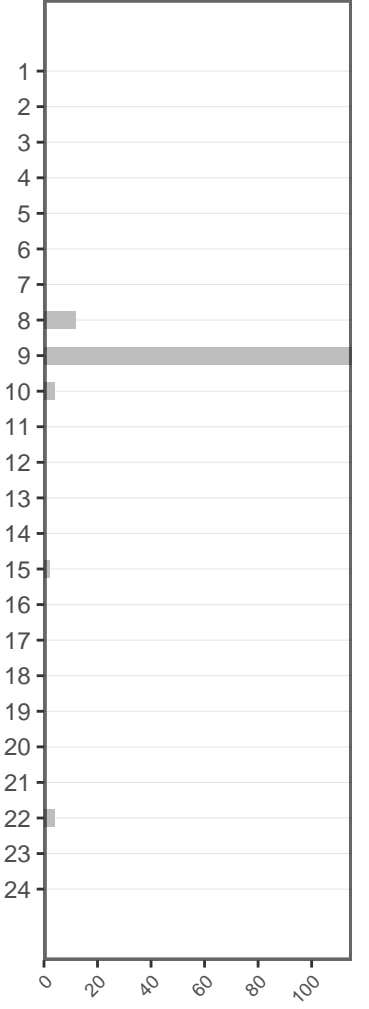
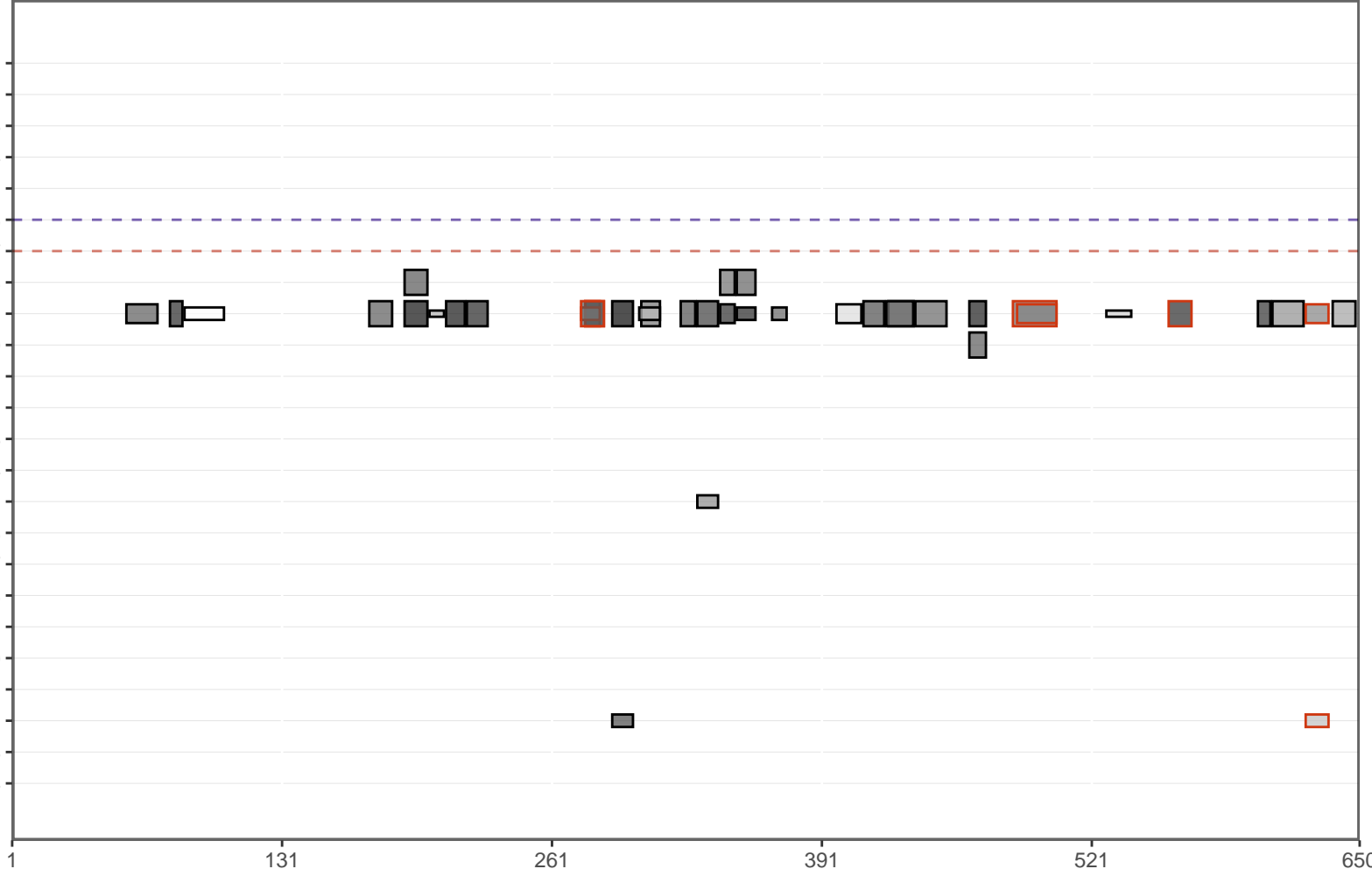
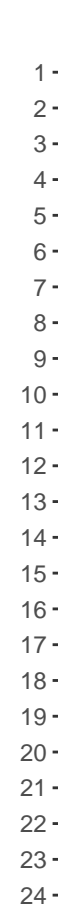
MW indication



Molecular weight

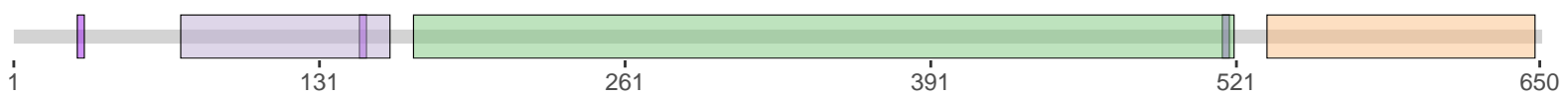


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SRKEFDKYYERLGVHLEEKGESEFNYPKALELLNEKGLIESEGARVIREGKKIPLVYKRDGGFNASTDLTALWYRLNEEKADMMVYTDVGGREHFEMFFSAKRAGVLPNENENPKASHVFGGLVAGEDGKRFRRTRSTEVKVLVDLDEAKSRKLALEERGKAKIEWTAEDELDDGTAEGVGVGAVKADLKNRILNTYTFNFDLMSDKGNATAVYLLVHARIGSIRKSGRDEELKKGAVDLAHDGERTLGLHLGFFPEIVEEAGTNLLPNLCEYLYKLSDFTKI

NbL10g01690.1 probable_lactoylglutathione_lyase_chloroplastic [MW = 40.16 kDa]

No. of times detected



log(intensity)



Values from



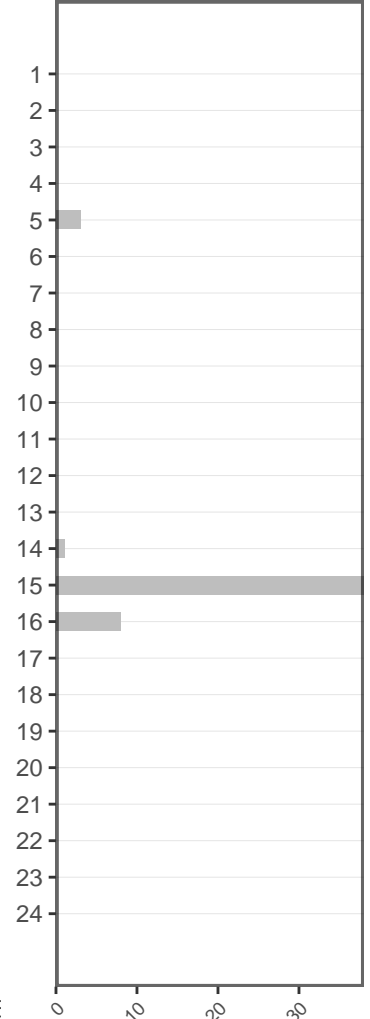
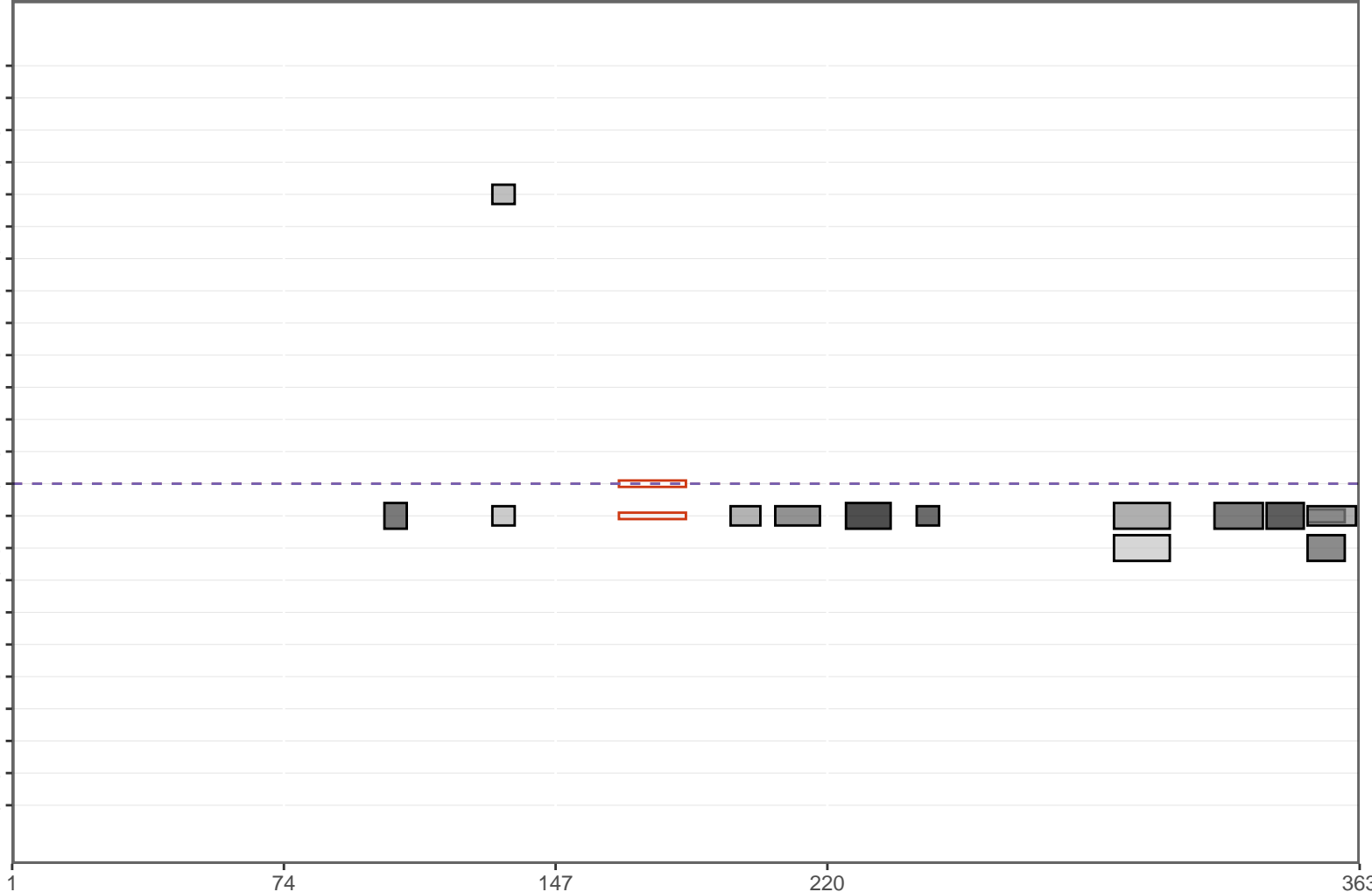
MW indication



Molecular weight



Gel Slice

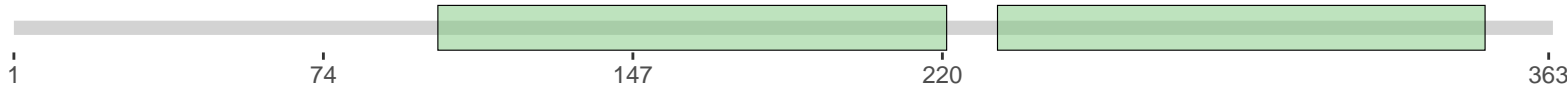


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SGFGHFGIAVEQIAKTVELVWAKGGKGVREKGGKTVARIEDPDGYNFELLERGGTPPEPLGGMLRVGDLERAINFYEKAYGMKLLRTRDNPYKYTIAMLGVGPESSAVMELTYNYGVTEYDKGNVAQIAGTDQVYKTAEARLRGGKTRPEGLPGIGSTKIVACLDPQGWKGVFVQNVDFLKELEI

NbL10g01430.1 aldehyde_dehydrogenase_family_2_member_C4 [MW = 54.67 kDa]

No. of times detected



log(intensity)



Values from



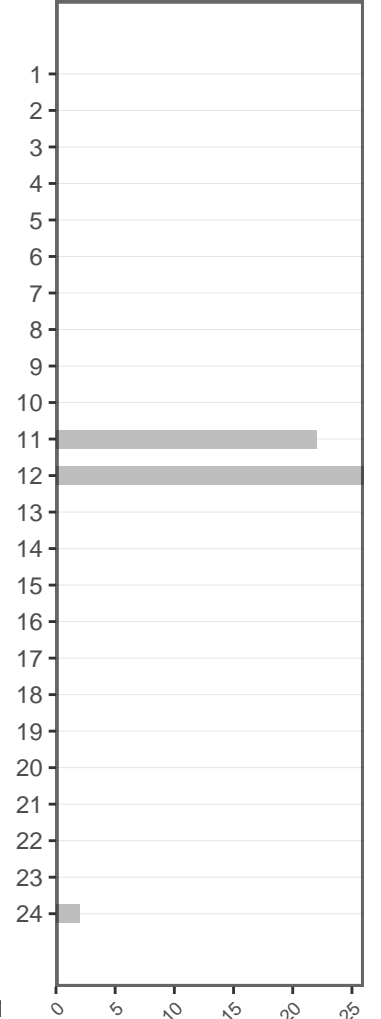
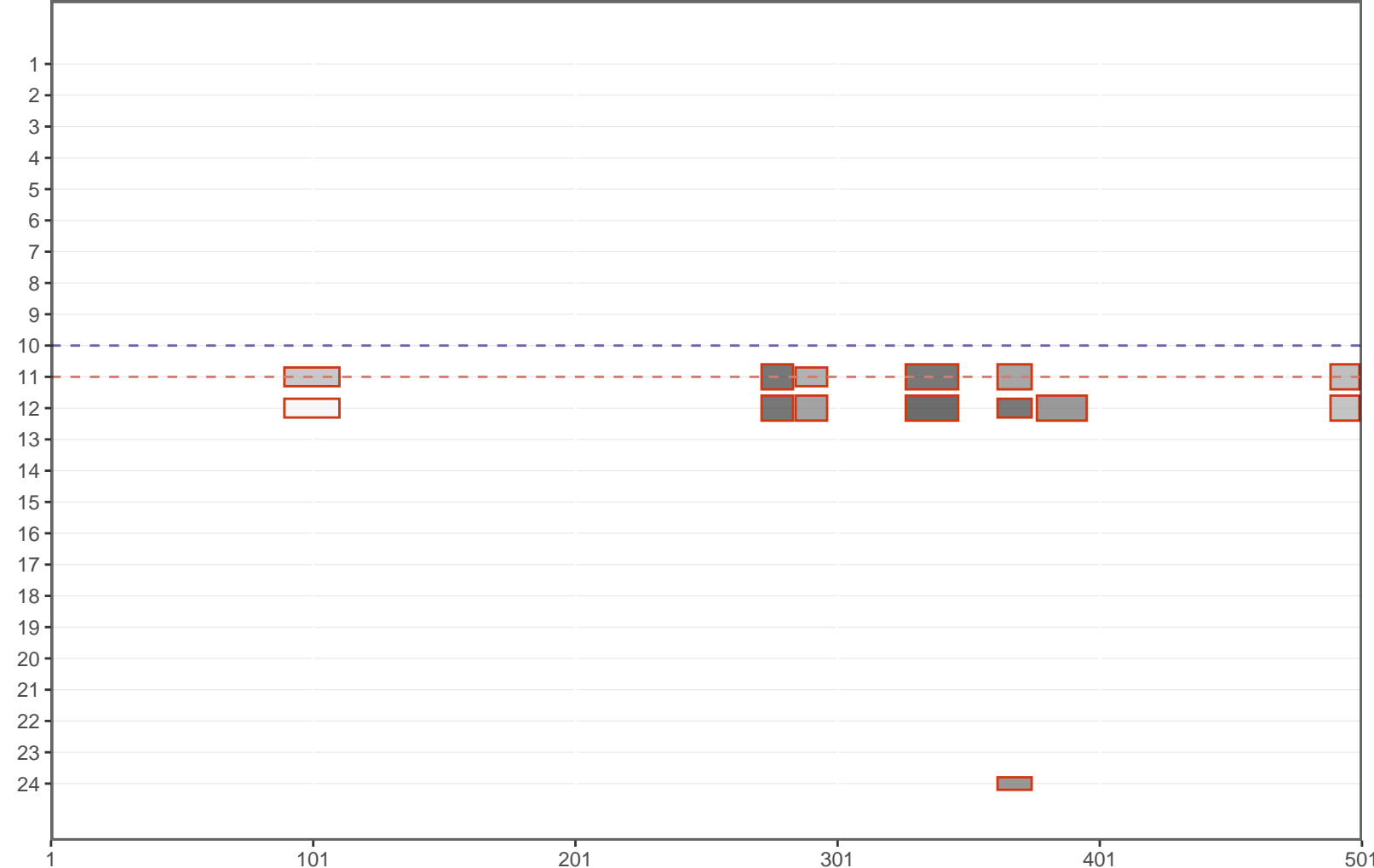
MW indication



Molecular weight

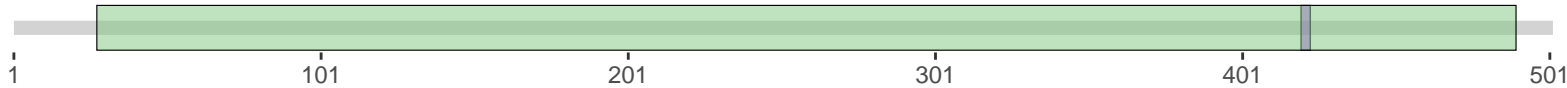


Gel Slice



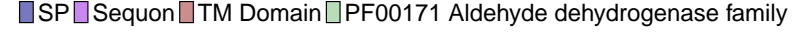
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DKISFTGSTEYGRIMMGAALSNLKPVLELGGKSPFFDFDQVKEKVPALALIGLYNKGECVAGSRLEFDGEGHYDKFVKKLVEFTKTVVGGDTFDNSHGQGPQVKKGFQFVLYEYHGRKCATVLTGQNALDRKDYFIETFTDVEDHMIKKEEFGPVLVMMKFKTVEEVKRNCTQYGLAAGVMTNLIANTVGRBRAGVWVWYFAFDPCDPYGGYKSSGFERDLGMEGLHKYLQVKBATPIYNSPWL

NbL10g01040.1 probable_ADP-ribosylation_factor_GTPase-activating_protein_AGD14 [MW = 65.84 kDa]

No. of times detected



log(intensity)



Values from



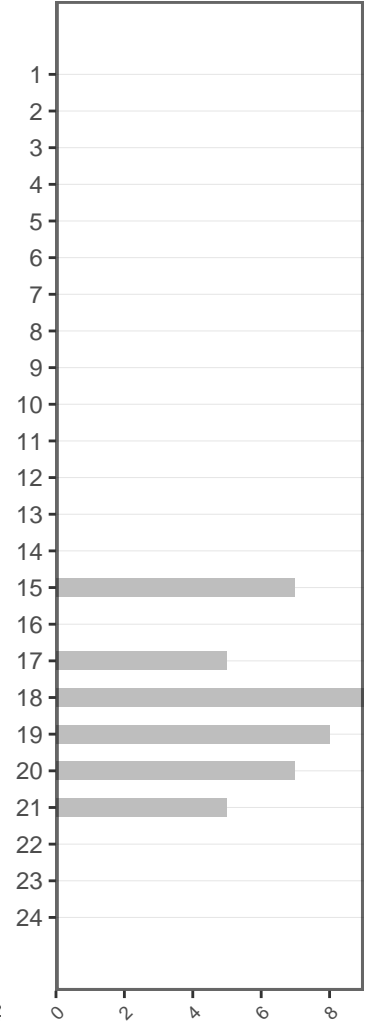
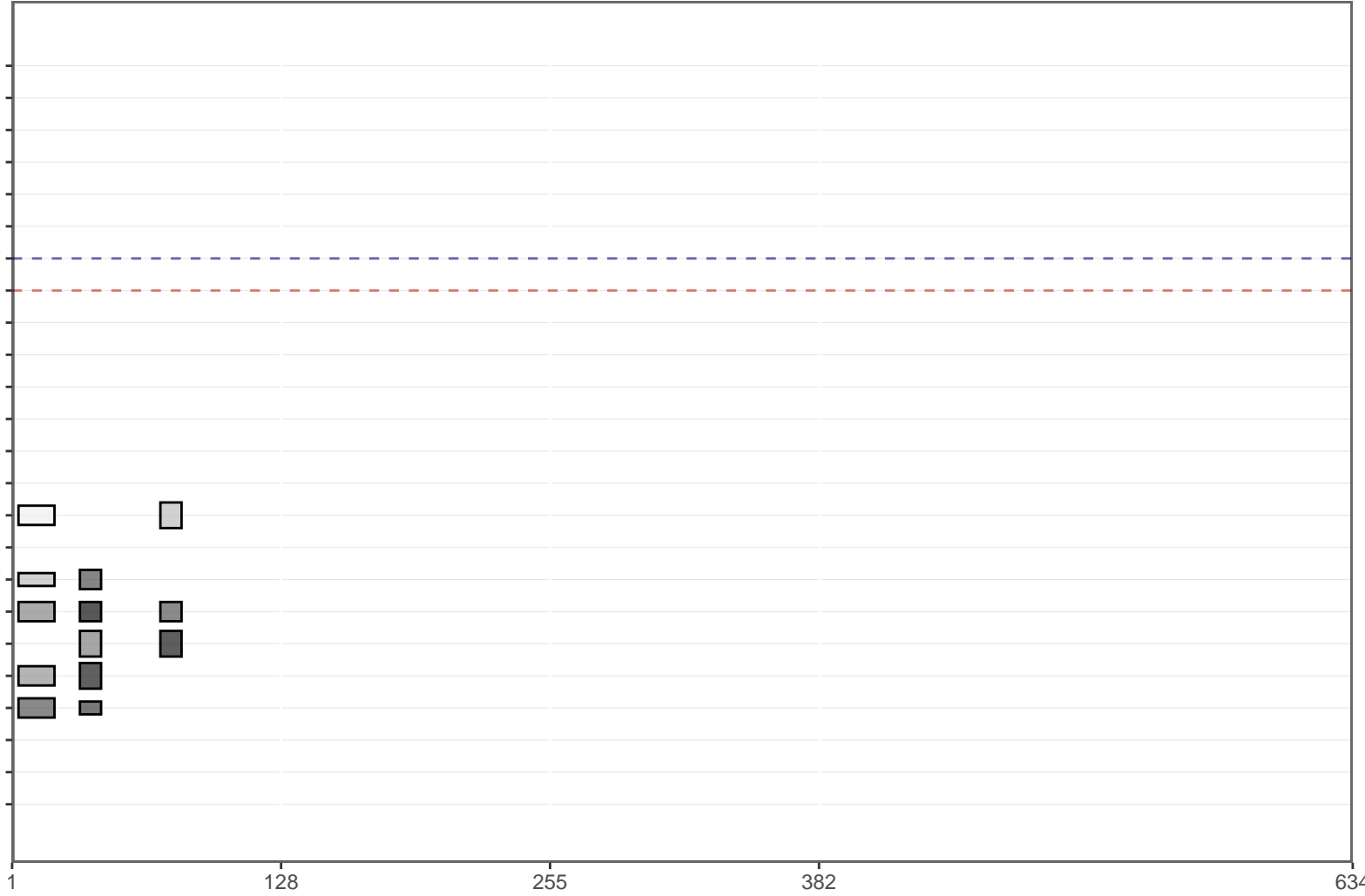
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

PATVYGHSAAPPGGGAPPVTPFSSFPVGGAAATVENSVFFPFGGASAAFTGPTPLPPVSGGNAFANHHGGMNMNLPQGGSLFPVITGPDQLGLSTPAAGGSPGNGQWVNFVATTATGFPETGTAQVGGDVNPNWVLGATSAVASGAAAPVEIKS6GRKGLPEDLFANVHSSIPGAFPDGWHITGPDQHYGVGFAMQYNMMSMTNALPQPKSANPFDFVNEPSSQAGSTFPMSASLGSTLPLNVPPTGLLHTSSLGAPTSYPRAMPQGGSPGVASAVPPGVMQLQVAGSMPQRPFP

NbL10g00910.1 protein_BUNDLE_SHEATH_DEFECTIVE_2_chloroplastic-like [MW = 14.02 kDa]

No. of times detected



log(intensity)



Values from



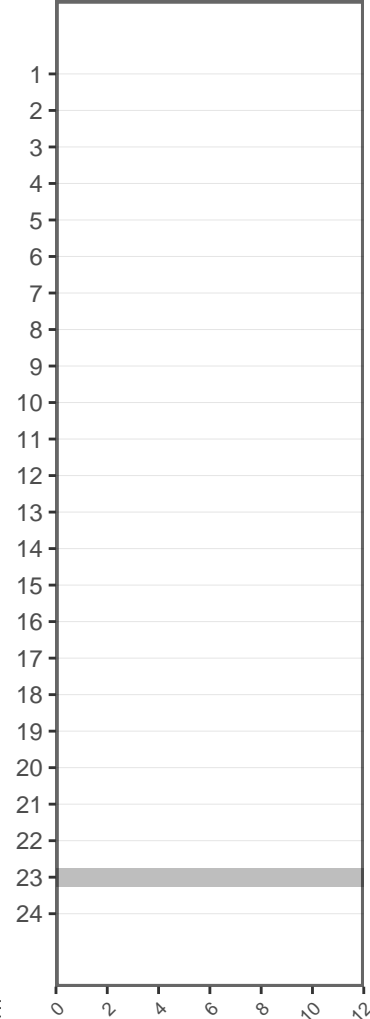
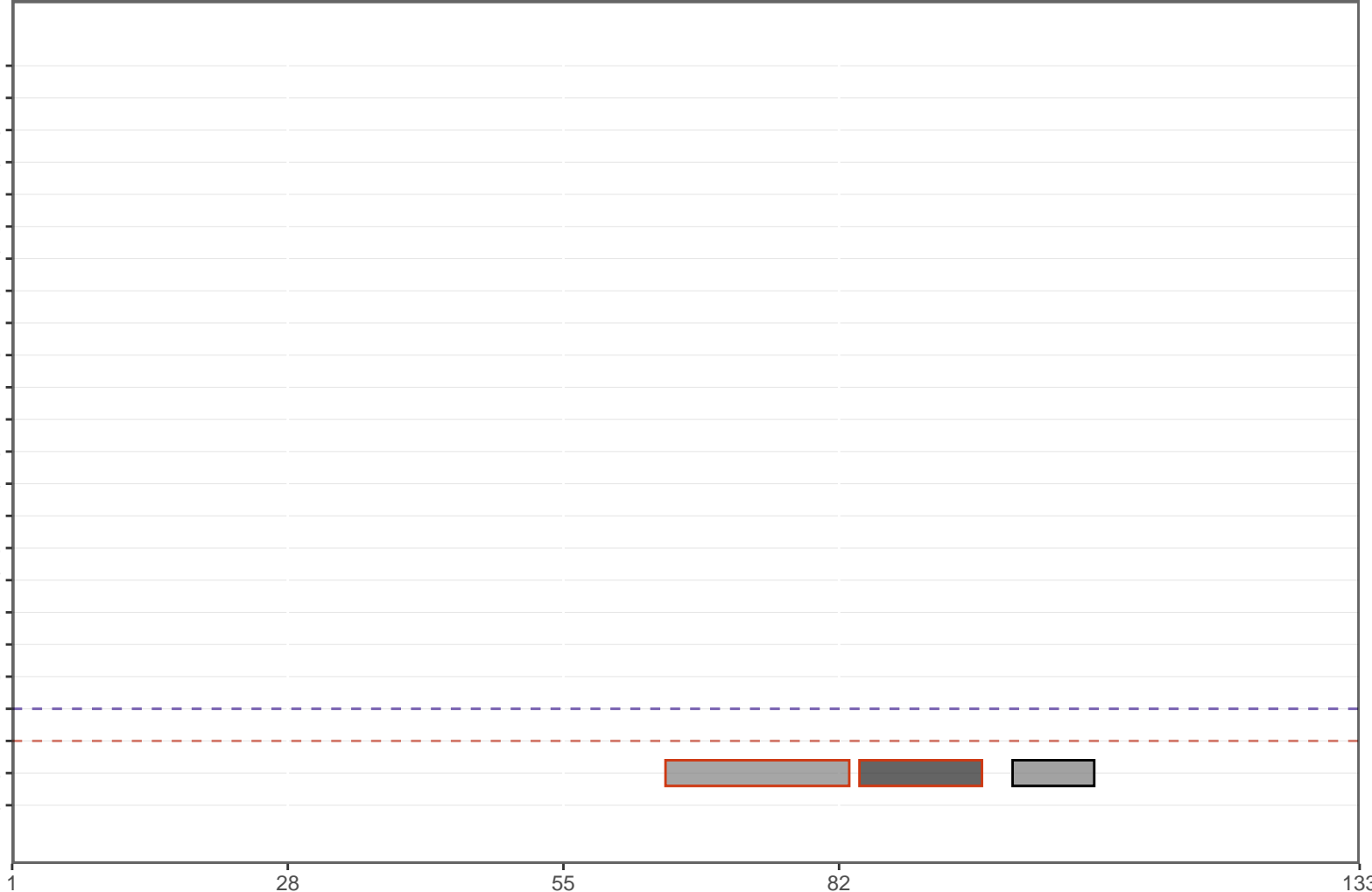
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

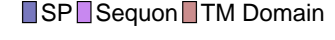
Protein length



Pfam domains



Pfam Description



Protein sequence:

SSDKDTKYSISVCGNEDGNGAVSGSGKGTGVNSVDHFNGRFKAGLGLWLGRGKIDMLGGDNGSAGFLGGFMSTFDE

NbL10g00880.1 oxygenase_1_chloroplastic-like_(LOC107792958)_mRNA_HQ690822.1_Nicotiana_tabacum_heme_oxygenase_1 [MW = 32.08 kDa]

No. of times detected
 1 2 3 4

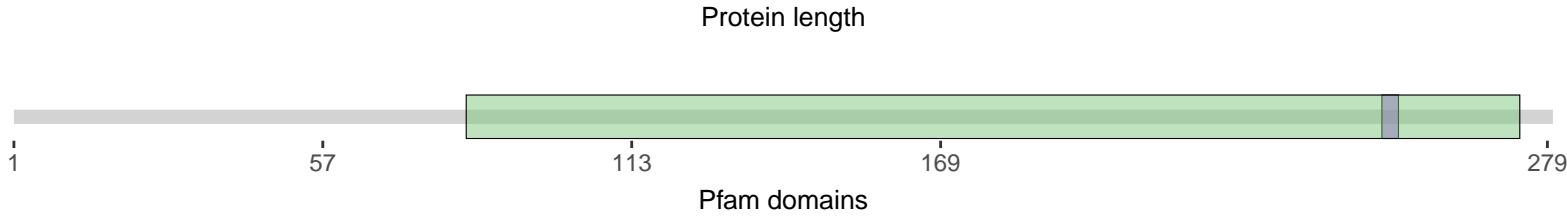
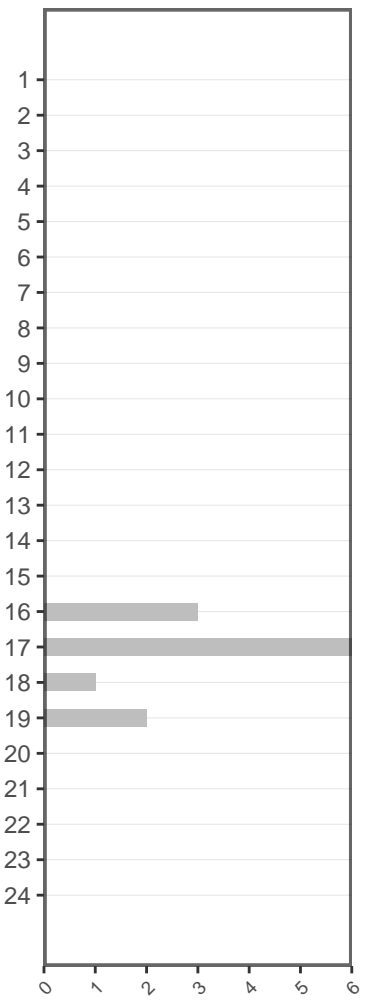
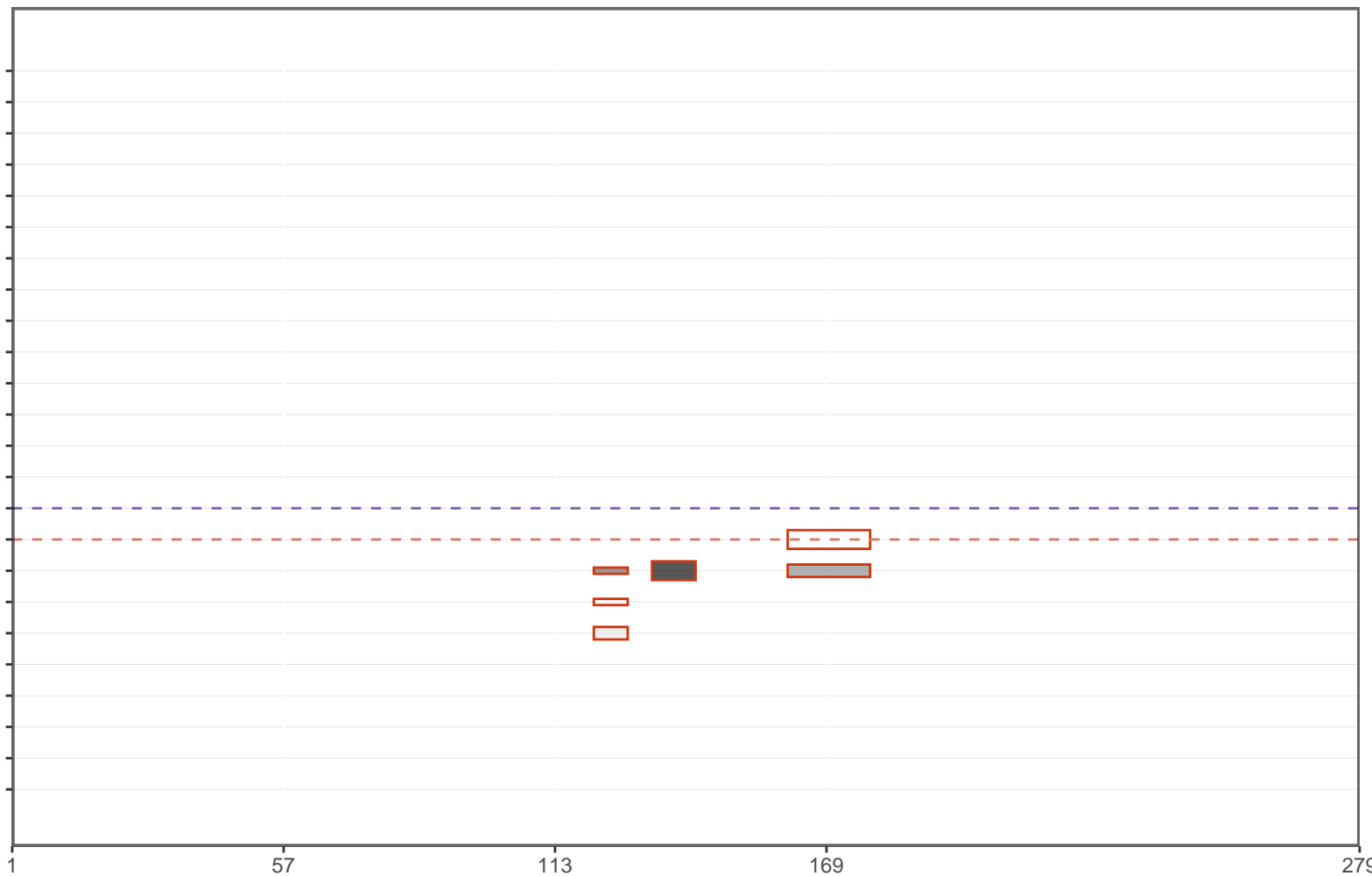
log(intensity)
 3.8 5.0

Values from
 Unique peptides
 Non-unique peptides

MW indication
 Predicted fully N-glycosylated MW
 Predicted non-glycosylated MW

Molecular weight
 180
 133
 100
 79
 62
 55
 48
 39
 30
 24
 19
 14
 0

Gel Slice
 1
 2
 3
 4
 5
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 7
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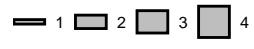


Pfam Description
 SP Sequon TM Domain PF01126 Heme oxygenase

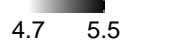
Protein sequence:
 LKIMKAPFPEYAFRNIGLERSEGLAKDLEWFRGGYAIPEPSSPLNVAHYAEELSEKDPQAFVCHFYNTYFAHSAGGRMGKRAEKILNKLELFYKWDGDLGQLLQNVREKLNKVAENVTREEKNHGLETEKSPKFKFSQELRLHS

NbL10g00790.1 repetitive_proline-rich_cell_wall_protein_1-like [MW - SP = 25.88 kDa]

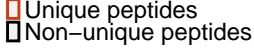
No. of times detected



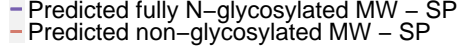
log(intensity)



Values from



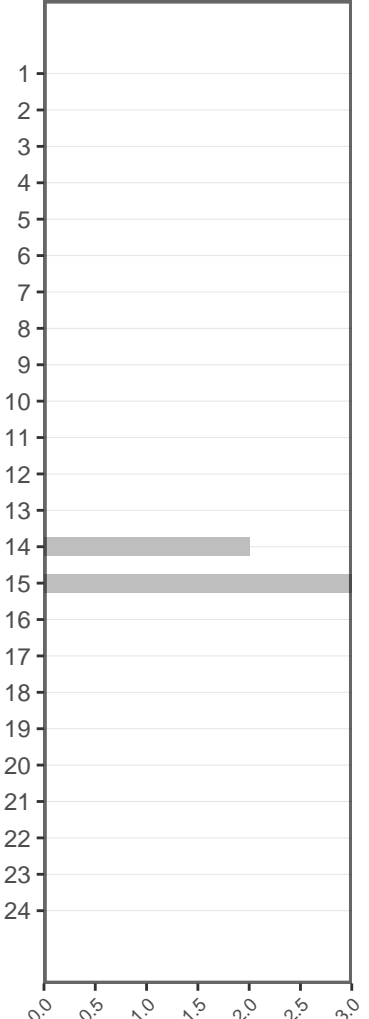
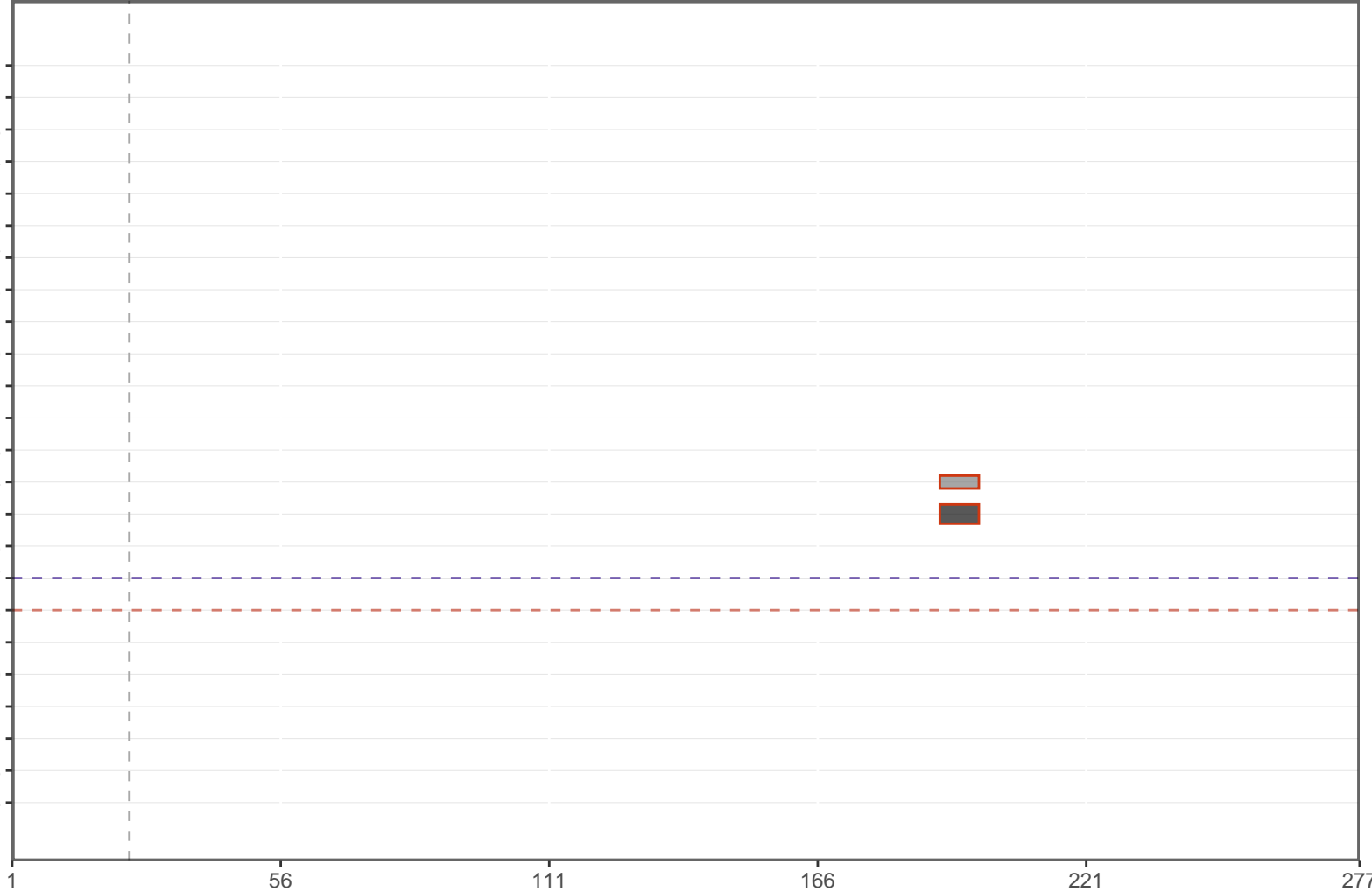
MW indication



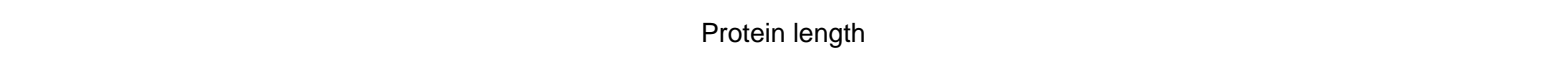
Molecular weight



Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

PPVKKPPGIPPVTVPPVAKPPNGLPPVVKPRNLPKPPGIPPPVITPPVTPSPKPKPCSPFPPTTKATGPDITLKLGAQVDLLGGVHVGGDPVAVNECGPILHGLVELEAAVGLGTTLKVLLNKKFVPLALQLLVTDGKTPPPGVTGEL

NbL10g00780.1 zinc_finger_BED_domain-containing_protein_DAYSLEEPER-like [MW = 89.66 kDa]

No. of times detected



log(intensity)



Values from



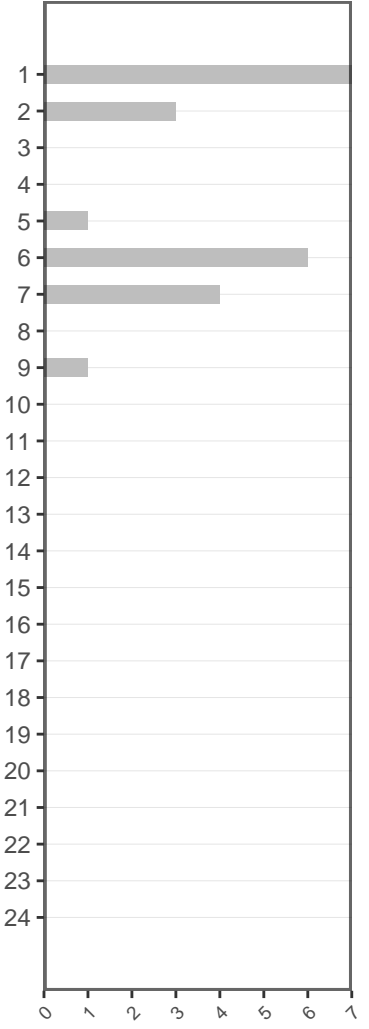
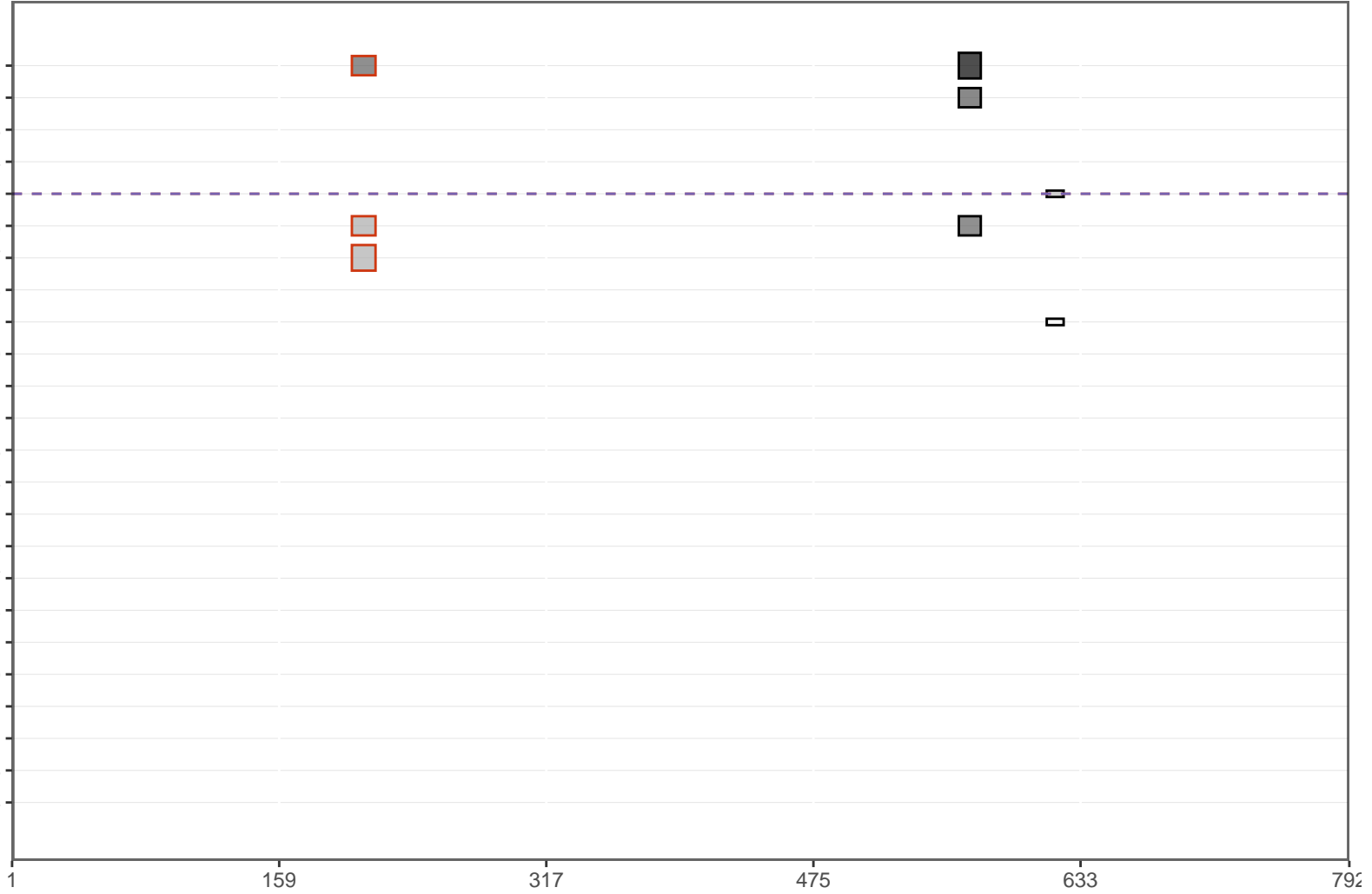
MW indication



Molecular weight



Gel Slice



Protein length

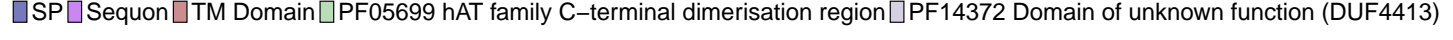


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

FSVITNIPGDAVQNLKALLSKNPLVLLGGLLVGNLARTLSSIALDAPHFLLHGTVMKVRDEVKYKTSSEHEENFMELKQGLQVPTTKRLALDDRTQWNTYEMLLAASELKEVFGSLDTSDDPKYKAPSEVEDWKGVEILGRYLKILFDTNLLTAPTPTNTFFHEAWKIQLELARAASEDPSISLTKTMQGEKFDKYYKTKGGLMLAIWVMDPREKMKLVEFSFTKYGEEAATYVWVEEGHLEFLVYVLPALPTFYAEAEANGDQKGENAQDNGASSNGAGLTFD

NbL10g00730.1 methyl-CpG-binding_domain-containing_protein_11-like [MW = 35.9 kDa]

No. of times detected



log(intensity)



Values from



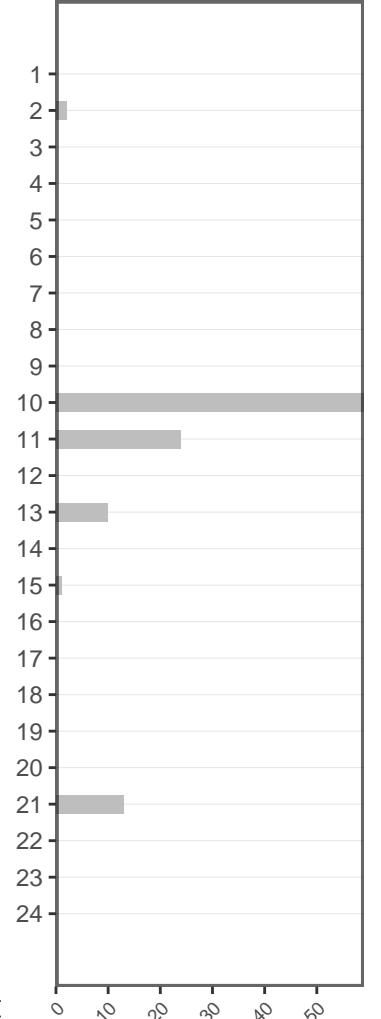
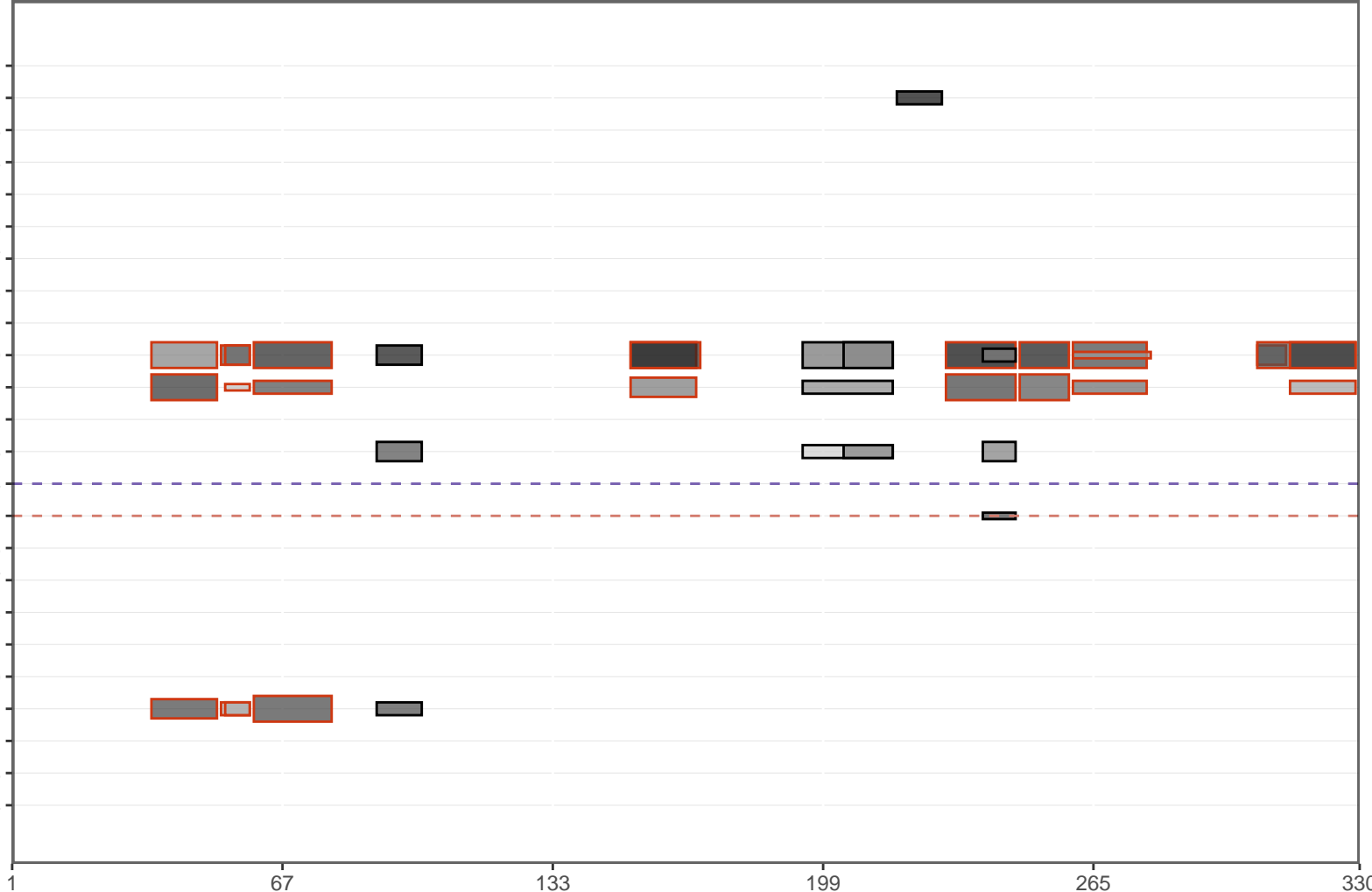
MW indication



Molecular weight



Gel Slice



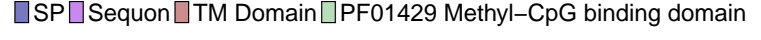
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKNDDETDGDSGVKVKKEAEATEKIVSKKDKKBSSEIDGKKDESQNDAGKVEDAFSEETQVKEKIVEMADNVGHSHKQVEEAAGDKVADDLKARTNNEEKQVQVEEKVENMPTFETVTLDSIAAEKKKQAEQEGKDEQKTSAAITGTFEDQHKLMNSEIKVKEGEVTEGNSGNTNEAKP

NbL10g00550.1 shikimate_O-hydroxycinnamoyltransferase-like [MW = 48.95 kDa]

No. of times detected



log(intensity)



Values from



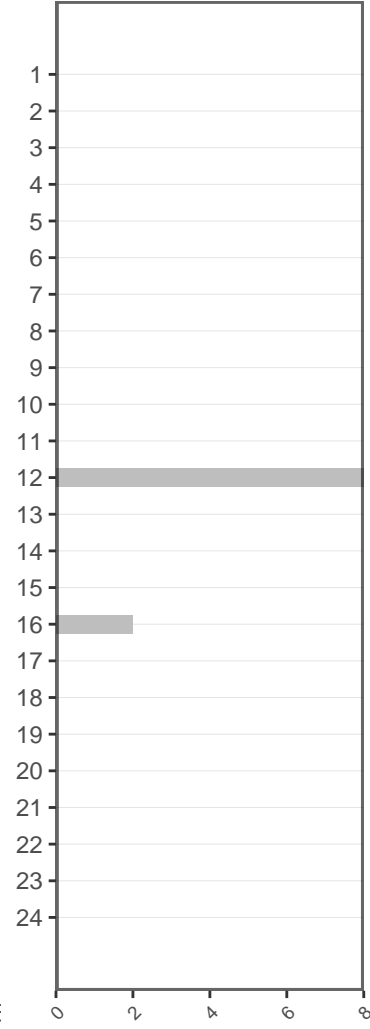
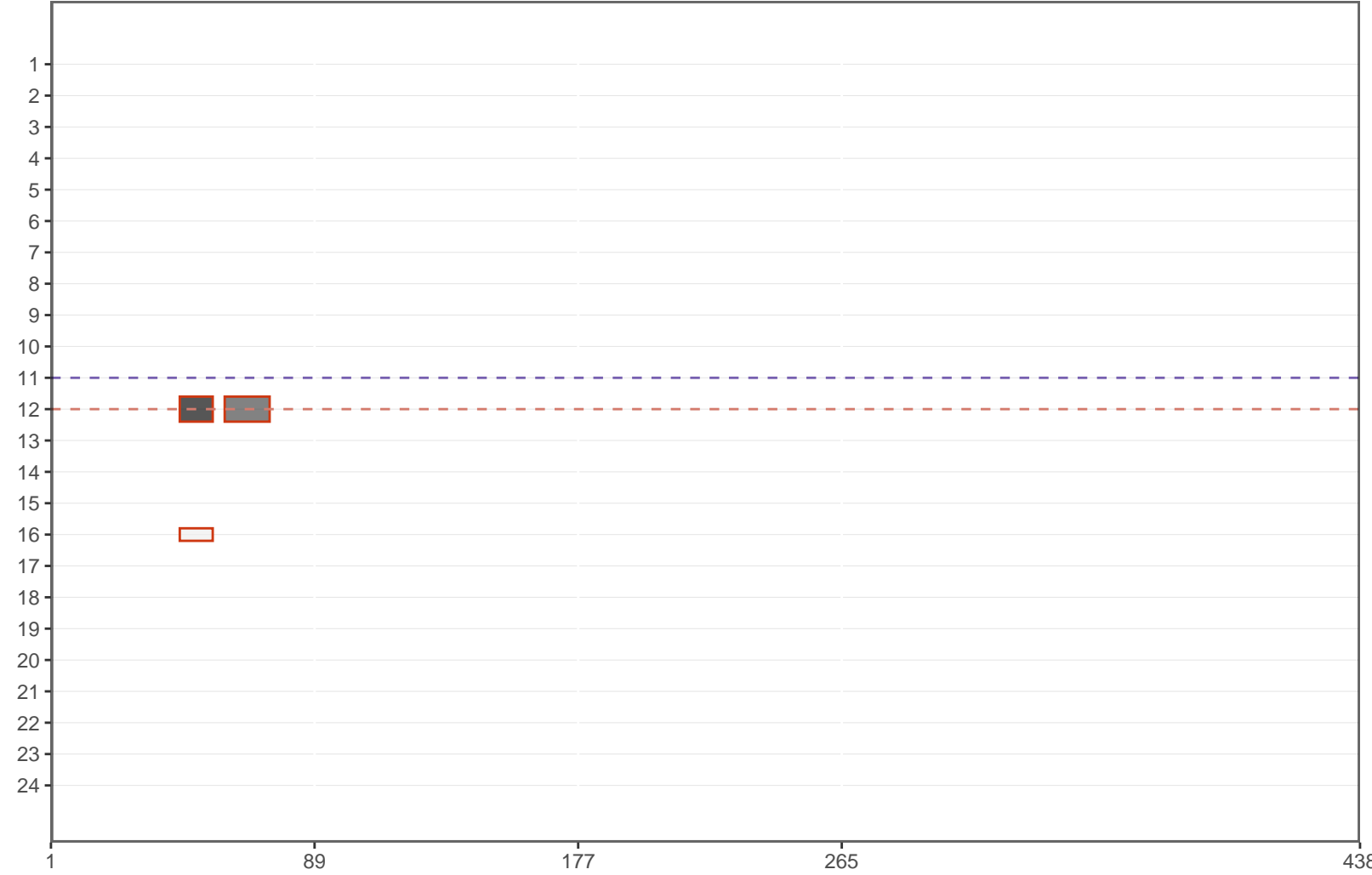
MW indication



Molecular weight

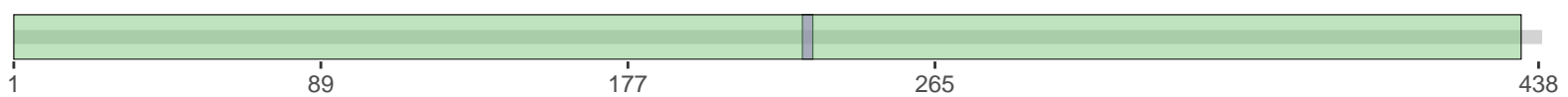


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEYHPPTLKLKLSGHVYDQVNGTKSSTAMFKITSDQLTKLTKSEHEGSTEYELAAHWGCTCKARGLDDQLTKLHWATDGRGRFPPLPPGLGNVFTATPIAKSGEILSEPLMNTAGRIHSEALARMDDDEYLRSADVLELGTDLGKLRGPTVFASPNLNINWTRLPVHDSDFGNGKPHMGPCALVEGTYYLPSPSNKNLRLAVGLDADHIFLFEKYLVDI

NbL10g00540.1 nucleoid-associated_protein_At4g30620_chloroplastic-like [MW = 20.01 kDa]

No. of times detected



log(intensity)



Values from



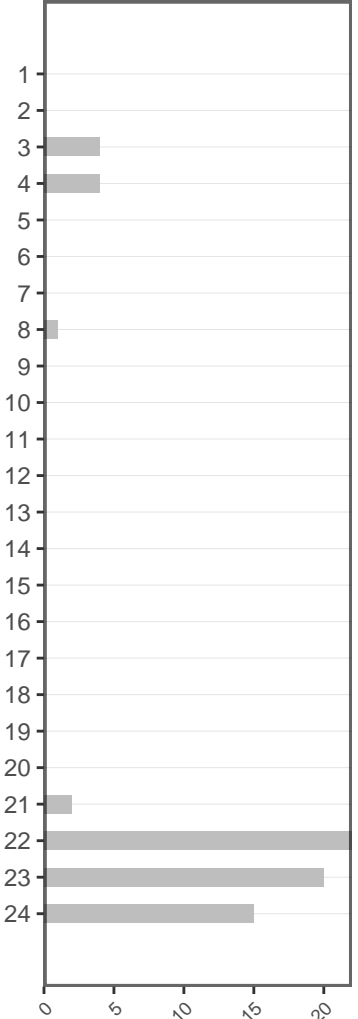
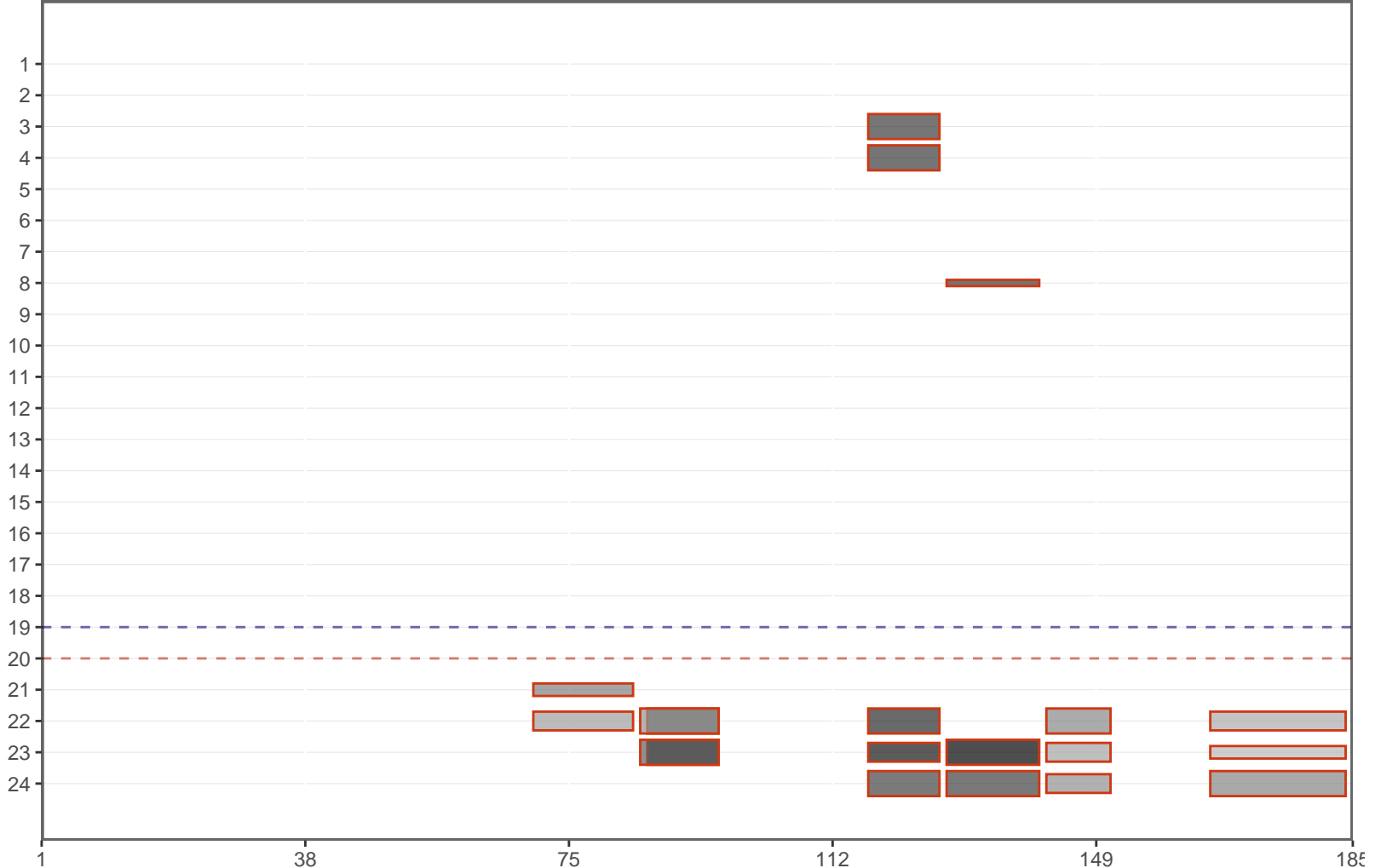
MW indication



Molecular weight



Gel Slice



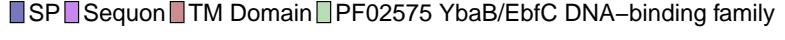
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILYETVYKAGNIVQVEAVRIVQKELALAEFDGYGEGELIKVTLGNGQPIRTEITETAAAMELGPENLISLLITEAYKDAHGKIVLAMKERMSDLAQSIGMPAGLGGFKQ*

NbL10g00510.1 leucine_aminopeptidase_2_chloroplastic [MW = 60.69 kDa]

No. of times detected



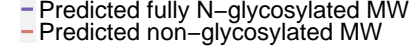
log(intensity)



Values from



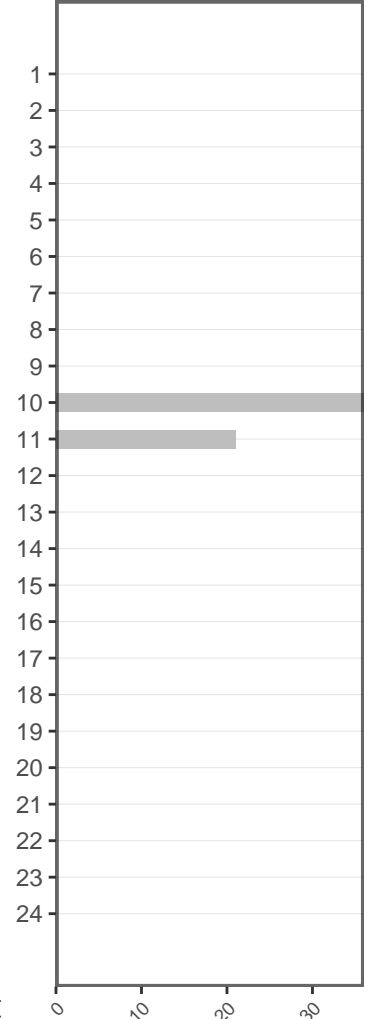
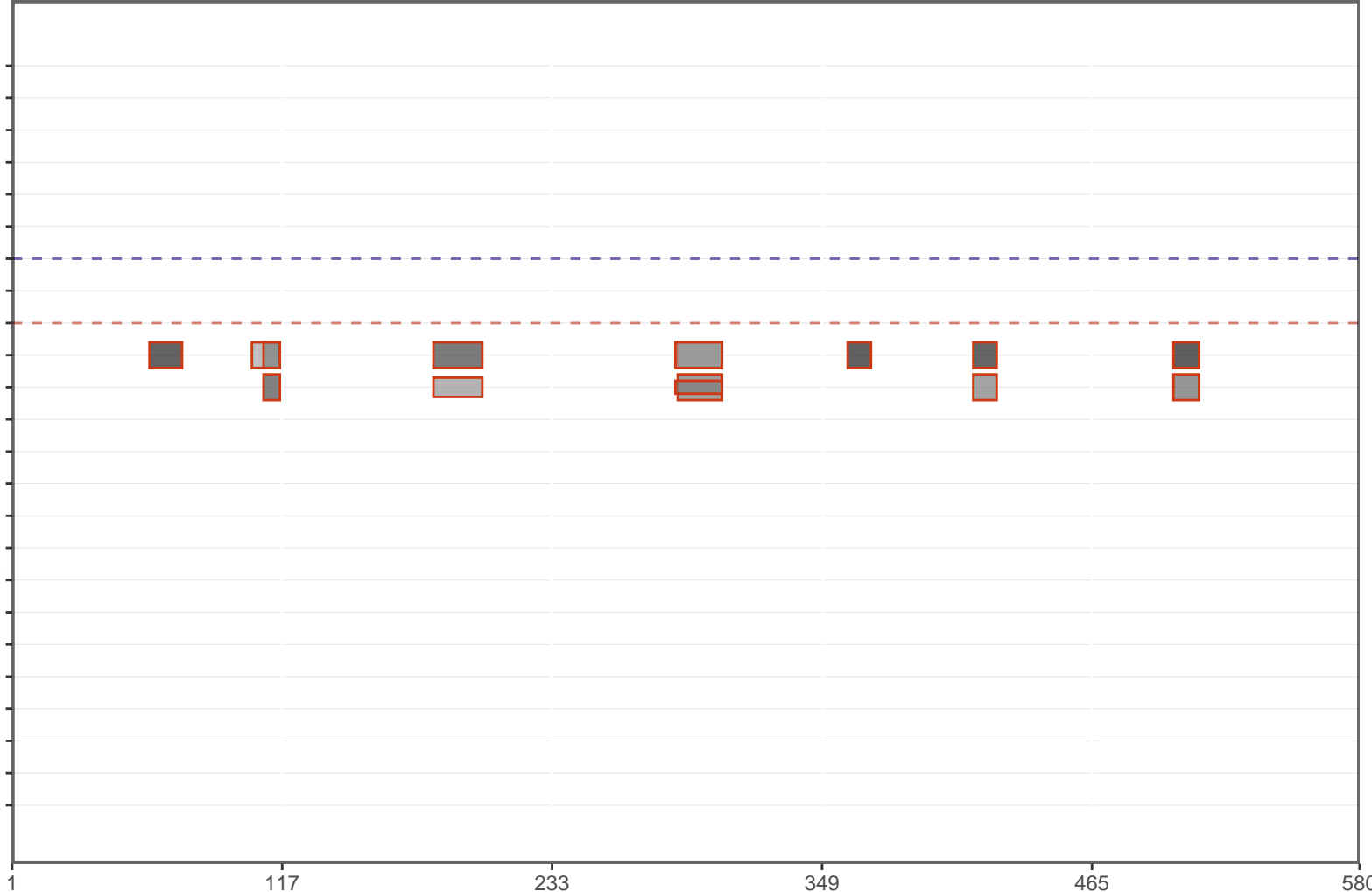
MW indication



Molecular weight

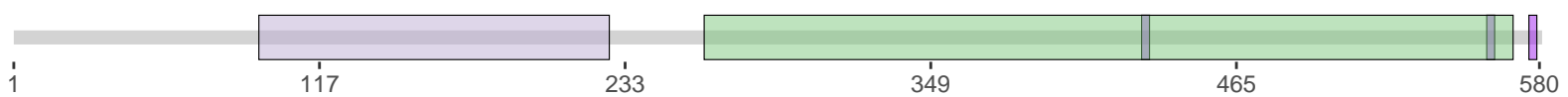


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00883 Cytosol aminopeptidase family, catalytic domain
- PF02789 Cytosol aminopeptidase family, N-terminal domain

Protein sequence:

EEAAKASTYSDVLSANLNVEGCKELMGGYVLAVGEASNPPIHILGYKPTGGEEKKLLALVKGKLTDFDGGYNYKTPGGGSELMKFDMGGAVALGAALKGQPKPAGVEVHFVAAGENMISGTMKRPDGVYTABNGKTEIENVNTDAEGRLLADALVACNGGVEKIVDLATLTGACVVALGPGIAGVFTPSDPLAKEVAWAASEVSGEKLRWRMPLEESYWDTKSGVADMANNTGRRGGAAVAALFLKGFVDEKVGQWMMHDLAGPVAWNBKKNKATFGVSTLVEW

NbL10g00500.1 probable_GMP_synthase_[glutamine-hydrolyzing] [MW = 41.05 kDa]

No. of times detected



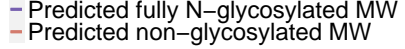
log(intensity)



Values from



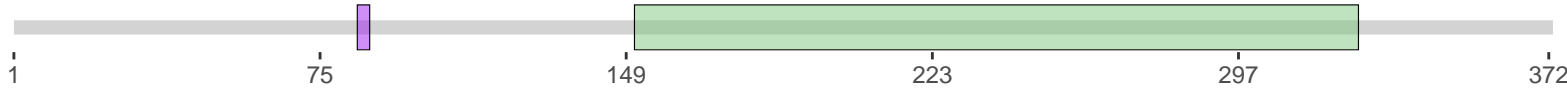
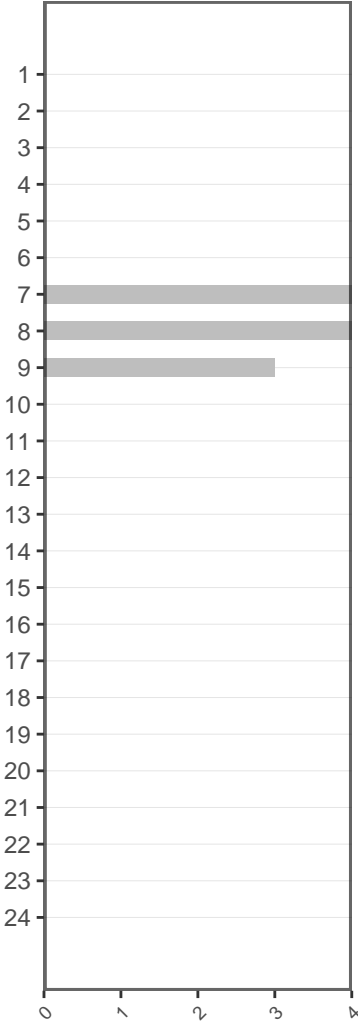
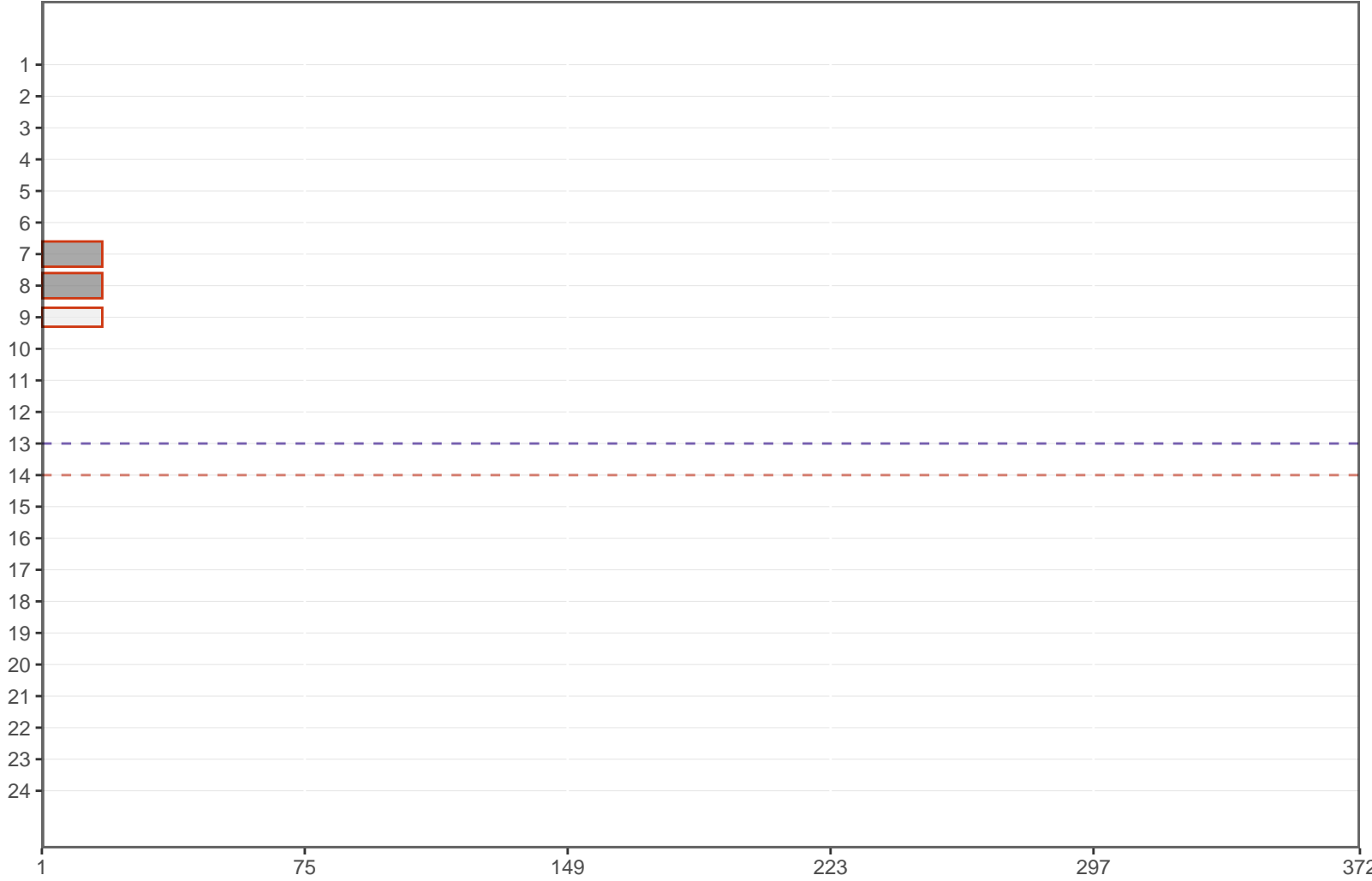
MW indication



Molecular weight

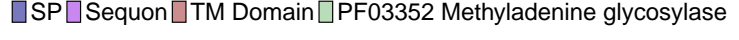


Gel Slice



Pfam domains

Pfam Description



Protein sequence:

PVHDDKLLFELLYLOGALAELEWPSILKRNIFREVFADFDPWVAKLEKNIKLAIFGSGTAGSLLSEKLRAIENARQMSKVIDEFGSFDKVIWISFVNNKPKVSGFRYPGRVPPVKTAKADLISKDLRRGRFRGVGPTVYYVFMQVAGITNDHLISGFRFRHGDVGEAEAKENKSNKDETEATKVDKDEAEAEICR6IDDL6FSSE

NbL10g00490.1 eukaryotic_translation_initiation_factor_5A-1/2 [MW = 17.51 kDa]

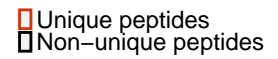
No. of times detected



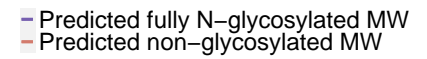
log(intensity)



Values from



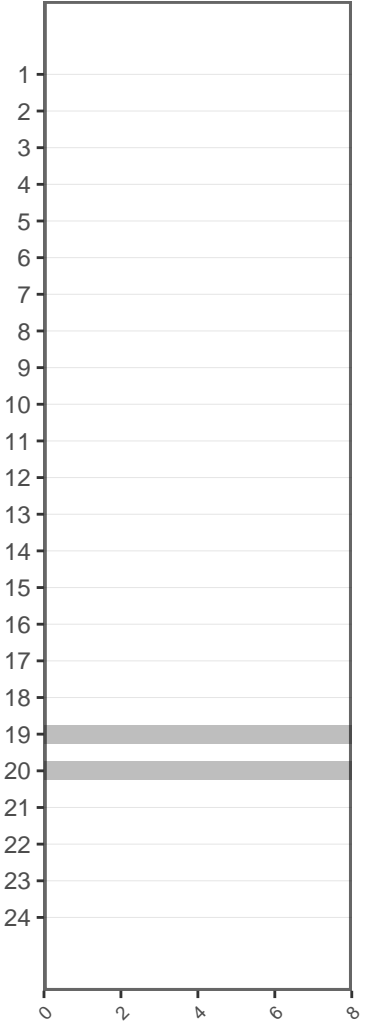
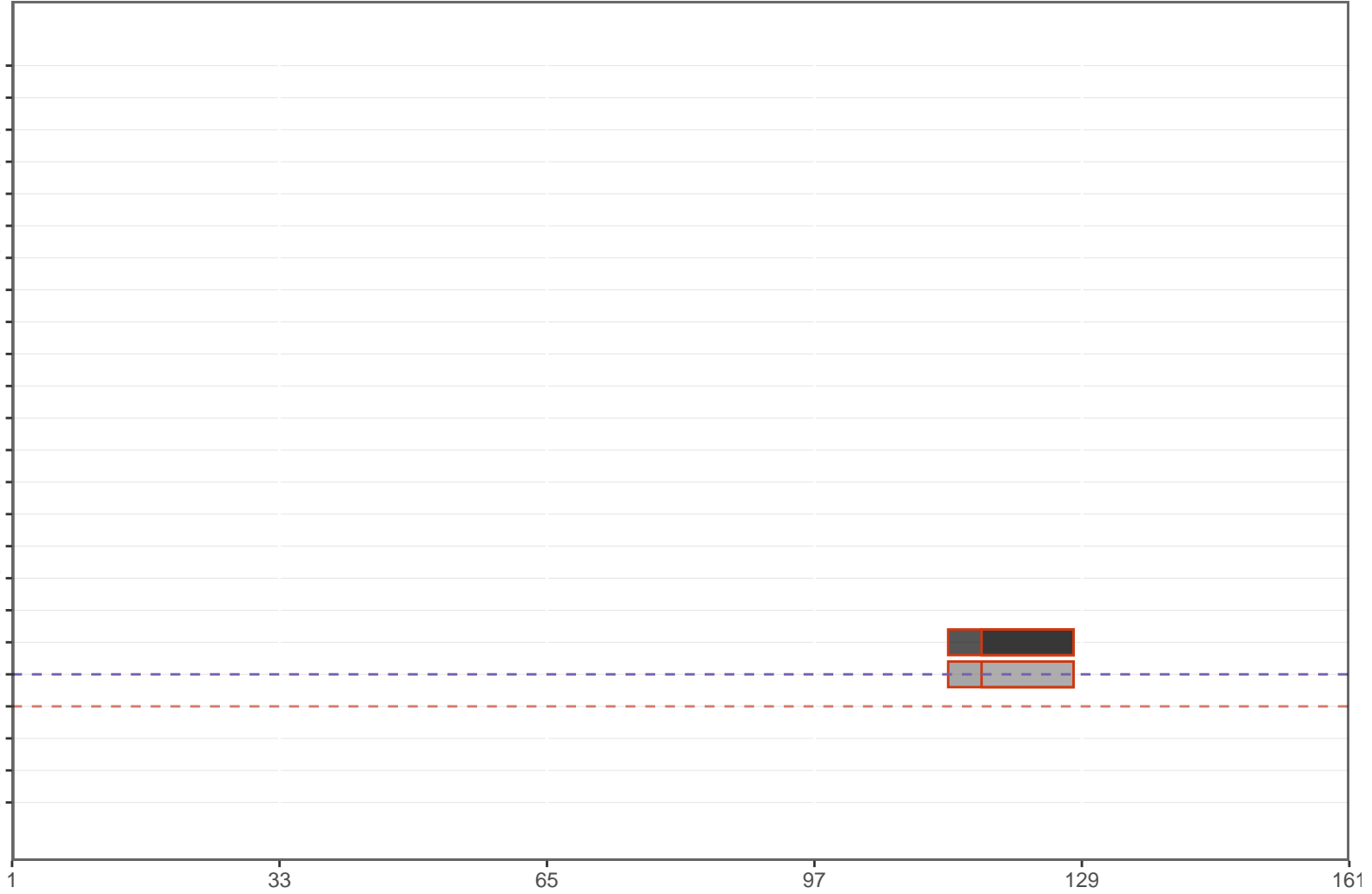
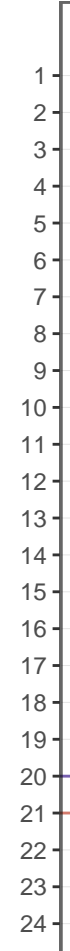
MW indication



Molecular weight



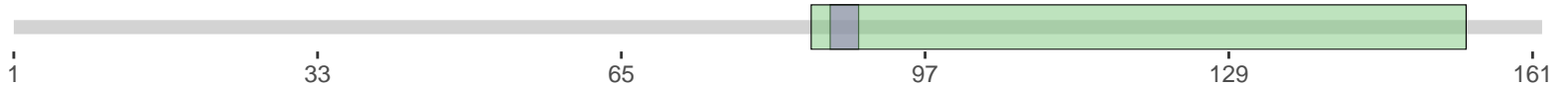
Gel Slice



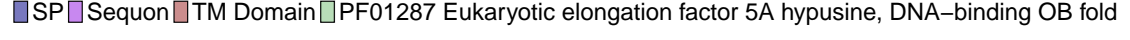
Protein length



Pfam domains



Pfam Description



Protein sequence:

IGKKLEIDVPSSTINGDVFHVNRTDYGQIDISEDGFVSLTFENGNTKDDLRLLPTDENLLNDVKGGFEEGKDLVLEVMAMGEEGIAWKGDTGKN

NbL10g00420.1 uncharacterized_LOC109225199 [MW = 11.96 kDa]

No. of times detected



log(intensity)



Values from



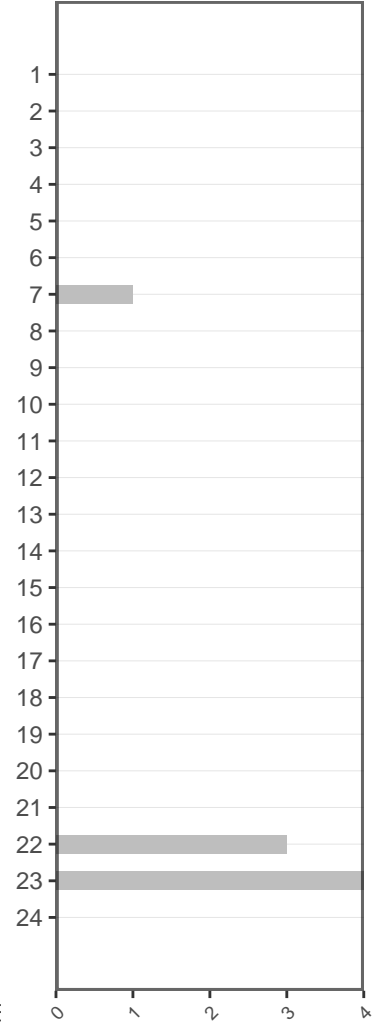
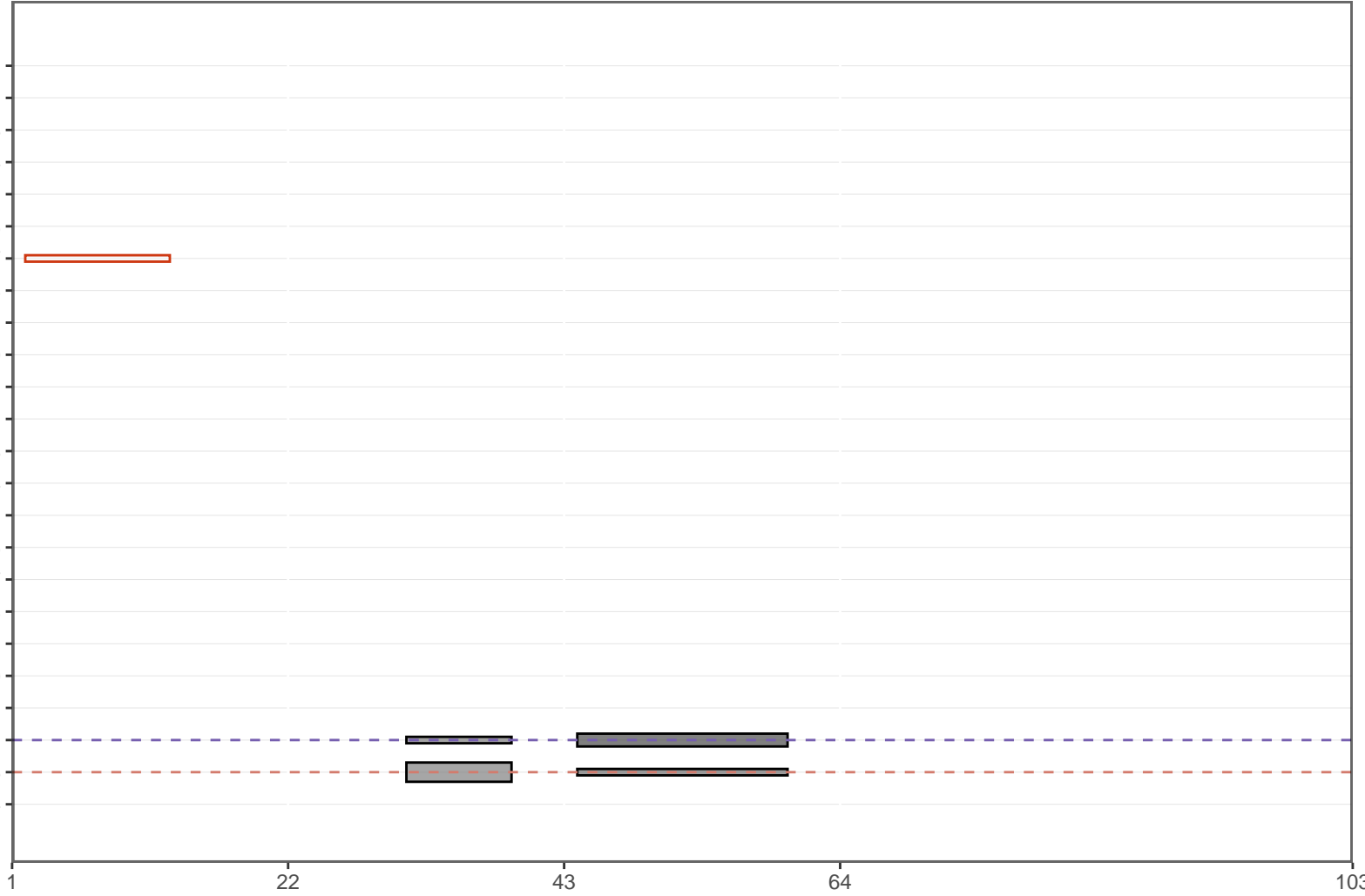
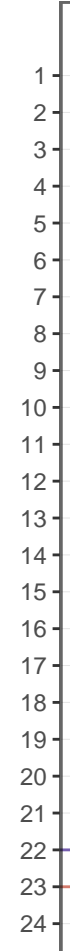
MW indication



Molecular weight



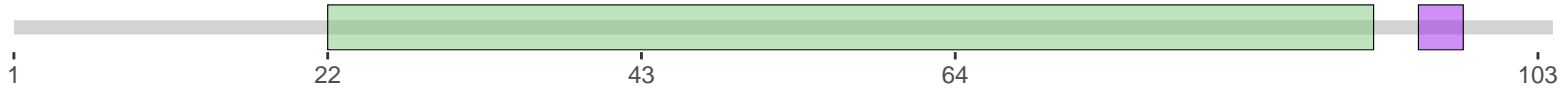
Gel Slice



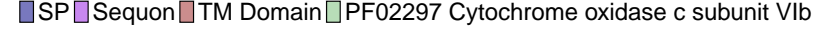
Protein length



Pfam domains



Pfam Description



Protein sequence:

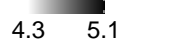
ISSSKPTEIATVGLLYPVEGKTRREYVKGQRPTWVHFDKRGYCAKMRVQRLLDNDSDRREQL*

NbL09g23590.1 uncharacterized_LOC107760951 [MW = 17.44 kDa]

No. of times detected



log(intensity)



Values from



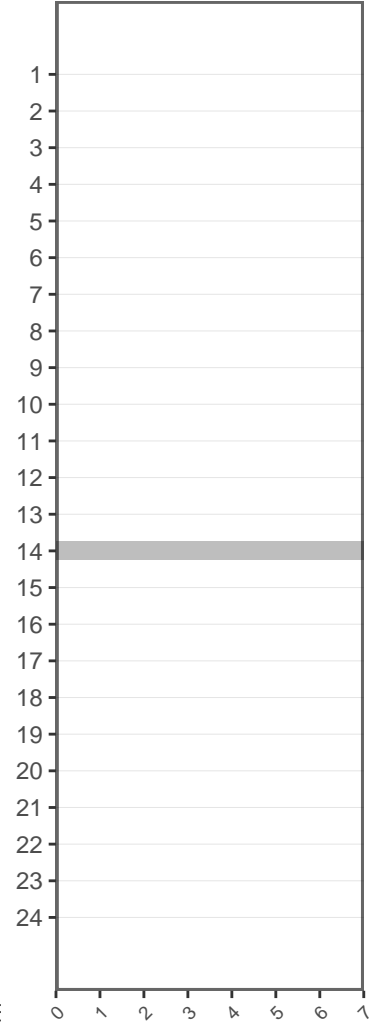
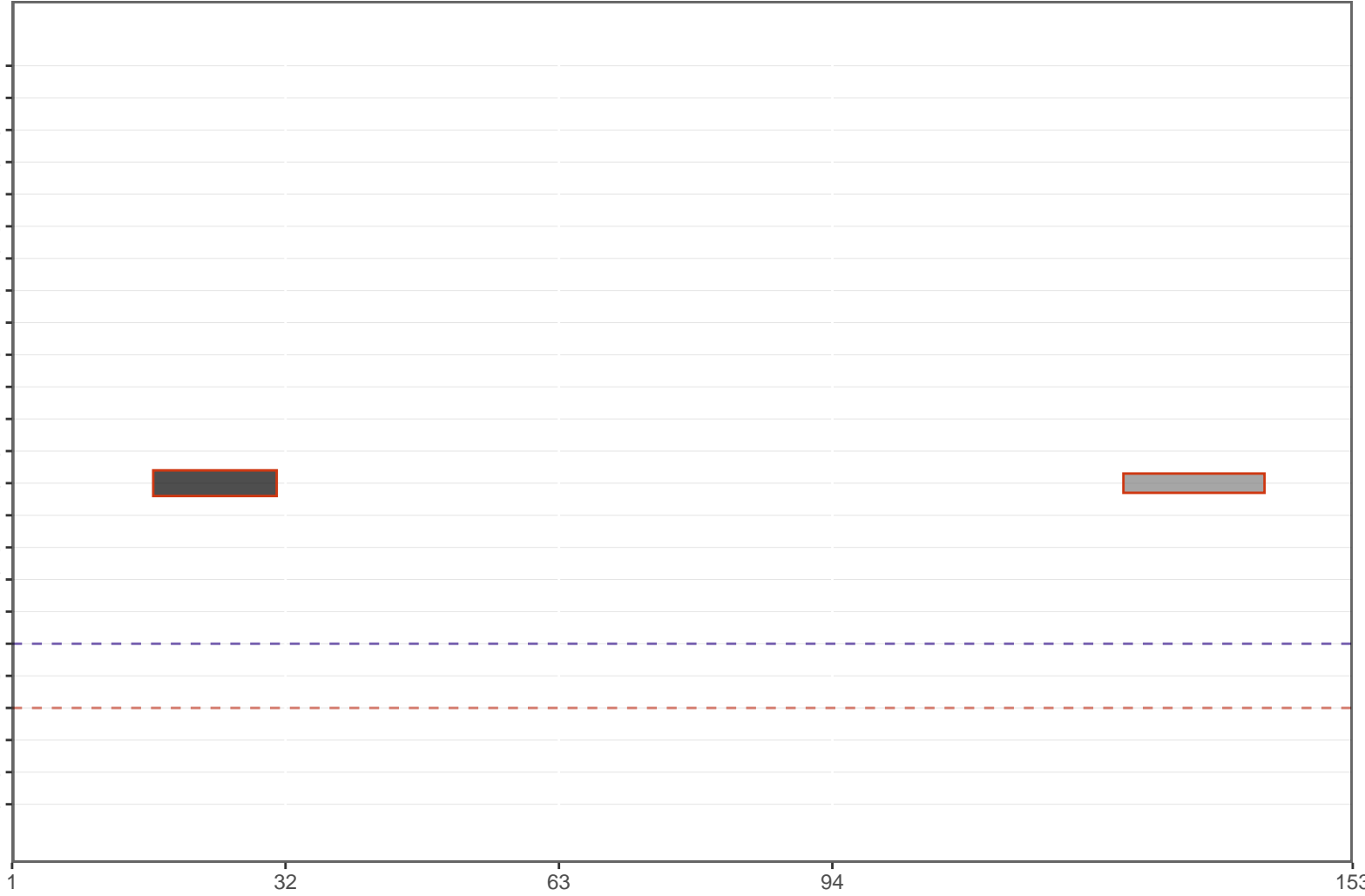
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PTLAQDDDAFDFMVKGRLLFTVGGDEADATRHSDERSIVDDNVEAFAYGSGGGYVAWVENKANPYIHWLEHCLIDPREKESRVRHQ

NbL09g23480.1 endochitinase_A [MW - SP = 32.73 kDa]

No. of times detected



log(intensity)



Values from



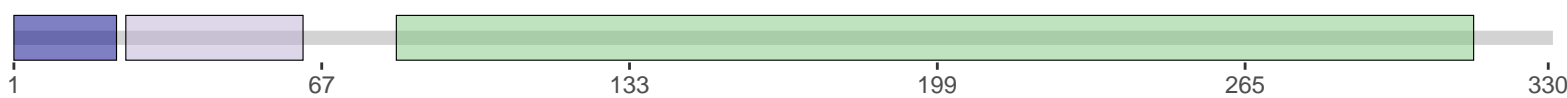
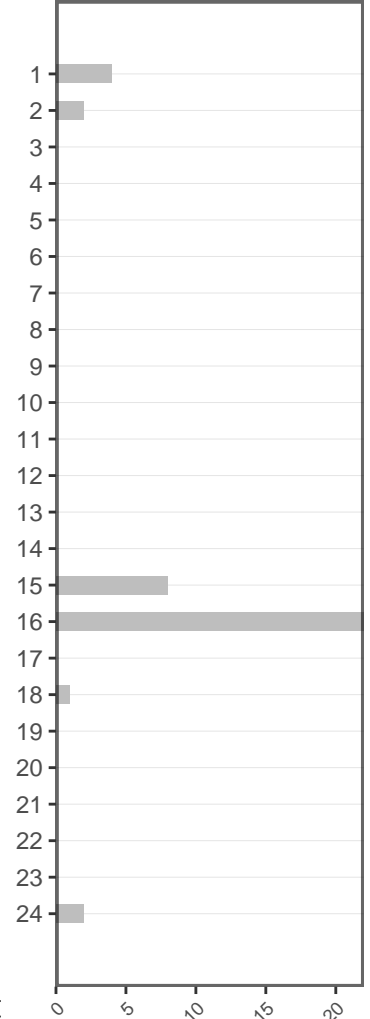
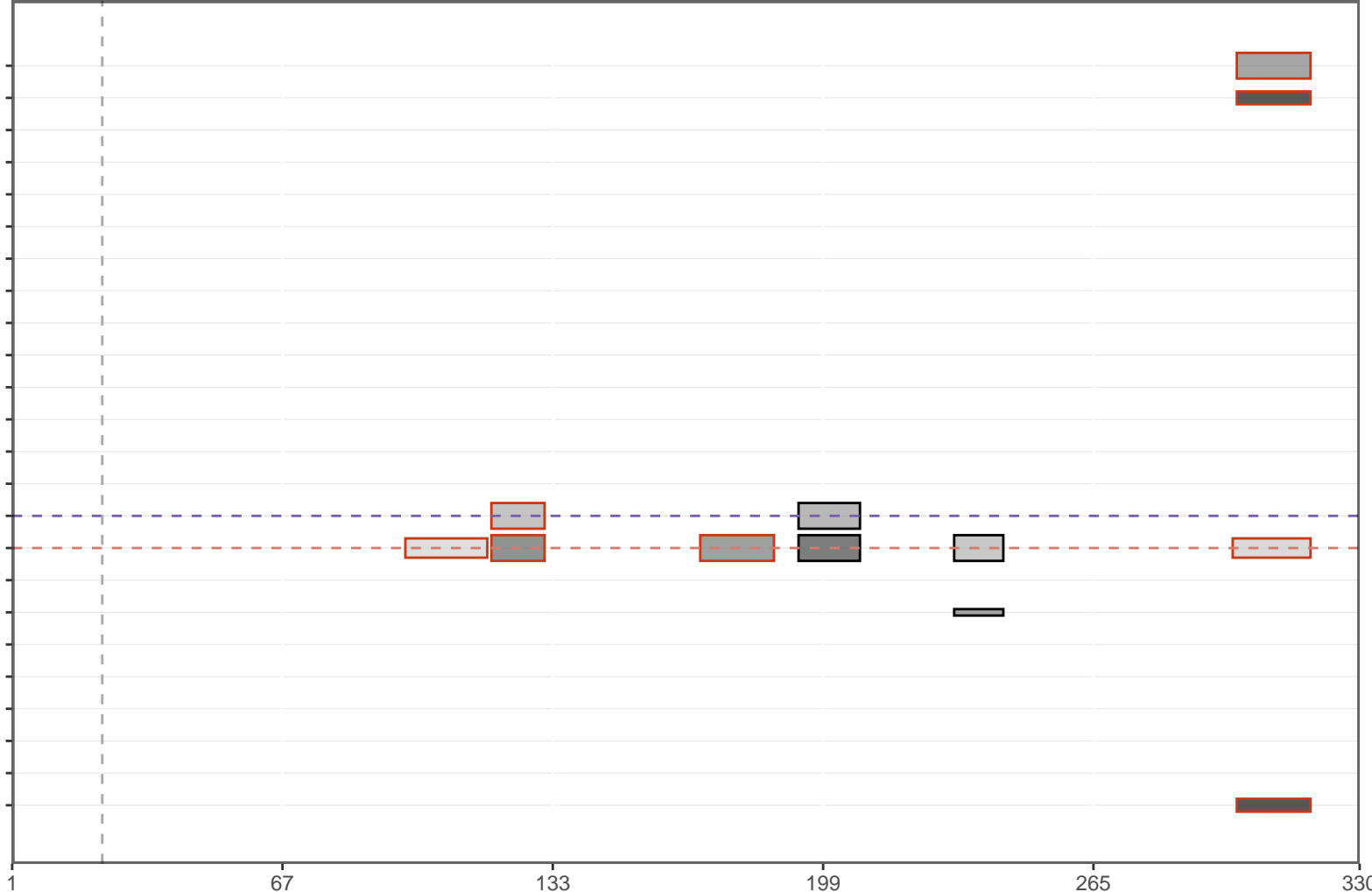
MW indication



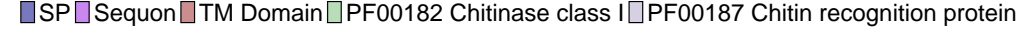
Molecular weight



Gel Slice



Pfam Description

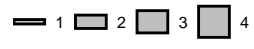


Protein sequence:

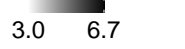
TAPOGPYAWGYCVLRERSSPGDYCTPSSGQWPCAPGRKYFGRGPIQSHNYNYGRCRAIGVDLLNLPDLVATDPVIFKALWFWMTPOGPKPSCHVIGRWGPSADRAANRLPGFVNTNIGLEGGHGTDERVQDRVGFYRRYSGLGVSPGDLDDGNGRFRFGNLLVDTM

NbL09g23370.1 V-type_proton_ATPase_subunit_B2 [MW = 61.05 kDa]

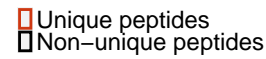
No. of times detected



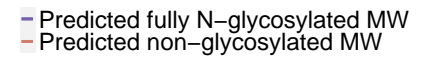
log(intensity)



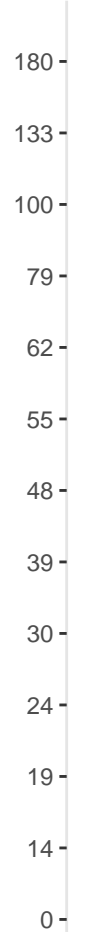
Values from



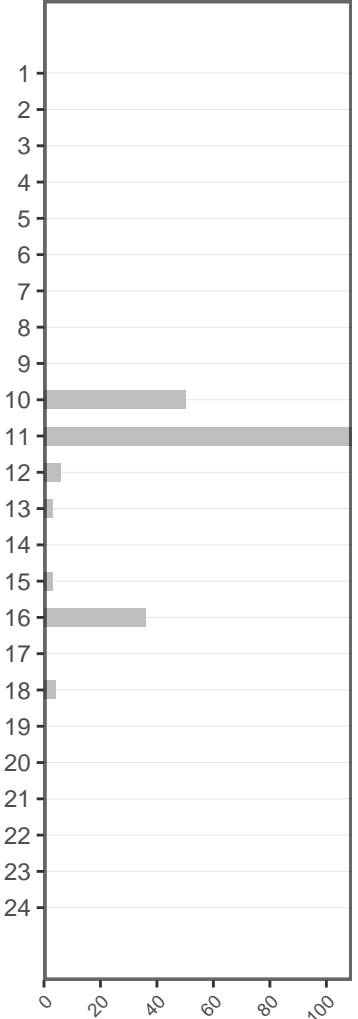
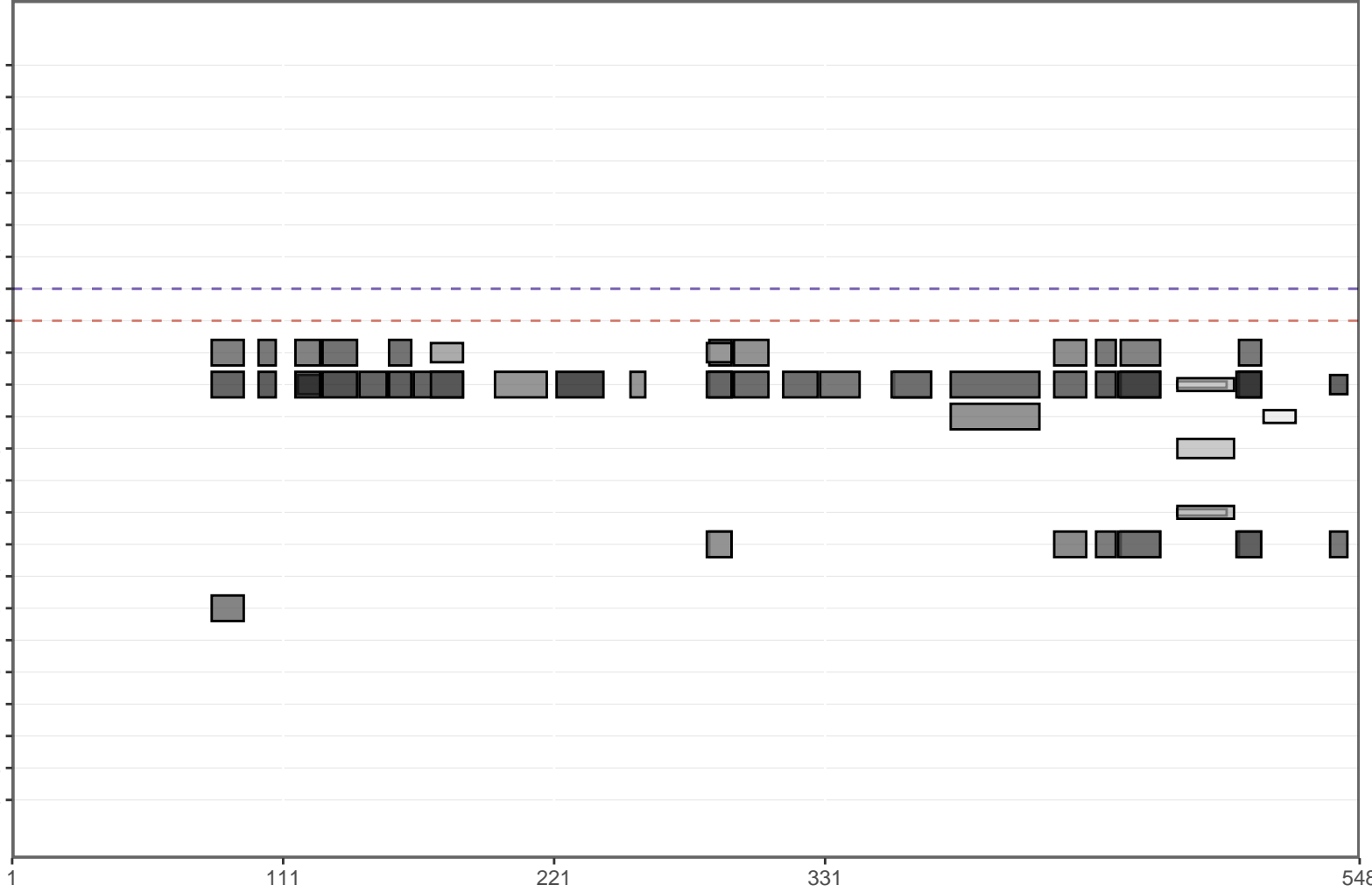
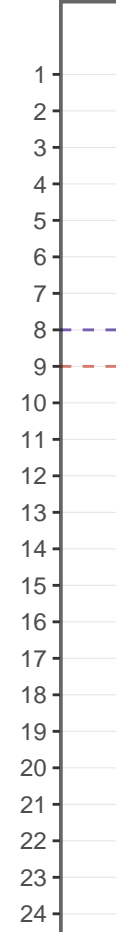
MW indication



Molecular weight

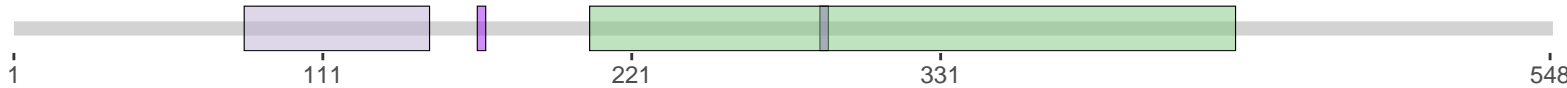


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00006 ATP synthase alpha/beta family, nucleotide-binding domain
- PF02874 ATP synthase alpha/beta family, beta-barrel domain

Protein sequence:

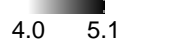
SEDDNFALVFAAMGVNMETAGFFKRDFFEENGSMERVTLFLNLANDPTERRITPRALTAETLAVLVEGGKHVLLVLTDMSSYADALREVSAREEVPRGRGYPGVVYLDLATIYERAGRIEGRTOGSITQPLTLPNDNDTHPTPDLTGYTEGGIYDROGLHNRGIYPPNVLPSLSRLMKAISGEGMTRRHDSDVSRNGLVANYAKGDVQAMKAVVGEELSSDELLYLEFLDKFERKFAVGGANDTRNFQSLDLAWTLRIFFPRELLHRIPAKTLGDQVYSRDSAY

NbL09g23340.1 aquaporin_PIP2-7-like [MW = 30.4 kDa]

No. of times detected



log(intensity)



Values from



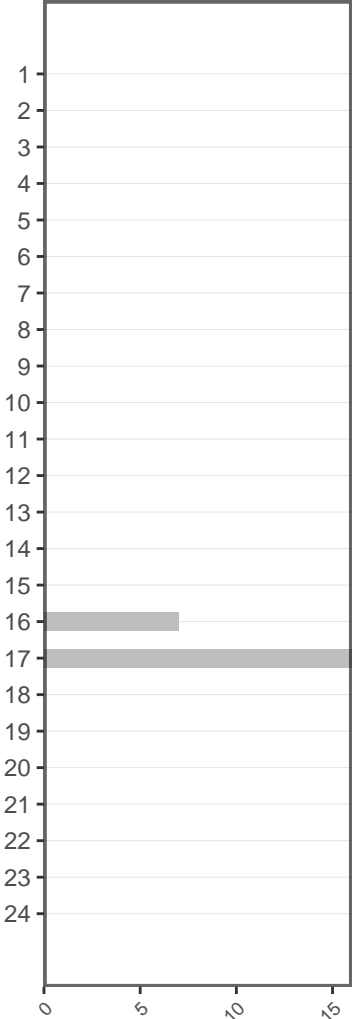
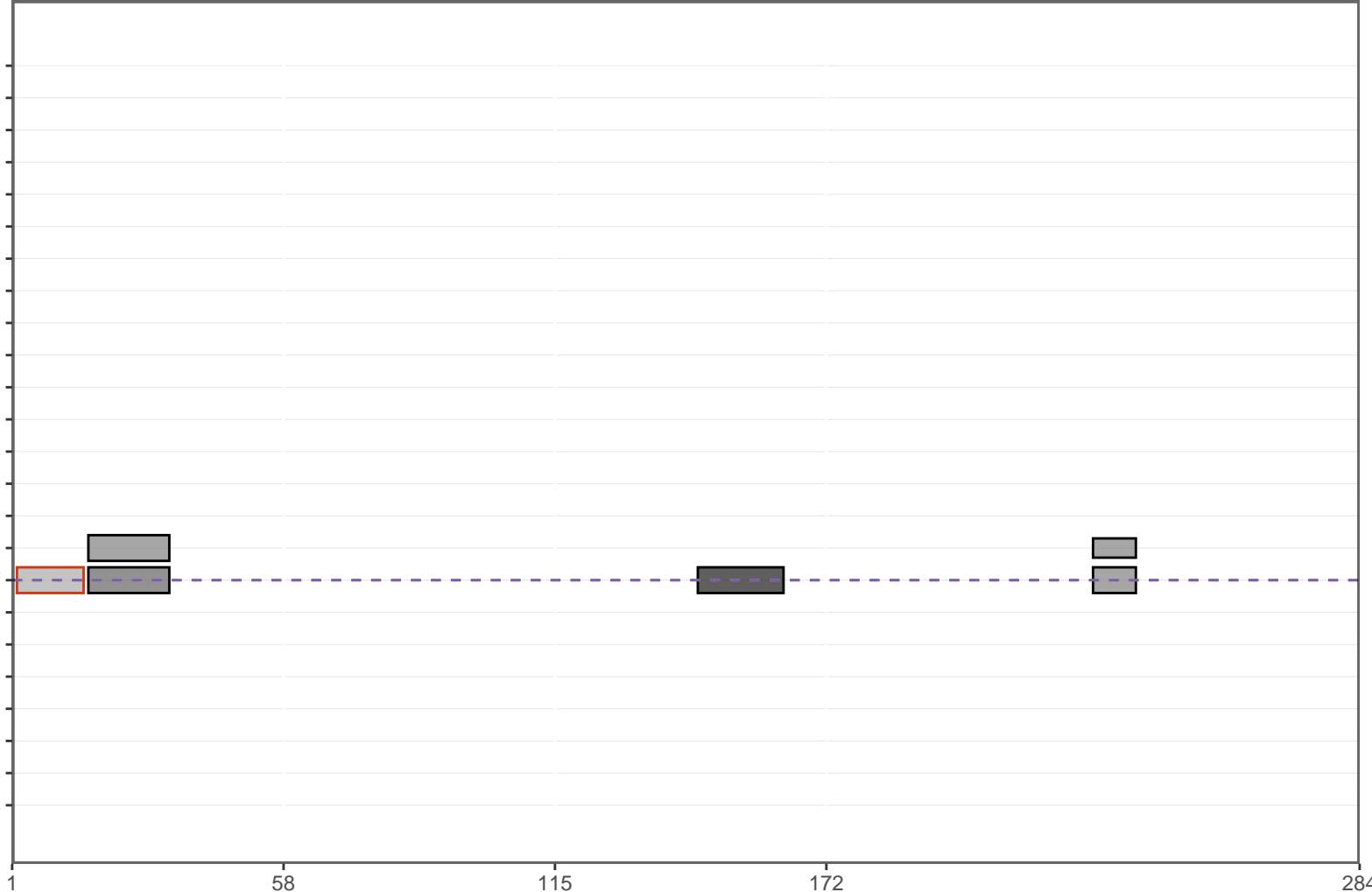
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

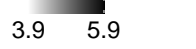
.GAICGVGVKAFMKHHYNLEGGANFVQPGVYKGTALGAEIKGTFLVYVTFESATDKRREARDSHVPLVPLPIGFAVFMVHLATIRPTGTGPNRSGFAAVYVYKEKIKWDDQWIFVYVGFVGLAAAIYHQFLRAGAVKALGSRFNPTN

NbL09g23170.1 peptidyl-prolyl_cis-trans_isomerase-like [MW = 18.05 kDa]

No. of times detected



log(intensity)



Values from



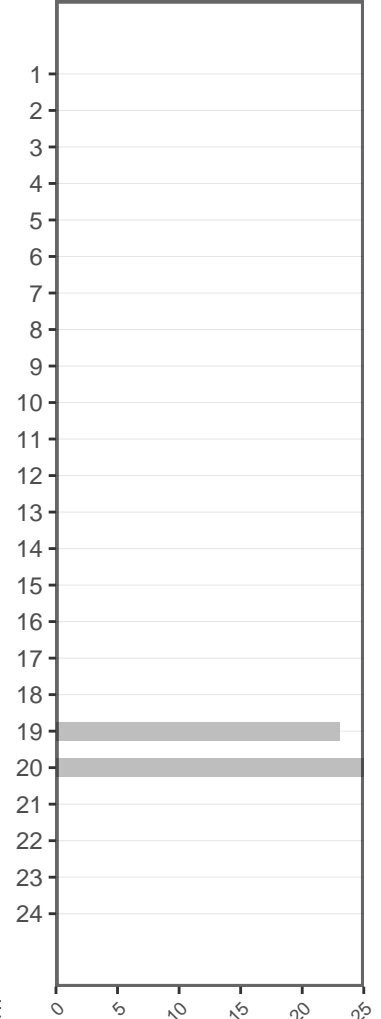
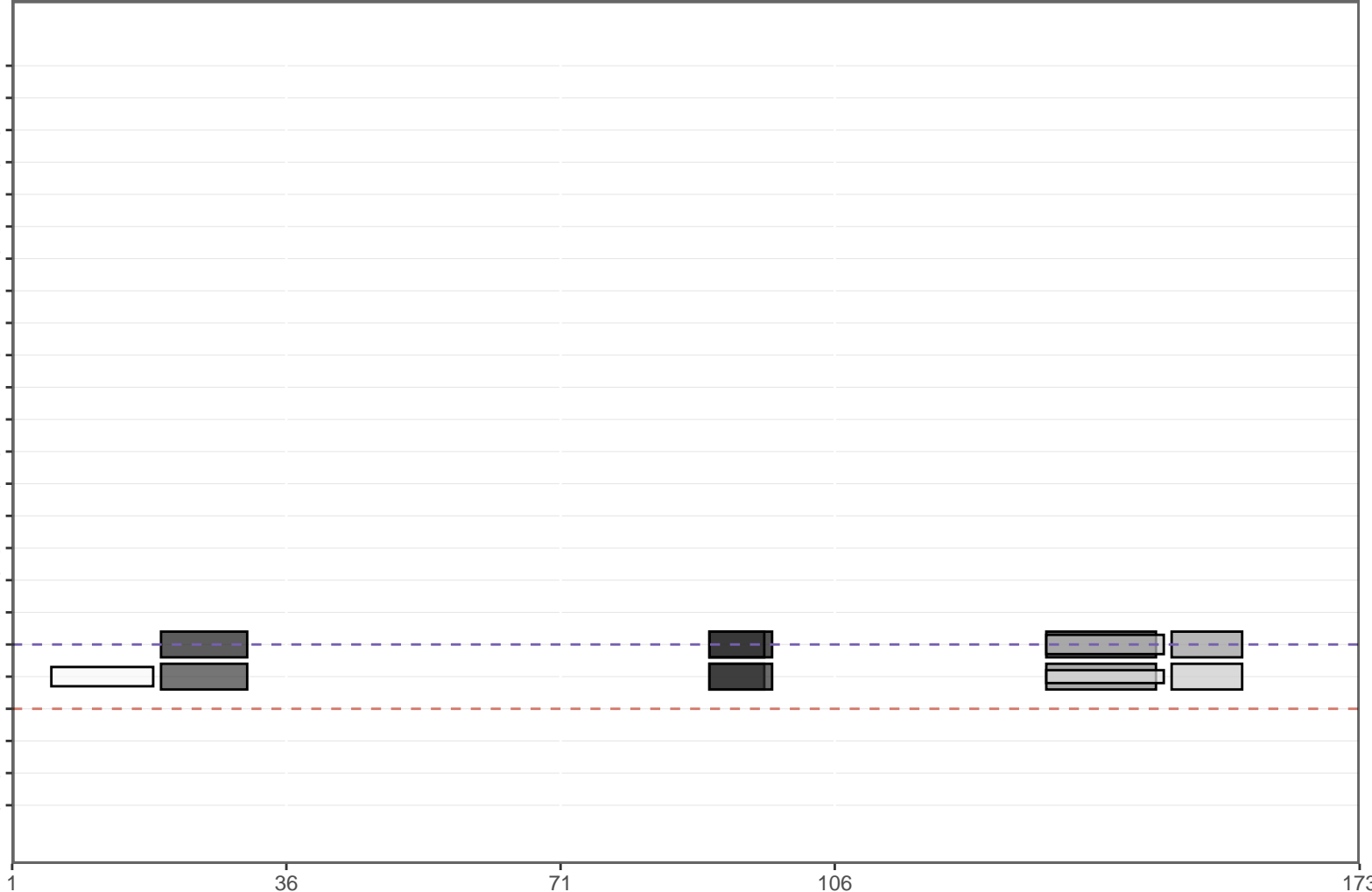
MW indication



Molecular weight

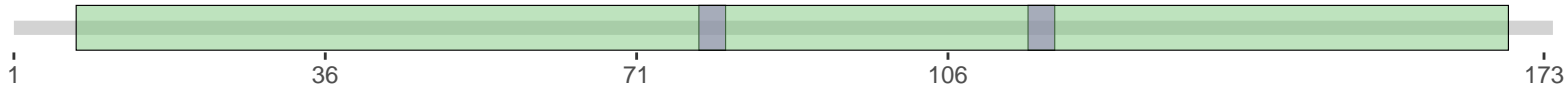


Gel Slice



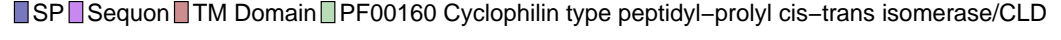
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

JFTAGNGTGGESISYGAKFADENFVKKHTGPGILSMANAGPQTNGSGFFICTAKTEWLDGKHVFDGQVIEGMVKKVVEAVGSSGRGKRPVVAADGGGLS*

NbL09g23080.1 NADH_dehydrogenase_[ubiquinone]_1_beta_subcomplex_subunit_9-like [MW = 13.77 kDa]

No. of times detected



log(intensity)



Values from



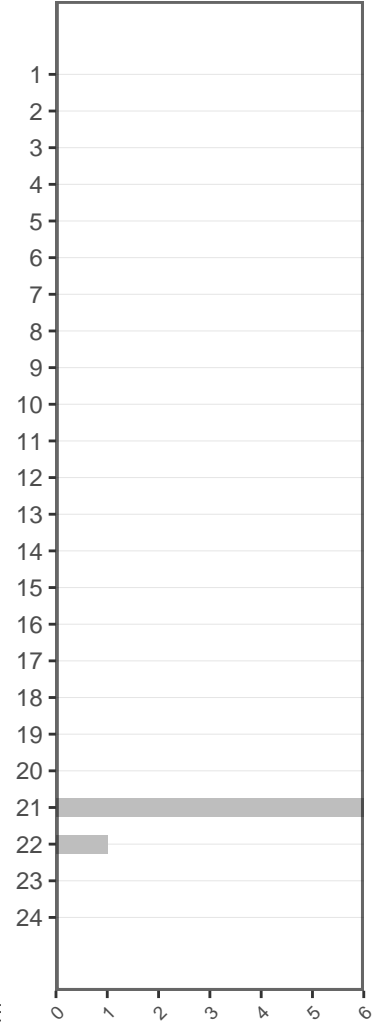
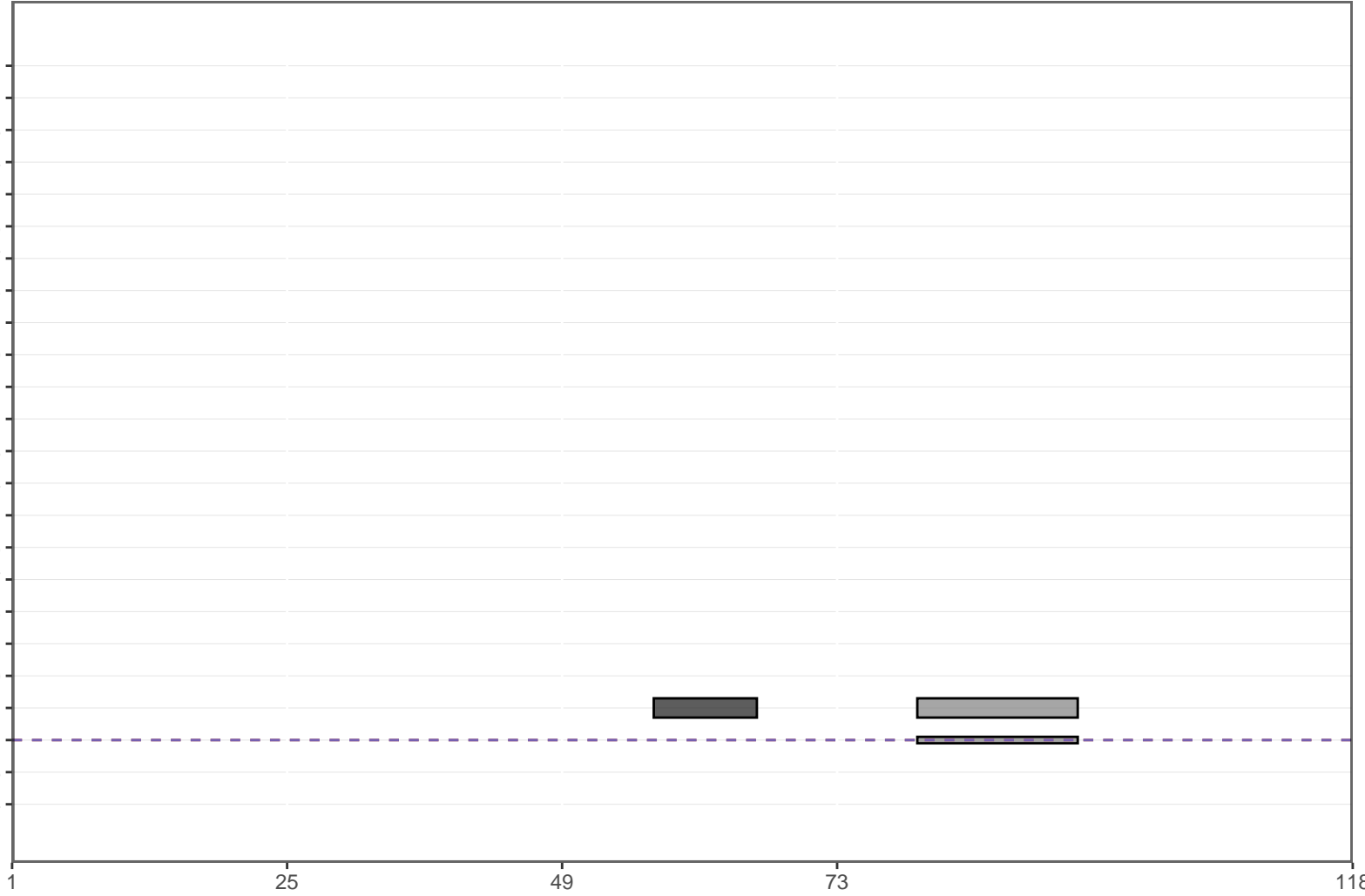
MW indication



Molecular weight

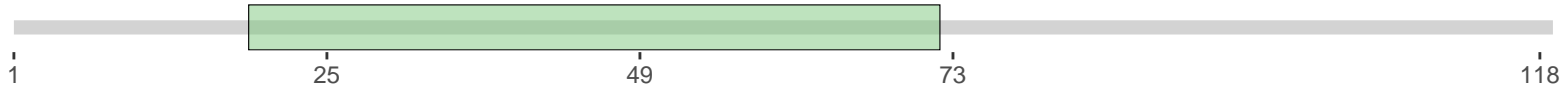


Gel Slice



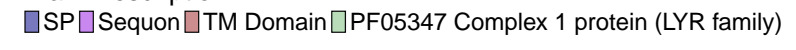
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

JALRERFEANQIVEDVETIDRLIADGASVNWKRHPDPVIVFVAPGGSEKFNRPVPPPEGLYFGRFMHQLLVE*

NbL09g22930.1 isoflavone_reductase_homolog [MW = 33.89 kDa]

No. of times detected



log(intensity)



Values from



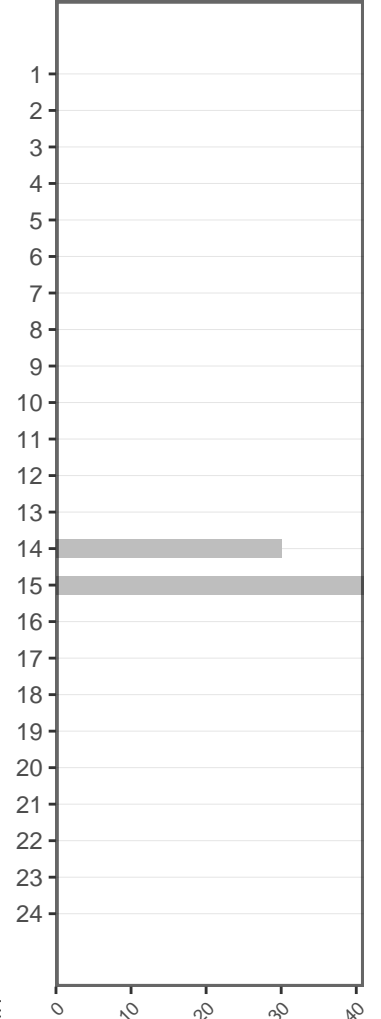
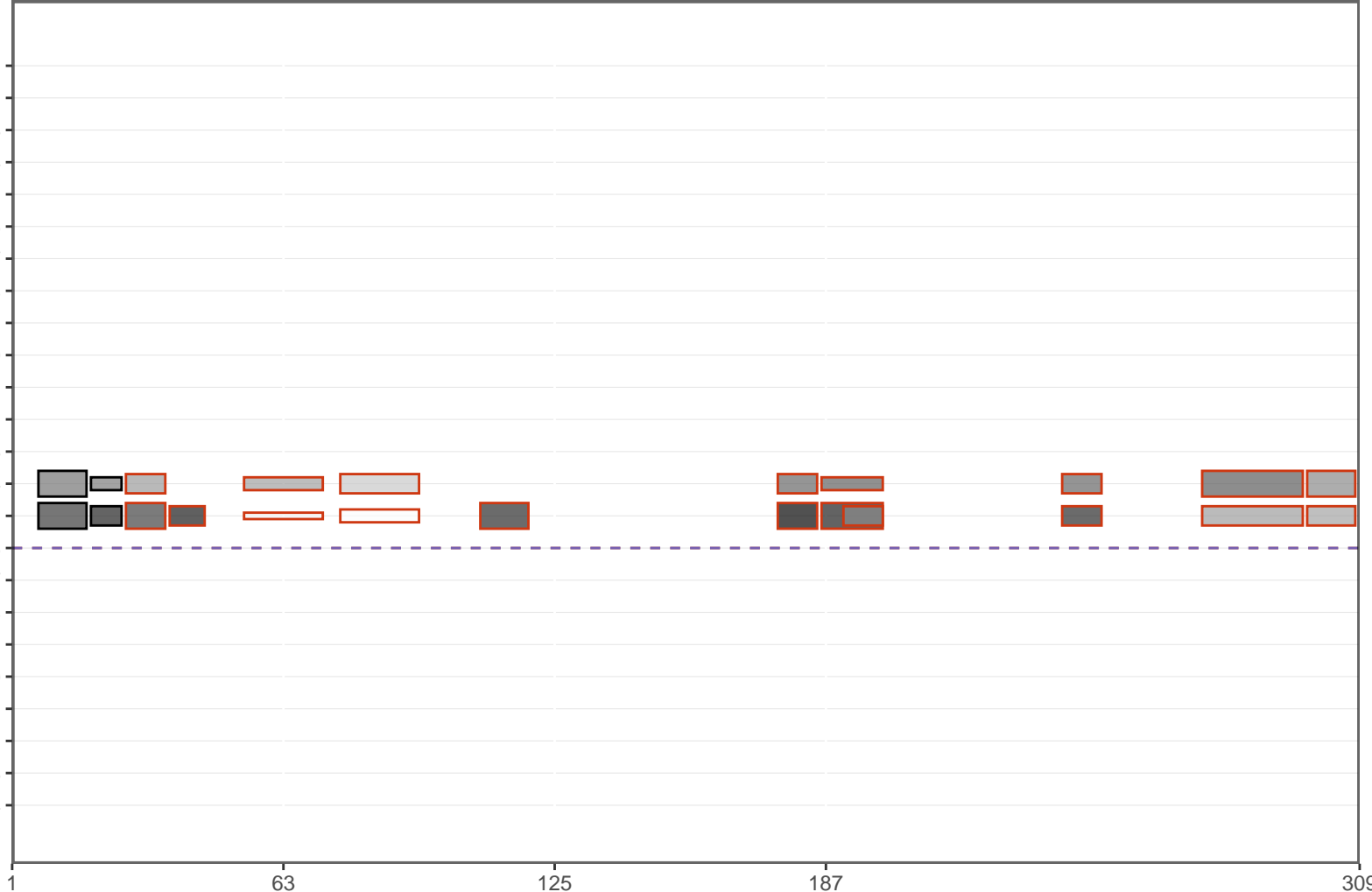
MW indication



Molecular weight

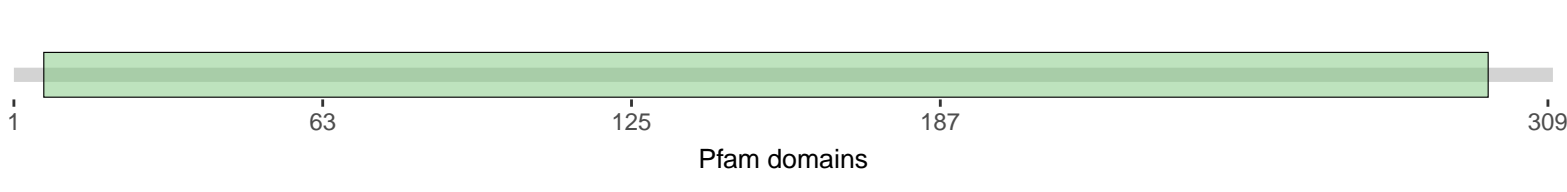


Gel Slice



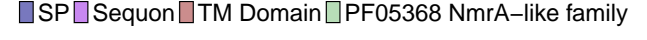
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IAEGIPFTYVANTFFADYFLNLAGPCASGPPDKVILGDGNTKAVFNKEEDIAVYTKAVDPRKTLNKLIRPPIHIVTLNDVLSWEEKTKGNLIRVYVPEEGVLNKDGEASFLNVLISHTAFVKGDDHTNFAIEPSPFGVEASEAYPDVKYTPVDELNGVY

NbL09g22880.1 glycine-rich_RNA-binding_protein-like [MW = 17.32 kDa]

No. of times detected



log(intensity)



Values from



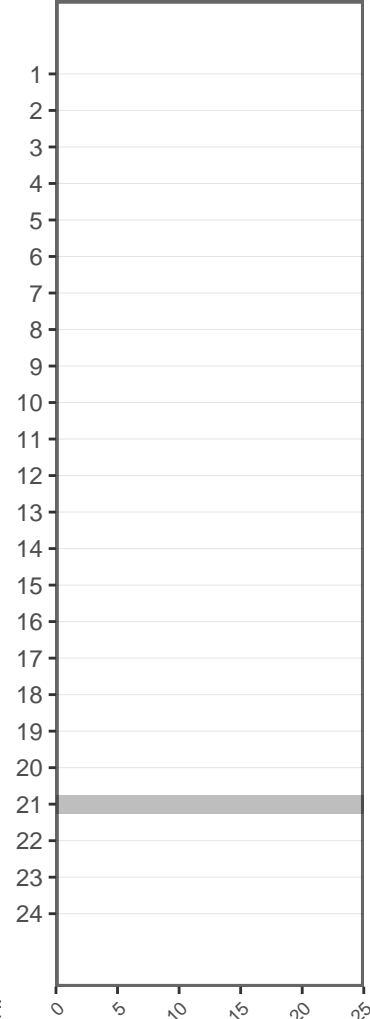
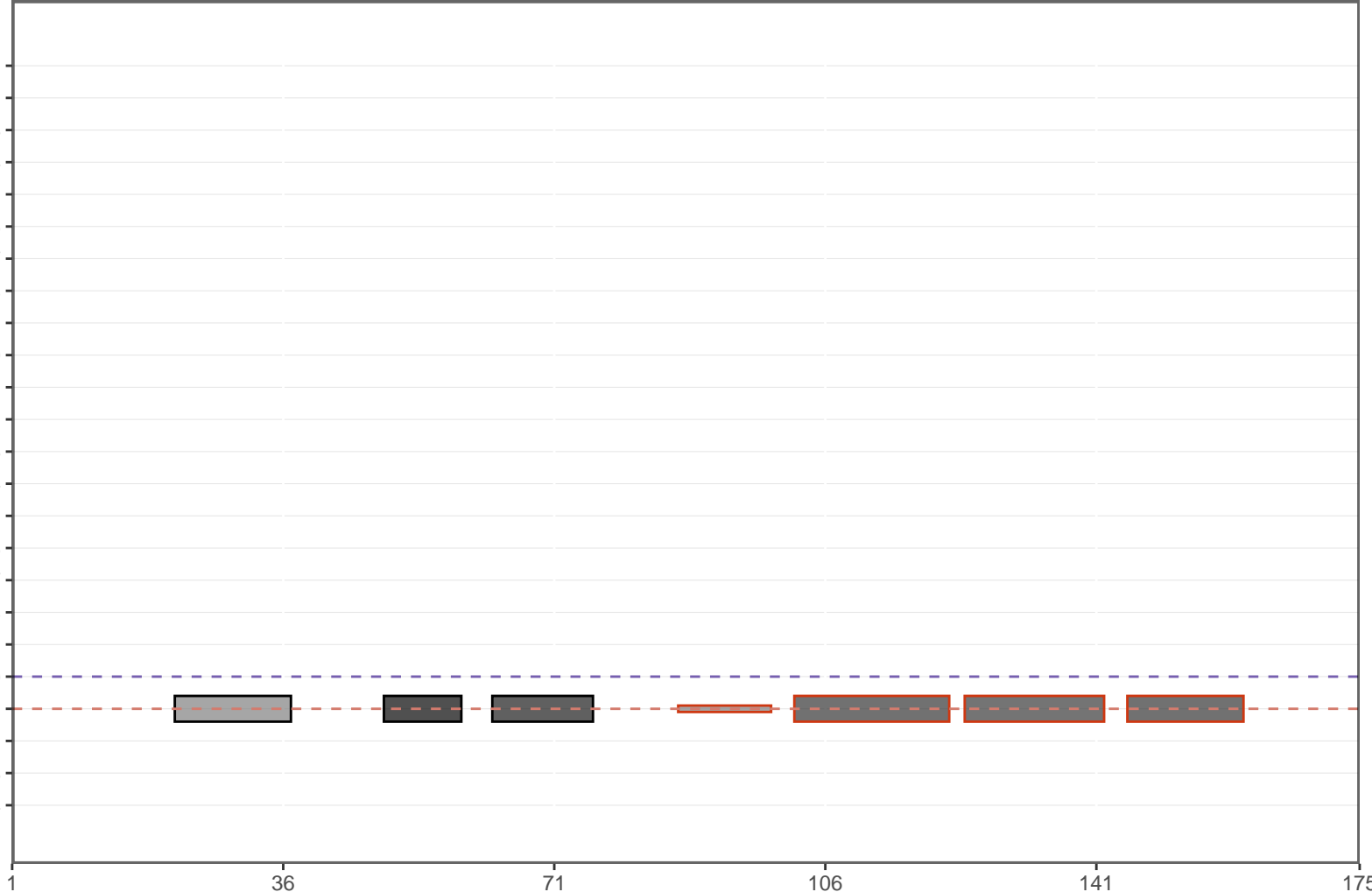
MW indication



Molecular weight



Gel Slice



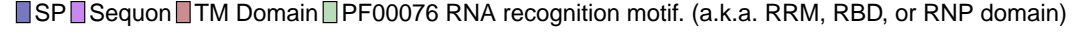
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VNEAGSRGSGGGGFGGRRREGGYYGGGGYGGGGYGGRRREGGYGGGGYGGGGYGGGRNRGYYGGYGGGGDGGSRYSRGGAGEGWRN

NbL09g22800.1 protein_TIC_62_chloroplastic [MW = 61.87 kDa]

No. of times detected



log(intensity)



Values from



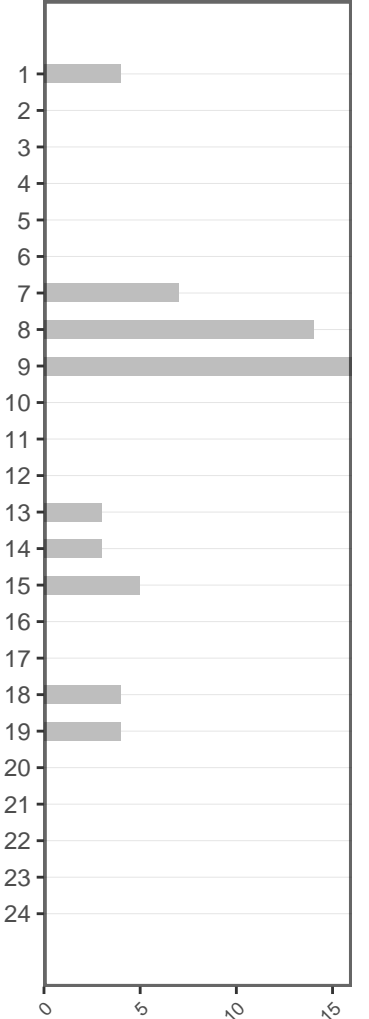
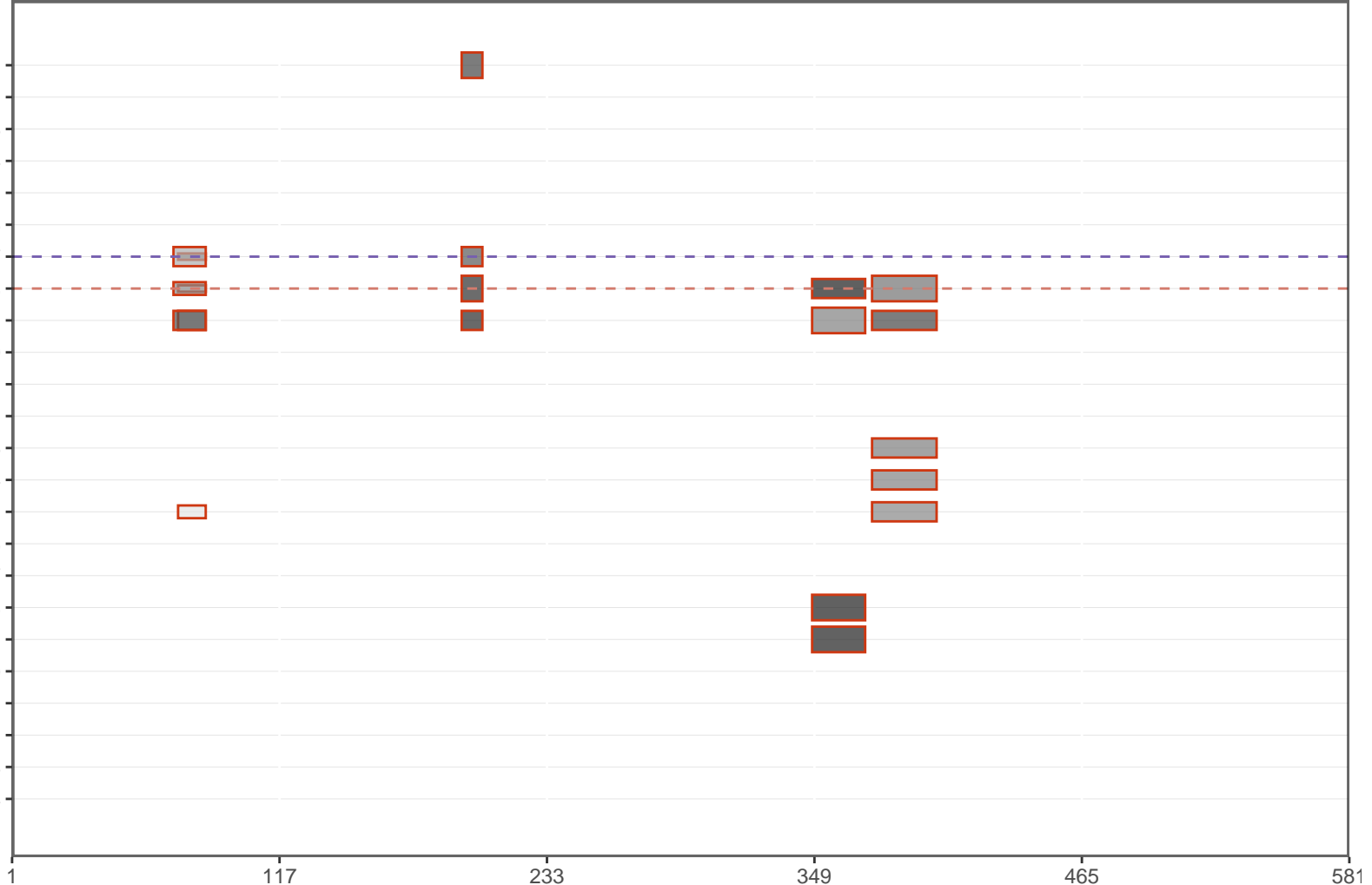
MW indication



Molecular weight



Gel Slice



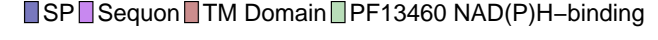
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TLFGGQVSNLQVAELLAVMAKMLSLGYGVVEVAETAPLTPMAGDLLAKIPPRQVEVSPKAEAGDGLKLAASSGTSSEIPSTSEKEMETKLAAPALSPYAVEDLKPASPTPTNPPGGSRVRSASGAEDGKTTMFASVYVDGTSKAELELTRPLSPVTAYEDLKPASPTPTSPGKASISAEIETGDLGAGNDISPGITTSAEKDPHHTVAFCHGSPFFPYEDLKPPTPTPTTPEGGAGSTTVETVSLHGNDVAIGSAADSTKEDTSKGLASGRSPYMYEDLKPPTSPPTS

NbL09g22750.1 ferredoxin--nitrite_reductase_chloroplastic-like [MW = 65.61 kDa]

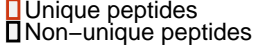
No. of times detected



log(intensity)



Values from



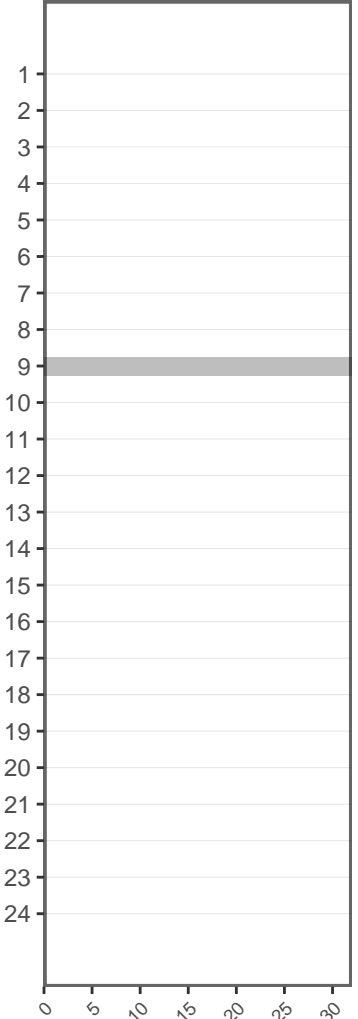
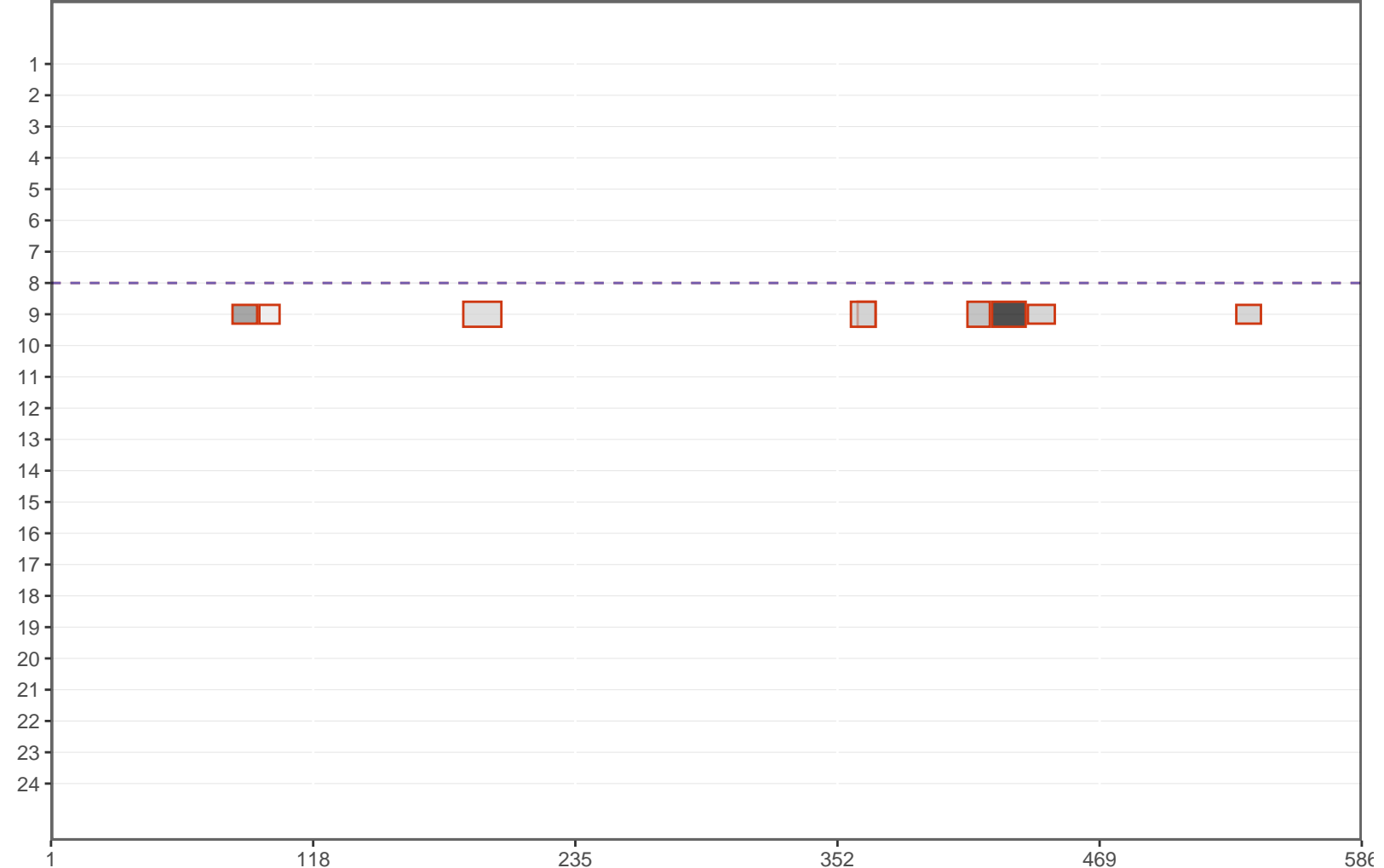
MW indication



Molecular weight

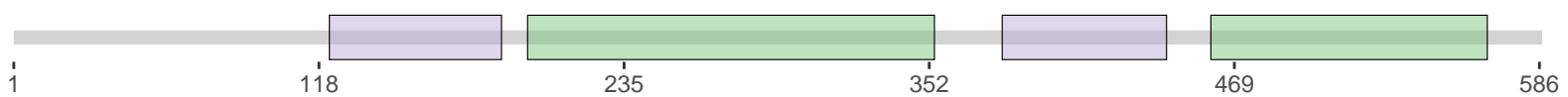


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

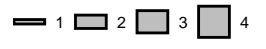
- SP
- Sequon
- TM Domain
- PF01077 Nitrite and sulphite reductase 4Fe-4S domain
- PF03460 Nitrite/Sulfite reductase ferredoxin-like half domain

Protein sequence:

LLVGGFFSPKRCASAVFLDAWVFDADVAVPVCKALEAYRDLGTRGNRQKTRMMWLVDELVEGFRAEYVKKRMLQKLDRESTDLDVQKQWERREYLGHPKQKGEYGFVGLHPIVGRVQADMDDELARLADNYGSGELRLTVEGNIHPVENSKIAALLNEPLIGNRFDSTDPILMKNLVAGTGNFGGGAIETKARSMKITEEVQRLLVSTKPKVRMHVHTGCFNSGGQVQVADIGFMGLTRKEGKTVEGADVYVSGRIGSDSHLGDVYKKSVPCEDLPIIVDLLVNA

NbL09g22720.1 uncharacterized_LOC109206941 [MW = 73.38 kDa]

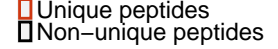
No. of times detected



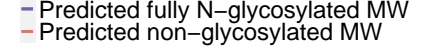
log(intensity)



Values from



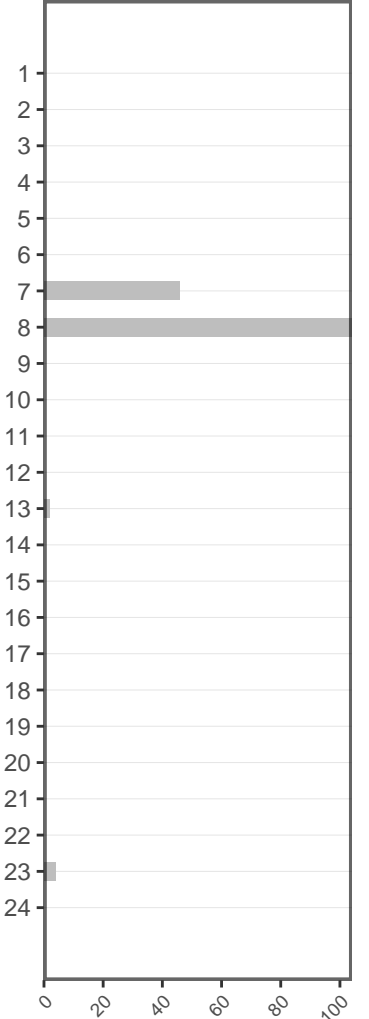
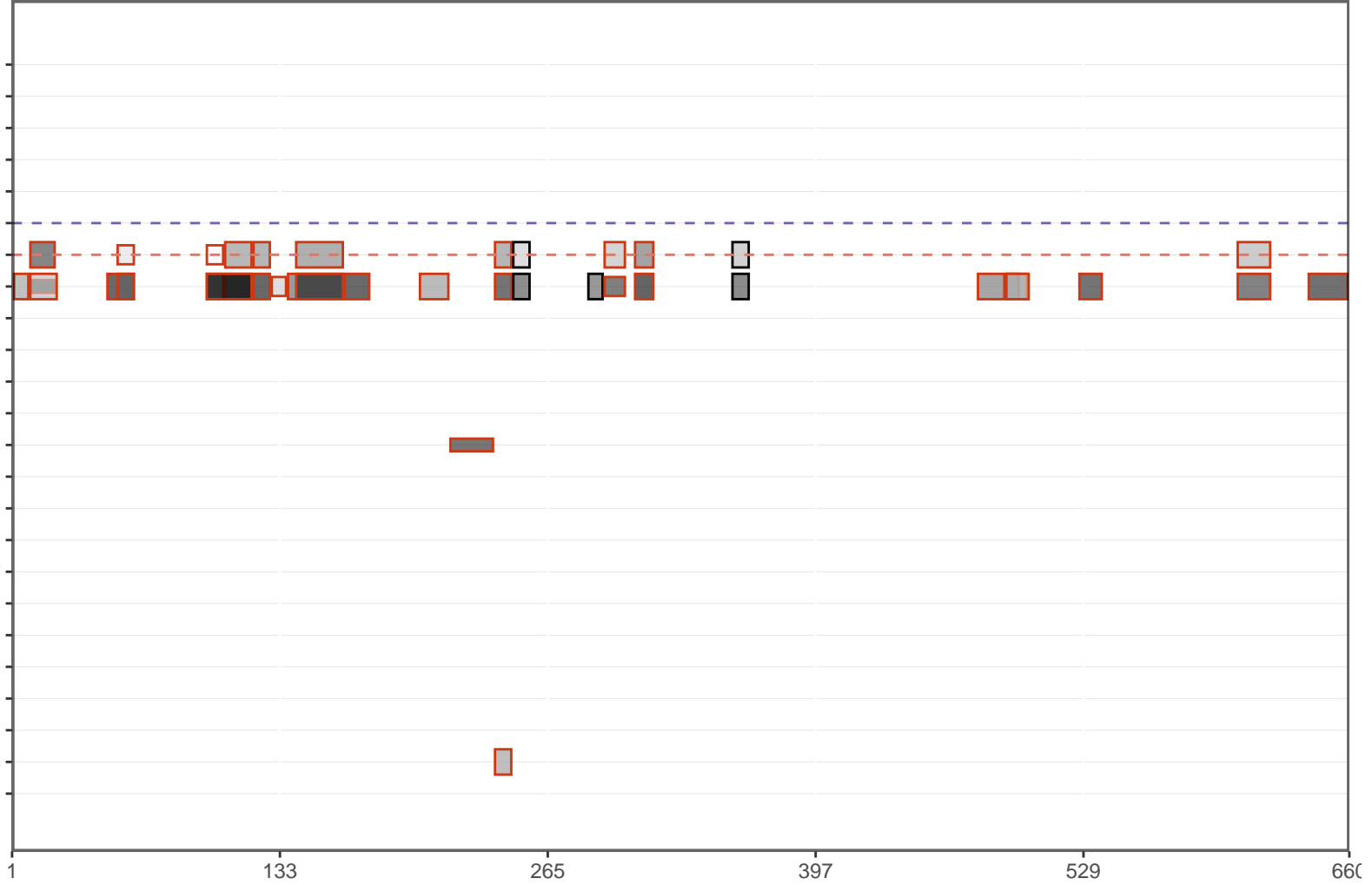
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

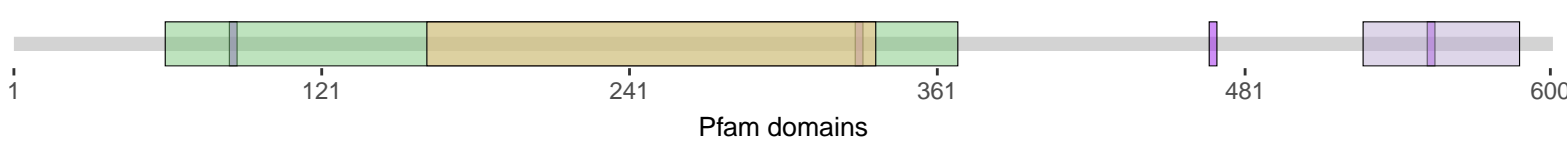
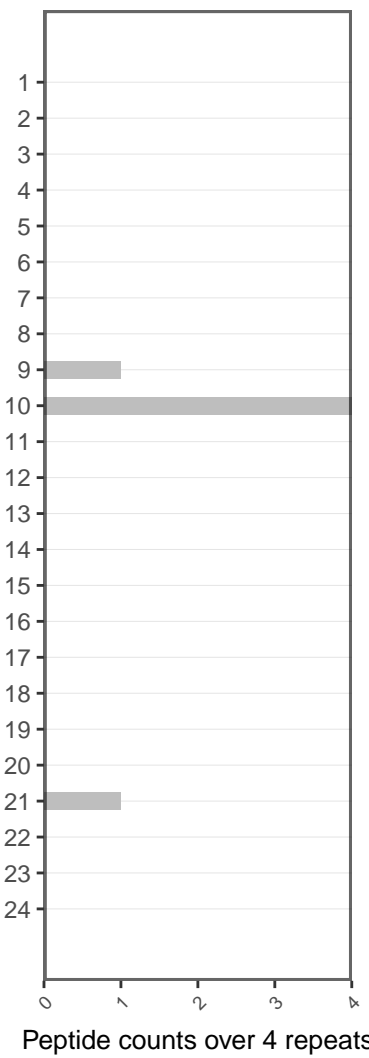
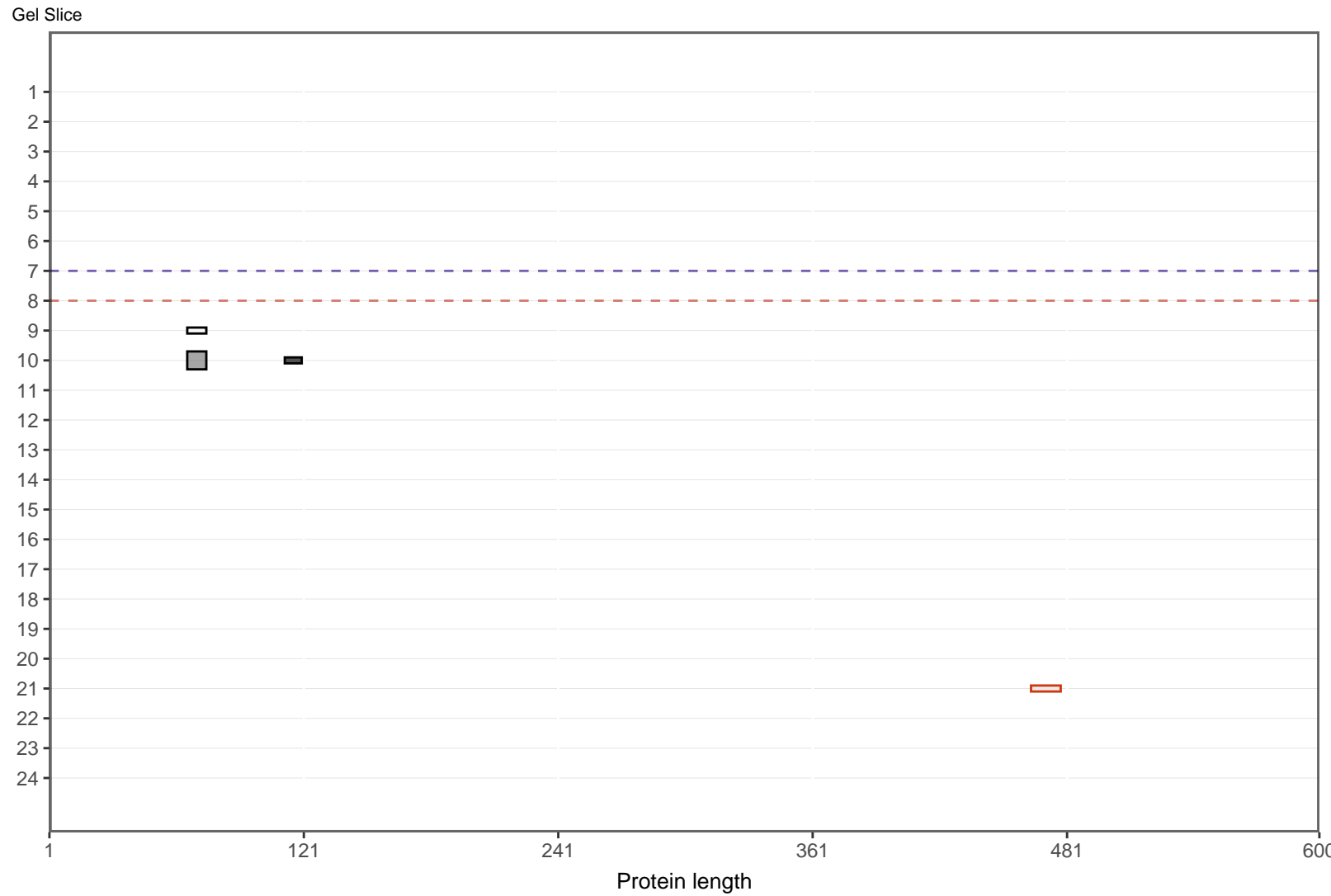
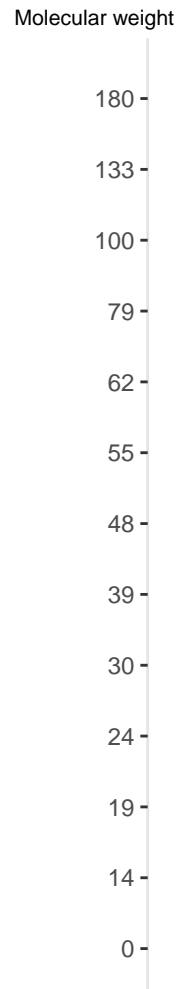
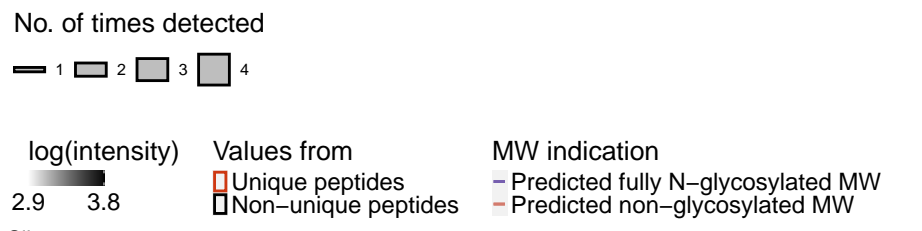
Pfam Description



Protein sequence:

DAKNSFCSDVDFPTFTHANLASGQQLVIEGASVLPSTLAKVVLDDHMSKVVDFSMWSSSSDSDGKYHVFSLPELIEFFPTGVAGGNAYVYFPCNPQVYKSGDEKPKLLLESHGPTDEAHGTLNLSQVYTSRQWAFVQVNVYGGSSGGRAYRERLLGKVGQVDVNDCCGCAKYLVDGEGKVDKRLGTTGGAGQVYTLASLAFRDTFRAGASLFGIADLKLSDKMKKFESYHLLNLAGNETALYERSFNIFDIHFSCPIHFGQLEDVTVQPEGAQKYQALXXXGLPVAH

NbL09g22520.1 D-3-phosphoglycerate_dehydrogenase_1_chloroplastic-like [MW = 63.39 kDa]



Pfam Description

- SP
- Sequon
- TM Domain
- PF00389 D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain
- PF02826 D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain
- PF01842 ACT domain

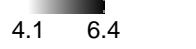
Protein sequence:
 IIVRGGVDELDLVRALDAGVADGALVFTVEPPKDKLQIHNVTATPHLGASTMEAGEGVWIEAEAVVGAALKGELAATAVNAPMVAEVLSEKPPVLAELKRLRAVQLVTGGSGVKKVYVYGSARAPDLDLTRLIRAMITKGLIEPISAFVNLVNAFTKAGRLRAEERSHLNGSPESPLEFRVQIANNVSKFASADSGEIRVGGKVDIPHLTKVGSFVVDVBLEGSLGRGVDDQPMIGKVSILSEENVWVGFMSVGRVAPRKHAVMAIGVDEQPSKESU

NbL09g22370.1 heat_shock_70_kDa_protein_mitochondrial [MW = 73.02 kDa]

No. of times detected



log(intensity)



Values from



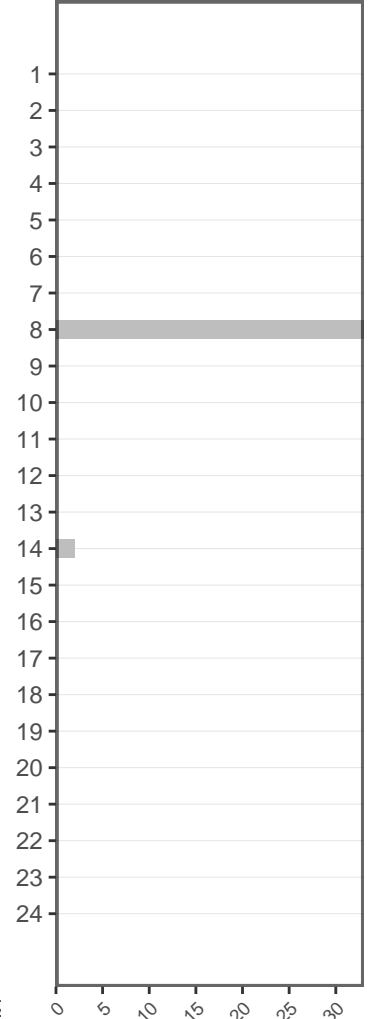
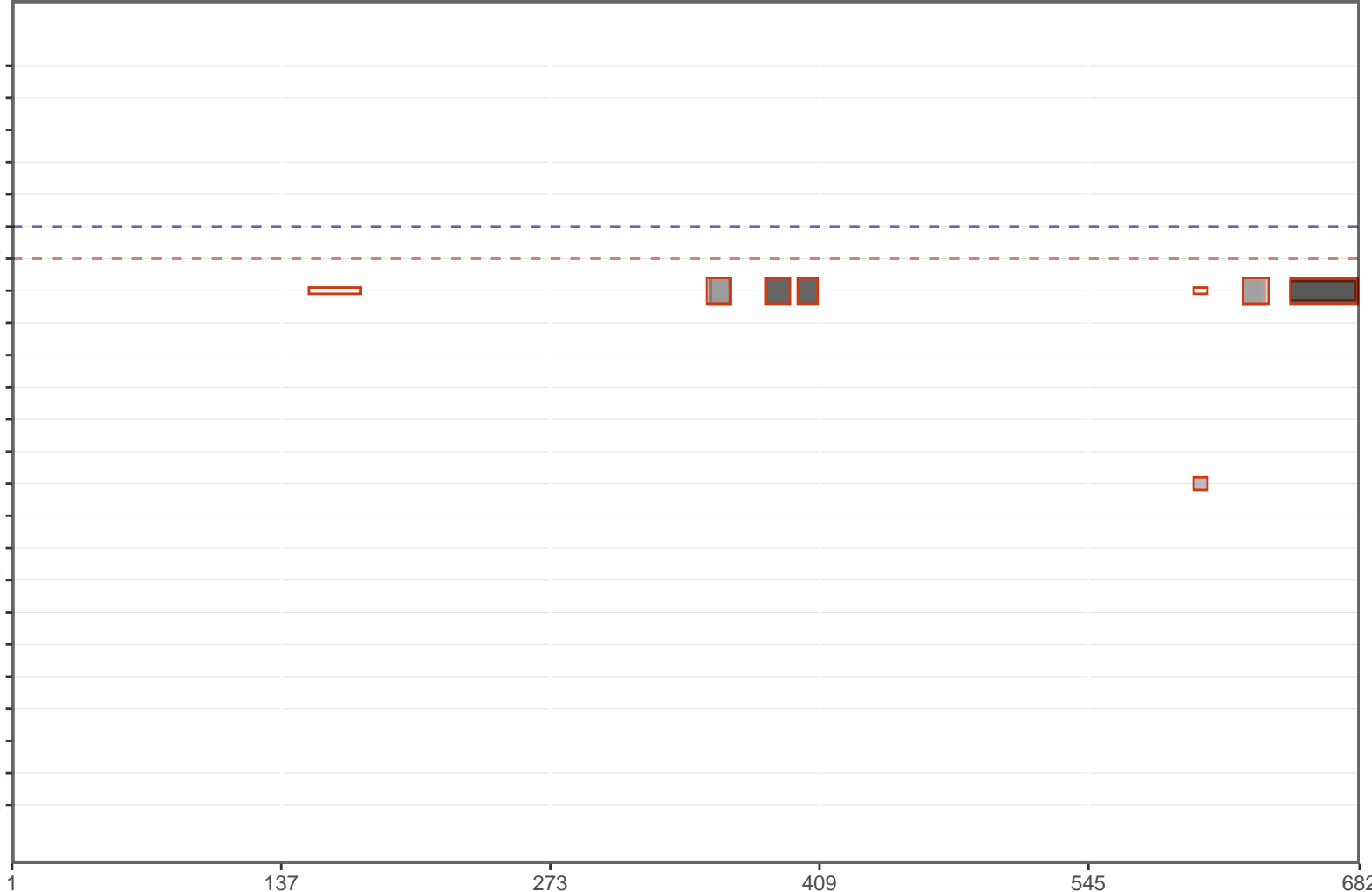
MW indication



Molecular weight



Gel Slice

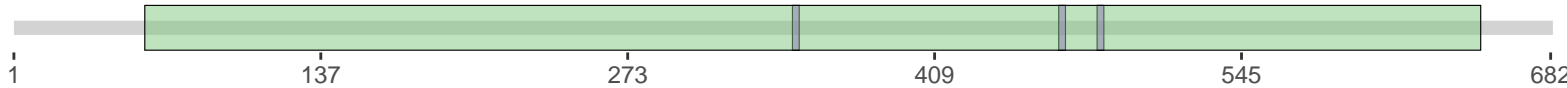


Peptide counts over 4 repeats

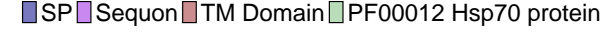
Protein length



Pfam domains



Pfam Description



Protein sequence:

QTEINLPTTADASGAHNLNLTFRKFEIIVSLIERTDPCKNGLKDGISTKEVDEVLLVGMTRVYKVDQNVSEFGKSPKGVNFDPEAVMGAAGGGILRGDVKELLLLDVPLSLGETLGGIFTRLNIRNTTPTTKKSGVFTAADNGTQVGVKVLGGEREMASDNKMLGEFELVGFPAFRGMPQIEVTFDDIDANGLVTVSAKDKATGKEQQITRSGSGLSEDEIDMMVKEAEMHQRDRGERKALIDRNSADFTTYSIEKSLNEYRDKVPEVATEITAVSOLRTAMGC

NbL09g22320.1 elongation_factor_1-delta_1-like [MW = 28.98 kDa]

No. of times detected



log(intensity)



Values from



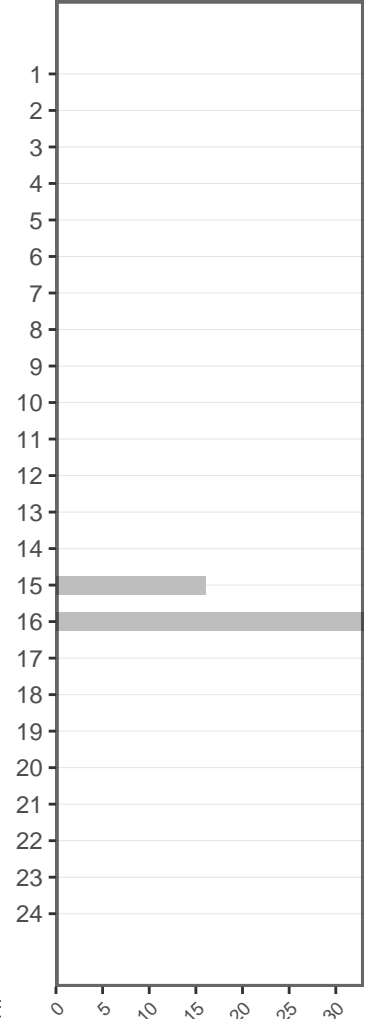
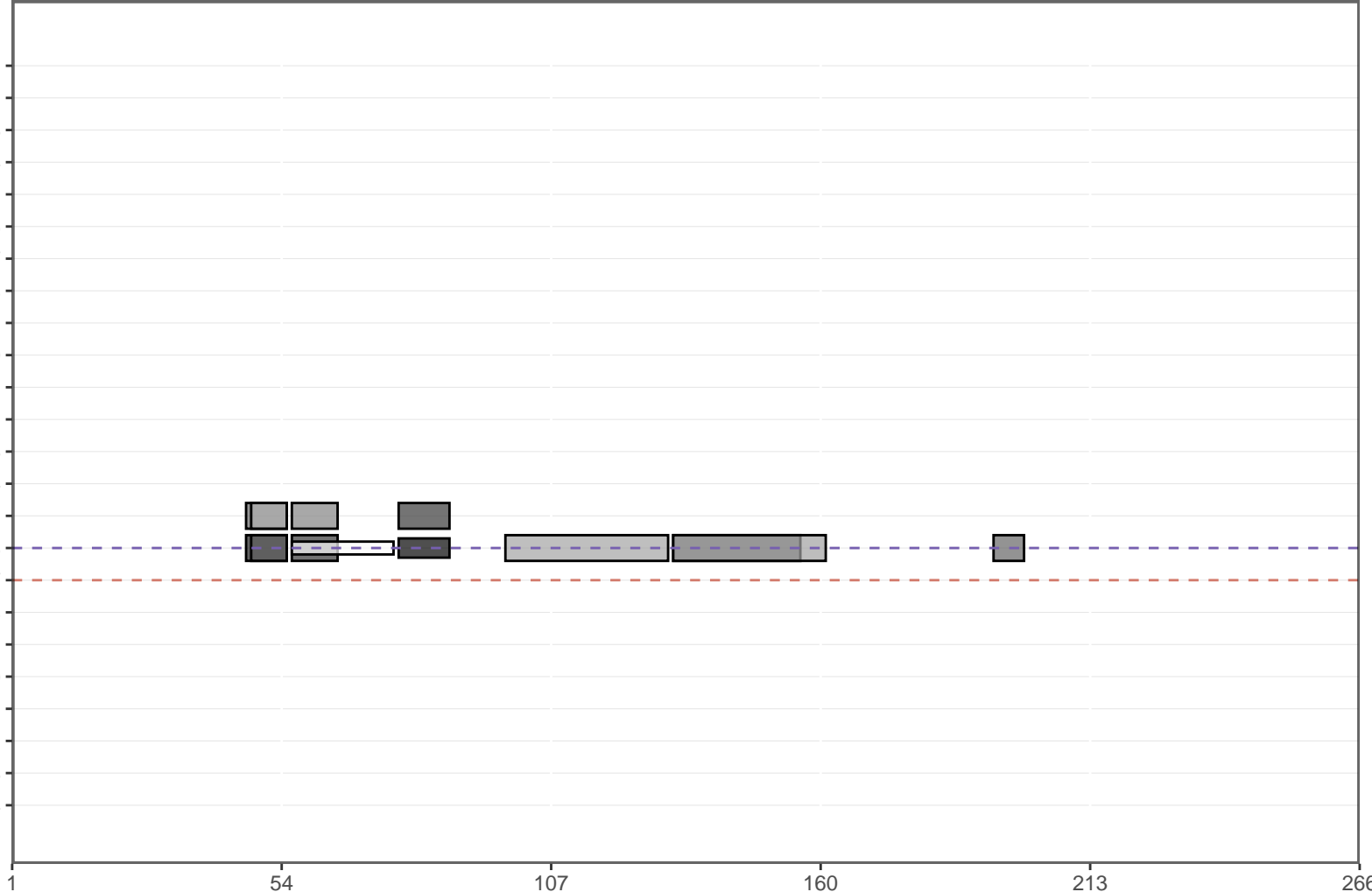
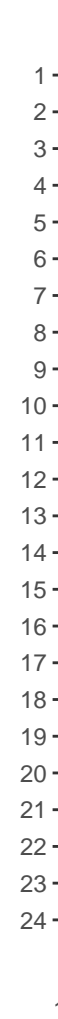
MW indication



Molecular weight



Gel Slice



Protein length

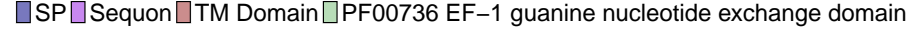


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VATPPAADTKASAAEEEEEDDDVDFGEEETEENKAAEERAAKAKSGKKKESGKSSVLLDVKPVDDEDTMKKLEEAIVRSVQMEGLTYGASKLIPVGVYGIKLIQMLTIIVDLSVDDLVENYFMAERINEVYVQSGDVAFNKI

NbL09g22150.1 L-galactono-14-lactone_dehydrogenase_mitochondrial [MW = 66.94 kDa]

No. of times detected



log(intensity)



Values from



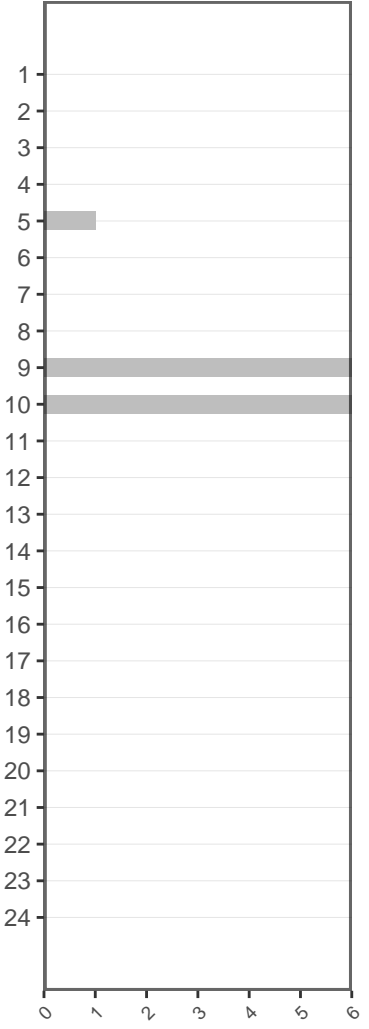
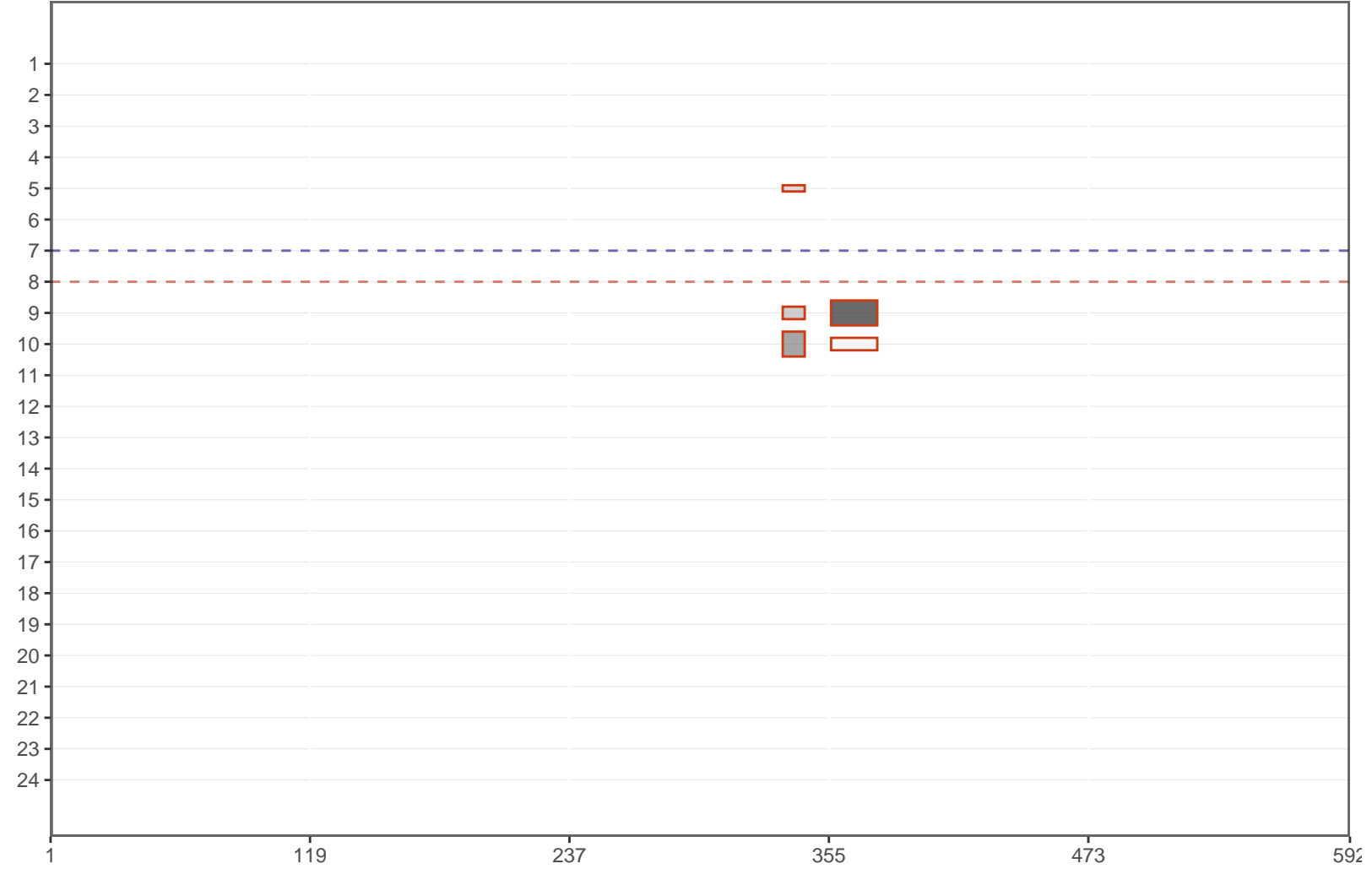
MW indication



Molecular weight

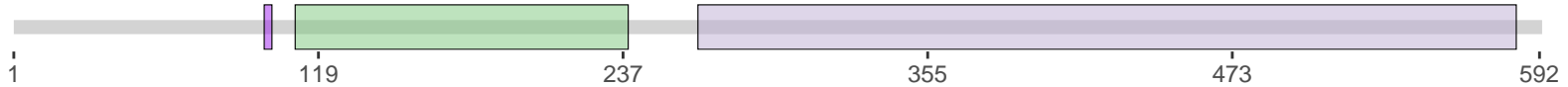


Gel Slice



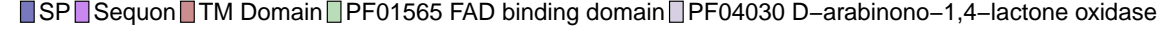
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MDIKDNH9KFLSENKHVYKLFHPYTDVVVVTENPIGKRGPPKPKYKTYTEALGHVRLVYREALKRYRGGVADGSSSEPEIDELSFTELKLLALDPLNKEHVEVNAKAEFWRKSEGVYRQVWSDLELGFDCGGHQWVSETGFFAGTSLKPKMKOLEVYIEELMQLAKEVYPAFPIEQRWATACKSRMRMSPYSSADDDIFSWVGMIMVLPMDARQRQGTIEFFHYRHMTOAQLWHDHYSSFEHWAKIEVPKDKEELAAALQARLKRFPVDANVQARXELDPKRLS

NbL09g21940.1 cystathionine_beta-lyase_chloroplastic [MW = 51.41 kDa]

No. of times detected



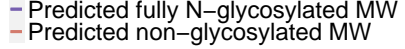
log(intensity)



Values from



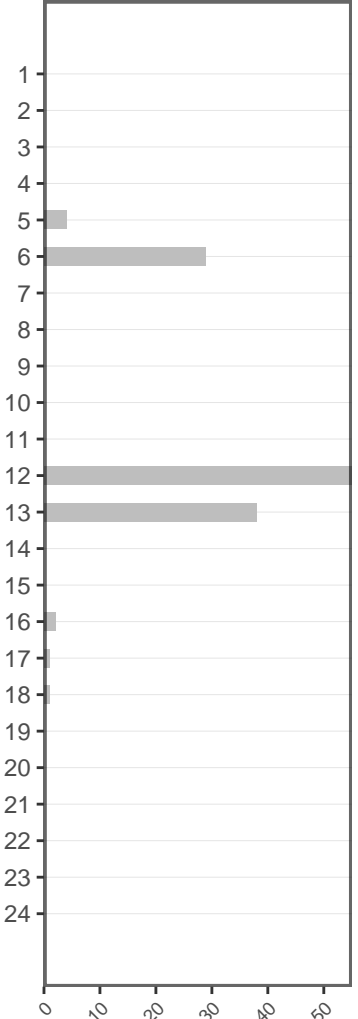
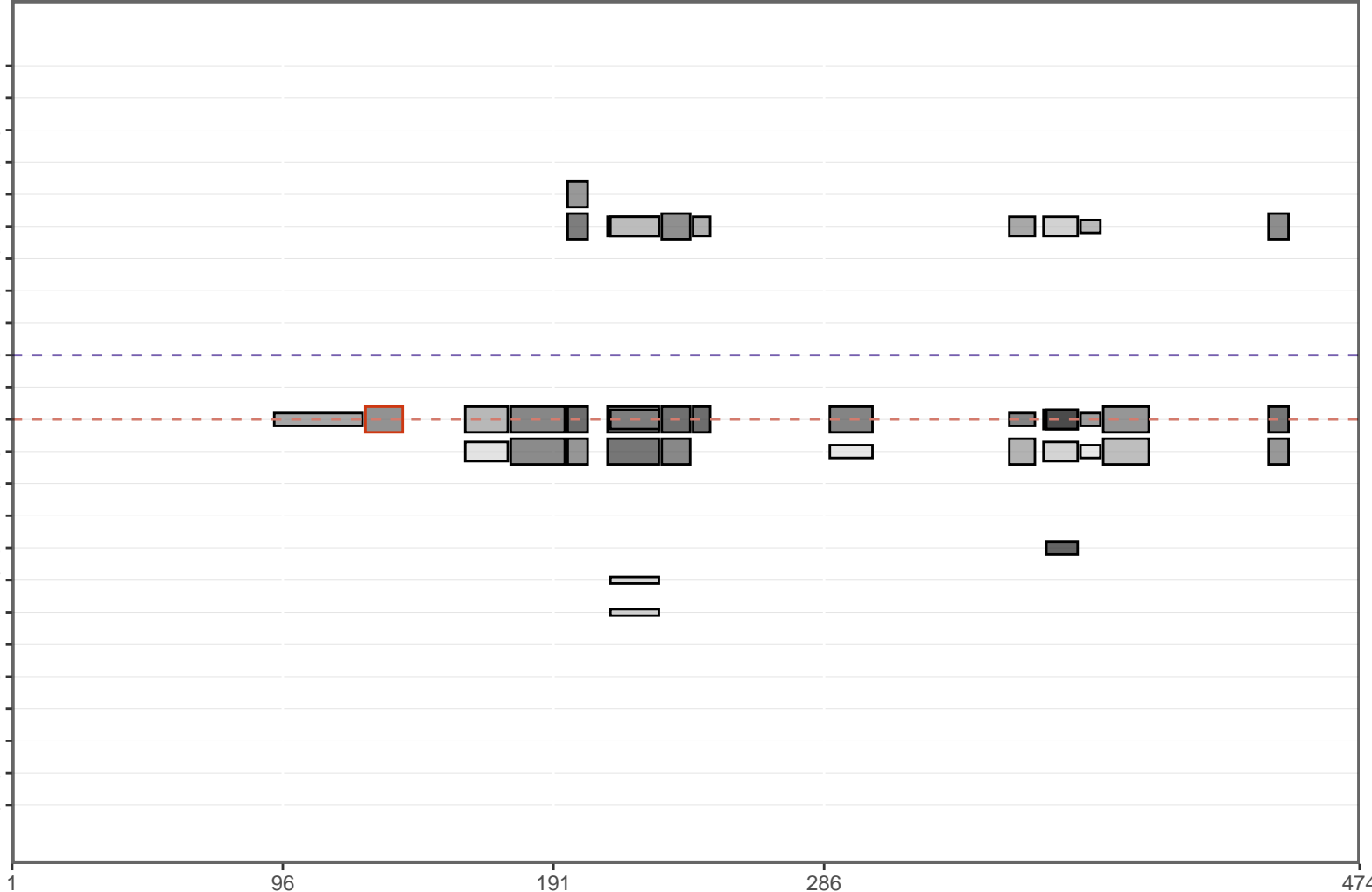
MW indication



Molecular weight



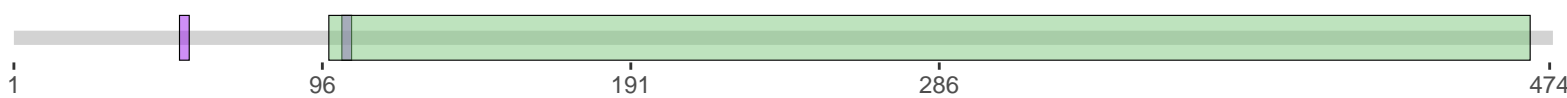
Gel Slice



Protein length

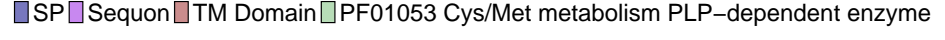


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SAINPOTKLVYLESPFNPRGGQCDIRKAKIAHAAGALVLDNIMSPVLSPHLELGADIVMHSATKFIQSHSDLMAGVLAIRGSELTKEIVFLQNESEGAGLAFDDWCLLRGKTMALRVEKQGENAGKIAEFLSSHPRVKKNVYAGLPHDIPGRSLHFSDARGAGSVLFLTGLALSKHVAETKVFSTVSGGSKGLISLPCFMHSHASIPVEVREARGLTEDLVRISVIGIEDNDLIDDLVALRTGPA

NbL09g21920.1 SNW/SKI-interacting_protein-like [MW = 69.59 kDa]

No. of times detected



log(intensity)



Values from



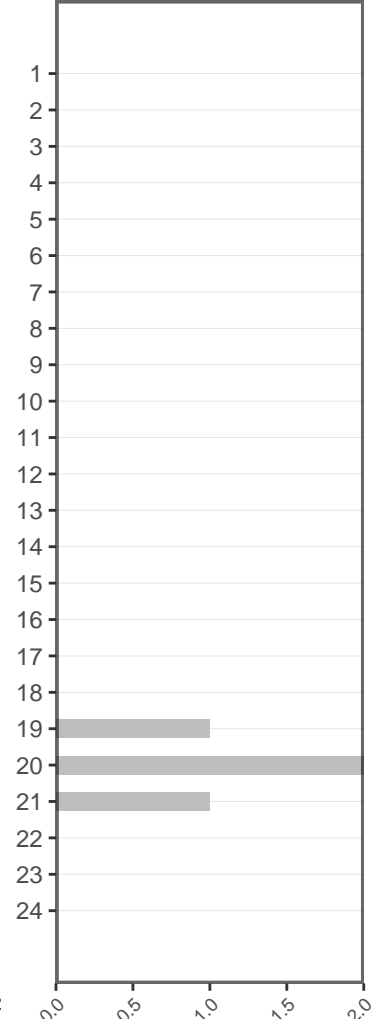
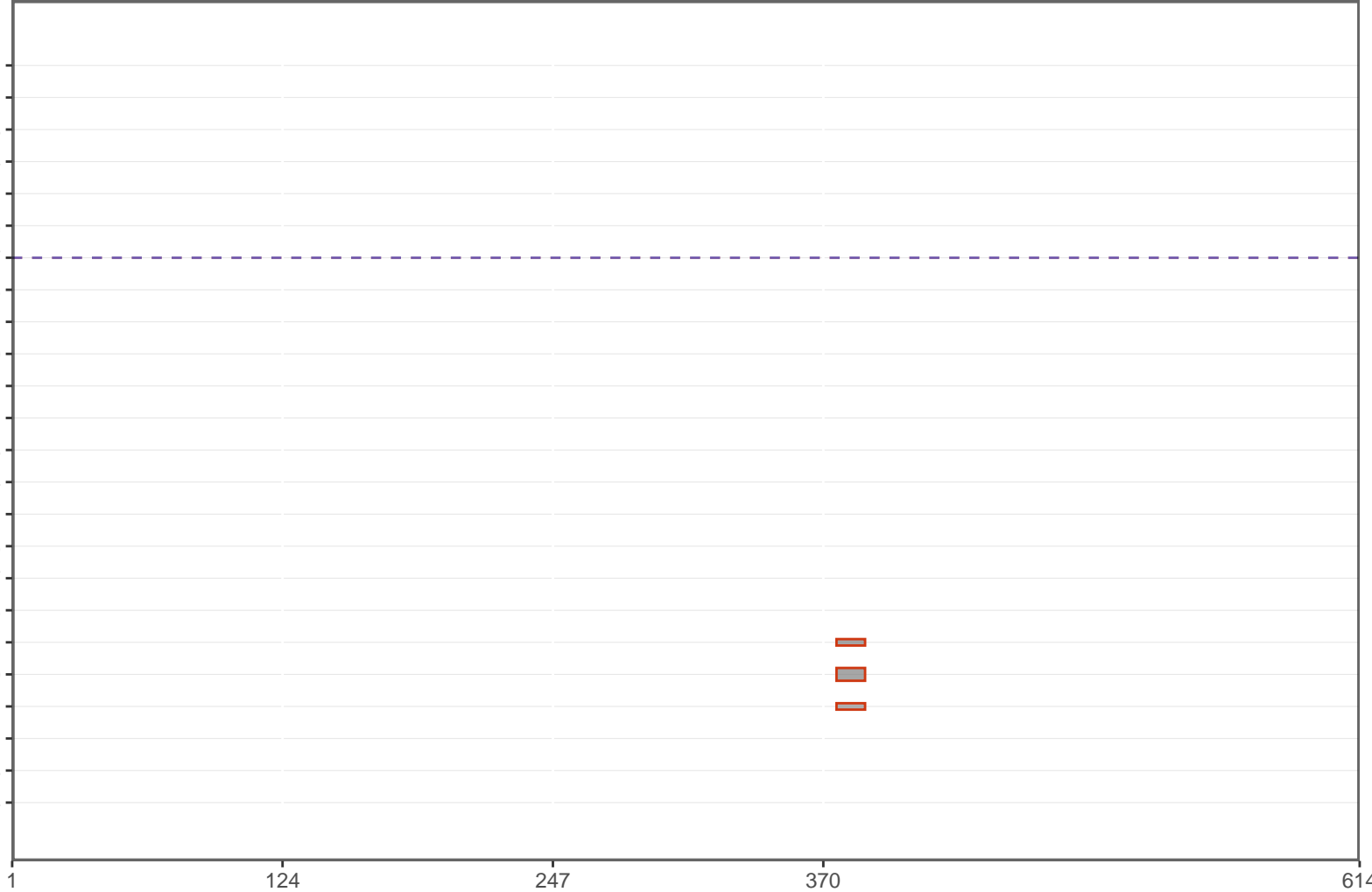
MW indication



Molecular weight



Gel Slice

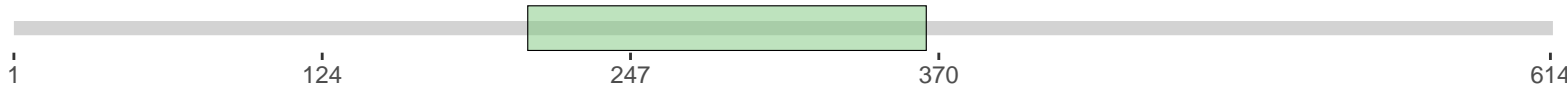


Protein length

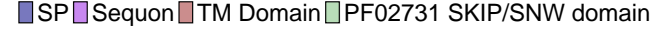


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LAADGRGLQIEYQINDNFALKEALYVAEQKAREAWMRBKVQKEMMKKEKEKEMELRELARKASERTGVAPPAERGTMMDDMSVDYERARDPFPKESREDREERSQREKMRREERRERERARRLEAKDAAMGKKKSKITRRDRDRVSEKVALGMAGTGTGRGEVWYDQRLFNQEKMGKMDSGFATDDAYWYDKGLFTAQPTLSTLYRPKKQADSEMVGGADEGLEKMKTERFKPKAFAGTSERAAPRDGPGVQFEKEVEEADPFGLDQFLTEYKKGKAMAS

NbL09g21630.1 thioredoxin_reductase_NTRC-like [MW = 59.43 kDa]

No. of times detected



log(intensity)



Values from



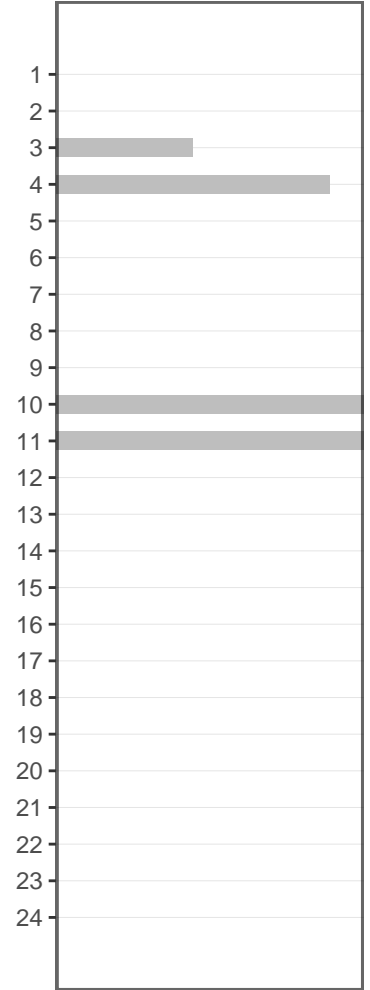
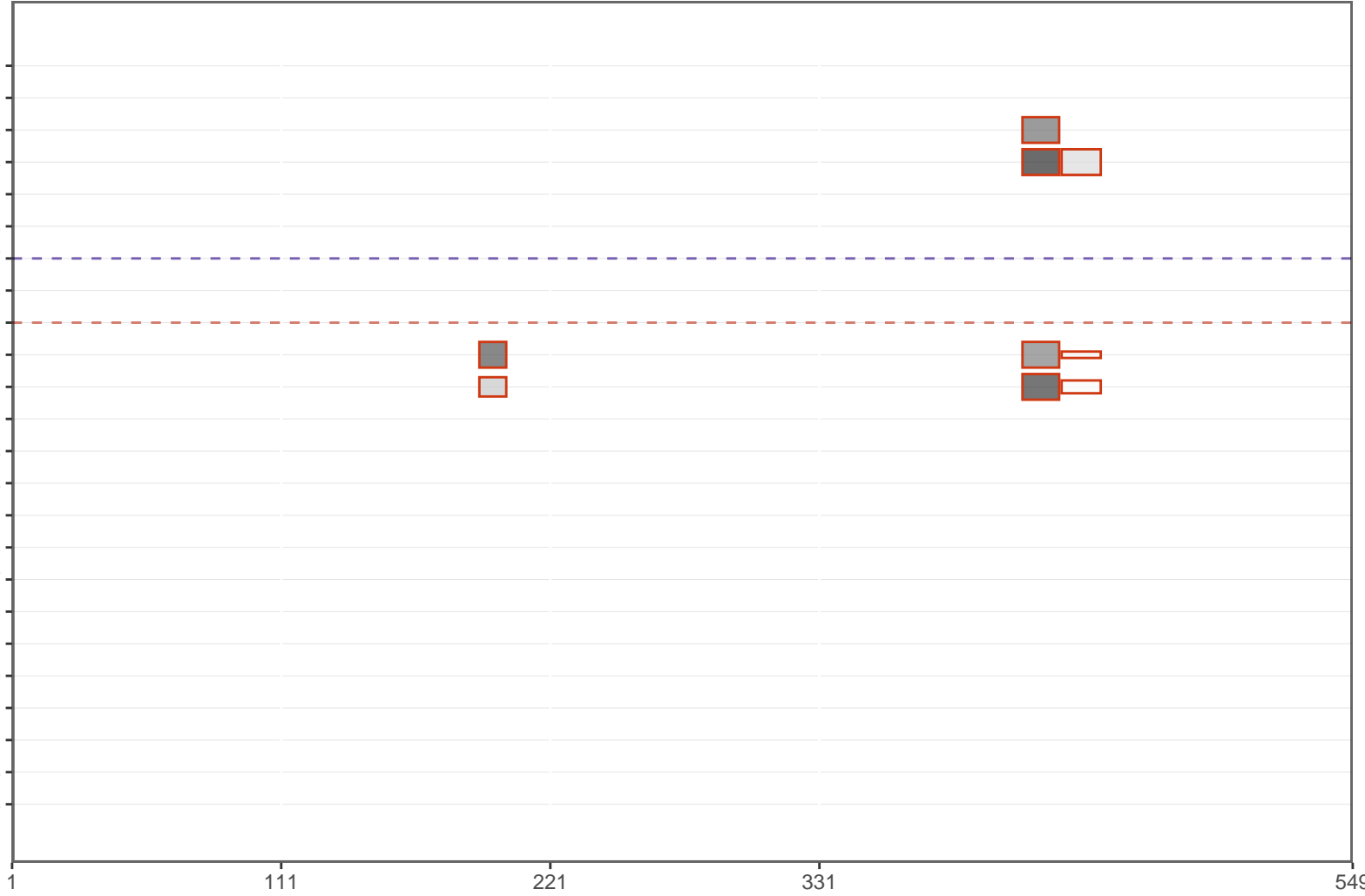
MW indication



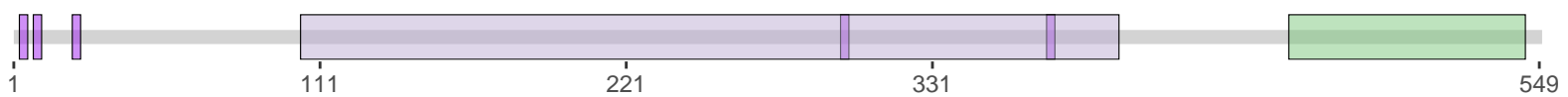
Molecular weight



Gel Slice



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MTTEAAYLTKYARHYVHLVLRKDKQLRABRAMQDRVFNPNPITVHNTETVDVSNPKGMSGLIRKADTQEESEVIEAKGLFYGGHSPNQLLEGQVLDSSGYLWKEGTANTSEVGVFAAGDNDGHEWRGQNTAAGSSGVAALGVERYLTKNLLIEFHQPSTEEVWKELTENKDYQEGFDLTKHKGQVALRKLWHESSRICVLYTSPTCGDPRTLKPILSKVIDEFDGHHVHFVEIDTDEPEIAEAGIMGTPOVQFFRNKEMLRVTSQVWMMKREYRELAEAK*

NbL09g21500.1 adenylosuccinate_synthetase_chloroplastic [MW = 55.1 kDa]

No. of times detected



log(intensity)



Values from



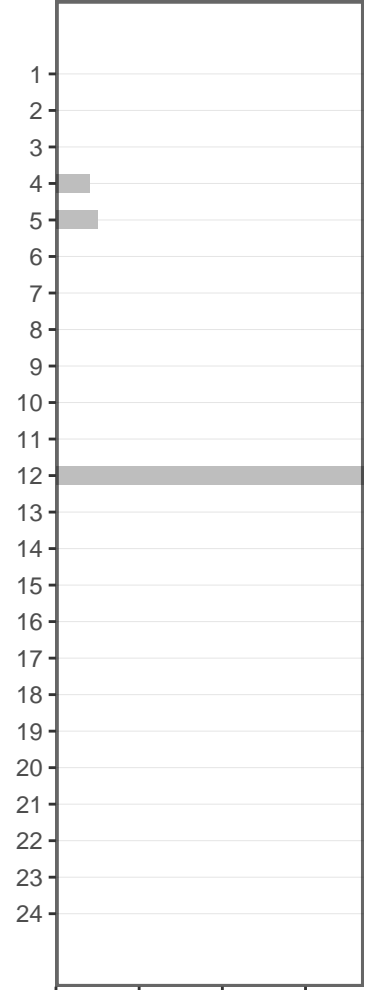
MW indication



Molecular weight

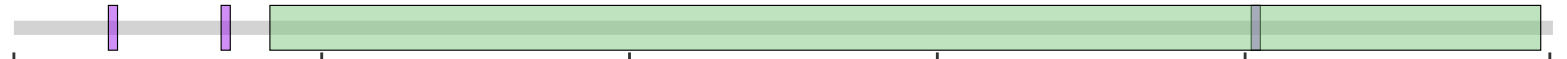


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

QLDLLLSDAASRFQGFNYGFDMLREEVERVKKFAERLEFFDTVHFMDAISGKKHILVEGGQATMLDIDFGTYPFVTS66SPSAGIGCTGLGAPRVGDLVGVVWATTRVSGSFPFTEIMSGKGDLLRFAGDEFFGTTTGRPRRCGWLDIHALRFQGGINGFASLNLTKLDELVDL6DL6SEQLGVTRYRHPDGTLSNFPDRLLEQIKVEYEVMPGWSGDS6SVRKYSDLPKAAREYVERIEELVGPVHHYIGVSPGRDALVYK

NbL09g21360.1 zinc_finger_CCCH_domain-containing_protein_14-like [MW = 30.66 kDa]

No. of times detected



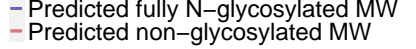
log(intensity)



Values from



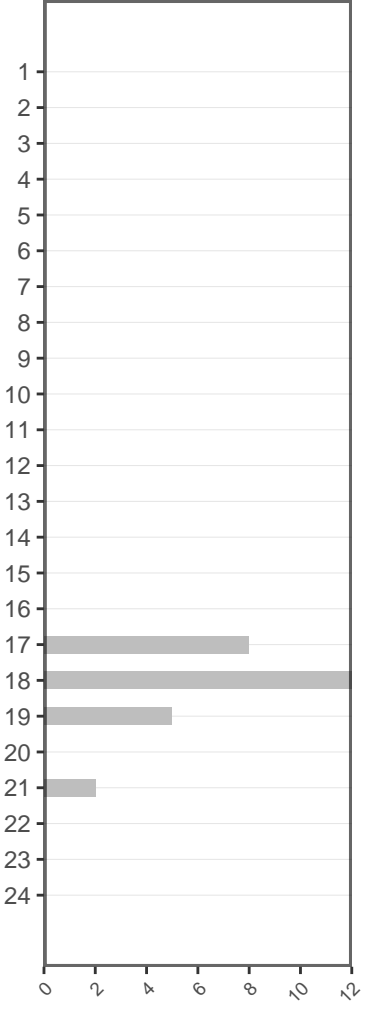
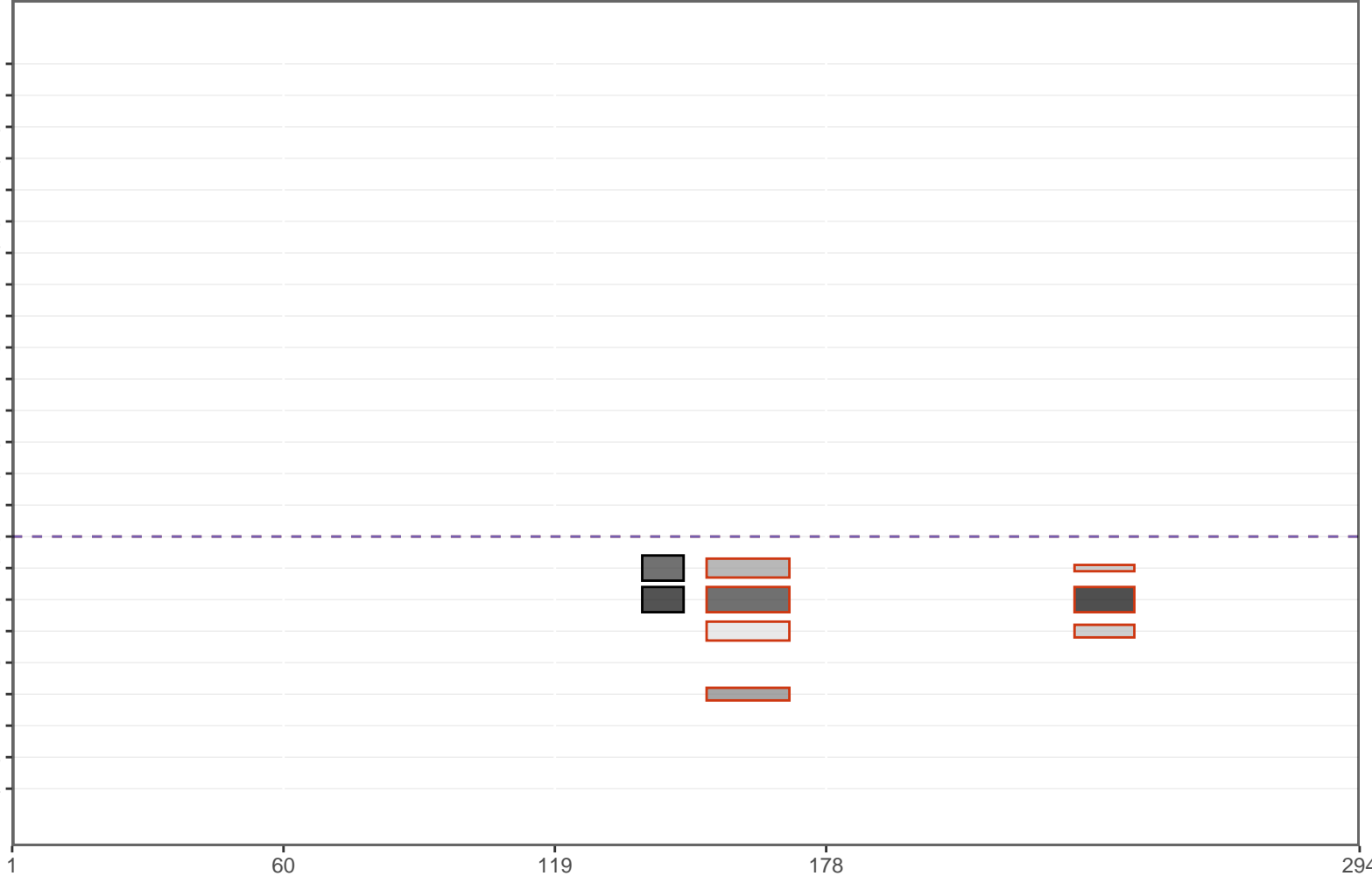
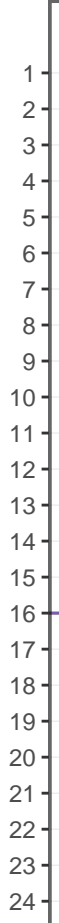
MW indication



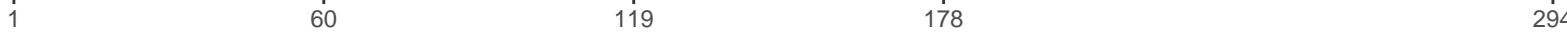
Molecular weight



Gel Slice



Protein length

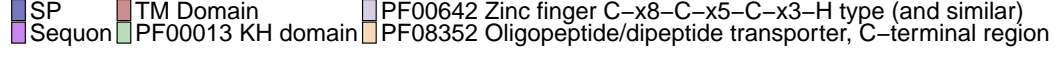


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IQEDPRAMGVGPVGRFRGRIERFWSGGPVAISFGTSATANKIVDSASLAGAIGKGGVHDKKIGRTGAKLAIRDHETDKNLRNLEEGTFEQISQASAMVRELINLGGVGGPGRTRFAPGGAAAPPGSNFKTKLGENFAKSGSCTFGDRGHFAHGAALRKTGV

NbL09g21340.1 probable_plastid-lipid-associated_protein_13_chloroplastic [MW = 35.9 kDa]

No. of times detected



log(intensity)



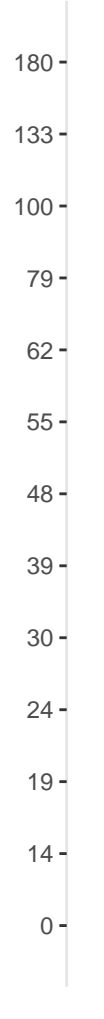
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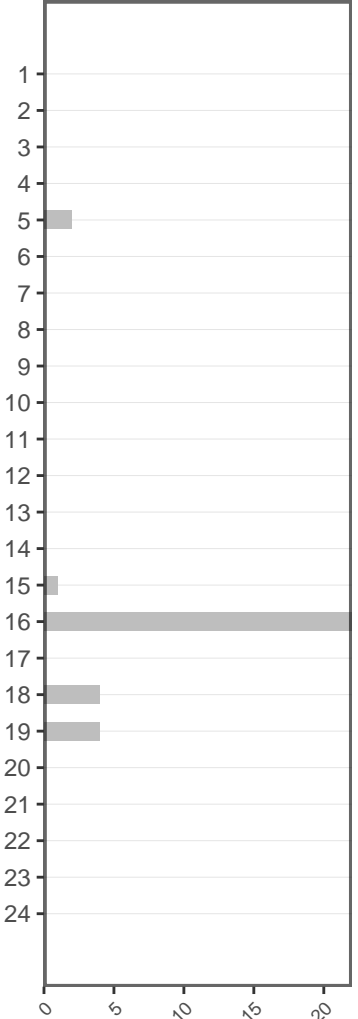
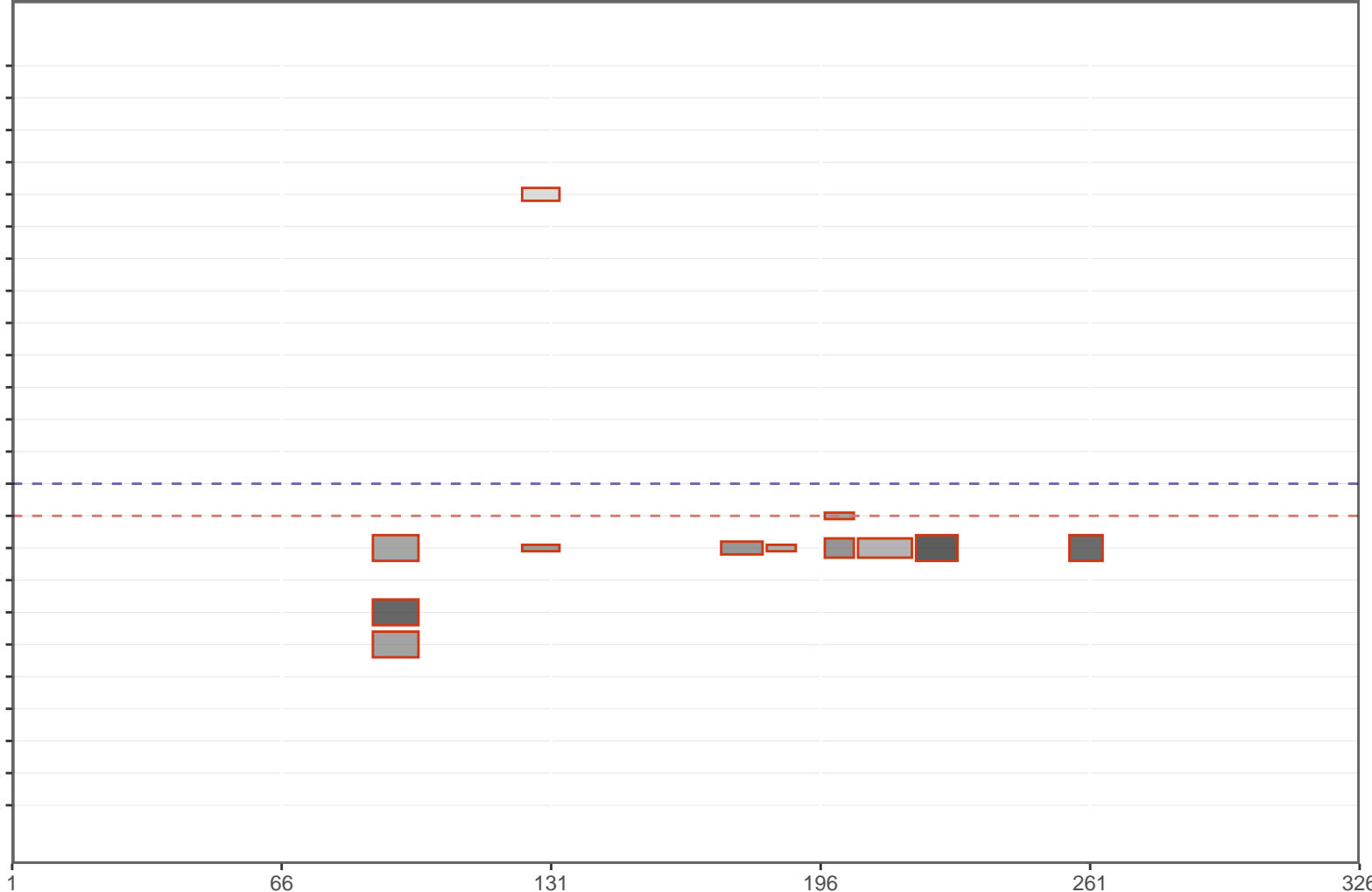
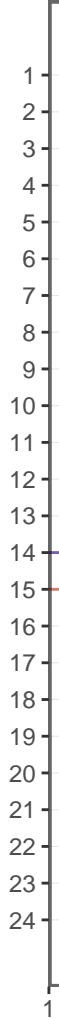
MW indication



Molecular weight

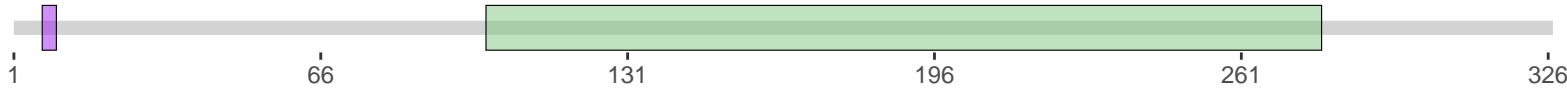


Gel Slice



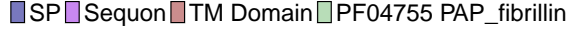
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LATRLLFGRIPPTLALSLKLLLRINYYGTAAHAKLLNSIEKFKVLGSKFVVEGFLRMKEEYEGIFETPKVNEEDTMEPEQLRQALGQAVSTLQGLPVPHKDTVSSGLKPLGFAFRQLRMSEKYLDEELVSPGLVLAQALLKDDGYQTRNIPISGHEGENTFINAKTKPQRLVLLNY

NbL09g21330.1 actin-like [MW = 41.7 kDa]

No. of times detected



log(intensity)



Values from



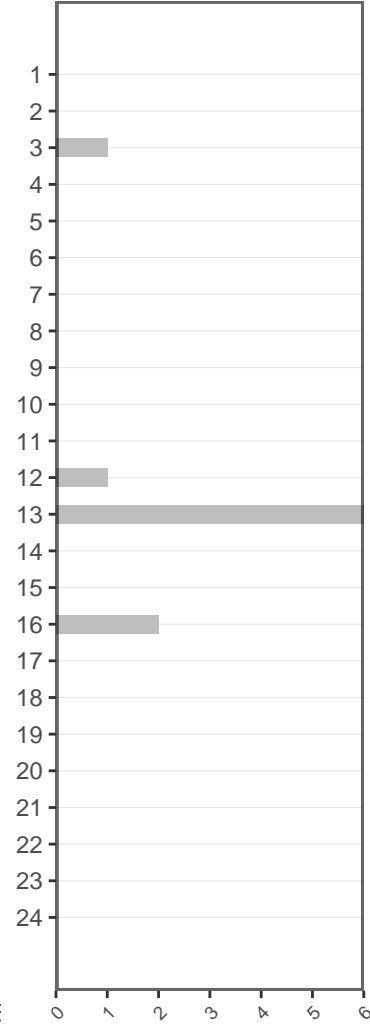
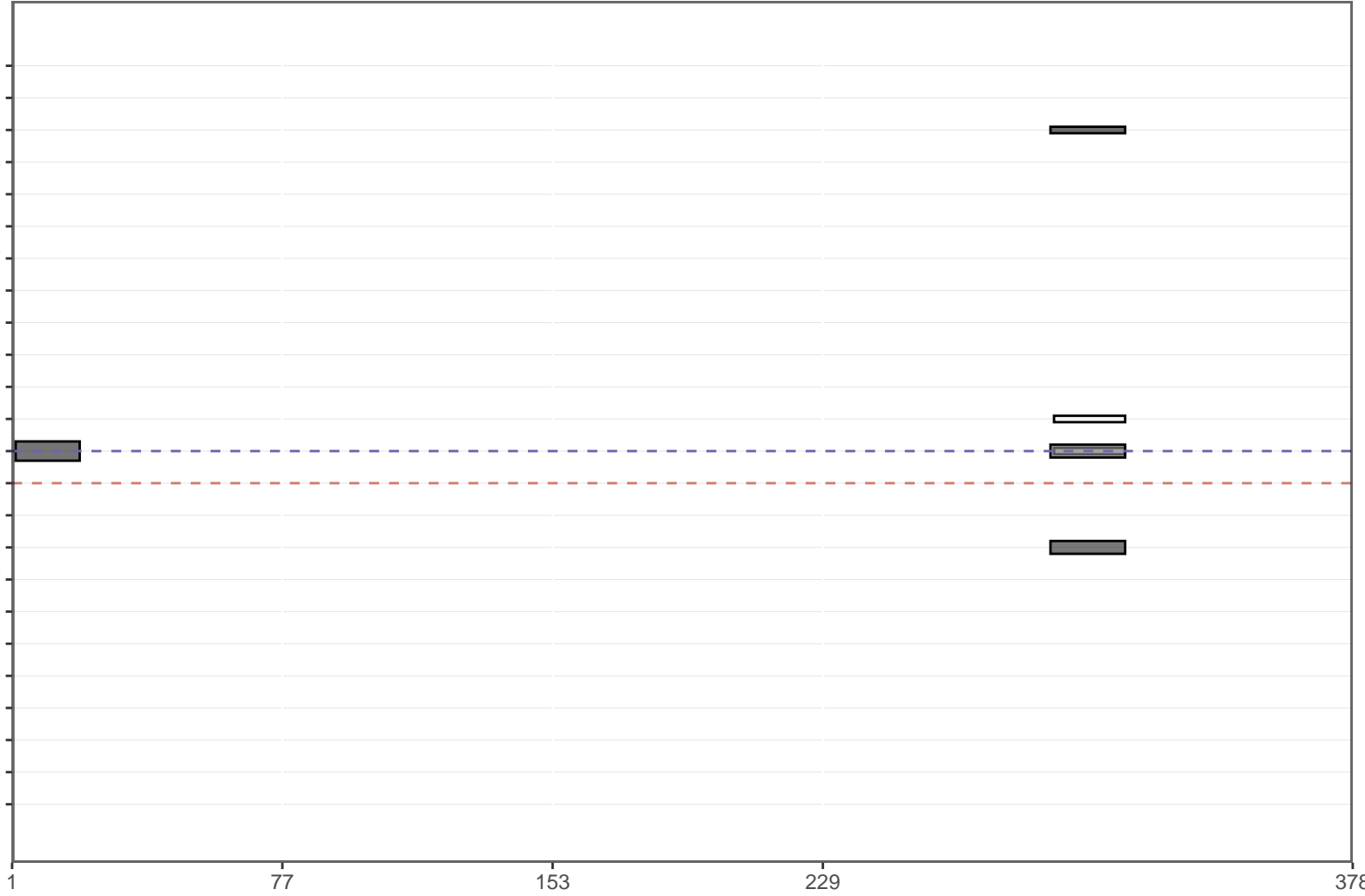
MW indication



Molecular weight

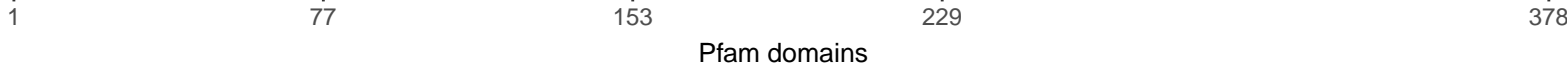


Gel Slice



Protein length

Pfam domains



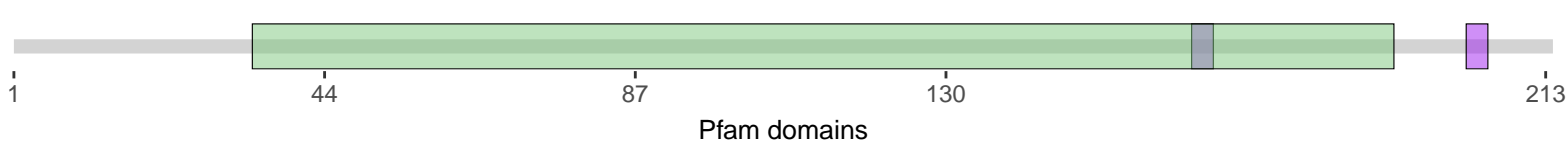
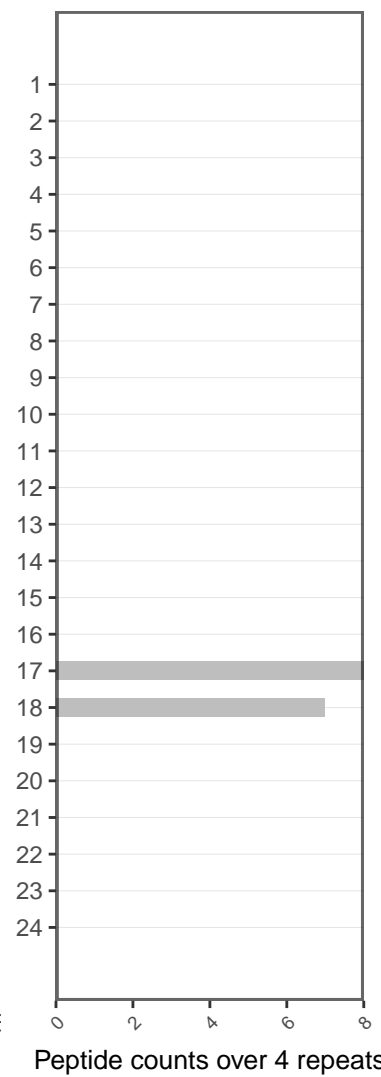
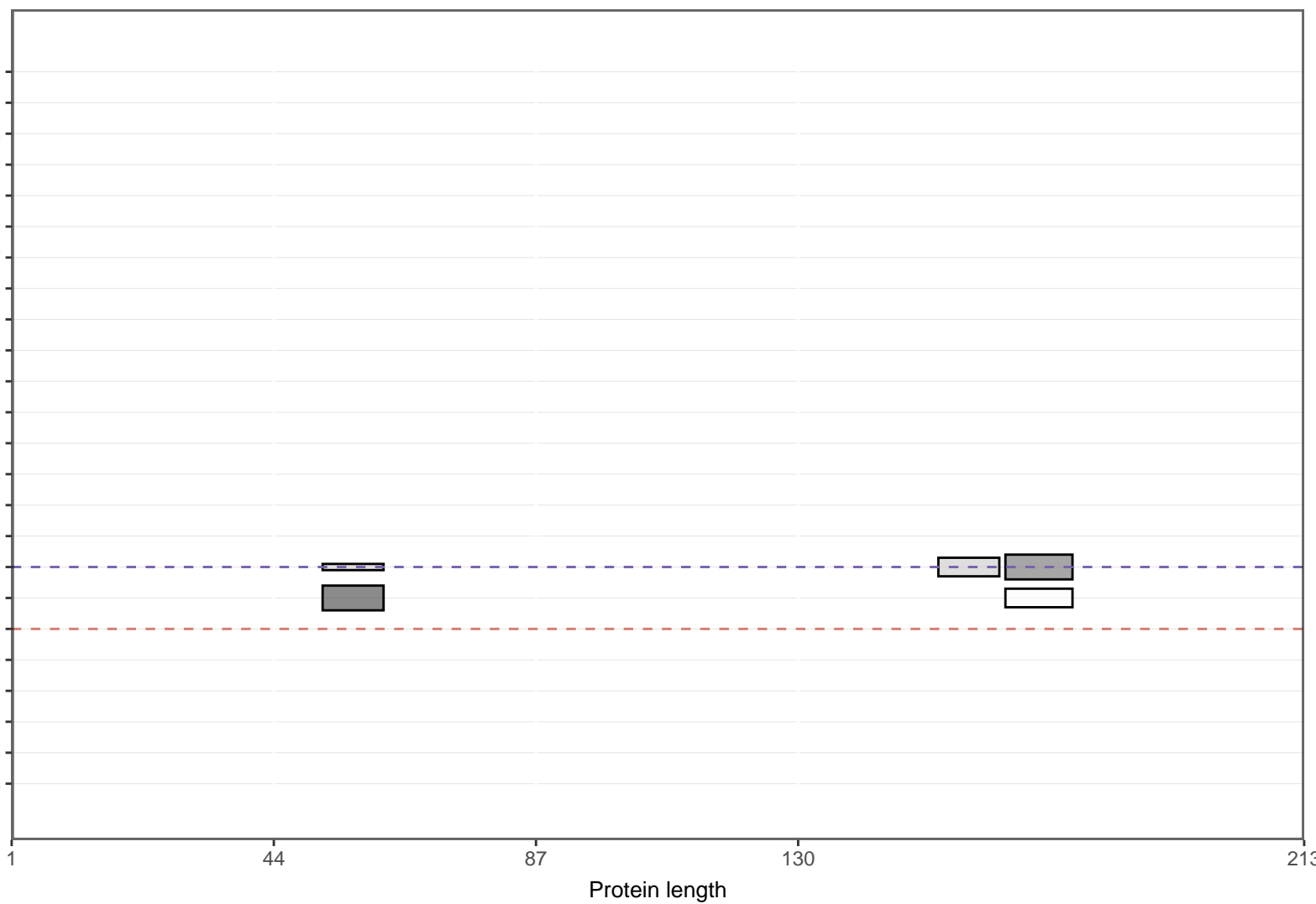
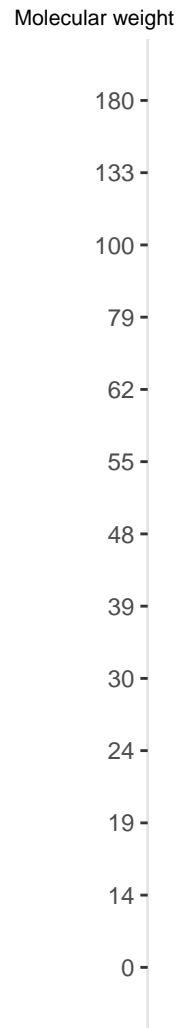
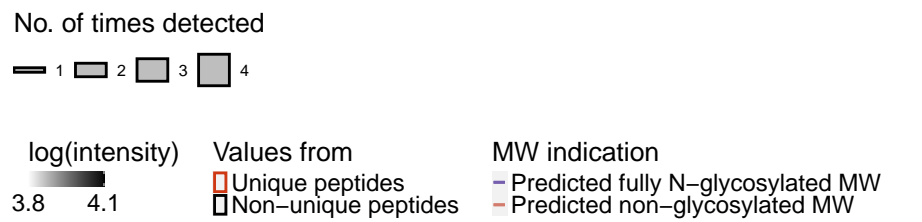
Pfam Description



Protein sequence:

MHAIKRLDLAQRDLSFDHLMKILTERGYSFTTAEIRVIRVDIKELAYALDYEQELETAKTSSSVEKSYELFDGGVITGAERFRCPREVLFPQPMIGMGAAGHETTYNSIMKGDVDIRKDLVGNVLSGGTTFMFGIADRMSKKEITALAPSGMKIKVVAAPERKYSVWIGGSLASLETFDQGMMAKAEYDESGPSVHRKCF

NbL09g21180.1 translation_initiation_factor_NCBP-like [MW = 24.47 kDa]

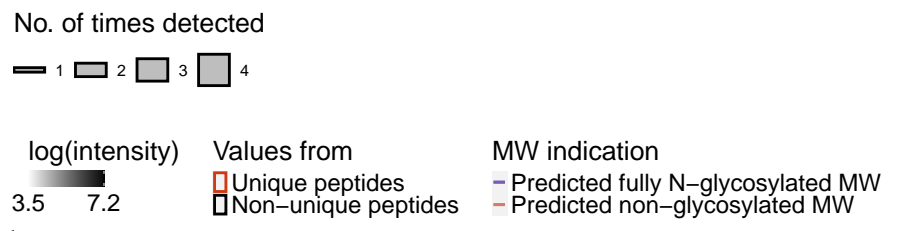


Pfam Description

SP Sequon TM Domain PF01652 Eukaryotic initiation factor 4E

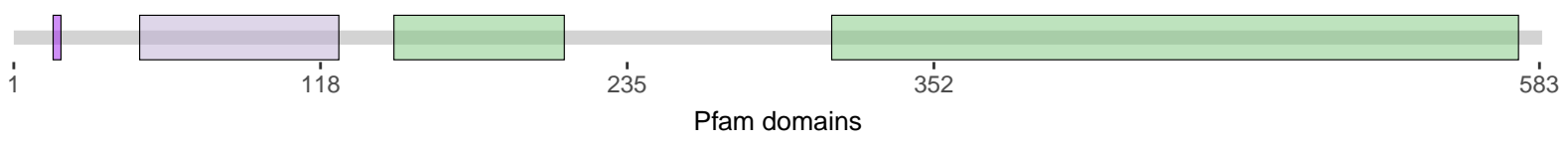
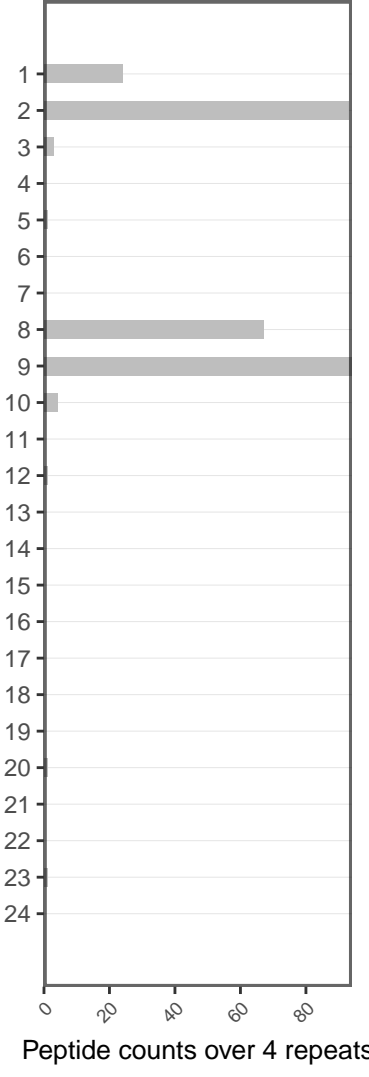
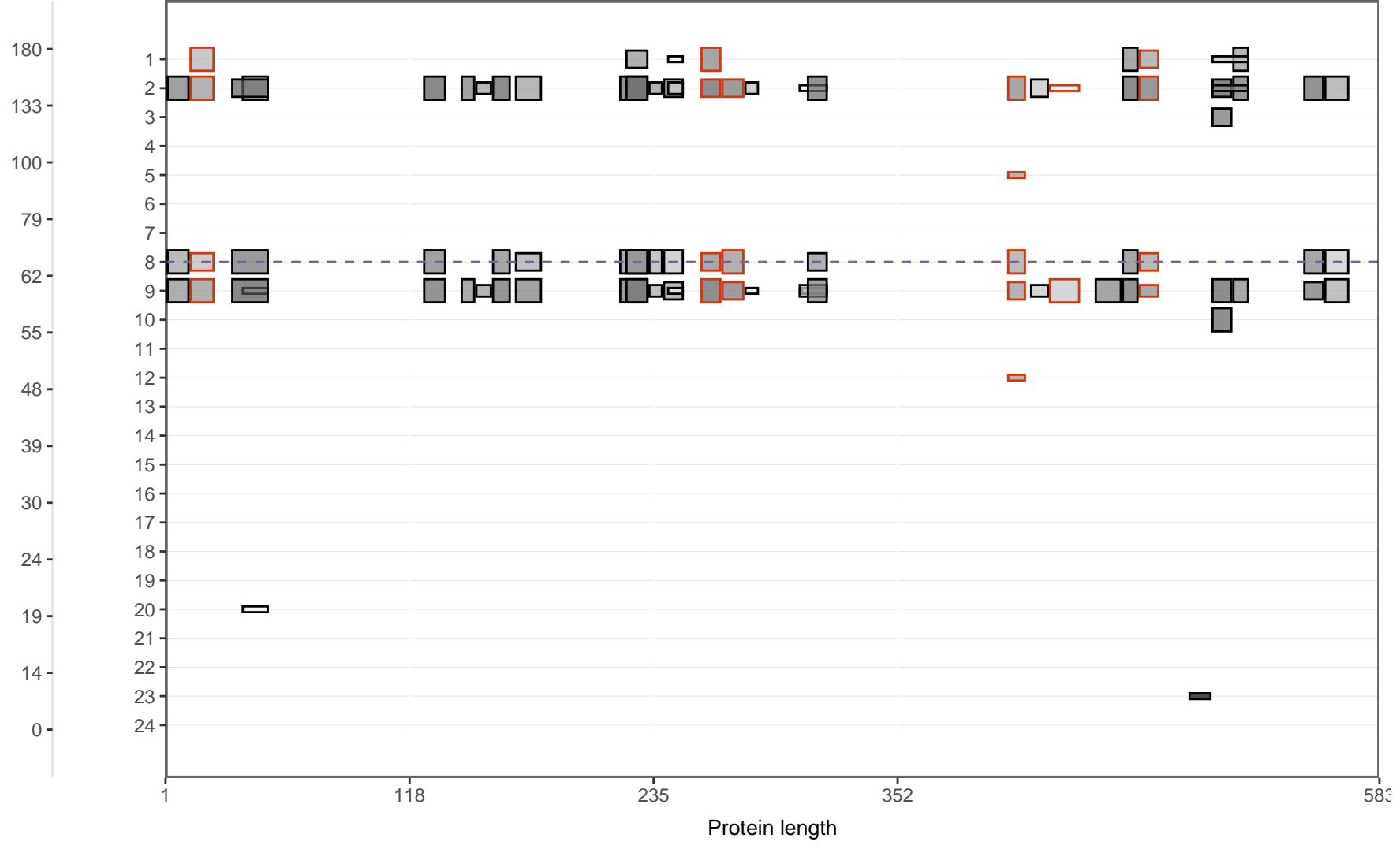
Protein sequence:
 KEGIRPLVEDAANNGSGKWRIRFKKAVSGRFWEDLVLALVGDGLDYGNIGGAVLSIRFNEILSVWNRNASDQAVMALRDAIKRHLKLPNGVYMEYKADASLRNNGSYRNTWRG

NbL09g21110.1 asparagine--tRNA_ligase_cytoplasmic_1-like [MW = 64.92 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00152 tRNA synthetases class II (D, K and N)
- PF01336 OB-fold nucleic acid binding domain

Protein sequence:

 CENLLKLDKFKLGERGLGGPKDKVDYDSEDFARQAFVTVSGGLGVETYAGALSIVYFGPTFRAGQSHSRHLAEFWVVEPEIAFDLGGDMKCAEAVYKFLQWLLDHLGCLDDMEFTKFKDKDLSRLRMVASSNCCYRITYSEAIALVEAAKWKFFENKVEVWGLDASEHERVYTEEHFKAPVIVFNYPKGIKAFYMKVKNEDKKTVAAMDLLVPRVIGELIGSSGREGEDVEVLRTRILEMGLPLEPVEWYLDLRRYGVTKHSGFGLGFERMIFATGIENRDYVPPR

NbL09g21080.1 protein_SMG7-like [MW = 108.07 kDa]

No. of times detected



log(intensity)



Values from



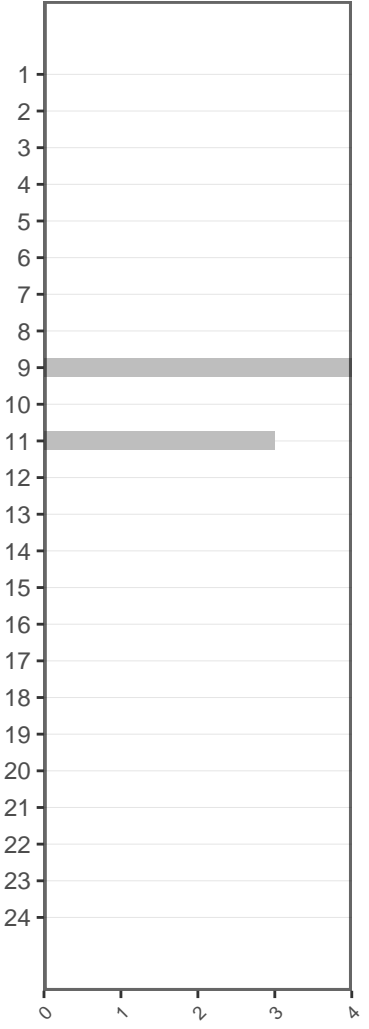
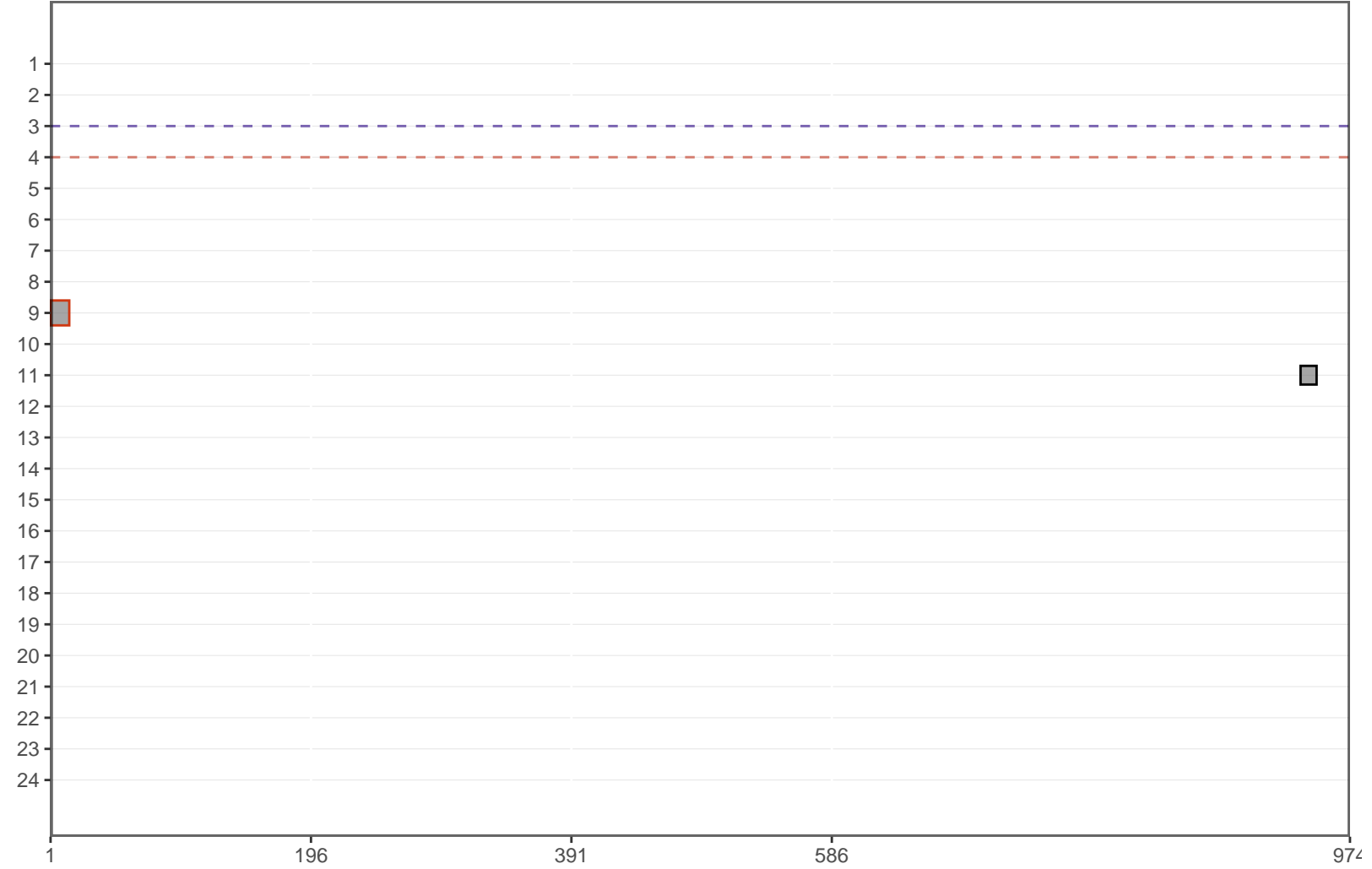
MW indication



Molecular weight



Gel Slice

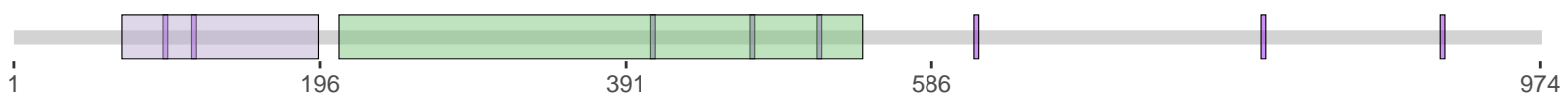


Protein length

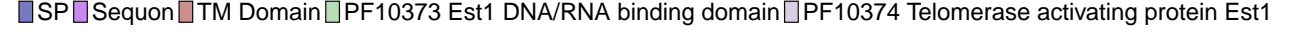


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ARSFYWKNCITFFNLLLATGKFKVDEDEDETCFFNMSRYDESEGNRLALPEDFELRGVPLLPAGLIDFSRKHDFGGDSGNKEKARLQRMIAAGKALANVVRVVEEGGDFDTRGKFKVGLPEQAADDHQLNGSREVAKLSGIELENFDAGLMMVGDLPKQQLVECEEEDEVWFKPVMKVMKNGISSNTLAVPVVVISASVVPGGVMAASINQSEMSPFSSALDGLGLGNWASAVRQRRTSIAHTNTGVVQPIGTSAMMWSVEGDVAMNGLVGLNLIQNRLL

NbL09g20930.1 3-oxoacyl-[acyl-carrier-protein]_reductase_FabG-like [MW = 31.22 kDa]

No. of times detected



log(intensity)



Values from



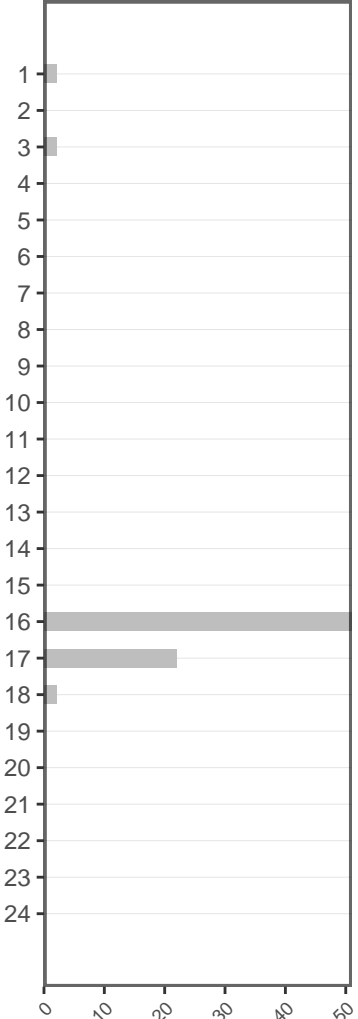
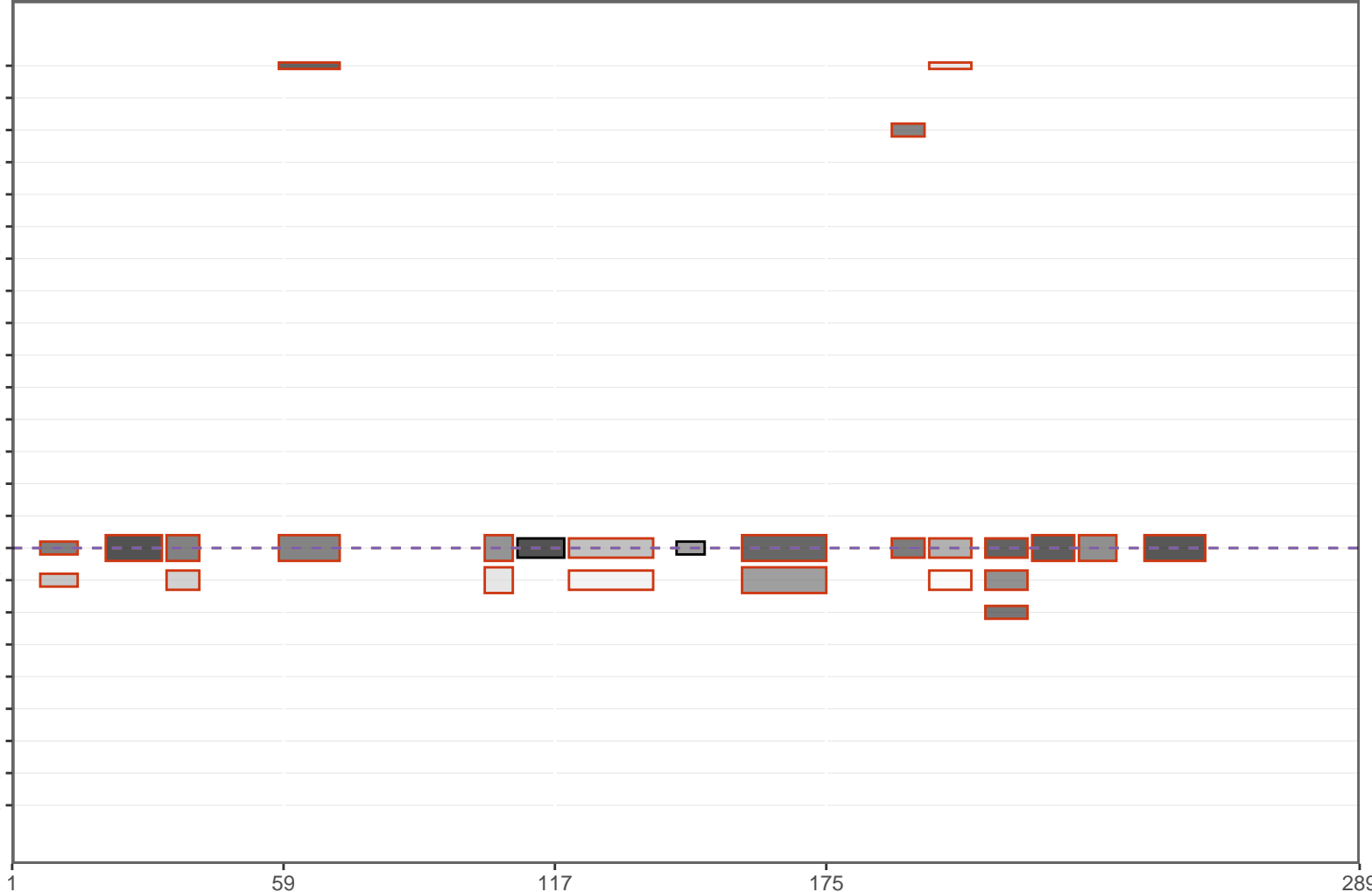
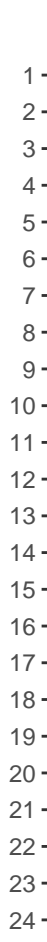
MW indication



Molecular weight



Gel Slice

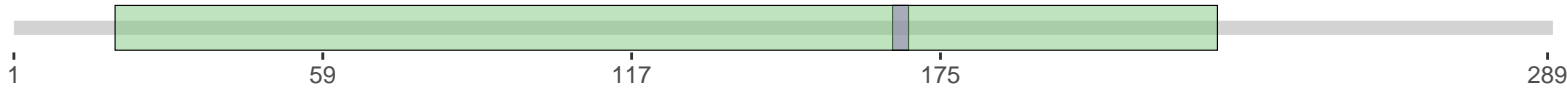


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IEEWDNIYRNLKGAALVSKYVGIIRMDANGGGIVINISSIAGLNRRGGVPSGLAYSSSEKTAINTVMMMAIEELGPKYKRVNSISPLFRSEITEGLMGKDWLPNIALRTPLRTHGTSDPALTSEVRRVLIHDSSEYVSGNIFVEAGATLPGVPIFSSLI

NbL09g20870.1 tubulin_beta-1_chain [MW = 50.19 kDa]

No. of times detected



log(intensity)



Values from



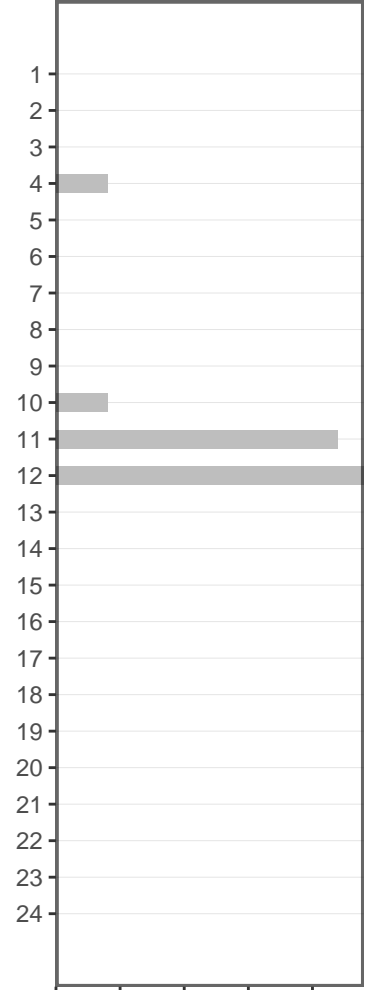
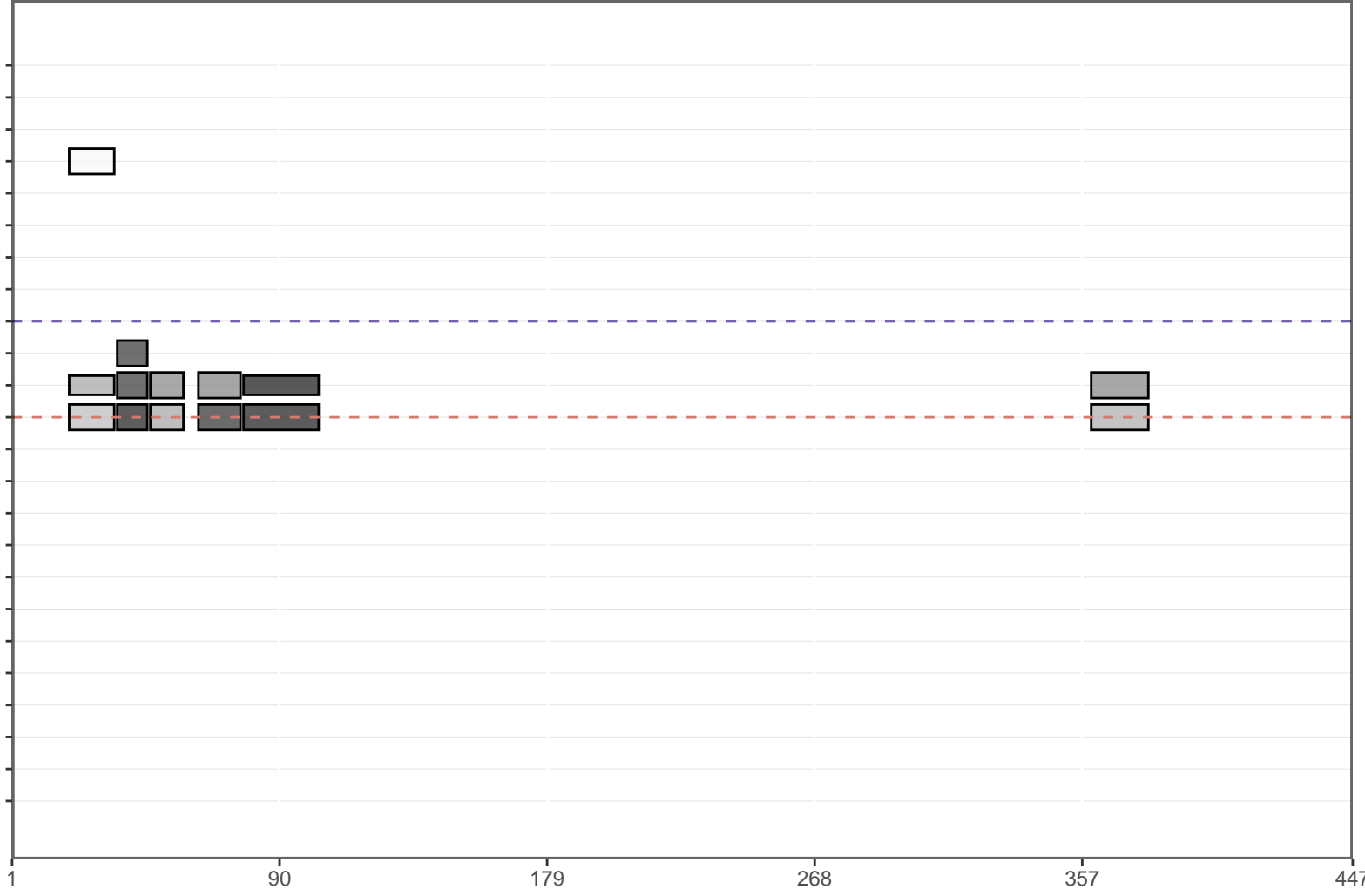
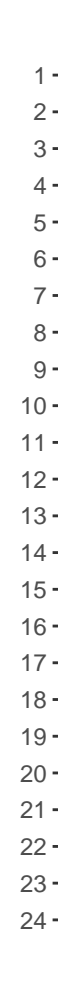
MW indication



Molecular weight



Gel Slice



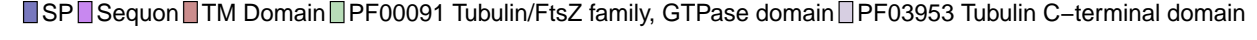
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CFRTLKLTPSFGDLNHLISATMSGVTCGLRFFRGLNSDLRKLAVNLPFRLLHFFMVGFAFLFRGGQYRALTVPETLQGMVDKNNMCAADPRHGRVLTASAMFRGKMSKEVDEGMINVGNKNSVFEVWIPNNKSSVGDIPPRGLSMASTFRIGNSTSIQEMFRRVSEGFAMFRKKAFLHWYTGEGDMEMETFAEAGNMNDLVEYQQYGDATADDEGEVEEYEDHEGN

NbL09g20840.1 bifunctional_protein_Fold_2-like [MW = 32.2 kDa]

No. of times detected



log(intensity)



Values from



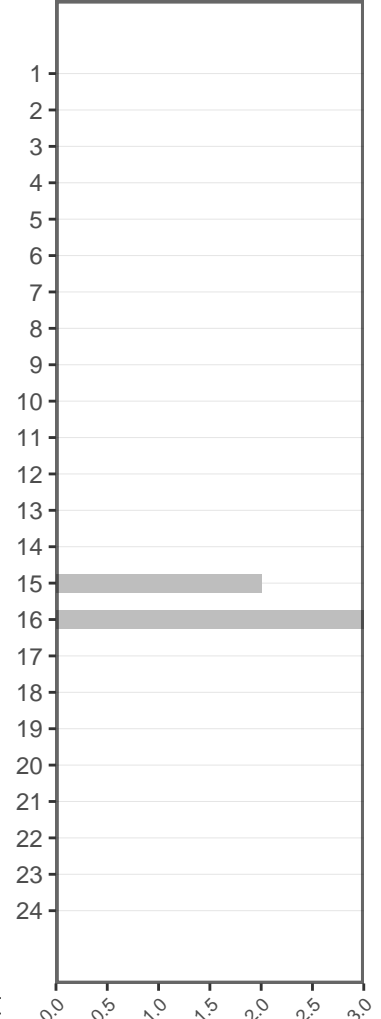
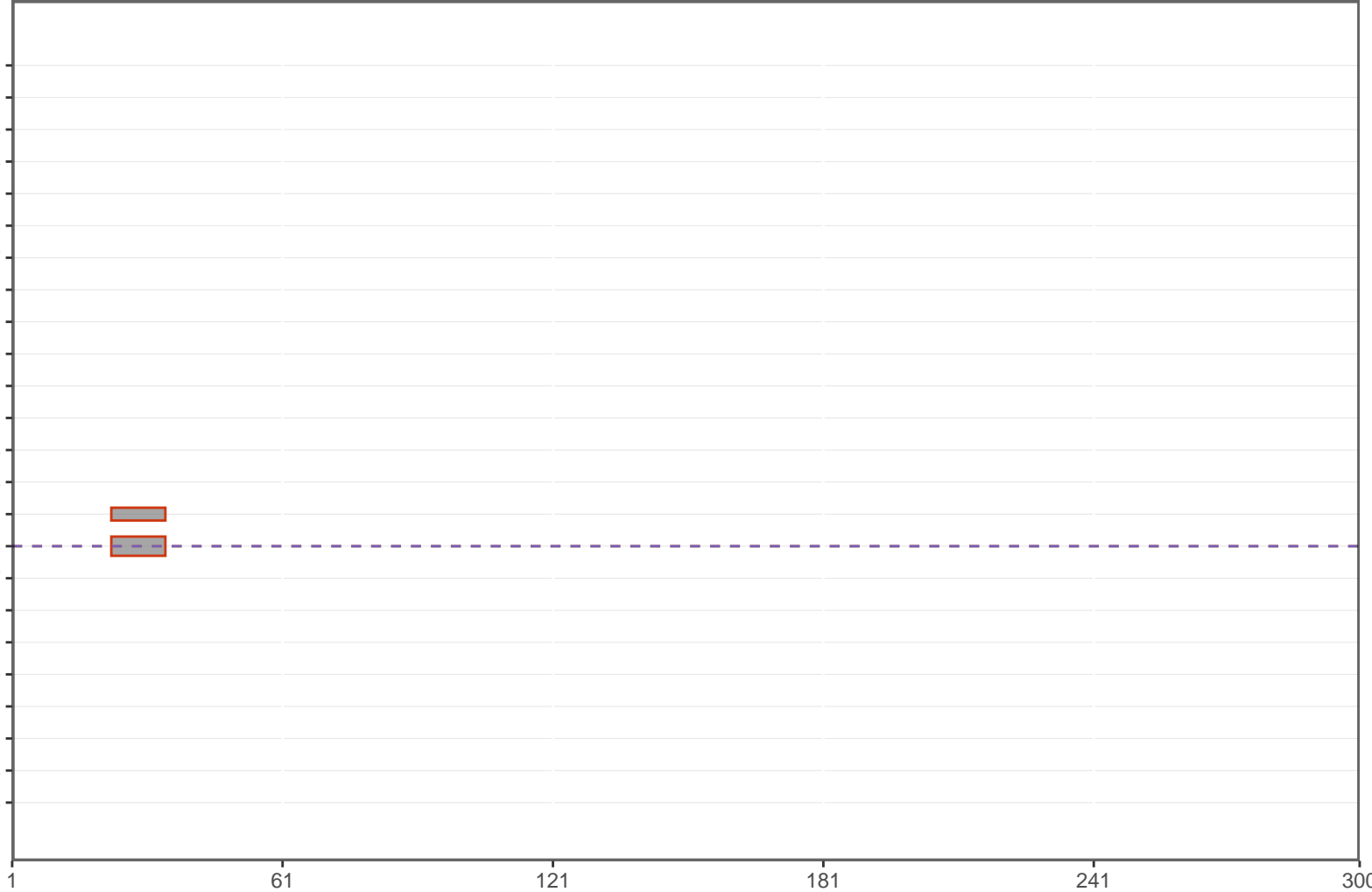
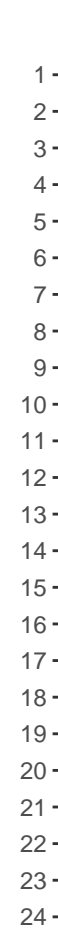
MW indication



Molecular weight



Gel Slice

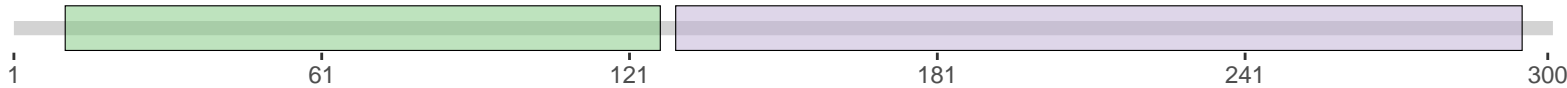


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

- SP Sequon
- TM Domain
- PF00763 Tetrahydrofolate dehydrogenase/cyclohydrolase, catalytic domain
- PF02882 Tetrahydrofolate dehydrogenase/cyclohydrolase, NAD(P)-binding domain

Protein sequence:

AMKGRPLFLPCTPKGIELLHRGSGIKGNAAVGRSNIVLPLVLLLLKEDATVTHSRTRKEPEKIVREADIIAAGDAMMKGSWKPGAAIDVGTNAVDPTRKSGYRLVGDVNFGEAGKAGWTFVPGGVGFMFVAMLLKNTLDGAKRVEK

NbL09g20780.1 transcription_elongation_factor_SPT6 [MW = 186.02 kDa]

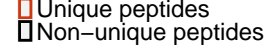
No. of times detected



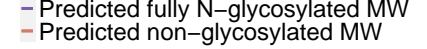
log(intensity)



Values from



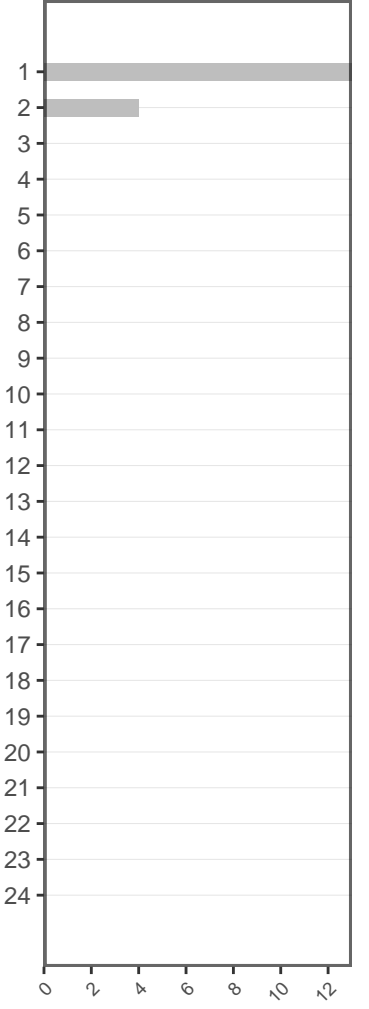
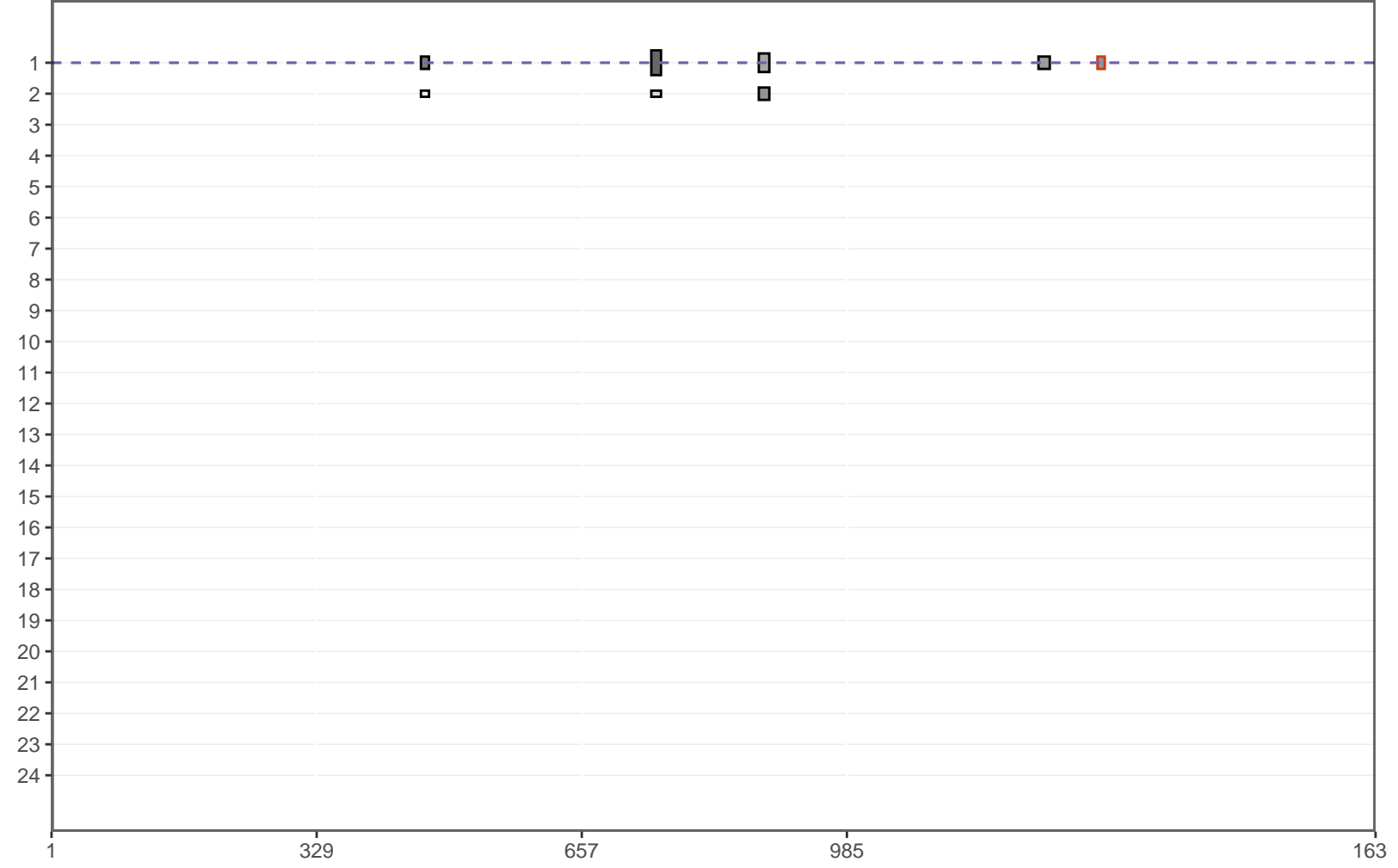
MW indication



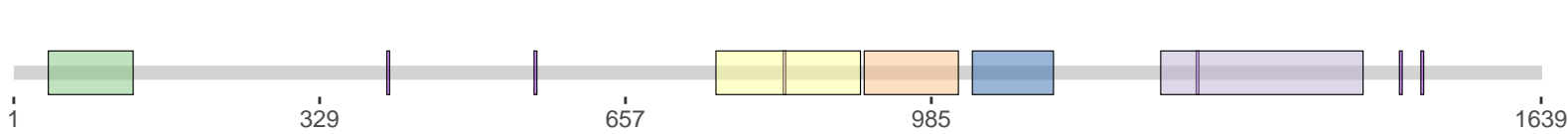
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

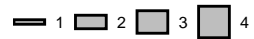


Protein sequence:

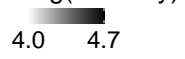
LLKFMMDHDPHYVWLGAVNLGSTRLKEDEYEIFKMWEDNPRDVGHEMDNLNIFYGDETLPLHYENSRISVDQLPGDGGVRRRAVALGRYLQNLPLAMWATLGGPGREILSWKLGSTLDLFLTPQEKYGMVEQVMAVDVINGVGVDLNLAISHEWLFAPLGFISGLGPRKAAASLQRSLSVROGTFTRKDLTEHRLGKVVFNVAVGFRLVRRSGYTSNSTYIDLGDTRHPESYGLAGELAKDIYLVNDIGEENDDDELLEMAIEHVREKPHLARLLKVPVNAKAKRQDKEETLND

NbL09g20770.1 nascent_polypeptide-associated_complex_subunit_alpha-like_protein [MW = 21.92 kDa]

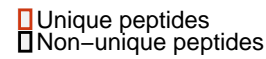
No. of times detected



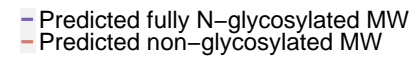
log(intensity)



Values from



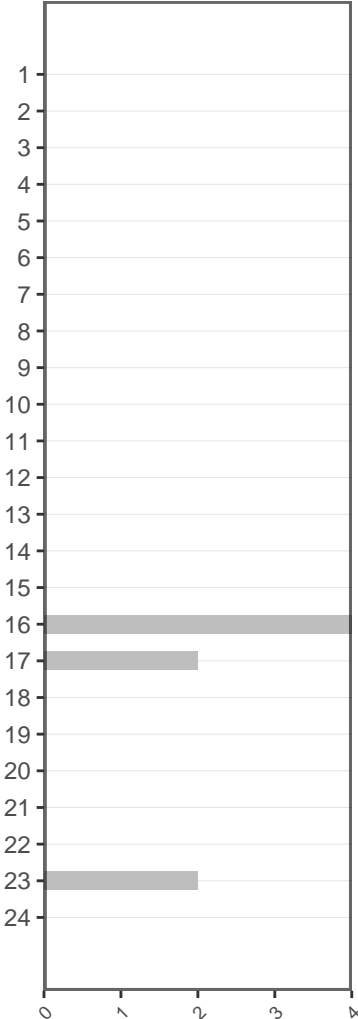
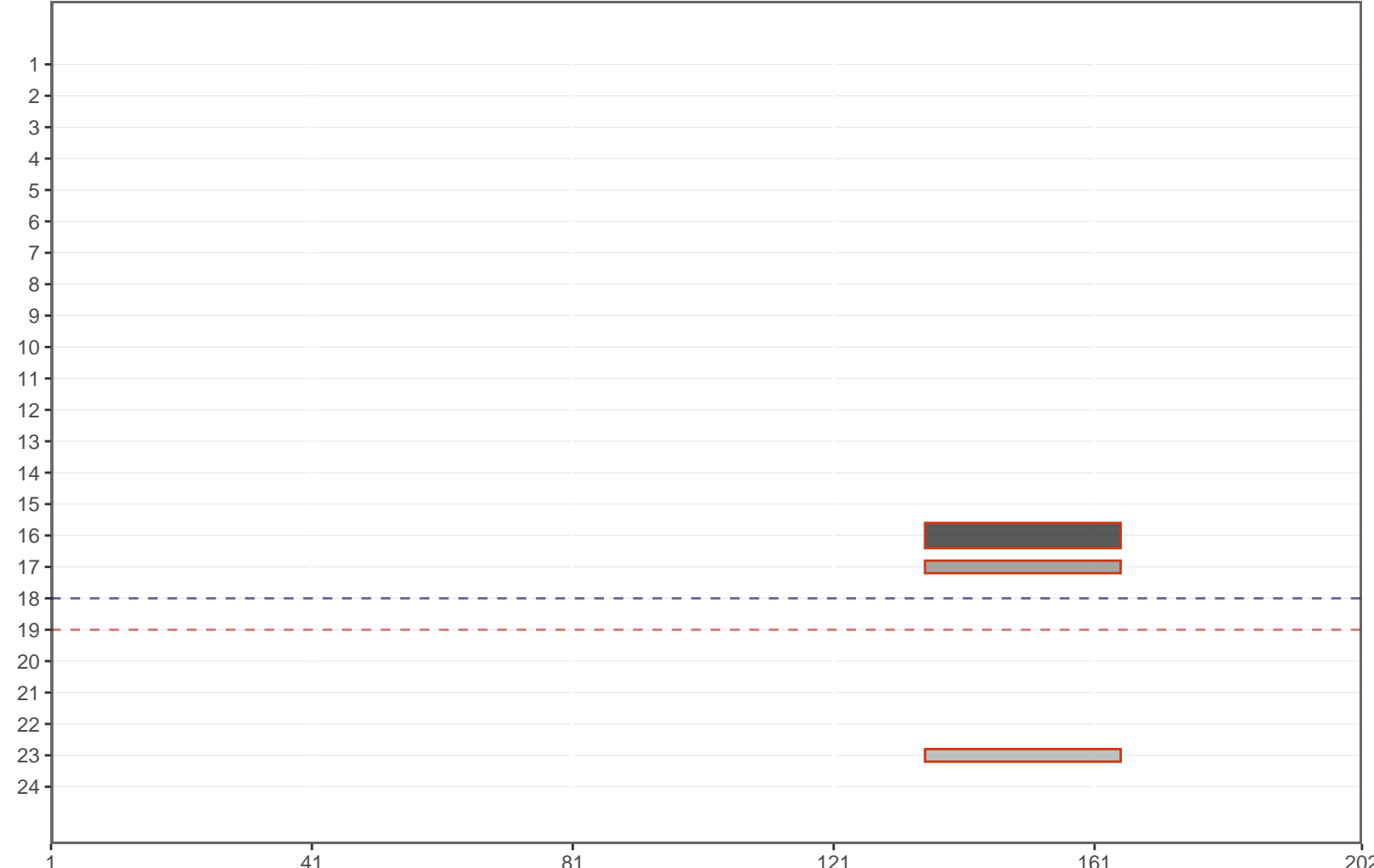
MW indication



Molecular weight



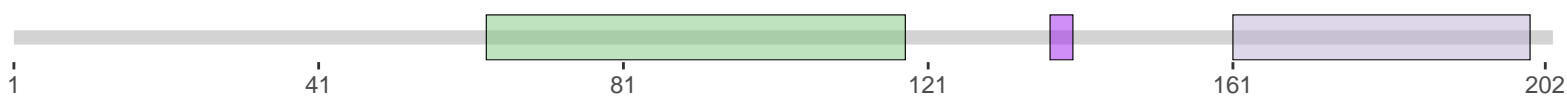
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

AKSKNLFVSKPDKVFKSPNSDTHVIFGEANIEDLSGLGTQAAEQFKAPLNSNVISKPEPSTVAGDDDEDVDDTGVEPKDIELMTGAGVSRKAKVAKAAADGDNASIMELTN

NbL09g20720.1 alpha-L-arabinofuranosidase_1-like [MW - SP = 70.83 kDa]

No. of times detected



log(intensity)



Values from



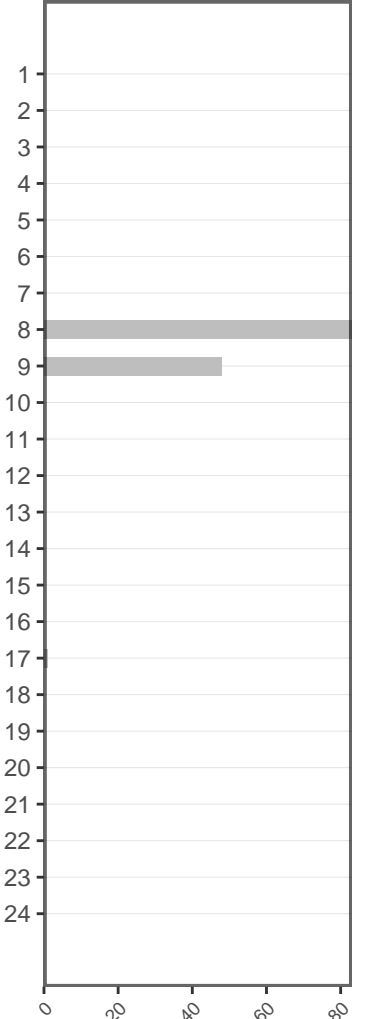
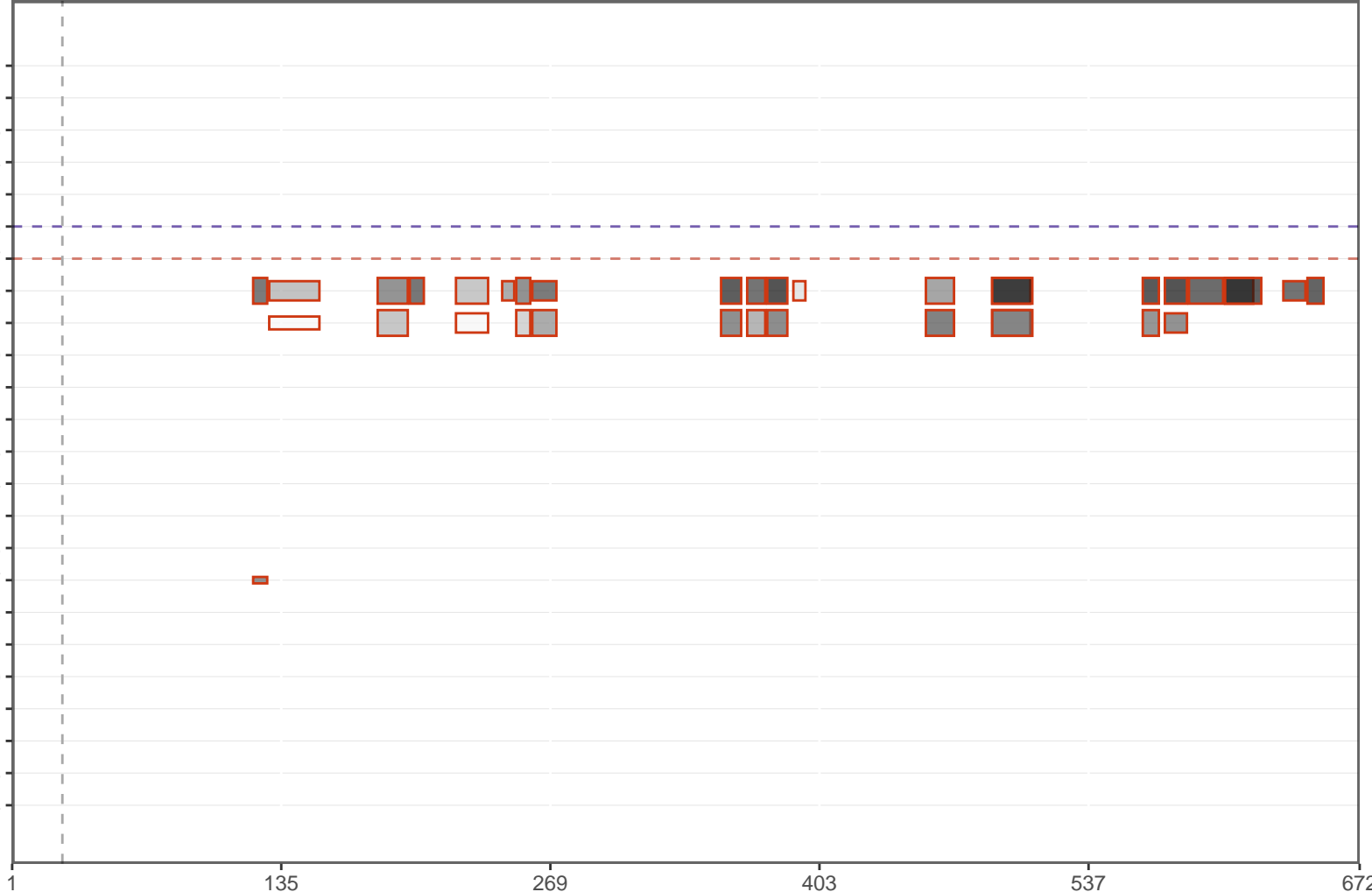
MW indication



Molecular weight



Gel Slice



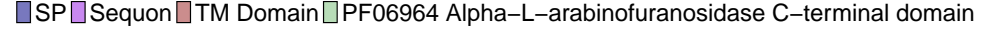
Protein length

Peptide counts over 4 repeats

Pfam domains



Pfam Description

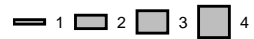


Protein sequence:

VFVNGVSHIDEVDTSAILPFVGEIDGLDFARGDPTSTWGEVRAKMGHPPEFDLKYAIGNECCGKSKYRGNLYKFSYSAKDVPDIRISGDCGSSPLDHPADLVDFHYVSSASVFSNARHFDRTRRGFKAFISEVAVTQNDGKGSLLAALAEAGFLIGVKEKSEAEIEMASVAPLFDVNDNRIRWNPDAIVFTS6QMYGTPSYVMGHFFKESNGATLLS6SLGANPNSLAEAITWRNSVNEVYLRKIVWFQGTAVTLKIGISGLDQNSLES66SAIKTLLTSTNVMDEN

NbL09g20710.1 proteasome_subunit_alpha_type-3-like [MW = 27.2 kDa]

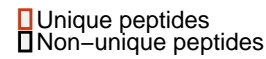
No. of times detected



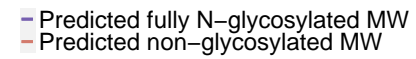
log(intensity)



Values from



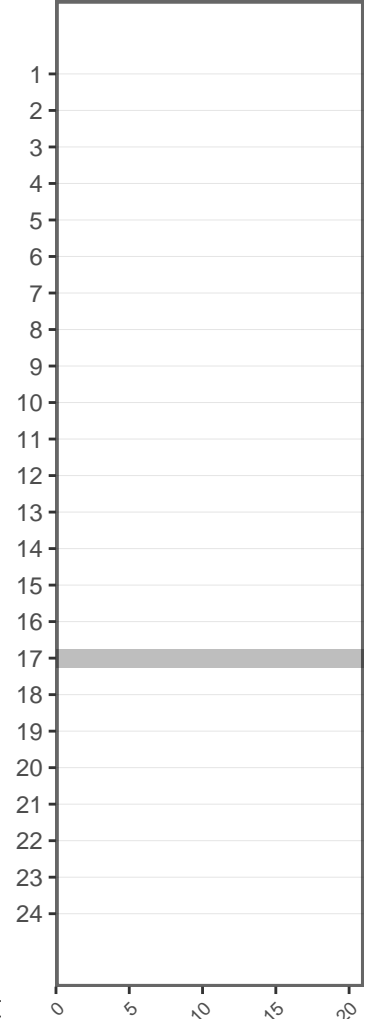
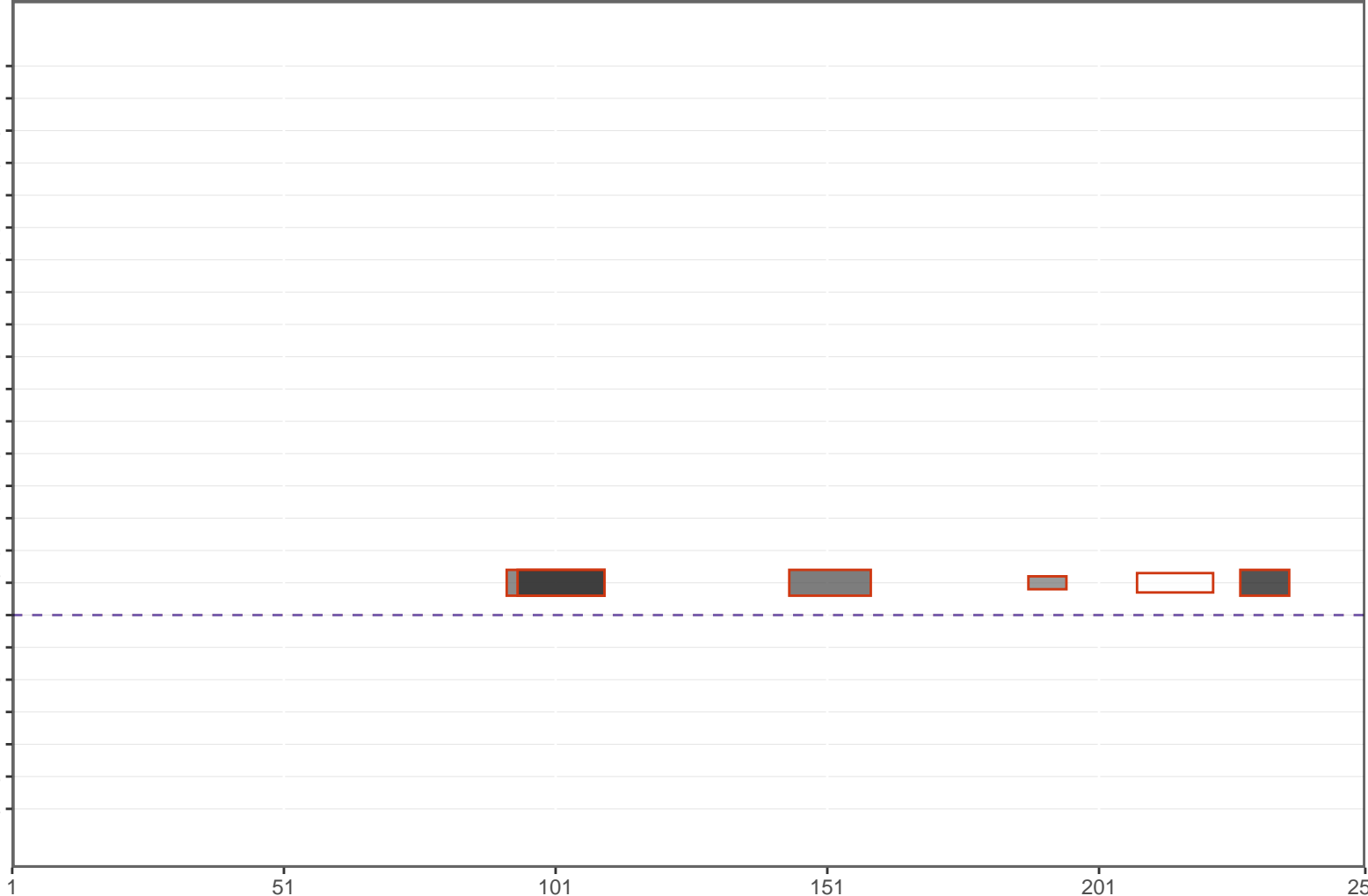
MW indication



Molecular weight

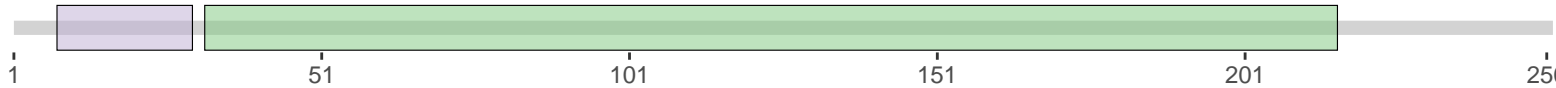


Gel Slice



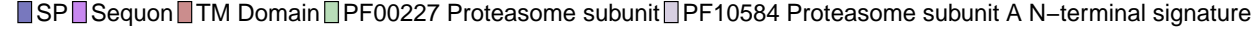
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LERVASYHLCITYWLLRPFGGVGGVYDRDGPQLMVEFSGVYRFRFGAANGKGRQAAKTEIEKLLKLSMTGRGGVIEAKIRYGVHDEAKDKAFLEMSVWGDSENRGHQKVPDLLEAAKAAKAALEEMDAD

NbL09g20660.1 calmodulin-7 [MW = 16.83 kDa]

No. of times detected



log(intensity)



Values from



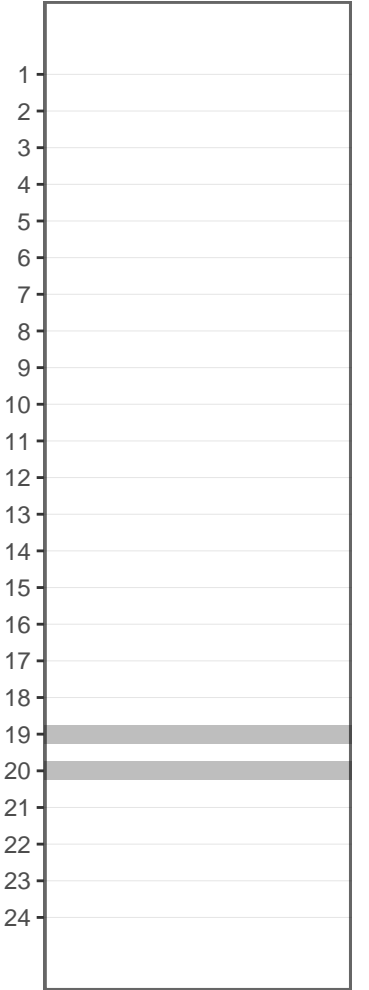
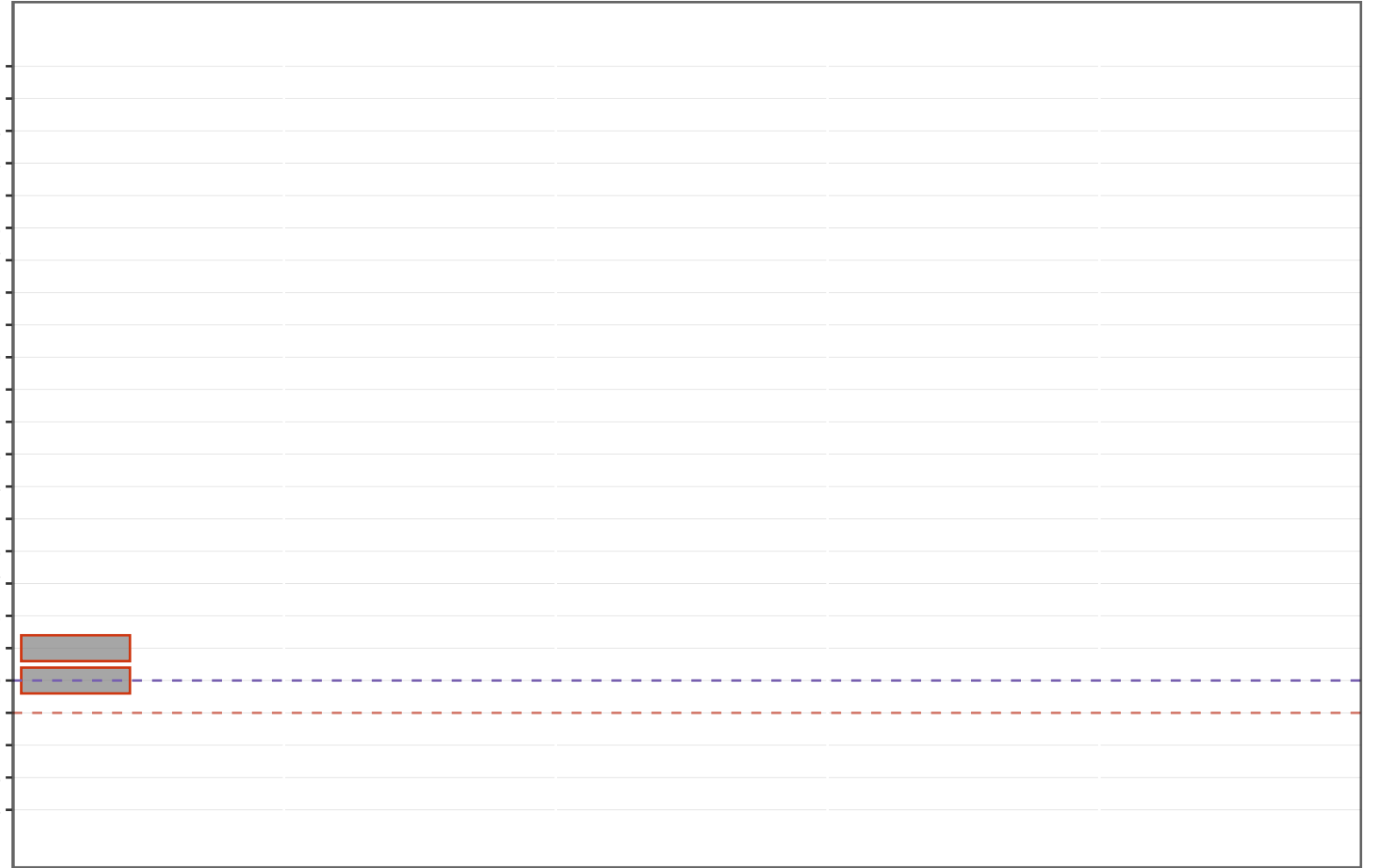
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



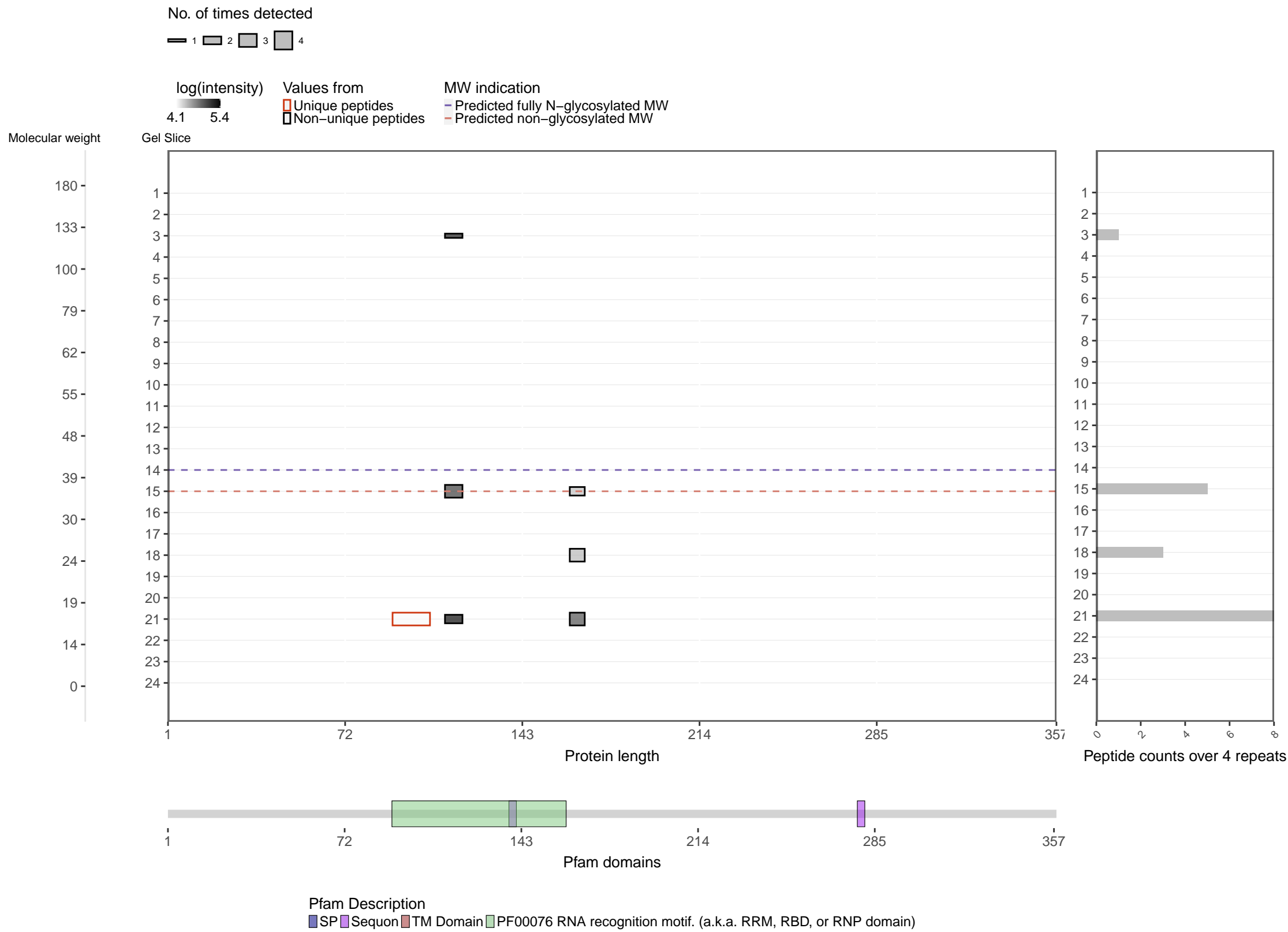
Pfam Description



Protein sequence:

GTIDFPEFLNLMARKMKDTSSEELKEAFRRVFDKDKNGFISAAELRHVMTNLGEKLTDEEVDMEIRADVDGDDGQINYEFFKVMMAK

NbL09g20650.1 glycine-rich_RNA-binding_protein_2_mitochondrial-like [MW = 35.79 kDa]



Protein sequence:

5GGGGGFGAGGAGGGGNYGAGGAGGGGNYGAGGAGGGGNYGTGGYGGGGNYGAGGAGGGGNYGAGGAGGGGDDAVAGSYGANNYGSGESSFGFTSGGNFFSGDNDTGENQNLGAAAAGSGDVTGTGEAASNSAFSGFGNDQFNVDTSNGAETGDAVNSPVDAGEDFRDQVVEGGDVAARRA*

NbL09g20620.1 protein_GrpE-like [MW = 42.71 kDa]

No. of times detected



log(intensity)



Values from



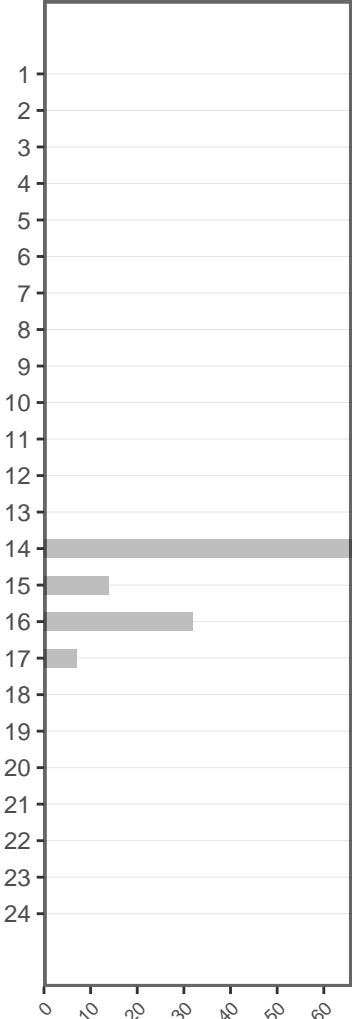
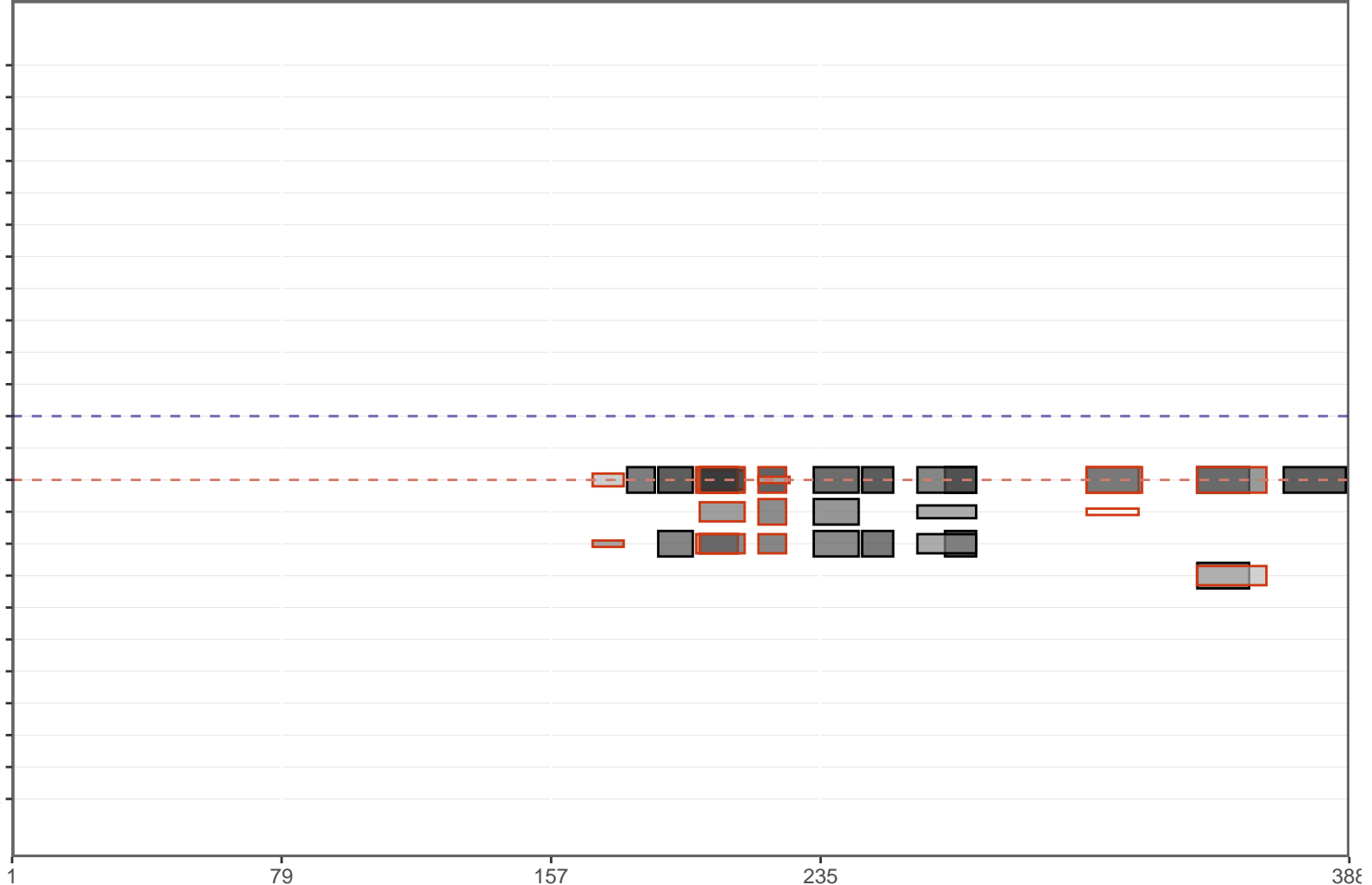
MW indication



Molecular weight

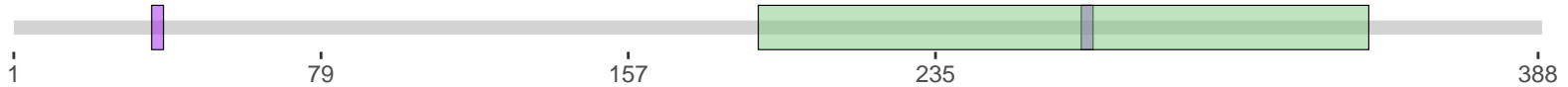


Gel Slice



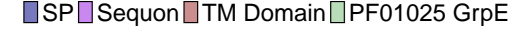
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEISLKSIEKIELGRRVASTLEELNERDLVLRVSDFDNFRRKRTERRERLGLVTNAGGSEVVEKLLGLVDNFRANMQIKVATGEKININSEVQSSIKGFEILGSLGVETVETVYKGFDFLLHEAIMREDSSEEFEGVLLVEYRKGPKLGDRLLRPSMKVVSAGPQPKPETAEPKEEQNKVQENKSEEGTAETAGDEGTGEGGN

NbL09g20510.1 14_kDa_zinc-binding_protein [MW = 17.62 kDa]

No. of times detected



log(intensity)



Values from



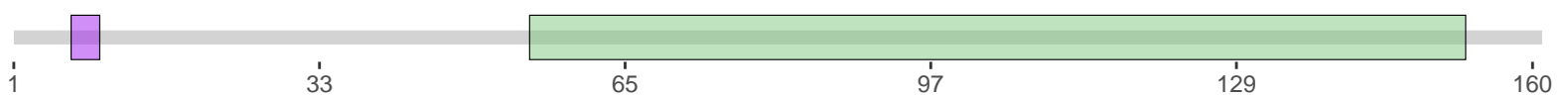
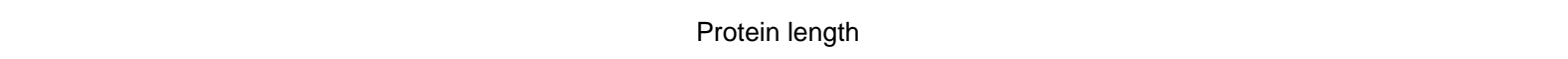
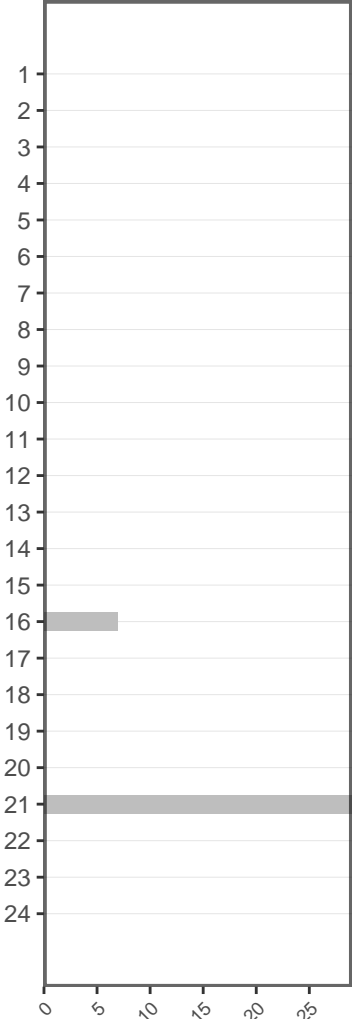
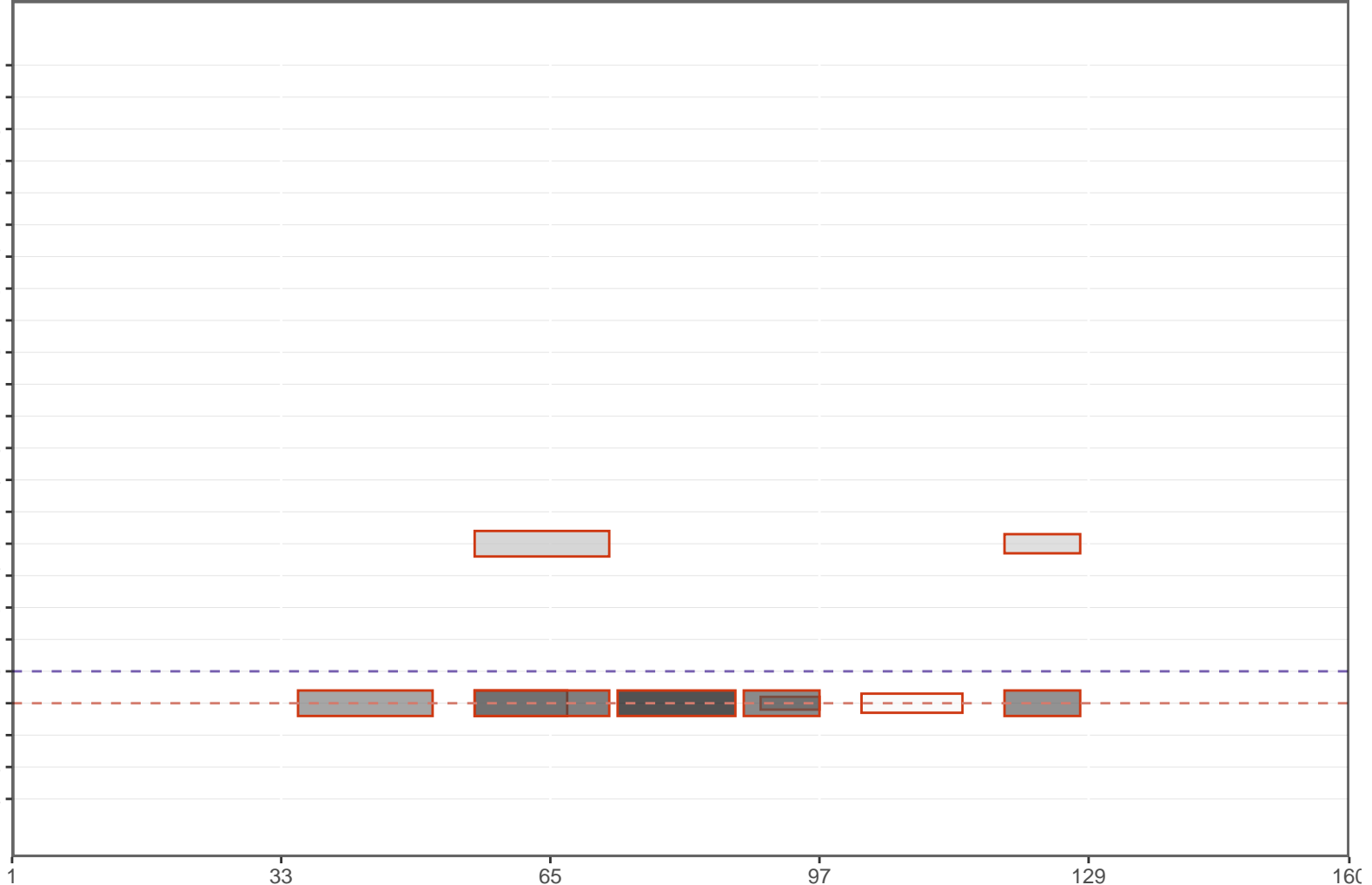
MW indication



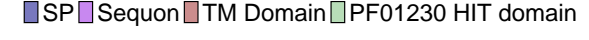
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

VLAFRDINPOAPVYHLLIPKVRDGLTGLSKAEKHCEILGQLLYTAKLVAKGEGLLENGFRLVNDGFSGGGVYHLLHLLGGQRMWPPG

NbL09g20450.1 secoisolariciresinol_dehydrogenase-like [MW = 29.45 kDa]

No. of times detected



log(intensity)



Values from



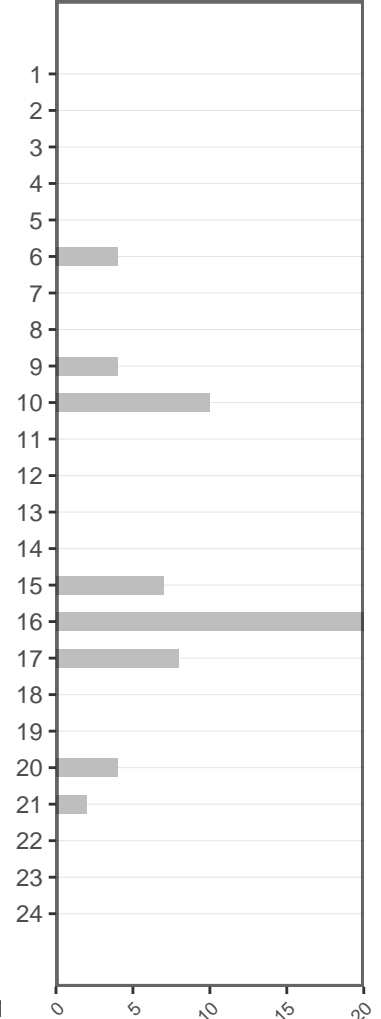
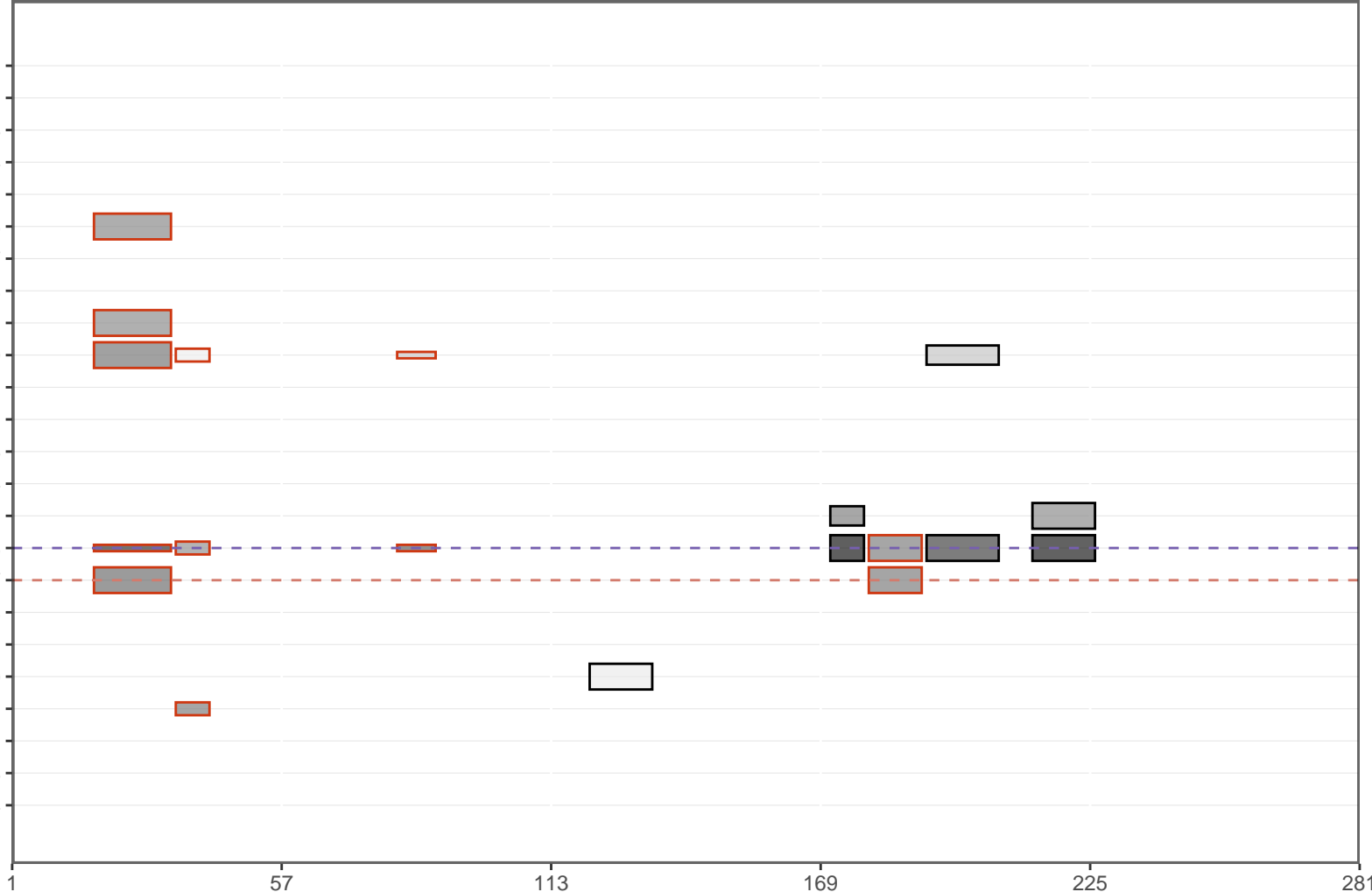
MW indication



Molecular weight

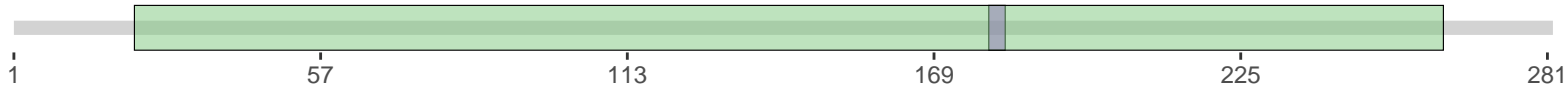


Gel Slice



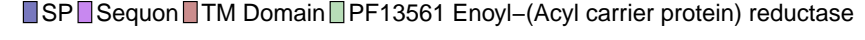
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGSFLGAKYARVIMPAKKGWILFTSSAAVNAAGEAPHHSYTVGKHAVVGLTKNLGAELEGGYGRVNGVSPCAWATPLLVKAMGDKSVVDGIGSSANLKGAVPTAEDAEAAALASDESKFYVGLNLVIDGGYSTNGAVMKTIQGVLFSSV

NbL09g20210.1 sucrose-phosphatase_2-like [MW = 47.99 kDa]

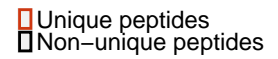
No. of times detected



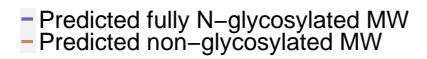
log(intensity)



Values from



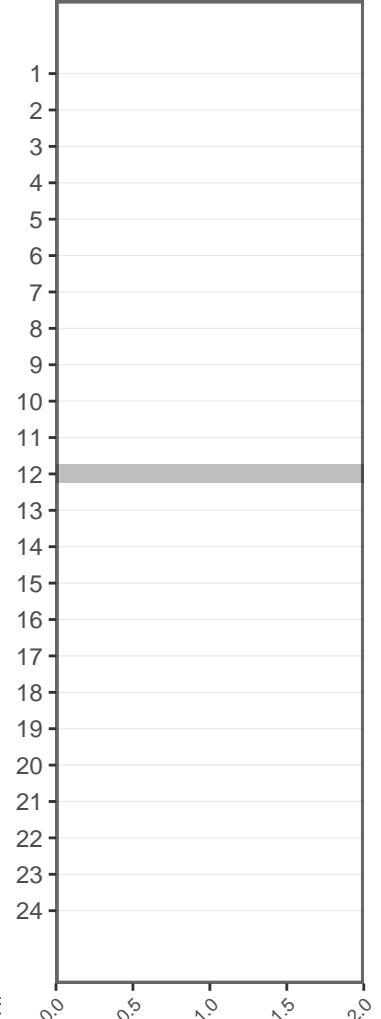
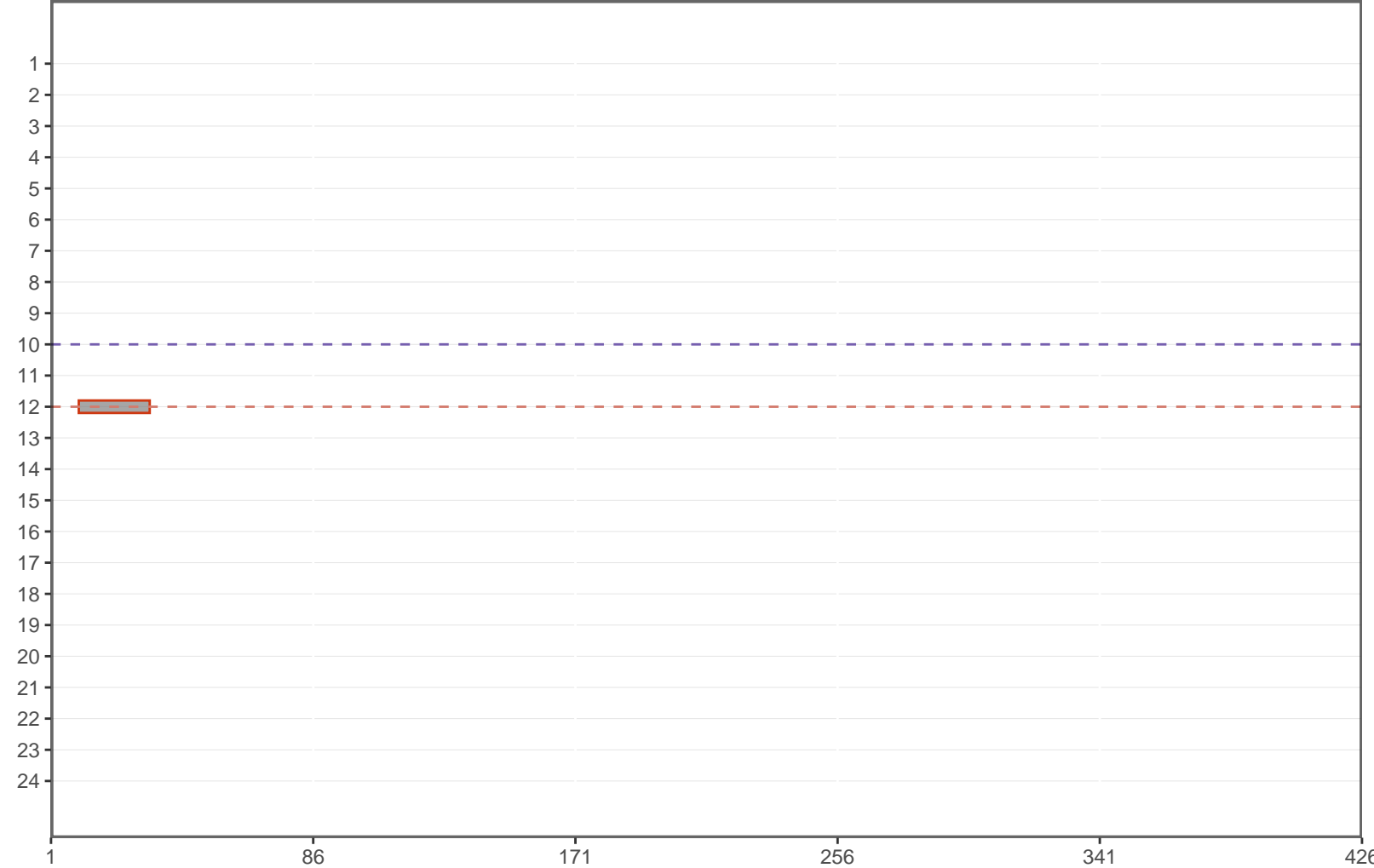
MW indication



Molecular weight



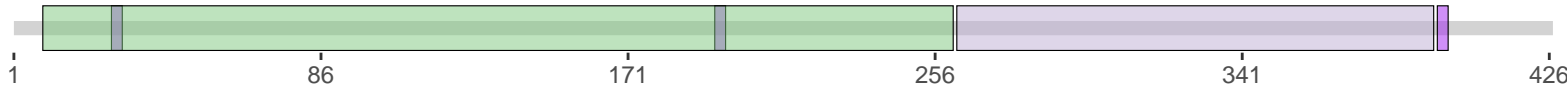
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF05116 Sucrose-6F-phosphate phosphohydrolase
- PF08472 Sucrose-6-phosphate phosphohydrolase C-terminal

Protein sequence:

DSGNDALFSPDVGVMVAANAGEELLGWHAANAKNNPKVHATERGAAGIGAGHFNLPSTSPRDVMDLSDCKMENFVYVEVKFKYLFKEKRRGEIEHSEHLENLKAVGRP6GTFVHPFGVEKSLGECVTLFRTHGSDKGGKGRFRIWDDVLFVQVGSDSWLVSPKXWELSGEDRHGCIITVLLSKNKTVADGLTWTWHVHGFWLNGAAAAD6GTTWFE

NbL09g20090.1 protein_WVD2-like_4 [MW = 48.52 kDa]

No. of times detected



log(intensity)



Values from



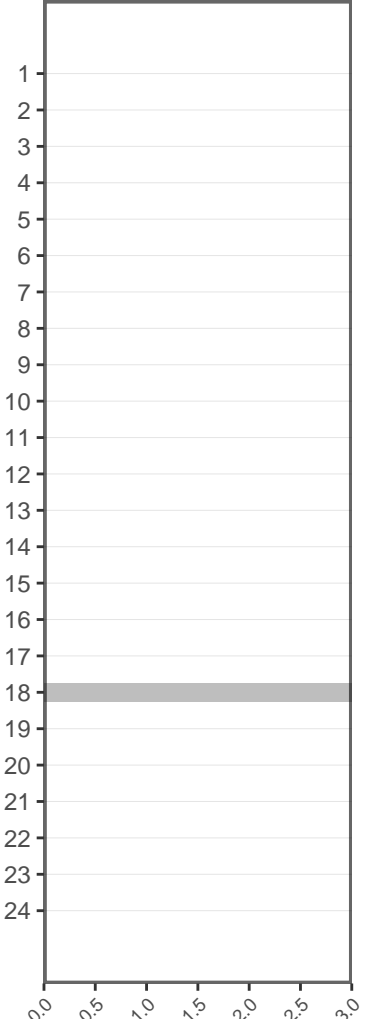
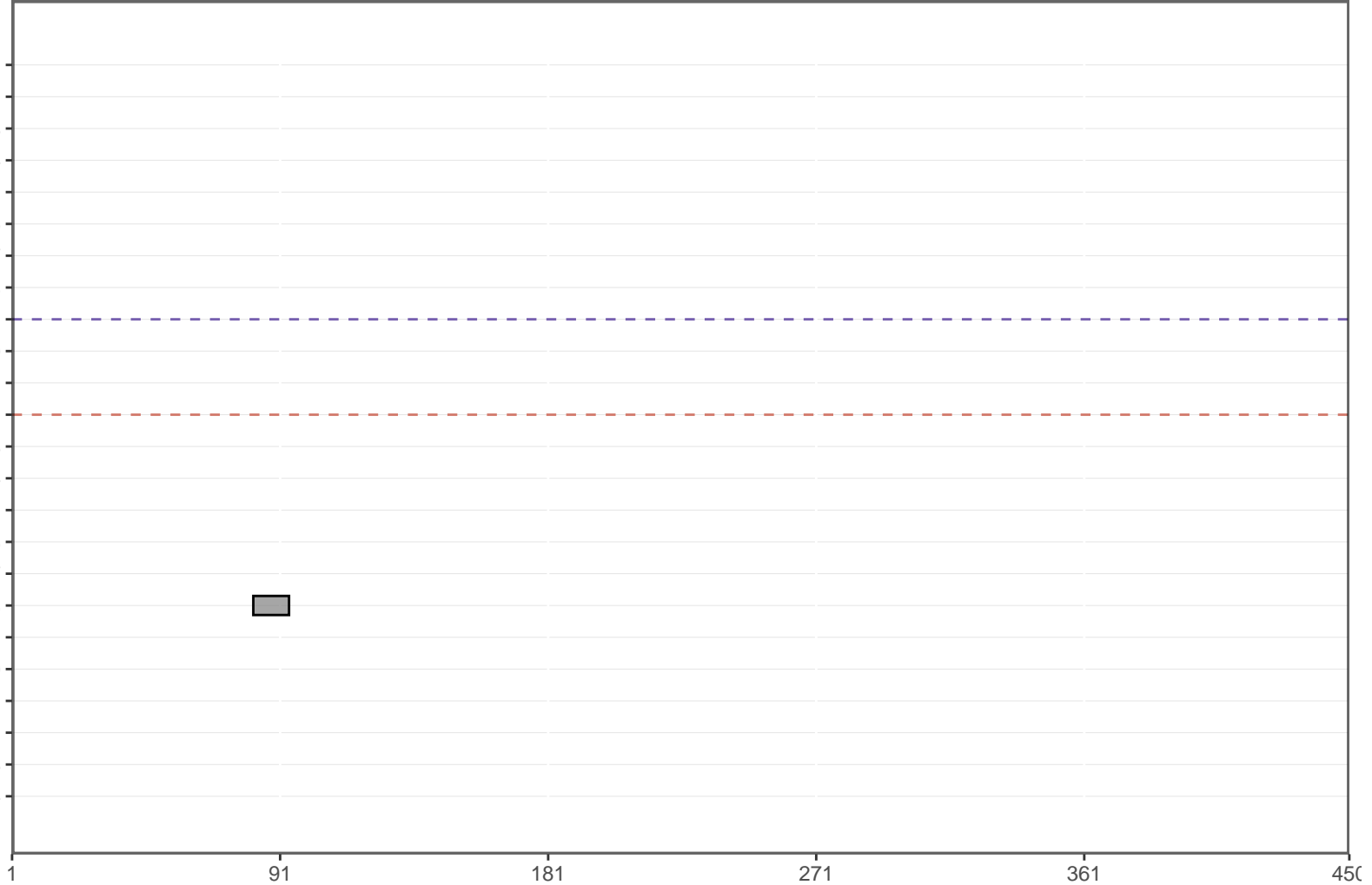
MW indication



Molecular weight

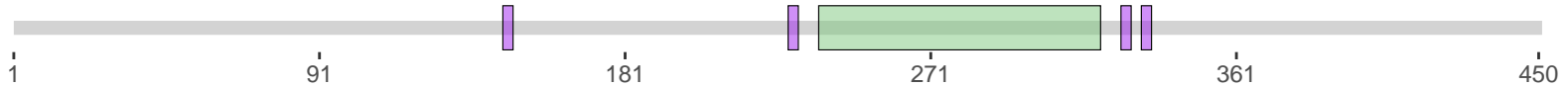


Gel Slice



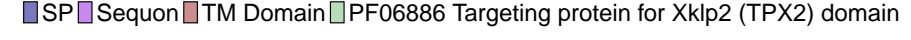
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

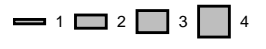


Protein sequence:

ATSPLKDDSDARSATSSNTTRTSTGGFSLRLEERAERKREKFLAKMEERIGAREEKKNNLLAKSKENDEEEVWQFRKSLTFKATPMNPNFYKEPPPKVLELKIPIRTRASPKLGNKKNSTATNGSEGGGSSFSFRKVKDRKSPRTSKDITATKGGKPVVEIKKPKVNSHTIGQSPKSTTKGSAETKLPKPAEKSGSDEKTEEMDQIPDSVPKPKPMNSVEDNVPFRPSNPFVVQAEVTVVEV

NbL09g20000.1 ubiquitin_carboxyl-terminal_hydrolase_12 [MW = 131.5 kDa]

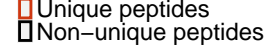
No. of times detected



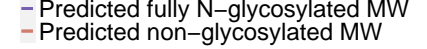
log(intensity)



Values from

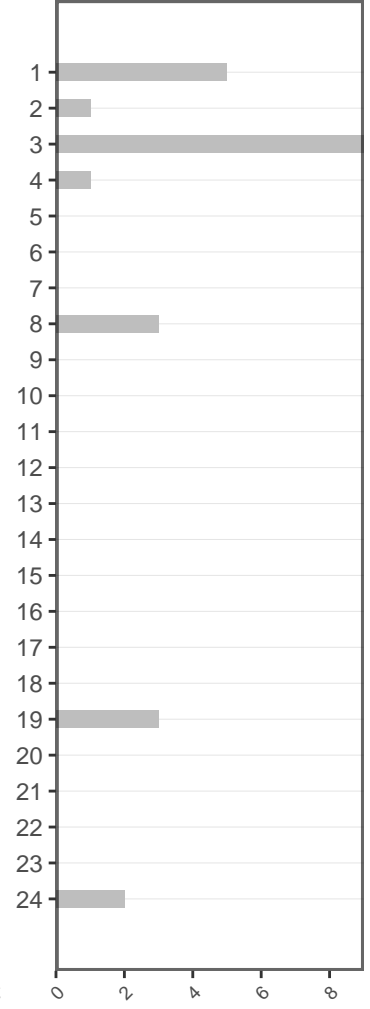
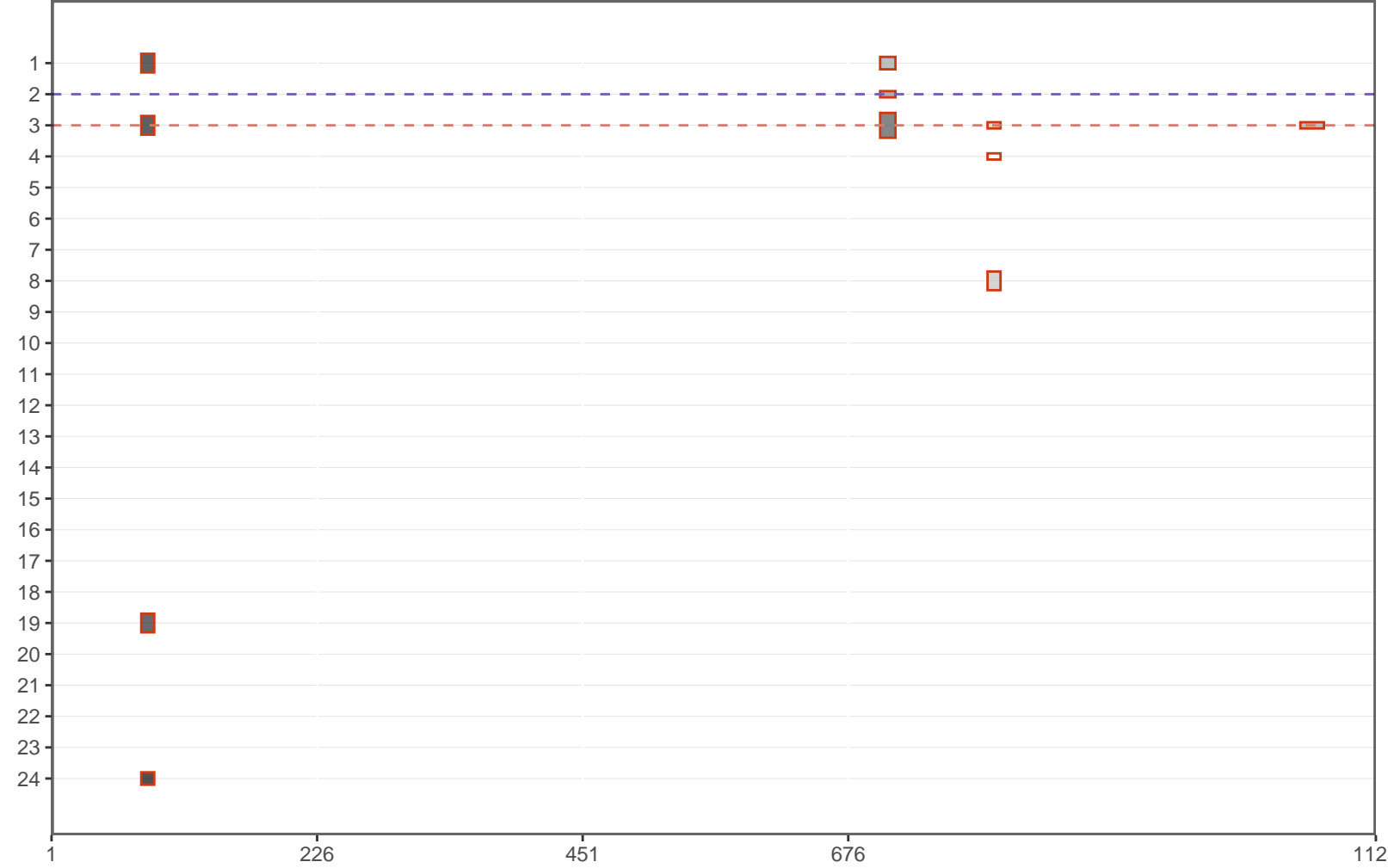
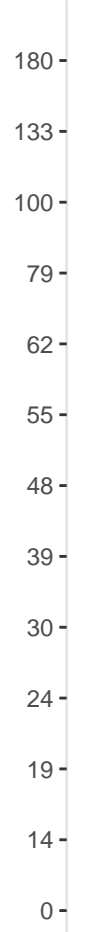


MW indication



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

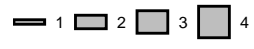
- SP
- Sequon
- TM Domain
- PF00443 Ubiquitin carboxyl-terminal hydrolase
- PF00917 MATH domain
- PF12436 ICP0-binding domain of Ubiquitin-specific protease 7
- PF14533 Ubiquitin-specific protease C-terminal

Protein sequence:

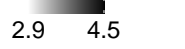
DIAEHLRRLKXCECEKEKRRYKAGAHLYTIKVARDELDREIQGKEVFDLVHDHKVRFRIQKQMPFNLFKEEVAKELGIPVQGFQRFWAKKRNQHTYRNRNPLTPQEEGLQTVGDLREVSNTNNAELKLFLEVDQGLDLPSPDPDKSKDDLLFEKLYDSEKEELGVYGRLLFKVSTKFPSELPLKLNELAGFAPDQDEIDLFEIEKFPFVMDERLNDKASFRFQIEDGSDICFQKQASPEVEEGVRFDPVYKLEWYKNRGIVHFRALFKPKEDDFLELAKSDTYDDVVEI

NbL09g19970.1 syntaxin-132-like [MW = 35.38 kDa]

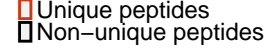
No. of times detected



log(intensity)



Values from



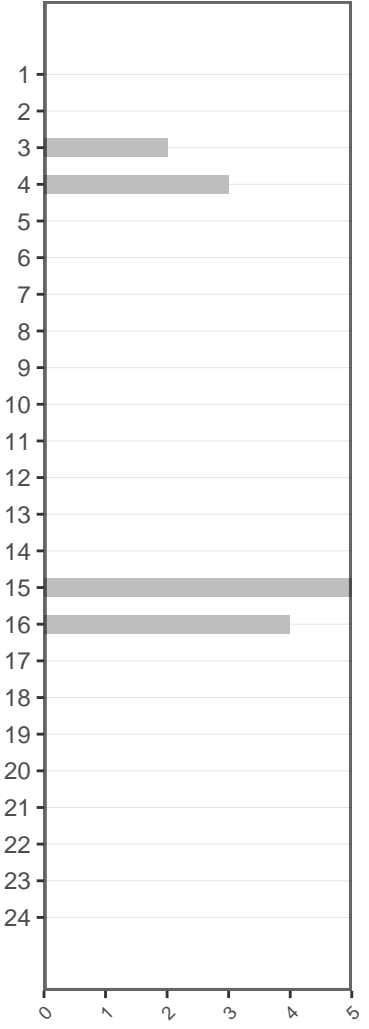
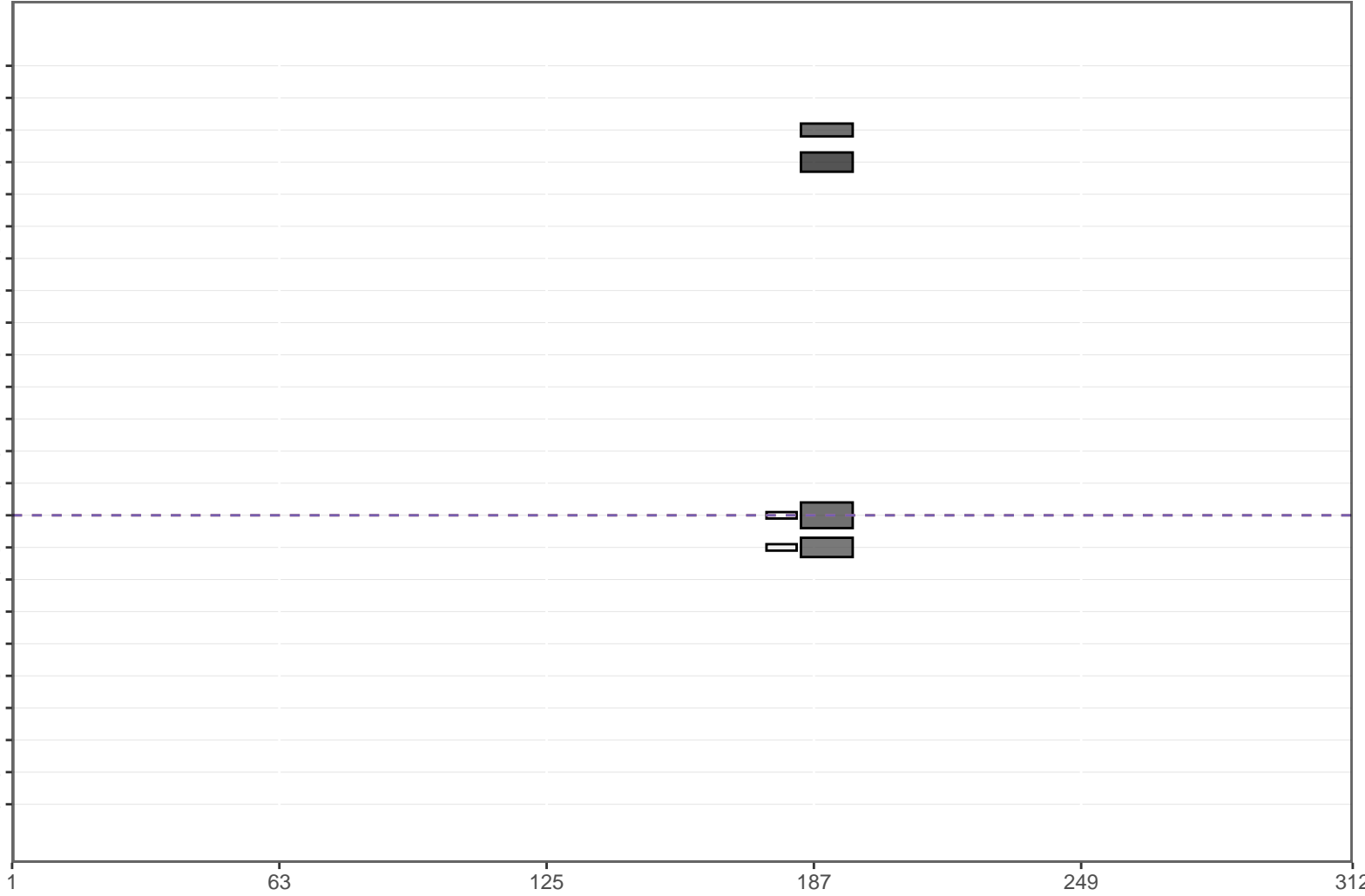
MW indication



Molecular weight

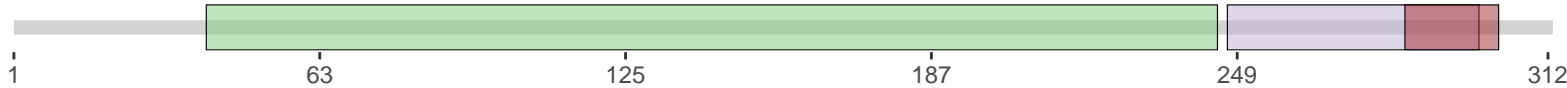


Gel Slice



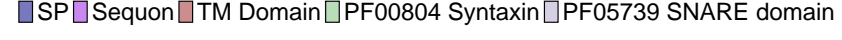
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

QKFKDAEAFQTLRENIQHEVYRERRVETVIGNRADEEETHRLIETGDSQGFQKAGDGGGRGGMGTLAIEIGERHDAVRELERKILELQGFLDVAIYVDAQGDMLDNIEGGVSTAVDHYDQGNALGKAKKLRNSRWKMFIAILLIIVRIVGVKIPWNSNGA*

NbL09g19950.1 tropinone_reductase_1-like [MW = 29.95 kDa]

No. of times detected



log(intensity)



Values from



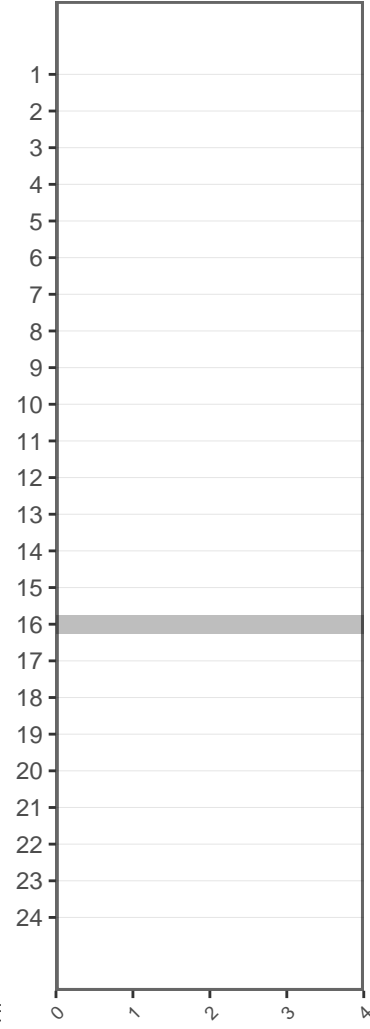
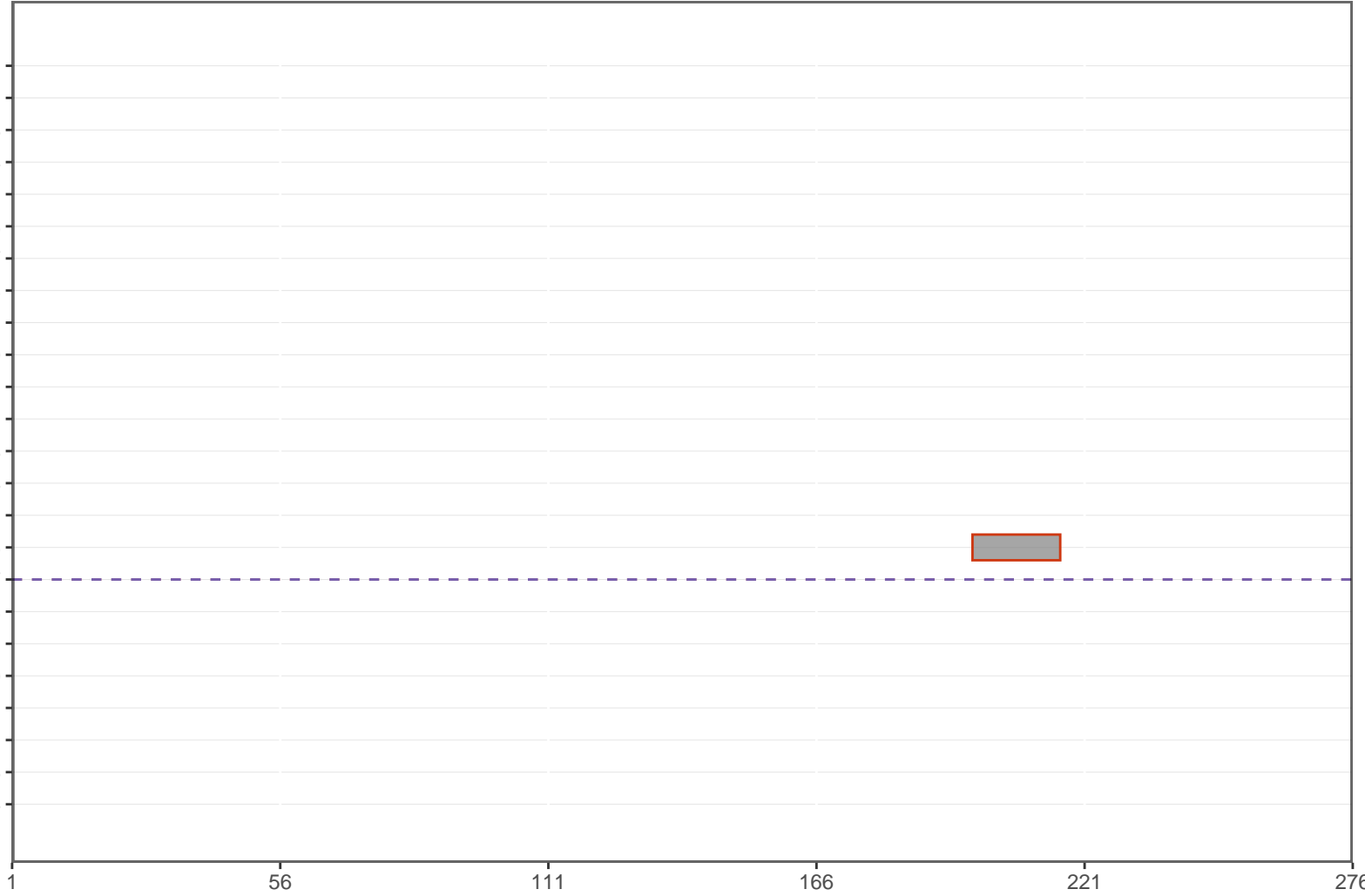
MW indication



Molecular weight

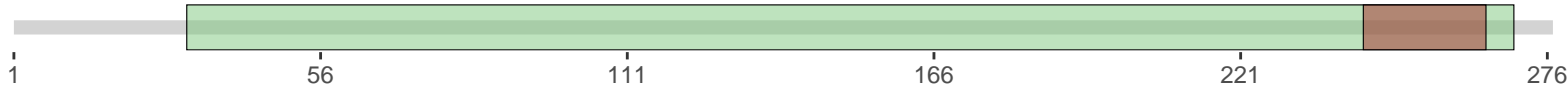


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

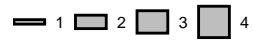


Protein sequence:

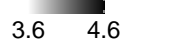
.EDIDIVAGTNTFEGHFLGSLAYFLKASENGNIFLSSAGFSLPLSLVLSASKGAINGMTKSLAGEWAKDNRVNSVAPGVMTPLVETANKNPKHKKDKIDHFIAKTPMRRTGKPEEISALMAFLGFPAASVYTGQIHWDDGGFTANGGP

NbL09g19720.1 protein_ABHD11-like [MW = 37.15 kDa]

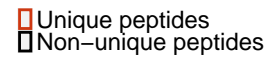
No. of times detected



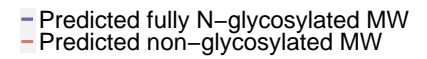
log(intensity)



Values from



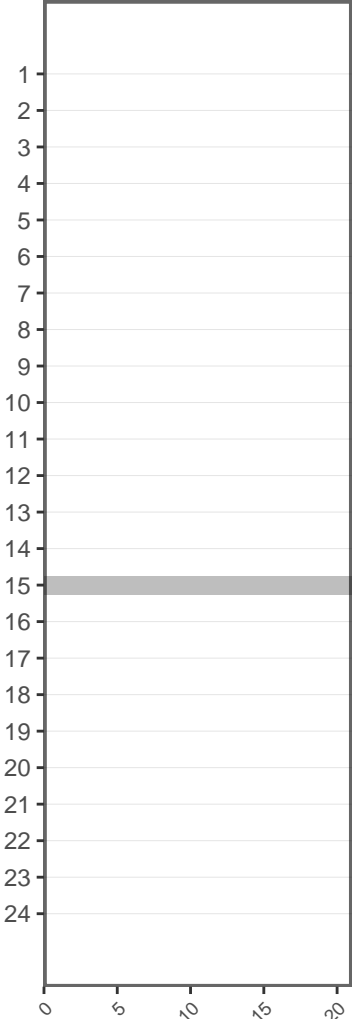
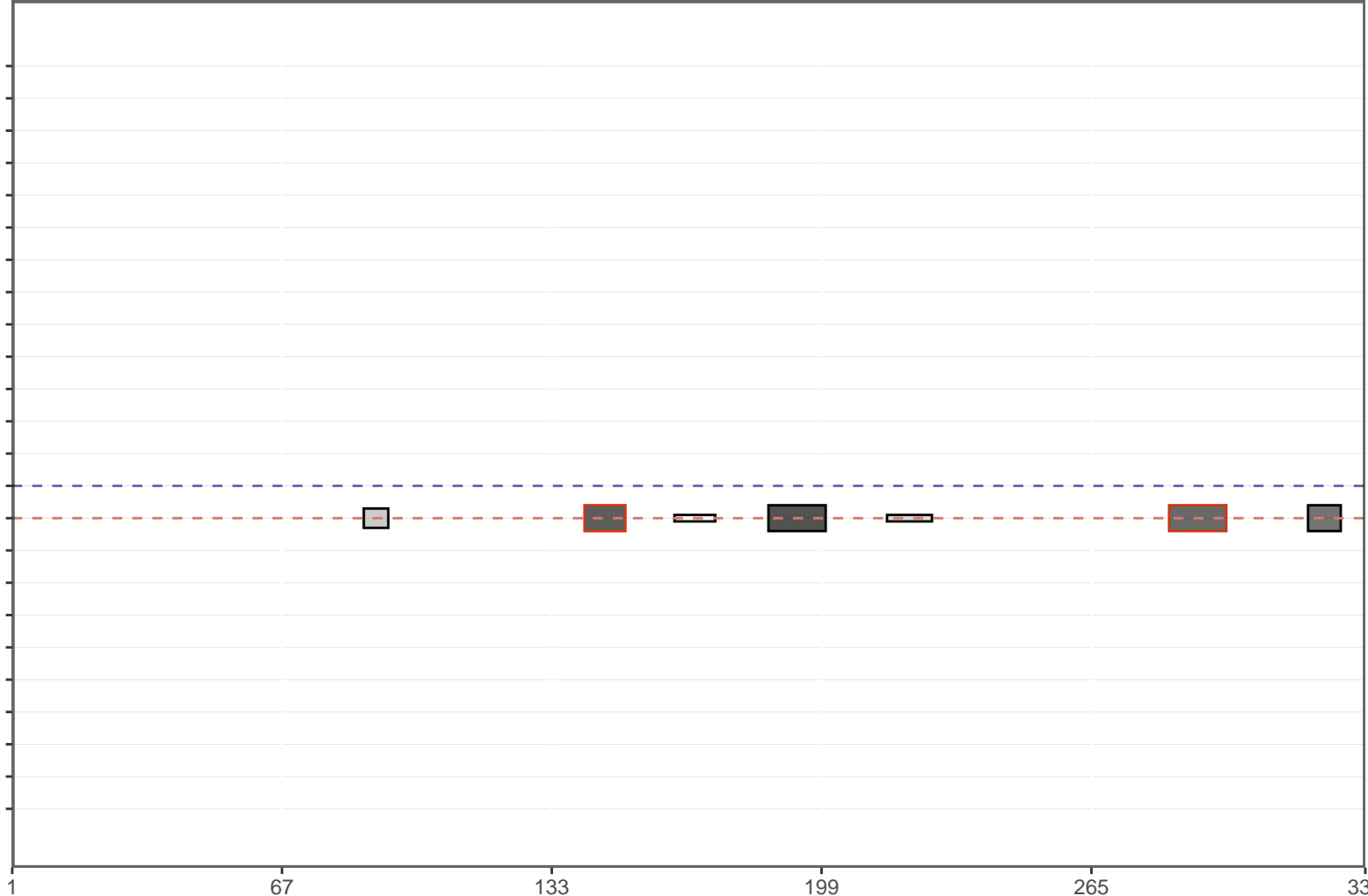
MW indication



Molecular weight

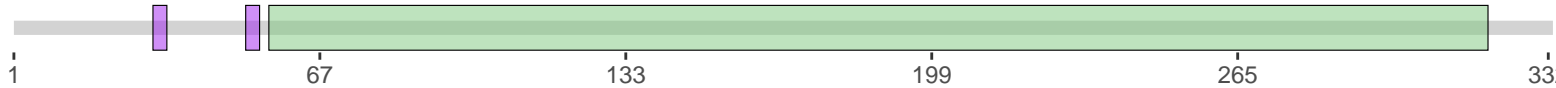


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

YQGSAALPKQLLYVLDGVPKVDREDSREVEKVMQTLQSLPSBSPSRKWLMDGMKLGFSKALSEWLGSLGKSGDGMKWTFNEMAEEMFNQYREKDYCPLEHPKGTETAVRAEKSDRWDPVTYQKLESLASNGGSEGEKMSYHLPLNSGHVAVHVENPRGELLEITPKLALVY

NbL09g19700.1 beta-fructofuranosidase_insoluble_isoenzyme_1-like [MW - SP = 63.54 kDa]

No. of times detected



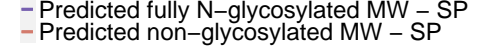
log(intensity)



Values from



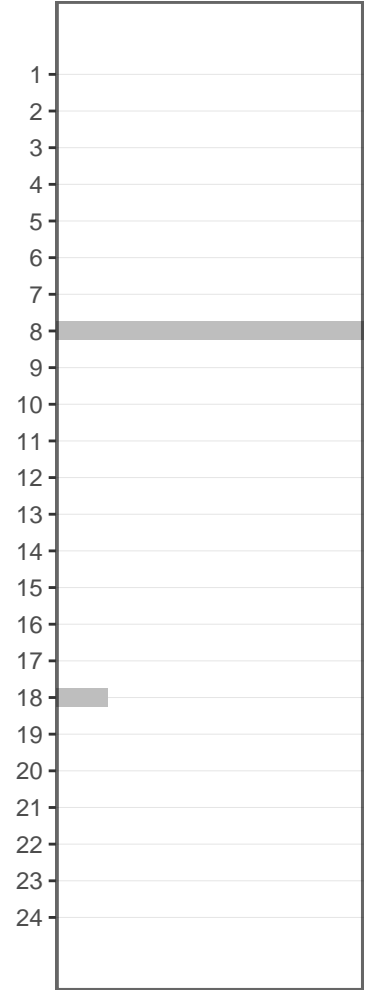
MW indication



Molecular weight



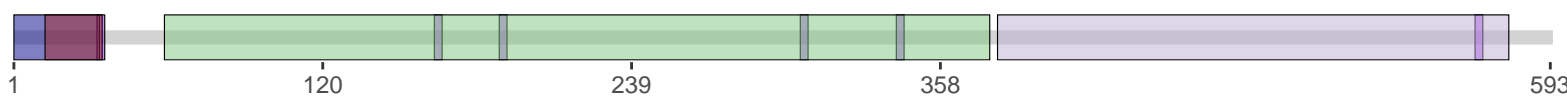
Gel Slice



Protein length

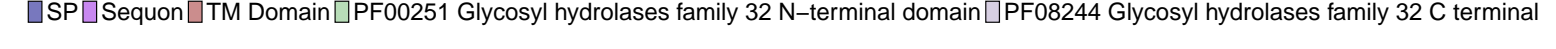


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RFEYTYGTQYDIKDKRYPINPTNSIDGWKGLRLDYGNYAKSFDYDPCRRRIIHWGWANESDITVDDVRRKGVWAGIGTIPRKLWLDPSGGKQIWDVWPVKELDTLRQKVLQKNHKLKNGENIEVKGITPAGADVEVTFASLQKAEFFDLWTDLVYGGDVCAGKSTVGGGIGPGLLLLAISEKLEETVDFRFRVKAQNKYKVLKMSDASRSLENDKIMKYPFAGVVDVLDLANNKLSLRSLDHSVVEFSGAGGKTQTSRVPYPTLAVDVAHFAFNNGTETIKELKAVSM

NbL09g19500.1 enolase [MW = 27.92 kDa]

No. of times detected



log(intensity)



Values from



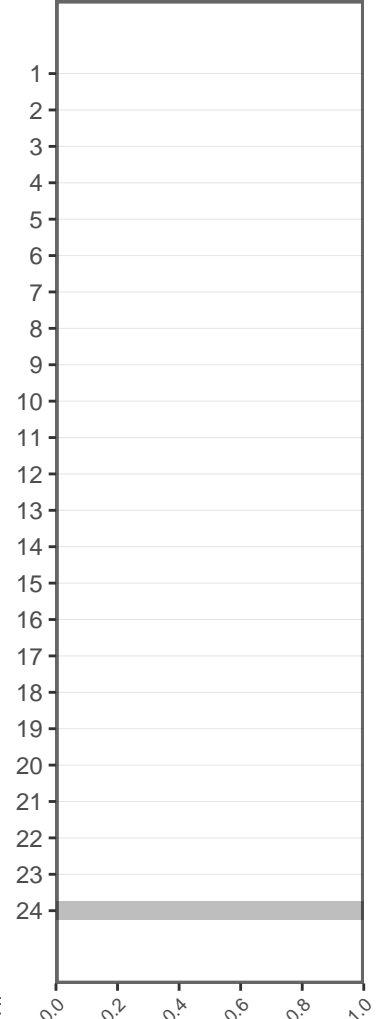
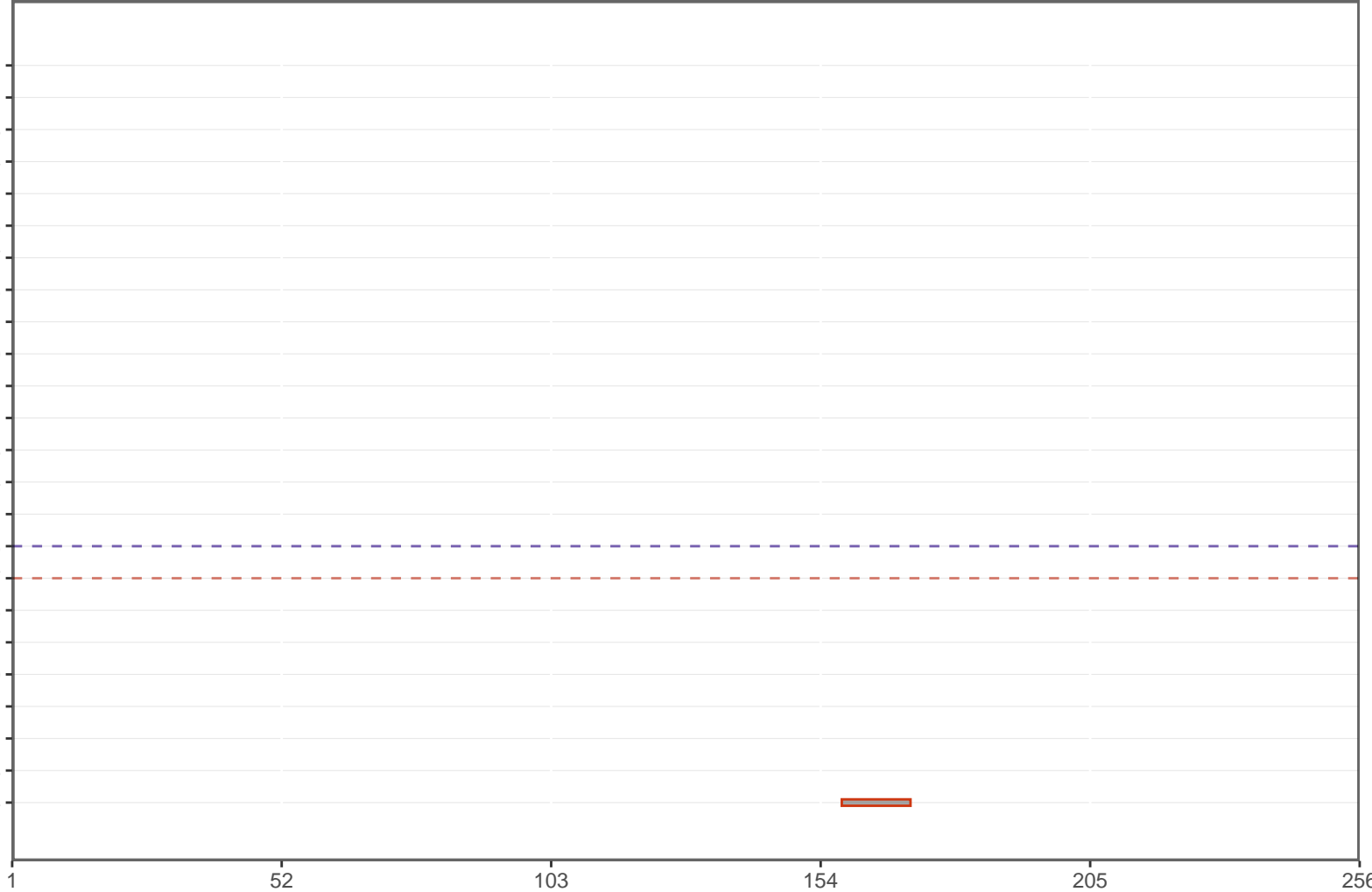
MW indication



Molecular weight

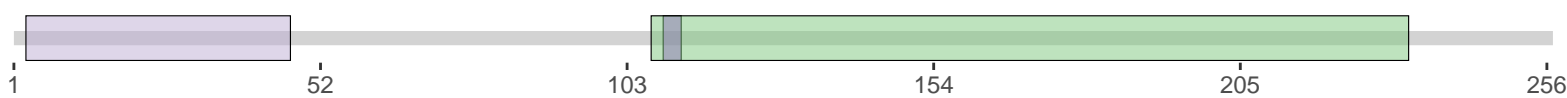


Gel Slice



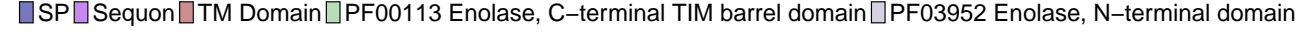
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KISGDQLKDYKSFVSEYPIVSDIEPFDGDDWETVAKLTAIEGKVKVIGDILLVTPKRWAKAIEGMTGNALLKVNQIGVTESEIAVWMSKRAGWGLMTSHRSGGETEDFDIAALVYVQLDKSRLELPVGGSVGGSIARF

NbL09g19490.1 peroxiredoxin-2E-2_chloroplastic-like [MW = 28.71 kDa]

No. of times detected



log(intensity)



Values from



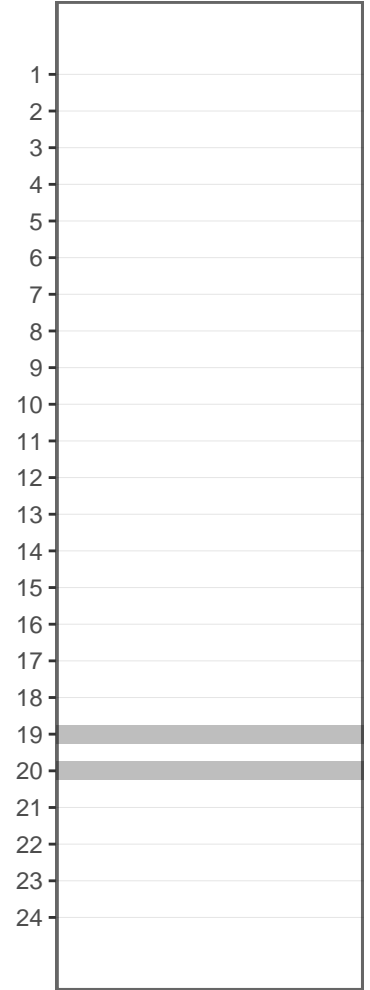
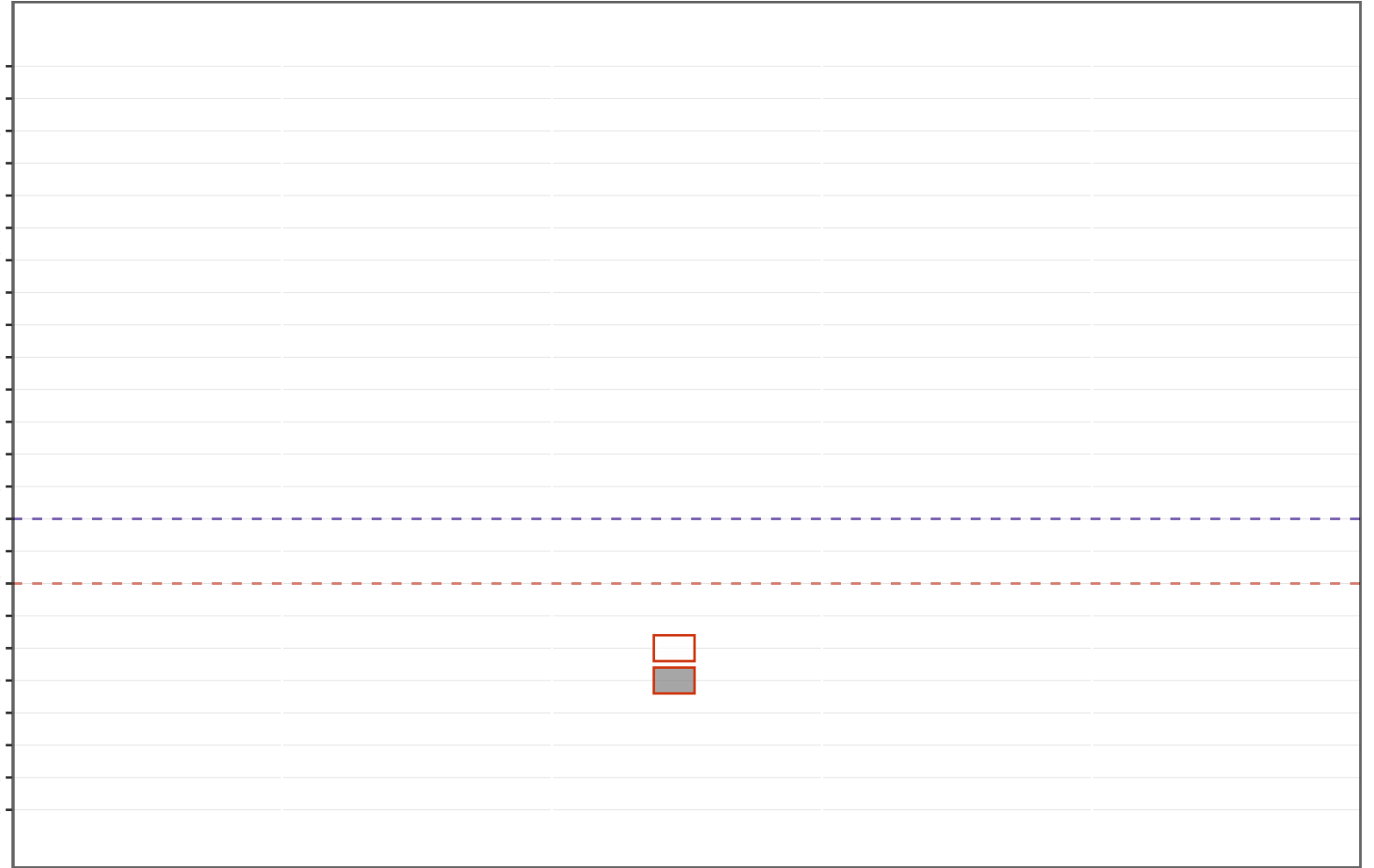
MW indication



Molecular weight



Gel Slice

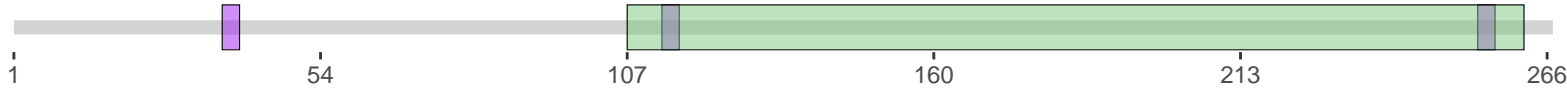


Protein length

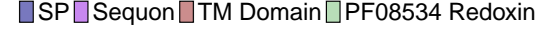


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ISDELKTLISIDLTGKQKVLFAVPGAFPTGSGKHLPGFVEKSKELKSGKGVDTAGISVNDAFVYKFKWENKINDEVLVLLSDGNLEFTKAGCELDSDKPIGLGVRBRVYMLVDDGVVYVNLLEEGGAFNVSSAEDLKTU

NbL09g19470.1 pyruvate_kinase_cytosolic_isozyme-like [MW = 63.09 kDa]

No. of times detected



log(intensity)



Values from



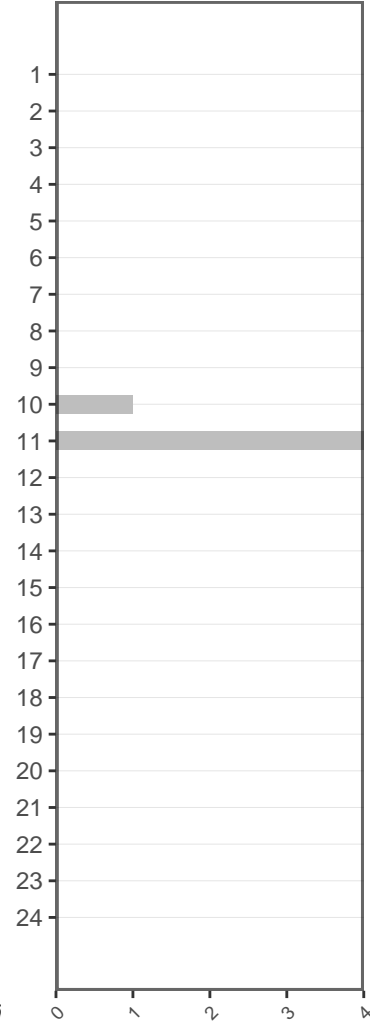
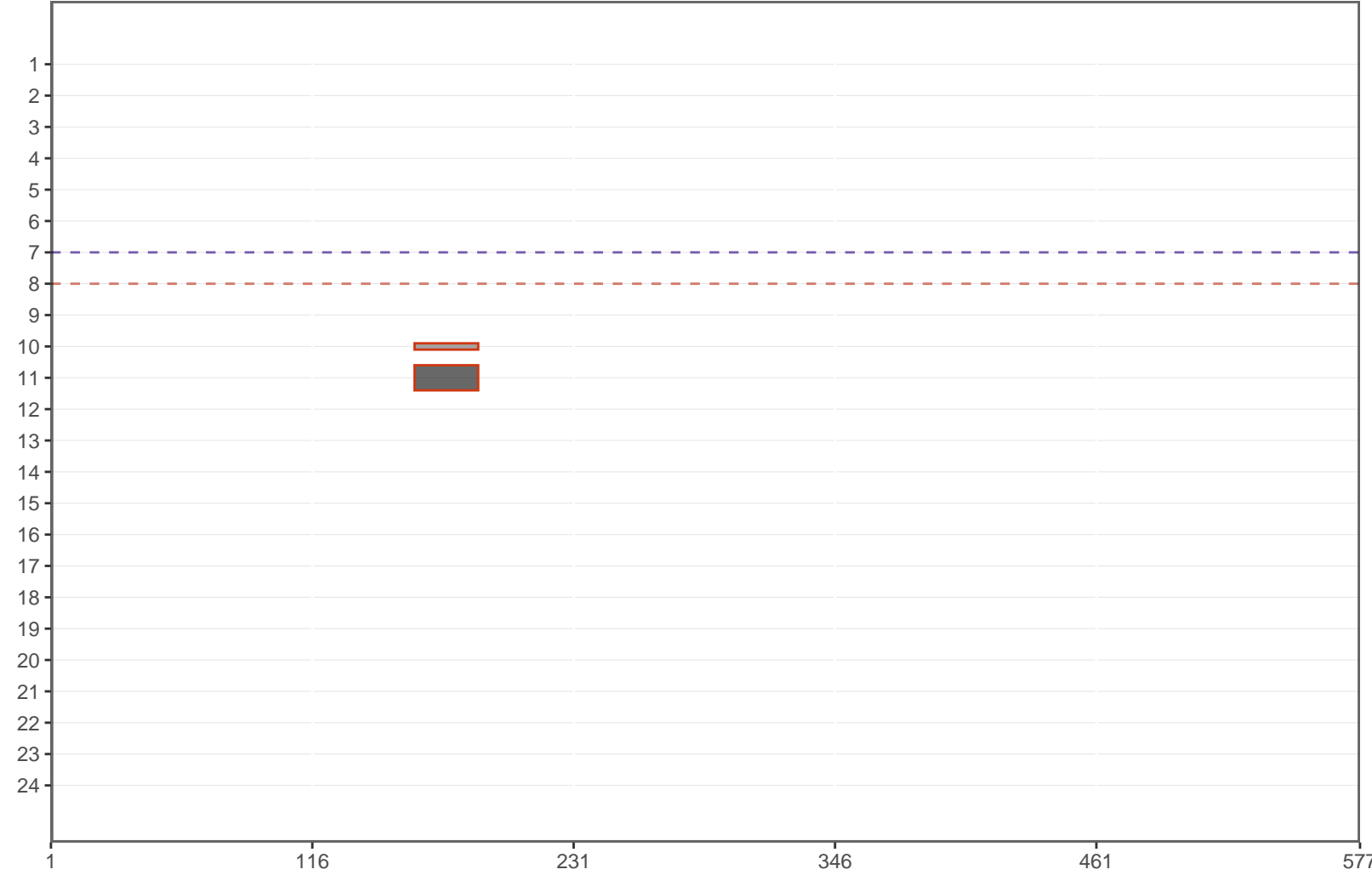
MW indication



Molecular weight



Gel Slice

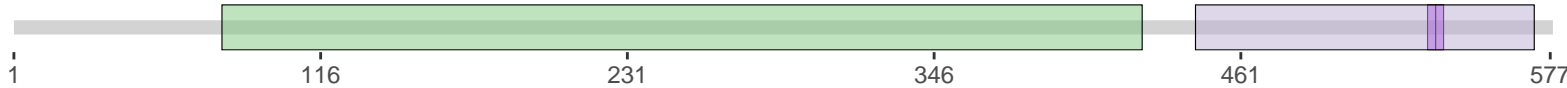


Protein length

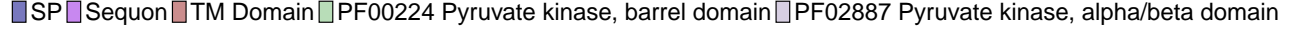


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

.SYTRHAEDVREAREFLKLGDLGDSGTGFAKIEVGLGTHFDLKEADGILSRGNLGIQLPPEKVFLLGKAIAVHKGNAAGKPVVYTRVVDGMTDNLRRTRAEATDVAVALDGTDAILLGAETLFGLYPVETISTVGRGFEAEKVFNDQLFKKTKVFGVEPMTLLESIASSAVAAKVAASVIGFTSSGRARLIKAYRPTMPVLSVIFRRLKTNGLKWFSGFAEARGSLVRLGFPMLADPRRHFAGETNABNESVLKVALDHGKAAGVYKSHDRVAVKCKVGDASVYKIELI

NbL09g19410.1 threonine_dehydratase_biosynthetic_chloroplastic-like [MW = 66.37 kDa]

No. of times detected



log(intensity)



Values from



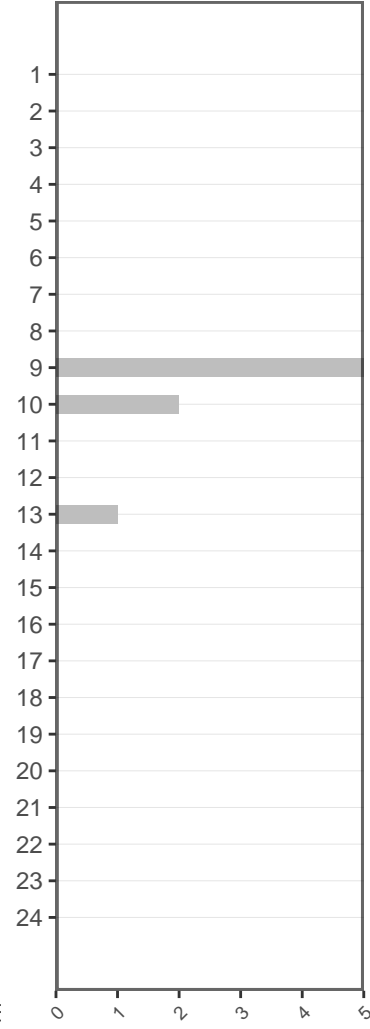
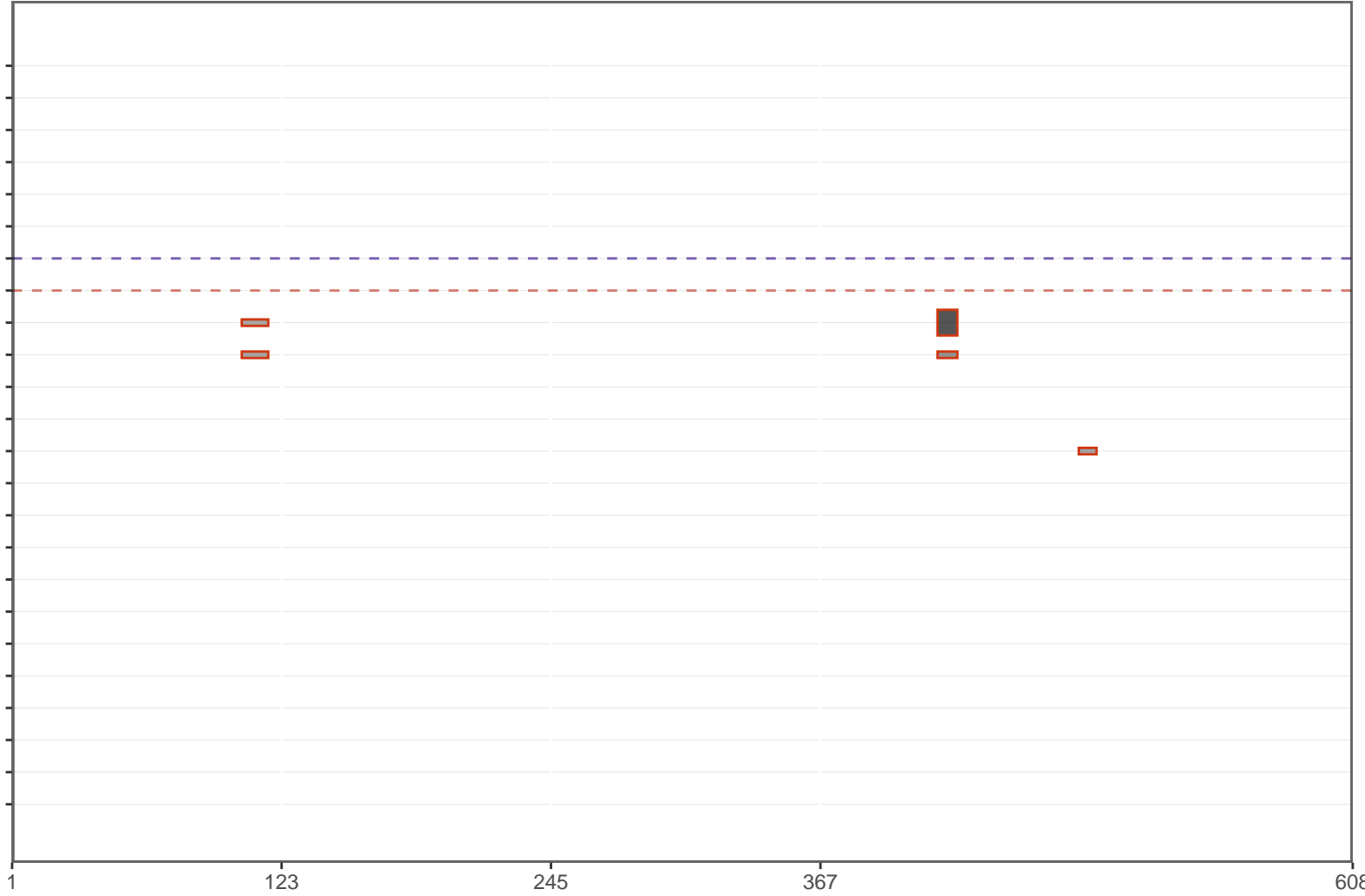
MW indication



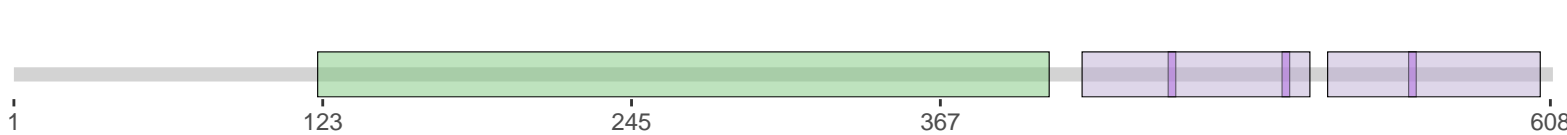
Molecular weight



Gel Slice

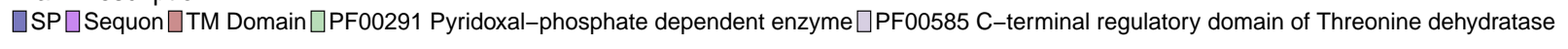


Protein length



Pfam domains

Pfam Description



Protein sequence:

YLKRVAPDKIKIGVEPLDANAMALSLGHGQRVMDLGVGFGADGVAWKVYVGEETVRLGKELIDGVYLVGRDAGASKDMFEENRSLPEPAGALAGAEVYKYLKSGENVAITSGANMNFDRLRVLTSLADVGRQREAVLATFMLEEPGSGKFKFSEMVGPMNTEFKYRYSAKENALVYVGLHTKLEEMVERMKSALHGTINTDNDLVKHLRHLMSGRTNHNELLCRFTFPEKPGALMKFLDAFSPRWNSLFLHYRAGDGTGANVAVGQVPOAEVDFEQR

NbL09g19390.1 protein_fluG [MW = 93.43 kDa]

No. of times detected



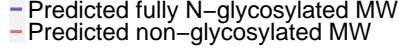
log(intensity)



Values from

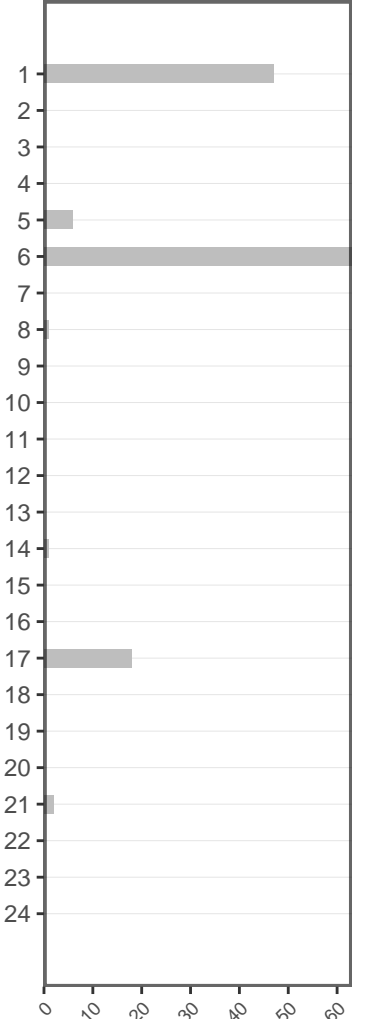
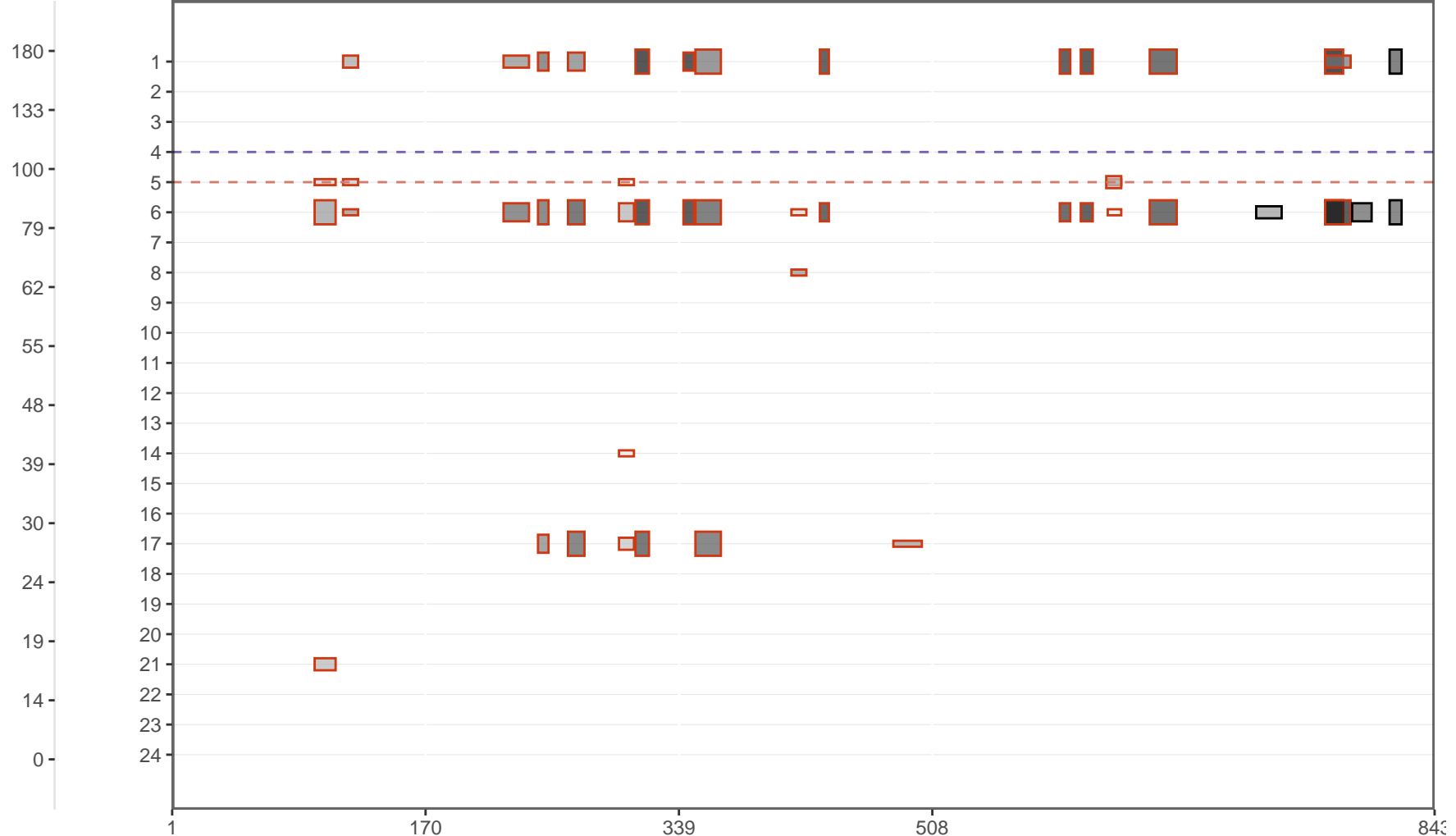


MW indication

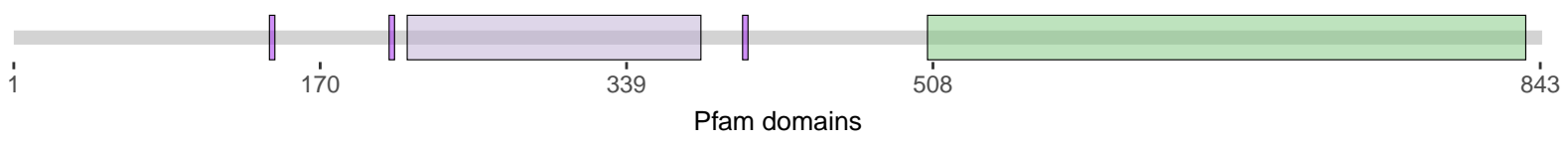


Molecular weight

Gel Slice

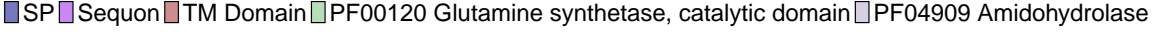


Protein length



Pfam domains

Pfam Description



Protein sequence:

LVRIIVVDSGQIRGRVVPQGRFYGSVWVHKGVLGTLGACMGMSASDGPVDTLTATSGEIRVPLDLSFKGLRPLVWNGGEMVLADMFEIPEGLKIWEYCPREALRKVSKLKDDEFDLVNVNAGFENFFLLKSVLRDQKEEWAFFDQTSYVGSTAFAFDAAFFILEEFABGLQLLNIVEGLQHAEGKGFPEALKYTDGCRRAANGLIFREIVRAVARKHGLLATFTVFKYKLDGSGSGHVNISLRNGENVFMA5DGS6QVMSKIGEAFMAGVNLHPLPFTAPLPSNYDRCPNMM

NbL09g19180.1 synthase [MW = 34.22 kDa]

No. of times detected



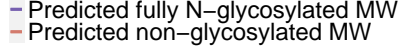
log(intensity)



Values from



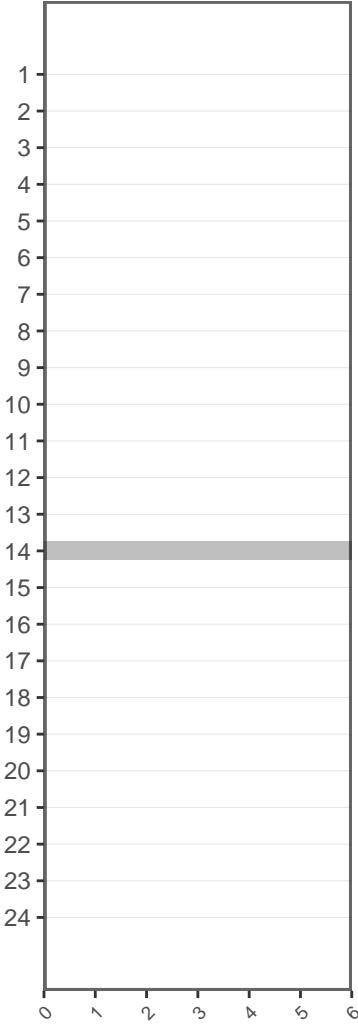
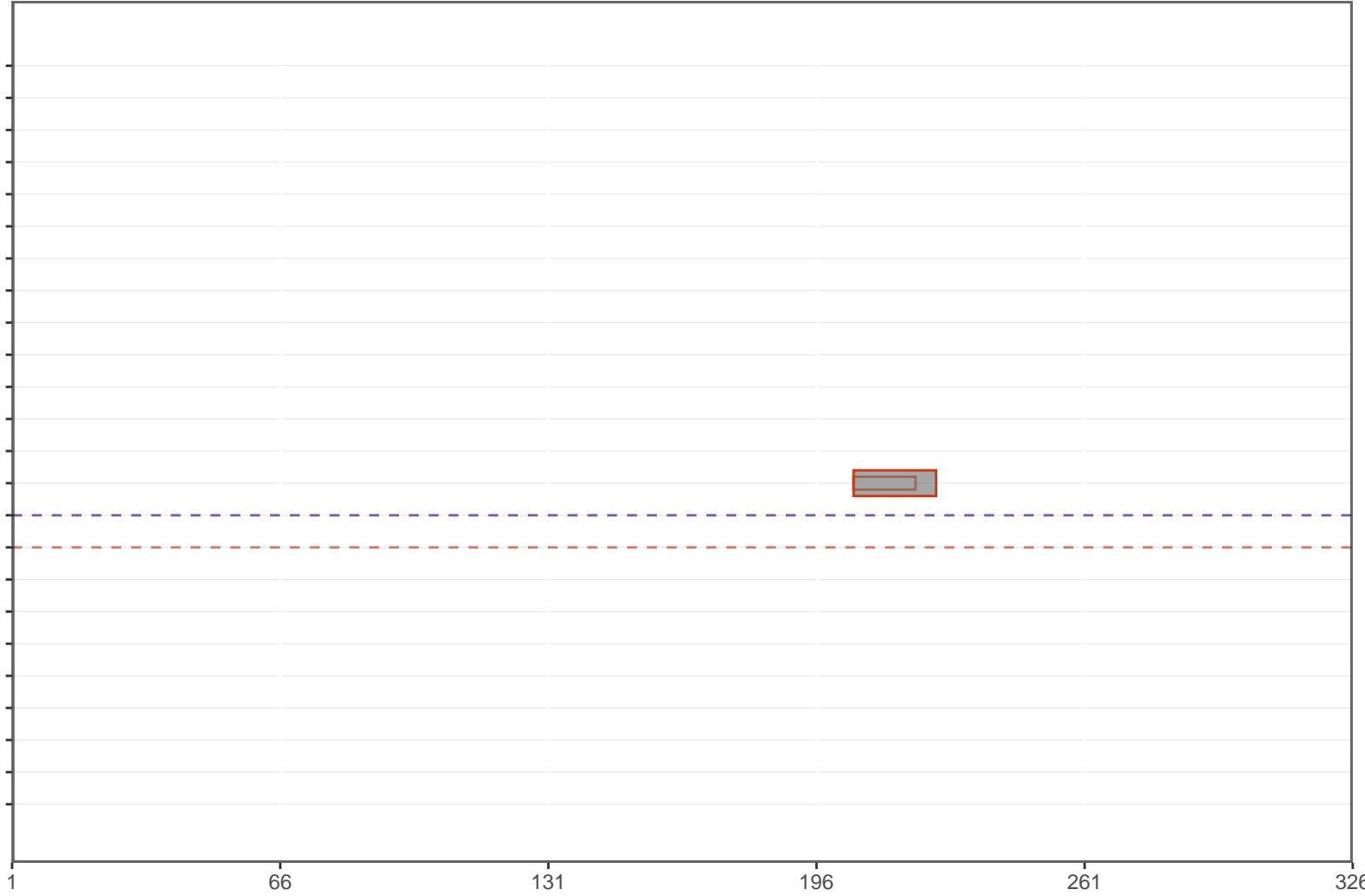
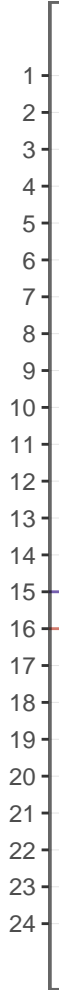
MW indication



Molecular weight



Gel Slice



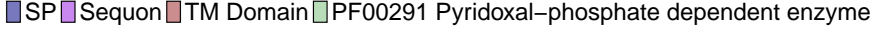
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

JFENPANPKYHYETTFGEIWKSGNGKVDALVSGIGTGGTIGSGKYLREQNPKILVGVPEVSAALSGGKPGPKKIDGIGAGFIPGVLEVLIDEVQVSSSEANETAKLLALKEGLLVGSSGASAAAANKLAKRPNENAGKLVAVVFPFGERYLGSVLFESVRRREANMTVEP

NbL09g19060.1 proteasome_subunit_beta_type-2-A [MW = 22.6 kDa]

No. of times detected



log(intensity)



Values from



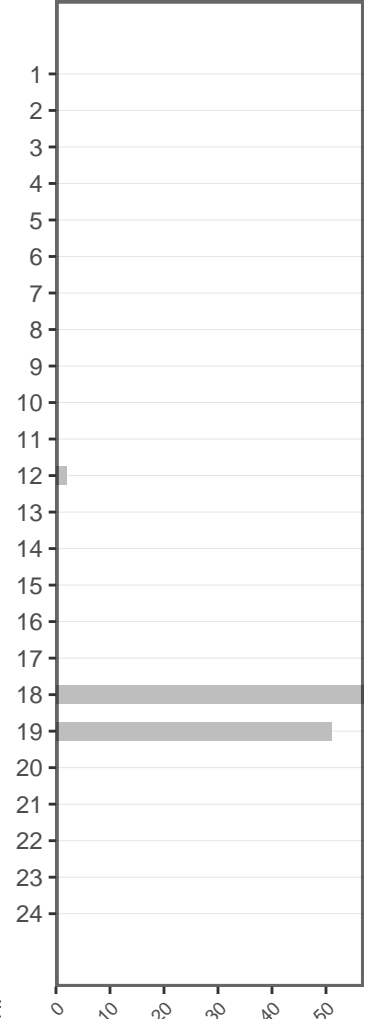
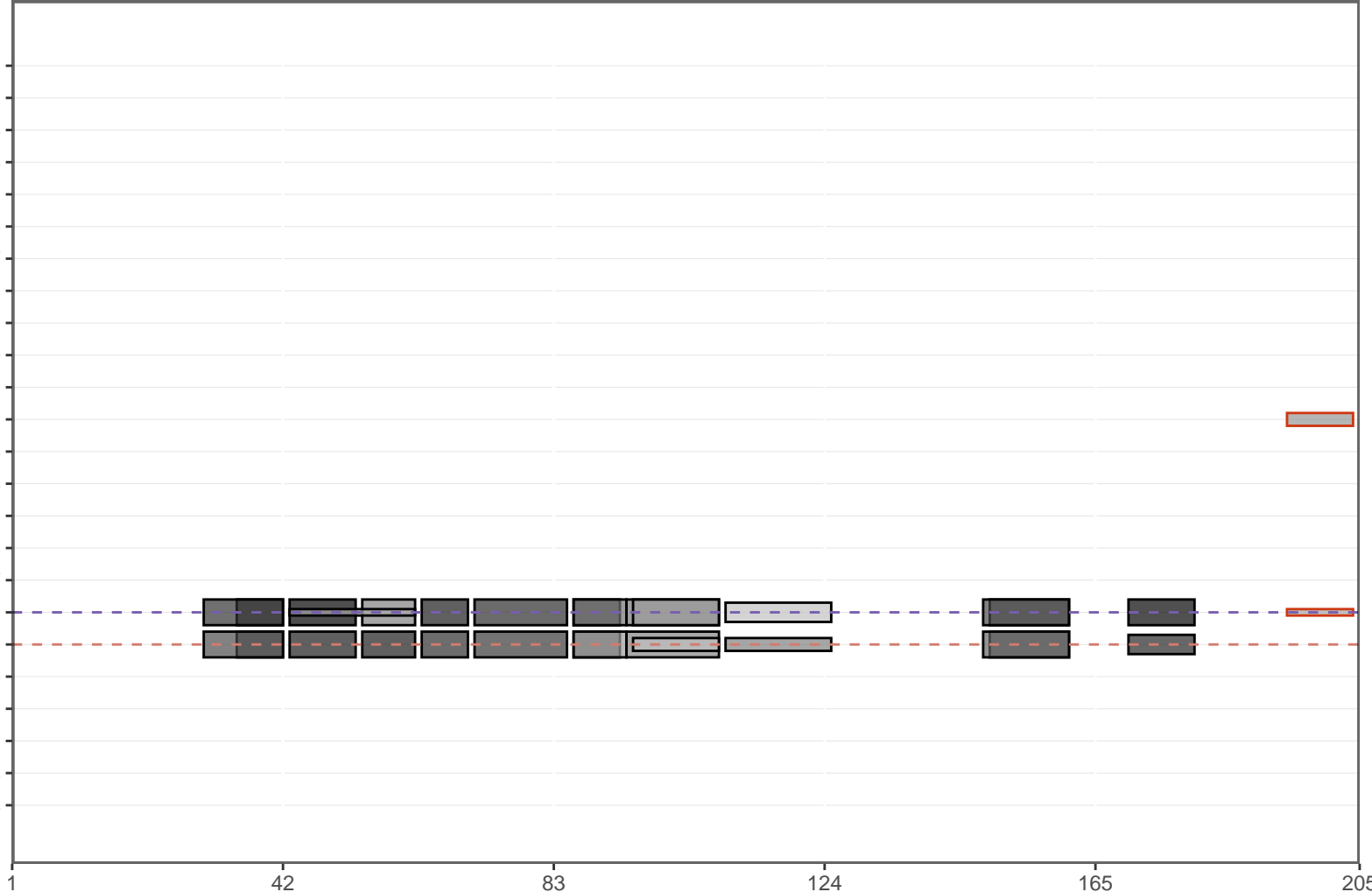
MW indication



Molecular weight

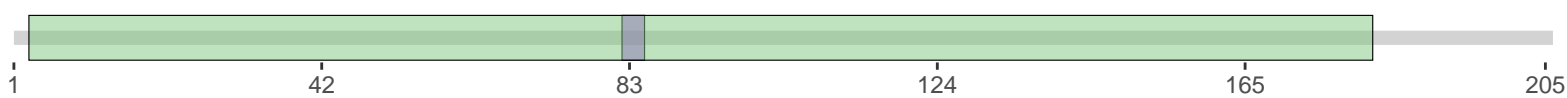


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ITALRKNPYM/NILAGYDKETGRSLVYVDVHATLHKVDKAAGVGYGVSFLAMMDRHYRKDMTVEEA/DLADKQMEIRBRLLVAFPNFVKIKVDDKDGAREVAVRGGVKDAPVENS*

NbL09g18860.1 12-dihydroxy-3-keto-5-methylthiopentene_dioxygenase_2 [MW = 25.62 kDa]

No. of times detected



log(intensity)



Values from



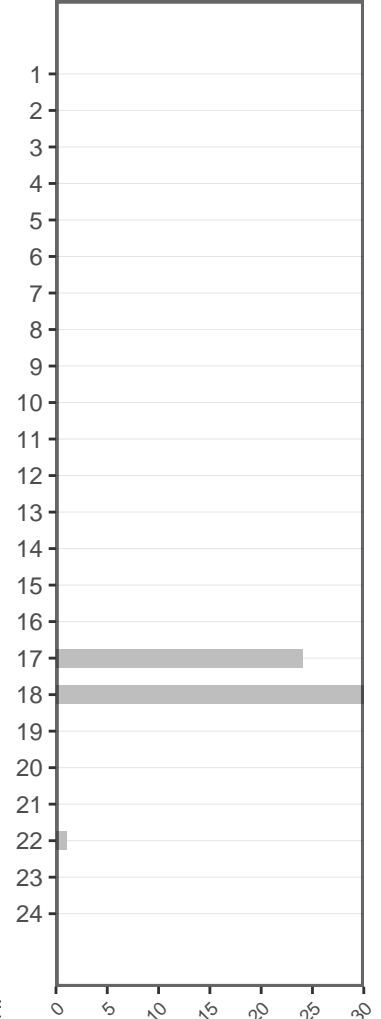
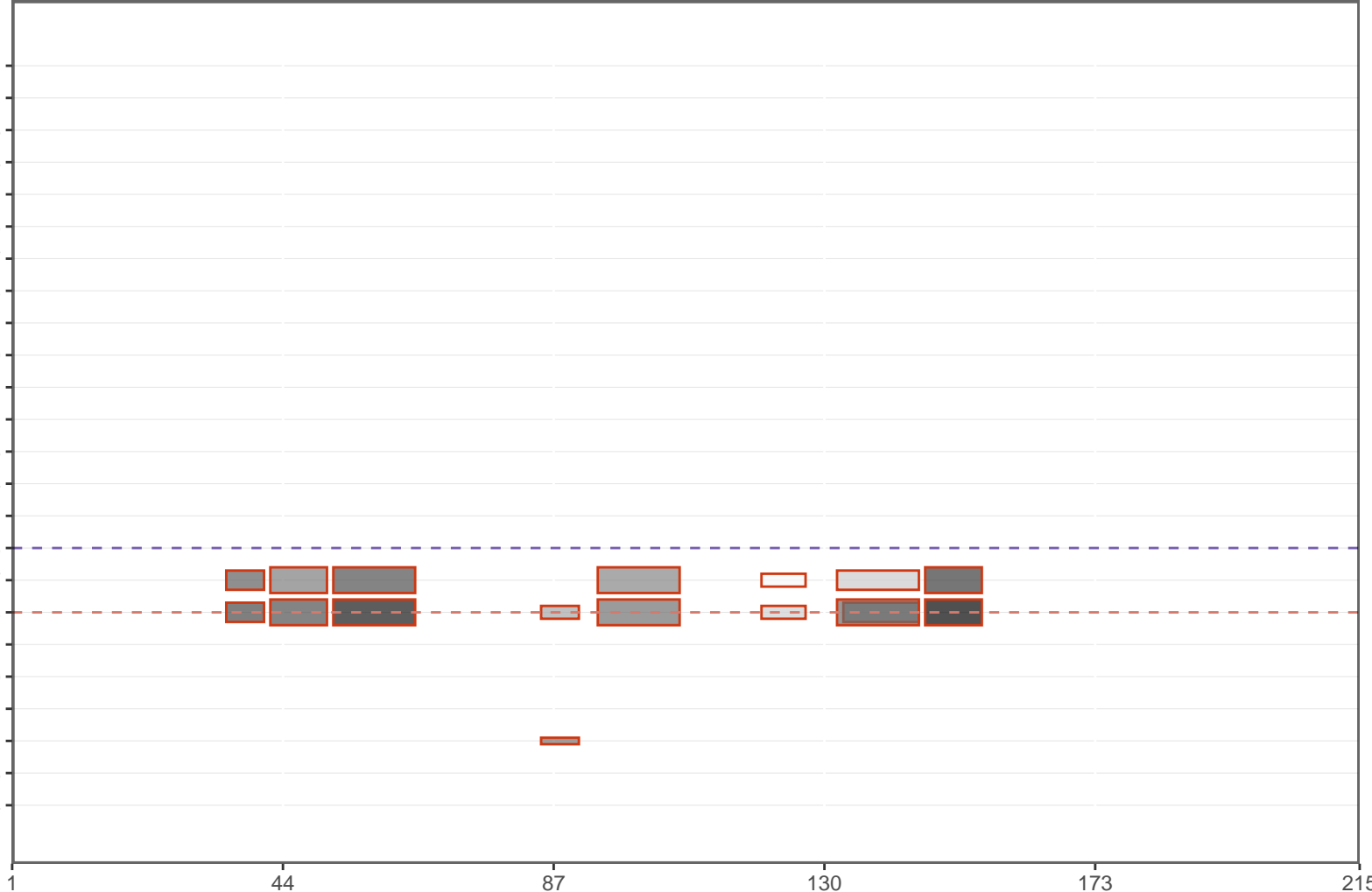
MW indication



Molecular weight



Gel Slice

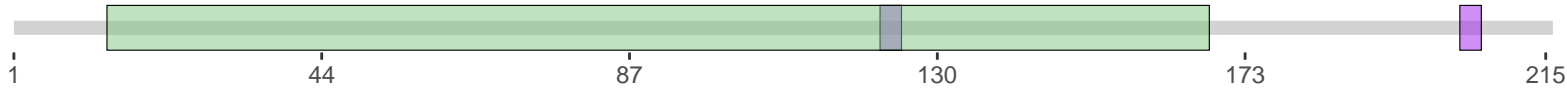


Peptide counts over 4 repeats

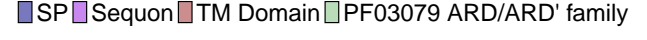
Protein length



Pfam domains



Pfam Description



Protein sequence:

NFFEELHTDEIRWQWGGYFDLRDNDTWRWVKKGGMVLPAQYHRFTLDSNNYKAMRLVGDPIWTPYRPHDLRAREVSRHLYSIFLNDGKHSWVEANESFLIMQERY*

NbL09g18800.1 stem-specific_protein_TSJT1-like [MW = 27.29 kDa]

No. of times detected



log(intensity)



Values from



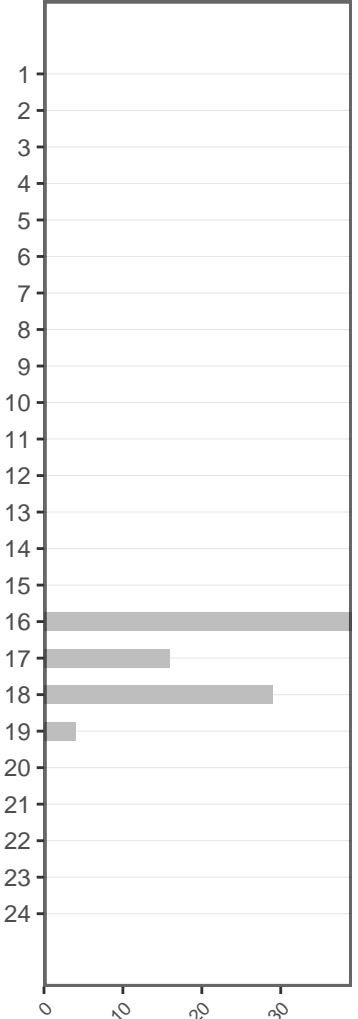
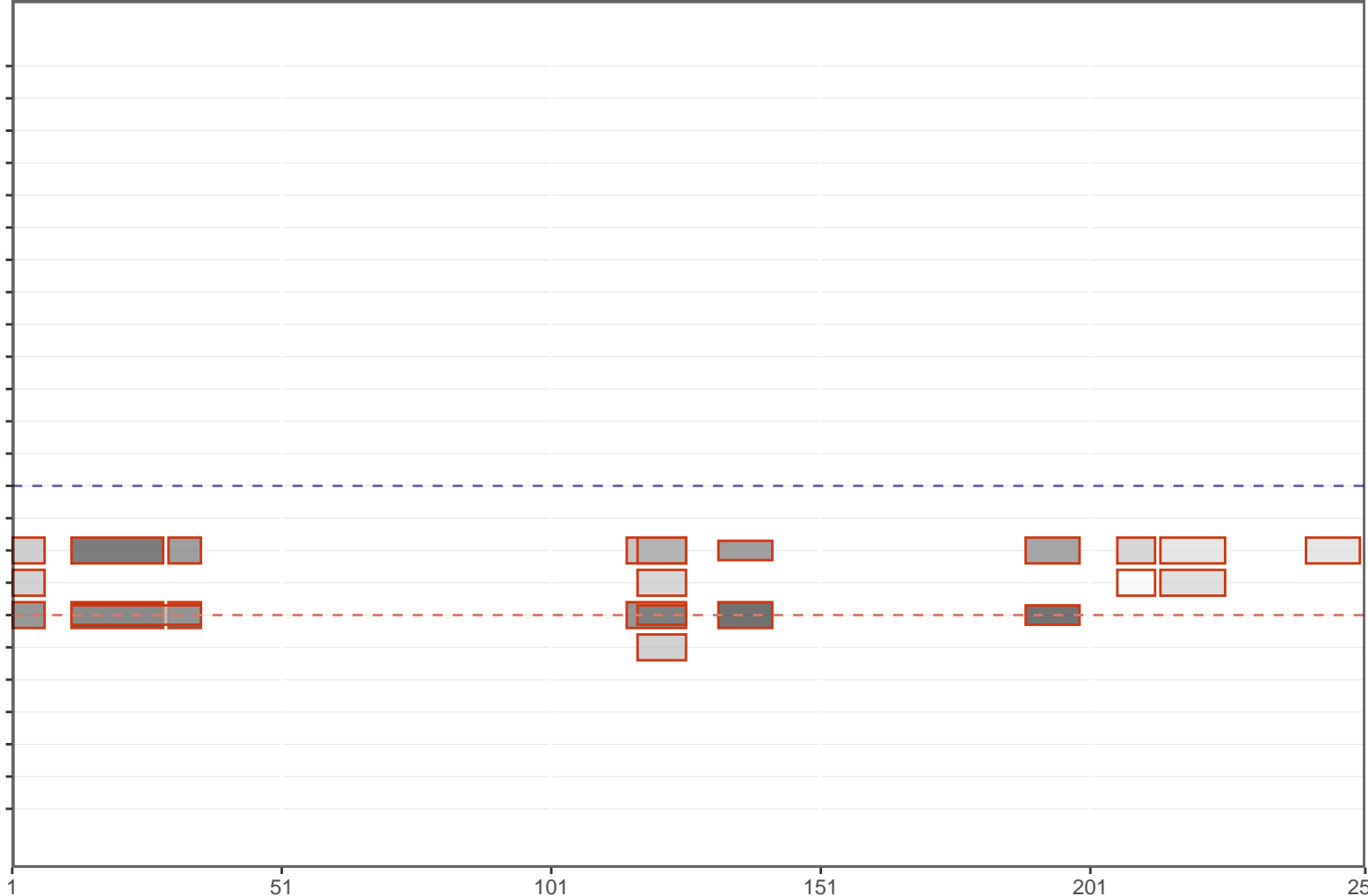
MW indication



Molecular weight



Gel Slice



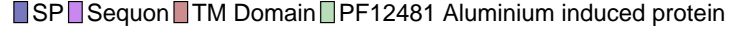
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGPYPPDQVVRDINHGKFAFVLDSSKTSFLASGVGGVPPFFWGTDSHGHLVLDSDMDIAHGKGGKSFAPFFKGGFTTS66GLRVEYHPRNELKPVPRVDS66EYVGGKFRVDAE6KGGTGMPRVDS6AANW6SHY

NbL09g18660.1 peroxiredoxin-2F_mitochondrial-like [MW = 20.97 kDa]

No. of times detected



log(intensity)



Values from



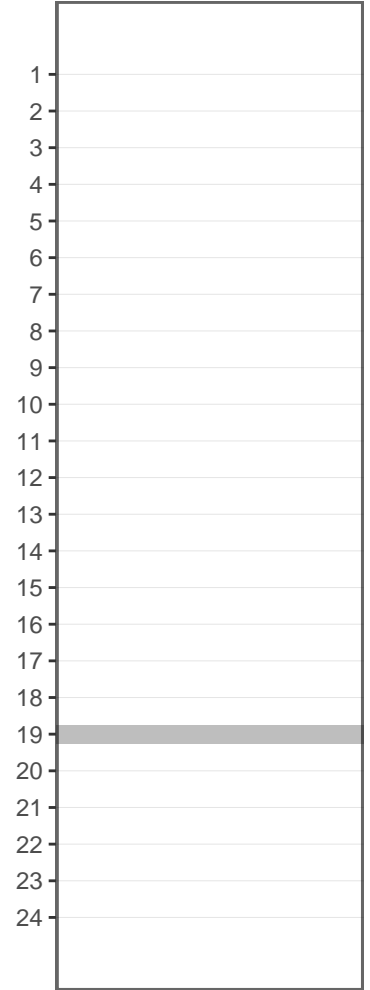
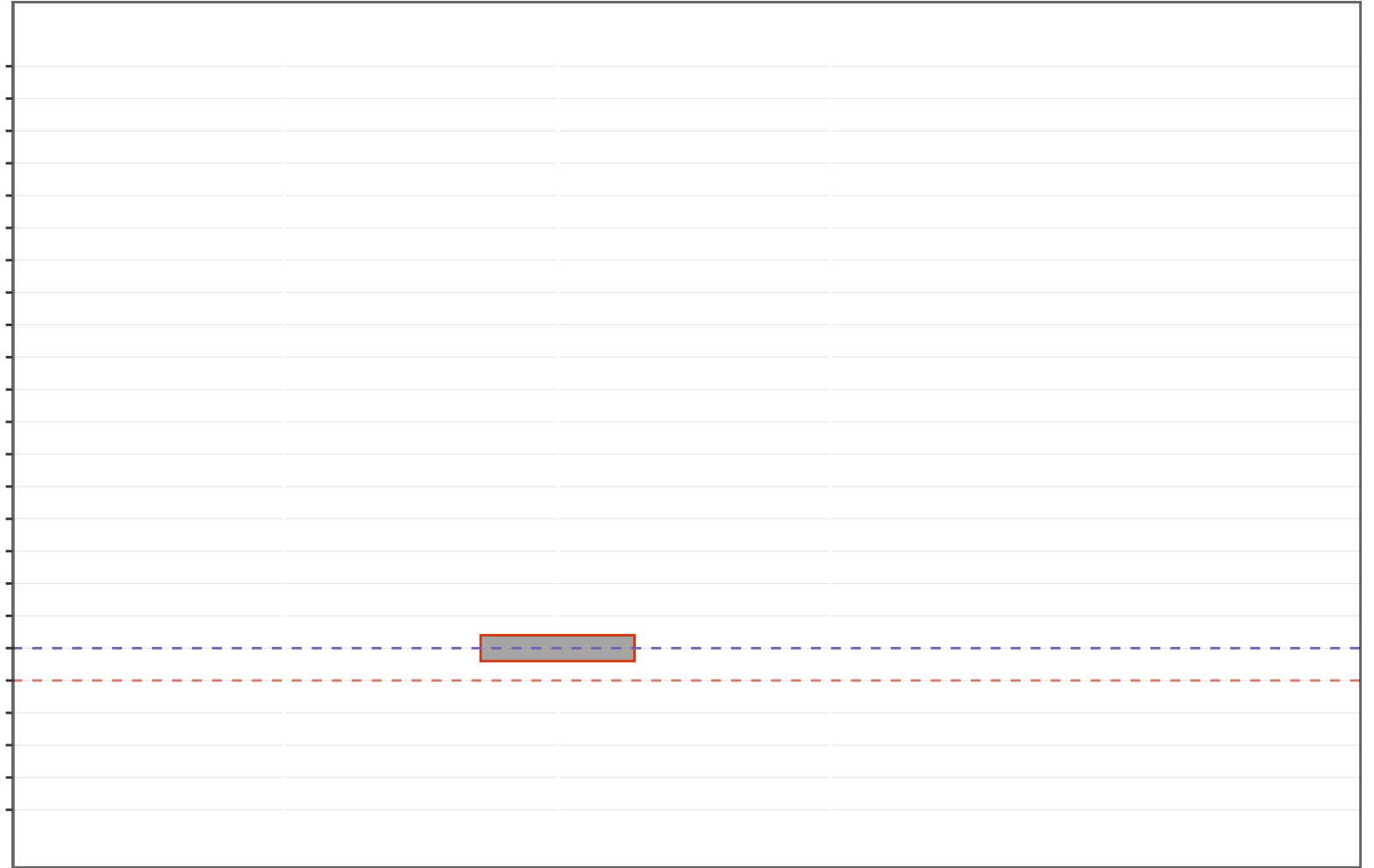
MW indication



Molecular weight



Gel Slice

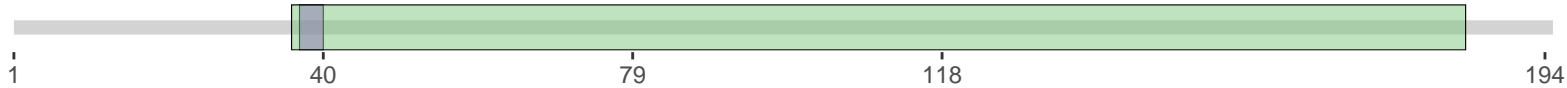


Protein length

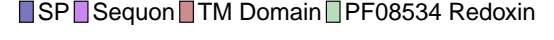


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

QHVPSTYKNNIDKFKAKGIDWICWVNDPYYMNGWAEKLGAKAEAFYGFDFGDFHKSLEDTQLSAALLGPRSHRWSAVYDDGNKVALNVEEAPDFKYSGGDVLGGI

NbL09g18640.1 glucose-1-phosphate_adenylyltransferase_large_subunit_3_chloroplastic/amyloplastic-like [MW = 57.32 kDa]

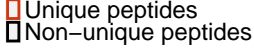
No. of times detected



log(intensity)



Values from



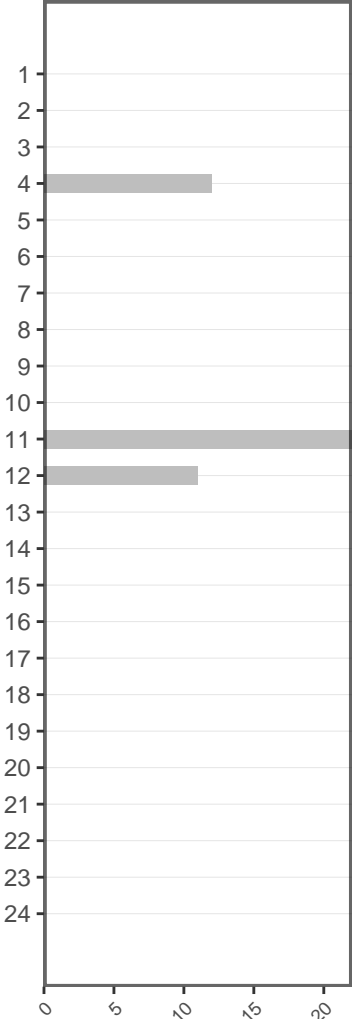
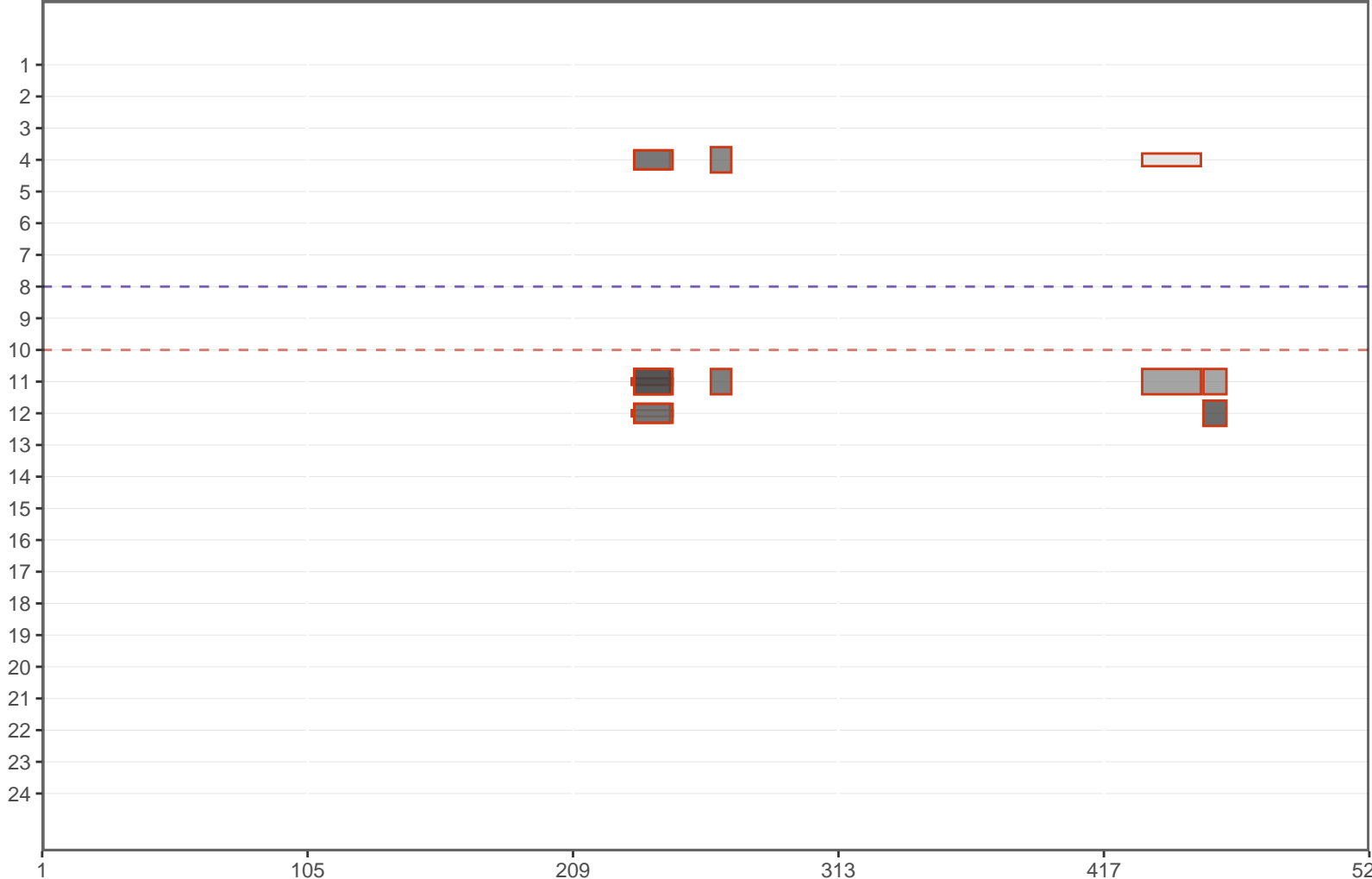
MW indication



Molecular weight



Gel Slice



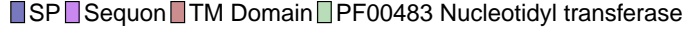
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

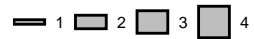


Protein sequence:

DDRRASDFGLMKIDDGGRVGSFSEKPKGGDLKAMAVDTSVLGLSPPEAKKPKYASMGVYVFKKEILLNLRWRFPETANDFGSEIIPSAKEFLKAYLFNDYWDGIGTRFSEANLALTEHPPEFSFYDANKPYTERRNLPFAIDNSKIVDSIVSHGSLTNGFVHVSVGRBRIGSNVHJKDTMALGADYVETDAEIASGLAEGKVPHGIGENTRIKCEGDKNARIGKNVVAANSEGVQEAADRSEEGFYRSGFTVILKNTSIDGLVW

NbL09g18630.1 uncharacterized_GPI-anchored_protein_At3g06035-like [MW - SP = 18.34 kDa]

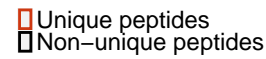
No. of times detected



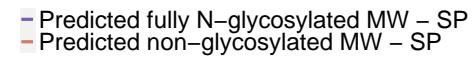
log(intensity)



Values from



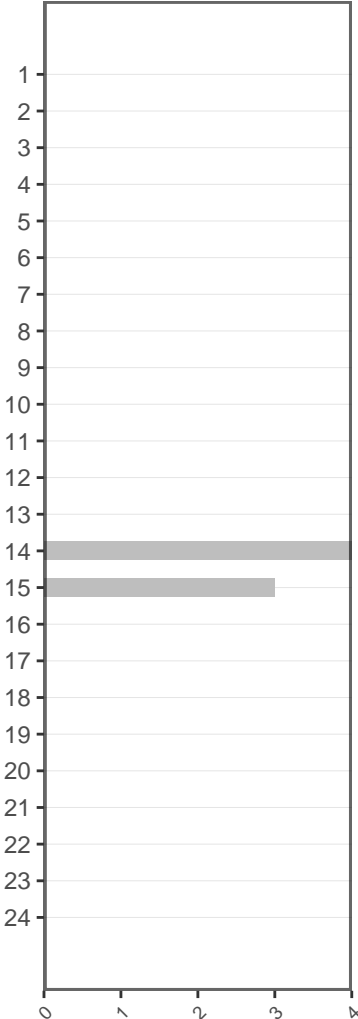
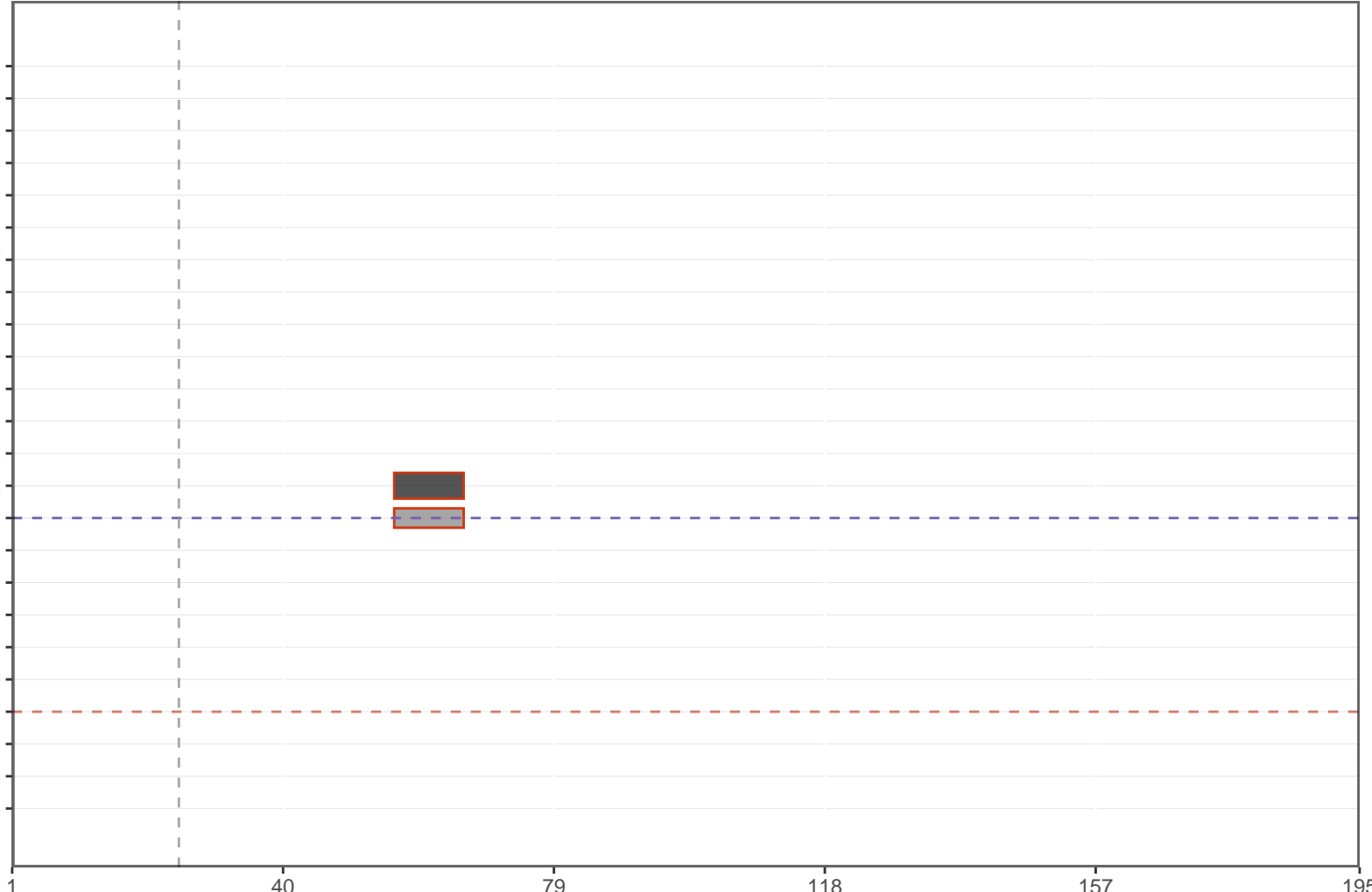
MW indication



Molecular weight

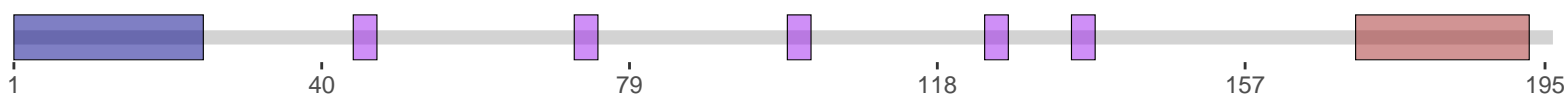


Gel Slice



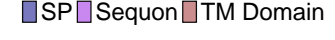
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

QFSQYPKLLSKCDLNATTTTRDGMMPGVPNLVSDLVLENYTKSGYSNLYNDTKFSGVGGSDNWWWLTTNPEGSFTPTSSANLIFGLGLHAWFILVAFVLL

NbL09g18530.1 RAN_GTPase-activating_protein_2-like [MW = 67.48 kDa]

No. of times detected



log(intensity)



Values from



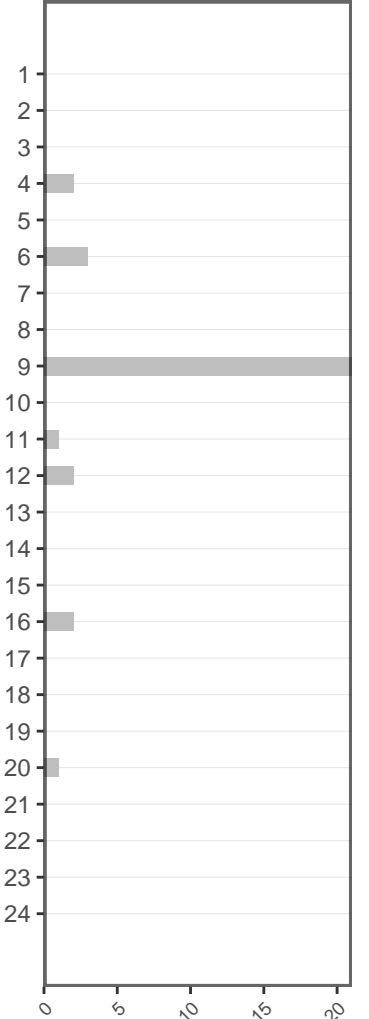
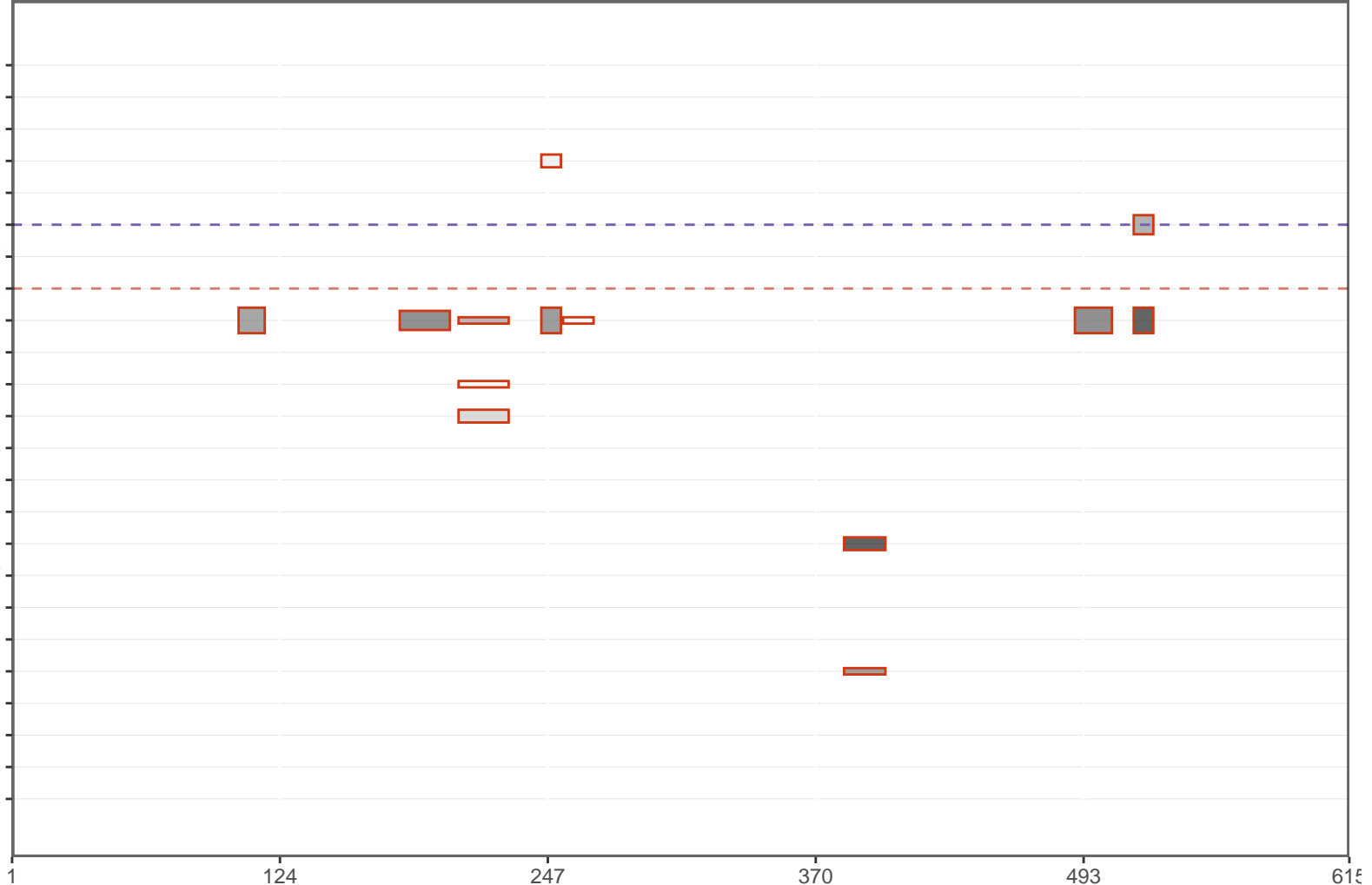
MW indication



Molecular weight

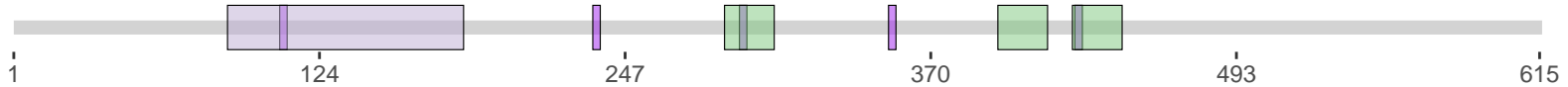


Gel Slice



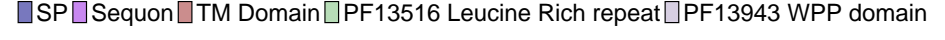
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

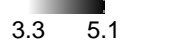
LGEKGVRAFGLKLGSGTNEELVYFINDGSDGEAARAVSELVPTTEKLVLFHFNMTGDEGAWIAEIVNRSPLEDFRGSSTRVSGEGSGALGKSGHKKLDRNMFQPEAGLVKSKALSKHENLTVYLVYLNLEDEGAIAVNTLKDAPSLGVLEMAGNDTEEAAPIASGIAAKGFLSKLSLGENELMDGGAIQAKALRGHNLKVEDMNTALRRAGARVLARTVYHKDFEKLINVNGNFRSEEGIDELKDFEKPPELLASLEDNDPVRDEDDDDDEEKEKSI

NbL09g18400.1 heat_shock_70_kDa_protein_8 [MW = 62.45 kDa]

No. of times detected



log(intensity)



Values from

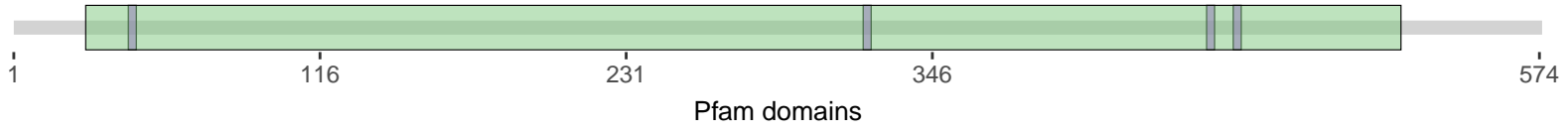
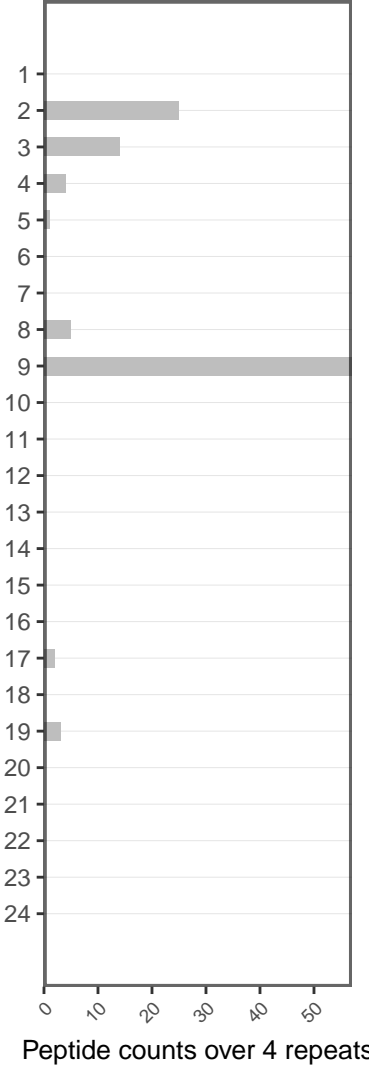
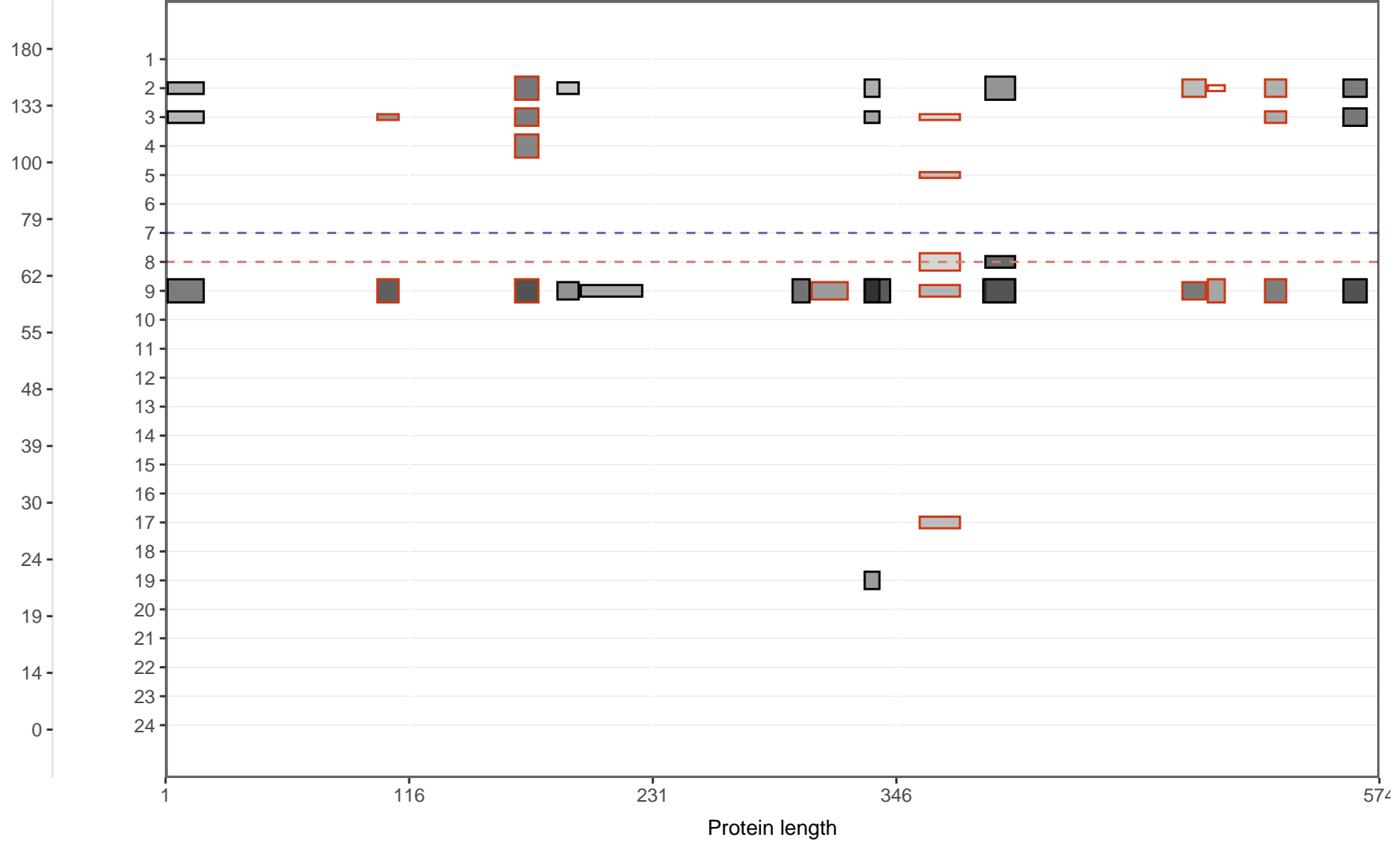


MW indication

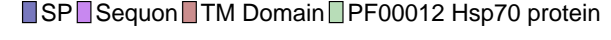


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

HLLPSMDDIFSSHGEEIKRMGLLRVATQDAHKLSSEMSEVPIQVDLNGTKHFKFLERAEEFEVYKEVFGKCEFLKQDLRDAKLEAEQVHDIIVGGGSHVPRNIVMSKIKREELYSGMNPLEAAVIRGAALGVAASGSDPFGSLDLITGATPLSGHQAQDSGNFVAIHKNTFTTTPVRKEGNFTTVDHNGAEALHFVVEGDEKTVEDNHLLGYFKITGIPPLPKGVPEINVCMDIDASNLVLRVAGVVPVGAAGKPPPEVMPFTVDDGHAWSAQTLKRTYGSTLDLVTVXXXK

NbL09g18360.1 probable_serine/threonine-protein_kinase_WNK9 [MW = 83.02 kDa]

No. of times detected



log(intensity)



Values from



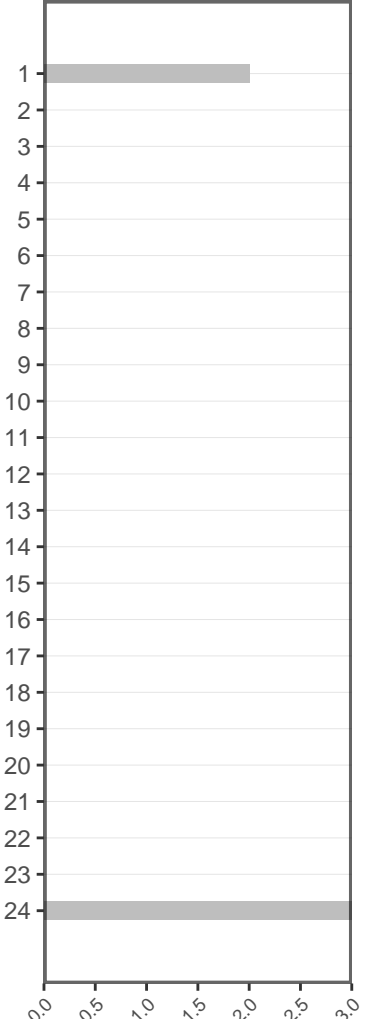
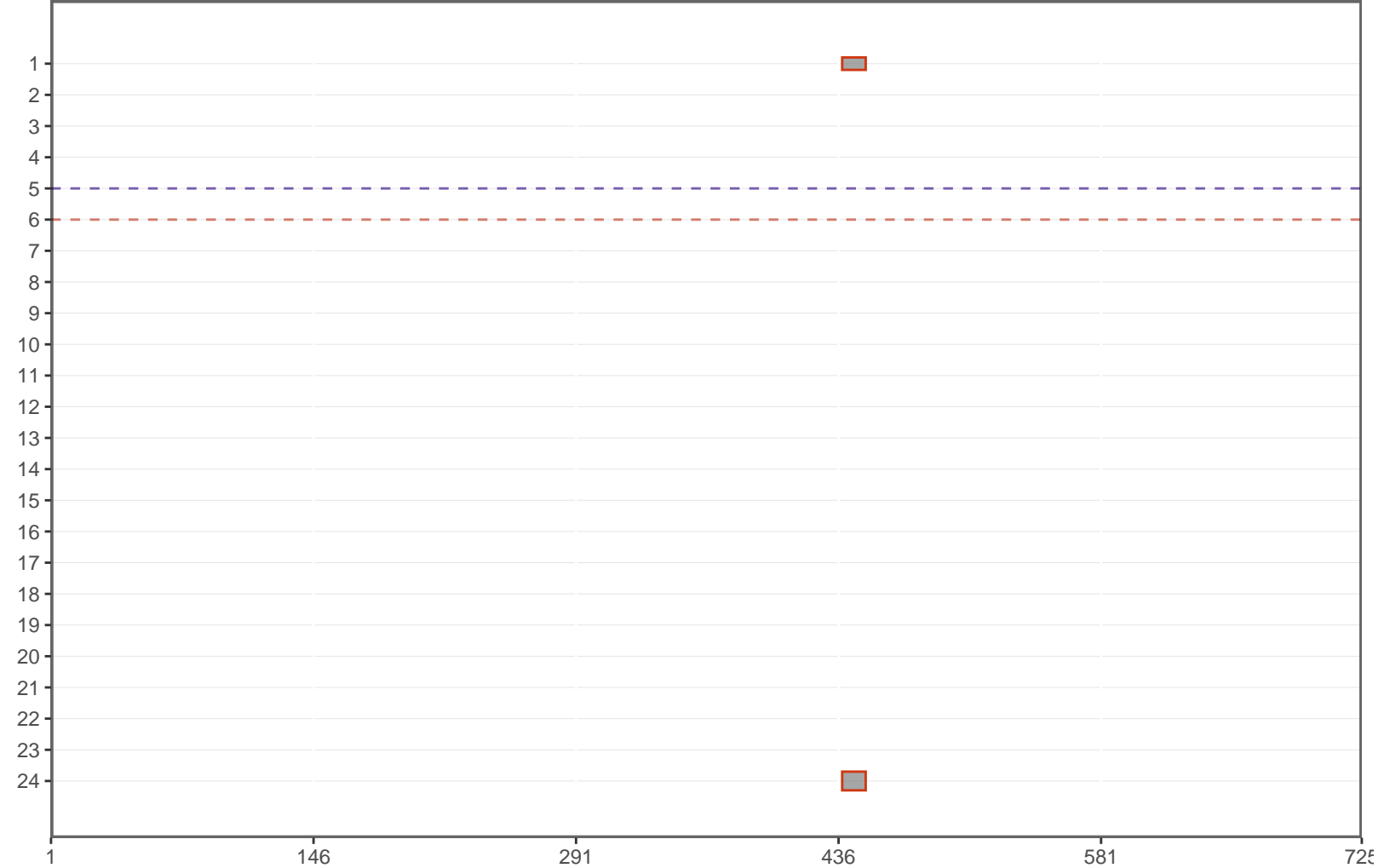
MW indication



Molecular weight



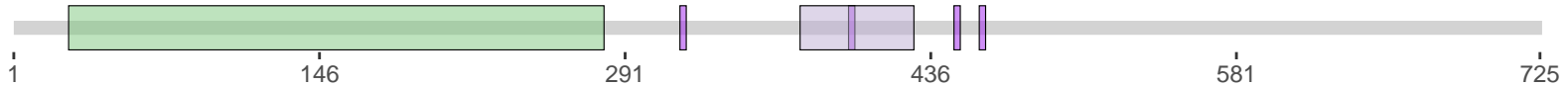
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

IEDDDMENVDISIKGRRRREDDGFLRLRIADKEGRVRRNYFFPDEVNDALVATEMVAELGITDGDVTKIADMDGEIASLVPVWKKGFQMEENLNHTRGKHGASGSLVNYLLFDGPRNLGVLHCGSKHGGAMHGRFEEIMYHLDRSEGGITDAPEGIWESEDDGVHYTDMWAQDKTKSRARSGVDYHSDVKDKLVDESIDGGEELTFVDKDDKSHVRLQDSSPSKSSGARTPVEDYENIRRELRLWKAKYQMLGLKLDORLGVDRKYGRGSSSNKPRDKYS!

NbL09g18340.1 imidazoleglycerol-phosphate_dehydratase [MW = 30.22 kDa]

No. of times detected



log(intensity)



Values from



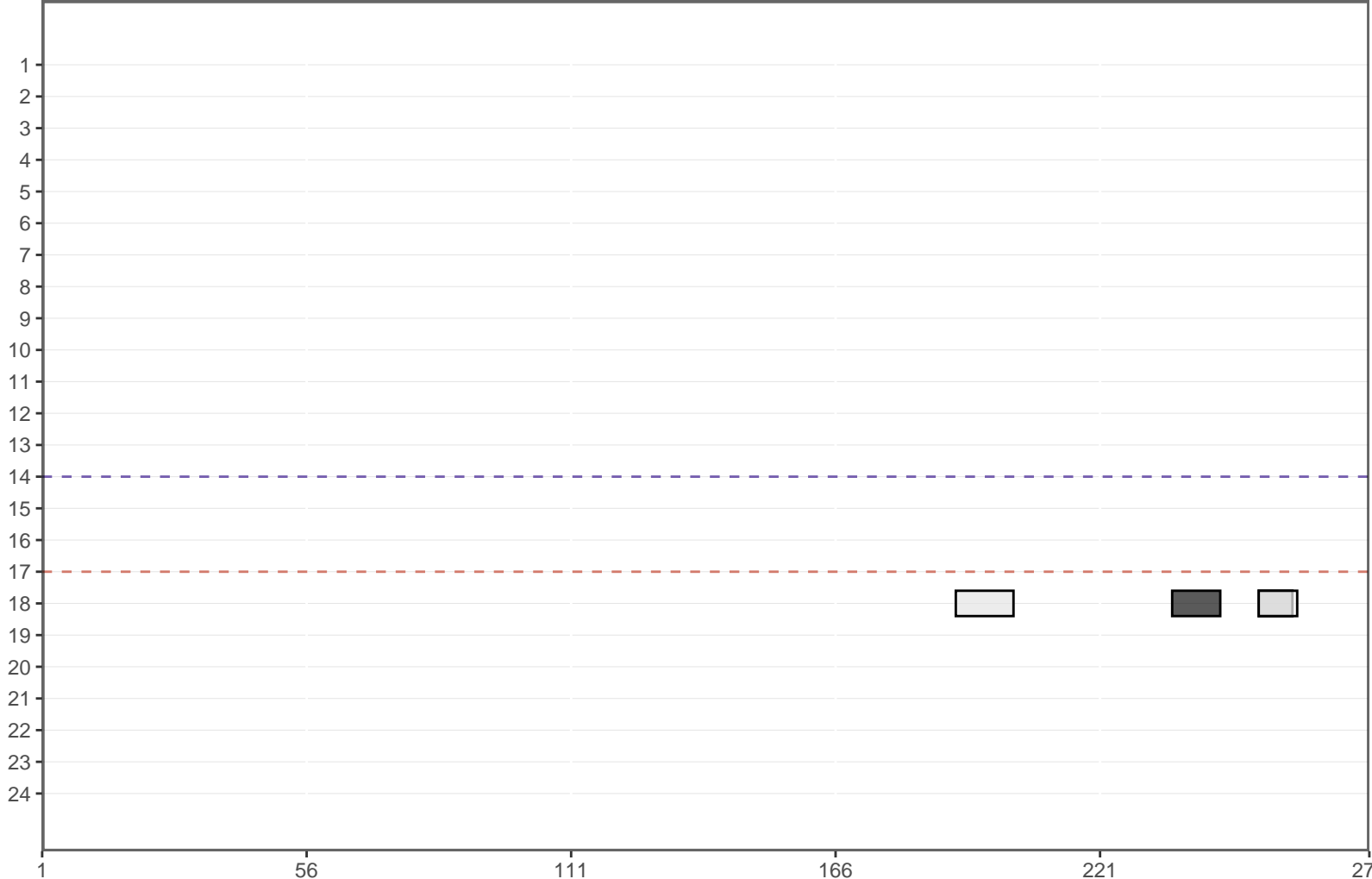
MW indication



Molecular weight

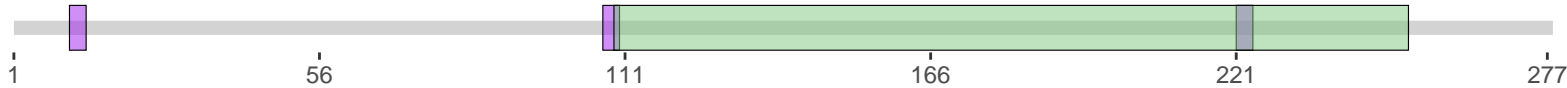


Gel Slice



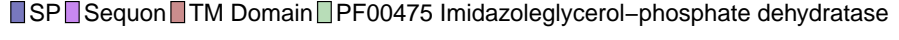
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SLFDVHVKATGDHSDHHTNEDVALAGTALLGALGDRKGINRFQDFSAPLDEALHVSLELDSGRPYLGYDLGIPTRVGTVDYQLVEHFFQSLVNTSGMTLHRLQLAGKNSHIEATFKAFARALRQATEYDLRRGGVSPSGKGLSRG

NbL09g18330.1 photosystem_II_D1_precursor_processing_protein_PSB27-H2_chloroplastic [MW = 22.64 kDa]

No. of times detected



log(intensity)



Values from



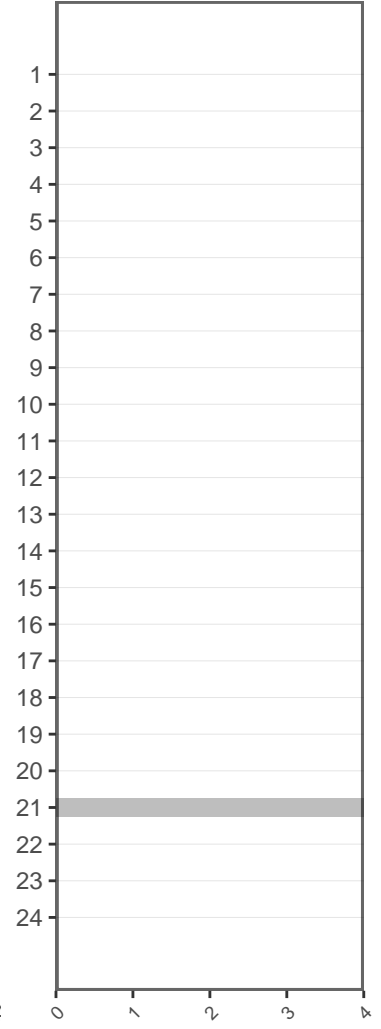
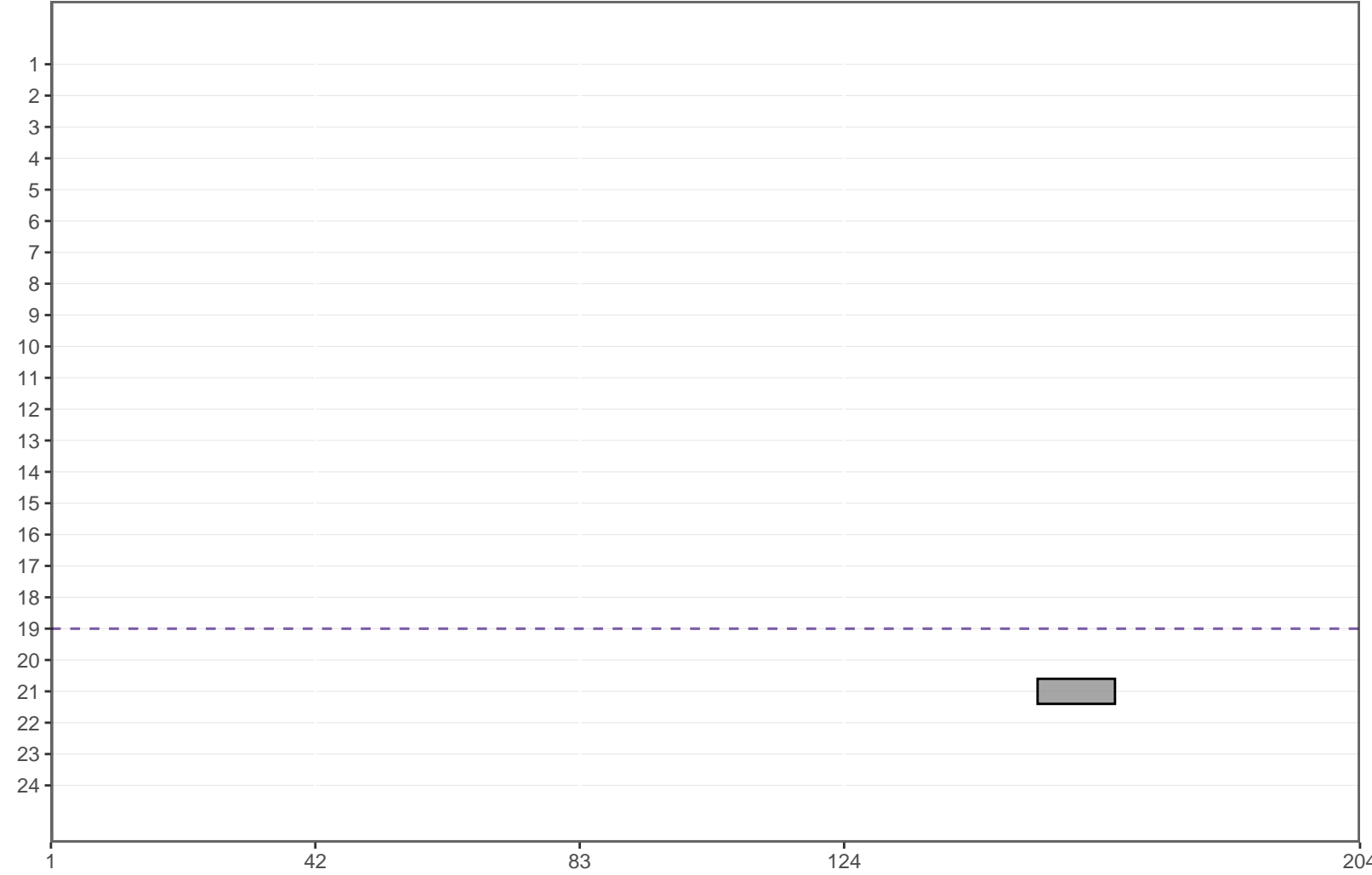
MW indication



Molecular weight

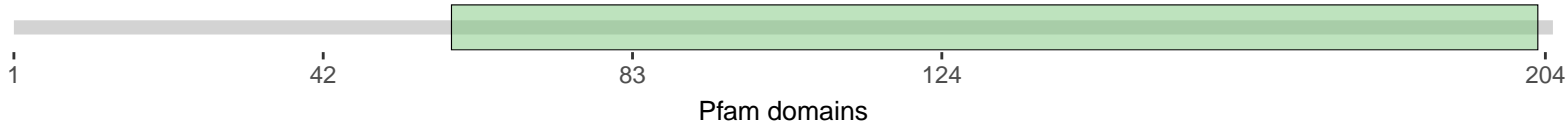


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DPNEKTKSGKILPKEDYKSAIEVWKTLRSEVKEDPNDMSKFRRTADAAKESIREVLGWRGQKSVNEESYVMLEKARBLASFYSKAGSPALPREEIKLELDLDDKAAEAL*

NbL09g18200.1 protein_TPLATE-like [MW = 129.42 kDa]

No. of times detected



log(intensity)



Values from



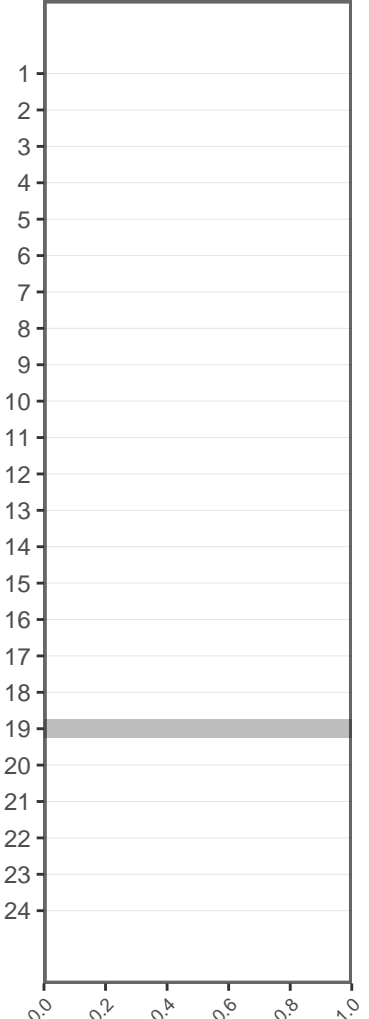
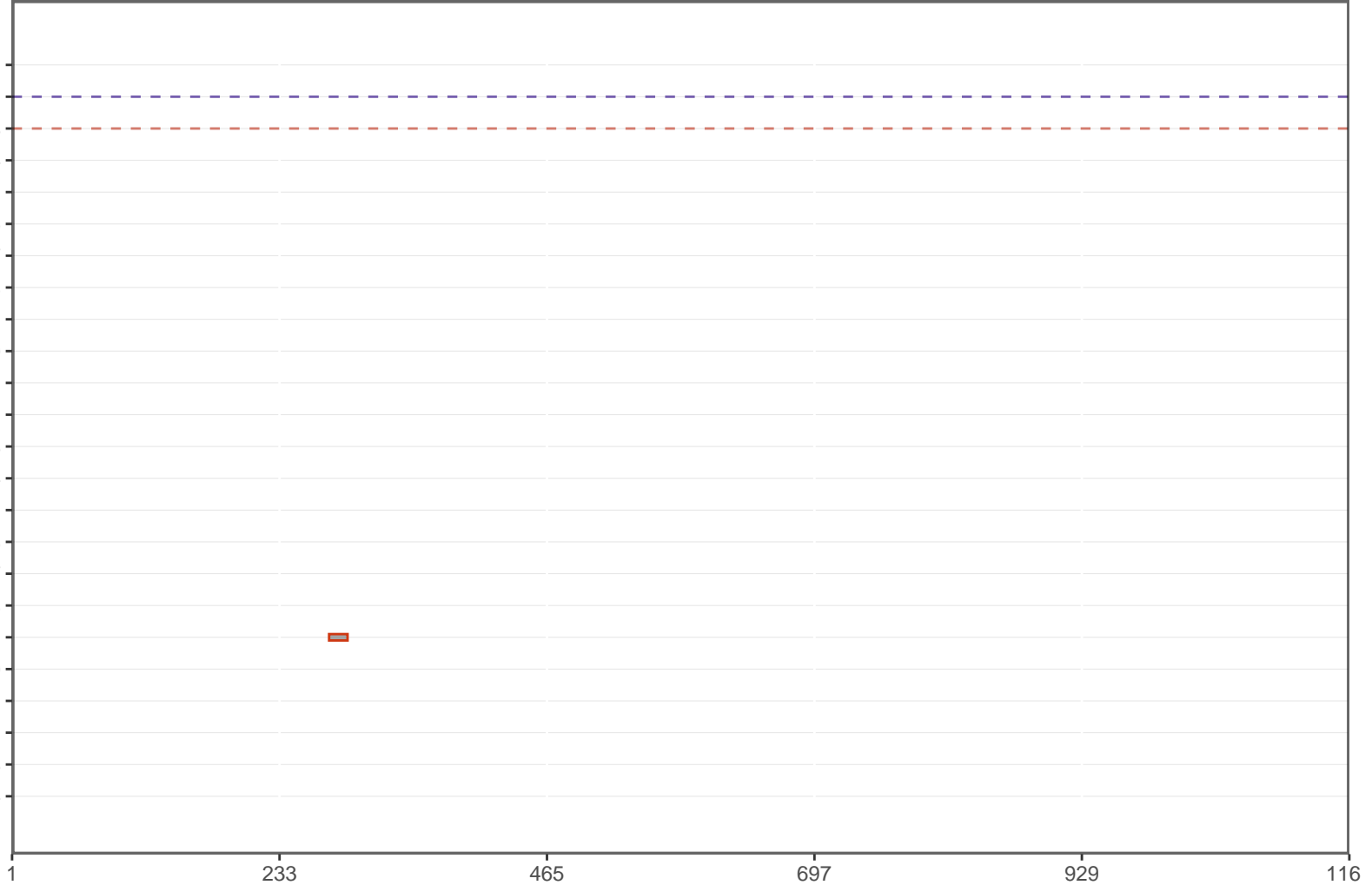
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

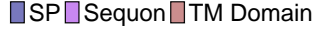
Protein length



Pfam domains



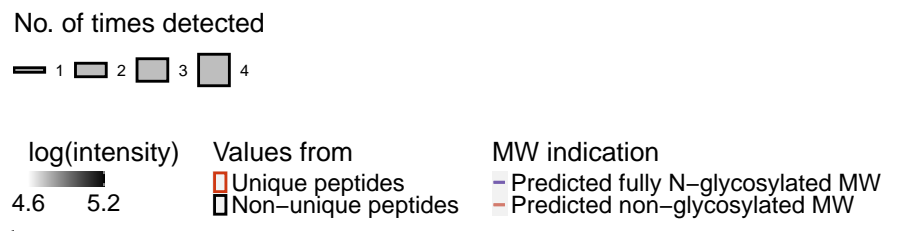
Pfam Description



Protein sequence:

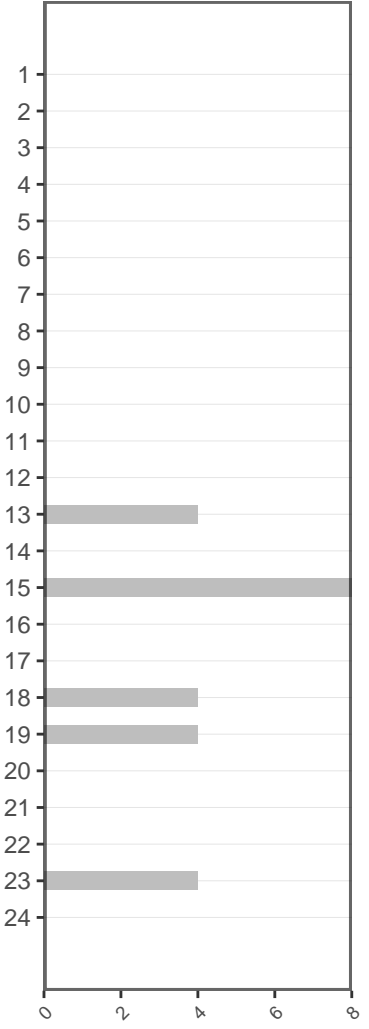
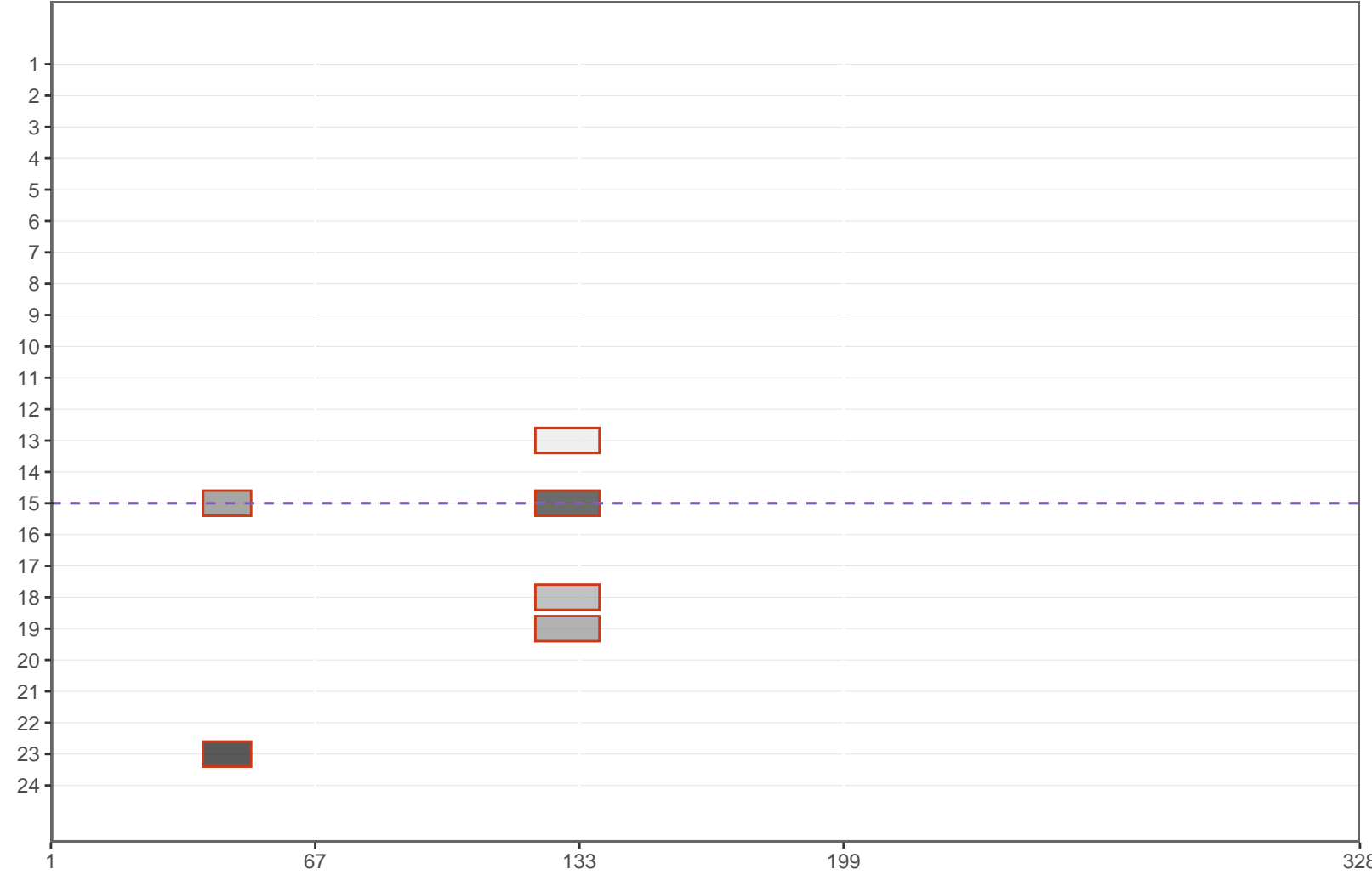
RDLREMNTPVYCTRLWAWSEHIDLEGLDPLADDDPEPLNHSNHKLVFNDSGASTNRLGGVQAVLLCAGRLGSRNARADGQLLKELEDFRNFADSVNKHQGRLLGRKYVSNHSEKWAHVAEGEARGDVPFSSHKLTVGFYEAAAAGDRKLEGLVHKALELWRPDSLALLAKRVDLTLKVPSPAYTLTGSDDPQVVEAYHLDTPSDGRITLHKVNLTEIELNRVDRVGLSGGLYFMDGSPQAVRQLRNLNSGPEVLSGVTGVGVAHFERCDLWVQVLYYPFY

NbL09g18190.1 uncharacterized_protein_At4g15545-like [MW = 35.9 kDa]



Molecular weight

Gel Slice



Protein length

Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain

Protein sequence: PPQTGISTEGSHSYGEEDEMESETSRPRISPGLLASGDTSTRLTPPGSPPLSASVSPERSPRPLRHSISFSTFRGMFDRSISVYSSSTSSGYSMSGLETSSGOTARARVDGKEFFRQVRSISLVEYGFQAFILNPKELNSHGKGTEDTLRKAEIFGDENKOLYTFIEGLTRNAP

NbL09g18170.1 probable_prolyl_4-hydroxylase_4 [MW = 35.62 kDa]

No. of times detected



log(intensity)



Values from



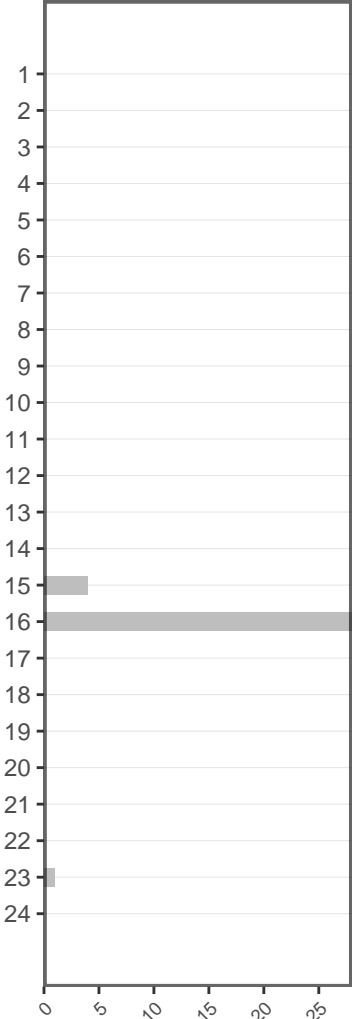
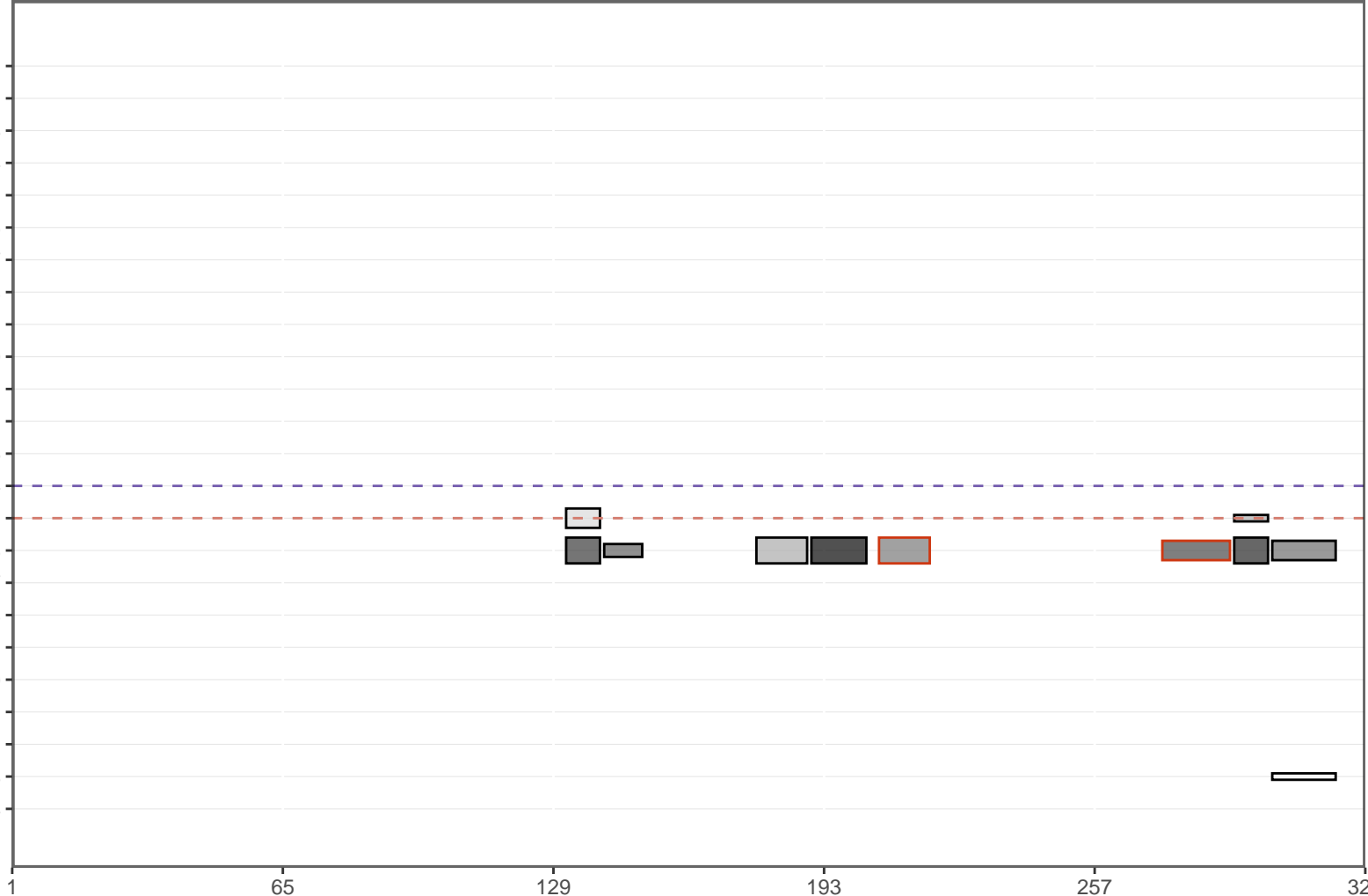
MW indication



Molecular weight

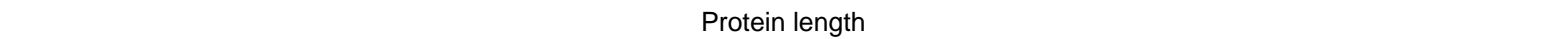


Gel Slice

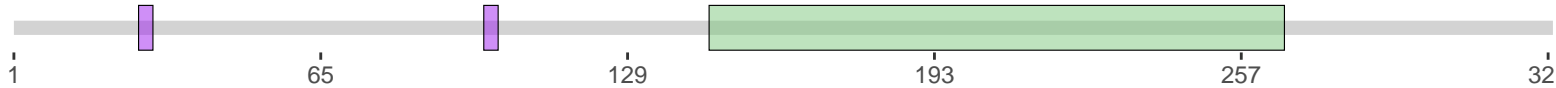


Peptide counts over 4 repeats

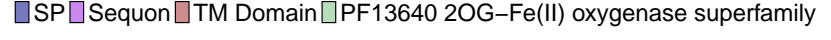
Protein length



Pfam domains



Pfam Description

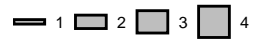


Protein sequence:

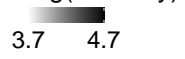
IEGQKYEPHYDYFSDKWNVHGGHRLATVLMYLSDEVEKGGSETVFEAEESTRRRSMADDLSECGARKGIANVPRKGDALLFSLHPNAVDPDMSLHGCGFVIEGKWSATKWIHVDSFDKIVGSGESCADQNGENCERWAALGECTKNPEVMVGS66DLPGSCRKSGKAD

NbL09g18090.1 ABC_transporter_C_family_member_14-like [MW = 169.55 kDa]

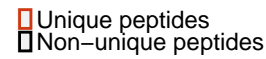
No. of times detected



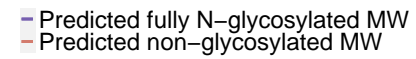
log(intensity)



Values from



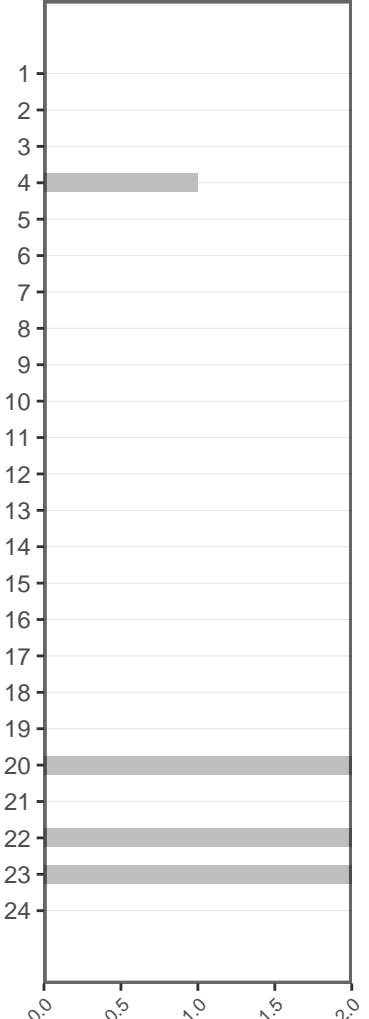
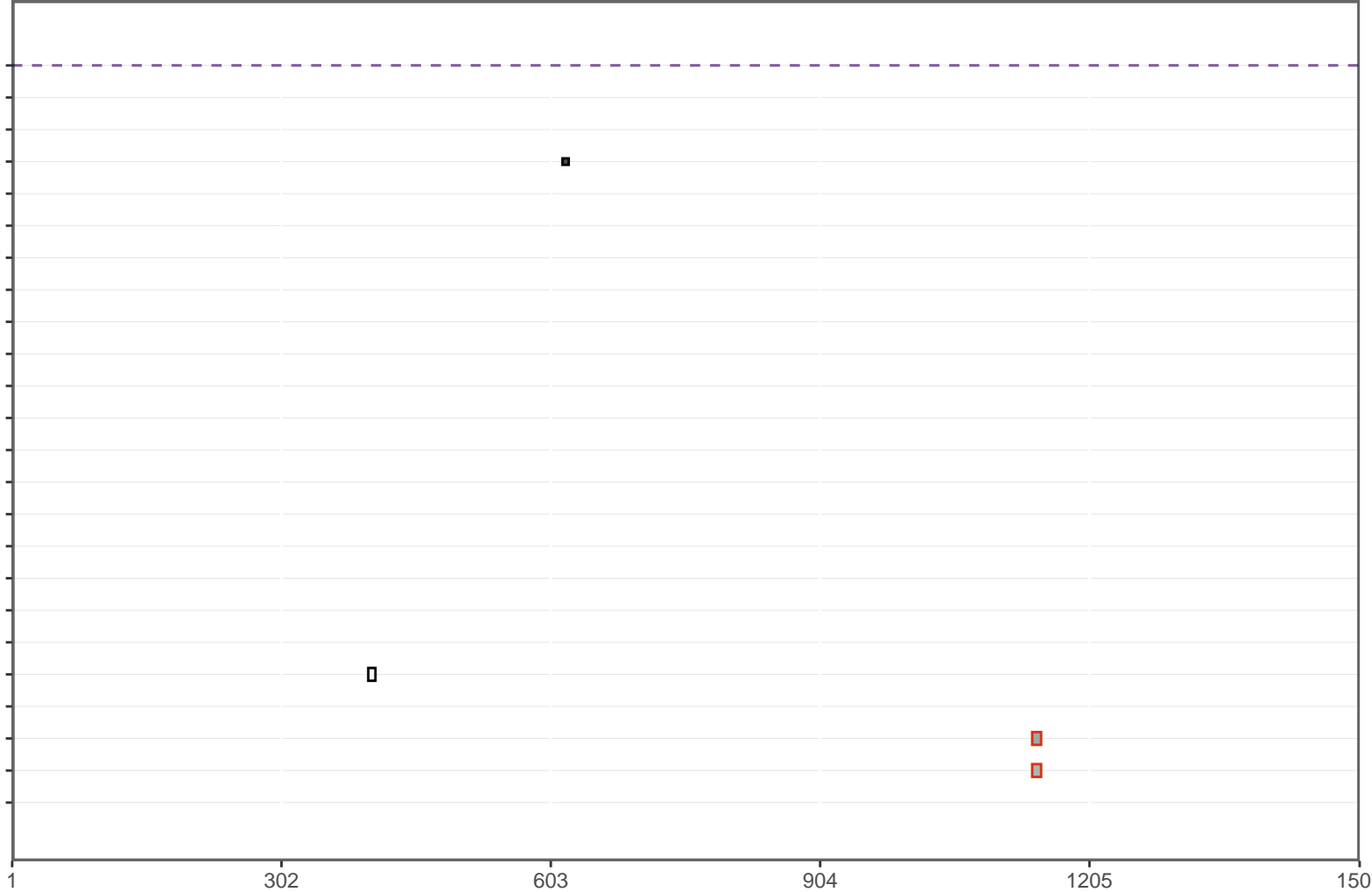
MW indication



Molecular weight



Gel Slice

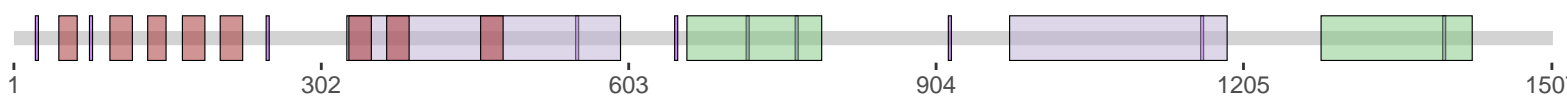


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

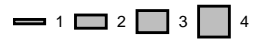


Protein sequence:

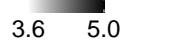
DVRYCSLEKDLKLEHGGDTGEIGERINLGGGKGRIGLARAVYQDRVYLLDDIFSAVDAQTGSEFKCVRGALDKDTNVLVTHQVDFLHNADLHVMRDGEIVQSGKYEELELGMDFGDLVAAHENEMELVESSAENLPGTRRPHQVQVTPKSPQKSGEETNGESTSLDGGPKNSKLEIEEERETGHVDFVYKGYGTEAFGWVGVVLLISALWQDSTMLEDVWLVAYETKDKHIFSPFLFNVYGHAAIGSIFVIRSLVAFGLKTKAGFFDGLDSLHAPMSFFDT

NbL09g17990.1 isoleucine--tRNA_ligase_chloroplastic/mitochondrial [MW = 123.94 kDa]

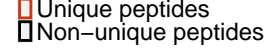
No. of times detected



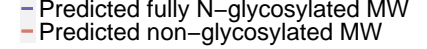
log(intensity)



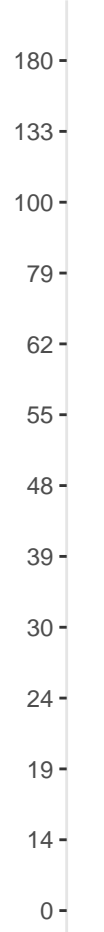
Values from



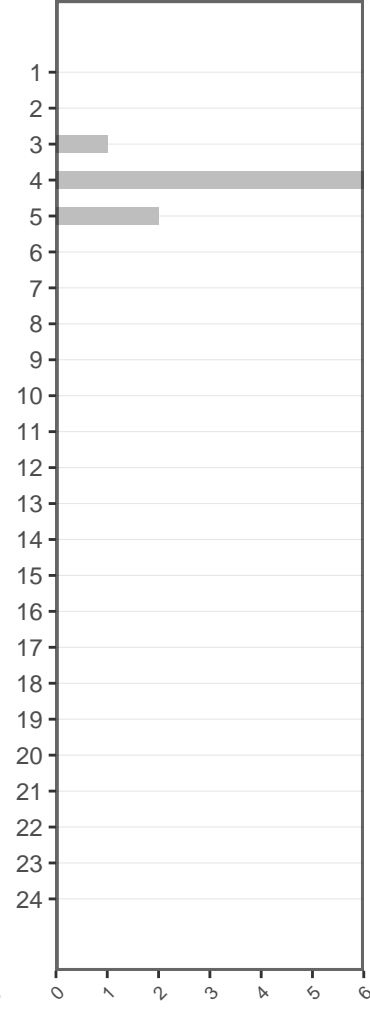
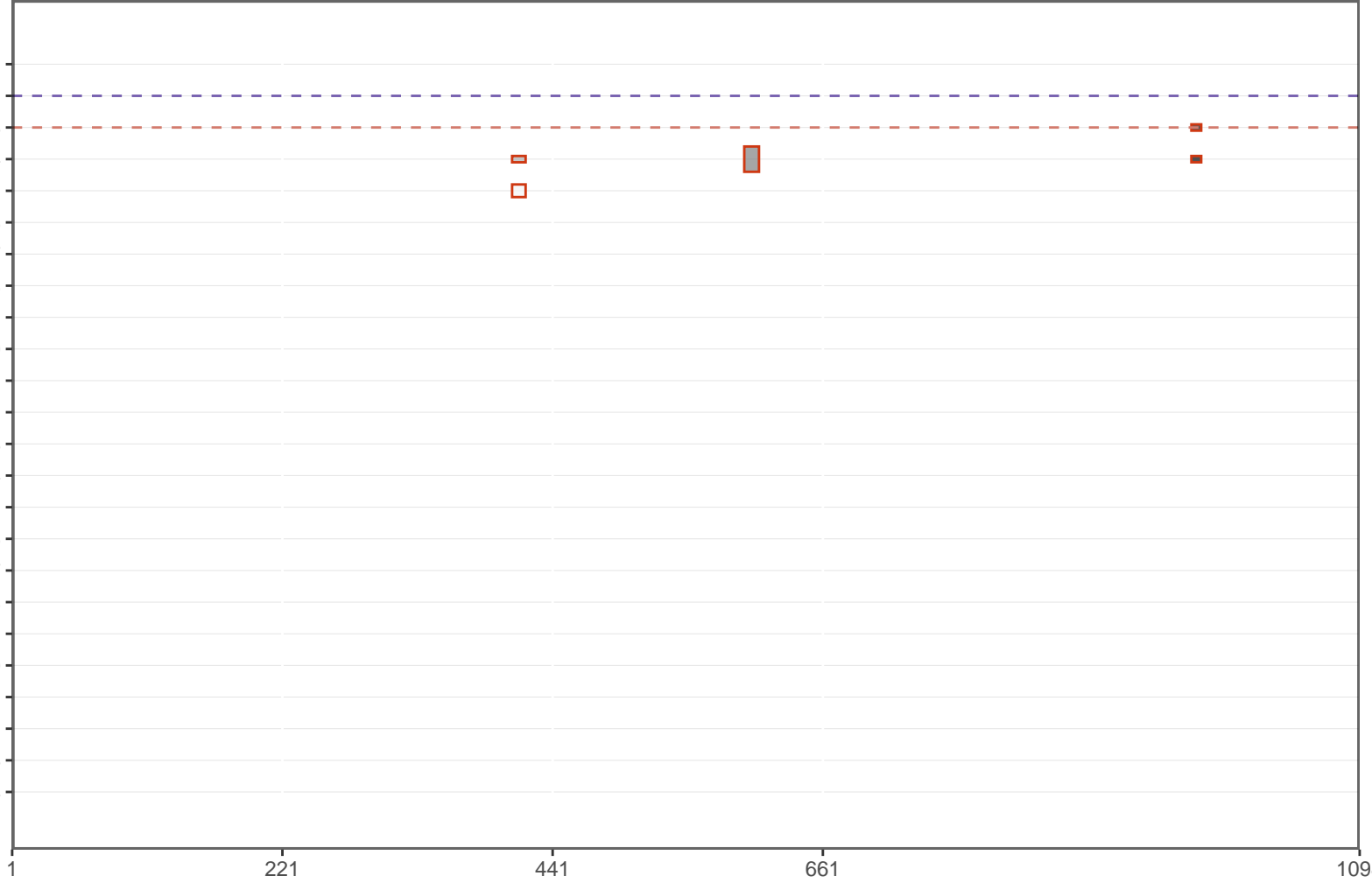
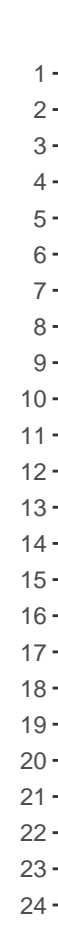
MW indication



Molecular weight

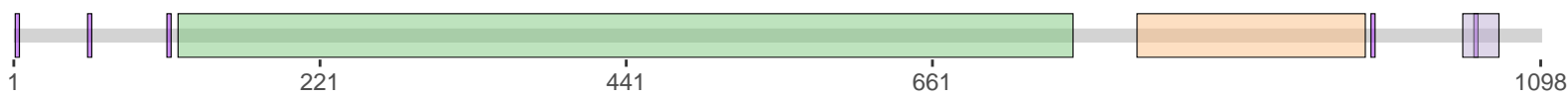


Gel Slice



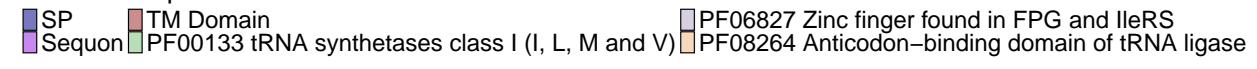
Protein length

Peptide counts over 4 repeats



Pfam domains

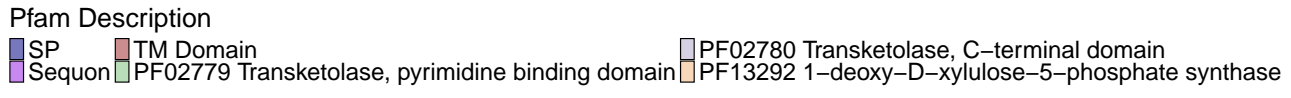
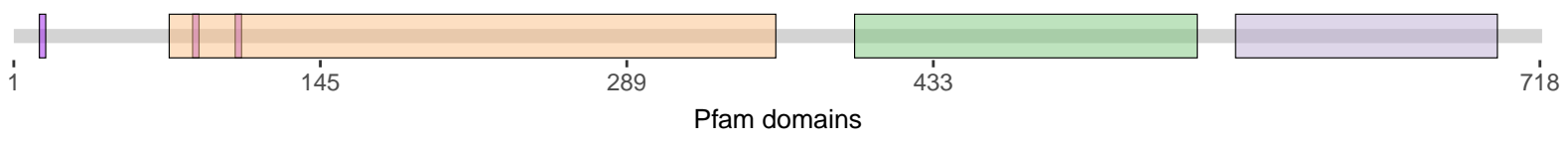
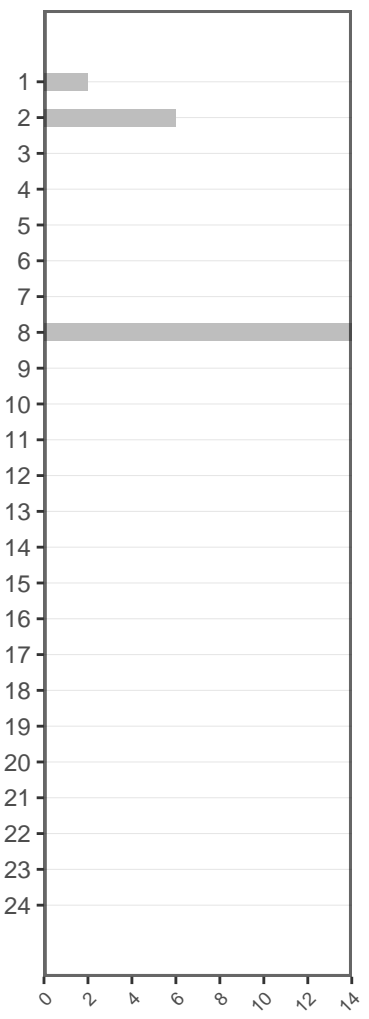
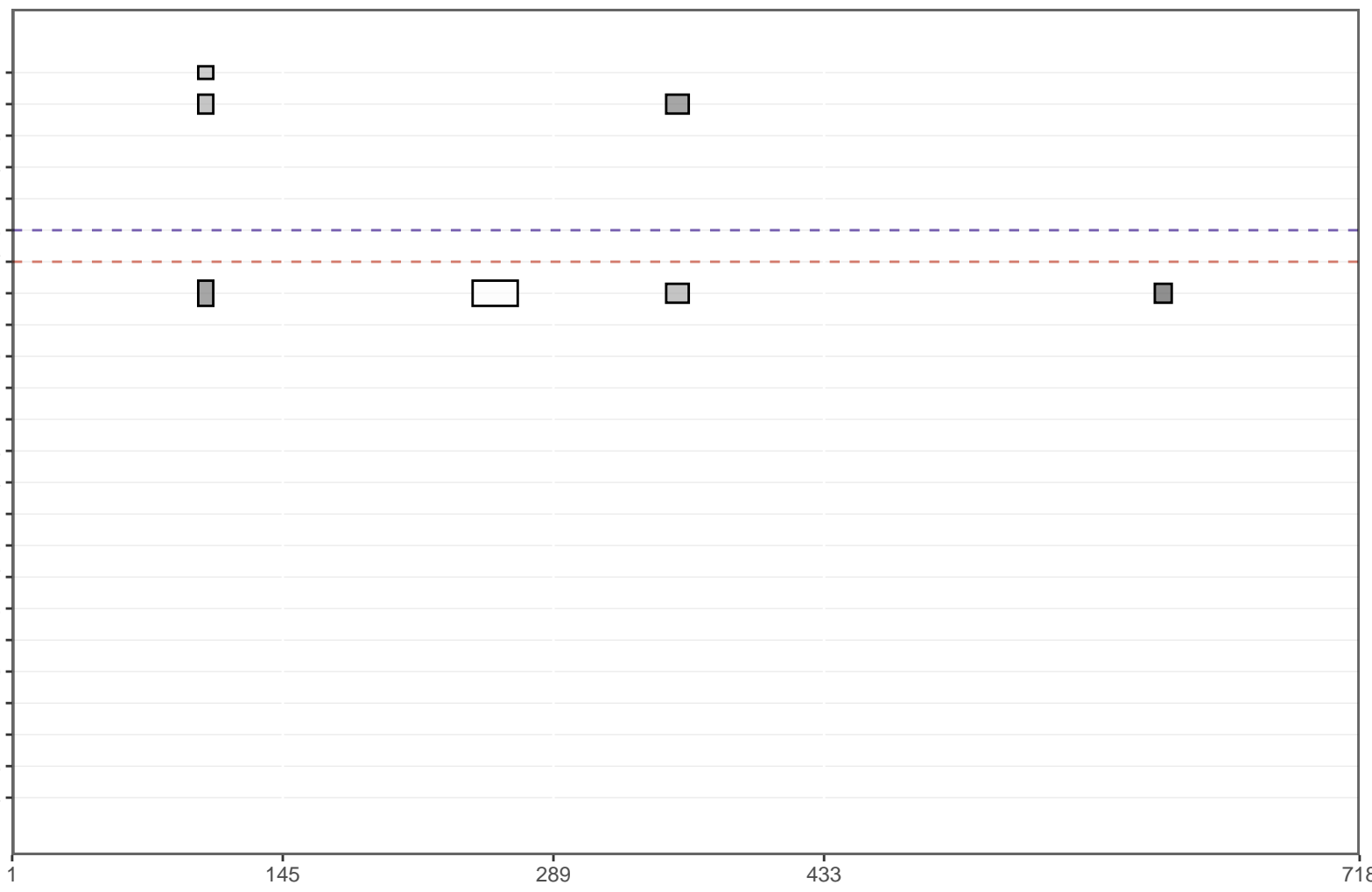
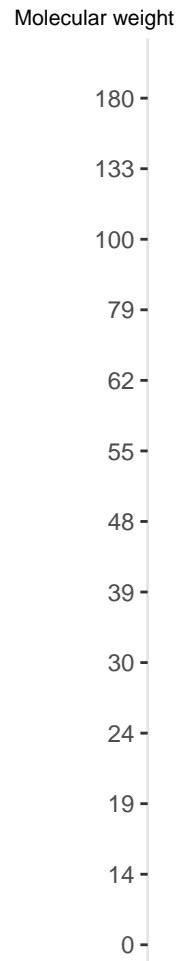
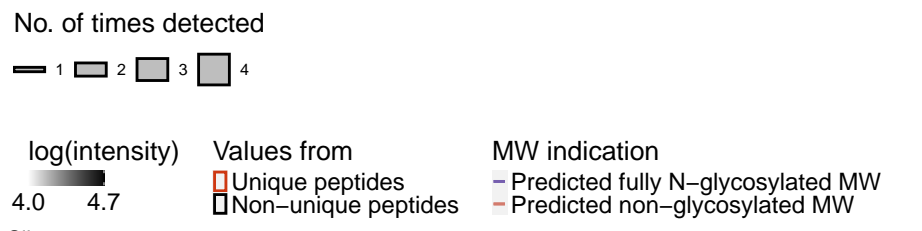
Pfam Description



Protein sequence:

WFASVEGFRDAJMDAINGVITWPTFGAVNRISAMTSGRSEVWISQRRTWGVPIFYHVESKEPLMNEETIDHKISISQKGSDDAWWMSVEELLPEKYDKASNYEKGTDTMDVWFDGSSGAAWLVKLRRESLNPADLYEGTDQHRGWFQSSLLSIAITGMAPYRQVWTHGFLVDERGLKMSKSLGNVDRPMVIEGKNGKESPPYSADVLRLWVSSVDYTGDLVIGPQVLRQMSDIYRKLRLGTLRFLANLHDWKADGAVPYSDLPMDQVLFOLANVYNNRE

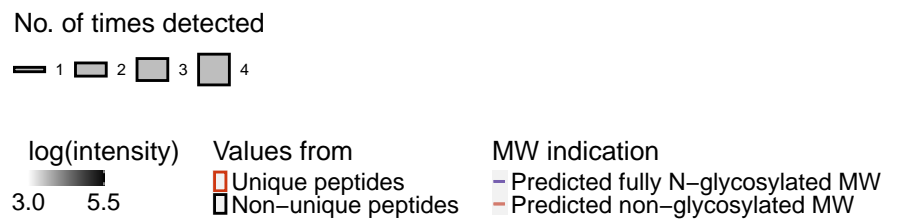
NbL09g17950.1 probable_1-deoxy-D-xylulose-5-phosphate_synthase_chloroplastic [MW = 77.4 kDa]



Protein sequence:

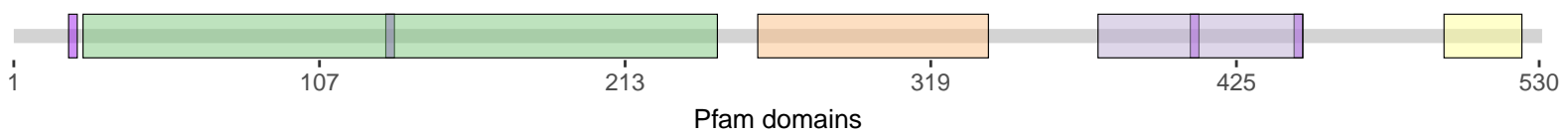
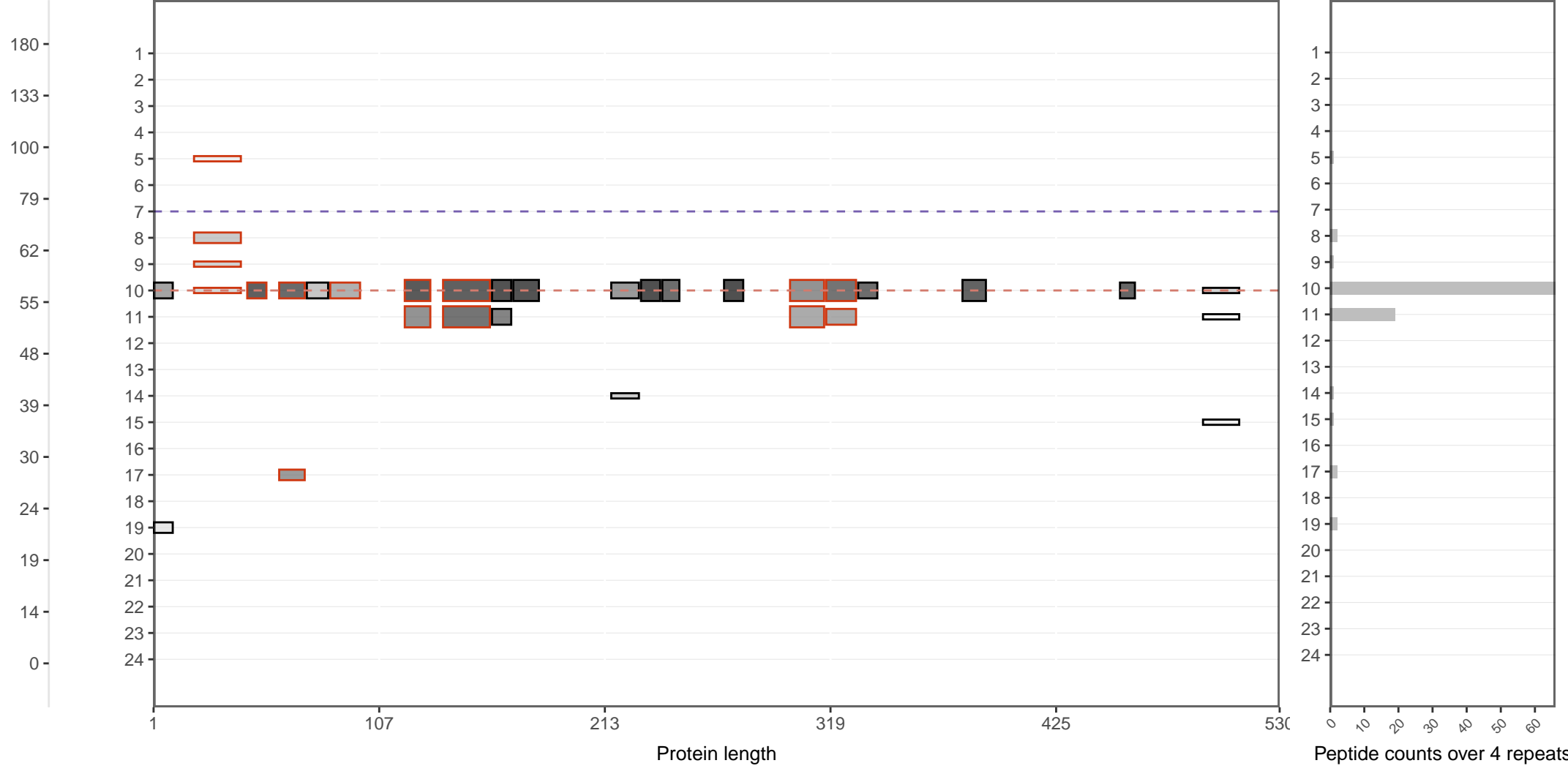
STKTTGPIIIVITENKRGYFPAERAADKYHGVAKFDPMTGKGVKSAKTSQYTTTFYAEALIAEAEADKDAIAHAAAMGGGTCMNLFHRFPNRFDFVAGIEGHAVTFAGLACEGLKPFCAVSSFLGRAYDGMHVDVDMGKLPVRFAMDRAGLVGADGPTHGAFDVFMAQLNMYVMVAPSDAEALFHMVATAAADDKPSGFRYPYRPNRNGGVELPVENKGRIFLEVKGKGRILVEGERVALLGYGSAVGNGLTAAVLETRGLQVTVADARFCKPLDGLAIRSLAKSHVEL

NbL09g17860.1 bifunctional_3-dehydroquinase_dehydratase/shikimate_dehydrogenase_chloroplastic-like [MW = 57.53 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF01487 Type I 3-dehydroquinase
- PF08501 Shikimate dehydrogenase substrate binding domain
- PF01488 Shikimate / quinate 5-dehydrogenase
- PF18317 Shikimate 5'-dehydrogenase C-terminal domain

Protein sequence:

SPDTRFGIGKPYSHKREPLLYNEAFRIVGFGVGLPLPLDDVNFRTYSBLDFAGFSGCTPHKEAVDDGDEVDPAKLGAVNGVRRPDGKLFQDNTDYSVAISEALQSGSPMSGSLAGKLFVVGAGGAGKALYGAKEKGRVAVNRTYERARELADVYGGALGLDELNHFPEQDMLANTTSYGMQPKVDDTPSKALRYYSLVDAVYTPKTRILLRGAQESGKVVTVGEMFVGGQAYEGYERFTGLPAPKELFKKIMAGVY

NbL09g17850.1 superoxide_dismutase_[Cu-Zn] [MW = 15.27 kDa]

No. of times detected



log(intensity)



Values from



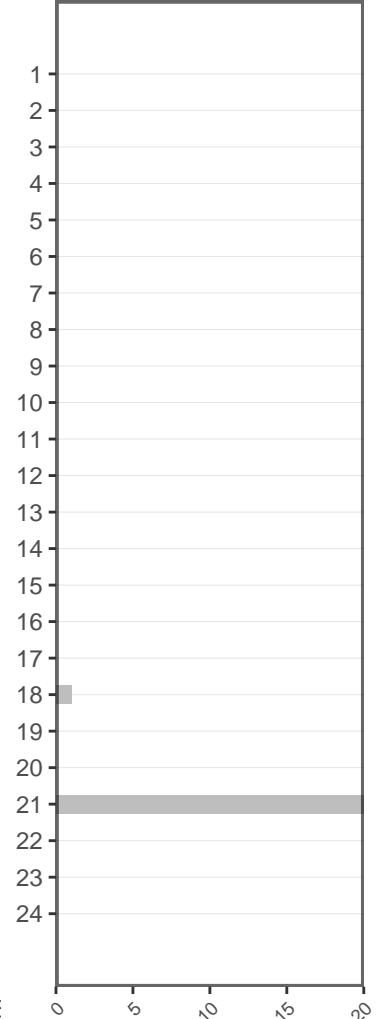
MW indication



Molecular weight

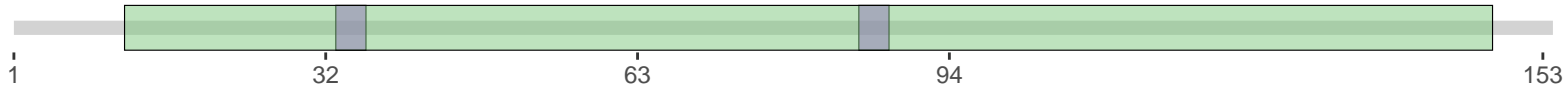


Gel Slice



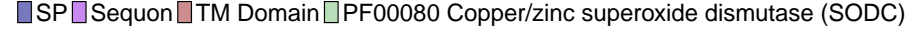
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YNPAGKEHGAFEDVVRHAGDLGNITVGEDGTAFSTFDKQIFLAGPQSIGRAVVVHAPDQDLKGGHLEKTTGNAGGRVAGGKLGQ*

NbL09g17840.1 acyl_carrier_protein_1_chloroplastic-like [MW = 13.99 kDa]

No. of times detected



log(intensity)



Values from



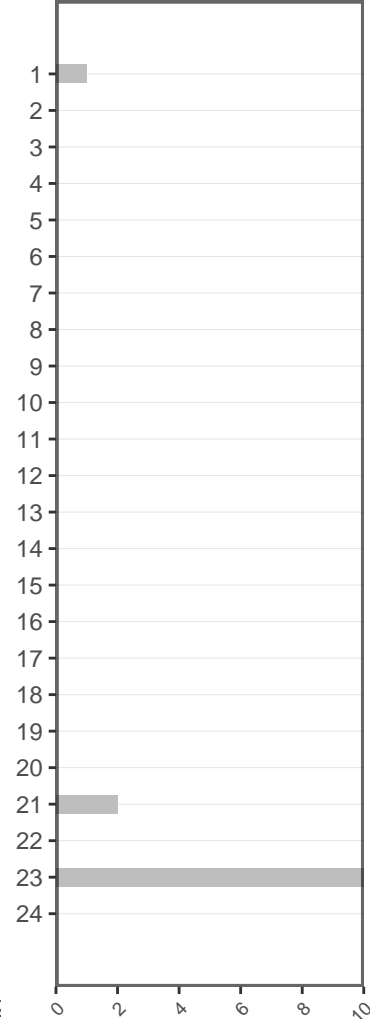
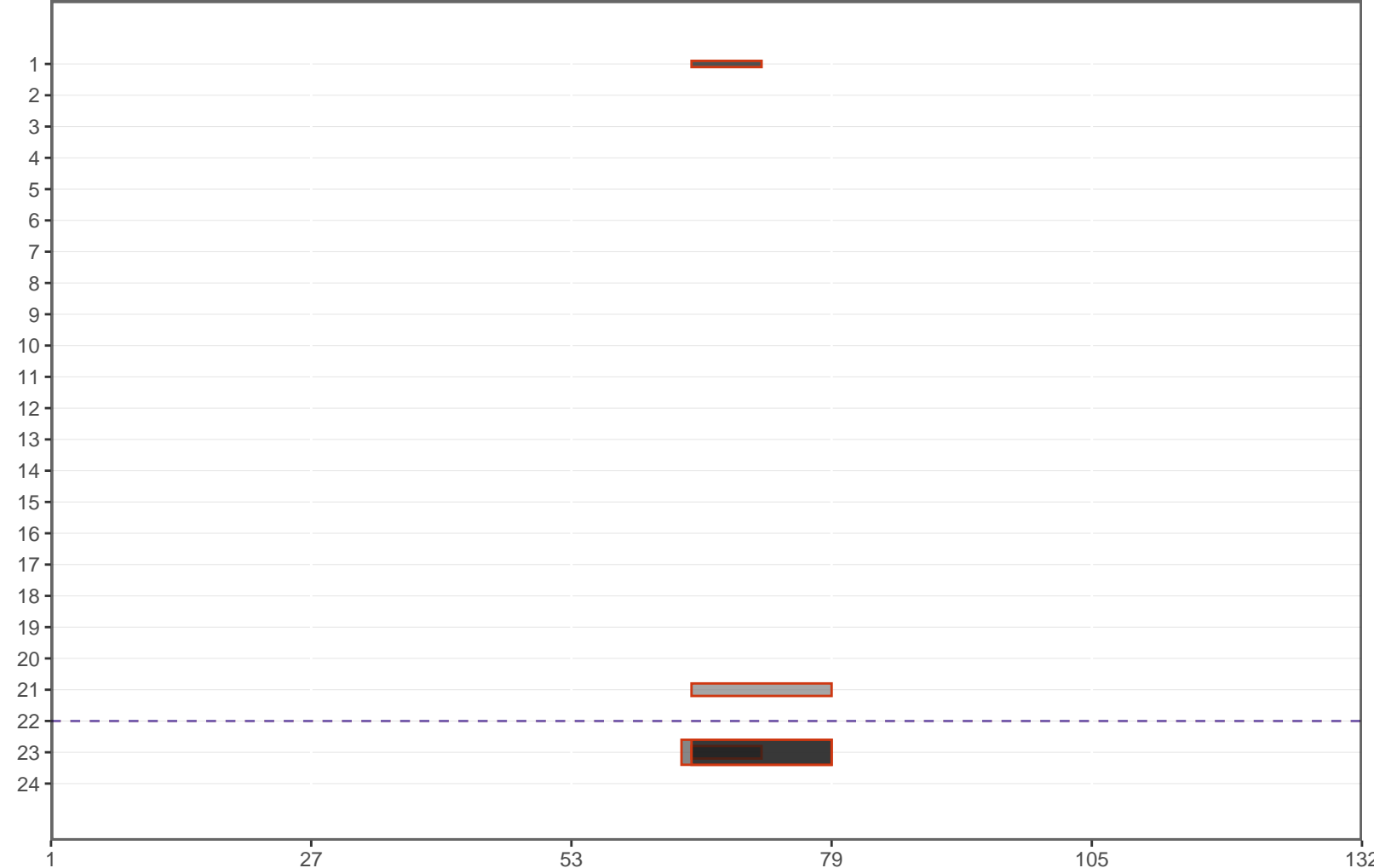
MW indication



Molecular weight



Gel Slice

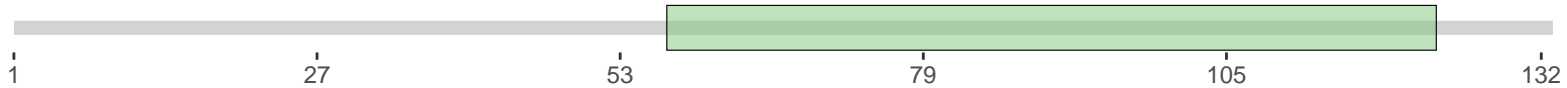


Protein length

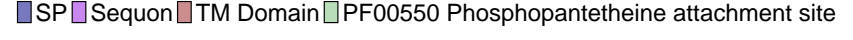


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ETVNVKVEIVKXKQALALTDKIVVNGESKFTALGADSLDTVENMGLLEAFGFTVEEENAGTATVGDAAADJEDLISKKA*

NbL09g17760.1 uncharacterized_LOC109208031 [MW = 26.81 kDa]

No. of times detected



log(intensity)



Values from



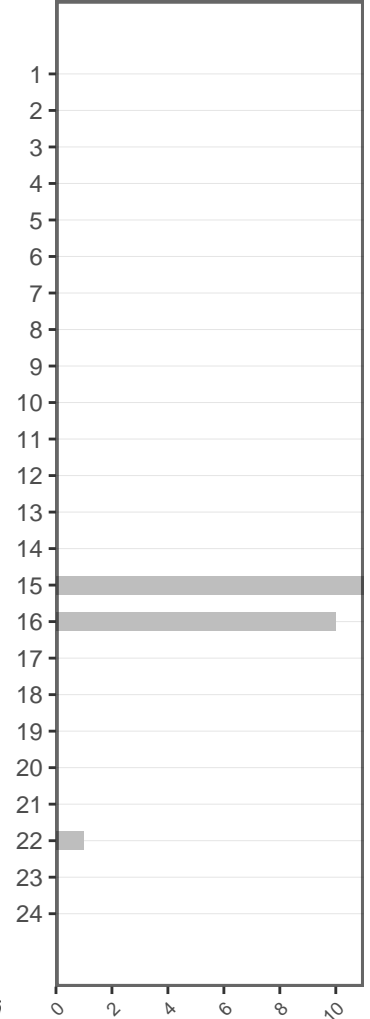
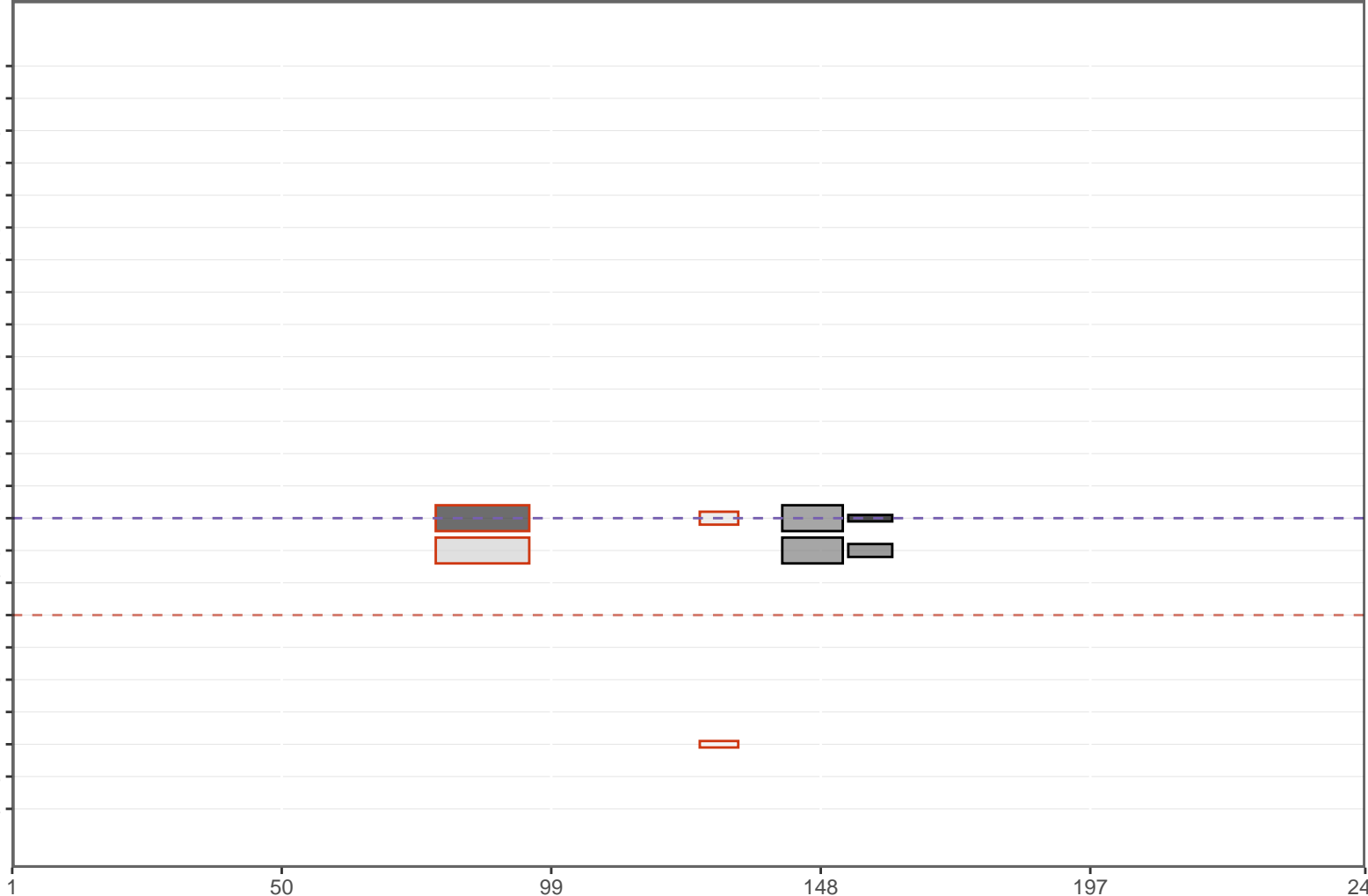
MW indication



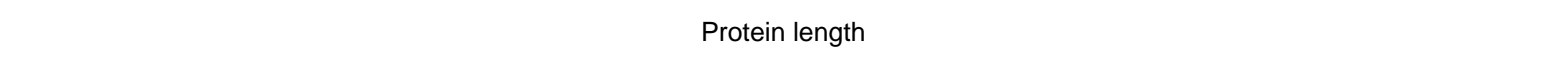
Molecular weight



Gel Slice

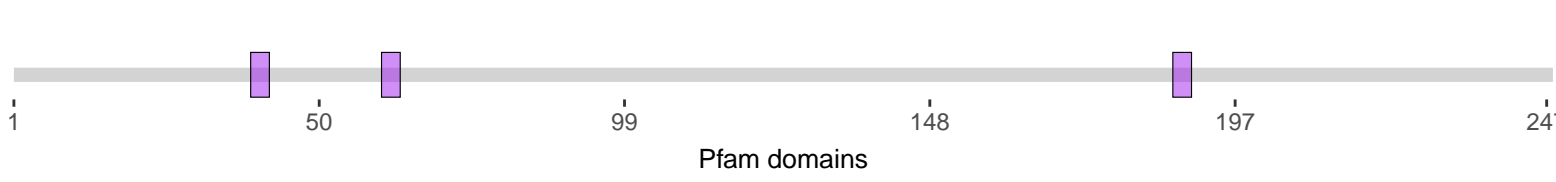


Protein length

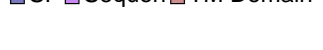


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IFGQTMITDHIHDELKMGISPSRETKFTSKFFYVFCAPPSPRTEDVPGDREAAKHWGEGSFLFTSSSAPYDCEDNGSVDEEDGPIVPIGRSPRTDLKAAEEVLEFGGCVIRLAGYISLDMDFKELGFFLCSL

NbL09g17320.1 uncharacterized_LOC109205690 [MW = 17.24 kDa]

No. of times detected



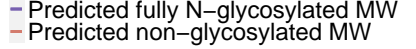
log(intensity)



Values from



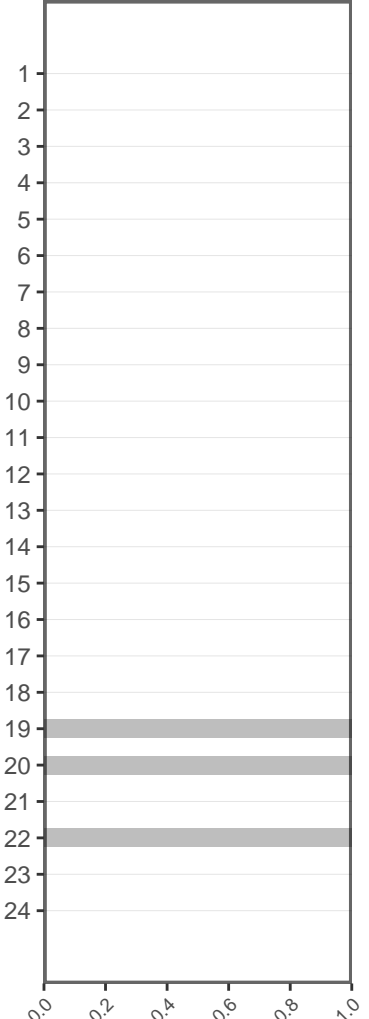
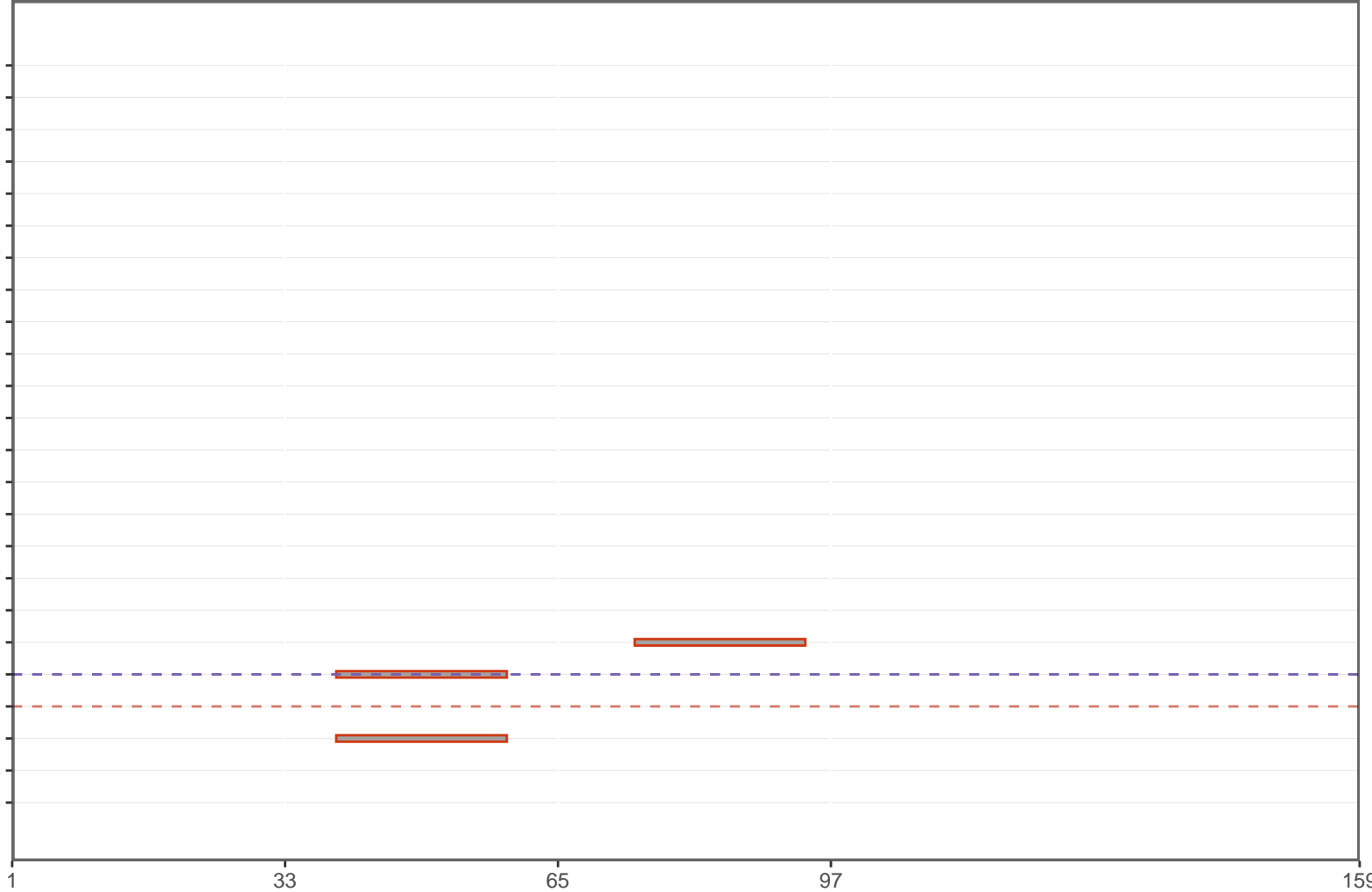
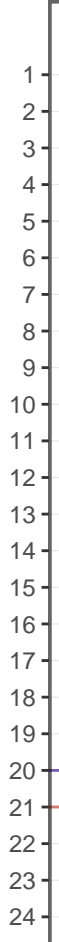
MW indication



Molecular weight



Gel Slice



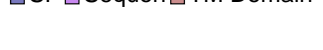
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VGASMRGEMGEKPGLEGVSPGENEALKTYVNSNFGSINNSIMLGGSSVETNDPGVHLDSDDYDQETPTPKGHGKKKERGSSKHYYHSQHSF

NbL09g17090.1 acylpyruvase_FAHD1_mitochondrial [MW = 26.79 kDa]

No. of times detected



log(intensity)



Values from



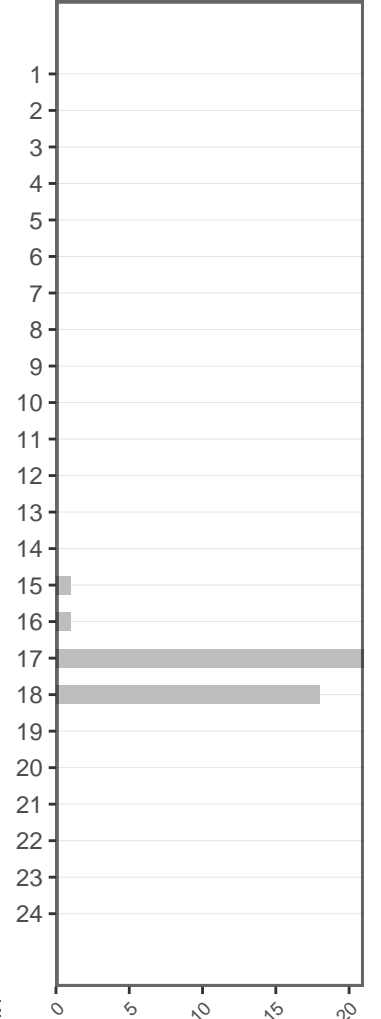
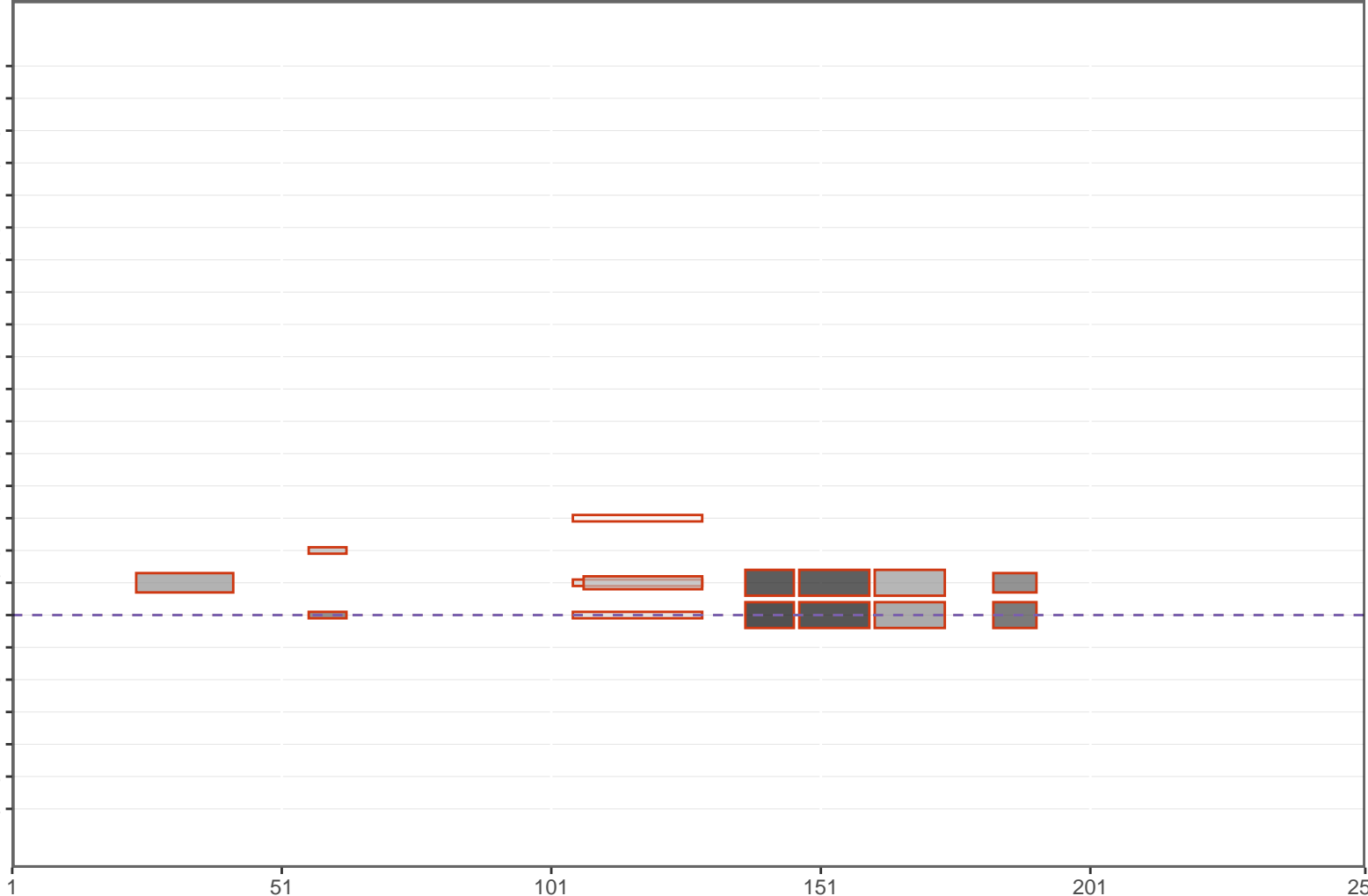
MW indication



Molecular weight

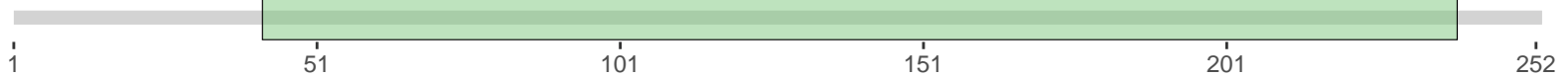


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AMIDYGGYALALDMTAREIQATARSAGLPWTVAKGDDFTFRP6SVLPKSMVDPDFHDIELWLVKNGEIRQKSGTSDMIFRIFLUSHISSMTLFGGDVLTGTPKGGVGVKVGGEIDAGITGLLDVHFVDVGRRPGAKGG

NbL09g17020.1 probable_acyl-CoA_dehydrogenase_IBR3 [MW = 91.27 kDa]

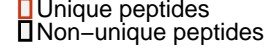
No. of times detected



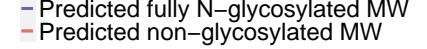
log(intensity)



Values from

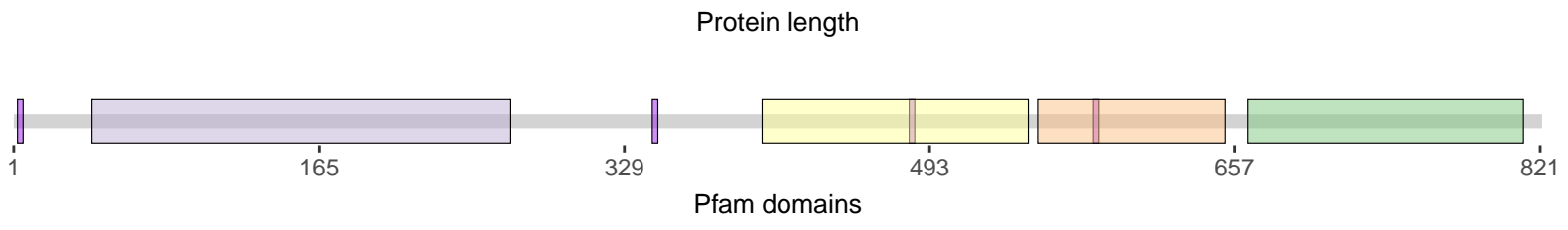
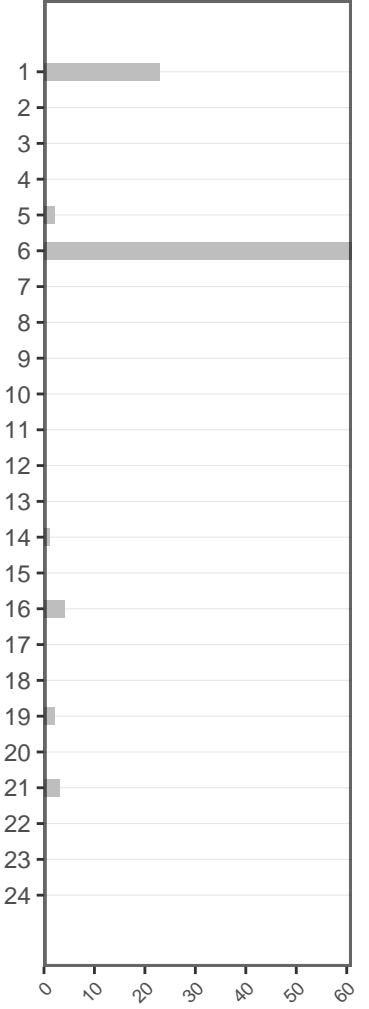
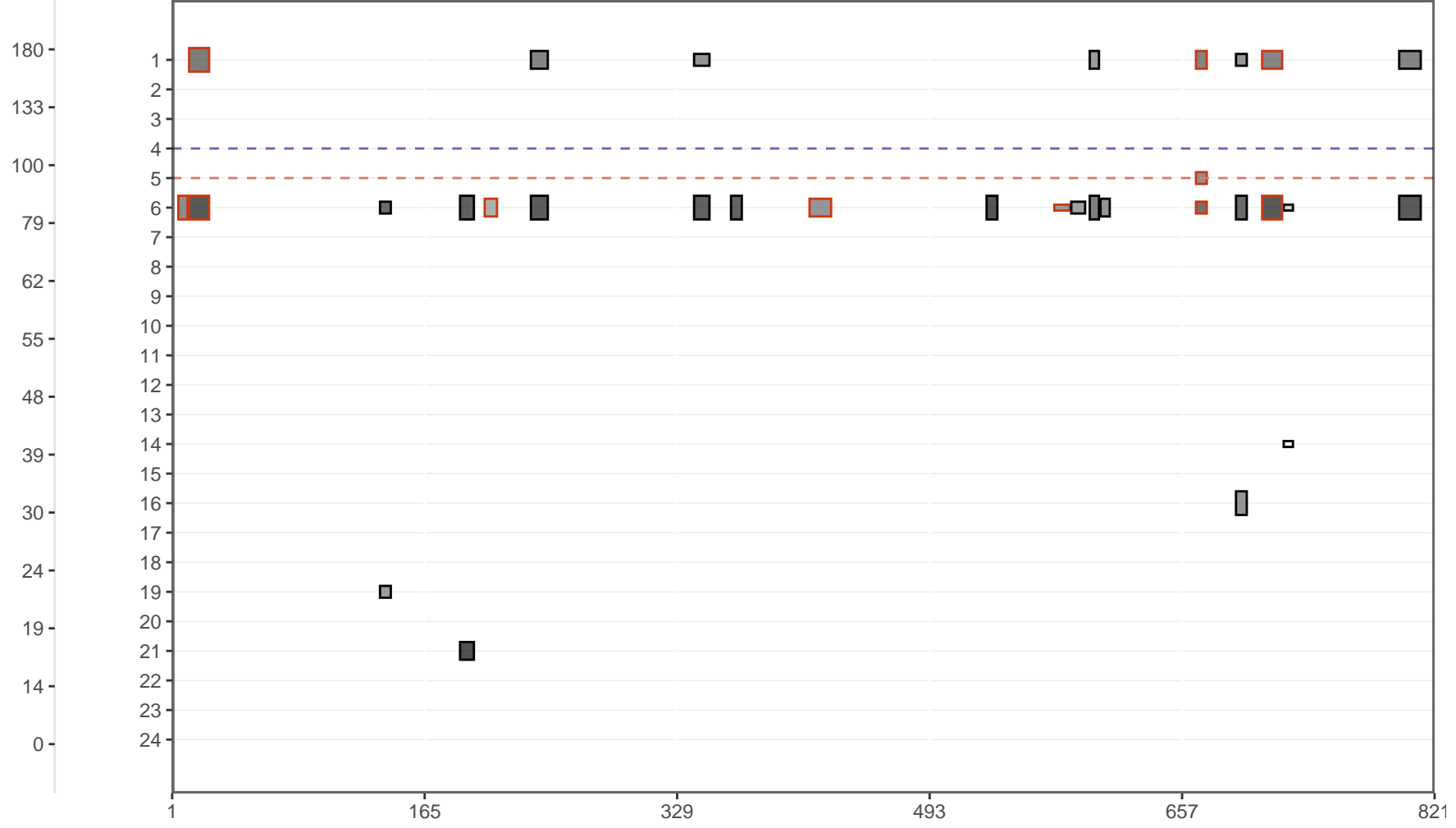


MW indication



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00441 Acyl-CoA dehydrogenase, C-terminal domain
- PF01636 Phosphotransferase enzyme family
- PF02770 Acyl-CoA dehydrogenase, middle domain
- PF02771 Acyl-CoA dehydrogenase, N-terminal domain

Protein sequence:

RFMPSEKYQKLRQKIKFMEDHYVWENEFKLAGSNMRWTHIFDDEEKLKELAKKEGLWNLWIFPDSAAARARELIYGSRLNGLSNDSDRLLGASLNLEYGLGEIMGRSVAWPAQIFNGGAFDTGNMEVLLRYGNEVQMKVLPVLLLEGKIRSGFAMTFEPQVAASGDATNEGSKRHGGSYINGTKVWVTFSGAMDRPKILVMGKTDLAAPKHKGGSMILVDINSPGITVQRPLTVFGFDPAHGHAELFENWCVPAINILLGEGRGEIAGRLGPRLIHCCMLRIGAAC

NbL09g16800.1 probable_UDP-3-O-acylglucosamine_N-acyltransferase_2_mitochondrial [MW = 33.8 kDa]

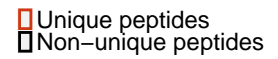
No. of times detected



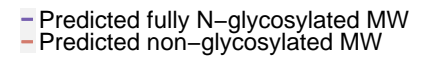
log(intensity)



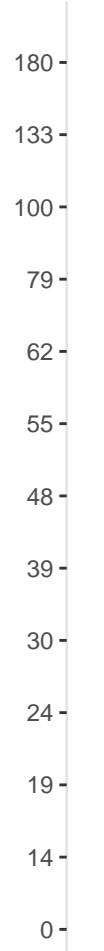
Values from



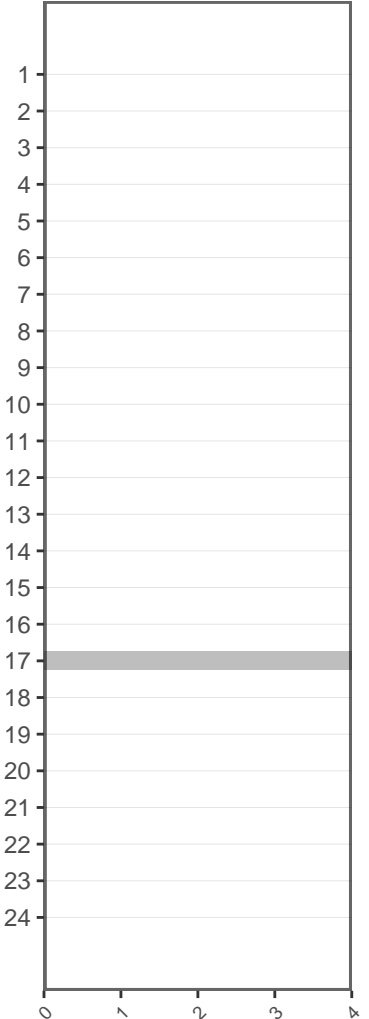
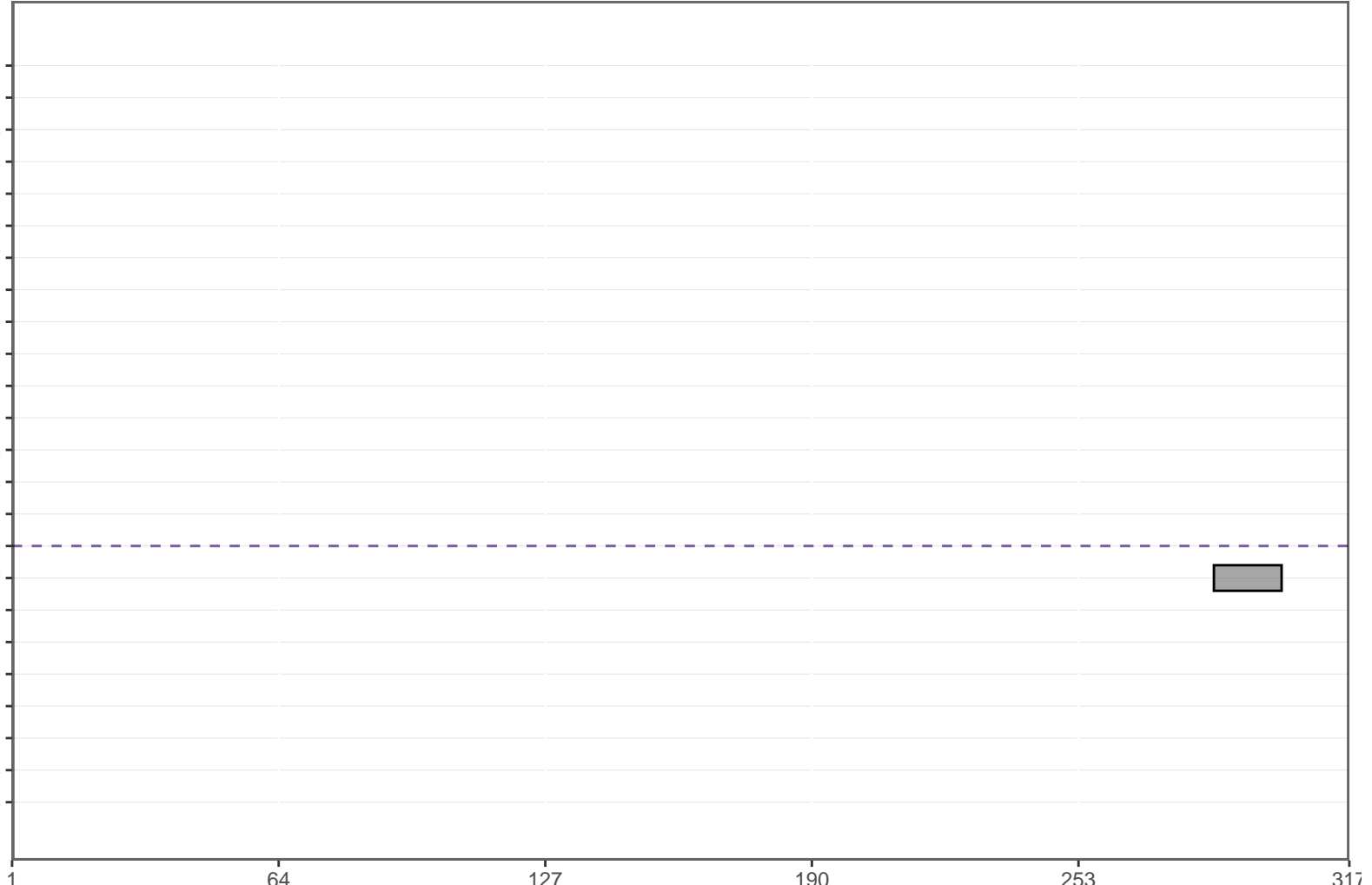
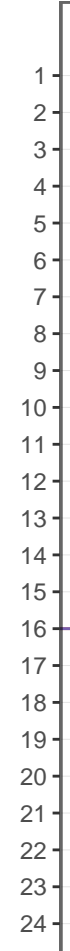
MW indication



Molecular weight



Gel Slice



Protein length

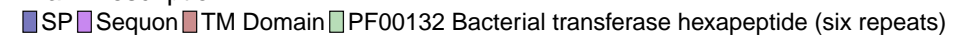


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

YINVALANGLMVGDFVHSGVGVGGDGGFFVDEGGNMKKPQTLNRIENHVEIGANTGIDRGSWRNTVVEHTKIDNLVQIGHNVVIGRSGICGGGVAGSVTGSDVYTFGGGRVGRDHNVNAASKVRLAANSGVTKDISEPGDYGGFPAIPRDWRRRQAMHRQELKS

NbL09g16730.1 UPF0051_protein_ABCI8_chloroplastic-like [MW = 61.26 kDa]

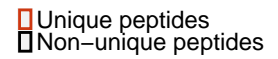
No. of times detected



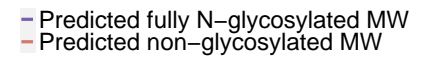
log(intensity)



Values from



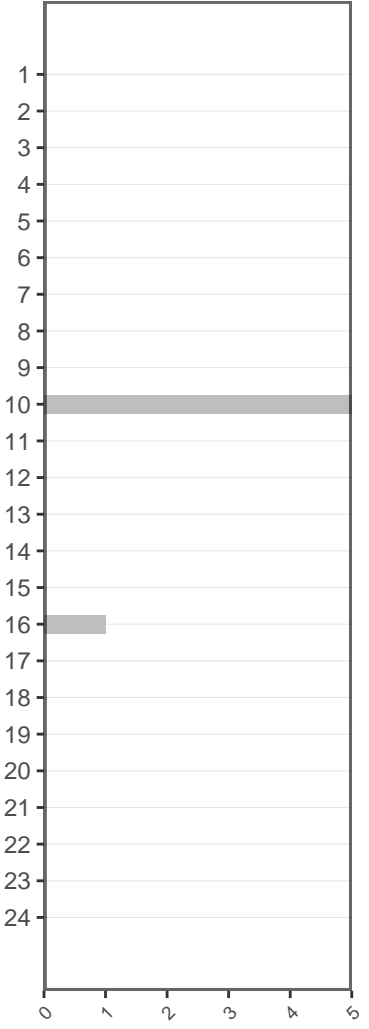
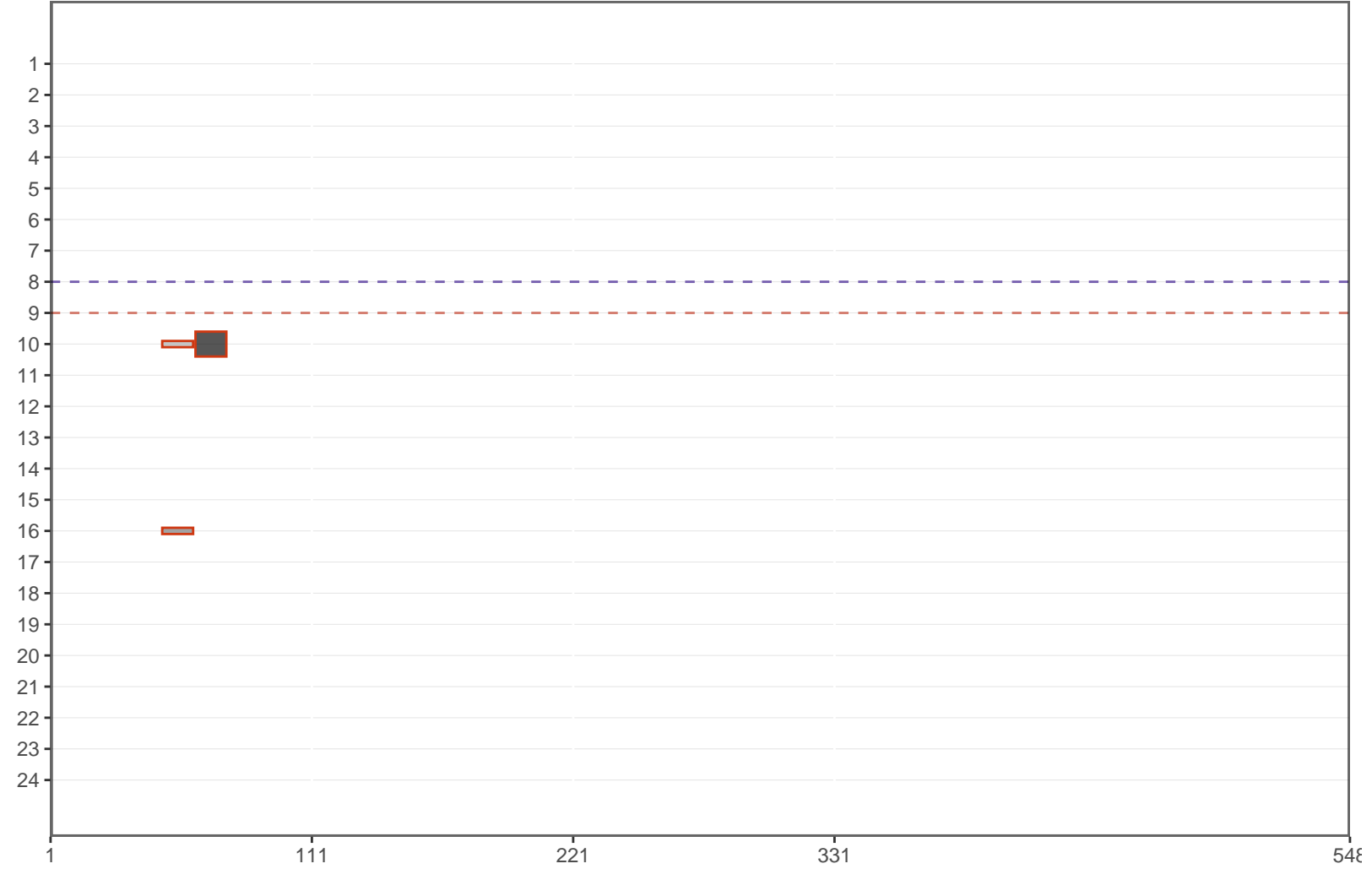
MW indication



Molecular weight



Gel Slice

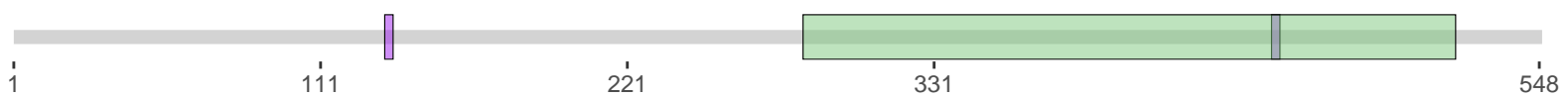


Protein length

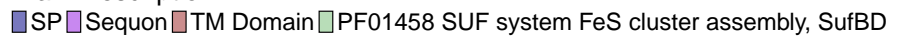


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KNTRCPMQISTYFRINAMETGGFERTVIAEEGSFVEYLEGGTAPVDNQLHAAVVELVGDGAEIKYSTVGMWYAGDEEGKGGHNFVTRKRLGAGARSKISWTVGTSATWYKPSVVLLEGDESVGFYSLVNTNNGQADTGMHMKGNTRSRISKIGSAGHSRNCYRGLVQLSNAENKNS6QGD6MLIGDTAAANTYFVIGVKNPTARIEHEATTSKIGEDQLFYFQGRGDYKAMAM6GFGRDVFNELPDERGAEVNQLMLKLEGSVQ

NbL09g16550.1 ubiquitin_domain-containing_protein_DSK2b-like [MW = 58.79 kDa]

No. of times detected



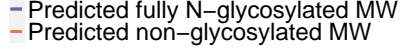
log(intensity)



Values from



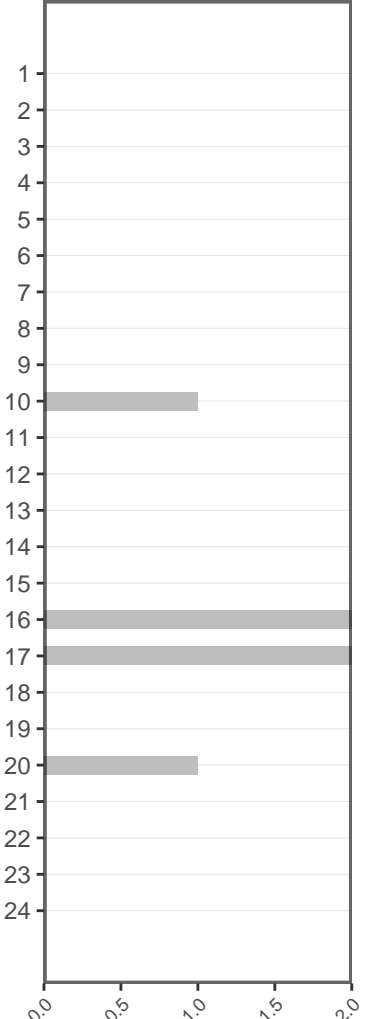
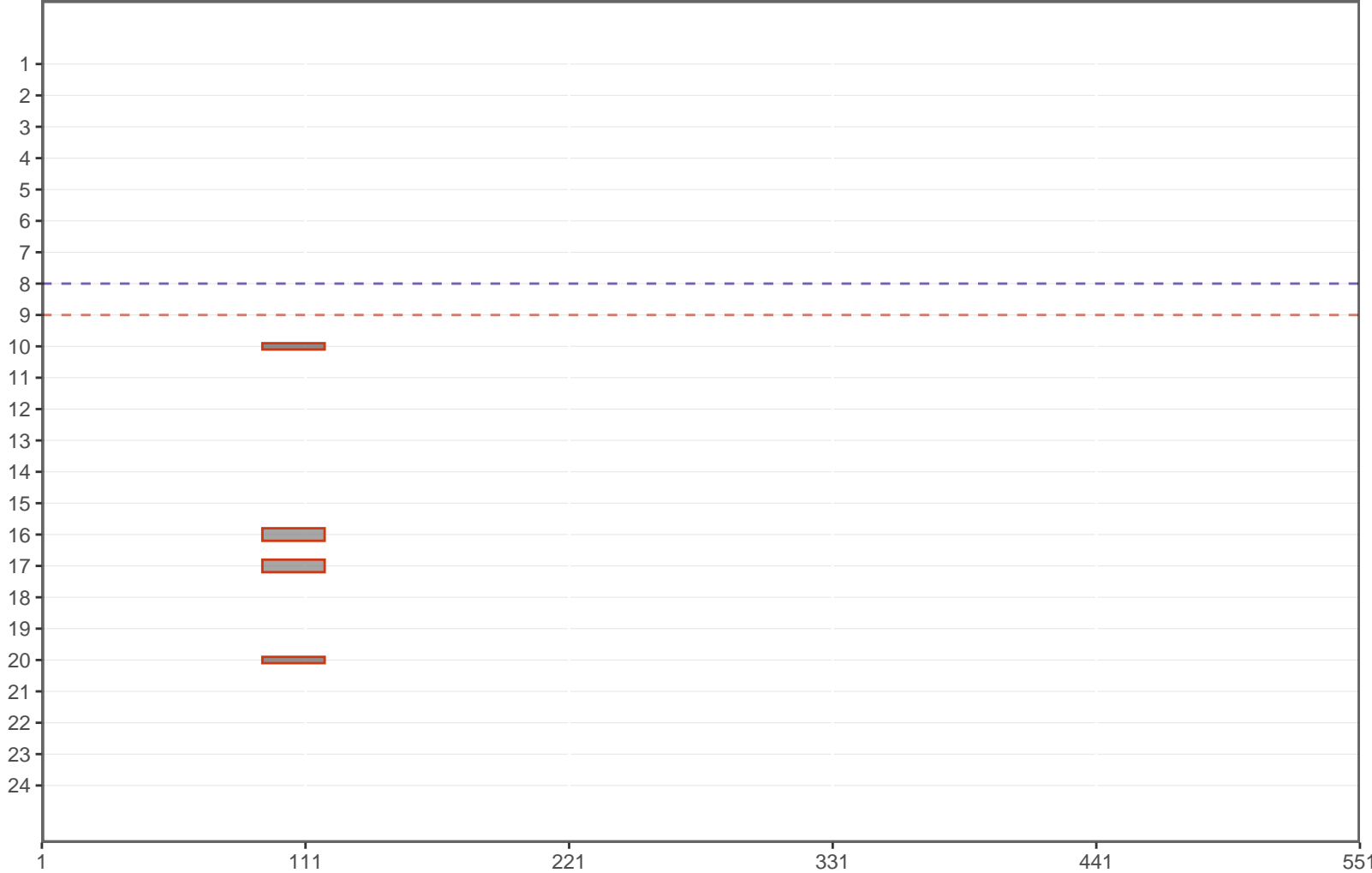
MW indication



Molecular weight



Gel Slice



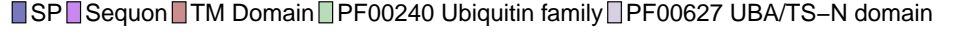
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IIVQPELLNATLISGDIIRNDVGNPFPAALLGAGGGGGGRHGGNNPPTGGSETTDNPPAPNTNPLFNPNFNASADTGAAGANTPARENTAADTRAAPLGGGLGLASPLGELQMPGMPDPTTSLNQMMPNPSISMMQGLLENPQYMNIGILGNLPQLRMLDSEHLEEMMGNPEFIRGLTSPETMQLMFEFQHGLLGSAWRQGTNGQVGNAGGAAGDNGMEMLMNMFGLLETGGLGVNRSNVPPEELVATQLTGLGEMGFDTGENRALIAAGNVIHAAVEQLGIP

NbL09g16530.1 heterogeneous_nuclear_ribonucleoprotein_H2 [MW = 30.17 kDa]

No. of times detected



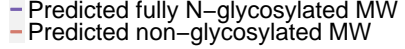
log(intensity)



Values from



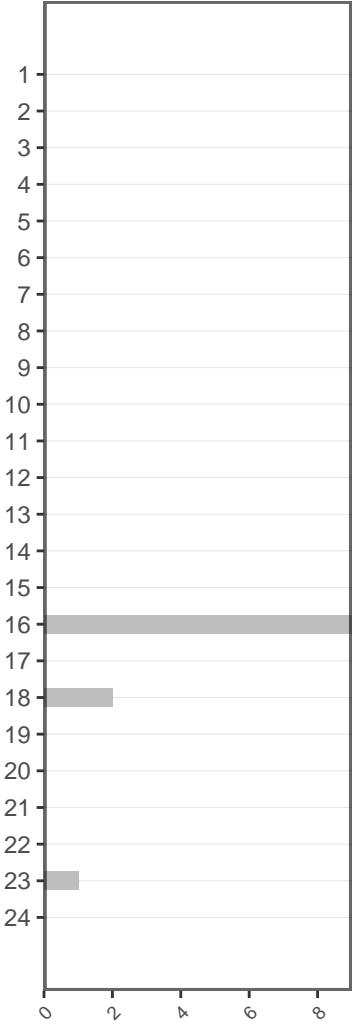
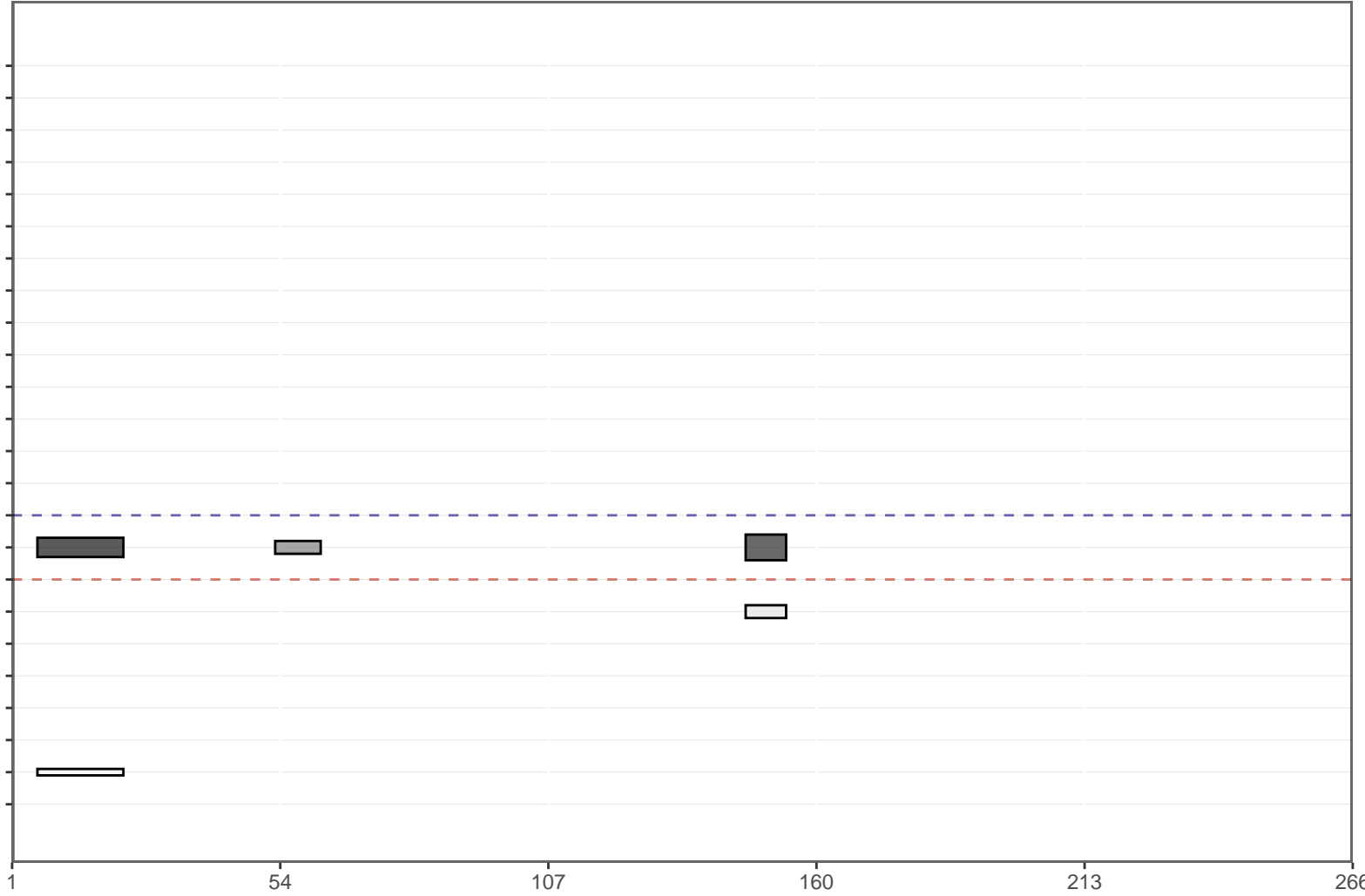
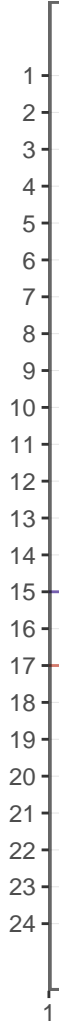
MW indication



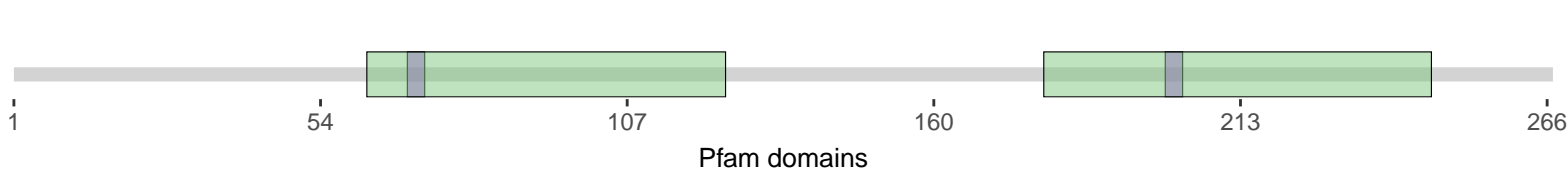
Molecular weight



Gel Slice

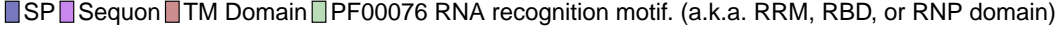


Protein length



Pfam domains

Pfam Description



Protein sequence:

INMSRRRYEVFSCKKEEYVEAAMDVKEGGDYVEYRTSPPPRKRSMNKDQMEYTELKLRLGLPYSVRRDIARFEGEEFNVEADKVHAYRPDQKATGEAVVEFASSEEAKKAMCKDKMKKGRVYELFPHDPDEARRAESRGRG

NbL09g16340.1 fasciclin-like_arabinogalactan_protein_4 [MW - SP = 42.1 kDa]

No. of times detected



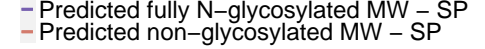
log(intensity)



Values from

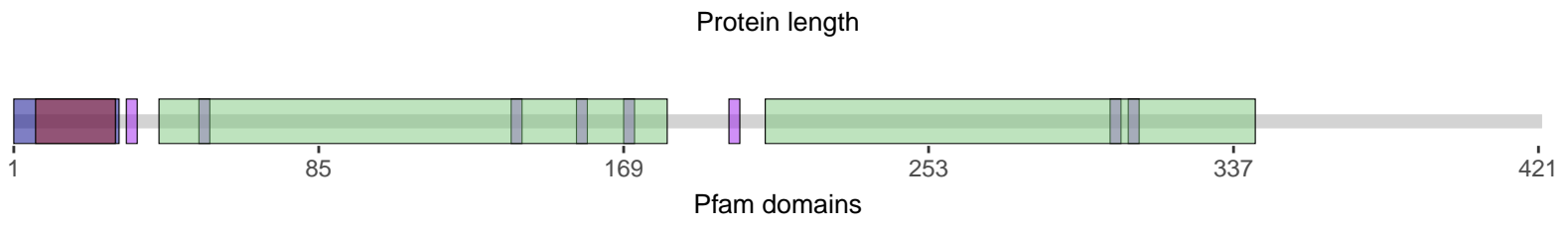
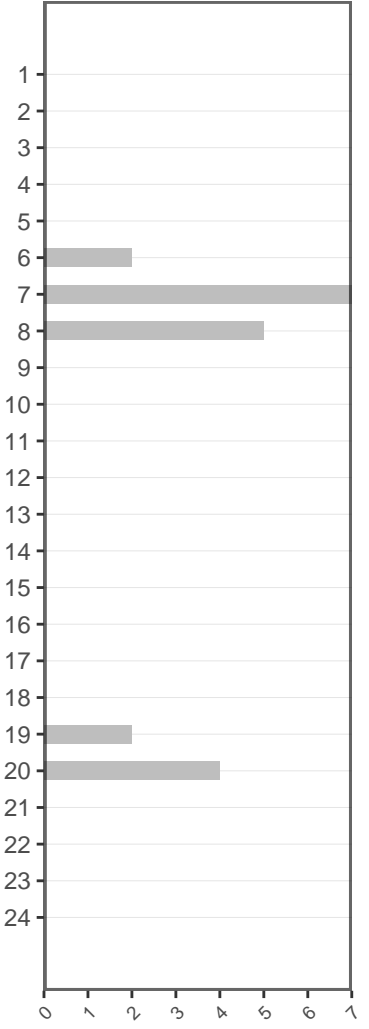
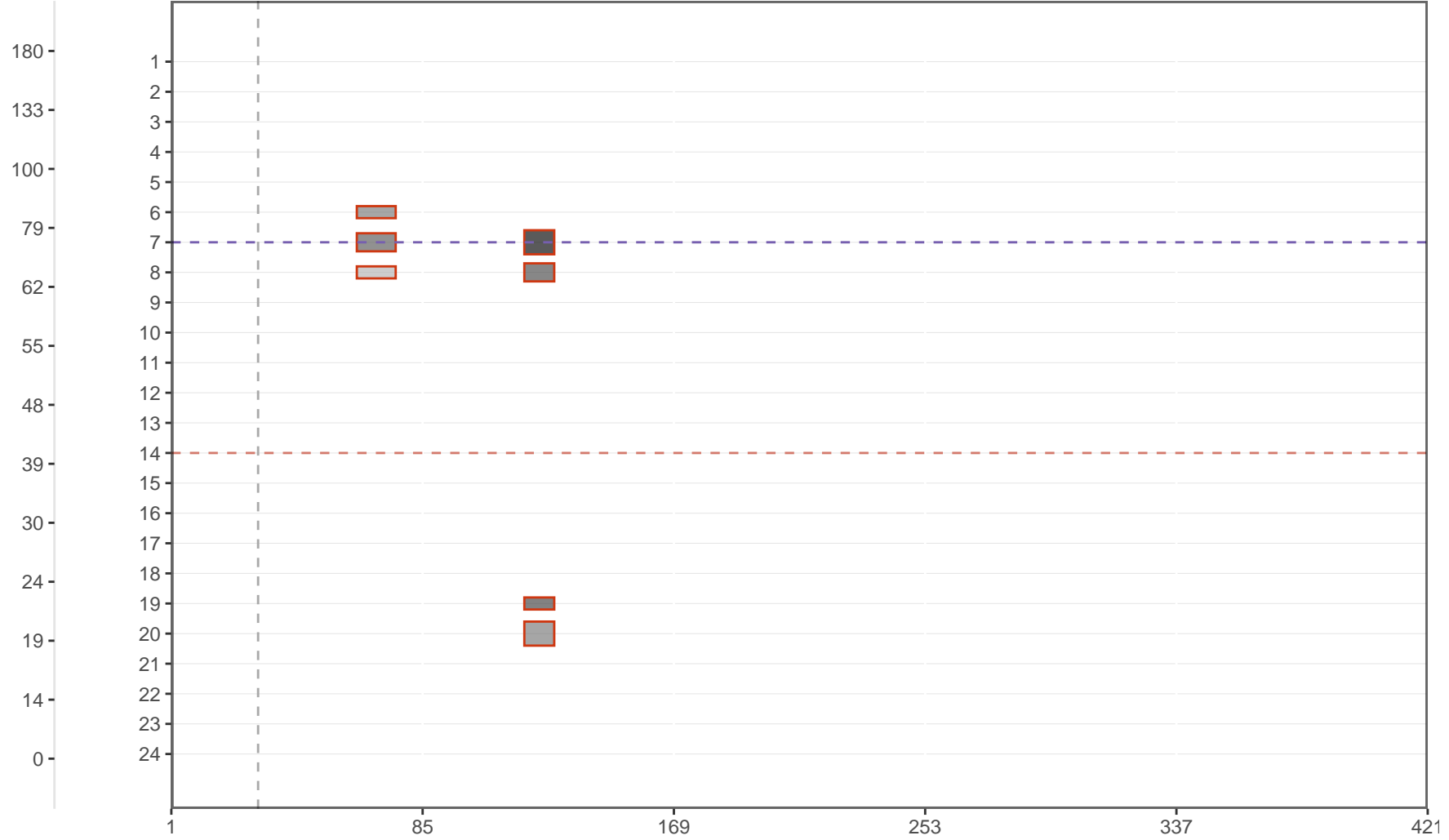


MW indication



Molecular weight

Gel Slice



Pfam Description
 ■ SP ■ Sequon ■ TM Domain ■ PF02469 Fasciclin domain

Protein sequence:

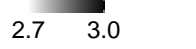
KTLDGHNFNVAASMTAGVVEEERFDEGGAGTFLVPTDEAFSEMSASNNFQGLFMEKKAVALRFRVHLSYFLGSLDSVNFVQPTLATDQNGAGSETLNSRVDNDSVGTGVAASVTQTTFDQNPVAFVGVKVLPRFFGKNPVIEVKNRPTGVASRPEISLPPENSGIYGPPEHLSEPPGLGIEASSANWKKGGFLWGRFFVLLLVN

NbL09g16260.1 heat_shock_cognate_70_kDa_protein_1-like [MW = 47.96 kDa]

No. of times detected



log(intensity)



Values from



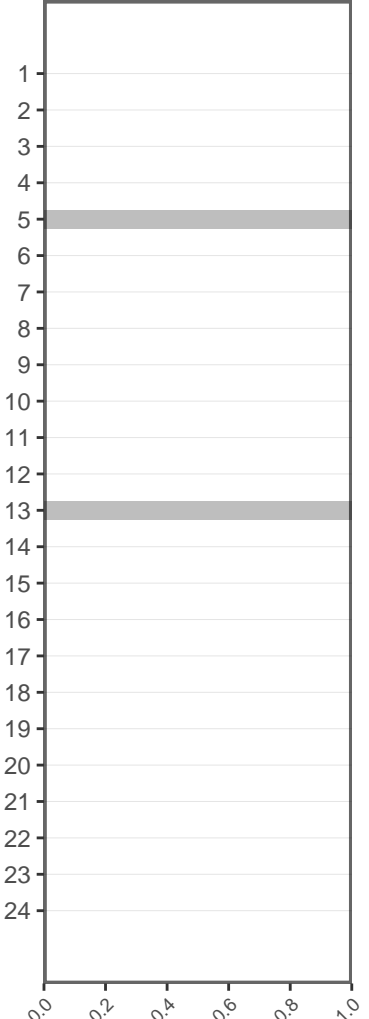
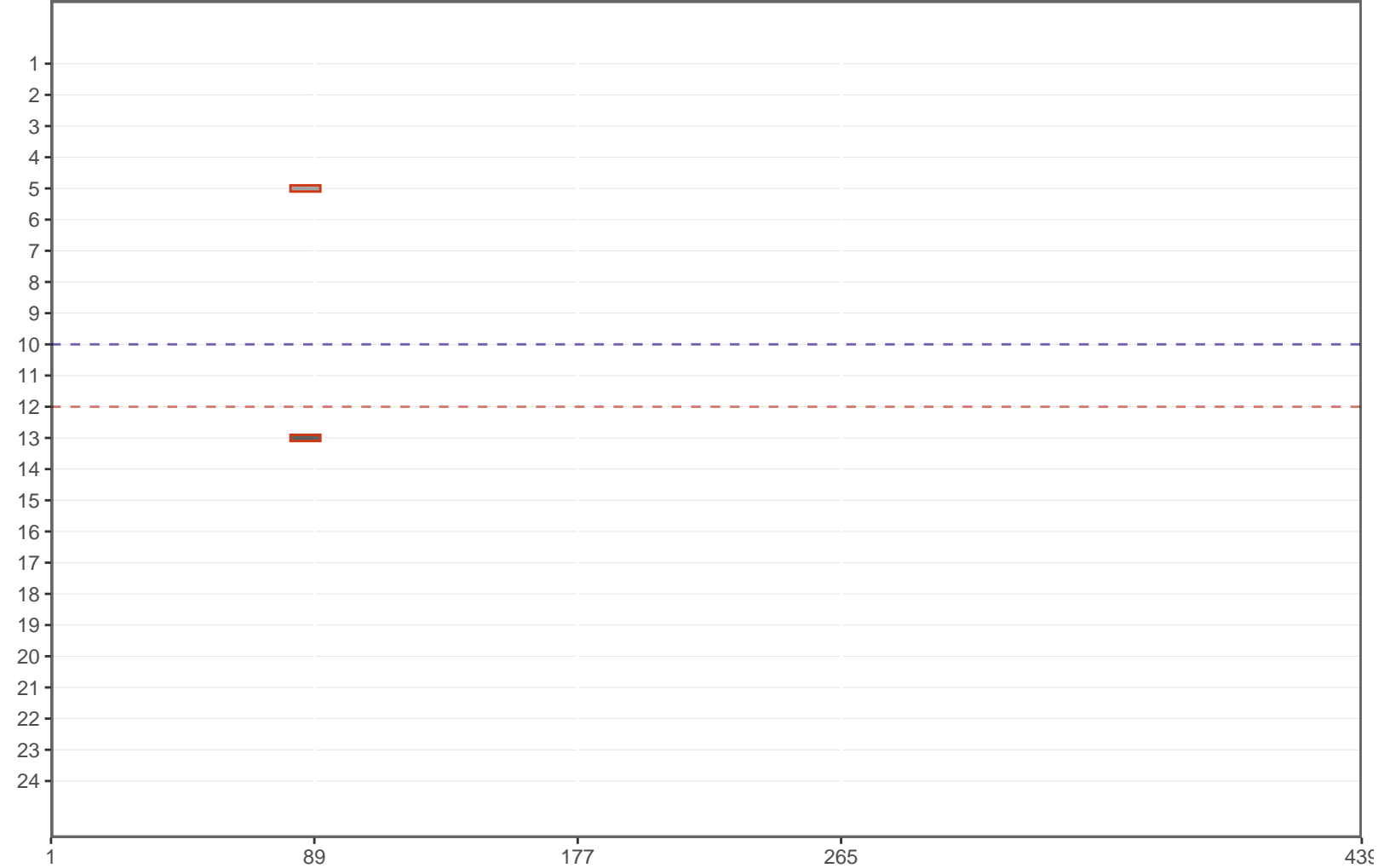
MW indication



Molecular weight

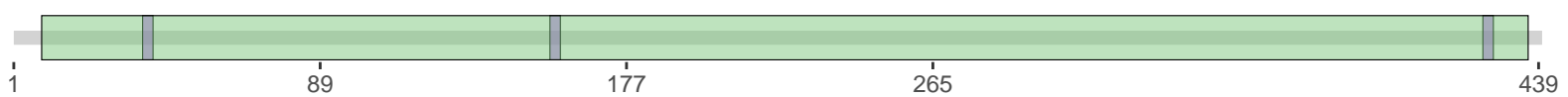


Gel Slice



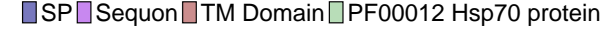
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LGGGTFDVSLLTIEEGFVEKATAGDTHLGGEDFDNRMMVHVFVGEFRKHKHKDIGNPRALRLRRTSGERAKRFLSSTAQTIEIDSLYEGVDYFSTTRARFEELNMDLFRKGMPEVVKGLRDAKMDKSTVHDDVLLVGGSTRPKVQGLLQDFNFKELGKSNPDEAWAYGAAGAAALSGEANEKVDLILLDVTFLSLGLETAGVMTVLPINPTTPTKQEGVFSHL*

NbL09g16200.1 NADH_dehydrogenase_[ubiquinone]_1_alpha_subcomplex_subunit_2-like [MW = 10.97 kDa]

No. of times detected



log(intensity)



Values from



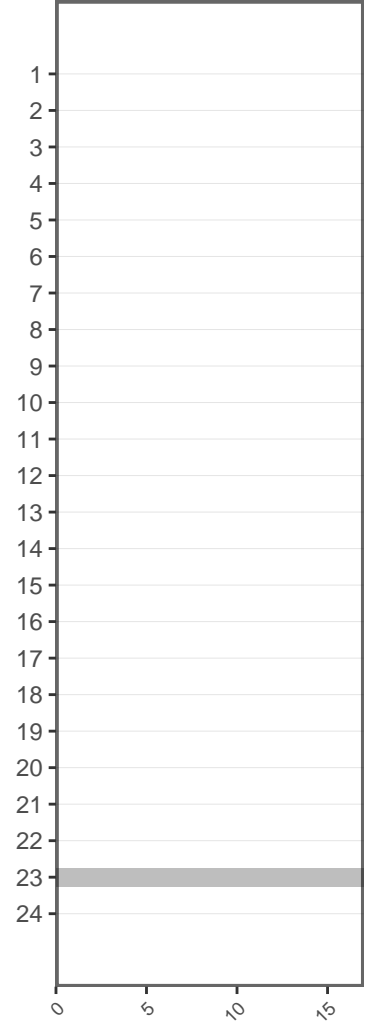
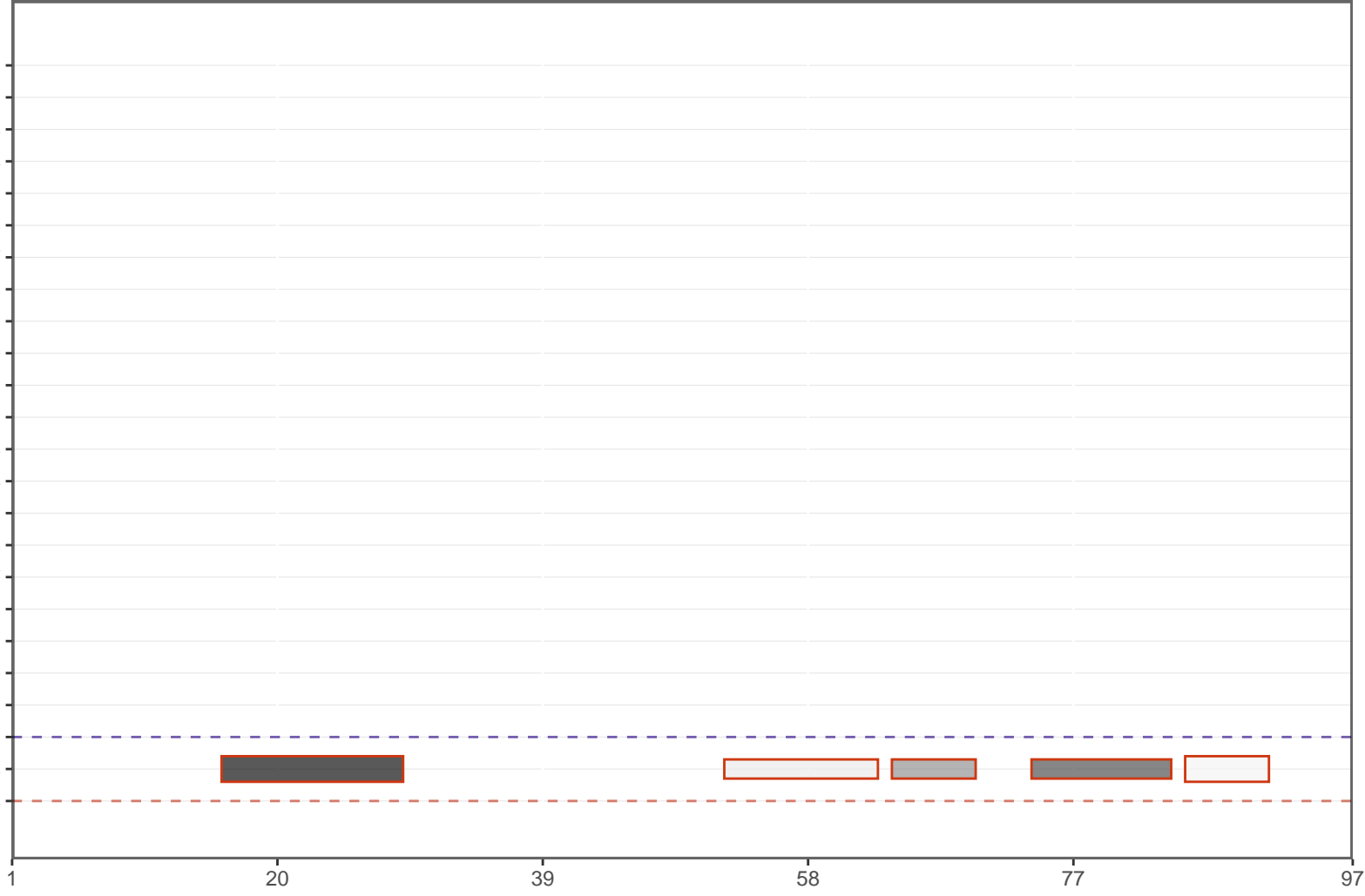
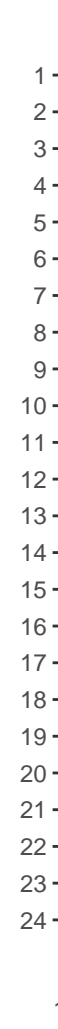
MW indication



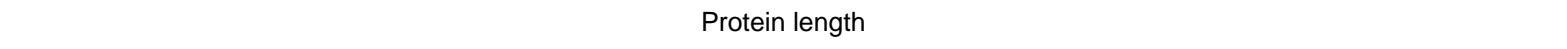
Molecular weight



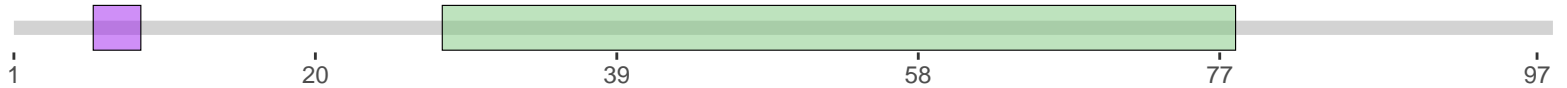
Gel Slice



Protein length

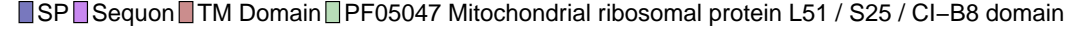


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NYRDLKTHNPKLPKRIEATSEIPEQLWARYDLGVGRIGRLGEGTEQISKALEDLWYVGSRI

NbL09g16180.1 probable_histone_H2B.1 [MW = 16.22 kDa]

No. of times detected



log(intensity)



Values from



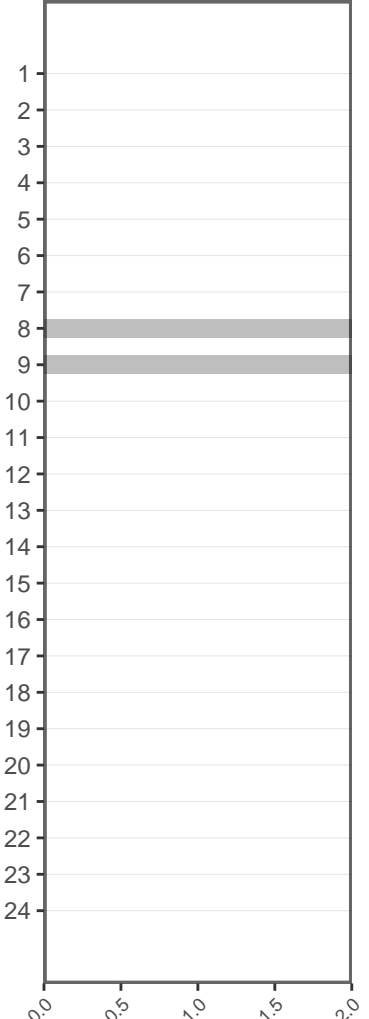
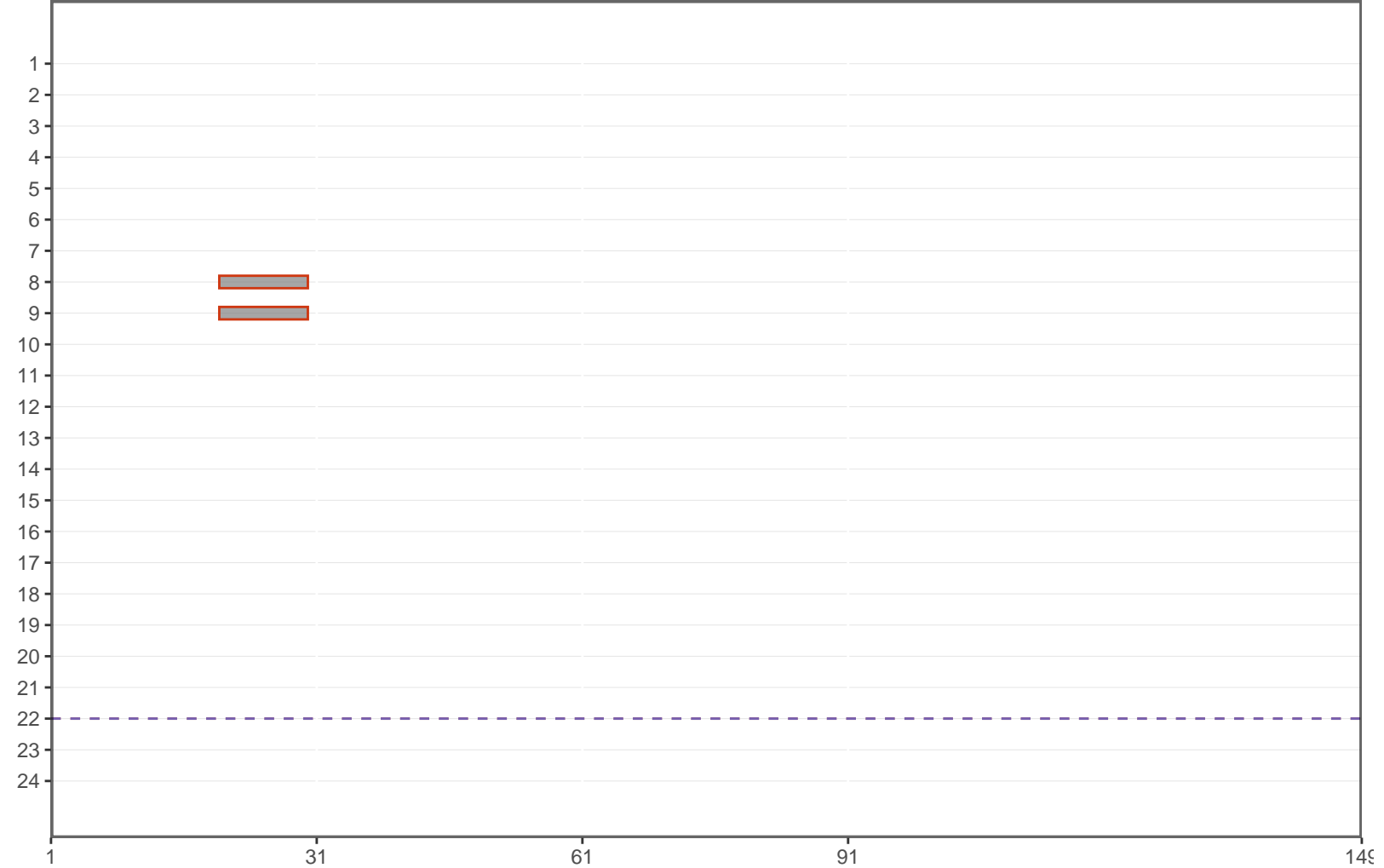
MW indication



Molecular weight

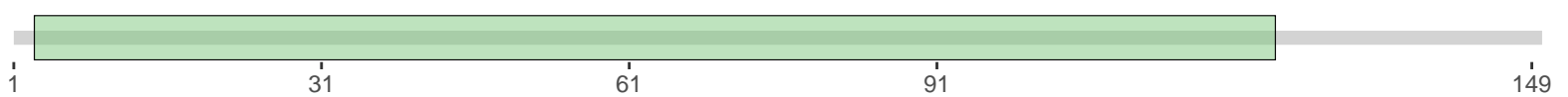


Gel Slice



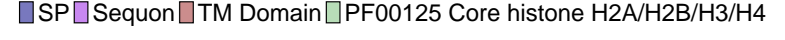
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ETYYKDYIFKVLKQVHPDVGISSKAMGIMNSFINDIFEKLAQESSRLARYNKKPTTFSREIGTAVRLVLPGLAKHAVSEGTAKVTKFTSP

NbL09g16100.1 aquaporin_TIP1-3-like [MW = 25.9 kDa]

No. of times detected



log(intensity)



Values from



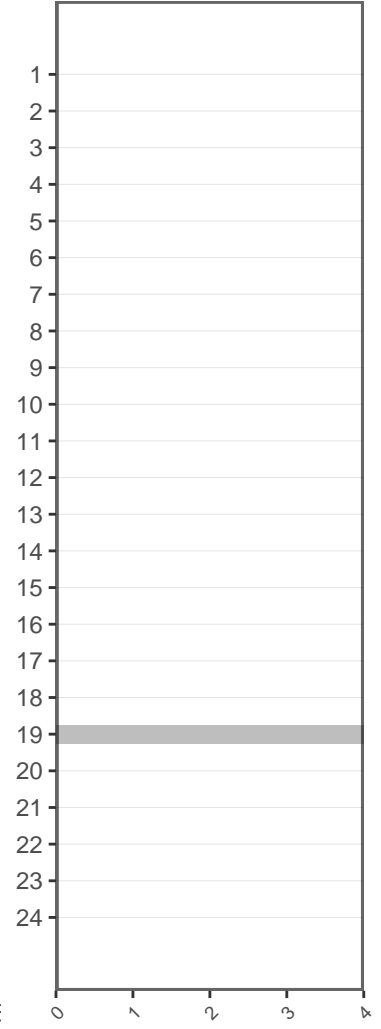
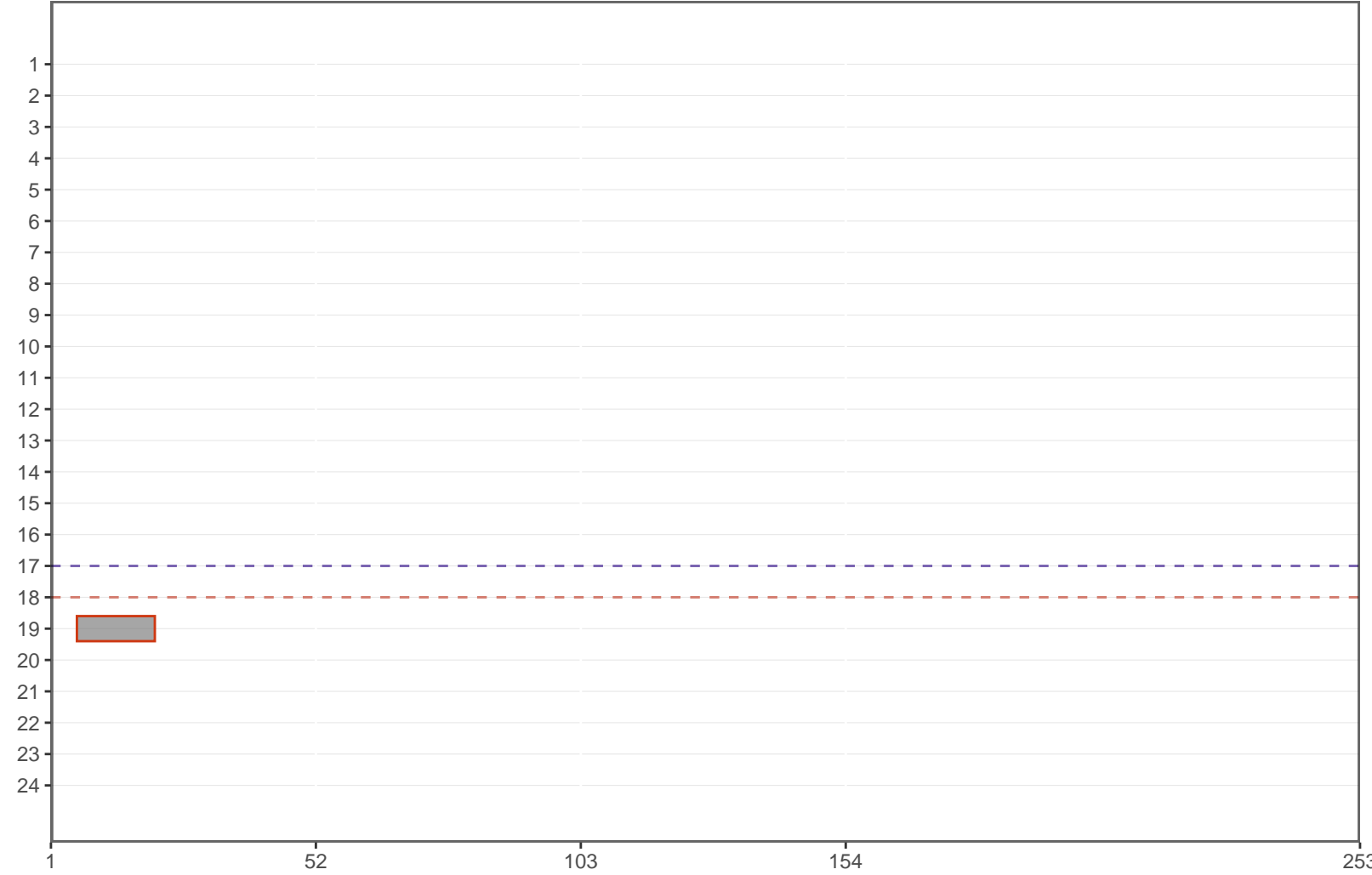
MW indication



Molecular weight

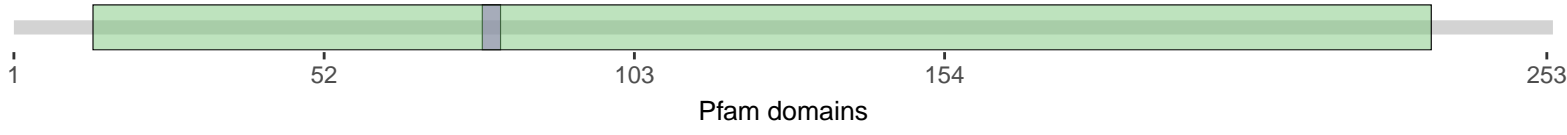


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

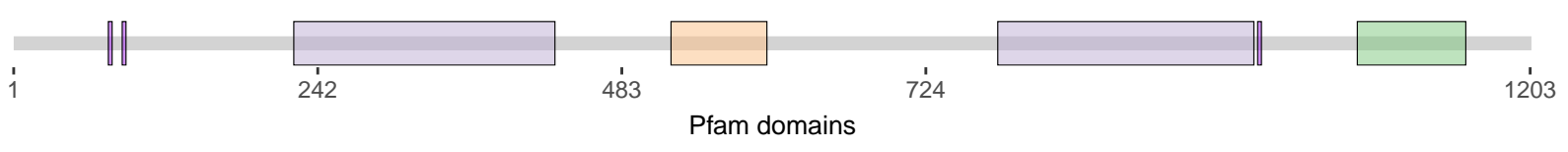
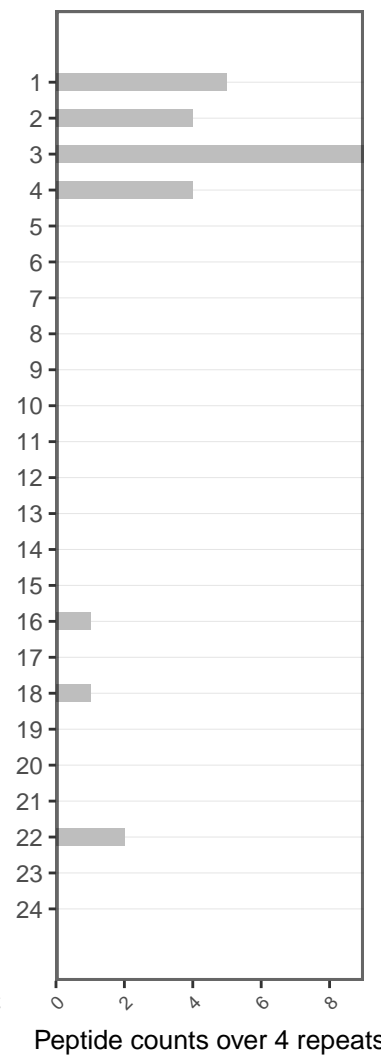
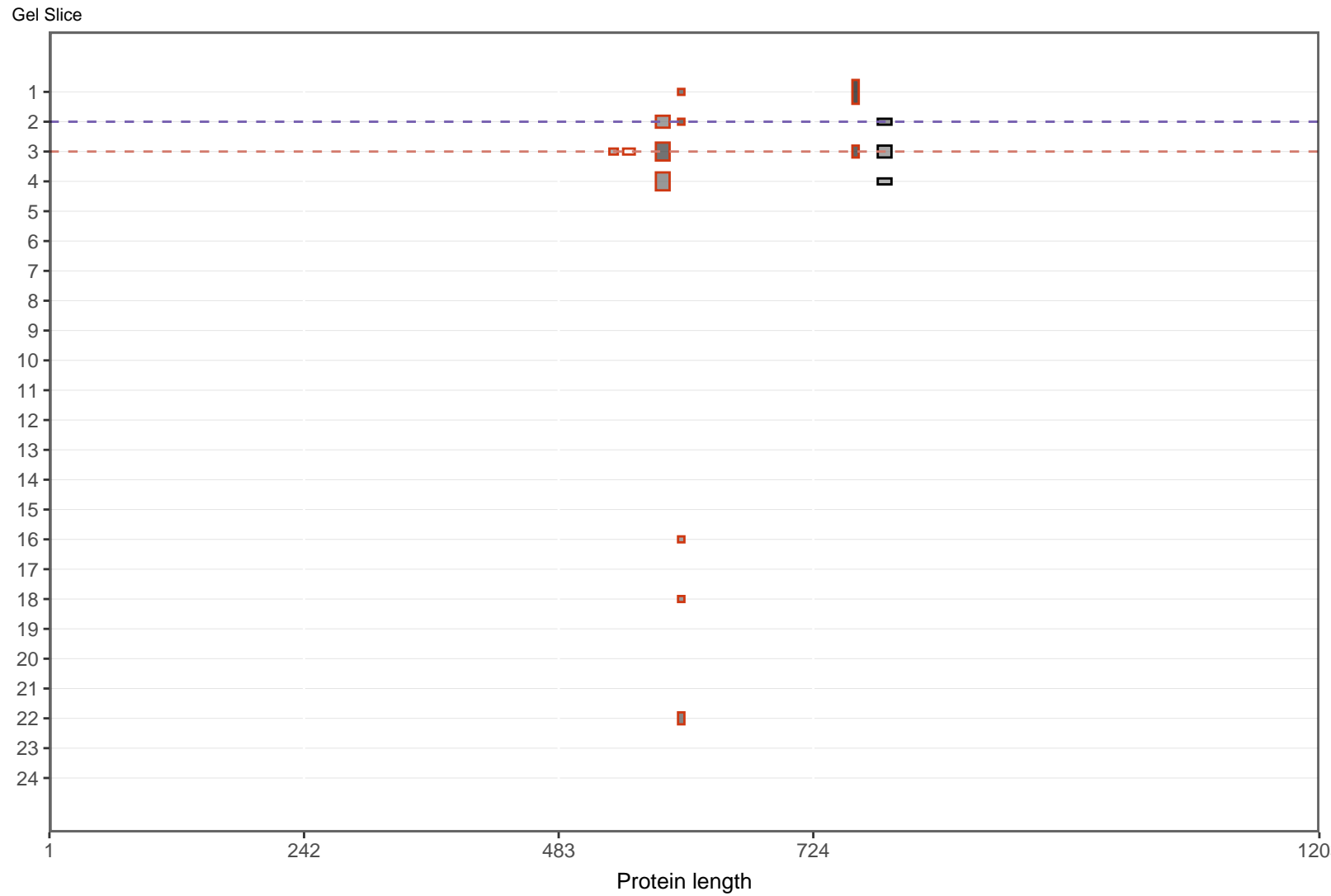
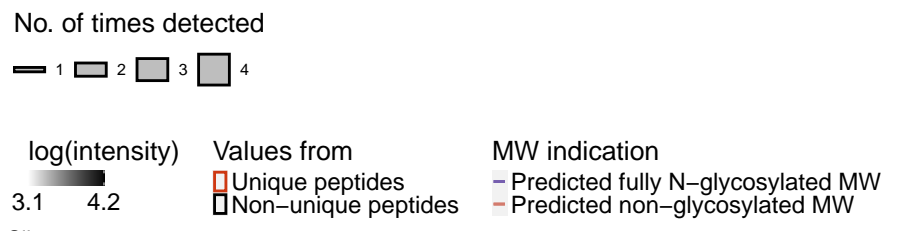
Pfam Description



Protein sequence:

SVVACVLLKATGGLTSAFALSTGVTPWNAVFEIWMTFGLVYTYVATVDPKRGNGIAPAIAGFVIGANLAGGAFDGAQMNPVVSFGRVVSIVTWNQHWVWVWVGFVGAALVYEIFIGDTHLEQLTADV

NbL09g15940.1 carbamoyl-phosphate_synthase_large_chain_chloroplast-like [MW = 132.09 kDa]



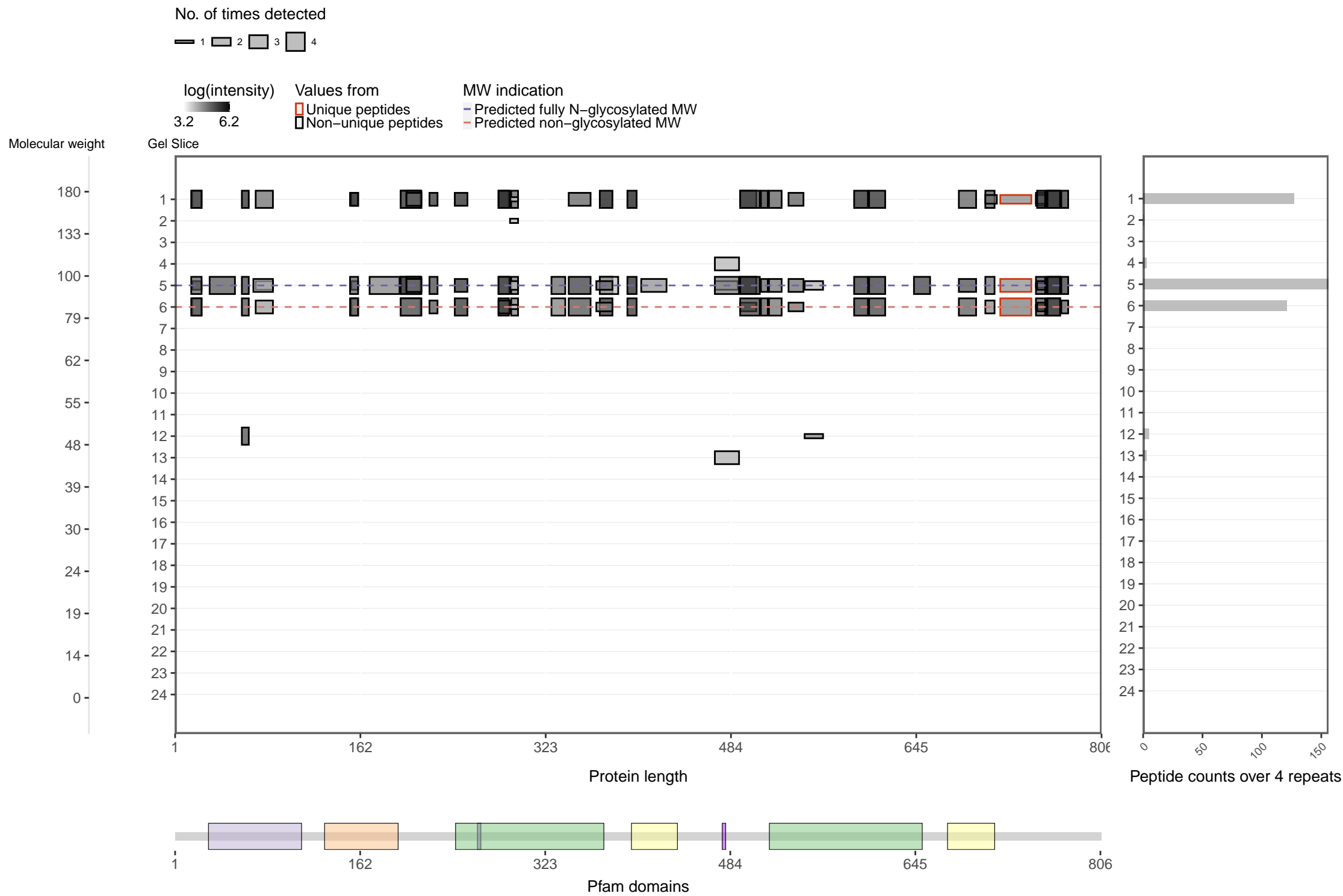
Pfam Description

- SP
- Sequon
- TM Domain
- PF02142 MGS-like domain
- PF02786 Carbamoyl-phosphate synthase L chain, ATP binding domain
- PF02787 Carbamoyl-phosphate synthetase large chain, oligomerisation domain

Protein sequence:

KKRGFSDRDQISFATKSSSEEVSRRLBLGPKPKRVDTGAAEFADPTPMYSBVDHECESAPTGRKKVLLGGGNRIGGGIEFDYCGGHTSFALQDAGYETIMMNSNPETVSTDTSDRLYFEPLTVEDVNLNIDLEGPDGIVFGGGTFLKLAIPQNLDERPKTRSGASFVRWGTSPDGDAAEDRFNAILNELGIVGPKGGIAKSEKDAVAATEVGYFPAVVRPSVYLGGRAMEVYVNDKLVYKLENAAKVKDPERPVLIDKYLTDVAEIDBALADLHGNYVGGI

NbL09g15770.1 cell_division_cycle_protein_48_homolog [MW = 89.38 kDa]



Pfam Description

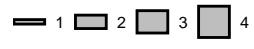
- SP
- Sequon
- TM Domain
- PF00004 ATPase family associated with various cellular activities (AAA)
- PF02359 Cell division protein 48 (CDC48), N-terminal domain
- PF02933 Cell division protein 48 (CDC48), domain 2
- PF17862 AAA+ lid domain

Protein sequence:

IKLAEVLDLERISKDTHGVVGDAAALGTEAALQGRKEMDVIDLEDDSDIAELNBMATVNEHFOTALGTSNPSALRETVVEVFNVSWEIDGGLENKRELGETVQYVPEHPEKFKFGMSPSKGVLYFVPPGGCKTLAKAANEDGANFISVKGPELLTAMVFGESSEANVREFDKARGAFCVFFDELDSIATQRGSVVDGAGGAADRVLNOLLTEMDGMNAAKTVFISGATNRPQIDFALLRPGRLDQLNPLPDEDSRHGFKAQLRKRPLSKVLDLRALAKYTGQF

NbL09g15740.1 ABC_transporter_F_family_member_1-like [MW = 67.55 kDa]

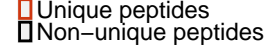
No. of times detected



log(intensity)



Values from



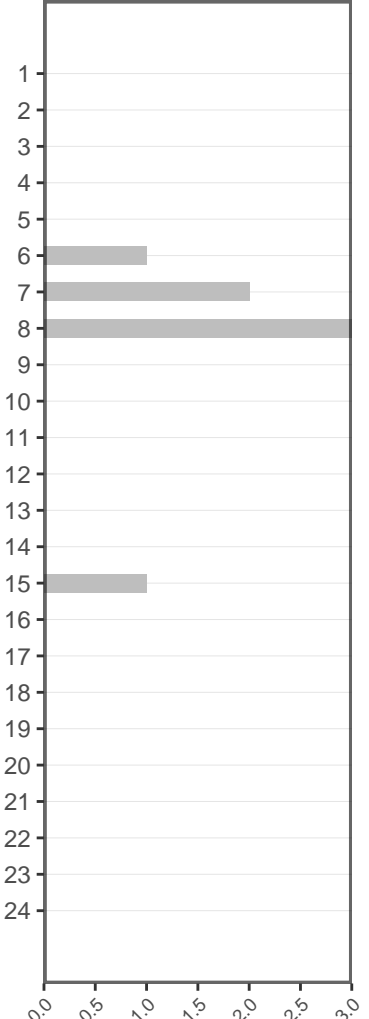
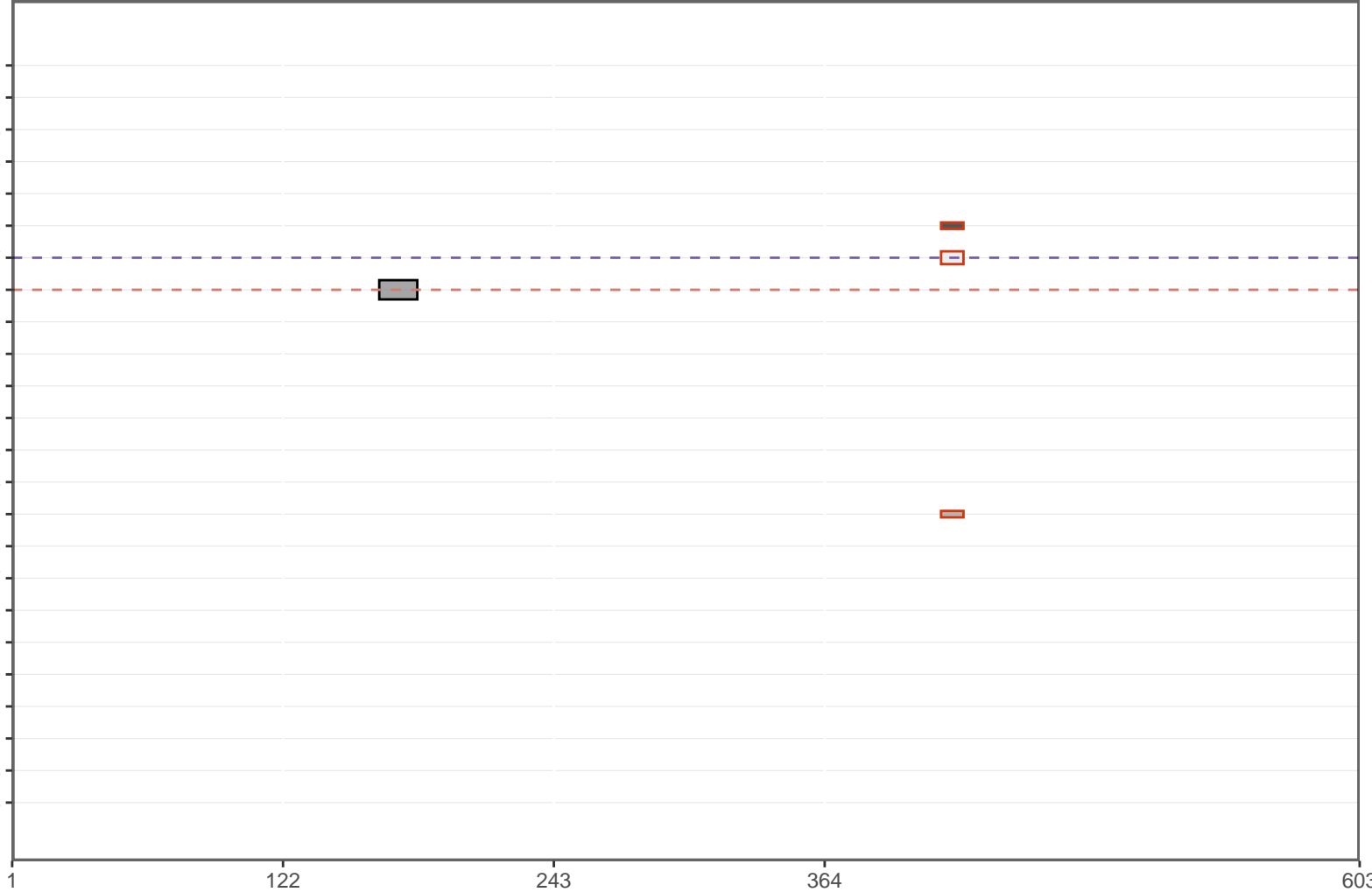
MW indication



Molecular weight

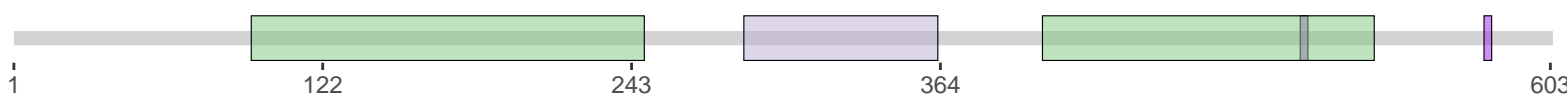


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KKLKYLTGNYDQYVDTREELEENQMGFRWEEQEGASMKYIARFGHGSAKLARGAGSGKENTLAKMERGGLTETKYYKDKVLVFRFPDVKLPPPLVGFVEVTFGYPDNLKYMDFGVDLDSRVALVGNAGKSTLKLMTFGDLVPLDGMVRRHNLRIAGFQHLAEKLDMEMSALQYMIKEYVPGNEEKMRRAIGRFGLTKGAGVMPKMLSDGGGRSRVFGWLAFRGPHILLDEPTNHLDIETIDSLAEALNEVDGGMVLVSHDFRLNGVAHEIWCENQTVI

NbL09g15690.1 probable_aquaporin_TIP1-1 [MW = 25.74 kDa]

No. of times detected



log(intensity)



Values from



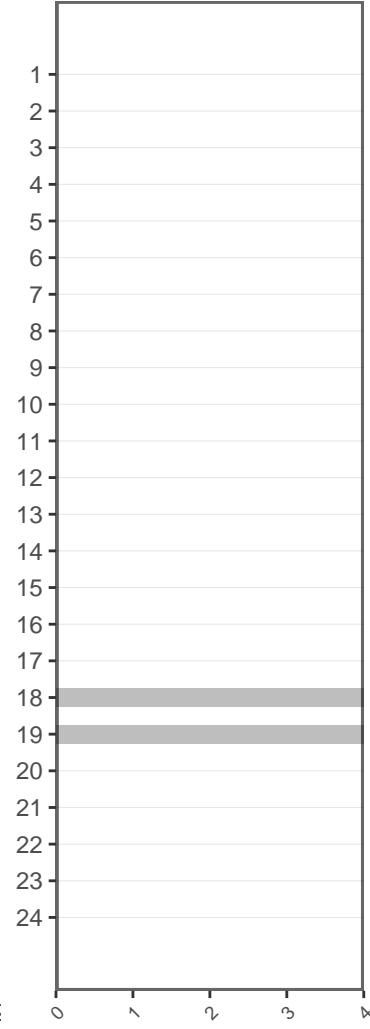
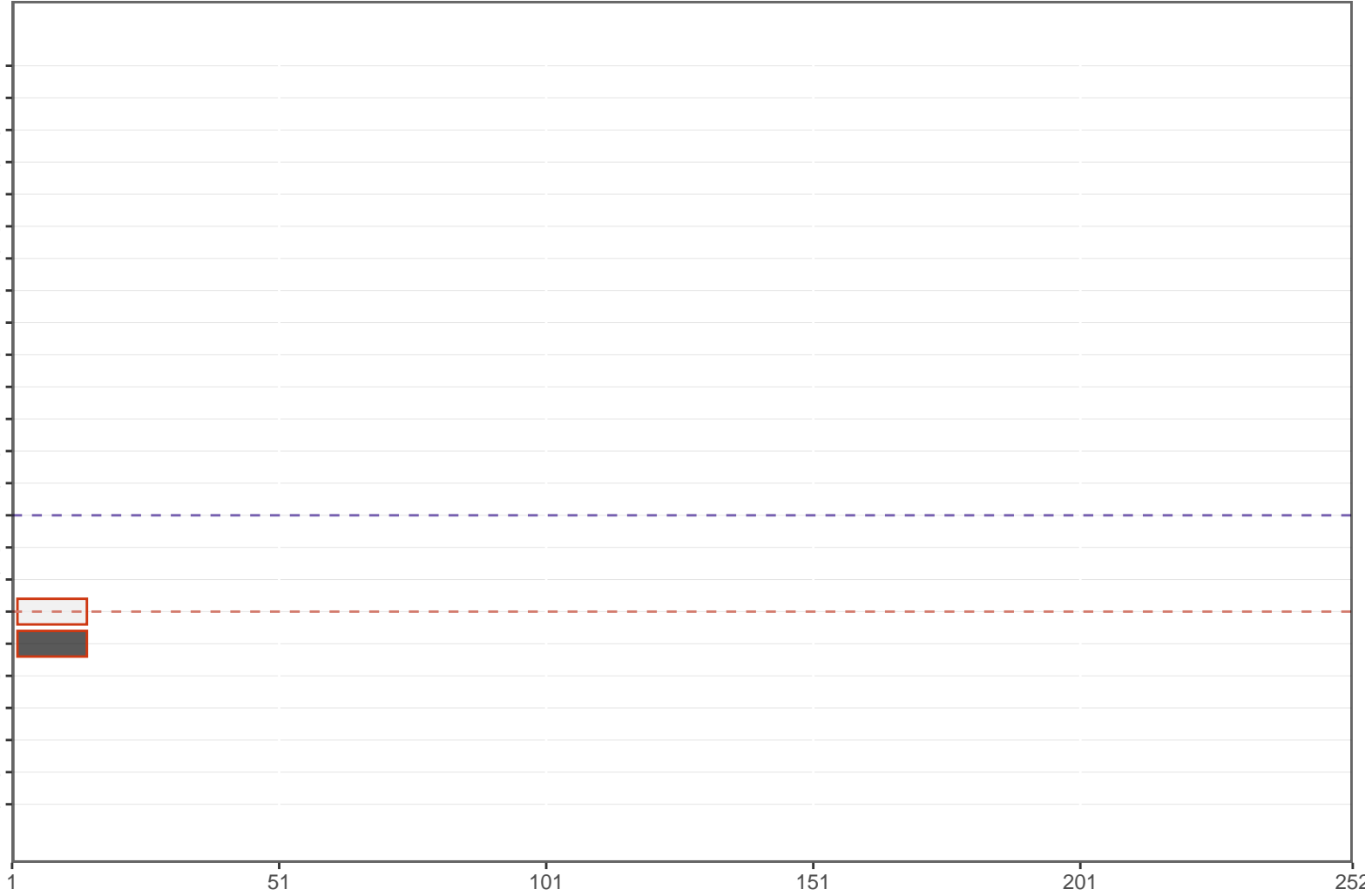
MW indication



Molecular weight

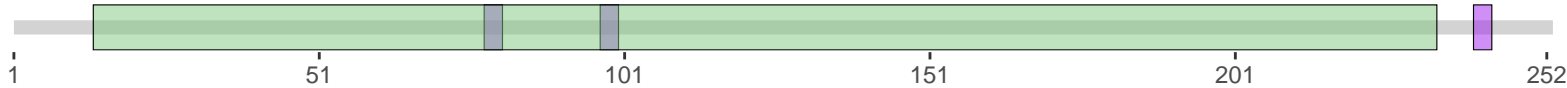


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

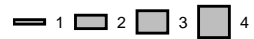


Protein sequence:

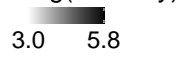
TVACLLLEFATGGMSTGAFVAVSAGVSEVWNAFVEIMVTFGLVYTVYATAVDFPKGGDLGVIAPIAGDFVGNLANLAGAFTGASMNPAWDFGPAVSWTWTNQQWVYVAGPLVGGGANGVYVYELFFNHSHEPLPSGDF

NbL09g15610.1 UDP-D-apiose/UDP-D-xylose_synthase_2-like [MW = 43.26 kDa]

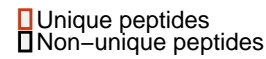
No. of times detected



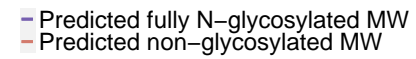
log(intensity)



Values from



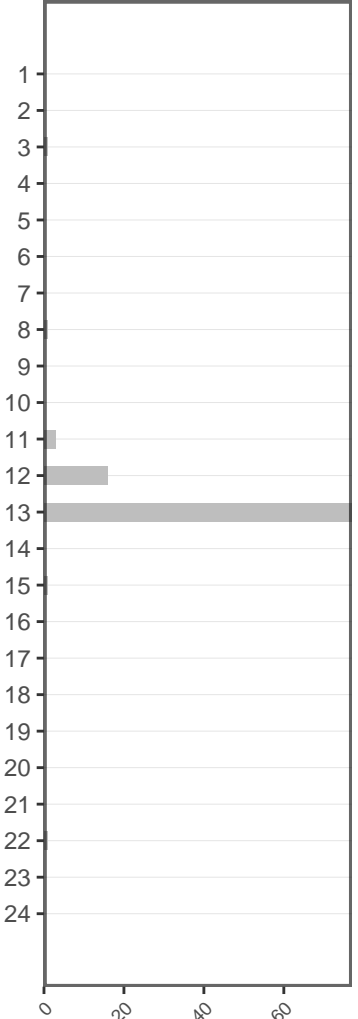
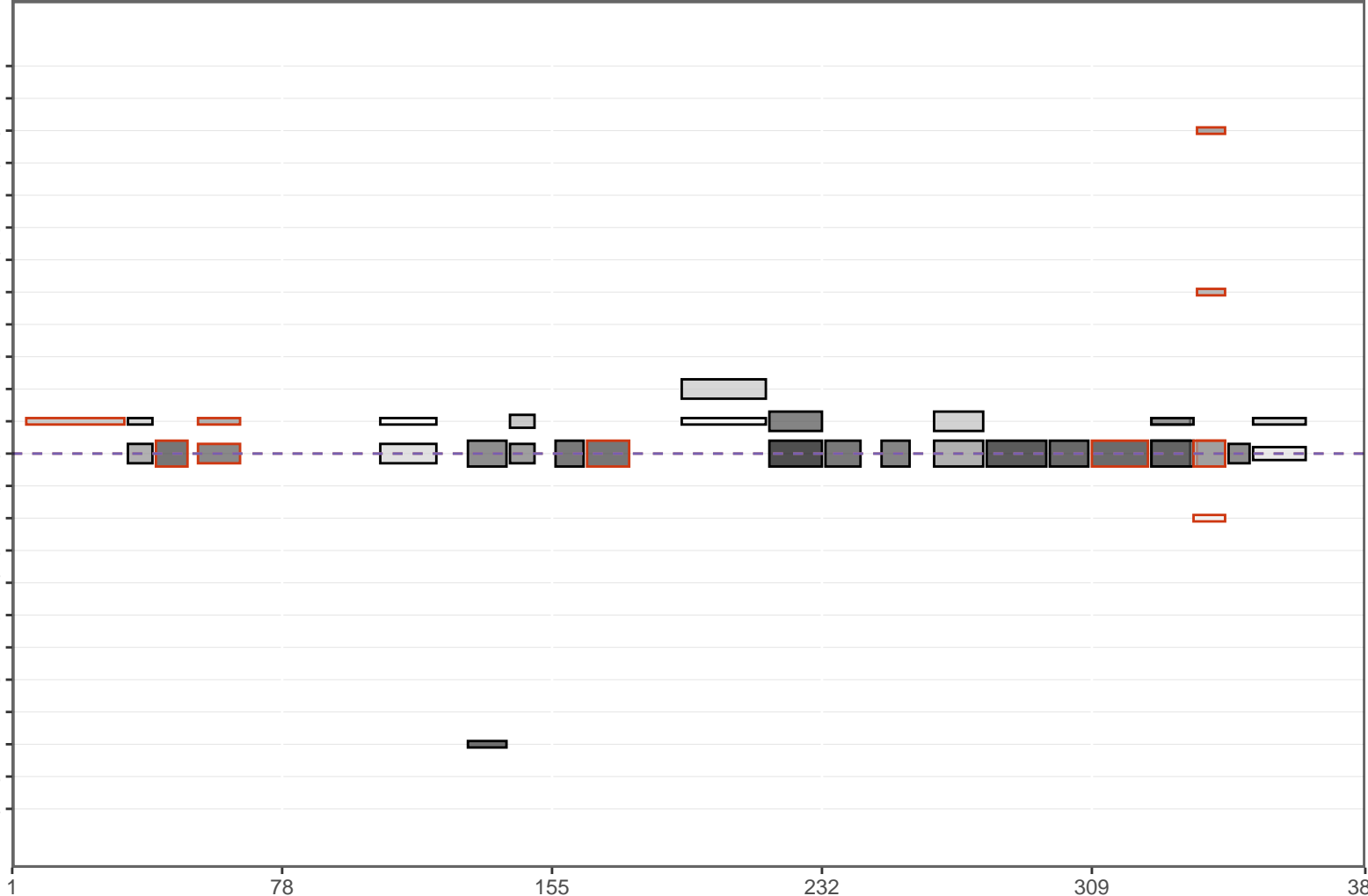
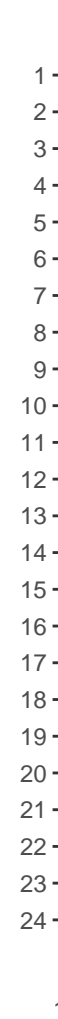
MW indication



Molecular weight

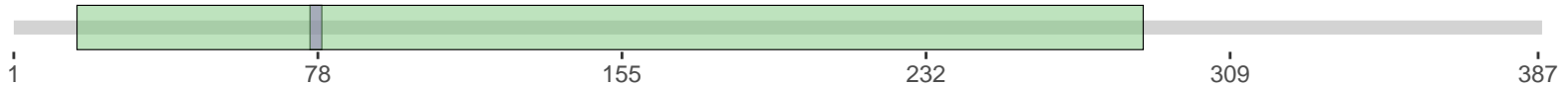


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ACAKQLIERLYAEGAENGLFTVRRFNWGRPRMDFIPGIDGSPSEGVPFRVLGFSNNLRRERPLKLVDDGSGRFTFYIKDAEAVLLMIENPARANGHIFVGNPNNVEITVRQLAEMTQVYKVKVSGESSELETPTVDVSSKEFYGEGYDDSDKRIPDMTHNKLGWPKTSLWDLLESTLYQHRITYAEVIKQAMSKTTAN

NbL09g15540.1 arogenate_dehydratase/prephenate_dehydratase_6_chloroplastic-like [MW = 47.27 kDa]

No. of times detected



log(intensity)



Values from



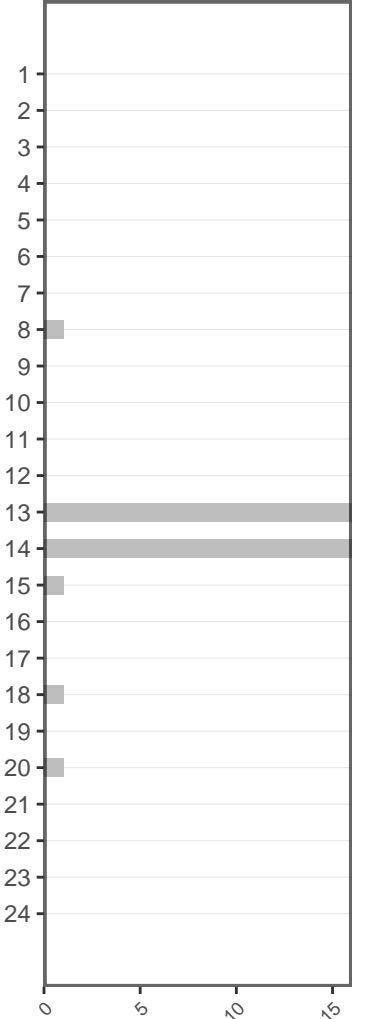
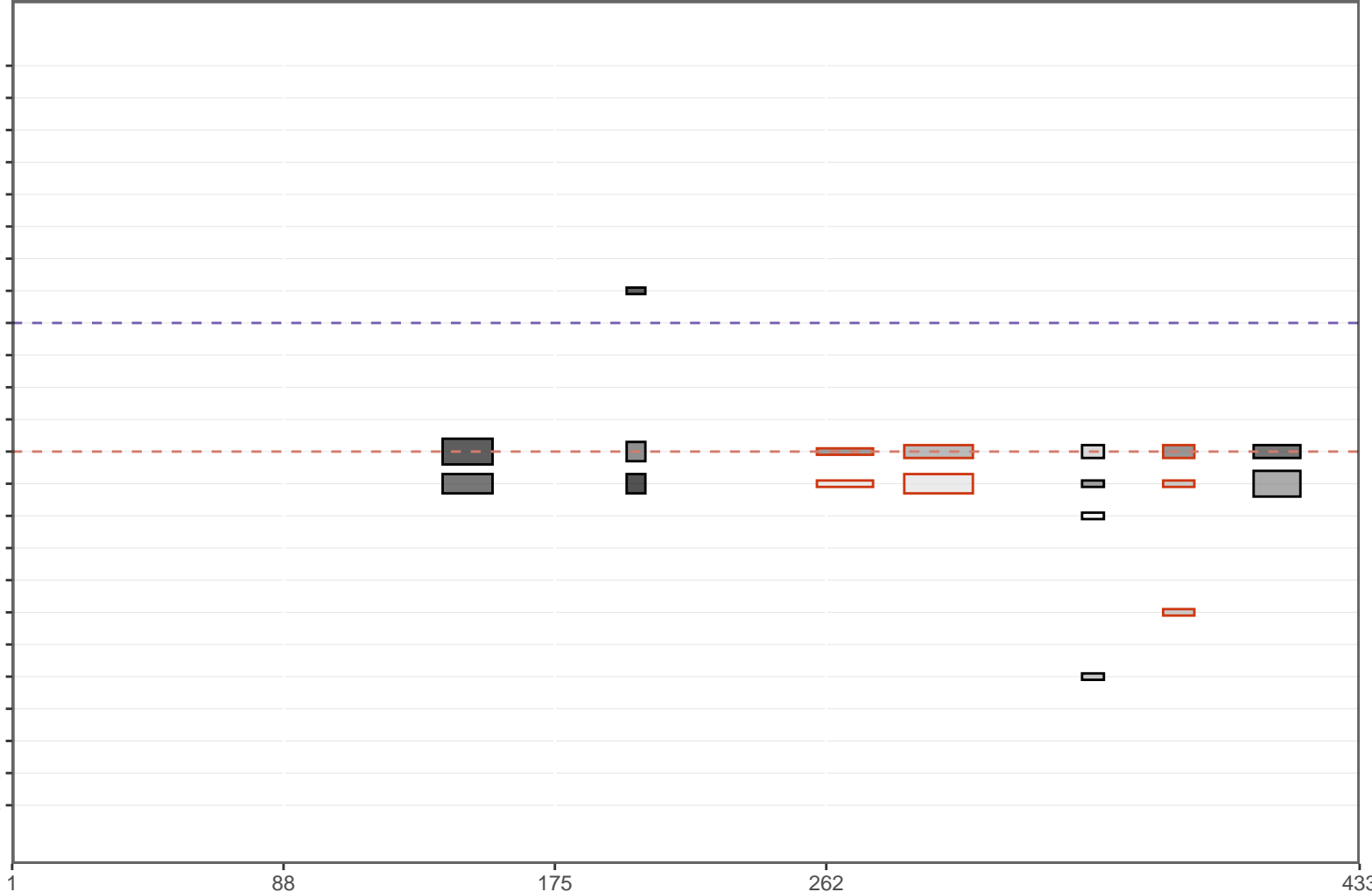
MW indication



Molecular weight

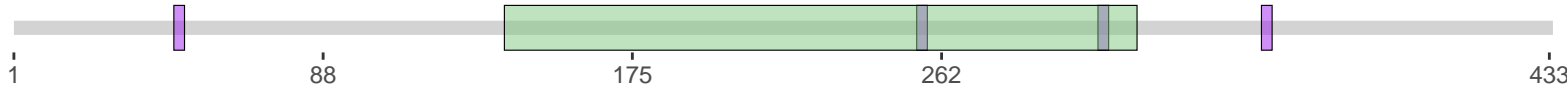


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LLRIRLHYGEVQLPVIHGLLALPGVRIKELTRVISHIQALAGCELITLTKLGLNVSREAVDDTAGAAEYVMAANNLRDTAAIASARAAEYVGLQLAEGIQDDSSNVTRFVMLARDPIRTRDPRFKTSVFAHDKGMVLFKVLGSAFRNIBLTKIESRPHRNRPIRLVDDANNVGTAKHFEVMEYVDFEASMAADVRAQNALAEVGEFTSFLRVLGVPMDMTPWCPGREE

NbL09g15530.1 probable_2-carboxy-D-arabinitol-1-phosphatase [MW = 55.89 kDa]

No. of times detected



log(intensity)



Values from



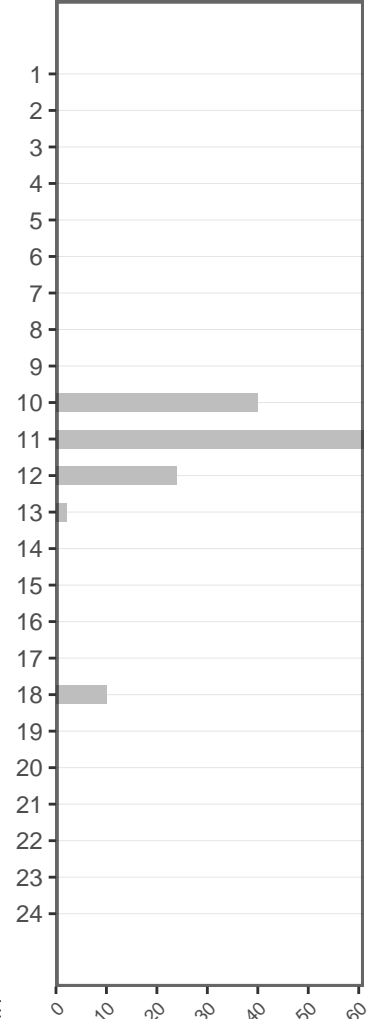
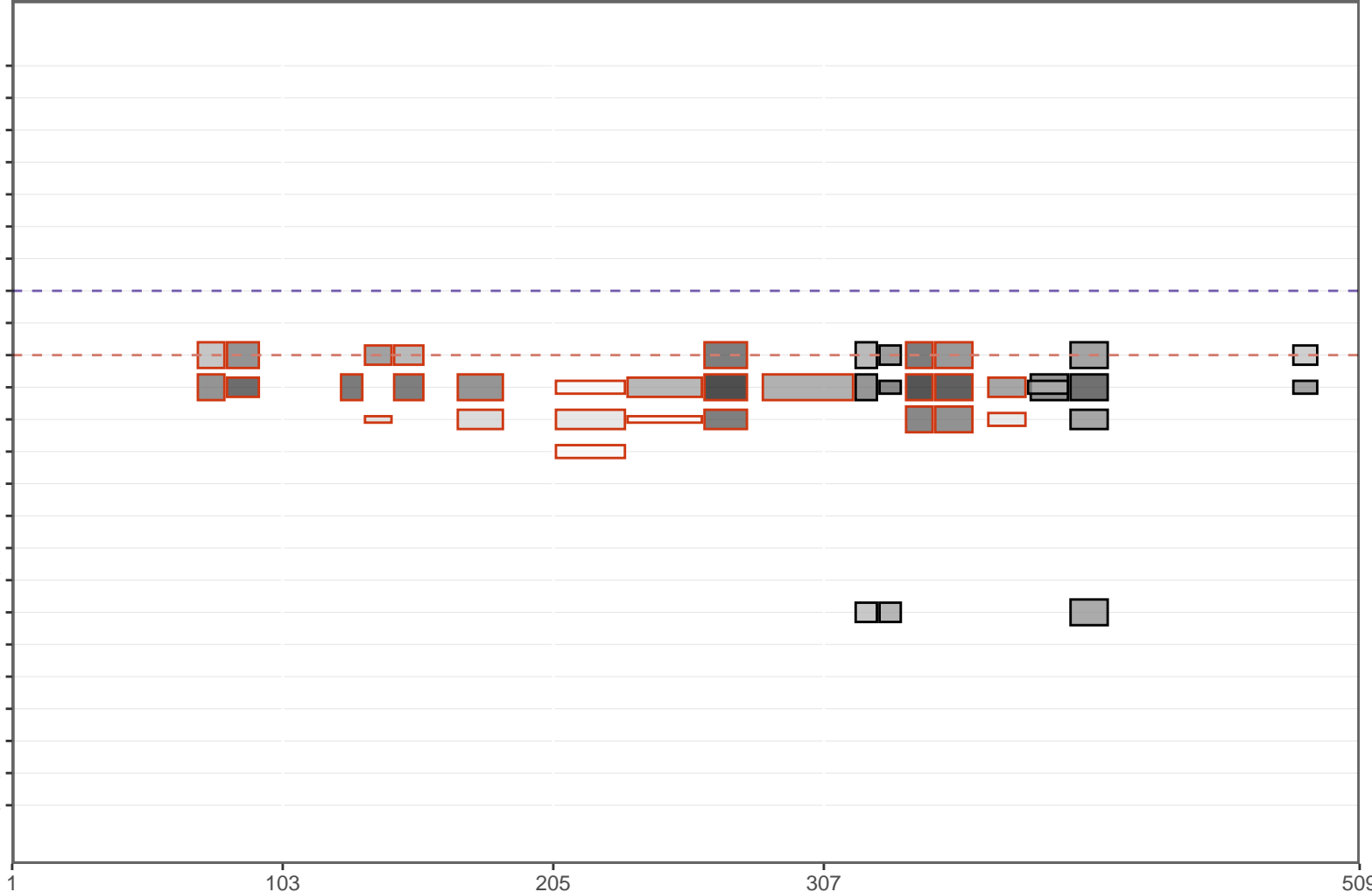
MW indication



Molecular weight

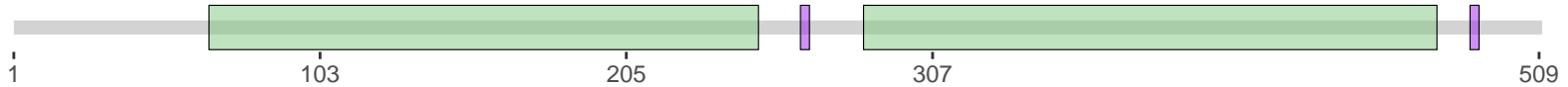


Gel Slice



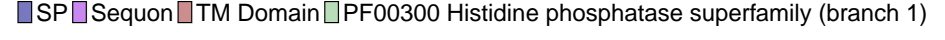
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VLDFTPEEGGTPSGLNRLNQTGSPVAGGSSGGKAKRKLVLVGHVSESDLENEMPYTGNFMNMLGVGDAKIAELLDLKLVSTIVSGTKRSTVETADTSIKVGEAADDLGDGIPRVYVETKQIPDLVETILTQSKKDAAGMGNVPSGWLNRLENDVTTSLVVDQSGKAWKHLLELSESSDEESVAVGHDPALHAMMGGHDLTKELVLSGFHLDAQSTVDFDPGSGRGVYVRCINVTALGRWSPITRSTGADEEV

NbL09g15470.1 60S_acidic_ribosomal_protein_P2A-like [MW = 15.01 kDa]

No. of times detected



log(intensity)



Values from



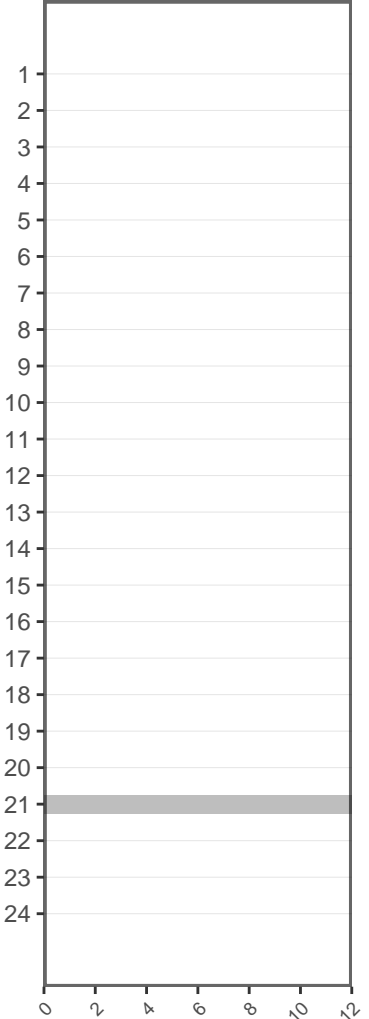
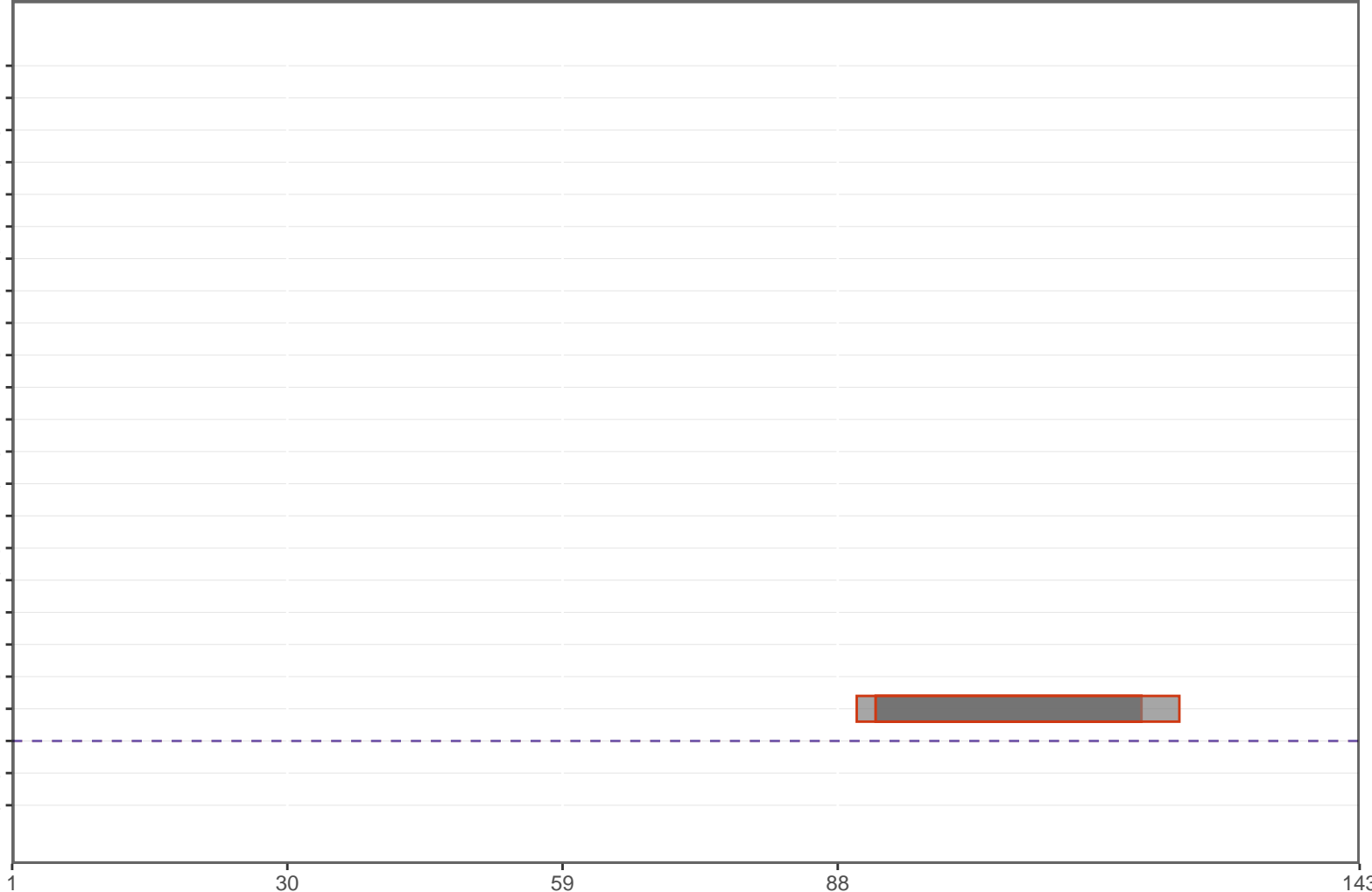
MW indication



Molecular weight



Gel Slice

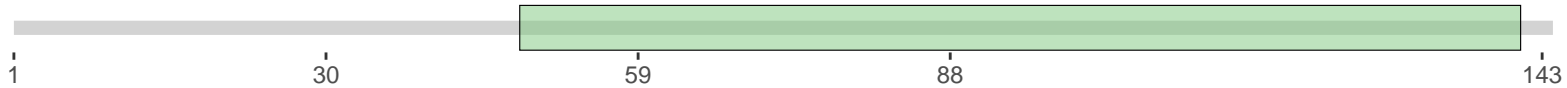


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VGAEADDRIELLGGVEGKDFELIANGREKLAVPAGGGGVAWAAPTSGAAAPAAEENKEEKVVEEKESDDDMGFLFD*

NbL09g15210.1 protein_CDC73_homolog [MW = 45.37 kDa]

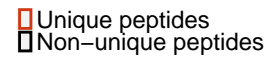
No. of times detected



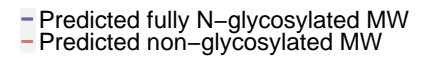
log(intensity)



Values from



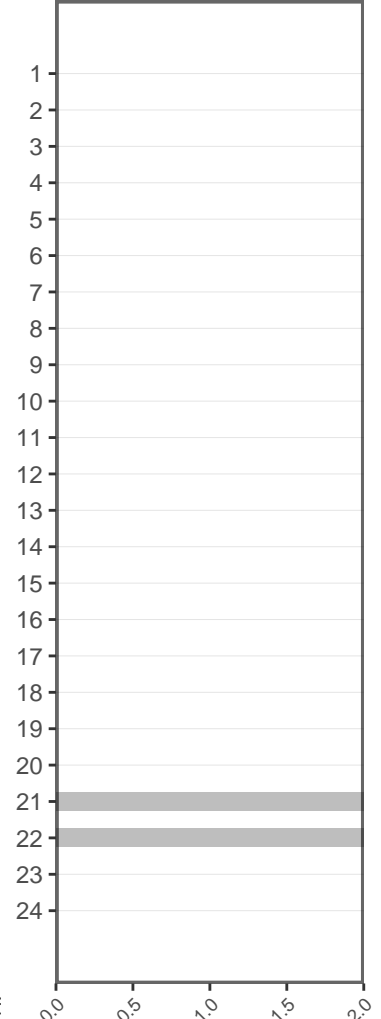
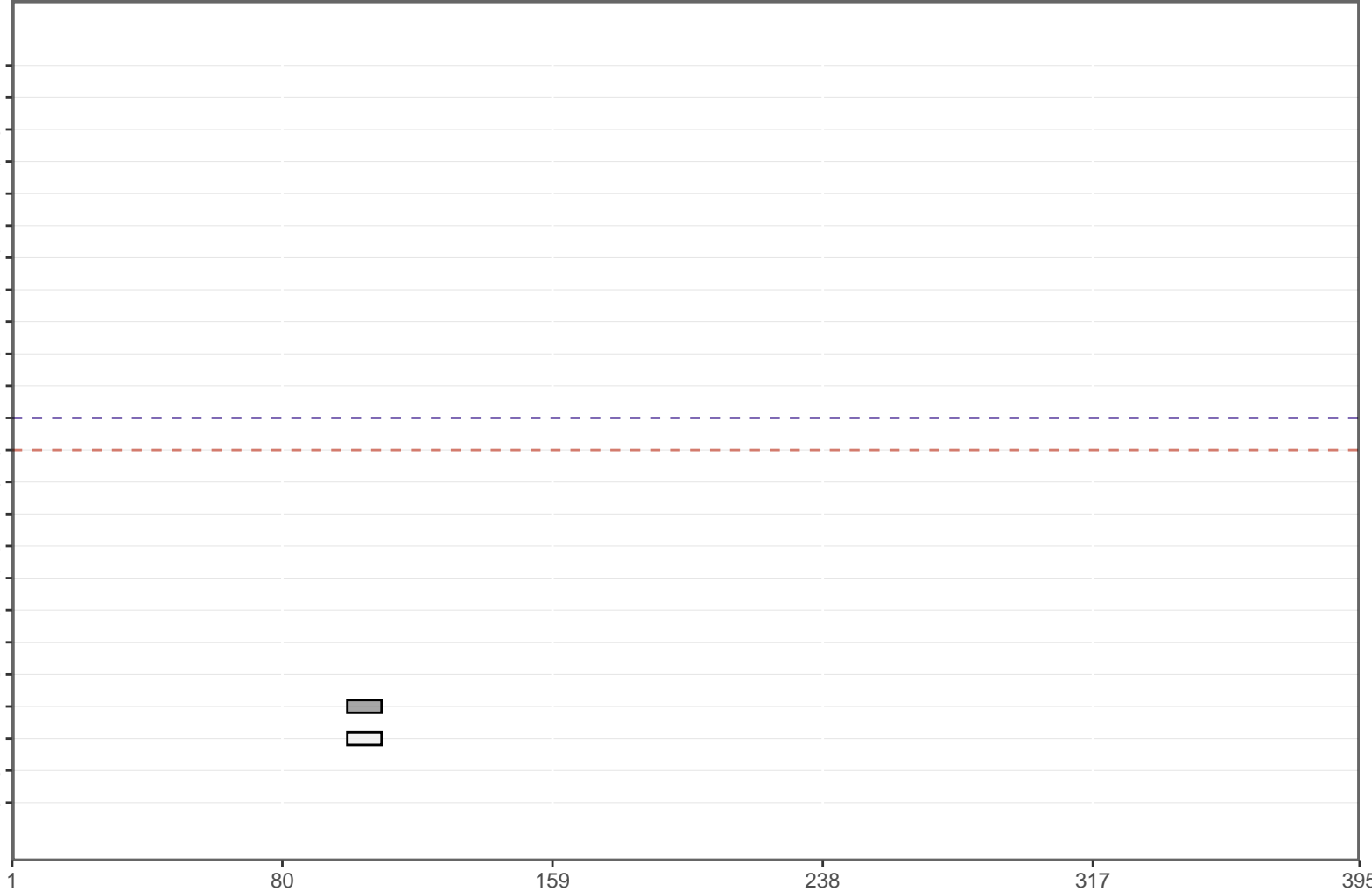
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF05179 RNA pol II accessory factor, Cdc73 family, C-terminal
- PF16050 Paf1 complex subunit CDC73 N-terminal

Protein sequence:

ESLQRKDLVAKNRIRGGFGGDELGYDGGPKAKMHLKGGKIGEGVPHLPKAFGLTFTYNNKEFLLEDGVFIPDVKLQKMGKMPDGTVQKIKFRDRVYTAVERDKPSALKAEDWRVWVFLVGLKEWGFKDWPFKNHVEIFNKVGFLLRFEDDSVESAKTANGWNVQIISIKNKHQDRAAAALEVWEKLEEFMRSRH

NbL09g15110.1 uncharacterized_LOC109240313 [MW = 65.51 kDa]

No. of times detected



log(intensity)



Values from



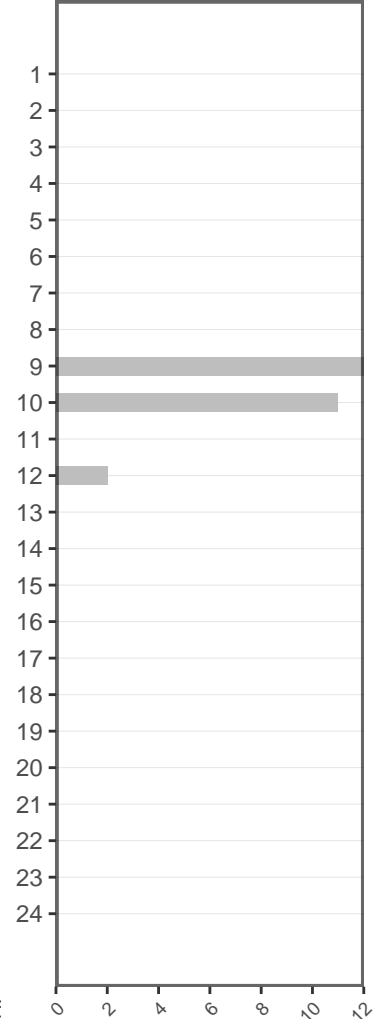
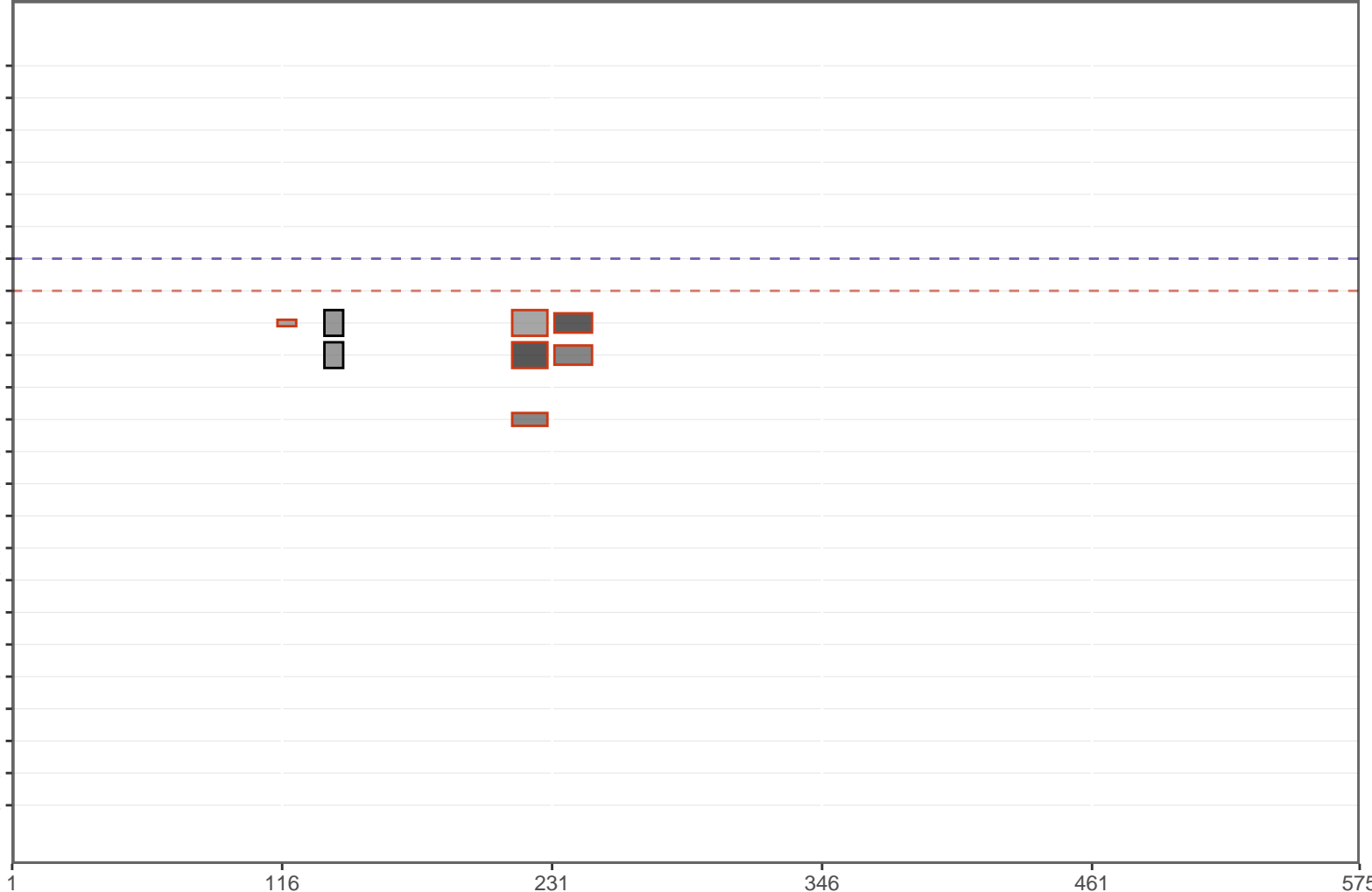
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

FSTNAEAAVALSQENEASSGGINPDSRRWIKWETGTEKRPDGVVCRWTLTRGVASDKTVEWEDKYWEAADFQHKELGSEKGRDAAGNVAHFEFVKEBMWQSGGLVHEKTDKQGRNKKGEWQEKWWEHYGAGGQAEKWAHKVGSIDFNTFLAAGHAHVHHERWGEKYDKGGSTKYTDKWERFEGDQWVKWGDWDEHFDLNAHGKQGETWVWAGKSGSERWRTWSEGHNGSGWVHKYGH66SGEHWDTHTNEERYFERFPHYGFYK

NbL09g14990.1 60S_ribosomal_protein_L19-3-like [MW = 24.56 kDa]

No. of times detected



log(intensity)



Values from



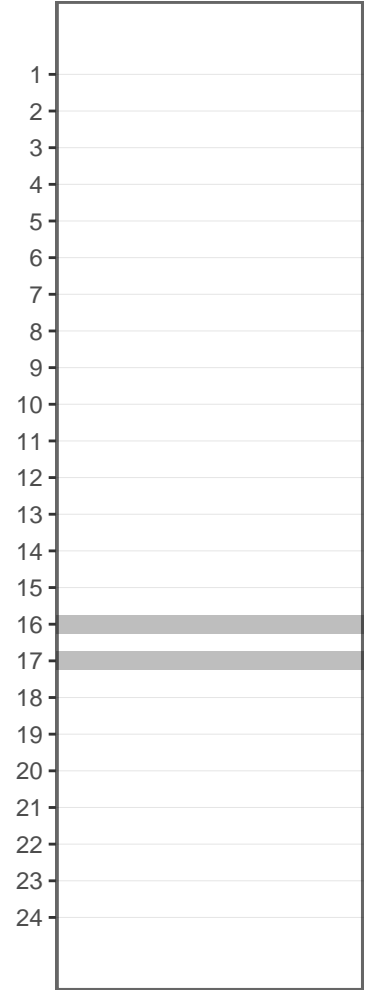
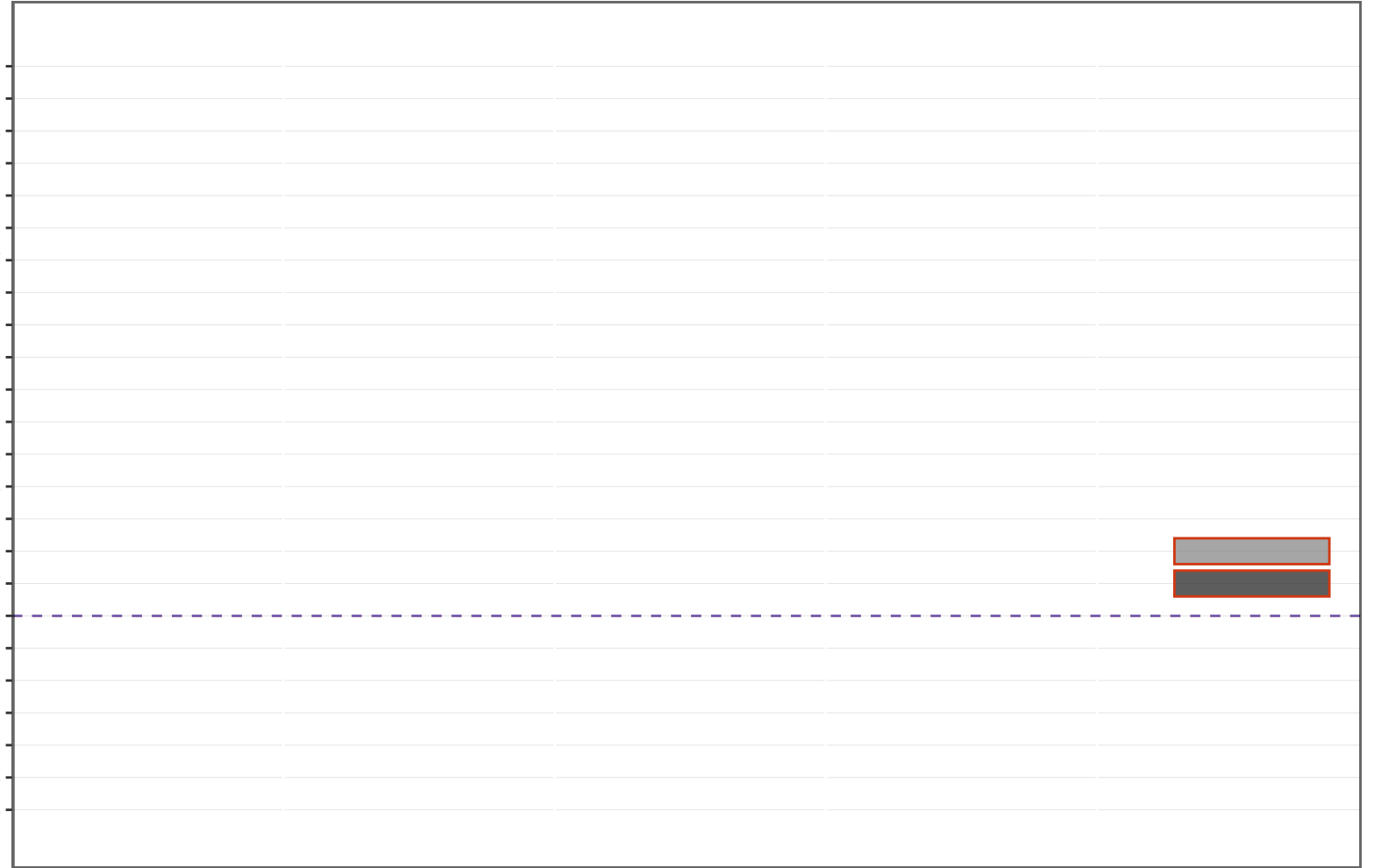
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length: 1, 43, 85, 127, 169, 210

Pfam domains: 1, 43, 85, 127, 169, 210

Pfam Description



Protein sequence:

/LWRRMRVLRRLRKYRESKIDRIMYHDMYMKVKGIVFNKIKRVLMEHDKTKAEKAREKTLSDGFARRAKNKASREKFKARRERLGGPGRPVQPAATEAPQAGGSKKIKK

NbL09g14980.1 uncharacterized_protein_At5g01610-like [MW - SP = 15.98 kDa]

No. of times detected



log(intensity)



Values from



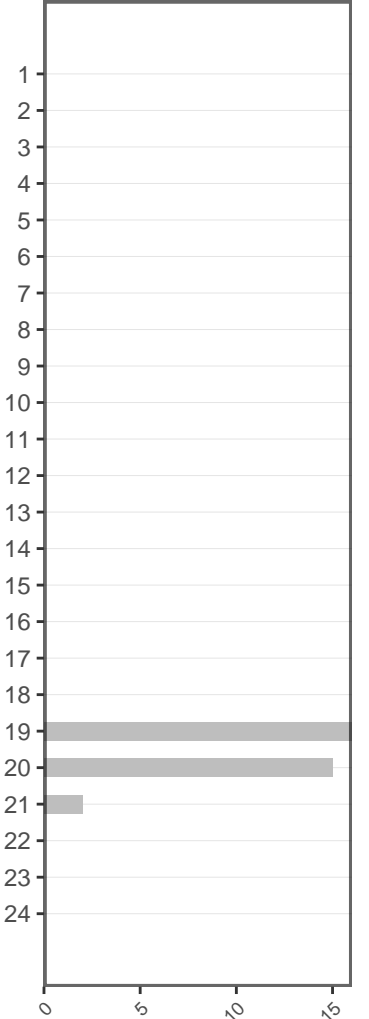
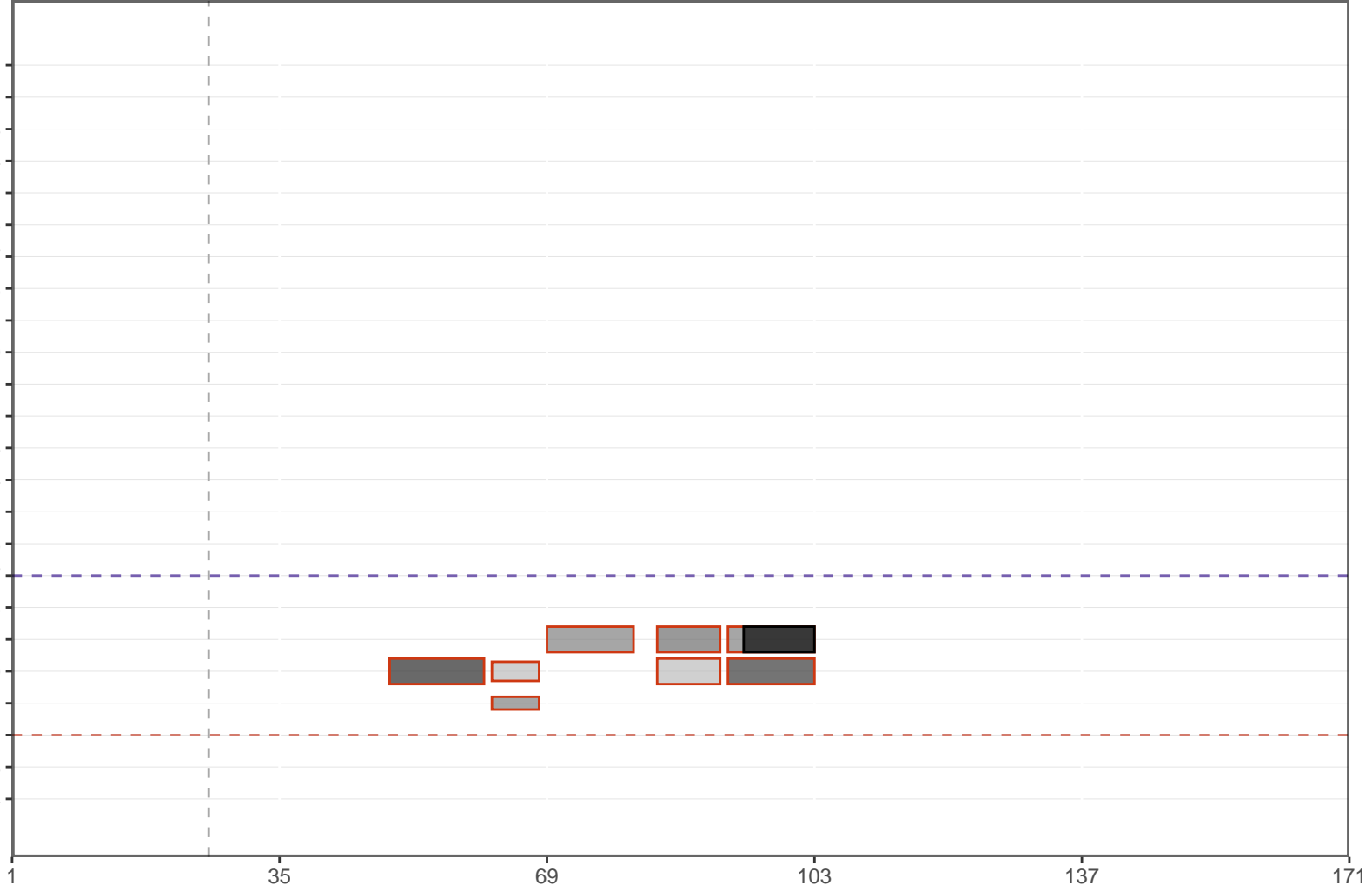
MW indication



Molecular weight

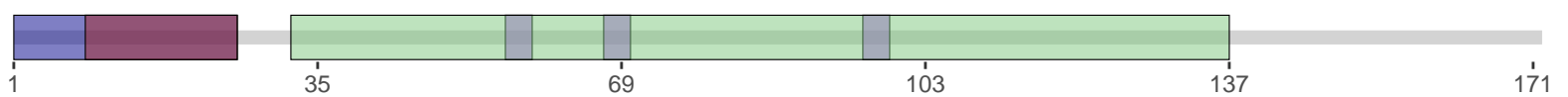


Gel Slice



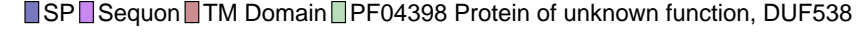
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

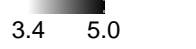
IEESYSLRYKSKITGTLKDKLKNLGGVQVWVLFVFWNIGEVARVDDLELDFYGVNSADFPDINFYEGSPGGCCGDCVNSGGKSTGEIRGNEMKEHK

NbL09g14800.1 short-chain_dehydrogenase_reductase_3c-like [MW = 31 kDa]

No. of times detected



log(intensity)



Values from



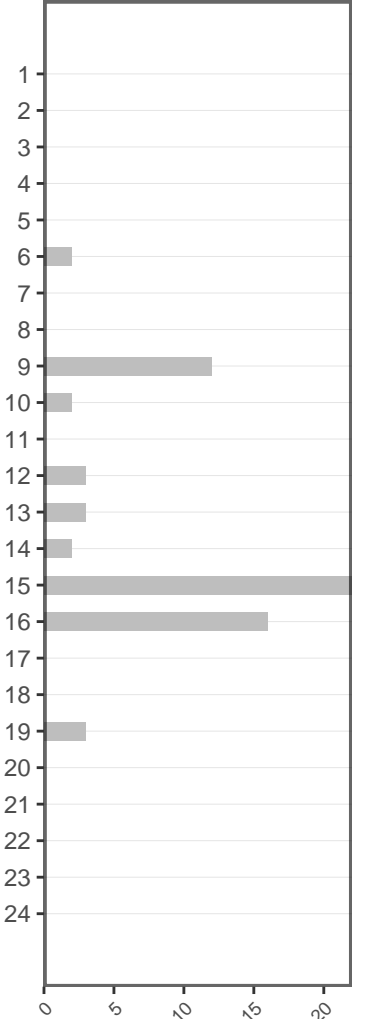
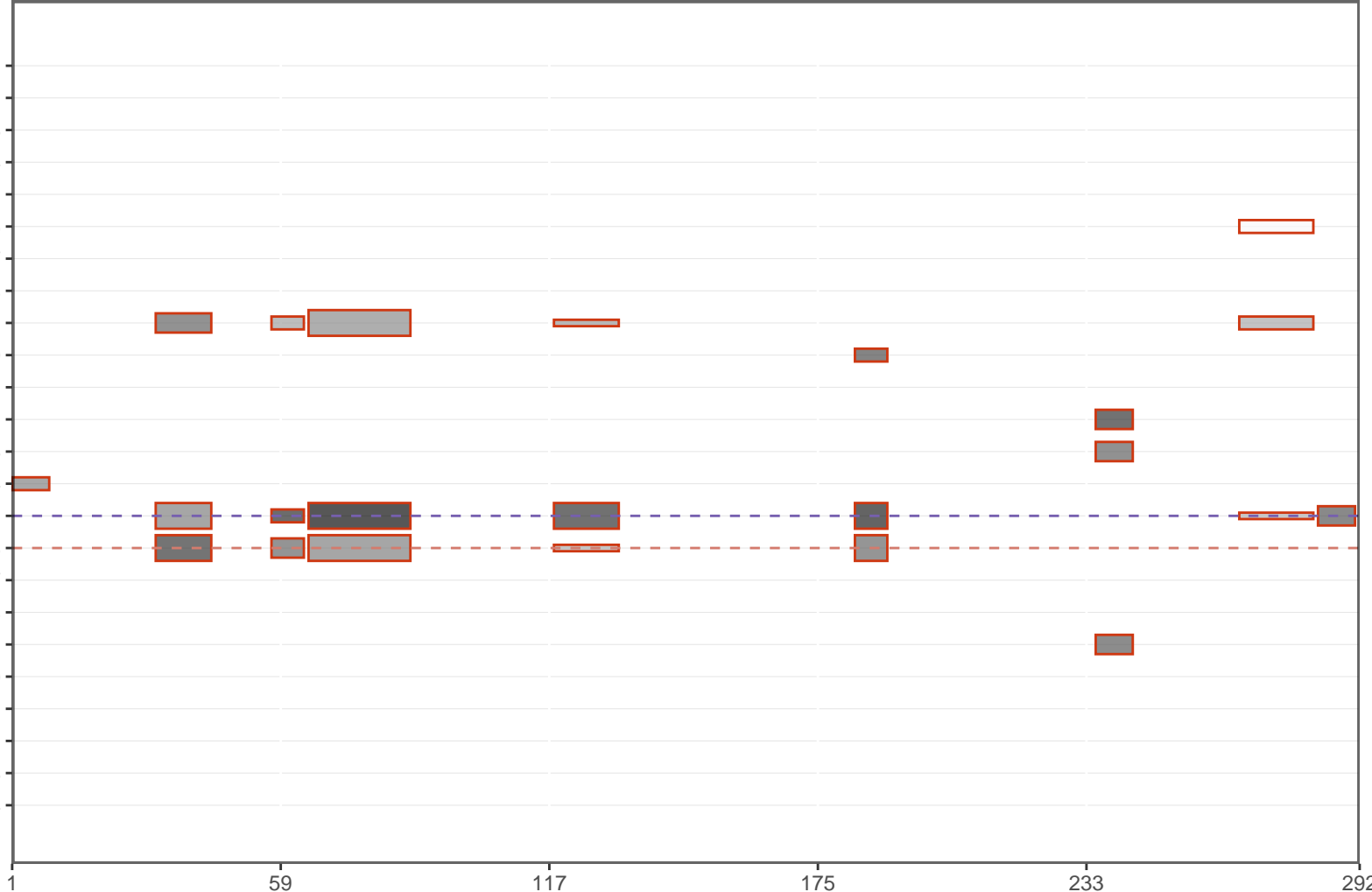
MW indication



Molecular weight

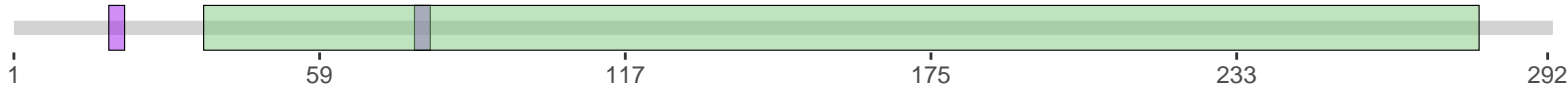


Gel Slice



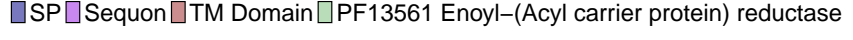
Protein length

Peptide counts over 4 repeats



Pfam domains

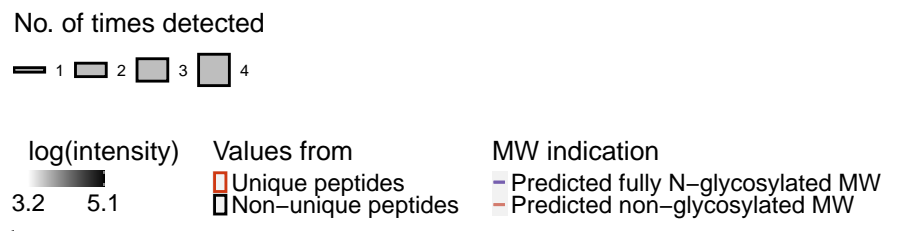
Pfam Description



Protein sequence:

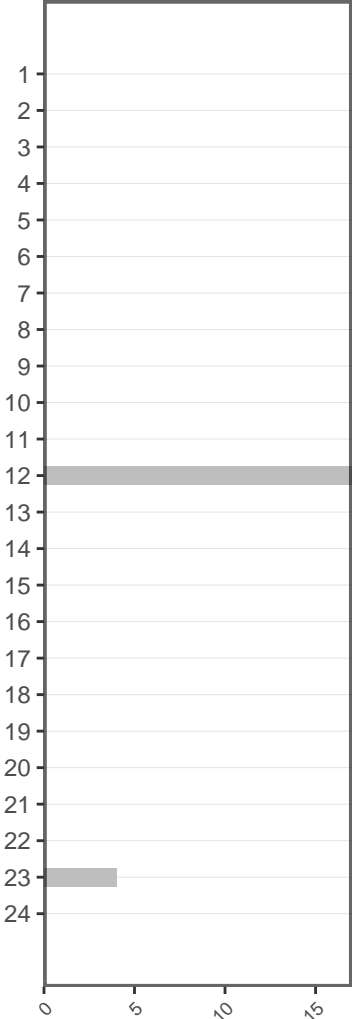
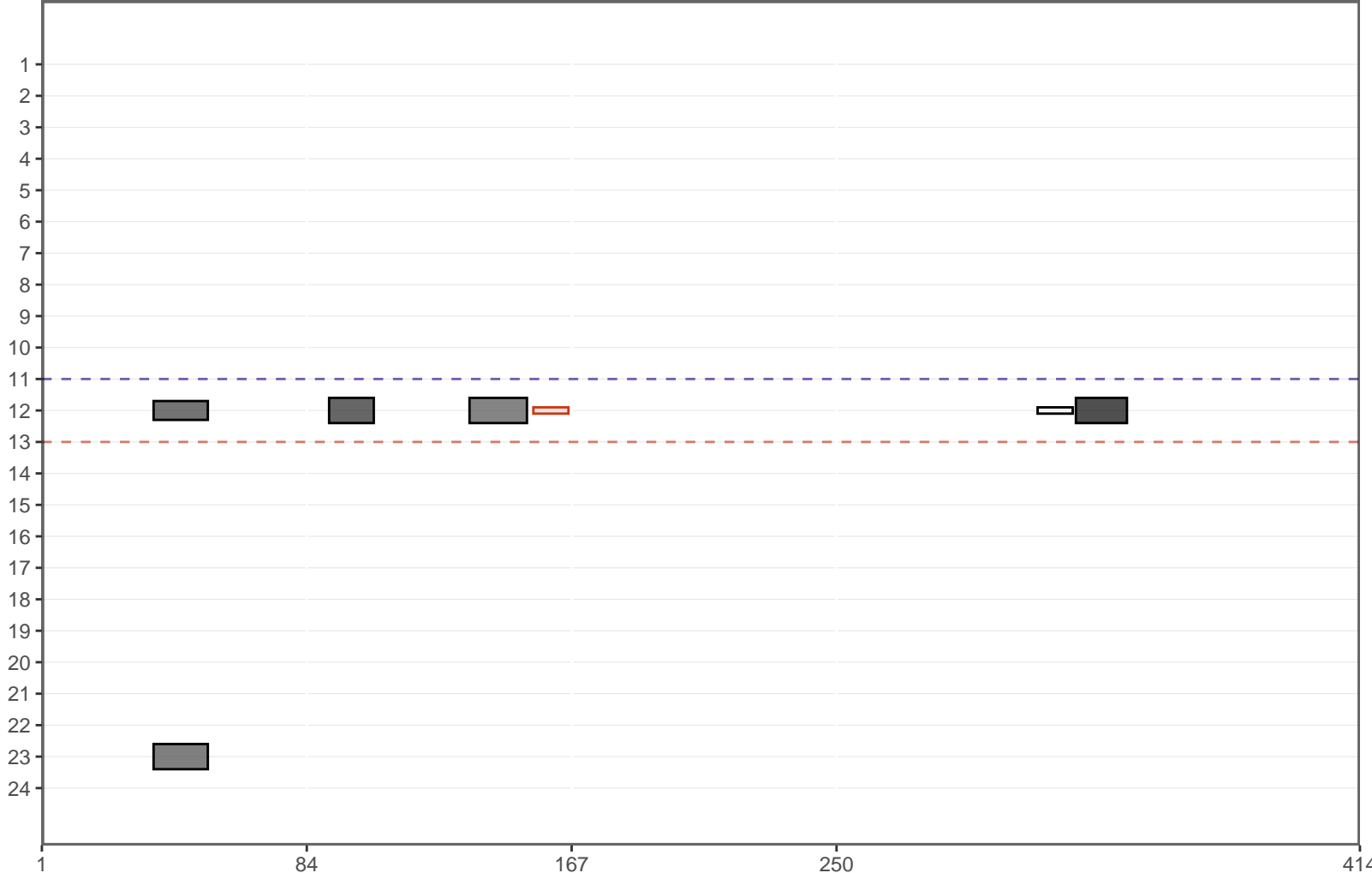
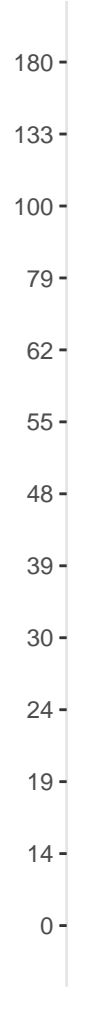
RVMANVROGVVAGKHAARVMPRGSGGLGCTASVTFGVIGGLAQRVYVTSKSGSVGVKSLTAQLCKGGIRINDGSEFFAIPFPFSLDEMKNHYFDGVEPQGLANLHSTSELKGVAYGEPDVAANAALFLASEDAKFRFSGHNLVDDGGFTSKSLNLAQVQV

NbL09g14740.1 NPL4-like_protein_1 [MW = 46.36 kDa]



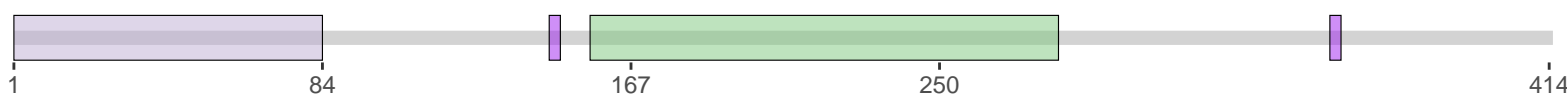
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF05021 NPL4 family
- PF11543 Nuclear pore localisation protein NPL4

Protein sequence:

EKVVDALAIQLGMRRVGFFTQTISGDKDYTMSTAEVLGAELHAEGDLKEWVTAVKLEVNEDGAADVHFEAFQMSGDMCVRLFKEGWFETEYKNDKEMIEFKLQKMKKDVLVGVKDTREVNDVDFLVVVKIADHGGPLSGSFPIENRNPVSMRALKDHFNRTKSLSFVKRISDFHLLLLAKFLDINADVPLAEQVHTQTAVPEGYQLLIESMASAS

NbL09g14580.1 small_nuclear_ribonucleoprotein_Sm_D1-like [MW = 12.61 kDa]

No. of times detected



log(intensity)



Values from



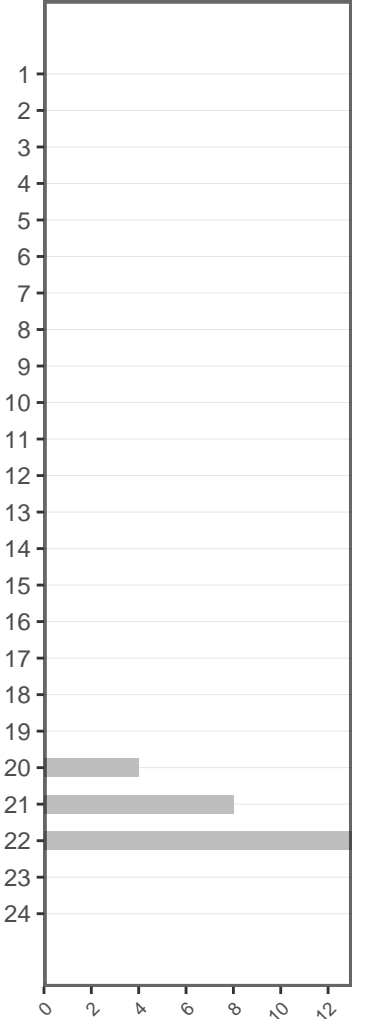
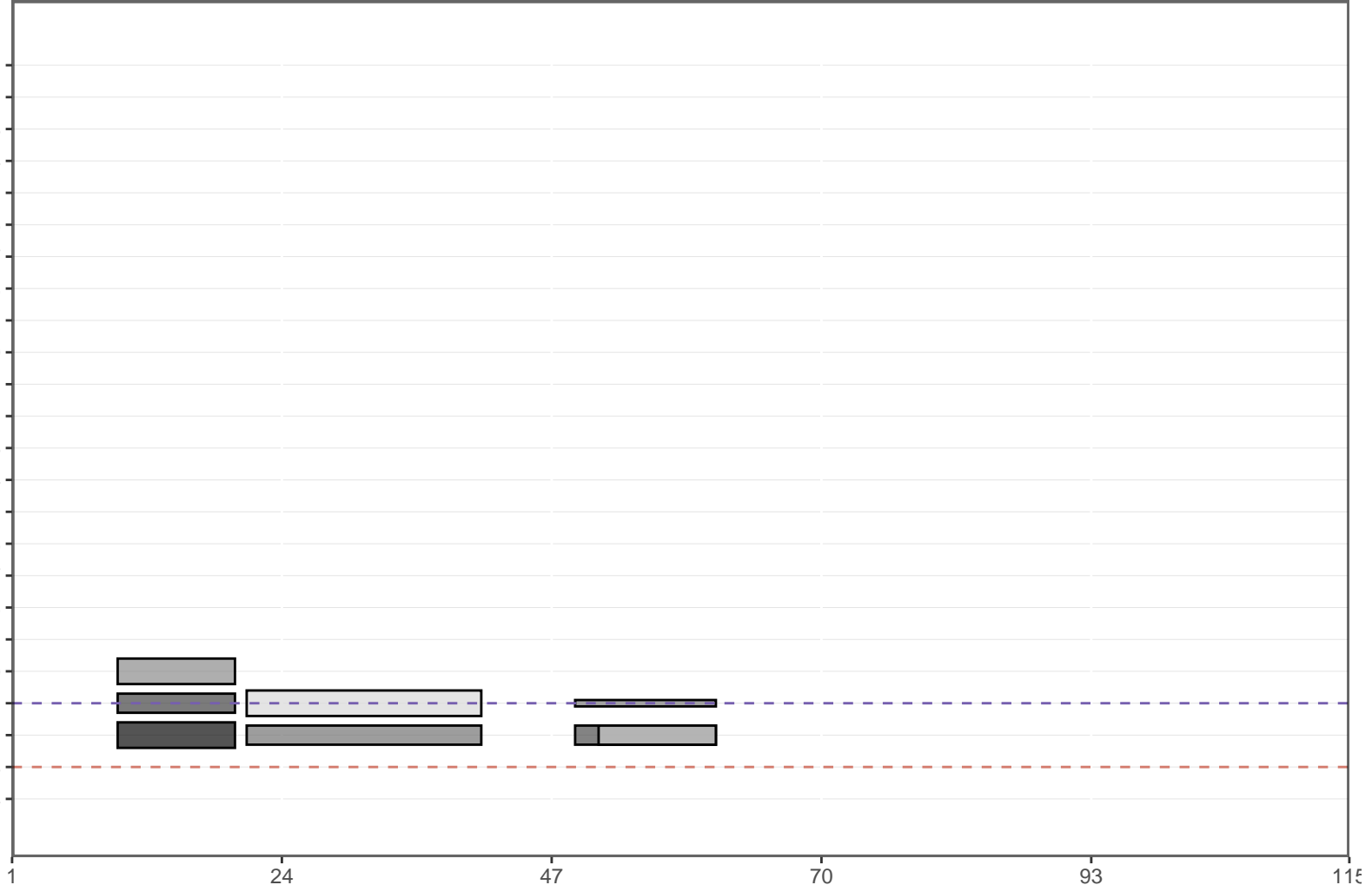
MW indication



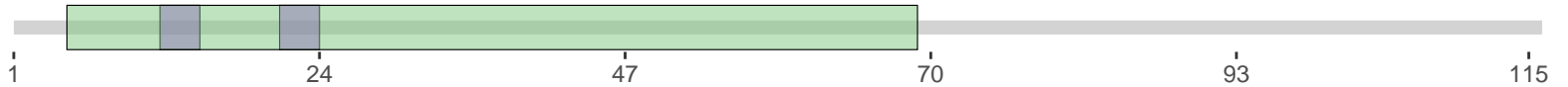
Molecular weight



Gel Slice

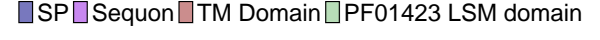


Protein length



Pfam domains

Pfam Description



Protein sequence:

LTLLGKQNPVTLDIHLVLRGNIRRYLFDGLNLETFLVVEETPRVWPKPKTAGKPLGRGRGRGRGRGRGR*

NbL09g14530.1 fatty-acid-binding_protein_1 [MW = 32.3 kDa]

No. of times detected



log(intensity)



Values from



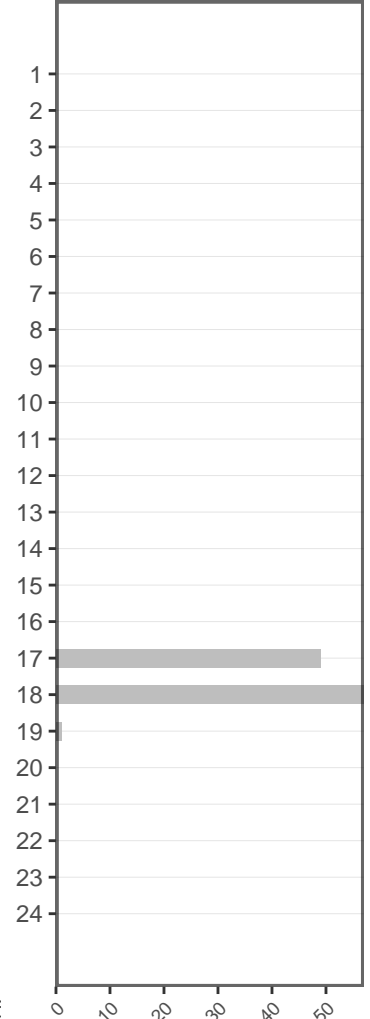
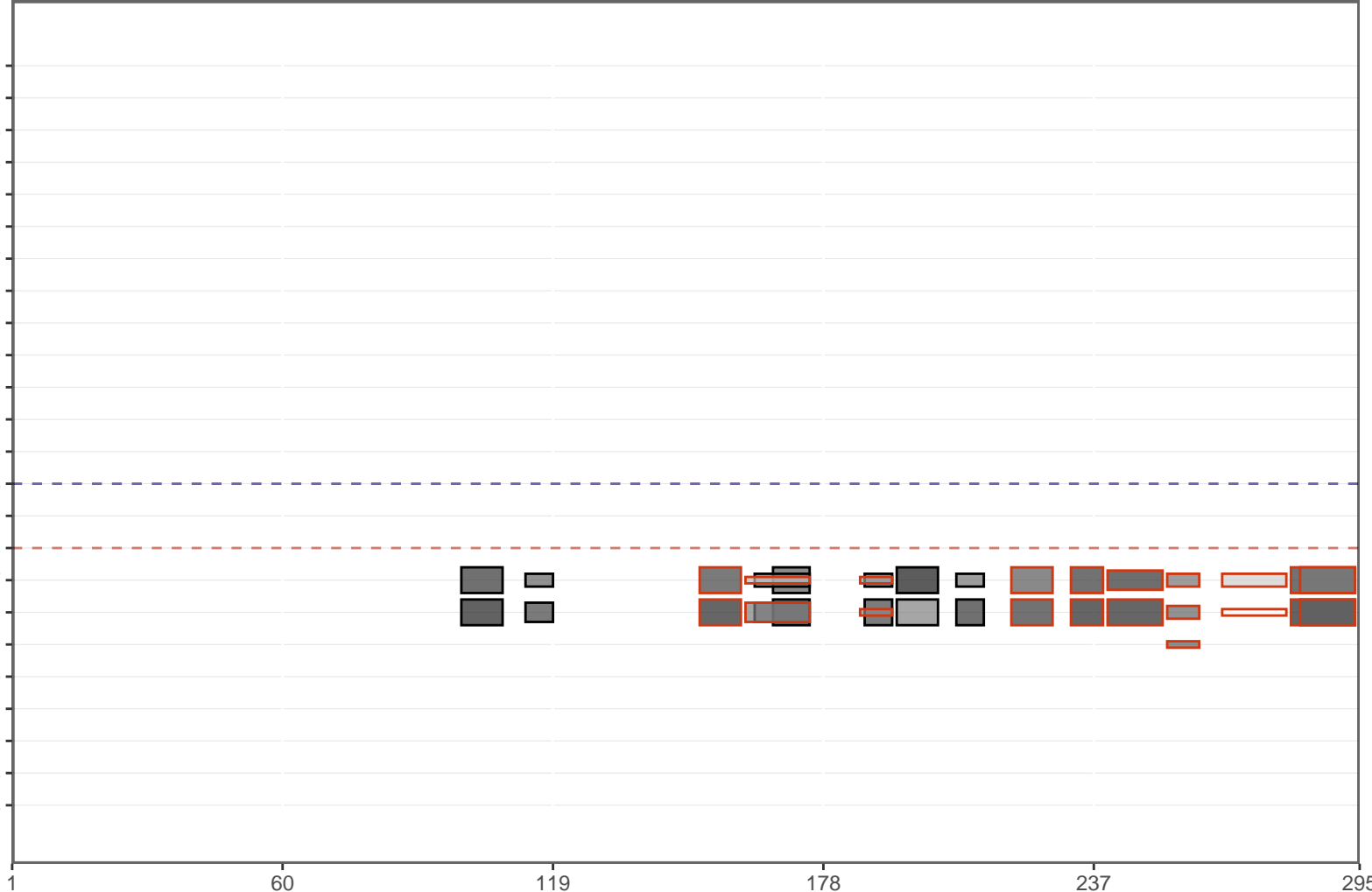
MW indication



Molecular weight



Gel Slice

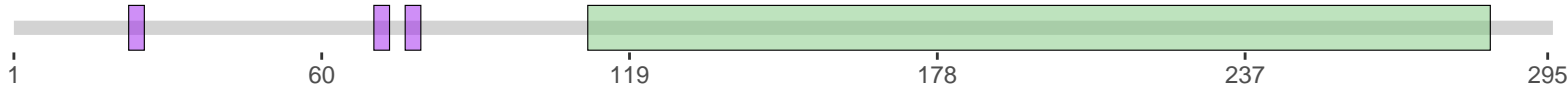


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

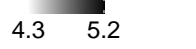
FGVYADDEVEYXXCLAGKHVGPDSSELKSKELRDHLMENDIRMTVRLGQVYRRLSIGSVRSFAFEESVGSRLKLFQGYDKNKKLLHRFTSGQFKDKIPRGSIELGRDHGVLHTFDGKEVSGSGKLLRBLDLVIGEEFQKAKEDEENLALSHK

NbL09g14420.1 non-specific_lipid_transfer_protein_GPI-anchored_2-like [MW - SP = 13.62 kDa]

No. of times detected



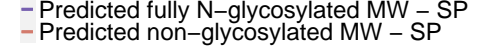
log(intensity)



Values from



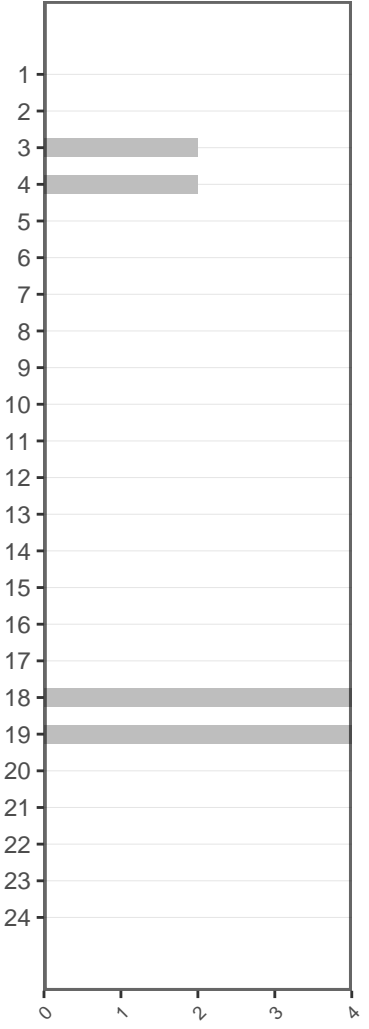
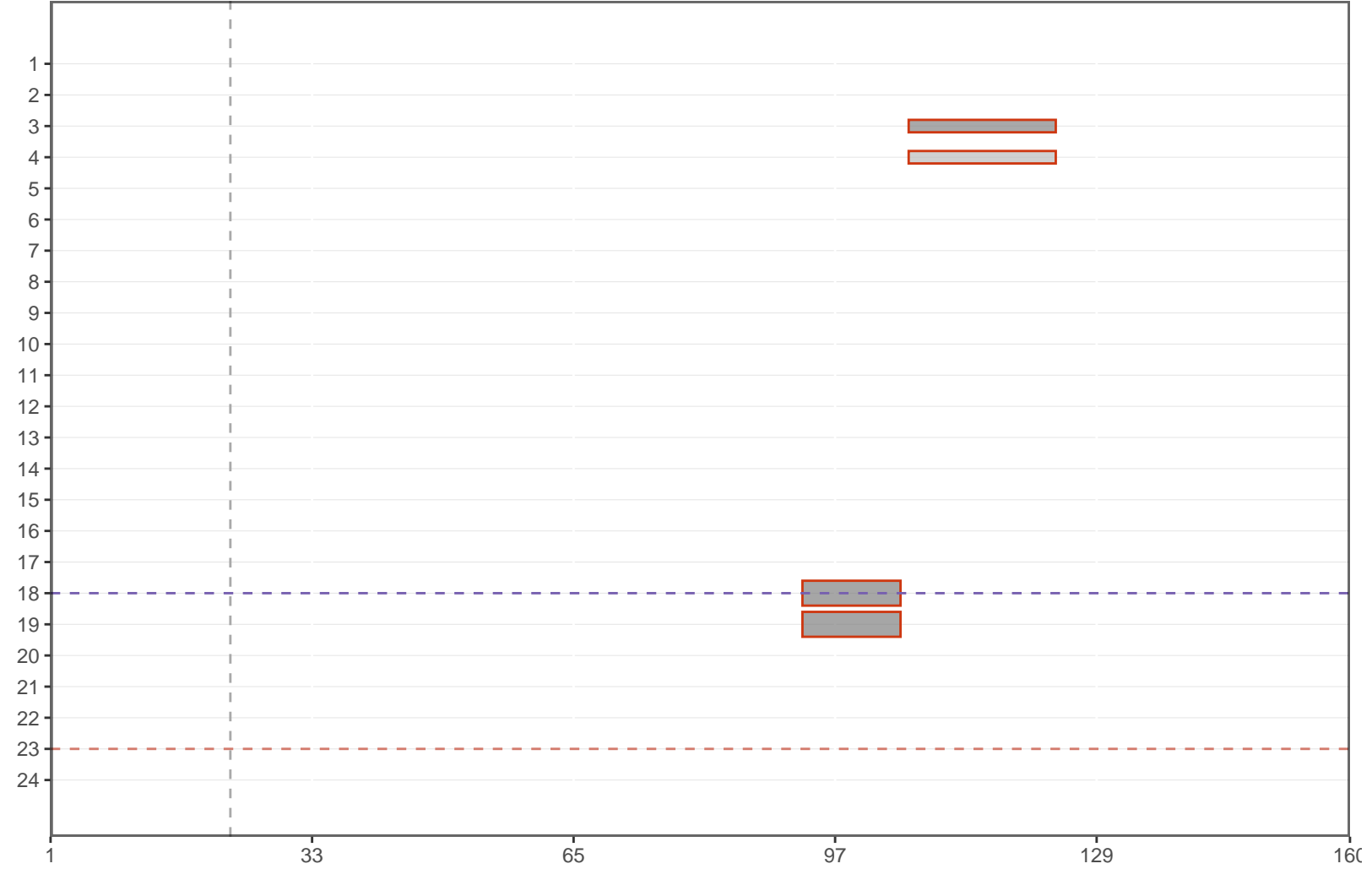
MW indication



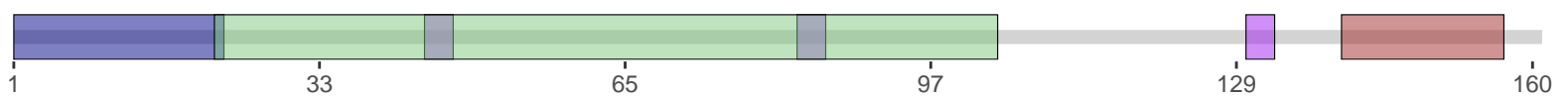
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

COVYNGGGSNLSGNVNGTQAMALPKAGNVGTPVSLGKGTTPSGS6S6SNFSGGKGEPE6GNS6GNEVMPYSLFLVMAASLATVETPI

NbL09g14140.1 glycolipid_transfer_protein_1 [MW = 24.68 kDa]

No. of times detected



log(intensity)



Values from



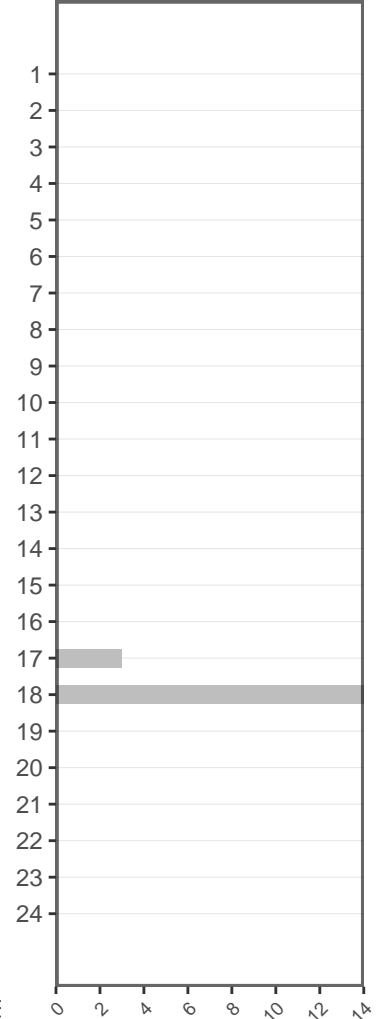
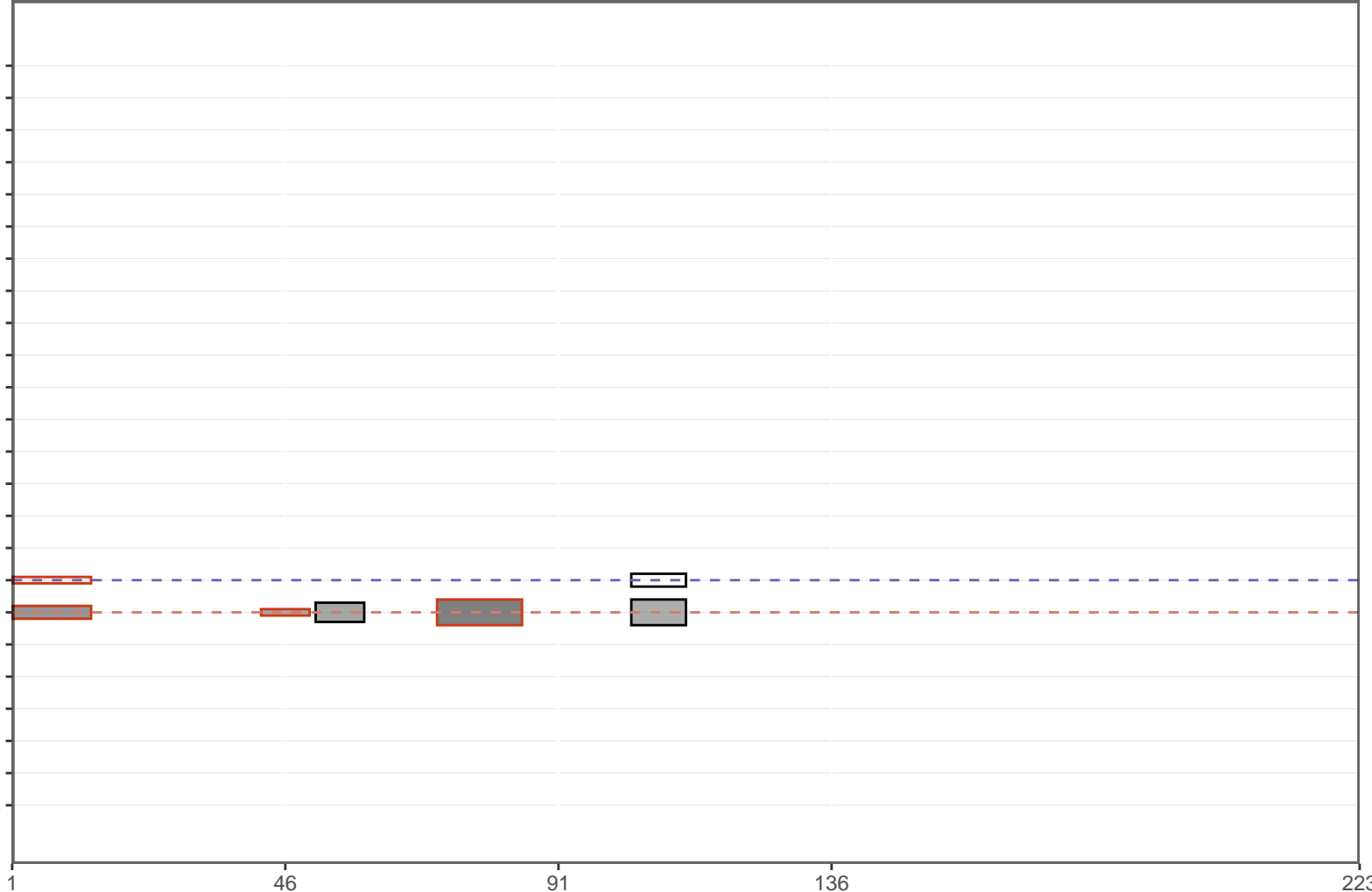
MW indication



Molecular weight

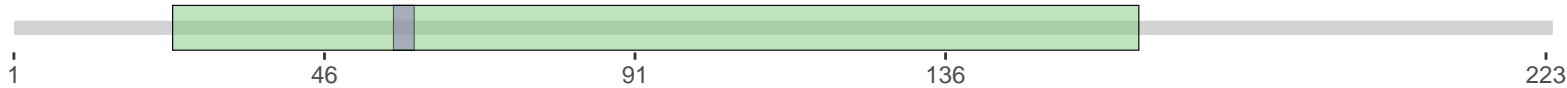


Gel Slice



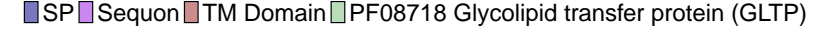
Protein length

Peptide counts over 4 repeats



Pfam domains

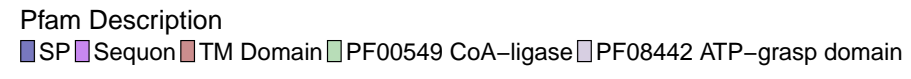
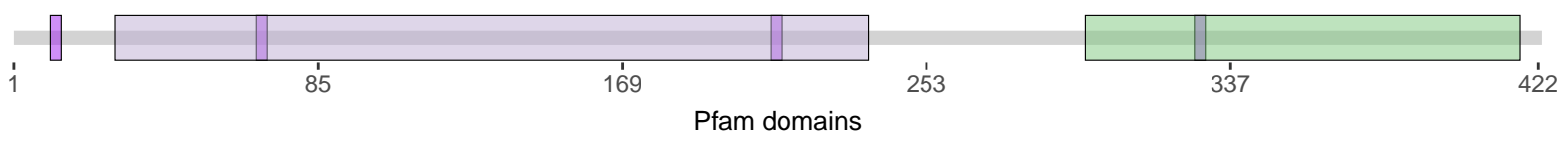
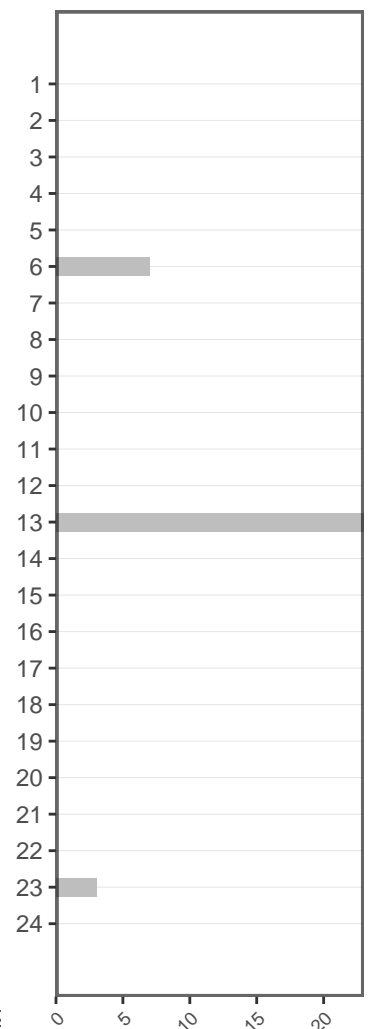
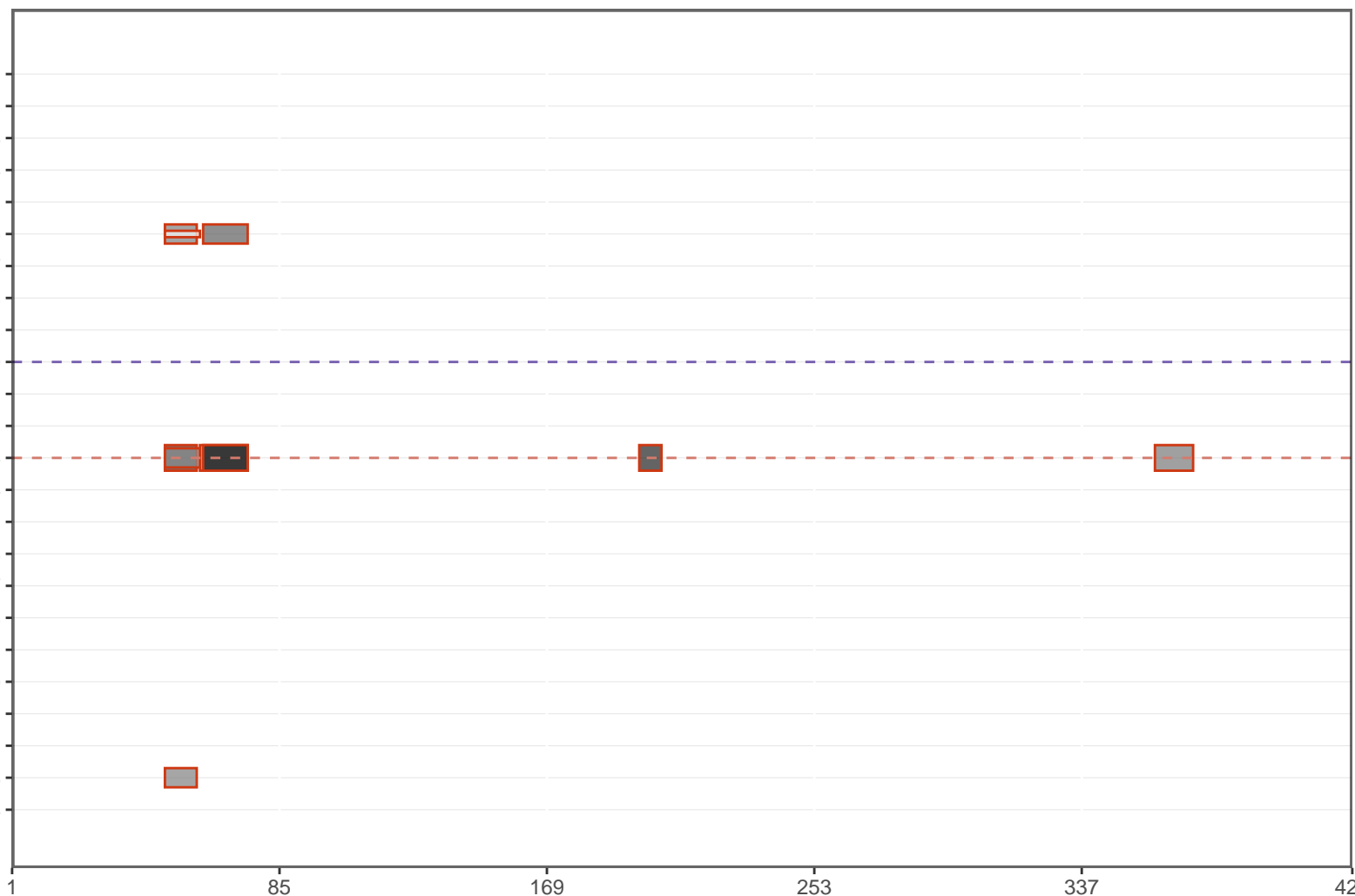
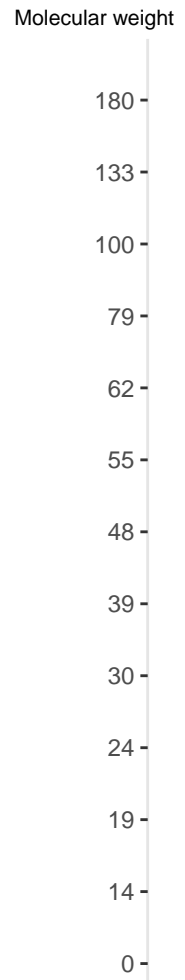
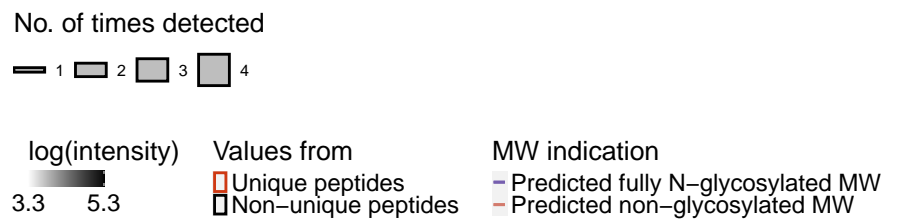
Pfam Description



Protein sequence:

.TRAMDVLYELFRNLEHGDMAMEGACSDSVDYKTLKFKHGWLASGFSVAMKLPDRKKFMVIGGTGDDSDGGGCTTFSPLEENKFLWKLGGYSDDRLDFFLGLHYGSGSFPAPT

NbL09g14120.1 succinate--CoA_ligase_[ADP-forming]_subunit_beta_mitochondrial [MW = 45.27 kDa]



Protein sequence:
 KVVYDGFAPKVALDRNDSIEGKWKLYLGFCESDGTMLEINFLAETSQNKLVADAKLFDQNAAYRQKEIFLRDSSGSDPREVAAMAKADLVYGLDGEIGGMVNGAGLAMATMDIKLHGSTRNFLFVLDVNGATEGGVVEAFKILTADKVKALVNFGGIMKQGVASGVNAKGVQKVPVAVRLEGTNVEGGRILKESGMFLTAEDLDLDAEKAVKALA

NbL09g14000.1 monothiol_glutaredoxin-S10-like [MW = 28.11 kDa]

No. of times detected



log(intensity)



Values from



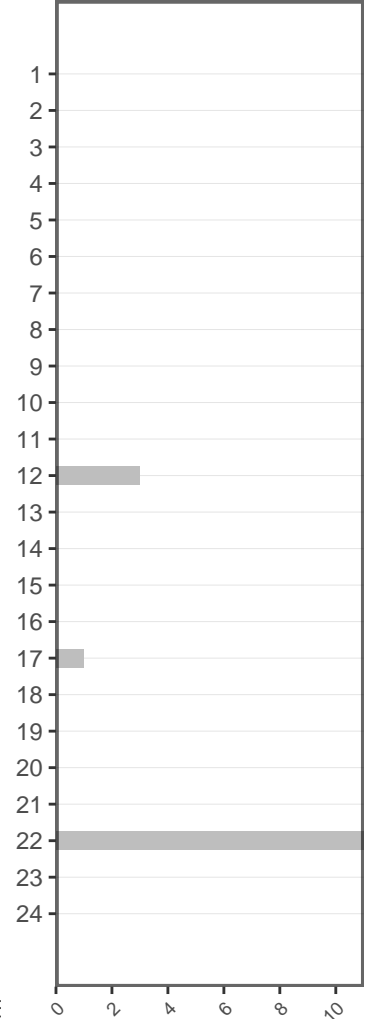
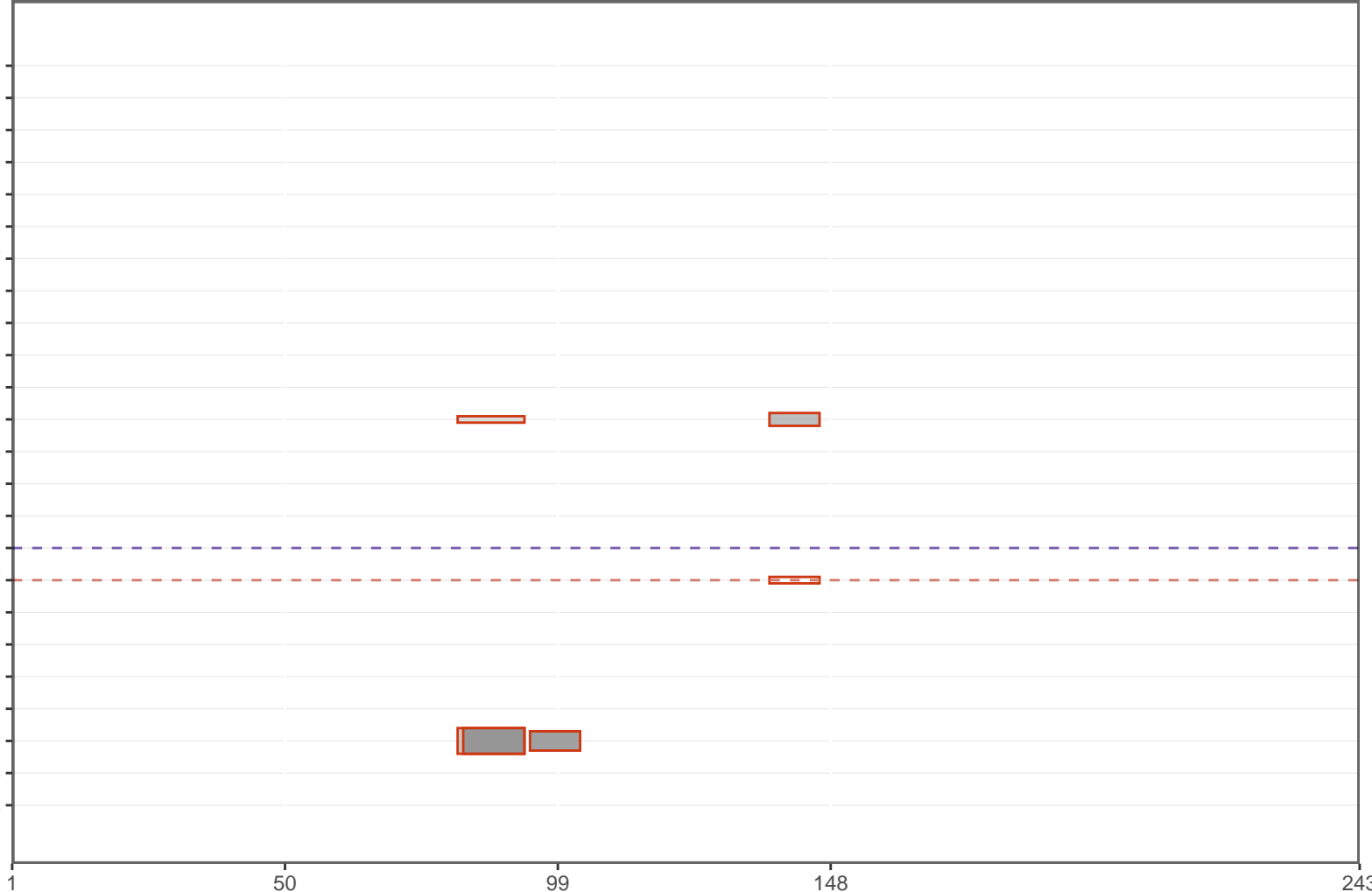
MW indication



Molecular weight

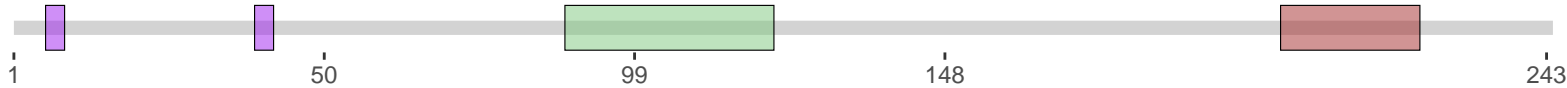


Gel Slice



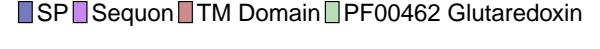
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

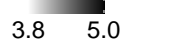
QLGVDPLVLEDEIVDMWFGVQPKDHSGRKGVNGLLDIRFPMVSLPNTLVVQILLGGIGKENLDCRQLMLEKGRKAPSWVSMKRRVHMLSLVYALFFQISLTPSYLMLFLYKYLILLKLTVEAEMLM

NbL09g13890.1 probable_pectate_lyase_8 [MW - SP = 46.28 kDa]

No. of times detected



log(intensity)



Values from



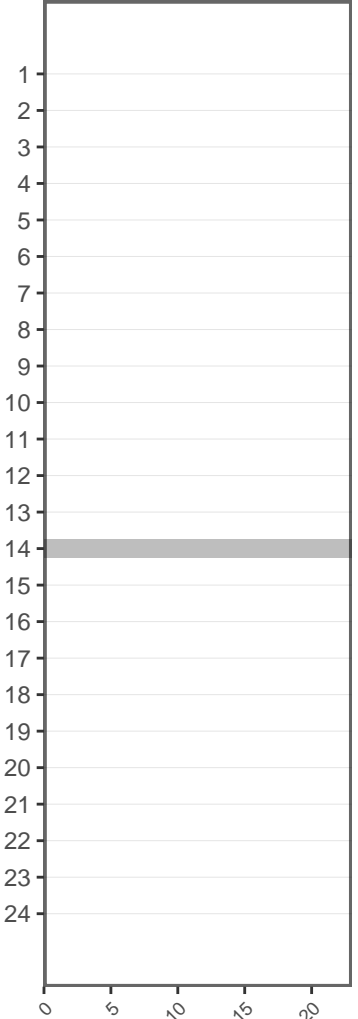
MW indication



Molecular weight

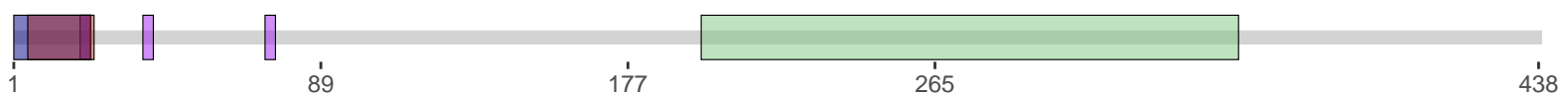


Gel Slice



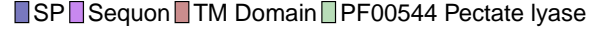
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

JHIDCKPTGNMIVRNSPSHYGWRIMADGGDGFIFGSGSHWIDHNSLGNAGDLIDMGSSTATISNYYETHNEVLLGHSDYIRDKVMQVTFARNHFGEGLIQRMPRCRNGYFHYVNNDKYTHVEMVAGGSADPTINSQGNRYLAPVNFPAKEVTKRVEPVEWEGSWHWVWRRSEGDMLNGAVFTASGRAAPRSVARABSLAAKSSSMVGTITENAGALSCHGFGD

NbL09g13540.1 peptidyl-prolyl_cis-trans_isomerase_FKBP62-like [MW = 63.37 kDa]

No. of times detected



log(intensity)



Values from



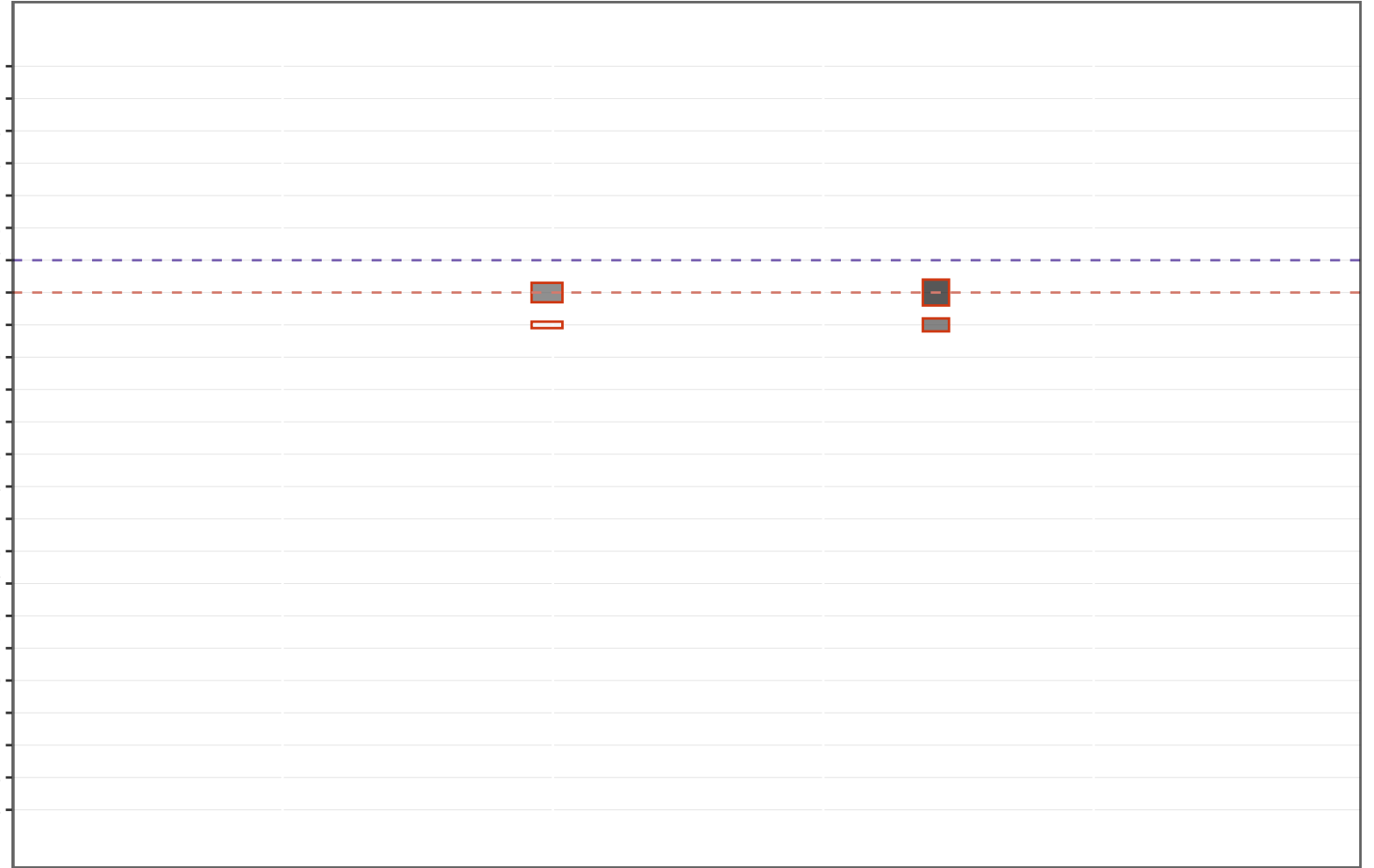
MW indication



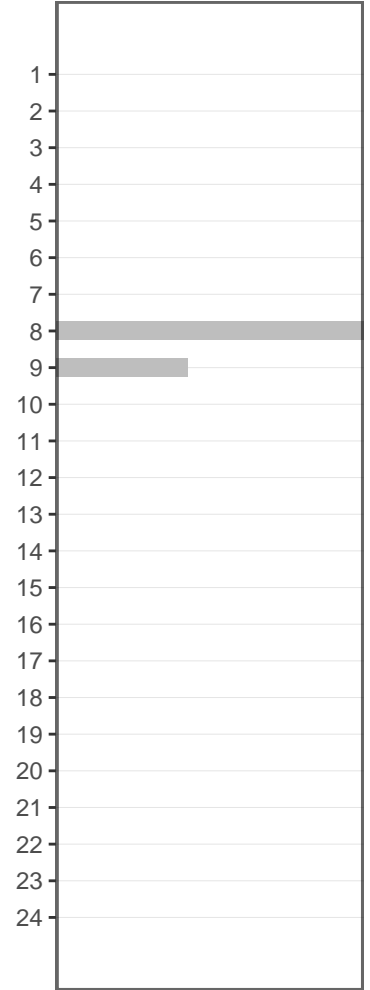
Molecular weight



Gel Slice



Protein length

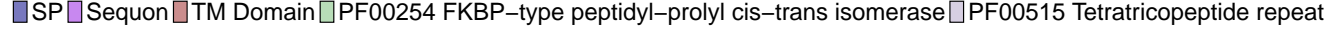


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

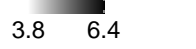
/VKKLKEGEGYKFNKNEGAVKLLKGLGDDGTVFKKKGHDGENEDELFFKTKDEEQVIDGLDRVMTMKGEVALLTAPEYVFGSSEKQDGLVIPPNGSTHYEVELVSPVWIKESWDMNTQCKIEAAGKKKEEGNALFKAGKYTRASKRYEKAARFIEYDTSFSEEEKGKALKISGNLNAAGLKLKDKYGAEMQTKVLELESTNWKALYRRAGAYMNMADLDLAEFDKKALEIDPNRDRVLEYKALKGKDKDFNKKDAKFKYGNMFANLNLESESPKPEPEM

NbL09g13440.1 serine_carboxypeptidase-like_20 [MW - SP = 52.86 kDa]

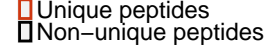
No. of times detected



log(intensity)



Values from



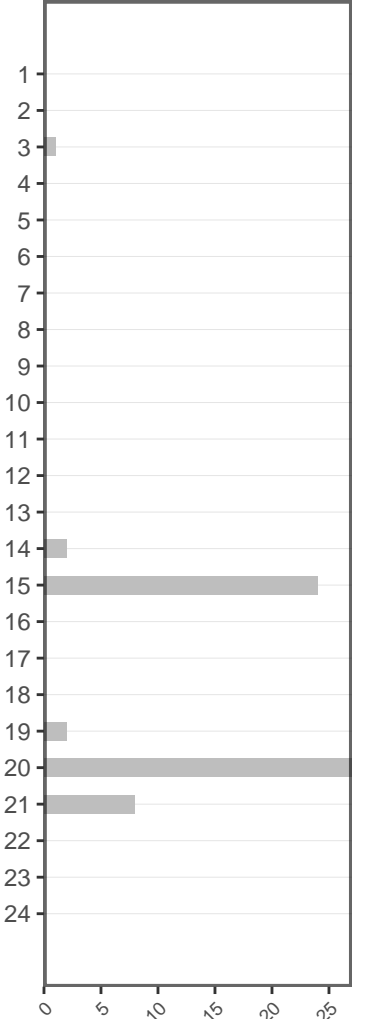
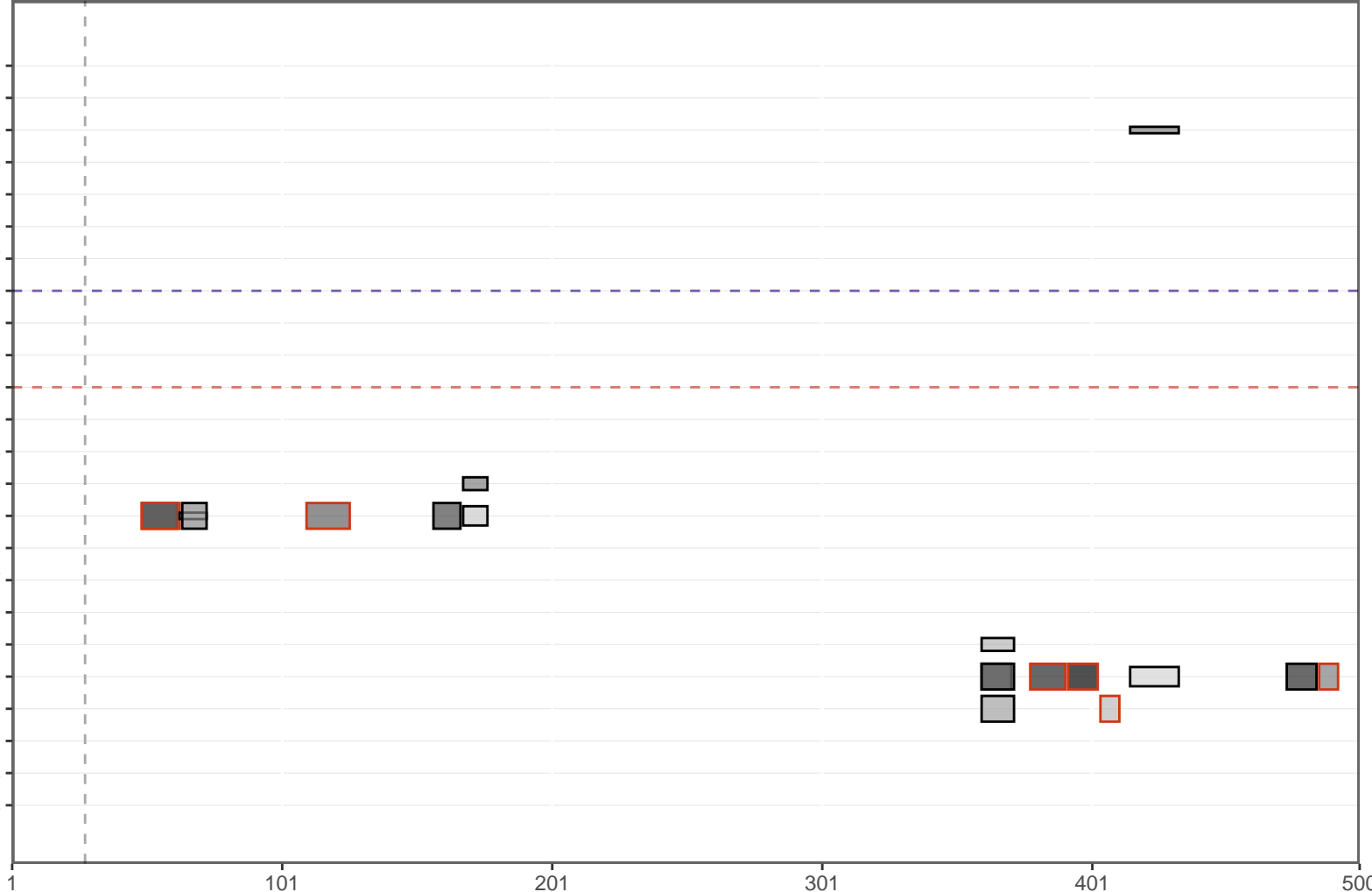
MW indication



Molecular weight

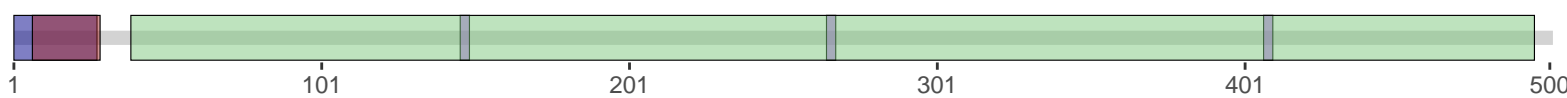


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MLISDELFEVYVSTLGNQNFYEPANNGNSKLNQVDDGDIADLNLYDLEPCYHSIDPQVISTGNSRLPTFSRKLGETERPFPRKRIMFGRSWPFRAPVKEGRVPTPELNGVHPCTDORVATWALNNEEVKKAHAKETTFTGPELGTGKLNLDHSGSMIKYHNNLTARGYRALYSGDHQDMCVPTFGSEKWTSLGYKIVDEWRPWWYNEQVAGYGGYDNNLFLTKAGAGHTVPEYKPREALTYSRWLEKNI

NbL09g13430.1 dicamba_O-demethylase_ferredoxin_component-like [MW = 18.01 kDa]

No. of times detected



log(intensity)



Values from



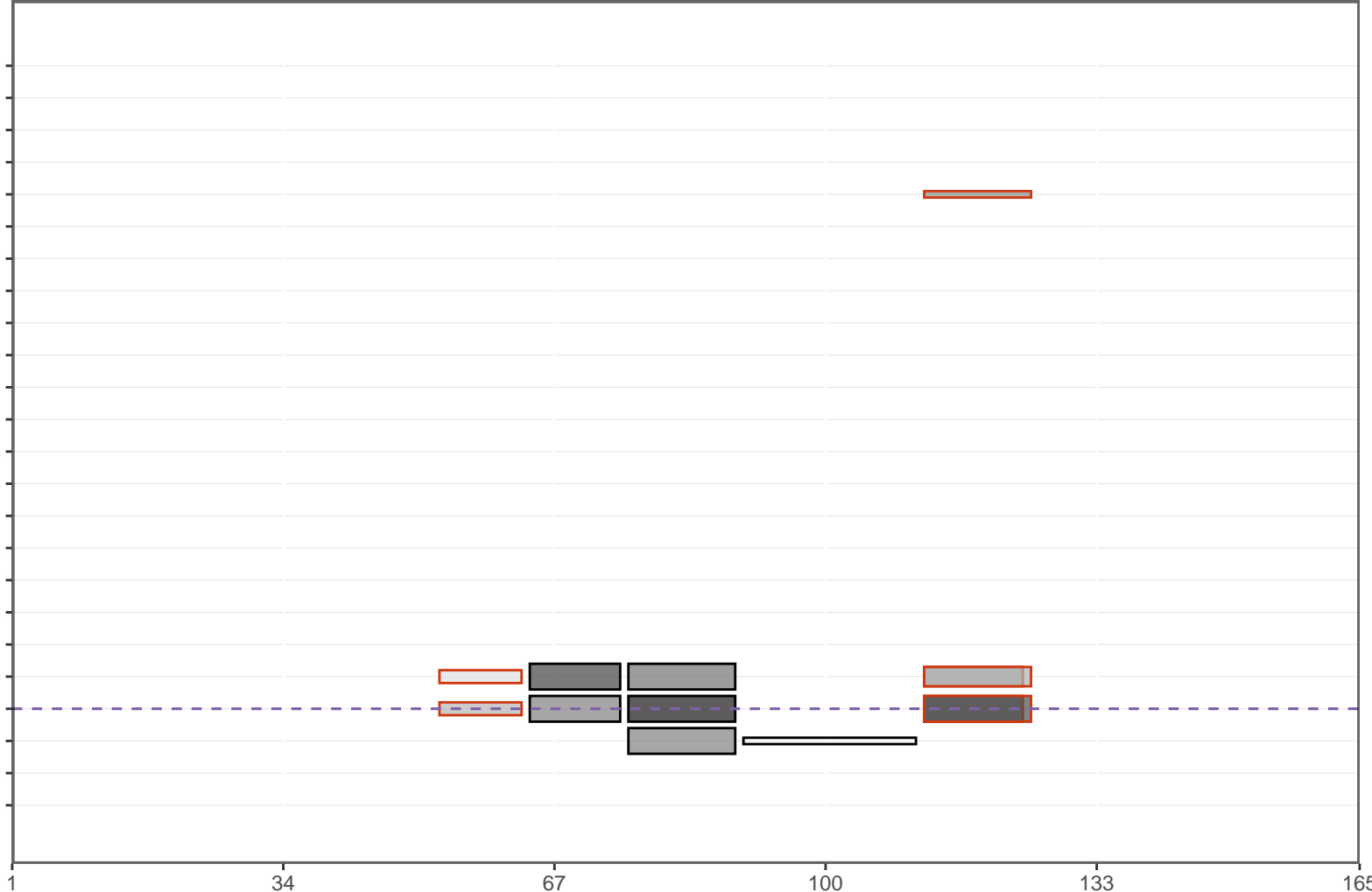
MW indication



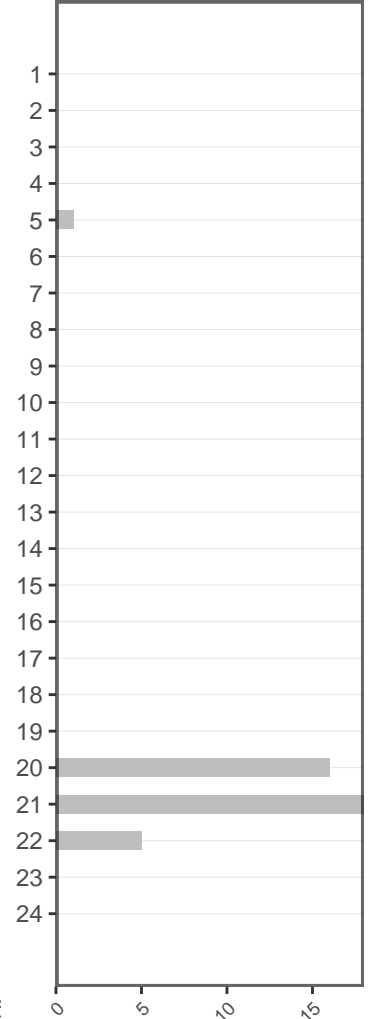
Molecular weight



Gel Slice



Protein length

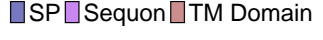


Peptide counts over 4 repeats



Pfm domains

Pfam Description



Protein sequence:

DTLLKALTNHGLIDPDSHRLEEDIDAGSBECEVHAGEVLEKLEPEASVDEQYVLLKKNRSRRLNKHSLRGGVYVLSQELQGMVAIPEAKPWDP

NbL09g13400.1 photosystem_I_reaction_center_subunit_XI_chloroplastic-like [MW = 23.26 kDa]

No. of times detected



log(intensity)



Values from



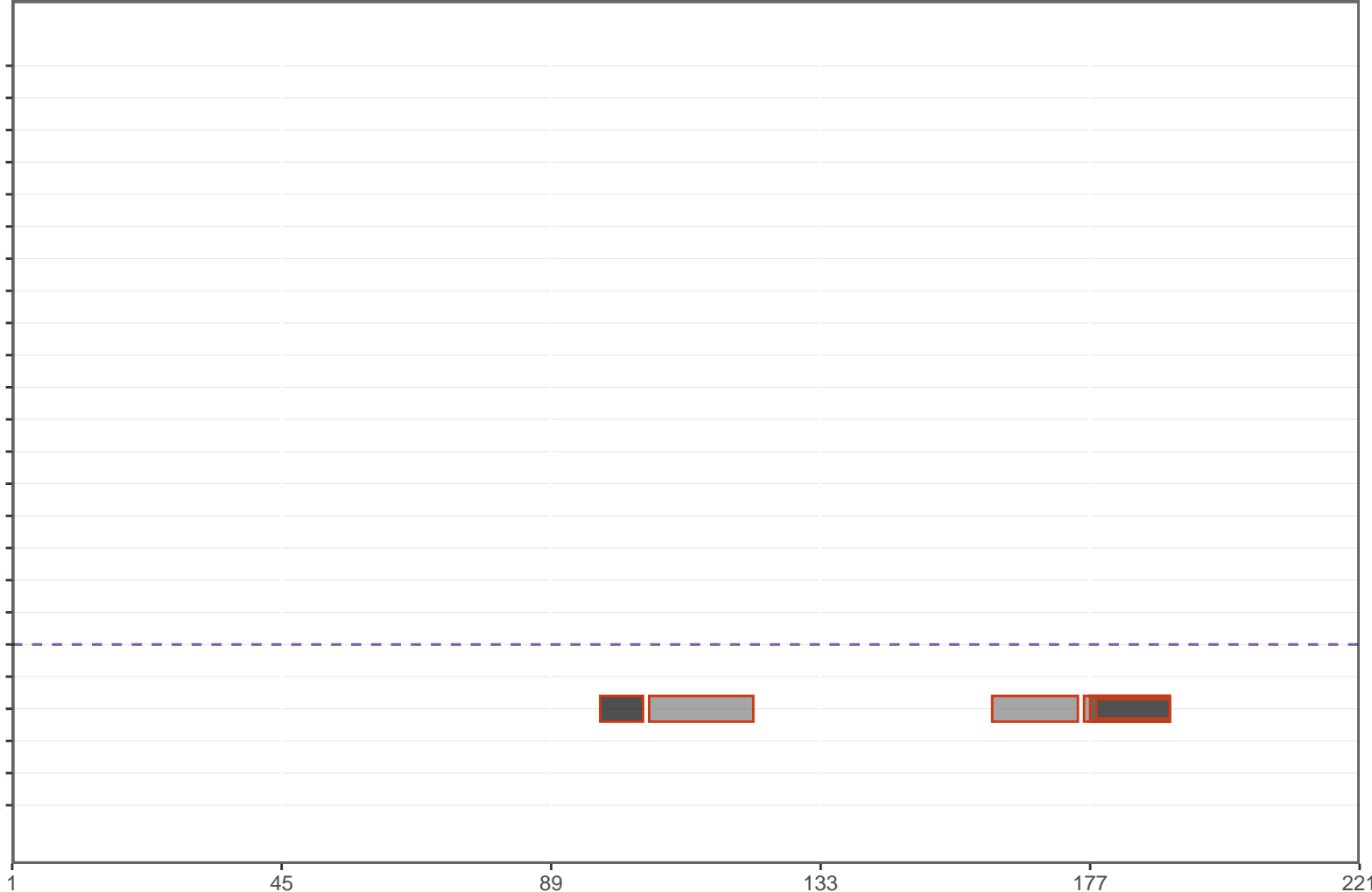
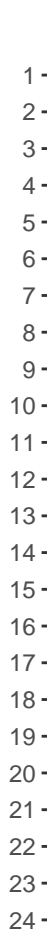
MW indication



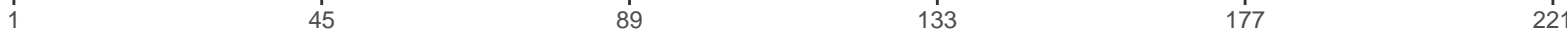
Molecular weight



Gel Slice

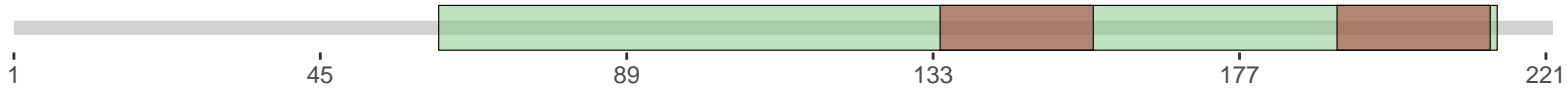


Protein length

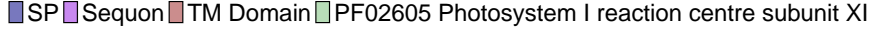


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

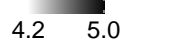
LVNPLLRGVVGLAHGFLLVGPFVYKAGPLRNTEVAGGAGSLAAAGLVVLSMGLTYGIGSFKEGGASTAPALTLGRKKVDPDQGTAEGWBSKFTGFFFGIGIGVTVWVFLVLDLPIYVW*

NbL09g13380.1 probably_inactive_leucine-rich_repeat_receptor-like_protein_kinase_At5g48380 [MW = 68.4 kDa]

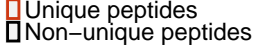
No. of times detected



log(intensity)



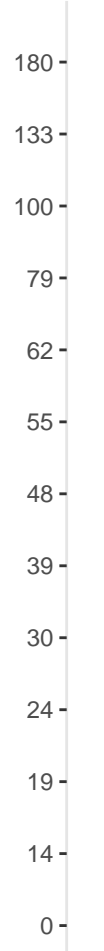
Values from



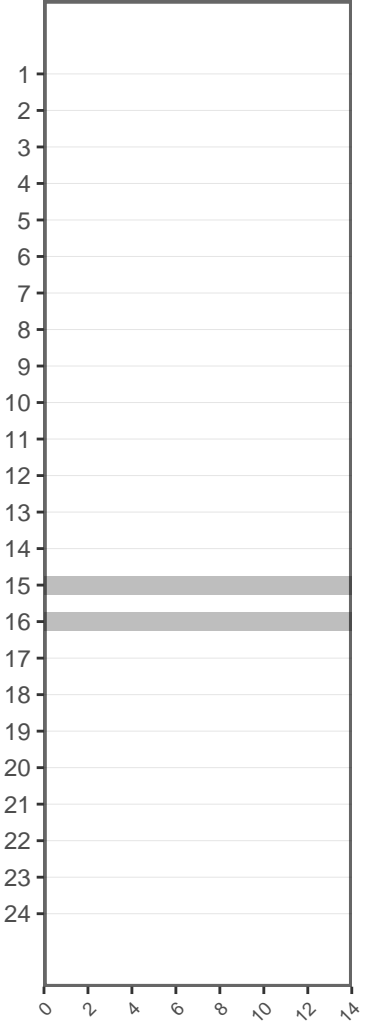
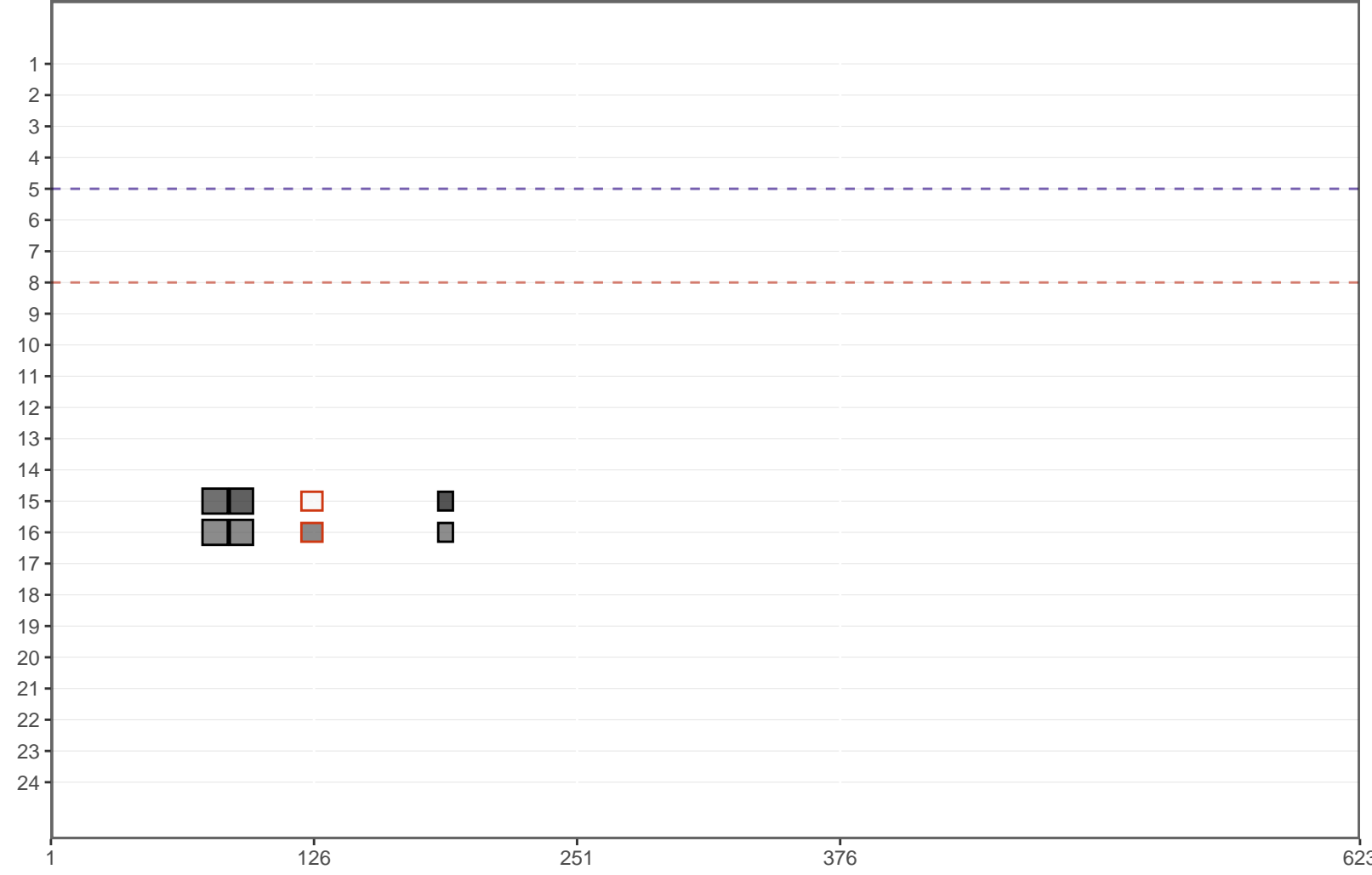
MW indication



Molecular weight

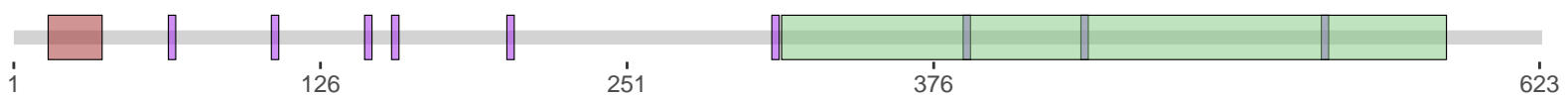


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISLTKATNFSSKSNIGSASTGTFFKAVLDDGTSLMKRLNQTQHSKEFEVSEMDTLGKVKHRNLPFLGFGMAKKEKRLVYKQMLNGTLHDKLHVSVEGEKTLKLEWPMRLKIGLGAAGKFAWLHHCNPNRIHRNIGSKILLDFEFEPKISDGLARLMLNPIDTLSTFYNGEFGDFYVAPEVARTLMATPKGDVYDFGVVLELVLTGERFTSVTKAPETFGKALVEWISNLSGEEKLHDAHDSLSGKGYDSEIFQVLKACRQVLSAPKERPTMFEVYQFLRAIGERYHT

NbL09g13220.1 elongation_factor_1-delta_1-like [MW = 25.19 kDa]

No. of times detected



log(intensity)



Values from

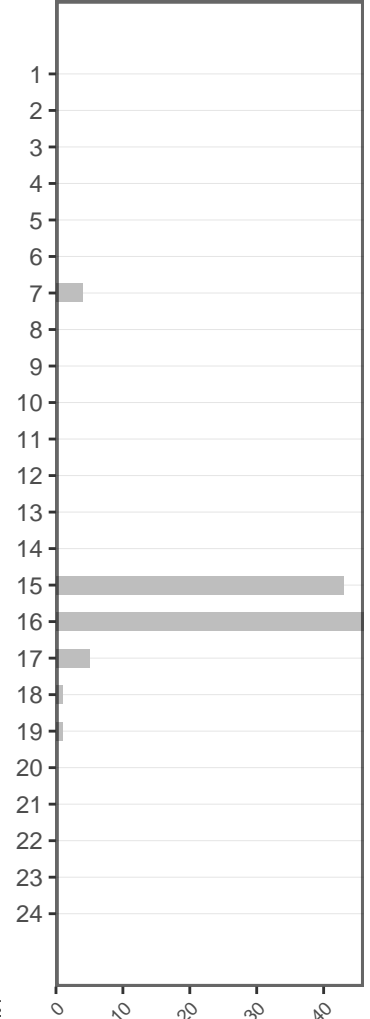
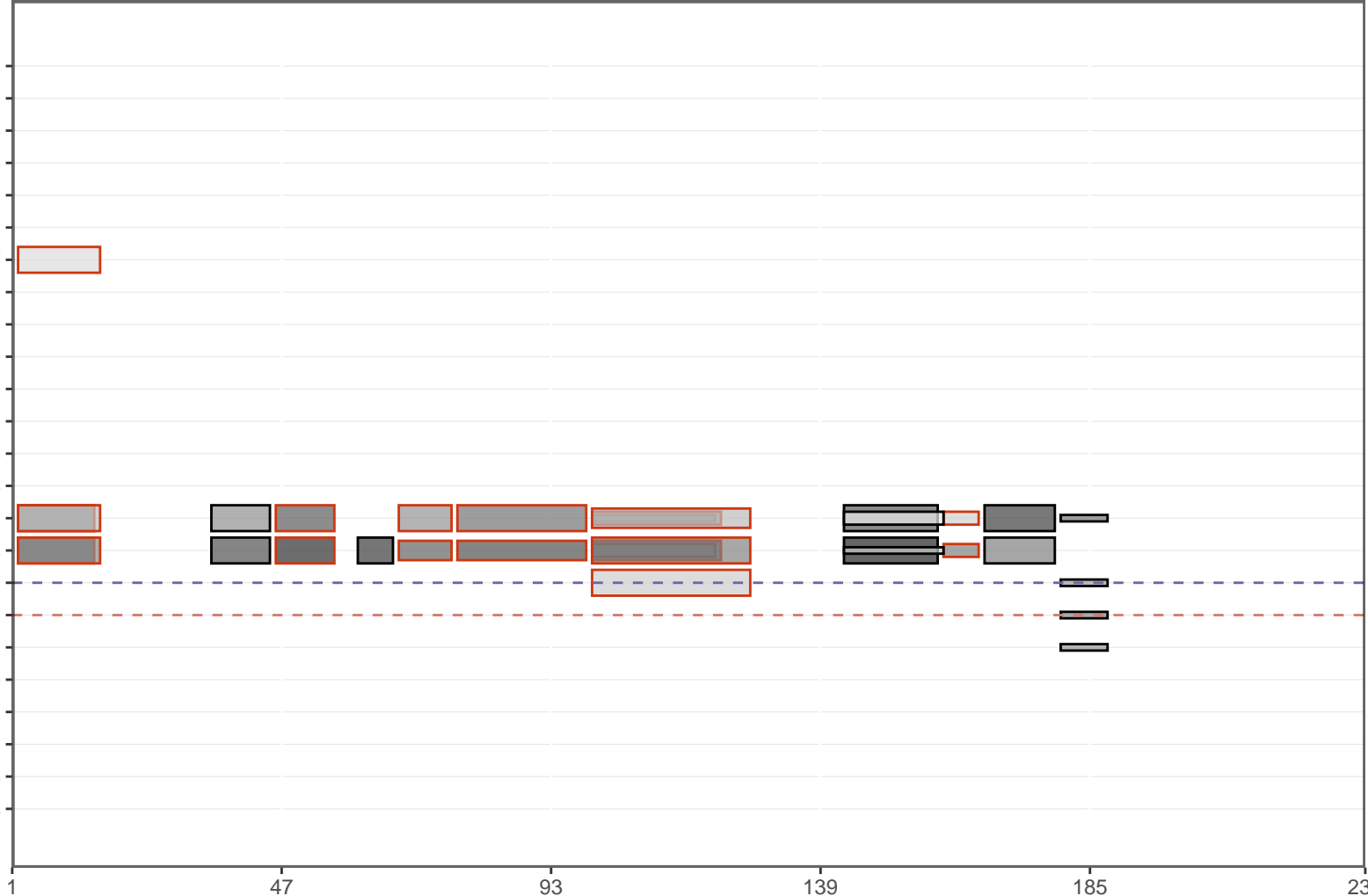
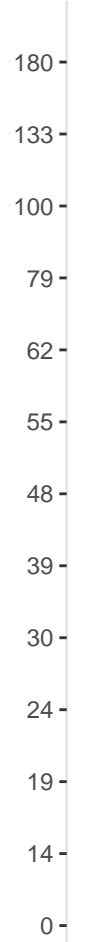


MW indication



Molecular weight

Gel Slice



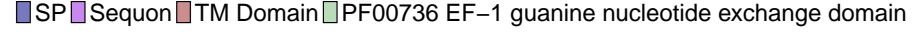
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LEEDDDVLDLFGEEETEEKKAAEERAAWAKASGKKKESGKSSVLLDVKPWFDEDTMKKLEEARISVQMEGLTYGASKLVFVGVGKIKLQMLTIVDDLVSVDDLVENYFTFEPINEYVQSGDAWAFNIP

NbL09g12940.1 U2_small_nuclear_ribonucleoprotein_B" [MW = 26.14 kDa]

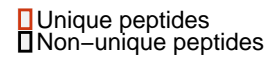
No. of times detected



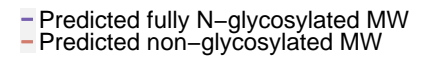
log(intensity)



Values from



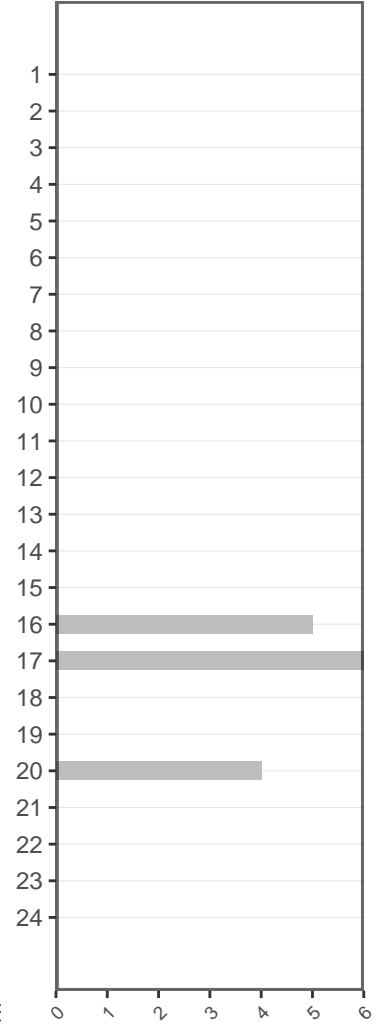
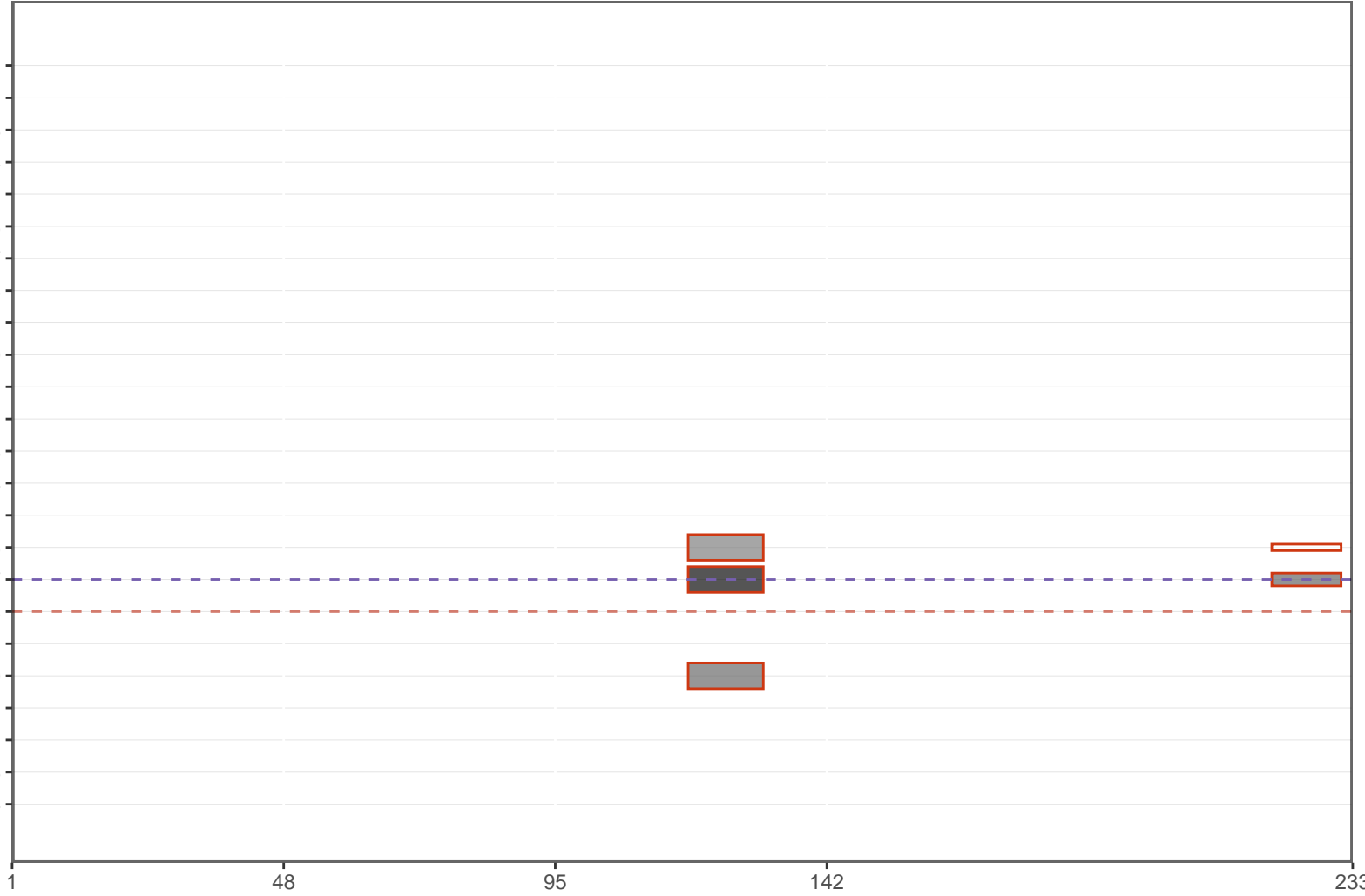
MW indication



Molecular weight



Gel Slice

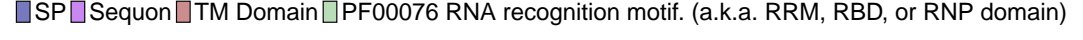


Protein length



Pfam domains

Pfam Description

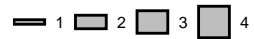


Protein sequence:

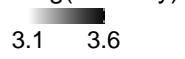
KKKQEEKVEKRRTEETPTGGAANGPRADSNNGPRAAAPROGRPSAQETVAEPNLFQGLPHIETTSMMLEVLFGYPGFREVRIEAKPGIAVFDFDDVQGSVAMQALQGFKITPQNPMAITWKKK

NbL09g12890.1 UDP-glycosyltransferase_87A1-like [MW = 51.6 kDa]

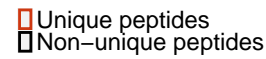
No. of times detected



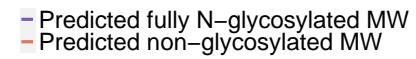
log(intensity)



Values from



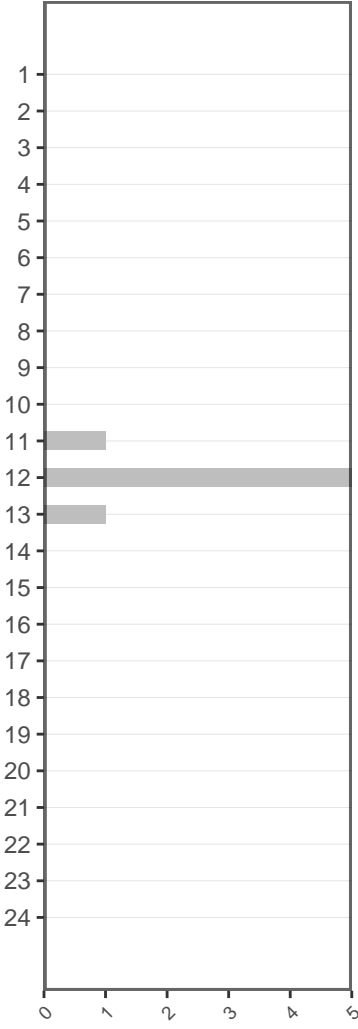
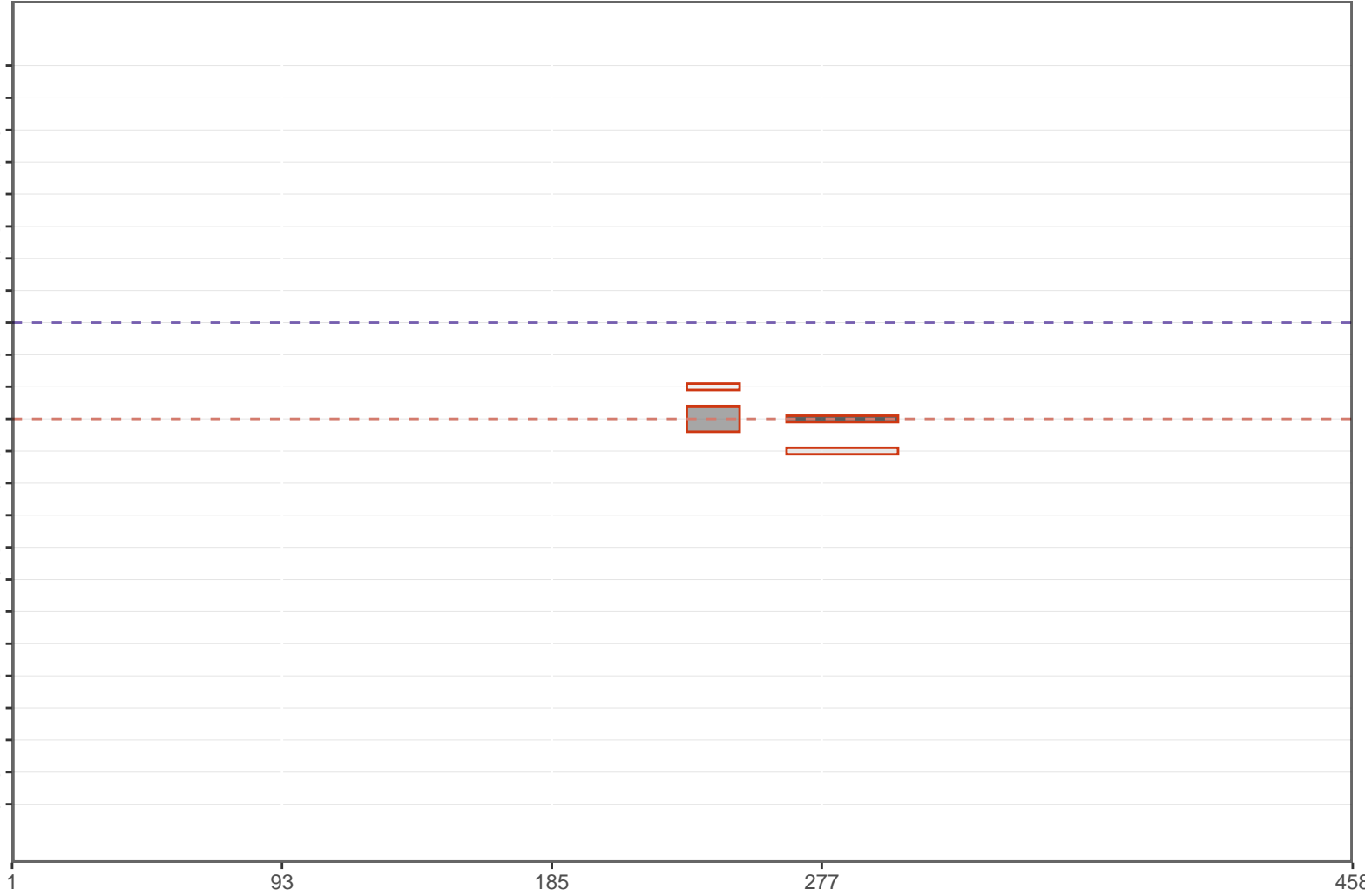
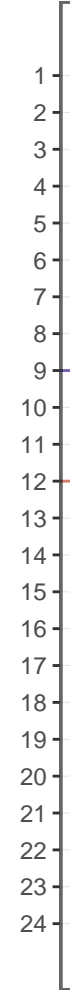
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

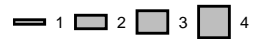


Protein sequence:

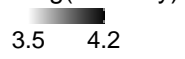
ISSVVDALKQKIFIPYIPGIPMPYFTSEKHS66TTSVDEPEYIKWLNAGPNDVLYH90GSLFASPAELDEWAGVHDSGVRFVWARDETVRFQNGSGEGLVFPWGDQKVLHPISGIGFVHSGWSTKAAAFSGFLMITYPIFDWGGTNSKGIQVWYKGVYKVKDDKSGIAREEISLLKWFMDENDEVMETRRRAKEIKIGKGGSTVNGGSSSEINDAFYKDVSSHKFP

NbL09g12830.1 transcription_initiation_factor_TFIID_subunit_15b [MW = 43.64 kDa]

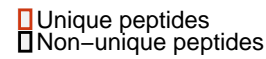
No. of times detected



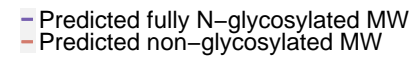
log(intensity)



Values from

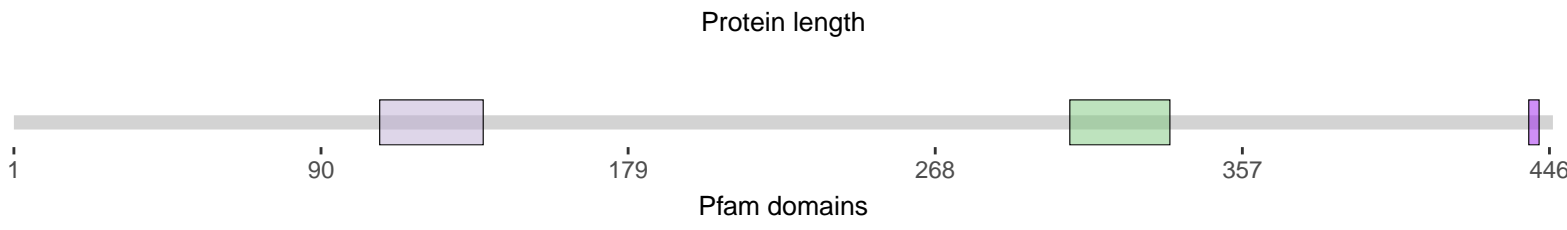
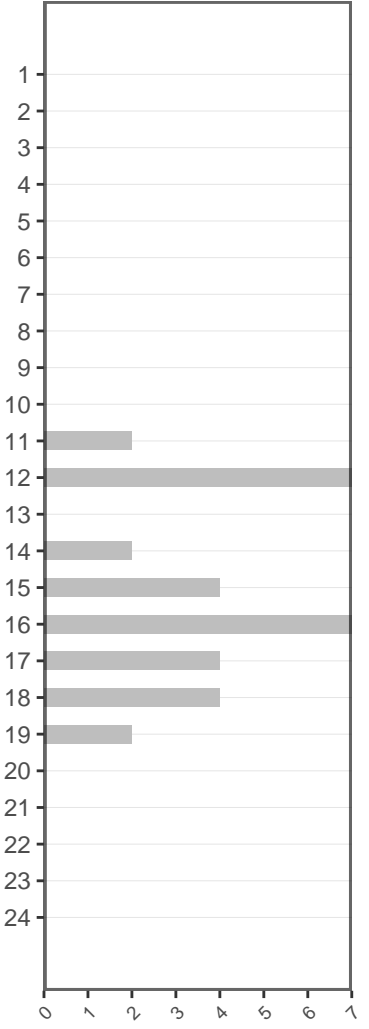
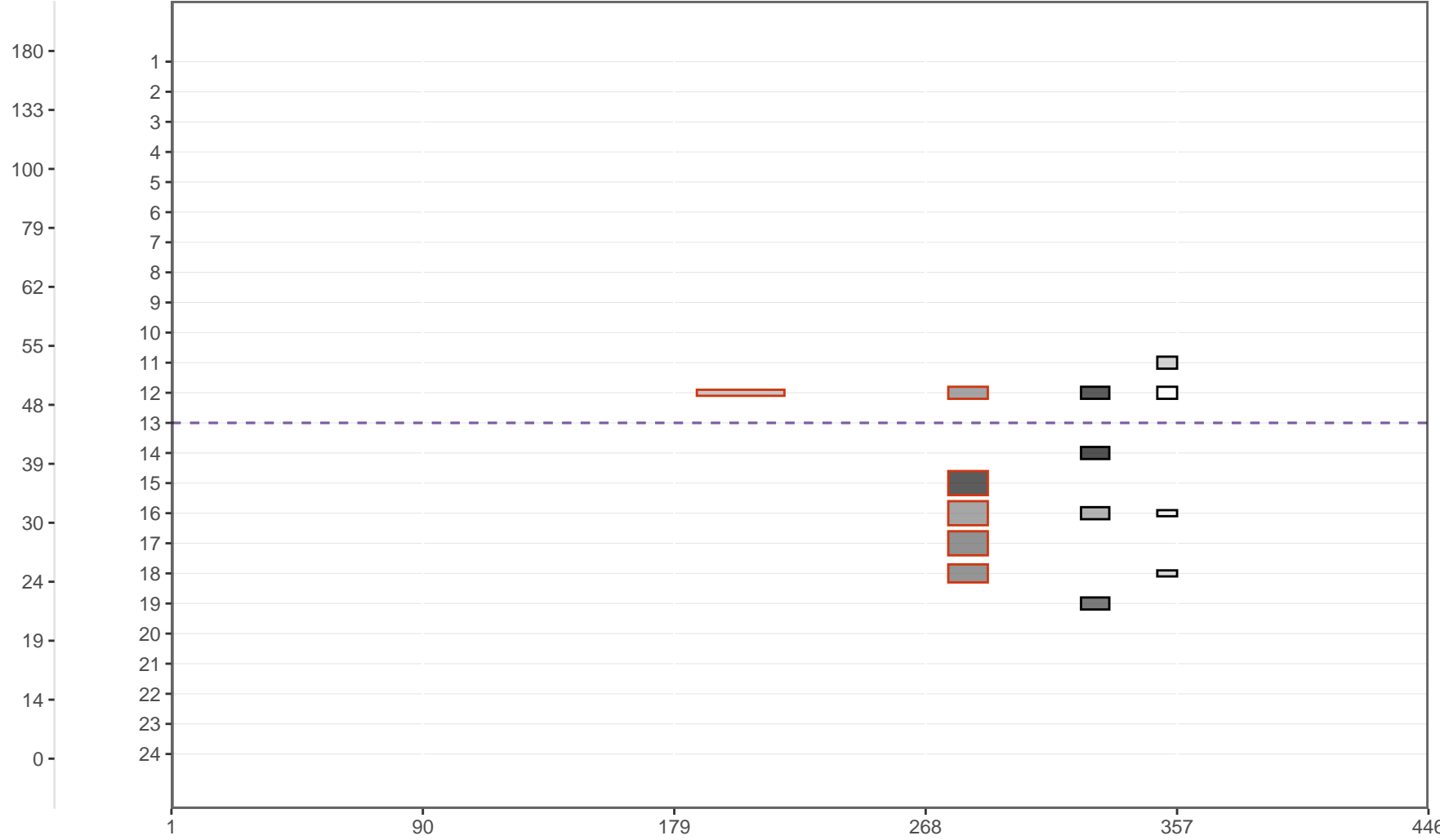


MW indication

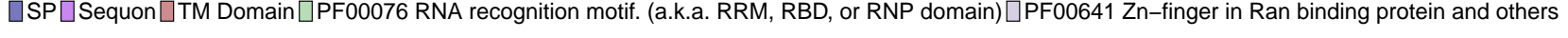


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

IADSNYPSPNITYGRNFDAPPPFTSEYVGGAAAYVPSYVYAGPGYGGDKTANARGGRRDPPGGYDGGYGGGRNAGGYDSSPNEAPEKVKYGGDENEGDFCDNARIYENLPPDVTIEELRELFGSISGQVARIKQKRYGDKDQWPVSKILYTDGQGNKGGDAVLSYEDPSAAHSAGGFFNHDFRYKISVAMAEKAPKPAFAGSGRGRGGYGGGGRDNRDGGGGSGPDRGSHGNGRSPV

NbL09g12780.1 protein_DCL_chloroplastic-like [MW = 26.54 kDa]

No. of times detected



log(intensity)



Values from



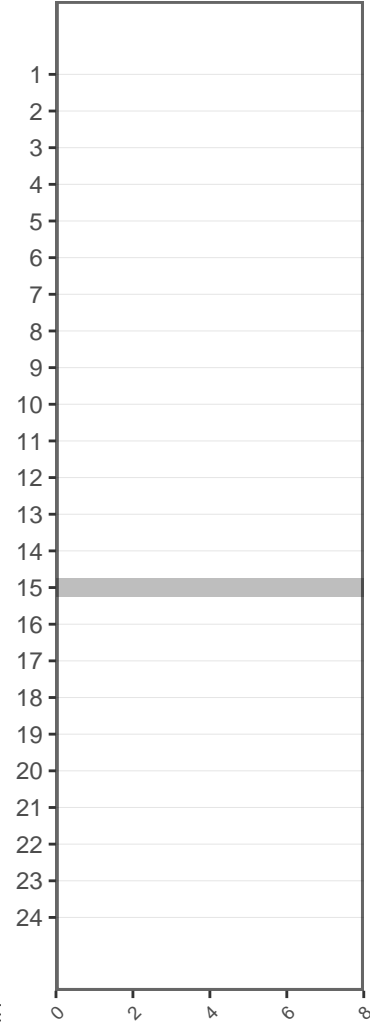
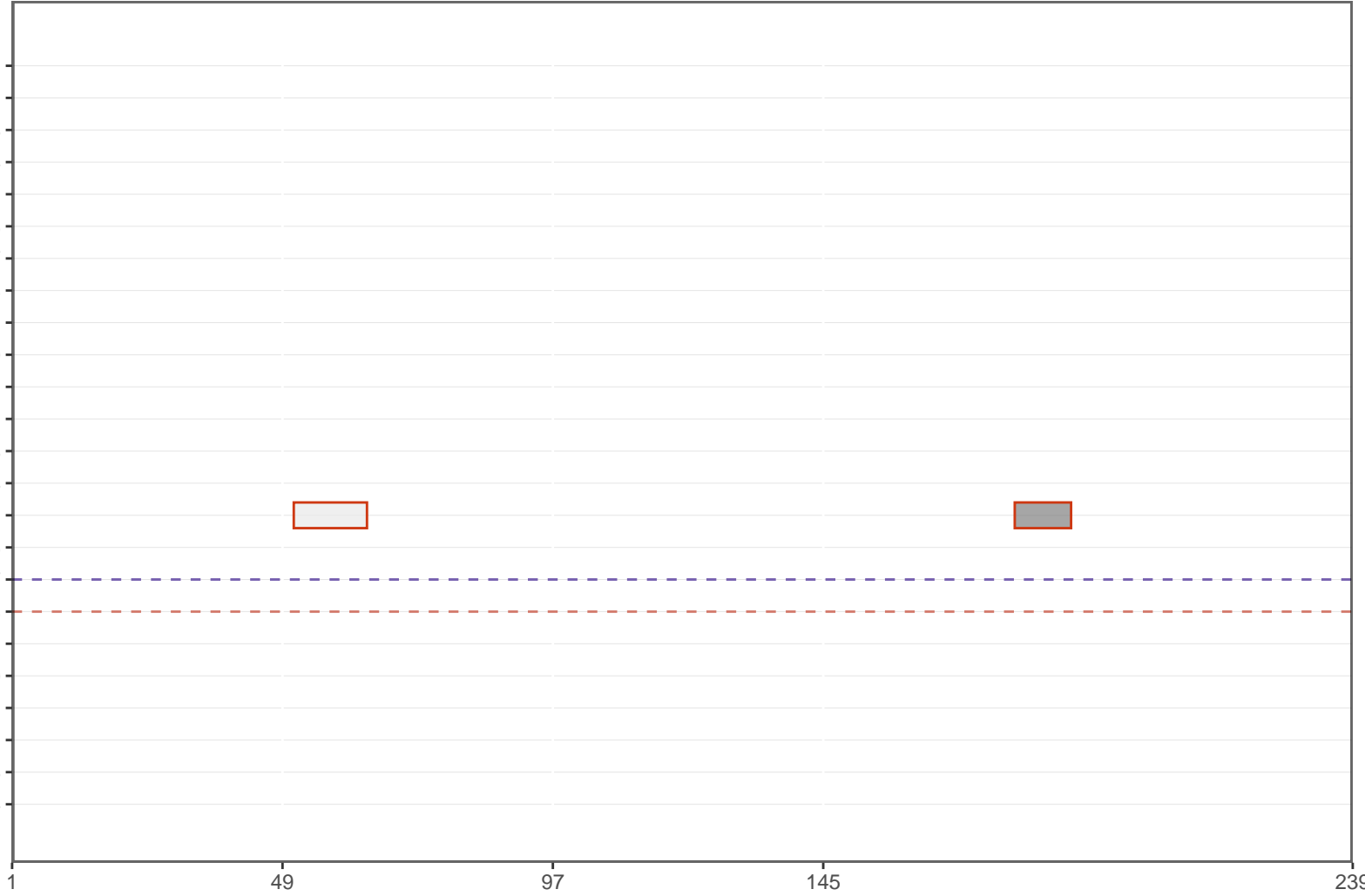
MW indication



Molecular weight

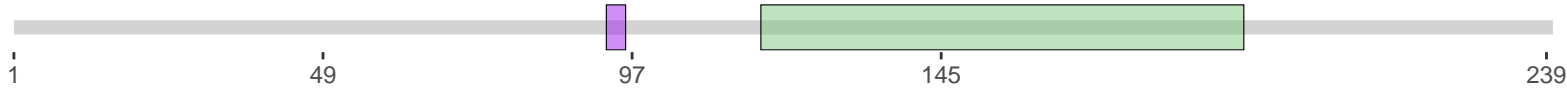


Gel Slice



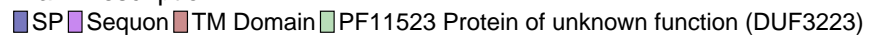
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISSVEMFDYFYKLLHWSFNLNKNNLQYEHLLVLLKLLKKGHLEPRKIGTGRIRAFQIRFHPQFKSRGFFVIREDDVDVDFSRKGVHILFLPENMQVKEANKALAHSGKGRGRKGGGGRDSEGGNGKSRVY

NbL09g12760.1 chlorophyll_a-b_binding_protein_4_chloroplastic-like [MW = 27.61 kDa]

No. of times detected



log(intensity)



Values from



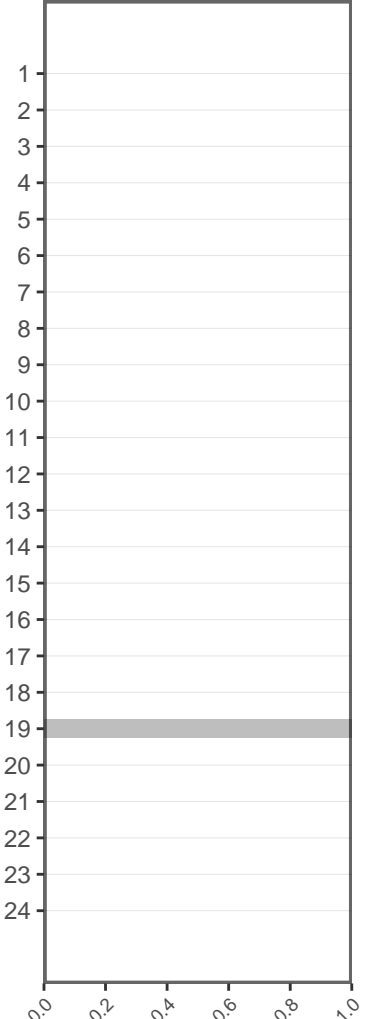
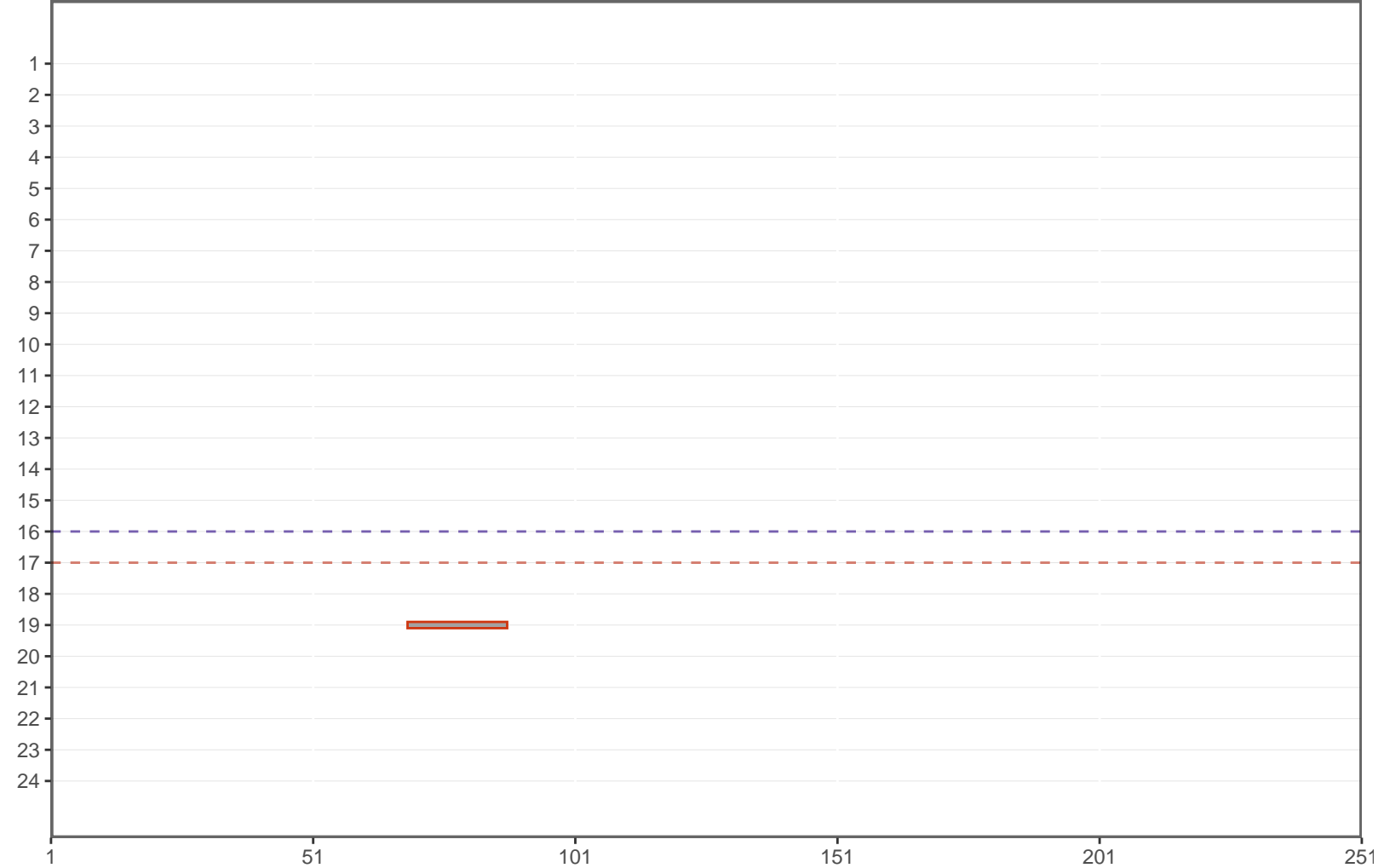
MW indication



Molecular weight

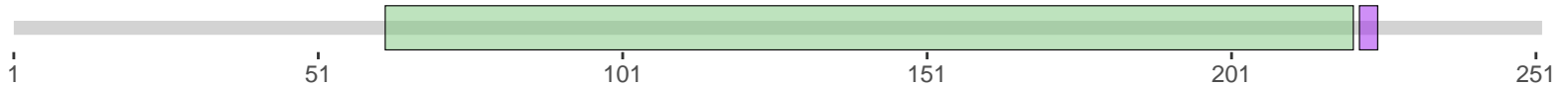


Gel Slice



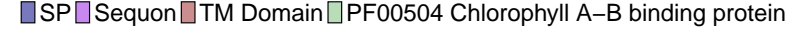
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LPEVLTSAQLLNVPWVYDAGKSDYFASBSFLFVIEFILFHYVEIRRWDDIKNPGSVNGDPFKFVSLFPNEVGVGGFNFNFAPFTLEAKEKEVNRGLAMLAFGLFVQHNVTGKGFDDNLGHSIDPWNTWGTFAV

NbL09g12590.1 biotin_carboxyl_carrier_protein_of_acetyl-CoA_carboxylase_1_chloroplast-like [MW = 27.53 kDa]

No. of times detected



log(intensity)



Values from



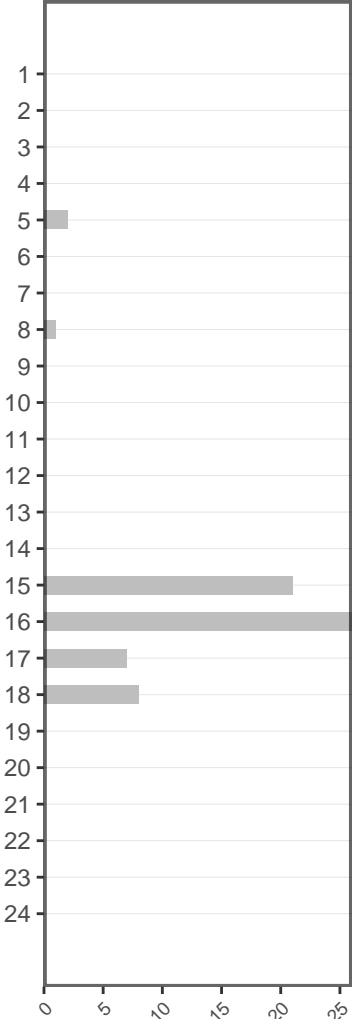
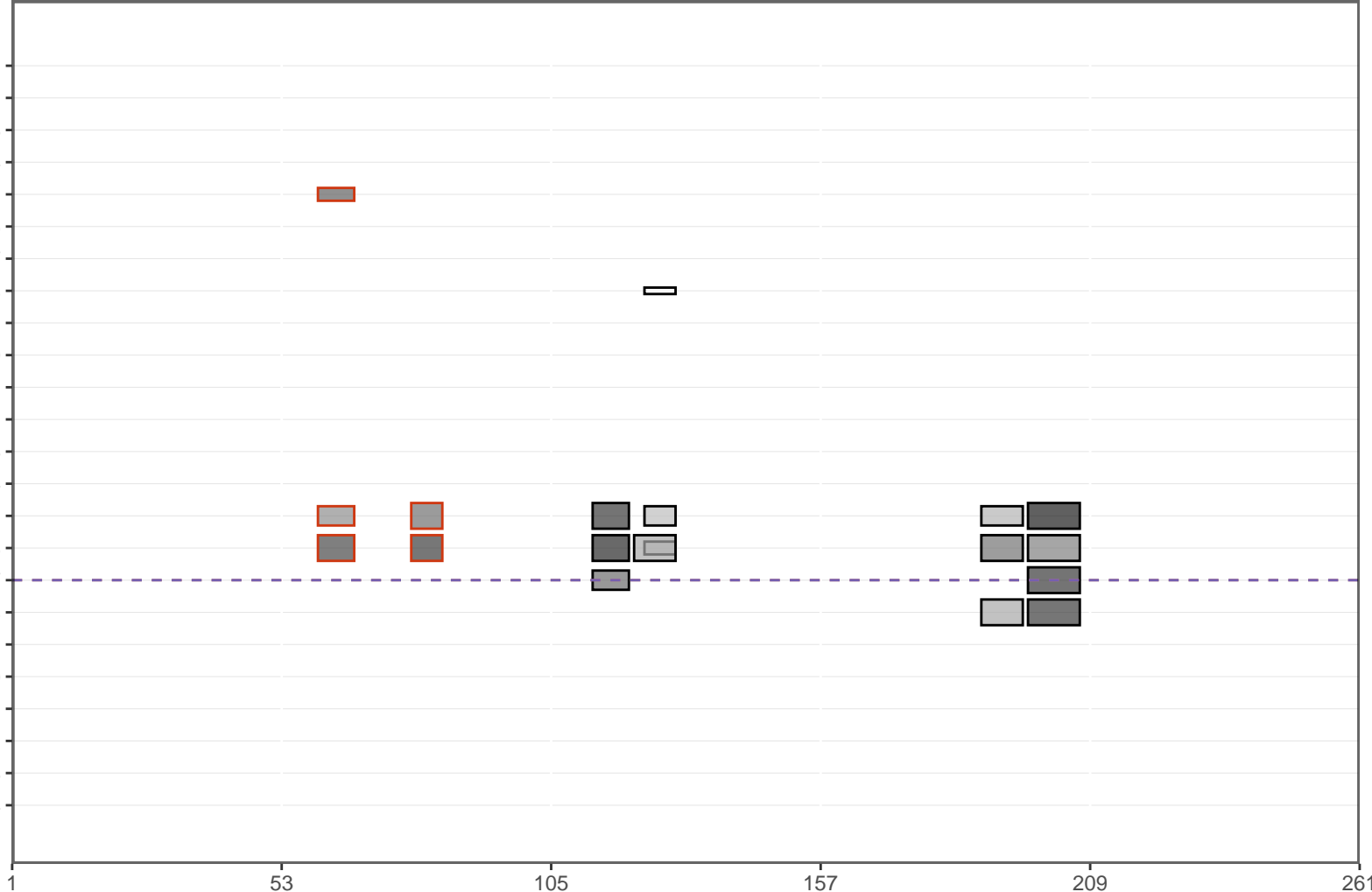
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

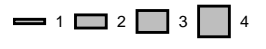


Protein sequence:

DLKQKDCLELRKKAALPQPPVMAAPFVVOGGFVQPLPPAPAPAPAPAPALPPAPSKPKESHPPMKGFMAAGTFYRSPAPGAPFPVVKVGDKQVQKGVVCIIEAMKLNIEIADSSGTTVDIADGGKPVSEVDTPLFVIEP

NbL09g12580.1 uncharacterized_LOC104224938 [MW = 237.3 kDa]

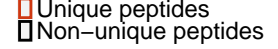
No. of times detected



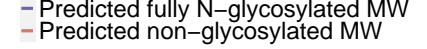
log(intensity)



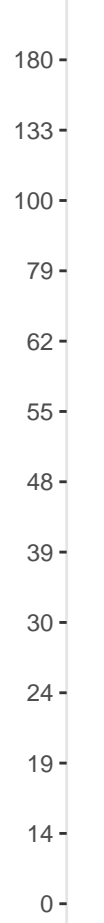
Values from



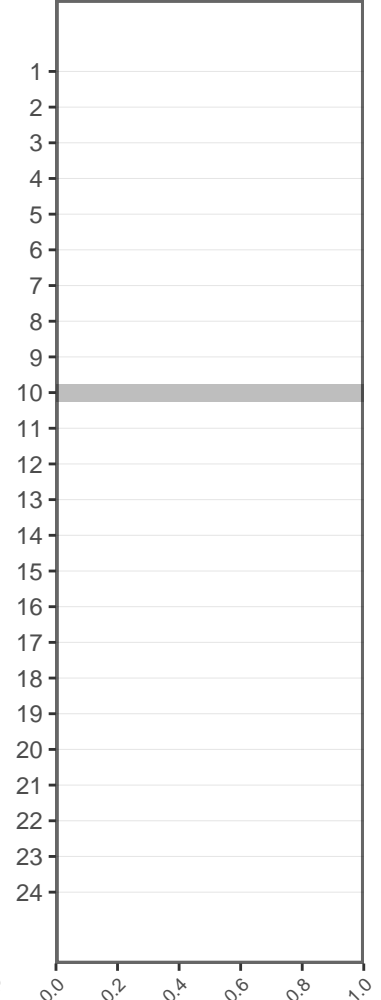
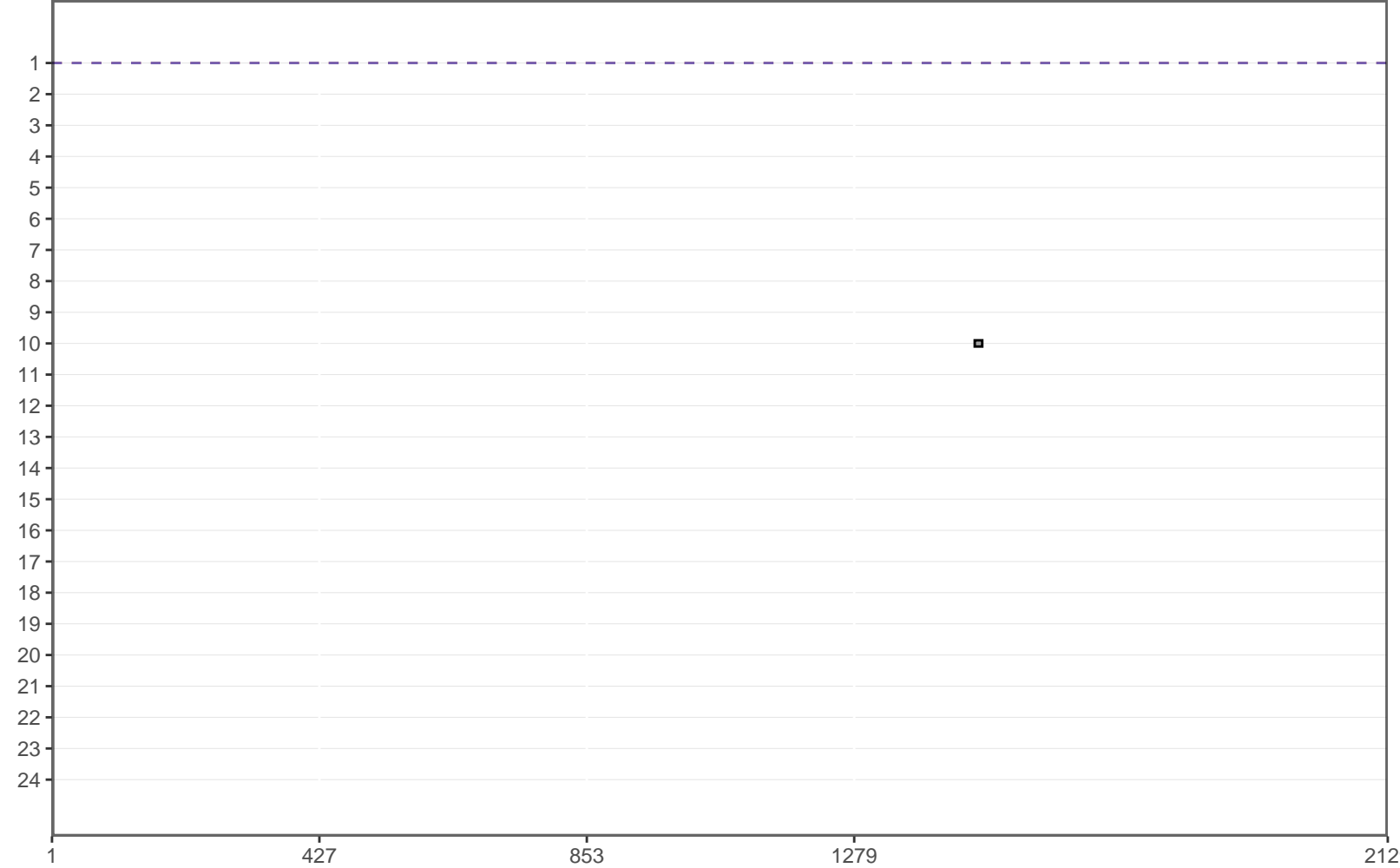
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF07727 Reverse transcriptase (RNA-dependent DNA polymerase)
- PF13966 zinc-binding in reverse transcriptase
- PF13976 GAG-pre-integrase domain
- PF14111 Domain of unknown function (DUF4283)

Protein sequence:

SGSVDNRASHITMEYRGGGFRGRSRPKGVGYNLGHTRDVCHSLHGRPTKNAYVAGTEPTGNQGFVSEREYNFLKYRAKQTSPOVATVAQPDTSVWAGNSFAGVSGSSPLEGQVWVDAASDHSGNKLLSDHYSGFLPNFLANGSGDTAKAGVGGATPLPSEVTLDEVLVYVGGPFNLASDRSTGGTGTGLESDGIVYLNLSLSEKAGLAADPPDLLHSRLGHPSLKLQKMPRLSLSLSTLECEGSQQLGKHTRASFPRBSRAEIVFELVHISDWVWSPSRQFM!

NbL09g12510.1 glycerophosphodiester_phosphodiesterase_GDPD6 [MW – SP = 43.59 kDa]

No. of times detected



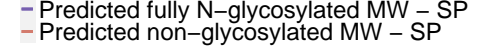
log(intensity)



Values from



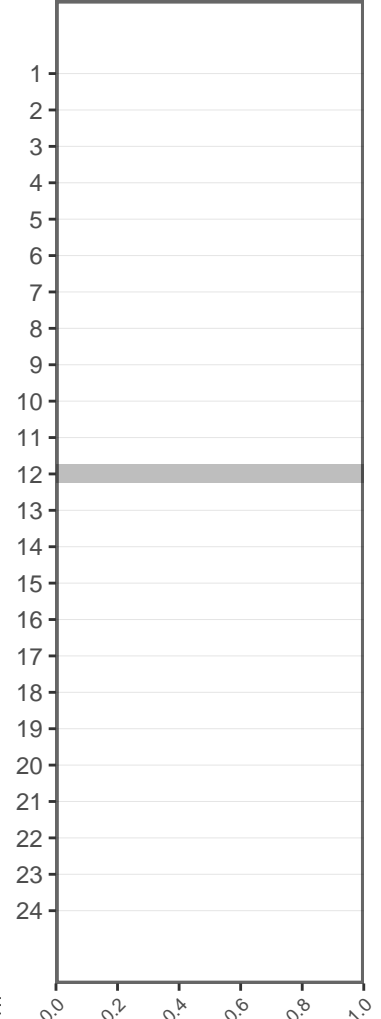
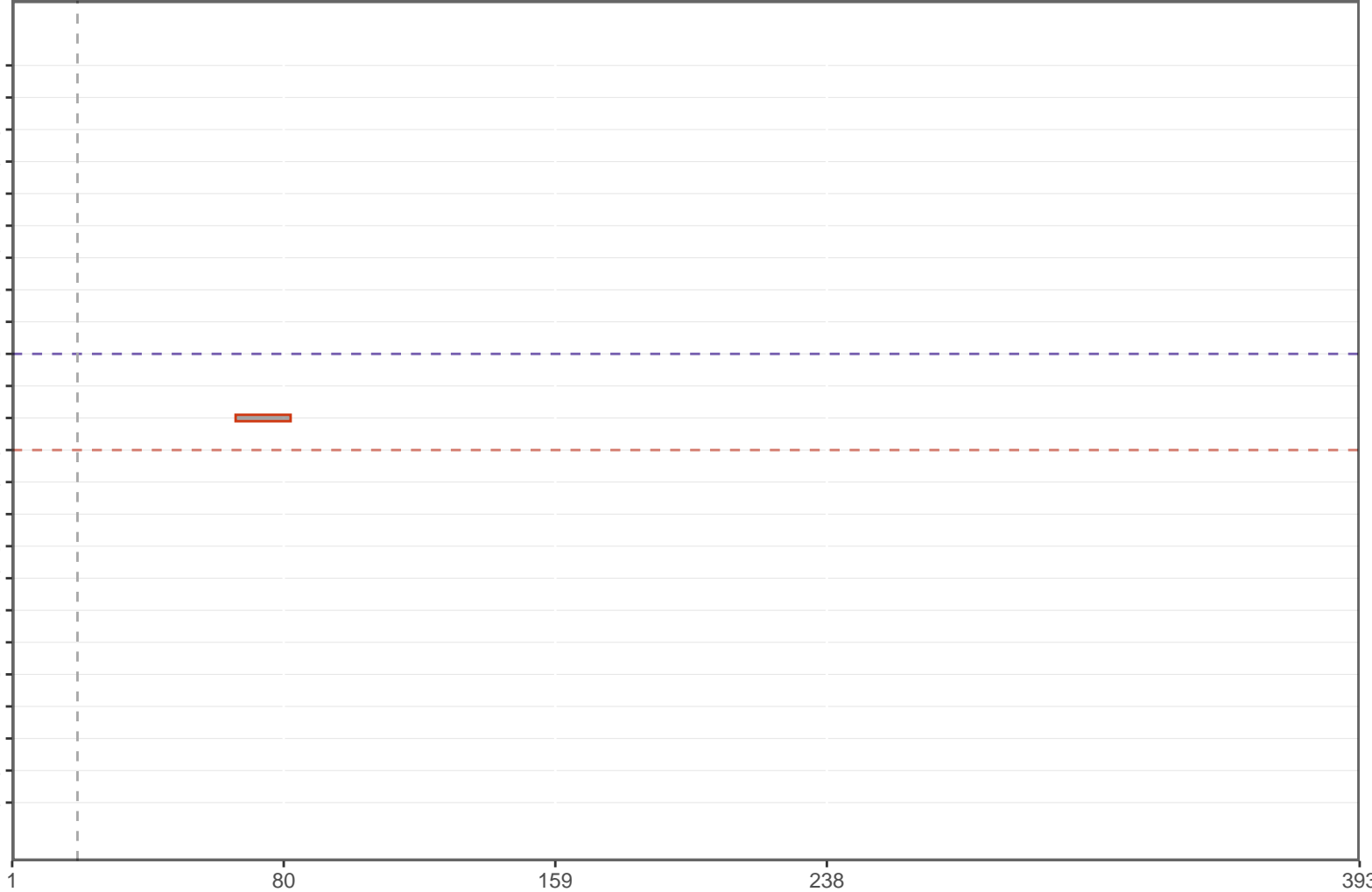
MW indication



Molecular weight



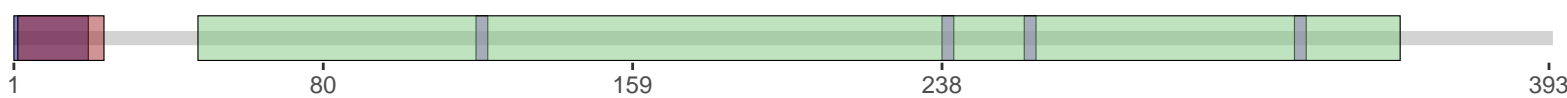
Gel Slice



Protein length

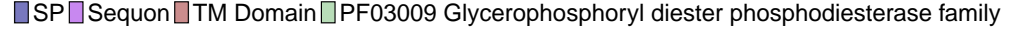


Peptide counts over 4 repeats



Pfam domains

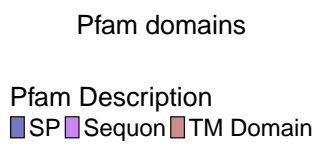
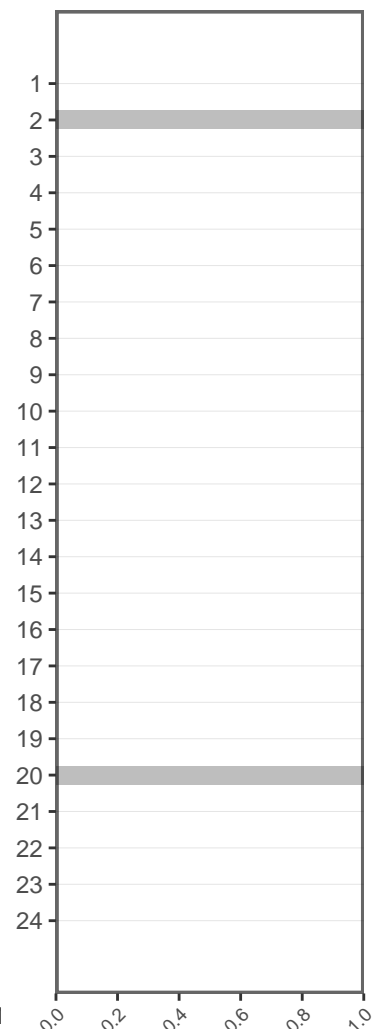
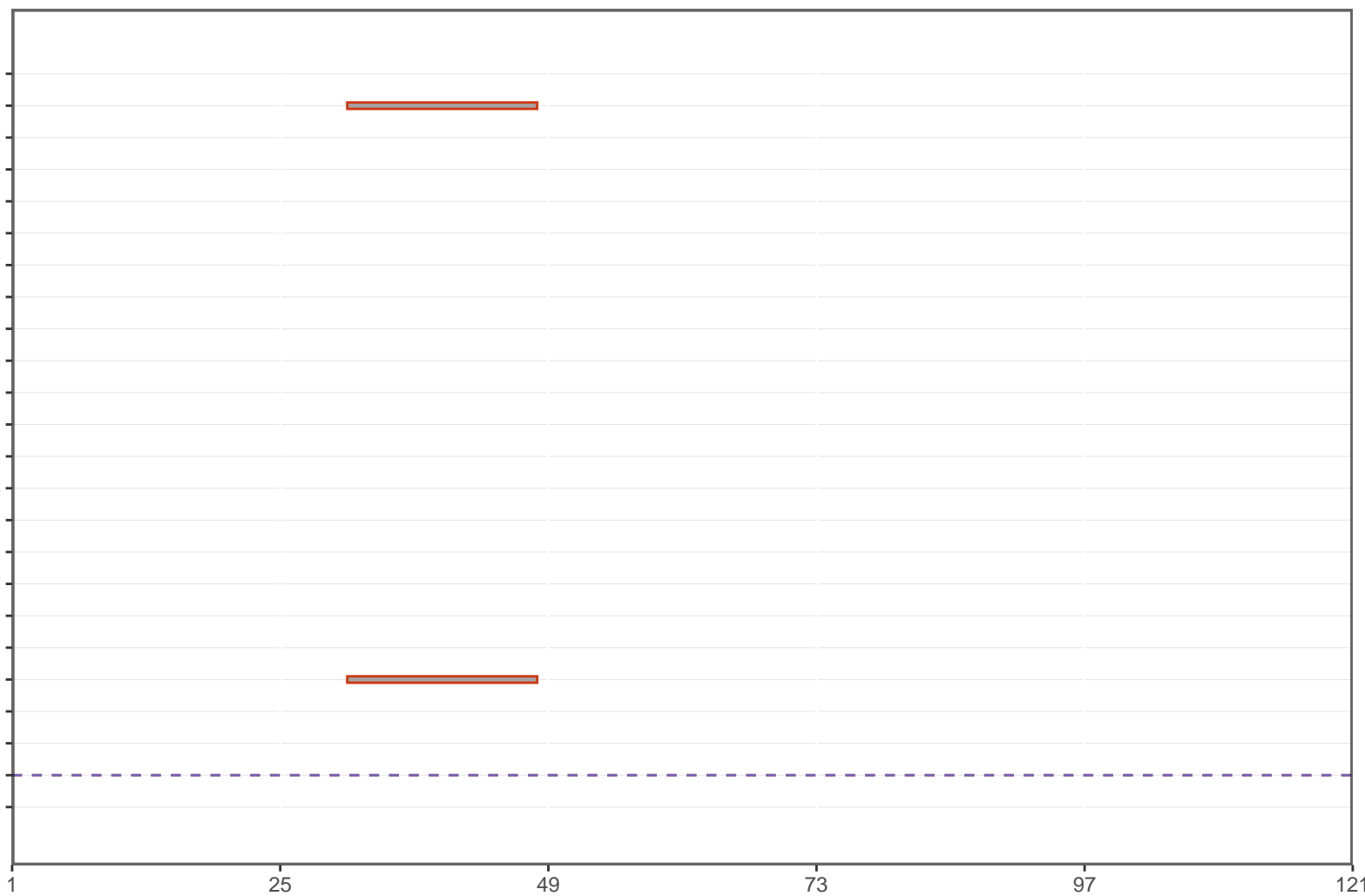
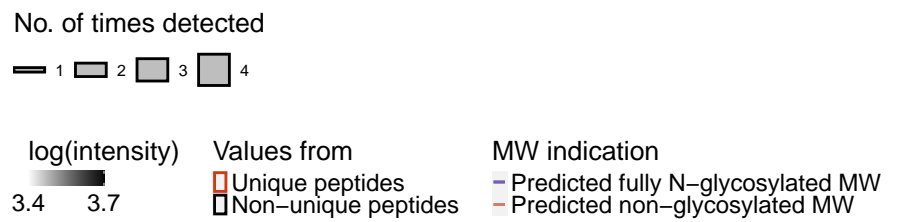
Pfam Description



Protein sequence:

QVYKVPGGKRFEDKPFVETLKKYGYRGSYMKQKWLKGFAPFGSFPAPTSLSYVINGTDLKPFILDDVDMPTQDTNGSVDWITSDEYVDFRIKEVYVGGIPKKNIPVSNYLGTPSDLVARAAHNLGQHPVYTFRRNENKFLHNFSEDPVNEYDQWINKIGDVLGFTDFTGSLHHYGEWTRNPFASGEKEATRLLHIELMLSKRYFN

NbL09g12470.1 uncharacterized_mitochondrial_protein_AtMg00810-like [MW = 13.71 kDa]



Protein sequence:
TKLSKFDGKGVDPFFRISLGVGLRYLTKNPDLFVAGVWGRMEAPRTSTQLKVTGRILHYLKGTDIFRLEYS*

NbL09g12250.1 serine/threonine-protein_phosphatase_2A_65_kDa_regulatory_subunit_A_beta_isoform-like [MW = 64.79 kDa]

No. of times detected



log(intensity)



Values from



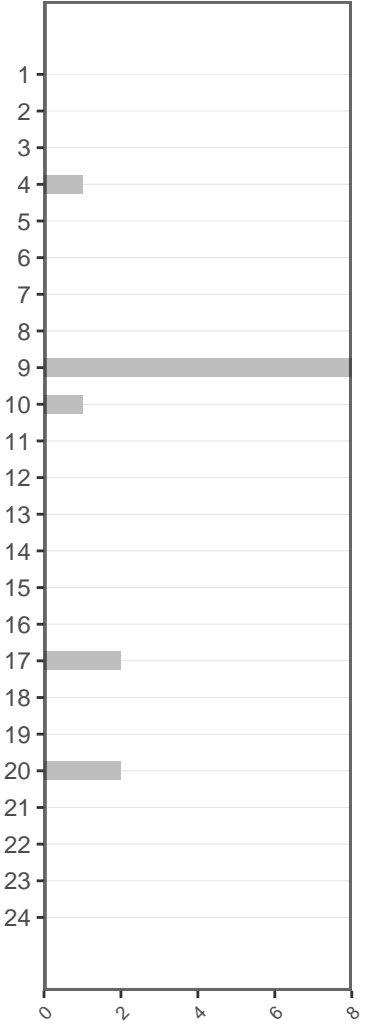
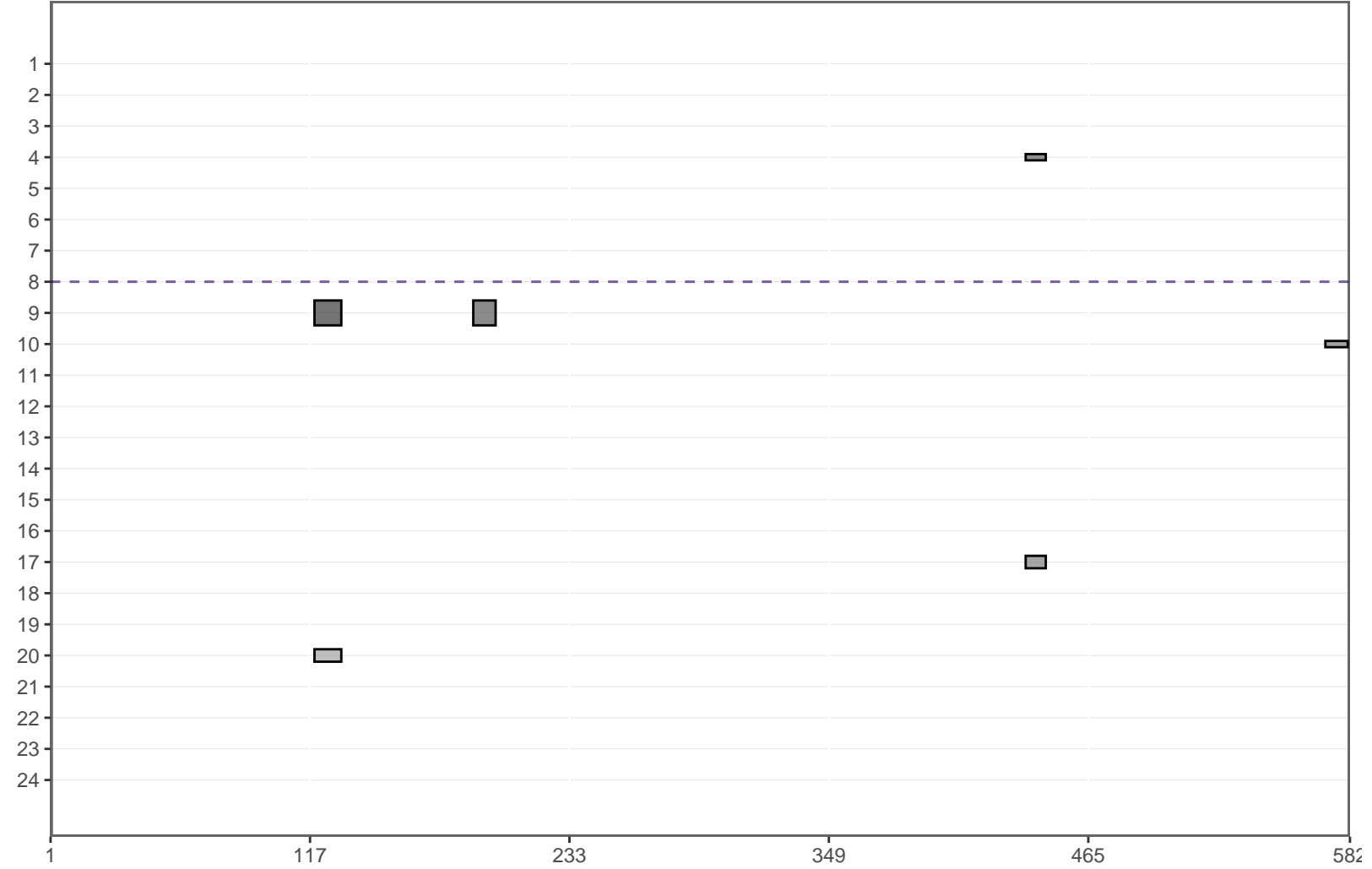
MW indication



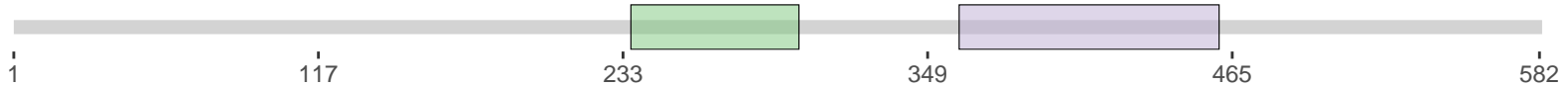
Molecular weight



Gel Slice

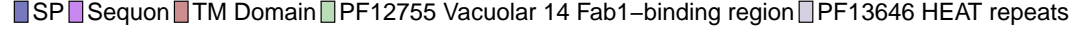


Protein length



Pfam domains

Pfam Description



Protein sequence:

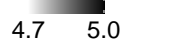
*EATRTDLYRIVYRLLRDNEAEVRIIAAGKVKFKFDRILPELAIQHILPCVKELSDSDSQHYRISALASVMGMAPLGGKDATEIGLLPFLSLLKDFDPVRLNHSKLDQVNGVIGILLGSGLLPAVVELAEDRHWRVRLAIEVYPLLASGLGCVGFFDDKLGALCAQVWKDKVYSIRDAAANNVYKRLAEFGFTWAMEHIPQVLDMNDPHYLVRMTLHAIISLLAPVMSGETCSKLLPVVITASKDRVFNKFNVAKYLQSLPIVEGQVYVETTRPGLVELSEDDPQVDRFFANALQ.

NbL09g12160.1 40S_ribosomal_protein_S7-like [MW = 22.07 kDa]

No. of times detected



log(intensity)



Values from



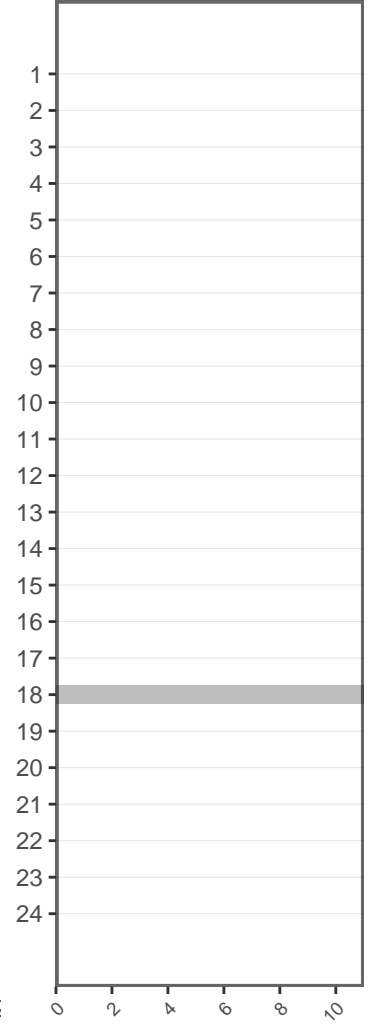
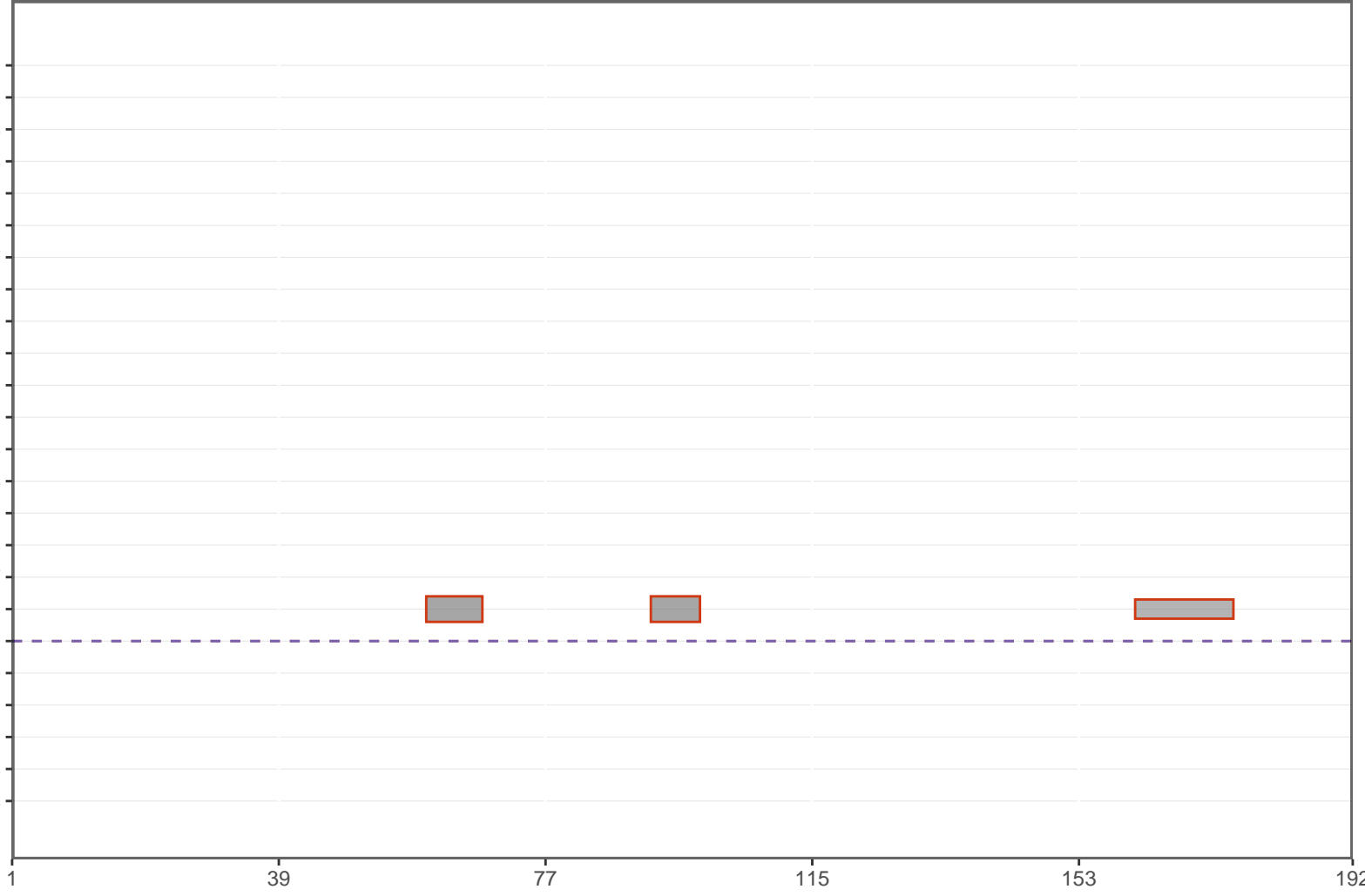
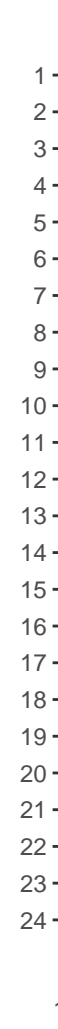
MW indication



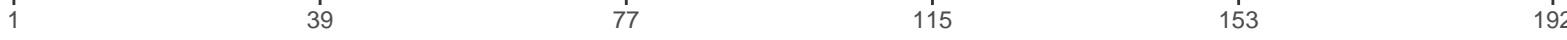
Molecular weight



Gel Slice

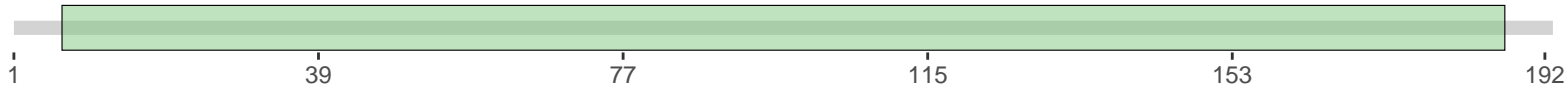


Protein length



Peptide counts over 4 repeats

Pfam domains



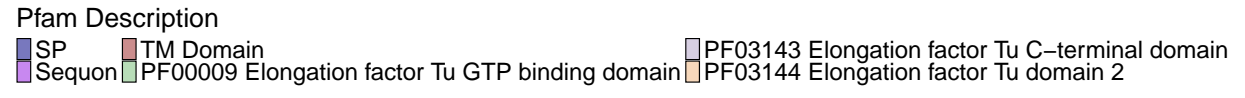
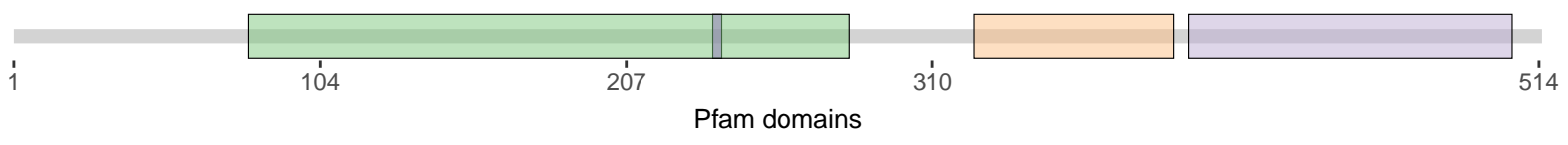
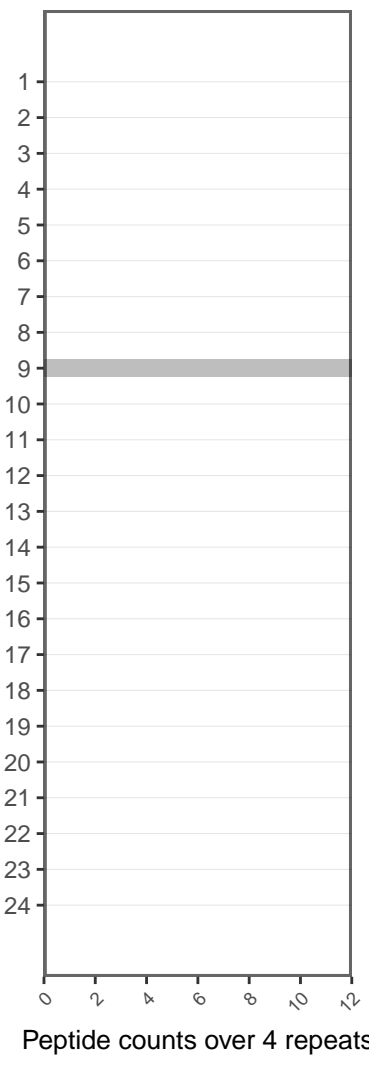
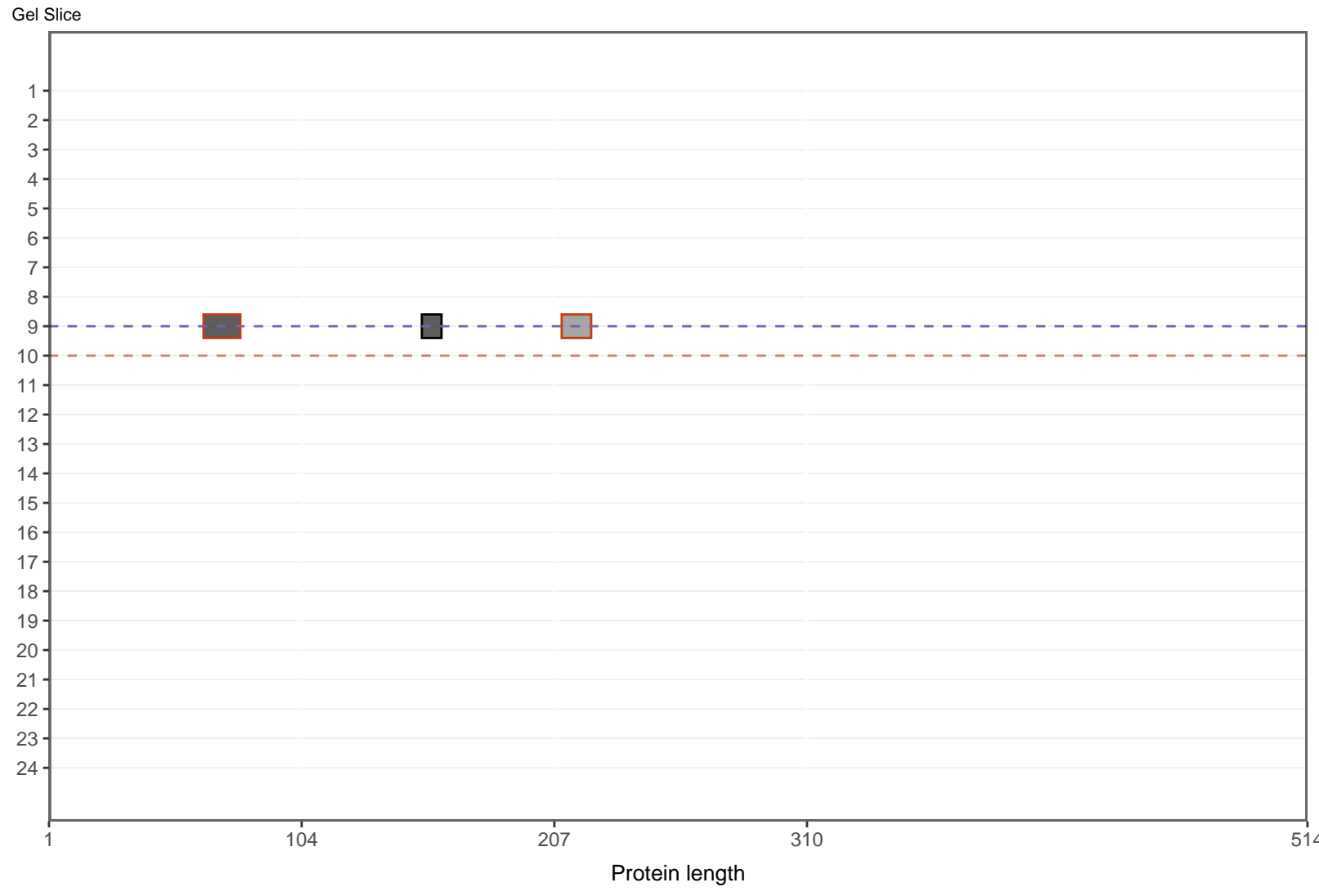
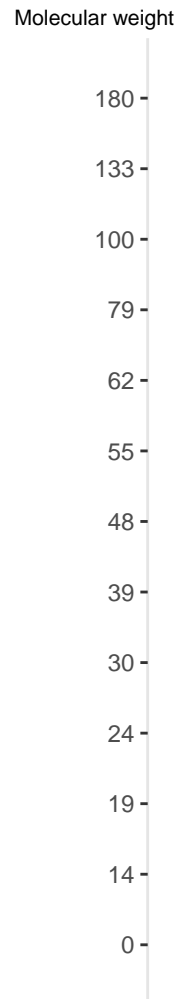
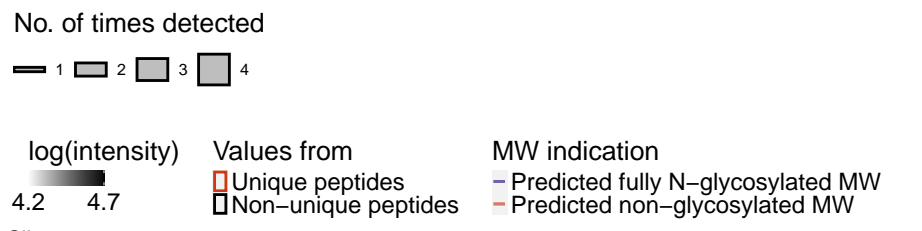
Pfam Description



Protein sequence:

RELEKXFGKDIIFATRIARPPKRGGAAGRPRBRTLTSVHDAILEDLVVPAEIVGKRTIRYRIDGSKMKVFLDPKERTNTEYKLETFSSAVYRKLGGKDVVFVEYFTEA

NbL09g12100.1 eukaryotic_peptide_chain_release_factor_GTP-binding_subunit_ERF3A-like [MW = 56.97 kDa]



Protein sequence:
 YDIEESKMVFLRSSEGVNKKDVGFLPIBGLLGSNLIKTRMEKSVGPWWNGPGLFETLDVPEVPPDFNGLRPLMPIDKFKDGMGTVMGRIEESGSIREGDNLMPNKAAYKVAIFGDEDKVRHVGCGENVRRLSGVEEDDILSGFLGSAKPHAVTEFVAGLQILELLDIAFTAGKVAKLVHHSVVEEGEIVELMQGIDKTKKPKMKKPLFVKNGANILGRVQVNNLICVEKFSDFAGLGRFTLRTEGKTVWGWKITALPTVADNA

NbL09g11980.1 serine_carboxypeptidase-like_45 [MW = 39.28 kDa]

No. of times detected



log(intensity)



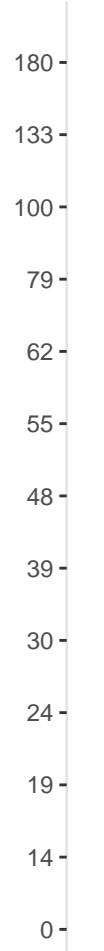
Values from



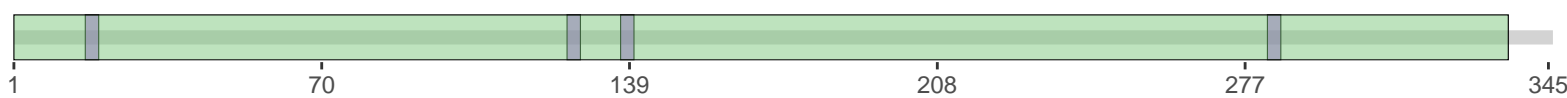
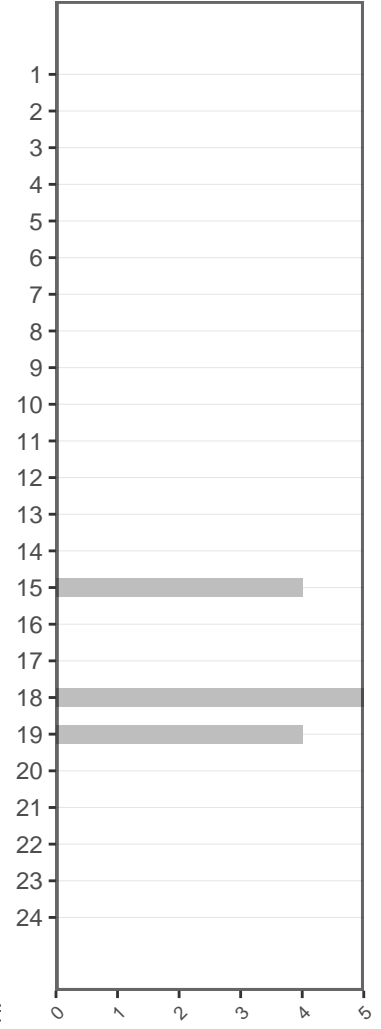
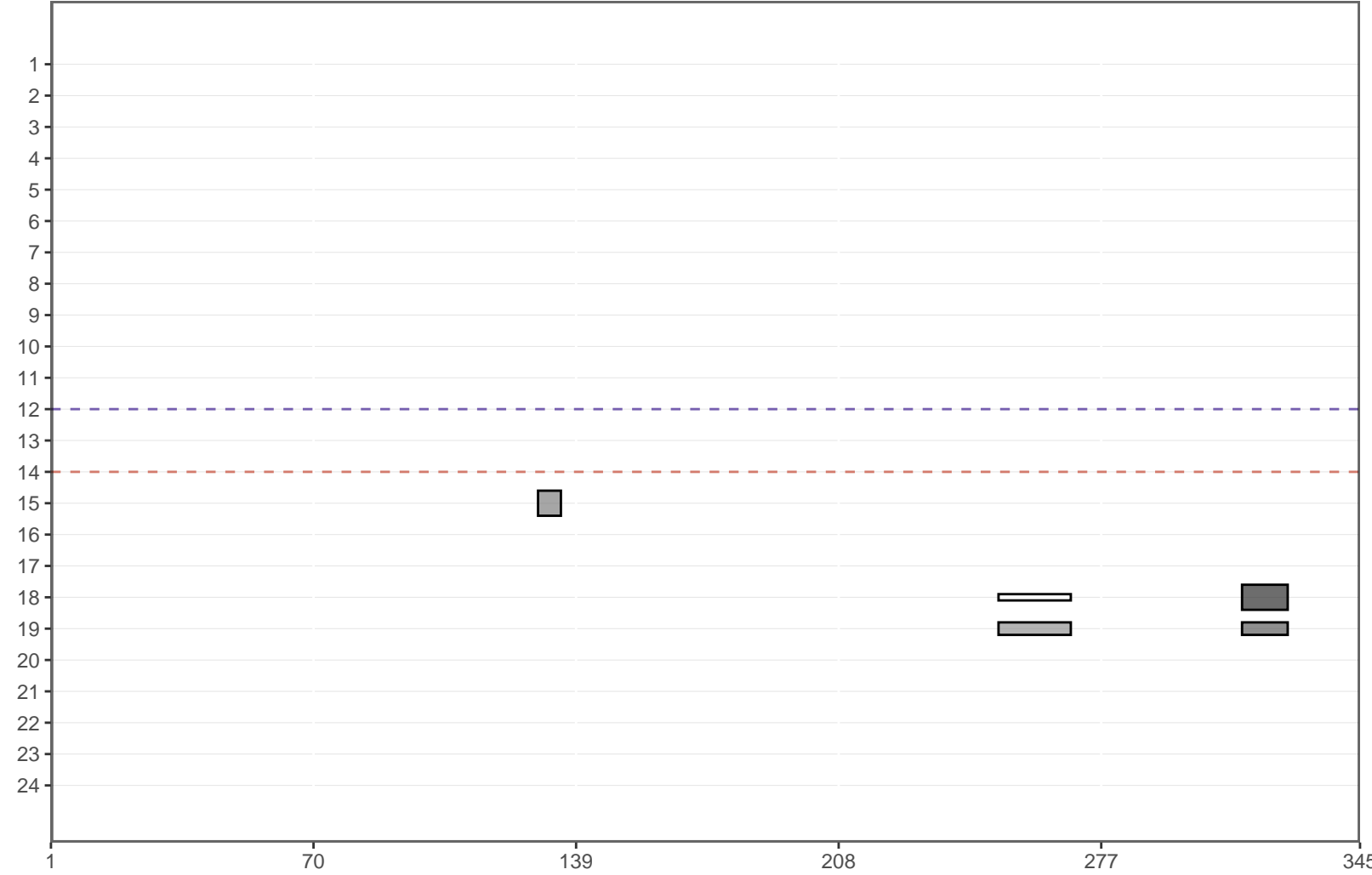
MW indication



Molecular weight



Gel Slice



Pfam domains

Pfam Description



Protein sequence:

DKYDYTLQVCLSSVLSGGKISPGENADAEEKIDGDKKTVNLYNRGQVRRALHANLVGVRRWQVGSNLDVQLLDEIPTISVGLLKERIPVLYSGDQDQVPLTGTGRTVVHQLAKRMLNTTVPYRWFAGQGVGGWTVYDNLISFATVRGAHVEVFFSGPERSFVLFKSFLEGRALPEVF

NbL09g11910.1 probable_beta-14-xylosyltransferase_IRX10L [MW - SP = 44.9 kDa]

No. of times detected



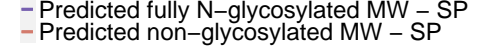
log(intensity)



Values from



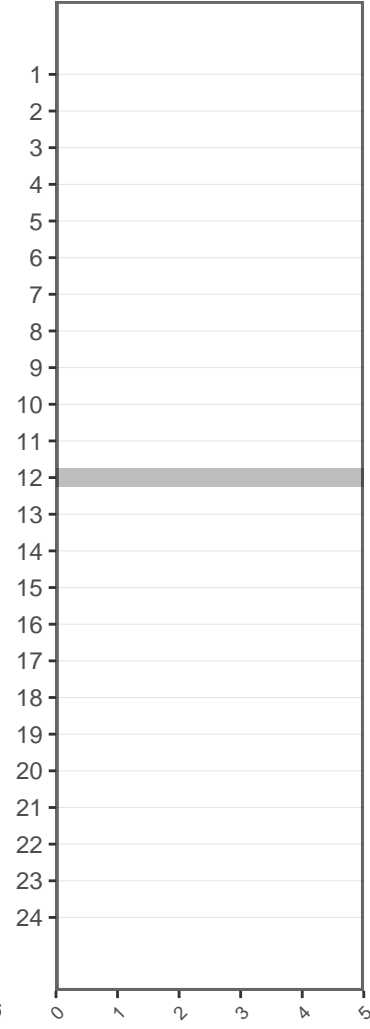
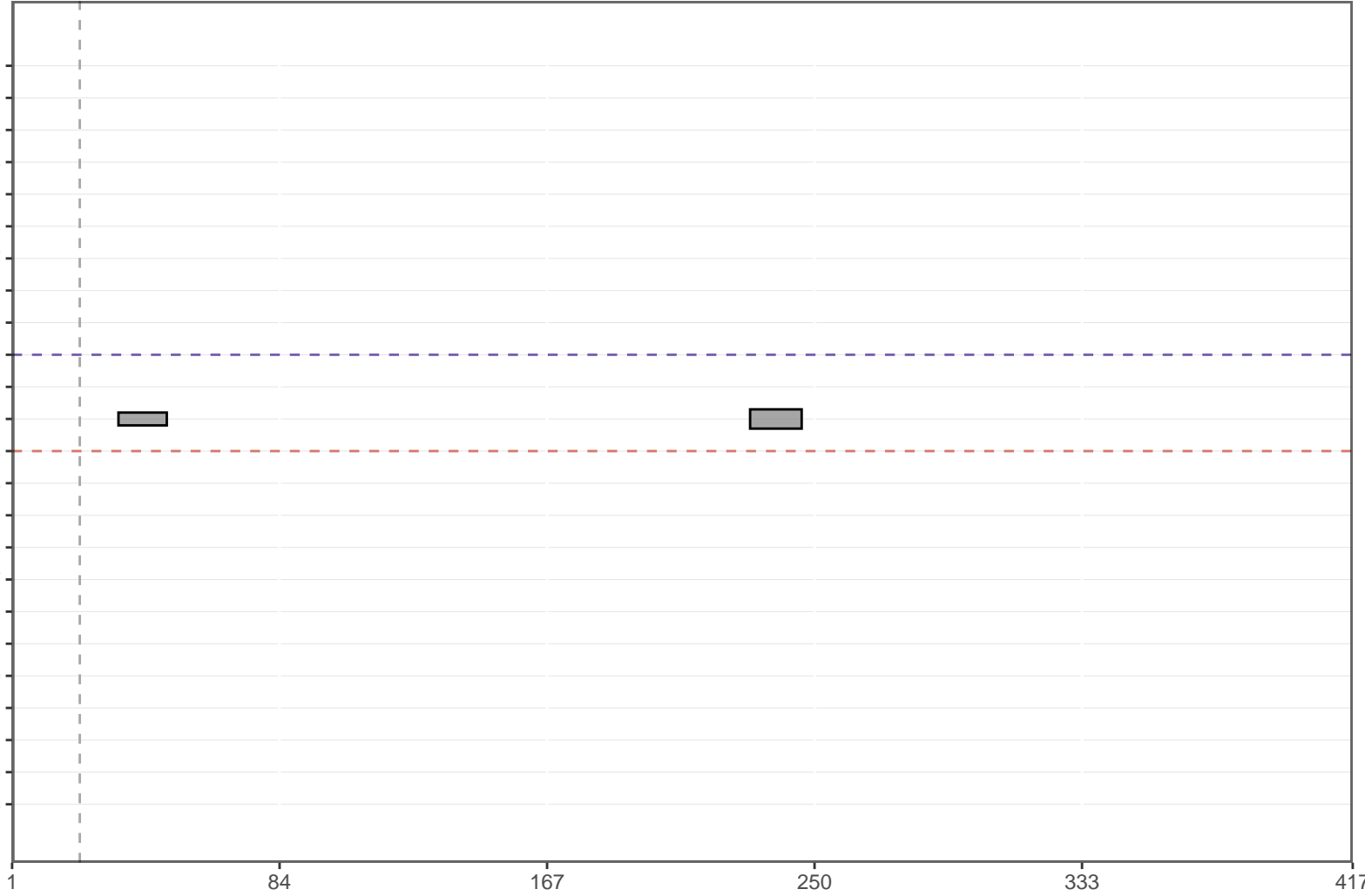
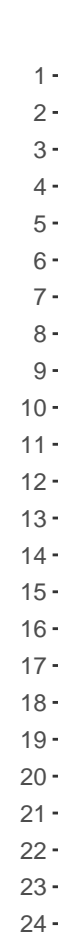
MW indication



Molecular weight

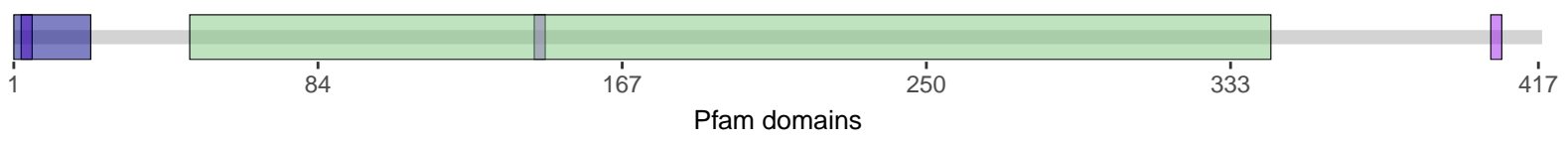


Gel Slice



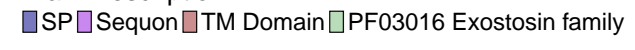
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MLKDGSLTPPPYAPPKMQSHLIPFDTRRSIEVYRGLFYDVGNDREGGYARGARAAWENKDNPLFDISTEHFTTFYEDMDRFAIFGLGLPGLWAPWSPRLVEAVIFGCGPIVADDDVLPFADAPWEDIGFVAEKDVNPLDITLTSIPREILRKRLLANFSMKQAMLPQRAQSSDAFHQLNGLARKLPDKSTYLPKQVALLNWTAGPVGDLKPW

NbL09g11890.1 uncharacterized_protein_At4g14100-like [MW - SP = 22.68 kDa]

No. of times detected



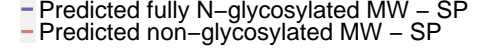
log(intensity)



Values from



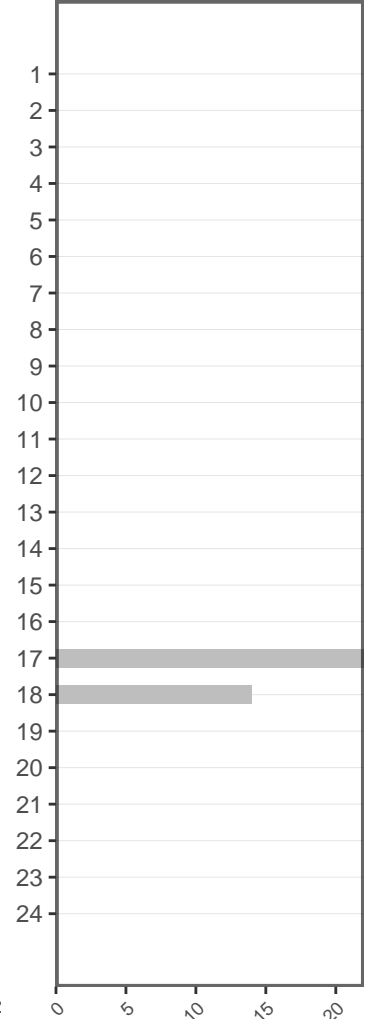
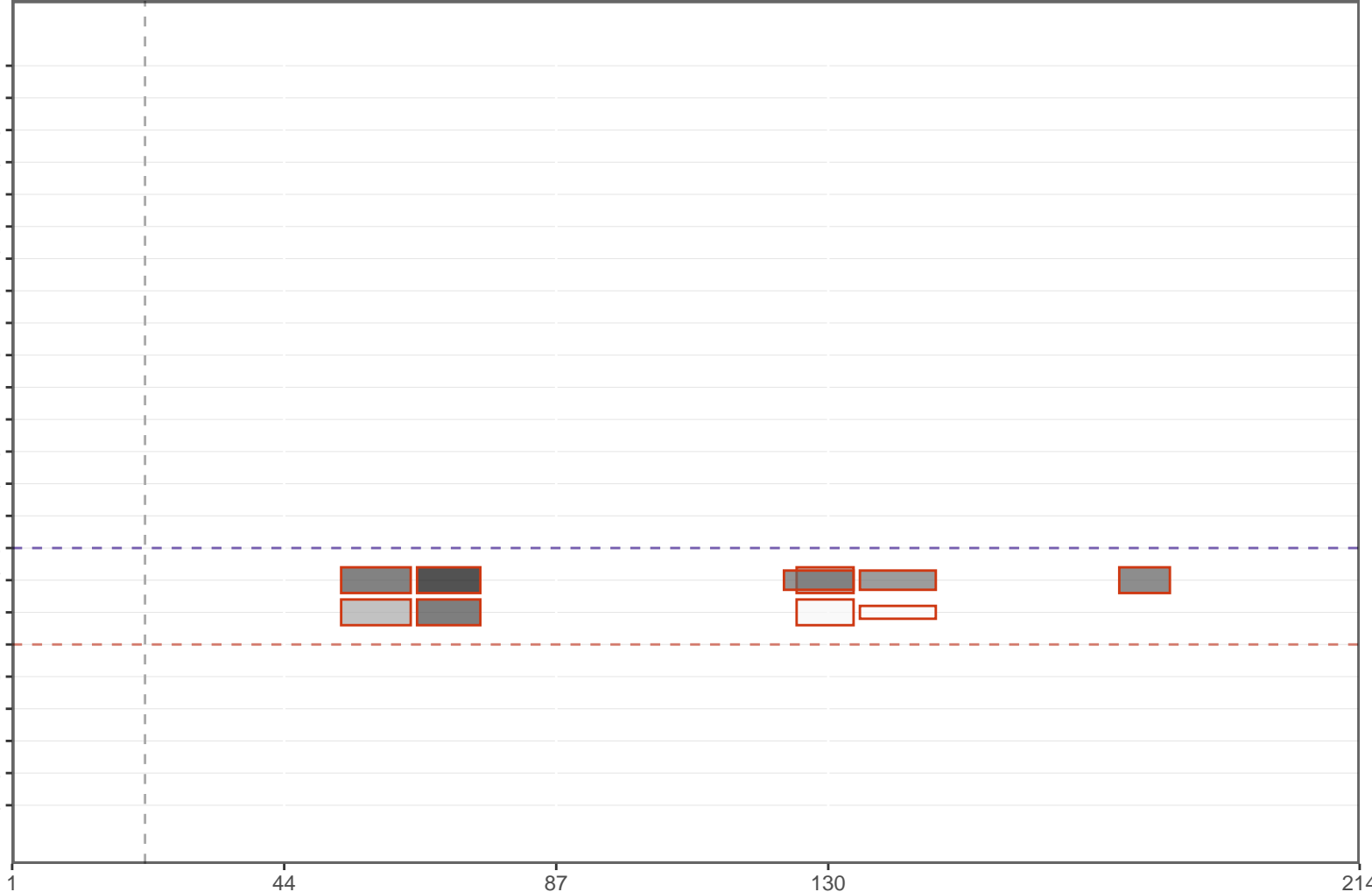
MW indication



Molecular weight



Gel Slice



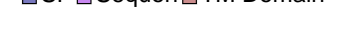
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TOECTRIFFPVGLRPNWLEGSNHYGHKYKIDGFLGNWWEKVGFLQYYEDAFTRIPVWVHFYDGLVEHMTFEVGVKLEDSKVGAPVYGFKEVEKERISLENLATHFRDVAWNGEVAEN

NbL09g11850.1 calnexin_homolog_1-like [MW = 65.68 kDa]

No. of times detected



log(intensity)



Values from



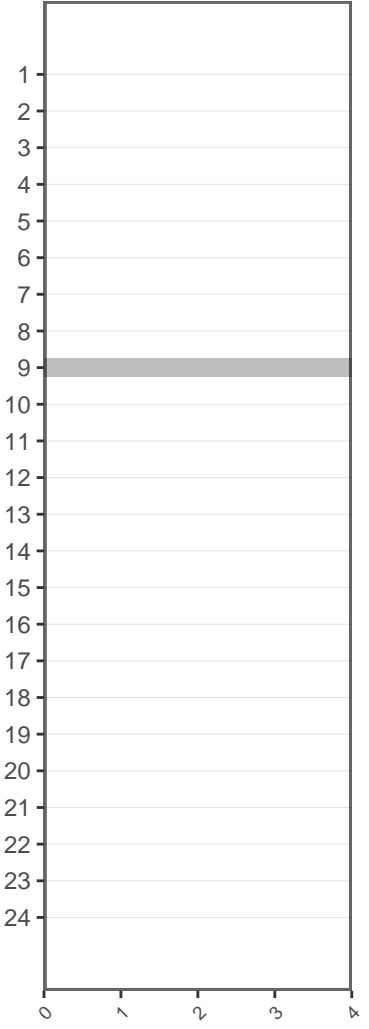
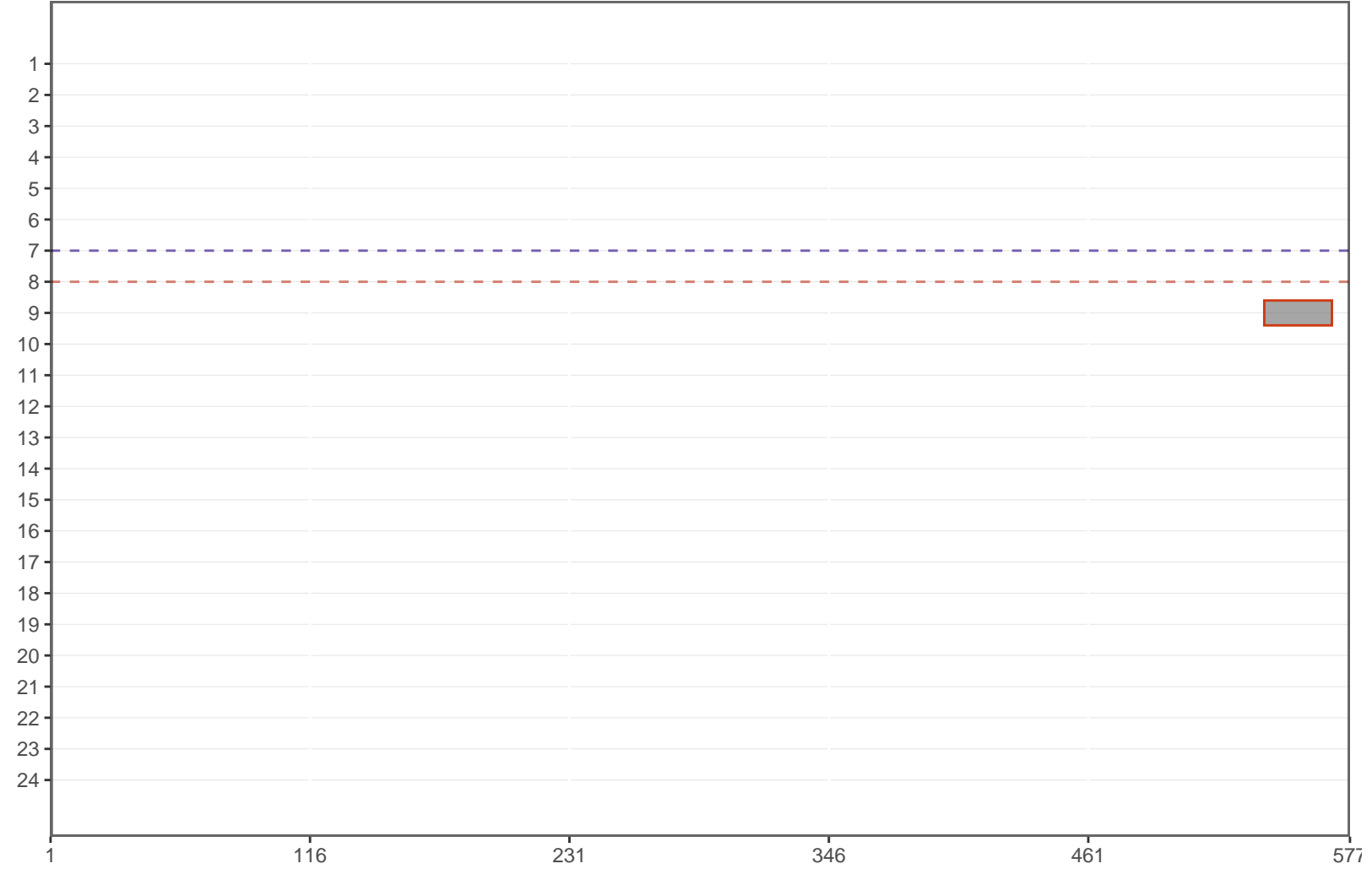
MW indication



Molecular weight



Gel Slice

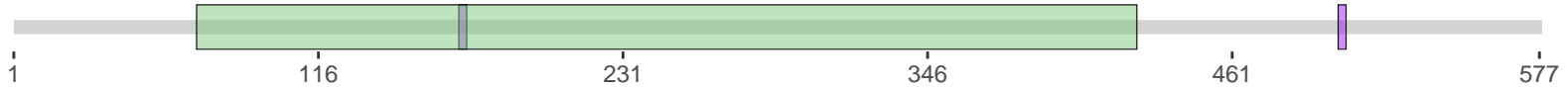


Protein length

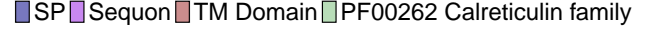


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

EKIPDPDAKPCDWDDEAPMEDEEAEKPEGLWDDPEEINDEATKPEDWDEEDGEWEAFNIDNPKGAEGPCGGEWRRPMKSNPKYKQKWHAPLIDNPNYKGGWRKPRDIPNPFELNPKNPEFPAAGIEIWTMGDGLFDNLLASDEKVAESYRKTWPKKFAEAEKQKAEATISGGLKGFQKVFDDLKYKADIPLLGEHKVLDLLEKAEIOPNLTVGVVSIHIFTVLLKLFGGKQKQPARATEEPKRSDVAEASTSN6GGATEEKEECNEDAAAAPRRR

NbL09g11830.1 calnexin_homolog_1-like [MW - SP = 57.94 kDa]

No. of times detected



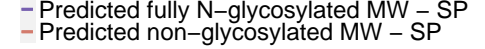
log(intensity)



Values from



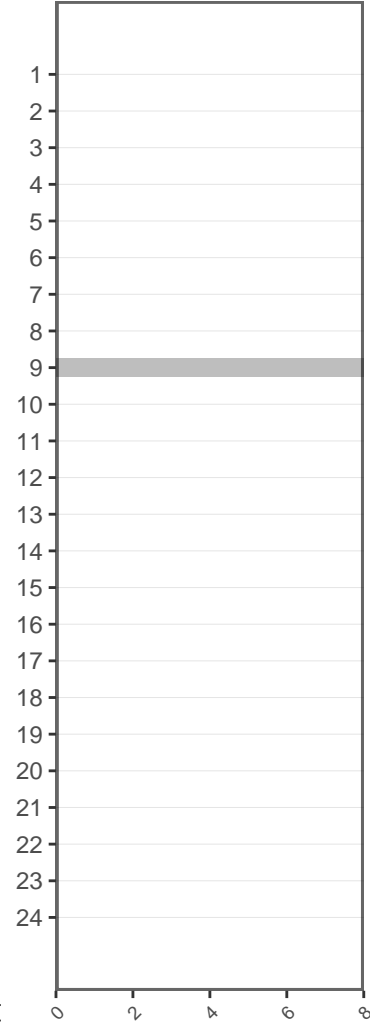
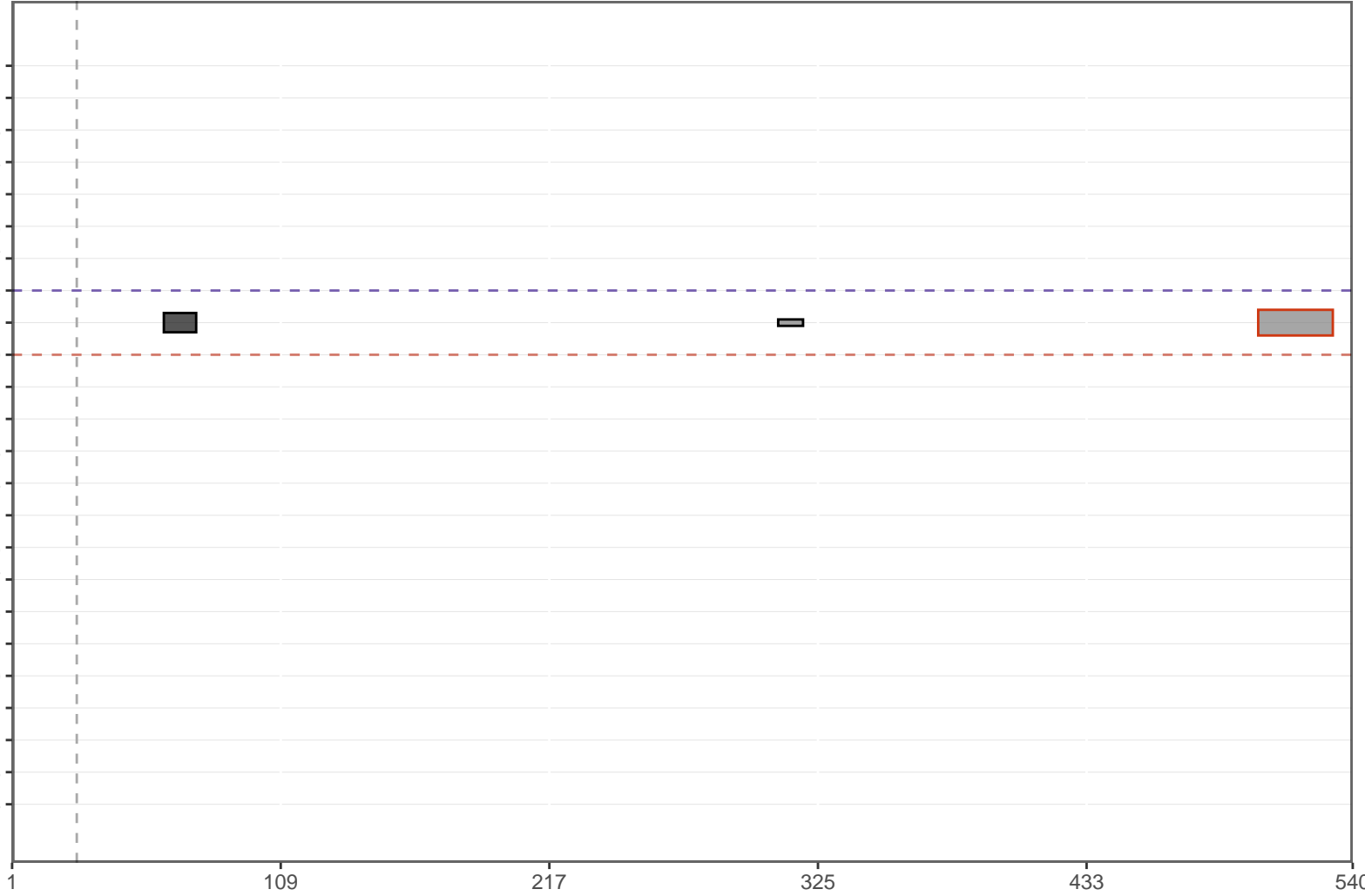
MW indication



Molecular weight

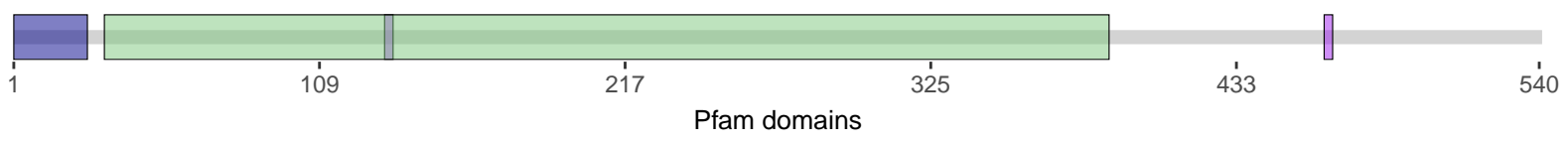


Gel Slice



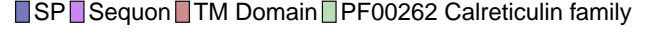
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

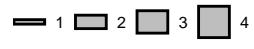


Protein sequence:

MAPMEIEDDAEXFEGWALDDPEEIDDPEATKPEDWVDEEDGGEWEAPKIDNPKGAEGPQGGGEWRPDKSNPKYKQWVHAPLIDNPNYKGIWPKPRDIPNPNYFKLDRPNFPIAIGIEIWTMDGGLFDNLIASDEKVAEYGRKTAWKPKFDAEKEKGAEEVANSGLKGFQKVVFDLLKVKADPLLGEHRSKILLLOKAEIQPNLTIGVVISIVVFTVLLKVFQGGKQGPRAATAEPRKKSDDGAEASTENNDGATEEKEEENEDAAAAARRRRRDN*

NbL09g11290.1 beta-glucosidase_BoGH3B-like [MW - SP = 65.67 kDa]

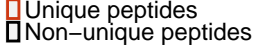
No. of times detected



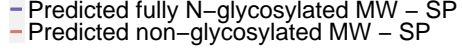
log(intensity)



Values from

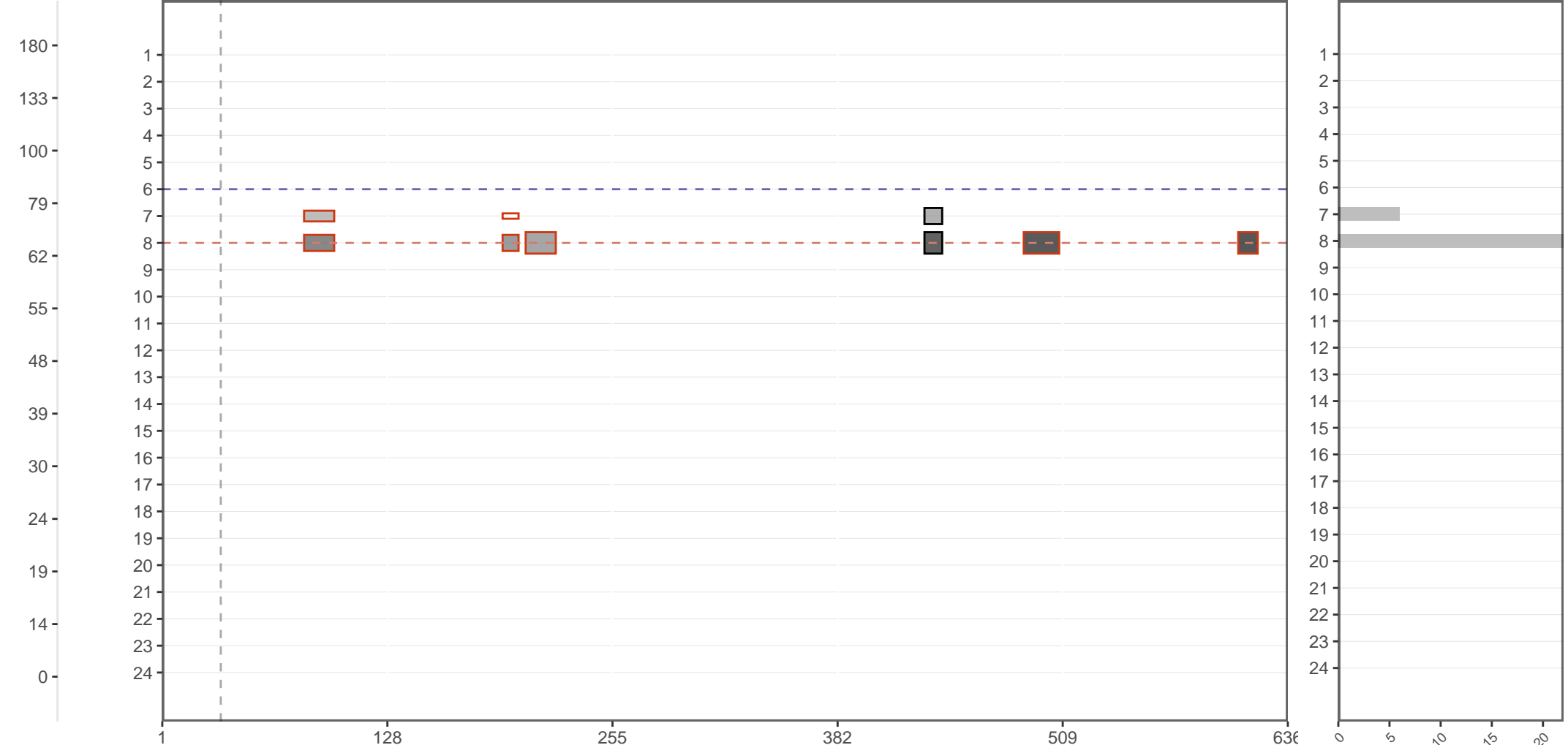


MW indication



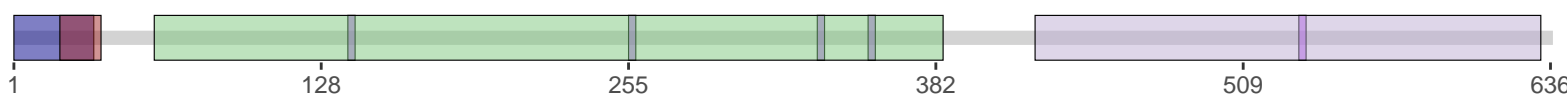
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

SP Sequon TM Domain PF00933 Glycosyl hydrolase family 3 N terminal domain PF01915 Glycosyl hydrolase family 3 C-terminal domain

Protein sequence:

IGFLKDRLLKFRGFLVHSDWGGSDIRTSPIHANYTVSVQAGVSGAGIDMIMVPEHYTEFDITLQLVKDNIPVSRIDDAVKRILRKFETMGLFENPLADL6YVNGL6GSD6EHRRLARAVRKSLLVLLKNGKST69PLLPKPKAKILVAGTHADNLGYQGG6WTIEWGGVPGNDLTVGTTLSAANKTVDPATQAVYEGNPD6NFVKSNEFS6AVWIKGEVPEVPEMFGD6TNLTTEAGP6TINN6GEAVK6V6V6V6SGR6P6VLEP6YVEKID6L6W6L6P6T6EG6W6DAL6FG6Y6T6G6K6

NbL09g11260.1 beta-glucosidase_BoGH3B-like [MW - SP = 65.7 kDa]

No. of times detected



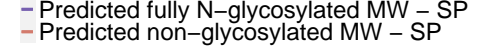
log(intensity)



Values from



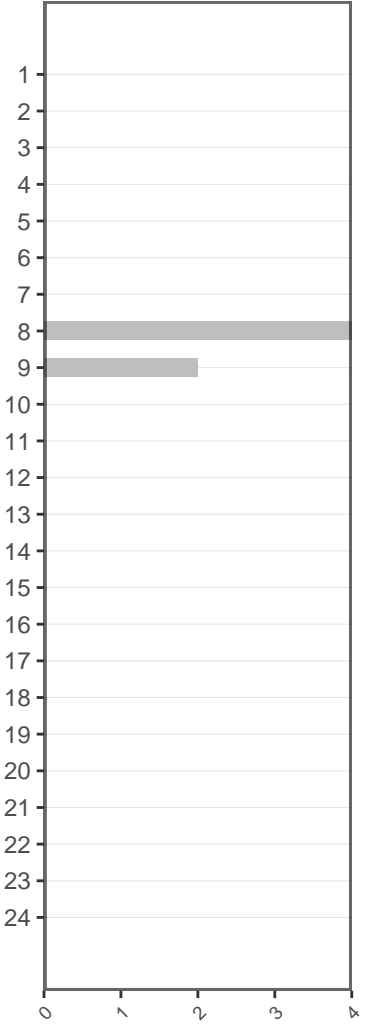
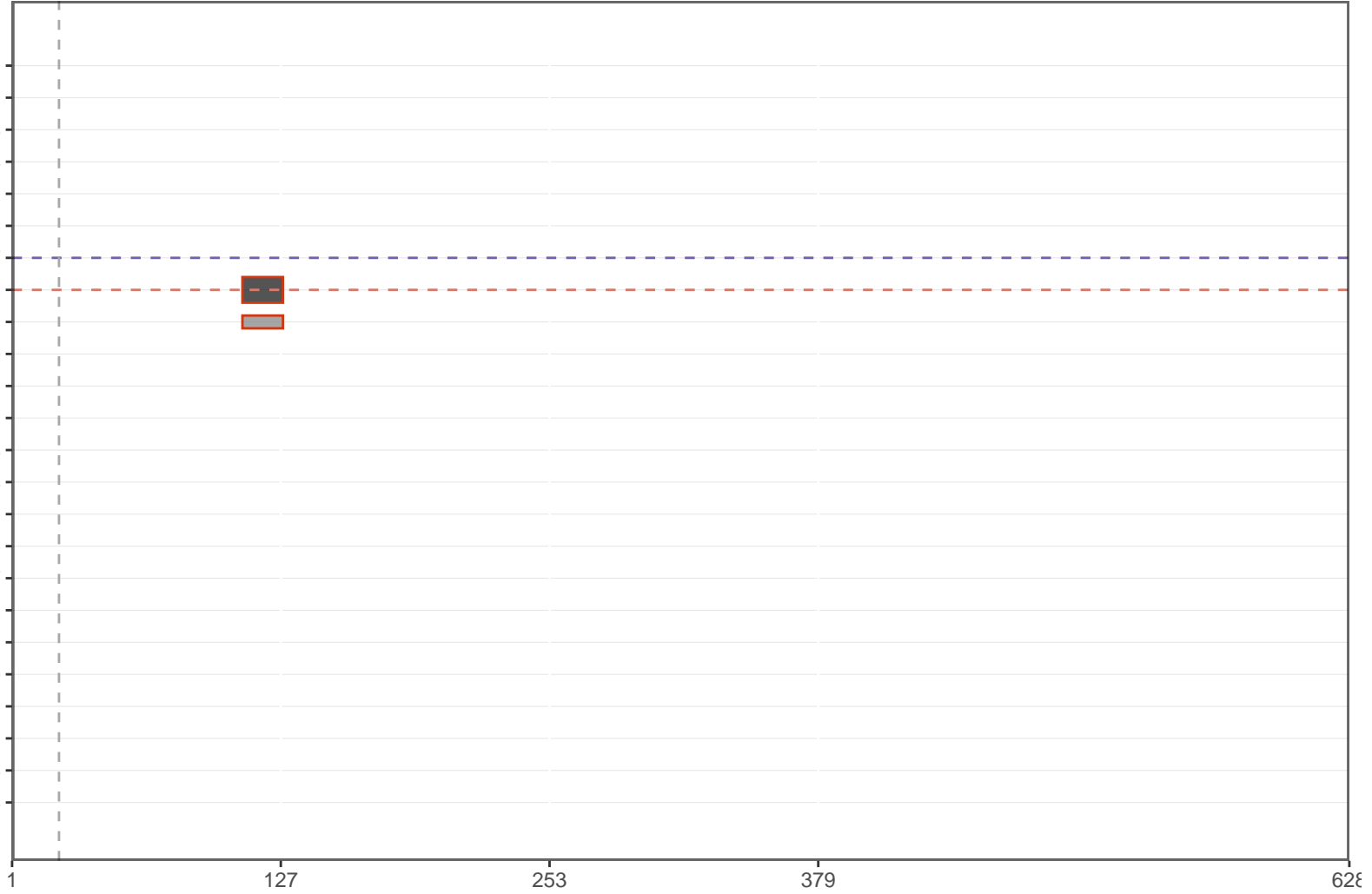
MW indication



Molecular weight



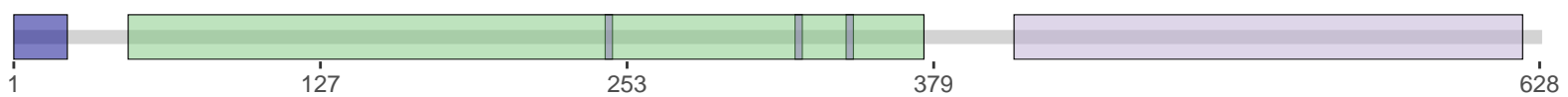
Gel Slice



Protein length

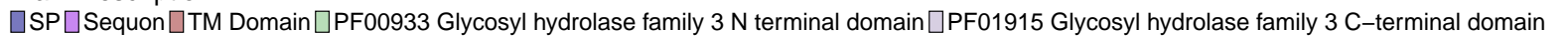


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

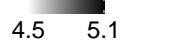
RGFVSDVEADKIDPPRANYSYGAGVLAGIDMMGGENTFELGDLAFLVRKNIIPMSRIDDAWRILRVRKVFVGLGFENFLADLSLANGLGSGEHERELARAVRKSLLKNGKVTSGPRLFLPKVMKMLVAGSHTDNLGYGGGWTGIVGGIGDNLTTGTTLSAVKNTVHPSTQVYVGNPQANFVKSNHFSVAIVAGETPYAEVFGDSAKLTAEPGPSTINVDGWWKQVAVVSGRPFVIEPYLANDALVAWLPSSGGGADVDFGDFGTGKARTWFKSI

NbL09g11200.1 60S_ribosomal_protein_L30 [MW = 12.38 kDa]

No. of times detected



log(intensity)



Values from



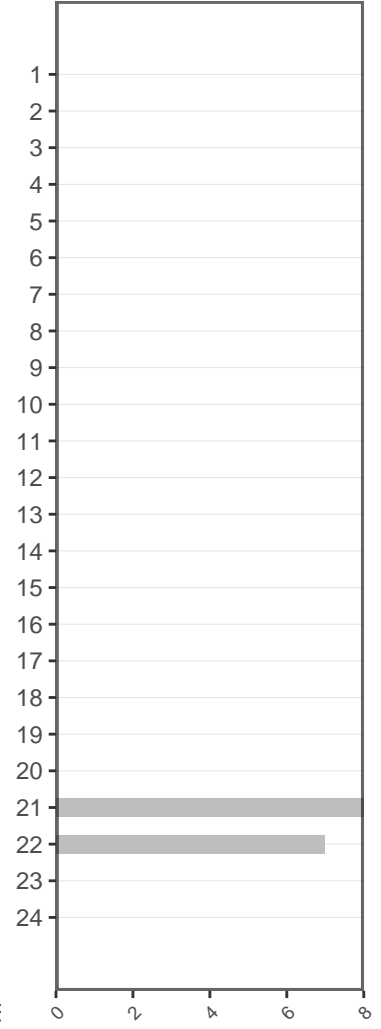
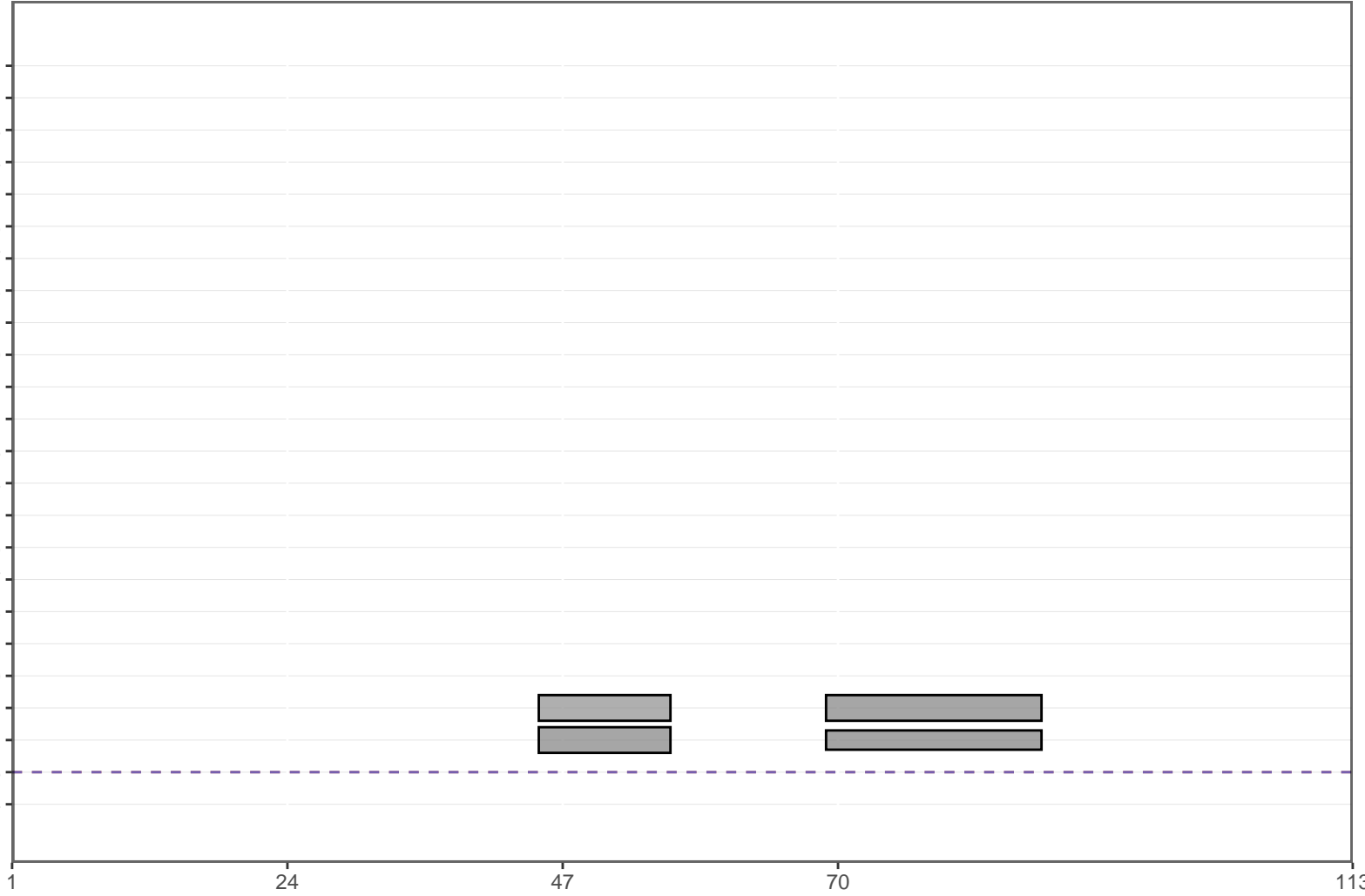
MW indication



Molecular weight

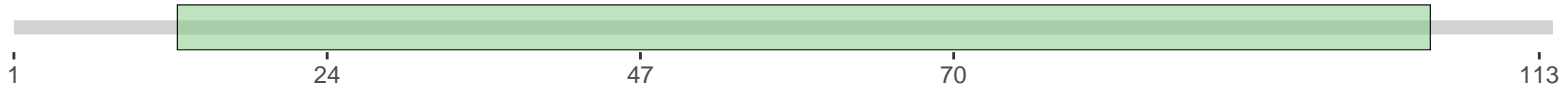


Gel Slice



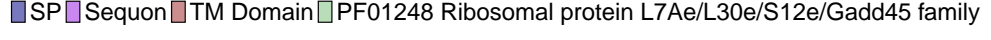
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

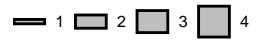


Protein sequence:

GKLVIANNCPLLRKSEIEYVAMAKIGVHHYNGNNDLGTAGKRVFRVCLGSHDPGDSDHKSMFGDQ*

NbL09g11180.1 NADH_dehydrogenase_[ubiquinone]_flavoprotein_1_mitochondrial-like [MW = 53.67 kDa]

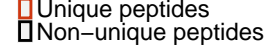
No. of times detected



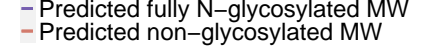
log(intensity)



Values from



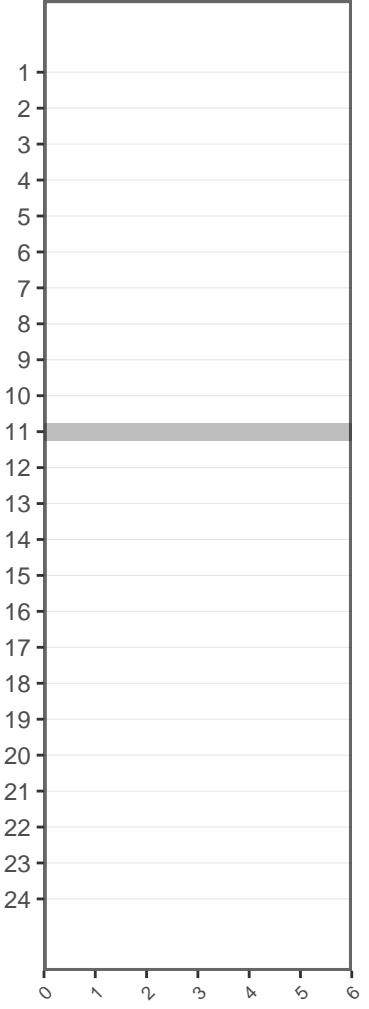
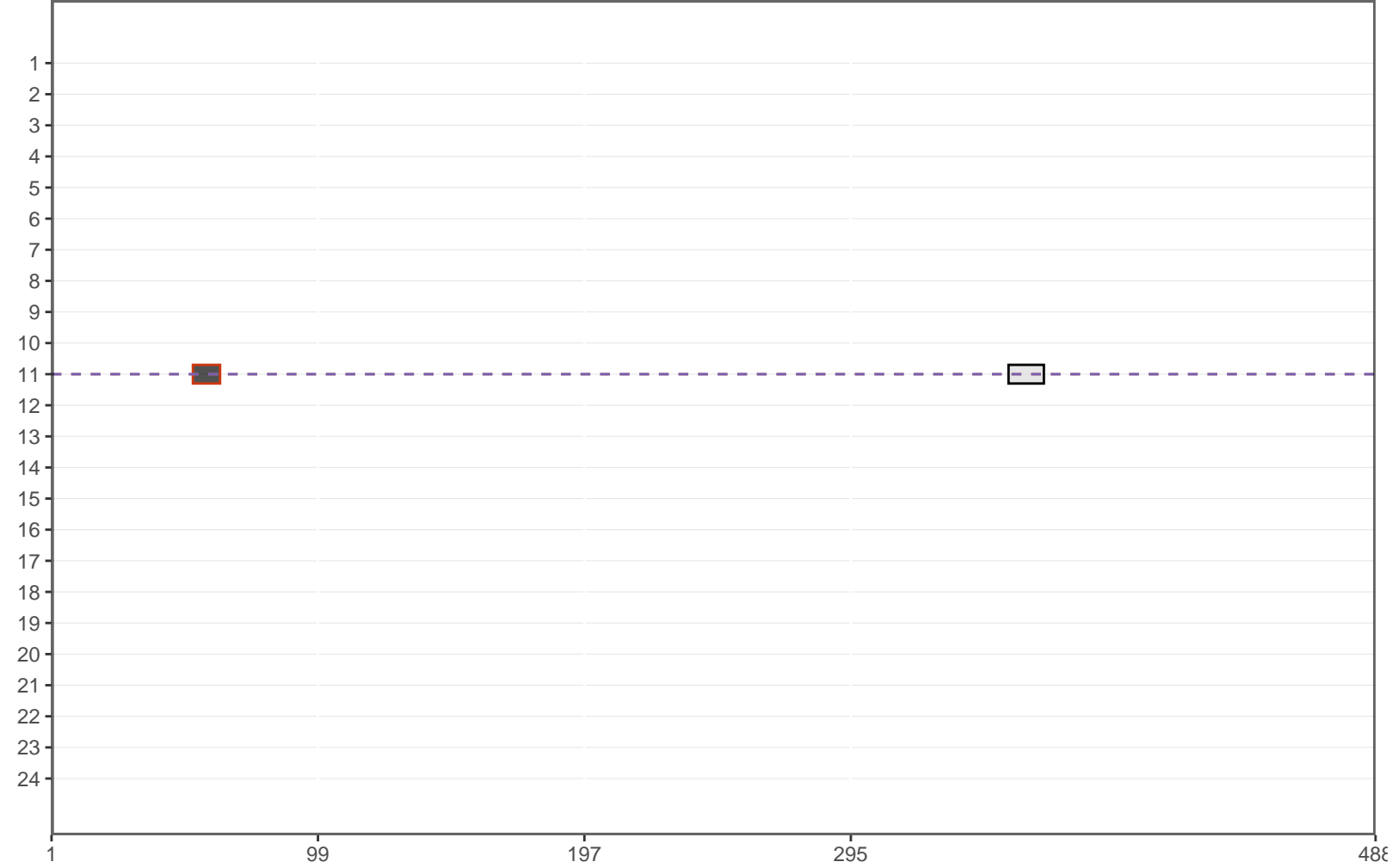
MW indication



Molecular weight

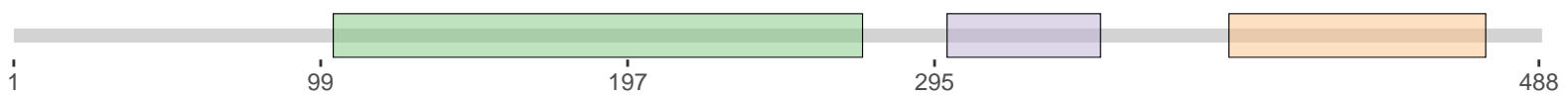


Gel Slice



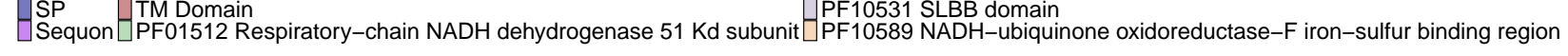
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GEETALLSLELGKGGKPKLPPFPNAGLVGGPTFTVTVETVAVSPTLRRGPEWAFSGFRKNNAGTKLFCBGGHVNKPCFVEEEMSIPLNELIEKHGGVRRGGWDLNLLVPGGSSVPLPKNVGEDLMDFDALKAVQSGLGTAAVWMDKSTDIVDAIARLSYFYWHESCGGCTPCREGTGWLVMMERMKVGNKLEEDMLQEVTKQIEGHTICALGDAAWVPGURHFPRPELERRIREHAEREIQGAAV

NbL09g11160.1 non-specific_lipid_transfer_protein_GPI-anchored_2-like [MW - SP = 14.64 kDa]

No. of times detected



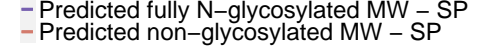
log(intensity)



Values from



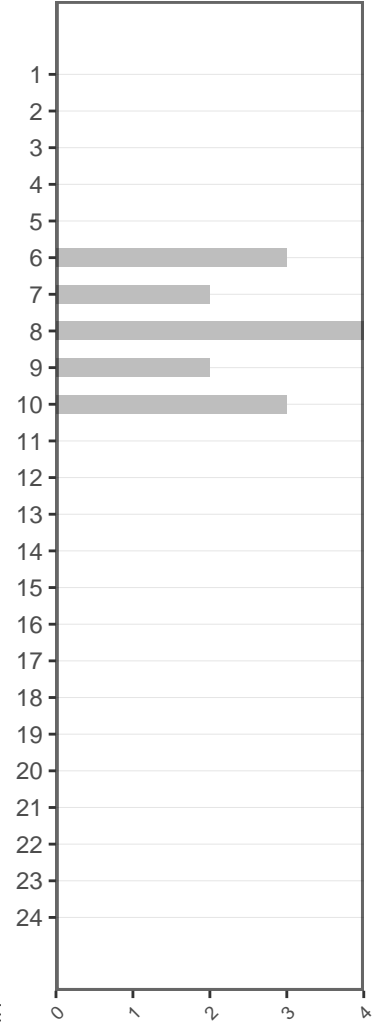
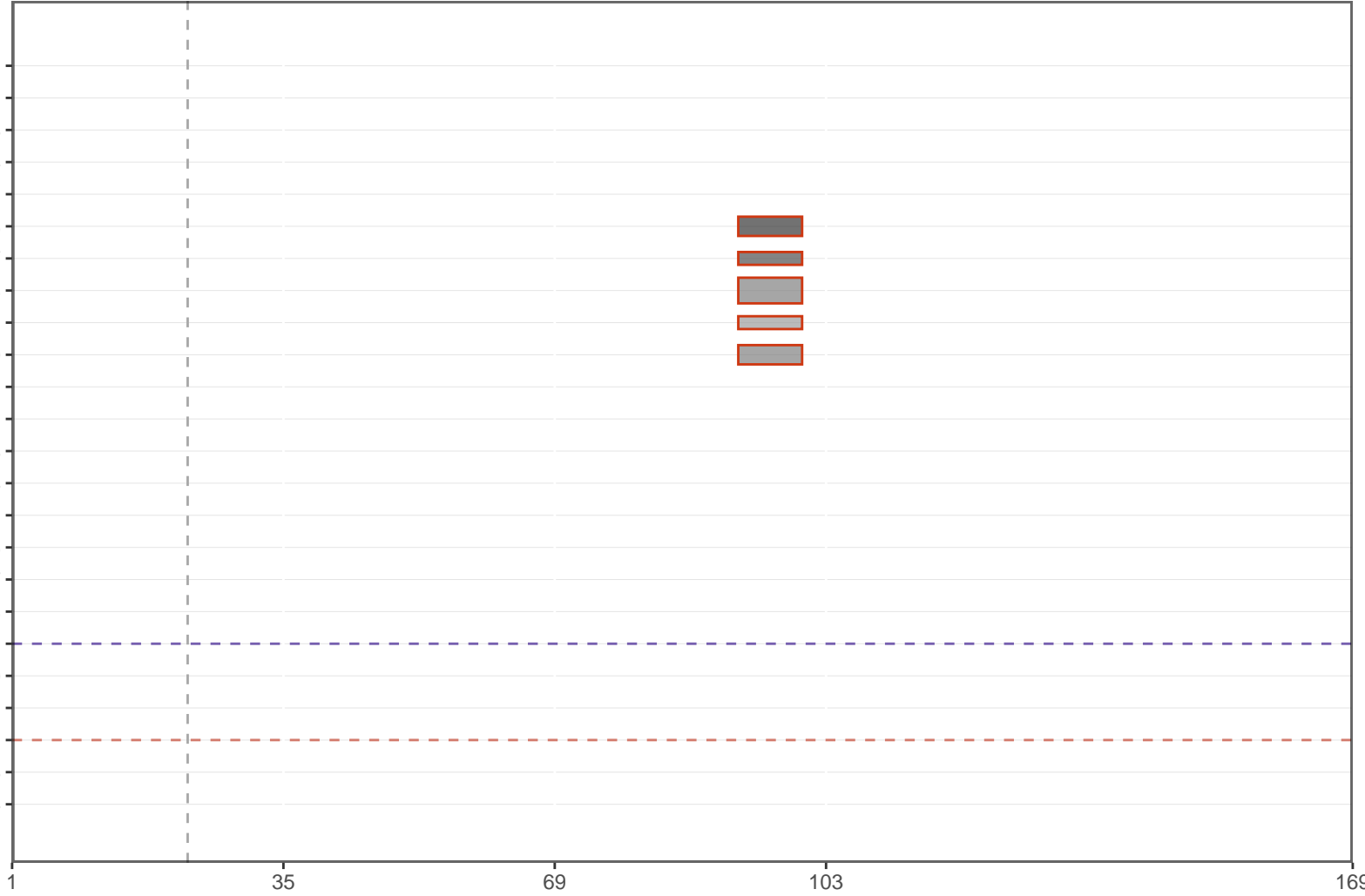
MW indication



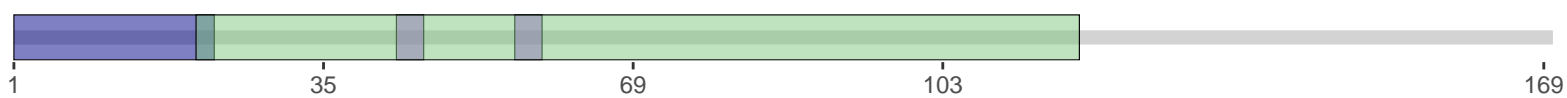
Molecular weight



Gel Slice



Protein length



Pfam domains

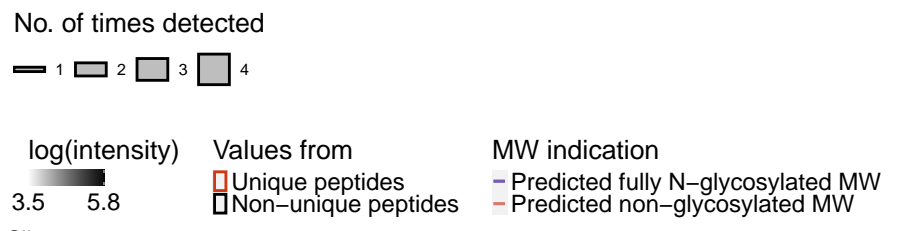
Pfam Description



Protein sequence:

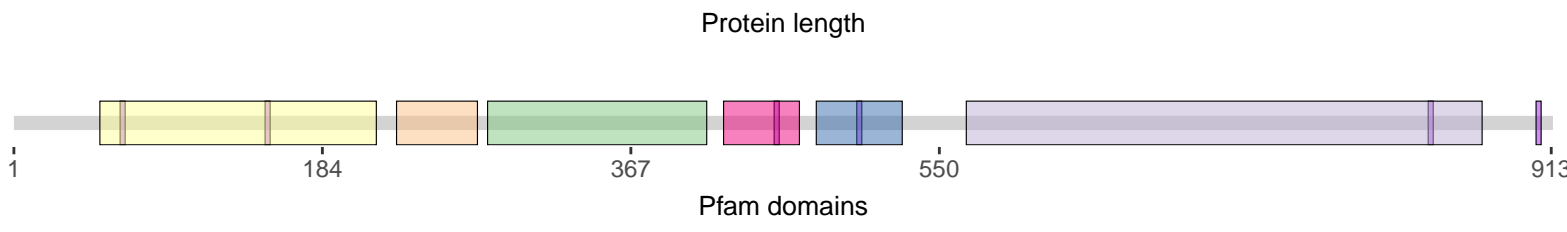
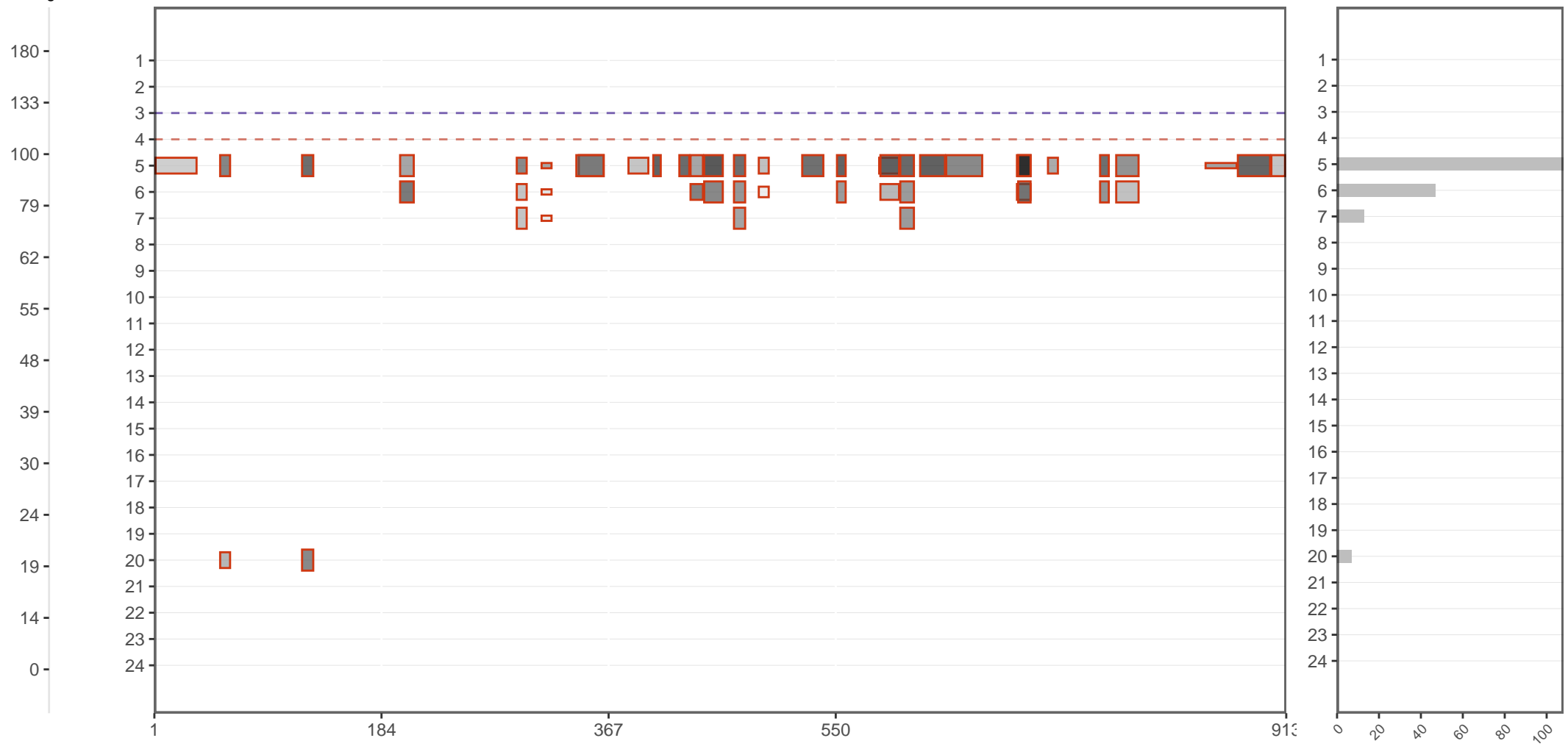
DSNPICLCQMLGRASSGAKIGFNIDVQKALKLPSVQGLEIPWATGSDLGVPVIGAPIASDDGPMPLPGGFATSFPTSDNKNAASTMAGLMTVSVSEI

NbL09g11050.1 protein_argonaute_4-like [MW = 101.85 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- TM Domain
- PF02171 Piwi domain
- PF16486 N-terminal domain of argonaute
- PF16488 Argonaute linker 2 domain
- Sequon
- PF02170 PAZ domain
- PF08699 Argonaute linker 1 domain
- PF16487 Mid domain of argonaute

Protein sequence:

ASGVYSSNFTQVEGRVLPAPKLGKAGNGDGLFERNRGRWFRNKRFFDPAKVERWAWNFNSARCDIRGLVRLTRIGEMKGISVEAPFEVFEESQLRAPRLVRVEKMFEEEGKLPQAFKFLKLLPERKNDYGRPKRKNLADYGVFTQGLAPGRVNDQYLTNLLKINAKLGLNSVLAIEHSPSPIMVSKVPTMILGMDVSHSGSPGSDVPSIAAVSSRWPSISGRVRSASVRTQSPKVEIMDNLFKHVSDTEDDGMRELLLDFFVSSGKRKPEHVFRDGVSESDI

NbL09g11010.1 biotin_synthase [MW = 36.85 kDa]

No. of times detected



log(intensity)



Values from



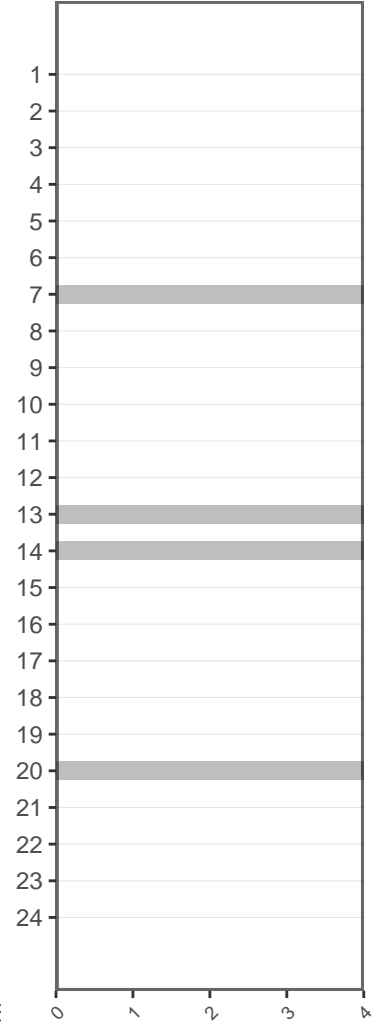
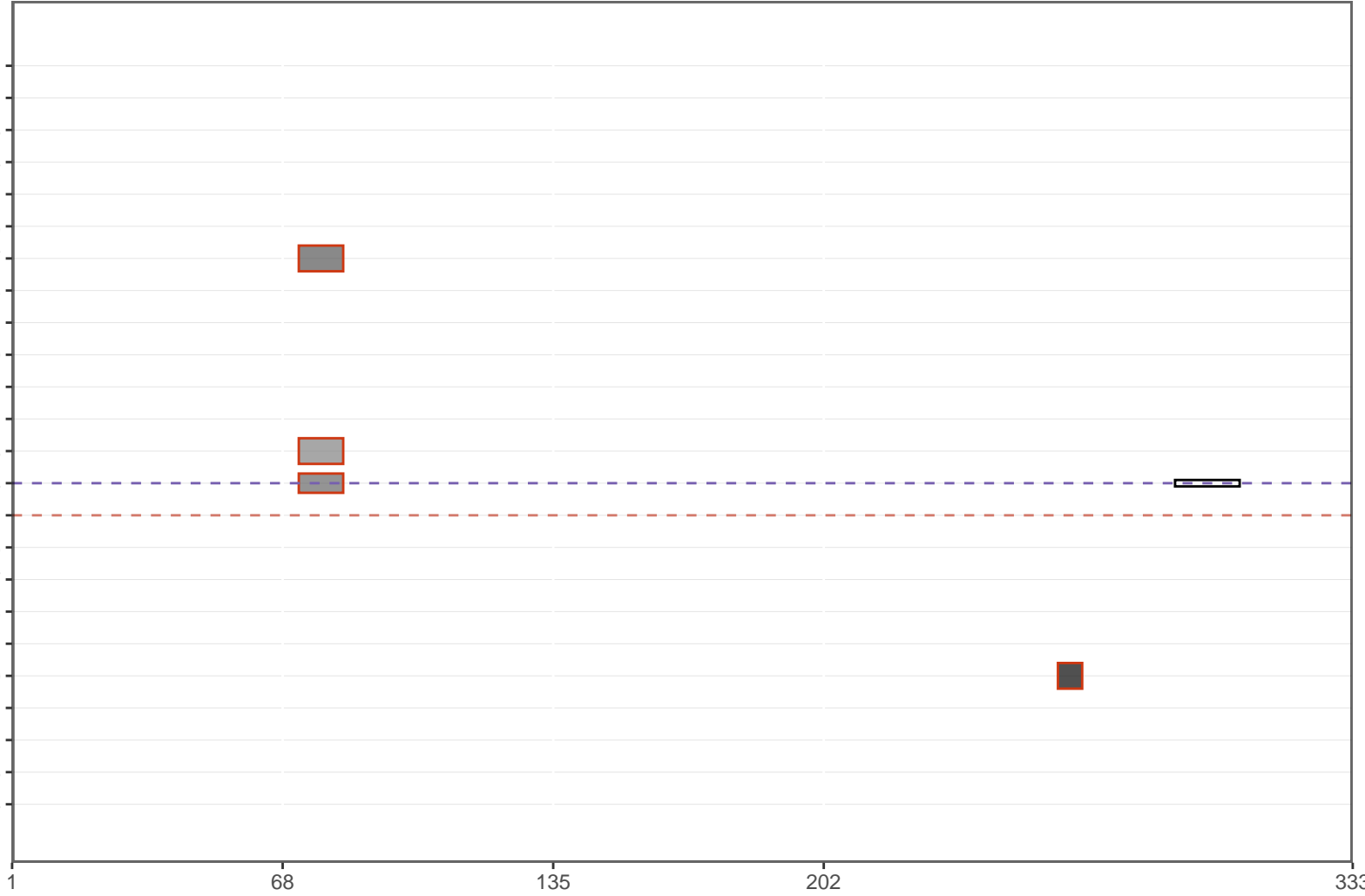
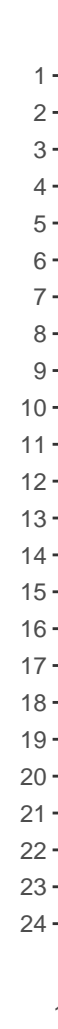
MW indication



Molecular weight



Gel Slice

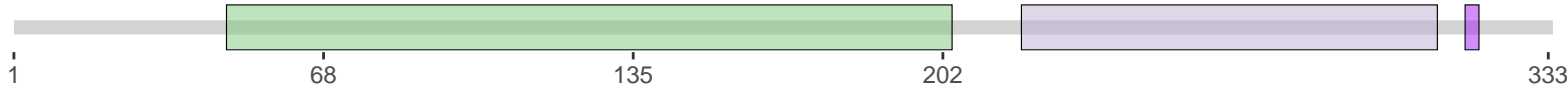


Protein length

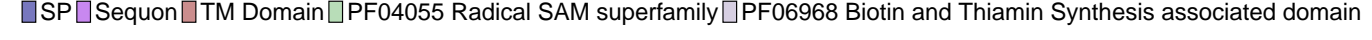


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

NINLDTSR EYYPNITRTYDERLETAKHVRKAGINVCSSGHGLGEAEEDRIGLLTFLALPHPEGSVFNALIAKGTPLEDQKVEVWDMRMSTARITMPSAMVRLSAGGVRFSPEDALCFLAGANSIFGDKLLTFNNQVDADQYMFKLLGLVFKAFNFSADKDEDEKLEAF

NbL09g10960.1 nuclear_pore_complex_protein_NUP50B-like [MW = 47.6 kDa]

No. of times detected



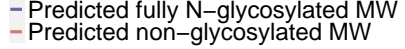
log(intensity)



Values from



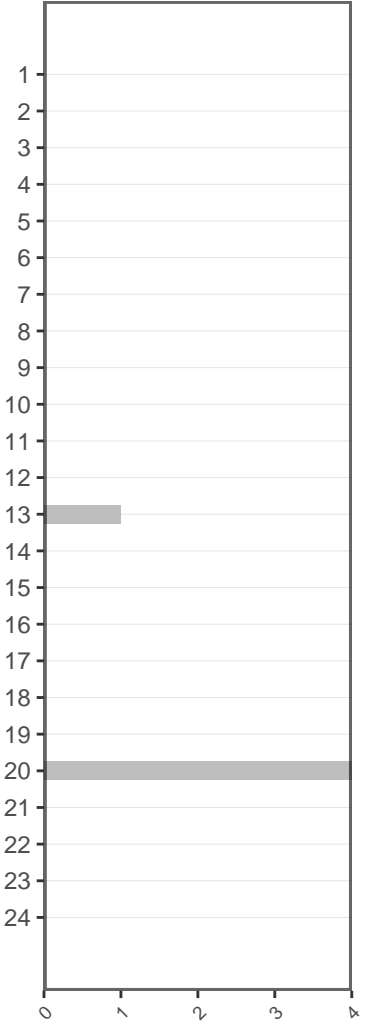
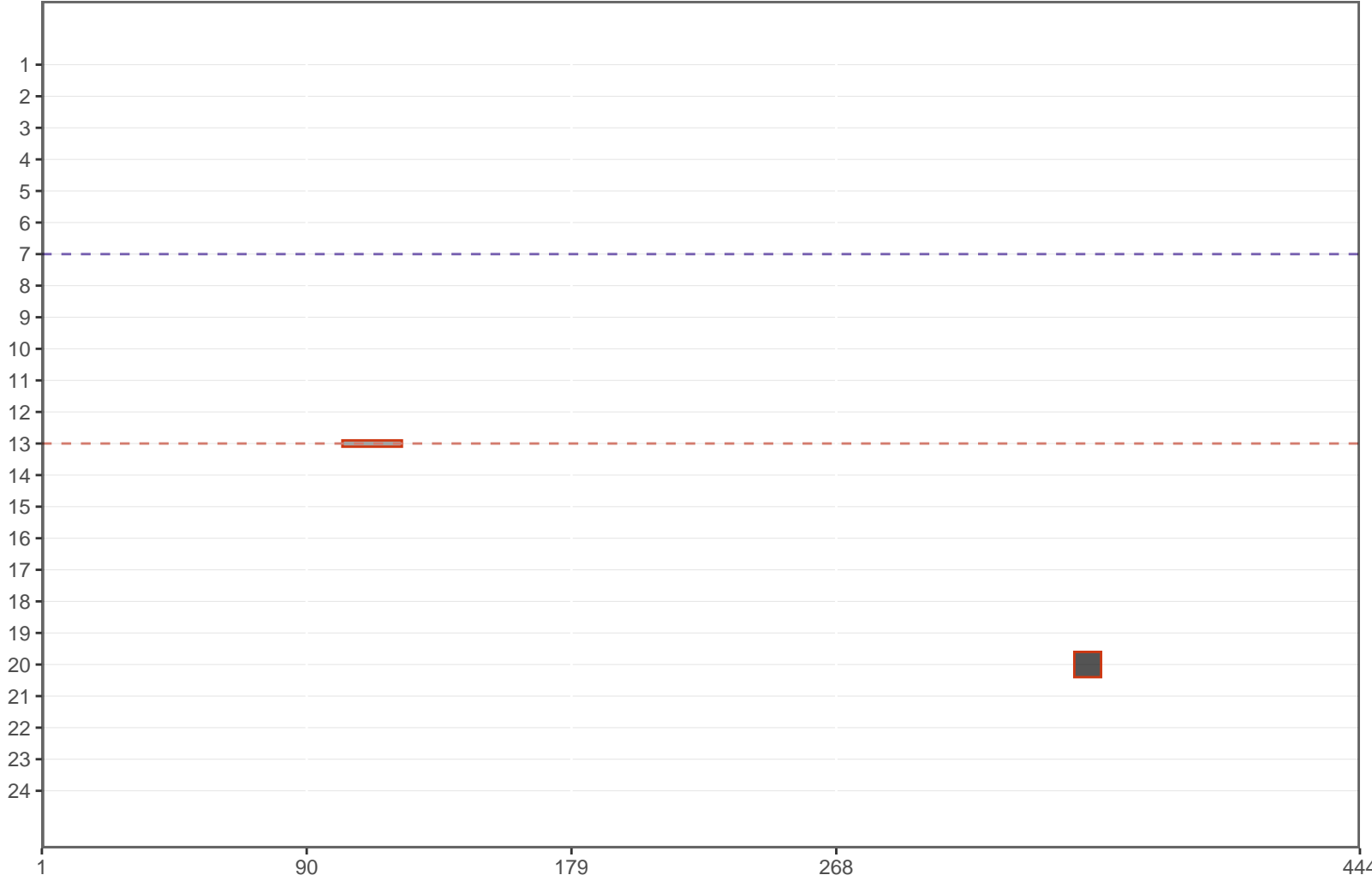
MW indication



Molecular weight



Gel Slice



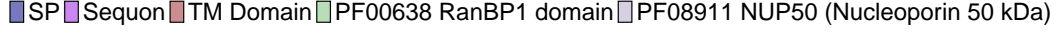
Protein length

Peptide counts over 4 repeats



Pfam domains

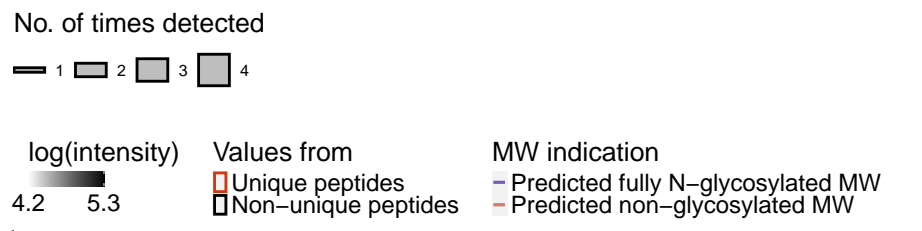
Pfam Description



Protein sequence:

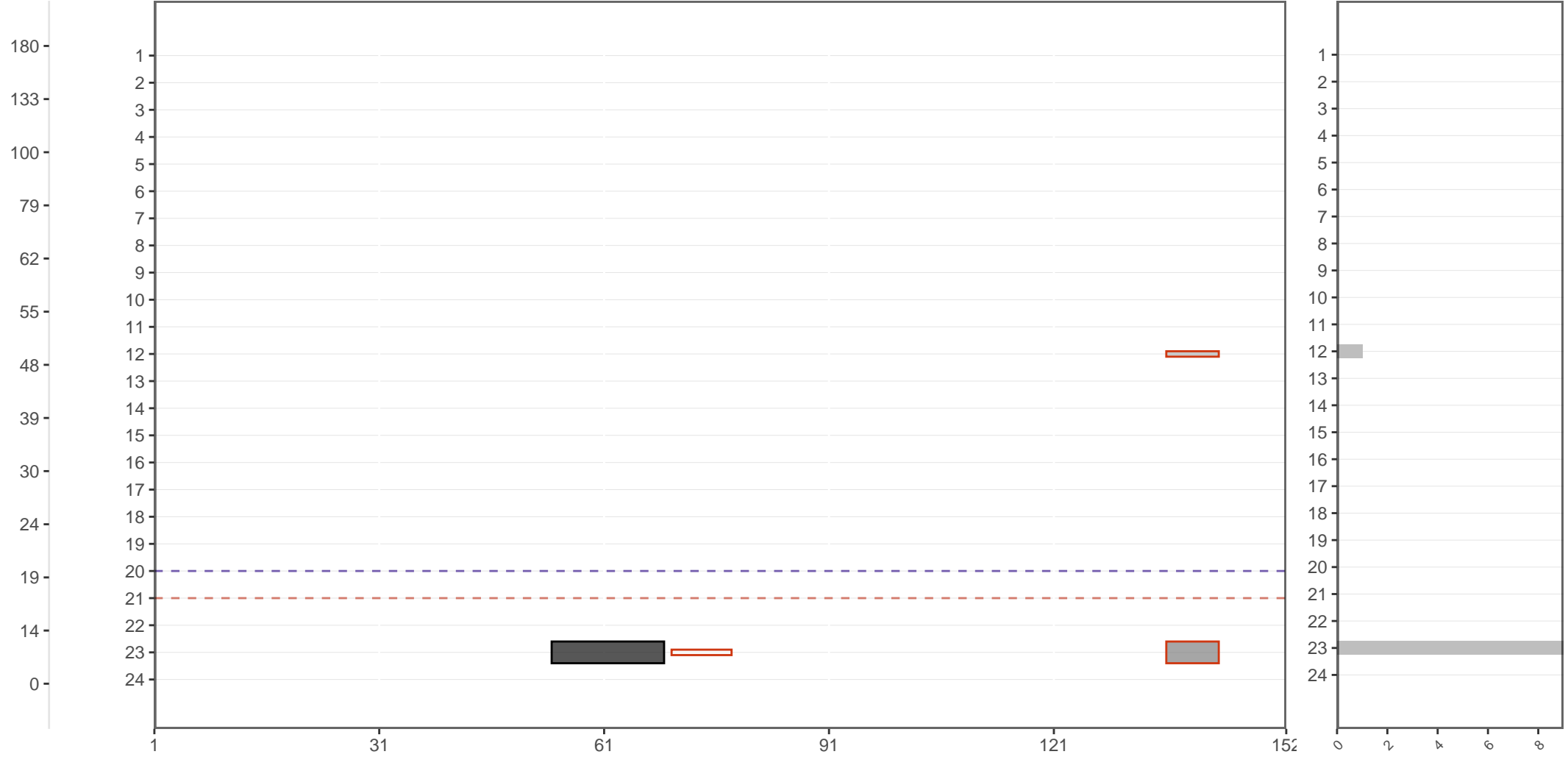
GNGENKGAETASFSFQQL666QNAFTGLAGTGFNNTFFSFGASSKESPLGSGGLFGVKSDGDFPGLNLSTNGNALSIFGNKGS66RVNKGEGEIPKMGVEFVETGSEENKAIFTADALFEFLNGGWKERKKGELKWNISSTETGKARLVLRTRGNYRLINANLYPEMKLTMKDKGVTFAGMNSAGDQKDGLETLAKFKDASIEEFRAVVAHEKDKMPGSLKTPQNSD

NbL09g10840.1 protein_CURVATURE_THYLAKOID_1C_chloroplastic-like [MW = 16.68 kDa]

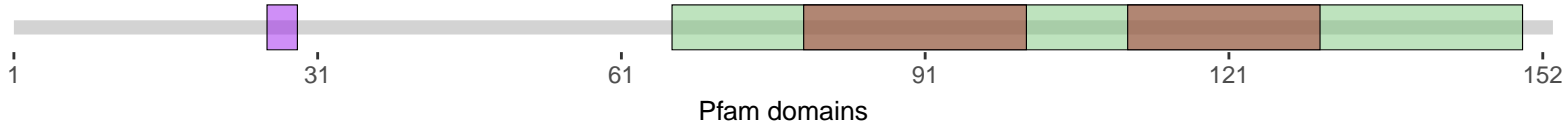


Molecular weight

Gel Slice



Protein length



Pfam Description

SP Sequon TM Domain PF14159 CAAD domains of cyanobacterial aminoacyl-tRNA synthetase

Protein sequence:
SSVVQSVKNIWDKPEDRWVWGLGAAVGFVWASNLAAIDRLPLPVSVEFVGLFSWVYRVYLLFKPKRKELFQAISKISDILGQI

NbL09g10830.1 golgin_candidate_5 [MW = 112.09 kDa]

No. of times detected



log(intensity)



Values from



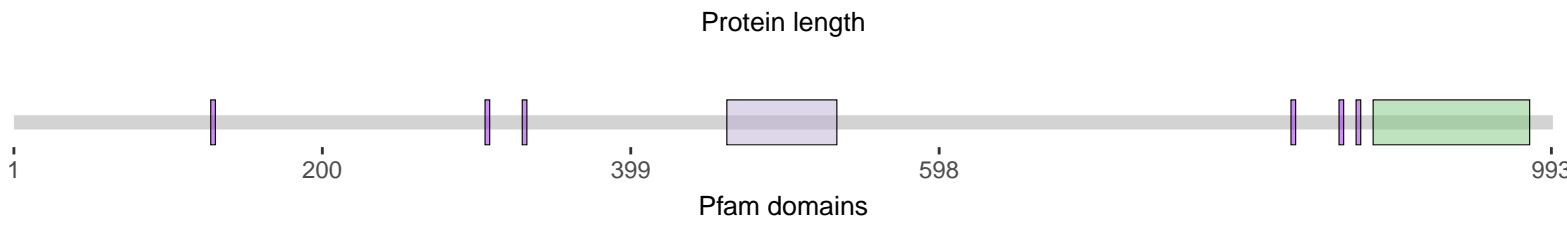
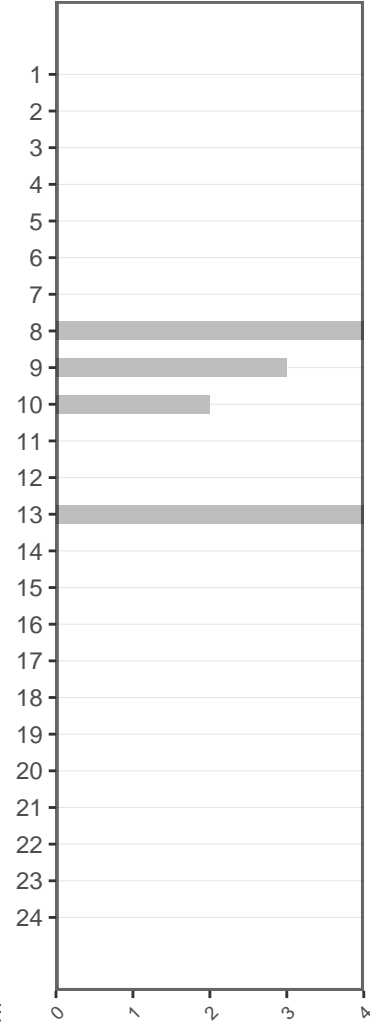
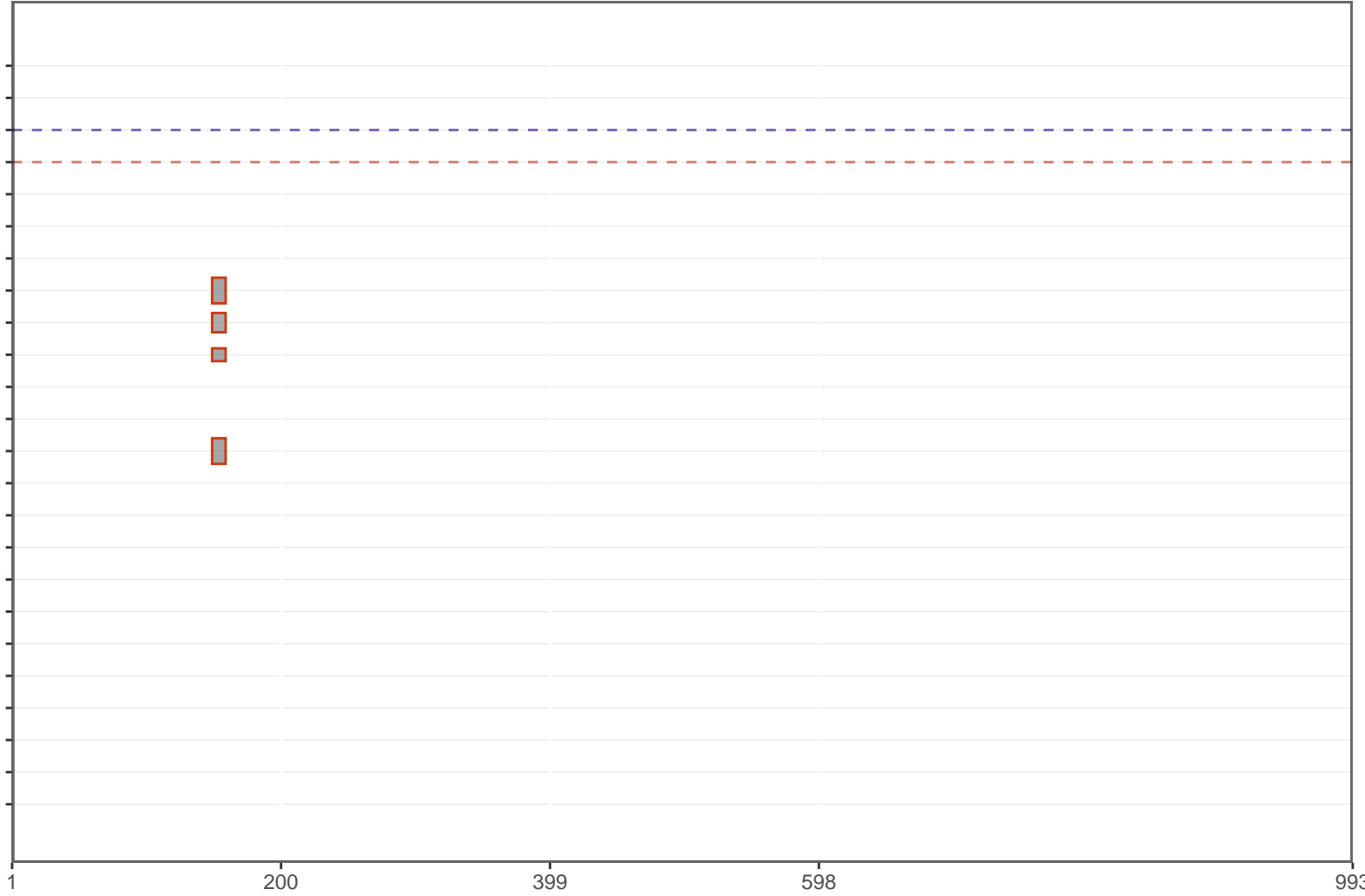
MW indication



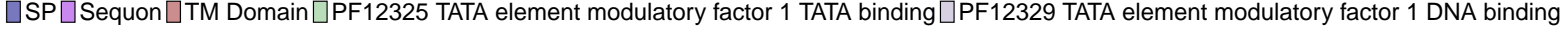
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

IQLSKYDAQAEADMRLKLRAGIRELEEEKGLLTKLLEVENKVESIKRRDKAATEKLLHETVEKHQAEIQTQKDYFTNALNAREAEALAEARANNEARTQLEGRLEAEADREAMLVDALEELRQTLRSRTQDAVFRFEDMLRRDIEDLQKRYQASERRGCEELTGVPESTRPLLRGIEAMQGETNARKTEAWAAVVERTLNSRLQEAEEAKATAEKKERSIGERLSQTLSRINVLEAGISGLRAEQTLRGLDKERQGRAGENRQEVYALKEEAETNEGRVNLQLEEEIKVRSRHKI

NbL09g10720.1 hexokinase-2 [MW = 54.34 kDa]

No. of times detected



log(intensity)



Values from



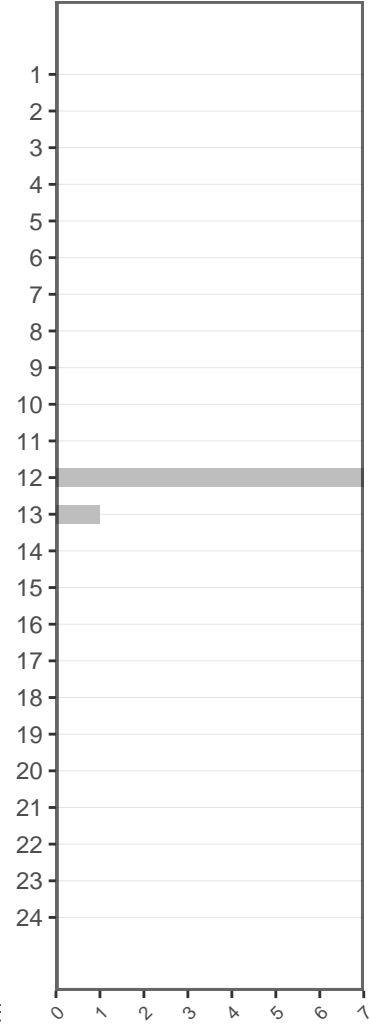
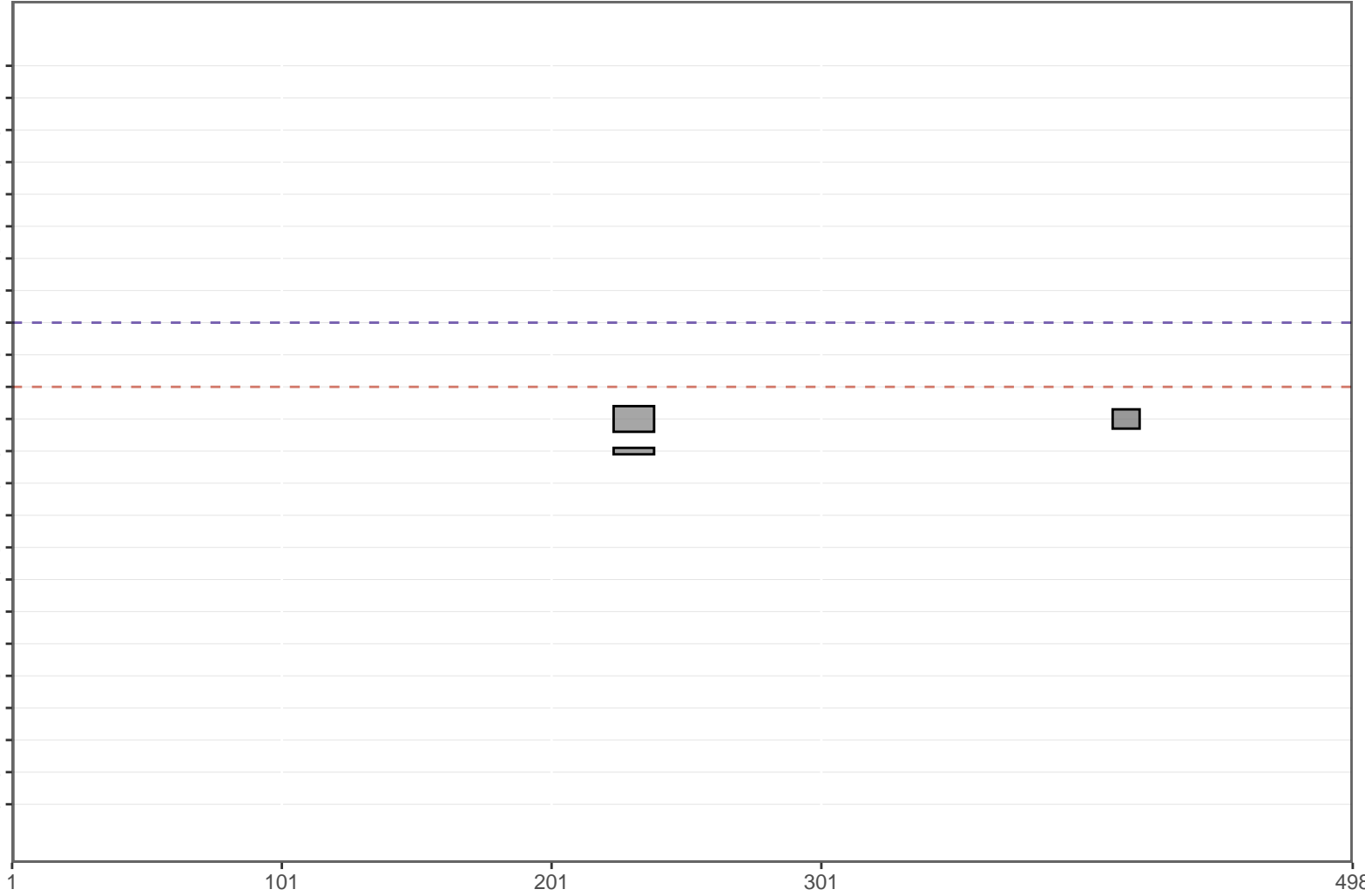
MW indication



Molecular weight

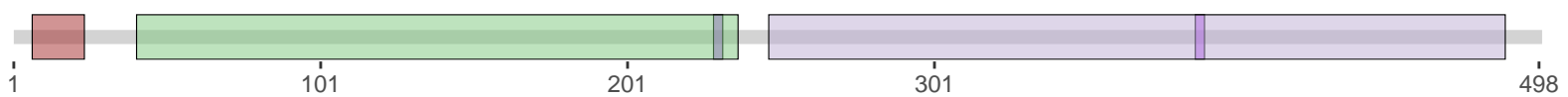


Gel Slice



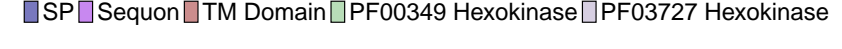
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LAGGRFSNKDYSIIVLGTGTNAAYVERAGAPKWHGPLPKSGEMVINMEWGNFRSHLPLTEYVDHAMDTSLNPGDFEIKIGSGMYLGEILRRVLRMAEEDAFDGEVPPRLKNGFLRTPEMSAMHHDTSDDLRVVGDKLKDLKILEISNTSLKIRRVLVELGNVATRGARLAAAGVLGIVKMGDRDTPRESGGGKIVVAMDDGLVYHYTEYRKLKLENTLVELLGEEMTSVFEHNDGSGGSAALLAASNSLYVEDK67

NbL09g10590.1 ESCRT-related_protein_CHMP1A-like [MW = 22.65 kDa]

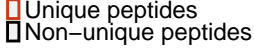
No. of times detected



log(intensity)



Values from



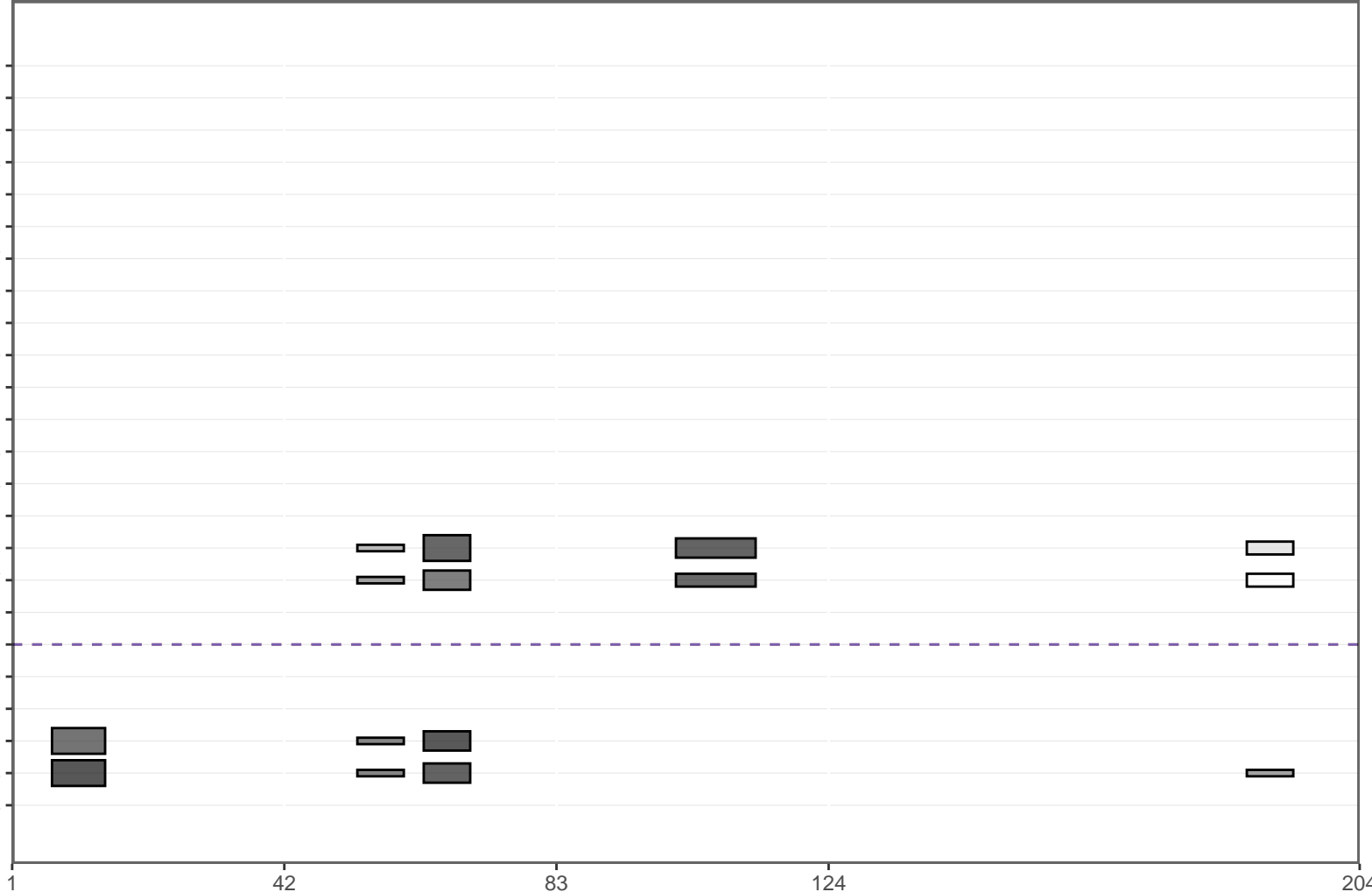
MW indication



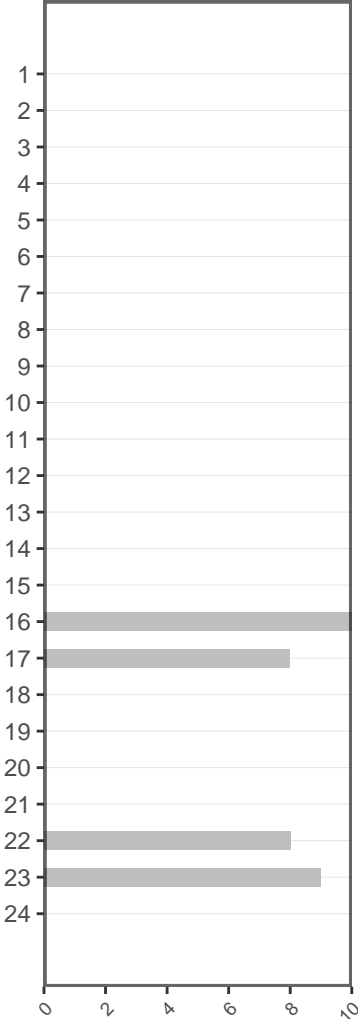
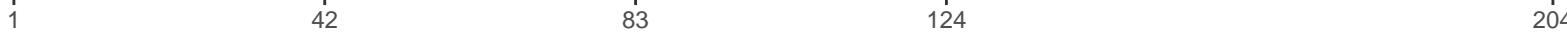
Molecular weight



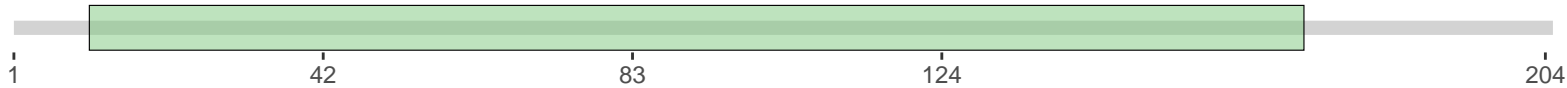
Gel Slice



Protein length



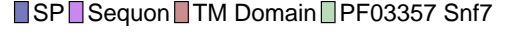
Peptide counts over 4 repeats



Pfam domains



Pfam Description

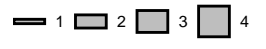


Protein sequence:

TTSKSMSSIVKLSLESLLNTGNLQKMEETMDGFERGFVNMVEVGAEFMESSMAGTSLSTPTFDQVGLMMDGVDDVGLGVSVGLPQPAHNSISKNEKVNEDDLKRRRLAELEKARG

NbL09g10540.1 beta-galactosidase-like [MW = 93.89 kDa]

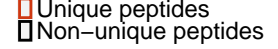
No. of times detected



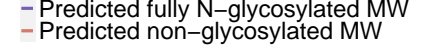
log(intensity)



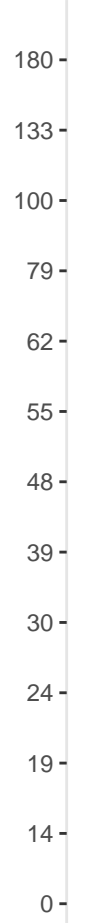
Values from



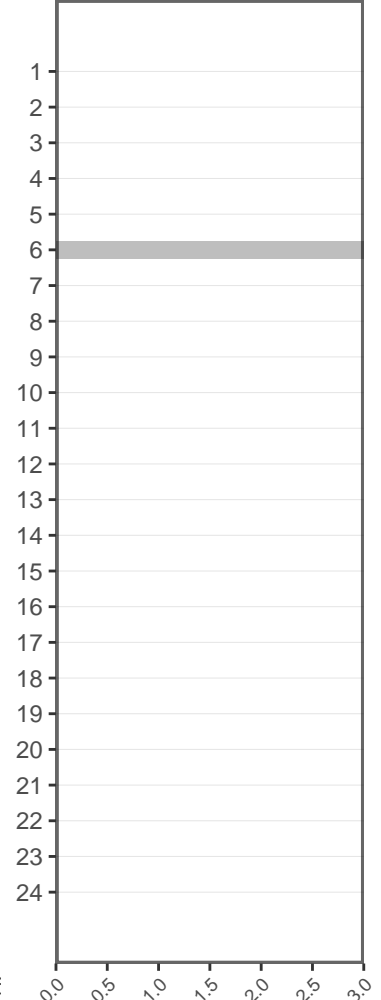
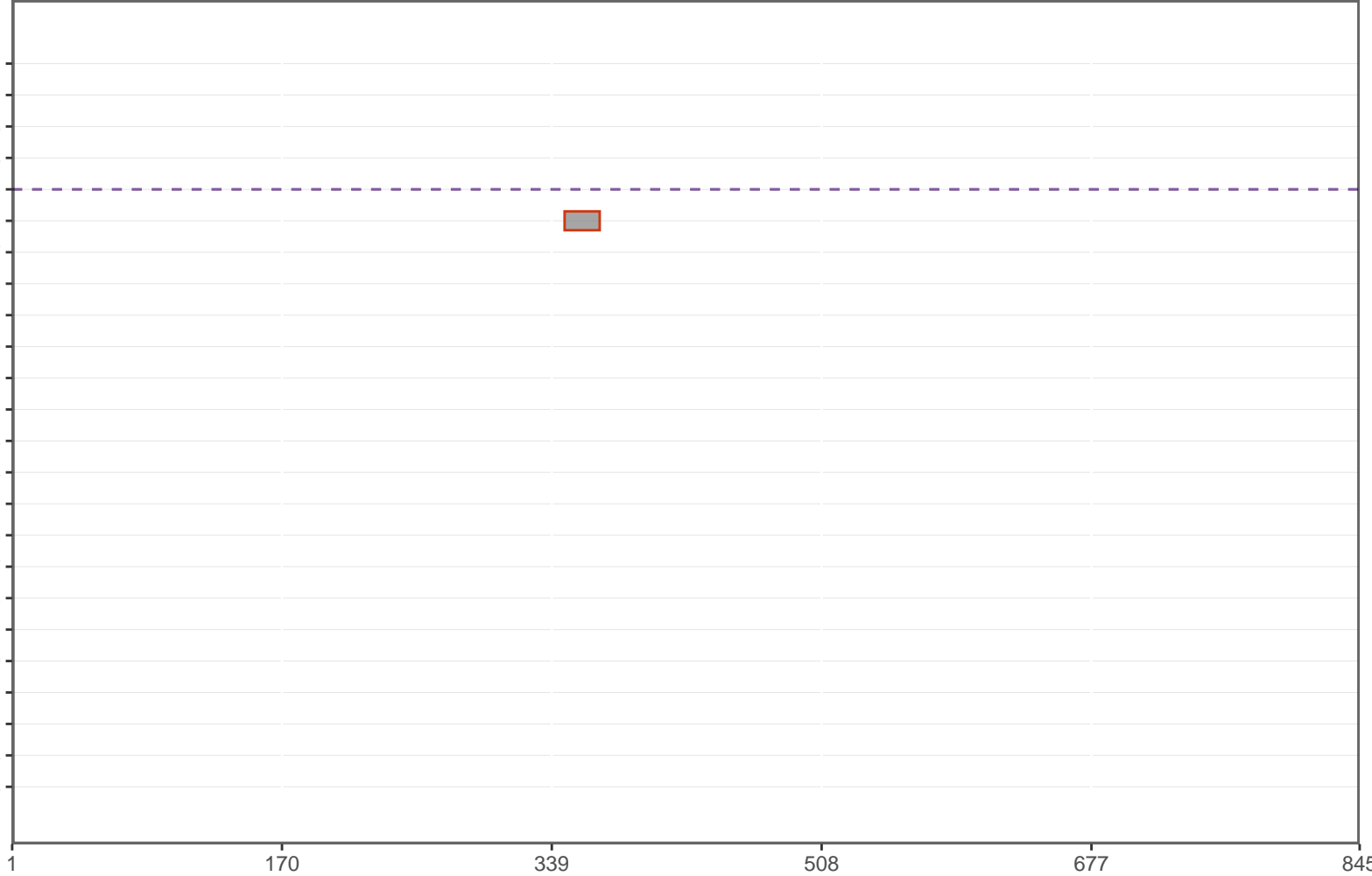
MW indication



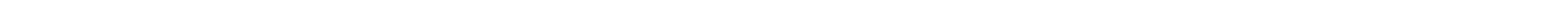
Molecular weight



Gel Slice

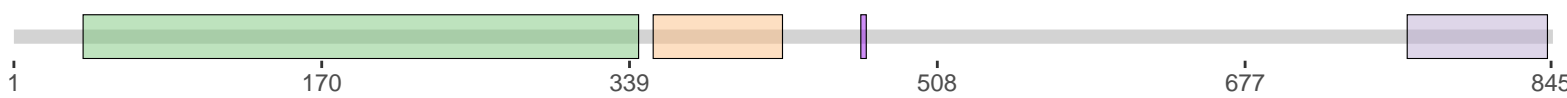


Protein length



Peptide counts over 4 repeats

Pfam domains



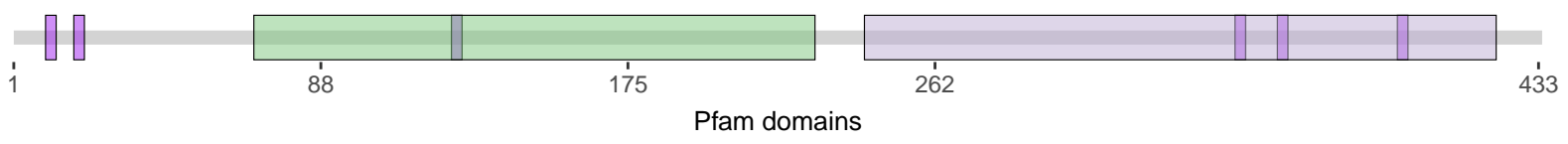
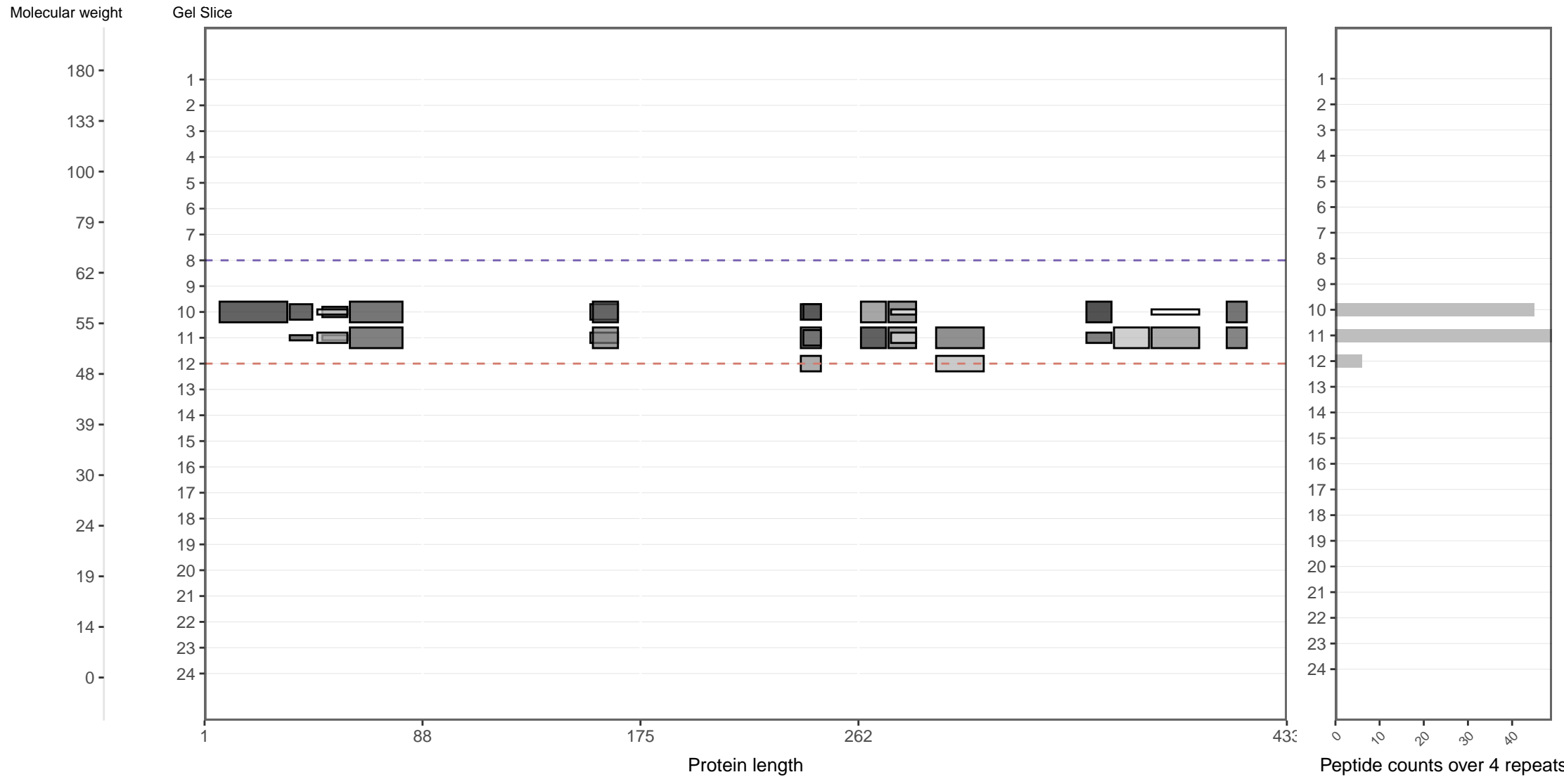
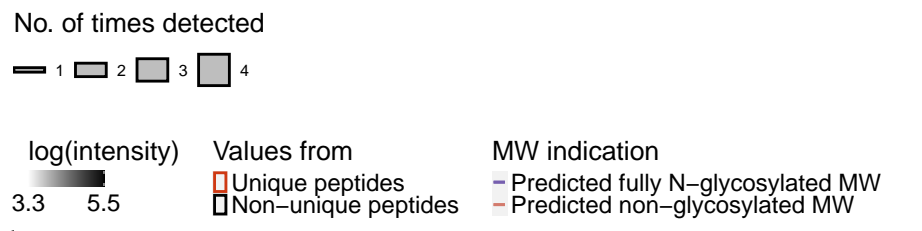
Pfam Description



Protein sequence:

DKNTLYNTARVCAQDALMKMTPVNRGFSWGSYNDPEASVEDNFTFVGLLEQINTRDSDVLYMMDKIDPREGLRSGKWPWLRVSSAGPALHVFVNGLQACTVYGSGLKSGKTFNKAVNLKAVLRAGVNRKLLLSIAVGLPNIQPHFETWNTGILGFVLSGLDEGKRDLTWQKWSYKVLKGEALNHLGLGSSSEVSEWVEGSLVAGRQPLTFWRTFTFNAPAGNEPLALDMMNAMKGGQVWINGDGSIGRVPQYKASGTGGAGNAGYFNEGKGGNCEATORWYH

NbL09g10400.1 glycylopeptide_N-tetradecanoyltransferase_1-like [MW = 49.66 kDa]



Pfam Description

- SP
- Sequon
- TM Domain
- PF01233 Myristoyl-CoA:protein N-myristoyltransferase, N-terminal domain
- PF02799 Myristoyl-CoA:protein N-myristoyltransferase, C-terminal domain

Protein sequence:

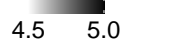
TRRVLKNIWCAAYTAGVLLPTTSTGGVYHRLBNPKKLDVGFSLGPRMTMSRTIKLYKLPDGTVPGRFRMEPHIVVTRLLRNLYKGFAPDFDENDEVEHWLLPKEDVYDSEYVSESTHETHTDFGDFYTLPSGLGNVSTLKAAYSYVNSTKTSWGLMNDALVAKGKDFDFVFNALDVMHNETFLKELKFGDGGKLYHYLYNRLKHVLRSEELGLVLL

NbL09g10390.1 glycylopeptide_N-tetradecanoyltransferase_1-like [MW = 49.76 kDa]

No. of times detected



log(intensity)



Values from



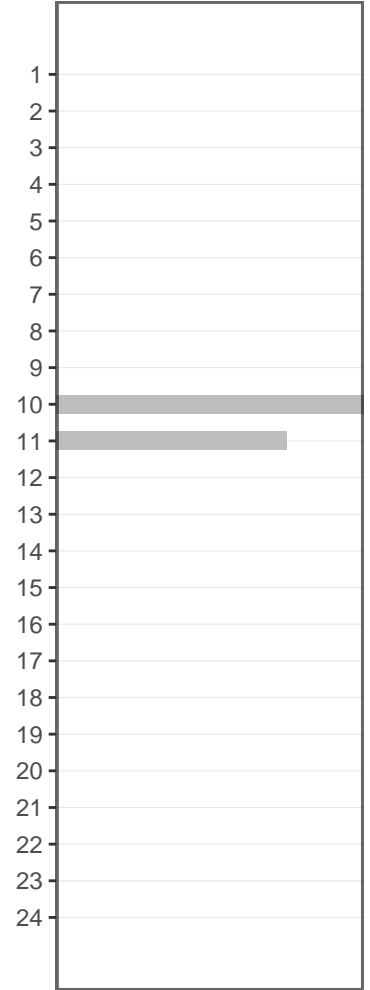
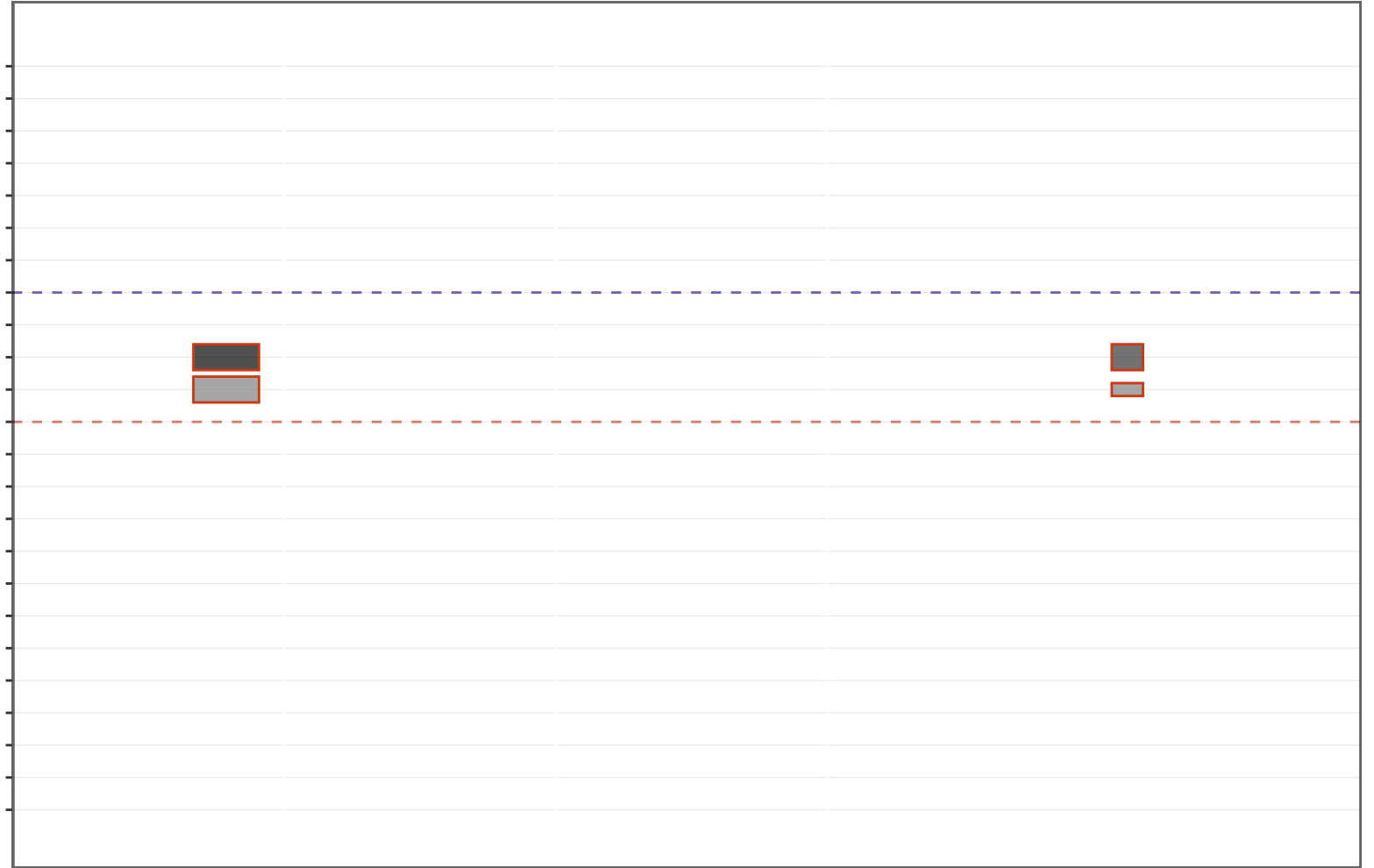
MW indication



Molecular weight



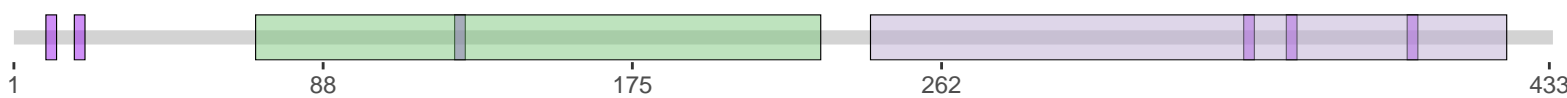
Gel Slice



Peptide counts over 4 repeats

1 88 175 262 433

Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01233 Myristoyl-CoA:protein N-myristoyltransferase, N-terminal domain
- PF02799 Myristoyl-CoA:protein N-myristoyltransferase, C-terminal domain

Protein sequence:

TRRVHLENWQAAVYTAGVLFPTTSTGGVWHRBLNPKKLIIDVGSRLGPRMTMBRTIKLYKLPDQTVTPGFRKMEPHDVPWTRLLRNLYKGFAPDFDENDEHLLPKEDVYDSEVSEPTHEITDFGDFYTLPSGLGNQYSTLKAAYSYVNSTRTSWQLMNDALVAKGKDFDFVNALDMMHNETFLKELKFGPGDGKLVYLVNRLKHLRBSSELGLVLL

NbL09g10360.1 threonine_synthase_chloroplastic-like [MW = 60.4 kDa]

No. of times detected



log(intensity)



Values from



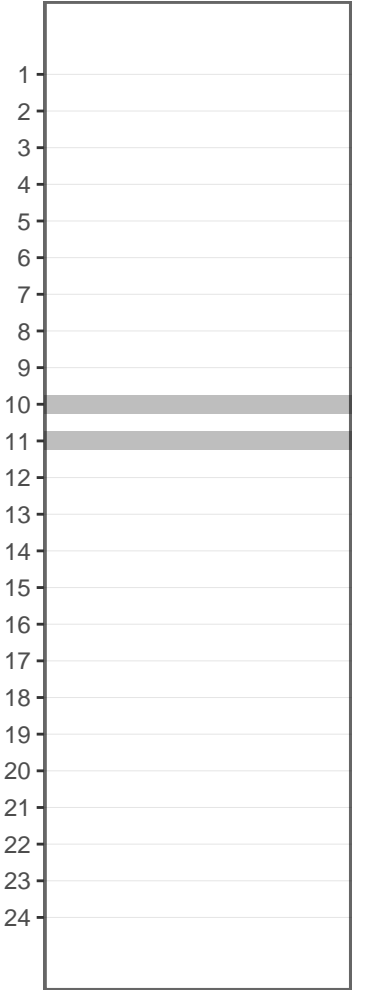
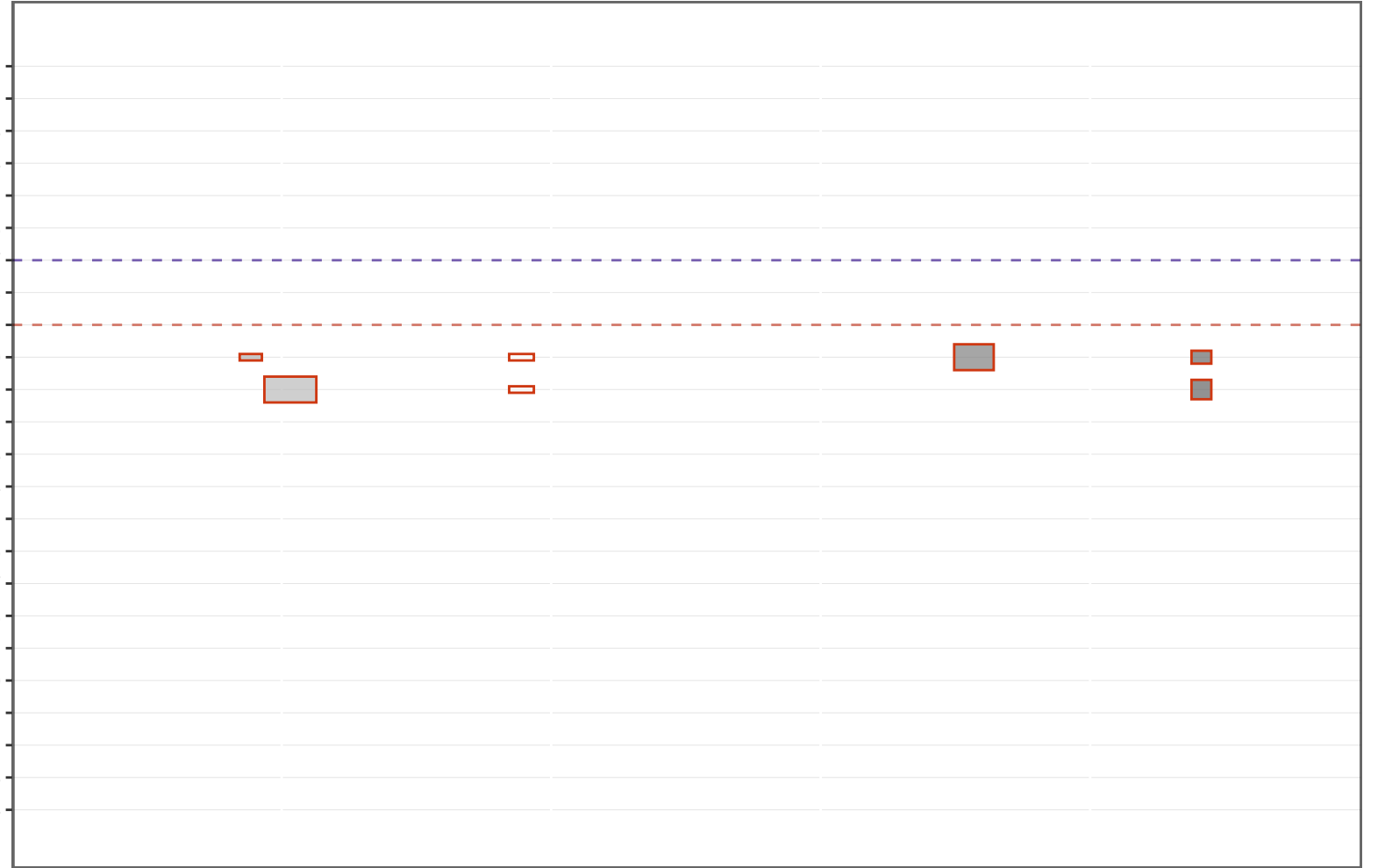
MW indication



Molecular weight



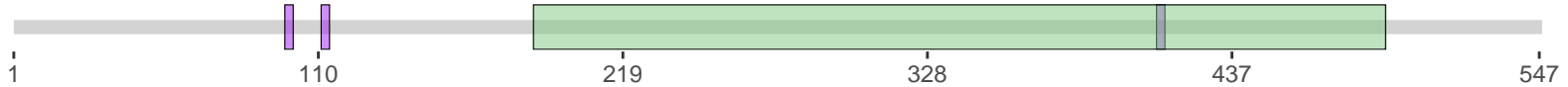
Gel Slice



Peptide counts over 4 repeats

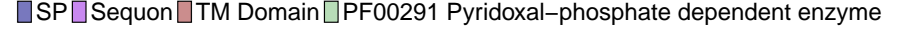
Protein length 1 110 219 328 437 547

Protein length



Pfam domains

Pfam Description



Protein sequence:

TSAAALSAYCASAGIPSPVFLPANKEMAGLQPIANGAFVLSLDTDFDGGMLIREVTAELPFLYLANSLNSLRLEGGKTAALAEIQDFDWEVDPVVWIPGGNLGNVYFYKGFQDMCKELGLVDRIPLRVGAGAAANPLYLHFKSGWKEKVKKANTTFASAIGKDFVSDRAVYALKNNGSIVEEATEEELMDMAGADSTGMFIFGPHGVALTALSKLRKGVIRPTDKTVVSTAHGLKFTGFRVQVHSHKEIKNMEGRFANRPVQVKAADFQGMVMDLKKYLLSKNSKFP

NbL09g10160.1 alanine_aminotransferase_2-like [MW = 59.35 kDa]

No. of times detected



log(intensity)



Values from



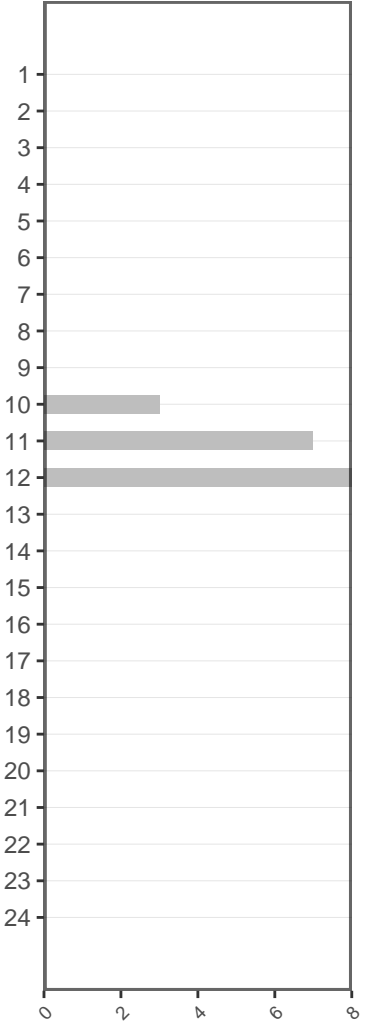
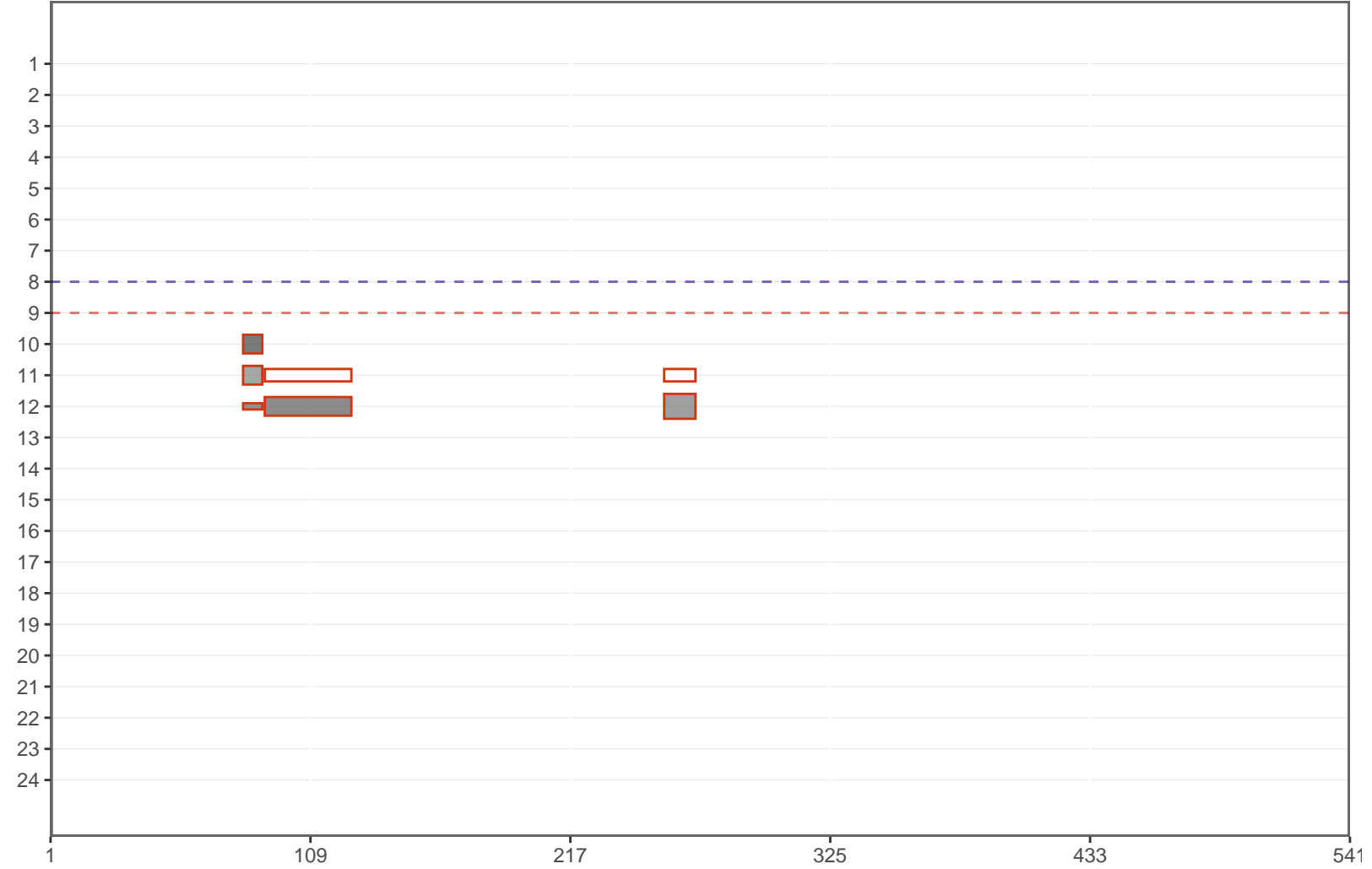
MW indication



Molecular weight

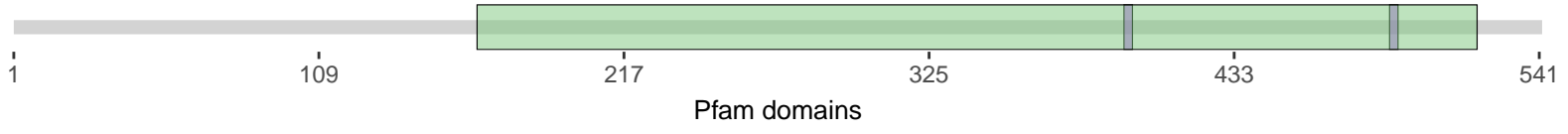


Gel Slice



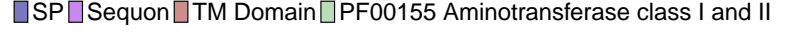
Protein length

Peptide counts over 4 repeats



Pfam domains

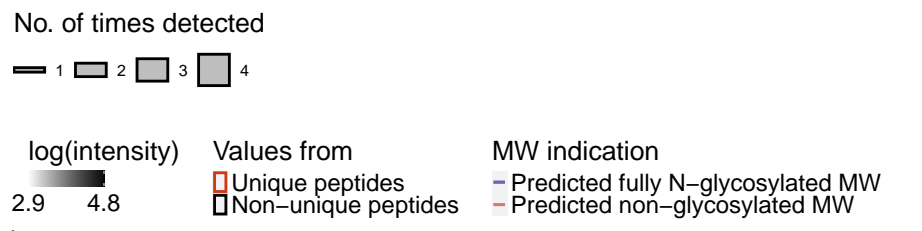
Pfam Description



Protein sequence:

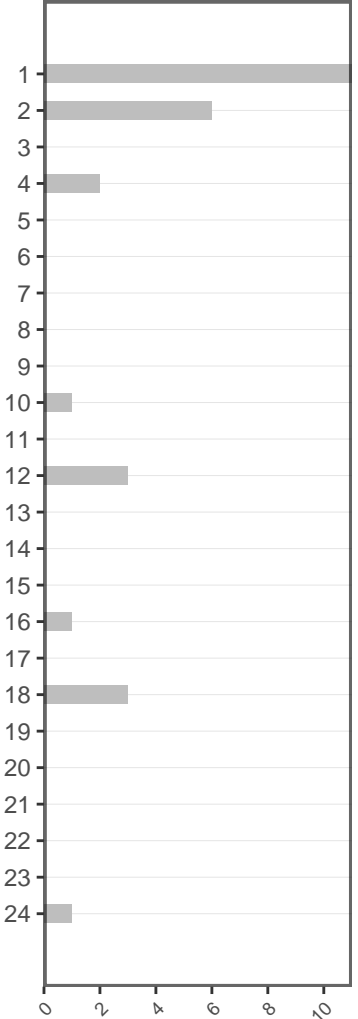
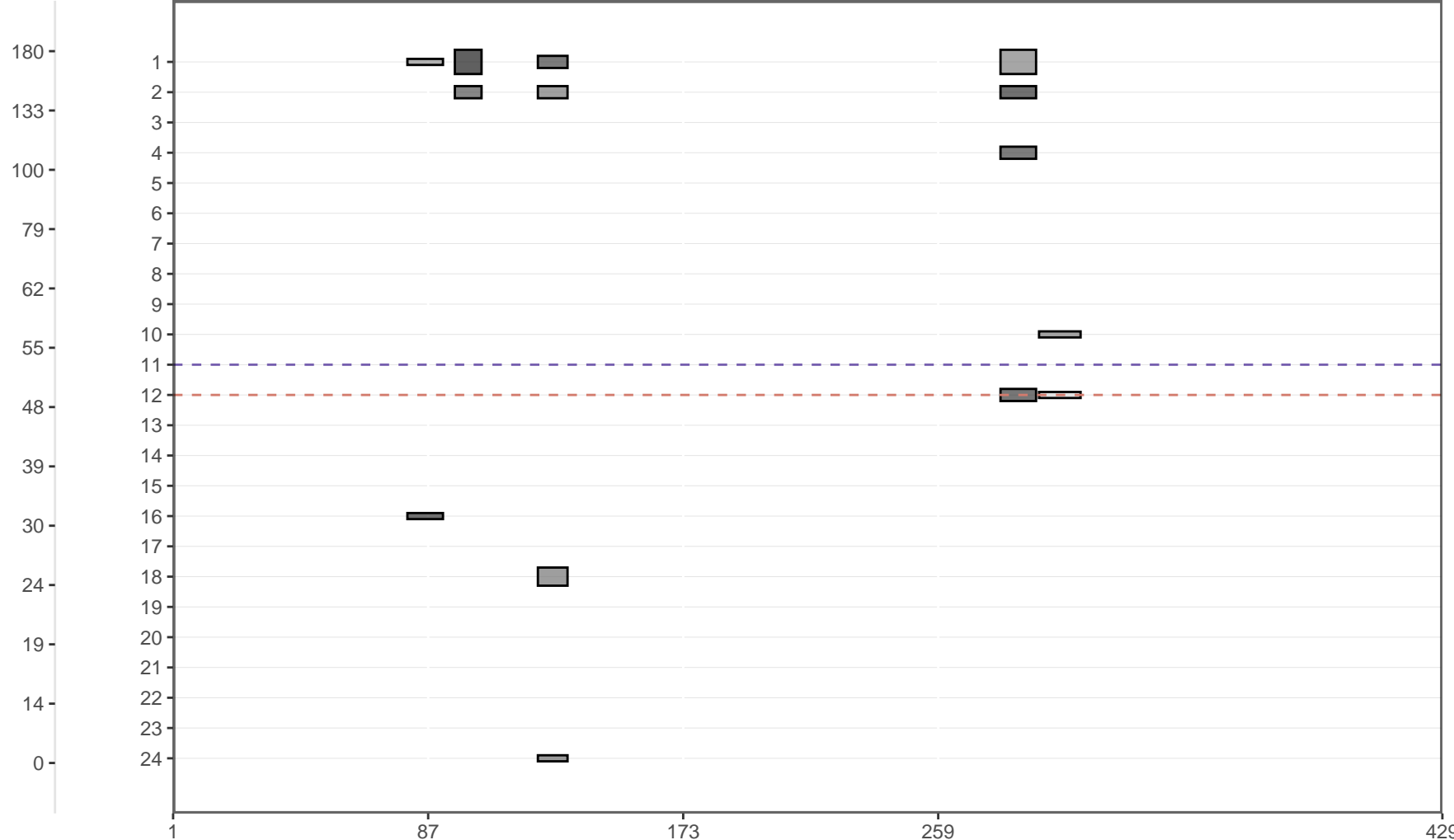
EISELEQQQLTAKSKGIDVRLVYVNPQPTGQVLGEANGRIEVEFKKREGLVLADEVGVENYVYPPKKFHSFKVSRSMGVGKDHLSVFGSVEKGFYEGEGKRGQGVMEVTFGFEVREQHYKVASVNLGNSGGQLABLMPKPKVGDSEYVESFAEKEGILSLLARRAKTLEDALNSLEGVTONRAEGAMVLFPRVNLPNKAVAAEAAKTAPDAFYAKGLLNATGIVVYFGSGFRQVPGTWHFRCTLPDQEEKPVAVSRITFEHEKFMNEFRG*

NbL09g10120.1 26S_protease_regulatory_subunit_7_homolog_A-like [MW = 47.77 kDa]



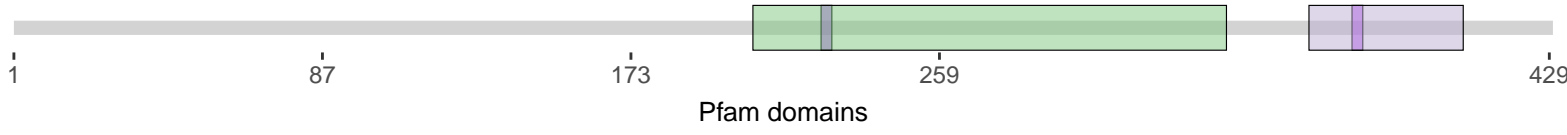
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain PF00004 ATPase family associated with various cellular activities (AAA) PF17862 AAA+ lid domain

Protein sequence:

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NbL09g10030.1 mannosyl-oligosaccharide_12-alpha-mannosidase_MNS1-like [MW = 56 kDa]

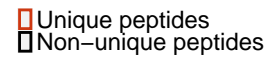
No. of times detected



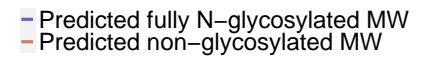
log(intensity)



Values from



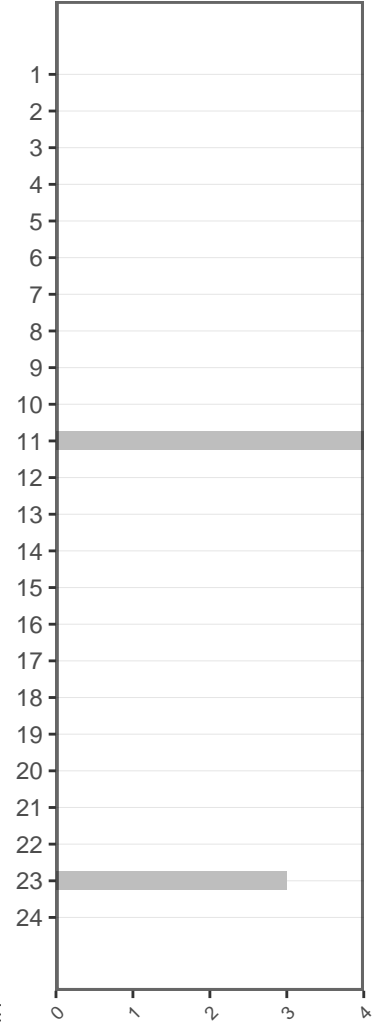
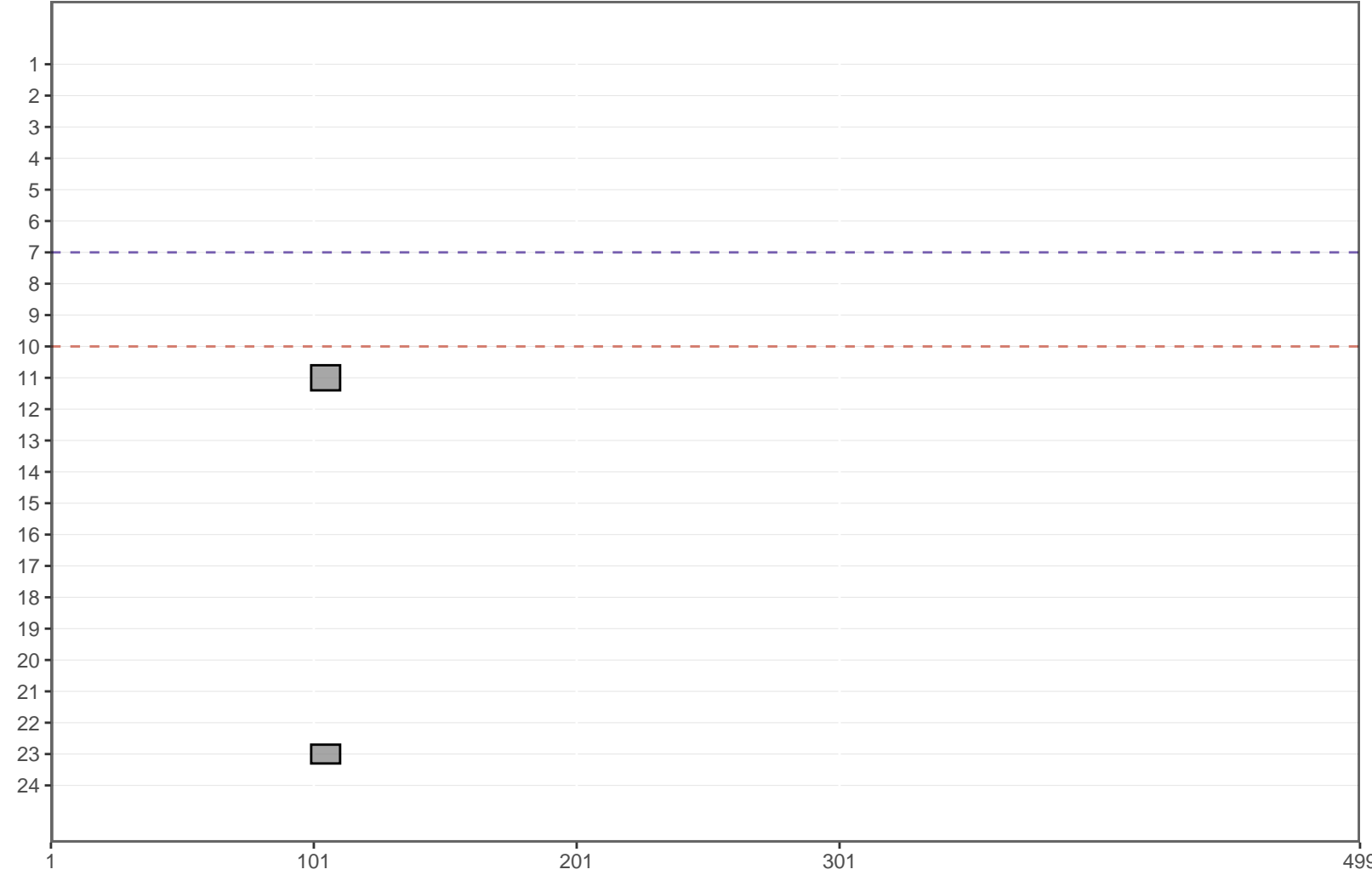
MW indication



Molecular weight

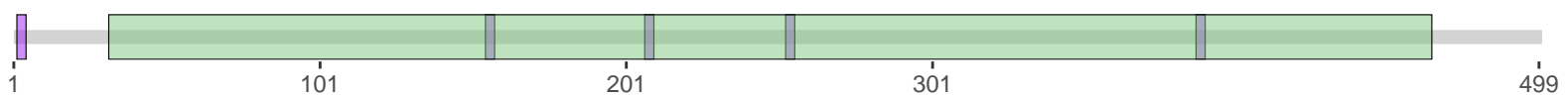


Gel Slice



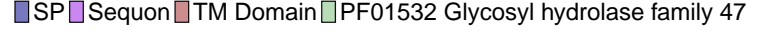
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DSFYELLKAWIQNGSTAVVGHYRKMWETSMKGLLSLVRRTTPSFAVIGEKIGSLNDMMDELACGAFAPGMLALGSSGYPESQKFLGLAEELAWTFQNFYQSTPTKLAGENYFFNDGGDMFTVGTSWNLRPETVESLFLYWRITGNKTYGEVQWVNFQAFENKSRISGGYVGLKDNVTGVRDDMMGGFFLAETLKYLLLFSPGSLPLDEWVWNTAHPRIWRSRNDPWVSSGRVGGAKYKQPRVRRREGFGNK

NbL09g10010.1 uncharacterized_LOC109227356 [MW = 44.98 kDa]

No. of times detected



log(intensity)



Values from



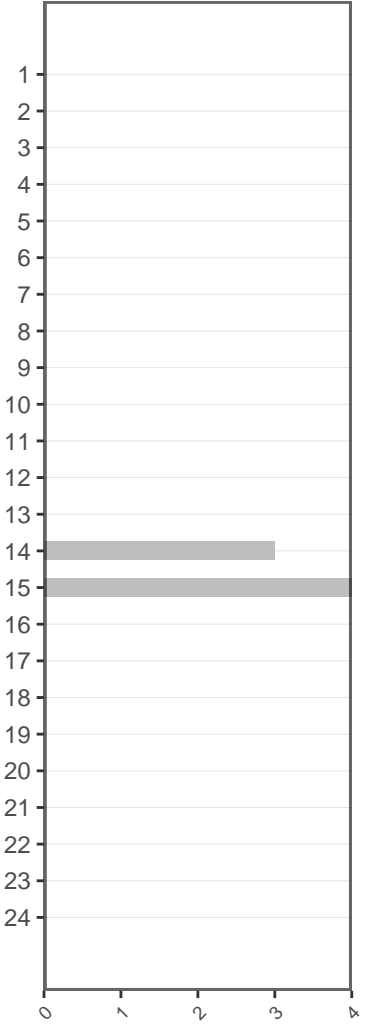
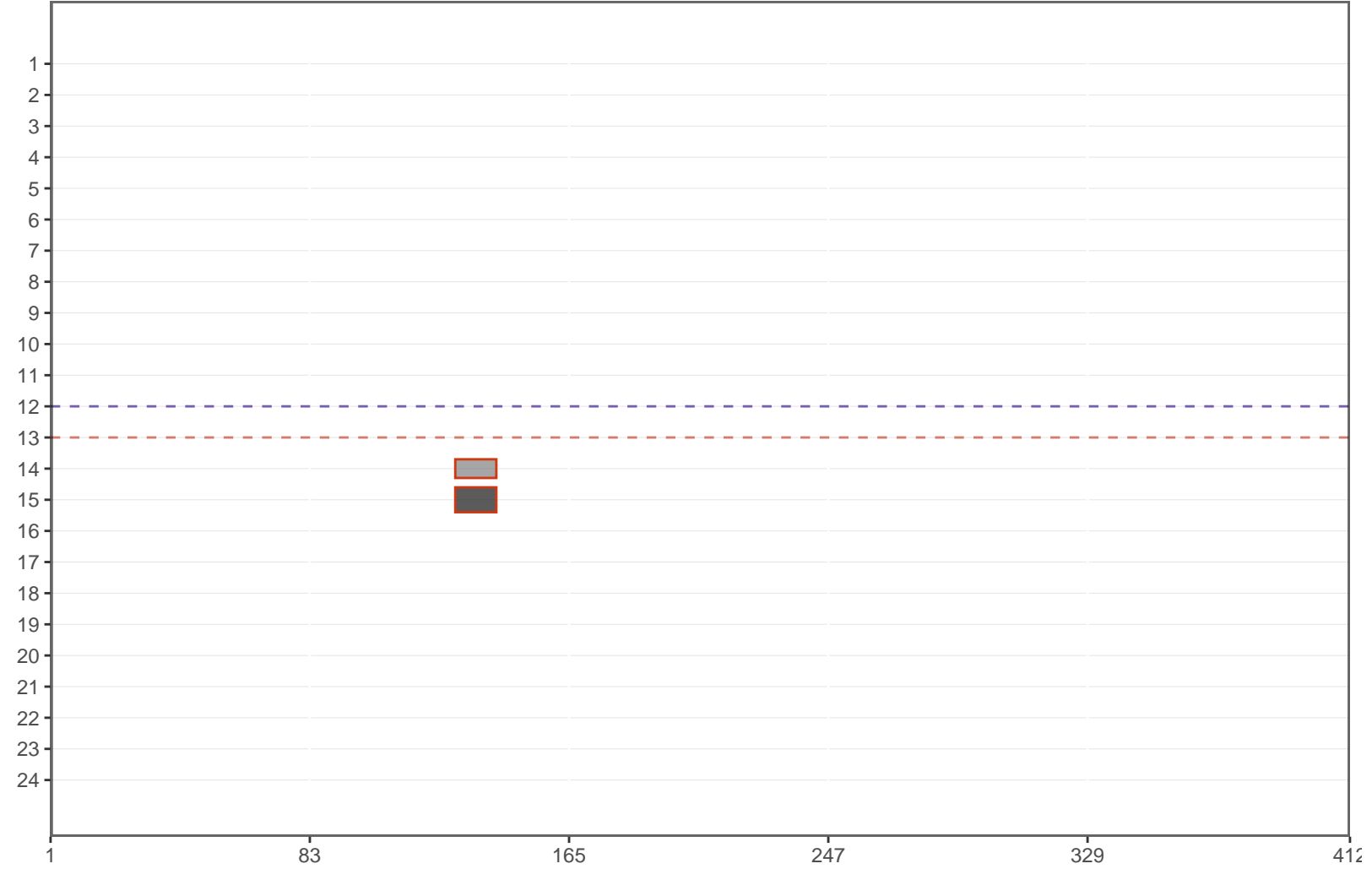
MW indication



Molecular weight

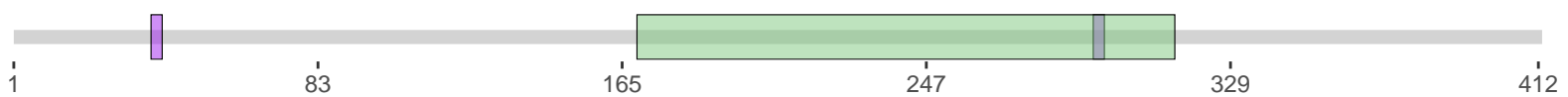


Gel Slice



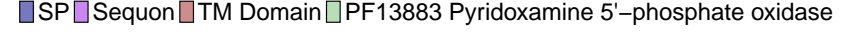
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

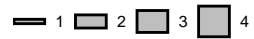


Protein sequence:

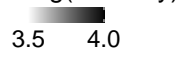
RREGYPTFGLVDFAPDSMGHPFISFSLAHTRNLLADPRCTLVVQIPGWISGLSNARVTFGGDYVPLPEDQQAIAWAHKGQYIAHQQGPFSGQWGNFFYFRMGNISDIYFISGGFTVWVWVWVKEVETLQPDNIAVDGEGEQLKELNAFISKPLKDLLEGSEVDDAALISIDSKGTDVRRVRRGGQGFNQRISFEVSHVGTLEEAKAAWKLINGGGVYVNLQK

NbL09g09970.1 V-type_proton_ATPase_catalytic_subunit_A [MW = 200.76 kDa]

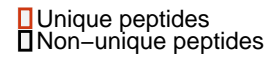
No. of times detected



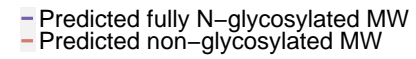
log(intensity)



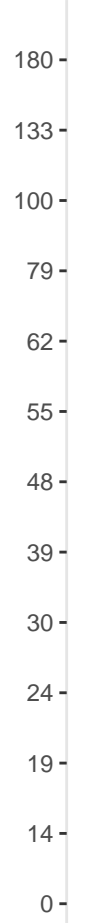
Values from



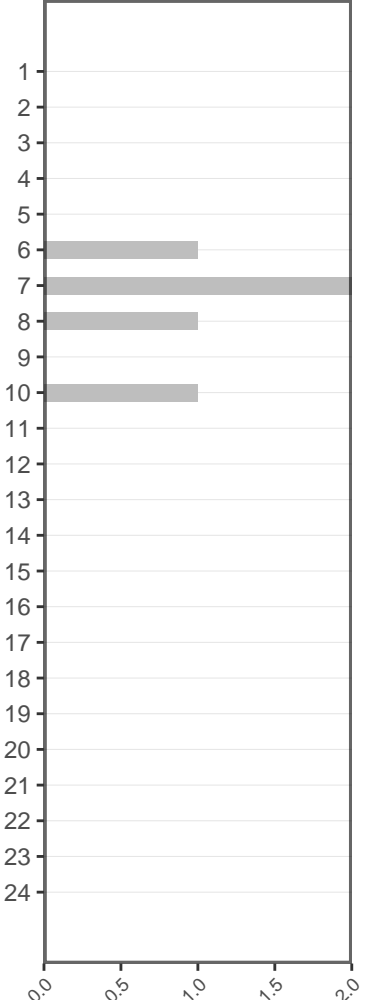
MW indication



Molecular weight



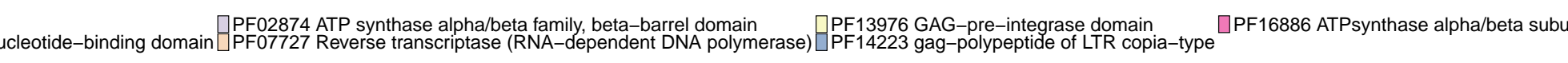
Gel Slice



Protein length



Pfam domains



Protein sequence:

ITGKQLKCLGSDNIGGDTLPGSSMFIADHMAFDMRRRMVWLPKPFWGEAVRAACYLHRSRSPVPLNSEVPEKLVWGGKYPYSYFRIFGCLAYAEKHKVIRKRDVFNHENTQIEDKPTSGKPNVAPPVPEATTEGFMRNEDTVREDFPEVEDNEEEDGFEGGEPQLALPDVPEP6DDDDGGSPHLEVKRKRGRIPRRYRYPESYLLLTEDGEPESFQEAVSHKDKEGWLLAMGGEMESLQKNGTYEVELPKGKALKKNWVFKLKKDDGGRWVKKYKARLVKYGFI

NbL09g09910.1 chlorophyll_a-b_binding_protein_CP26_chloroplastic [MW = 30.41 kDa]

No. of times detected



log(intensity)



Values from



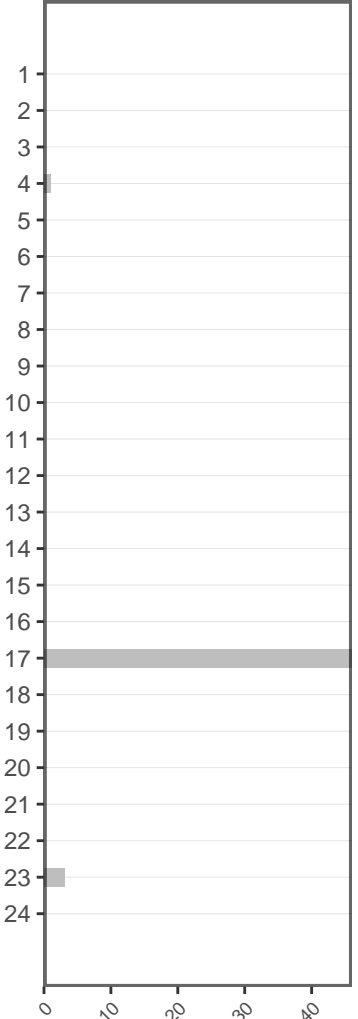
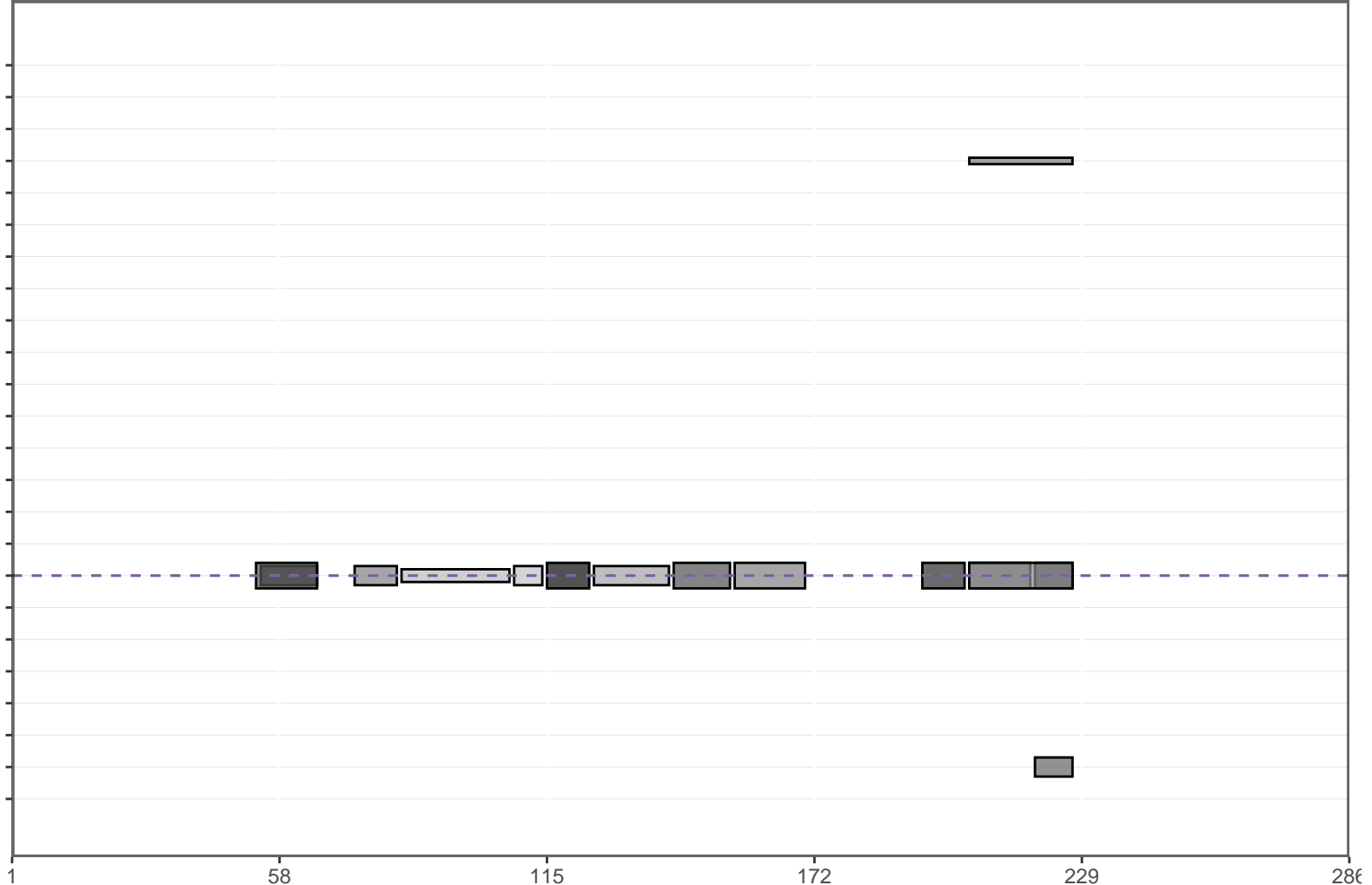
MW indication



Molecular weight

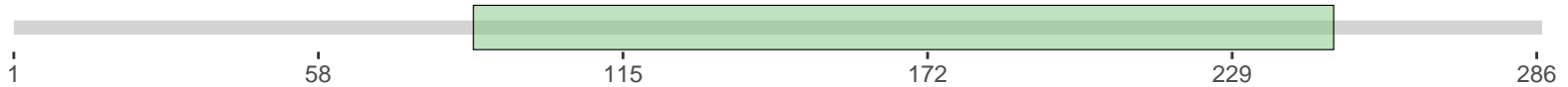


Gel Slice



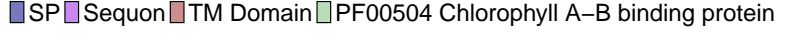
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IAAGFVPEAFNKGADGGPEAWFKTGAALLDQNTLNFQKINPILVWVAWEVLLGGAEYRITNGLDLEDKLHPGGPFDPLGLAKDPDQAALKVKEIKNGRLMFMALGFPIQAVYVGGGPVENLAHLEDFPGNNLLETVIGGTAERVPTL

NbL09g09840.1 trans-resveratrol_di-O-methyltransferase-like [MW = 40.43 kDa]

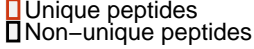
No. of times detected



log(intensity)



Values from



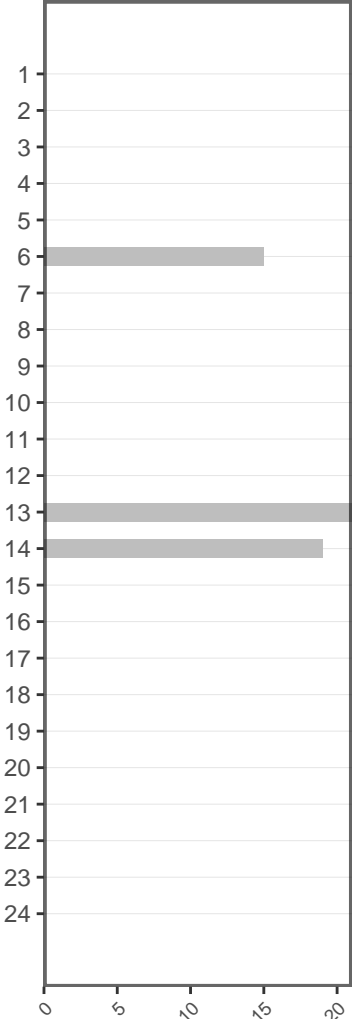
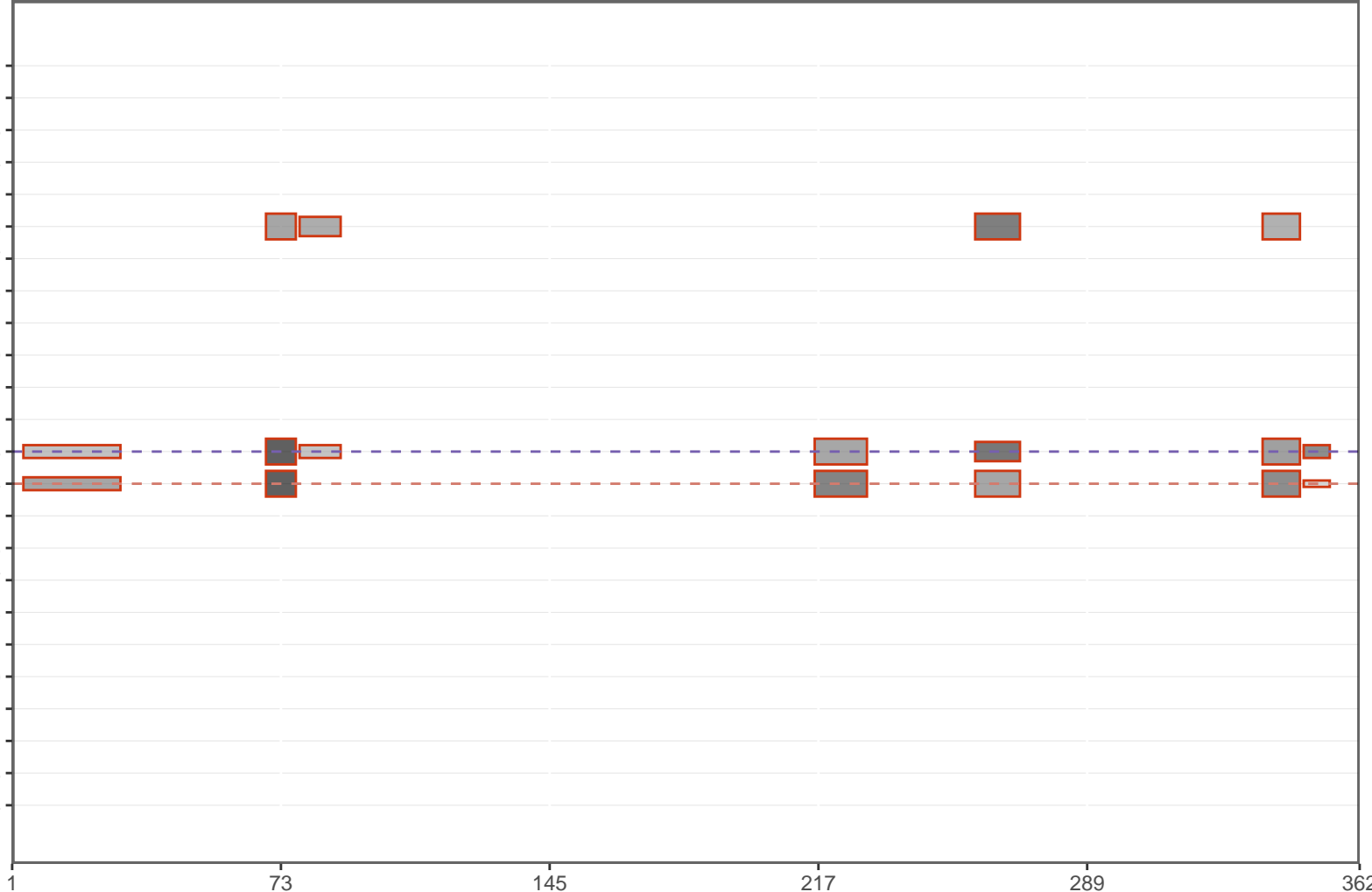
MW indication



Molecular weight

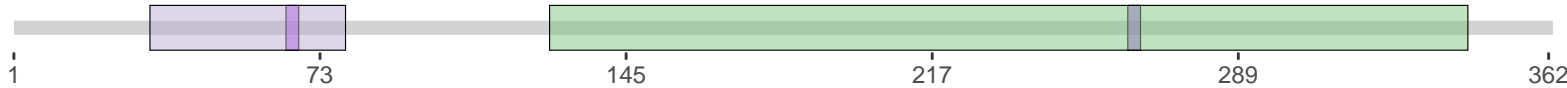


Gel Slice



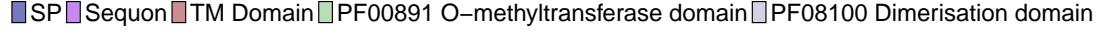
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

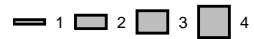


Protein sequence:

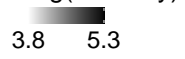
MAASDKLISHLLINSEGDQKHVFEGLTSLVIVGGGTGLMAIANAFPRLLNGVLDLPHVIGDREGITTEVEFVAGMFDNIPYANAVLLKYLHNWSDDEDGVLLKKGRESIPKESKGGKVAIVDVMEDYSSNNINEQLLGVQHLMHVVMKITYGAKERTKTEWKLFLDAGFSEYKWTANFGLRLIEYPT

NbL09g09570.1 patellin-3-like [MW = 63.9 kDa]

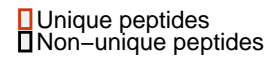
No. of times detected



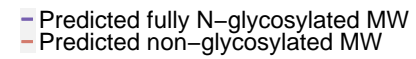
log(intensity)



Values from



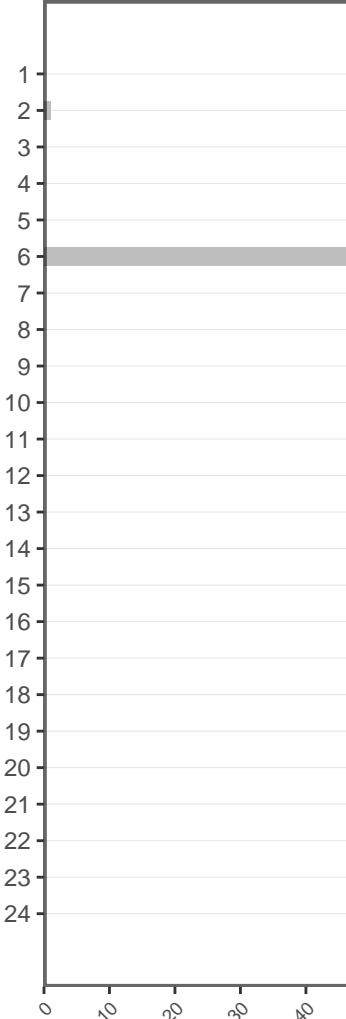
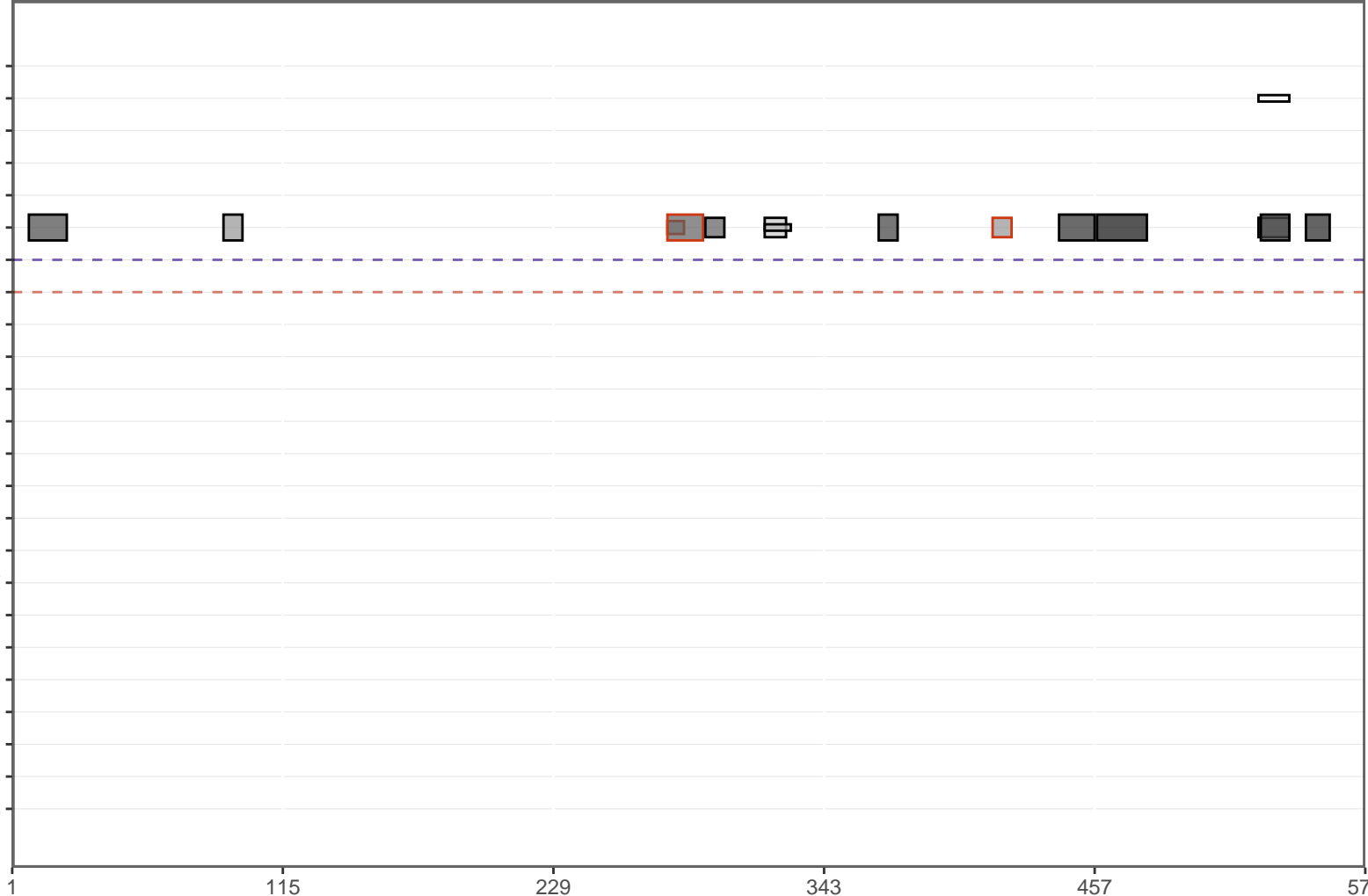
MW indication



Molecular weight



Gel Slice

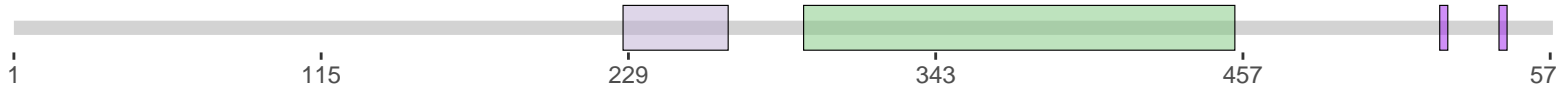


Peptide counts over 4 repeats

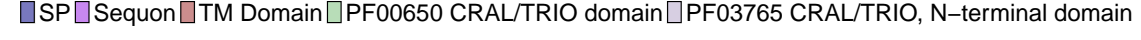
Protein length



Pfam domains



Pfam Description



Protein sequence:

IEFKDLDLDELKELGGLEKVVNYGLDKEGHPGVNAPGEGFNKELVQNTFADKELTKFLRWRIRGFMKESIRNLDFSPDGGICTFVQVIDLKNPSGLFFKFKELRQATNRALQLLQDNYPEFVAKGVFNVPVWYRPRYRMINAVFTTRTKSKFVAGPSRSRSETLTKYITPEQGVPAQYGLSKEGEGEFTVAEPATEDIKKPAKHTIEFPVTEKGLVWEARVTGWDVSVYGAELVPTAEGGYTHIEKSRKVGANETVSNFTYKAGEGKVVITFDNGS6KXKLLVYRSKNKPS

NbL09g09440.1 uncharacterized_LOC104248794 [MW = 13.72 kDa]

No. of times detected



log(intensity)



Values from

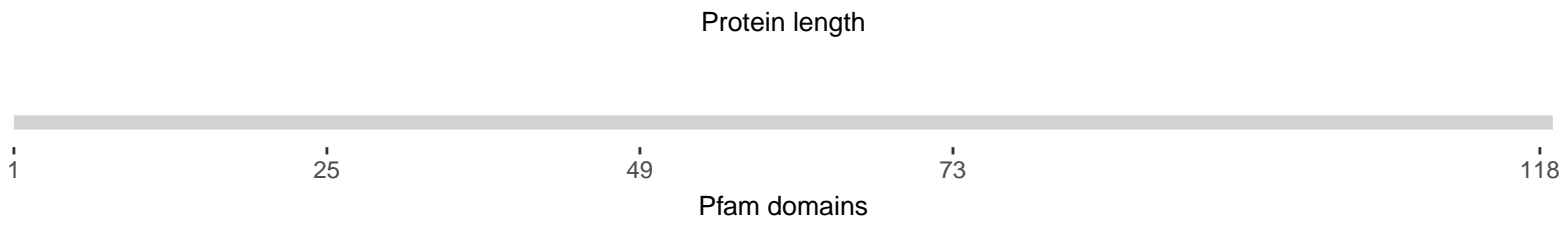
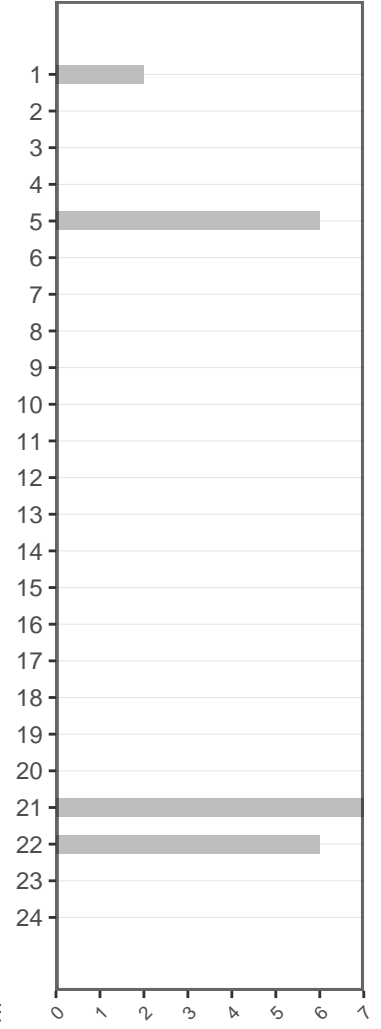
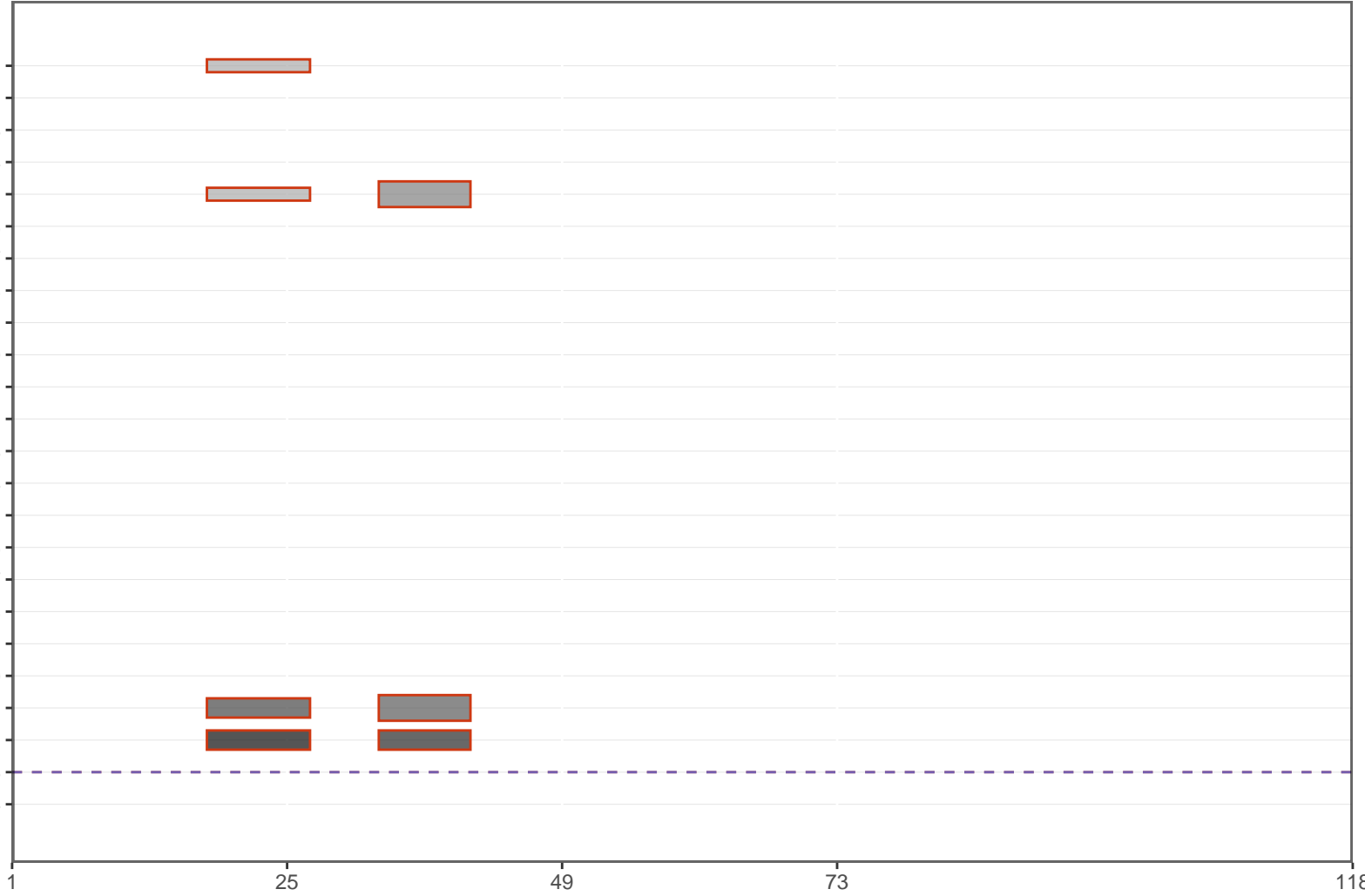
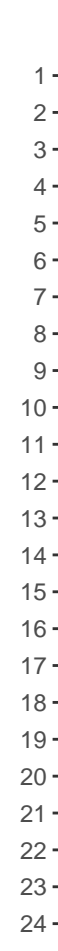
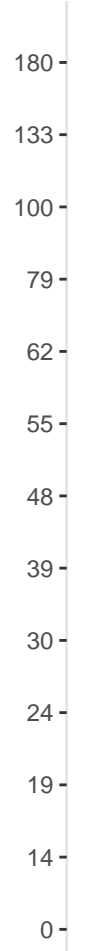


MW indication



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain

Protein sequence:

IREAAWKAEISRREAEIARGEARLKMERENLEKENVLMGTASNDNDGGALEITVSGEKYRGLRFANAKK

NbL09g09310.1 50S_ribosomal_protein_L21_chloroplastic-like [MW = 23.46 kDa]

No. of times detected



log(intensity)



Values from



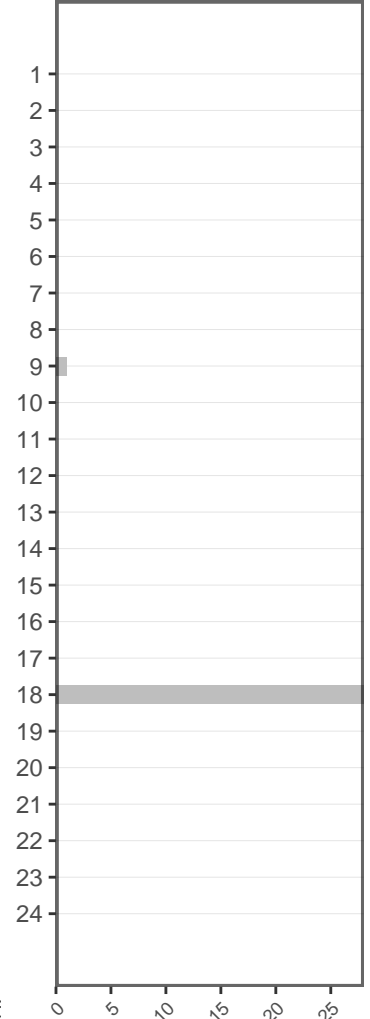
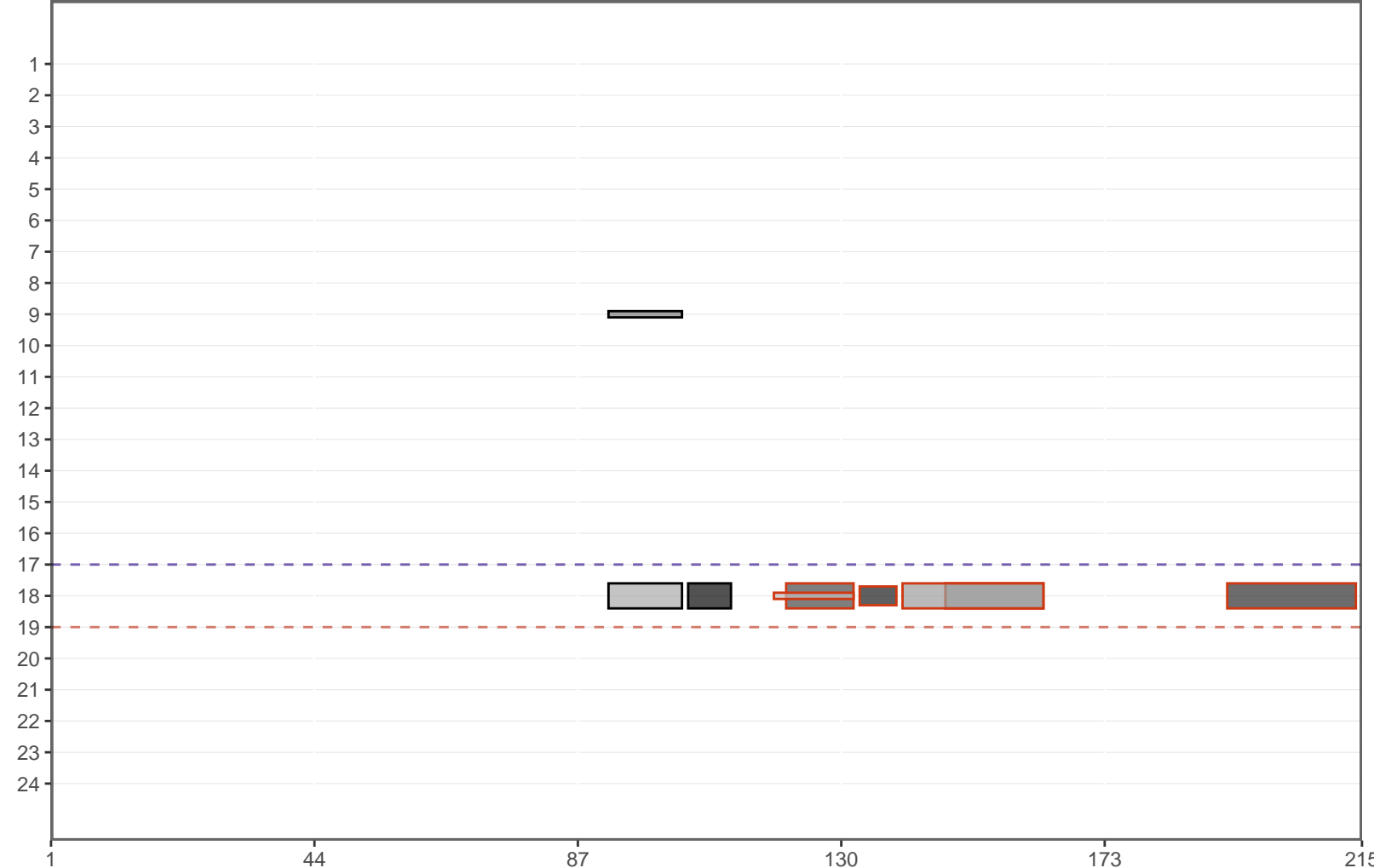
MW indication



Molecular weight

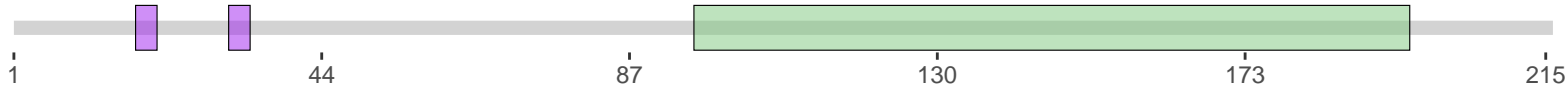


Gel Slice



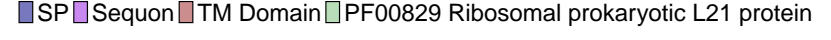
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LVFAVVMIGSRQTYVFPGRVYVFGRLKGANVNDKILNKVLLVGTKTSTFWGKPIVQNMVAHVAVEDQLKDKKVVFFKYKKNKNYRRNIGHRQPTIRIRIMGITGYGDSPWFLDLEAAK

NbL09g09120.1 60S_ribosomal_protein_L18a-like [MW = 23.71 kDa]

No. of times detected



log(intensity)



Values from



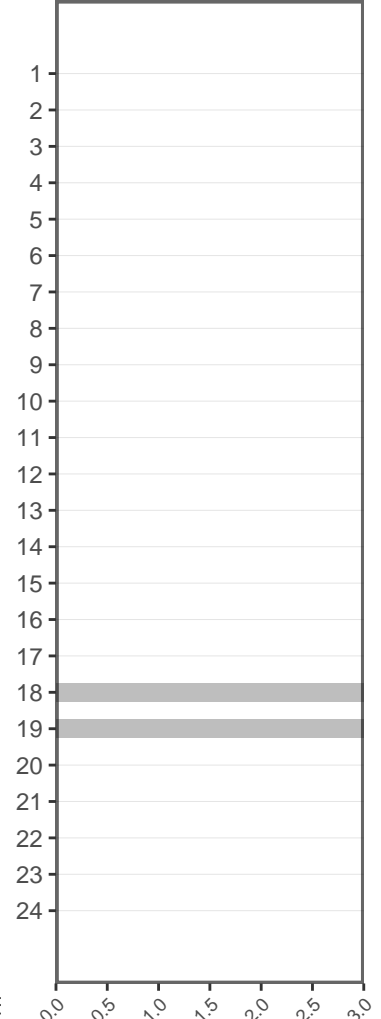
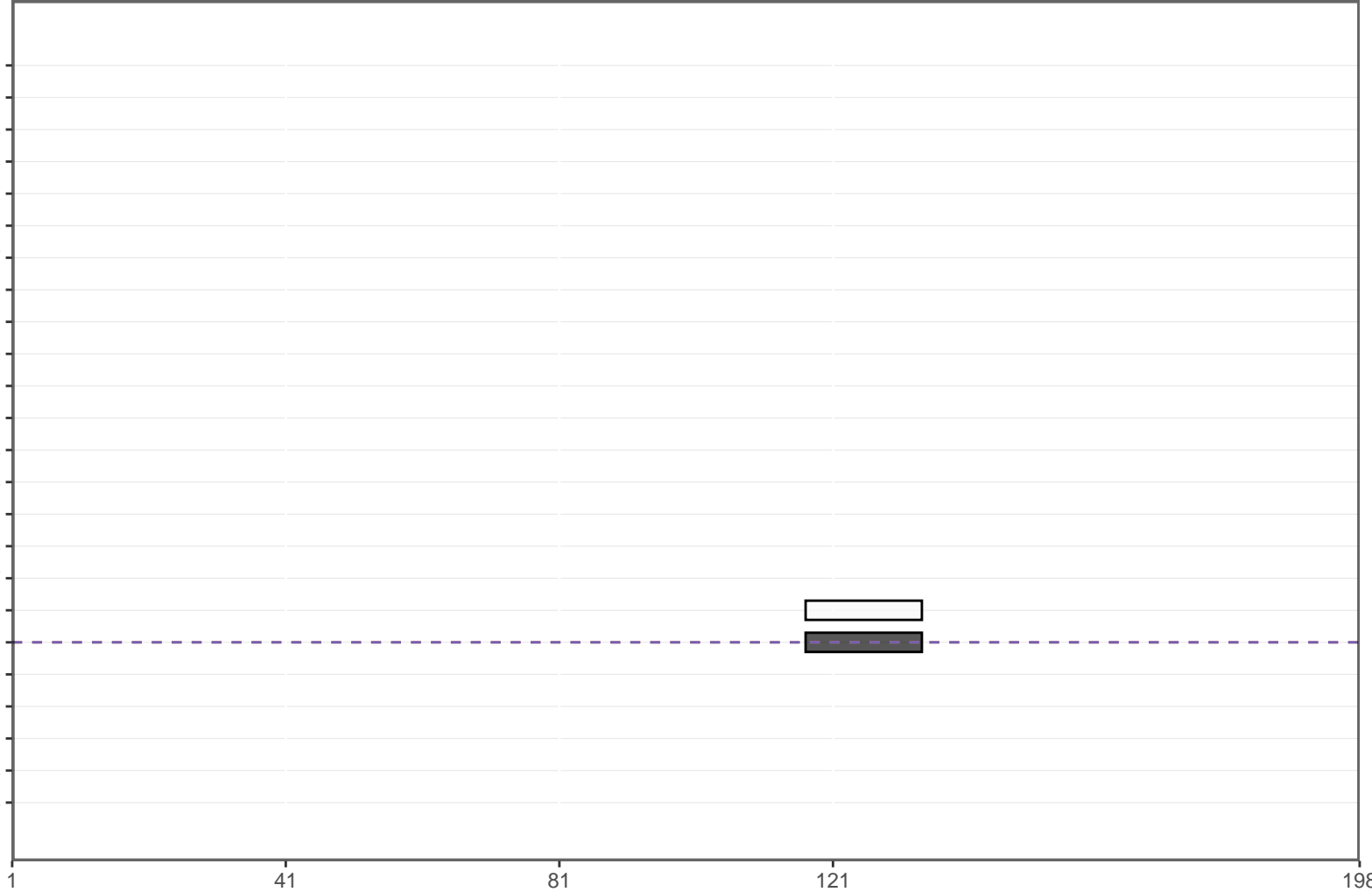
MW indication



Molecular weight



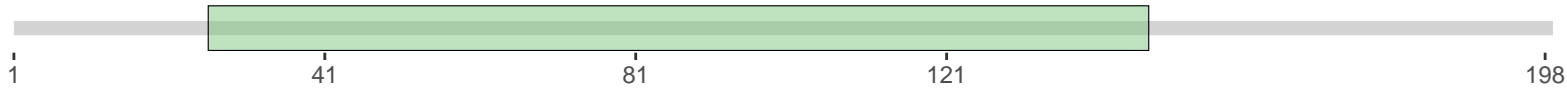
Gel Slice



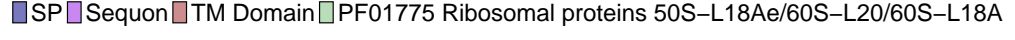
Protein length



Pfam domains



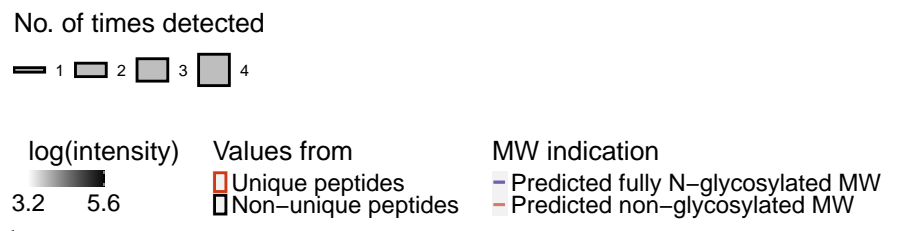
Pfam Description



Protein sequence:

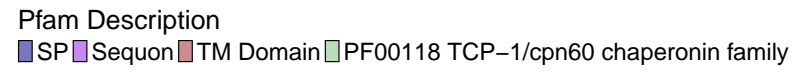
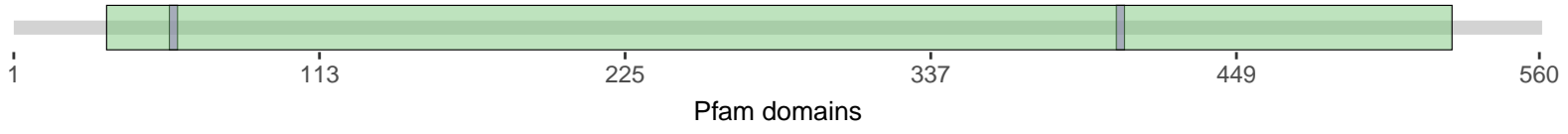
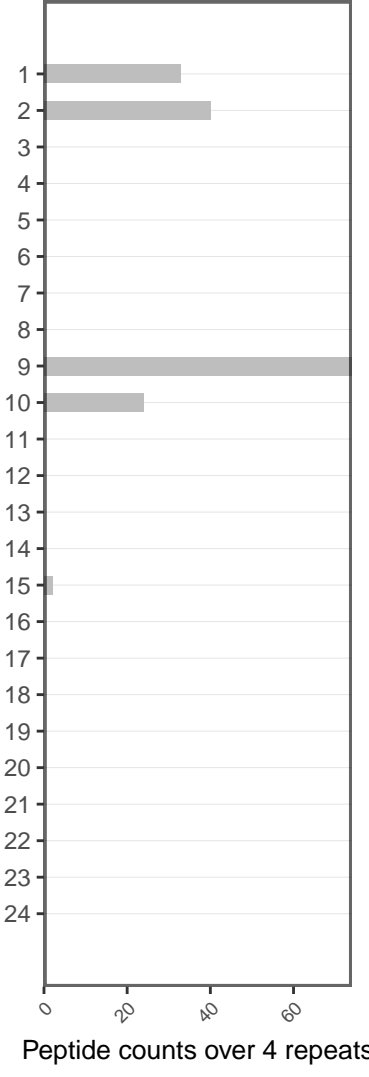
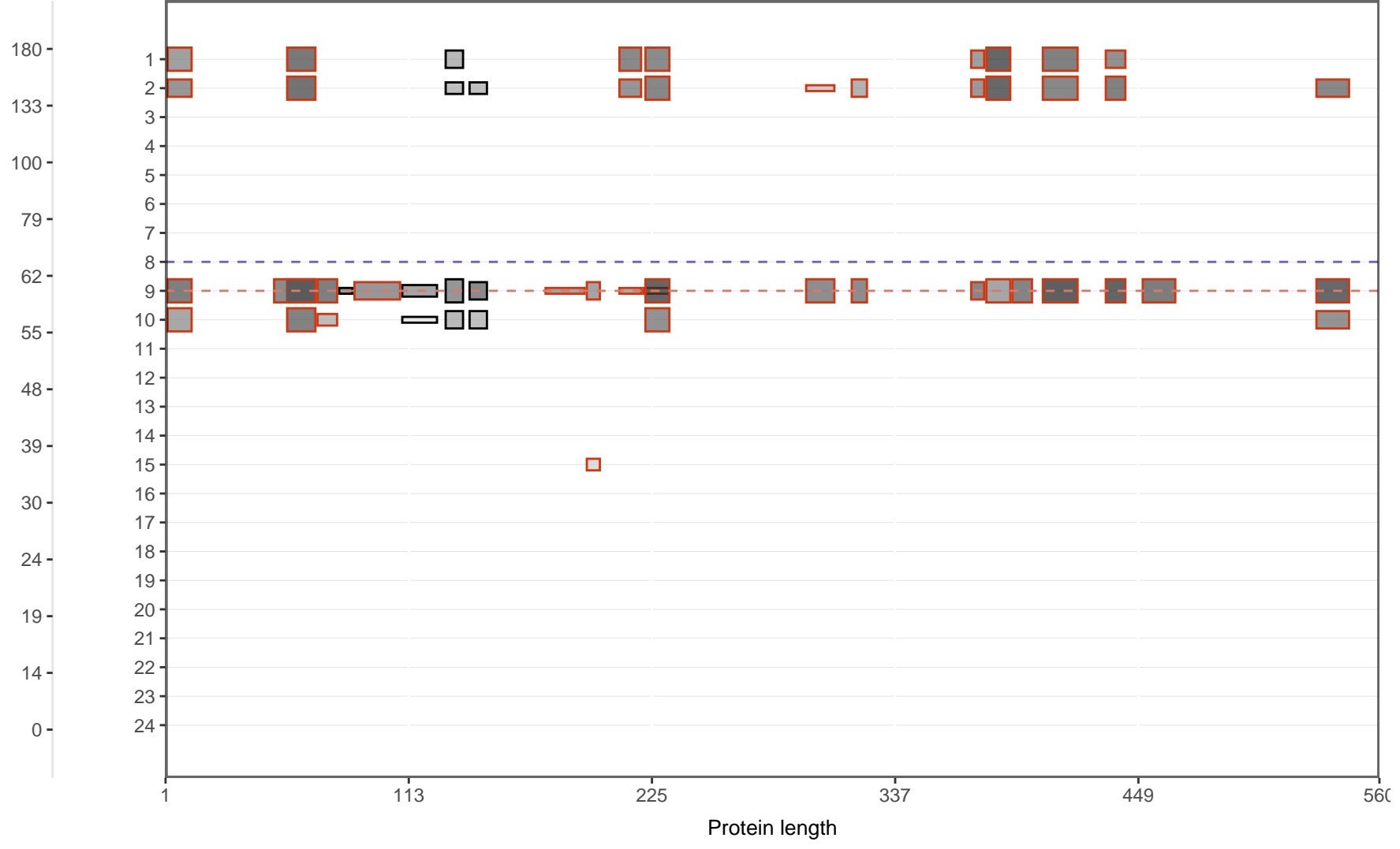
EFEKQPTKIKNYGWLRLYQSRGTGYHNMKFEFRDITLNGAVEQMYEMASRHRVRRHHCIGIKTATIPKLLKREKSTKGFHDEKIKFPLVFKVVRPPSRKLLKTTTKATRNPLFM

NbL09g09040.1 T-complex_protein_1_subunit_eta [MW = 60.35 kDa]



Molecular weight

Gel Slice



Protein sequence:

DAEIVNIYKLDKGVKSGANVLSRLAIGDLATGYFADRIDFGAGRVAEEDLHRVAATGGTGTGTTVNNVIDELGGCELFEEKGVNERFNIFSGGSGKATATVLRGGADPFIEESERSLHDAIMVRRALKNSTVVPGGGAIMERFLRHARTIQGKSGQLFINSYAKALEVYSRQLGDNAGFDATDVLNKLRLQKHALPSSGEGAPYGVDTNGGADAFANFVWEPVVKINAINATEAAGLILSVDETNNPKSESAGGDAASAMGGRRGGRRGMRRR

NbL09g08960.1 neurofilament_heavy_polypeptide [MW = 100.52 kDa]

No. of times detected



log(intensity)



Values from



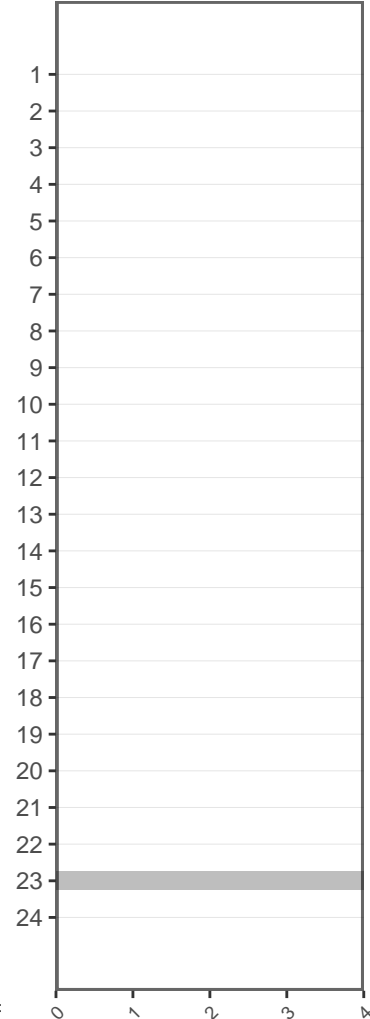
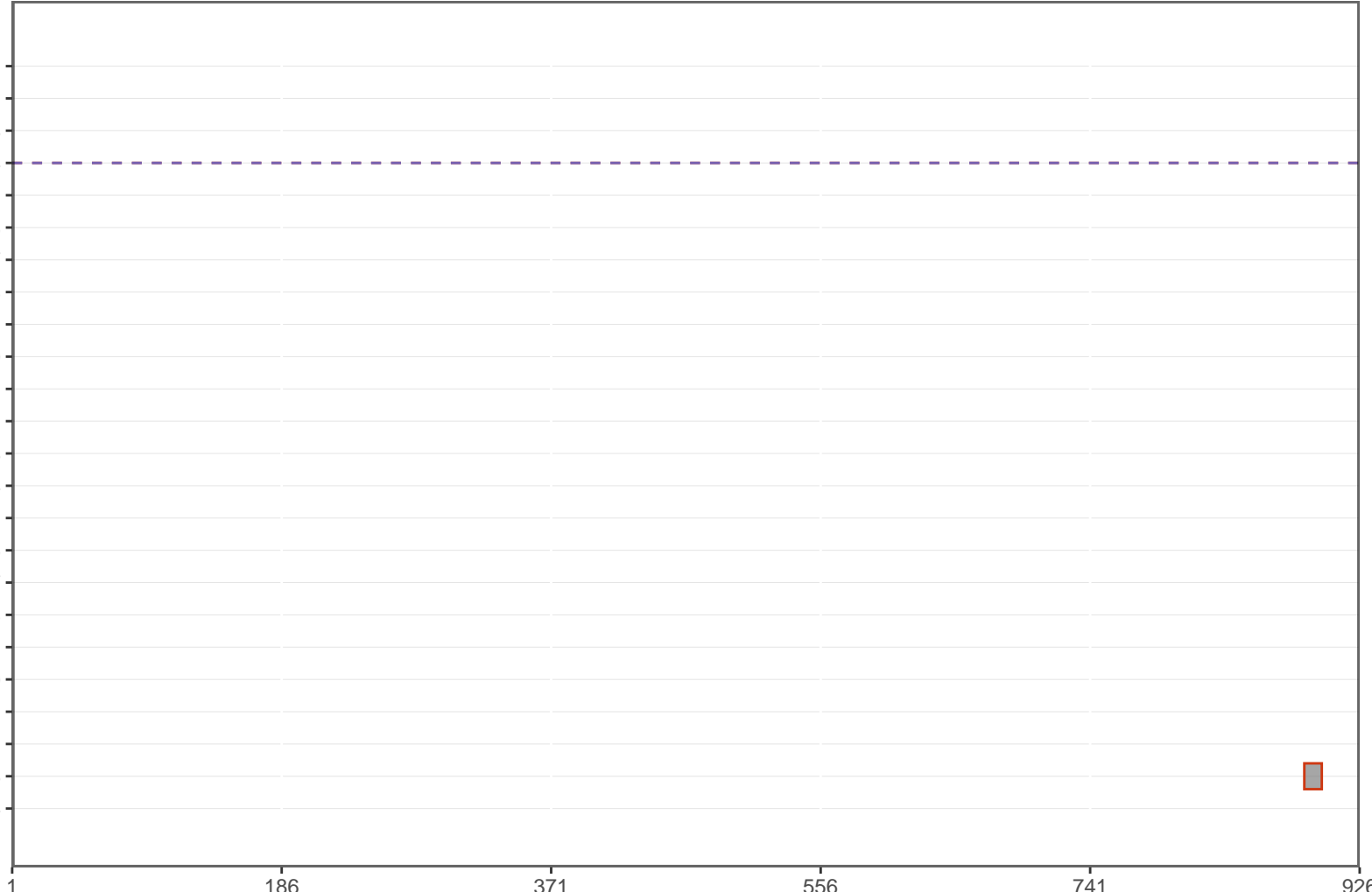
MW indication



Molecular weight



Gel Slice



Protein length

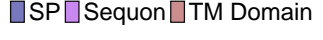


Peptide counts over 4 repeats

Pfam domains



Pfam Description

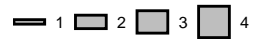


Protein sequence:

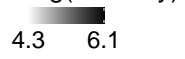
MSAPKESSEGEAVNYAPLYTDLBSPDESAPKNGGRRQKEDLNQEEGVSEEEPEATSDLELVKQVRRPDKKAPAEPSHKENEGVSTSDVEAKKQKSGSKIDTKNKQVGPVNRNKEDSKRGRGKASPETAPPOEESPDDSAKHFEENEDIPKTSAKKKPLSGKGRERVPSPLDINTAKHENNEEATPRTSAKRKRSGKDKVGGTVQHGESLGVKKVWWPLDKPEFYGVVEKFDPAKKKYRWYTDGGVVEHNLTEERWKLVEDDTMSEGEQMASADAASERQKXX

NbL09g08800.1 14_kDa_proline-rich_protein_DC2.15-like [MW - SP = 10.71 kDa]

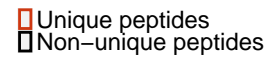
No. of times detected



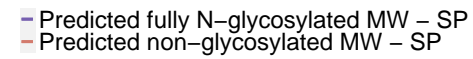
log(intensity)



Values from



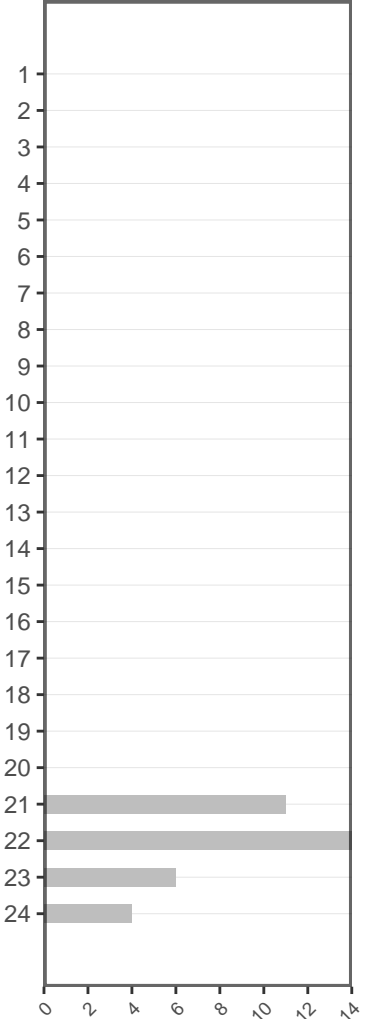
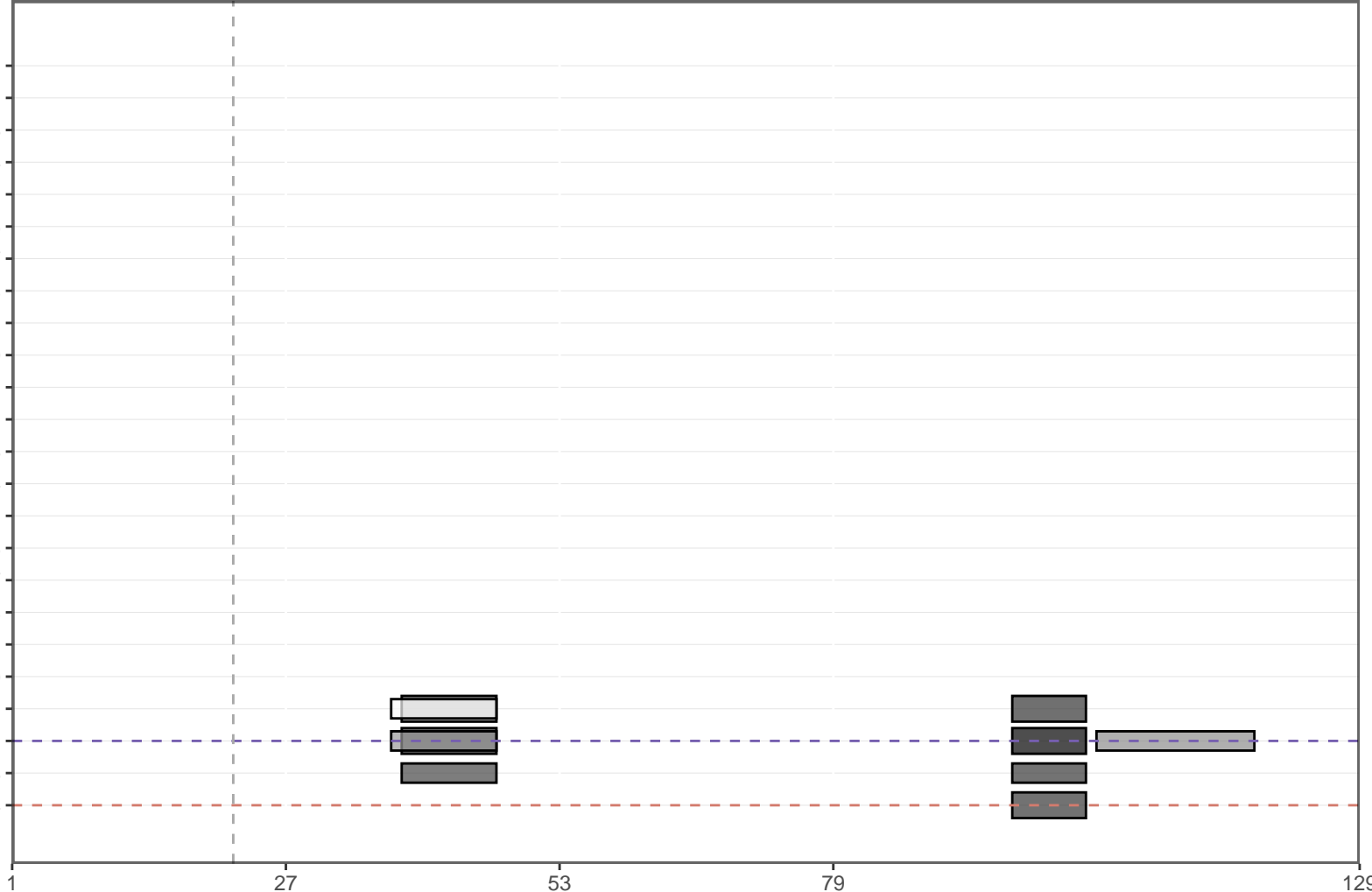
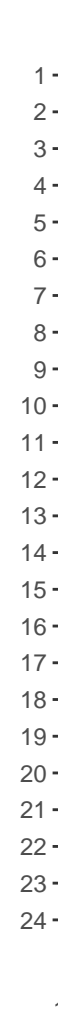
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LGVCADVLLGYNWVGGVTFSPDSSLLGGADLEVAAGLCTAIKANKVIGIKLDIPVLSALVSACAKTFTGFKGN

NbL09g08710.1 DEAD-box_ATP-dependent_RNA_helicase_56-like [MW = 48.42 kDa]

No. of times detected



log(intensity)



Values from



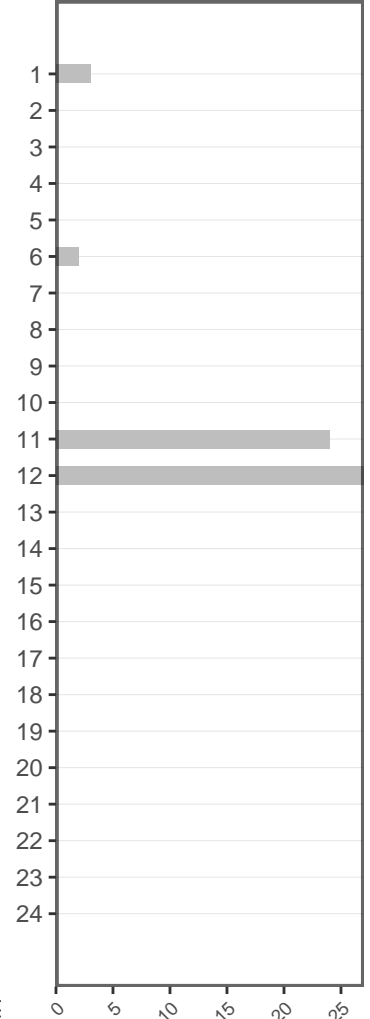
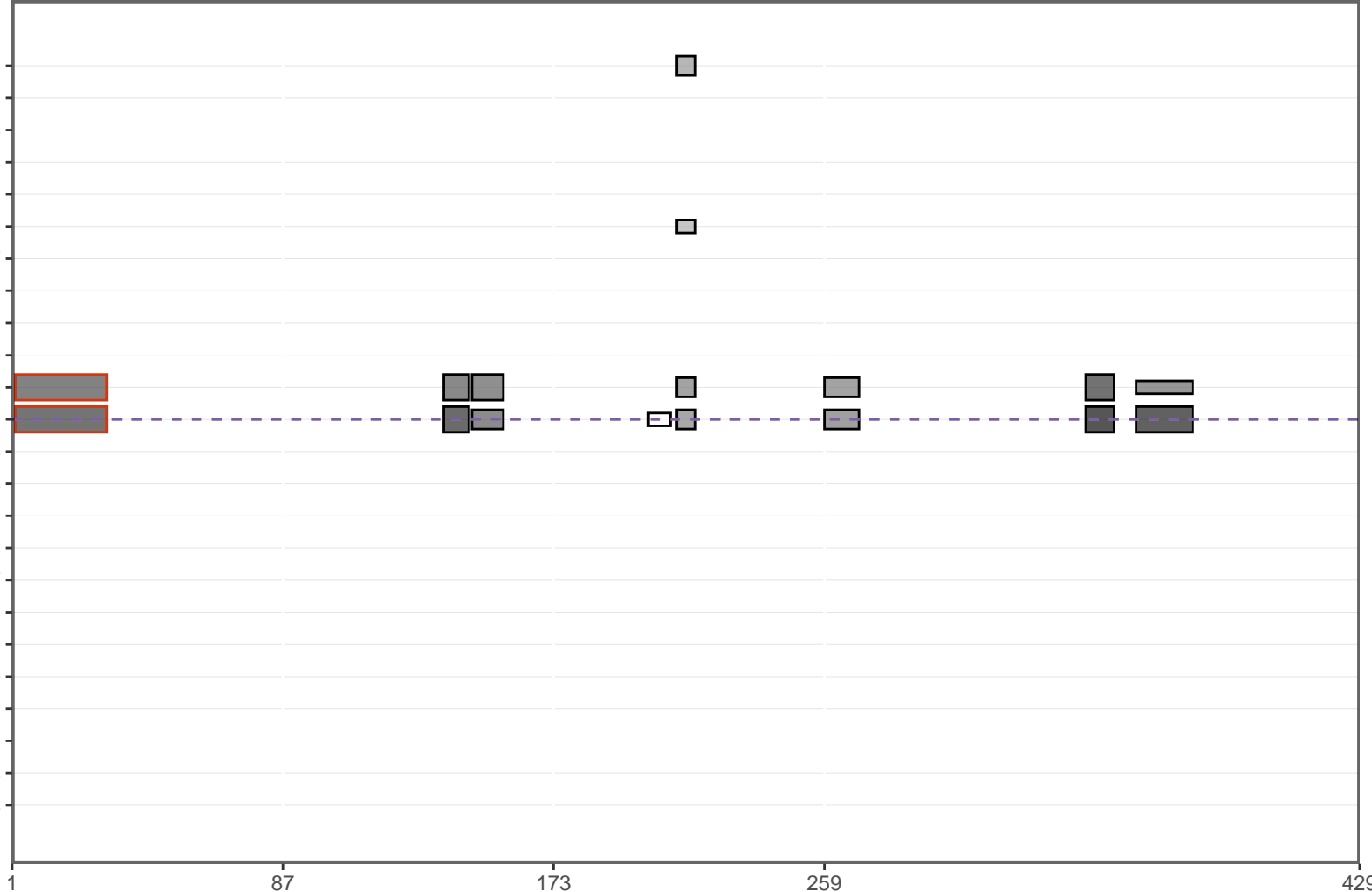
MW indication



Molecular weight

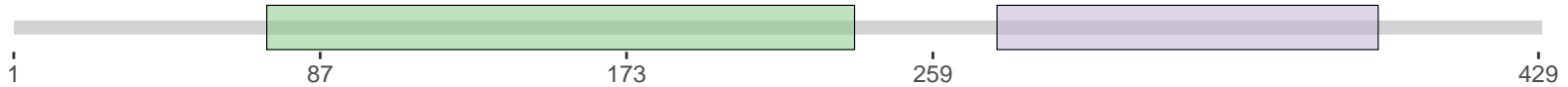


Gel Slice



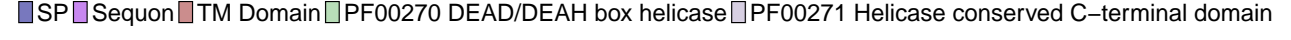
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DKMLLESLDMRRDVGDFKMTPHDQGVMMFSAFLSKEIRPVCKKFMQDFMEHYVDDEAKLTHGLVGHYKLSGETEKNRKLNLDLDDLFNQQVVFVKSVSRAAGLQKLLVEGNFFSICHSIGMTQEERLTRYKGFKEGKRRILVATLVLVGRGIDIERVNVVNDMPDSADTYLHRVGRAGRFGTGKGLATTFVSSASDSVLLNQVQERFEVDIKELPEGIDTSTYMPK

NbL09g08640.1 uncharacterized_protein_At2g34160-like [MW = 17.49 kDa]

No. of times detected



log(intensity)



Values from



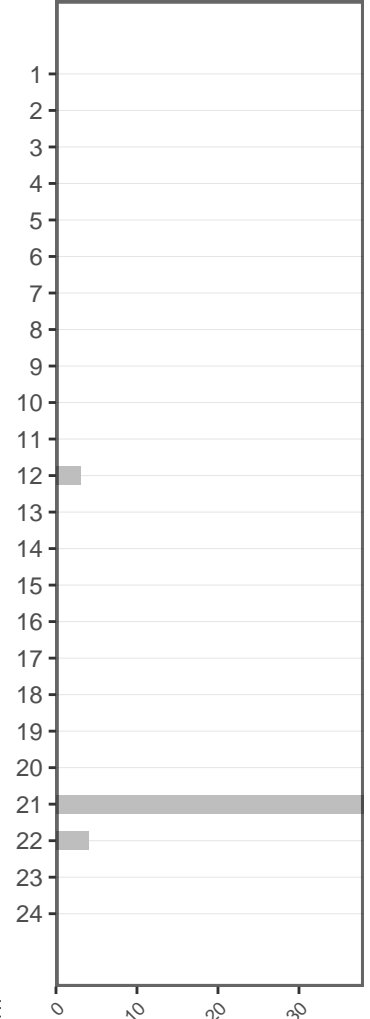
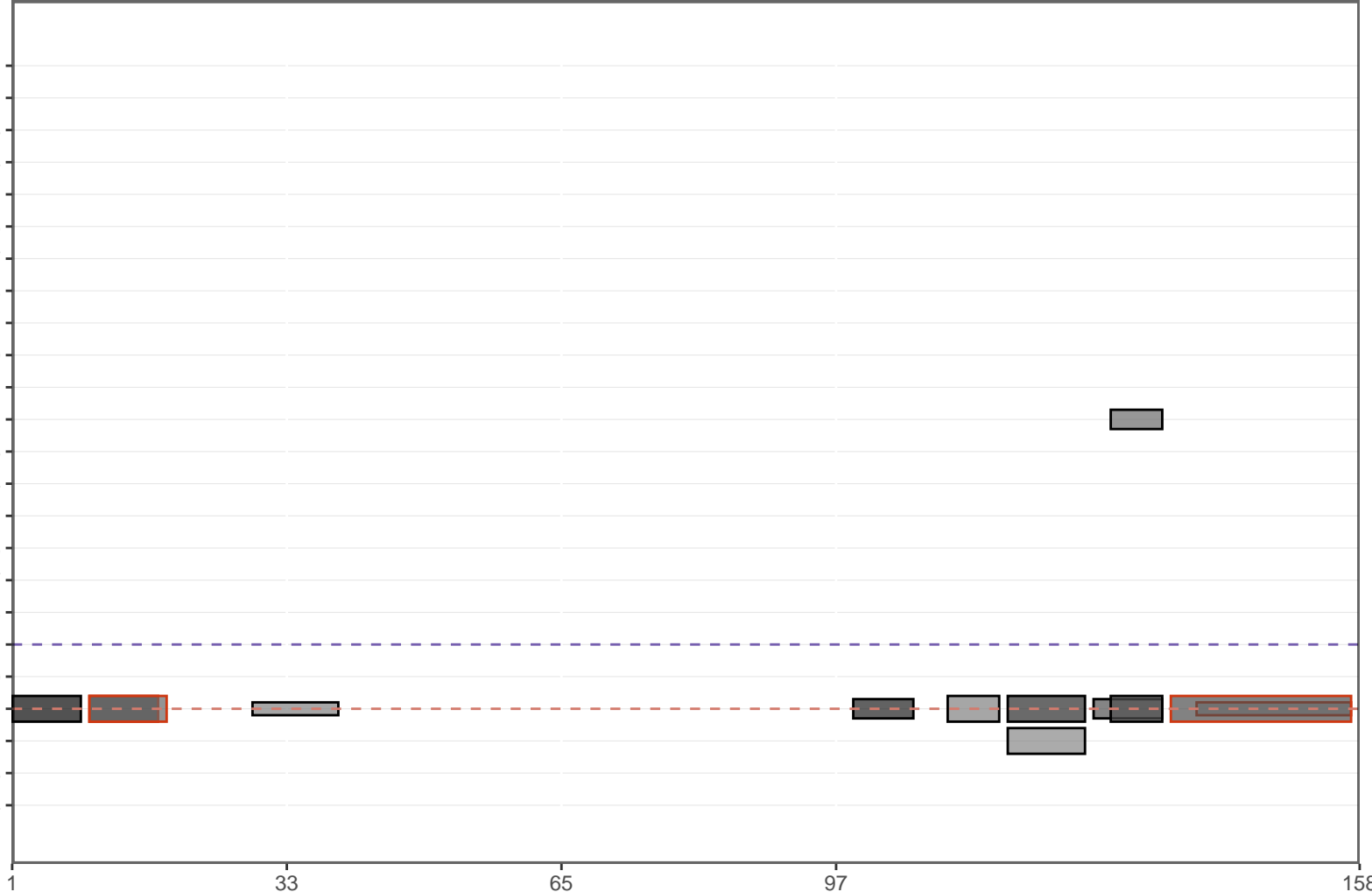
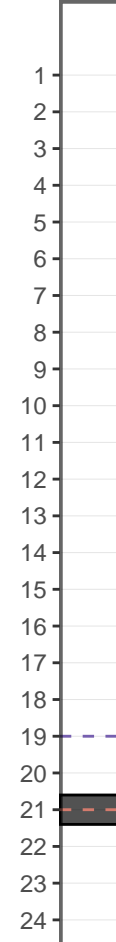
MW indication



Molecular weight



Gel Slice

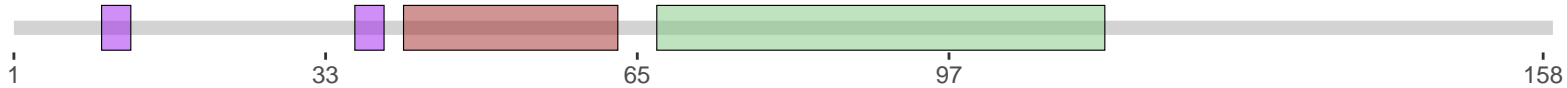


Peptide counts over 4 repeats

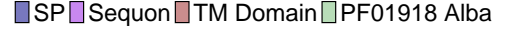
Protein length



Pfam domains



Pfam Description



Protein sequence:

IMGRYMQQYNEVELSALGMAISTVTVAEILKKNNGFAVEKKIRLFTIDMRDEPGARPIPKAKIEVLGKTEKFDLMAAEAGNGDSEEGT

NbL09g08500.1 protein_IWS1_homolog_1 [MW = 58.65 kDa]

No. of times detected



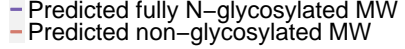
log(intensity)



Values from



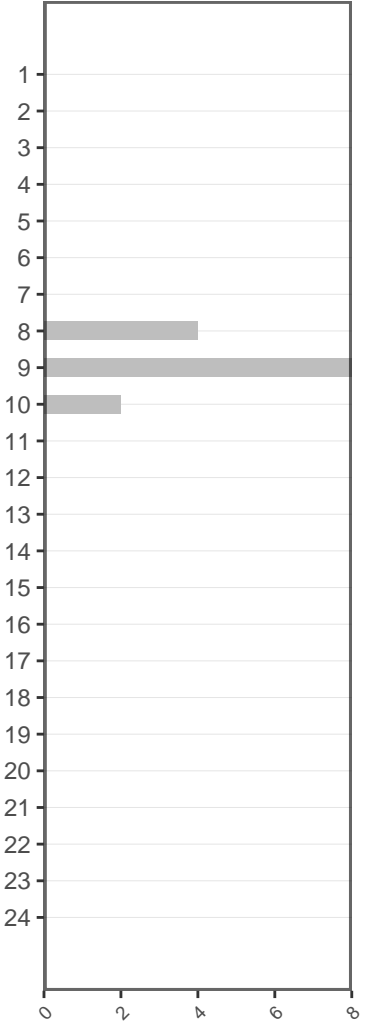
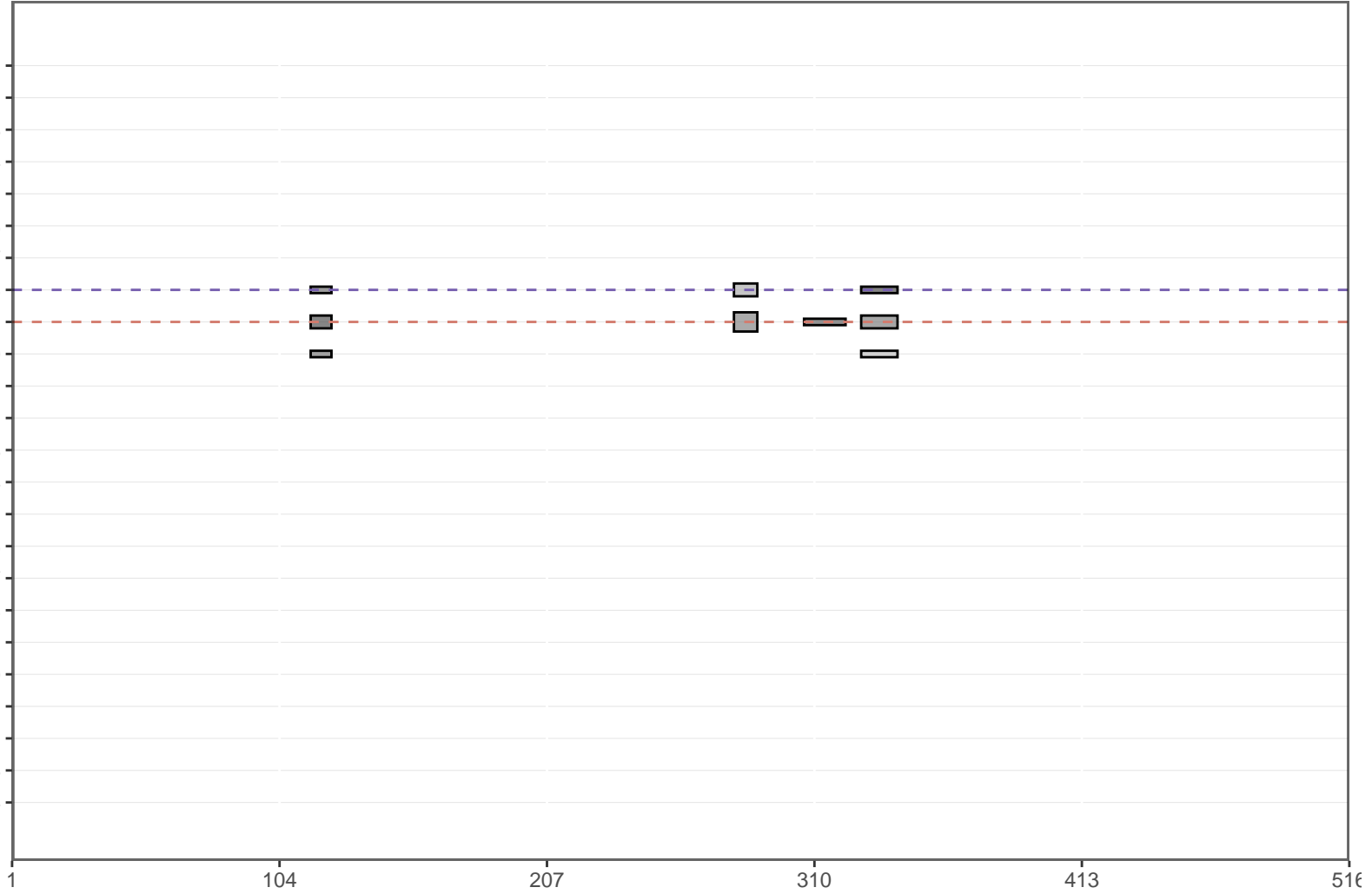
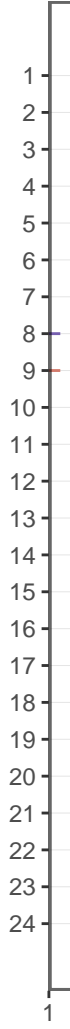
MW indication



Molecular weight



Gel Slice



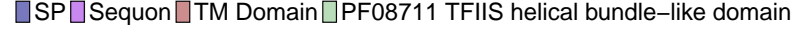
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VAEIALLVENVAEAELEVVAAEEDAEELNRGSKPANKLKKLLPLLDVLSKKGIGGEEFLDHGVLTLLRTVLEFLPDGSLPNINRAAILKLTDPIDLEQVDRREQLKKGSLGKVMFLKSKSEDEETTANRKLAKDLVKKWRSPFNKSTRFEDMRNFDERAAGFRPSPMKKPMNKASGMEGRDDLDLAGFGDGGKSGSPSSGSLQTSRPEAFMSMDFLVRPQSKIDPEEVRRARAKAMVDDGRRMMNKKLQGLKAPKKKKLQATKLVVEGRGMWYK

NbL09g08360.1 uncharacterized_LOC109238939 [MW – SP = 6.01 kDa]

No. of times detected



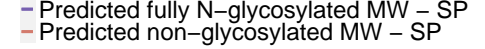
log(intensity)



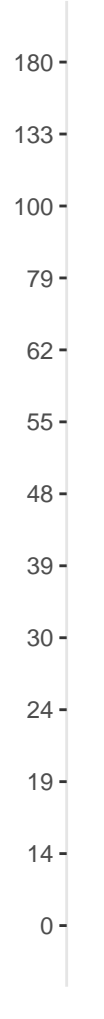
Values from



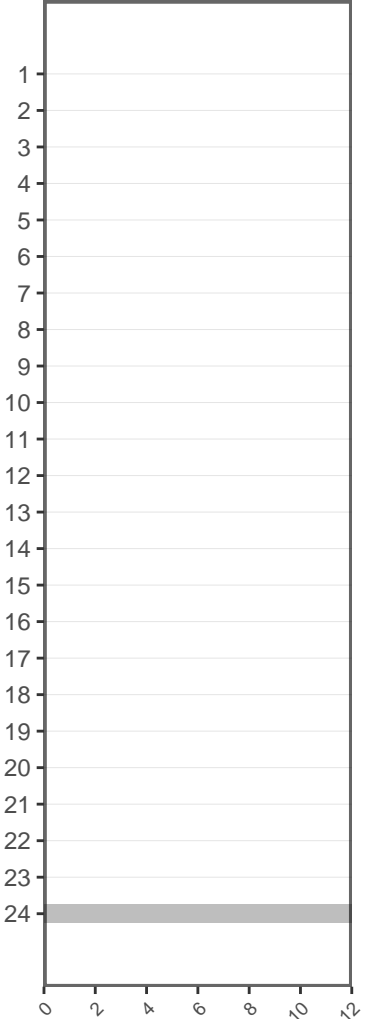
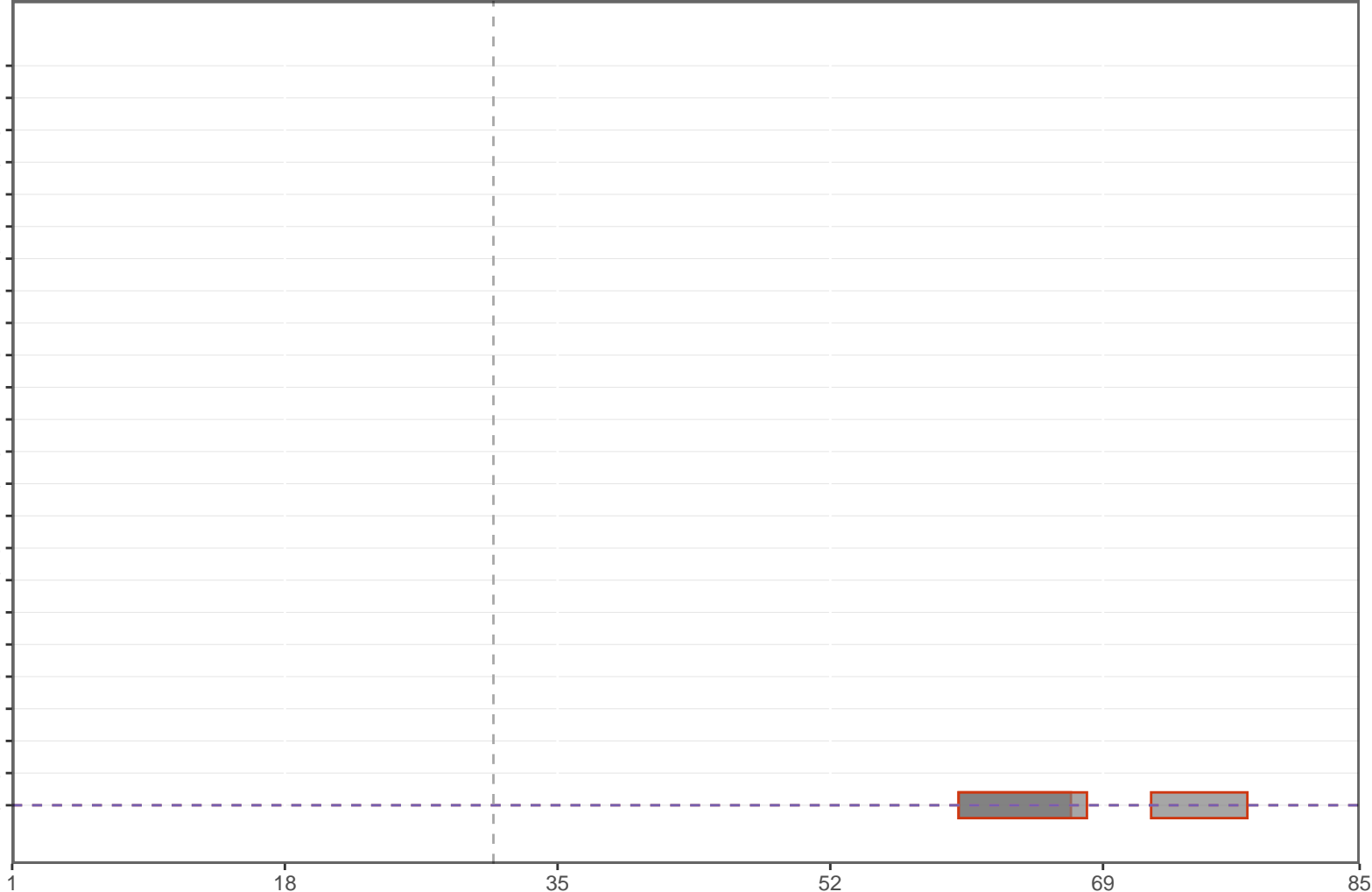
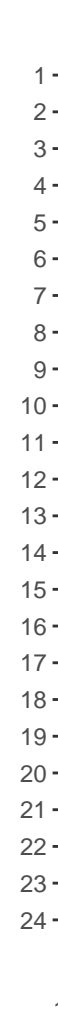
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

VARDVSRITAELEKSKLSDPTLMGGGGVGRGASDGFDRRCPRGYVDWIKLTYGCR

NbL09g08340.1 abscisic_acid_receptor_PYR1-like [MW = 28.56 kDa]

No. of times detected



log(intensity)



Values from



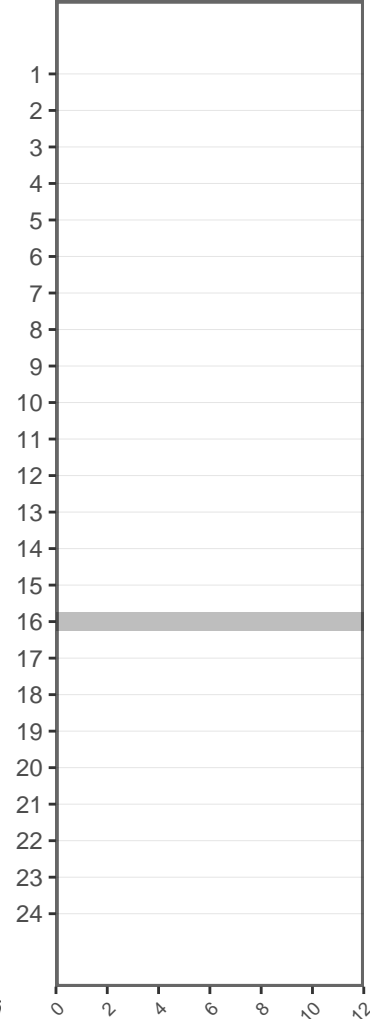
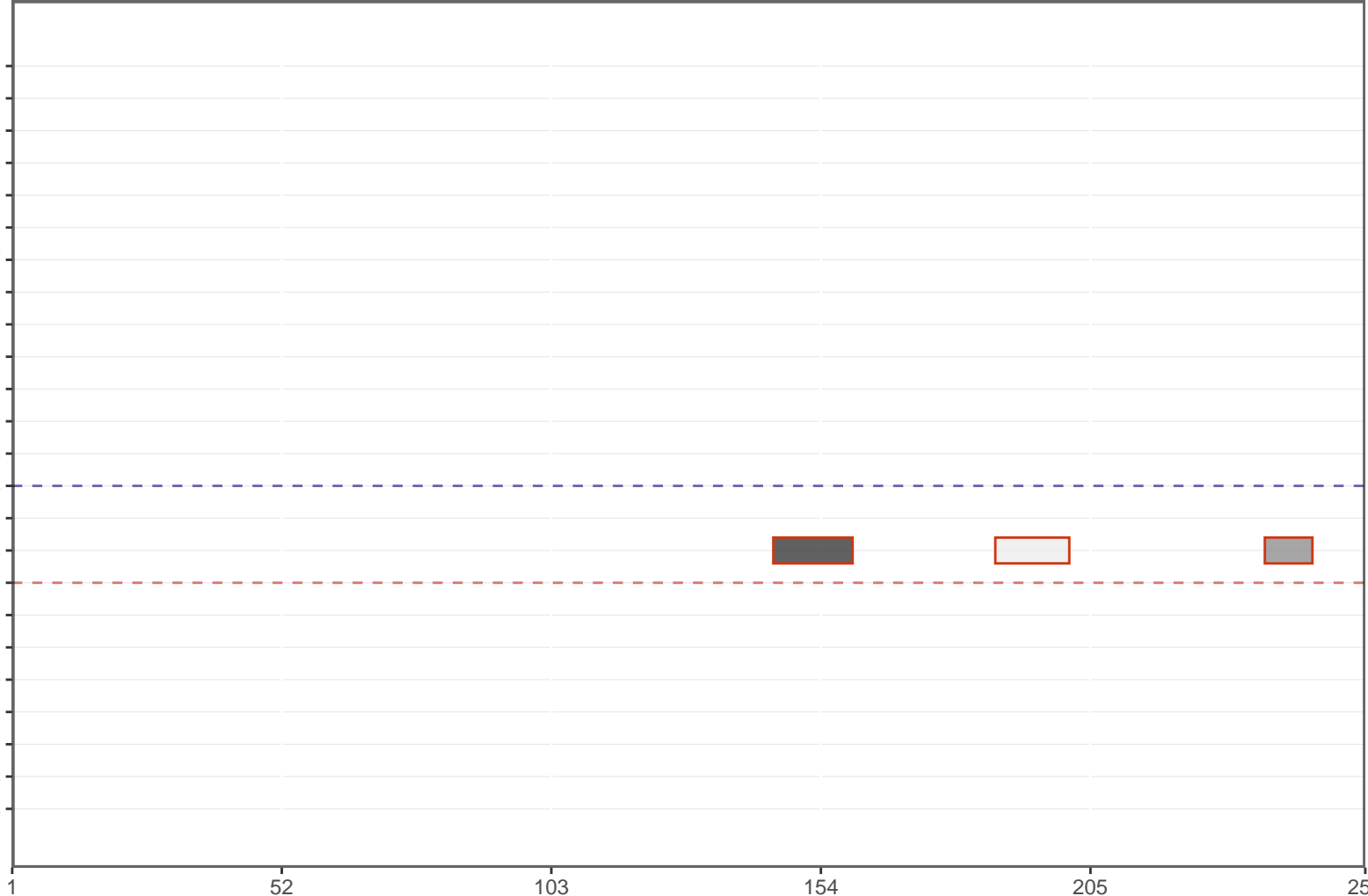
MW indication



Molecular weight

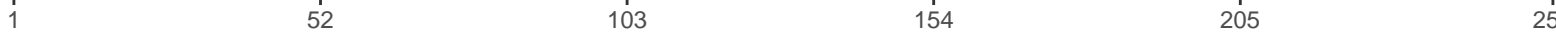


Gel Slice

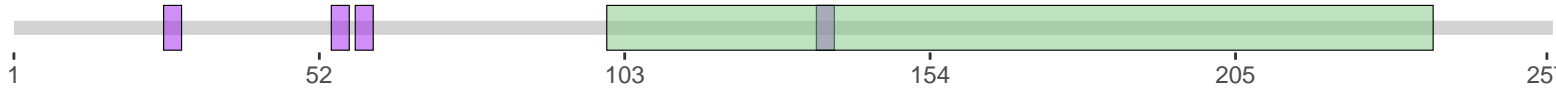


Peptide counts over 4 repeats

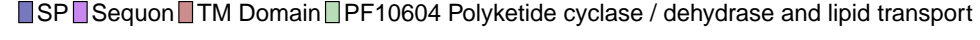
Protein length



Pfam domains



Pfam Description



Protein sequence:

IRFDKPYKHFKKSGVGENFSGVATRVVWVIGLPAATSTERLDLDDKYYTGFSGIGGHEHLRNRVSTTVHGFYQGLDKVSTVALESVVVDVPEGNTFEEDRLFADTVKLNKLGVAEAIVRGGKGVSEEN

NbL09g08310.1 glycine_cleavage_system_H_protein_mitochondrial-like [MW = 17.43 kDa]

No. of times detected



log(intensity)



Values from



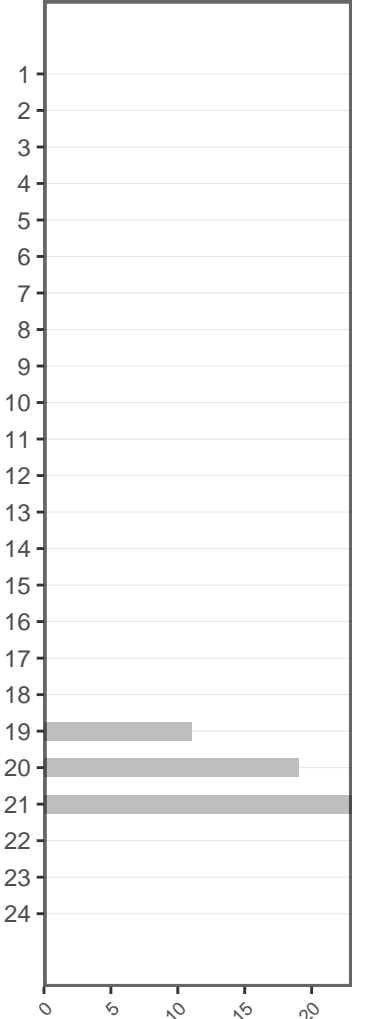
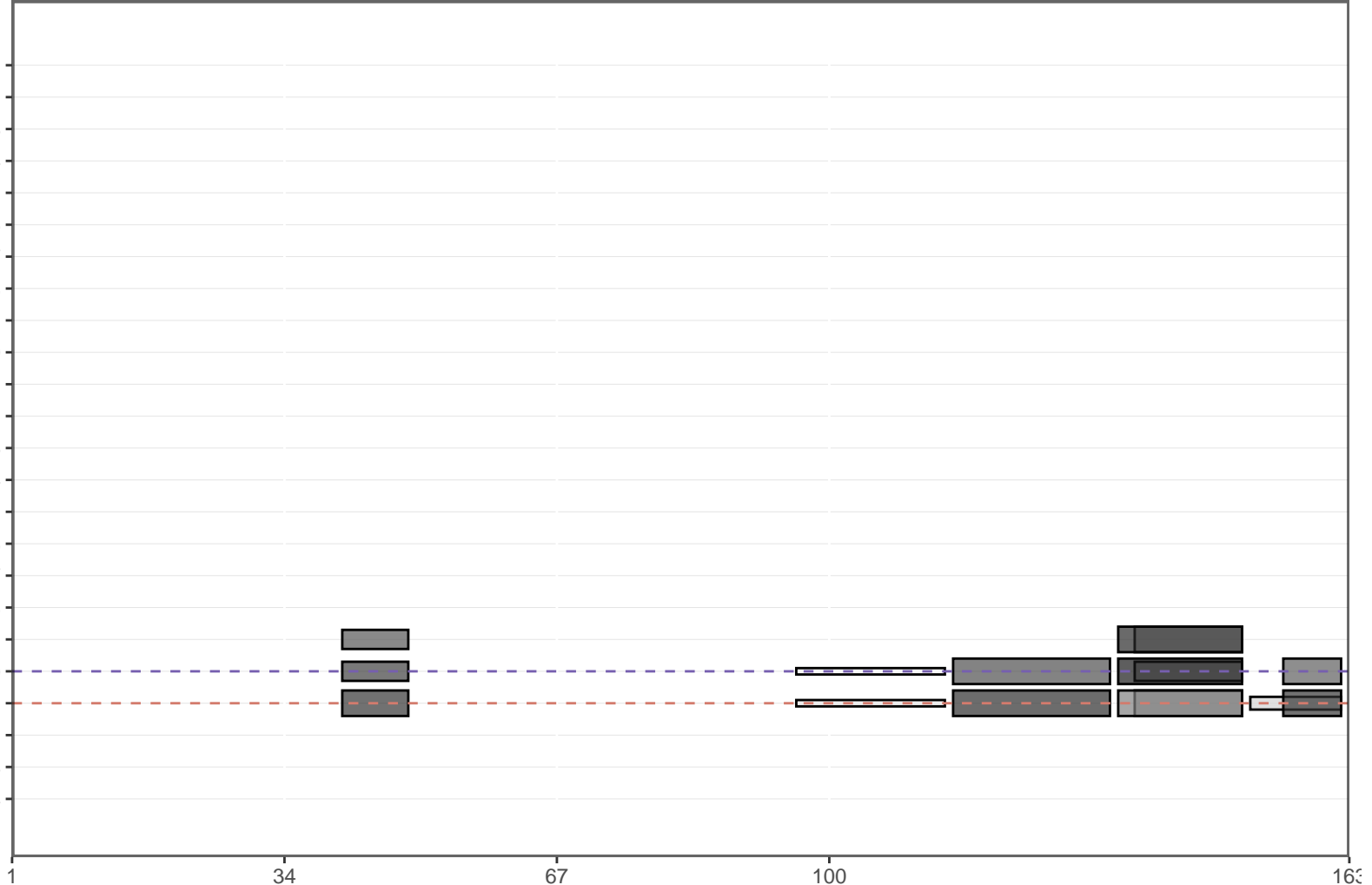
MW indication



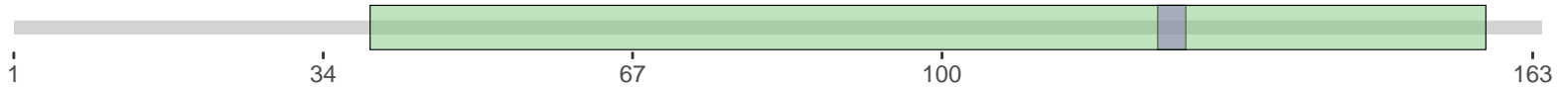
Molecular weight



Gel Slice

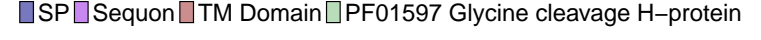


Protein length



Pfam domains

Pfam Description



Protein sequence:

EVVFDLPETGGSVGGSSFGAVESVKATSDNCPHGEIVEVNTKLTETPGLVNSPVEDGWMKIVKPSRPELESLMSKEYTKFCEEDSHI

NbL09g07990.1 U3_small_nucleolar_RNA-associated_protein_25 [MW = 39.2 kDa]

No. of times detected



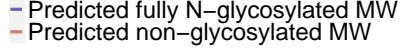
log(intensity)



Values from



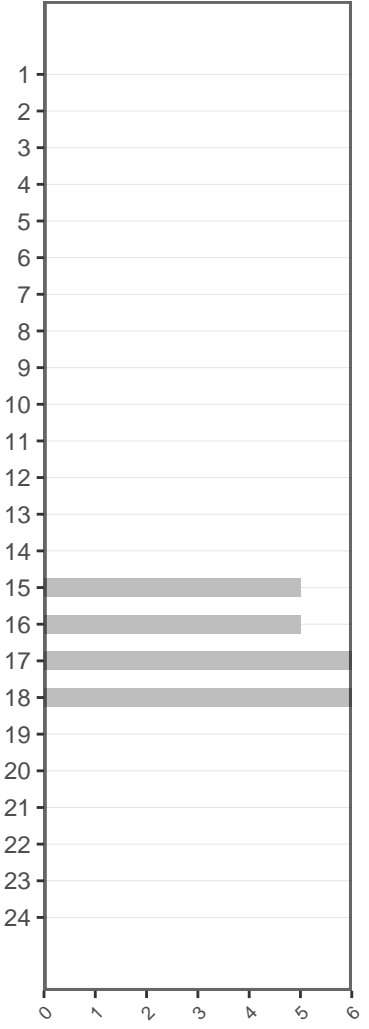
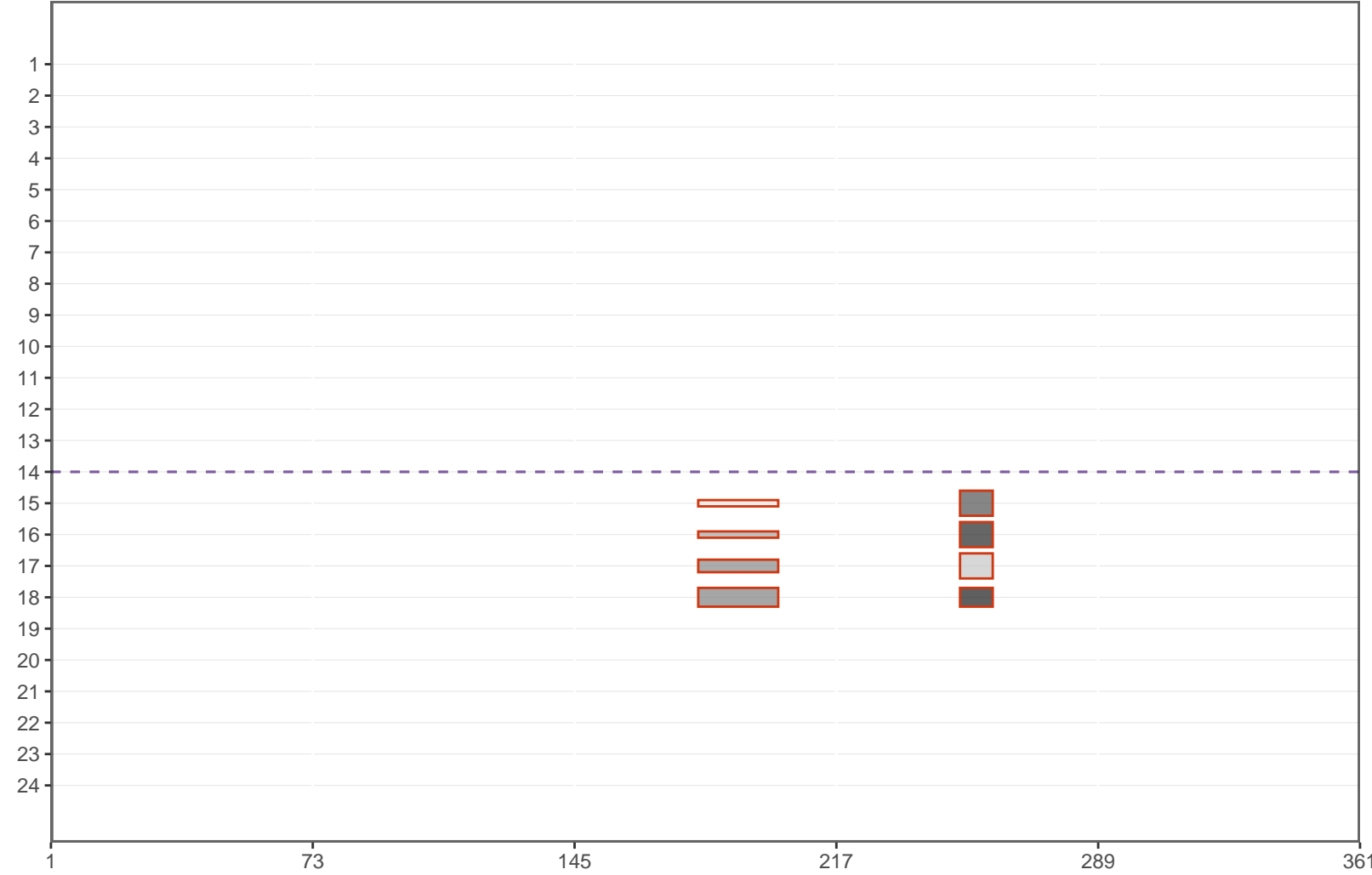
MW indication



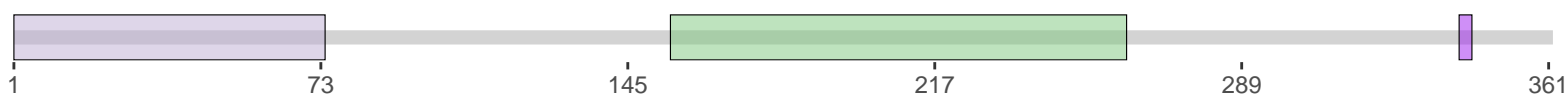
Molecular weight



Gel Slice

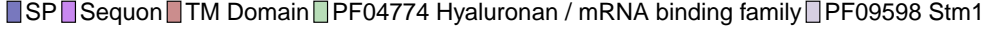


Protein length



Pfam domains

Pfam Description



Protein sequence:

SRGNEFKREGAGRGHWGTRDFEFAPEKEEPPVNEGEKIVDTEKAGAGQADIEDTKDQDPAEFPQEKPEEKEMTLEEYKLLLEEKRKGLLALMAEERKVNLDKEFESMQLLNKSDDEVFKLGSEKDKRKEAVEKAKTKSINFLPADGSEVYRGGGRGRGRGRGRDGFVGNNEVSPSIEDVRFPSLGAAY

NbL09g07960.1 ubiquitin_carboxyl-terminal_hydrolase_3-like [MW = 25.84 kDa]

No. of times detected



log(intensity)



Values from



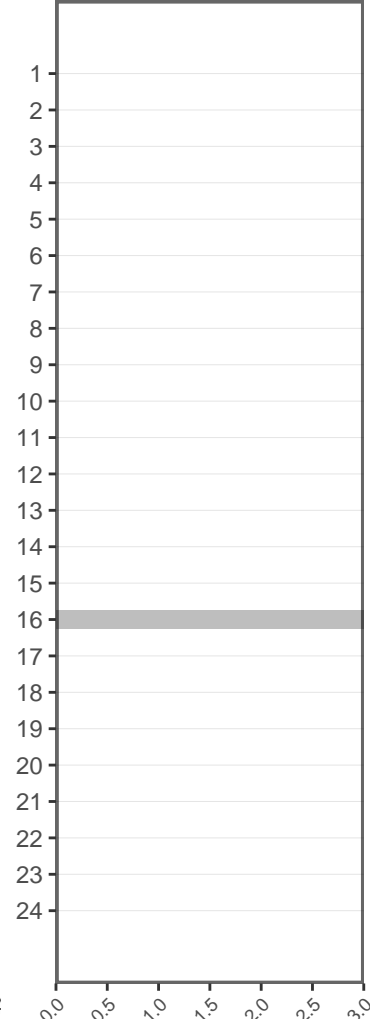
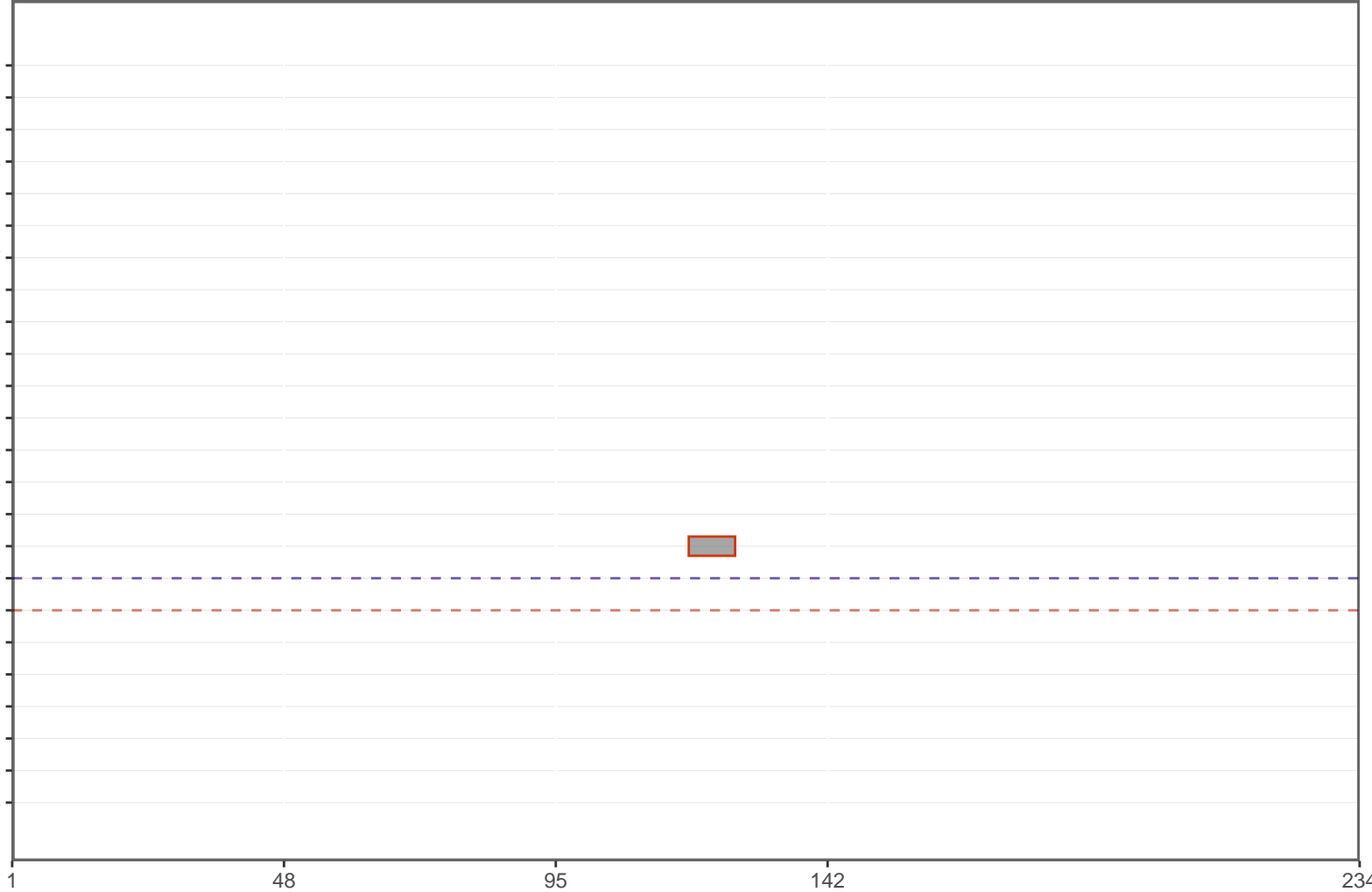
MW indication



Molecular weight



Gel Slice

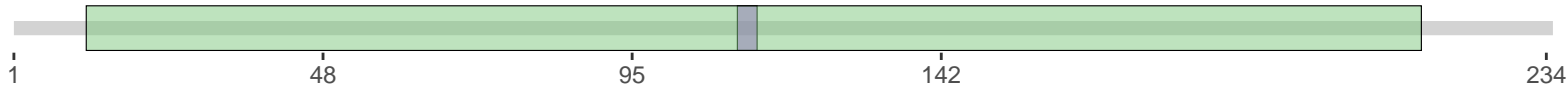


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

STIGLLHAIGNITSOAKLTFEESFLDRFFKSTAMDPKQRAFLFLENDREMEVAVHSWATAGETEASEEDVNTHFICFTCADGQVYELDGRREAPHSIGASBPNNLKDPAKVIQKMKIEKNPDSINFVVAISKRPD

NbL09g07880.1 formyltetrahydrofolate_deformylase_1_mitochondrial-like [MW = 36.4 kDa]

No. of times detected



log(intensity)



Values from



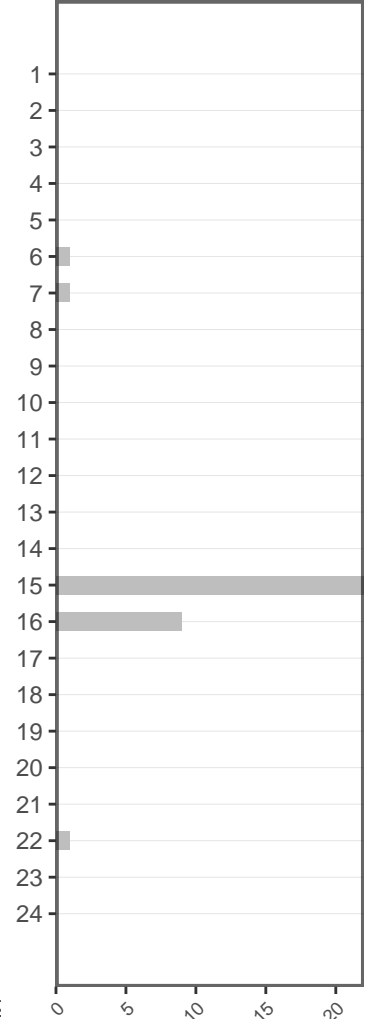
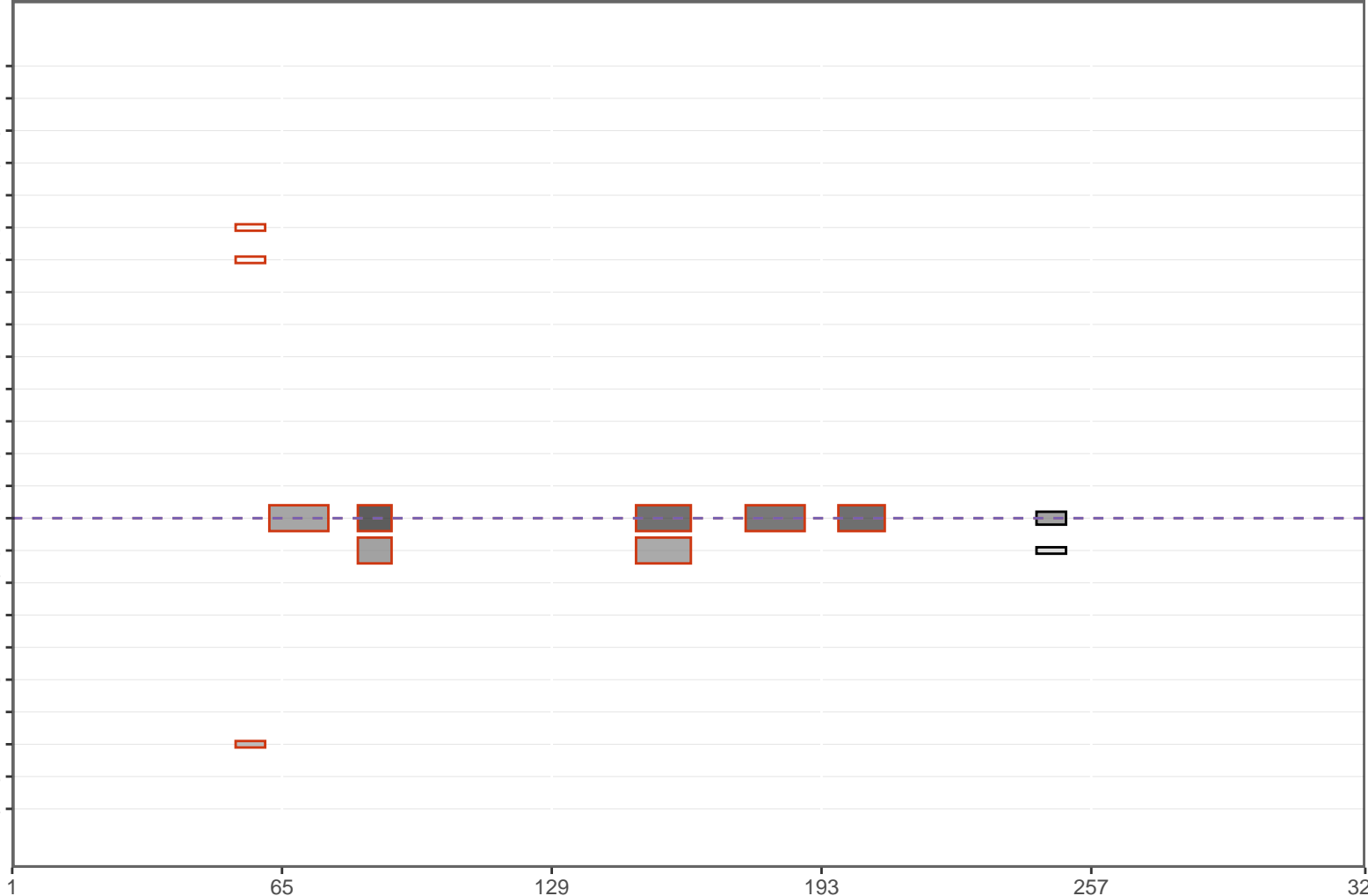
MW indication



Molecular weight

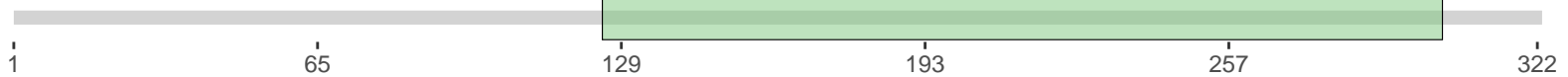


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NGRLPVDITSVSNHQRGPDAAHWLLERHGPYYLPTTMTGFKREVEIKLVHDTDFLALRYMDFSAEFLSEYCKDINHGHLLPSFGKGGSPKQAFAGVKGIGATSHFVSEGLDAGPIEQMVERVSHRDLRFQKSEDELEKQGLAKAKSYGELRVLPPYKDKTVVF

NbL09g07740.1 protein_disulfide-isomerase-like [MW - SP = 52.58 kDa]

No. of times detected



log(intensity)



Values from



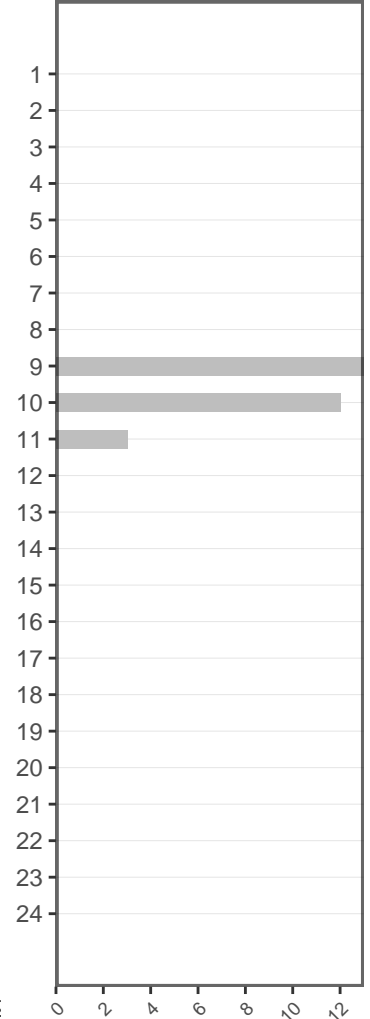
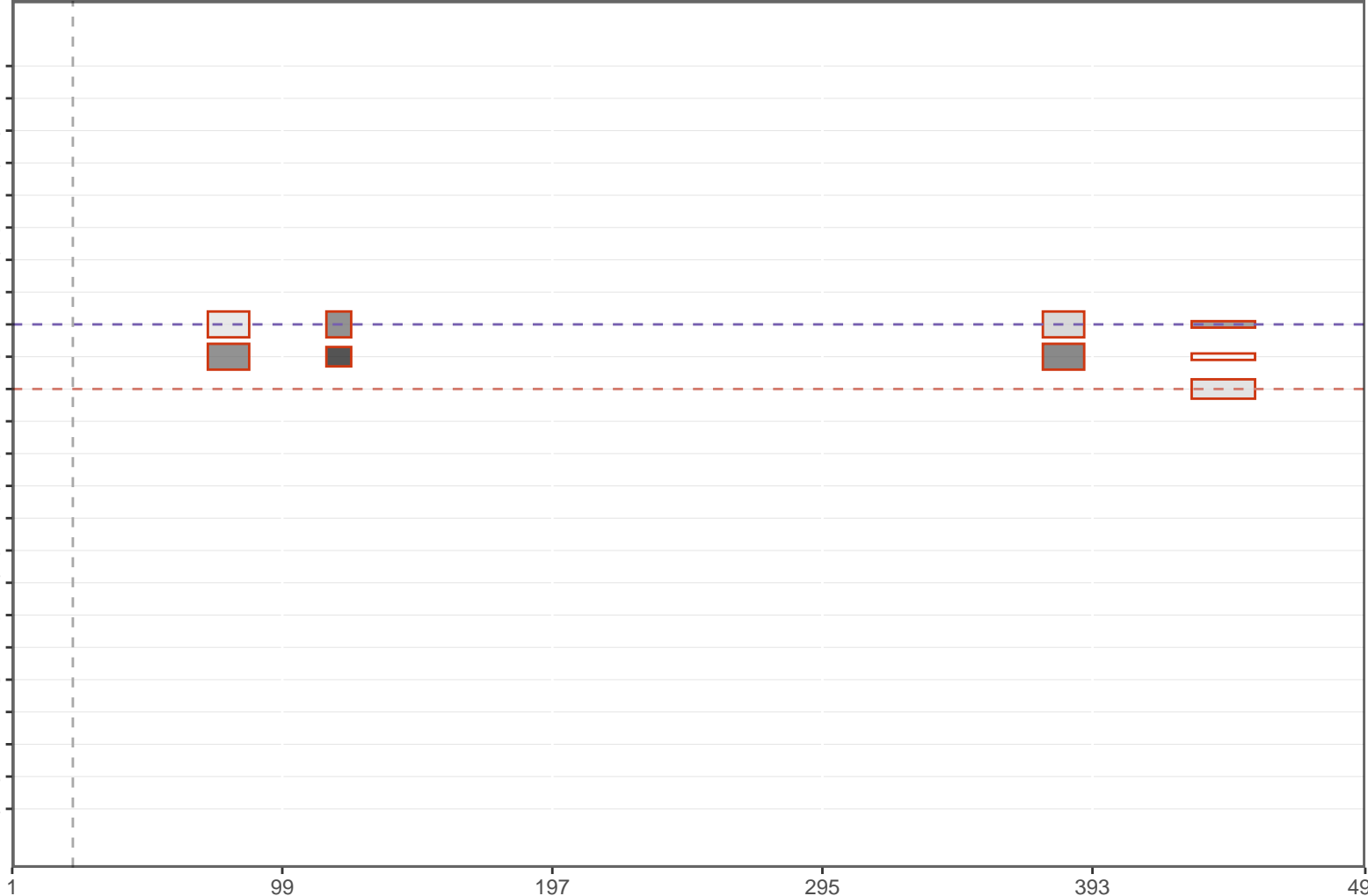
MW indication



Molecular weight

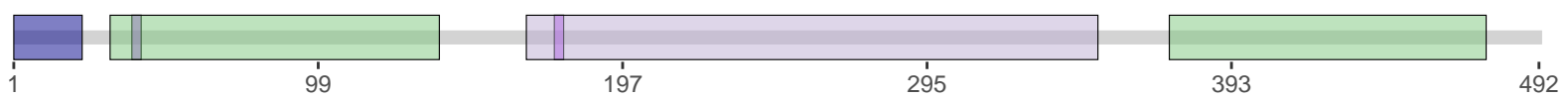


Gel Slice



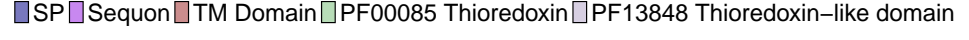
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

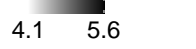
LVEAASPTVTLFNDPNNHFFVWFFNPNKAMLFVNFNSDLIDTFKSKYHEVAEQYKGNDFLKGDEASQGAQYFLKEDQVPLIIGTNDGKYLKPNVPEPDHIAHWKDKDKKPKFKKSEPIPEVNSEPKVVAADTLQDMVFNISVWVLEEFYAPWGGHGGKGLAPLDEVAVFEFESDADVMMAKIDATANDIPQGTDFDVGQYPTLFTKATASGKISQYEGDRTKEDIDFHKNRDKAADGGRKEEL

NbL09g07690.1 photosystem_II_22_kDa_protein_chloroplastic [MW = 29.26 kDa]

No. of times detected



log(intensity)



Values from

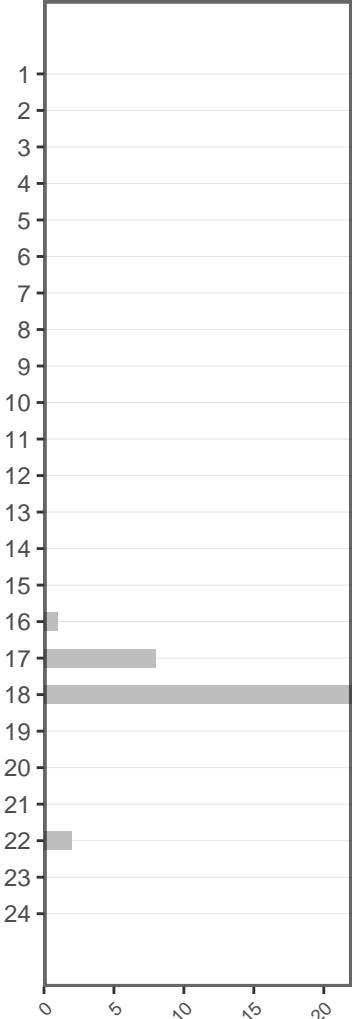
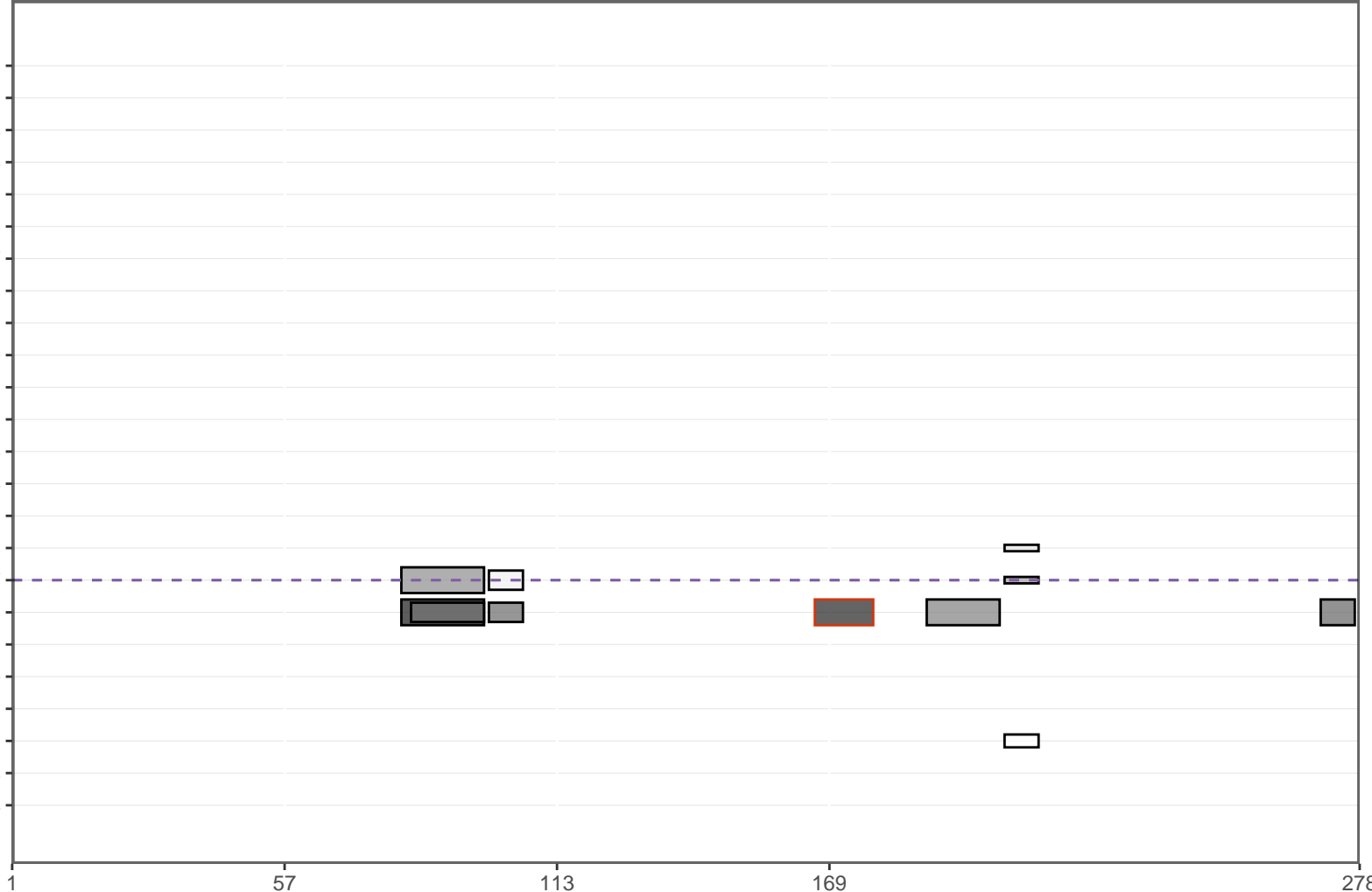
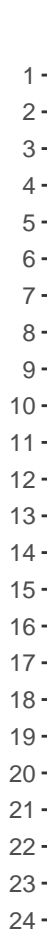


MW indication



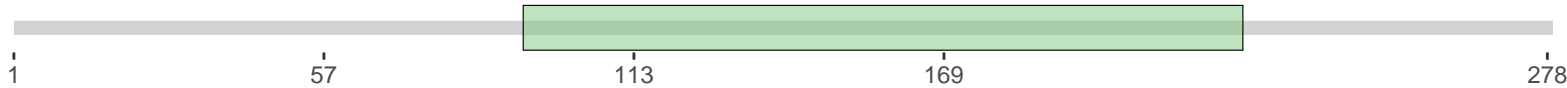
Molecular weight

Gel Slice



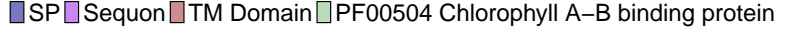
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SKGLAQNLLETGIPHYEAEPLLLFFILFNLLGAGLGDGRGKFDPPPTPTGLDQKAVIPPGKGFKSLGLSEGGPLFGFTKANELFVGRLAGLGIASFHIGIEHTQKGLAQLNFETQVPIIEIPLLFNIVFFVVAANPQTGKPFVDEEEE

NbL09g07290.1 acetolactate_synthase_1_chloroplastic-like [MW = 71.78 kDa]

No. of times detected



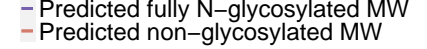
log(intensity)



Values from



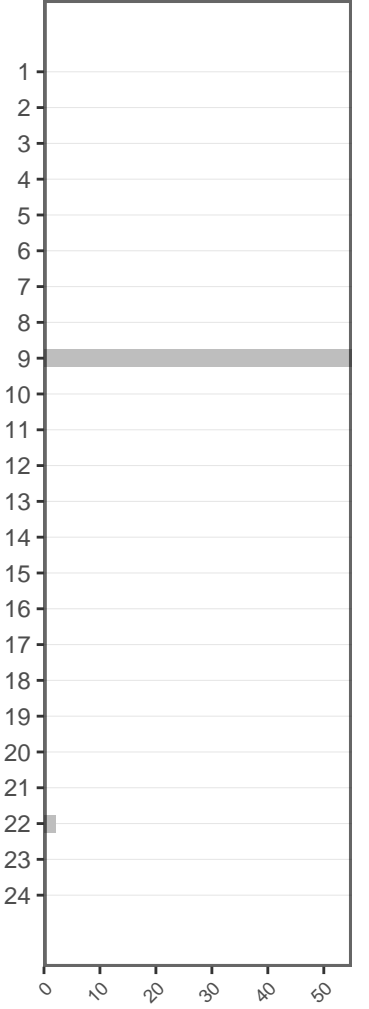
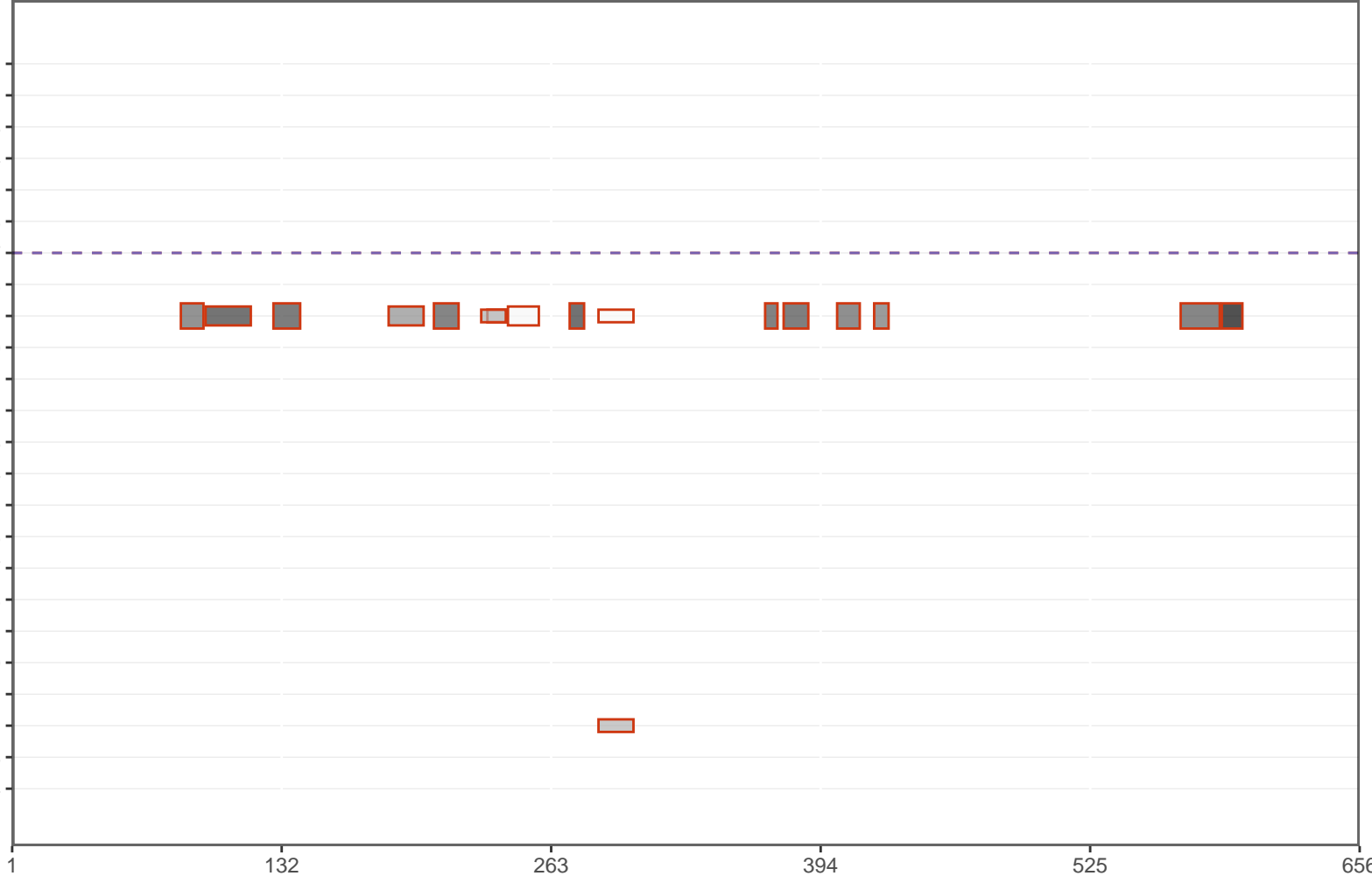
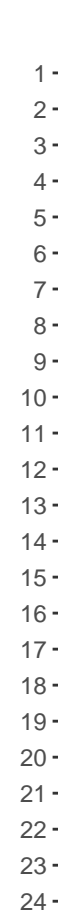
MW indication



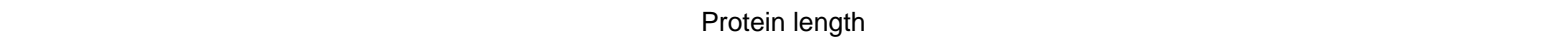
Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00205 Thiamine pyrophosphate enzyme, central domain
- PF02775 Thiamine pyrophosphate enzyme, C-terminal TPP binding domain
- PF02776 Thiamine pyrophosphate enzyme, N-terminal TPP binding domain

Protein sequence:

LMGLVFTTGDLSLGMIGMHTVYKSNVAVDS6DLLAFGVRFDRVTKLETTFASRANVHDDIDPEIKNKLPHLGGCTDKLALGGNLBILEREIGKIKLNFSPWTKELTEQKLYPLKYKSGDMPQVAQVLDLSTNGNAHSTGVGQHGMAAGYKYYKNSRQWLTSGGLGAMGFLPAMGAWAARPNKVVDDIDGDSFMMNVQELATIRVENLFPVKMMLNQHLSGMVGVWEDRFYKANRAHTYLGNSIEAIFPDMKFAEADIPGRVTKRTVRAAQI

NbL09g07260.1 40S_ribosomal_protein_S2-3-like [MW = 30.04 kDa]

No. of times detected



log(intensity)



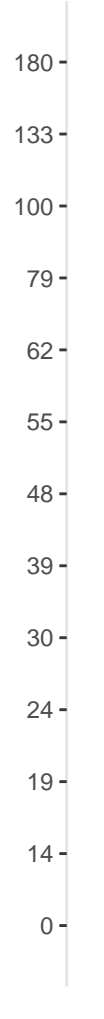
Values from



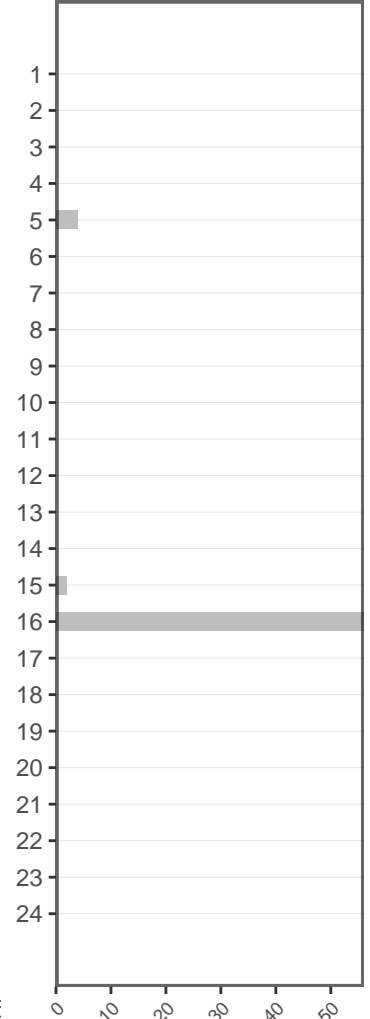
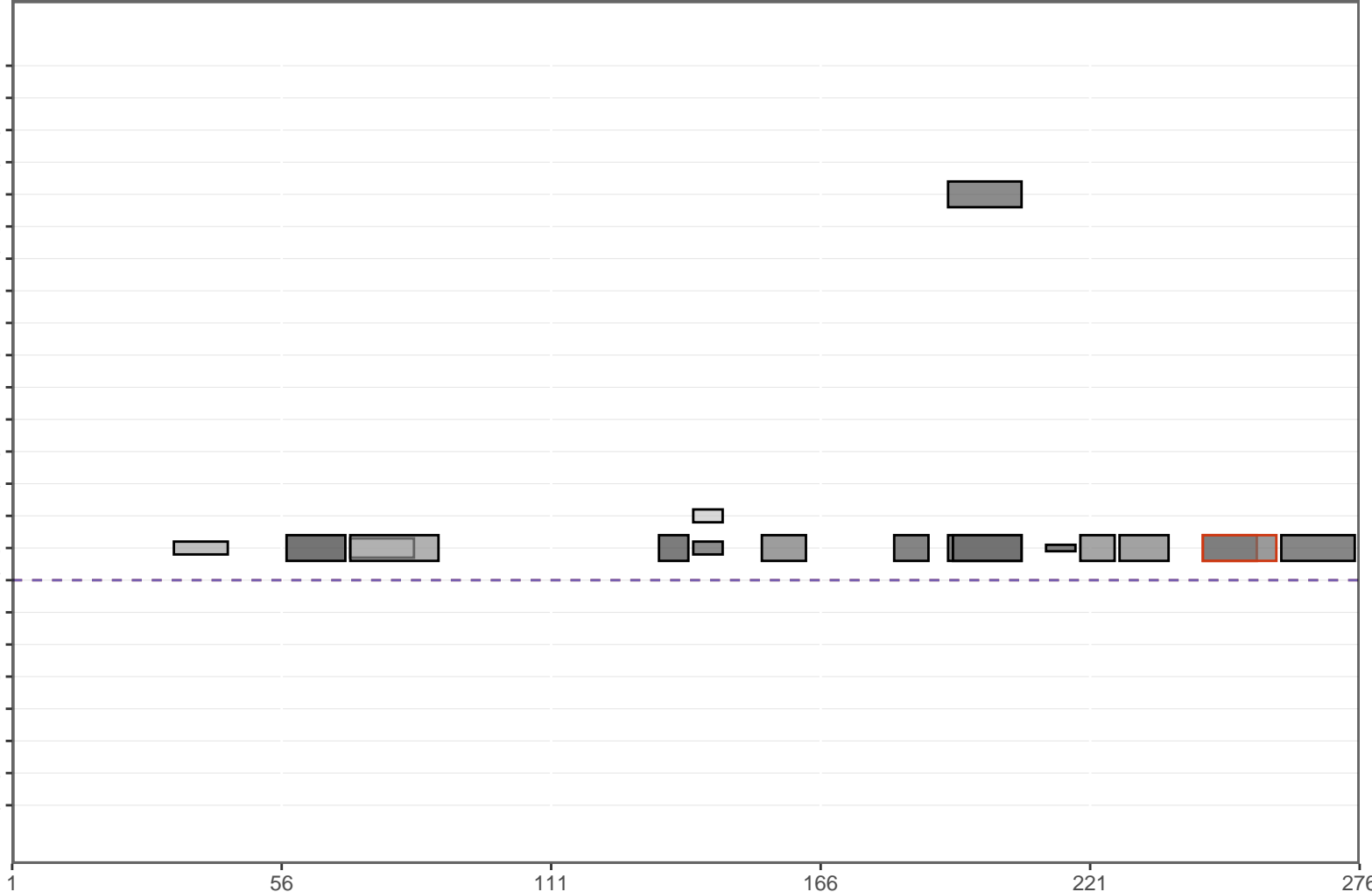
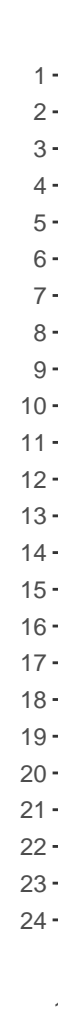
MW indication



Molecular weight

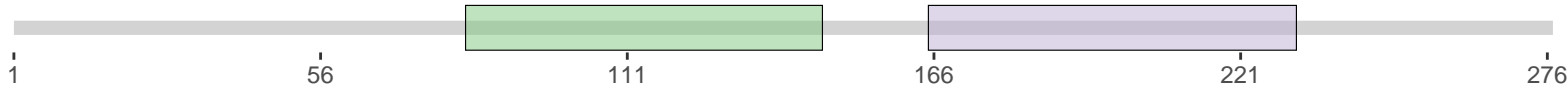


Gel Slice



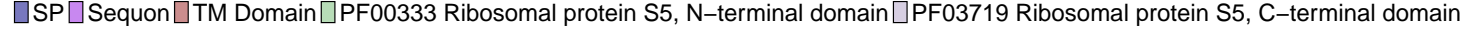
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CCSKEVATAIRGAILAKLSEVIVRRGIVWNGKIKPHIVPKVITGKGGSVTVRMVPPRAGAVIARVPKKVLGFAGIEDVFTSRGSKTLGNFVKATFDLUMKTYGLFTDPDFWKETRFKSPFQEVADLLKPKSKVIVYITTEEAAPETVQA

NbL09g06990.1 scarecrow-like_protein_14 [MW = 84.73 kDa]

No. of times detected



log(intensity)



Values from



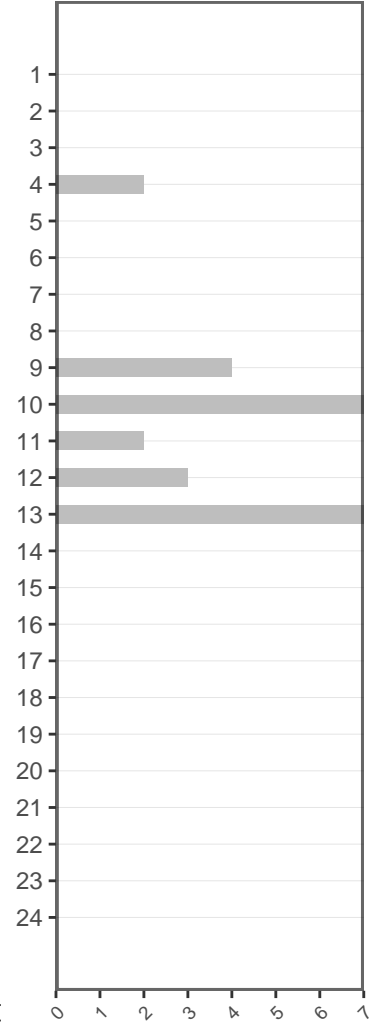
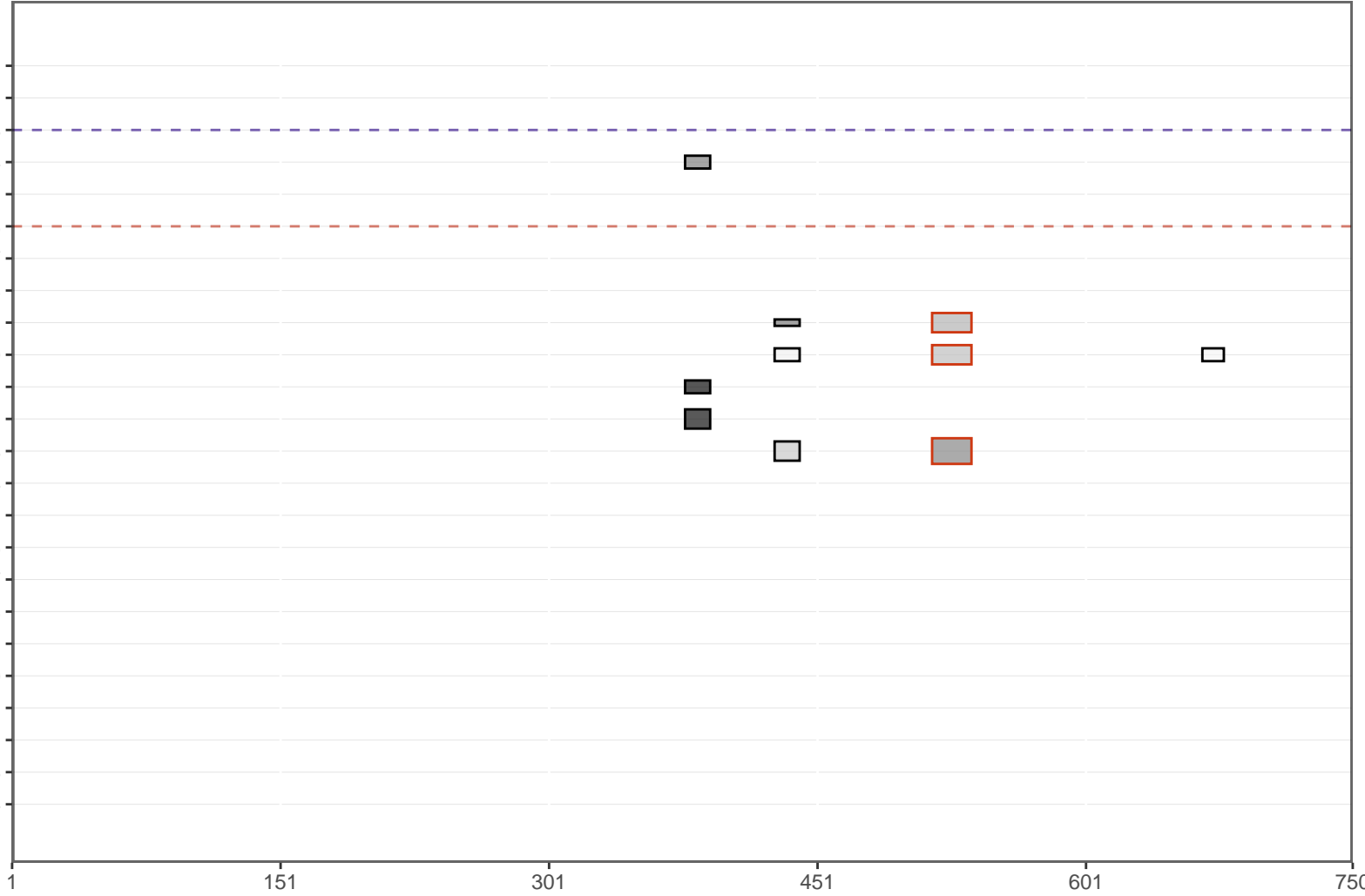
MW indication



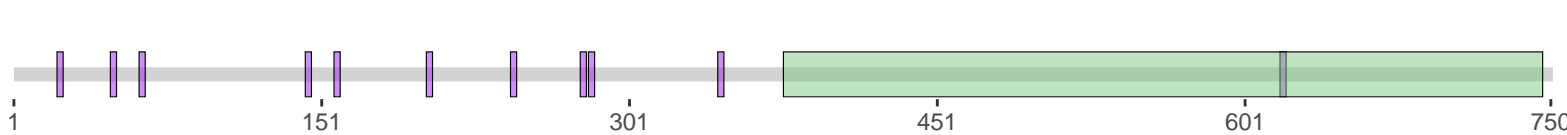
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

SKTRAKCGTKNEAVDRITLISGAGSVAADDRRTAVYEQLKQIRGHSPTGDAYQRLASVTFADGLEARLAGTGTGGYALAPKRITAEKIKAYQVYLSGSPFKKISIFFANKMIFHTASNARTLHLIDFGITYGFGWPIQLQLSGMPGPGPKLRITGIDLSGPGFRPAESLEGTGNRLAKYGERFHPVPEFYTAATGNWENIKEDLKLASGETVAVNGLFRKLNLLDETYYVDSRDAVGLGIRKMPDFIVGAVVNGSYPAPFFVTRFREALPHYSTLFDMFDATLPRDOOORLH

NbL09g06980.1 uncharacterized_protein_C24B11.05-like [MW = 33.12 kDa]

No. of times detected



log(intensity)



Values from



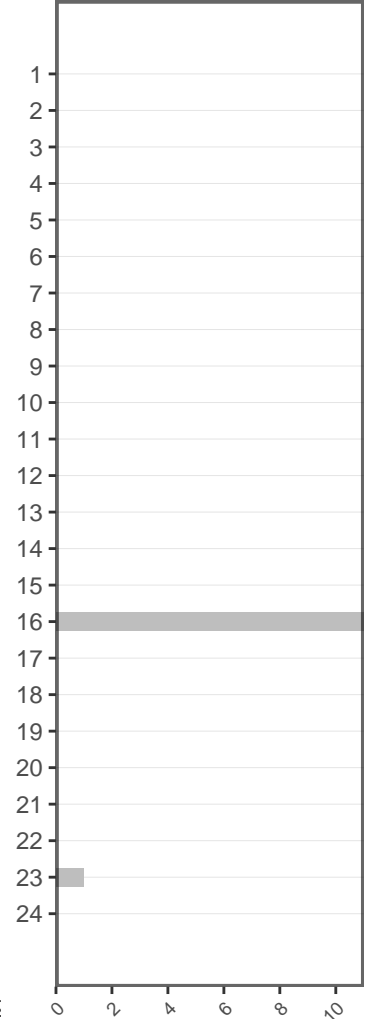
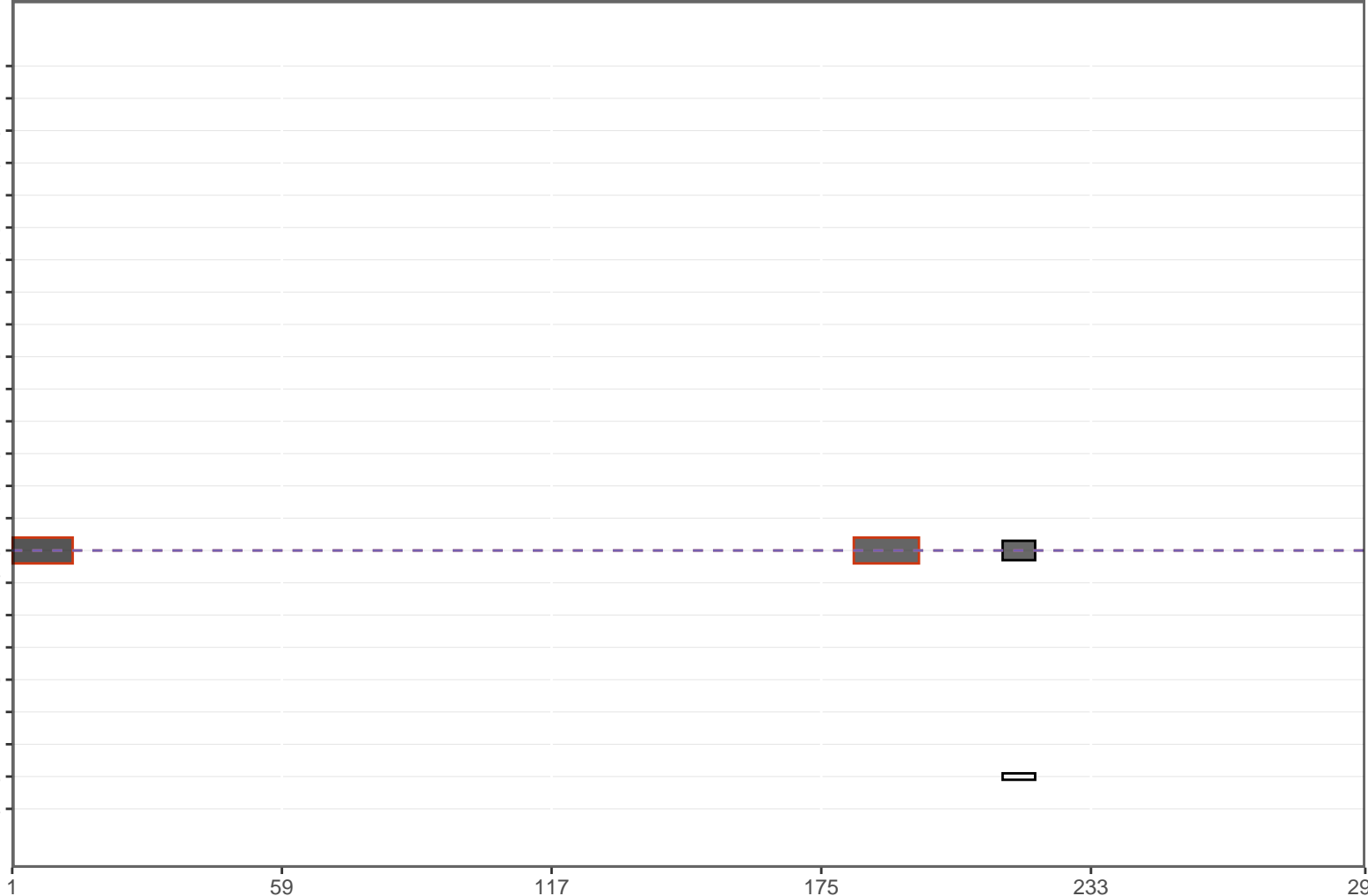
MW indication



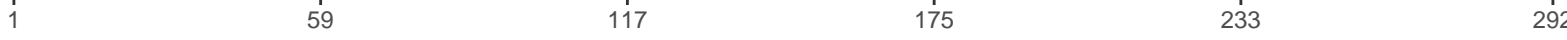
Molecular weight



Gel Slice

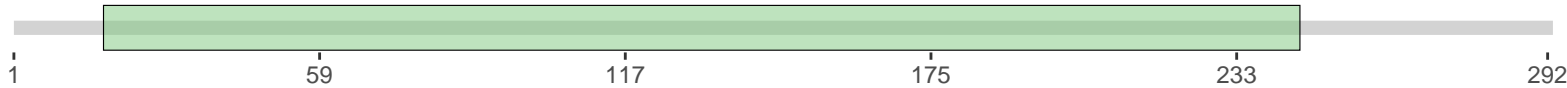


Protein length

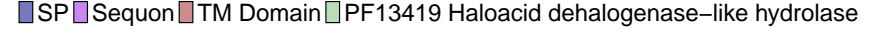


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LRNLLHSLPFRKVFQSNANEAHVAVKVLRLGLEDFDDICGFETVNPTRNSVALDNINGESARTLVVCKPFEAEVAFKIANINPKQTLFFDDSVIRNLGTAKLMLGHTLVWVGHSHRTKGIYALESHINMKEALPELWEGVRFQVHISEKTAIEVRV

NbL09g06800.1 phosphoserine_phosphatase_chloroplastic [MW = 35.31 kDa]

No. of times detected



log(intensity)



Values from



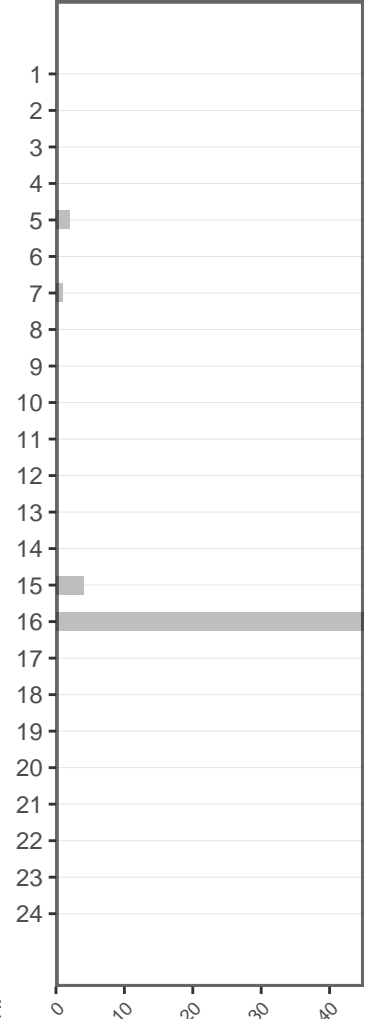
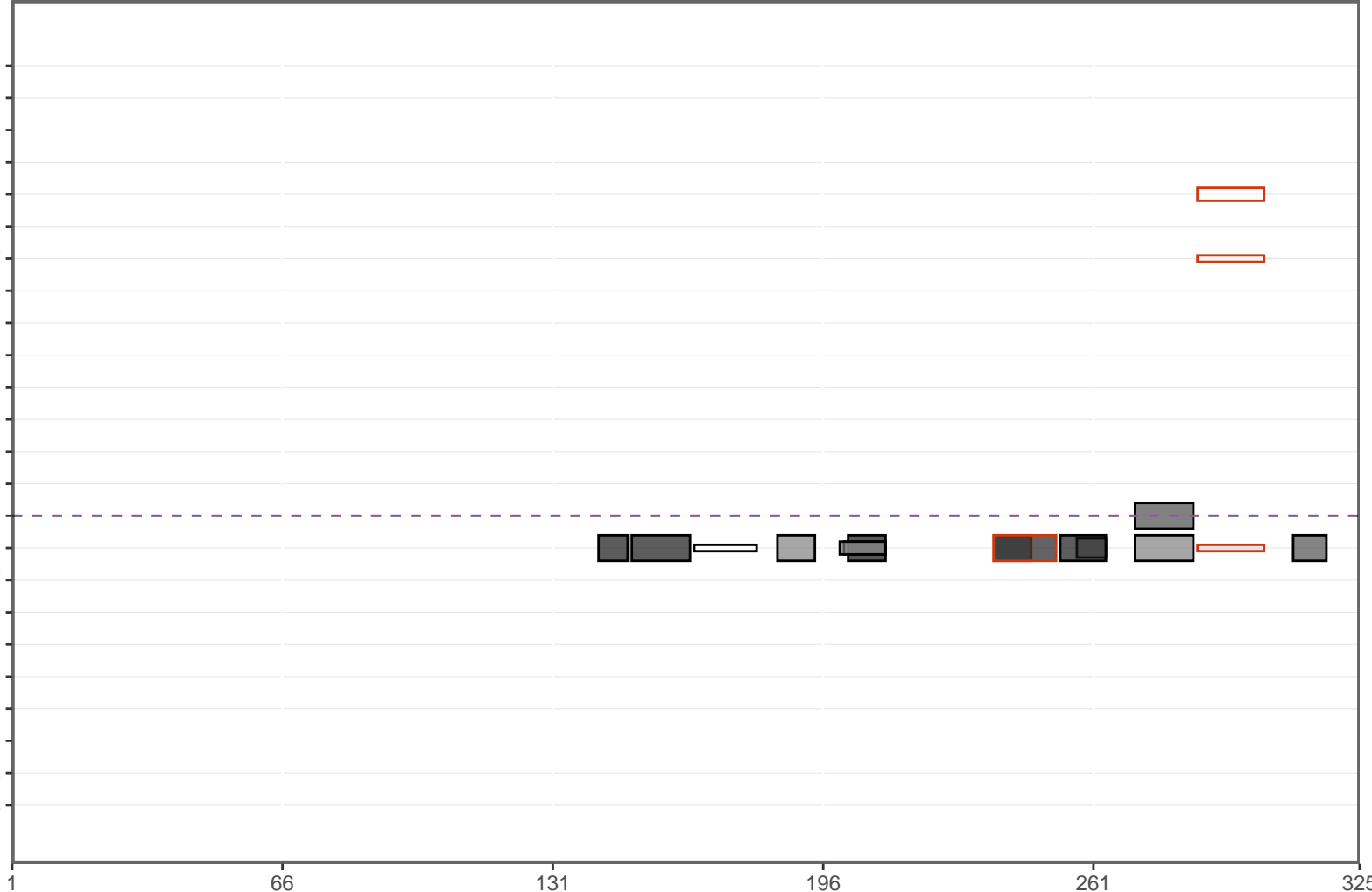
MW indication



Molecular weight



Gel Slice

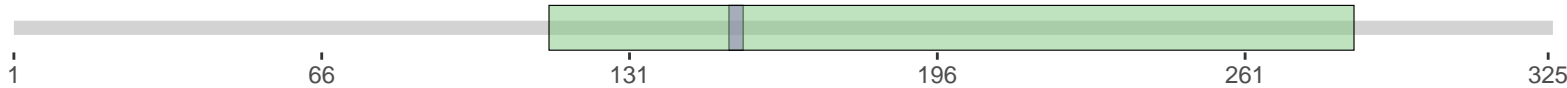


Peptide counts over 4 repeats

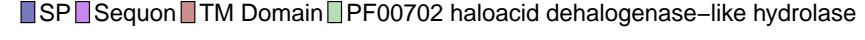
Protein length



Pfam domains



Pfam Description



Protein sequence:

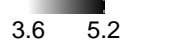
IAAMNGSVPFEDALAAARLSINPELGGLODFLKRPPRLSPGIDLLVKKLKKKKDYLVLGGFRGMNPAVSLGITLENFANGMLFRSNGEFAGFDKNEFTSRGGKPTAVGQKKARGYKSVVMIGDCATDLEARLPGGADLFICYGGVQLREPVAAKADWLWVFNFKDLINSL*

NbL09g06730.1 cytosolic_enolase_3 [MW = 51.71 kDa]

No. of times detected



log(intensity)



Values from



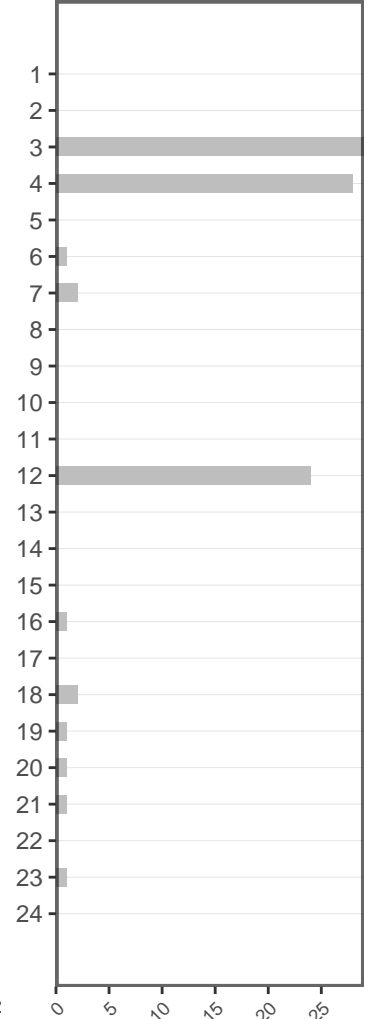
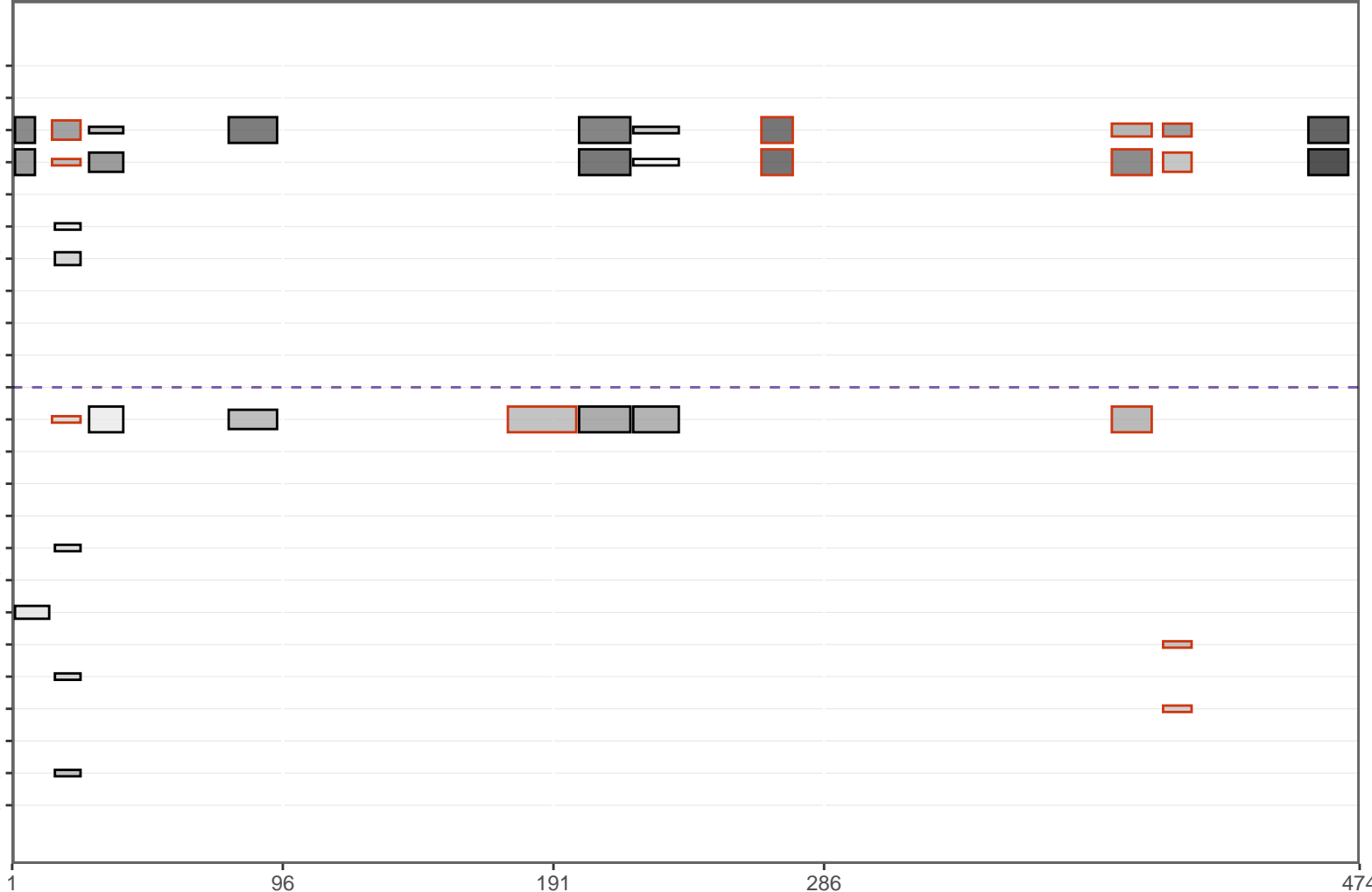
MW indication



Molecular weight

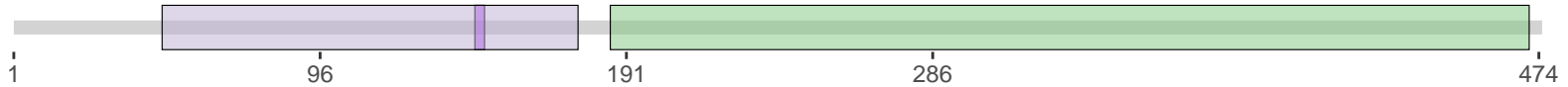


Gel Slice



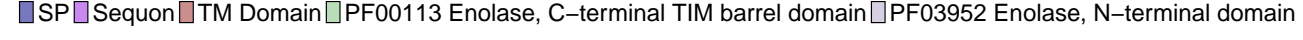
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGSETYHRLKLVITEKYGAGGNVGEDGGFAPDISLRDLVGEAGRTGYKEKHAIGVAATEFGIGTKYDLKLTPTKHSQGNFKSGGDMIMYKELCADYPIVSIEDPFKEDWEHVYFSSLGMCQVVGDDLLMSPKRIERAQENACNALLKVNQIGTVEFTEVVKMAKDAQWGVVMSQRSGEETEDSFIADLSVGLATGGQKAGAPGRGERLAKYNGLLRIEDELGGQAFYIGEKWRT

NbL09g06720.1 proliferating_cell_nuclear_antigen [MW = 32.2 kDa]

No. of times detected



log(intensity)



Values from



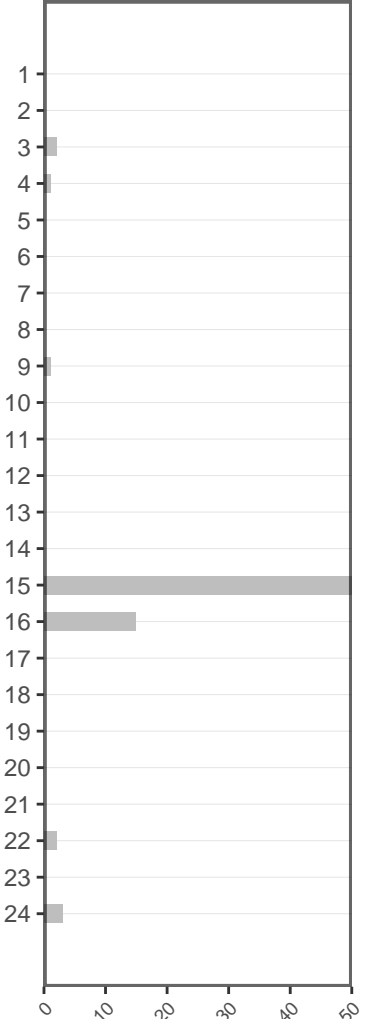
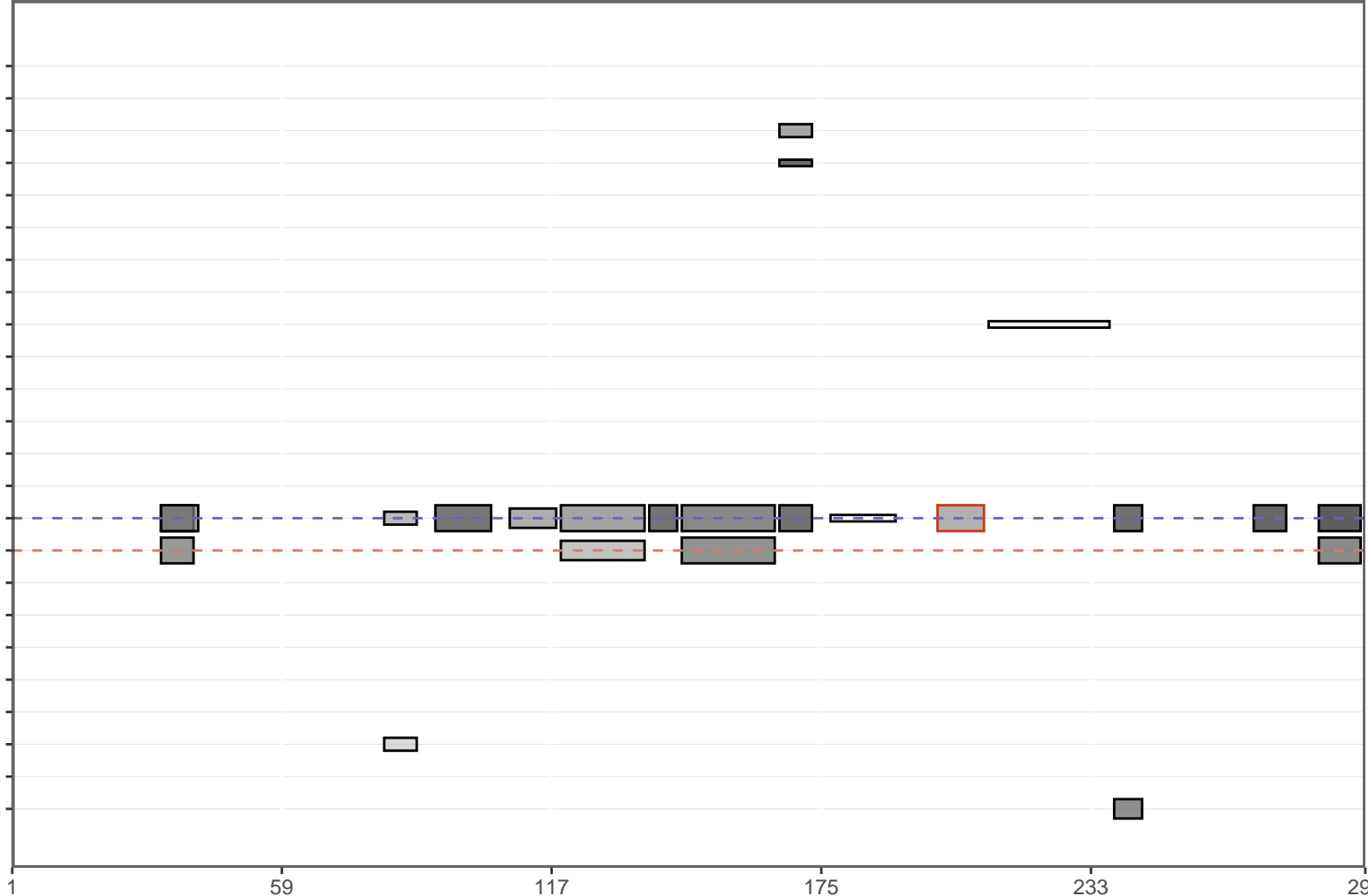
MW indication



Molecular weight



Gel Slice



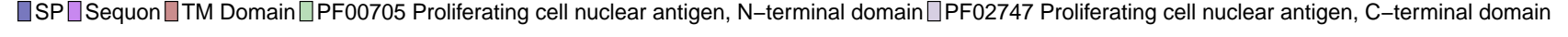
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ESPTQDKADFEMLMDIDSEHLGIPAEYHAHVRMPSAEFARIGKDLSSIGDVTVISVTKEGVWFSTRGDTANVCRGNFTVDKPEEATVIEMNEPVSITFALRYLNSFTKATPLNNTVITLSSSELPVIEVKKIEMGQYIRFLAPKIEDEEETKPT

NbL09g06690.1 acyl-coenzyme_A_thioesterase_13-like [MW = 17.19 kDa]

No. of times detected



log(intensity)



Values from



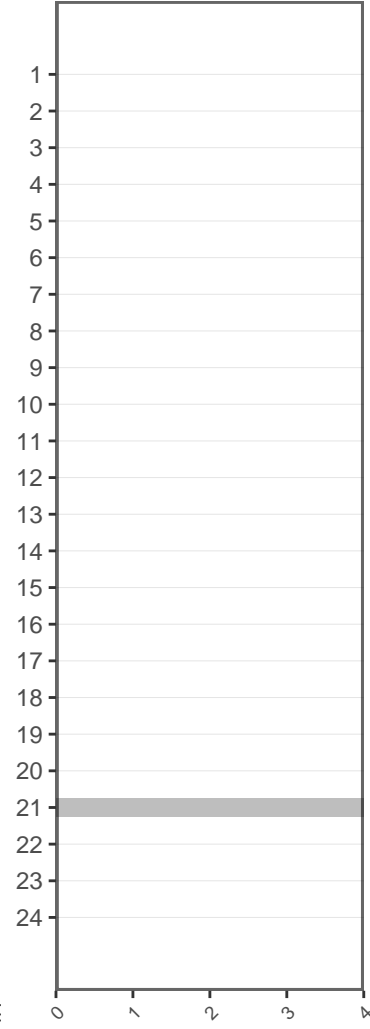
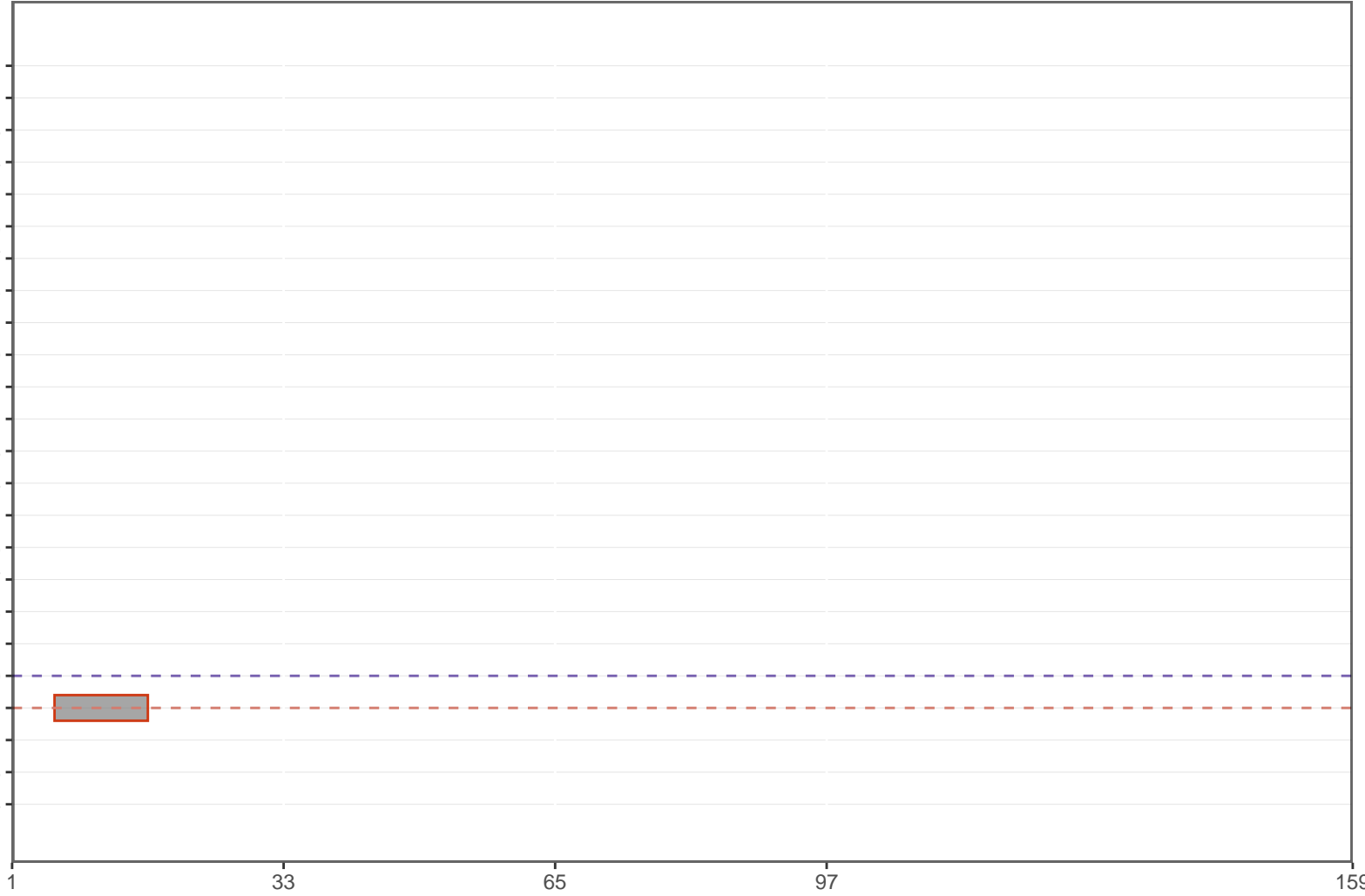
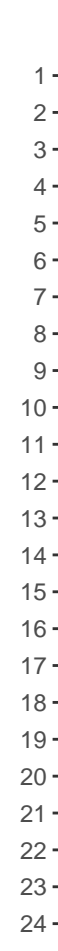
MW indication



Molecular weight

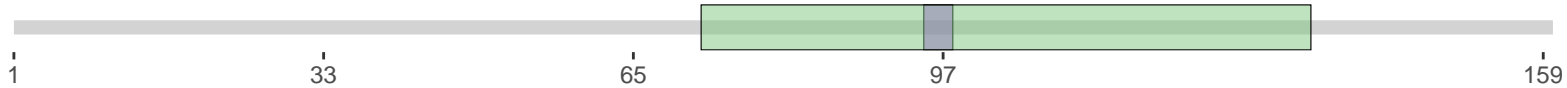


Gel Slice



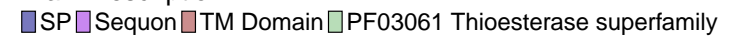
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

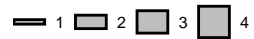


Protein sequence:

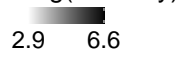
EEGLASGAIANLYDEVEGAVFVEGLPMNVSVDMISIFLSSAKADDELEIGRVAQGRKRGVSGTEVYVKNKATGELIAEGRHSLFGKHASKM

NbL09g06630.1 beta-glucosidase_BoGH3B-like [MW = 65.71 kDa]

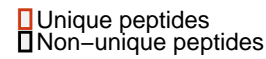
No. of times detected



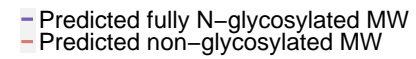
log(intensity)



Values from



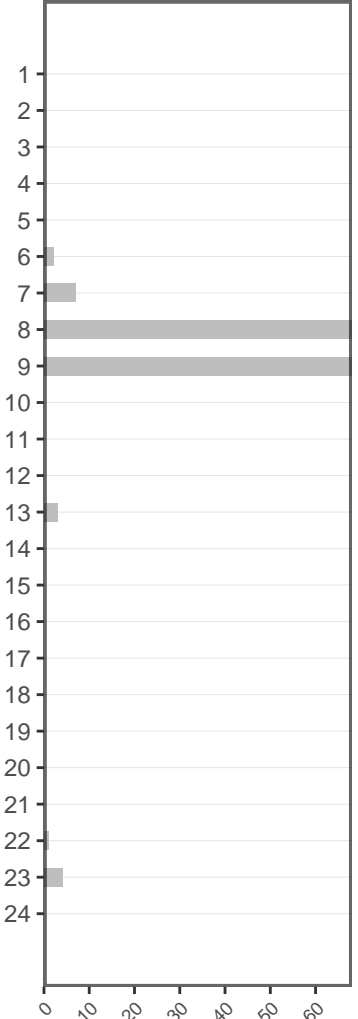
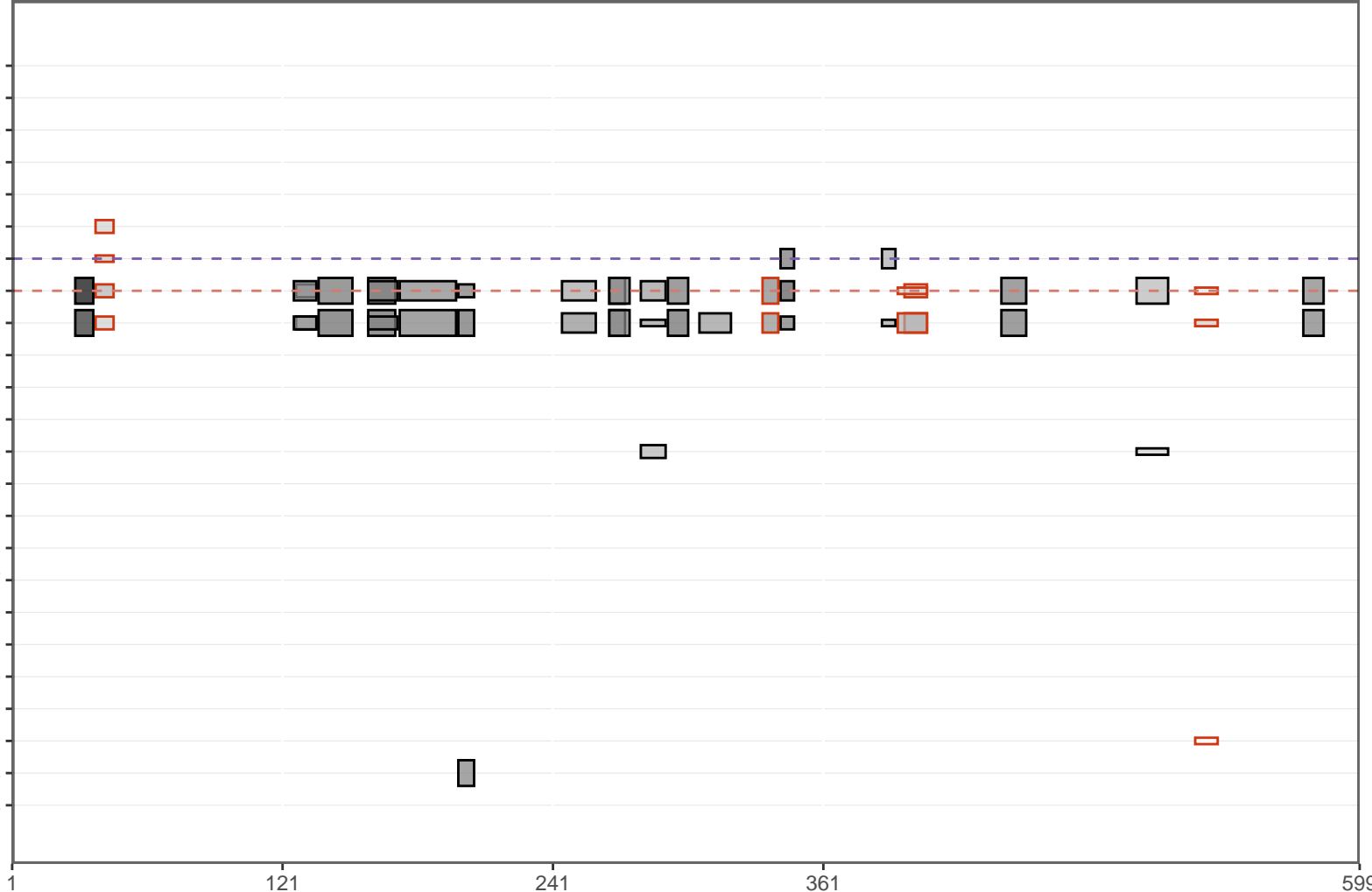
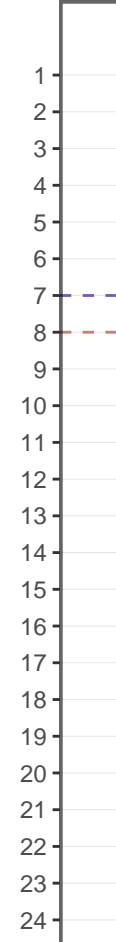
MW indication



Molecular weight

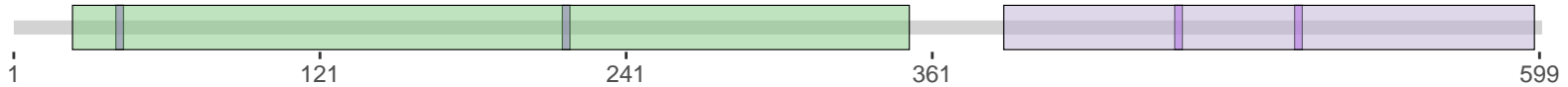


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

SP Sequon TM Domain PF00933 Glycosyl hydrolase family 3 N terminal domain PF01915 Glycosyl hydrolase family 3 C-terminal domain

Protein sequence:

ITDVEALDRITDPHGSDVRSKSTFNAGIDMMVFRVYELFLEELLKSLKSGEISMARIDDAVERILRVKVFAGLFEHPFTDRSLLELVGGEAHRDVAEARKSLVLLKNGKDPTRKPLFLDRNANKKLVAGTHADDLGYOCGGWTATWTGEGSRITVQTLLEALKKVGNETEIVFEPNPTAETTFANQDFSAVAWAGEGPGVCEGTGGDDPELRIPFNTEATFVADRVPTVTLISGRPMVLEPALLEKVDAPVAWALPGTEGAGITDNLFGDYPFGQKLPV/TWFKTYDQLPMH

NbL09g06520.1 pleckstrin_homology_domain-containing_protein_1-like [MW = 16.64 kDa]

No. of times detected



log(intensity)



Values from



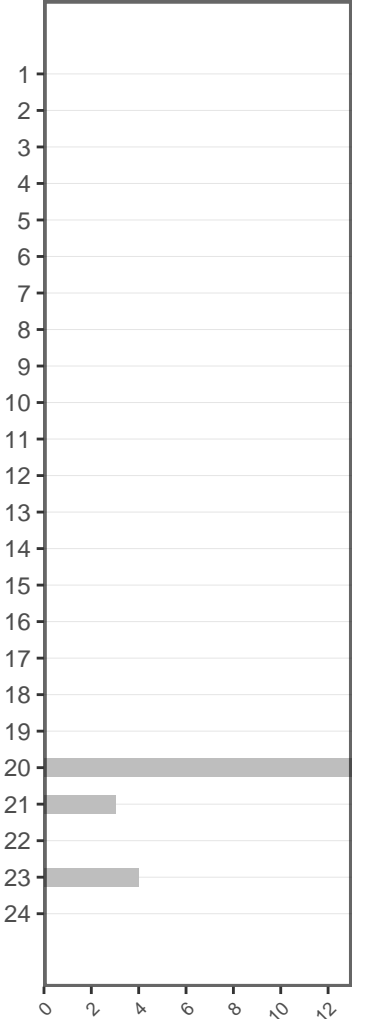
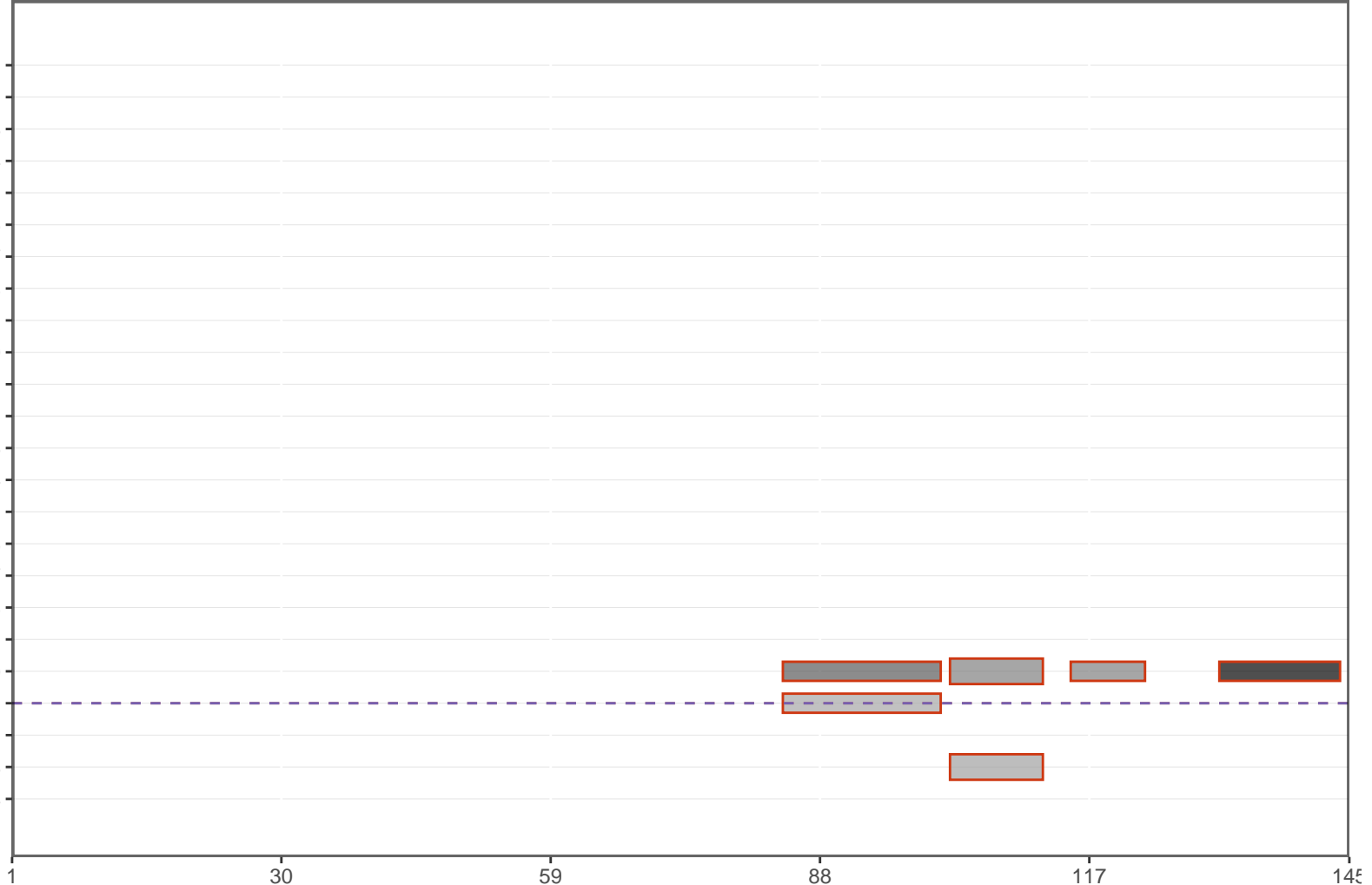
MW indication



Molecular weight



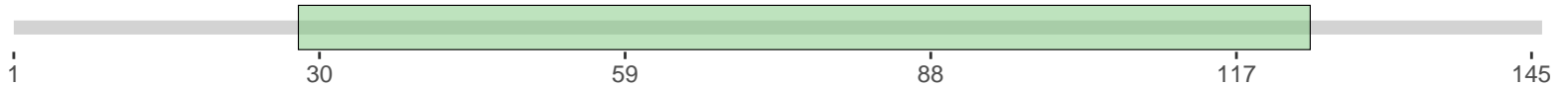
Gel Slice



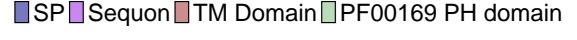
Protein length



Pfam domains



Pfam Description



Protein sequence:

KDPSSVTRAAPRGVGVVVAEGLTVKGAEDVINKPFAFELTGRDITMYFIADSEKEKEEWINGRGSIVQHSRSVTDGEVVDYDRP

NbL09g06430.1 peptidyl-prolyl_cis-trans_isomerase_CYP19-4-like [MW - SP = 19.54 kDa]

No. of times detected



log(intensity)



Values from



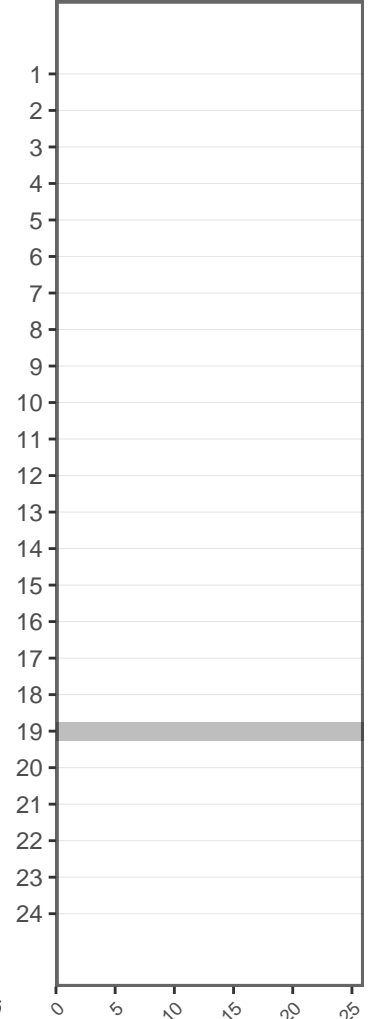
MW indication



Molecular weight

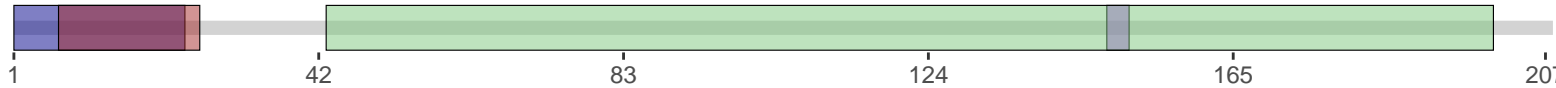


Gel Slice



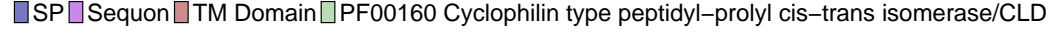
Peptide counts over 4 repeats

Protein length



Pfam domains

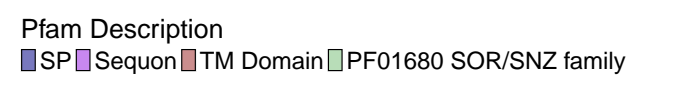
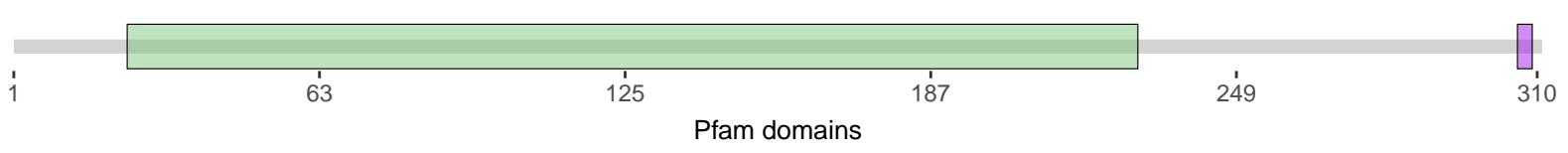
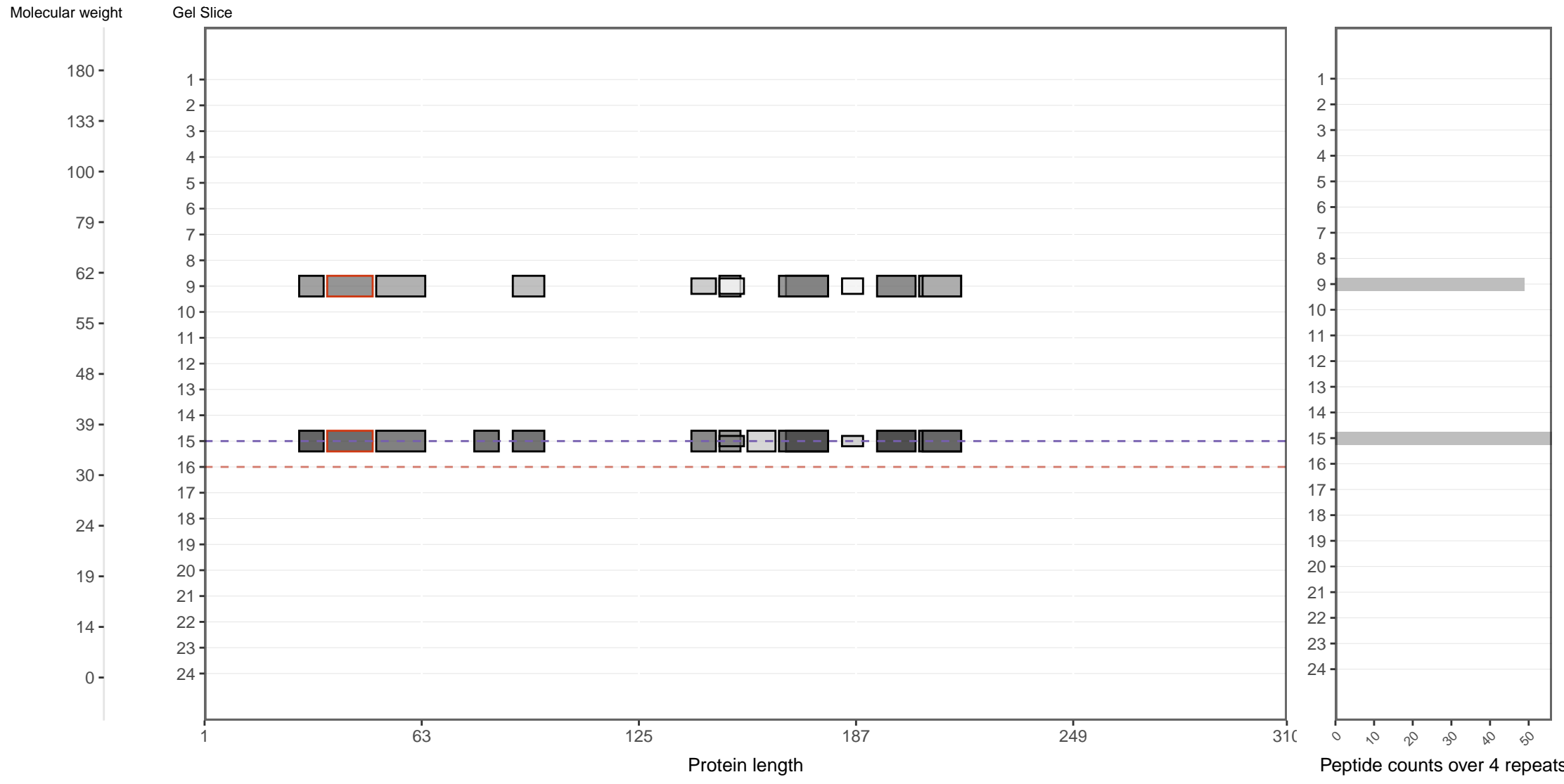
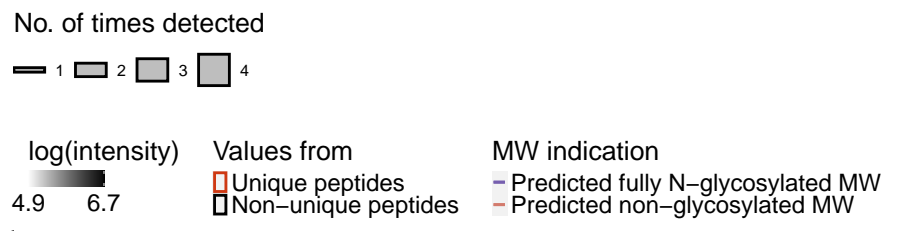
Pfam Description



Protein sequence:

STFHRIPSEMLQSGDFTLGDGRGSEBYGEKFDENFKIKHTGPLELSEMANAGPDINGSGDFFITVTSWLDGRHVVFGKVLGMDVYVYKIEAEGRGGSTPKSKVVIADSGELPL*

NbL09g06410.1 probable_pyridoxal_5'-phosphate_synthase_subunit_PDX1 [MW = 33.09 kDa]



Protein sequence:
 CCRCNLGELRRIRREGAMIRTKGEAGTGNIEAVRHVRBVMGDRVLRNMDDEVEFFAKKLGAFYDLVMGKQLGRLPVVFHFAAGGWATPDAALMMLQGGDGVFVSGGFKSGDPMKRAIVQAVTHYSDPQLLAEISGGLGEAMVGINLDDKVKERYANRSE

NbL09g06350.1 ERBB-3_BINDING_PROTEIN_1 [MW = 42.78 kDa]

No. of times detected



log(intensity)



Values from



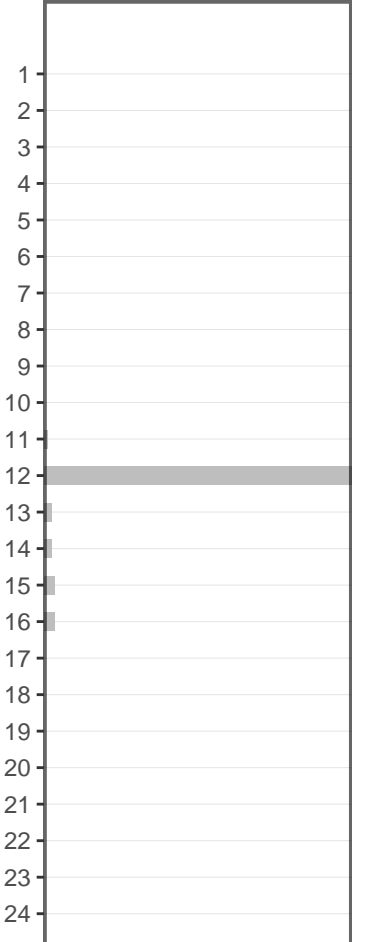
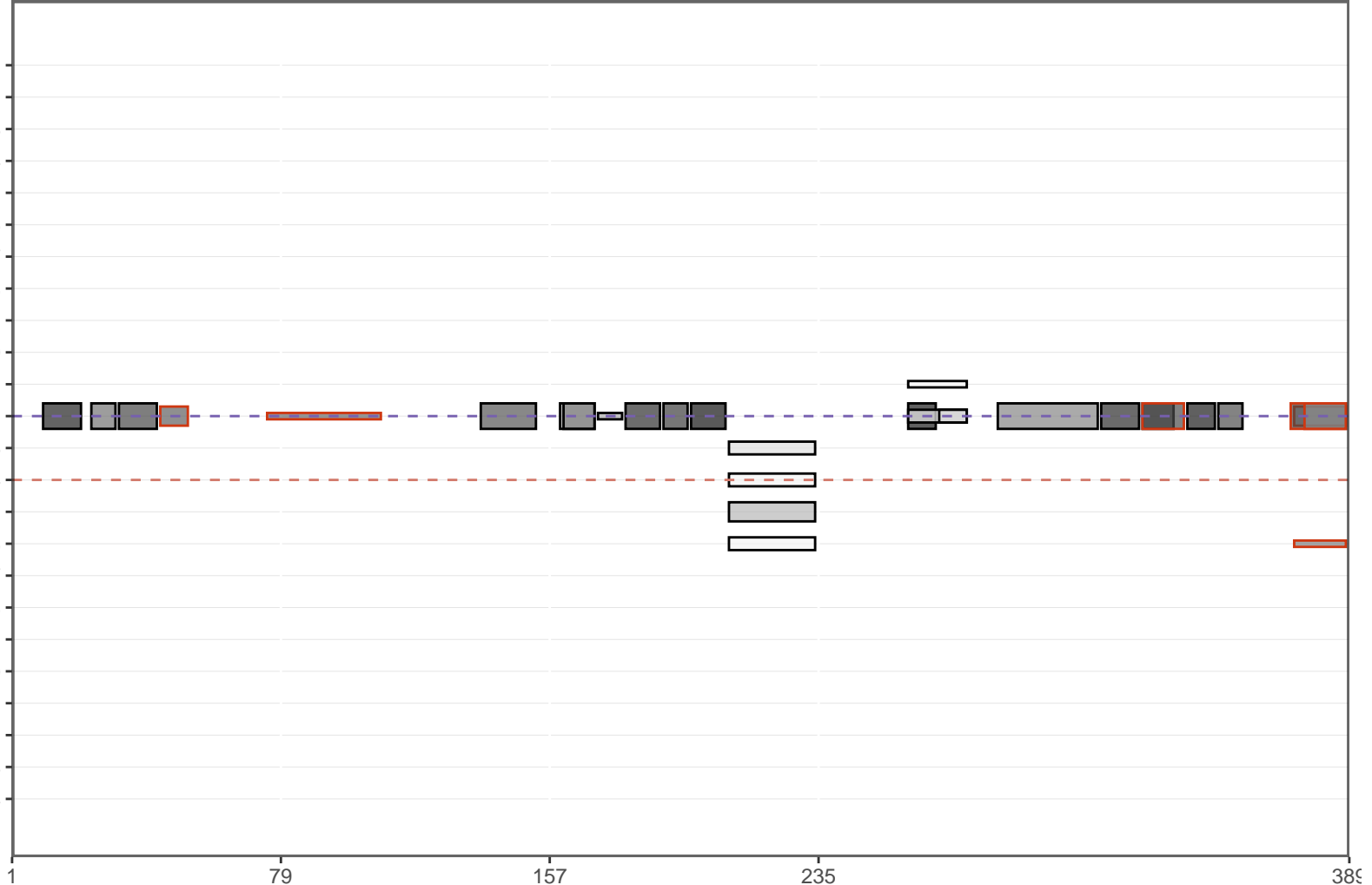
MW indication



Molecular weight

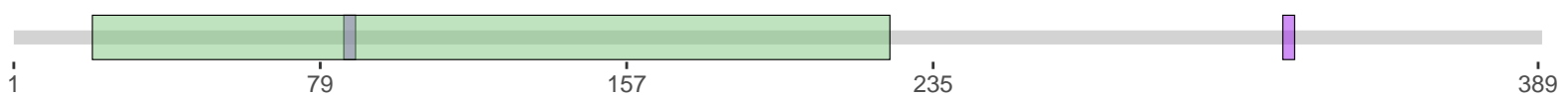


Gel Slice



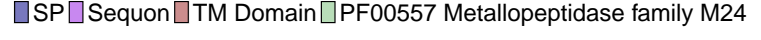
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

VLSHQMKQFVIGAKVAVLSEVTFNPEIRVDEAEFEENEVYSIDVTSTGEGPKLLNEKQTTIKRAVDKSNLKKMKASRFISEISQKPIIMPFTARDLLEKRRARLGLVEGVNHELLOPYPVLHEKPGDLVAHKFTVLLMPNGSDRVTSALGELKPAKTIENEPEKAWALPVTAKKGGGKXXXXXXXXXGDKTDEDSGAAEPEG

NbL09g06340.1 U5_small_nuclear_ribonucleoprotein_200_kDa_helicase-like [MW = 247.4 kDa]

No. of times detected



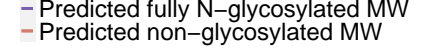
log(intensity)



Values from



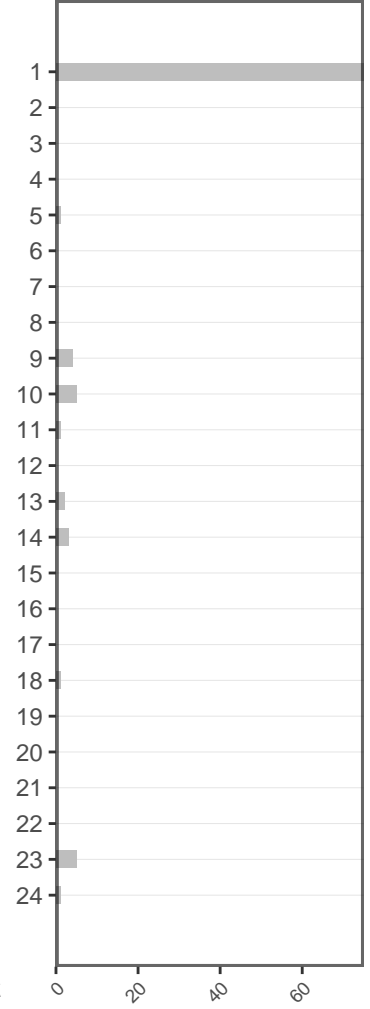
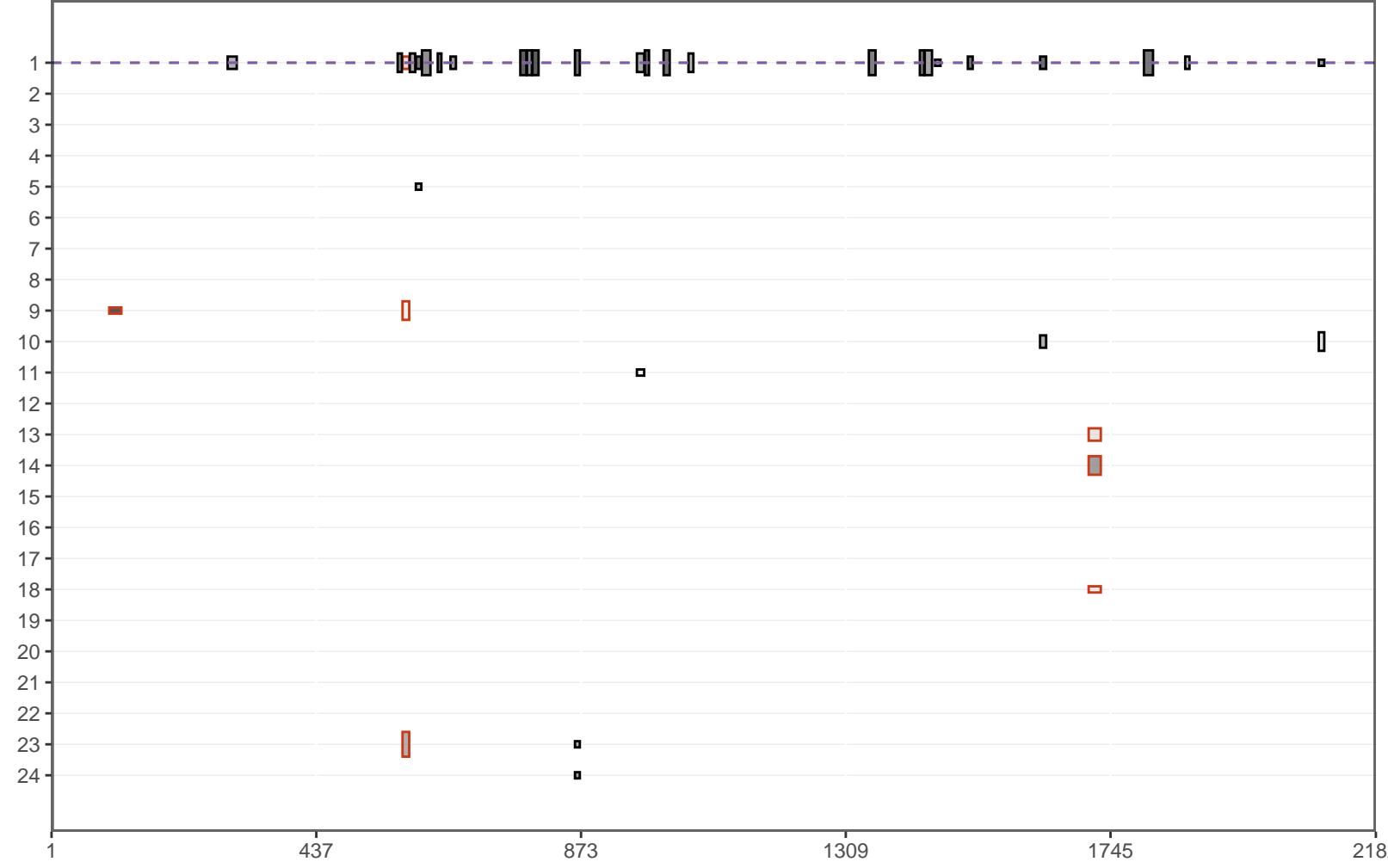
MW indication



Molecular weight

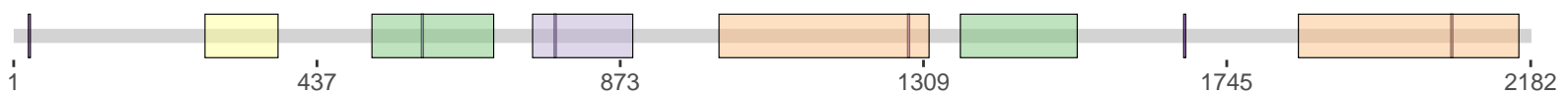


Gel Slice



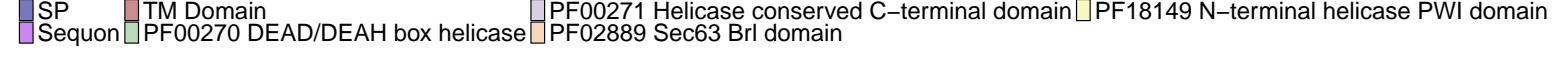
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

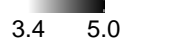
PVKEISLEEPSAKINLLGAEERLKEGLSLSDDMYYTGSAAARLMRALFENLKRWAGLAEKALKWCKMISKMWSVQTLRQGHGIPNELMKLEKDLAWERYDLSGSELGELRFGKMGRTLHKFHGFPLNLAHAHQPTREKRVRLVELTITPDPFGWDDKVKHGFVEFPVWVVEDNDGVEYLIHEYFMKKGVIDEDHTNFTVPIYELRFPQYFRRVSDRWLGGQTLVPSFRHLLPEKYPPPTTELLDGLPLVTALRNPVYEAAYGDFKHFNPVQTVQTVFLYNSI

NbL09g06330.1 6-phosphofructo-2-kinase/fructose-26-bisphosphatase-like [MW = 83.16 kDa]

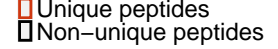
No. of times detected



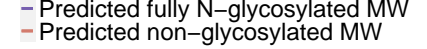
log(intensity)



Values from



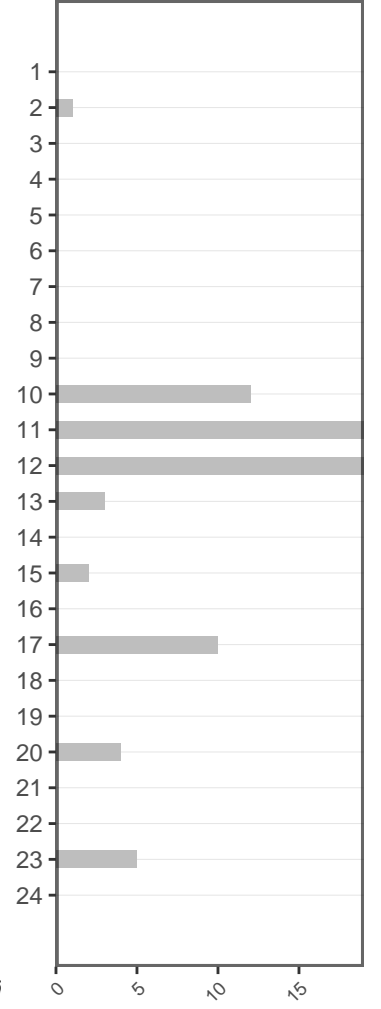
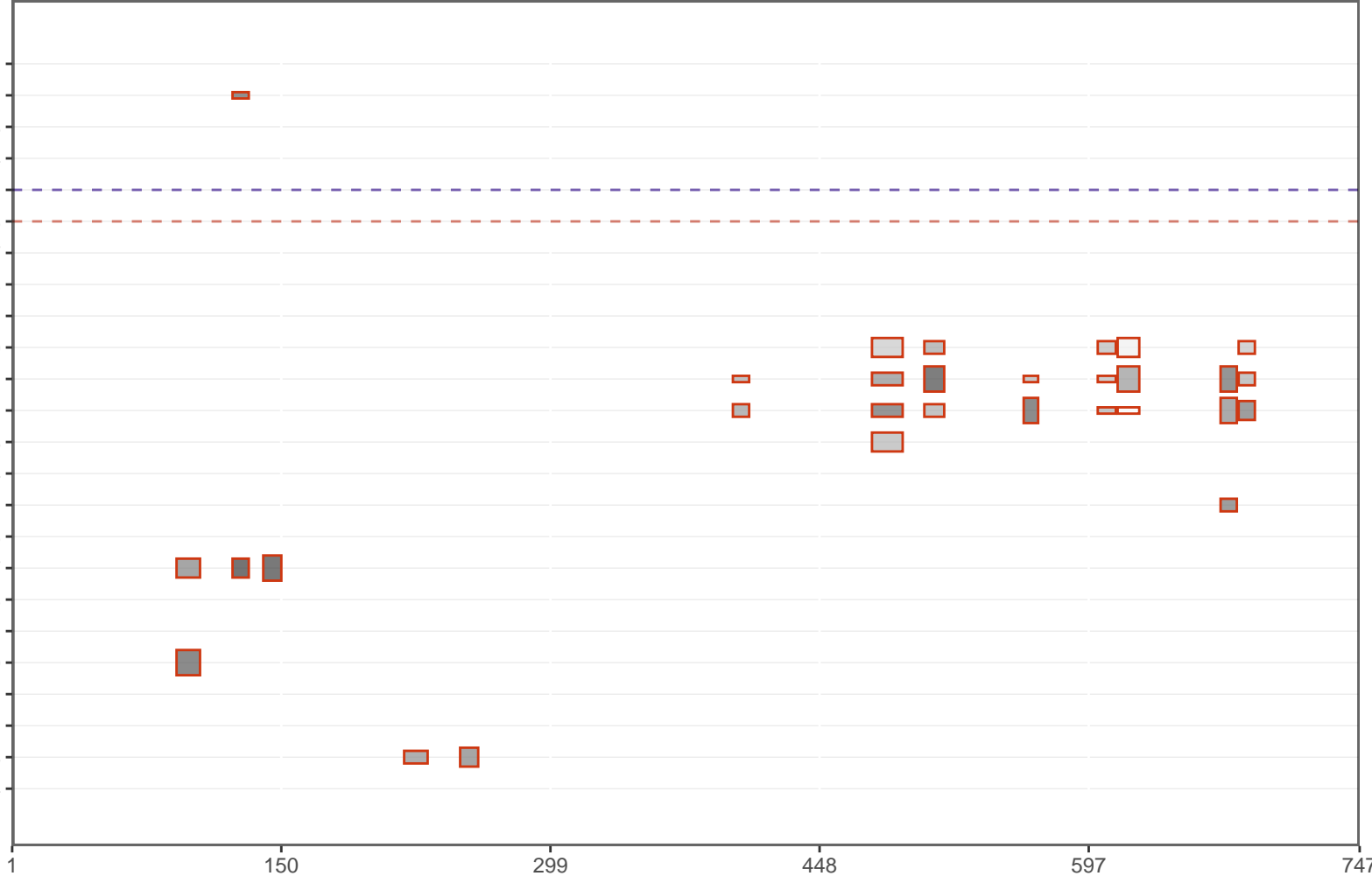
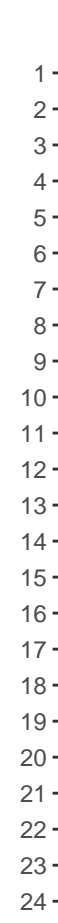
MW indication



Molecular weight

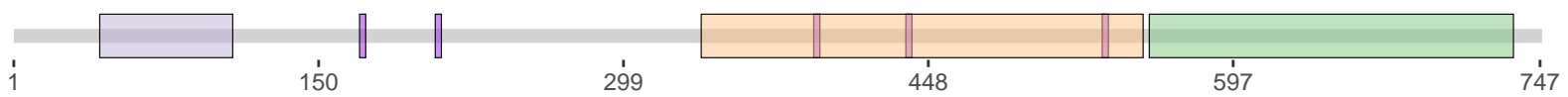


Gel Slice



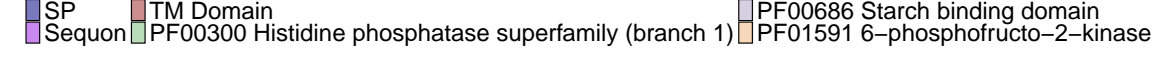
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KTFTAAKLTTRYLRWLGHDTKHFNVGKYRLKHGSMNSADFFRRDGNPEGLEARNVEAALAMEGDMTAWMDEGGGVGIFDATNSGRQRNMLMKMAEGKGIKIFLETGNDKIKIERNRLKVGQSPDVAEEDFAEGRDKNRLNDEKVEYEPVEEGGYKMDMVGSGGGGQVNNISGGLPGRVFFLWNTLHTPRPIFLTRHGESLYNFRGRNGDTSASEAGELYAKKLANFVEKRLNKEAKASIVTSTLQRTLTASPIAGFPKQWRALDEINAGVGDGMITYEEKKQMP

NbL09g06280.1 NAP1-related_protein_2-like [MW = 28.94 kDa]

No. of times detected



log(intensity)



Values from



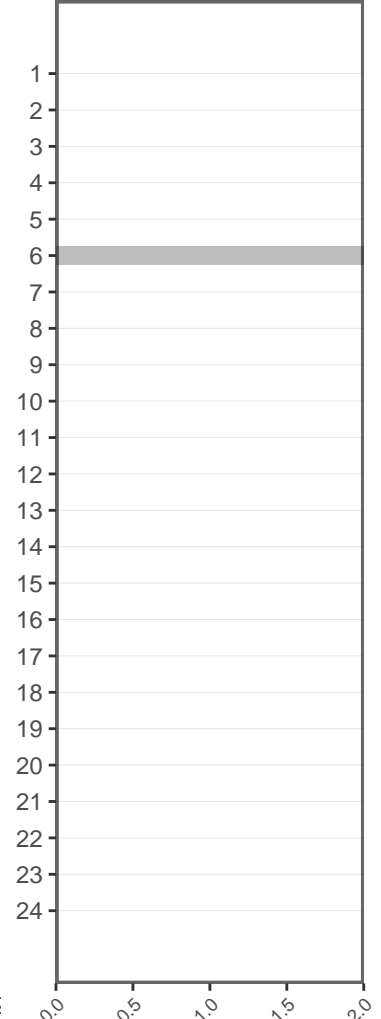
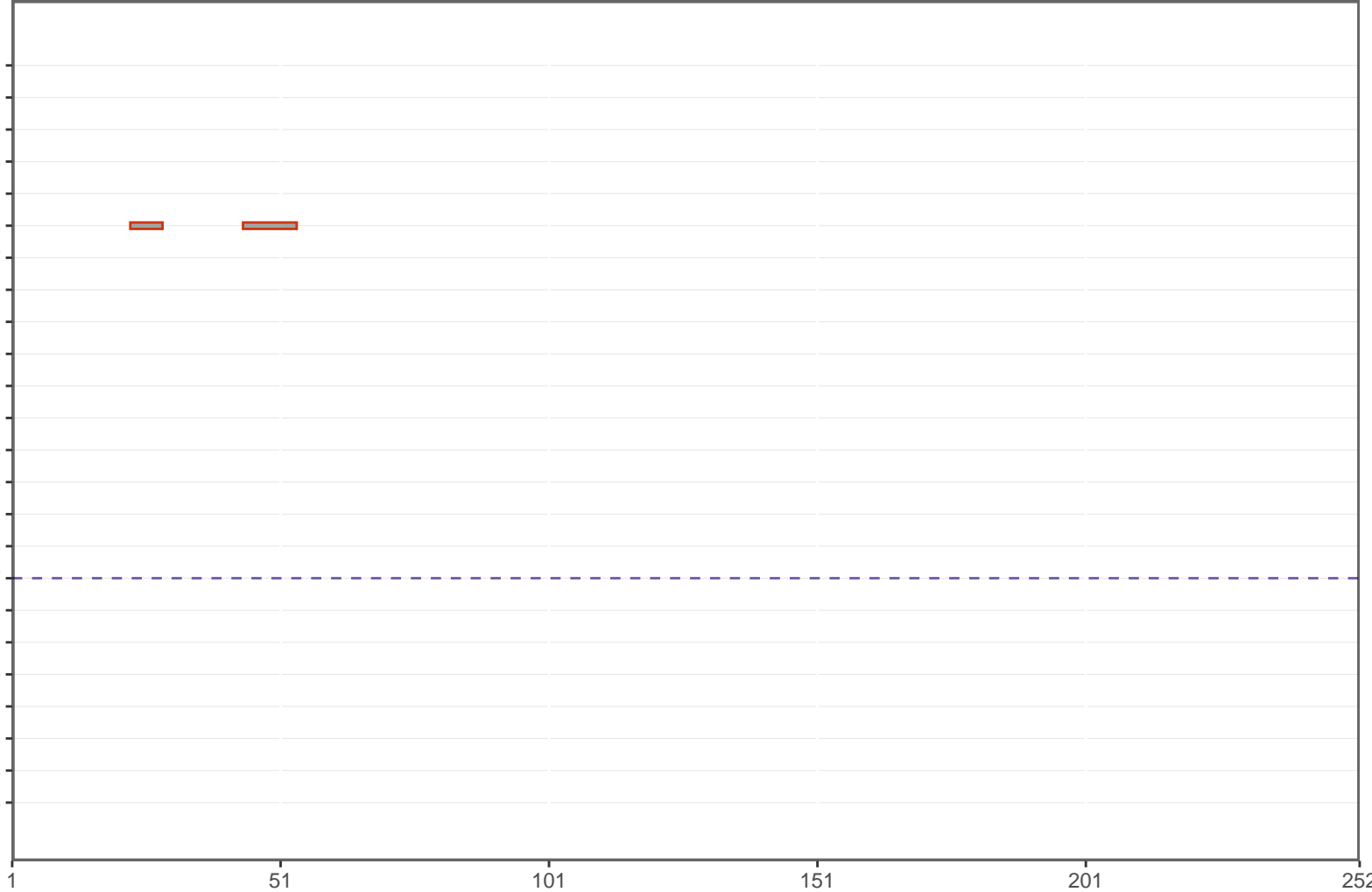
MW indication



Molecular weight

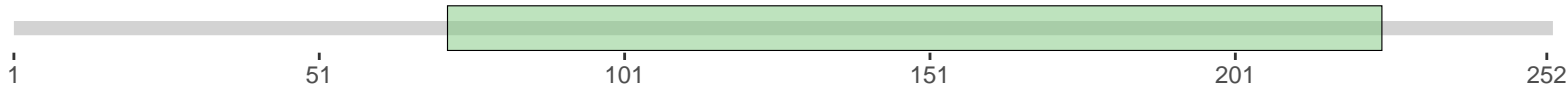


Gel Slice



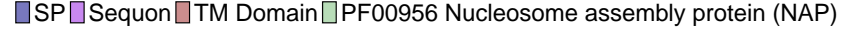
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISGHISITNFKPNPWFENSKLTKTYFLEEDGPTKNTATTKIKWKEGMAIPNGVADKNKGNKRHAEESFFTFWSEVNGKGDVDDENEILDGDDVAEIKDOLWPNPLNYFDHPDEEDIEGDEVGGHSGFIAAKLS*

NbL09g06210.1 delta-1-pyrroline-5-carboxylate_dehydrogenase_12A1_mitochondrial [MW = 60.84 kDa]

No. of times detected



log(intensity)



Values from



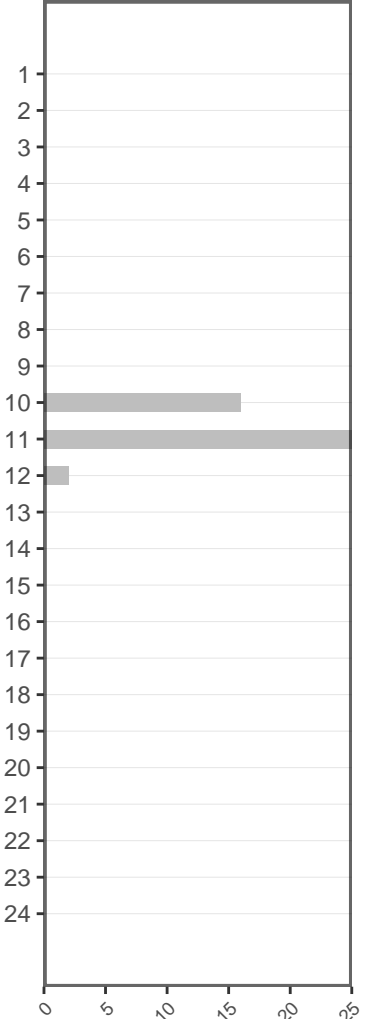
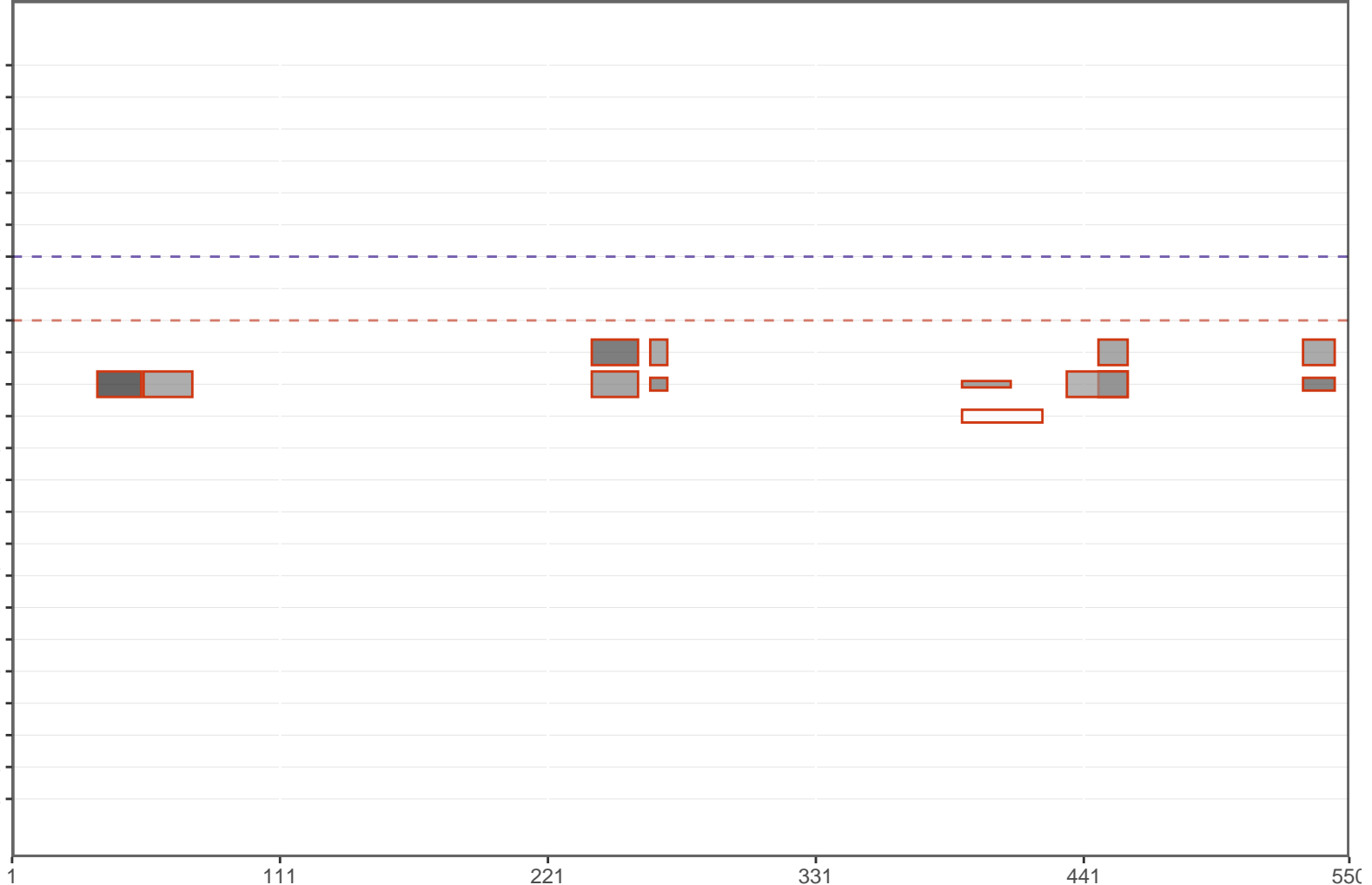
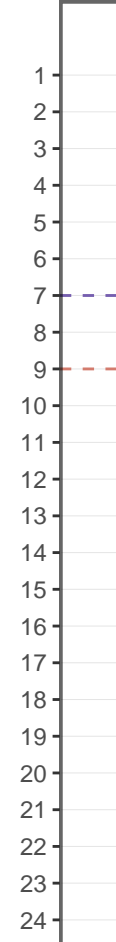
MW indication



Molecular weight

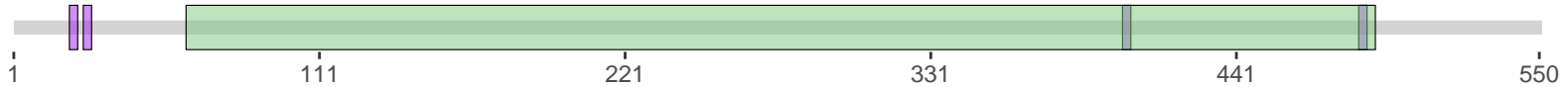


Gel Slice



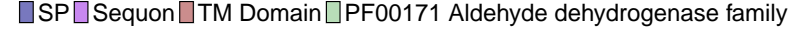
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TMINLLVEGKPRMFLFTGGSSRVAEKLADLGGKRVKLEDAFGDWKLGPDVHEVDVWVWDDGDAWAGSGGKSAQSILFMHENWGRSSLLDKMTELAARRKLDLDTGIPVLTVTEVMLEHAAKLLQIPGSRLLFGGSEALGNHSIPAYGAIKPTAIFIPLEELKEGHHVLTKEFGPFQVVEYKDNGLPLVLDALAKMHAHLTAAVVSNDLFLGEVIGNSVNGTAYGLRARTTGAPQNHVFGPAGDPRGAGIGTPEAKLWVSGHREVYVDGVPVPLGIVRTAST

NbL09g06120.1 plasma_membrane_ATPase_2 [MW = 70.41 kDa]

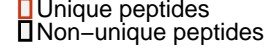
No. of times detected



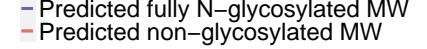
log(intensity)



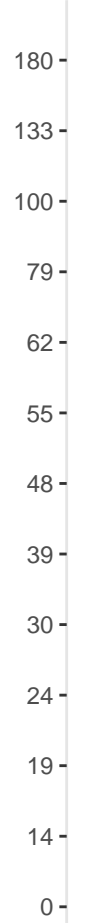
Values from



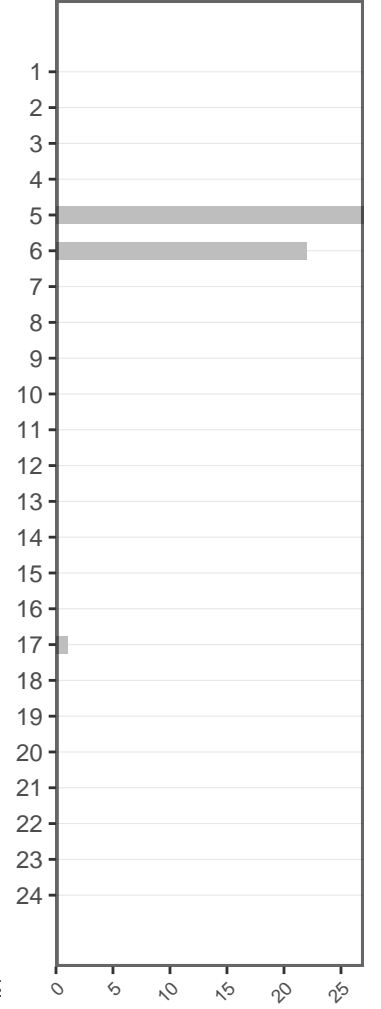
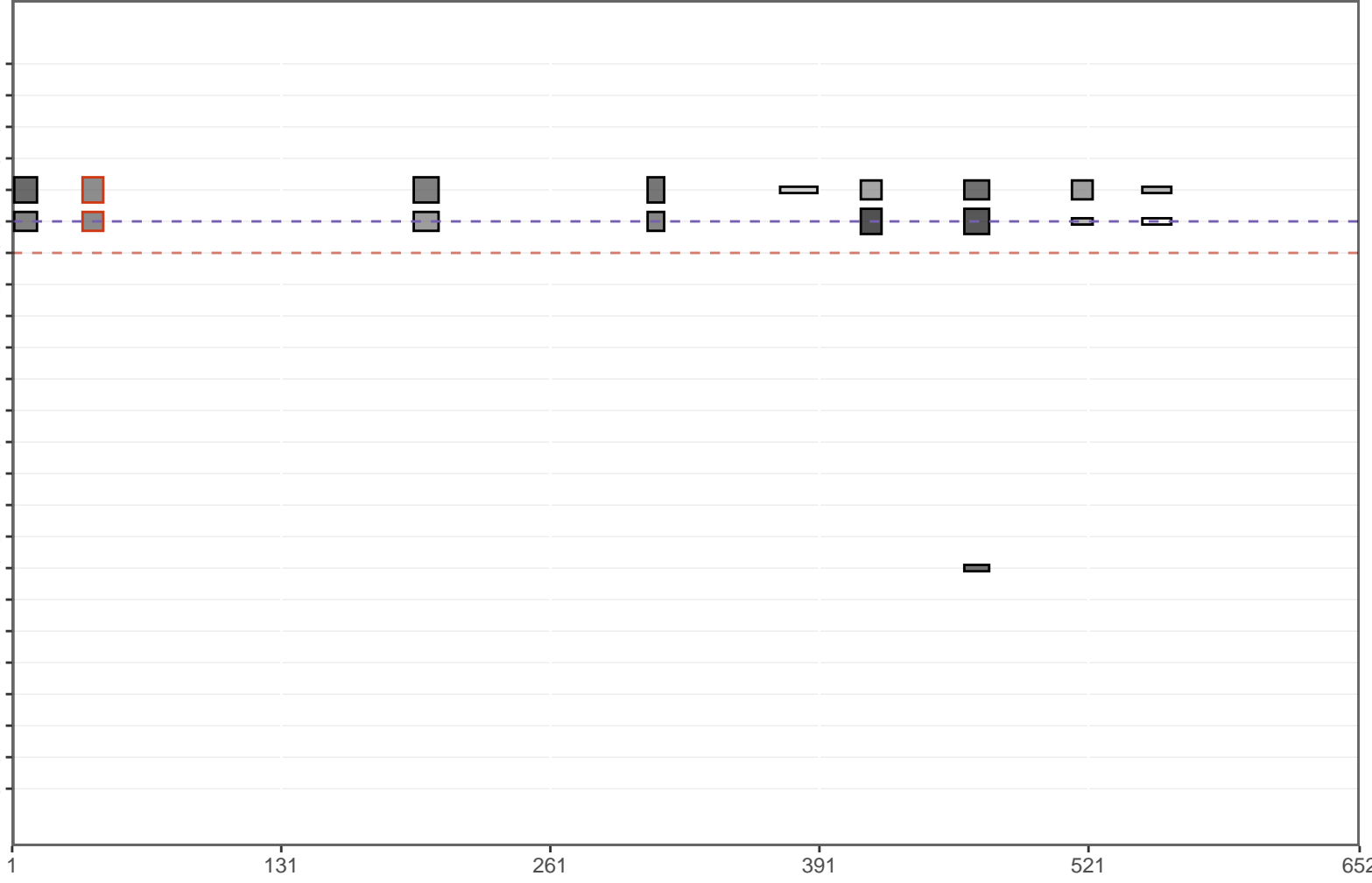
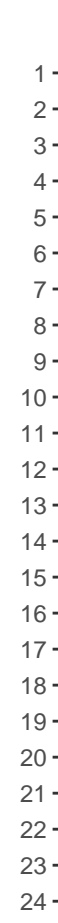
MW indication



Molecular weight

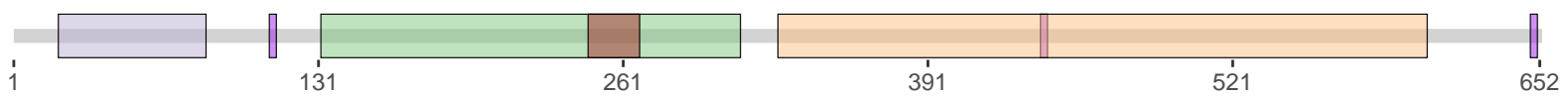


Gel Slice



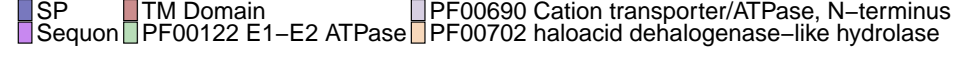
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKRMTAIEEMAGMDVLSGSKTGLFNKLVQKNIIVEVFAKGVADPTVWMAARASRTENGDADTAIVGMLGDPKKEARAGREHFLPFPNPTDKRRTALTYLDGEGKMHHRVSKGAFEGQLNAHNKSDERRRHVAIDKFAERGLRSLGWAVGEVPEGRKKESTGGPWFQIFGLLFLFDPPRHDSAEIIRRALNLGVNKKMITGDQLAIGKGTGRRLGMGTNMYPSALLGGTNDDESASLPIDELIEKADGAGVFPPEKYEIVKRLQARKHGGMTGGDGVNDAPALKKADIGIADV

NbL09g05810.1 60S_ribosomal_protein_L13-1 [MW = 23.71 kDa]

No. of times detected



log(intensity)



Values from



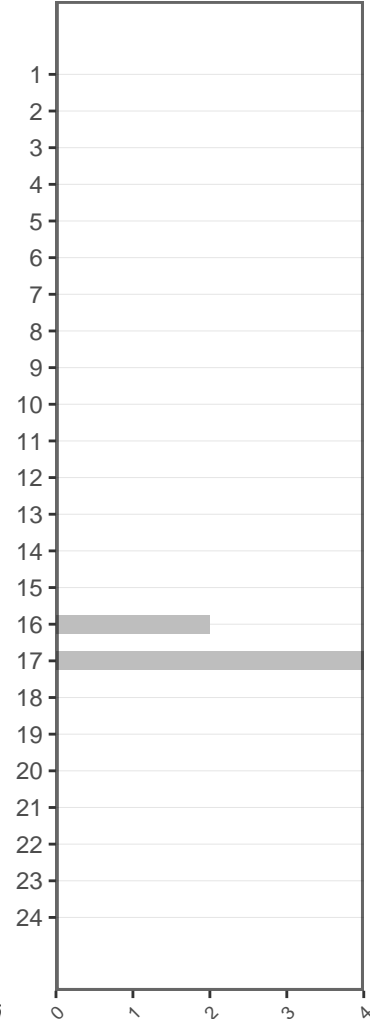
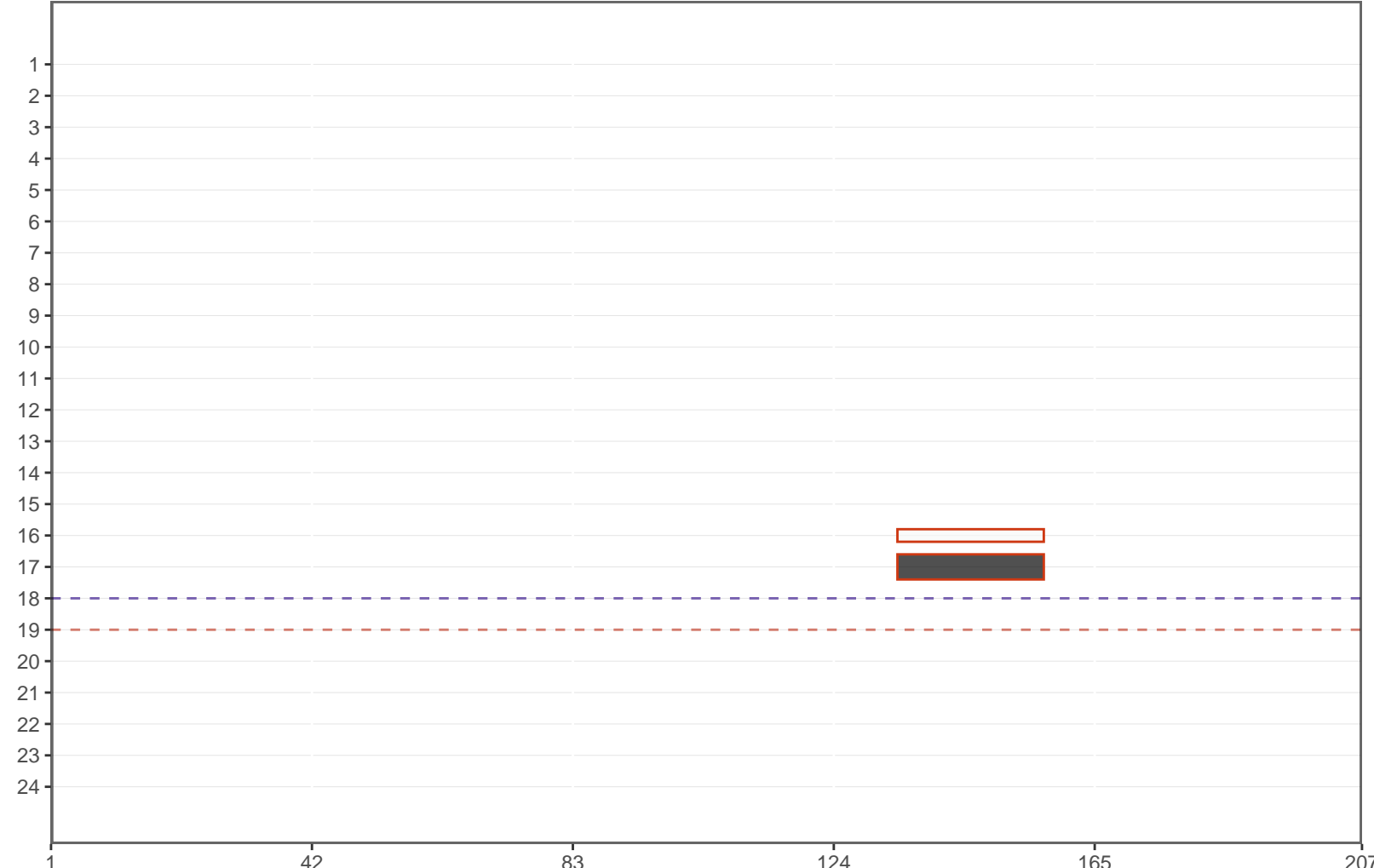
MW indication



Molecular weight

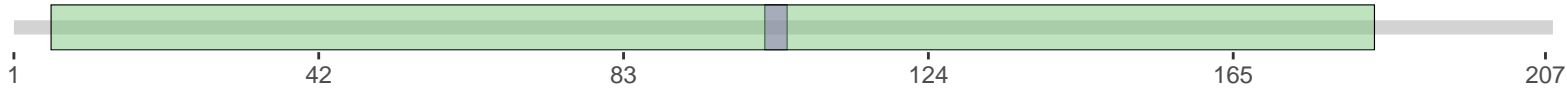


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TIGIADHRRRNRSLSEGLGTNVGRKTKYKAKLVFPRRARKVKAGDSAPEELATATQVHGDMPIAREKPSVDLWVTEEMKSFNAVYKGLRVERTNERHIGARMKRAAEAEKEEK

NbL09g05580.1 pyruvate_dehydrogenase_E1_component_subunit_beta-1_mitochondrial-like [MW = 39.42 kDa]

No. of times detected



log(intensity)



Values from



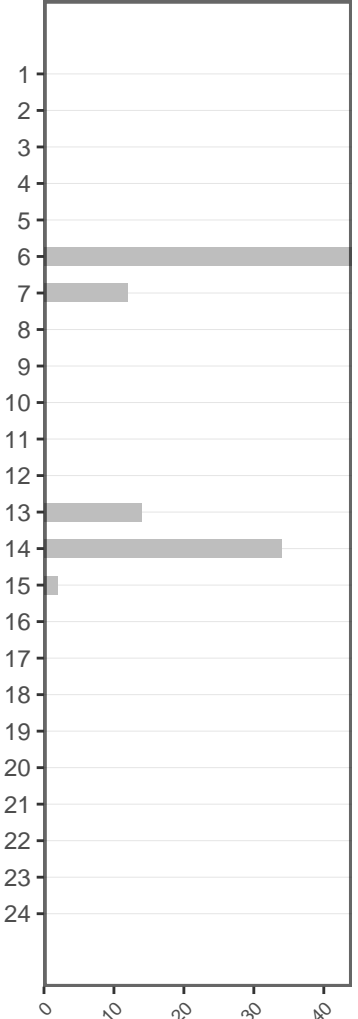
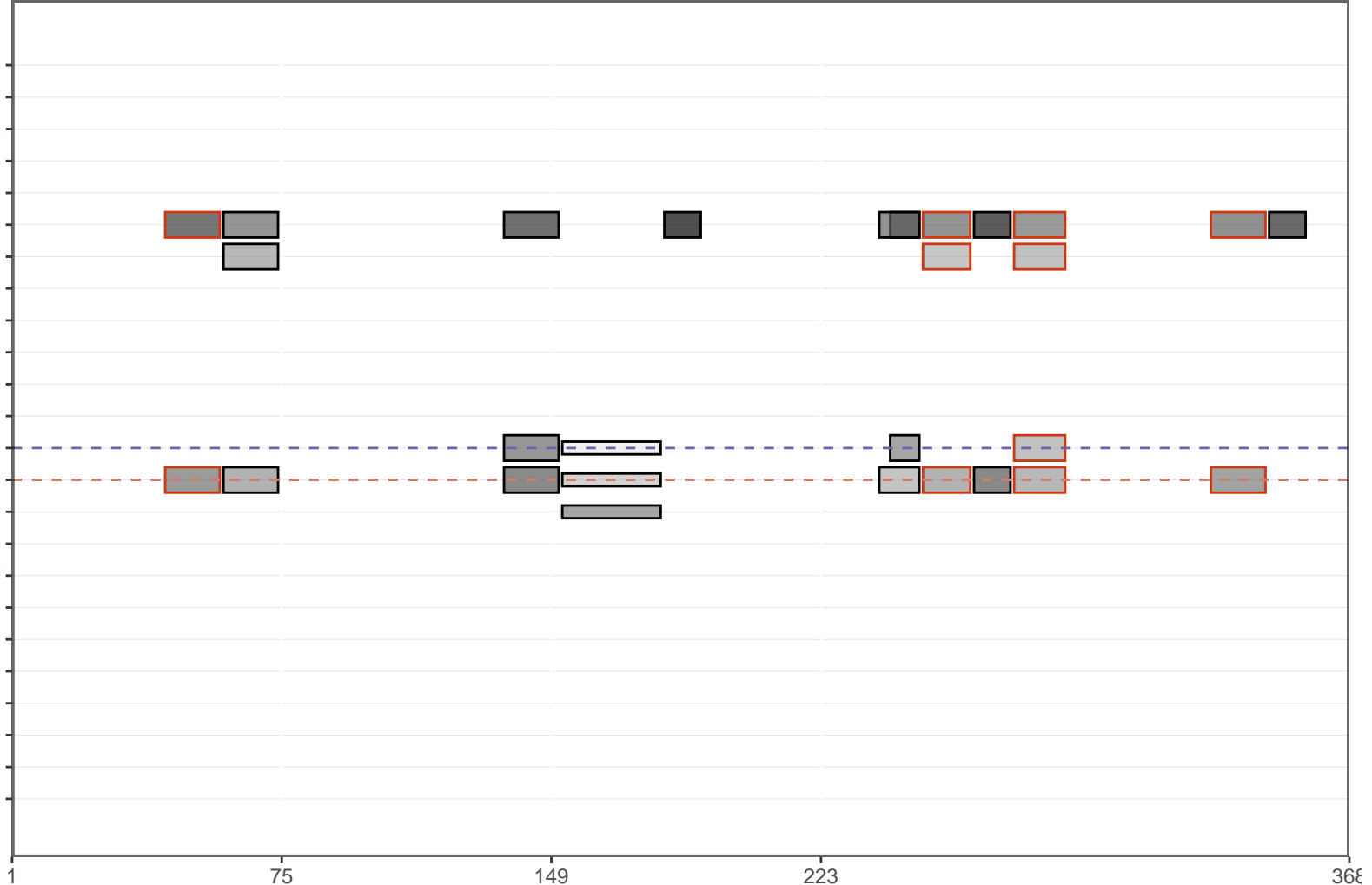
MW indication



Molecular weight

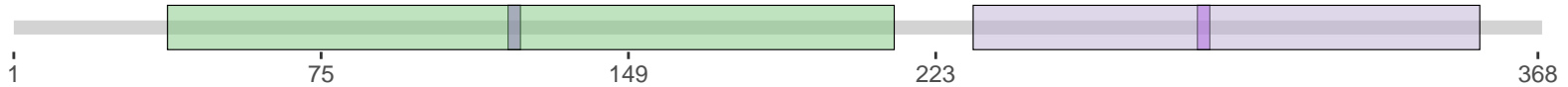


Gel Slice



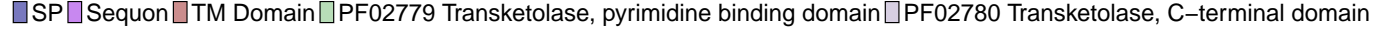
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

WVFGSCPGLKLVLPYVSEEDMRGLKKAIRDPDPVFLLENELLYGESFFVSAEALDSFCLPQKAKIEREGKDVTTTAFGKMGVYALQAEILAKEGSIAEVNLRISRLDRPAINTEVVRKTNLIVTVEEGFPQHGVAEGCASVVEESFEYLDAPVFRITGADVPMPVSNLERMVAQVQEDNVAKRACVRSST

NbL09g05530.1 40S_ribosomal_protein_S3a [MW = 29.77 kDa]

No. of times detected



log(intensity)



Values from



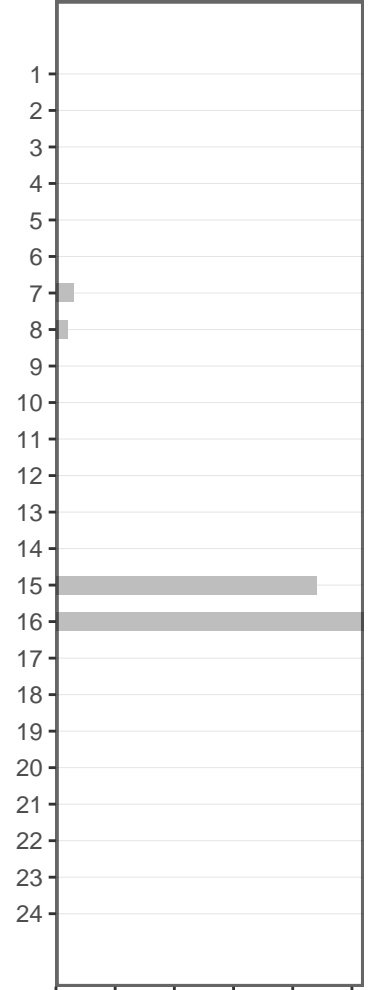
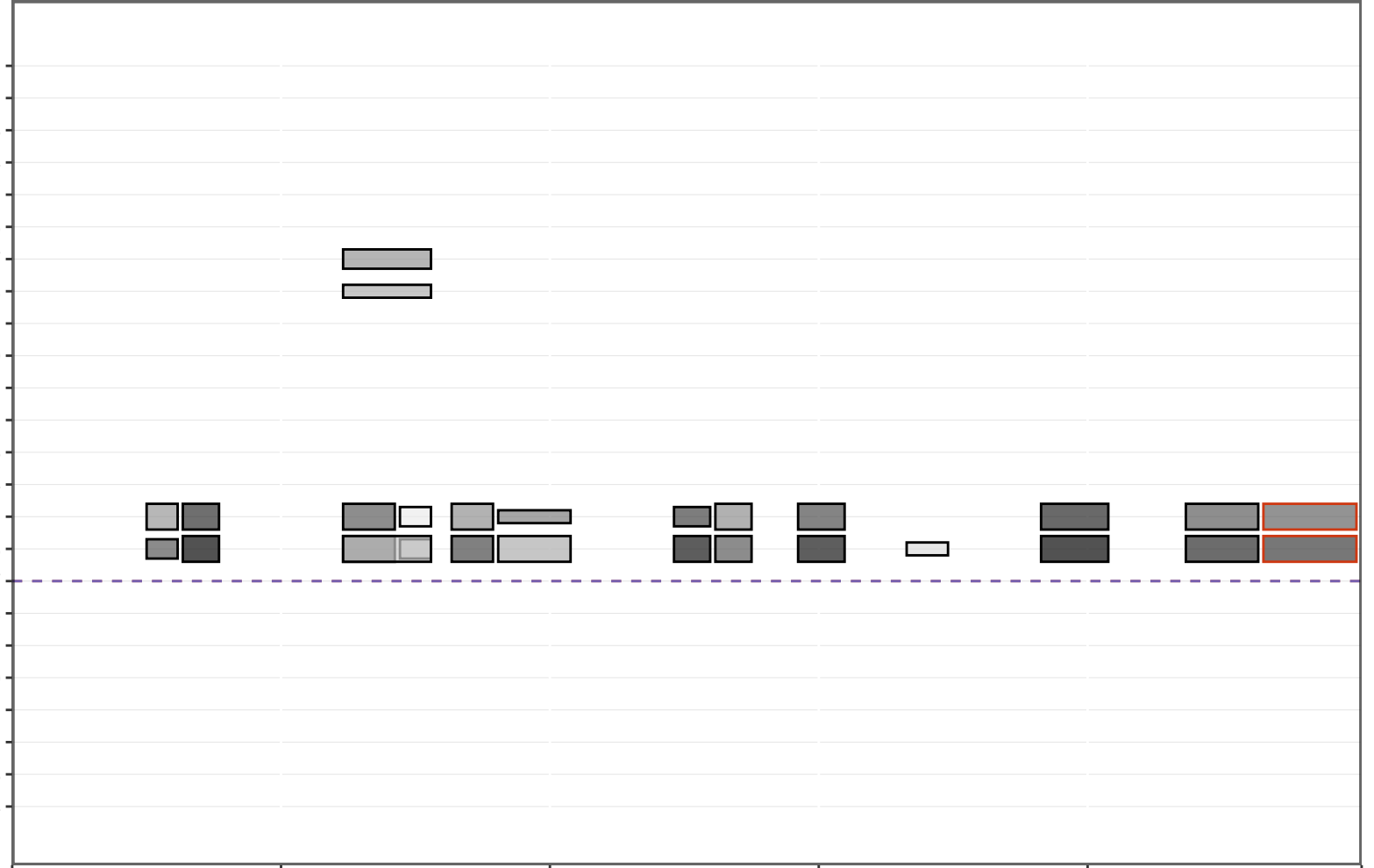
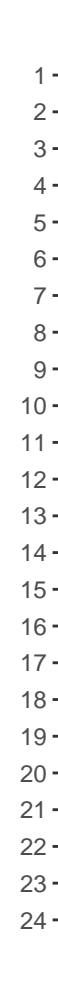
MW indication



Molecular weight

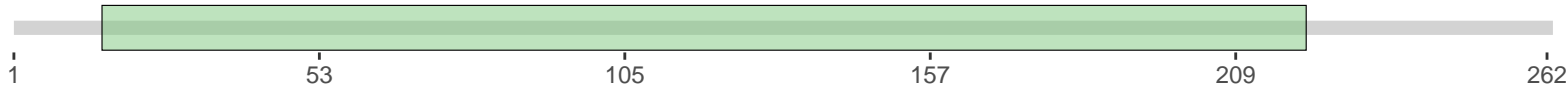


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

WQTLIEAHVDYKTFDEVTLRFMGAFTRKRRPNDGKRTGYAGSSGIRGIRRMVEMIRNGASSCDLKLKAFKPEISGRIEKATSSIFPLGNVYIRKWKILKAPKFDGKLMVEVHGDQSEDFGVKLRDPDENWAEAEPEIPGA

NbL09g05510.1 50S_ribosomal_protein_L29_chloroplastic-like [MW = 19.06 kDa]

No. of times detected



log(intensity)



Values from



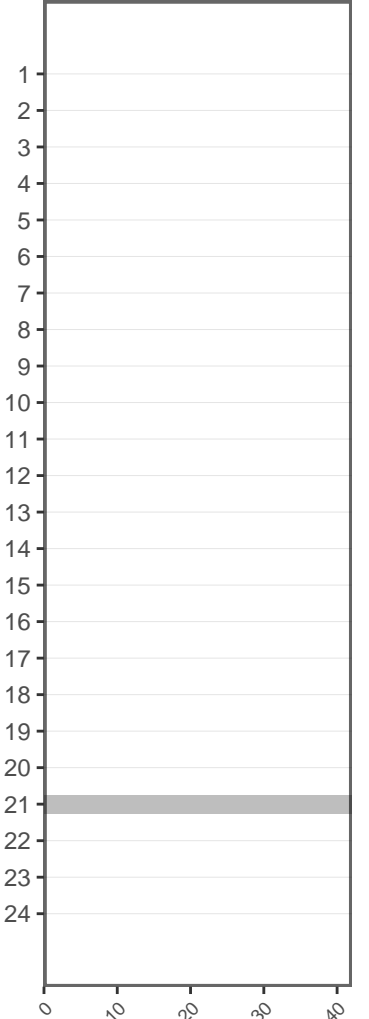
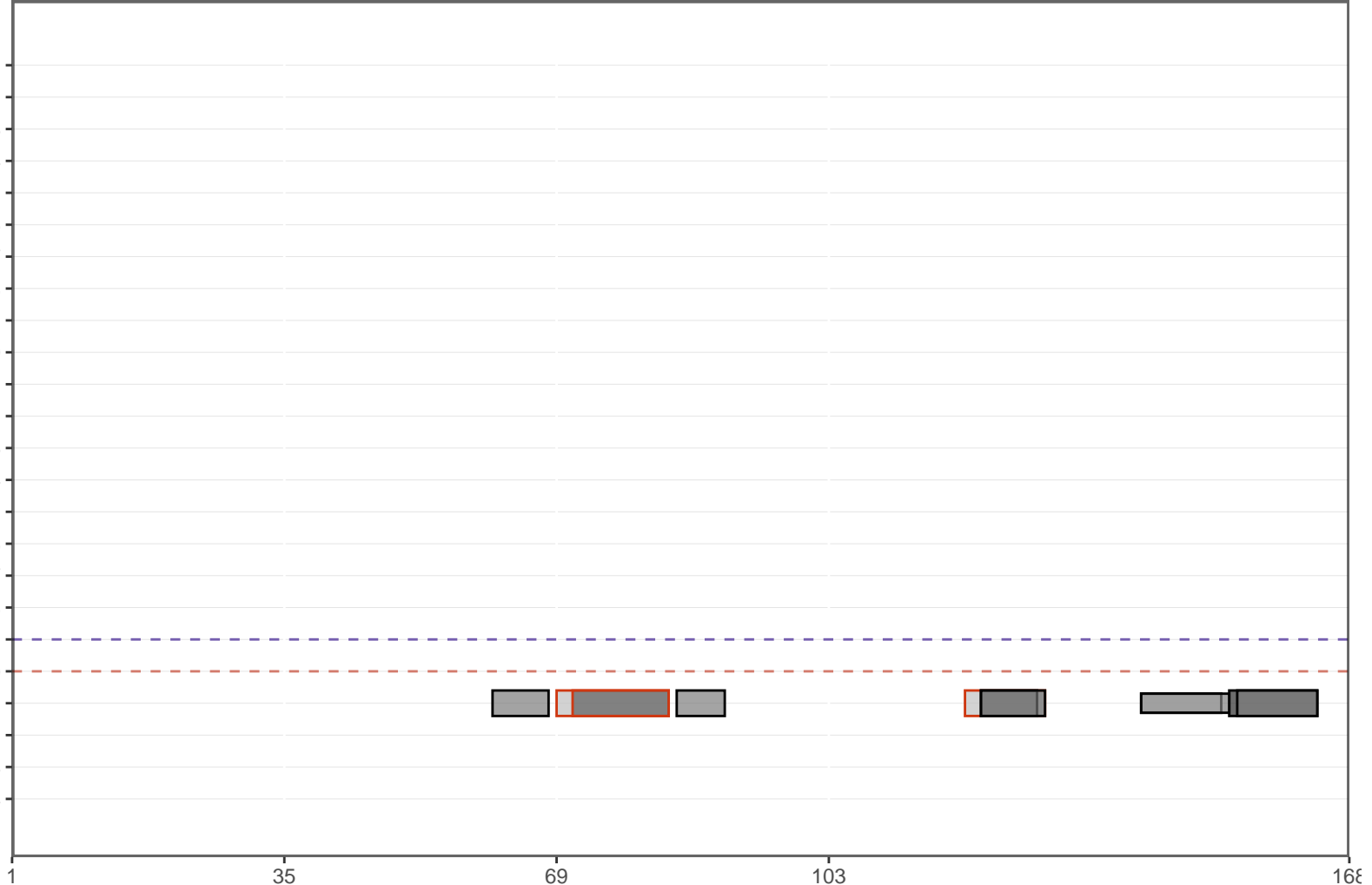
MW indication



Molecular weight

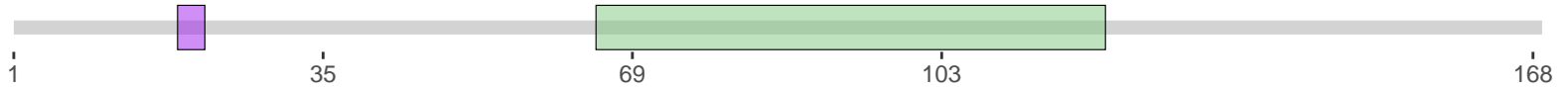


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

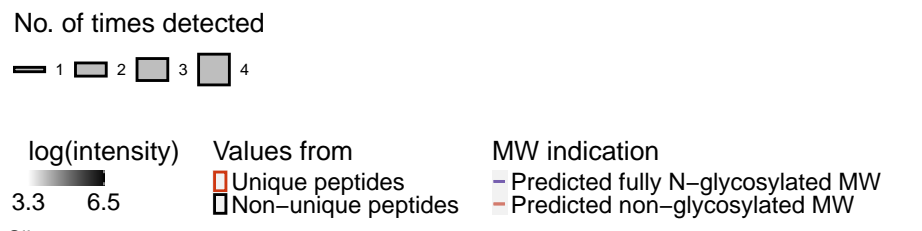
Pfam Description



Protein sequence:

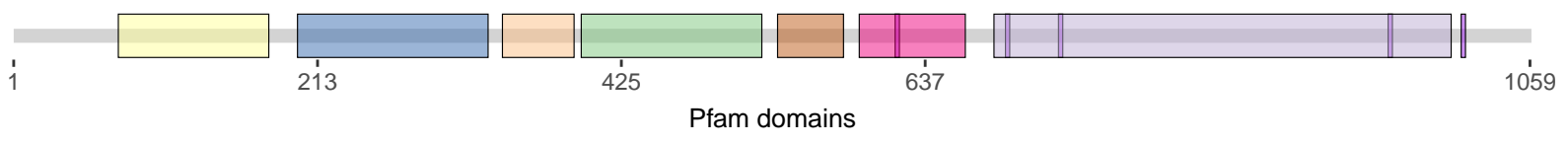
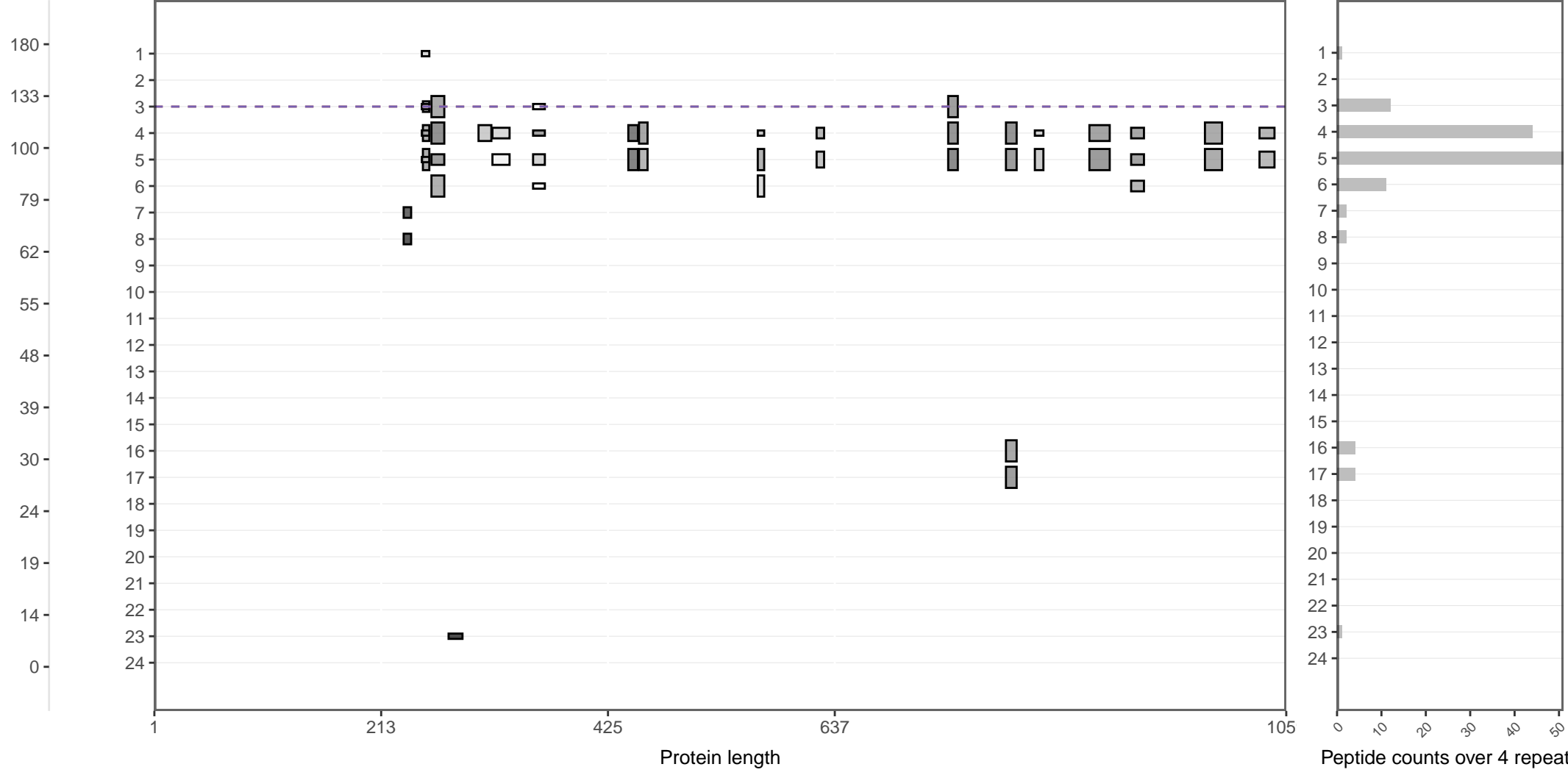
TEELQEEIVDLKGLGELFMLRLRGRSARNEFKSSEFLMRKRIRARMLTVKRDRELEEGINKRISRLDRKWKKSIVPRPPPSLKKLQEEEAAMAAEKES*

NbL09g05430.1 protein_argonaute_1-like [MW = 117.76 kDa]



Molecular weight

Gel Slice



Pfam Description

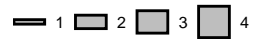
- SP
- TM Domain
- Pf02171 Piwi domain
- Pf12764 Glycine-rich region of argonaute
- Pf16487 Mid domain of argonaute
- Sequon
- Pf02170 PAZ domain
- Pf08699 Argonaute linker 1 domain
- Pf16486 N-terminal domain of argonaute
- Pf16488 Argonaute linker 2 domain

Protein sequence:

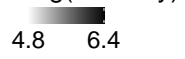
RYSKRLNERQITALLKVTGGPQERERDLQGVHNNAYADDPYAKFEKIKSEKLAGVEARVLPAPVAKVYHDTGREKDLPLQVGGWNNMNMKMMVNGGTNWNWICVNFSSRVGDTVARGFCSELADQMMISGMNFPNPLPVSARPDQVVERVYKTRFHDMATKLPQNGRELDLLVLPDNNGSLYGLDKRIGETELGVNQGGLTKHFVKMSKQYLANVSLKINWVGRNTVLDALSRPILVSDRPTIFGADVTHPHPGEDSSPSIAVAVASGQVPEITKYAGLVSI

NbL09g05410.1 pEARLI1-like_lipid_transfer_protein_1 [MW = 15.69 kDa]

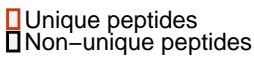
No. of times detected



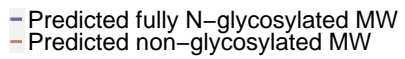
log(intensity)



Values from

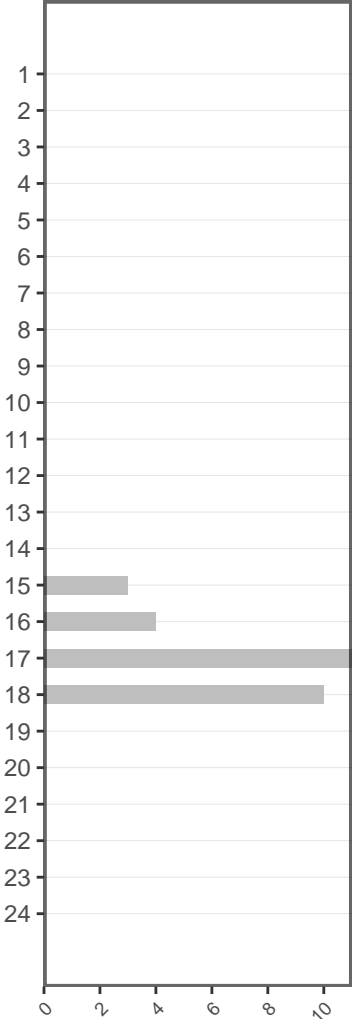
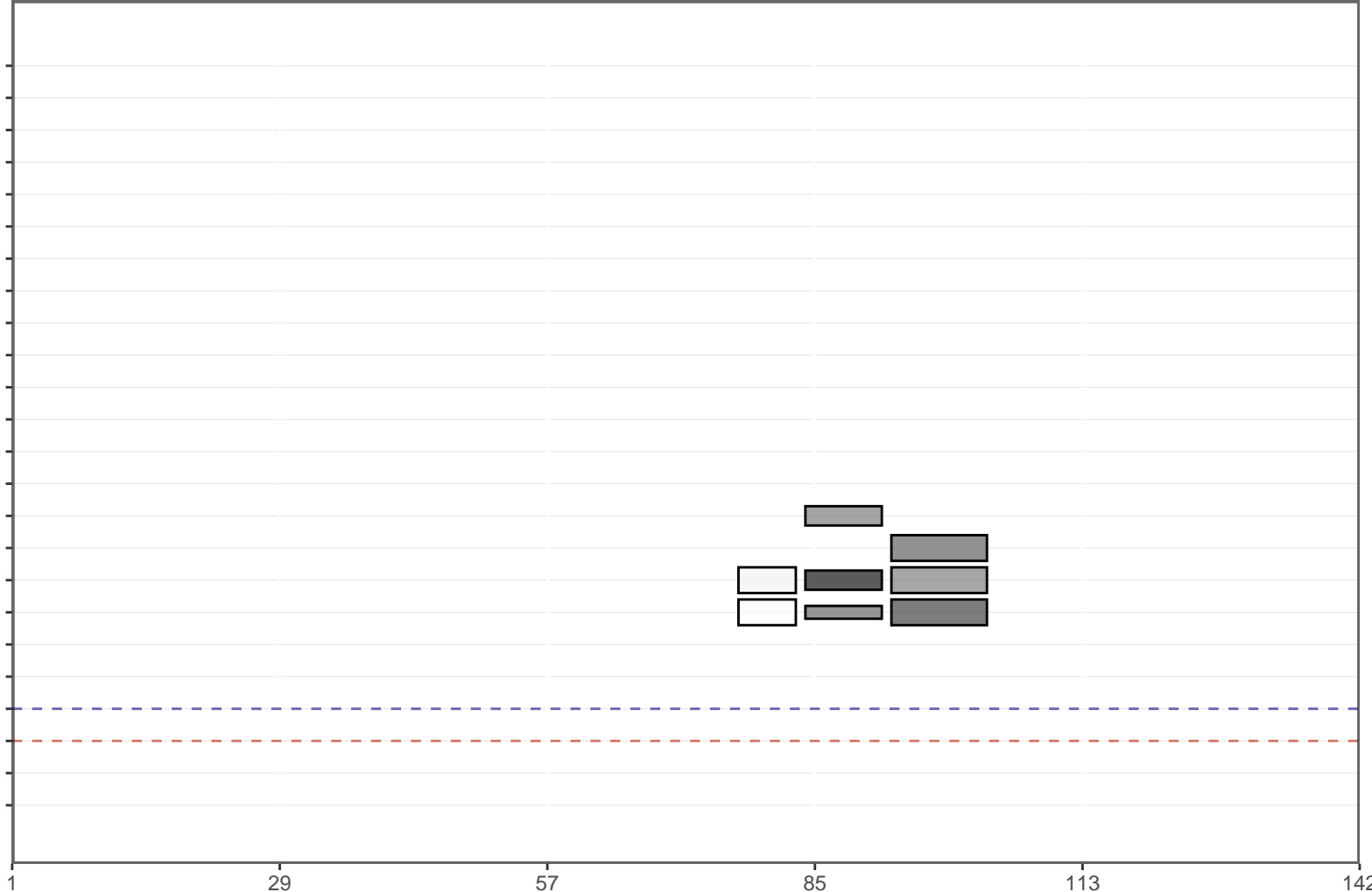
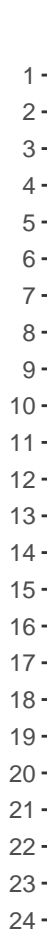


MW indication



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



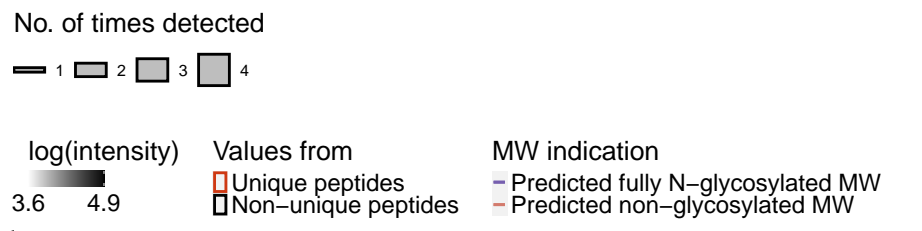
Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

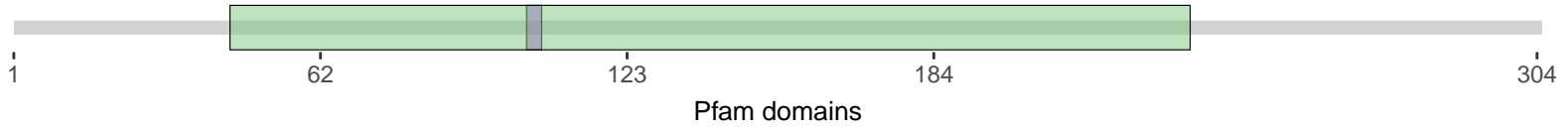
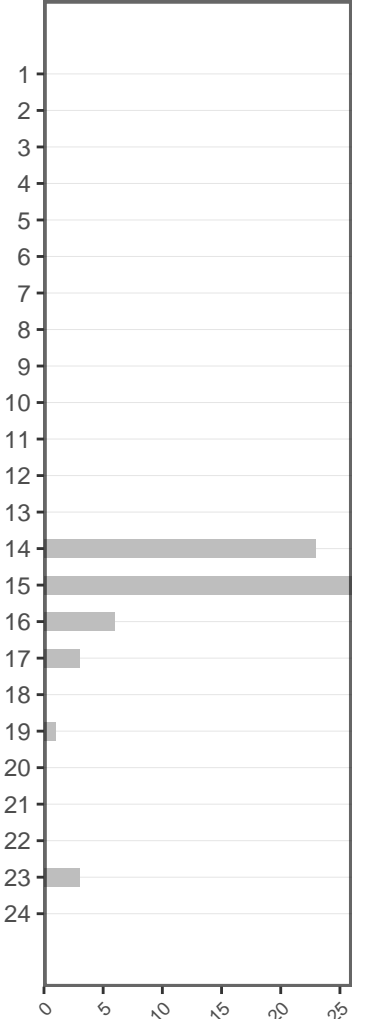
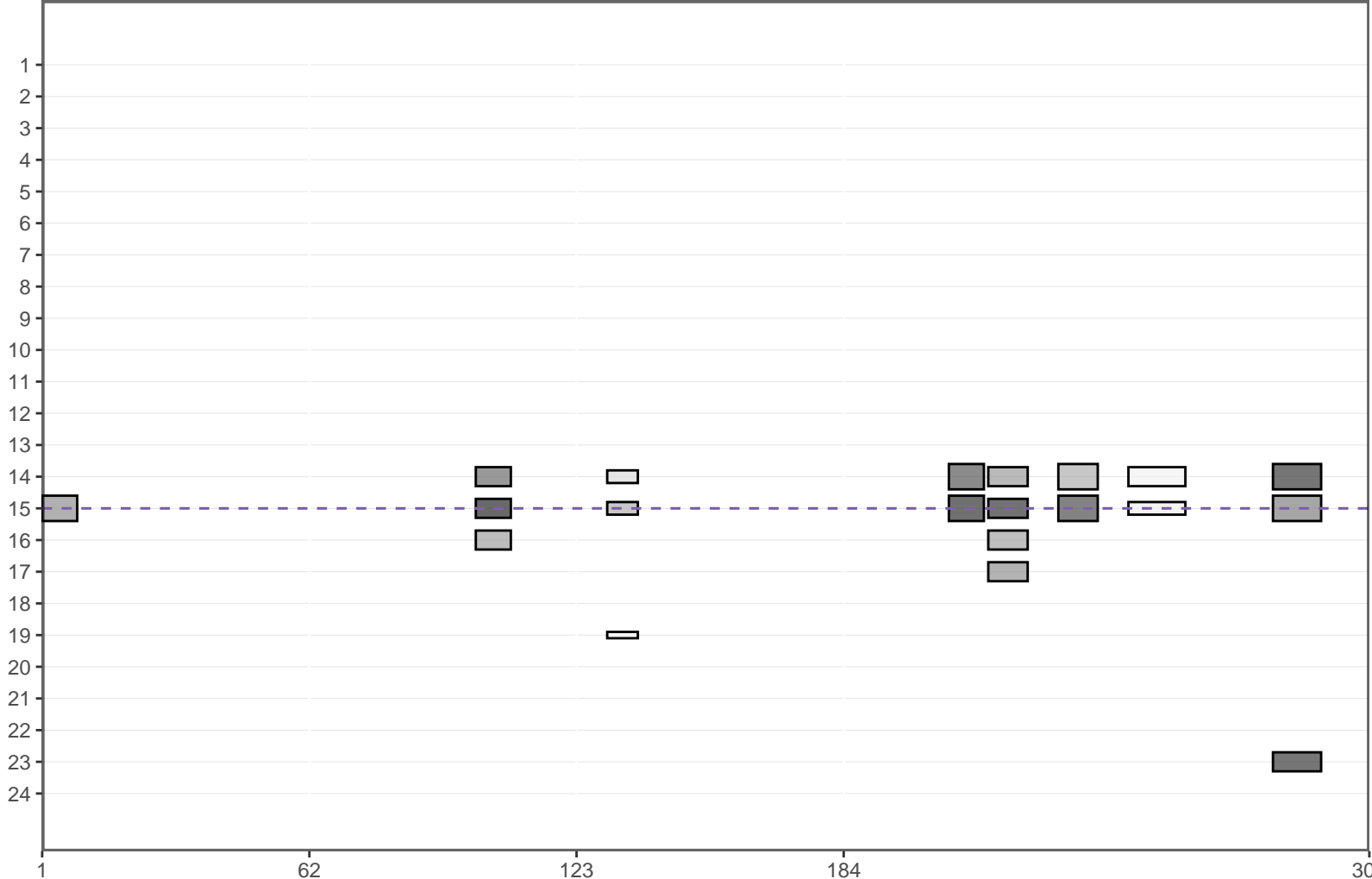
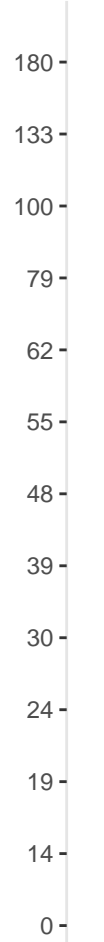
PPPPAPSSSCSASDSEANVYKGMFNETKIDPQPTFFKSLGTSGPCYKVAENLINDQVLTIEAVGDVYSPCKLGLQIKLSKEEYK

NbL09g05350.1 phytochrome-associated_serine/threonine-protein_phosphatase_3-like [MW = 34.87 kDa]



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain PF00149 Calcineurin-like phosphoesterase

Protein sequence:

CTDVFDYLTLSAIDGTALGVHMGGLSPDVRFDQIRVIERNCEIPEHGPFQDLMWSDPEDIETWVSPRGAGWLFGRVITTEFNHINKLDLVRAGHLVGEGLKYMFDKGLVTVVWSPAPNYCYRQGNVASILSFENMEREVWFFTEENNMGRGFRGTGVPVFL*

NbL09g05330.1 40S_ribosomal_protein_SA-like [MW = 32.21 kDa]

No. of times detected



log(intensity)



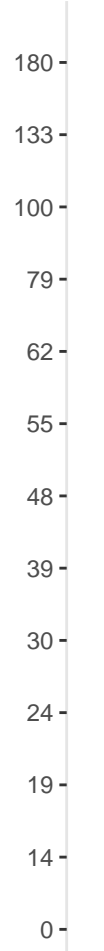
Values from



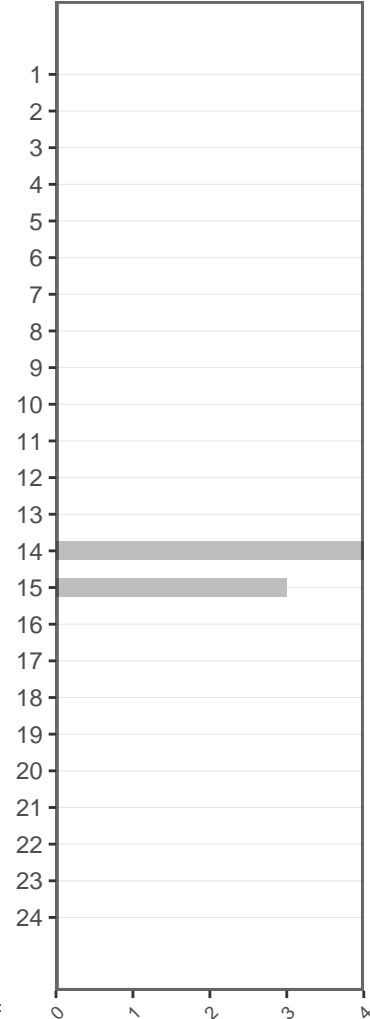
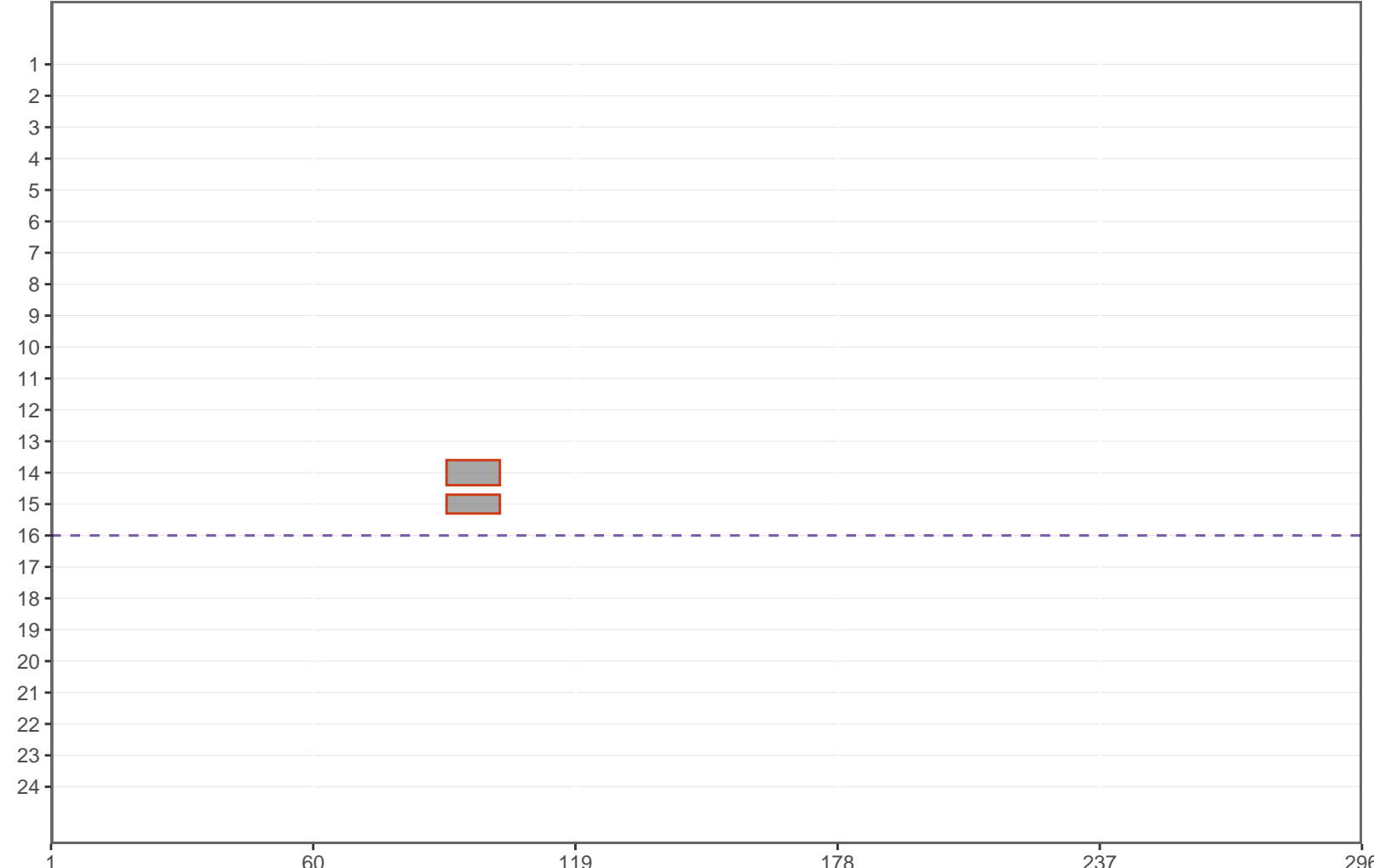
MW indication



Molecular weight



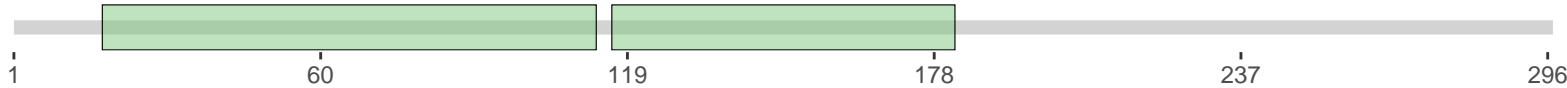
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

ALGNPTIAFCDDTDEPMRVYDGIIPANKGKHSGVLFWILARMVLDGMRGSSINGGKHWEVMVDFLFYREPEEAKEQEEEEPNDVADYSAGAAALGGDWSSSQIPEAGWTGDAAPSGPVAASGWSGEGVAEGGWDTAAAPVPIVVDAAPTAGATGWE

NbL09g05250.1 glyceraldehyde-3-phosphate_dehydrogenase_cytosolic [MW = 36.66 kDa]

No. of times detected



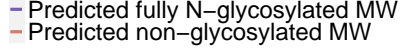
log(intensity)



Values from



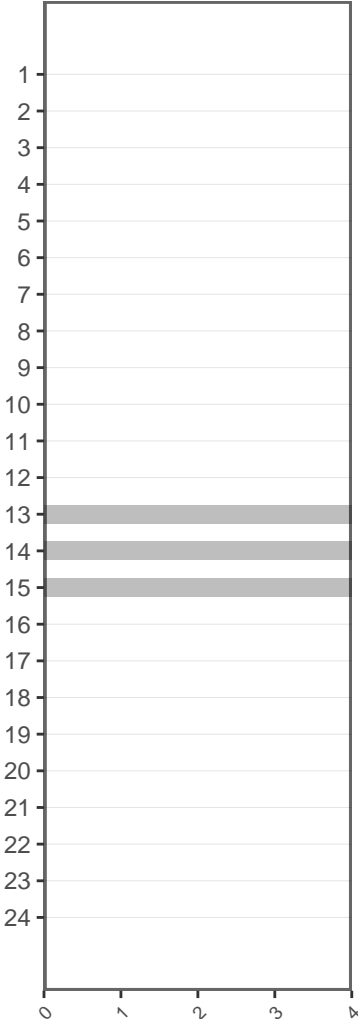
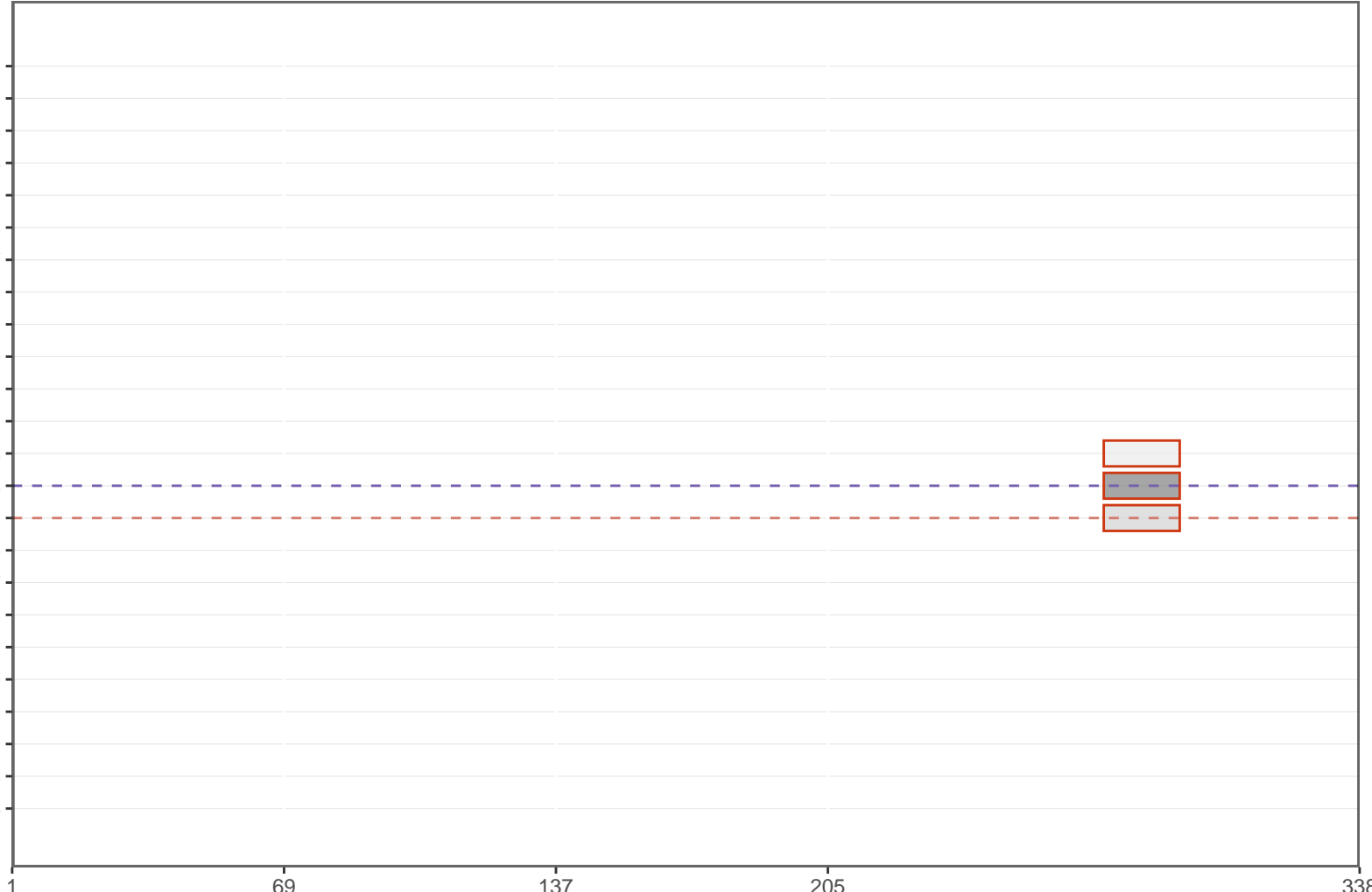
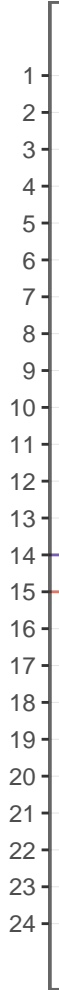
MW indication



Molecular weight



Gel Slice

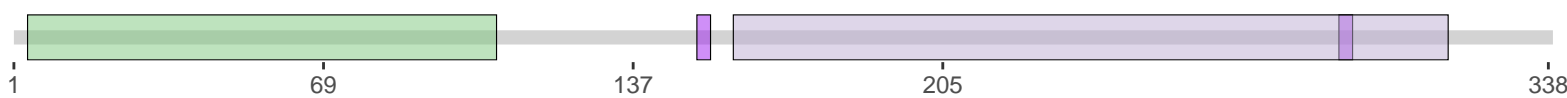


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description

- SP Sequon
- TM Domain
- PF00044 Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain
- PF02800 Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain

Protein sequence:

TNCLPLAKYIHDRFGVEGLMTTVHMTATQKTVDGRPAKDWRRGRAAGFNIPSETGAAKAVGKVLPSLNGKLTGMFRVPTVDVSVDLTVRLEKEATYDEIKAAIKESSEGLKGLGYNEDDVYSTDFDGNRRSIFDAKAGIALSKNFVKLVSWYDNEMGYSTRVVDLKHMAASVQ

NbL09g05240.1 3-oxoacyl-[acyl-carrier-protein]-reductase_4-like [MW = 34.17 kDa]

No. of times detected



log(intensity)



Values from



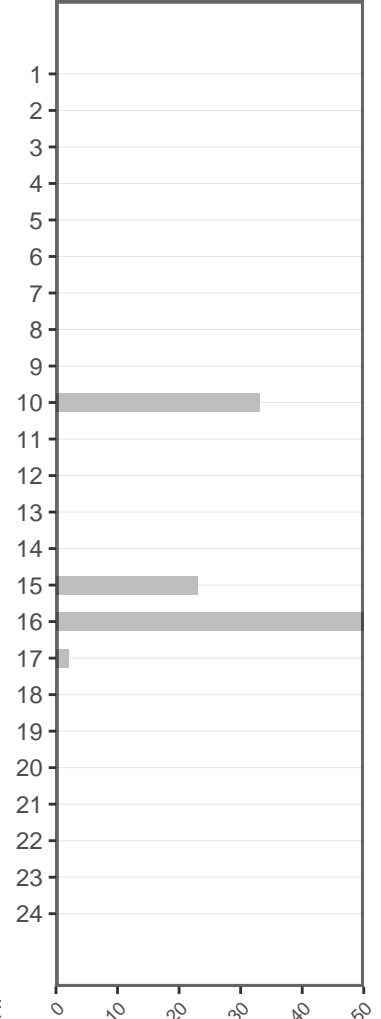
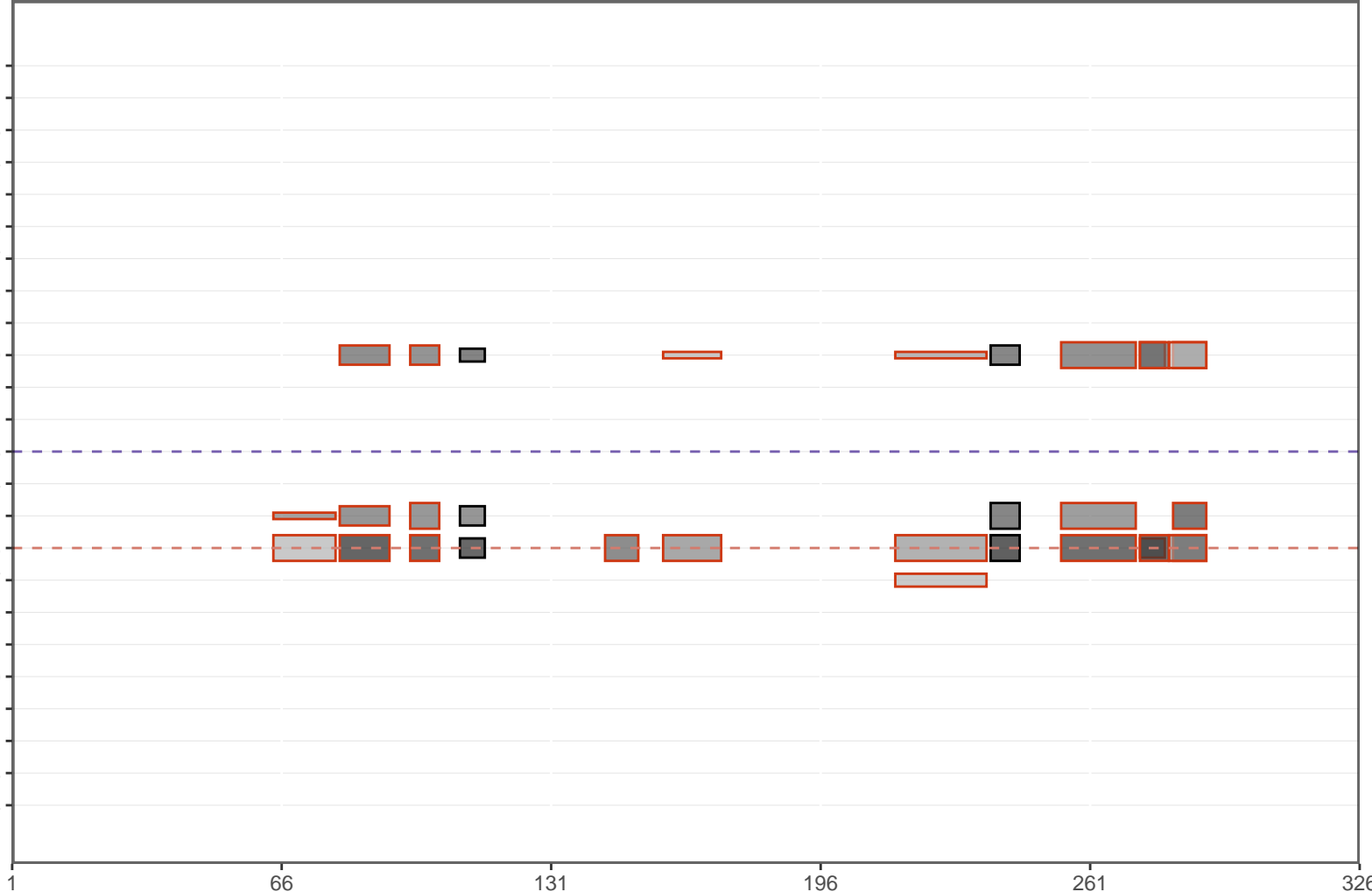
MW indication



Molecular weight



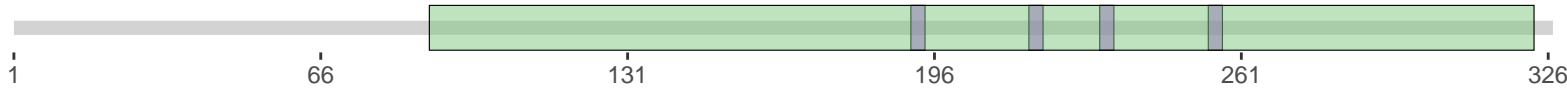
Gel Slice



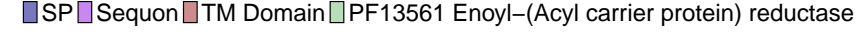
Protein length



Pfam domains



Pfam Description



Protein sequence:

SMKTAVDRVIGTVDLNNAGITRDFTLLMRMKGGWQGEVIELNLGTVFLCTGAAAKMKMKKKGRINISSEVVLGNAGDANYSAAKAGVIGLTKSVAKEVAGRNTVNAVAPGRASDMTAKLSEDEKKLQSVPLGRYGGPFEVAGLVEFLALNPAAYFTGGVLTIDGGMMV*

NbL09g05220.1 60S_ribosomal_protein_L17-2-like [MW = 20.09 kDa]

No. of times detected



log(intensity)



Values from



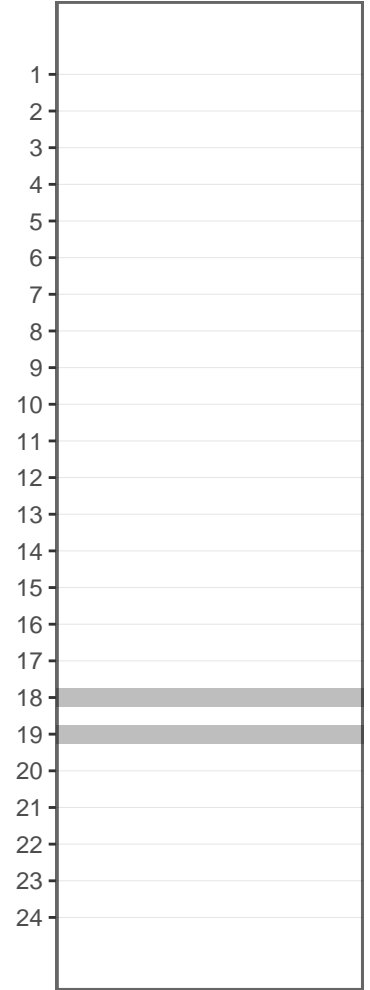
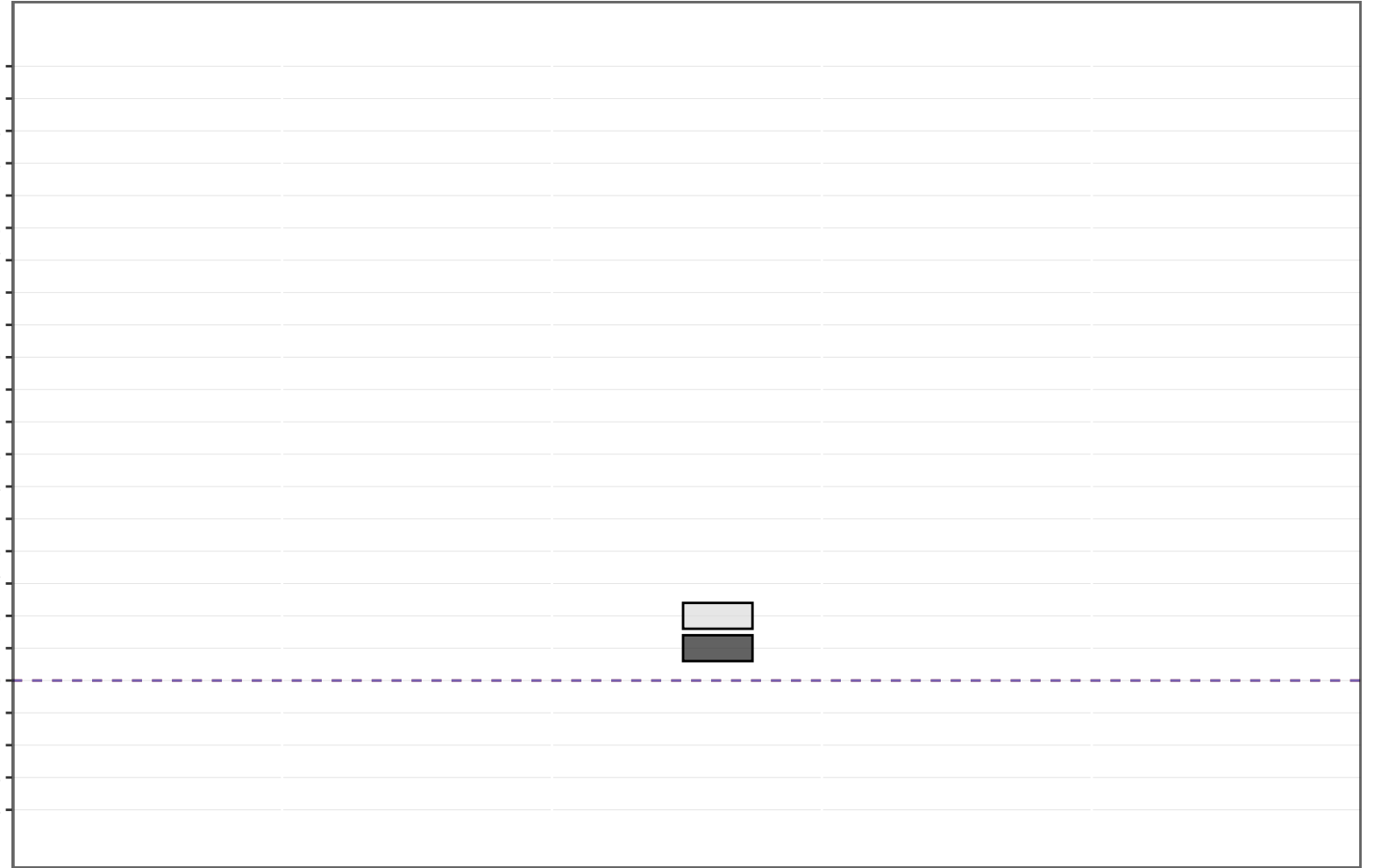
MW indication



Molecular weight



Gel Slice

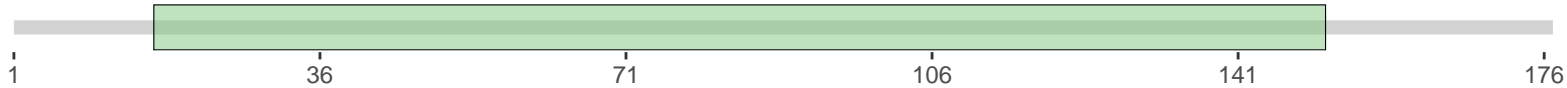


Protein length

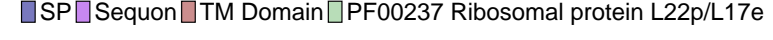


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IRHSNGQGRVWPVNSAGFILDLKNAESNAEVKGLVDBLYTHIGVNGAQKRRRTYRAHGRINPYSNPCHIELTSEKEESVRIKEPETQLAPRRTKASS

NbL09g05160.1 peroxisomal_membrane_protein_PEX14-like [MW = 57.29 kDa]

No. of times detected



log(intensity)



Values from



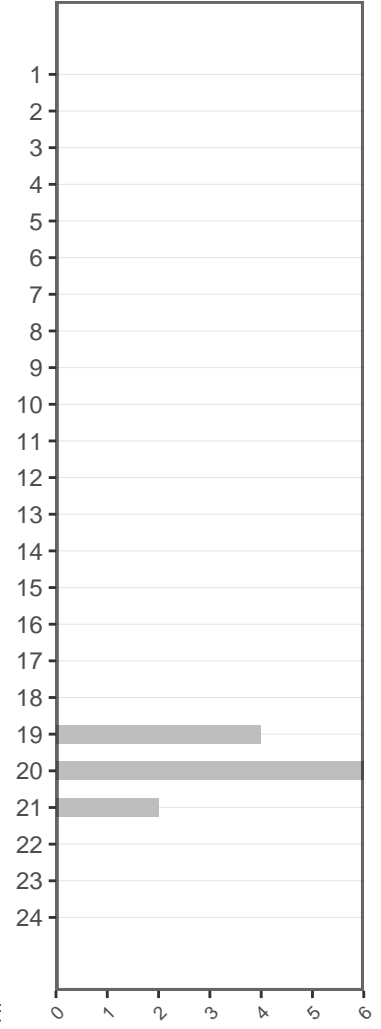
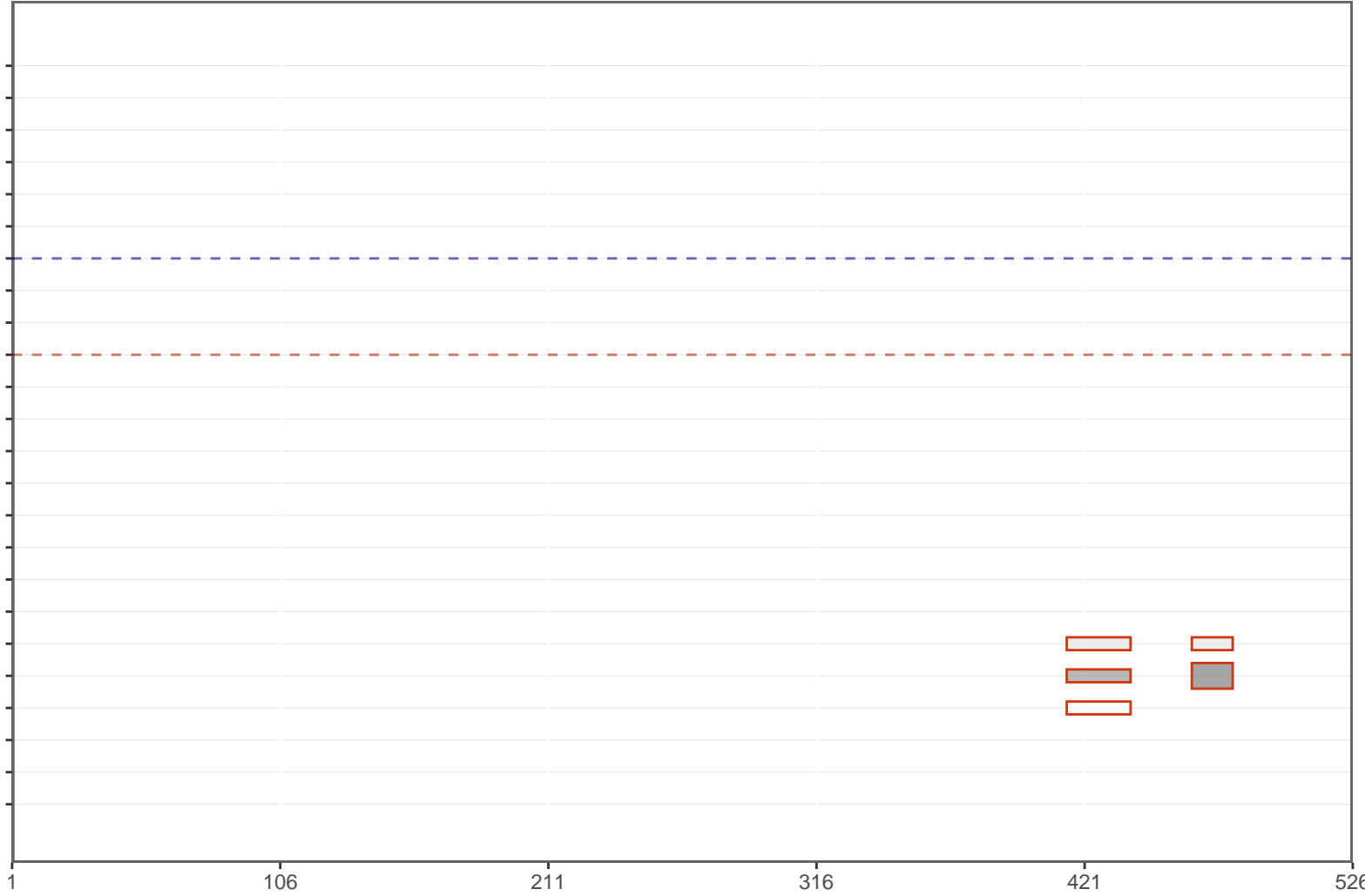
MW indication



Molecular weight

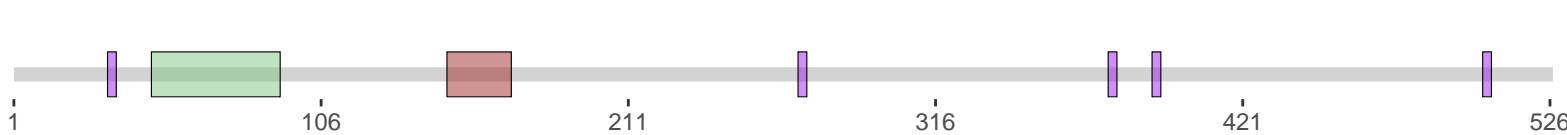


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

REMKSMTSALAEKLEGGSNFSGRPITELDDRRRISVTOGRGSVYNGKVDGDARSVRLSLPASVEGSAFHPKGVMEIMAMVORGEKPNQDNDGPPNPKPVSDFRIVFKPKPVEVGGIGENSTLQFGGSGDGLNYSVQDSLTNGDSSAAWWWGRNRNARTEISEGEQNFQSGPAPVQERPKQRSWPPQPPVAMAEAAAIRGPRKPKVLQNEQVTDQQLMARSSSEITDELGRVTRFSESGDAPEANGSSALHSETPIGEGDQLS-

NbL09g05110.1 GDSL_esterase/lipase_At5g62930 [MW = 27.43 kDa]

No. of times detected



log(intensity)



Values from



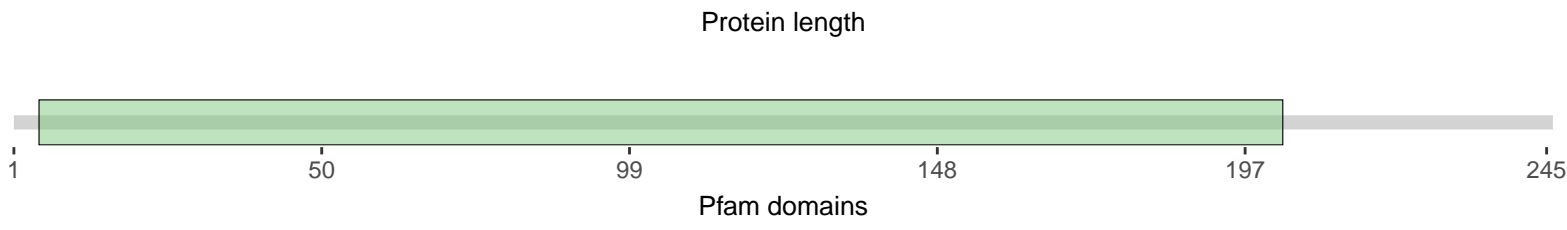
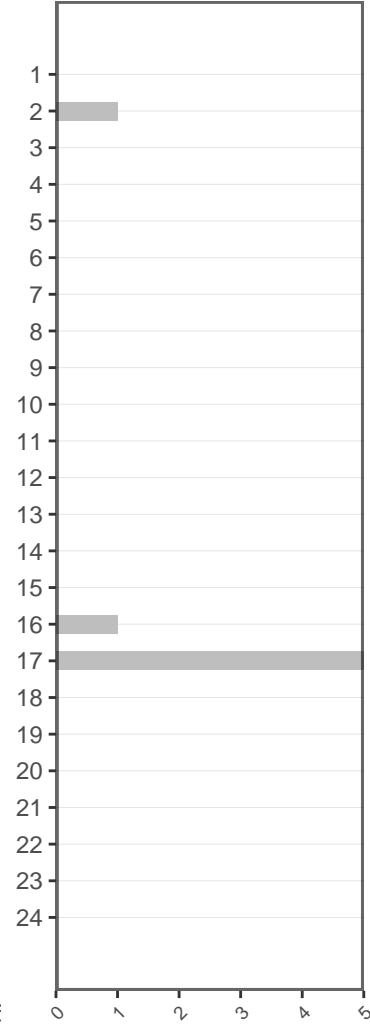
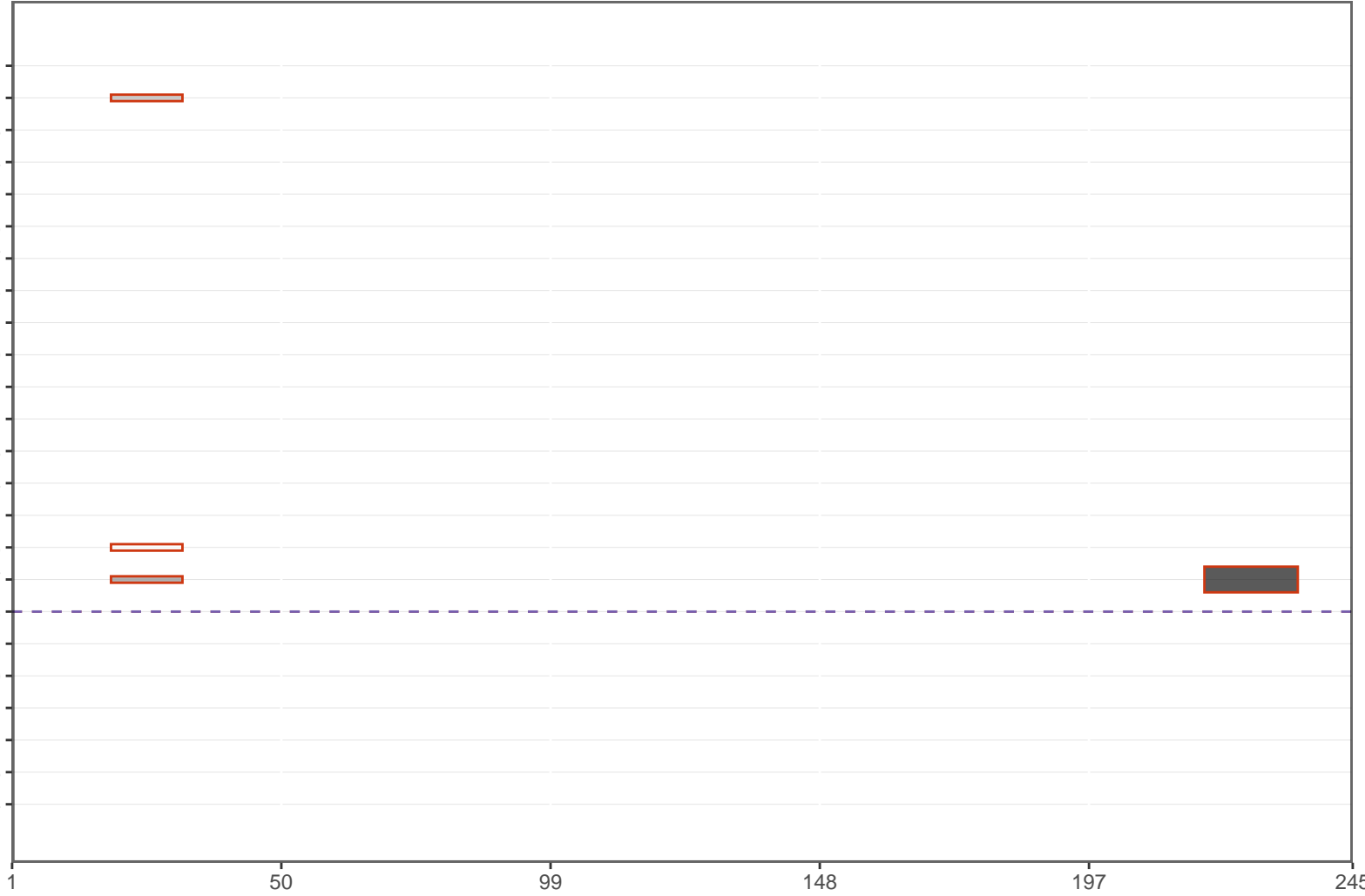
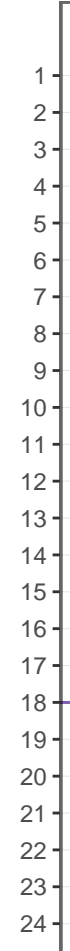
MW indication



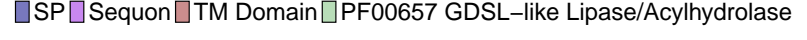
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

SILVLLITPPVDEAGRFEQARSMYGDKAMELFPRTNEVYTGVAKQGVLELARELGLPSINLWSKMGTEGWDKFLGDGLHLEAGNAVHGEVVAKFAEAGFSADKMPYDYPHISEIDGGHPKAFQLGGPW

NbL09g05050.1 uncharacterized_LOC104247359 [MW = 39.88 kDa]

No. of times detected



log(intensity)



Values from



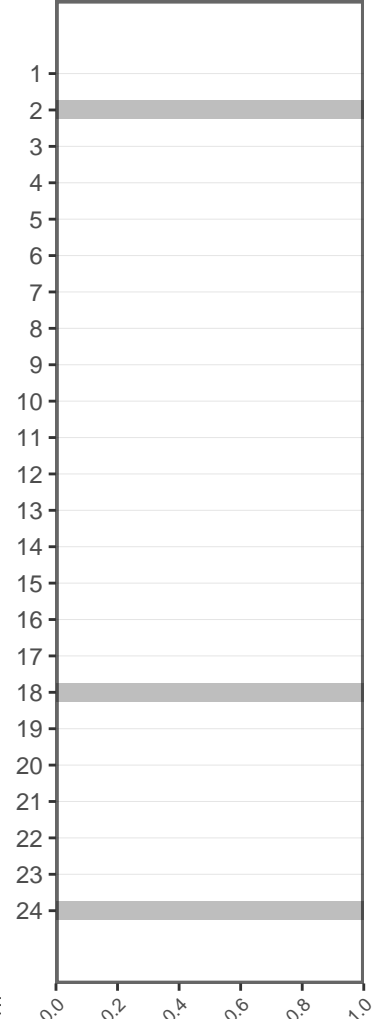
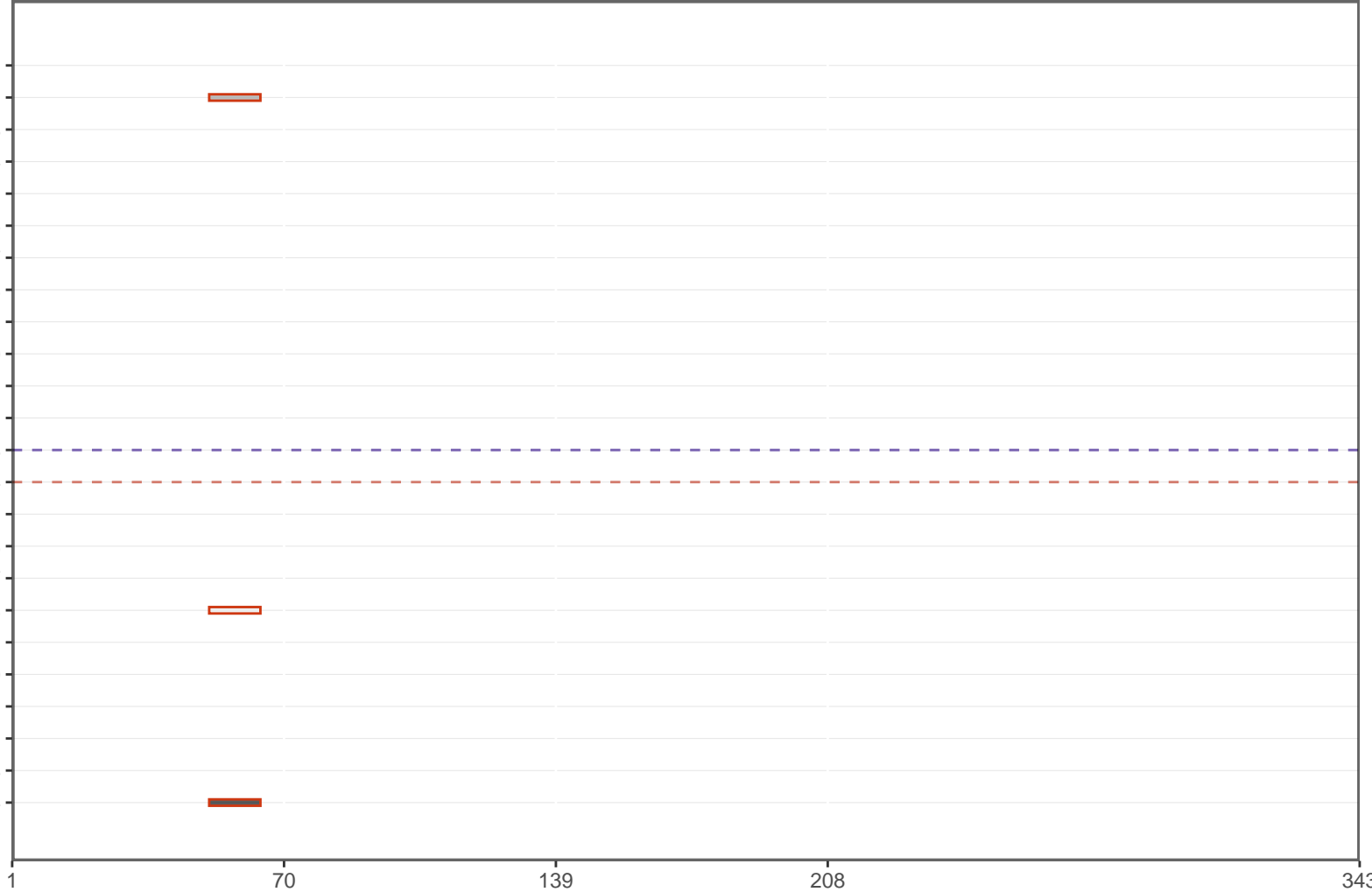
MW indication



Molecular weight



Gel Slice



Protein length

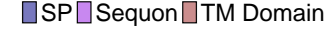


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

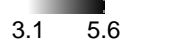
DAEYGSQGLAESISSDAKHGEGAEQPYHRKTDADFVGVVFRQIFQMNAGAVMLTDCYFVFLVPLVTKGKYNLNFWINMHSVNVFLSDTALNGLRFPWFRIGYFFIWTGTGVVIFQWVHACISGWWPYPFLDLSALAPLWLLVAFMHPDYGIFVLMKLNKHLFSKWFQGEYQGAR

NbL09g04950.1 60S_ribosomal_protein_L27a-3-like [MW = 19.69 kDa]

No. of times detected



log(intensity)



Values from



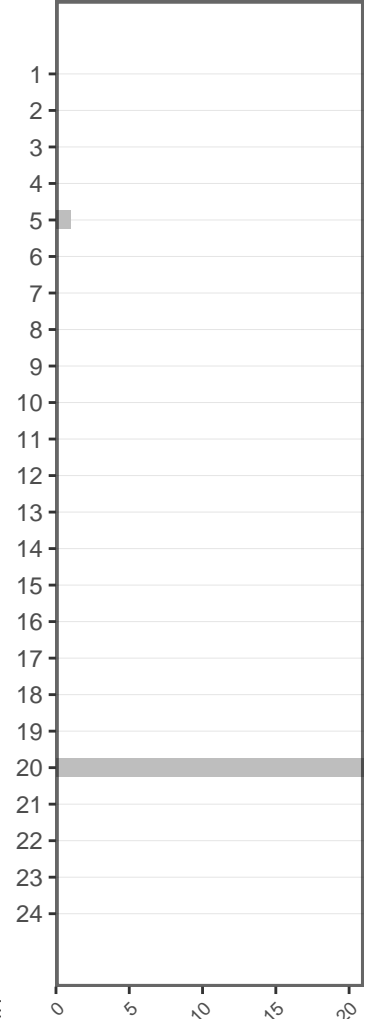
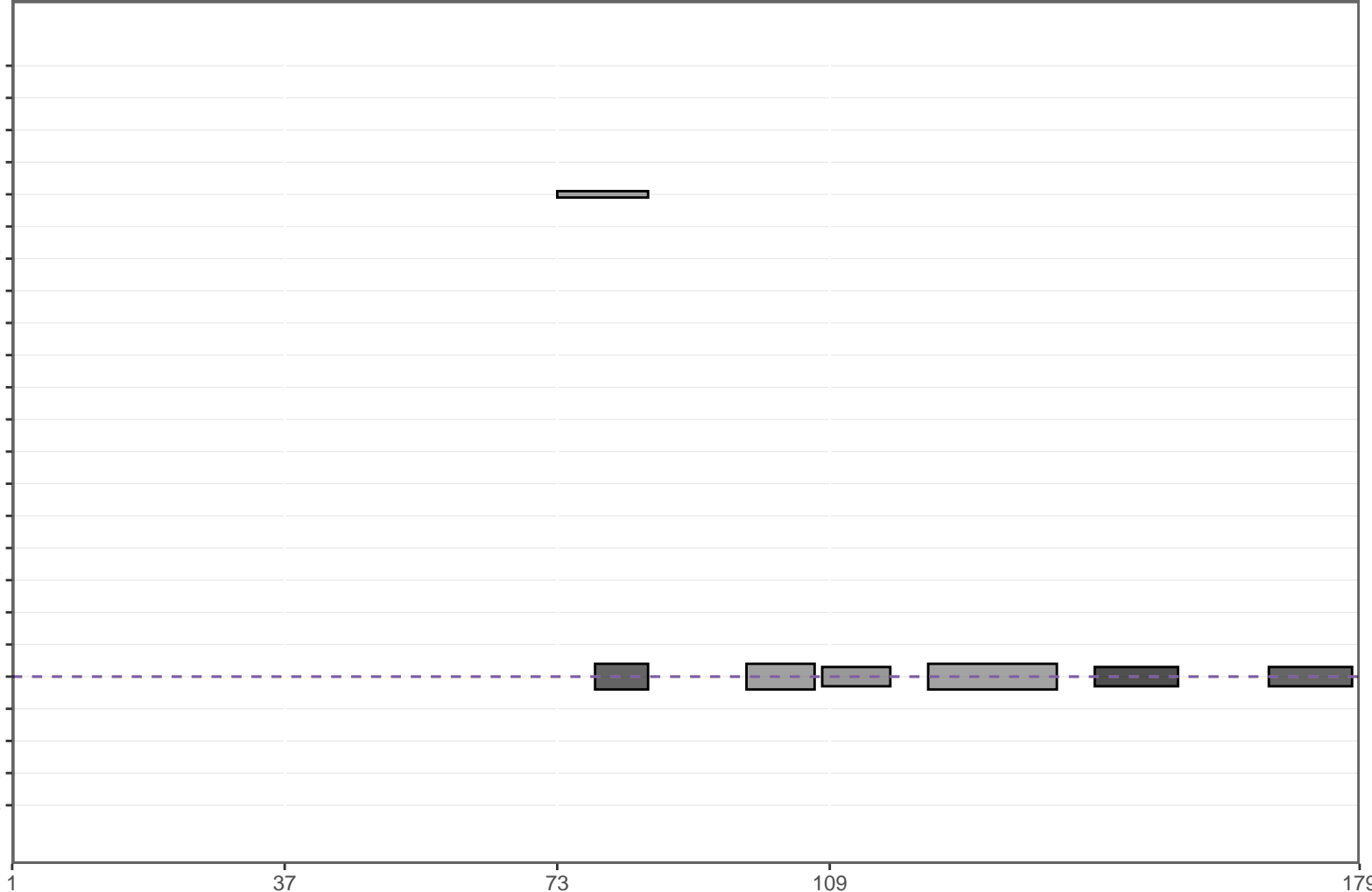
MW indication



Molecular weight

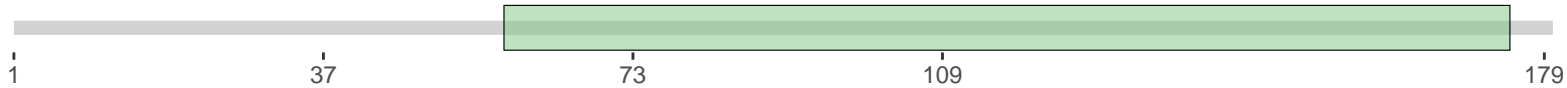


Gel Slice



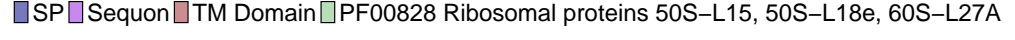
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

KYHFGYFGKVMRYFHLKLNKFKPTVNDKLSLFPQEVKDKAKANNGAAPLIDMTQFGYFKVLGKGLPTGQPVVAKAKLVSKNAEKKEAGGAVLTA

NbL09g04760.1 IAA-amino_acid_hydrolase_ILR1-like_5 [MW - SP = 44.57 kDa]

No. of times detected



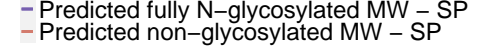
log(intensity)



Values from



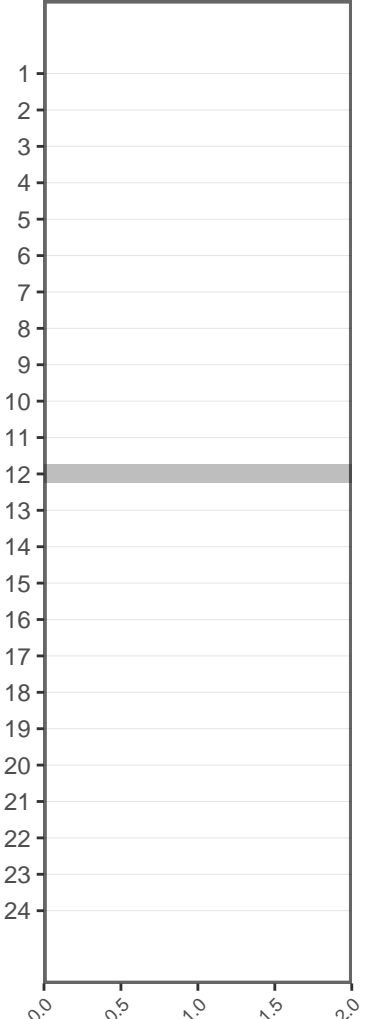
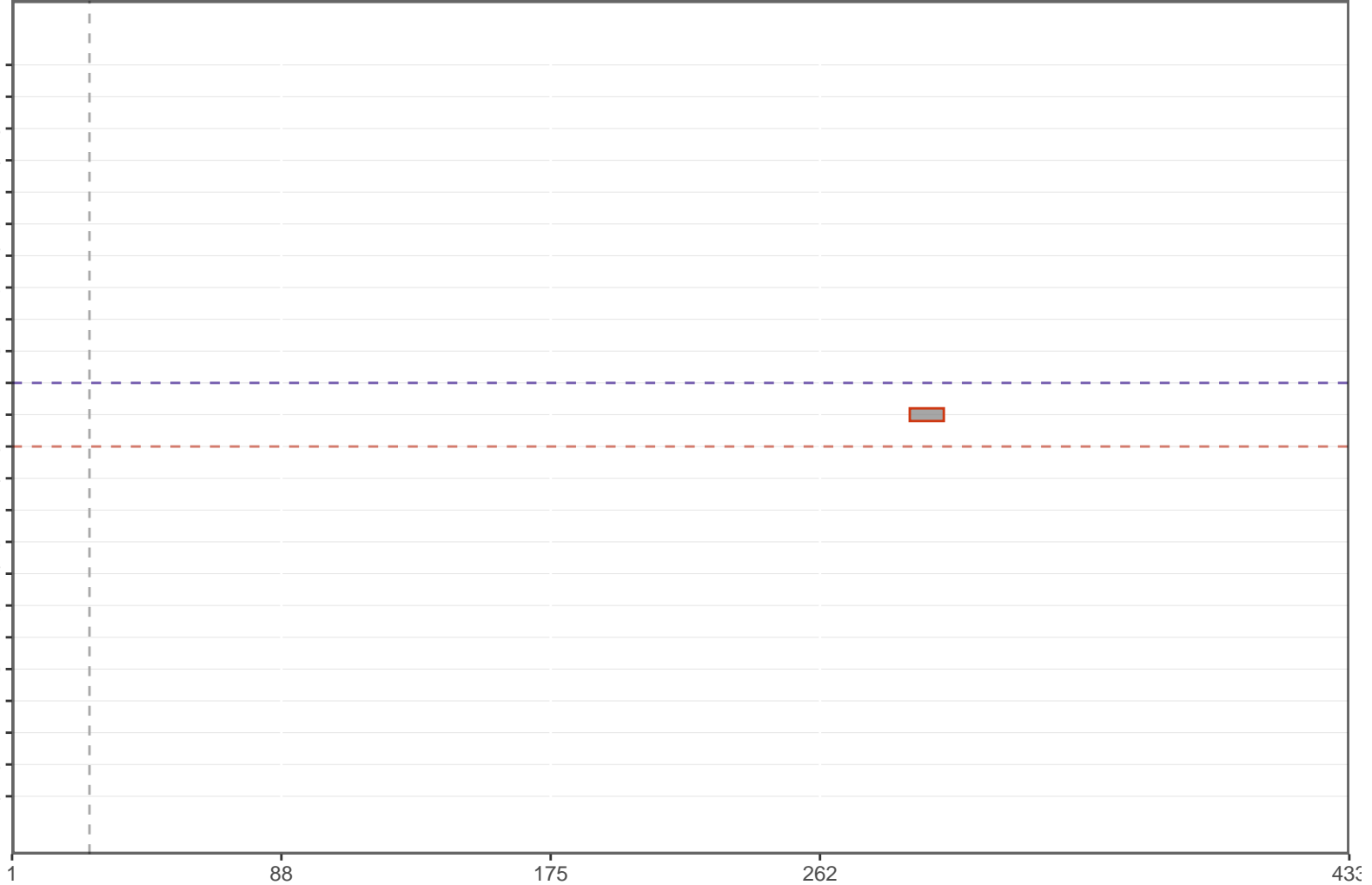
MW indication



Molecular weight



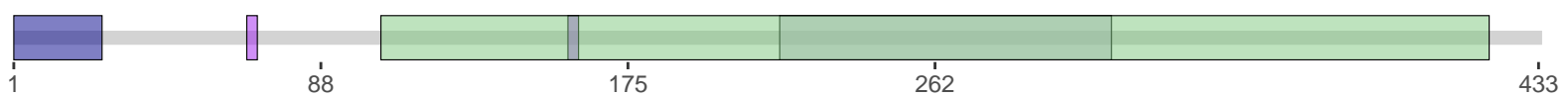
Gel Slice



Protein length

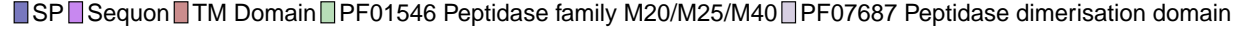


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SSIGTSPGPIAAV/SFFEAKIEGKGGHAAEPHATVDPLAASFAVALGGLISREVDPLHSGQLSVTYRGGSAENWPPYVFGDGLRLFTTEGLLQIQKRFKEVEGGAAVHRKQAVGMKEEDFPVYAGINDERLHQHVGRVQKLLGSENKEAEKVMAGEDFAFYQELTQVVMFDQIRNEKVGSTHAPHSPHFLEEDVLPGLWHTAAEMVLDKQHPVAV

NbL09g04620.1 RNA-binding_protein_2-like [MW = 25.38 kDa]

No. of times detected



log(intensity)



Values from



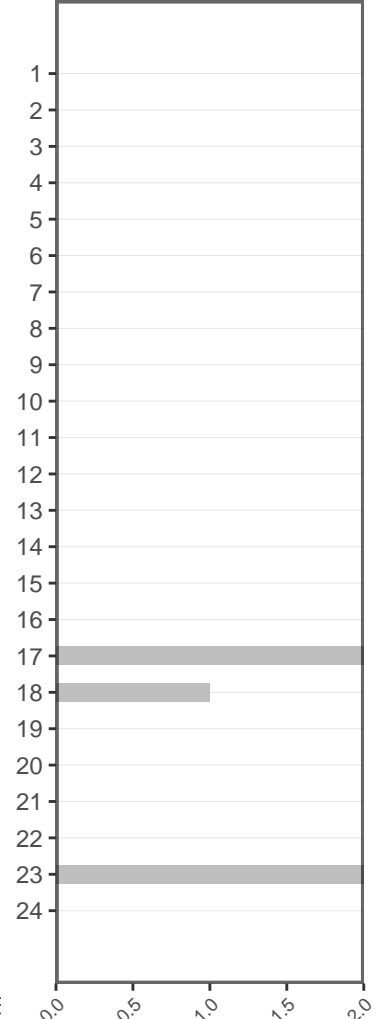
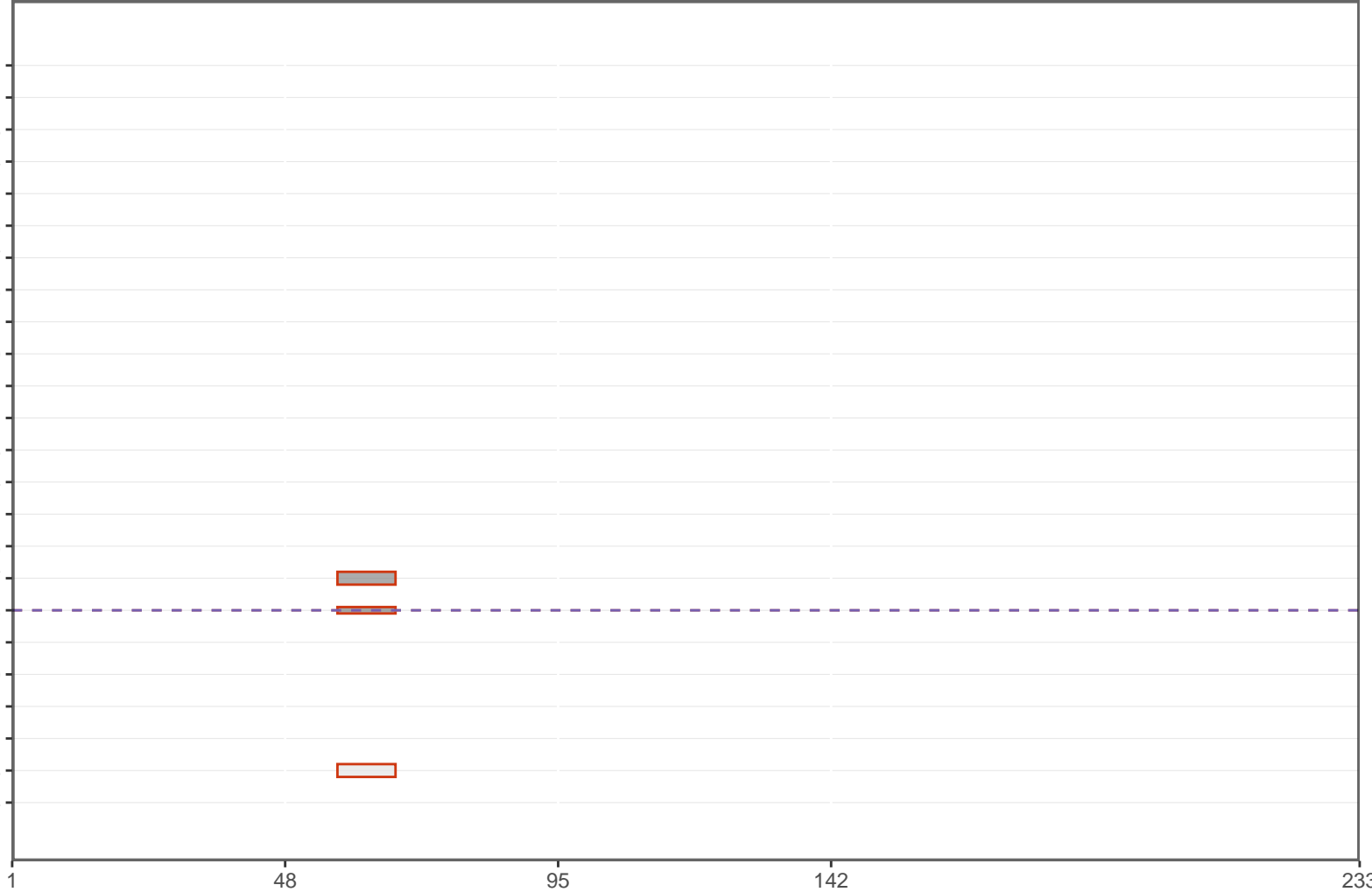
MW indication



Molecular weight



Gel Slice



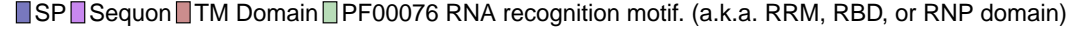
Protein length



Pfam domains



Pfam Description



Protein sequence:

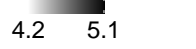
IGPDPLALKSRNIGMVGGRPEISLPDASSTLFEGLPADCTRETVSHFRFPVGVYKEVRLPKGSRHLGGDPLLCFVDFVTPLRAAAAMDALOGYKFDHQRDEVSRLRMQYARNFGARSGGNGRKR

NbL09g04550.1 importin_subunit_beta-1-like [MW = 96.14 kDa]

No. of times detected



log(intensity)



Values from



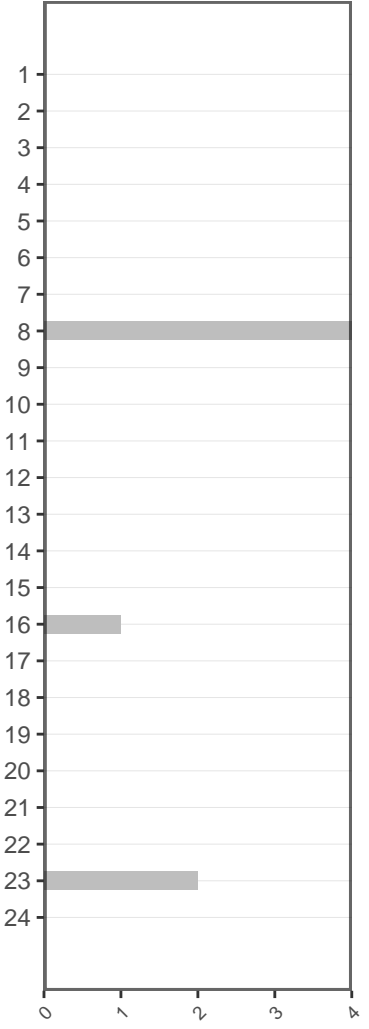
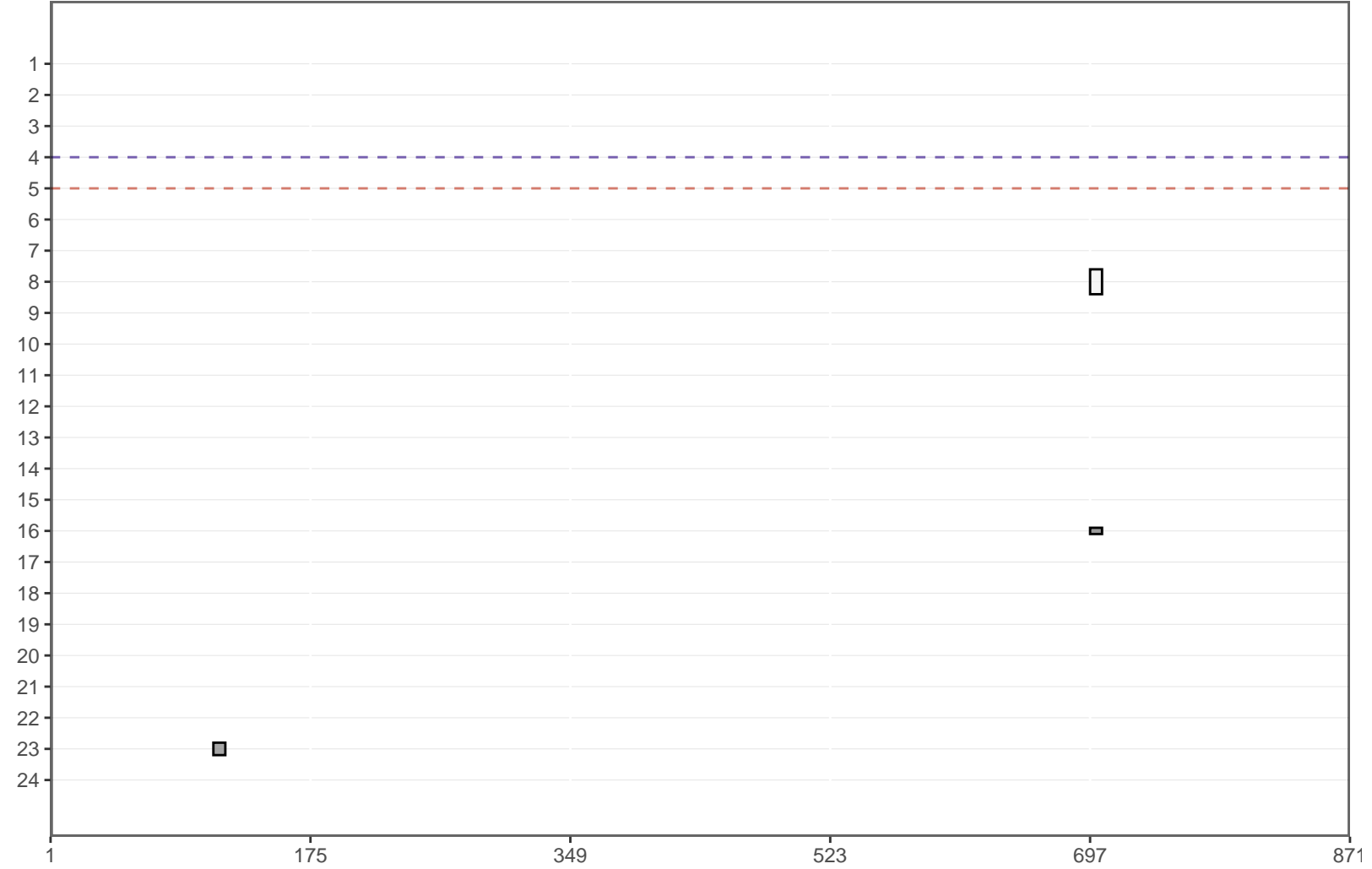
MW indication



Molecular weight

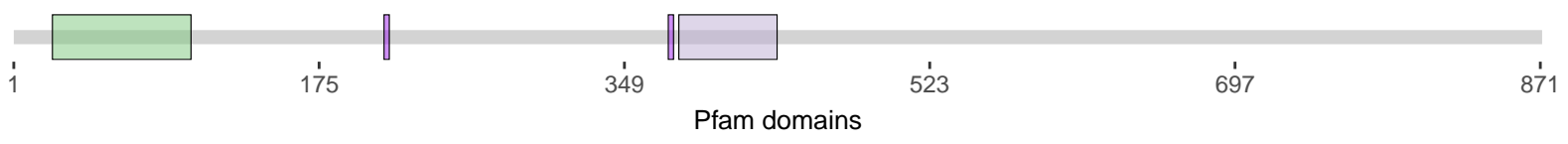


Gel Slice



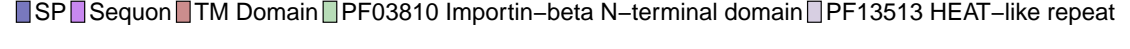
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISIVKDTTAVTLGRIFELHSGTVEIPITFANGCGQIFVLLQSMKDPANVAEKTCGALYFLSGDYGDNVGSASPLTFPFQGVQGLLTVTHRKDAGEERLRTAYAEALNEVVRGSDTETAPMLVQLVPMIMMELHQCLEAKLSSDEREKQSELOGLLCGGLGVHIGKLGASEPTKYVFLGVDQIMSLFFKVFAGRSATVHEEAMLAIGALAWTGADFAKYMPPEFYKLEMLQNFEEYGVCAVTIGVWGDVCRALERDLRYDGGIMTQLKDLKDLSSNQLHRVYKPIPFSCGDIAI

NbL09g04290.1 T-complex_protein_1_subunit_gamma-like [MW = 67.82 kDa]

No. of times detected



log(intensity)



Values from



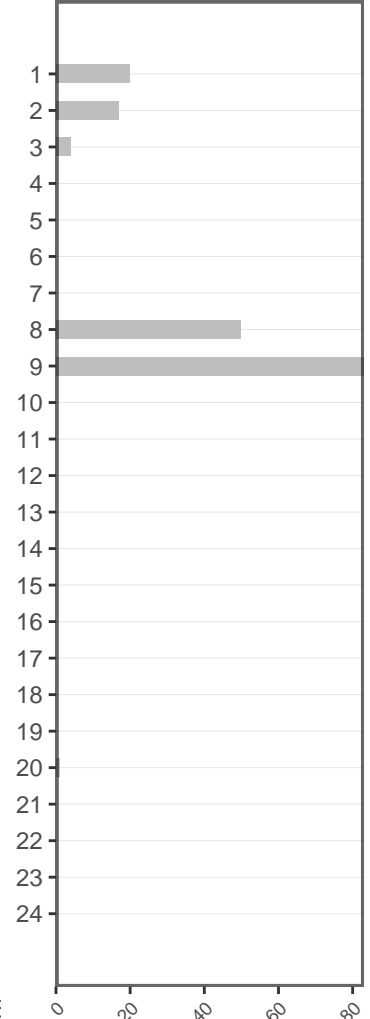
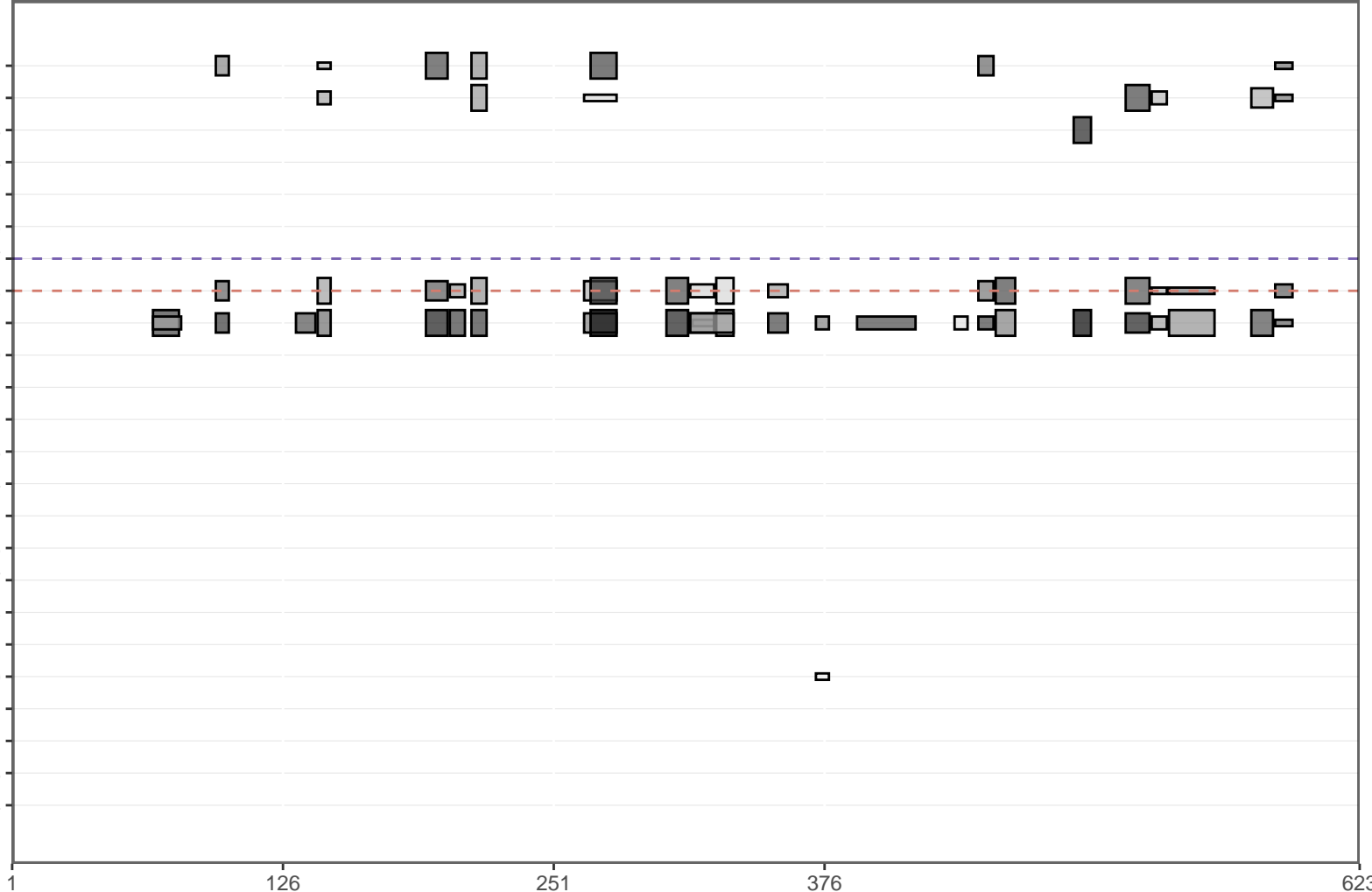
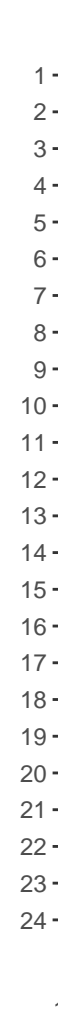
MW indication



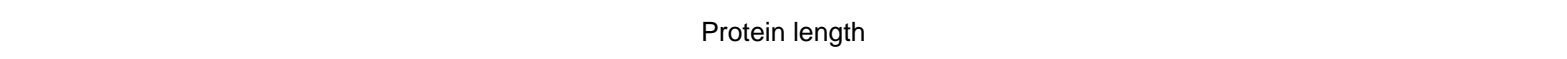
Molecular weight



Gel Slice

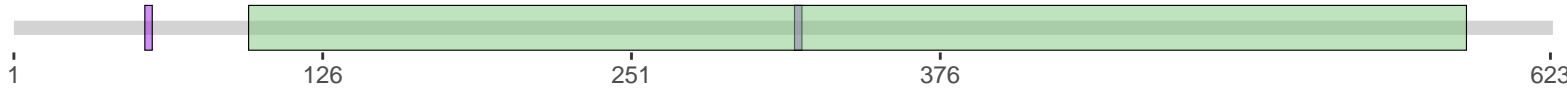


Protein length

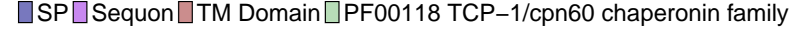


Peptide counts over 4 repeats

Pfam domains



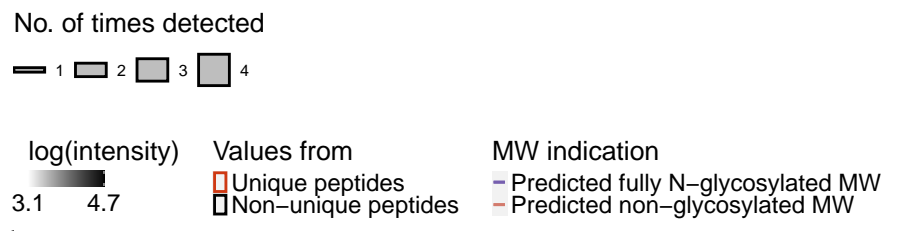
Pfam Description



Protein sequence:

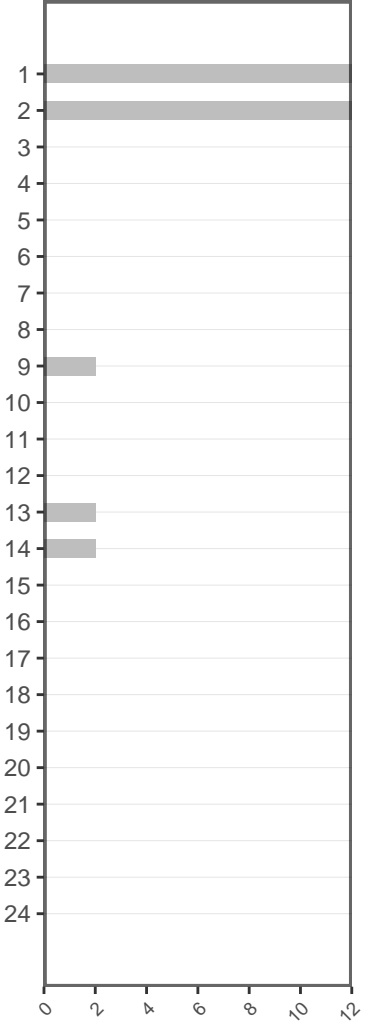
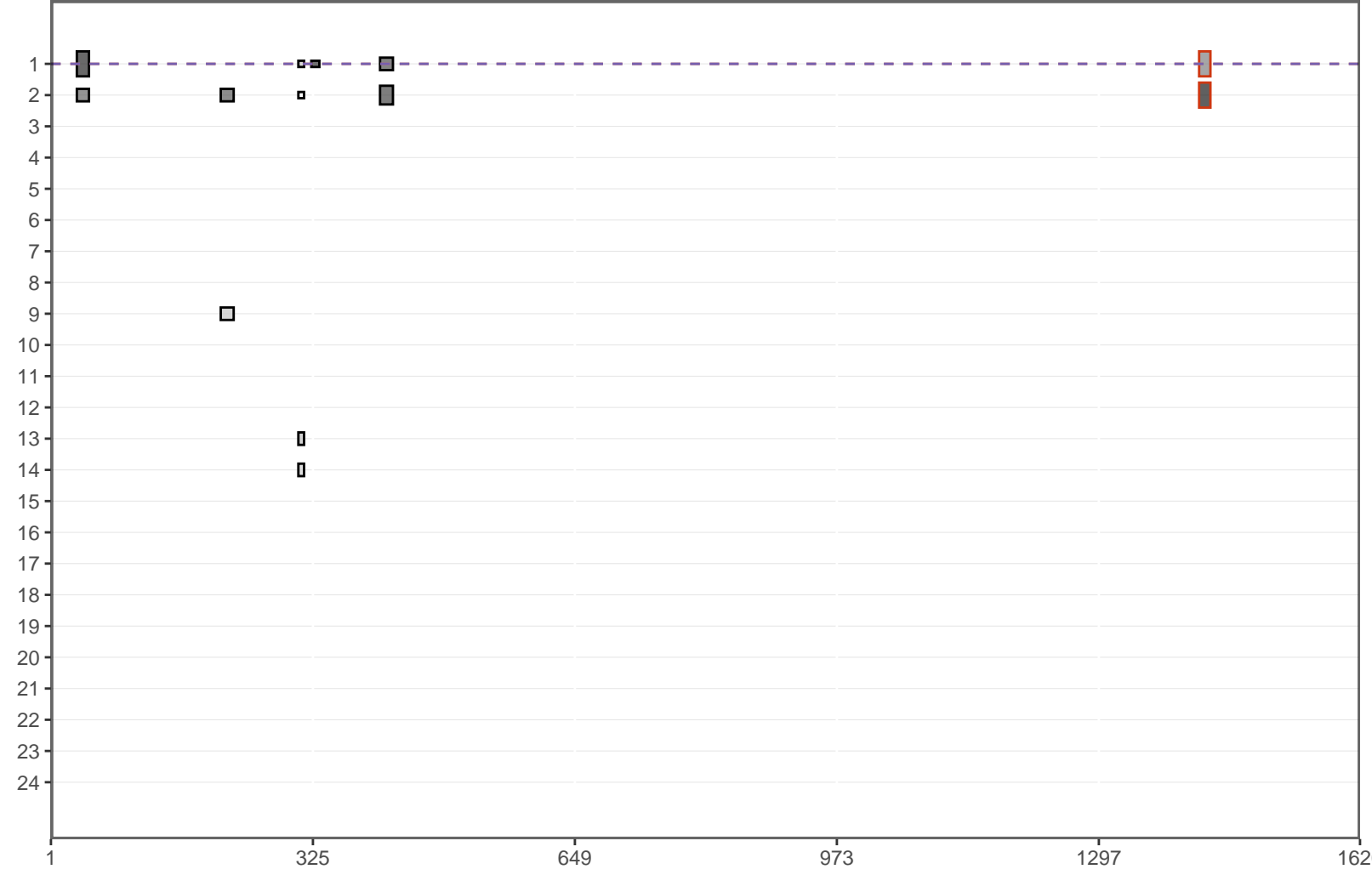
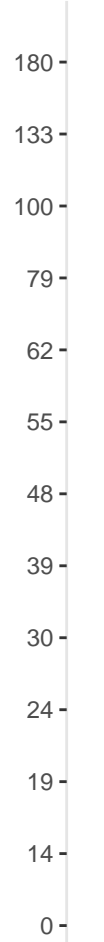
IPRILLDSFLEYKGGNGTMAELLREEDWNLLKMEEEYENMCAGIKFKPDAVITEKGLSDLACHYLSKAGVSAIRRLRKTDDNNAKAGGAVVNNRDELQESDVGTSAGLFEVKKIGDEFFTFVYDCKDKPKACTVLLRGAQKDLLEVERNLQDAMSVARNIKNPKLVPGGATELTVSAMLKQKSSSIEGIEKWPYGAAMAAFEAFPRTLAAGNGGVNVRTMTALOGKHANGENAWGIDGNTGEIADMKEGKIWDVYTVKAGAFKTAIEAAGLLRIDDIYSGIKKXQAPG

NbL09g04030.1 probable_phosphoinositide_phosphatase_SAC9 [MW = 179.04 kDa]



Molecular weight

Gel Slice

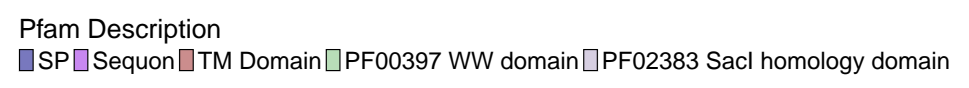


Peptide counts over 4 repeats

Protein length



Pfam domains



Protein sequence:

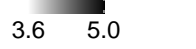
EELEGEVDFLTRVAVLTFYPMADGGGPTLGEHELGVPLPWRFLKHHEGVSYTRFAEQAEAHIDNNPFLTETENPFASALATDAGENSADLVWLLTGERISRDINRGSATETVPHGGDDLLDFLDDAIVGGPKVENSFSKTSKGFPTDNNHTGHYLNCFKLLVSPOMERKLSYMAAMKLEIERFRVNLGAAERDRALLSGVDRNIDPNIILLDDSRIGLGRRIANLALLGHASLEDKTASGSEFADDSANDFNWAGVSEICMGGTGGVHAENGPVLIHTLSYSTTQAQSF

NbL09g04010.1 peroxidase_47-like [MW - SP = 33.84 kDa]

No. of times detected



log(intensity)



Values from



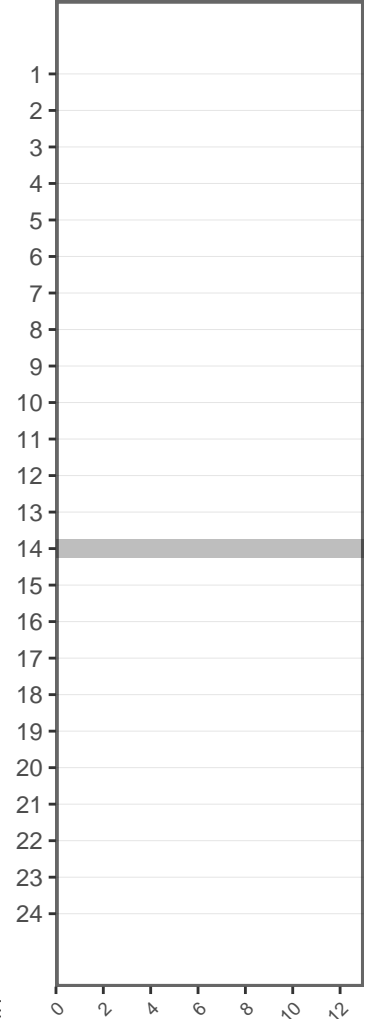
MW indication



Molecular weight

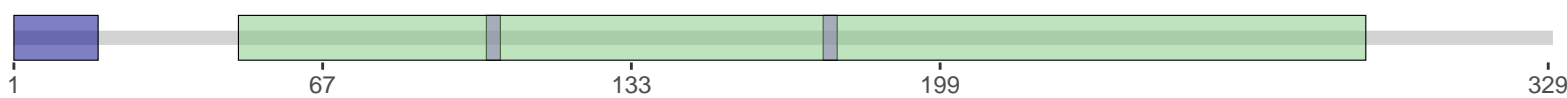


Gel Slice



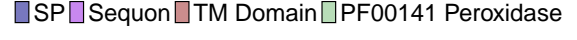
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

KGRKDGRRSRIEDTINLPRLNNSSELRIFAGHGFSGAGEMVALSGAHTLGVARGSSFKRRLSNFDSHTHGVDPFLDAGFAKLSKTCGGGGDKSEGAFTDTKNDFDNNVYFALORRSGVLFSDQTLVNSPRTRGVNGVAFNGAMFFLDFGQAMVMMGLLDVKEGLDGEVRSNGRIN'

NbL09g04000.1 probable_calcium-binding_protein_CML20 [MW = 21.22 kDa]

No. of times detected



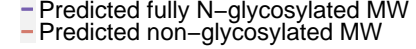
log(intensity)



Values from



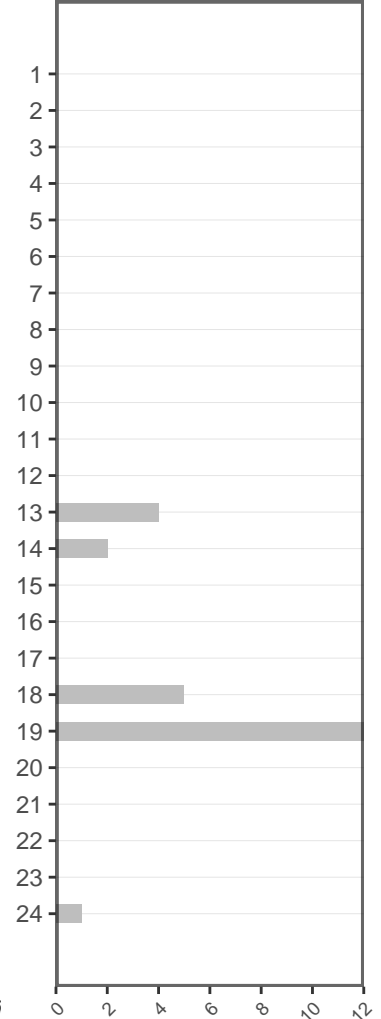
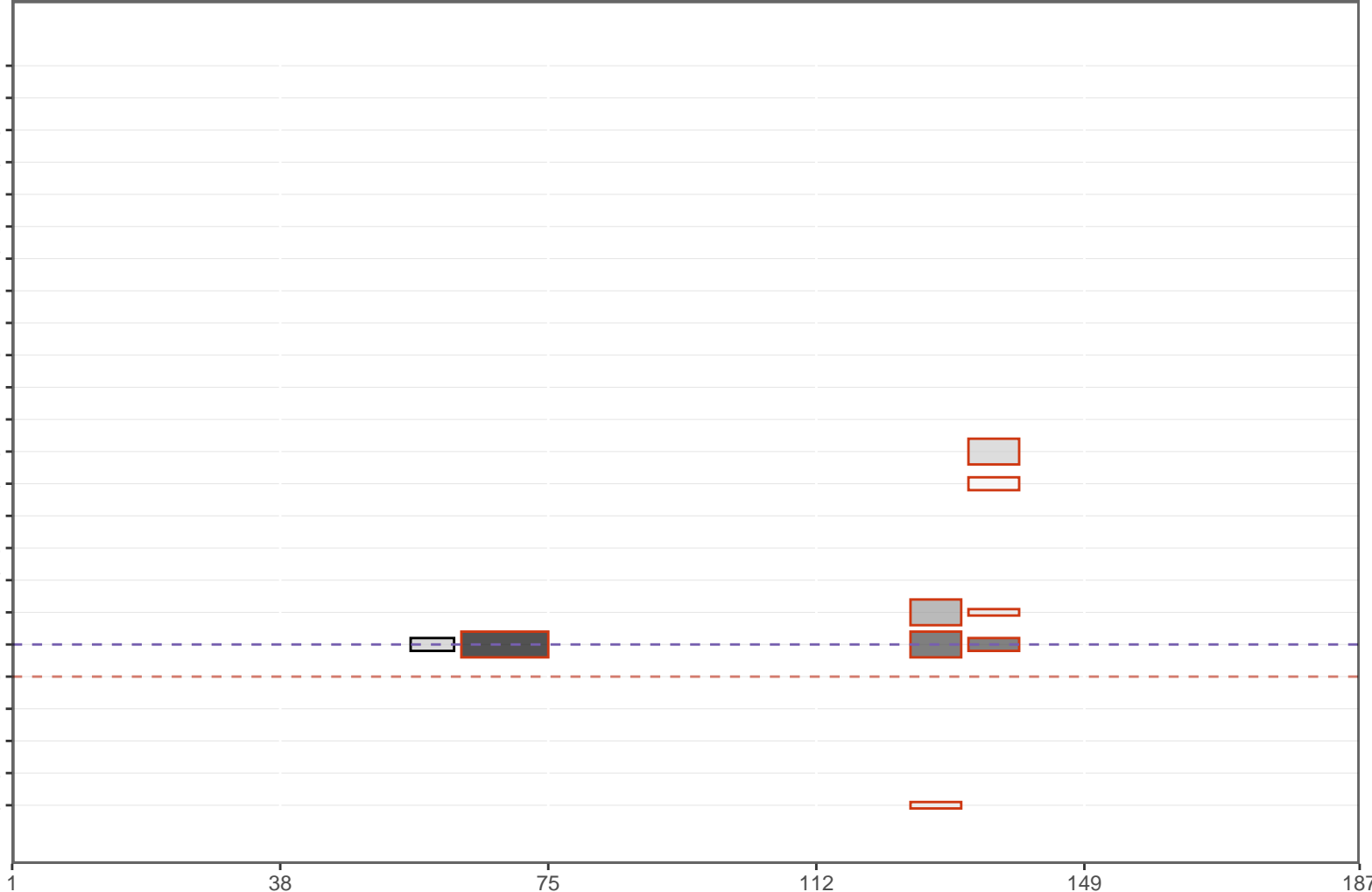
MW indication



Molecular weight



Gel Slice

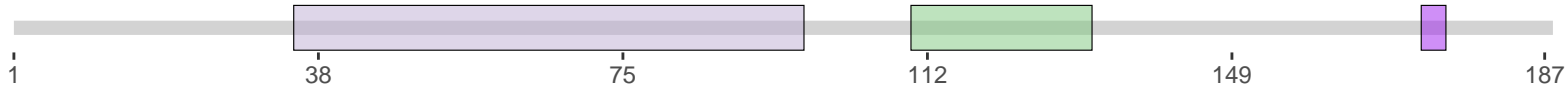


Protein length

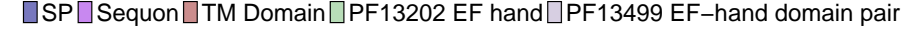


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VQKDGSGAIDFDLDFVHMMFAKFGDRDKKEELKKAFFVDDGDKNGKISFADGRIADELGERFDRDQEMIEAANDGRRVCGLSIFSLWMLLNITTHSAPLGLSP*

NbL09g03970.1 2-alkenal_reductase_(NADP(+)-dependent) [MW = 37.83 kDa]

No. of times detected



log(intensity)



Values from



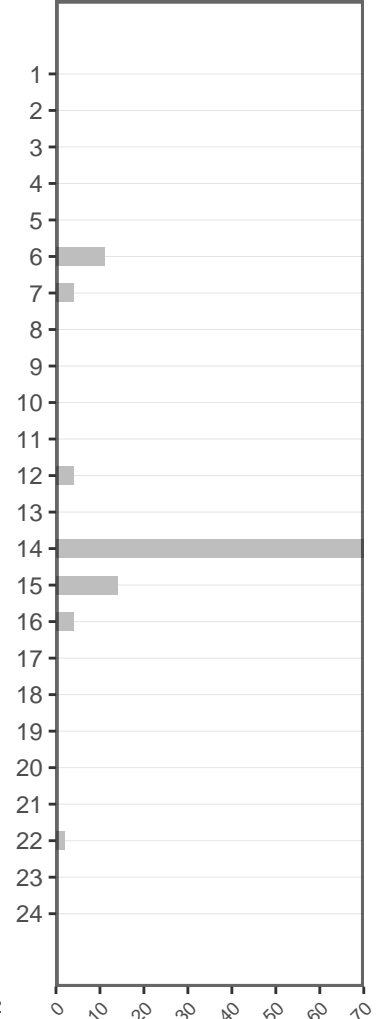
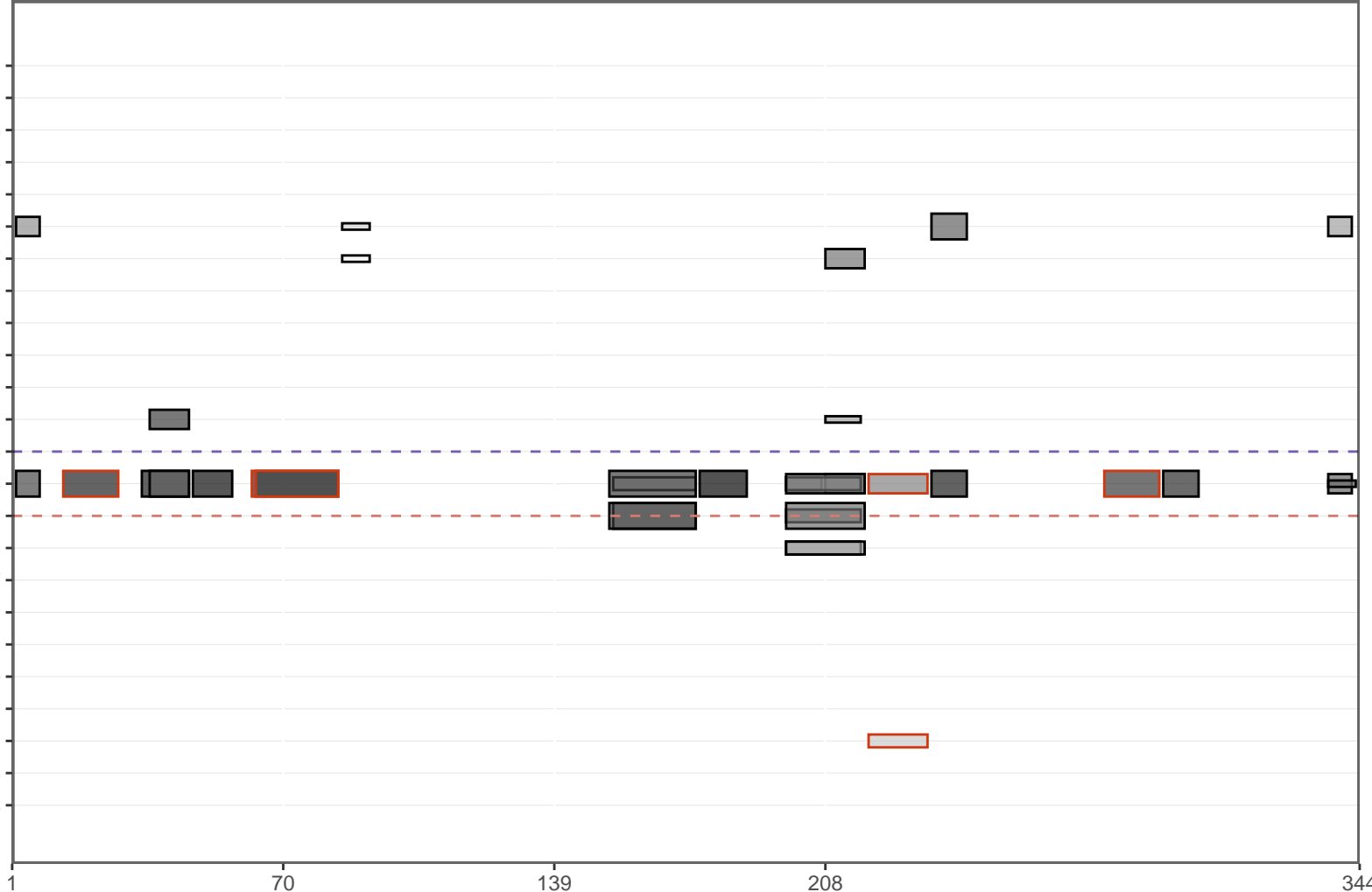
MW indication



Molecular weight

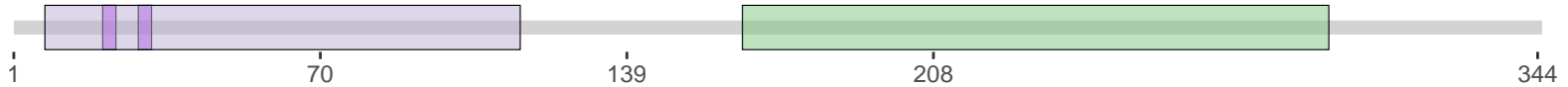


Gel Slice



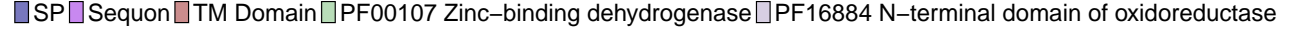
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YSAASGAVGQLVGGFANMLGGYHYVGSAGSKEKVDLLKPKFGDFEAFNYKEEGDNLAAIKRFPDGGDYVFENVGGKMLDAVLLNMLHGRIACGMISGYNLEQNEGIVHNLGFLTKRIRMEGLVSDYHYLKYKLEMVPIQKAGKVVYVEVDADGLEAPALVGLFSGRNIGKGVVYVREI

NbL09g03860.1 valine--tRNA_ligase_chloroplastic/mitochondrial_2 [MW = 109.88 kDa]

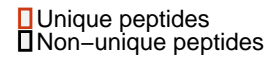
No. of times detected



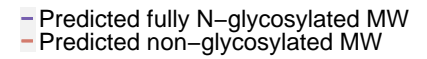
log(intensity)



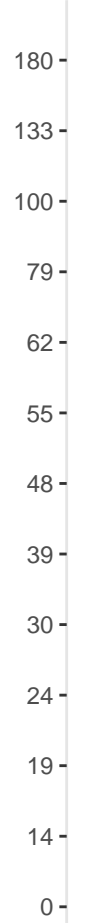
Values from



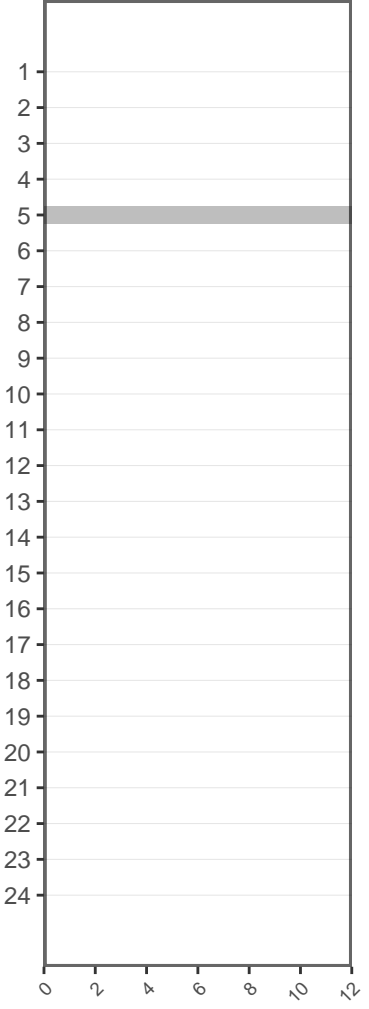
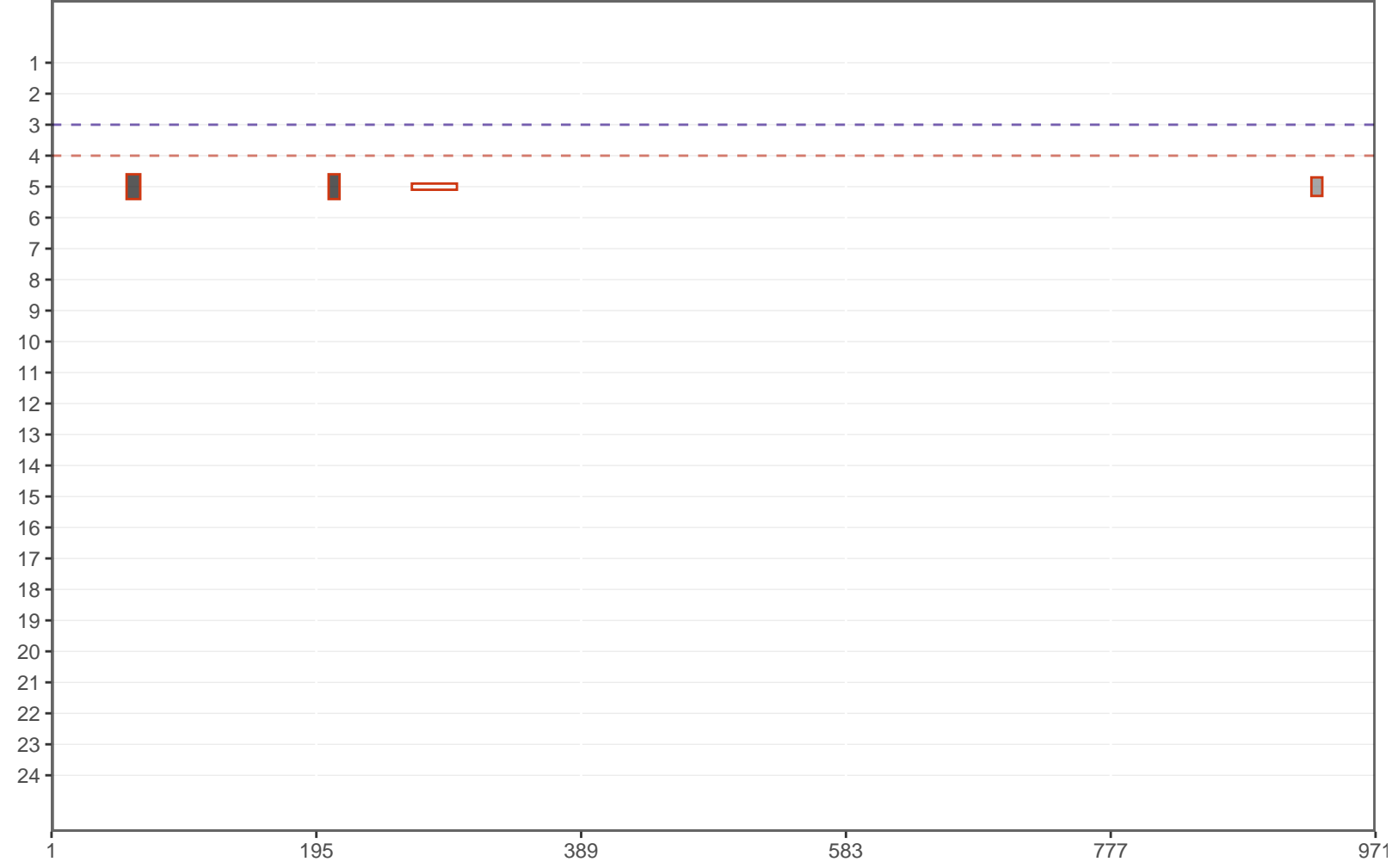
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

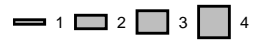
- SP
- Sequon
- PF00133 tRNA synthetases class I (I, L, M and V)
- PF10458 Valyl tRNA synthetase tRNA binding arm
- TM Domain
- PF08264 Anticodon-binding domain of tRNA ligase

Protein sequence:

VGHRIPVWYASGKDCDEEYWARSHREALSKAGEKYGNVVEIQDPPVLDTWFS66LWPFSTLGNWPD6SAEDFRKRFYPT6VLETHGDIILFFWARMVMMGIEFTGTVPFNSVYHGLIRDSGGRKMSKTLGNVDPIDTAEVGTDLRF7LALGTAGQDLNLSMERLTSNKAFTNKLWAGKIFLRNLP4LDDTVAWKALLAKFKDKV6GVKPLPEGQWVSKLHVLDVDTADYENLFFGDNGREYDFFWADPADWVIEVSKARVHSGDHV6SEV5QAALLYFTGLI

NbL09g03640.1 ABC_transporter_D_family_member_2_chloroplastic [MW = 80.38 kDa]

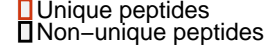
No. of times detected



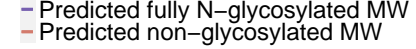
log(intensity)



Values from



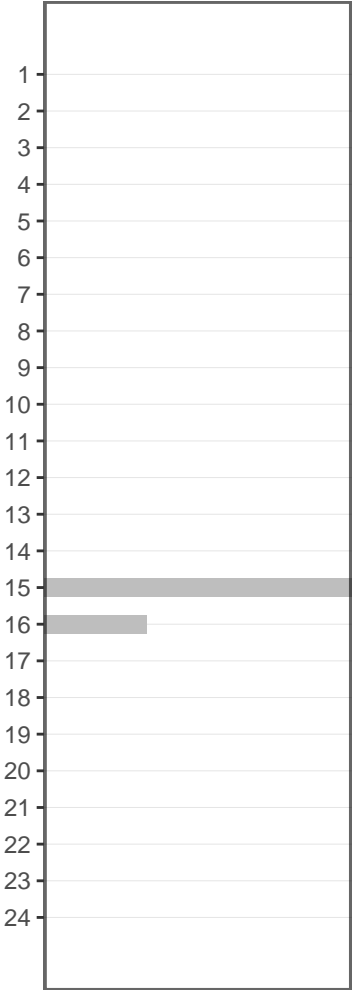
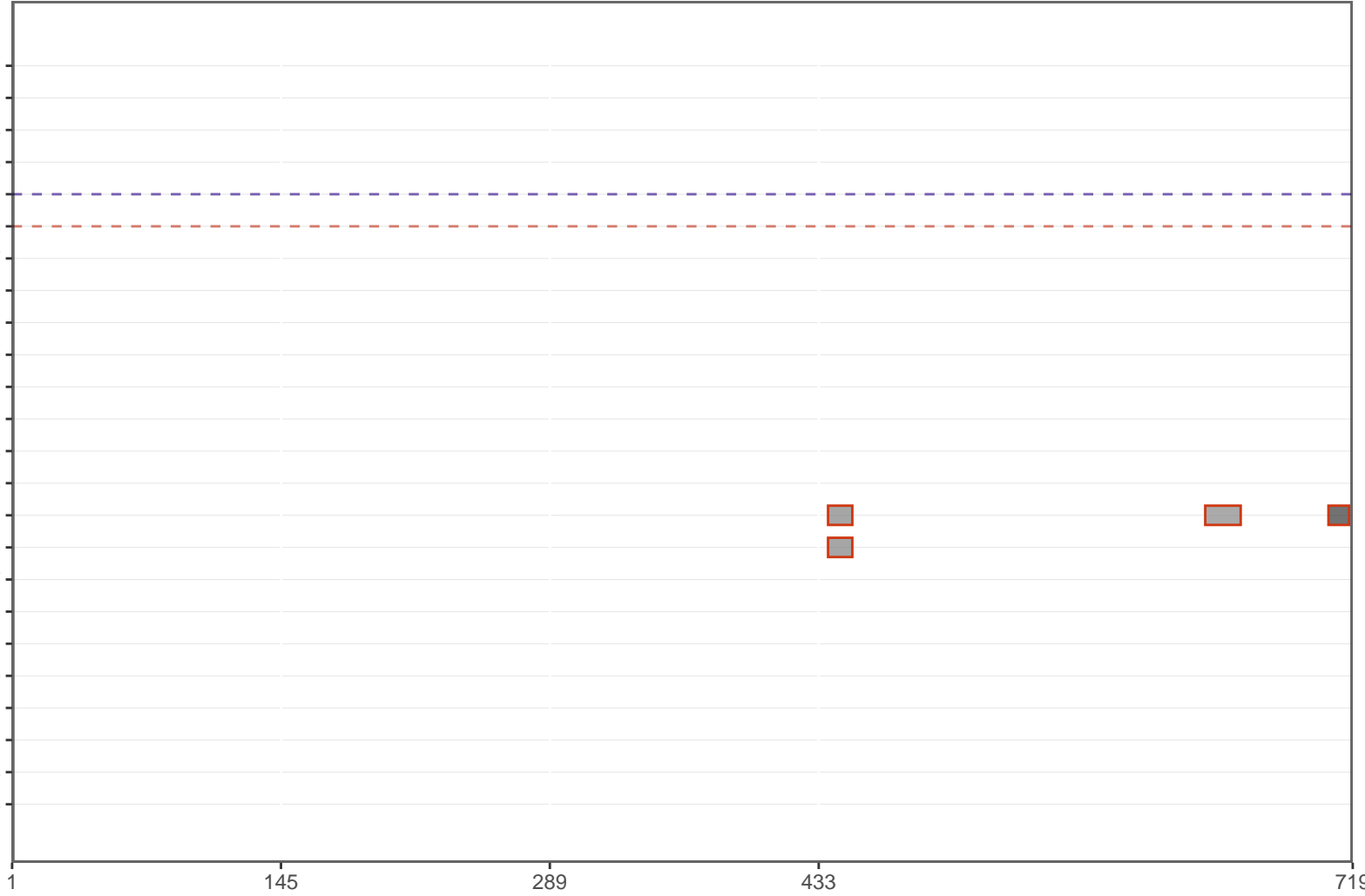
MW indication



Molecular weight

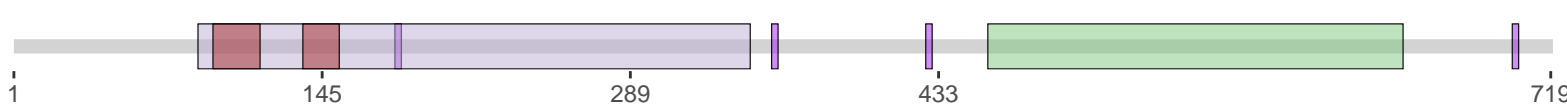


Gel Slice



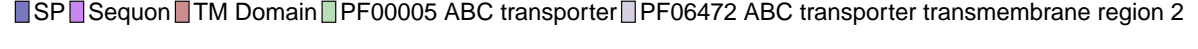
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

KIEFGVYVNSASAFNHLGDFSLHYVGFQAFSAFSAVDRLGEPDVLDSNRRKKGHDHLEKEKLNFLDLISGSNLSGNSGNSMPLSRRVKLLDVEQLTGTTPSKATLKDLSFEIYEKDHLLITGPGSGGSKTSLLRVAAGLWVFGSGATIVYRPRGELMPREPDVHSGGVSTNEIHWDTGRRNSEGVFLPKPKYAVLGTLRGQQLLYPTWTEDESDNVAVDDAKGSGDVGVGNERPMPGTSDDLRVLDVSLRHLLSRFDGLDSTYEWSSVLSLGGGRLAFARLLAKPLTJ

NbL09g03290.1 fasciclin-like_arabinogalactan_protein_1 [MW - SP = 26.26 kDa]

No. of times detected



log(intensity)



Values from



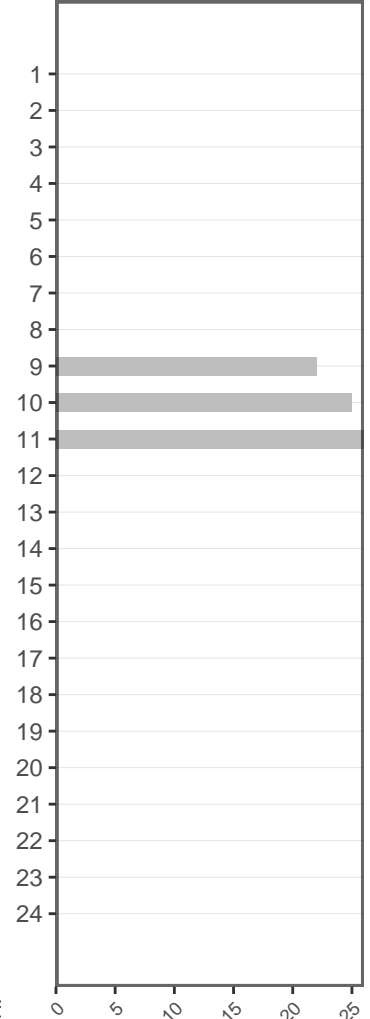
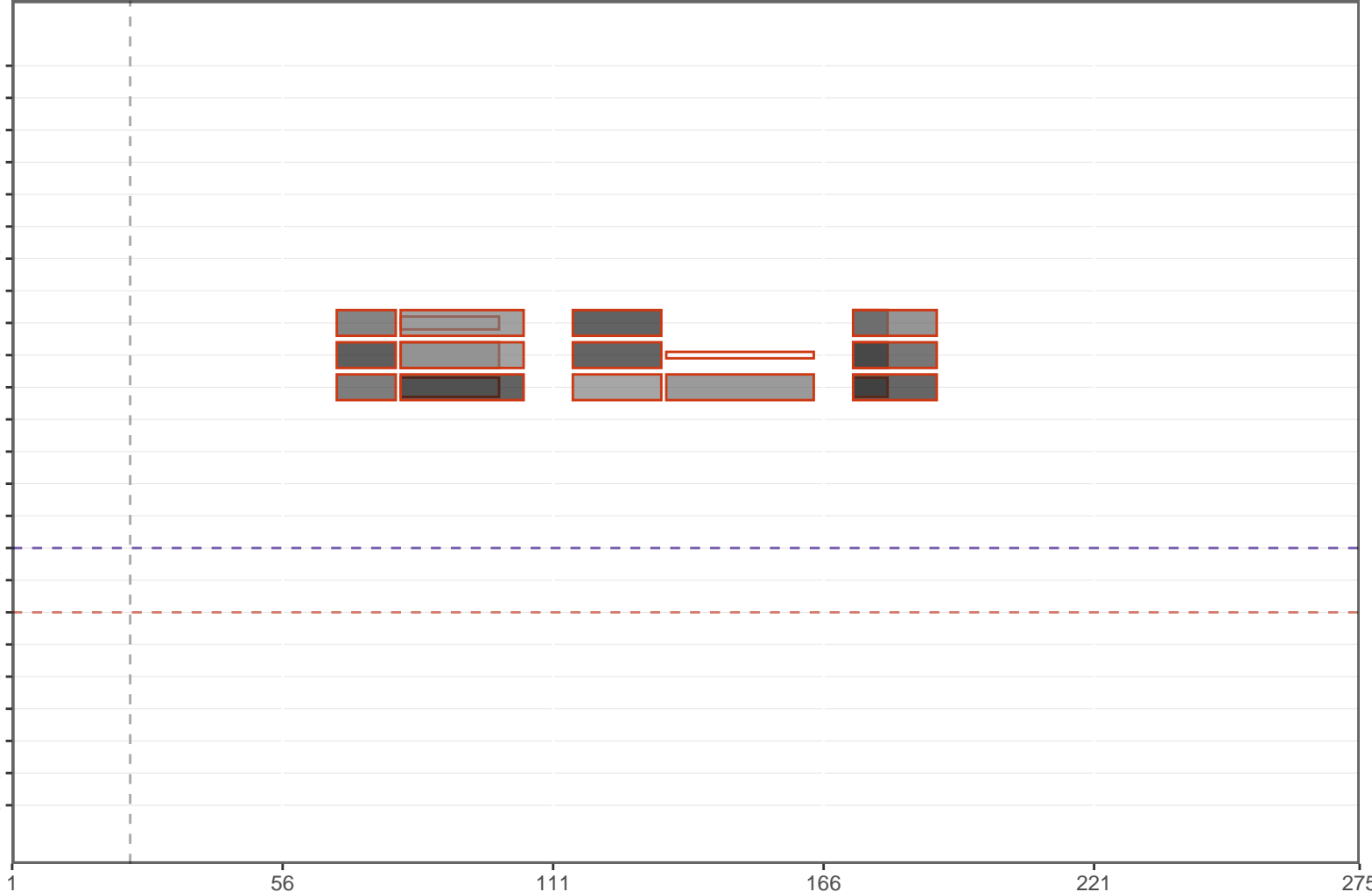
MW indication



Molecular weight



Gel Slice



Protein length

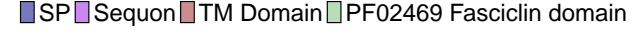


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PVYQSLSLRTSNGLMNLTAFDGNANNDFVQNDGGDWTLRTKIDTAKITGTVIDEKLAFISDQVLEPKELFKGAPTAPAPAPAPAESPKPALKKHKKPPAPSPADSPDGFDTDDVADSKADKNGAFRRYNAGALVLPVVGWFGHLLI

NbL09g03050.1 porphobilinogen_deaminase_chloroplastic-like [MW = 40.08 kDa]

No. of times detected



log(intensity)



Values from

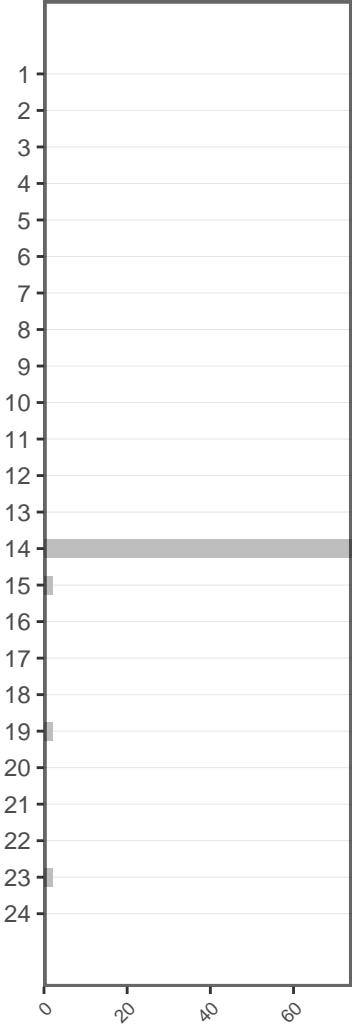
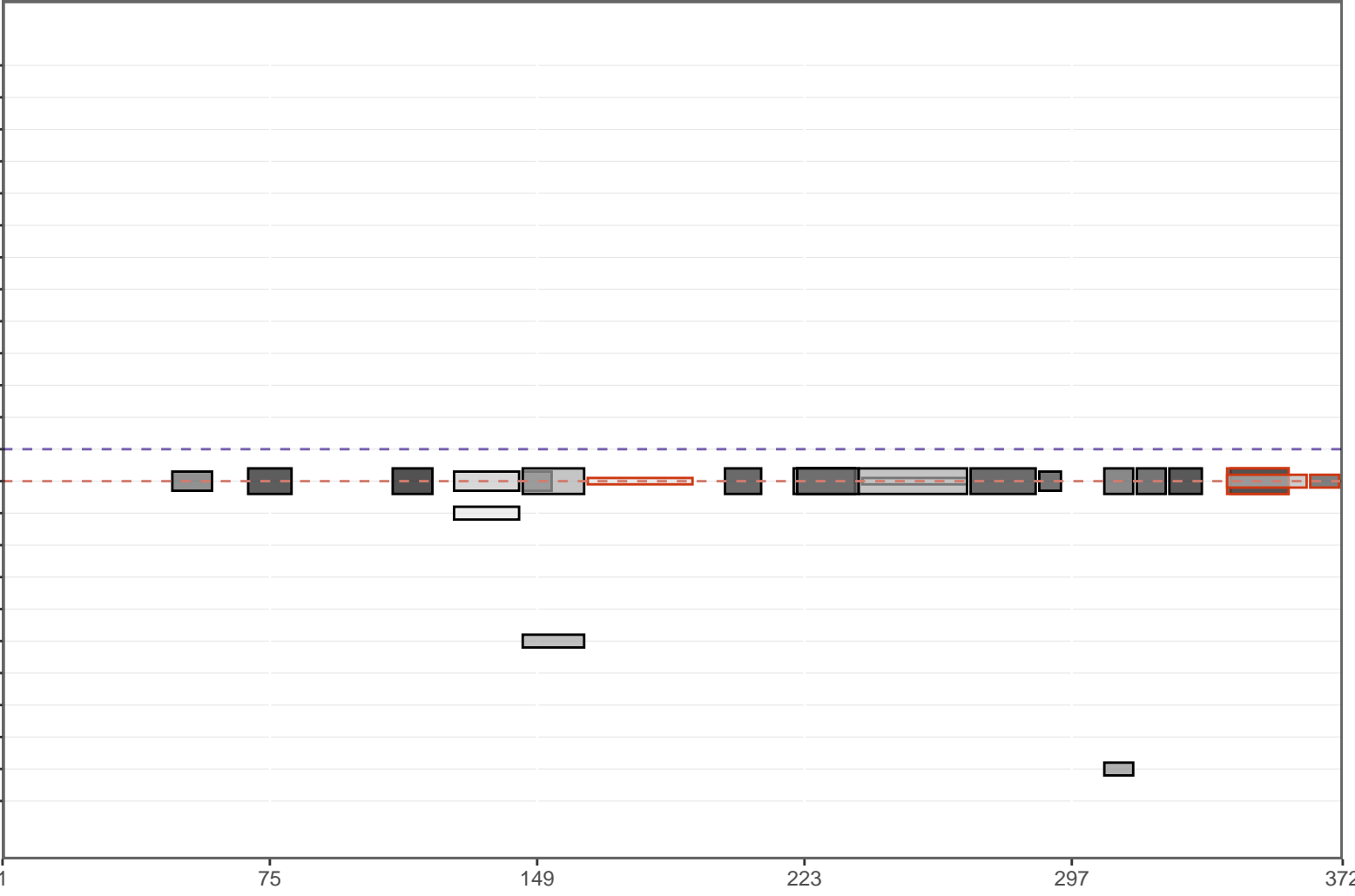
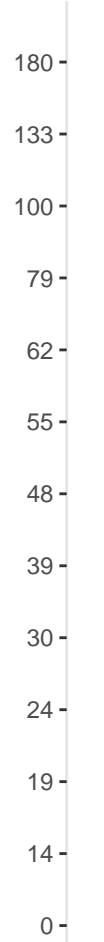


MW indication



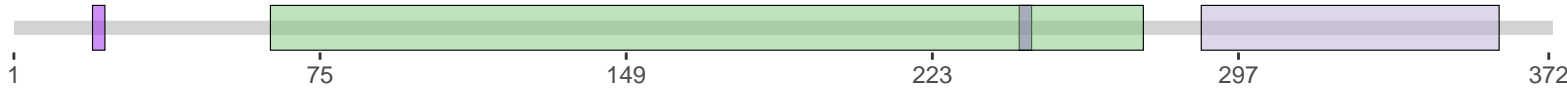
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01379 Porphobilinogen deaminase, dipyromethane cofactor binding domain
- PF03900 Porphobilinogen deaminase, C-terminal domain

Protein sequence:

AQLPSGSTVGTASLRKSGQLHRYPSLNVLENFRGNVQTRLRKLNKNEGVQATLLALAGLKLKLDMTENVTSLPIEDMLFPAWQAGAIAGRSDDETMANVYALLNHEETRLAWAGERAFKLTLDGSGRTPIAGVAGRGEDDDCFKGLVASPDGTRVLRLETSRKGYPYFEDMTVMQEDMGKELLERAGPQGFQTKV

NbL09g03010.1 phosphoglycerate_kinase_cytosolic-like [MW = 42.48 kDa]

No. of times detected



log(intensity)



Values from



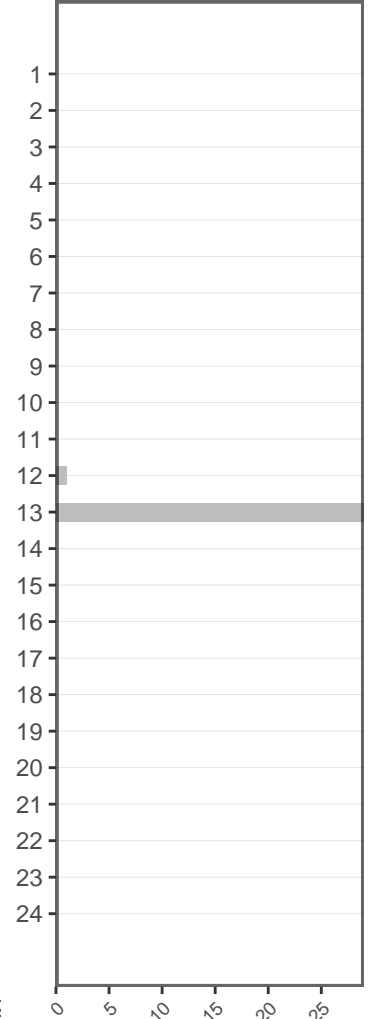
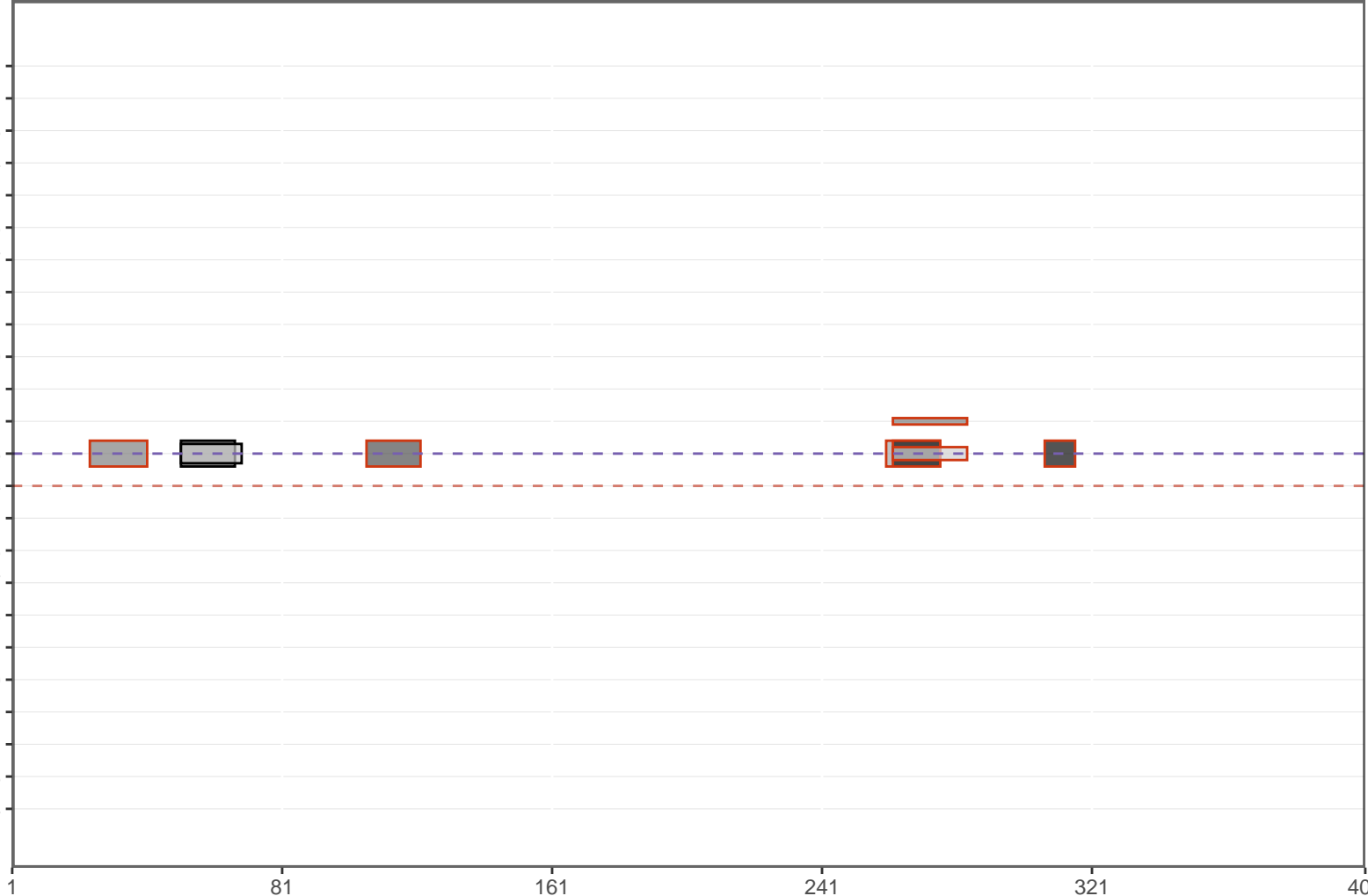
MW indication



Molecular weight

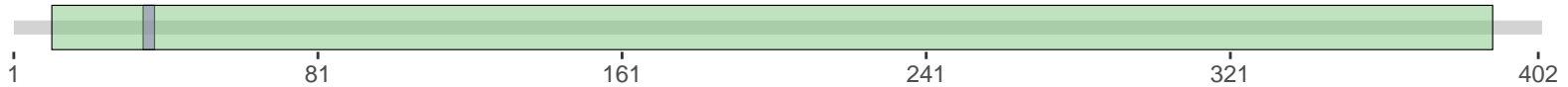


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VSINPKPFAAIVGSGKVSQKGVHSELEKVNLLGGGMIFTFYKAGGVYVGSLSVEEDKLDLDTLSLEKAKKAGVSLLLPADVADNFADANSKVPASEIPDGMVGLDNGPDAIKSFGSEALDKTIWNGPMGVFEFEKFAAGTEAAKHLAELSGKGVTTHTGGGDSVAANEKVLADKMSHSTGGGASLELLEGGKLPGLALDDV

NbL09g02980.1 glucan_endo-13-beta-glucosidase_12-like [MW - SP = 49.49 kDa]

No. of times detected



log(intensity)



Values from



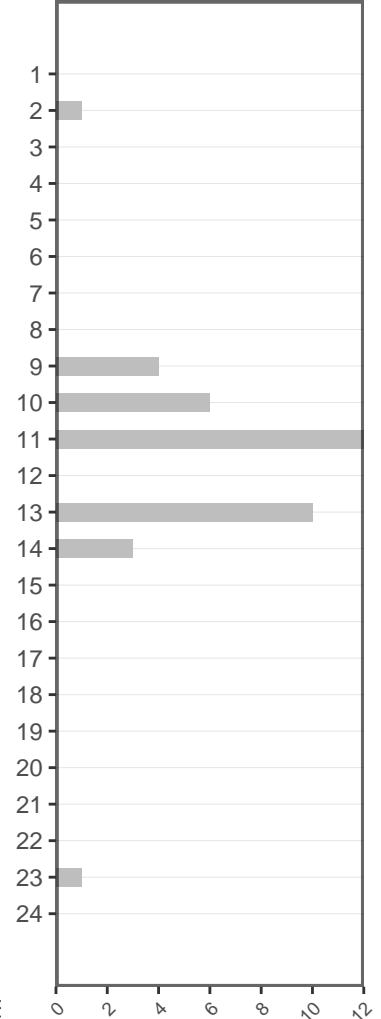
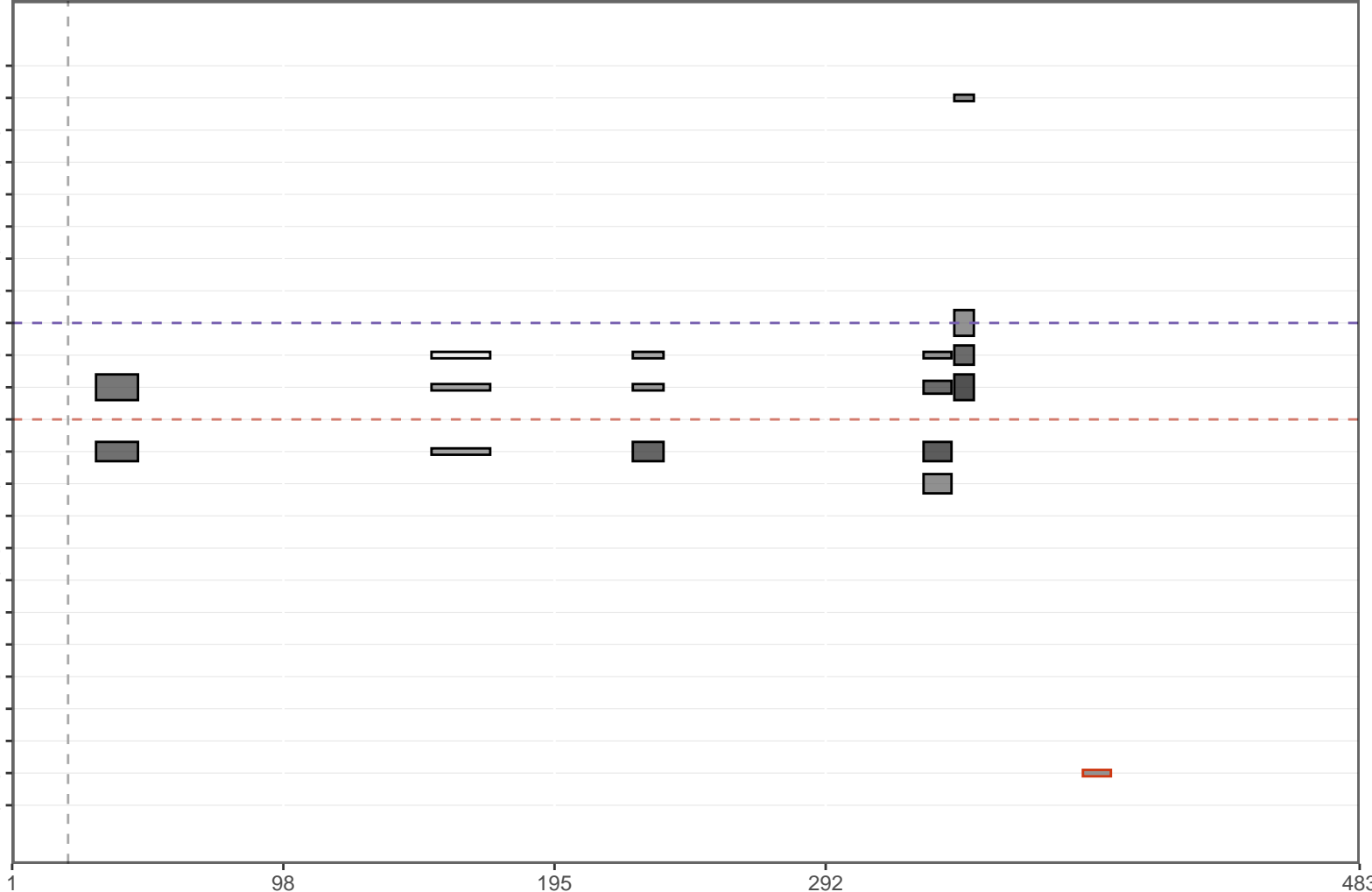
MW indication



Molecular weight



Gel Slice



Protein length

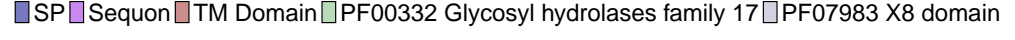


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

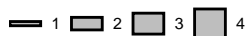
KSLFEAQIDVYIAMKAVGFGDVAHSVSETGWPSKGDENEAGAGADAAAYNGNLVRRVLTGSGTFLKNEPLDVFLLFALFNENKPKPPTSERNYGLFVYNEQVYDIALTKEGLNGPTMNMNSKSTVVTAPEKAEAPVSSGGDVEVSKVNTWGVWANEKAAREKLGAALEDVACDGGKGDGDRPQQGGATGVNPDLEAHASVAFNSVYQKNTKTRGVGTGDFNGAAVYVTDHPSEVSGFCFNNKHTIQ

NbL09g02930.1

dihydrolipoyllysine-residue_succinyltransferase_component_of_2-oxoglutarate_dehydrogenase_complex_1_mitochondrial-like

[MW = 51.42 kDa]

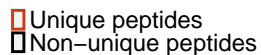
No. of times detected



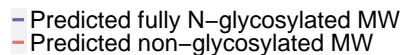
log(intensity)



Values from

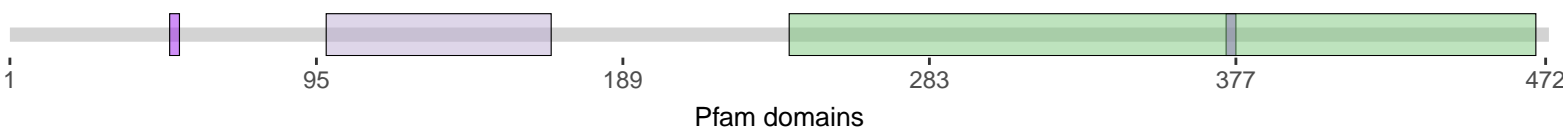
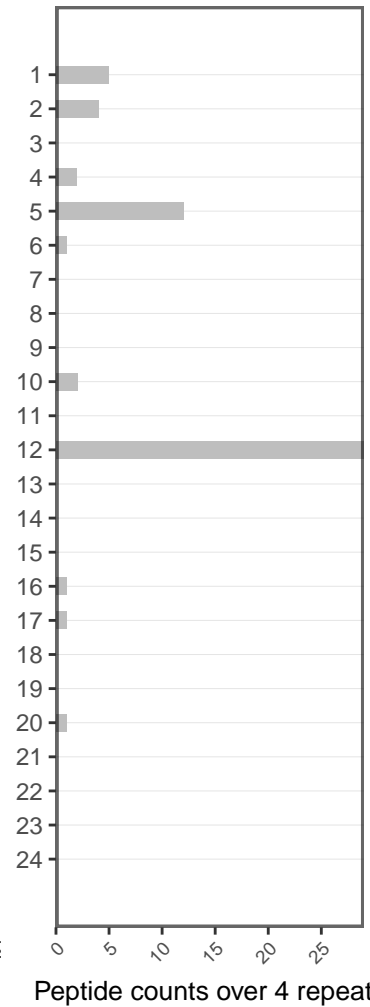
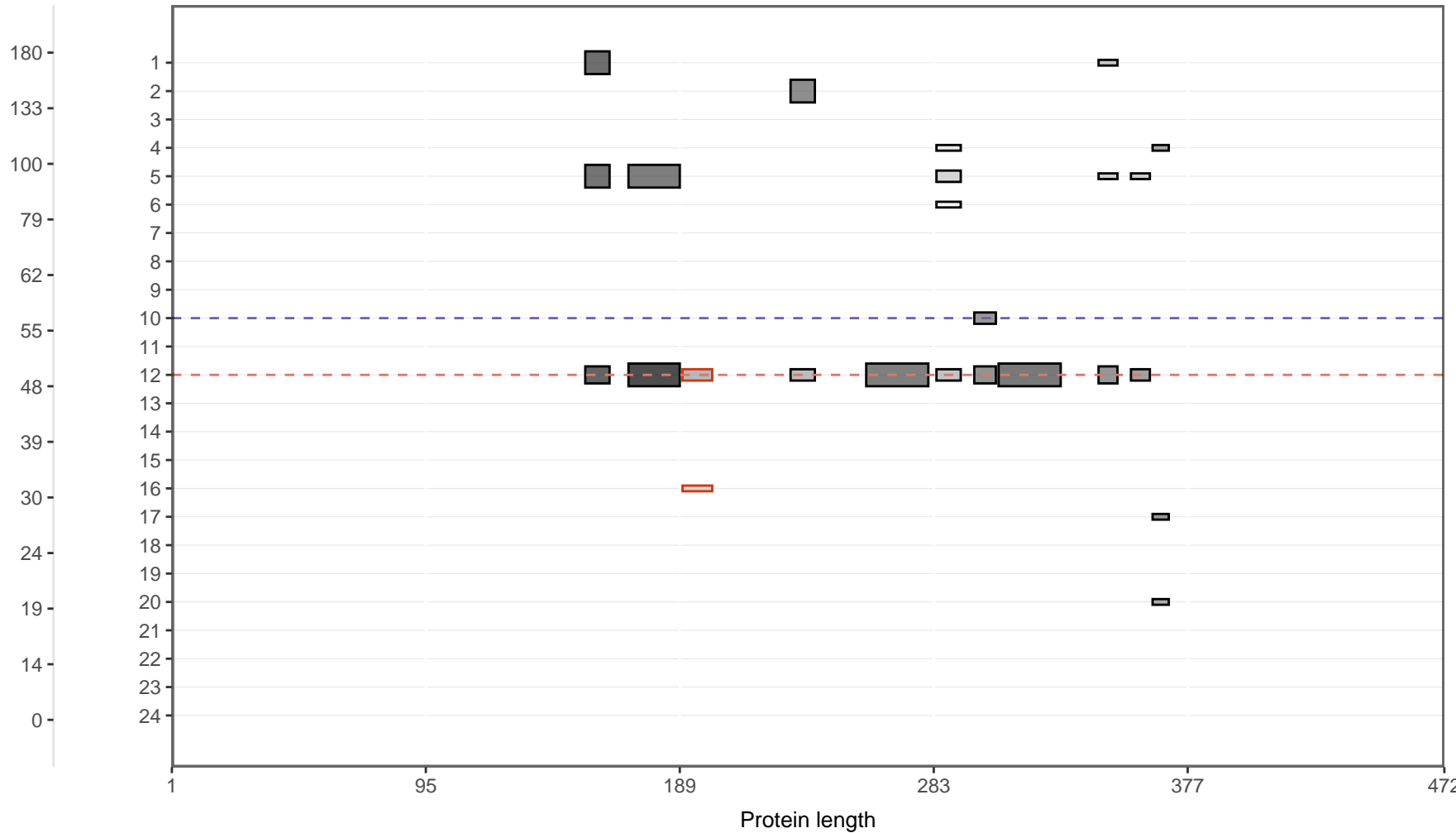


MW indication



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain PF00198 2-oxoacid dehydrogenases acyltransferase (catalytic domain) PF00364 Biotin-requiring enzyme

Protein sequence:

TSPPPPKRSATEPOLPPKERERRVPMTRLRKRVRWLRKDSQNTFALLTFNEVDMTNLMKLRSDYKDFVEKHGVKGLMSGFVAAVYALGNQDPVAVWIDDDHVRDVRVDSISWYVTKGLVYVYLRNAEKMNFAEIKTINSLAKKATNGTISIDEMAGGQFTINSGVYVYVGLLSTPINPPOSALGMHSIVNRPMMVYVGGNVYSRPMMVYALTYDHRLEIDGREAVYFLRRKDYVEDPRRLLEDV

NbL09g02790.1 ras-related_protein_RABB1c [MW = 26.66 kDa]

No. of times detected



log(intensity)



Values from



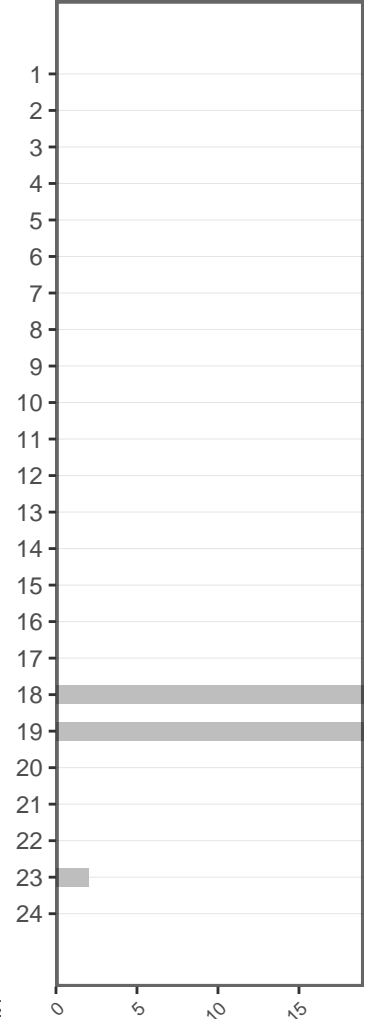
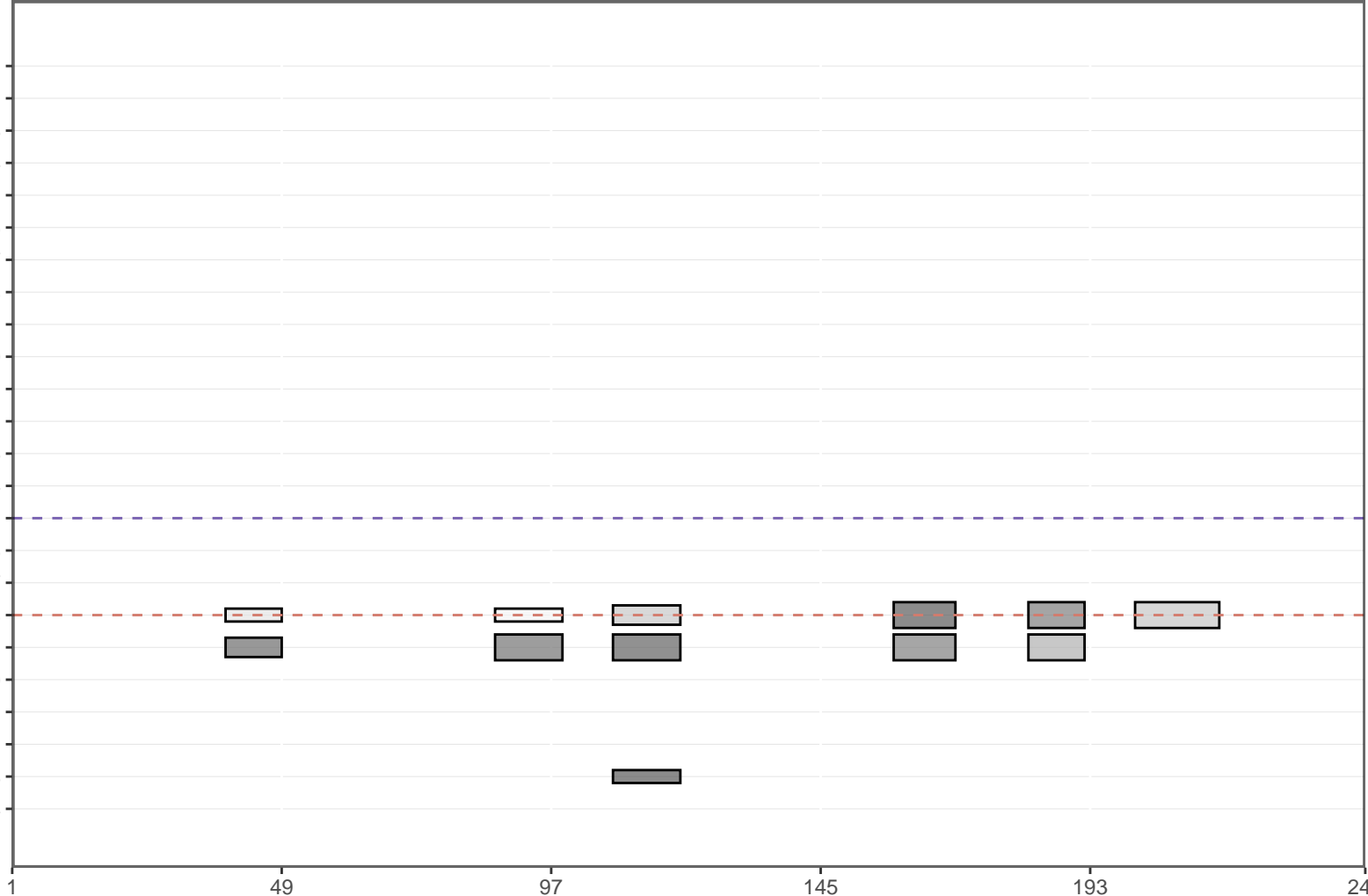
MW indication



Molecular weight

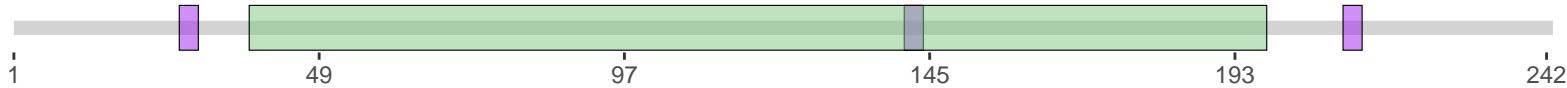


Gel Slice



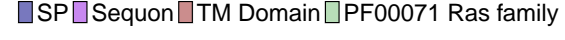
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

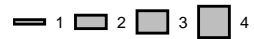


Protein sequence:

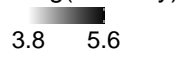
AGALLYDITRRETFNHLASWLEDRGHANANMTMLIGNKDLAHRRAVSTEEGGQFAKENLIFMEASAKTAGNVEEFARTASTYKKIQDGFVDSNESYGIKGVYGGIPGPGGGRDGVASGGGGGGG

NbL09g02750.1 elongation_factor_Ts_mitochondrial [MW = 43.29 kDa]

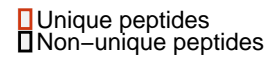
No. of times detected



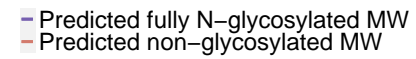
log(intensity)



Values from



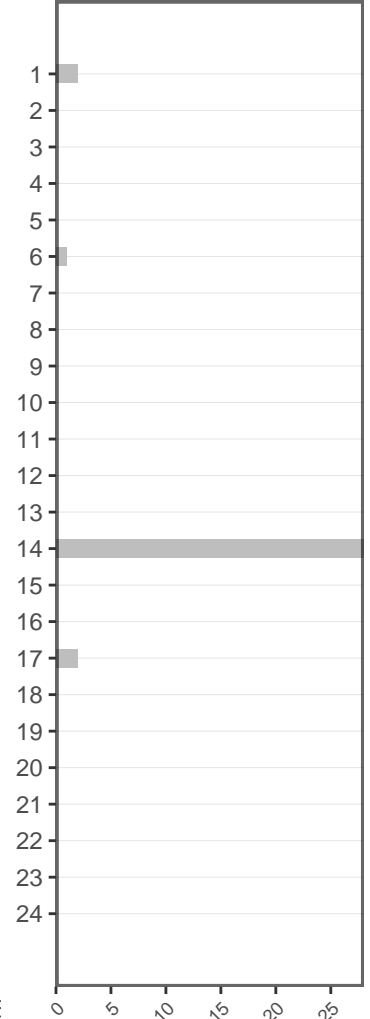
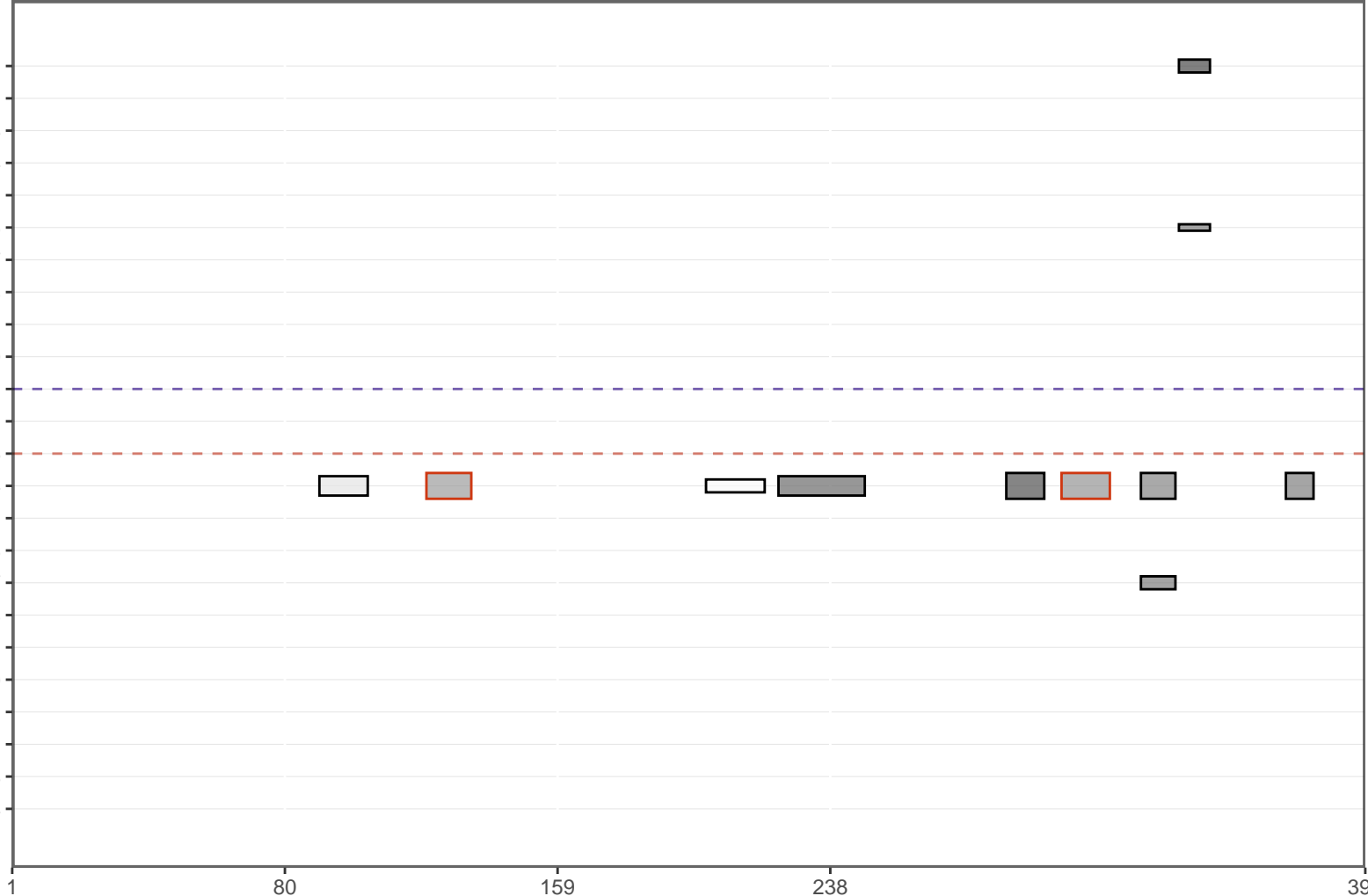
MW indication



Molecular weight

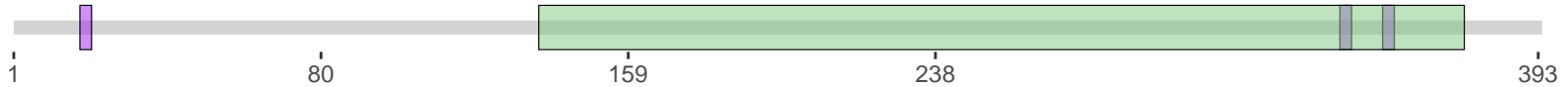


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IHLNMLDHPKLSGEKSVNATEVAAMNGENKLRGFAMTRPSIGVISTYLHTSPQPGVGRIGAGLSELEVEDGNVQDLAGRVSSEIAMHVAAPKFLTKEDVSSDALSNERELKSDAELSGRPOIAEKMVEGRMRKYFEEVALMEGKFFVNDTINVKTLISNLKSEKVPWIGSFLRMEVGEGLGRLEASNEPLNAA*

NbL09g02650.1 persulfide_dioxygenase_ETHE1_homolog_mitochondrial-like [MW = 33.04 kDa]

No. of times detected



log(intensity)



Values from



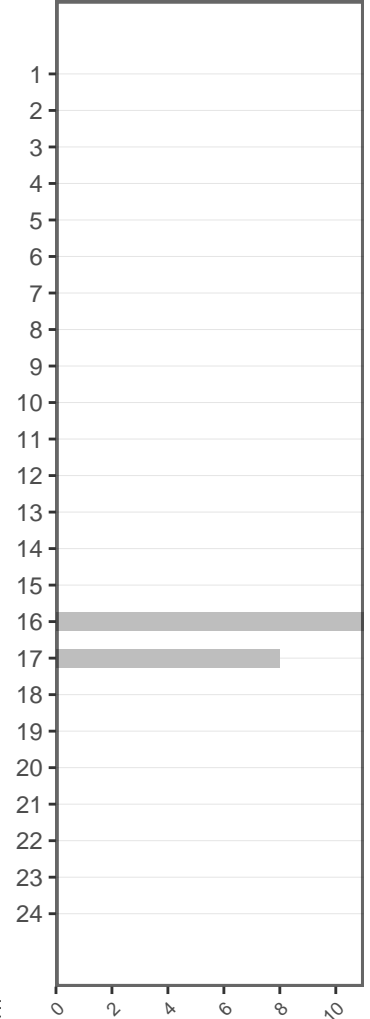
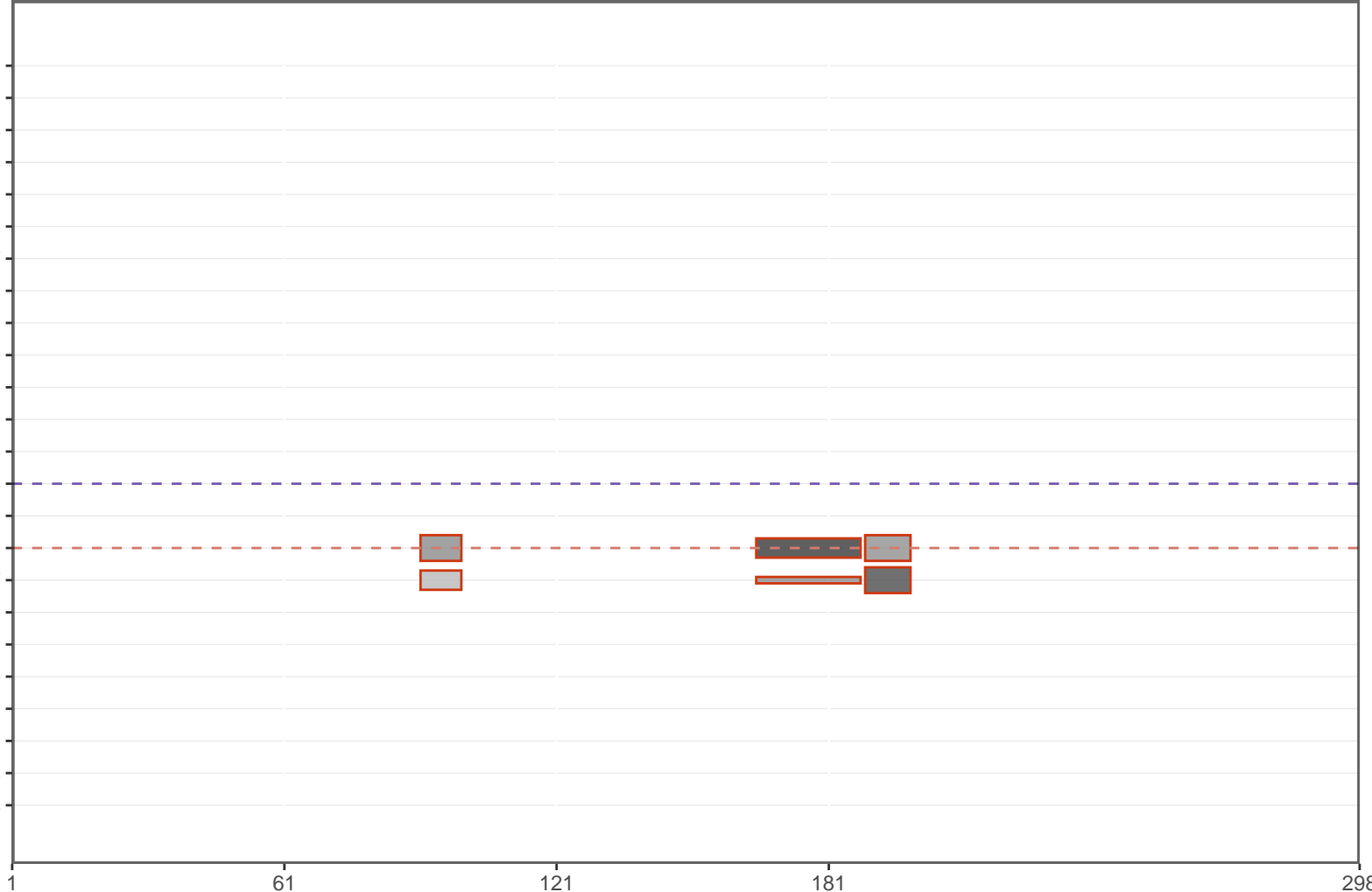
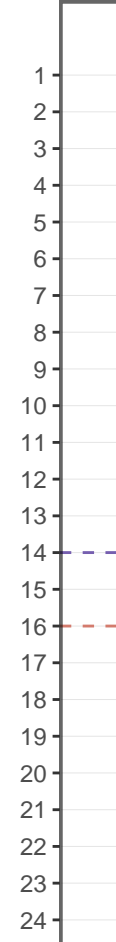
MW indication



Molecular weight

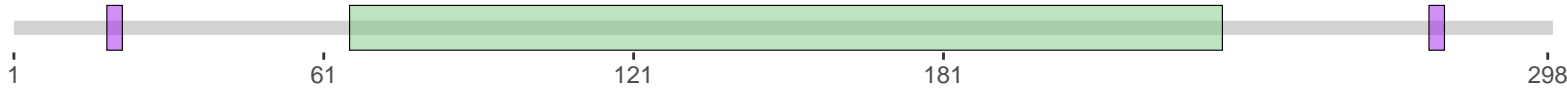


Gel Slice



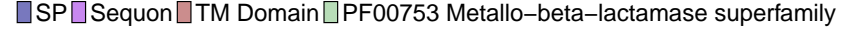
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ASNAKADLVFEPGDKYFGDFLEVRATPGHTLGGVTVYFGDGPNGPQRIAFDGMALLIRGGRTDFDGGSSDNLVDSVHSDIFLTKDYLWPHDKGFTVSTVGEEMLYNPRLEKDEQFLQETFNIMONLNLGYPKMMQAVPSPMLGGLQET

NbL09g02630.1 a-b_binding_protein_13_chloroplastic [MW = 28.5 kDa]

No. of times detected



log(intensity)



Values from



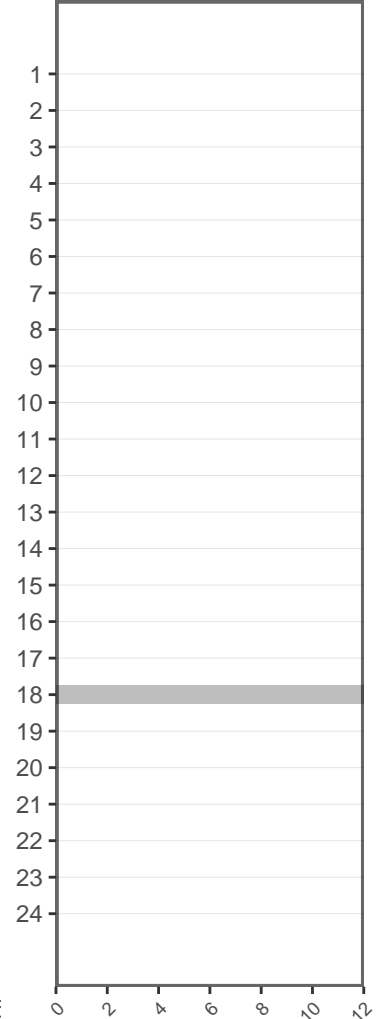
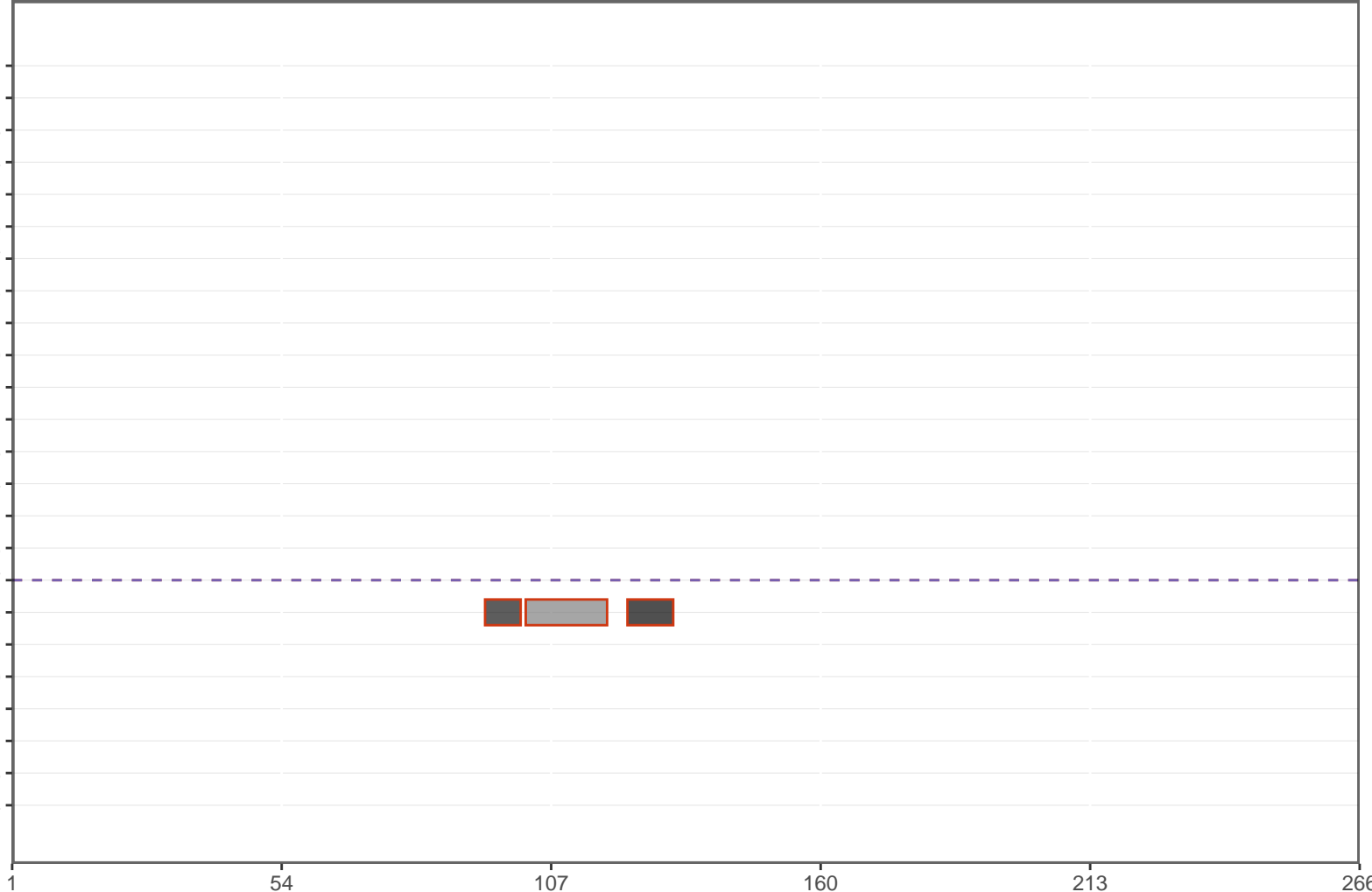
MW indication



Molecular weight



Gel Slice

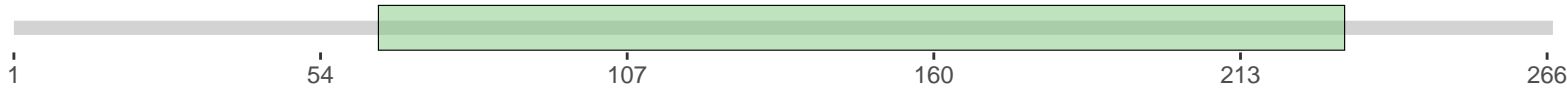


Protein length

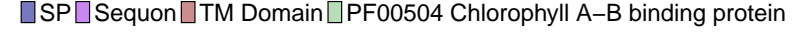


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IKVYDKEPWFYKAGIFSEGLDHLGNPLNHAQBIHLVLFQVVLMSLVEGFRINGLPVVEGNNLYPGGDFDPLGLADPPTFAELKVKKEKNRGLAMFSMDFGVQAVITGKGLLENLHLDNPNVANNVWATKVPGA

NbL09g02580.1 peptidyl-prolyl_cis-trans_isomerase_CYP37_chloroplastic [MW = 53.15 kDa]

No. of times detected



log(intensity)



Values from



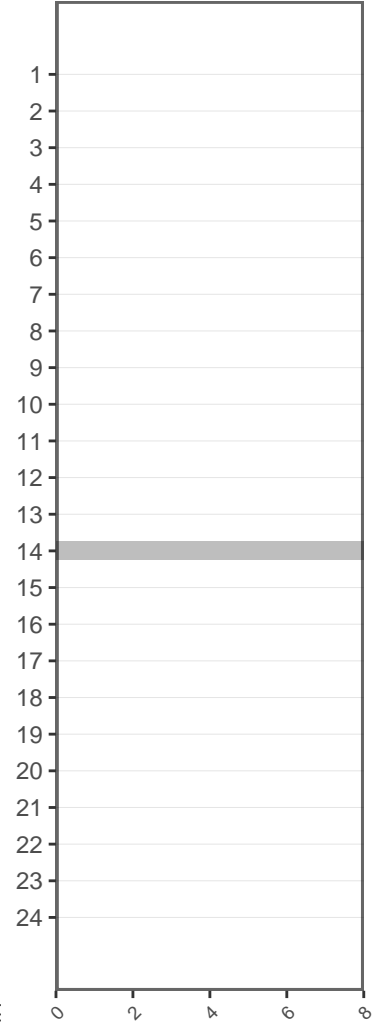
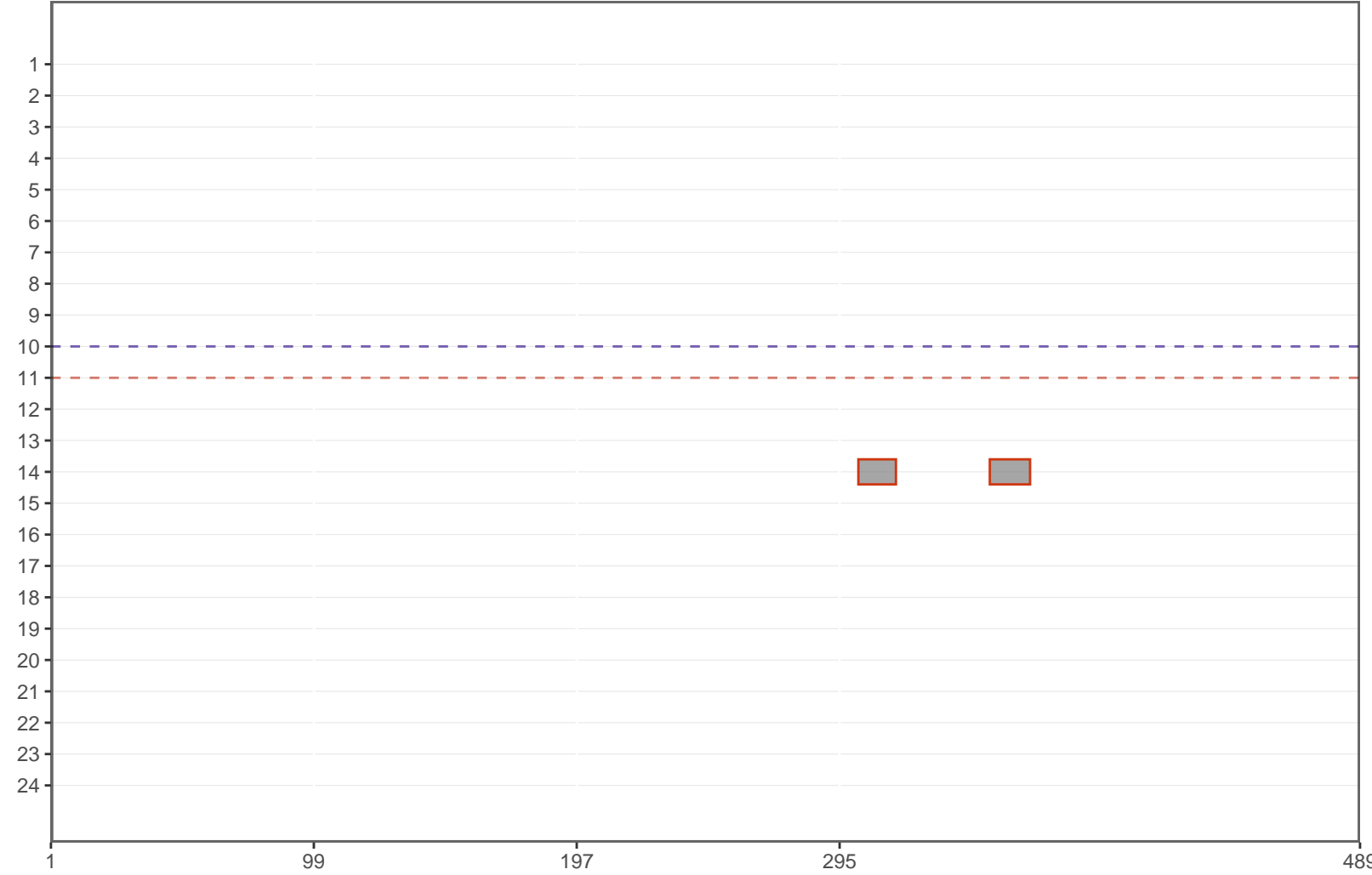
MW indication



Molecular weight



Gel Slice



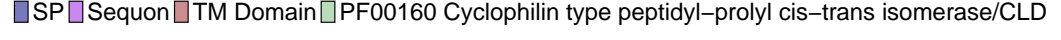
Protein length



Pfam domains



Pfam Description



Protein sequence:

IKGSLQNLLOYKDKDPDKVSVGLASTLDTVALELLGAPGLSFLPQQVLYKPRLTGRGIVFEFTVEKVDGSTFYFEAAGVAKSTAKIQVYLDGYSAPLTKNFALVIDGAYDGMKLTGANQALSDSELGKATGYSVPLEKPKSGGFEPFLYRTLSVQDGELPLVPLSVYGAWAMAHSDVSEELSSPQGFYLYDKRNSGLGGLSFEEGGFVFGYTTIGRDVLPQIKTGDIRSAKLVGGDRLLVPPGEN

NbL09g02350.1 early_nodulin-like_protein_2 [MW - SP = 34.11 kDa]

No. of times detected



log(intensity)



Values from



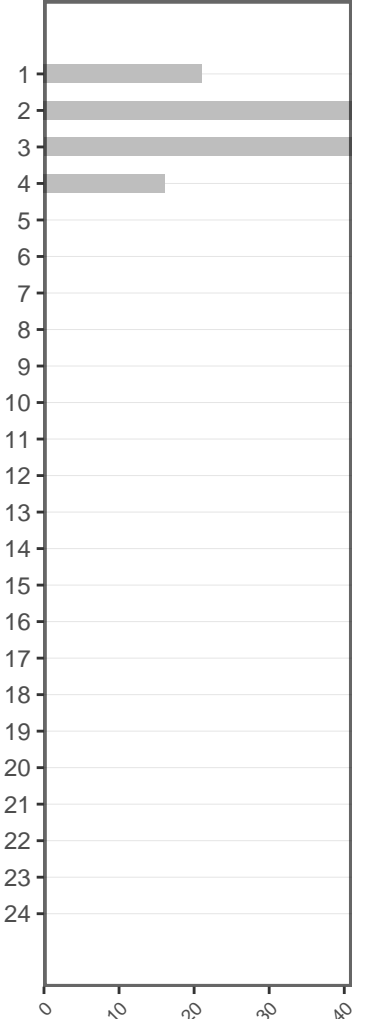
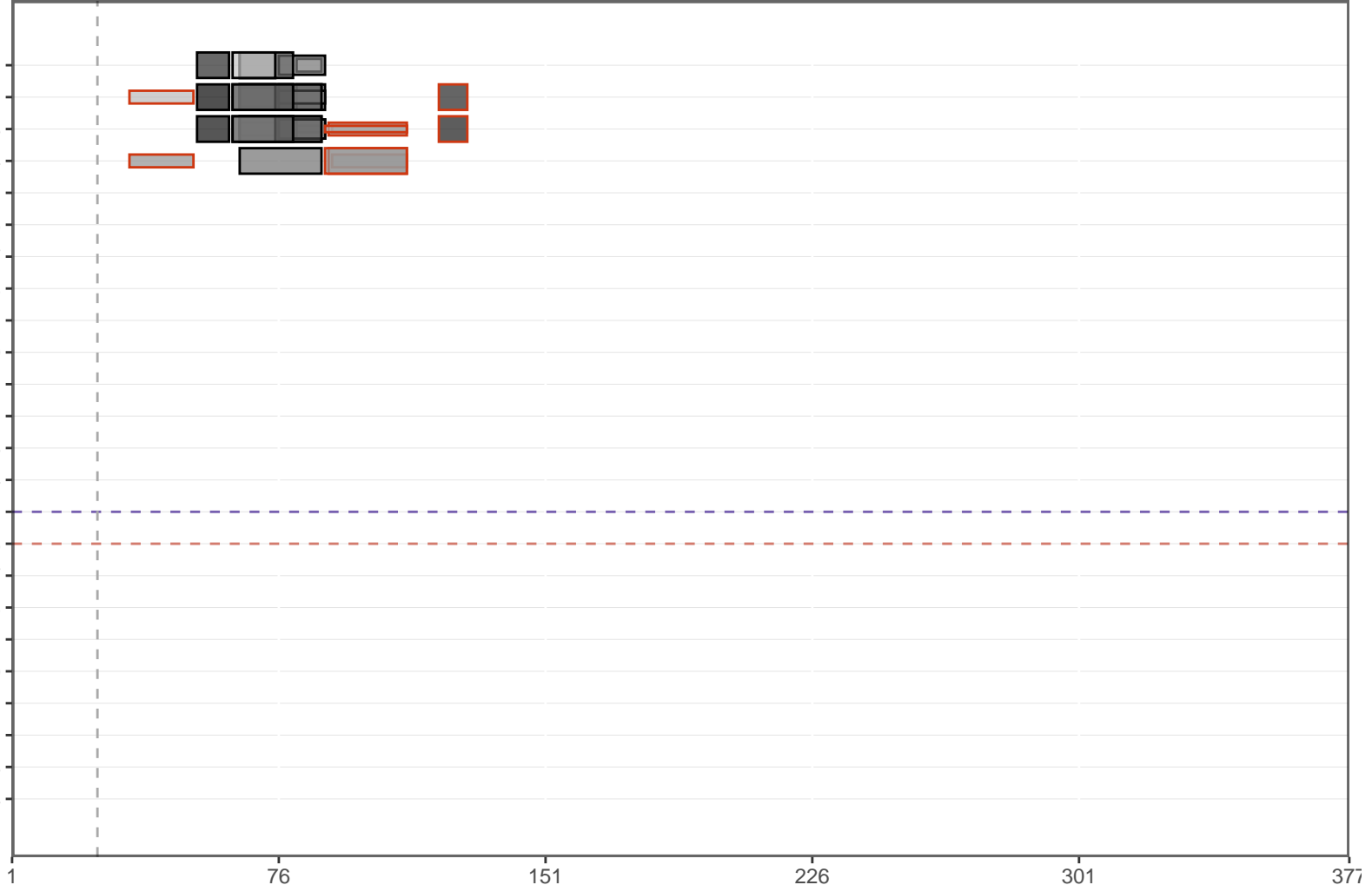
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GSFGSSSTPSPFSGAPPEPSAGSTTPPPPTTSAPPTTTTPAGPTKGSATPGTSSPNGAPVVPFPPAGKSPSTSSPTTNGSTVSRATNAPAPVITFMSPTGSPAPAGGASDLSPSPSSSLSPGSSALSPGGMAPAGGPTSSMAPGTMAPGAGAGSTPADINSFGAPSNPNSFAVKAFTFVALLSTVLSULTMAFGFHSIP

NbL09g02270.1 reticulon-4-interacting_protein_1_mitochondrial [MW = 39.65 kDa]

No. of times detected



log(intensity)



Values from



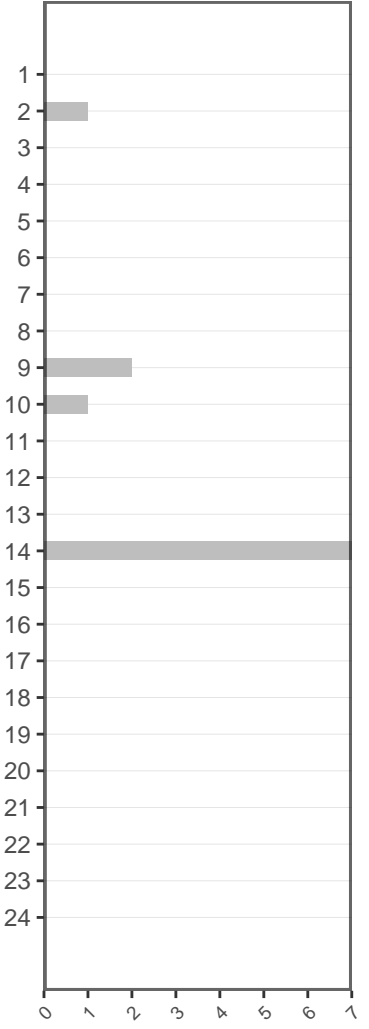
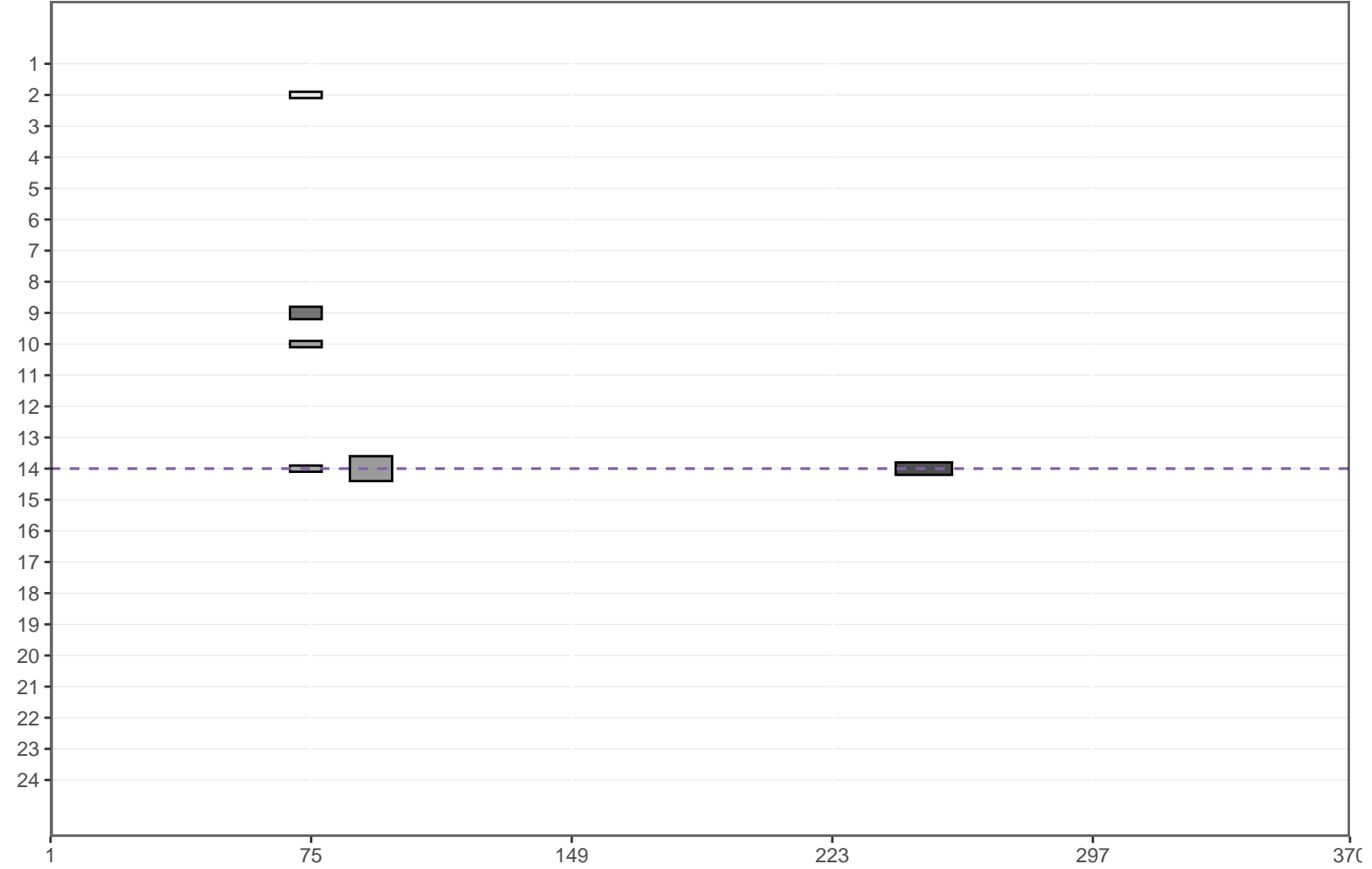
MW indication



Molecular weight



Gel Slice



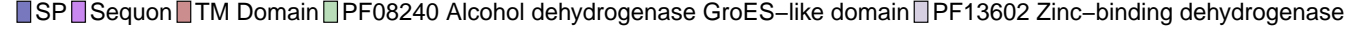
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISTARIREGHRVLYVGGGGAVGFSQAQLAAWAGHVSSTGEGESISIRILAAAGAEAVDYTTDECEALMGHFDVLDLTGIVPETERINGINLLKRGGHYMTLGGEEAASLTDRYGLAFGLPLATALKKQIQYRYSHGIEYWWNYMRADAEGLEHRRLESEAKLRIPVDKTFPLSGAREAHAEKDRRQIPGKVVLEID

NbL09g02210.1 UBP1-associated_protein_2C-like [MW = 45.76 kDa]

No. of times detected



log(intensity)



Values from



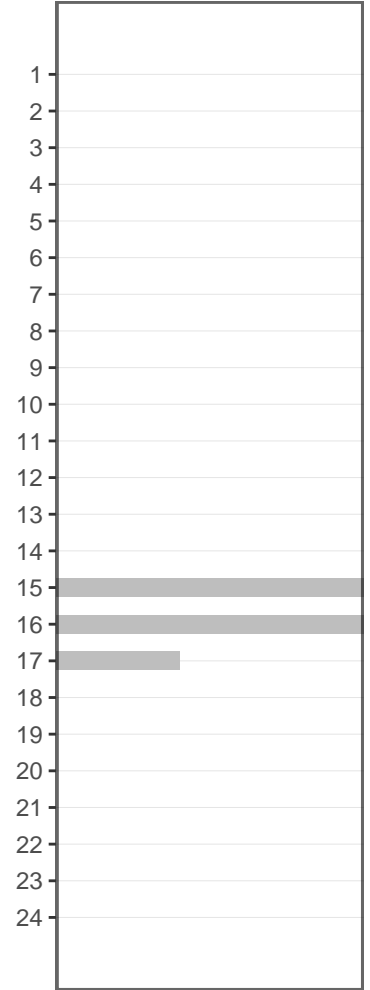
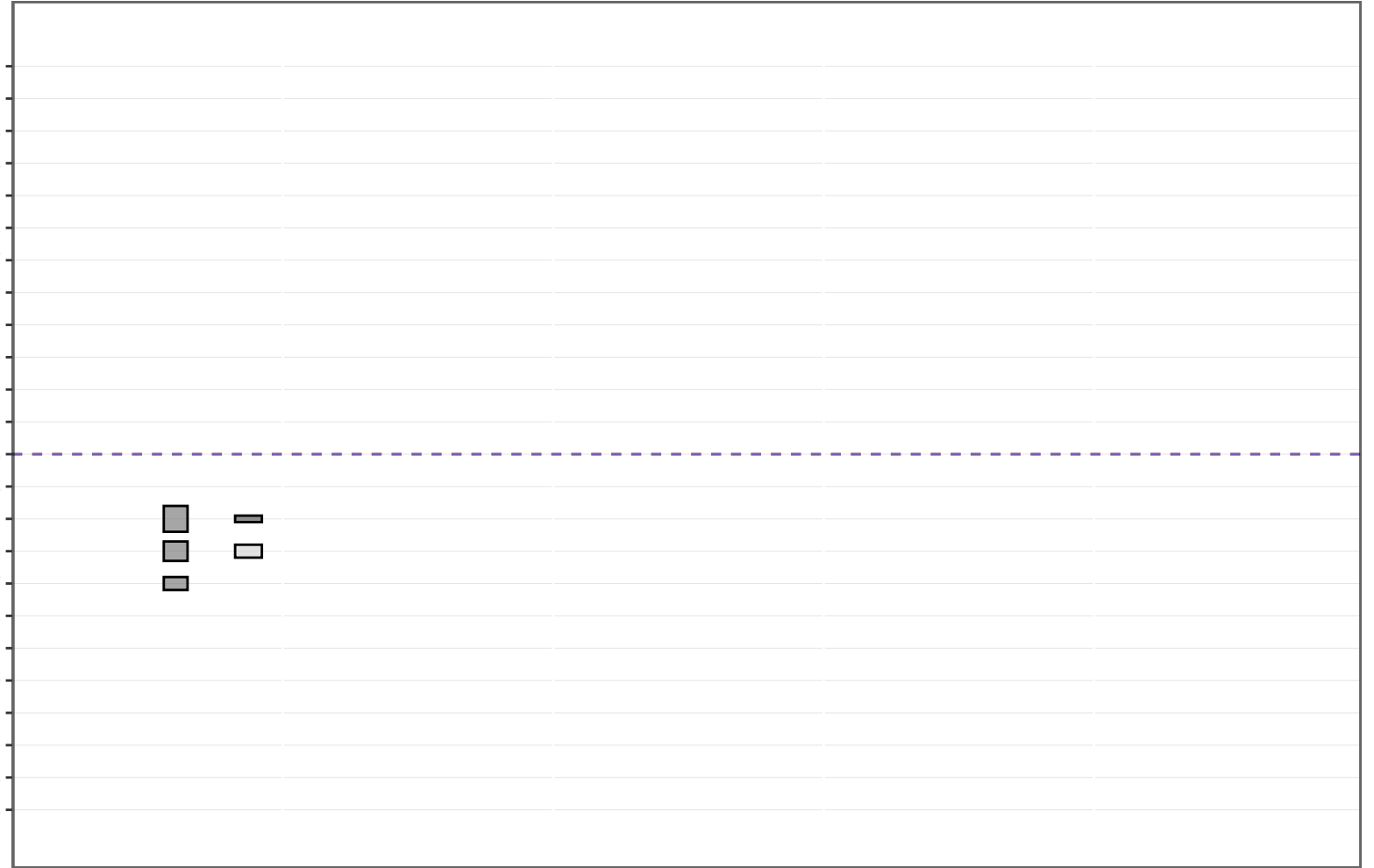
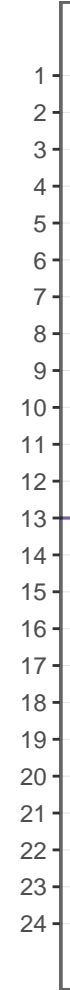
MW indication



Molecular weight



Gel Slice

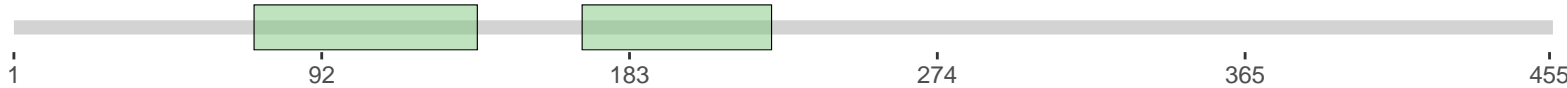


Protein length

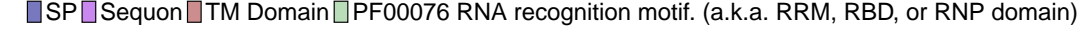


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ASLVDPVYKIDGHLNGLKLDGKPKGGGADVQTDGHVYGVGPGQYGGPESGTFGYGGFFPGHSTFGDGVHGLNSAVGSGNGKGVGGPQGGSEYVGGSGPGGSGVGGVAGPYPGGGGSHYGGPDSAGYALASTATGGGGGVYSPGALGAGGVTGTDALGGGLSGVGGALGAGRGSSMYGLPPSSTGLASGDDYPPGGRHYSGQNGVPGVSPFRVAPGGMVQGMHEVY

NbL09g02180.1 malate_dehydrogenase_2_mitochondrial [MW = 35.63 kDa]

No. of times detected



log(intensity)



Values from



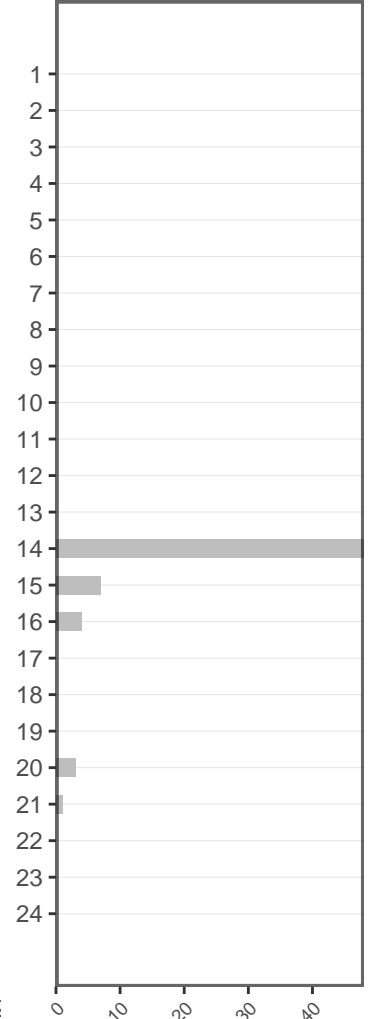
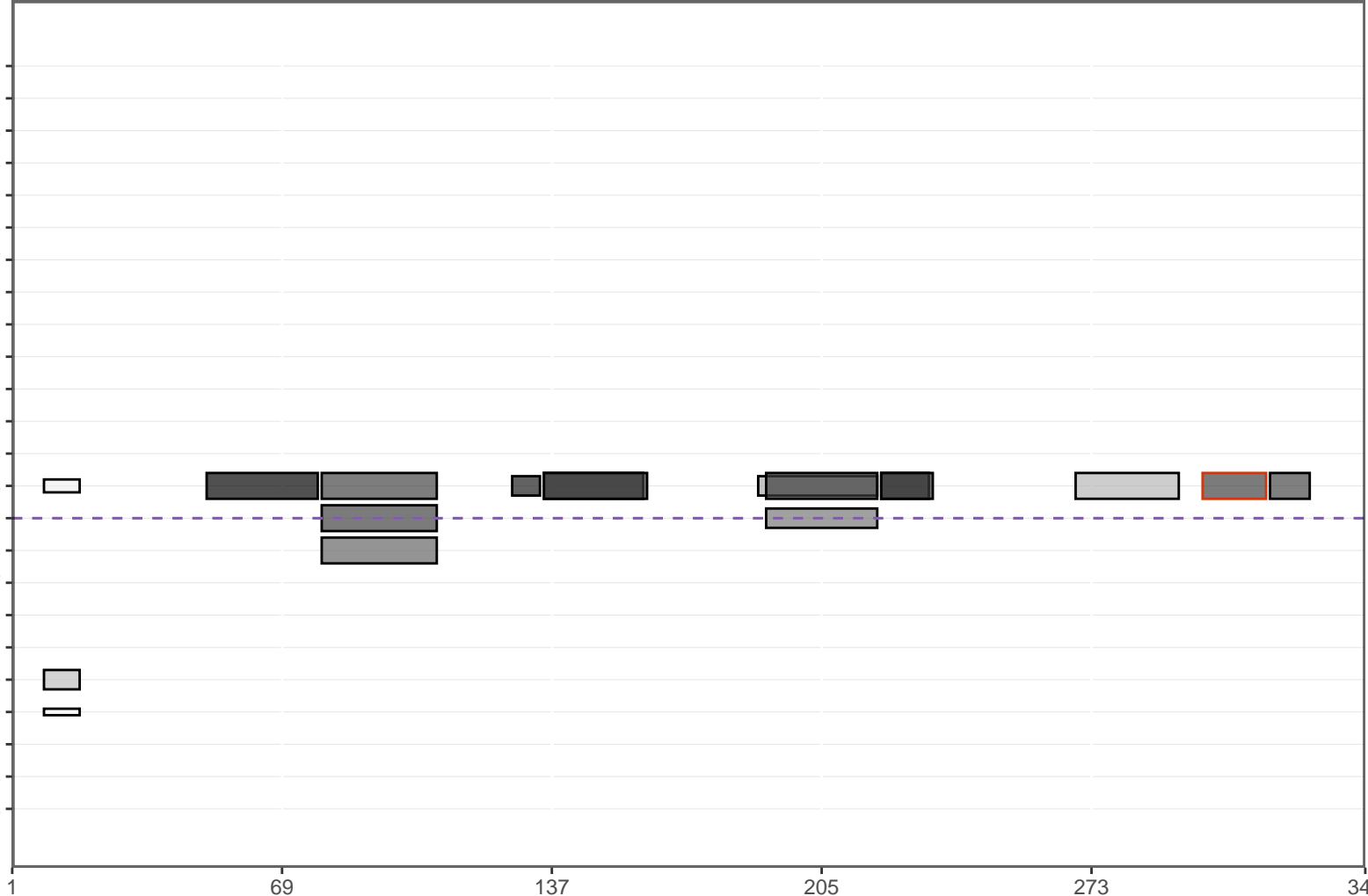
MW indication



Molecular weight

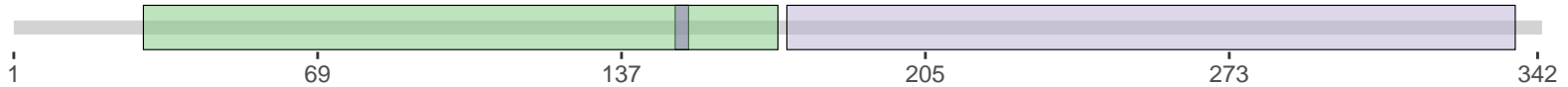


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF00056 lactate/malate dehydrogenase, NAD binding domain
- PF02866 lactate/malate dehydrogenase, alpha/beta C-terminal domain

Protein sequence:

FKKAGTYDEKRLFGVTTLEIVRAKTFYAGKAKVNVADVIVPVVGGHAGITLPLFSGDAPKANLQDEEIEALTKRTQDGGTEVVEAKAGKGSATLSMVAAGAFADAGLKGNGVDPVVEGSEFVQSTVTDLFFFAKVRLLGKNGVEEVLGLGPLSDFFENQGLEALKPELKSSEIKGKIFANDN*

NbL09g02100.1 homogentisate_12-dioxygenase-like [MW = 52.36 kDa]

No. of times detected



log(intensity)



Values from



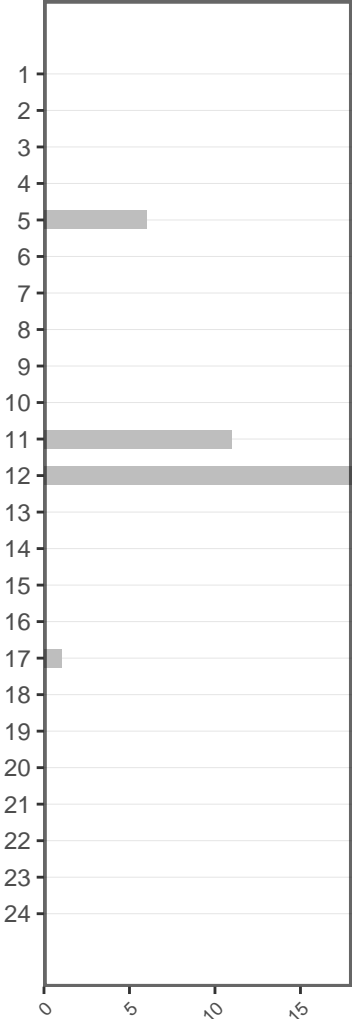
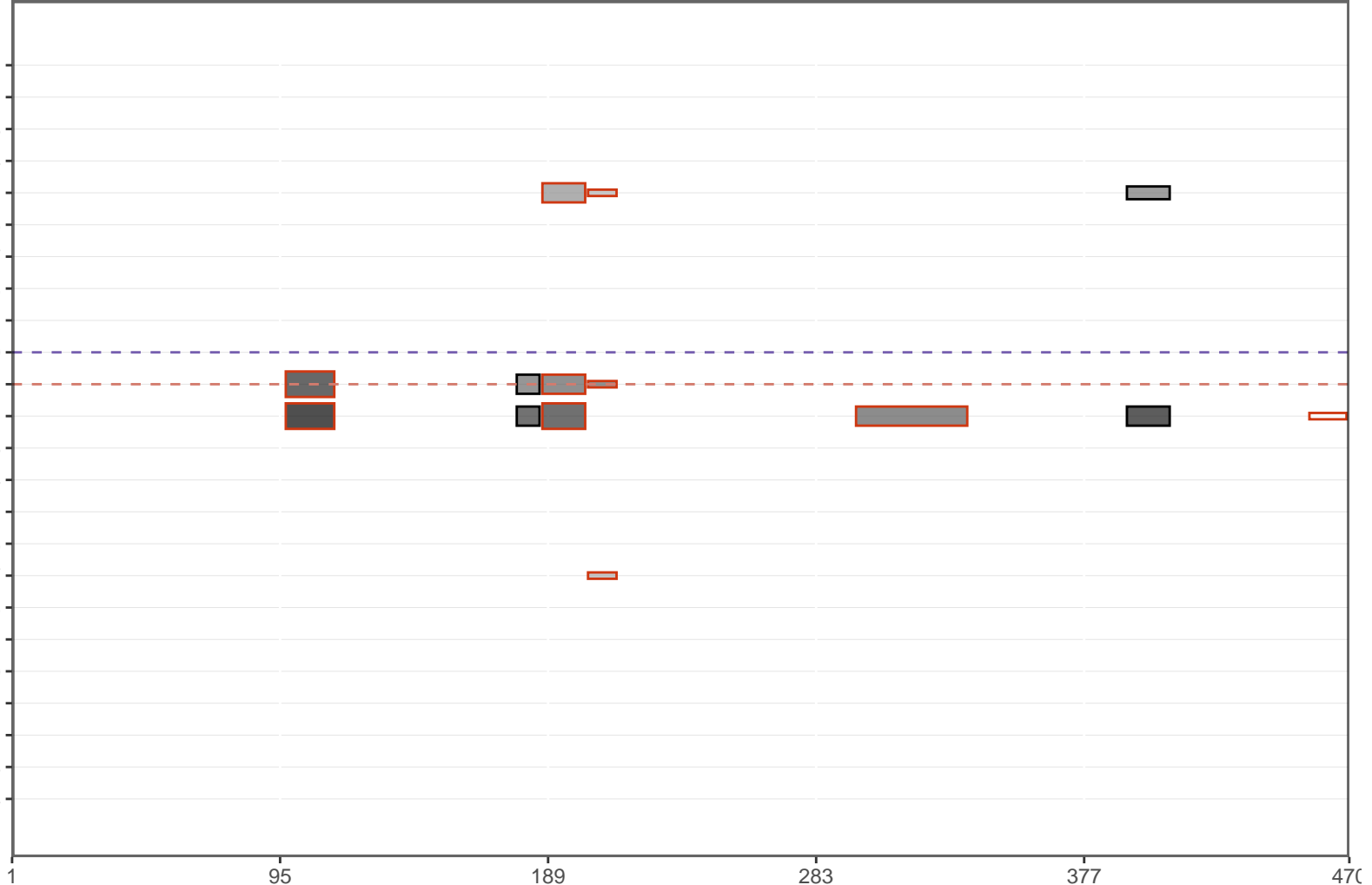
MW indication



Molecular weight

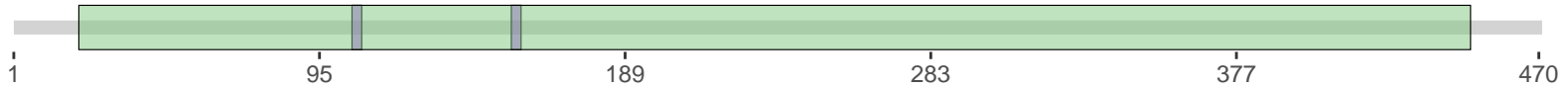


Gel Slice



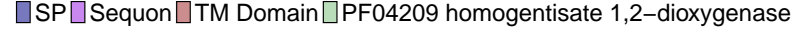
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

.QLPDLGGVANGLAAPRDLPLVWAWYEDGSRPGYTVQKYGGLFTAKGDFSPFNVAWHGNYVYKYLKSKFPYNTVLDHSDPSINTVLTATDKPGVALLDFVIFPPRRVLVAEHTFRPPYVHRNCASEFMGLYGGYEAKADGSRHGGABLHSGMTPHGDPTKTYEATIALGNEAGPHKIGDTMAFMFESGLIPRVCFWALESPFMKHQYQGWHLKSHFSGLEMKMDNRDFQNGKPVET

NbL09g02080.1 ras-related_protein_Rab11B [MW = 24.24 kDa]

No. of times detected



log(intensity)



Values from



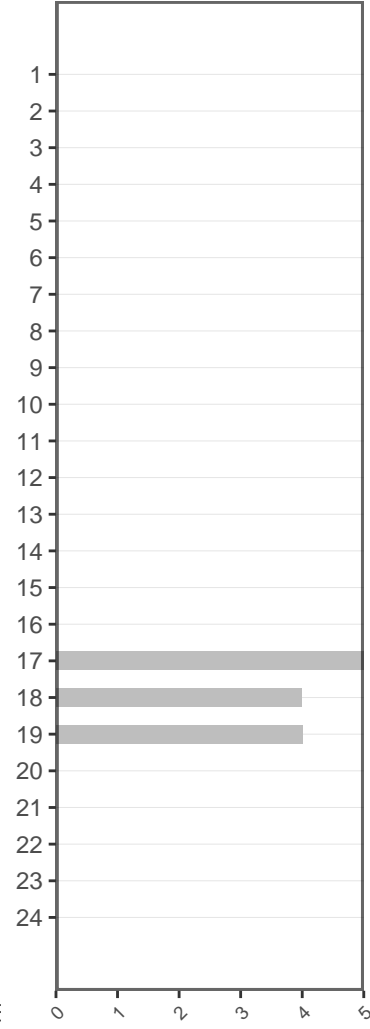
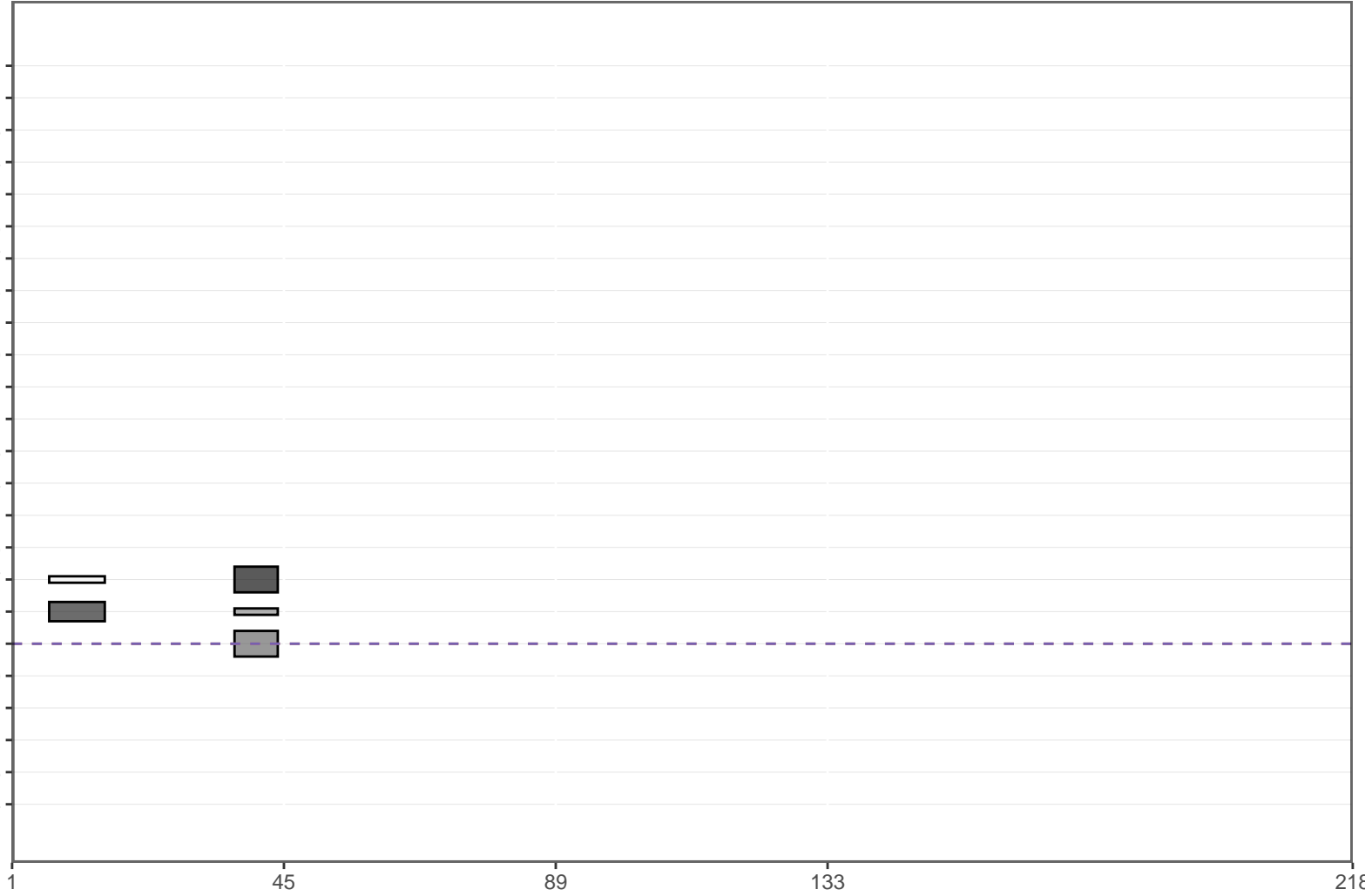
MW indication



Molecular weight



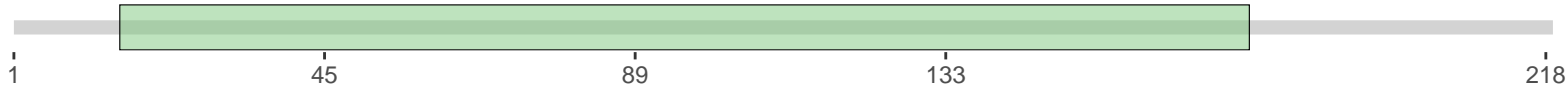
Gel Slice



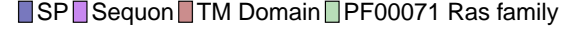
Protein length



Pfam domains



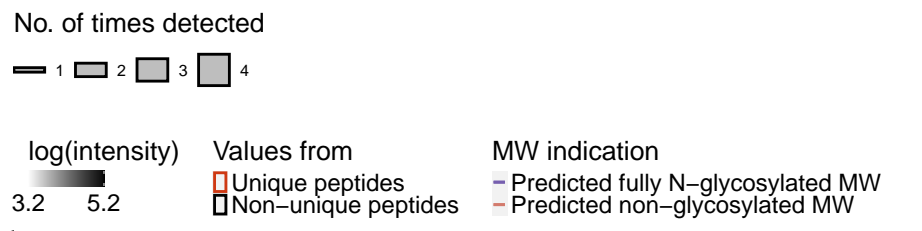
Pfam Description



Protein sequence:

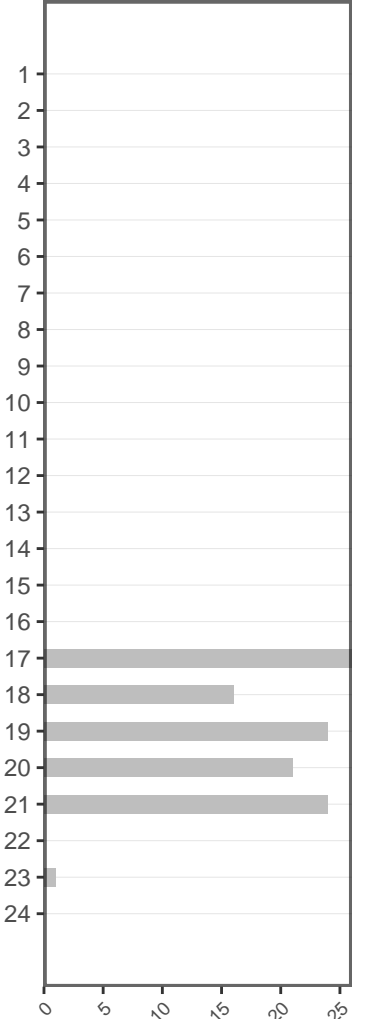
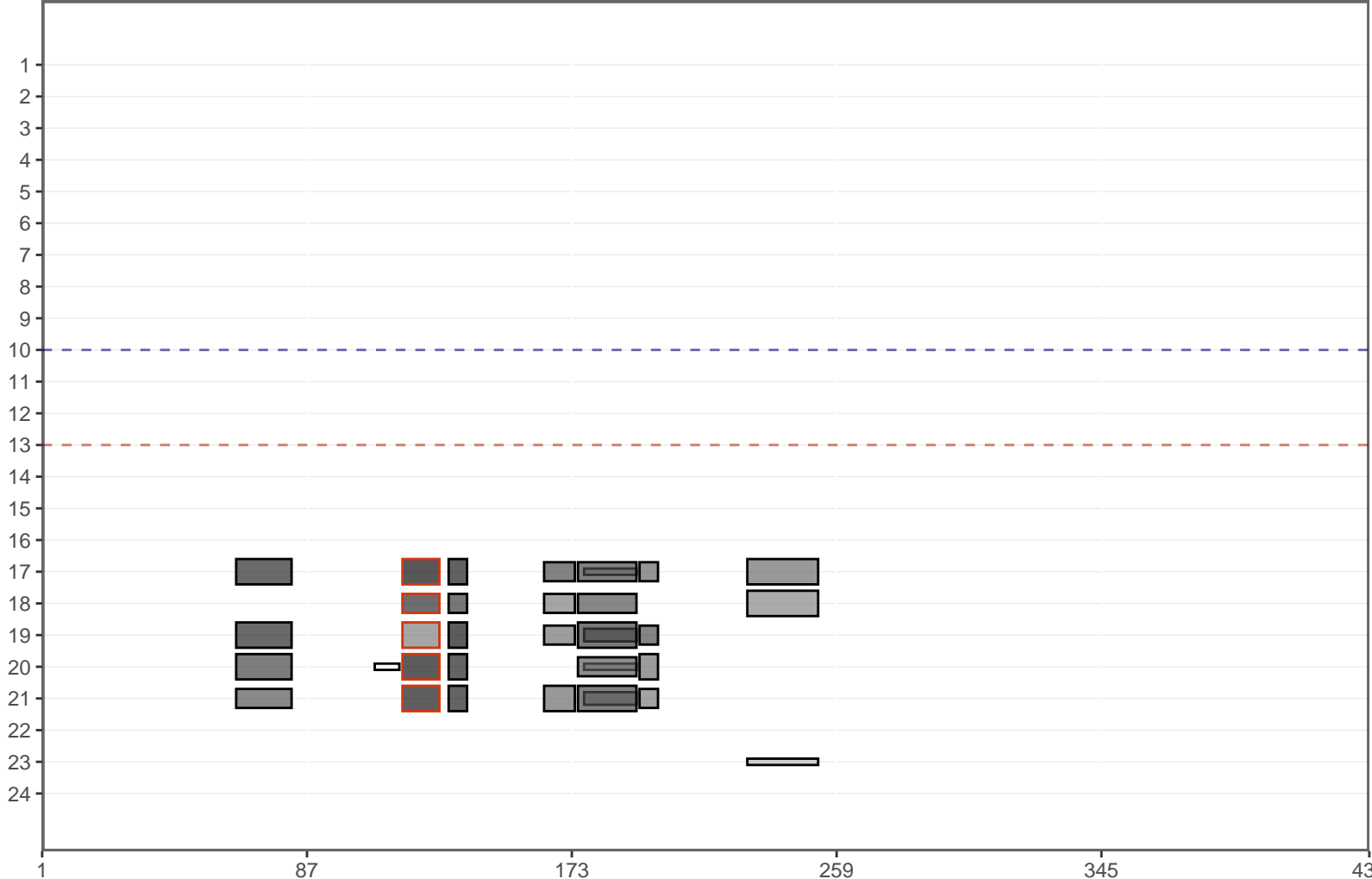
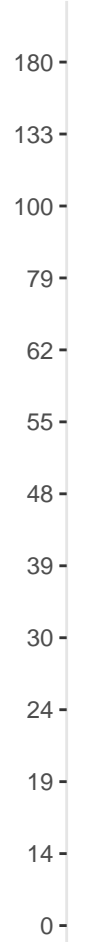
IRHVTFFENVKELRDRHTDQNVIMLVGNKADLRHLRAVSTEDAKAFARERSTFFMETSALSLNVENAFTEVLTETKVVGRKALEVGDDPAALPKGGTFNKGKDDVSAKKVGGGSV

NbL09g02050.1 multiple_organelle_RNA_editing_factor_8_chloroplastic/mitochondrial [MW = 47.2 kDa]



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

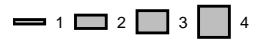
Pfam Description
 SP Sequon TM Domain

Protein sequence:

IPRNFDRSRNFERRRDMGTNIGNSGPNPGENMPPGGPPNMRNPPPPNMMVGMGQPNMAGGPPNMGSMHQGPNMGGPPNMGSMHQGQGGPPNMGSMHQGQMGGPPNPGGSMHQGPMGGPPNPGGSMHQGPMGRRPHVSGMGGPPNMPPTTGGVPPNMGGGPPNHYGGVFNAPNFQVNSGNSGGTPTPTGPRPNNGSYSPNPGDGNPYQGNLPGRDMPPNY

NbL09g02010.1 phosphoenolpyruvate_carboxylase [MW = 110.33 kDa]

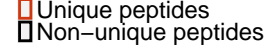
No. of times detected



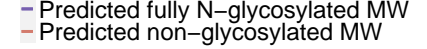
log(intensity)



Values from

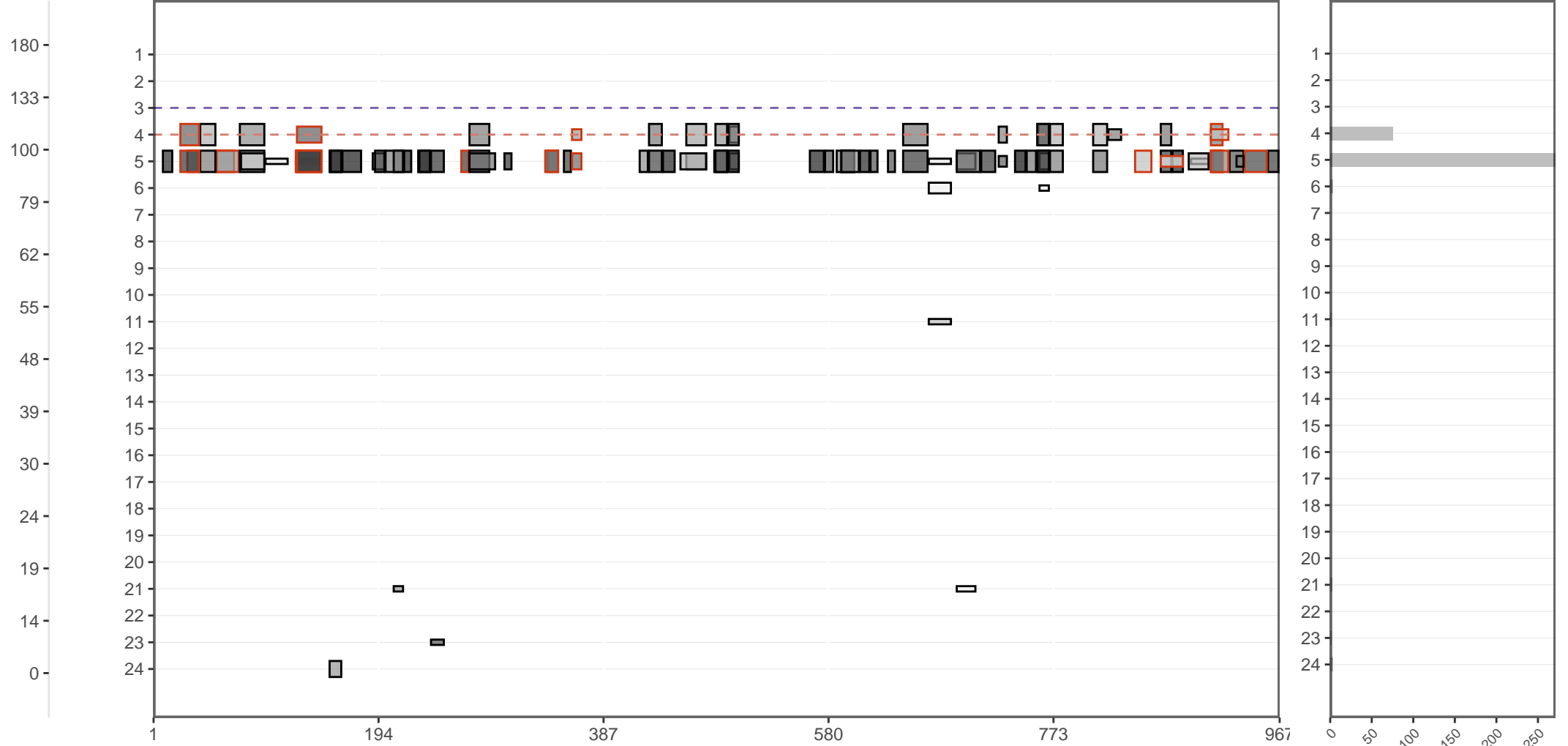


MW indication



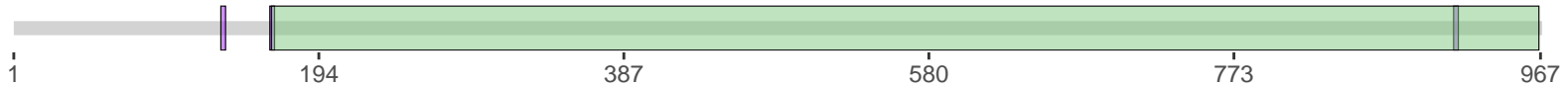
Molecular weight

Gel Slice



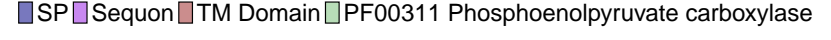
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

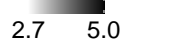
IIGSYREYVSEERKGEWLLSELGSKRPLFGDLPKTEIADVLDTFHVAELFADGFGAYISMATAPSDVLAVELLQREGRVKGPLRVVPLFEKLDLGAFAAWARLFSEVYRNRINGKGEVMYSDSGKAGRLSAWQLKAGQELVWVAKEYGVKTMFHRGAGGTVGRGGGPTLAILSGPPDTHGNLRVTVQGEVIEGGFGEEHLGFRTLQRFTAATLEHGMHPPVSPKPEWRALMDEIAWATEKYRISIVFKRPRFVEYRLATPELEVGRMNIGSRPSKRPKPSG

NbL09g01990.1 multiprotein-bridging_factor_1b-like [MW = 15.27 kDa]

No. of times detected



log(intensity)



Values from



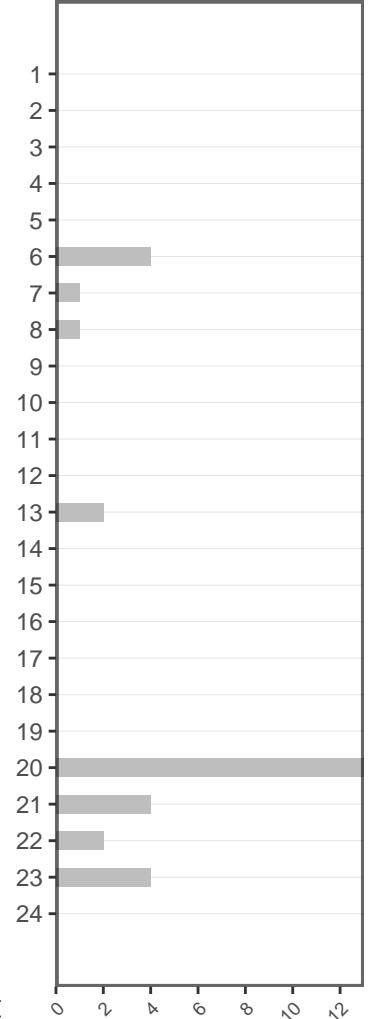
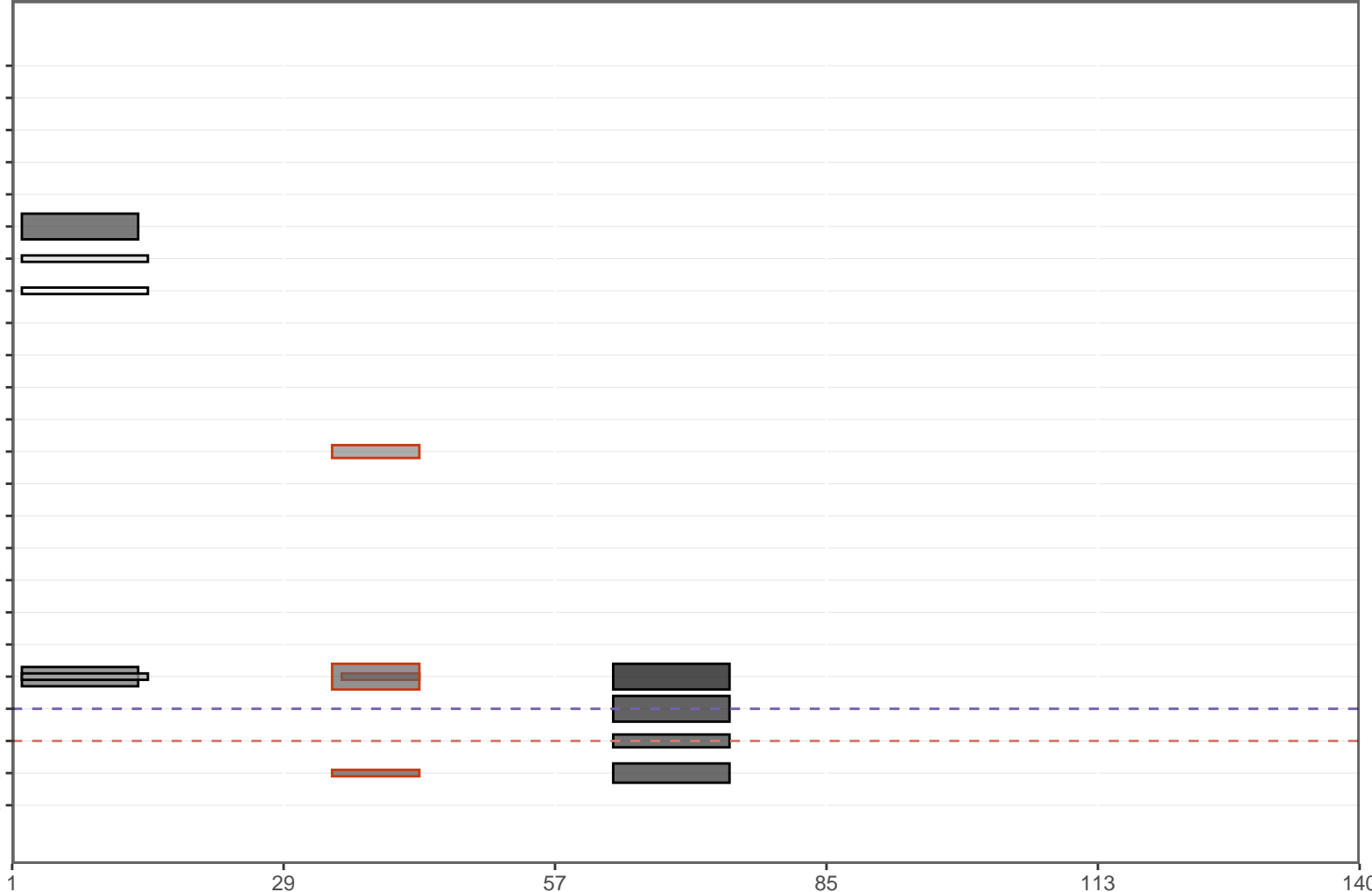
MW indication



Molecular weight



Gel Slice



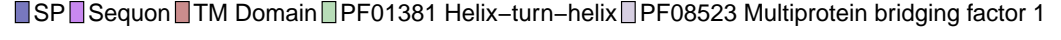
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

STLNTNRKLDLEDTENLSHQKVPTELKKAIMGARQDQKLTGSGLAGLINEKPKQIQEYESGKAIPNQIQIKLERALGAKLRGKK

NbL09g01900.1 50S_ribosomal_protein_L13_chloroplastic [MW = 27.12 kDa]

No. of times detected



log(intensity)



Values from



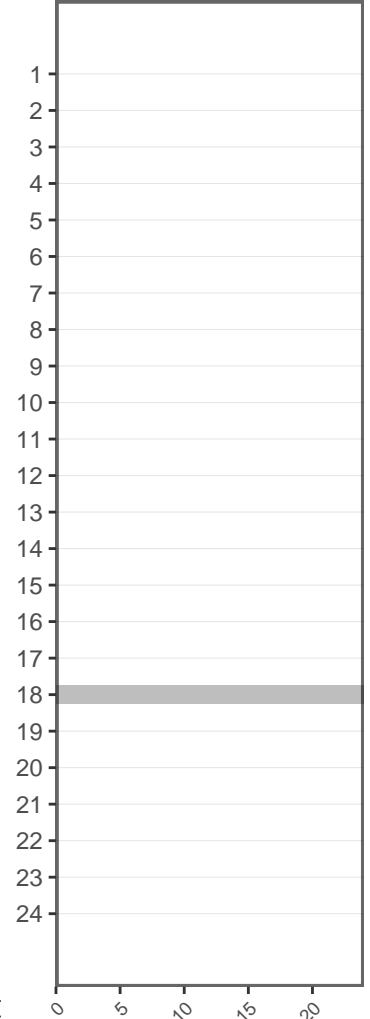
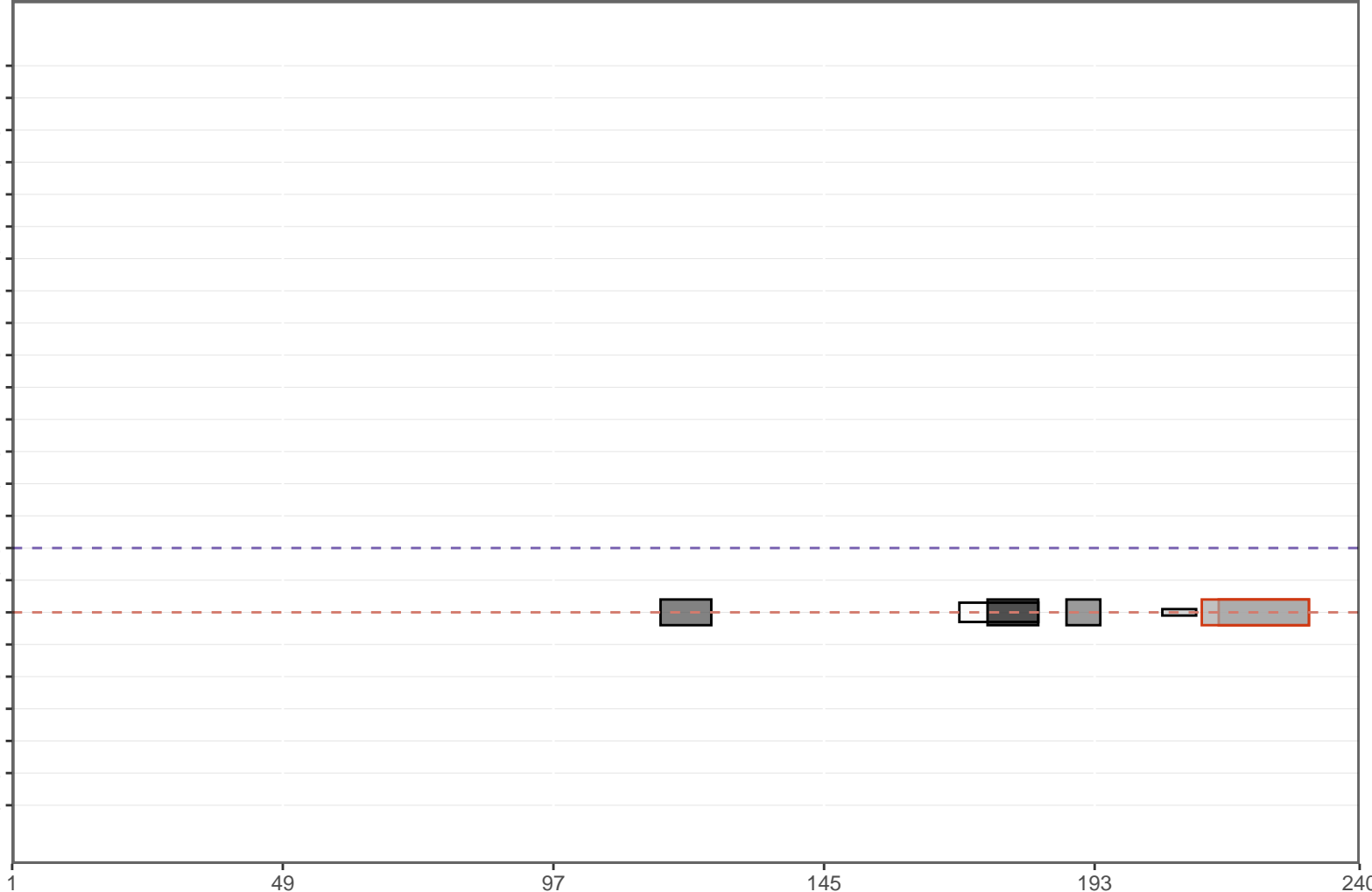
MW indication



Molecular weight

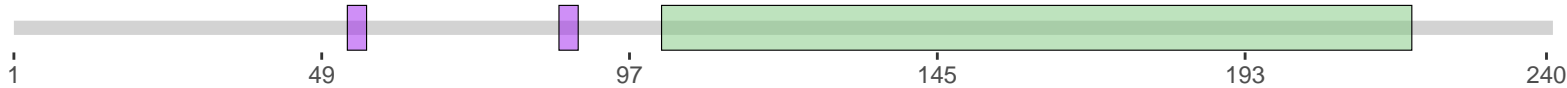


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

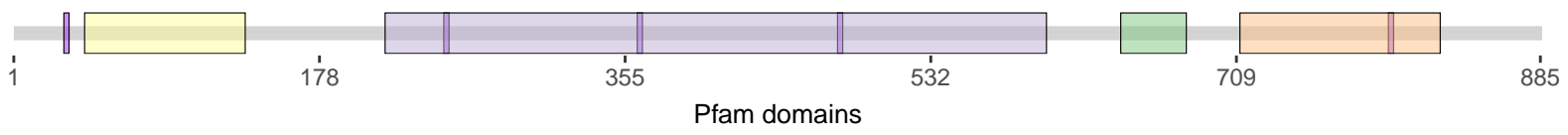
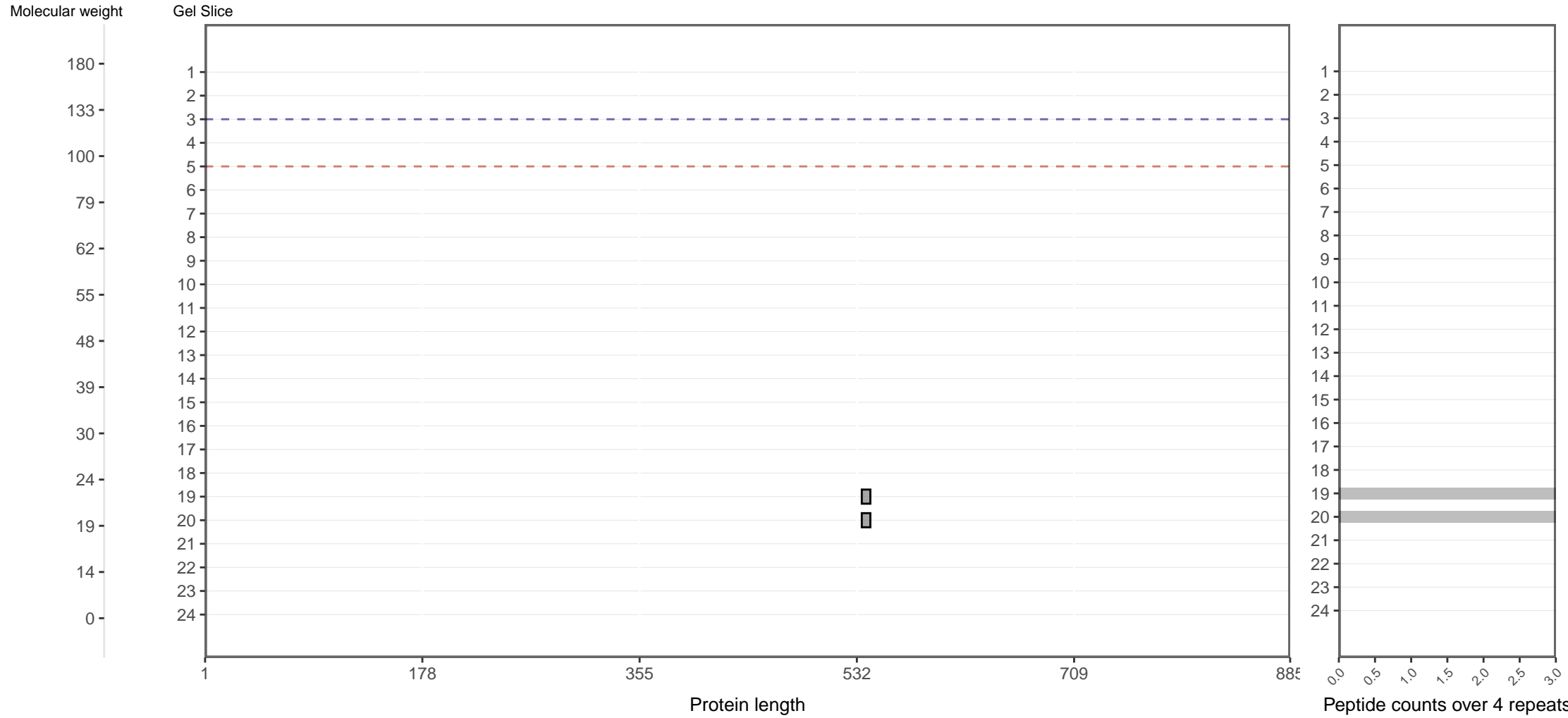
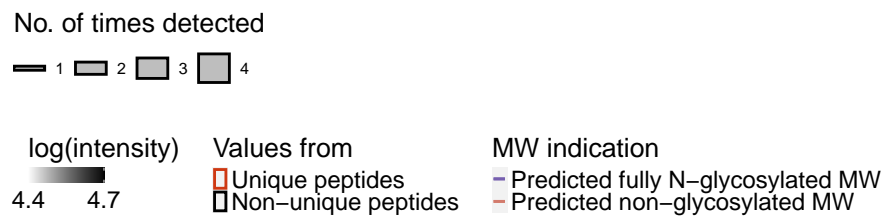
Pfam Description



Protein sequence:

/DATDLILGRMASTIAHMRGNLATYTPVDMGAFVIVVAEKVAWSGKRTQNLVRRHSGRFDGMAKVFYFDQLQGRIPERIEHVARGMPLKGRIGRGLFTHLKVYKGDHPHAEAKPIELPRDKRIKQGR

NbL09g01710.1
 putative_SWI/SNF-related_matrix-associated_actin-dependent_regulator_of_chromatin_subfamily_A_member_3-like_1 [MW = 99.39 kDa]



- Pfam Description
- SP
 - Sequon
 - TM Domain
 - PF00097 Zinc finger, C3HC4 type (RING finger)
 - PF00176 SNF2 family N-terminal domain
 - PF00271 Helicase conserved C-terminal domain
 - PF08797 HIRAN domain

Protein sequence:
 WDSPIKKEWWRVLDENHYKYNMGDSRAVNNLAKRRKVVYVTFPIGNISFDLYSLMAFLRFEPLSKAYWNSLDRPLAOGDEKGVSRGLVMSFTMSLRRTKEKALIGLPSKSIETFFVLSGEEIREYDQMESEAKRYKGYISSDSMKNNYVFLSVVYLRKQICDLALCPSDLRSLSLPSNKGIDVHNSFOLLKMLSVLQDDEGIDCIPFPPTDSVITCDGDFHFKSGLKTKTKRAKPOCLCRHPLSESDLFPCLPEASNWNWNGSSSTASIKYKALLKLLCASRDEI

NbL09g01660.1 photosystem_I_reaction_center_subunit_II_chloroplastic [MW = 22.65 kDa]

No. of times detected



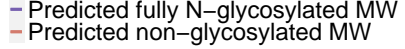
log(intensity)



Values from



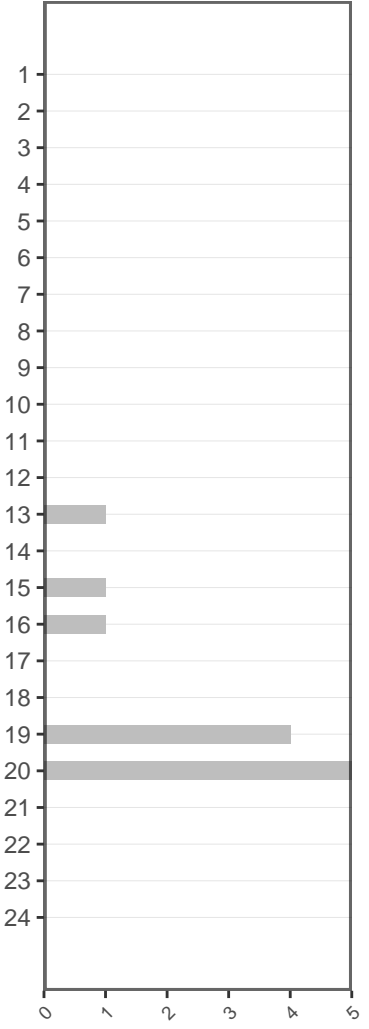
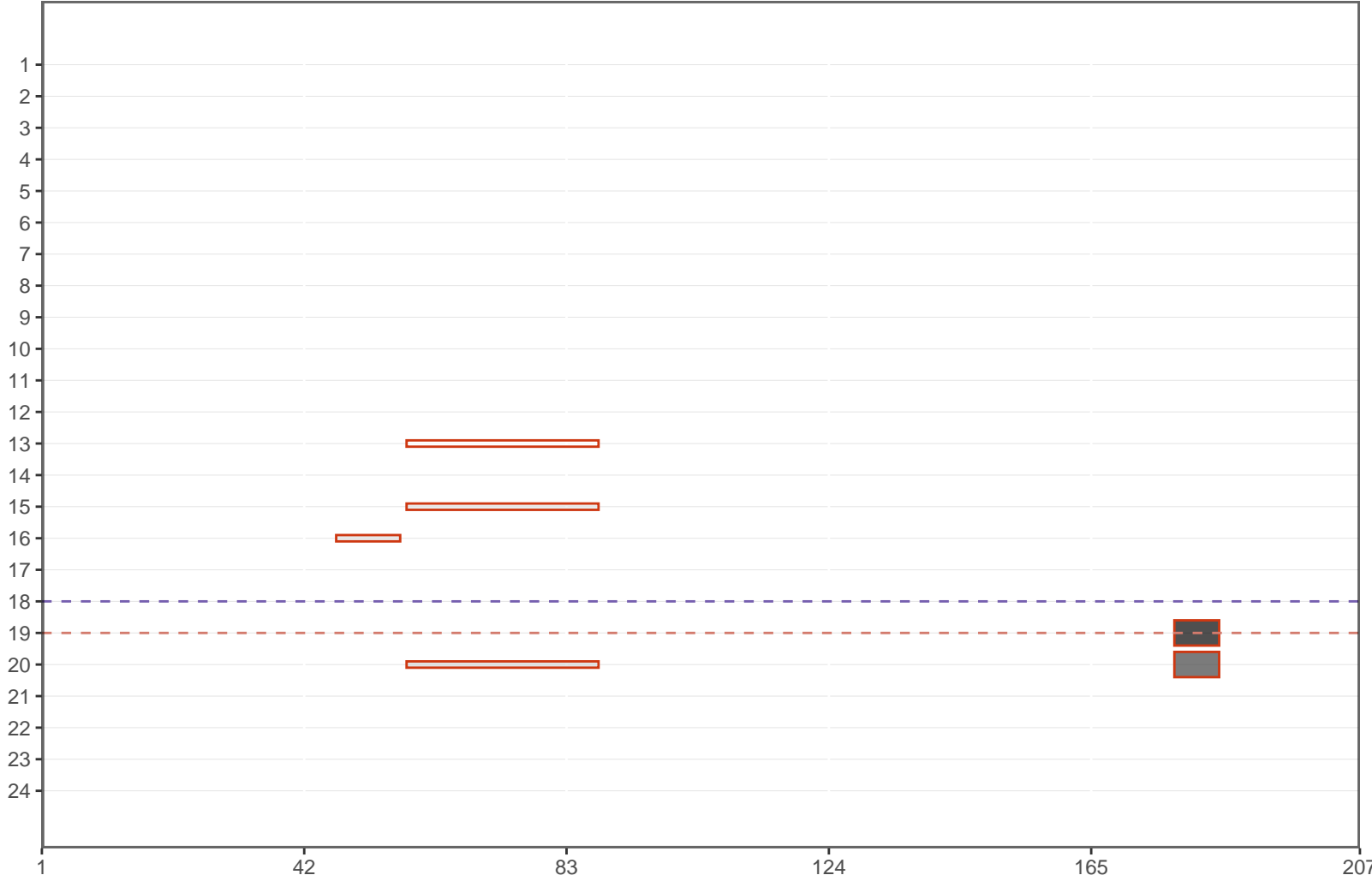
MW indication



Molecular weight

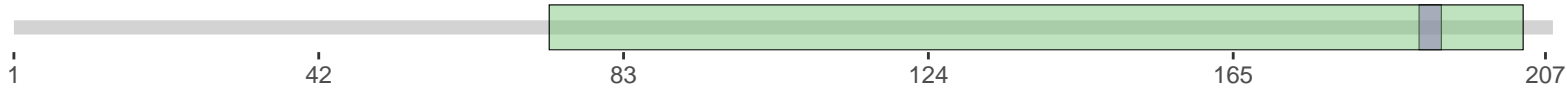


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DVEEFYVITVESPKEGFEMPTGGAAIMREGANLLKLARKEGQLGTRLRBKYKINRFRVRFNNGEVGYLHPKDDVYPEKVNAGRGGVGNFRBIGNKNSPEVKFTGKGVYDL

NbL09g01500.1 triphosphate_tunnel_metalloenzyme_3-like [MW = 26.78 kDa]

No. of times detected



log(intensity)



Values from



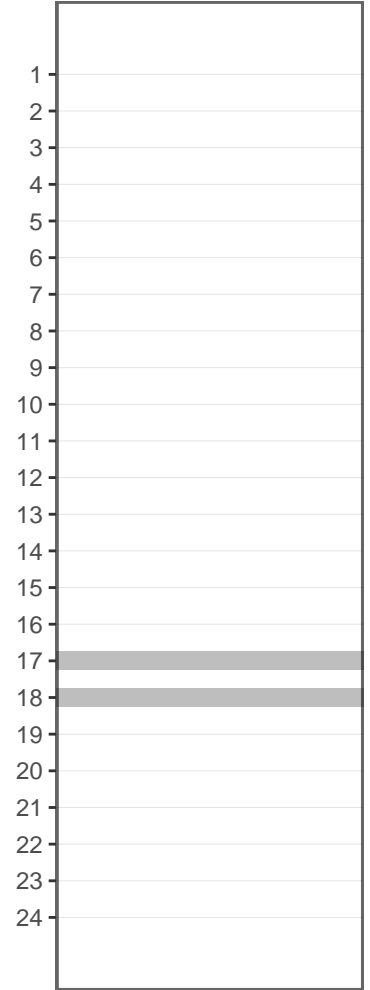
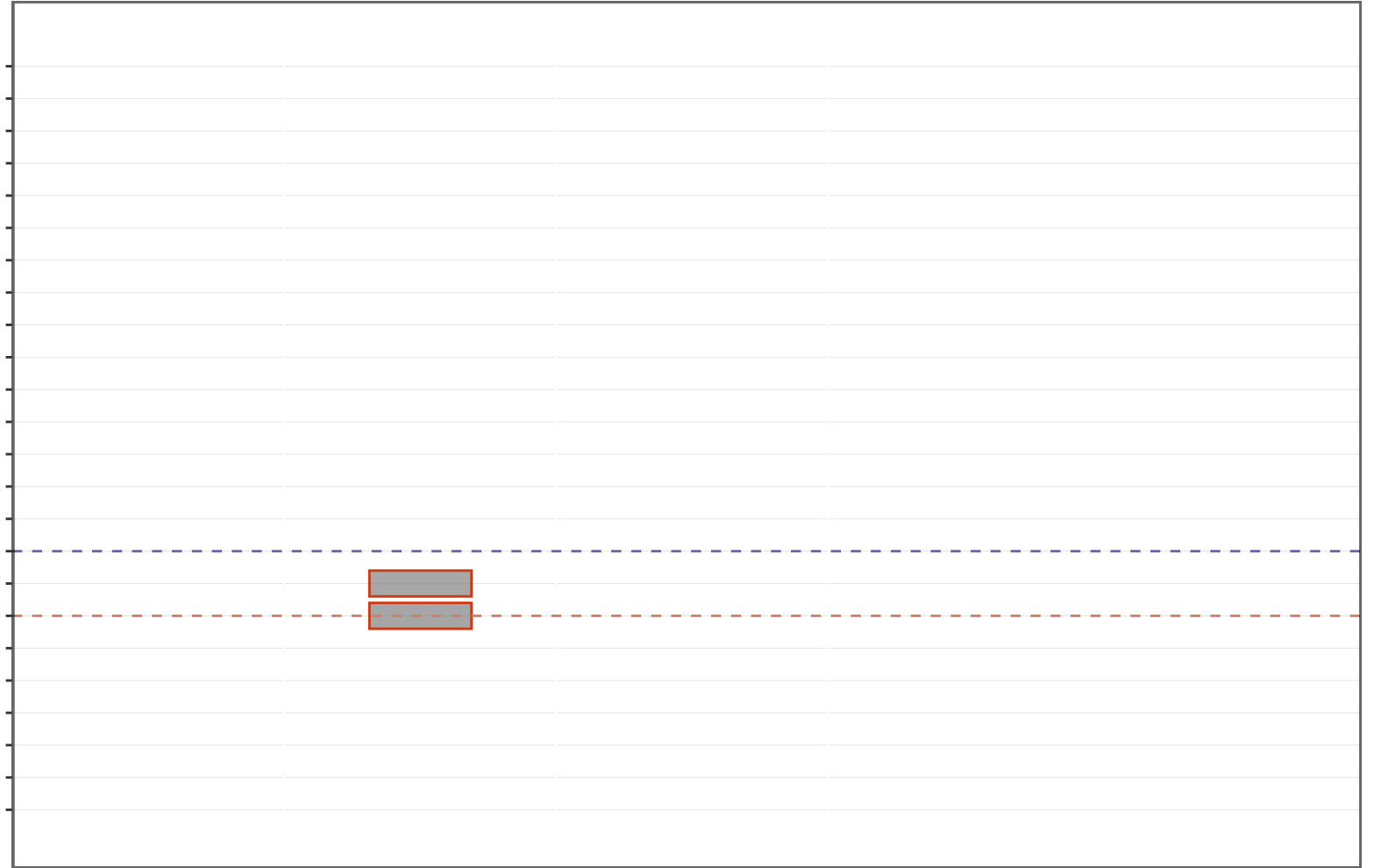
MW indication



Molecular weight



Gel Slice

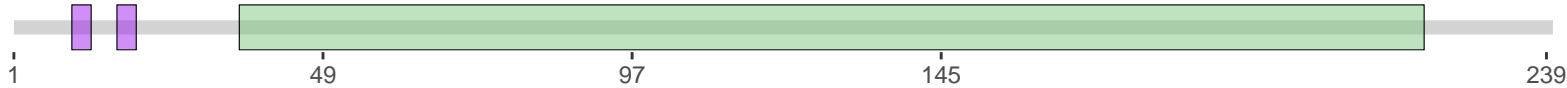


Protein length

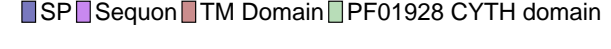


Peptide counts over 4 repeats

Pfam domains



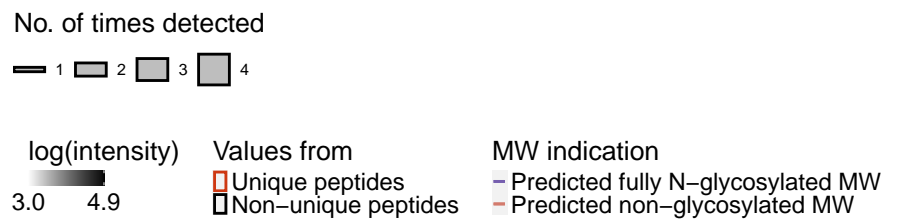
Pfam Description



Protein sequence:

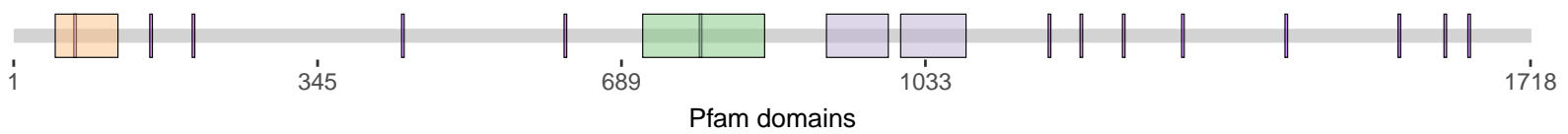
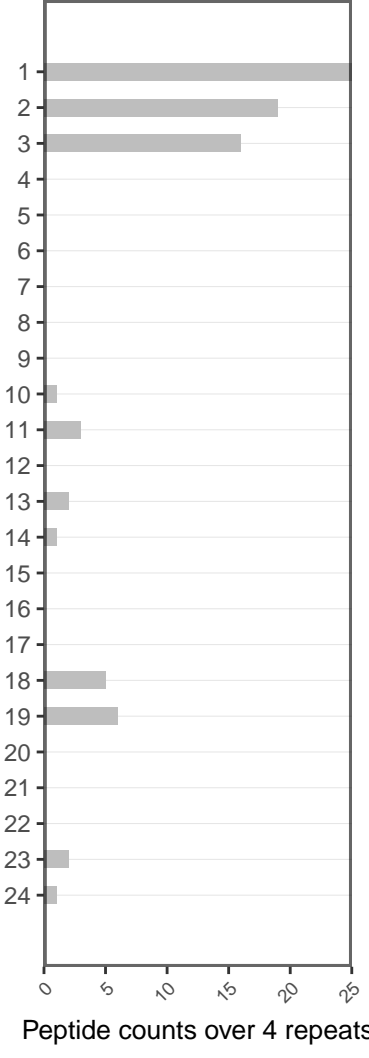
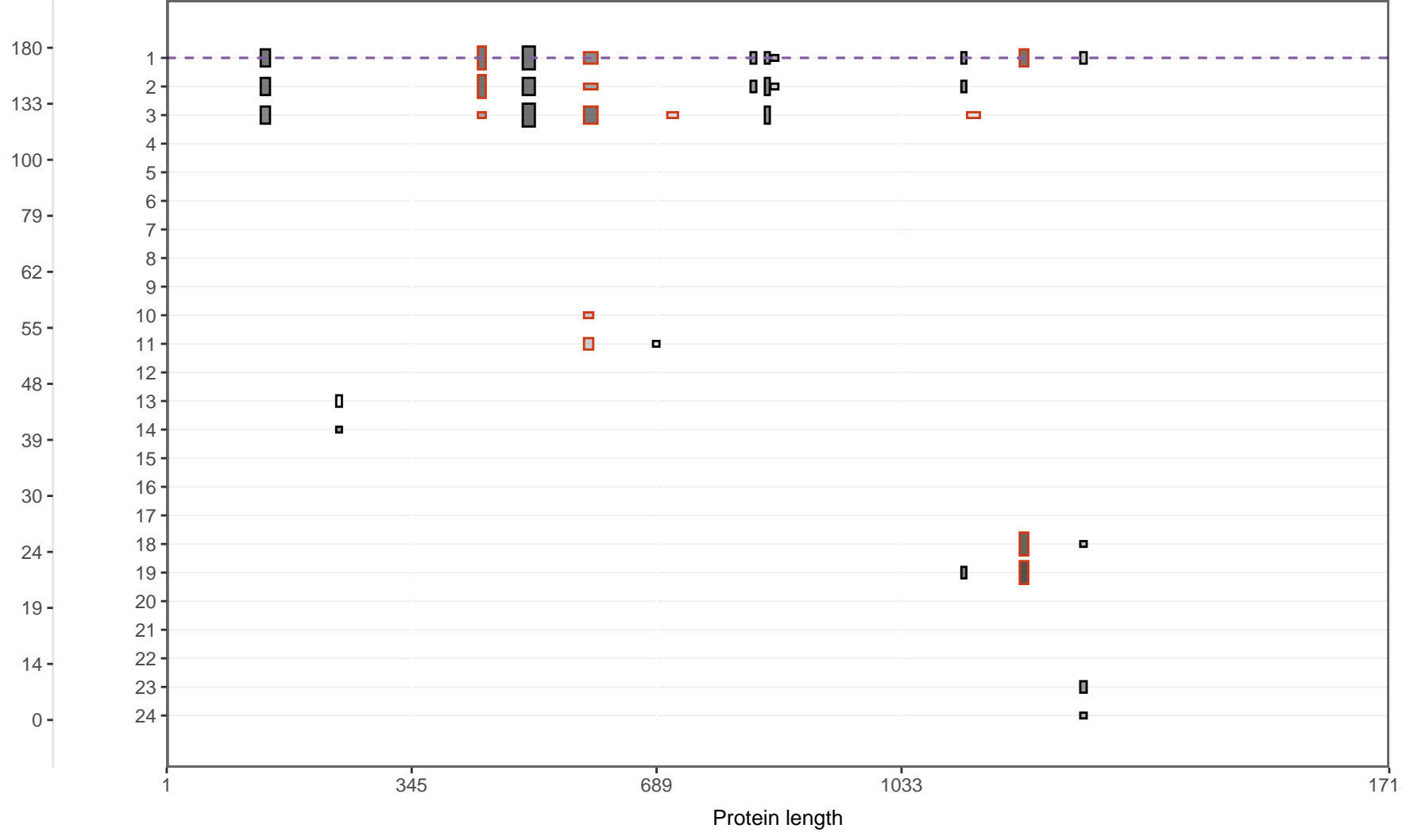
ISNGISRIIEDEEPDPSIGRADVSDPWRLLLDSDSRVQRKDEYGFGEKQGLVGLGFRNVRVYEWKGLGLALDETHYEGMNFIEGEGSDPERAKDLLEELKSHGIEYVSTVSKFAFRGKLPQ

NbL09g01470.1 clustered_mitochondria_protein_homolog [MW = 189.08 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF12807 Translation initiation factor eIF3 subunit 135
- PF13424 Tetratricopeptide repeat
- PF15044 Mitochondrial function, CLU-N-term

Protein sequence:

*KDYDMESEPPYFSKTDVHVVPLGNHVGCSADGRLLLESKVALDKGKLEDVWVGTAKALAIWQGPVHRATASAVSLLVAIVLHVGDFNQATVGGKALDINERELGLDHPDTMKSVDLGVFYRQLQHELALKVYVNRALFLHFTGGLSHPTAATYINWAMMEEGMGNVHIALRVLHEALKGNORLLGVDRHQTASVYHAIAMLSMEAYSLVQHEGFTLQIGLQAKLGAEDLRTGDASAWLEYFESKALEGGEAARTGAPRLDQATASKGLHSVPLDLLDIYSPGGQSSP

NbL09g01460.1 haloalkane_dehalogenase-like [MW = 35.75 kDa]

No. of times detected



log(intensity)



Values from



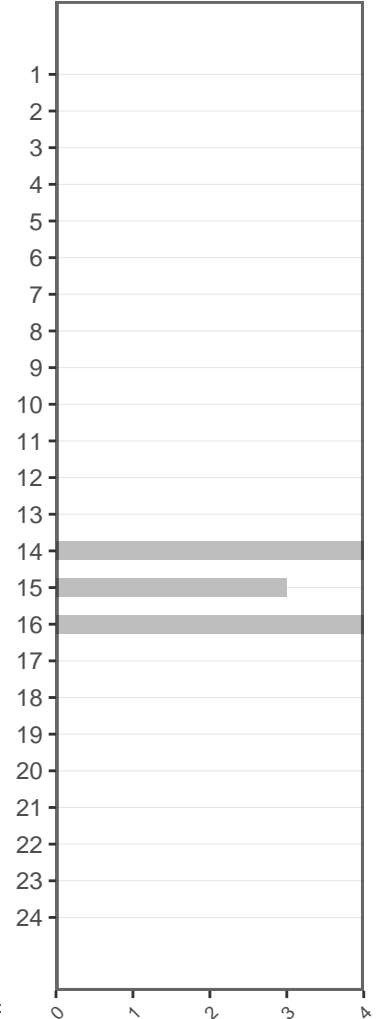
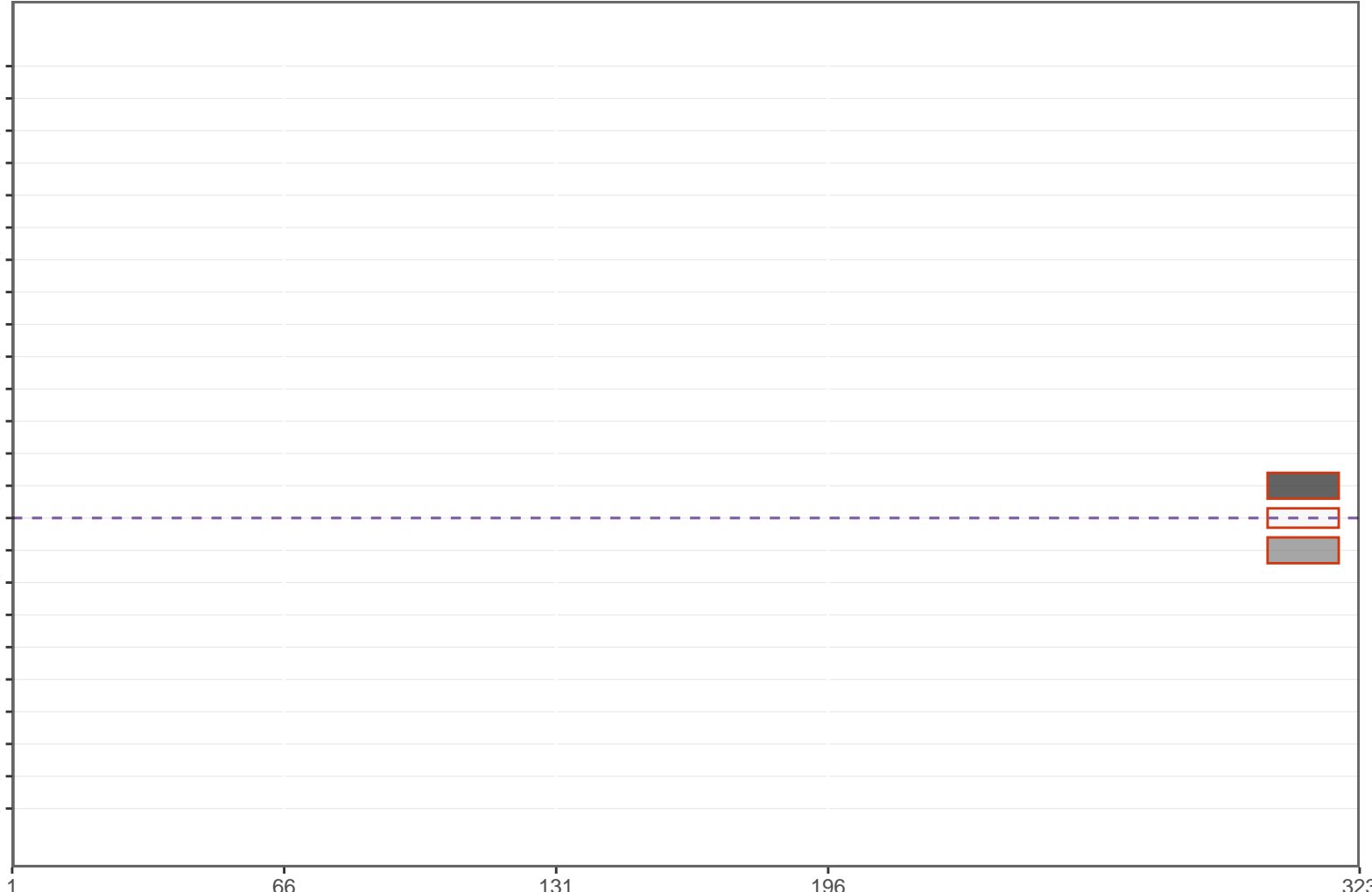
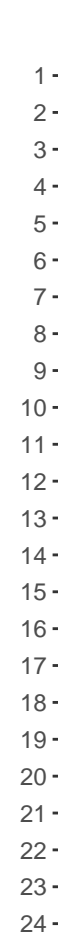
MW indication



Molecular weight



Gel Slice

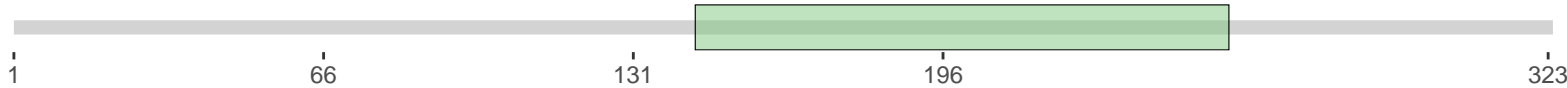


Protein length



Peptide counts over 4 repeats

Pfam domains



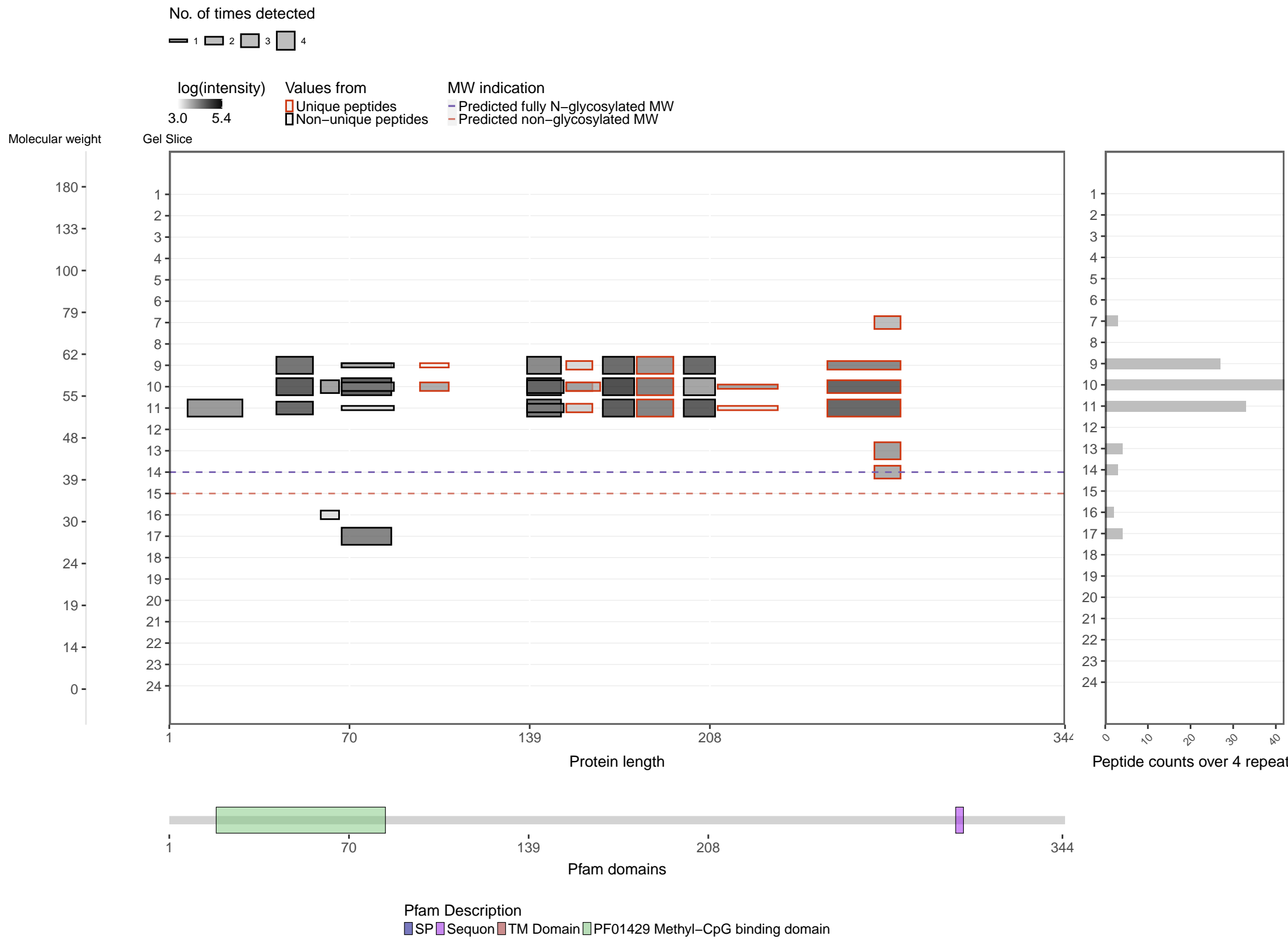
Pfam Description



Protein sequence:

LHGAPTSYSYRVAIMSQMDTGFHGFAPWGFQGFSDKPPQPGYGFDTKEKFEFEKLELVGVTSFFLVVGGFLVGGVGLTWLKNPKSKISLAINTPLTVSSPIGLFQQLRIPFFGEFTQGNVMAERFIEAGSAYVLUKLEKADVYRFLPYLAASSGPGFALLETKLQI

NbL09g01410.1 methyl-CpG-binding_domain-containing_protein_11-like [MW = 37.56 kDa]

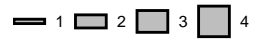


Protein sequence:

DDKGGKVEYEAADDEEAEGMKGAEHLHEEKPMDDKGGKVEYEAANEEAEGMKGDELHPEEKPESEPEKVDSDADDGGKGGKSENAKIEKQVSGEKLESGDSKESPAADNENKPEVVTAEIGNKGVGGSSKQKVEHAGNGEENNGENSGREEEKEMIGTDLVIGNKKNKQDGPMSGGHGRPISG

NbL09g01370.1 phospholipase_D_alpha_1 [MW = 92.1 kDa]

No. of times detected



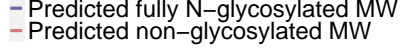
log(intensity)



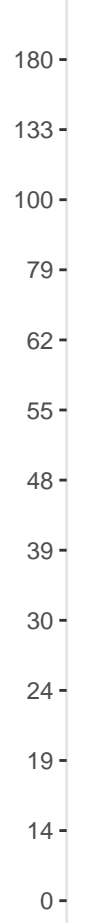
Values from



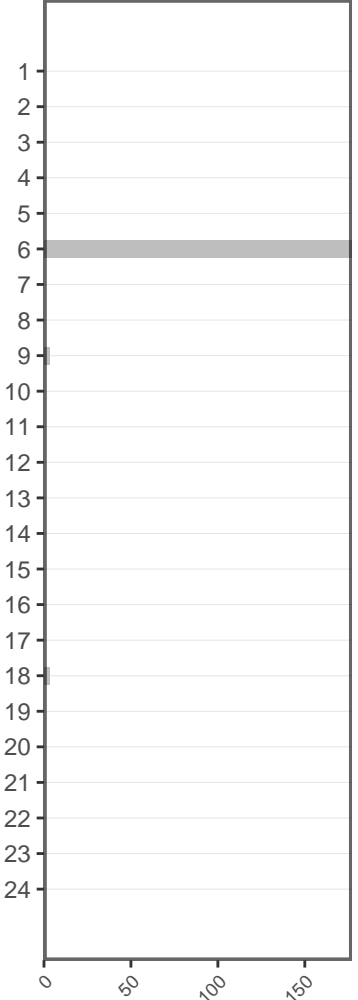
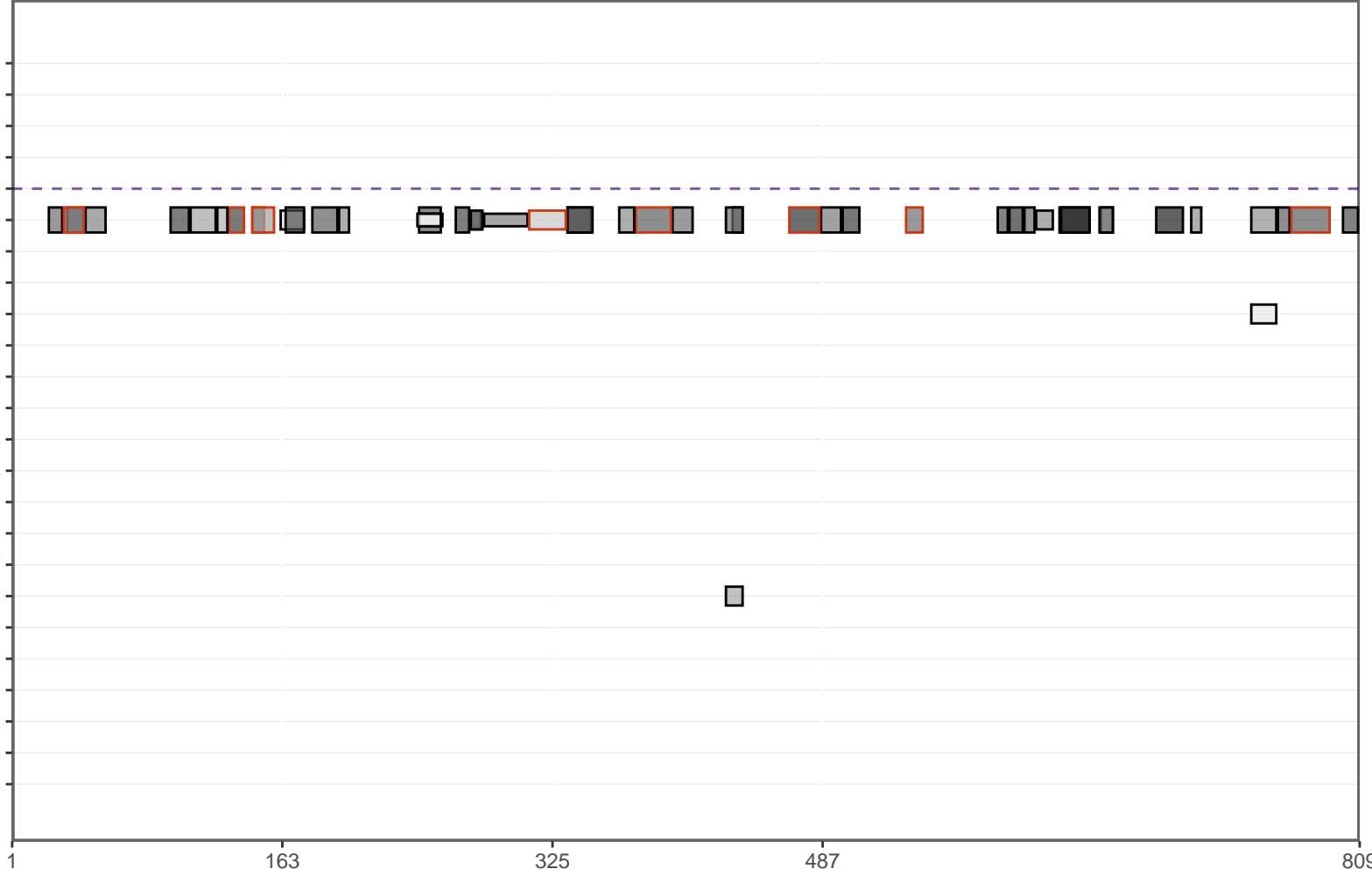
MW indication



Molecular weight



Gel Slice



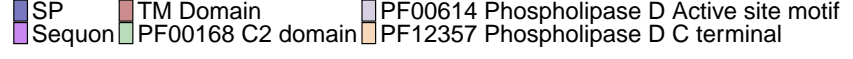
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

GAITXGSPREPFWIDHSRLRLEGPWADVLFNFRGWRKGGKQKDLVNFRELDNHPSPVMYLDSETWVYQLFRSDEGAAGFGFPETEDAAGKLVGSKNIDRSIGDVAHARRAKNFYIENGYFLGSSVDWQSDDKKEIGALHVPKELALKVSKIEAGERFTYVVVPMFEGIPESASVQALDWRRTMEMMYKHVQALNAKQIEEDPRNYLTFDFGKREYVKKSGEYEPSETPEPDSQYMRAGEARRFMVYHSHKMMIVDDEYHIGSANNQRSMQARD

NbL09g01350.1 trafficking_protein_particle_complex_subunit_2-like [MW = 15.32 kDa]

No. of times detected



log(intensity)



Values from



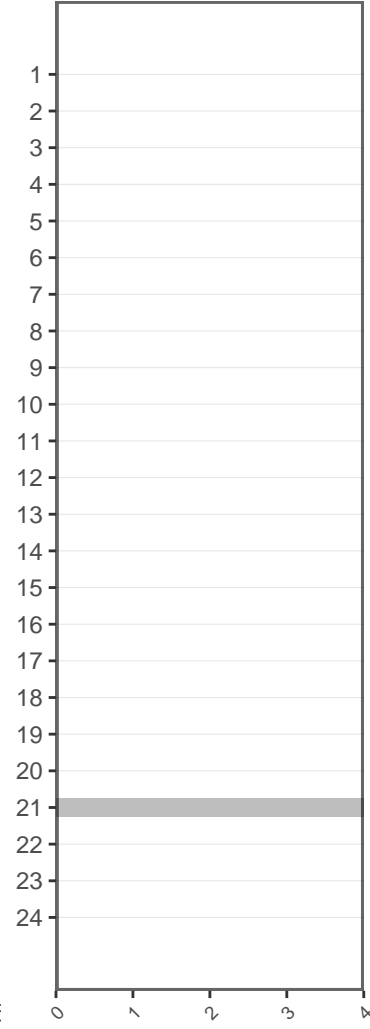
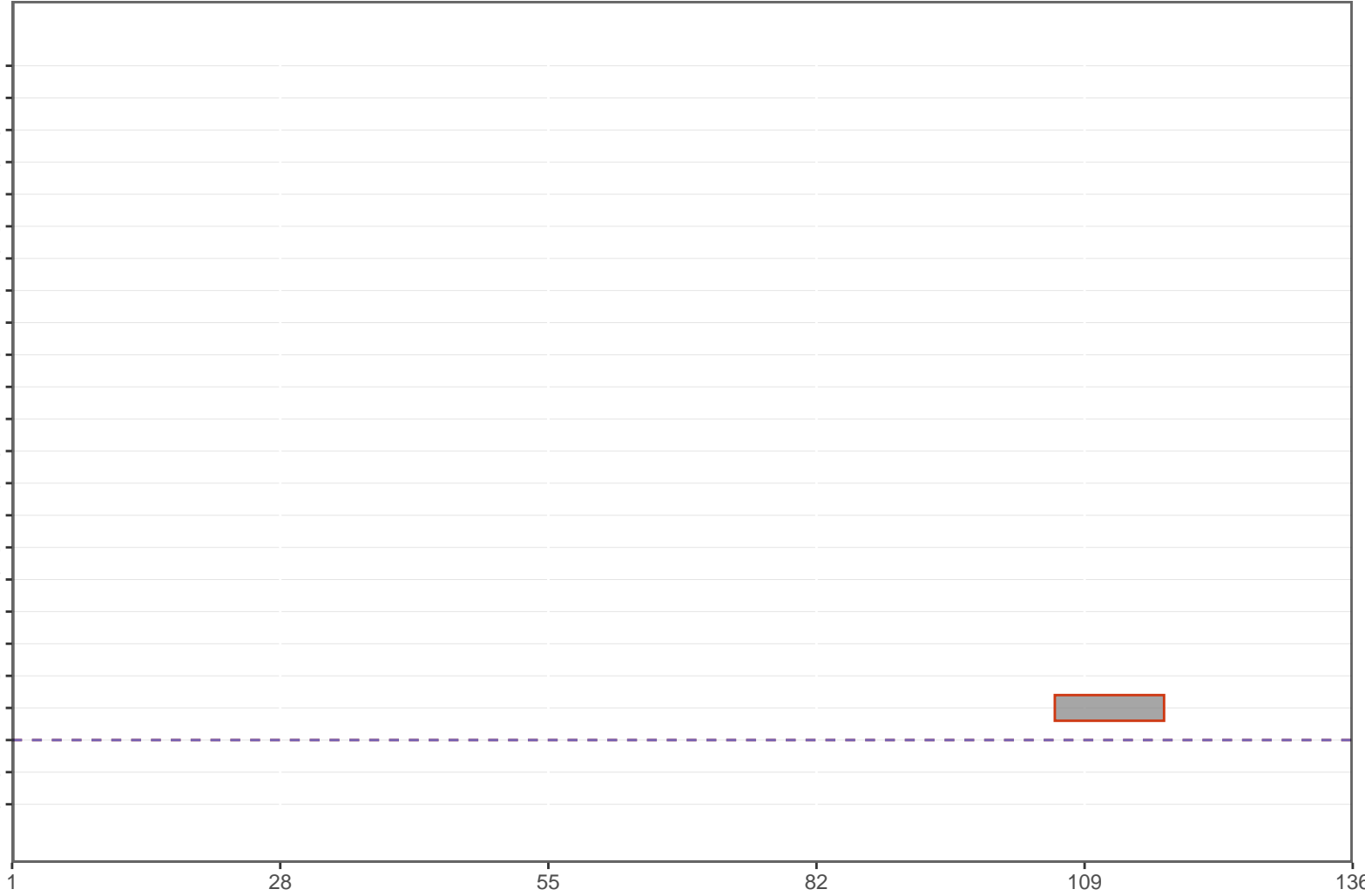
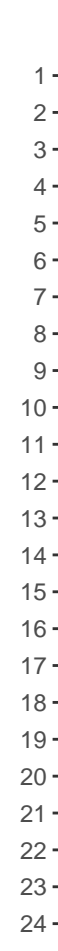
MW indication



Molecular weight

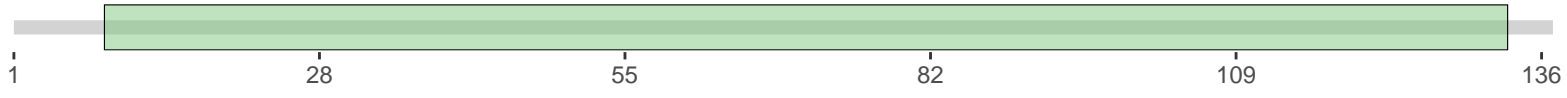


Gel Slice



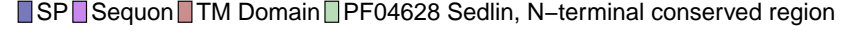
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AMFLKSIDRFNDLVAQVAVTAGHTRMLMLHDSRINDDGKIFFQEVHELYKVLNPLVLPGRITSSHFDTKVRALARKYL

NbL09g01330.1 uncharacterized_LOC107826806 [MW = 46.3 kDa]

No. of times detected



log(intensity)



Values from



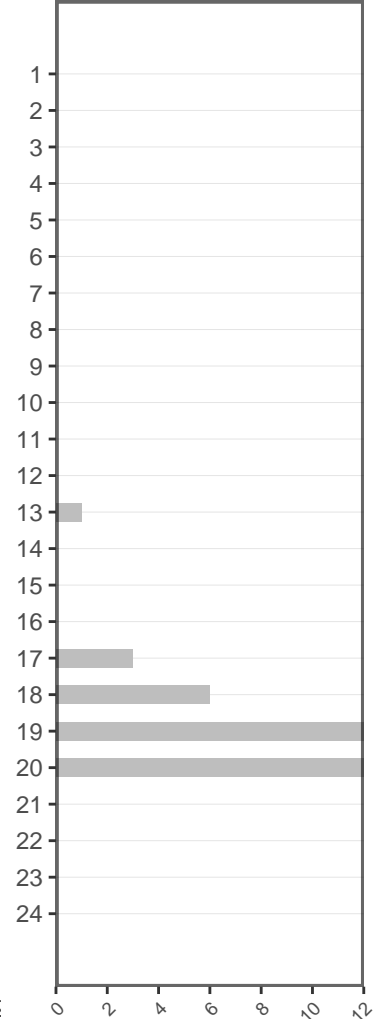
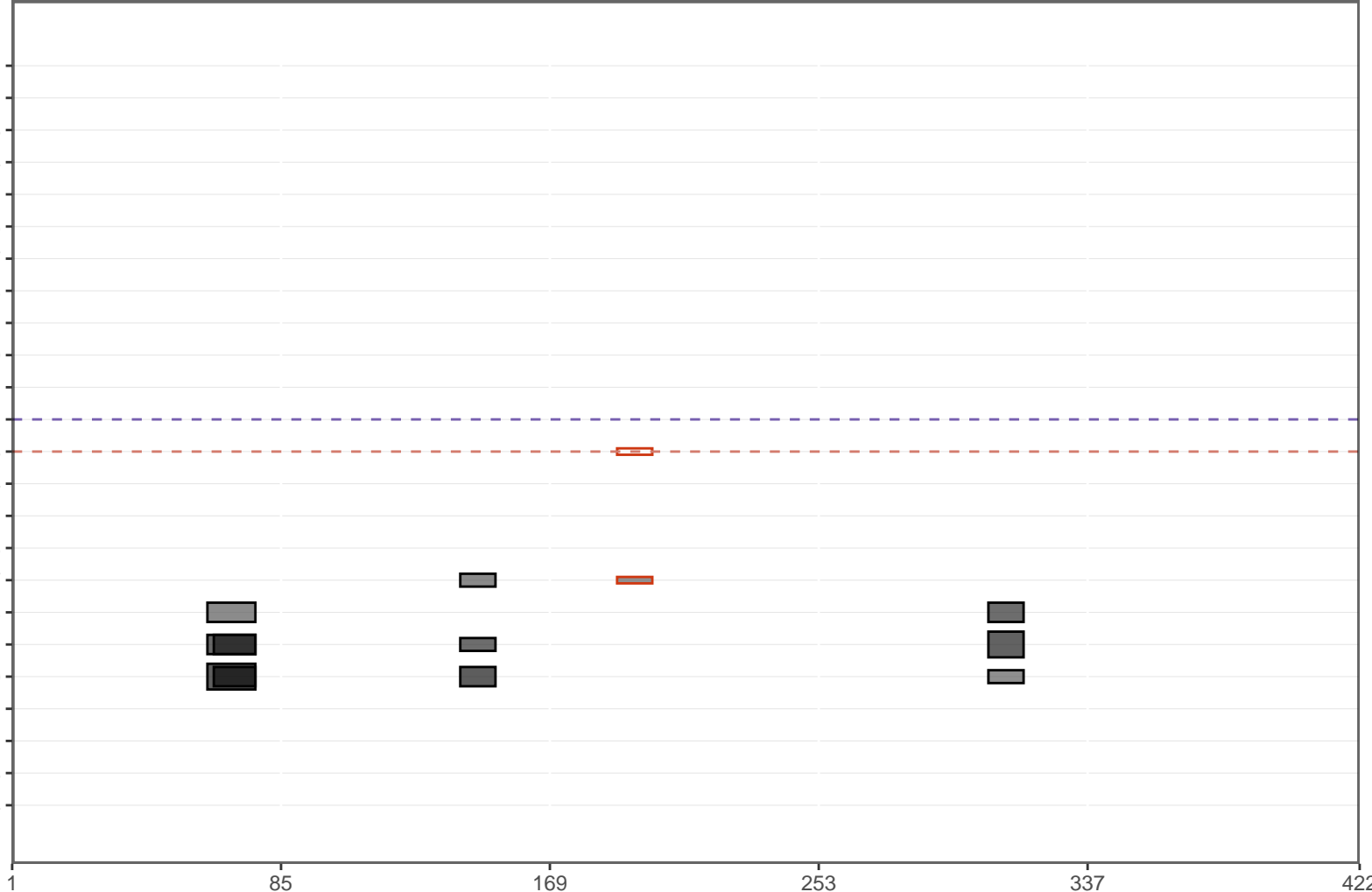
MW indication



Molecular weight



Gel Slice



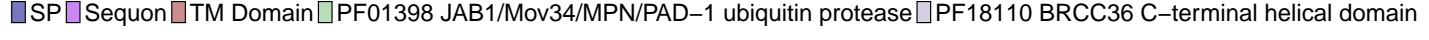
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

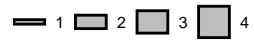


Protein sequence:

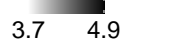
MSRAALASKGGARSTDLGNFFANVDNRVGENLQANSLNGLDVPDMMDSDMQEAMHRSNLEMDSGAEYVRKEIPLVLPSSLLNLDAPLNSFTDLQRVLFEEERTAYNDQAVVTNMRREGKARHLTFHHTFTYQASMKRLMEVQLSPWALQDHLRENEIRLKMLEEAKVLETEITKGEPTSSPRRSTLGRDLVSPTELSMKVSGSGSRKRKA*

NbL09g01190.1 protein_CDI-like [MW = 29.42 kDa]

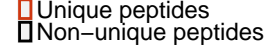
No. of times detected



log(intensity)



Values from



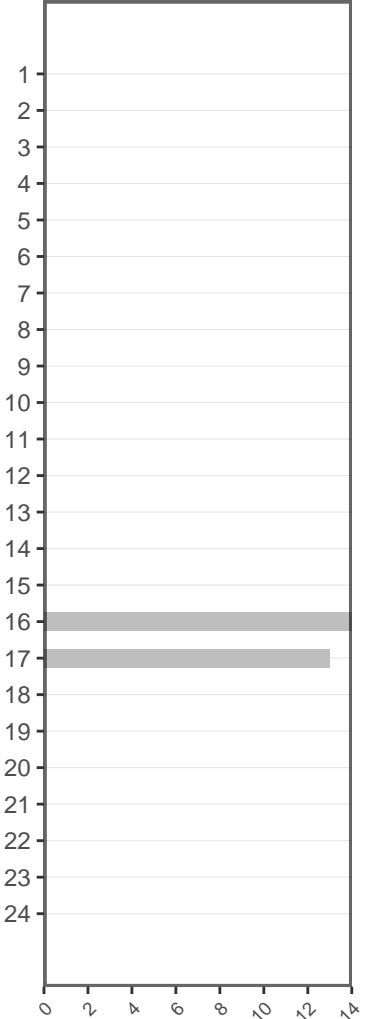
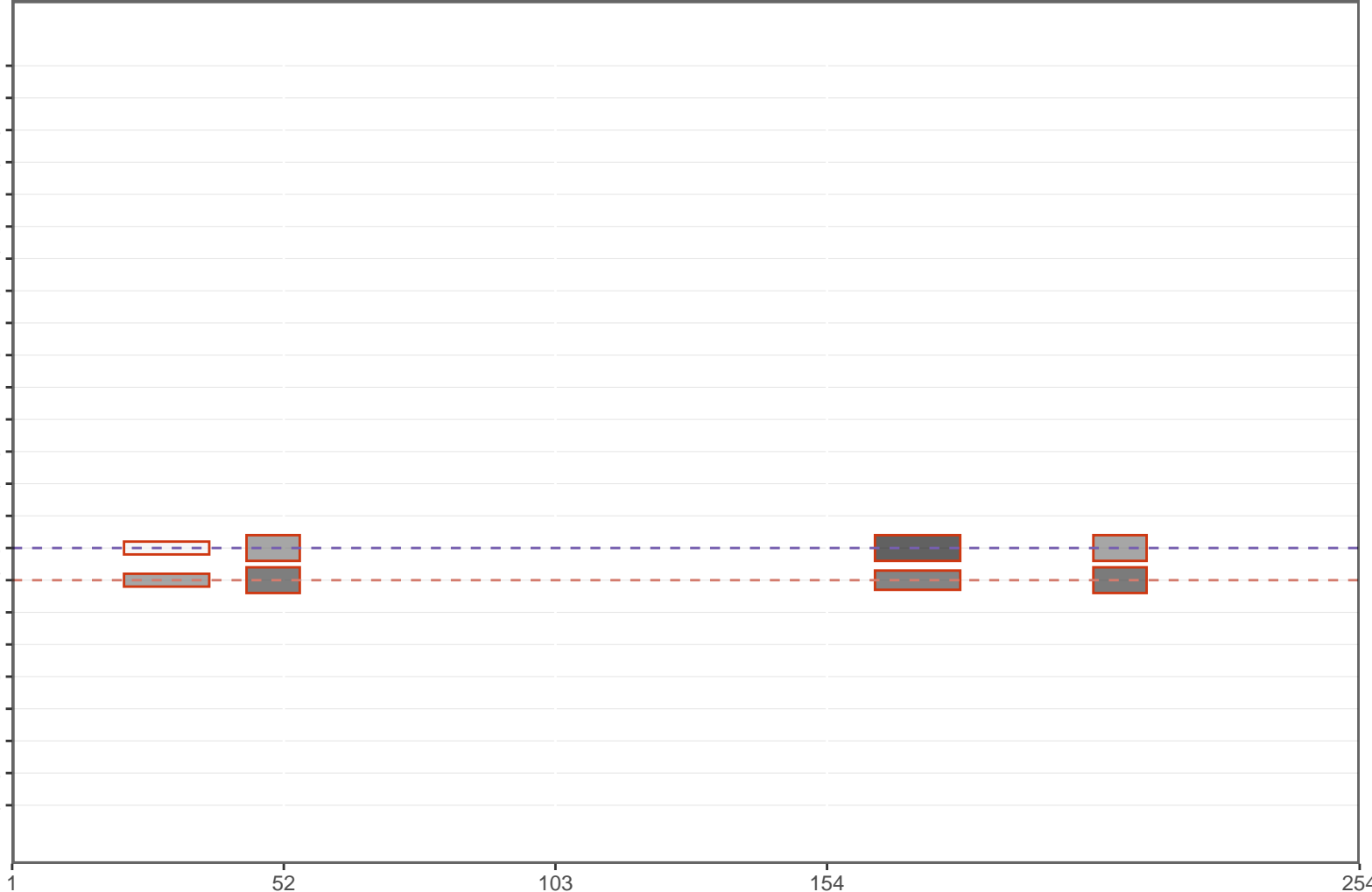
MW indication



Molecular weight



Gel Slice



Protein length

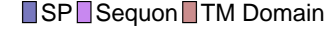


Peptide counts over 4 repeats

Pfam domains



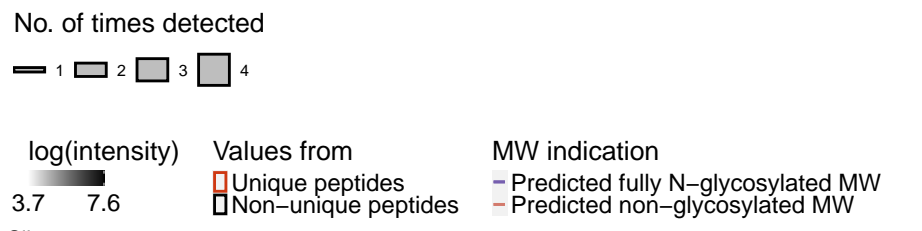
Pfam Description



Protein sequence:

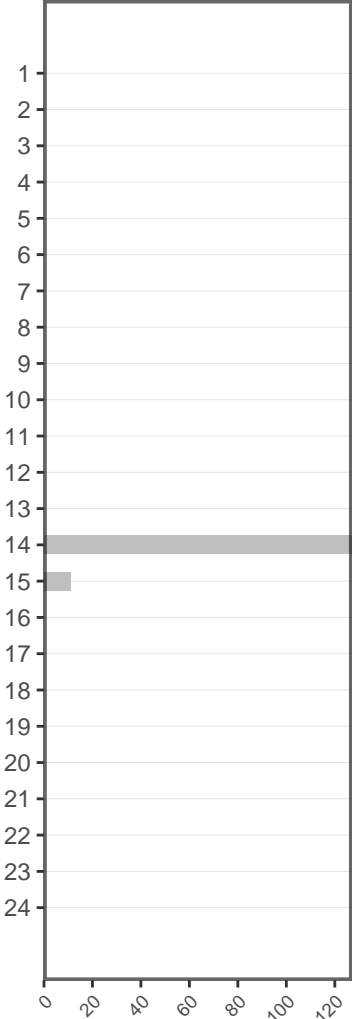
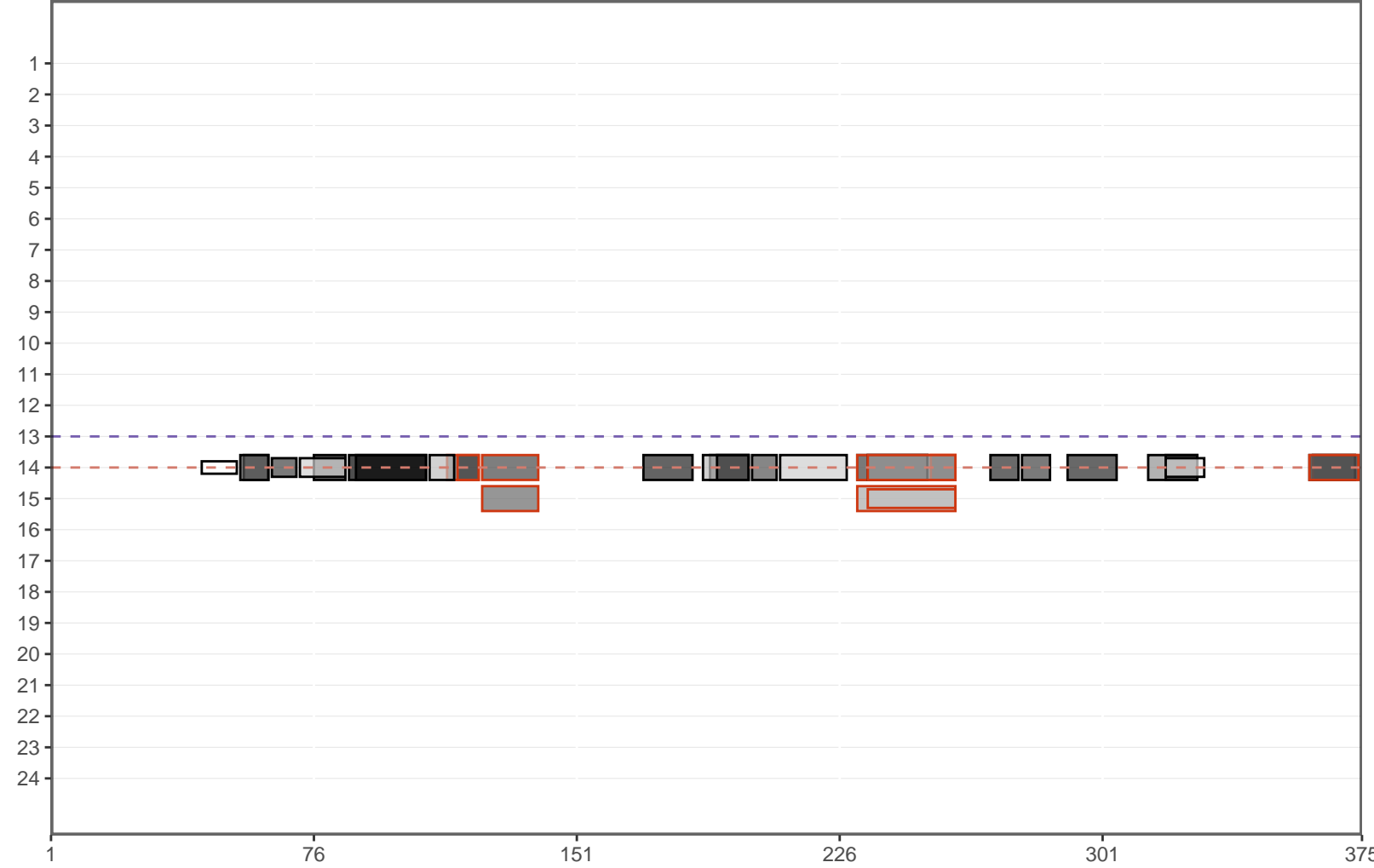
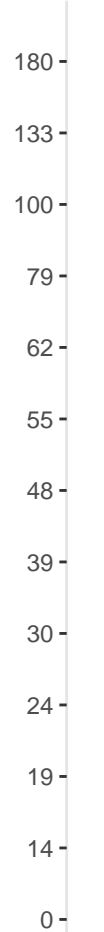
KYVA/MCVYIHID/APKETTMDGAVGTVPYPRKNWSSMVAIYNGGHPRKNVLTPEIWNTEGSAFLHRFMVLLEDNEIGEVPFVWVNFVGHKNVVEGDPTFRKSHYTLGGPWFVAWKDDGFGDLWKELEEYKKSIDKKAD

NbL09g01110.1 chloroplast_stem-loop_binding_protein_of_41_kDa_b_chloroplastic [MW = 41.72 kDa]



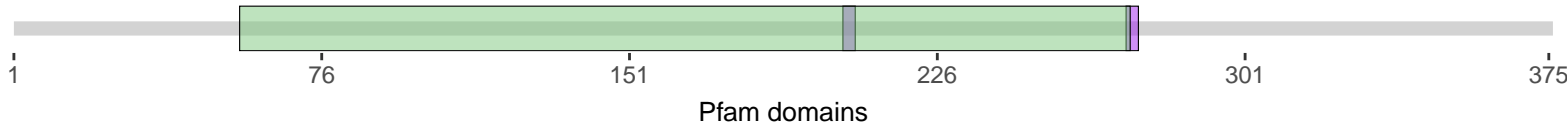
Molecular weight

Gel Slice

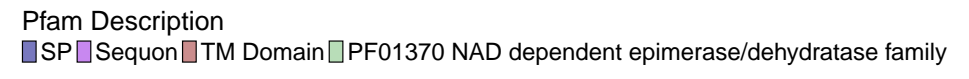


Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:

IFEADVDPKSRHKGKLETESLLESDRWNTSVPVYVYGLNINPVEEWFHRLKAGRPPIIPNSGLGTLQGHYKDLATAFKVLGNEKASKGVFNISGEEKYVTFDGLAKAKAGAGFFPEPEIHHYHNPKEFDGKQKAFPRDGHFFASVEKAKAVLGVWPKPEFDLVEGLTDSYNLDFGRGTRFKEADFSTDDLGLGN*

NbL09g01070.1 tetrapyrrole-binding_protein_chloroplastic [MW = 29.96 kDa]

No. of times detected



log(intensity)



Values from



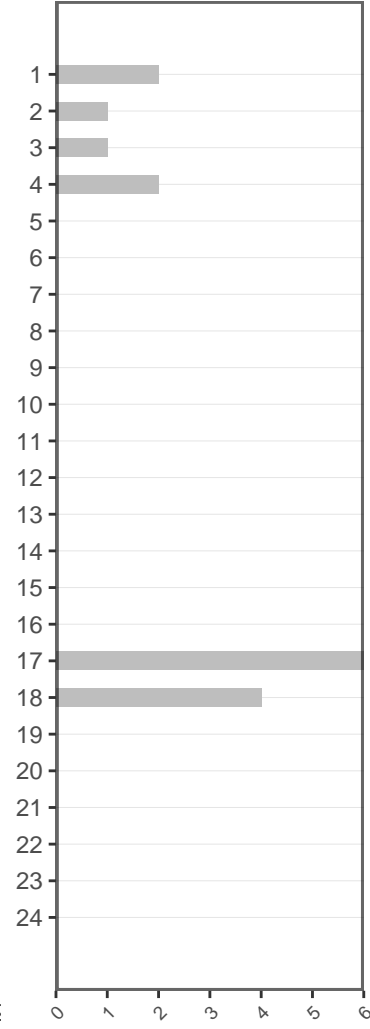
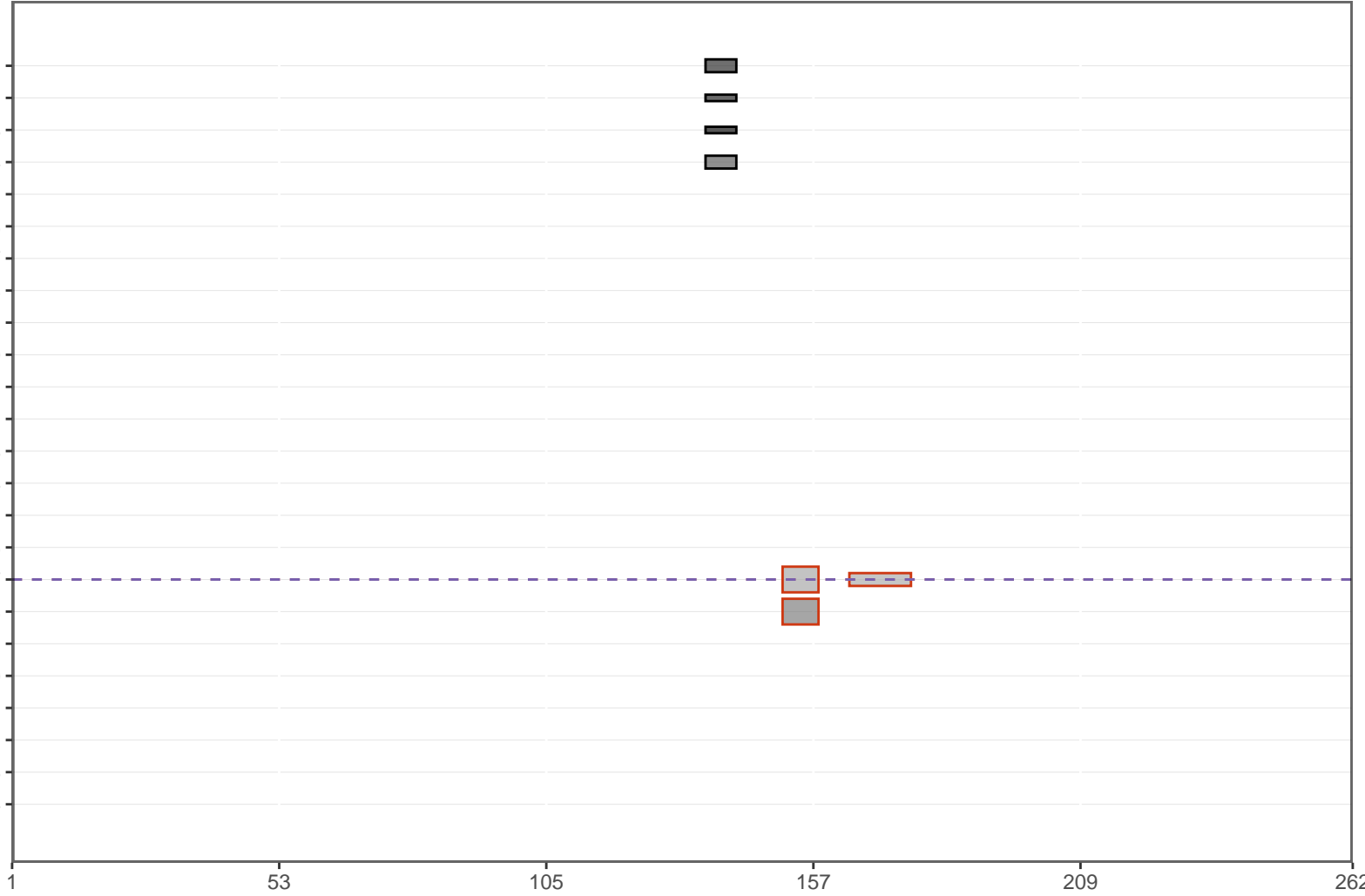
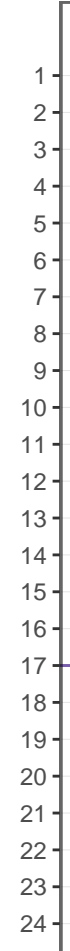
MW indication



Molecular weight

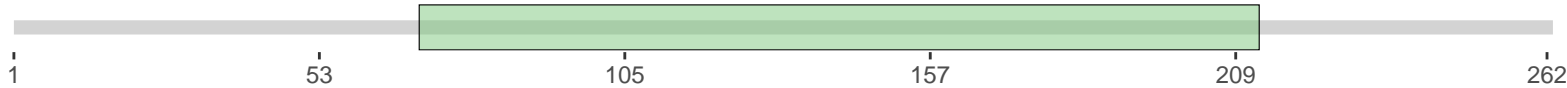


Gel Slice



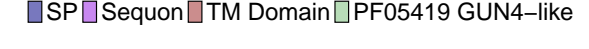
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KEIDSLWKYKYSQNFQYGVQKIKWIKVNRDFTSFFIKVGVWKKLESSEVEQYNYRPFNFIEWELNEETPEGHLPNTNLRGTQLLSIFTHPAFVEGGEEKDEEKQAFSGEIKKSVYKGGLLGLRSLKLFQKPDYSP

NbL09g01040.1 60S_ribosomal_protein_L9-1 [MW = 21.98 kDa]

No. of times detected



log(intensity)



Values from



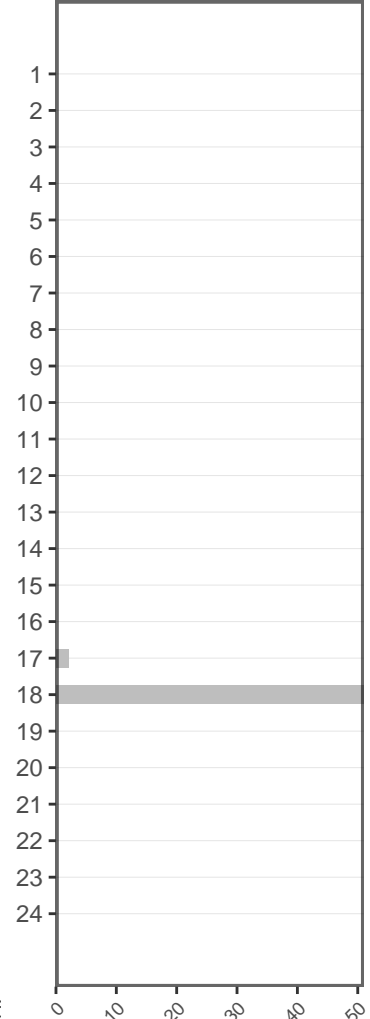
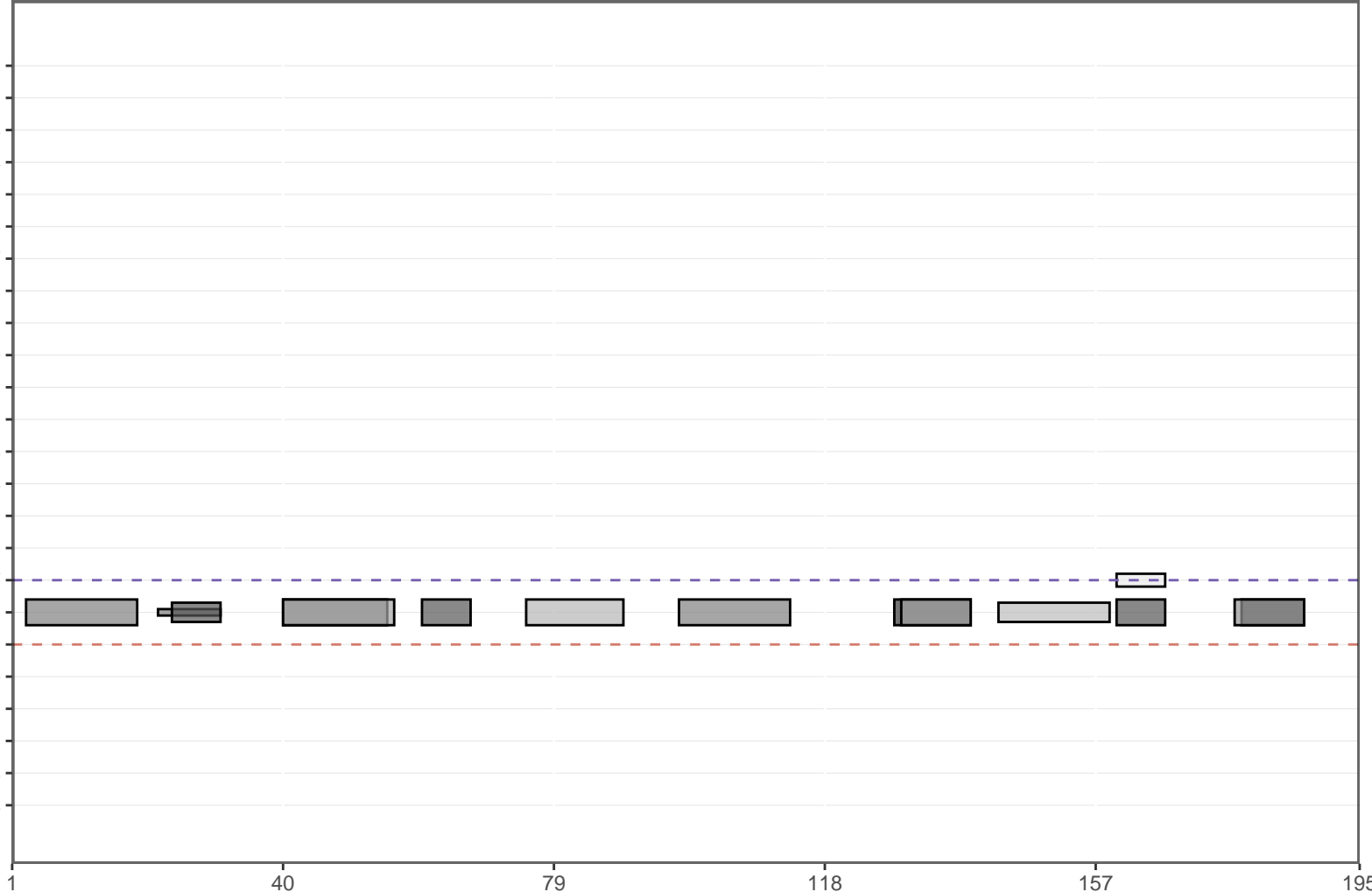
MW indication



Molecular weight

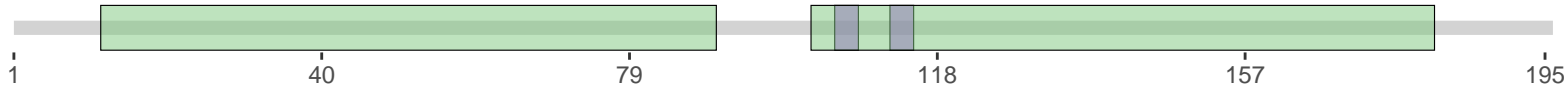


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGVITGQYRYKMRFLVYHFPNBSITGNGKBIERNFLGKRNVRKVDMLDGVTVVRSKVKDELVDLGDNDIELVRSAAALNGKHGKHNKDIRKFLDGIYVSEKGRIAEE*

NbL09g00870.1 nuclear-pore_anchor [MW = 229.22 kDa]

No. of times detected



log(intensity)



Values from



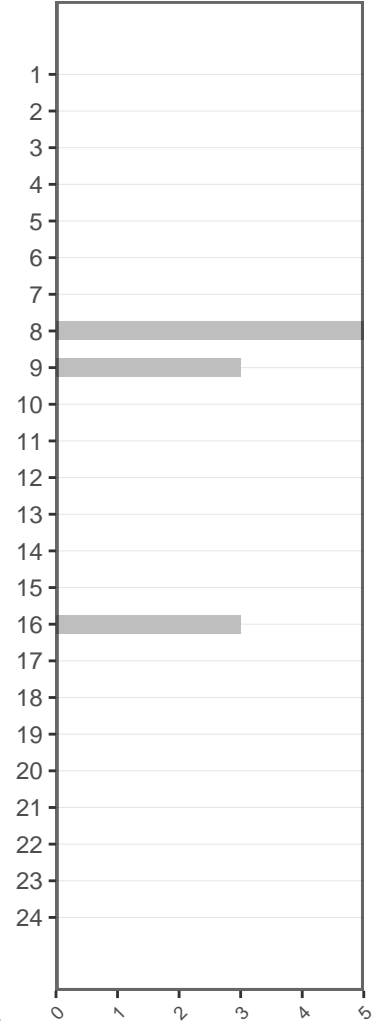
MW indication



Molecular weight

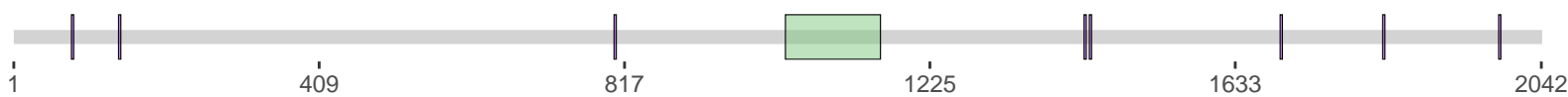


Gel Slice



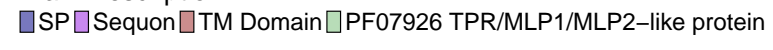
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ITVKSVEASATAGKEEAVGATLAEISLKEEDNAKMSQINLEAGITALKDDLEKHQRWRRAADVYVERQVILGSETIGELTRTSQALAAALQEESSELRKISDLETENELKAKWAGMSALEVSKTEAEKKYTEANEQNKILLDRLEGLHKLAEKDRSGLGTSSGDTTAEQDGLMMVYVLRFRSKDIAETELRDLRGEKLRIGSGLENAGRRADIAEASLSSERENSRADVINEEFKALQLGVRELNLLRESNLQRLREENKHNFEEGQKLRRAAGKMKIEVEGLQKLLN

NbL09g00820.1 protein_FAM136A-like [MW = 17.02 kDa]

No. of times detected



log(intensity)



Values from



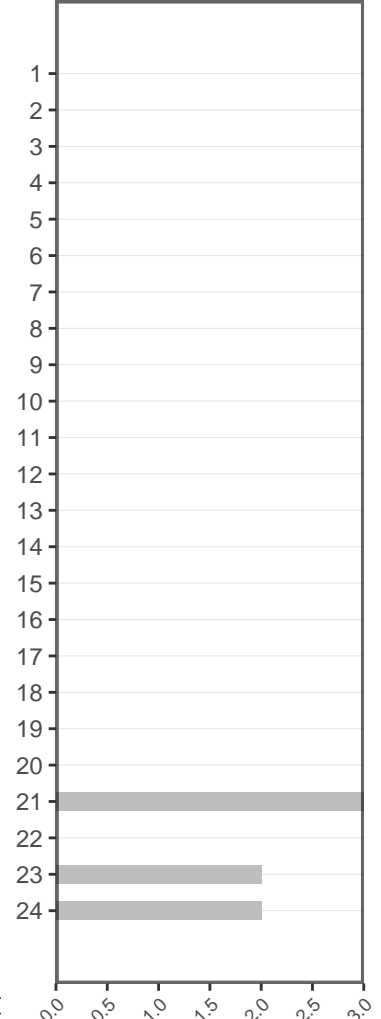
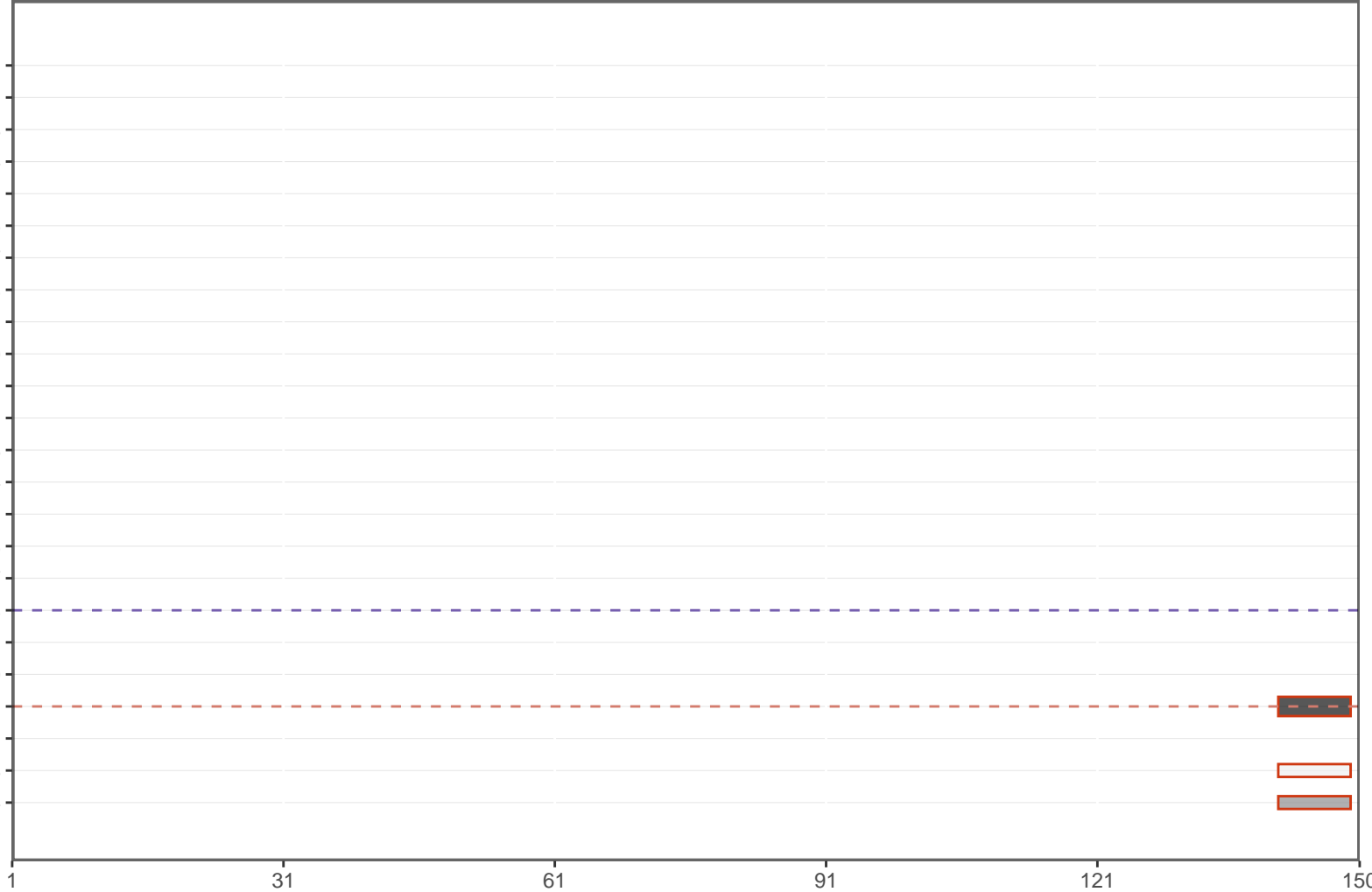
MW indication



Molecular weight



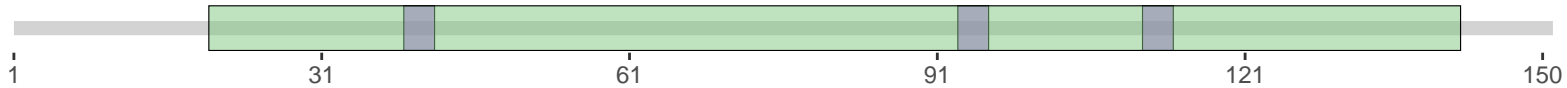
Gel Slice



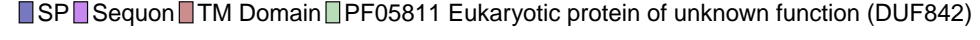
Protein length



Pfam domains



Pfam Description



Protein sequence:

IGHCVCCSYIIVHNAQNLVQNEAKFGERRMNRSLMVGGDKYETAKLQKRRSDATKDLKLESCVDDQVHDSNLFHLVARLKGSLGIAN

NbL09g00810.1 stearoyl-[acyl-carrier-protein]_9-desaturase_chloroplastic [MW = 47.78 kDa]

No. of times detected



log(intensity)



Values from



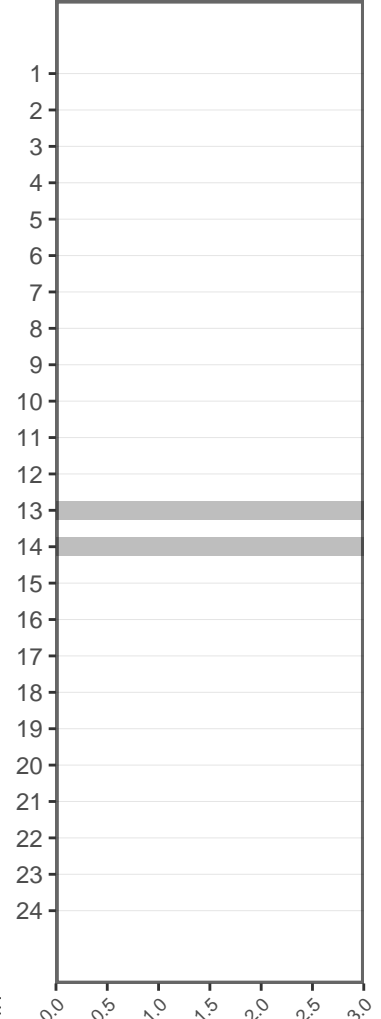
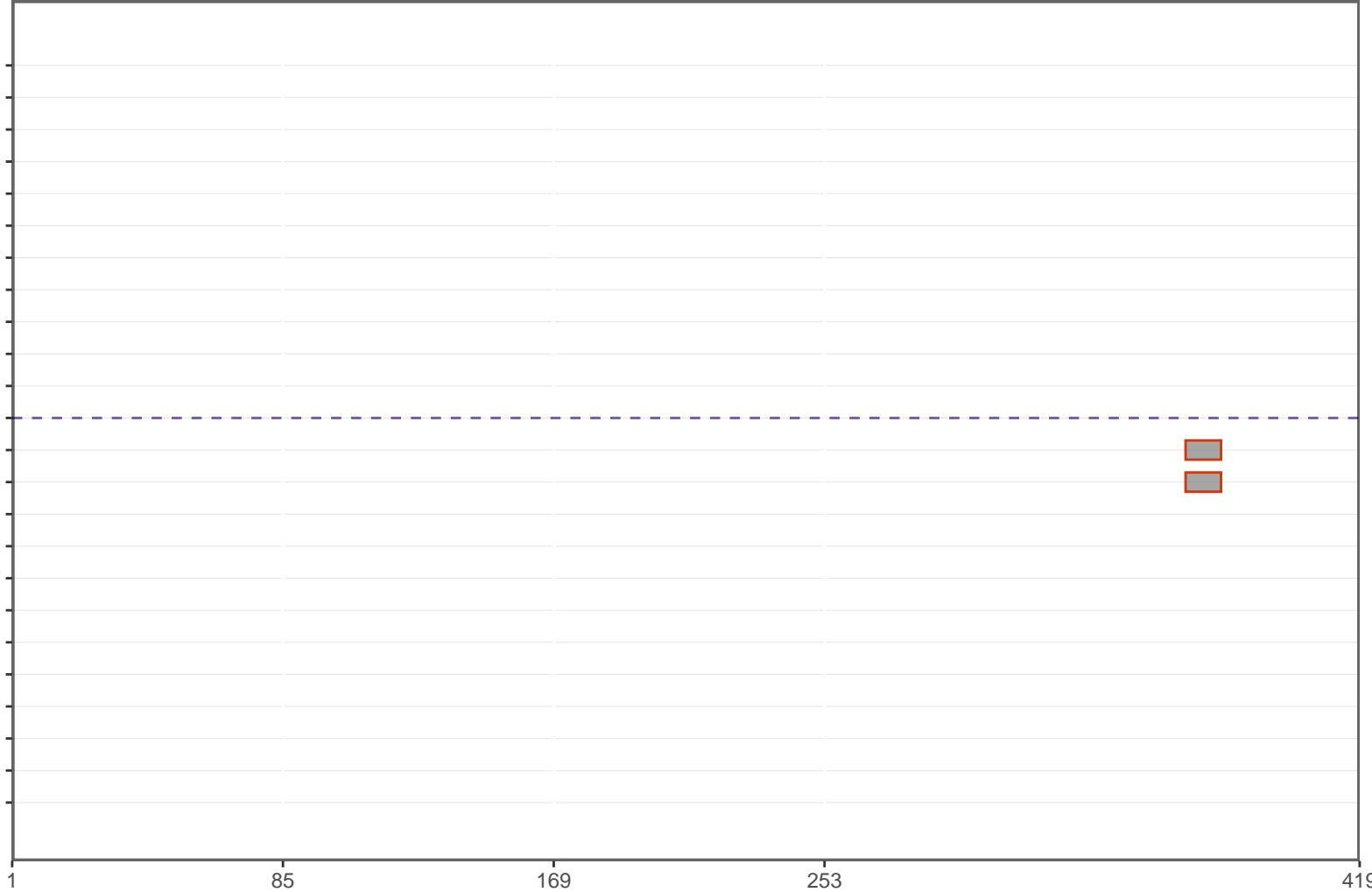
MW indication



Molecular weight



Gel Slice

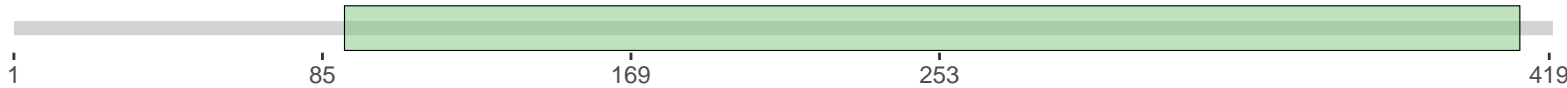


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VTAENRHGDLNLYLISGRVDMRAIEKIQYLIGSGMDPRTEPNPVLGFVYTSFGERATFVSHGNTARLAKEHGDKLAGKGGHAADEKRHETATKIVKLFKFEIDPDGTVLAFADMMRKKISMPHLMFYDGRDDDLFDHFSVAWGRLVVYTKADYADILEFLVGRWVADLTGLSGGGRKADEYKGLPRIRILEERAQGRAKGPEMFFSWYDREVKL

NbL09g00740.1 fructokinase-2-like [MW = 39.05 kDa]

No. of times detected



log(intensity)



Values from



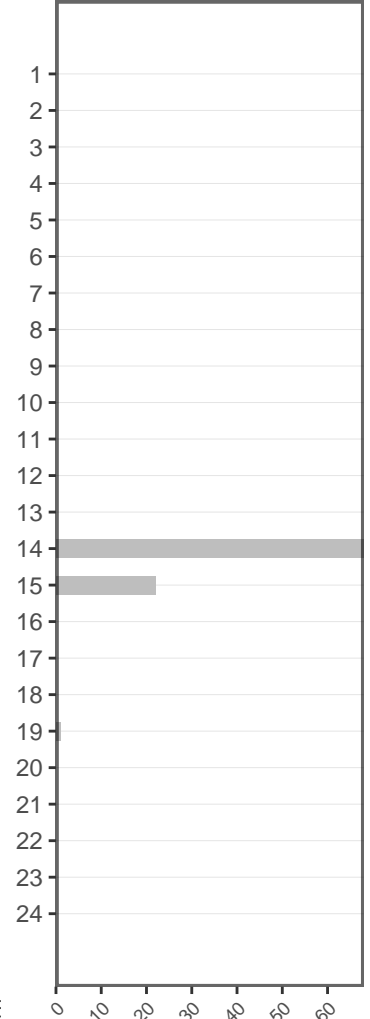
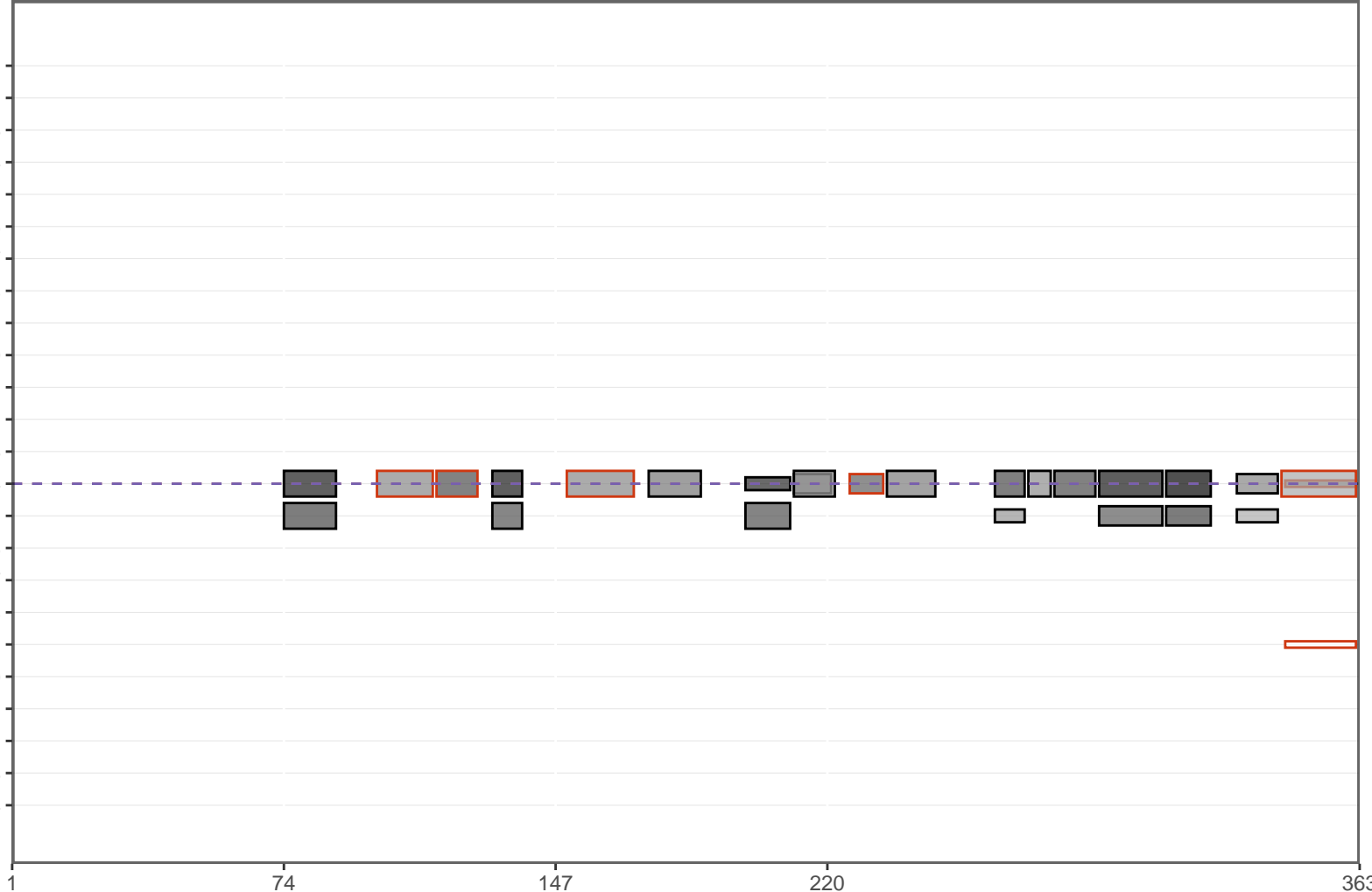
MW indication



Molecular weight

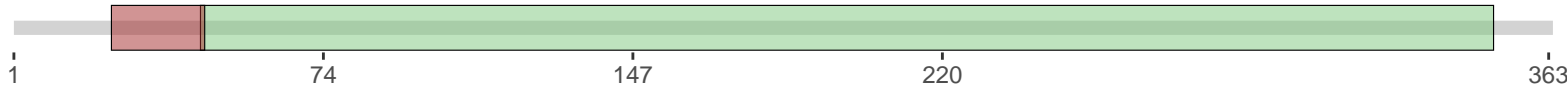


Gel Slice



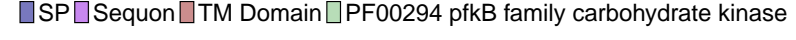
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IAKVFHYGSILVIEPDRBAHLKAMEVKEAGALLGVDPNLRLLPWSAEARKKQKSIWDEADVKVSDVLEFLTGSDDKIDDESAMSLWHPNLLKLLVLTGKGGCNYTKNFHSGGVFAFHVKTVDTTGAGDSFVGLLTKVDDGSDLEEARLKEVLRFAAGAGATTTTKGAPALPTESEALTMVYGA*

NbL09g00610.1 probable_hydroxyacylglutathione_hydrolase_2_chloroplastic [MW = 36.4 kDa]

No. of times detected



log(intensity)



Values from



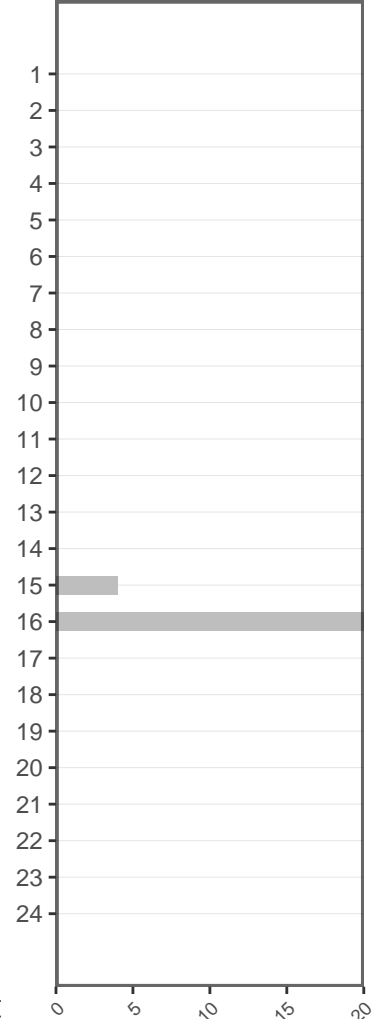
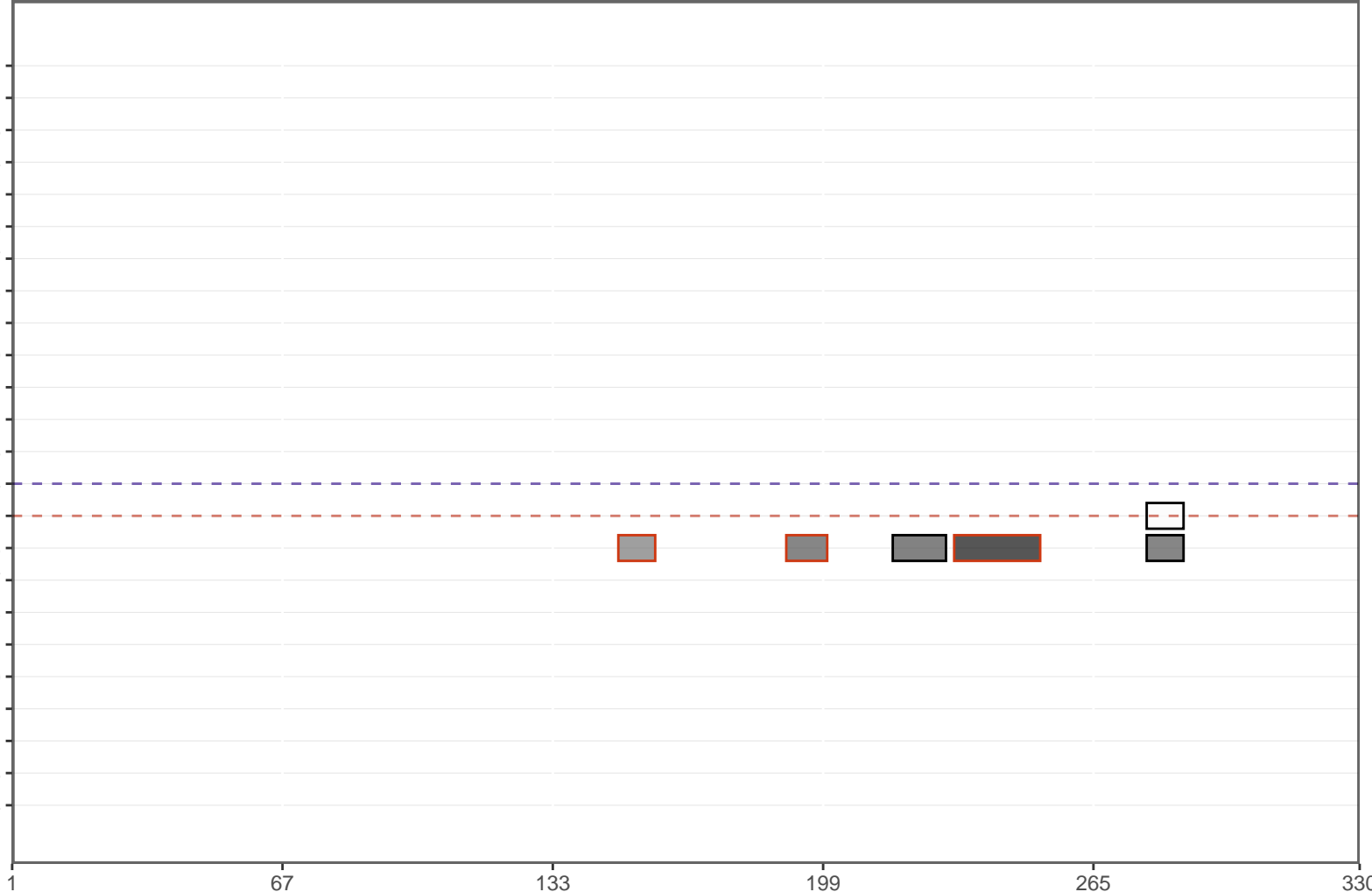
MW indication



Molecular weight



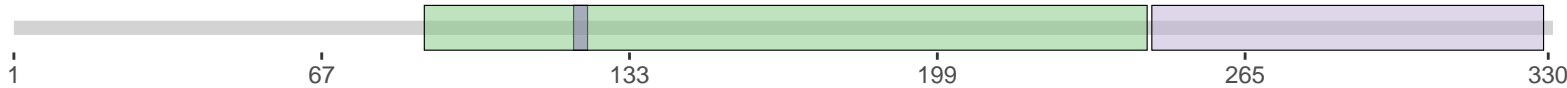
Gel Slice



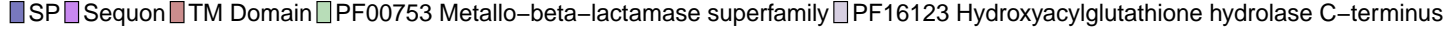
Protein length



Pfam domains



Pfam Description



Protein sequence:

ISGVDSDRIPGIDIALNDGGQWVFMFAGHEVIVMETPQHTRGHSHFYFPGKAITGDTLFSLGGKLFEGTQQMLSSLRKITSLPDDTNYVCGHEYTLNENKFKALGVEPQNEELGGVSTGVVNLRRKKGFLPTPTTLKAERLGNPFLRTSSTEIRKLLNIPPTADDEALGAIRRAKDF

NbL09g00510.1 2-isopropylmalate_synthase_B [MW = 66 kDa]

No. of times detected



log(intensity)



Values from



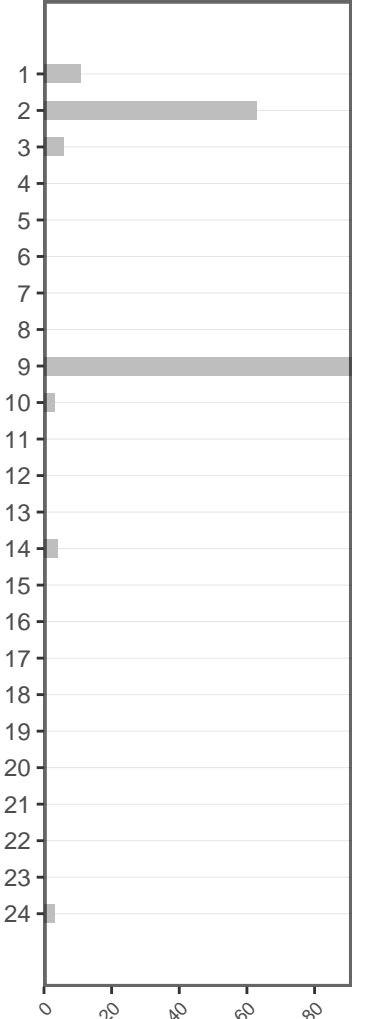
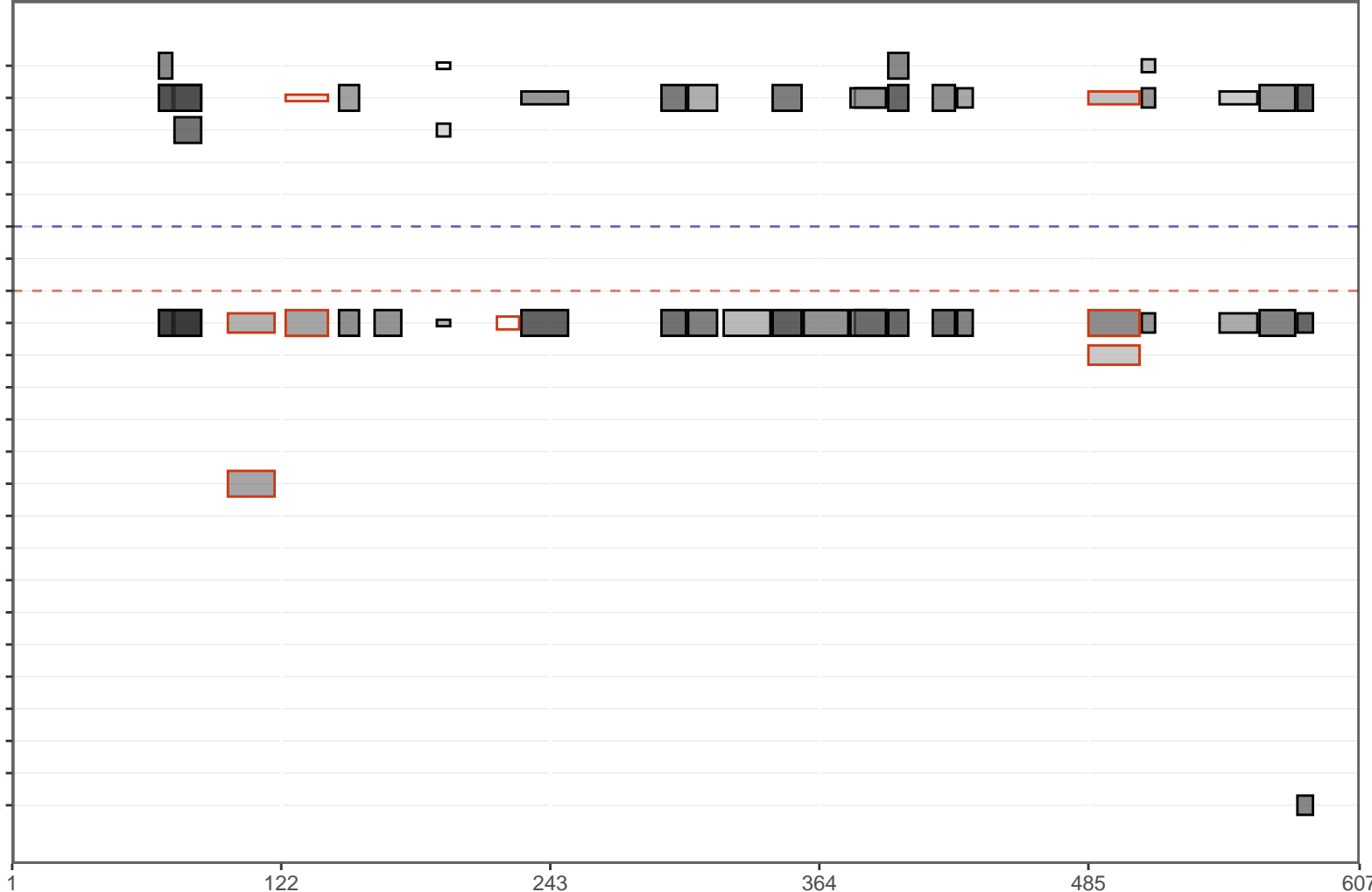
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

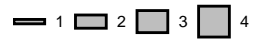


Protein sequence:

IVEVTNGIGERAGNASLEEVWALKGRGEVGLGIVTQINTGHILMSKMWEEYTGHLVDPKAVGANAFHESGHDDMLKHKDTYEISPEIDGLNRAVESGVLGKLSGRHAKKALELGYDIECKELEDLFWRFKSAEKKKKITDDLLALMSDEVFQPGFVWGLENVQVTOGSLGLSTATVKLIDTGGGHHVSGSVGTGPDVAAYKAVKDLKVPVVALLEYSLNAVTEGIDMASTRVYLRGENGHTSTHALTGETVHRFSFGTGADMDVISEVFRAYIGALNKLS

NbL09g00250.1 ATP_synthase_subunit_alpha_mitochondrial [MW = 49.53 kDa]

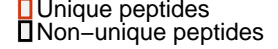
No. of times detected



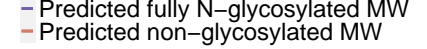
log(intensity)



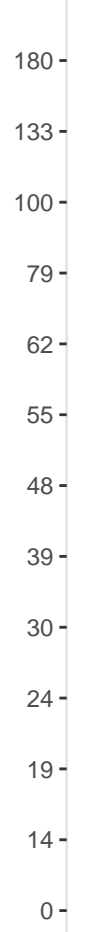
Values from



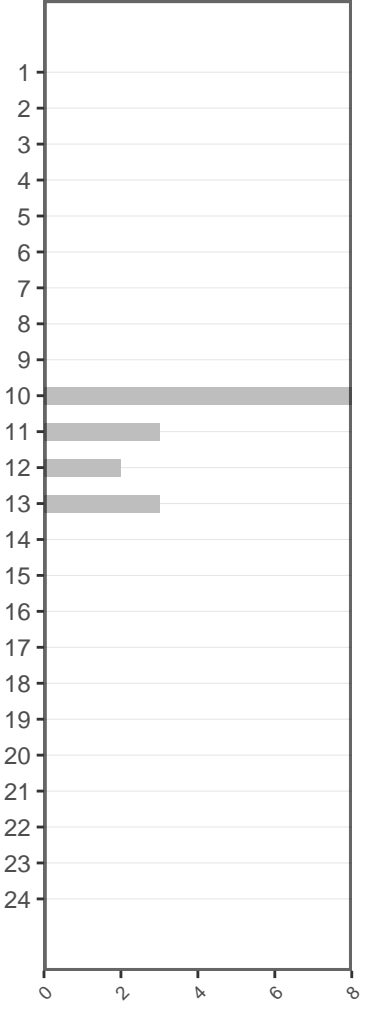
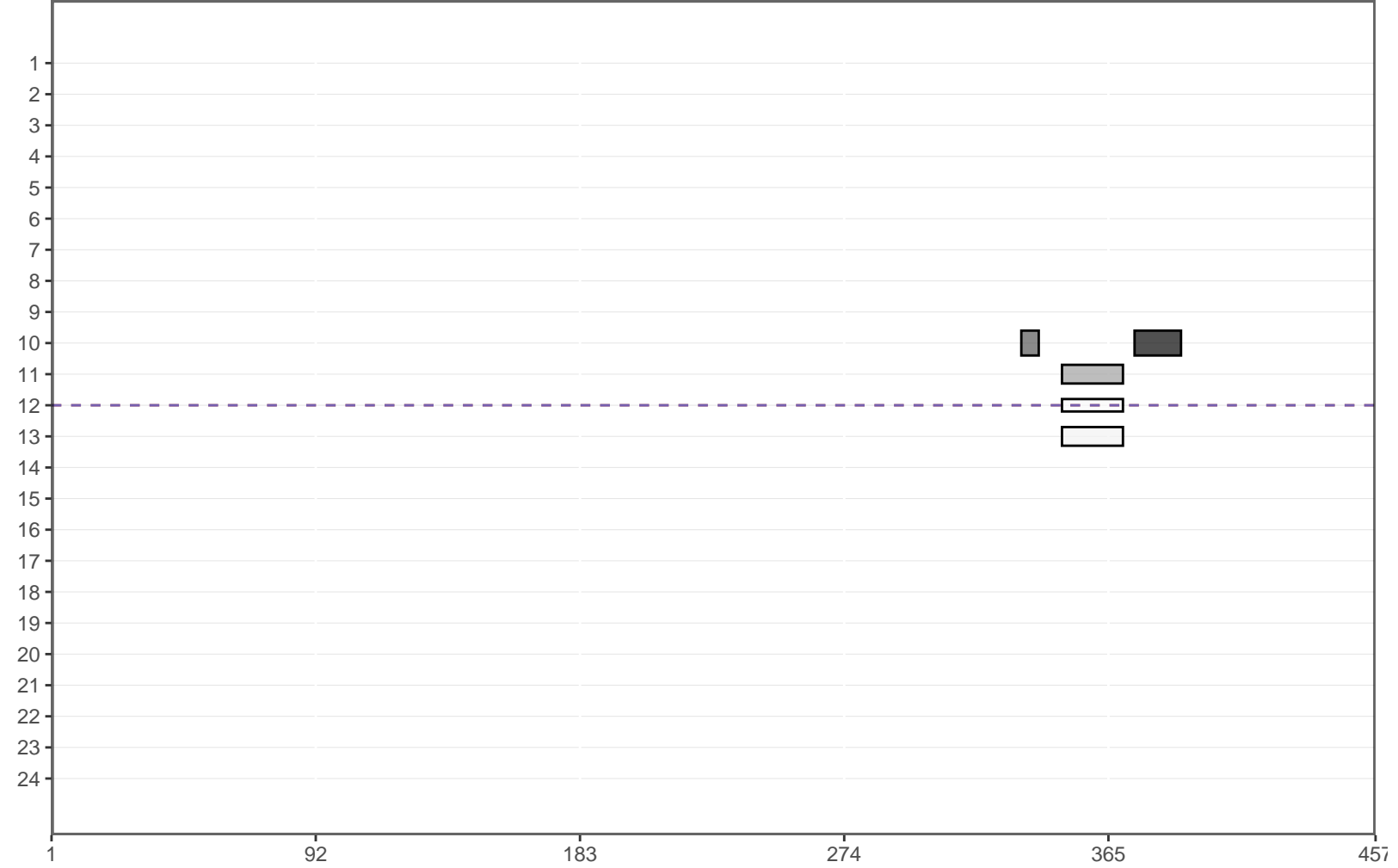
MW indication



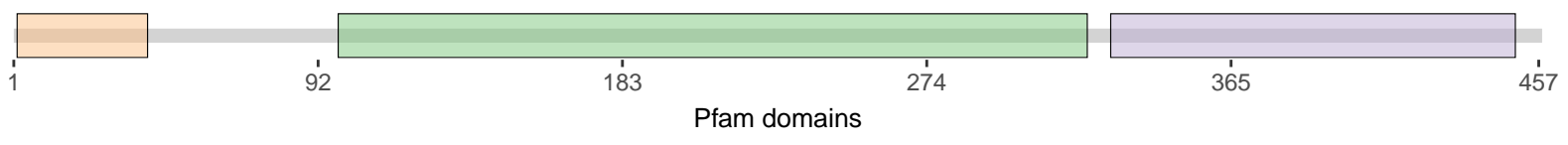
Molecular weight



Gel Slice

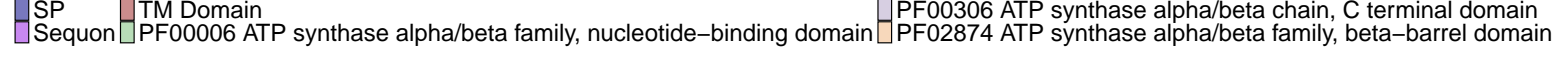


Protein length



Pfam domains

Pfam Description



Protein sequence:

LIYYDLSKQAWYROMSLLLRPPGREAFFPGDVFYHGRLLERAAKRSDQTGAGSLTLPVETGAGDVSAYPTNVISITDGGIGLETFLFYRGRIPAINVGLSVSRVSGAAGLKTMKGVCGSLKLELAGYREVAAFAQFGSDLDAQTGALLNRGARLVEVLKQDQVYALPLIEKQILVYAAVNGFCDRMPLDRISQYERAILNSVWPELLOSLFEKGGLTNERKMELODFLKEGALAFI

NbL09g00210.1 uncharacterized_LOC105138841 [MW = 49.25 kDa]

No. of times detected



log(intensity)



Values from



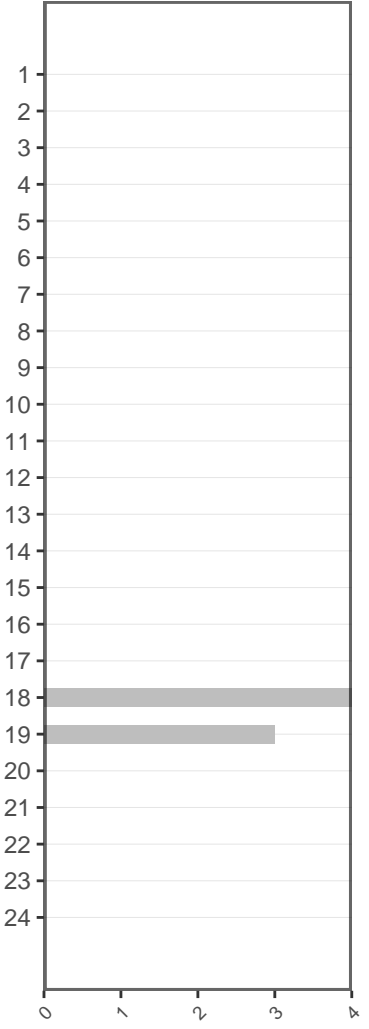
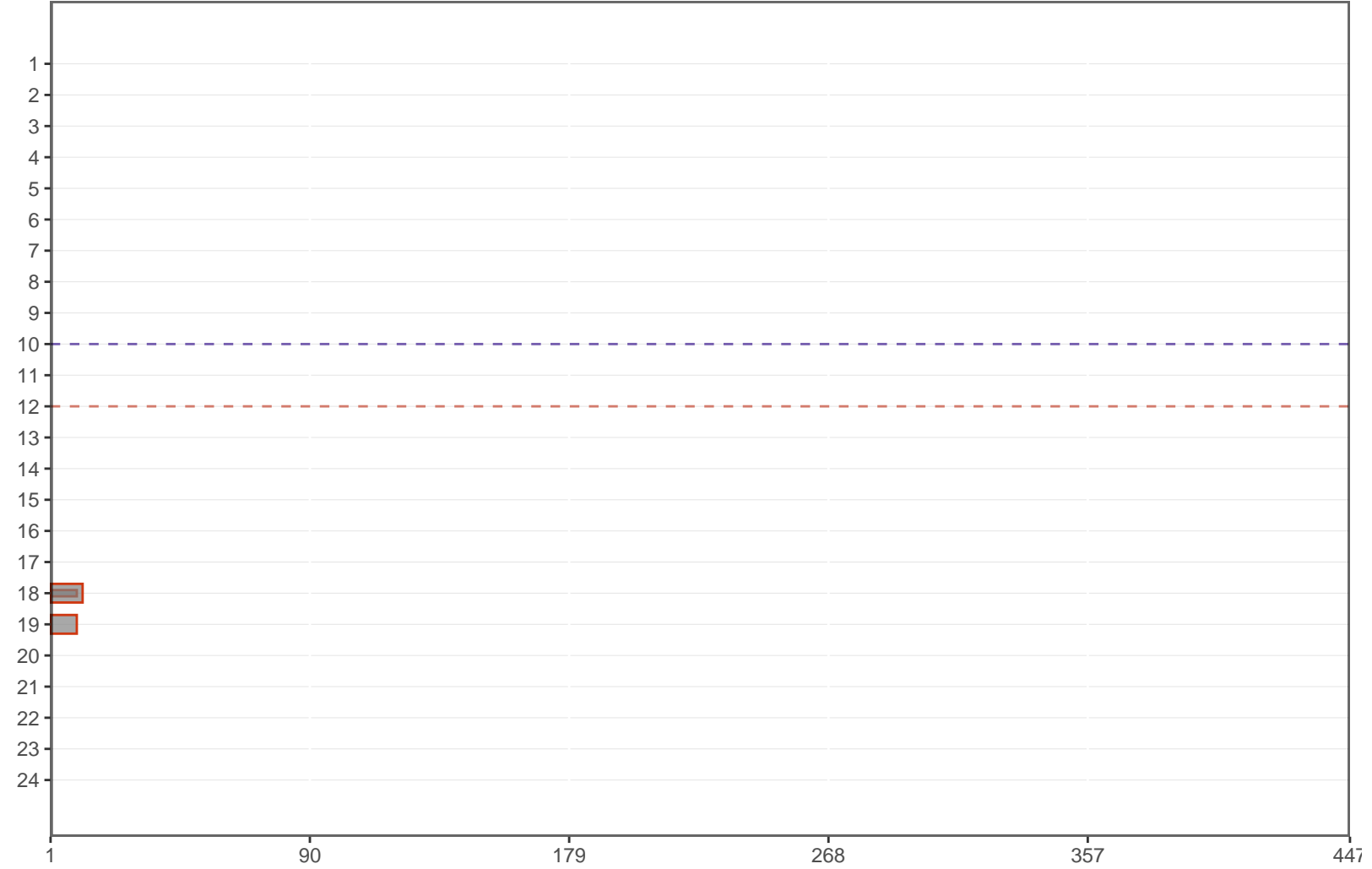
MW indication



Molecular weight



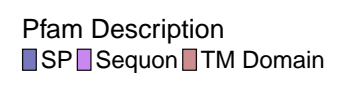
Gel Slice



Protein length



Pfam domains



Protein sequence:

MLELACVRRRHQSDNQEPCRSVFEPTGSGTSSGNKSKGLDTSGAGLGLQDRVSPNCFVLRDPRGEEAKMPDLTAEPEEISGRDEGLGNKAEEDGVKDRTLSESDLRGRSEDLTEETWYGGSDGDLFCQDKGMSNNDLRAEKRGEPKSKSKRSRSTRMTNKVEDPDLLESDKAALPSEKTKKGGTTPFFIDWLHPLPLTSLSTNKIRVVTAYRHYFKGDCLHTGMVSPSTEL

NbL09g00040.1 40S_ribosomal_protein_S15 [MW = 17.17 kDa]

No. of times detected



log(intensity)



Values from



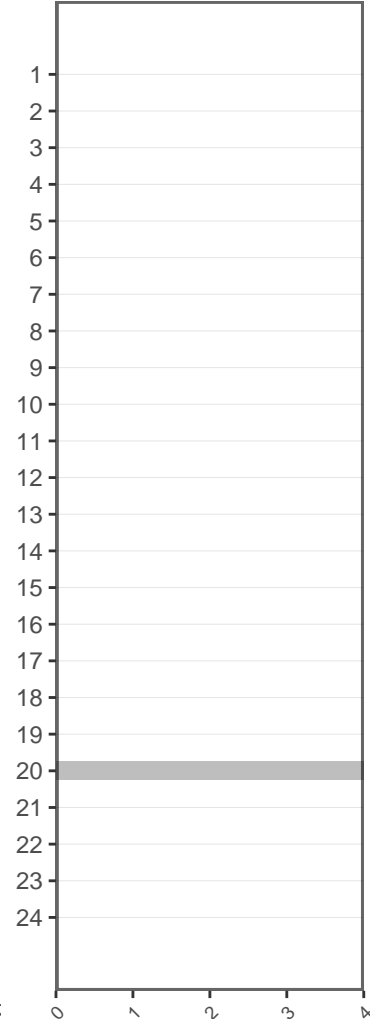
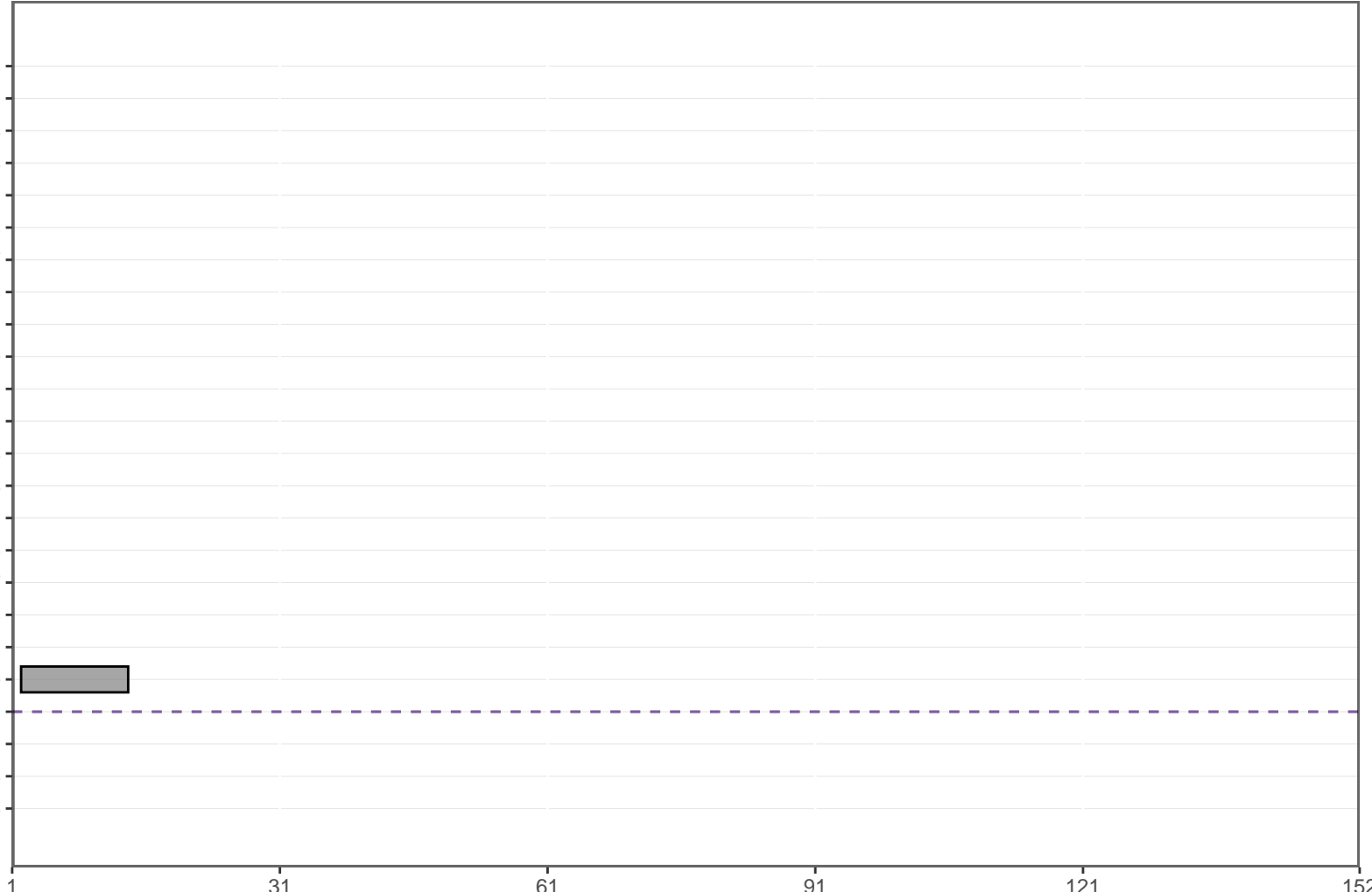
MW indication



Molecular weight



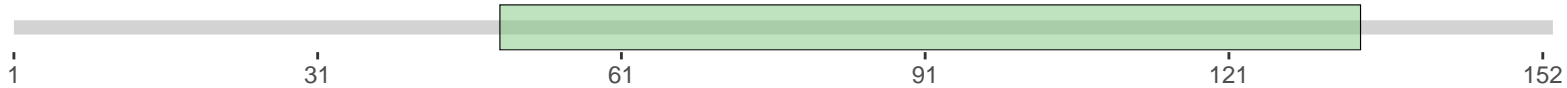
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

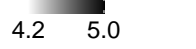
ALIKKLRKAKREAPPGEKPEPKVTHLRNMIIPEMIGSVGVGNGKTFNDIEVKPEMIGHYLAERFISIVKPKVHGKRGDGGATHSRFLK

NbL08g21680.1 phytanoyl-CoA_dioxygenase [MW = 32.27 kDa]

No. of times detected



log(intensity)



Values from



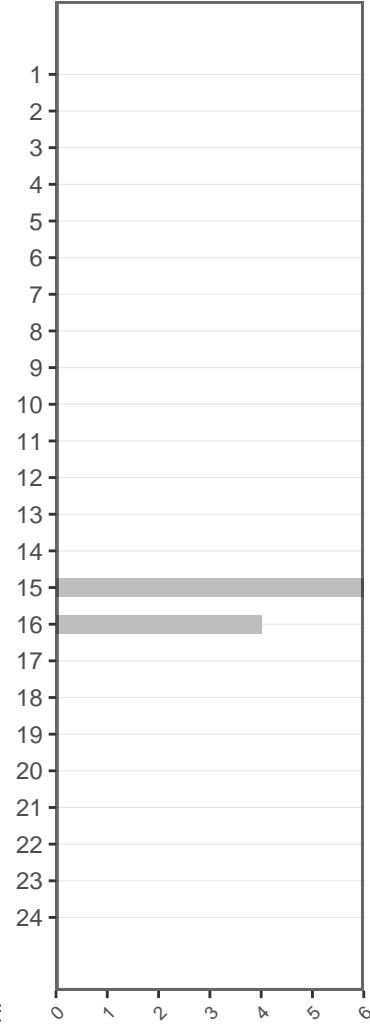
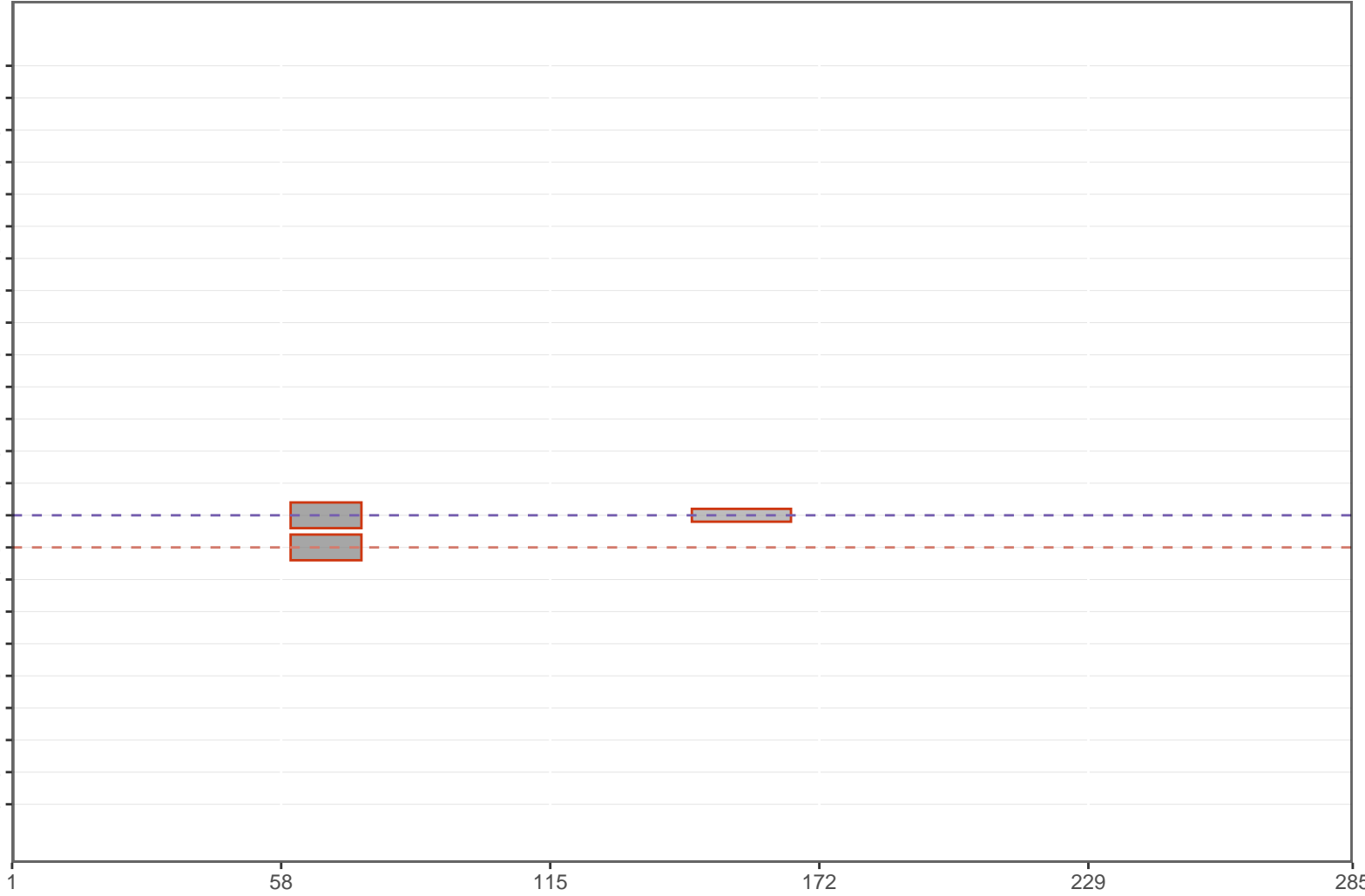
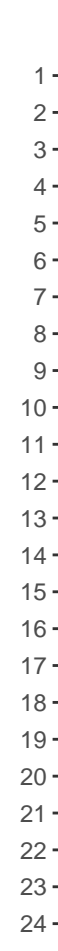
MW indication



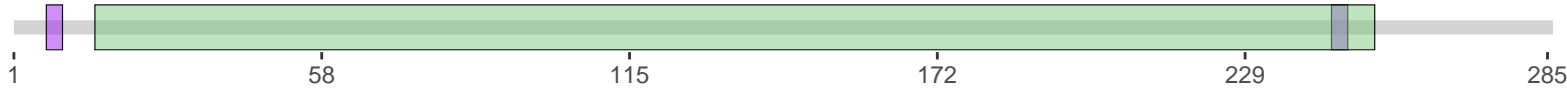
Molecular weight



Gel Slice

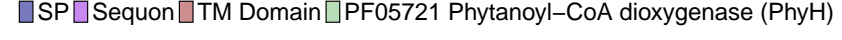


Protein length



Pfam domains

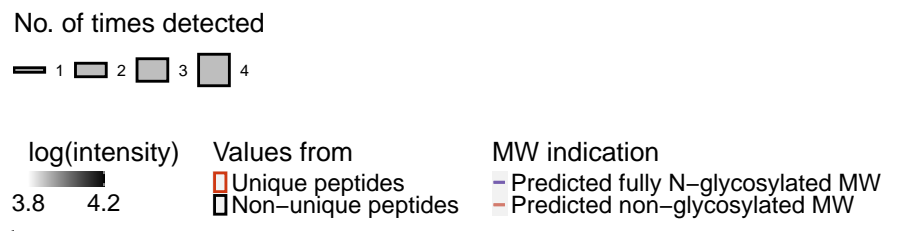
Pfam Description



Protein sequence:

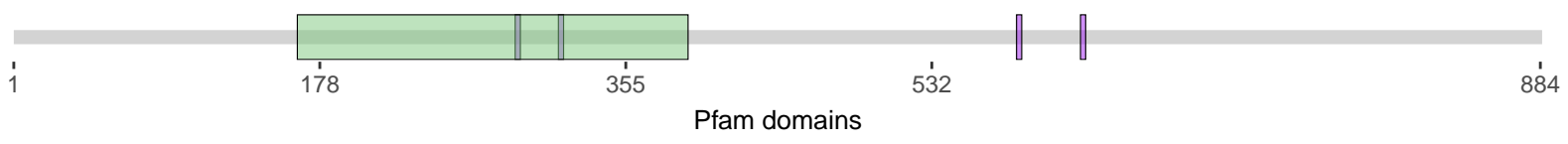
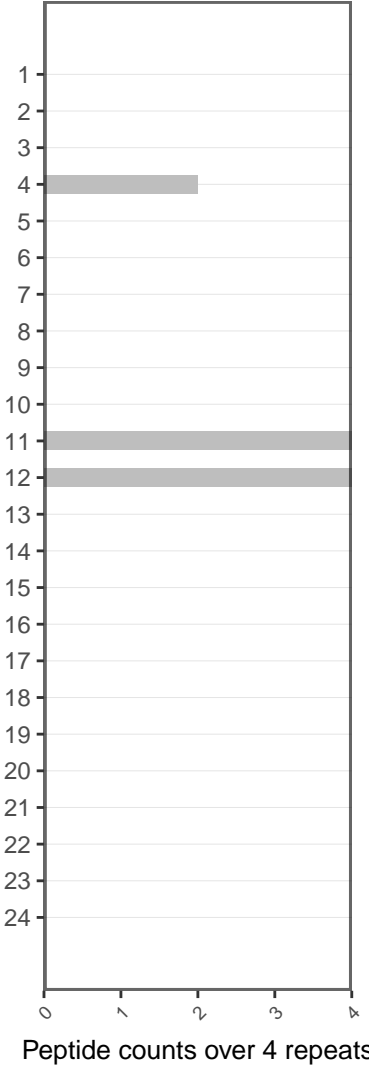
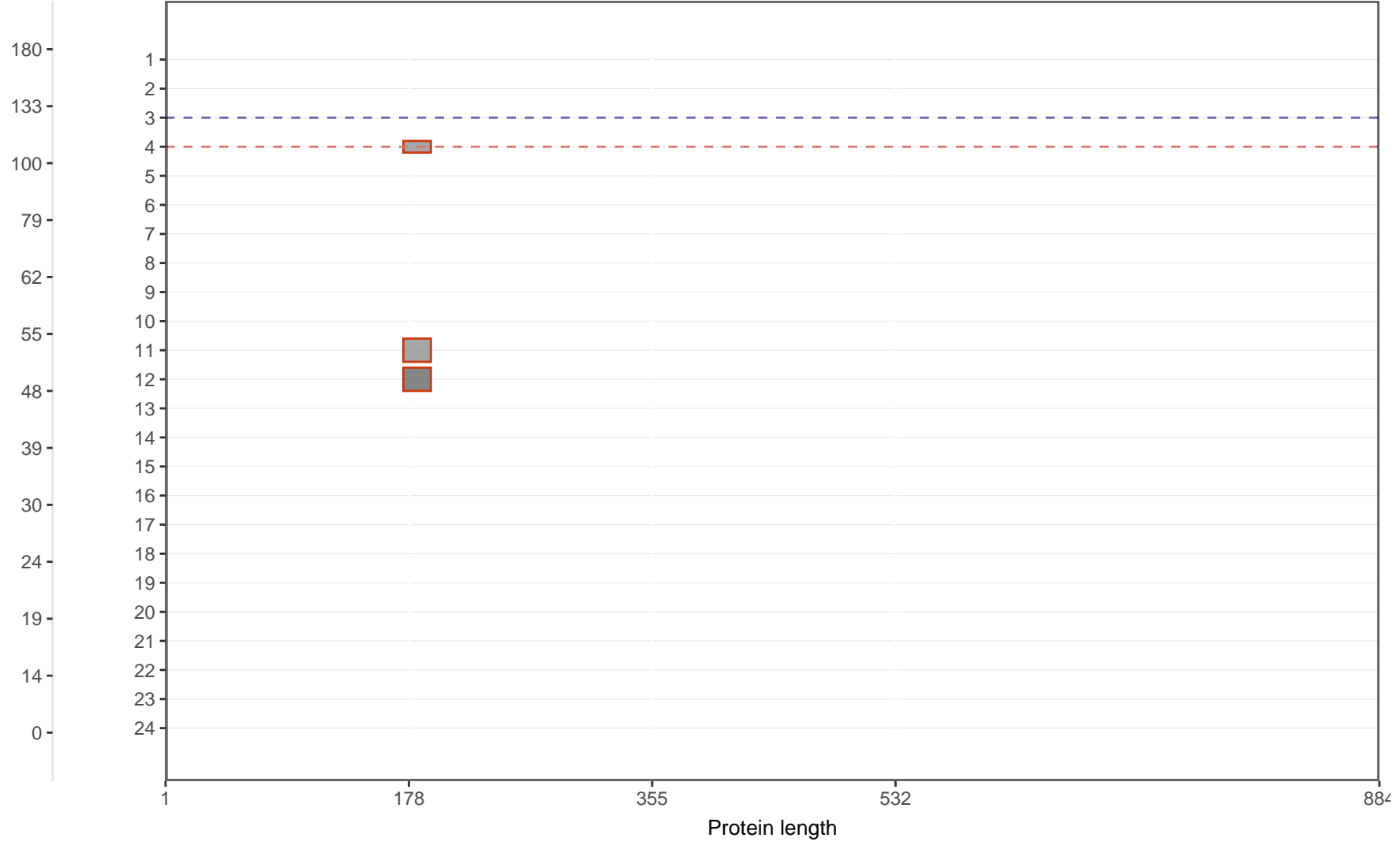
GYQRPVAVQSMYIFKQPGGGEVPHQGNFLYFETKTCGLWLALEEATVNGLWAIPIGSHKNGLVRRFLRDENGVHFDKPSDYNKQKDFVPLEVKAGSLVHHGDLHKGSEFNGSKSRHAYSLHVVDTNGCKWAEDNWRIRRVDPPELYSP

NbL08g21650.1 putative_late_blight_resistance_protein_homolog_R1A-10 [MW = 102.56 kDa]



Molecular weight

Gel Slice



Pfam Description

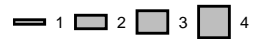
- SP
- Sequon
- TM Domain
- PF00931 NB-ARC domain

Protein sequence:

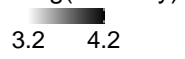
IGVSKLKWIAELFVRAENKRLMVAEYLEELIDRSLHAGKRRANGRMKTGKHLLRLGLRGAQFENFVHLSDDHSSSEKYYORRAMLSLGNHWNFYVPRHWRFFITRTNLSVFTGYSFGVSVMPDFVLGFKLLKLVLEVSEVDYVFGWVWPKLVHLRYAAKINAPSLKLVNLTGRIHNTRRDFHLPLEWVTMSKIRHLDDTGHMRNPLEAENLCIEGPELLNLGKLLALPSSPFLAEILRRTPNKLQVDMKHADWPALDGLLSELETLAKAERNDRV

NbL08g21570.1 nicotinate-nucleotide_pyrophosphorylase_[carboxylating]_chloroplastic [MW = 39.91 kDa]

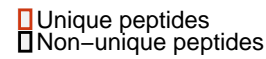
No. of times detected



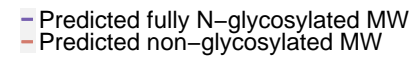
log(intensity)



Values from



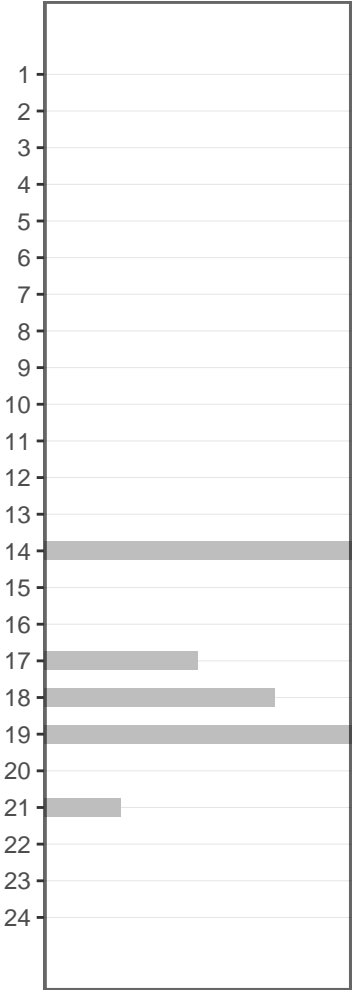
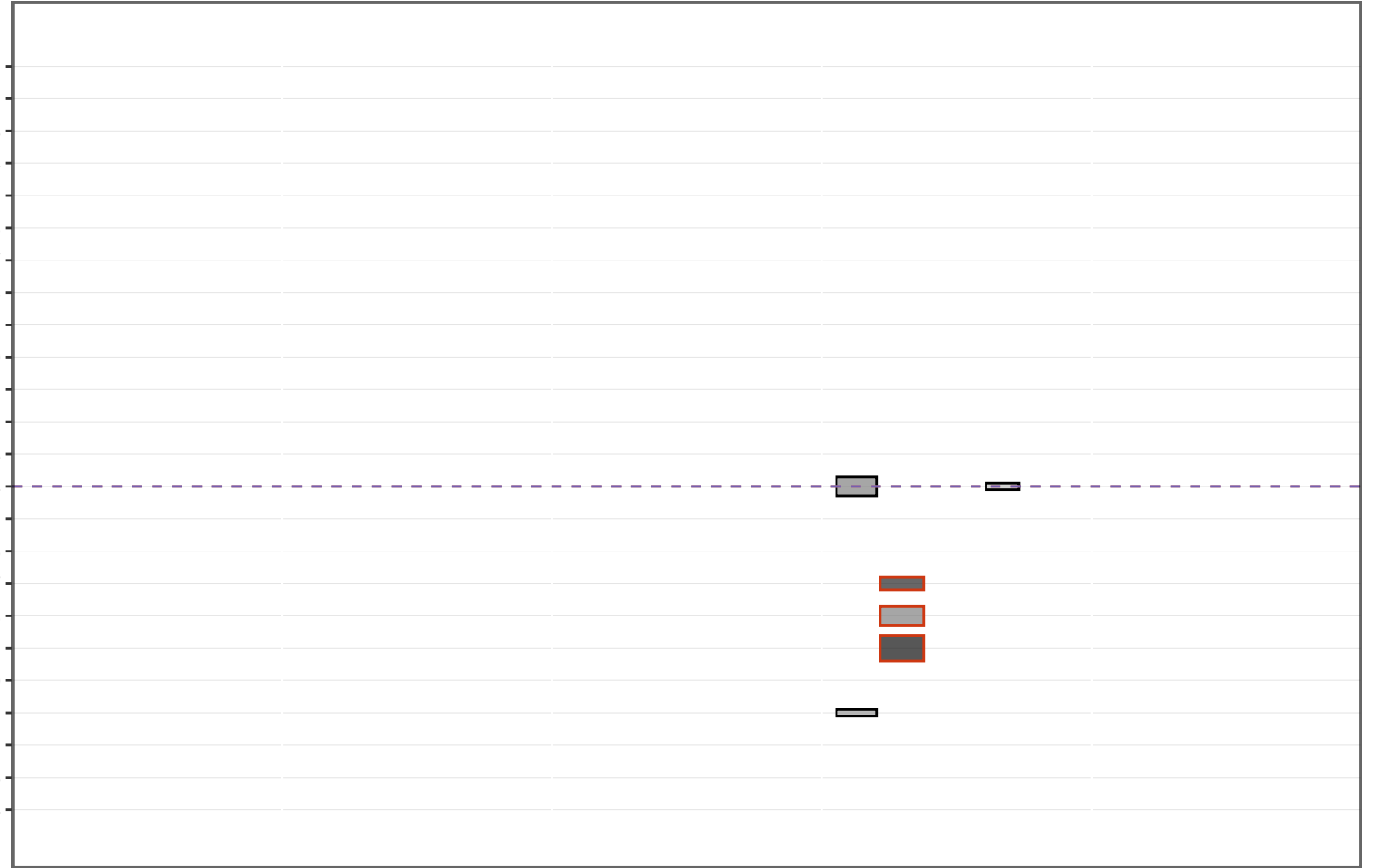
MW indication



Molecular weight



Gel Slice

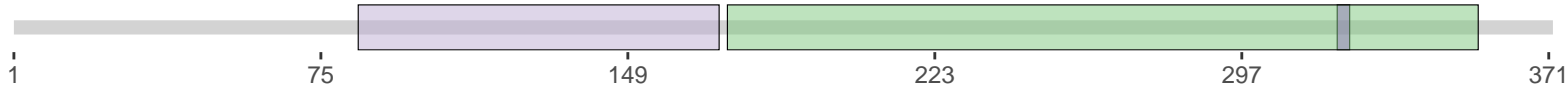


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

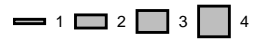
- SP
- Sequon
- TM Domain
- PF01729 Quinolate phosphoribosyl transferase, C-terminal domain
- PF02749 Quinolate phosphoribosyl transferase, N-terminal domain

Protein sequence:

ATLTAKMADAIAHPTALETRKTPAGLRILVDKVAIKGGGKHKHRLGFLDMVMIKDNHSAAGGVSKALNSVDYLEGNKLGMSVEVETRIHAEVREVLVDYASGTRKTLRMLDMMVPLNSGDDVDVSMLKESVDLNGRFETEASGNVLETVHKGGGTGVTVISSGALTHEVKALDISLMDTELAEVGRTRKRA

NbL08g21480.1 multicopper_oxidase_LPR1-like [MW – SP = 62.95 kDa]

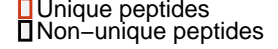
No. of times detected



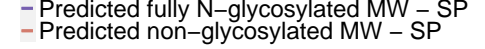
log(intensity)



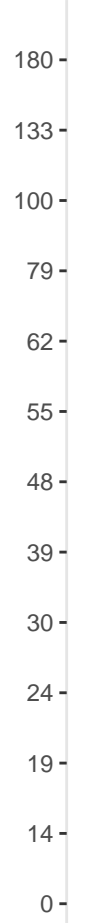
Values from



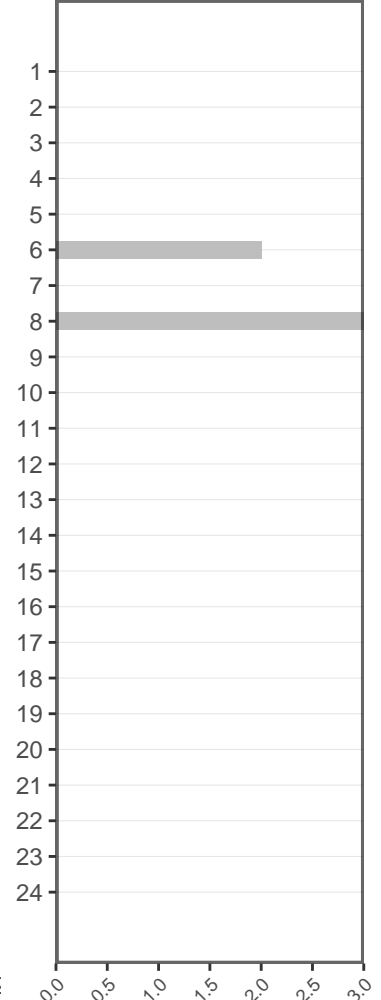
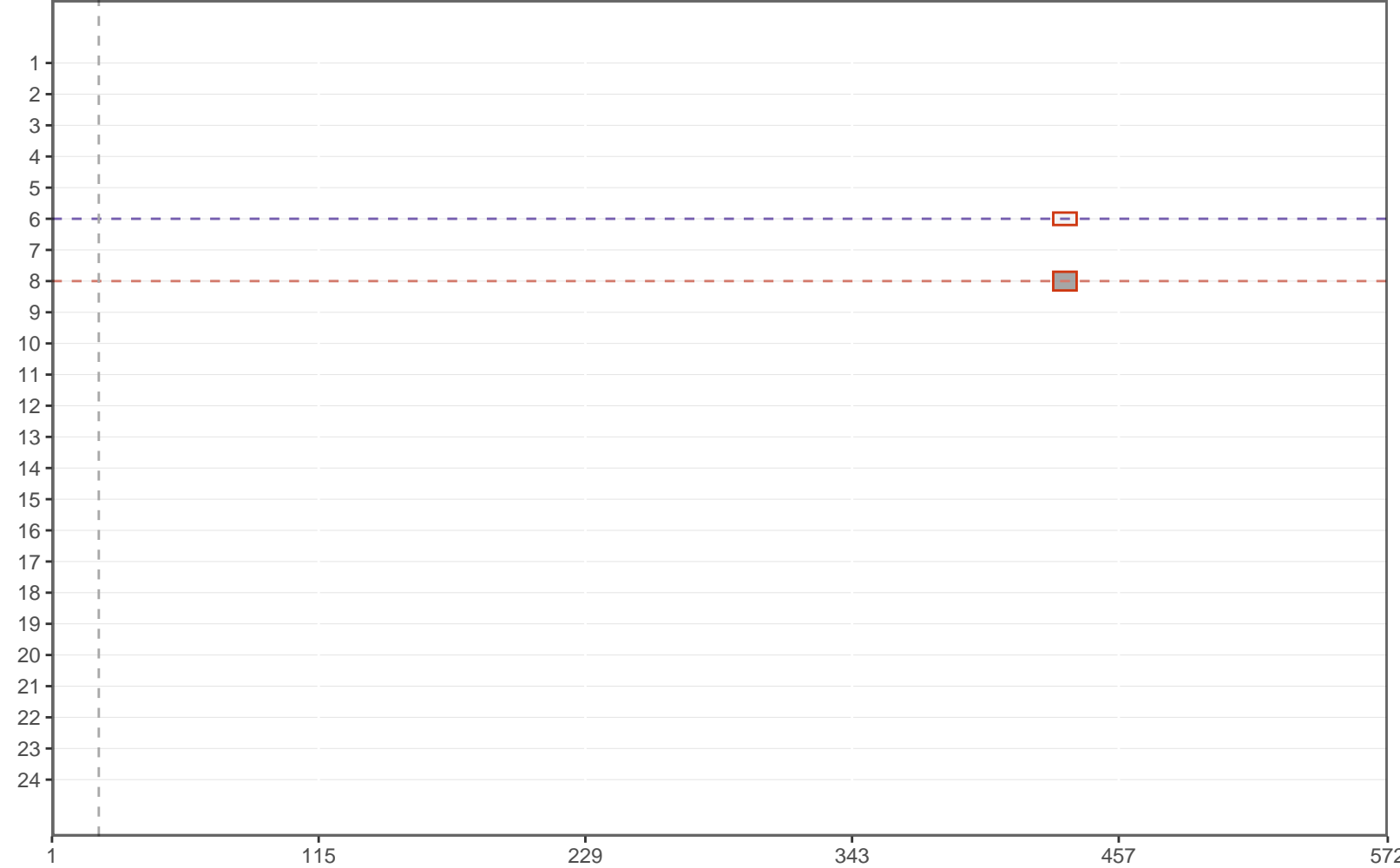
MW indication



Molecular weight



Gel Slice

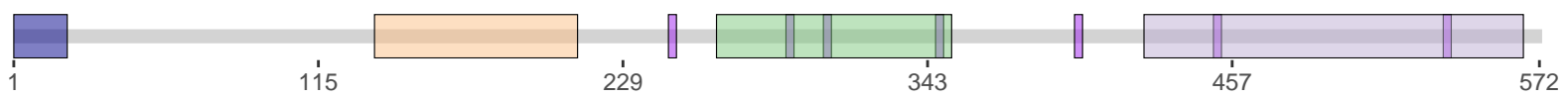


Protein length

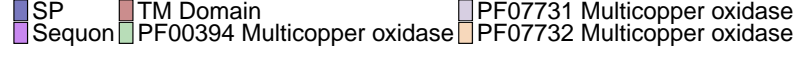


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IGKAWPYTVVRRKKYFRIRINASNAKRFKFFFTNNMTFHHVAGDSAVHERPVELHDLILPSEADIVVDFEKSNSNITLANDAAYPPSGDPPNEANRKYMKFIEFHHVVDTRIPRKLKMKHGGPNSSEASNRVIAFYEVASDIDEPHLYINGKSFSEAPVETPRVGTSEIWNINLTEGNIPLHLGLFVLDQTELINEEFPKAGMMKLNDAKMKKSKYTHGGKTKVFPVHEKGWNNYKMMMPGHVTRILVRFVYHSNASHYVFDATAEPGVYVHGHLDIEDNVMRPLI

NbL08g21420.1 probable_ribose-5-phosphate_isomerase_2 [MW = 28.33 kDa]

No. of times detected



log(intensity)



Values from



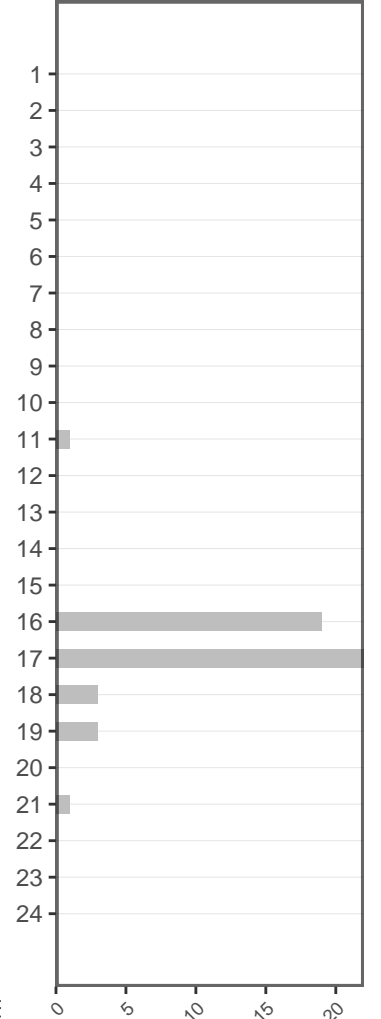
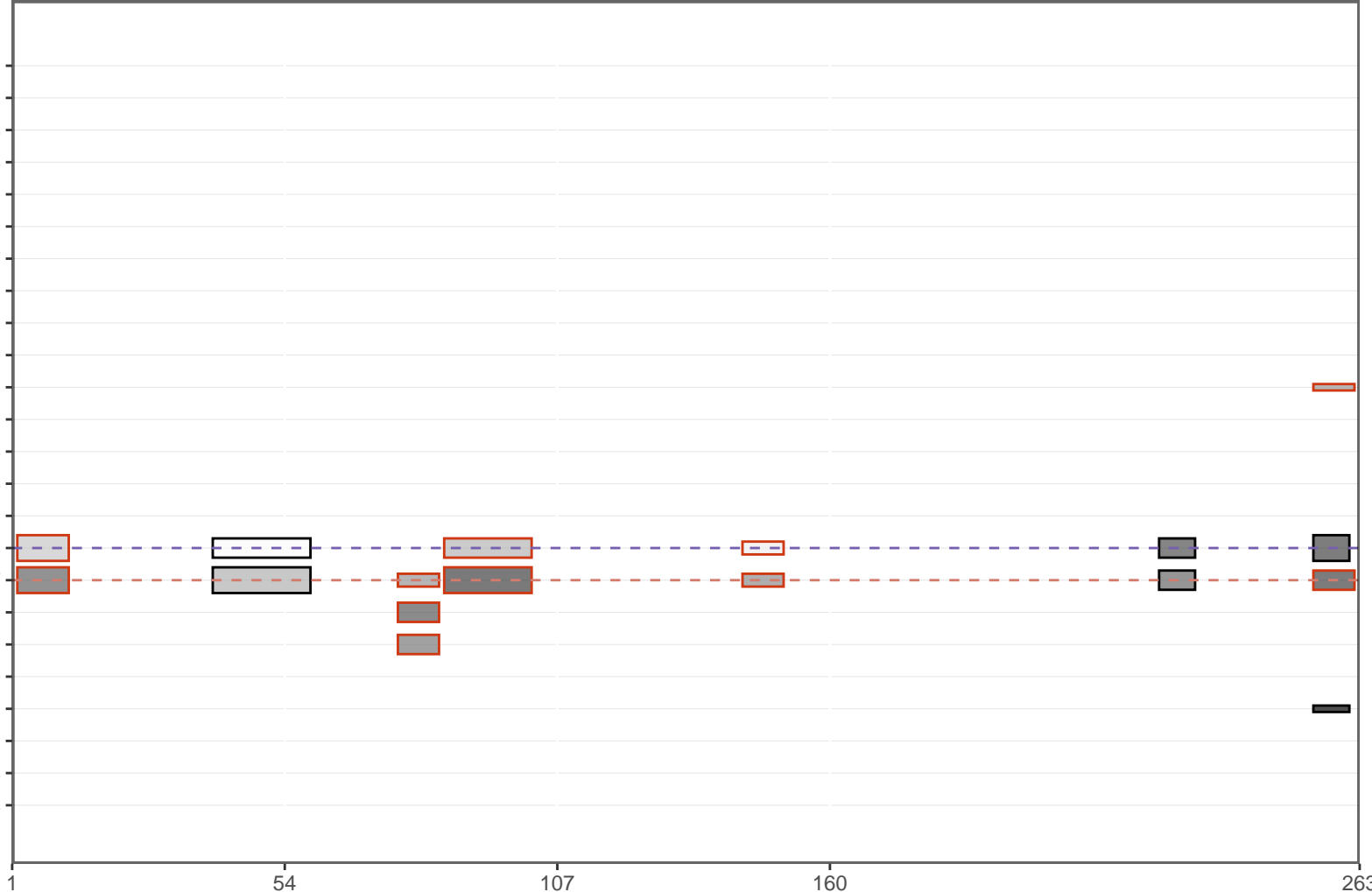
MW indication



Molecular weight



Gel Slice



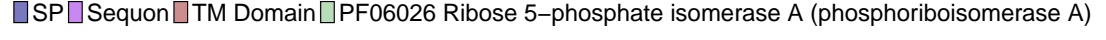
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

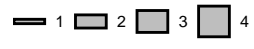


Protein sequence:

MNLVKGKGGSLLEKMMVEASKKFKVHDESKVNYLGGGSLAMPVEIVPFGWFTLKRLEMLFIEAGGVKLRITVGENGEVYVTDNGNYHIDVFKKMDGLKAASDAILRLAGVVEHGMFIDMTFVWAKLGVSVTNKEI

NbL08g21340.1 ATP-dependent_Clp_protease_ATP-binding_subunit_ClpA_homolog_CD4B_chloroplastic [MW = 102.26 kDa]

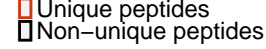
No. of times detected



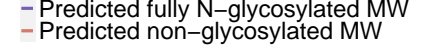
log(intensity)



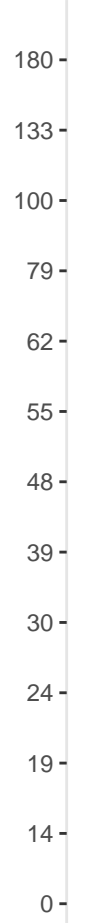
Values from



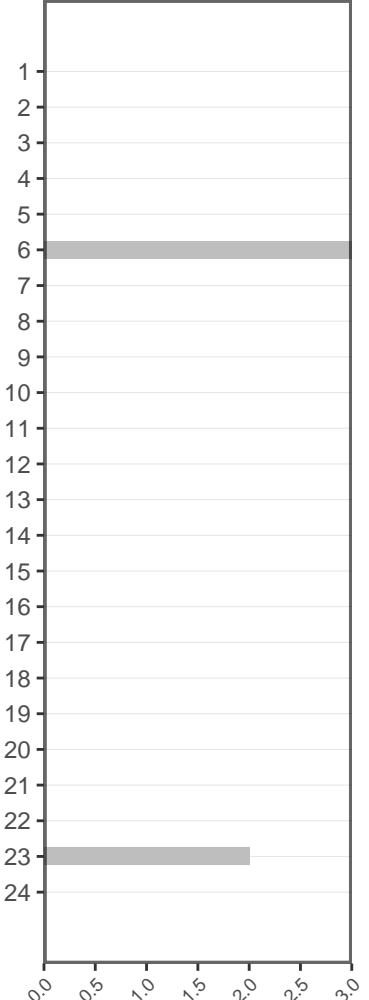
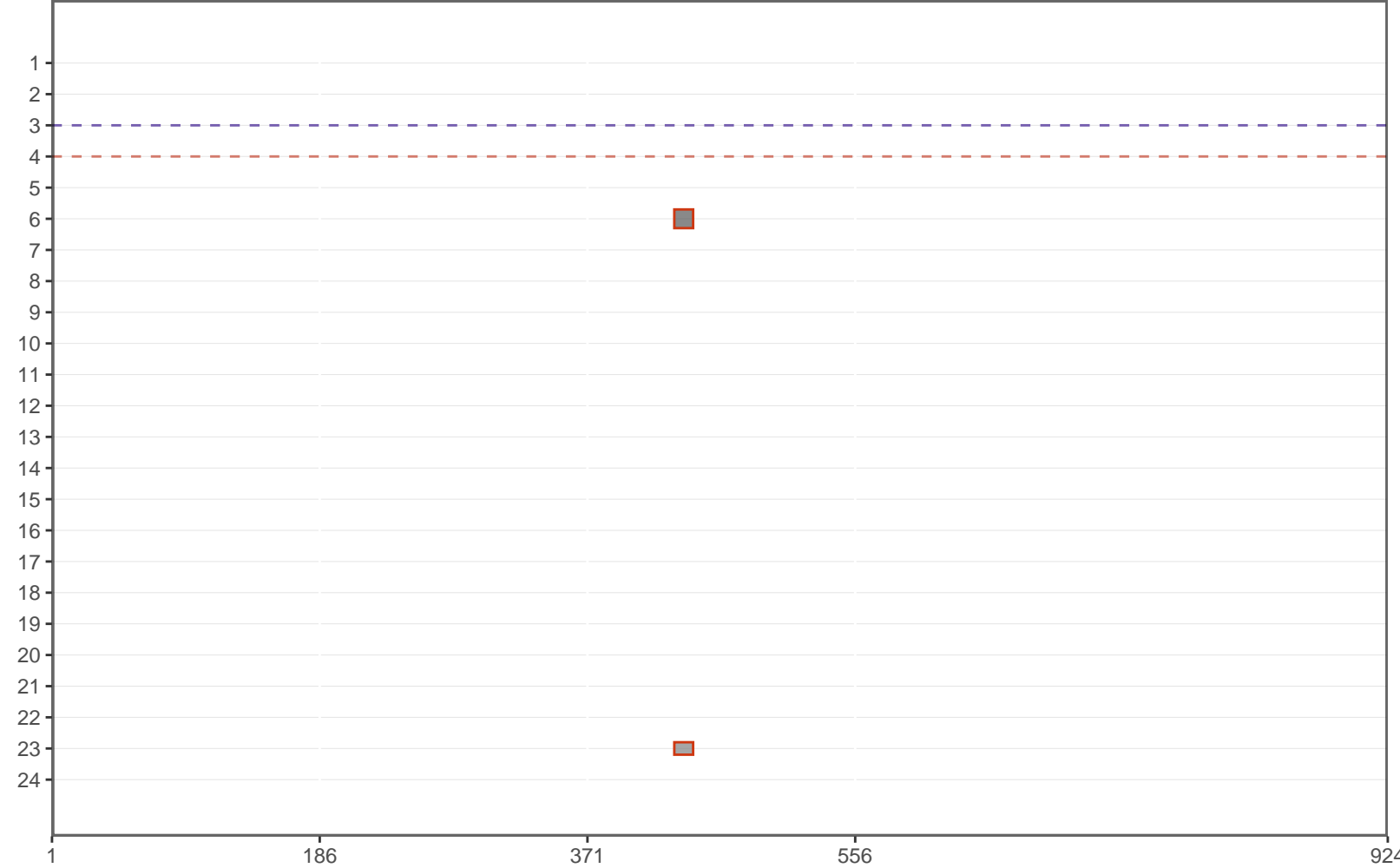
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF00004 ATPase family associated with various cellular activities (AAA)
- PF02861 Clp amino terminal domain, pathogenicity island component
- PF07724 AAA domain (Cdc48 subfamily)
- PF17871 AAA lid domain
- PF10431 C-terminal, D2-small domain, of ClpB protein

Protein sequence:

YERHKLRYTDEALEAAMQLSEVGYSDRFLPKAKIDLIDKAGSRVRLRHAGLPEEAKLEKELRGTKEKNEAVRGGDFEKAGELRDREMDLKAQITLIDKKNKEMKAASETGGTGPLVTEADIQHVSWSWFGIPVEKVSSTDESDDLKIMEETLHTRIGGDGAEVKAISRAIRRARVGLKNPNRPIASFIFSGPTGDKGKELAKLAAYFGSEAMRLDMSEFMERHTVSKLIGSPPGYVGYTEGGQLTEAVRRRPYFVLFDEIEKAHPGVFNMMALQLEDGRLTDSKGRTVK

NbL08g21220.1 uncharacterized_LOC107812854 [MW – SP = 48.81 kDa]

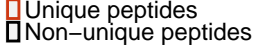
No. of times detected



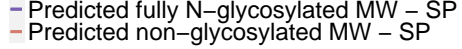
log(intensity)



Values from



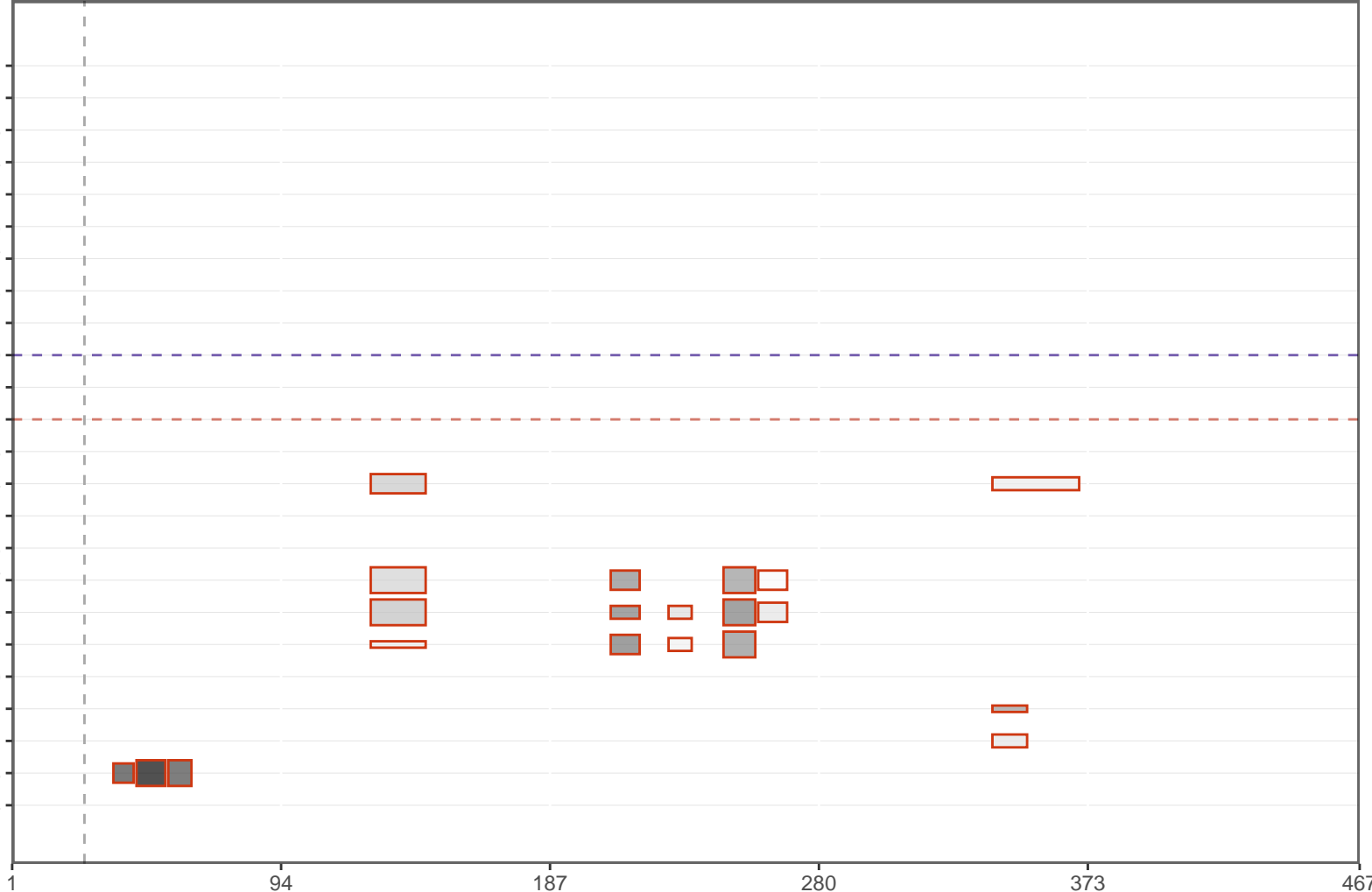
MW indication



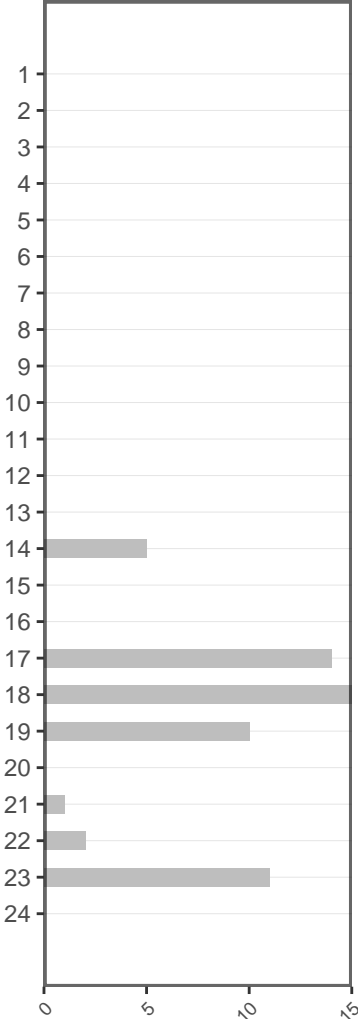
Molecular weight



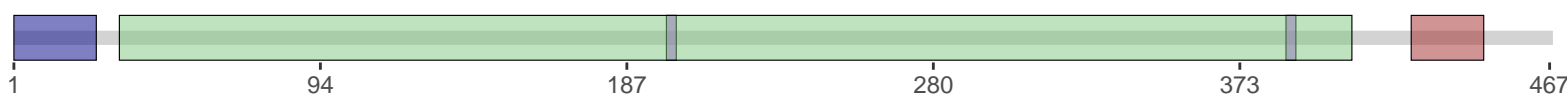
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

⋮CYDETRCKLYKGFQGARRELYLKYTKYIDWDPISVVPKXHLVDYDTWKKPKENSTATVSRHHKQKLVVEGSAEAEANADGHTFKKIVTTPPSGGDVIYVAHQHTGGTGSALHGEDGRIVCSGSPFYEGEKEPNEAGHYVGMSSGYPKRPSPKIKISEGETVFLSNYSAGRHGTGMGLFKYLVAEPKPKNSFLHSTDGTGEVILHNWGVLAVFGIAVLQAAWYQRRNGREEEGYEVLM⋮

NbL08g21110.1 shikimate_O-hydroxycinnamoyltransferase-like [MW = 48.09 kDa]

No. of times detected



log(intensity)



Values from



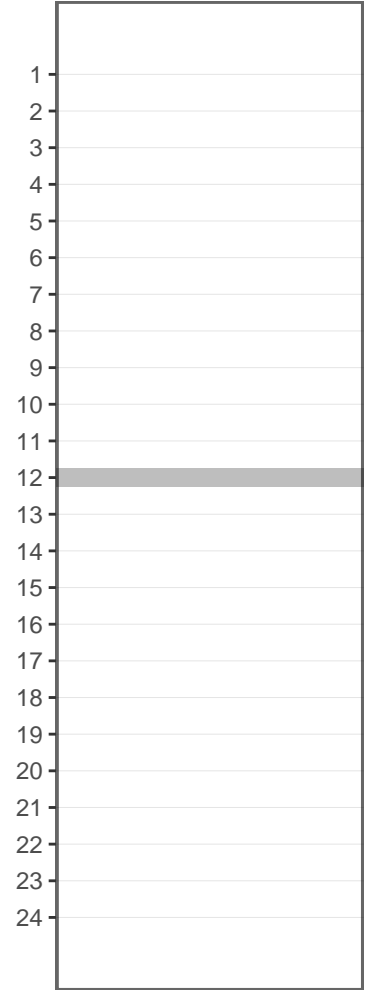
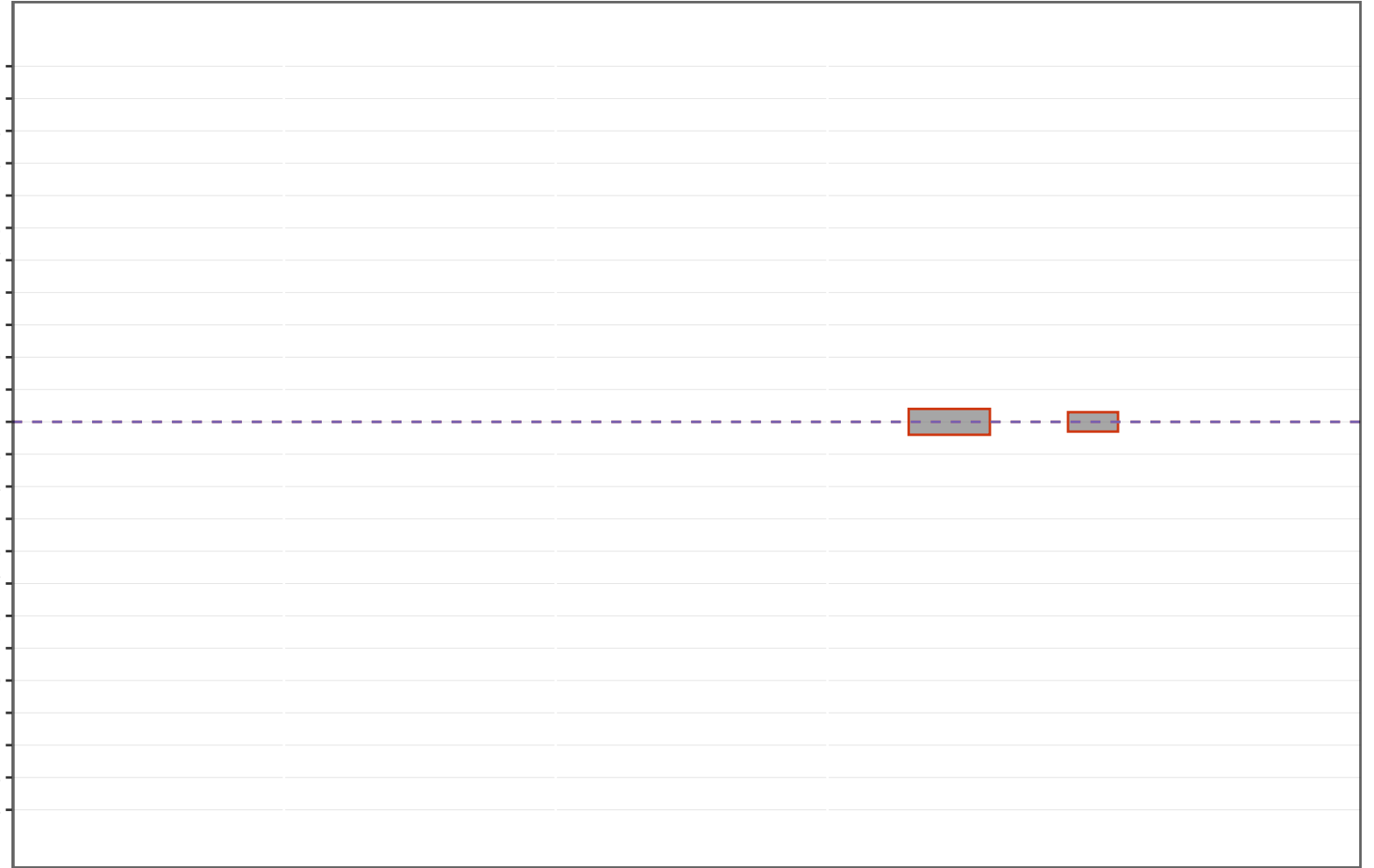
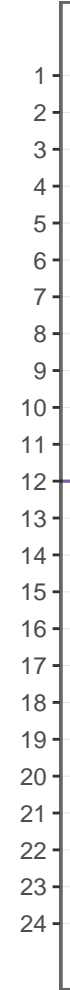
MW indication



Molecular weight



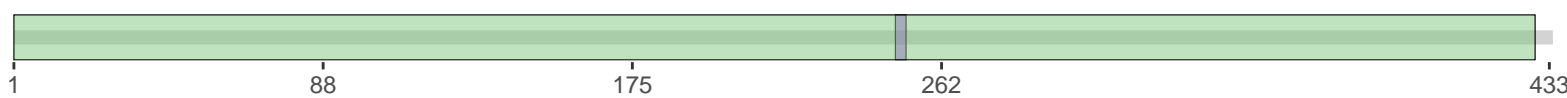
Gel Slice



Peptide counts over 4 repeats

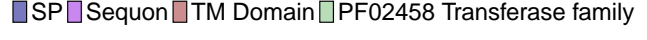


Protein length



Pfam domains

Pfam Description



Protein sequence:

IEYQPPPTLKNAKTEAVPETAVSIFKLRDQIDKAKKSKEDGNTVNYBSYEMLAGHWVRSTGMARGLEEDGSGKYATDGRSRRLPPTLPPGKYNVETATPIAVAGDKLSPKPIWVAASKIHDLARMDNDLRSALDYLLELQPDLTALVRGAHTRFCPNLIGTSWVRLPHDADFQWGRPRFIMGPGGIAVEGLSFLPSPTNDGSL6VAISLQADHMKLFEKLYDF

NbL08g21080.1 40S_ribosomal_protein_S12-like [MW = 14.95 kDa]

No. of times detected



log(intensity)



Values from



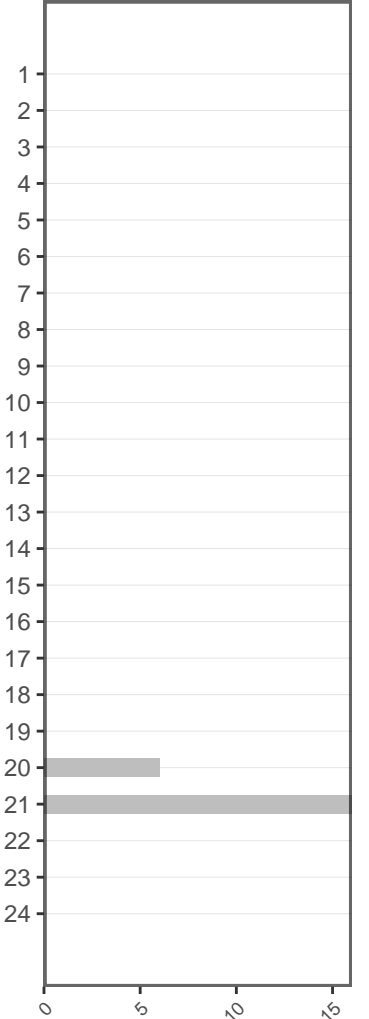
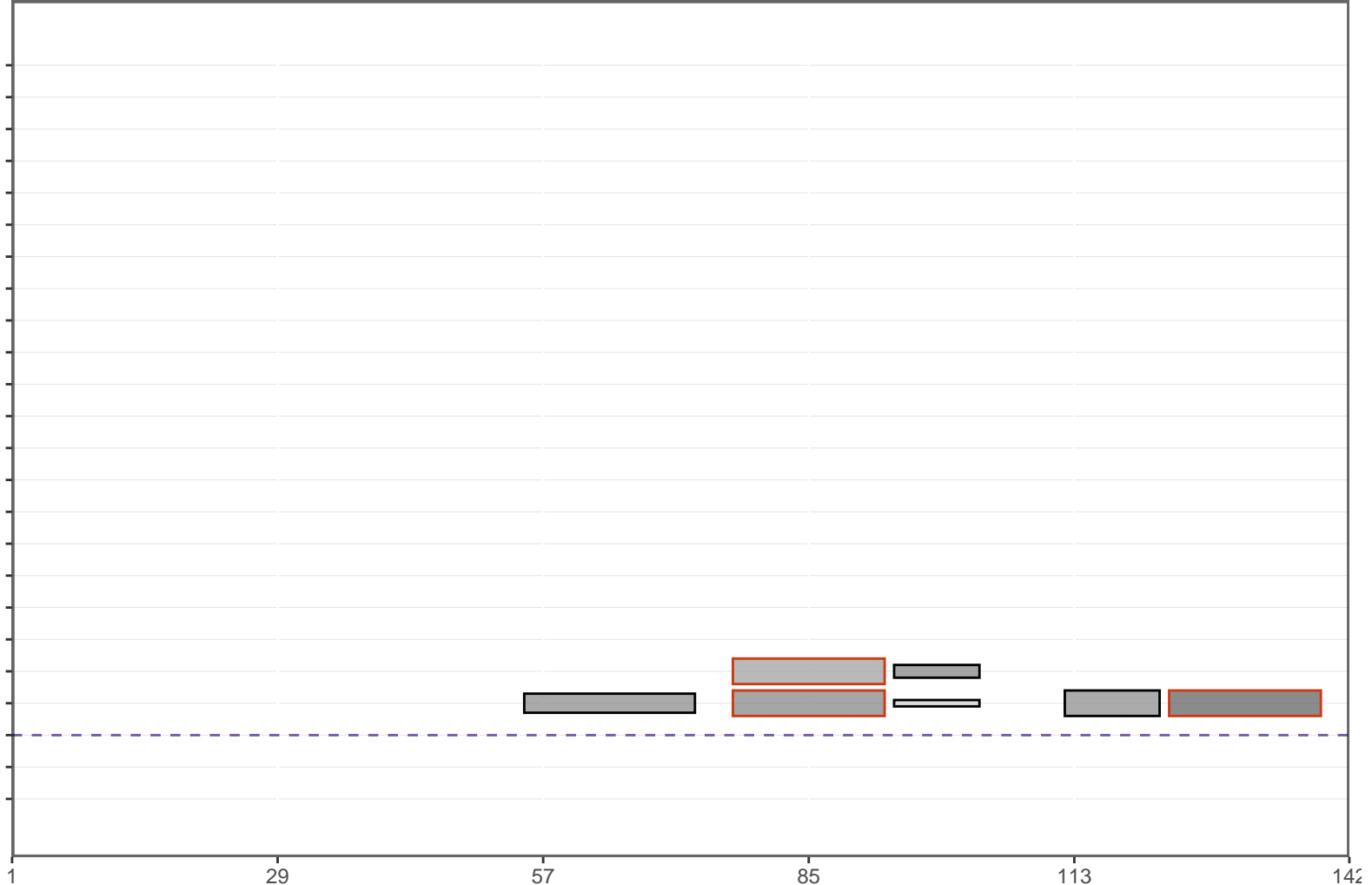
MW indication



Molecular weight

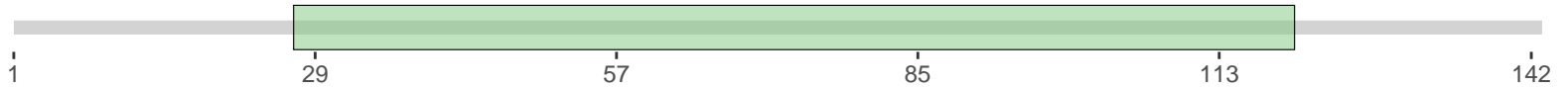


Gel Slice



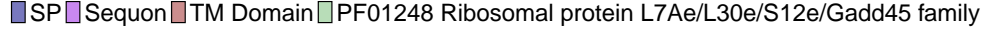
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LCVLAEDCCDDPDYKWLKALGADHNNLFTVPSAKTLGEWAGLGNIDEGKARKYVGGGGVVKDFGEEETGLHIVGEYKSHI

NbL08g20950.1 stress-response_A/B_barrel_domain-containing_protein_UP3 [MW = 34.43 kDa]

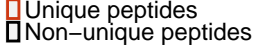
No. of times detected



log(intensity)



Values from



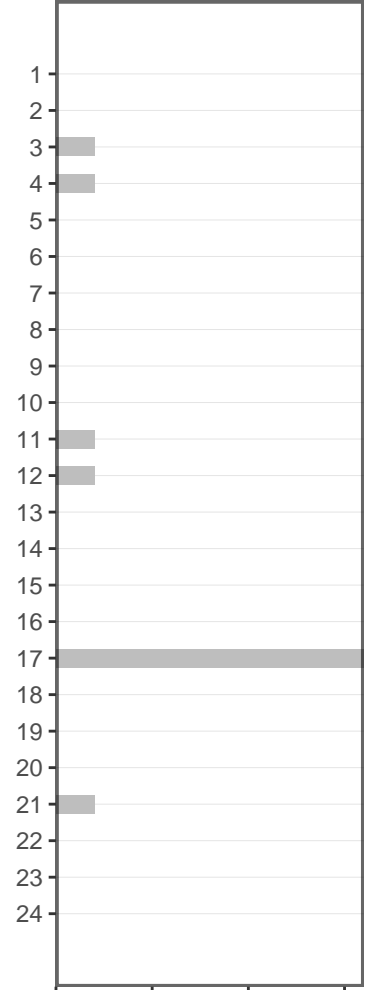
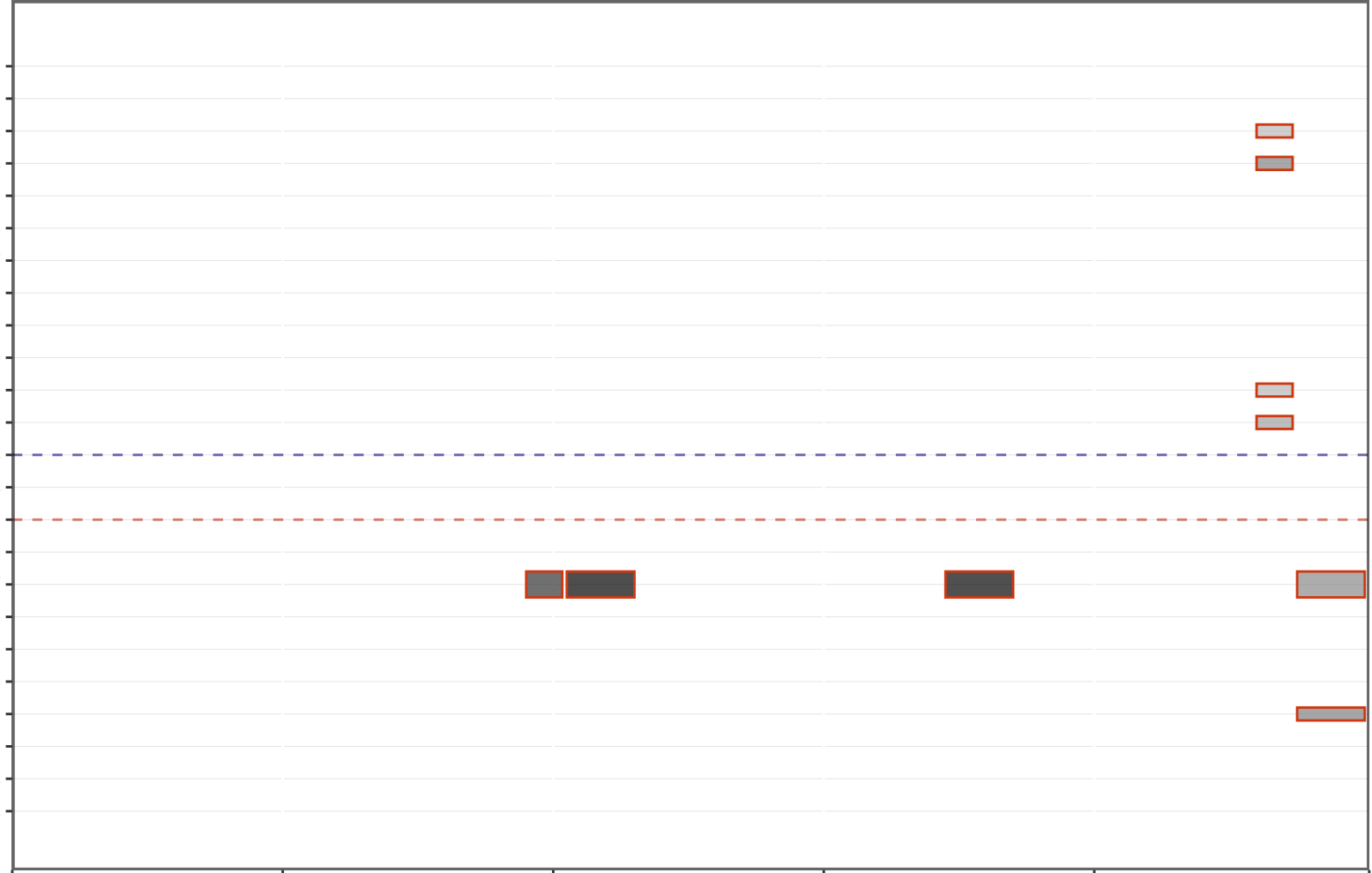
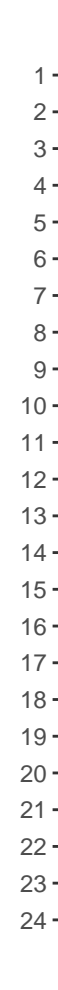
MW indication



Molecular weight



Gel Slice



Protein length



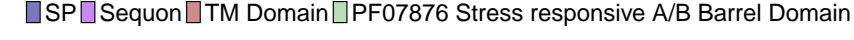
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

TYMRFQTKEDLSKFYENQFYGVLRDHALPYGHEINADFESEVEDDLPIFRKGEFFNYGVLELLLLAFVKSLLDGPMEALLVLSKLTFFPSLIVQATLGSINISVEYTHGIVIRFRSSEAFQMFINSSEYNTWRSKFQIPVQKHVSVHFSVDVPGTELM

NbL08g20940.1 thaumatin-like_protein [MW – SP = 13.65 kDa]

No. of times detected



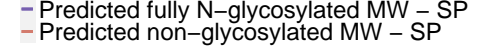
log(intensity)



Values from



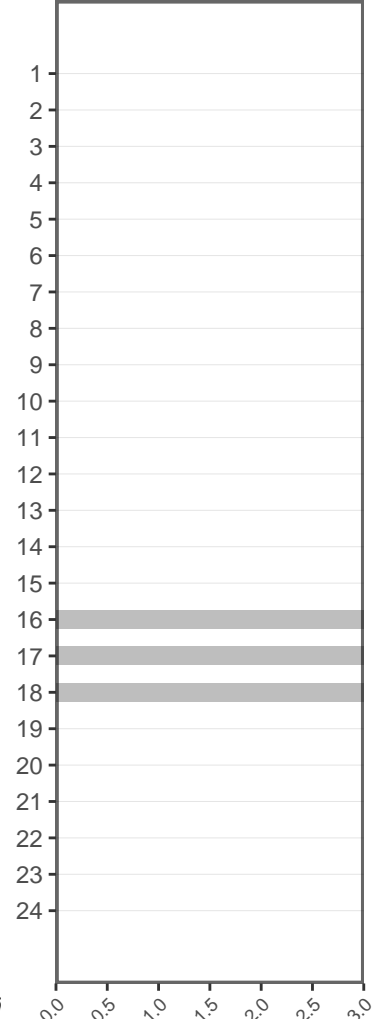
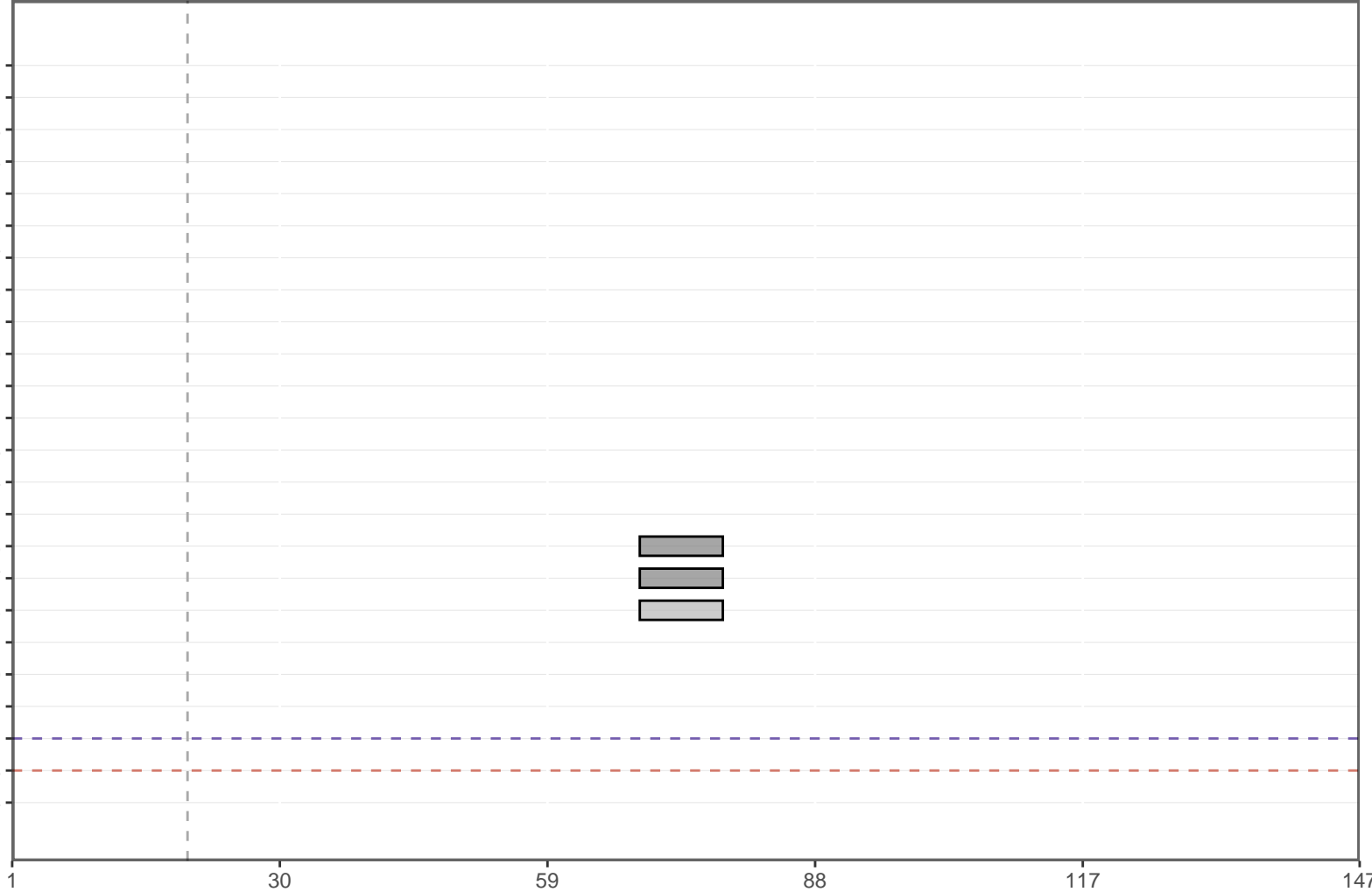
MW indication



Molecular weight



Gel Slice

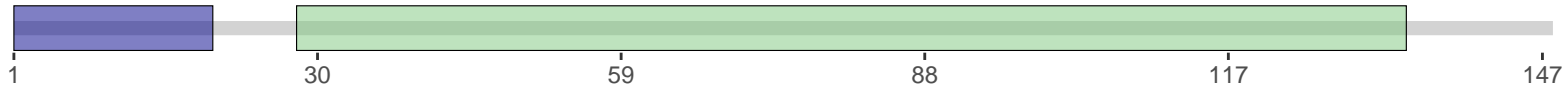


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ITKRIVSRITCNCFDASGRGGDDTGDGNGVLEGGAFGRPTNPNTLAEYSLSKGFNLDFFDISLVDGDFNVPMEFSPGTVLLRGAALPTP*

NbL08g20930.1 pathogenesis-related_protein_R_minor_form [MW – SP = 21.66 kDa]

No. of times detected



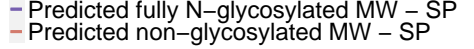
log(intensity)



Values from



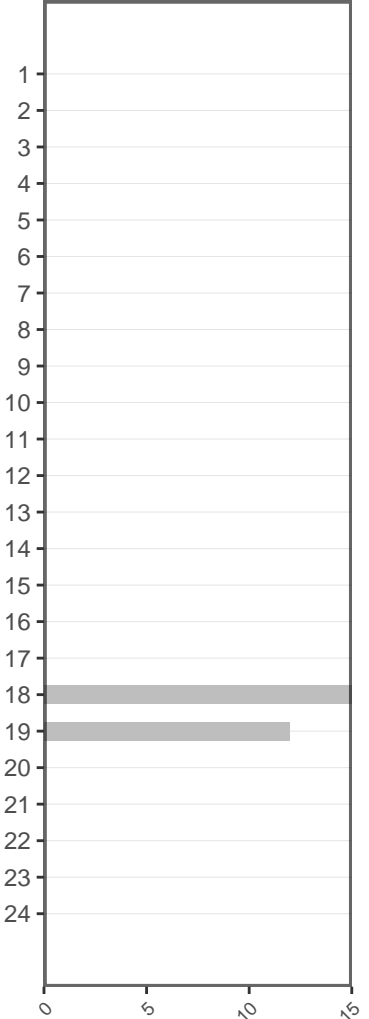
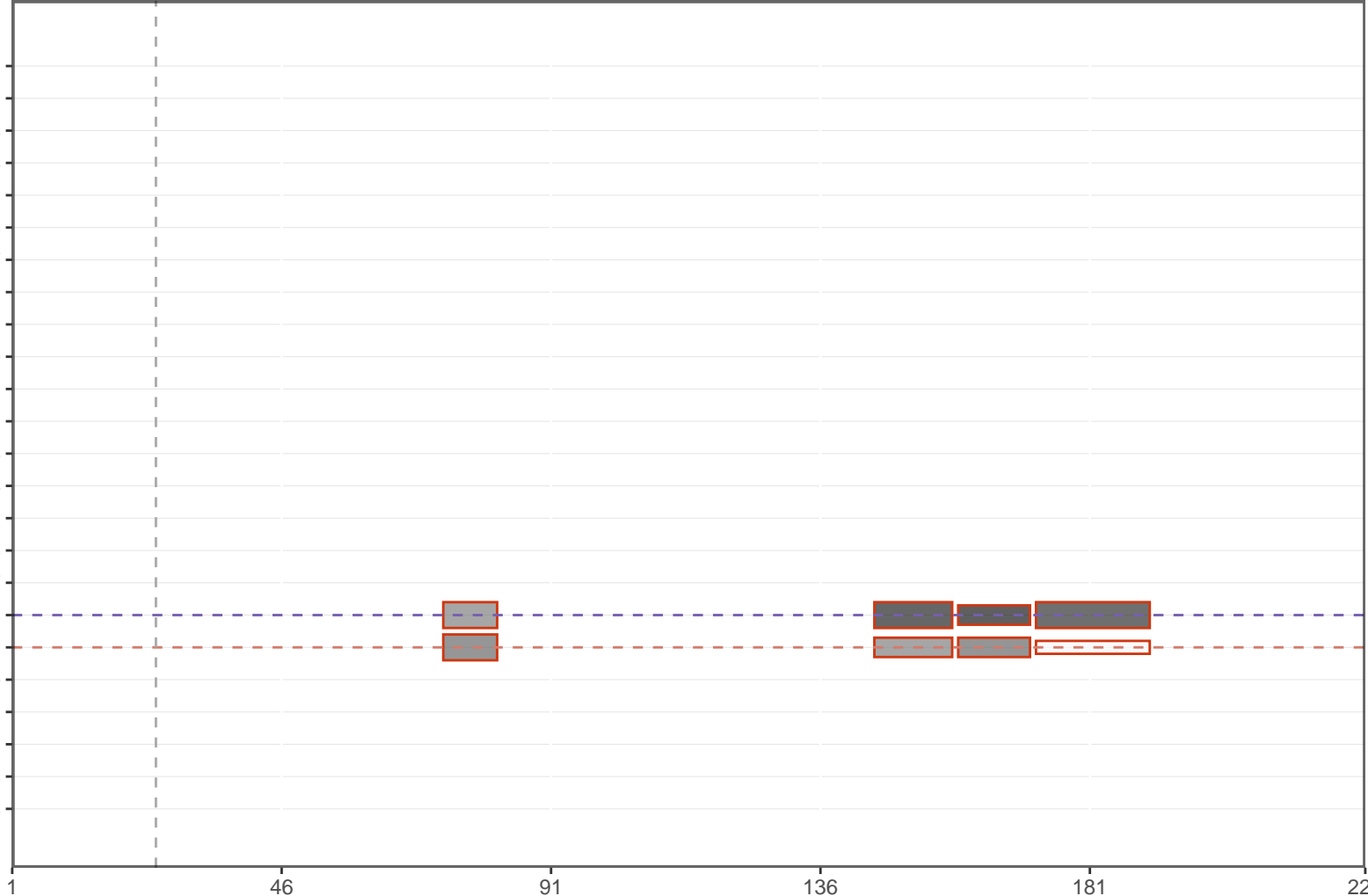
MW indication



Molecular weight

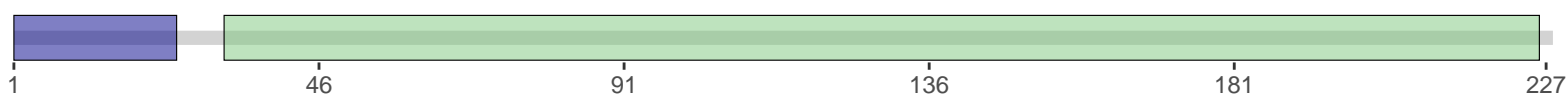


Gel Slice



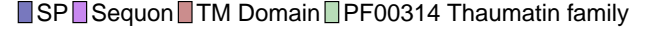
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GIKPPNTLAEFALNGPNDGDFVDSILVDGNIPIEMFSPITNGGCRNLKGAAPINEGGPAQKTFGGGNNPCTVKITNEYCGTNGPGCGPTLDRFFKRGPDAYSYPGGDPTLSFTGPGGTVRIVFQPI

NbL08g20860.1 octanoyltransferase-like [MW = 26.43 kDa]

No. of times detected



log(intensity)



Values from



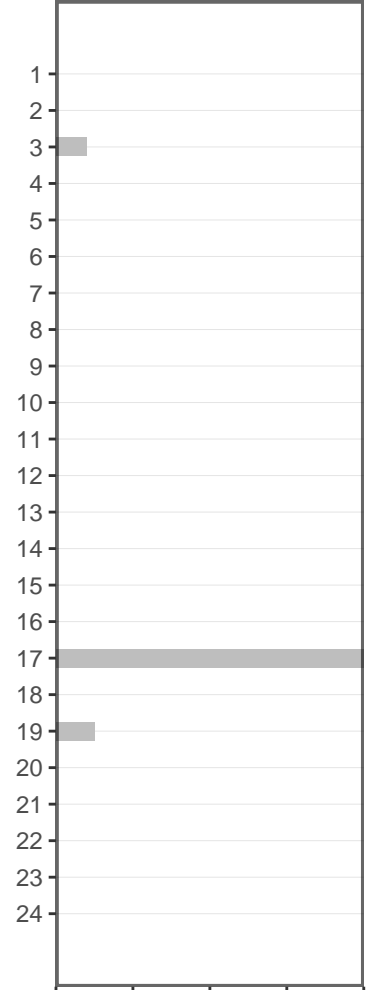
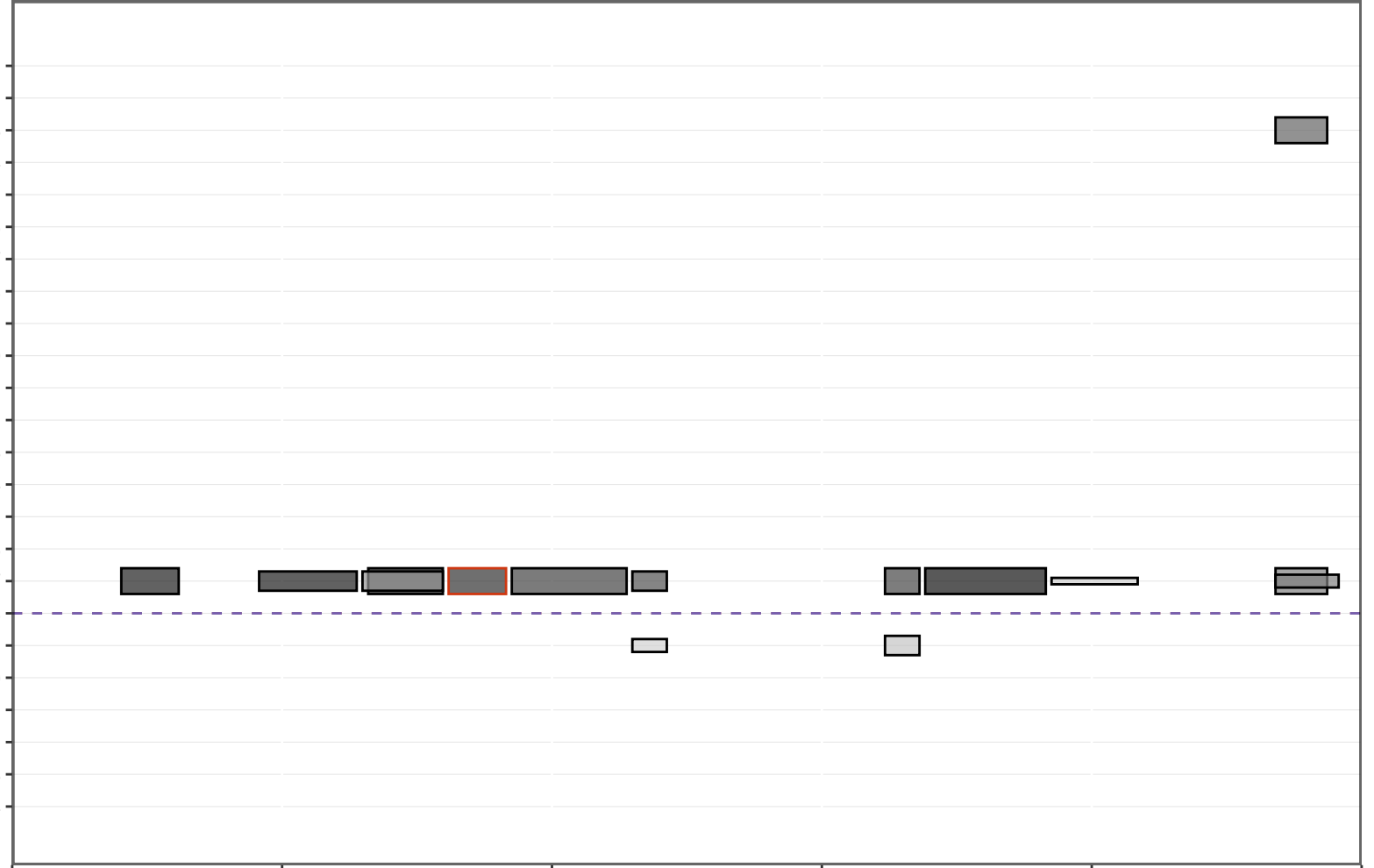
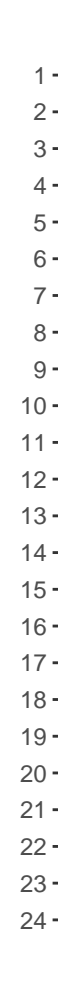
MW indication



Molecular weight

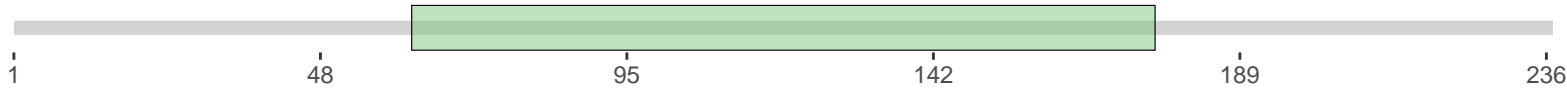


Gel Slice



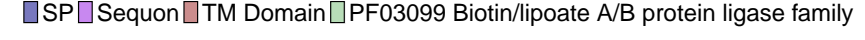
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PVLSLRDGLGARKVKEKLEETMELASIGYKAGVSKRGETGVWVEDRKGIGAGVRSSTSHGLAFNMDPOLNYFKHVPQGIADKDVTSLKAEADVLPKAEVIEIQIAGFVRFYDYNILKDKGVL*

NbL08g20690.1 ATP_synthase_delta_chain_chloroplastic-like [MW = 26.79 kDa]

No. of times detected



log(intensity)



Values from



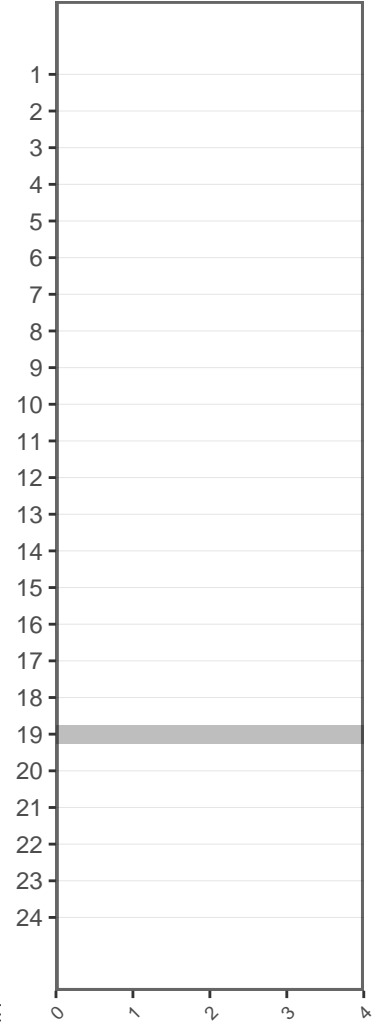
MW indication



Molecular weight

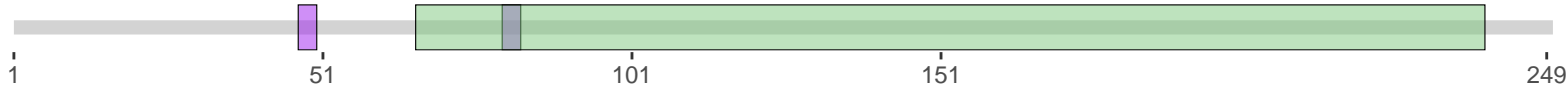


Gel Slice



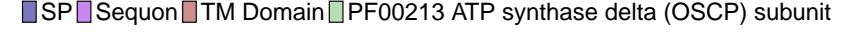
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PVIGEEKRELVDENSSSSGIPNFANFLNLDMKRVELKEVKEFEKVVNTTDTLAVVTSVVKLESDHLAGAKGVQRLTGSKNVRIKTAIDELVAGFTIRYGNSSGKIDMSVVKQLEDNAAGLEIGDQLAV

NbL08g20660.1 protein_tumorous_imaginal_discs_mitochondrial [MW = 32.85 kDa]

No. of times detected



log(intensity)



Values from



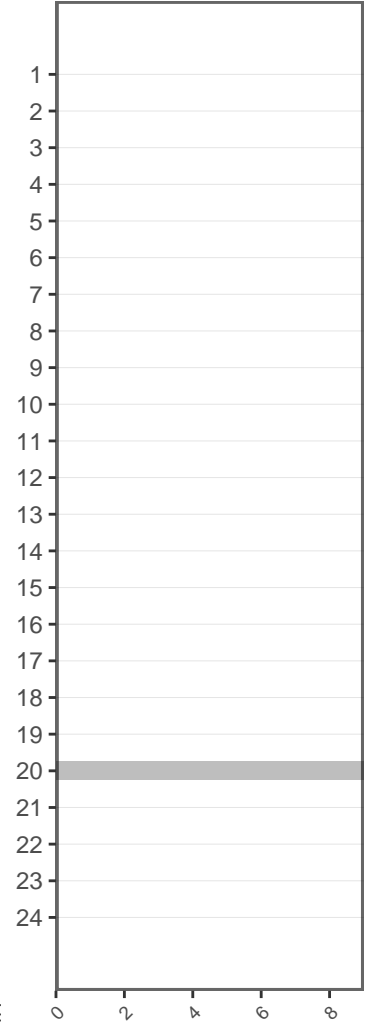
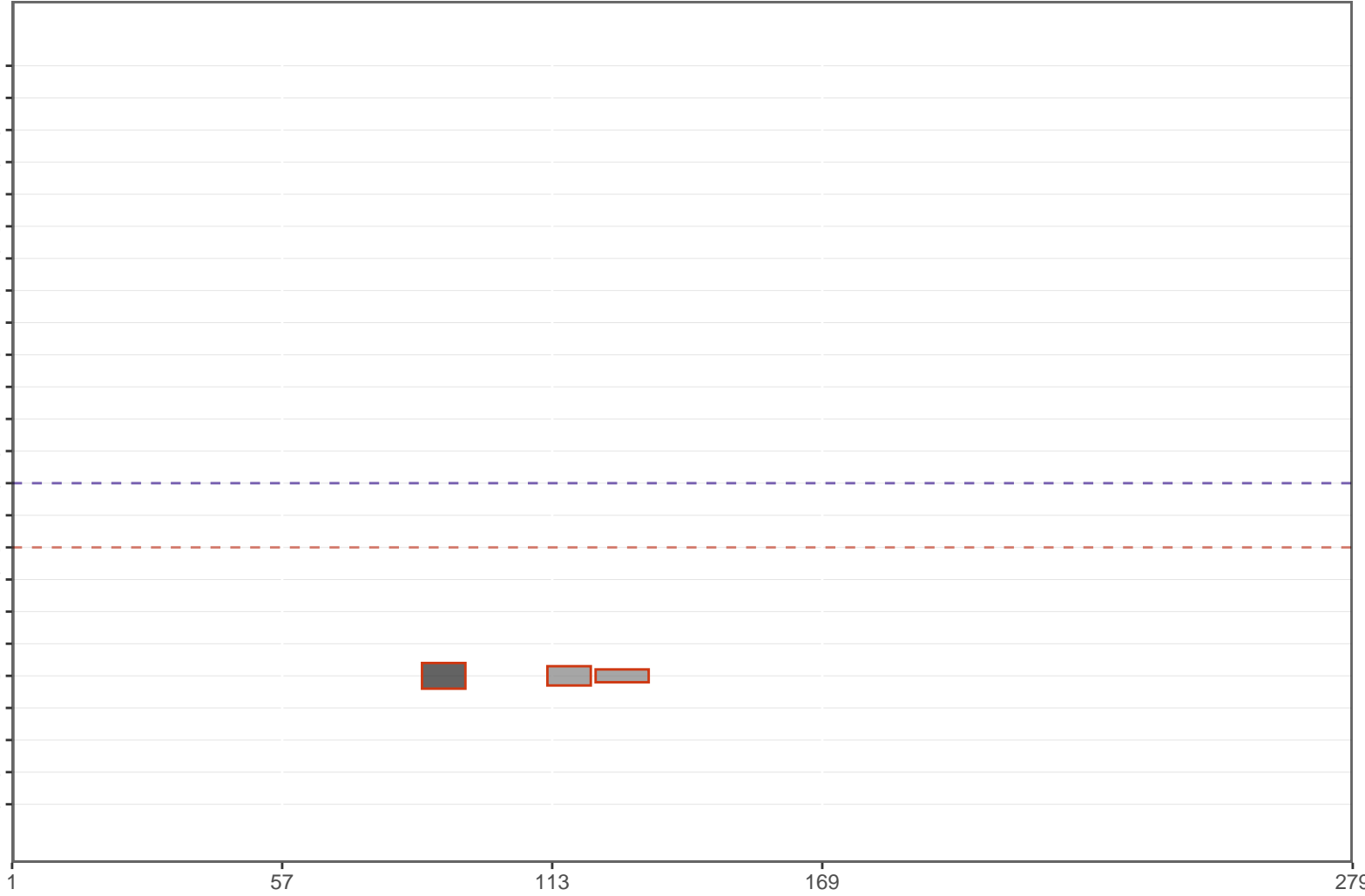
MW indication



Molecular weight

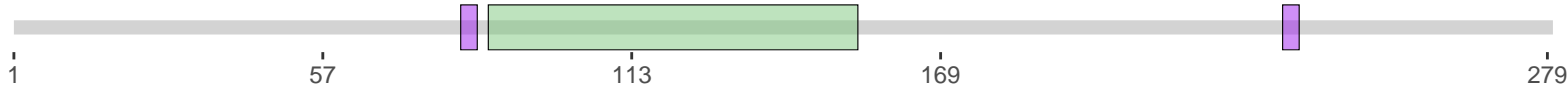


Gel Slice



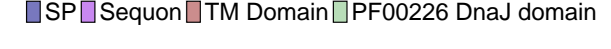
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IEGETAEARFKIQDAAVYELLIDEDERKKYDANRNPNPKASEAWMEVLRKKRKAFFDRGDMAAAWAEQGGLELNKVRRLARSGKMDPDEERRIAEKKASLENFNFLKRIHTLVLRKRDMRRKAEKKKKVISMLAAEGLLEEEEDDKNL

NbL08g20630.1 probable_glucan_13-beta-glucosidase_A [MW = 36.26 kDa]

No. of times detected



log(intensity)



Values from



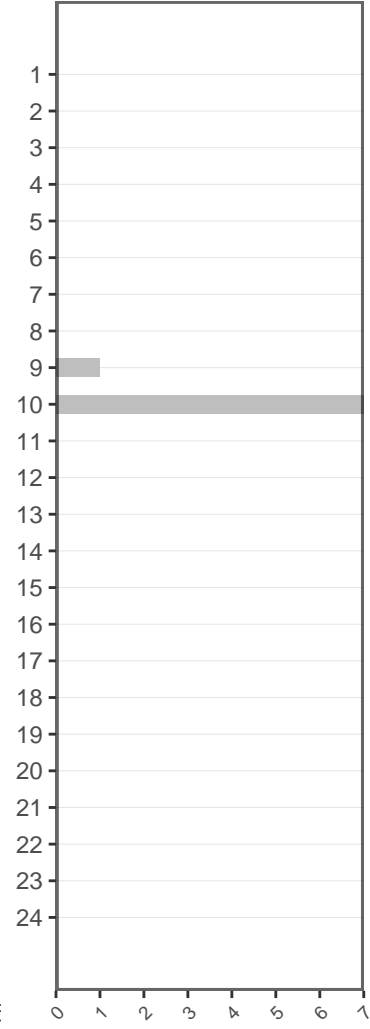
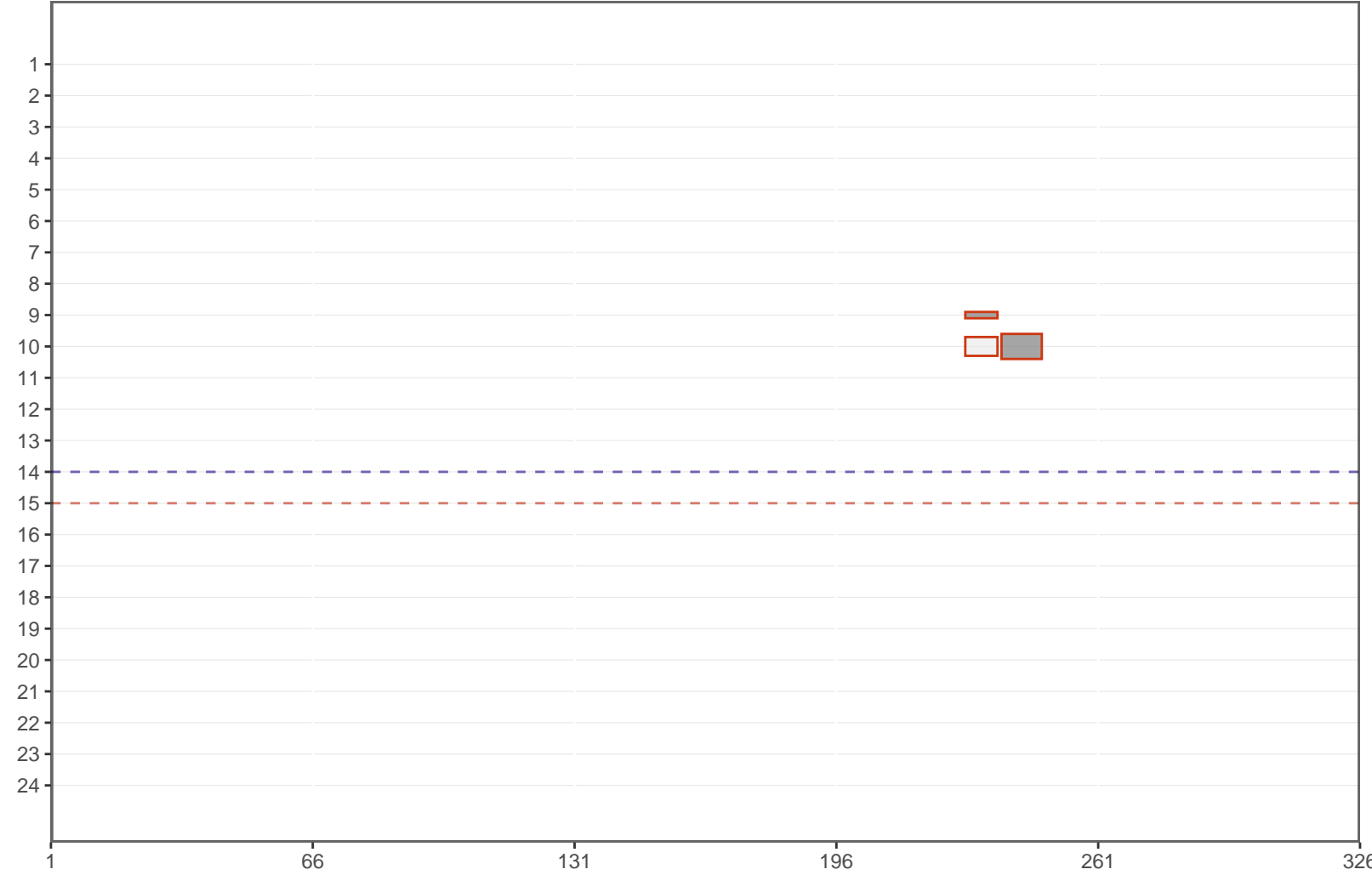
MW indication



Molecular weight



Gel Slice



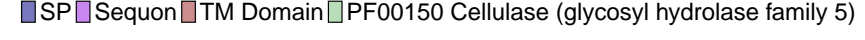
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

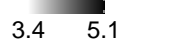
ISDNPGRVRIKASNGFFLQVWTEELVTDNSGNGWSDDDPFRVFMGTSGRLEGEFQITNGYGPMAQVMREHWKTFIVEEDPKFIASNGLNARIPRPGVWIASDPTPKPKPVGGSLHALDNAFFWAKYGLKVIDLHAAPGSGNPNWEHSANRDGTIEWQLMTTFNRLLEG

NbL08g20540.1 7-deoxyloganetin_glycosyltransferase-like [MW = 54.34 kDa]

No. of times detected



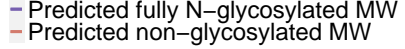
log(intensity)



Values from



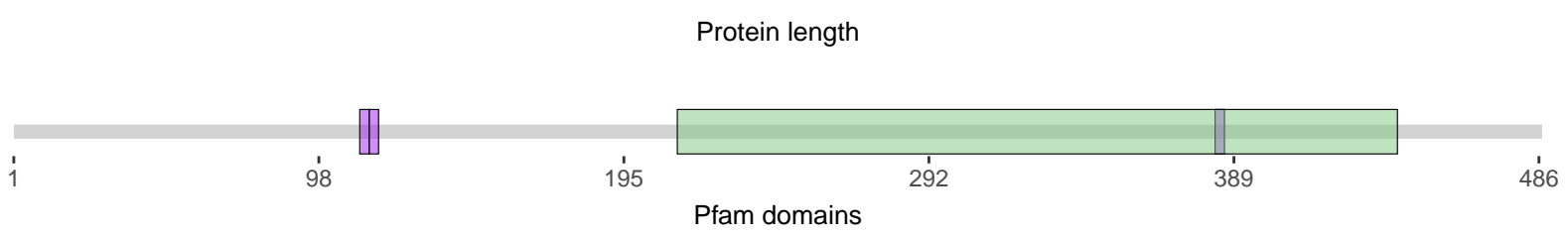
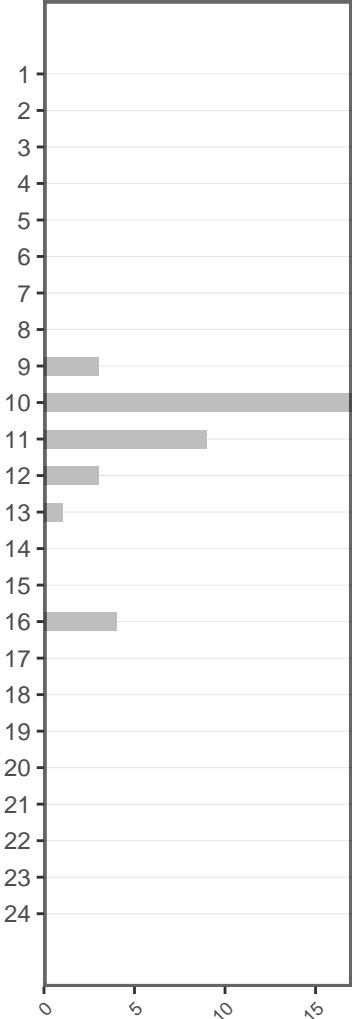
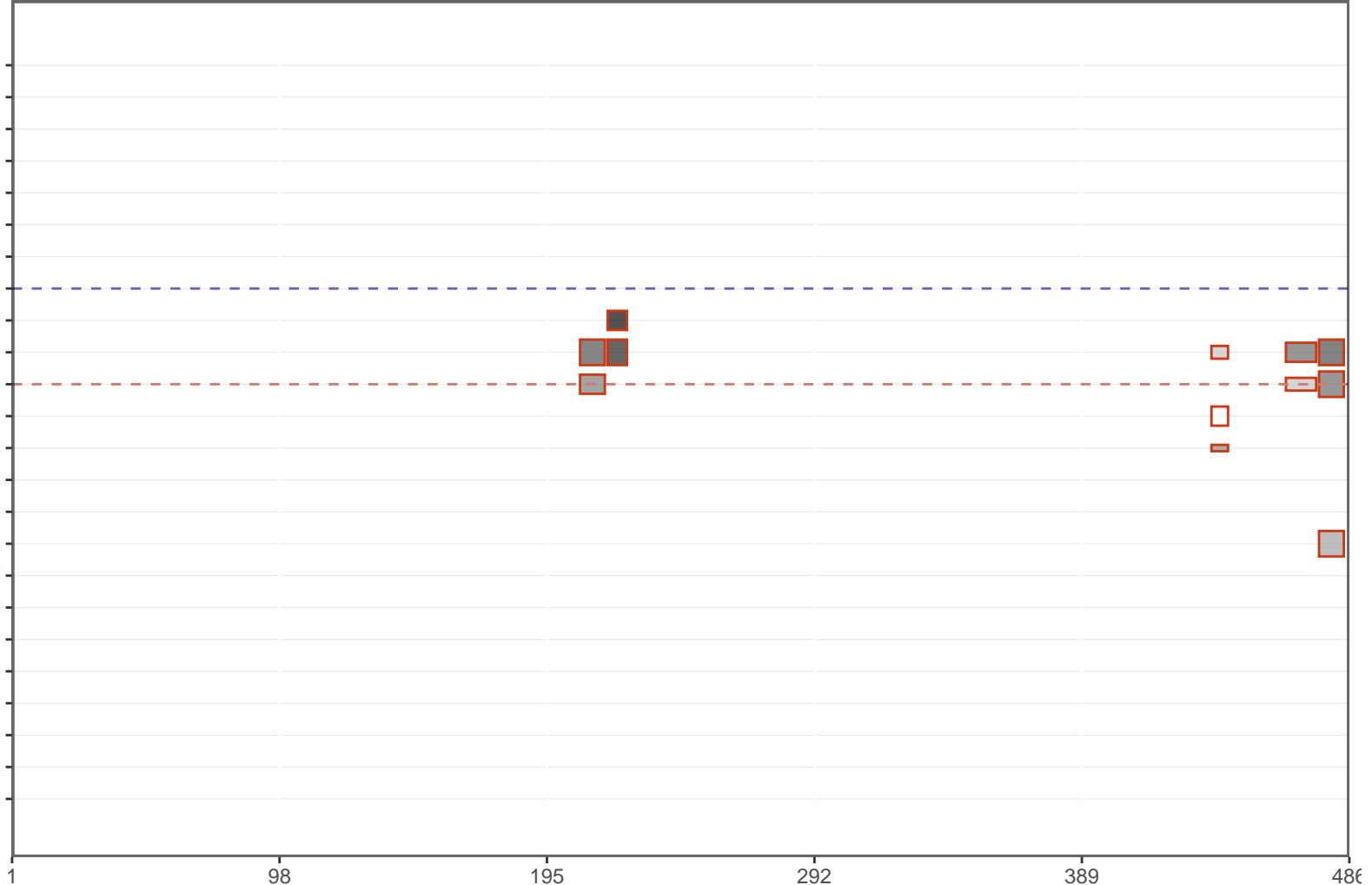
MW indication



Molecular weight



Gel Slice



Pfam Description



Protein sequence:

ILNFTETLEAVLEFLRNMLPPVYKGPLHFLVQHADDENLKLRSLLWKEEPEQIQWLDTKKFNSSVYVNFQGFVMTPTNQLIEFAWGLANSQGTFLWIRPDVSGDASLPPFVEETKTKRGMASVGSQDEVLKPAAGGLFTHSGVWNTLEISGSSVPMQVPPFFAEQGTNGVDFVTRWDGIMEIDGVKRDVEVGLVRELVMGEGKMKKKKAMEWKELAESAKEHSGLEYVNEKVVNDLLSKKH

NbL08g20530.1 14-3-3-like_protein_B [MW = 28.77 kDa]

No. of times detected



log(intensity)



Values from



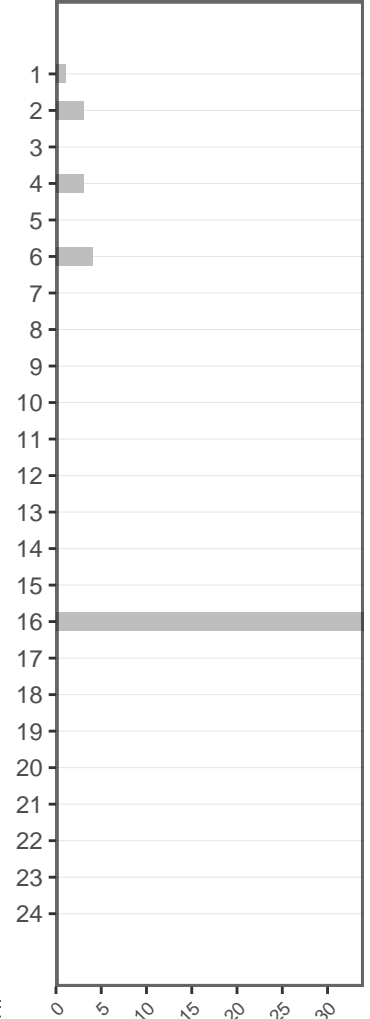
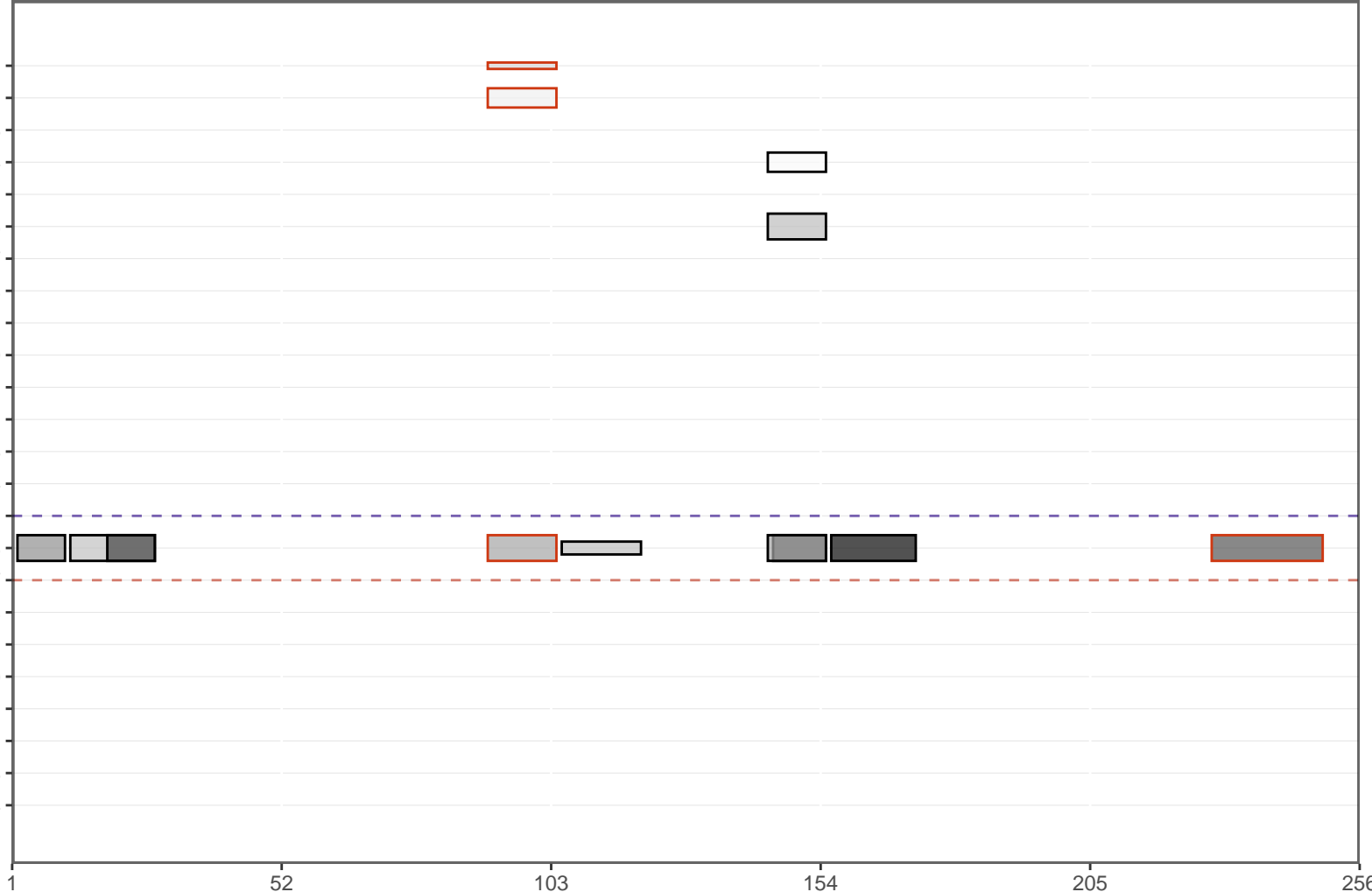
MW indication



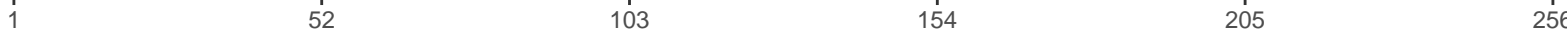
Molecular weight



Gel Slice

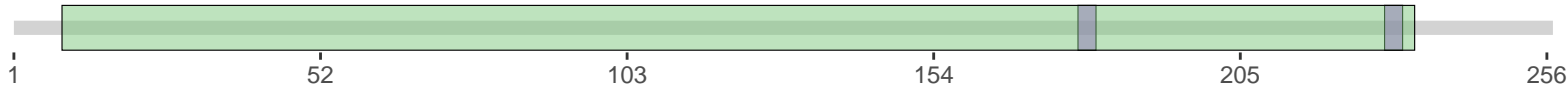


Protein length

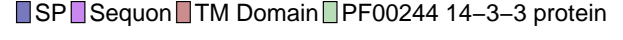


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

AGDSKVFYLMKGDVHRVLAERFKTGAERKEAAESTLSAYKAAGDIAELAPTHIRLGLALNFVDFYFELNSPDRAGNLAKGAFDEAAELDTLGEESYKDGSTLMLLRDNLTLVTSMDODDGADEIKETKADNEGG

NbL08g20300.1 LIM_domain-containing_protein_WLIM1-like [MW = 21.43 kDa]

No. of times detected



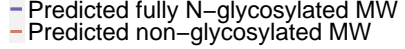
log(intensity)



Values from



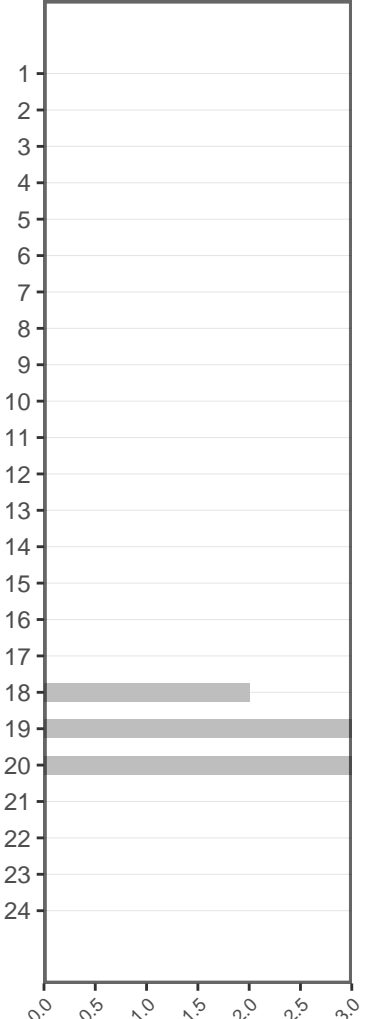
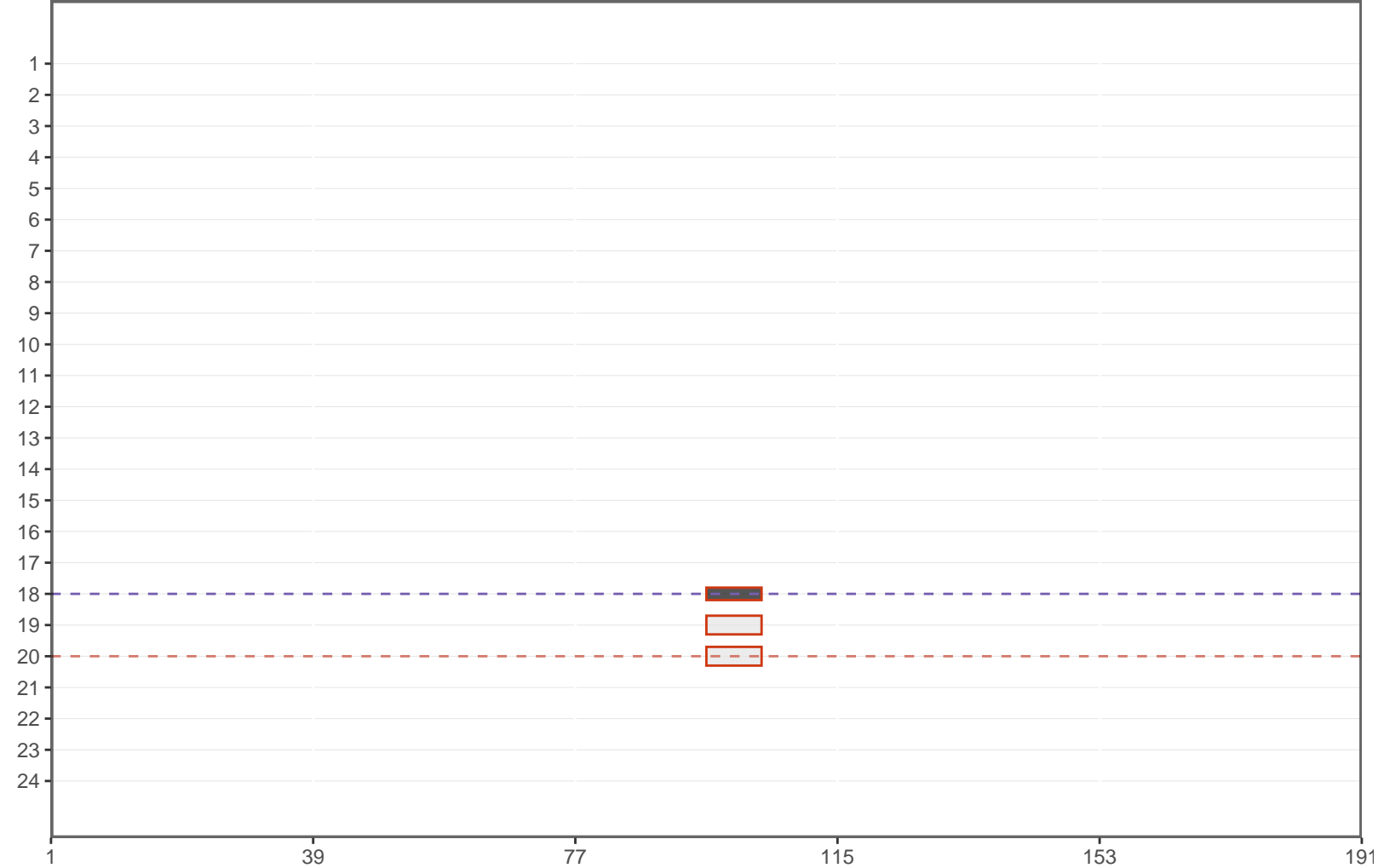
MW indication



Molecular weight



Gel Slice



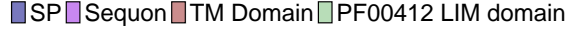
Protein length



Pfam domains



Pfam Description



Protein sequence:

VKPEKDEKPIAAKVKVSMFVGTREKFGGKNTVPTKESVWNGTPTVHKSGPKGSHGGCTSPENVAHHEGRLYGKHHHQLIKEKGNLSGLEGGHDNNTVTAQVWAEI

NbL08g19980.1 low-temperature-induced_cysteine_proteinase-like [MW = 56.48 kDa]

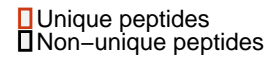
No. of times detected



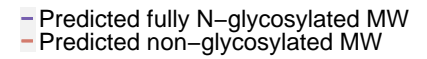
log(intensity)



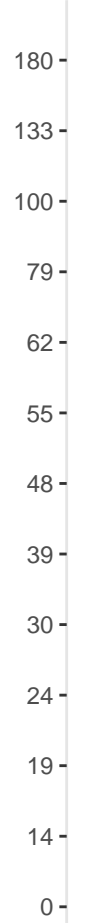
Values from



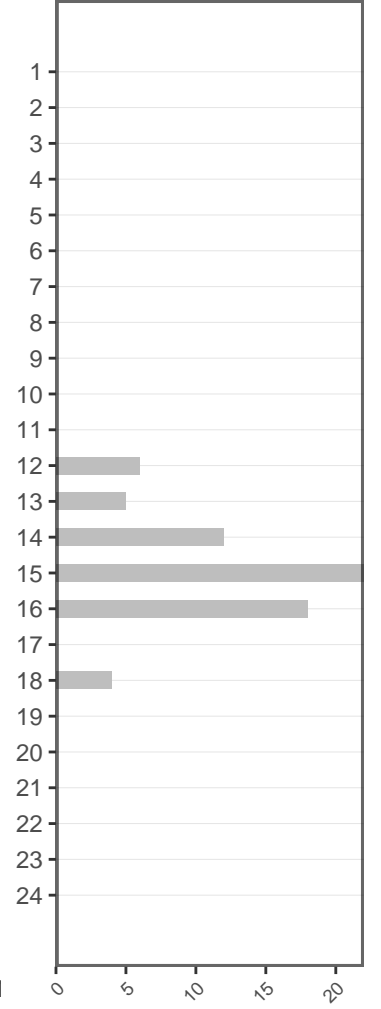
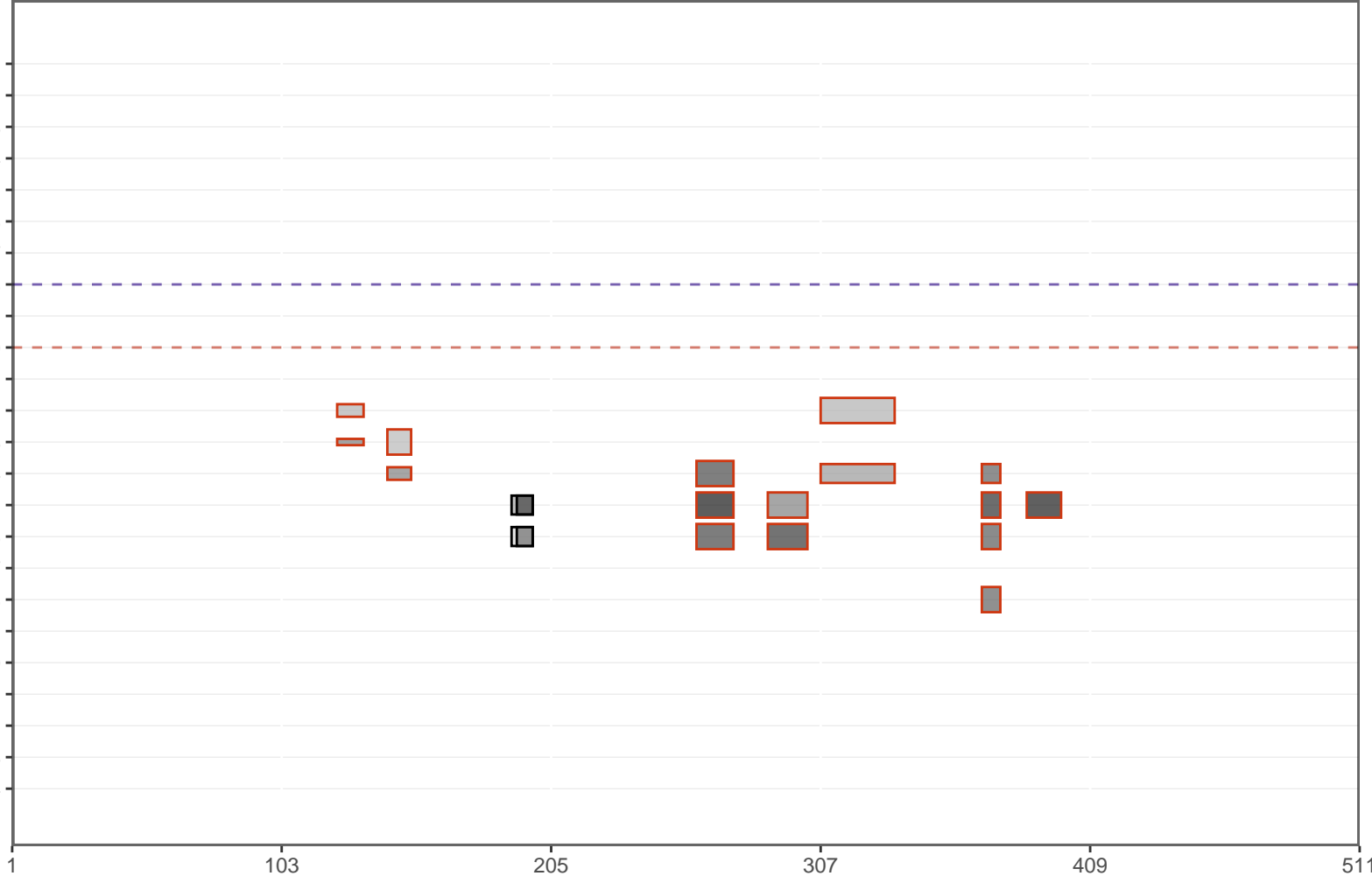
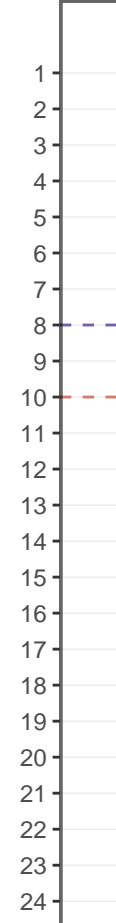
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

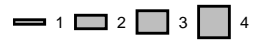


Protein sequence:

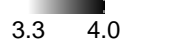
CNGLMDVAFDFIRKNGGIDTEEDYPTGRDGRDGRKNAKVVTDGGVEEIVANNEKALQKVAASQPVSAIEAGNDPQHYVSGIFGKGGTAVDHGVYAVGYSSEMSMDVWIRNSWGARVWGGEGYLRVQRNVA8SKGLGLAIEPEYVVKTGQVNPVPPKPPSPKPPFTQCDVWAGCEGTTCCDVEYVNSGFSWGGCPLGATCCEDHYSCGPHDYPVQNRVAGTGSISKDNPLGVKAMKHLAIEPIGAFINGGRK665

NbL08g19960.1 polyadenylate-binding_protein_2-like [MW = 71.97 kDa]

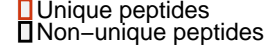
No. of times detected



log(intensity)



Values from



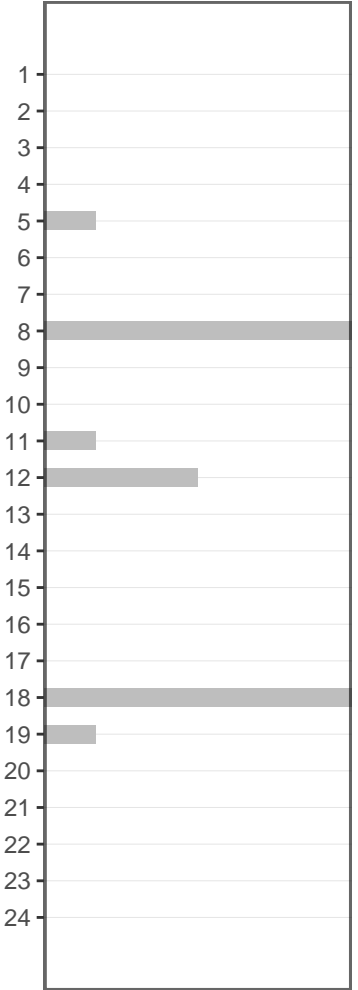
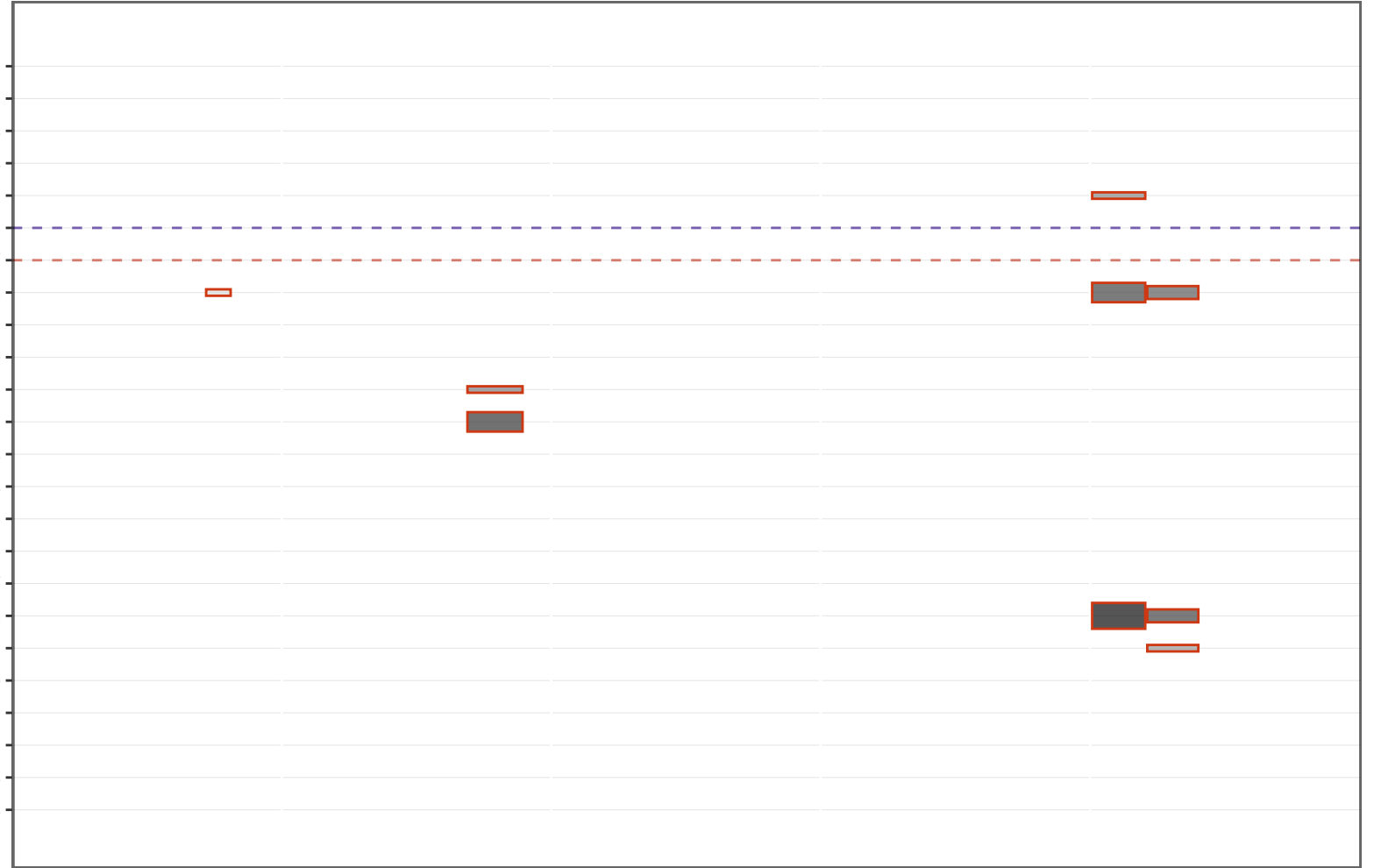
MW indication



Molecular weight



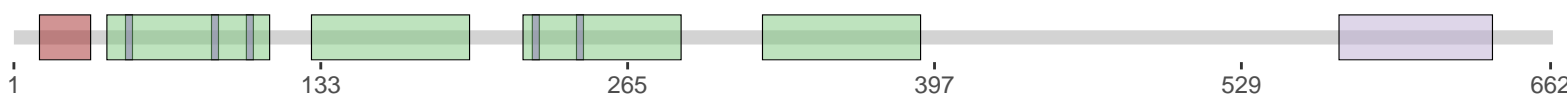
Gel Slice



Protein length



Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- PF00658 Poly-adenylate binding protein, unique domain

Protein sequence:

ILNLYVKNLDDTDIDDEKLEKLEFLEFGTTTSGKVMRDPGIGRGGGFVAFSTSEASRALSEMNGKMIYKPLVALADRKEERRAKLGLVQADFGQLRPLVAMPPLSLARMPYVPPGAPGIGGLFYGGGPRMPPGAGFYGGGLVPGMRPGGAPMNFMLPLVGGGGGGRRPGRRGAGPVGQGTGQPLMLGQGLMPLRGRMYRYPGGRNGPEGMPGVPGSMLSVYDMMGMLPRDSAMGGMPSTLALANAPPEGQRTMLGESLYPLVDDLEHEHAAK

NbL08g19950.1 50S_ribosomal_protein_L4 [MW = 34.3 kDa]

No. of times detected



log(intensity)



Values from



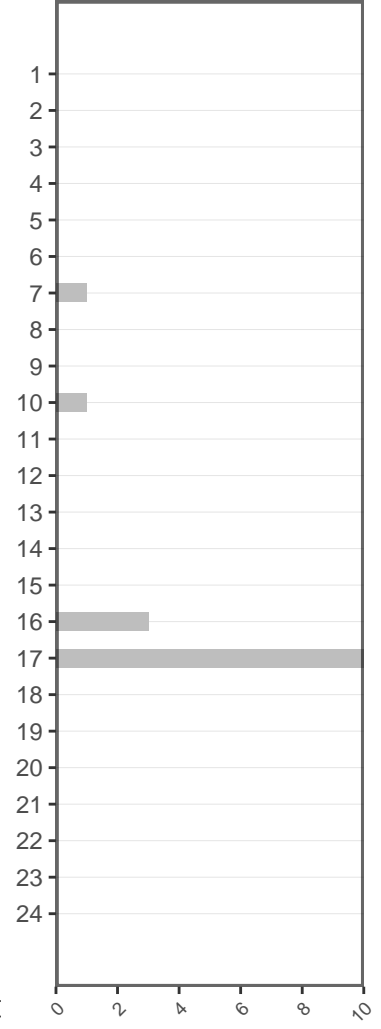
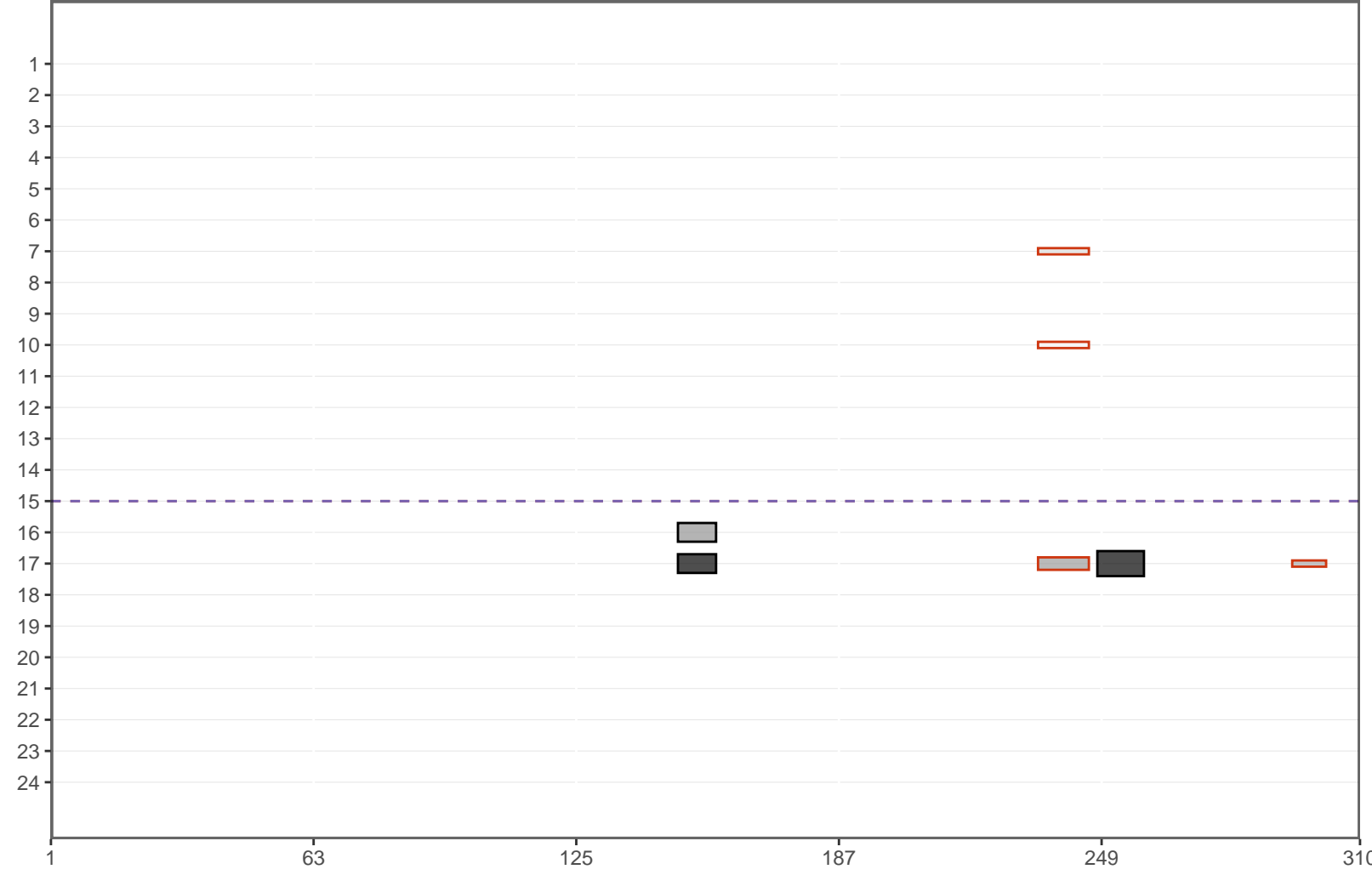
MW indication



Molecular weight

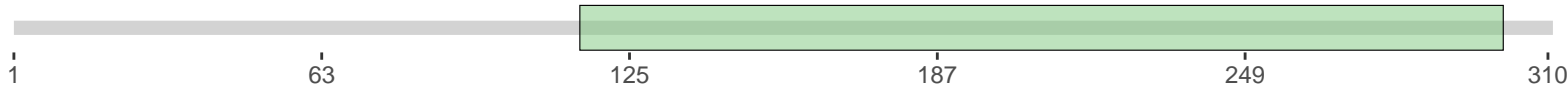


Gel Slice



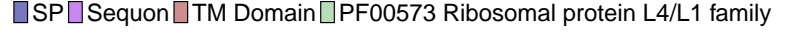
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGTHISTKTISEVSGTGRKMPWRKGGTGRARHGTLRGADFRGGATMGGPKPRSHAIKLNKQVRRLLGLKIALSARAAEGRLMVFEDLEISHSKTKNIVNRYFNQLMNTKLLLVDDGGPSEKIKLATQNVHYVNLPSIGLNVYSLLHDTLVMRDVAWNTIVERMHTFNRV

NbL08g19920.1 subtilisin-like_protease [MW - SP = 79.88 kDa]

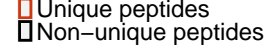
No. of times detected



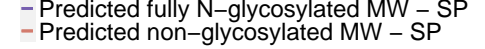
log(intensity)



Values from



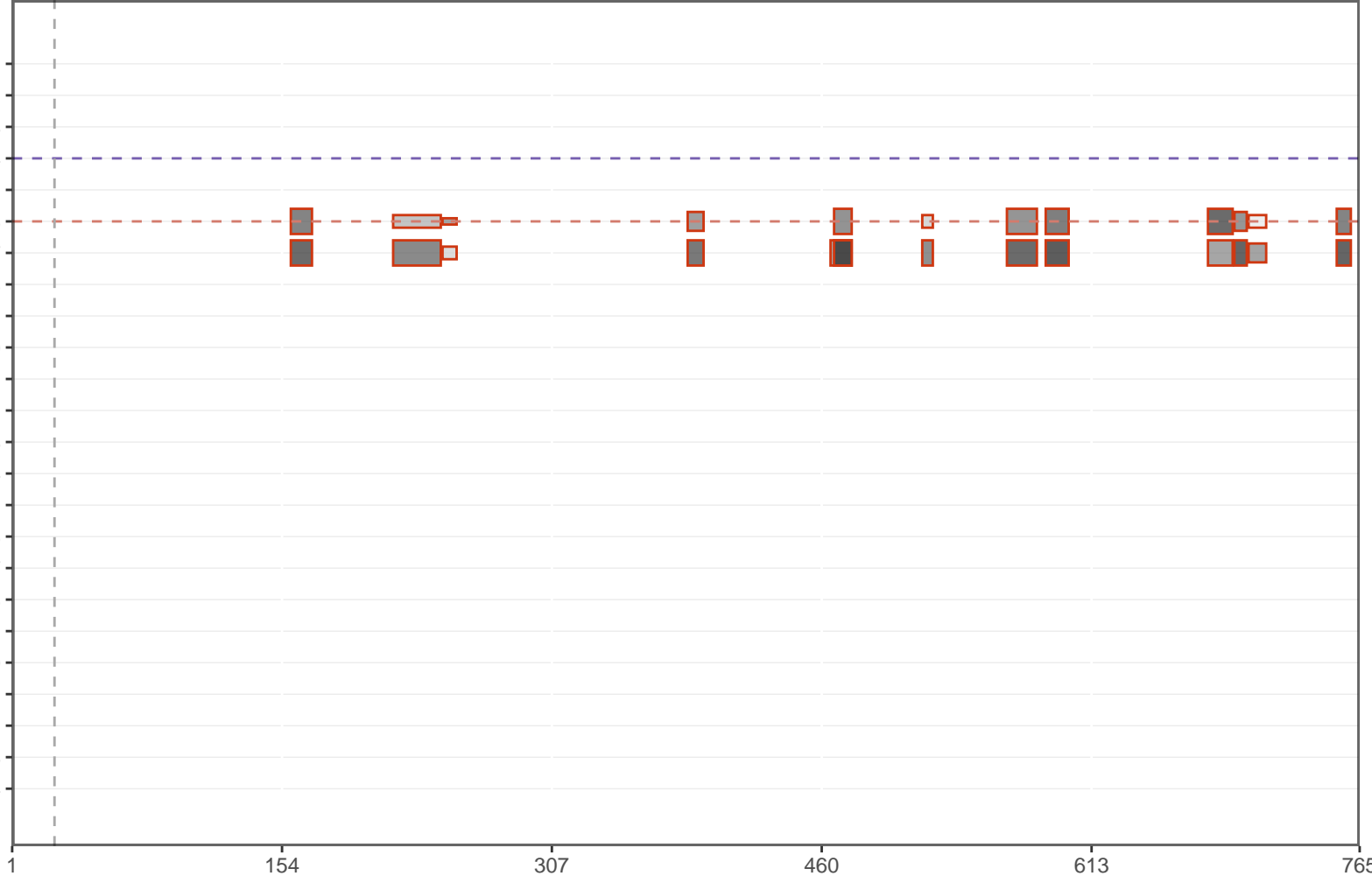
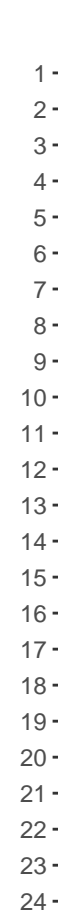
MW indication



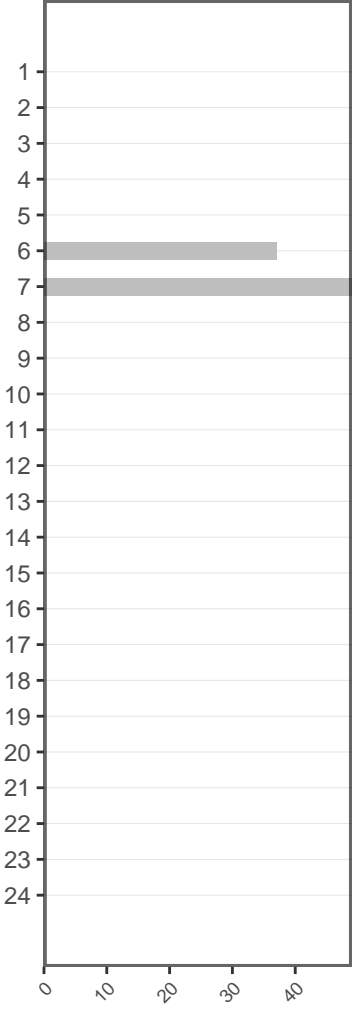
Molecular weight



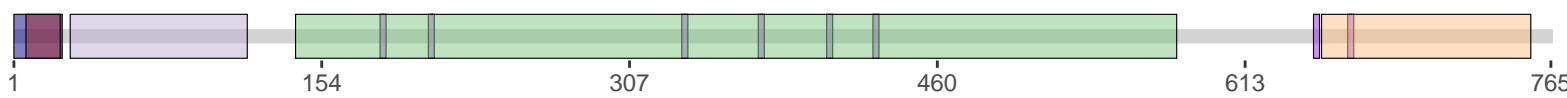
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGNSSSESSIVFLKTDLEKELEKNAHKFAVGYDTNNGVSDQLYVKNKTKVAGGIFITNTDLEFYLGQSEFPVFLNFEDGDKVLEIKRNSHSPKARLEFQVTHLIGAKPAKVAEYSRGRPESECFILKPDLMAPGALILAEWPKSPATQIRSGELFSFNINISGTSMSGCPMAAGVAALLKGAHPKWSPAIRGAMMTTADTMDNMGMPIRDIGRNNAASPLAMGAGRINPKALDPGLYDTSQDYINLLCALDFTSQGQKATR66SAVSGNSL66LNYPSFQYFNYSI

NbL08g19570.1 ornithine_carbamoyltransferase_chloroplastic-like [MW = 41.83 kDa]

No. of times detected



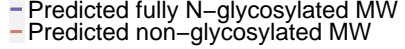
log(intensity)



Values from



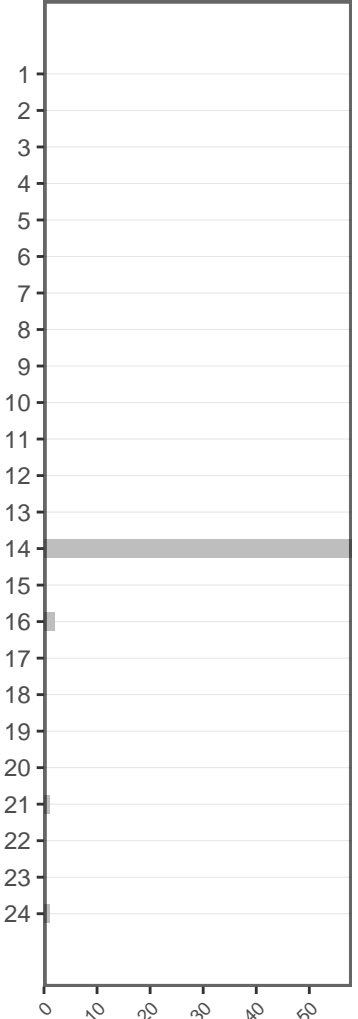
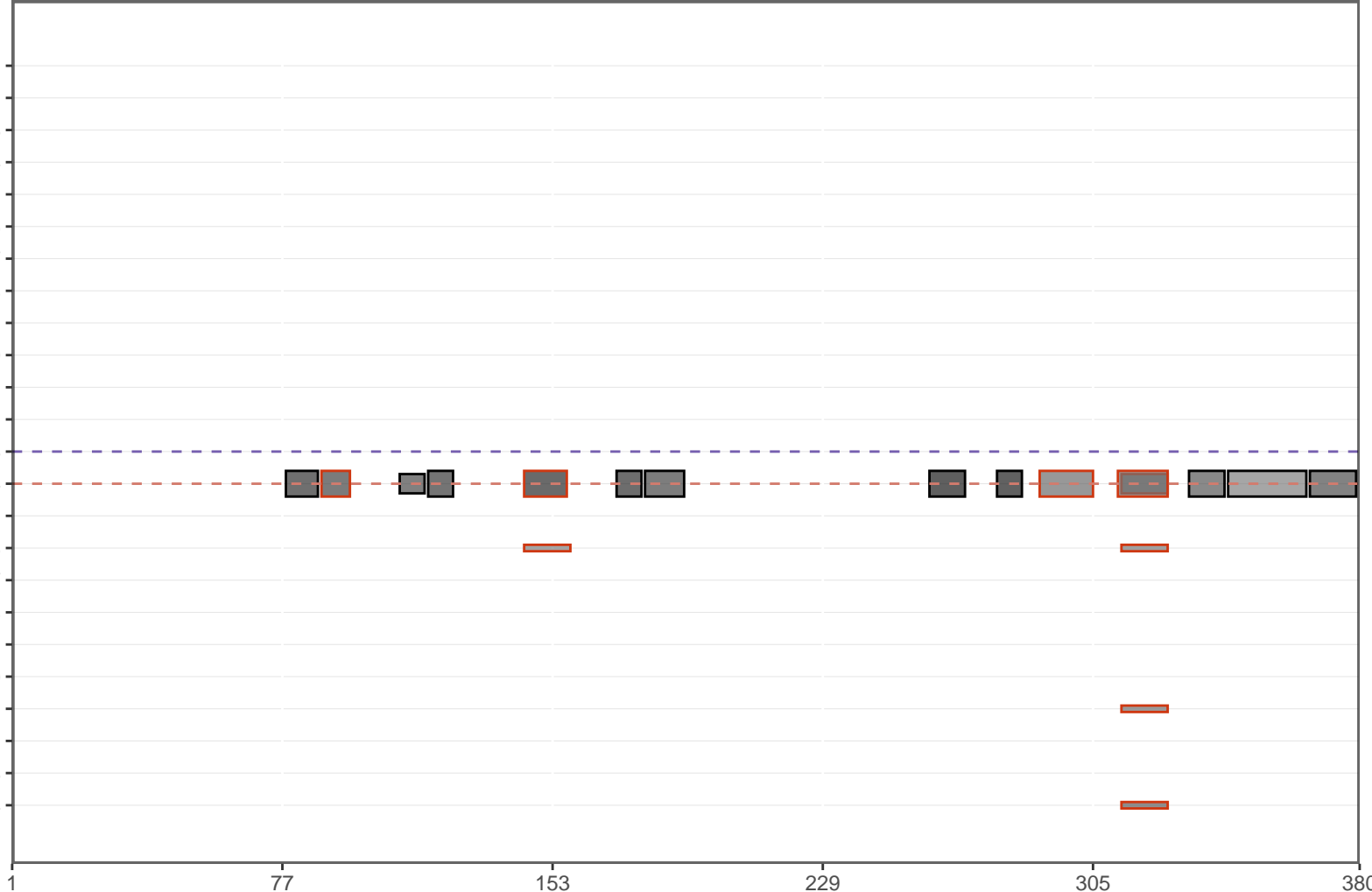
MW indication



Molecular weight

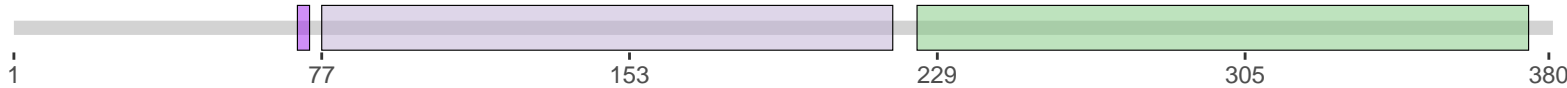


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00185 Aspartate/ornithine carbamoyltransferase, Asp/Orn binding domain
- PF02729 Aspartate/ornithine carbamoyltransferase, carbamoyl-P binding domain

Protein sequence:

FAHQDILDAAKYATVFPVINGLTDVNHFGQIMADALTMIEHVGLEGRKVVVYGGDGNVHSHWLLLSLVIPFHFVQAGPKGFEPDGETVEKARQAGVSKIEITNDPKAEVRGADVYVADVWASMGKKEEAHRRQVFGQFQVDEELMKLAGGKVFHMLGLFPERGVEVTDGVEAPNSVFPQENRMHAGNAMLHVLGL*

NbL08g19380.1 uncharacterized_LOC104222813 [MW - SP = 22.33 kDa]

No. of times detected



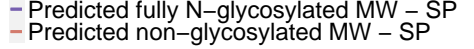
log(intensity)



Values from



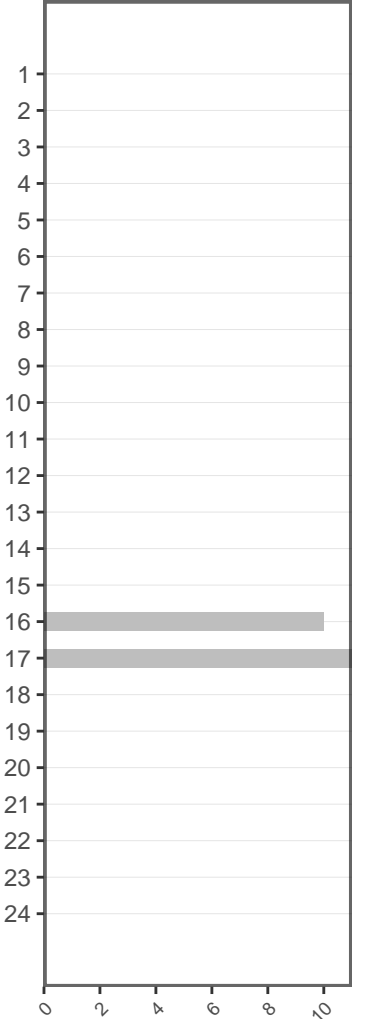
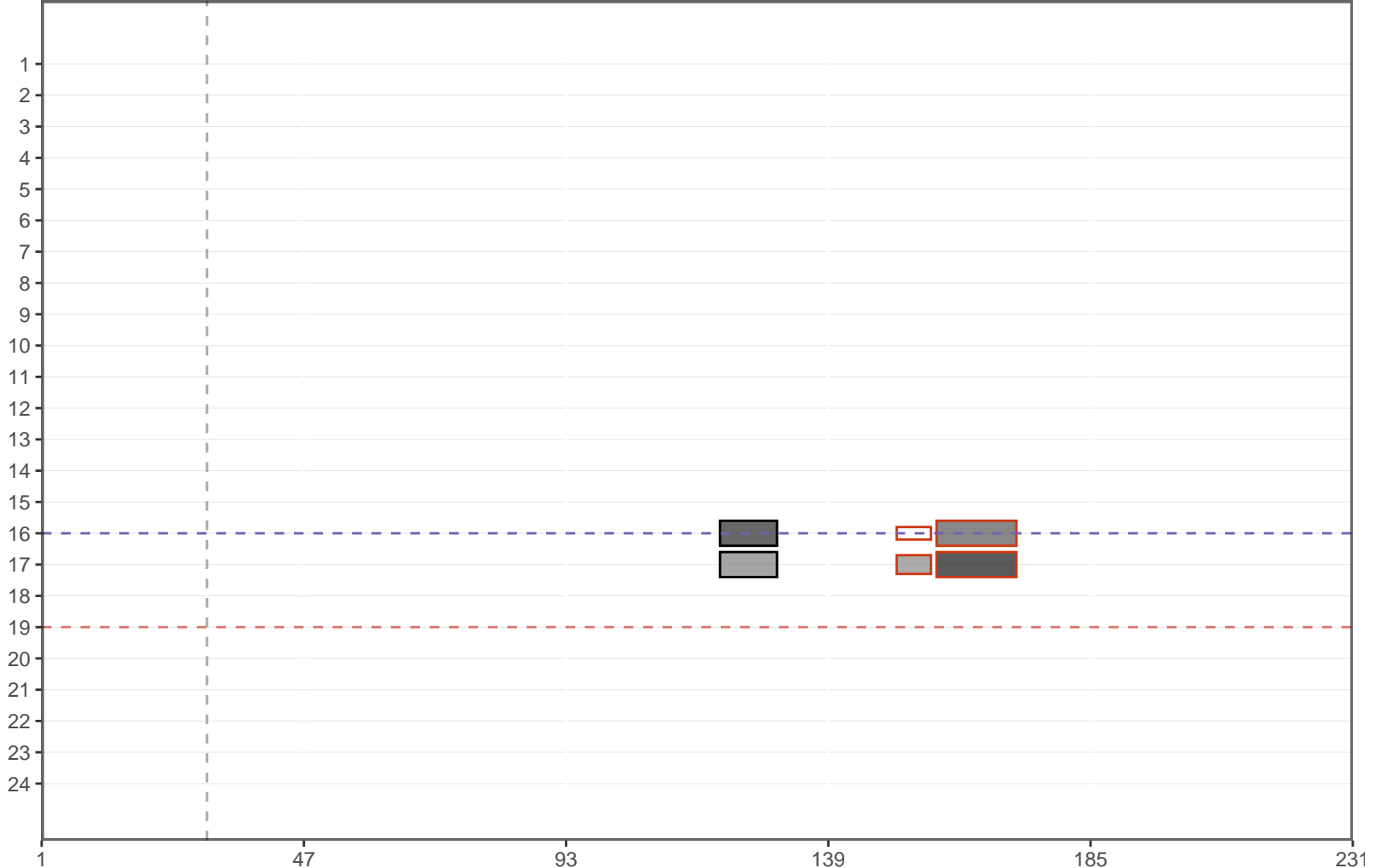
MW indication



Molecular weight

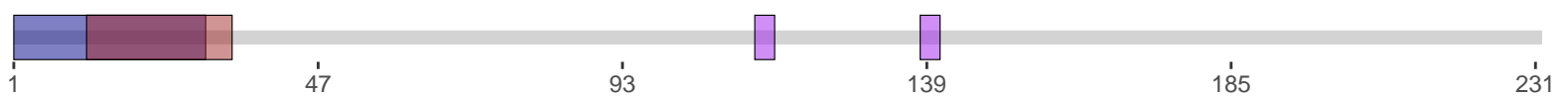


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

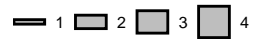
Pfam Description
 SP Sequon TM Domain

Protein sequence:

ISRALHINKLNTSATYRLLLEFFGGGDKFYGKATFNLSKASVVDKIKFTFSNAVRINSNYAAEAGFTDPKTDQATRIISFKYGVGKGVYGTPTFFVYNGRFLPADGSPLEKHWARNLIDPLVSPAGLQEG

NbL08g19330.1 glutathione_S-transferase-like [MW = 25.47 kDa]

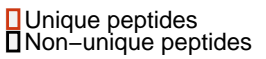
No. of times detected



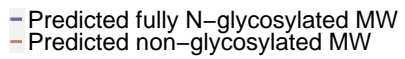
log(intensity)



Values from



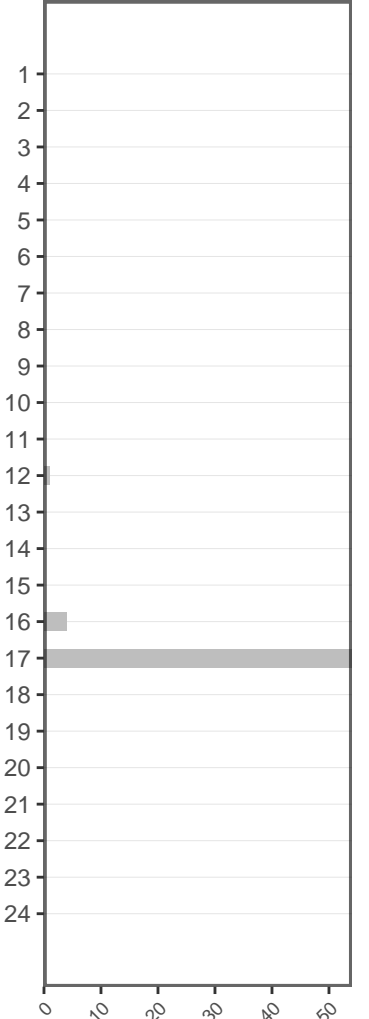
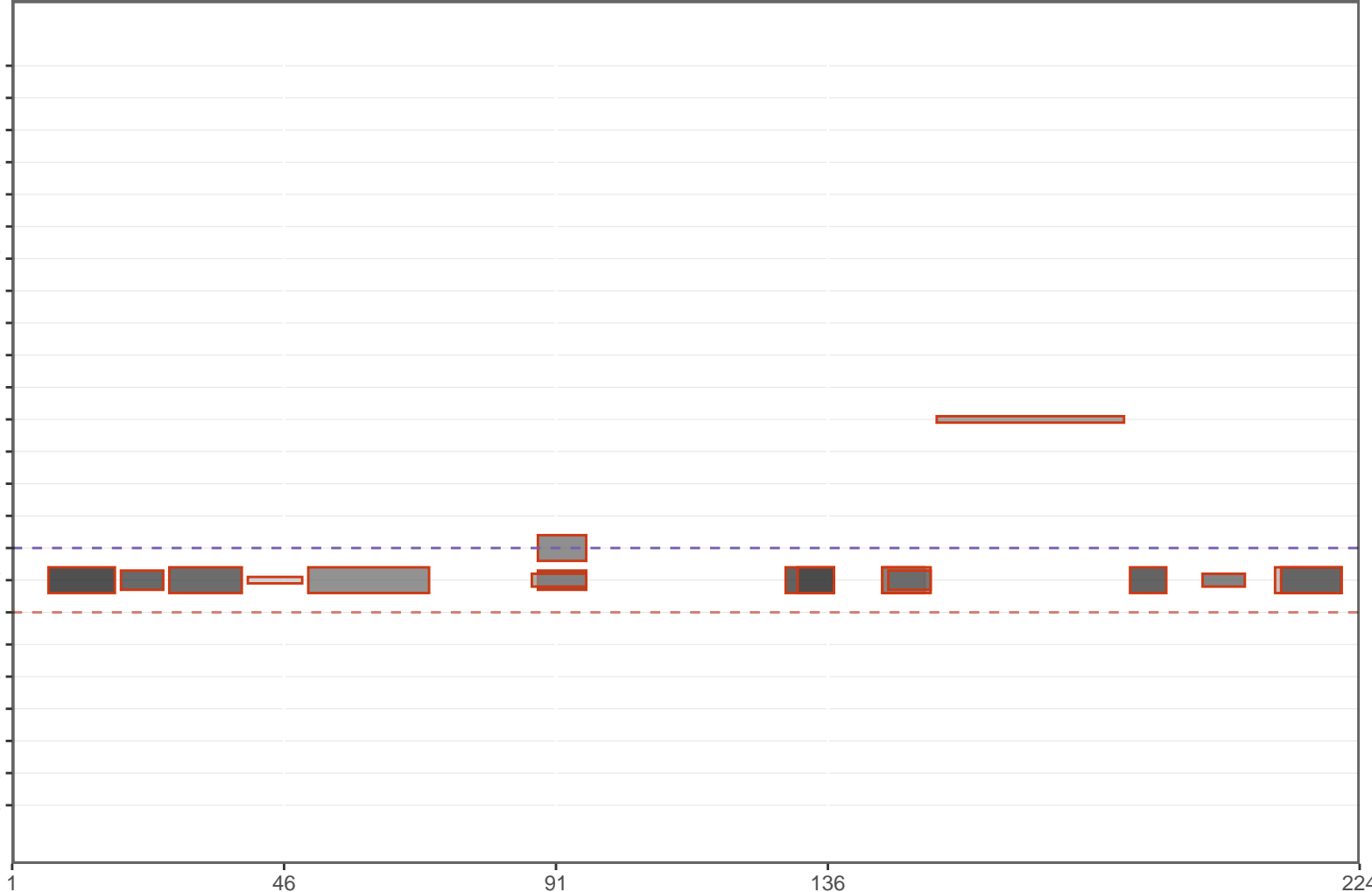
MW indication



Molecular weight



Gel Slice



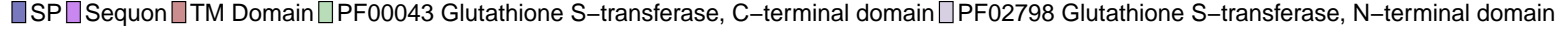
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

QXWIEAEGQSFNPPSSILVFGAFAPRMKIKGDNLRHQEELKIKVLDVVEKRLGESDYLADGDFSLADLSHPNQYLVNGTDRAELFTRKIVGRWWDHSSRESGKKVEMQTSPPPKTC

NbL08g19260.1 4-coumarate--CoA_ligase-like_5 [MW = 60.65 kDa]

No. of times detected



log(intensity)



Values from

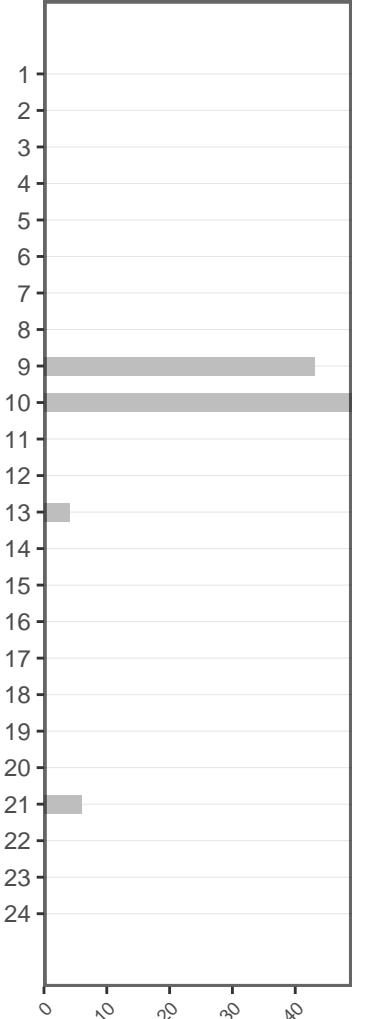
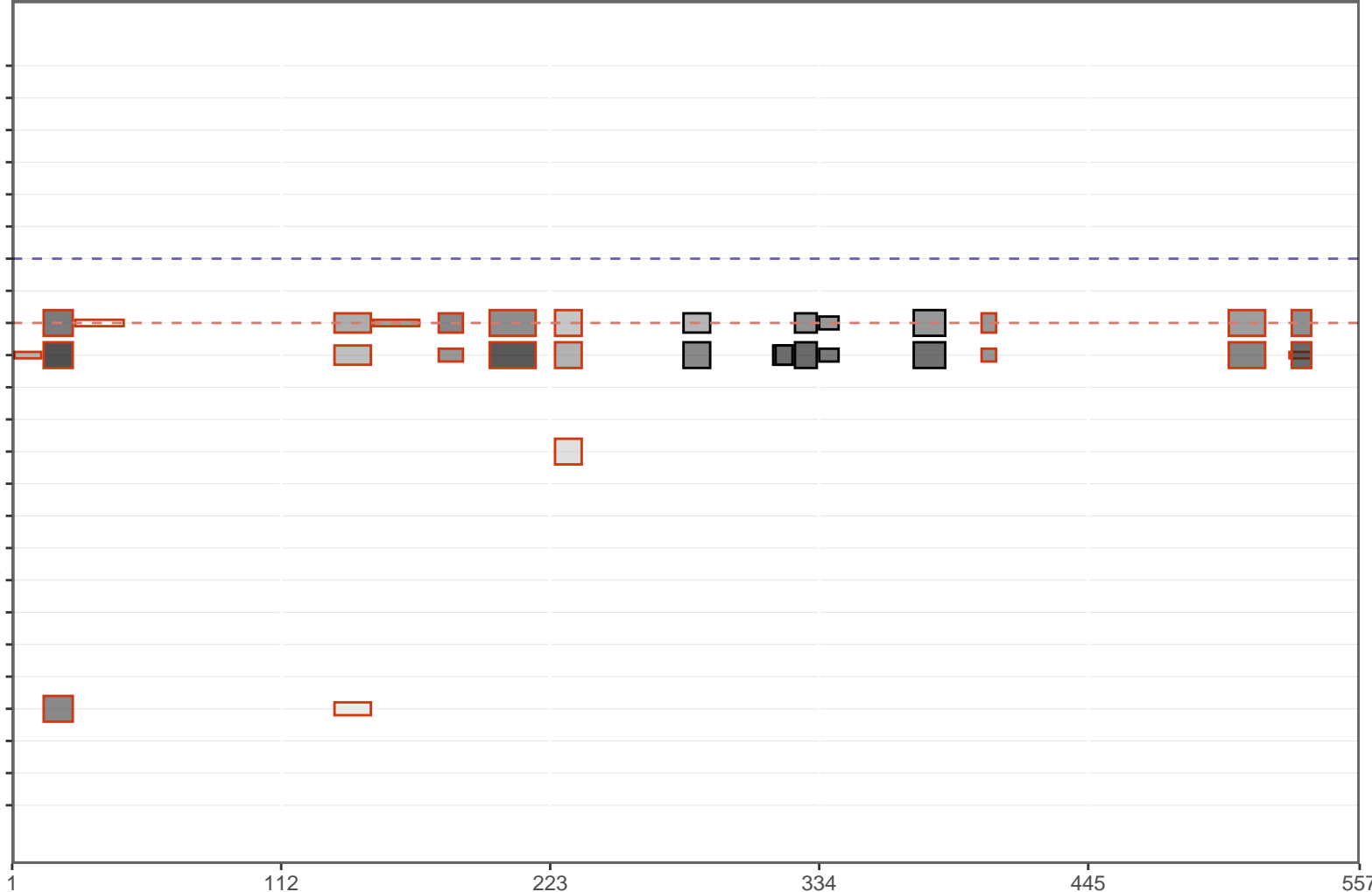
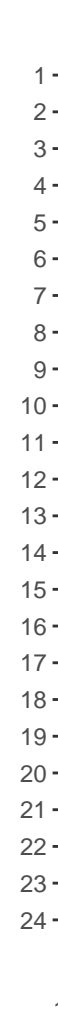
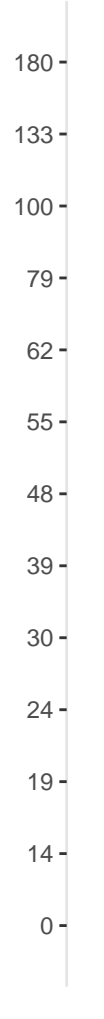


MW indication



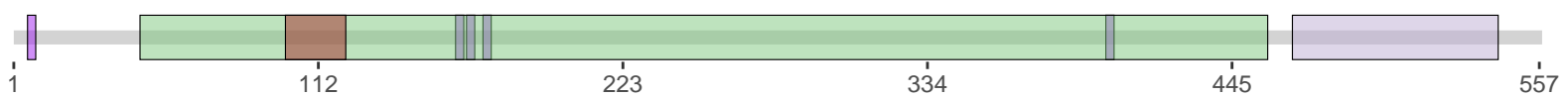
Molecular weight

Gel Slice



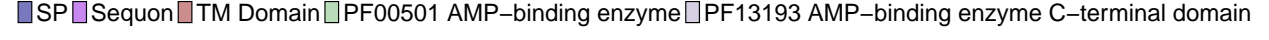
Protein length

Peptide counts over 4 repeats



Pfam domains

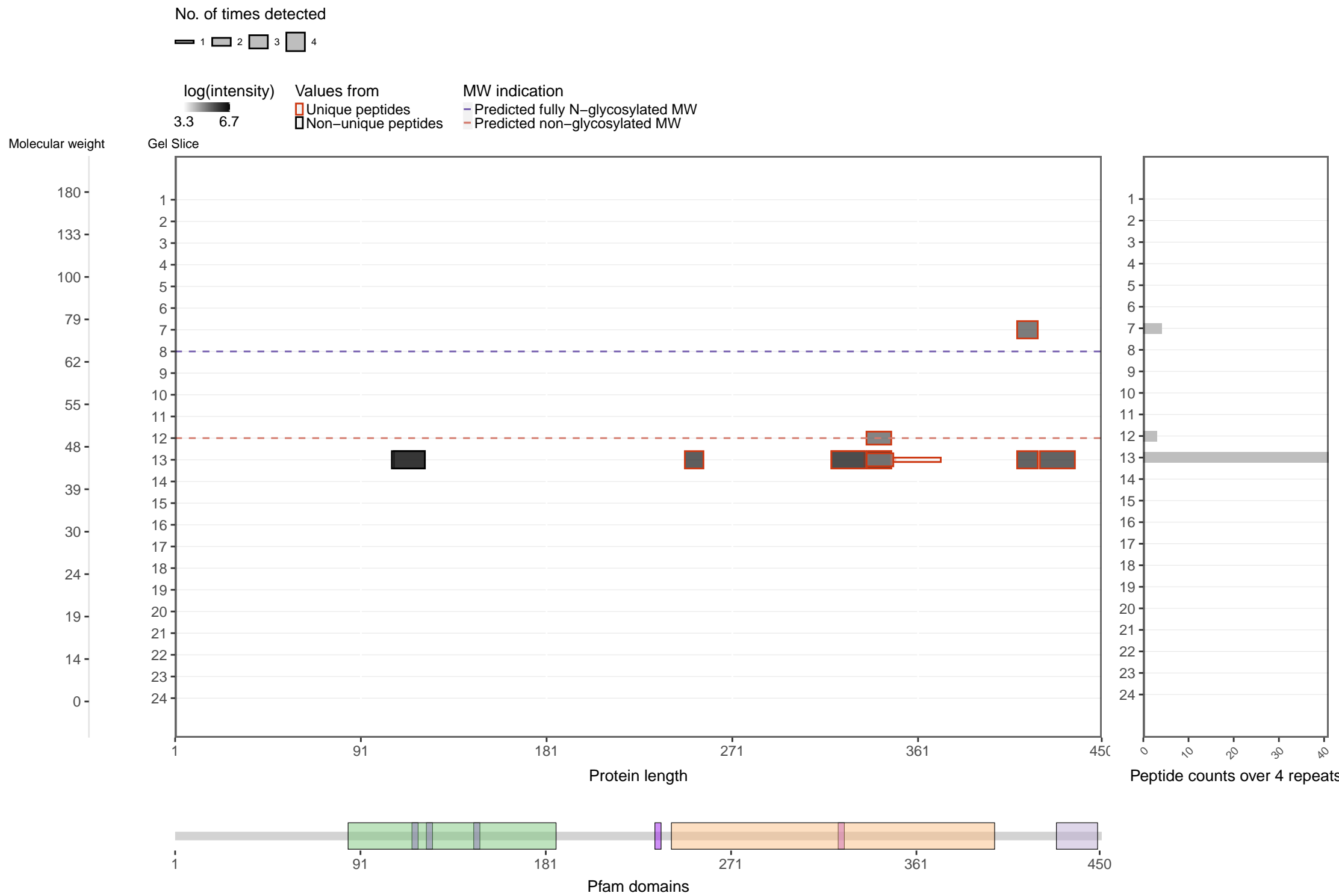
Pfam Description



Protein sequence:

ISGSTVYVLSKFEEMDEMLSSSHKHKATYLPVLPVWLVNNAEMIKKKYDLSSLKVVLSGGAPLEKEVEGFLKYPVTVLGGVGLTSTAGASTDSLEESRRYGTAGMLSPMSAKVVDPESGKAFVNTKTELWLRGPTIMKGYFSNEEATASTLDSGGLVRTGDLGYDEGDFVDRKELKYYGVVPPAELEALLTHPEIDAAVIPPFDKVGQGFPMAYVVRKSGSLSSESAMDFIAKGVAPYKRRRWFVASIPKNPESGKLRKDKLAKSL*

NbL08g19150.1 glyceraldehyde-3-phosphate_dehydrogenase_B_chloroplastic-like [MW = 47.92 kDa]



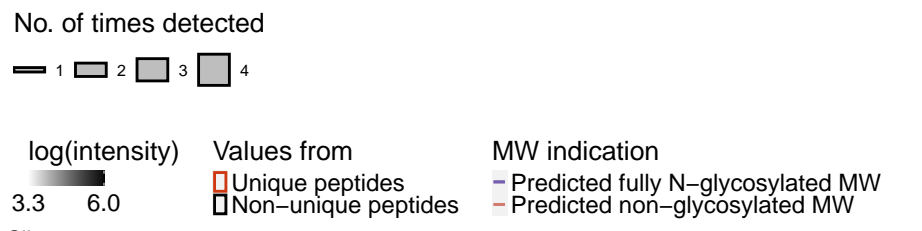
Pfam Description

- SP
- Sequon
- TM Domain
- PF00044 Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain
- PF02672 CP12 domain
- PF02800 Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain

Protein sequence:

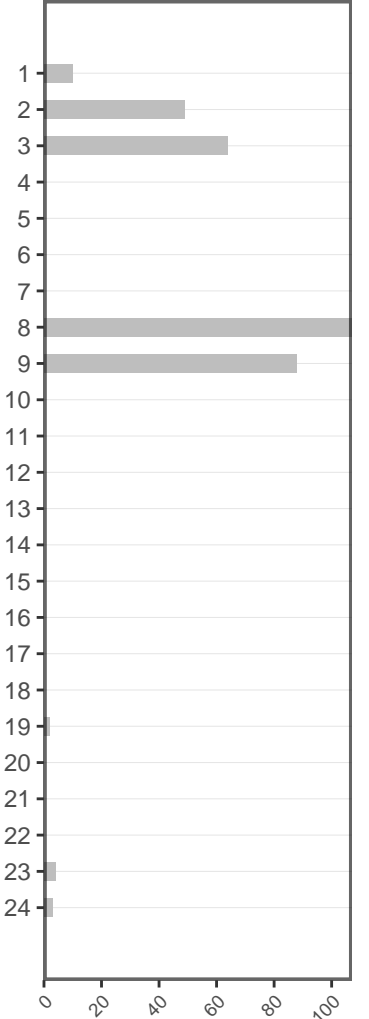
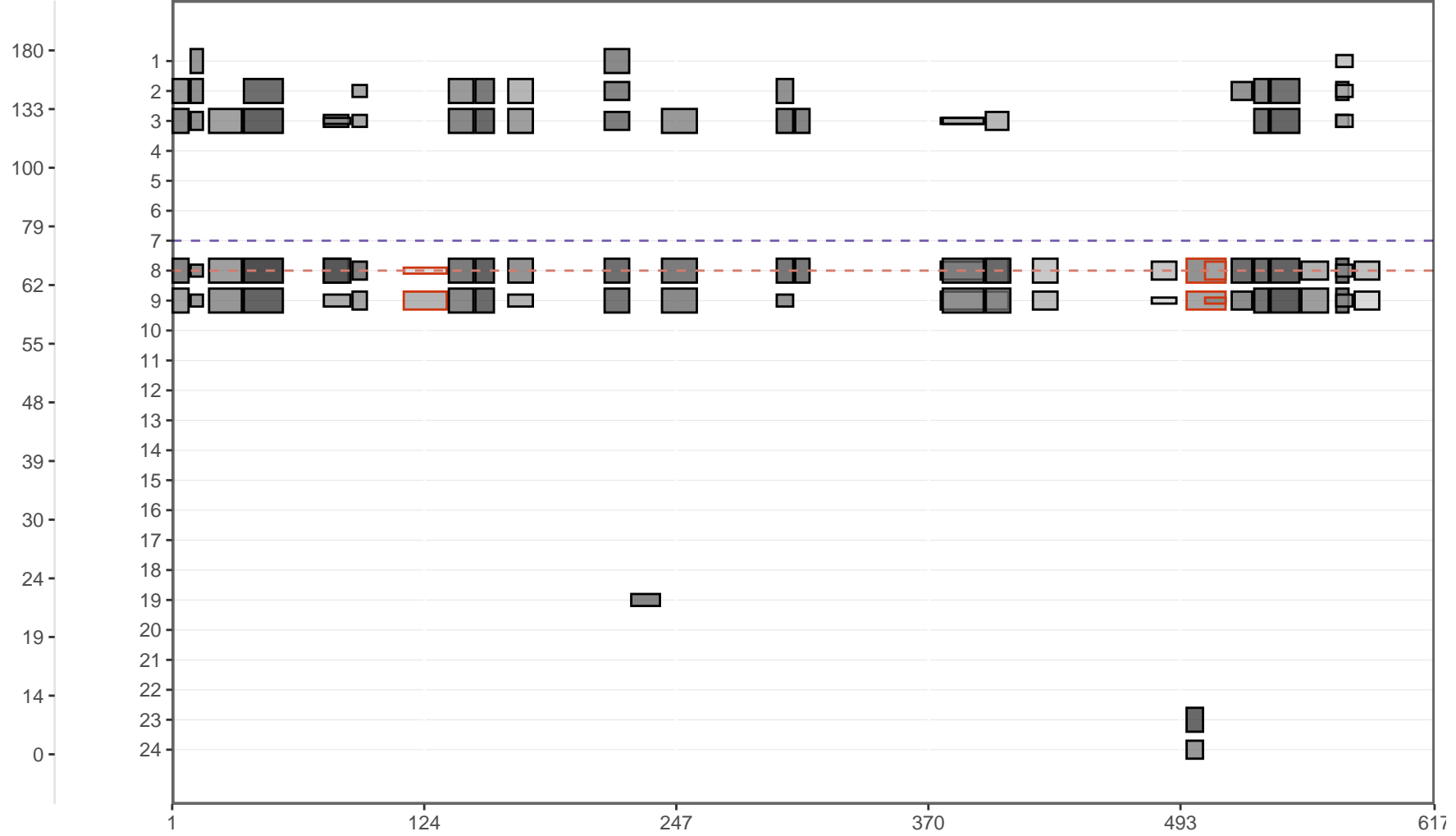
TYVGVNEQDYSHVANIISNASGTFNGLAPFVWVMDDELGVKGTMTTTHVYTGDRLLDASHRDLRRARAAALNVPTSTGAAKAVSLVLPQLKGLKNGIALRVPTRVSVVDLVVVERKGISAEEDVNAAFRKAADGLPLNGILAVGDVPLVSVDFRGSQVSGTDSLSLTVMGDDMKVYWWWVNEWGVYSGRVLDLHLVASKVWPGSSVEGSDALEVQKTNPAKKEGKVEE

NbL08g19050.1 pyrophosphate--fructose_6-phosphate_1-phosphotransferase_subunit_alpha-like [MW = 67.17 kDa]



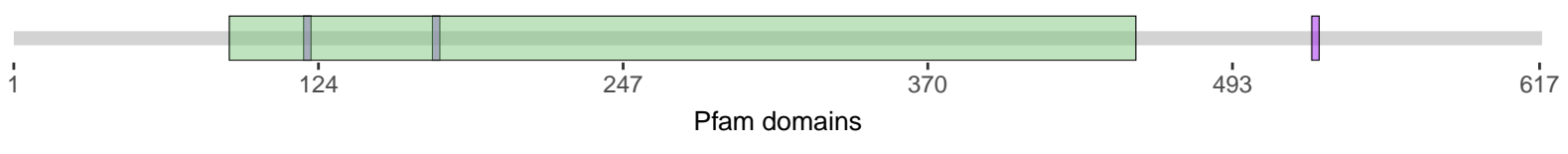
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:

SKLTLFDITKICCDVAGRAEGDKNHGIVLLPEGLGIEPIEVYALLGEGHGLLRGVSDAKISGLSPWASALFEFLPFPIKQLLLYFEGSDSALQSDIETKLIAHIVETEMNKRRLKEGTYYGKFKFAIGHFFGVGARGSLPKFDCDVAWYVLGHICHHYLAAGLNGYMATVTLNKNPYNKWRGAAAPITAMMTVKRYGRGPNANAKRPVHPVYDLKGGKAYELLSGNATKFLLEDVYRNPGLDFDGRGADAKAVTLGVEDGGYMGRIHKLGEVLEKAVRTVYKPGCSGDYLYK

NbL08g19040.1 UPF0047_protein_YjbQ-like [MW = 20.84 kDa]

No. of times detected



log(intensity)



Values from



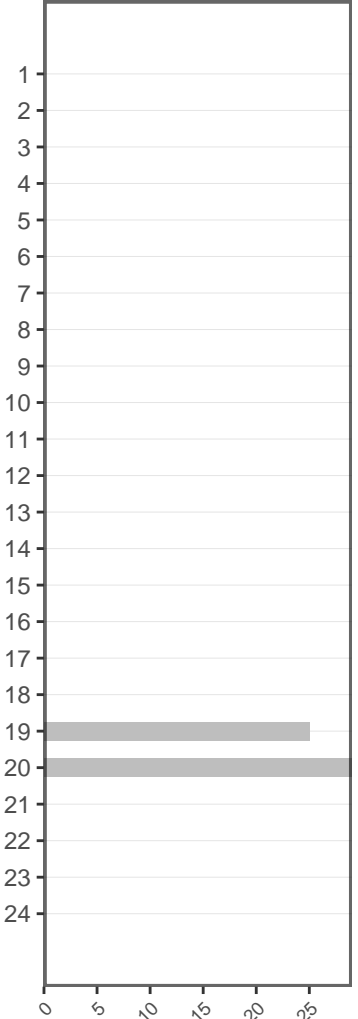
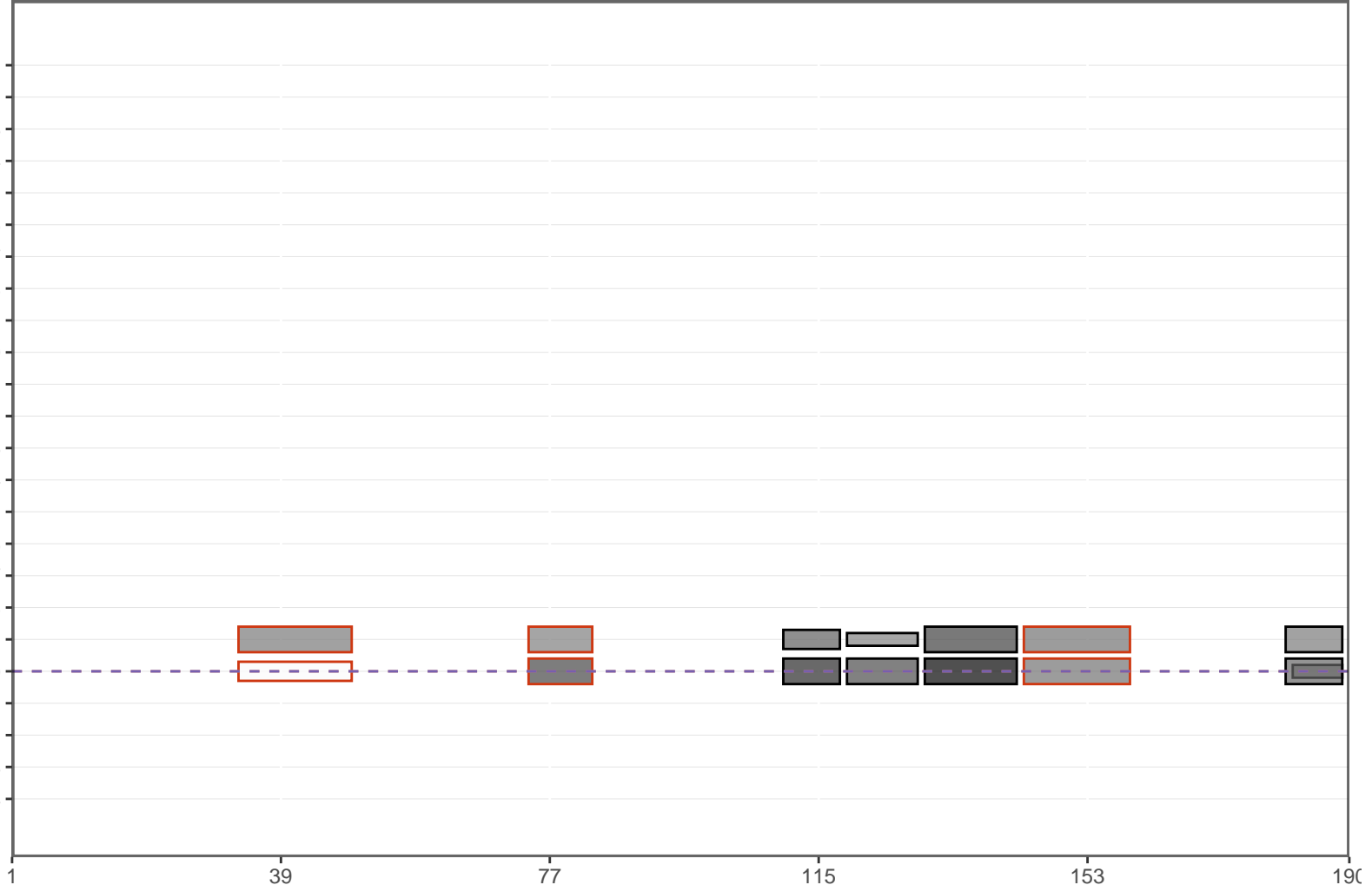
MW indication



Molecular weight



Gel Slice

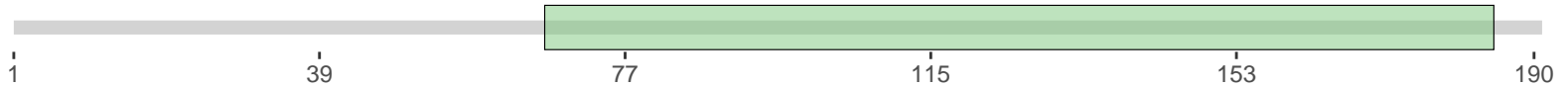


Protein length

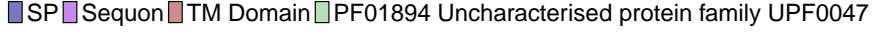


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KCCGLAHFLQHTSASLTINENYDSDVDDDTETFLNRRVVEGIGAPWKHFLLEGDDMPAHKISSMFGCTLTIPTDQKLNMGTVGGIWLGEHRDAATPRRIVITLNGM

NbL08g18970.1 tryptophan--tRNA_ligase_chloroplastic/mitochondrial [MW = 49.69 kDa]

No. of times detected



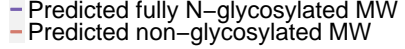
log(intensity)



Values from



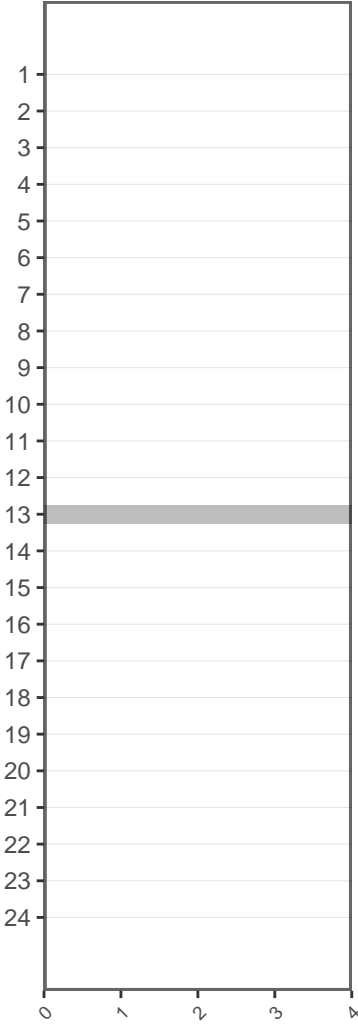
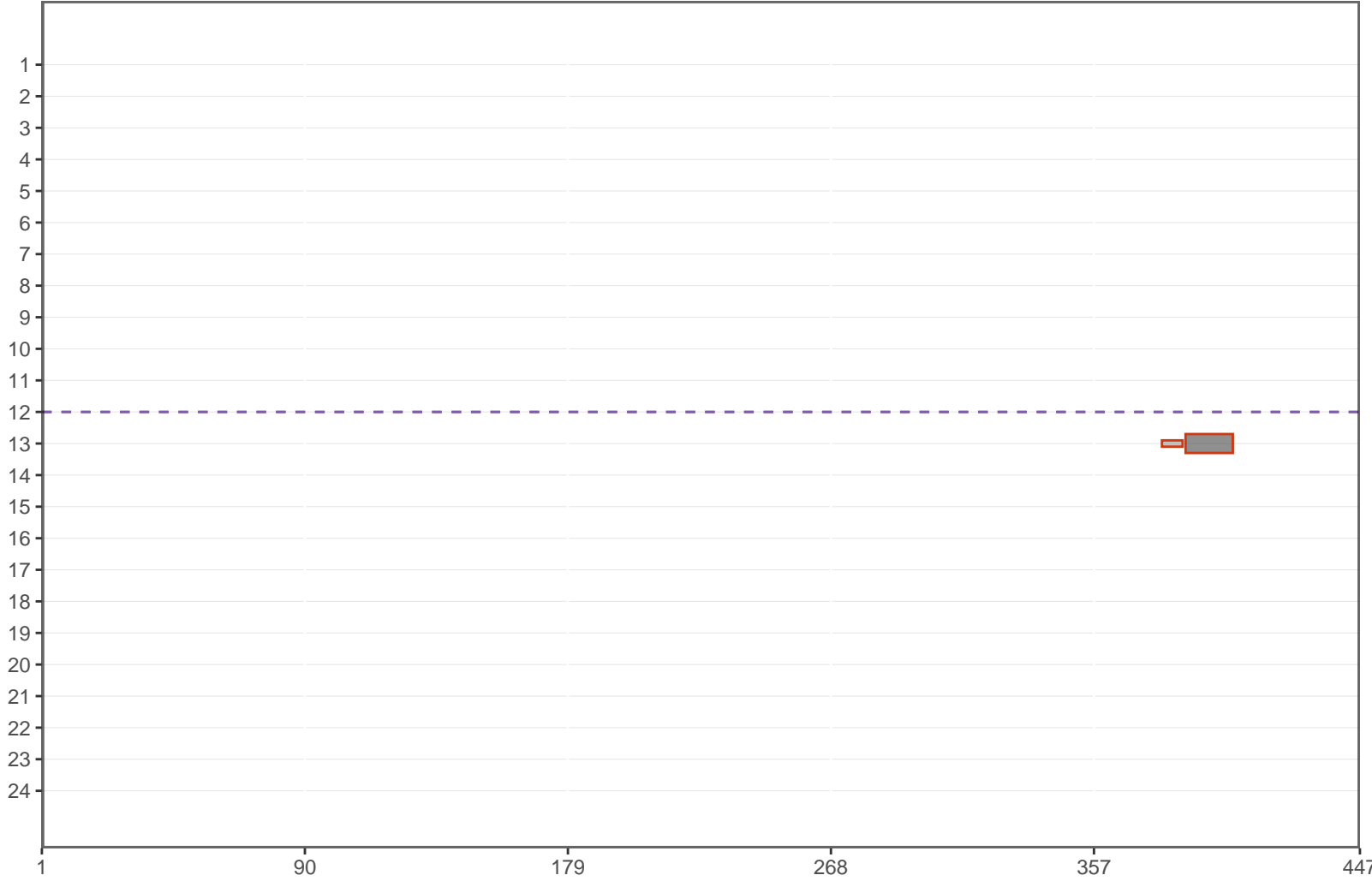
MW indication



Molecular weight

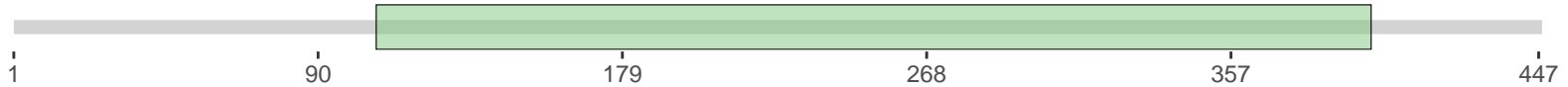


Gel Slice



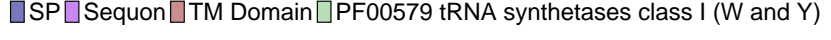
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

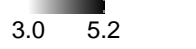
FKEKSRKAGDENVGVALLTPVLMADILLVYGSDFVPGVEDQKHLELRELAERVNLYGGRKWKLGRRGGSIFKVPPELPPGARGIMLTDGLKMKKAPBEGQRINLLDSKDVAAKIKRCKTDSFPGMEFDNPERPECCNLLSHVQLYGTGKGEVAEEGRHMHWGTFKLLVADALVDLHPQIVRYEEIVSDAVYLDGVLAEGRKAADVAVTVNIVFQMGFLRR

NbL08g18930.1 ATP-dependent_6-phosphofructokinase_6-like [MW = 57.05 kDa]

No. of times detected



log(intensity)



Values from



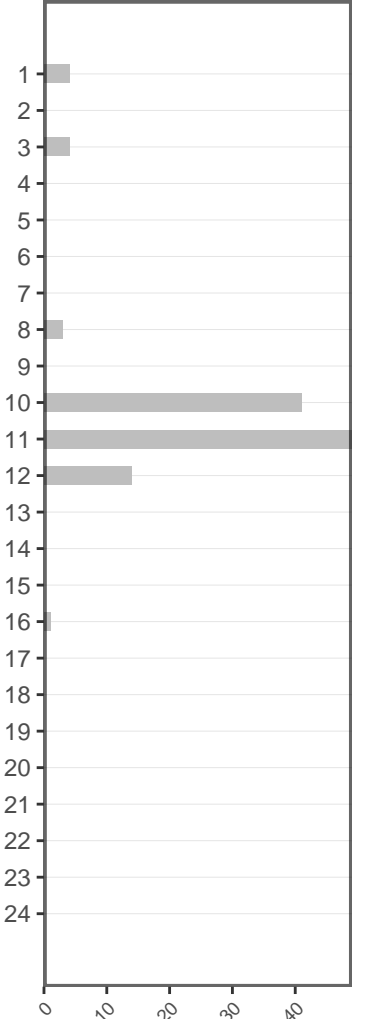
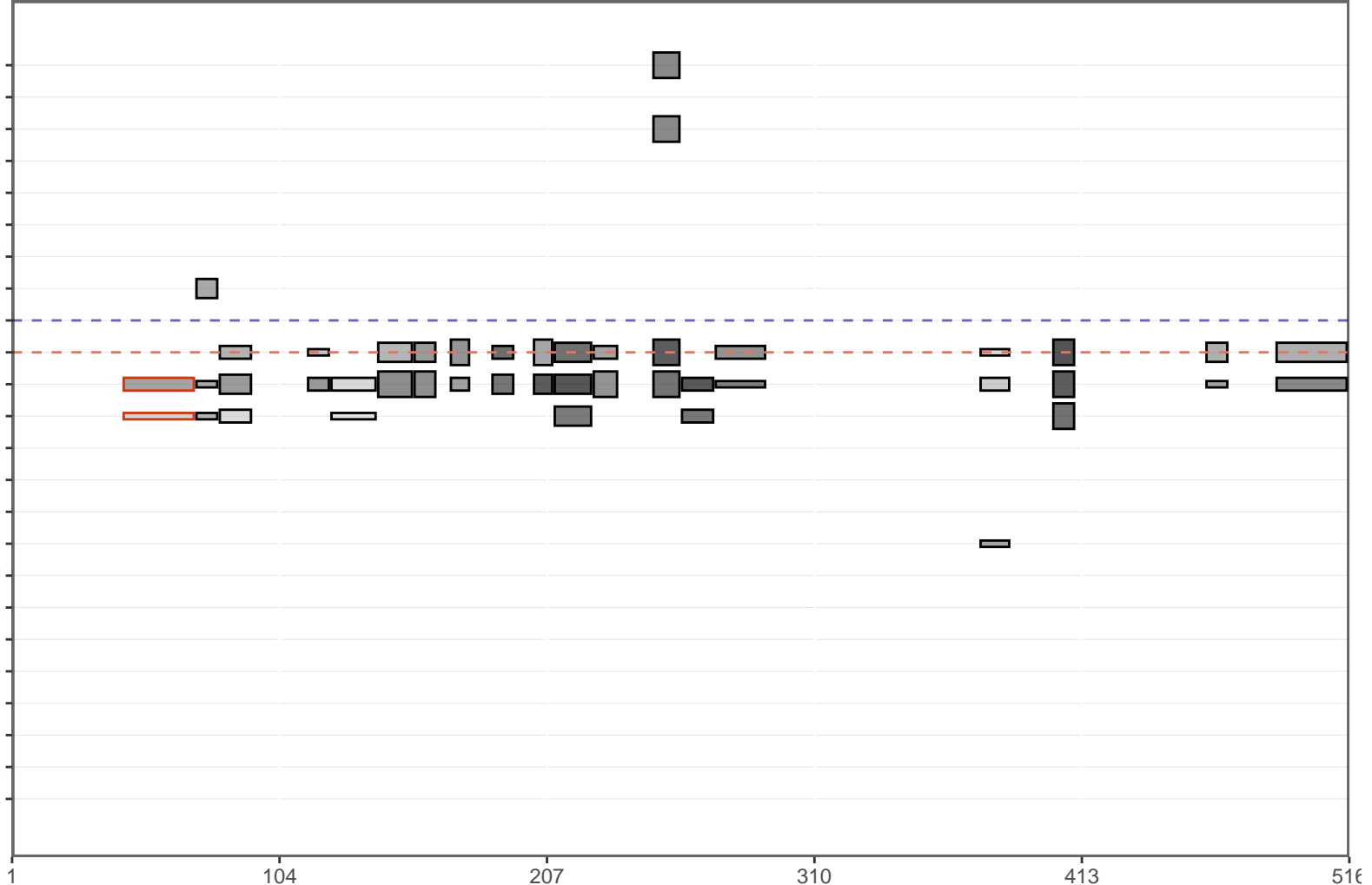
MW indication



Molecular weight

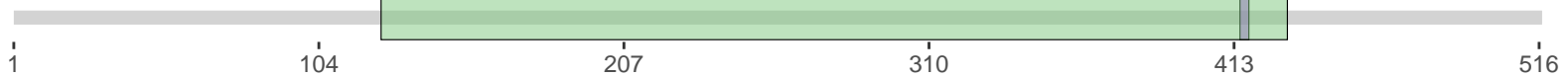


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKTKDNDIPVVDKSGFDTAEEAGRAINAHHVEAESAENGKGVVLMGRYSGFRAMVTLASRDVDCGLPESPFYLEGEGLVEYIEKRLKENGHMVVAEGAGGELLAENSLAKNEGDAAGKLLGGVLIWISQKIRDFHAKNPKMATLKYVDPTVMIRAVPSNAAGDNYCTLLAGGCVHGAAGYTGYSGLVNGRGTYPVFNRIETKGNMVFTRMMWRLLSSTNGPFLCPKDVVEEVNNEEGPQTQLLGDGNNVHENGSH

NbL08g18900.1 vacuolar-processing_enzyme-like [MW - SP = 51.1 kDa]

No. of times detected



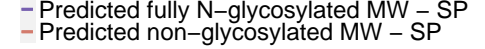
log(intensity)



Values from



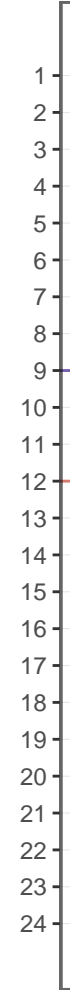
MW indication



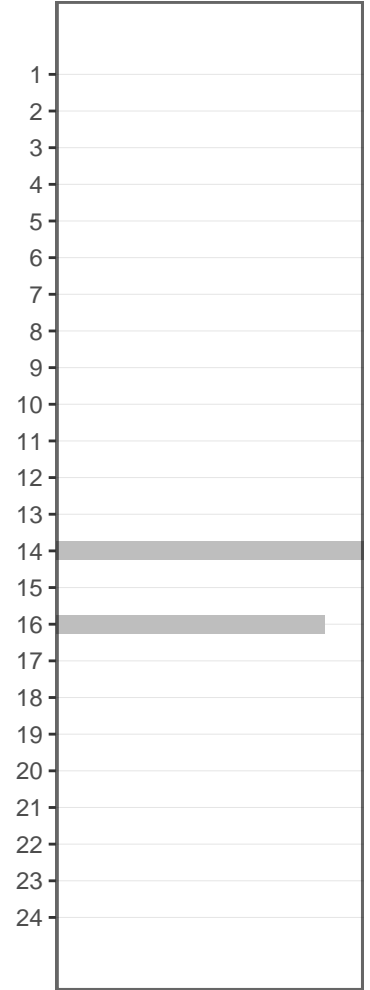
Molecular weight



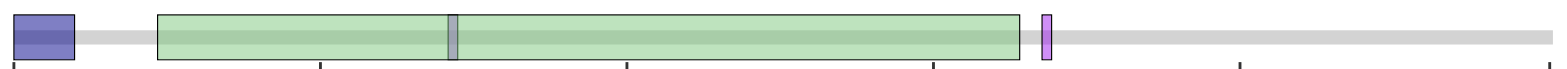
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

WGTYCPGDYPSLPDGYETGLDGLVAVGWMEDESEMHNLRTEFLRQGYHLVKGRTANGNSAVGSHLQFGDLQLEMDLFLMYMGTNPNANDNYTYVDDNLSLRASCKAVNGRDADLHFVWDFKFKAKAPEGSARKVEAQKQFTEAMSHRMLDNLNEMALVGLLFGDQKPEALKHFRPVGGPLVDVNTGLKSFVRFTEHCGSLGGYGMKHMRSIANIGNAGKMEQAVEASAGAQPEVPEPTWSSLRHGFA

NbL08g18880.1 far_upstream_element-binding_protein_2 [MW = 67.55 kDa]

No. of times detected



log(intensity)



Values from



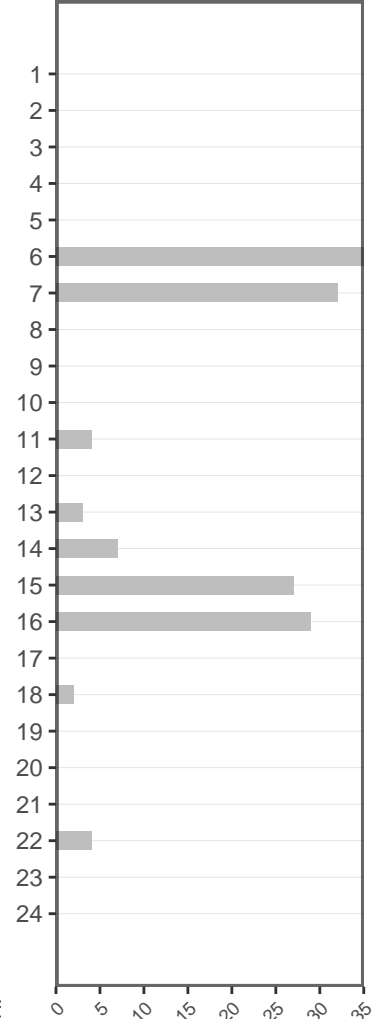
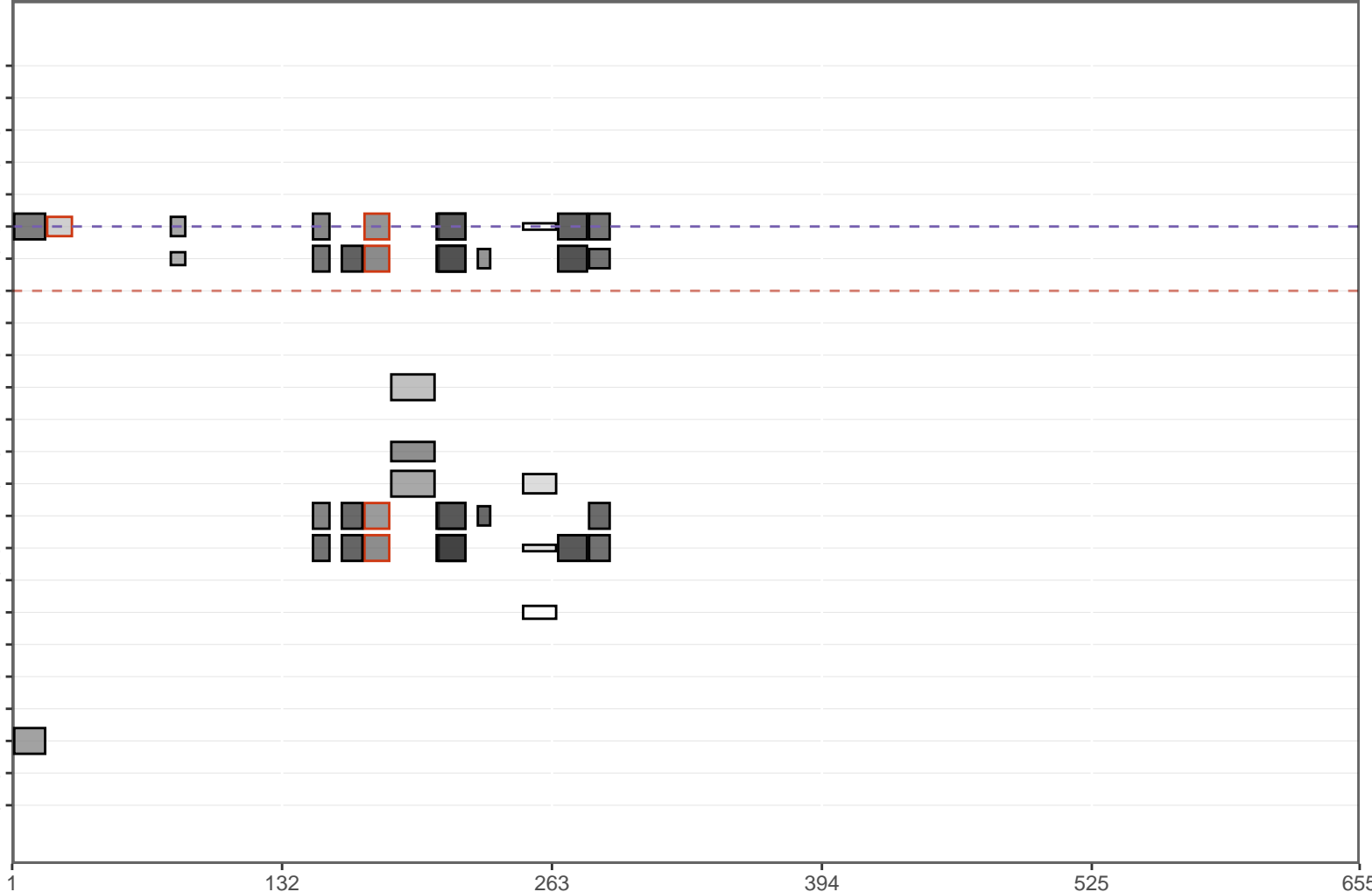
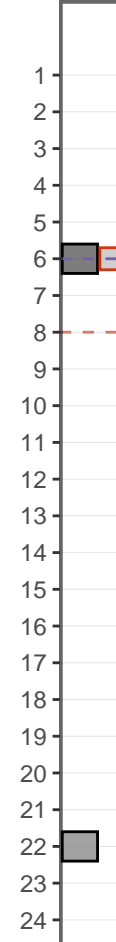
MW indication



Molecular weight



Gel Slice



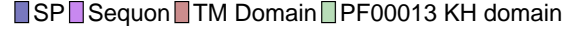
Protein length



Pfam domains



Pfam Description



Protein sequence:

IPDGYVQPGAYPGRPFHYHTSGQRPYGPYRQPSAGYSGWDGTAAGNQGSGGGGFHYNDGAPFGQGGTTPGGTAASTDNSAVGYNQGSASGYSQGGYSQGGYVGVGYNAAAPSGSGYGGTGYEQGGQYSSAAGYGNASNPSTSGDGNSEYGTGGGCGAAPPYVGSATGGQSGYPSQGSQAQYGMPTSGGQYGTTPRPAQVYANVYAPQTKPKPSPQYRWGGPQGSFSAQGGYAGPQPRMRYGYPQPAAGSGYAGPDSGSGRPRGYGAPTSQPGYC

NbL08g18800.1 60S_ribosomal_protein_L7-4 [MW = 32.93 kDa]

No. of times detected



log(intensity)



Values from



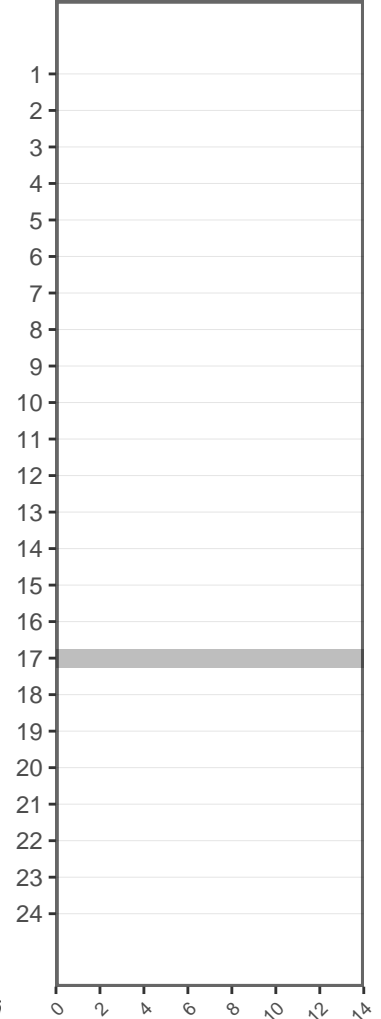
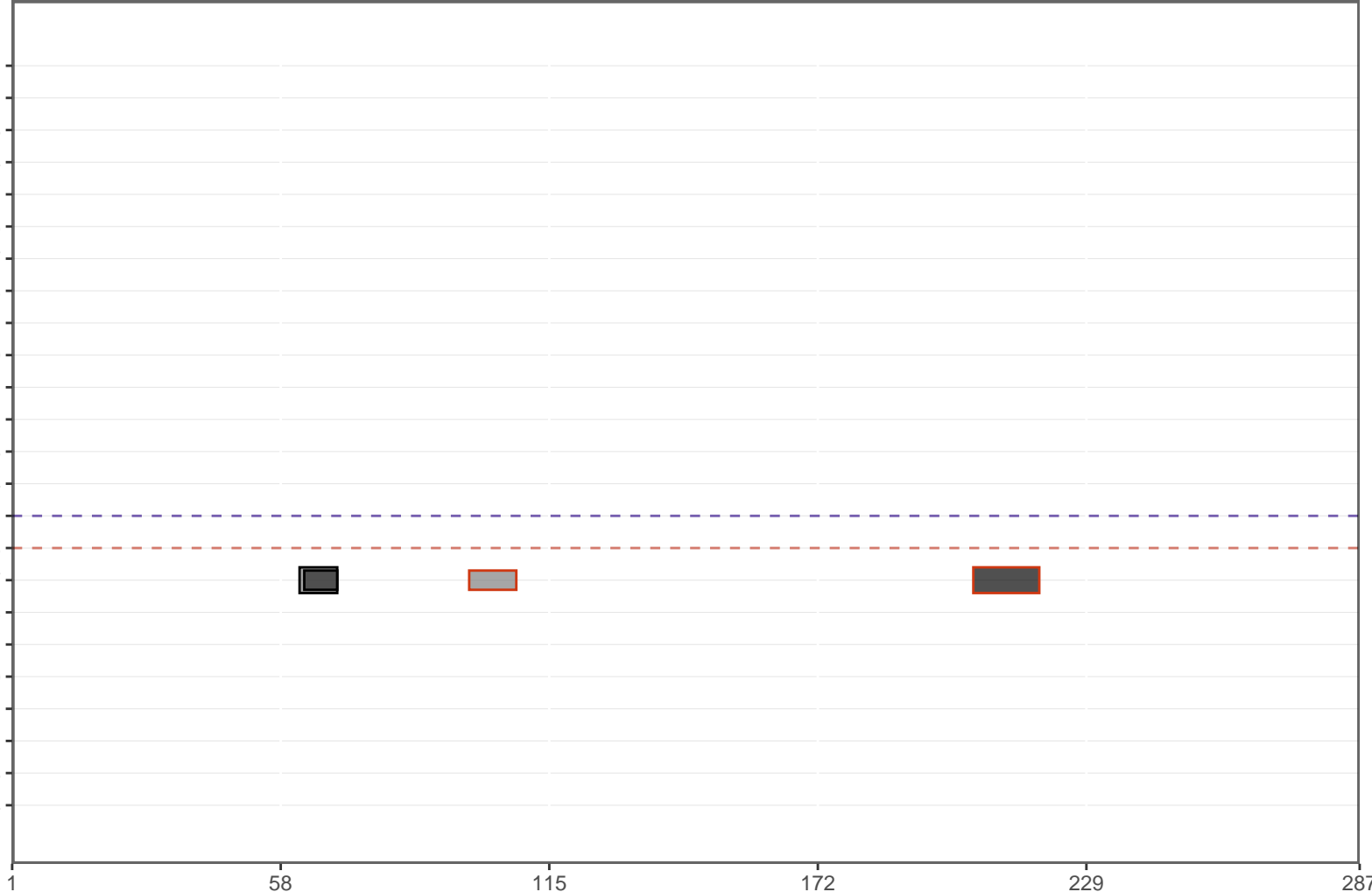
MW indication



Molecular weight

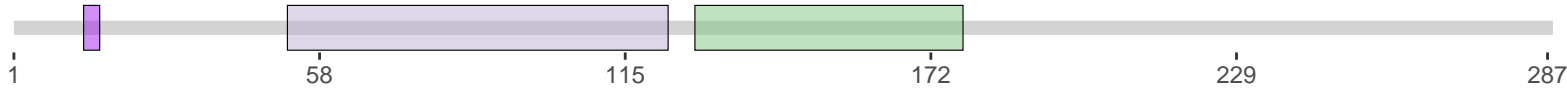


Gel Slice



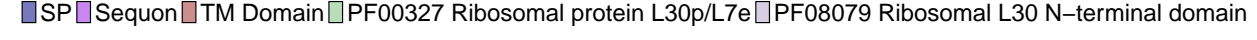
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MFIRIRGINAMAPDQFNKILQLLRDFNGVFLKVKATVNLHHRVPEVYTYGYPNLSKQVRELFYKRGYGLKDKRIALTONSISDQALGKHGIGCAEDLVHEILTVSPHKEANNLWPFQKAPLGGLLKKRKHVVEGGDAGNRENYNEIIRRMN

NbL08g18750.1 tryptophan_synthase_beta_chain_2-like [MW = 54.1 kDa]

No. of times detected



log(intensity)



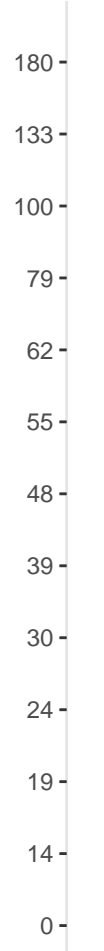
Values from



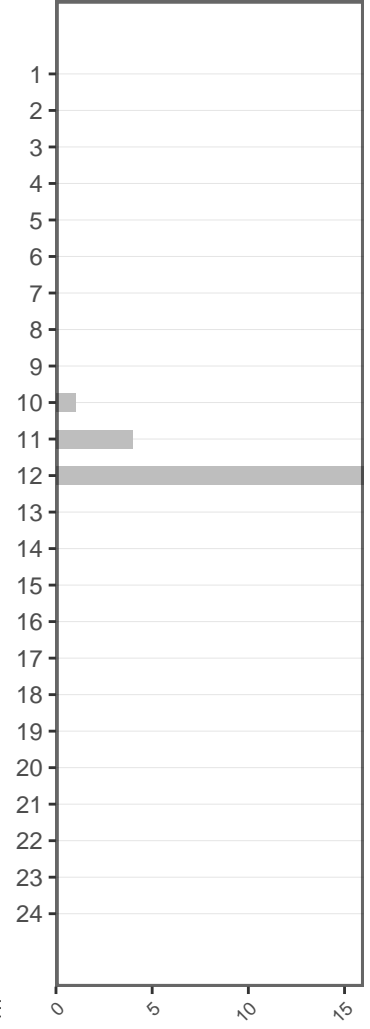
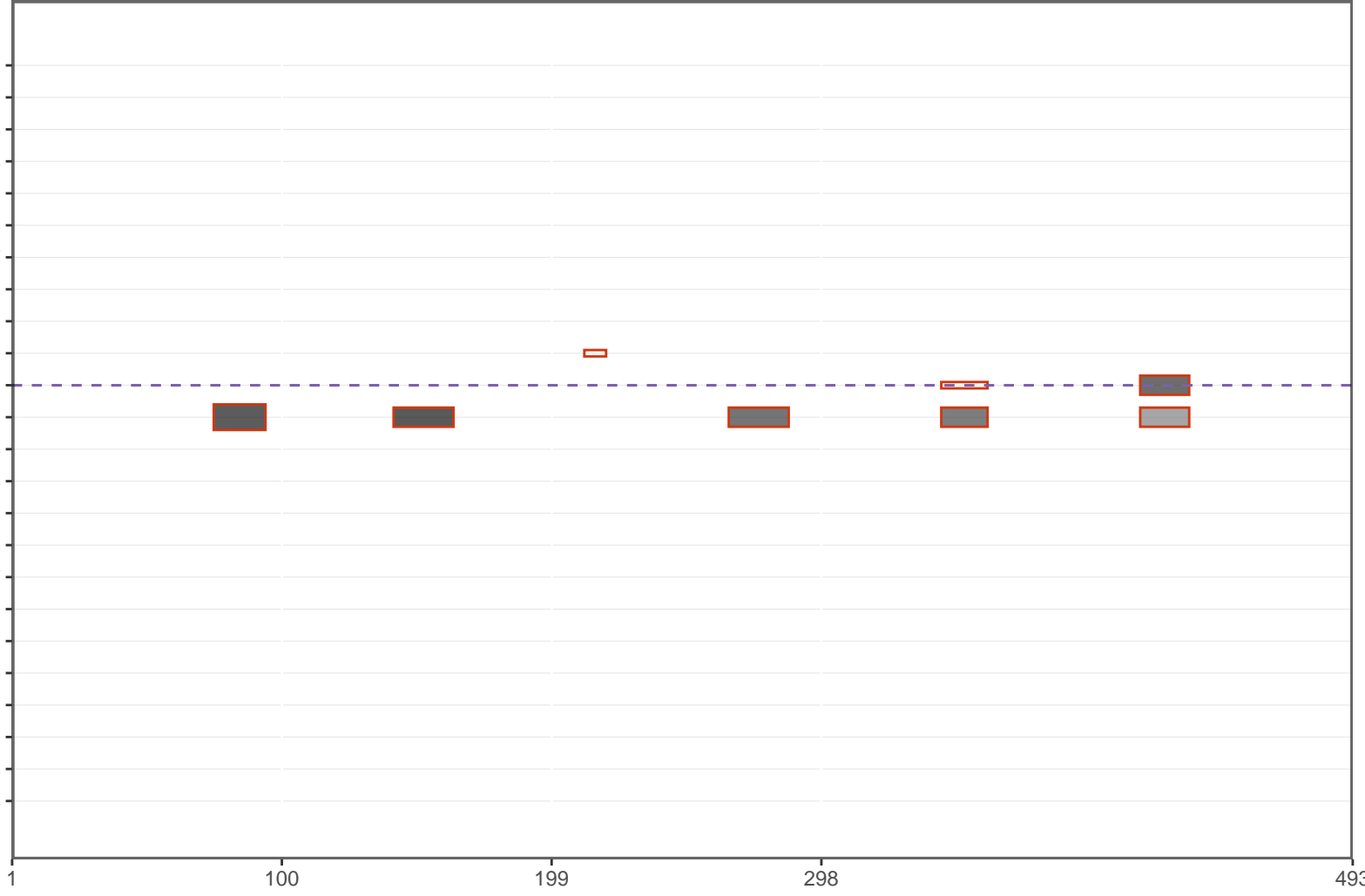
MW indication



Molecular weight

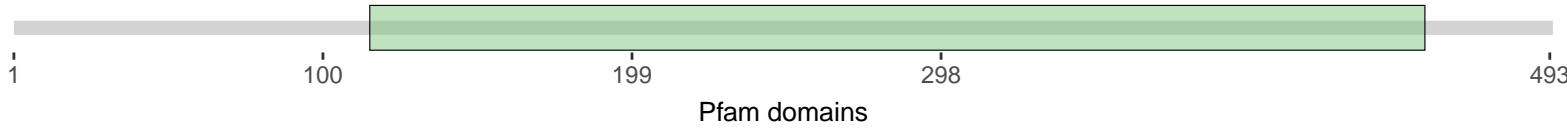


Gel Slice



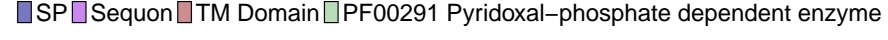
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

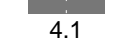
.GRTLRMDPSSPGLGIAISEAVEIATNADTKYVLGSEVNLNHLHQTIVGEEGKIMEGLGEIPVHIGCTGGGDFAGLVFFPIREKLGKGNLPIRAVEPACGSLTKGVYVYDGDGTAGMPLMKMHTLGHDRIPDPHAGGLRYHGMAPLHSHVYELGFMENISIPQTEGFKGAGFARSEGLIPKPEPTHAIAATIRALRCKTGESKVLMMAMGGHGHFDLSEYDKYLOGGMVDLSEEEKESLAKIPQVPE

NbL08g18700.1 60S_ribosomal_protein_L13-1-like [MW = 23.73 kDa]

No. of times detected



log(intensity)



Values from



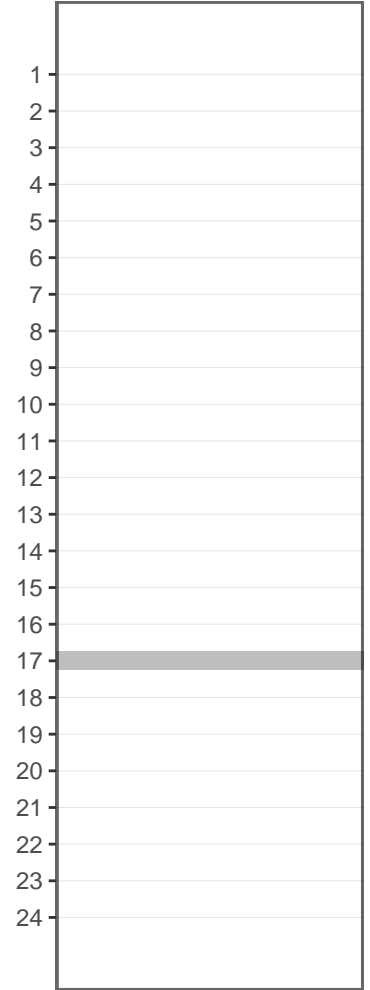
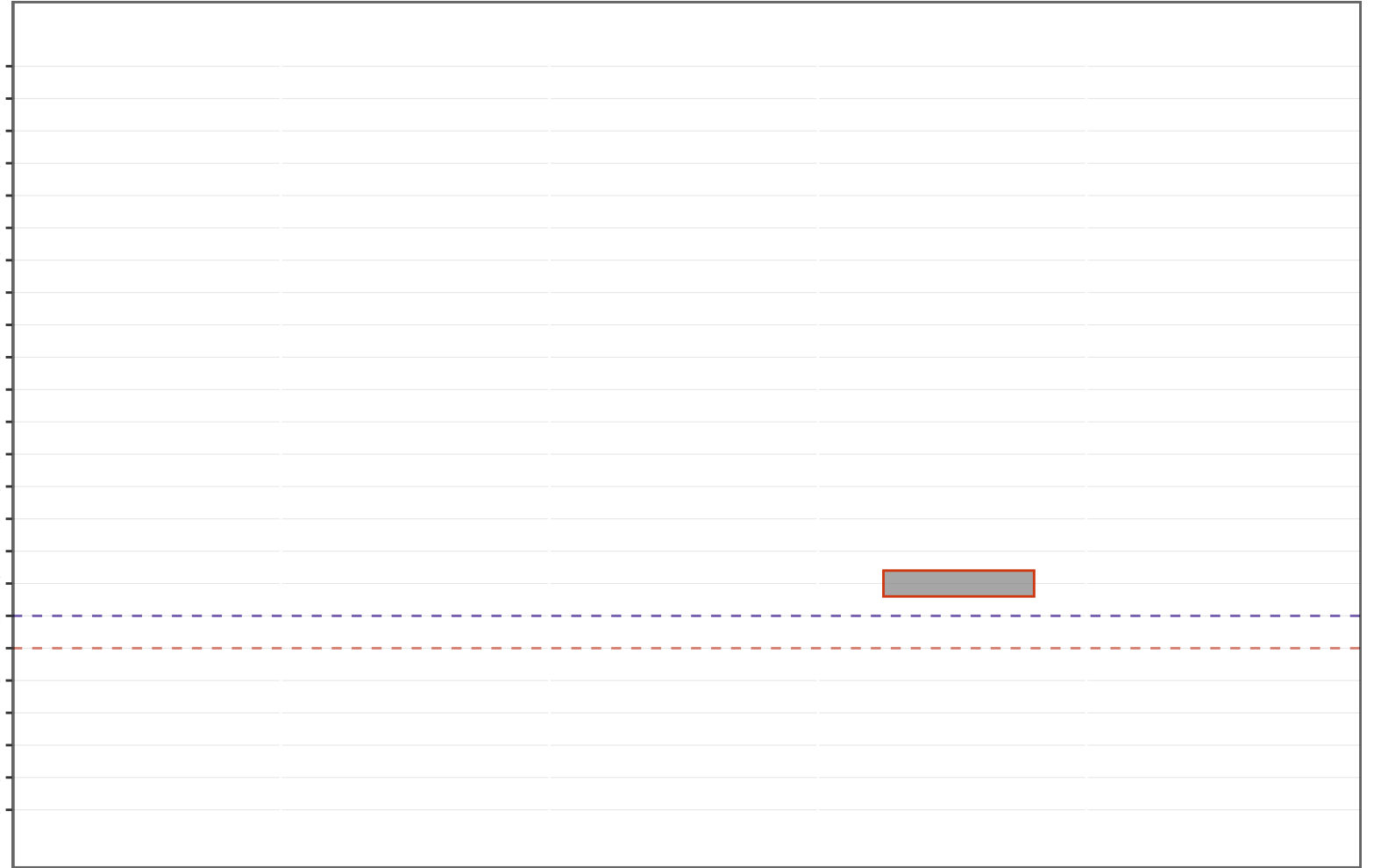
MW indication



Molecular weight



Gel Slice

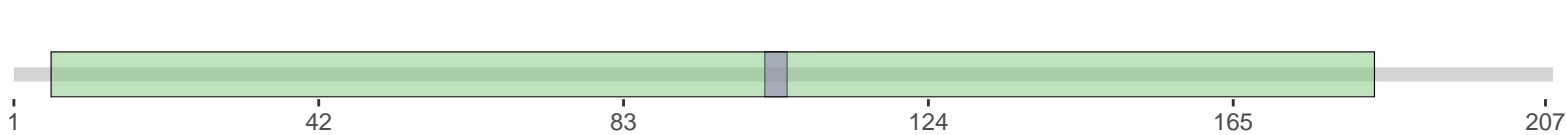


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

APITGIADVHRRNRRLLEGLTNVDRLKTYKANLIFPRHAKKWKAGDSSPEELATATQVGGTYMPTREGSTELVWVTDEMNSFNAYGKLIERTNERHIGERLKRAAEAEEKKEK

NbL08g18630.1 scopoletin_glycosyltransferase-like [MW = 39.54 kDa]

No. of times detected



log(intensity)



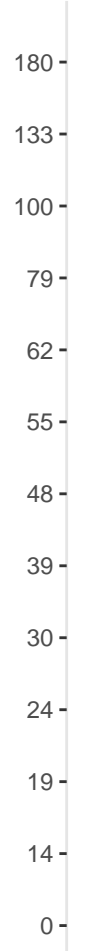
Values from



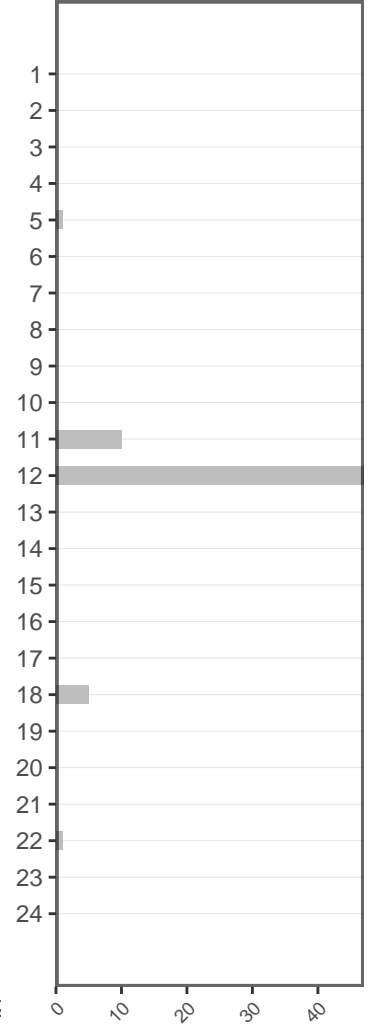
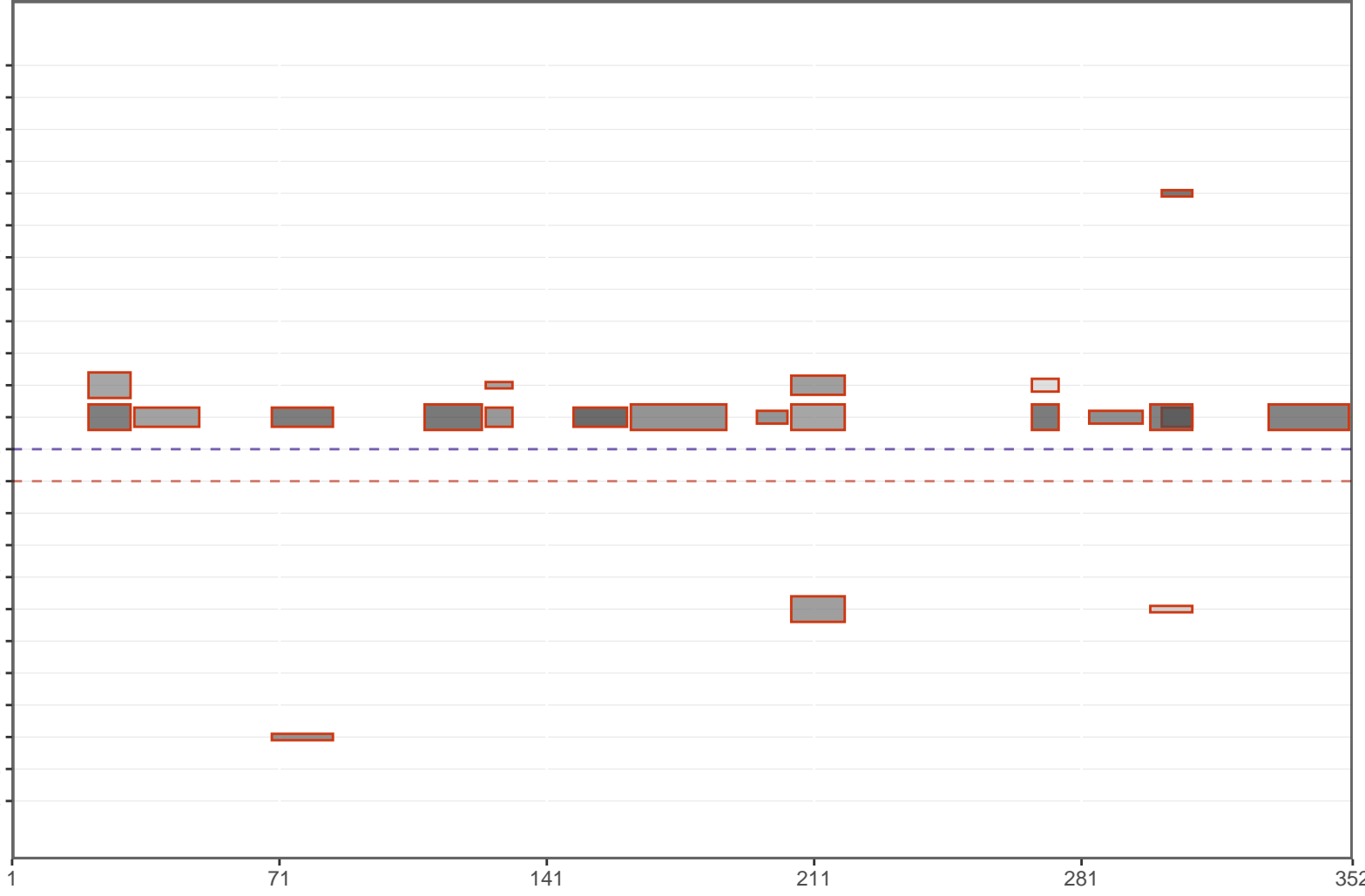
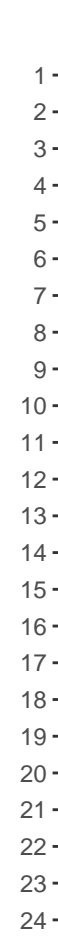
MW indication



Molecular weight

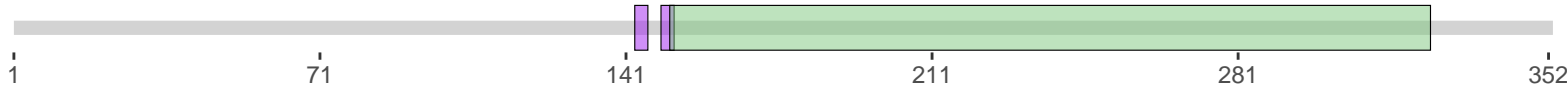


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

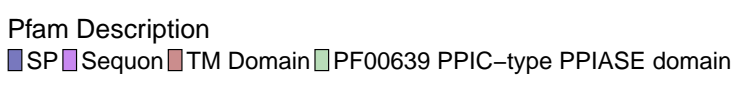
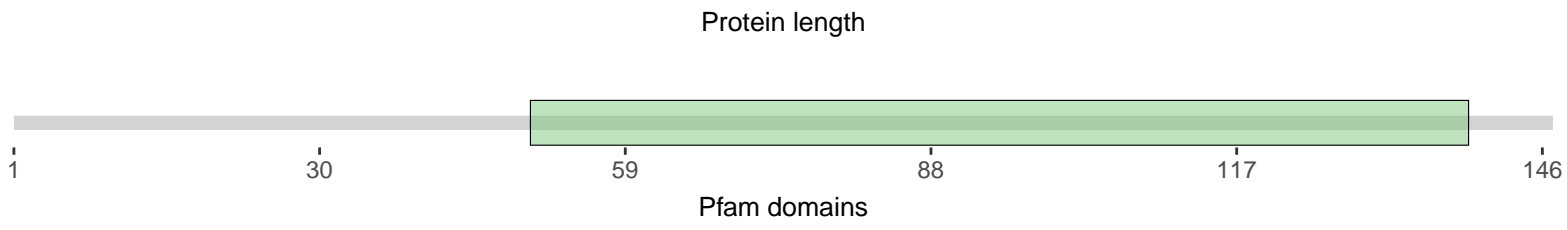
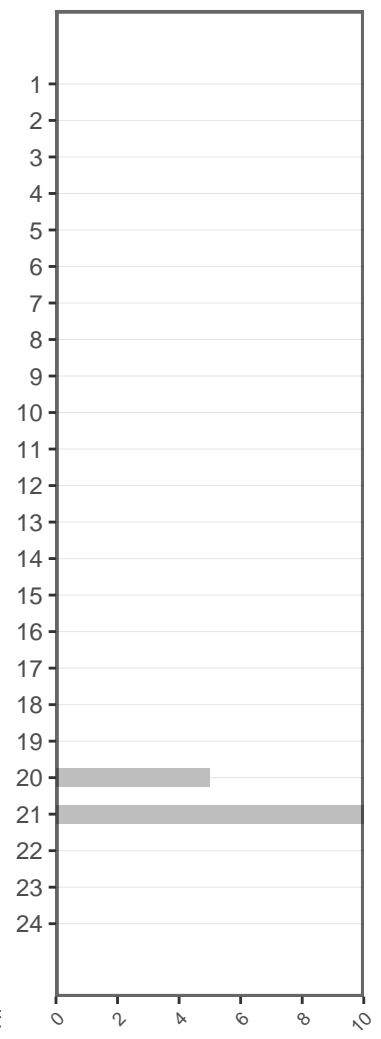
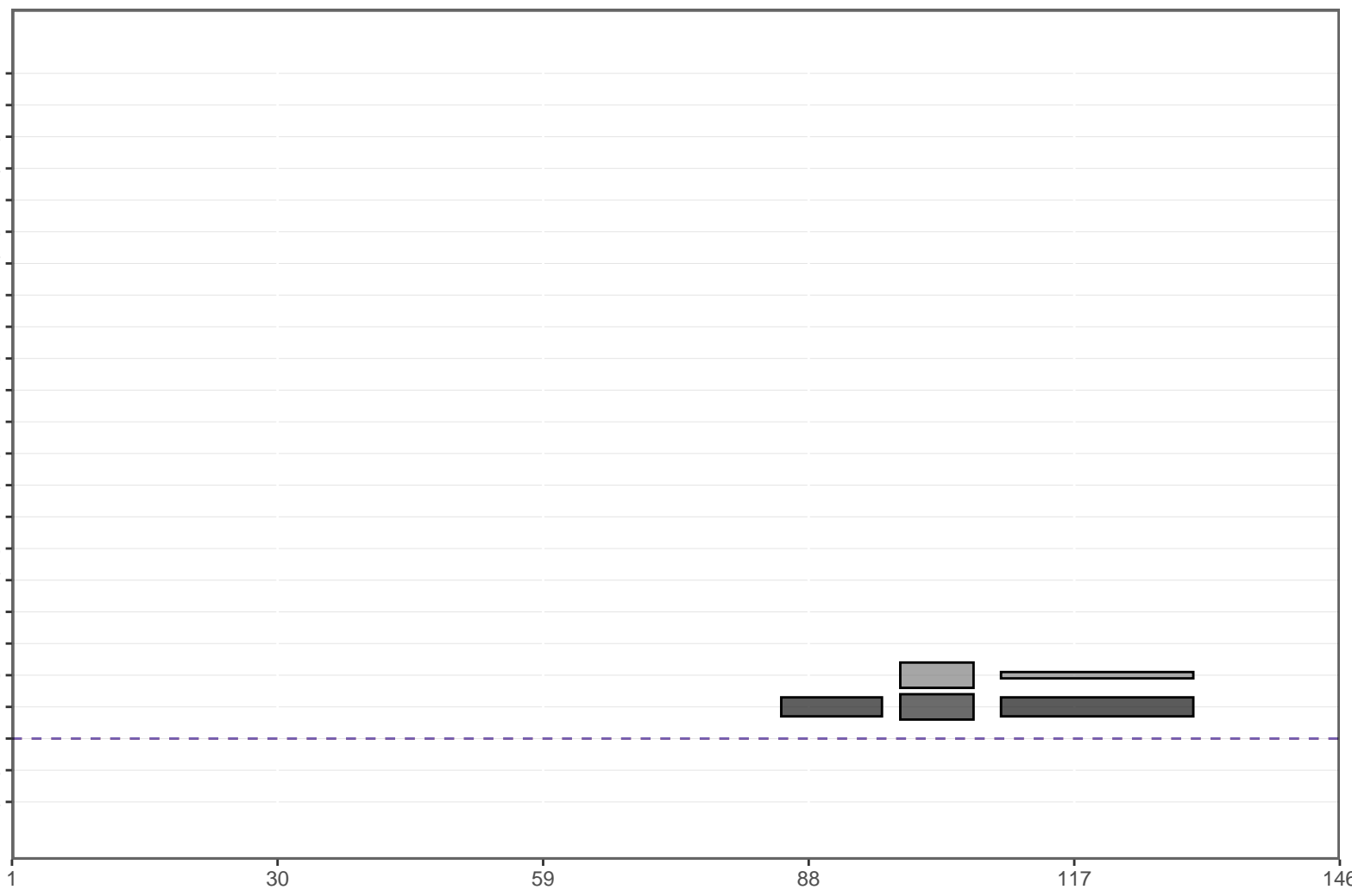
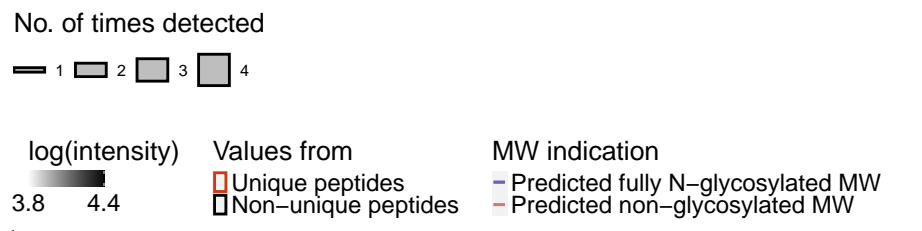
Pfam Description



Protein sequence:

SKSPSSIIYAFGSDVYPTLEEEHEEIAKALEEBSRGNFIWVSKNGDGYFNTLETQVGRGLINGWAPQLLLGHPSTGGFLTHCGVBSIMEAIGDGVPLLAWPIRGGDFYNAKLVNGLKIGHMVSISGENGLKRVKKEEIGGVGRIMEDKGVHNRWKLSDKFRHGFPISSAASLNDKDFRIMQA*

NbL08g18120.1 peptidyl-prolyl_cis-trans_isomerase_NIMA-interacting_4 [MW = 15.13 kDa]



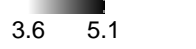
Protein sequence:
 INEAYKLGEGWLDGDKVPPAEFAKVAAYSECPGKGGDLGWFRGKMGAPFQEWNTFVGVTSAPFKSTHGWHILSEGRKN

NbL08g17940.1 NAP1-related_protein_2-like [MW = 29.02 kDa]

No. of times detected



log(intensity)



Values from



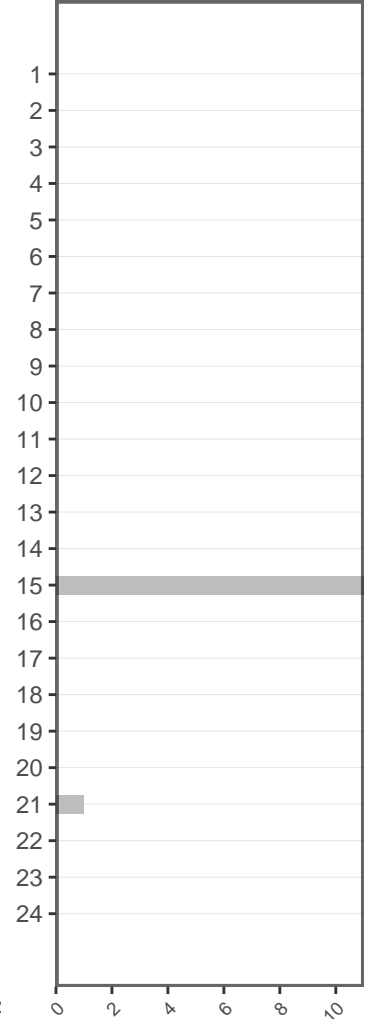
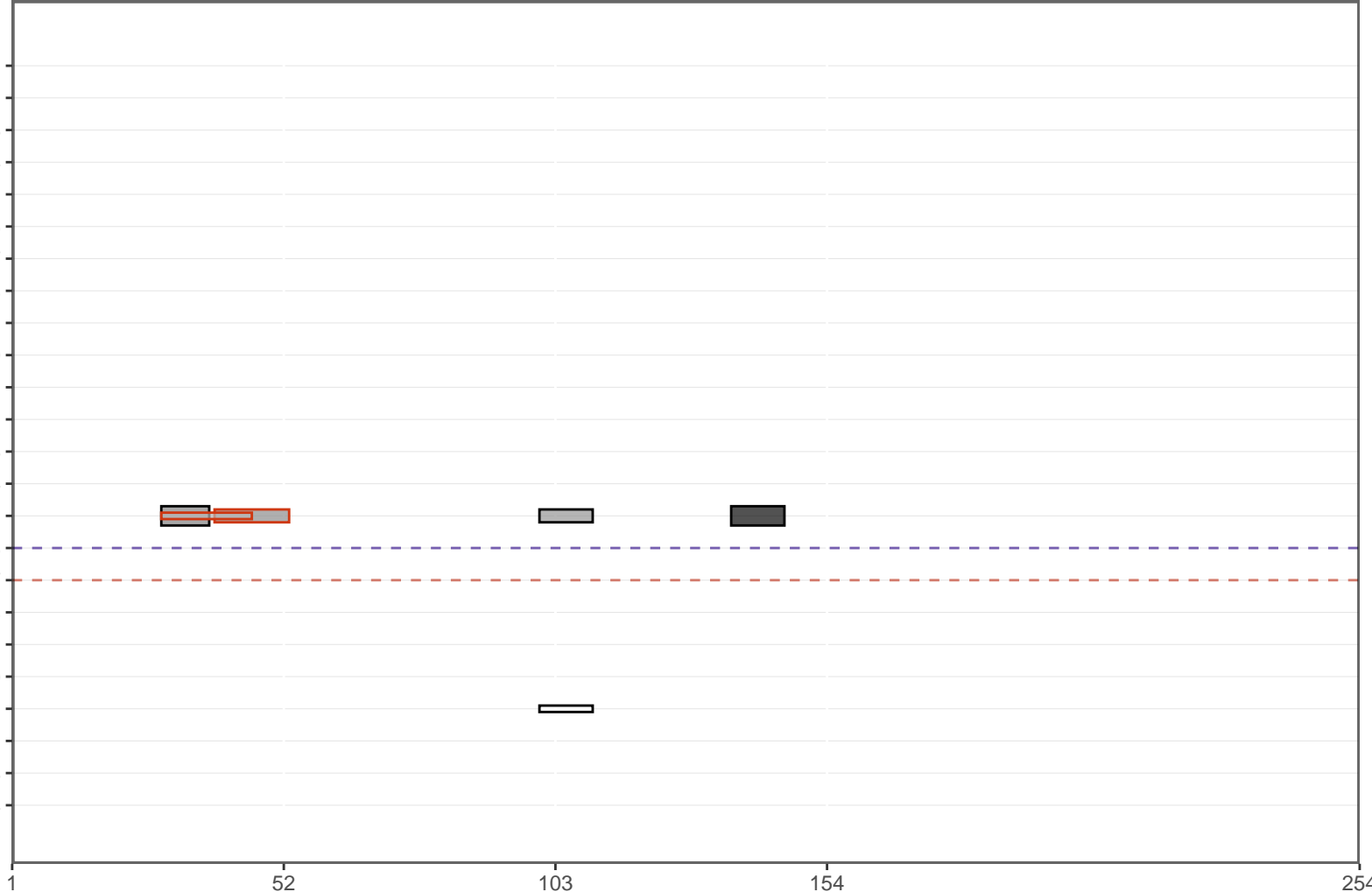
MW indication



Molecular weight

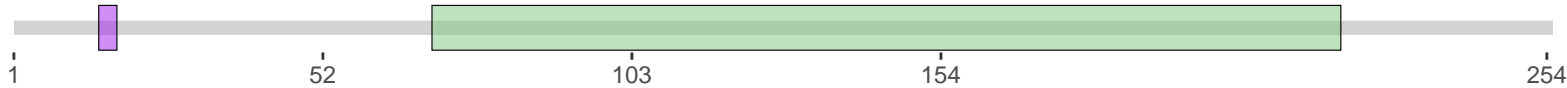


Gel Slice



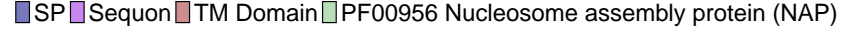
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

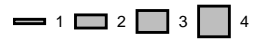


Protein sequence:

YSITTFNPNANPYLENTKLAKEYTFLIEDGPTKISATTKRWKEGTGIPNGVAHEKGNKRSHAEESFFTWFSVNVKDKDEALEHGDEVAHIKDDLWPNPLFYFNNEPDEEDFDGDKGDSGSEDEEEEEDEEDGGEE

NbL08g17820.1 plasma_membrane_ATPase_1 [MW = 105.24 kDa]

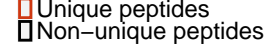
No. of times detected



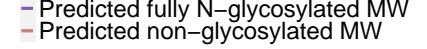
log(intensity)



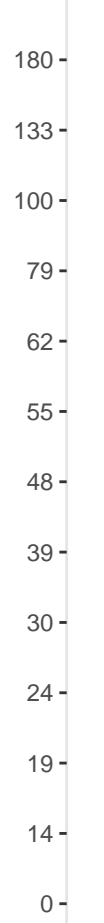
Values from



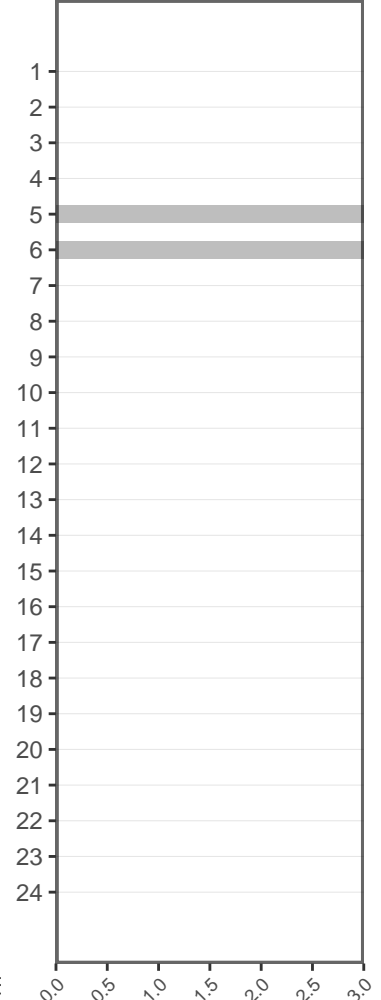
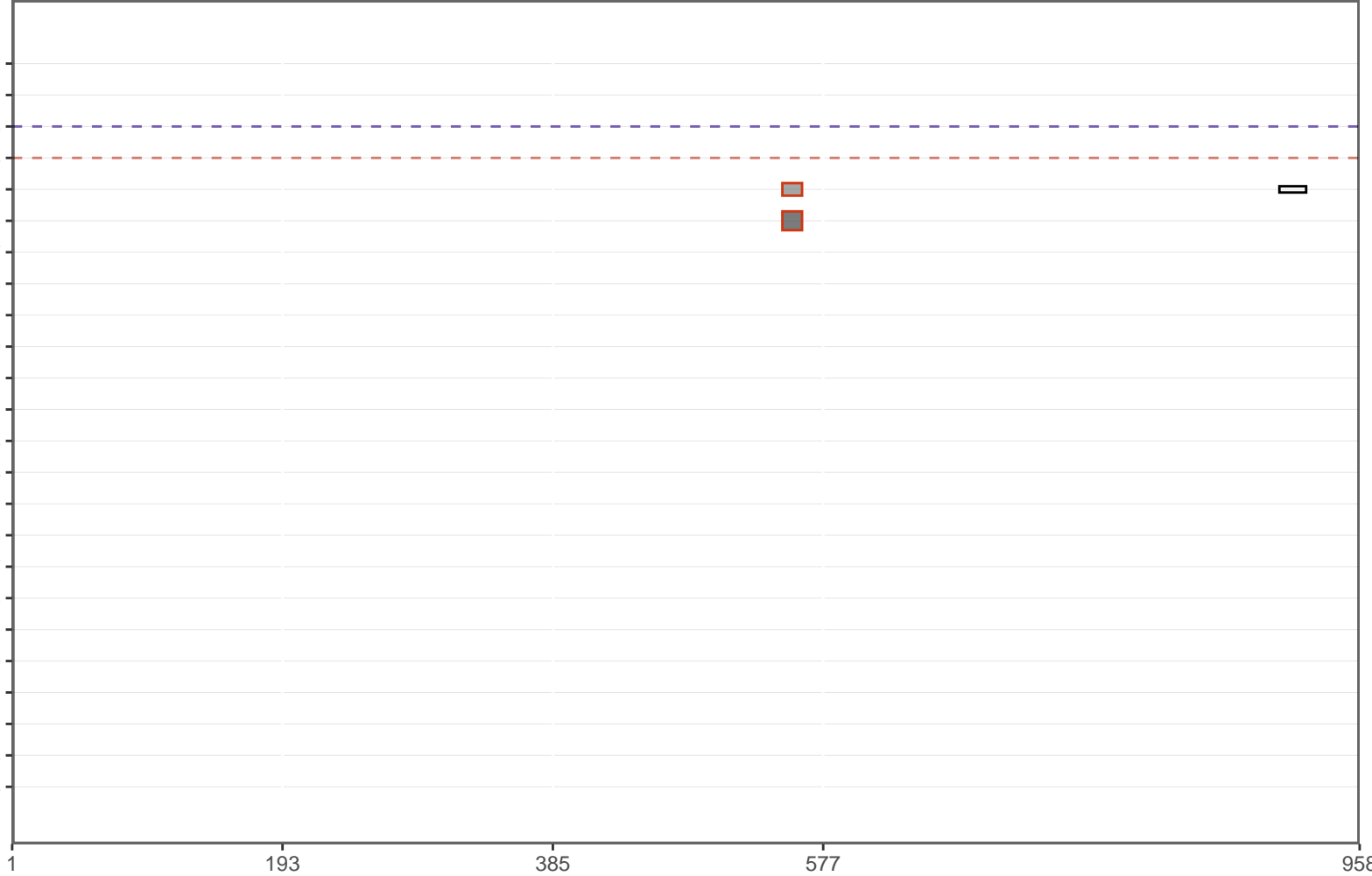
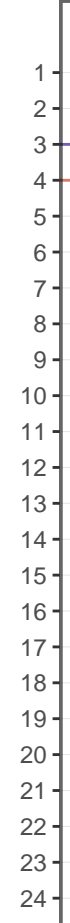
MW indication



Molecular weight



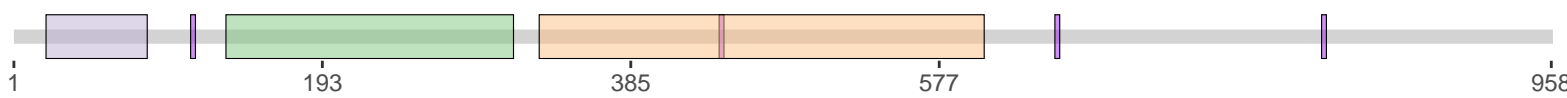
Gel Slice



Protein length

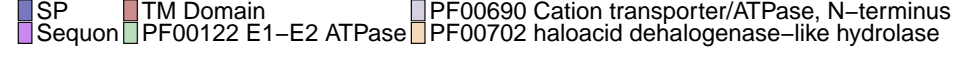


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SVAYQEVPEGRKESAGAPWDFGLPLFDPPRRHDSAEIIRRALNLGVNKKMITGDQLAKGKTRRLGAGCTNMYPSGALLGGTNDSEISALPDELEKADGFAGVFFEHKYEIVKRLGARKHCGMTGGVNDAPALKKADGIAVDDATDAARASQDAVLETEPGLGVHISAVLTSRAIFQRMKNKTIYAVSIRIRIVLGFMLLALWKFDFPFPMVLIHAIINDGTMITSGKRVKPSPLPDGKLAIEFTTGVAVGGYLAMMTVIFEWAKTFFFRVFGVSTLEKATATDOOFKRLASA

NbL08g17690.1 protease_Do-like_9 [MW = 63.34 kDa]

No. of times detected



log(intensity)



Values from



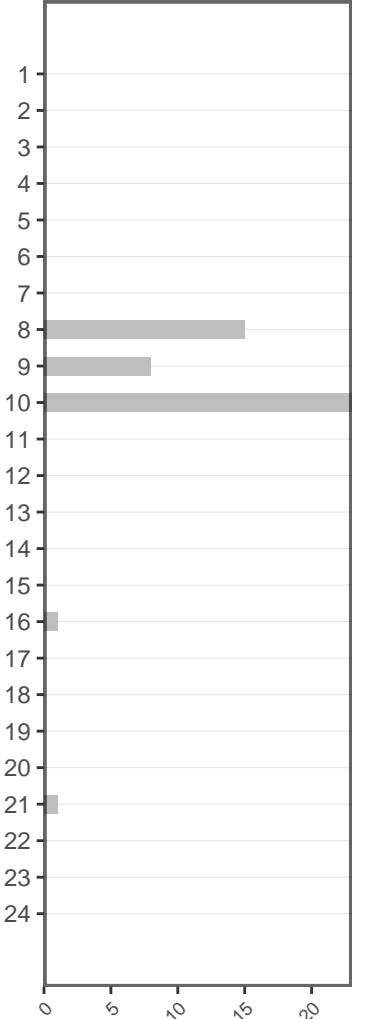
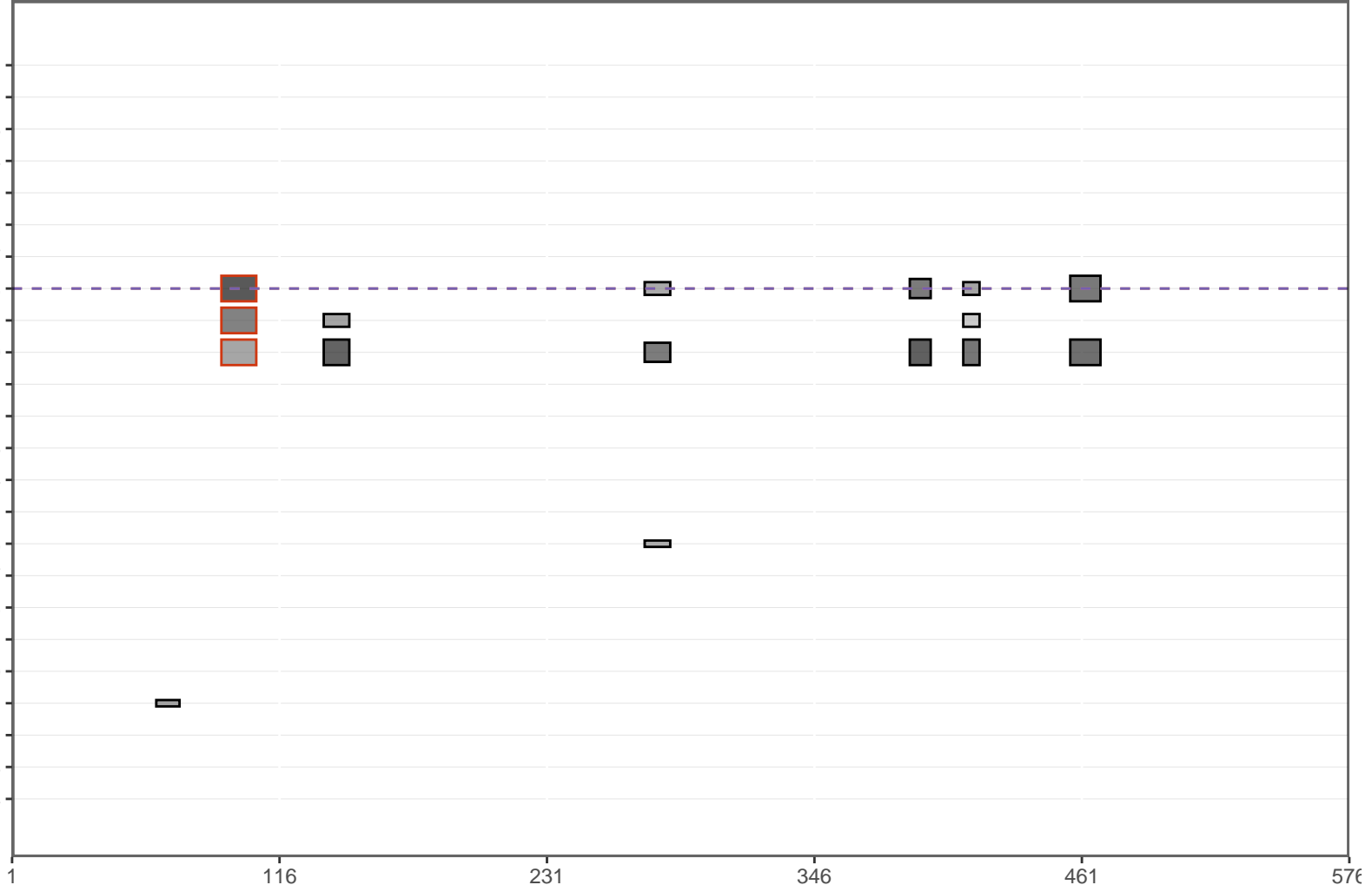
MW indication



Molecular weight

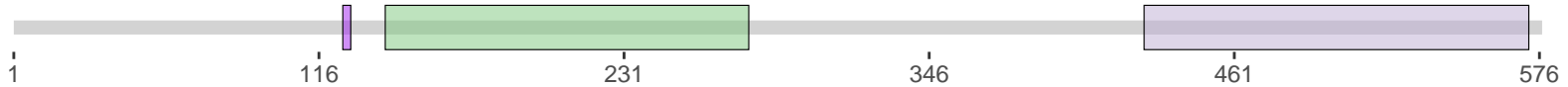


Gel Slice



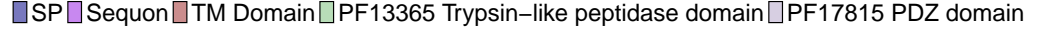
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NCVGIAFQSLGHEDEVNGYVWPTPMVHFQDYEKNGAYTGFPILGIEWQKMEKNDLRLSMSMKPDKGKGVRRIRIDTAPAEMLLMPDVLVLSFDGVDIANDGTVFRHGERIGFSVYVSGKYSGDEAAWVLRNSELNFKIKLATQMLRVLVPHNKGRPPSYVIAAGFVFTTVSVPLRSEYKDKVEYAPVQLLDKLLHEVYRQSPDEQVYVSGVLDVADNIGYEENNTQVLAFLNGKPKVNLKSLASVMEVNGNDFELKLDLEYQQVYVLTQTKTAKSATDILTHICPSAMSE

NbL08g17680.1 iron-sulfur_cluster_assembly_protein_1-like [MW = 18.19 kDa]

No. of times detected



log(intensity)



Values from



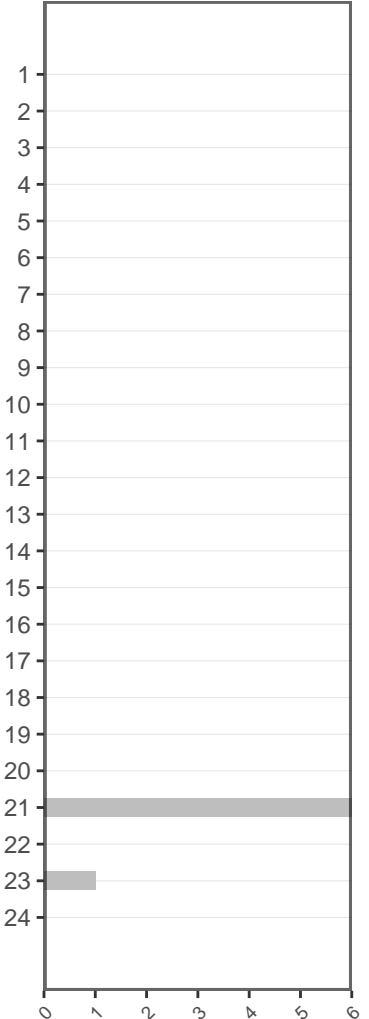
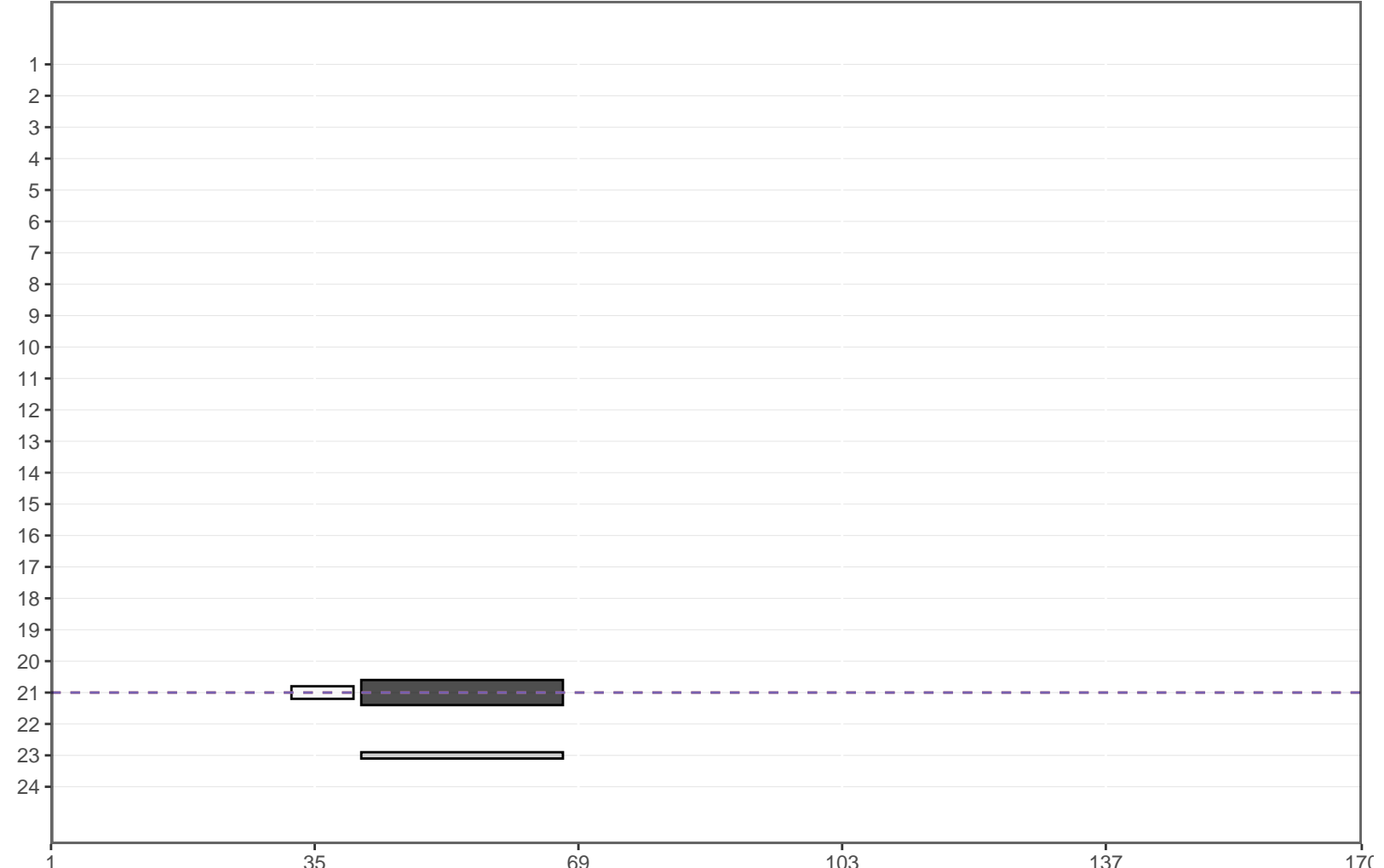
MW indication



Molecular weight

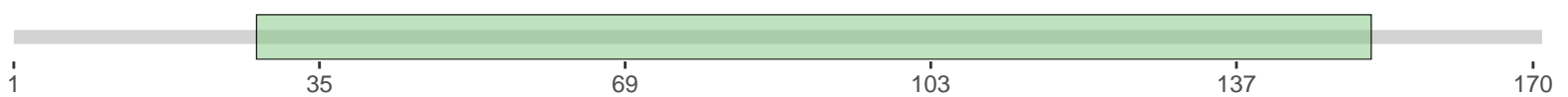


Gel Slice



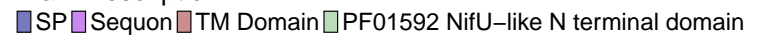
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YDEETGKTDACFKYFGGSAIASSVATEFWVWKGQMEVLSIKRTEAKHLSLPPVWLHGSMLEDAIKAAWKDYSAKRAKLSDNAIDGQMGKAVDA

NbL08g17510.1 31_kDa_ribonucleoprotein_chloroplastic [MW = 45.08 kDa]

No. of times detected



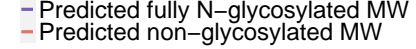
log(intensity)



Values from



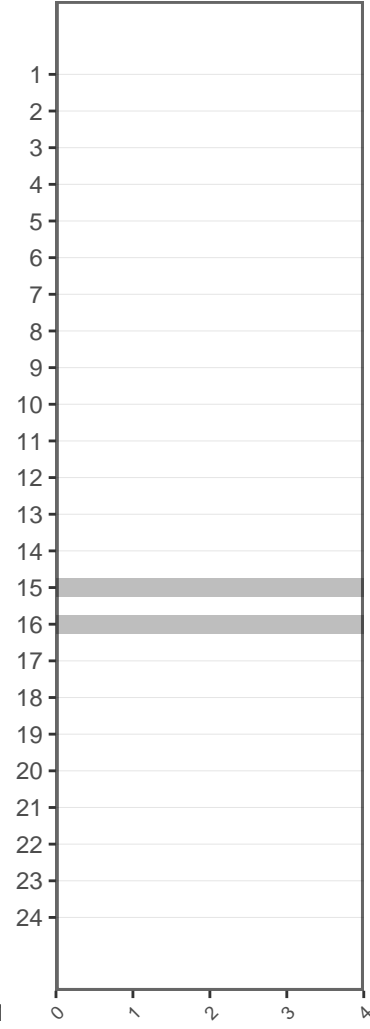
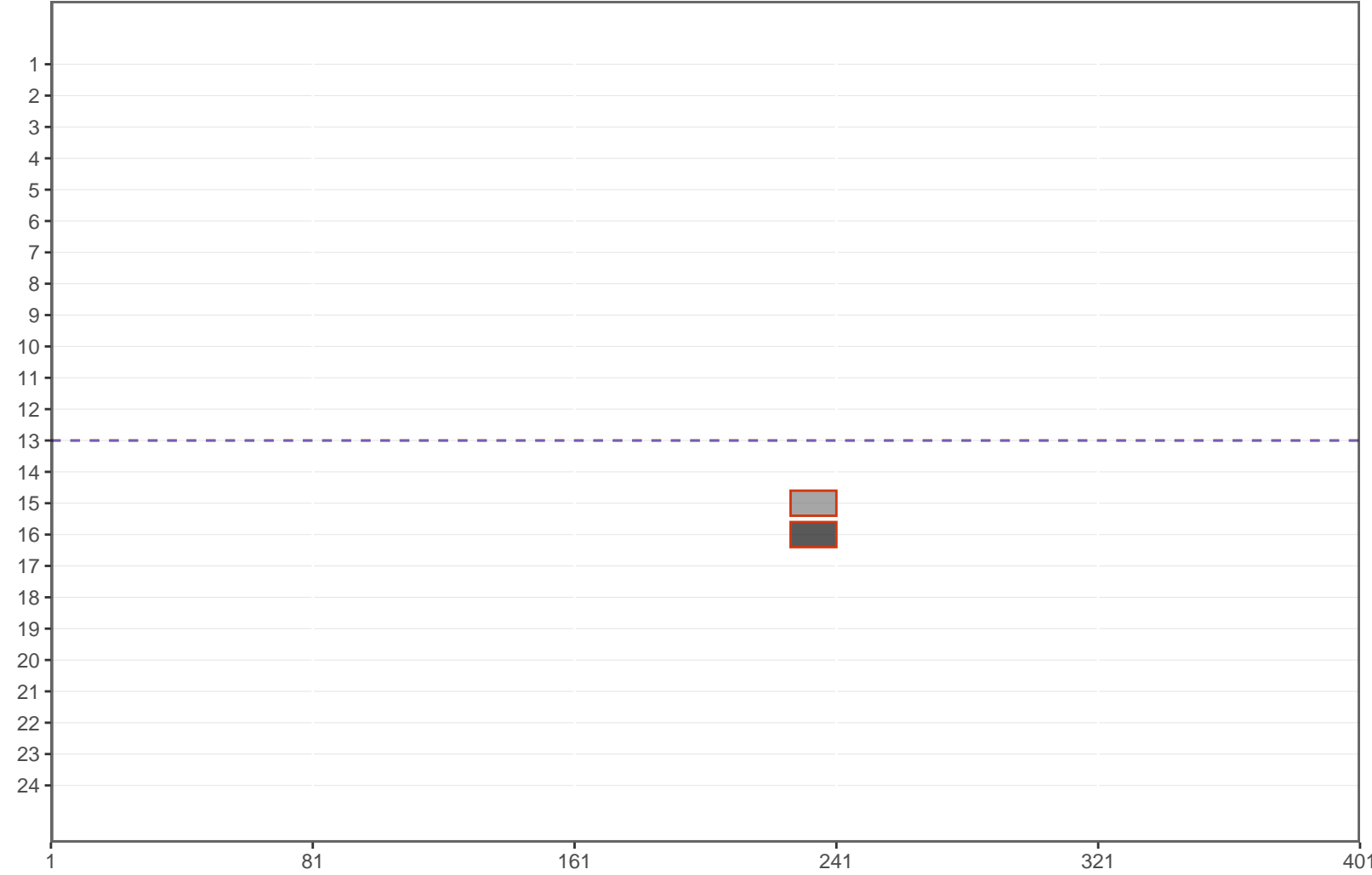
MW indication



Molecular weight

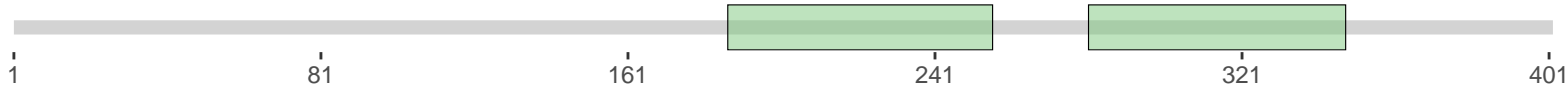


Gel Slice



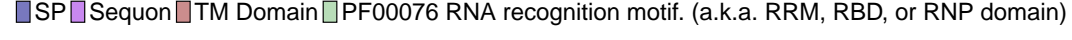
Protein length

Peptide counts over 4 repeats



Pfam domains

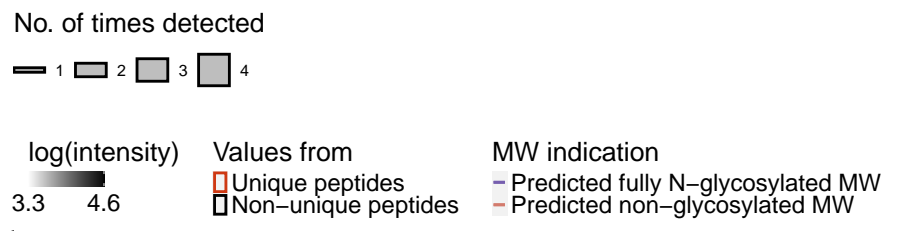
Pfam Description



Protein sequence:

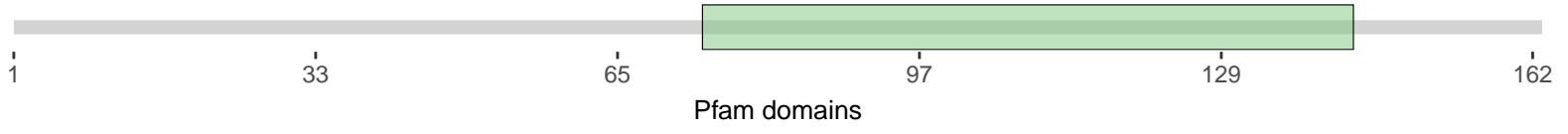
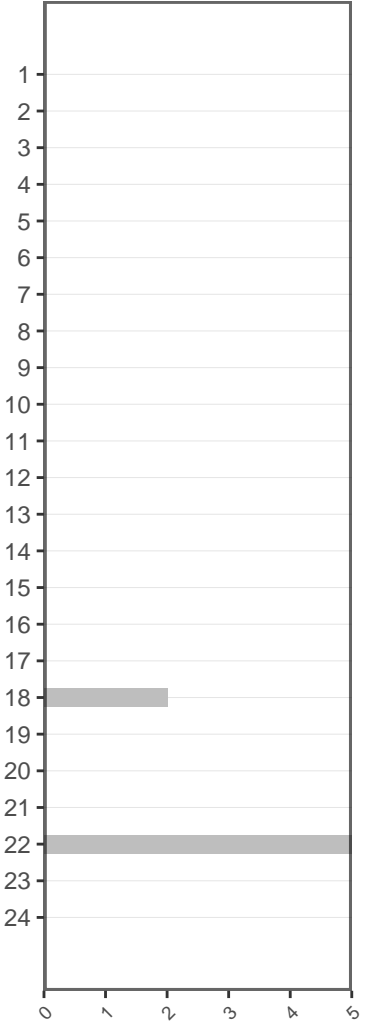
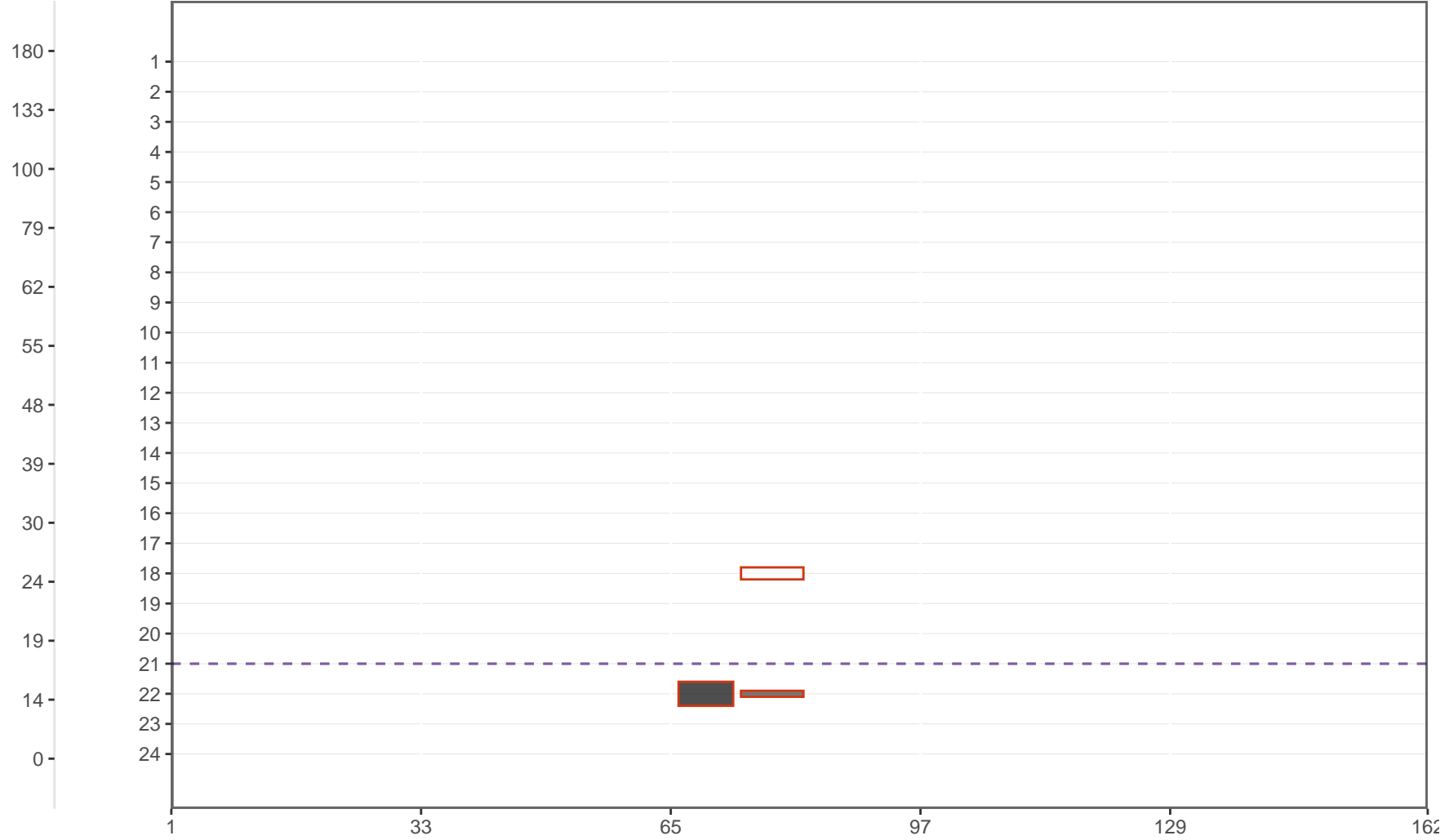
INLPYDIDSEGLARLFEGAGVEAEVYNNRDTDGRGRFGFVMTSTVEEAQKAVEMNRYDVNGRLLFTVNAKARRGERPERPPOTFEGQVRYVGNPNWGDARLEQLFSEHGKVSARVYVDRETRGRSRGFGFVTMAGEAEMSDAIANLGGVHARRFLTHNQHAHLHIVFEETRKGQGVLSIAFHIFHLNHFHSFGRGSDP

NbL08g17390.1 glycine-rich_RNA-binding_protein_4_mitochondrial-like [MW = 18.32 kDa]



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

Protein sequence:
 NPSTKLVVSGLSFRITTEESLKAFAFDGELVEVNLMDKIANRPRGFALRIVATEEESQKAIEGMHGKFLDGRVIFVEVAKPRSELRRITARDQ

NbL08g17080.1 GDSL_esterase/lipase_At5g03980-like [MW - SP = 38.77 kDa]

No. of times detected



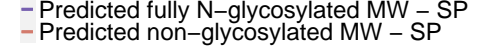
log(intensity)



Values from



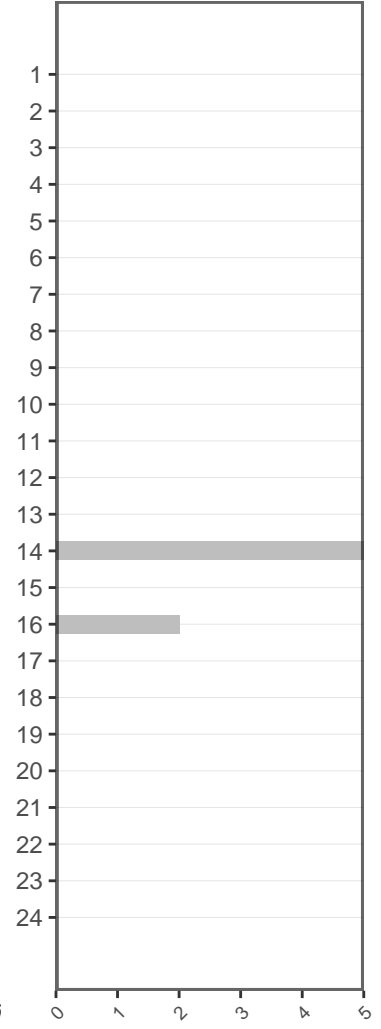
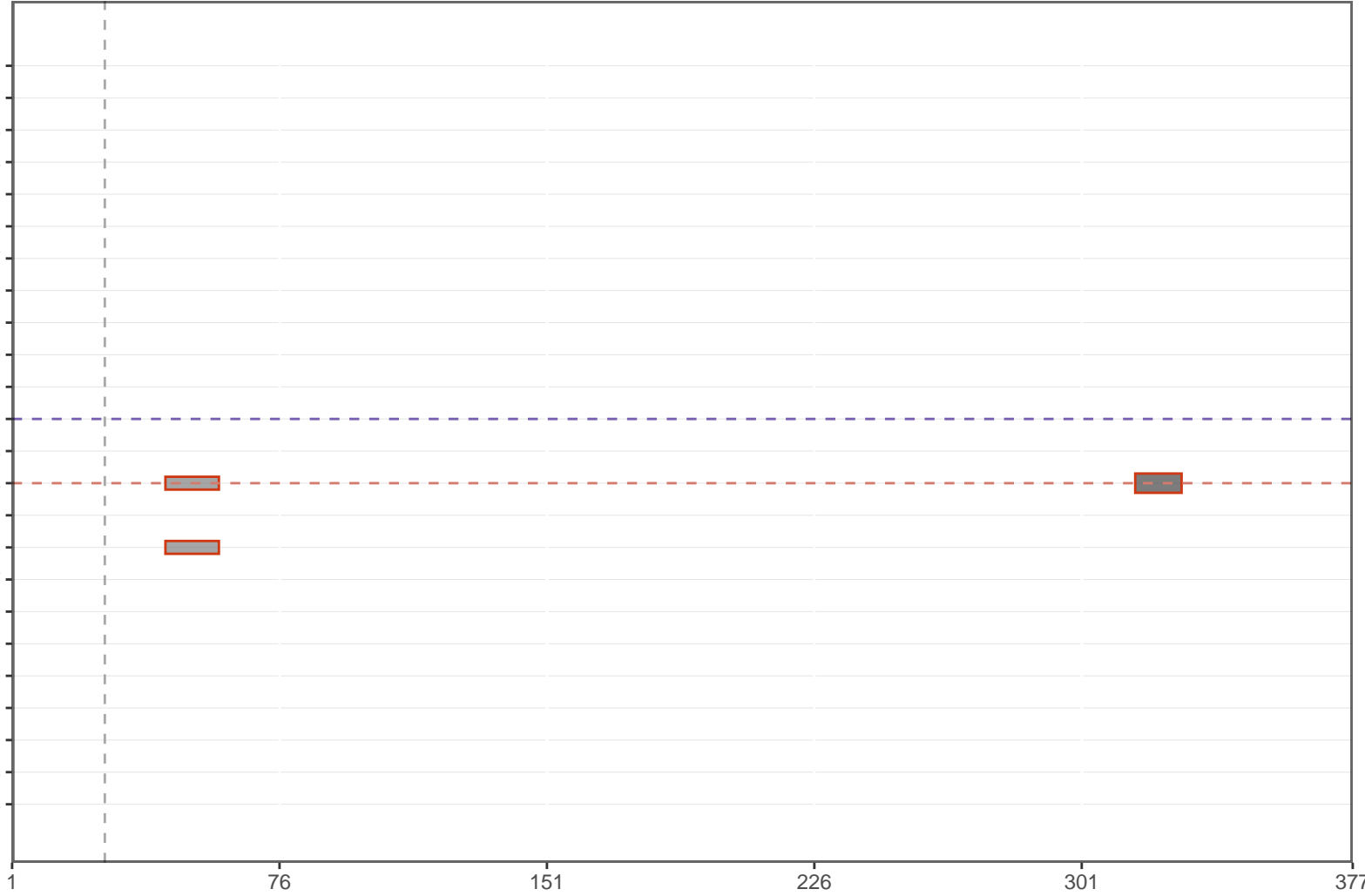
MW indication



Molecular weight

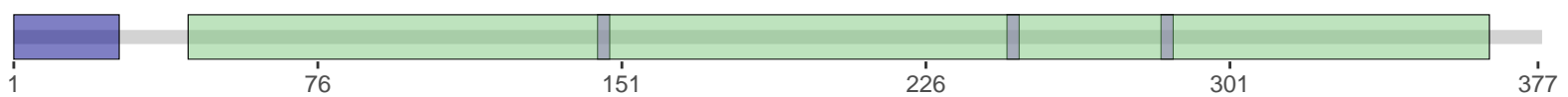


Gel Slice



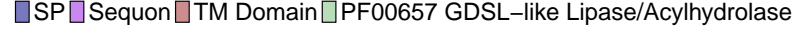
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

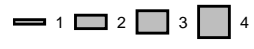


Protein sequence:

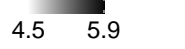
.FLVGGGGNEFFYGLTGGKMEELRNMVPEVQINVEAVNTVTFGFGAIRLIPGNFPIGGLPMTLTFLELNMSMAYDENHGLKDLNLAIFYNEHGGAEIDKKNKPNVFLVYGDYNNAYGWLLGHTVYNGGFDGNSLLKACGGEGGYNYDAKRGCGFFDGVFVCGADPGTHSEWDDGVHTEKAYSIIATWLHDDLPQLKG

NbL08g17070.1 probable_U6_snRNA-associated_Sm-like_protein_LSm4 [MW = 15.76 kDa]

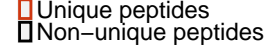
No. of times detected



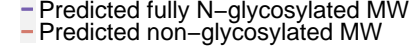
log(intensity)



Values from



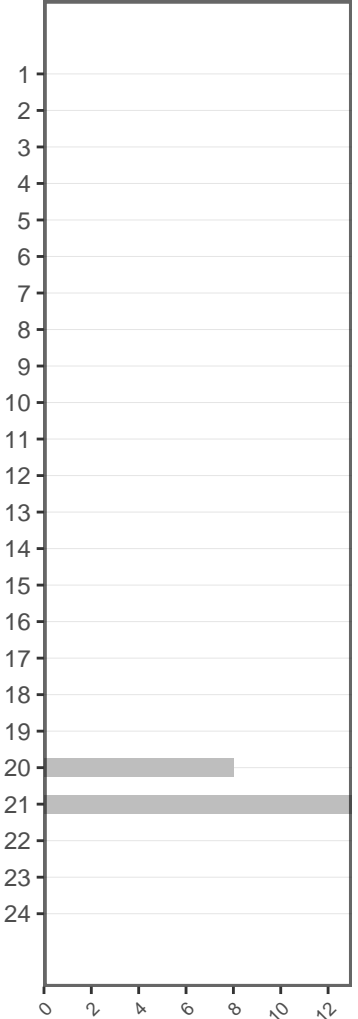
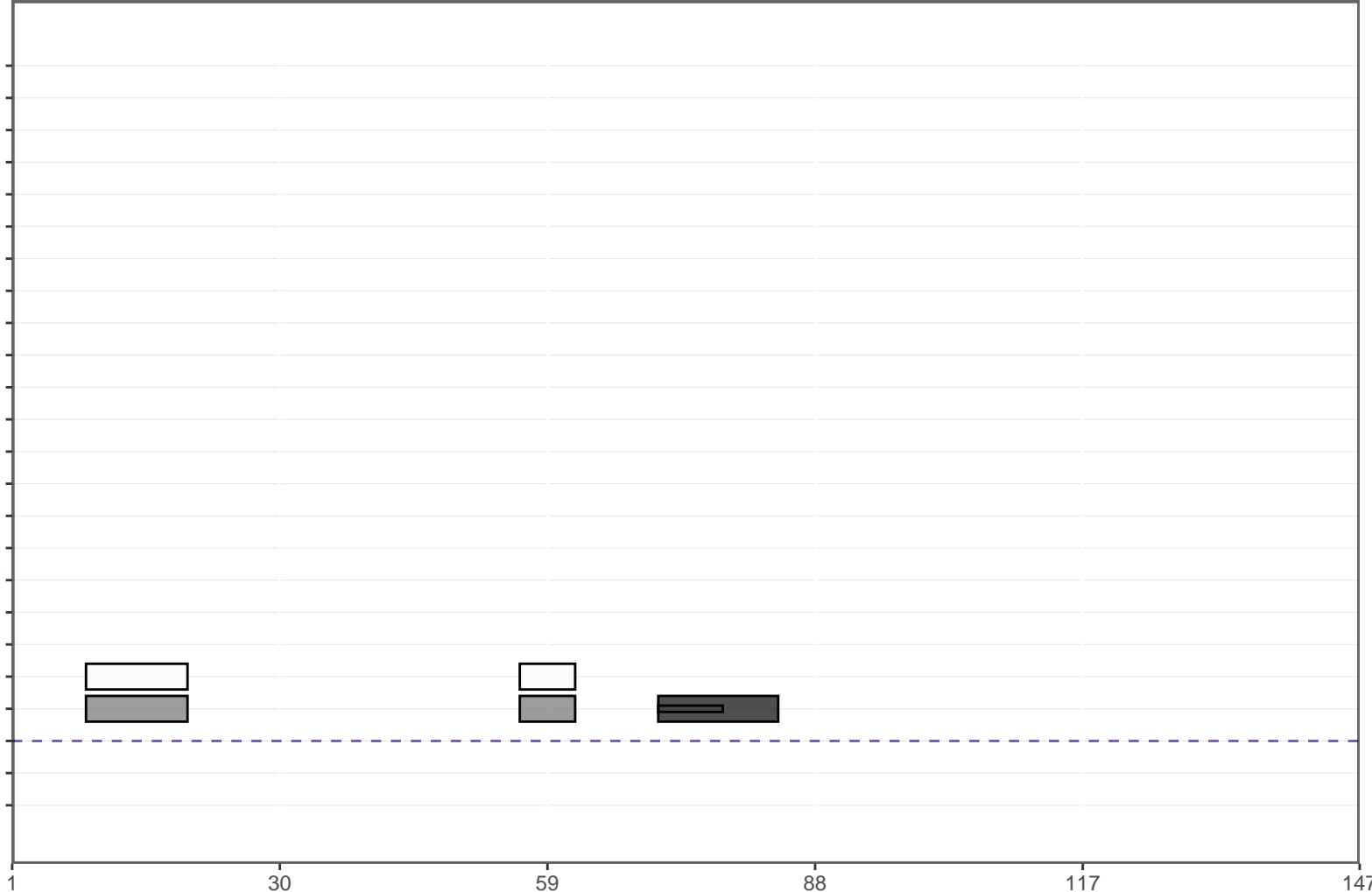
MW indication



Molecular weight



Gel Slice



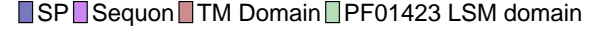
Protein length



Pfam domains



Pfam Description



Protein sequence:

ISNTIKYLRYVDEIVSKVQEEAKSRTRDKPPGVGRGRGRGRDDSAAGRQAKGIGRGMDDGGANGRGRGGPSAKSGGRGGGRGRG*

NbL08g17020.1 proteasome_subunit_beta_type-7-A [MW = 34.74 kDa]

No. of times detected



log(intensity)



Values from



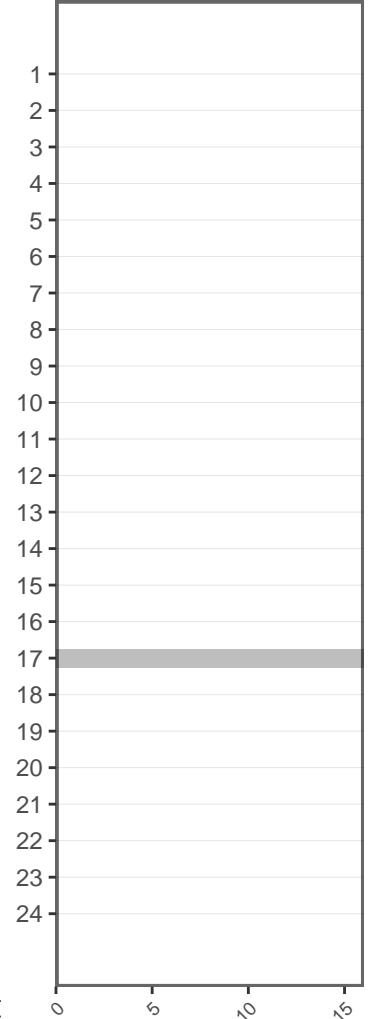
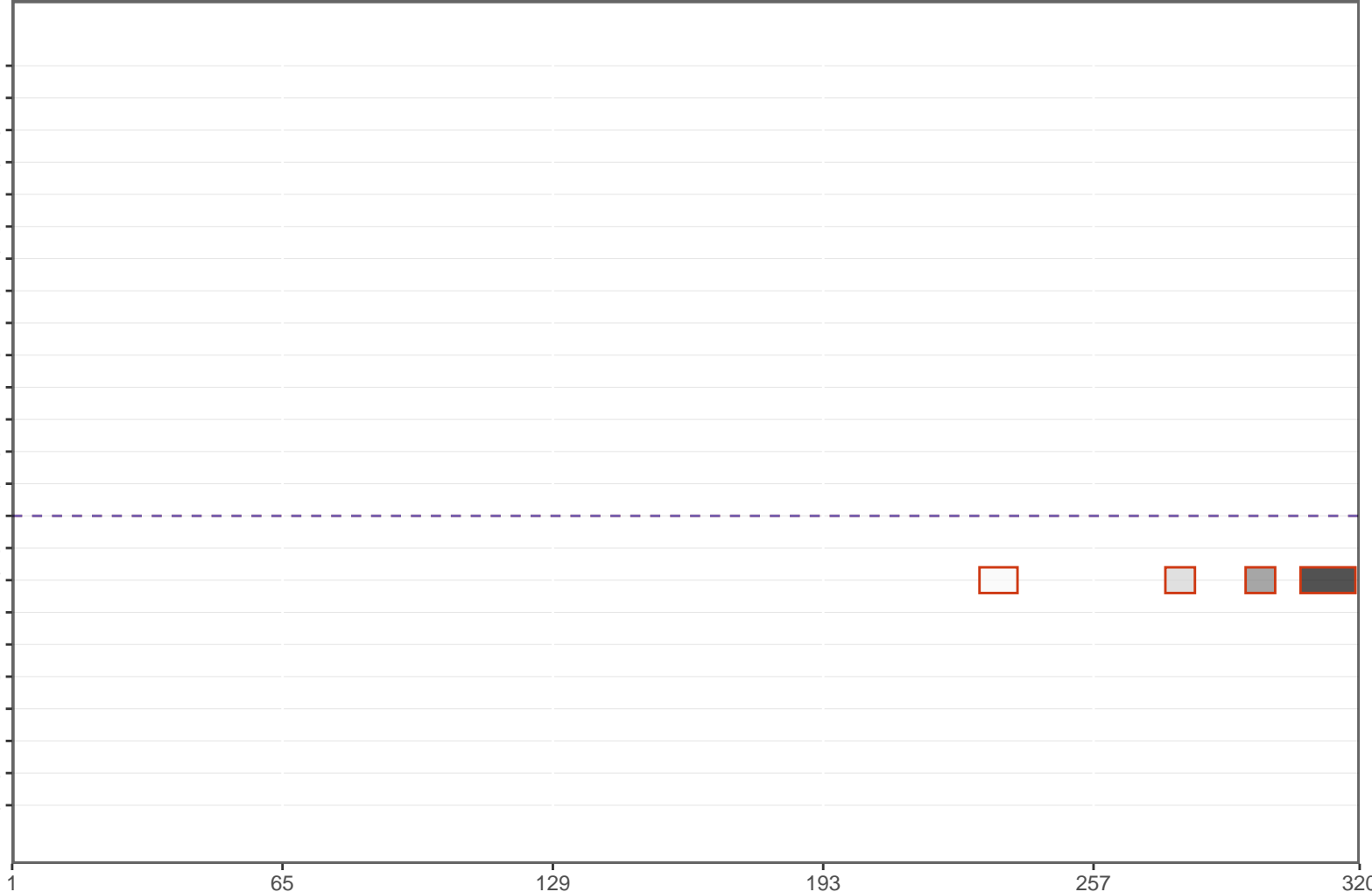
MW indication



Molecular weight

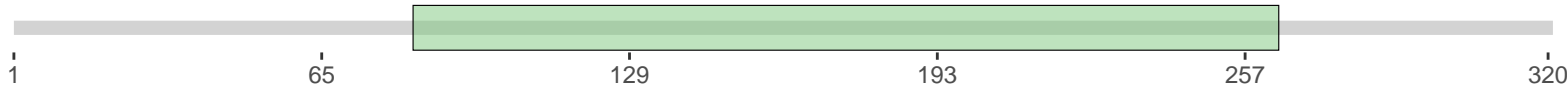


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IQLKLRFHFTGRESRVVYVYALTKLKHLEFYQGHVSAALVGGVDVYTGPHLHTYFHGSDTLFVATMGSGSLAAMAFESKYREGMNRDEGKIVAEALGGVFDNLGSGGNDICVTKGTEYLRNHLSPNRTYVQKGVYFQPKTEVLLTKITPLREIVQVIEGGDAMEE

NbL08g16870.1 peptidyl-prolyl_cis-trans_isomerase_CYP18-1 [MW = 26.82 kDa]

No. of times detected



log(intensity)



Values from



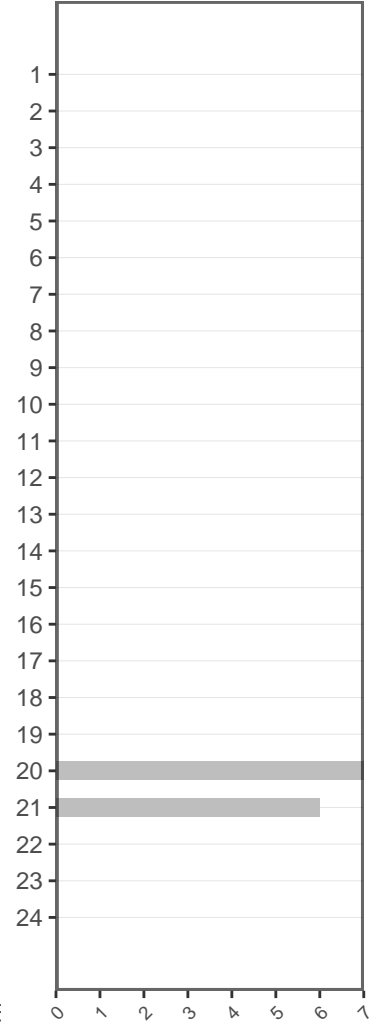
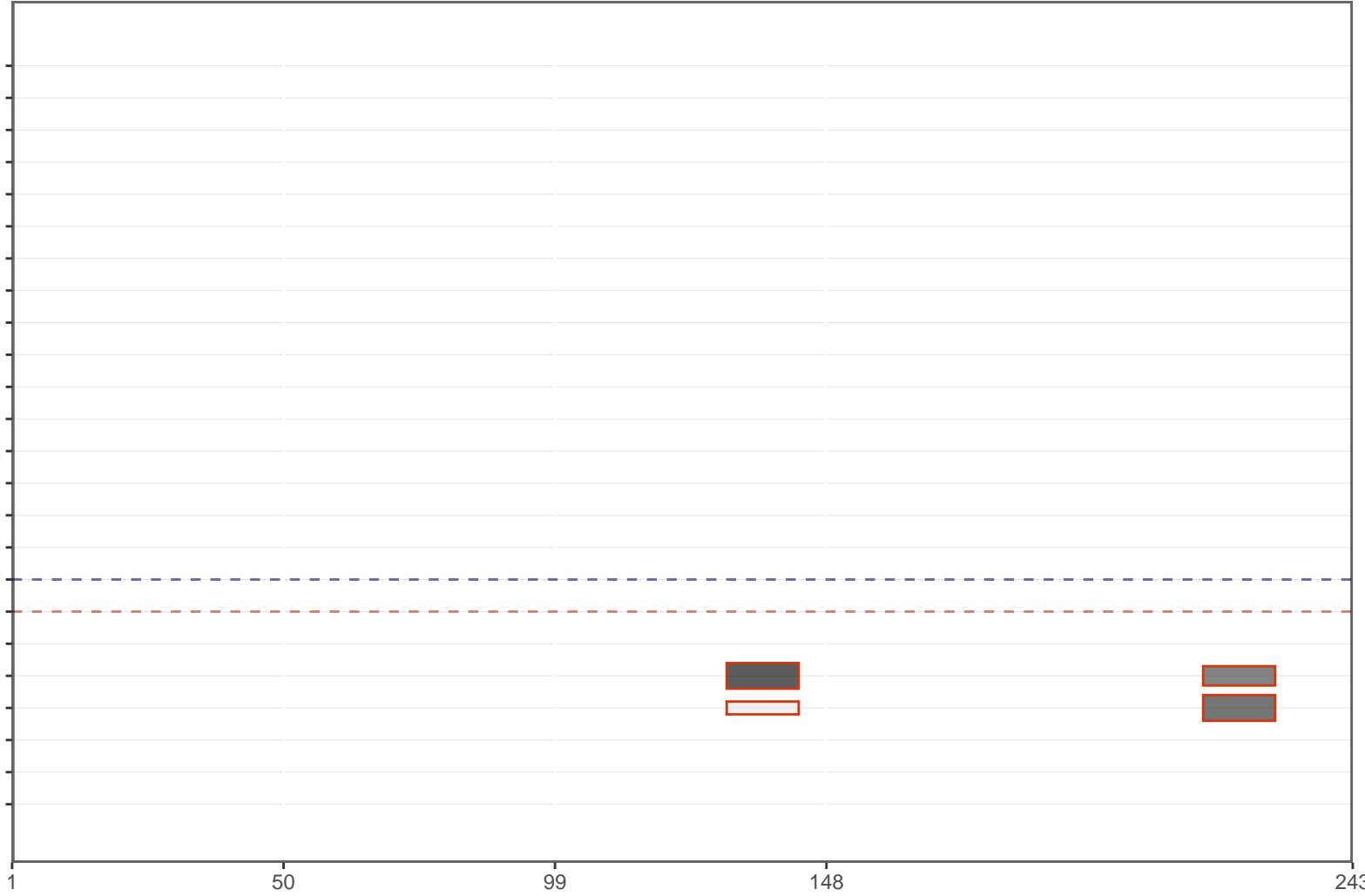
MW indication



Molecular weight

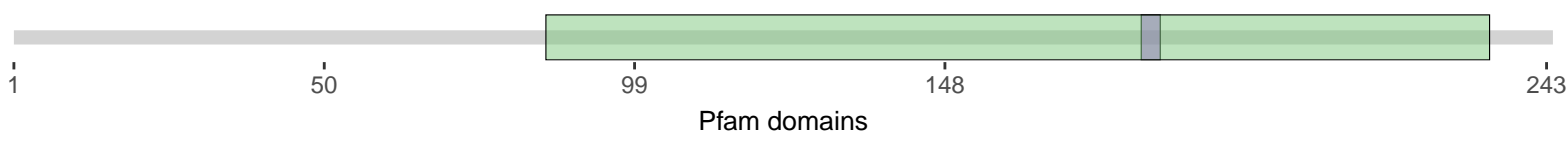


Gel Slice



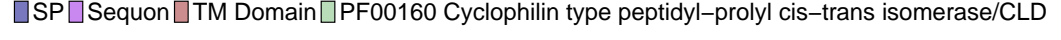
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

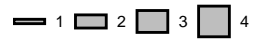


Protein sequence:

FLALCASGYDGTFRHNKGFMDGGDSTGTRGGTSHWKKFNDERELKHNARGLSMANSQNTNGSGFFMTYAKGPHNLGLYTFGRVHGFVLDIMKNTPTGPGDKPLAERLNRYVTHANPLAG

NbL08g16540.1 D-3-phosphoglycerate_dehydrogenase_1_chloroplastic-like [MW = 63.48 kDa]

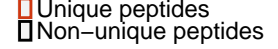
No. of times detected



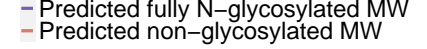
log(intensity)



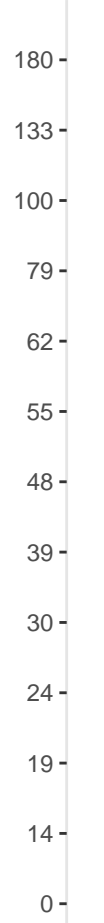
Values from



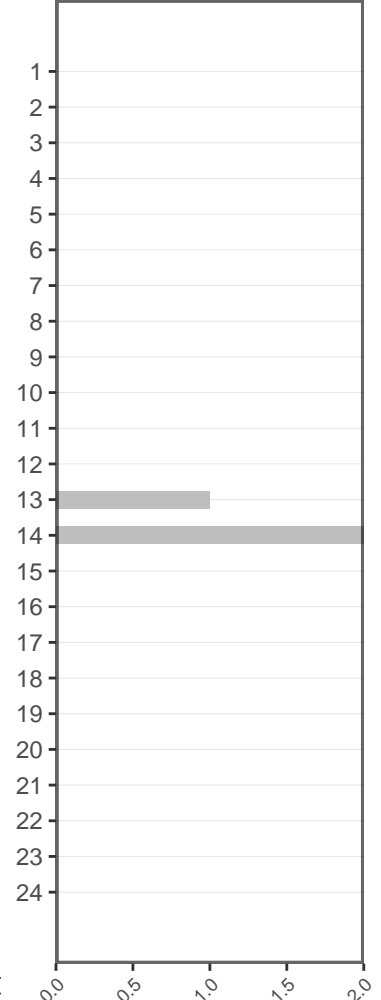
MW indication



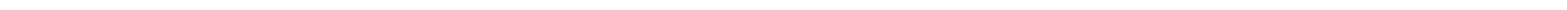
Molecular weight



Gel Slice

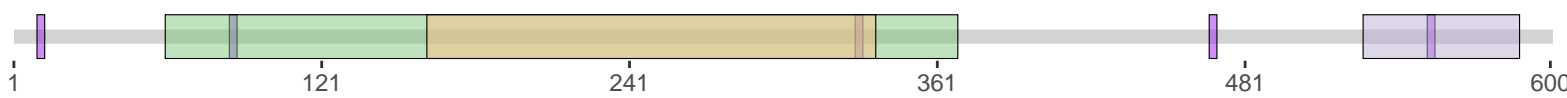


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

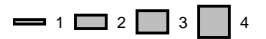
- SP
- Sequon
- TM Domain
- PF00389 D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain
- PF02826 D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain
- PF01842 ACT domain

Protein sequence:

IARGGVIDEDALLVRLDMGRVADALEDFVTEPPKDKKLVQHENVATPHLGASTMEAGEGWNEAEAVGALKGELAATAVNAPMVAEVLSEKPFVLEAEKLGRLAVQLVTGGSGVKSIVKYVGSARAPDQLDTRLLRAMITFKGLIEPISGAFVNLVNAIDFTAKGRGLRAEERLLNGSPESPLEIRIVQIANVESKFAISAIDLGEIRVEGKWDGPIHETKVGSEFVDSLEGSILGRQVDPQPMGKVDGILSEENVNISFMVGRVAPRKHAWMAIGYDEQPSKESLKI

NbL08g16530.1 pathogenesis-related_protein_1A [MW – SP = 69.41 kDa]

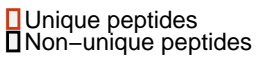
No. of times detected



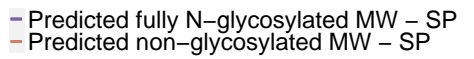
log(intensity)



Values from



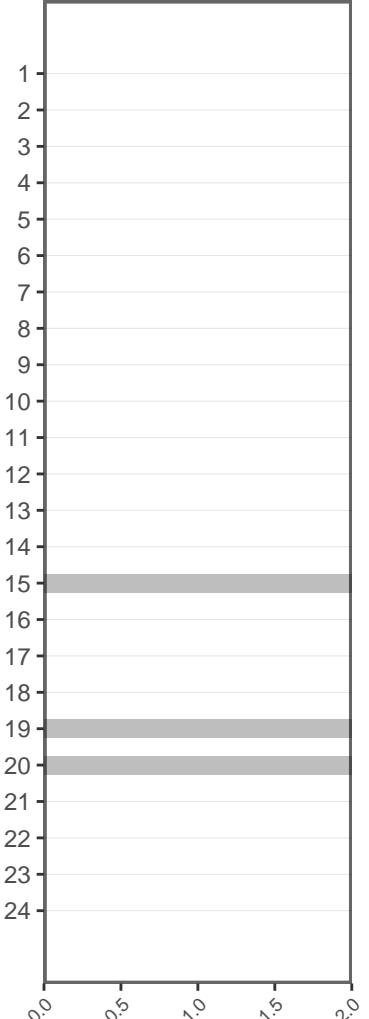
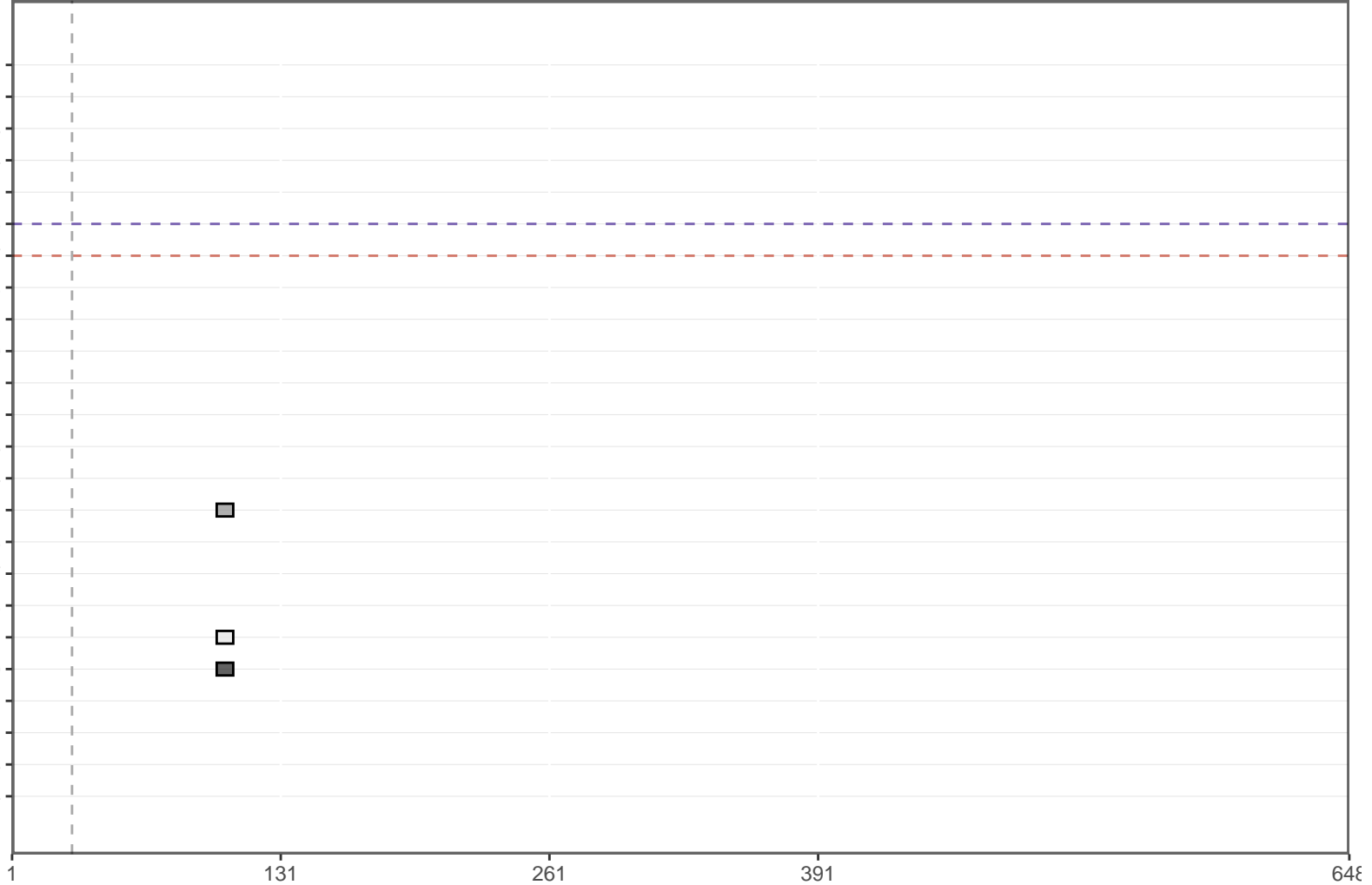
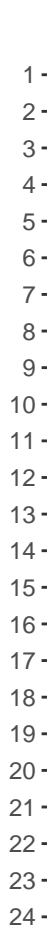
MW indication



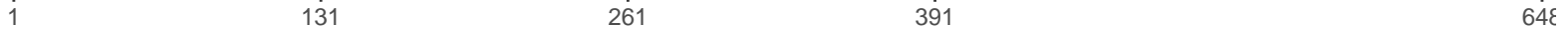
Molecular weight



Gel Slice



Protein length

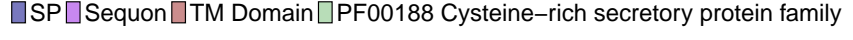


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FRIDMGRGTYHQLLGGGGVHTPIPEPQSSPRRSREGTDPGGSHNANAGFNNDKALGNTLNTLENPRRGLVNSGGGGISGEGSRDRPEPHMTAFRTGKGNLTKGDDEGLVKKFGEPLTKGAFITWYDHRSRNRREGGSSRFQNGRNRRESGDDDRNLKARFGGYNFNVSTSELVVSRMRMGDKELVFKERISNPNRNFNHWGEFHDDHRHKTAGSSMILLRLLREMGAEEDKLVKHEHLSGFENASIVTMGEVILFTFTKGVKDKFQVWVMEIACNMLGRP

NbL08g16430.1 uncharacterized_LOC107772566 [MW - SP = 23.53 kDa]

No. of times detected



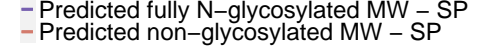
log(intensity)



Values from



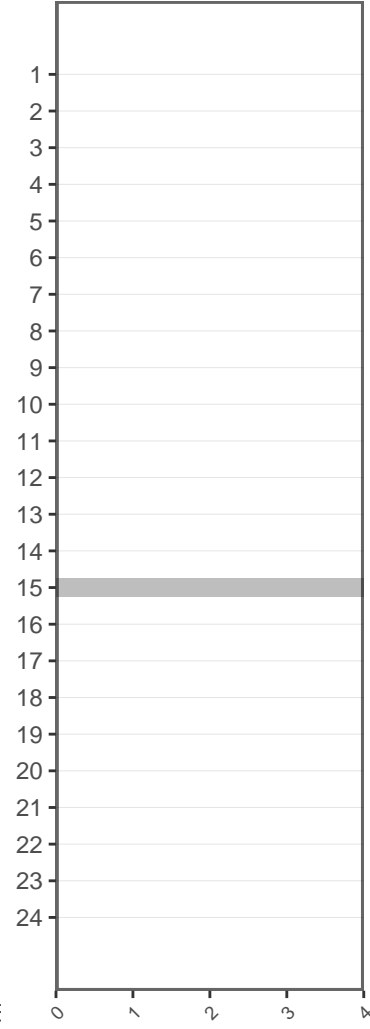
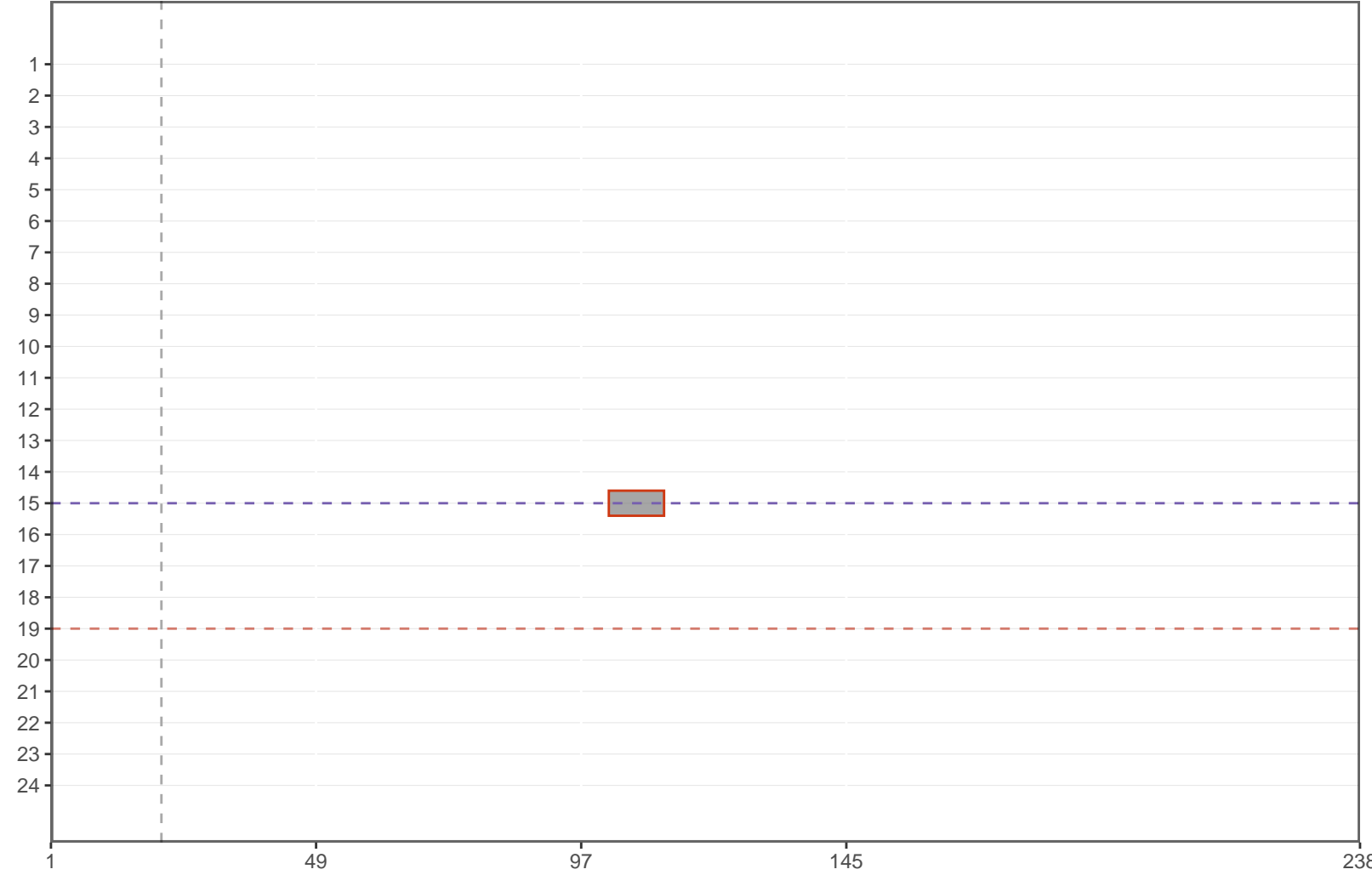
MW indication



Molecular weight



Gel Slice



Protein length

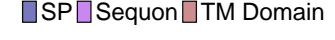


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

...AFAGRCYAAARSLRFVADNTHITTSFTLWLEFGKGLQNLFWKFKFGGSSGTTGGSFVGLNITTDCAVFNKNGNGSGVDCNMGIGLAFSGDTKNDVNLNSWYEVKMLRGLSYLGLFGDVSDELTFPKNLF...

NbL08g16390.1 isocitrate_dehydrogenase_[NAD]_regulatory_subunit_1_mitochondrial [MW = 40.48 kDa]

No. of times detected



log(intensity)



Values from



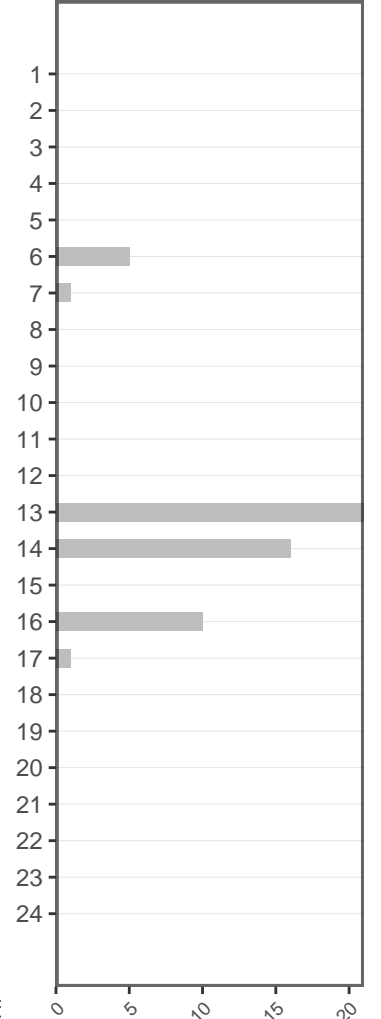
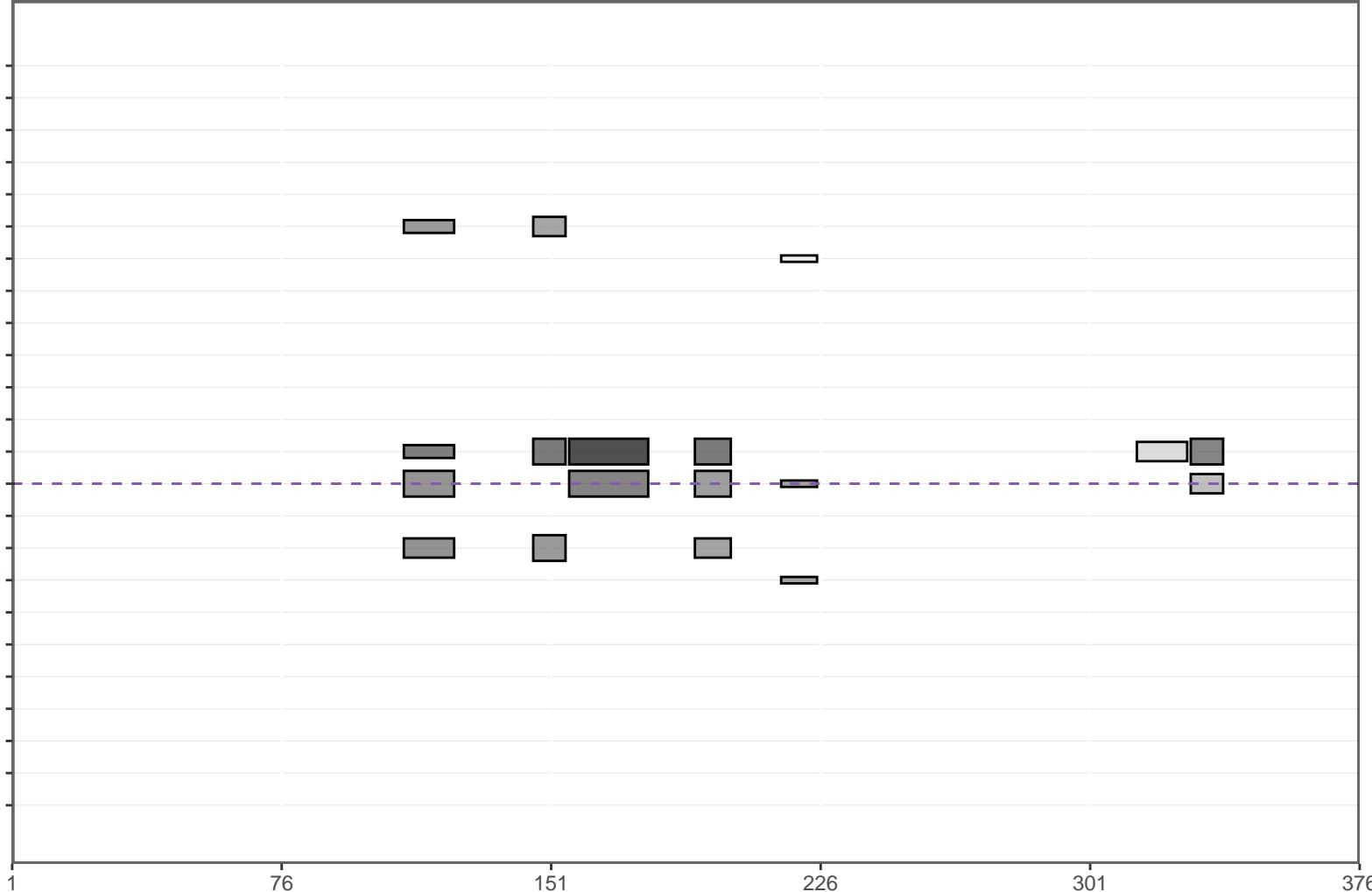
MW indication



Molecular weight

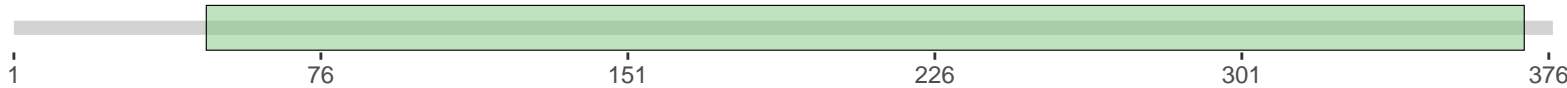


Gel Slice



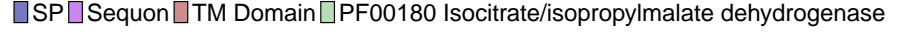
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

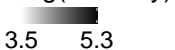
VELSLKVMTKFCSERIAKYAFEVYLNLRKRVYTAHKANIKMLADGLFLESCREIVASKYPGIKYNEIIVDNGCMQLVSRPEQFDVMTPTNLYGNLWNTAAGIAGDGTGVMPGGNVGADHVFEGGASAGNVGNENKLEKQKKNPVALFLSSAMMLRHLQFPFADRLKTSVSRVAEGKGMTRDLGGGCTTQETDVAIANLDI

NbL08g16130.1 glycine-rich_protein_2-like [MW = 21.24 kDa]

No. of times detected



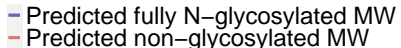
log(intensity)



Values from



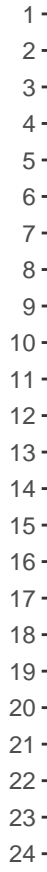
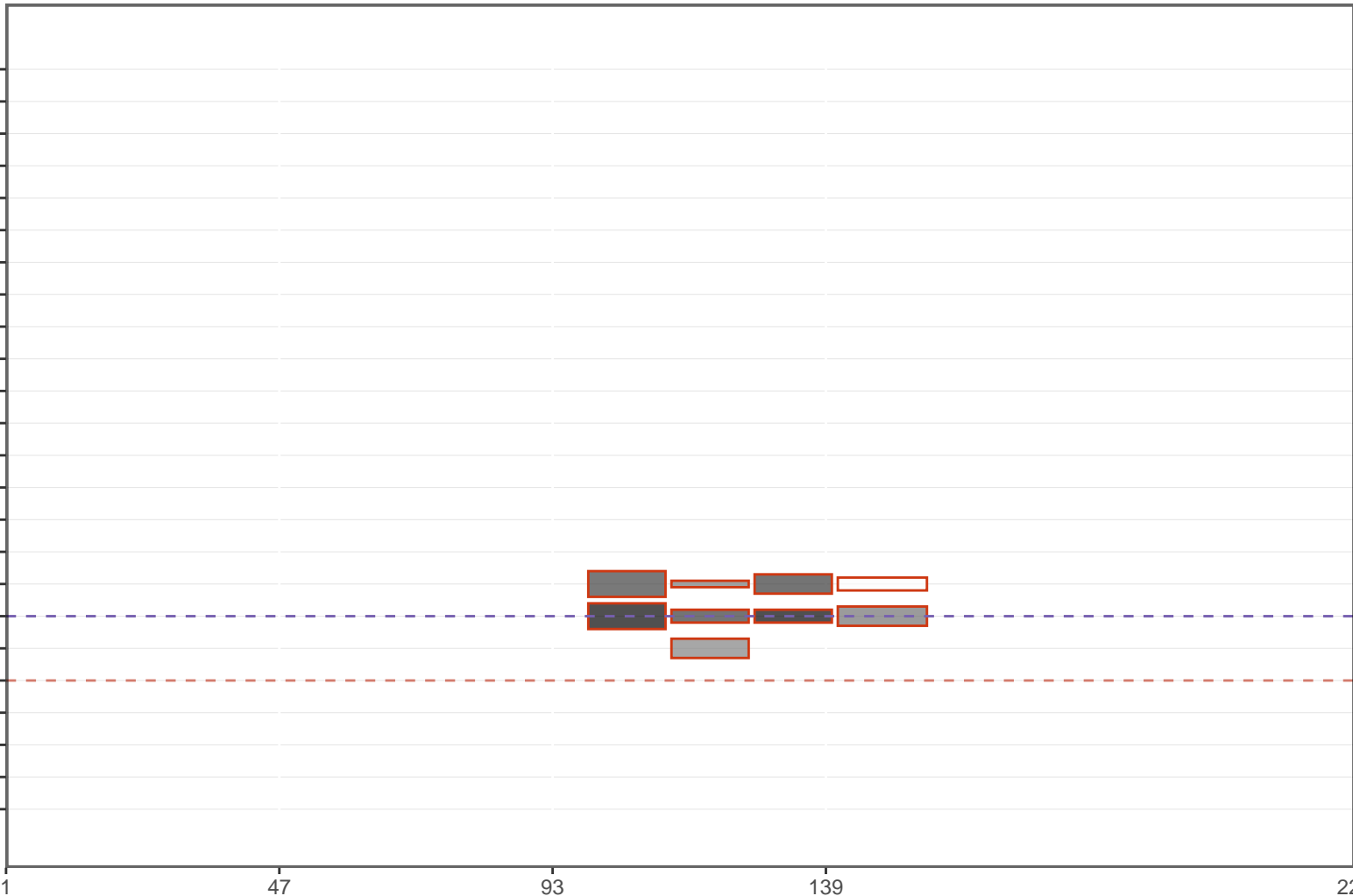
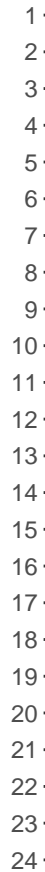
MW indication



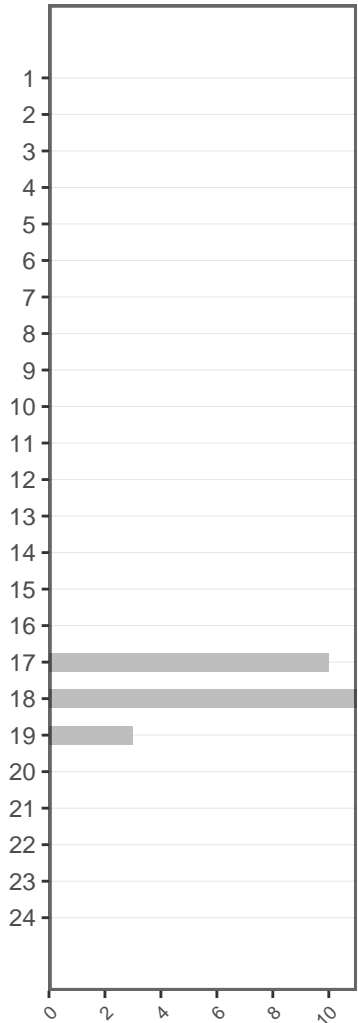
Molecular weight



Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains



Pfam Description



Protein sequence:

IGGGGGRYGGGSGYGGGGGRYGGGGYGGGGGRYGGGGYGGGGSGGGYGGEEGHFAREGSGGGGGYGGGGYGGGGYGGGGYGGGGGRYGGGGGGGGCFKDEEGHFAREGPNSSGR

NbL08g16080.1 triosephosphate_isomerase_chloroplastic-like [MW = 34.16 kDa]

No. of times detected



log(intensity)



Values from



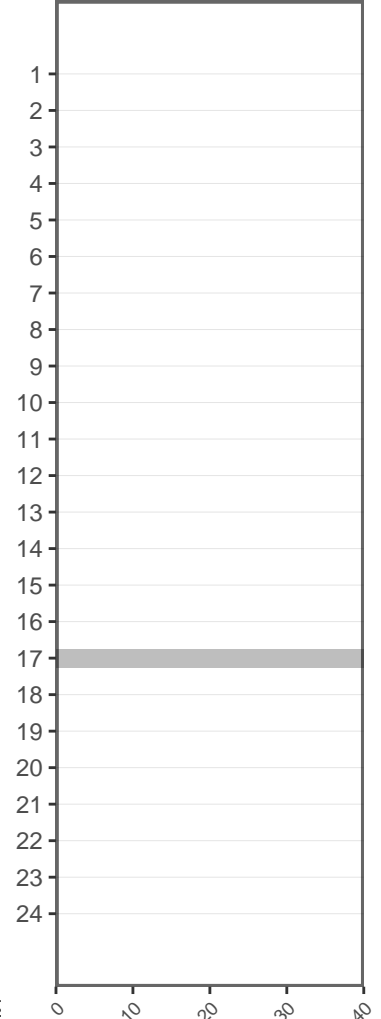
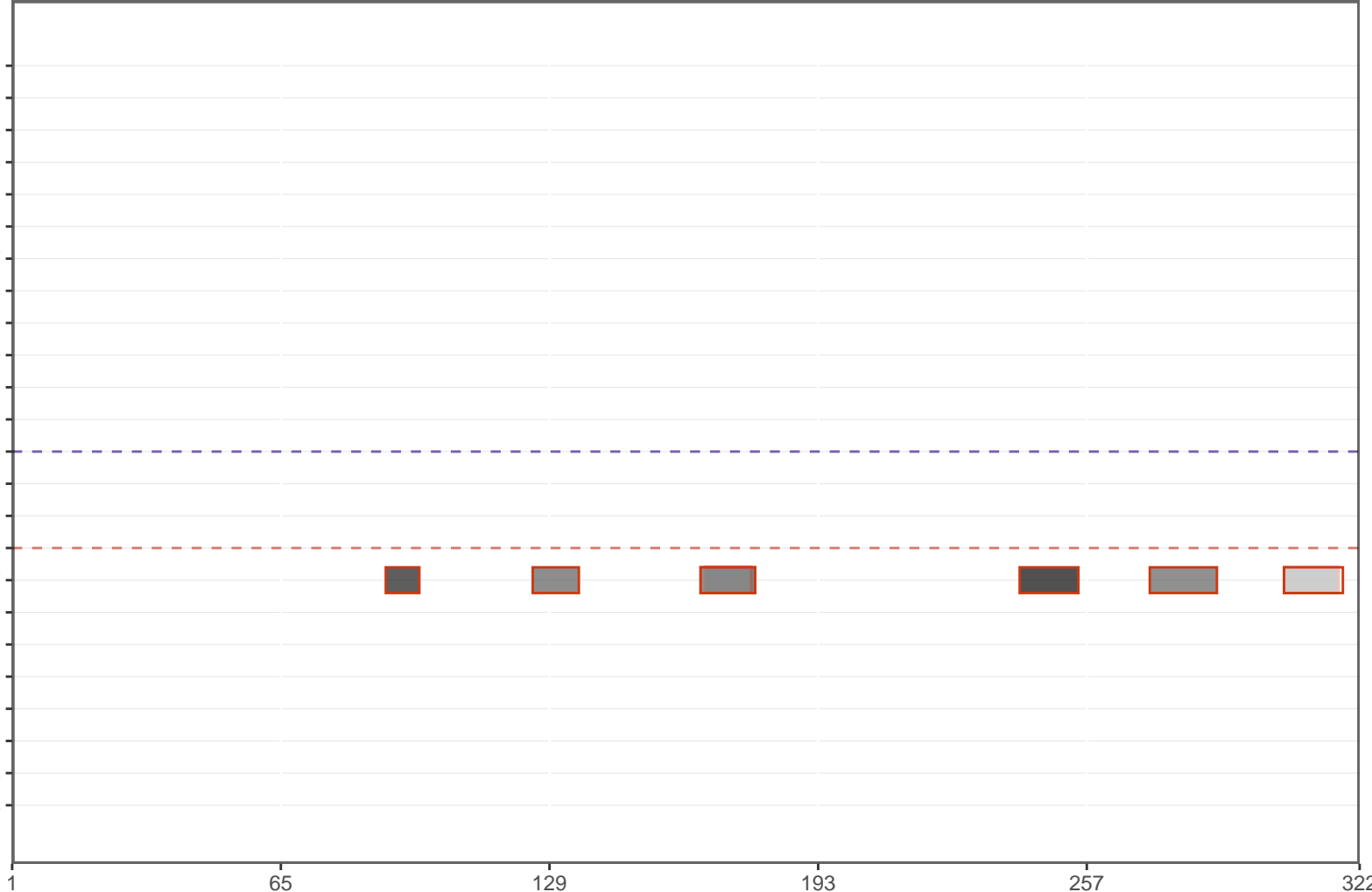
MW indication



Molecular weight



Gel Slice

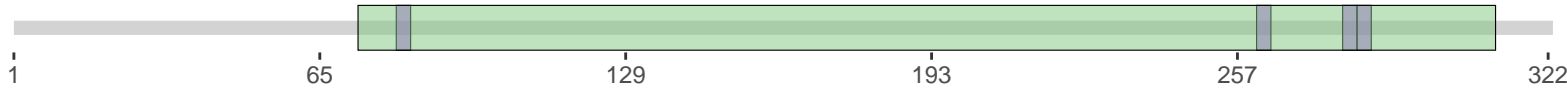


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IQKLDLCKYVILGHSERRHIGENDEFGRKAAAYALSGNVGVAGIGELLEEREAGKTFDVGFGQLKAFADALPSWDNVVAEYEPVVAIGTKWATPEGAQEVHAAVRDVLGKNVSAEVAASKTRIIYGGGANGSNGDGLAKKEDIDGFLVGGASLKGPFEFASIVNVTSKKAAV

NbL08g15890.1 60S_ribosomal_protein_L4-1-like [MW = 44.7 kDa]

No. of times detected



log(intensity)



Values from

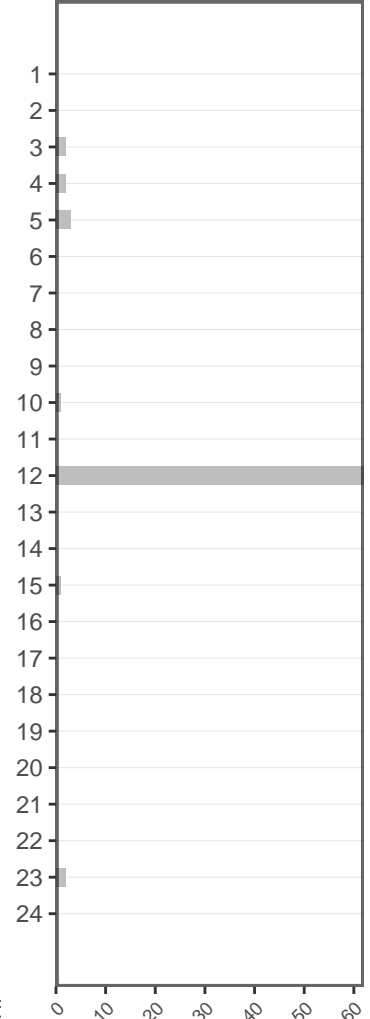
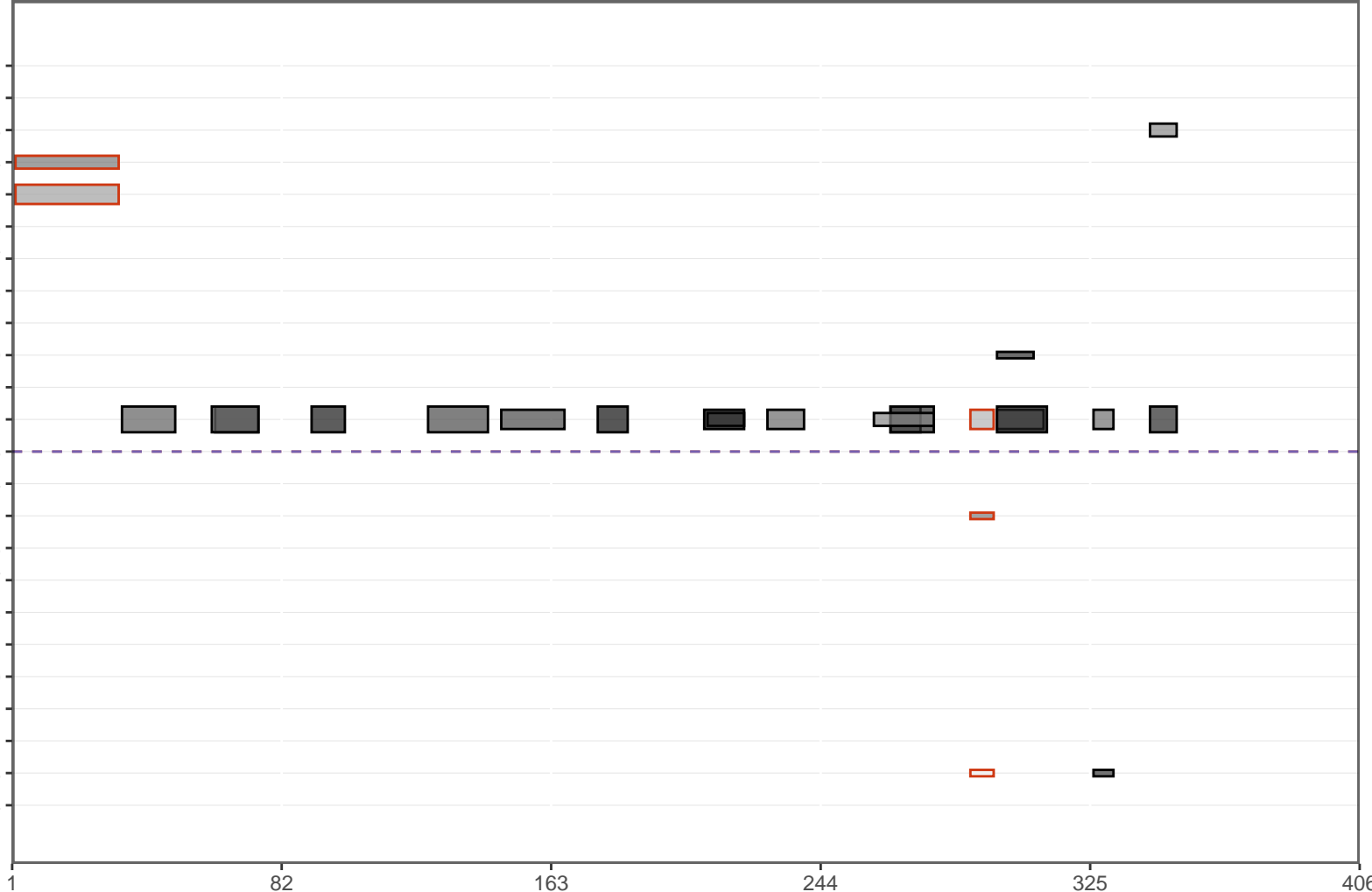


MW indication



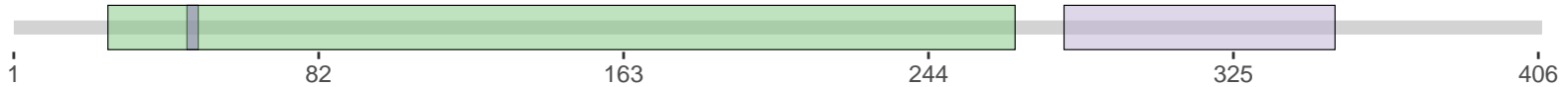
Molecular weight

Gel Slice



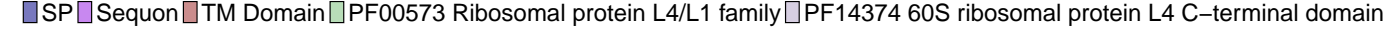
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SHAIRPGGKMRNRRIYHSRKGFLVYGTGEGAKLKAFRNIPGVEICHVERLNLLKLAPOGHLGRFVWTKSAEKLDEHYGFDFKPEKKKGYLPRAKMANADARIINSEDEVGSVVRPIKQDKRATLKKKPLKLNLLKLNIPYAKTARRMSELLAEGRVKAKKEKDKRHHVYTKEEASAIRBSAAWYKTMISDSGYTEFDYFKWLGVTQ

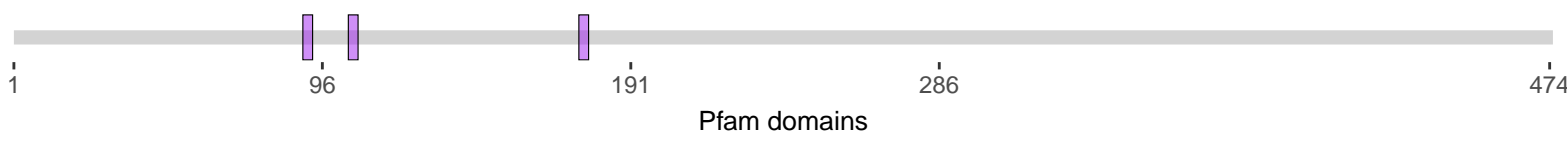
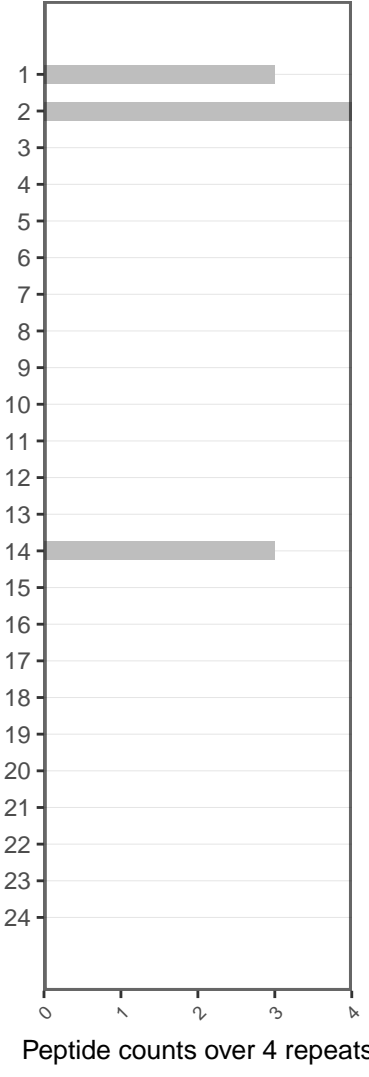
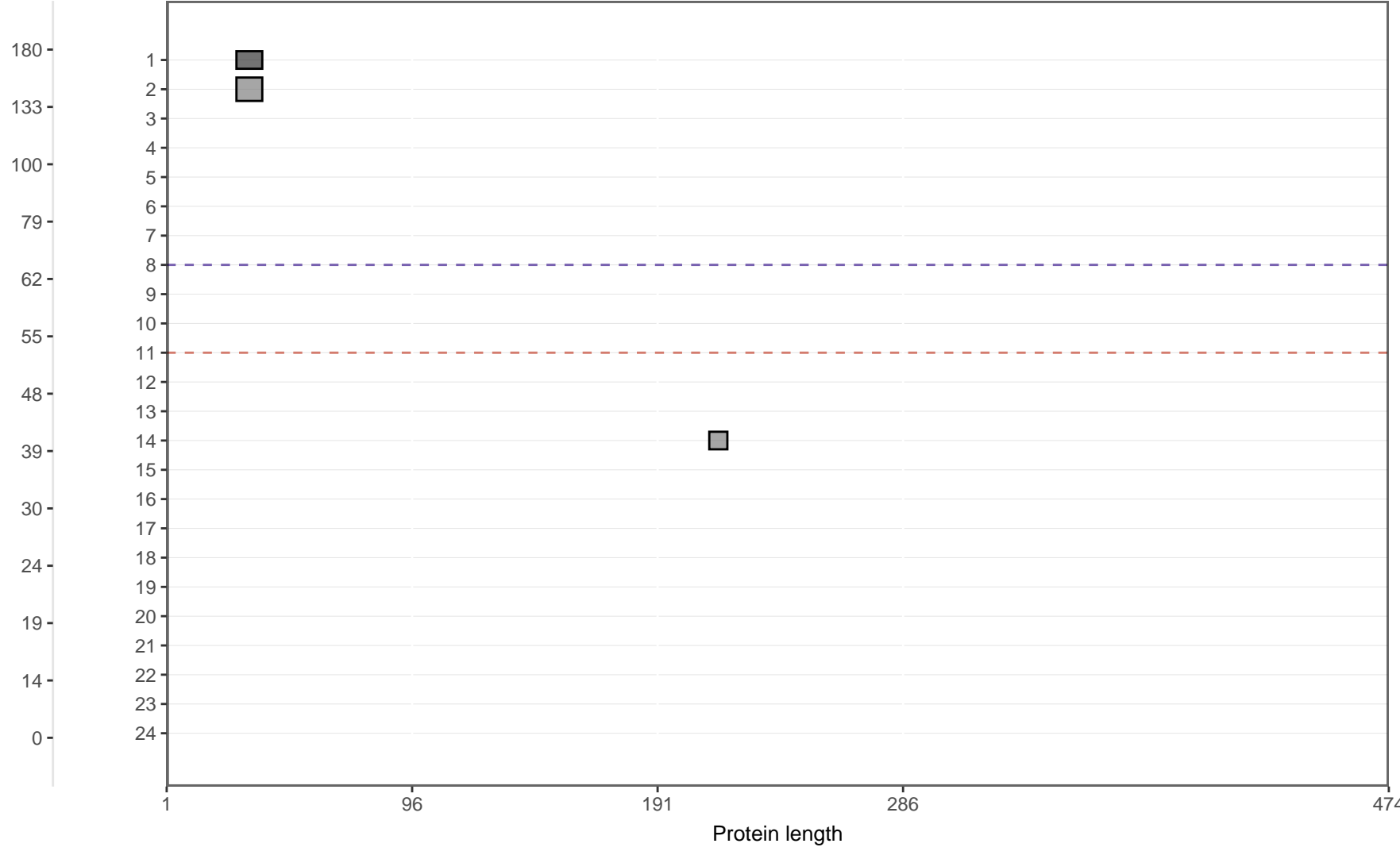
NbL08g15860.1 interactor_of_constitutive_active_ROPs_2_chloroplastic-like [MW = 52.84 kDa]

No. of times detected
 1 2 3 4

log(intensity) 3.2 4.8
 Values from Unique peptides Non-unique peptides
 MW indication Predicted fully N-glycosylated MW Predicted non-glycosylated MW

Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain

Protein sequence:

CSLTGLTSAVEIVETGKSESGRDTFENWKNLNAKADVEELTGTLMNKEAELQKSDENKGLNQLVVEIQADDDGDTKLGAEUKKSESLADLRASLFDKTEVQSTTEENMLKSEMKRREMSTKVNDEVLALAEAAKTSEREAALMKLGYLTFEADKRSRKAARVIELDAAGAAANSEAEALRRLKVGSDQWRKAAEAAAAMLSNNGKYVERTGSLDHTTGGKLRSPLSDDMDNDPRRRMAQ

NbL08g15740.1 cytokinin_ribose_5'-monophosphate_phosphoribohydrolase_LOG3-like [MW = 24.01 kDa]

No. of times detected



log(intensity)



Values from



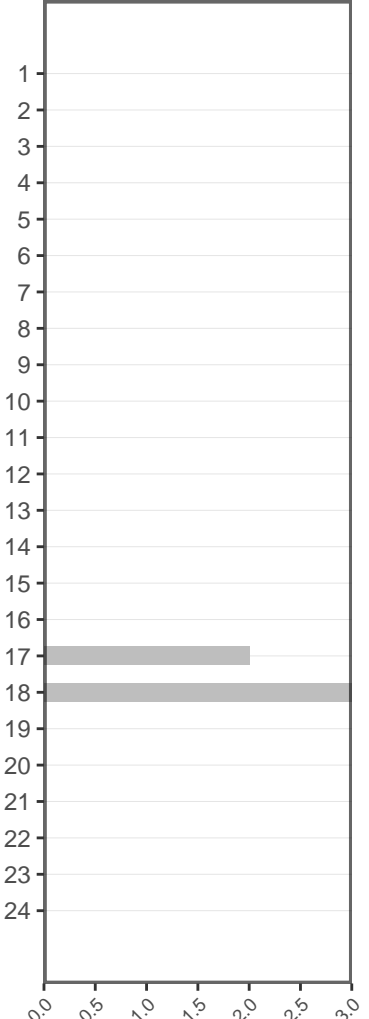
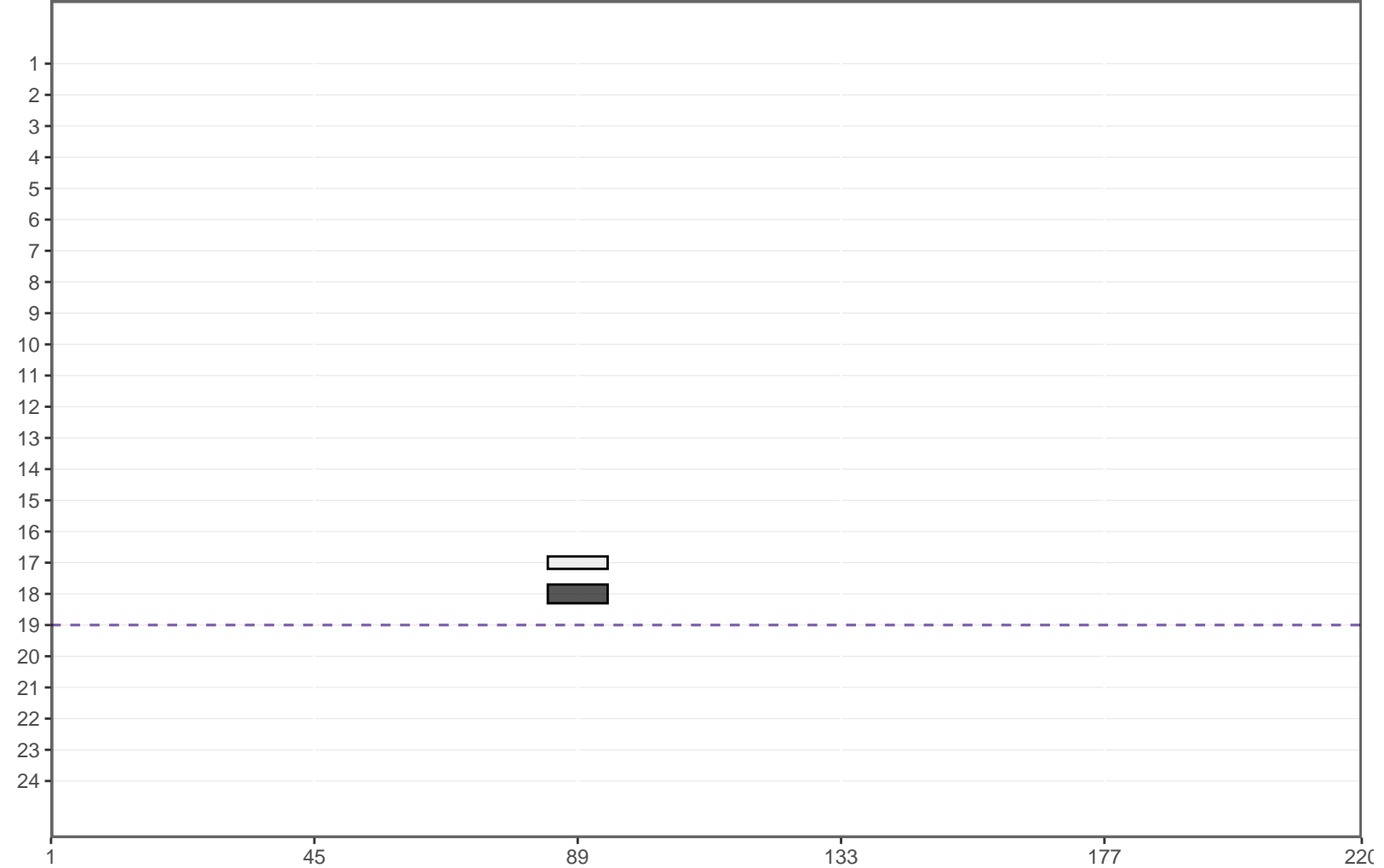
MW indication



Molecular weight



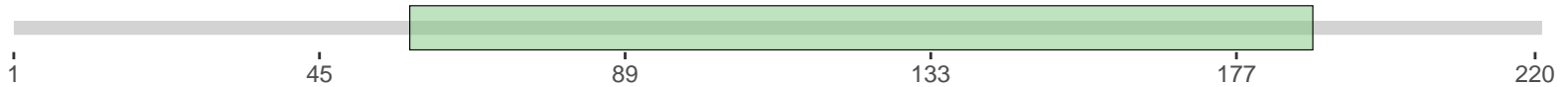
Gel Slice



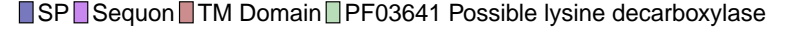
Protein length



Pfam domains



Pfam Description



Protein sequence:

LDMLQRKAEAMAKHSDAFALPGGYGLEELLEVITWQLGHDKFVGLLNDGYYVSGLLSFDKAVEEGFICPNARHIVSAPTPKELVANKLEEYVPCHERVASKLSEWEMEGLYGPOAGEMAR

NbL08g15640.1 thylakoid_luminal_15.0_kDa_protein_2_chloroplastic-like [MW = 24.77 kDa]

No. of times detected



log(intensity)



Values from



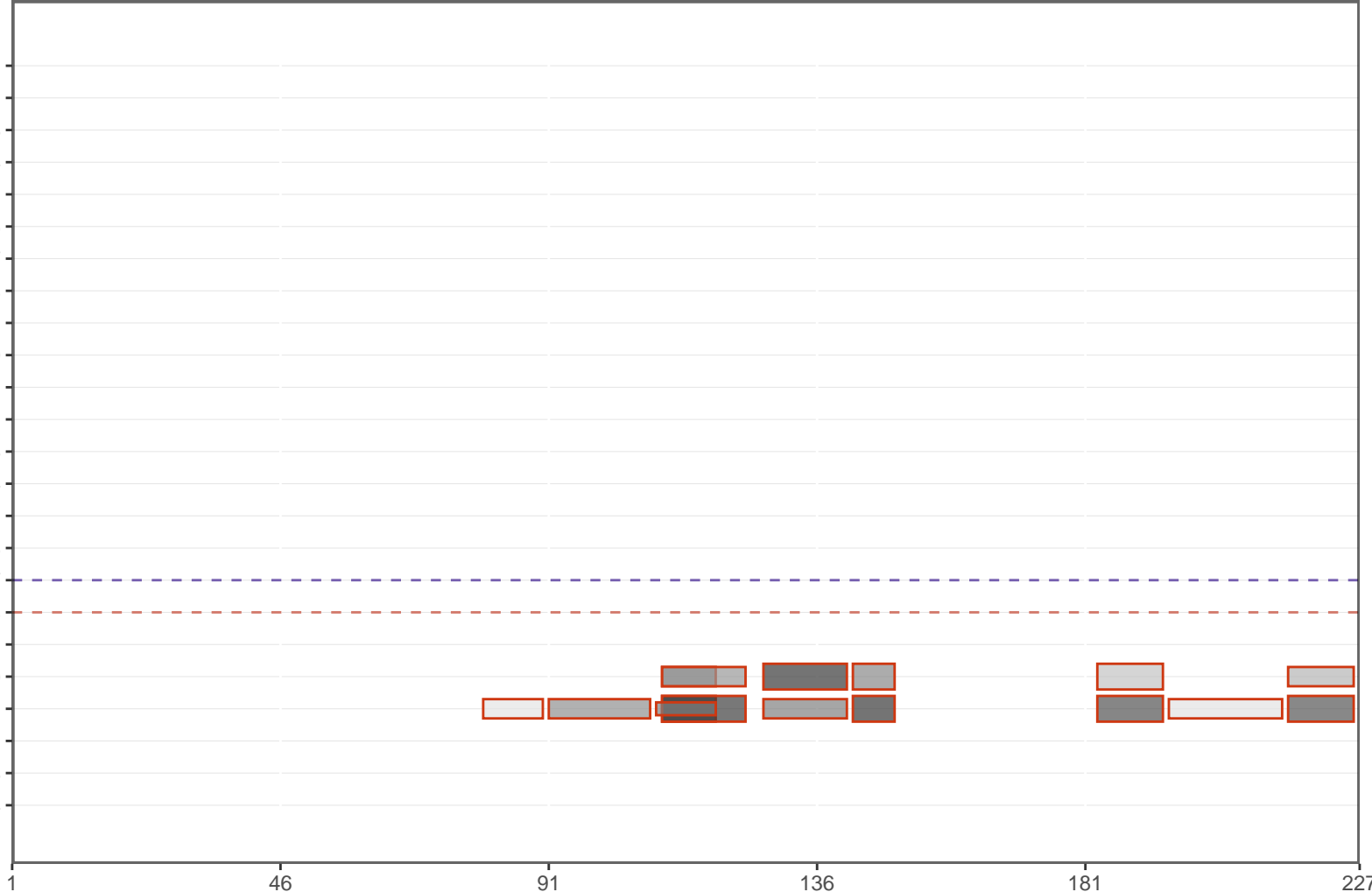
MW indication



Molecular weight



Gel Slice

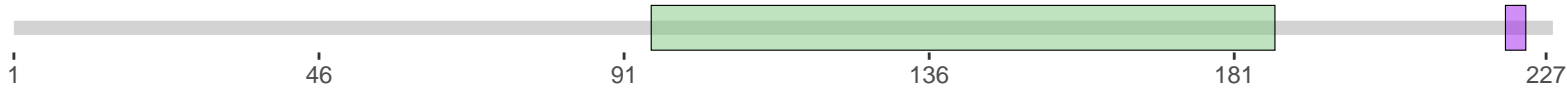


Peptide counts over 4 repeats

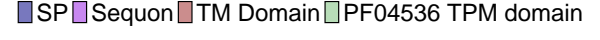
Protein length



Pfam domains



Pfam Description



Protein sequence:

.SDGGEKRLAGEITDEKDTGFKLRVLAGNYPTPTGLAIKDFWGVDDRTVVFVADPTFGNLFNFVGVATVLDLIPRFVSRLAGTYGNMFYWKKEGEDASIEAAVMAISTGLRPEVGPNNDEEW

NbL08g15490.1 poly_[ADP-ribose]_polymerase_tankyrase-like [MW = 21.86 kDa]

No. of times detected



log(intensity)



Values from



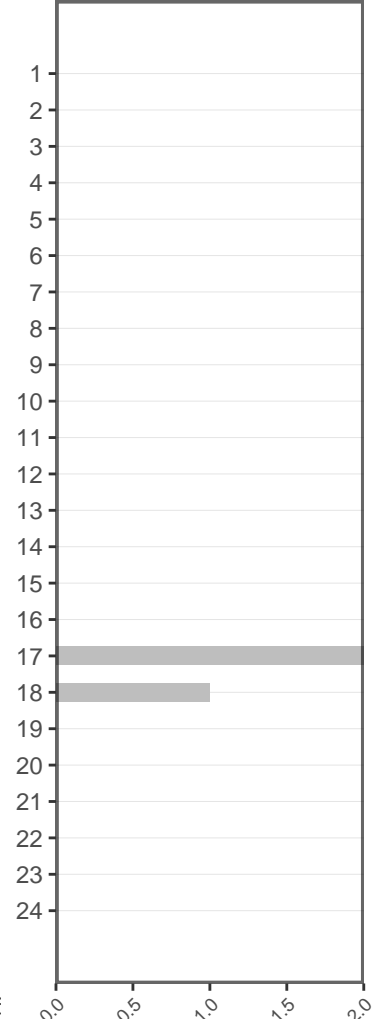
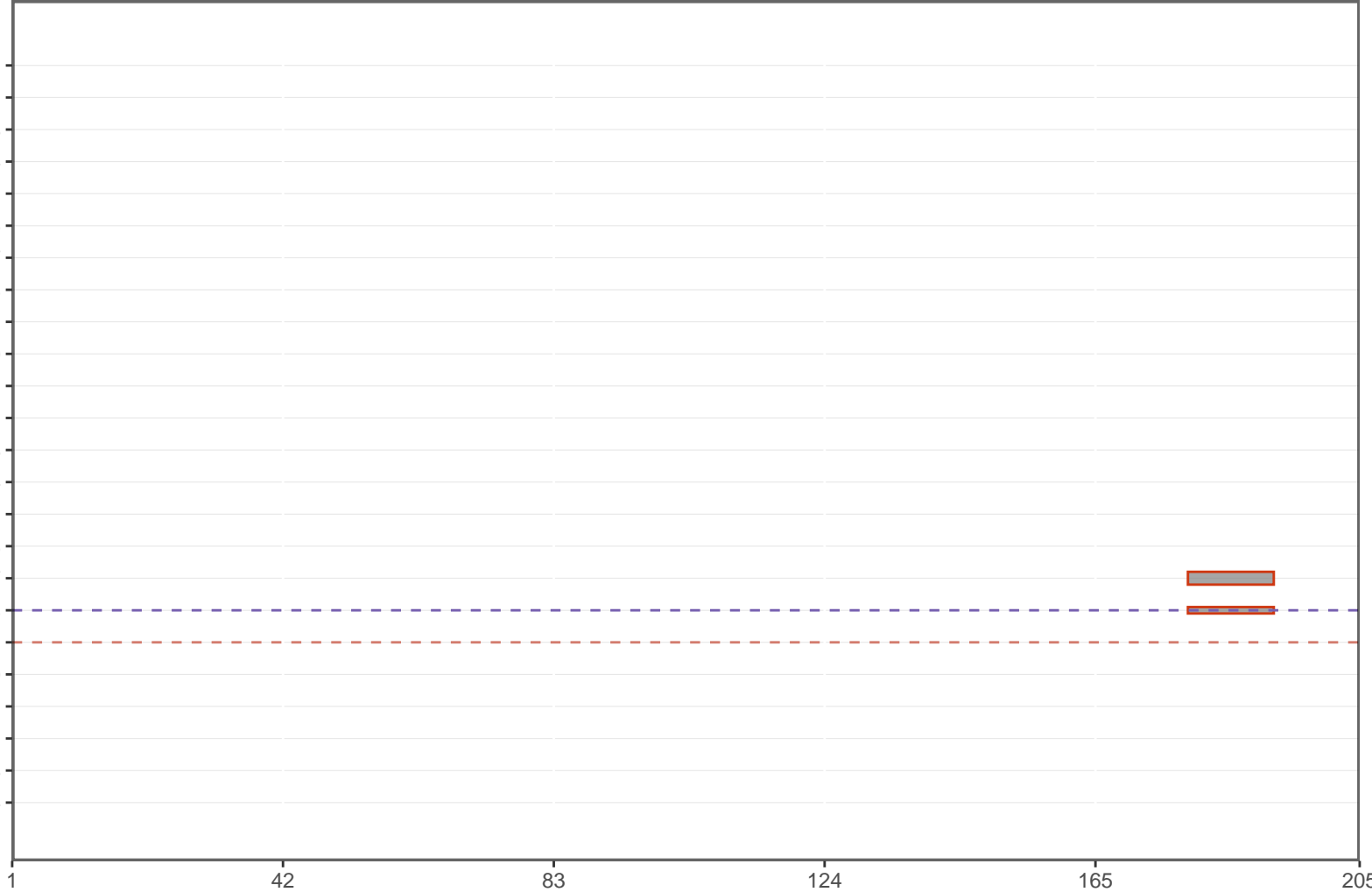
MW indication



Molecular weight



Gel Slice

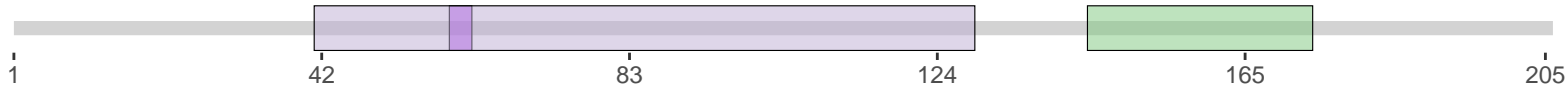


Protein length

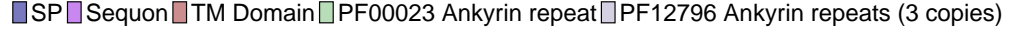


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LLERGASLEPKDEEGAPLHDAGAGGYEIAQLLINSAPDPEGVKRMLDSEVDEGDTPLHHAARGDHVTYVRIALLASGACPRRTNIVGKTPGELAEPPDGEAGRILDETARAFPSH

NbL08g15440.1 carotene_epsilon-monooxygenase_chloroplastic [MW = 60.82 kDa]

No. of times detected



log(intensity)



Values from



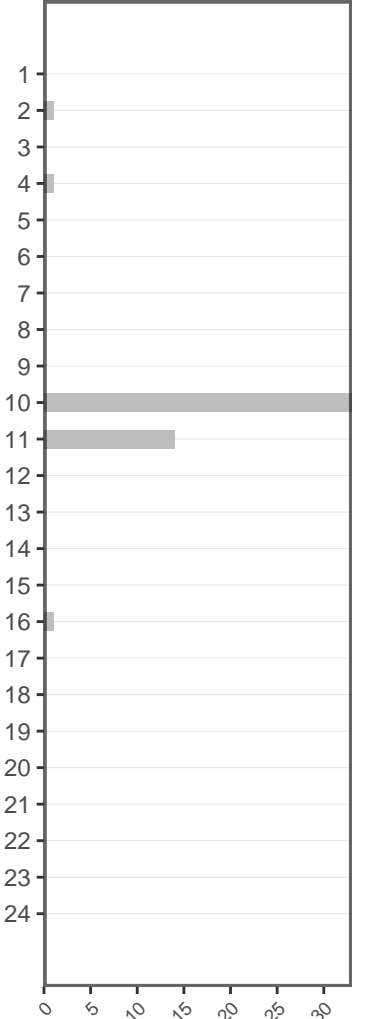
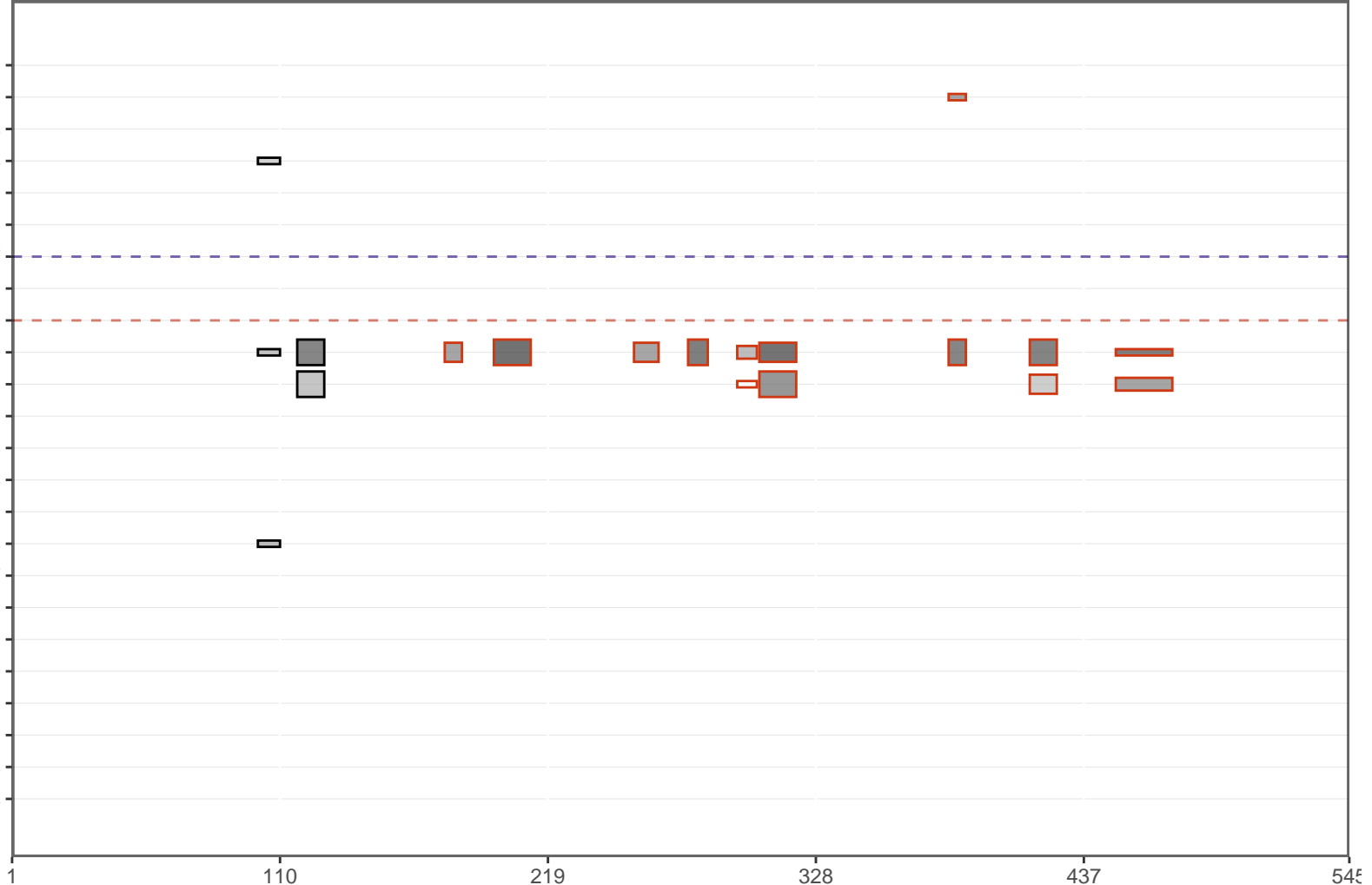
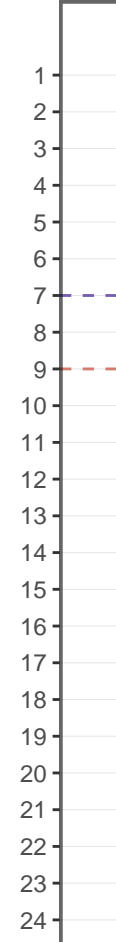
MW indication



Molecular weight

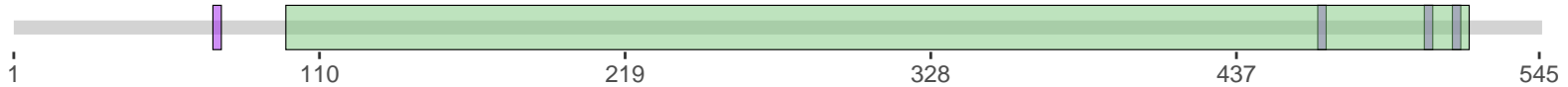


Gel Slice



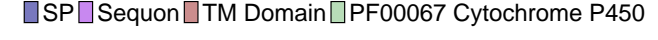
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FWQIKALCKYIPROKAGNAVSLRGTVEELGKCRIVEISGDERINEDEYVNDNRDPSILRFLLAGREEVSSVGLRDDLLSMLVAGHETTGSVLTWTSYLLGNPSTLKKAAHEEVDVLLGGRNPTYEDMRNLKFLTRGITESLRVHPVPLIRRALVADLPGNKKVYVAGDDMSVYVYHHSSEVVERAAEEFDFERFDLEGPVFNETNDFRFRIPFSGGPRKVGDDQFALLEATVALAFLQNFSELPDQNSMTTGATHITNGLMKVKWGRQKEVLA*

NbL08g15400.1 threonine_dehydratase_biosynthetic_chloroplastic-like [MW = 66.07 kDa]

No. of times detected



log(intensity)



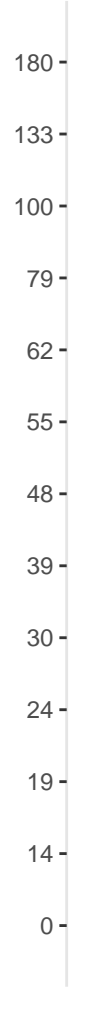
Values from



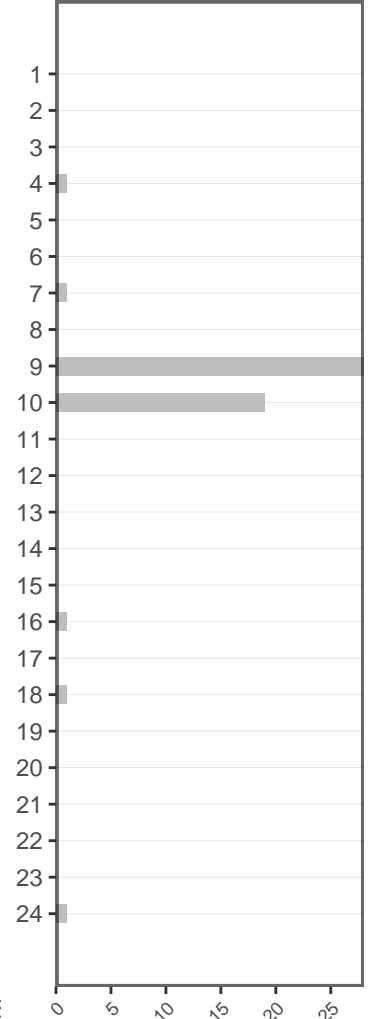
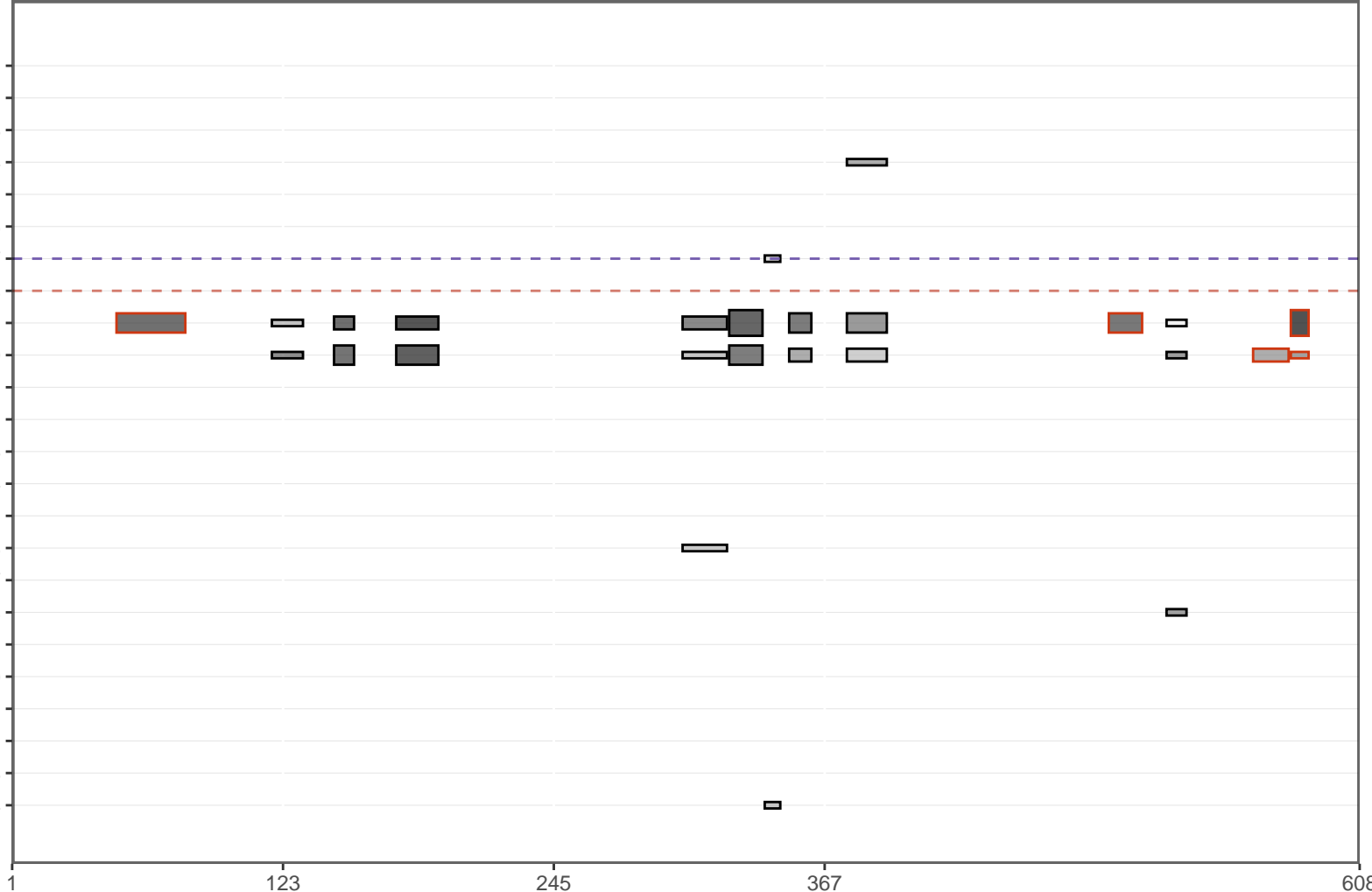
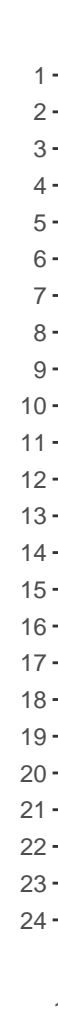
MW indication



Molecular weight

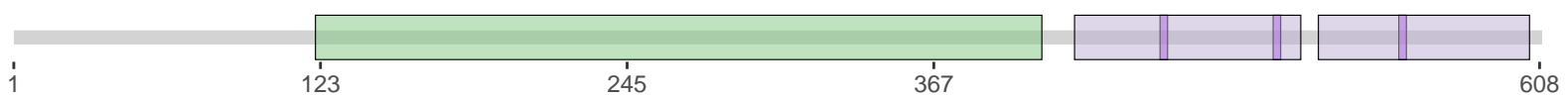


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon TM Domain PF00291 Pyridoxal-phosphate dependent enzyme PF00585 C-terminal regulatory domain of Threonine dehydratase

Protein sequence:

YLLKRVAPDKIKGVEPLDANAMALSLGHGGRVMLDQVGGFADGWWKVVGEETRYRCKLEDGVVAVVGRDAACASKDMFEERKSLERPGALALAGAEVKKYVGLKGENIVATSGANMDFRRLVTELAAVGRGREAVALTFMAEEPGGRKFKFSEMVGPMNTEPKYRYSGGKKAIVVSVGLHTKLEELERMKSANLGTINTDNLVNDHLRHLMSGRTNVAHELLCRFTPEKPGALMKFLDAFSPRWNSLPHYRAGDGTGANVAVGGVPKAEVDFGGR/

NbL08g15350.1 pyruvate_kinase_1_cytosolic [MW = 64.64 kDa]

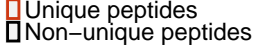
No. of times detected



log(intensity)



Values from



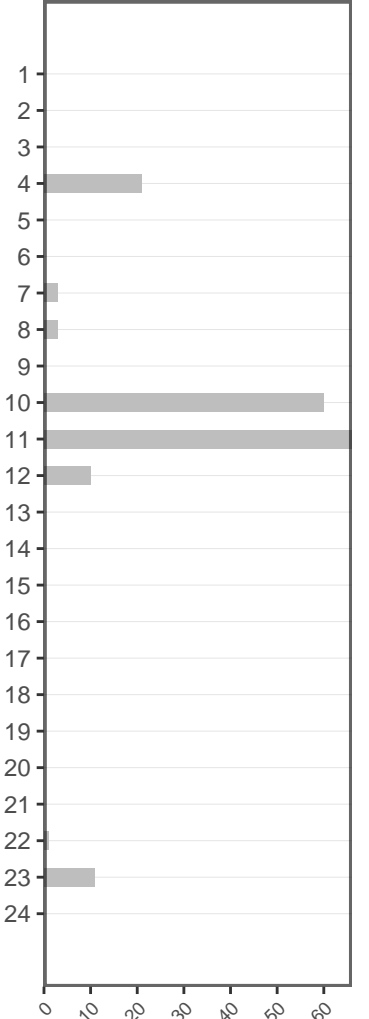
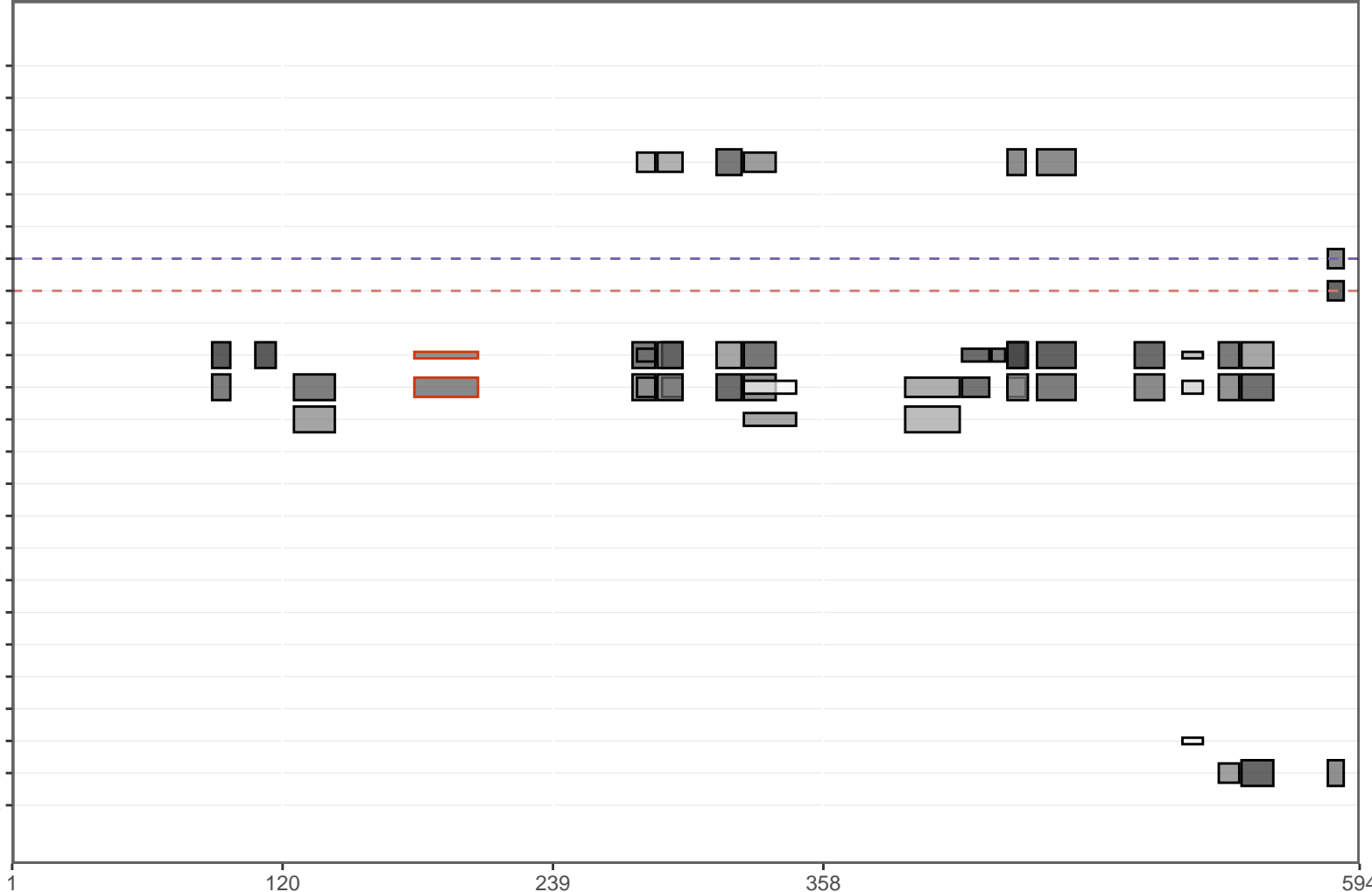
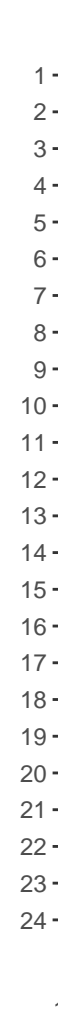
MW indication



Molecular weight

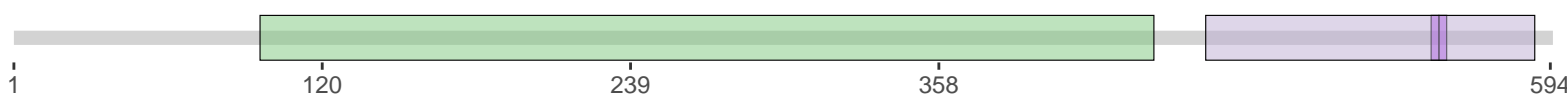


Gel Slice



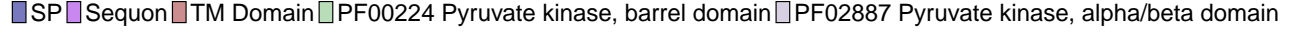
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SVKNDIFSLSYTRHAEEDVREAREFLKLGDLGDTQIFAKIENVEGLTHFDEILKEADGILSRGNLGDLPPEKVFQKSAVHKGNMGNKQVAVTRVVDGMDTDLRPTRAEATDANAVLADGTDAILLGAETLRGLGYPVETISTVGRIGFEAEKVFNDGLYFKKTKYKVGEPMTLHESIASAVRAAKVAVSVICFTSSGRRARLIKAYRPTMPLGVVIFRLLKTNLQKWFSGAFEARQSLVRLGFLFPMADPRRHPAEETNABNESEVLKVALDHGKAGVWIKSHDRVVICQKVG

NbL08g15300.1 peroxiredoxin-2E-2_chloroplastic-like [MW = 24.25 kDa]

No. of times detected



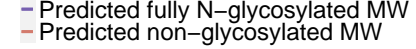
log(intensity)



Values from



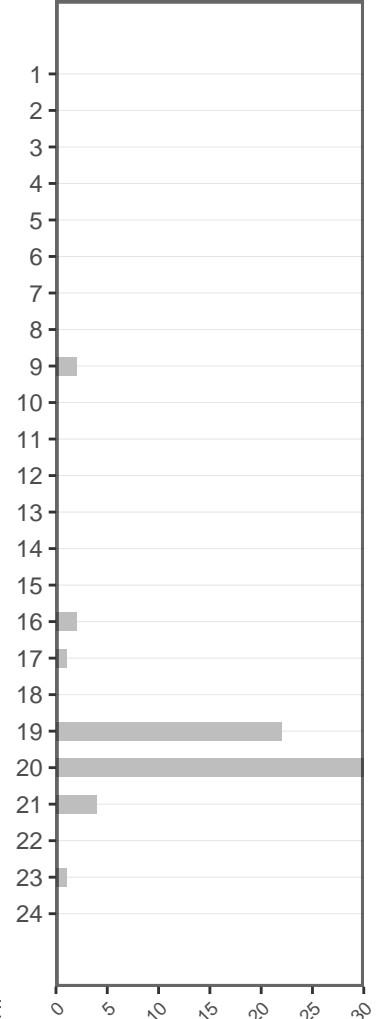
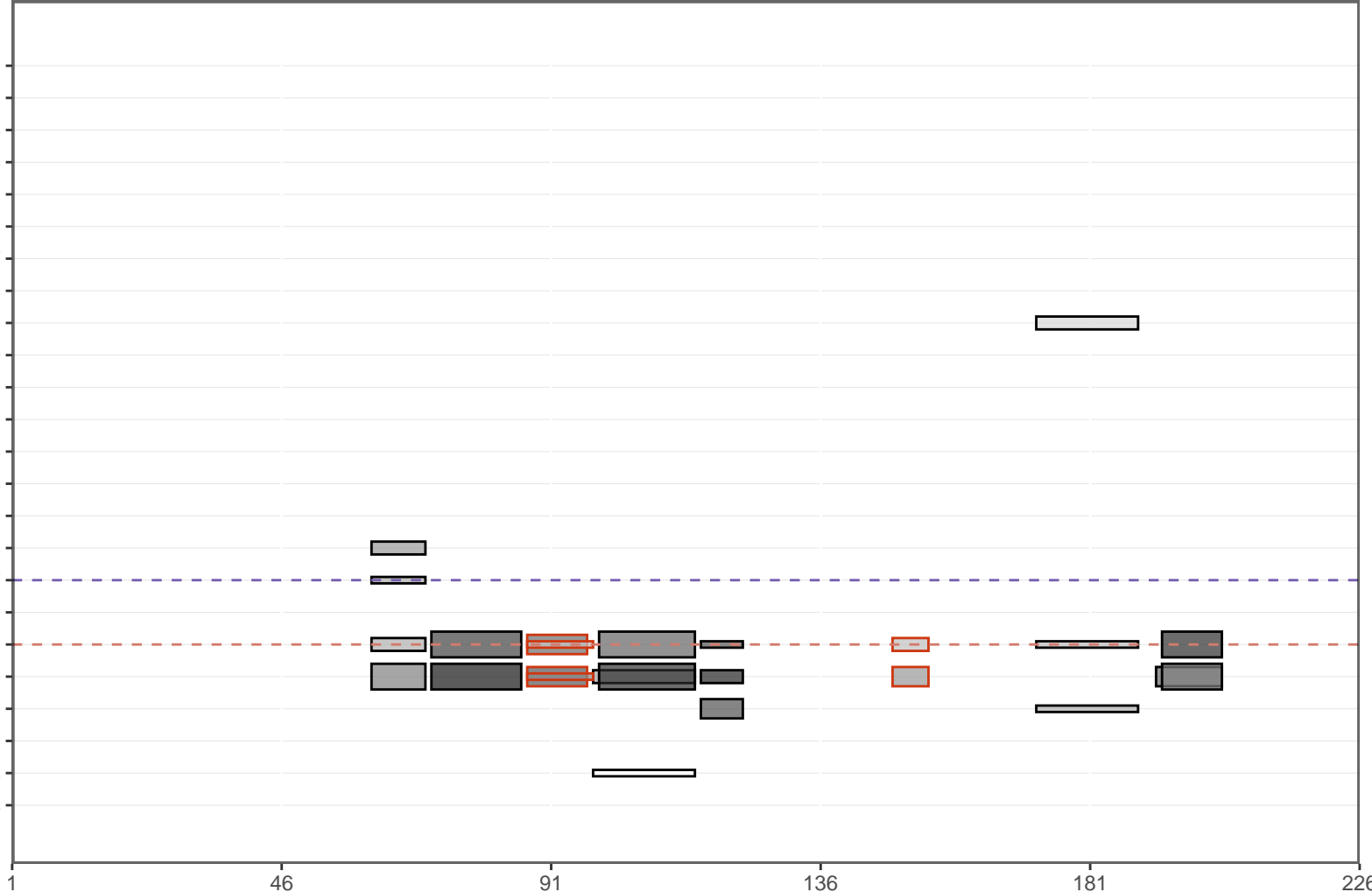
MW indication



Molecular weight

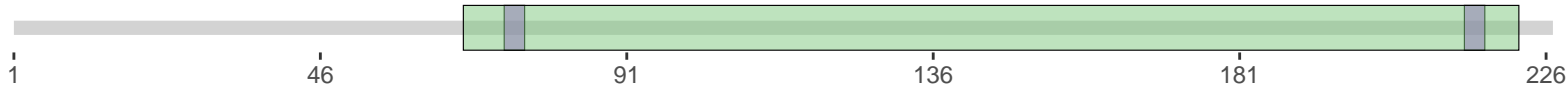


Gel Slice



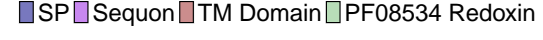
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FAVPGAFPTTCSQKHLPGFVEKSKELKSKGVDTAGISVNDAPFVMSKWKENKINDEVLLSDGNLEFTRKAGCELDLSDKPIGLGVRBRRYAMLVDDGKWKVNLNEEGGFANVSSAEDIKTL*

NbL08g15270.1 calcium-dependent_protein_kinase_4 [MW = 61.78 kDa]

No. of times detected



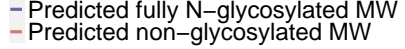
log(intensity)



Values from



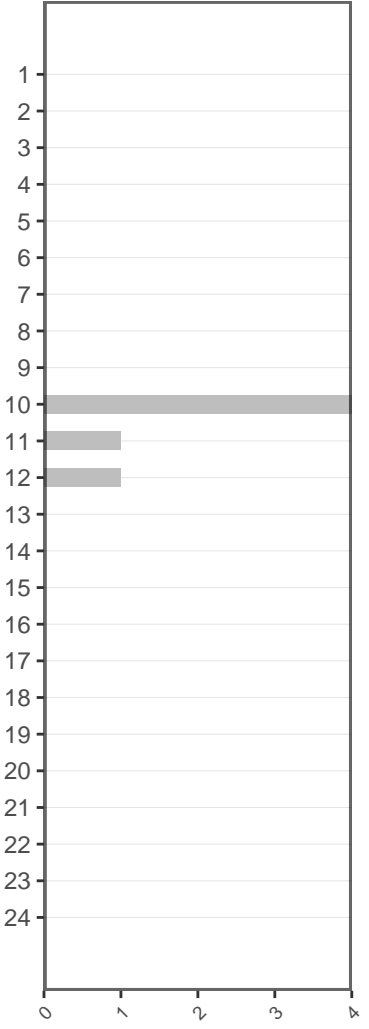
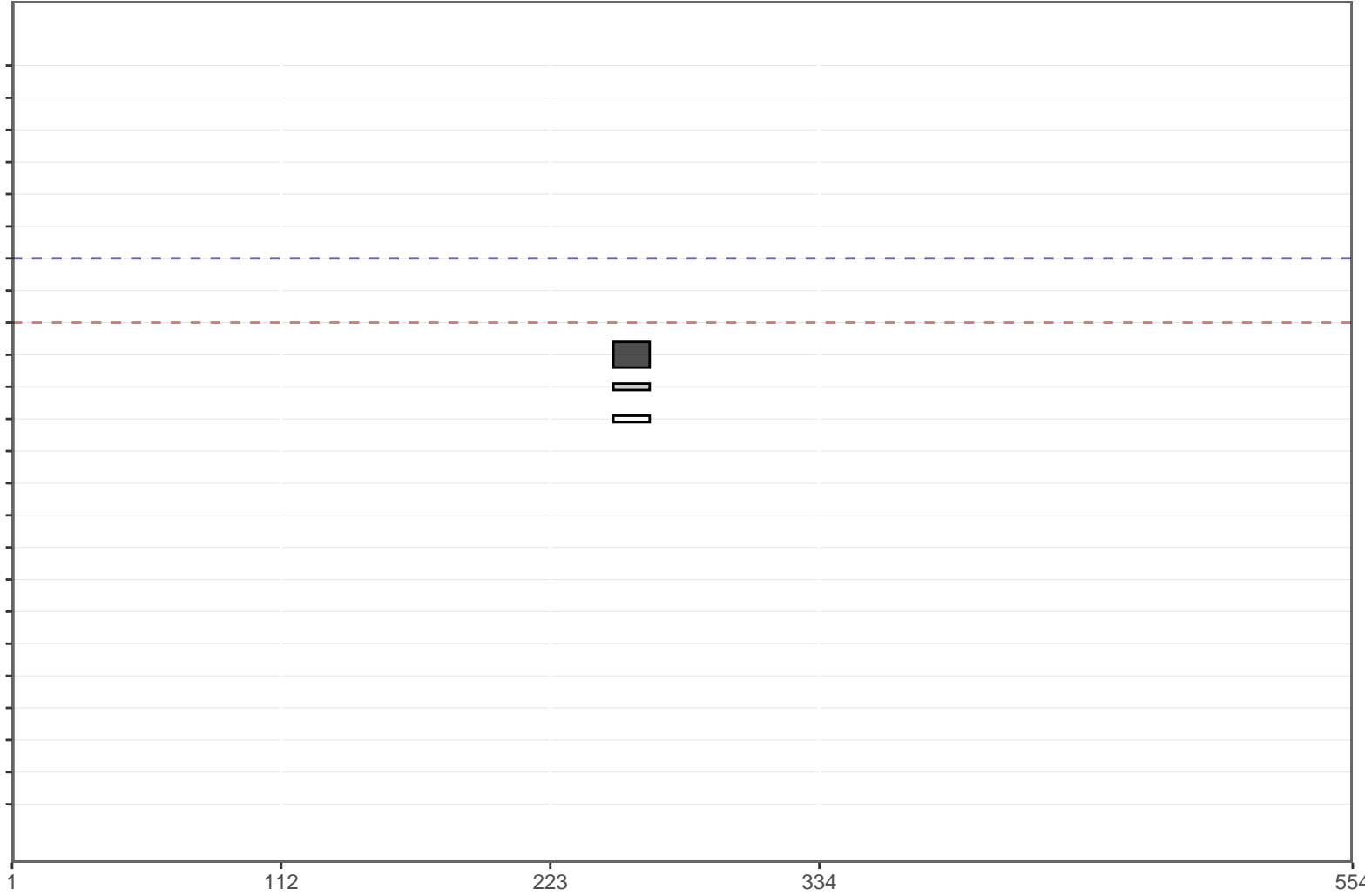
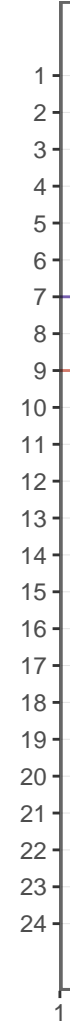
MW indication



Molecular weight



Gel Slice

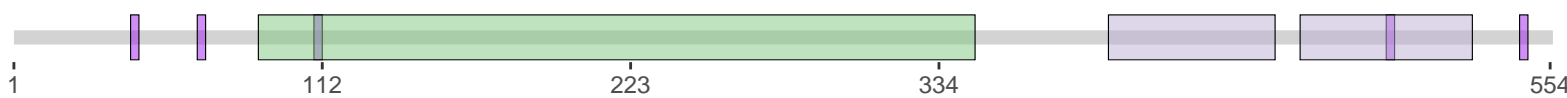


Protein length

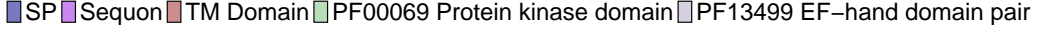


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

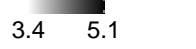
Q1YGEADVWTAGVILYLLGGVPPFAETGGGIFDVLKGHDFDSDPFWPLISESAKDLRKLKMGMPSEKRTAEVLCHPWCENGVAFDRAALDPLVLRKLGFSAMNKLKMMALRVVAESLSEEEIAGLREMFKAMDTONSGAITFDLKKAGLRKYGSTLKDTEIRGLMNAADVNSGTDYGEFIATVHLNKLREELHMAAFQYFDKGGSGYTVDEVGGAGAEHNTDNYFEDIRREVGGDNDGRIDYGEVAMMGKGNPCGGVRRTRMNSLMSRDAAGAI*

NbL08g15260.1 uncharacterized_LOC107760951 [MW = 34.16 kDa]

No. of times detected



log(intensity)



Values from



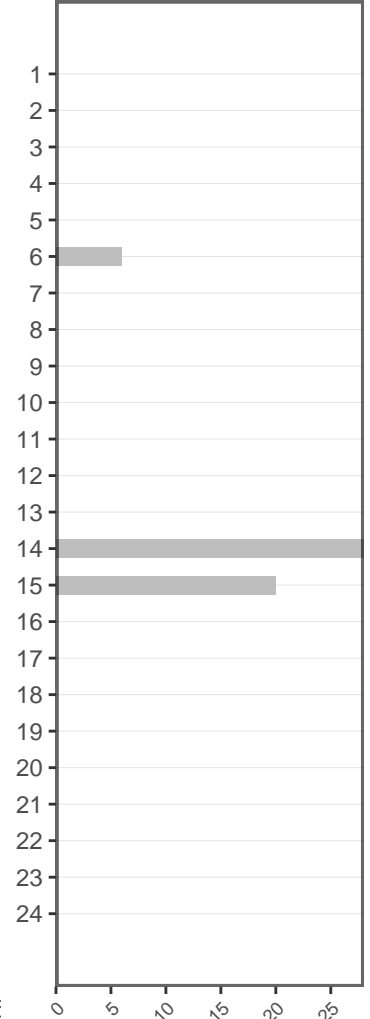
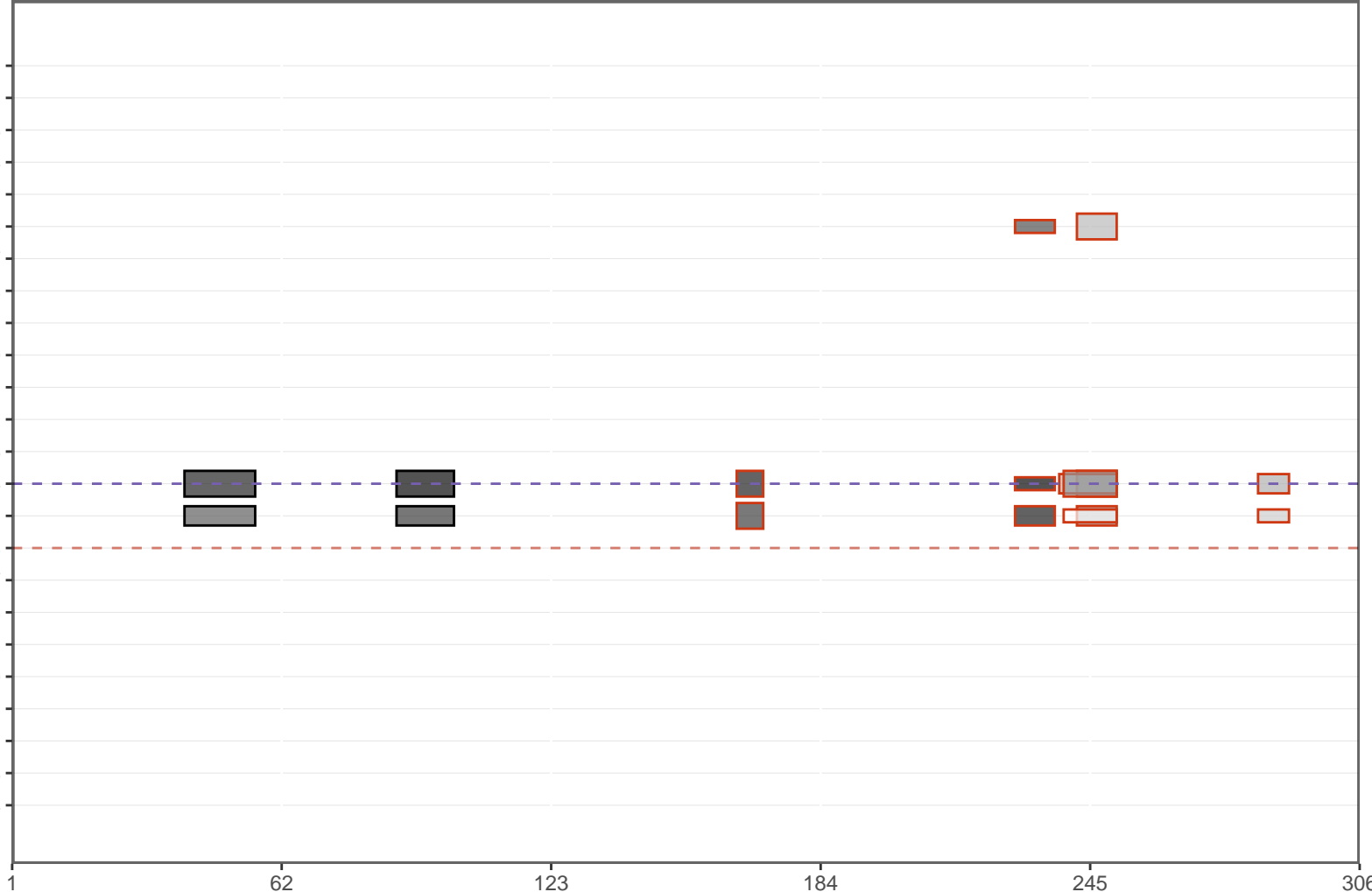
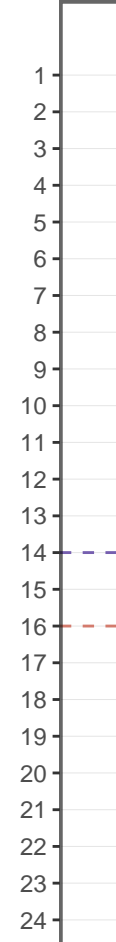
MW indication



Molecular weight



Gel Slice



Protein length



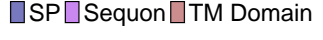
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

HCILDPRKXESRVRHQVVRLEDSKLVGNVVFGEHWYGFPRNGDGLGGCAQDSAFASQALDPTQVGVWEGKHAFSGFDPNAPQKVQELVDGSTRKTVRDELQVLLPRGLWDLKQKVAAGGETGCEVGVLFKGRAMTSKQIFRSDDGKLEIAGESASAE*

NbL08g15250.1 uncharacterized_protein_At2g17340-like [MW = 44.41 kDa]

No. of times detected



log(intensity)



Values from



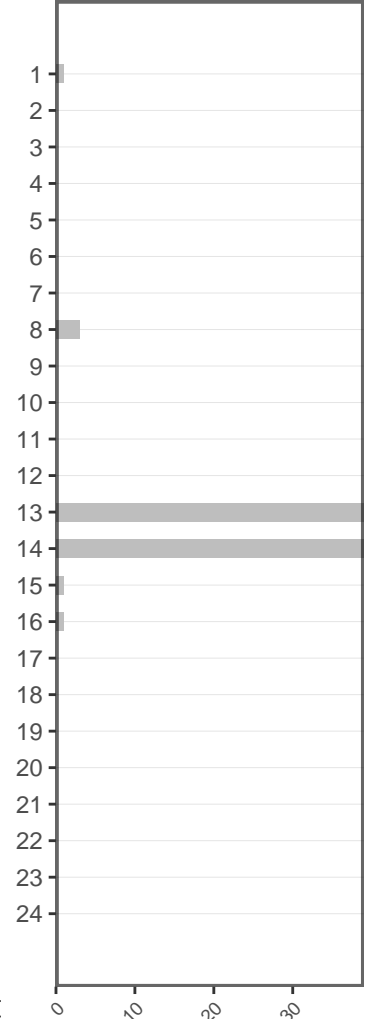
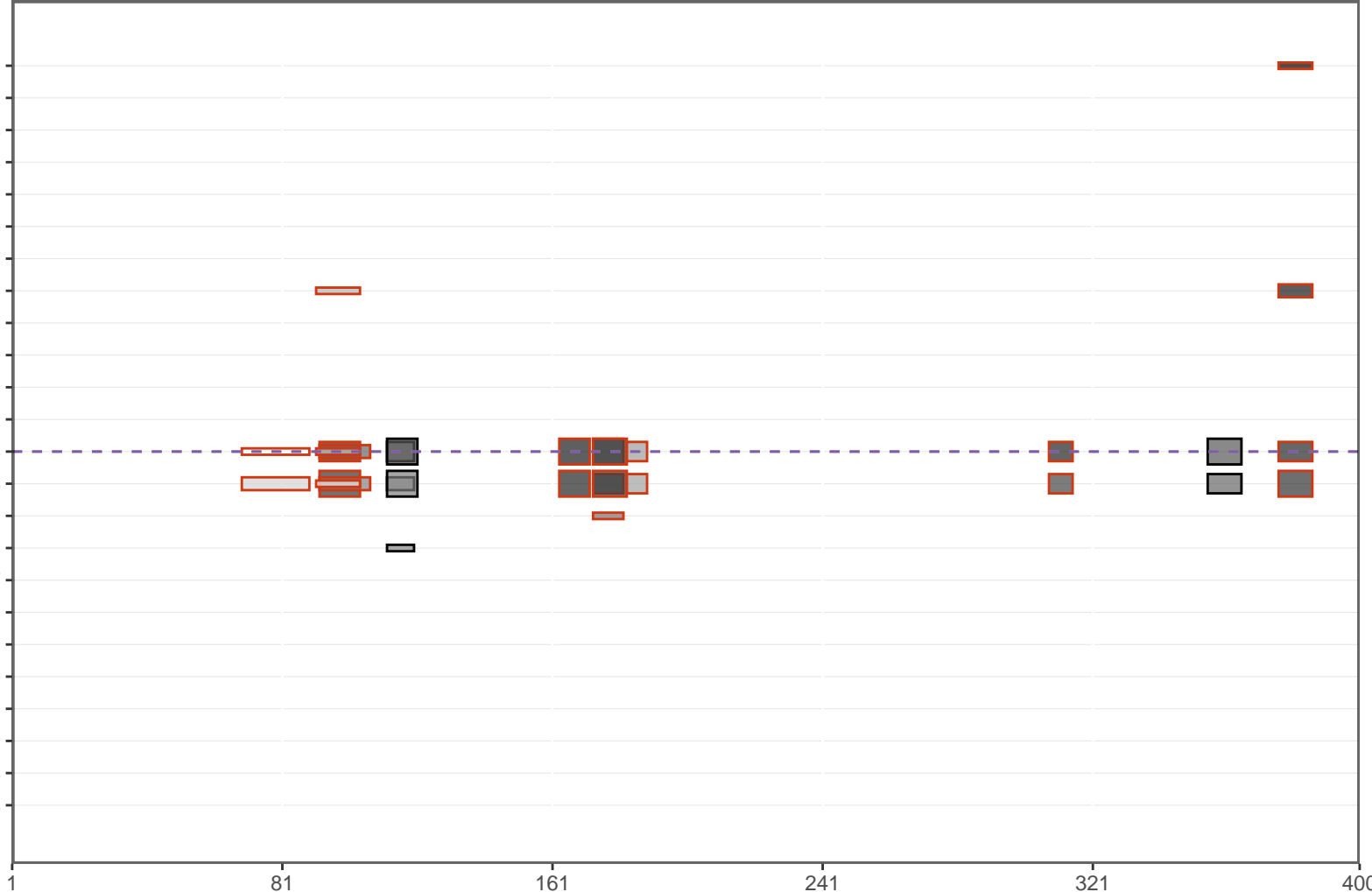
MW indication



Molecular weight

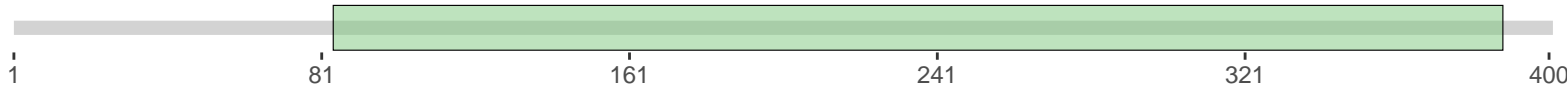


Gel Slice



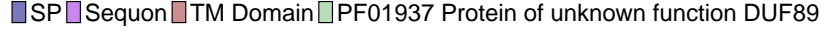
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

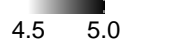
ENLYRQGFAGNFDLGSANLAELFSEDDMSFLASGQNLVPRPWVDDVDTFTKWRKTKWKAIVFVDSGADILGILFFARELLRQGTQVLAANDLPSINDVYTELVELSKLKDHEHGKLVGDTFKLLVANSQNDLPVLDLTVSQELVYLABDADLVILEGMRGIETNLVAGFKDSEKIGMVKHAEVAGFLGGRIVDGVKFKNEALS*

NbL08g15030.1 acetyltransferase_NSI [MW = 28.25 kDa]

No. of times detected



log(intensity)



Values from



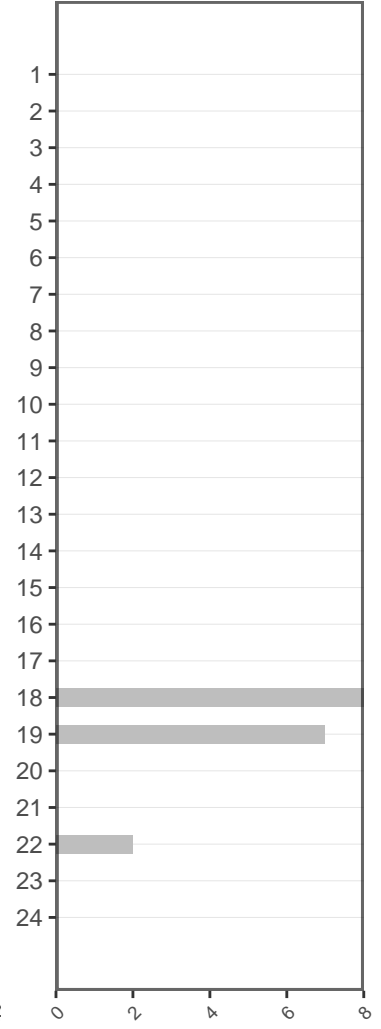
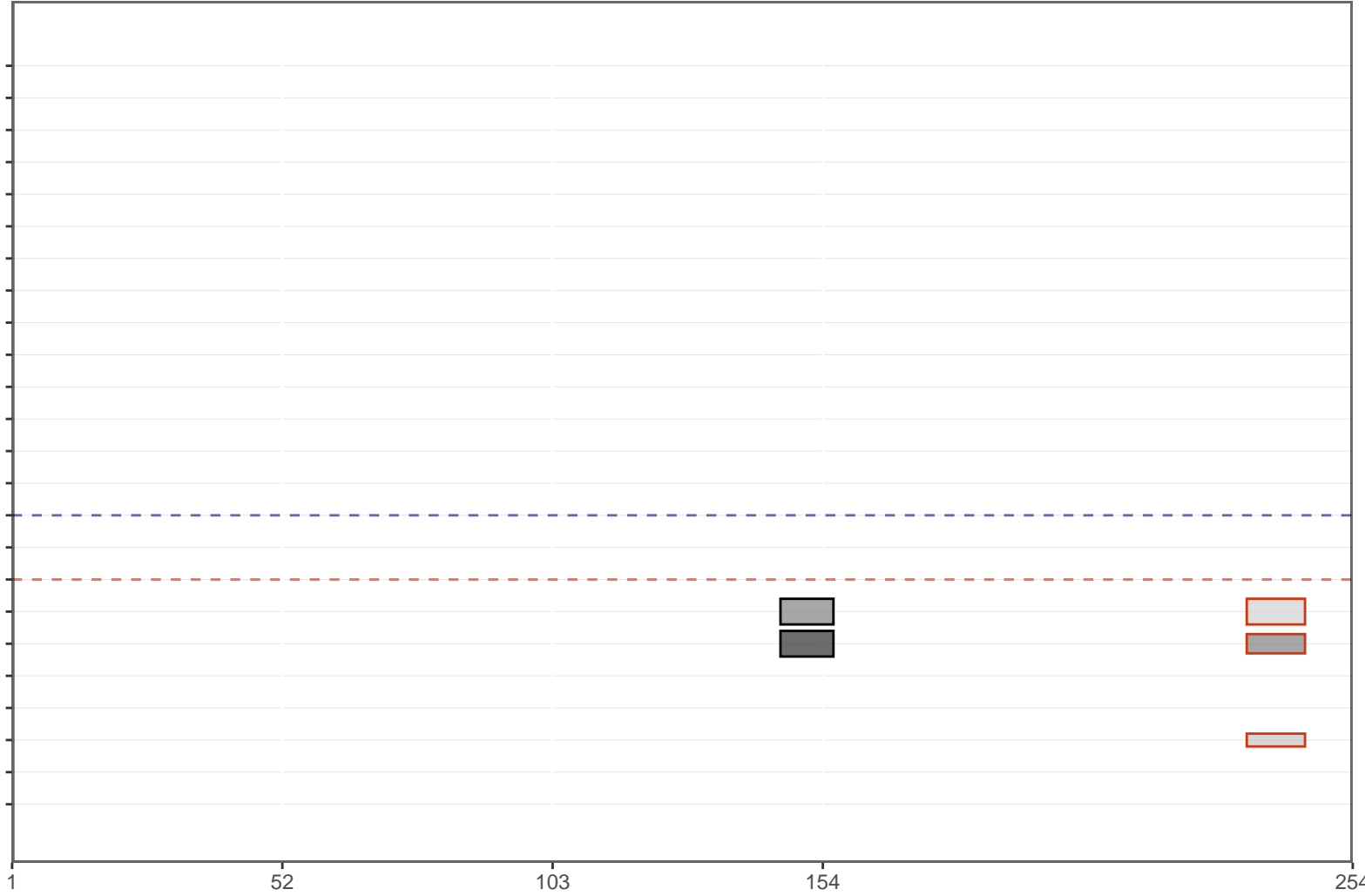
MW indication



Molecular weight



Gel Slice

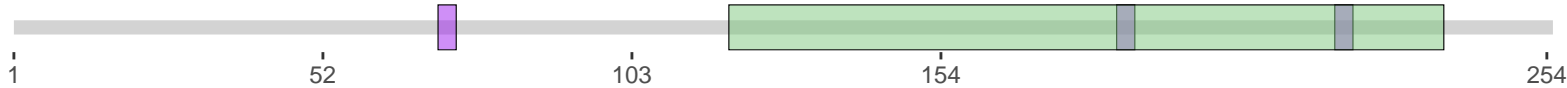


Peptide counts over 4 repeats

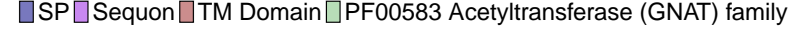
Protein length



Pfam domains



Pfam Description

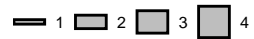


Protein sequence:

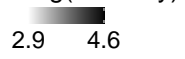
IGGDVYDYLALGDKVWFRRLPLSLAAALKNBIVATLHBRKFSGSEEGNGEKKLIGMARATSDHAFNATIWDVLDPSYGGGGLKALIEKIRTLQORDGNLSLFDASQVVEFYKNLGFEPEDEKGMFWYPMV

NbL08g15020.1 mannan_endo-14-beta-mannosidase_6 [MW - SP = 46.4 kDa]

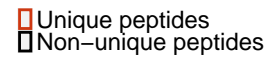
No. of times detected



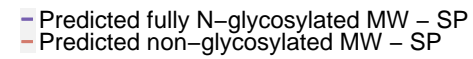
log(intensity)



Values from



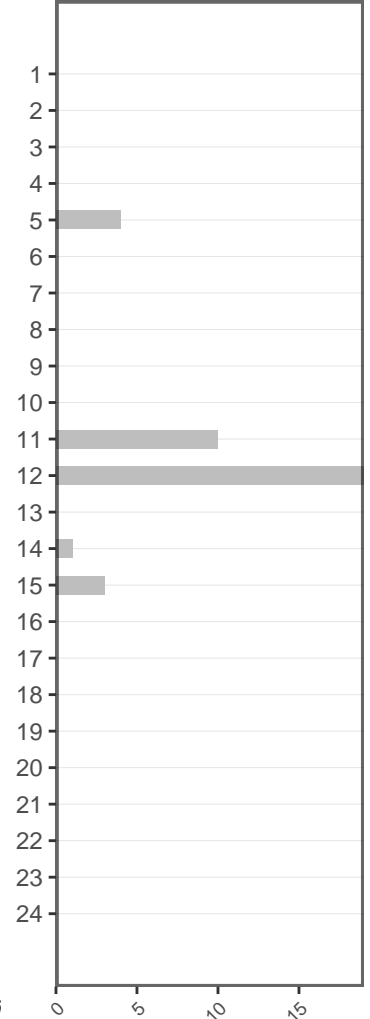
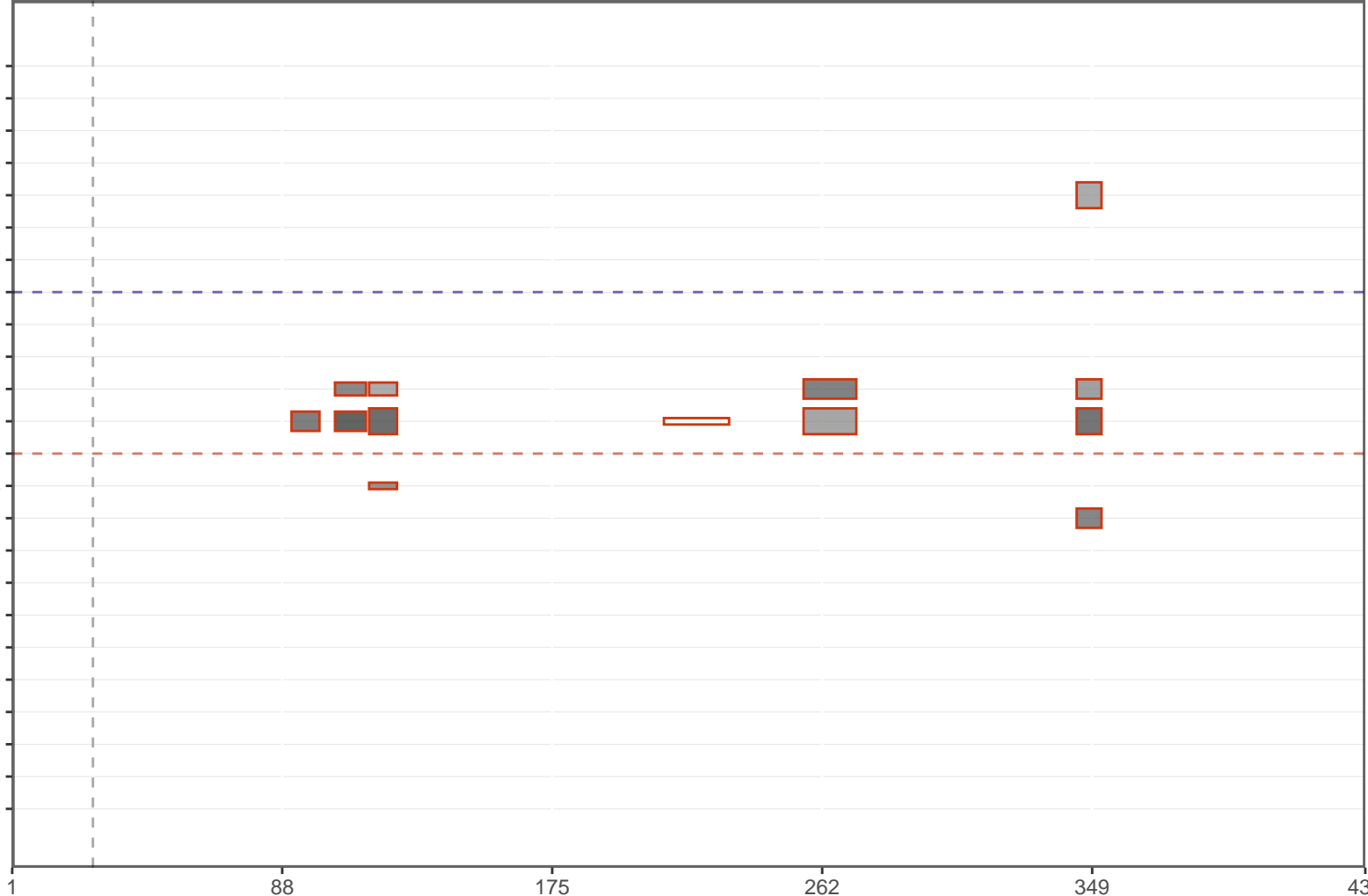
MW indication



Molecular weight



Gel Slice



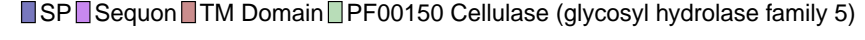
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ELMNEPRCESDPSGDKLQAWVEEMAVYVKSIDPKHLVEIGLEGFYGLSTPNRAGVNFNSVAGQVGTDFIRHQVLGVDFASVHYHPSWIEGSGSEAHVEFTKSWMGSIHDDAEKYLMPVYFAEFGVSTKDPGVNSTYRDLTLMYVKTILNSTRKGGAGGSGLLWQVYFEGTDVMDGGYAVLSEKLSISNIVSLHSHKILNTNFSGVSKWGHVWGRKKHVLLEDFQSRDEL

NbL08g14990.1 vacuolar-sorting_receptor_1-like [MW - SP = 67.2 kDa]

No. of times detected



log(intensity)



Values from



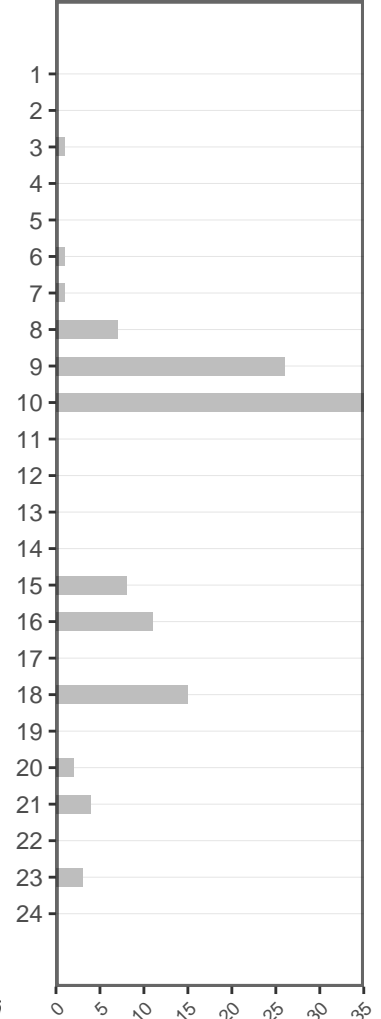
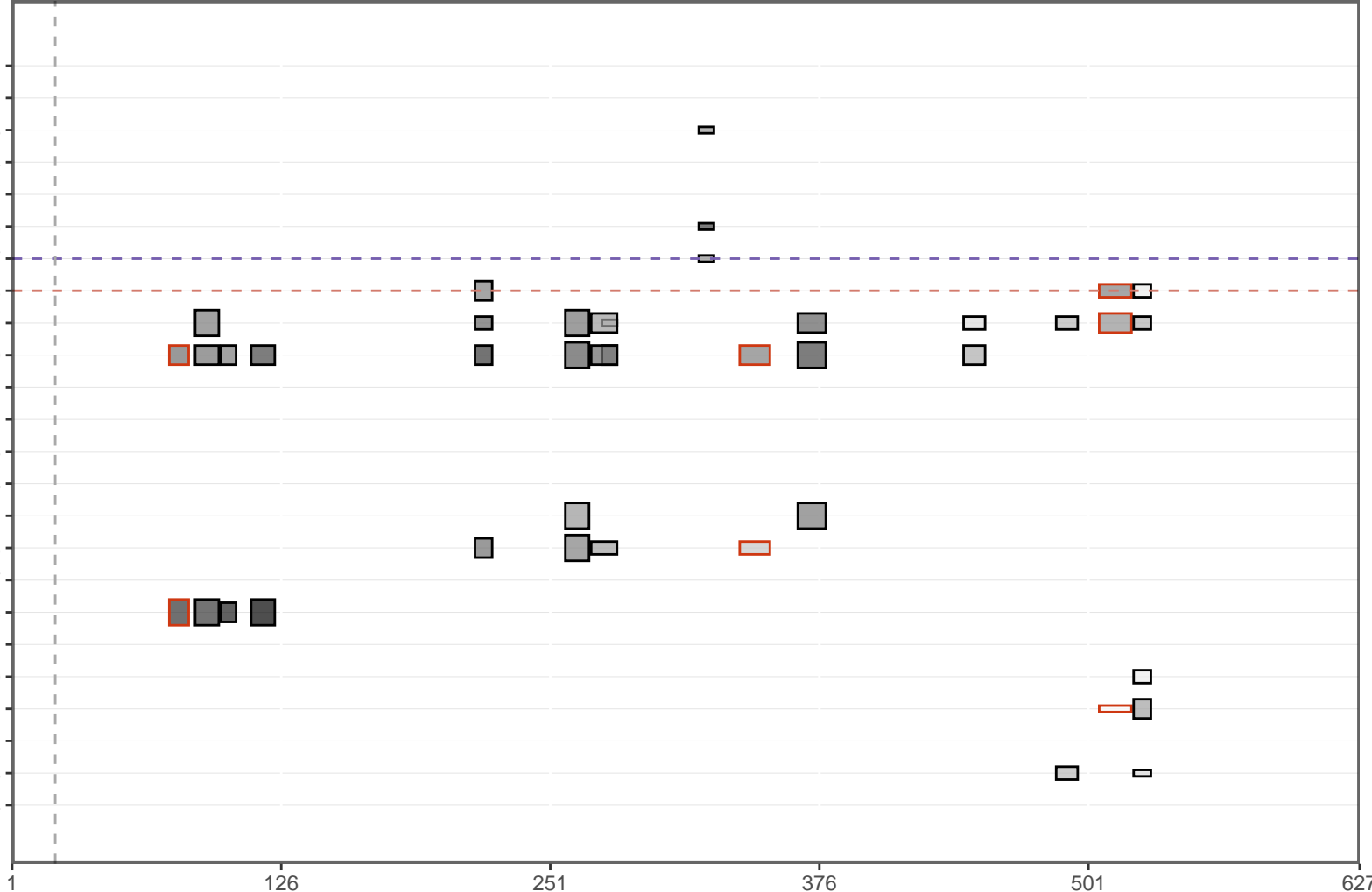
MW indication



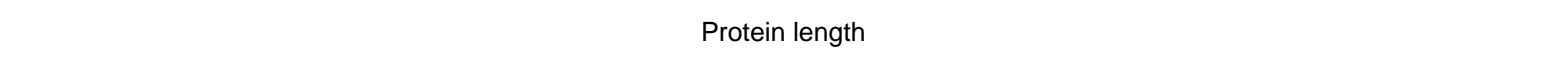
Molecular weight



Gel Slice



Protein length

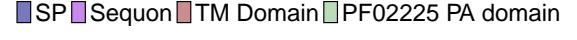


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

YVTFDIRCPIMKEKYVTKEGADGVVKKLGFDFVKGIDKGVGDPPEADANPNVKAEGAEQKIDSRGSDVTLPELVNINRQVYRGLDKGAVLKAIGSGFEETTEPAKLTDDIQITNEGLSENGGWDKKAANTAGRDTRFRKVGCECPMAVGGVWFVGDGYTHDEASGALRGINNGGQWVGWGTGDRTRFSAGIDDHTRKGGKPPDFKGDGVNCGEDIDEGNERLADQCFEKGKNTWGGYDGSQGNLVMHEHDTQINAGKDKTEFSWGFVWVWIKGLAAAGVAVYI

NbL08g14940.1 67-dimethyl-8-ribityllumazine_synthase_chloroplastic-like [MW = 24.65 kDa]

No. of times detected



log(intensity)



Values from



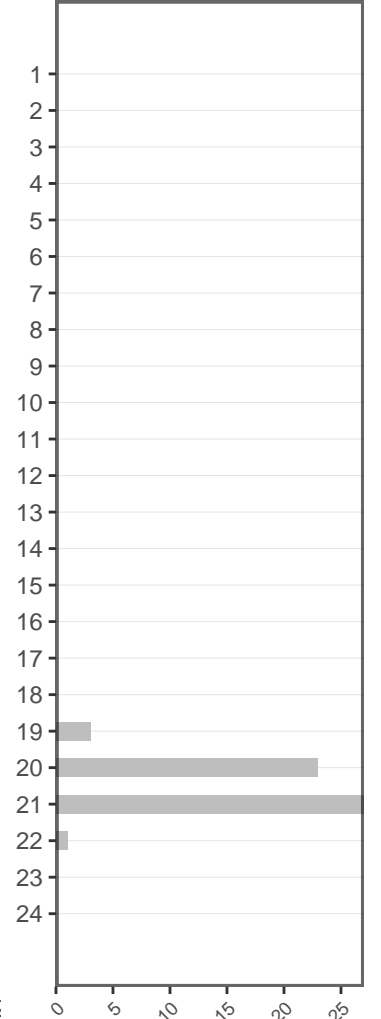
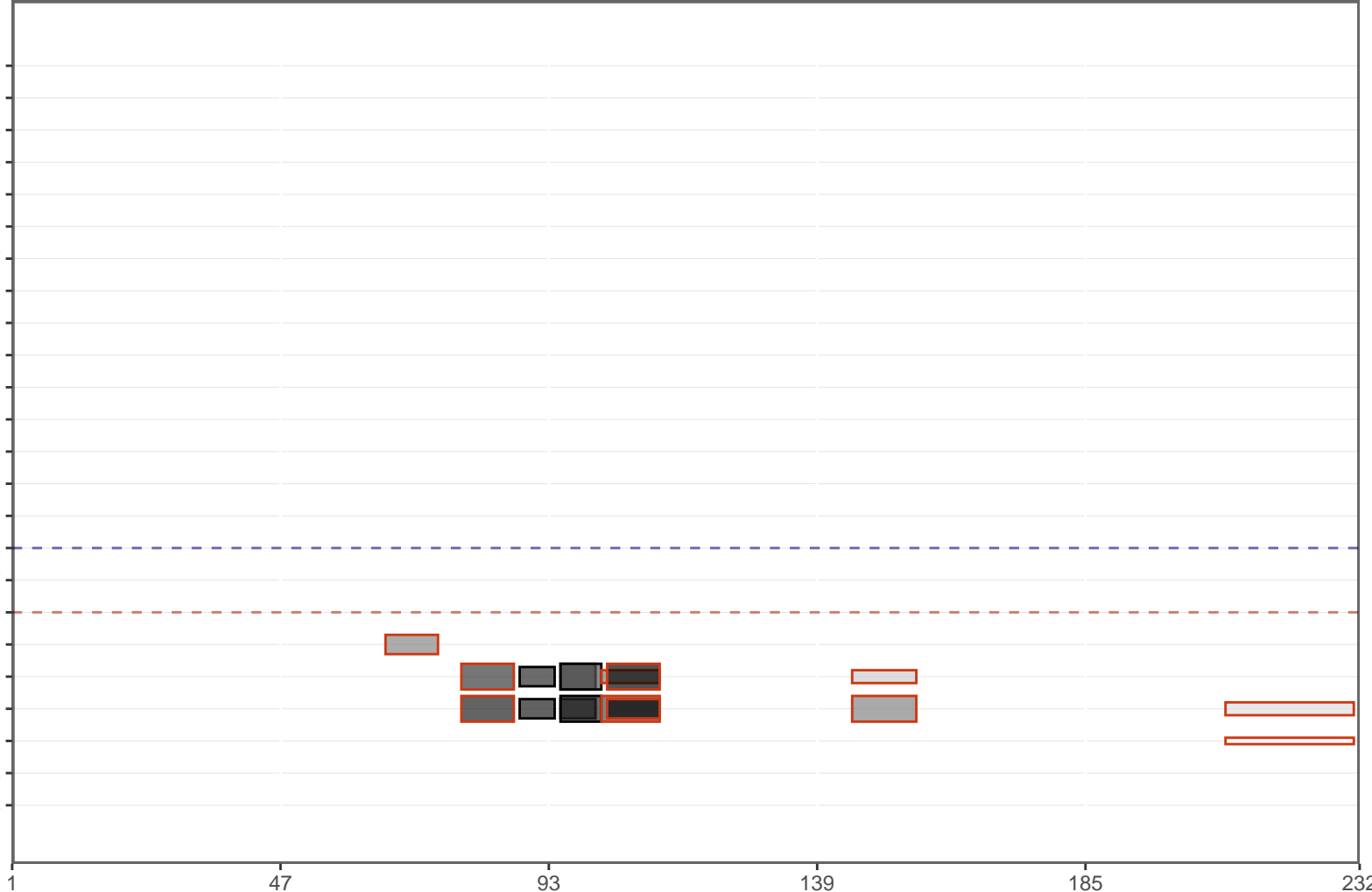
MW indication



Molecular weight

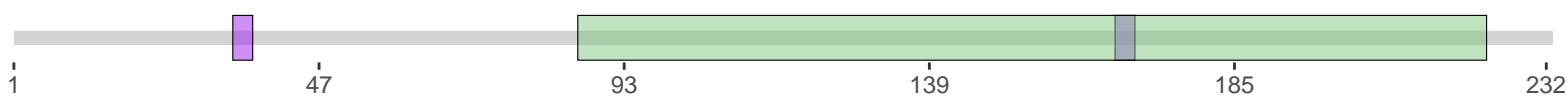


Gel Slice



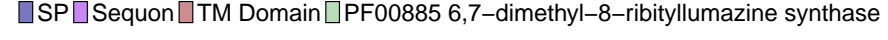
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LEGALDTFKYSYSVREENIDVWVWPGFEGVVAQGLGKSGKYGBLGGVAVKGGTSHYDAVVAWTFSGVLSAGLNSGTFPGFDVLTGDTLEGAFNRAGGKSGKNGKAEALTIEMASLFEHHLKPLE*

NbL08g14920.1 pyruvate_dehydrogenase_E1_component_subunit_beta-3_chloroplastic-like [MW = 44.49 kDa]

No. of times detected



log(intensity)



Values from



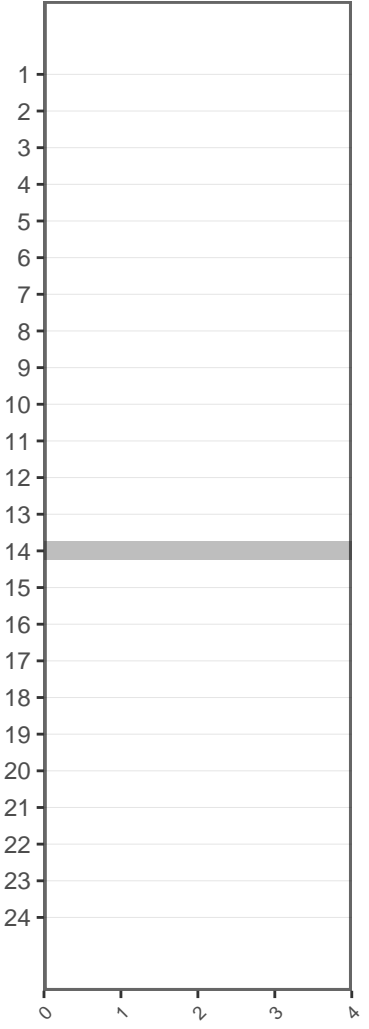
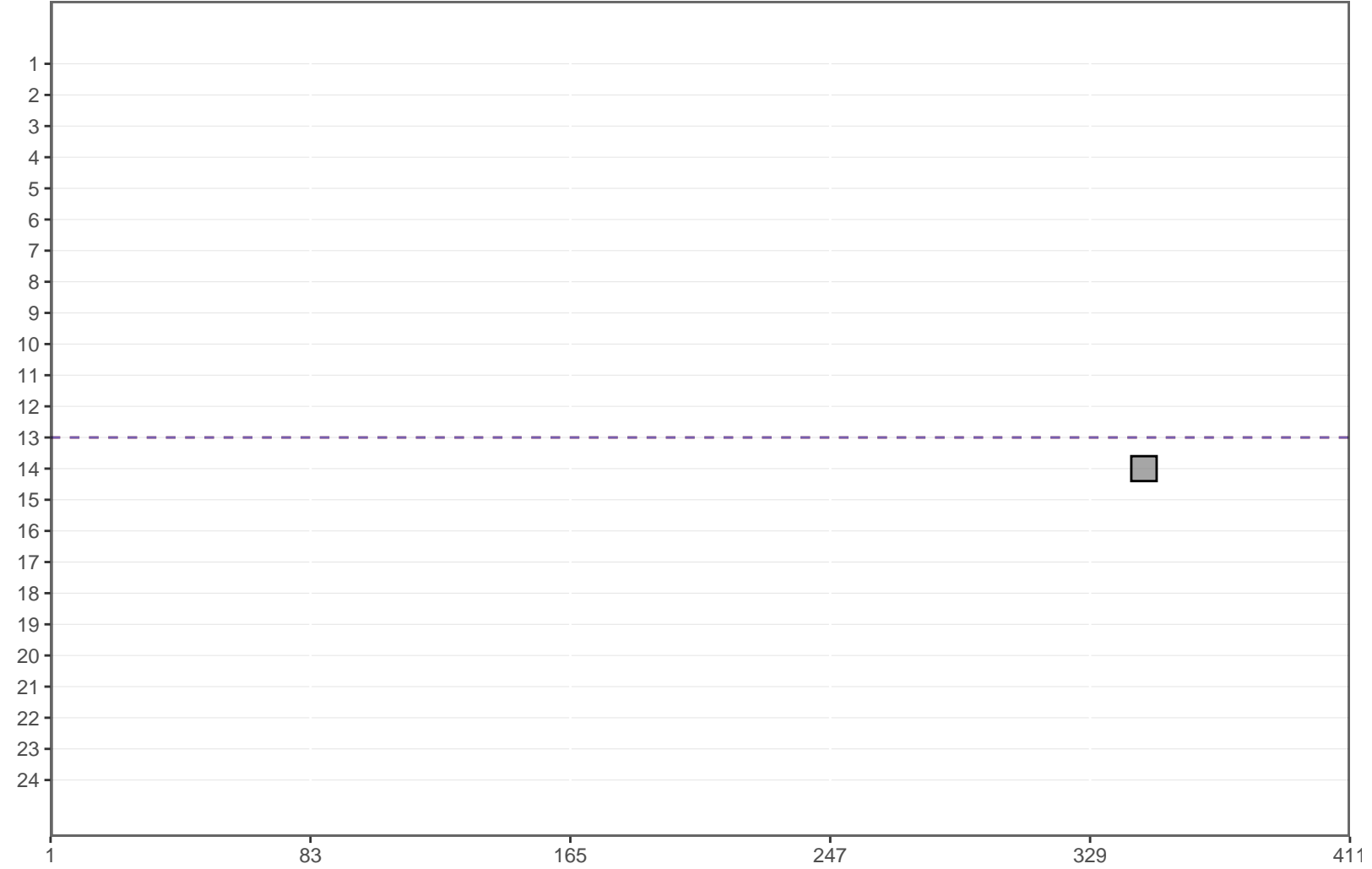
MW indication



Molecular weight



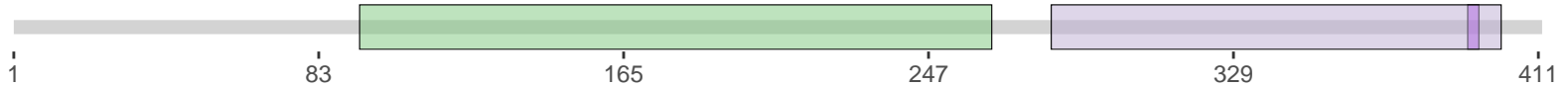
Gel Slice



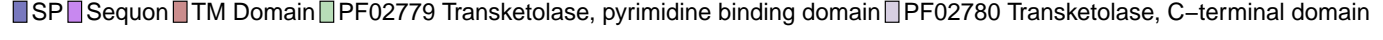
Protein length



Pfam domains



Pfam Description



Protein sequence:

SGGGPKFVIRGPGGVRQLGAHSGRLSEYFQSPFGIMVAGSTPYNAKGLMKAAIRSDNPNVLFHVLVNLKERIPDEEYVNLLEEAEMVRPGEVTLTYSRMRYHVMQAAKTLVDKGYDFEVIDRSLKPFDLHTIGNSVKKTRHVVVEECMRTGGGASLTAATENPHDLDPANVQLSGGDPTTPYAGTLENWTVVQRPQGVAVTEGLQR

NbL08g14850.1 uncharacterized_LOC107820649 [MW = 30.78 kDa]

No. of times detected



log(intensity)



Values from



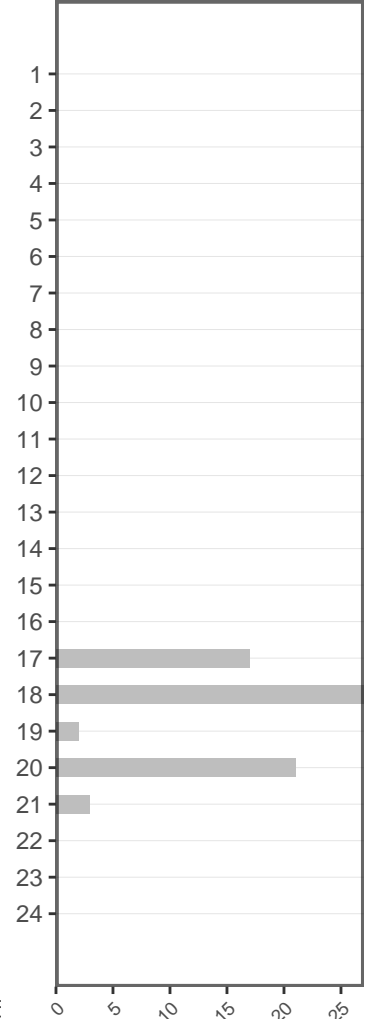
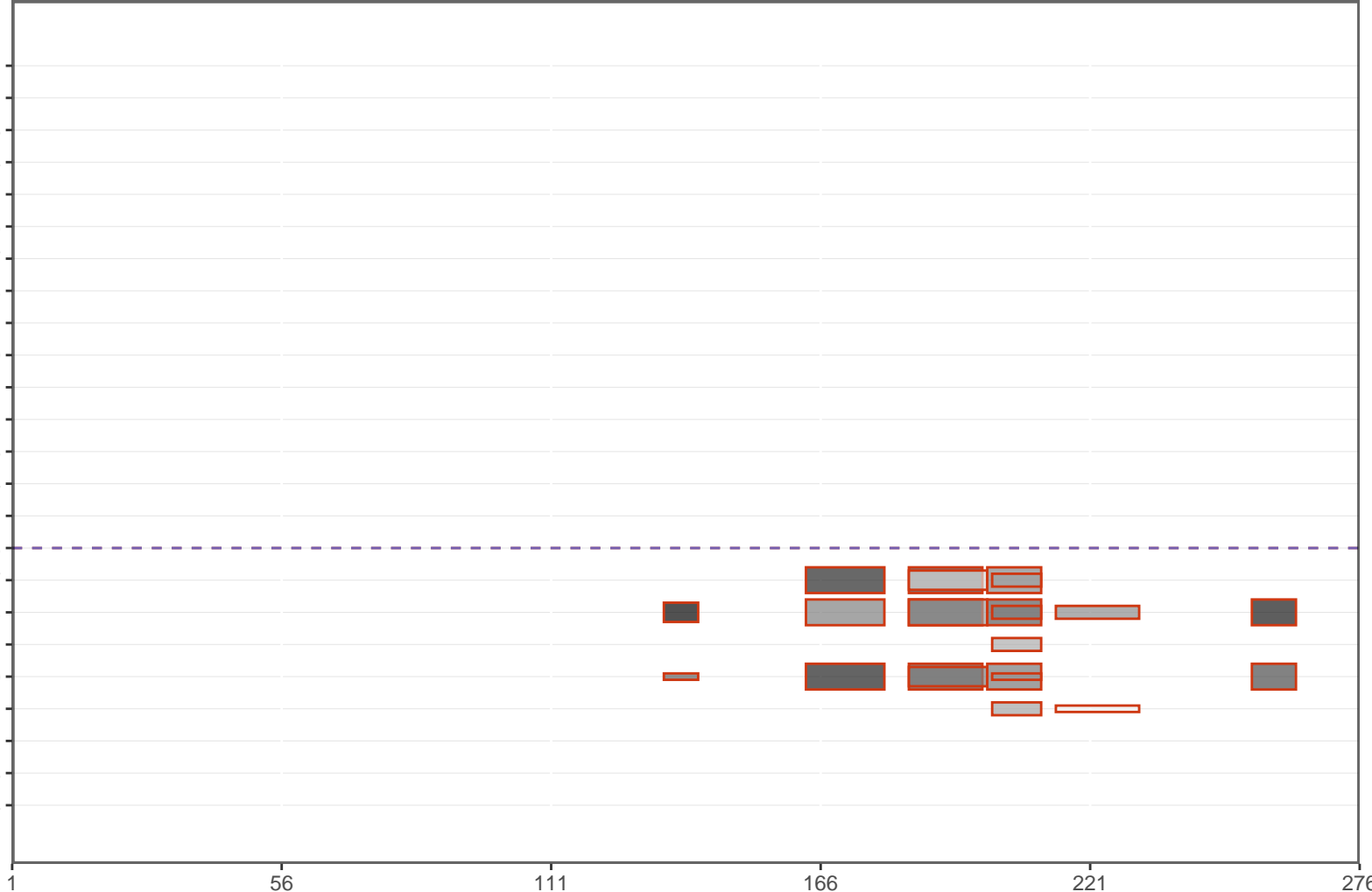
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



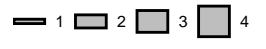
Pfam Description
 SP Sequon TM Domain

Protein sequence:

ELLAIQQGGPRNIGFFGTRNMGFMHGELELVALVITKNHFTSGAAGTNAVIRGALRAEKPELLVLPGLKKQPPESGELLKWKVHIEKPHNDHLSLEASRLGNMDFIQVGGVGFVAFHDSRLMETGQEAANKLRKIVLELD

NbL08g14810.1 ATP_synthase_subunit_beta_mitochondrial-like [MW = 59.7 kDa]

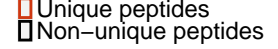
No. of times detected



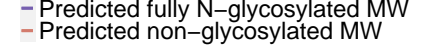
log(intensity)



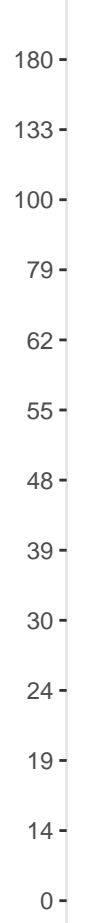
Values from



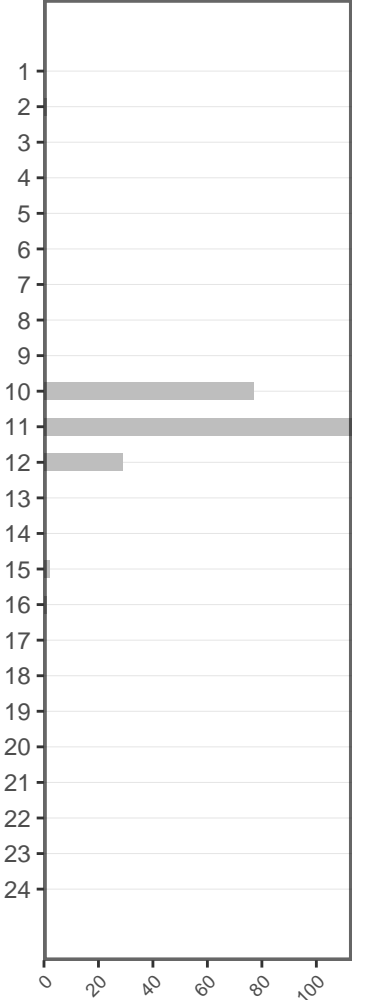
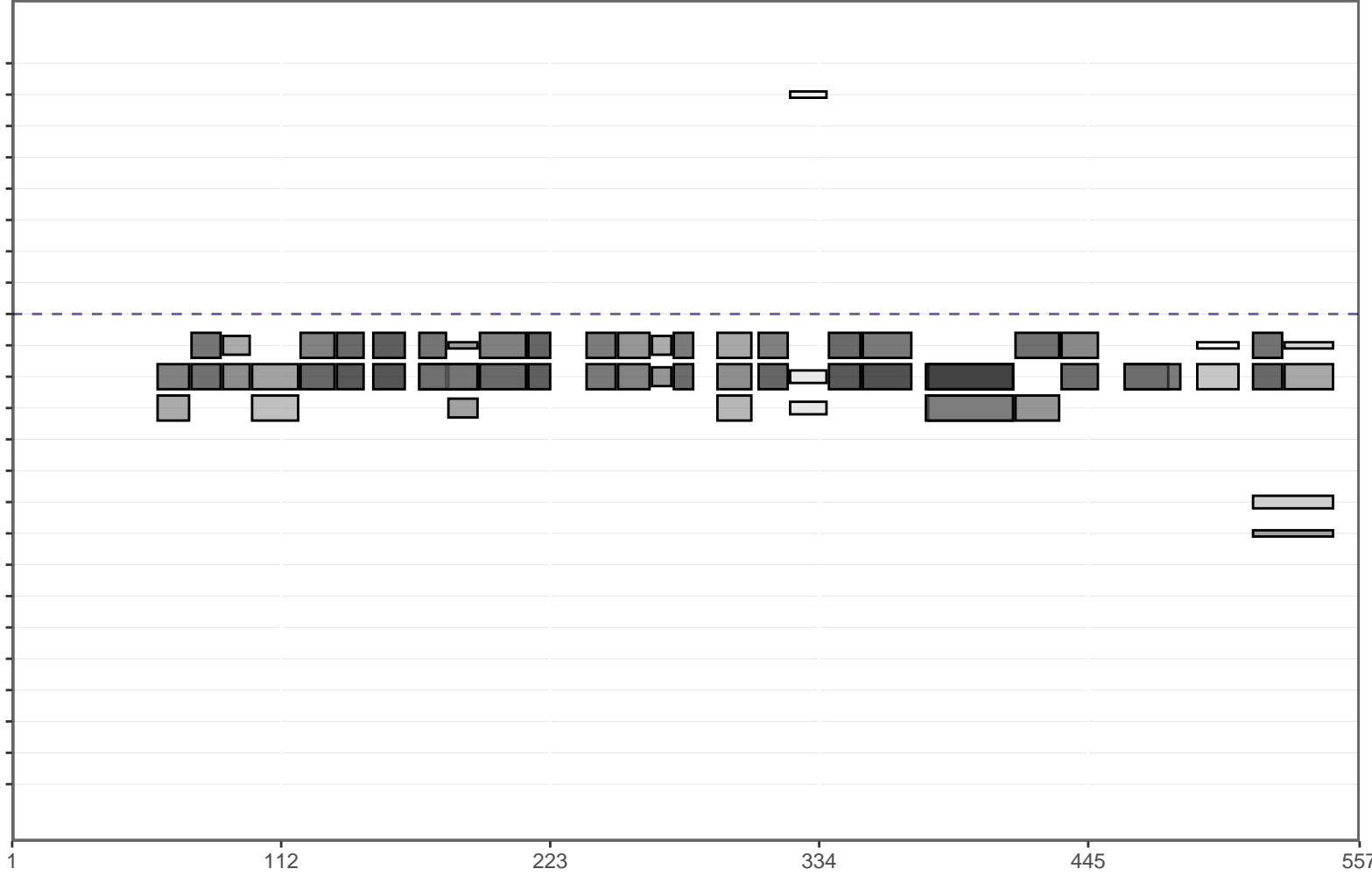
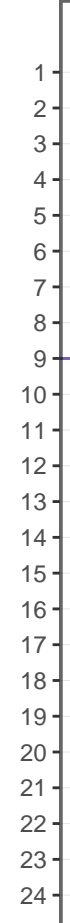
MW indication



Molecular weight

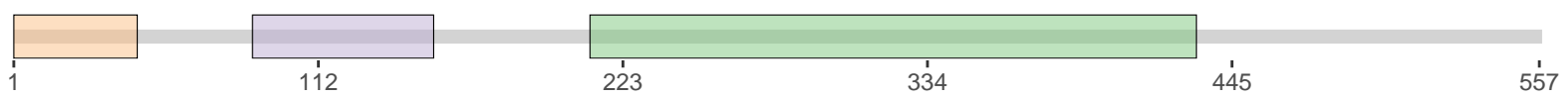


Gel Slice



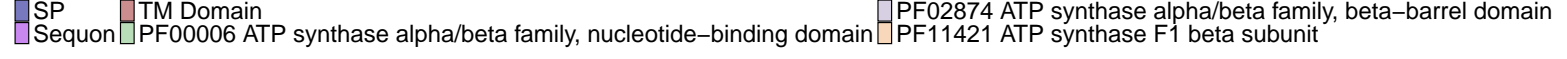
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

REGNDLYREMEISGVRLGDKDQSEKALVYGMNEPPGARARVGLTGLTVAEHRFDREGGDVLFDINFRFTQANSEVSAALLGRIPSAVGYGPTLATLGGIGERITTKKGGFTSVQAIYVPADLTDPAATFFAHLDTTTLVSRQISELGIYVADPLDSTSRMLSPHLGSDHYNTARGVQKVLGNVKNLGDIALGMDLSEDDKMTVARARKIQRFLSGPFAVIEVFTGAPGKYVLDKESINFGQVLDGKYDDLSEQSEYMYVGGDEVAKAKEIAKESAA*

NbL08g14800.1 fruit_protein_pKIWI502 [MW = 33.42 kDa]

No. of times detected



log(intensity)



Values from



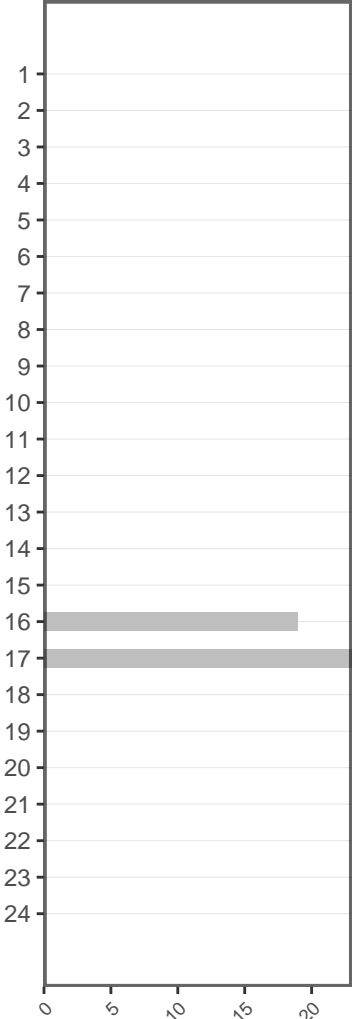
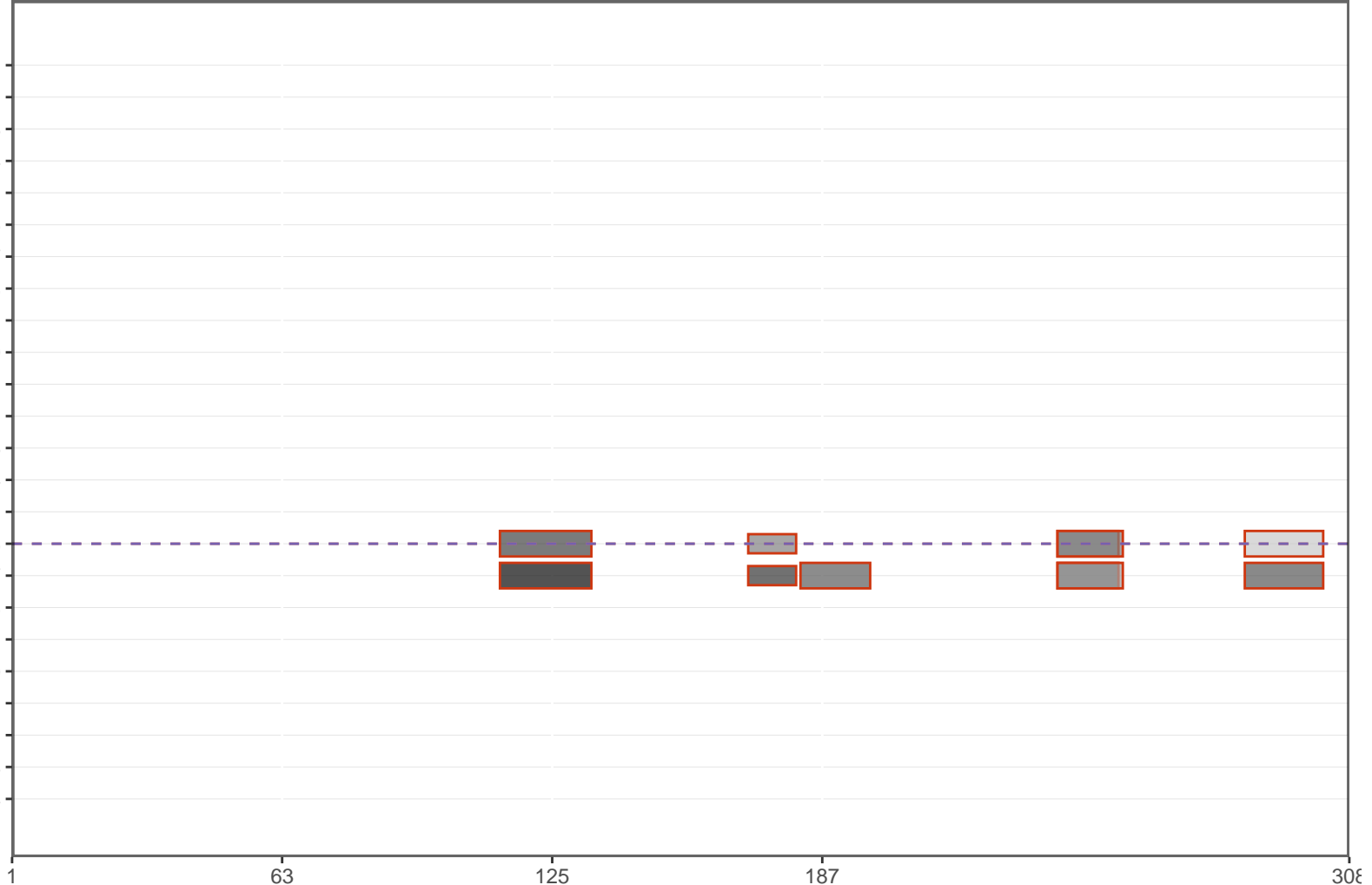
MW indication



Molecular weight



Gel Slice



Protein length

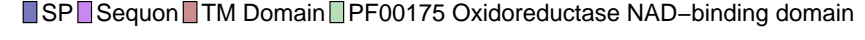


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SSGSAELLCLLQKNGDVELSGVMGKGFDLQKISPPKYGTVLIFATGSGISPIRSLIEAGFSADKRSQVRLYVGARNLKRMAVGDGFENWASSGQWVYVPLSGPDDAWTGRKGFVQAAFARANNFSPQSTGAVLGGQKQMAEEVITALLVADGVSTENLKNF

NbL08g14690.1 fructose-bisphosphate_aldolase_3_chloroplastic-like [MW = 42.91 kDa]

No. of times detected



log(intensity)



Values from



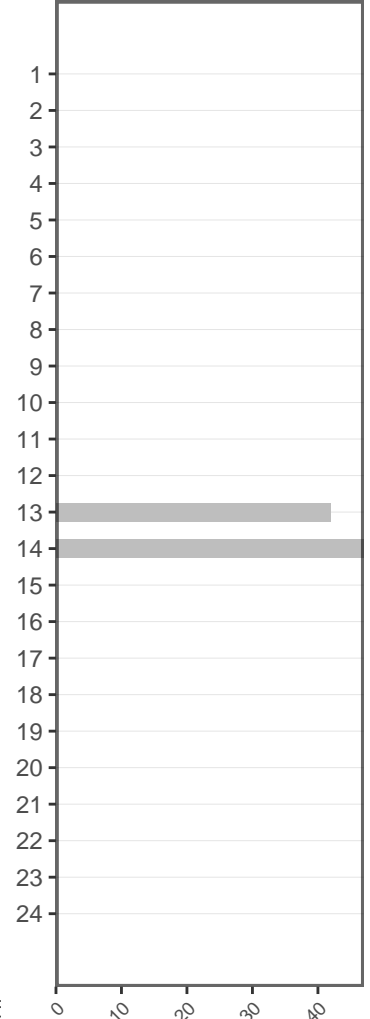
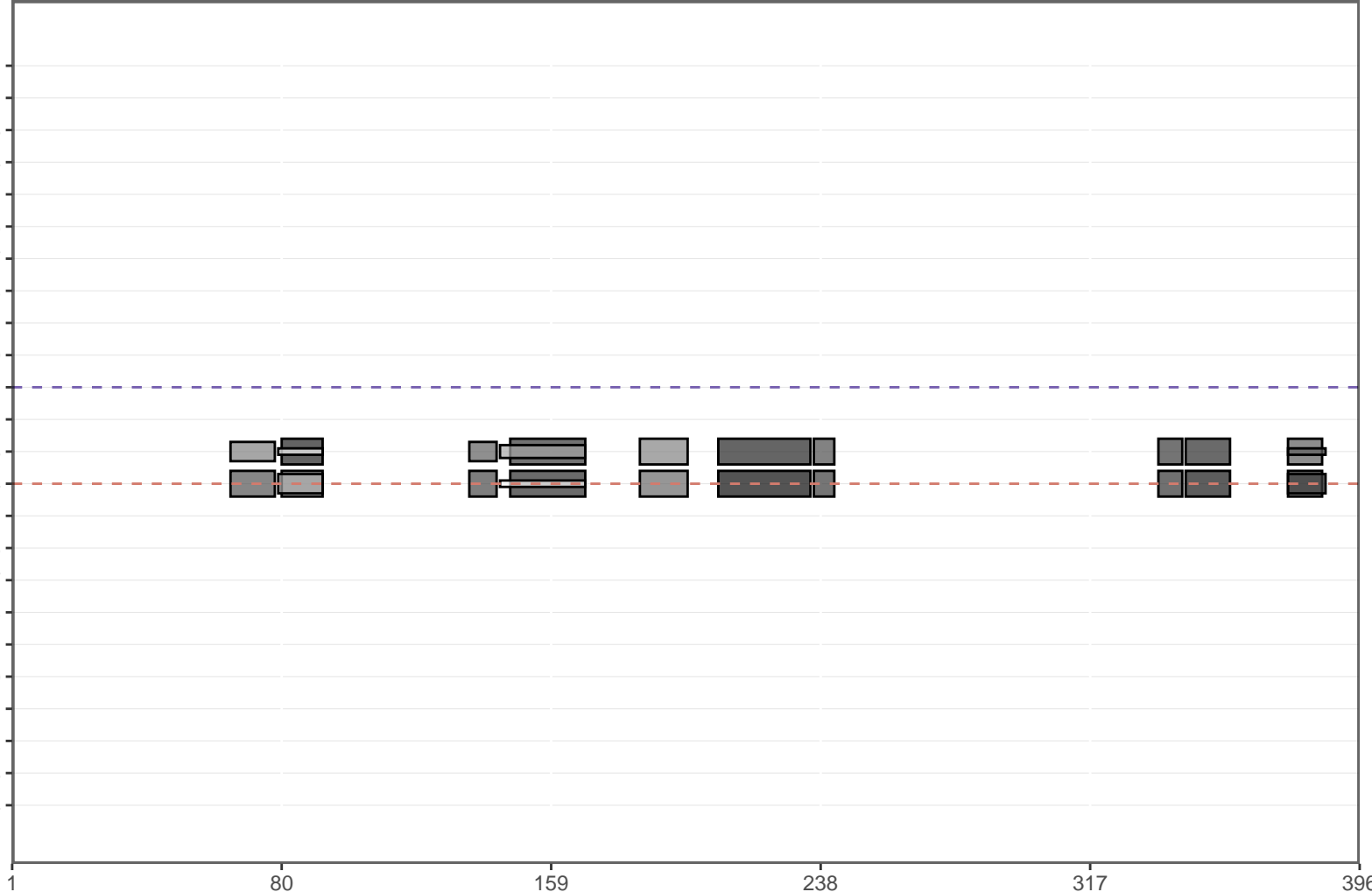
MW indication



Molecular weight

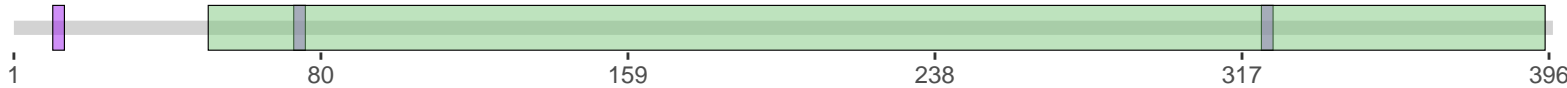


Gel Slice



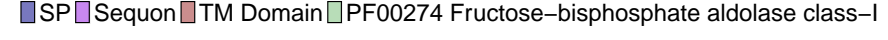
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TVSPICGFSALAVKEAAWGLARWAIBDNGSLVPEPEILLGGDHPRIETLEVAERVWAEVFFYLAENNVFEGLLKPSMVTAAEHKEKESFDTIAYKTKMLKRRVPPQVPGIMFLSGGGGSEVEATLNLNAMNGSPNFWVHVFYSYARALGNTVYKTKWGRPENVAAGKALLIRAKANSLAGLGGYKAAAGESEEAANKGMFVKGYTY

NbL08g14320.1 uncharacterized_LOC107766948 [MW = 55.01 kDa]

No. of times detected



log(intensity)



Values from



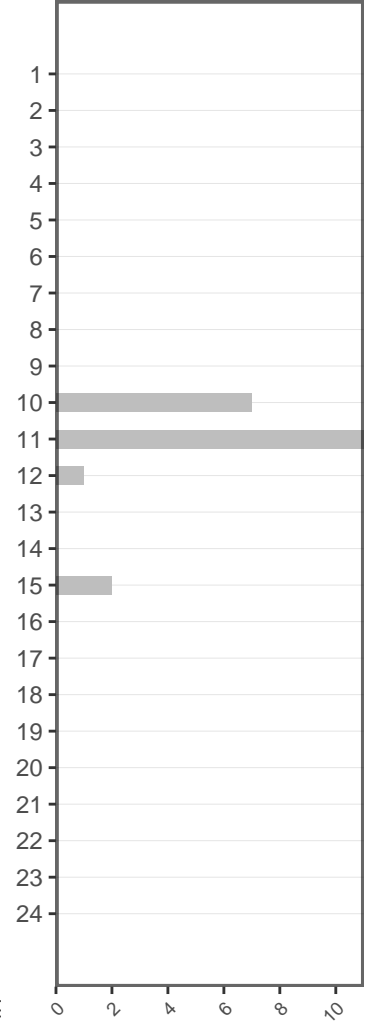
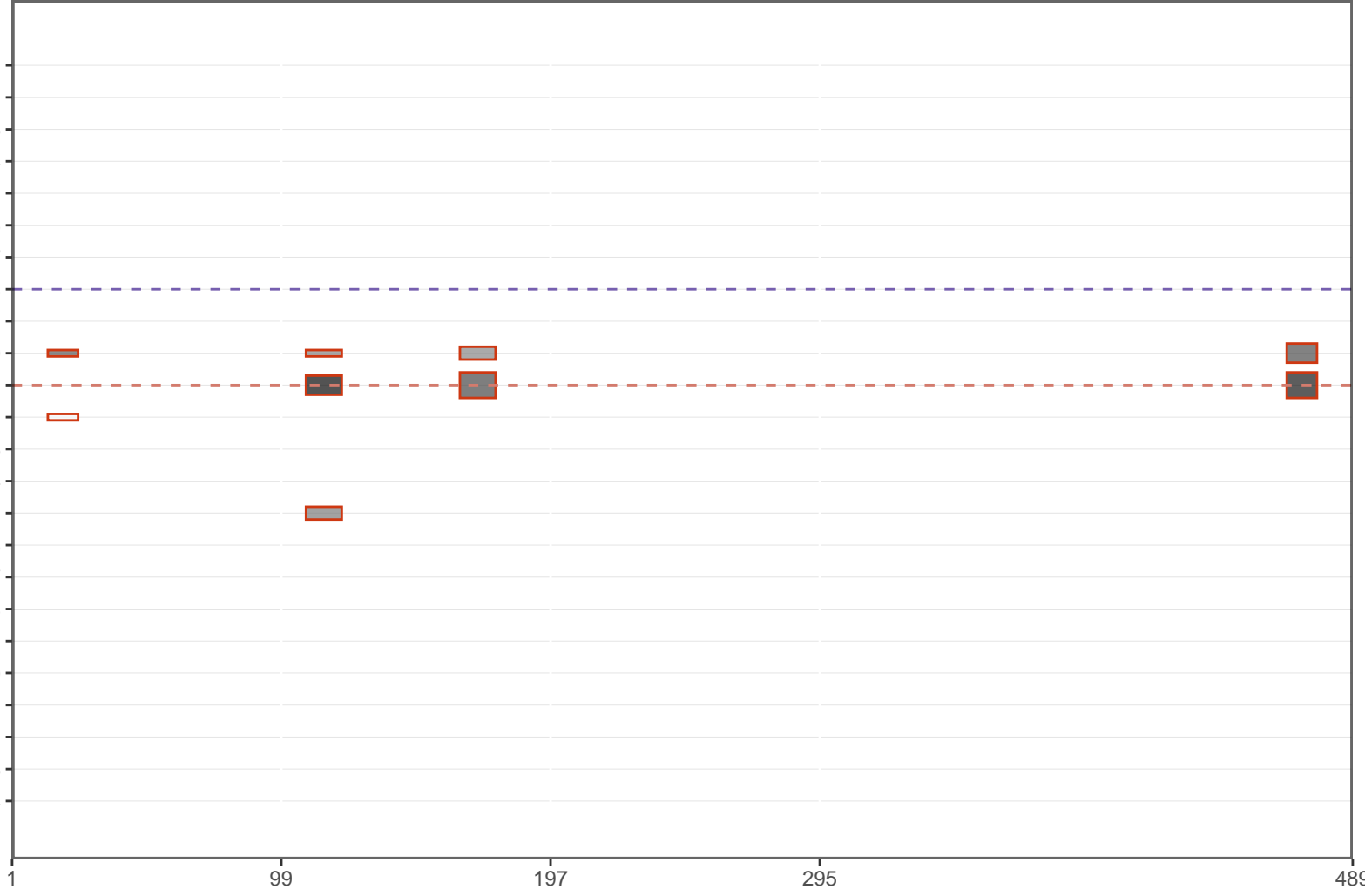
MW indication



Molecular weight

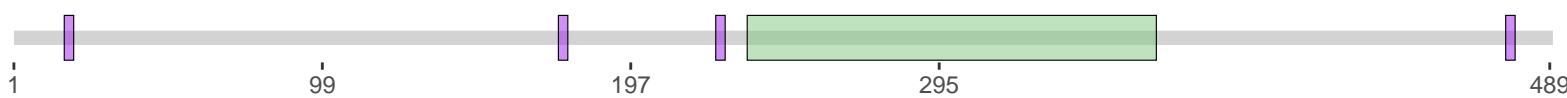


Gel Slice



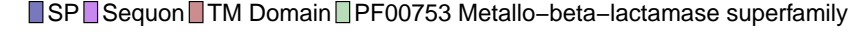
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

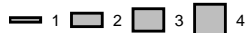


Protein sequence:

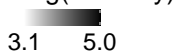
SFVAHGELIVDPGCKSASVEGLKEIKALPRKLVVFTVTHHHNDHVDGLSVQKYSPOAGLLAHEHTIRRRKDDWSLPCVYVSGSEECIGSGORLRFWTFPGHGDGMGLLHVSTNLSLVGDKVGGSGALLDASGGNMRDVFETTYKFIELPHALIPMGRINMWPKMLGGLKRRRYRESTLKAIEGAKTLFDWVYTAEVDRSLWYFASNNRLHVHDLALGDKLPNDFSELENFNRSGVEFADKVVHKK

NbL08g14270.1 cysteine--tRNA_ligase_cytoplasmic [MW = 66.62 kDa]

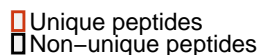
No. of times detected



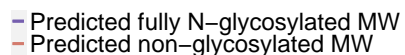
log(intensity)



Values from

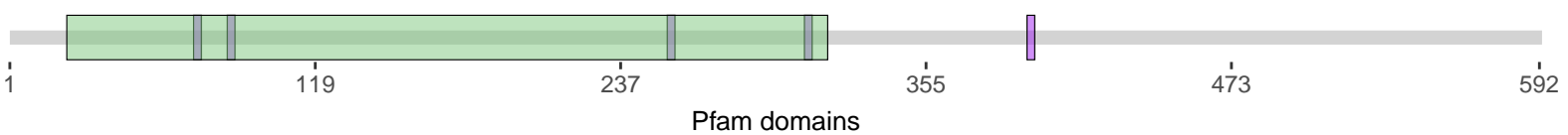
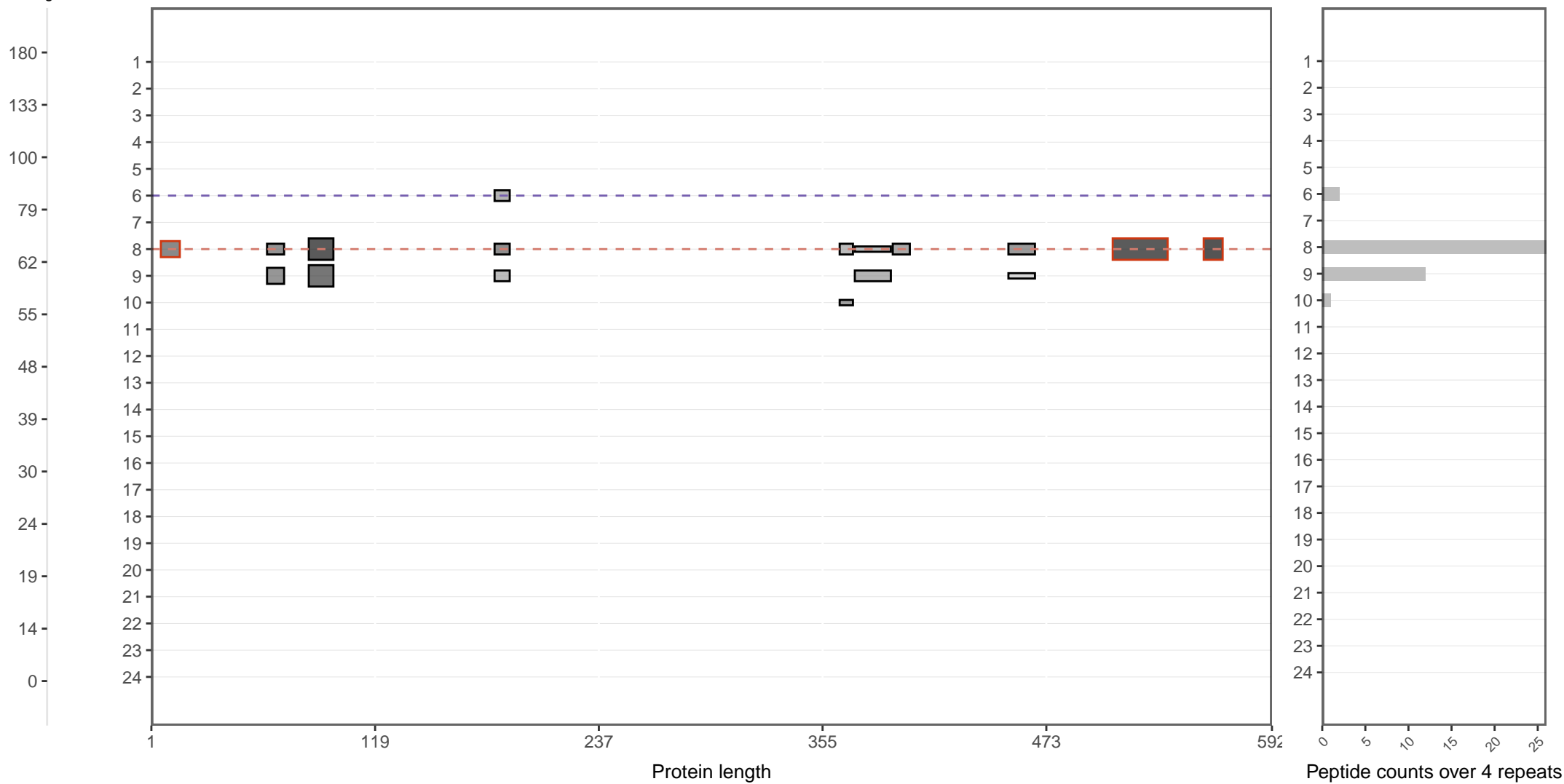


MW indication



Molecular weight

Gel Slice



Pfam Description

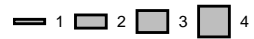


Protein sequence:

IRVETRLYHPALRYFLGGMHYRSPNYSBGGHIAEBSEVFEVYGLQTLDDGEALSVFQGGTETETETEVKGVIRVSSQVQECNKLHNELETKLSDLLHTPTLILNAALGELRALRMNSSLNMLKQKQKQDLGAVLGLAELLKEVKAVIDLGLLSSTGAEVLDGPKERALKRAELTEEDILHAEERTLARKNKEFARSDQIRSDLVAKGIALMDIGAEVWRPCVRAQGGEPAPAGQGGEPAPAGQGGESAAAMQKEKVPASQKQKGSAGAPKQEPVAAPSPKQISAAAPQKE

NbL08g14260.1 glutamine--tRNA_ligase [MW = 95.97 kDa]

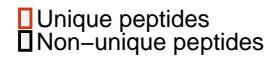
No. of times detected



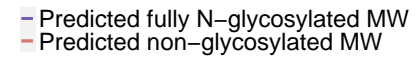
log(intensity)



Values from



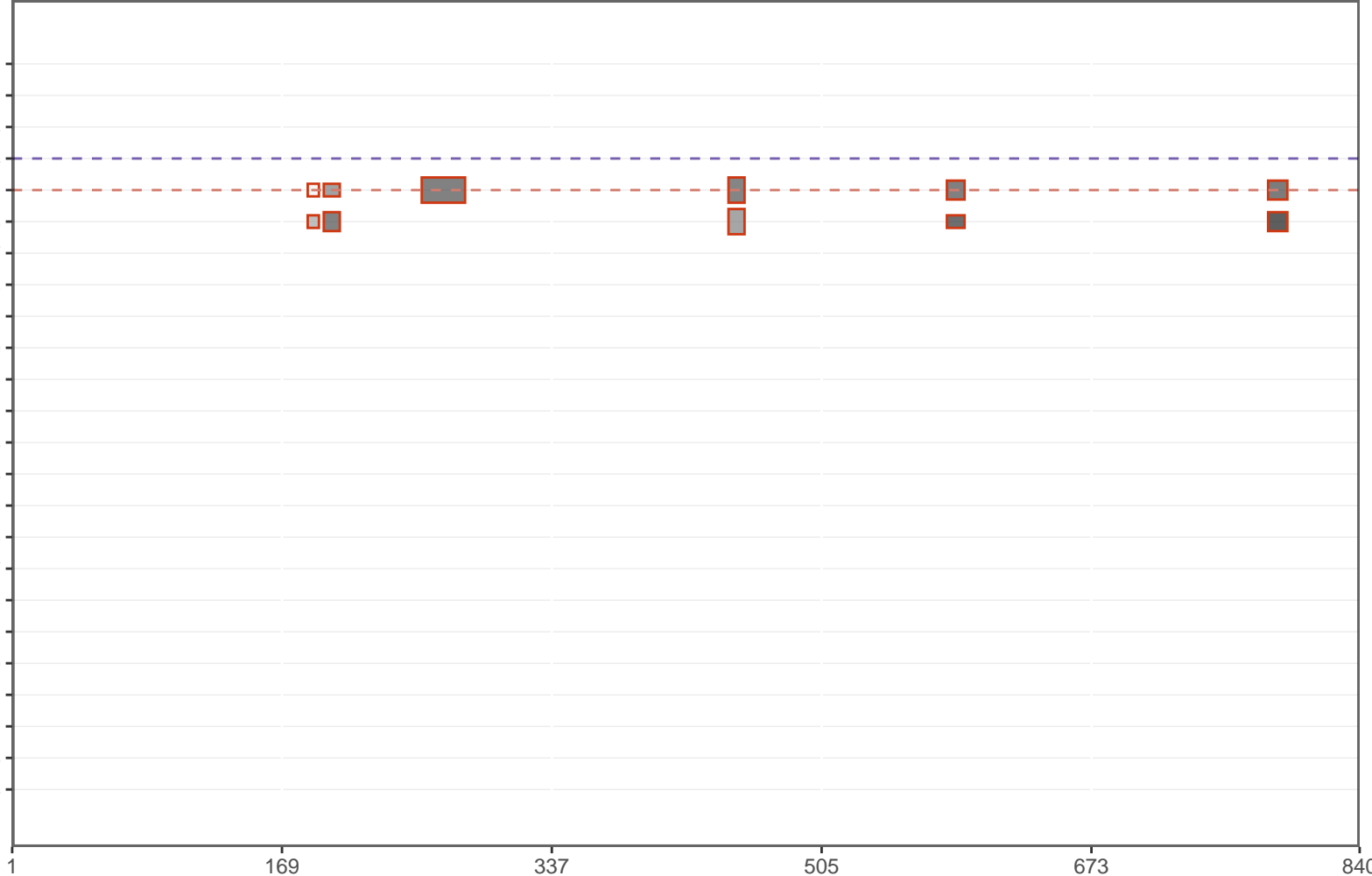
MW indication



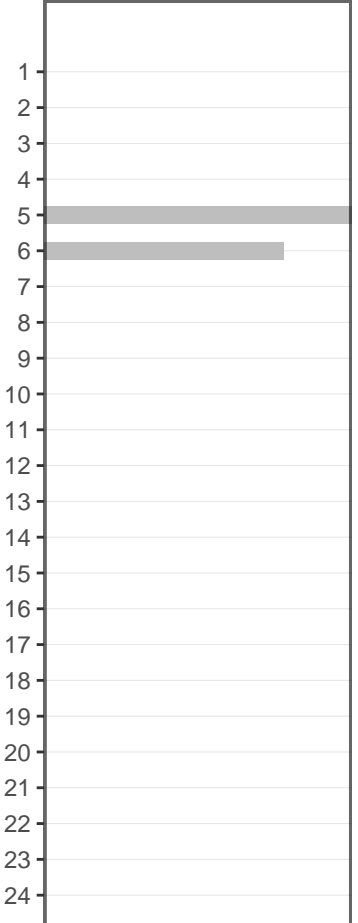
Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Description

- PF00749 tRNA synthetases class I (E and Q), catalytic domain
- PF03950 tRNA synthetases class I (E and Q), anti-codon binding domain
- PF04557 Glutaminyl-tRNA synthetase, non-specific RNA binding region part 2
- PF04558 Glutaminyl-tRNA synthetase, non-specific RNA binding region part 1

Protein sequence:

[DHQTEPEEKYREKKNMSPWRDRPIEESLRIFDEMKKGMINEGNATLRMKQDMQSDNFENMDLVAIRKFTTHPHAGDKWGYPSYDVAHGVDLENTHBLGTFEFETRRAASYWLLDGLGLYGFVFEVYGRNLVGNVTVMMSKRKLNRLVTEKWDGWDPRLMFLAGLRRGVYSTAINAFVRIQIGTRSDGEMIHVSRLEVHIREELNKAPRTMVAVLPKVVITNLEAGLVTDLDAAKWKREAFANDASGFYKVPFSRWVYIERTDFRLKDKDKDFGLAPGKSVLLRY

NbL08g14190.1 50S_ribosomal_protein_L15_chloroplastic-like [MW = 28.53 kDa]

No. of times detected



log(intensity)



Values from



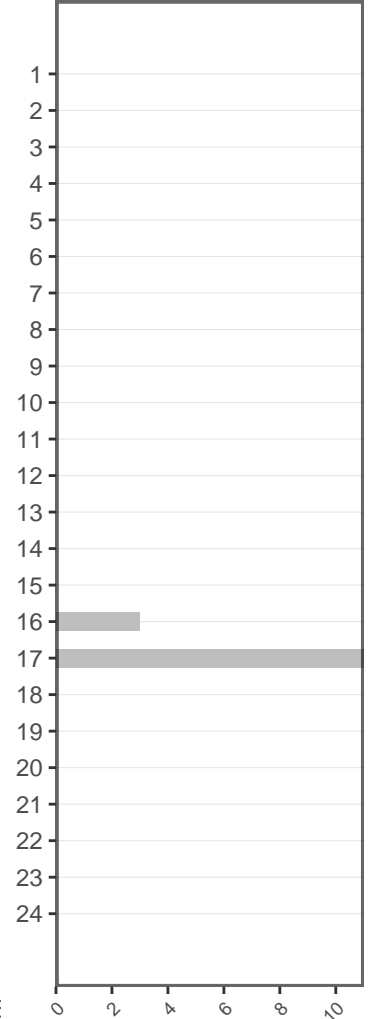
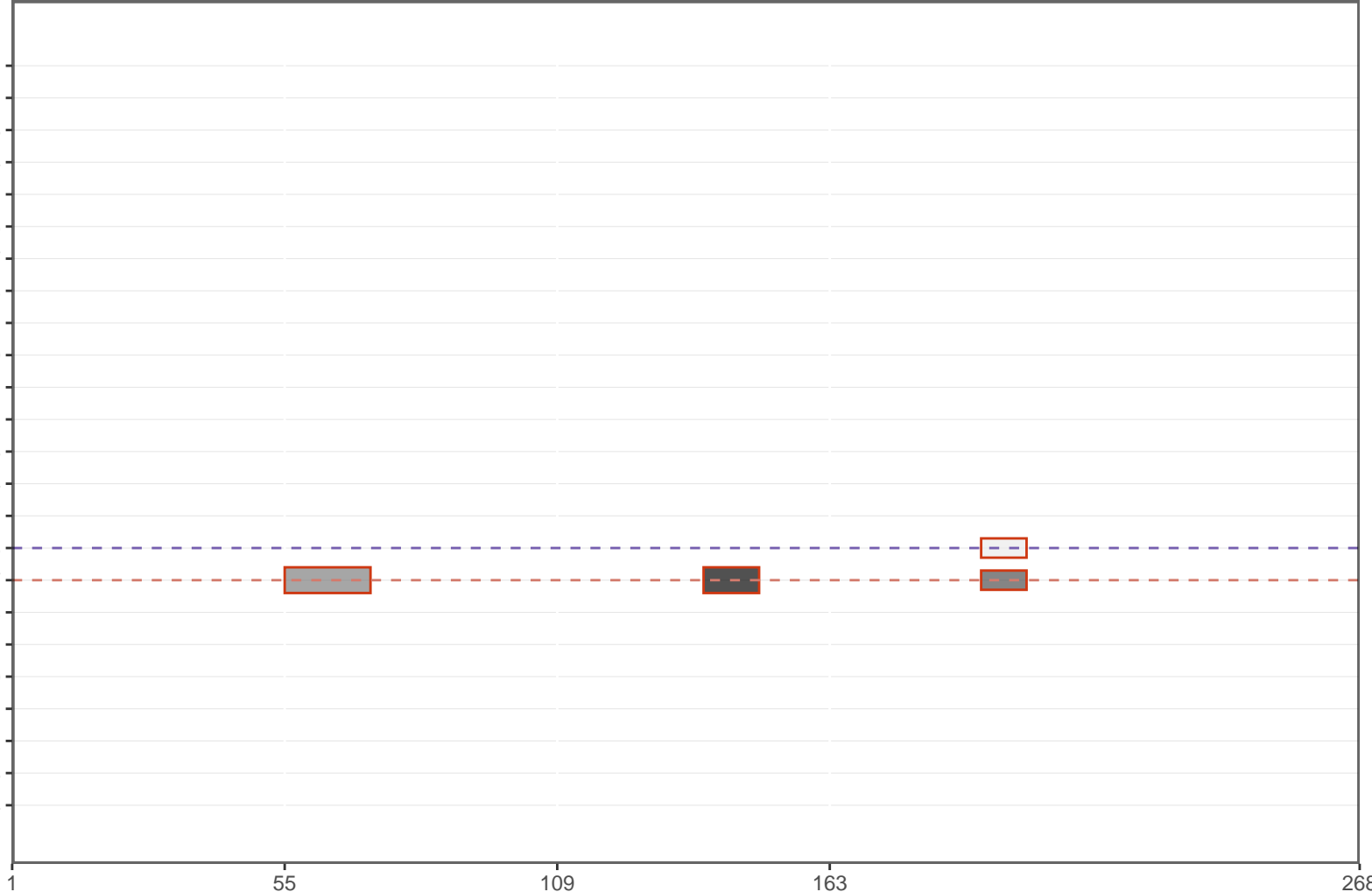
MW indication



Molecular weight



Gel Slice

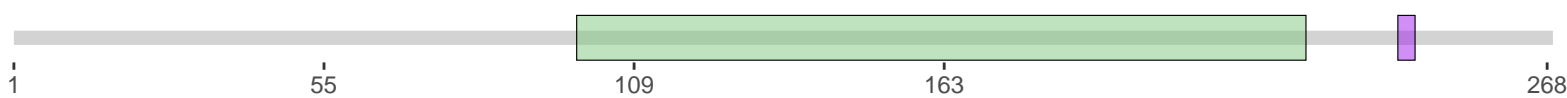


Protein length

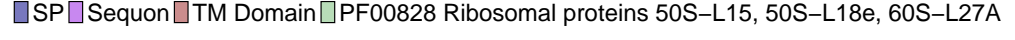


Peptide counts over 4 repeats

Pfam domains



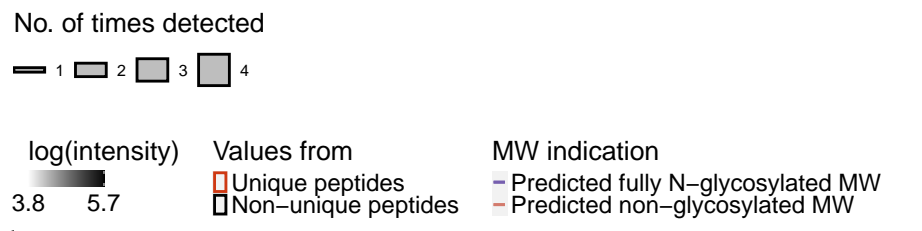
Pfam Description



Protein sequence:

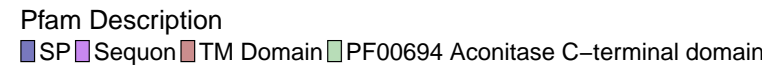
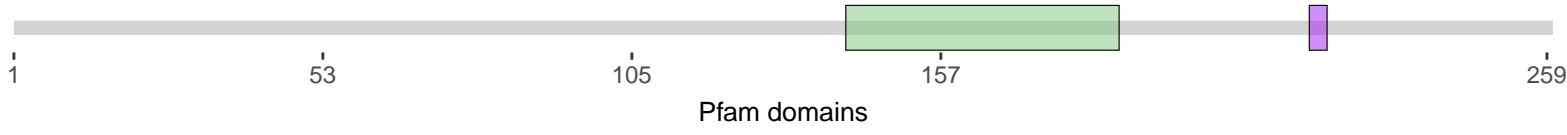
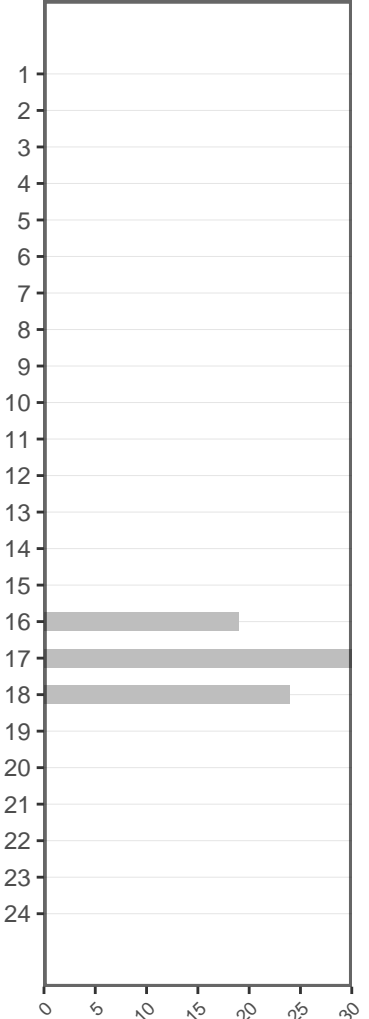
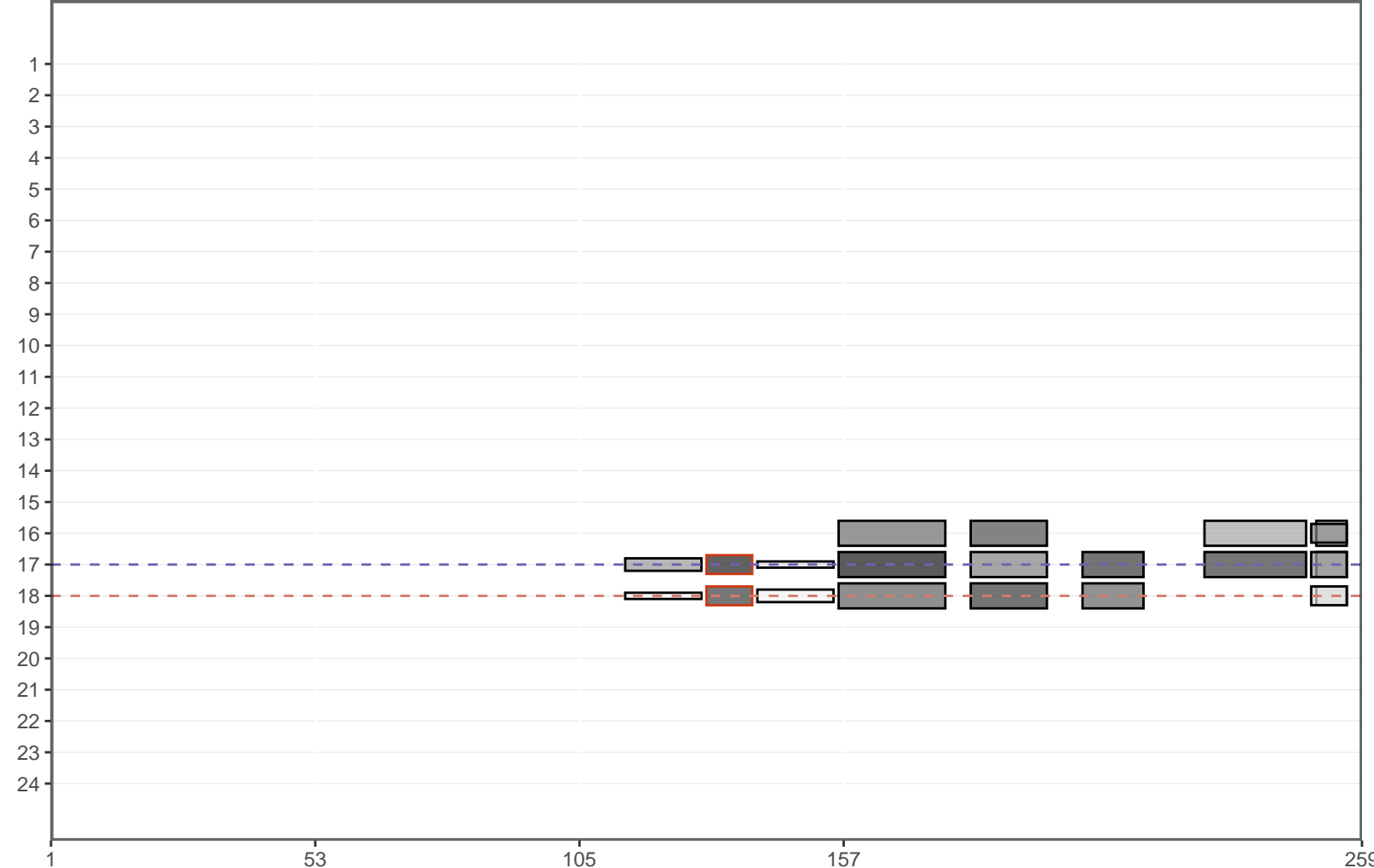
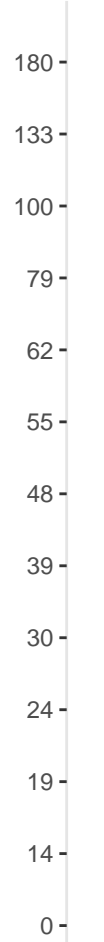
IFEGGQMPLYRRLPKLRGAGGMAAGLPKYYVFNLDKDEEAGFQEGEEVBLESLKQKGLNPSGRERRLPKLRGDGELSVNLFKARAFETSAAKELAEAGSLTLPGRKQWYKPVVANNLGRADEVFAKKRAAAASEAADPSA*

NbL08g14180.1 3-isopropylmalate_dehydratase_small_subunit_3-like [MW = 27.23 kDa]



Molecular weight

Gel Slice



Protein sequence:
 /ALCLPSSYOTRFVDPDEFKSKYSHGGDNFGGGSRHAPALGAAGWVAVESVARIFRRNSVATGEVYPLESEVRICEEGKTDVAVTVLGEGRNLNHTTKKEYLKPQDAGFVIEAGGFAYARKAGMPSRDV

NbL08g14010.1 serine/threonine-protein_phosphatase_2A_65_kDa_regulatory_subunit_A_beta_isoform [MW = 65.55 kDa]

No. of times detected



log(intensity)



Values from



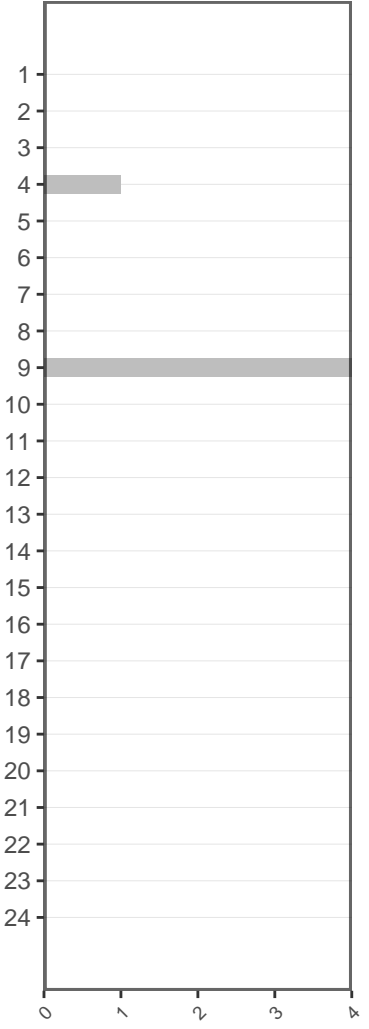
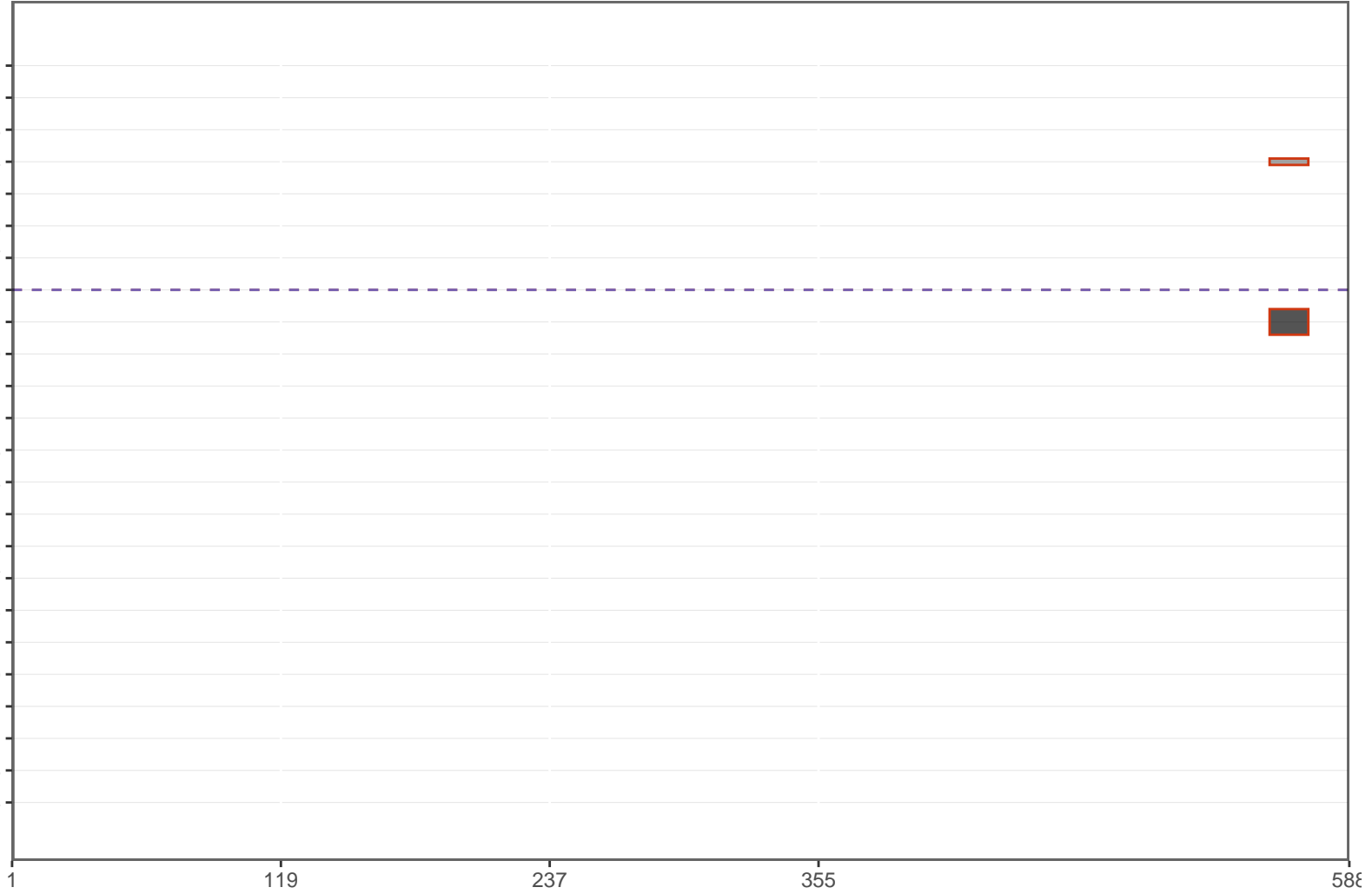
MW indication



Molecular weight



Gel Slice



Protein length

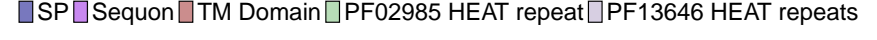


Peptide counts over 4 repeats

Pfam domains



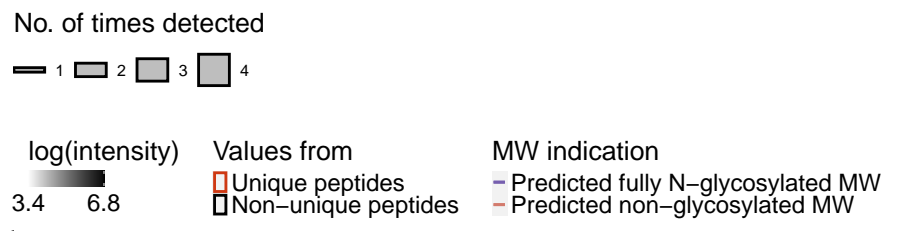
Pfam Description



Protein sequence:

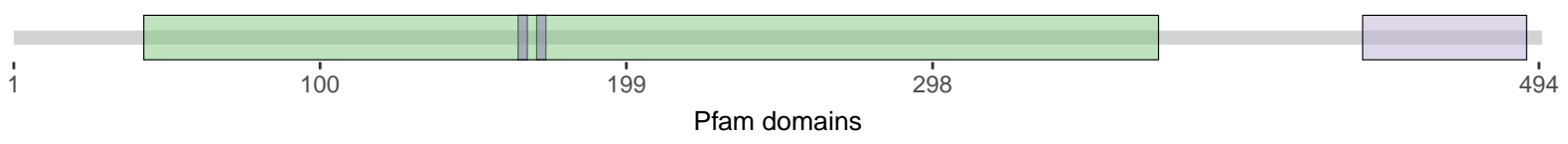
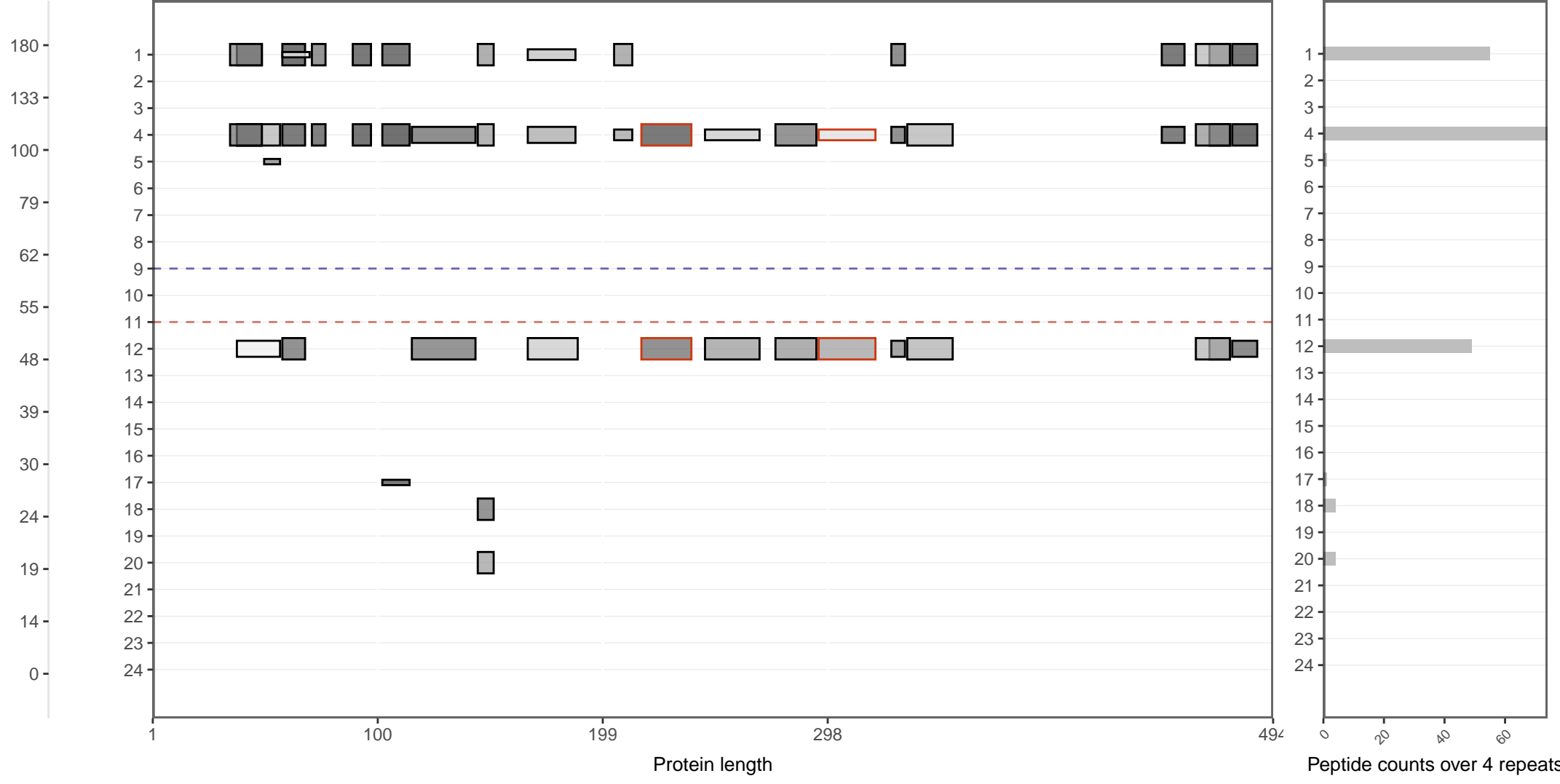
RTDLPYVYVLLRDNEAEVRIIAAGKVKTKFGRILSPELAIQIHLPCVKELSSDSGQHYRSALASVMGMAPVLGKDATEIHLPLFLLSKDEFDFVRLNIHSKLDGVNQGVDLLEQELFPAIVELAEEDRHWRVRLAIEVYIPLASGLGIGFFDNLGALCMQWLGDKVYGRDAANLKLAEFGPEWAMQHIPOVDMTTSFHYLYRMTLRRAISLLAPVMGSEFGSKLLPVITATKDRVFNKFNWAKVLSLPIVDHSVVEKTVRPSLVELAEDFDVDVRFYANQALQSD

NbL08g13930.1 fumarate_hydratase_1_mitochondrial-like [MW = 53.35 kDa]



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain PF00206 Lyase PF10415 Fumarase C C-terminus

Protein sequence:

YAAQYKIDRVLGFLPHMYGLADGGTAVGTGLNFKKGFDRKAAVAEETNLPVTAENFEALAAHDAFVETSGAINTVAASLMKYGDRIIRFLGGPRGLGELILPENEPGSSMPGKVNPTDCEALTMVCAQVMGNHWVITGGSGHGFELNFKPMIANALLHVSRLGDSASFENKCVIRIGQANRERAKLLHESLMVLTGLNPKIGYDNAVAAKKAKHEGKTSKDAALNLGVLKSEEFDLVLPKMGPTD

NbL08g13660.1 protein_decapping_5 [MW = 62.31 kDa]

No. of times detected



log(intensity)



Values from



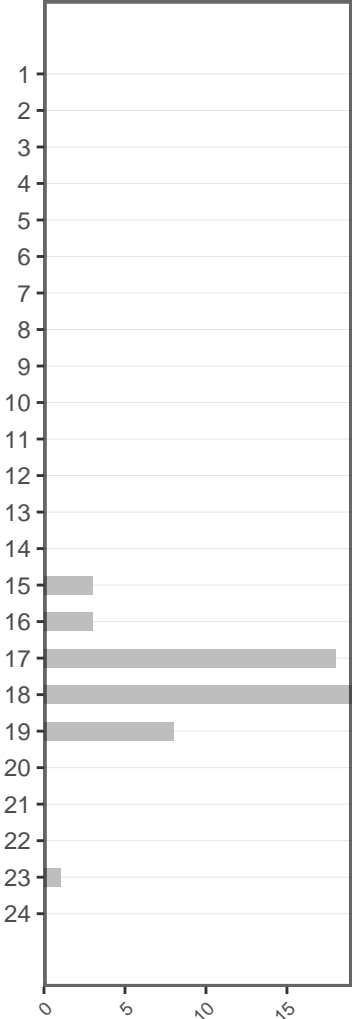
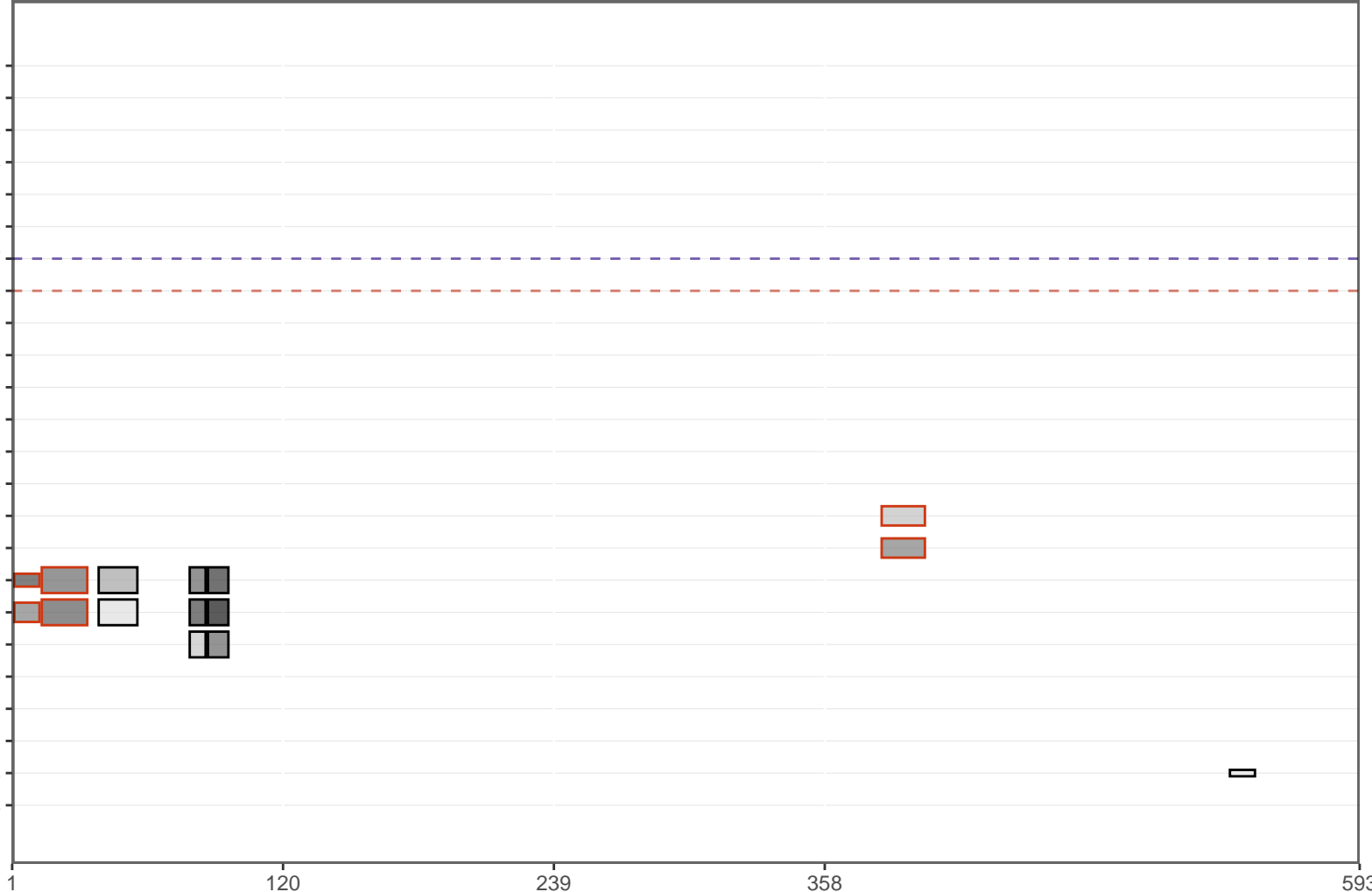
MW indication



Molecular weight

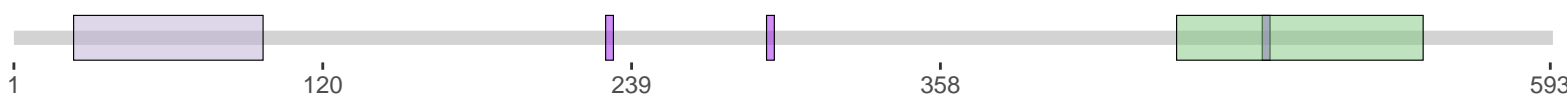


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

STLANKTSVSAUSGSLGASLPLPLPLTTPFRDVAISIKRNPVPSPALSGSIVSTMVGPSSNLVETPTPLSLVTPGQLGSGPDIIVPSTGSETGTAQKDEVEVQVLPAPSETPAPVKTEDGPPILPLPPTQTRVQKTNQAFVQARVYNNYRGRGSGMGVSRVPTKFEEDDFMAMNEKFKDEWGHGKSNREGGDNGSGDEDFSNVEYDDVLPKIDVPPVYKNDKDFDLSLNSALINDPNHGRTRFSEGRKIDVETFGDFSRVYRGRGGRGRGSGEYYRGGYGGNGY

NbL08g13560.1 HD_domain-containing_protein_2 [MW = 36.35 kDa]

No. of times detected



log(intensity)



Values from



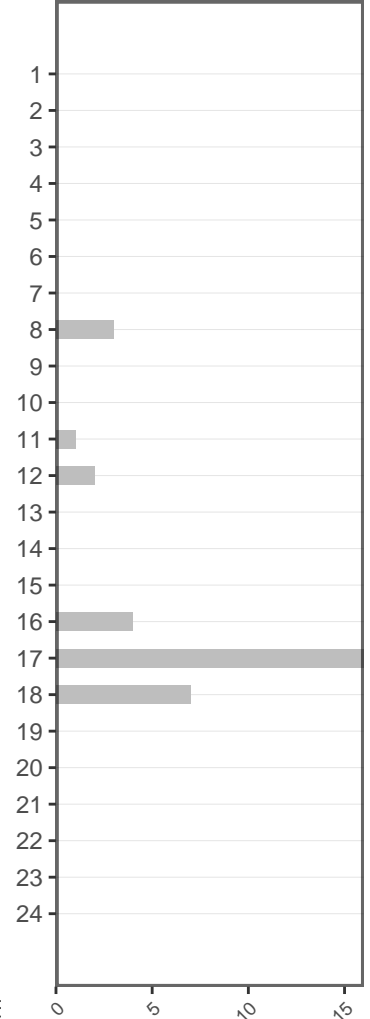
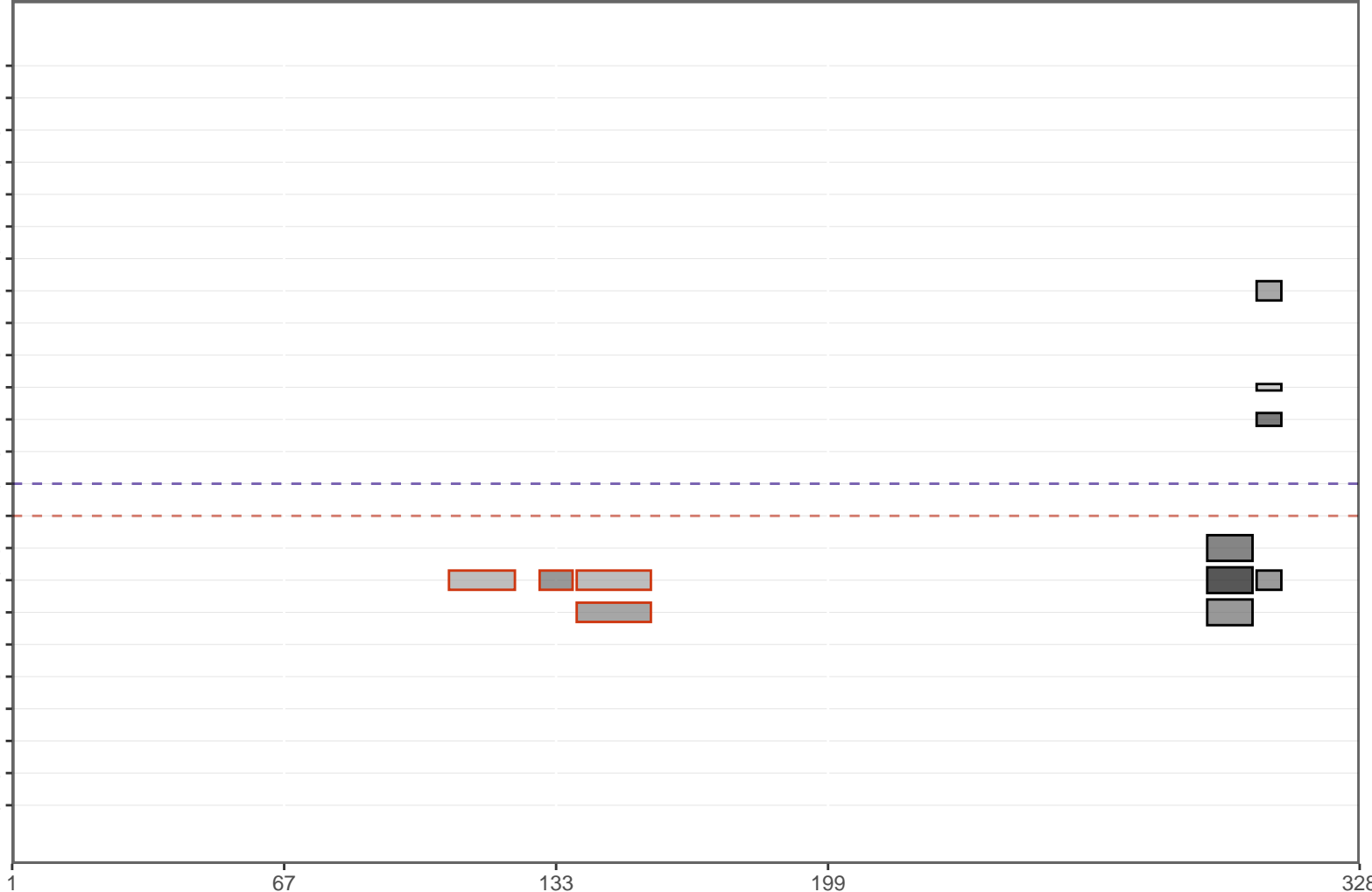
MW indication



Molecular weight



Gel Slice

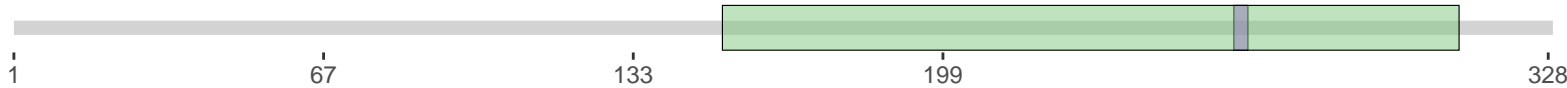


Protein length

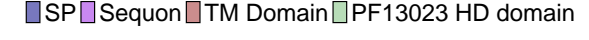


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

1:SLKTKQKRGWVNHGKGFESADHMYLMSVMAIAISDLPGVNRERCKMAIVHDIAEAVGDITPDDGVPKAEKRRRLAALNEMCKLGGMRAREEIKELWGEYENNASLEANLVNDFKVMILDALEYESEHGKVLDEFLLSTAGKFTQEGKSWAEIHRRNSRSENRL

NbL08g13370.1 UDP-glycosyltransferase_89A2 [MW = 51.39 kDa]

No. of times detected



log(intensity)



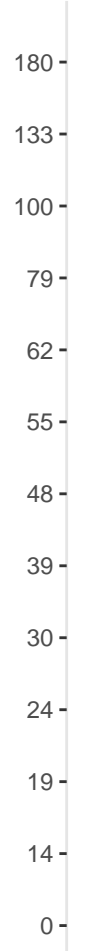
Values from



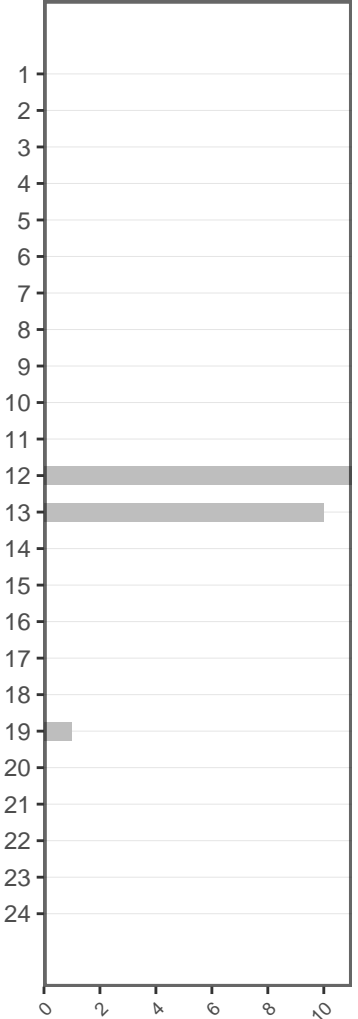
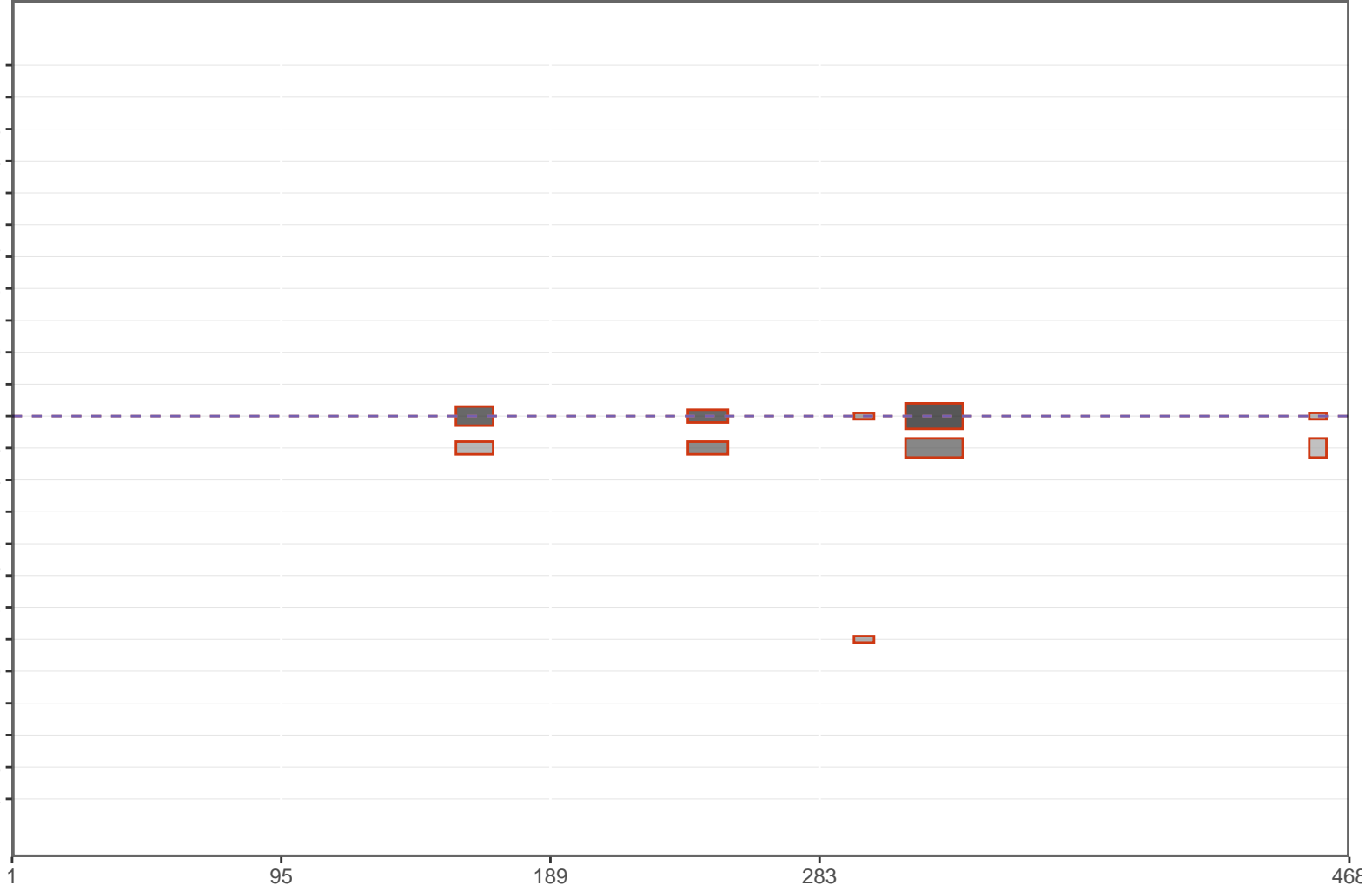
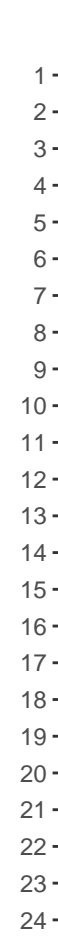
MW indication



Molecular weight



Gel Slice



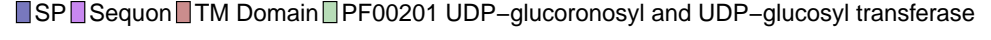
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ELYLFLKXKMGHERVYSGIPNLVGGPGRNGKENVQGVNERVFTWLDEGGDGVVYVAFSGSKLTKAMKALTGLEKSGVRFILVKQLTAQGLEEGYGVPEGFEDRISGRGLKGVWAPQVVELGHRAGVFLSHQGVNSVLEAVAGIQLGWPFMEADQFNWLLVENMKTLLVRFVCEGADSVDPDLELGRGTGEAMSNELFKERAKLIRDEAHEAVKIGGSSKRDLEIVRELALQIKC

NbL08g13350.1 heat_shock_protein_90-5_chloroplastic-like [MW = 91.01 kDa]

No. of times detected



log(intensity)



Values from

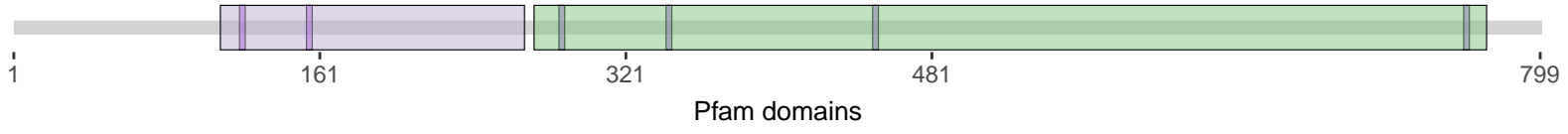
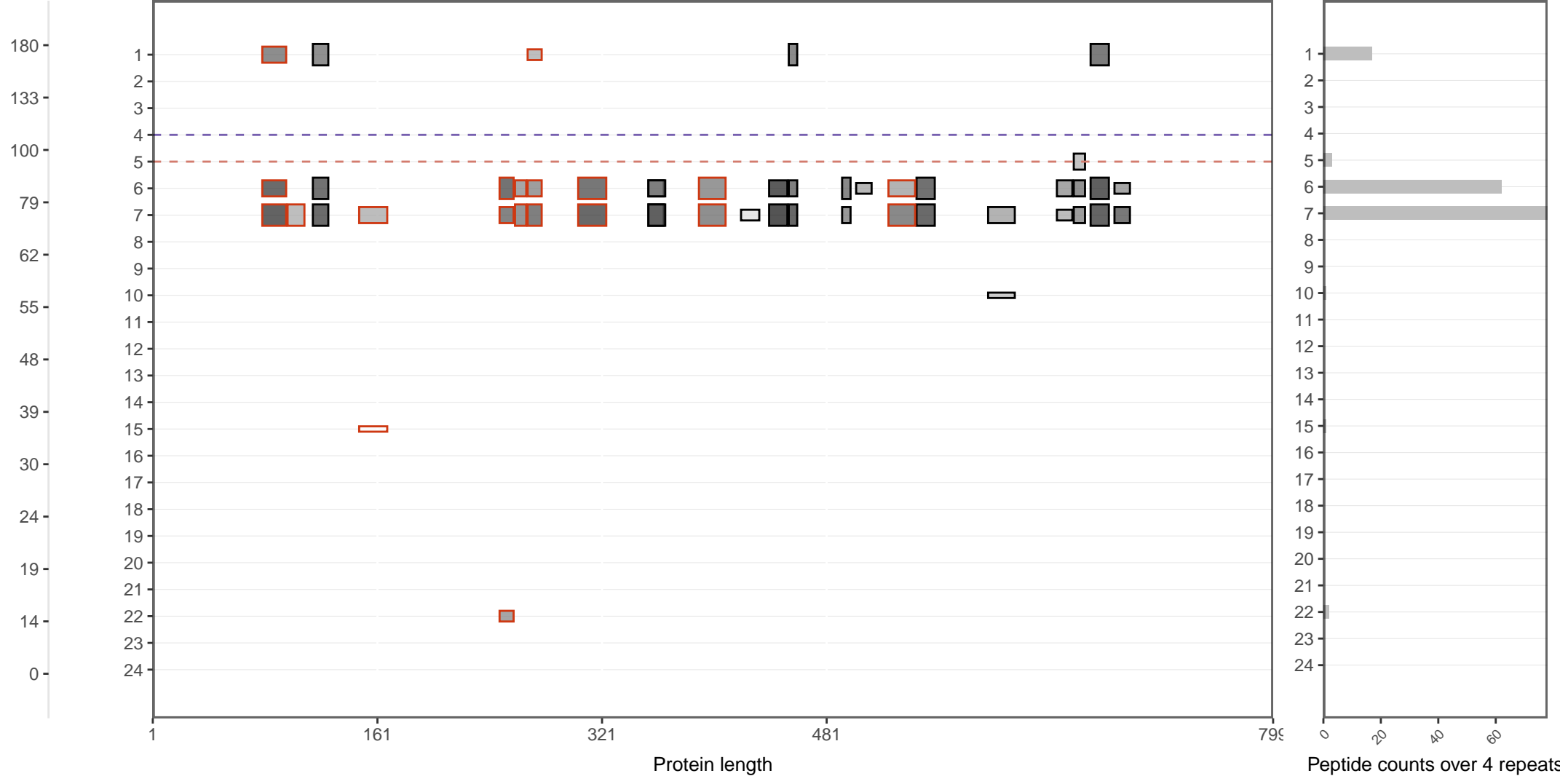


MW indication

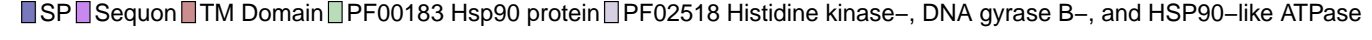


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

MFERSVLYIPGMALPNNNEEVNPKTKNRLHVKRVFISDFDGFLLFRYLSFVKGVVDDDDPLNVSREILQESRIVRIMRKRRLVRFKAFDMIQDLSESEKEDQYKFWENFGKFKLQIEDTGNHRRITPLRFFSFKKEELISLDDYENMGENGKAIYLLATDSLQSGARTAFPLEKLVQKQIEVLYLVDPIDEVAKGLQTYKEKFKVDSKEDLELDDDDDEVKEREAKGEVNNLLGDVWQQLGDVYAKVGVSKRLVLSGSPDLVSGKFGVSWANMERLIRAGTLGDTSTLLEFMRG

NbL08g13240.1 chaperonin_60_subunit_beta_4_chloroplastic-like [MW = 65.73 kDa]

No. of times detected



log(intensity)



Values from



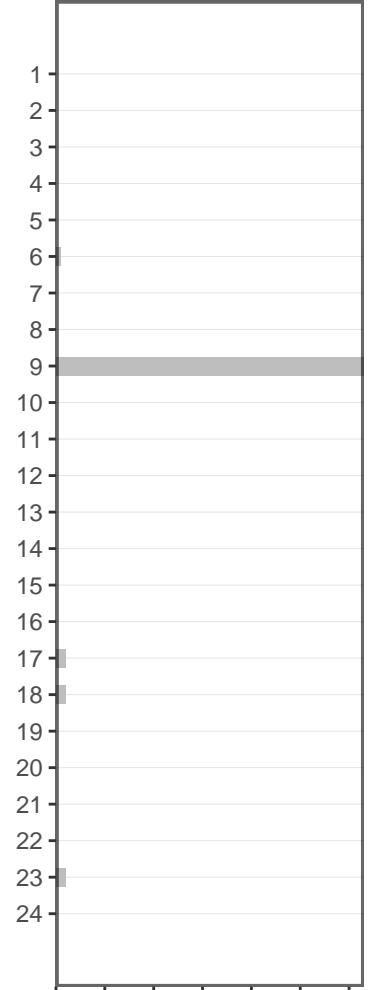
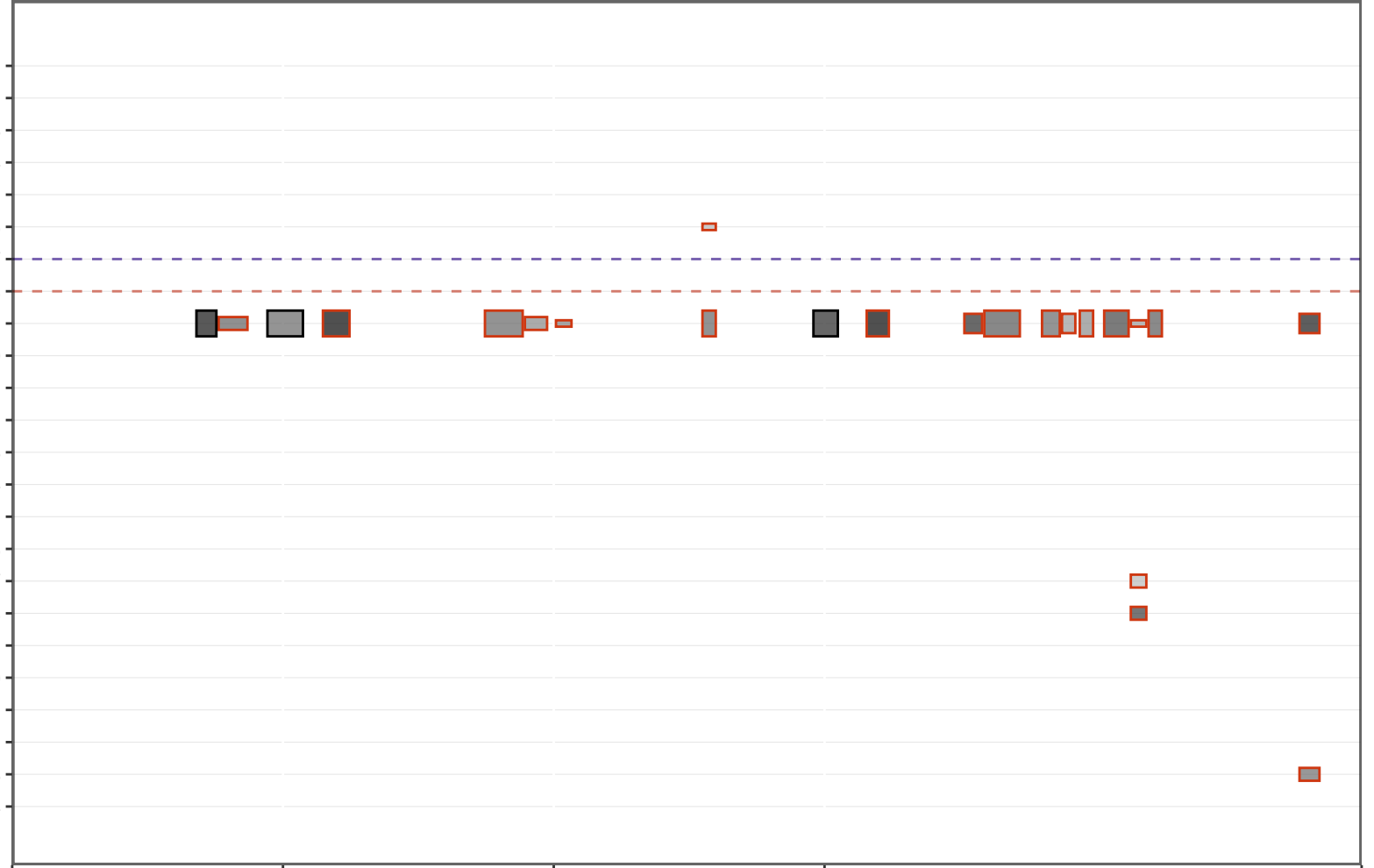
MW indication



Molecular weight



Gel Slice



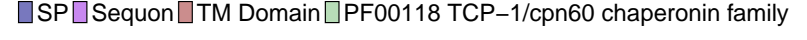
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

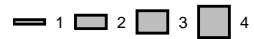


Protein sequence:

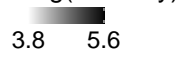
SDALAPVIRNKLRLGVKVAIAKAPDFGERKSLGLDDIALTGCTVIRDDMGLTLENAAHKDLGSAKVVITRDTLIVTDGNTREAVMRRVTFGKQKLVENTFENFQKILNERIARLGGIAHQVAGTQVELKDLRIEDALNAARATEEGVYVGGGGCLLRLLSKVDIAKEMLDNEDKKGADIFKRLSEYPAKGIKAKAGVNGNIVVEKILSVNMQYGYNAARDRYEDLMAAKLDPKAVYRGLGHEAAVAAKTFLSDAVVDPQPVSRGMRRFPMPRTSGSRLDLTGGG

NbL08g13220.1 serotonin_N-acetyltransferase_2_chloroplastic [MW = 21.69 kDa]

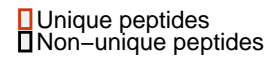
No. of times detected



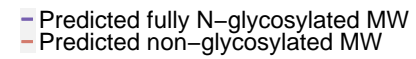
log(intensity)



Values from



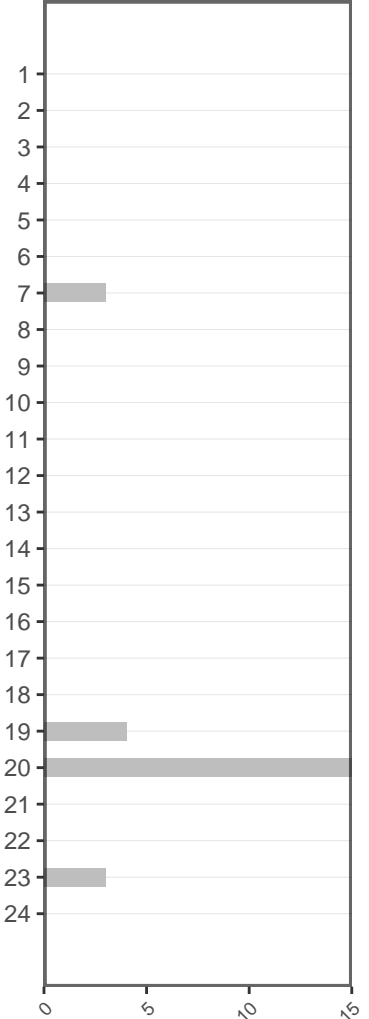
MW indication



Molecular weight

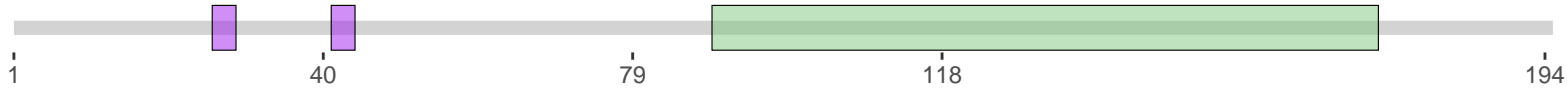


Gel Slice



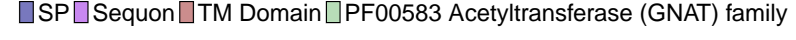
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

QLALENTDSLMIIEYEKTRKRPVAFARATGDGVFNAIWDDVDFPFGIGLGLKAMERLVTLLGKGINNIALYSEPRVLGFYRPLGFVADPDGIRGMVYGRKKKKR

NbL08g13210.1 6-phosphogluconate_dehydrogenase_decarboxylating_3 [MW = 54.04 kDa]

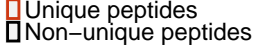
No. of times detected



log(intensity)



Values from



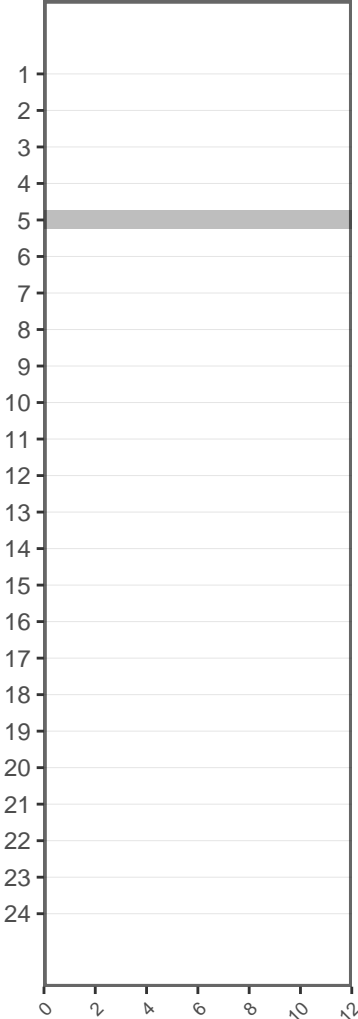
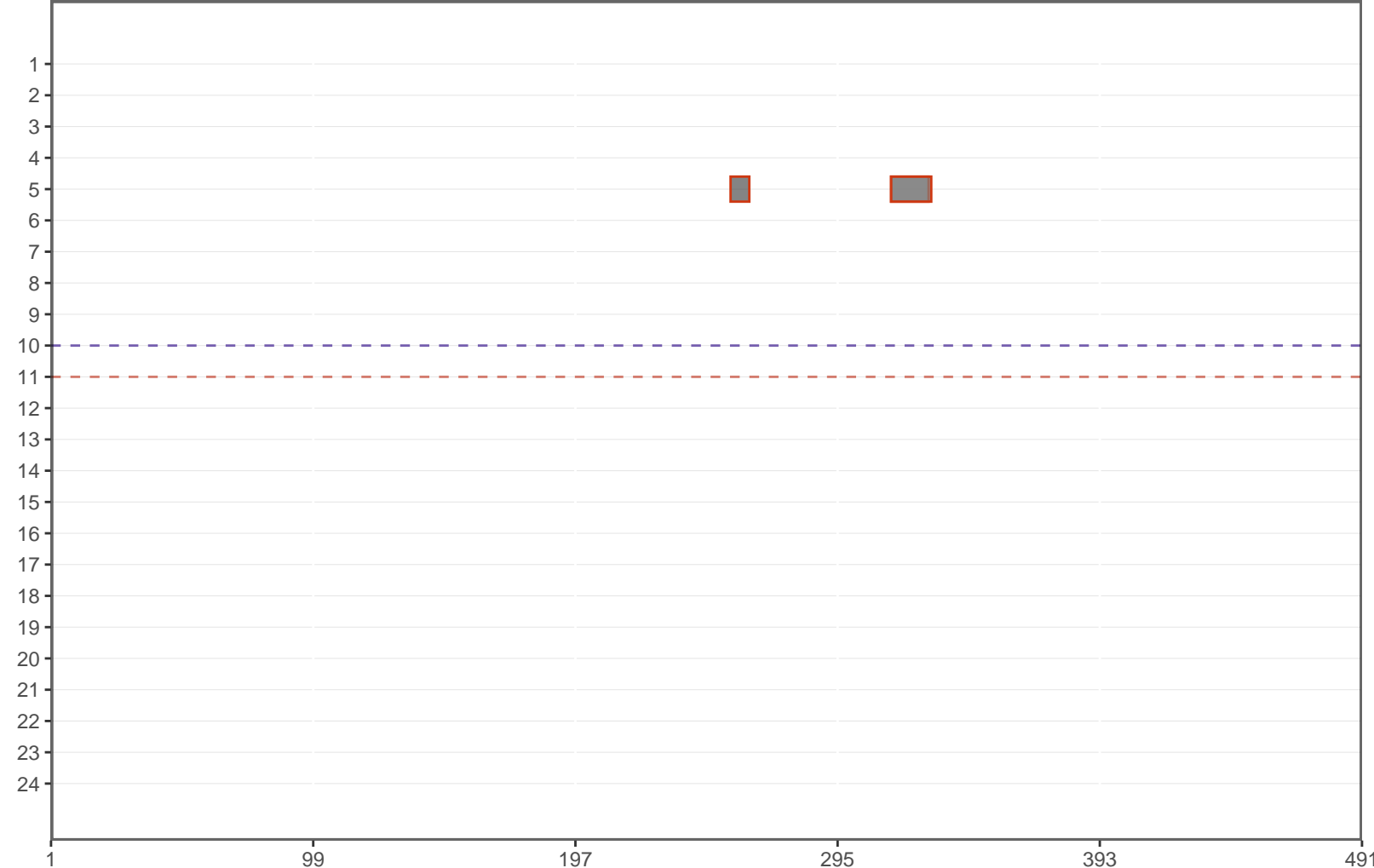
MW indication



Molecular weight



Gel Slice

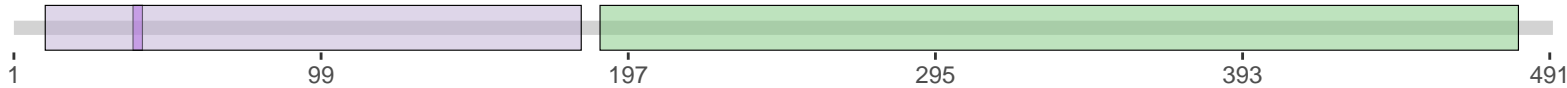


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

- SP Sequon
- TM Domain
- PF00393 6-phosphogluconate dehydrogenase, C-terminal domain
- PF03446 NAD binding domain of 6-phosphogluconate dehydrogenase

Protein sequence:

VNKGELLSFLIEITDFGKDKADGVLVDKVLKTKMGKGTGKWTVQGAELSVAAFTASLSDRFSLGKDERVGAQAKVFKSGGVNDLVEGSDVKKLIQDDVRKALYASKIGSYAQGMILIRAKSVKQKGVLDKLGELARVWGGGCHRAFLDRIKGAYDRNFDLANLLVDEEFAKEVVERGSAWRRVVLAISSGISTPQMSSSLAYFDEYRRELRIPANLVQAGRDVFGAHTYERTDMPGAFHTEWFRKAKGSKI

NbL08g13170.1 uncharacterized_LOC104099690 [MW = 29.71 kDa]

No. of times detected



log(intensity)



Values from



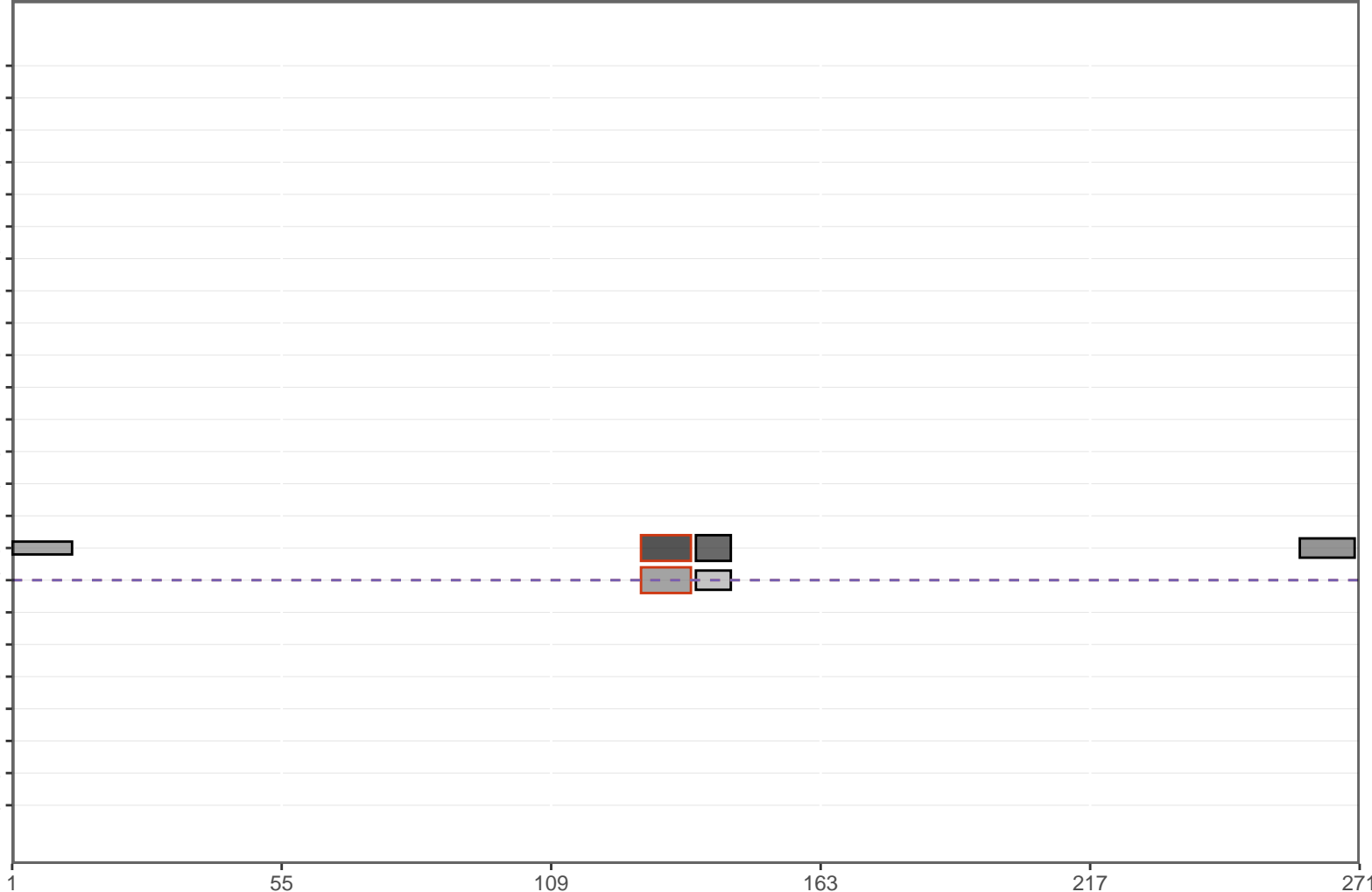
MW indication



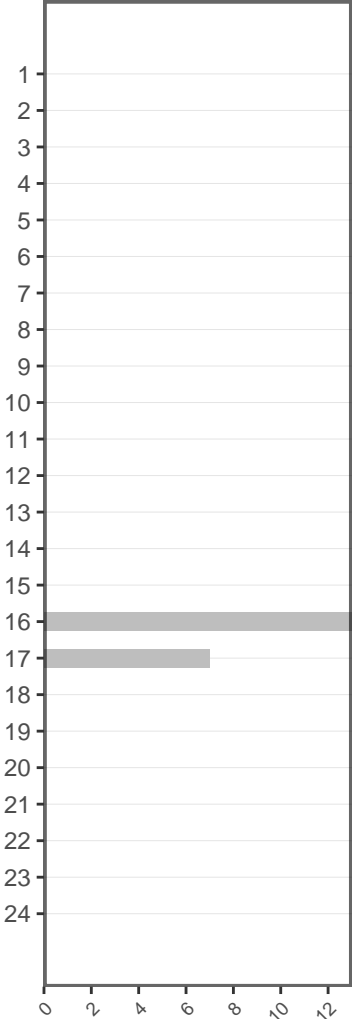
Molecular weight



Gel Slice



Protein length



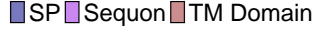
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

AAWAKLLIGEQIPEKVKVLDSIRSNFRGKLSPEDEAFKLESSAERKAKKADGHGDSPLVKGTDYPLPSGSSVVDGLAALLERQKIKIRGTLGVSWEPEAGISVISIKGLLLKDKVLSGVNHNVDLEEEFKLSRKNKDFLLDSELVT

NbL08g13160.1 DNA-directed_RNA_polymerases_II_IV_and_V_subunit_3-like [MW = 35.68 kDa]

No. of times detected



log(intensity)



Values from



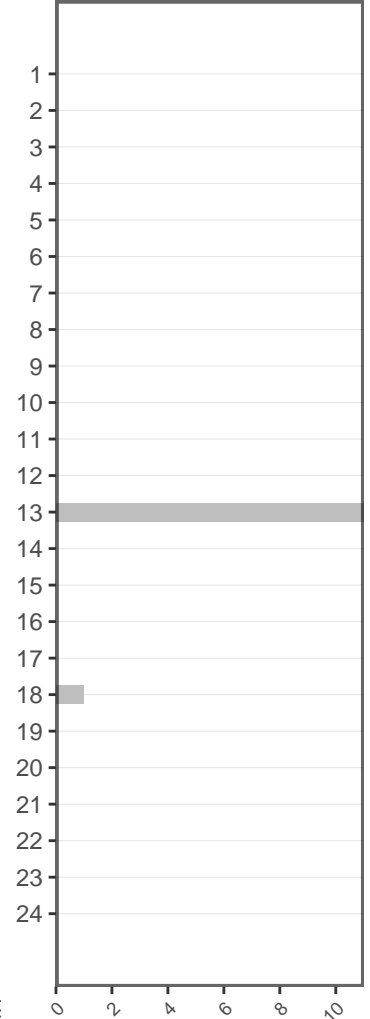
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF01000 RNA polymerase Rpb3/RpoA insert domain
- PF01193 RNA polymerase Rpb3/Rpb11 dimerisation domain

Protein sequence:

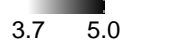
NSTNKGIIVKLRGGELRLRAARKGIADHAKWSPATVTFMVEPDVYINEDMMETLLEEKRELVDSSTPEVFGIDPENKVVVDPKATYDDEVLVKGEAMGKPLQLEIHAREDSFFITVETTGAVKASQLVLAIEVLKQKLDVRLSDDTVEADDQFQELGAHMRGG

NbL08g13150.1 chalcone--flavanone_isomerase [MW = 26.53 kDa]

No. of times detected



log(intensity)



Values from



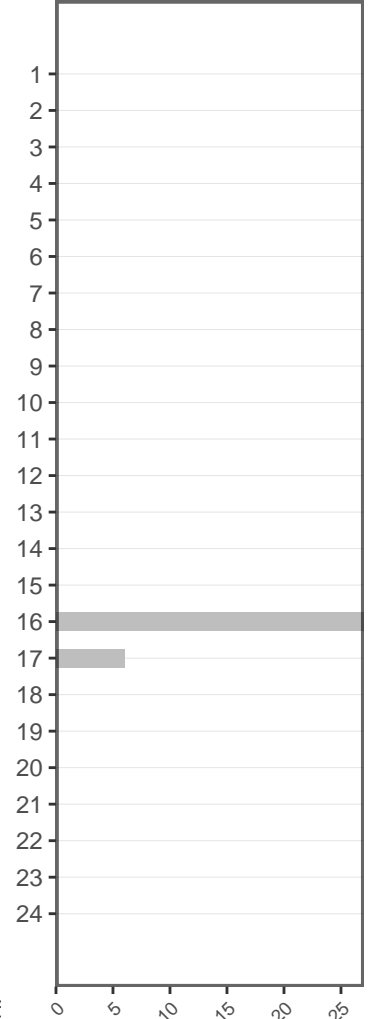
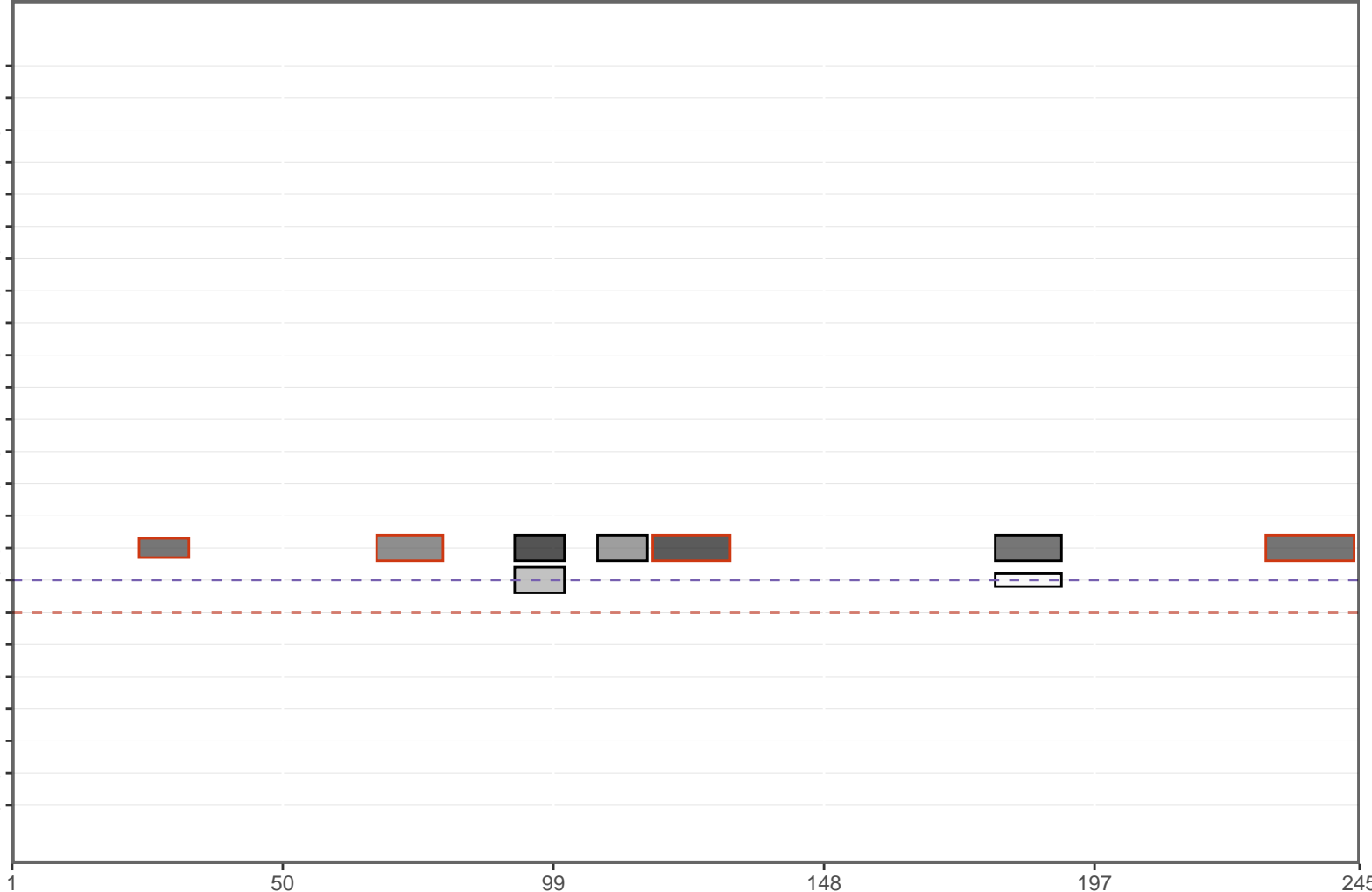
MW indication



Molecular weight

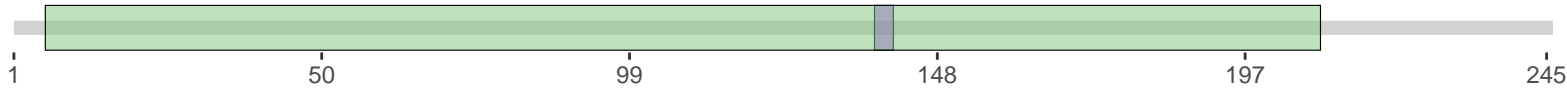


Gel Slice



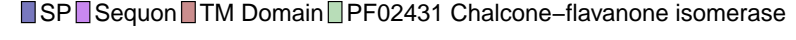
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AEKNCVAHWKAGTQYTNMESQAEKFLNIFQNETFLPGASILFTQSPVGAITRIFKDDSDITGTGNWIKENKQLSEAVLESIGKHGVSPPAAKSGIAERVSELFKPKYADAVGCEKPGIENSSDPVIEEKPTPEIGV

NbL08g12840.1 probable_UDP-arabinopyranose_mutase_1 [MW = 41.13 kDa]

No. of times detected



log(intensity)



Values from



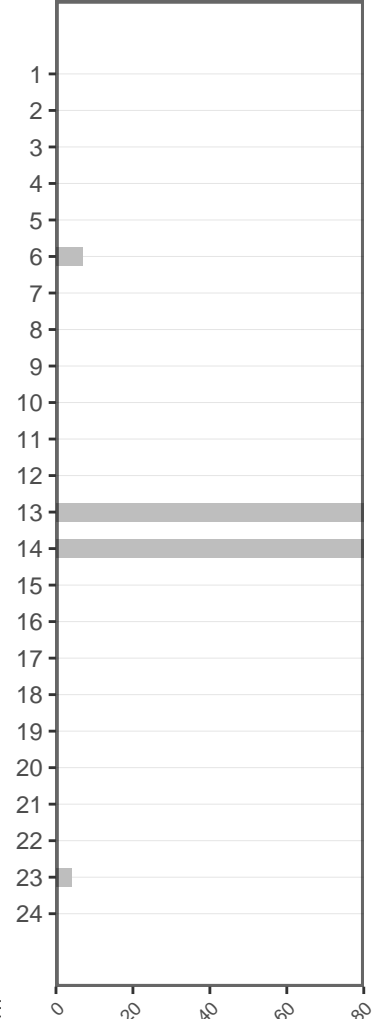
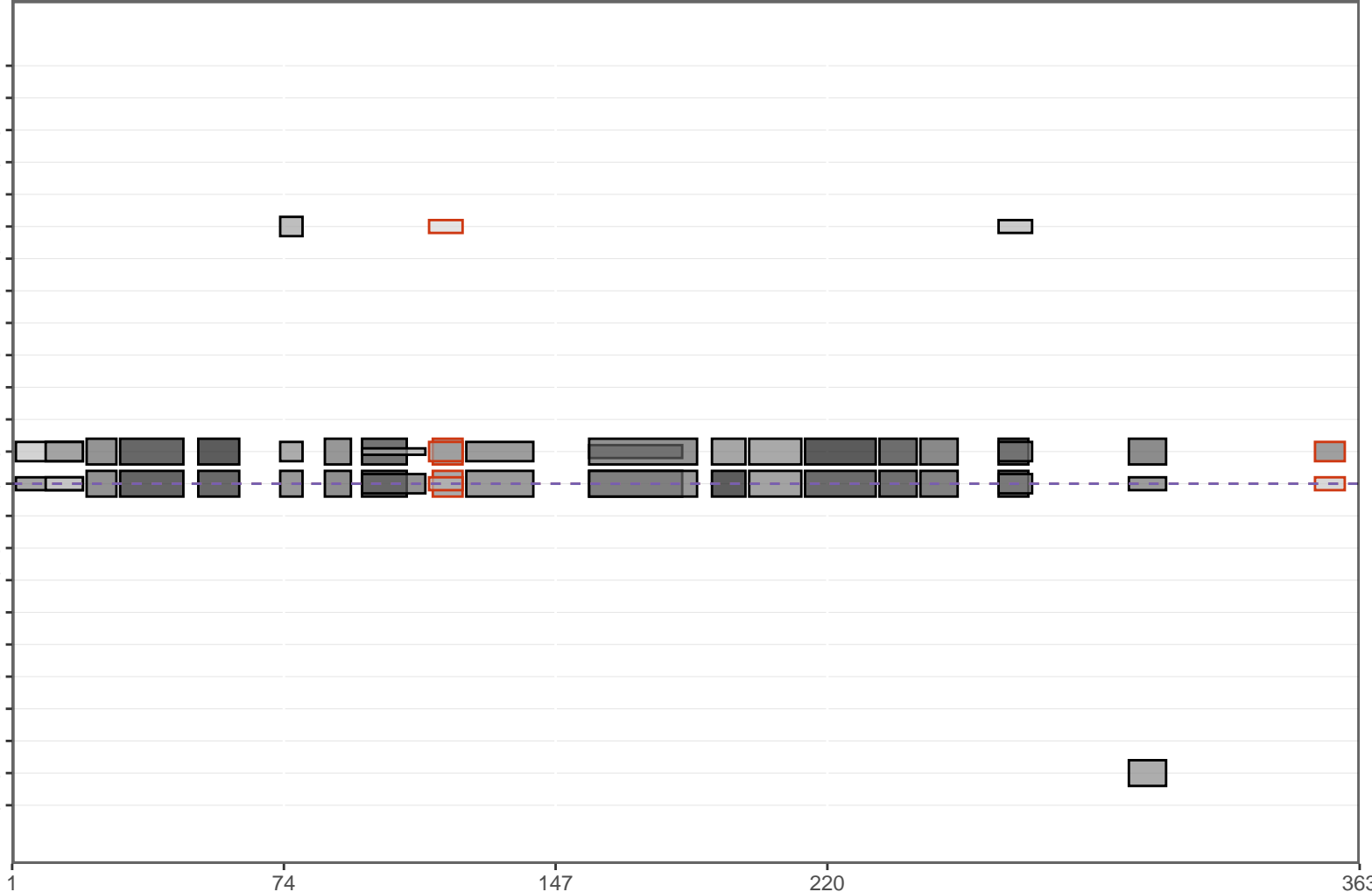
MW indication



Molecular weight

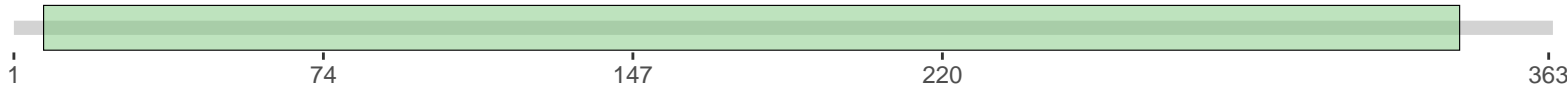


Gel Slice



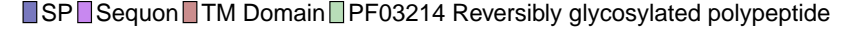
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

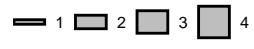


Protein sequence:

POYDPTQLVXPHERNTRVYDAVMTFPGKTLFFMGGMNLAFLREILGPMVYFLMGDGGPGRVDDMMAGWCTKVICDHLGLGKIGLQVFWHSHKASNPVWHLUKEVNGIFWGEIIPFFQAATLPEKCKTVGGCYLELSKGVKDKLKDIPYFTKLGDAMVTWIEAWDELNPETGESLAKLISIDGPKAAK

NbL08g12830.1 splicing_factor_YJU2 [MW = 37.43 kDa]

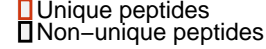
No. of times detected



log(intensity)



Values from



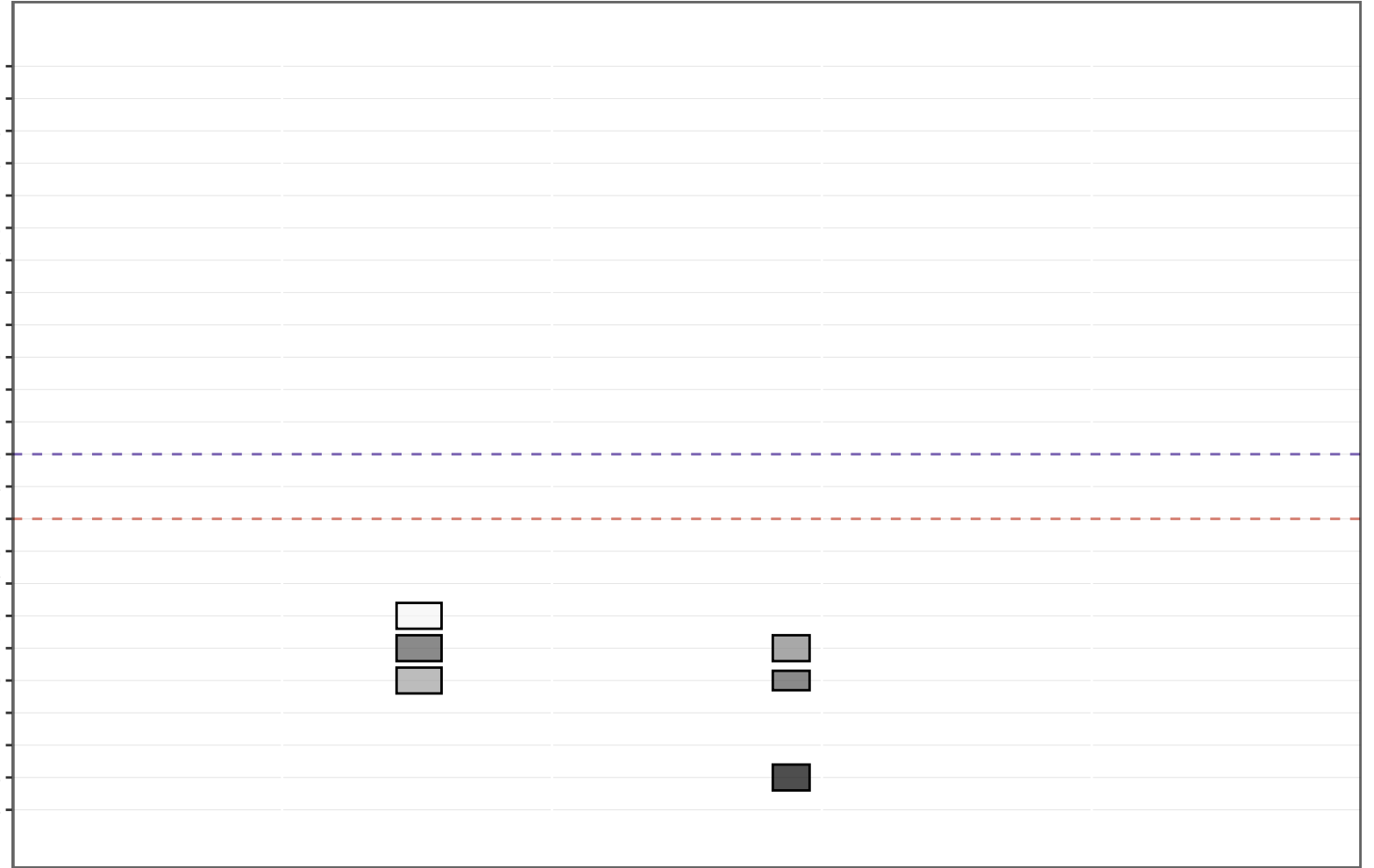
MW indication



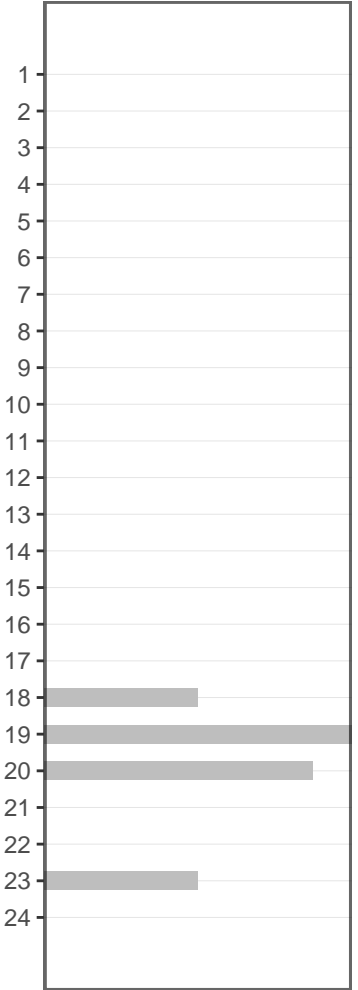
Molecular weight



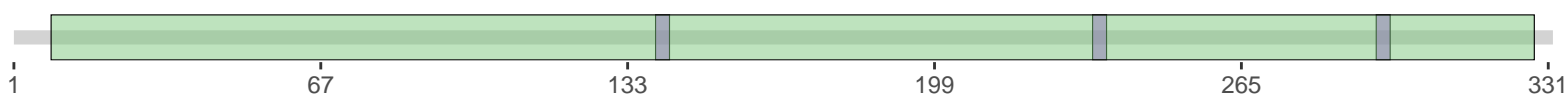
Gel Slice



Protein length

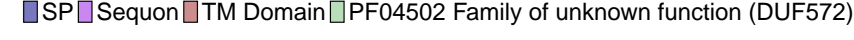


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IAALDEMKSKSRHATVGVVDAMLEALGRADEAKARKLEEKDEALIRSVFGGSRDRKRIPIDELEEDDGDIAFFAPESGGSENNLKRKRKVESEENKPTNFTLKAVTDSGINKKAKSSSDGKHFKSSSVKISVVKKPSDDNNSKKTVEGNGQAEKTKGTSNGLLSLOGQYEGSEDDP

NbL08g12790.1 fructokinase-like_2_chloroplastic [MW = 74.85 kDa]

No. of times detected



log(intensity)



Values from



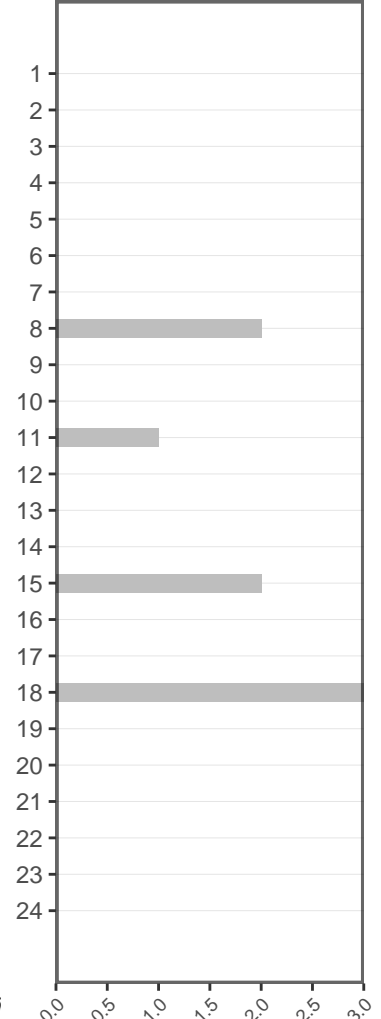
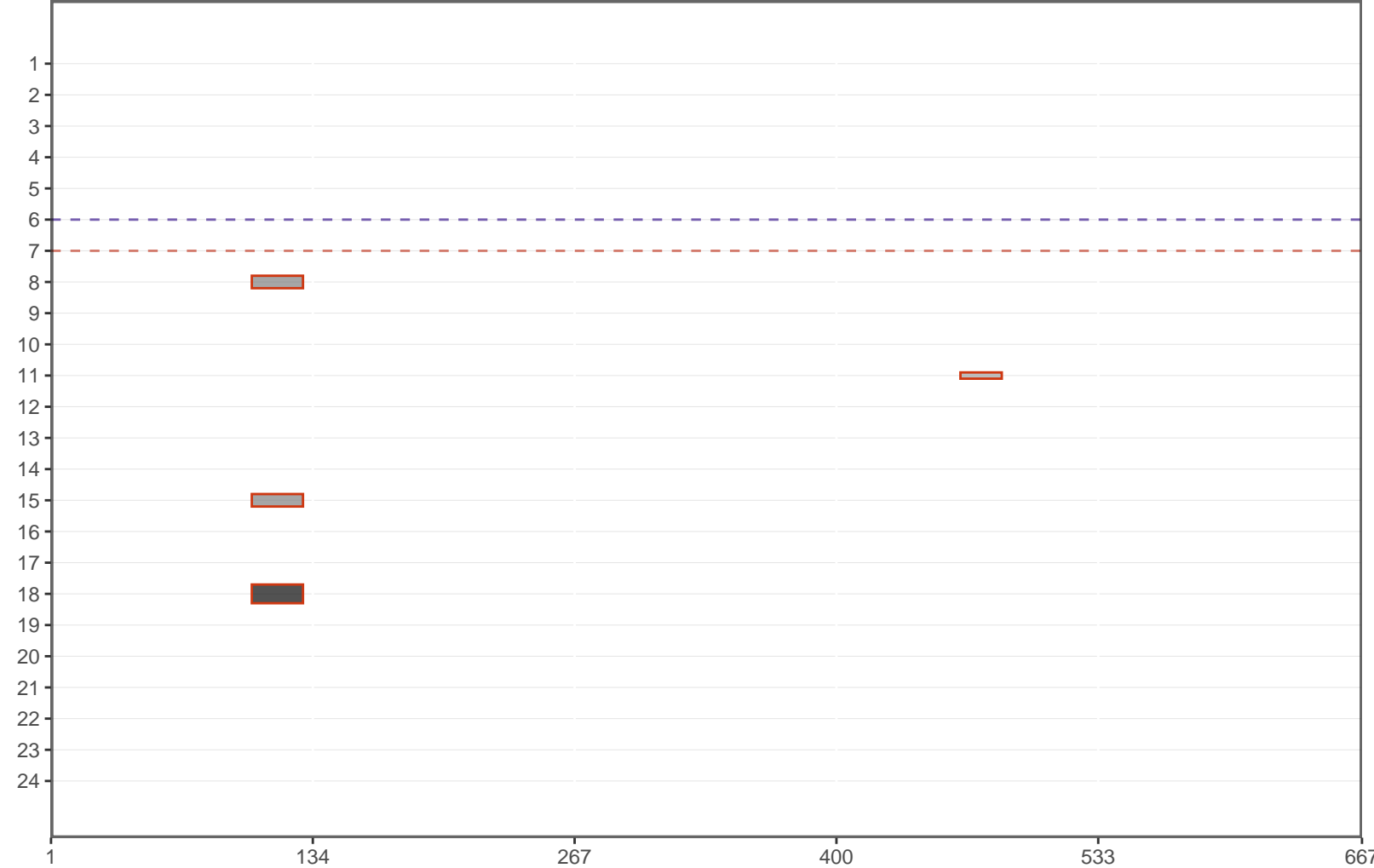
MW indication



Molecular weight



Gel Slice

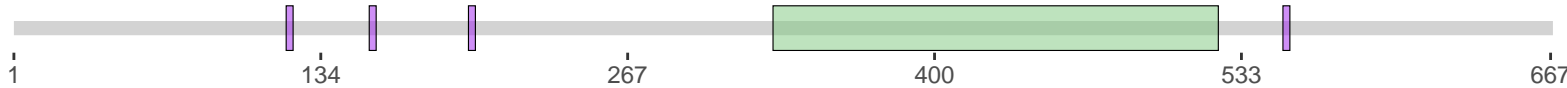


Protein length

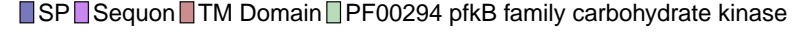


Peptide counts over 4 repeats

Pfam domains



Pfam Description

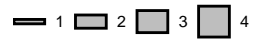


Protein sequence:

LVDHEWHERIKDAWDEPKFTRSPGGGSSNVAVALSLGGKVAFMKGLGDDDFGGSLVYFMNNKQVDRVRFDDKKATAITHMKIKGRGGLRMTTKPSAEDSLKSEINNVLKEAKMVFYNTFSLDDPNMKLTLRATKIKKLGDDVVFYDVNLPFLWESGGDKAKTFIQGAWDLADIEVTKQELFLGGIKPSEKFDKDNDRSKFTHYPPEVIAFLWHENLKVLFVINGTKRHHYTKKHNGAVLGLLEDVPLTPVTSQMSASGEGHAGHRMPTVQPHLMTDKGYLERTL

NbL08g12630.1 probable_inactive_purple_acid_phosphatase_1 [MW – SP = 66.42 kDa]

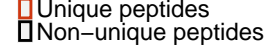
No. of times detected



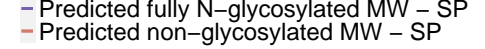
log(intensity)



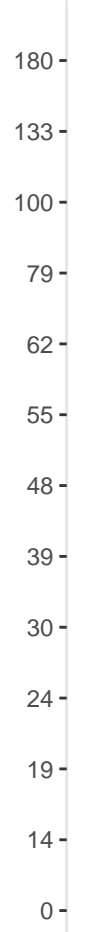
Values from



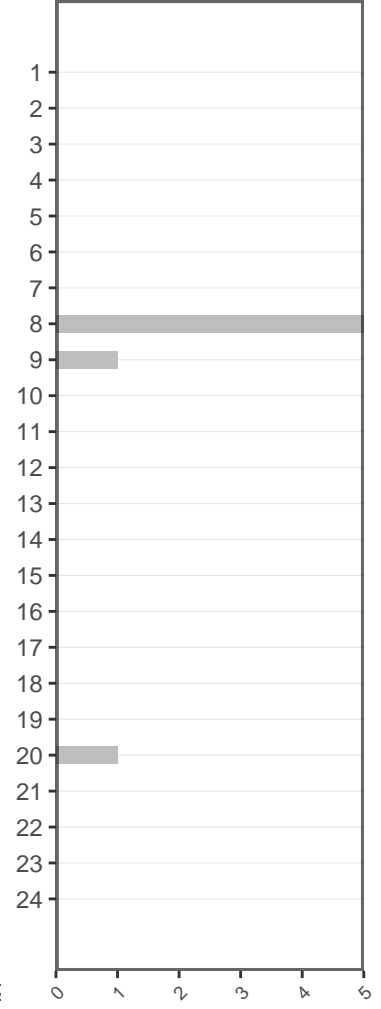
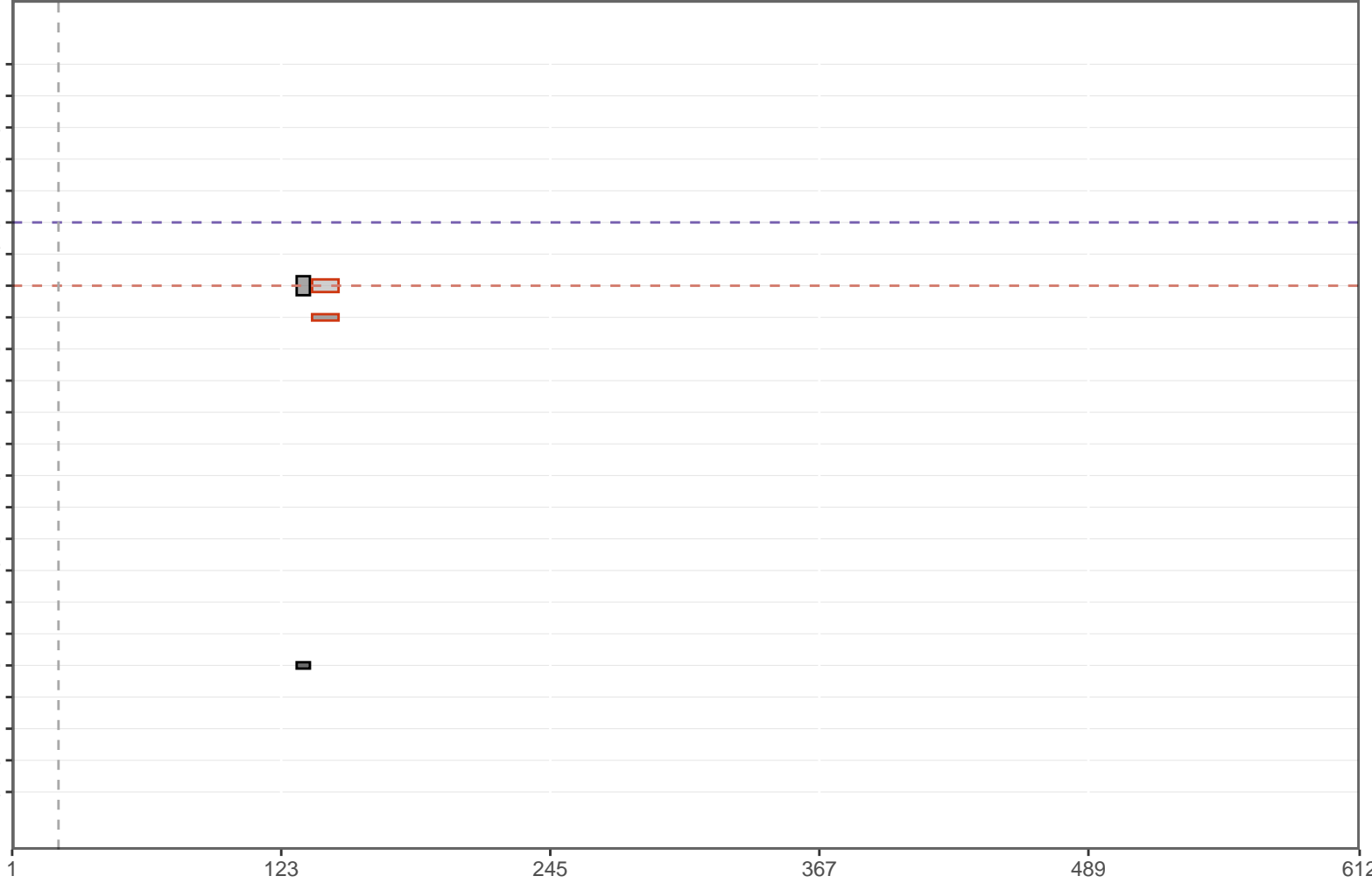
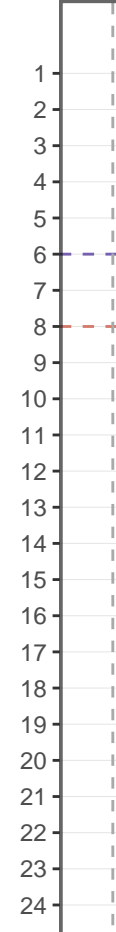
MW indication



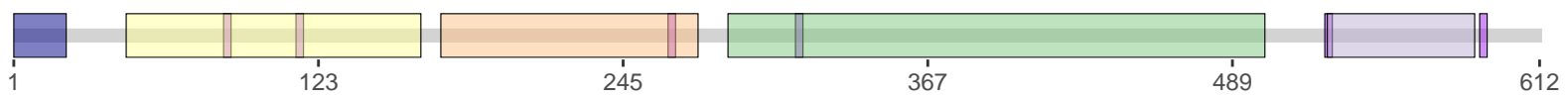
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

- SP
- TM Domain
- PF00149 Calcineurin-like phosphoesterase
- PF16656 Purple acid Phosphatase, N-terminal domain
- PF14008 Iron/zinc purple acid phosphatase-like protein C
- PF17808 Fn3-like domain from Purple Acid Phosphatase

Protein sequence:

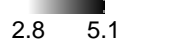
GKEEADCSNYYNQYQGLNFTTKQIBDLKNDIVFHIGDLYANGYLSQWDQFTSQVEQTSRVPYMAASGNHERDWPDSGSFYGKKDSGGEGGVLAQGTMEYFPAENRDKFWYSTDYGMRFRGDIADTEHDWRREGTEGYERIEHCFASVDKQKSPVLFLLAHRVLYGSSGDFVADEGSGFGEFPMGRESGLKLVGKYYVDIAVGHVHNYERTGPIYQNTGTMNEKNYSYKGLNGTHVAVGGGAGLVKFTPLGTRWBFKDYGFVKMTAFDHSNLLFEYKSRDGV

NbL08g12620.1 argininosuccinate_synthase_chloroplastic [MW = 53.85 kDa]

No. of times detected



log(intensity)



Values from



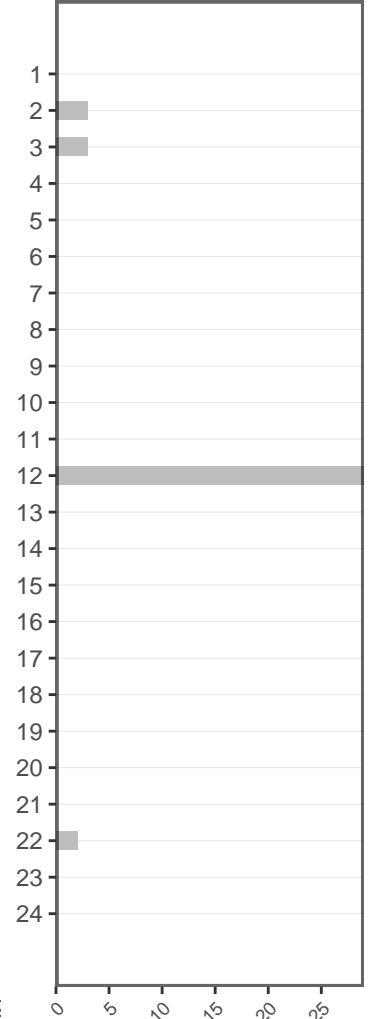
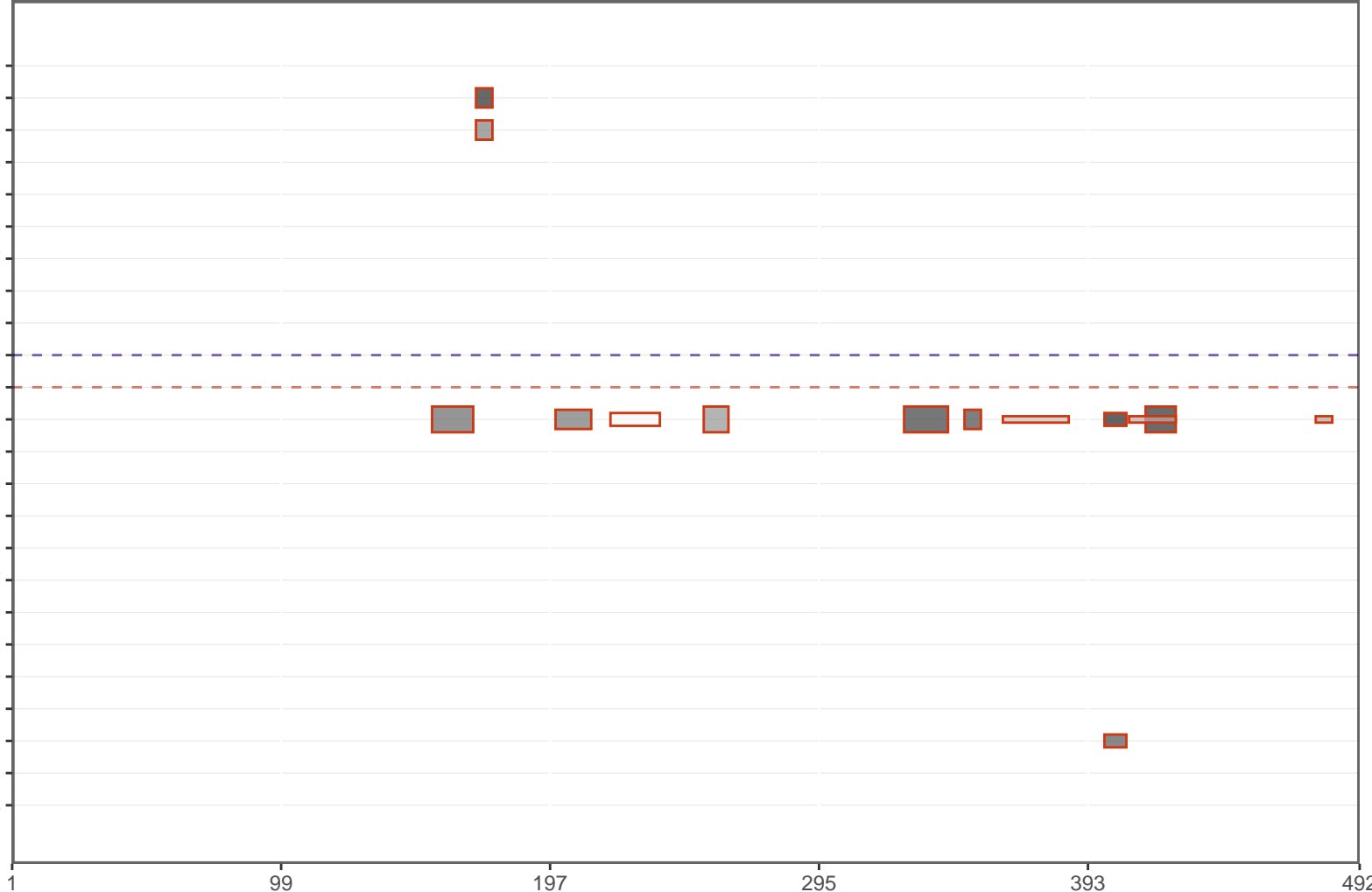
MW indication



Molecular weight

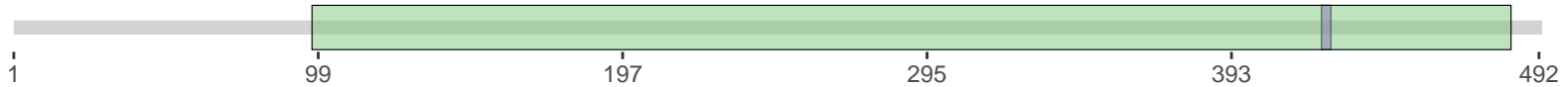


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VAPVREVEITGRGDMIEVAKKHVVPVPTKKSIVSRDRNLWHLSEGGDLEDPANEPKMDYMMMSIDPQDAPODPEVYVNGVAGVGVVNGKELSPATLLSELNEIGRRHGIGRIDMVENLIVMKSRGVYETPGGTILFTAVGELSLFLDRDTQVYKDLAKYAEVLYAGRWFDPLREGMDAFMENTKTTTGSVTLKLYKGVSVTGRQSPHLYRQDSSFEFGDHYNGADAAGFRLVGLPMRVRAMLEKGL

NbL08g12550.1 PLASMODESMATA_CALLOSE-BINDING_PROTEIN_3-like [MW - SP = 17.79 kDa]

No. of times detected



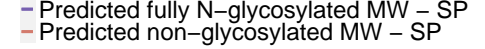
log(intensity)



Values from



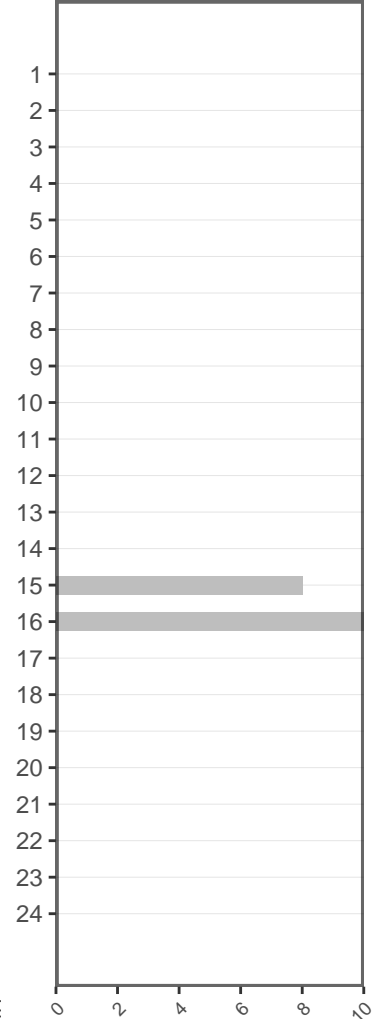
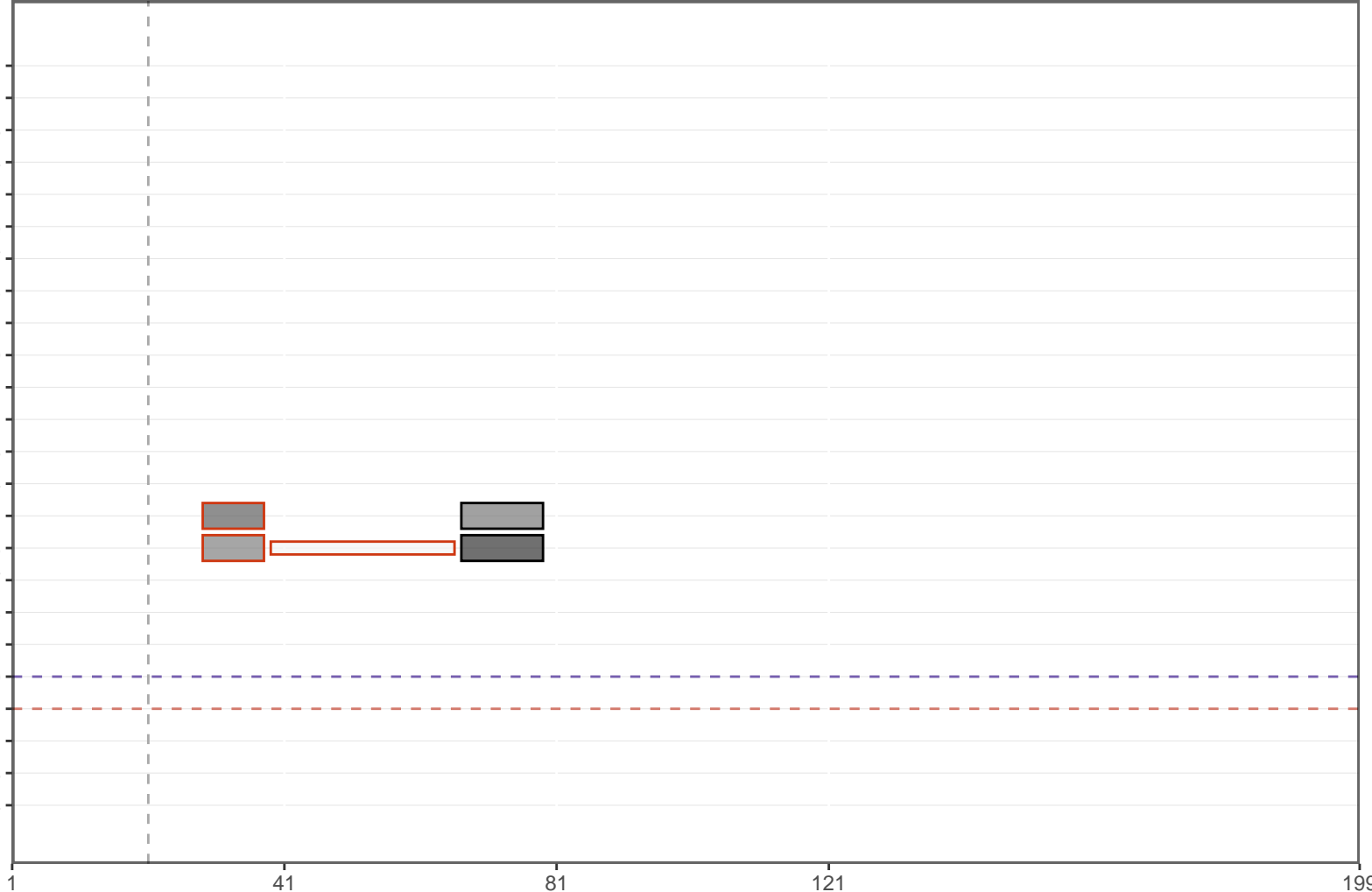
MW indication



Molecular weight



Gel Slice



Protein length

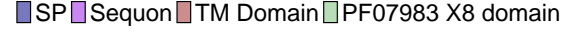


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CDPSGATLSSNPF66ST6GGYQFTTQNTAGGTTVPQTTFVPGITTFPGIGTGTGTGTGTGTTGGNNPTFGLGPTG6GGFNPQ66GTELHQNTVFFTIALFTSLVLR

NbL08g12520.1 14-3-3-like_protein_GF14_iota [MW = 29.94 kDa]

No. of times detected



log(intensity)



Values from



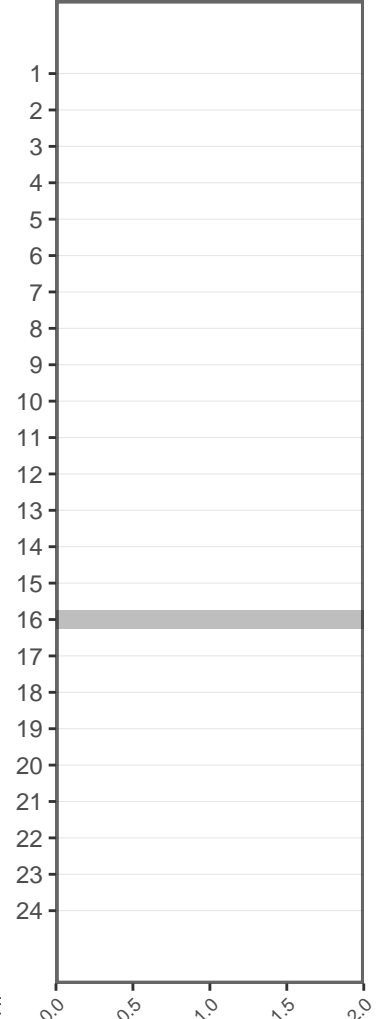
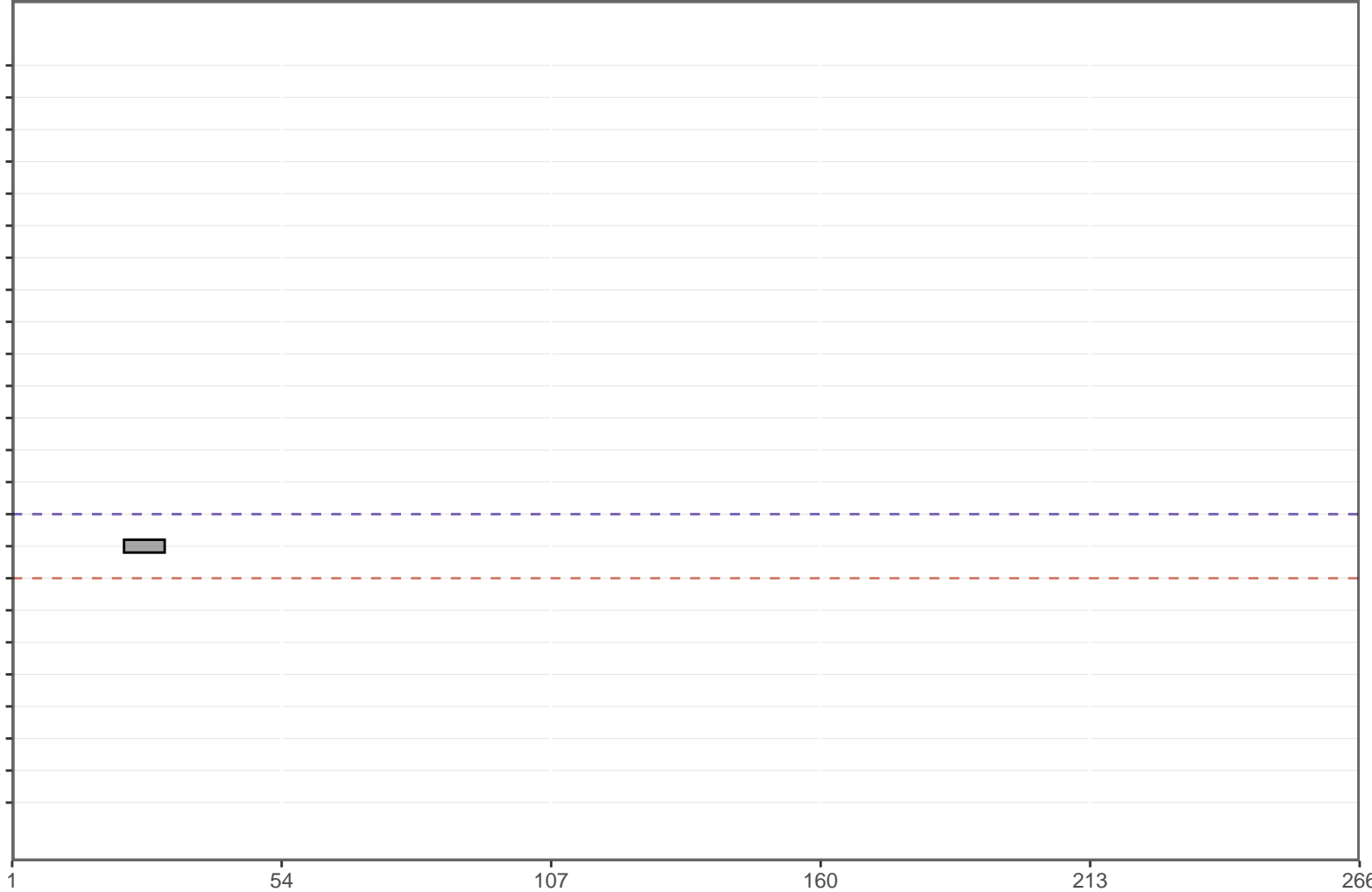
MW indication



Molecular weight

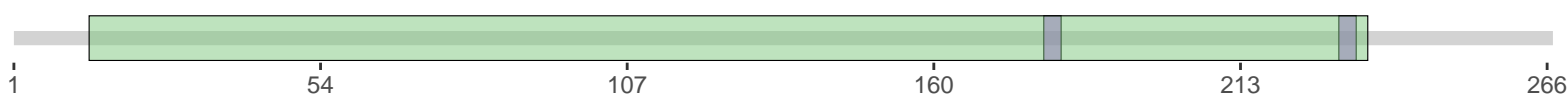


Gel Slice



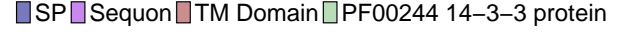
Protein length

Peptide counts over 4 repeats



Pfam domains

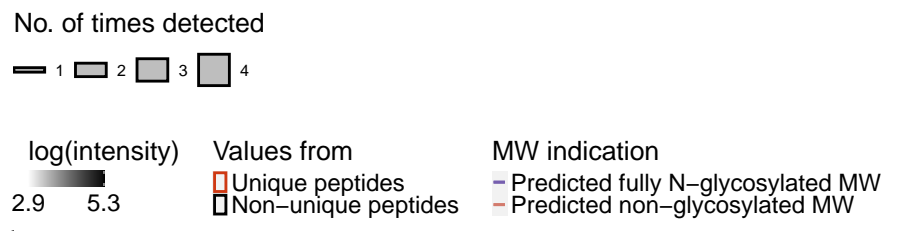
Pfam Description



Protein sequence:

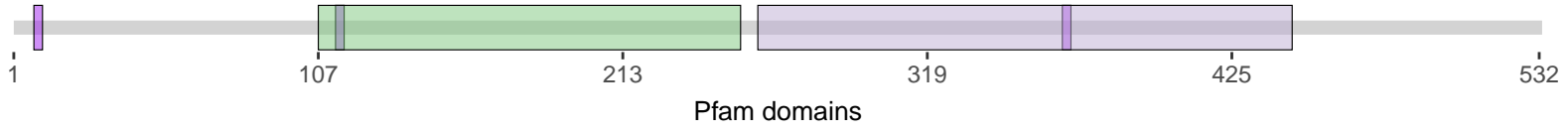
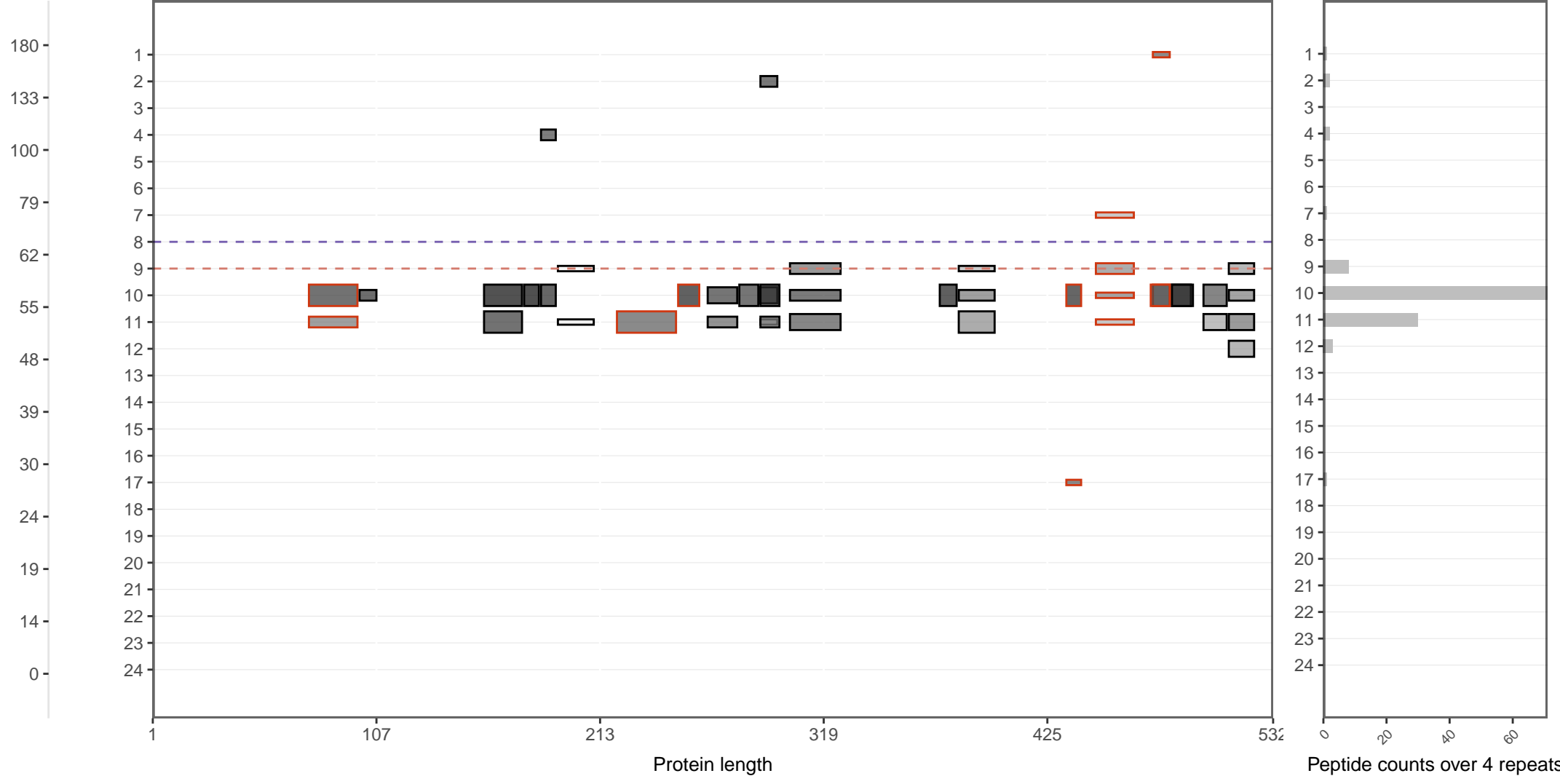
ITVYYKMGDYRRLAEFKTDSERKEAAEQSLKGYEATATANTDLSSDTHPIRLGLAALNFVYFYEIMNSPERAGHLAKGAFDEAAEIDLSEESYKIDSLIMGLLRDNLTLWTSQDLPEDGGEEENWGDPEKGAEPKSDAKAC

NbL08g12460.1 probable_mitochondrial-processing_peptidase_subunit_beta_mitochondrial [MW = 59.43 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00675 Insulinase (Peptidase family M16)
- PF05193 Peptidase M16 inactive domain

Protein sequence:

IPQNGKMTTRAHIGDQVSTHYGAHRMVISAAAGAVKHEDEVLVKHKHFKLGSNPITTSQLVADPEAFITGSEIRHDDDLPLAQFAVAFSGASWTDPPDSILMMVMQGMGKSWNKTSGGGGHMGSELVGRVAINEAEVGSMAFNTNYKDTGLFGVVAEAKPDGLSDLAYVMGGKGLQYRVSEADIRARNGLKSSILHHDGSGPAEDIGKQLTYGRRIPHAELFGRIDRVQADTYKRVANRIFEDRDIAISARGPQGLPDNYWFRRTYWLRY

NbL08g12400.1 skin_secretory_protein_xP2-like [MW = 23.71 kDa]

No. of times detected



log(intensity)



Values from



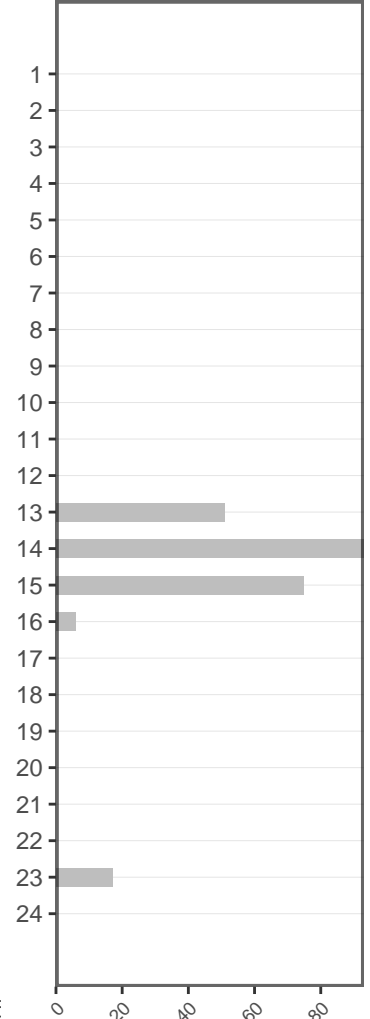
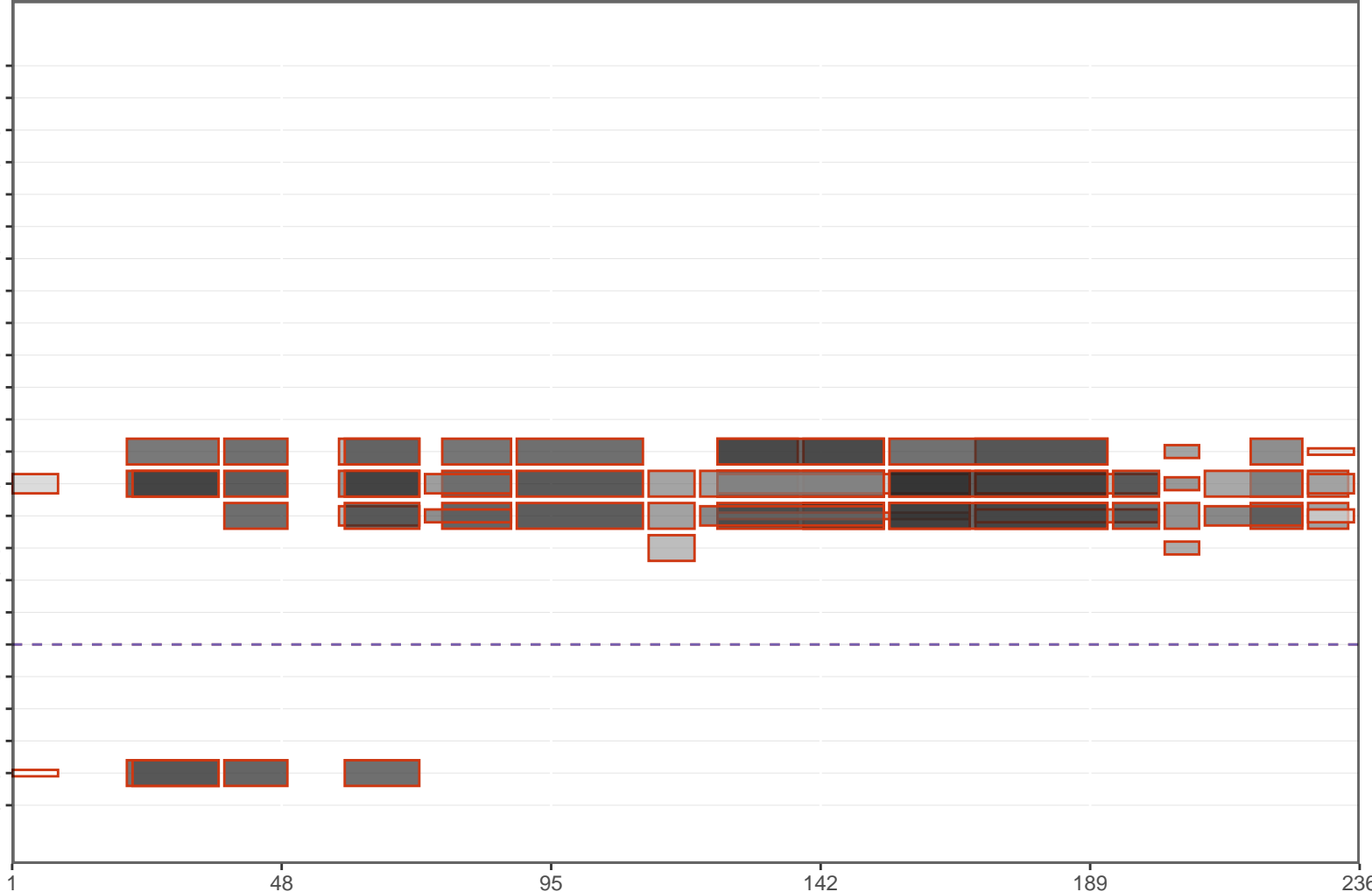
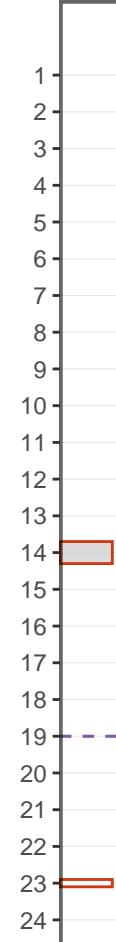
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

ITDAALAKAPVATPDTKDTKAPTRAPAAADTDETKAPAPAPAAADTEETKASAPAPAAADTEETKAPATADTDEEPAPAPAPAPAPPEEKGGEGYGVKMAEGFLKGGDDSAKASEGGSDHKKMAGDFLGGK

NbL08g12390.1 26S_proteasome_non-ATPase_regulatory_subunit_10 [MW = 25.23 kDa]

No. of times detected



log(intensity)



Values from



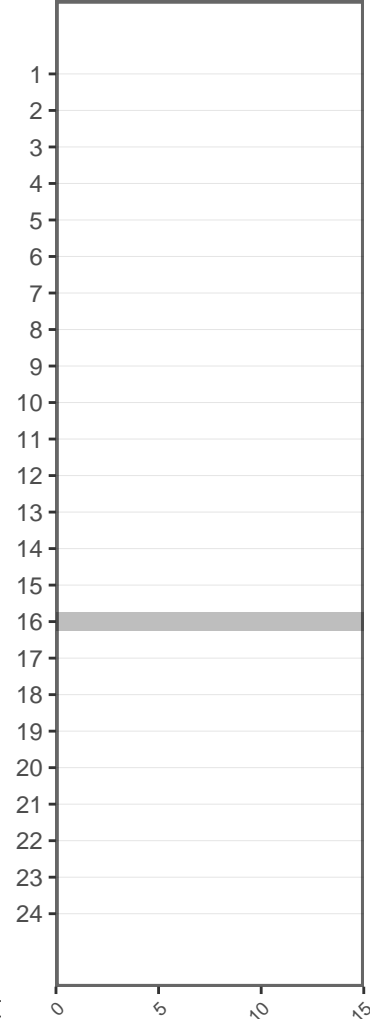
MW indication



Molecular weight



Gel Slice

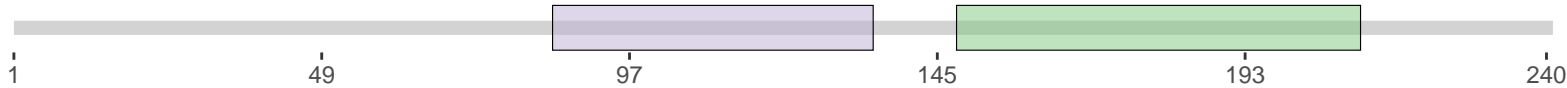


Protein length

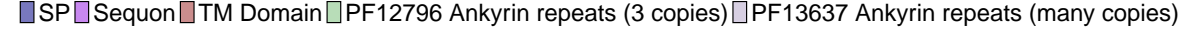


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

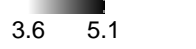
JAALKNDGGRTALHYAASKGRVKAPELLSHGAKINAKDKVGGTFLHRAASTGNSELGELLUEECAEIDEVDKAGETPLMTAVVCGNKEVAMLRHIGANVDAEKEGYTVLGRASNDLRPLVDAAKTMLEG*

NbL08g12360.1 uncharacterized_LOC109212061 [MW = 37.96 kDa]

No. of times detected



log(intensity)



Values from



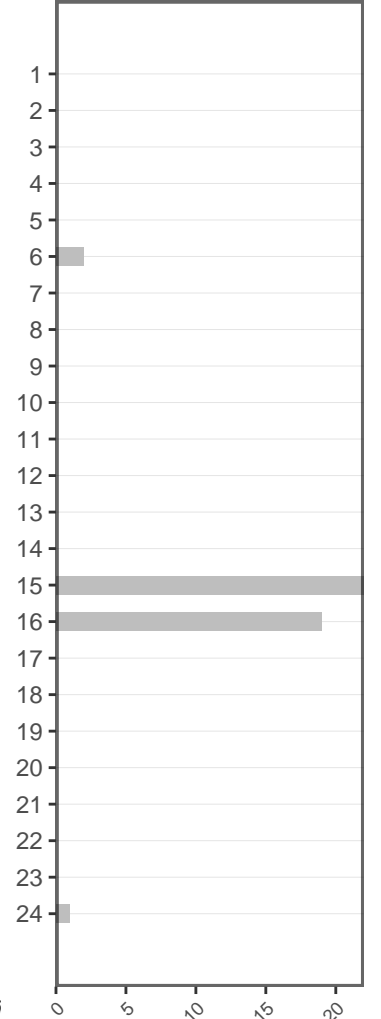
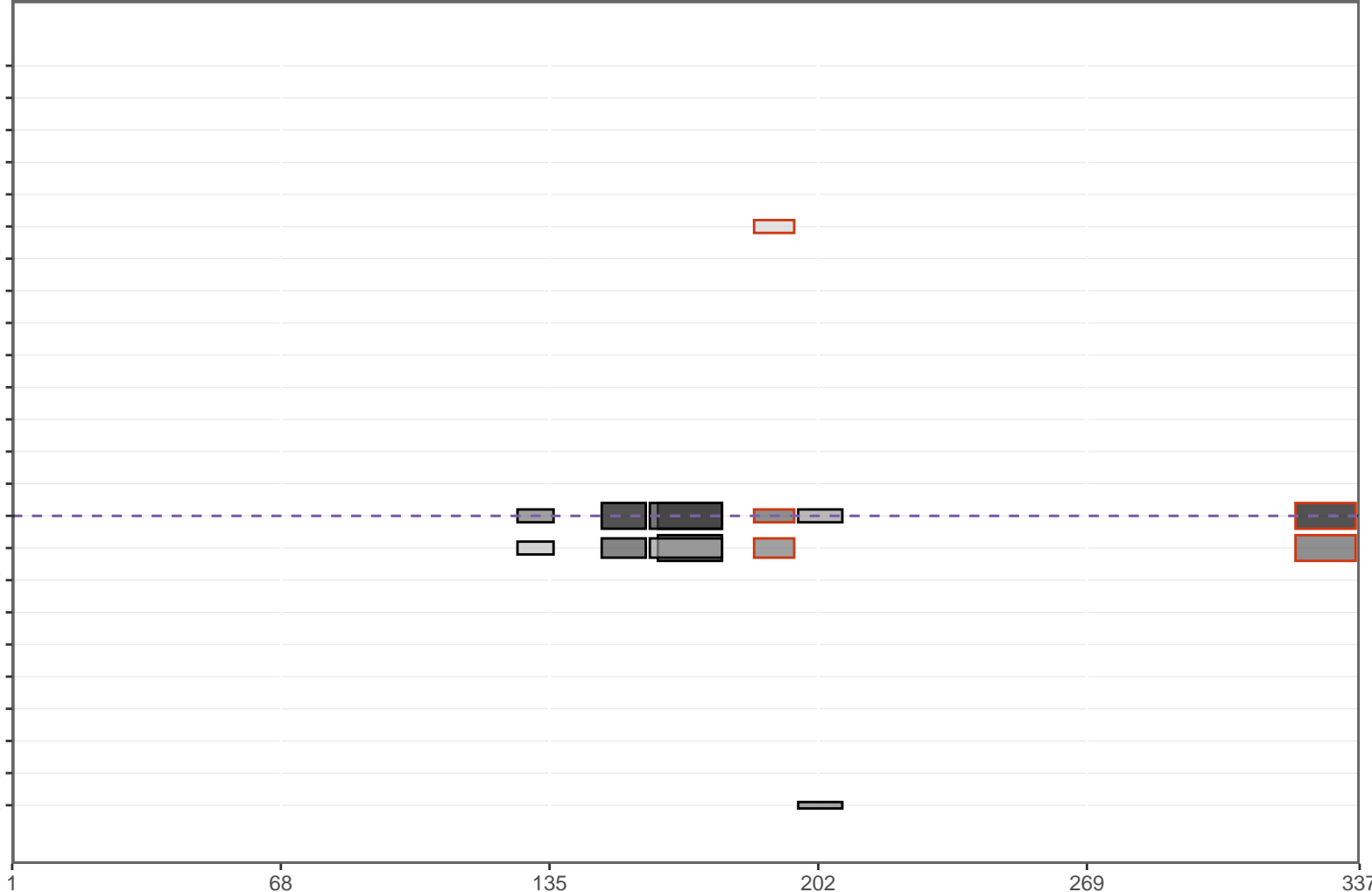
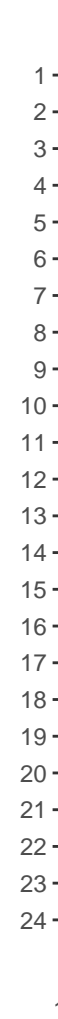
MW indication



Molecular weight



Gel Slice

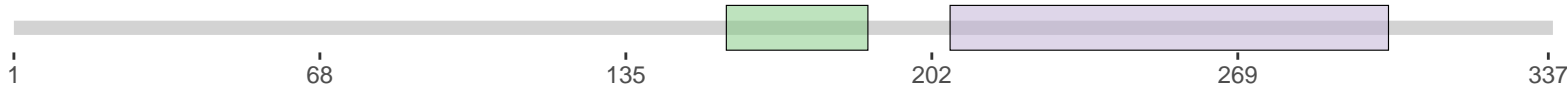


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ASILRLRADLQNAVQSENDAANKLRDEIKLEAELSTAEVRAGAVYNAQVAFRLGGKVRKKNFGYRGGVGMDFPICGESSWMTAQVOKLGRGDPGFYQVVLVDVHTDPNLLVAVYPEESLVAPEPDKDRFDHPYTSFLFFGMDAAGDFIPKGLREKYNRPRHEVPYDPEDEKSGEGS

NbL08g12190.1 probable_L-cysteine_desulfhydrase_chloroplastic [MW = 49.09 kDa]

No. of times detected



log(intensity)



Values from



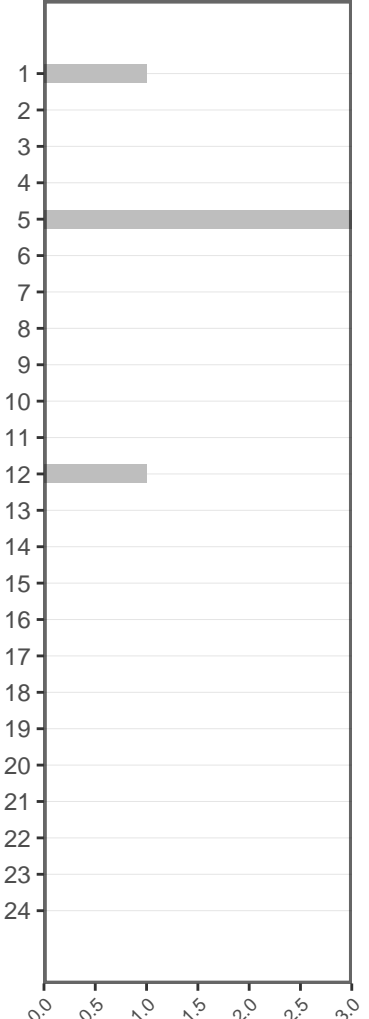
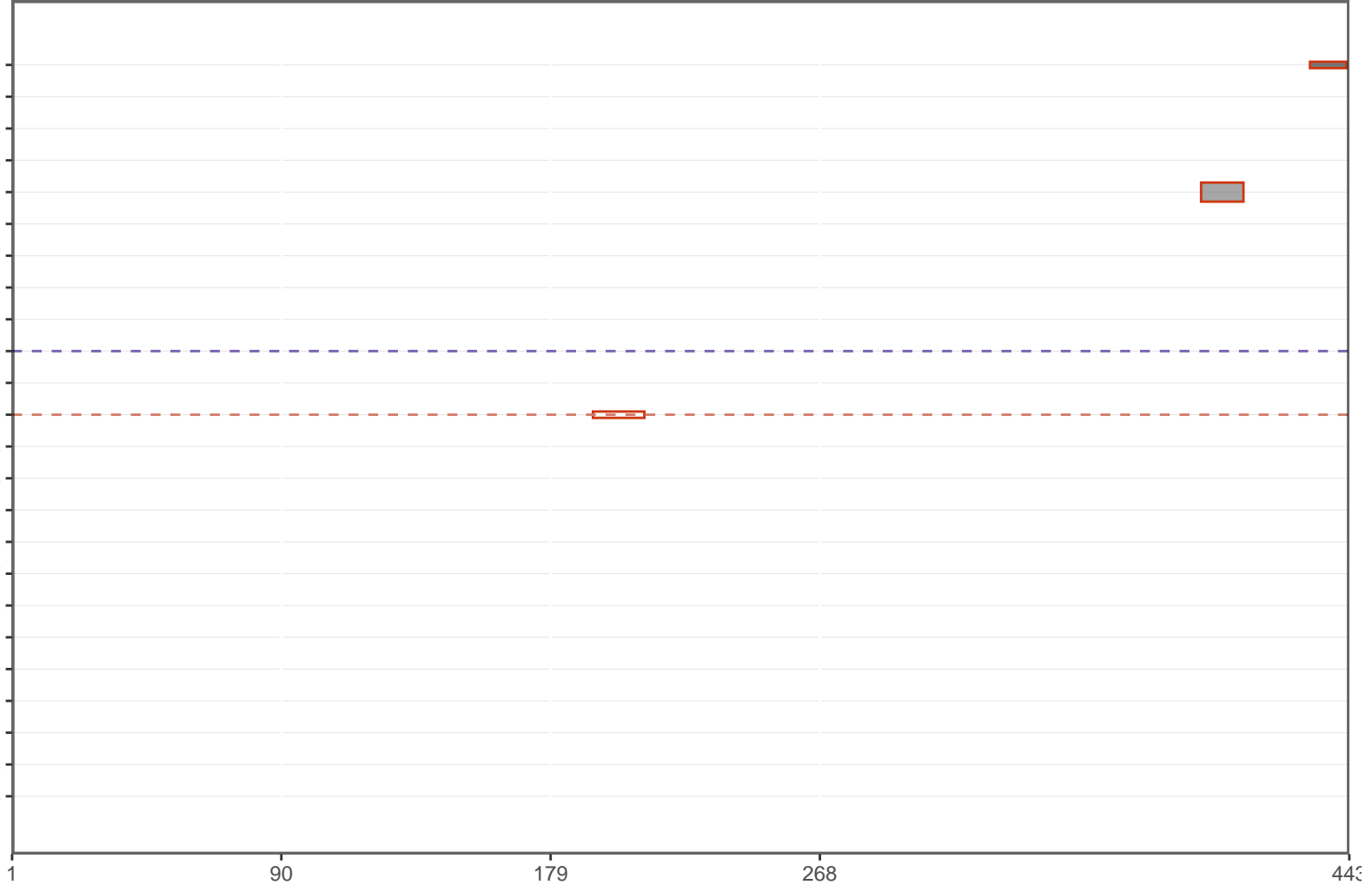
MW indication



Molecular weight



Gel Slice

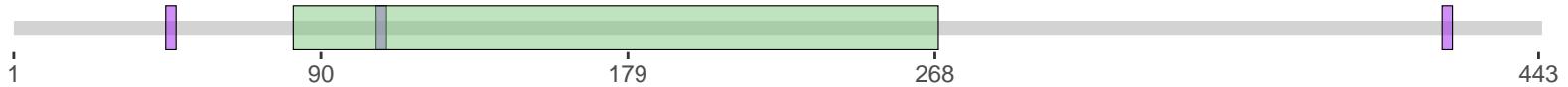


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ELLVKMRDEGVDFVDSGAHAGNQQVVDGIDAEVYTNLHKWFFSPPSAFLYCKKSDKVLDLHPVVSNEYGNGLPIESAWIQTRDYSAGLVPEVLEFVNRFEFGGIEGIRRRNHGKVVEMAEMLVKAWGTLGTPPEMCSAMMVGMPDGLGISDSDALKLRHLRVSFKVEVPIYVRAPLEGLNSFTGVARISHQVYNTTEDGVYRFRDAIKLNDGFTCALSN

NbL08g12150.1 uncharacterized_LOC109214568 [MW = 32.7 kDa]

No. of times detected



log(intensity)



Values from



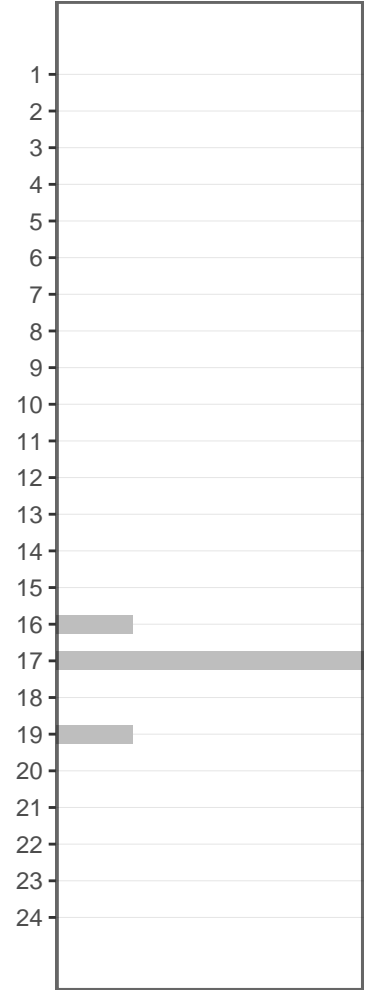
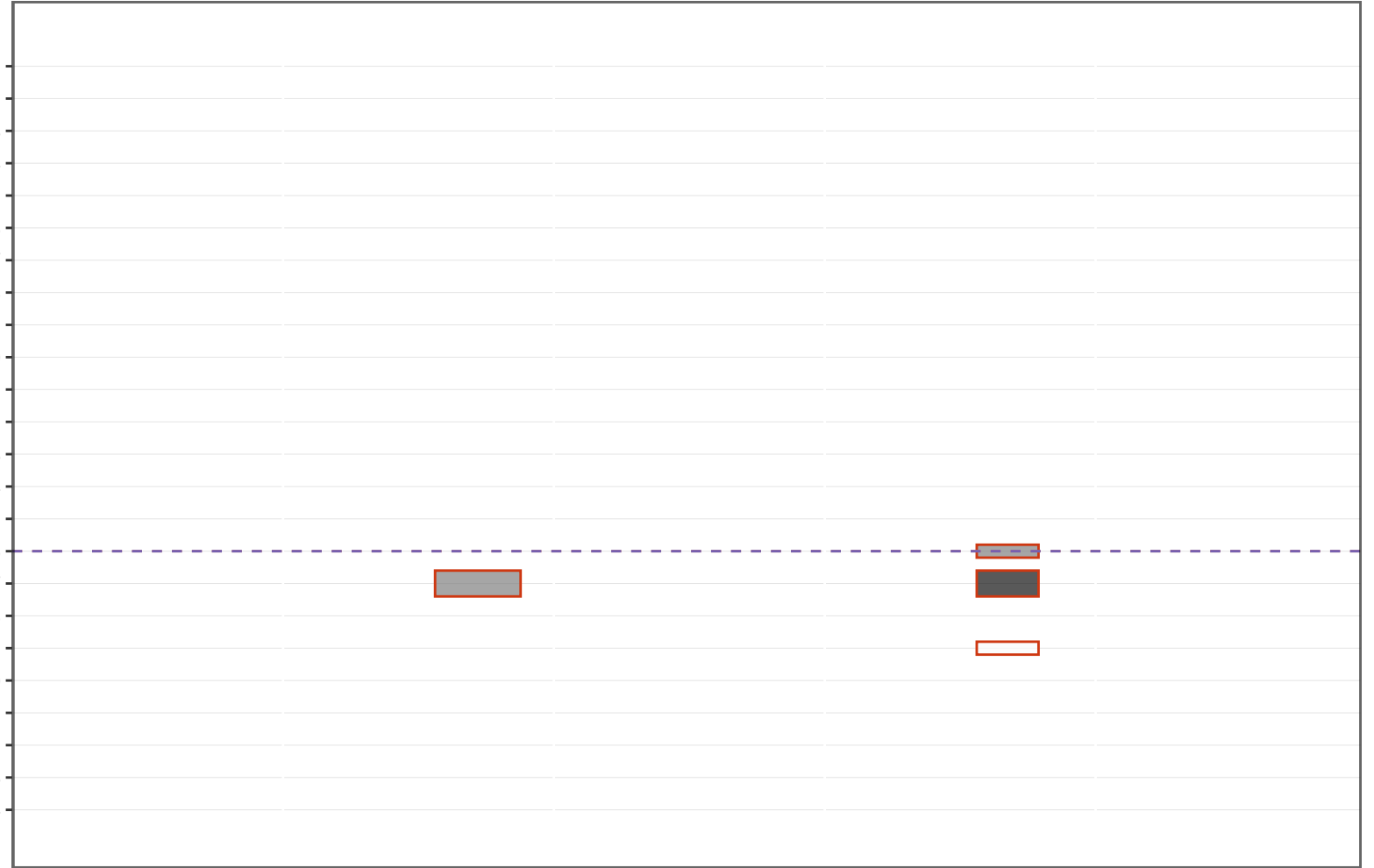
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

1 58 115 172 229 285

Protein length

1 58 115 172 229 285

Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

NPVIRETPKPYVYVLTQRENQLCTMKTRKNRFFFEAGSEVERELGMLFSKGGKWKRAKQPEPTDTRFQMLVEDIREGLVFEDENEAARYDGLGGGGGGEGVAIEAASVDFDLGRKMRALAVLFRFRGRTPLPELKLNRARKRSLDDGENLM

NbL08g12070.1 extracellular_ribonuclease_LE-like [MW - SP = 22.65 kDa]

No. of times detected



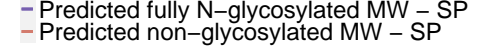
log(intensity)



Values from



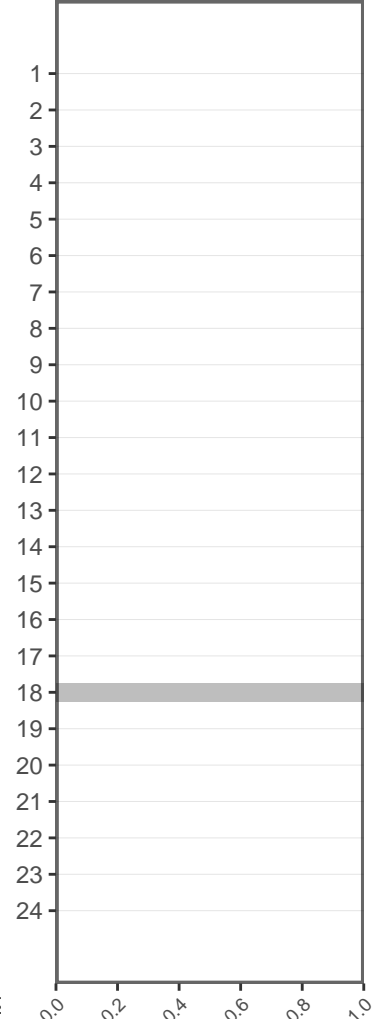
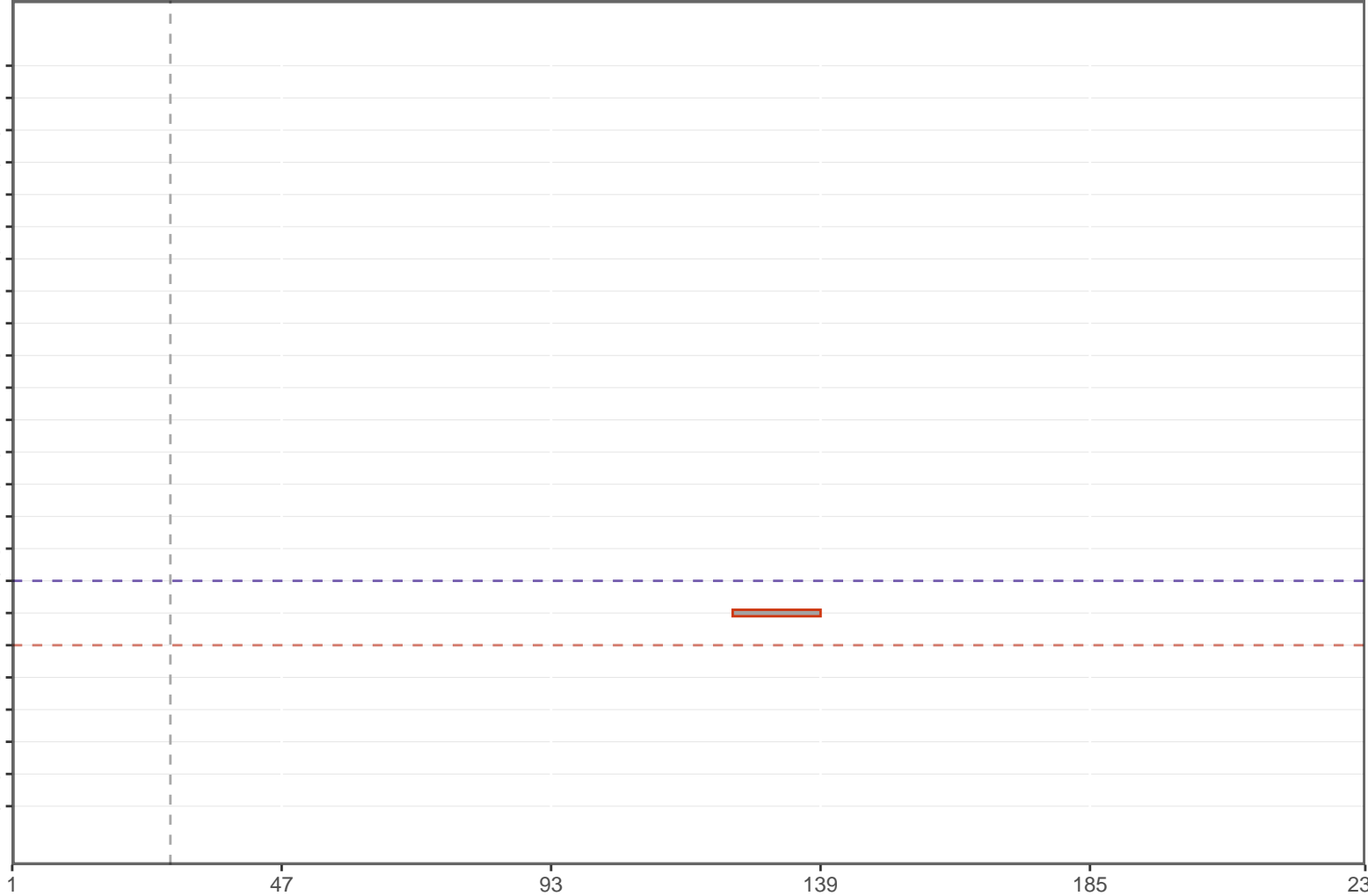
MW indication



Molecular weight

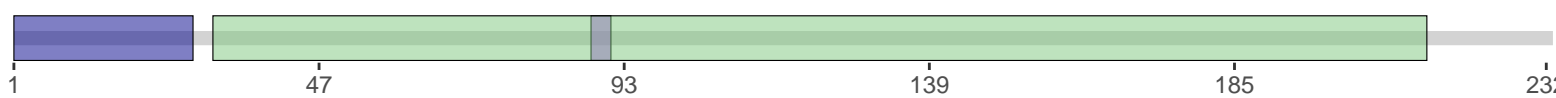


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

NWPTLACPSGTGSAFWHSEWEKHGTGSEIFDGHGFKKALDKLNQNLLELQGLADINPDGGGFYSLNNKNAIRBAGYTPGIEGNDESGNSQLYVYVHVDGSGSNLIEGPIVFRPKGGSSIEFFPTF

NbL08g12060.1 intracellular_ribonuclease_LX-like [MW = 28.86 kDa]

No. of times detected



log(intensity)



Values from



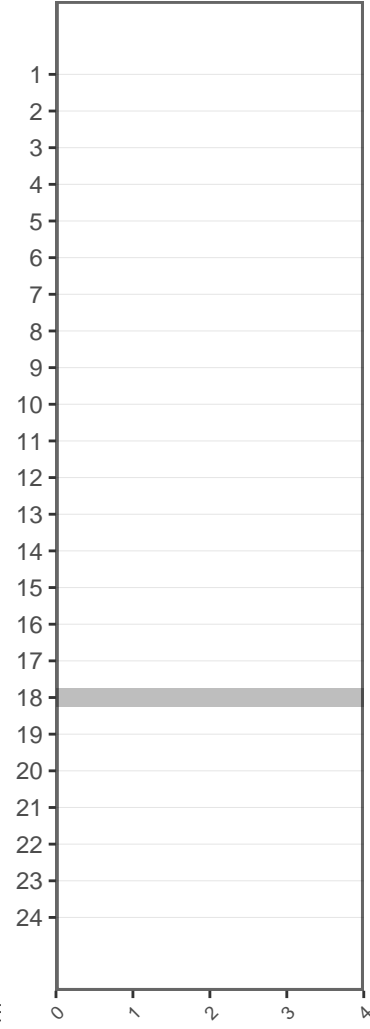
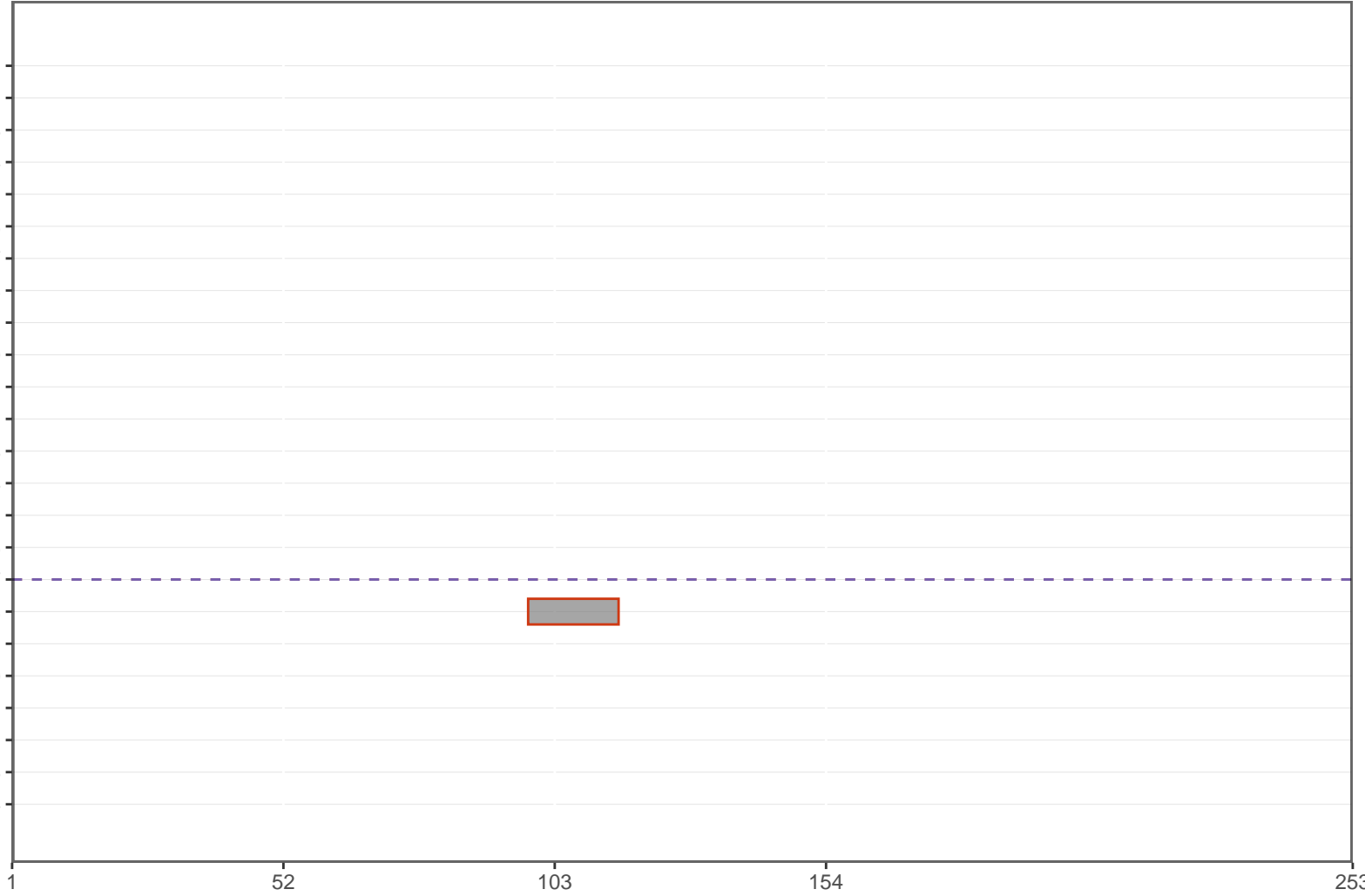
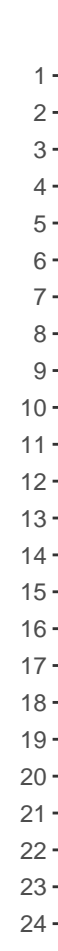
MW indication



Molecular weight

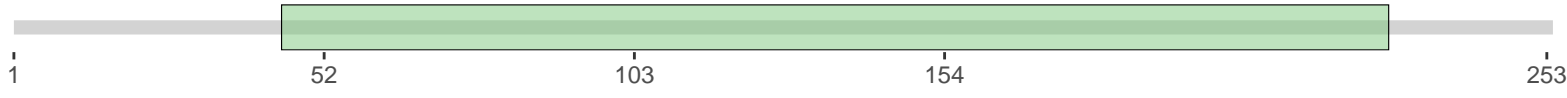


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EKNVPSLACPSDDGVRFWSEHWLKHGTGSAIGERAYFGAALDFRKKNNLLENLKNAGITPRNGEHYELESIKKAEEGVGHPIYIEGNVDTQGNHGIYGVYLVGDKTASHFDGPFVPHGRGGGAWIEFPFSSDHDEF

NbL08g12030.1 methylecgonone_reductase-like [MW = 36.48 kDa]

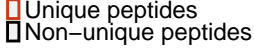
No. of times detected



log(intensity)



Values from

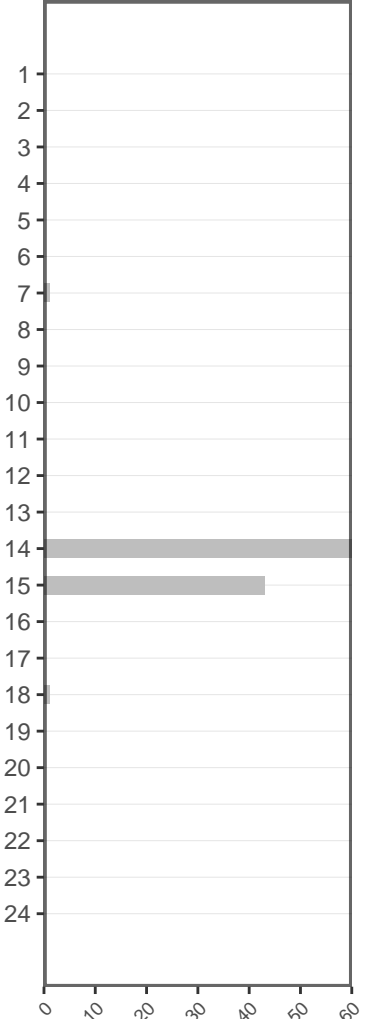
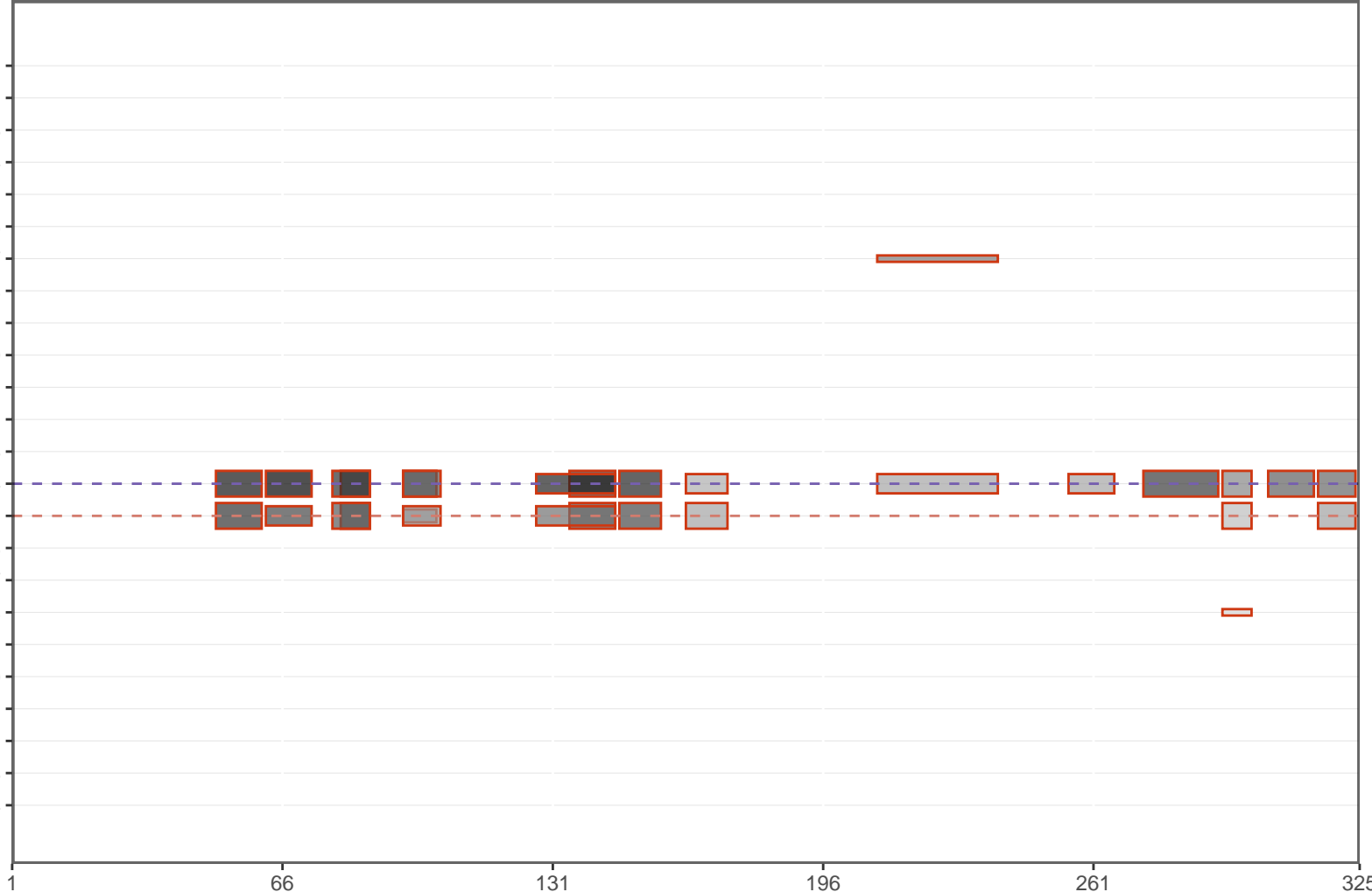
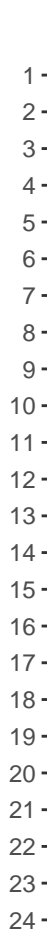


MW indication



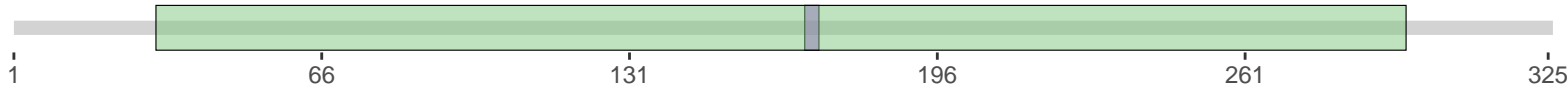
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MEECHRLLGLAKSIGVNFSGTLAGLLHHTIPPAVQVEMHVTWRQDKMLEFGKEKGIHSAWSPLGANGIPLWGNHVMQDGPVLKDAFGKQKSIAGVALRWYYEODGVILVWKFNDKRMKENGLDQWELSNEMEARKEIPQCRGFKAEVFIHHPNGPYKVDQDFWDEGL

NbL08g11930.1 KH_domain-containing_protein_At4g18375-like [MW = 57.42 kDa]

No. of times detected



log(intensity)



Values from



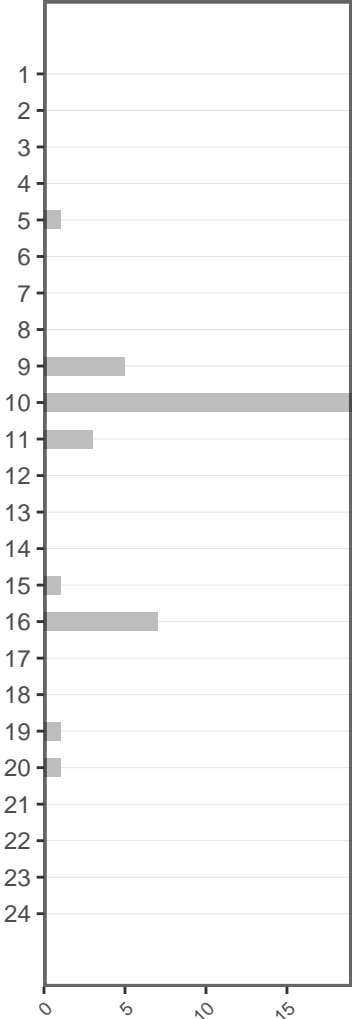
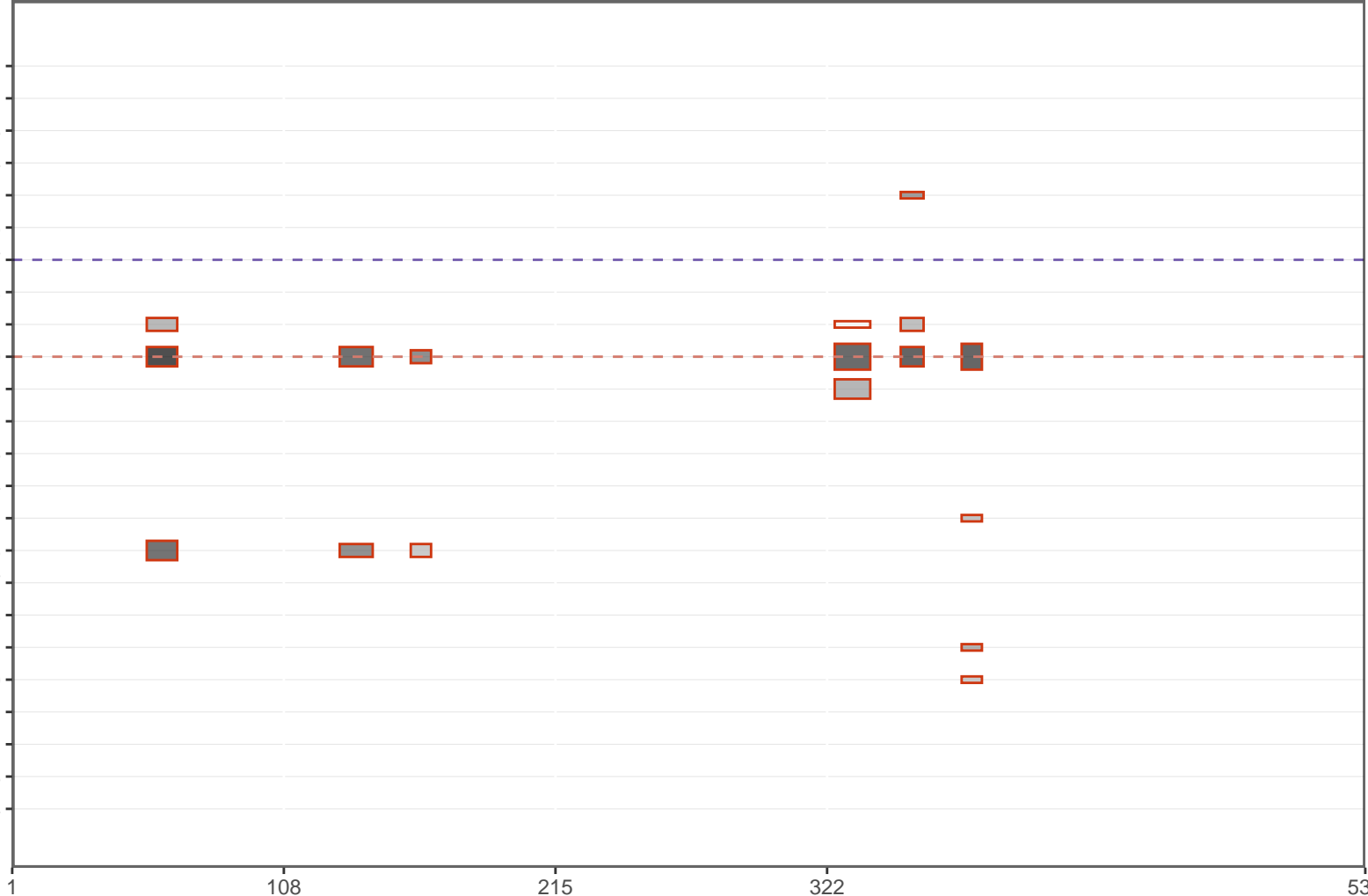
MW indication



Molecular weight



Gel Slice



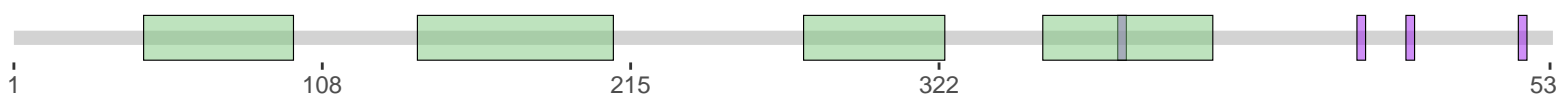
Protein length



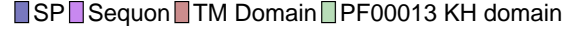
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

GSYKSDGRSRSSASVKEFAVRLVGFTEVIGAVIGKGGSHKLRGEGSGASIKVDSAAAEGDDCHVVSAAKEAYEDGSPDTQATMLRQPRSEKTEKDSGDALITRLLVPSERVGLGKGGGIVNEMRNTRFASIRLKENLPIKVAEEDDEMVFQITGDVAVAGNALLGLMLRLRANIFEMEGSFATFSPFVYVPLPSFMSDGRVYANRDNKSRRHGVSEVYSGGHVNDSDGSDSYGGSGVGGGGYAPVYVYVSGGRS66AGVSNHNS6AYGKVRP*

NbL08g11820.1 uncharacterized_LOC107767450 [MW = 53.83 kDa]

No. of times detected



log(intensity)



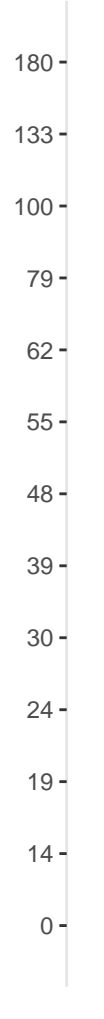
Values from



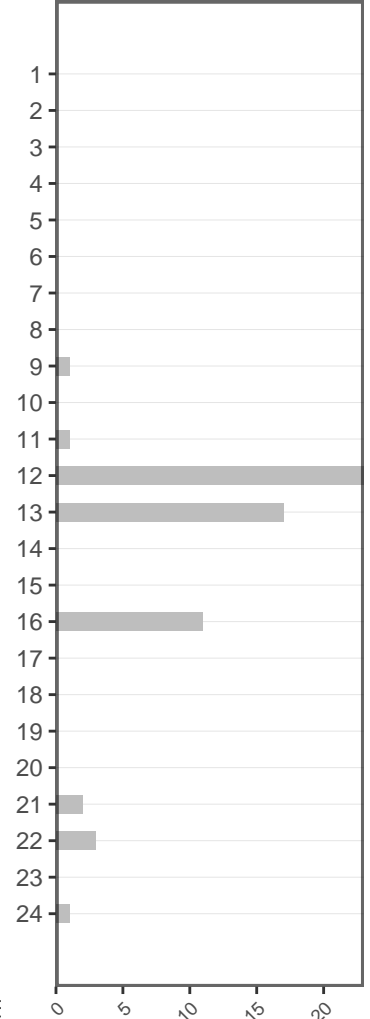
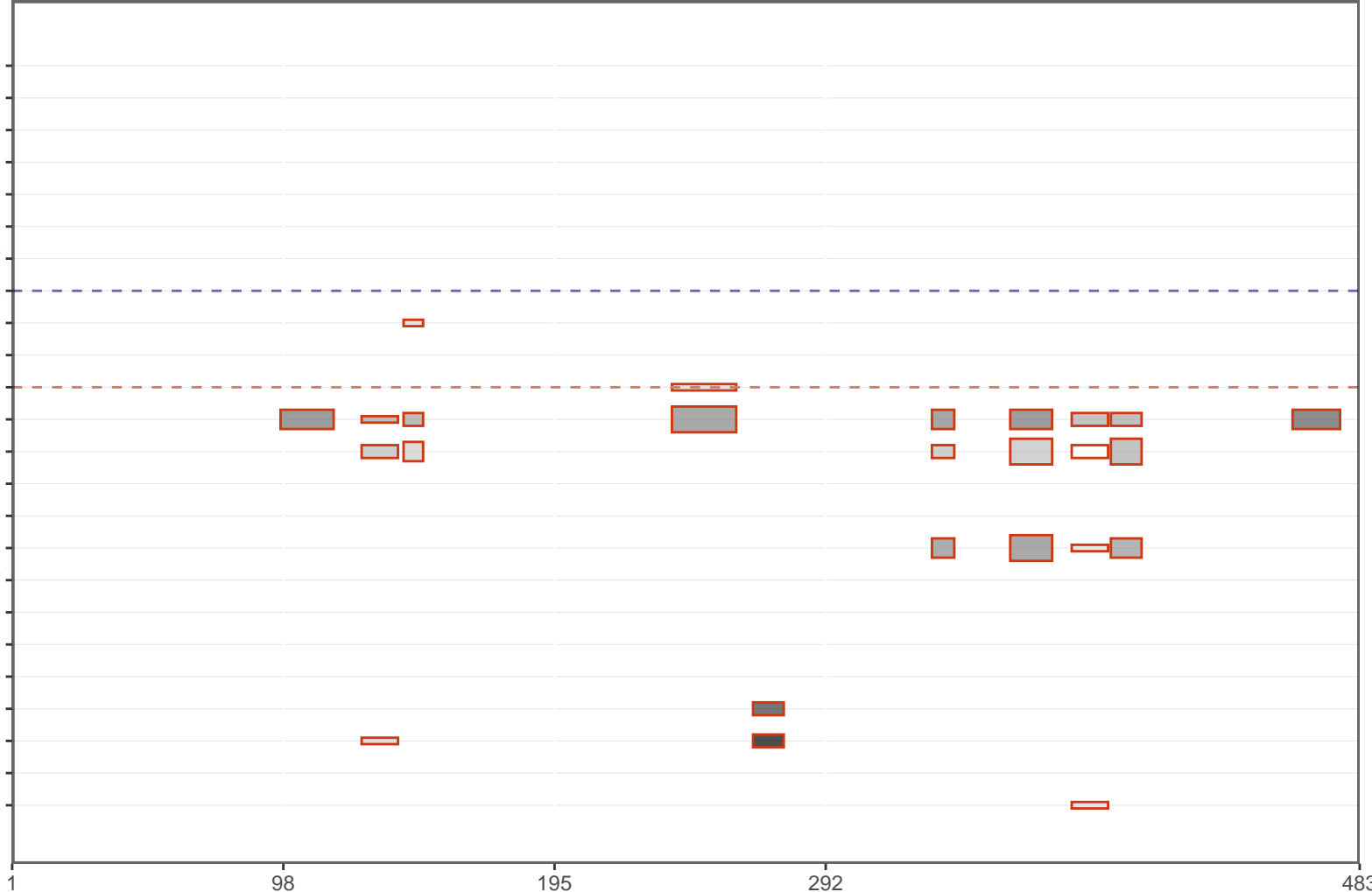
MW indication



Molecular weight



Gel Slice



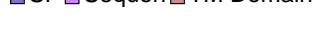
Protein length

Peptide counts over 4 repeats



Pfam domains

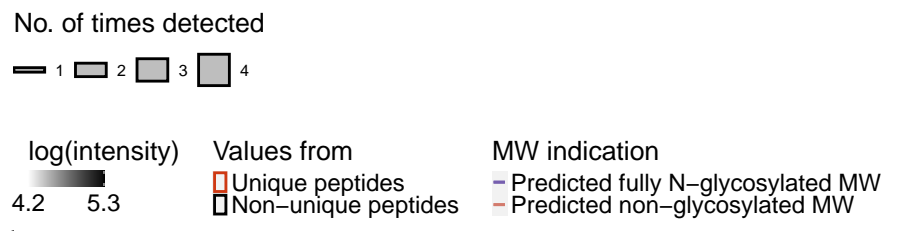
Pfam Description



Protein sequence:

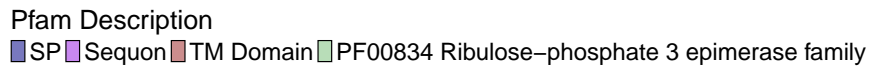
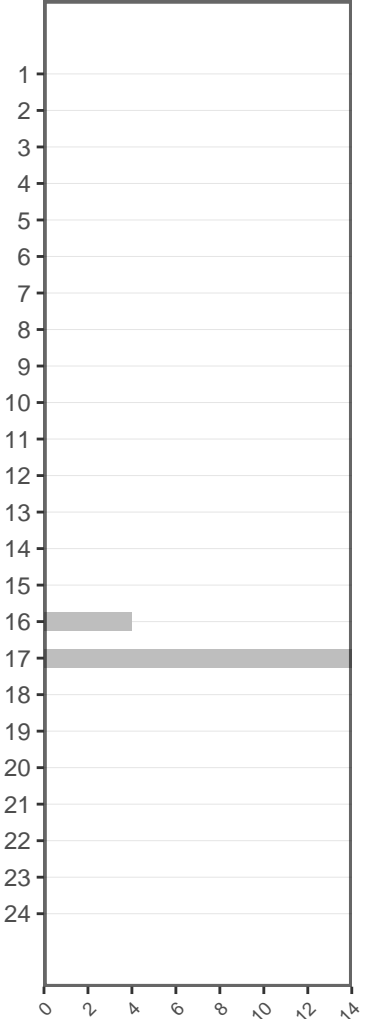
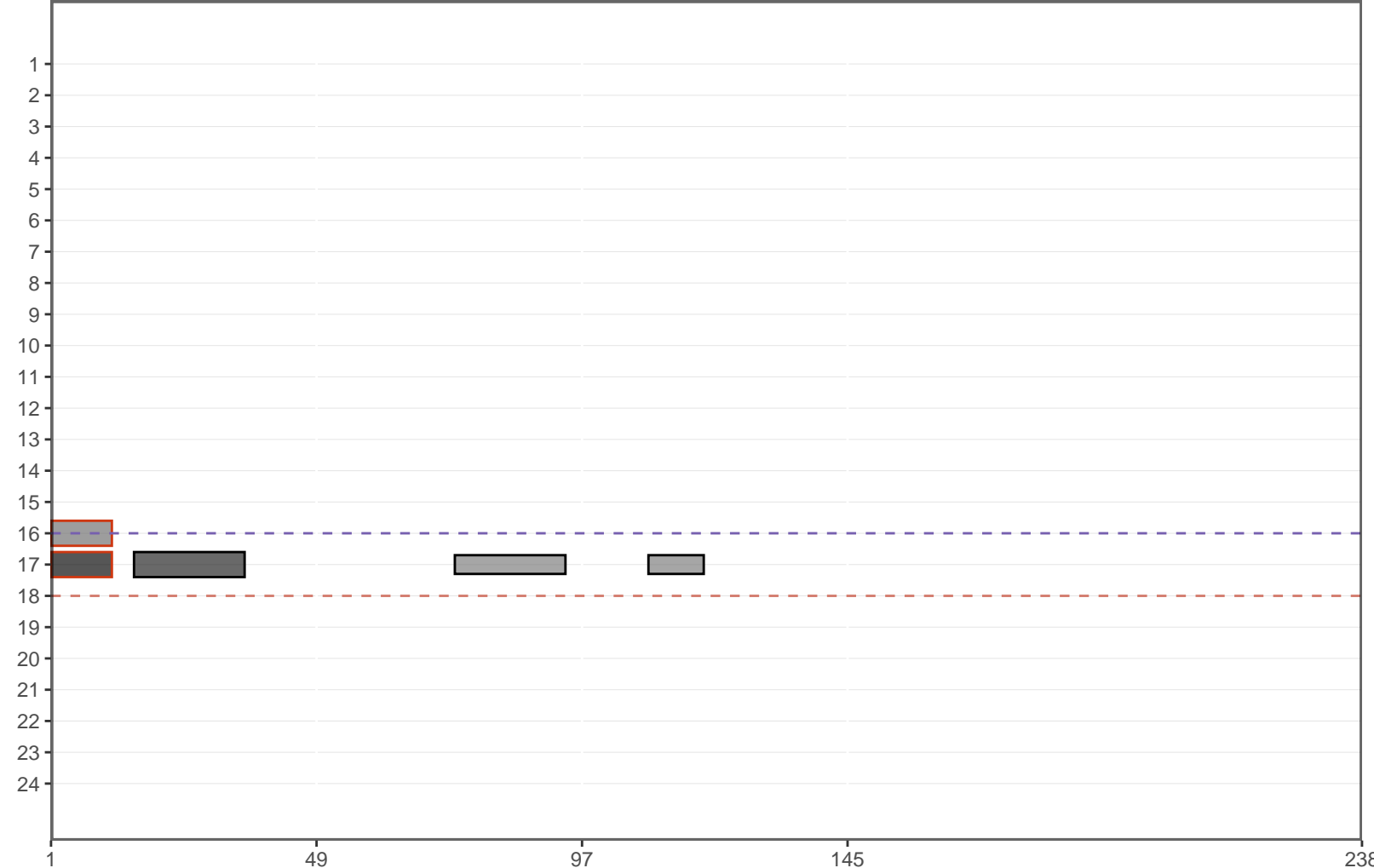
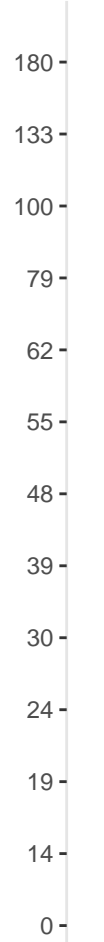
3FSSEKIDFLDNLDFELDNPELHSGNGKGFKPLPLGLAMSDGRHWARIEGEHSGALFDVGEIWEWDSLFASPKVVFHSSGDLRMVYHXYDVEKNGFGIARSRDGMKWLKLGKGGGGKGFDELGMNPHYWRNRKDGKYLVMYEGVDNGERSIGMAISSDGLKGVKRVGDNVAVLKKCEEDRWDSGVSPLVGMDDDDDDHEWRLYRGGVGNKRTGIGMAASGGDEFQDFQRWTFHL

NbL08g11590.1 ribulose-phosphate_3-epimerase_cytoplasmic_isoform-like [MW = 25.7 kDa]



Molecular weight

Gel Slice



Protein sequence:

SRDNYGELLVQCKKSKGKMGKPGVSLKPGTPEEVYVQLDGDGNSVEILVMTVEVPGFGGQKFMPEMMDKVRTLRRKYPBLDEVDGGLGSPSTIEAASBAGANGVYAGSSVFGSPDPQGVISLMRNVEEAGKIS

NbL08g11310.1 alpha-amylase_3_chloroplastic [MW = 101.8 kDa]

No. of times detected



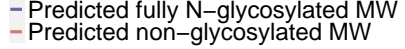
log(intensity)



Values from

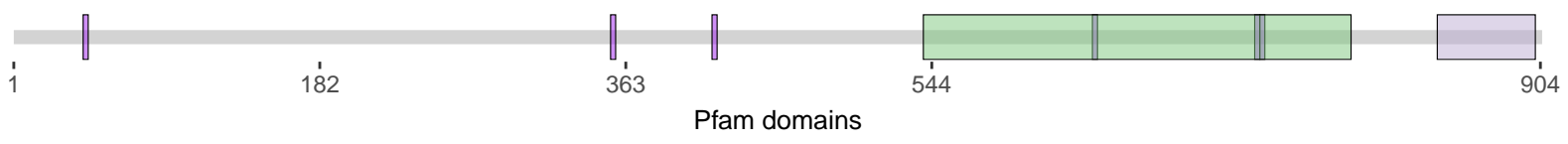
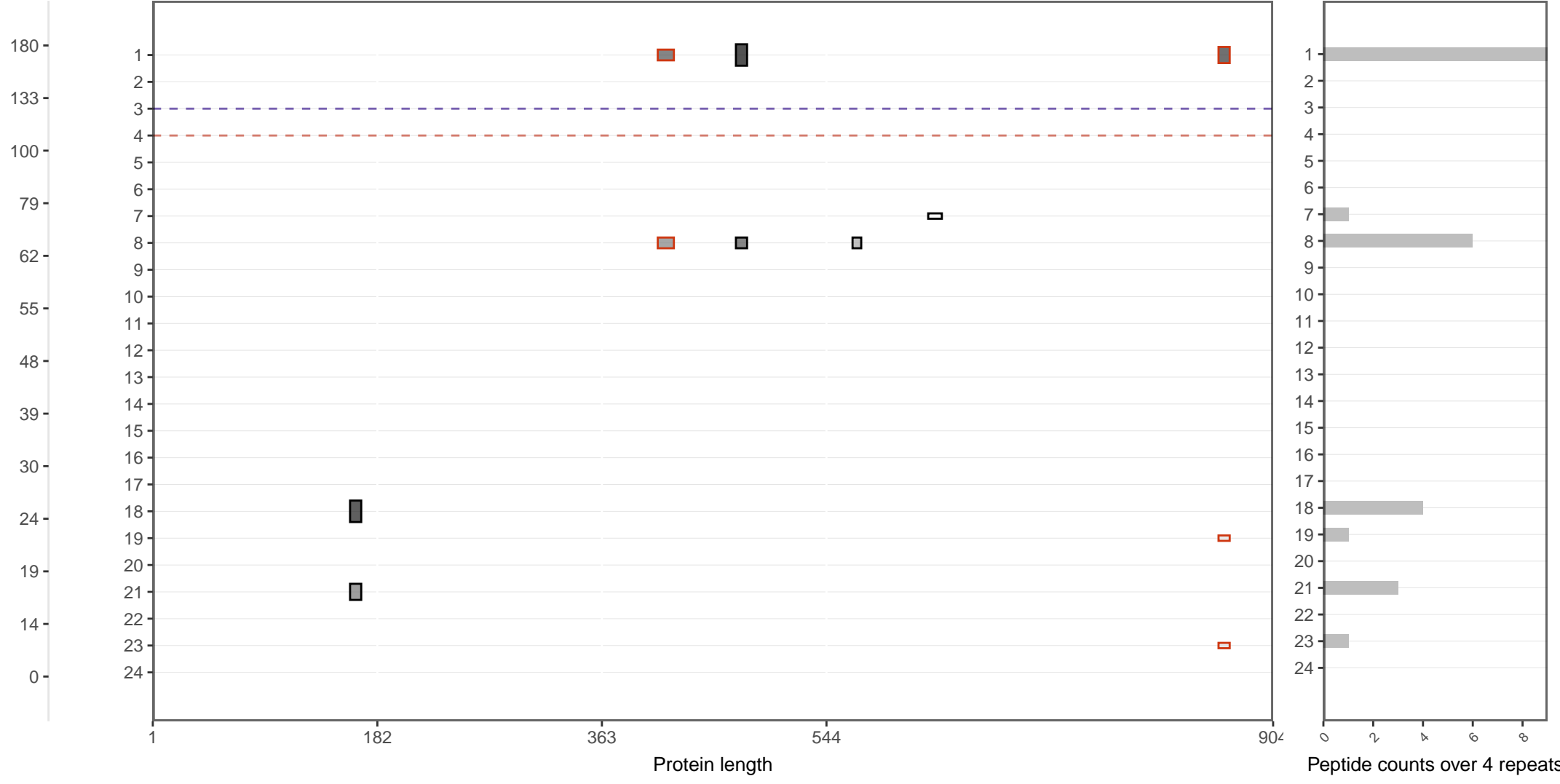


MW indication

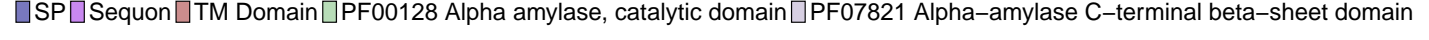


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

TDISSEKSRKTKSKETQENLDEEKLAAEAVSIFRNSIPTBSEDVYVSEAEVSGDPDKVYSSGTGSGFELCOGFNVEHSHKGRWYVELHEKAAELSGIHFVIVLPPPTDGVSPGEMPRDLNLSNRVGSFDELKVTWKFKHEVGVKVLGDVVLNHRGASERNQNGWVFGGRNLWDRVAVADDPHFQGRGNKSSGNFHAAPNDHSGEPFRKDKHWLRWLRREEIGYDGVRLDFRFGFVGGVYKDYLDATPEYFAVGEYWDLSYTYGEMDINQDAHRORVYD

NbL08g11290.1 uncharacterized_LOC109219735 [MW = 42.67 kDa]

No. of times detected



log(intensity)



Values from



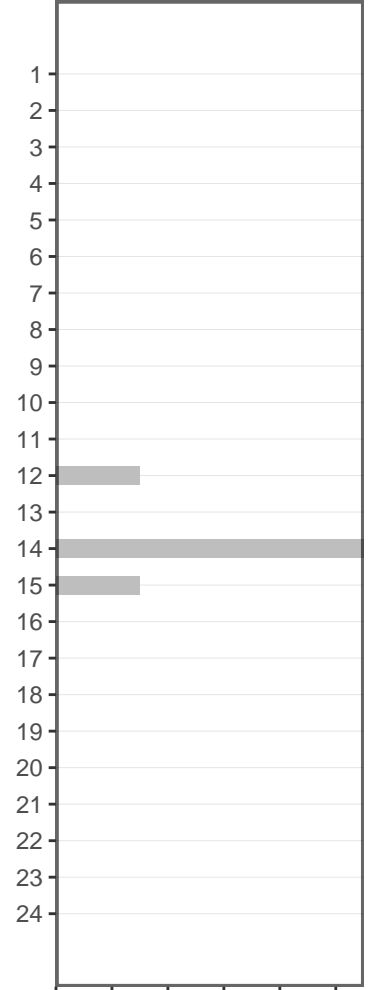
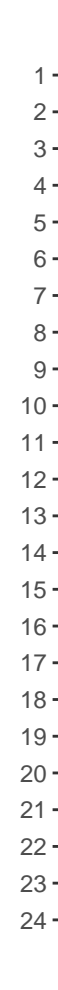
MW indication



Molecular weight

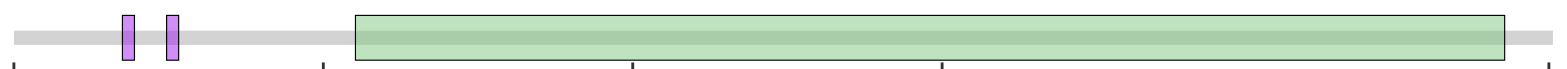


Gel Slice



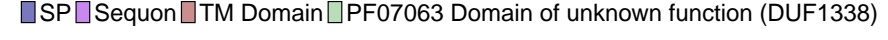
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IRGSGVDDPLPRIFSELLVDQLSPEAGDINKYTDISRCGKEVALASAFGLVWTERPVSSEFQGLARESEYAWTLVNGYALNHVTISHTRLFSIGNLNGFEKTFNLNSEGGLKVPDGLLLGSSVADSTSFQFSDGITEAWPCGVIEFAERLVHPQYKDLPAEEVEEFHRRDGFVSNADKIFESTKDLTRAAV

NbL08g10850.1 serine/threonine-protein_phosphatase_PP2A-2_catalytic_subunit-like [MW = 34.98 kDa]

No. of times detected



log(intensity)



Values from



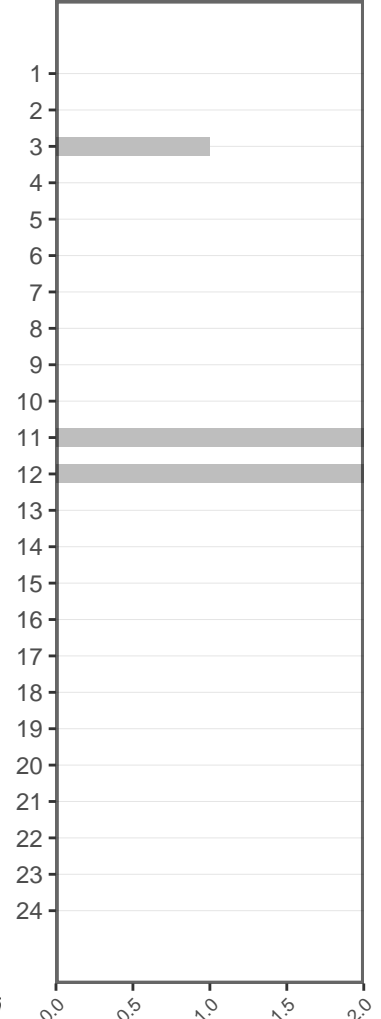
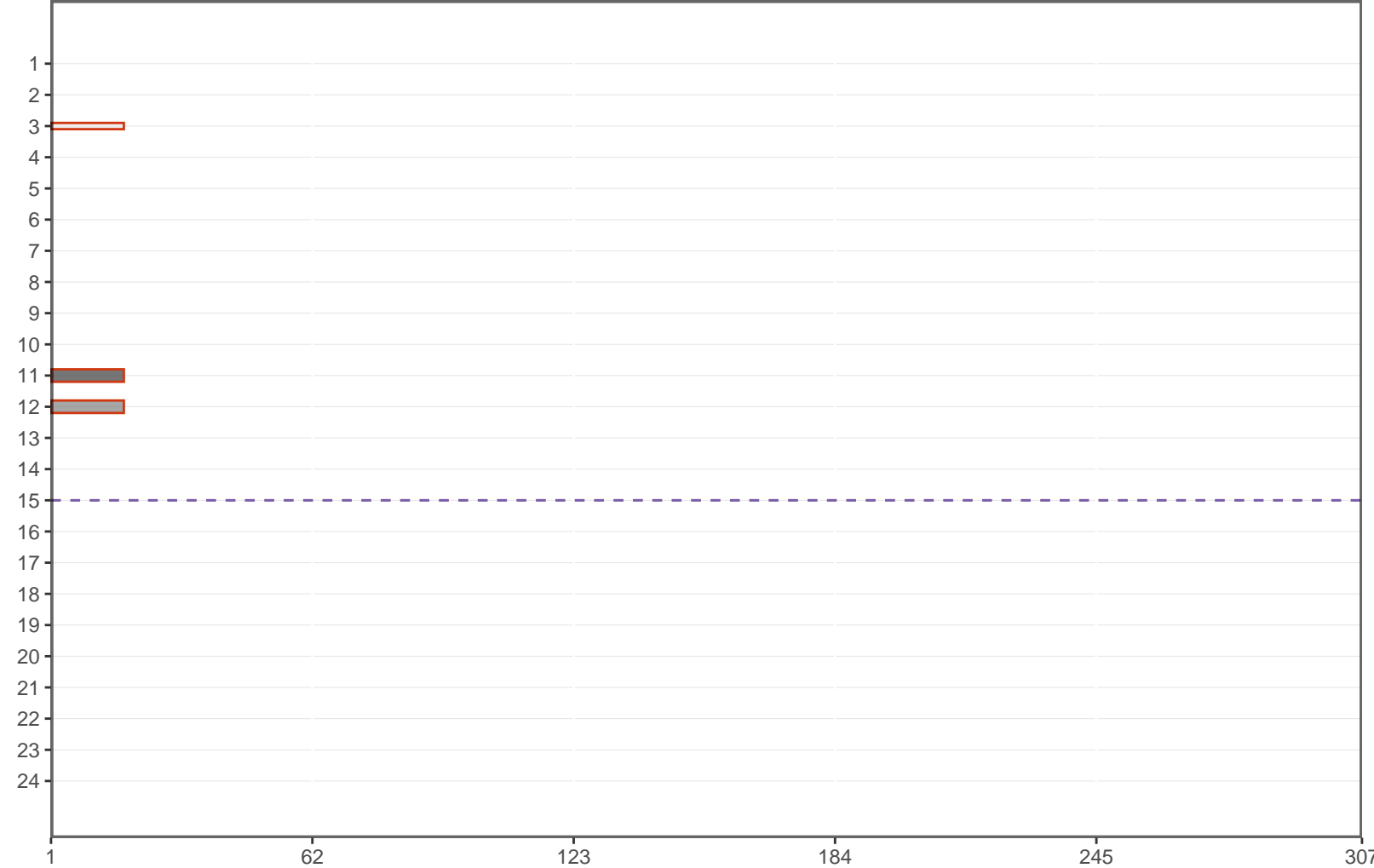
MW indication



Molecular weight



Gel Slice

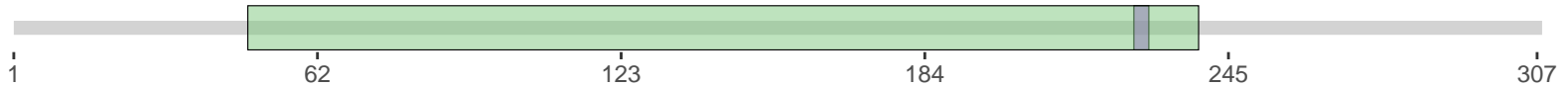


Protein length

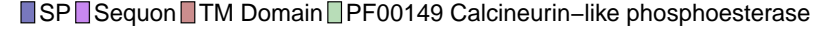


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IKHFTDLFDYLFPLTAIEGQIFGLHGGLEPSELDLDIRALDRIGVEVPEHEGFMCDLLWSDPDRGRGWGISPRGAGYTFGDDASGFNHTNGLTLISRAHQLMVEGFNMGDDKNVYTVFSAFNYCYRRCGNMAALEIGENMEGFLGDFDPRGIEPDTTRKTPDFL

NbL08g10780.1 pyruvate_dehydrogenase_E1_component_subunit_alpha_mitochondrial-like [MW = 44 kDa]

No. of times detected



log(intensity)



Values from



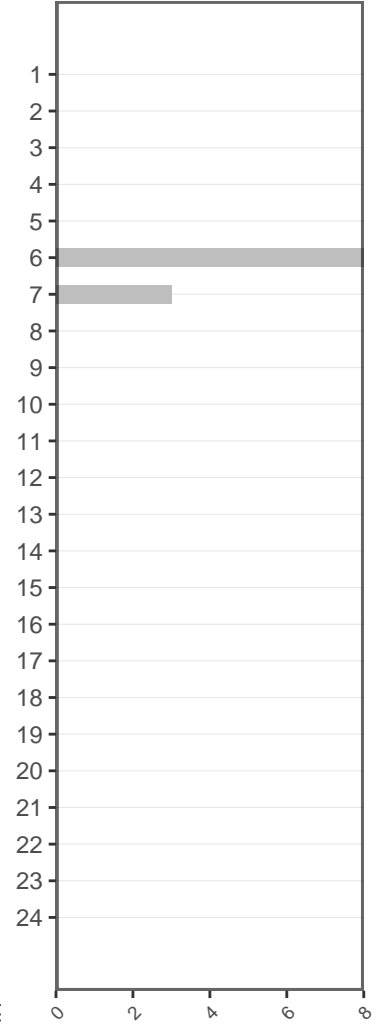
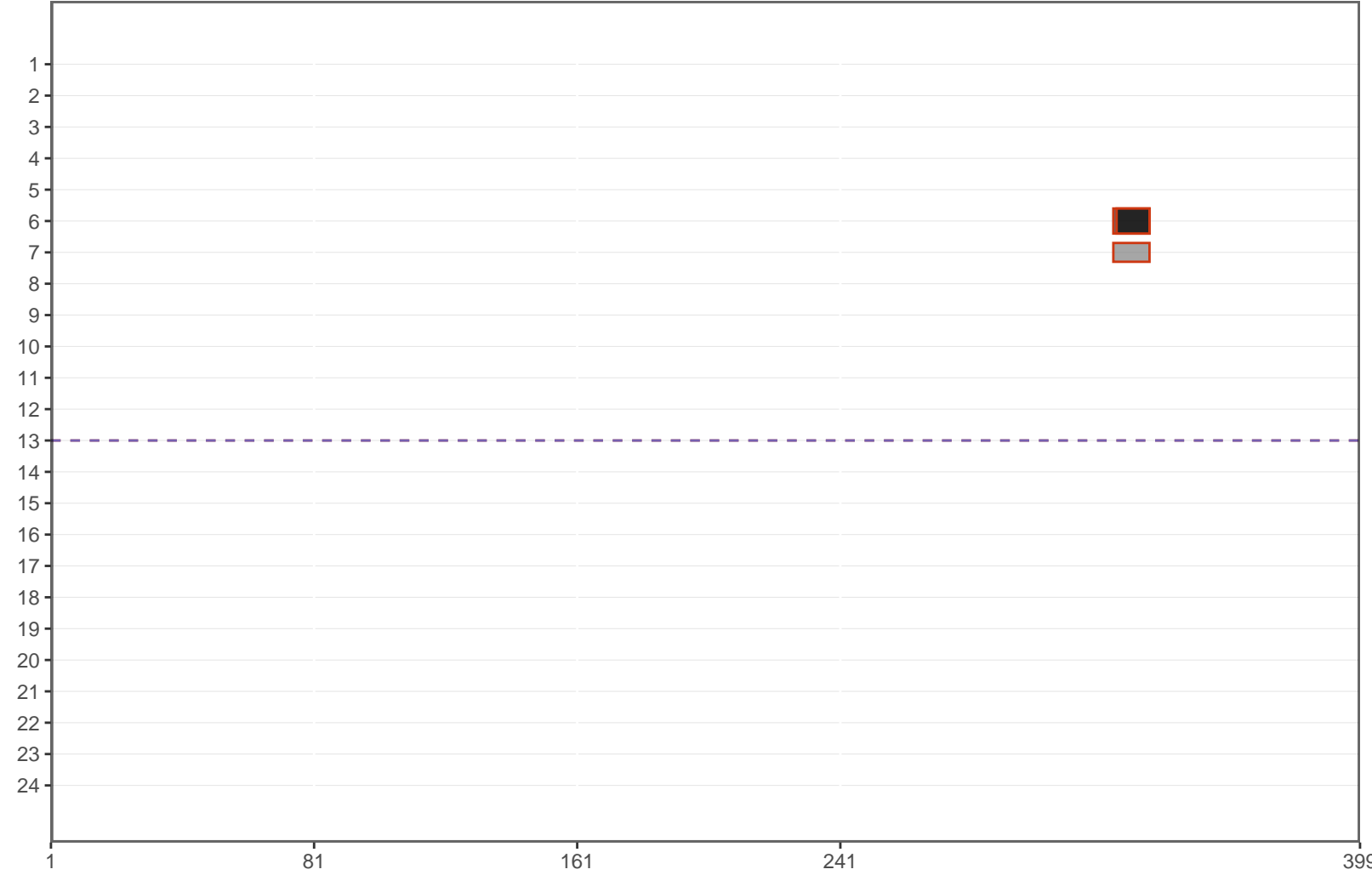
MW indication



Molecular weight



Gel Slice

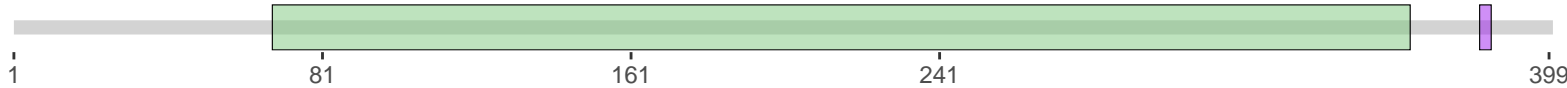


1 81 161 241 399

Protein length

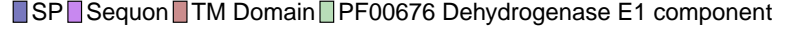
0 2 4 6 8

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KEEIHVSFAMYCDGAANGGLFEALNMAALWDLPAIIVGNNHYGMGTAEWRAAKRFAYYKRGDHYVPLGKVDGMDALAVKQACKFAKEHALKNGPILEMDTYRYHGHSMDFGQSTVYRTRDEISGVRRGDRPIERIRKLLAHDIAATEKELKDKIEKRRKVDIAIAAKESFMPDPELFTNYYVYKGFQVVEVCGNSNHFIPKLFYGGII

NbL08g10270.1 glyceraldehyde-3-phosphate_dehydrogenase_cytosolic [MW = 36.36 kDa]

No. of times detected



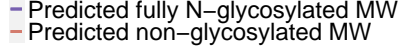
log(intensity)



Values from



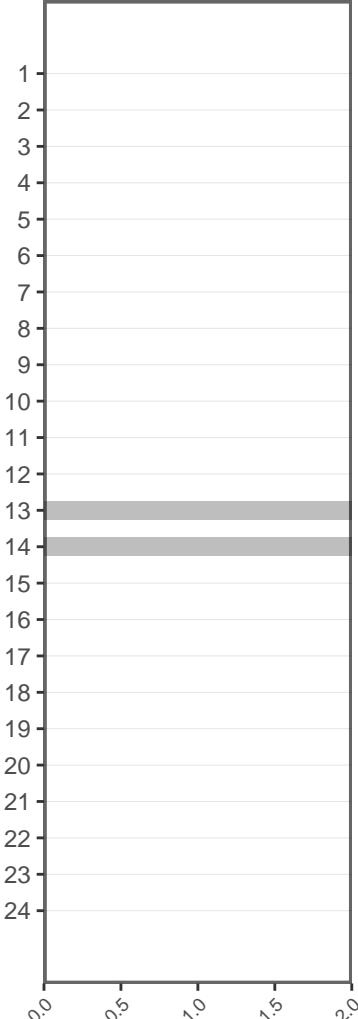
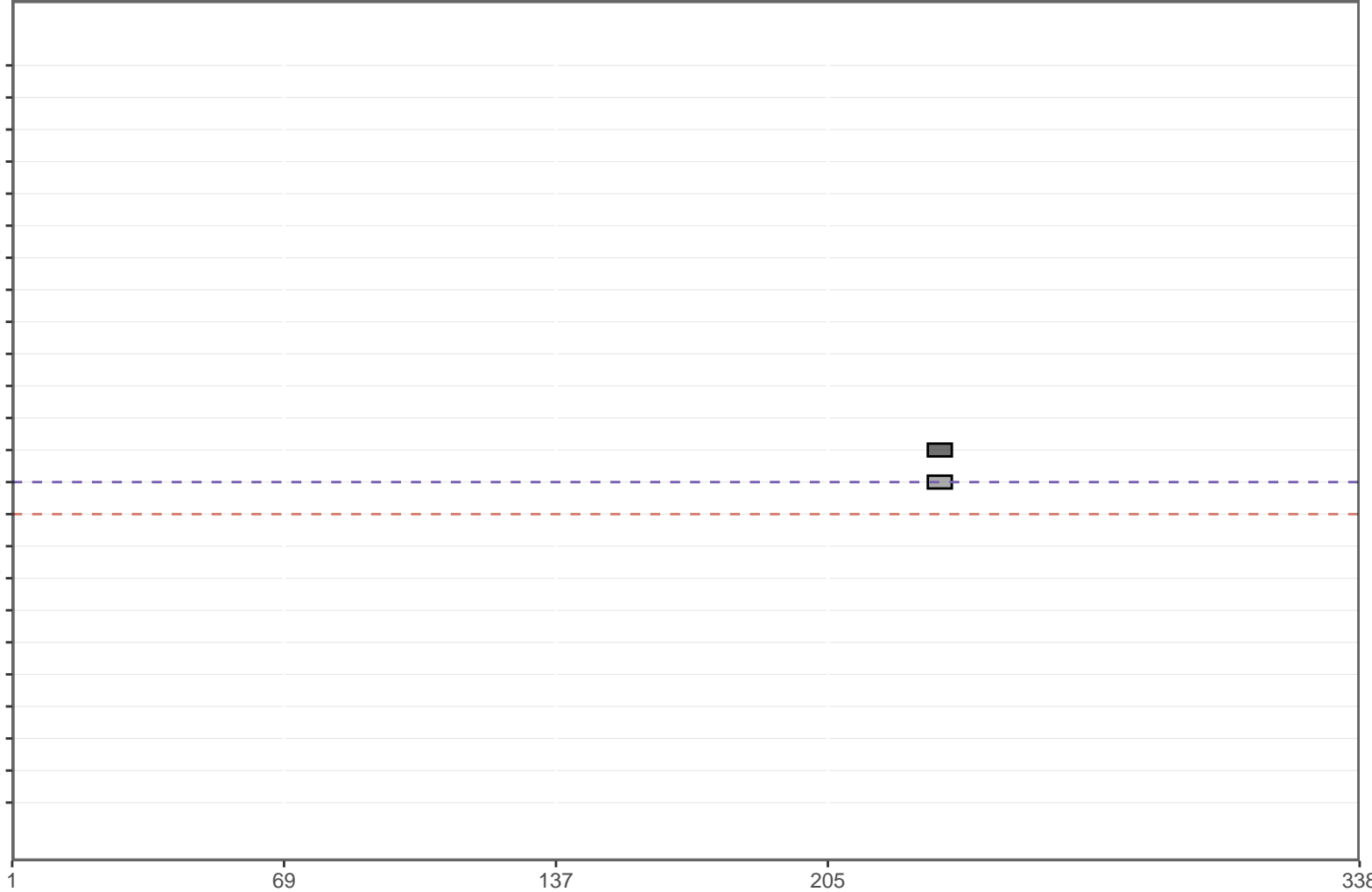
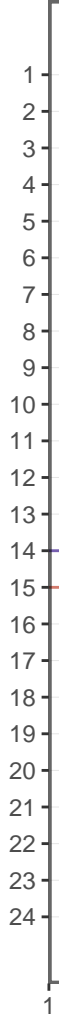
MW indication



Molecular weight

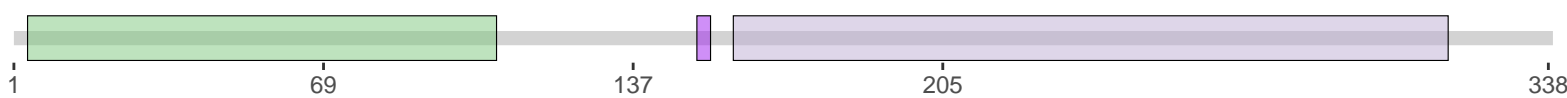


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

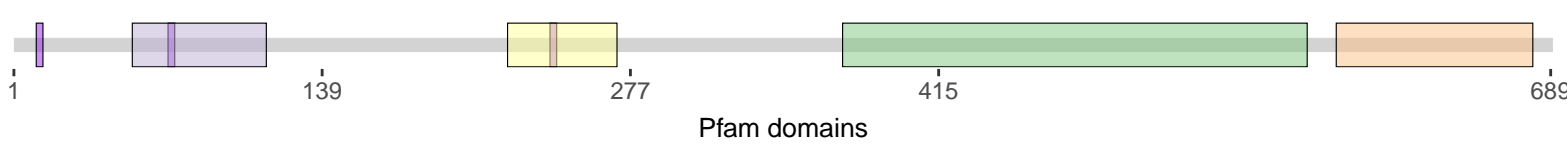
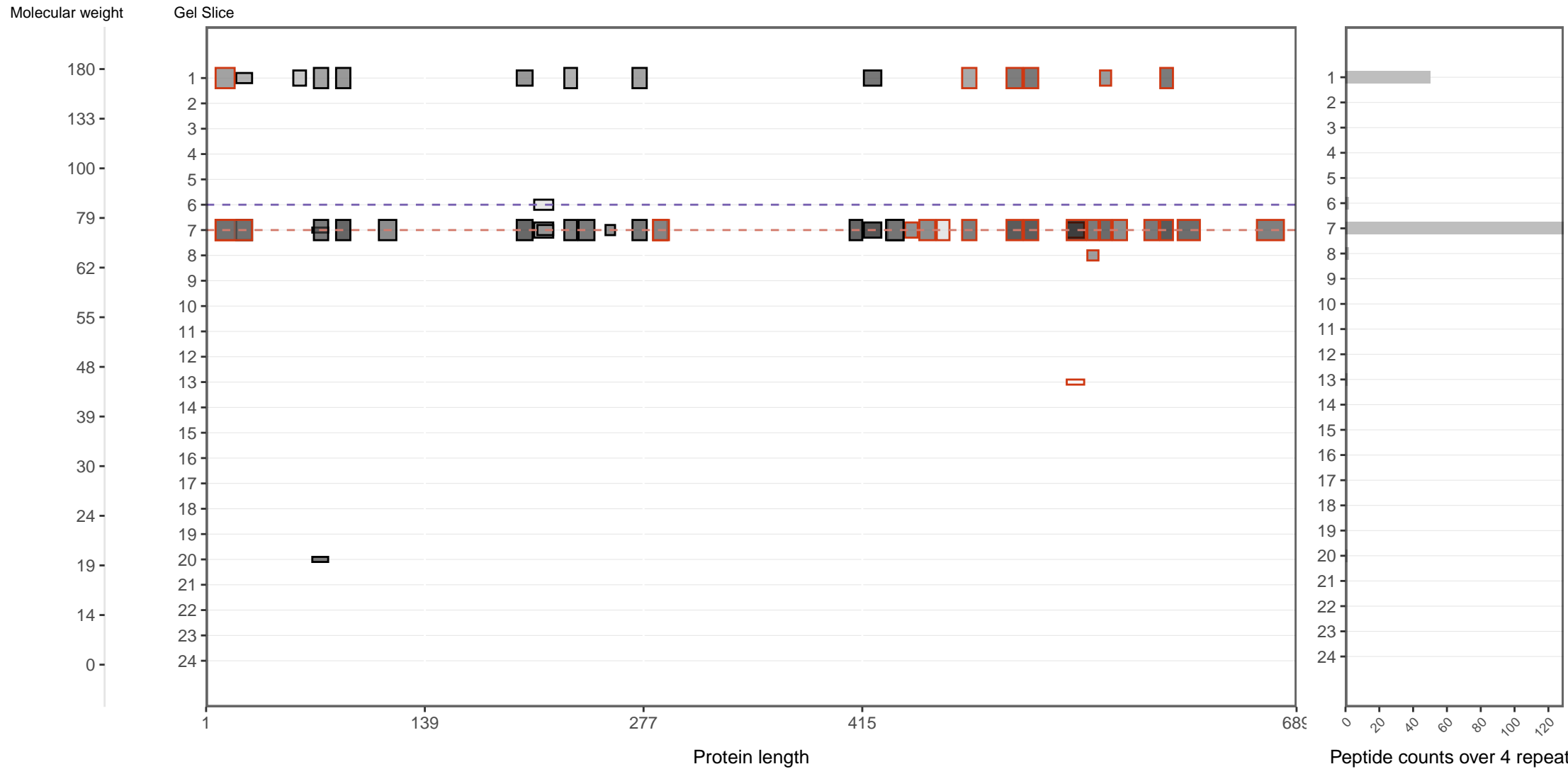
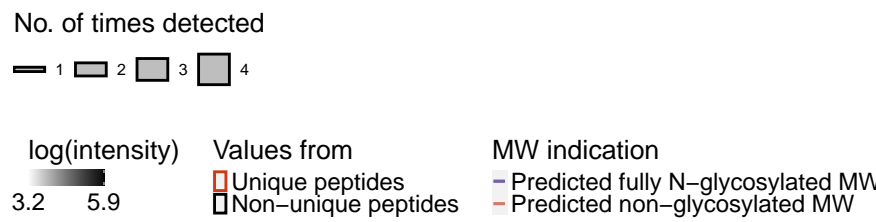
Pfam Description

- SP Sequon TM Domain PF00044 Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain PF02800 Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain

Protein sequence:

TTNCLAPLAKVINDKFGIVEGLMTTVHSRATQKTVDGRPMKDWFRGAAAHNIPSSGAAKAGKVLPLNGKLTGMFRVPTVDVSVVDLRLAKAATYDEKAAKAESEGNKMGILGYSEDDVVSDFVGDGRSSIFDAKAGIALNGNFVKKVSVWYDNEWGYSNRVLDLRHMATVA

NbL08g10230.1 threonine--tRNA_ligase_mitochondrial_1 [MW = 79.01 kDa]



- Pfam Description
- SP
 - Sequon
 - TM Domain
 - PF00587 tRNA synthetase class II core domain (G, H, P, S and T)
 - PF02824 TGS domain
 - PF03129 Anticodon binding domain
 - PF07973 Threonyl and Alanyl tRNA synthetase second additional domain

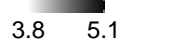
Protein sequence:
 SQIYKRGVEEVWSPMMYNAQLWETSQAANNKENMVEFDKIQEFLKPMNCPGICLFDHVRVSYRELPLRLADFGVLRHNEASGALGTLRVRRFGQDDAHIFCRGQKIDVYKGLDFISVYKIFGFTFDLKLSTPPEKYLGOLESWNAEDAALAEALDEFQKPEWKEGGDGFYGNKIDVSDAMRRKFGQATLQLDLPQRPORFNLYSAEDENKRERFVAMHRAILGVSVERMFAILLEHFKGKWPFWLSPROAMVGPVSDKGGVVALELRERHIDAGYYVDV

NbL08g10050.1 aldehyde_dehydrogenase_family_2_member_B7_mitochondrial-like [MW = 58.6 kDa]

No. of times detected



log(intensity)



Values from



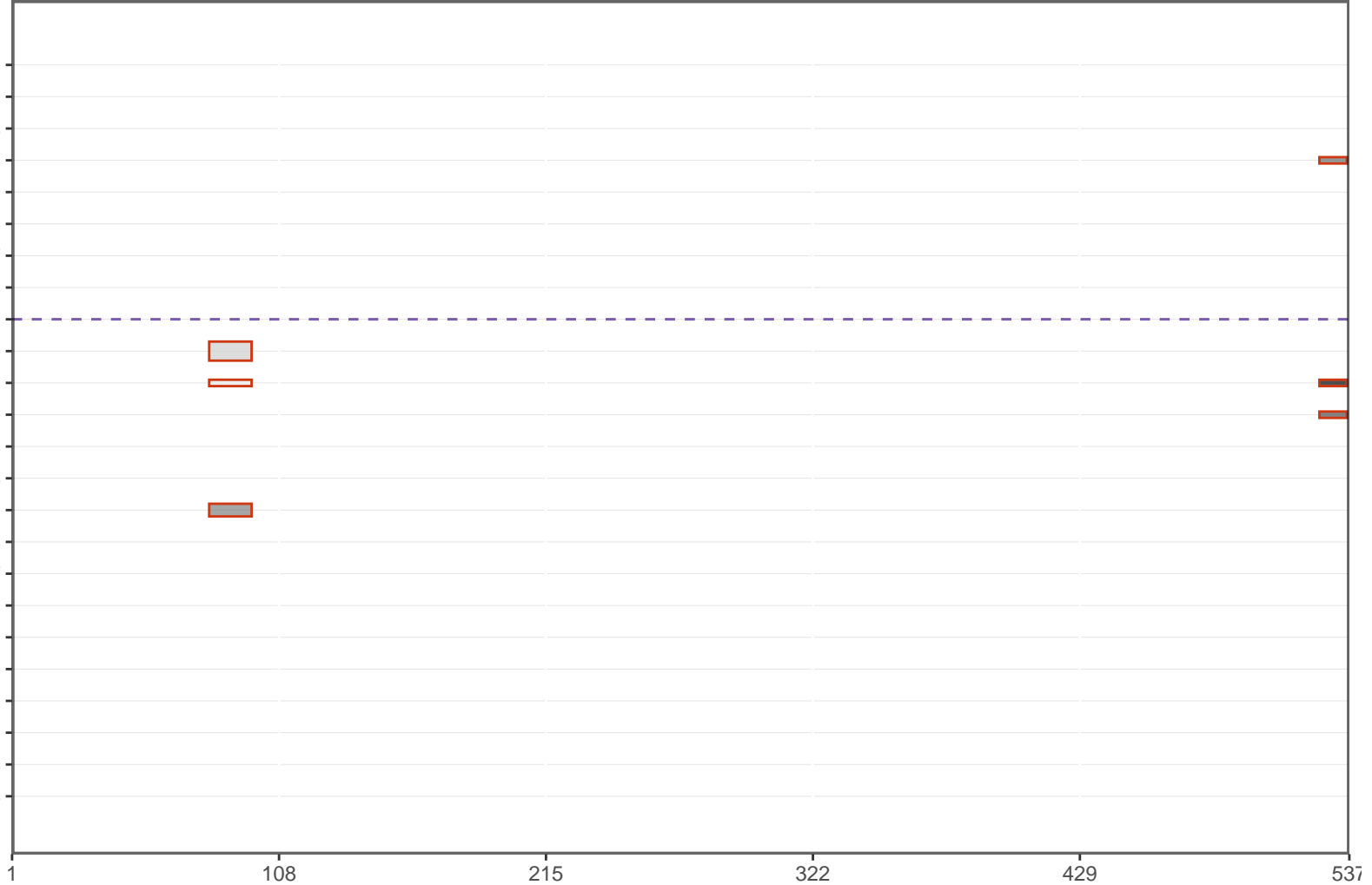
MW indication



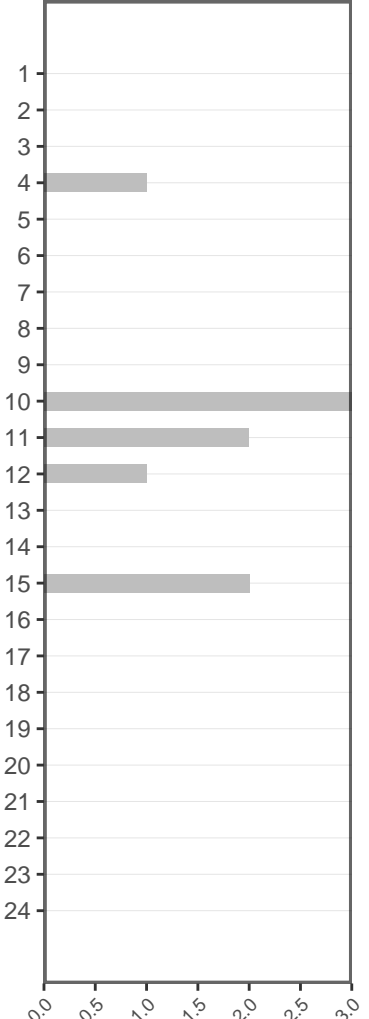
Molecular weight



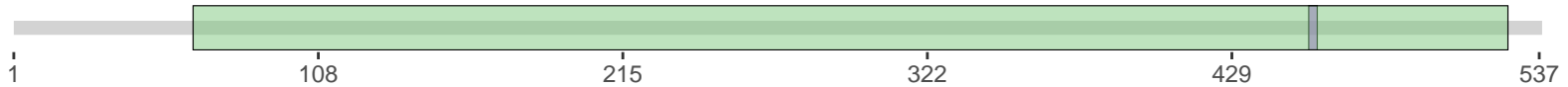
Gel Slice



Protein length

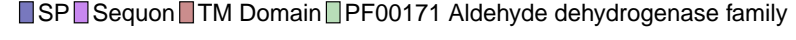


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

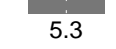
IGFGPTAGAPLCSHMDVYKLAFTGGSDTQKALSLAAKSNLKPVLELGGKSPFVCEADADITAVEQAHFALFFNQGQCGGASGRVYHEKVVDEFLEKAKARLRKRVYDPPKSGTEGGPQIDSKGDKIMNVRGINSGATLETGGERLGERGVYKPTVFSNFKDDMLAQDDEFGPVQSLKFKDLDDVRRANRKYGLAAGVFTQNDTANTLTRALRVGTWVYNGDFDQATFFGGYKMSGHGREKGEYSLKNVGLQKAVVPLKNPALV--

NbL08g10040.1 40S_ribosomal_protein_S16 [MW = 16.7 kDa]

No. of times detected



log(intensity)



Values from



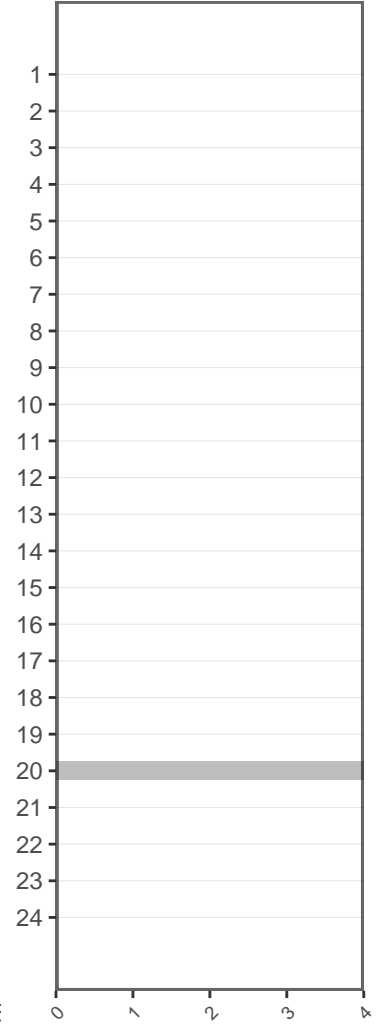
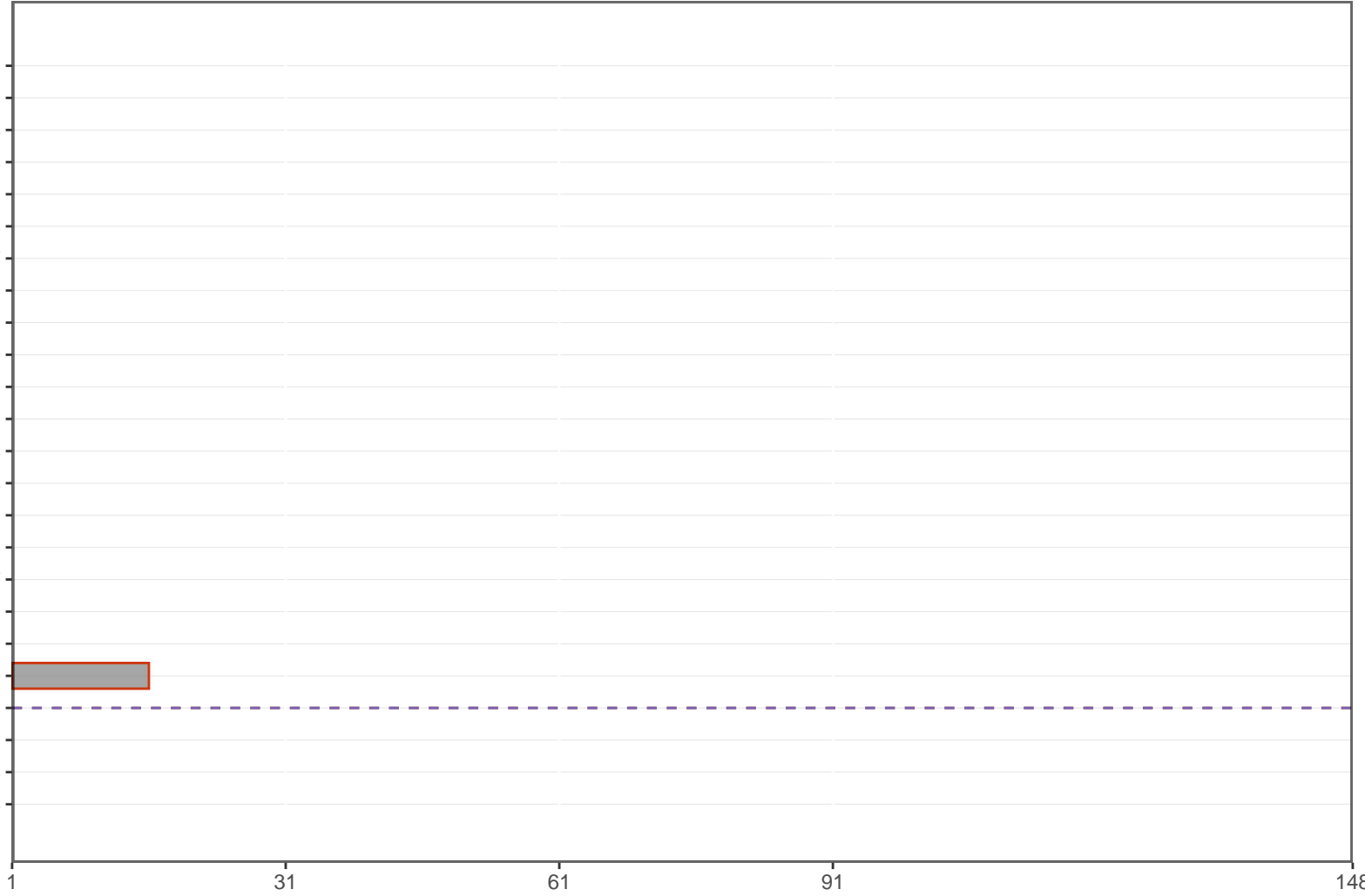
MW indication



Molecular weight

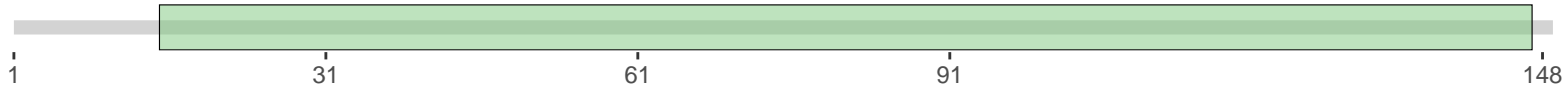


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

HRFAGVDMRIRVYGGGHTSQVIRGSAKALWAFYQKYVDEGQKKEKDLVRYDRTLLVADPRRCEPKVFGGRGARARFGKSYR

NbL08g09860.1 uncharacterized_protein_At4g28440-like [MW = 18.07 kDa]

No. of times detected



log(intensity)



Values from



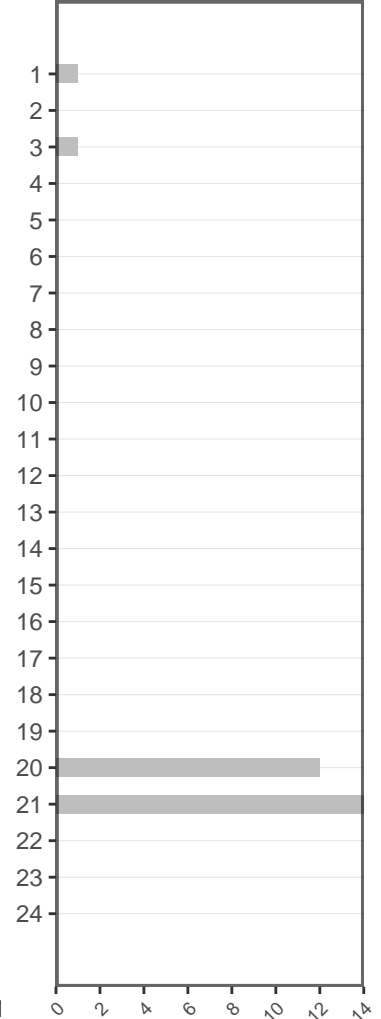
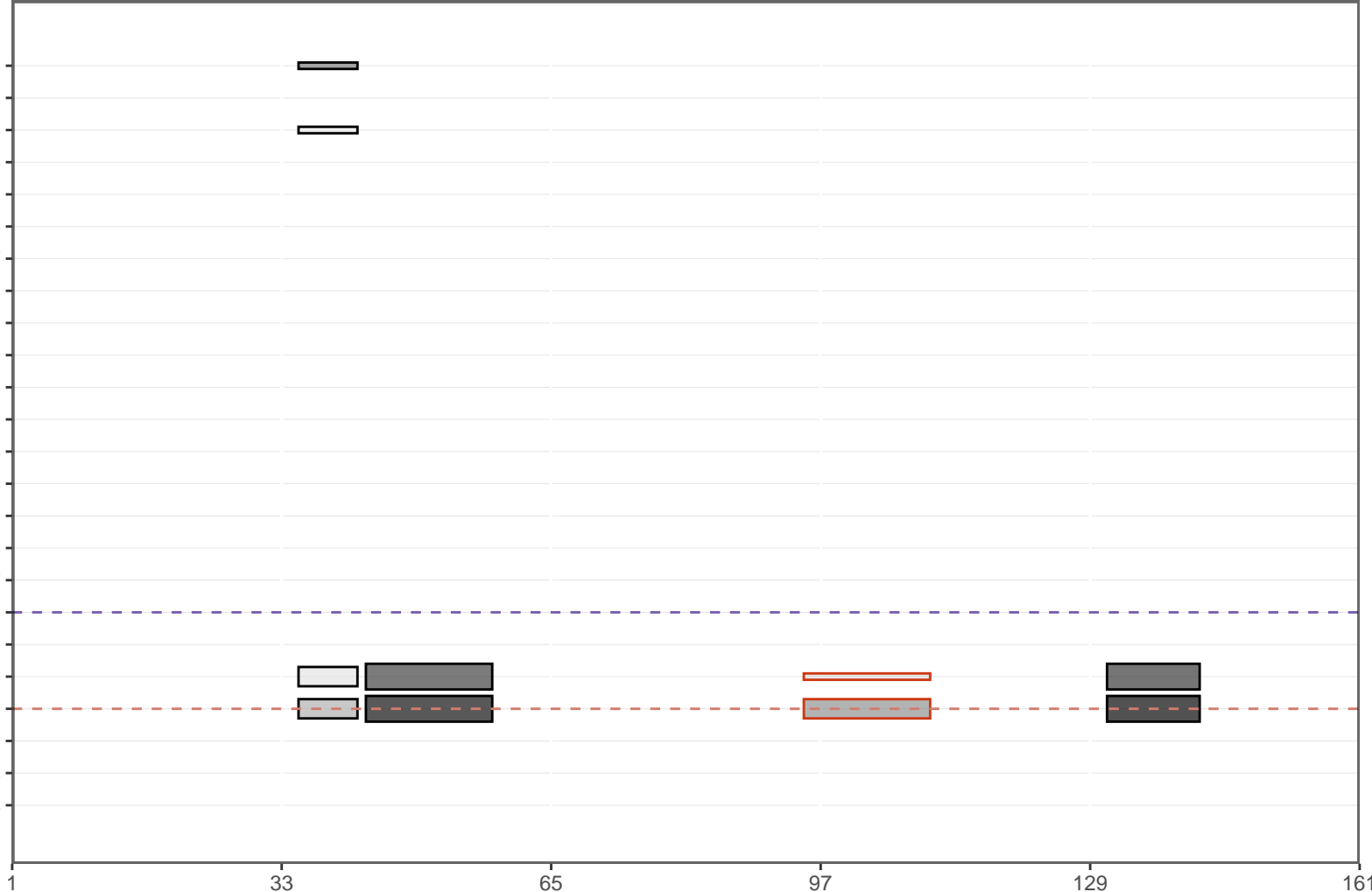
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RGNGSRMRLAELGLVSDFTGMIFATRNDDQEMMTEGATVLRNKAIDMFKGSMRLAVDRWGRVETPASFVSKEDNNLLEIEFGQTVVEG

NbL08g09850.1 carbonic_anhydrase_2-like [MW = 34.59 kDa]

No. of times detected



log(intensity)



Values from



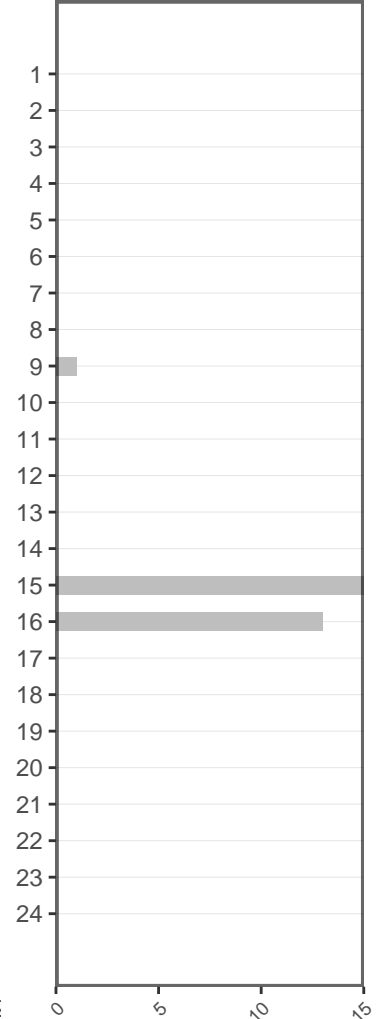
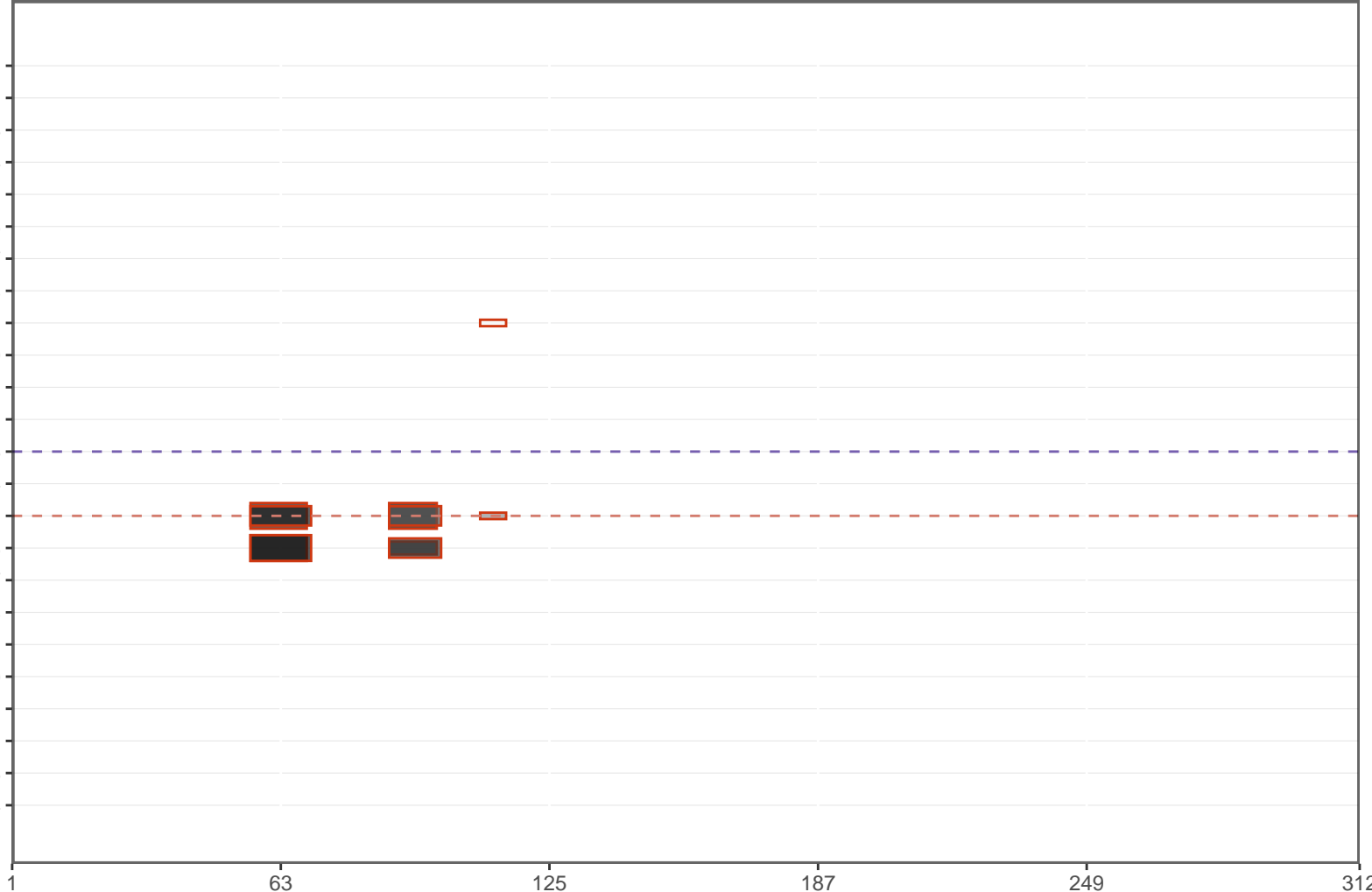
MW indication



Molecular weight

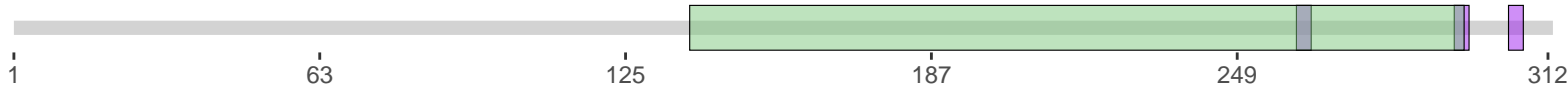


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

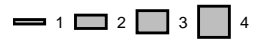


Protein sequence:

DSRVCPSHLNFQDGEAFVVRNANMYPFDGTYKYGSGAAVEWVYHLKVENLVGHSGGGKGLMSPDGGSTNSDFREWVKGLPAKAKVKAEGCHLDPTTEGQTKLEKAVNWSLGNLLTYPFVREAVVQKSLAKGGHYDFVNGSFELWIDFNLTPEVSL*

NbL08g09830.1 2-methylene-furan-3-one_reductase [MW = 41.2 kDa]

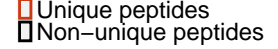
No. of times detected



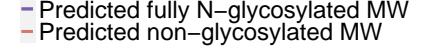
log(intensity)



Values from

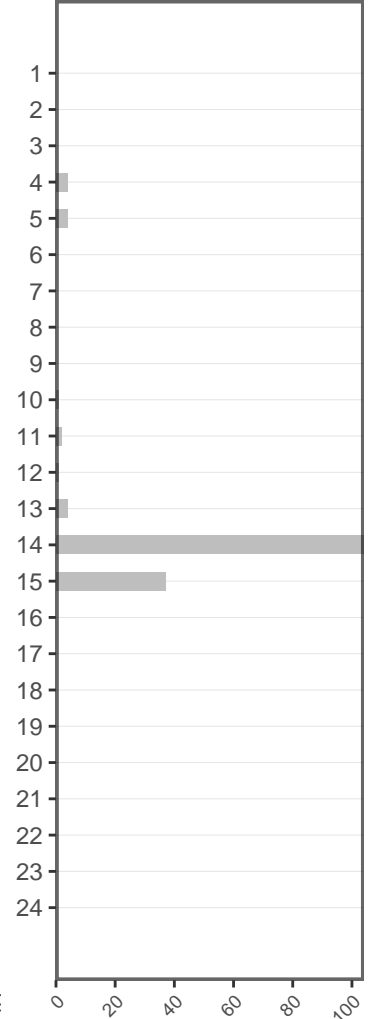
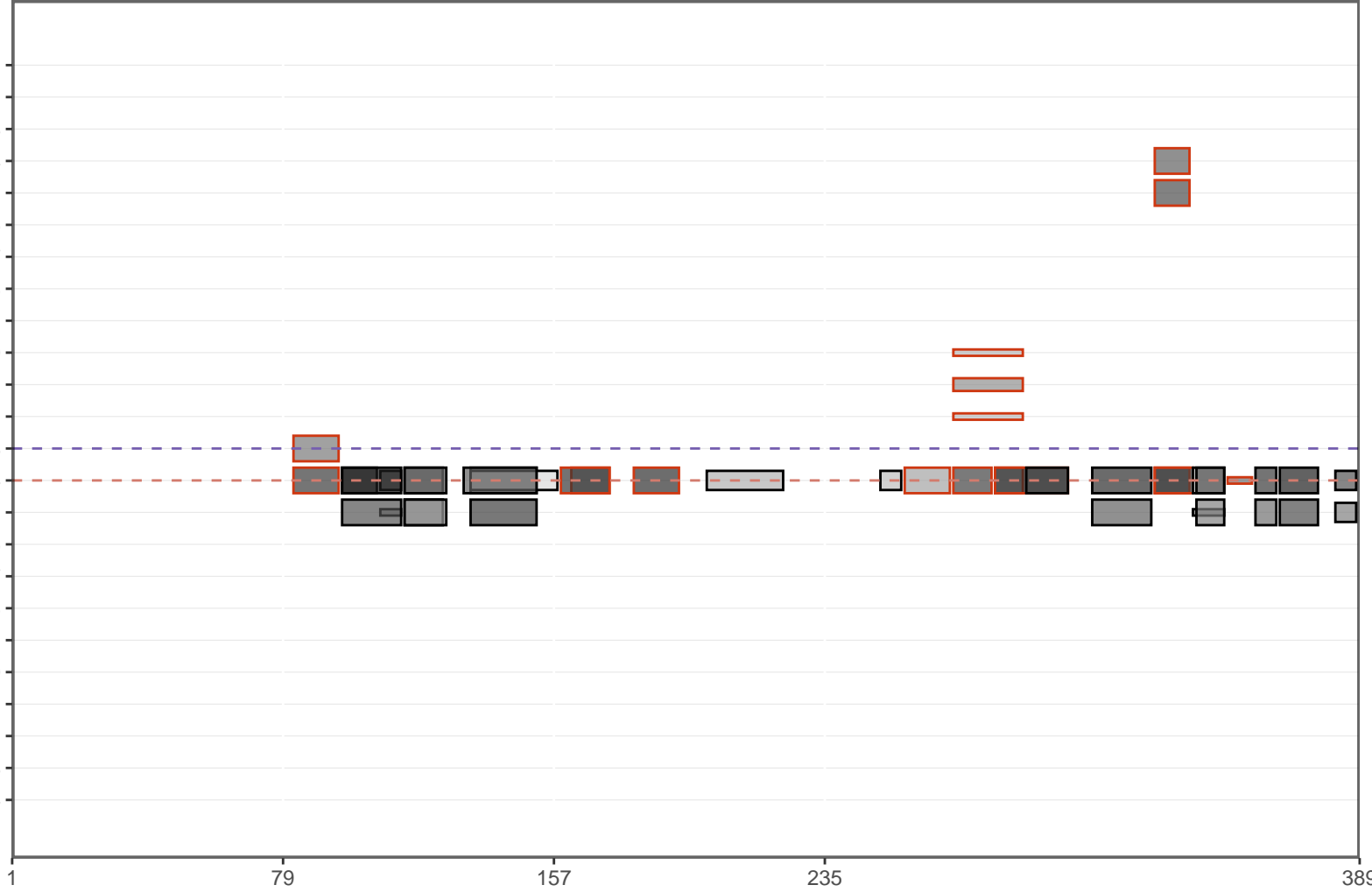
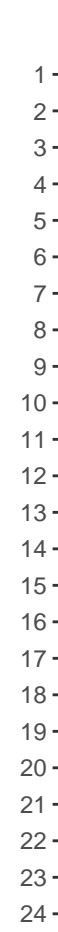


MW indication



Molecular weight

Gel Slice



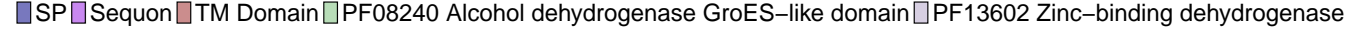
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DFGSLAEYTAVEENKLVAKPKNLGFAEASGLPLAETAVVEGLEKAGFSAQKSLVLDGAGVGSLSLVQKXKHVFGASKVAATSETGKLDLKLKSLGADLADYTKENFEDLPEKFDVVDYDTVGGGEKAKKAVKEGGSVAALVTGAVTPPGFRFRVTSNAEMLKIKPKYLEGGKTPVDPKGPFDFDKVEAFSLYLETGRATGKVVHPII

NbL08g09690.1 pyrrolidone-carboxylate_peptidase-like [MW = 23.64 kDa]

No. of times detected



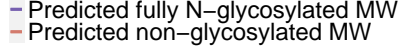
log(intensity)



Values from



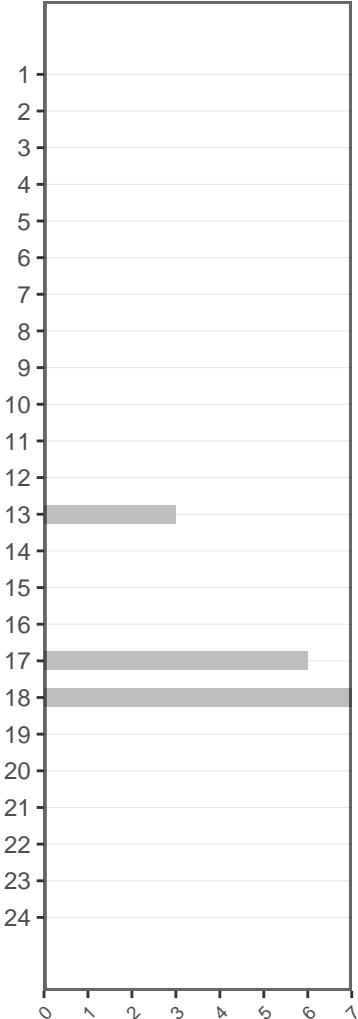
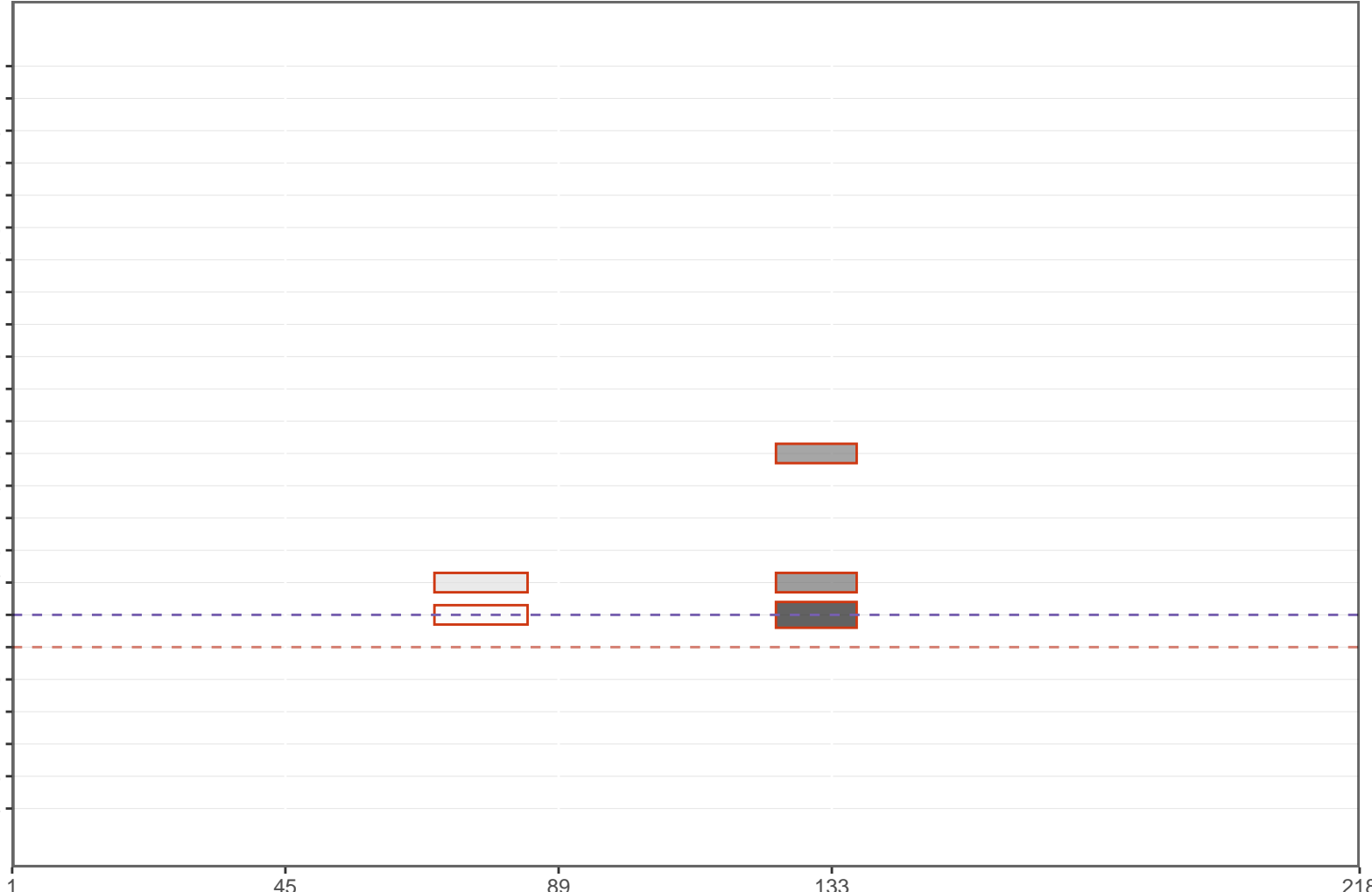
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

STKFAIERLAVNEAFRRGAEDELGWQRPRLPVPEFDGGINGARKTSGSAEGILEFLKKKGFVETMSDDAGRFDVNYVYHSLRFAEKKGHSIFVHVPTFRVWQETQMEFVWALLEAAATG

NbL08g09670.1 14-dihydroxy-2-naphthoyl-CoA_synthase_peroxisomal-like [MW = 36.72 kDa]

No. of times detected



log(intensity)



Values from



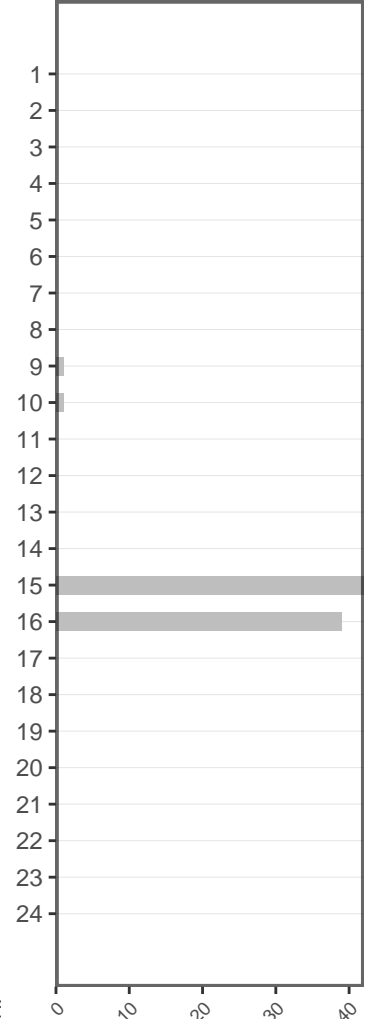
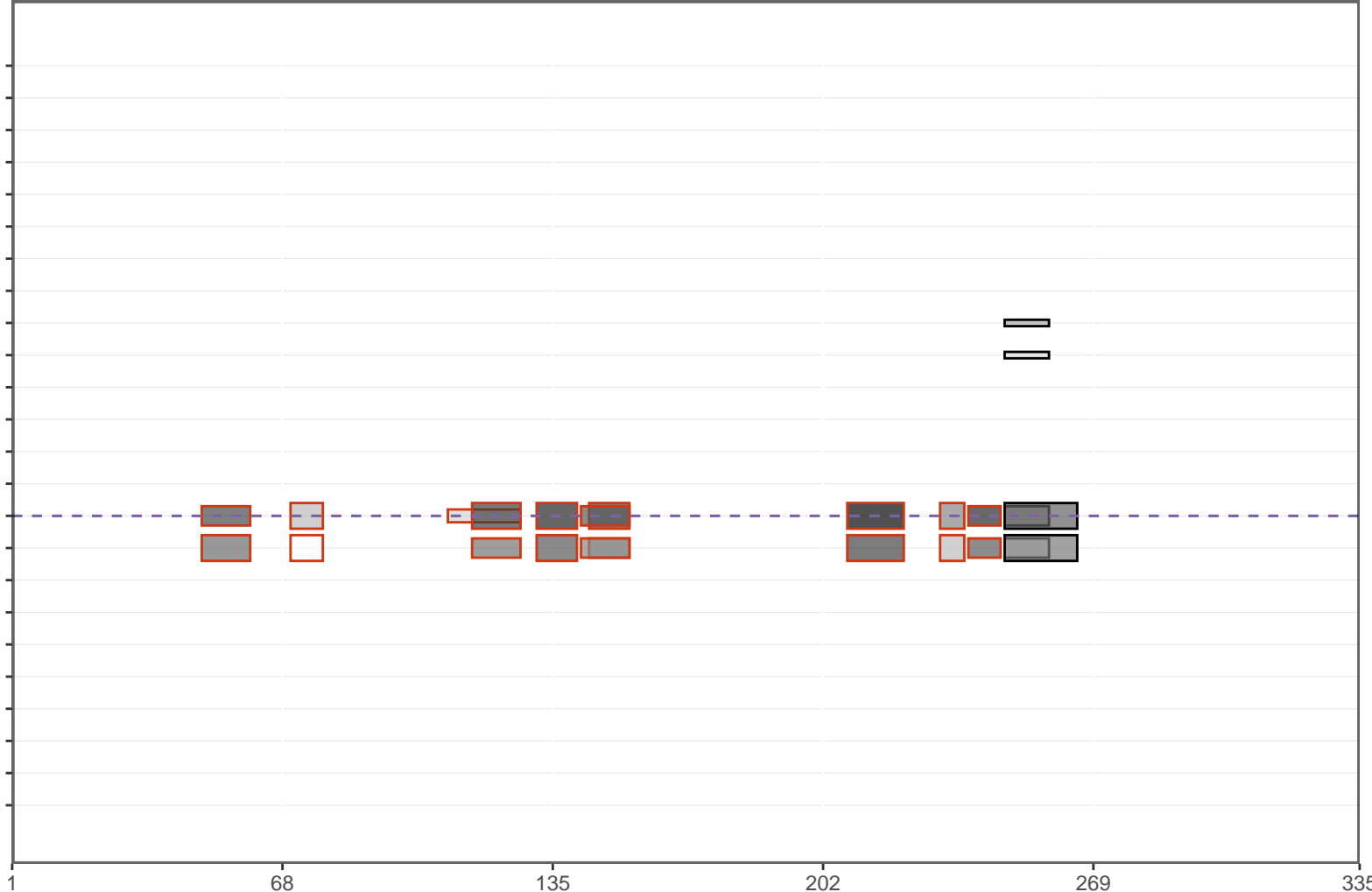
MW indication



Molecular weight

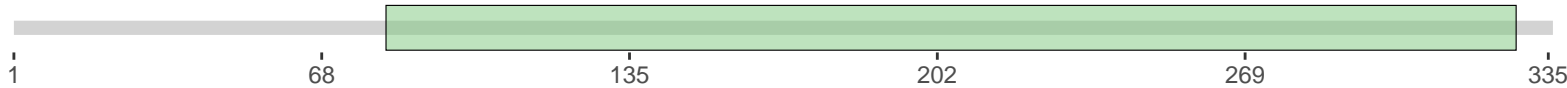


Gel Slice



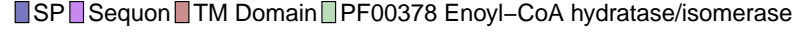
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NVLDLQVQIRLRPKPVAAMVAGYVGGHILMVCDLTAADNAIFGGTGRKVGDFDAGYSSMSRVLVGPVKAREMVFTRFYTASEAEHMGVNTVPLDKLEGETRWGRELRNSPTAIRVUKSALNWDGHHAGLOGLDGDTLLFYGTETEGEGKNAVNERRRPDKFKRPLP

NbL08g09640.1 ATP-citrate_synthase_alpha_chain_protein_2 [MW = 46.53 kDa]

No. of times detected



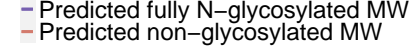
log(intensity)



Values from



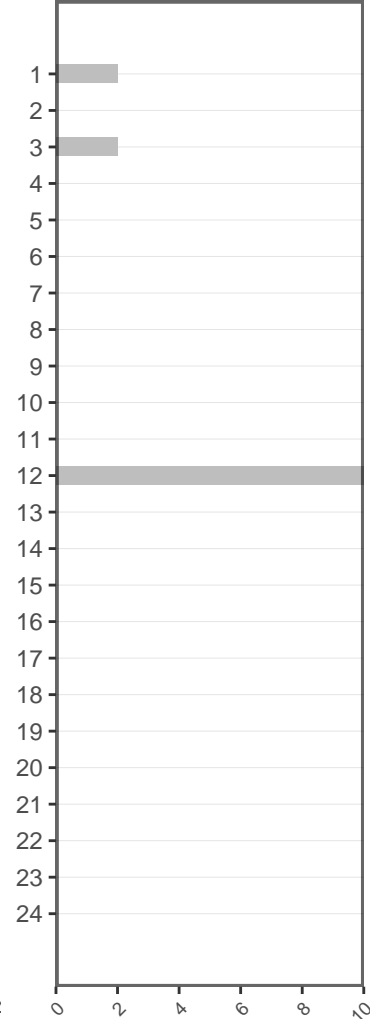
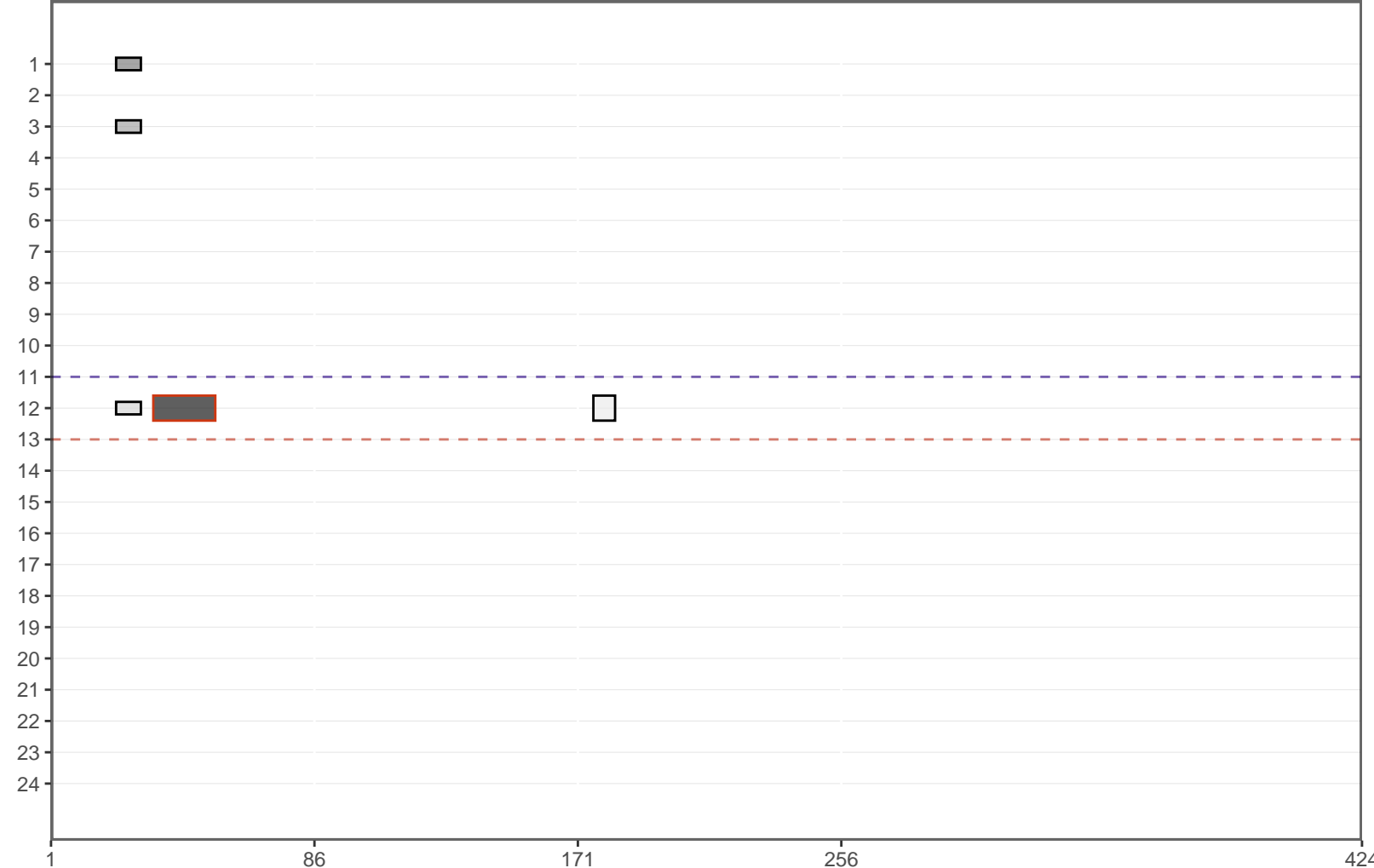
MW indication



Molecular weight



Gel Slice



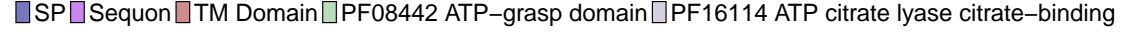
Protein length

Peptide counts over 4 repeats



Pfam domains

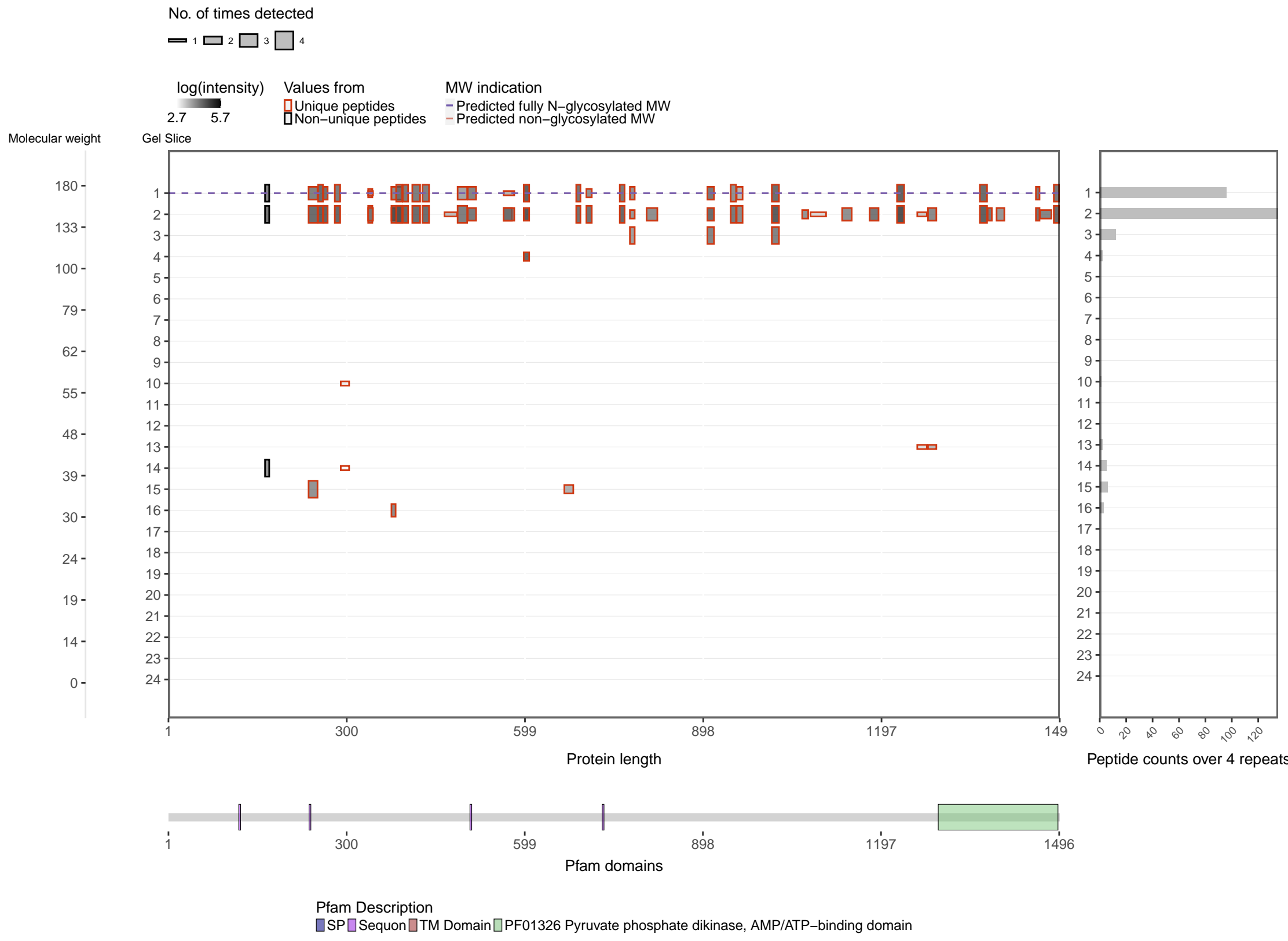
Pfam Description



Protein sequence:

INPFAIVEGKPYPLDMRGELEDDTAFAFNFKWGNIEFPLPFGFRVMSATEFRIHGLDEKTSASLKFTVLPKGRWMTMVAAGGGASVYADTVGDLGYSSELGNYAEVSGAPNEEVLQVARVVIDCATANPDGRKRRAIVGGGIANFTDVAATFSGHRALKEKEKSLKAARMQIFVRRGGFNVYQKGLAKMRSLSGEEIGPIEVYGPATMTGICKQAEIGTPAA

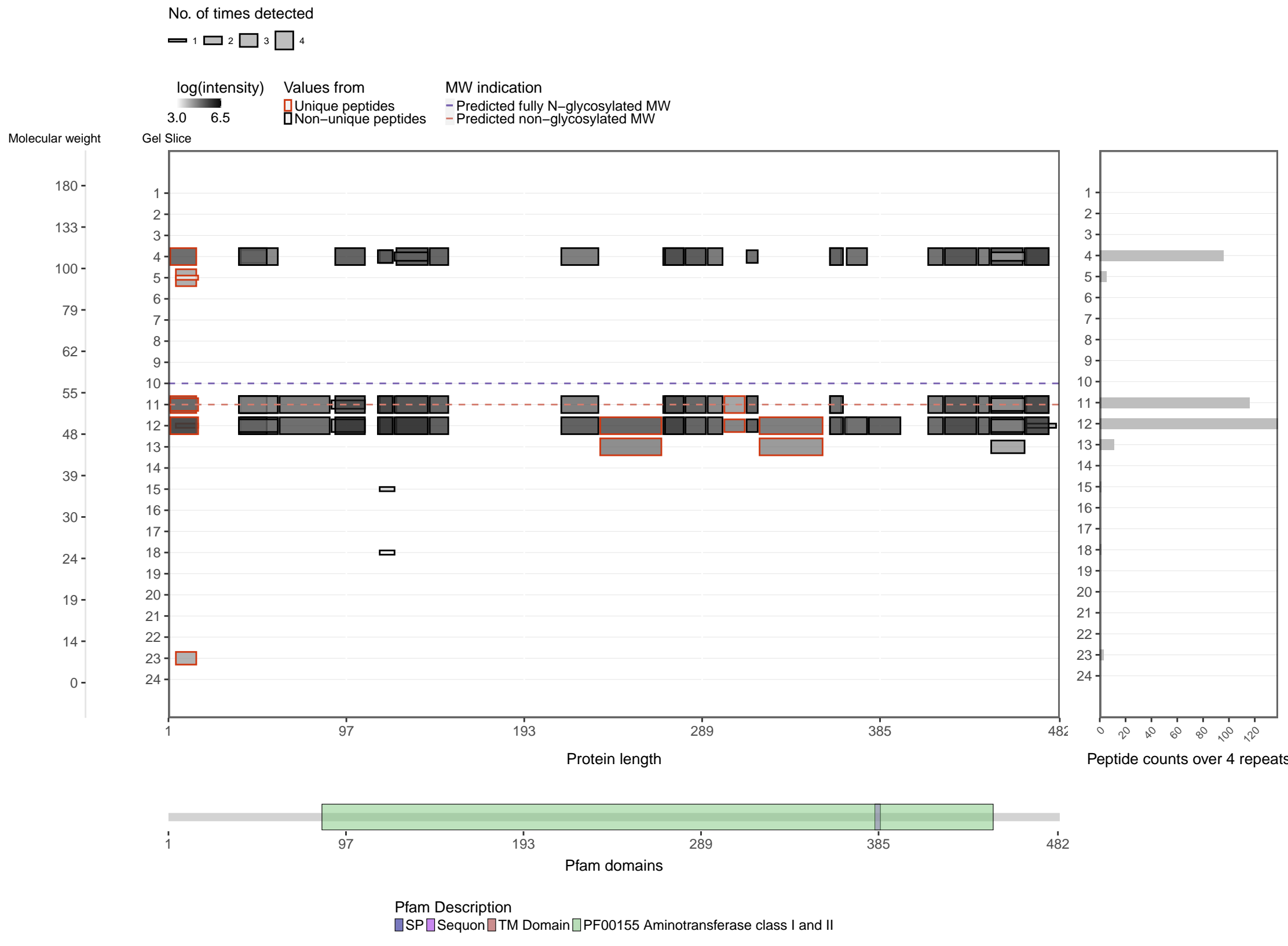
NbL08g09520.1 alpha-glucan_water_dikinase_chloroplastic [MW = 166.69 kDa]



Protein sequence:

IPDDVVICGALIDYIKSDFDGYWKTFLNENGINKEKLLSYDRAHSEFNFRDDQKEGLLRDLGHYMRFLKAVHSGADLESAAIANMGYRTEGGFMVGVQINPVSGLPFGFDGLHFVLDHVEDKNVEALLEGLEAREELRPLFLKPNRRLKDLFLDIALDSTVAVRGEYELNANPEKMYFISLVLENLALGVDDNEDLVYGLKGVWNGAIMEKDDGNHWLFAKAVLDRTRLALAKAEWYHHLLGPSAEVLSGLGVDQWALNFTTEIRAGSAASLSSLLRLD

NbL08g09480.1 glutamate--glyoxylate_aminotransferase_2 [MW = 53.5 kDa]



NbL08g09090.1 uncharacterized_acetyltransferase_At3g50280-like [MW = 49.43 kDa]

No. of times detected



log(intensity)



Values from



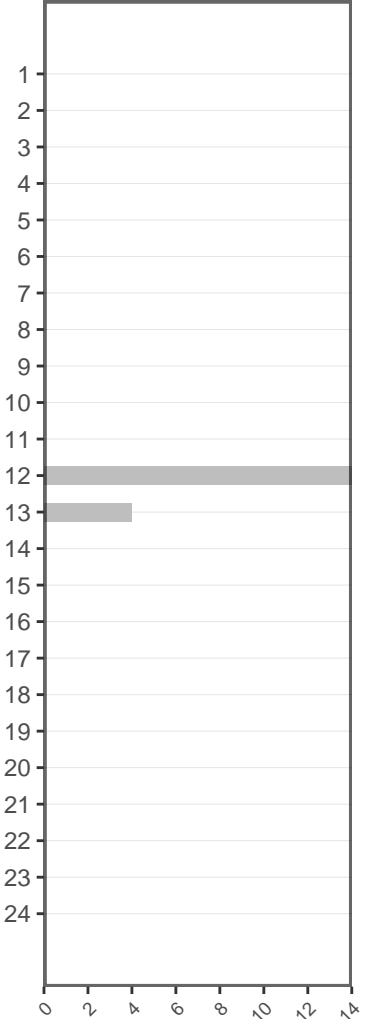
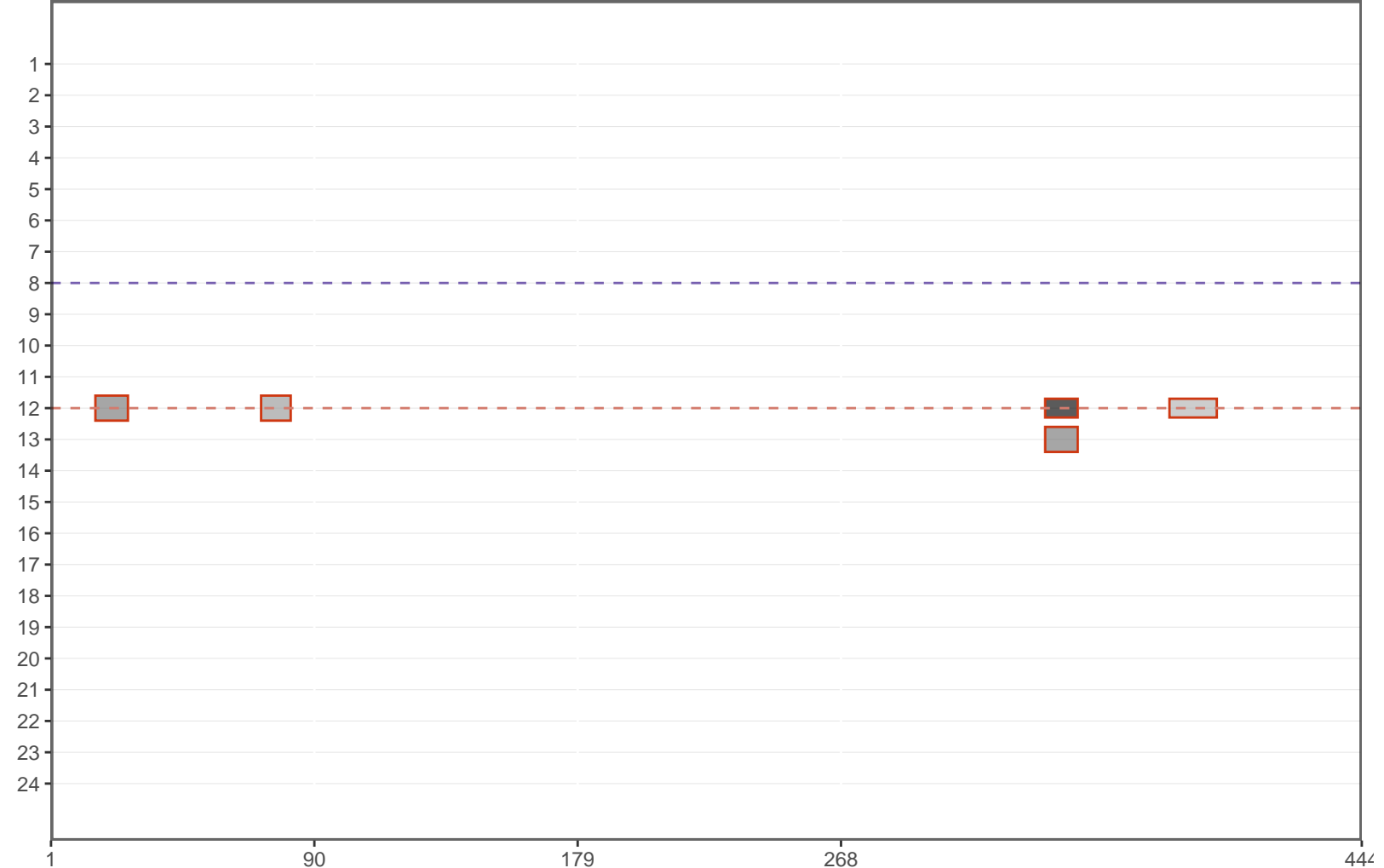
MW indication



Molecular weight



Gel Slice



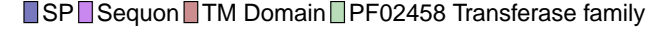
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

HLPIKLDDEKLFVFEFPHKERIFHLKESIAKLEKANSEMGIKBSISLGAFLAHLWRBVTGRKLDAAKEEVVGLIGTRSRNLNPPLEFGYFQNAHAKRVTKTAGELLEGLGWAAAMELNKYVNSQNSEEVKIKYKEVAENPVLFSKSTVFGSKLAIS6SPRYNYGTFDVGWGPVAVR6GMANKSDGKITLFPDVEEGSDIEVGLPKTLGAMENDESEFMEAVTN

NbL08g09050.1 40S_ribosomal_protein_S6-like [MW = 28.36 kDa]

No. of times detected



log(intensity)



Values from



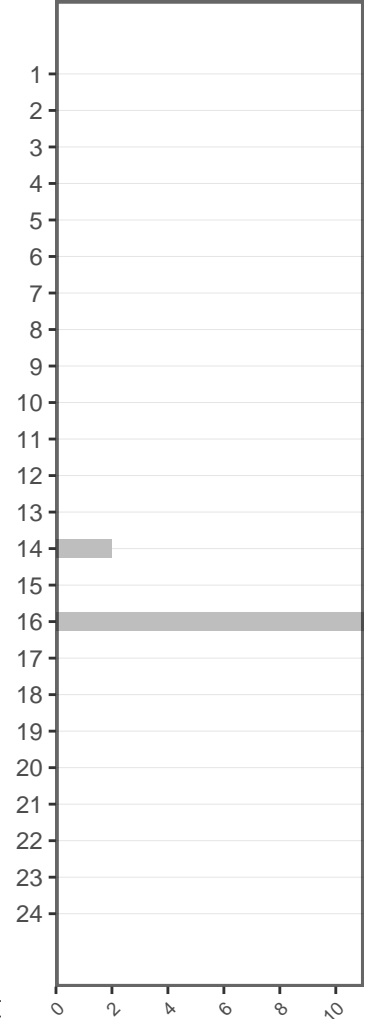
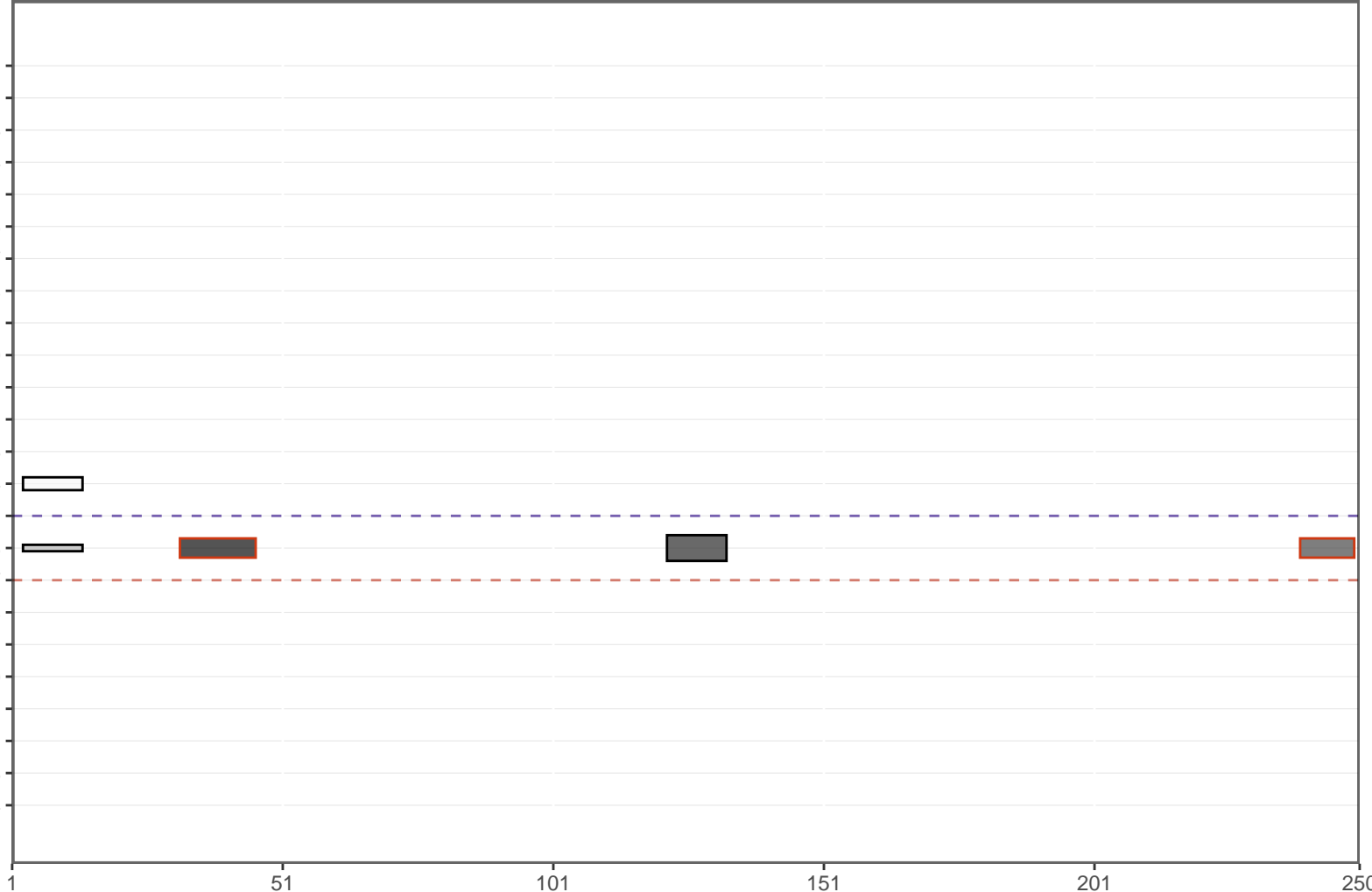
MW indication



Molecular weight

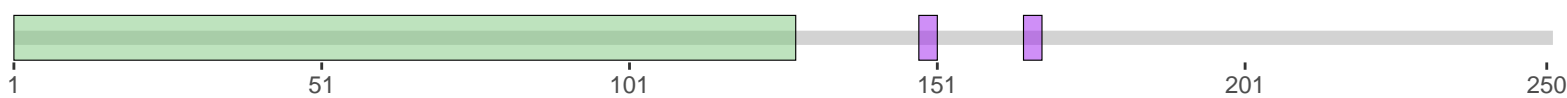


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

/NLIVYKXGKDLPGFDTEKPRMRGPKRASKIRKLFNLSEKEDDRKVVNYFYRIRNFTTKSGKKAKAPKIQRLVPLFLQKRRARIADKKRIAKAKBEAADYQKLLATRLKEGRERRBEELAKKRISLSAASKPEVA*

NbL08g08920.1 upstream_activation_factor_subunit_UAF30-like [MW = 13.22 kDa]

No. of times detected



log(intensity)



Values from



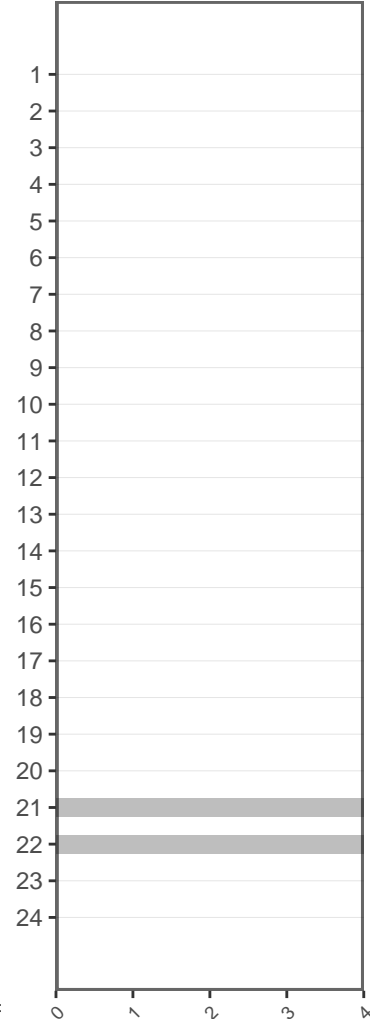
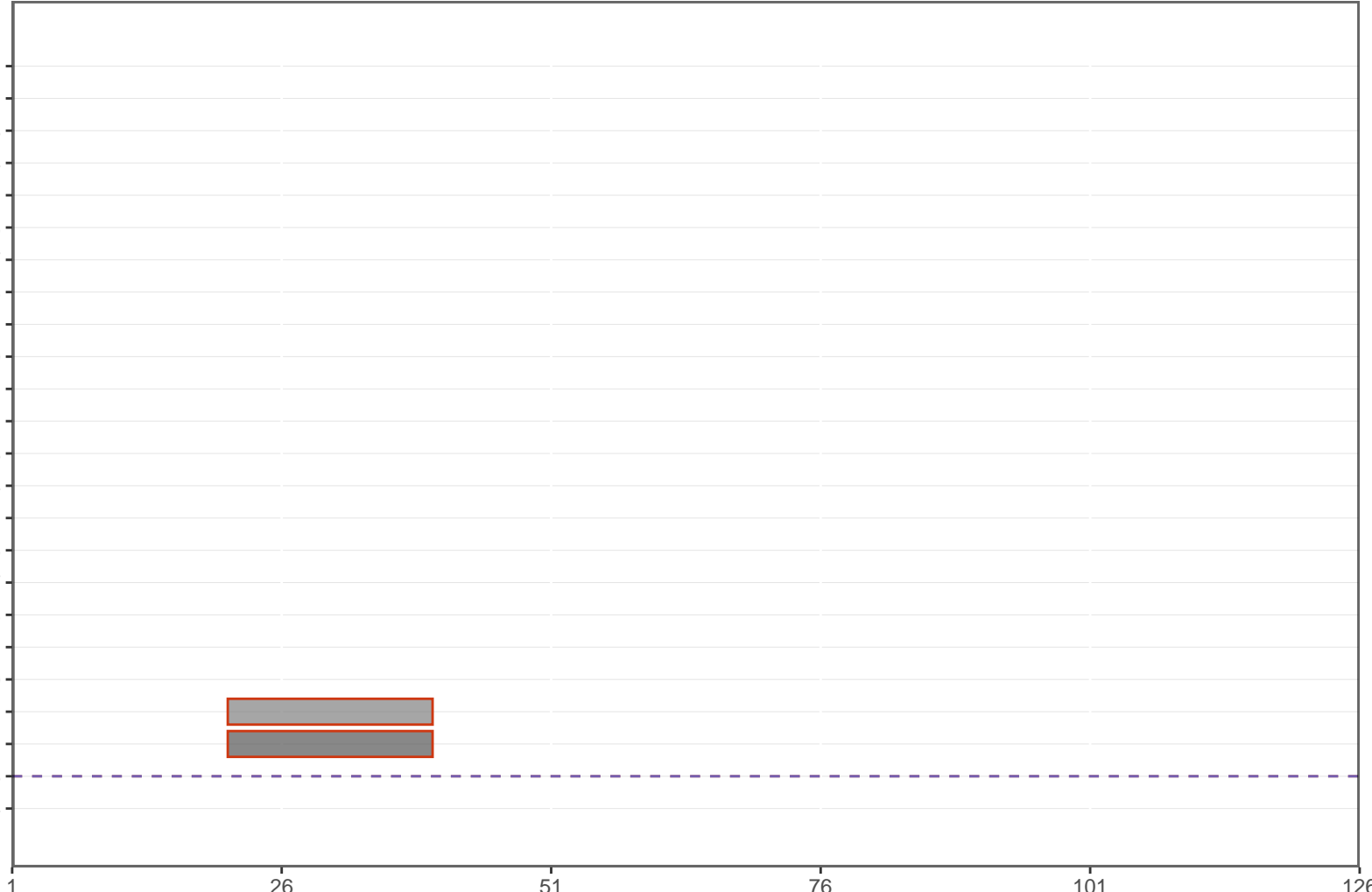
MW indication



Molecular weight

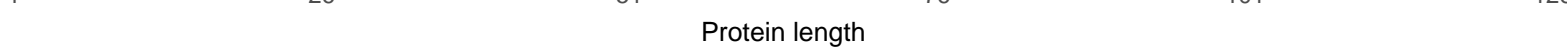


Gel Slice

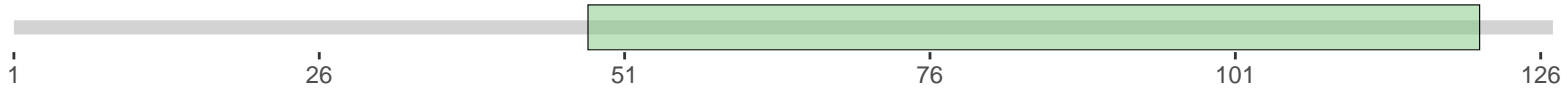


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

LPVSPALGKLVGSEISRTDAKVKVWDVKTNLGNPANKKEGGDDKLTIFAGKDKVGFLEAKLSSHFQKAS

NbL08g08790.1 probable_methyltransferase_PMT20 [MW = 56.91 kDa]

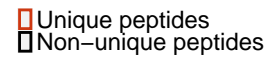
No. of times detected



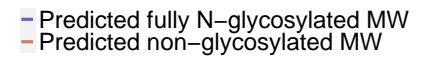
log(intensity)



Values from



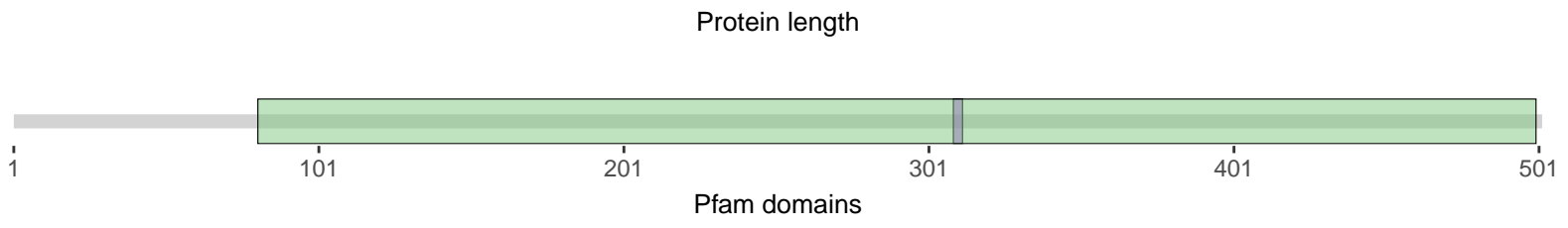
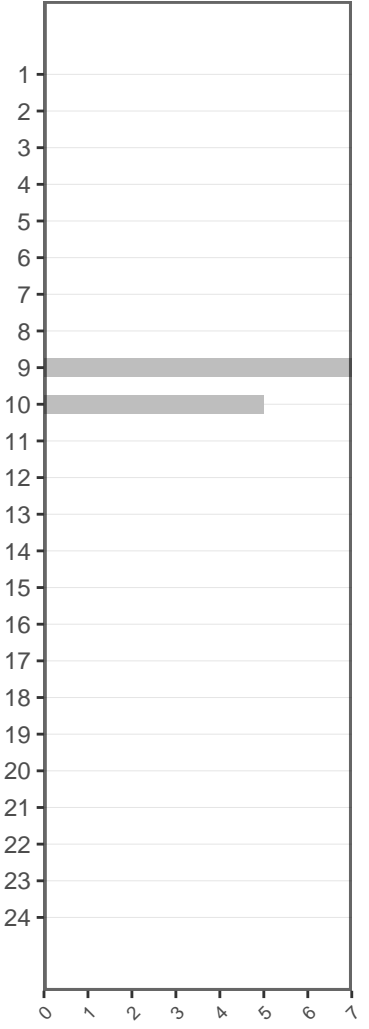
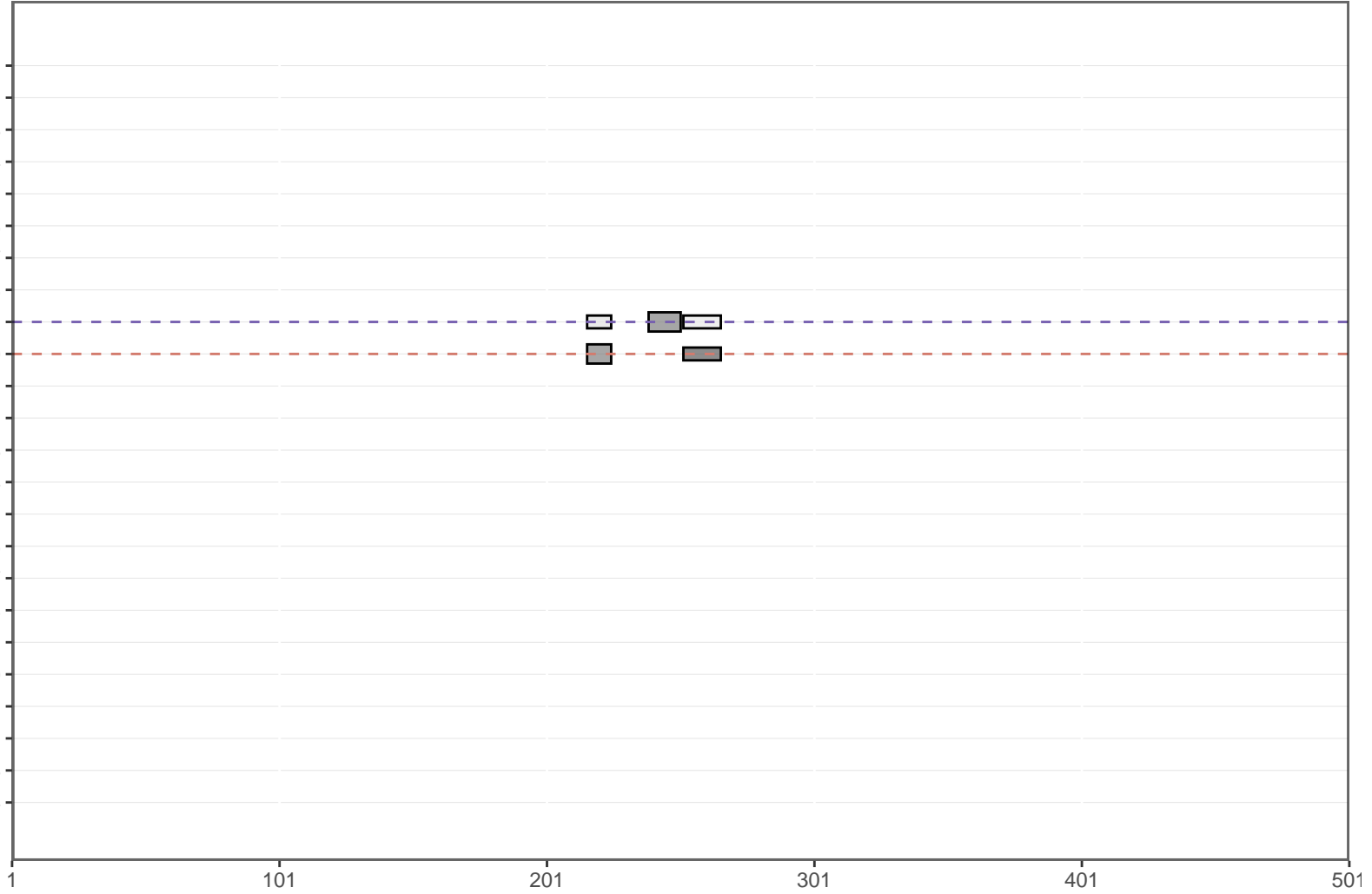
MW indication



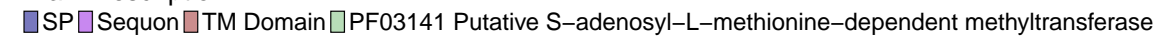
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

.ERIGFALGISTORLFFPSNFDMAHCSRGLPWTEFGVYLLHHRILRPGDFVWLGSPPNVYEHRRWRGWNTTIEEGKSDVLDLGEELTSMGKFLNKKDDIIVWQKLGSDSNCKKLNPNFDPKDKDDGTEPDSAWYPLRPCVVVFNPAKLLKLDALAKWPERLHWAPERVSDVIRGGGAGAFKHDDKWKVIRAMHYKLLFALGTEKIRNVMMDMNTLVGGFAAAVDAFVWVWVNVSSVYVNTLPVWYDRGLGTHDW

NbL08g08510.1 lipoyl_synthase_2_mitochondrial-like [MW = 42.51 kDa]

No. of times detected



log(intensity)



Values from



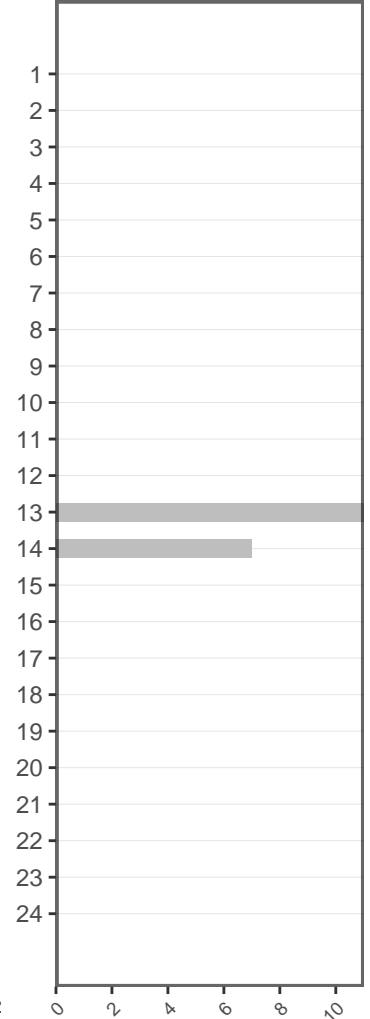
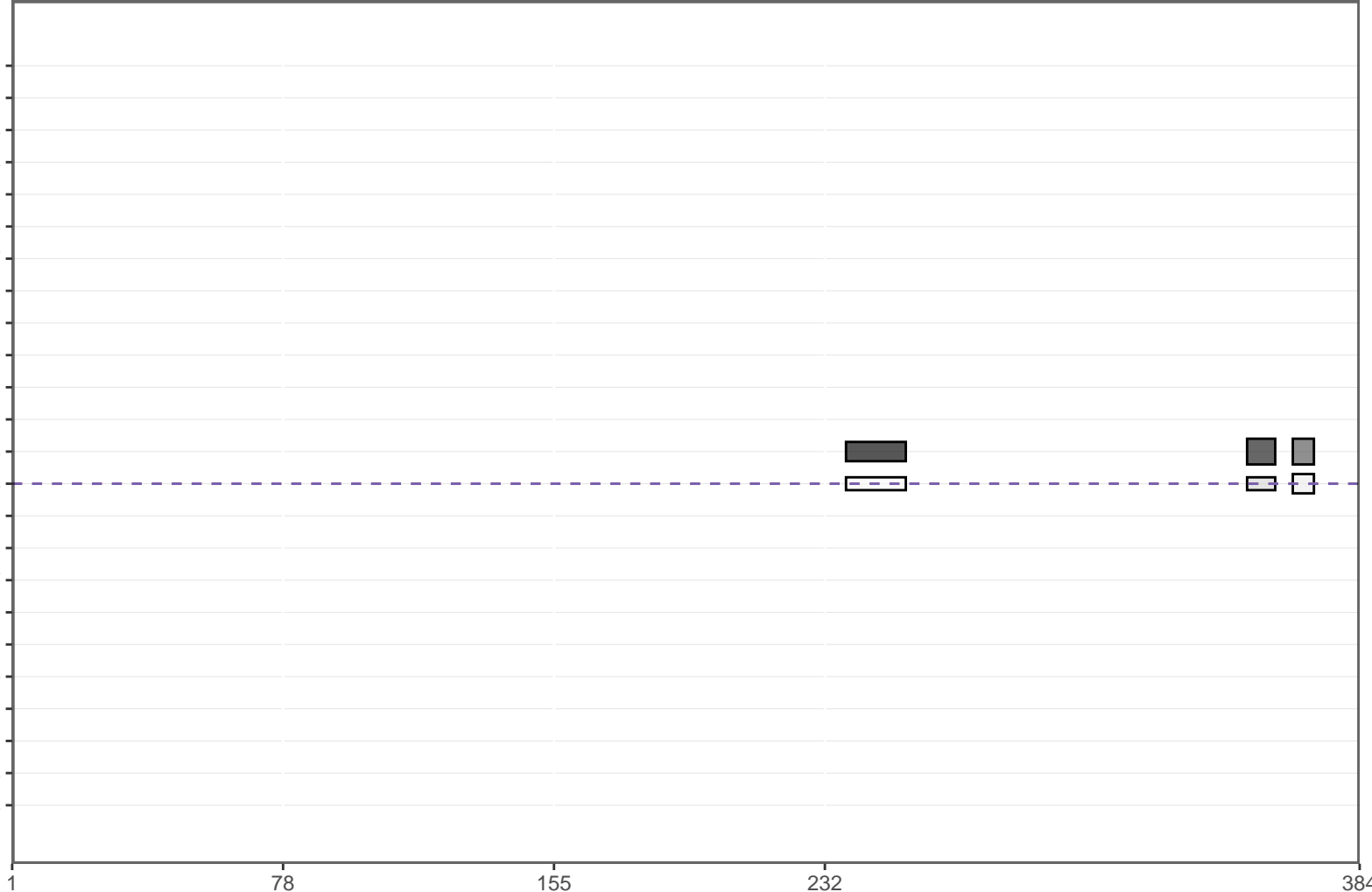
MW indication



Molecular weight

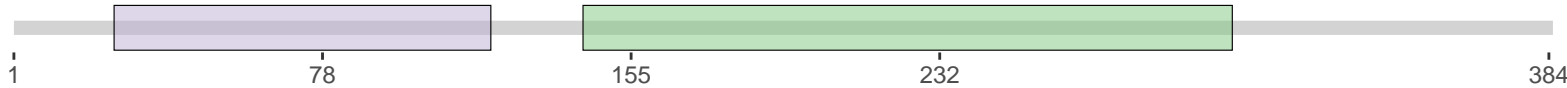


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILDYVYITSDVDRDLDLPGGGSGHFAETVQKIKALKPKMLLEALVDFRGGDPCIEKVAHNSGLDFAHNIEVTEELGRVVRDRHRANFKGSDMDLMMKAKGAPATLTKTSVMLGGGETPDGAVKTKMEKVRAGVDVMTFGGVMRPTKRHHMPVSEYITFEAFENHYRLVLMGEMGFRVYASGPMVRBSYKAGEFYKSMESDRAASVY

NbL08g08460.1 5–aromatic_acyltransferase–like [MW = 50.22 kDa]

No. of times detected



log(intensity)



Values from



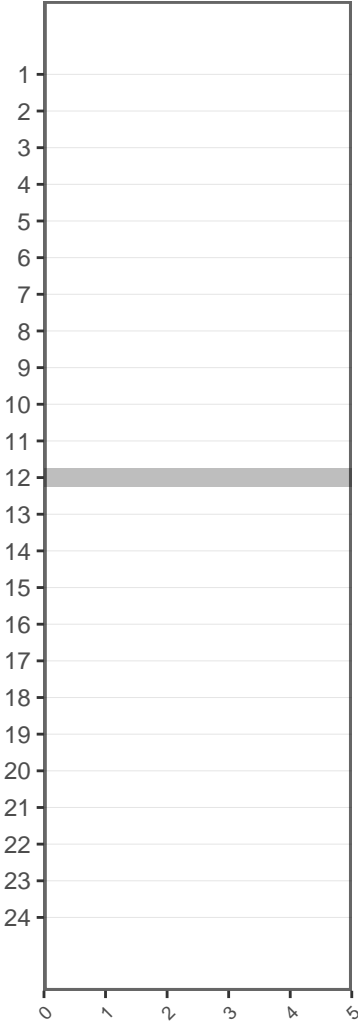
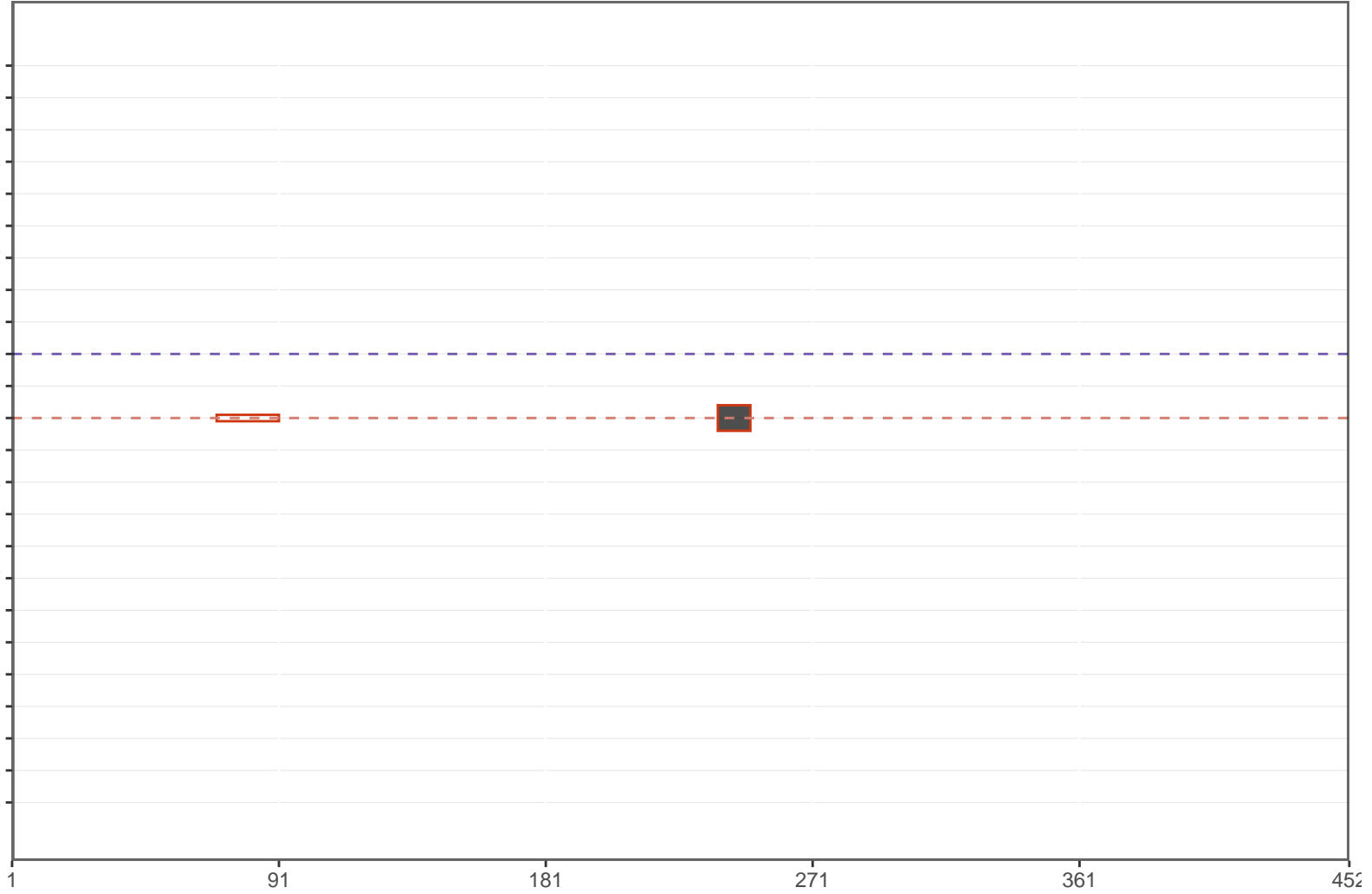
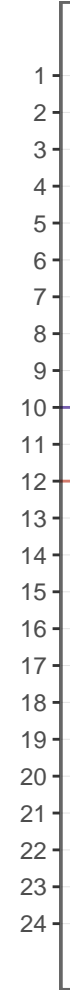
MW indication



Molecular weight

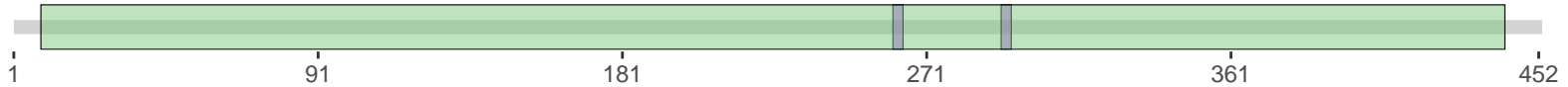


Gel Slice



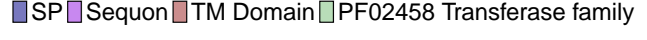
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MISIVDEMOKFKLEMCIDVITPLDKVIRGTFHFDQDGTLLKLNMLSRPPLSHVTSFTVTCAYVWTGLIKSEDSRIIEEIEENVTELFGGVADCRRLNPLPSPVDFGNCLVPLVARAGHADLAGKEGFTWVYVIGETIQKRMKDEDVLSGKWFKEFGSDVDKRTLISAGSPKLELVAADFQWRPEKLEFVSDINGDGVSMLSLKEKDDGNGLELGLPKTRMNAFAALFTHGLSEFL

NbL08g08250.1 26S_proteasome_non-ATPase_regulatory_subunit_2_homolog_A-like [MW = 98.12 kDa]

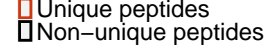
No. of times detected



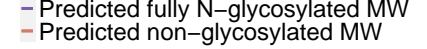
log(intensity)



Values from



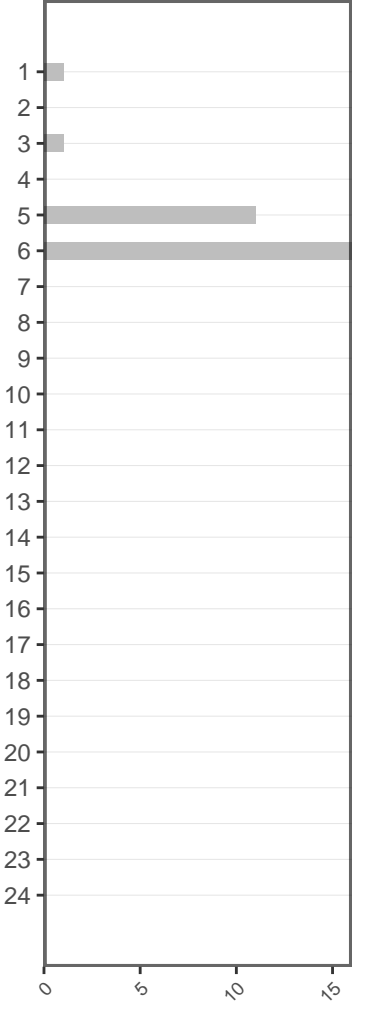
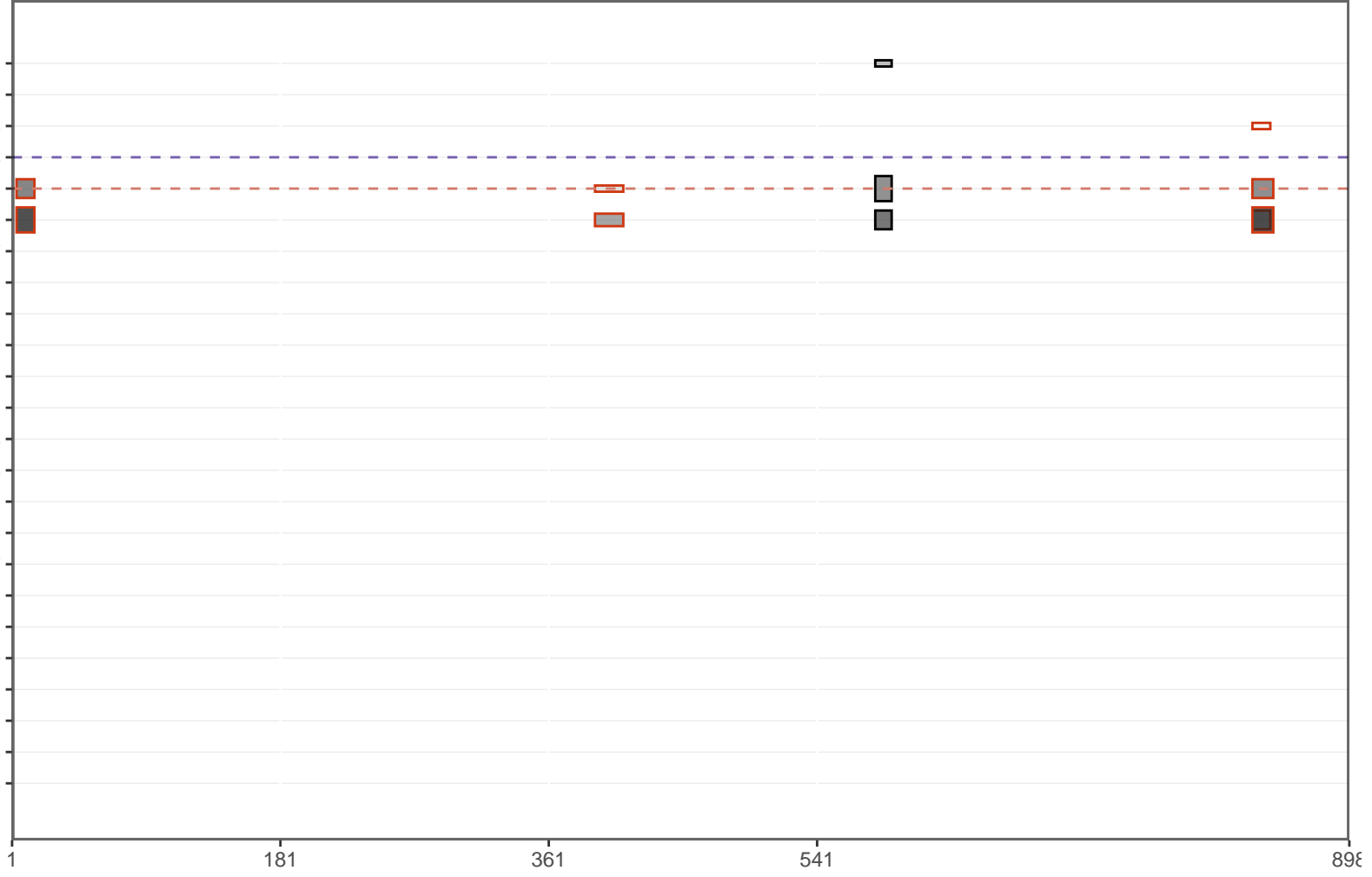
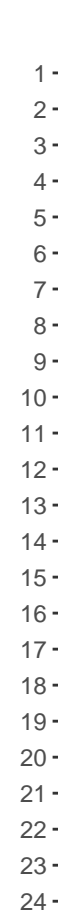
MW indication



Molecular weight

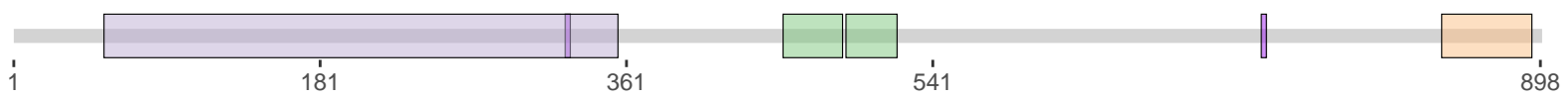


Gel Slice



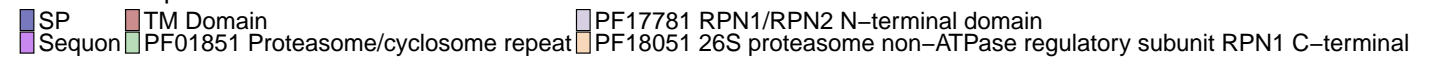
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

/D/DSGLAQLDKVFHSDTHVAGALLGVGVNGGKNDGDFALALLAEVYDKDDPSRIGAIMGLGLVAGAGNEGRSILTPILGDKKASLDVIAFAASLGLVYVSGNEIEAQAIFALMERSESELGEPLARLLPLGLGLLYLKGQESVEATAEIVSKTFHEKIRKHCMTLLSGAVAGTGNLVKQVHFLGDCAGHLEKGETYGGPWLGIAMVAMSEELGEMTRLSLEHLQYGEQNRRAVPLALALLGDSNPKVNVMDTLGRLSHSDTEVMAAISLGLIGAGTNNRIAG

NbL08g08200.1 acyl-coenzyme_A_oxidase_3_peroxisomal-like [MW = 76.03 kDa]

No. of times detected



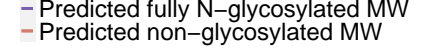
log(intensity)



Values from

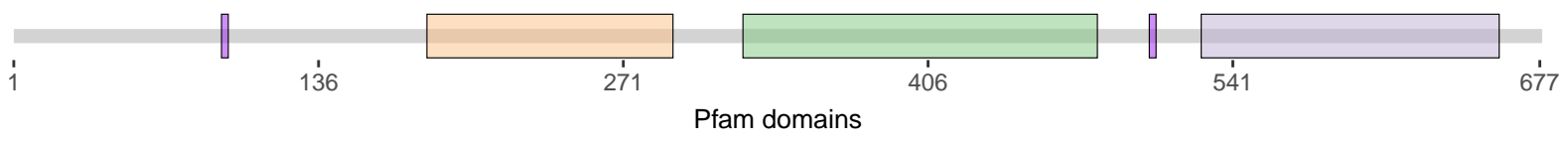
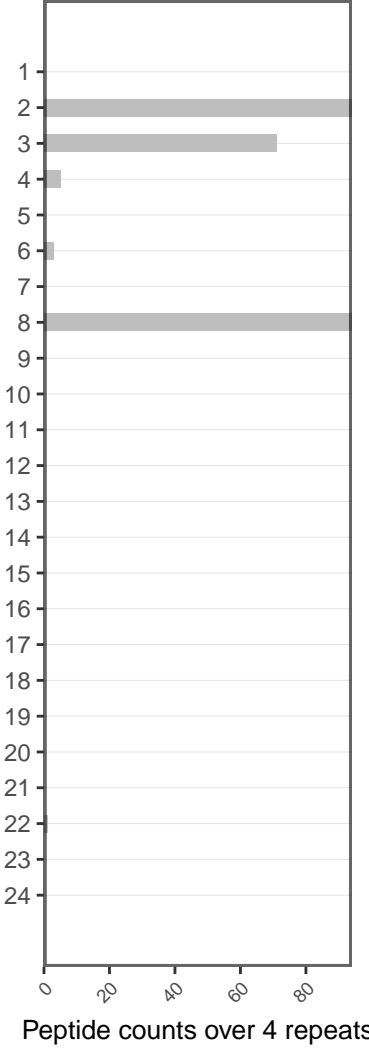
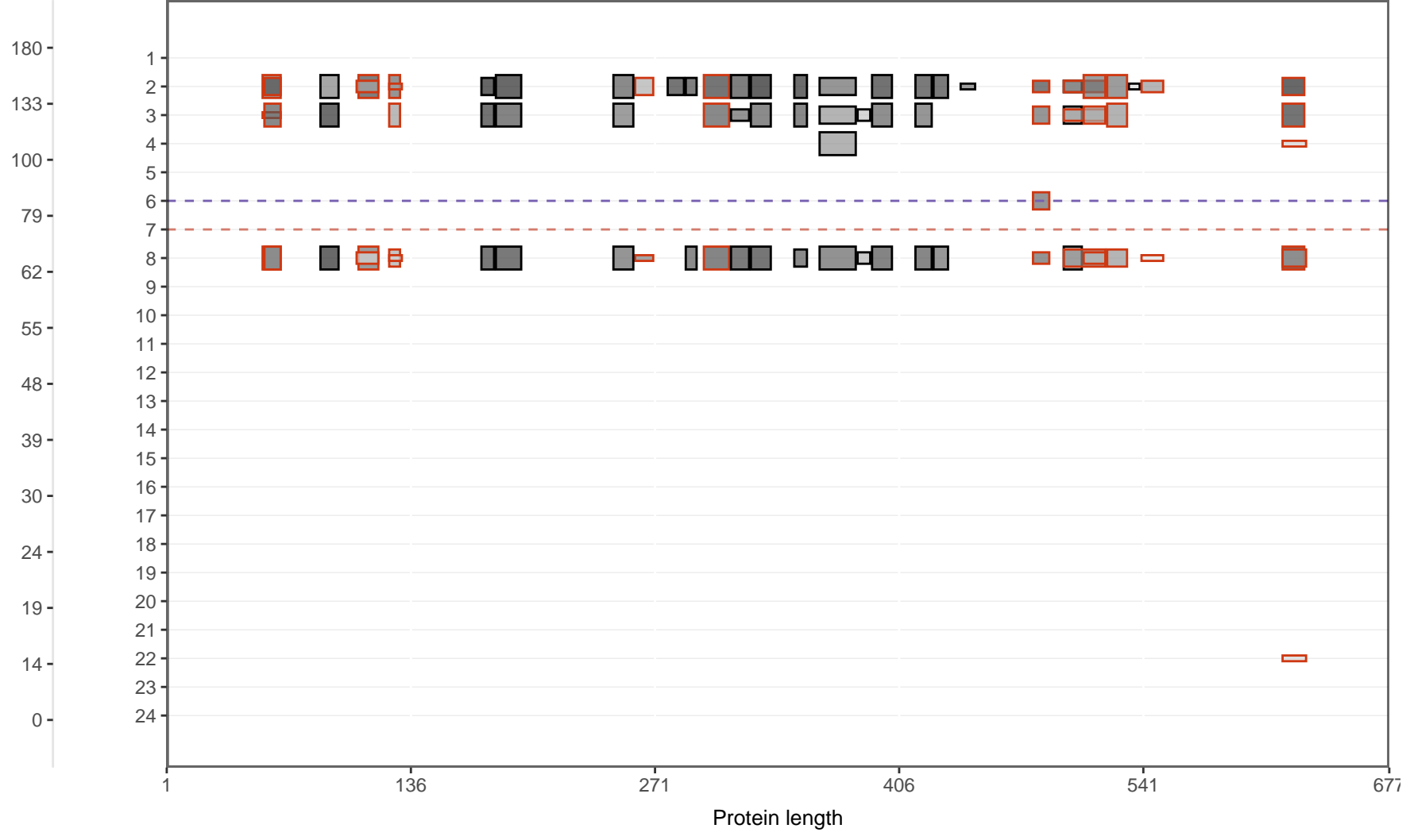


MW indication



Molecular weight

Gel Slice



Pfam Description

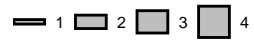
- SP
- Sequon
- TM Domain
- PF00441 Acyl-CoA dehydrogenase, C-terminal domain
- PF02770 Acyl-CoA dehydrogenase, middle domain
- PF01756 Acyl-CoA oxidase

Protein sequence:

AAFMPLTSGRVTAVSATPSAKIGLATALRYSLTRAFVSTPNGPEVLLDYPHQRRLLPLLAKTYAMSFANLKKYVWRTPENMKVPHWISSAFKATASWHNMRTLGEGREAGGGGLKTEKRVGDKLGEFDVQSTFEQDNNVLMQGVSKALLGEYVTAKRSKKPKFKGLGLEHMMNSRPVWPSQLTSTMRGAGFGNDIFGLRERDLERFAEVALGGGKNEVAFTLNYQLAEDLGRAFSDRAVLTFLAEVTSVTSQPLKNLGLVRSMLVLTLEEDVAFLRY

NbL08g08030.1 ubiquitin-NEDD8-like_protein_RUB2 [MW = 17.09 kDa]

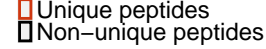
No. of times detected



log(intensity)



Values from



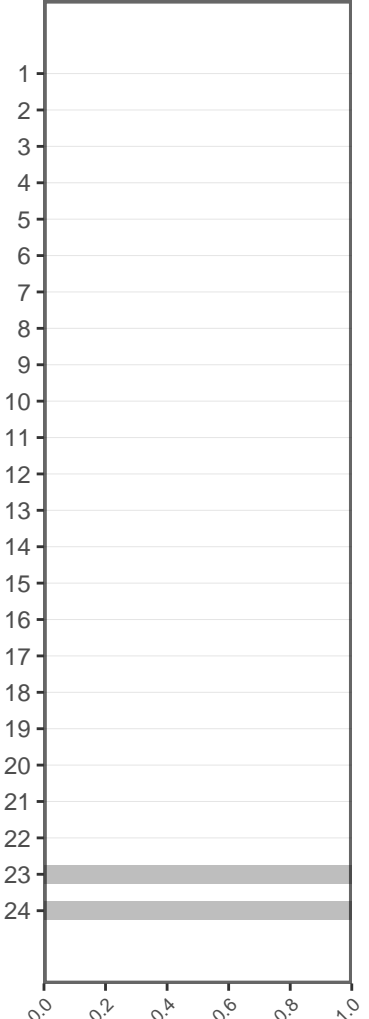
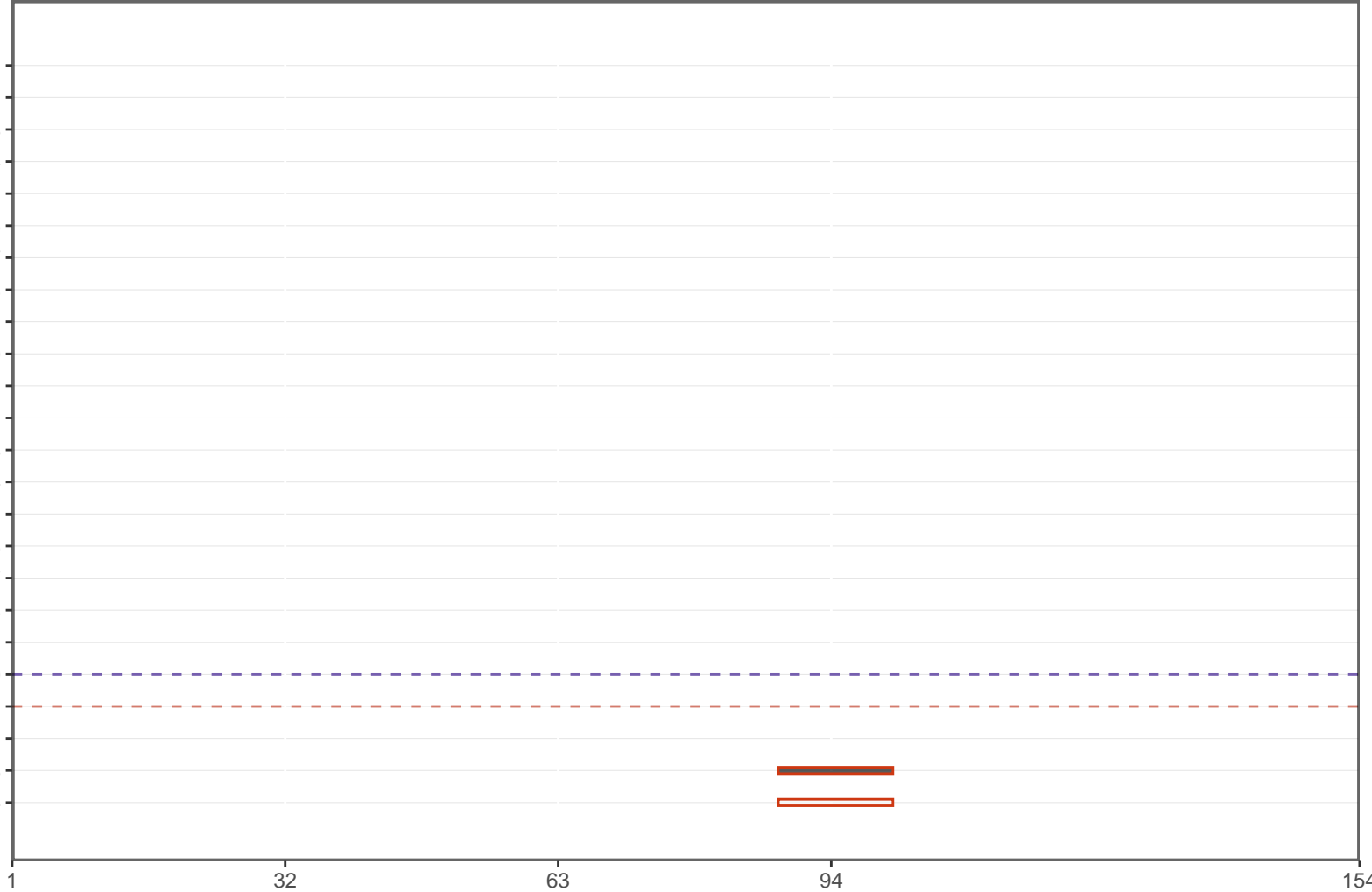
MW indication



Molecular weight



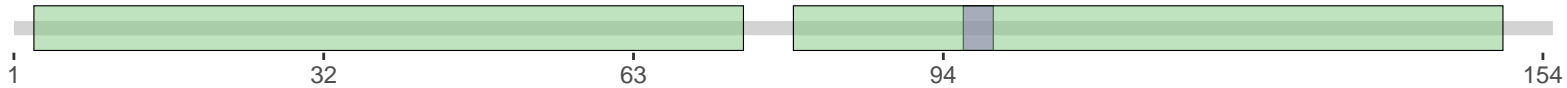
Gel Slice



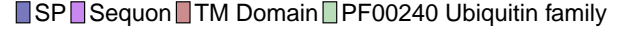
Protein length



Pfam domains



Pfam Description



Protein sequence:

ESTLHLVLRLRGGTMMKVKTLTGKEIEIDPNIDIRKERVVEEKEGIPVQQRLLYAGKGLADDKTAKDYNIEGGSVLHLVLRGGN

NbL08g07930.1 putative_4-hydroxy-4-methyl-2-oxoglutarate_aldolase_3 [MW = 20.55 kDa]

No. of times detected



log(intensity)



Values from



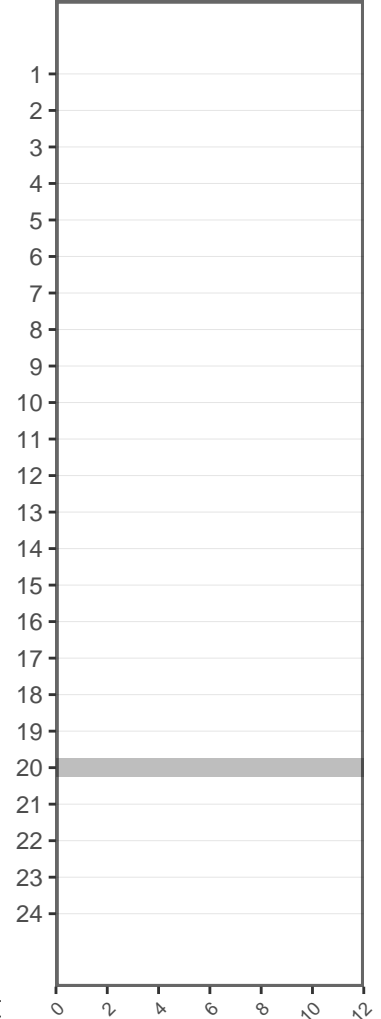
MW indication



Molecular weight

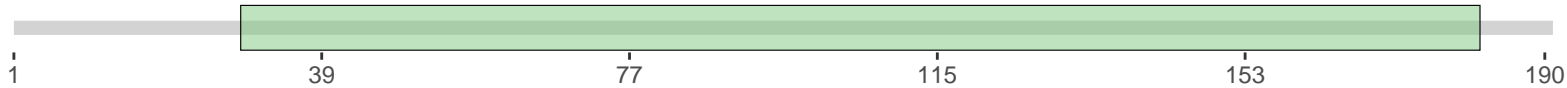


Gel Slice



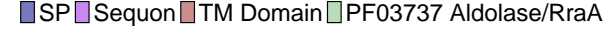
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IRDEGRVLYIDGGEMRFALVGGNLGGLADNMWAGVWVNGGIRVDVEINGDCDGVRLASHPKGSSKSGHDEKHVFPVYGGMLIREGEWLYADSDGHLVKTETEVV

NbL08g07880.1 photosystem_I_reaction_center_subunit_V_chloroplastic-like [MW = 16.21 kDa]

No. of times detected



log(intensity)



Values from



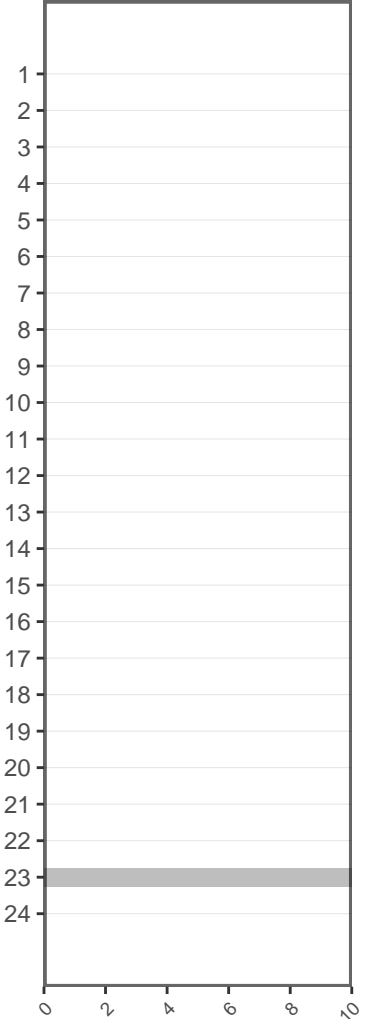
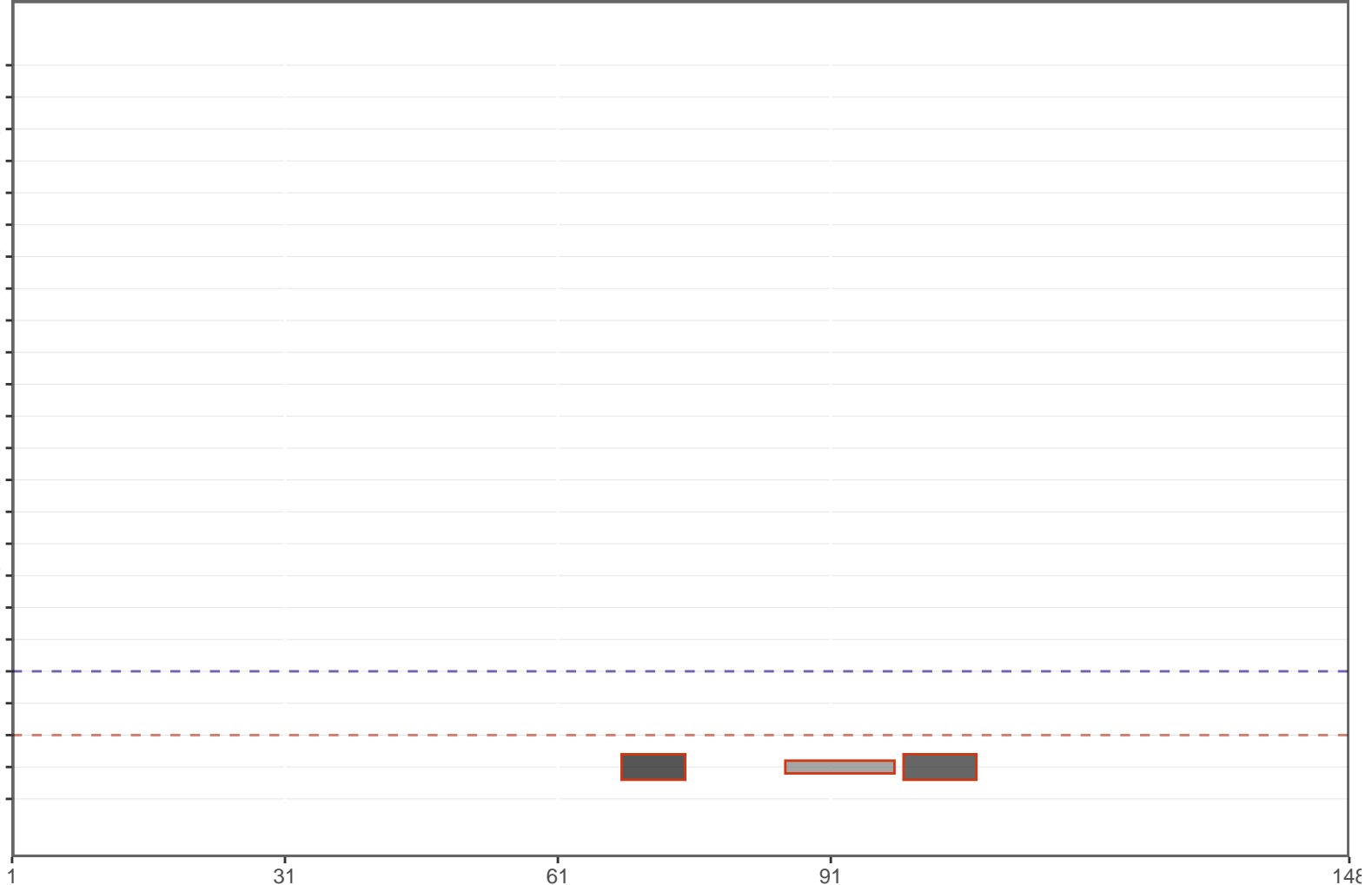
MW indication



Molecular weight

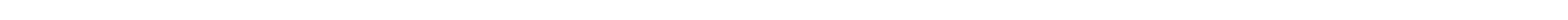


Gel Slice

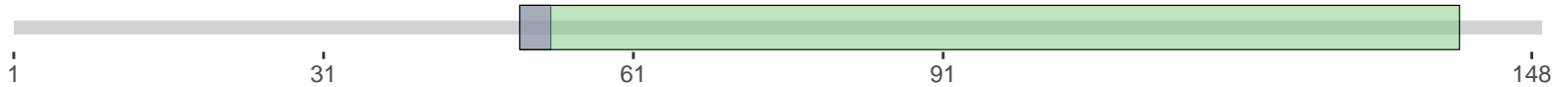


Peptide counts over 4 repeats

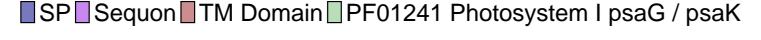
Protein length



Pfam domains



Pfam Description



Protein sequence:

LSLFLGRFVFNFGRENVAKQGLPKNGKNGSHFEAGDSRAKEVVELLKNKNDPVGFNVDVLAWSSGSHVWYHILATSSNGYDKPKFGD

NbL08g07810.1 DNA_damage-inducible_protein_1 [MW = 44.75 kDa]

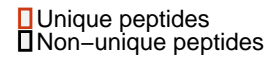
No. of times detected



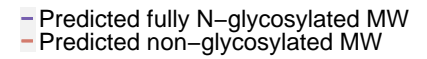
log(intensity)



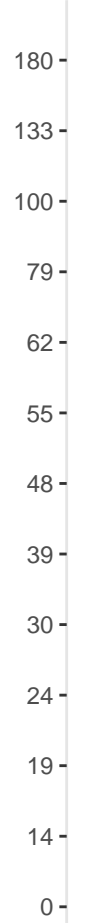
Values from



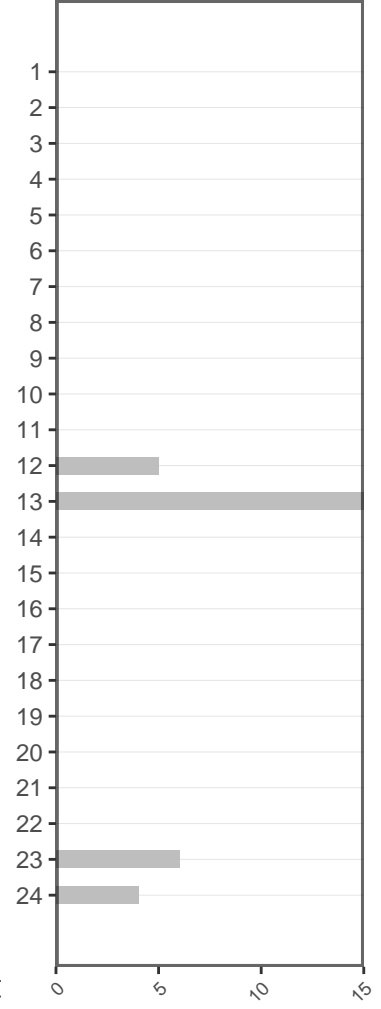
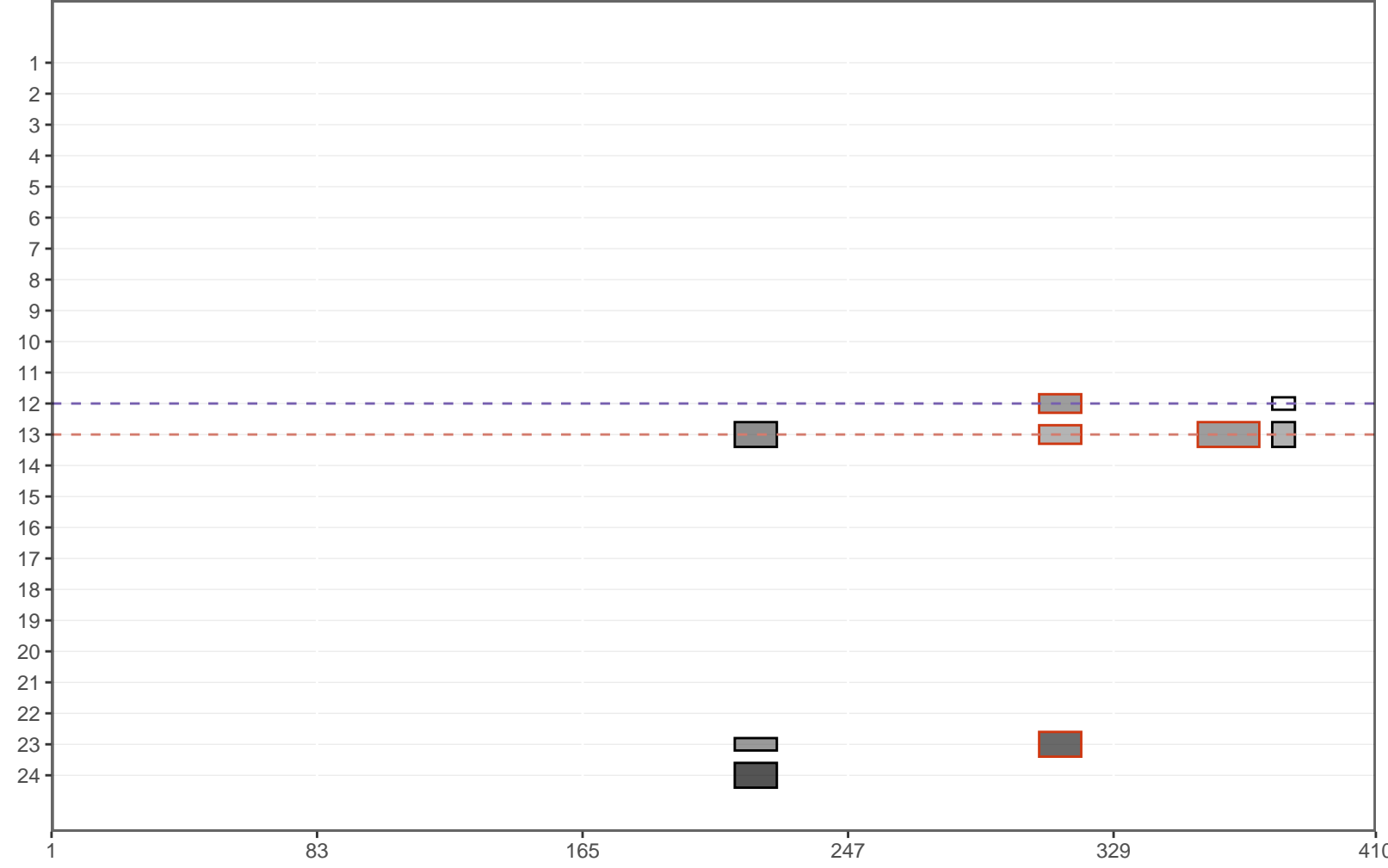
MW indication



Molecular weight

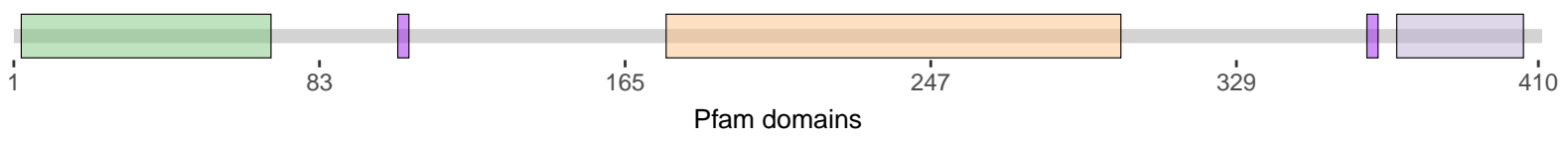


Gel Slice



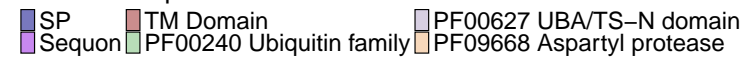
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EAFARVYMLYYDMEVNGHPLKAFVDSGAQGTHTKSGAERDGLLRLLDTRVYKGAHGVGQSELRRIHVAPIKGGIFYPGSRVVLDSRNMFLFGLDMLRKHGCDMLKENLVRVGGGEVAVPFLQENDPQGHFLDEERFAKEASSGGAATSGAKEKTPRAKGGP6GGAPGNSIQGTFFEAARVRLVELGFRDVAIQALKFFDQNEEQAAGVLFGG

NbL08g07780.1 heat_shock_cognate_protein_80-like [MW = 80.18 kDa]

No. of times detected



log(intensity)



Values from

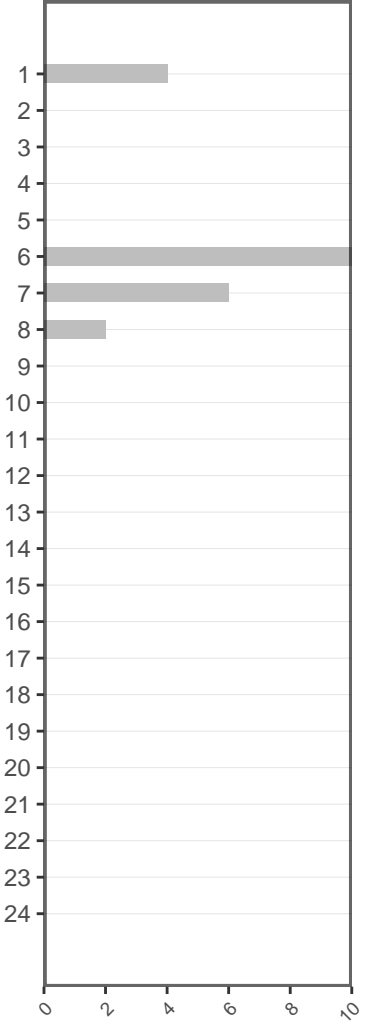
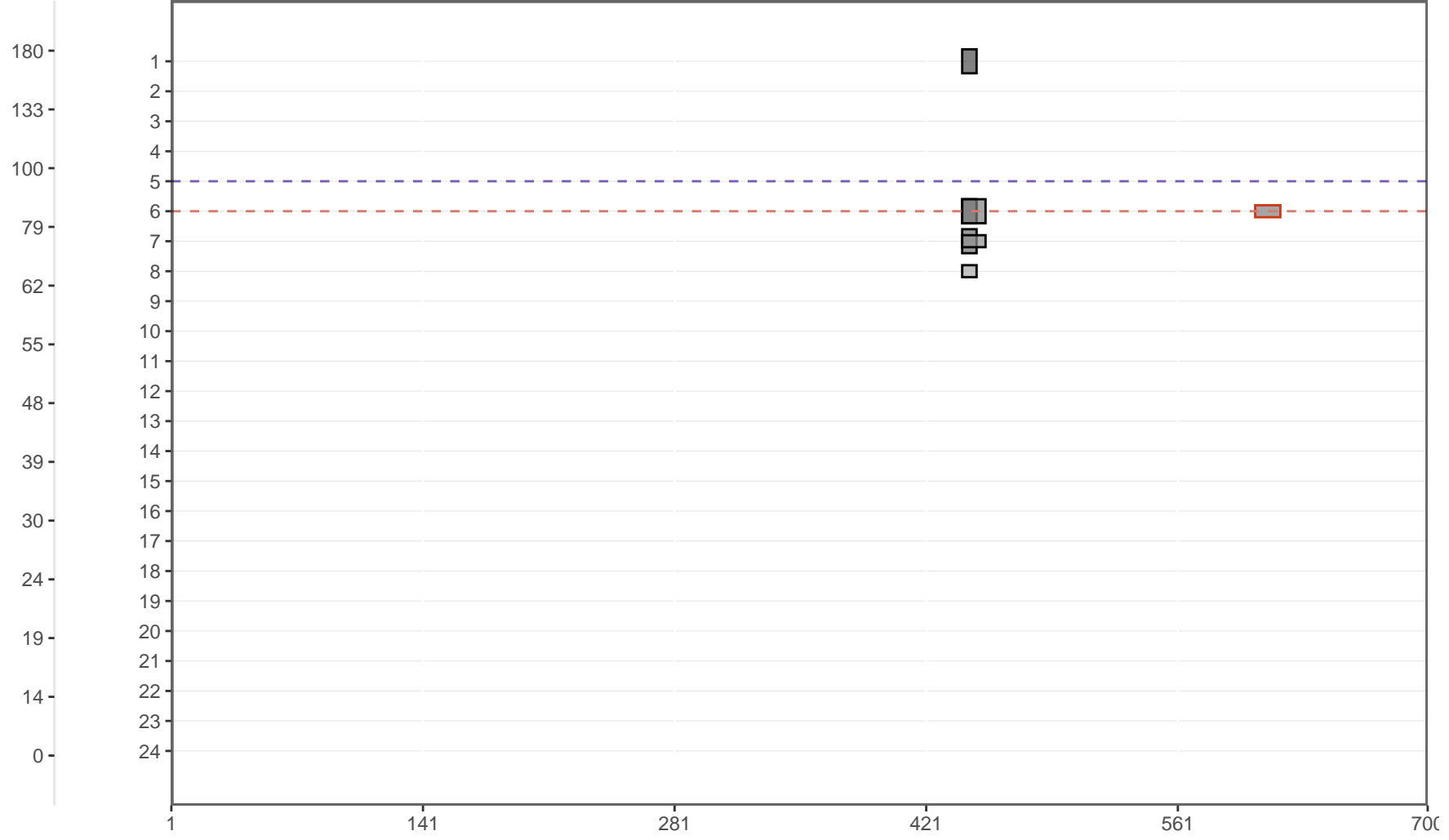


MW indication



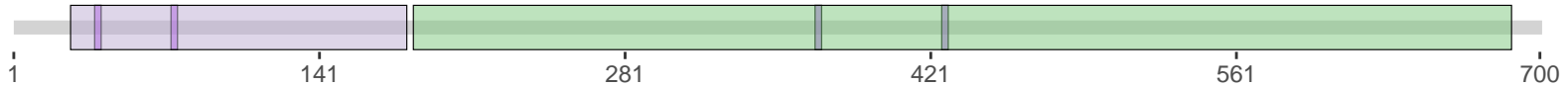
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00183 Hsp90 protein
- PF02518 Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase

Protein sequence:

/FIMDNCEELPEYLSFVWGVDSDELPLNISREMLQQNKIKVIRKIKVKKGEELFFEIAENKEDFDKIFYEAFSKNKLGHEDSGNRFKFAELLRYHSTKSGDDMTSLKDYVTRMKEGQNDHYVTGSEKKAENSPFLEKIKKGVYELVMVDAIDEVYGGQKFEFGKIKLSATKEGLKLDSEDEKDKKKEELKEKFEGLGKVKVDVLDGKVKVYVSDRVVDSFGGLTGEYGVFTANMERIMKAGALRDSMAGVMSKTKTEINFDNIMDELKRRADADKDKSYKDLV

NbL08g07740.1 protein_CWC15_homolog [MW = 26.86 kDa]

No. of times detected



log(intensity)



Values from



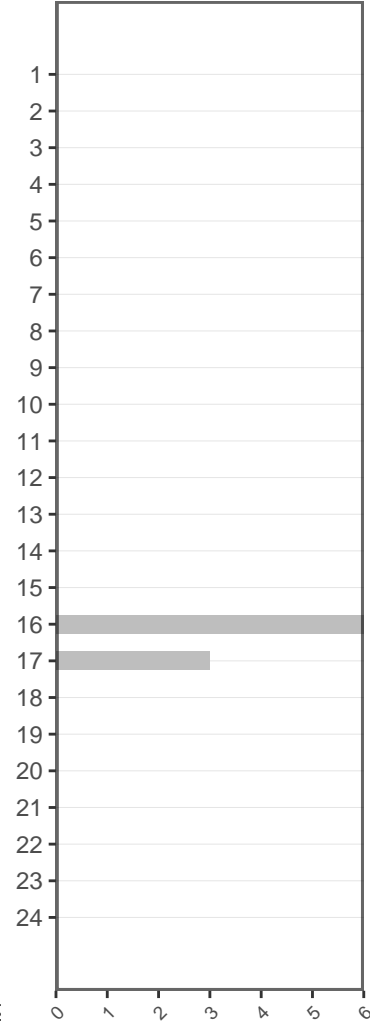
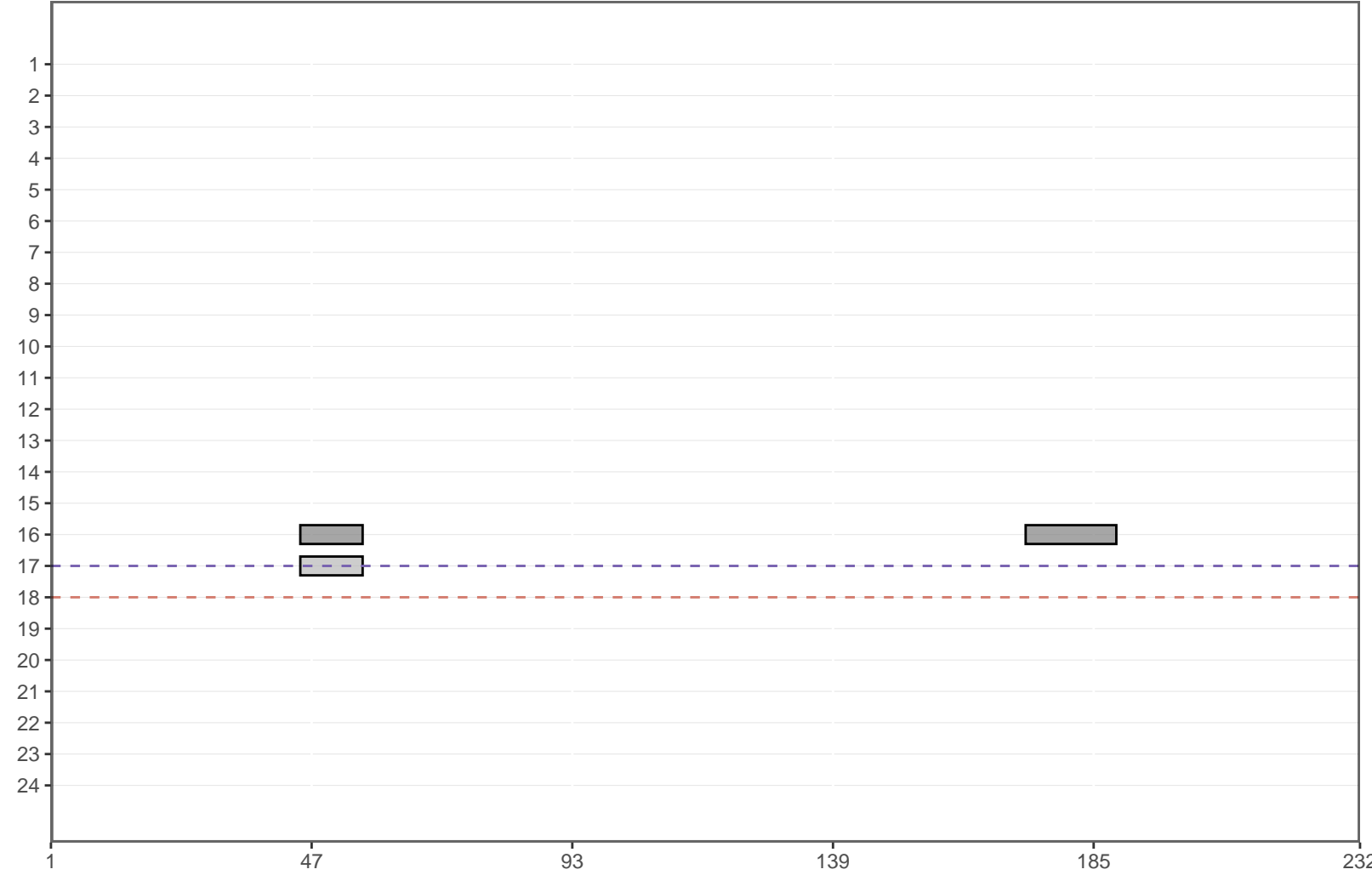
MW indication



Molecular weight

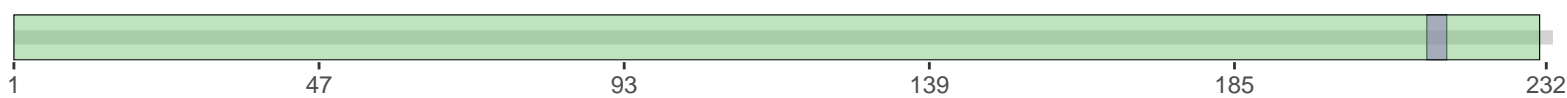


Gel Slice



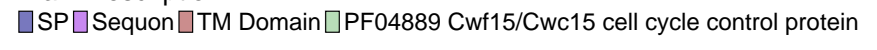
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IPRSADADDADVDVNSGDESDDDDDDDDDTEALLAELEQNKKEAEKLRKERDQEEELKAKAEALLRGNPLLNHGAGPTFSFVRRRWDVVFKNGARGEMKAAKRFINDTRNDFHRFLGKYMK

NbL08g07710.1 nudix_hydrolase_2-like [MW = 31.93 kDa]

No. of times detected



log(intensity)



Values from



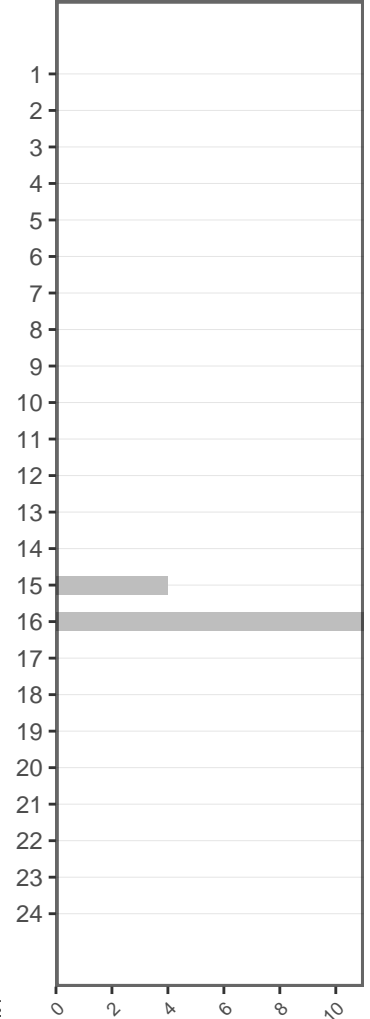
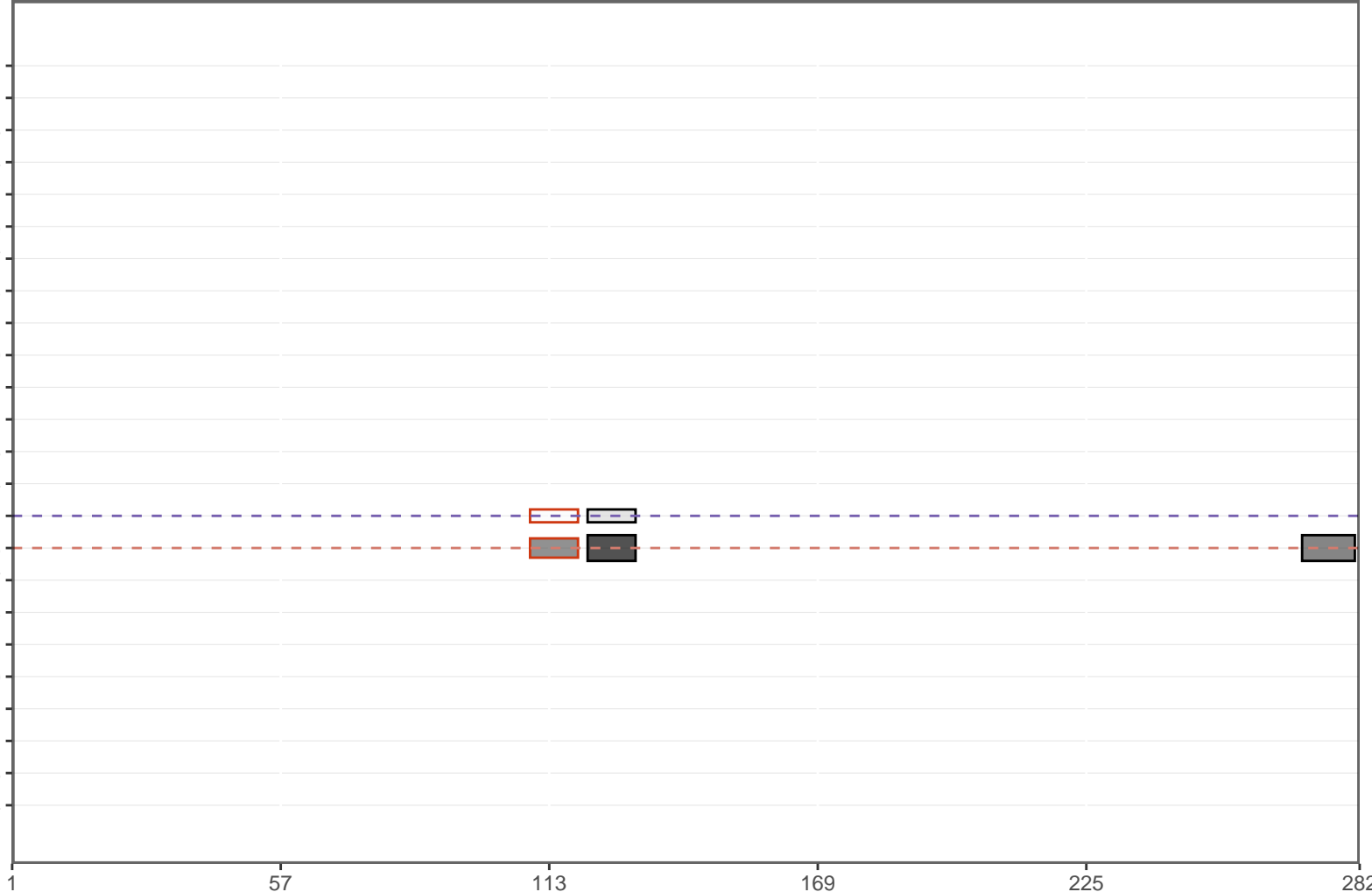
MW indication



Molecular weight

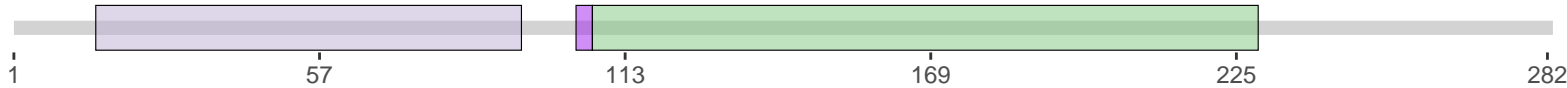


Gel Slice



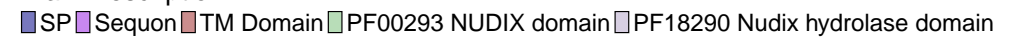
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ENSGRLKGTAVWKIPITGLEEGEDIFEGAIREVKEETGIDTEFLVLAFRQTQKALFGKSDLFFRCMMHPLSFDIQKQKDLIEAAGWMPLEEVAAQRPVQKHGIRKYTKDLGLVKAERNYPGFPTVPVITSFDFDQSTFLVYVNDKDLDDQESSAHL*

NbL08g07460.1 autophagy-related_protein_8C-like [MW = 13.74 kDa]

No. of times detected



log(intensity)



Values from



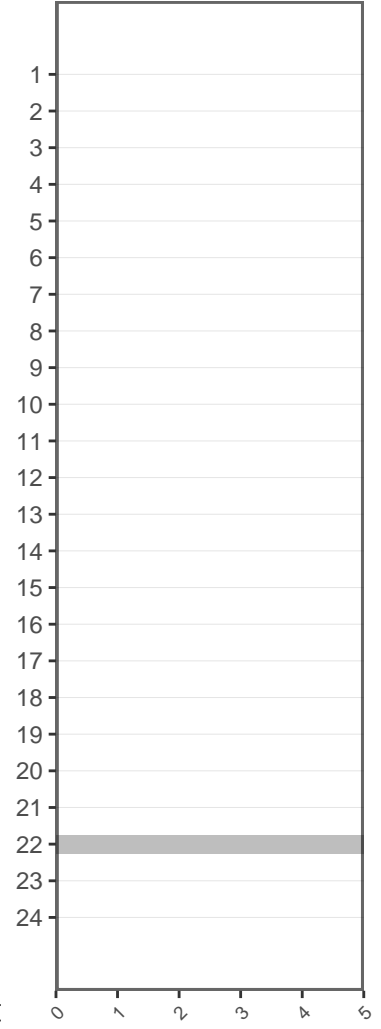
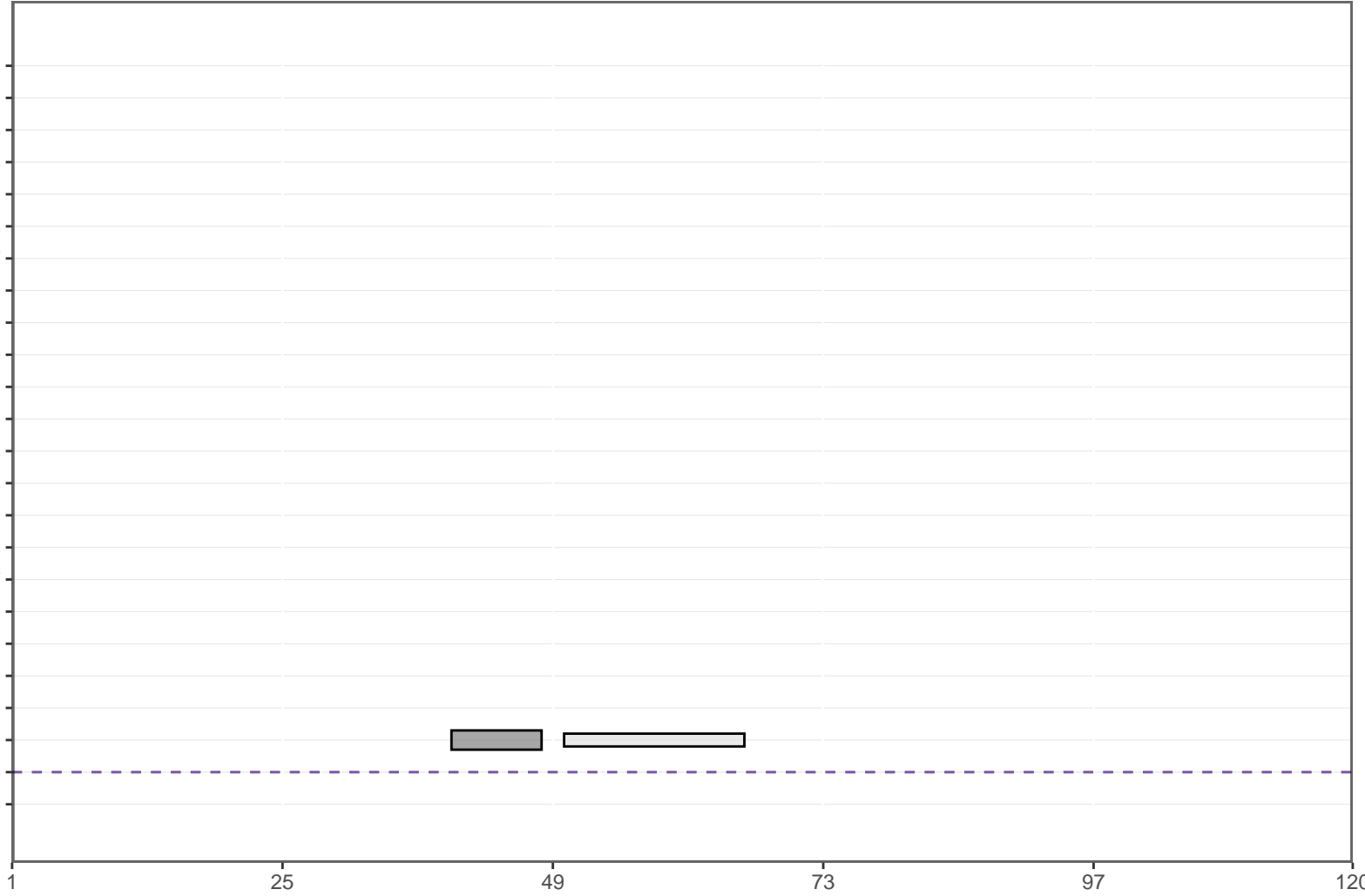
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

KKKYLVPADLTVGQFVYVVRKRRLSSEKAFIFVKNLPTAAMMSAIVEEHKDEDFLMTFYSSENTFGSP

NbL08g07370.1 tryptophan_synthase_beta_chain_1 [MW = 51.19 kDa]

No. of times detected



log(intensity)



Values from



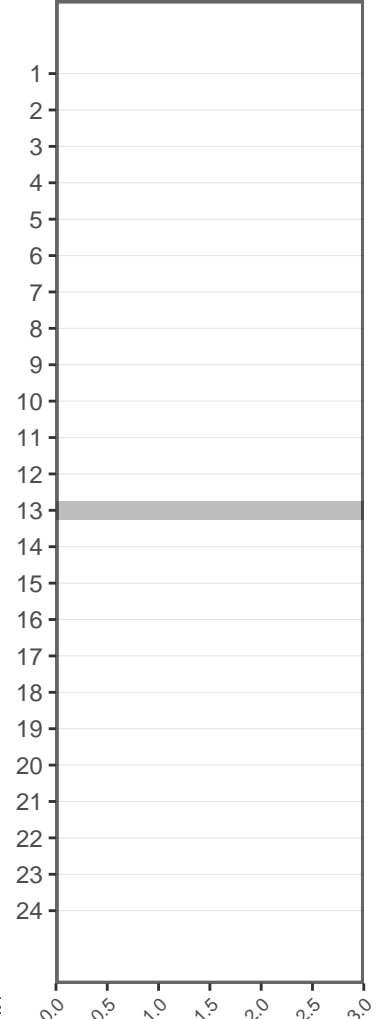
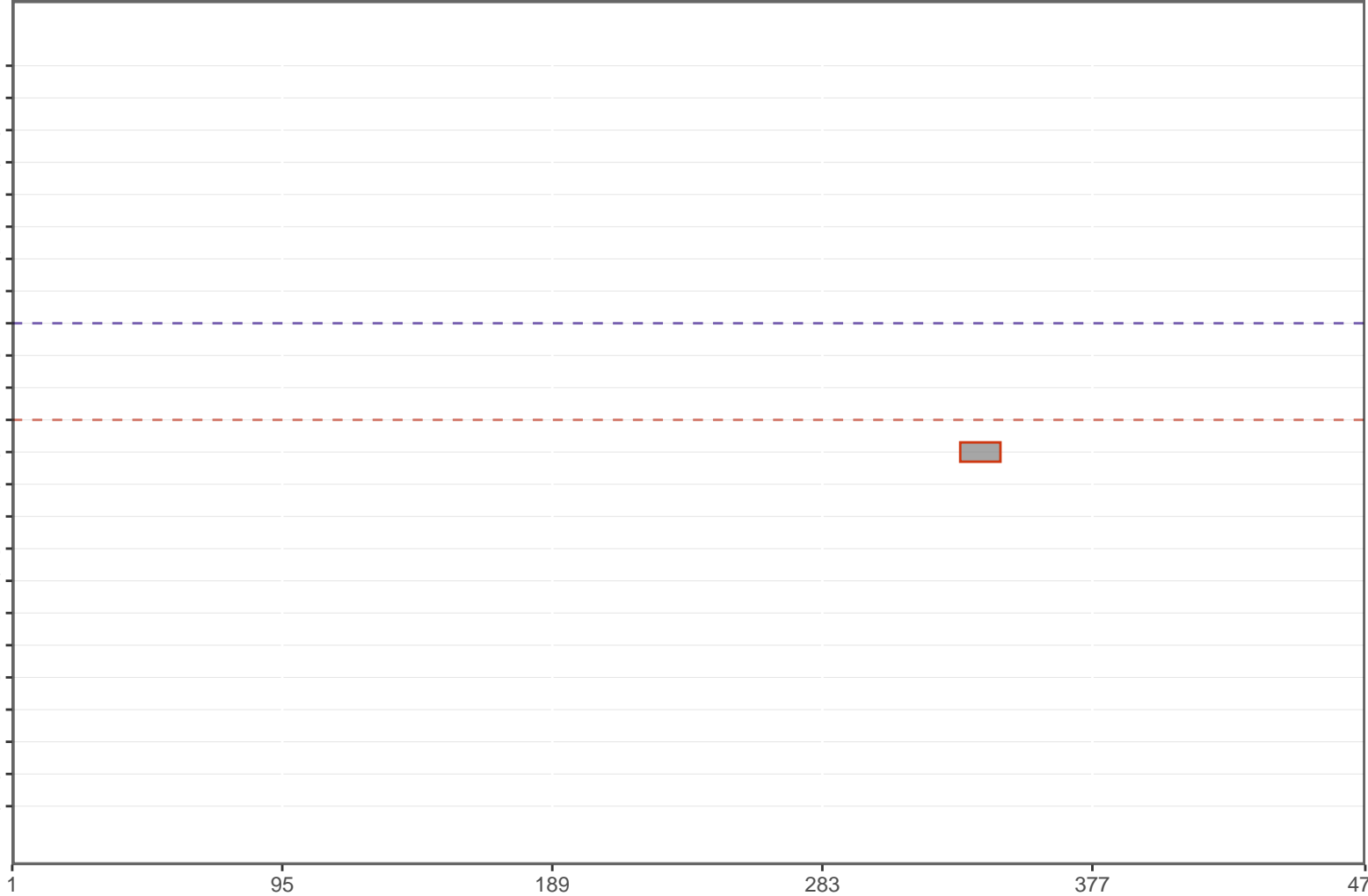
MW indication



Molecular weight

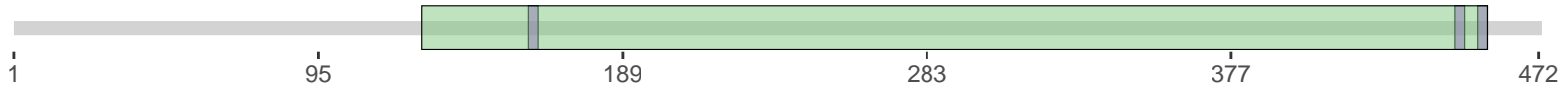


Gel Slice



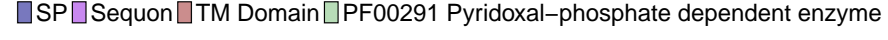
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IVTRMLLGAELVIRGVHSGTATLKDATSEAIRDWTNIVETHYILGSAVGHPPYPMVMVREFHAWIGKETRKALEKRWGKPDVLAQVGGGNNAMGLFHEFVDEEDVRLVGVVAAGFGIDSGKHAATLTKGEVGVLHGAMSYLLQDEEDGGIVFPHSISAGLDYPGVPEHFLKDLGRAEYVYGTDEEALFAFKRLRLEGIIPALETSHALAVLEKLCPTLPNGTKVVLNCGSRGDKDHTAKYLVY

NbL08g07290.1 trafficking_protein_particle_complex_subunit_3-like [MW = 20.89 kDa]

No. of times detected



log(intensity)



Values from



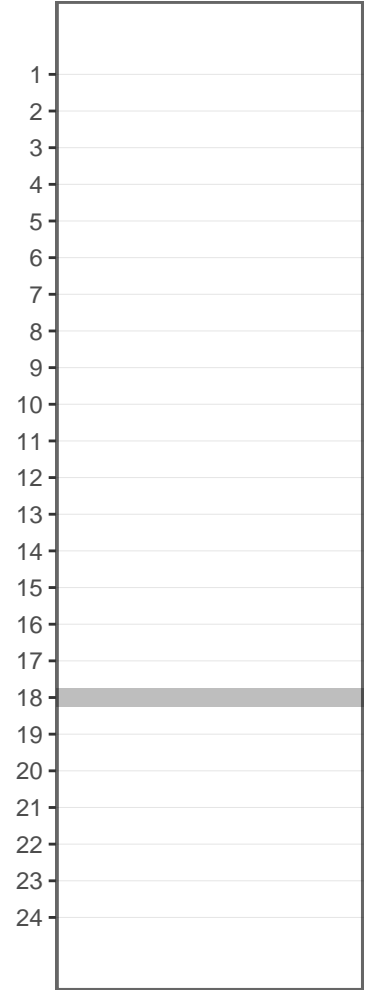
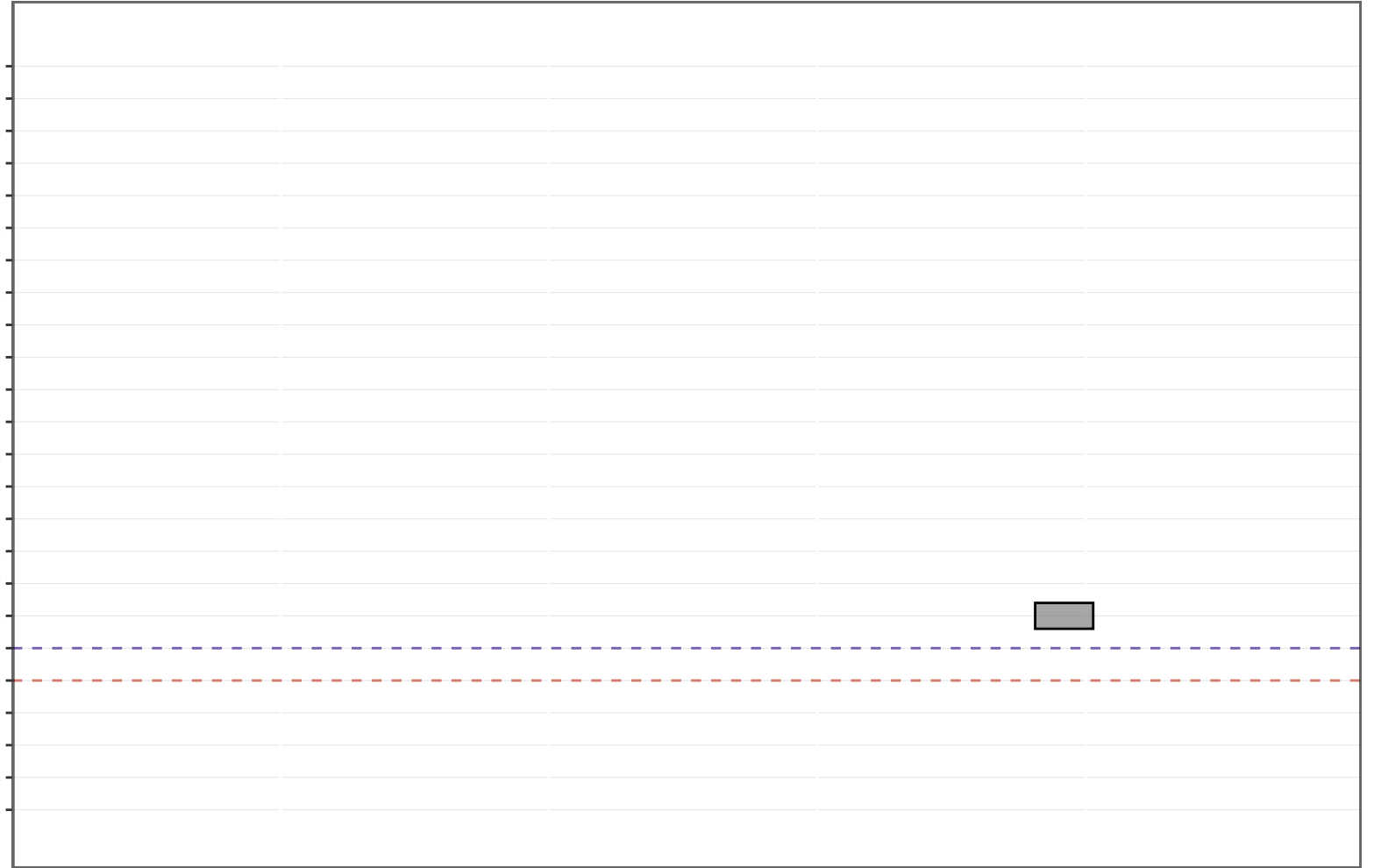
MW indication



Molecular weight



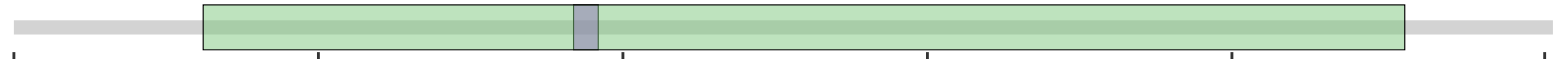
Gel Slice



Peptide counts over 4 repeats

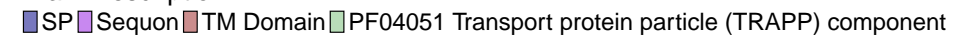


Protein length



Pfam domains

Pfam Description



Protein sequence:

VIAKVLKMLFLQVATVGNWDAEGFTTCSLIEDNPLVDFVELPDTCCGGLYCNLGGVIRGALEMVSMKTEVTWRDMLRGDDAFELQKILRGVPEEYPPKDEE

NbL08g07230.1 50S_ribosomal_protein_L24_chloroplastic-like [MW = 21.15 kDa]

No. of times detected



log(intensity)



Values from



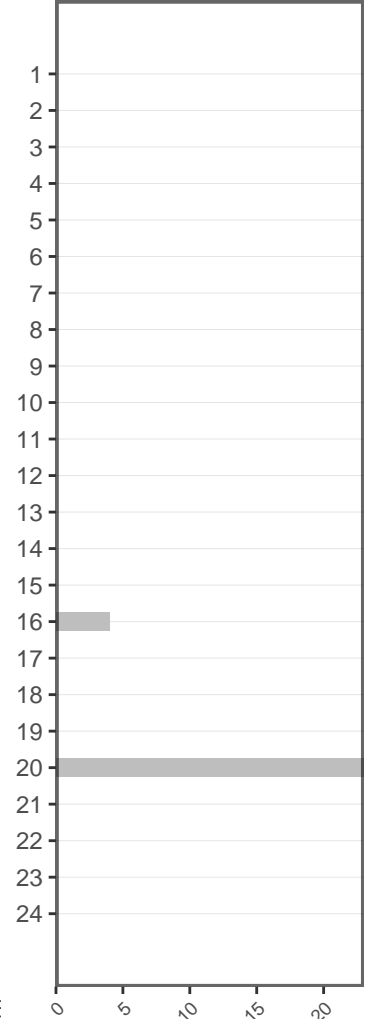
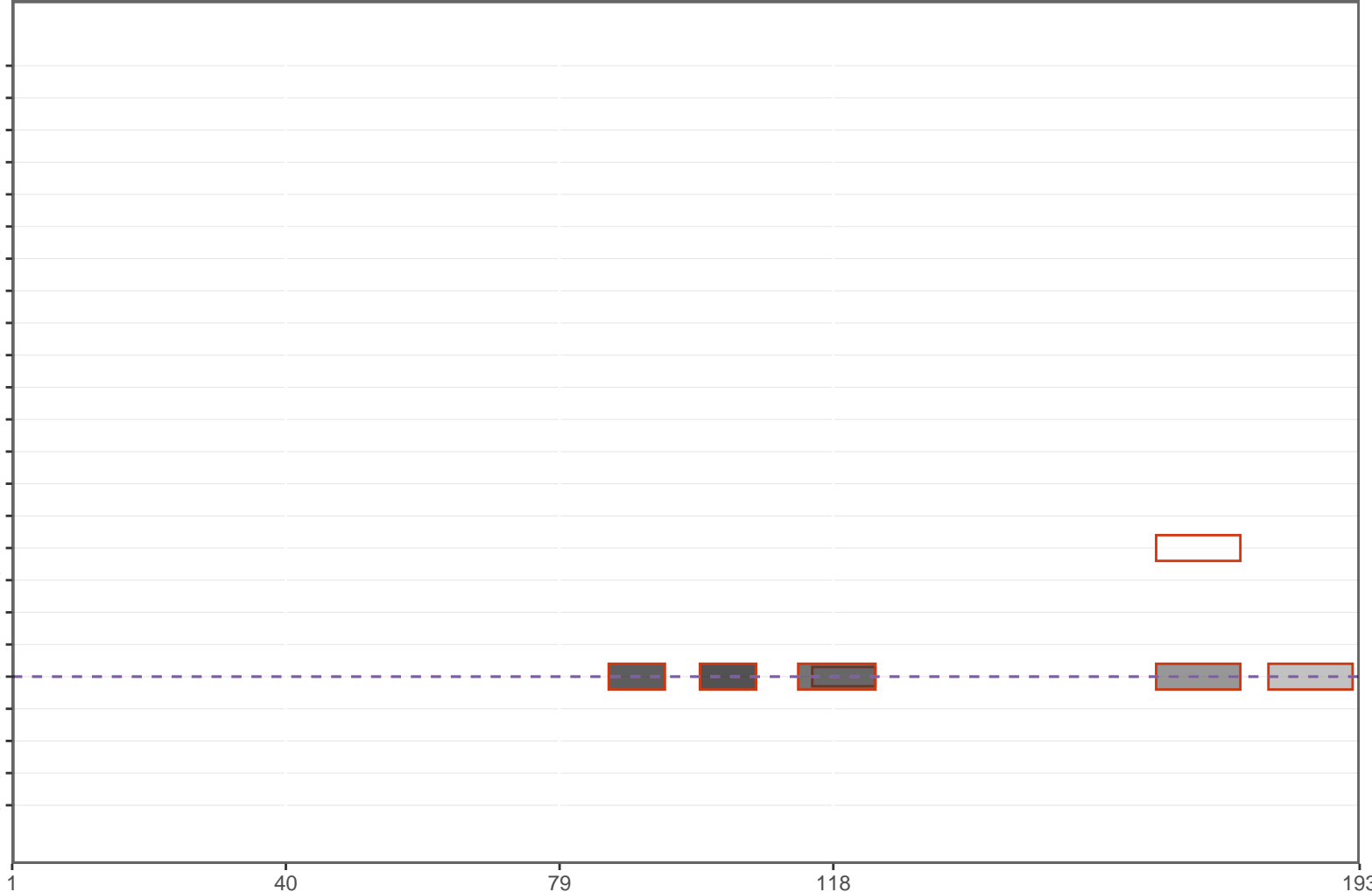
MW indication



Molecular weight

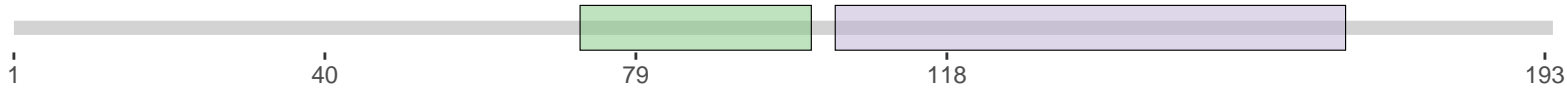


Gel Slice



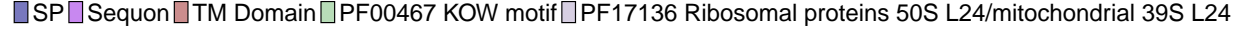
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

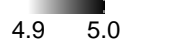
DKGKGGEITEIKQINRKYVVEENLKRTHVKSRENEPQQIKIEAPHISNMLVSKGKVASRVGHKTLONGKRVRYLVKLTGEIDSAENWKRRAVKETKTEFAVAATP

NbL08g07210.1 60S_ribosomal_protein_L8 [MW = 34.62 kDa]

No. of times detected



log(intensity)



Values from



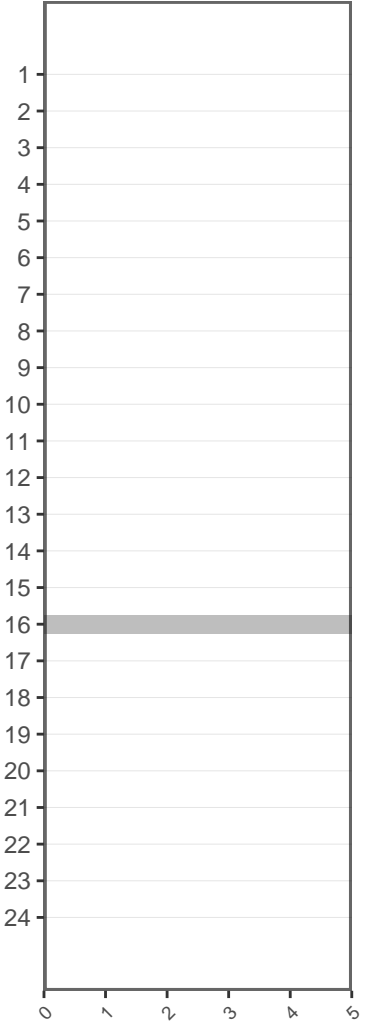
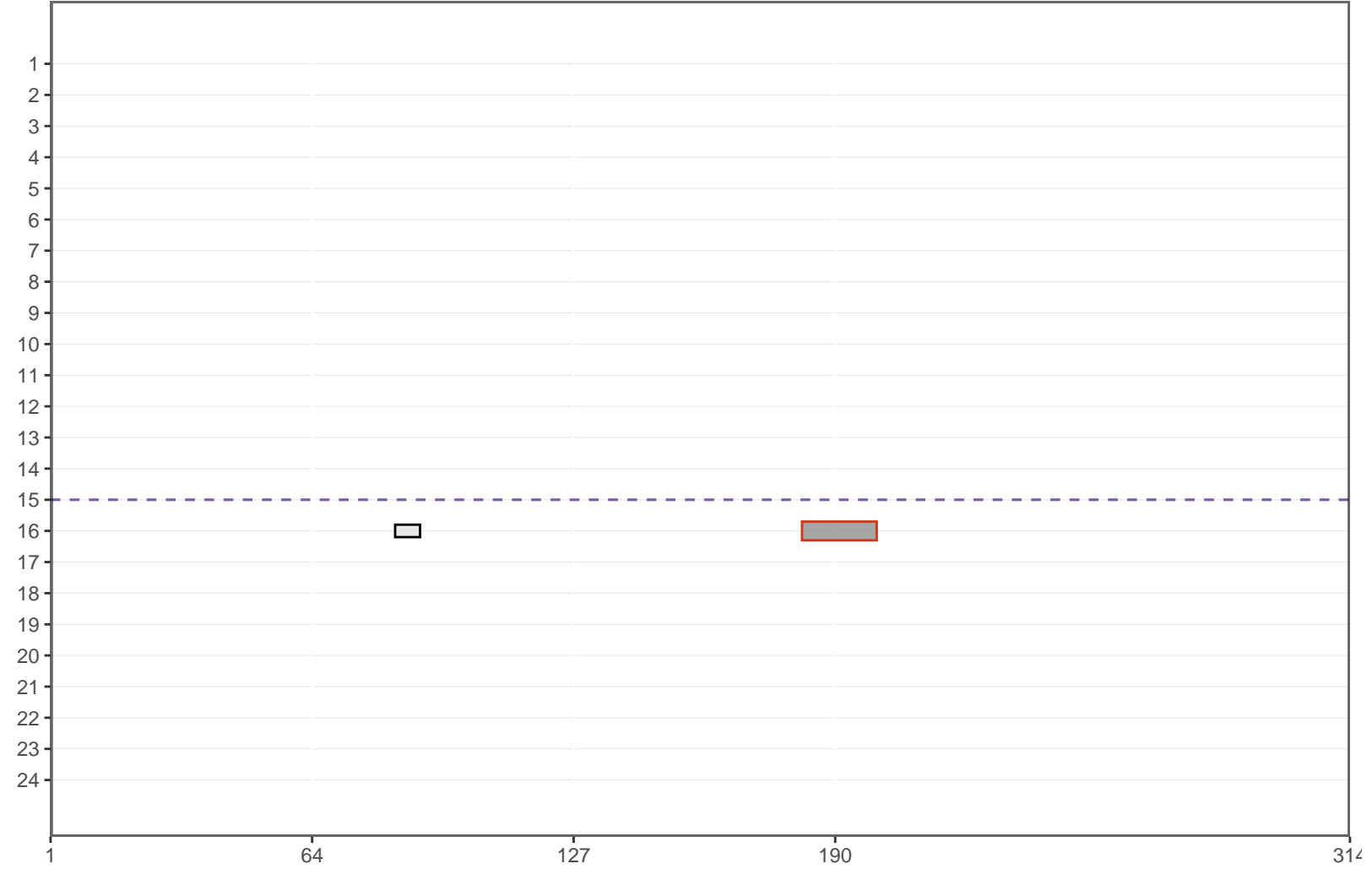
MW indication



Molecular weight



Gel Slice

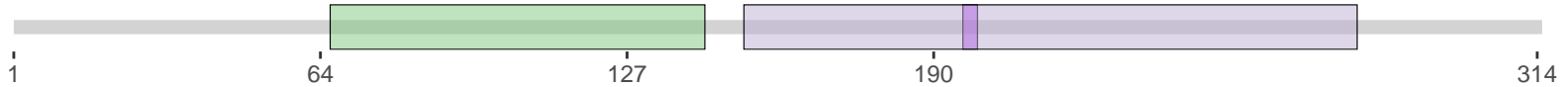


Protein length

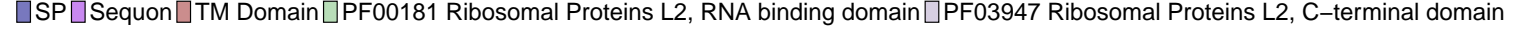


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KKATLMVGNVLPRLRSPFEGAVVGVNVEHKVGDGRGVFARSGSDVAIWHHPDNGTTRVWLPESGAKKVPESGRAMIGVAGGRTEKPKMLKAGNAYHKVYKRVKRWKPKVGRVGMNPFVEHPHGGNHQHGHAHSTVRRDAPPDQKVLIAARRTGLRGGAAATAKAKA

NbL08g07080.1 uncharacterized_LOC107808755 [MW = 27.53 kDa]

No. of times detected



log(intensity)



Values from



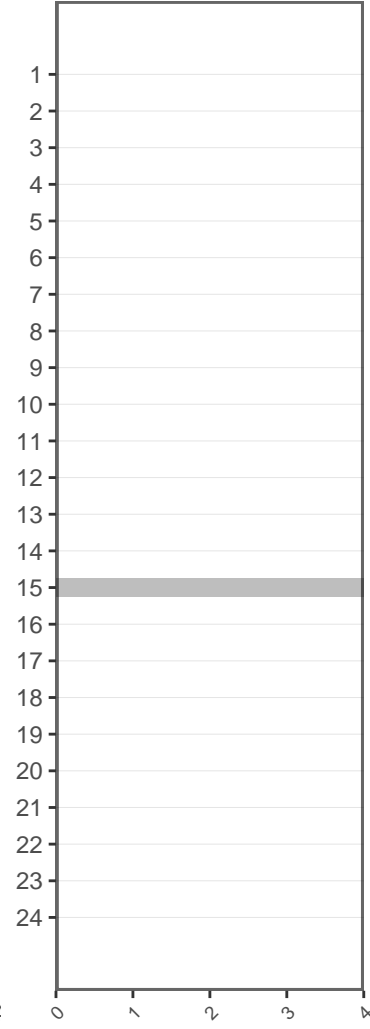
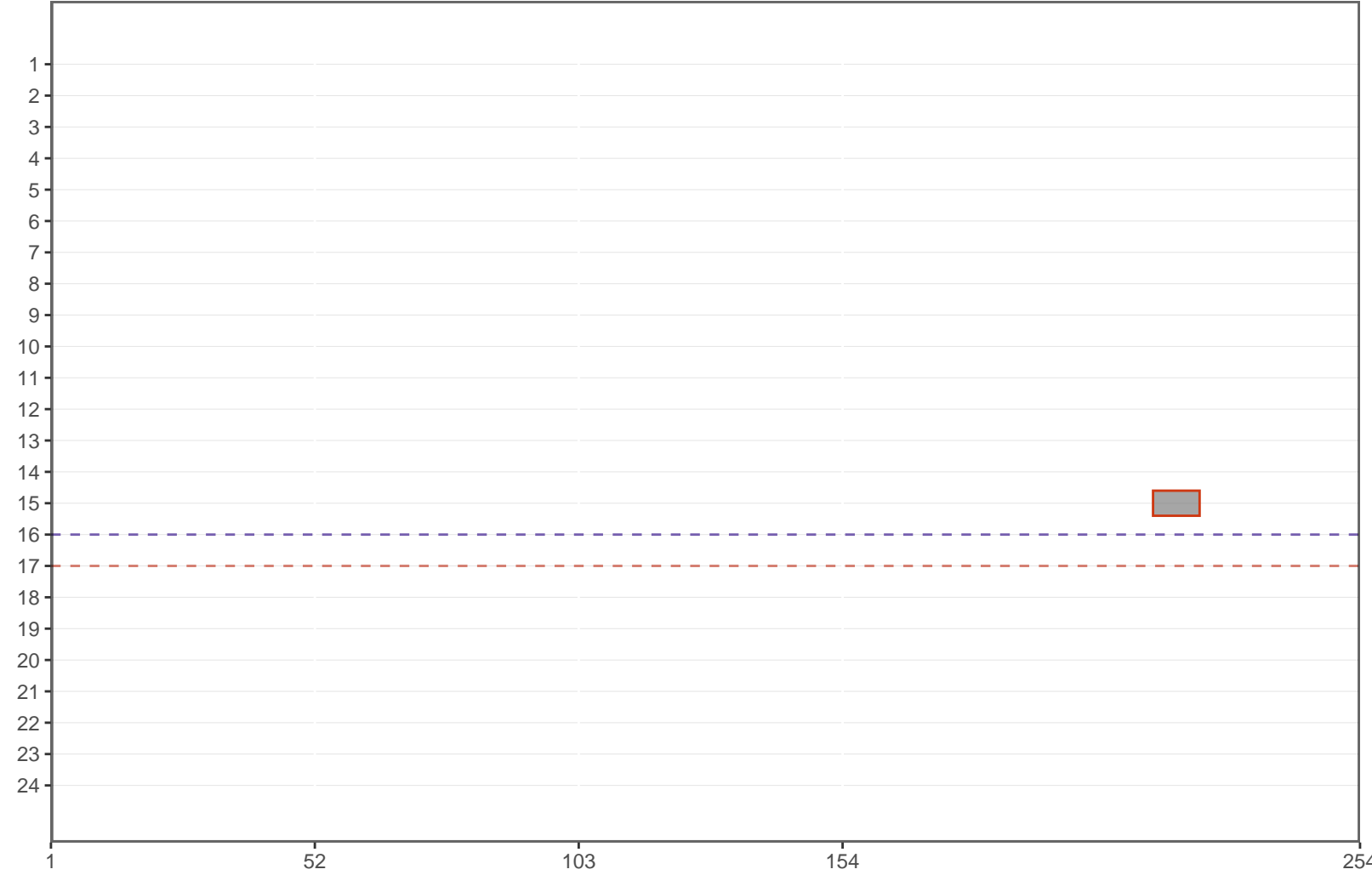
MW indication



Molecular weight

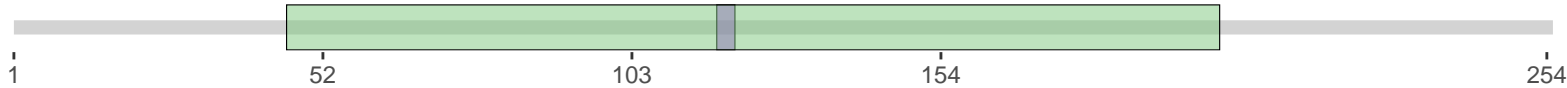


Gel Slice



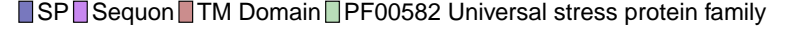
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

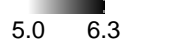
DNFTATYKSSALAQPLVDAQIPYKHIVKDKDMKERLGLVEVRLGLSAVIMGSRGFGATKRGNDGRLGVSVDYGVRRHGVPLVAVRRYPDEKDGGAARKVGVGVAASAAKEEETEYHDAEDDRGGGPAKGGKTDN

NbL08g06850.1 thioredoxin-like [MW = 19.92 kDa]

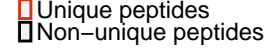
No. of times detected



log(intensity)



Values from



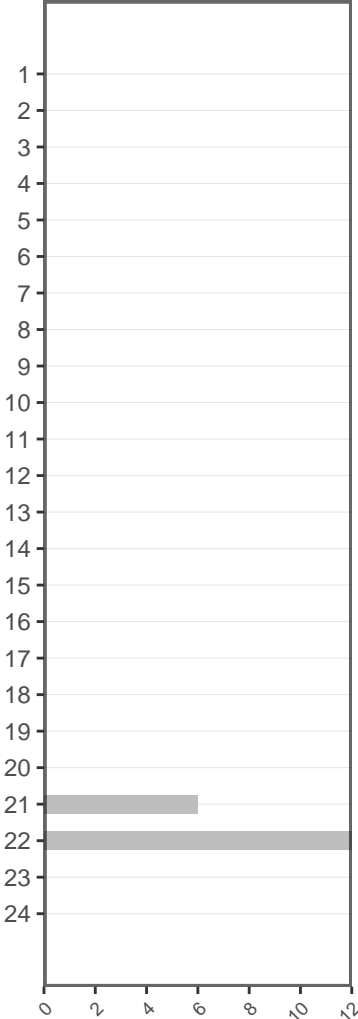
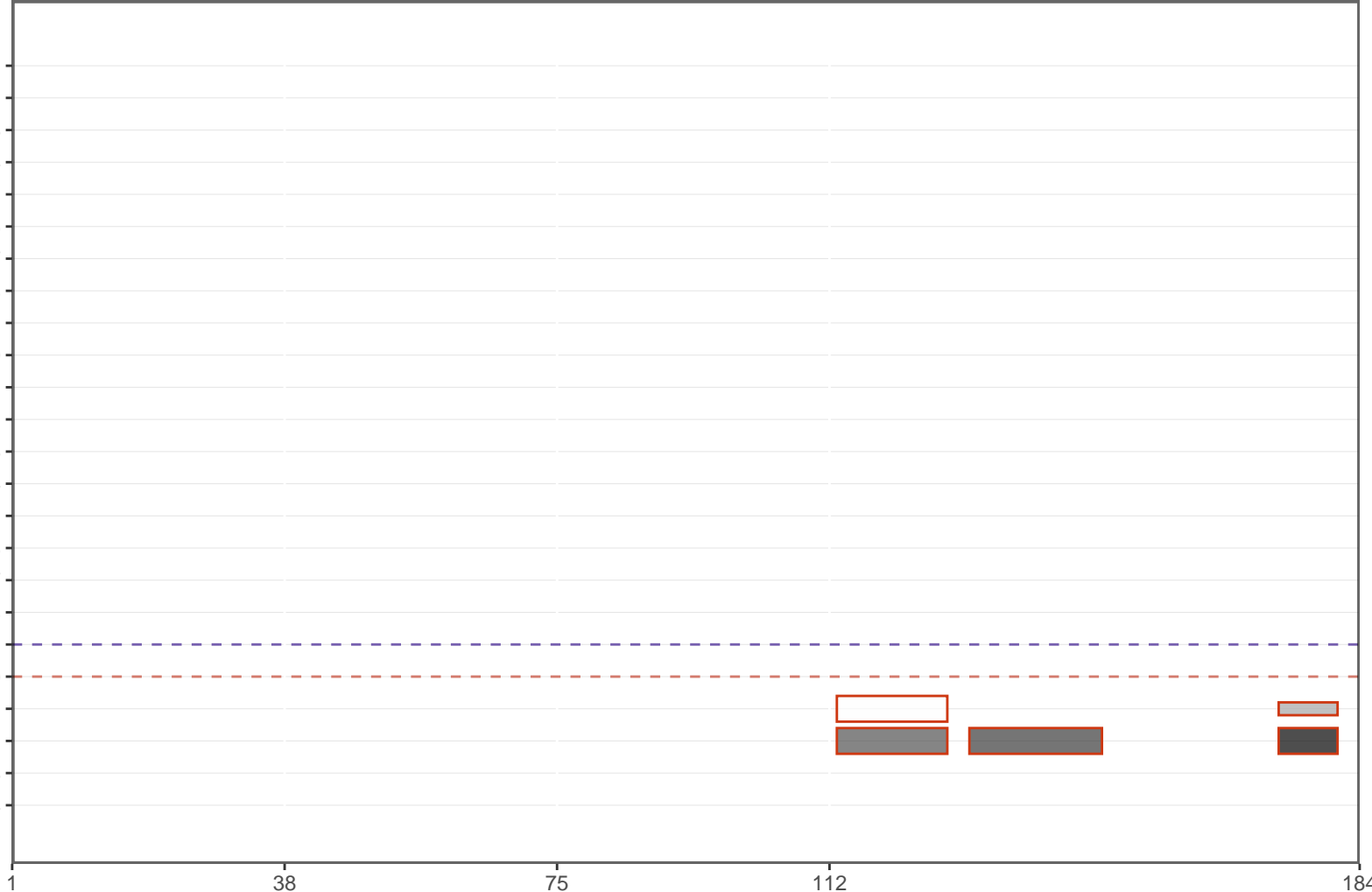
MW indication



Molecular weight

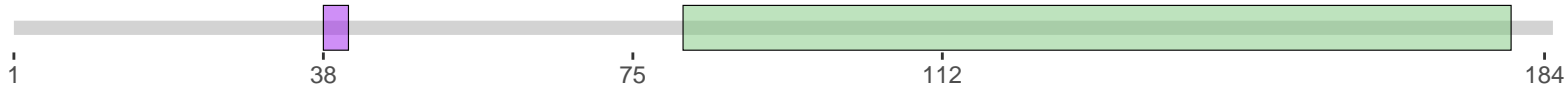


Gel Slice



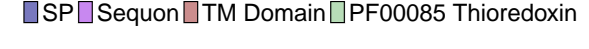
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

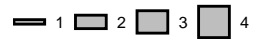


Protein sequence:

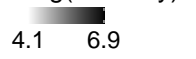
IAVQVPAVTDKTYKGLVIESDLPVLFVFWAPWGGPCRMHPVIGELSGEYAGKFKFFQLNTDESPSTASEYGRISPTVMIFKGGKEDAVIGAVPKTTLTSEIKFL

NbL08g06660.1 malate_dehydrogenase_mitochondrial [MW = 36.23 kDa]

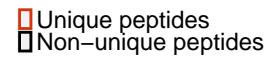
No. of times detected



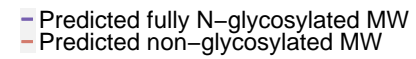
log(intensity)



Values from



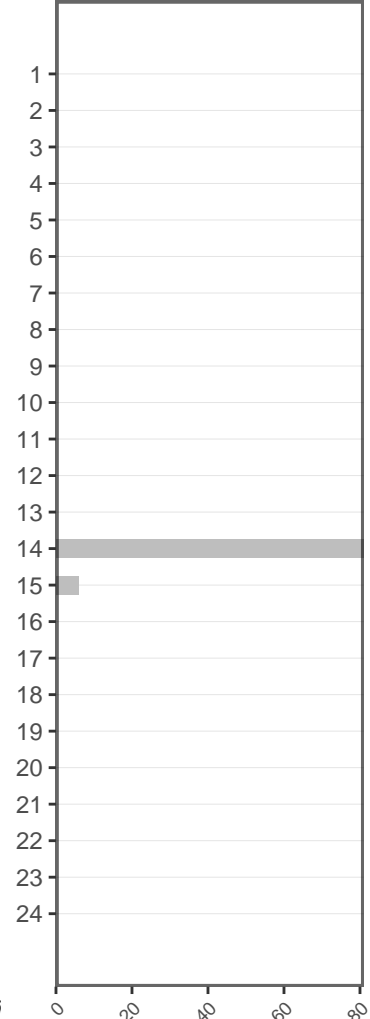
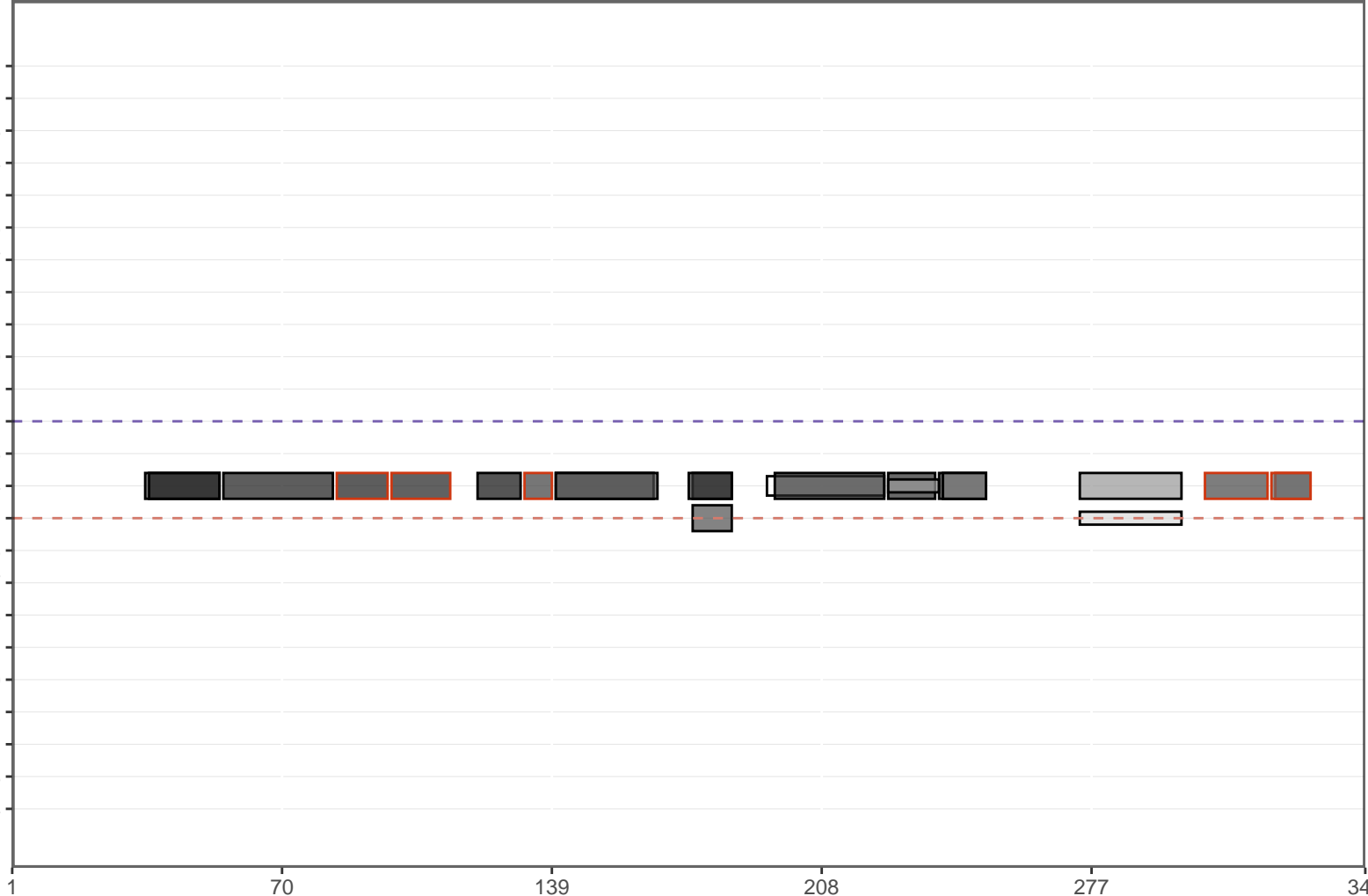
MW indication



Molecular weight

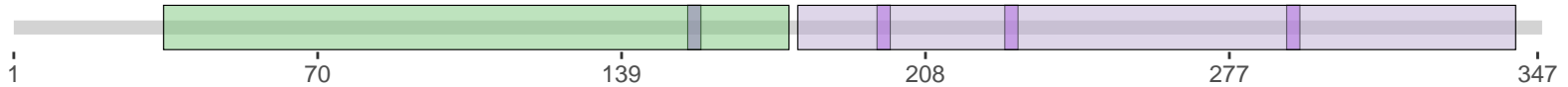


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00056 lactate/malate dehydrogenase, NAD binding domain
- PF02866 lactate/malate dehydrogenase, alpha/beta C-terminal domain

Protein sequence:

LEVFKAGTYDEKRLFGVFTLDAVRAKTFYAGKAKVNVSDVWVWVGGHAGITLPLLGATPKANLSDDEEVALTKRTQDGGTEVVEAKAGKGSATLSMAYGAIFAAGLKLNGVDPVVEGTFVQGNVTELPFFAFKVRLLGKNGVEEVLGLGLSDVKEKGLLEALLPELKSSEKGGKIFANEN

NbL08g06580.1 uroporphyrinogen_decarboxylase_1_chloroplastic [MW = 46.32 kDa]

No. of times detected



log(intensity)



Values from



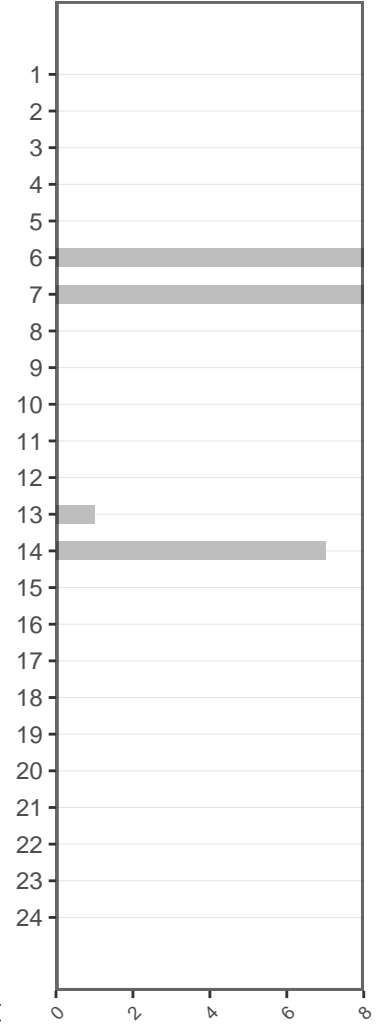
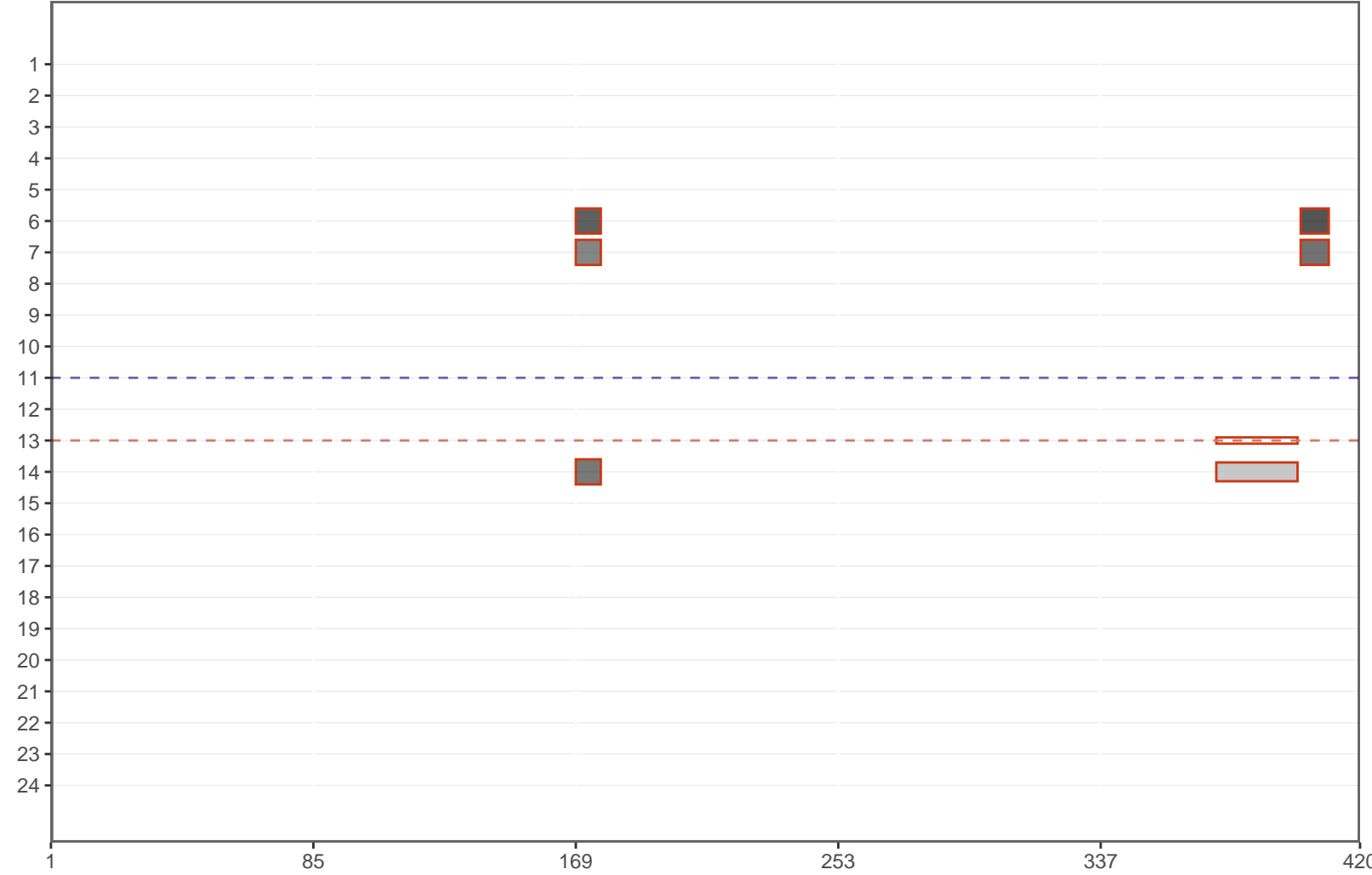
MW indication



Molecular weight

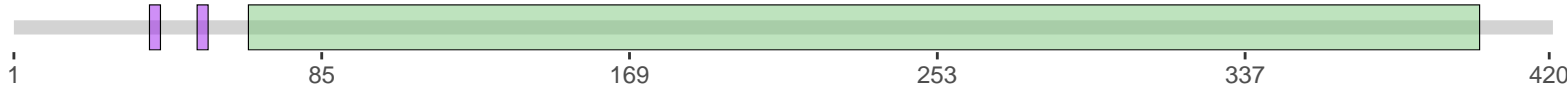


Gel Slice



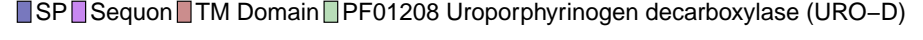
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

JAALVLFVGPWITATYVEGGTRFRYTRIKDGMGHTAPHVLRALLSHLSKAAIEYVQVEGSAHGDGFDGSGGQLPHMMWDGWSKPYDEIVATKRKCPQPTFLVLYINGNGLLERMKETGVGVGLDWTVDMEGRKRLGTDKGGQGVDPAGLFGPLPALTDEIERVVKASGTRGHNLGHGVALVGTPEEAAVHFFDVAKEGFNFDKVEDRISEANTVAAL

NbL08g06560.1 multiprotein-bridging_factor_1b [MW = 15.25 kDa]

No. of times detected



log(intensity)



Values from



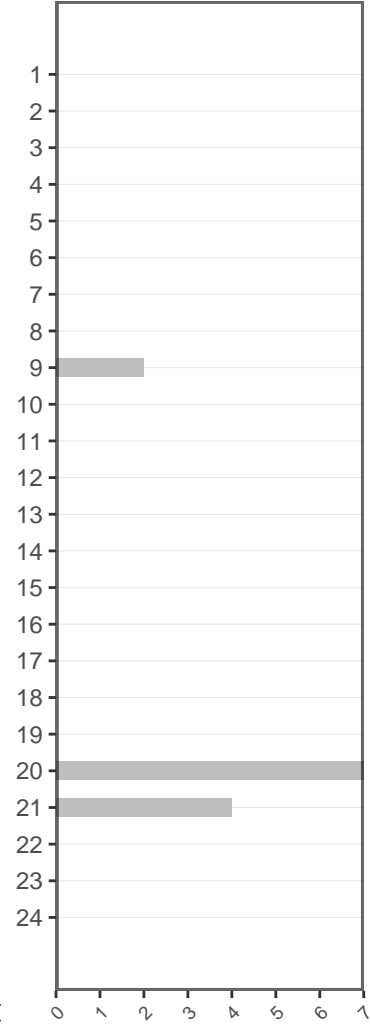
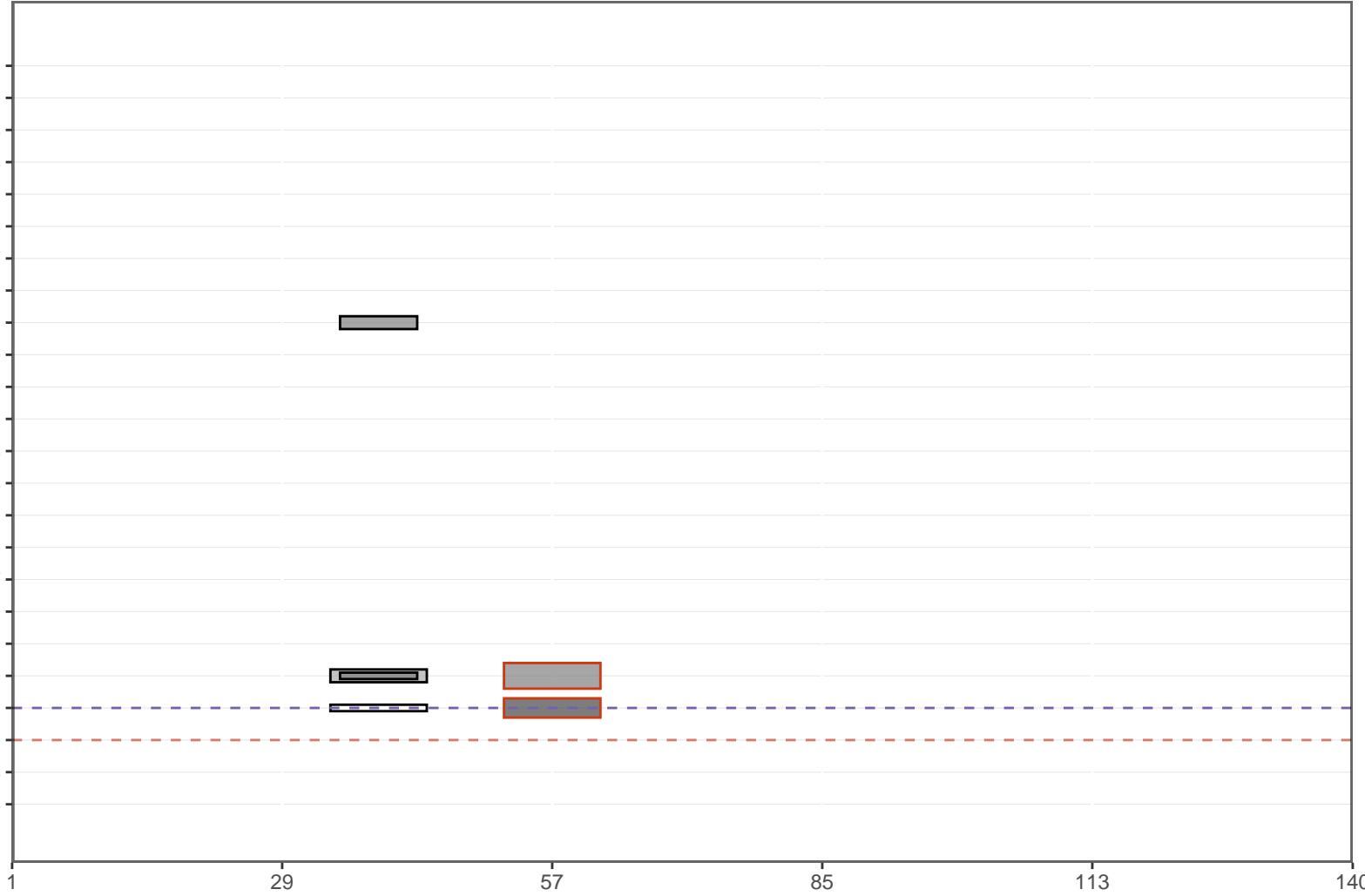
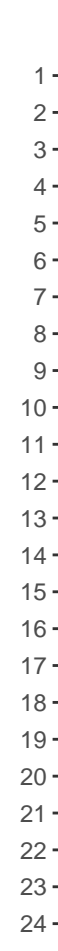
MW indication



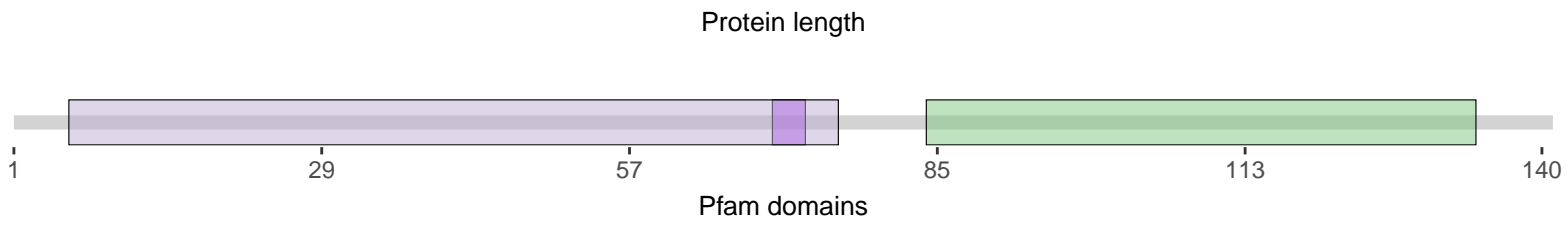
Molecular weight



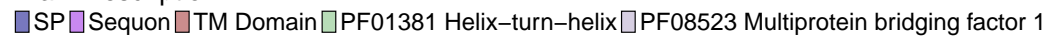
Gel Slice



Peptide counts over 4 repeats



Pfam Description



Protein sequence:

STSLNTRTLDEEDTENLSHEKVPTELKKAIMGARQDDKLLTQAGLAGLINEKPKIQIEYESGKAIPNGQHSKMERALGAKLRGKK

NbL08g06510.1 gamma-glutamyl_hydrolase_2-like [MW - SP = 35.7 kDa]

No. of times detected



log(intensity)



Values from



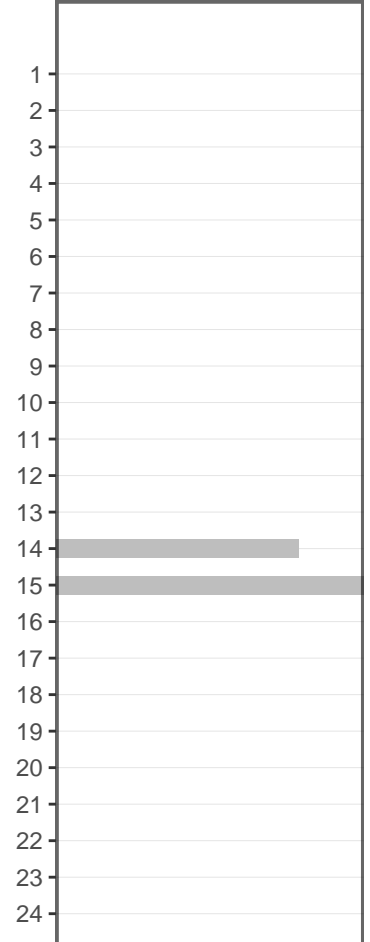
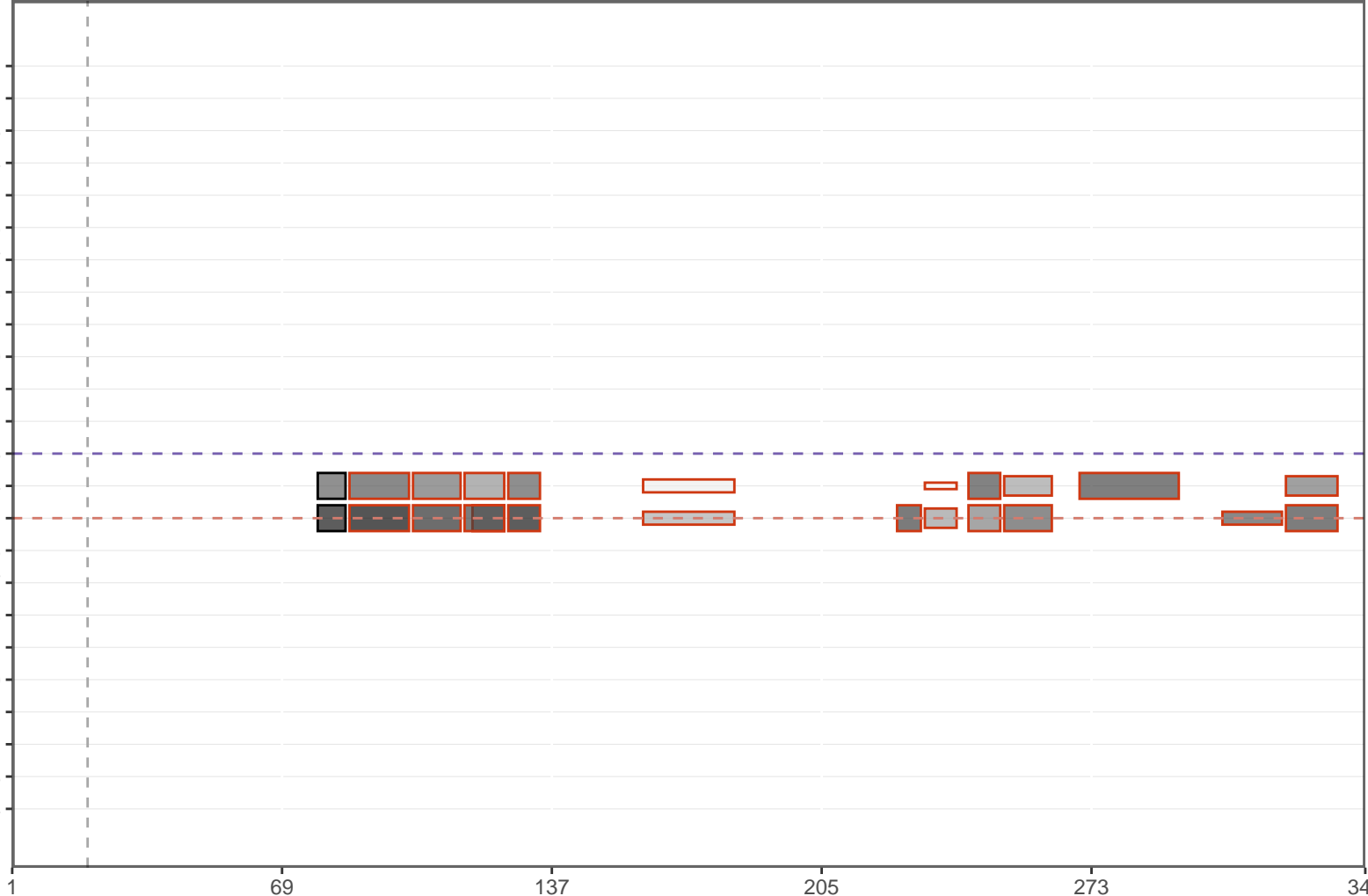
MW indication



Molecular weight

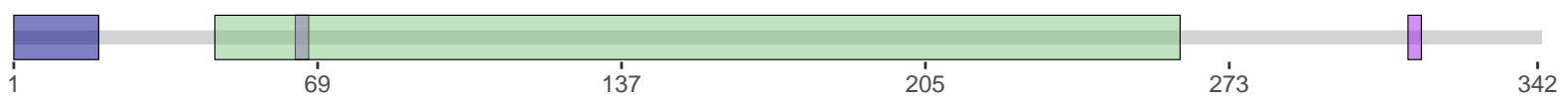


Gel Slice



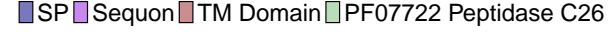
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



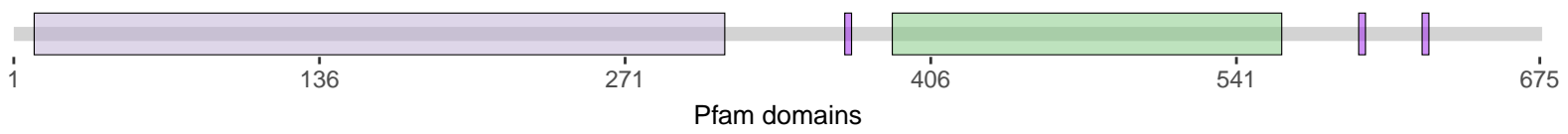
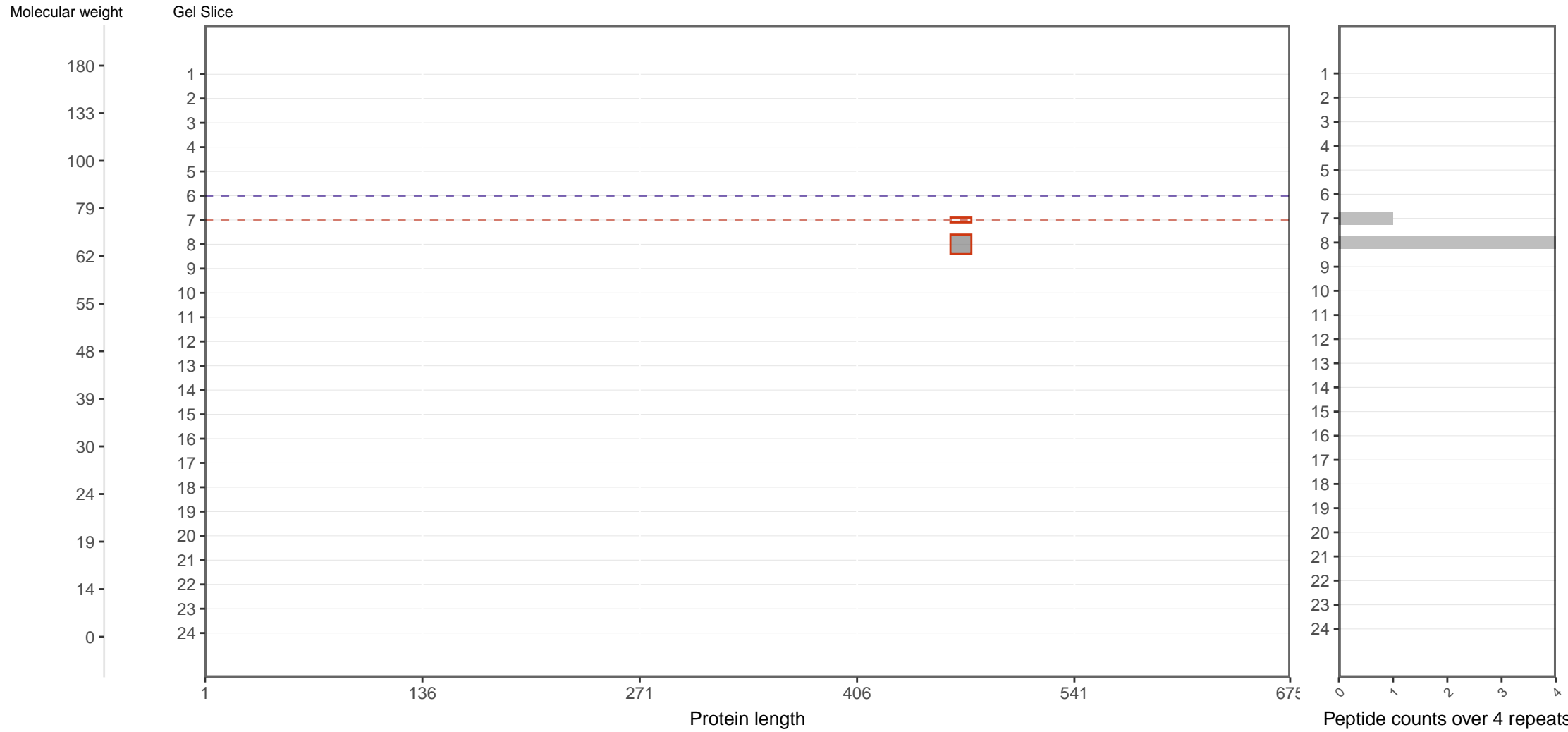
Protein sequence:

NNILEEFAANDASTVQVFNKLERIVFGRFPVLLKMKMSTHGLVMQNHFGISPERFQANKDLSFFRLTSTDKNKVYVSTAGARRYPVITALQWHPEKNVFEWRSGQPHTEDAIGVTGHVANNVFESEGRKSSNKPVPSKLLDNLNNYSPFGAKGAGGGFDEVLVFSRPRALSEL

NbL08g06470.1
 trifunctional_UDP-glucose_46-dehydratase/UDP-4-keto-6-deoxy-D-glucose_35-epimerase/UDP-4-keto-L-rhamnose-reductase_RHM1
 [MW = 76 kDa]

No. of times detected
 1 2 3 4

log(intensity) 3.7 4.1
 Values from Unique peptides Non-unique peptides
 MW indication Predicted fully N-glycosylated MW Predicted non-glycosylated MW



Pfam Description
 SP Sequon TM Domain PF04321 RmlD substrate binding domain PF16363 GDP-mannose 4,6 dehydratase

Protein sequence:
 /GDVSGALLPFRMLMMPGGHERHLDGSEKYDGGSSSEFSAKSNETKTVAPAPKSSDVPKSPFKFLYGRGTGWGGGLKGLCEKGGIPVEYGRGRLDRSKLLADNAVYKPTHYVNAAGYGRPNVYDWSHSPETIRTNAGTLELADVCREHGLLMMNFATGCFEYDANHLGGSGFKKEEKPFNFAGSFYSKTKAMVEELLKEYDNYGTLRVMPISDDLNPFRNFKISRYNKVYNPNPSMTLDELLEPSEIMANRNLKGNVFNFPQVYSHNLELMEYKYNPEF

NbL08g06350.1 peroxisomal_(S)-2-hydroxy-acid_oxidase [MW = 40.66 kDa]

No. of times detected



log(intensity)



Values from



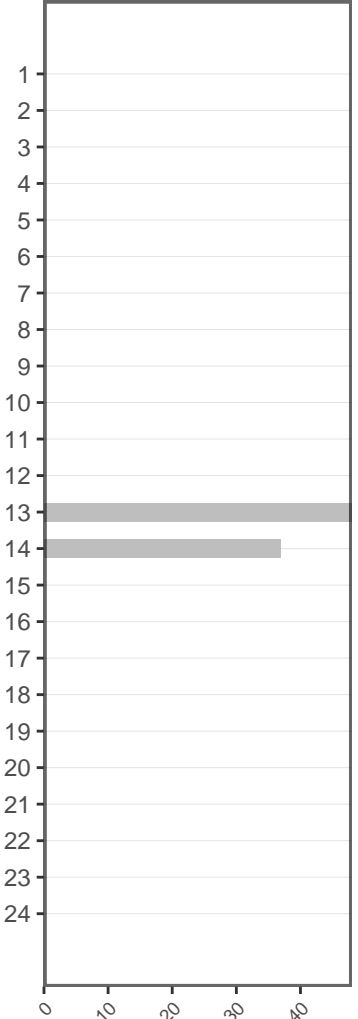
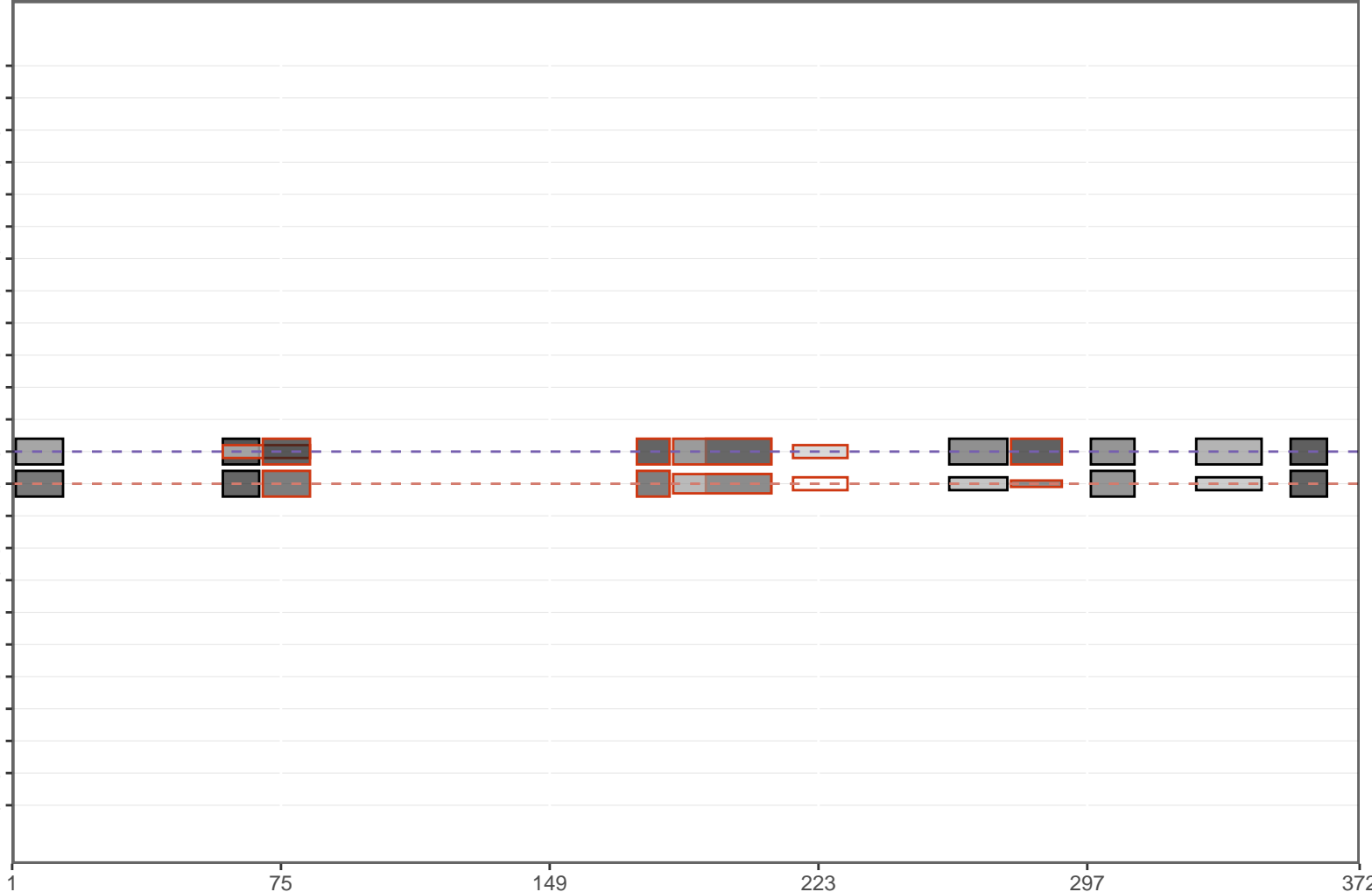
MW indication



Molecular weight

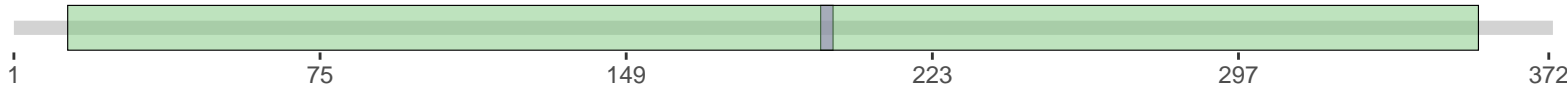


Gel Slice



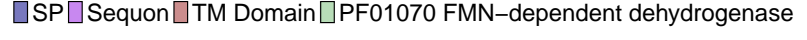
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

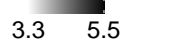
LLOPFLTLKNFEGLELGLKMDKDEANDSGLSGYSVAGGIDRSL6WKDQGLQTTSLPLVKGVLTAEDARIWVGAGAGIVSNHGARGQLDVPXTIMALEEVKKAAGGHVPLFDGGVRRGTDVFKALALGASGVFGRPFVFSLSLAEEGEGIRKVLQGMMDREFELTMALSGGRSLKETRNIHVAQWDAPRAALPTPRL

NbL08g06280.1 ultraviolet-B_receptor_UVR8 [MW = 46.97 kDa]

No. of times detected



log(intensity)



Values from



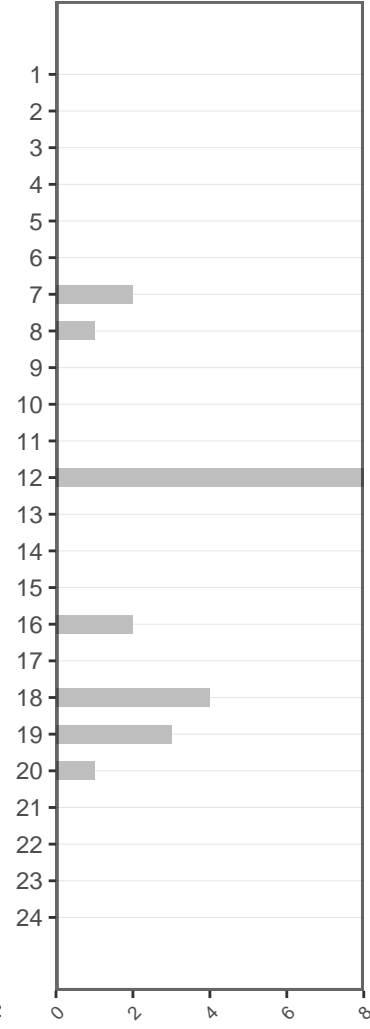
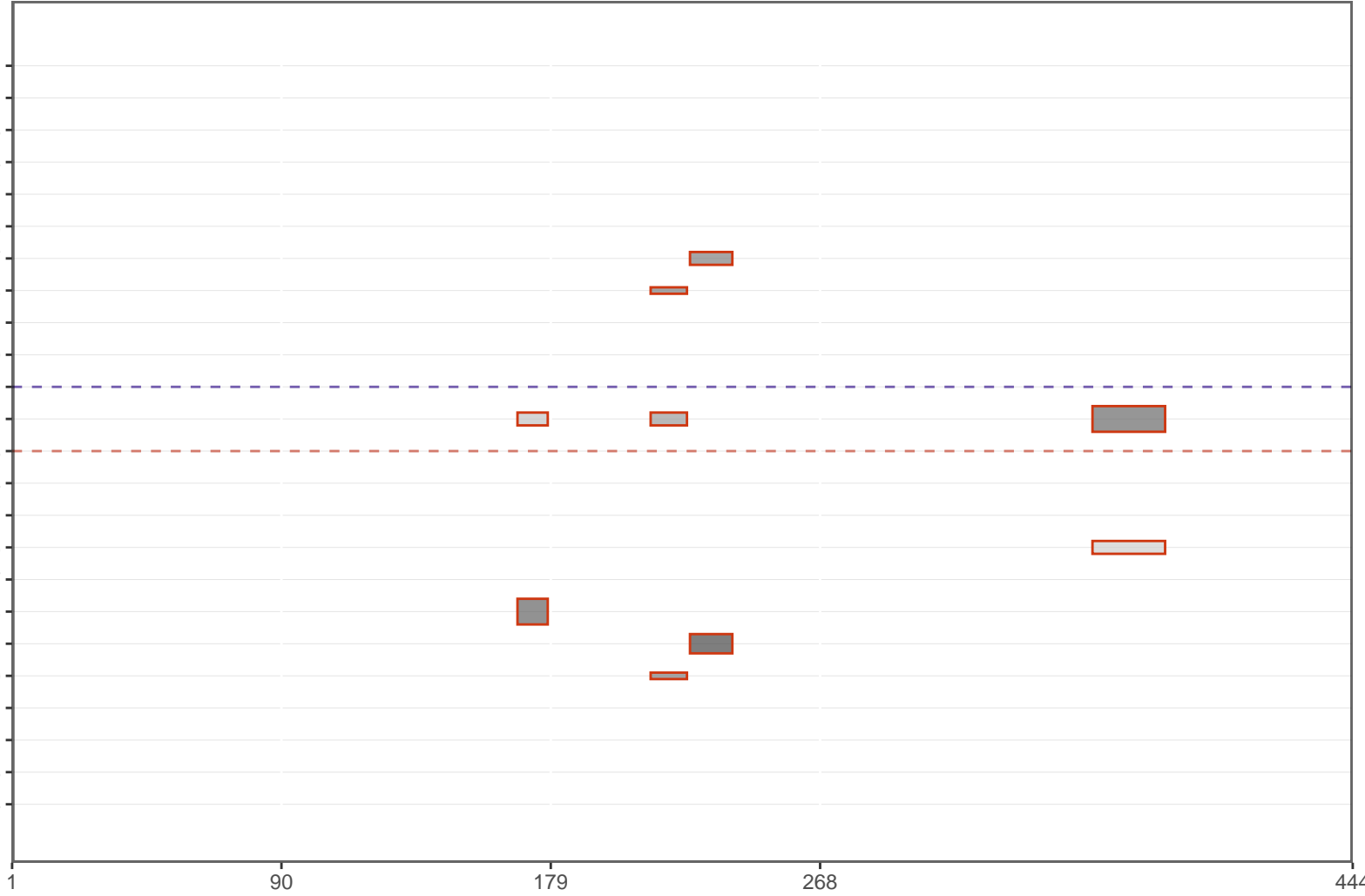
MW indication



Molecular weight

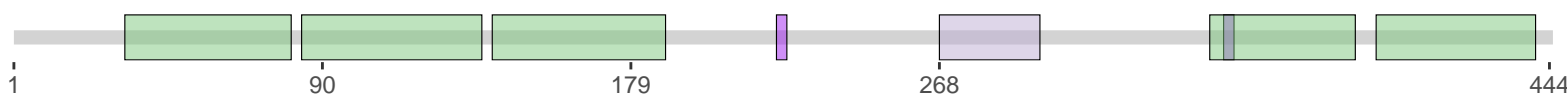


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00415 Regulator of chromosome condensation (RCC1) repeat
- PF13540 Regulator of chromosome condensation (RCC1) repeat

Protein sequence:

IQGRELESSPLESNTKLSGGEGSSAEAAEKSKVMEAMEKEKDMPLIWEFGVVEELHGLKLVADVAGGLDHSLLVGRDGTLSFGGSNYYGQLGRLNKDLGMGPVDQDFRPLIASGLGHSLLVCHGASSETTEDATSVVSGWGNRRSSQLGREGPEHIPQVVEGLSGETPIEVSGGRAHSLALTTKELVWVGGGKNGRLGLGSSDDEAFPMLEVELECTEVQAVAGLDHSLVWEE

NbL08g06270.1 chlorophyll_a-b_binding_protein_8_chloroplastic [MW = 29.34 kDa]

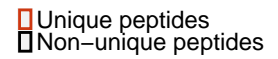
No. of times detected



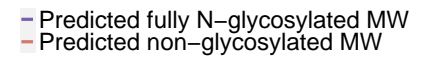
log(intensity)



Values from



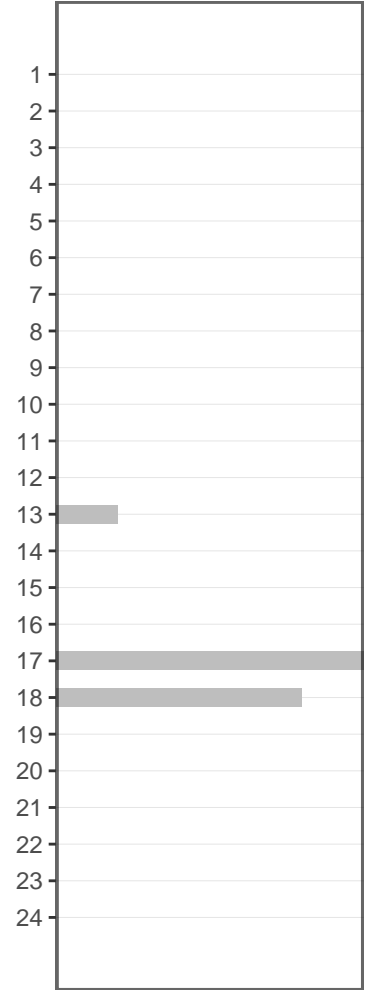
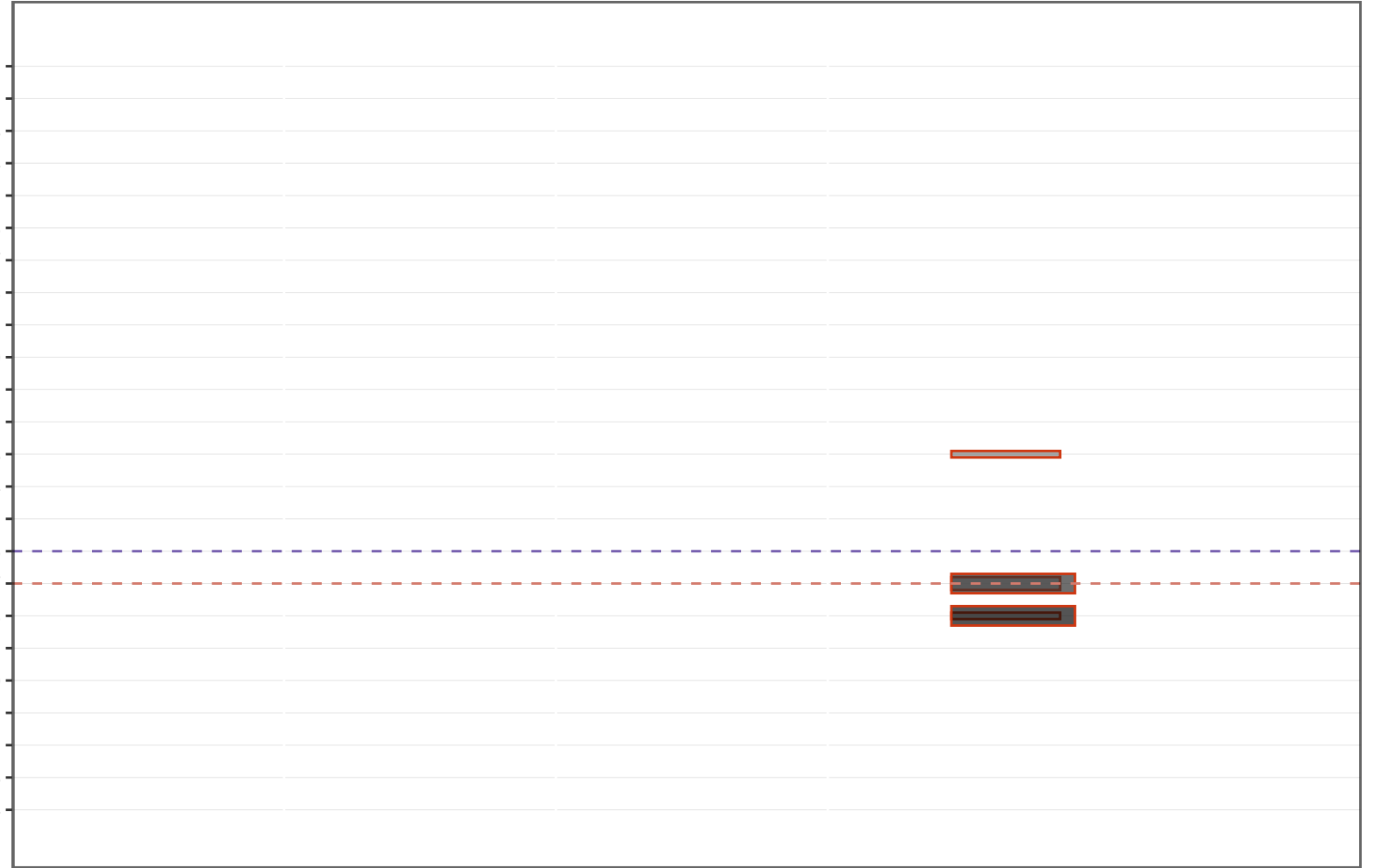
MW indication



Molecular weight



Gel Slice

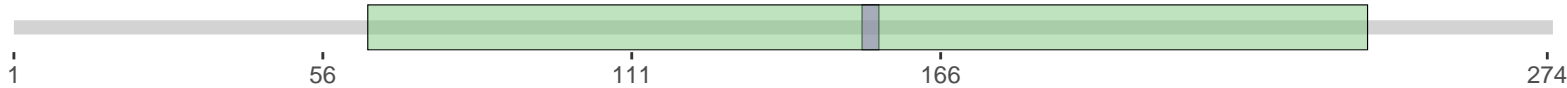


Protein length

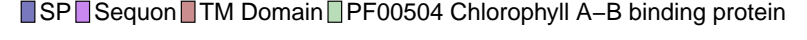


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LIPPETALPWFOTGWRPRAGTNYWADNVTFLVLEMLMGFAEHRFRFGDWAQKPGSMGKQVFLGKLGKGGSGEPWVPGPPFFNPLGFGKDEKSMKDLKLEVKVNGSRLLMMLALGYFIQGLVGTGVSQVQNLLEHLADPVRNNILNFKFH

NbL08g06260.1 ras-related_protein_RABB1c-like [MW = 23.15 kDa]

No. of times detected



log(intensity)



Values from



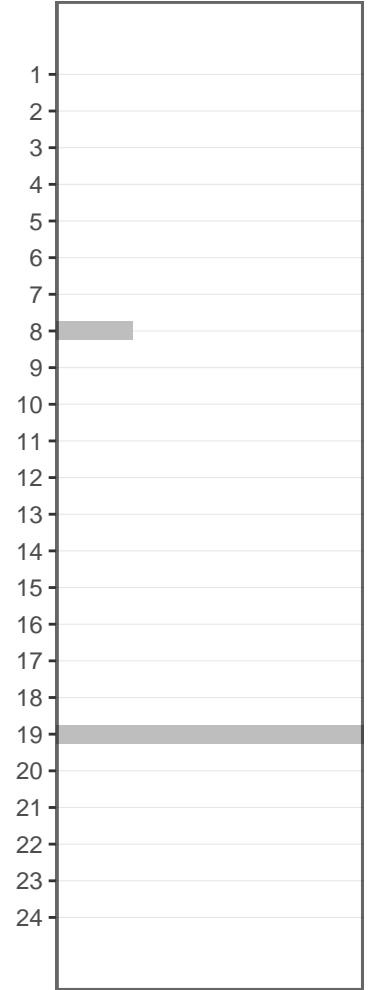
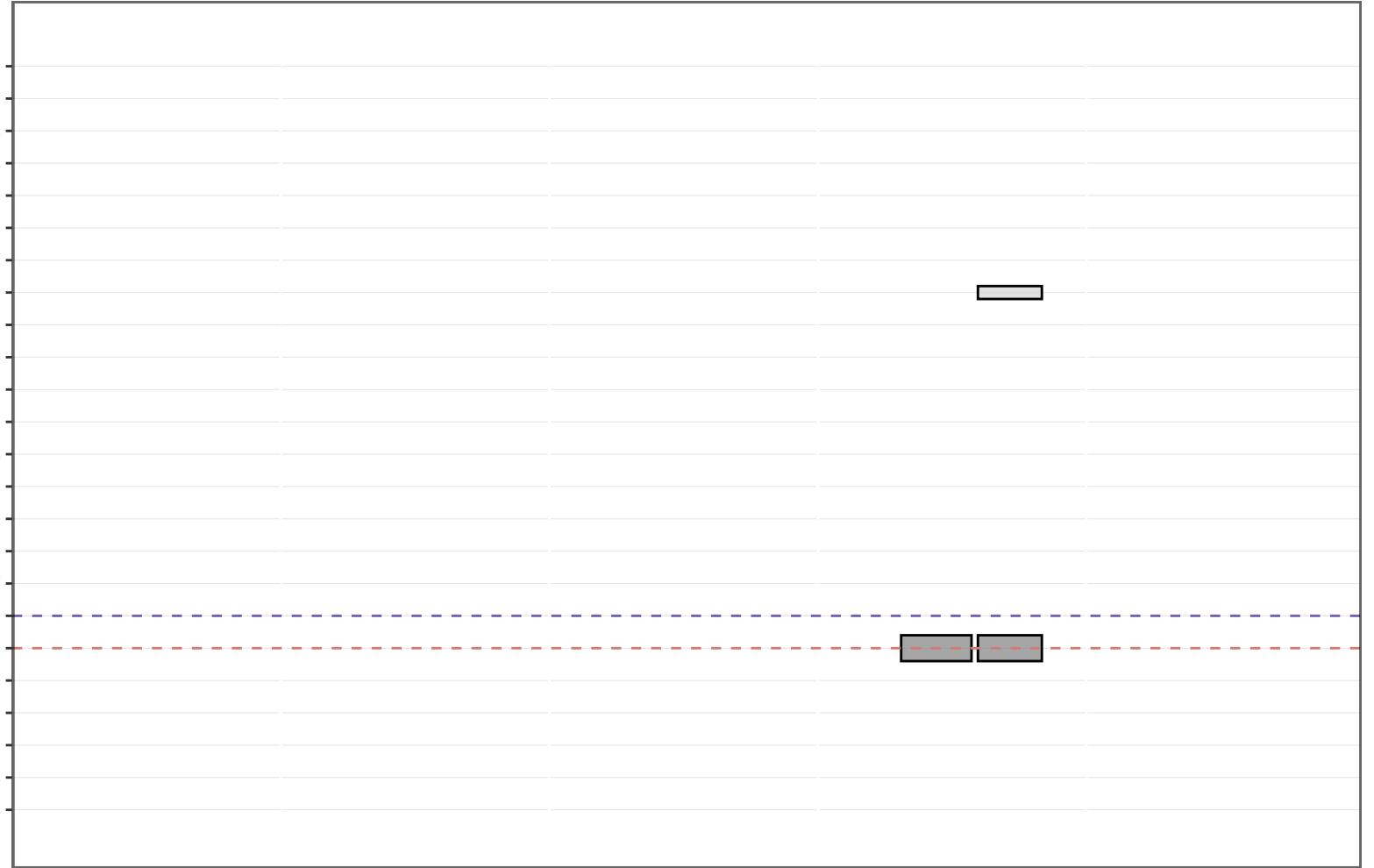
MW indication



Molecular weight



Gel Slice

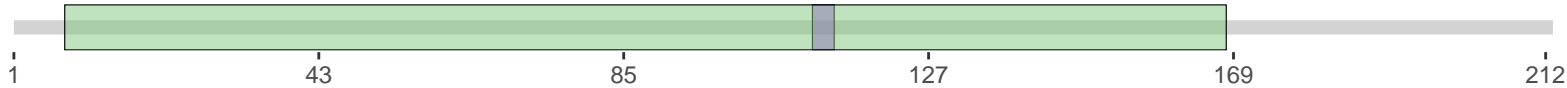


Protein length

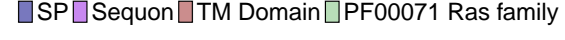


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

HLASVLEDAHQHANAMTILMIGNKGLAHRRAVSTEEEGGFANEHGLFMEASAKTAGNVEEAFIKTASTHYKKKGGVFDVSNANGIKFDYGLLPGSGGDRGAAAGGGGGGGS

NbL08g06160.1 ribose-phosphate_pyrophosphokinase_4-like [MW = 35.93 kDa]

No. of times detected



log(intensity)



Values from



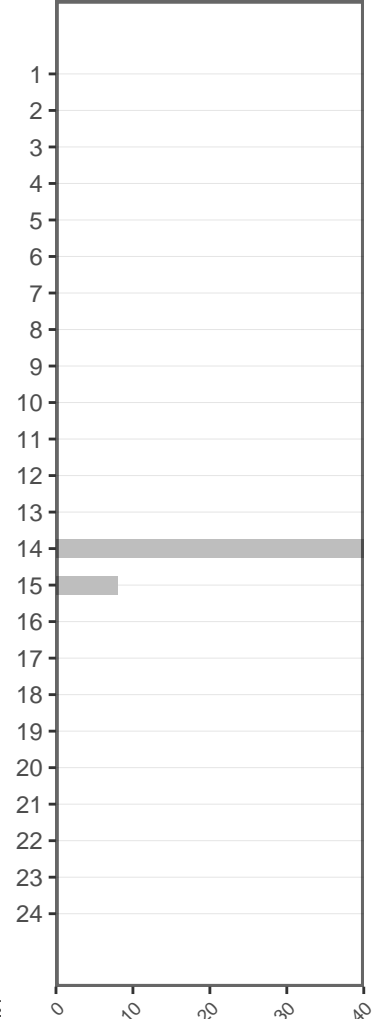
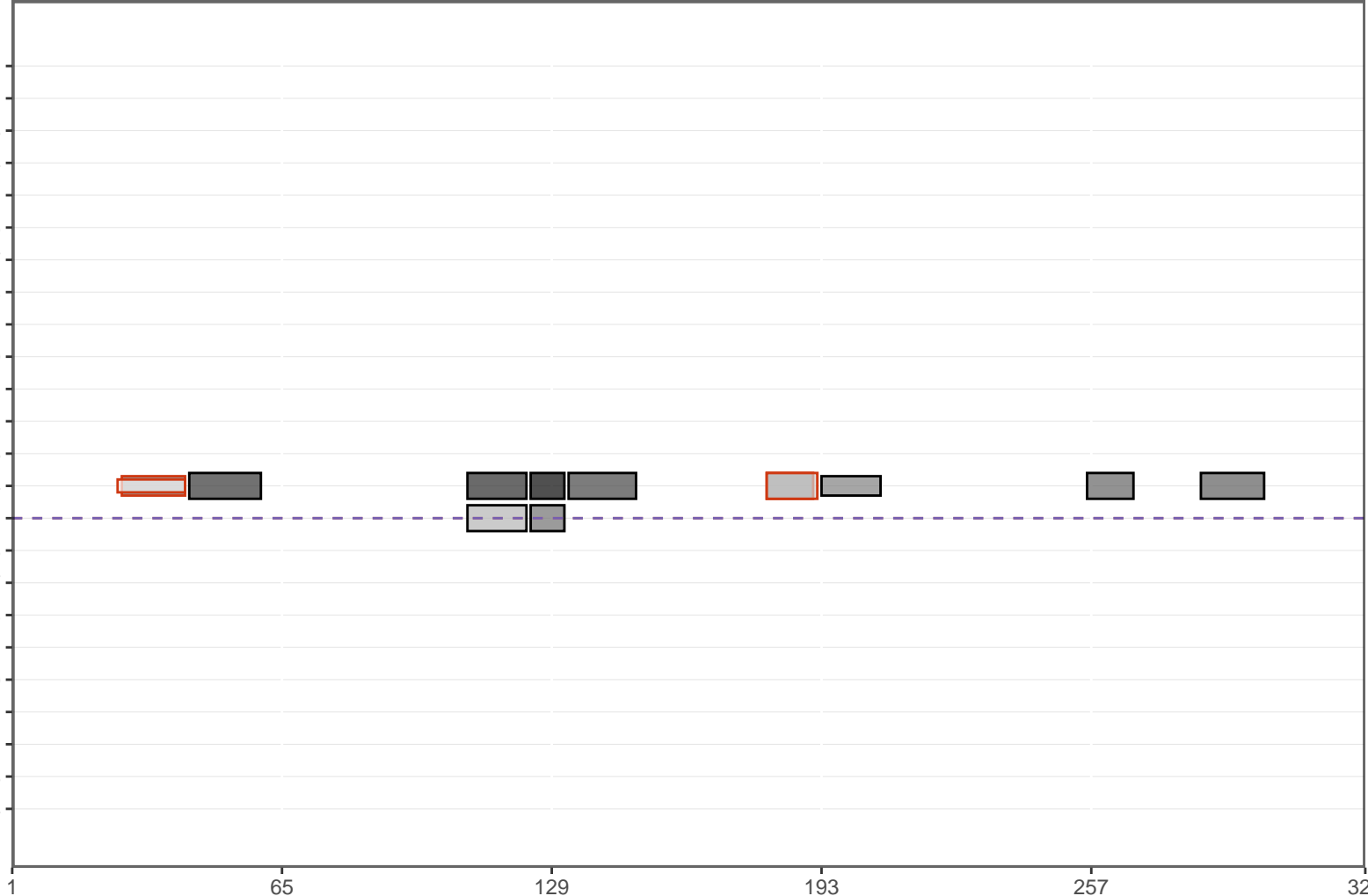
MW indication



Molecular weight



Gel Slice



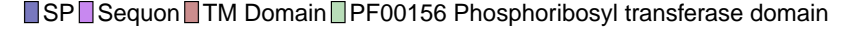
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YFGDNVLPFETGIPLLKGRIGLQPKSEKIIAPDDGAWKRFRHNLQVDPVPTVIGTKVREGDKRIRLKEGNPDGGHVVVDLQVSGGTLGCGKVLAAHGASKVQAVYTHGIFPKRQWERFLHKNDSSEKAFYVFTTDSCHPTVYKAVANKGPFVSLAGSIADALQI

NbL08g06070.1 glutamyl-tRNA(Gln)_amidotransferase_subunit_A_chloroplastic/mitochondrial [MW = 60.72 kDa]

No. of times detected



log(intensity)



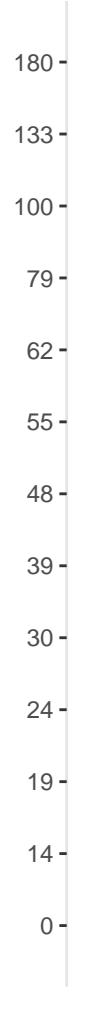
Values from



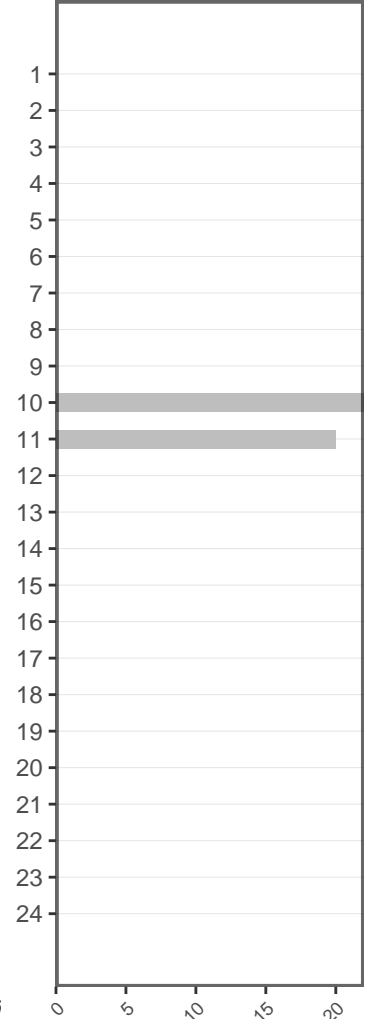
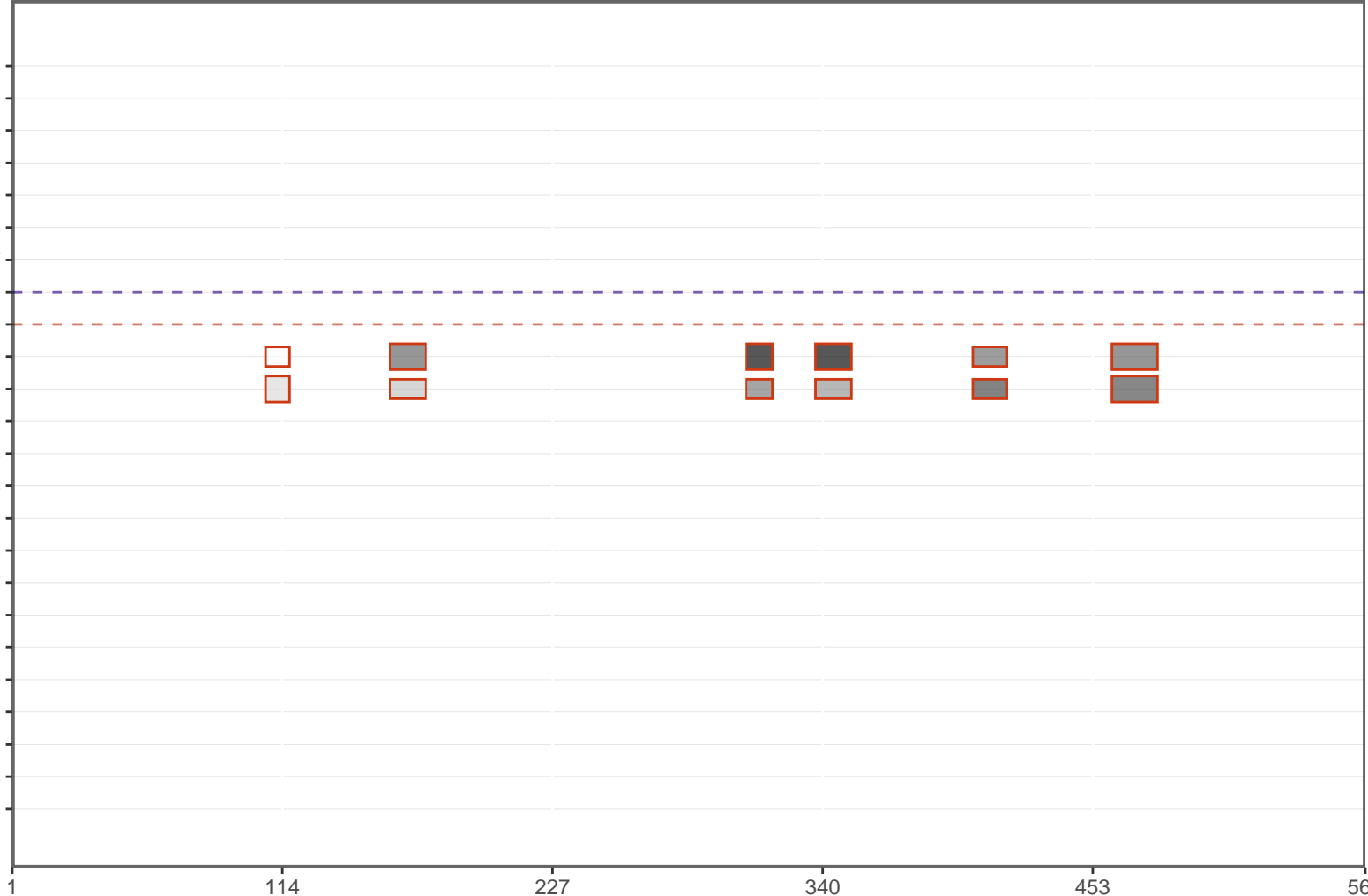
MW indication



Molecular weight

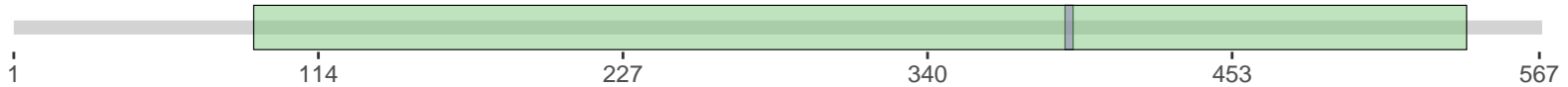


Gel Slice



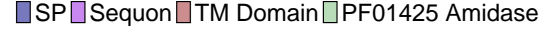
Protein length

Peptide counts over 4 repeats



Pfam domains

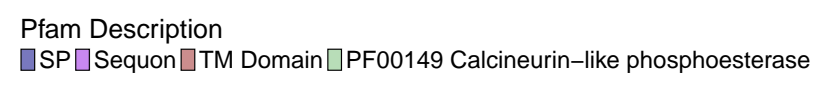
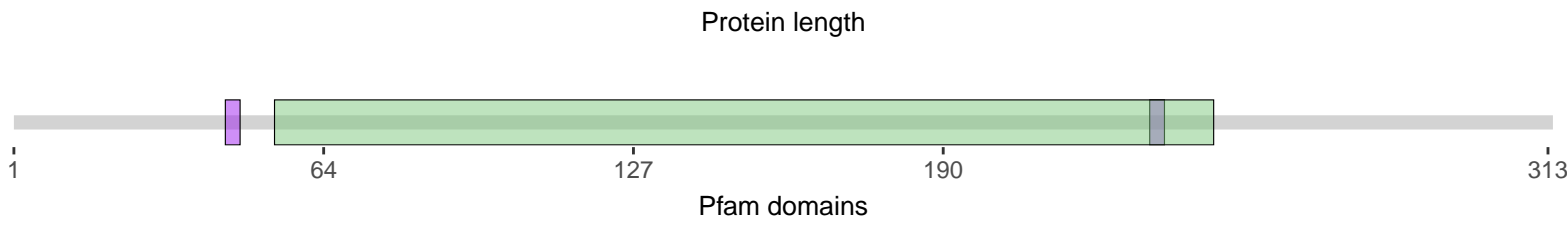
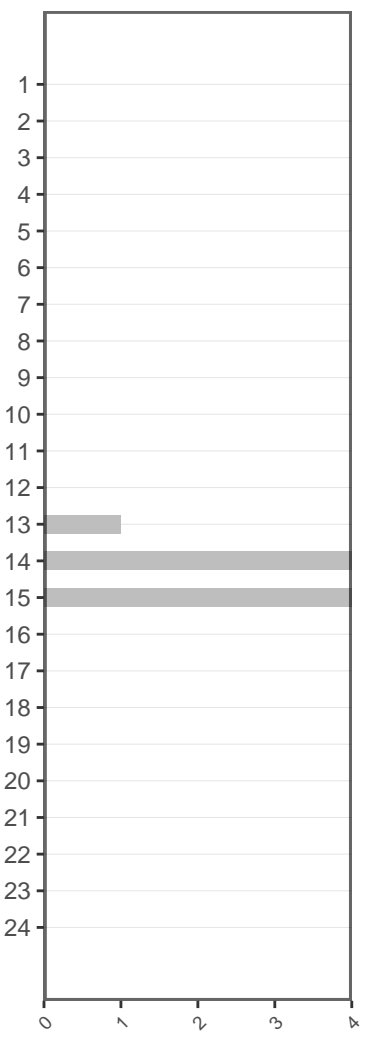
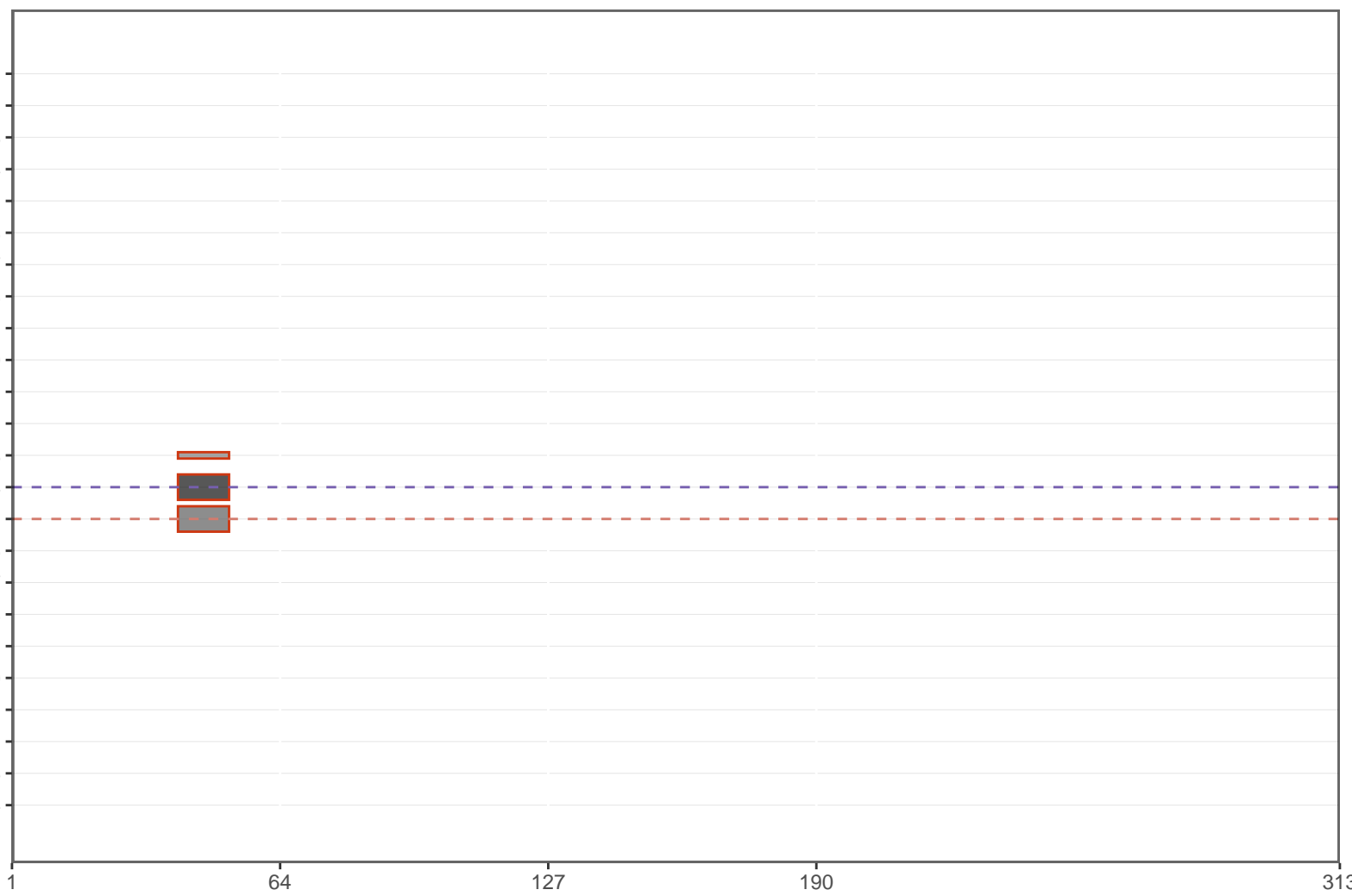
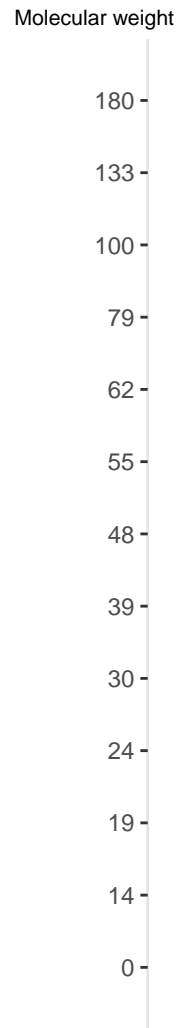
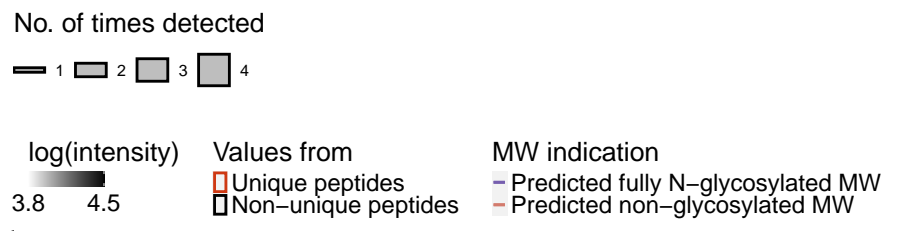
Pfam Description



Protein sequence:

MAVSSLDVIGCFGSSVADAGILLHAISGHDKFDATSKREVDFAFSGFIARDHLDDKPKLGLRVGLURETIEDGVDPETSRIRGAASHLEELGCTVTEVLSLRFSLGLPAYILASSESSSLNLSRYDGRIRYKGVVADELNSLVGESRAGGFGSEVPMRILMGTVALSAGYVDAYYKRAQGVRTLVRNFRAALENDLSAPAPSAAYRIGKEKNDPLMAYAGDMTVNVLNLAGLPLVLPQGFVDSSEVLPVGIQMGIAAFEEKLLKVKHFQTLGGGFFPPVVADELCA

NbL08g05820.1 serine/threonine-protein_phosphatase_PP2A_catalytic_subunit-like [MW = 35.47 kDa]



Protein sequence:
 NVWKTFDLFDYFPLTALVESEIFGLHGLSPSIELDNIINRFRVDEVPHEGAMGDLWSPDRDRGSGWISPRGAGYTFGGDSEGFNHTNKLKARAHGLMEGFNWAHDQKVTFESAPNYGYRGGNMAISILEVDDGNGHTFQGFAPRRGEPDVRTRTPDFL*

NbL08g05740.1 protein_YLS3-like [MW = 25.74 kDa]

No. of times detected



log(intensity)



Values from



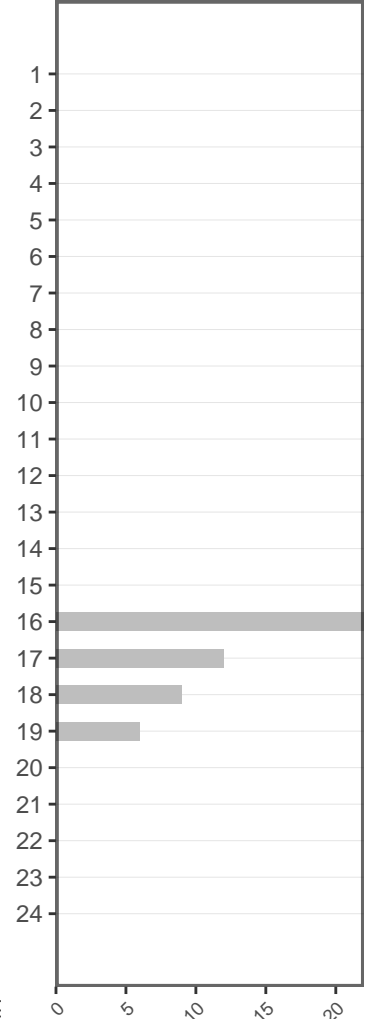
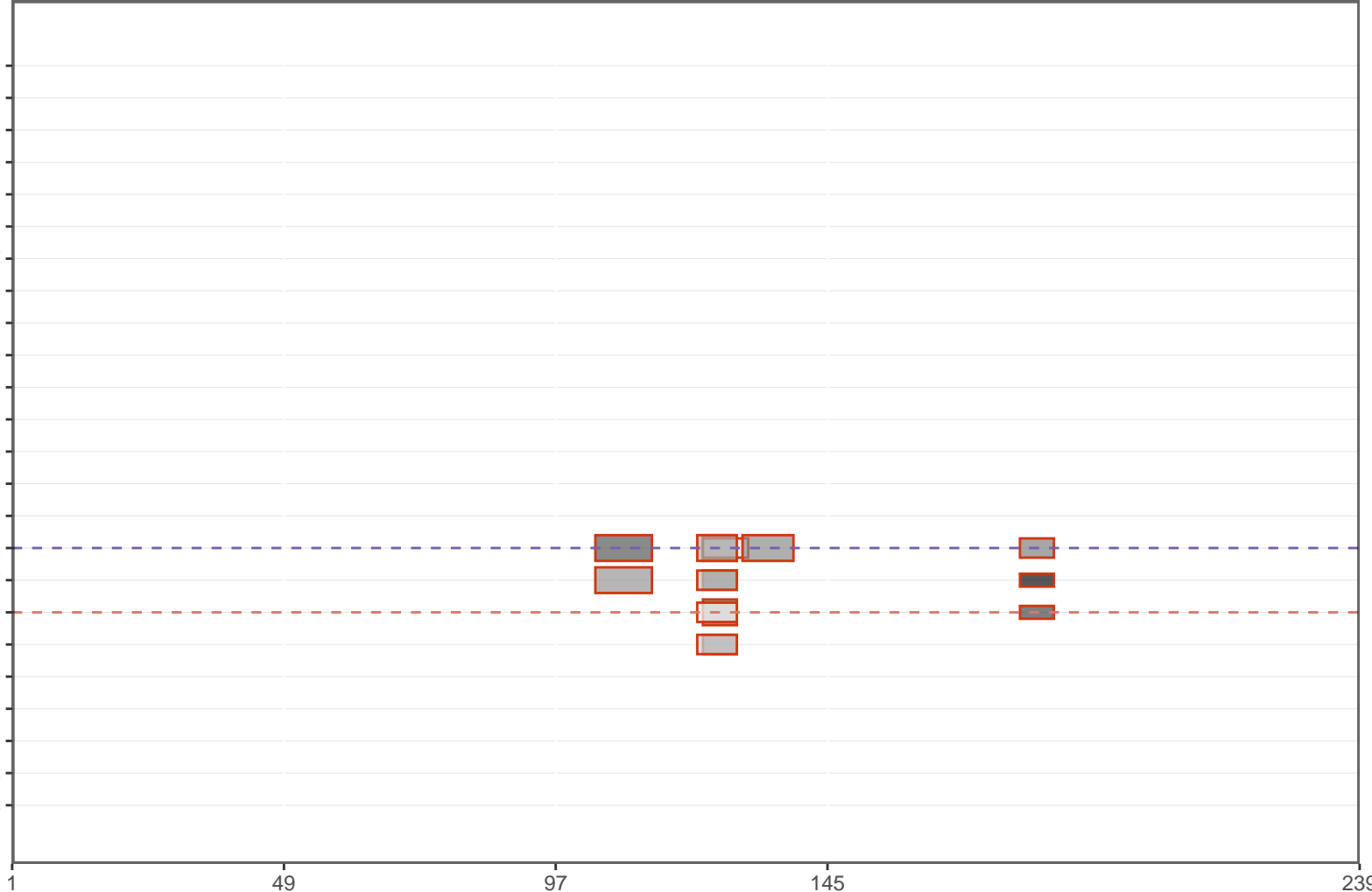
MW indication



Molecular weight



Gel Slice

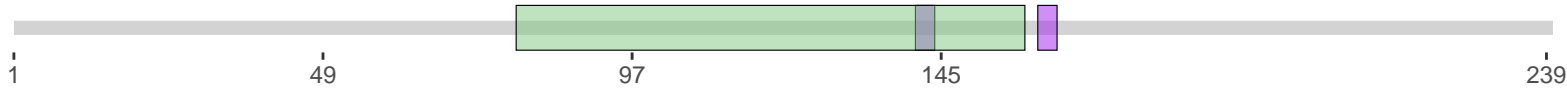


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

CTGLKEVLDKSKKGLGVLVKDRNPDLGLKINATLALSLPTLGHAPVSAITNVMSCPELLHLPNNSPDAKVFEAFSAKSGSTASSAPVSGSSNGKTATTANEKNDGGDRRKMVGMEVTMGFLFIMLV

NbL08g05350.1 peptidyl-prolyl_cis-trans_isomerase_CYP28_chloroplastic-like [MW = 35.57 kDa]

No. of times detected



log(intensity)



Values from



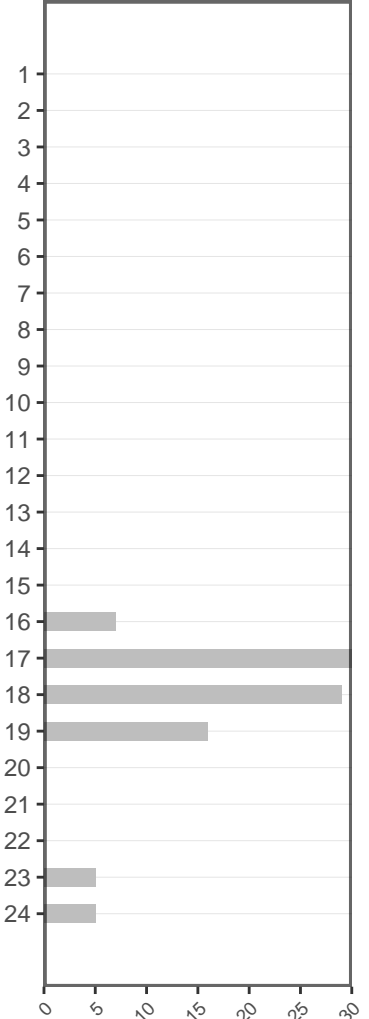
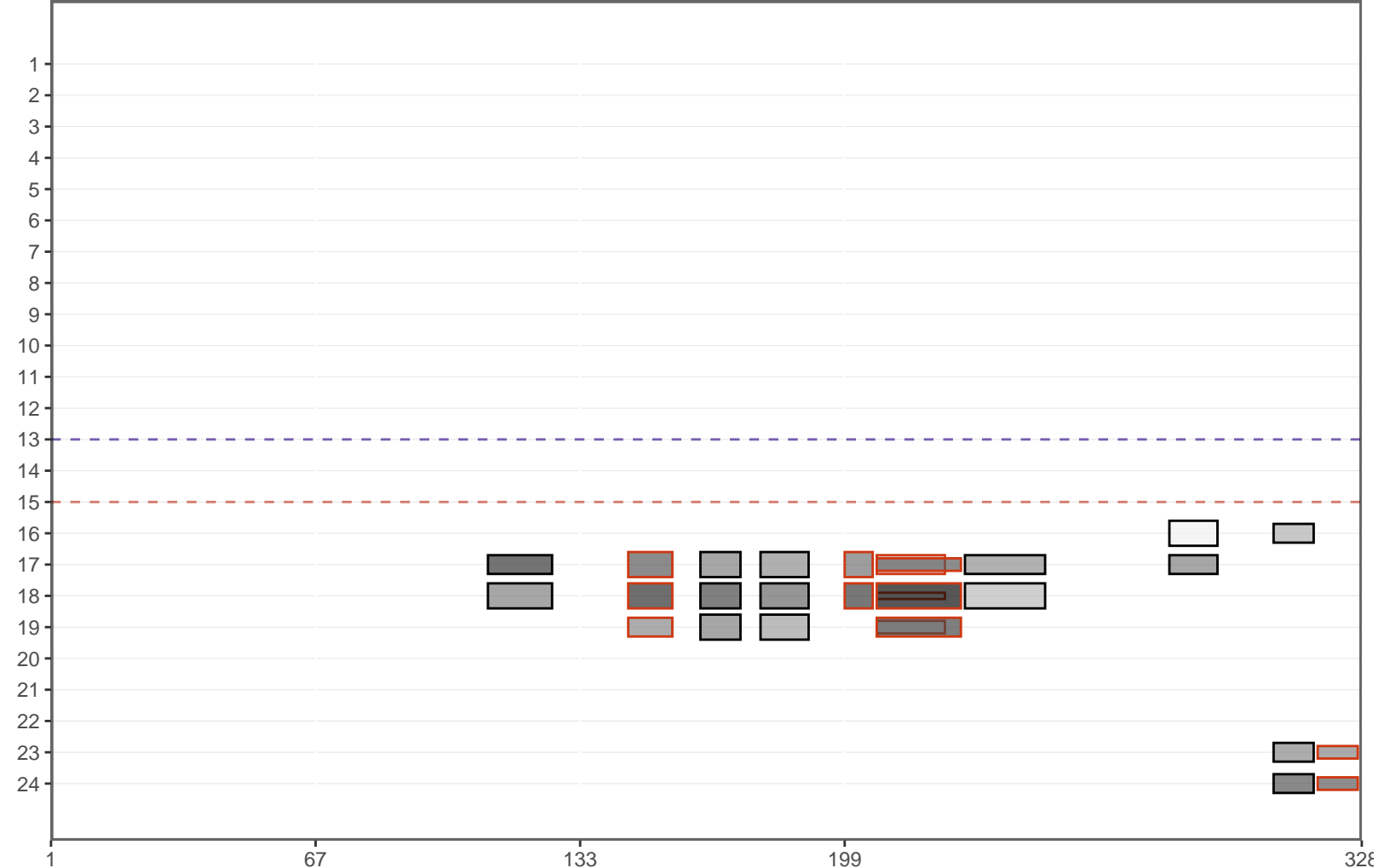
MW indication



Molecular weight

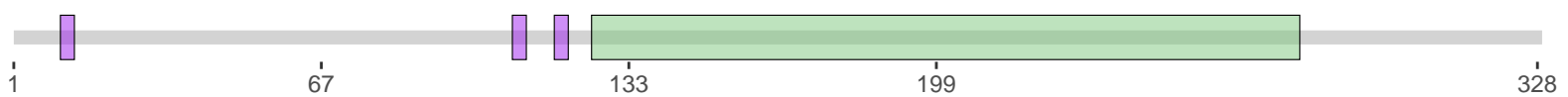


Gel Slice



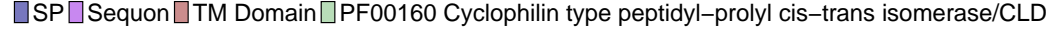
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISTYKGLTVQKIFPGQFFMAGRGGRRDKGEVKKPPELIRNTEIESKAFLEHNRGGVSLPLSENDDDDDKLNPKYHNVFLFTTGGPVPQLDKNVIVGTVLEGMDIVTSAIPTYKPSNRHQVYNGFAELLGDGRAKTARAIAWKNPKQKTVVHSDDGEELKWKPTLSPSLP

NbL08g05220.1 4-coumarate--CoA_ligase_2-like [MW = 61.82 kDa]

No. of times detected



log(intensity)



Values from



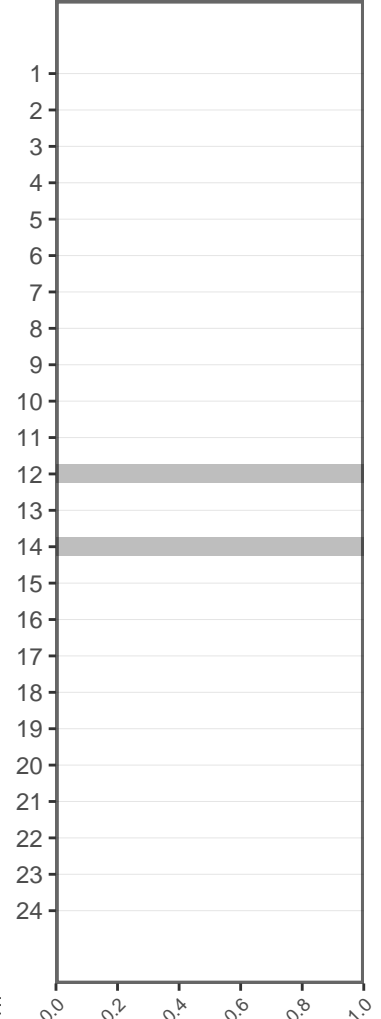
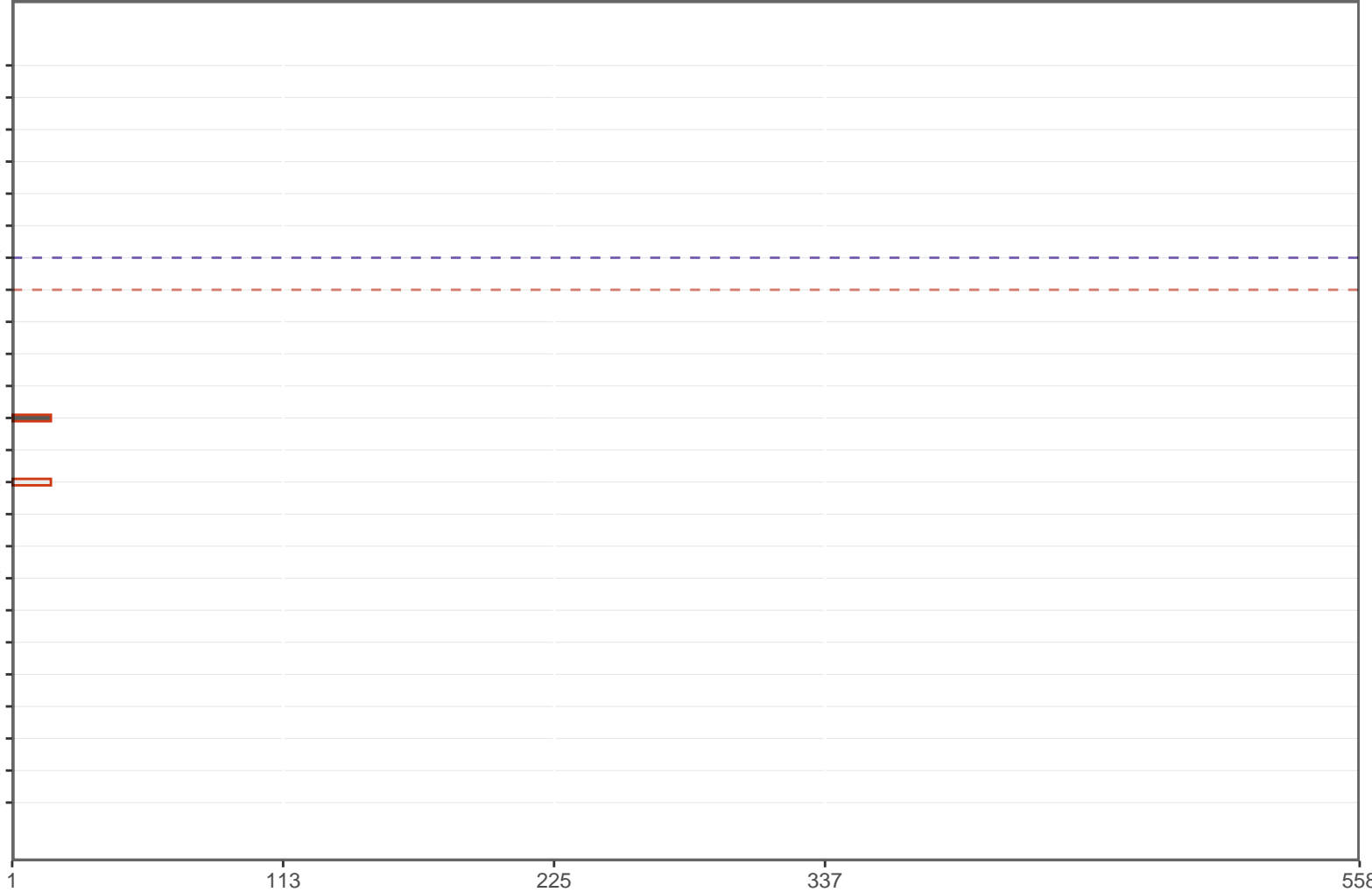
MW indication



Molecular weight



Gel Slice

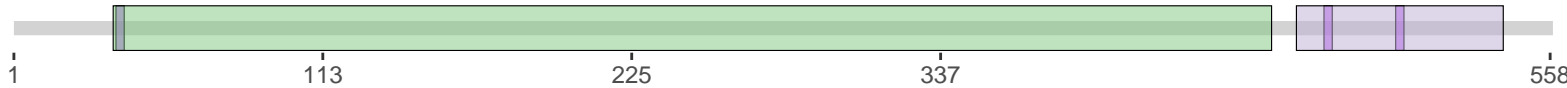


Protein length

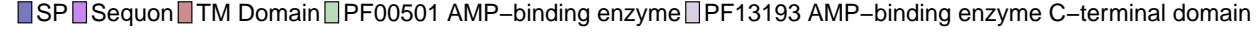


Peptide counts over 4 repeats

Pfam domains



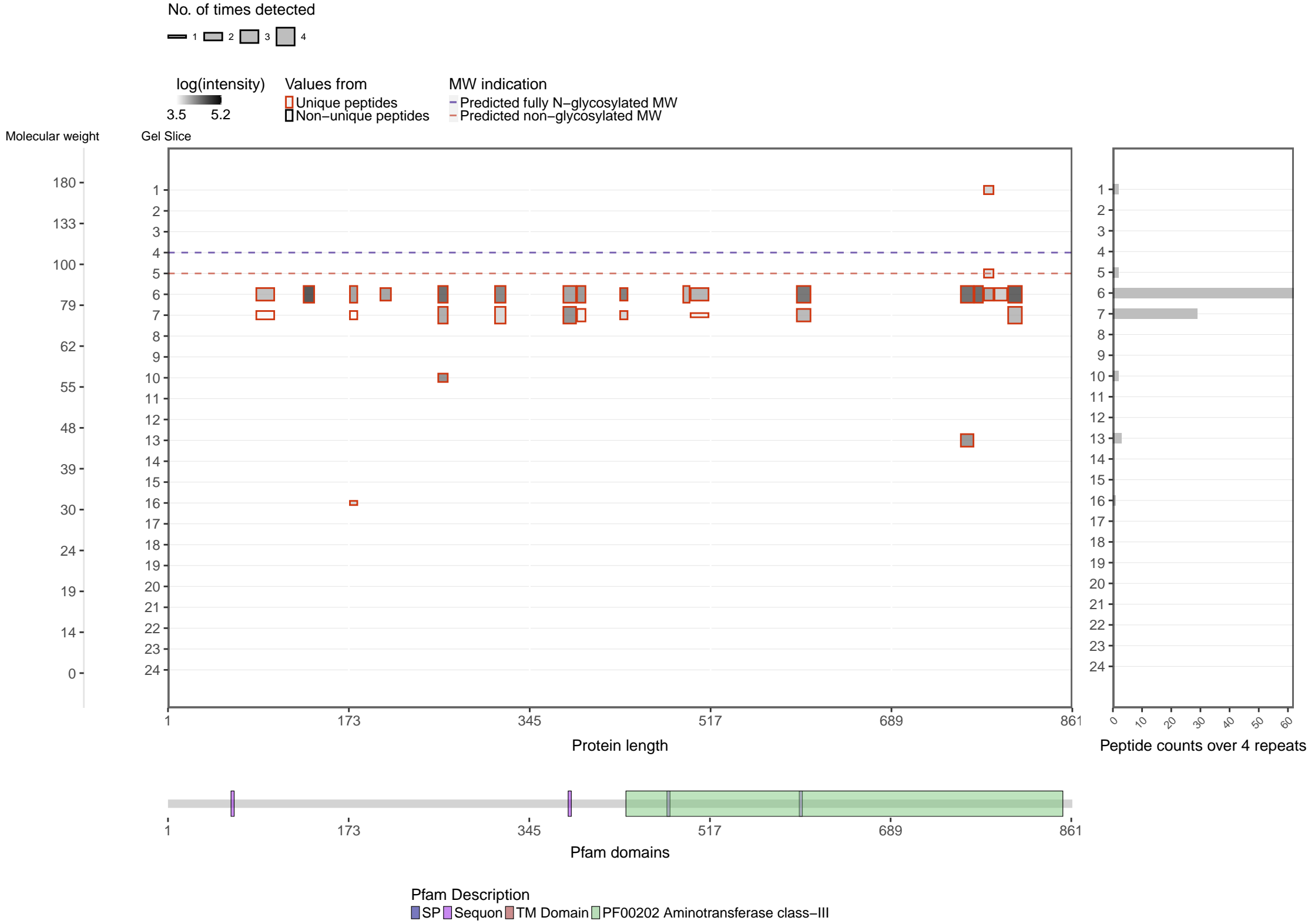
Pfam Description



Protein sequence:

IGAAIIMQKFEIKGLMELVEKVKYTAFFVPPVLAIAKPLVHKYDLSSIRMMMSGAAFMKKELEDTVRAKLPNALGGGGVMTAEPVLSMCLAFANQPFEEVKGSGGCGTVVRNAEMKIVDIDTGAISLPNHAAGEIGIRGDDIMKGYLNNPEATEETIDKEGWLHSGDGIYDEDDGGVFDVDRLEKIKYKYGQVAPAELEALLISNPNTDAAVPMDEVAEGEVPVAFVVRANGSKISEEEKIKYISEQVIFYKRIKRIWFFTEAIPKAPSGKILRKDLRAKLAAGLAC

NbL08g05090.1 bifunctional_dethiobiotin_synthetase/78-diamino-pelargonic_acid_aminotransferase_mitochondrial [MW = 95.8 kDa]



Protein sequence:

MTGGPDTLQIELARDVQVATARYGHVAFPPENVYEPALGECALLLEGVKGVKQWASRVYFSDNGSTAEIEMKMLRKLFLDHRIRISDDLVAESAESEHYDLKVALRGSVHGGDTLGAMEAGAFSPVYTFGVQGFVWYKGRGHFLDPPTVAMGDGVVWKLGLPQEIETGKPNIEDLTFSLRENFKESRDNLSLSEHYHVRIRRLQLMDSGGSTGTGALHEPVIQGGAGGEMVDFLQRFQVLRVKECRGQKIPVDFEVFTGFWRLGAESETEFGKPKDAGVAMLTGGVPLAVTLA!

NbL08g05050.1 FGGY_carbohydrate_kinase_domain-containing_protein-like [MW = 69.08 kDa]

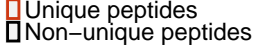
No. of times detected



log(intensity)



Values from

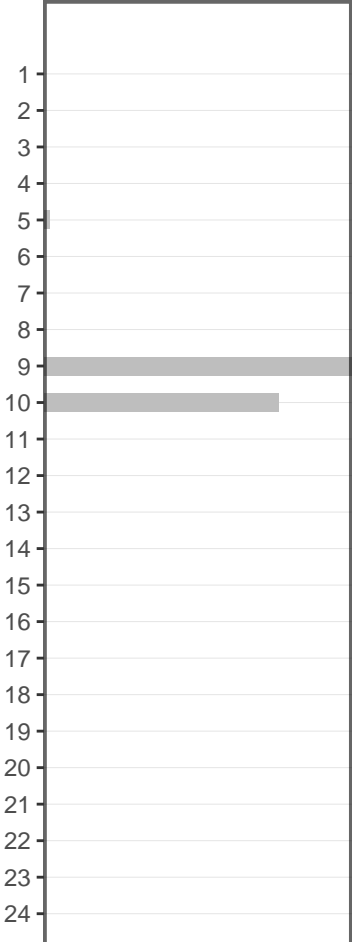
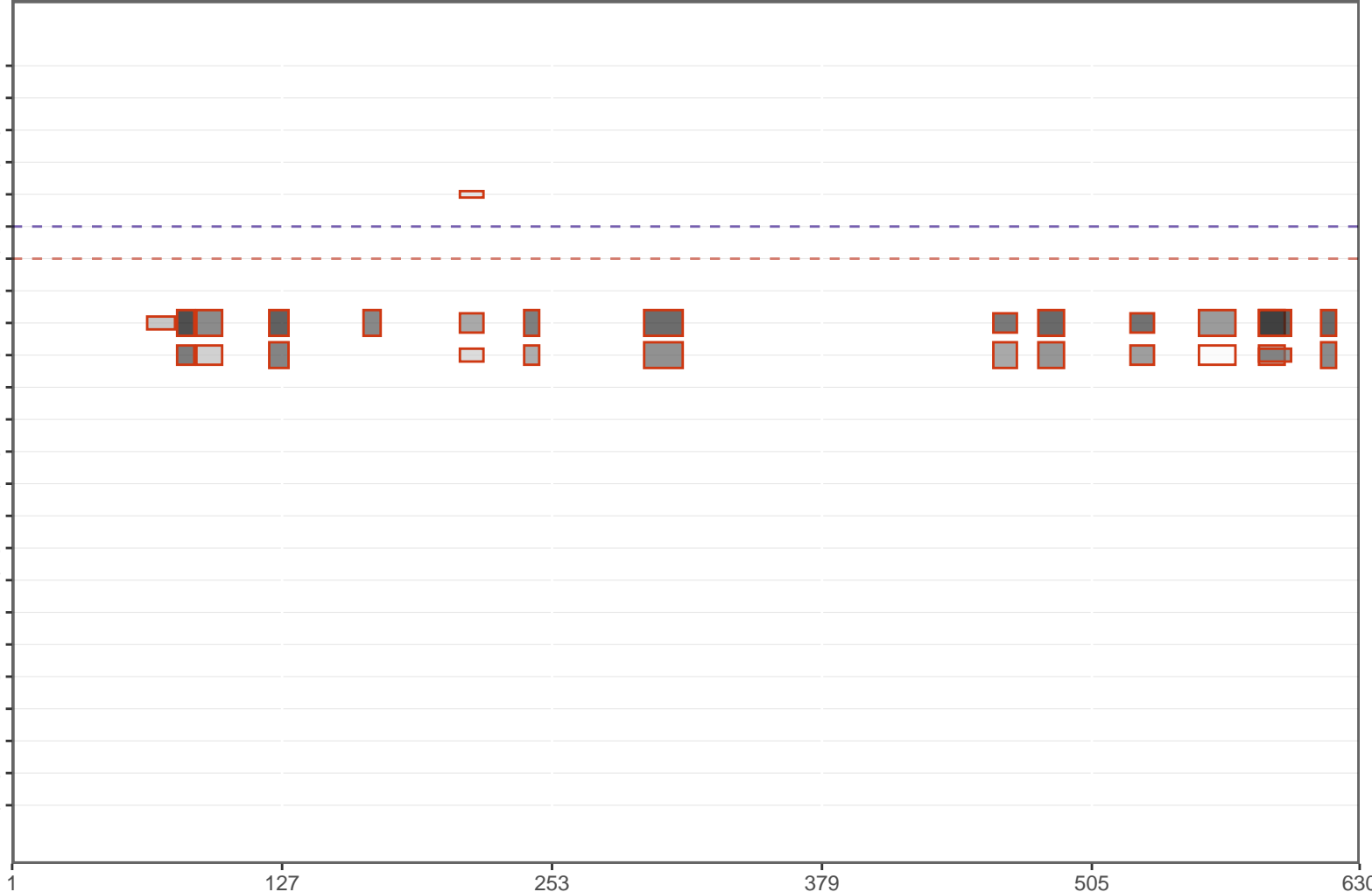


MW indication



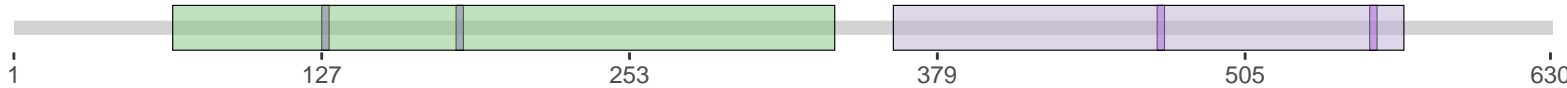
Molecular weight

Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00370 FGGY family of carbohydrate kinases, N-terminal domain
- PF02782 FGGY family of carbohydrate kinases, C-terminal domain

Protein sequence:

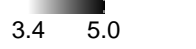
VAIFPGHALGSGSLTDAAKELGLMAGTPVGTALDHAAGGQGVMEVPADESEGVDEDAERRMVLVGGTSTCHMAVGRTRKLFIPGVWSPFFVWGMVPEYVLTGGGSGATGALLDVIENHWASPHLANRAASRRISIFDLLNELLESKQEEGGGDFISALTKDLHLPDFHGNRPIADPKSKGMISGLFDTSEKQLALLYLATVGGVAGTRHVEHNSNANGHKKIDTLACGGGLANNHLFVQEHVDIGYVPIPRENESVLLGABLGAVASKYKPTVREAMKAMNAAGOVVYV

NbL08g04960.1 xylose_isomerase-like [MW - SP = 50.79 kDa]

No. of times detected



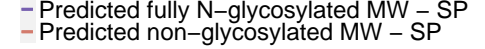
log(intensity)



Values from



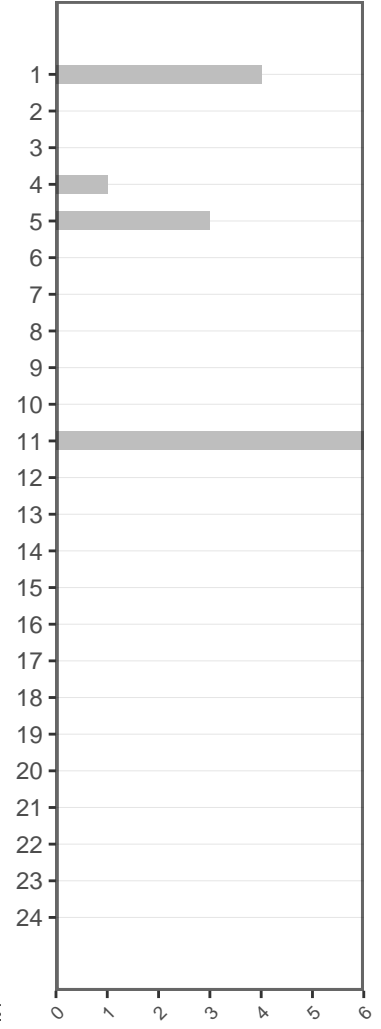
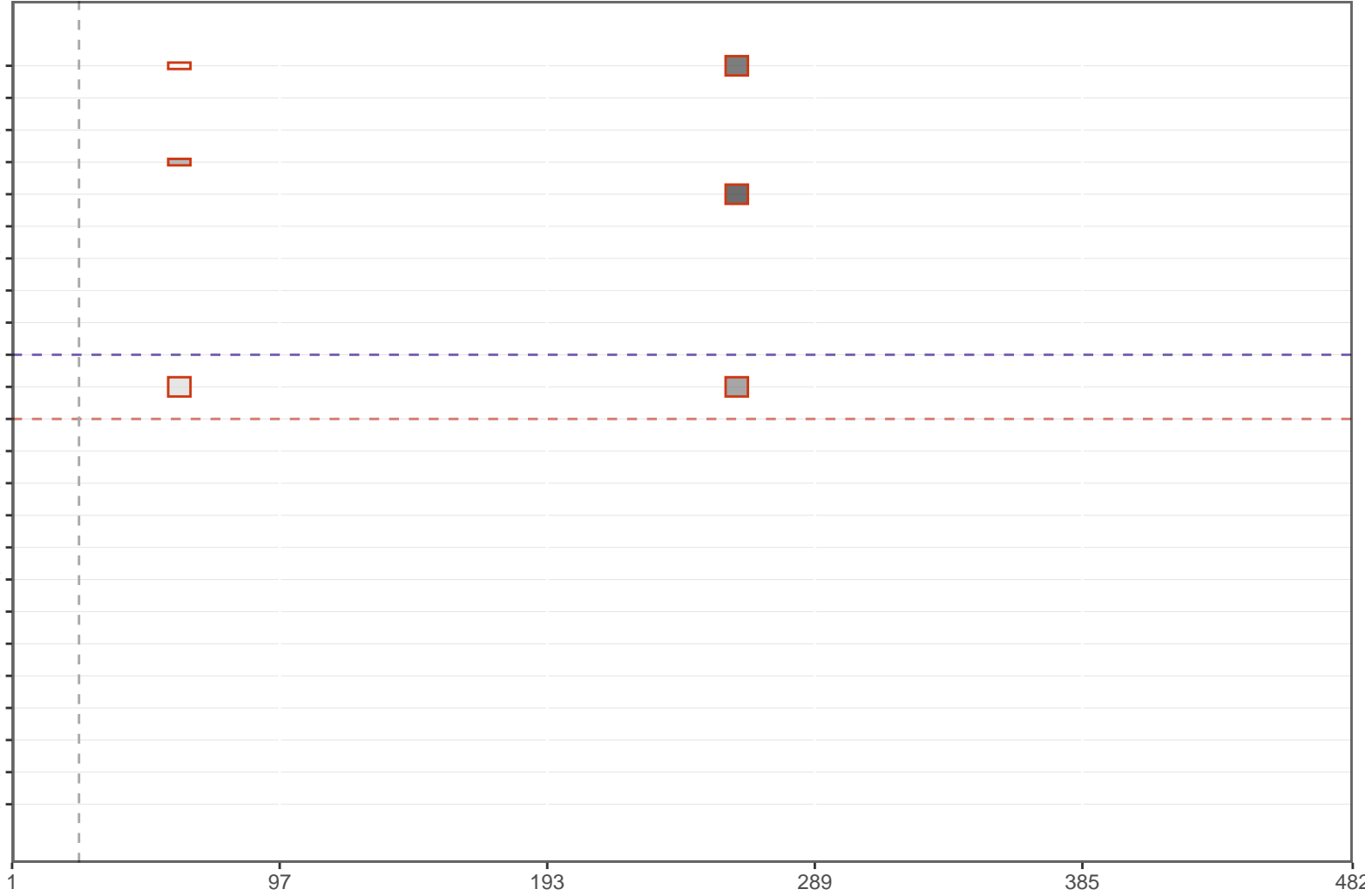
MW indication



Molecular weight



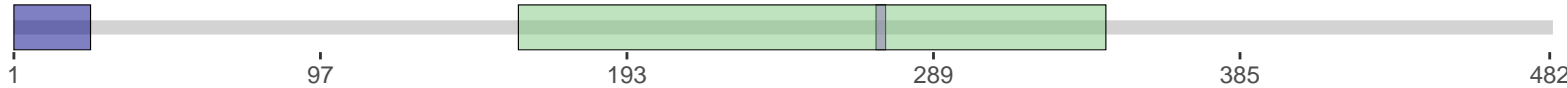
Gel Slice



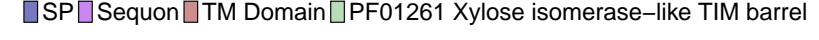
Protein length



Pfam domains



Pfam Description

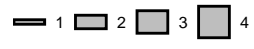


Protein sequence:

GENYFYVGGREGVQGLLNTDMERELDHMRFMEEAAWYKKIGFNGTLIEPKQDEPTKHQYDWDVAATSANFLRKYKLGIEFKLNEGNHATLGHSHCHIELETARINGLLGNIDANSGDPOVQVWDTQDFLMDVAEATLVAGTIVKNGGLAPGGFNFDAKLRRESTDVEDLFIAGMDTLARGLRANAALIEDGSLGELVLRKRYGDFTELGAAEAGKADFELLEKVALEWGEPKVPSGKGLAEMFQSAI

NbL08g04950.1 ADP-ribosylation_factor_1 [MW = 20.31 kDa]

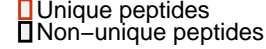
No. of times detected



log(intensity)



Values from



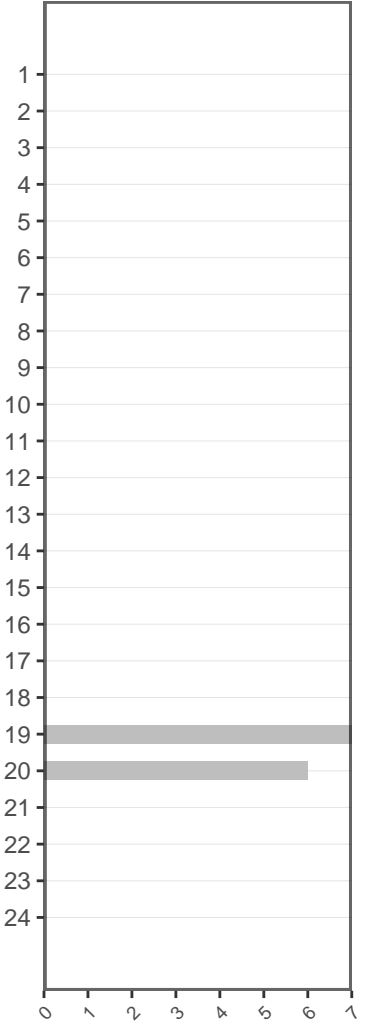
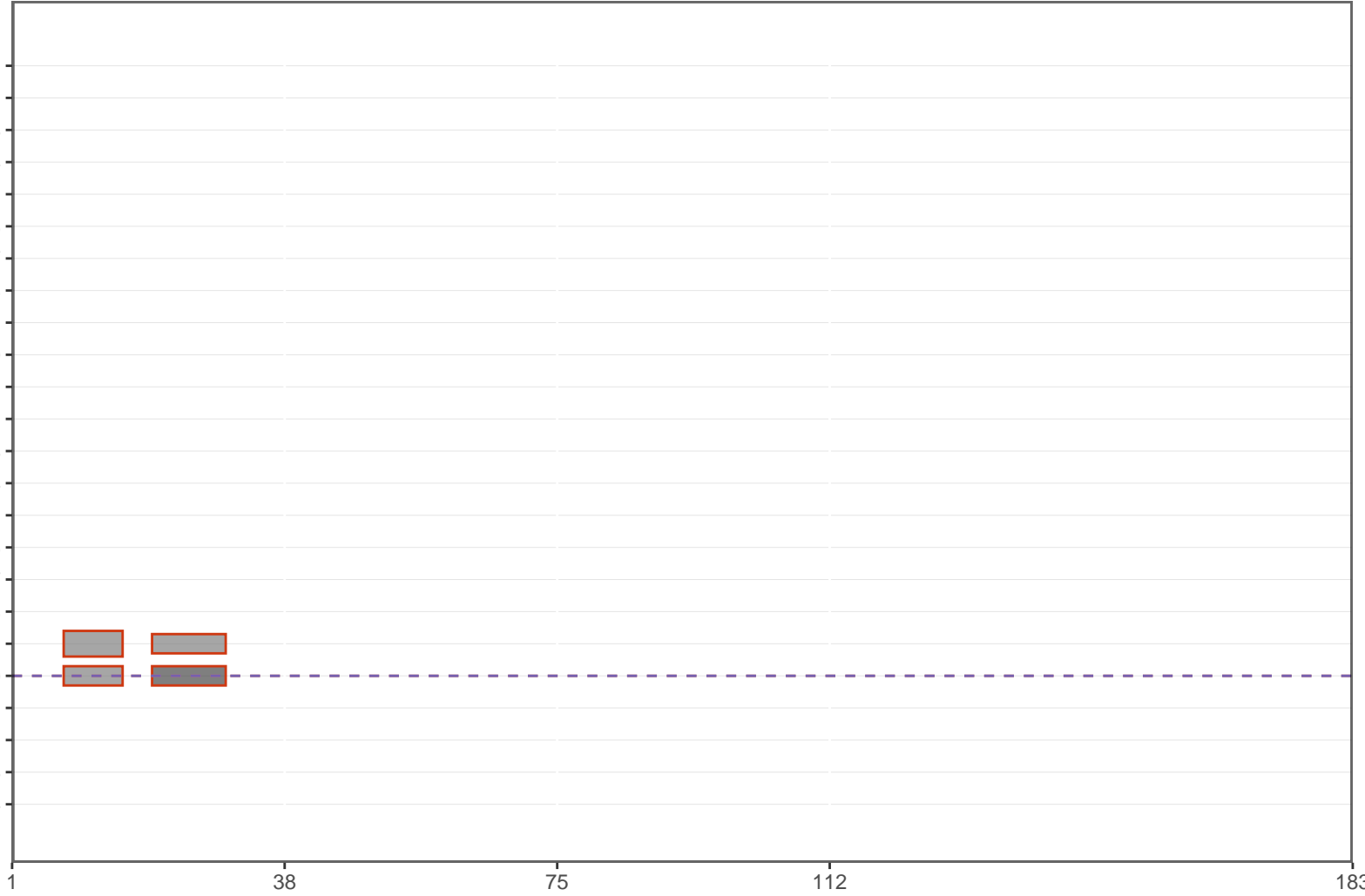
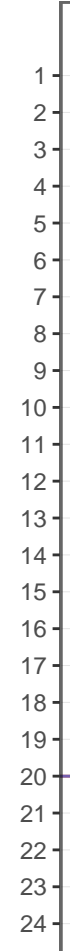
MW indication



Molecular weight



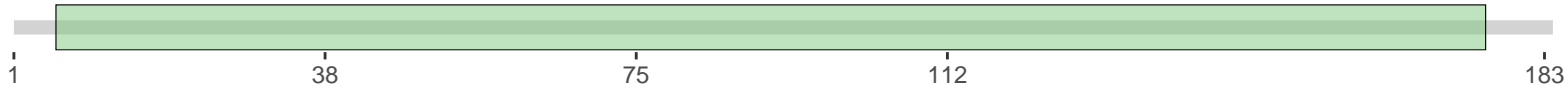
Gel Slice



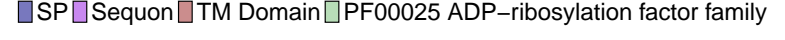
Protein length



Pfam domains



Pfam Description



Protein sequence:

/RCYFPNTQAIIVYVDSGSDRRLVAKKEFHAILEEELKGAIVLVYANKODLPGALDDAVTEALELHKIKRQWAFKTSARKGELFEGLDLWLSNTLKGGGQ

NbL08g04810.1 adenylosuccinate_lyase-like [MW = 60.93 kDa]

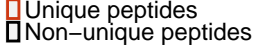
No. of times detected



log(intensity)



Values from

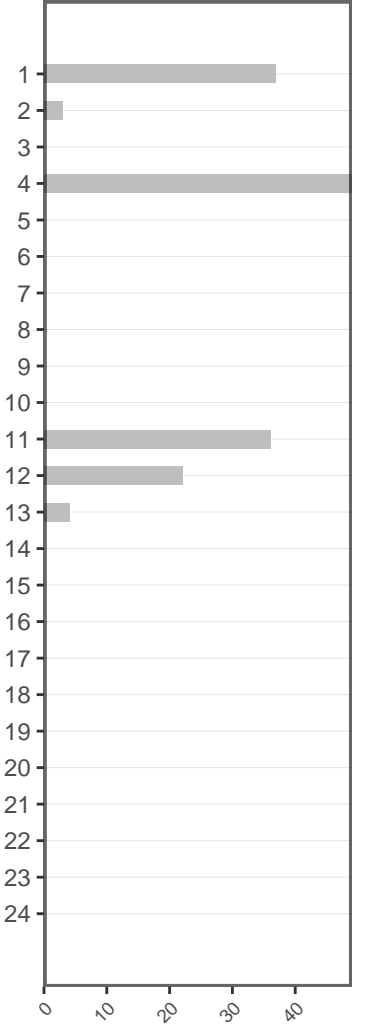
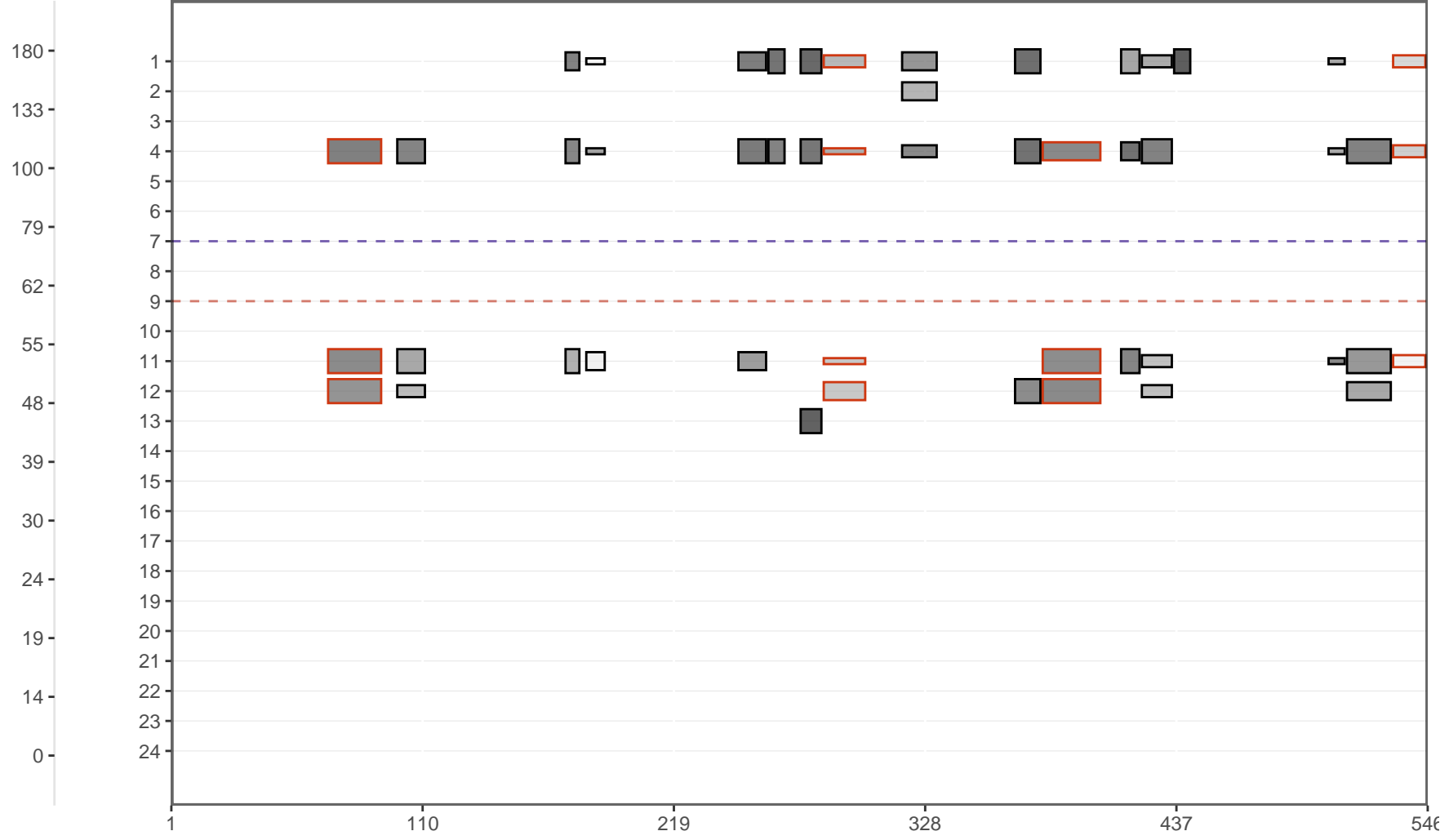


MW indication



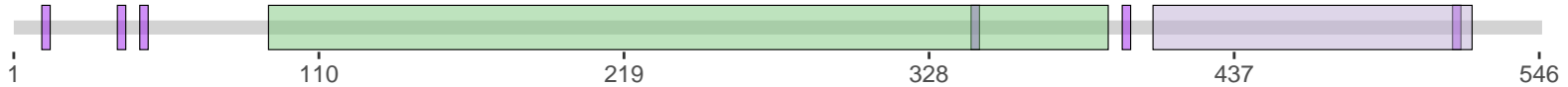
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00206 Lyase
- PF08328 Adenylosuccinate lyase C-terminal

Protein sequence:

IMAFAYRLSRERRRISQIEMLGKFKAGAVGNVYHAAVPEVVKWQIAEFLVMSLGLKFNFPVYVQIETHQVMAKLFHSIVDFNNSVDFDRDVGWYHISLGYFKGTAKGEGSSTMPHKVYDFDFENSEGNLGVANGNLSHLSTKLPISRWQRDLTDSVLRNMGVGLGHSLLAVALREALGGKLGVNEALTEDLKQWEVLAEPQGTVMRRYGVPEPEYKIKALTRGRVTVKEIKREFIKLDIRPDAKTALLNLRPHVYVGAALAKSINDANLENGAQVF*

NbL08g04560.1 tetraspanin-8-like [MW = 30.12 kDa]

No. of times detected



log(intensity)



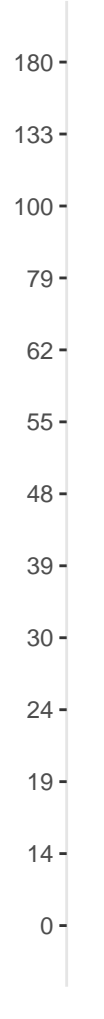
Values from



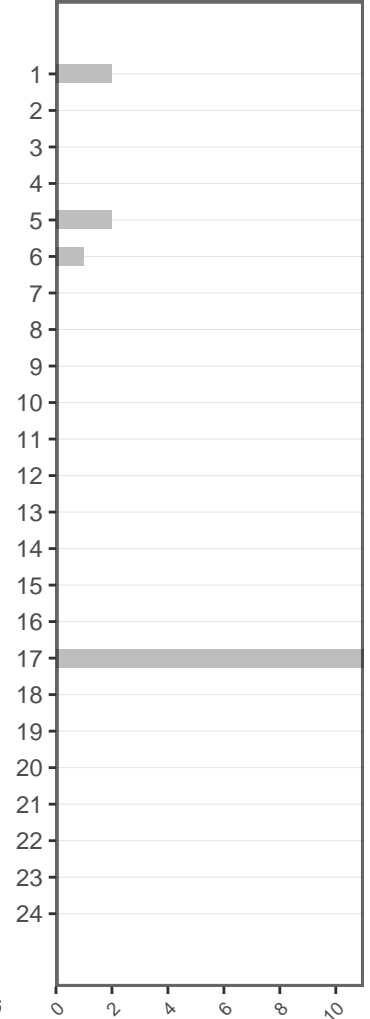
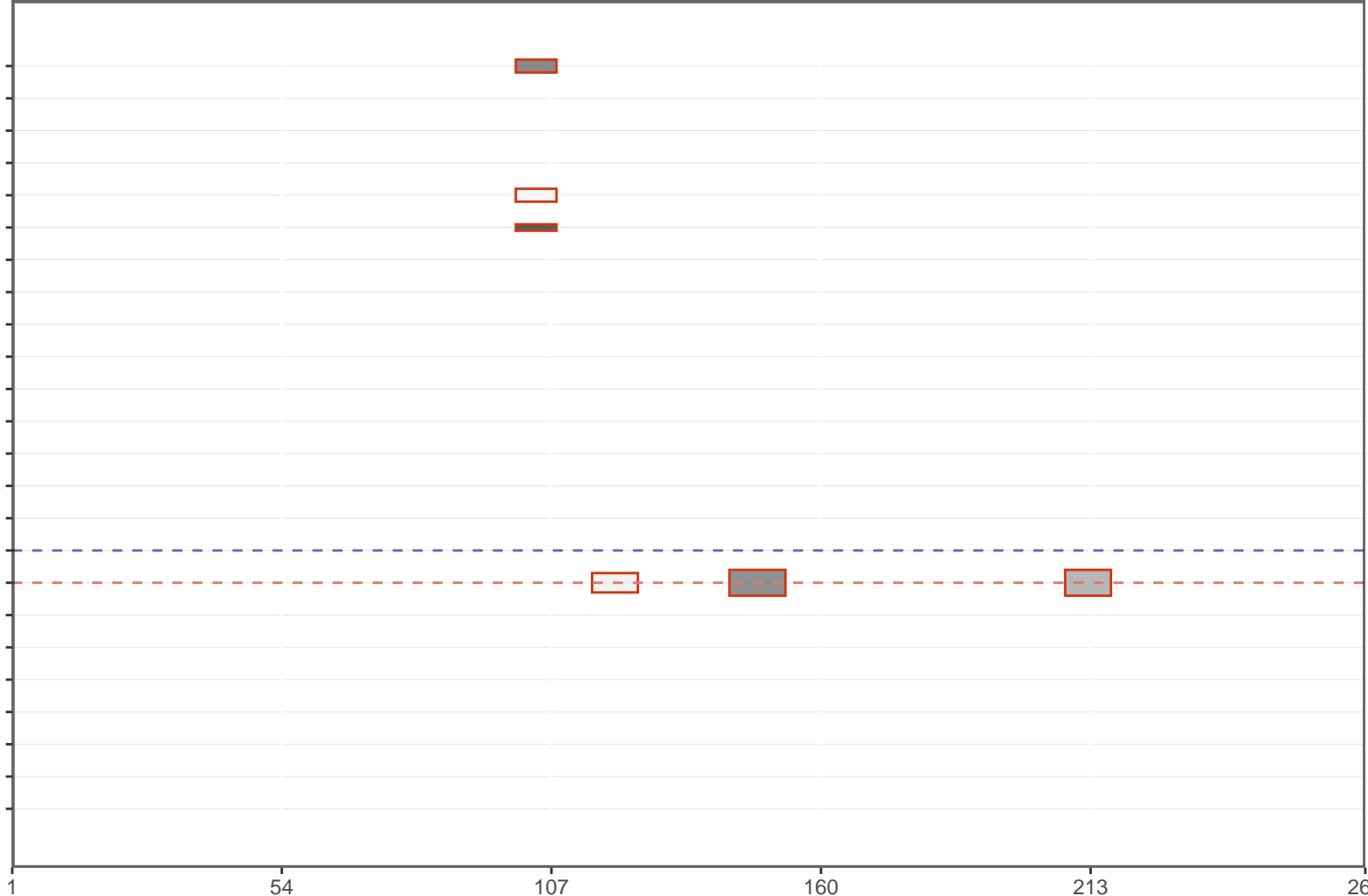
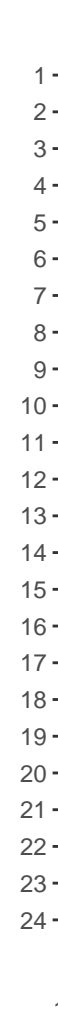
MW indication



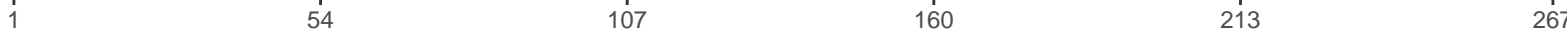
Molecular weight



Gel Slice

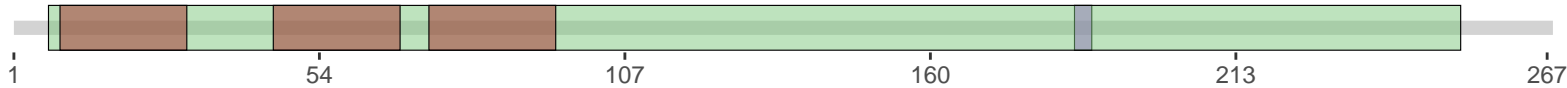


Protein length

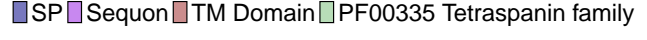


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IRVNDNHYSRHISCLGDSKIGSLIEGNTKADDFKHLISALGSGCKPMSNDCHFEYVSPNTWTRTPSSLENDPDCITAWSNDPKILOYGDSGKAGLLDLKSDKRWAVLNIHLVFLVIVYSIGCCAFRNNREDNAWKRP

NbL08g04470.1 tetratricopeptide_repeat_protein_1-like [MW = 31.06 kDa]

No. of times detected



log(intensity)



Values from



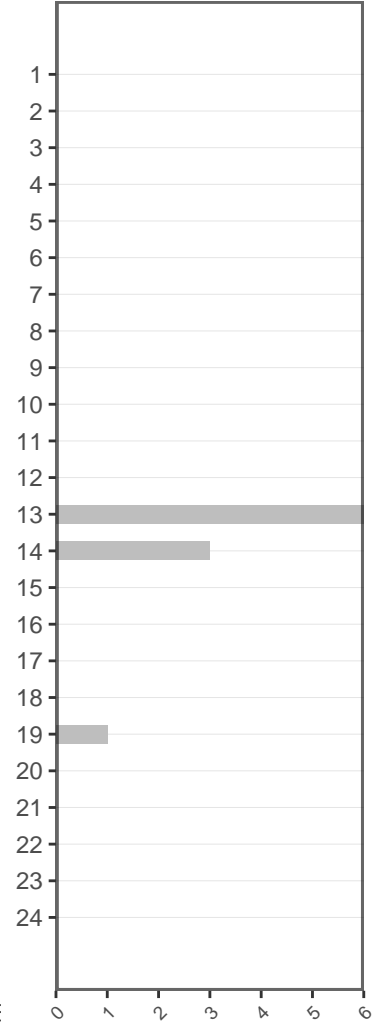
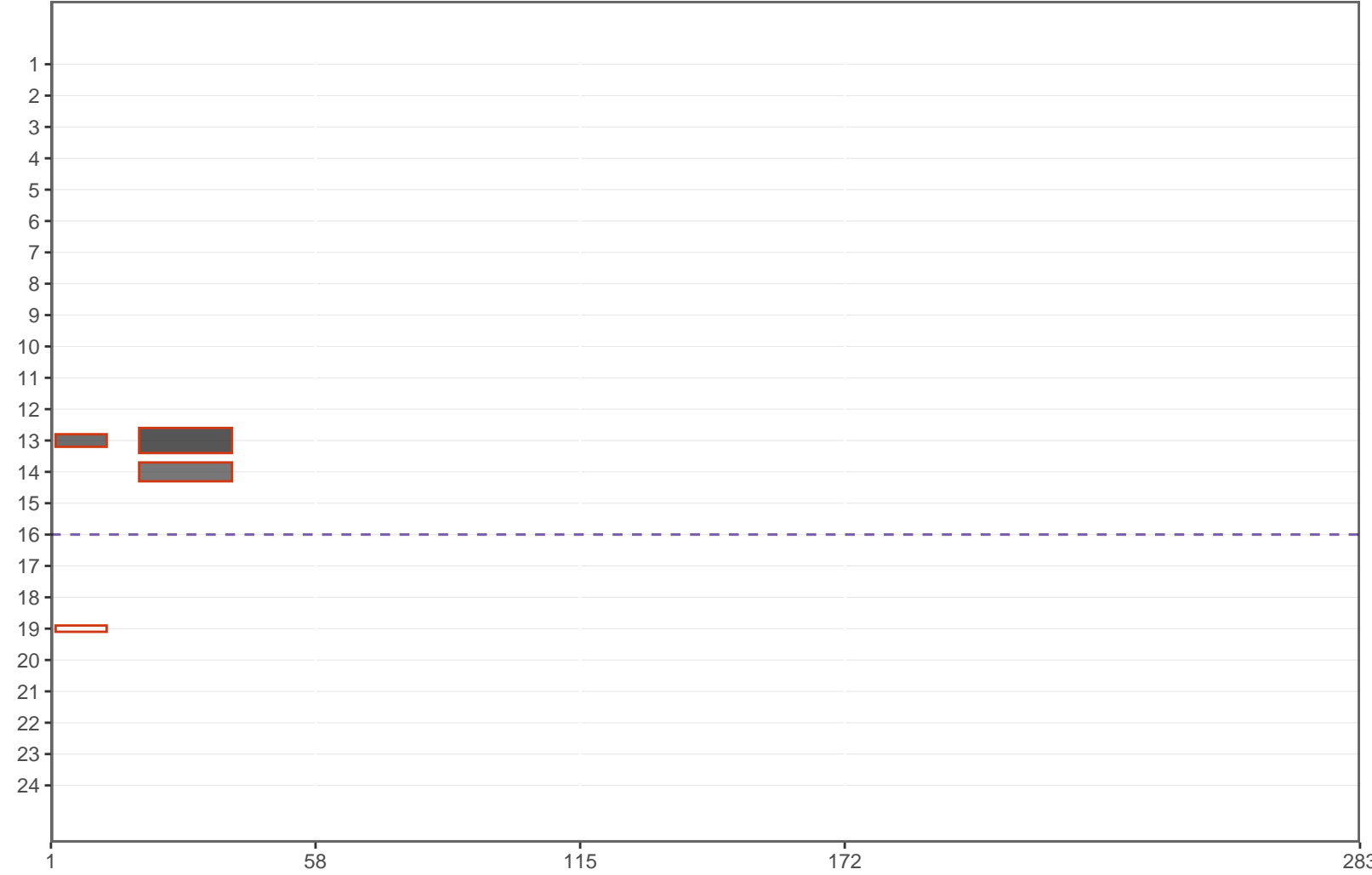
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IALSKYELALQVADIPSSSTERSIRGIANRAACFKLGHGHTKEGKTKALELNPTFKMALKVRRRAEAHEKLEHYDEAVTDMTKIMELEPNDQARRRVSMLRKLPADEKREKMKEMIGLKEKMGNSLGRFGMSVDNFKVAKDPTNGSYVSFGK

NbL08g04360.1 putative_GDP-L-fucose_synthase_2 [MW = 34.78 kDa]

No. of times detected



log(intensity)



Values from



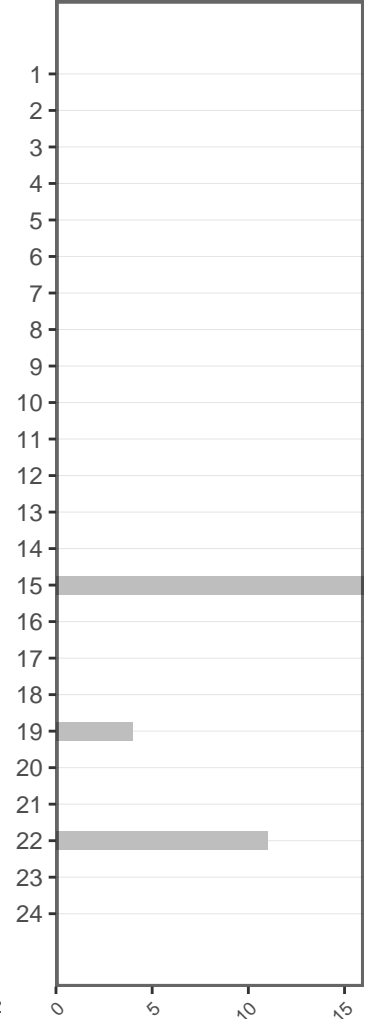
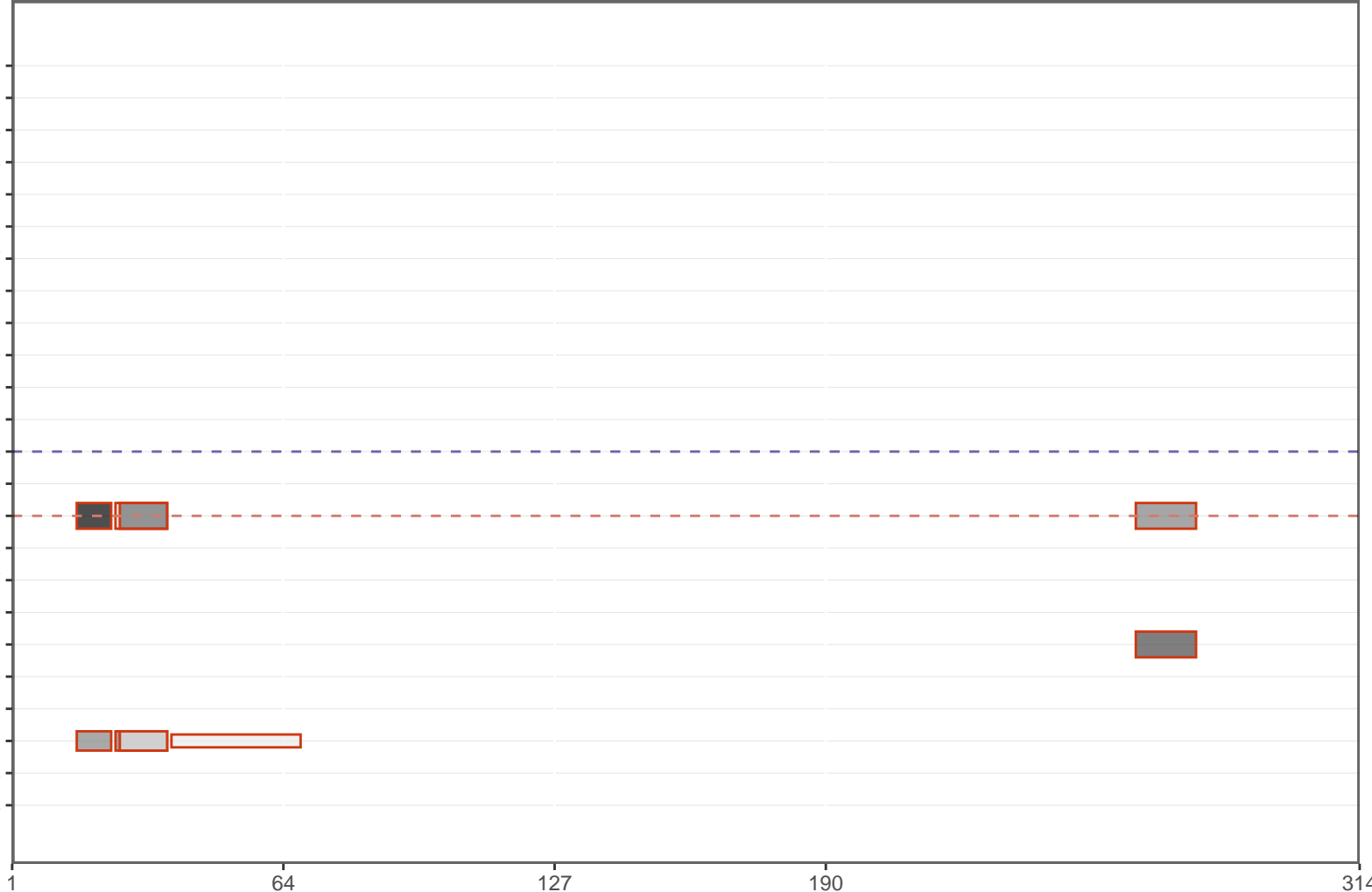
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKMCCAYRLQHNFDAISAMPTNLVGTNDNFHPENSHVLPALLRRFHEAKINNKLVVYWGTSGLREFLHVDDLDADAVIFLLENVSDLEHVVVGGSGEVTIKELAEIVKEVVGFKGELVWDSKPKDGTFRKLMHTSKLLVGLGWTFKISLRDGLVDTYKHWVLENYGKQ

NbL08g04330.1 clustered_mitochondria_protein [MW = 202.26 kDa]

No. of times detected



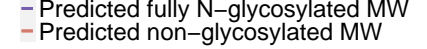
log(intensity)



Values from

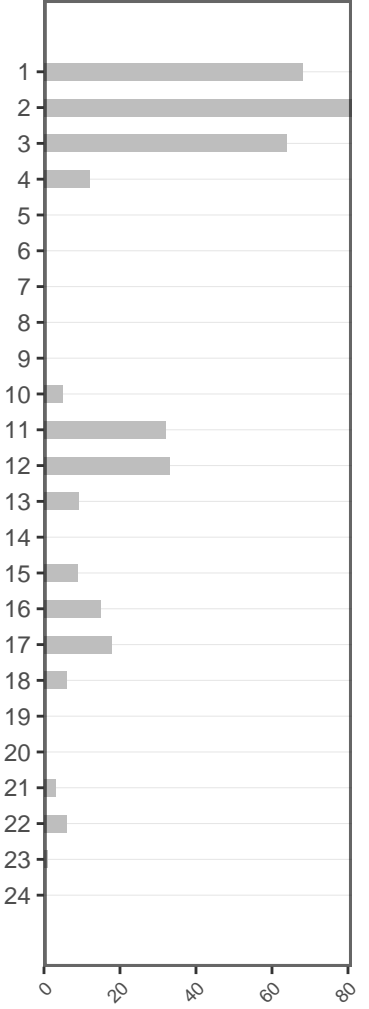
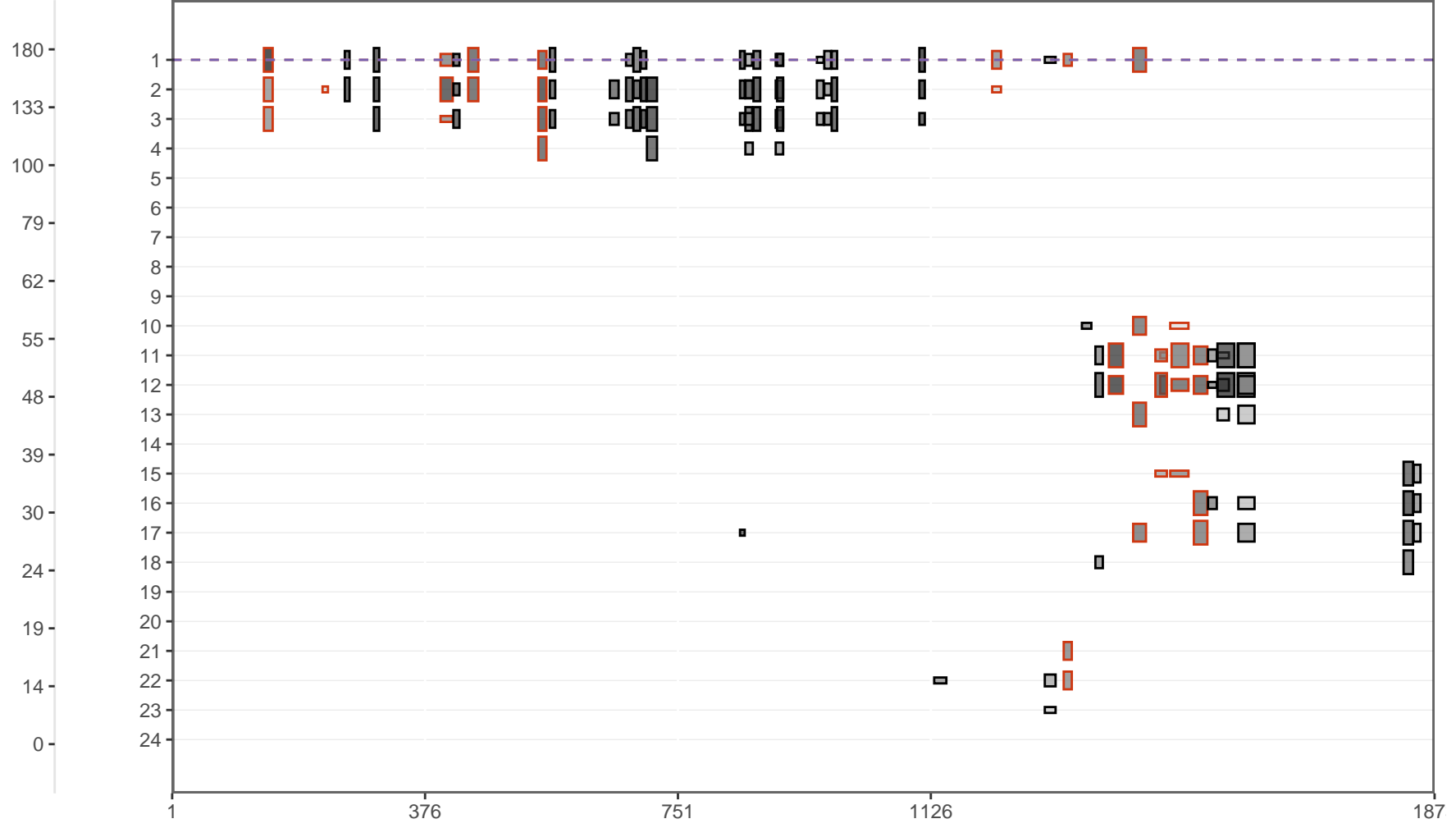


MW indication



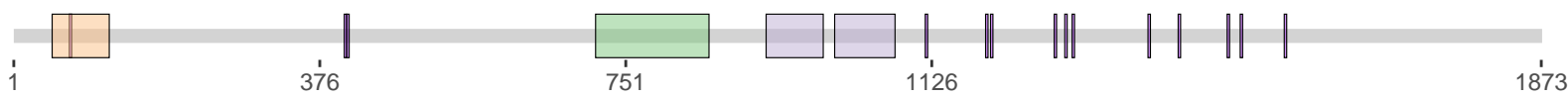
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

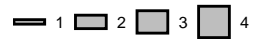
- SP
- Sequon
- TM Domain
- PF12807 Translation initiation factor eIF3 subunit 135
- PF13424 Tetratricopeptide repeat
- PF15044 Mitochondrial function, CLU-N-term

Protein sequence:

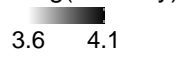
ISLLAVLYHTGDFNQTIVGQKALDINERELGLDHPDTMKSVDGLAVEYRRLGHTLALKYVNRALRLLHLTQGPHPNTAATYINVAMMEELGNHVALRVLHEALKNGRLLGADHIGTAASHYMAAMLSLMEAVSLVQHEQTFLQLQAKLGPDDLRTGNFLQDAAVALEVFESKALEGGEAARNGTTPKPDASISGKHLGVSDDLQVAFDPAEMKAREAQKKGARAKVGGKAGONGGIATDEFEKDELLSPNSPVAVENSQDKENKSELQNLLELQIADSTAKQSDHII

NbL08g04250.1 V-type_proton_ATPase_subunit_H-like [MW = 51.53 kDa]

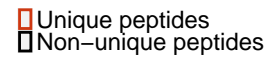
No. of times detected



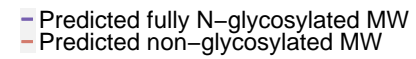
log(intensity)



Values from



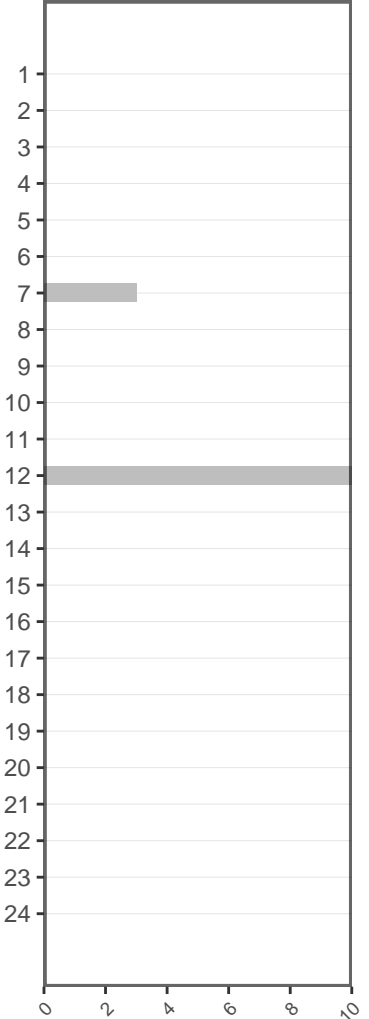
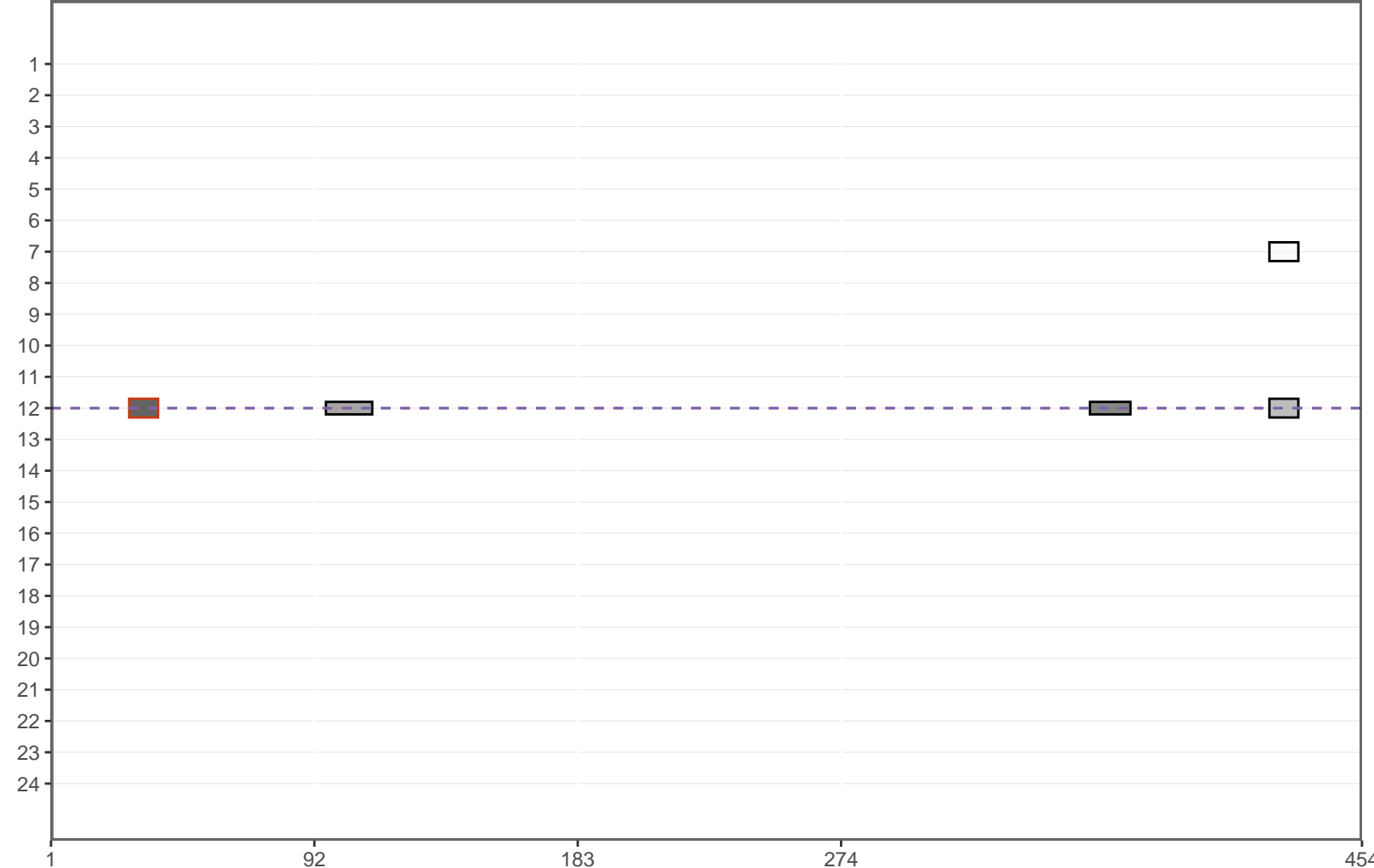
MW indication



Molecular weight



Gel Slice

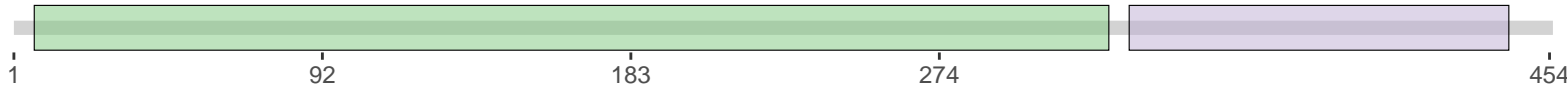


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

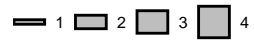


Protein sequence:

LVP LSP LST QOS IGL YET QG WLL S V Y E P A E V L A T S R A L P R L I E V V K G S T K E K V V R V V L T R L N L L S K G S F S I L M V D L G V L G V S L K A G A W S D E D L L D A L N O L E E G L K N K N K L S F D K Y K G V L L G H L D W S P M H K D P L F W R E N N S F E E N D F Q I L R V L I L T D S E D P R T L A W A G Y D L G S F Q I G H S A G R I V N D L K A K E R V M K L L N H N E A V T R N K A L L G I R L F L G A K Y A S F L Q V

NbL08g04080.1 DNA-directed_RNA_polymerases_II_IV_and_V_subunit_11-like [MW = 13.62 kDa]

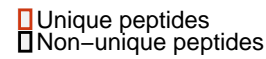
No. of times detected



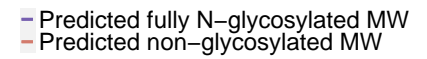
log(intensity)



Values from



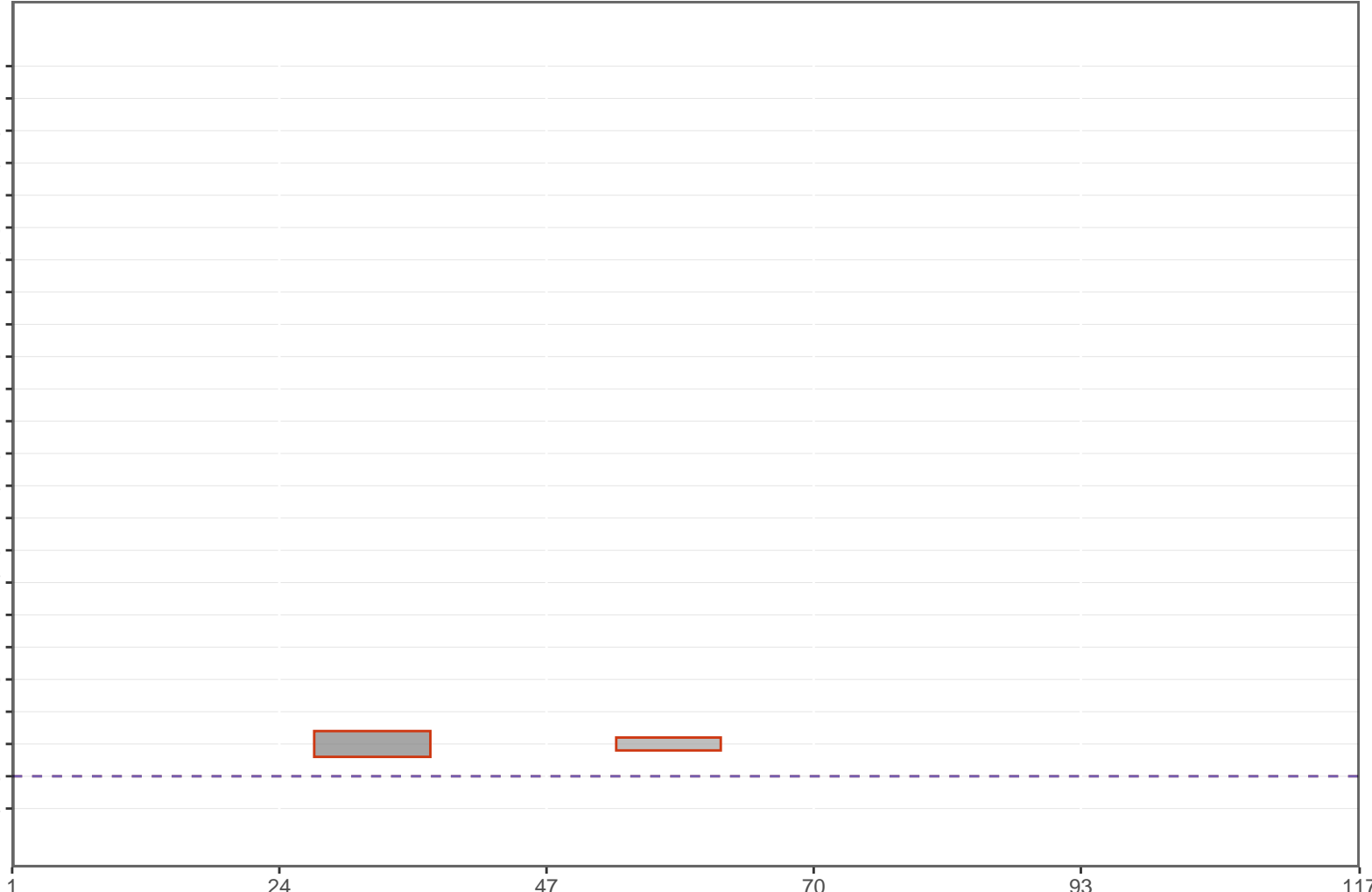
MW indication



Molecular weight



Gel Slice

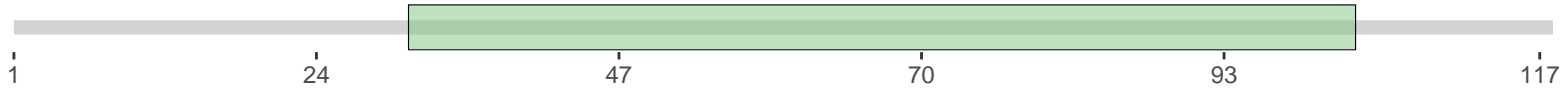


Protein length

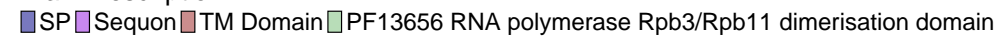


Peptide counts over 4 repeats

Pfam domains



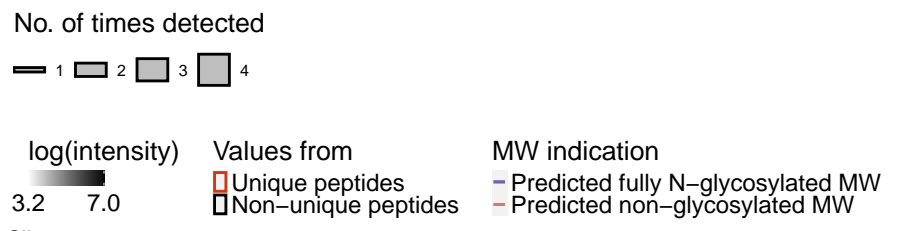
Pfam Description



Protein sequence:

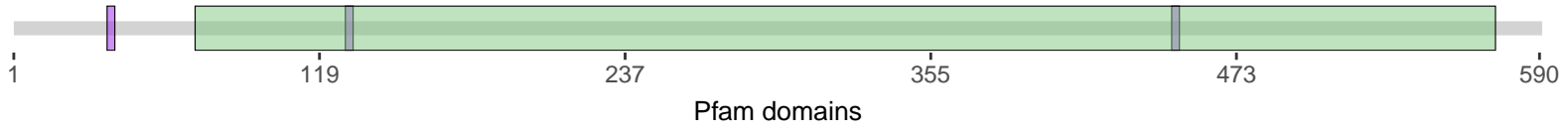
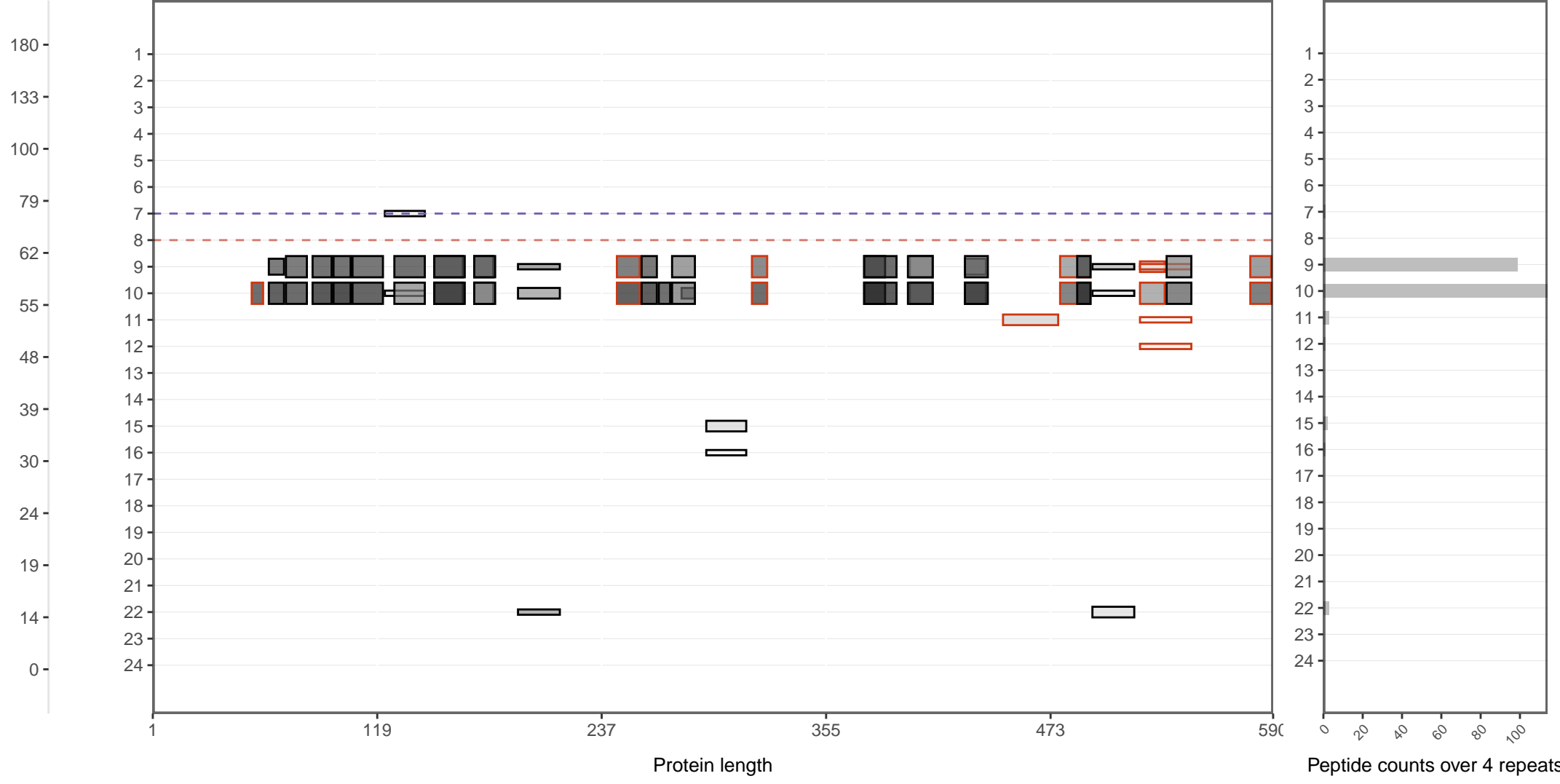
.RMQLHRDDNYLFAQYKLPFLQYKILLRIQFTSQQSFMQAYNGAINDLKELDHLKNGFEGELAKHSREY

NbL08g03960.1 ruBisCO_large_subunit-binding_protein_subunit_alpha-like [MW = 62.11 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00118 TCP-1/cpn60 chaperonin family

Protein sequence:

⋆IPLLEKTTQLRSPLIIAEIVTGEALATLVNKRIGLNVAIKAPGFGERRKALLQDAIVTGAIEYQATDLGLLEIETPVEALGIARKVITIKDSTTHADAASKDEIQARAGLKKELSETDSVYDSEKLAERIAKLSGGVAVKVGATEALELDRKLRIEDAKNATFAIEEGVPGGGAFFVHLSTVYVPAIKKLELDSDEKLGADIGRALKVAPSLIAGNAGEGEEVVEKVKREAEWEMGYNAMIDKYENLVDAQVIDRKYVTRGALGNSASVAGMVLFTQAVVEKAKPKTAAPAP

NbL08g03760.1 cell_division_cycle_protein_48_homolog [MW = 89.57 kDa]

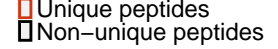
No. of times detected



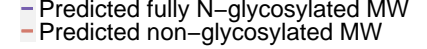
log(intensity)



Values from



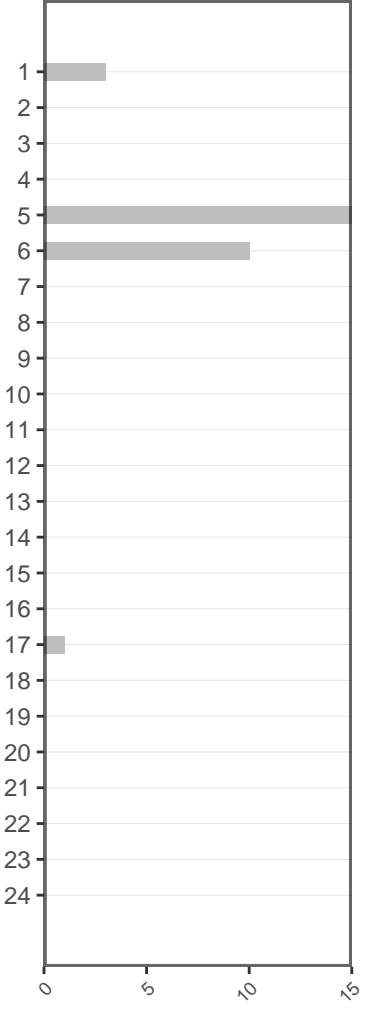
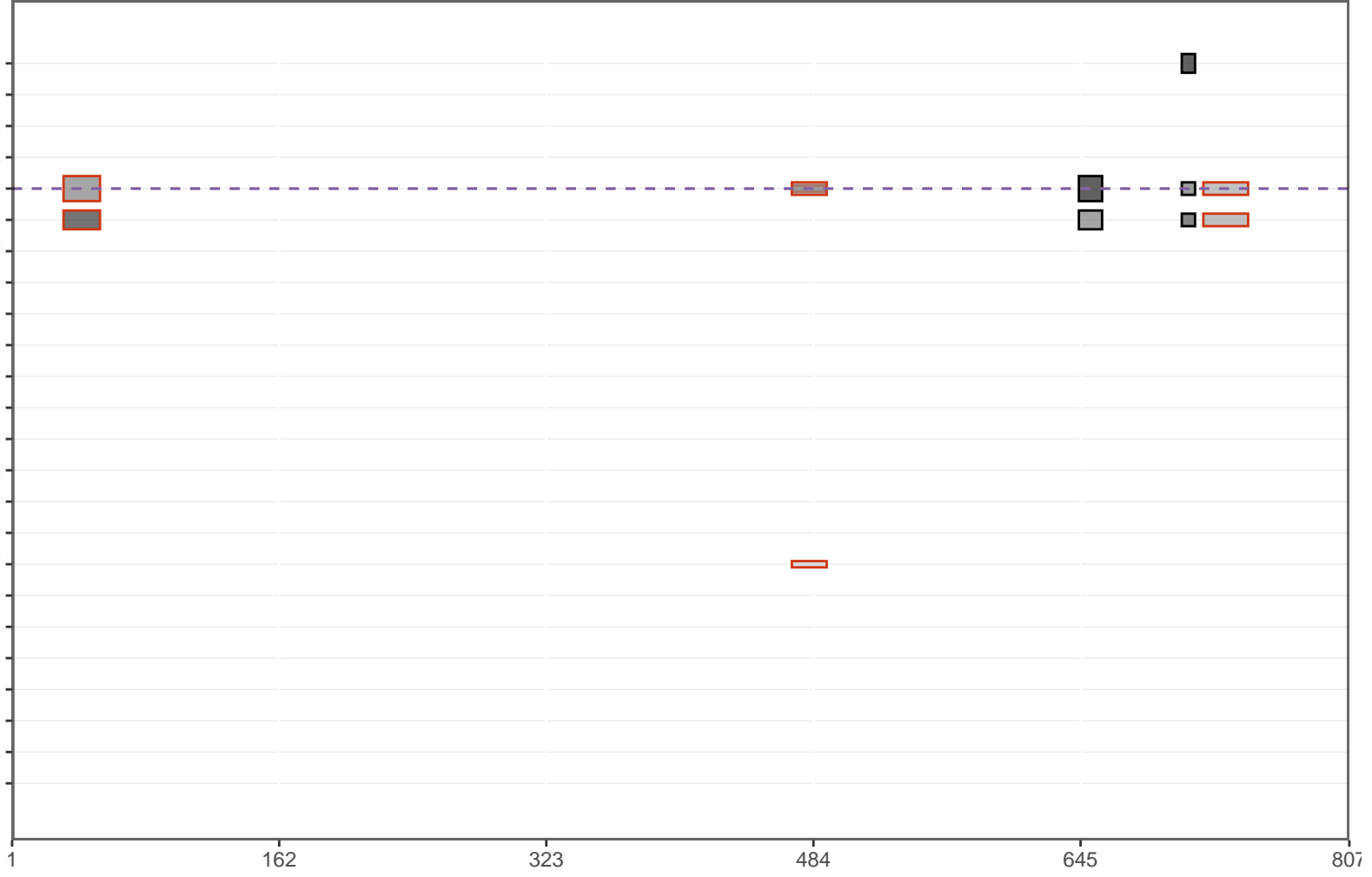
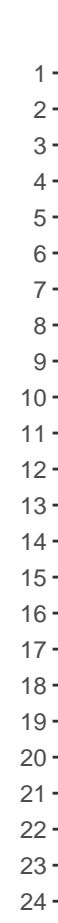
MW indication



Molecular weight

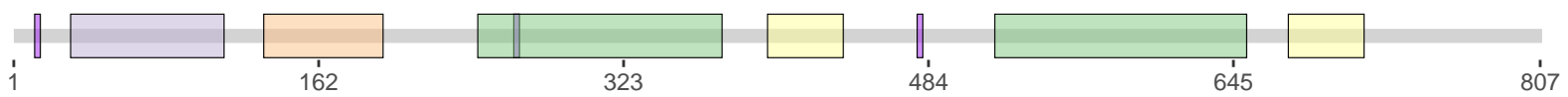


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

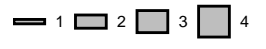
- SP
- Sequon
- TM Domain
- PF00004 ATPase family associated with various cellular activities (AAA)
- PF02359 Cell division protein 48 (CDC48), N-terminal domain
- PF02933 Cell division protein 48 (CDC48), domain 2
- PF17862 AAA+ lid domain

Protein sequence:

MKLAEEVDLERIGKQTHGIVGADLAALCTEAAAGGIREKMDVIDLEDSDTDAEILNSMAVTNEHFDALGTSNPSALRETVVEVPNVSWADIGGLENVKRELGQETVGVYVPEKPEKFKGMSPEKGVLFYVPPGCGKTLAKAAIANEGGANFISVYKPELITMWFGESEANVREIFDKARQSEAPGVLFDFELDSDIQRGGSSGDMGGAADRVLNGLLTEMDGMNAKKTVFIGATNRPDIIDPALLRPGRLDQLHYIPLPDEESRHQIFKALRKSPLSKQVDLRALAKYTOGF

NbL08g03740.1 elongation_factor_1-alpha [MW = 49.34 kDa]

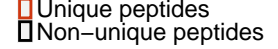
No. of times detected



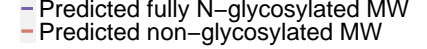
log(intensity)



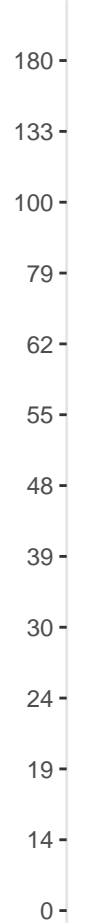
Values from



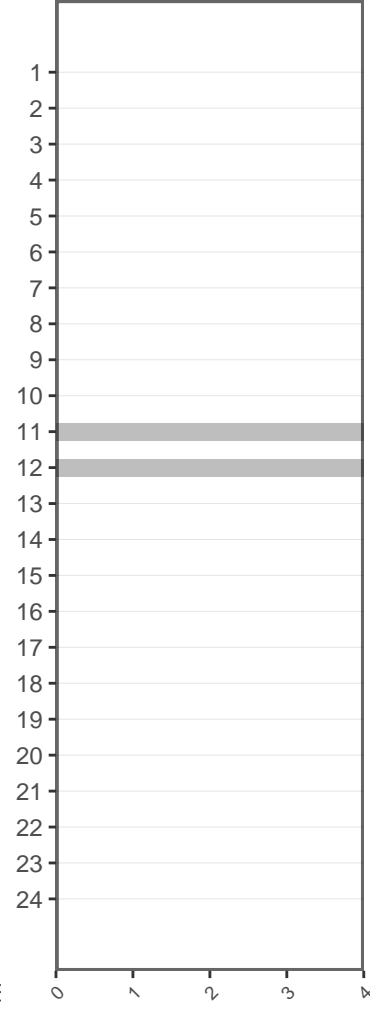
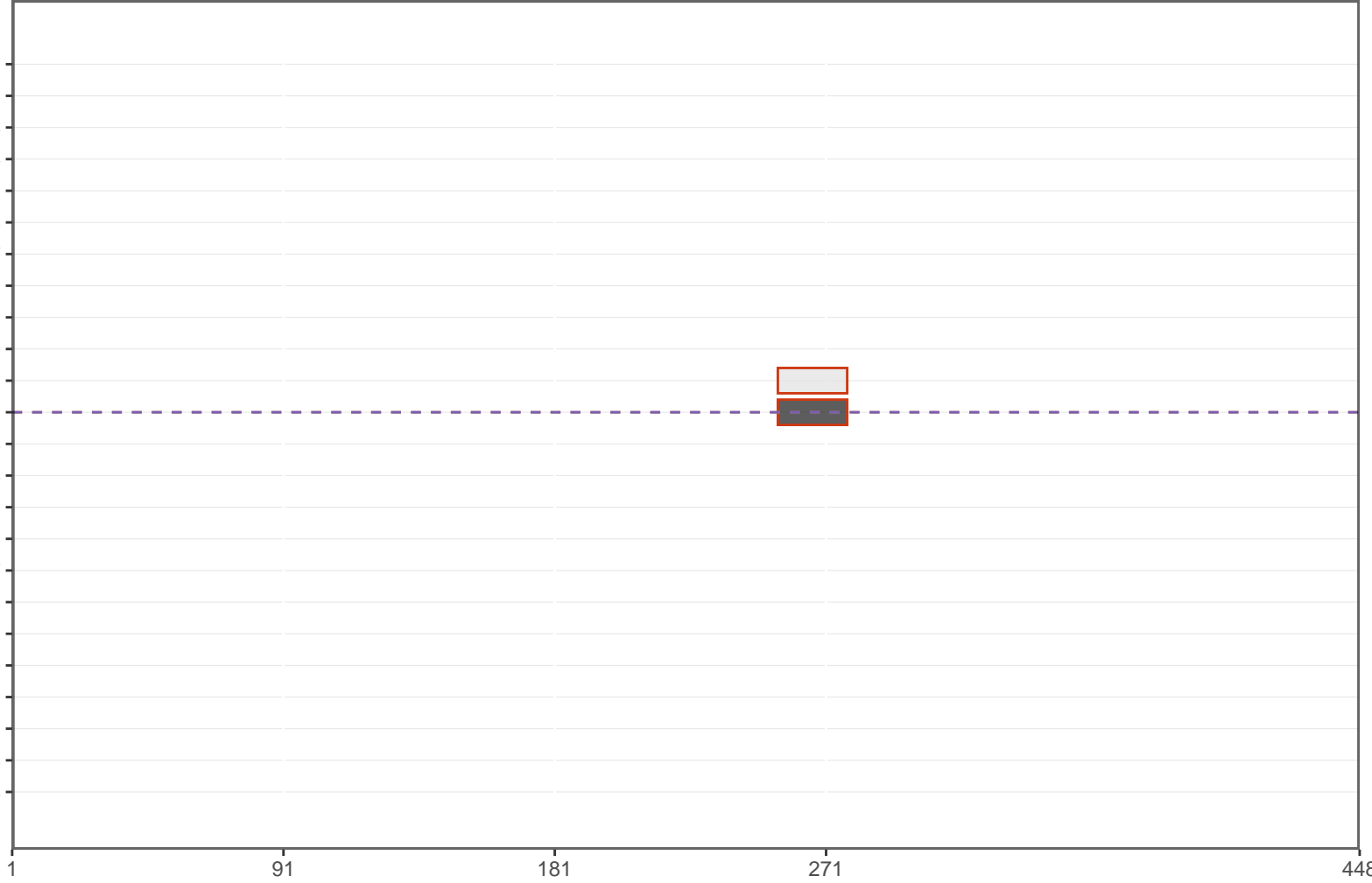
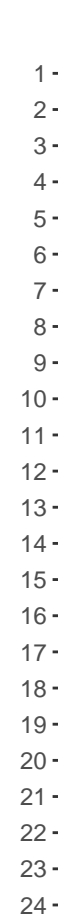
MW indication



Molecular weight

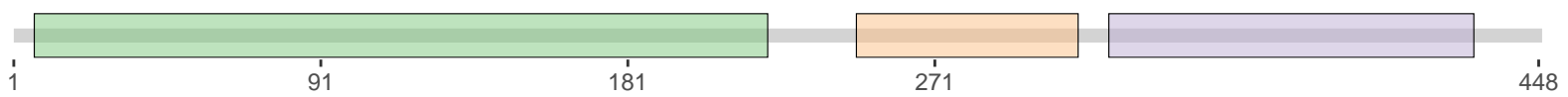


Gel Slice



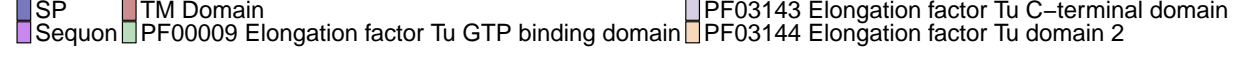
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GPTLLEALDONENKRPBQKPLRLPLGDDYKGGIGTVPVGRVETGLKPGMVTFGPTGLTFEYKSEVMHHEALGEALPGDNLGPNVKNVAVKDKRGEVAGNSKDDPKGAASFQSGVHMNHPPGGIGNGYAPVLDGHTSHAVKFAELTKIDRRSGKEIEKEKFKLNGDAGMVMMLPTKPMVVEVFSEYPLGRFAWRDMRGTVAGVYKKNVQKDKPTGAVTKAAQKKK

NbL08g03640.1 uncharacterized_LOC109233996 [MW = 130.24 kDa]

No. of times detected



log(intensity)



Values from



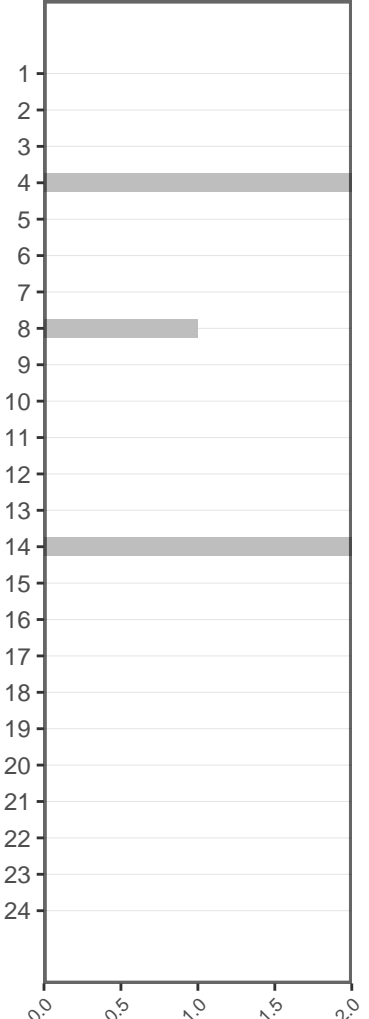
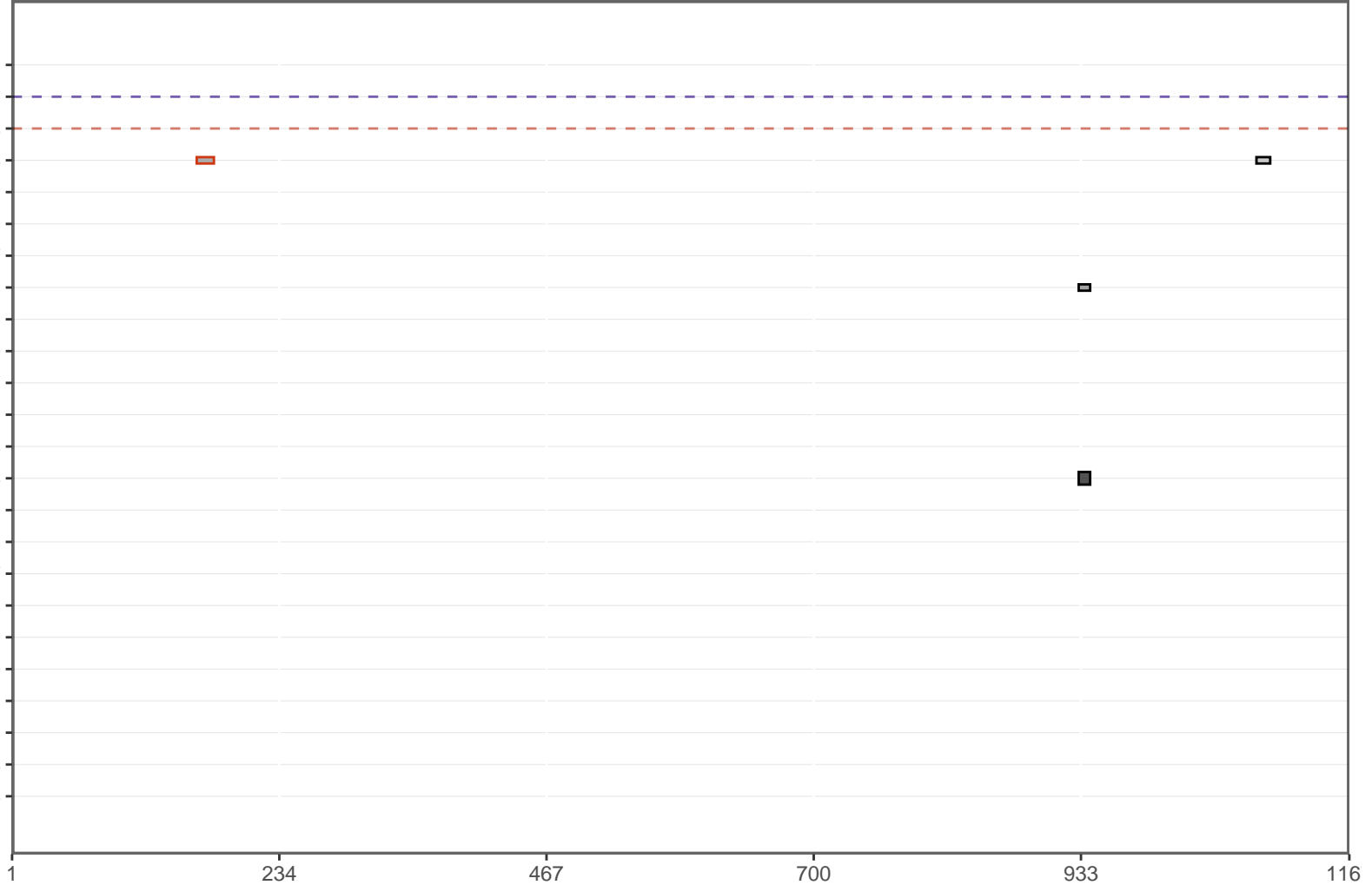
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

DLFKANEKAAEMVQSSDHWKNSGESSLADEADANLMLKFLAYLKRTRFLRNGSLFLKFGPEAVRAYLRQMKWNTSAKQRELSKMLDEWVHRRKYGNKPLSSSTYLSAEFLFQYAKREPQNGALIGAGNFYKVEDFMVAVEGDDEEGDLETKHAPSSPSFKDMVAKNEGLVFFPGIPGAKSALGKELNVPGLGDDRPVHSLMGDLKGRYVQKVADERRRKPYSIMLADKQAPNEEVRQIENMGLSTKASAPVVPDSEGTENPFSVDAL

NbL08g03530.1 interactor_of_constitutive_active_ROPs_3-like [MW = 70.85 kDa]

No. of times detected



log(intensity)



Values from



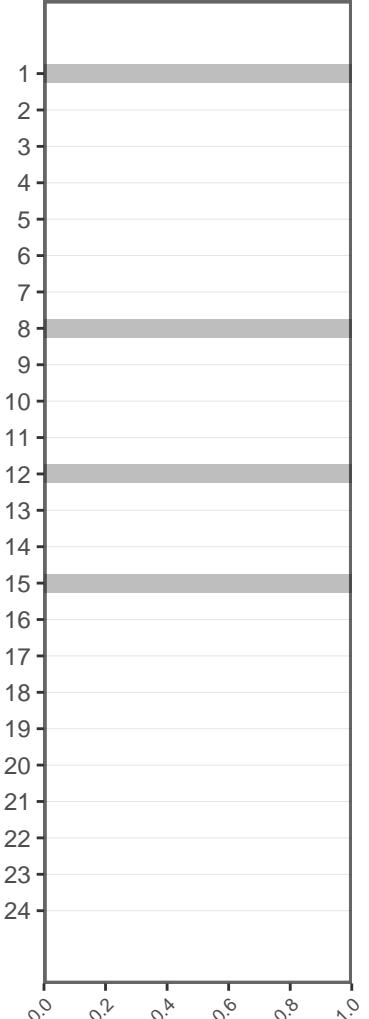
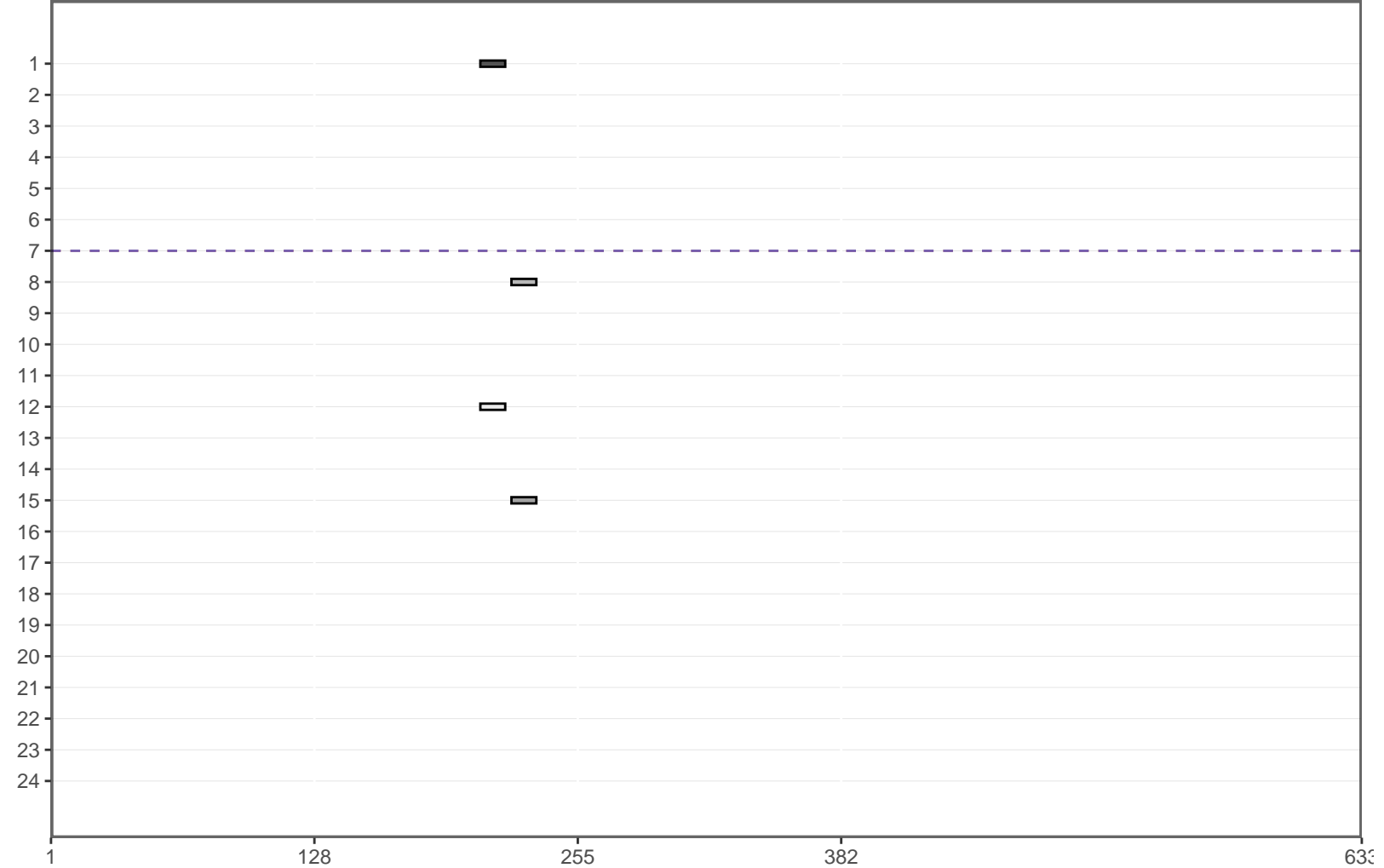
MW indication



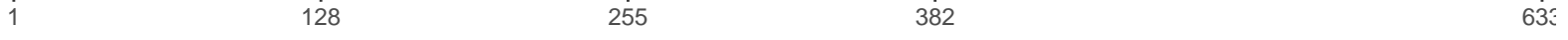
Molecular weight



Gel Slice



Protein length

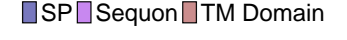


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KARANLWEEIVCKLQDTFNSVGETEVEVDESKETIEAEL68SLKBEVERLKAADLEAAEITFYNEKTRBTLEIRSAVELVEGKAMSKQKDELDKGLQKFKTQIDELKANLMMKNETELGGICKEKENEITMKLENNAKSGKGENELEKELGRSLDIENMKANLMDKTELGNIILEENELKLETNKKENNRGKWKDEVAAELEGAKTAEREAGDMKLVYMKKEVDKSNRRVAVTEGLDAAQASNAEMEAELRKLKLVQSNQWRKAAEVATMLNNGNNGKFMERTGSMDSQYSS

NbL08g03500.1 arogenate_dehydratase/prephenate_dehydratase_2_chloroplastic [MW = 43.21 kDa]

No. of times detected



log(intensity)



Values from



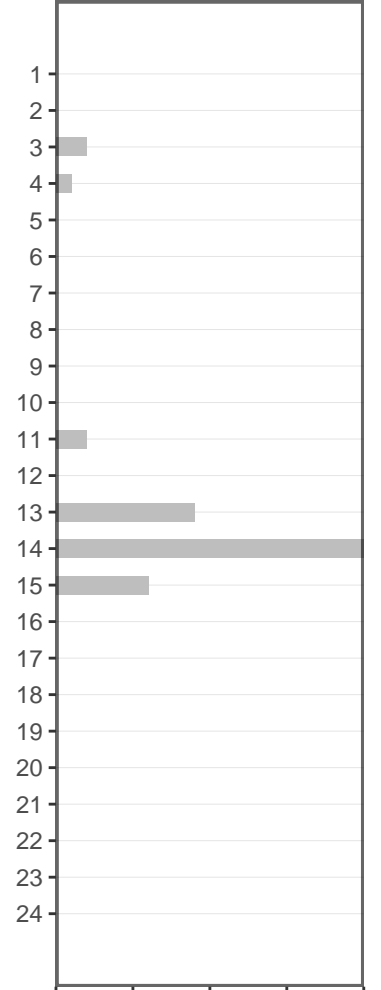
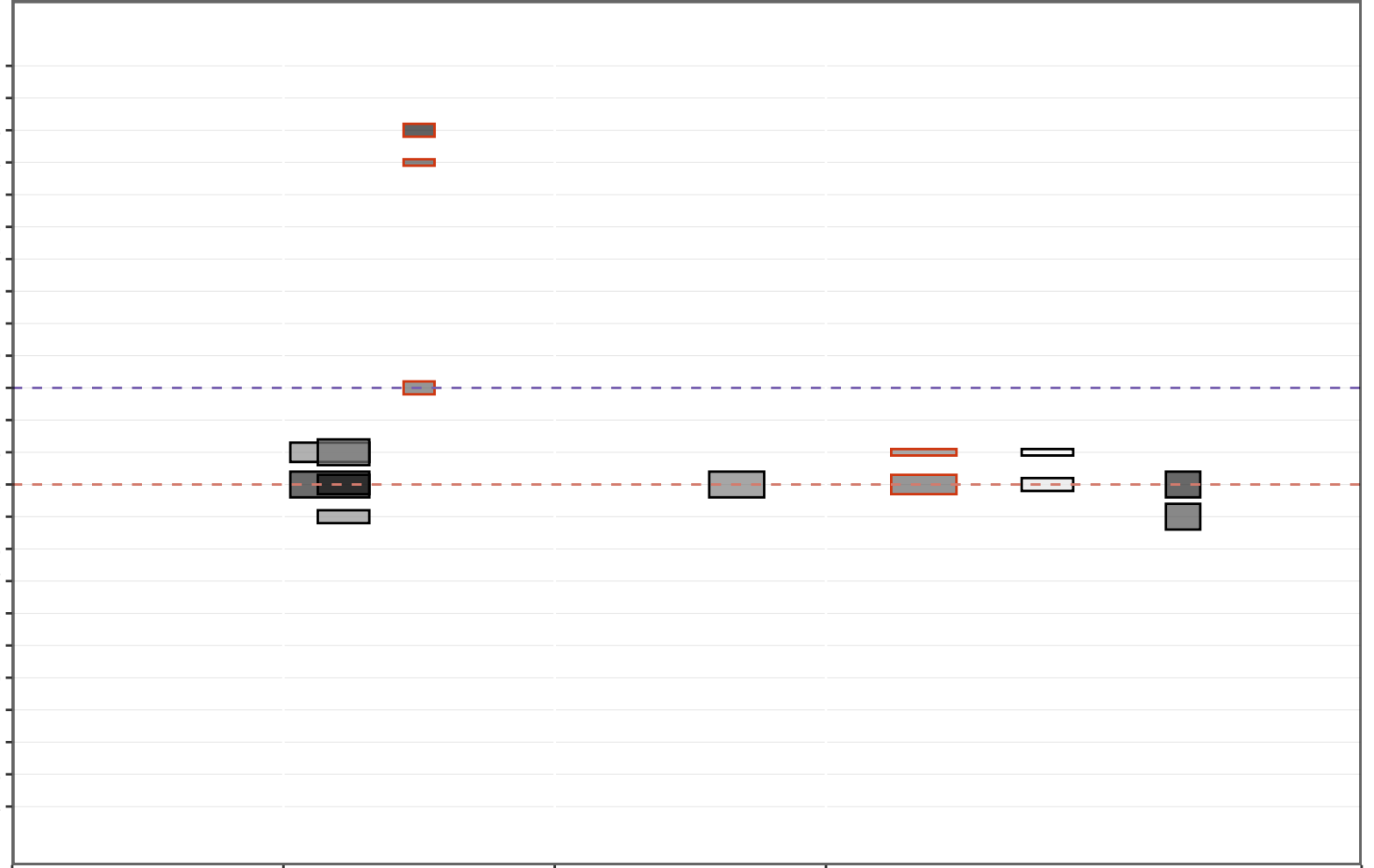
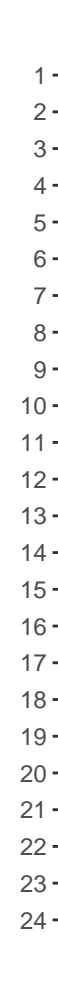
MW indication



Molecular weight



Gel Slice

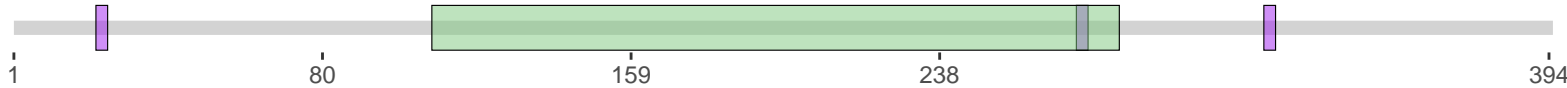


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LAIRHCLMANNNGVYKIEDLKRVLKSHIPQALAGCENTLTKLGLVREAVDDTAGAAYVAFQKLDAGAVASLAARIVGLNVLADGDDSDNVTFRFLMLAREPIPTGDKPFTKTSVYVSLDEGPGVLFKALAVFAMRNINLTKESRPLGKQALRVLDDSDGFPKYFPLKLVVDFEASMDADRGNALGHKEFATFLRLVGGVYPSDSSVA

NbL08g03250.1 2-dehydro-3-deoxyphosphooctonate_aldolase_1 [MW = 31.9 kDa]

No. of times detected



log(intensity)



Values from



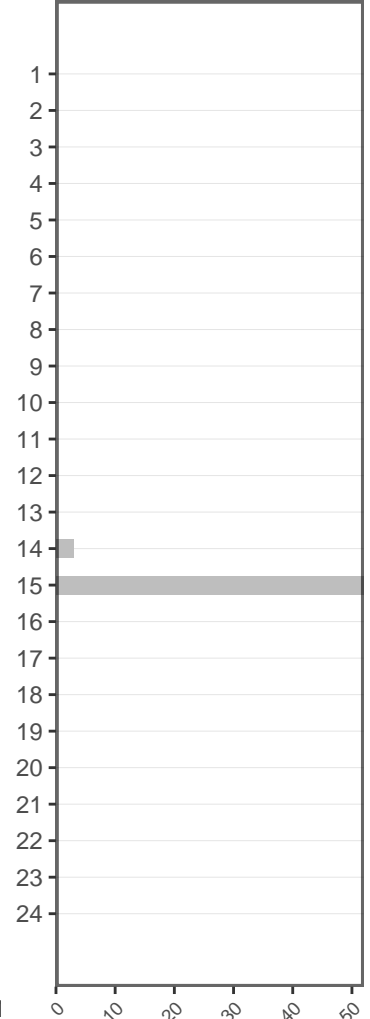
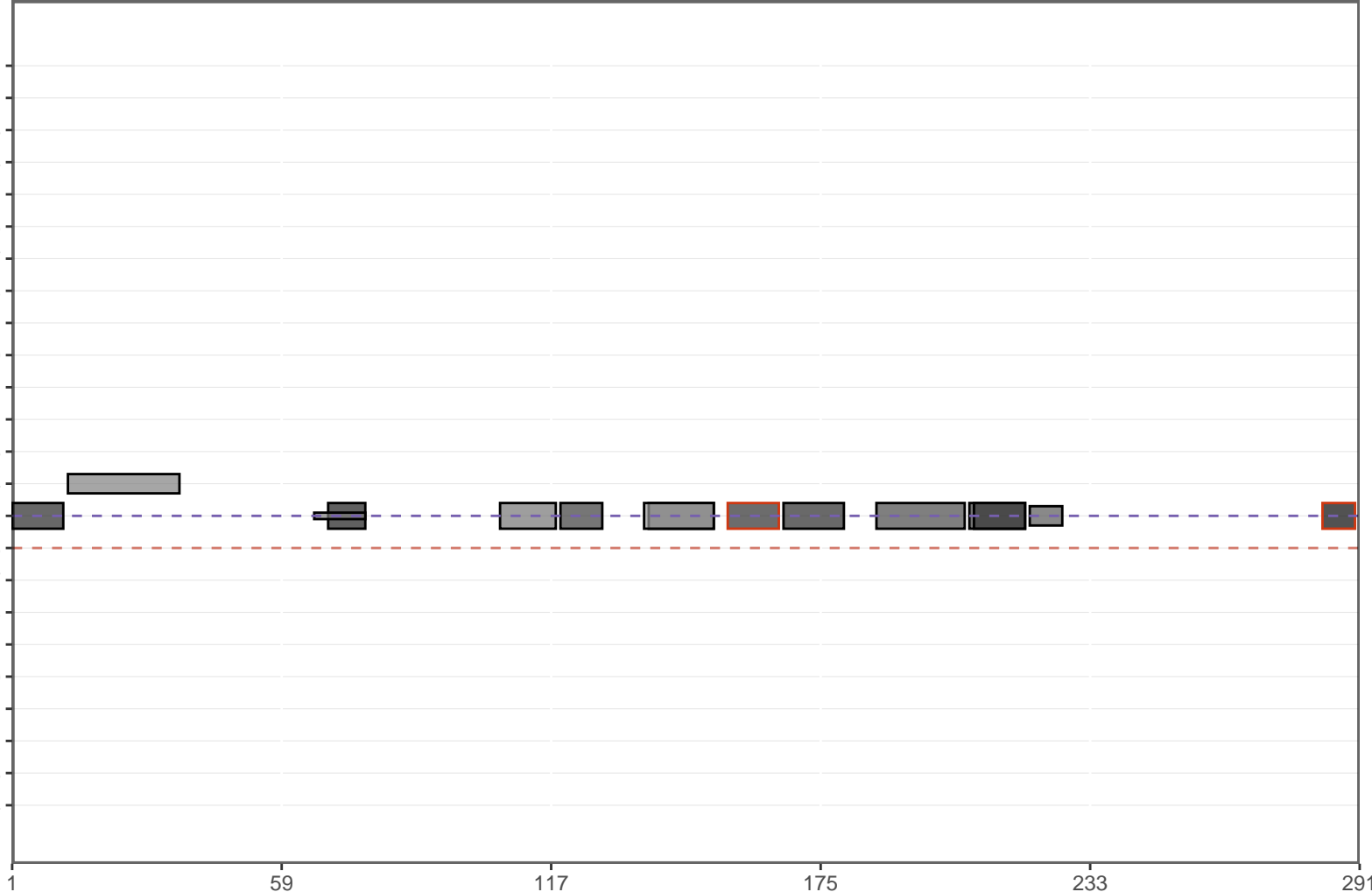
MW indication



Molecular weight



Gel Slice

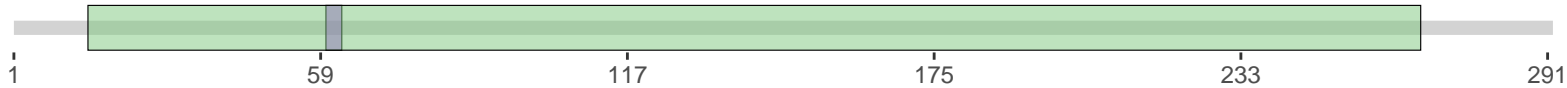


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

KGQFCAPSVMANSAEKVRLAGNHNVMVGERGTMFGYNDLVDPRNFEWMREANGPVAADTHSLGGPAGKLEGGVAVSGGLRELPICARTAWAVGIDGIFMEVINDPLSAPVDGTQWPLRHLEELLEEELVTLGRVSKGKGGQFDHIDTFRFDI

NbL08g03010.1 receptor-like_protein_kinase_HERK_1 [MW - SP = 89.5 kDa]

No. of times detected



log(intensity)



Values from



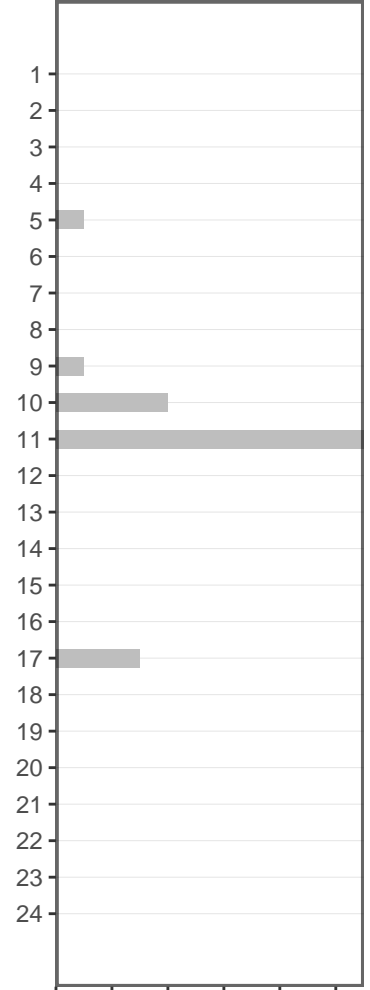
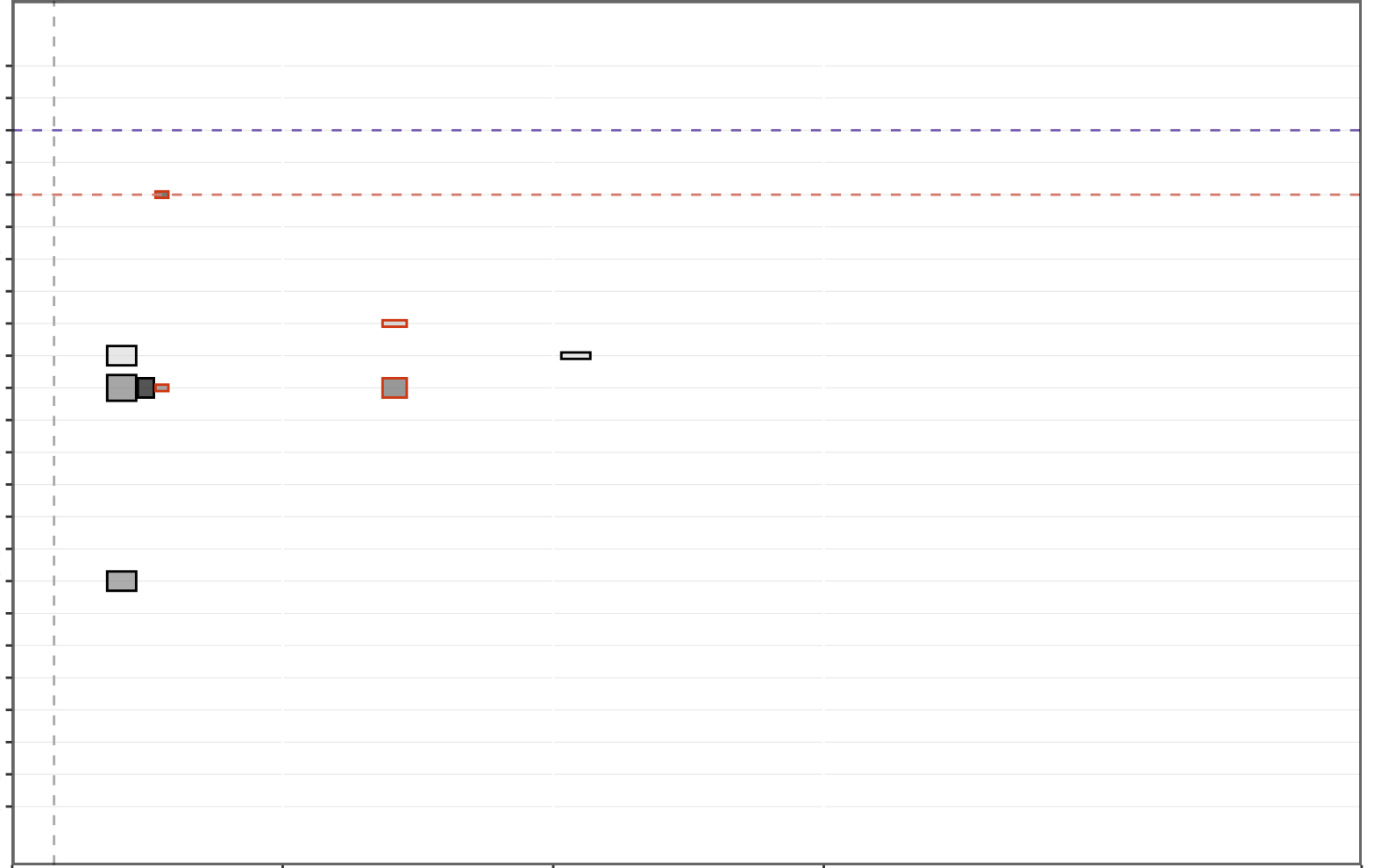
MW indication



Molecular weight



Gel Slice



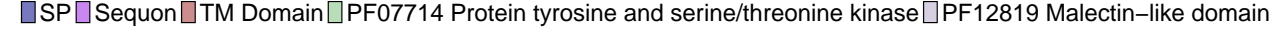
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SRRAKNVGVTVGVSVGVPULLLVGLFCMHRKRRKAGELLAAQKWIPLSVNGNSHTMGSKYNGTTTSAANL6YRVPFALLEATSNFDESLVIGIGFGKYRGLVCDGDTKVAWRGNPK9DQGLAEFRTEIEMLSGFRHRLHLSLMGYCDEKNEMLVYEVMEKNTLKSHLVGSDLPMSBWRQLRLEIGIGSGARGLHYLHTGQYAKVHHRDVKGNANILLDESFMAKVAADFGLKTPPELDQTHVSTAVKGF6FYLDPEVFRROGLTEKSDVYFGVYVFEVLCARPVDFSL

NbL08g02920.1 60S_ribosomal_protein_L35-like [MW = 14.19 kDa]

No. of times detected



log(intensity)



Values from



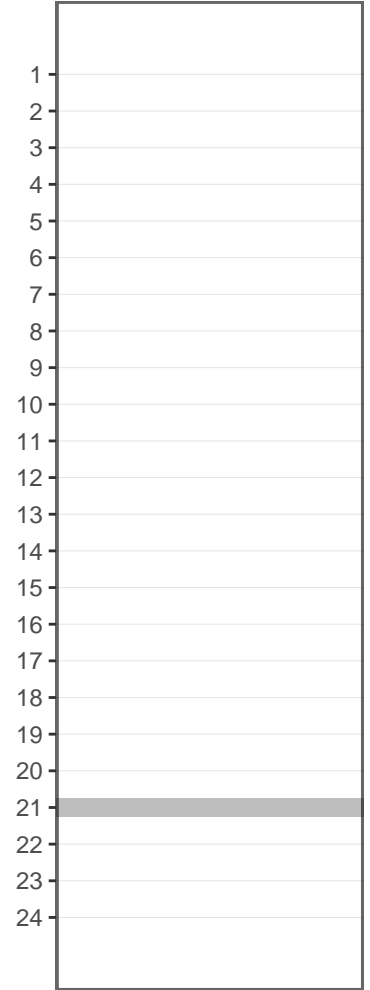
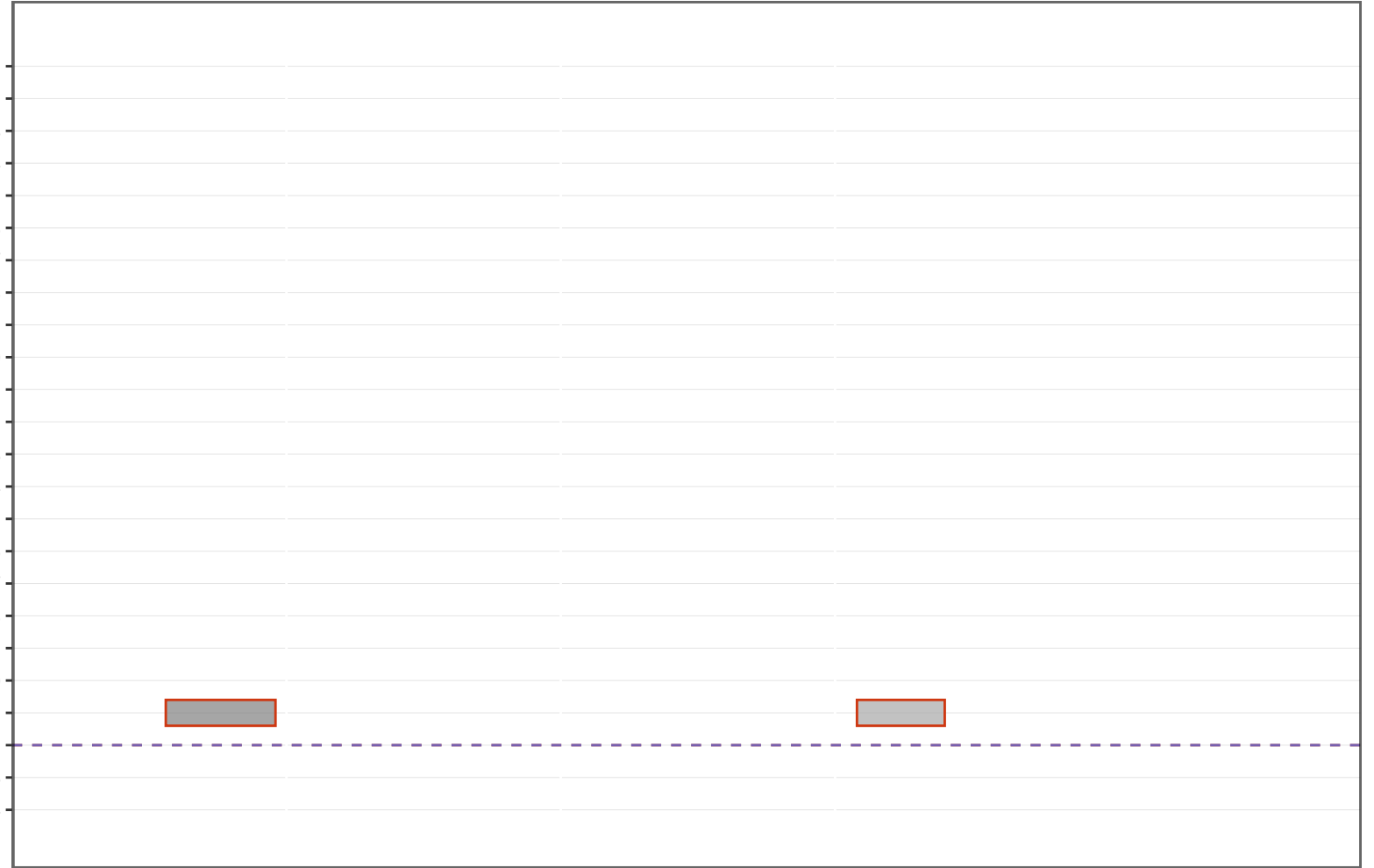
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

1 26 51 76 124

Protein length



Pfam domains

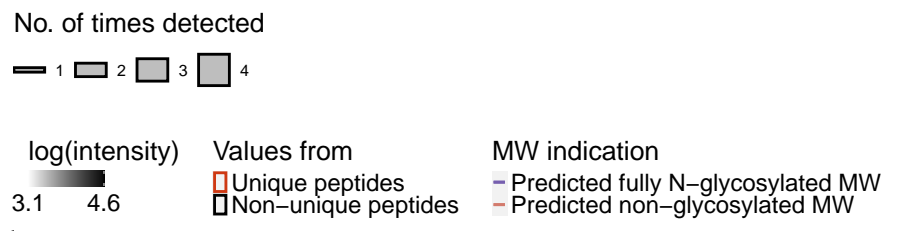
Pfam Description



Protein sequence:

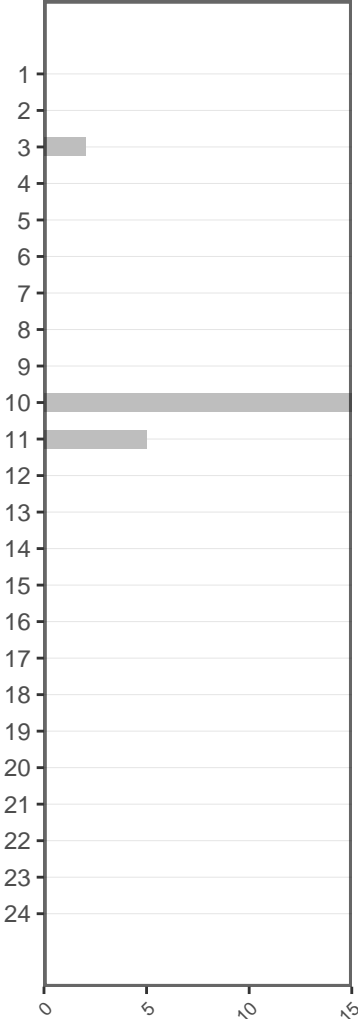
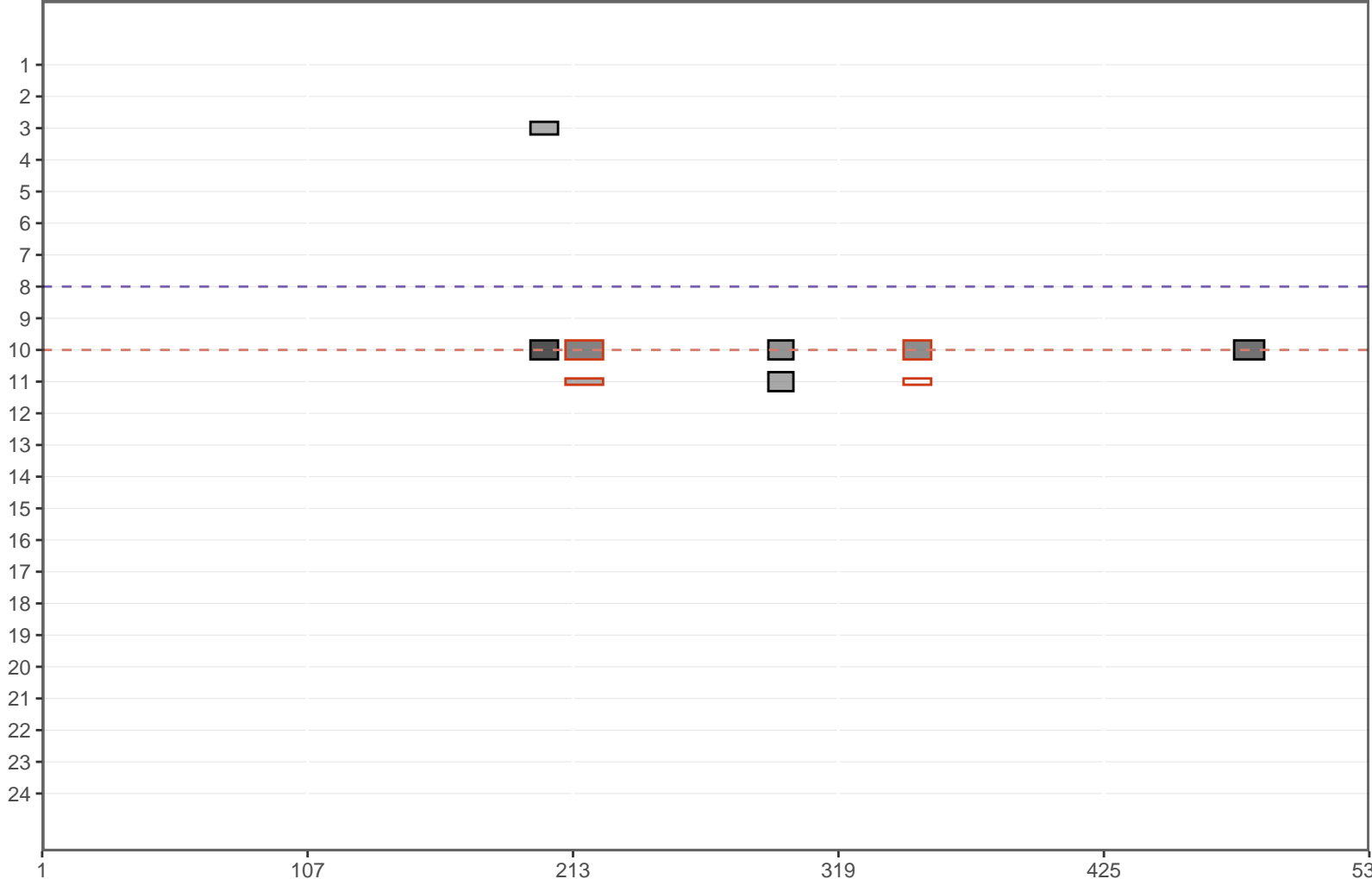
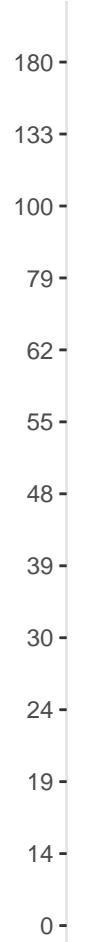
VVRLSIAQVLTVISGKIKTALREAYNNKYLPLDLRPRKTRAIRKRLTHGASLTEREKKEMFFPRKYAIKV

NbL08g02790.1 monofunctional_riboflavin_biosynthesis_protein_RIBA_3_chloroplastic-like [MW = 57.86 kDa]



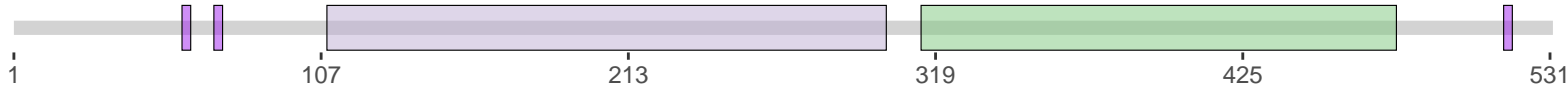
Molecular weight

Gel Slice

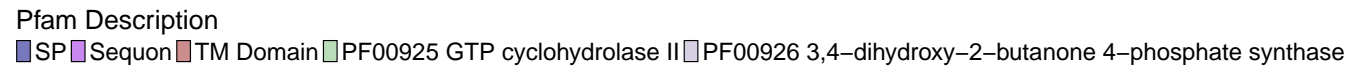


Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:

DLVMSAGLKPYSVLSAFAVDKNDGSSASMLLNLALENKPIVGIIDLVRYRRKRRENVERTAVSRPLTFKWLFEAYCYRSLKDGTEHAIVKGGIDNGDGDALVRHSEGLTGDGFSRRRDCGNGLDLAMLQIEEAGRGVWVYLRGHEGRIGLGNLGAAYNLGGDGHDTVEANLELGFADAREVYGGAGMLRDGIVRTMRLMTNPNKFTGLKGGVGLAVIGRVPVLTPTFEENRKYLETGRTKRMHSHYVGSVGGPKASINRSLKQDPDGRKES

NbL08g02600.1 actin-depolymerizing_factor_2-like [MW = 15.94 kDa]

No. of times detected



log(intensity)



Values from



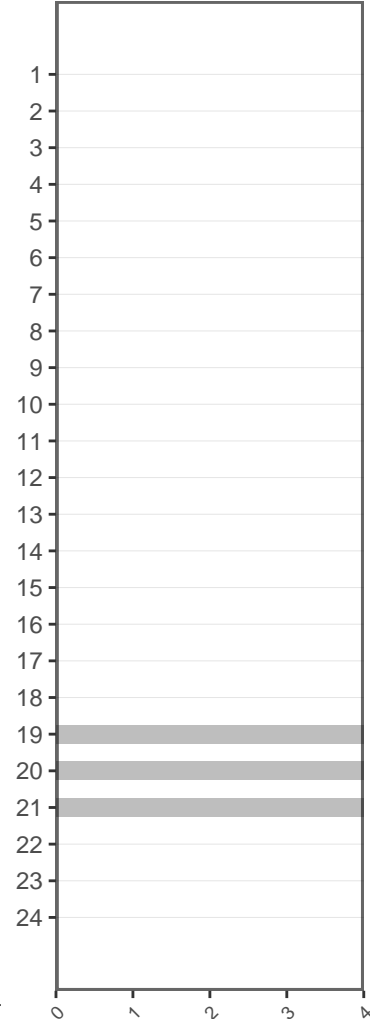
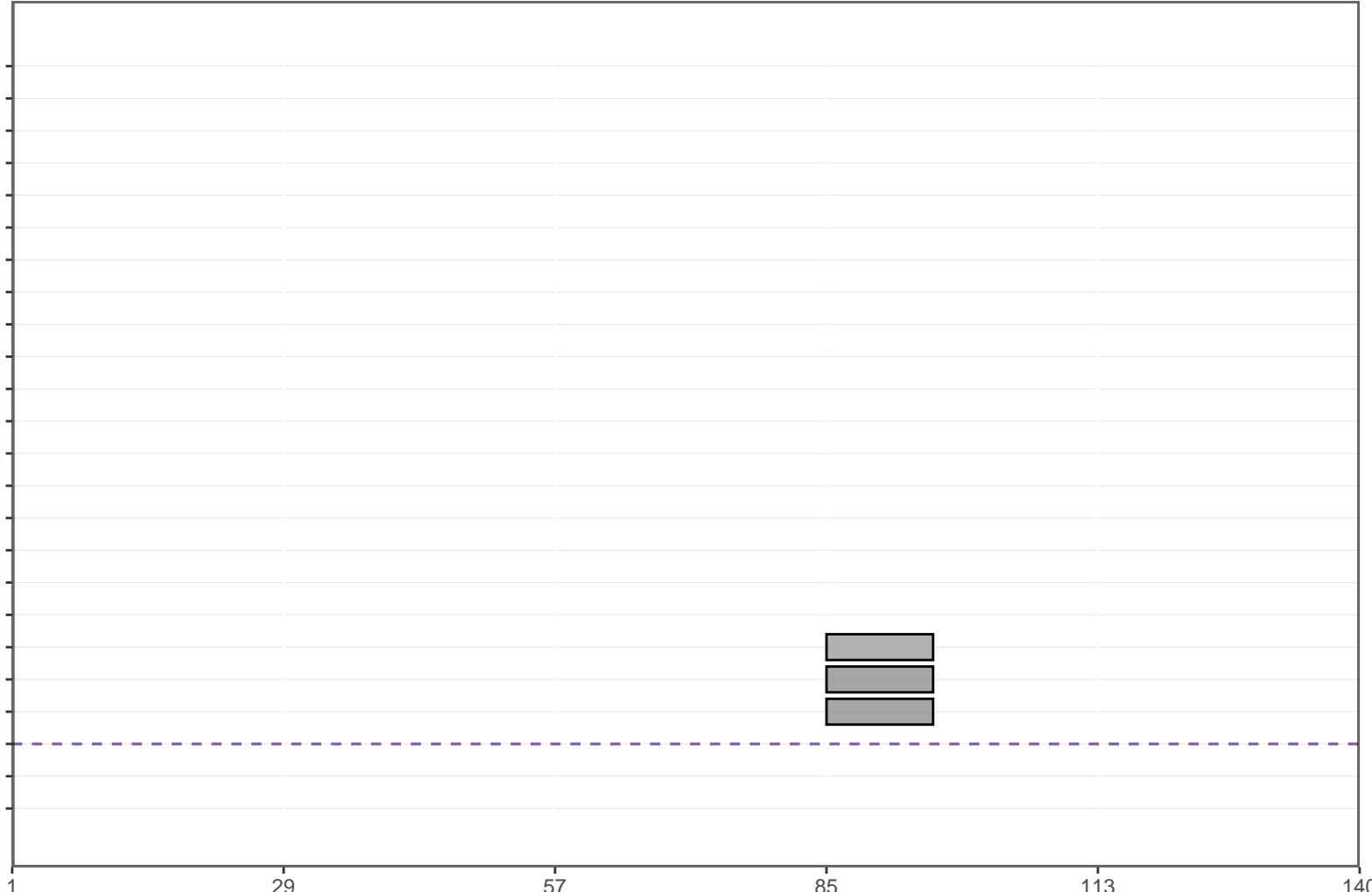
MW indication



Molecular weight



Gel Slice

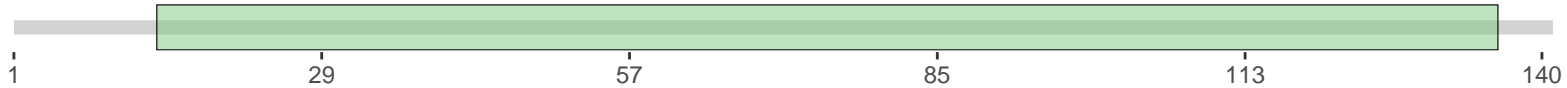


Protein length

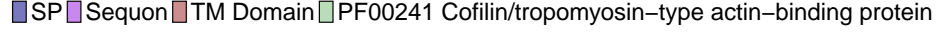


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

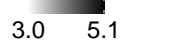
MAQLPADECRYTVFDLFDVTEEGGGKGIFFIAWSPDTAKVREKMIYASGKDRFKRRELDGKVELGATDPTMGLGVFKERTT

NbL08g02560.1 UDP-glucuronic_acid_decarboxylase_6 [MW = 39.13 kDa]

No. of times detected



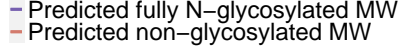
log(intensity)



Values from



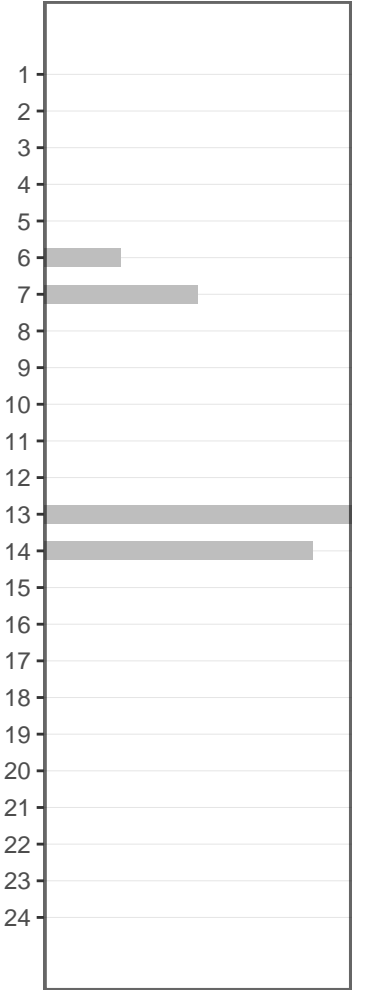
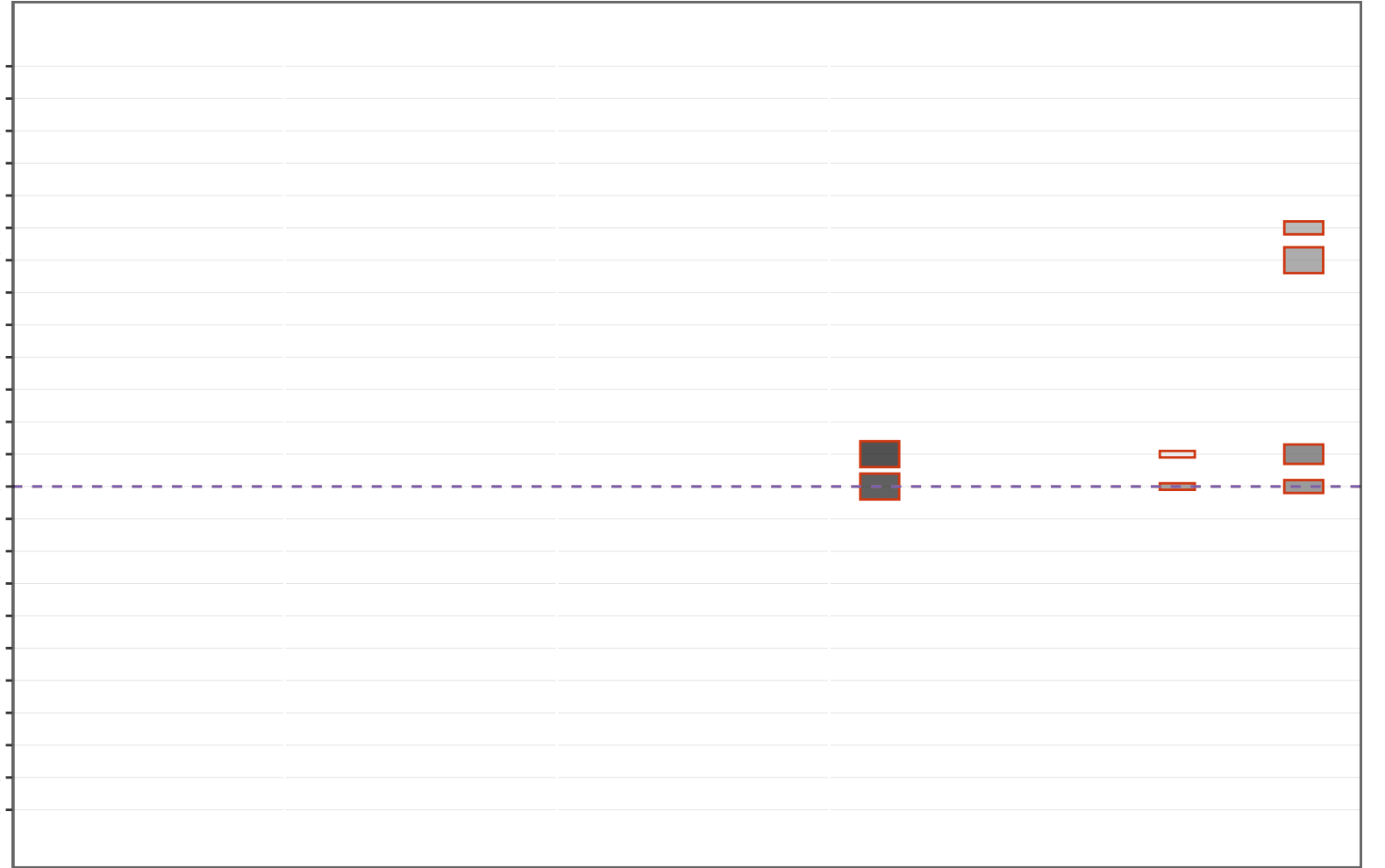
MW indication



Molecular weight



Gel Slice

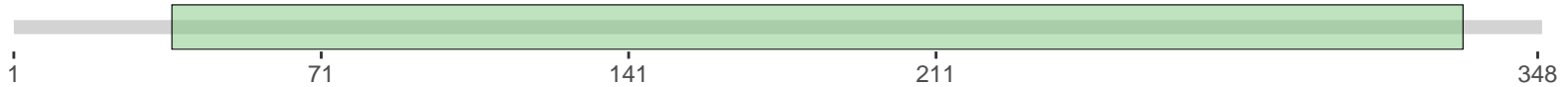


Protein length

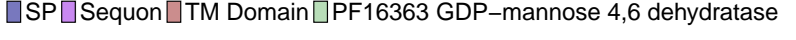


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IEIYWGQVNPQGVRSQYDEGKRAVETLMDYHRHQHIEIRIARINFTYGRMINDGRVSNFIAQALRDELFTVQAPCTQTRRFQGVSDMVMNGLIQLMEGEKTPGMNIGNPGEFTMELAEELVKELNPKVKEIKSVENTPDDPRGRKPDITKAKELLGWEPKVELRDGLFLMEEDFRLRLGVSKK

NbL08g02520.1 osmotin-like_protein [MW - SP = 24.46 kDa]

No. of times detected



log(intensity)



Values from



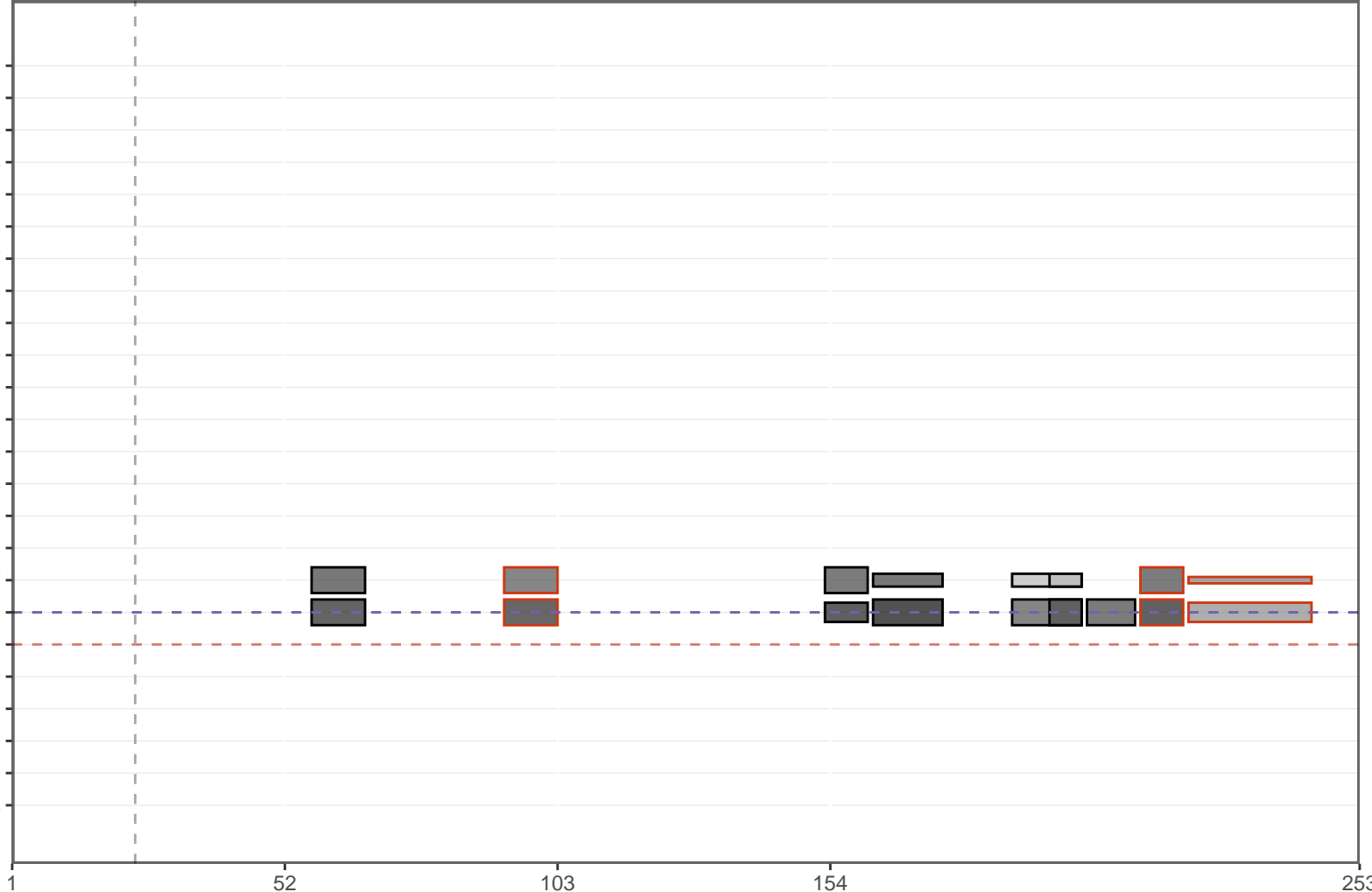
MW indication



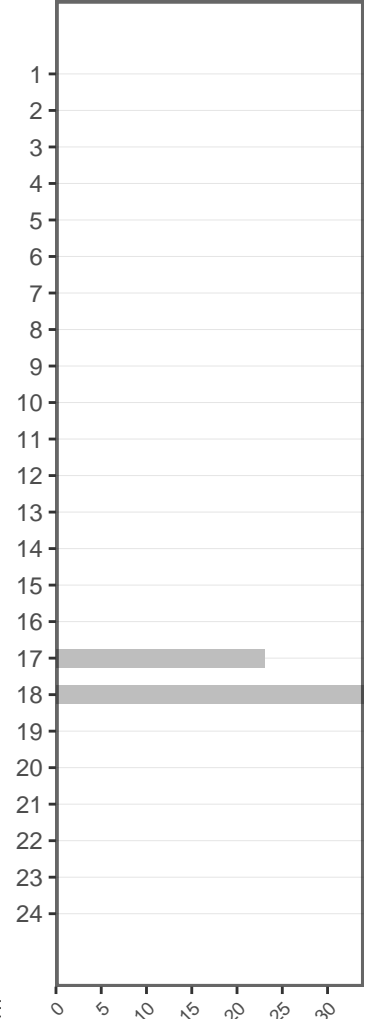
Molecular weight



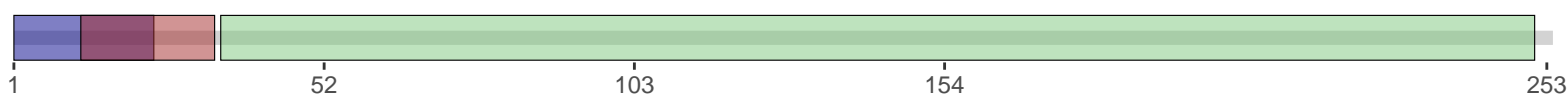
Gel Slice



Protein length

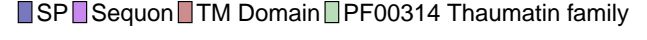


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YTLAQFALHIGHADDFSEYGVSLVDGFIPLVTFPIHEGKGGKCFVVGGRRAEILGTGPVALQLRSHGSHGHPVVGCKBGGGEAFKTDDELGCRNHFNSPQTCKGGSYSEFFPKHACPAITFFAHDSPLMHEGSSPRELKVFCI

NbL08g02380.1 actin [MW = 41.71 kDa]

No. of times detected



log(intensity)



Values from



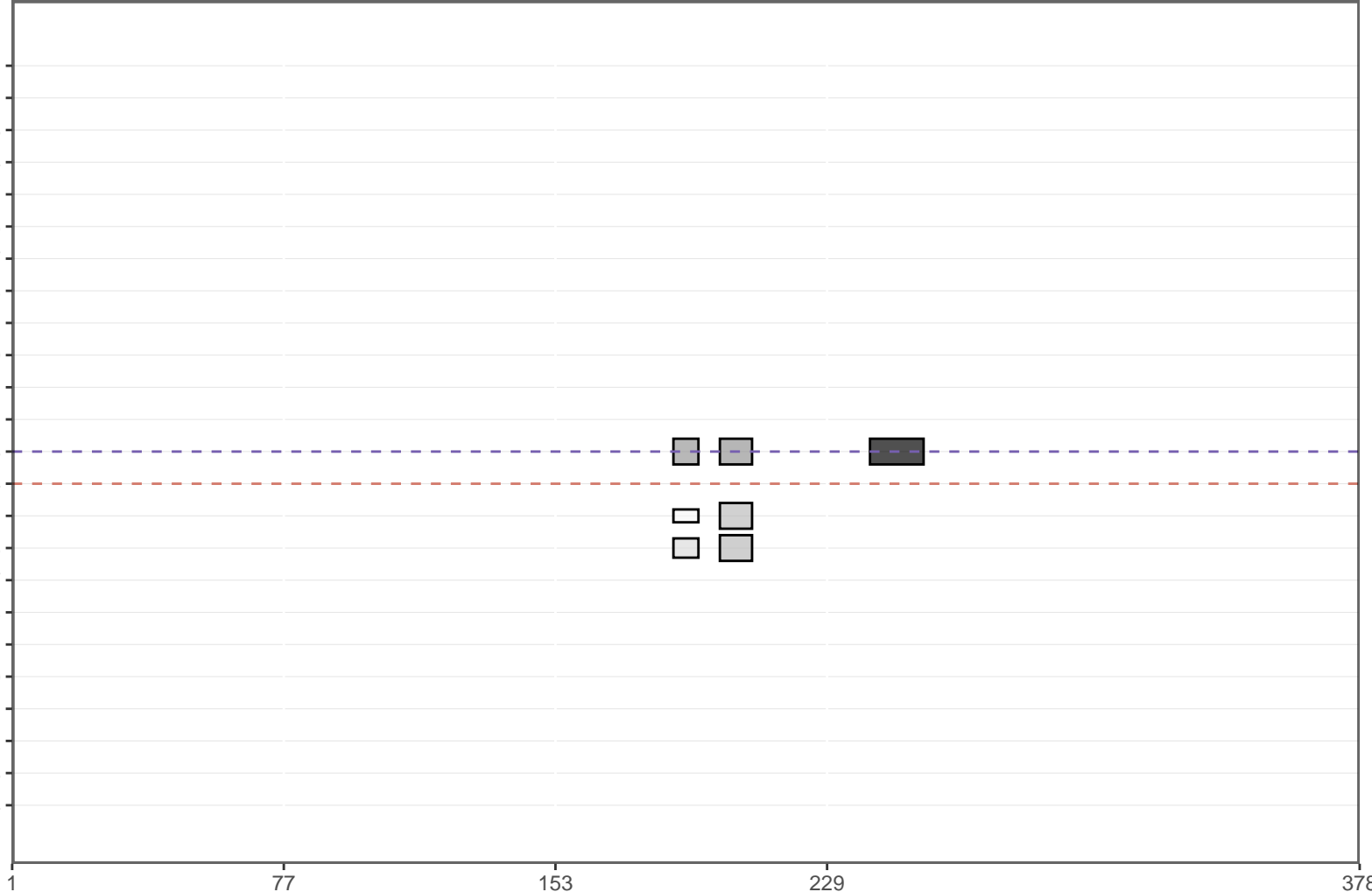
MW indication



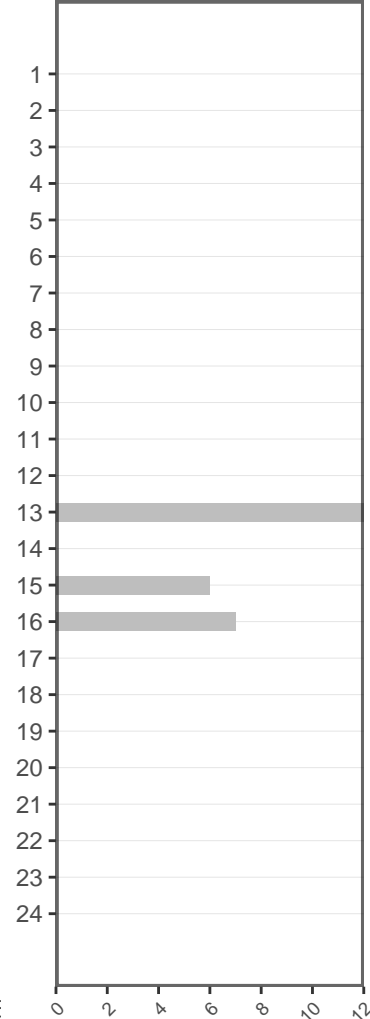
Molecular weight



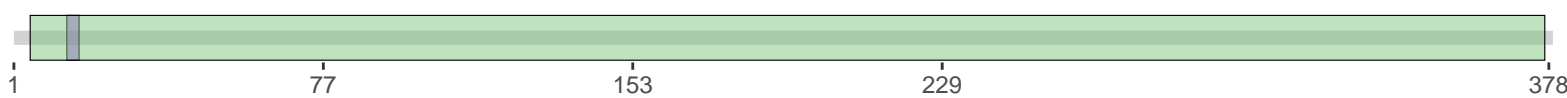
Gel Slice



Protein length

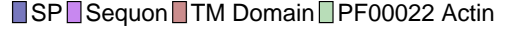


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

HALLRLDLAGRLDTHLAKILTERGVYFTTSAERENVRDKEKLSVALDFEQEMDTSKTSSSVKESVELPDGQVITGAEFRFCPEVLVQPSMIGMEAAHGHETTYNSIMKGDVDRKDLVGNVLSGGSTMFGIADRMEKEITALAPSEMKIKVVAFFPKYKYSVWIGGSILASLSTFGQMMVIAKAEYDESGPSVHRKGF

NbL08g02290.1 dicarboxylate_transporter_1_chloroplastic-like [MW = 62.78 kDa]

No. of times detected



log(intensity)



Values from



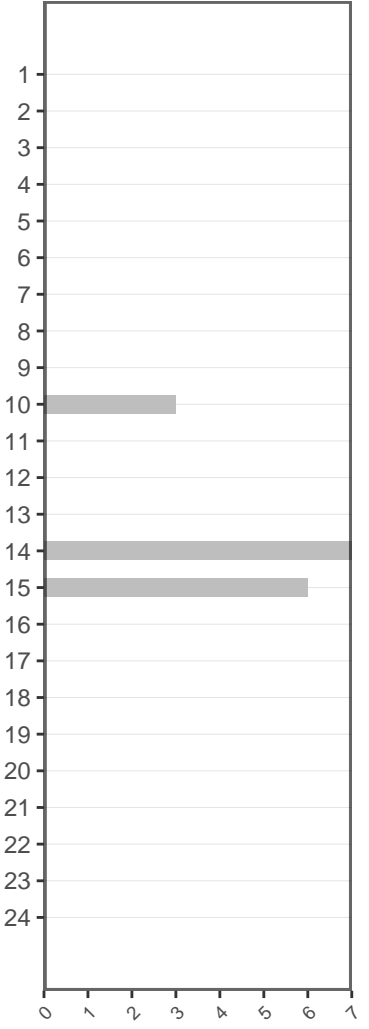
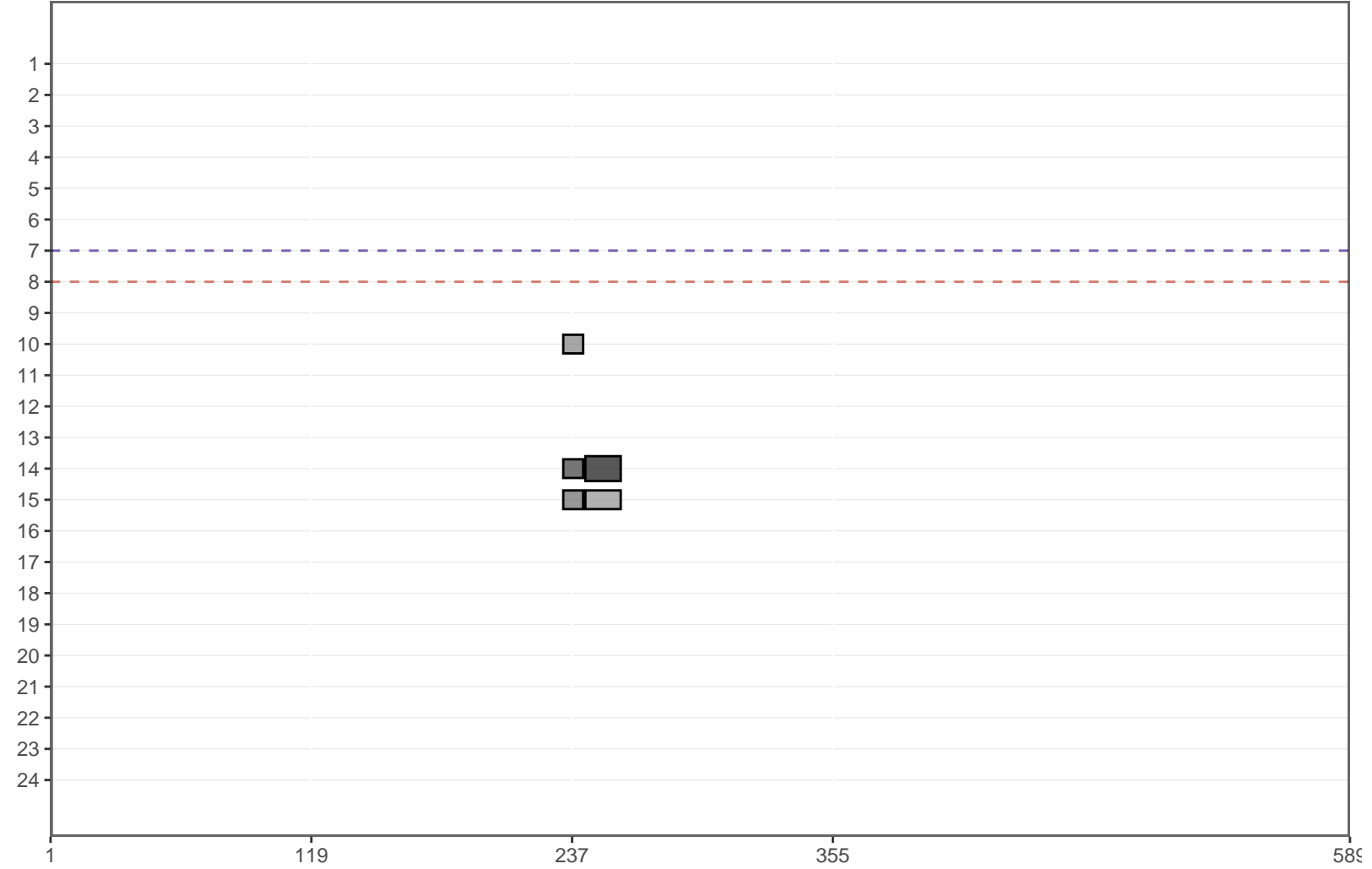
MW indication



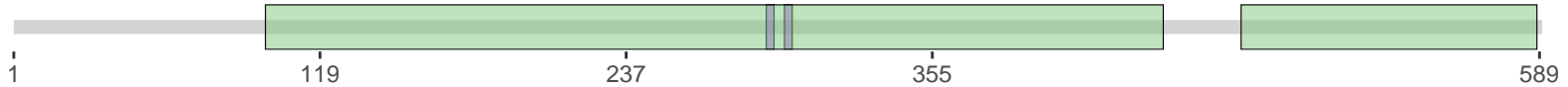
Molecular weight



Gel Slice

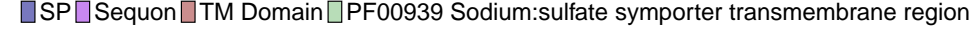


Protein length



Pfam domains

Pfam Description



Protein sequence:

AAANPLSANLTLSTINGTIGMDWAKAAVPLGLVSLVIVPLLLVHYVPTVKSDFAPRLAKENLEKMKCFMSKNEEMMAGTLLLVSLWIFGSLKVDVTAALGLSLVLLITGVVSWKELGEAAWWDLTWFAALAMAGVLNKYGLISWFSSETVYKDRSTRGTGTRLESEGLVYLNLSKSKVVDGLSLWQLSFGLLVLYFVSHYFFASGAHHGAMFTAFLEVAELGTPPVLGALVLSFLSNLMGGITHYGGISAPVYFGANVPLAKWVGKGFVSNLIIIVLGVGGIWK

NbL08g02260.1 uncharacterized_LOC107821402 [MW = 25.51 kDa]

No. of times detected



log(intensity)



Values from



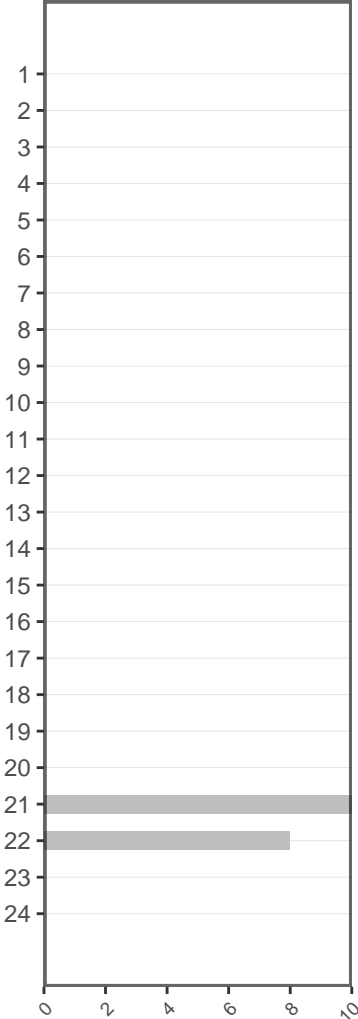
MW indication



Molecular weight

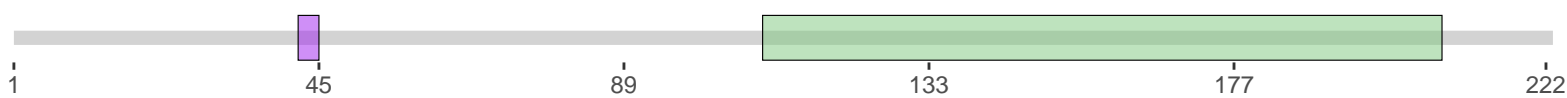


Gel Slice



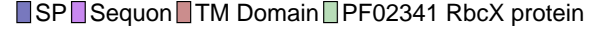
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EQEYEGFDDIKTQALNFFKAVRILNQLNEMDSPGVGFNDVYVANKLRDGRFRIRLAKKELAEKVMVTRILSLVAKWKKGDHEEIVNRISDGNVEVMRERLMEYVWPSDDTNSERVG

NbL08g02170.1 sulfite_reductase_1_[ferredoxin]_chloroplasic [MW = 82.25 kDa]

No. of times detected



log(intensity)



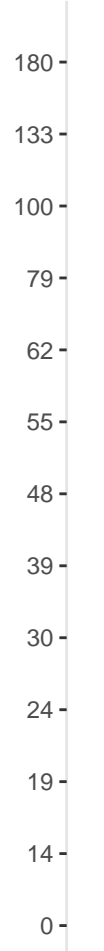
Values from



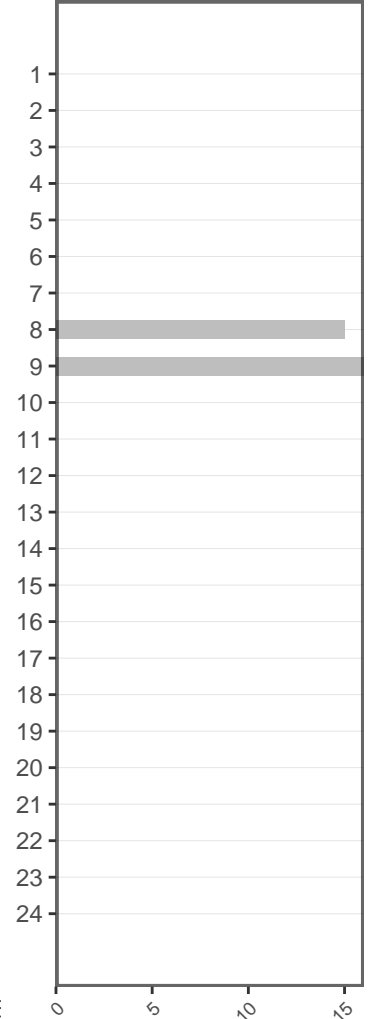
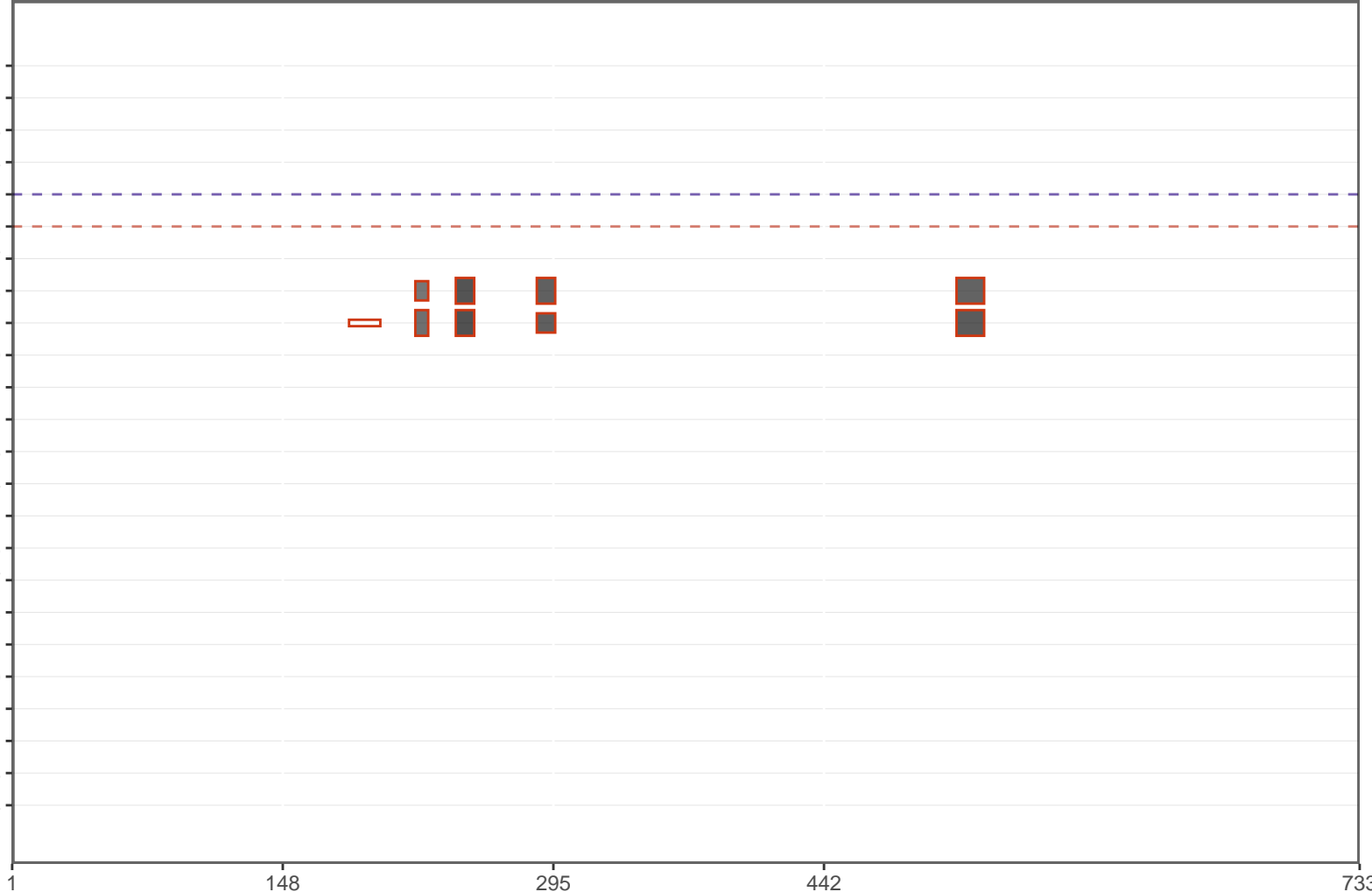
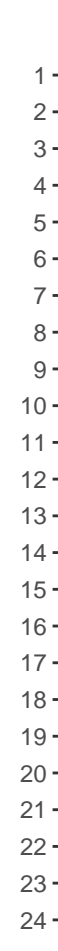
MW indication



Molecular weight



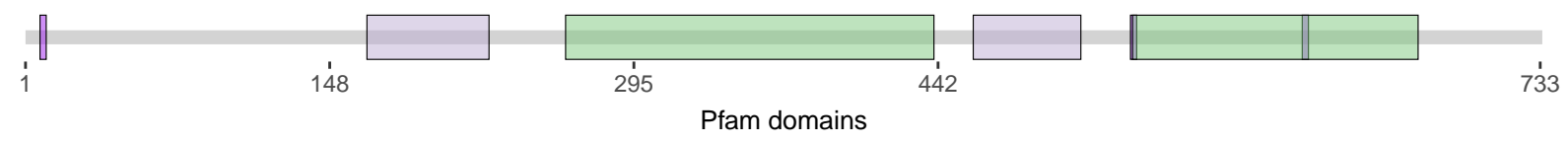
Gel Slice



Protein length

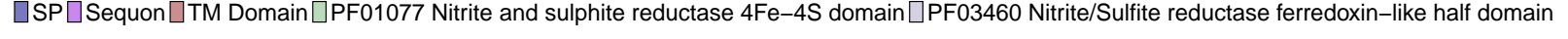


Peptide counts over 4 repeats



Pfam domains

Pfam Description

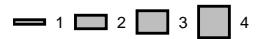


Protein sequence:

IFNIYGGGMGRTHRMETTFPRLAELGIVPKEDLWVAVKAVTGRENGRRDDRRYSRLKYLSSWGEKFRSIVTEQYYGKFKFEPRELPEWFEKFRSLGWHEAGDGSGLFGLHVDNGRKGAMKKALREVIEKYLNVRILTPNGNHLGNIRQAWKRPTITVLGGGLMQRVYDPLNLTAMACPAFLPLCLPLATEAERGIIDILKRVAFERVGLKYSSEVVRITGGPNNGARPYMELGLVGDGPNVQIWLGGTPNGTSLAKTFKDKKVVQDLEKYLELPLFFHWRRM

NbL08g02150.1 glucosidase_2_subunit_beta-like [MW - SP = 65.13 kDa]

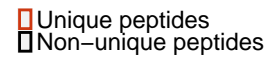
No. of times detected



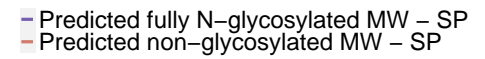
log(intensity)



Values from



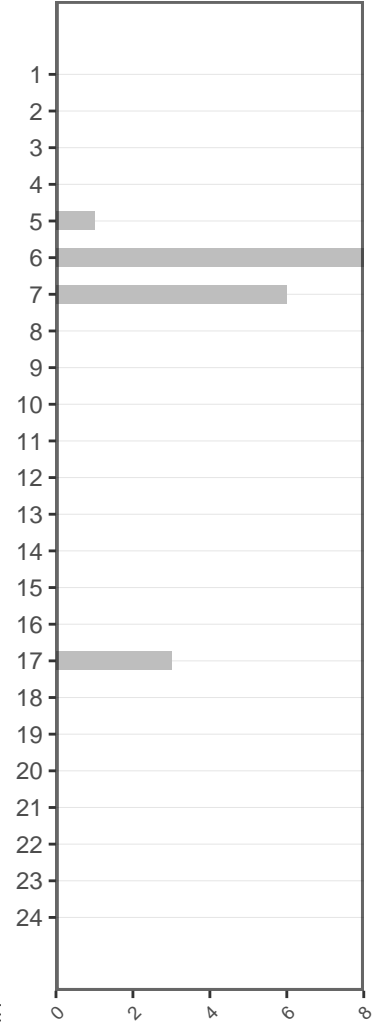
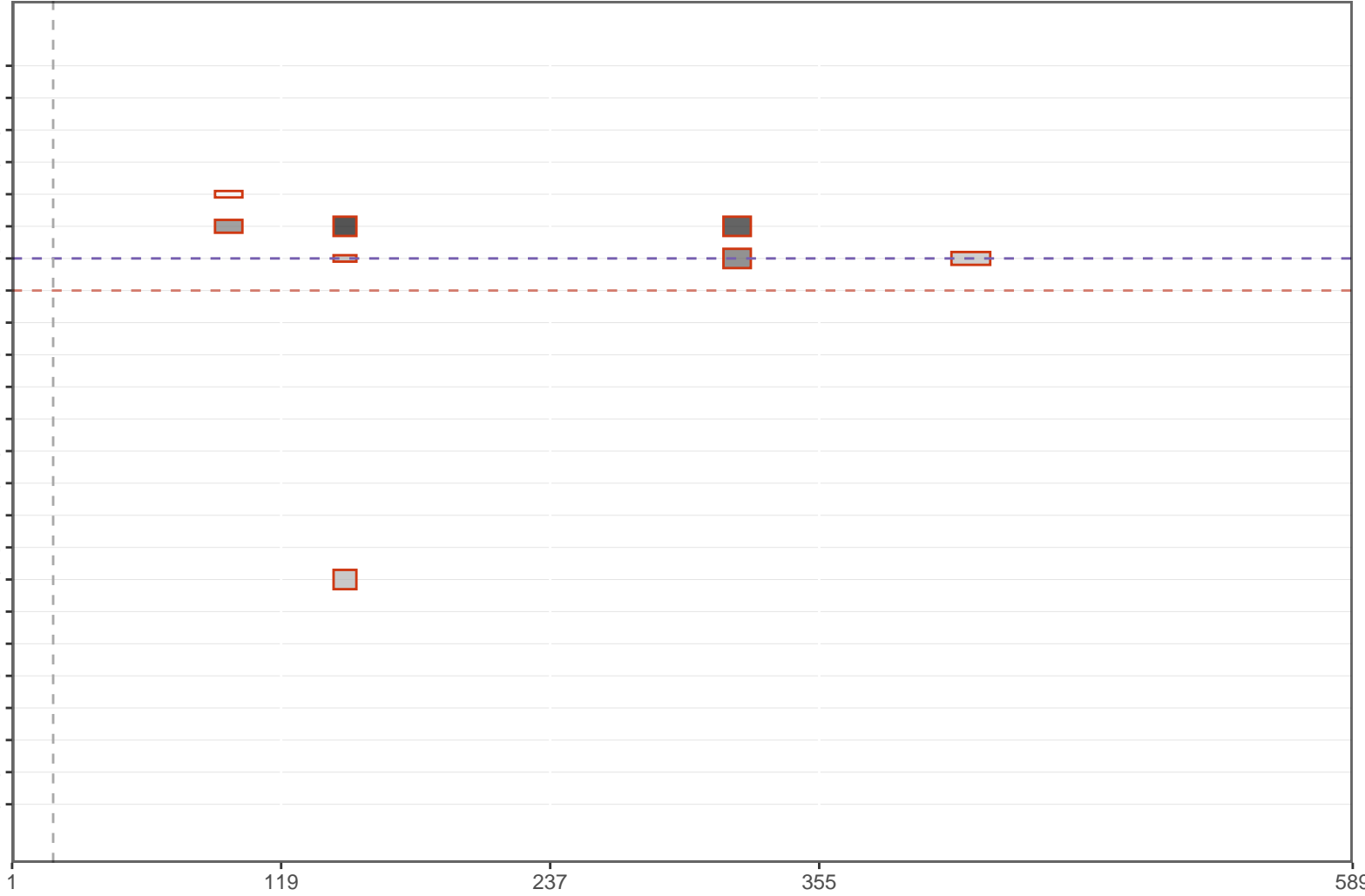
MW indication



Molecular weight



Gel Slice

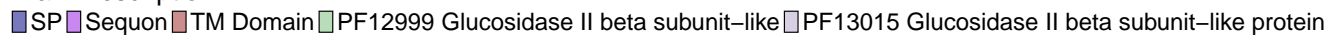


Protein length



Pfam domains

Pfam Description



Protein sequence:

SEKDTTENTESLSKEELGRVIGSRWLQKKBELANEEVDAGTKSNYDSSDEGATDSHEEEYHGYDSEDDHKKYEDDEDEPVEDLGGEDHDSSSSYKAESEDDDDDFSDVMTGNPDMMEKQKRTMKRIFRQVNLFGQTPVNSIDAAHRIKEDLSAKLGLKLRISLSEKLLKGGDFPEKEFYGFYGGGFSKQNKYTYKIGPFKATQVEGYSSTRLGNWDKFDYRALQFSSGDKWNSPDRTLKVKLRGLKLNELTDVDEPSRGEYMAFLSTPALCLEEKLEKLC

NbL08g02070.1 glucan_endo-13-beta-glucosidase_4 [MW - SP = 50.3 kDa]

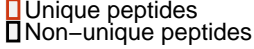
No. of times detected



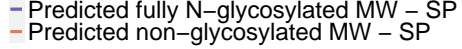
log(intensity)



Values from



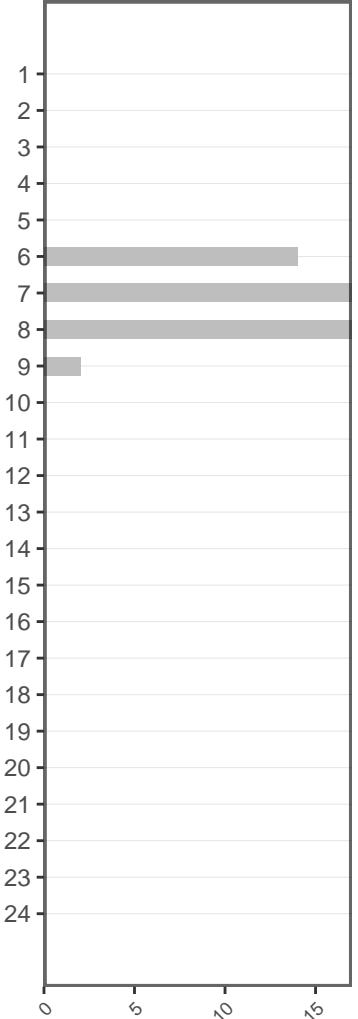
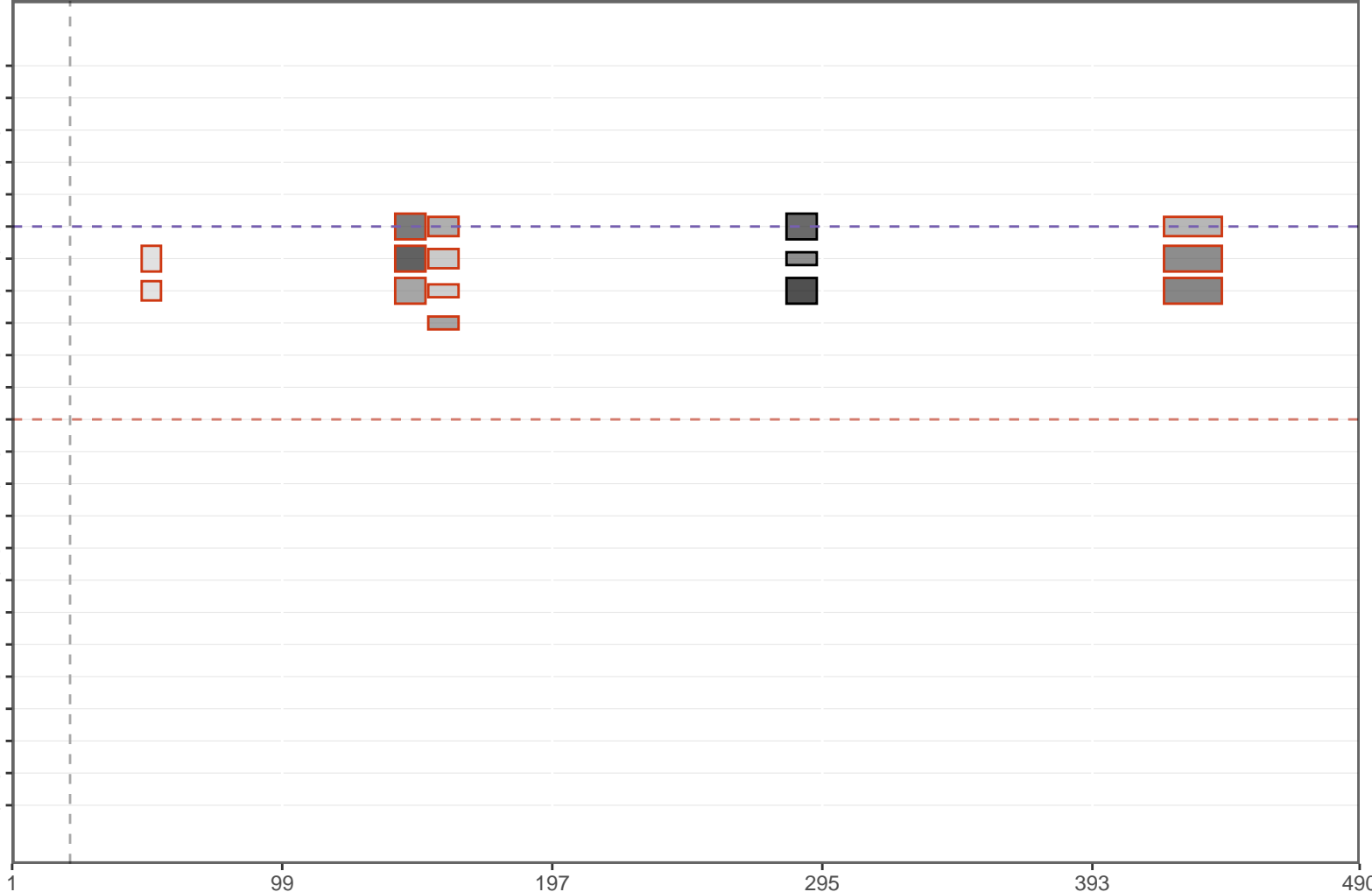
MW indication



Molecular weight

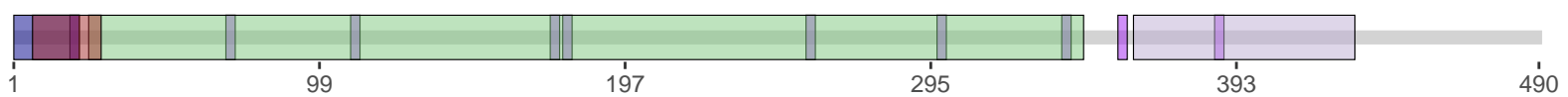


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YVSMFDALVDAYNEAALNFSDPVPVETGTGWPFDGQVNEFPDATKENAETFNHNRVENDTGPSPGPKNPINTFFIYEMFNEDKRPGISERNWQIFSTNGSSEVYSLKLGSSAGISDNSTAVFCIAKKGADENKLDGGINWAGGGHANSAGSAGSGPCYFPDPLQNHASWAYNDHYGRMRSEVGGTCDPFDGATTTTQDPSKTKTKFTGSGSTPGGLFPPAALFQPSPTSGSSTIRASVIVLAWFFCFVDAI

NbL08g01770.1 CDT1-like_protein_a_chloroplastic [MW = 66.1 kDa]

No. of times detected



log(intensity)



Values from



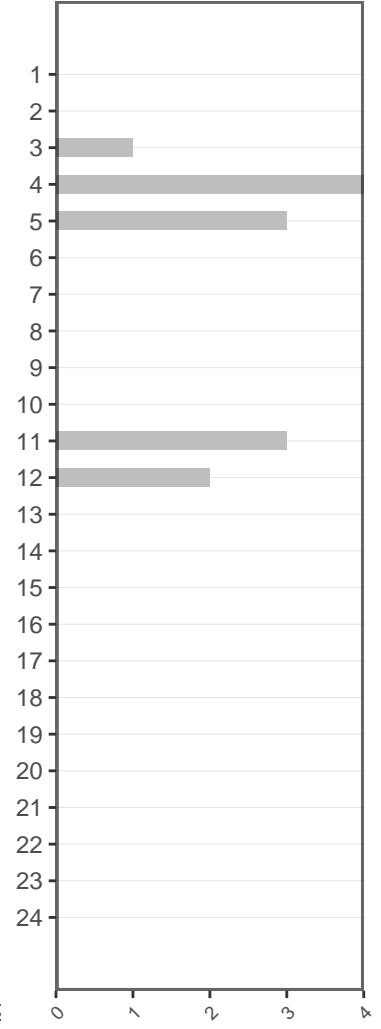
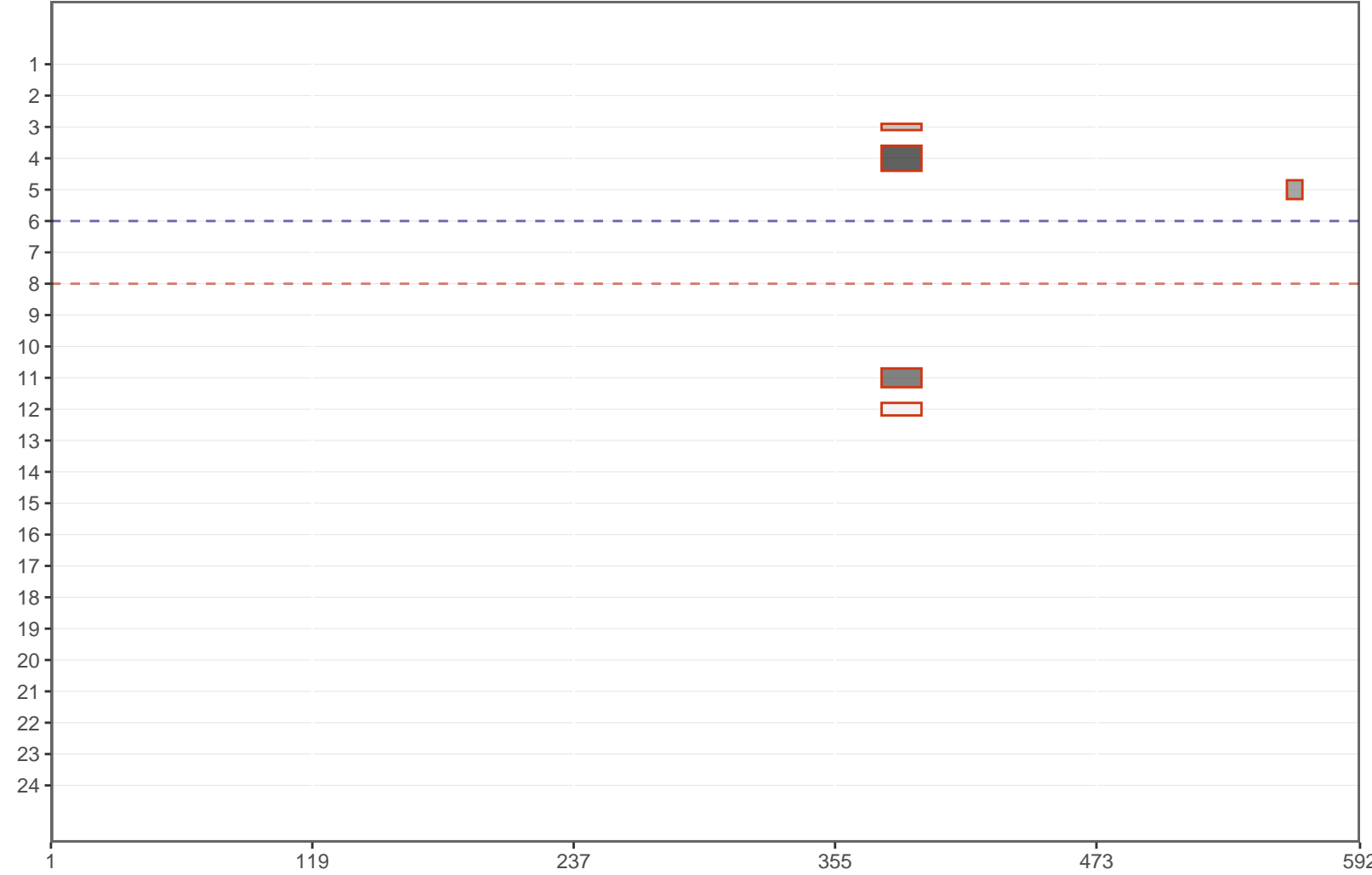
MW indication



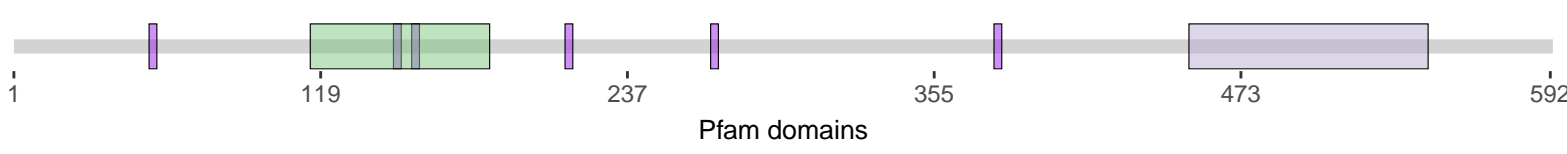
Molecular weight



Gel Slice



Protein length



Pfam Description

- SP
- Sequon
- TM Domain
- PF08839 DNA replication factor CDT1 like
- PF16679 DNA replication factor Cdt1 C-terminal domain

Protein sequence:

LSHLGGFRRCFSKGGASITGGNAEEDRAGLVFVSPVDFVLEVESGKTKKPVAGADAPMLGSGKGTMMKYSSGGVVSASLGGHPAPPMSSEAKKGENDSMSAPATMPLLEPPKRCYMSPPDNPMSPELAKLHPSTRRSLGDFDTPVGNANAADGVGENERFSTNDFDLPENLLKSGIKESKELEEQQDPAISGAKRRKGMIAGLPRLFDMYVLFQGRIRRVMTKEELMRRLISGKTELDADKREVEEQULLGKLAPEWYIEKPTSSAILLGVNKNISNPDRSRRLAEAKLEKGE

NbL08g01650.1 formate--tetrahydrofolate_ligase [MW = 67.33 kDa]

No. of times detected



log(intensity)



Values from



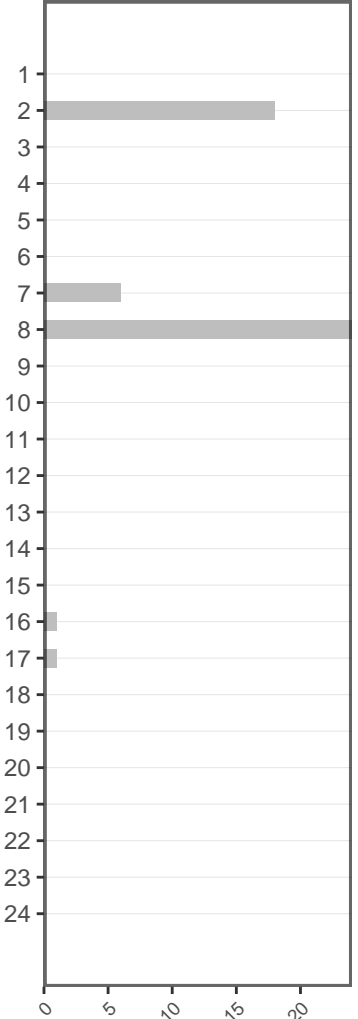
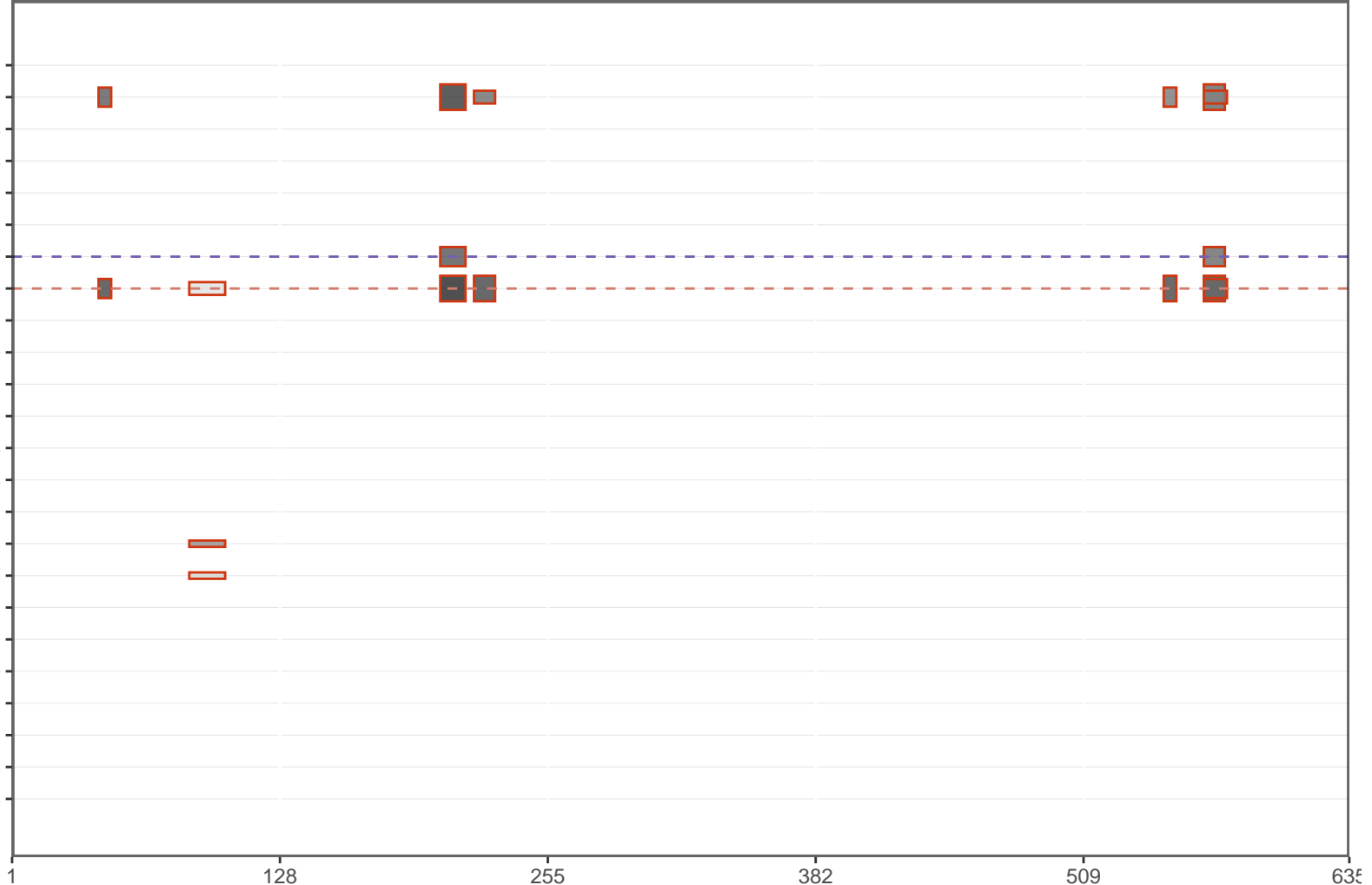
MW indication



Molecular weight

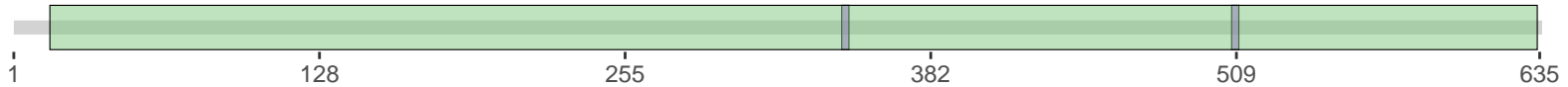


Gel Slice



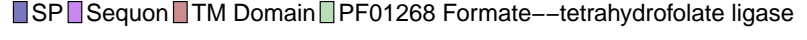
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DLGVGGALTYLLKIDANFRLMOTLEGTPVAVHAGFPANIAHGNSIVADKIALKLVPGGPFVYTEAGFGSDGTEKFMNKRYSGLKPQCAVIVTRALKMKHGGGPDVTAGRPLDRAVVTENVALVEAGVNLARHNSNTKAYGANVVAWVAFATDEAELNKKVWAFAGAFDAWIGTHAAHGKGAVDLGIAMGKAGENATQPLRFLRFLPLDGIKDKIAIAKKGKADGVEYSEGAENKDIEMVSKGGFSLNLPKMAKTGYFSFHEAAKKGAPSGFILPRDVRGSGIGAGFYI

NbL08g01610.1 peroxidase_N-like [MW = 18.03 kDa]

No. of times detected



log(intensity)



Values from



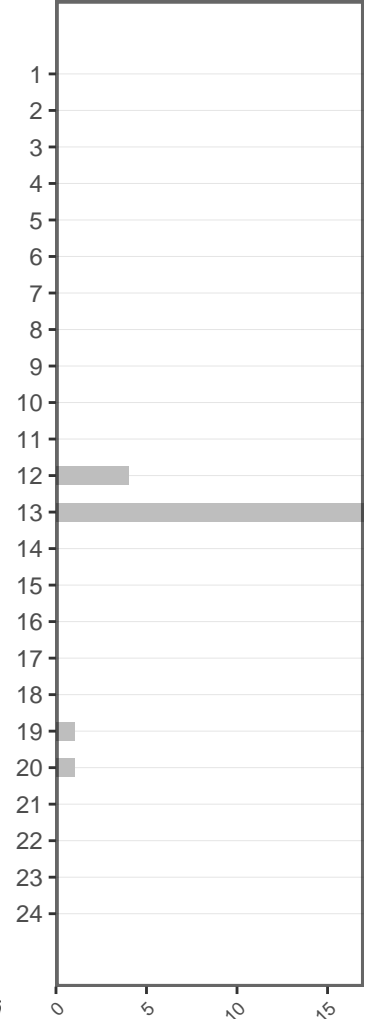
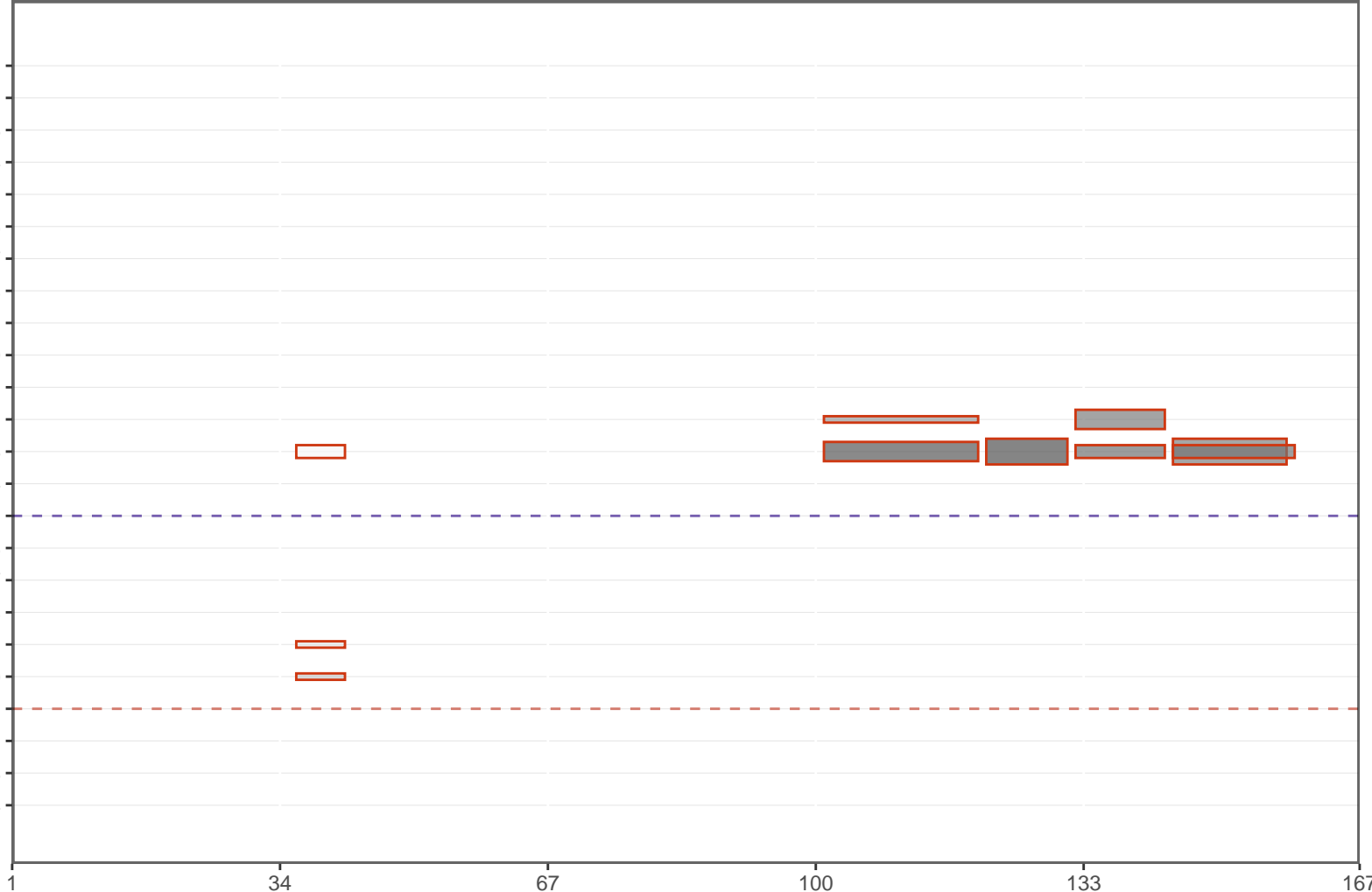
MW indication



Molecular weight

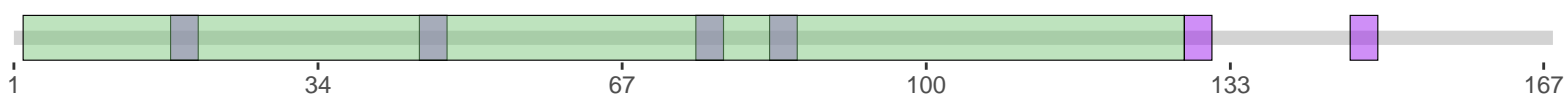


Gel Slice



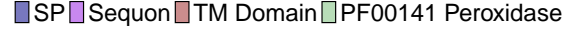
Peptide counts over 4 repeats

Protein length



Pfam domains

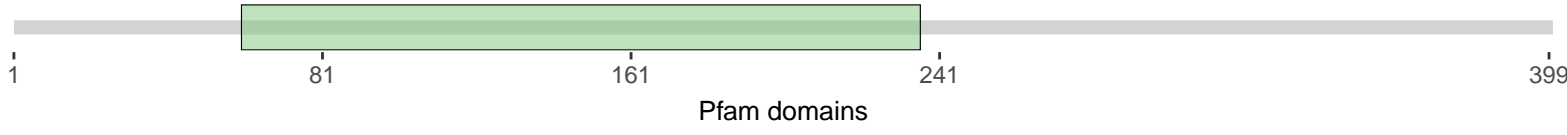
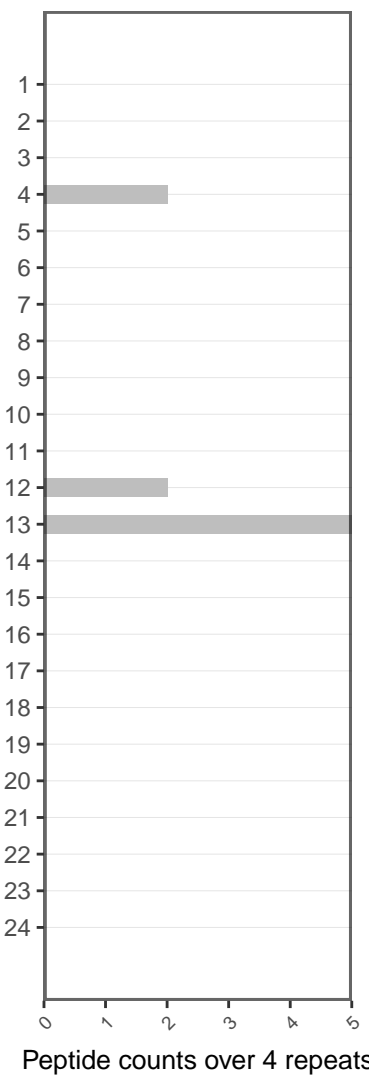
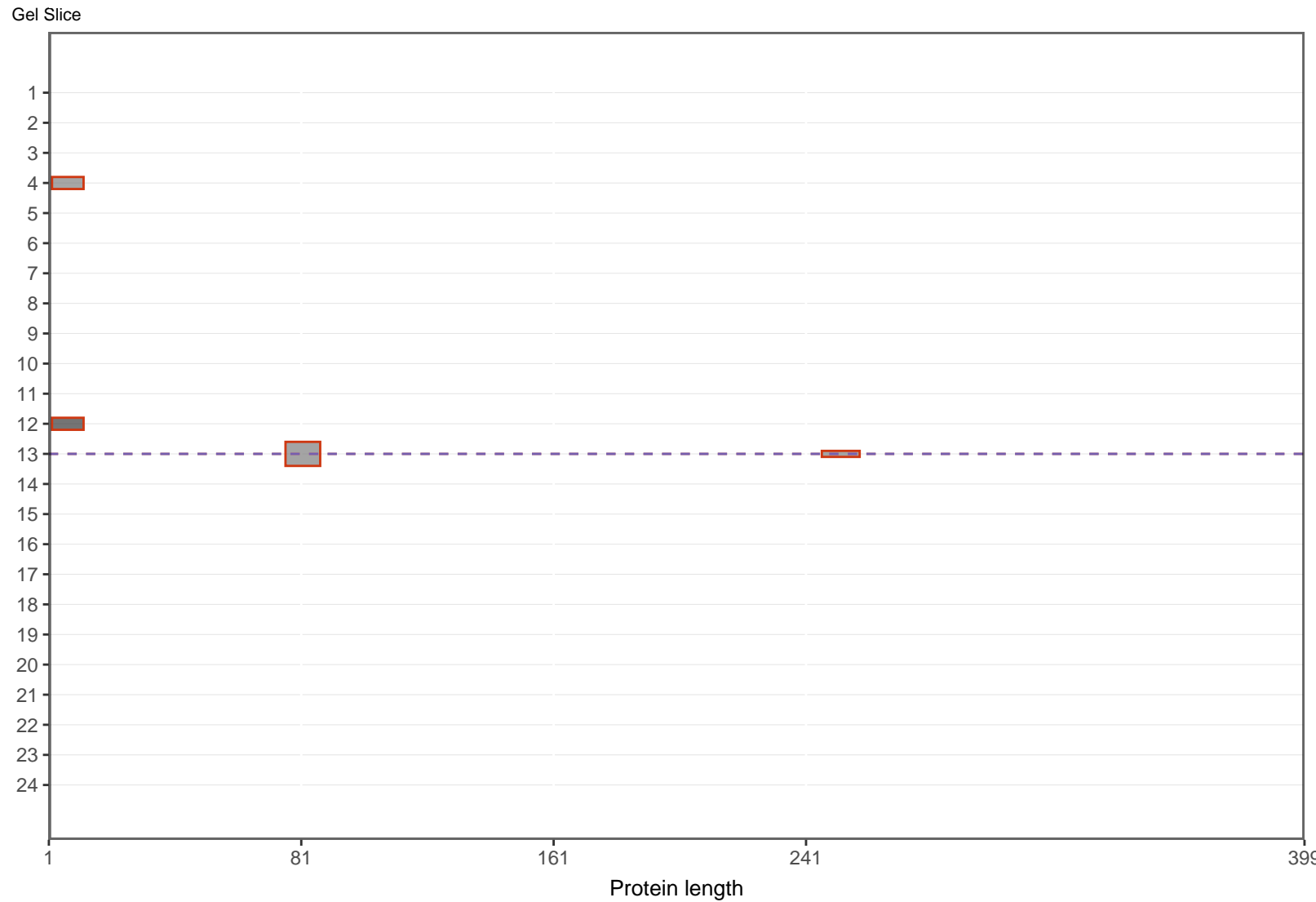
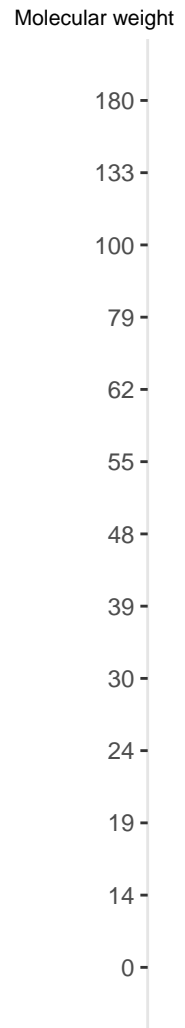
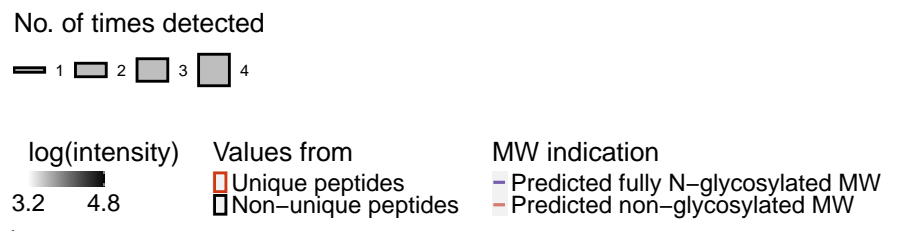
Pfam Description



Protein sequence:

ISDGNITAPLDRNSTDFDINHFRNLNGLLEGGDLVLFSSDDAVGTTKLVETYSNSKFFDFVNSMKMGNSPLVGGDGEIRKNGRVVNS

NbL08g01590.1 probable_plastid-lipid-associated_protein_12_chloroplastic [MW = 44.66 kDa]



Protein sequence:
 SFKFLPVCVPPYPVFRLLGDEAKGWLDTFLSPSGNLRIRGNKGTTFVLQKEADPRQKLLSSISGTGTSVEKAIDEFISLNGNVAANPELEFEGEWQMIWSSGQVETDSVVENAGNGLMGMDQYKPNQGLKFLVEFFGIRFMTGQYKESGNTYDVMDDGAFVADYGIPIVEMSKFTIELYTDKKRIRSRGYNKILFVHVRDDGSKKK

NbL08g01470.1 enoyl-[acyl-carrier-protein]_reductase_[NADH]_chloroplastic-like [MW = 41.8 kDa]

No. of times detected



log(intensity)



Values from



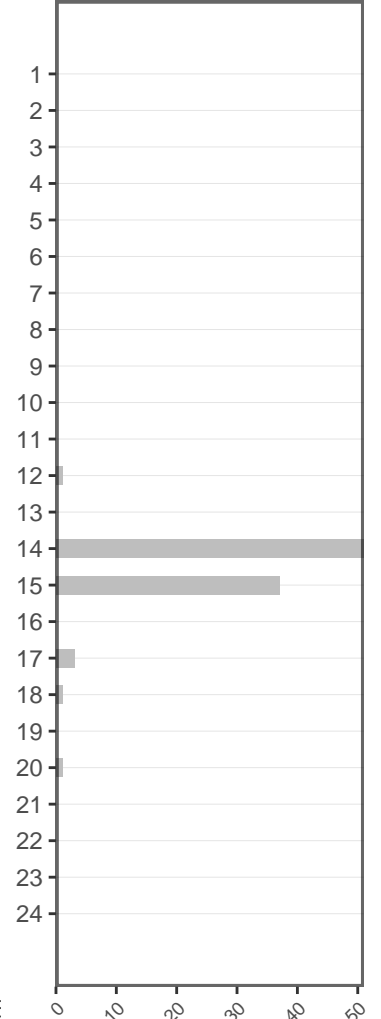
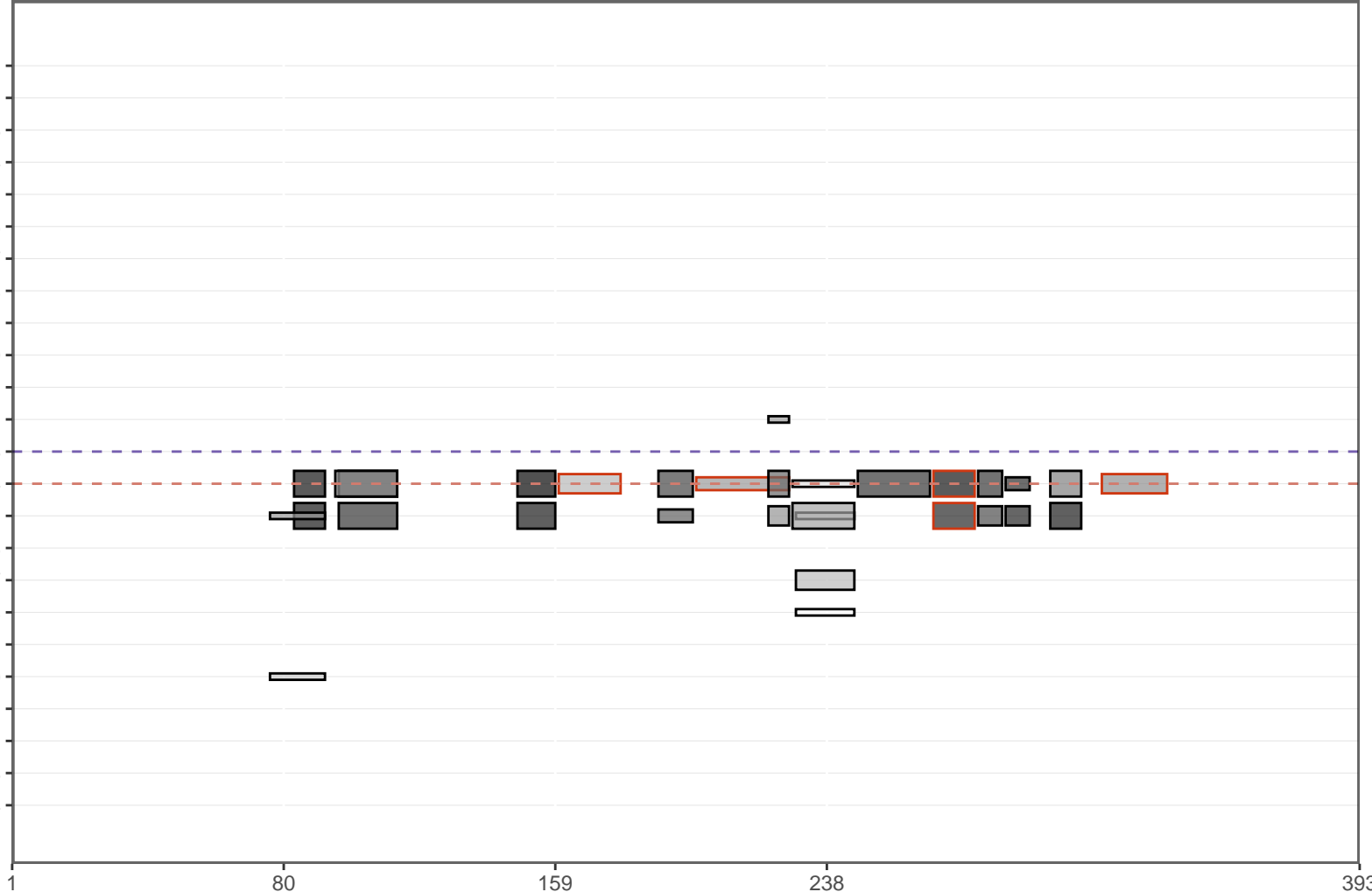
MW indication



Molecular weight

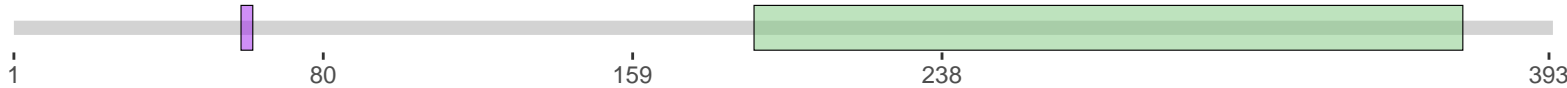


Gel Slice



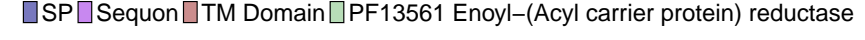
Protein length

Peptide counts over 4 repeats



Pfam domains

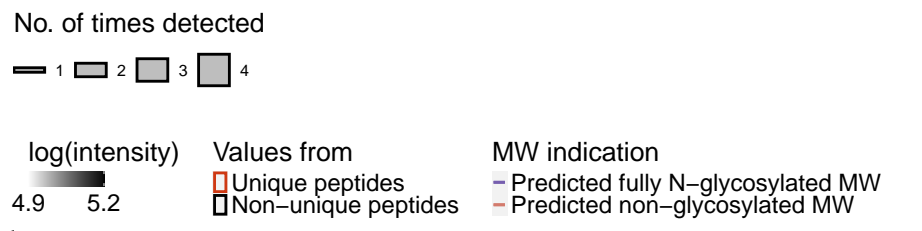
Pfam Description



Protein sequence:

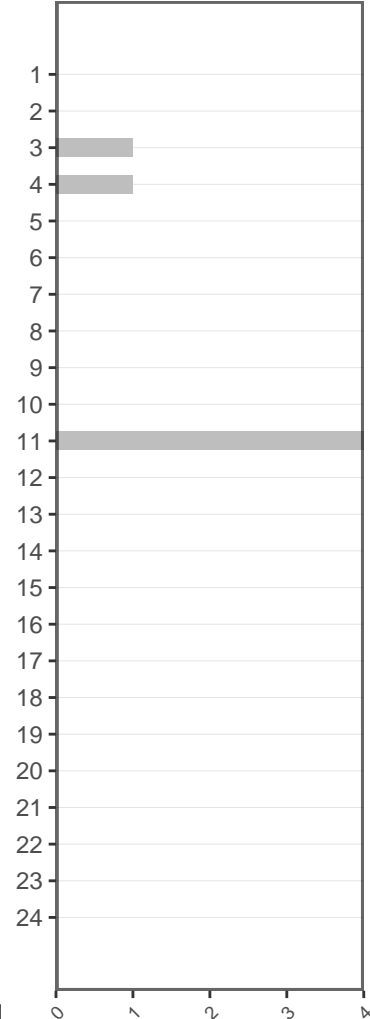
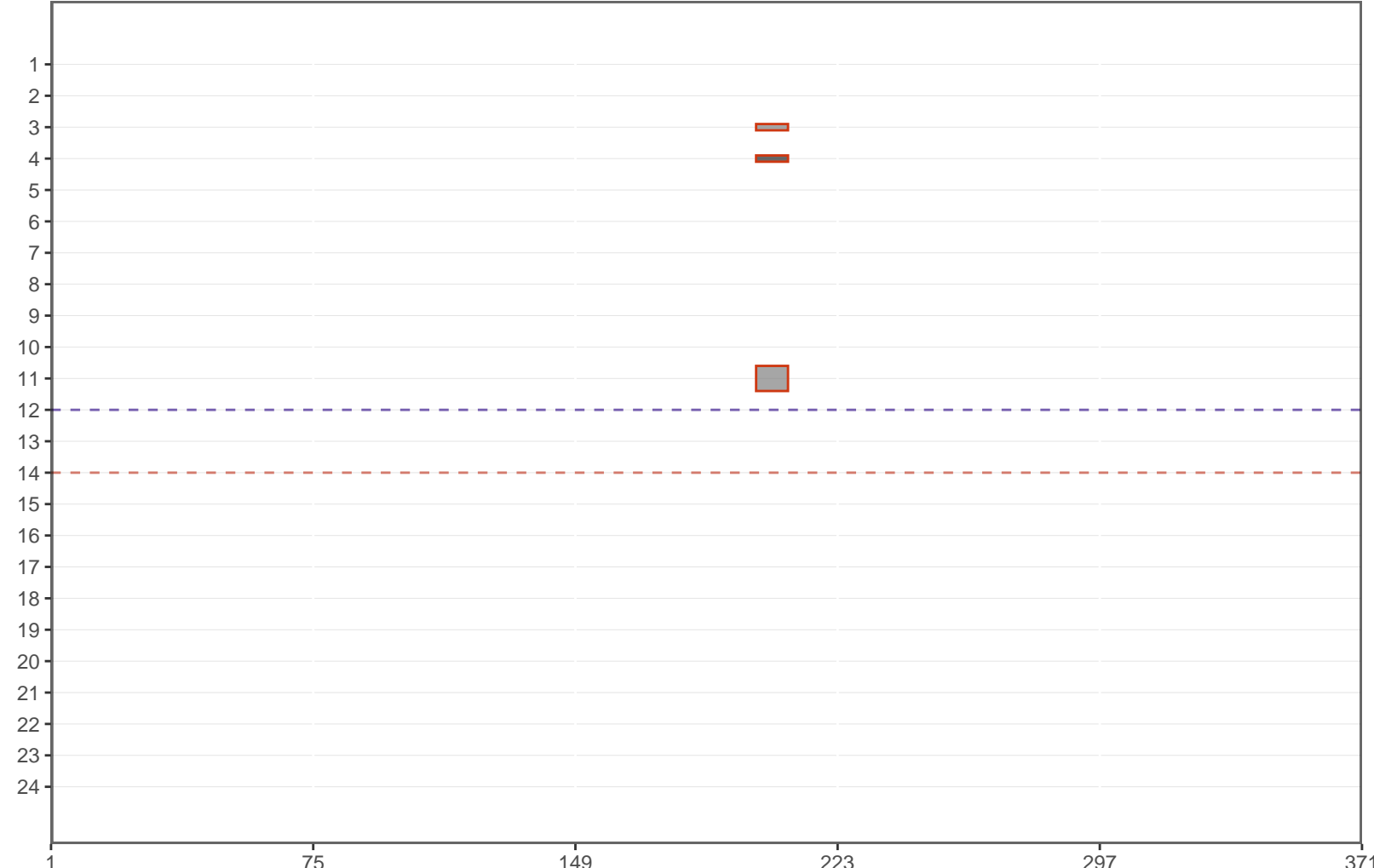
YAGSSKVTYSEVASEVKEDEFGVDLHLSLNGPEVTRKPLLETFRKGYLAANAS6SY6YV6LLKHFLPIMNPGG6SISLTYASERVIPG6G6M6S6A6LES6DR6L6FA6E6AG6R6KK6V6R6NT6IS6AG6PL6R6R6A6A6IG6R6D6M6D6Y6I6AN6AP6L6K6E6L6S6A6D6E6G6N6T6A6F6L6A6S6I6A6T6G6V6Y6V6N6G6L6N6M6G6V6D6S6F6K6E6L6N6I6K6A6E6

NbL08g01460.1 non-structural_maintenance_of_chromosomes_element_4_homolog_A-like [MW = 41.72 kDa]



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:

RRRTKYHSRACPNELEVNTEEKTDFTDKNIGTMFGILRKKRKRKLESLMNRKSFQSGIENLFTLFLVKGDRVFDVDEGGSHFVSPRNGPSAAAVKSGEVKYSHFVCRDLDFADWELMKNVPEGEELMPNRDILMNPGRITAEFVPTDGRPLNVTWVKKFSRNRGKVLKASEVDDSPREGDANINGSLKRRLL

NbL08g01420.1 UPF0061_protein_azo1574-like [MW = 70.97 kDa]

No. of times detected



log(intensity)



Values from



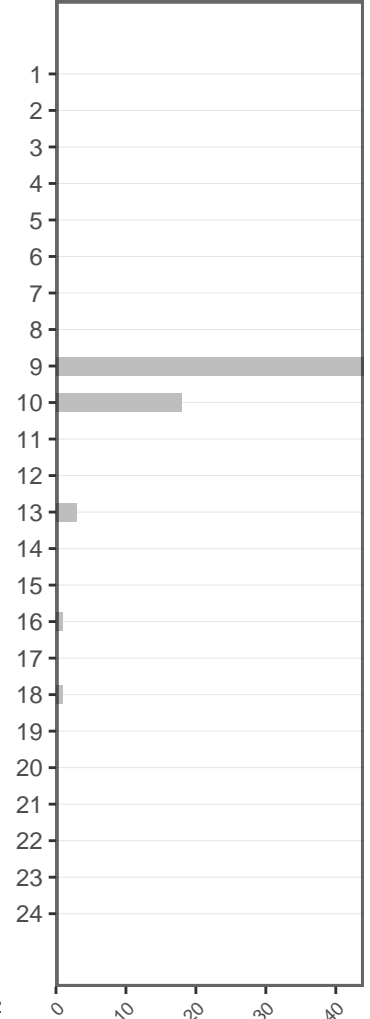
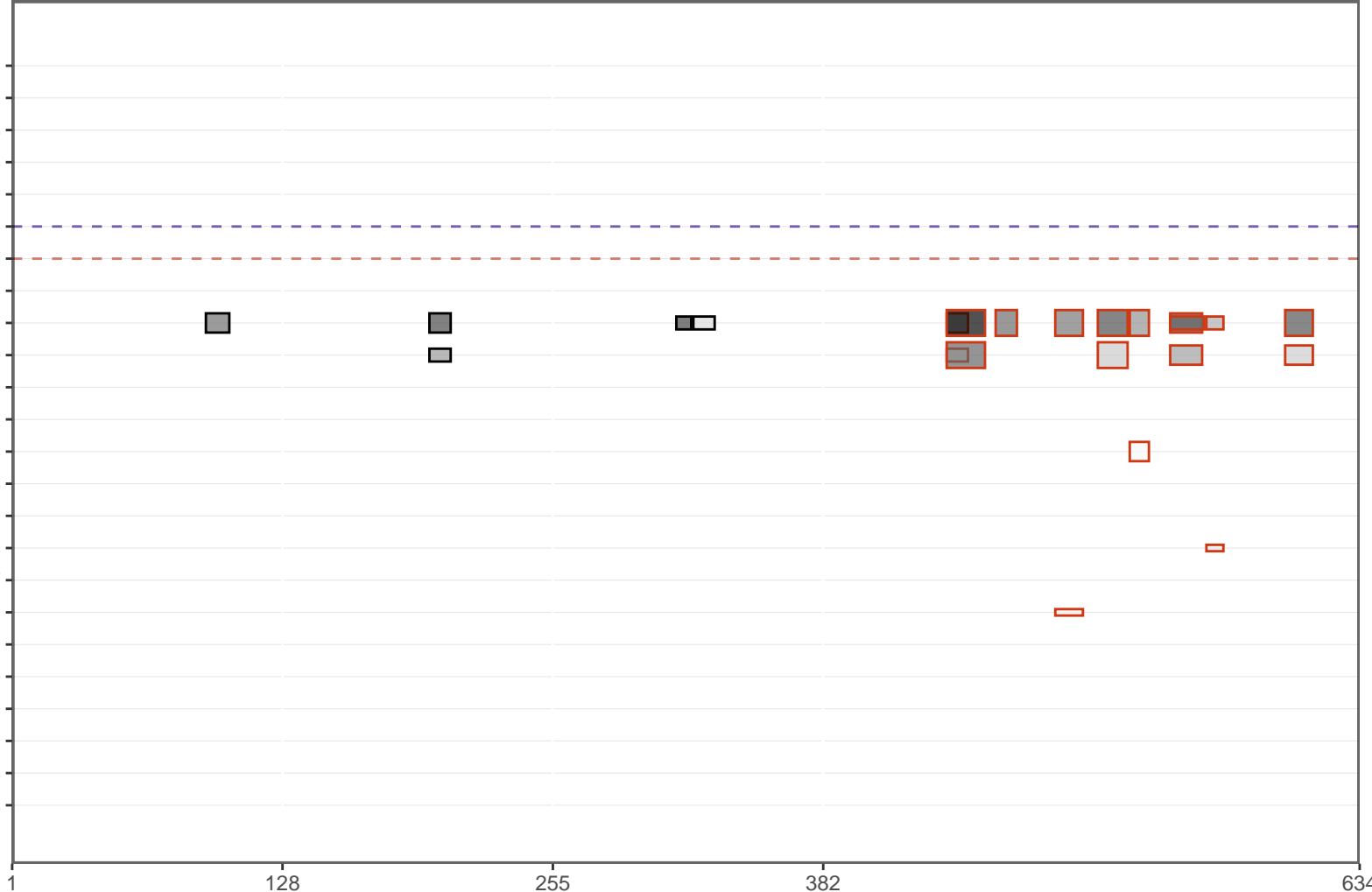
MW indication



Molecular weight



Gel Slice



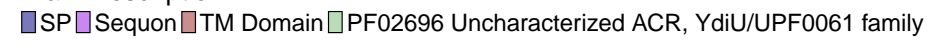
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

GKDLIEVRLTADYARHFFHLENMSKESISFSTGEEEDDSAVDLTSNKYAAWAVEAERTASMIARWQGVGFTHGVMTNDNMVGLLSTBYGPFGLDADFDPSTFNTTFLPGRRYVGFANGPDPGLVNWAGFAKTLSTAGLLNDKESYAMERYGKFMDDVEAMTRKGLAKYKQMGDLKNMVAQKVDVYTNFRLLSNVAKDLTPADQLLPLKAAALLDGMERKEAWTSWVKEVIGELSTSGVSDERKASMINVNPYVLRNKLGGGAIDTEGGDFGEVRL

NbL08g01380.1 G-type_lectin_S-receptor-like_serine/threonine-protein_kinase_RLK1 [MW - SP = 88.54 kDa]

No. of times detected



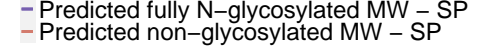
log(intensity)



Values from



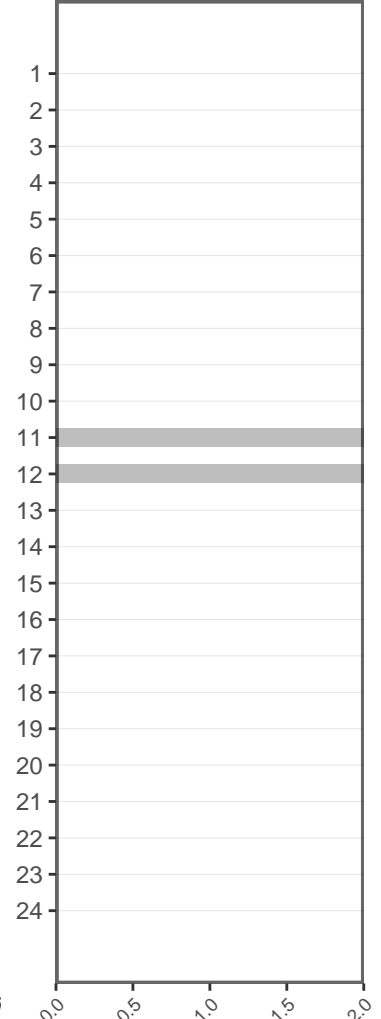
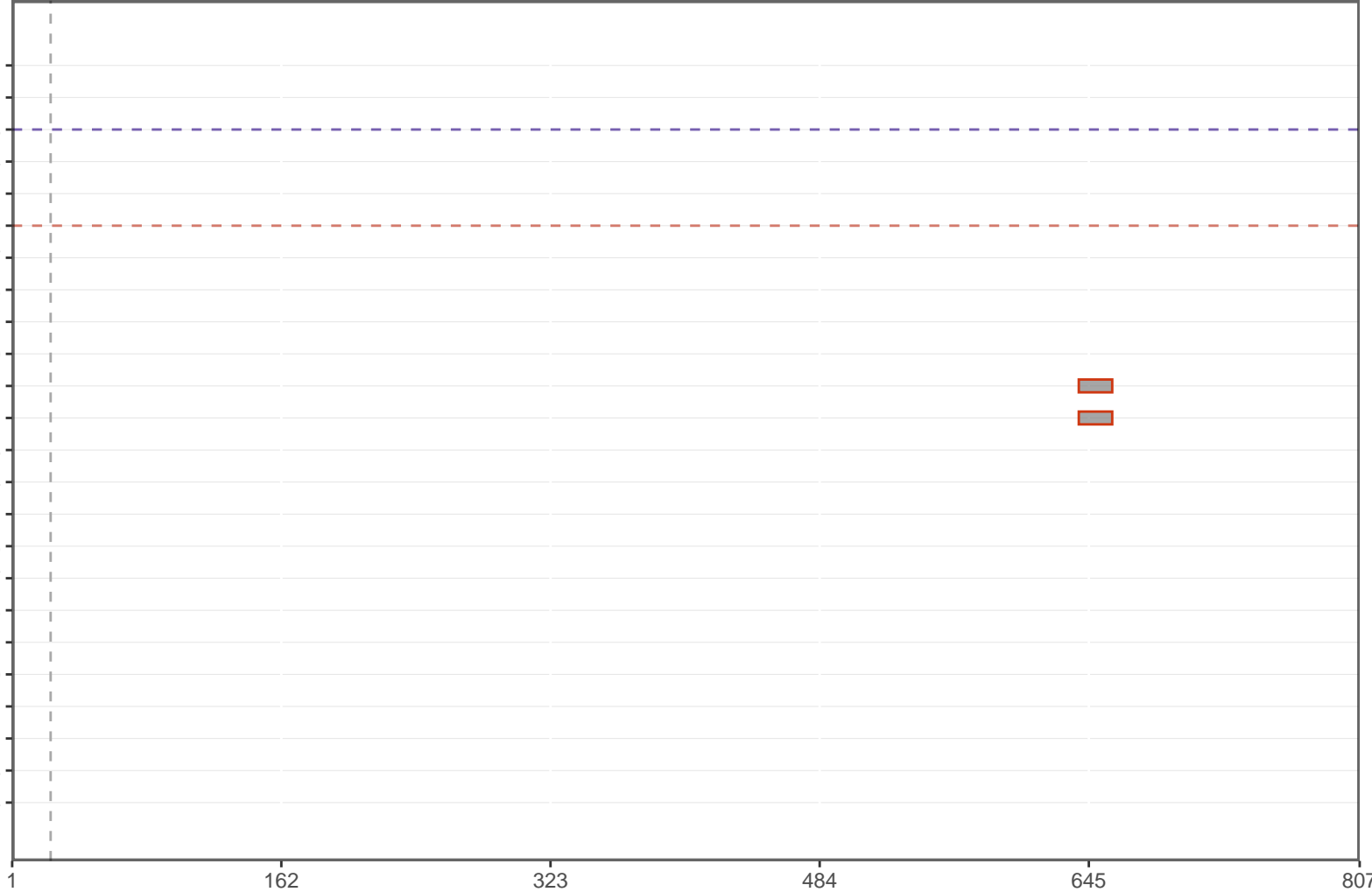
MW indication



Molecular weight



Gel Slice



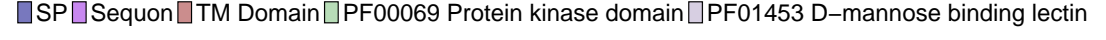
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

CLNDCMCAVSYFRENBSGKKKPLSNGRVDNRVNSKVFIKRKNKGNIAVEDPNSREFPKKNGDTRILHSVFLGSSVFVNGLLLVGLSLGFLVYRNKNSTFDRBKSMSMDQTLRFVSVGELSKATEGFKELNLRGAFGVYKGVGIEGKPIPAVAKKLDNRVDDGEEEFKTEVWVIGDTHIKNLRLLGFDGEGPHRLLVYEFLLNGTLASFLFGDLKLTWNRQTOVALGIARGLLYHDEGSTQIHGDKPKGNILLDNGYDPRIEDFGLANLRMDQGETQAIRGTGKYVAPEWFI

NbL08g01370.1 sorbitol_dehydrogenase [MW = 38.56 kDa]

No. of times detected



log(intensity)



Values from



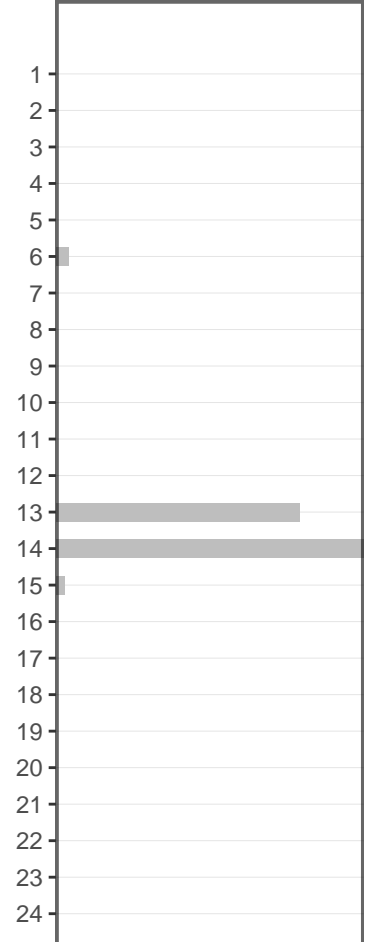
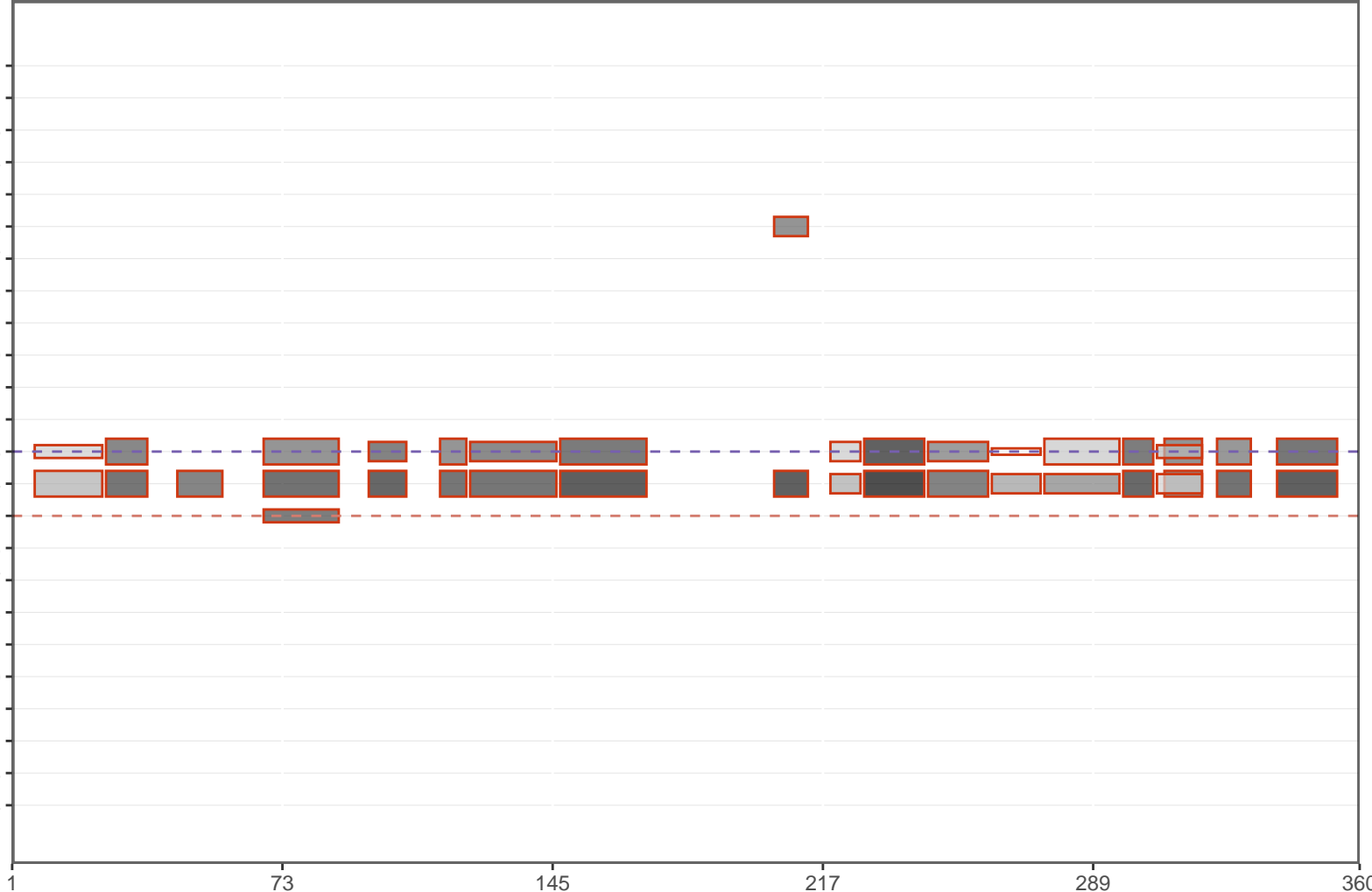
MW indication



Molecular weight



Gel Slice



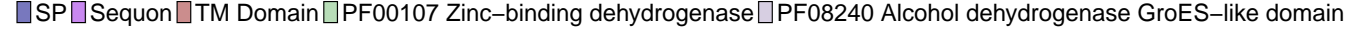
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

GVYHACRRANVGPETNIVLGGAPGLVTLAARAFGAPRIVVDVDRVLSWAKLGADETVKYSTNIDNADENIQKAMGAGIVSFDCAQFNKMTALGATCPQGGKVLGVMGSHHEMTVFLTPAAAREVDVIGIFRYKNTWPLGLEFLRSGKIDVKPLTIRFGFSGKEVEEAFETSAGGGDAKVMFNL

NbL08g01350.1 linoleate_13S-lipoxygenase_2-1_chloroplastic-like [MW = 102.16 kDa]

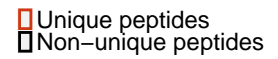
No. of times detected



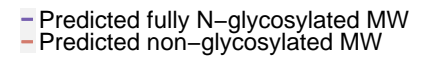
log(intensity)



Values from



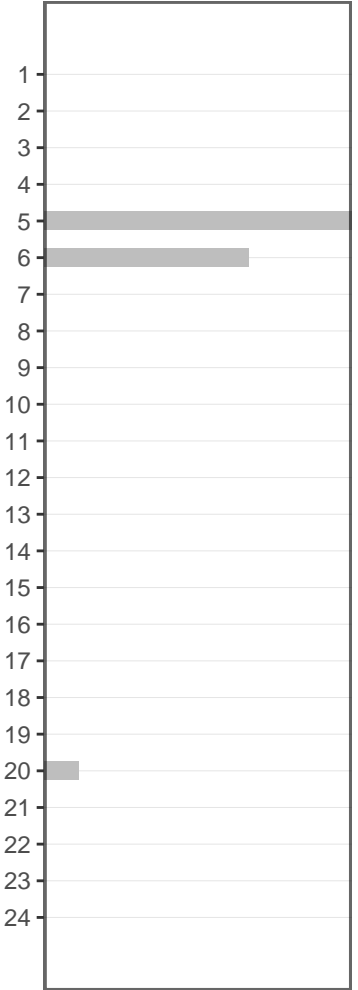
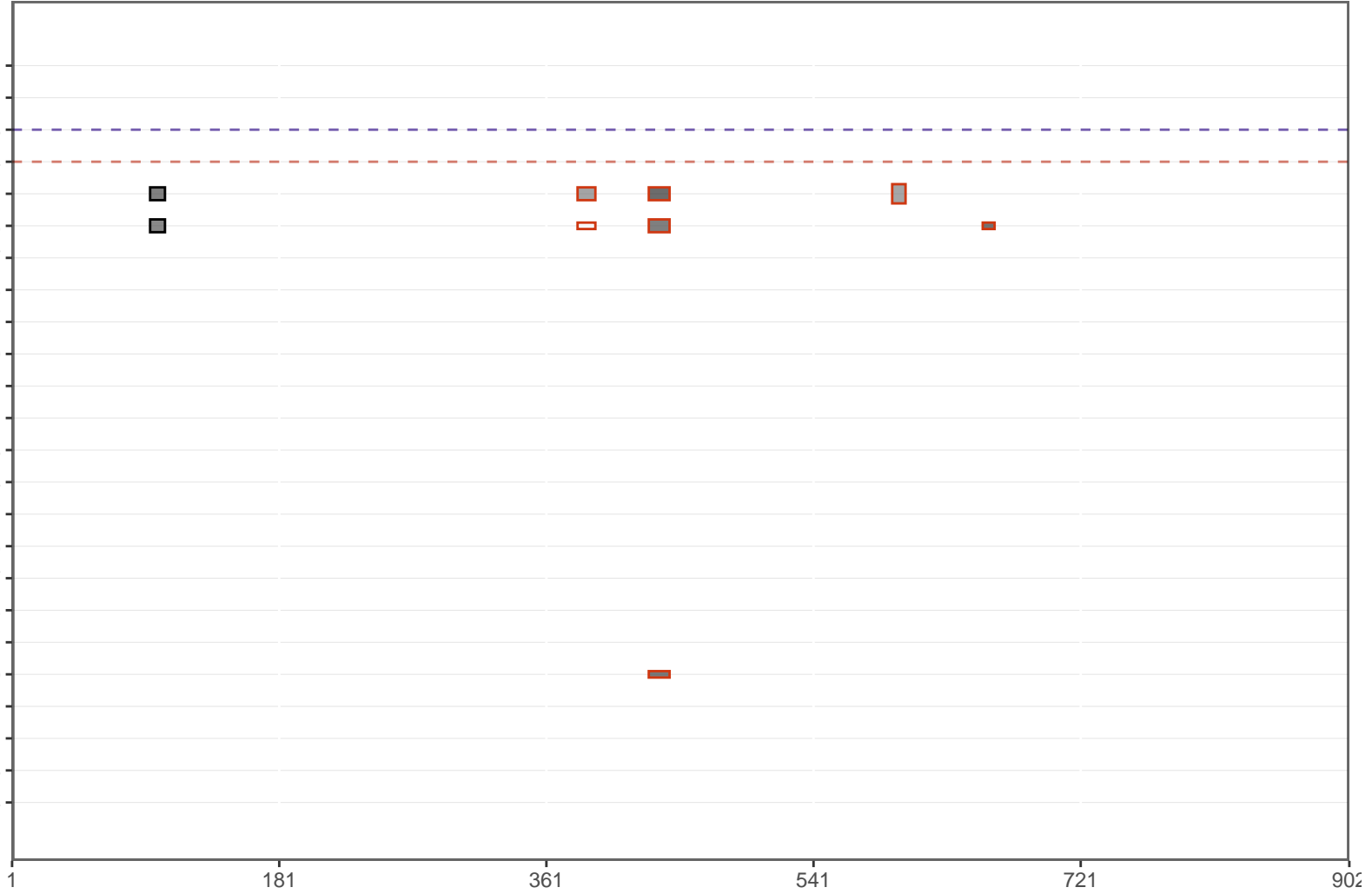
MW indication



Molecular weight

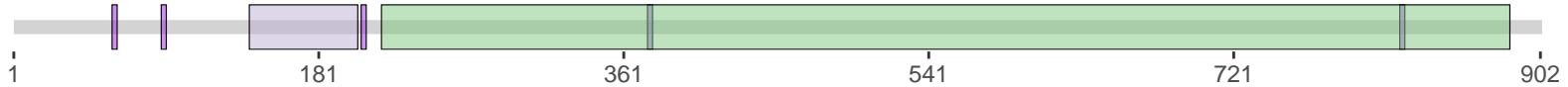


Gel Slice



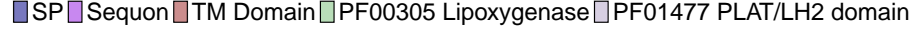
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SAITKELIELEIAGFMTVEEAVKQKLFIDYHDLILPYANKVNLKGRVLYGSRLLFFLTPDGLRPLAEIETRPPIYDKPQWKEVYQPTWHATGSLWIKLAKAHVLAGDGGYHGLVSHWLRTHCATEPYIATNRQLSAMHPYRLLPHFRYTMENSLARDALINANGIENSSFFPKYKSMELSSWAYDLEWRFDRQALPEDUSRGMMAKGDNAPYGLKITEQVFFANDGLMWDIKQWYTDYVNHVYETELEIEFDTELQAWWSEIKNVGHGDKKQAPWVPELXTPDD

NbL08g01330.1 uncharacterized_LOC107827241 [MW = 39.62 kDa]

No. of times detected



log(intensity)



Values from

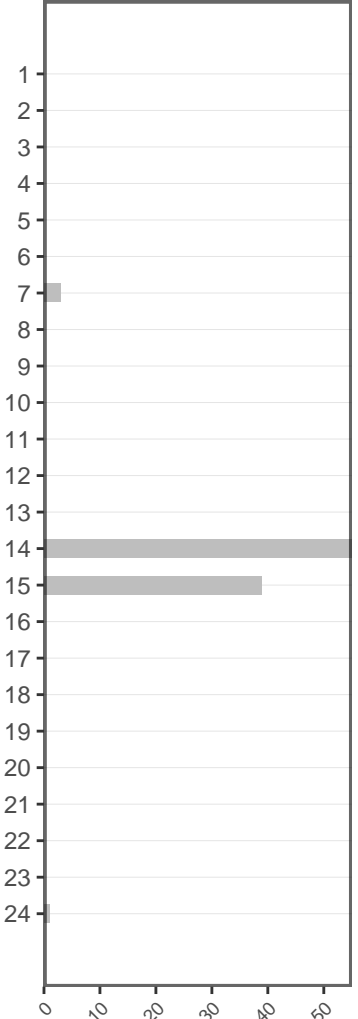
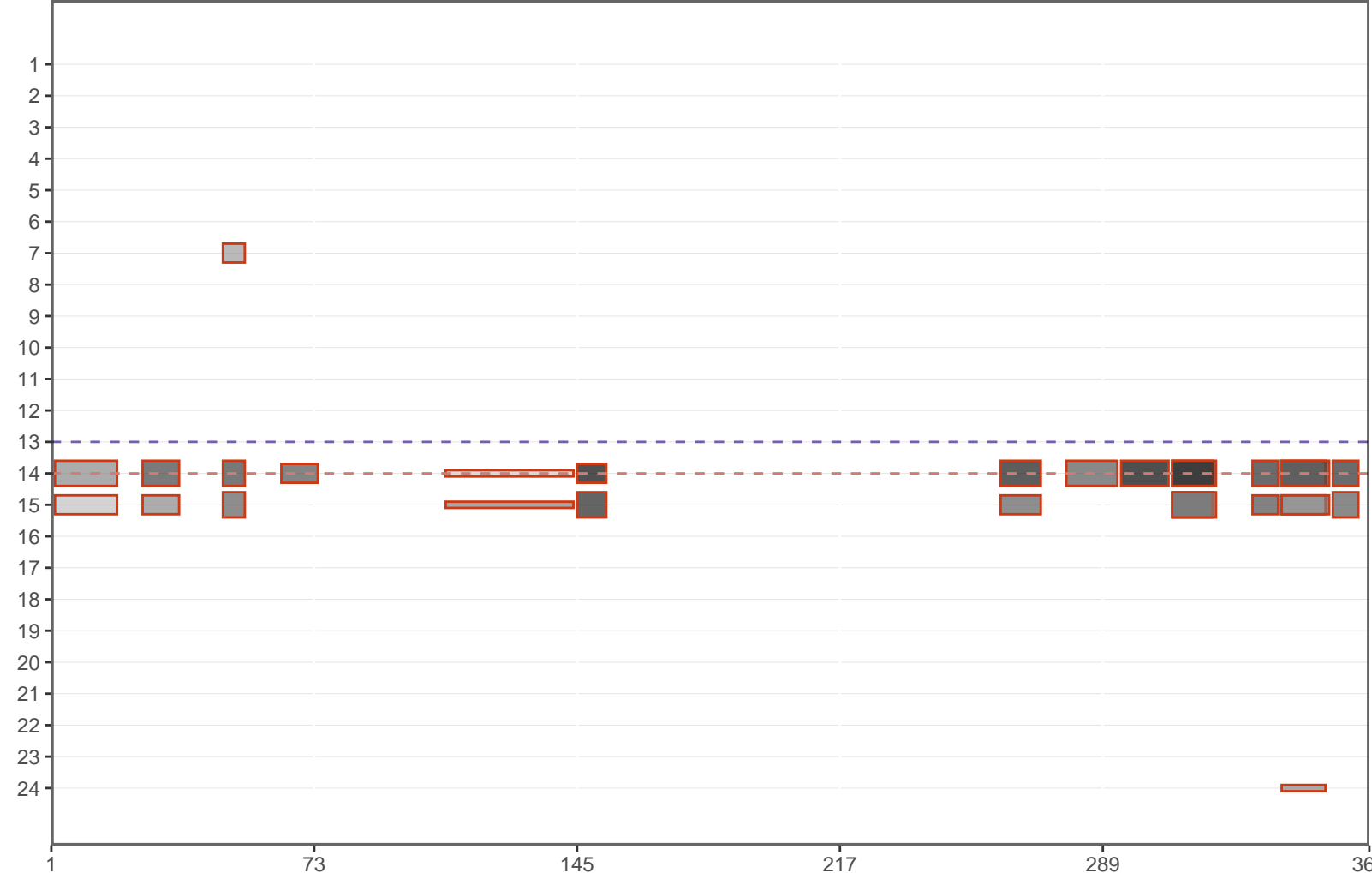
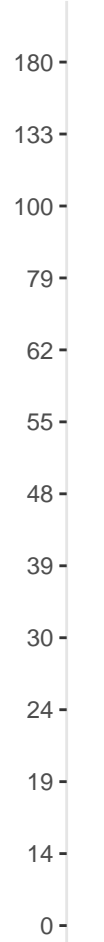


MW indication



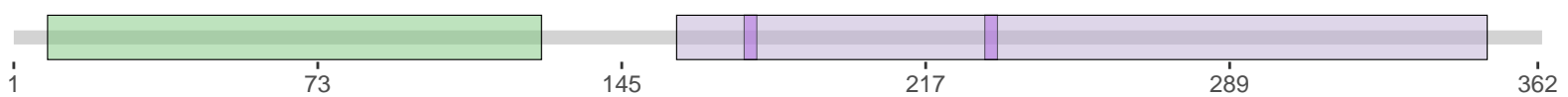
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



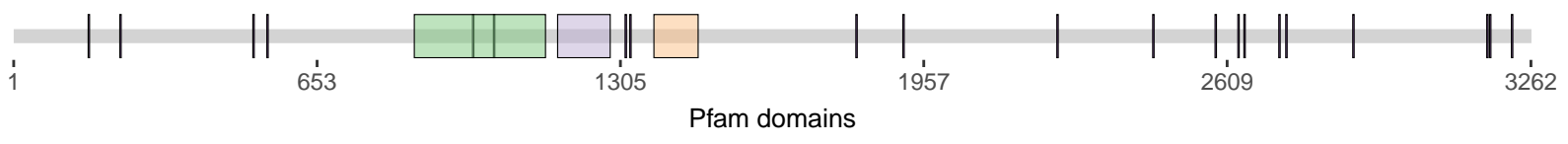
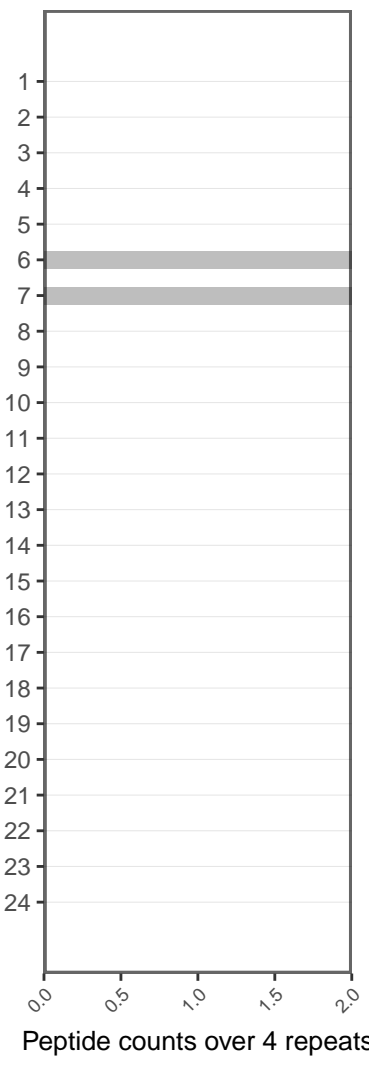
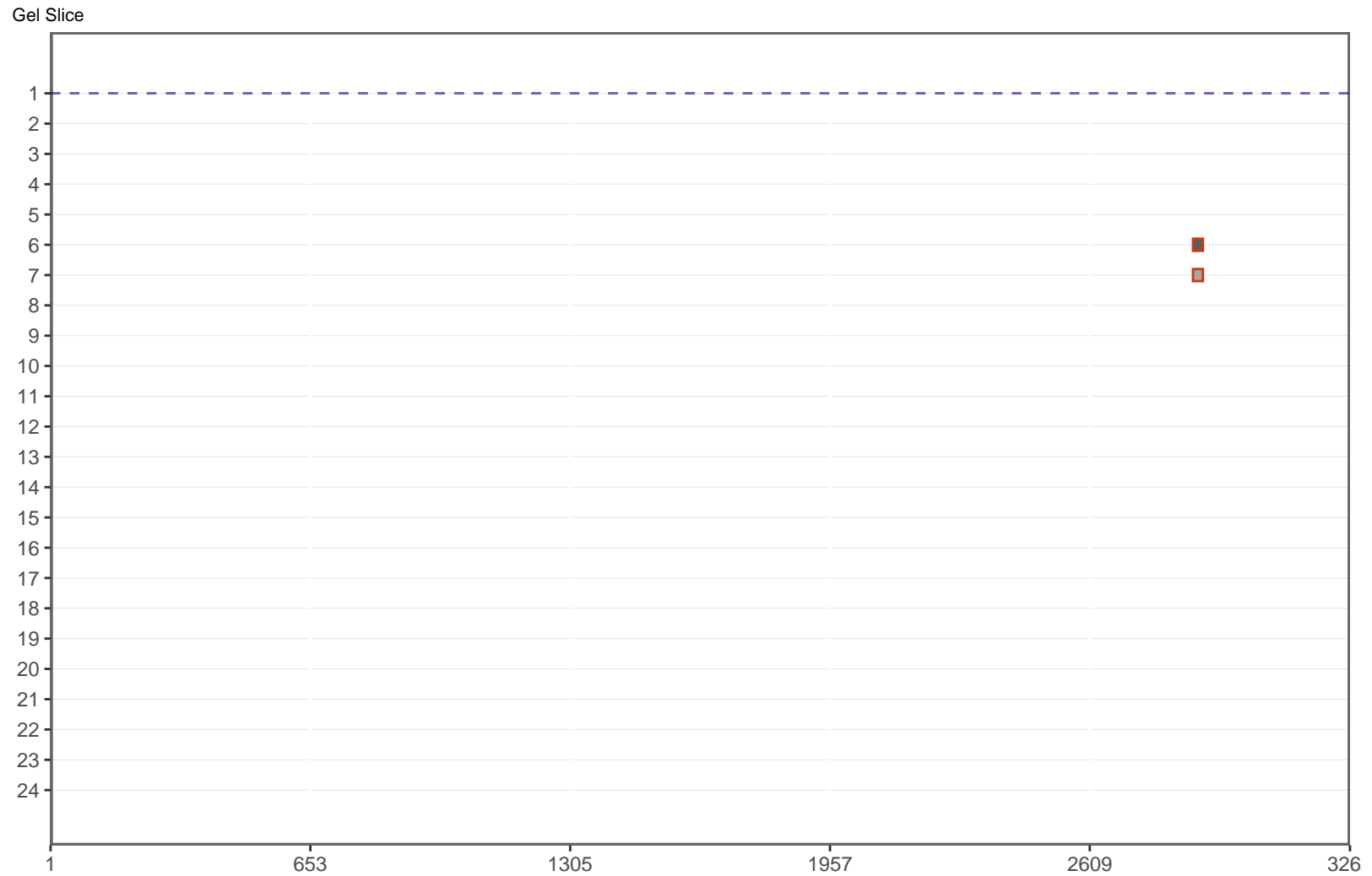
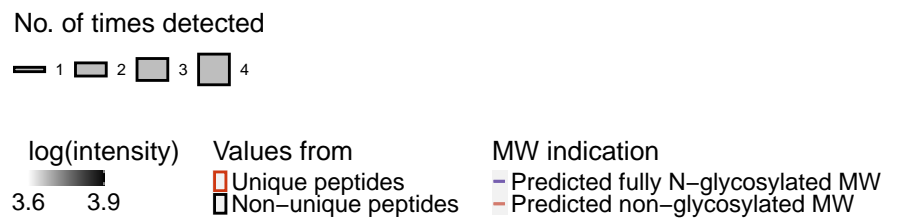
Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF01408 Oxidoreductase family, NAD-binding Rossmann fold
- PF02894 Oxidoreductase family, C-terminal alpha/beta domain

Protein sequence:

MSNNSNPFYSSSVRRGFGGFLDMGHEVAGLRMLVGGELIASMNSHVDKTLFPPDNISGMFQLENGCGGVFVMVSSKGPKIWRVVLGNGLVGERGNKDKHGYSIHLMADGGKFFYPFSGVDELKTLFSDVSTANLKKDHSIDPRLSFAEGARDVAVLDMLESGKRGGALVQVKPF



Protein sequence:
/ESTSPTLQSATAVAPCHGQVVPQVAVLSDPPPTTGGGRGRGRGRGRGRGRVVEGEAPGRGRGRGVVTEALLPPPTQAISEPVSAAGVNVVLS66SHMPPTTPGPKDLVPLVAVGLGKDLGHAPAMRDANKELNIVSGMPLASFFTKQKIVGVSTVVPVPS6666QDPSSISPAVH6666KLVH6666HDFSAQTEAIPQADAVSVVPHTSPSADTEPS6ATPGPLLLTFSKDG6GILPMPVPA666AGMELTVGCPVPA666G66AGPSSAPVPLLA

NbL08g00760.1 OTU_domain-containing_protein_6B-like [MW = 35.42 kDa]

No. of times detected



log(intensity)



Values from



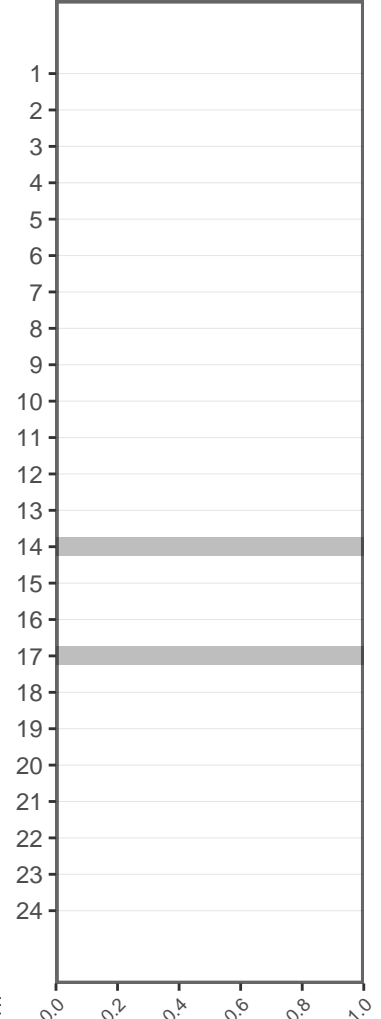
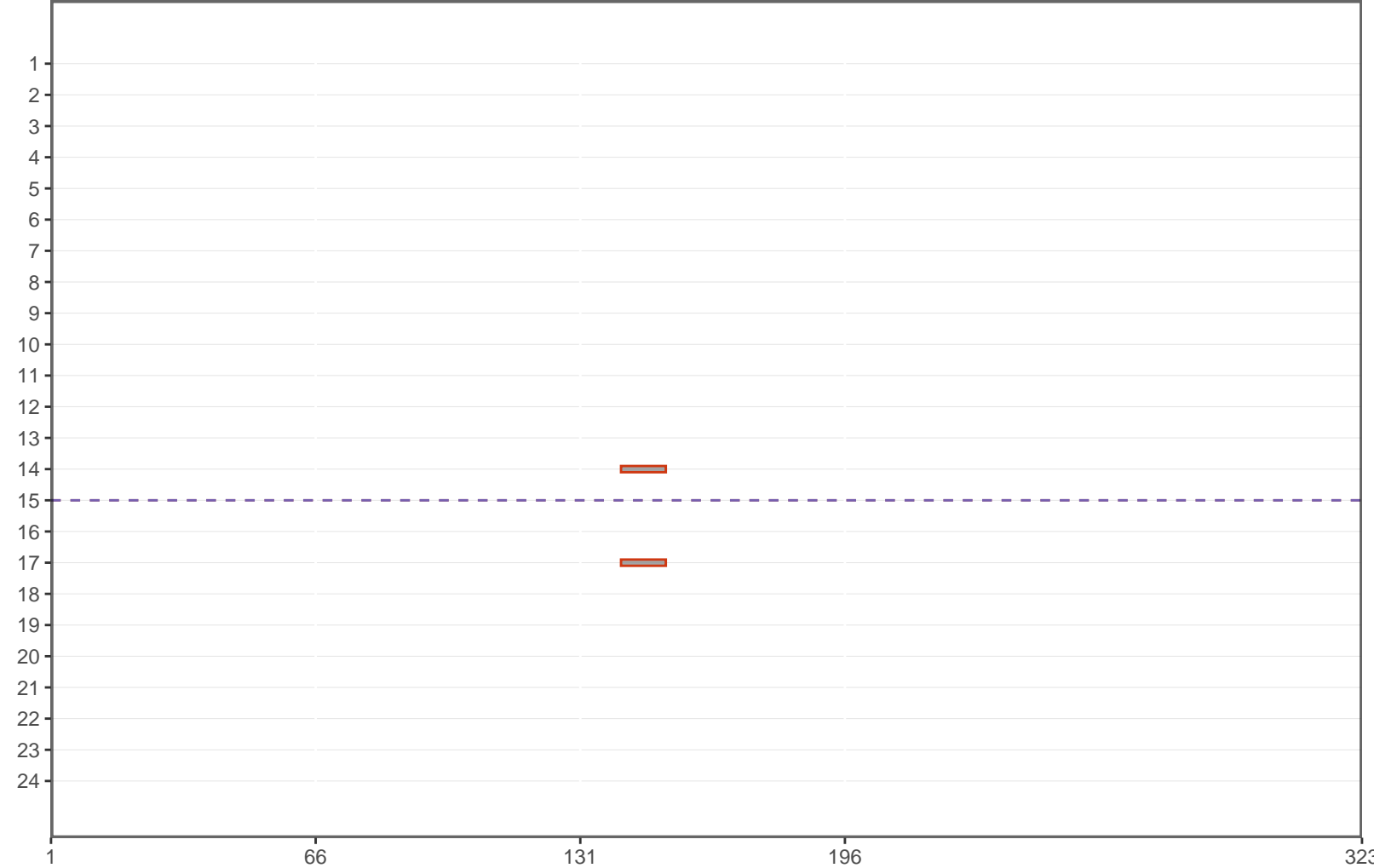
MW indication



Molecular weight



Gel Slice



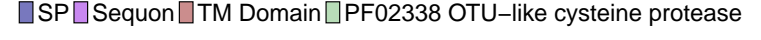
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IIVSDRVIEIKLDSKLEPLGLMVAEIKRPGDGHGIVRAIENQLAVGSGSSPVTYLELRQMAVAMRKHATDFLFFLSENAEGGSDGSLVERFENYCRVEVESTAAWGGOLELGAETHLKKHMFSGSFFDVEEMKKEYKSDNSGSGSSTGIMLSYHMHFGLGHEHNSIVPSSA'

NbL08g00710.1 L-ascorbate_oxidase [MW - SP = 61.76 kDa]

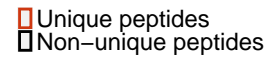
No. of times detected



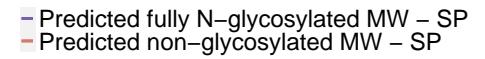
log(intensity)



Values from



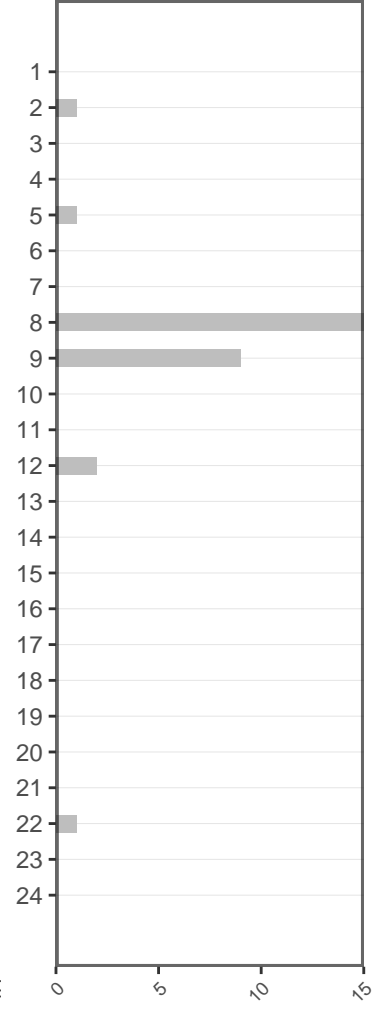
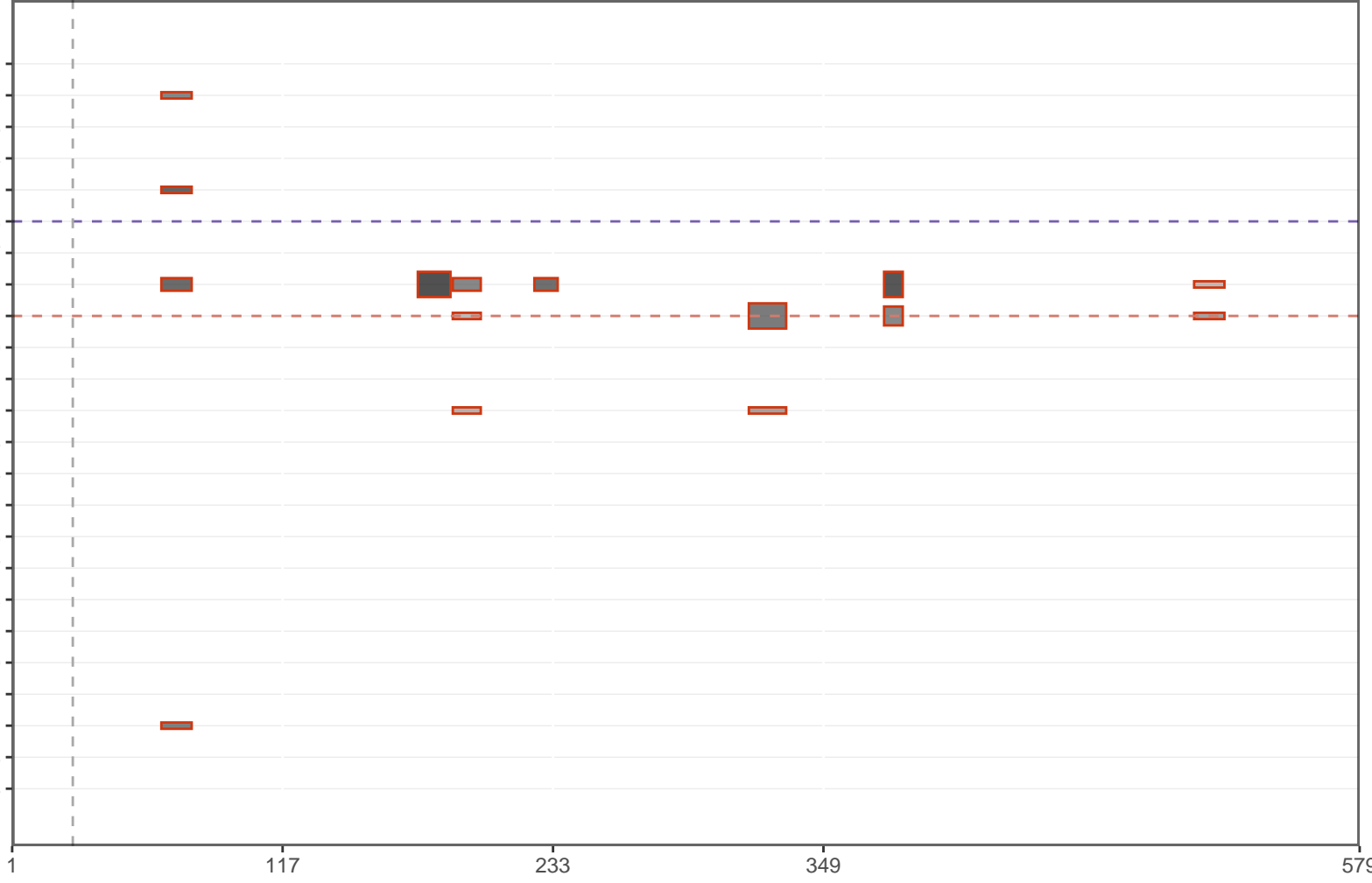
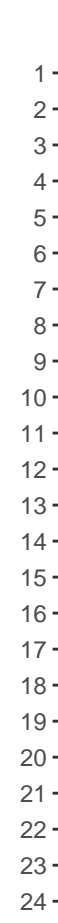
MW indication



Molecular weight

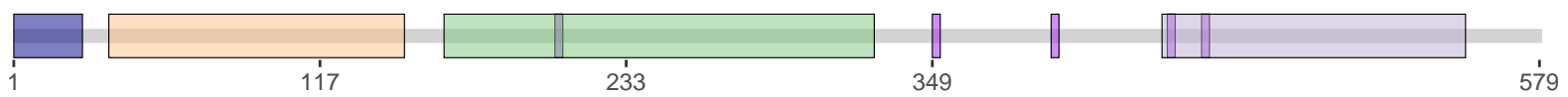


Gel Slice



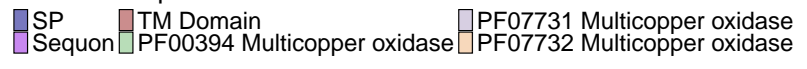
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PFVQDMIDYISGESYVLFKTDGDTKNYWSINVRGREPKTPGGLTLLNLPNSAOKFPTSPPLAPLWVDYVHSHKSFNKFALMGSPKPPQNHRRILLNTQNKIDGYSKAWANNVSLVLPFTTPLYGSRVGINAFDAKPPDPNFKDQYDLKGAQNSNSTYGNQVYLLKFKETIDILGNANALAKDVEIHPVHLHGHDFFVLYGYGEGKFKSEKDVNFKNPLKPLRNTAVIFFPGWTALRFVTONPGVWAFHGHIEPHLMGMGVVFAEGVHLWKKPKKEALACGLTGK

NbL08g00620.1 GDP-mannose_46_dehydratase_1 [MW = 41.73 kDa]

No. of times detected



log(intensity)



Values from



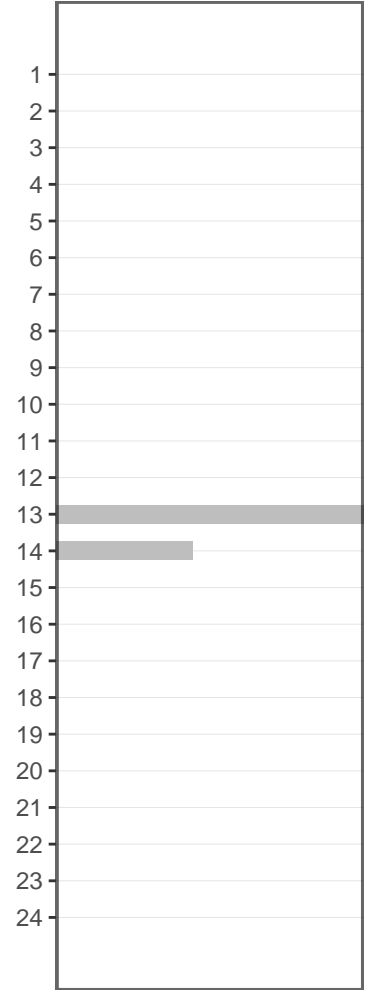
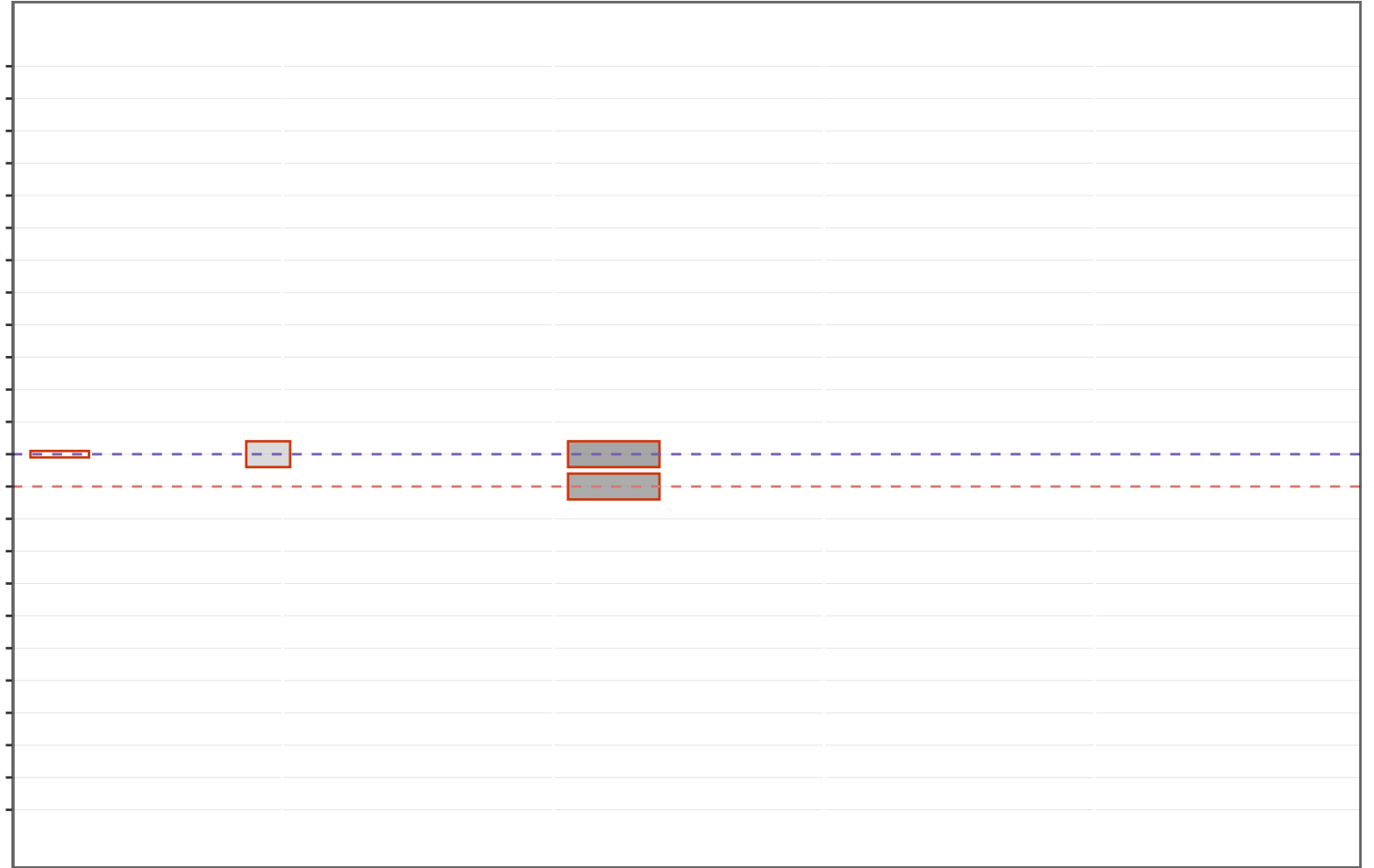
MW indication



Molecular weight

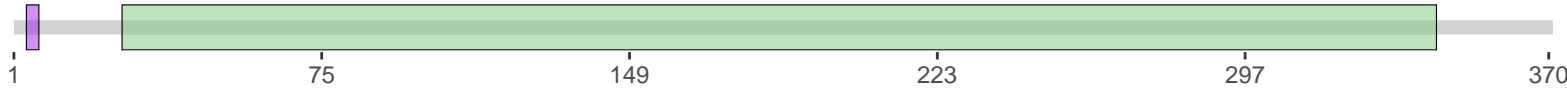


Gel Slice



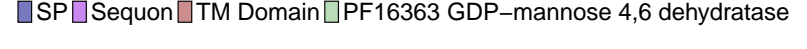
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FHPRSPYAVSKCAAHWYTVNREAVGIFAGNGLFNHEGPRRGENFVTRKTRAVSGRIKGLGSKLFLGNLQASRDWGFAGDVEAMMMMLGQEKPDVVWTEEAHTVEEFLEAFVFRVYGLNWKDHVIDKRYFRPTEVDNLKGDGSKARKVLGWKPRVGFEGLVKMMVDEDELAQREKVLVDAGYMDAGGGP

NbL08g00470.1 THUMP_domain-containing_protein_1-like [MW = 44.15 kDa]

No. of times detected



log(intensity)



Values from



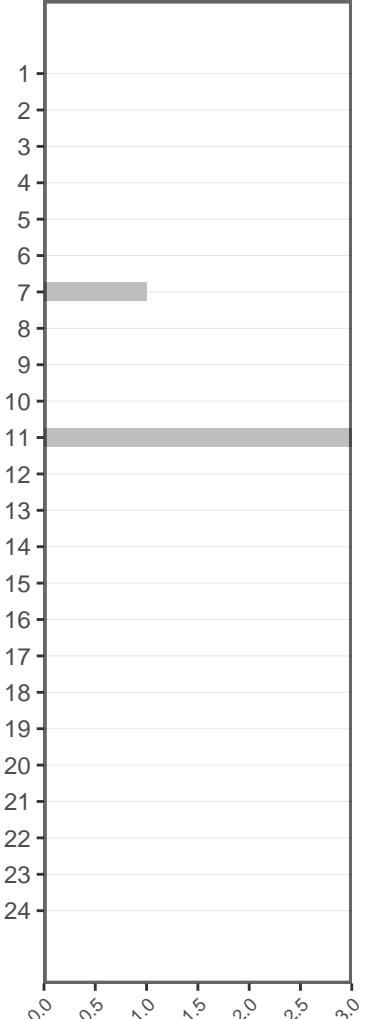
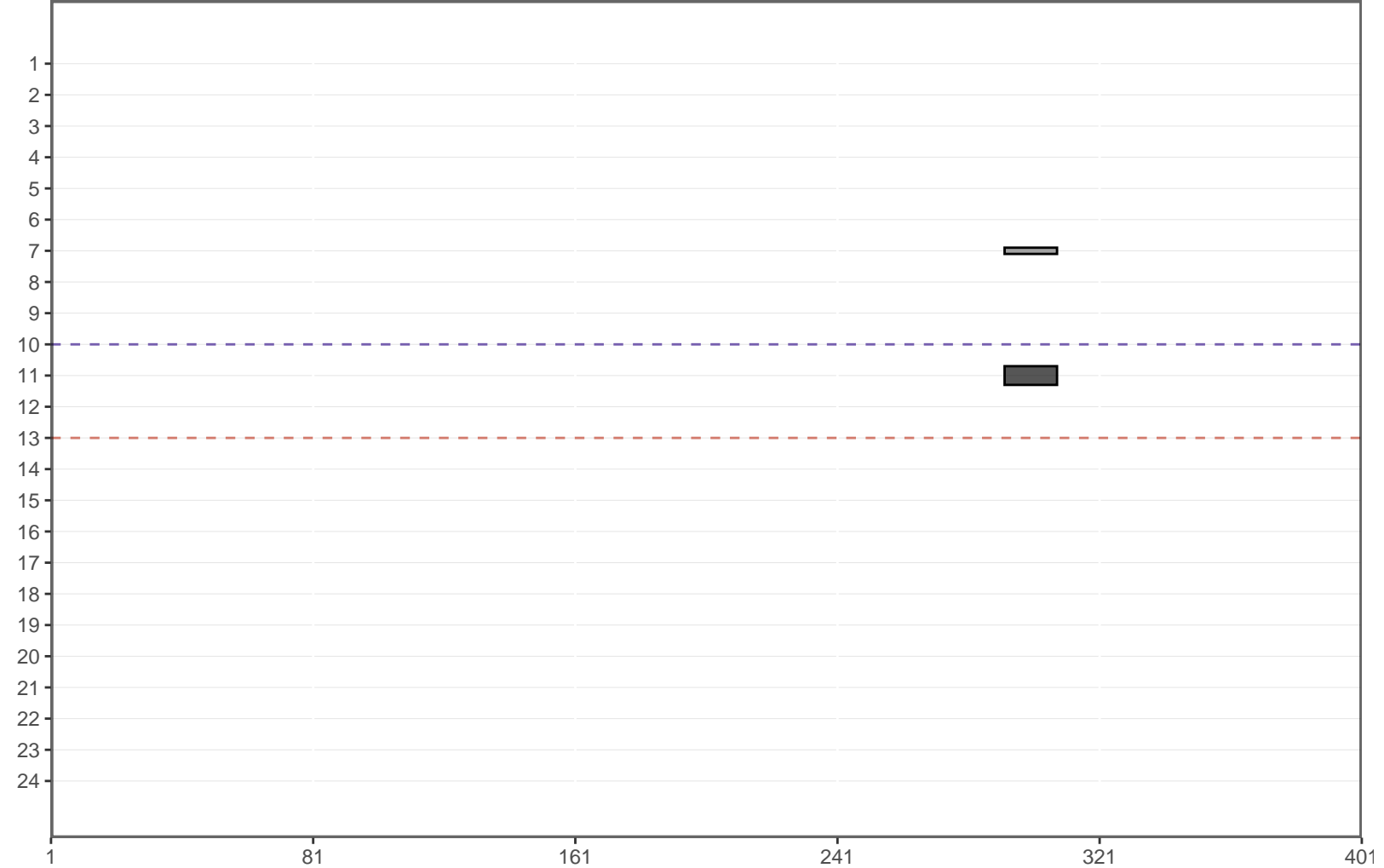
MW indication



Molecular weight



Gel Slice



Protein length

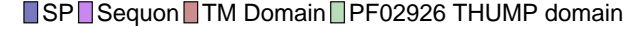


Peptide counts over 4 repeats

Pfam domains



Pfam Description

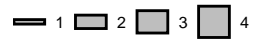


Protein sequence:

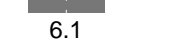
TTHEOKDGEAGEFPKPKKQGVREATKTKGNVAVGKTEKSVDKLHEAELAEELGDKSKRRFTYLDGGGNGVVFVQMRKKDGDNPKEIQQHMMSLSLAKTRHVRFLRLVLPVEVTCVASEEEIGRAIKPLVEQYLPVETDTPKPKFVLYEARANTGINKMKIDTVAKSVPSPKKVDLSNFEINVVQIVKTVGLLGVVENYKELSKYNIQLTSKN

NbL08g00200.1 importin-5-like [MW = 46.74 kDa]

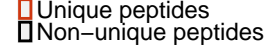
No. of times detected



log(intensity)



Values from



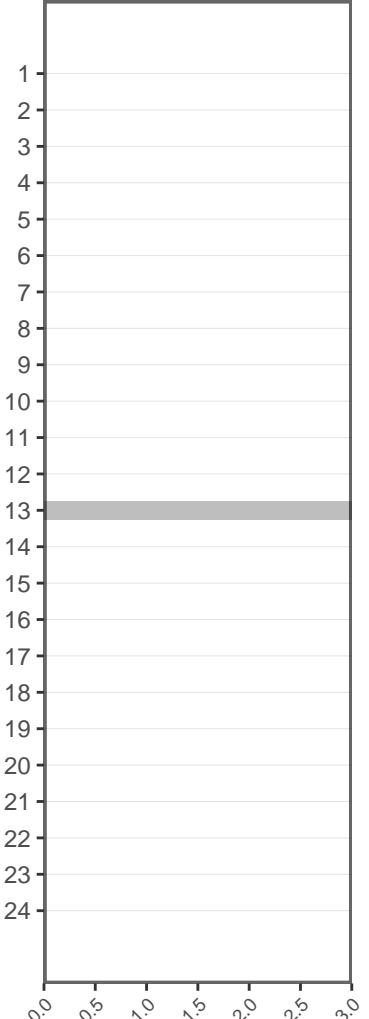
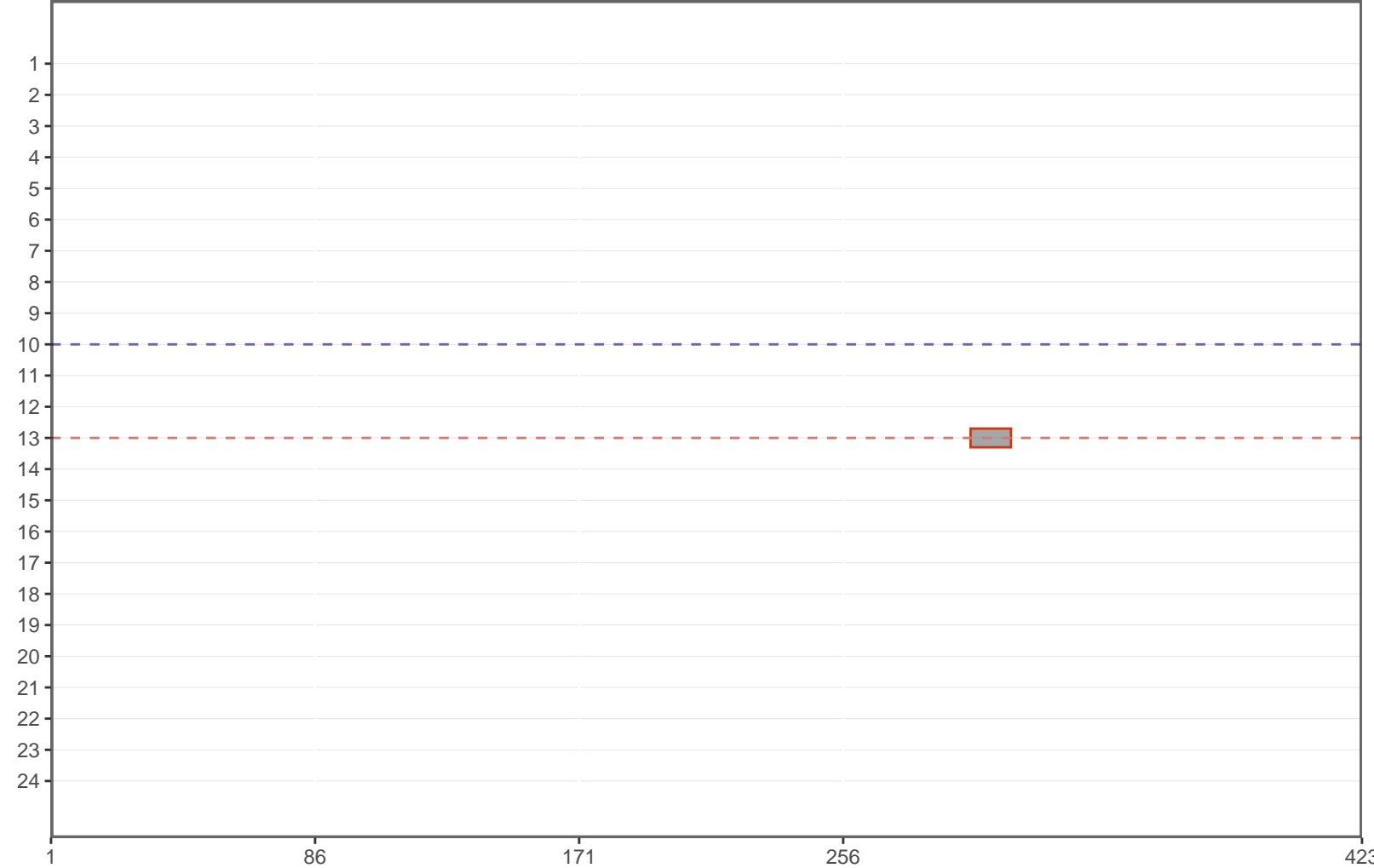
MW indication



Molecular weight



Gel Slice



Protein length

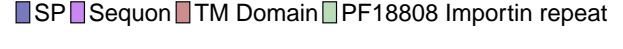


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

PSNDKDYVYQGLLQALLGLTEALTKGEEVYTRALELENFVEFAENFRFLRMQLVEVATMFEIAENESLEKETRHLAKFLLVEAKKEAPGMMKRLPLFTSNGFAMLLRLQGVDEDEPPWNNHKVAFREYGNVTVGIGVFDLLGRALGAKTIAPVAKEQLSVGLAAPGWQKRIHAALLALAVISECCPHGRILNVALGVYLLAGVFGSLPLSLPPPGS

NbL08g00130.1 mitochondrial_dicarboxylate/tricarboxylate_transporter_DTC-like [MW = 31.67 kDa]

No. of times detected



log(intensity)



Values from



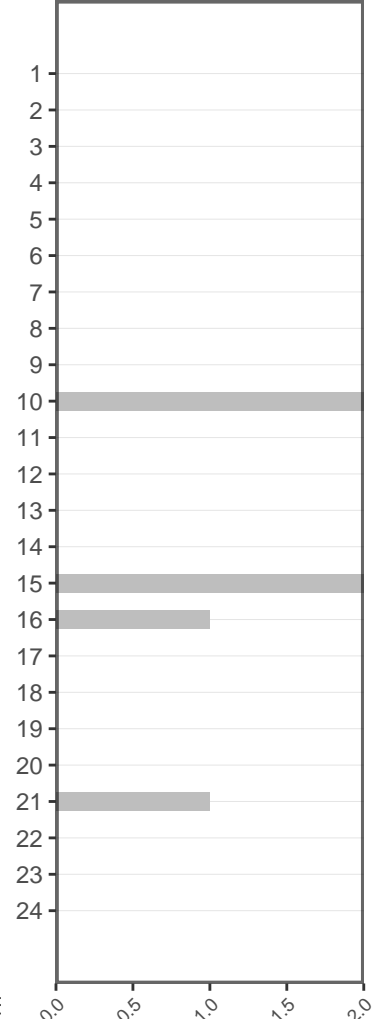
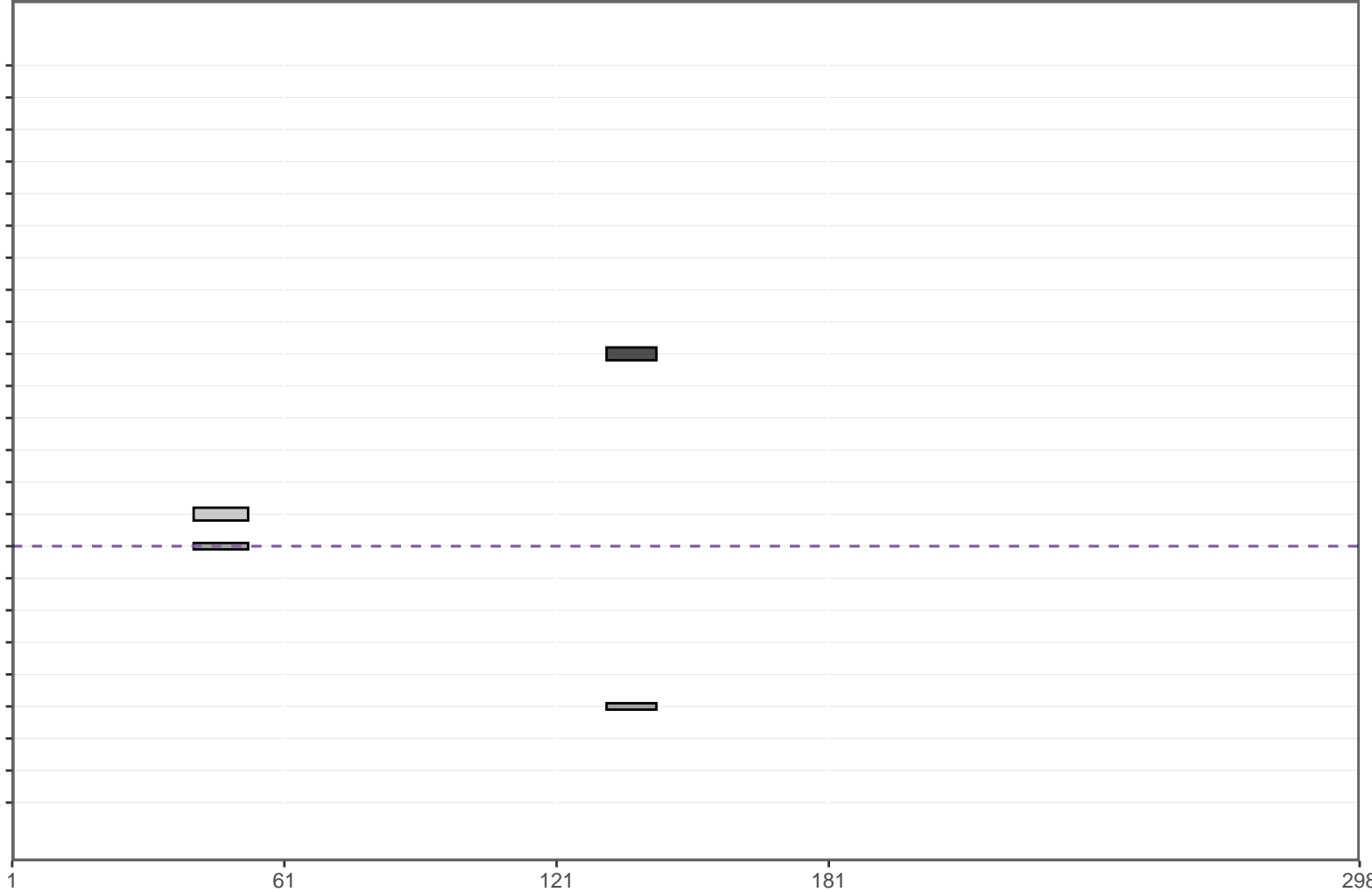
MW indication



Molecular weight

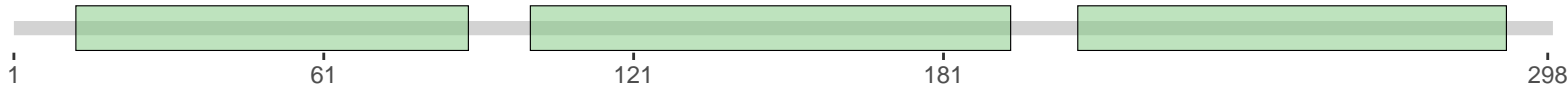


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PLAQRHYTNATFALSRIVADEGLALWKGAGPTVVRAMALNMGMLASVYDGGVEFRDRNLGLGEAATVVGASVSGFFAAAGSLPFDYVKTQIGKMGPDMEGKLPVSGSFDGAMKTLKAGGPFKFTGFPVYGVRIAPHVMMTWFLNIGKGAERKLGSL

NbL08g00070.1 isocitrate_dehydrogenase_[NADP] [MW = 46.84 kDa]

No. of times detected



log(intensity)



Values from



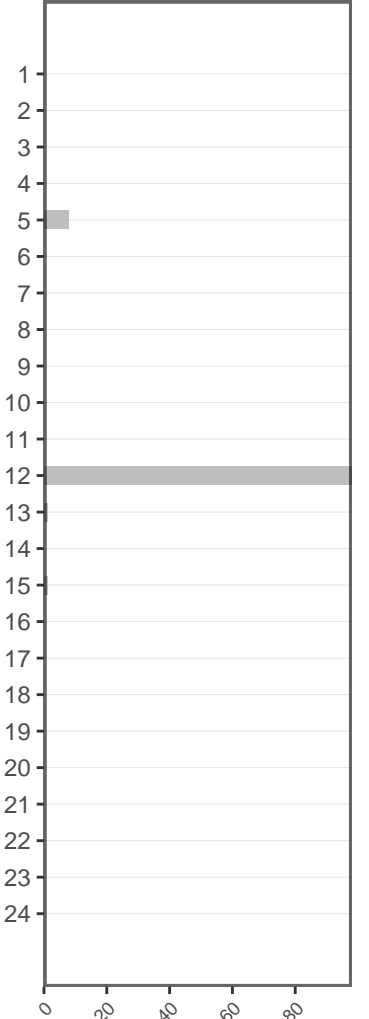
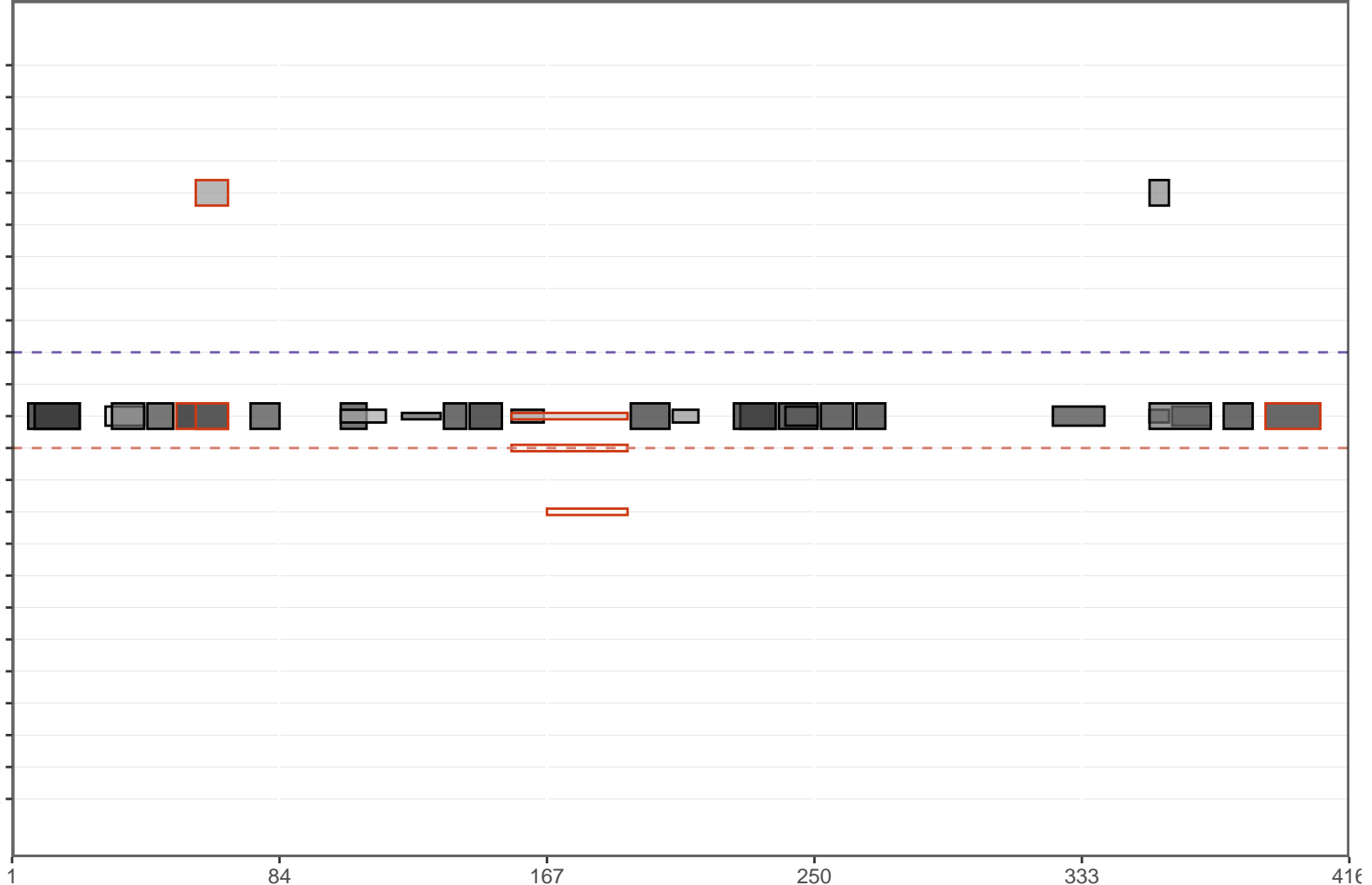
MW indication



Molecular weight



Gel Slice



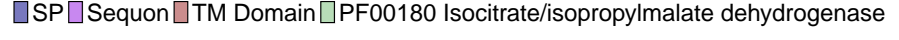
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ASINMAYQKYPFLPLSTKNTLKKYDGRFDGFEVYEAHWKSKYEEAGWYEHRLRDDMVAWLKSEGGYWAQKNYDGGVQSDFLAQGFGSLGMLTSLVLPDQDKTIEAAAHGTVTRHRYRVHQKGGETSTNSASIFAWTRGLAHRATLDKMERLLDFTKLEAAAGVESGKMTKDLALIHGSKLSREHYLNTFEFDITVADEKARLUKAKA

NbL08g00030.1 lysine--tRNA_ligase_chloroplastic/mitochondrial [MW = 27.41 kDa]

No. of times detected



log(intensity)



Values from



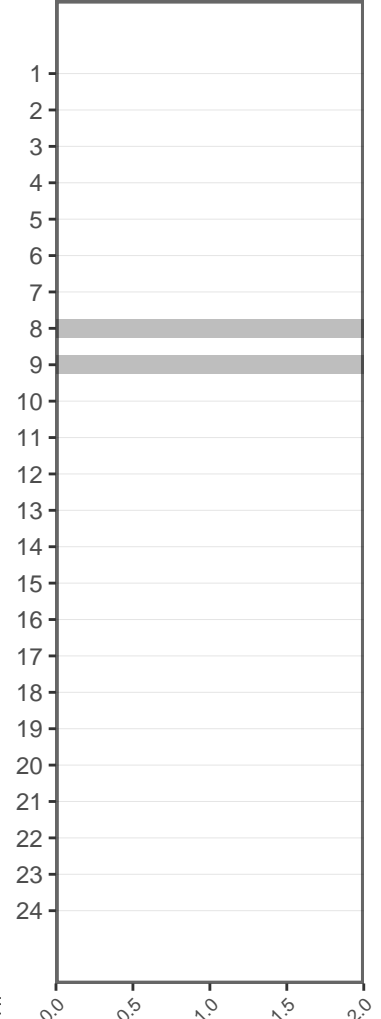
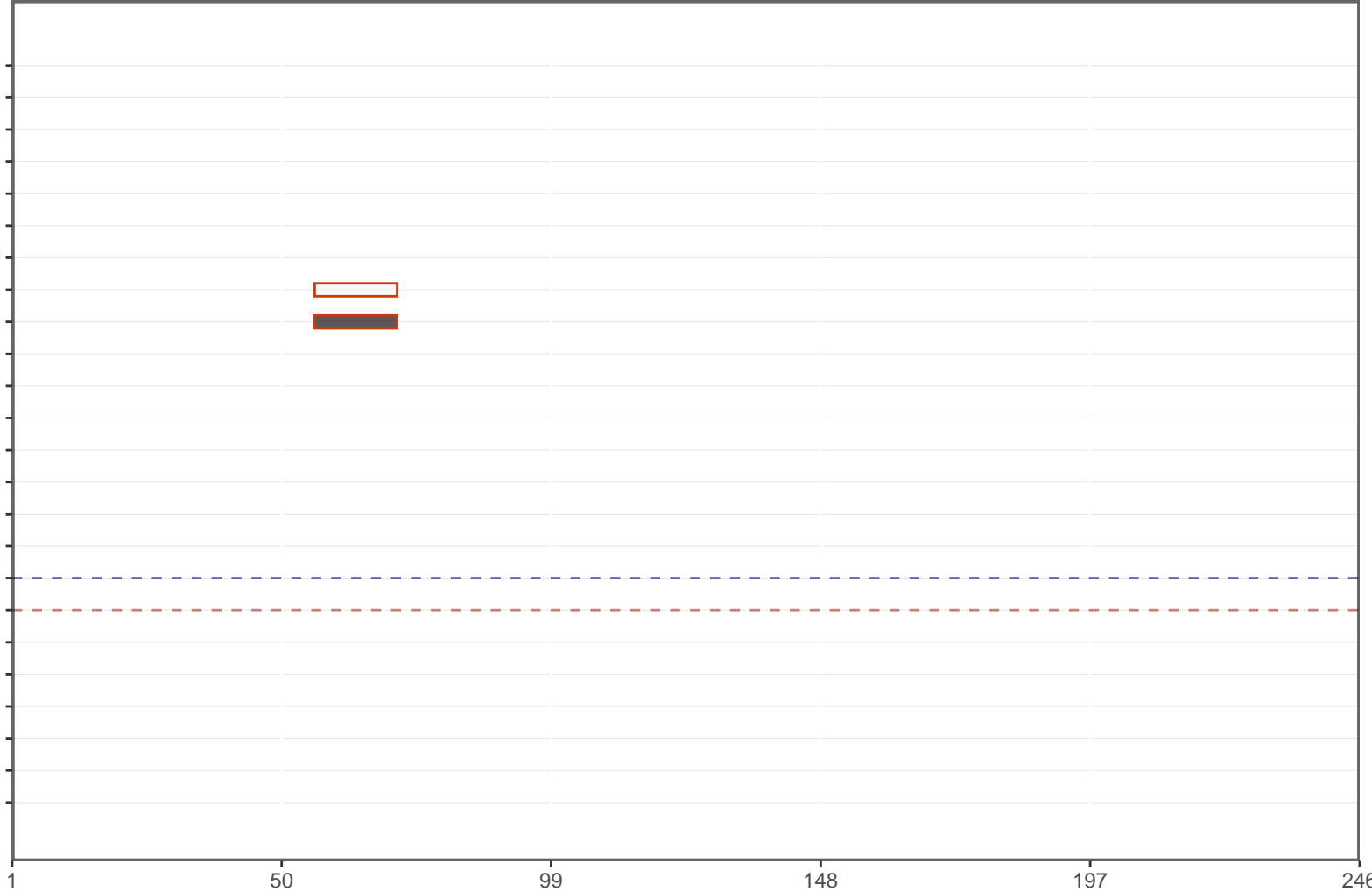
MW indication



Molecular weight



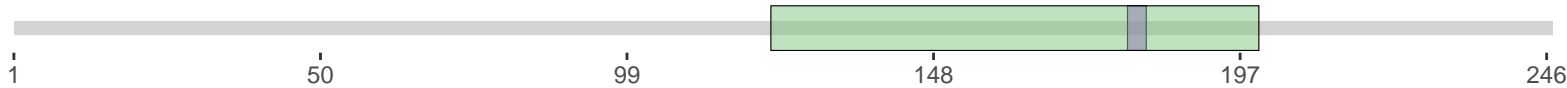
Gel Slice



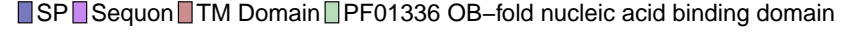
Protein length



Pfam domains



Pfam Description



Protein sequence:

SNNGEESNSENDYVSVSGRIVARRAFGLAFLRLRDDGSMQLYCEKERLVDDQFEQLKTLVDVGDLGANGSKIRTEKGLSVCVNSFSILTKSLPLPKYHGLTQVQKRYRQRVYDMIANPEVADTFRRKRAKVS

NbL08g00020.1 lysine--tRNA_ligase_chloroplastic/mitochondrial-like [MW = 32.79 kDa]

No. of times detected



log(intensity)



Values from



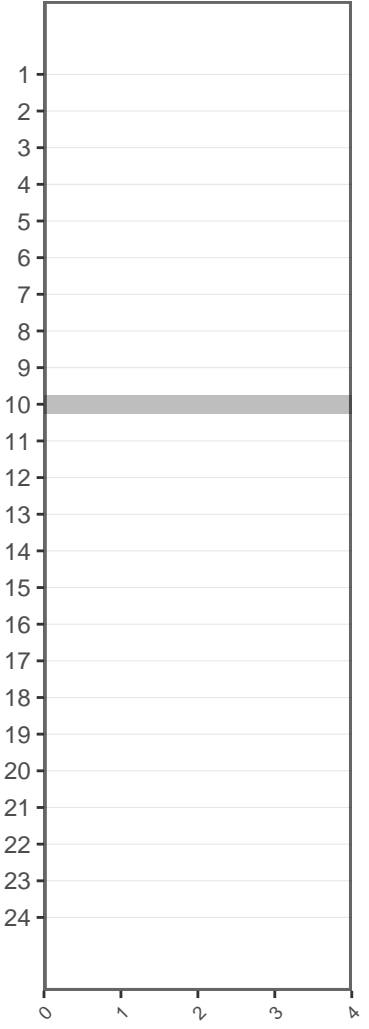
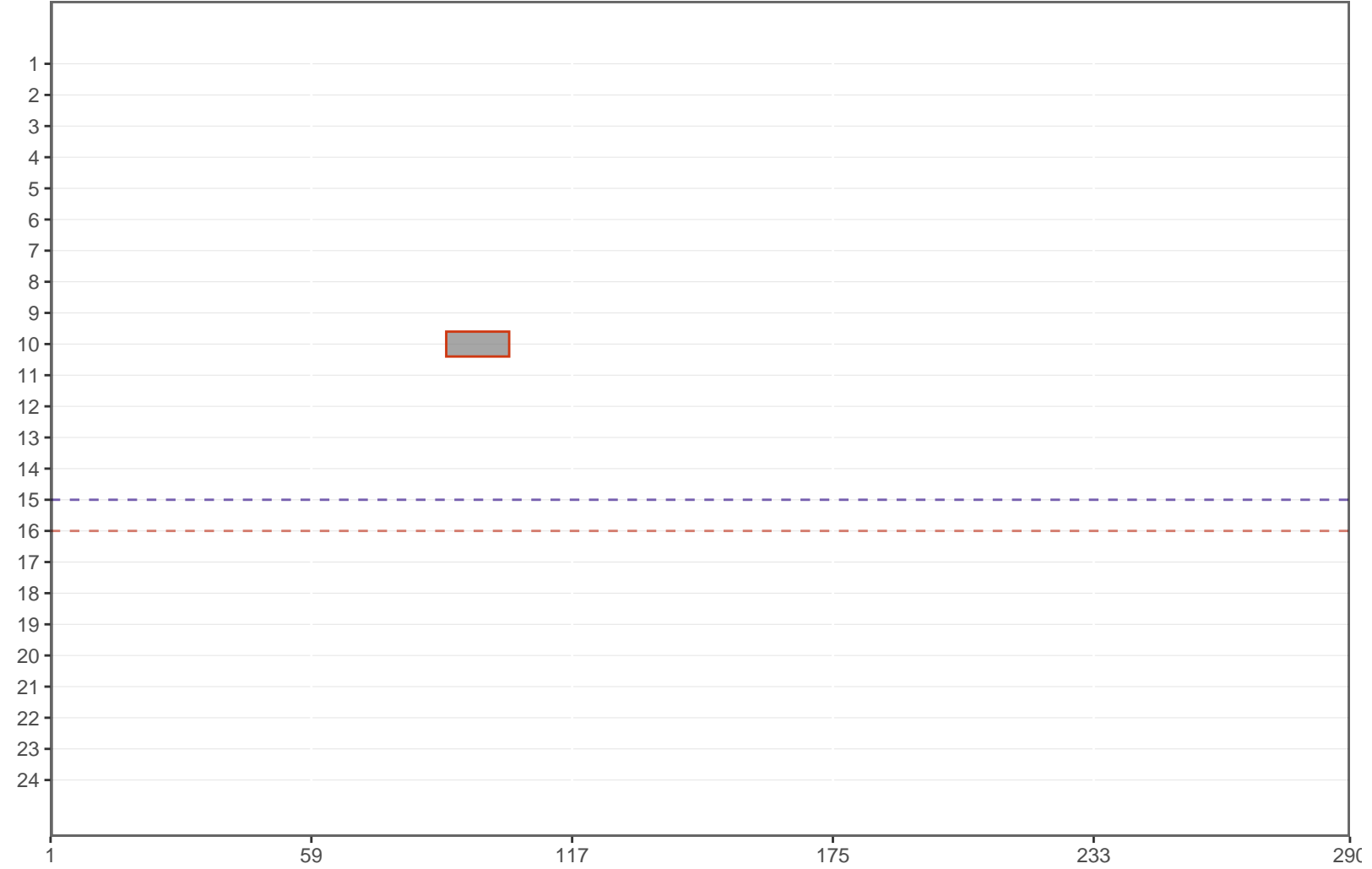
MW indication



Molecular weight

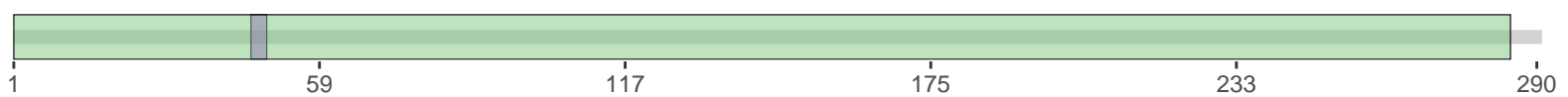


Gel Slice



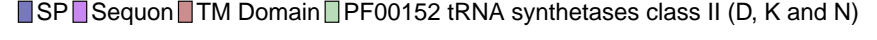
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SHLVNEVFEMVLEPWLGPFTFLVDYPIEISPLAKPHRRHSGLTERFELFGRELANAFSELTDPDRRLLEEYKQHNKKVASGLNMACAEGGKNDKDDSDYKFLDEDFITALEYGMPPASGMCLGIDRLVMLTNSASIRQVAFPVKIQGQ

NbL07g17970.1 ATP_synthase_subunit_alpha_mitochondrial [MW = 55.25 kDa]

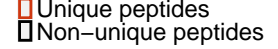
No. of times detected



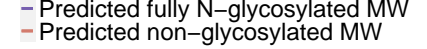
log(intensity)



Values from

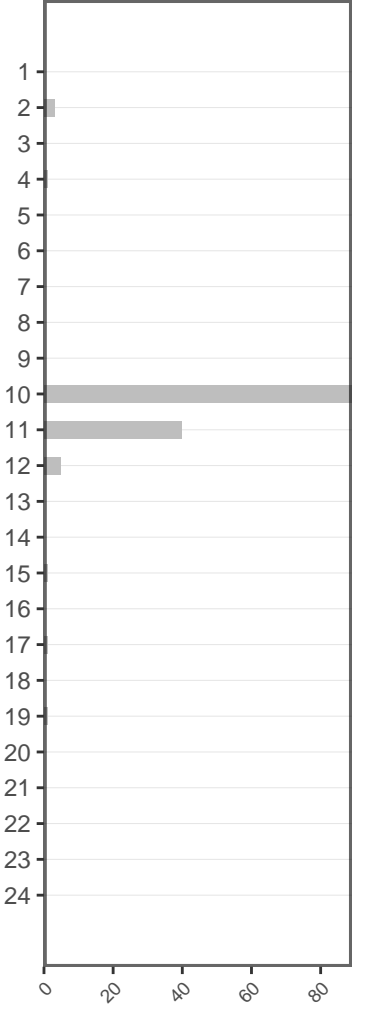
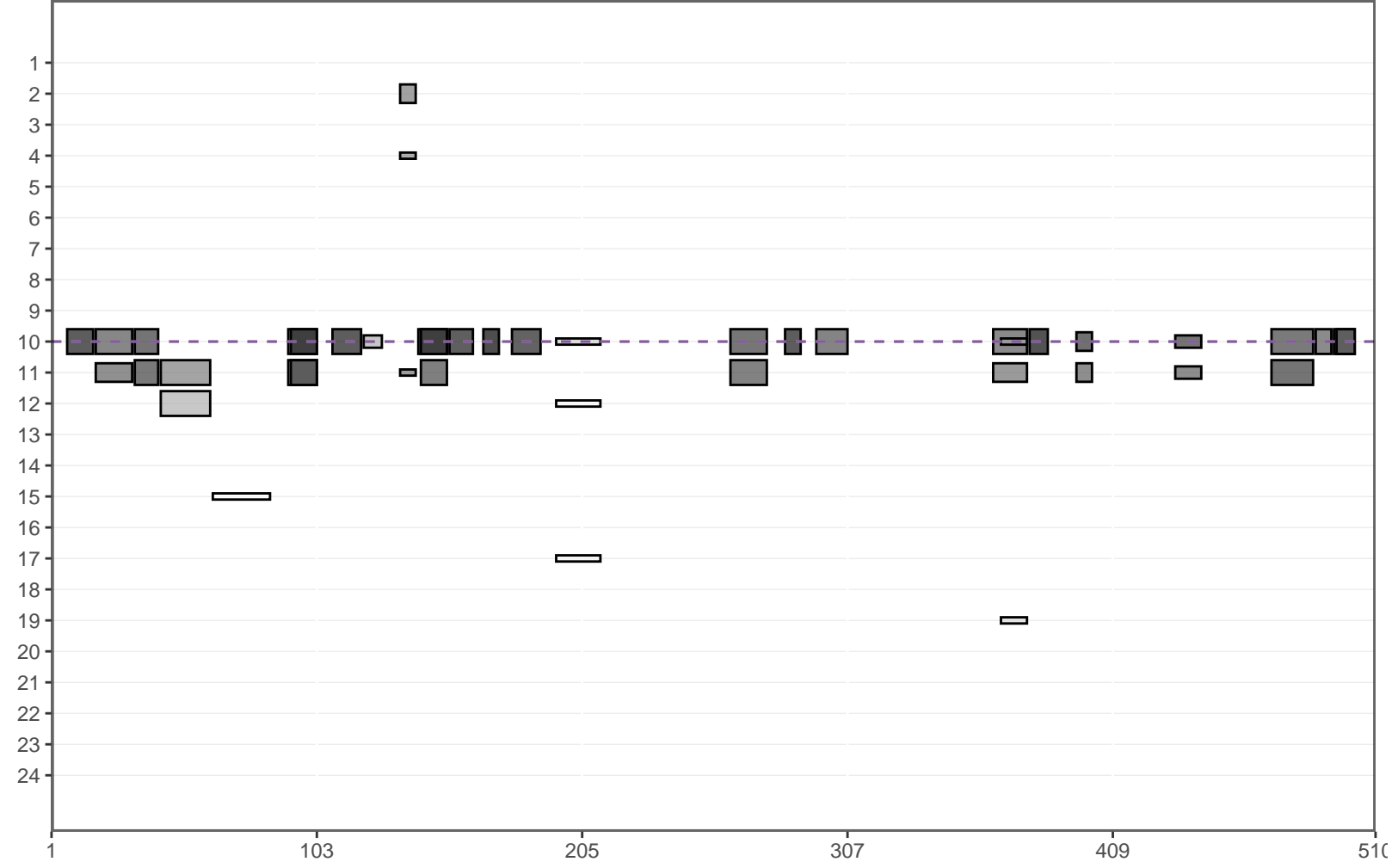
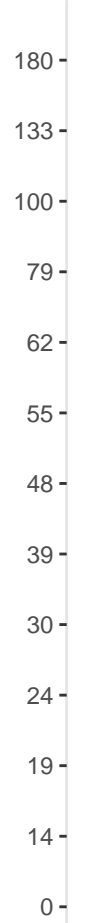


MW indication



Molecular weight

Gel Slice



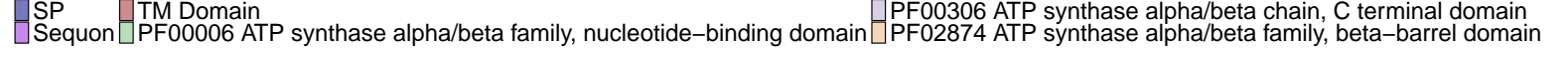
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

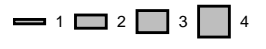


Protein sequence:

VPLQFLAPYSGCAMGEYFRDNGMHALHYDQLSKQAVAVRQMSLLLRPPDGRFAFFDGFYKLRLLERAAKRISDGTGAGSLTALPVIETQAGDVSAYVPTNIGIFDGGKLELELYRGRPAINVGLSRSRVGSAAGLTKMKVQVSSKLELAGYREVAALQFGSDLDATGALLNRGARLTFVWQVQVAPLPIEKQILVAVWNGFDIMPLDRHGVYERALNSVWPELQSFLEKGLTNERKMEIDTFLKESALAFI

NbL07g17960.1 ribosomal_protein_S3_mitochondrial-like [MW = 145.57 kDa]

No. of times detected



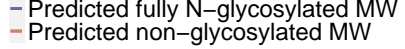
log(intensity)



Values from

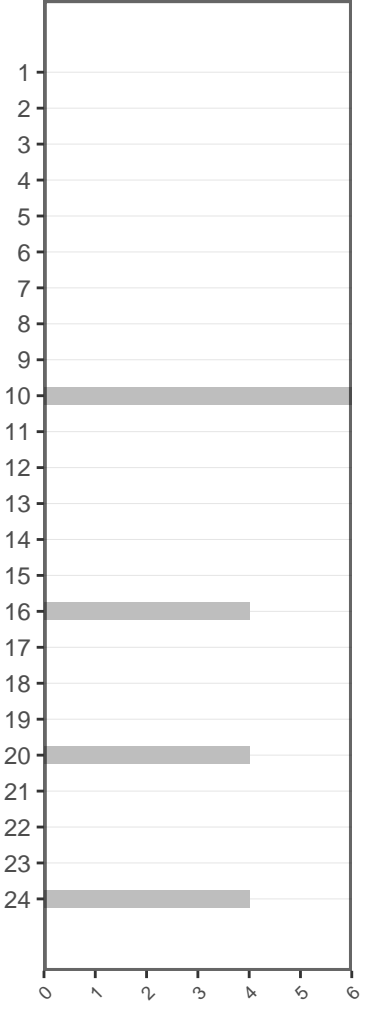
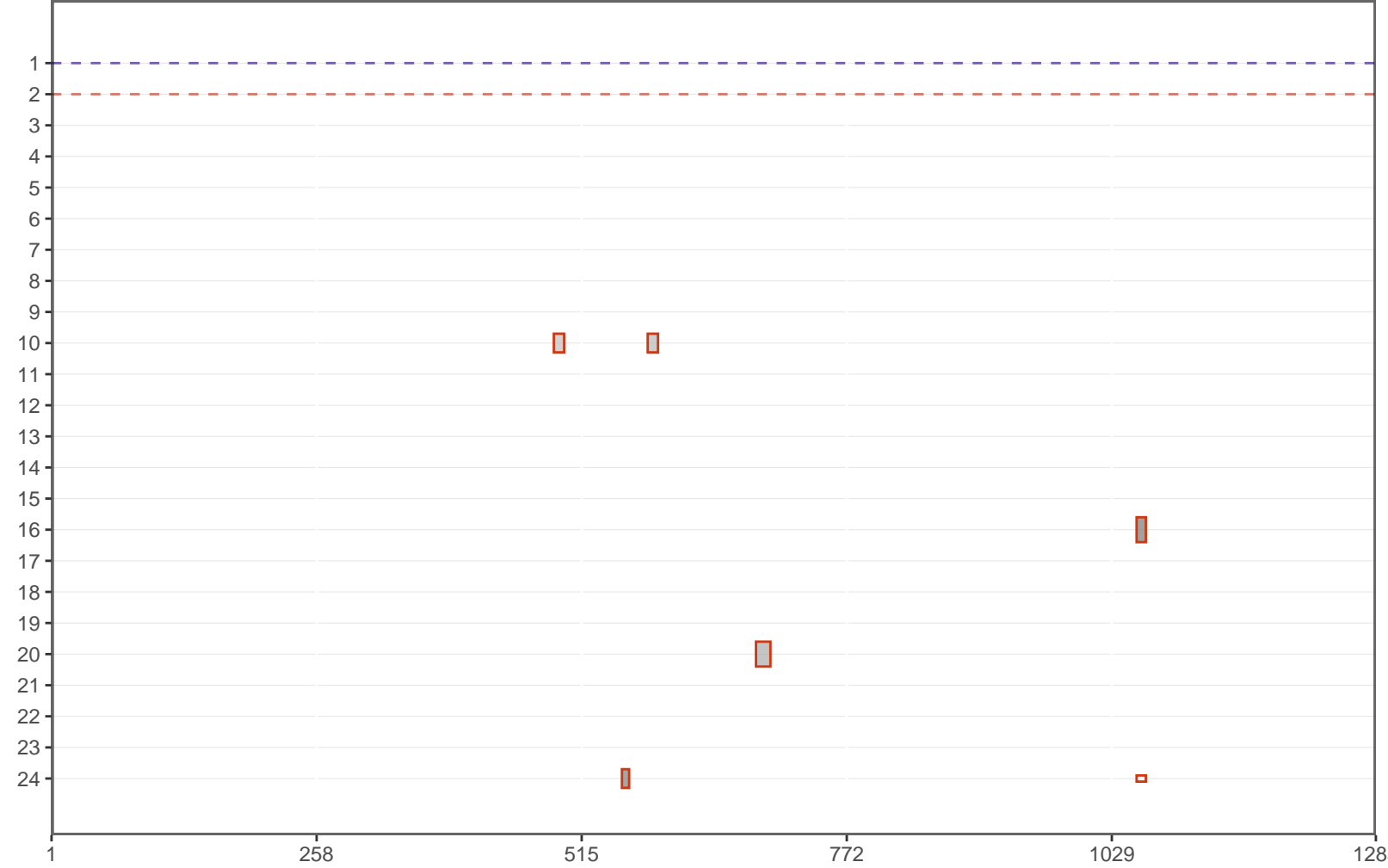


MW indication



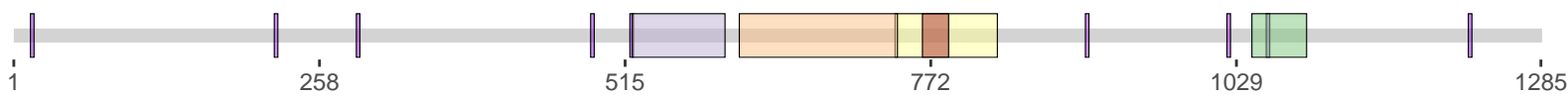
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- Pf00116 Cytochrome C oxidase subunit II, periplasmic domain
- Pf00189 Ribosomal protein S3, C-terminal domain
- Pf00252 Ribosomal protein L16p/L10e
- Pf02790 Cytochrome C oxidase subunit II, transmembrane domain

Protein sequence:

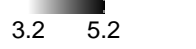
STQLGFGRYGKSCRAGRLSYRAEARRAIKHGFHRAMSGGFRNKKWVYRFADIPITGKPTVEMRGRGKGNFTGWARVSRGGLFEMDGVLSNARGAATLAAHKLSEPVWLGFDQATPIMGDIHLHHDVFFVILILFVILWLRALWVHFHYKKNIPQRIVHGTTTELWTFPBIILMFAIPSFALLVSMDEVVVDPAITKAGHWYRSLPALHEADGKRGVEVVRPFRINAPSGIAYGSLVAGVAVVYFQPNRPSNLSEWGPVGNHSGSCTTGPGEDELFI

NbL07g17940.1 NADH_dehydrogenase_[ubiquinone]_iron-sulfur_protein_3 [MW = 22.86 kDa]

No. of times detected



log(intensity)



Values from



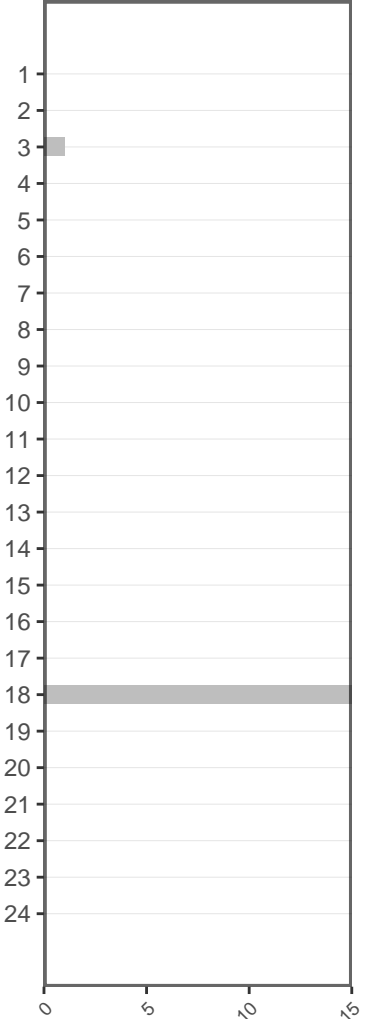
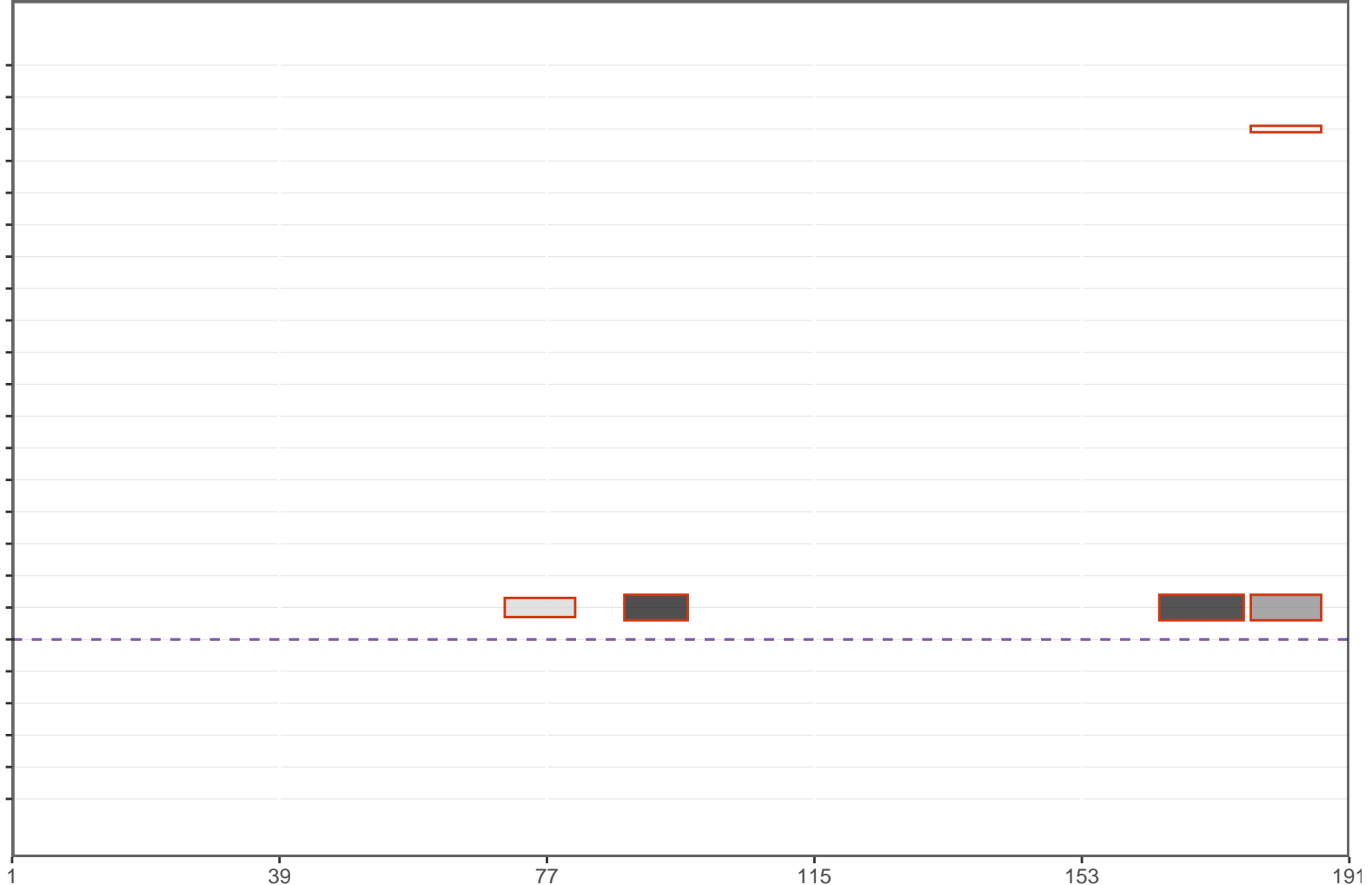
MW indication



Molecular weight

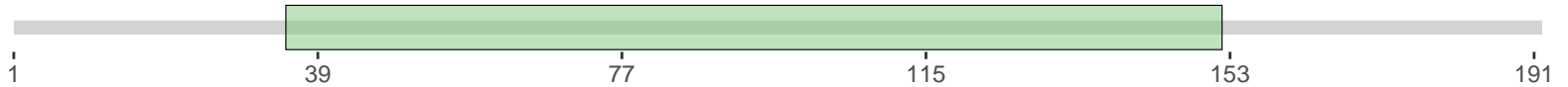


Gel Slice



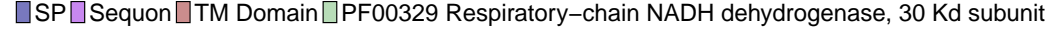
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISRIRVQTSADDEVTRISSEVVLFRAGWVEREVWDMFGVGFNHPDLRRILTDYGFEGHPLRDKDFLLSGYVEVRYDDPEKRVVSEPIEMTQEFRRYDFAFAPWEGRSGDQ

NbL07g17930.1 ribosomal_protein_S4_mitochondrial [MW = 32.36 kDa]

No. of times detected



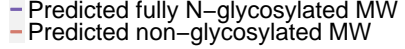
log(intensity)



Values from



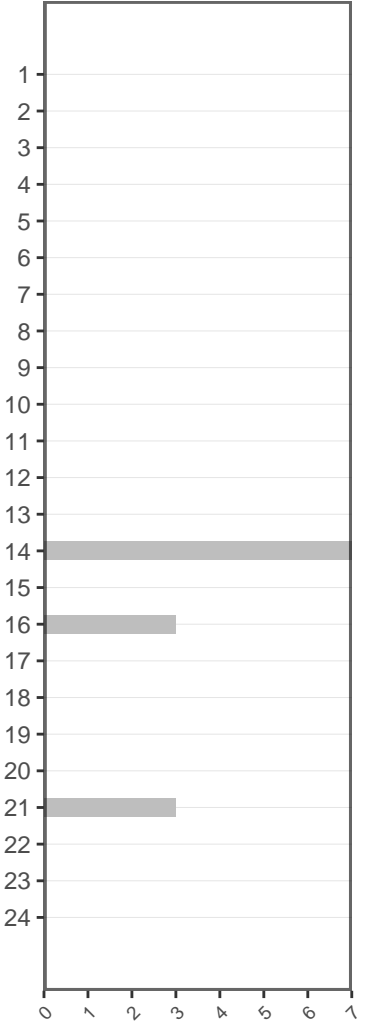
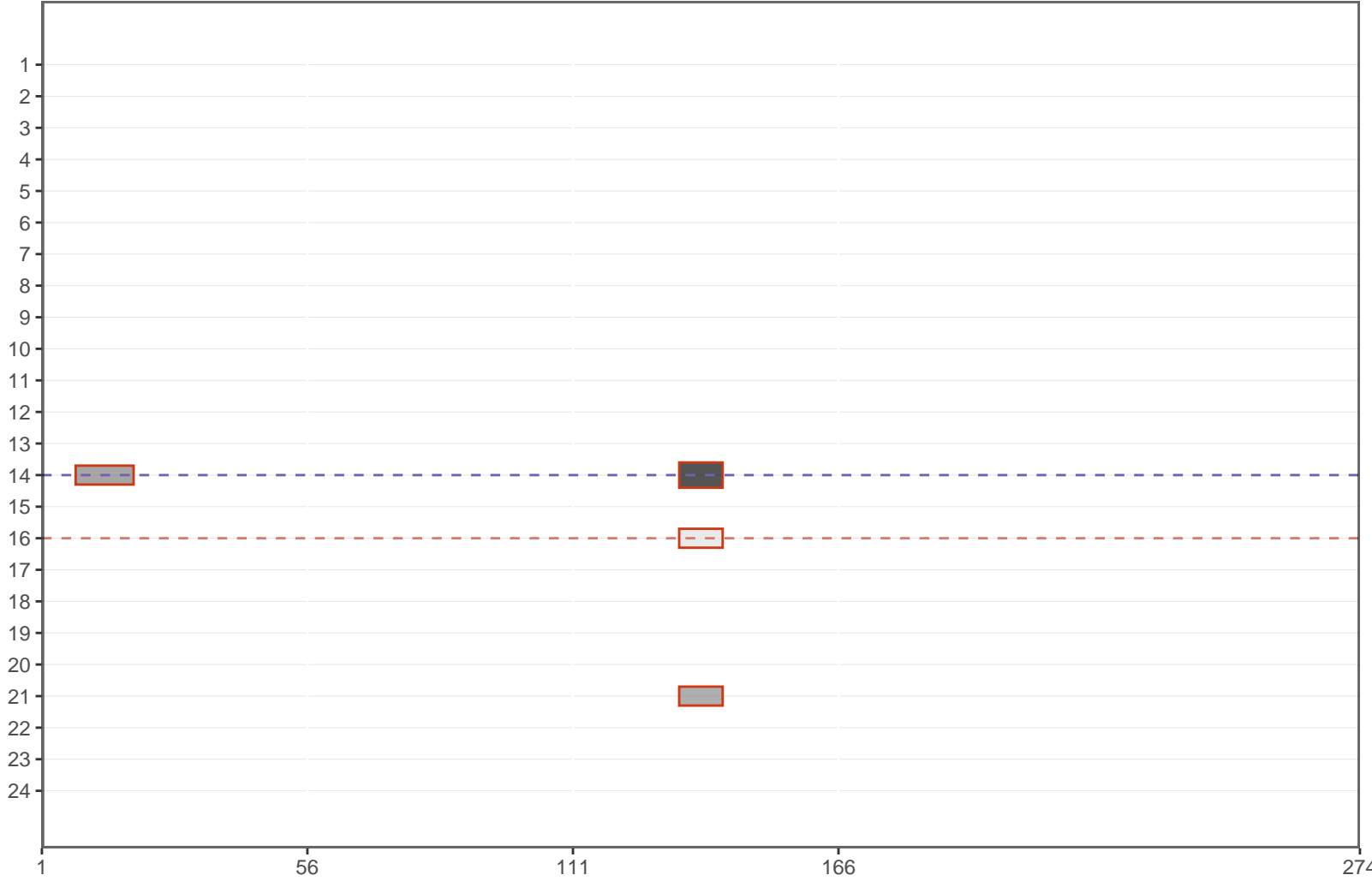
MW indication



Molecular weight



Gel Slice

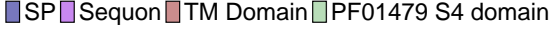


Protein length



Pfam domains

Pfam Description



Protein sequence:

IRFLQQLRSMQEEELERTKFKGSEKVCVLSGSSFAEHRMRKRNLYHFKSLFLSKRRNEKNRNPTRTRSPVYVNSLSYNSYSGASPHGFTKKIKRIELPTHYLEVNYRTPKAVVSYGPNIGHPHDIRLKDNLILLWSGKGRGGNI

NbL07g17900.1 photosystem_I_P700_chlorophyll_a_apoprotein_A1 [MW = 83.02 kDa]

No. of times detected



log(intensity)



Values from



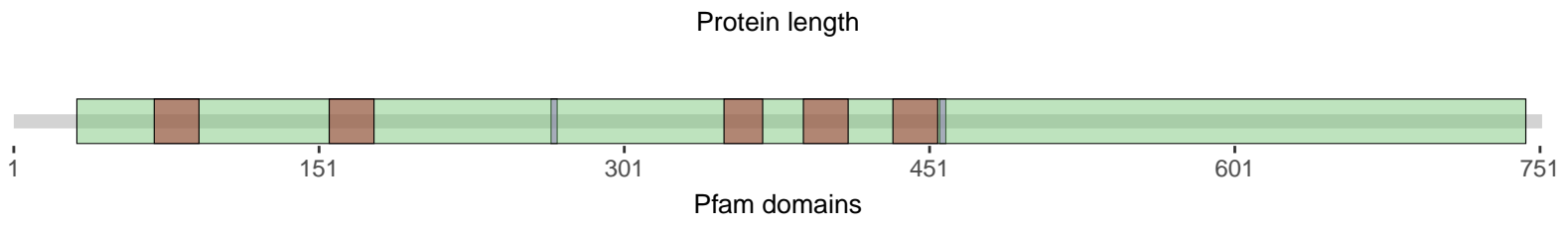
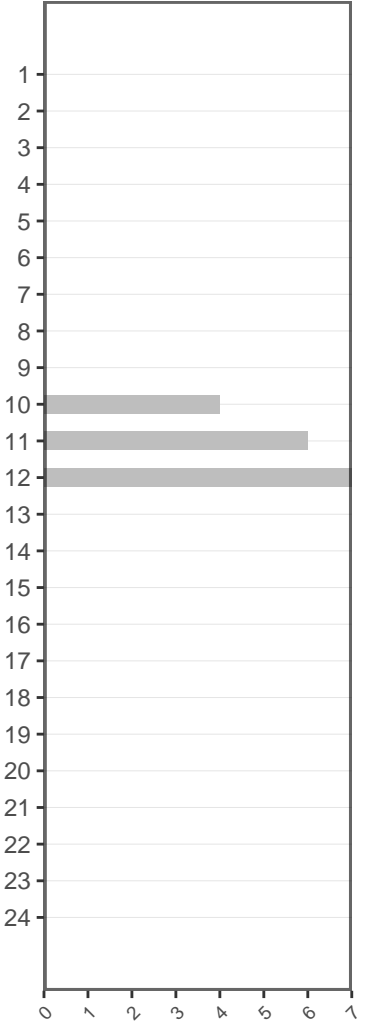
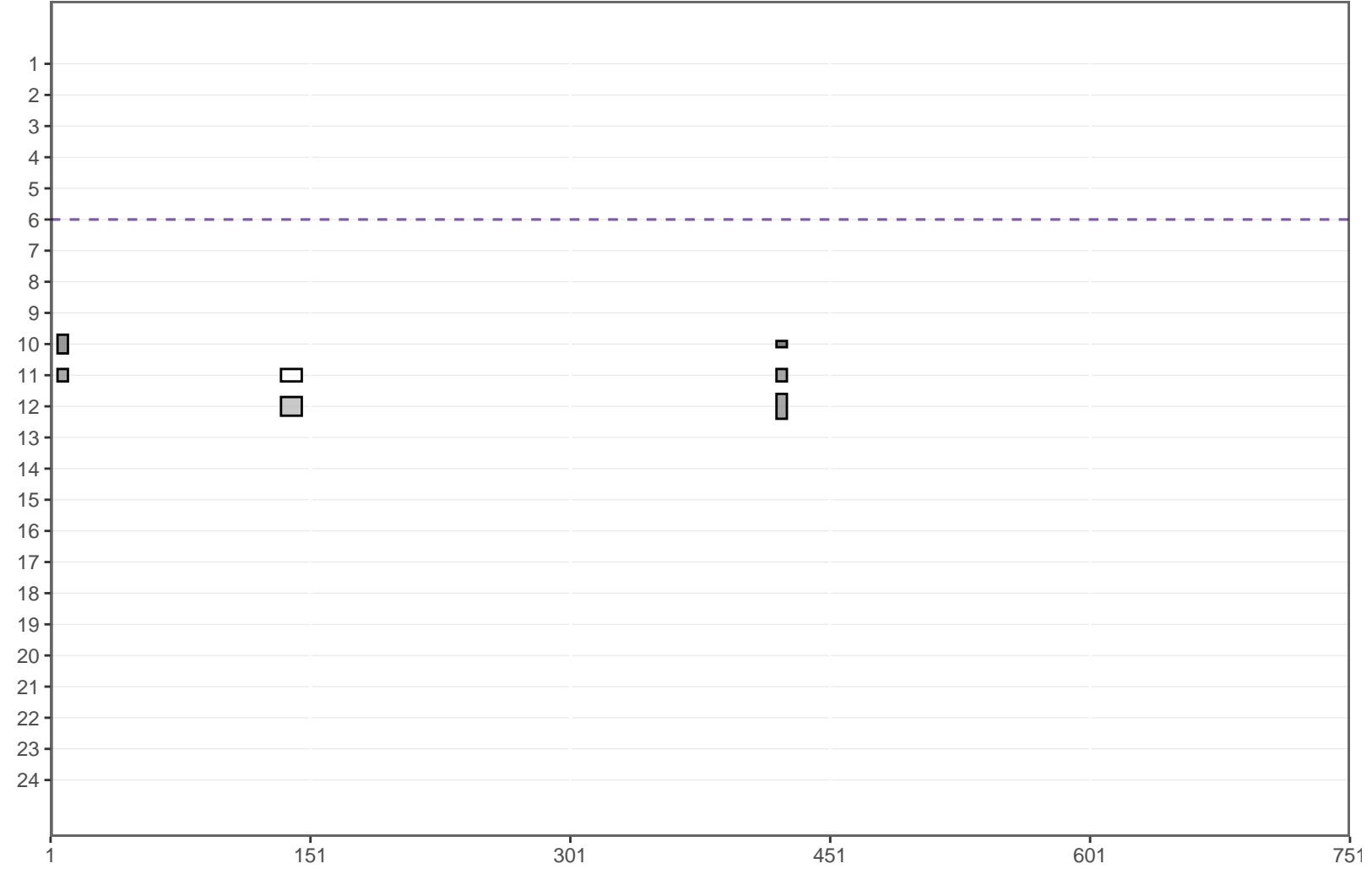
MW indication



Molecular weight



Gel Slice



Pfam Description
 ■ SP ■ Sequon ■ TM Domain ■ PF00223 Photosystem I psaA/psaB protein

Protein sequence:

/VAHIMYSMPYPYPLATDGTQLSLFTHHMWGGFLVGAHAAMFMRDYDPTFRYNDLLDRVLRHRDAISHLNWACIFLGFHSGFLYHNDTMSALGRPQDMFSDTAQLGQVFAQWQNTHALAPGATAPGATASTLTVGGGDLVAVGGKVALLPPLGTDARFLVHHAFTHVTVLLKGLVAFARSRLLPKANLGFRRFGDQGRGRTGQVSAWDHFLGLFLWMMYNAISVVFHFQWMMQSDVAVGVSVDQGVVTHITGGFAGSSTINGWLRDFLWQAQASQV

NbL07g17890.1 acetyl-coenzyme_A_carboxylase_carboxyl_transferase_subunit_beta_chloroplastical [MW = 58.28 kDa]

No. of times detected



log(intensity)



Values from



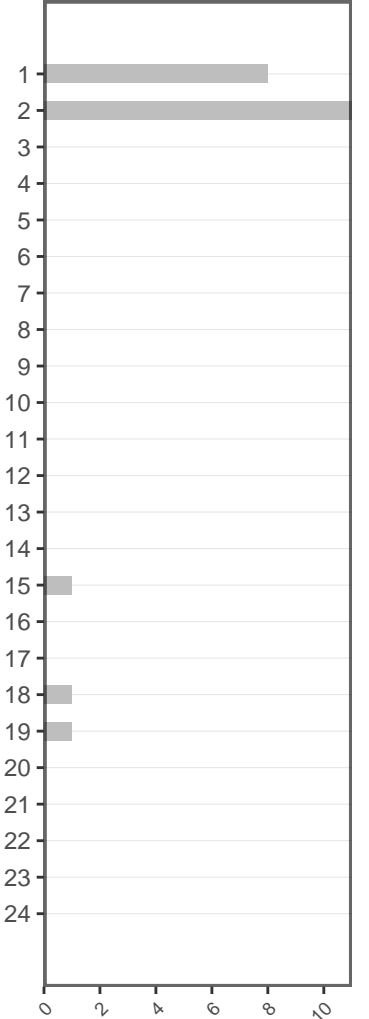
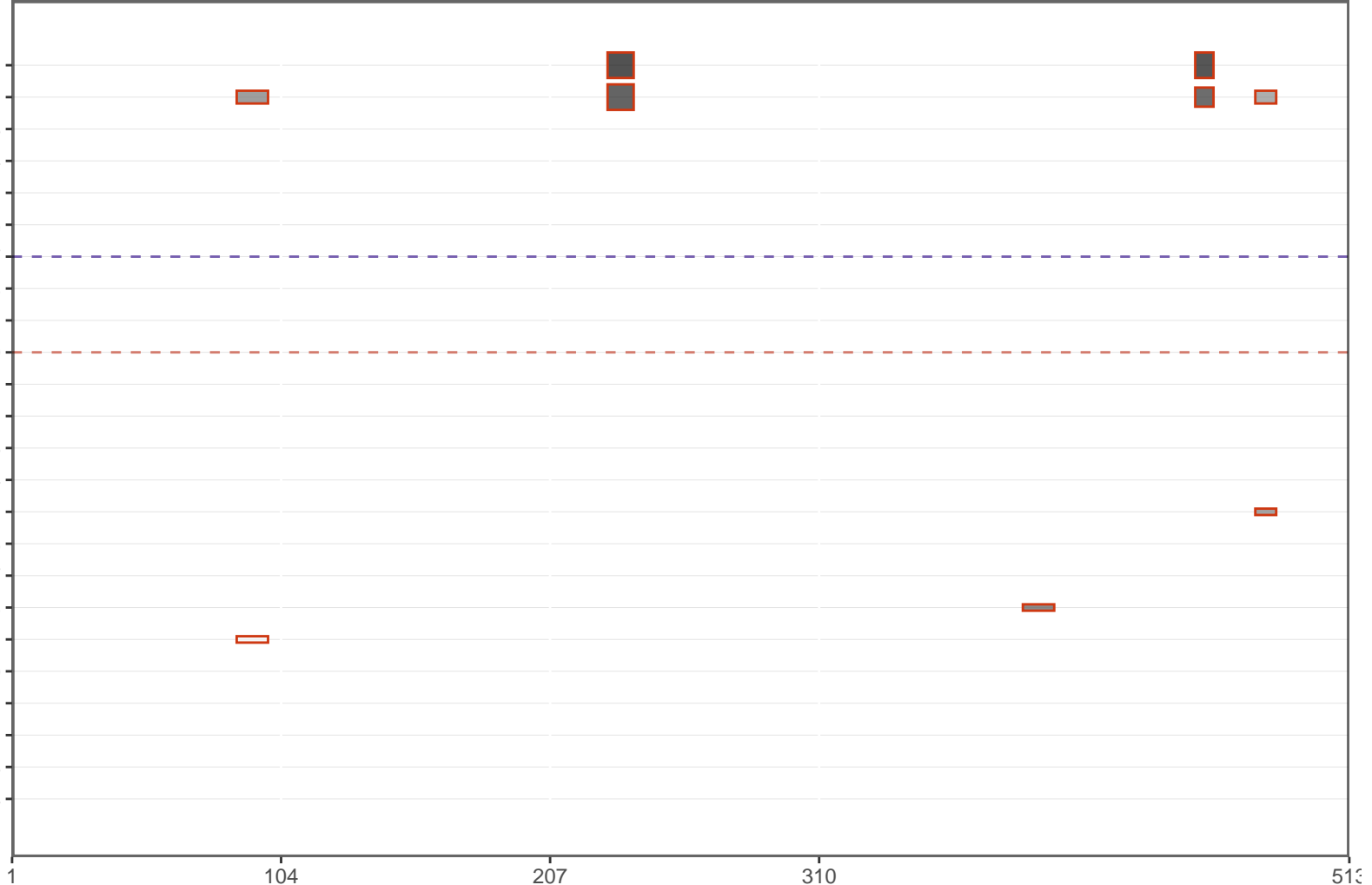
MW indication



Molecular weight



Gel Slice



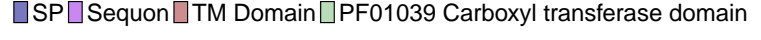
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

1:HLVVOECNYGLNKKFLKSKMNGEGGGYHLKMSSSDRIELLDPTGTDPMDEDMVSLDPIEFHSEEPYKDRIDGVRKTLGTEAVQTGQGLNGIPVAIVDFQFMGGSMGSEVYSEKTRLIEQAAHQILFLIVCASGGARMQEGSLMGMAMHSSALYDVLNKLFLYVSLTPTTGGVTAAGFGLMGDIAEPNVAIFAGKRVIEGTLNKTVPFGSSQAAEYLFQKGLFDLIVPRNLLKGVLSLFLKHAFFPLNKGSKIK

NbL07g17750.1 stromal_processing_peptidase_chloroplastic-like [MW = 140.54 kDa]

No. of times detected



log(intensity)



Values from



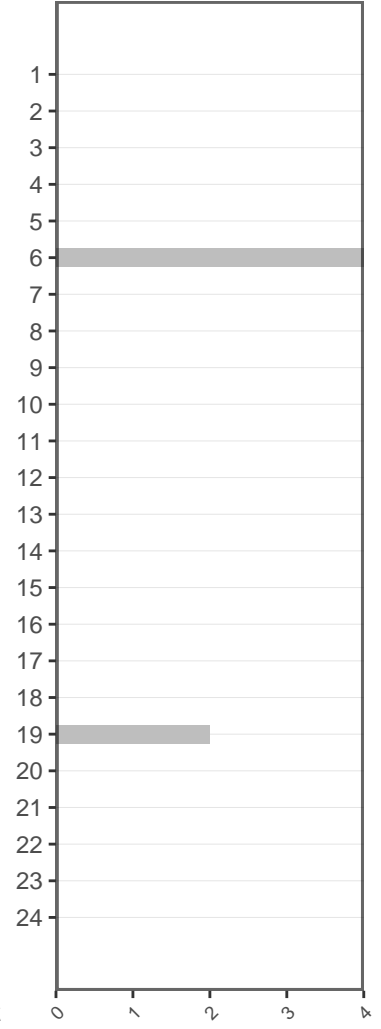
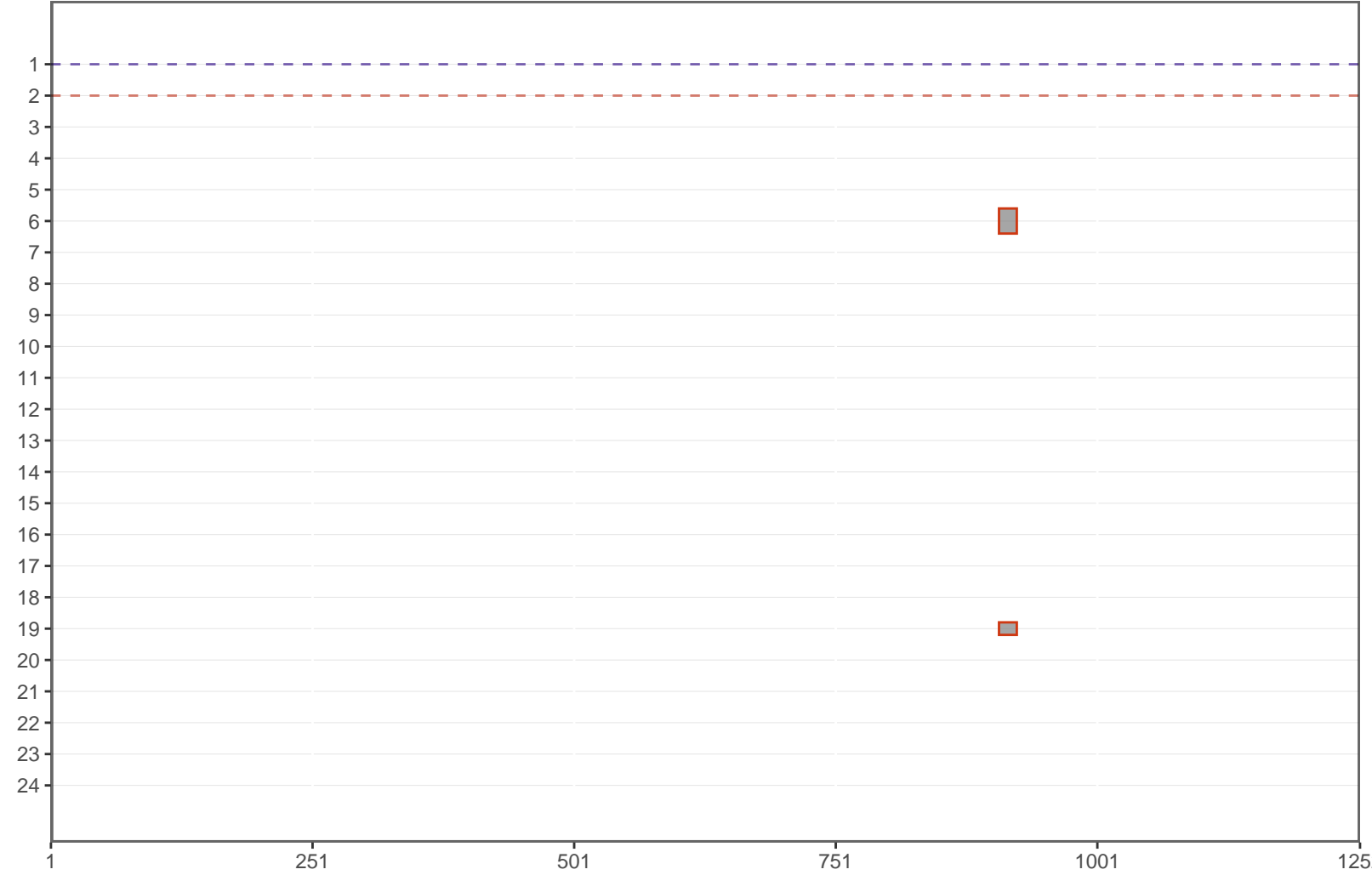
MW indication



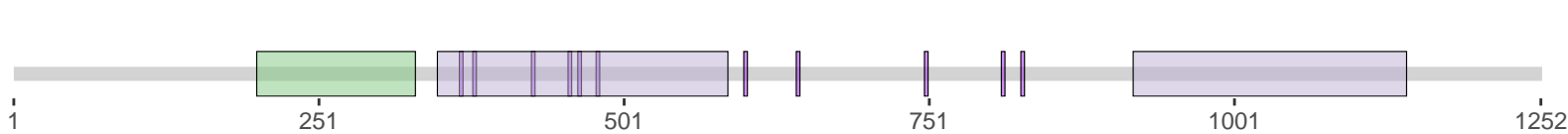
Molecular weight



Gel Slice

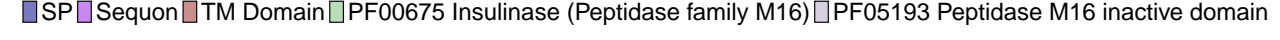


Protein length



Pfam domains

Pfam Description



Protein sequence:

*VMSDALGHITVMDRGRGHESLLIAGITLLEEVNATGAELVYISDFGKPSAPLPAVAACVPSKVVHVDGGGAEFRISPEEITAIISGLKESIEPELEVPTELITLTKLEELLRKRCPSFVPTGNSDVTKSYDNETGVDRRLSNGPILNYKTRNEANGVMDRLVGGGAAESSHKEGIVGVVTRTLEGGGRVGNFRSREGVVELFDVNHLSNGLESTEEFGMEFRFTLRDQAMRGAFOQLLHMVLEHSVWLLDDAFDRAKGLVMBYRSPKSLERSTAHKMLMLMNGD

NbL07g17730.1 acyl_carrier_protein_1_chloroplastic-like [MW = 14.99 kDa]

No. of times detected



log(intensity)



Values from



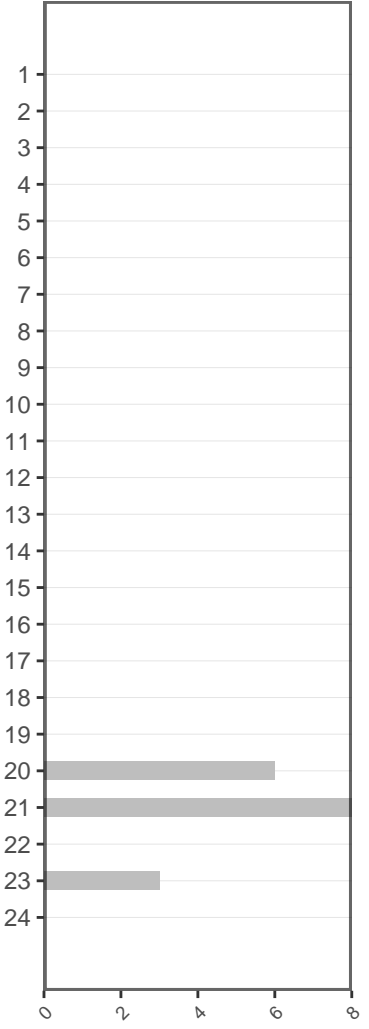
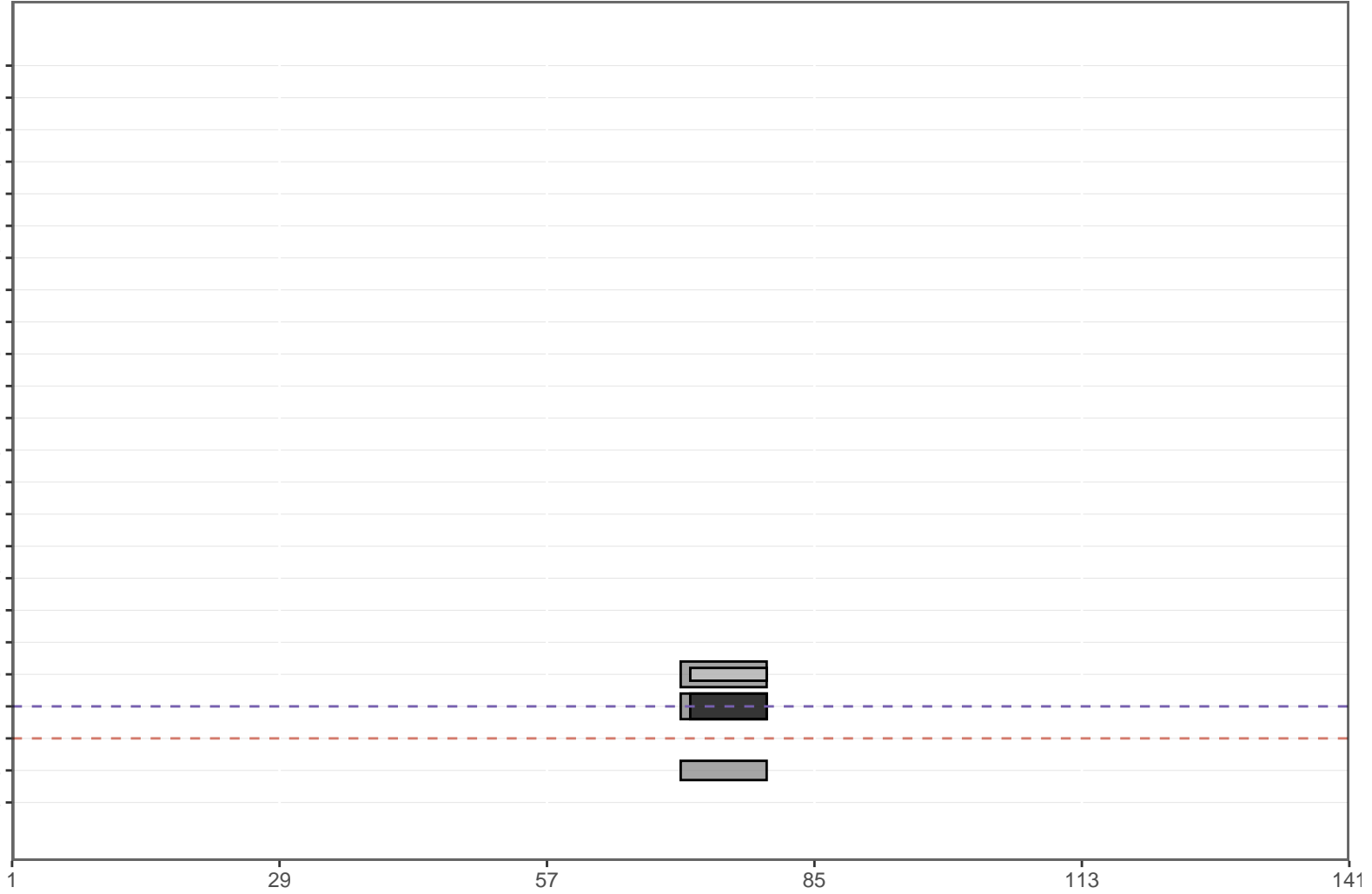
MW indication



Molecular weight

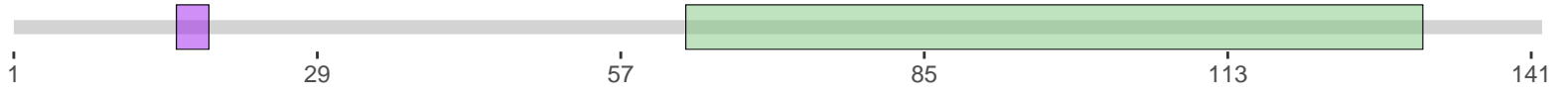


Gel Slice



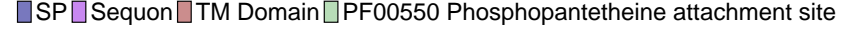
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

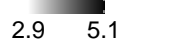
CAKPEYVEKVISIVRKGALPADTKVNAESTFNTDLGADLDTVEIVMALEEEFGIAVEEENSETIVTVDGAAQLIEKLVKKAA*

NbL07g17710.1 serine_carboxypeptidase-like_45 [MW = 56.08 kDa]

No. of times detected



log(intensity)



Values from



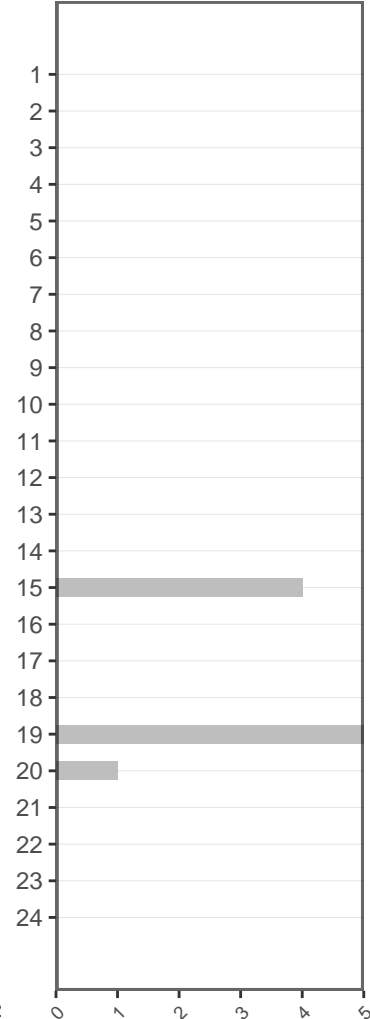
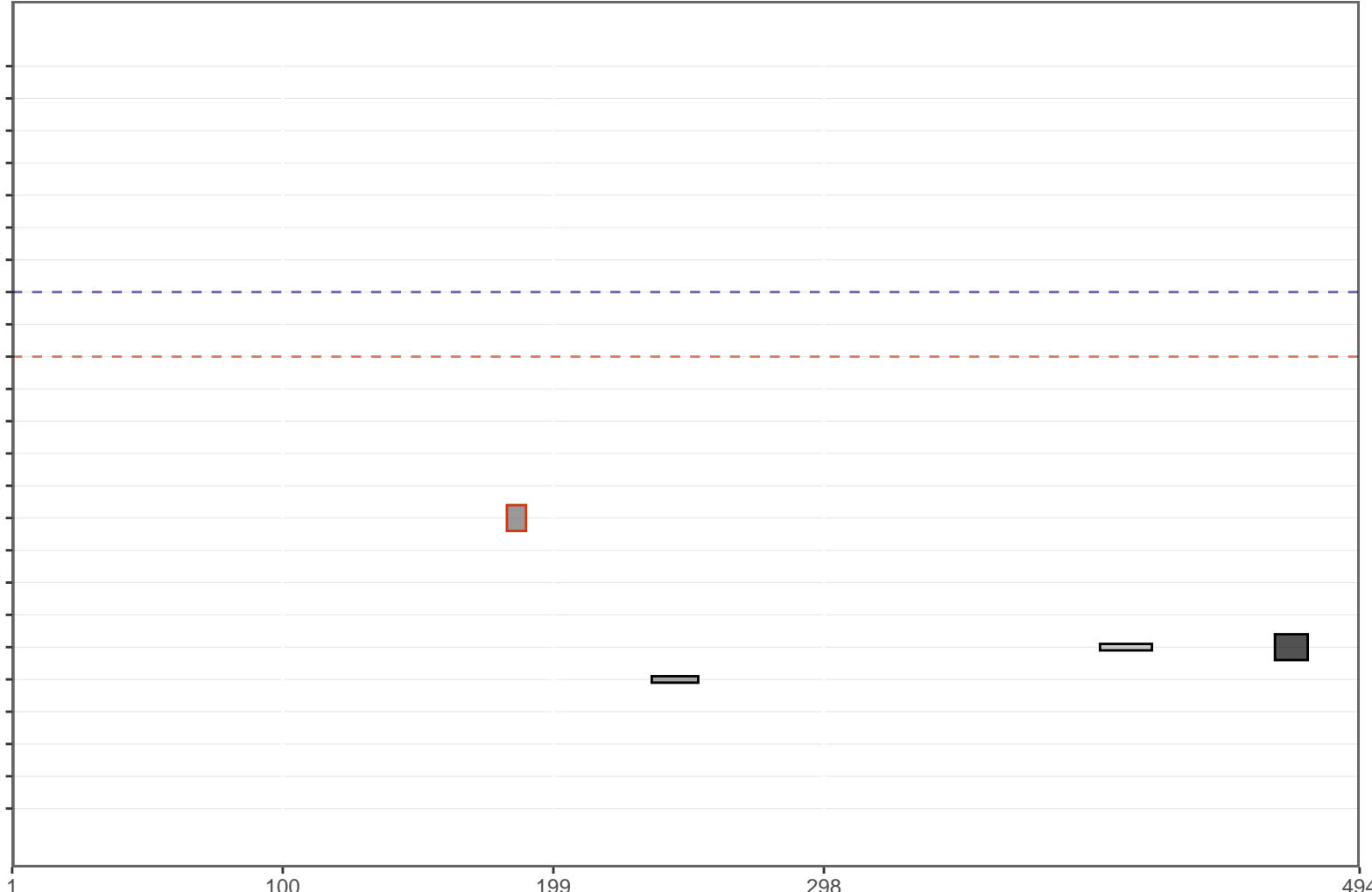
MW indication



Molecular weight

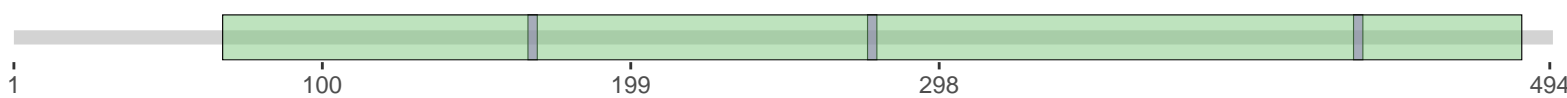


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

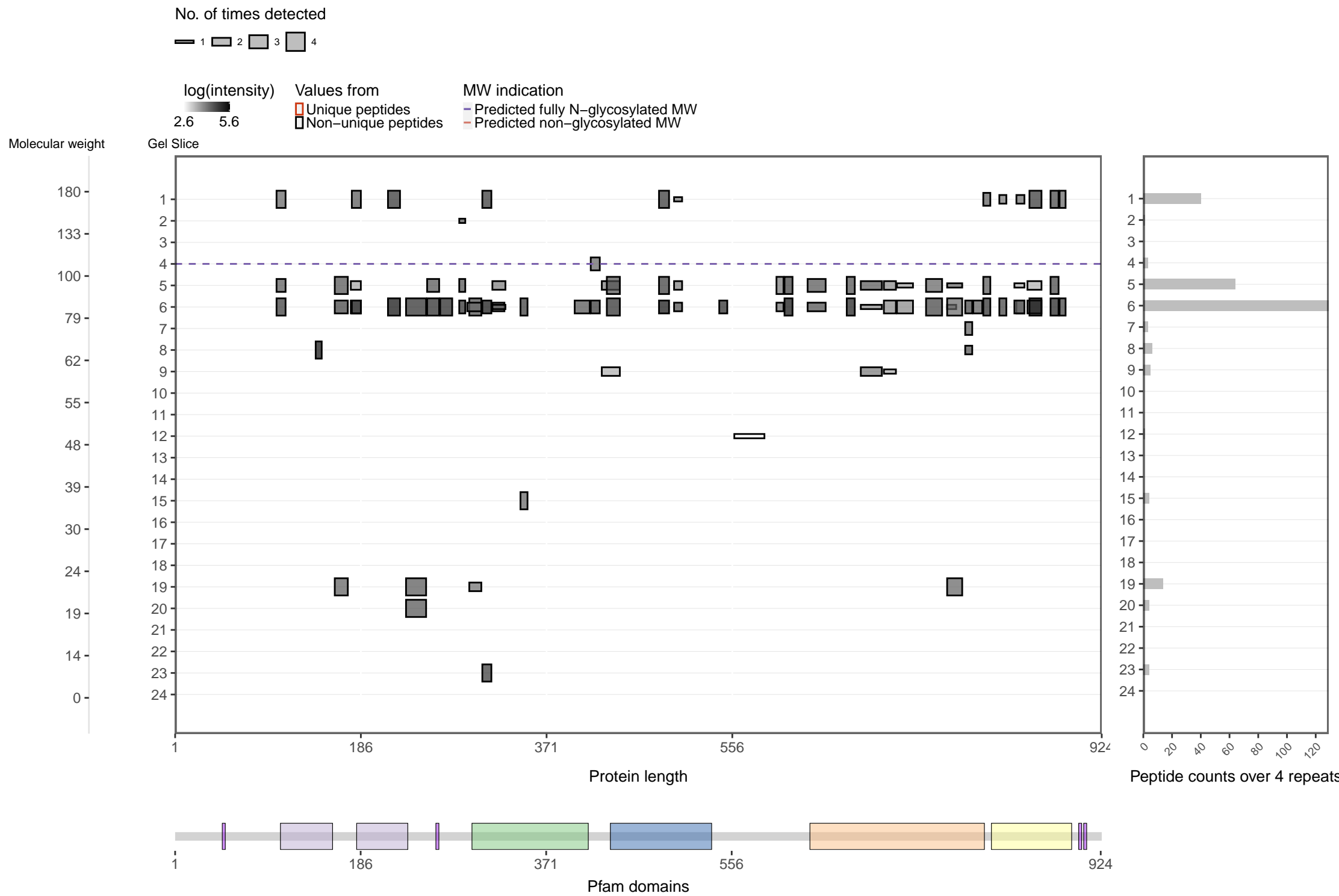
Pfam Description



Protein sequence:

ILKGVALGNPYLEFATDENSRAEYFVSHGLISDPTYRIMFSAQNYRIVYGVGEYRSGSPKSRVMBLVSRETSEFVDKYVGLDVCISVLSGSKHSPQGENVEKLDVGVVEDEINYLNRKQVRRALHAEELVGVRRVWVCSNILDVQLLDIEPTISIGMLVKEIPVLYSGDQDSVPLIGSRATHQLARRMRLNTPVYRWFVAGQGVGGVTHVYDNLFSFATIRGASHEAFFSGPERBULVFKSFLLEGRLPEVP

NbL07g17690.1 ATP-dependent_Clp_protease_ATP-binding_subunit_clpA_homolog_CD4B_chloroplastic-like [MW = 102.37 kDa]



Pfam Description

- SP
- TM Domain
- PF02861 Clp amino terminal domain, pathogenicity island component
- PF10431 C-terminal, D2-small domain, of ClpB protein
- Sequon
- PF00004 ATPase family associated with various cellular activities (AAA)
- PF07724 AAA domain (Cdc48 subfamily)
- PF17871 AAA lid domain

Protein sequence:

YEHKRLRYTDEALEAAAGLGGYHSDRFLPKAIDLIDEAGSRVRLRHAQLPEEARLEKELRGTKEKNEAVRGGDFEKAGELRDRREMDLKAQISALIDNKEMKAESEAGDTGPIVTEADIQHIVSWSFGIPVKEKVTDESDDLKMEETLHTRIGGDEAVKASRAIRRRARVGLKNPNRPIASFIFSGPTGVKGEELAKALAAAYFGSEAMIRLDMSEFMERHTVSKLIGSPPGYVGYTEGGQLTEAVRRRPYFVLFDEIEKAPGVFNMMALQLEDRLTDSKGRTV

NbL07g17640.1 magnesium_protoporphyrin_IX_methyltransferase_chloroplastic-like [MW = 35.24 kDa]

No. of times detected



log(intensity)



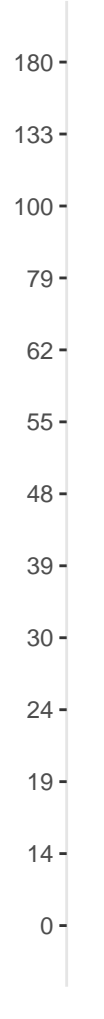
Values from



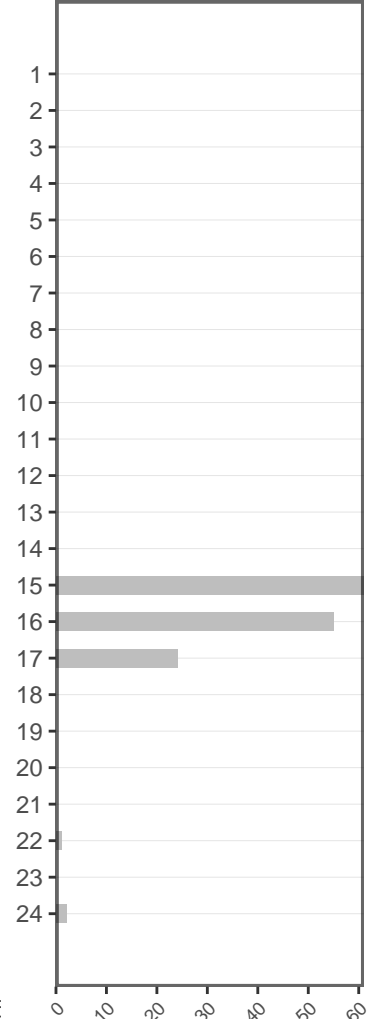
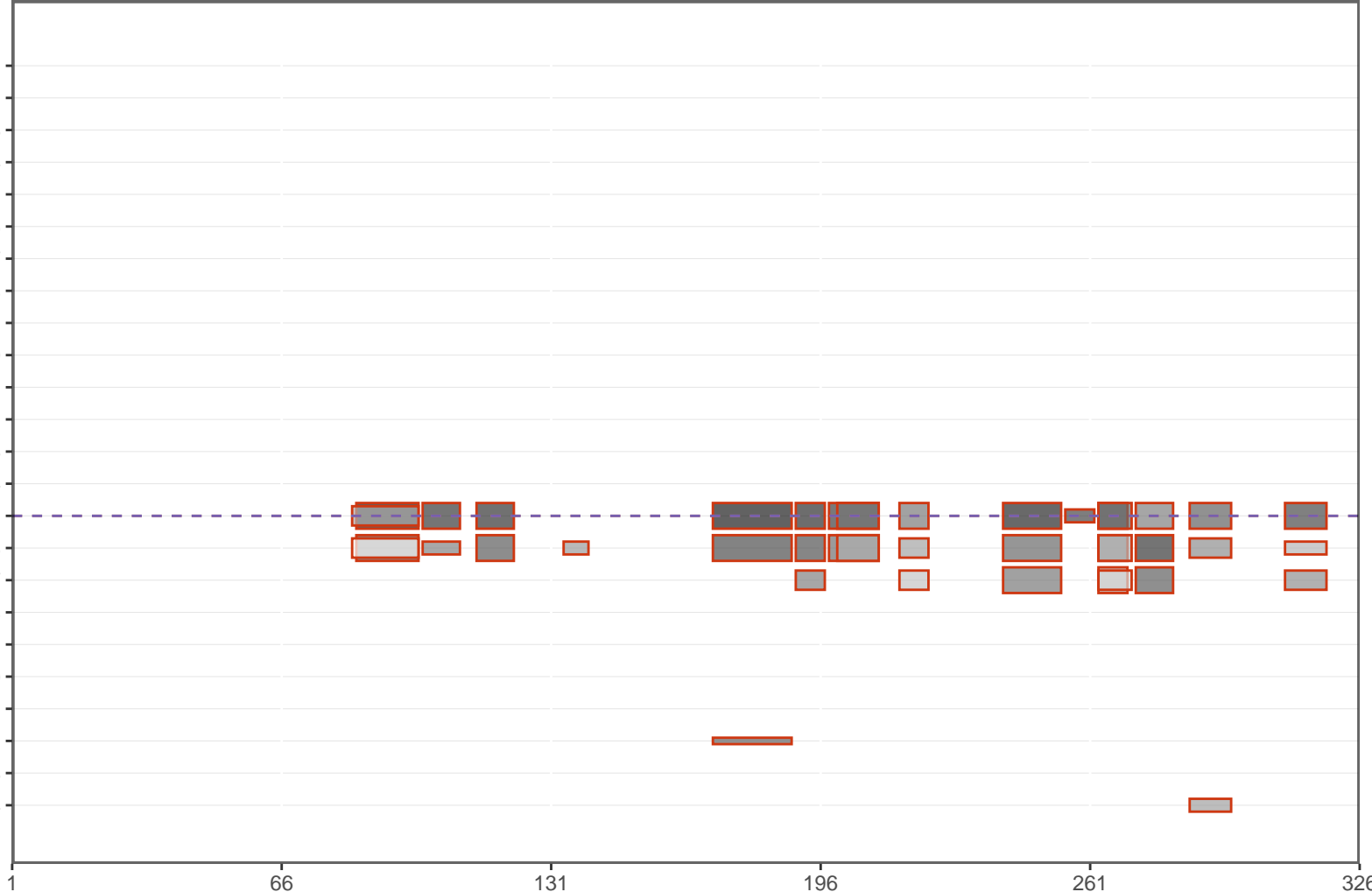
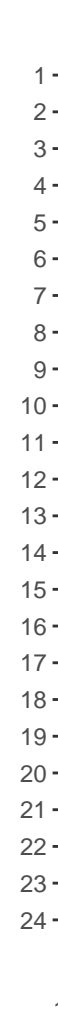
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfm domains

Pfam Description

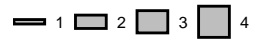


Protein sequence:

DSGVTVYCDAGCCGTGQLSPLAKGAVVSSGDISASMSVAEAKQKGAQEELFKAKDDGSPAPVMPKFEVWDLKESLDGKYDTVWGLDVMHYPQSKADGMIAHLSLAENRLLSFAKFTFYDLLKRIGELFFGPKSKATRAYLHAEADVERALQKAGWRIRKRLGLATQFYFAKLEAVPK

NbL07g17590.1 glycine--tRNA_ligase_1_mitochondrial-like [MW = 70.13 kDa]

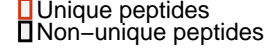
No. of times detected



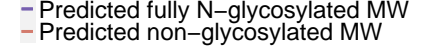
log(intensity)



Values from

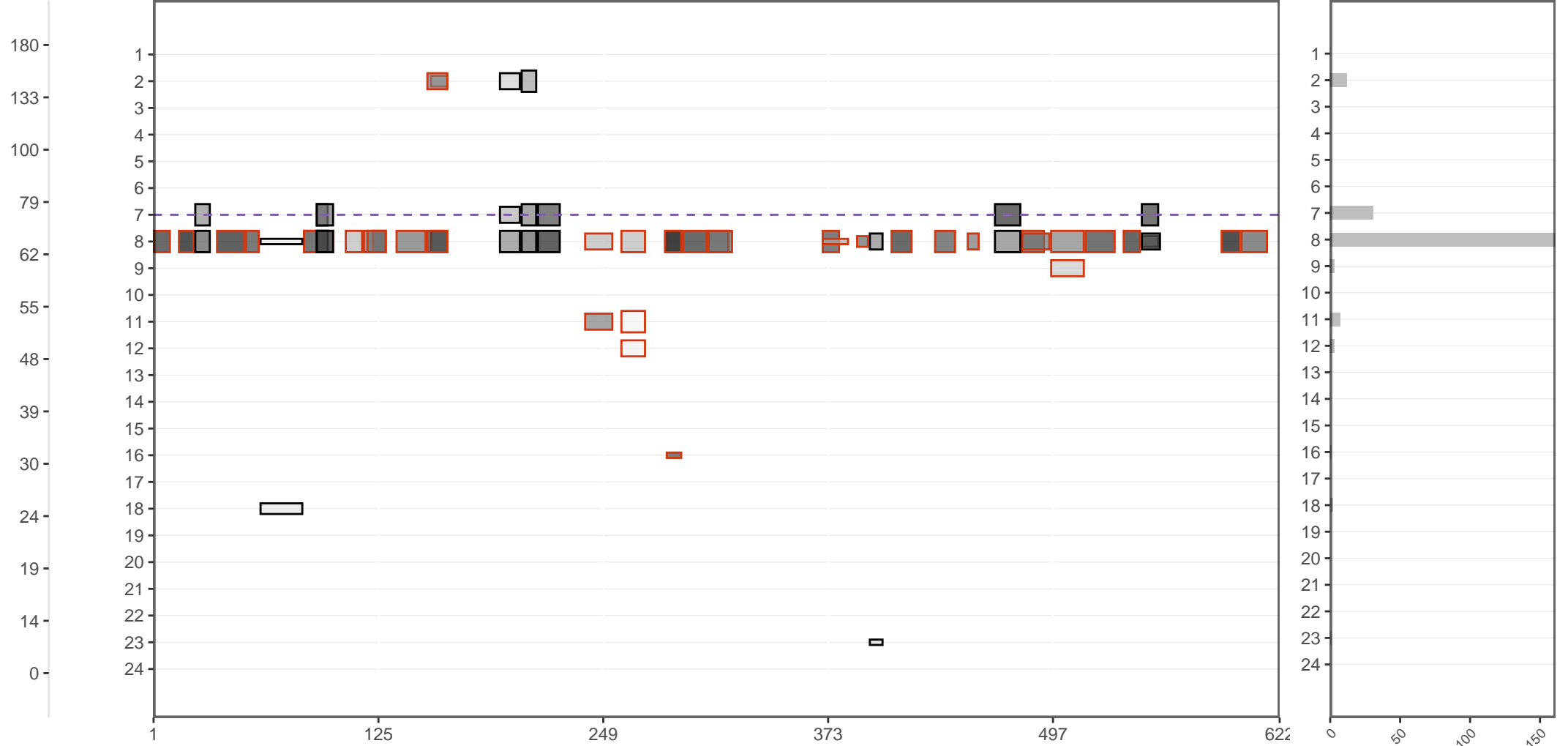


MW indication



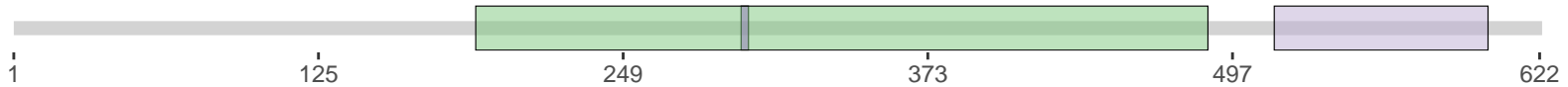
Molecular weight

Gel Slice



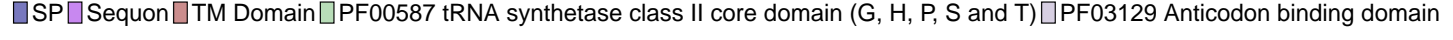
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

INETLQYFGRVYLFTHLGDGDKDLRFRRHLANEMAHYADQWDAEIEGSSYGVWEGVGSADRBAYDLRAHTKSGVPLVAHEKFPPEPREVEKLIITPAKKELGLAFKGNQKMWLEALEAMGEKEAMEMKATLEKGEAEFVCTLDRIIVANKNMVBIKEMKKEHQRVFTFPIVIEPFGIGRIYGLYEHFNTFRPSRDLGDEGMNFFSFPPIVAPKIGTVFPLVGNQGVYEEVARQIARLSTAYGISYKIDTGTSGKRYARTDELGVFFATVDSTSSVTIRERDSKQIIRVNYDE

NbL07g17560.1 uncharacterized_LOC107786132 [MW = 17.64 kDa]

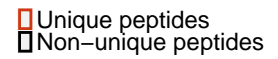
No. of times detected



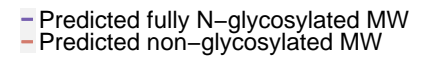
log(intensity)



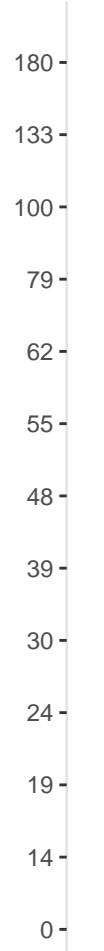
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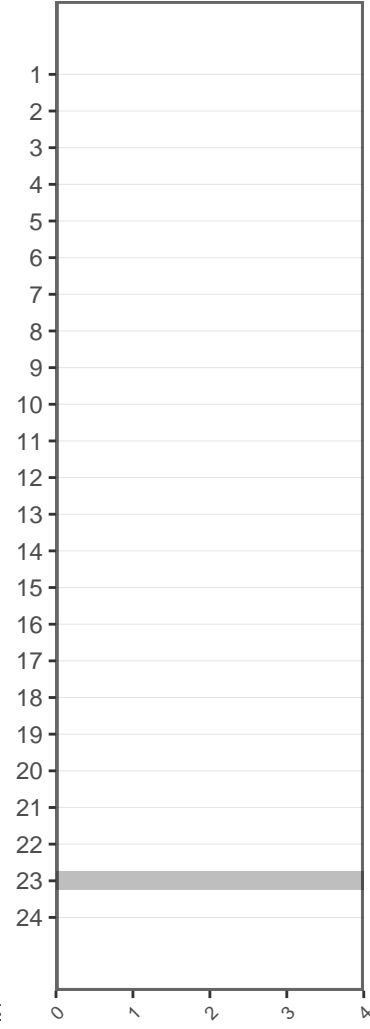
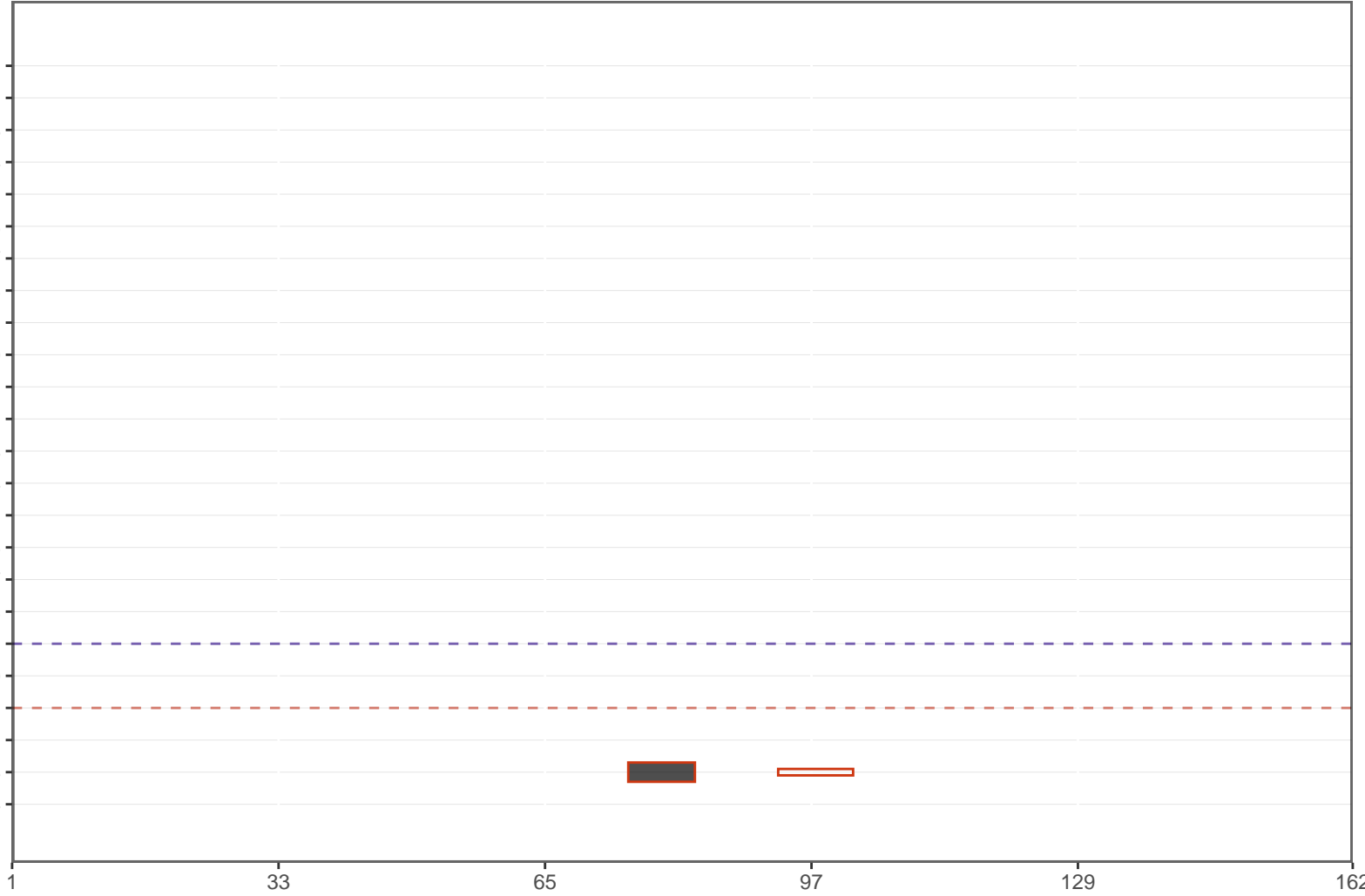
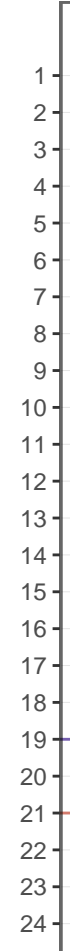
MW indication



Molecular weight



Gel Slice



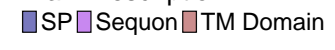
Peptide counts over 4 repeats

Protein length



Pfam domains

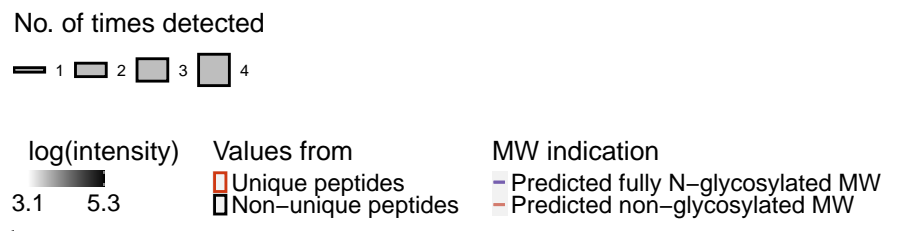
Pfam Description



Protein sequence:

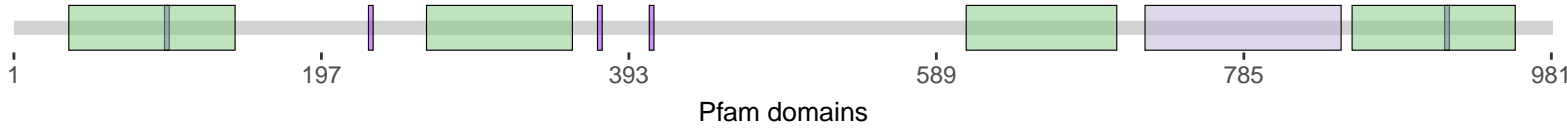
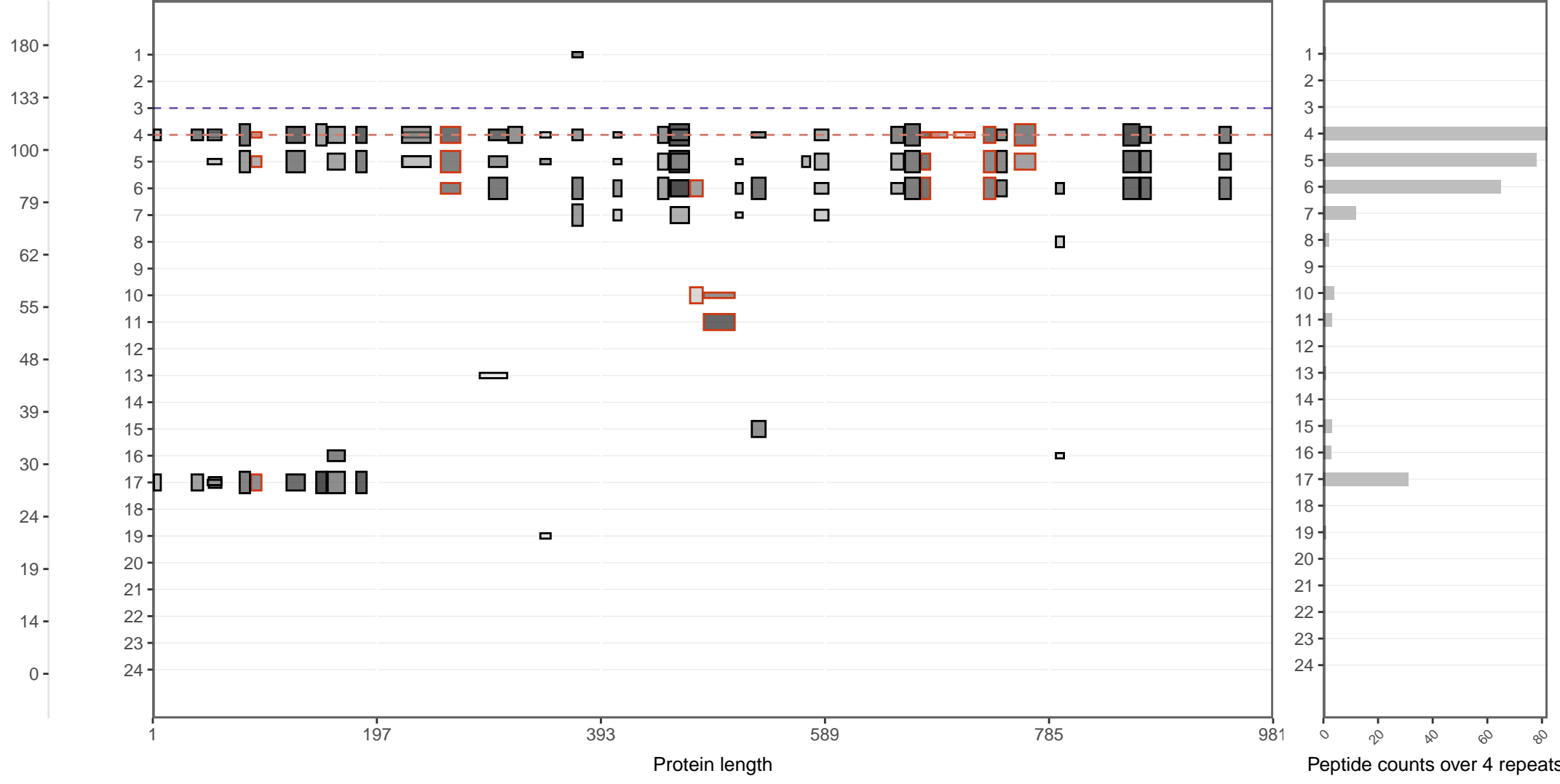
QAYICRDCGYYINRITFFKQPKYFQPVGAPKRRFRSVEPKVTKDANSTEVKARKEGLKRDSEIGNALPIAGVGVWLAALYFYVNNSS

NbL07g17510.1 staphylococcal_nuclease_domain-containing_protein_1 [MW = 107.79 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00565 Staphylococcal nuclease homologue
- PF00567 Tudor domain

Protein sequence:

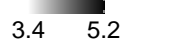
FLASKGGDDASPAAGAGNGLAGVWVWELLVVRGFATVVRHRDFEERNVYDALLSAESRAISGKKGKMHPEKPPVMMVTDLLAGSSEKKAQDFLFLQNRNRMSAVVEVYVLSGHRFKLFPKFKETGIAFSISGVRGPRDRDEPYSSEAAIMRRRMRGRDVEIEVTVORTGTLGTLWESRKNWVTLLEAGLARLQTSFGTDRIDHAHLLMGAEGAAKQKLVKVENVVEGEEVANGAAEKRQKEEVVTVTEIISGGKFPVGLVSDGKVAIQKGLASLNLOEAPVGA

NbL07g17500.1 glutamyl-tRNA(Gln)_amidotransferase_subunit_A-like [MW = 69.08 kDa]

No. of times detected



log(intensity)



Values from



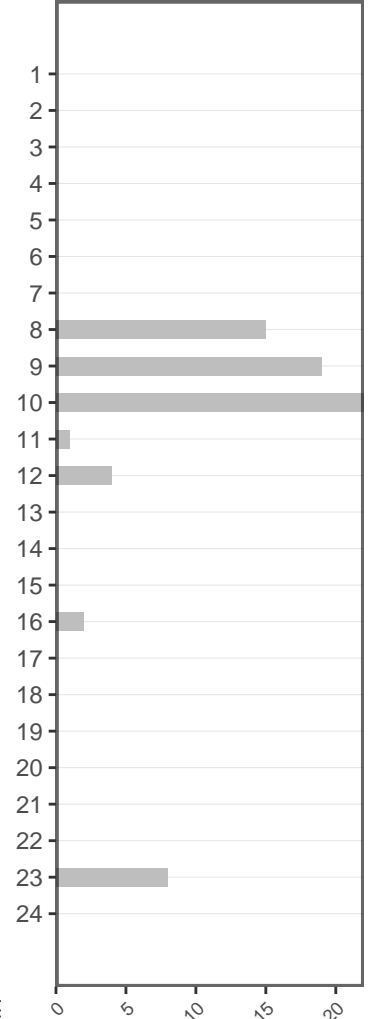
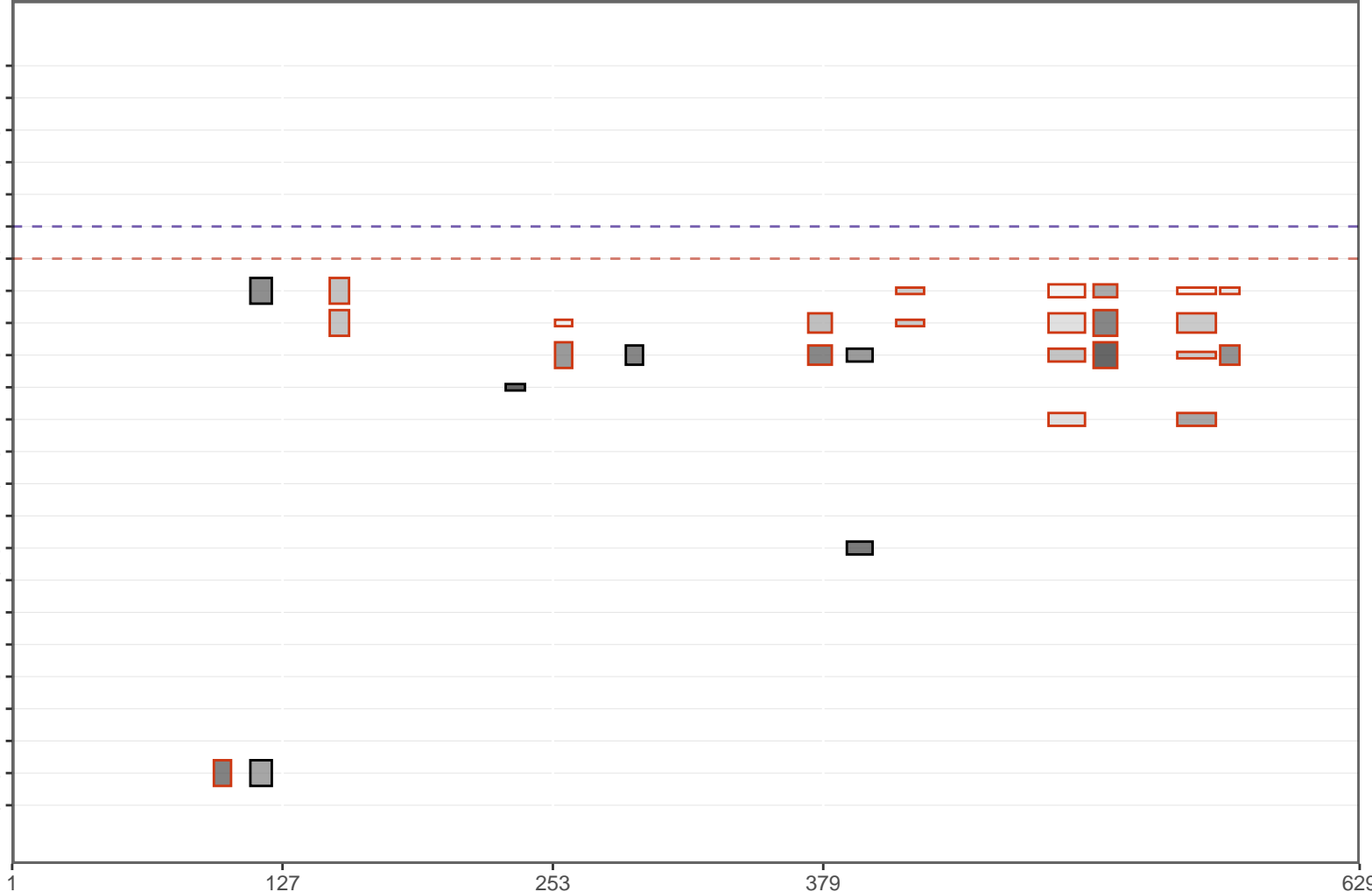
MW indication



Molecular weight

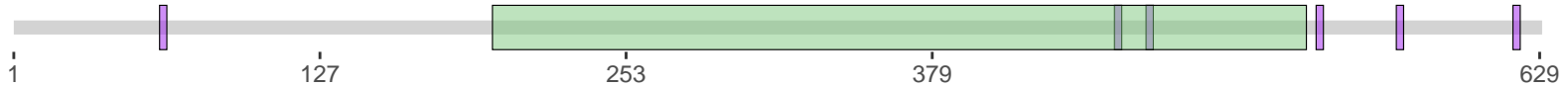


Gel Slice



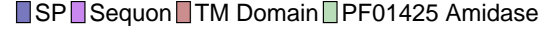
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IDDVWFGRTRINPWNKEYSTGSAGAPSGTSGAGLIPFAIGSETTGSITFYASRGGVTLRPTFGAVGRITGVMSVAEGLDKLGFGRNAVDCVLDITRIGKDPDVSRRDIPFSDPFVDAKLTGVYLEDVEMVHVLGSGKGVNMPFNLSVTVDSAGQVWFTMDVEMLAHFDKWRGRNLDDEVEAGDDQWPIELRRARVAVDVYLGAGRARGKLVGVRESFRVDFRGNATDWEKVCVGNLVGIPVAVVPTGFRKKISDAPSNDRTRRTITTTGGVAPPDRDHALAL

NbL07g17460.1 inositol_polyphosphate_multikinase_alpha-like [MW = 33.53 kDa]

No. of times detected



log(intensity)



Values from



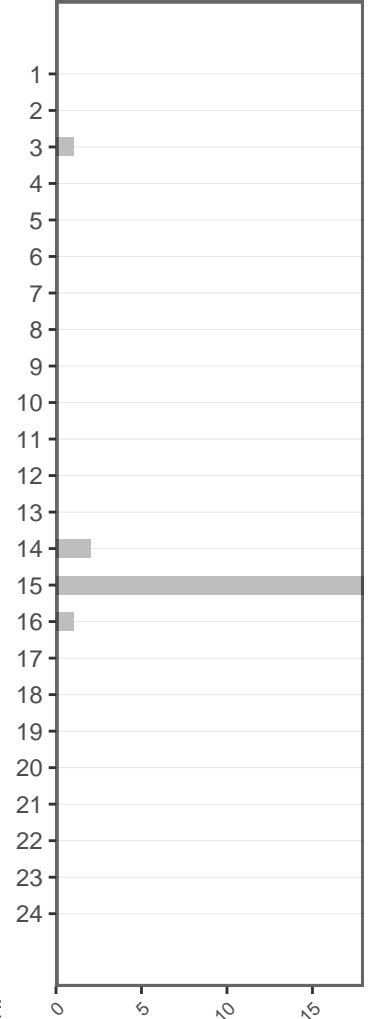
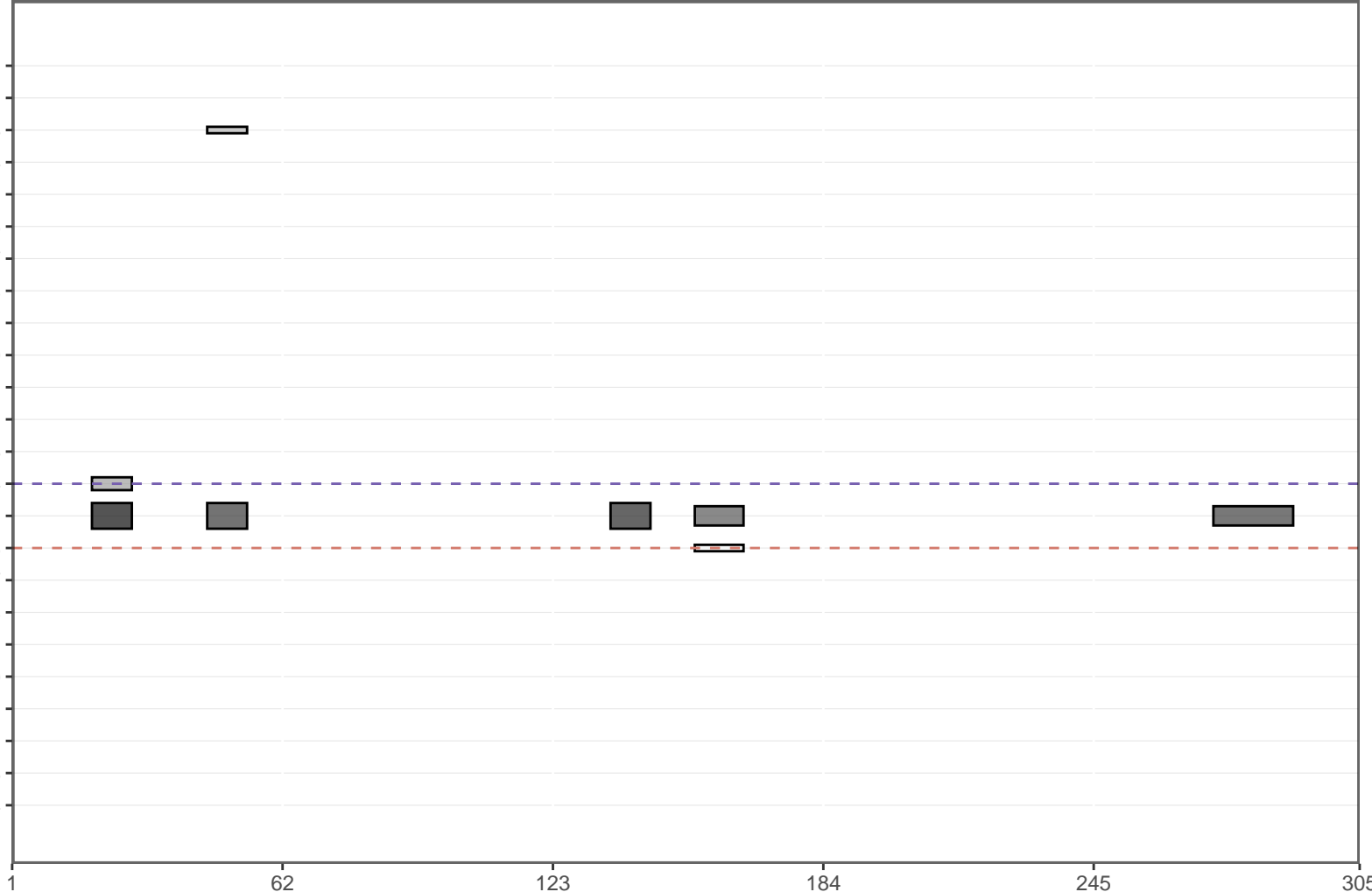
MW indication



Molecular weight

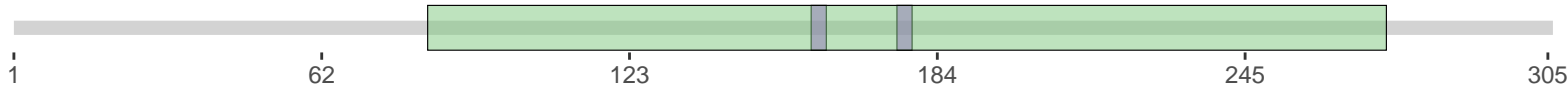


Gel Slice



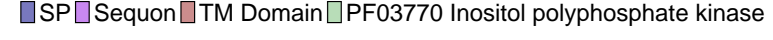
Protein length

Peptide counts over 4 repeats



Pfam domains

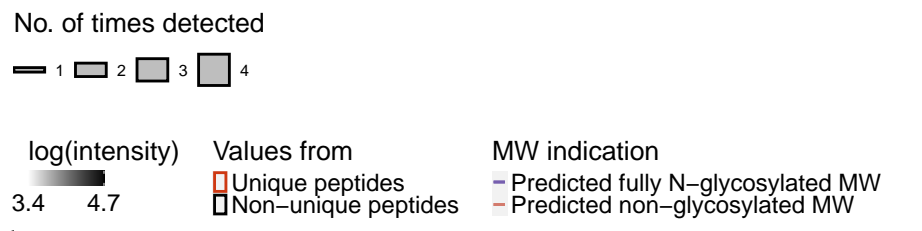
Pfam Description



Protein sequence:

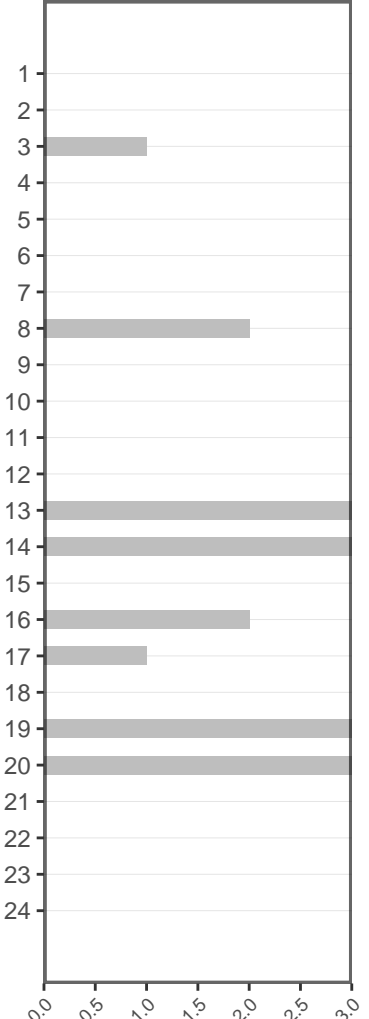
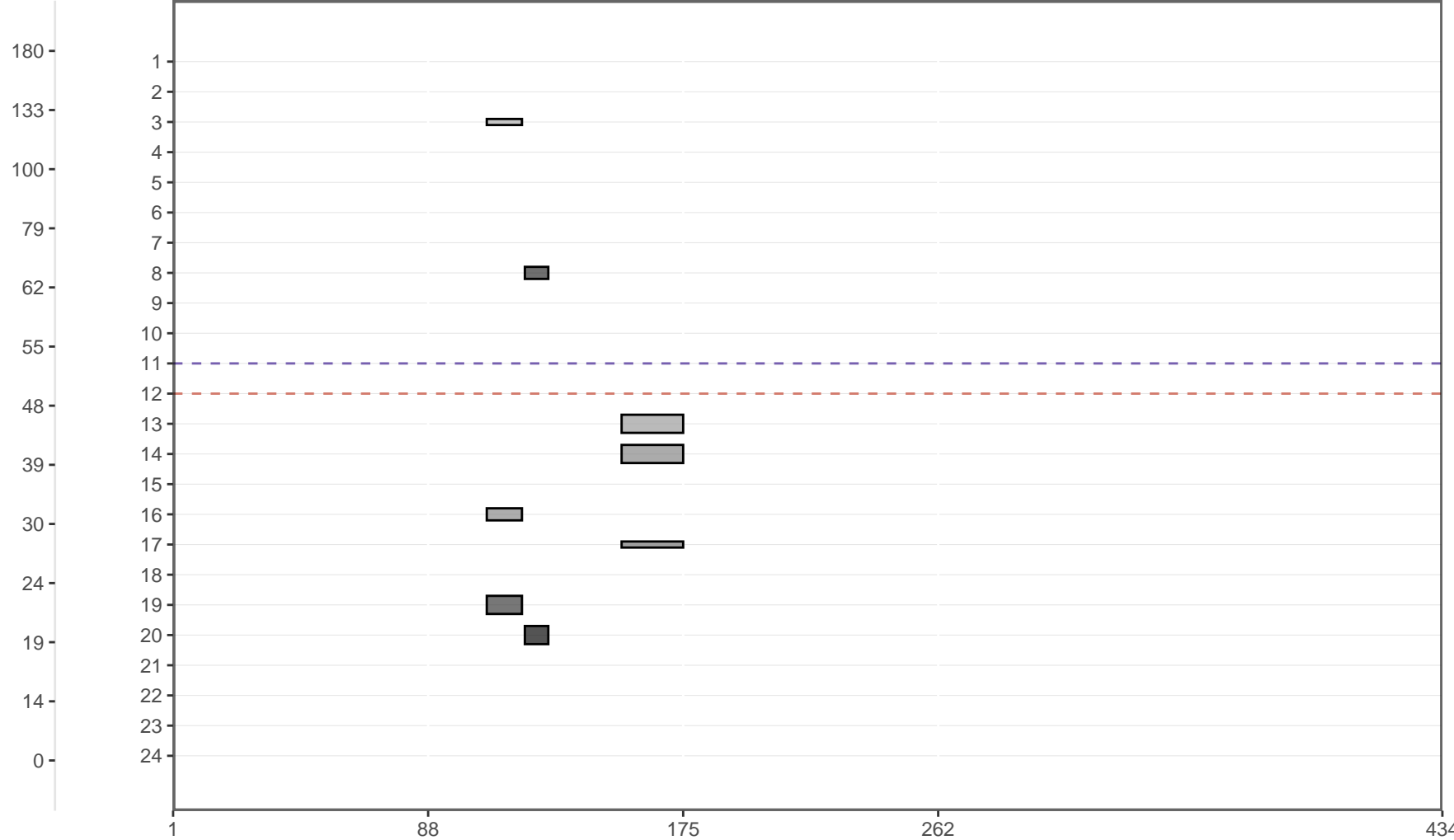
GIQIYQNKESGYIWKPERTSISGLSAEEVRLIKKFKFVSNASTDSLEPDCGAAATVYGGSTGLGQLLELKAWFEDQTMHYEYSGSLITFEKELALEGNPCGAIKILDFAHVSEGRGVDHNFVGLGLGSLIKFISELTPNEHTTEVSSKPDHNLISGDSNVN

NbL07g17430.1 multiple_organelle_RNA_editing_factor_1_mitochondrial-like [MW = 48.38 kDa]



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

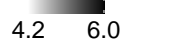
IGNYGPPQSPFQGNFPPQGFAPGLNFGPPQGFAPGQNYGAAGPFPQGNVAAAGPFPQGNVGGPRVYFPQGNVGGQYFPFPQGNVSAFQGFQGNVGRPNPLPQGGYSAFQGNVPSQWNHGFQGGFSPQGNVGGQAGDPWHGTPLGSGPQGNVNSGGGRQDSRQYQVNYNGEGGNYSPQRDRHGVAPEERGRFRGDNQHYAPPEQRGFRGDNQR

NbL07g17340.1 ACT_domain-containing_protein_DS12_chloroplastic-like [MW = 30.99 kDa]

No. of times detected



log(intensity)



Values from



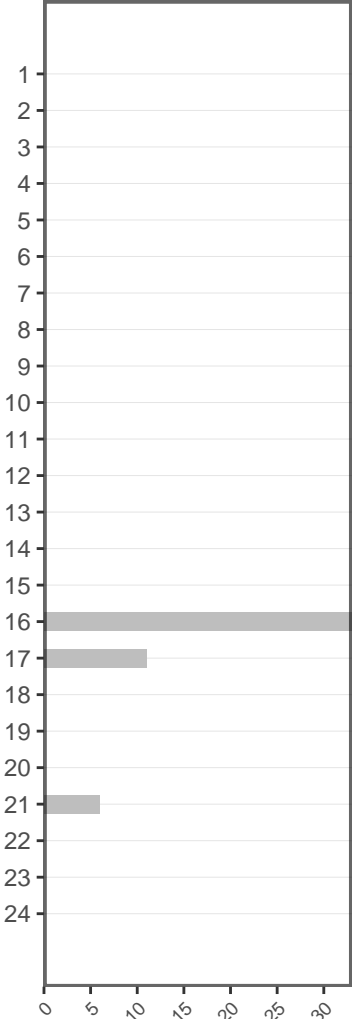
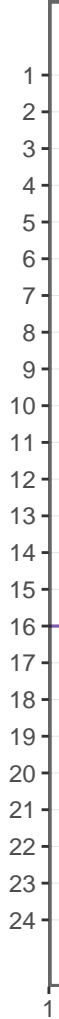
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

ISGKHITLCTINASTGRKVDQPEGLAERLTHINMIEFHPESBALLAMGEVFGAYQNEKLDVDIATHIKVYDDGPRRLVVEAADRPLGLVDLWRIEINIDVESGEFTEGLLAKAKFHVSYKNKALIKPQGVLANSLRYLRRPTTEESSEF

NbL07g17330.1 4-coumarate--CoA_ligase_1 [MW = 59.83 kDa]

No. of times detected



log(intensity)



Values from



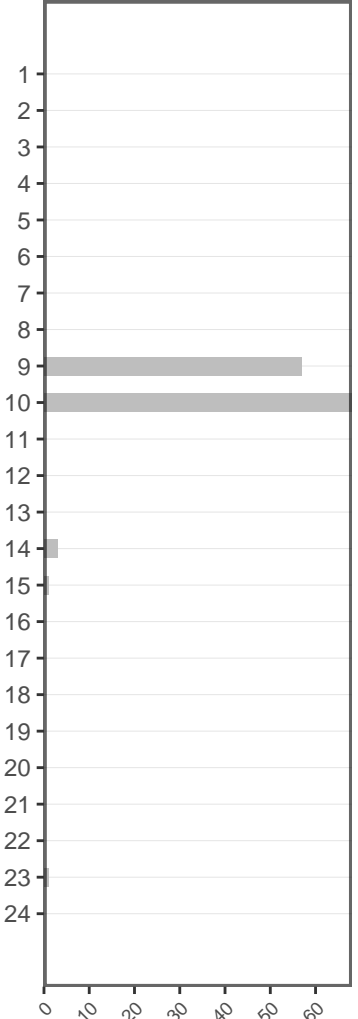
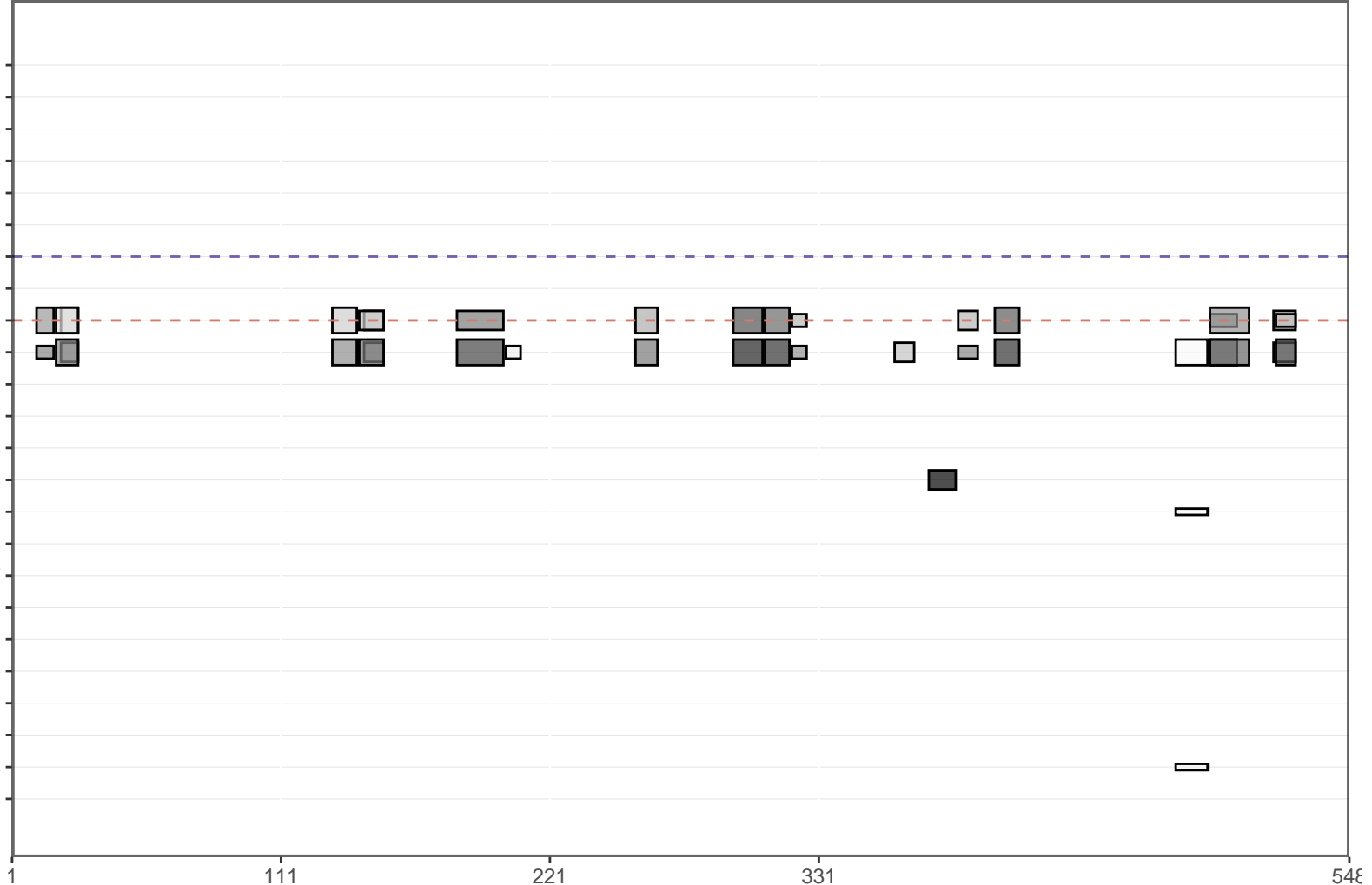
MW indication



Molecular weight

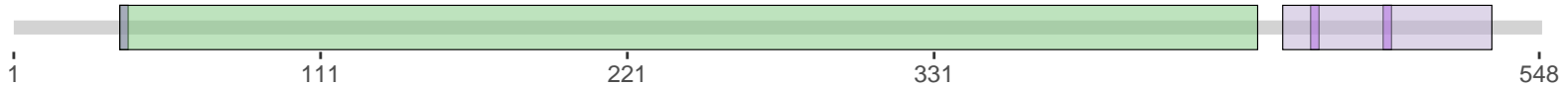


Gel Slice



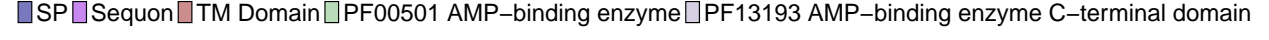
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

VQKFDIAPFLLEIQKYYKSGIPFVPPVLAIAKSPVDSYDLSSVVRTVMSSGAAPLKELEDVWRKTFPNAKLGQGGYGMTEAGPVLAMCLAFAPKPFDKSGAGGTVVNRNEMKIVDDPTGGSLPRNGPGEIGRIGDQIMKGYLNDPEATRTRIDKEGWLHTGDGDFDEDFVDRLKEIKYKGFQVAPAEIALLNHPNISDAAVVPMKDEQAGEVFPVAVVRENGSATEDEKDFVSKQVIFVYKRVRFVETVYKSPSGKILRDKLRARLAAGVFN*

NbL07g17240.1 uncharacterized_LOC107804369 [MW = 33.72 kDa]

No. of times detected



log(intensity)



Values from



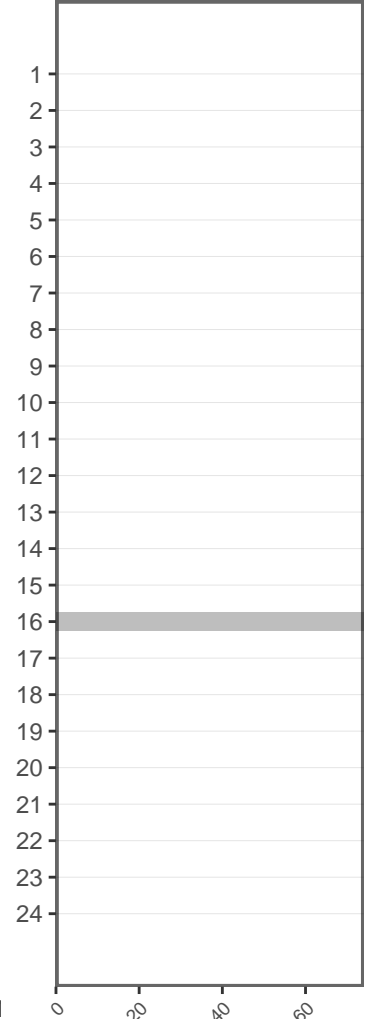
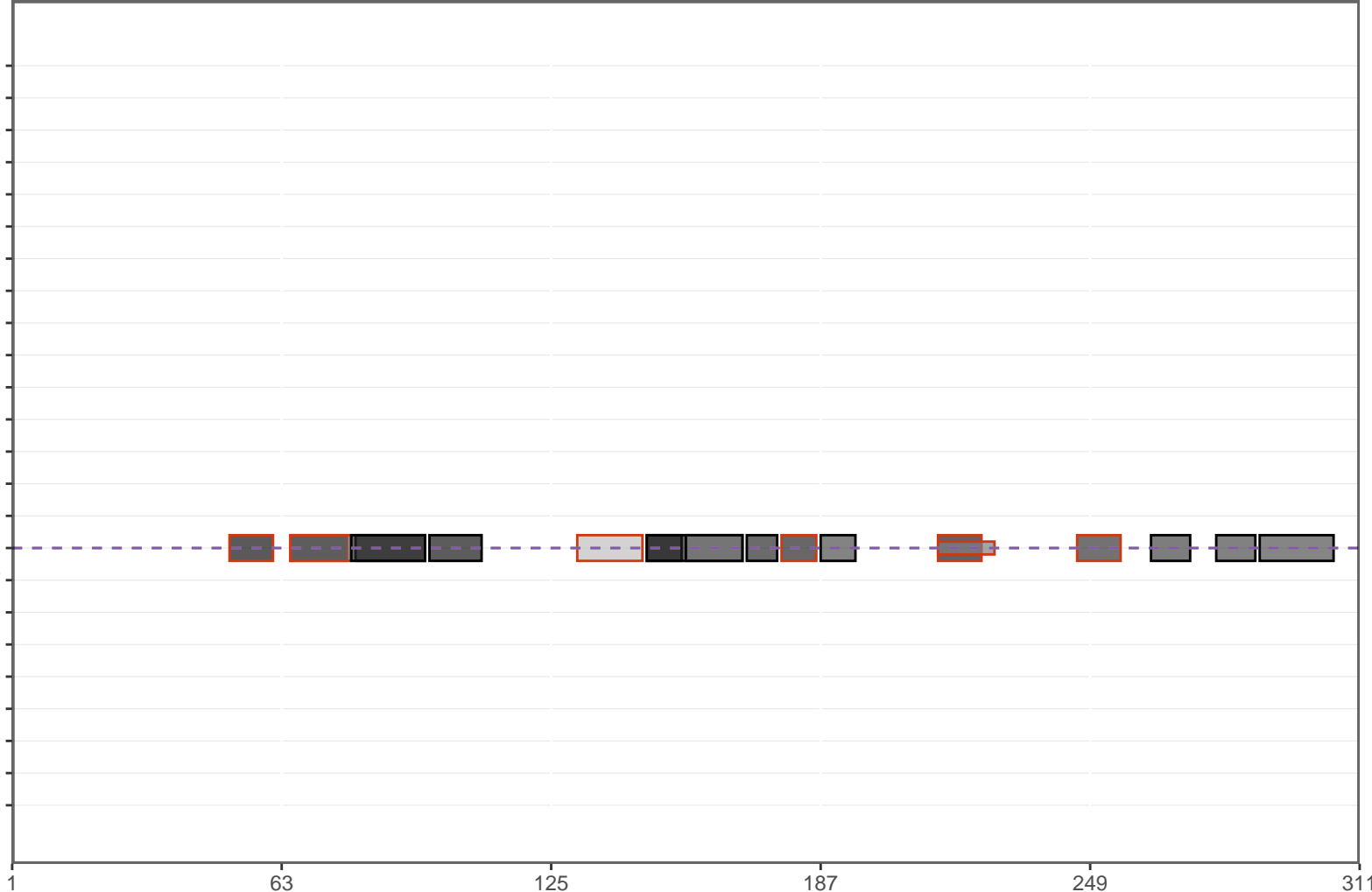
MW indication



Molecular weight

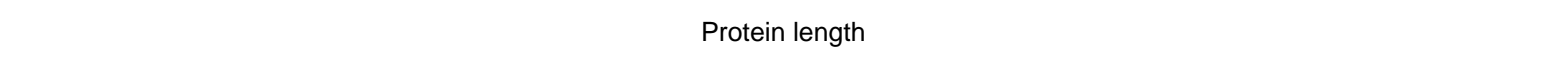


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description
 SP Sequon TM Domain

Protein sequence:

VSKLGEPTDQKTDNPEGLTAAYGKWBAAVRLQDTGLGSKVLEKFFQKMLEKLIWIGAFMLVGRHPGATVGAIVEKEYRSEVSGLIAELAAAAAEEKLVFEDAMEDRLGAVSRVAHFPTAVKEFKWRNGWPFYSLSEKAIAGEKPDPCPLHTAWLKEKIV

NbL07g17110.1 lamin-like_protein [MW - SP = 15.84 kDa]

No. of times detected



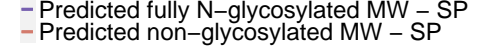
log(intensity)



Values from



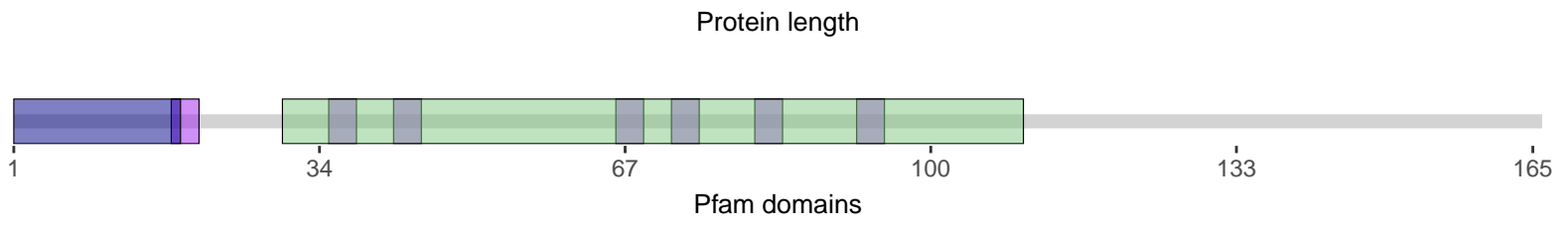
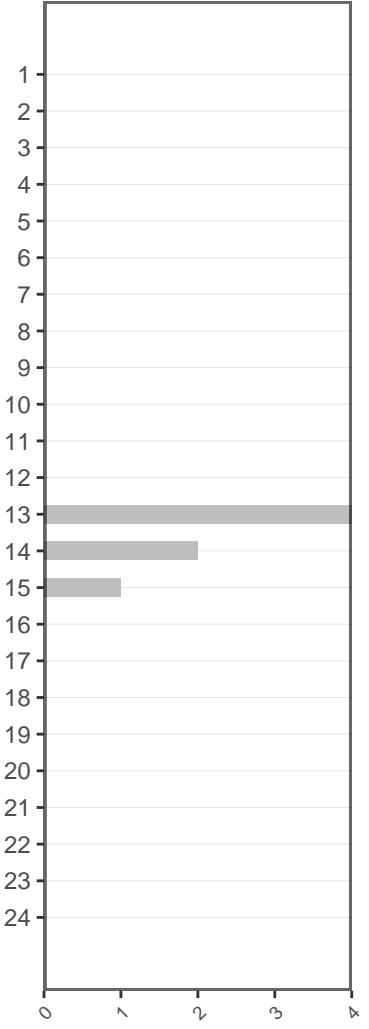
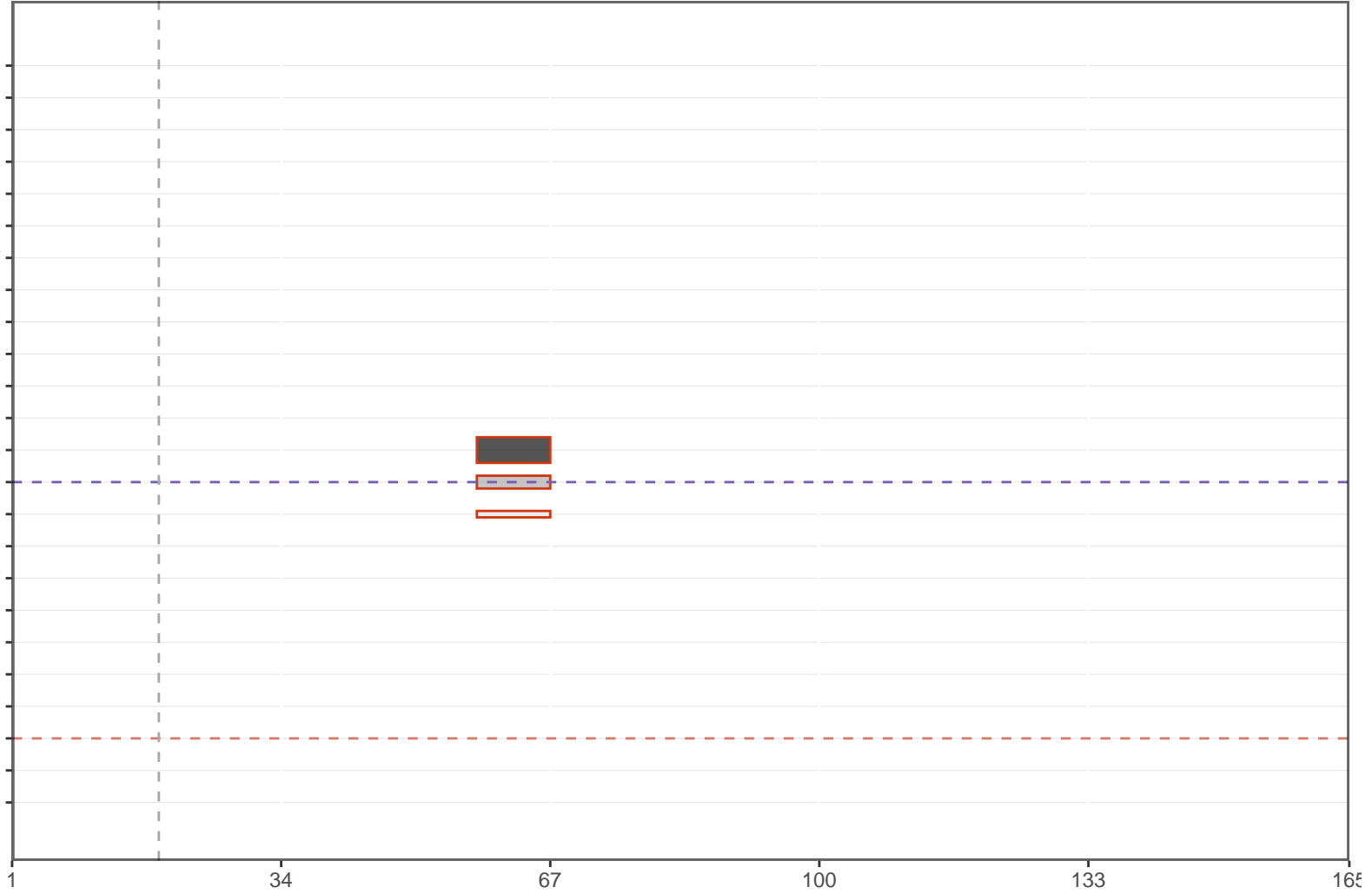
MW indication



Molecular weight



Gel Slice



Pfam Description

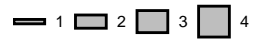


Protein sequence:

DNCTTEGALGNVFGGKDFIMLNKTRYYFIGTGGGLNGMKVWVWHPLEPSPKKAISAHSHSKSAAPVAARGFGLLMSFALGLTFSWVI

NbL07g16940.1 proline--tRNA_ligase_cytoplasmic-like [MW = 57.17 kDa]

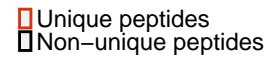
No. of times detected



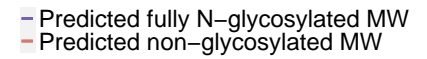
log(intensity)



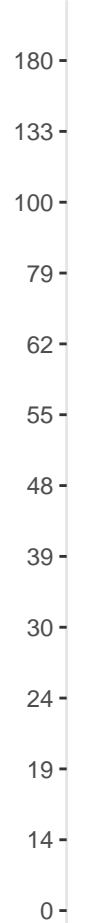
Values from



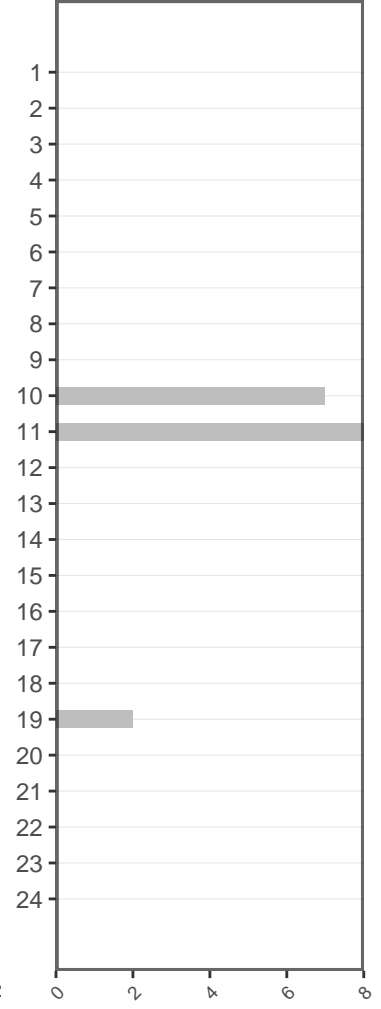
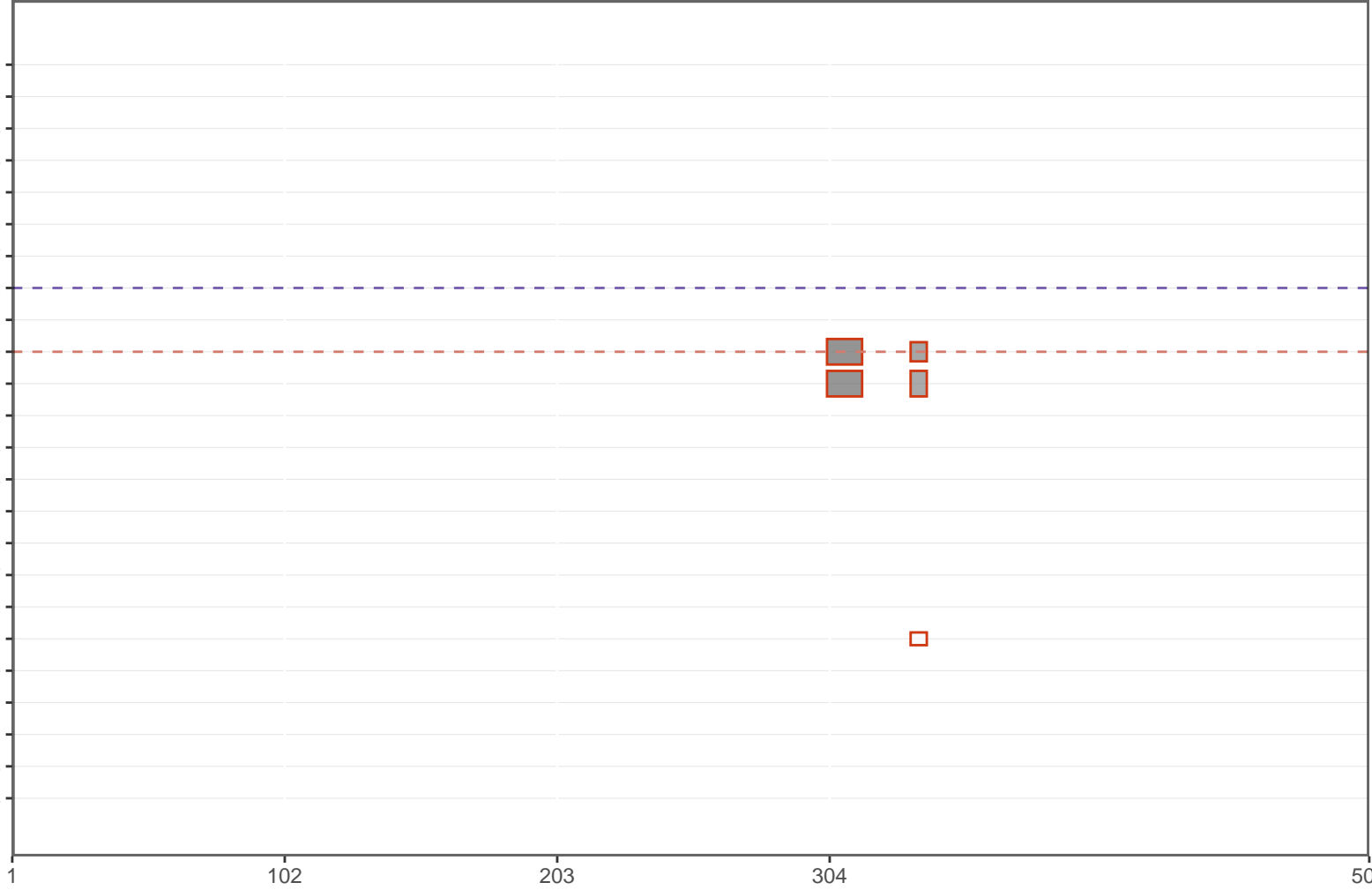
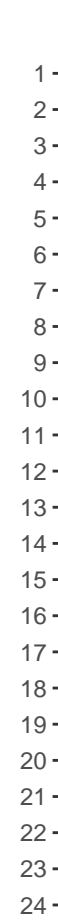
MW indication



Molecular weight

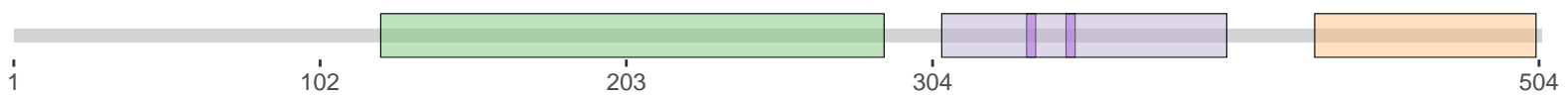


Gel Slice



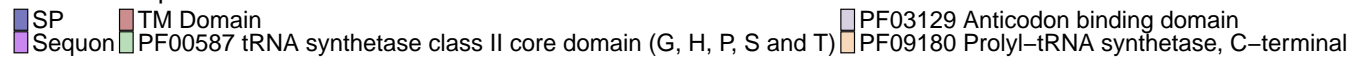
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

30GATSHCLGQNFAMFENFENEKGEKAMVWQNSWYTRTRTGVMIMVHSDDKGLVLPKVASQIVVIPPYKDNANTGGIFDAGATVEKLNESGRRAEADFRNYSPOQWKYSHWEMKGVPLRIEIGPKDLANNQVRAVRRRNGAKADIPMDNLAEGLEVLATDGNLFDVWAKGRDAGVQVVRTWDEFTVALGQKKLILAPWQDEEDEVKDKVARTKGEKGAATLGSFDDQPELPEGTLCFASGKPKMKWYVWGRGV

NbL07g16930.1 50S_ribosomal_protein_L3-2_mitochondrial-like [MW = 32.61 kDa]

No. of times detected



log(intensity)



Values from



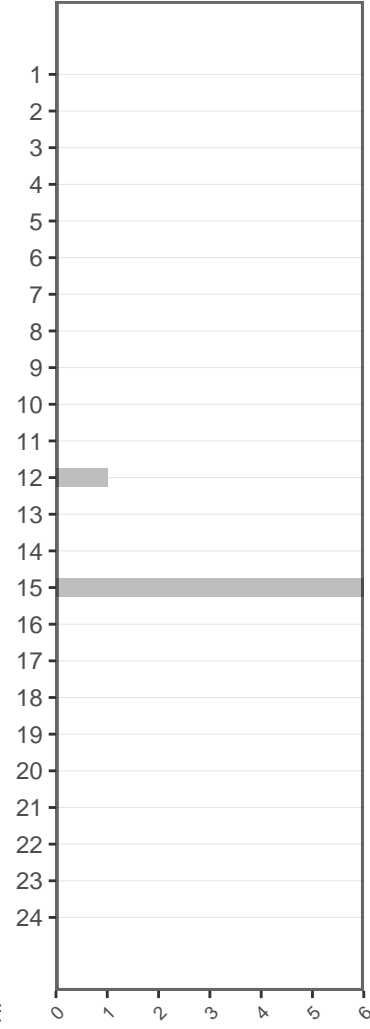
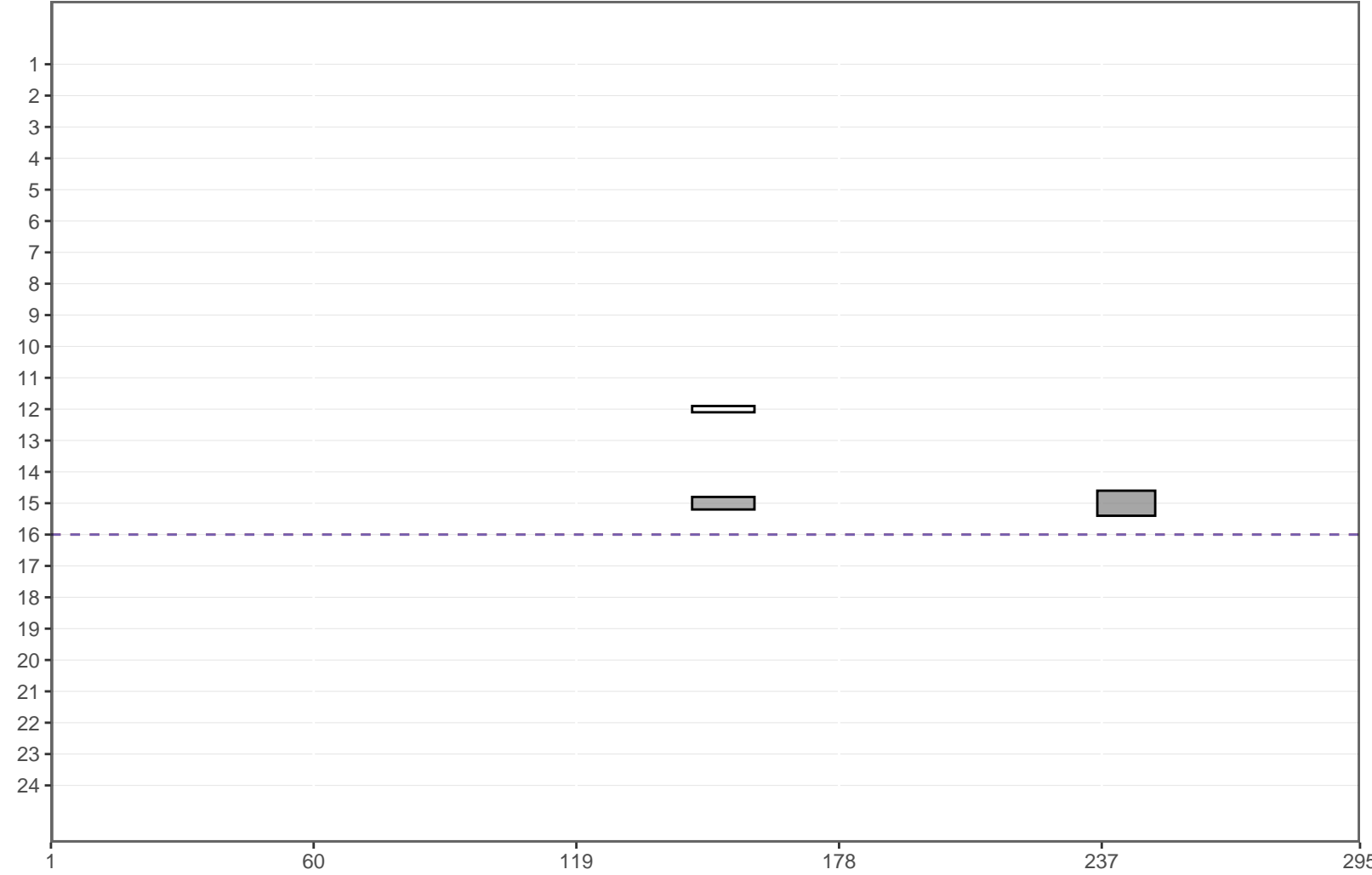
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GTSSIVRHFFVPGQYVDVTGTRKGFQGGMKRWGFKGMPA8HGABLSHR8IGSTGGRDAPGKVFKGKMPGRMGQVQRTVKNWVYKIDPARNLMMVKGQVPGAEGNFVFKDSVYKKPDISMLFFFTYFAPEDEDEDDLEPLVADLGGTDFPMAAD

NbL07g16880.1 uncharacterized_LOC109223891 [MW - SP = 55.3 kDa]

No. of times detected



log(intensity)



Values from



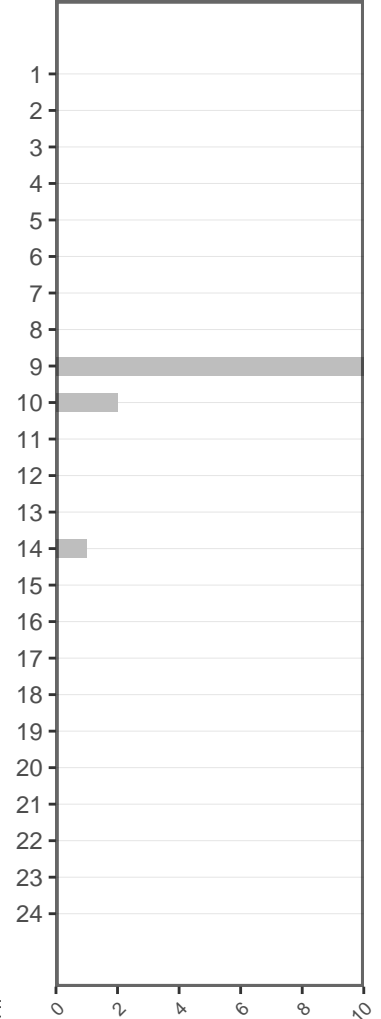
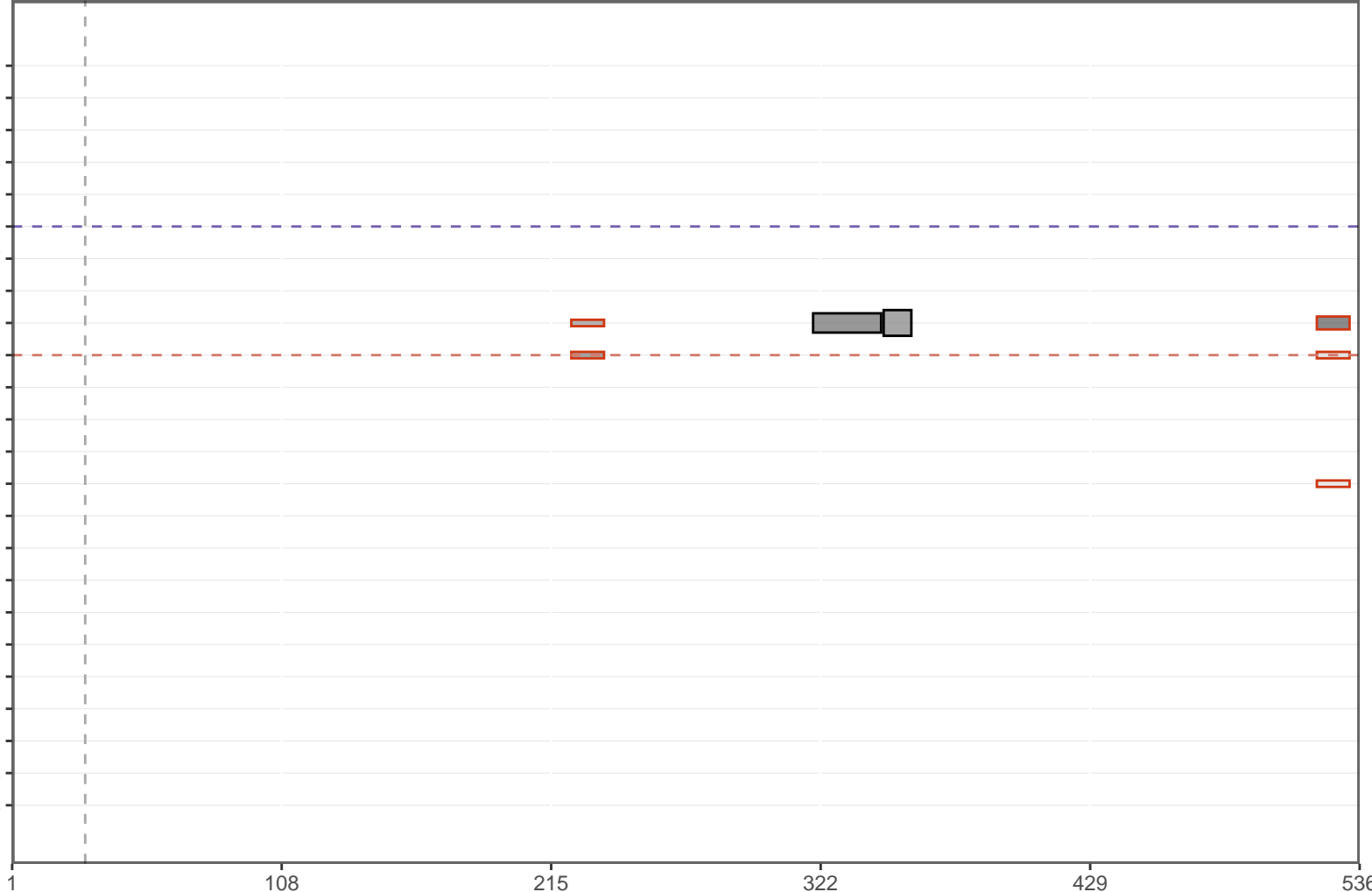
MW indication



Molecular weight



Gel Slice

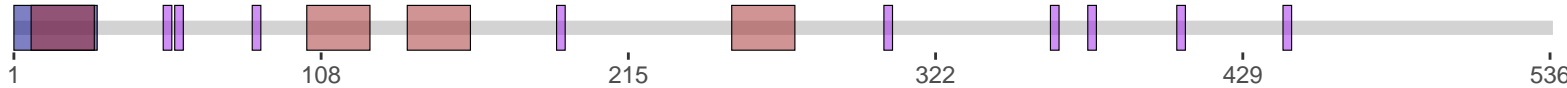


Peptide counts over 4 repeats

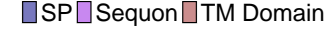
Protein length



Pfam domains



Pfam Description



Protein sequence:

VMLGLAALGFLFSILGGLQVLYILVGVWLVAVTRIGGVFLVLIHNTAGDGVAMNWDWKNPTAHTALDDIPCVDTATGETLSGSKEVTVQLVGVNRIITVNSINDPPSGVGVYNSGGPLVPLNLCNPNFNEDKTRKSGSEVELSNATGVWRNVYGVGSASNVGVSTVGRLTQPMYNGMTGVYVNSGLYHSGPFLSELLDCTFLRDTVGVHDEHCPDLTRYSKWYVIGLALVSAWMLSLKGVLYVARERRHRKVTKLVDATSGGSEFACKSGG

NbL07g16480.1 uncharacterized_LOC104218509 [MW = 31.46 kDa]

No. of times detected



log(intensity)



Values from



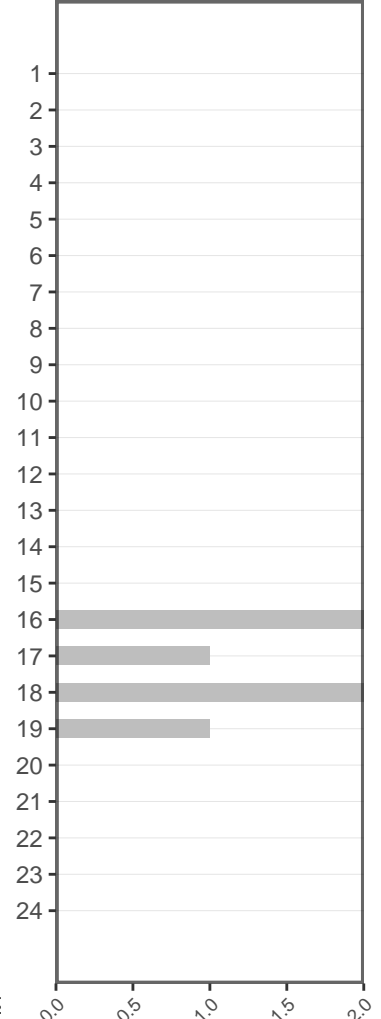
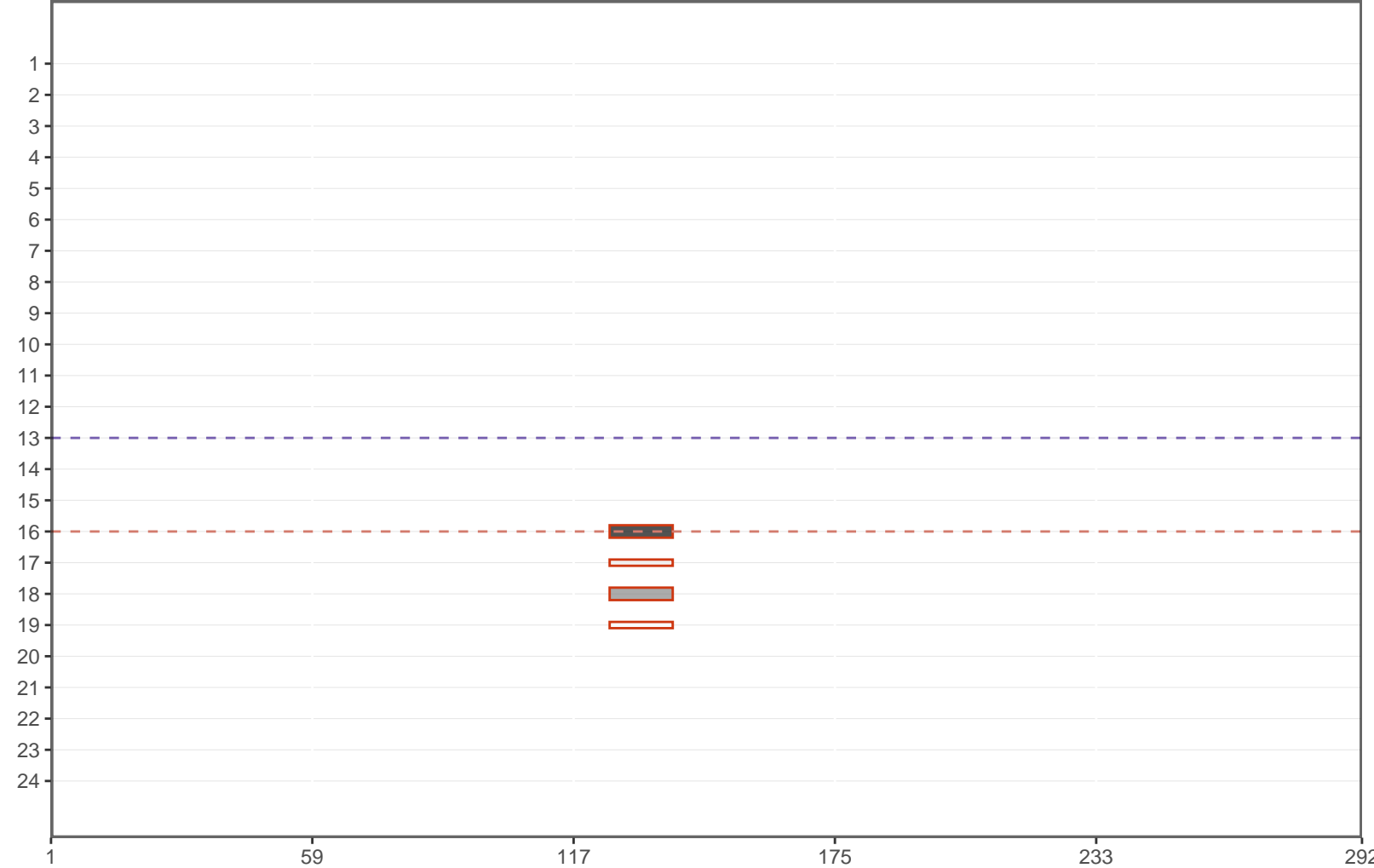
MW indication



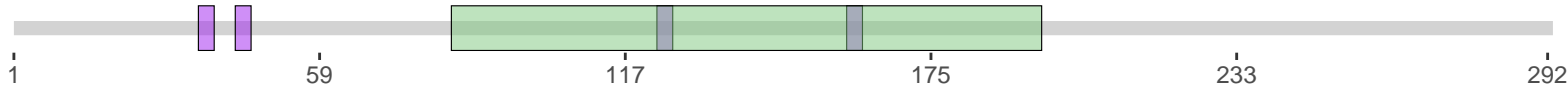
Molecular weight



Gel Slice

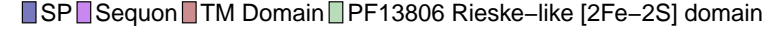


Protein length



Pfam domains

Pfam Description



Protein sequence:

EGLLNAKLTQDCGCVPTDSTFYLQNGSIKEWYPNPVLRVLRTRALRNLFVYVTKTDDENYEMRGGGKVDASAEIVFSGKAGPGVTASDNNVDEVRMVIDEGEAFGFTGRNELNGKAAVGFLLLDPELLTGKLLKGTGLLDFRIVSVDAPK

NbL07g16410.1 40S_ribosomal_protein_S5 [MW = 31.93 kDa]

No. of times detected



log(intensity)



Values from

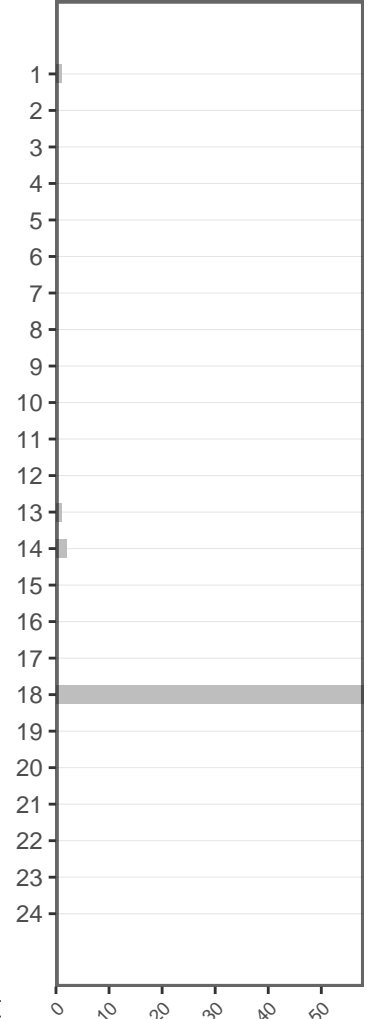
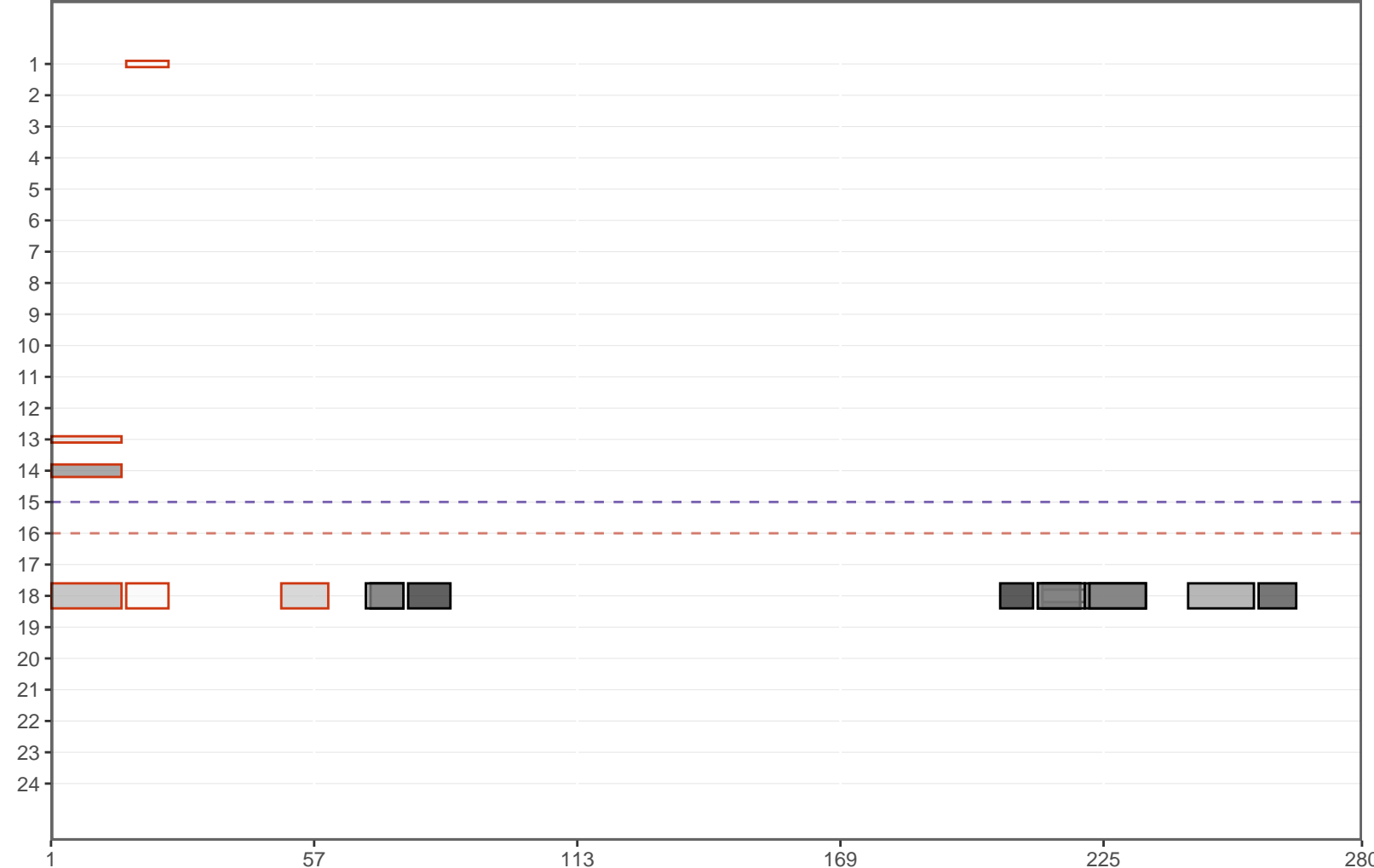
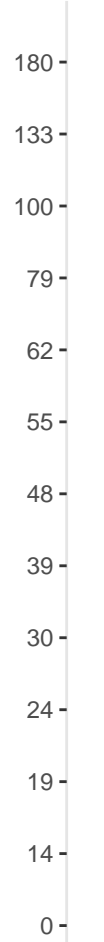


MW indication



Molecular weight

Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

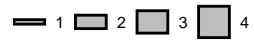


Protein sequence:

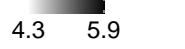
LDYFCIKLDAFLLRIGVRRFSEVHVFVLEFEGAKKKWFEHYHVAAGFRYFVSNFVSFSLQGPVQSSGSPREDATRIGSAGVRRGAVDIPLRVNDQAWLTTTGARESFRNKITAELADELINAAGKSSNRYAKKKDEIERWAKNR

NbL07g16360.1 cytochrome_c [MW = 12.12 kDa]

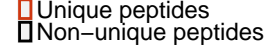
No. of times detected



log(intensity)



Values from



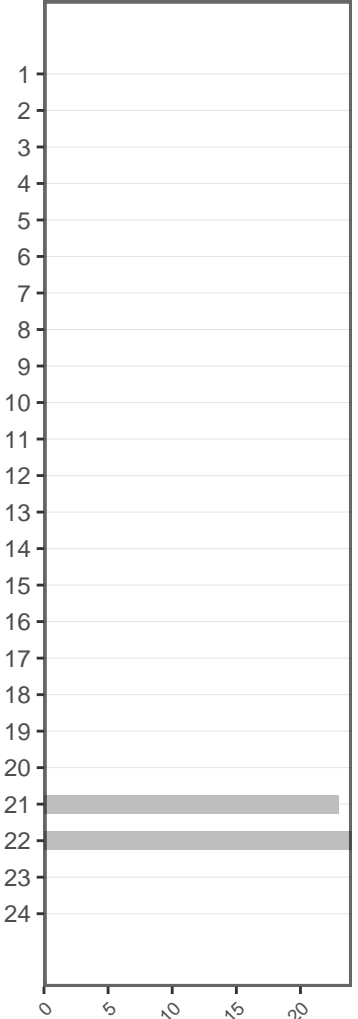
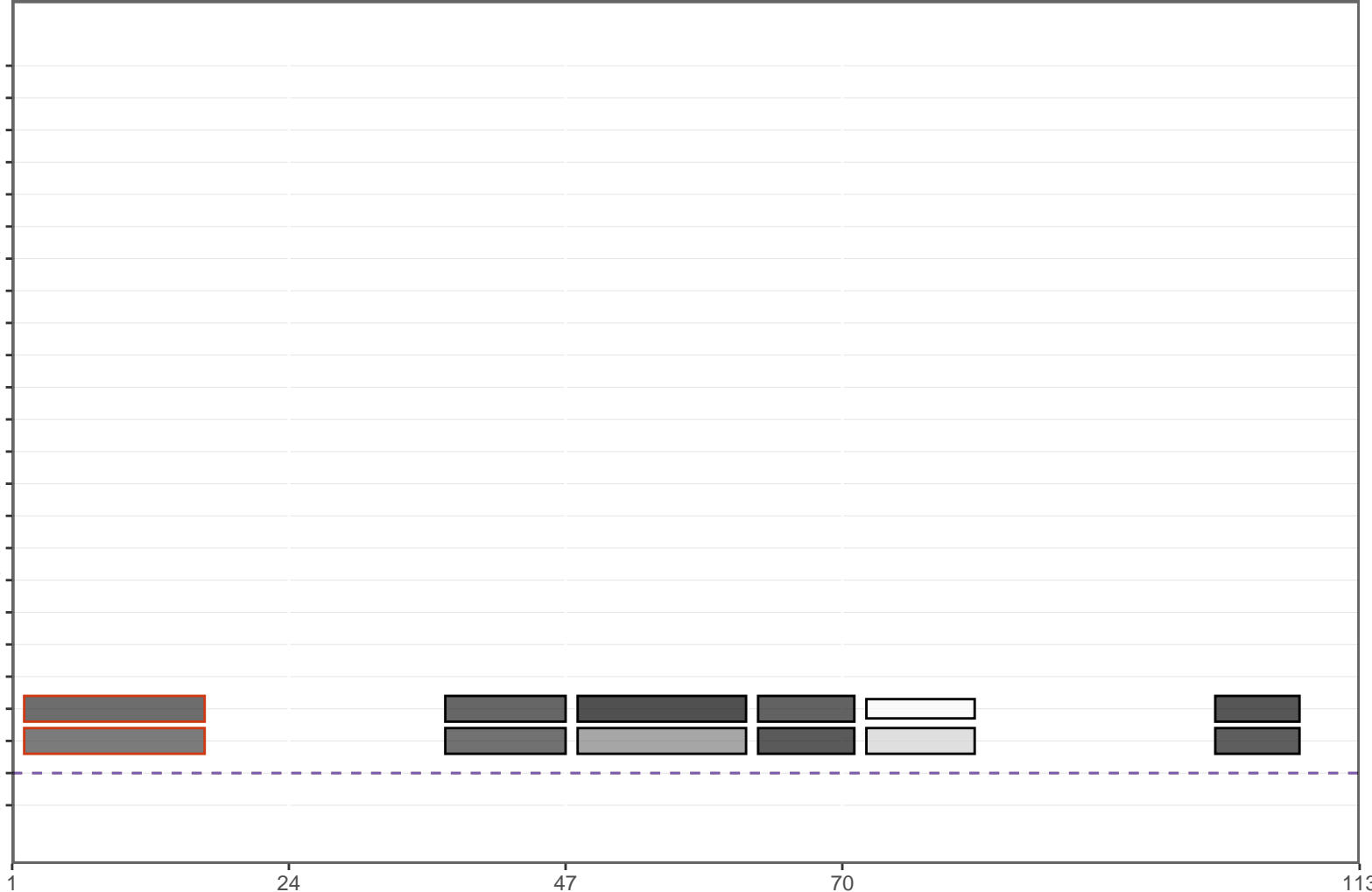
MW indication



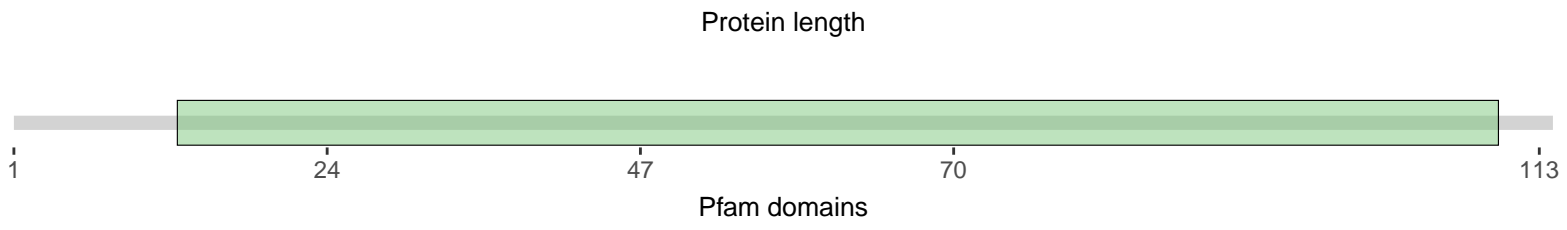
Molecular weight



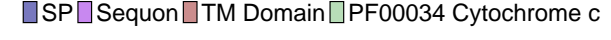
Gel Slice



Peptide counts over 4 repeats



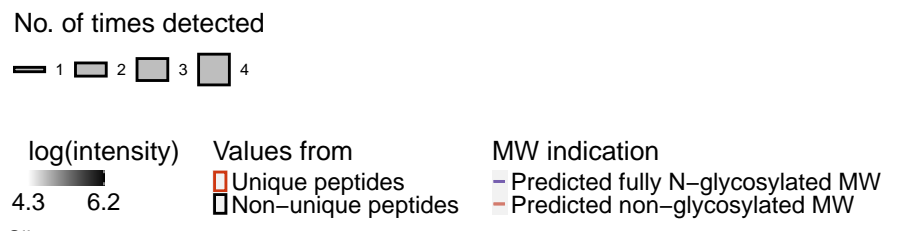
Pfam Description



Protein sequence:

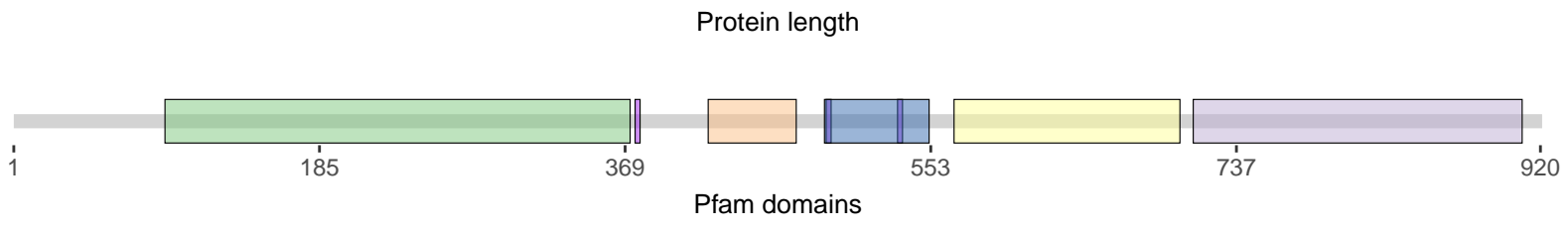
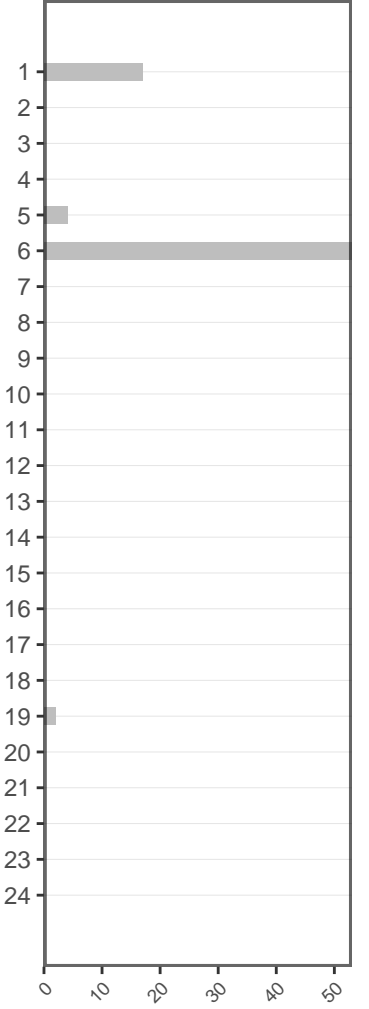
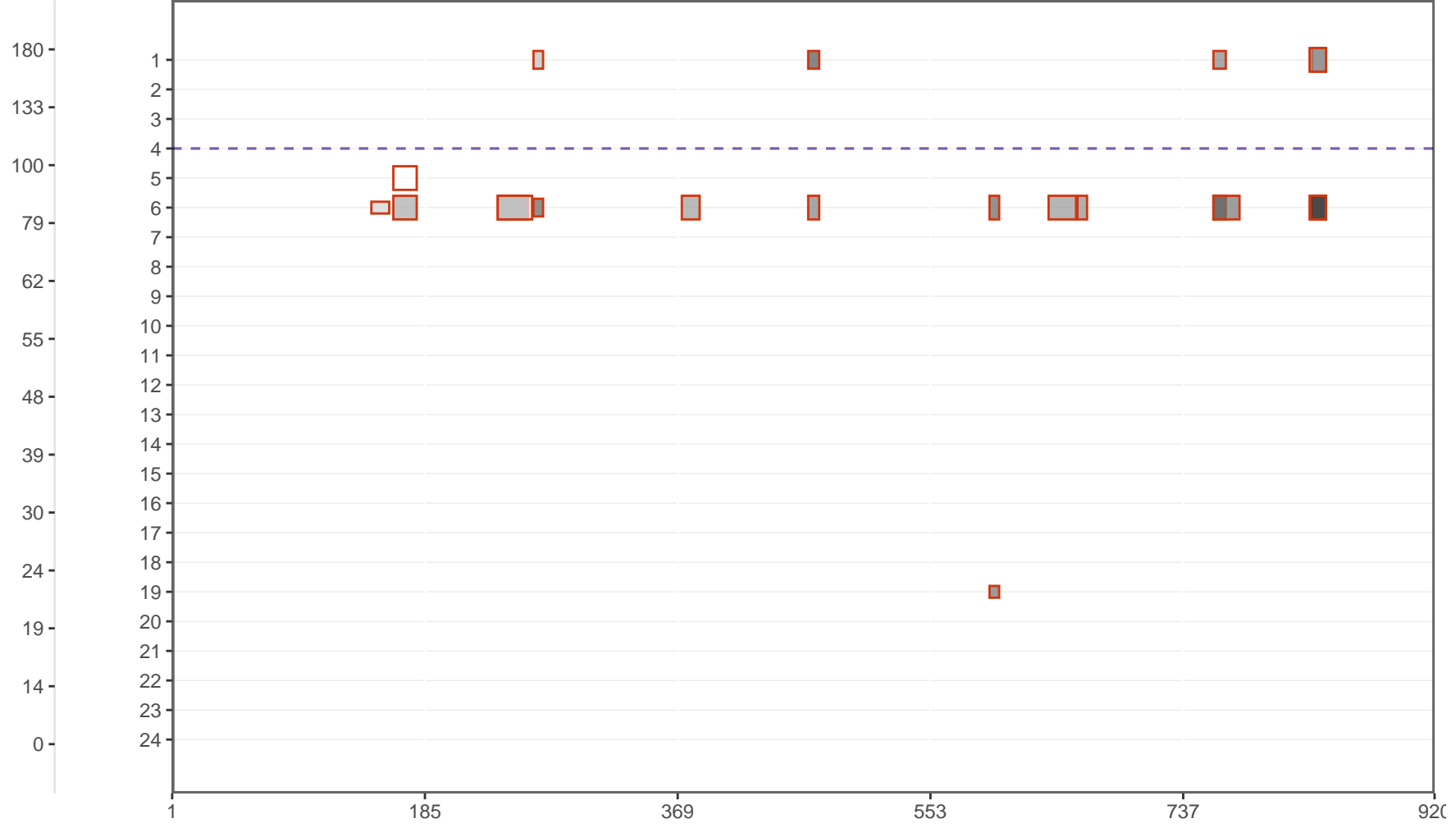
SLFGROSGTGTAGYSEYSAANKNMVMWEKRTLDYLLNFKKYPGDKMVFPLGKKPQERADLIWLSATV

NbL07g16260.1 bifunctional_aspartokinase/homoserine_dehydrogenase_chloroplastic-like [MW = 100.18 kDa]



Molecular weight

Gel Slice



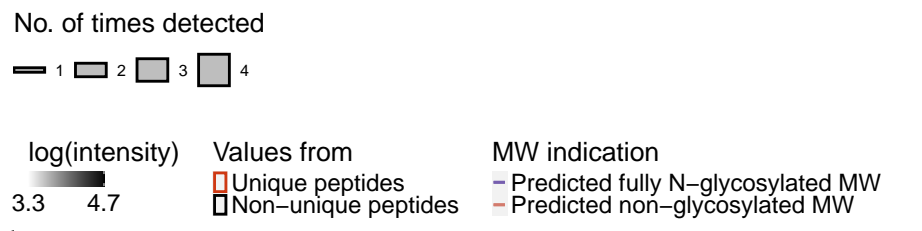
Pfam Description

- SP
- TM Domain
- PF00742 Homoserine dehydrogenase
- PF03447 Homoserine dehydrogenase, NAD binding domain
- Sequon
- PF00696 Amino acid kinase family
- PF01842 ACT domain
- PF13840 ACT domain

Protein sequence:

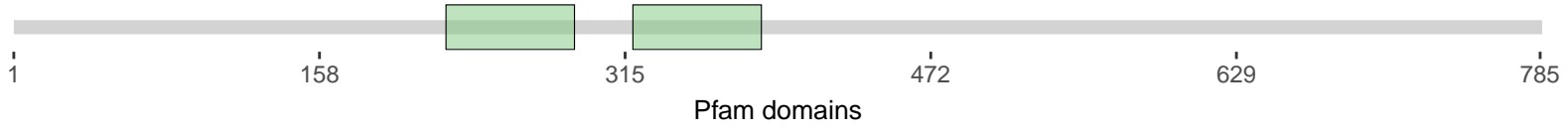
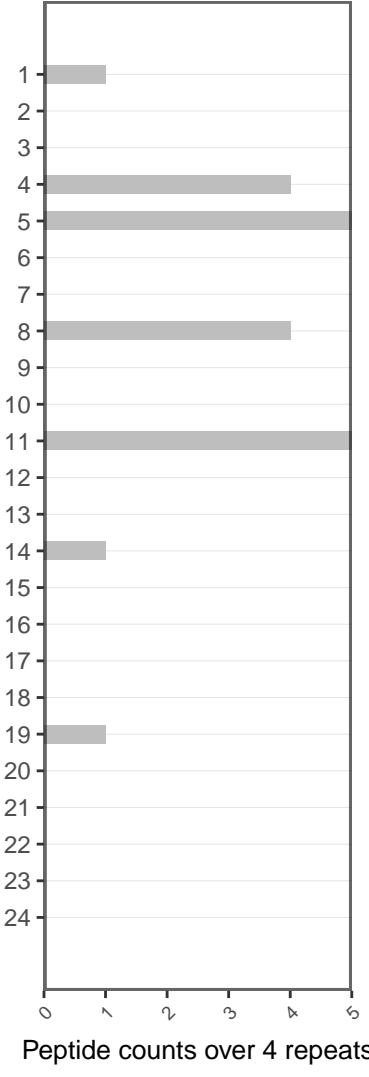
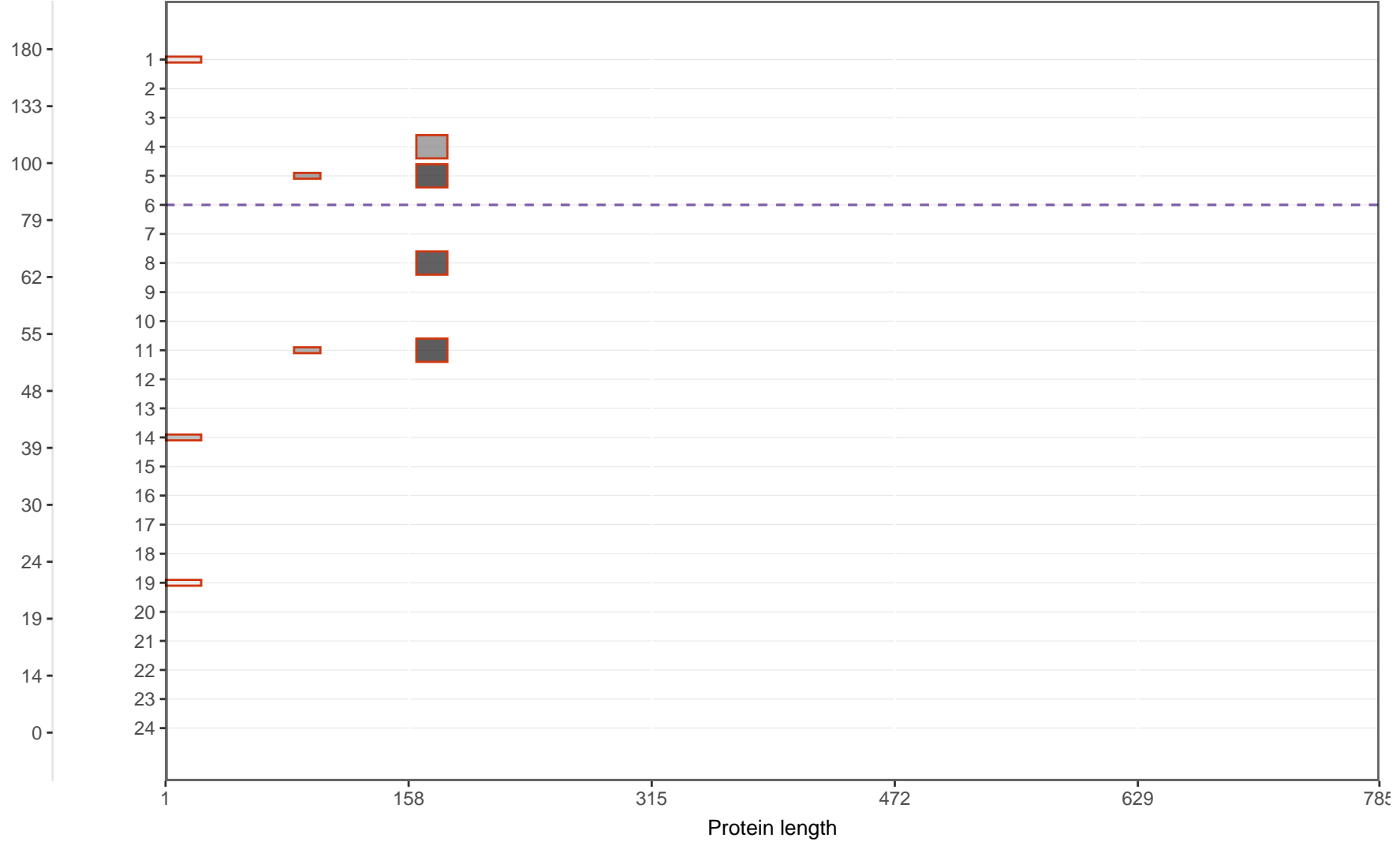
ISQASSEISVCTFAVPEKEVKWADVLESRFGGALSGRLGQAVFNGGILAAVGGQRMASSTPGVSAITLFTALAKANNIRAIAGDQCTENITVAVKREDDVRLRAVHSEKFLSRTHVAGVGGPLGATLLDGLKDTGTAVKEKFNIDLRVMGTFGRITMLLSEGGDLKWRRELLGLRGEMADLSEKFNHVRGNGHFIPNTVLVDCCTADGSHARHYYDMLKGGHVVTPNKKANSGPLDGLKLRALGRQSYTHYFYEATVAGAGLPHTLRLGLETGGKILRIEIGIFSTLSLYFNFA

NbL07g16190.1 far_upstream_element-binding_protein_1-like [MW = 84.18 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF00013 KH domain

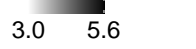
Protein sequence:
 RPSLSSGYGQCAFRRPRGGAAPPQWGRGRGCHPGGFPQVDHQRGGYSSRSPQYPPRVGNHYHQQAFPRGFGGQWGRPRRSMQGGPQSGNANNYVGAHGKDPVGGSYPHHGAGHGQGGYGHGKTEVRYVDHQMPPQNGYGGHGKPGPPTVYVPGSAHPVYGTGEGYKPFPEYGMHPQASHGQVYSHPRANGKPGVEVYVGGGAPRSTGGYGAEMPPFGQGGGGGGYVYASSGGMGQTYRAGVSTTTADGYNHPQAAAPASGPGYVPGQ6ADPVPQYGG5VY

NbL07g16110.1 receptor-like_protein_12 [MW - SP = 49.4 kDa]

No. of times detected



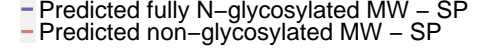
log(intensity)



Values from



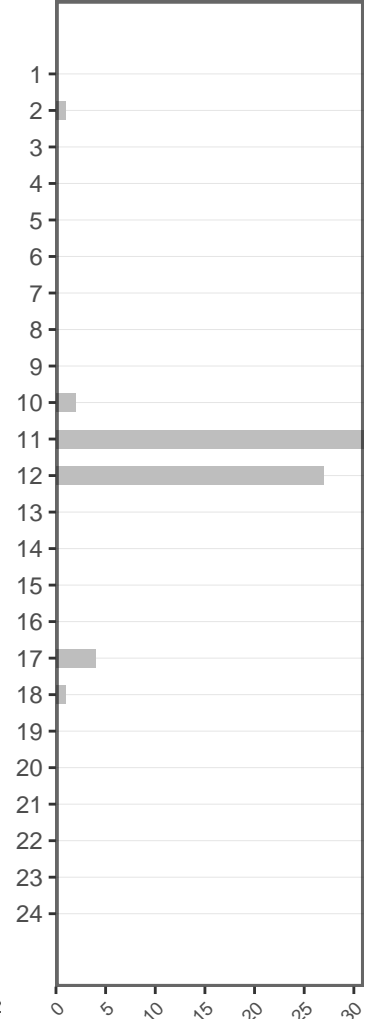
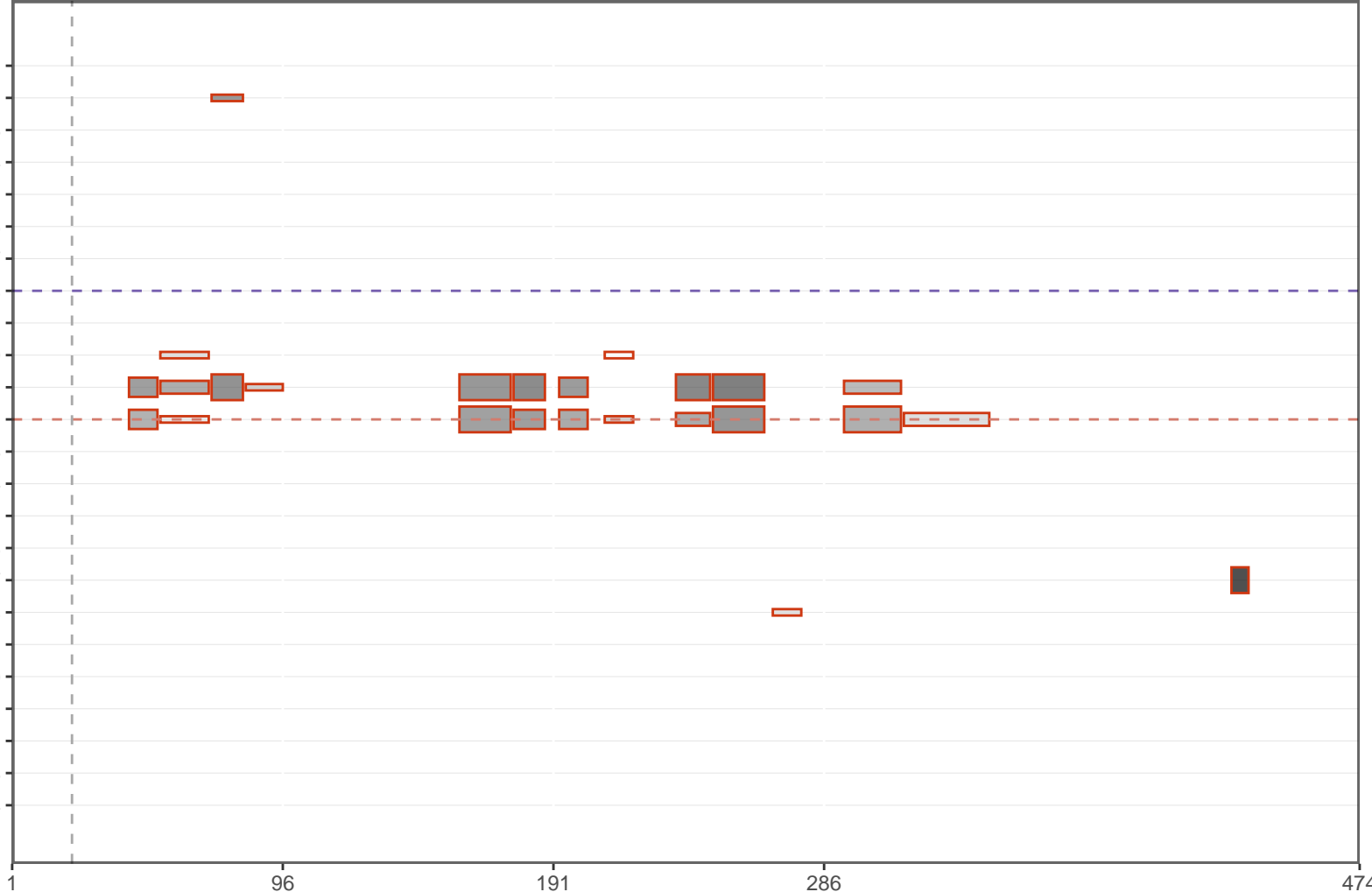
MW indication



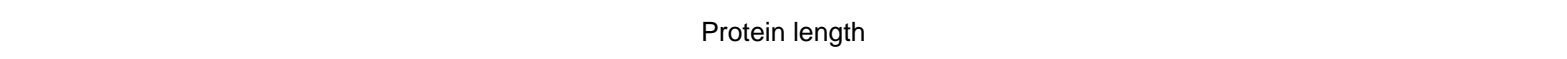
Molecular weight



Gel Slice

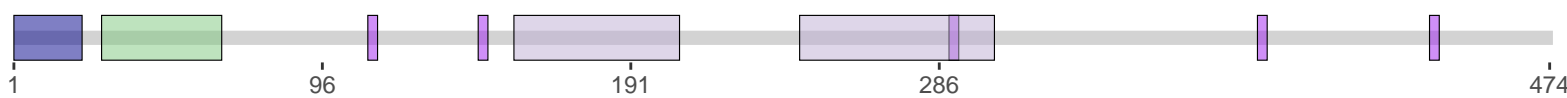


Protein length

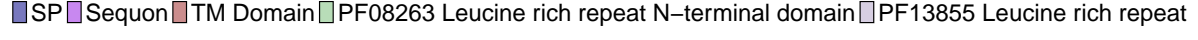


Peptide counts over 4 repeats

Pfam domains



Pfam Description

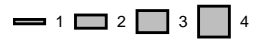


Protein sequence:

LSHNKTKTKPSSATLAPQLRVLRYLELGHNYLTGQIPDLGKFRFLDLDLSSNKFSGTVPKFSANLTKFNLELDSHNLNLDVPPDGLFKVIGIESLDELVNNFHLGTPISWITSSPIYSLKAKGDKIKLDDWPKPTTYFYDVIDLNNNEISGSPGLNKTDFLIGFYASGNKIKFDLEKLRIVGTLKDLDLERNMYYGKPKAISGLGKLNLSNHLGGGLPPTKFGANSFAGNAGLGGSPLPKPS*

NbL07g16010.1 probable_sucrose-phosphate_synthase_4 [MW = 118.64 kDa]

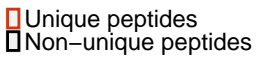
No. of times detected



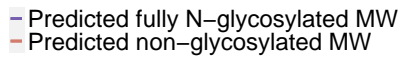
log(intensity)



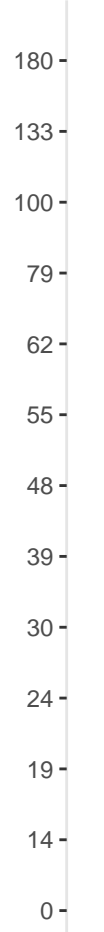
Values from



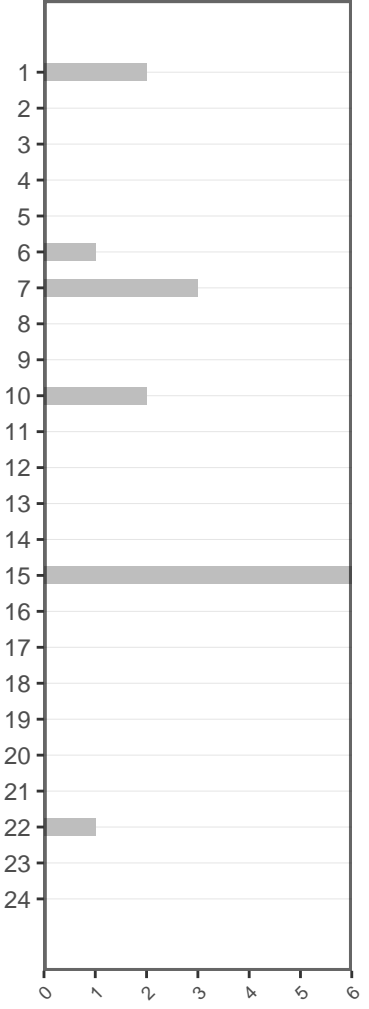
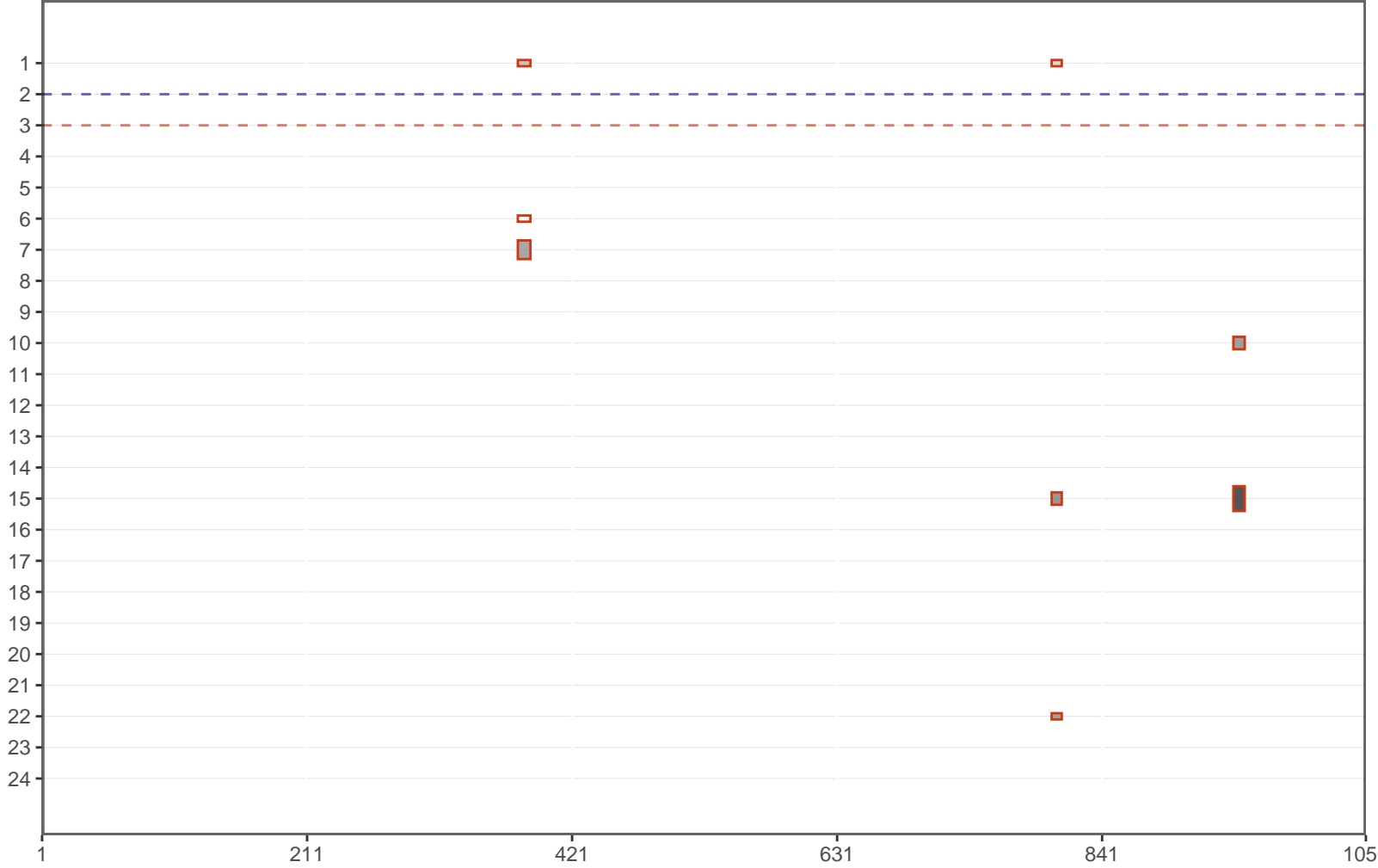
MW indication



Molecular weight

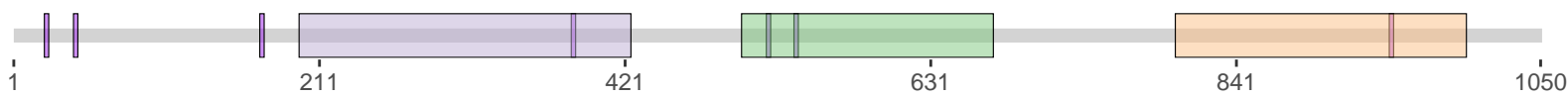


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

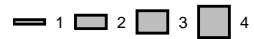


Protein sequence:

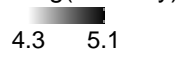
LSRPDPKXNVTTLLRAFGEGGALRELENLTULGNRDDIDMS666SAVFTVTKIKIDKYNLYGGVAYPKH*KGPDVDPDYRLAAKTKGVFNPNALVEPFGLTIEAAAYGLFVATRNGGPDVILKALNNGLLIDPHDQKAADALLKLVADKNLWLECRKNGKLNHRFSWPEHCRNLYLVYVGHCRNHPANRLEVMKPTLEEFMSESLRDMEDLSLKFSDVDFKANGELDMARRQDELVEKSRKANSSEKPIVYVCGPRGRQVLYVWTDGYNSEKTPPTETLSLTYXNMQVAGI

NbL07g15950.1 single-stranded_DNA-binding_protein_WHY2_mitochondrial [MW = 26.67 kDa]

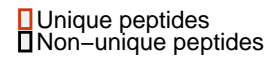
No. of times detected



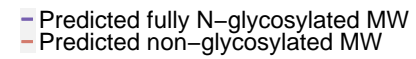
log(intensity)



Values from



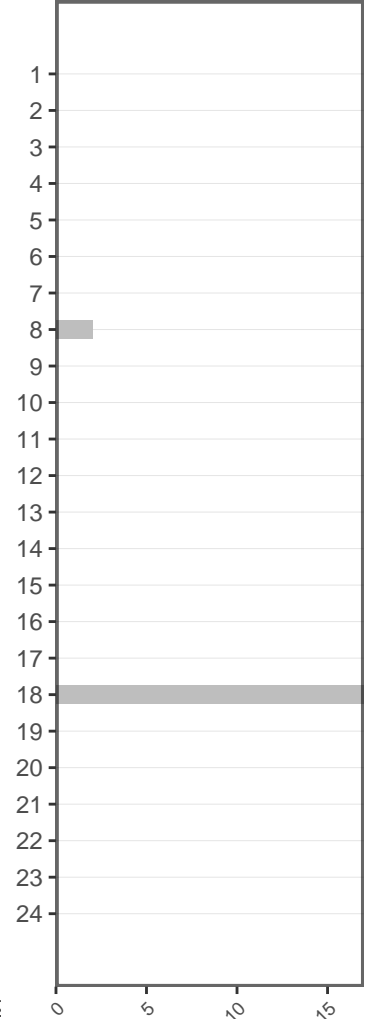
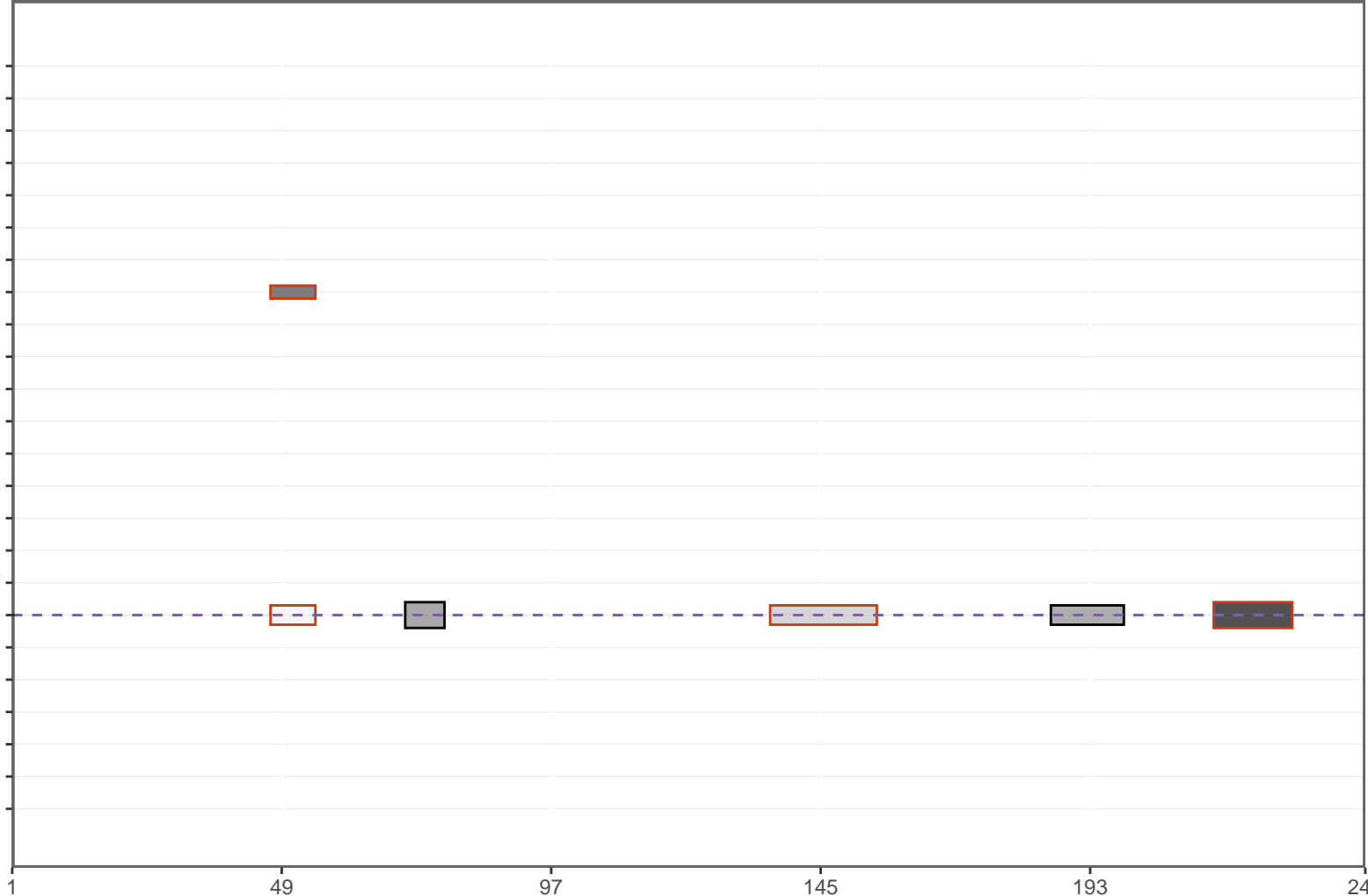
MW indication



Molecular weight

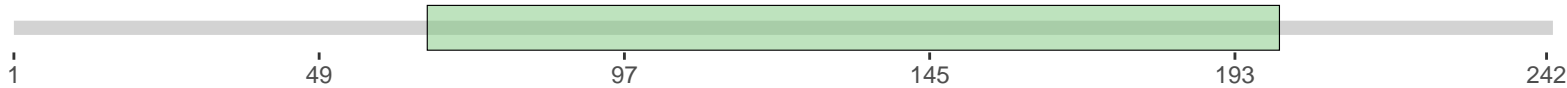


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RRKYDVEKRLQALFALGATEVGLISGTRDTGCEFFHDFSLSSNAGQVRKLSLSPKPNADSGGYFVLSLVVWNNLKTNDRFVFPVTTAEFAVMRTAFSALPHMGWDRFINPLESISGSSKVVLPOLMETEWDRI

NbL07g15820.1 endochitinase_3-like [MW - SP = 33.6 kDa]

No. of times detected



log(intensity)



Values from



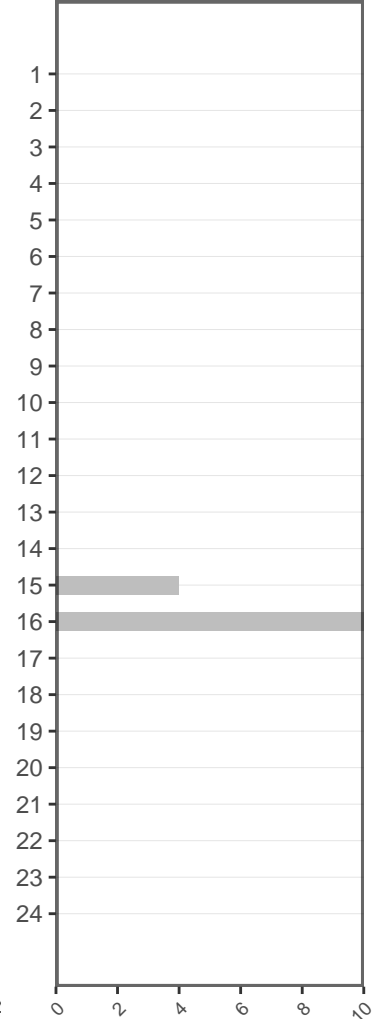
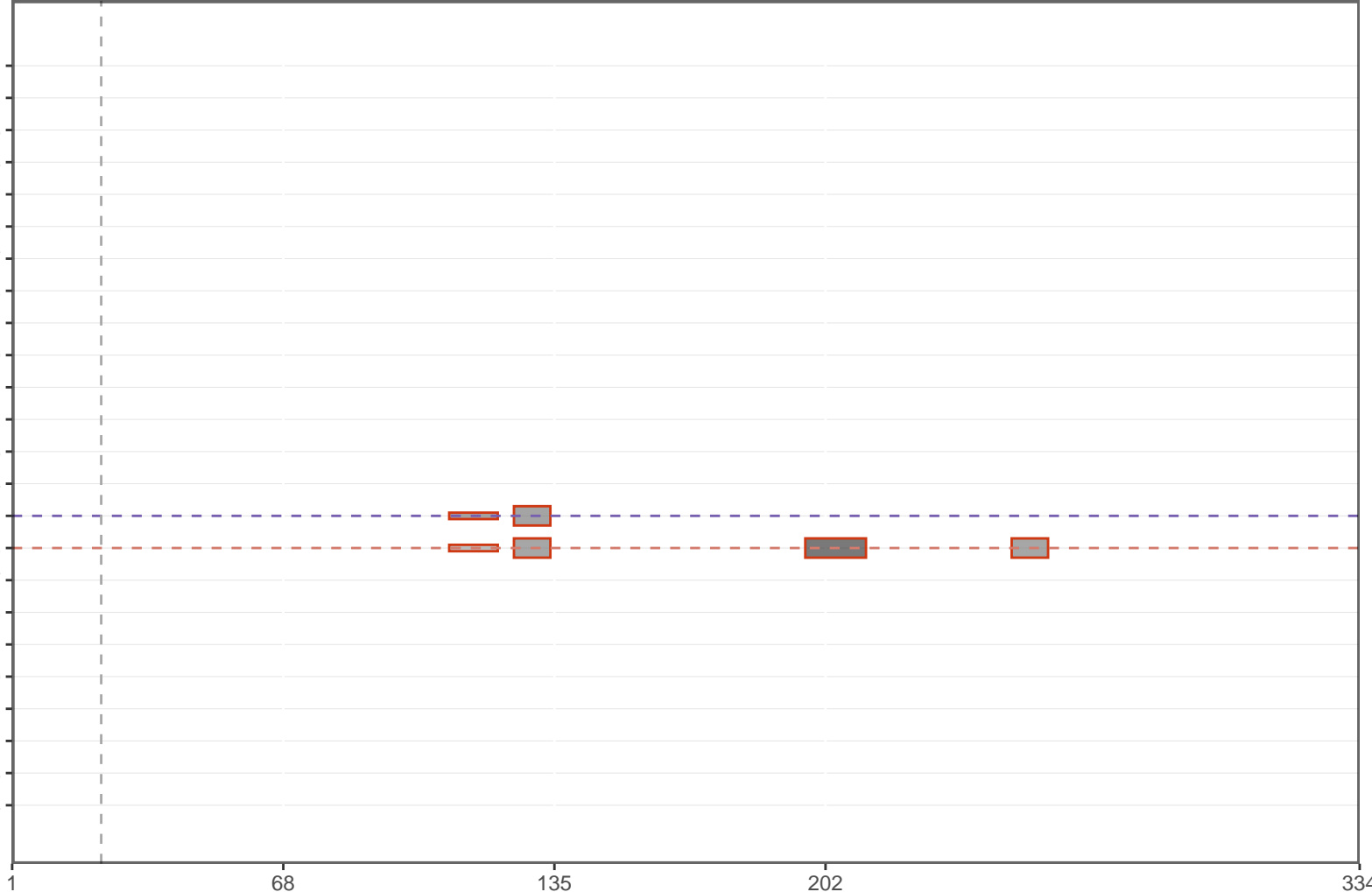
MW indication



Molecular weight



Gel Slice

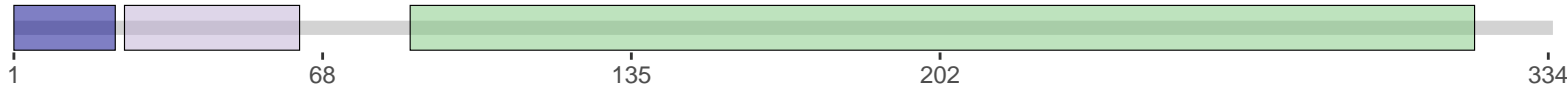


Protein length

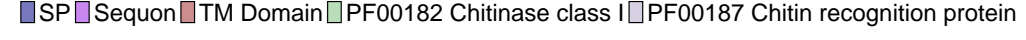


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ADTAPDGRYAWGYYKLRREGNPFPEYQSSGQWPCAPGKHYGRGPIQISYNNYKPCGRAIGNLLNFDLMTNAVYFKSAIWFVMTAGPKPKSCHDVTGRWTPSAADRAANRLPDYGVITNINIGLEGGHGGSDARVQDRIGFYRRVGSLSGVSPGDNIDCGNRPFPNSGLLLETM

NbL07g15700.1 SKP1-like_protein_1A [MW = 17.51 kDa]

No. of times detected



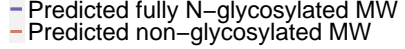
log(intensity)



Values from



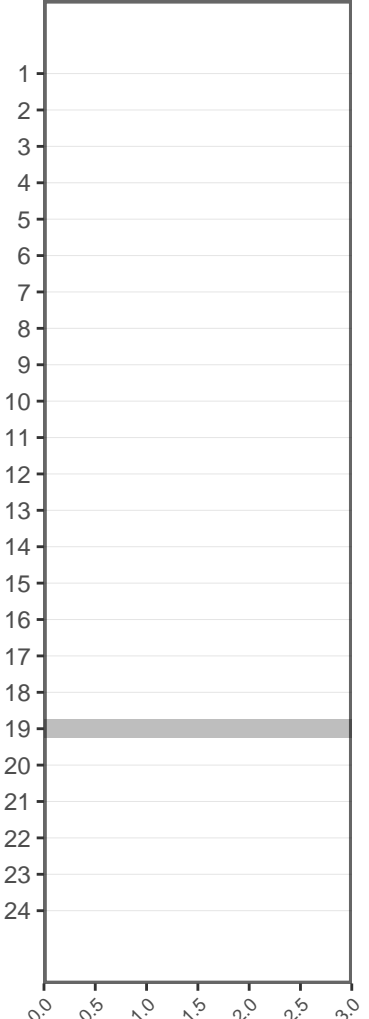
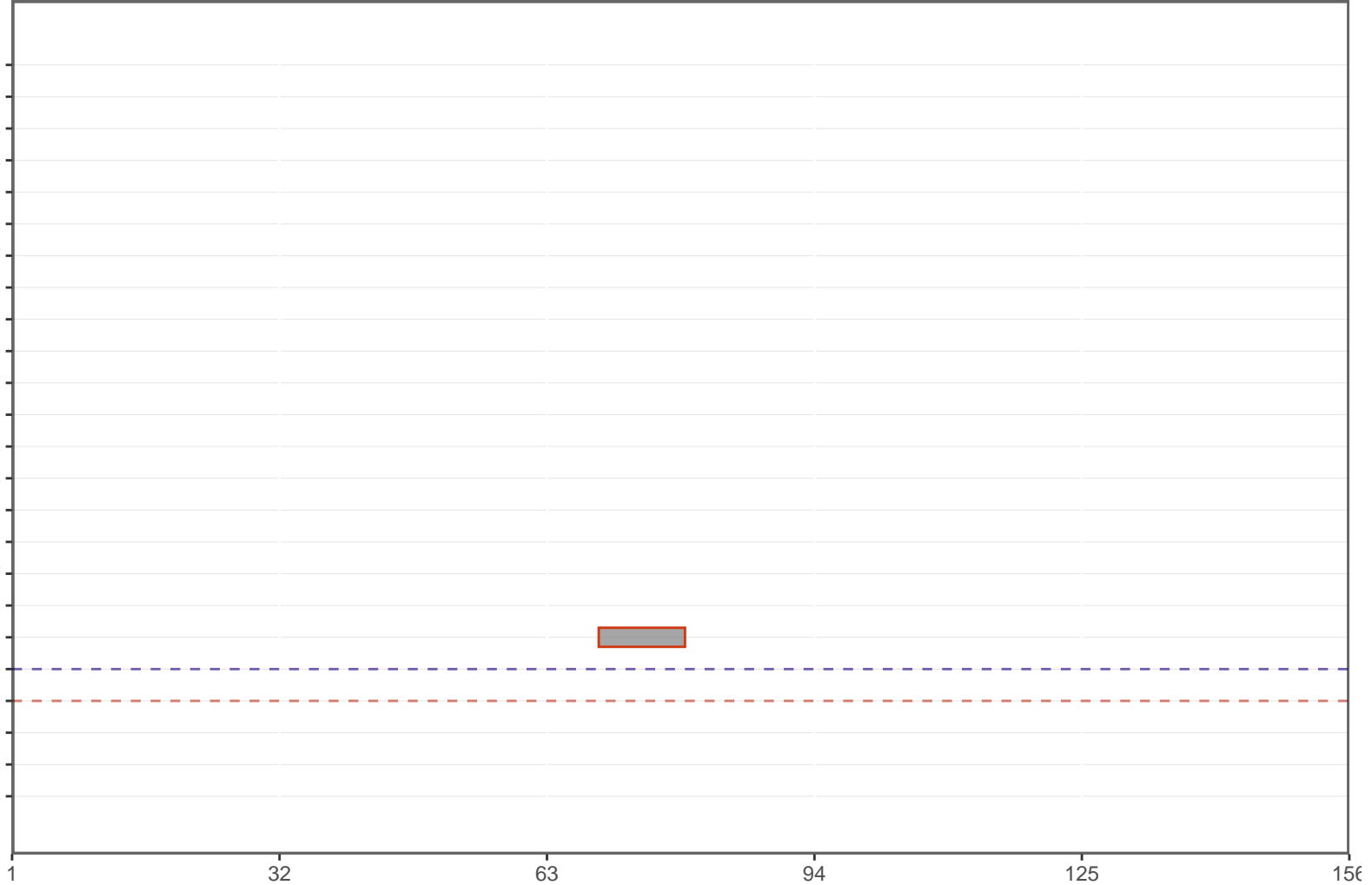
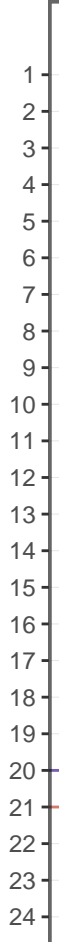
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DATKAEDKASEDELKAFDSDFKVGGATLFDLILAAHLYLNKIGLLDITGQTVADMKGKTPFEIRKTFNKNDFPPEEEEVRRNAAWAFI

NbL07g15500.1 ubiquitin_recognition_factor_in_ER-associated_degradation_protein_1-like [MW = 36.25 kDa]

No. of times detected



log(intensity)



Values from



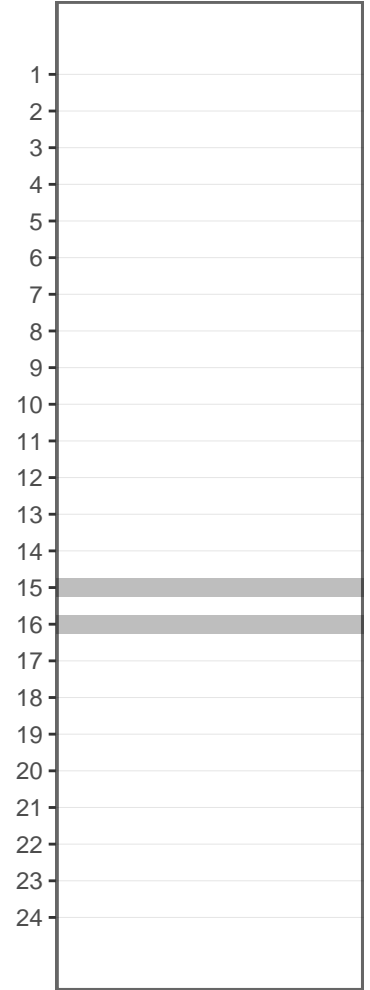
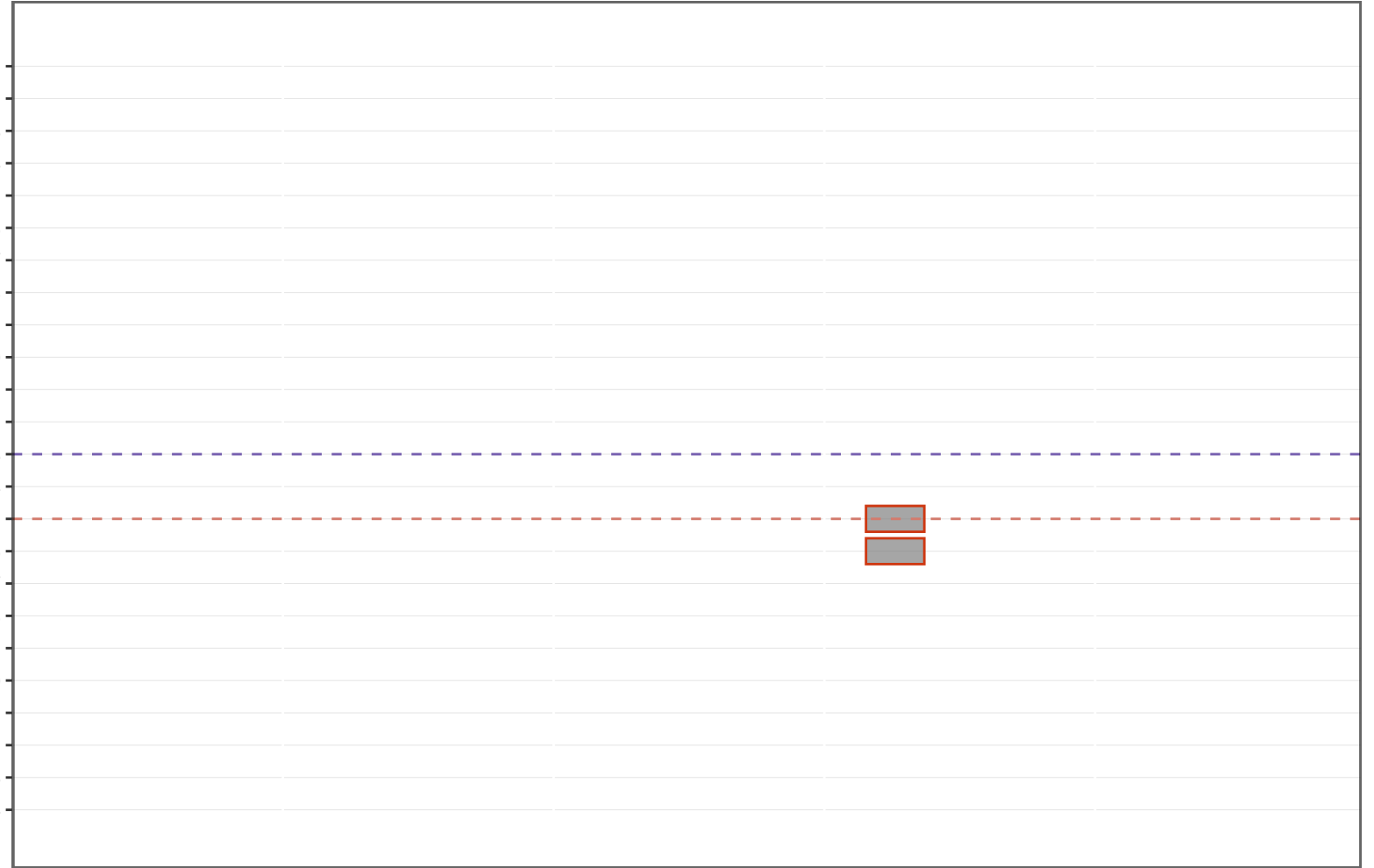
MW indication



Molecular weight



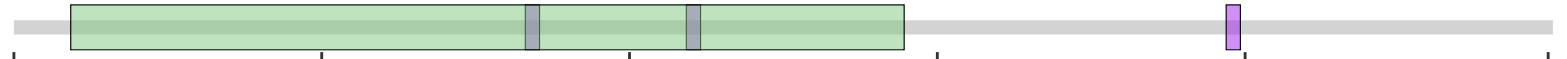
Gel Slice



Peptide counts over 4 repeats

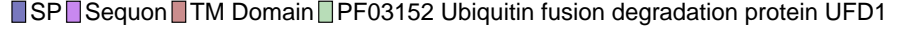


Protein length



Pfam domains

Pfam Description



Protein sequence:

ISMVAVYNNKCYIDVVEGAPSNASIEITDCEVDFAFLDYKKEPERFVPLPSKPAEGEEAAAEKPKFNPTFGSARRLDGKPLKGGPPVSTGSKDKRPMANATGGSATGSSGSSNRGTGGKLVFGSNANRNRPDKGKPEVKEEPPKKEEFPQAFQTKKYSLRG

NbL07g15490.1 epimerase_family_protein_SDR39U1_homolog_chloroplastic [MW = 38.97 kDa]

No. of times detected



log(intensity)



Values from



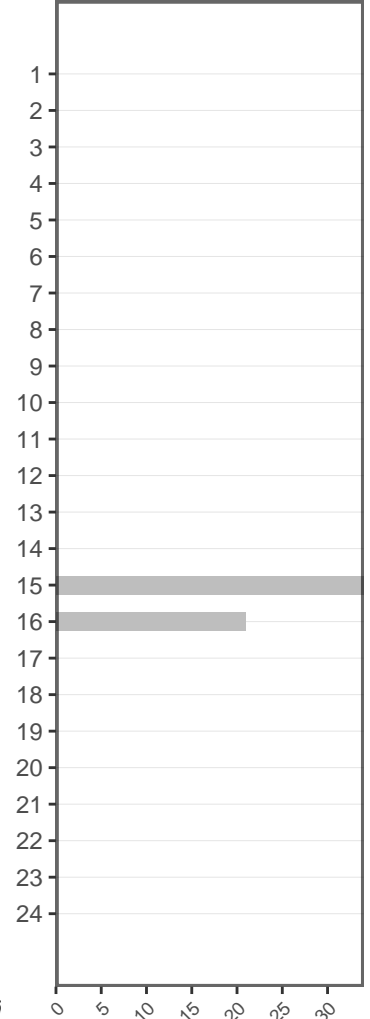
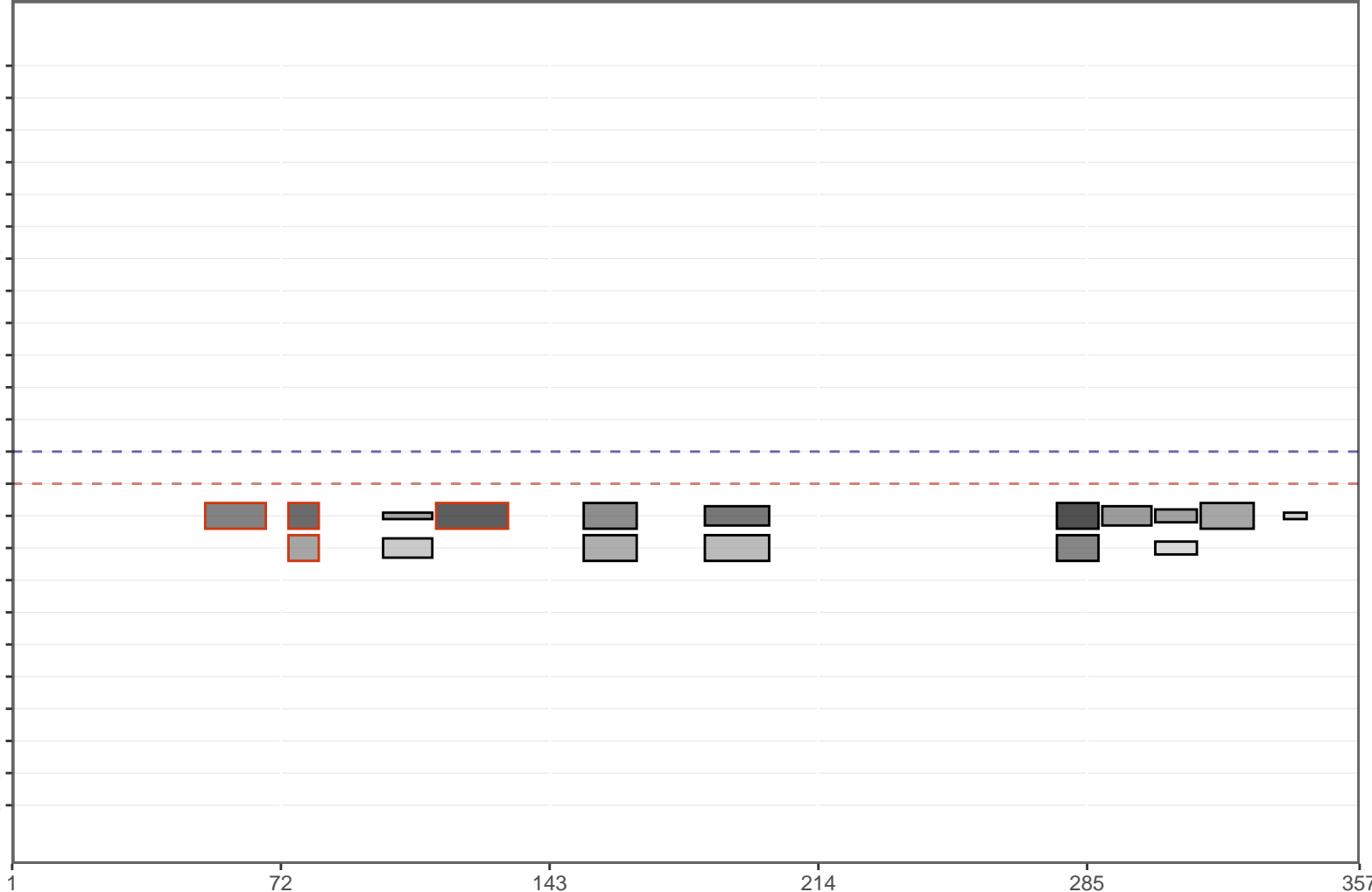
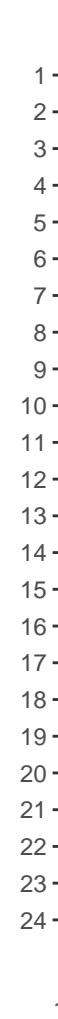
MW indication



Molecular weight

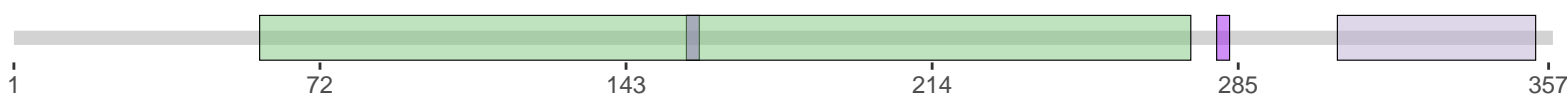


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

<small>CVLISAVGYGTYGTSETRVFDEGSPGNDVLAEVCREWEGAAKVKNDVRLALRIGVLLGKDDGALAKMRFMMFAGPLGSGNGWFSWHLDDVLVLYEALSNPQKGVNGTAPNPNVRLAEMCEQLGVLGRPSWLPVPEIALKAVLGGASVLDGGKVPTRVKELGFPFKYQYKDKALKAMS</small>

NbL07g15380.1 uncharacterized_LOC109223501 [MW = 23.51 kDa]

No. of times detected



log(intensity)



Values from



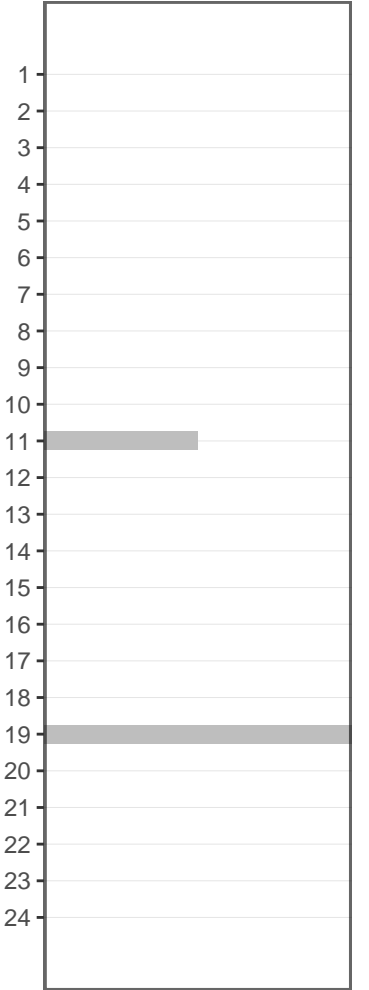
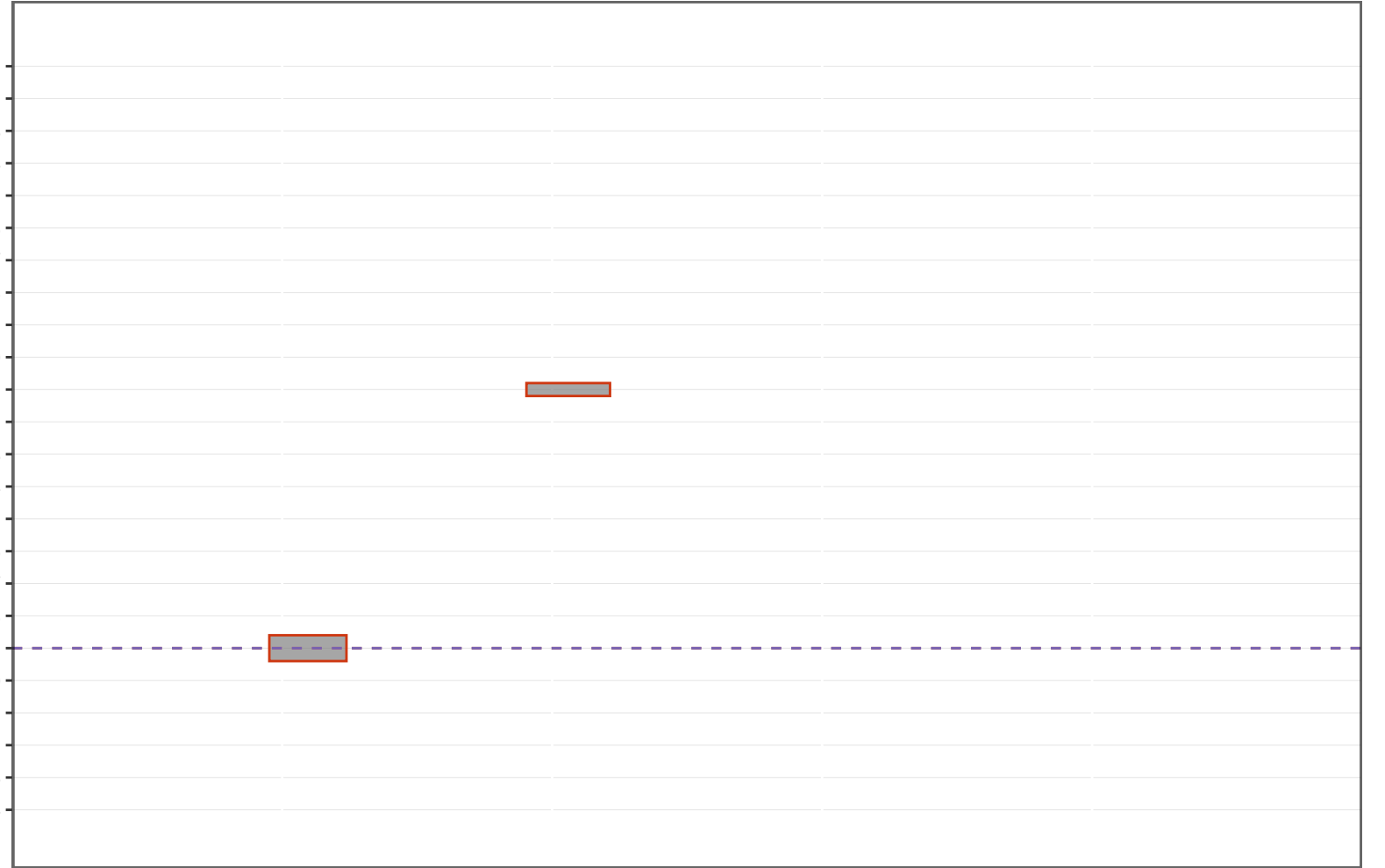
MW indication



Molecular weight

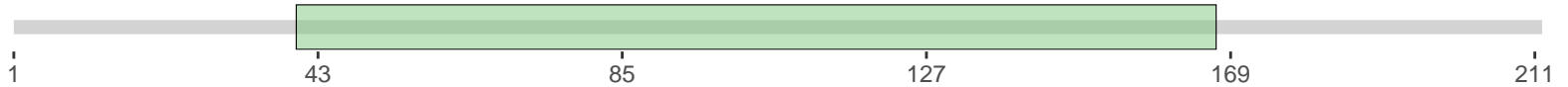


Gel Slice



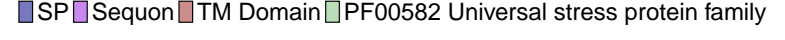
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEKLAIEAFEVAMVNTVARIVEGDAGKRWICKEAERLKPAAVMGTRGRRLIKVLOGSVSEHCFHGCKTAPIVPPGKGTLLHLFCFSKFFVWVGEQNVLLSRERGGICNLMTGQV

NbL07g15370.1 glycine-rich_RNA-binding_protein-like [MW = 17 kDa]

No. of times detected



log(intensity)



Values from



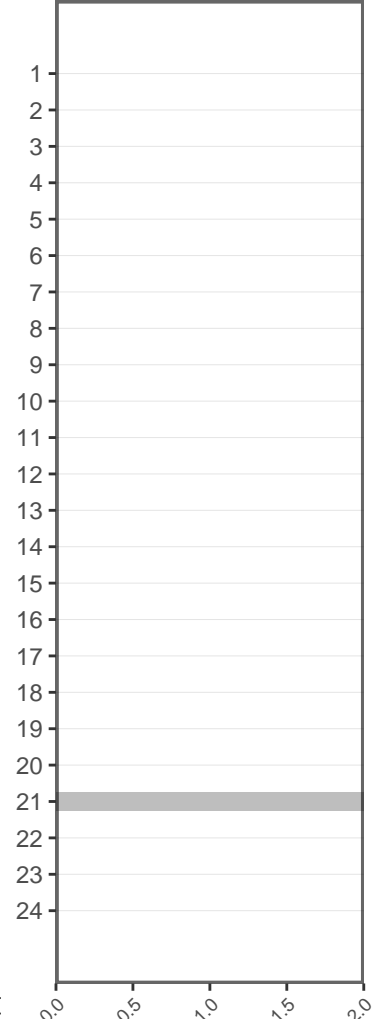
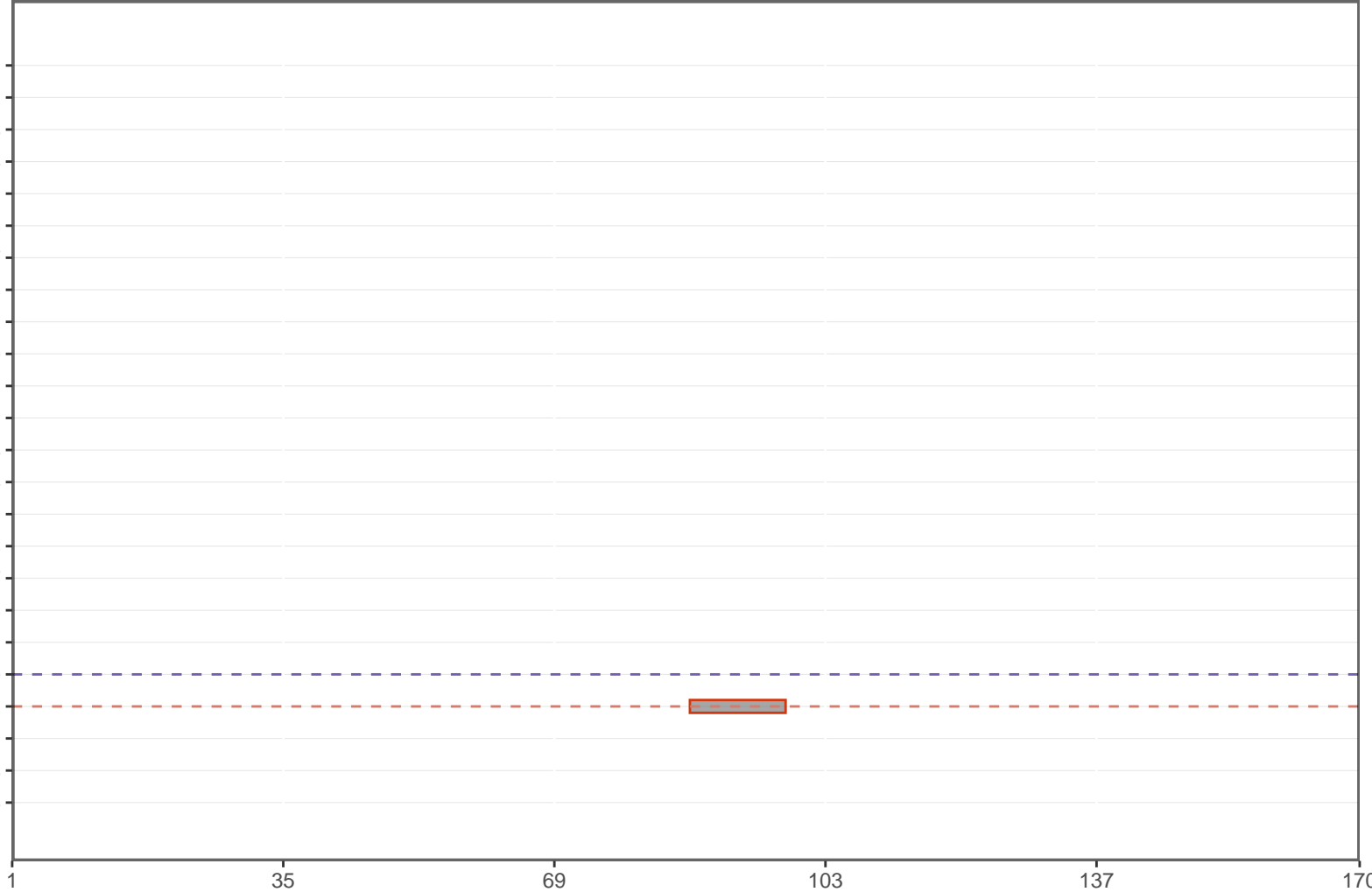
MW indication



Molecular weight



Gel Slice



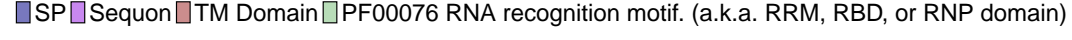
Protein length



Pfam domains



Pfam Description

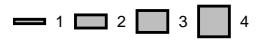


Protein sequence:

ITVNEAQRSGGGGGGGGGFRGRRGGGGYGGGGYGGRRGGGGYGGGGYGGGDRGYGGGDRGYGGGGGRYRGGGSDSDGNWNI

NbL07g15350.1 coatomer_subunit_gamma [MW = 98.44 kDa]

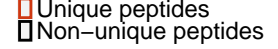
No. of times detected



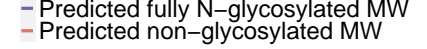
log(intensity)



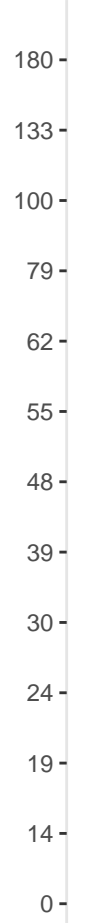
Values from



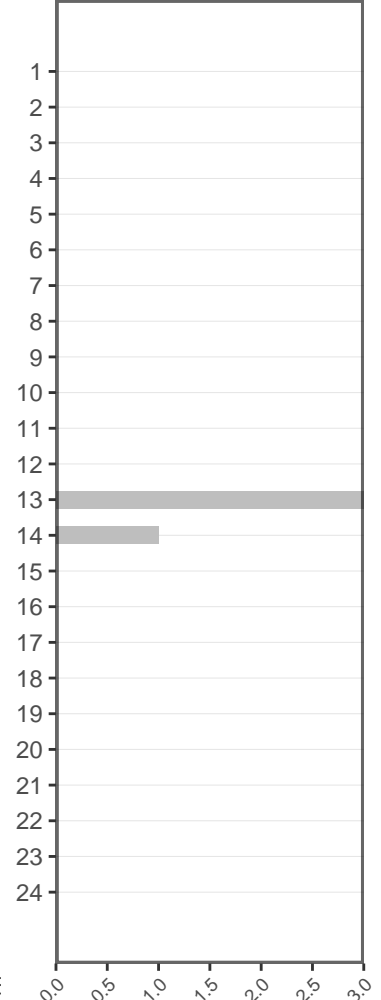
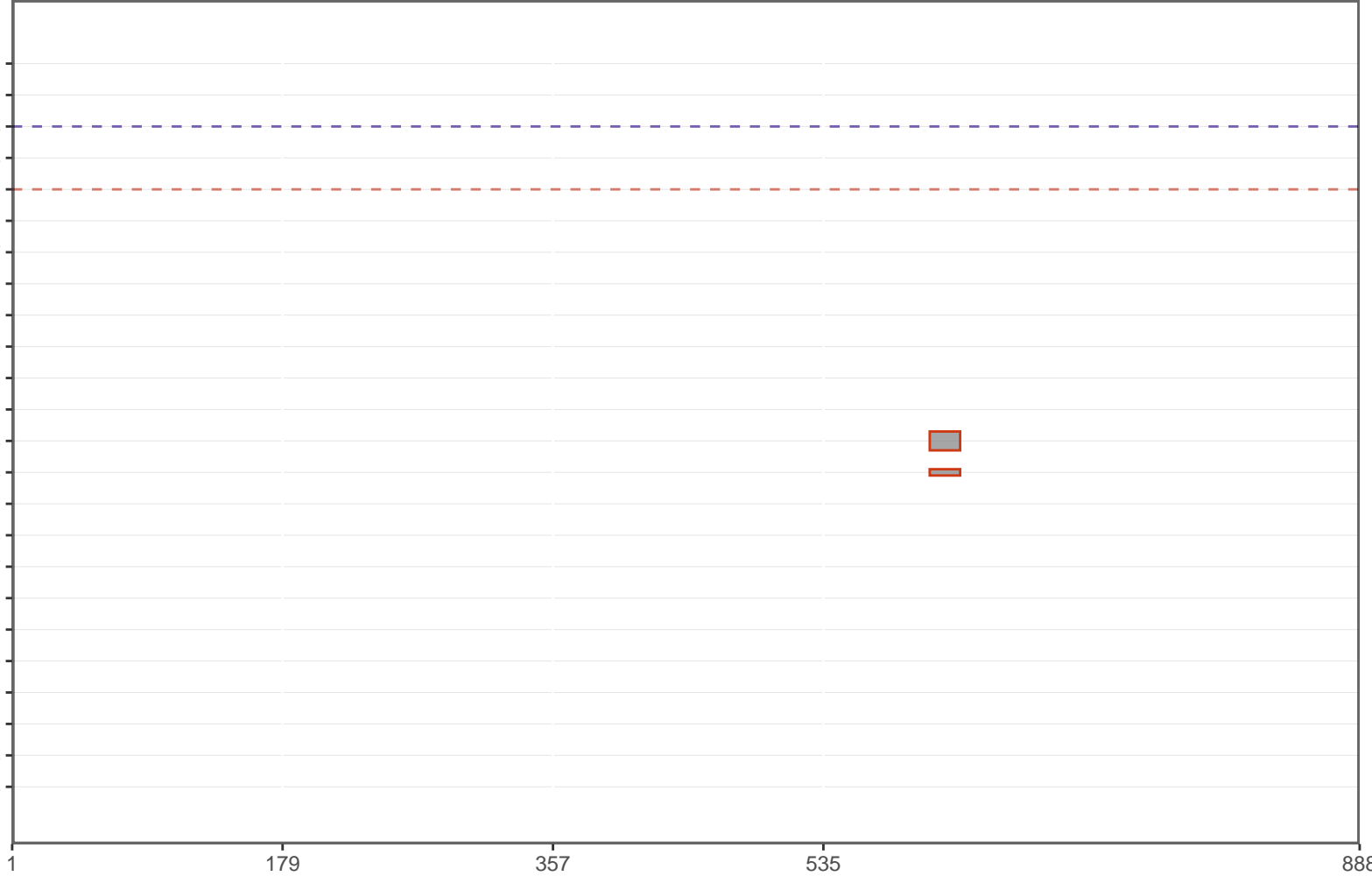
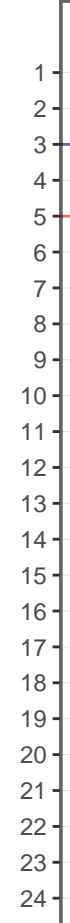
MW indication



Molecular weight



Gel Slice

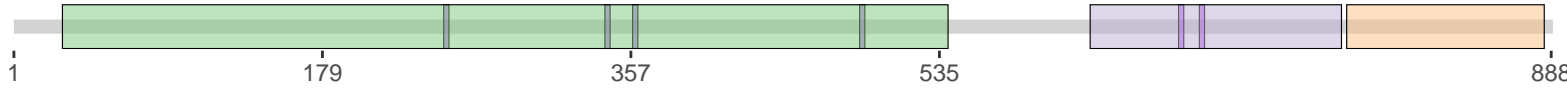


Protein length

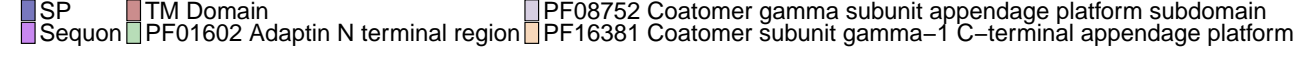


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

PDAAKESGLLILCEFHEDGDEFTVLSGTLHFLGNENEGPKTSDPSKYIRVYHNRIVLENATVRASAVSTLAKFKGALVDLSLKPRIEVLNLRGLFDSDDEVRDRATVLYNLTGGDGAIVETDDEVNEFLGSLVPLNLETSLKKNYEPSEEAFFDFISVPEVMSGQPLAEKAPGKXKPTGLGAPPVGPSTFVDSVERLLSSIPDFADYGLFKSSAPVELTEAEFEVAVNWKHFDGHVYFQYNGTNTIPEGLLENVSVIVDPSEAEFEFSIASKPLKLPVDTPTGQTFVAFEXLEGLGVRAVQKI

NbL07g15060.1 probable_cinnamyl_alcohol_dehydrogenase_1 [MW = 38.99 kDa]

No. of times detected



log(intensity)



Values from



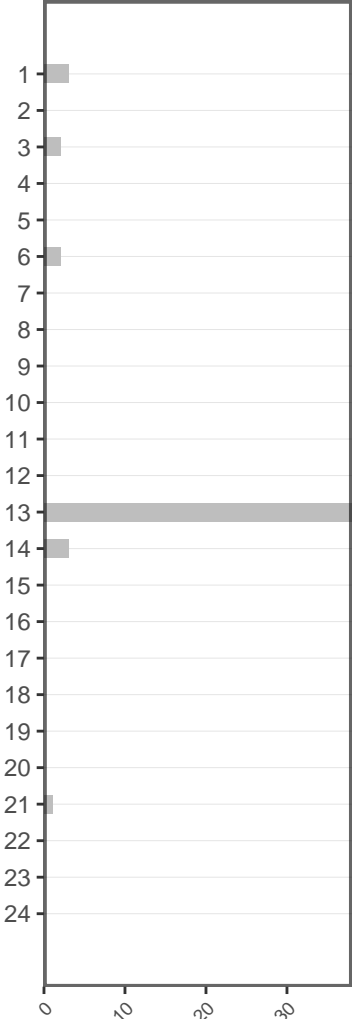
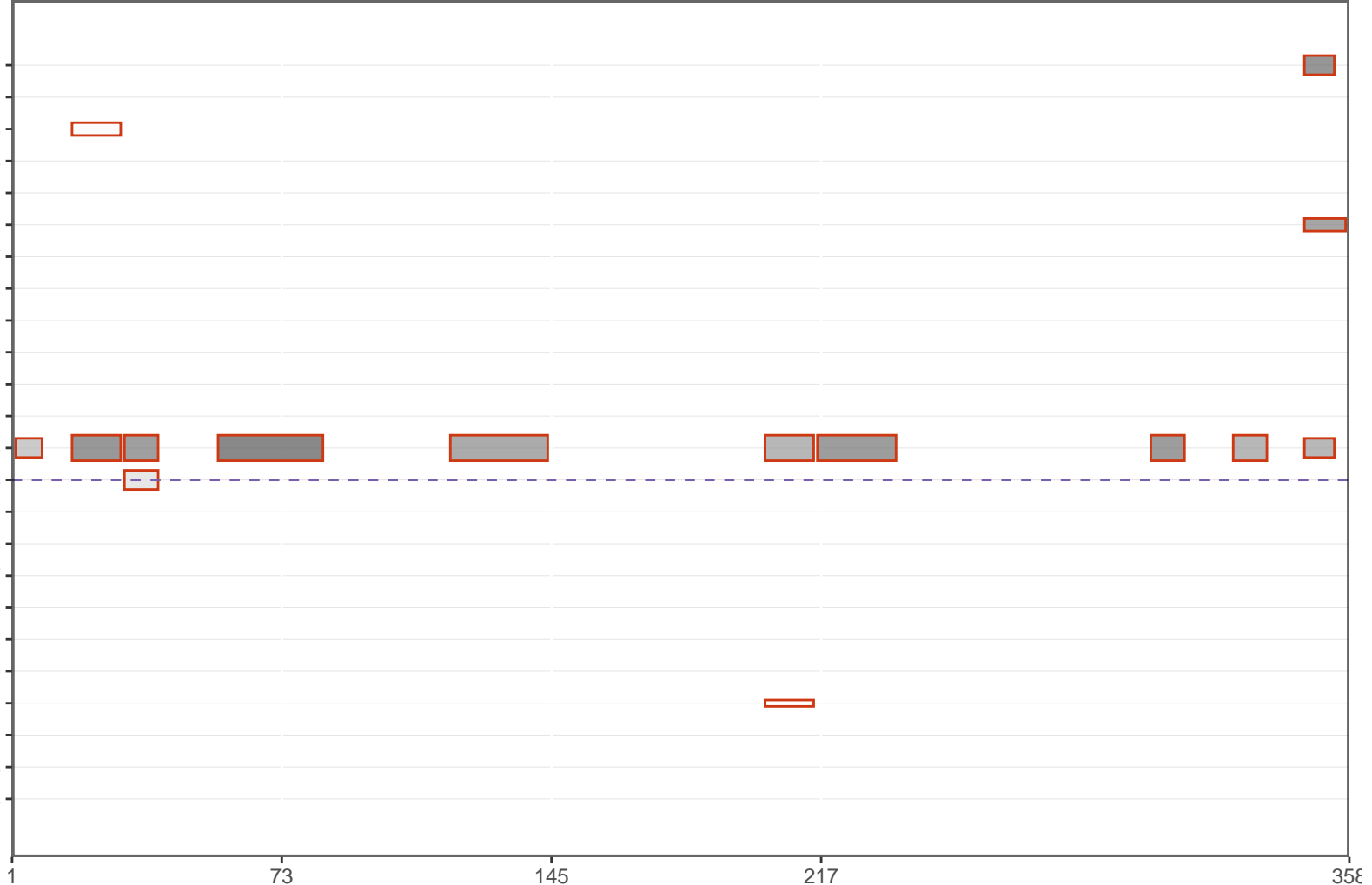
MW indication



Molecular weight



Gel Slice



Protein length

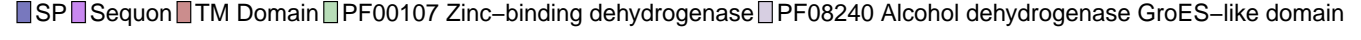


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LCAGLTYSPLNHFGLKQSGSLRGGILGGVGHMGVKKAKMGHHFVSSSDRRKKEALEHLGADEVYSSDTRRMGEAADSLDHDTPVHFHLEPYELLKLDKLLMGVINTPMQFITPMMLGRKTTTGSFGISGMKETEVEVLEFQKEKGLTSGHEVVMMDVNTAMERLEKNDRVRFVDAAGKLDQ

NbL07g14960.1 beta_carbonic_anhydrase_5_chloroplastic-like [MW = 33.54 kDa]

No. of times detected



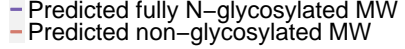
log(intensity)



Values from



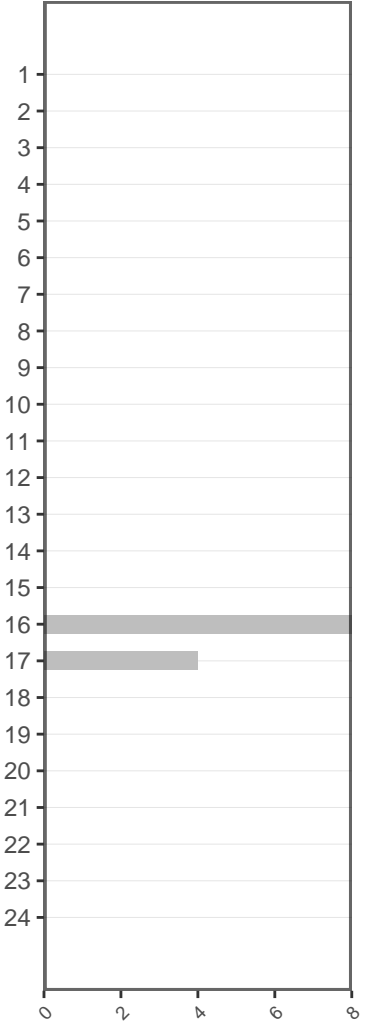
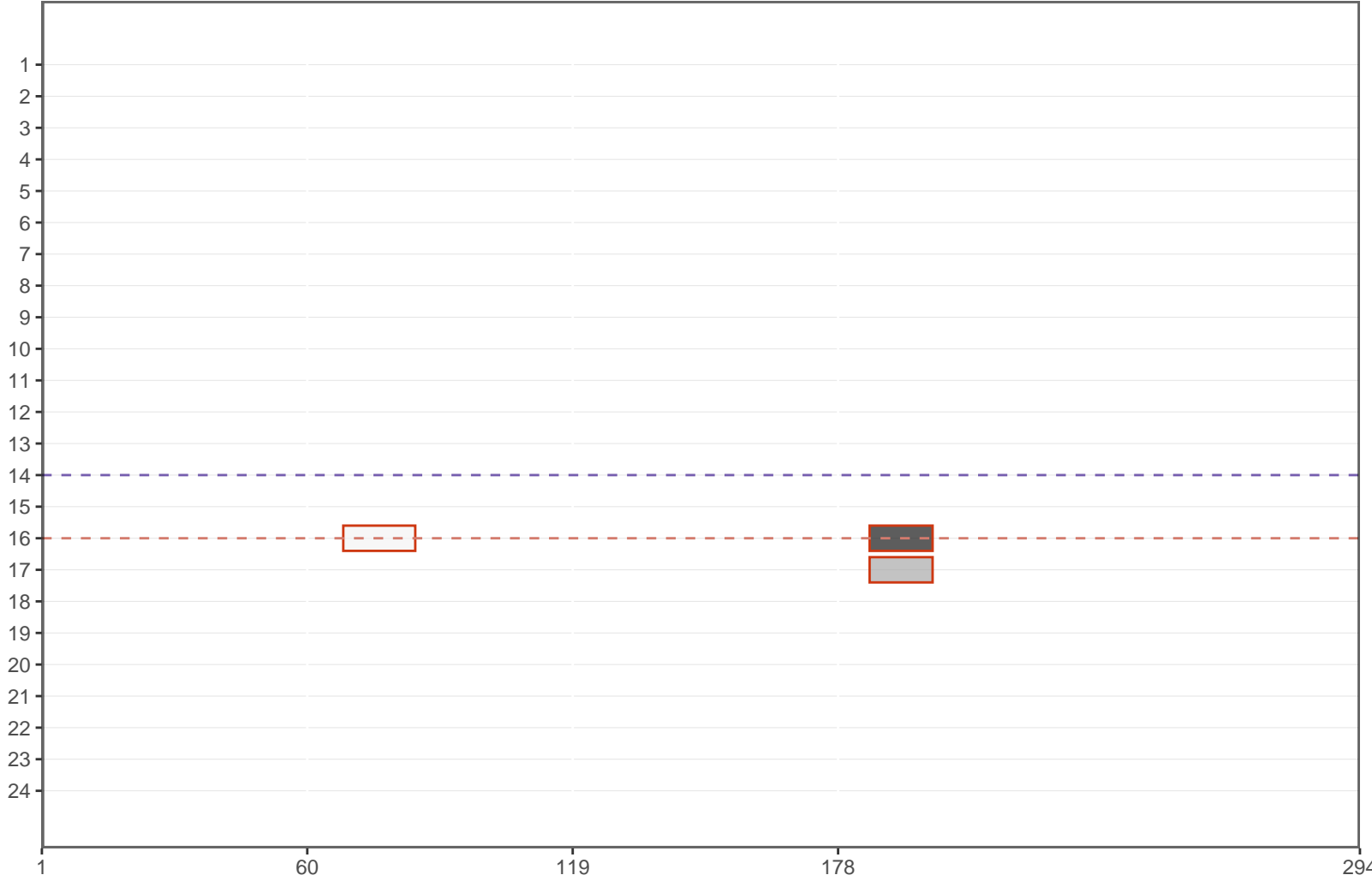
MW indication



Molecular weight



Gel Slice

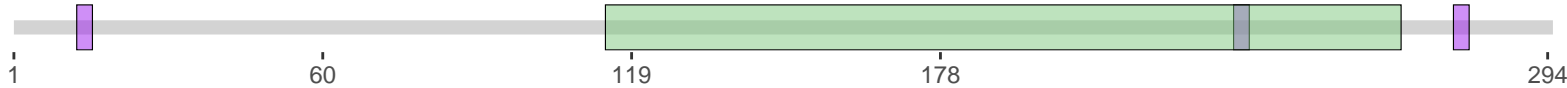


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

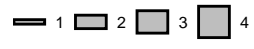


Protein sequence:

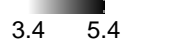
IAFVVRNANLYPPYENGPSSETMALEFAWNTLKVGNLHIGHRGGGRALMSMDSETPSSFRSWWWWGKSARARTKAAANLGFDDGCKHCKEKESVNGSLMNLFFYPWIKDKVYKNGELLHGGVYDFVDCSFEKWTLENNSRVDDGVSRINRFWQ

NbL07g14910.1 proline_aminopeptidase-like [MW = 48.03 kDa]

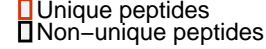
No. of times detected



log(intensity)



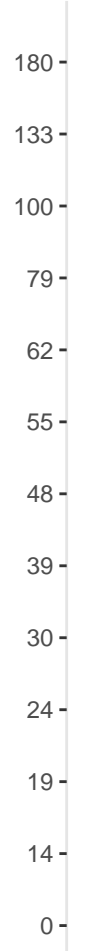
Values from



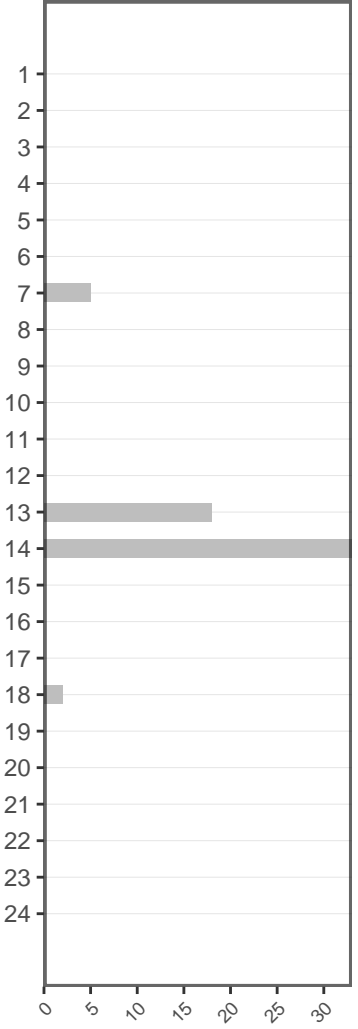
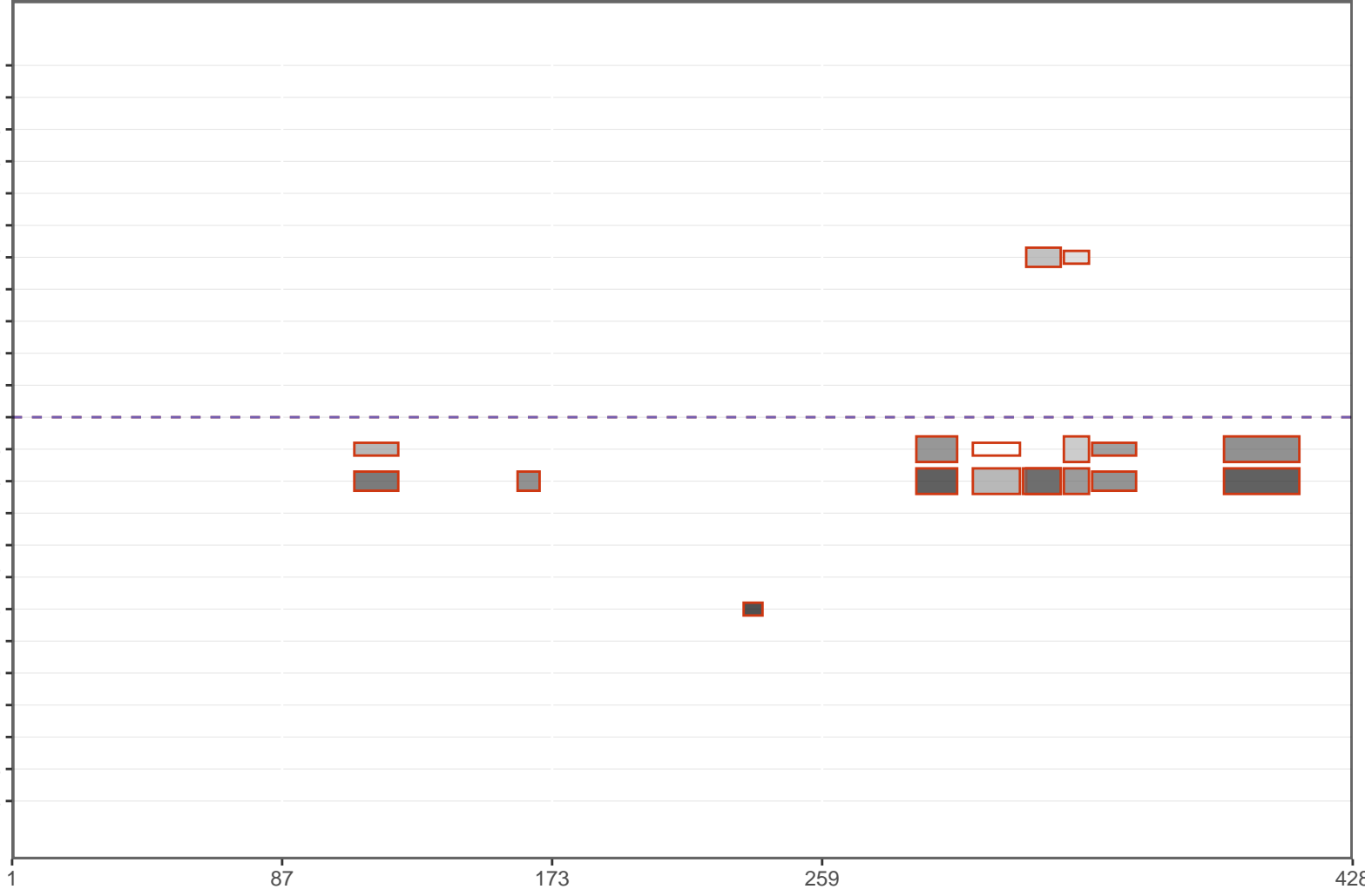
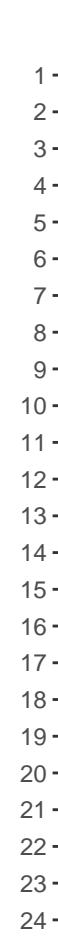
MW indication



Molecular weight

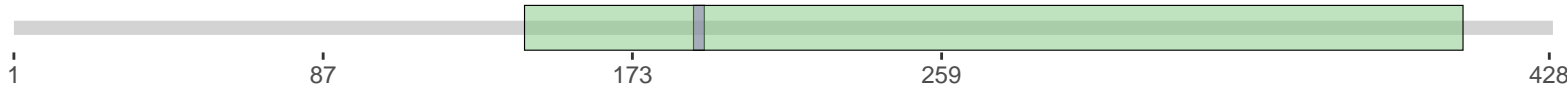


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LRHLEPEWQVYFGGWSGLALAYGSHPEKVTGHLRGIFLLRKKEDWFEVGGAAAFPDWVEPFRDLIPENERKGFVEAHKRLNDDLETQYAAARAWTKWEMMTAHLPEINEENKRGDDDDDFSWAFARINHYFNKGFSSDSEFLLDNVEKIKHKTTFVGRVYVCCPMSAWDLKAWPEAEFRVVPDAGHSANEPGAAKLVAAEKLNKIKGVG

NbL07g14860.1 glucan_endo-13-beta-glucosidase_8-like [MW - SP = 49.94 kDa]

No. of times detected



log(intensity)



Values from



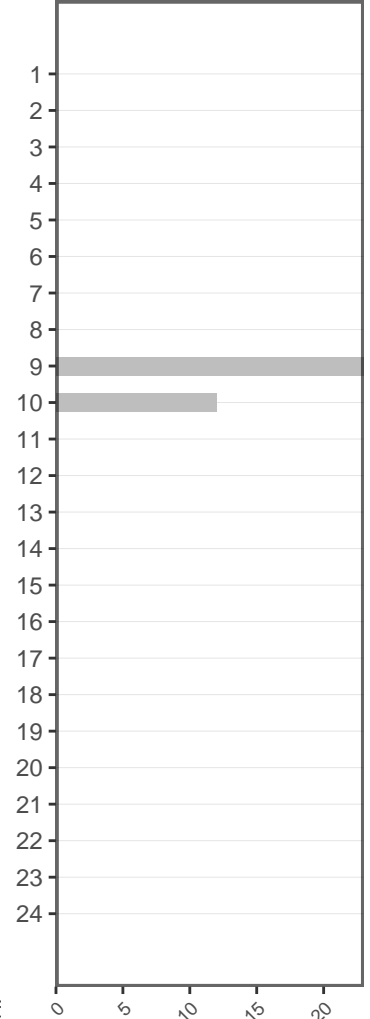
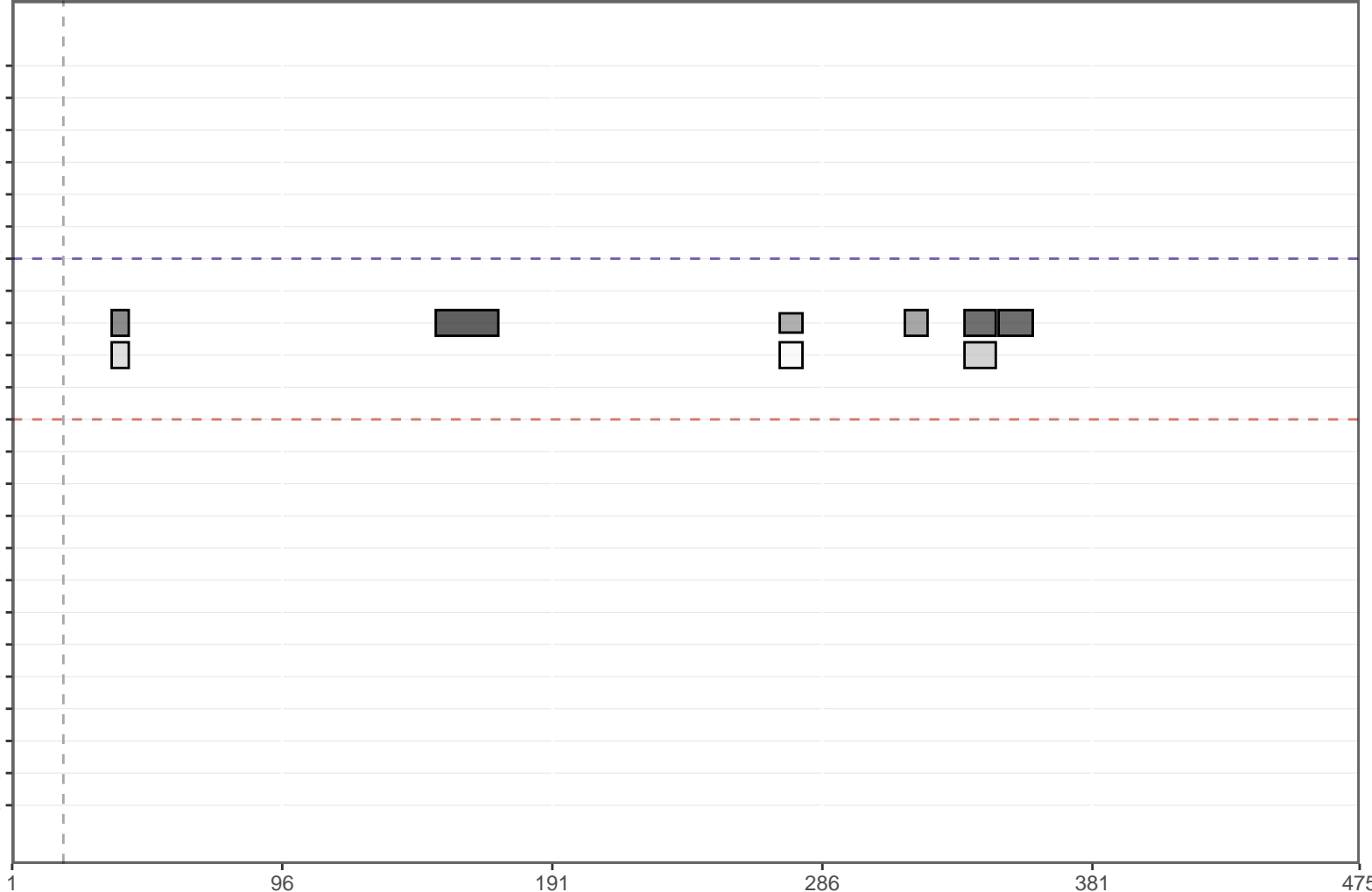
MW indication



Molecular weight

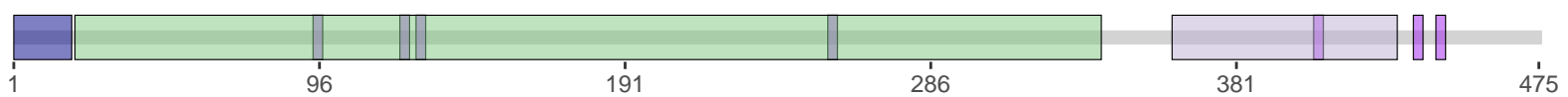


Gel Slice



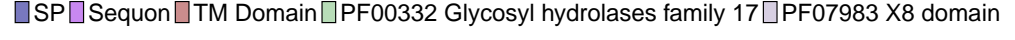
Protein length

Peptide counts over 4 repeats



Pfam domains

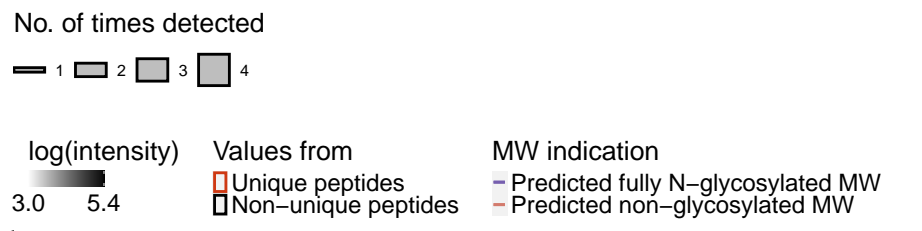
Pfam Description



Protein sequence:

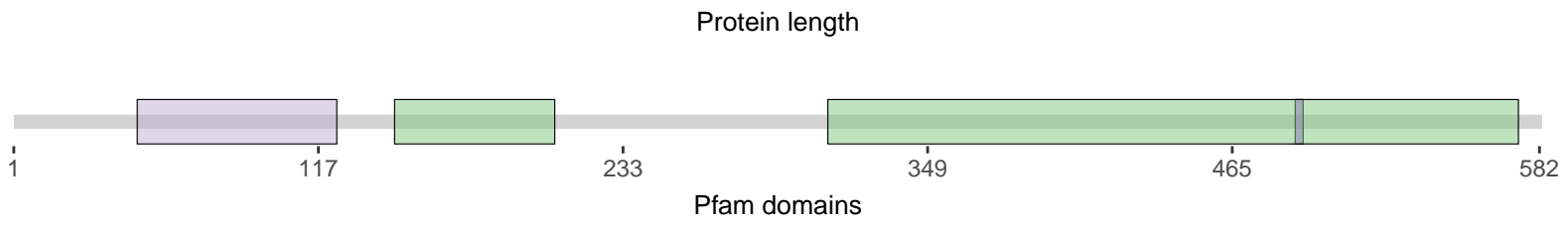
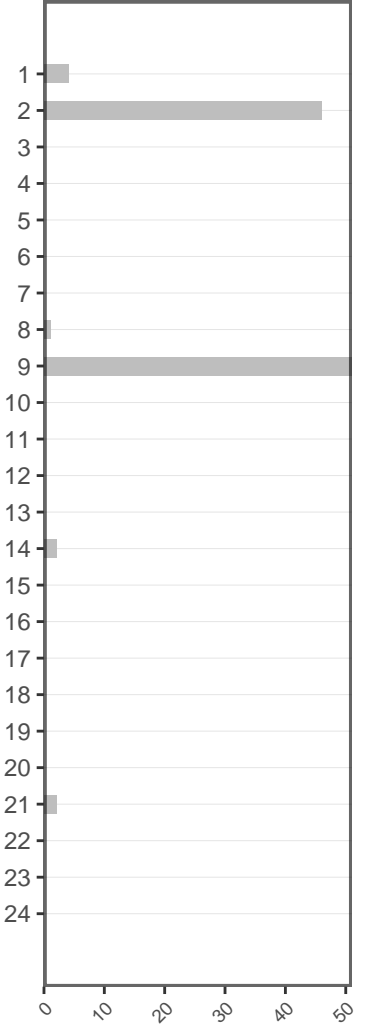
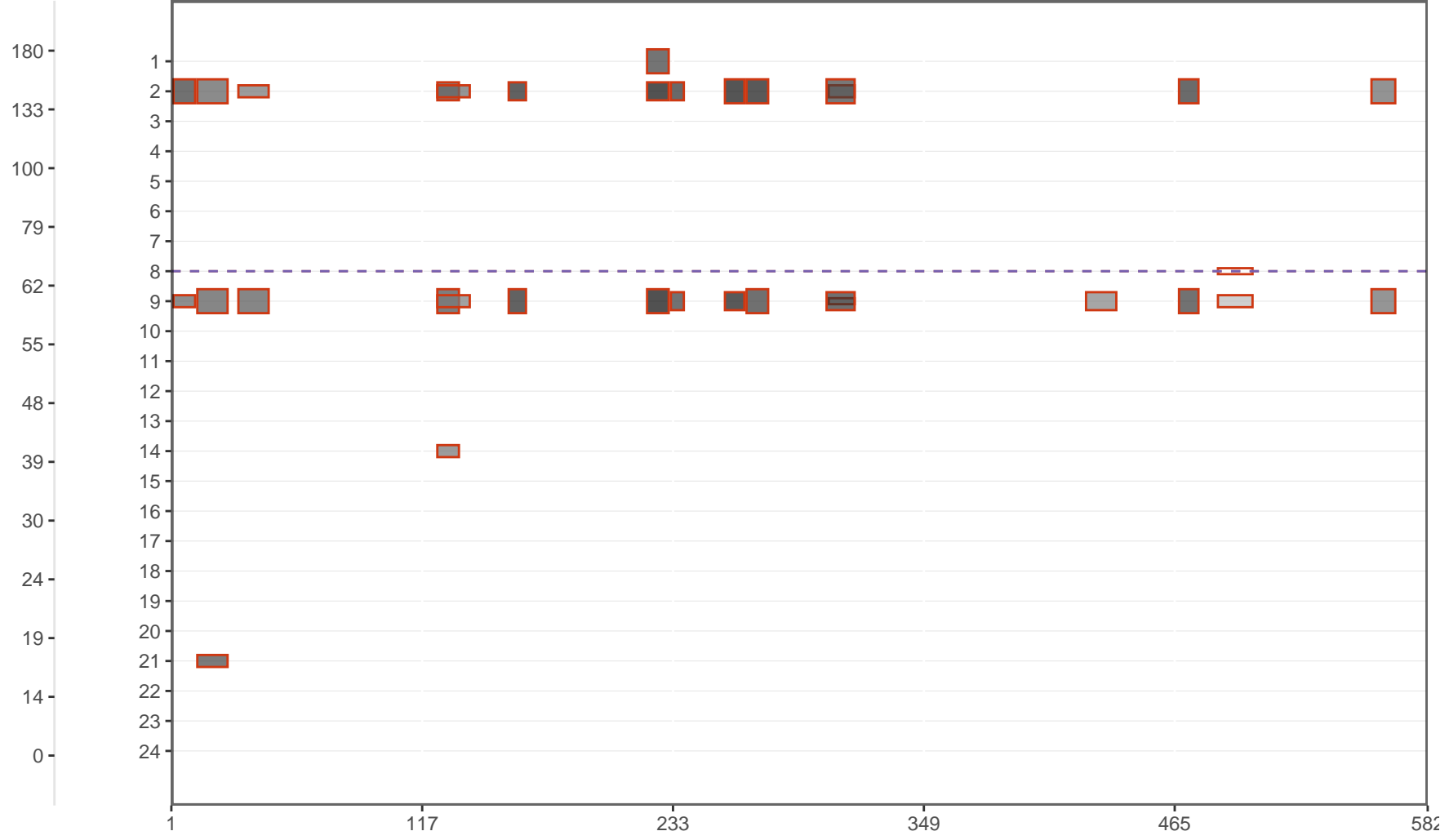
LDKGYTYTNVFDANFDLVSALRAAGVGNMTELVGEVGPWPTDGDKNANVNLAVRFFKGLLSRLAANTGTPLRPGYIEVYVFLGLIDEDGKSIAPGNFERHWGIFRYDGGPKFAMDLTGGGKFLVGAQNVIEYLPKHWMLNPNNAKDLKGLADNDIWAICTFSDGTLGYGSSGGLDANGNAEYAFNMYGAQNGGDFSGCGFQGLAMVTDQNGSQANGNFTQIAYFSQKWLPGPGVALFLTAFTFILL

NbL07g14810.1 asparagine--tRNA_ligase_cytoplasmic_1-like [MW = 64.8 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00152 tRNA synthetases class II (D, K and N)
- PF01336 OB-fold nucleic acid binding domain

Protein sequence:
 KENLLKLERFKLGERVKSAGIPKDGNDYTDFFARGAFLTVSGGLQVETVAGALSSTVTFQPTFRAGQHSRHLAEFVMVEPEIAFDLKDMMNCAEAVKFLDGLWLEHCLDDMEFTFKDKGALGRLRMVTSSKFRHLYTEAIAALEEASKTKTFENKVEWGDLSAEHERVLTTEHFKSPVIVNYPKDKAFVYMKVNEQNKVAAMDLLVPKVDELIGSGSREEDVEVALRSRISDMGLALEPEWYLDLRRYGVYKHSGFGLGFERMILFATGMENRDVIFP

NbL07g14780.1 costars_family_protein [MW = 12.13 kDa]

No. of times detected



log(intensity)



Values from



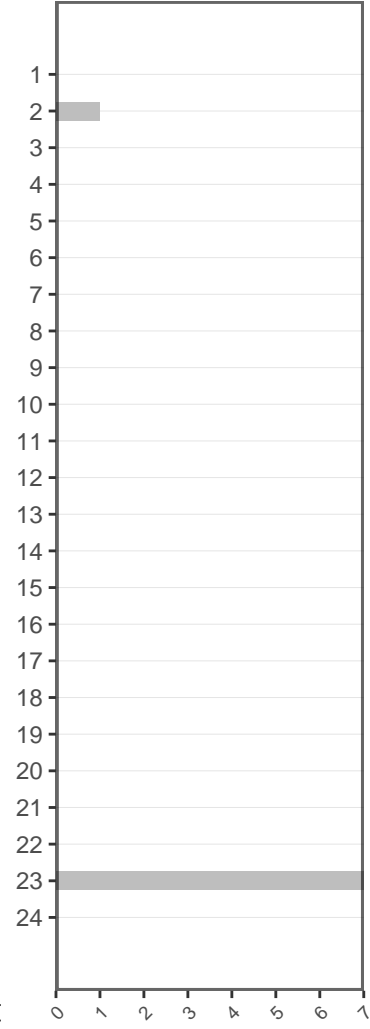
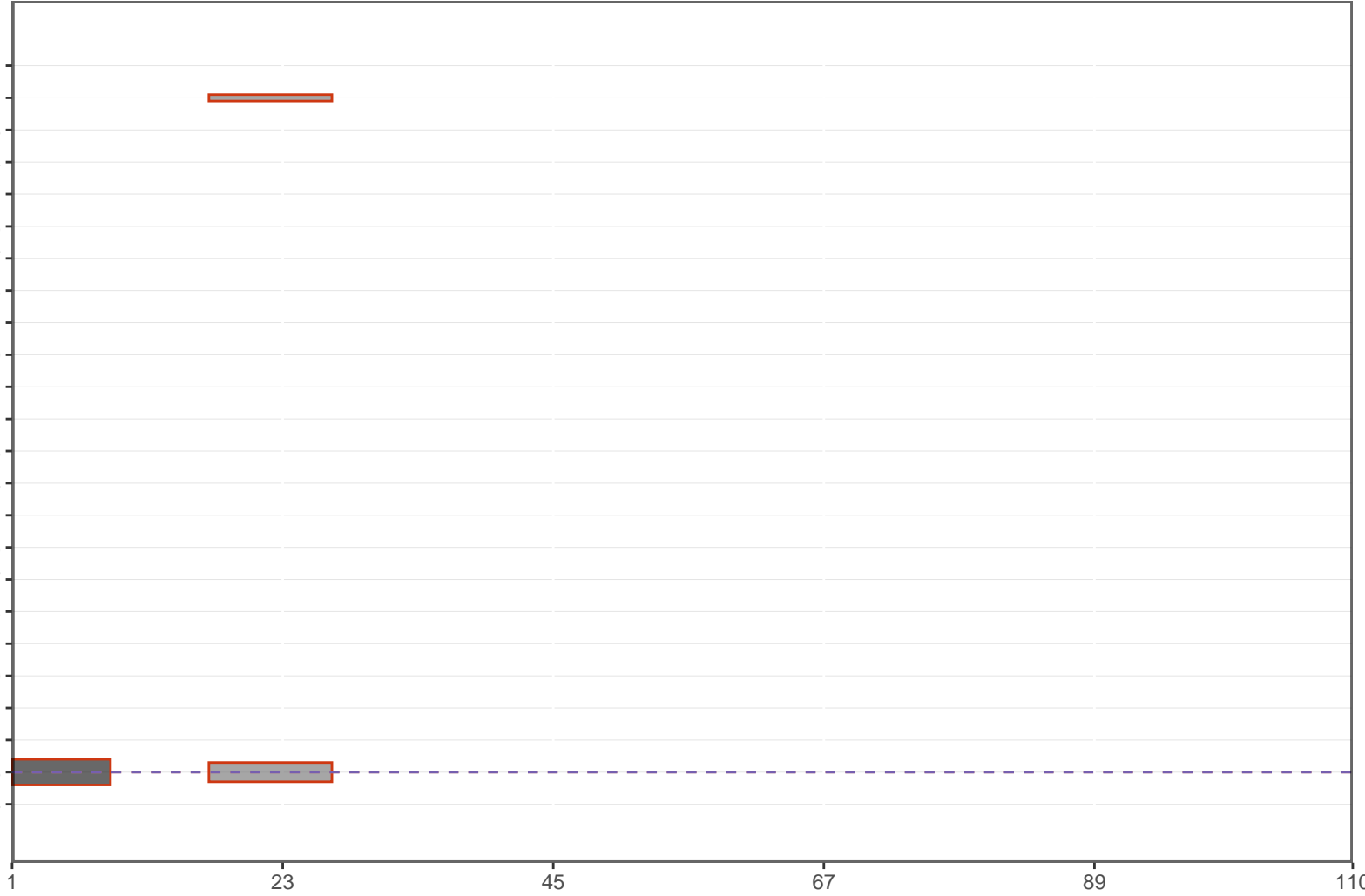
MW indication



Molecular weight



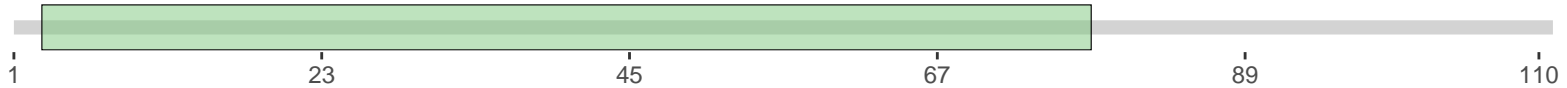
Gel Slice



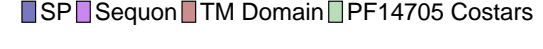
Protein length



Pfam domains



Pfam Description

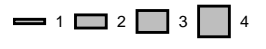


Protein sequence:

NIFEALVGLTRAAKKRKLAYDGEILLGGVHNDVEHLKPPSVTSGASALFILSVAPRVAAWKQLPFGP

NbL07g14700.1 polypyrimidine_tract-binding_protein_homolog_3-like [MW = 49.15 kDa]

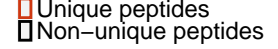
No. of times detected



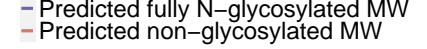
log(intensity)



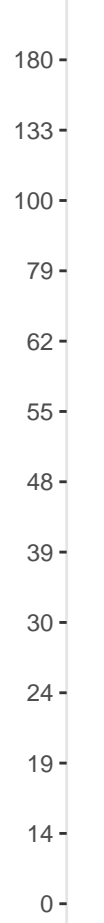
Values from



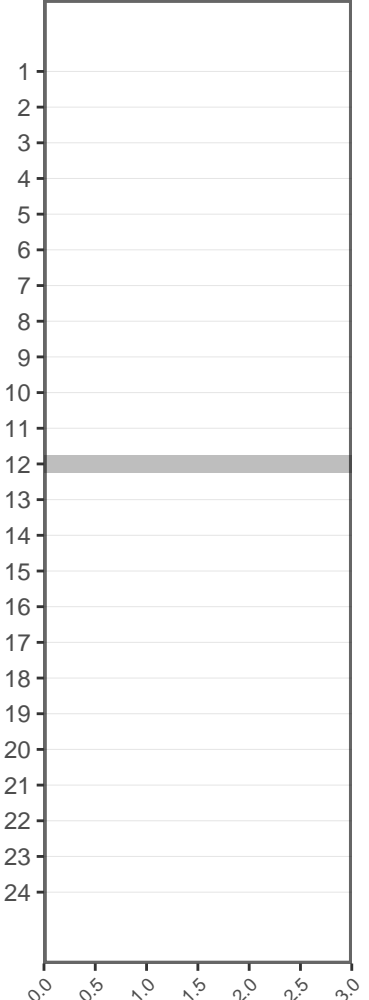
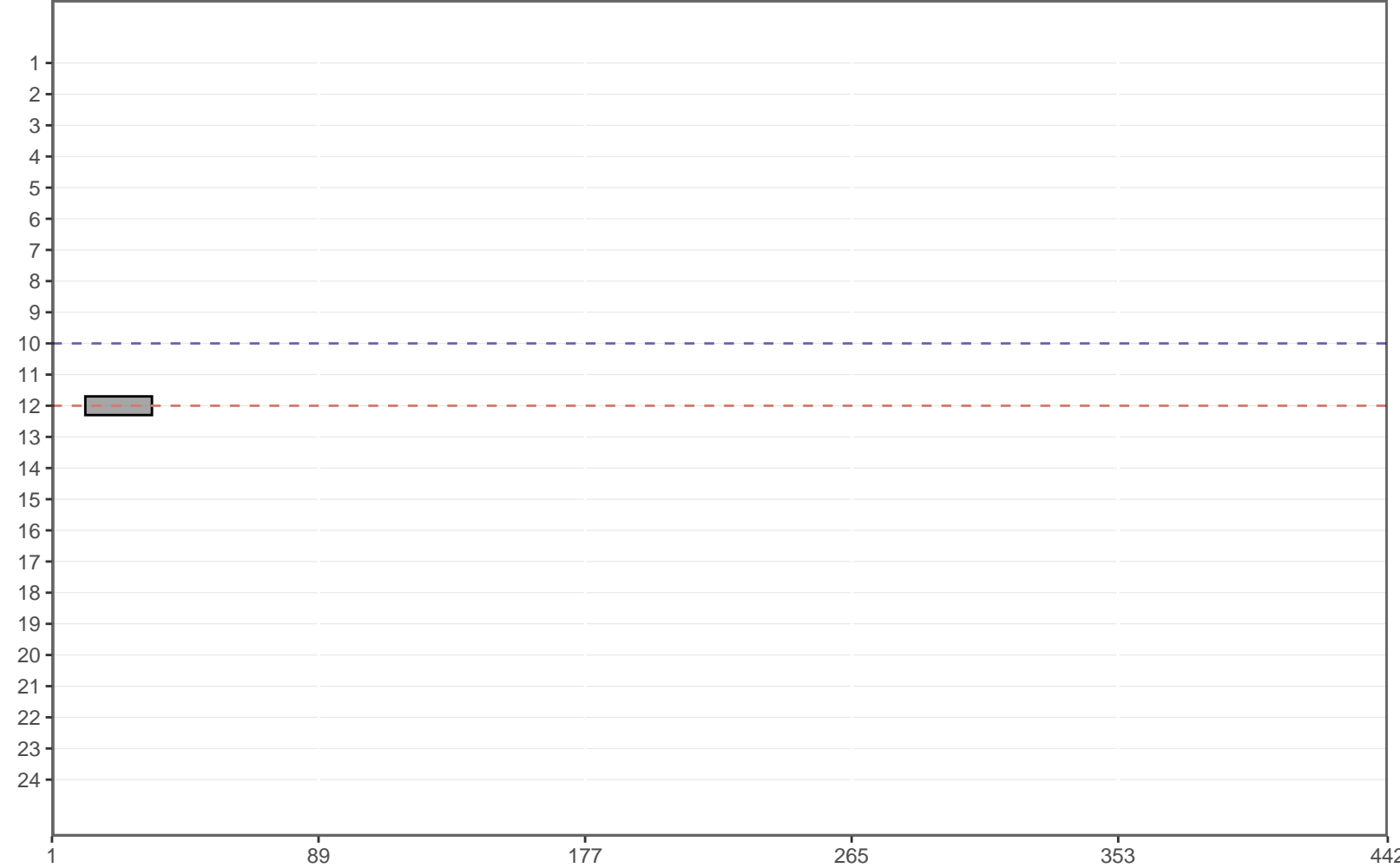
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- PF11835 RRM-like domain
- PF13893 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

Protein sequence:

IQOQYGDYSPQGGGAHAGGFPMGNNAEAMAAFAAGLPPGISGTNRDRTILVSNLDSDDRIDEDKLFNLSLYGNVKKIKLRKPDHALVQMGDFGQAEALVHFLKGAIFDKRLVAVNFSPKPNITTTGPDTHDYNSNLRNFRNRNAANNRYRGGSPTKMHLGSLPQDTEEEVAHLEEHGSIINRKLIFEMNGKQGAALVLFENEQEQATEALVQKNKATSLGGSTIRISFQQLQSI

NbL07g14600.1 adenylyl-sulfate_kinase_3-like [MW = 23.08 kDa]

No. of times detected



log(intensity)



Values from



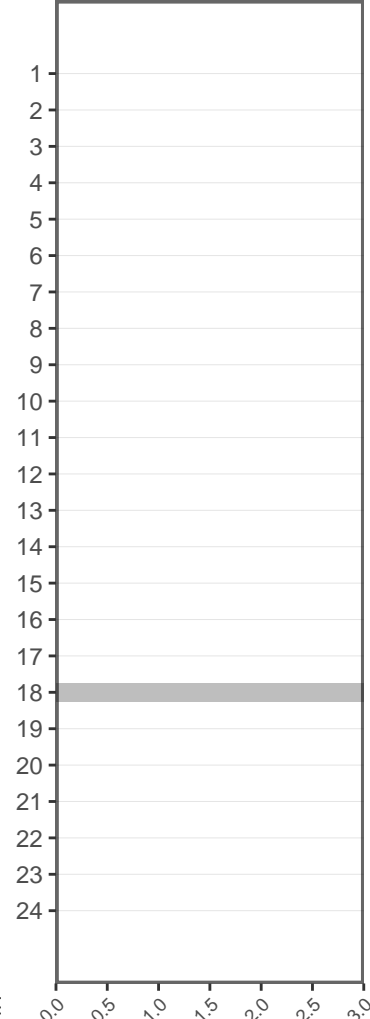
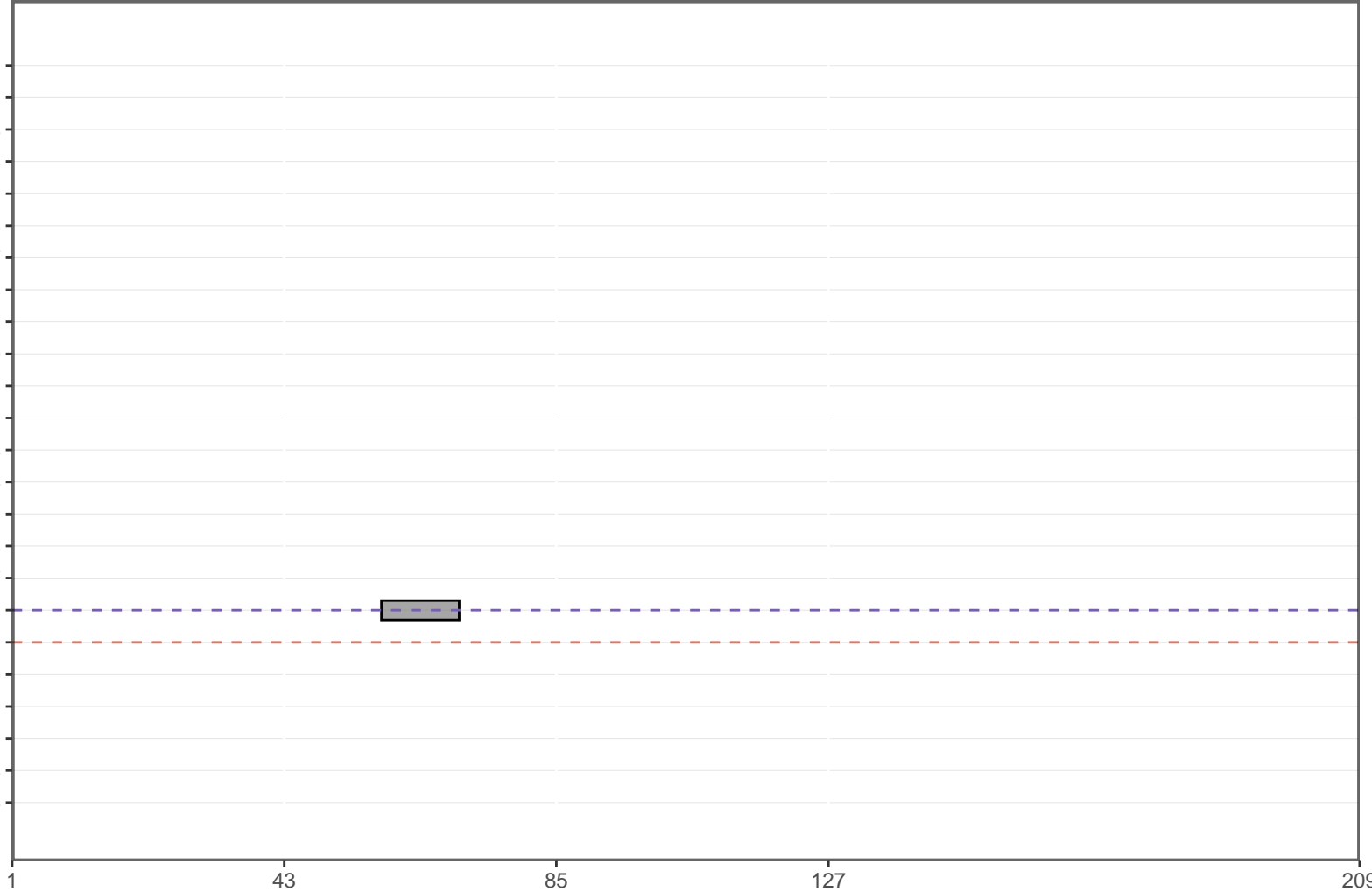
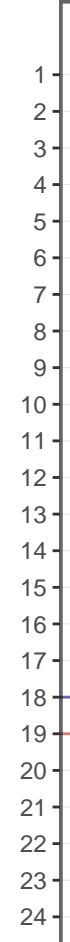
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

VVEVSKLFDADGLGICSLISPIVRRDRDAGRALFPDKSFIEVFMNMPLLELGEGRDPKGLYKLRAGKIKGFTGIDDPYEPPLNGEIEQKDGVPVPTHEMAGGVVPTMEDRGLKAG

NbL07g14450.1 photosynthetic_NDH_subunit_of_subcomplex_B_2_chloroplastic-like [MW = 38.82 kDa]

No. of times detected
 1 2 3 4

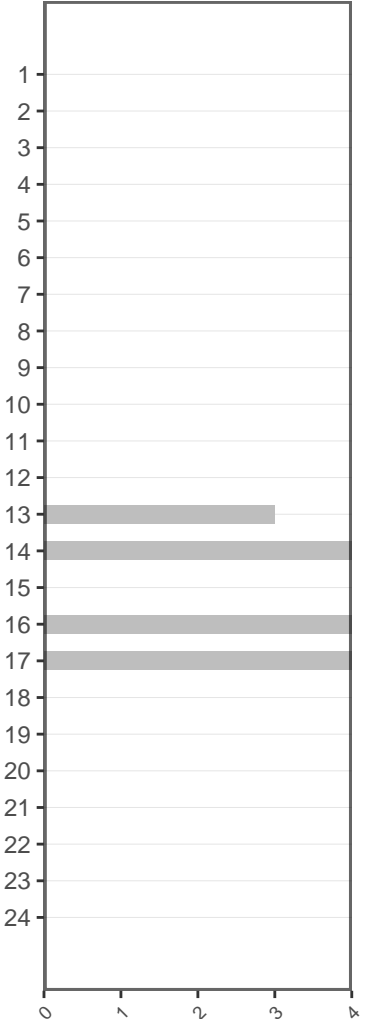
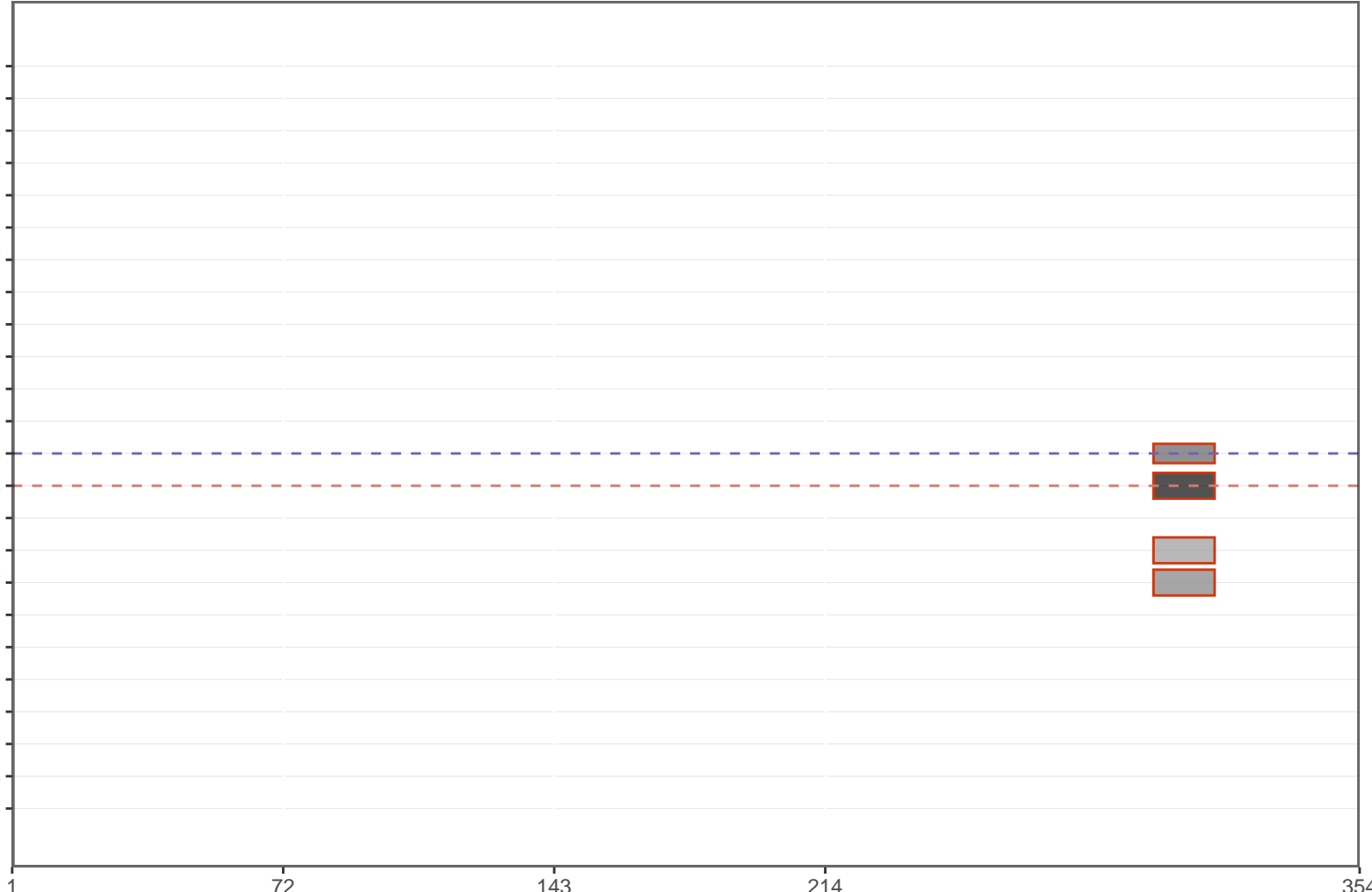
log(intensity) 4.0 4.4
 Values from Unique peptides Non-unique peptides
 MW indication Predicted fully N-glycosylated MW Predicted non-glycosylated MW

Molecular weight

Gel Slice

180
133
100
79
62
55
48
39
30
24
19
19
14
22
23
24

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24



1 72 143 214 354
 Protein length

1 72 143 214 354
 Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

MATAIVYVNGSRKPKLMSAILSHLKFTRTGIGLRSCTYCAHPLRSPFELSPGEAMKTEEPGLFSGWEPKPGIWSAODVPTLKHKLRLVYVPEERAKEFYNSIPSKYETDGGRELFFRIIRMGFEDIFLSSPFSKDYKGEYFICTGPAAMLVPLVNPNGEWRGAQVEHDNL

NbL07g14400.1 probable_phosphatase_SPAC5H10.03 [MW = 31.48 kDa]

No. of times detected



log(intensity)



Values from



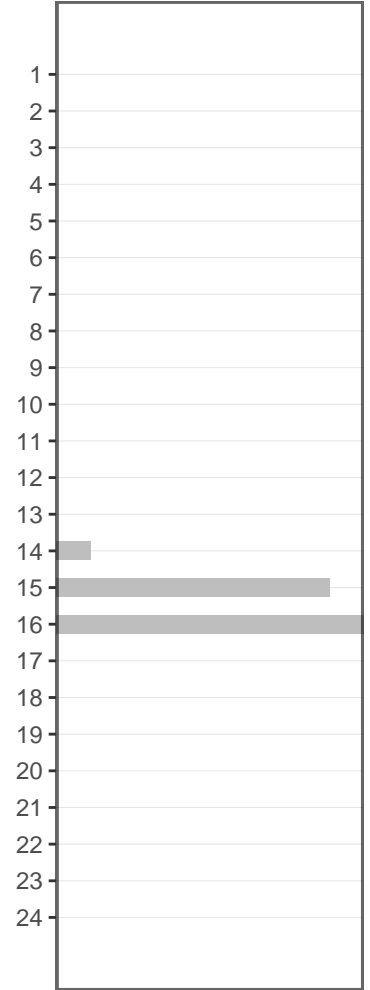
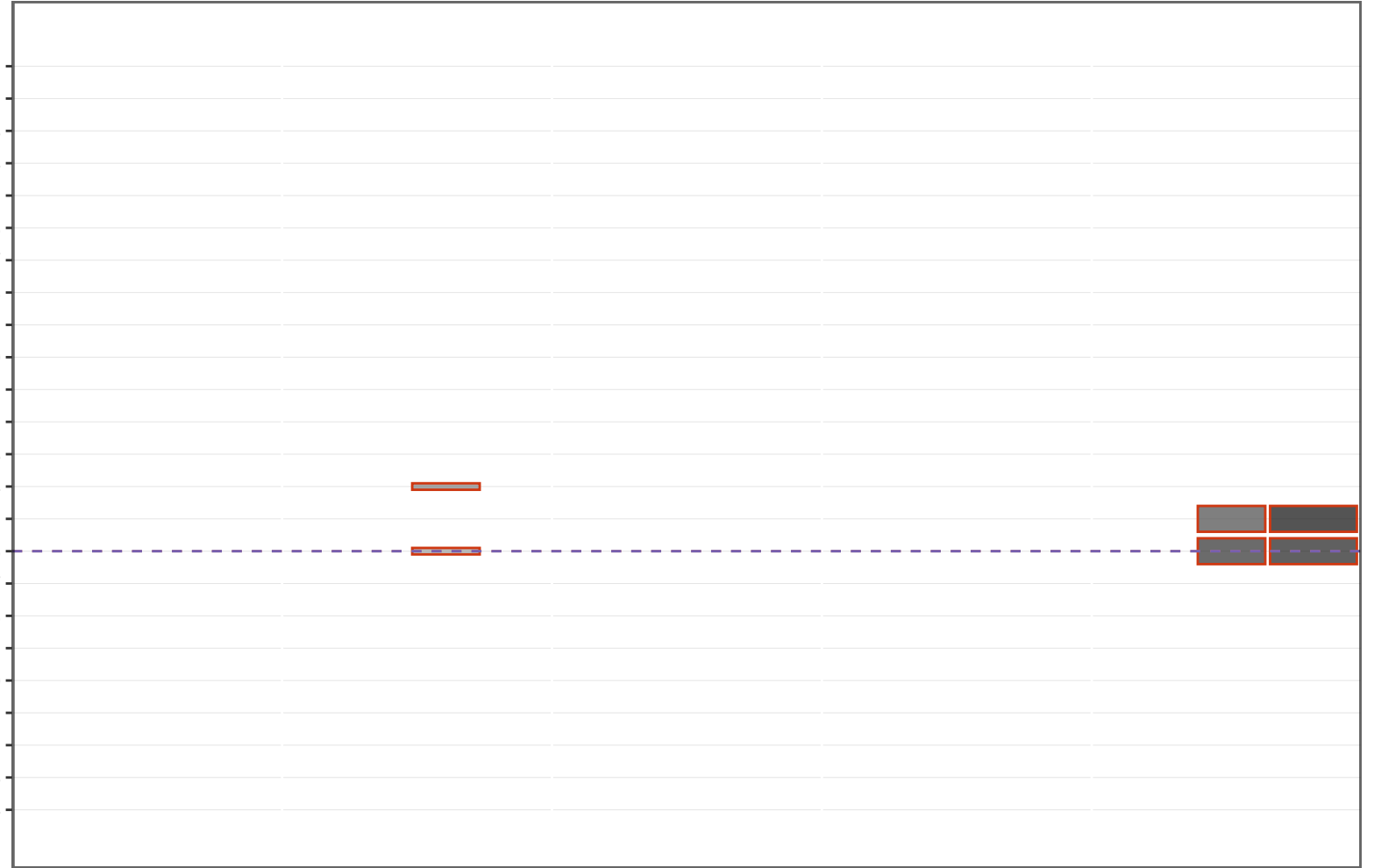
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

PIAHLELREHLGVHPGDSRRBVRREYVGLFFPADLSLIESDEDTLWKNVRETKEEVMARGKFLNWLTRKEKEIMVSHNGLFHTLNAFGTDCDHPFVKEICKRFDFNGLRSMVDFDRSMGSDSSITFYPGKIPGAAILPSEADESSGER

NbL07g14170.1 probable_receptor-like_protein_kinase_At5g24010 [MW - SP = 89.02 kDa]

No. of times detected



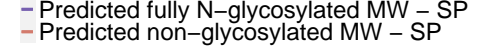
log(intensity)



Values from



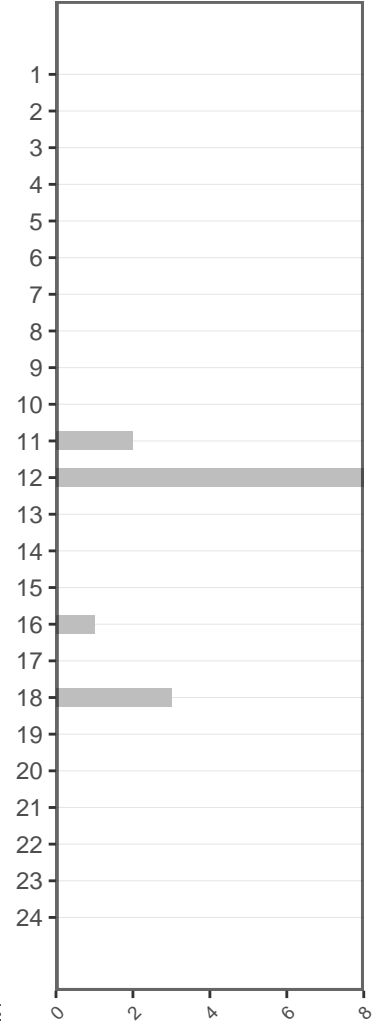
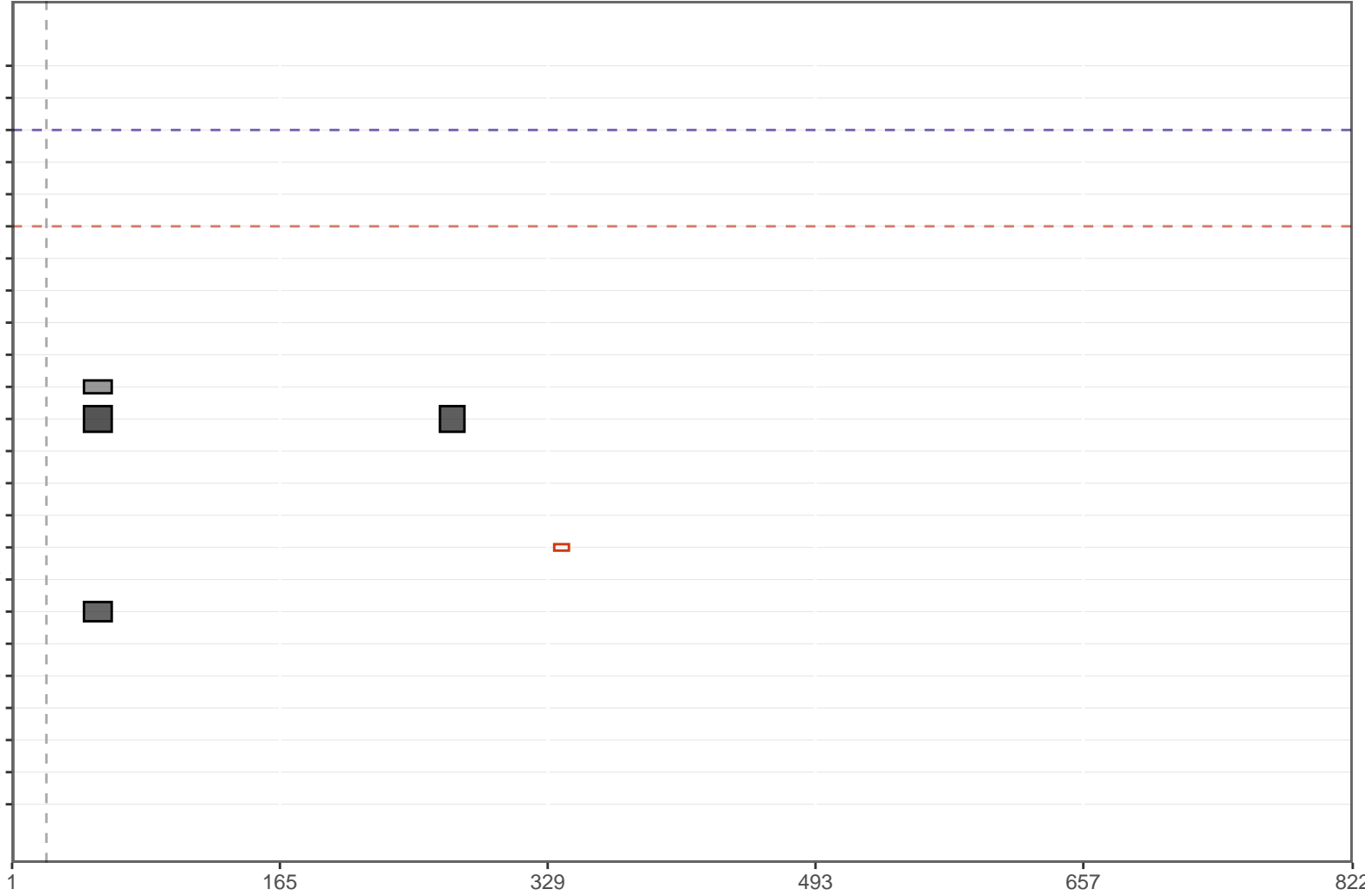
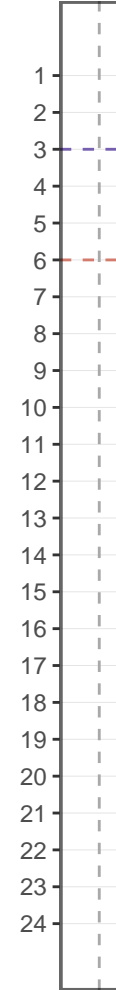
MW indication



Molecular weight

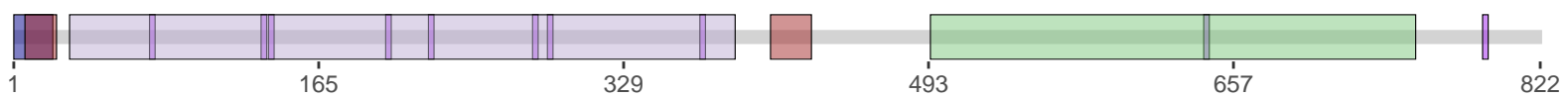


Gel Slice



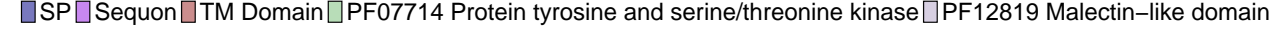
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKRRNVIIVSSVLSGFLLEVLVLLVLLVYGRKQKLNPKRSEBAGWTLRLRGYGSSTHGLSDGTSEVQPNGLGGRIPFAEIGSATNFDKSLVIGSGGFGMYYKAVLGNRRKVAIKRQVPSGRQGLPEFHTETVLSKIRHHLVSLVGYGCEGSEMLVYEMEKGLPKRHLVYGPITPLSWKGRVVEIGGAARGLHLYHTGFAGGIIHRDKSTNILLDENYKAVADFGLRSTGPGLNETHVSTGVKGSFGVLDPEVYFRQGLTKNEDVYVFGVVLFEVLCARPAIDPLLSRE

NbL07g14110.1 60S_ribosomal_protein_L21-1 [MW = 18.64 kDa]

No. of times detected



log(intensity)



Values from



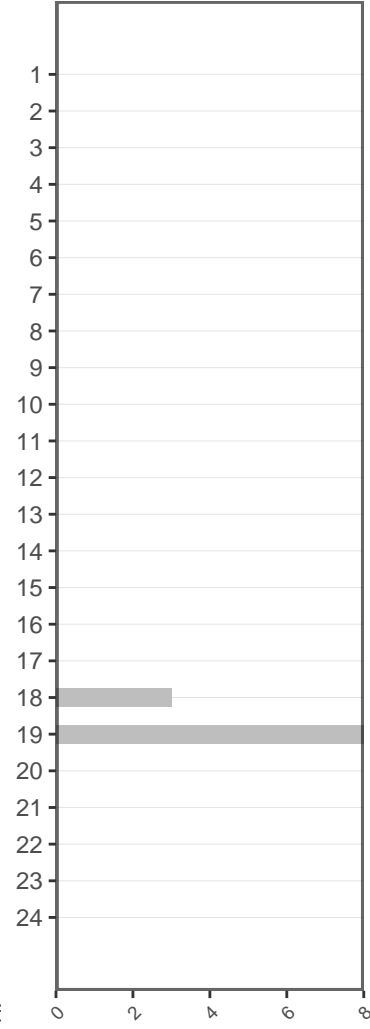
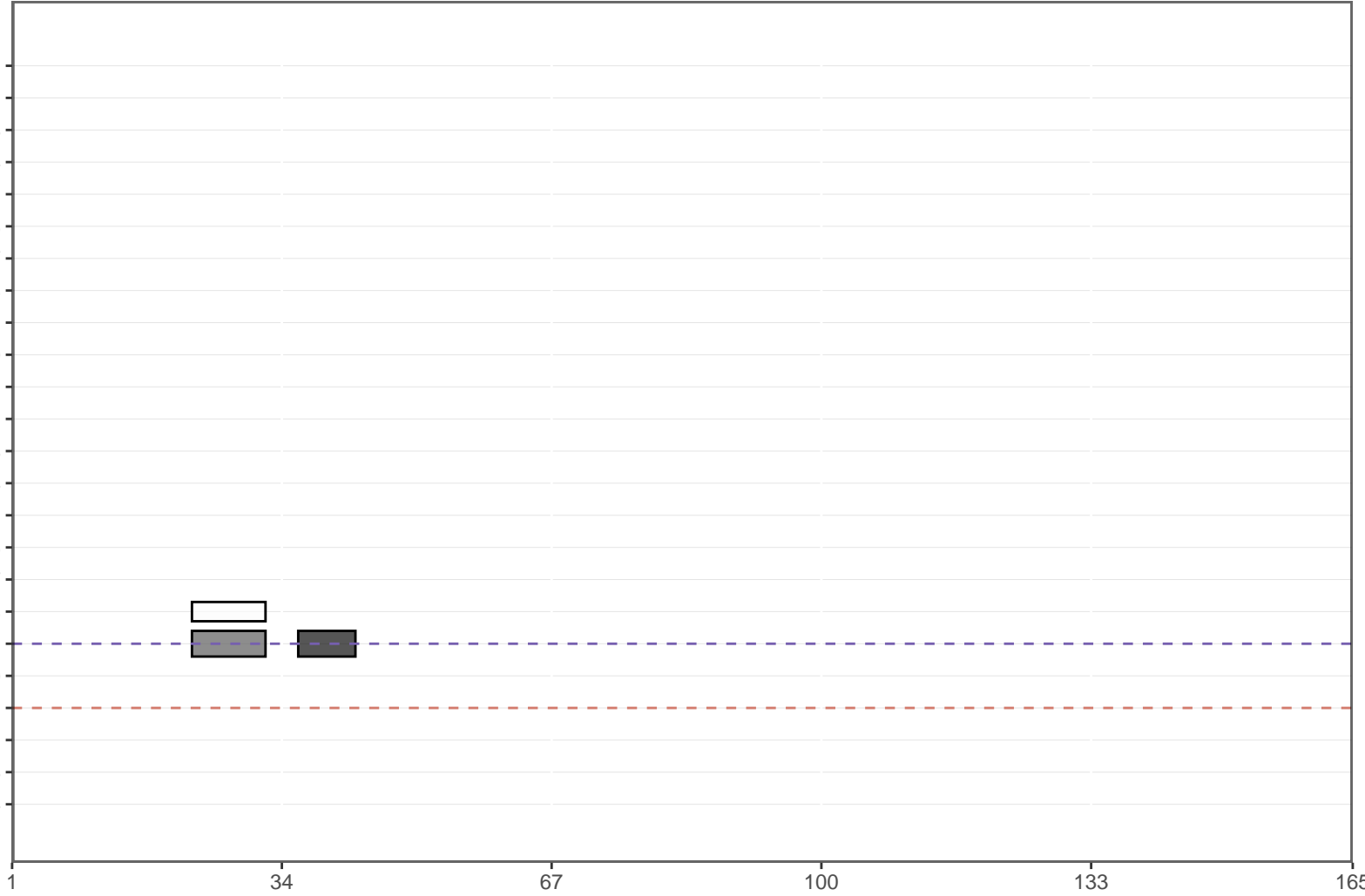
MW indication



Molecular weight

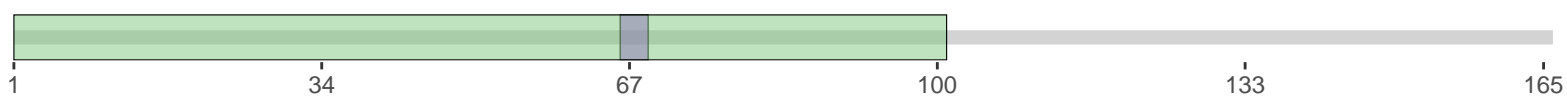


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

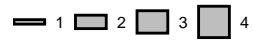


Protein sequence:

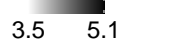
KRAVGVENVKQVFNKILKRIHRIEHWQLSRGTEEVKERIKKNDQLKAEAKARGEVSTRKQGGPKPGFMVEGATLETVPVVDVNDLKGKY

NbL07g14080.1 UDP-glycosyltransferase_74F2-like [MW = 51.4 kDa]

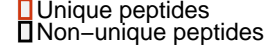
No. of times detected



log(intensity)



Values from



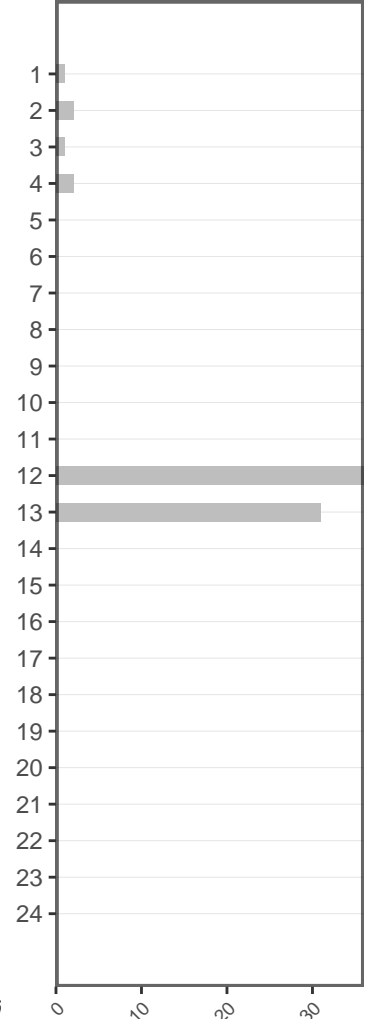
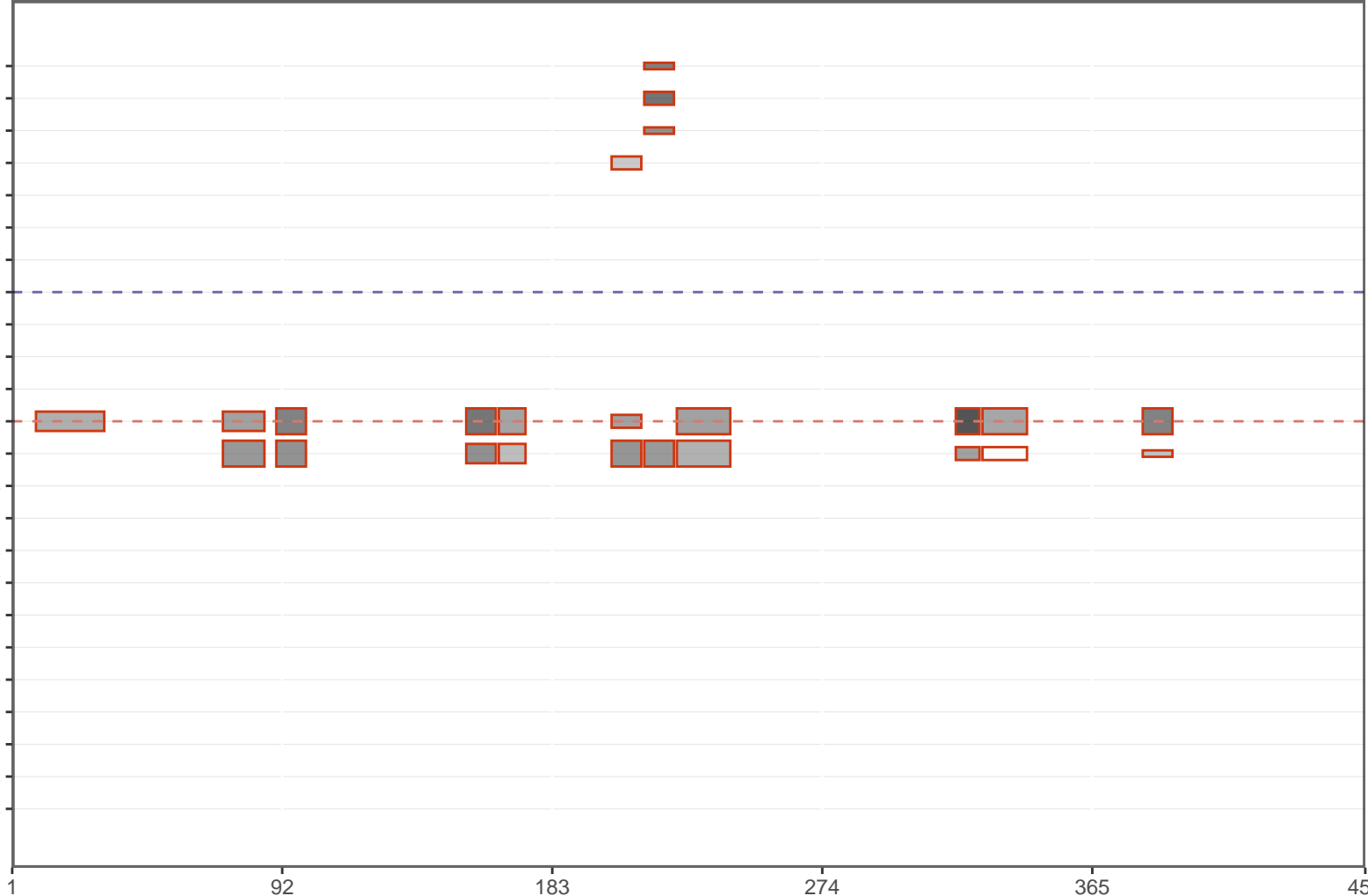
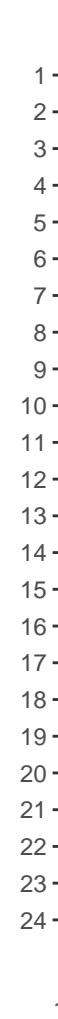
MW indication



Molecular weight

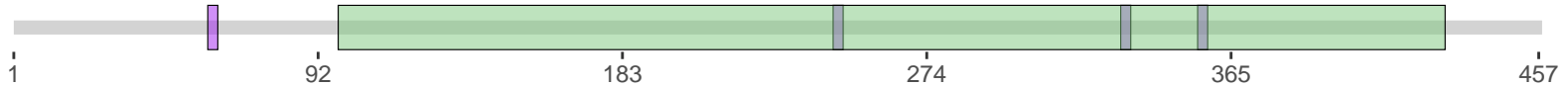


Gel Slice



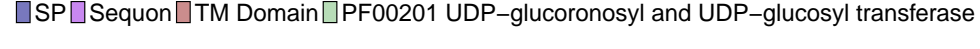
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IMSKVPMSTIGTFLPSLIDNRVENDTEYGLSLYQVDAFTGHWLNTKTEGSAVYVAFGDMSTMENQMEIEAWGLKATNYFLVWVRTODEAKIPKPIEETSEKGLVNVNSPQLGILSNKAAMFFSHGQVNSTTEALSLGVPMVWMLVFDGTTNAKLVGDVWVSGVYRVSVNEKGFAGREEIEKQVRIWMEGDKGKEMKKNLAKWDLAKEAVNEGGTSDKNIEEFVSKGTR

NbL07g14010.1 uncharacterized_LOC107782443 [MW = 42.27 kDa]

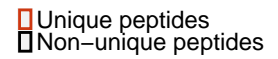
No. of times detected



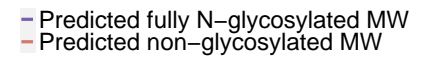
log(intensity)



Values from



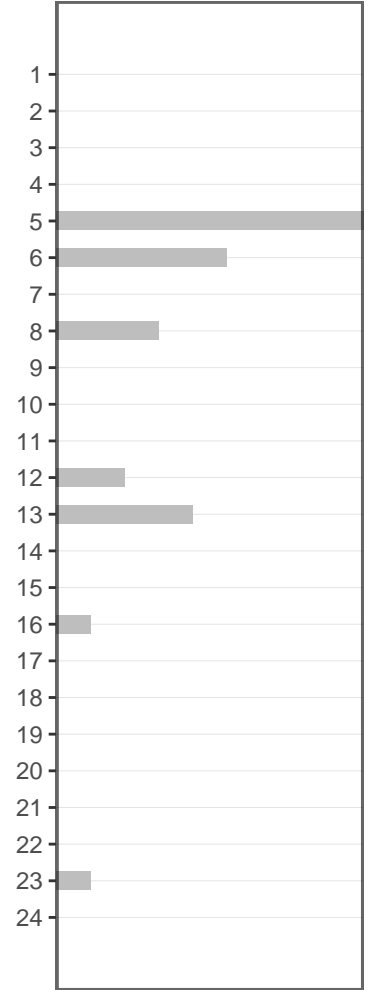
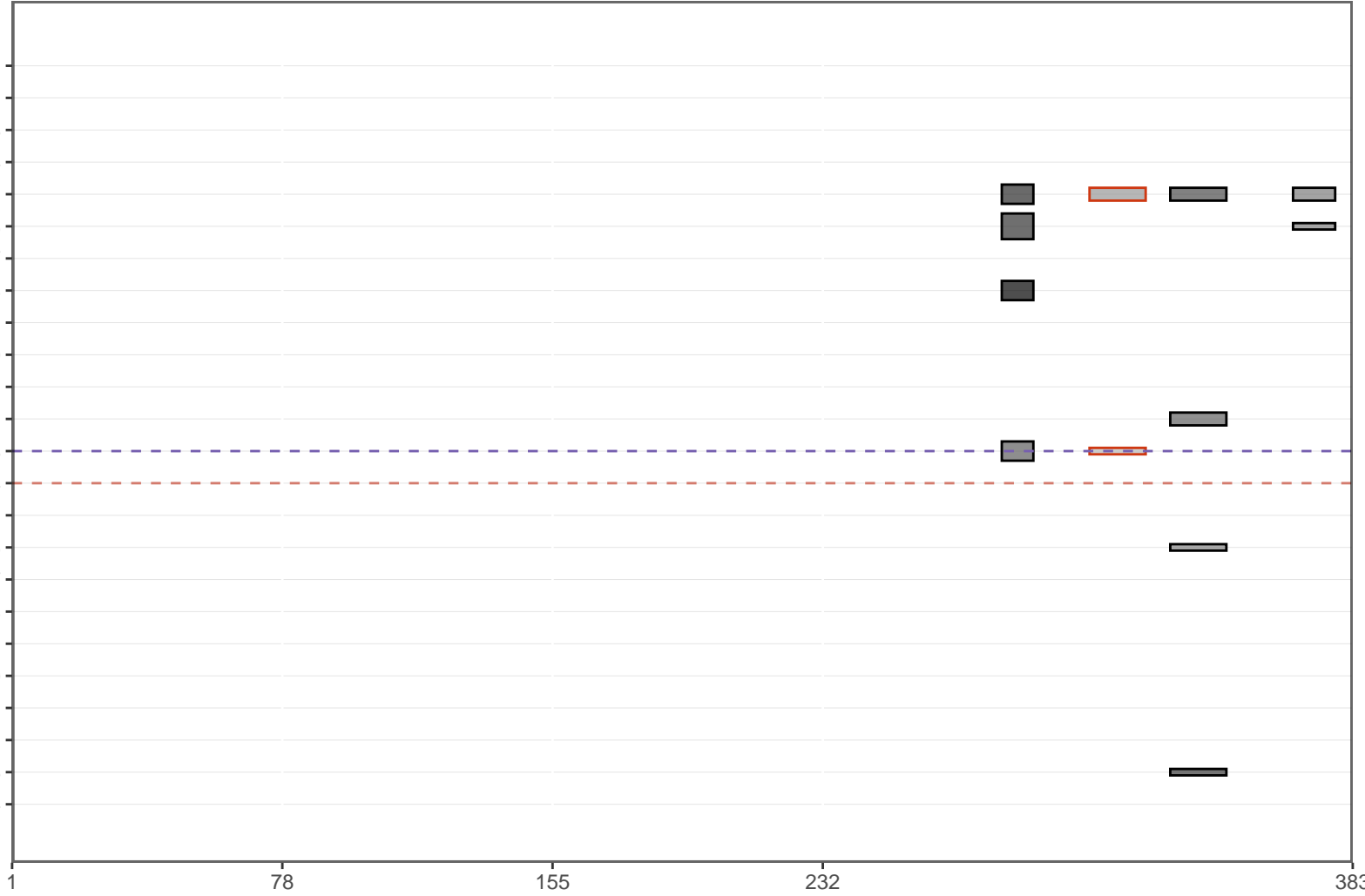
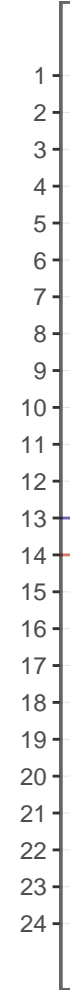
MW indication



Molecular weight



Gel Slice



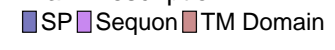
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

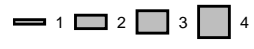


Protein sequence:

ERGAFLVQAMRAFRANNIDSAKRITMCAADDIRGQLERLGNTEBELGSLGVVLGMLGDCGRATGDAAASAVTYFEESVNFVWPKDDLEHTLTVSLNKGDKKYDDLEAARSHYKALDVRRNAIKGGAPSGHIDATSLAKWAVDRIKGNEDAIDGFEEAKMLELELNPEEASLEQRRLVIVGFLNSQMEKKGPA

NbL07g13950.1 nudix_hydrolase_23_chloroplastic [MW = 31.96 kDa]

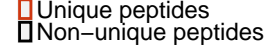
No. of times detected



log(intensity)



Values from



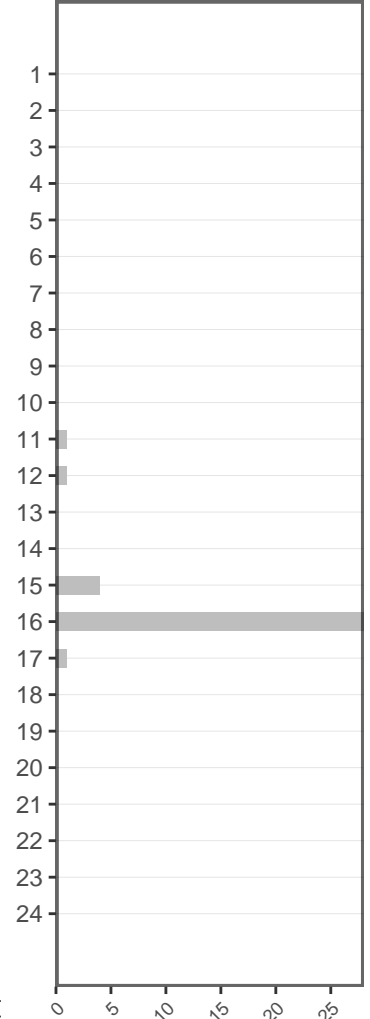
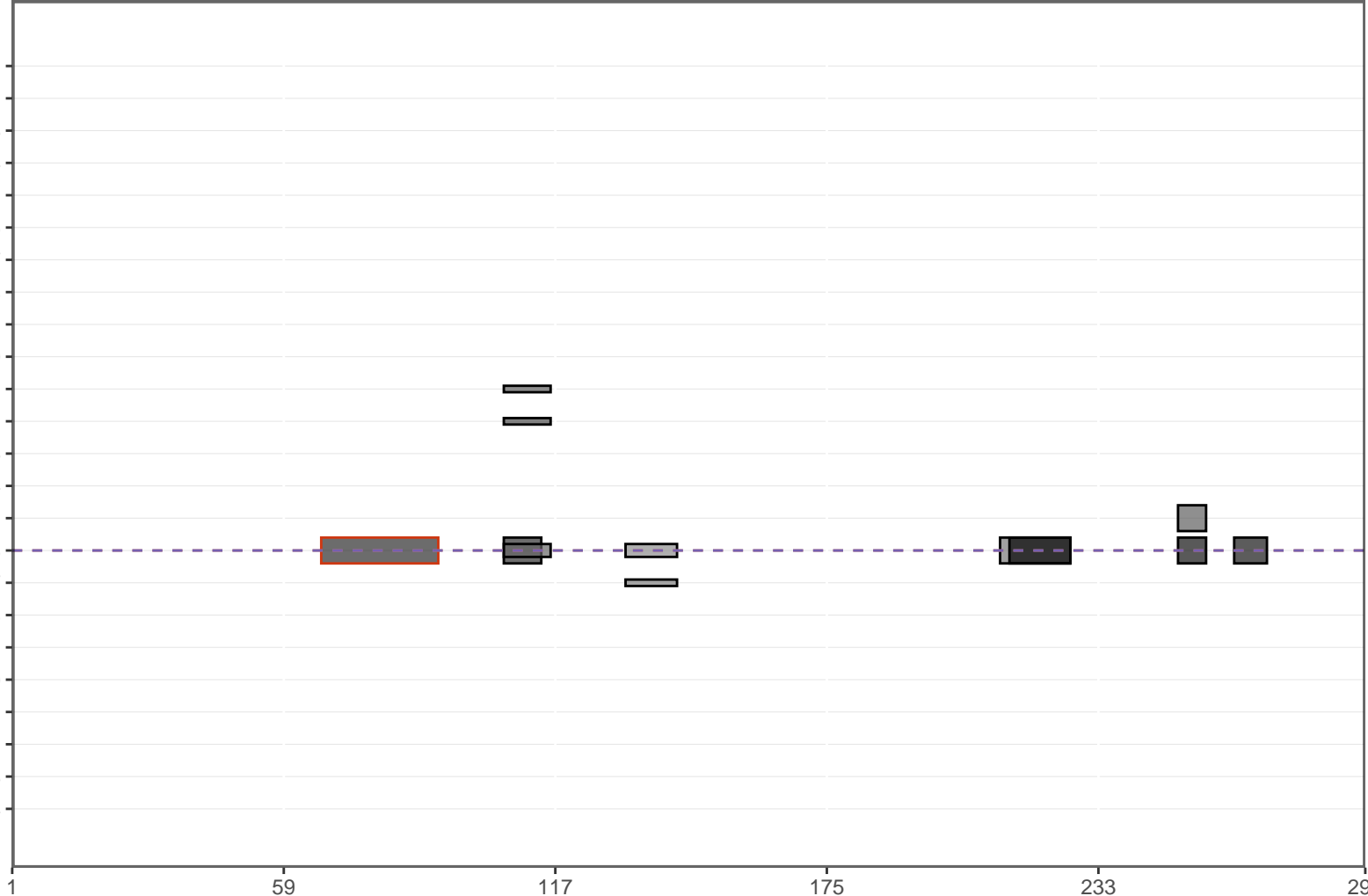
MW indication



Molecular weight



Gel Slice

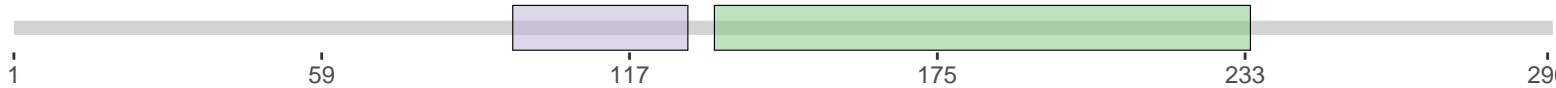


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

GMVVGCLLEIHDKKILMCRKRKQPSYGLWTLPLPGYMEIGESAAGEAIRELEEAANAEEVEVGGPFAGLDIPLHGDTYMFLLAKLKTTHFSPGPESEGRVLEDDIPFDSLAFSGMLVTLLKVEDIKVGRPKFYHYGINKRPGTSPSEIHAVTLQVHMGS

NbL07g13940.1 probable_plastid-lipid-associated_protein_13_chloroplastic [MW = 32.82 kDa]

No. of times detected



log(intensity)



Values from



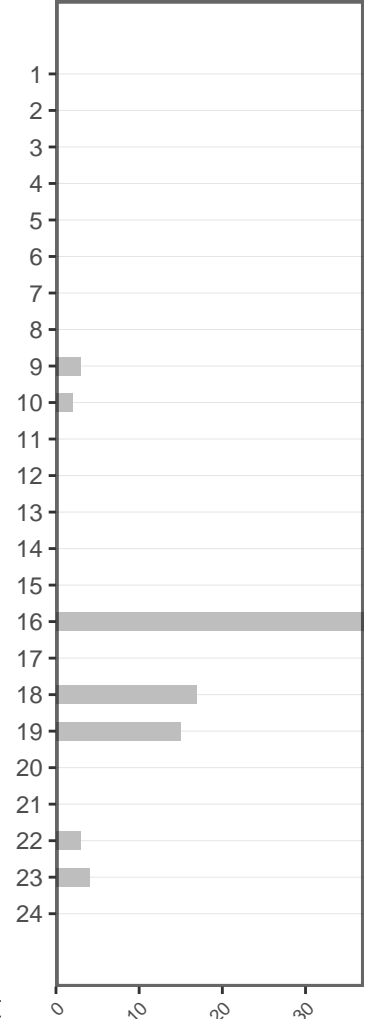
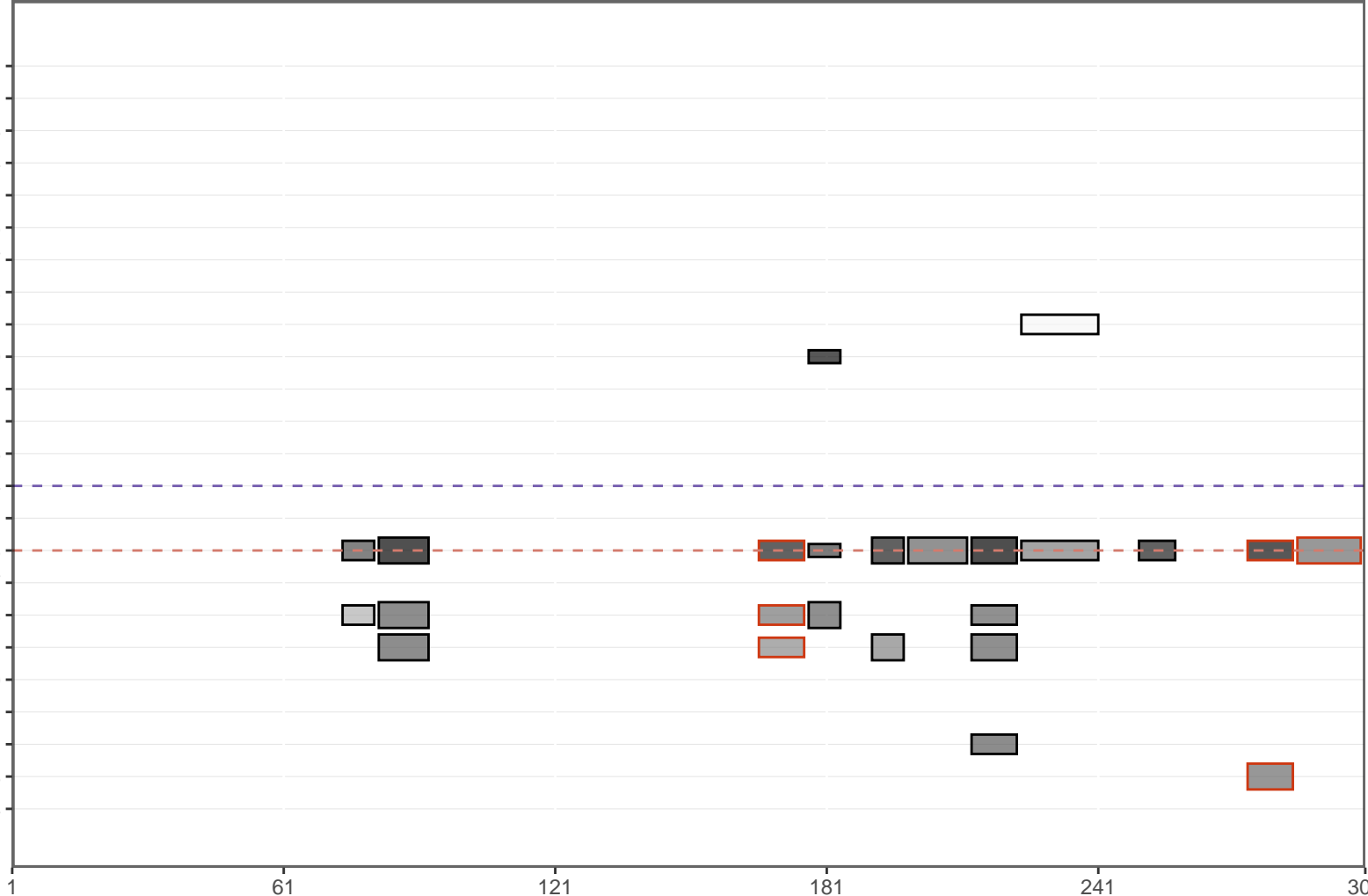
MW indication



Molecular weight

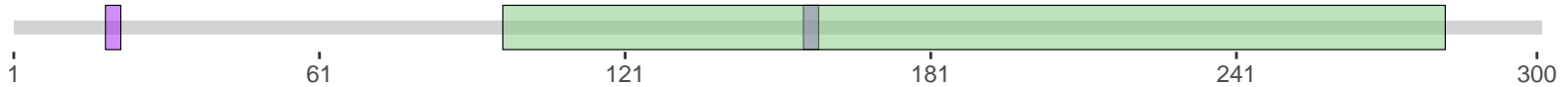


Gel Slice



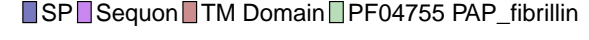
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

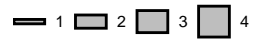


Protein sequence:

IGSPVLIFAKFLGRIPPTLVNLSKGLDVKDGYGTATAQVKKLNSIENKFIETKYVSEGPLRMKEEYVEGTFFSGPKVNEEAVPEQLRGAFGQAFNTVQQLPVPDRDAVSSGKVPVPLGGTFFQRLIMSYLDELIVRNAAAGEPVLTRLEAPPETETPEYEP

NbL07g13890.1 zinc_finger_CCCH_domain-containing_protein_14-like [MW = 30.67 kDa]

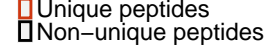
No. of times detected



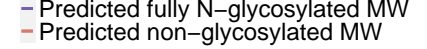
log(intensity)



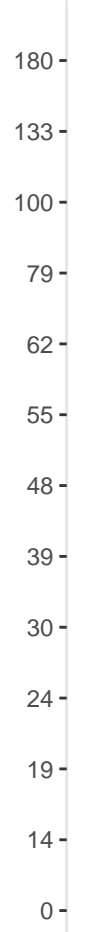
Values from



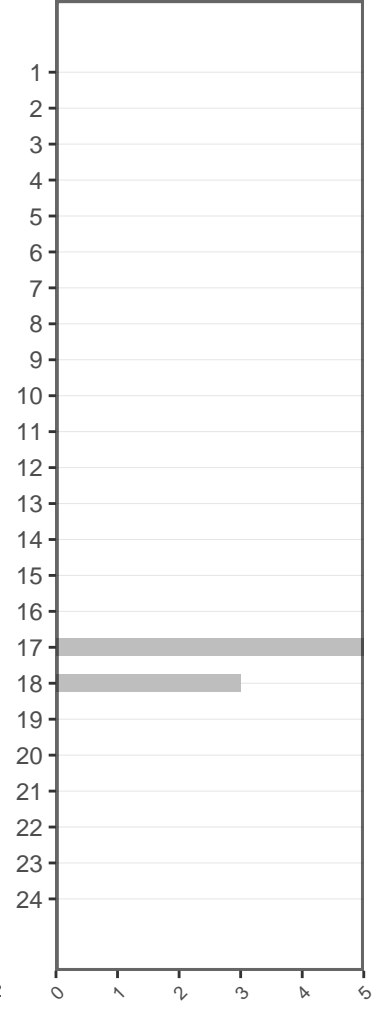
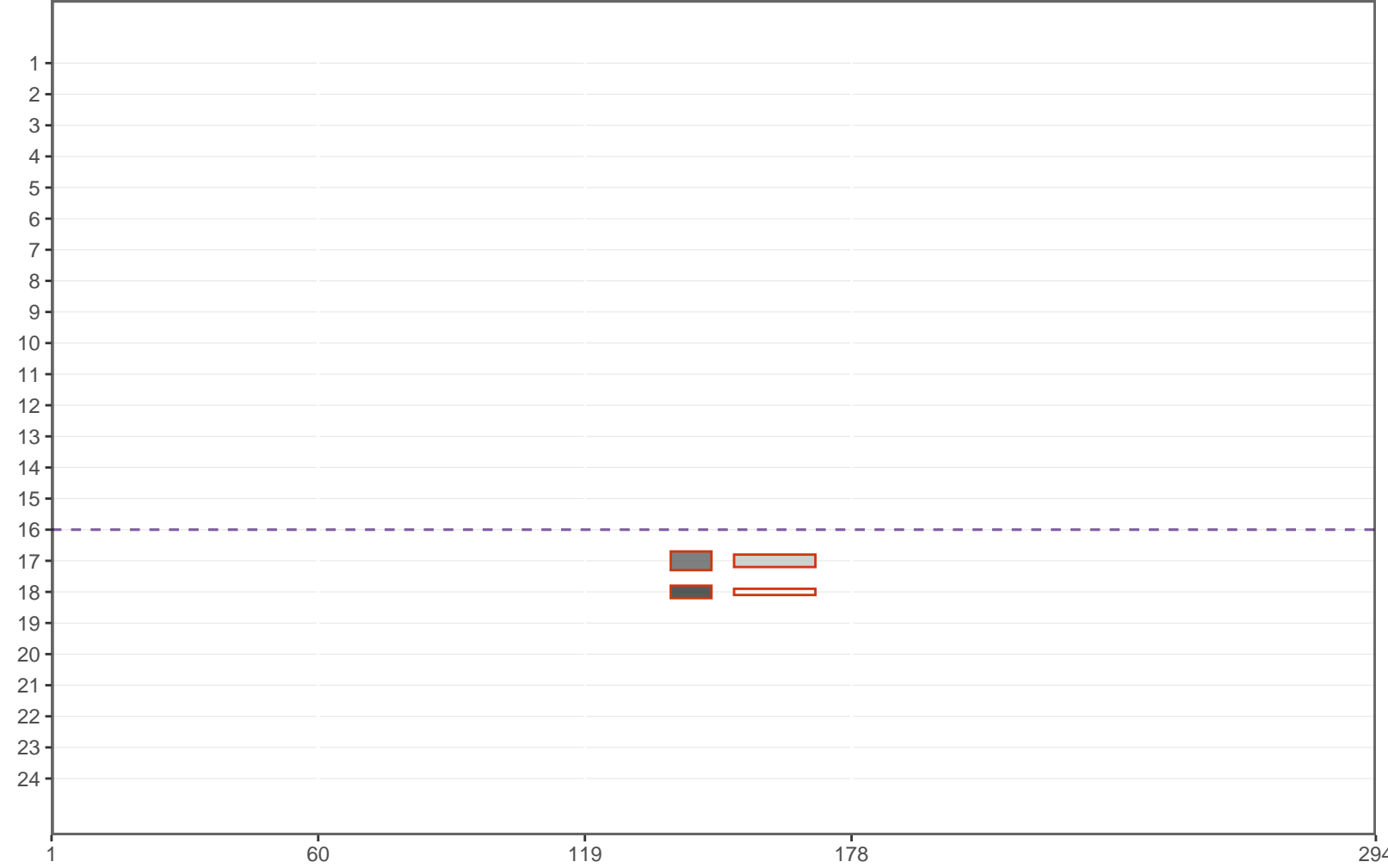
MW indication



Molecular weight



Gel Slice



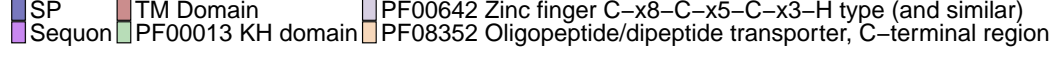
Protein length



Pfam domains



Pfam Description



Protein sequence:

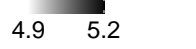
CEDPKMGGGPVPGRFGGRMEPPRGGPMASFGTATANKIVDASLAGAIGKGGVNSKQGRGTAKLAIREHETDKNLRNIELEGTFFEQI6QASAMVRELISLGGVGGPGRARFVGGPPPPQMSNKKTKLGNFAGKSGCTFGERGHFAHGAELRKTGV

NbL07g13880.1 enoyl-[acyl-carrier-protein]_reductase_[NADH]_2_chloroplastic-like [MW = 41.35 kDa]

No. of times detected



log(intensity)



Values from



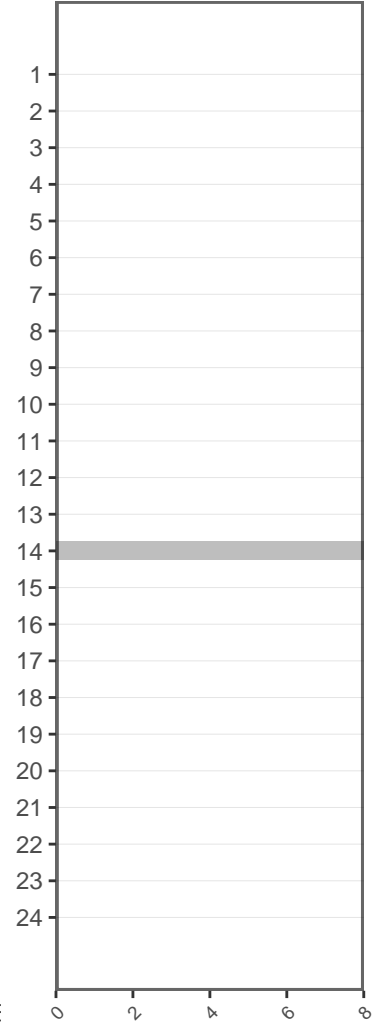
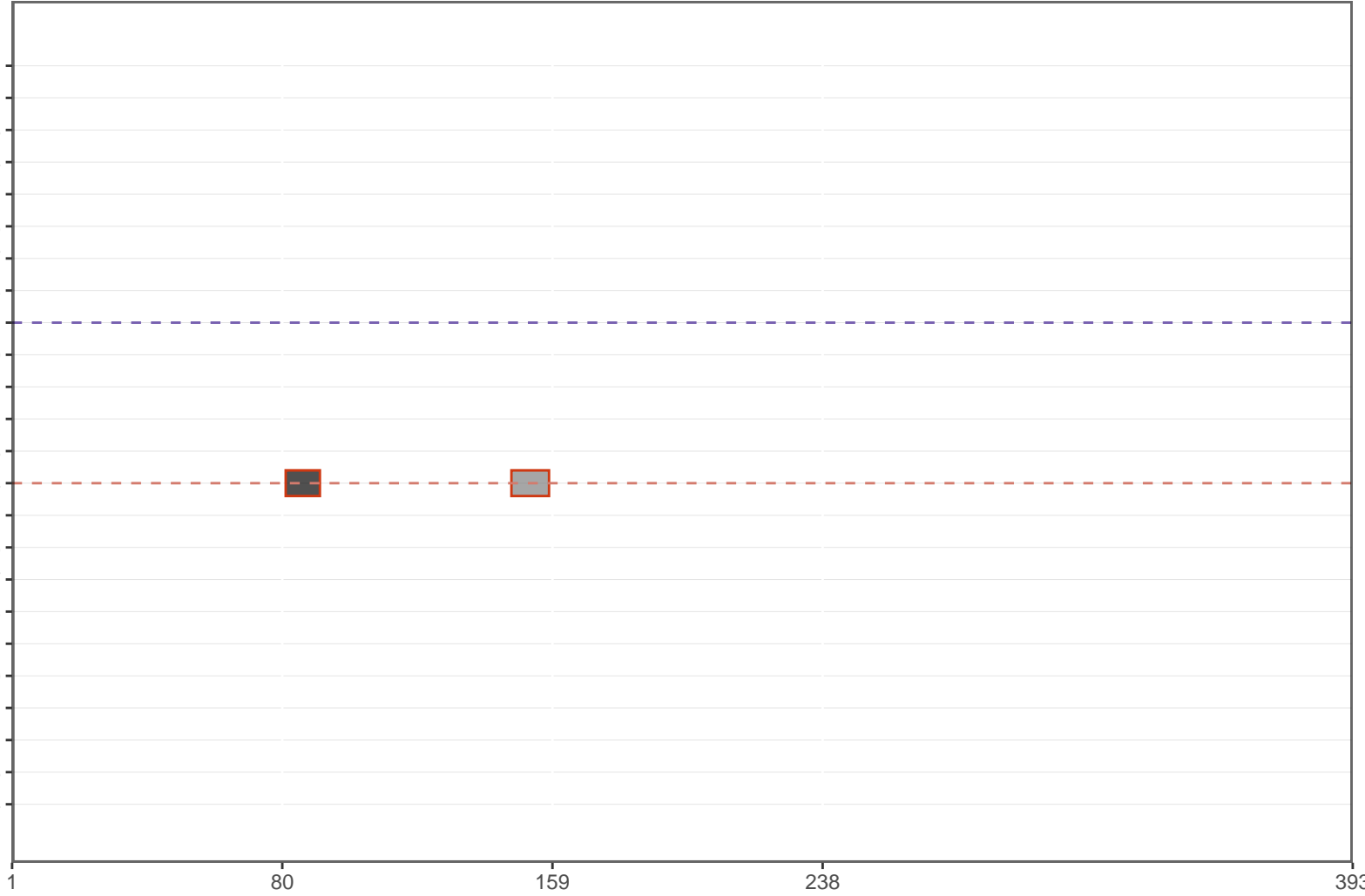
MW indication



Molecular weight



Gel Slice

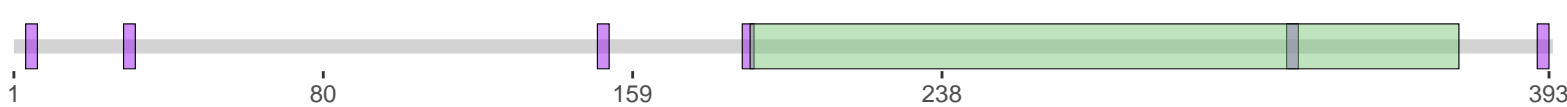


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IYAGSSNWTYKELVESVWQDFGTDILVHSLANGPEVVKPLLETSRKGYLAASVSA65YFVLLLRHFLPLINPGGASISLTYASERHPGYGGGMSAKAALESDTKVLAFEAGRNKRVNRTISAGPLGSRRAAKAKGFIDMMINYSLENAPLQKELVAEEVGNAAAFLVSPLASATGATYYDNGLNMMGVGVDFPAFEGLDIPKDKNS

NbL07g13690.1 phosphoenolpyruvate_carboxykinase_[ATP]-like [MW = 73.46 kDa]

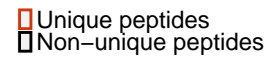
No. of times detected



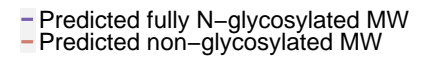
log(intensity)



Values from



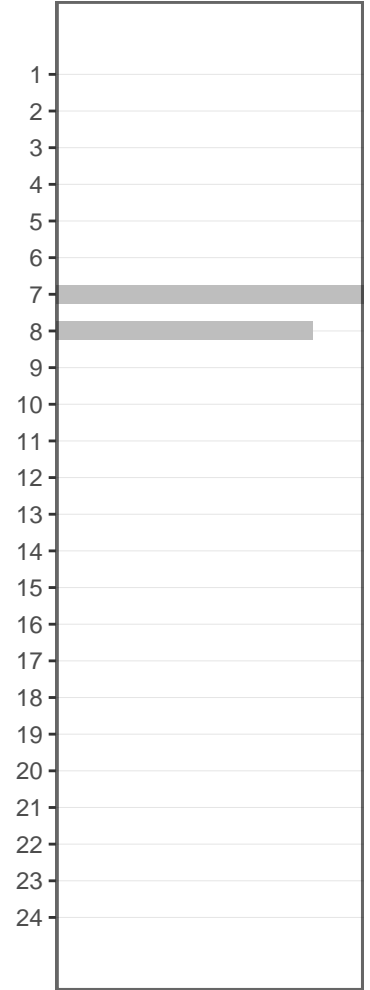
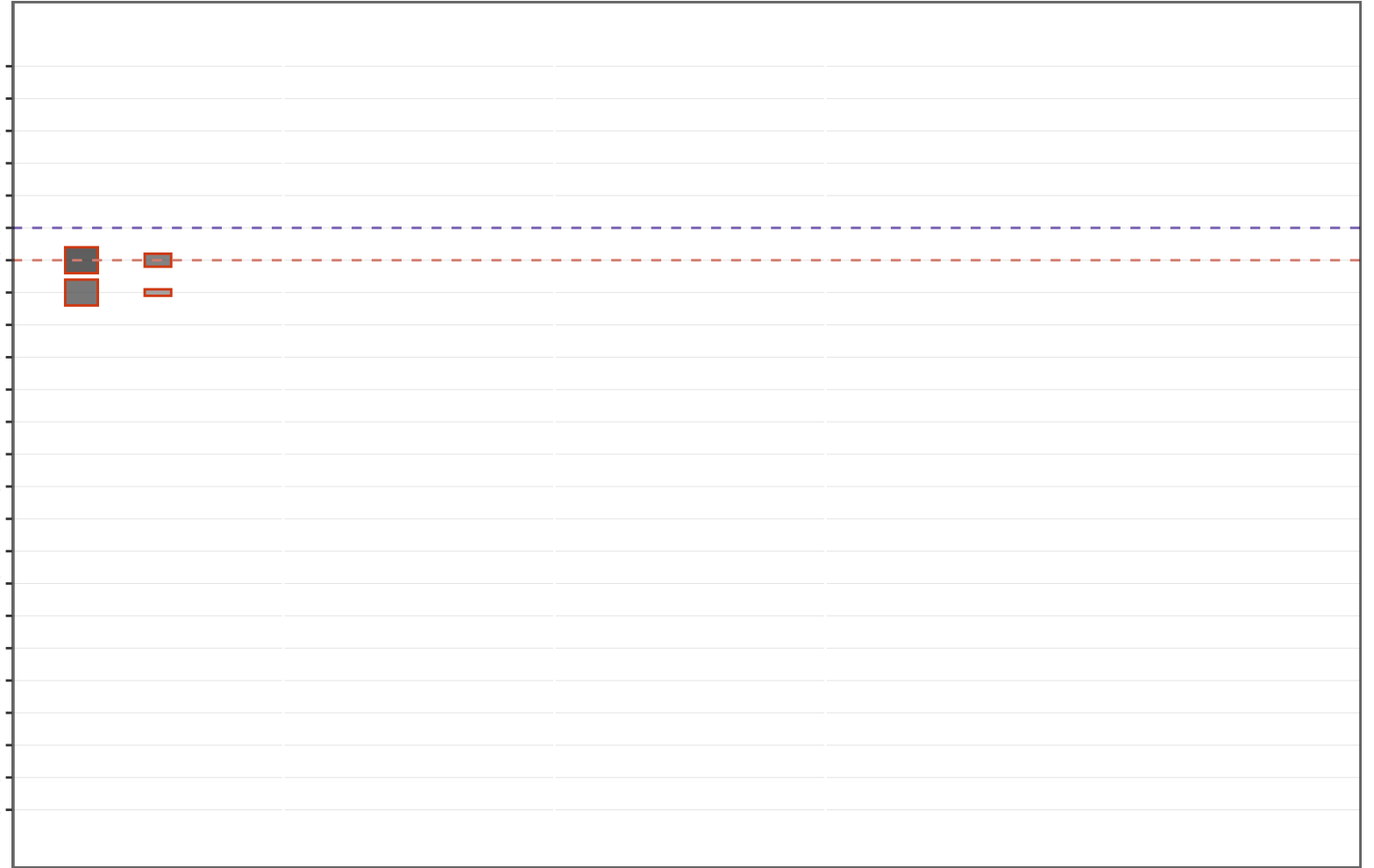
MW indication



Molecular weight



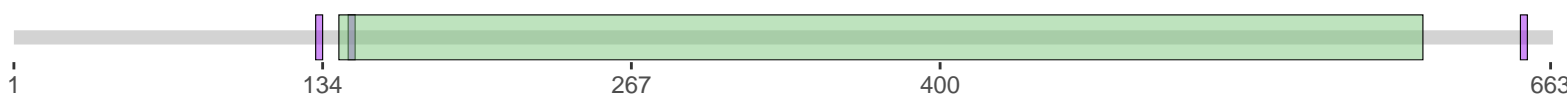
Gel Slice



Peptide counts over 4 repeats

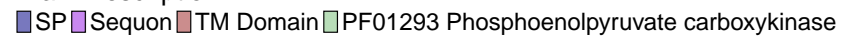


Protein length



Pfam domains

Pfam Description

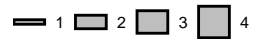


Protein sequence:

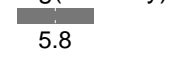
TOYAGEMKXGLFSLMRYLMPKROLSLHSGGNMKGDDVALFFGLSGTKTTLSTHNRRLVGGDEHGVSDHGVSNIEGGVYAKGDLAREKEPDIWNAIKGFTVLENVVFEHTRREVDAKDSVNTENTRAAYPIEYFNKIPDGVKPKNILLAGDAFGVLPVSKLNLAQTMVHFISGYTALVAGTEDEGKEPTATFSAGFGAAAFMLHPTKYAAMLAEKMKKHGATGWLVTGWSGGSGYSGSRRIKLAYTRKIDNIHSGALLSANVKKTEVFGLIPTLELGVPSLELPA

NbL07g13660.1 ATP-dependent_Clp_protease_proteolytic_subunit_4_chloroplastic [MW = 37.88 kDa]

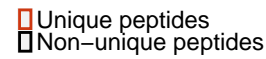
No. of times detected



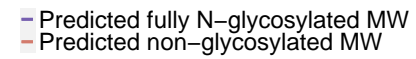
log(intensity)



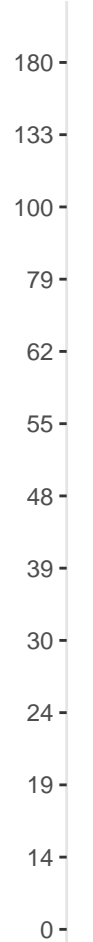
Values from



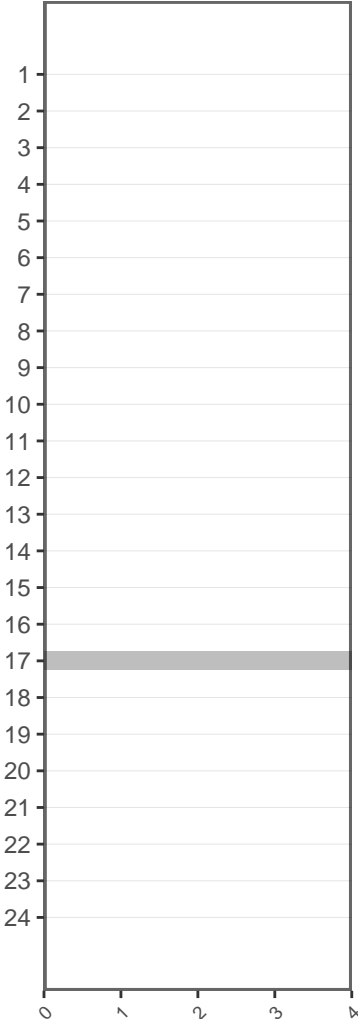
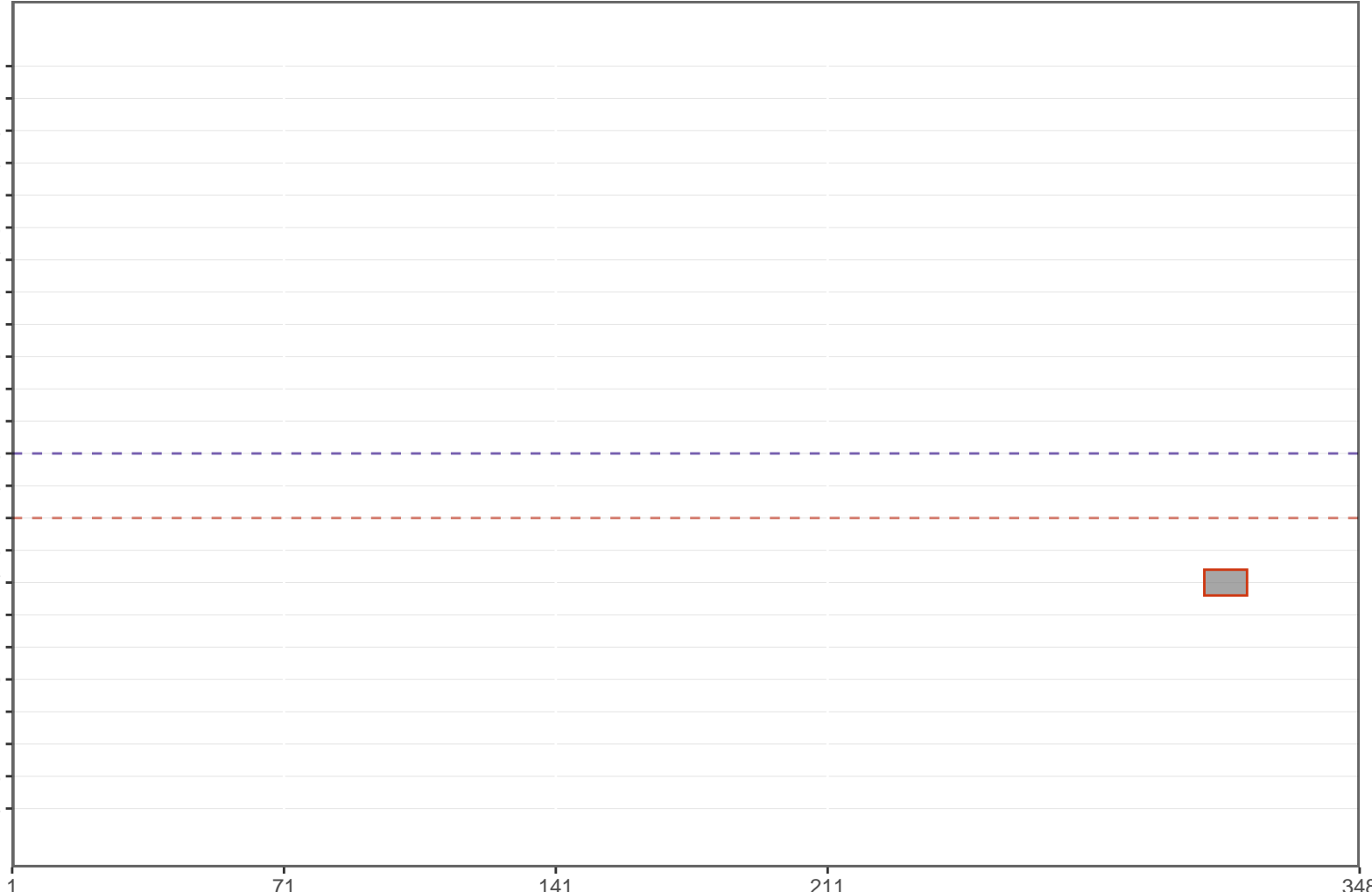
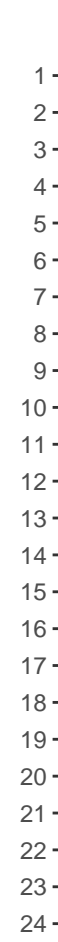
MW indication



Molecular weight



Gel Slice

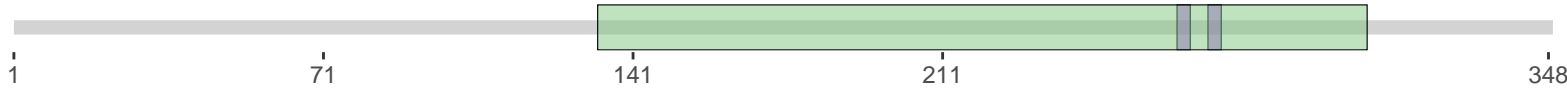


Peptide counts over 4 repeats

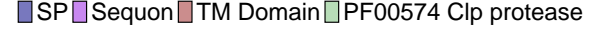
Protein length



Pfam domains



Pfam Description

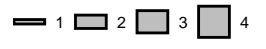


Protein sequence:

MSQLLLLDAMDSKDKIRLFINSPGGSLBATMIFKFDVAVKLRADVSTVALGHAASTASILGGGKGRVAMPFNARIMHQLGGASGGADVEHQAREIMHNKDNVTKISNCTGRVYEQVQKDDRDRIYMSPEAVEYGLIDGVDRHSIIPLEPVERVKGSTLNYGEISKDKPKFLNPEIPDEEY*

NbL07g13430.1 phosphoribulokinase_chloroplastic-like [MW = 45.31 kDa]

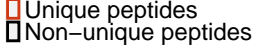
No. of times detected



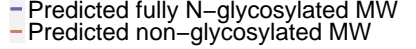
log(intensity)



Values from



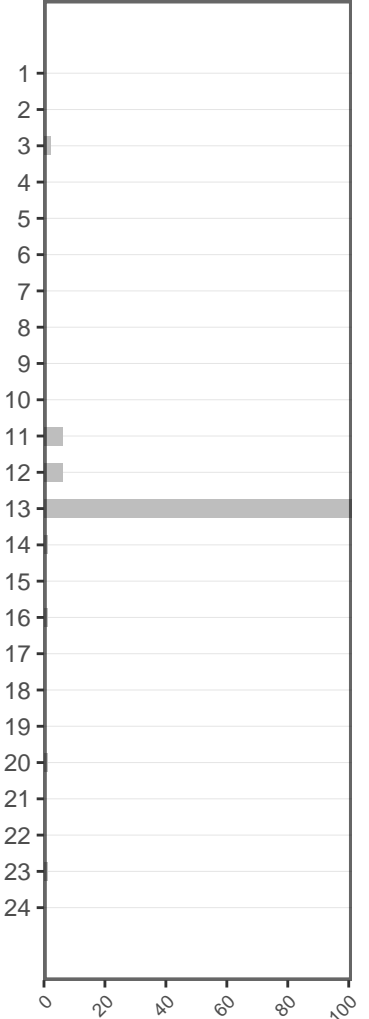
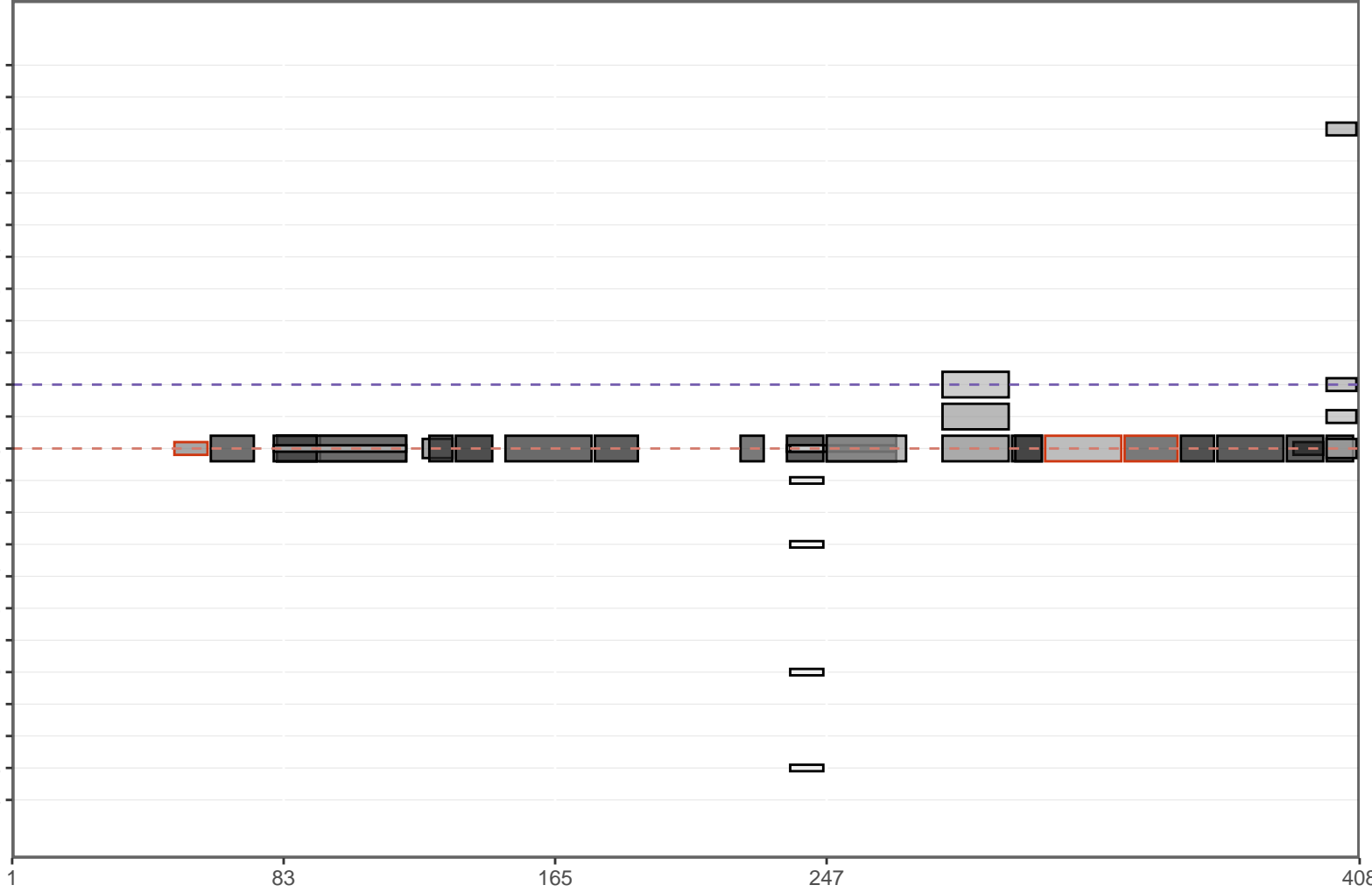
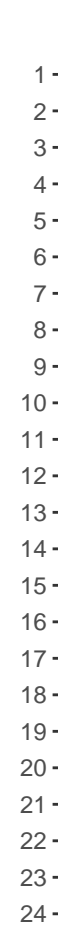
MW indication



Molecular weight

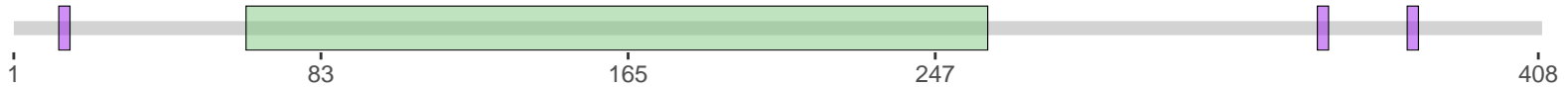


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VRELLDFSYLDISNEVKFAWIKGRDMAERGHSLSEKIAIEARKPFDFAVDLPQKQYADAVIEVLPFQLPDDNEGKVLRRLLMKEGWVFNPNVYLFDEGGTISWPCGRKLTGSGYPGKIFTYGPDTFYDNEVTVAEMDGGQDFDRDLDELIVYVESHLENLSGKFFYGEVFGQMLKHADFPGGNGTGFQTVGLKIRDLYEGWASRAAAPVQAAKA*

NbL07g13350.1 uncharacterized_LOC109217894 [MW = 34.88 kDa]

No. of times detected



log(intensity)



Values from



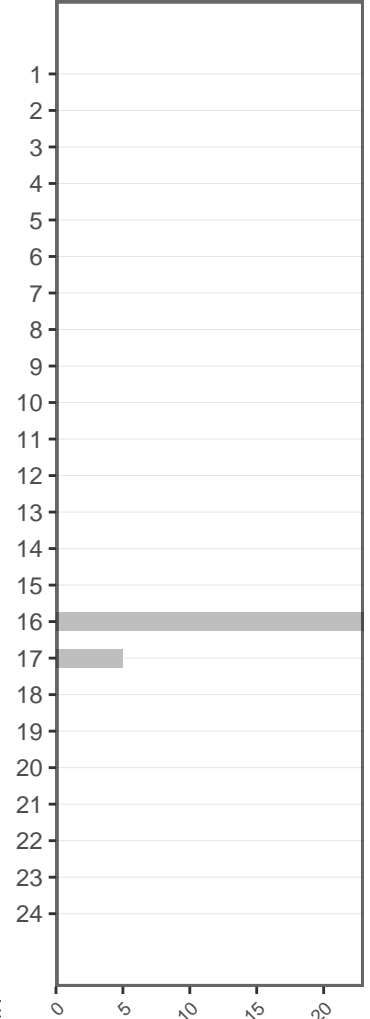
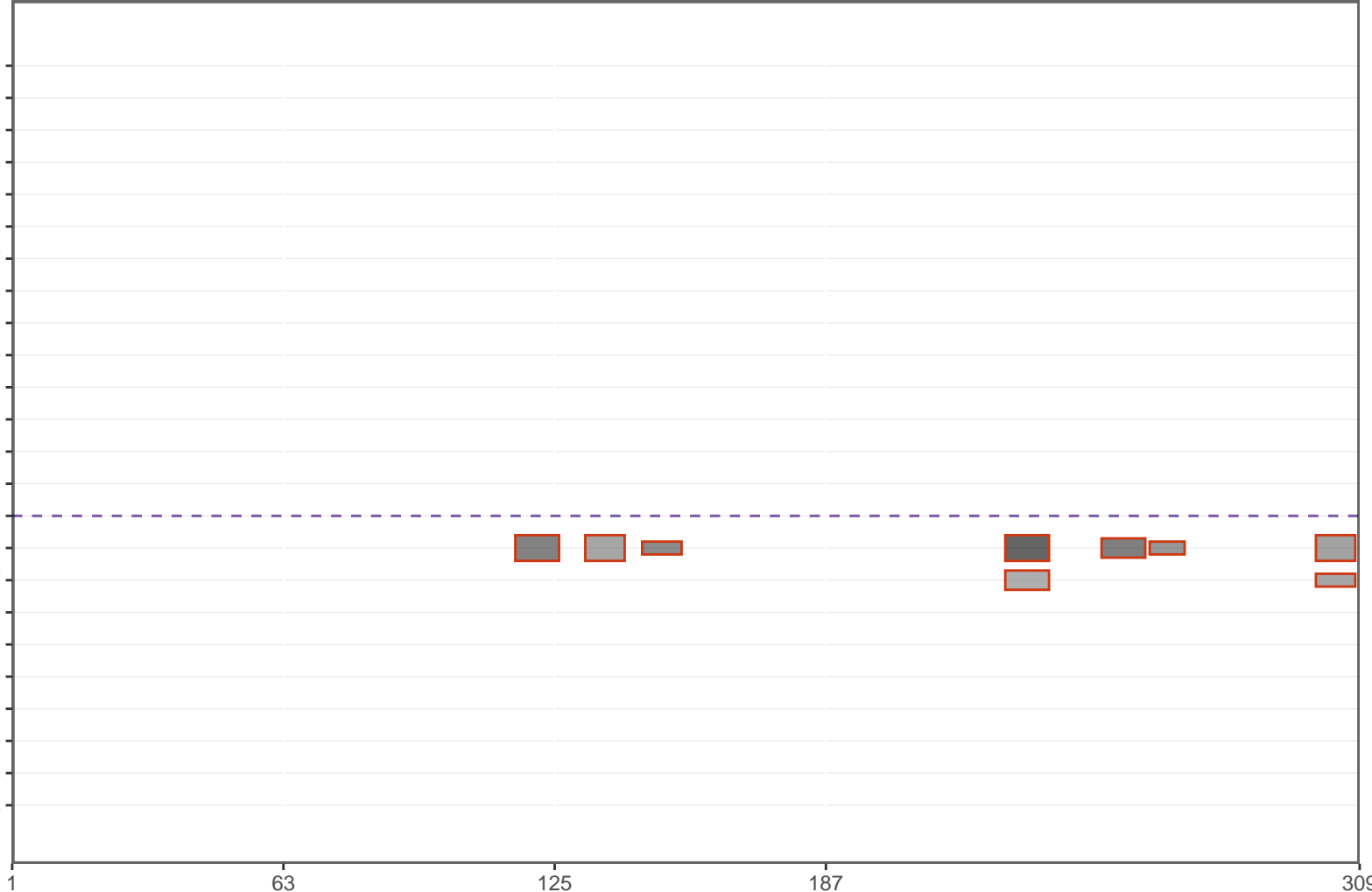
MW indication



Molecular weight

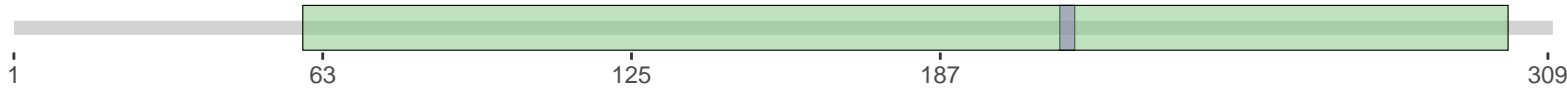


Gel Slice



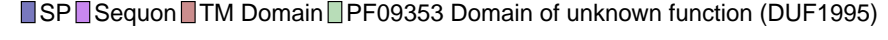
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KFARQSIFGASFLKLDLTKPFFEDDFGFEKVMADRKKPEDELFIWVYFVFNEMLVVEELKAAVSNTRKLIHFNGLDRIRSGYYPFFFYFKLAALKLTFPKMETVYYVHNFKGPNGVLFRCYVPGVWVLRVRRVNAVIGLHQEGEMPLKKEVALDPLA

NbL07g13180.1 ornithine_aminotransferase_mitochondrial-like [MW = 52.16 kDa]

No. of times detected



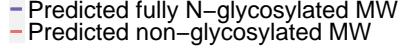
log(intensity)



Values from



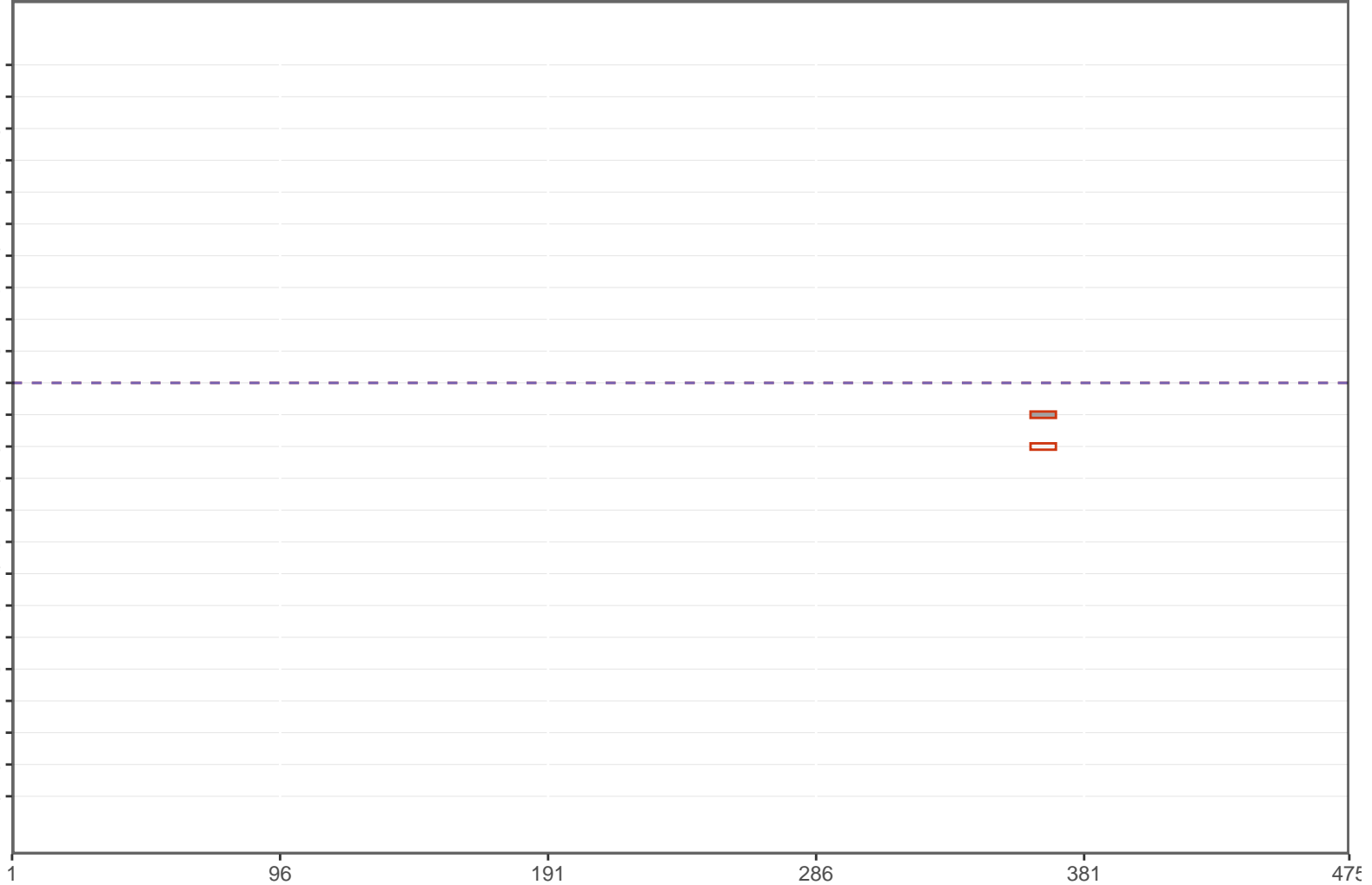
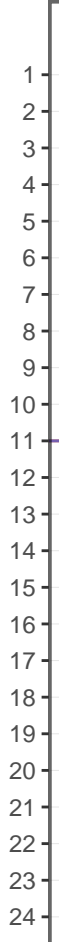
MW indication



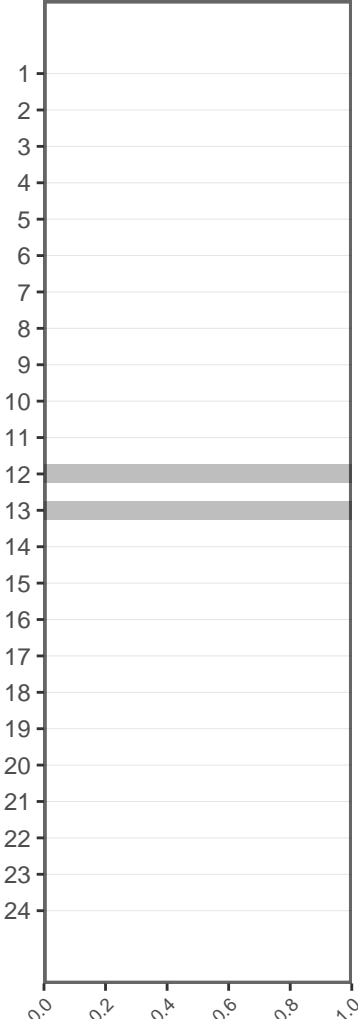
Molecular weight



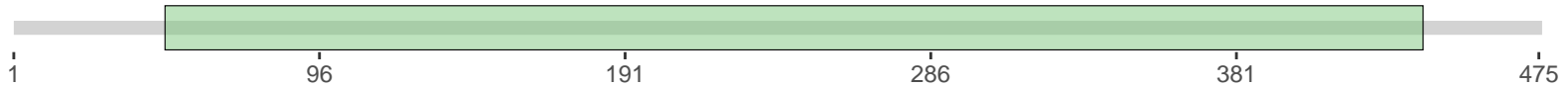
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IAAGFLFEPHQEGAVIPPEGYLKEVRDLGKYNILMADEIGSGLARSGRLLAGDWEERVDPVILGKALGGVLPVSAVLADKDMVMVQIGAGEHGSTFGGNPLASVAIASLVDVREEGLAERSAGMGEGLRHQLMKVGEQFPNFIKEVRGKGLFNVAVELNSKSLLPVTAVDICMLKERGLAKPHTDSIRLTPPLMSLDELQEGSKVLHDFELDLPKMGKEKPTVSHAASSVQDRGRNLYGSS

NbL07g13170.1 KH_domain-containing_protein_At4g18375-like [MW = 66.49 kDa]

No. of times detected



log(intensity)



Values from



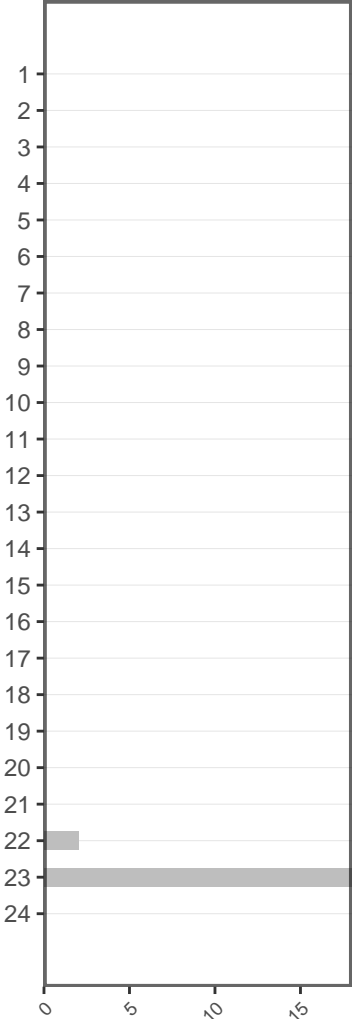
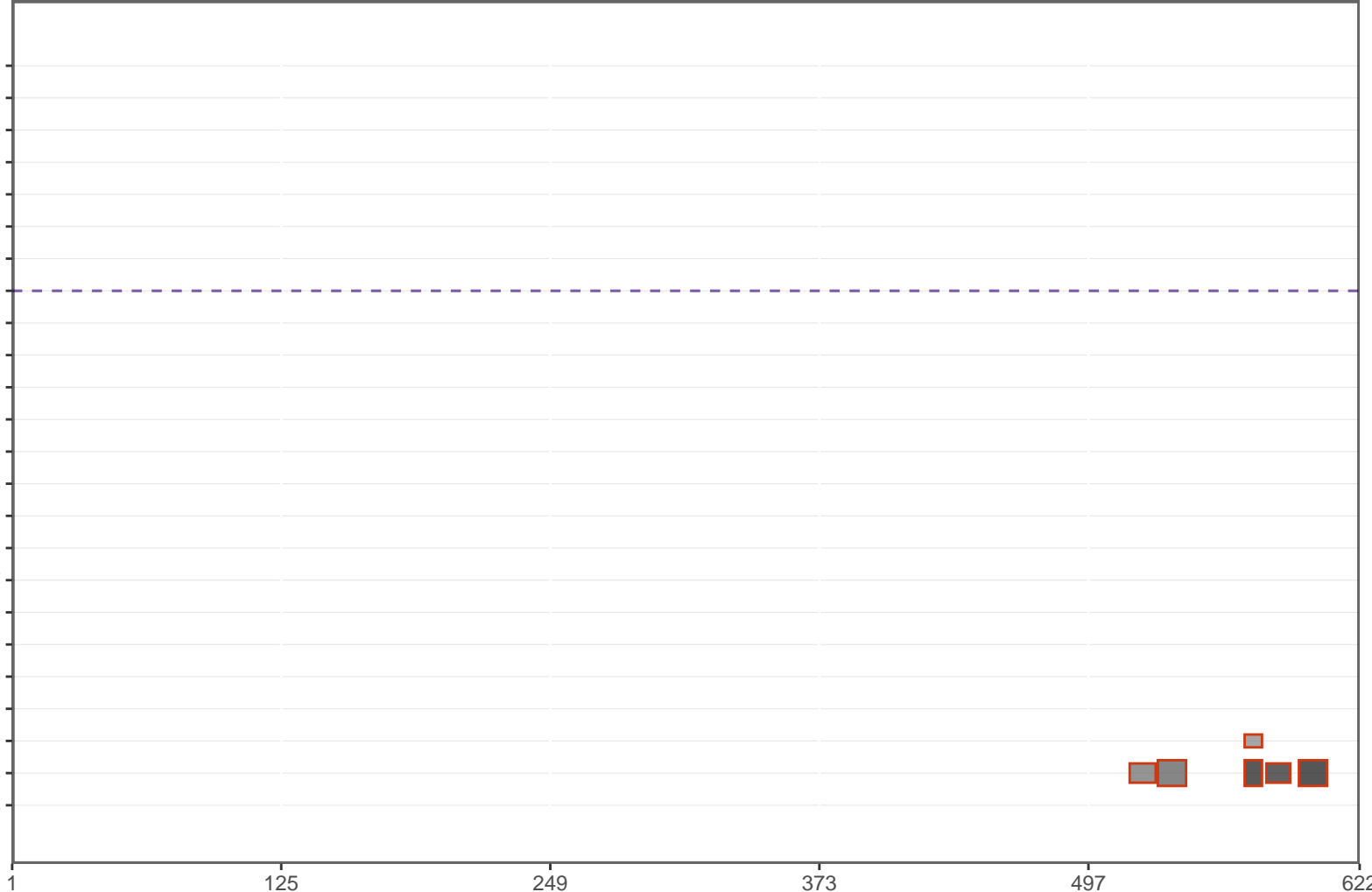
MW indication



Molecular weight



Gel Slice

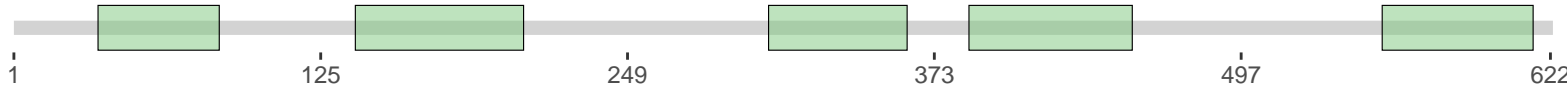


Peptide counts over 4 repeats

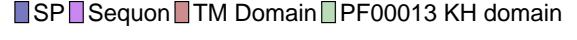
Protein length



Pfam domains



Pfam Description



Protein sequence:

IGASQTEELTRVYLGPTNNGRIVGKGGASIKSVRQASGARIEVGDMAKADRDQCHTVISTESVDDLKEMAVEAVLLLOGKINDDDDEVTFRLLVLPKIGKIGKGGSSVNEIRKRTRADVRISGDKPKKADENDELVEVAGEISVRRDALHIVLRIRDVLLKVRRESFNPNPAGADSLRAGGTGHSGLAPLVLPNVPPTASLVEYHRGETGNLGMRRSGGLYGHESFSRGGDDGYGAYSSYKHYGLPPTALEMVPQHAAGKVIKGGGENDNIRKIGASVYDIDSKSRGD

NbL07g13130.1 pyruvate_dehydrogenase_E1_component_subunit_beta-3_chloroplastic-like [MW = 44.58 kDa]

No. of times detected



log(intensity)



Values from



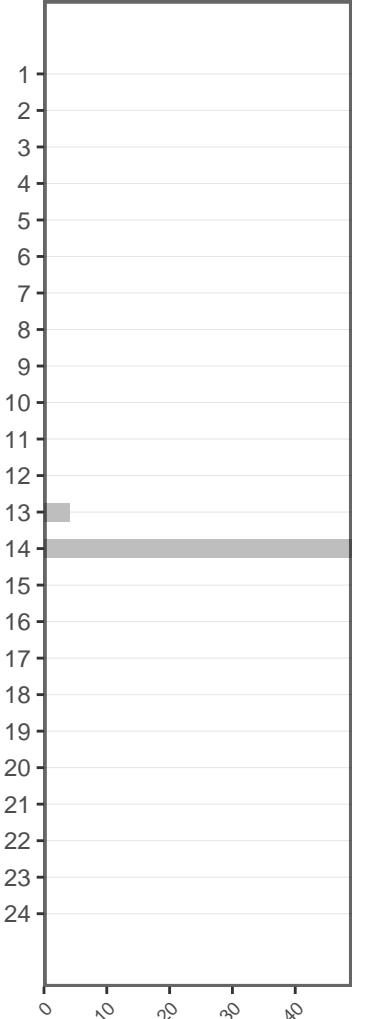
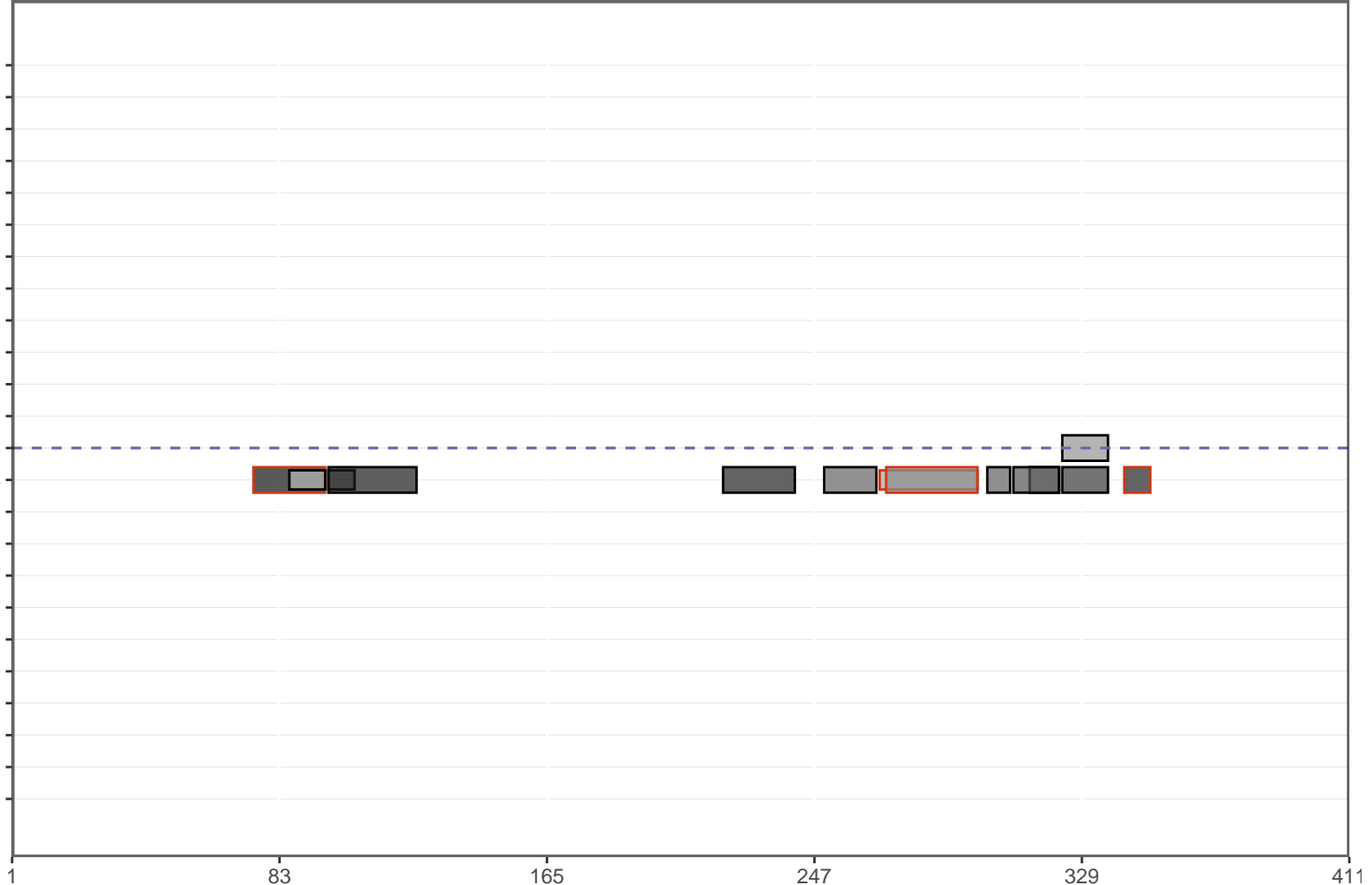
MW indication



Molecular weight



Gel Slice

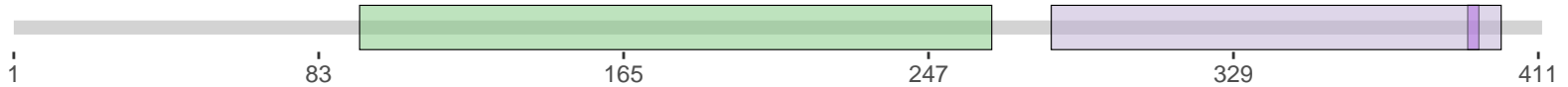


Protein length

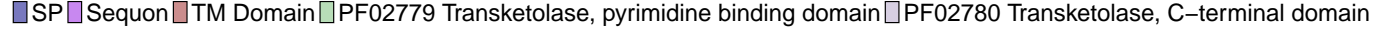


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ISGSGFQFVIRGPGGVRGRLGAEHSGRLSEYFGSPGPGMAGSTFYNKAGLMAKAIKRSNPNVLFHVLNLSKERIPDEEYVNLNEEAEMVRPGEHVTLETYSRMRYHMGAAKTLVKGVDPEVDIRSLKPFDLHTIGNSVWKTNRVLIVEECMRITGGIGASLTAITENFHDLDAPVLSGGDVPPTPYAGTLENWTVAGPQVYAVEGQD*

NbL07g13090.1 calcyclin-binding_protein-like [MW = 24.07 kDa]

No. of times detected



log(intensity)



Values from



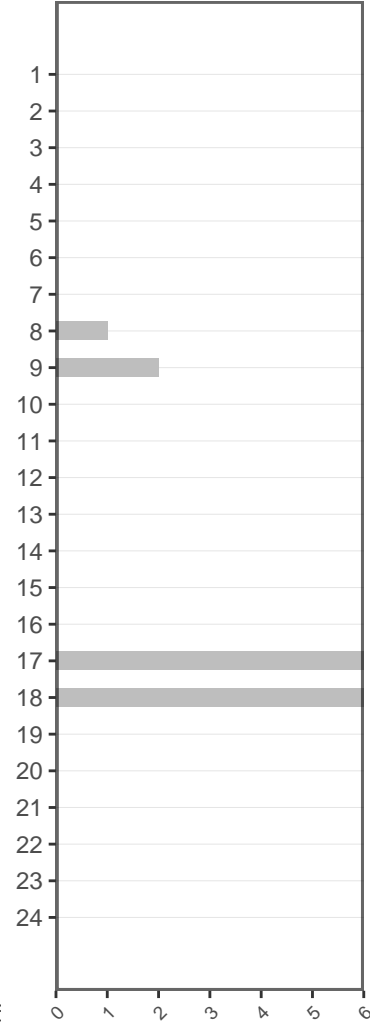
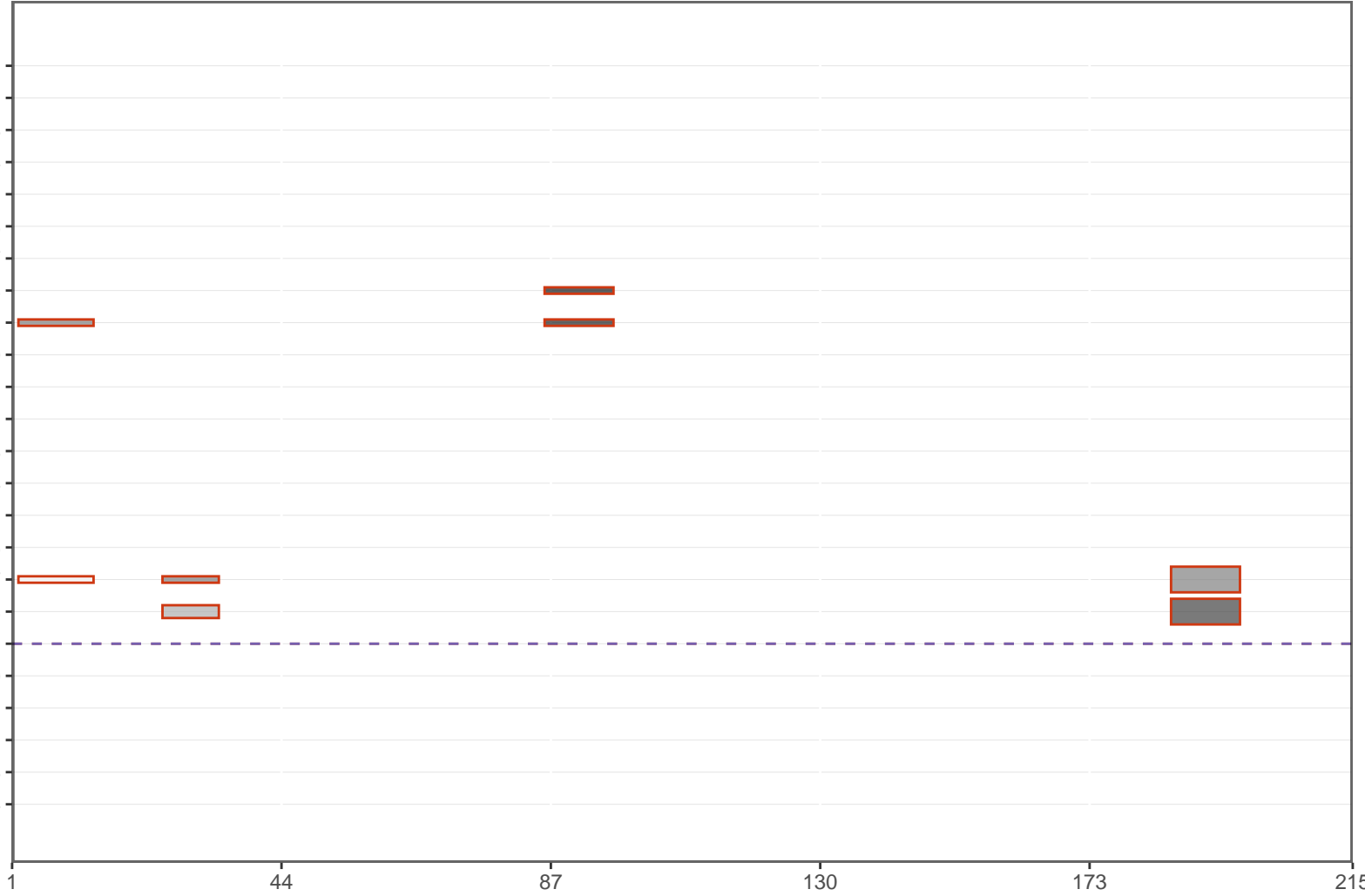
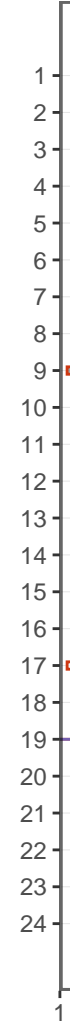
MW indication



Molecular weight

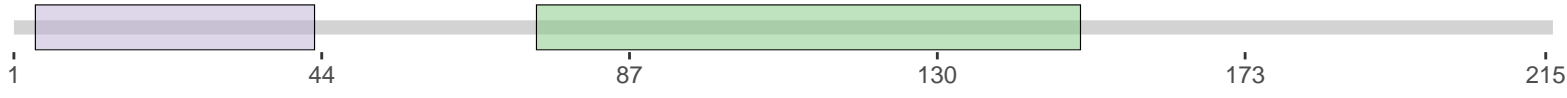


Gel Slice



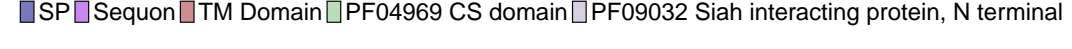
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKAETEFKPMISFDAMFHDHGHGKFNFRFLPLNKEIPEKDKVVKVPTFRVITLKAASKGNWLDLHYKEDKFKPLDKKEDPMAGIMDLKMKMYEDGDEEMKRTIAKAWTDAKSGKAADR

NbL07g13030.1 prefoldin_subunit_6-like [MW = 14.77 kDa]

No. of times detected



log(intensity)



Values from



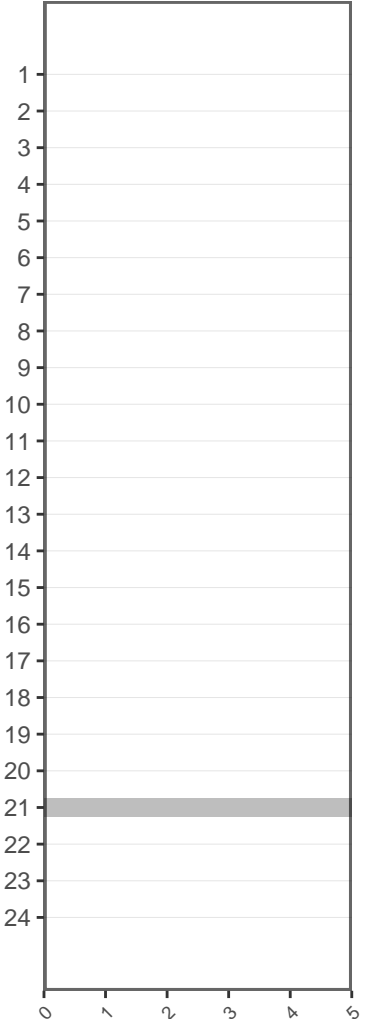
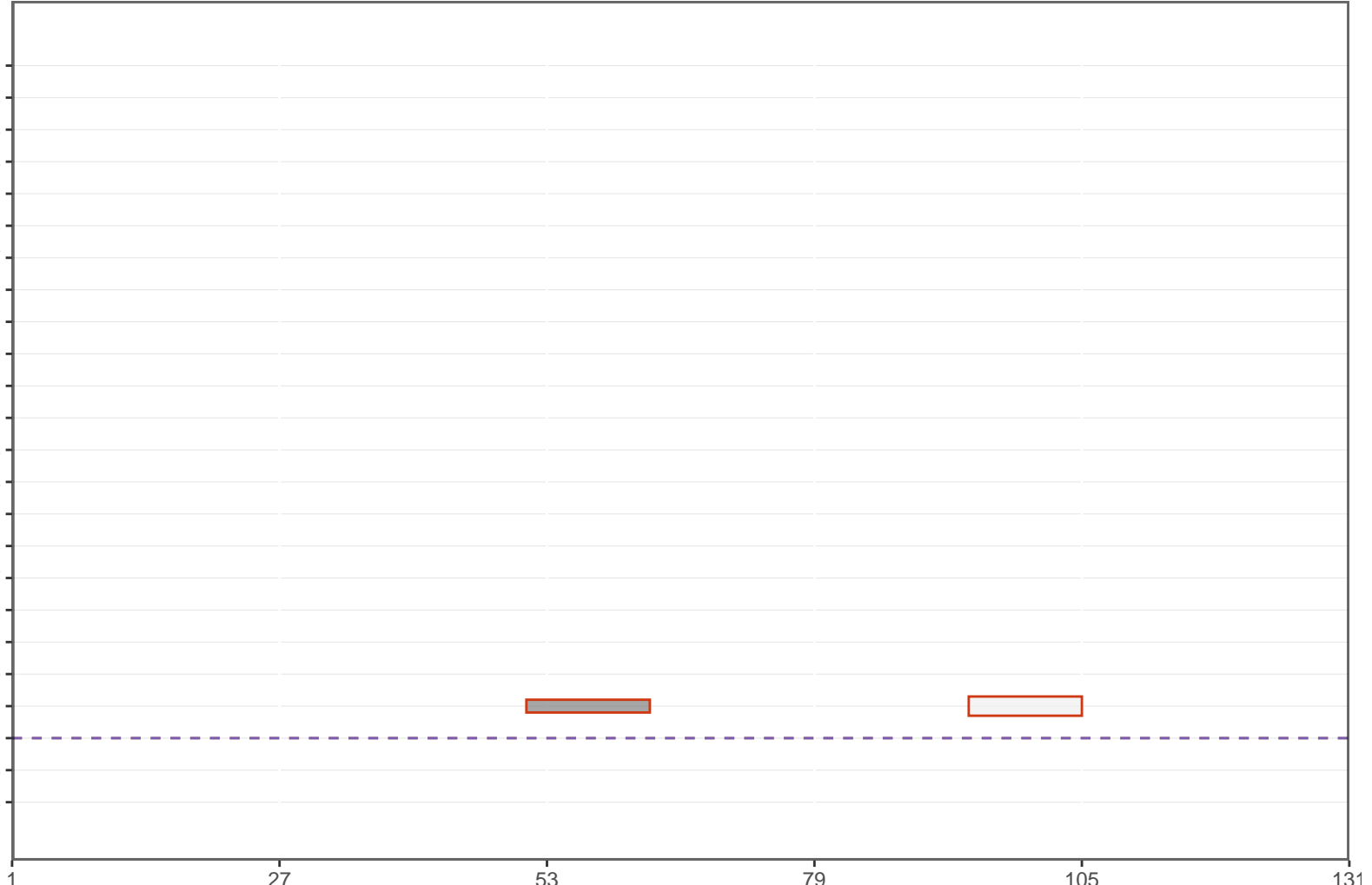
MW indication



Molecular weight

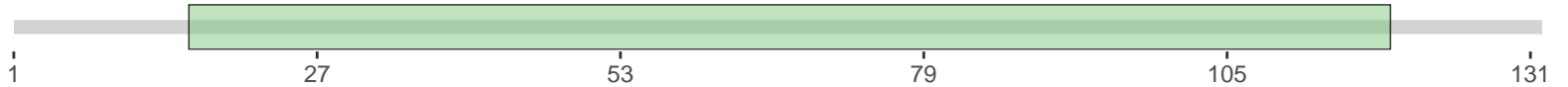


Gel Slice



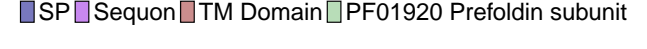
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LDPLNEDANYYKLIGPVLVWGDLEAFARANNKKRIEYHAEELKRLDSTLQDLEEKNSKKEIKLQKQKIGSLGAGKGA*

NbL07g13010.1 3-oxoacyl-[acyl-carrier-protein]-synthase_I_chloroplastic-like [MW = 49.93 kDa]

No. of times detected



log(intensity)



Values from



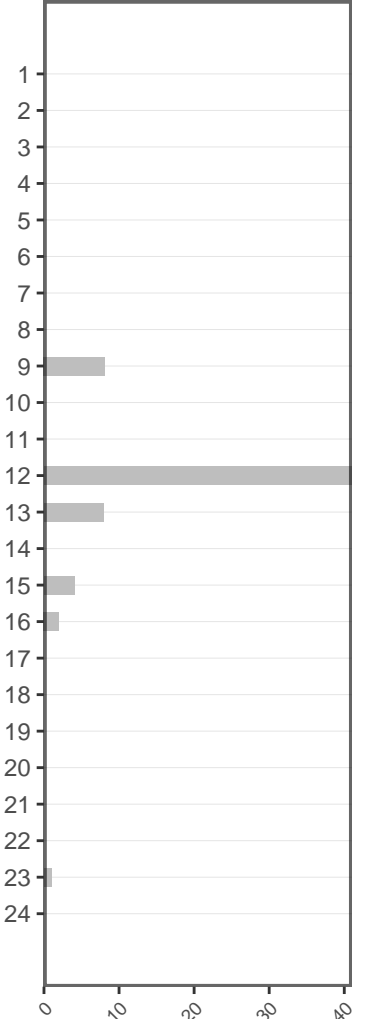
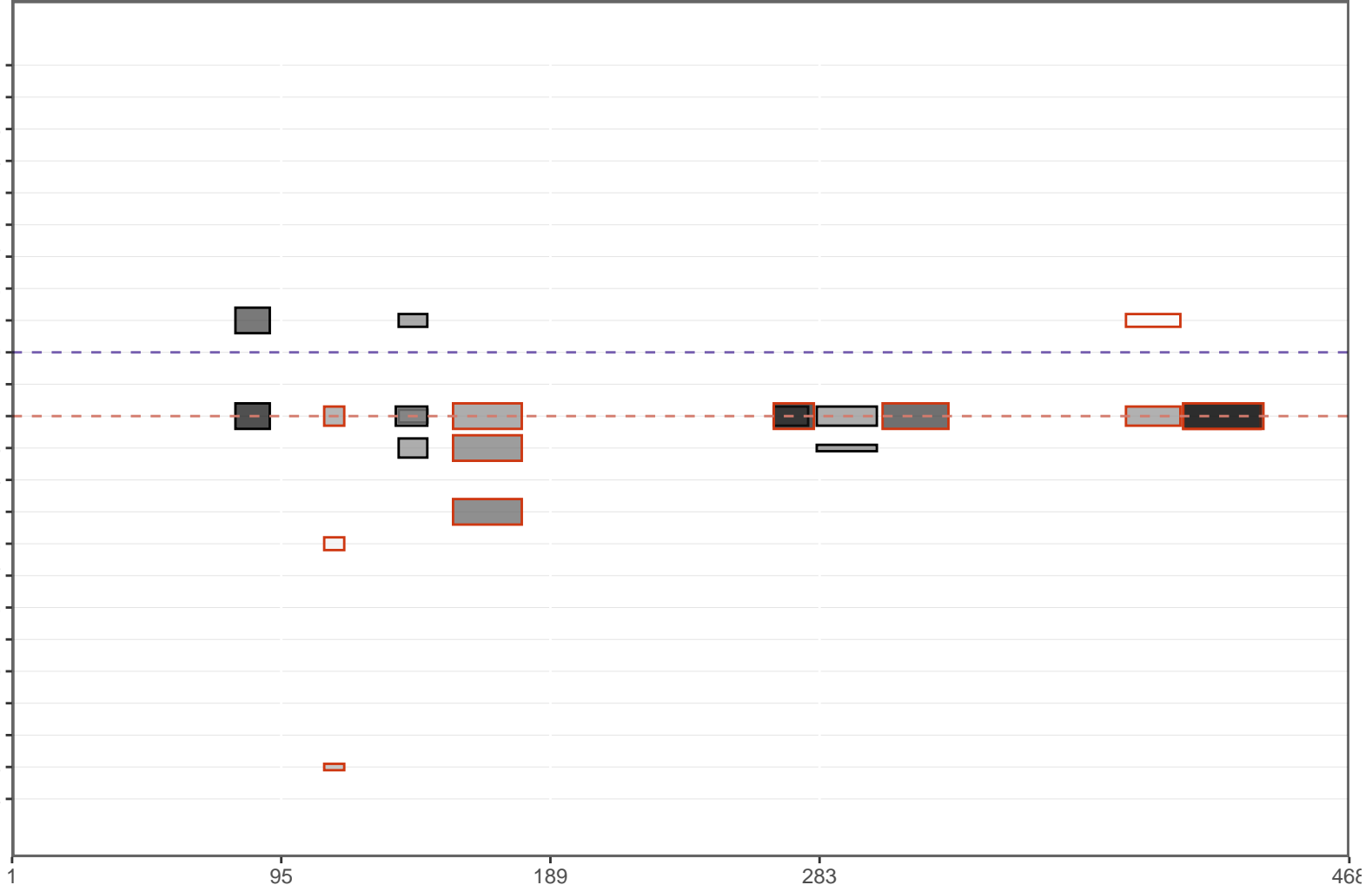
MW indication



Molecular weight

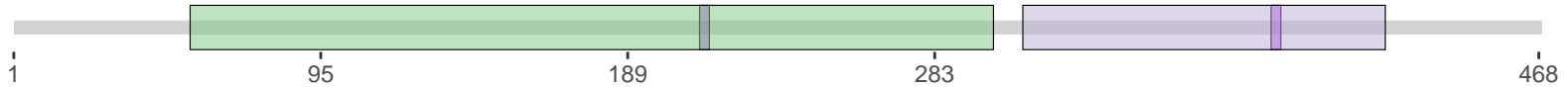


Gel Slice



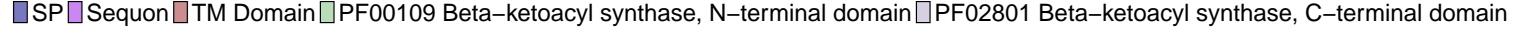
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YICFYAAAHRRRGEADLMAGSTEAMPIGLGGFVCRALGQRNDPQTAARFVWDRDGFVMEGEGVLMESLEHAMKRGAPIAEVLGGAVNDDYAHMFTDPRADGLVSSGILSLEDGVSPEEVNNAHATSTVIGDLAEVNAKKVFNKPNSEIKMNAKMSMIGHCLGAAGGLEIAATVKAITGWLHPBINGFNPPEPVEFDTVNKKGGHEVNAWSNFGFGGHNVVWVSAFKP

NbL07g12900.1 phosphomannomutase/phosphoglucomutase [MW = 67.34 kDa]

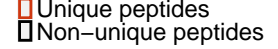
No. of times detected



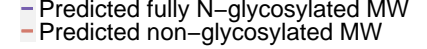
log(intensity)



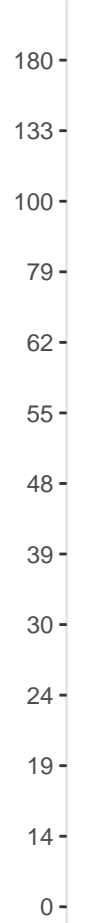
Values from



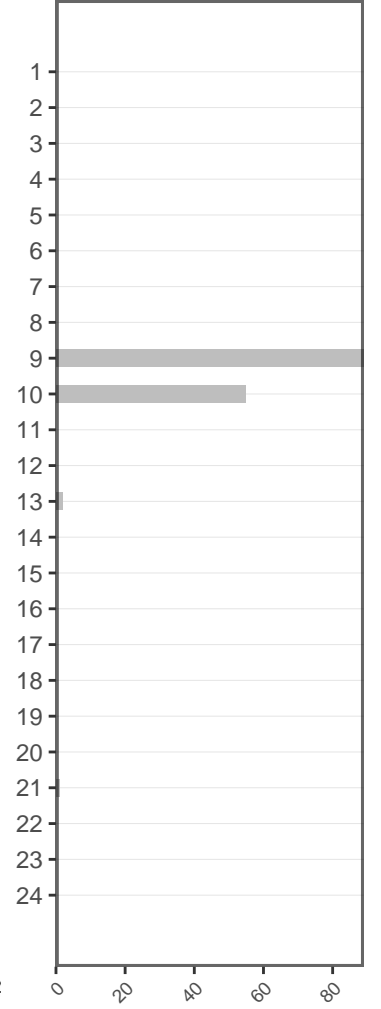
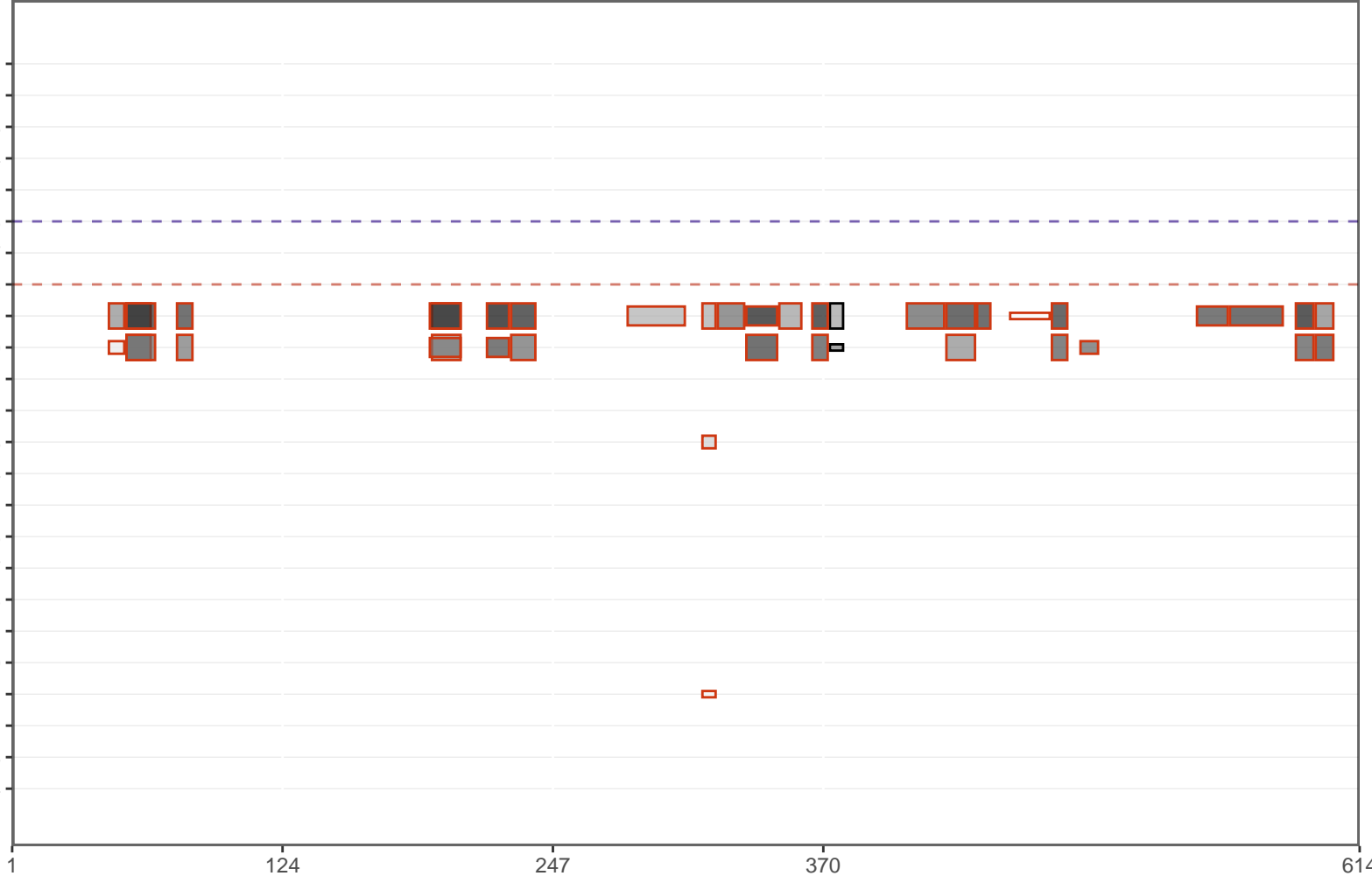
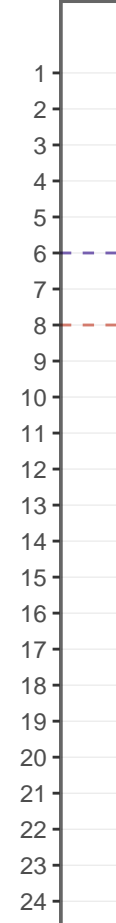
MW indication



Molecular weight

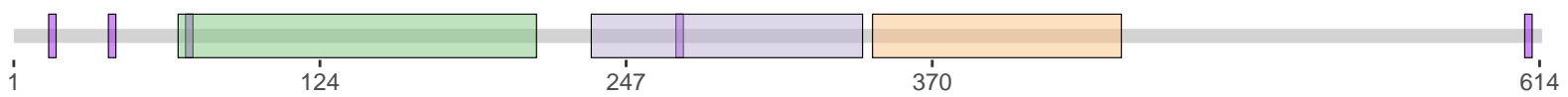


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF02878 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain I
- PF02879 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain II
- PF02880 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain III

Protein sequence:

SMFNNHPNPEKTKAMALTRAAVLENKADLGVFDTDVDRSGVVDSEGNPNDRLLALMSAIVLKENPRRTTIVTDARTSMALTKFKTKKGGQGLVRYGVYRNVKDGKLNKDGIEHLMMETSGHGALKENFLDDGAYMVKIHEMVRMLKLGSKRIGSLIEDLEPLESAEVRMVLSEPRNAKAKAVEAEAFRTHHEGGSLPQWELDTGGDCWVSDGGLVDTNDPDAIDAFMYRAKVSDEQNGEHWVHLRGGHNPNAVNLGRTIPGGGGFMAKVLDRFLPL

NbL07g12800.1 caspase_8_associated_protein_2 [MW = 53.19 kDa]

No. of times detected



log(intensity)



Values from



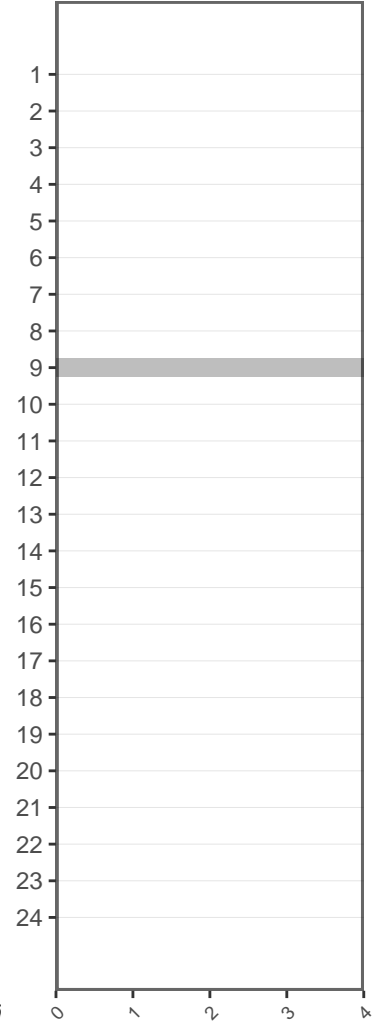
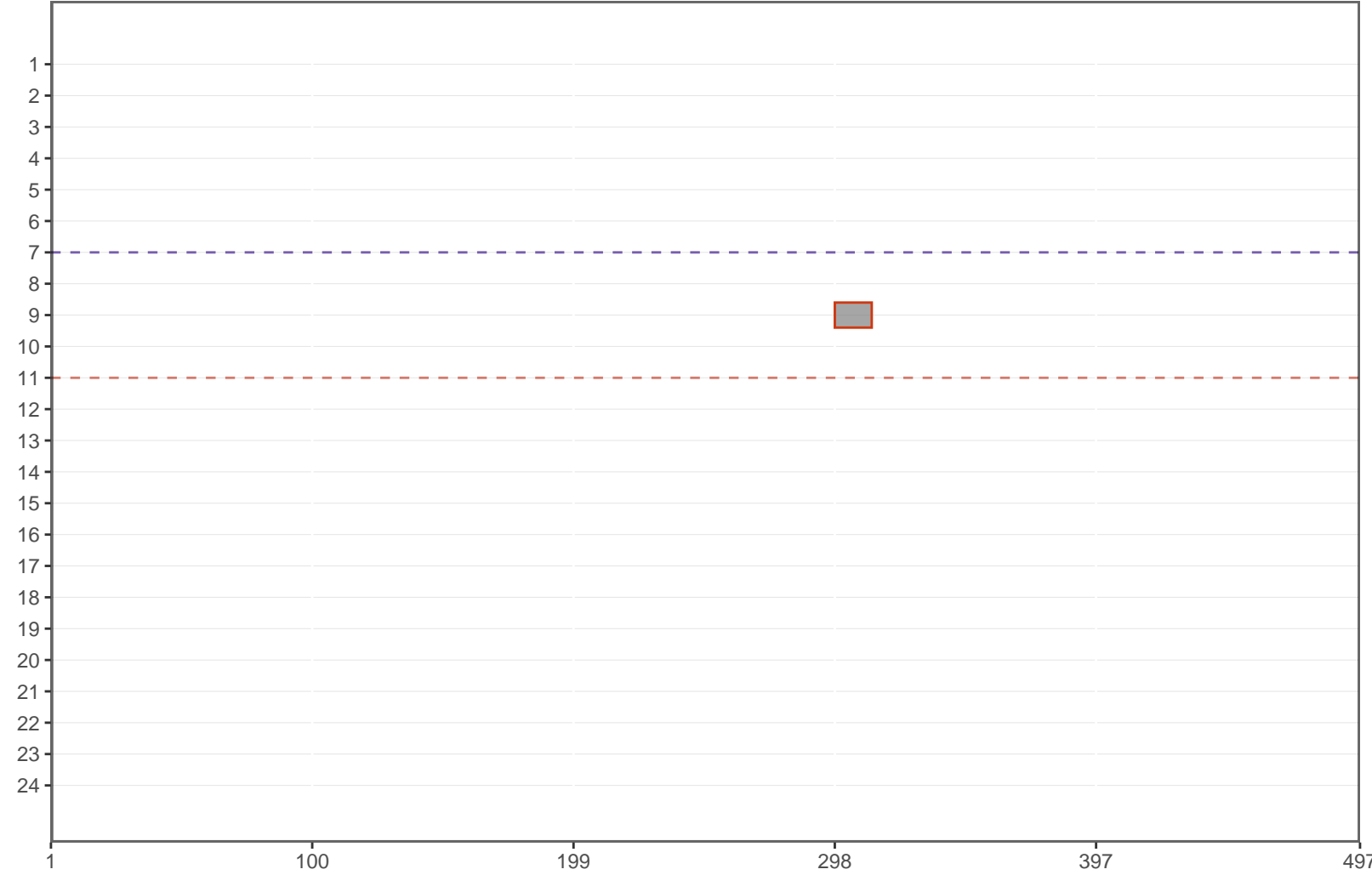
MW indication



Molecular weight

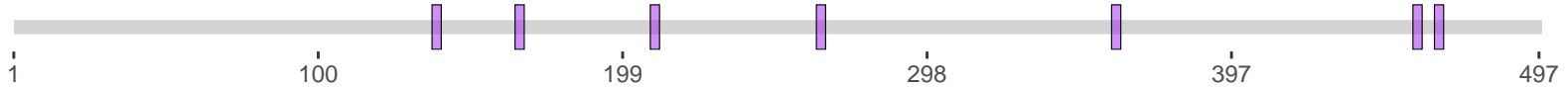


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

IQFLIGSNSPVICTEPVKEKPIPHSHNDLSLKEGVNFFNFGDGTFTTFLVLAGGPDFTTVDSKMASLNPGSDITGVKAKSLAKTNGDTAGTSGGAVTATNLETTTTPHAAVMEKGSQDHRQLNSSTVYDSDSASTTAVPTFTVTPISHNAQGYVMPSSGIVRQPLNPFSGNDLACGQHSPLVDKTDATDKESGSDPTGQKETTPEVSLKSGKPMNAEAGNNENRNLNETVFWLRFPEIGKLGSDANRPNVRRDDEGK

NbL07g12780.1 acetylornithine_deacetylase [MW = 52.99 kDa]

No. of times detected



log(intensity)



Values from



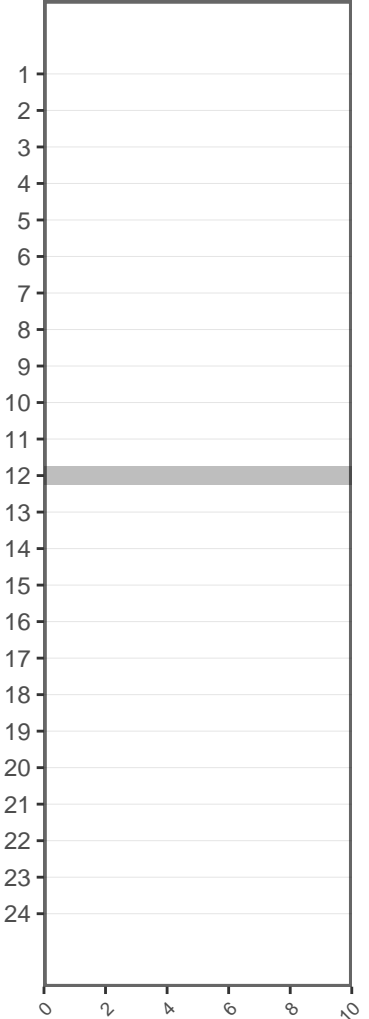
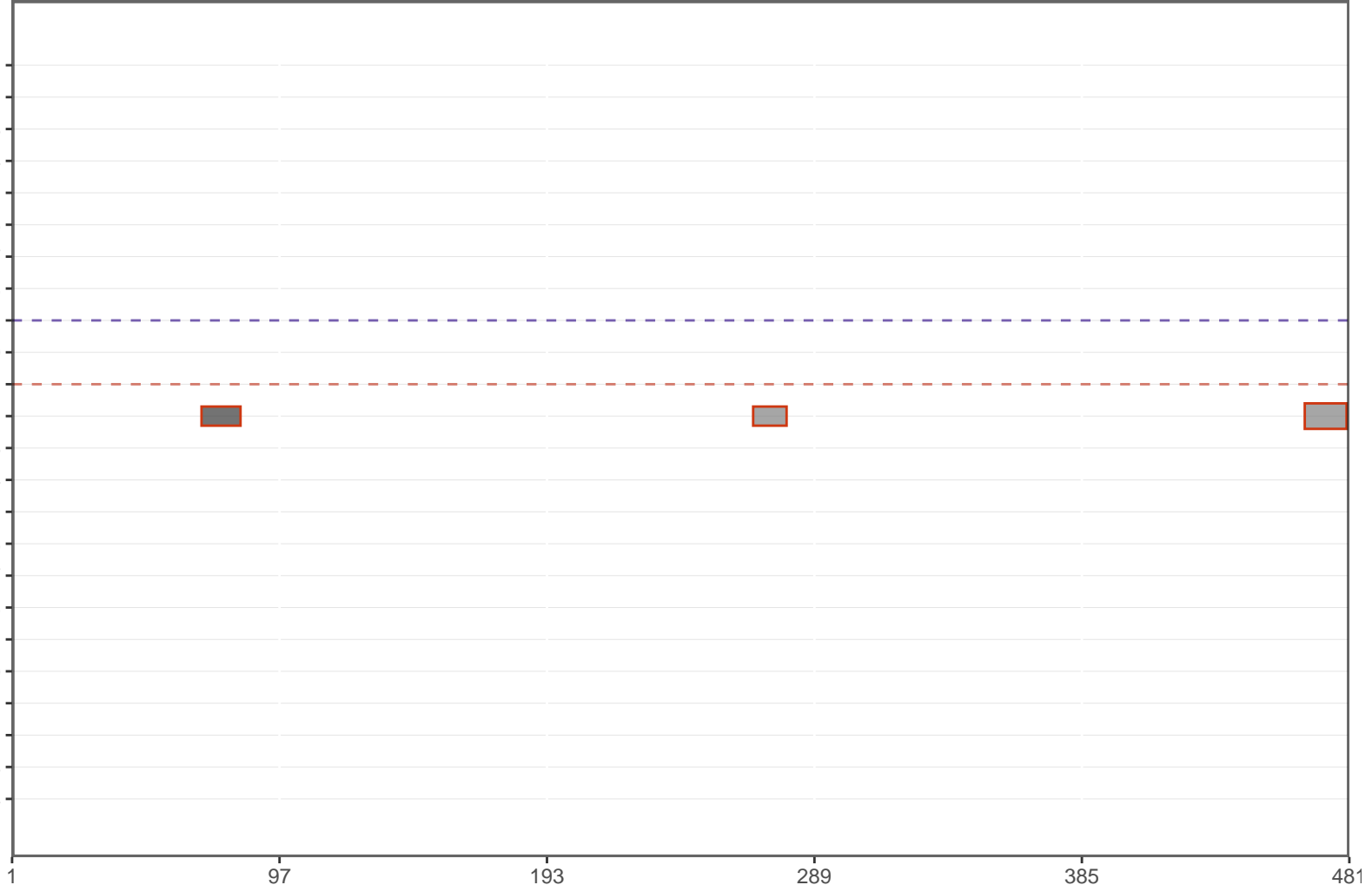
MW indication



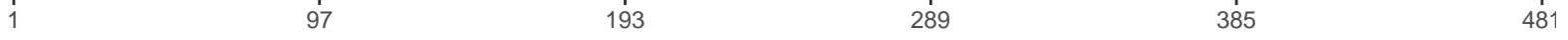
Molecular weight



Gel Slice

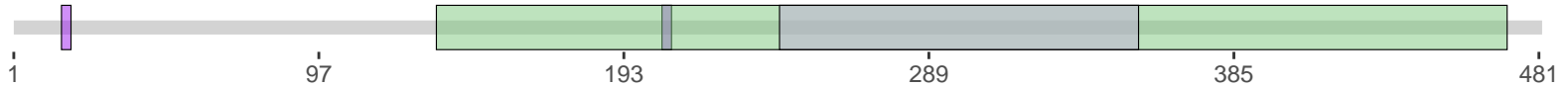


Protein length

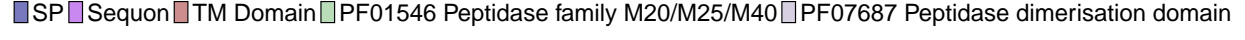


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LFVWDTADKQPCIGTGGSPKWLHYTGKLFHSGLAANKANPLLEAMETLKEIQSRFYRDFPHKPEQVYEFATPSTMKPTQWYFPGGGINDIPECTVSGDVRNLPFFYVSDAMKLGVEYDDNANNDKLDRCRGPVSKYVLPDENLRGRITRFDEA66GVAGDLNSRGPVHLGKATEEEVGHVWPYSITGTLPLRDLQDEGFVDVQTSVGLMATYHAKNEYGLSDMGGYRVTASVWGLEDDRYEV

NbL07g12700.1 28_kDa_ribonucleoprotein_chloroplastic [MW = 31.67 kDa]

No. of times detected



log(intensity)



Values from



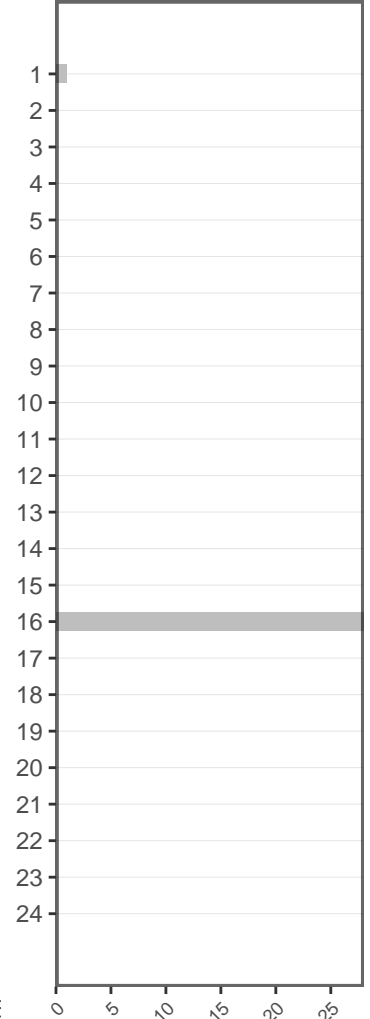
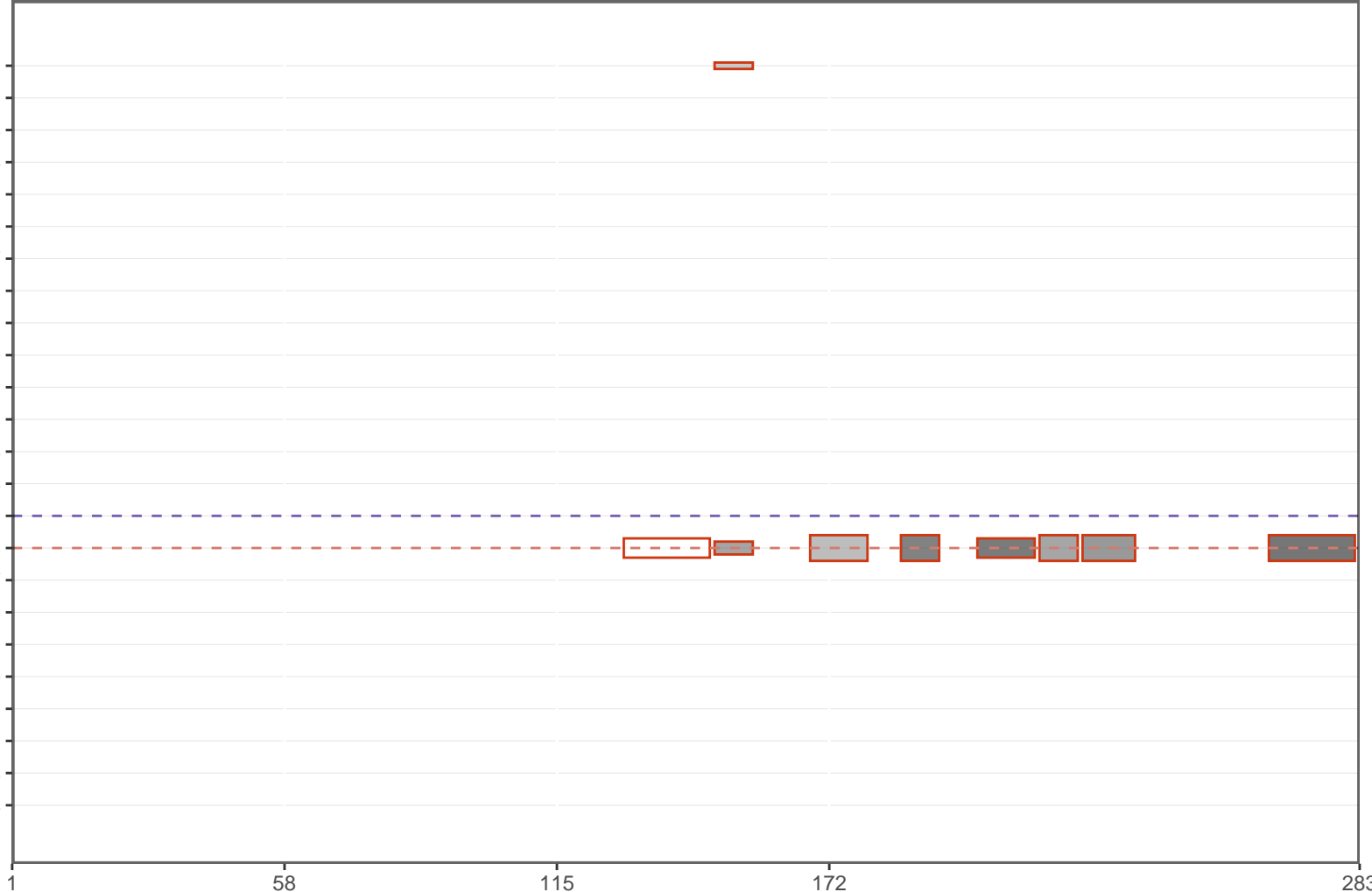
MW indication



Molecular weight



Gel Slice

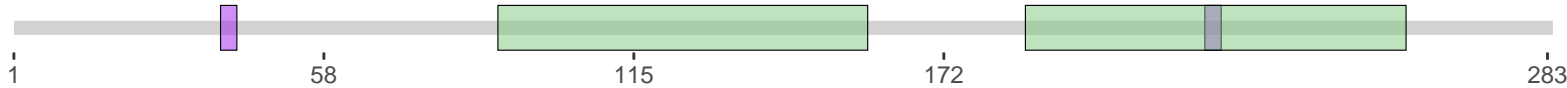


Peptide counts over 4 repeats

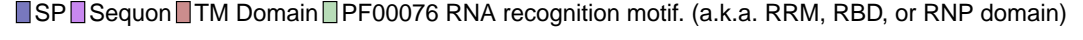
Protein length



Pfam domains



Pfam Description



Protein sequence:

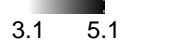
AFVYTMSSGEEAQAANDKLDVYTLGRIIRVFAHRFKPKAGAPPPPTPRGETRHKLIVSNLAWKVRBTHLRDFFSTNINPVSVRVVFDNAGRAAGYGVFSFDTKEEAEALSAFDGKELMGRPIRLKFSERDADGSENNEEPHGESPEEP

NbL07g12610.1 plastoglobulin-1_chloroplastic-like [MW = 37.21 kDa]

No. of times detected



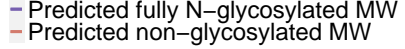
log(intensity)



Values from

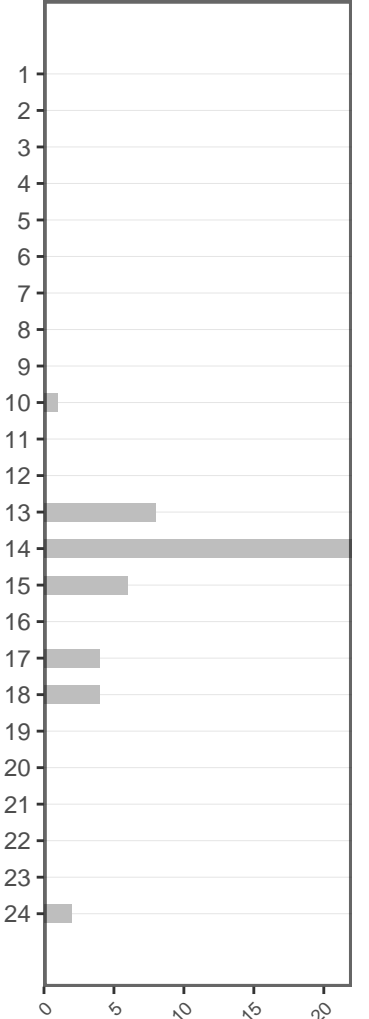
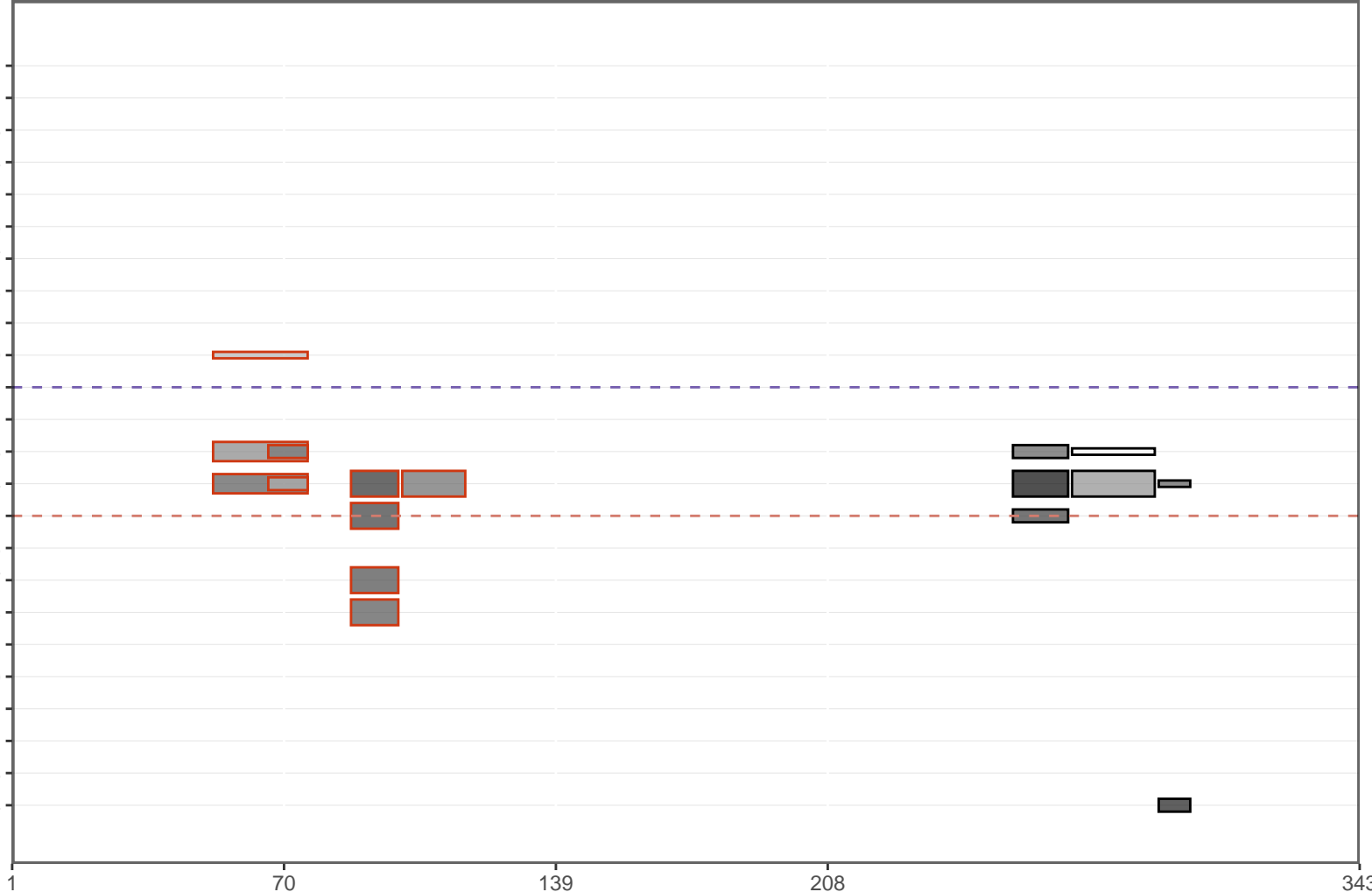
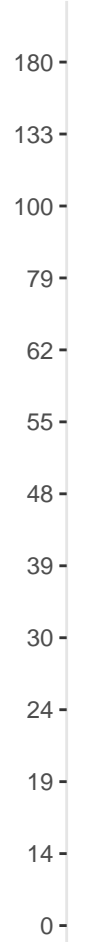


MW indication



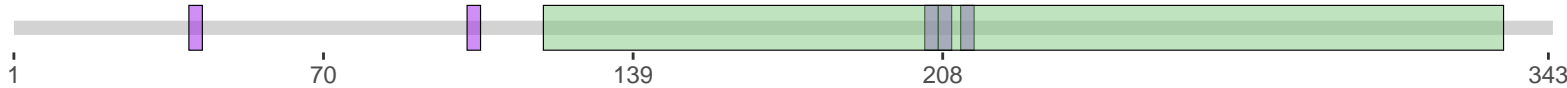
Molecular weight

Gel Slice



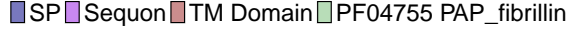
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

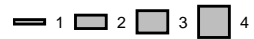


Protein sequence:

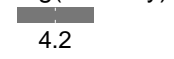
LVNPTPAETCEPELLDGNWLVVTFAPSELLFLAAGSIPLVKVEKISGGINTSNFTIENSTLSSPVATLFSFAAATFEVRSRPRGQVFKKEGDFKPKPEIKENIENLVNDFVGGKISLSPVQOGLGPLENVAAGARTISGGPPLKIPKIPGERTKSWLLFTVLEKDLRISKGGDGFVLYKGGSLLY*

NbL07g12530.1 nascent_polypeptide-associated_complex_subunit_beta-like [MW = 17.57 kDa]

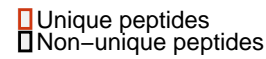
No. of times detected



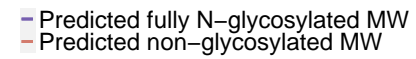
log(intensity)



Values from



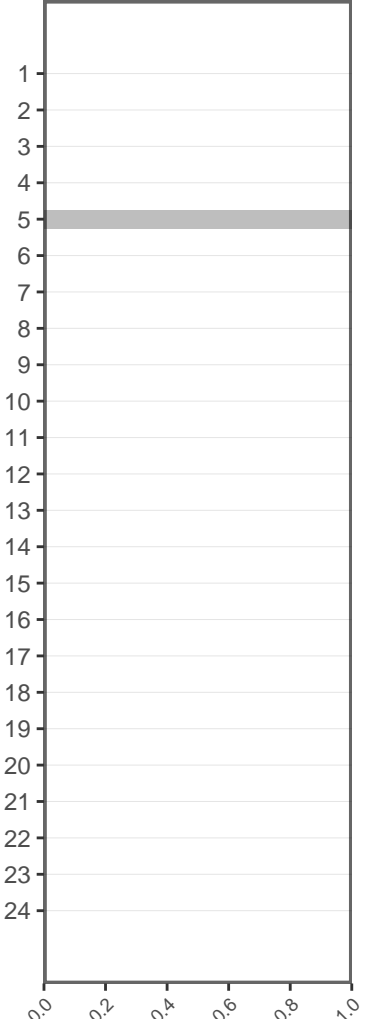
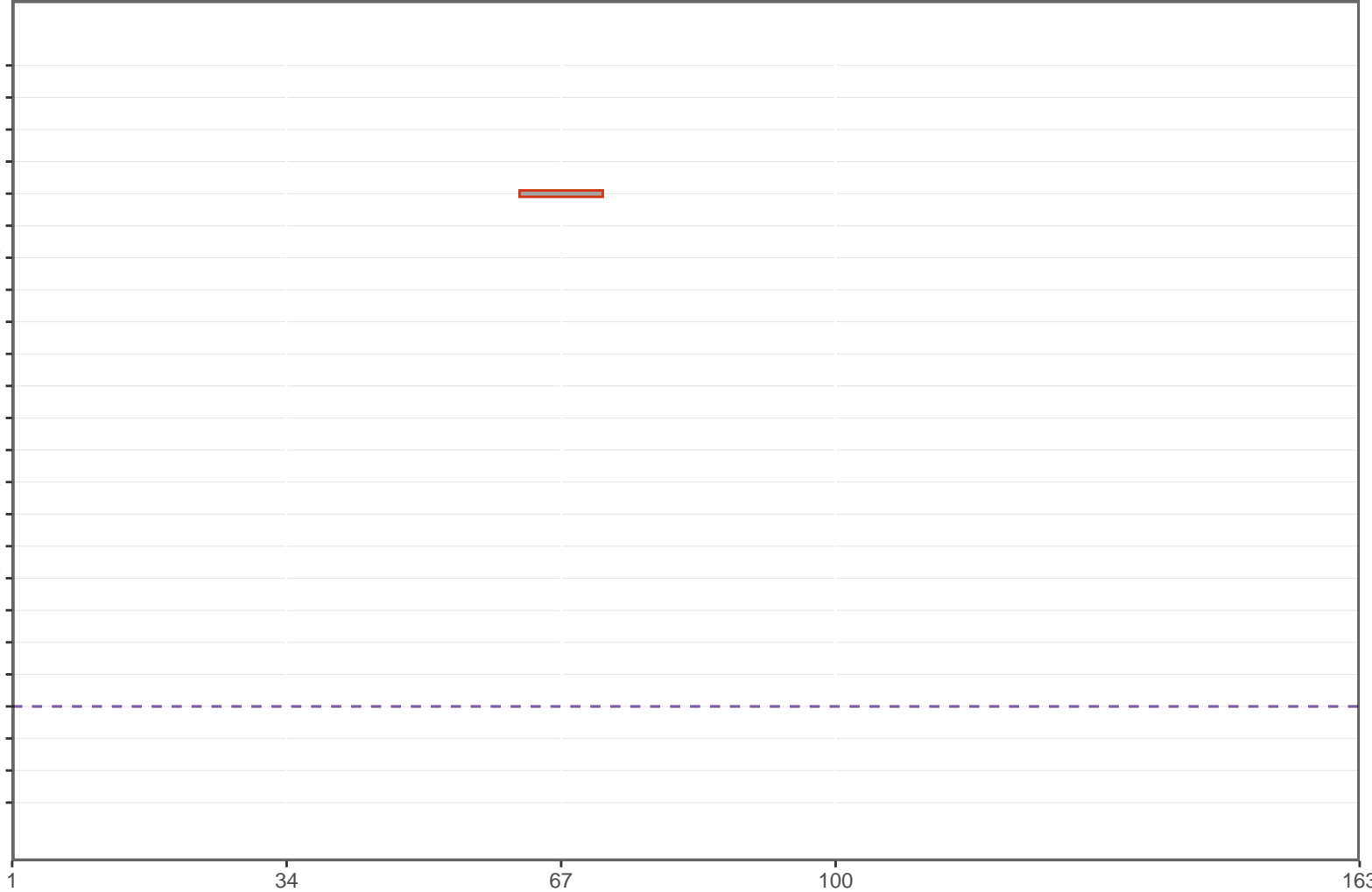
MW indication



Molecular weight



Gel Slice



Protein length

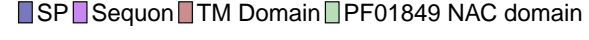


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

NPKYQASIAANTWVVGSGPQTKLGDLPQIHHLGPDNLENLKKLAEGFGKGAPTGAPEGGAAAGDEDDDDVPEPVGDTFEAAAEEGHTS

NbL07g12520.1 villin-4-like [MW = 109.25 kDa]

No. of times detected



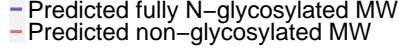
log(intensity)



Values from



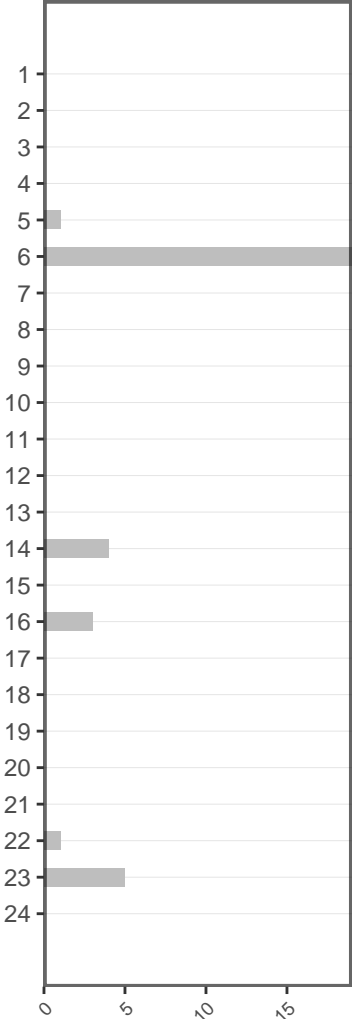
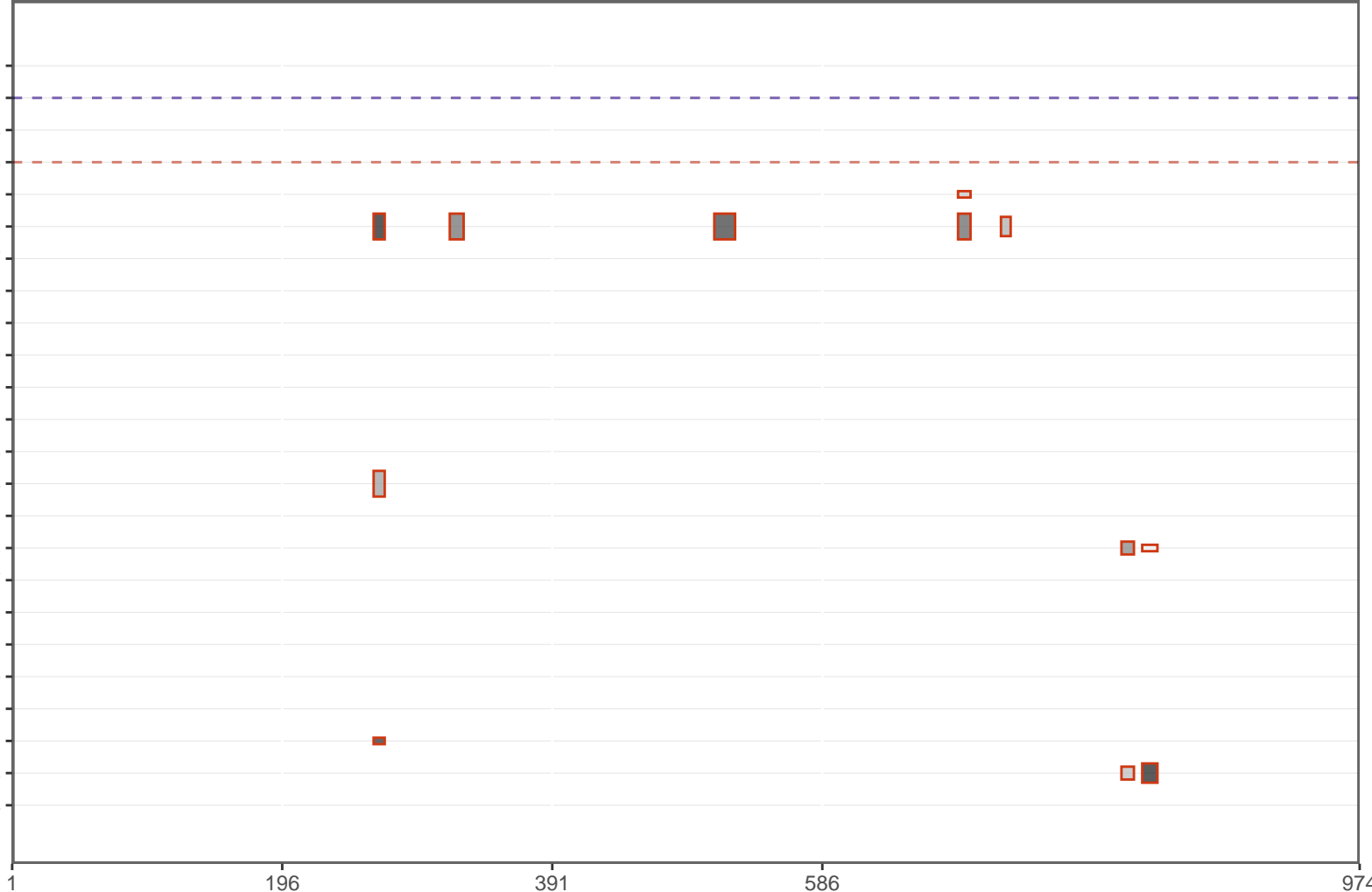
MW indication



Molecular weight



Gel Slice



Protein length

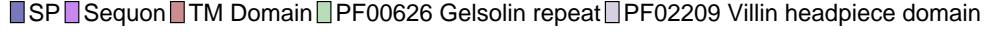


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

RIVYEGYEPLOFFVIFQSFVFNKGLSEGKHLVEKELADDTYKEDGIALFRHQGTGPDNMGSGQVEPVAASLNSISYCHLHSGSSVFTWTGNLTTSEGDQELVERGLDLKPDMDGSKLQKEGAEEGFWDLGGKSEYPEKIGKRAEAGDPHLFSGCTFSKGLKVTETVFNFGDGLMTEDFILDCHSDNYVWVGQLEVEYKMKQALSGIKFLDYDLMEKLSHGAPVYVMEGSEPPFFTRHFSWDSNKSAMHGNISFORKLTWKNKGPPPMKPKRRTVSYGGRSAPE

NbL07g12480.1 uncharacterized_LOC109237233 [MW = 39.83 kDa]

No. of times detected



log(intensity)



Values from



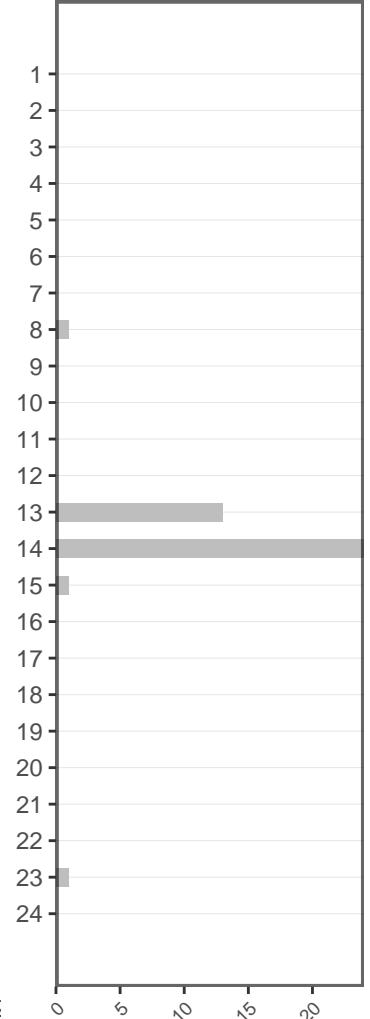
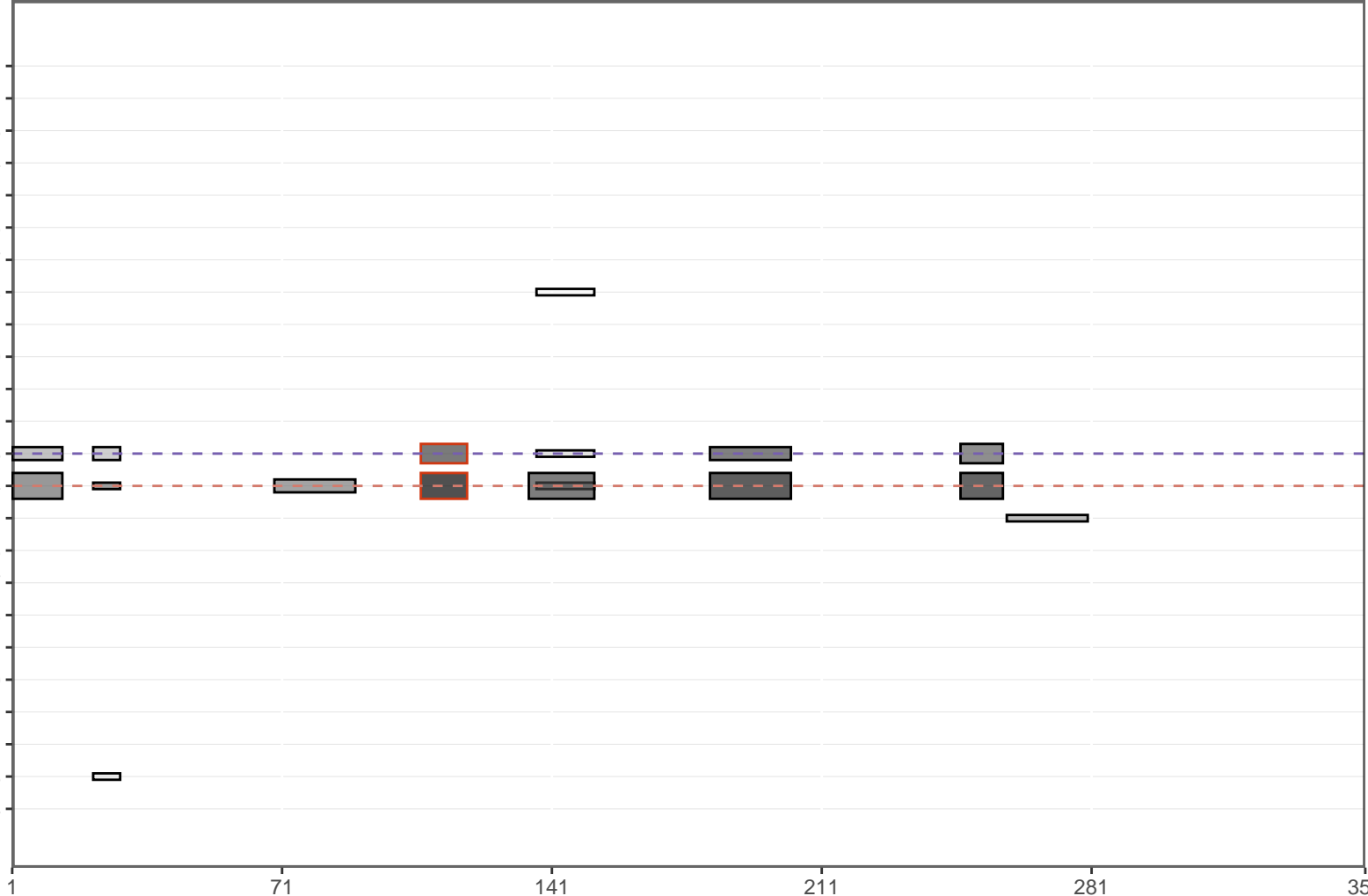
MW indication



Molecular weight



Gel Slice



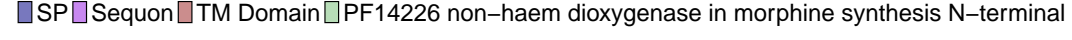
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MLAIECVAEIVANGFGLKDAFTSLMDGQPHLLAPRTGSDLRVYAKEGTVFAGVHYDLMFLTHIGRFRFPGLSLWLRNGQKMEKVPVGLLHOTGKQIEVLTAGECMAGMHEVVVTRRTTDAIRRALEQNRSLWRVSTLFAHIASDVLKPLGHFSDTLASKYPPIDAGEFVVEGELAINLKCANGA

NbL07g12460.1 kirola-like [MW = 16.54 kDa]

No. of times detected



log(intensity)



Values from



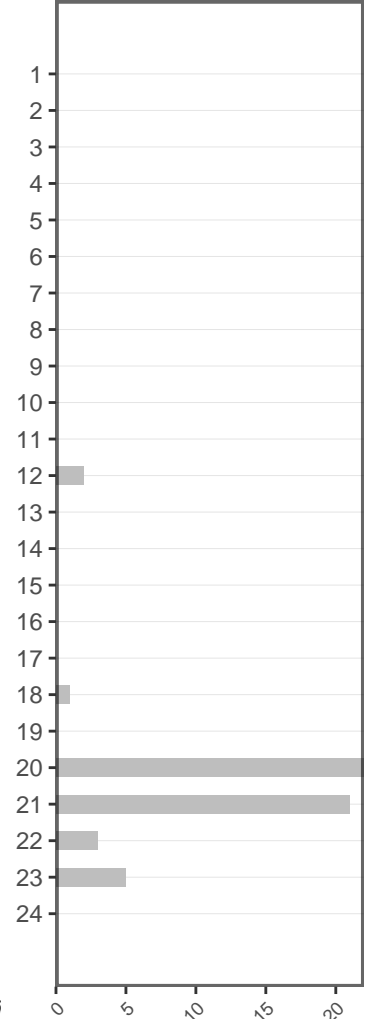
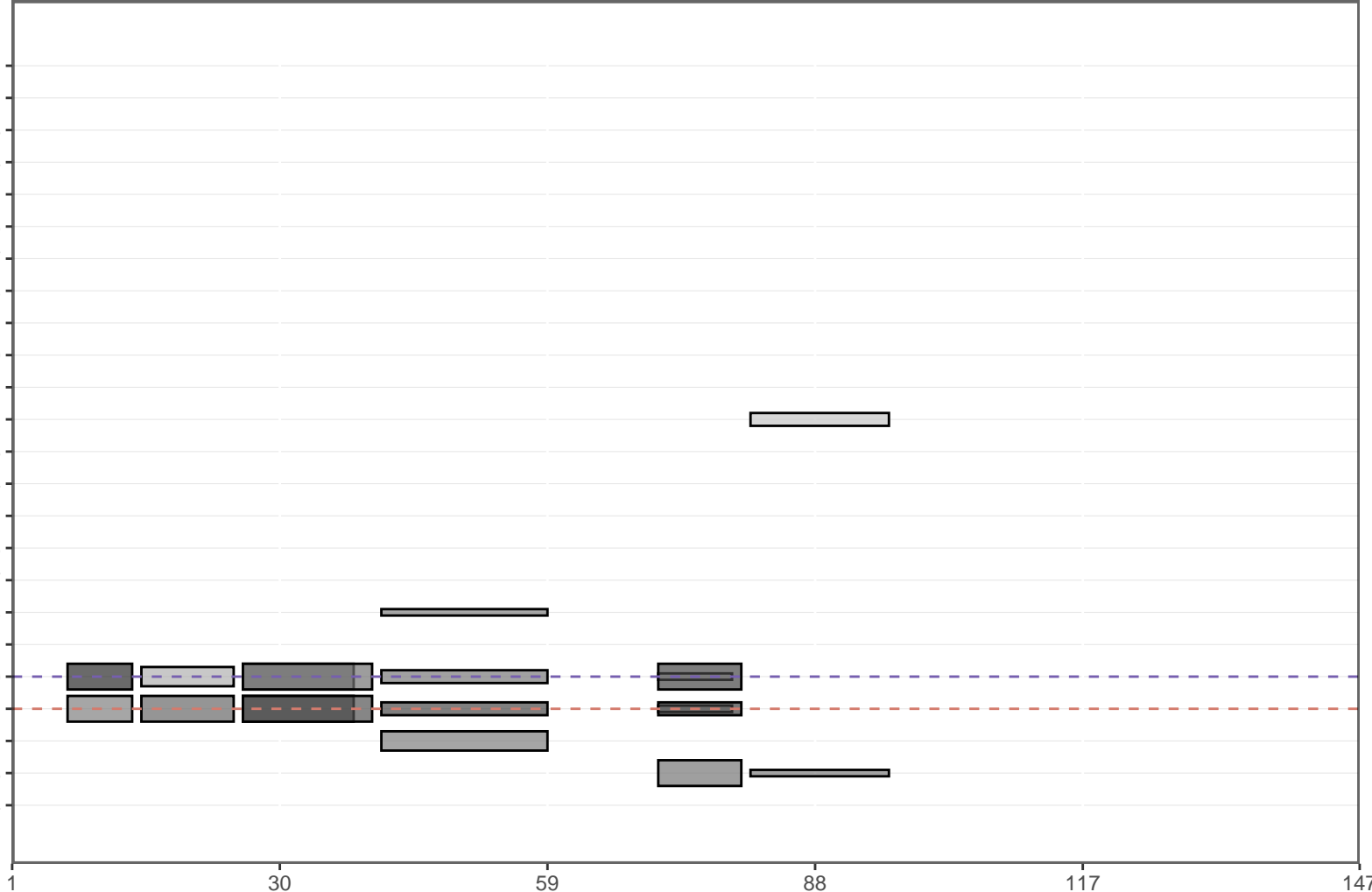
MW indication



Molecular weight

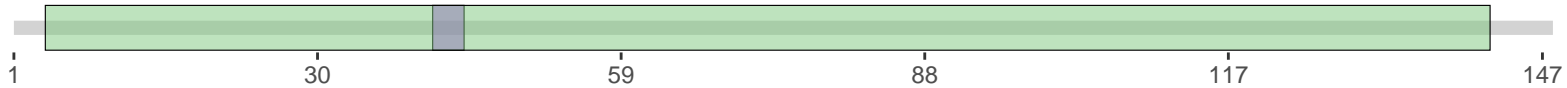


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YVVGKERRIAKQVAVHVDAAKSGITFNVEGVMNELVKSITATLTAEGNWMFTWLVYEKLNENTPEFLDLLEFACLLDIEPHVGVK

NbL07g12170.1 14-3-3_protein_9-like [MW = 30.04 kDa]

No. of times detected



log(intensity)



Values from



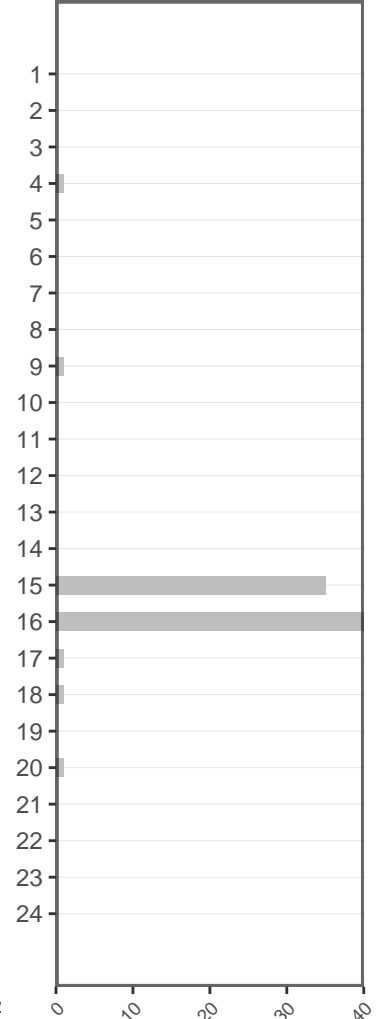
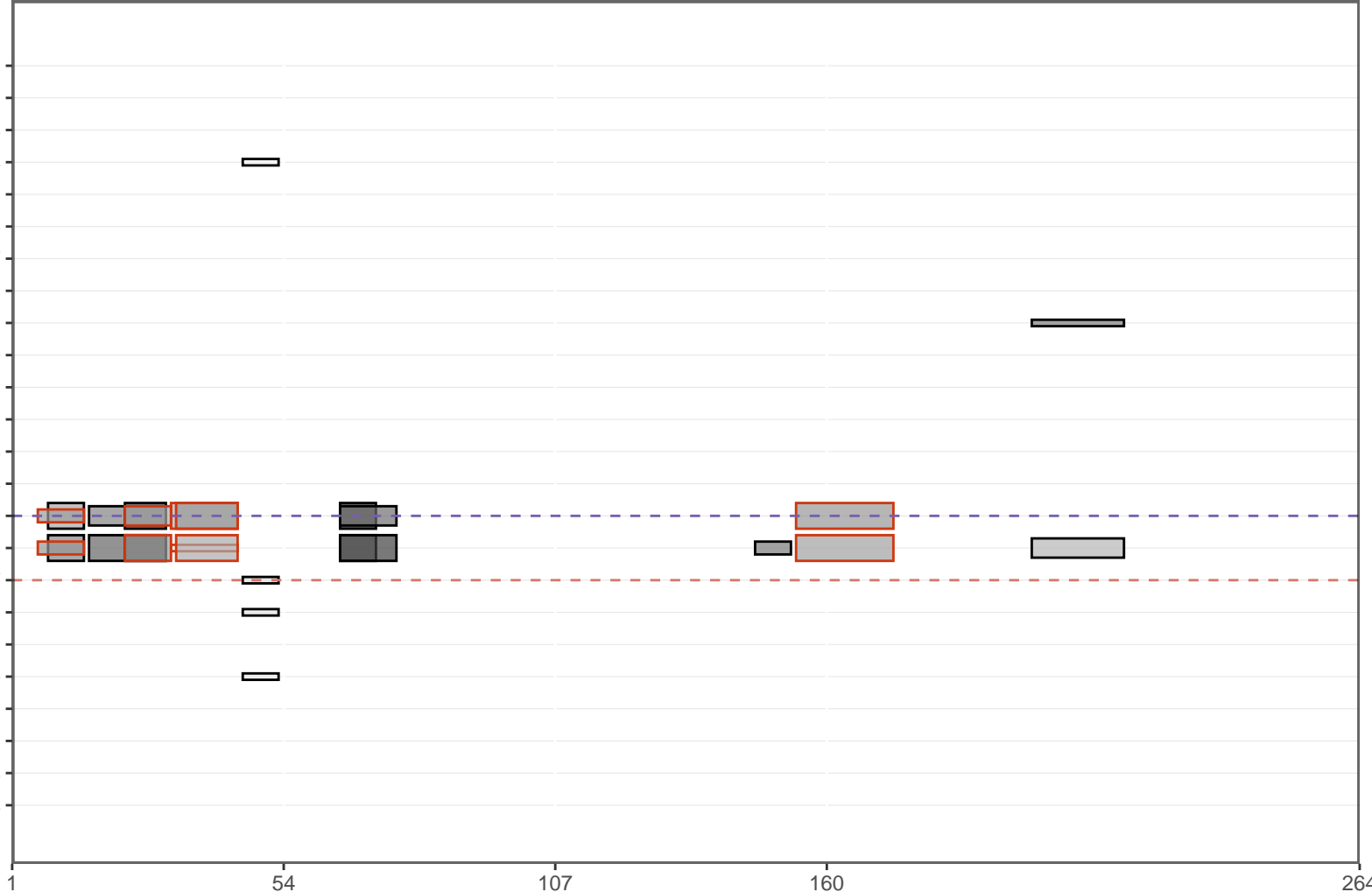
MW indication



Molecular weight

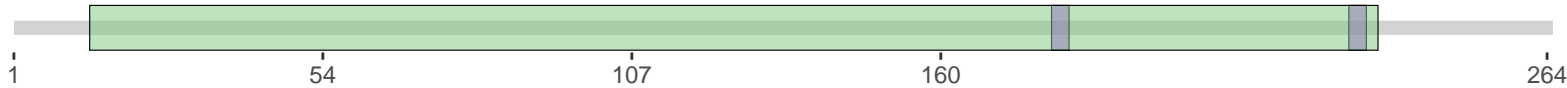


Gel Slice



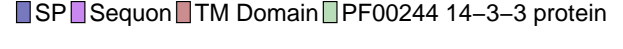
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GESVFFYXMGKGDYRVLAEFKTGTGDKKEVSDLSKAYGSAATTAEALPPTHPIRLGLALNFVYFYEILNSPERADHLAKQAFDEANSELDLNEDEBYKDTLMQLLRDNLFWTSDIPEDSGIREVIFSLGVFVYGTTCG

NbL07g12160.1 uncharacterized_LOC109215312 [MW = 41.09 kDa]

No. of times detected



log(intensity)



Values from



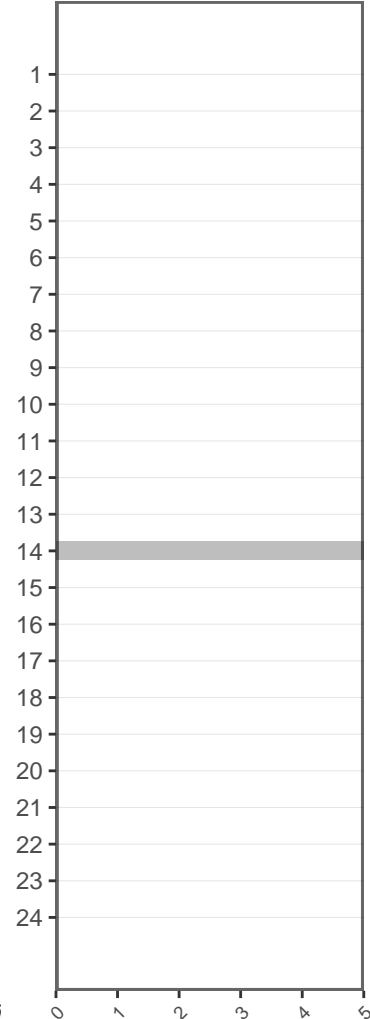
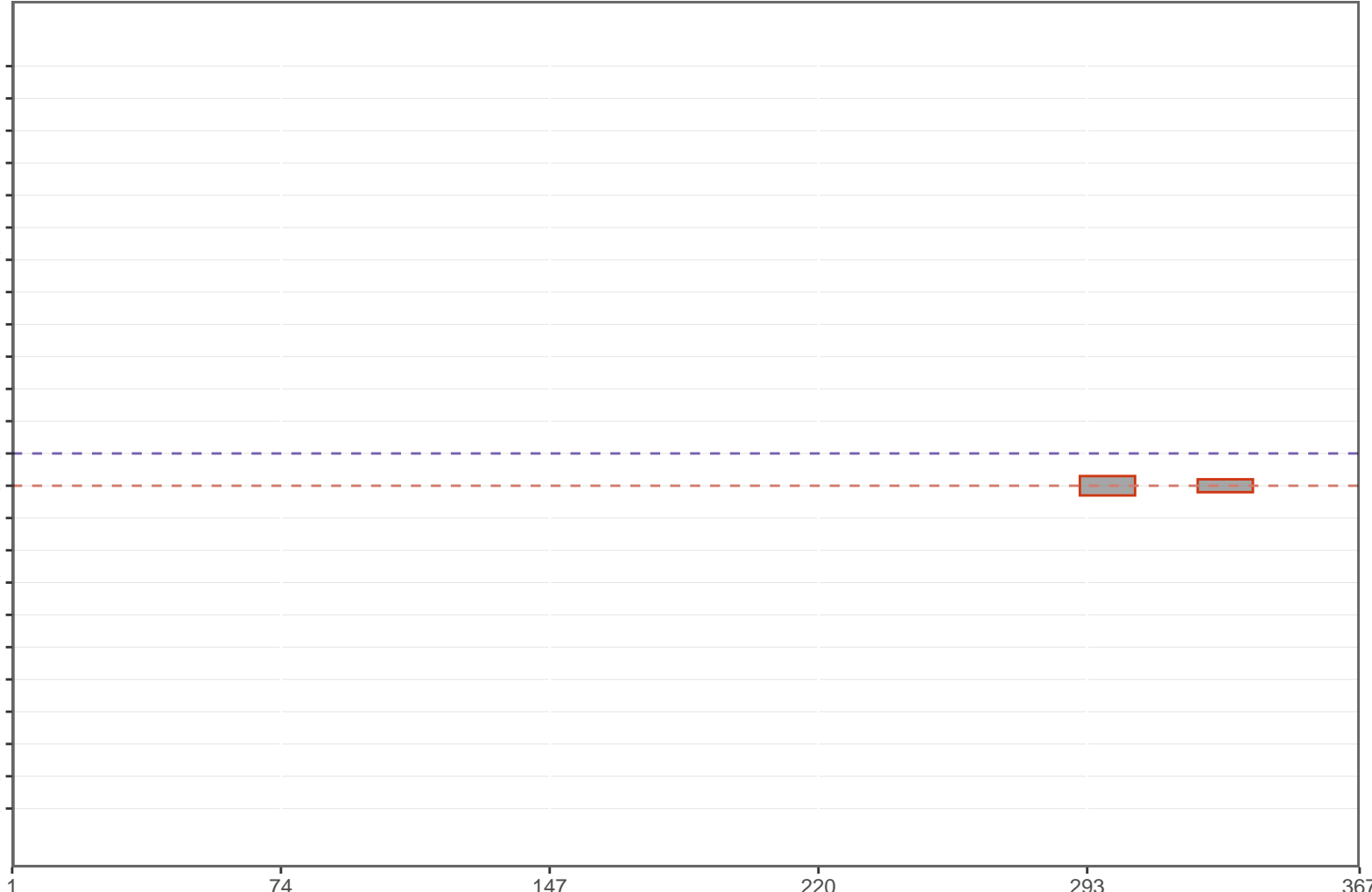
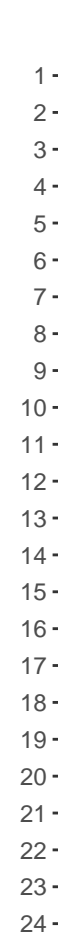
MW indication



Molecular weight



Gel Slice

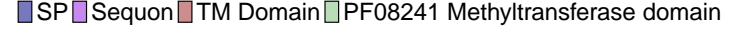


Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

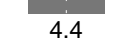
IQIVRGNVLDIAEKHDDQVGGDFSRDILDGCGVSTGYLADRYPSAKVTGLDLSPFLAWAGYKEKKRNGRKNPISWHANGENTGLPSKSFDLVSHYVFHEGPERAIRNLVYKESFRILRPGGTVATDNGSPKSLGELPPVLFETLMKSTEPFLDEVYLTDLERVMKETGFANVQTVLDRHRVETATVPV*

NbL07g12040.1 cytochrome_b-c1_complex_subunit_9-like [MW = 11.68 kDa]

No. of times detected



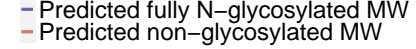
log(intensity)



Values from



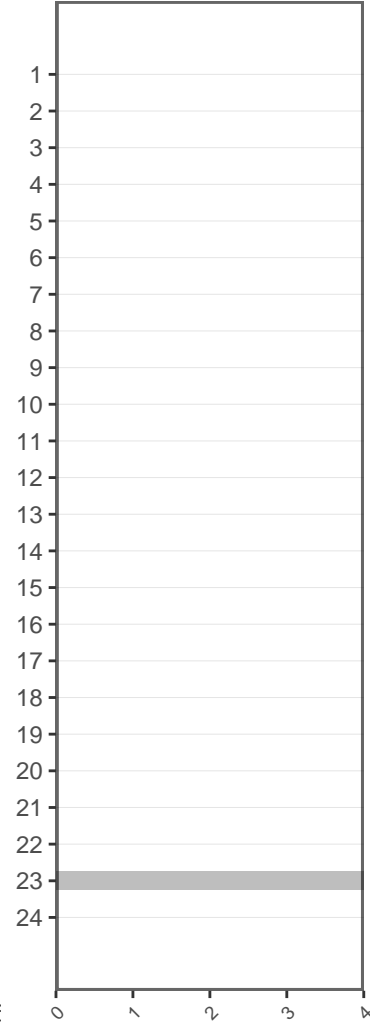
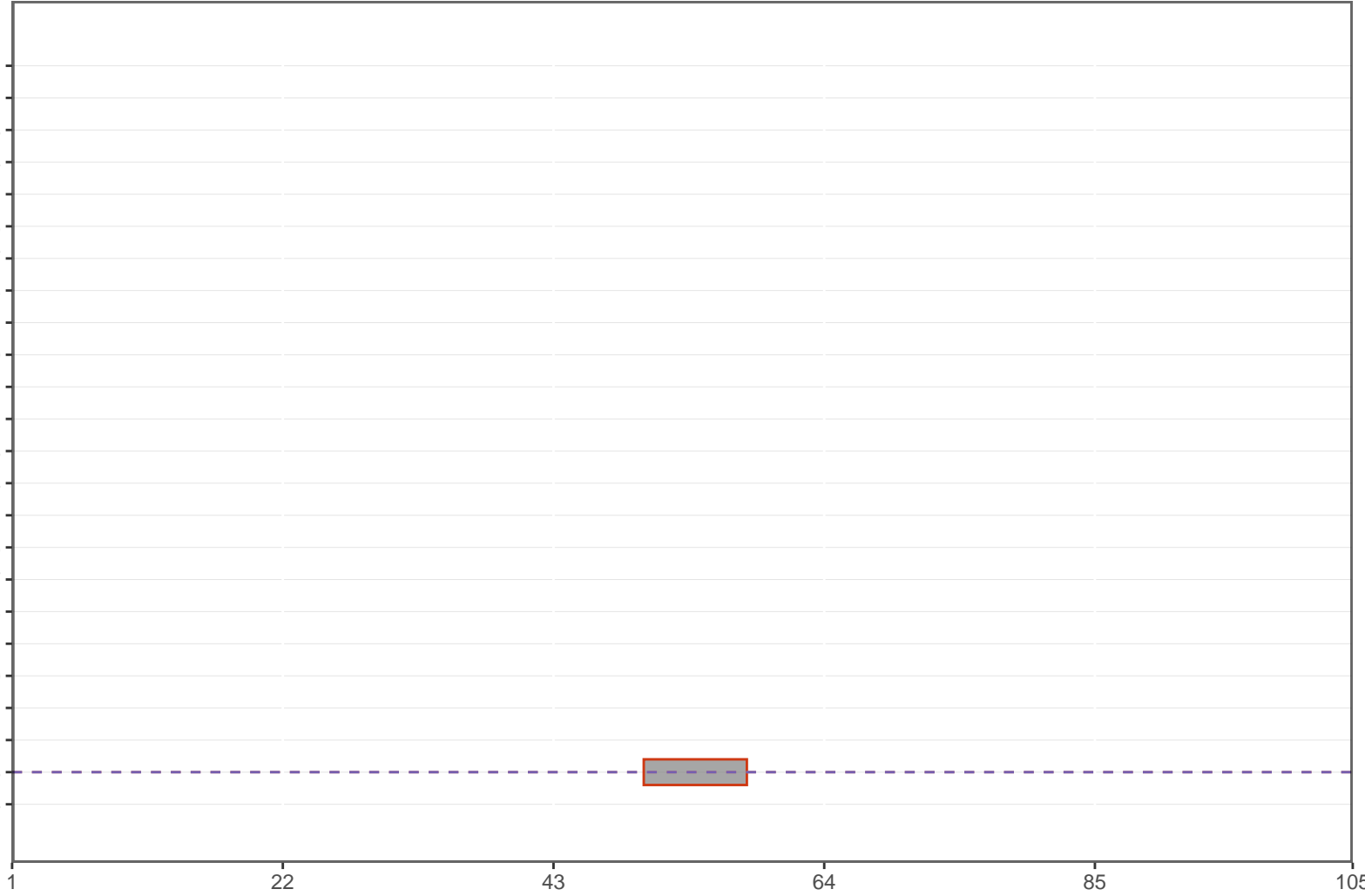
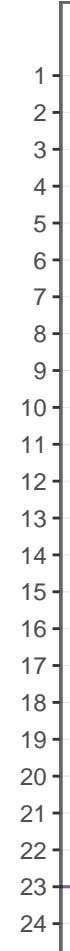
MW indication



Molecular weight

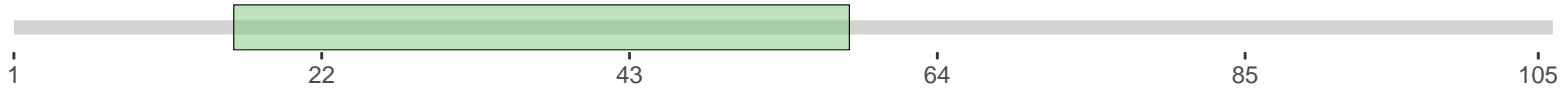


Gel Slice



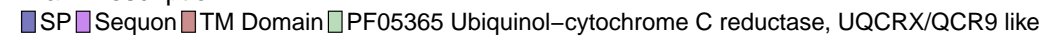
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SEKAVDYGVHRLVEMNNVSKTKGKGLQVLPVVSFSEKRFVHLSLSLDVLPDLLLYKLVGFCULIA*

NbL07g12010.1 glucan_endo-13-beta-glucosidase_14-like [MW - SP = 39.55 kDa]

No. of times detected



log(intensity)



Values from



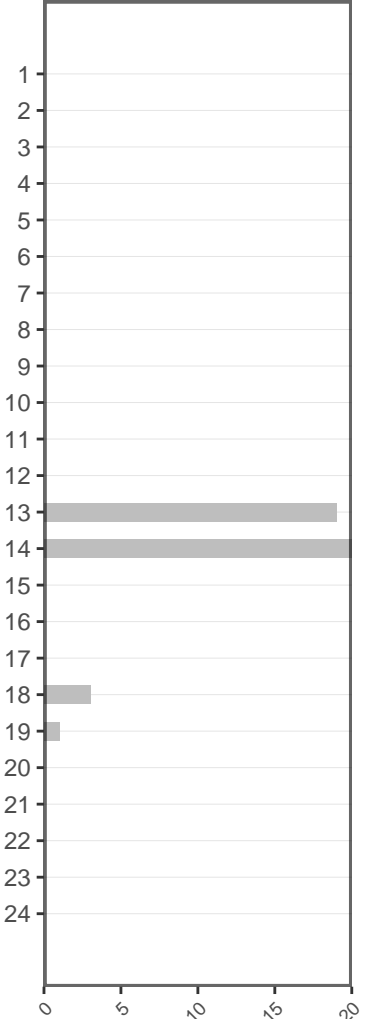
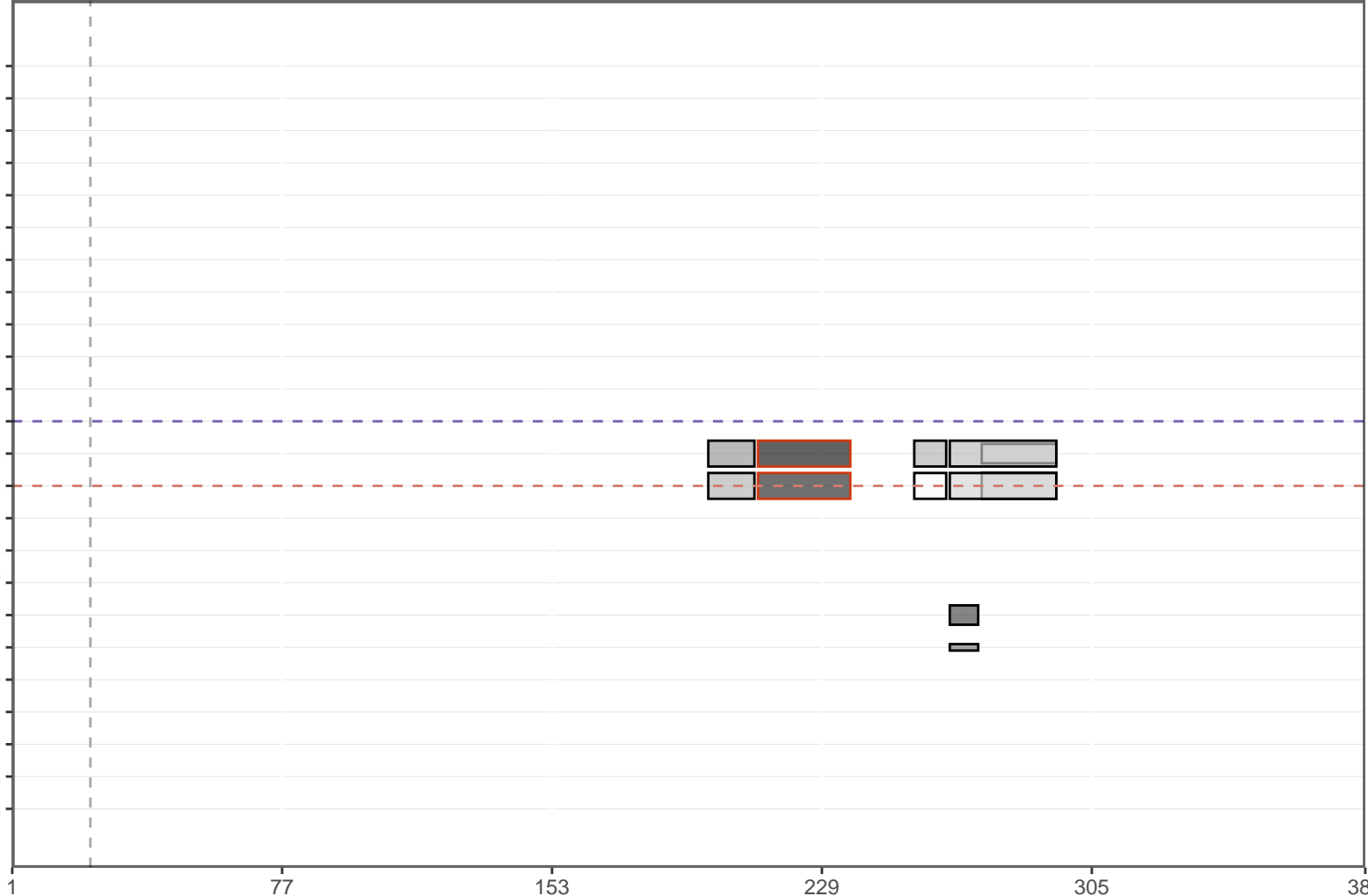
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RDGLAEYHGLNFMAGTKFPLINAYFFFAKDPDQVFLDYVLRFRNAGTLDPTNKKYDNNMVAQIDAVHSAAKAMGYSDGVKVSSETGWPSKGDPPNEFGATPENAAQGNLFRRIQGNQGTFRKPSPEIDVYVFALENENLKPDPASERNYGLYDGTPTVYINGLGGFLPRMDVSAAKNALSISAILLILVFLQF

NbL07g11910.1 N-carbamoylputrescine_amidase [MW = 33.53 kDa]

No. of times detected



log(intensity)



Values from



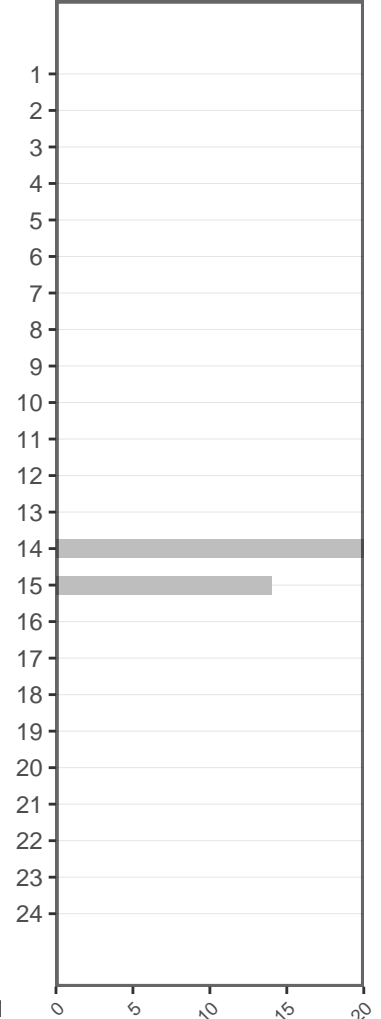
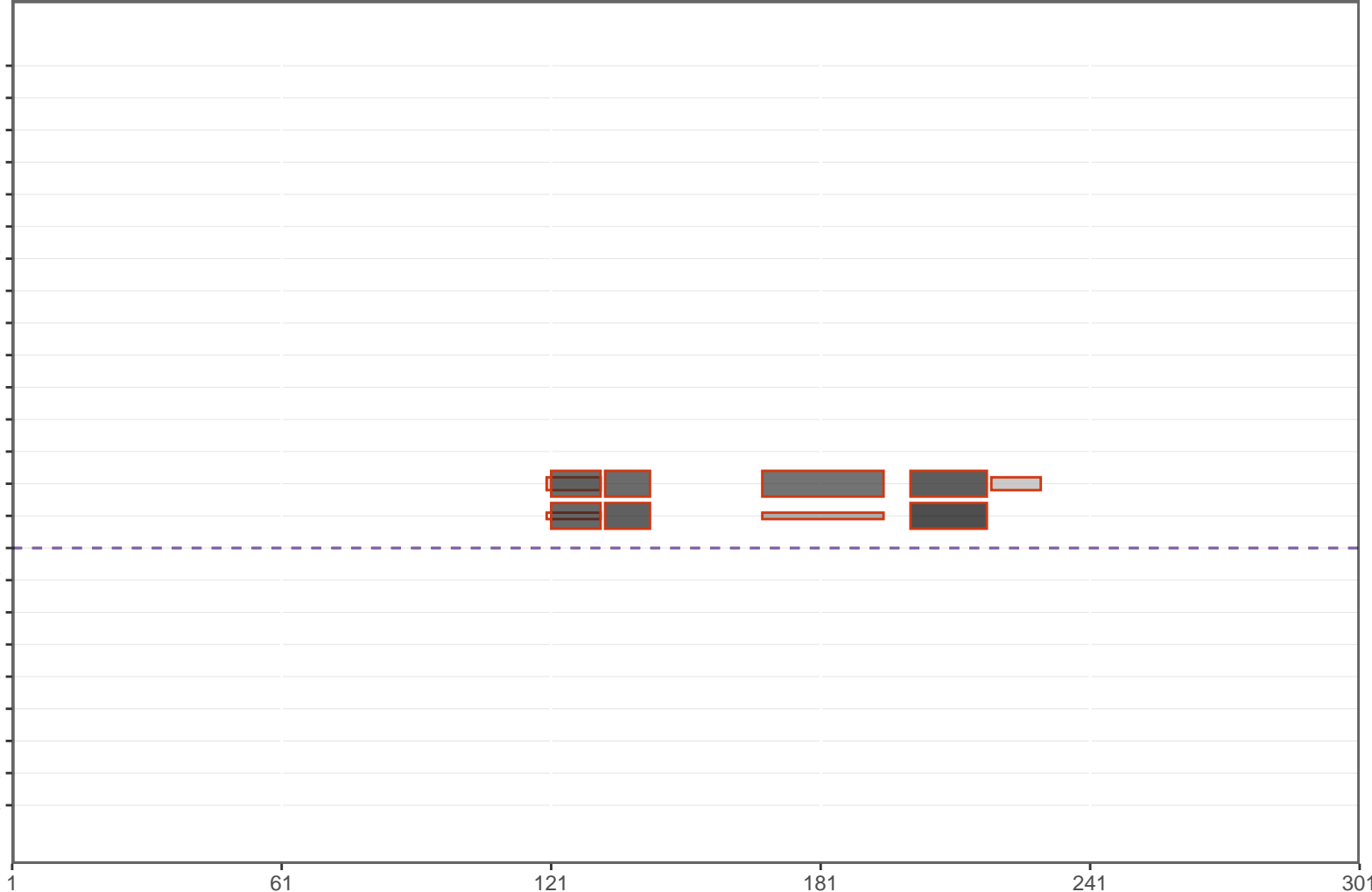
MW indication



Molecular weight



Gel Slice

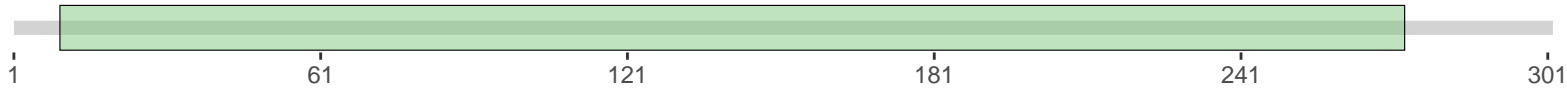


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

JTGFKYFTKYAKIGVAGDQWDFPEARRAMALGGAEVLFYPTAIGSEPDQDGLDSRDHWRRVMQSHAGANVPLVSNRIGKETIETEHGSAFFYGYGFIAGPTGELVAADQKEEVLLWDFLDKIKSKRGWGVFRDRRDPDKVLMFLDGSNPVY

NbL07g11830.1 long_chain_acyl-CoA_synthetase_4 [MW = 51.08 kDa]

No. of times detected



log(intensity)



Values from



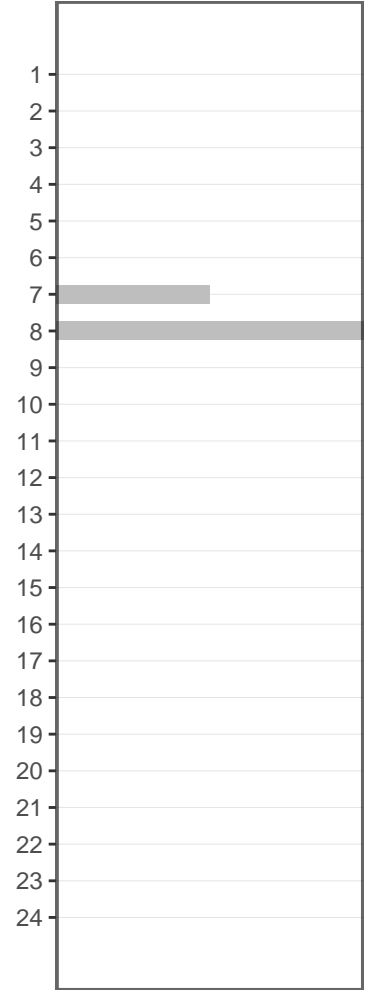
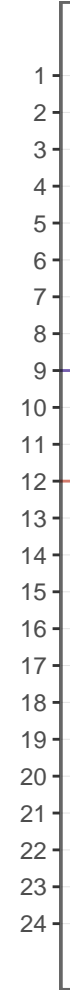
MW indication



Molecular weight



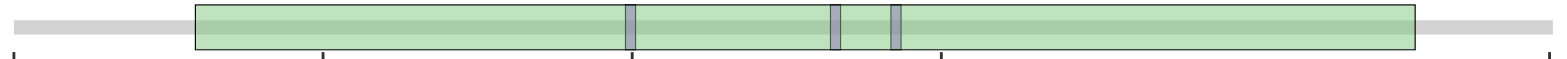
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

CFDLPVXXKEDICTIMYTGTTGDPKGVLENSNIVLTIAGVQRLLGVSNEGLTVDDVYLSVPLAHFDRVIEECFNHGASGIFVRGDVLLTEDEIGELKPTIFGAVPRVLDRIYSGLOQKISSGGLLKSTLFLAYAKHHLNKKGRKHFEASPLSDKVFYSKVKKEGLGGKVRLLSGGAFLAAHVEAFRLRVACGKPVLDGYPFPFQNIIMLAEIMMKFLAFSFKHRRWVWVWVPSRCRT

NbL07g11700.1 nitrilase/nitrile_hydratase_NIT4B [MW = 37.67 kDa]

No. of times detected



log(intensity)



Values from



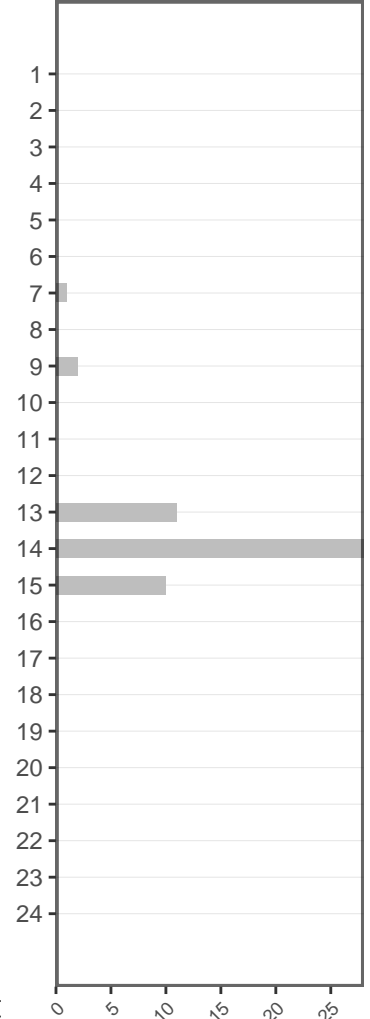
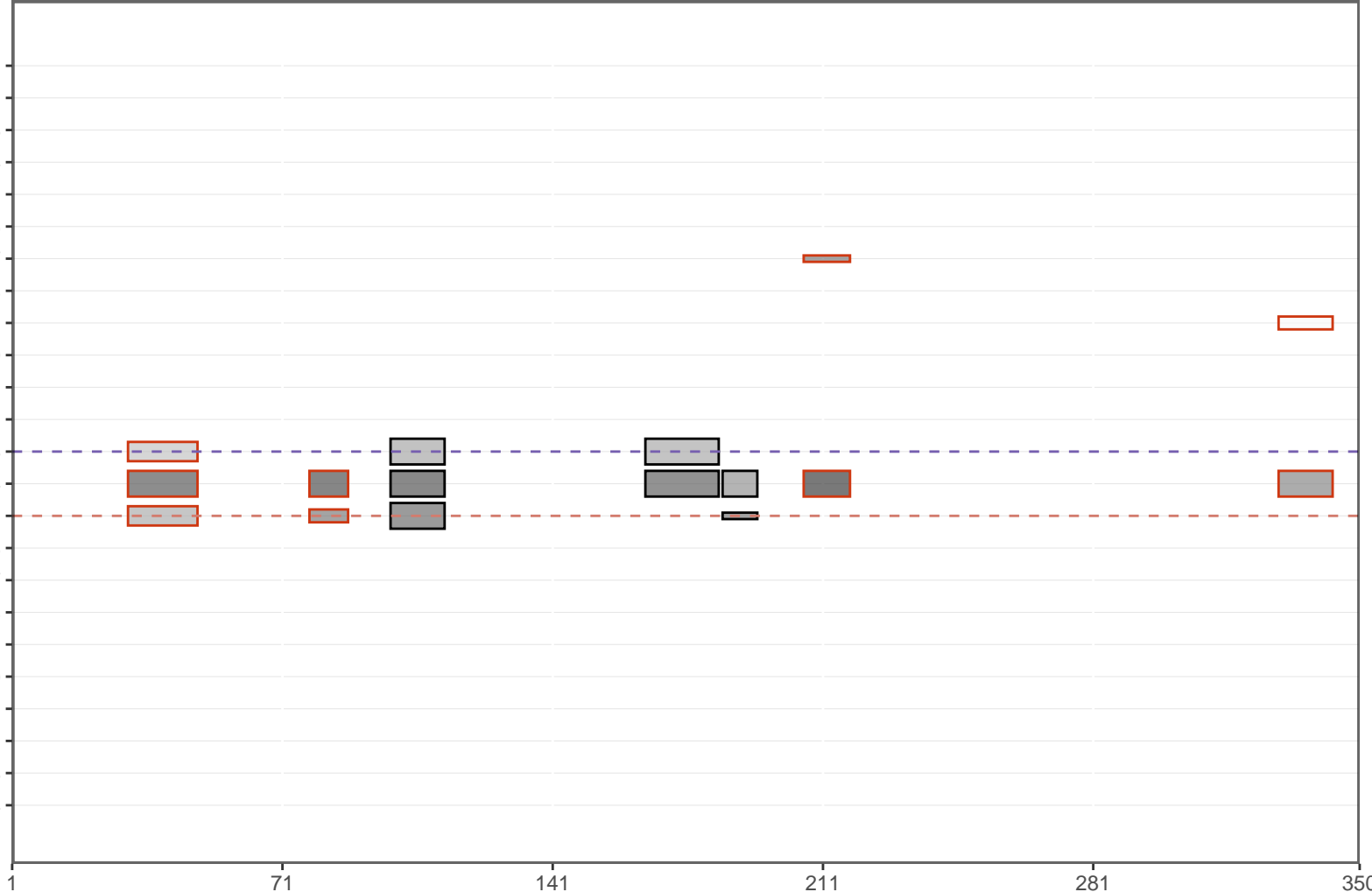
MW indication



Molecular weight



Gel Slice

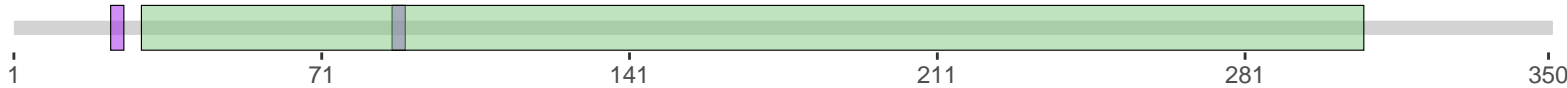


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ALERIRWFGDGGSTPVDYDFLGNKGAACWENRMLLRMTAMVYKGIIEYCAPTADARDVWQASMTHALEGGCVLSANQFCRRKDYPPPEVYVFSQTEEDLTPDSVCAAGGVVHSPGAVLAGPNVEGEALISADLDLGEIARAKDFDVAVGHYARPEVLGLVLRDHYVSPVFTSTSEKAESSPK

NbL07g11610.1 uridine_5'-monophosphate_synthase [MW = 51.56 kDa]

No. of times detected



log(intensity)



Values from

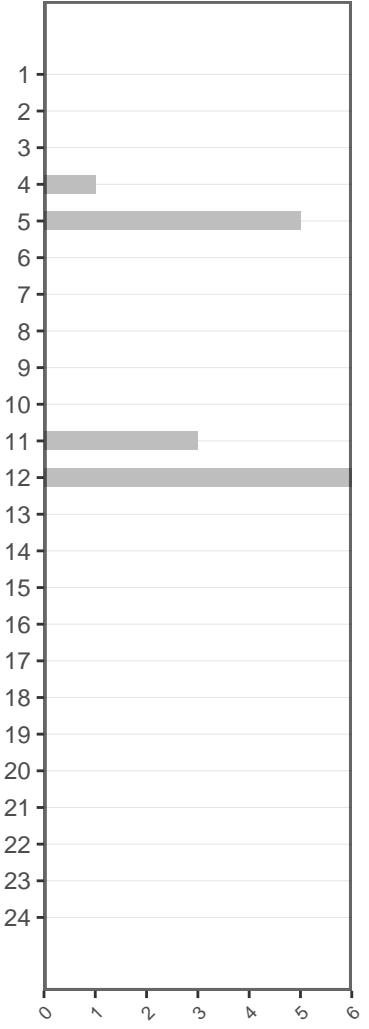
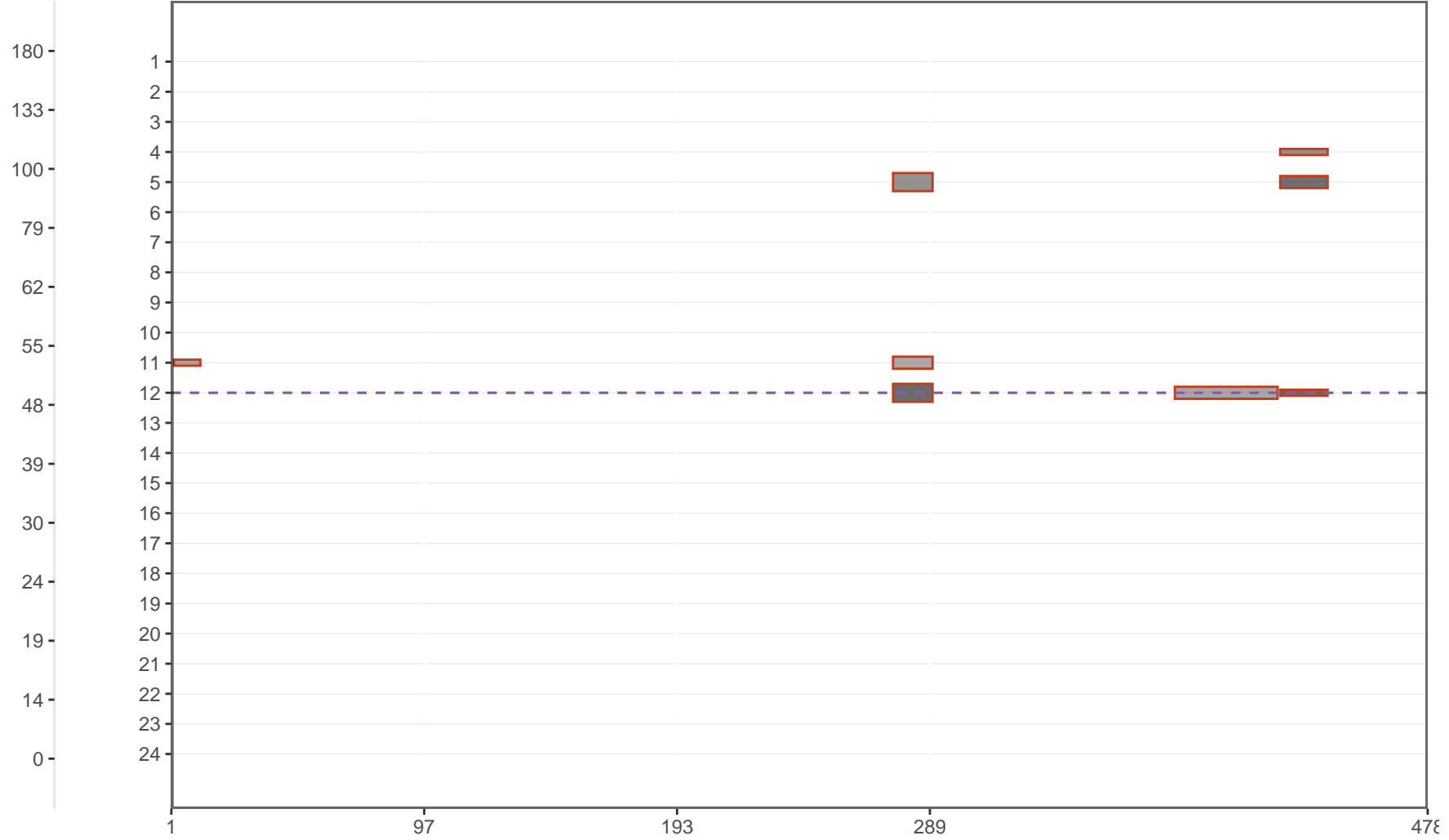


MW indication



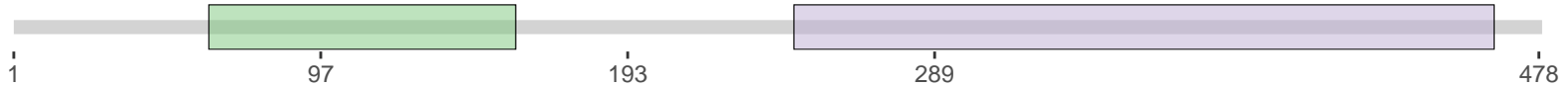
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

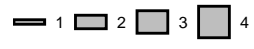
- SP
- Sequon
- TM Domain
- PF00156 Phosphoribosyl transferase domain
- PF00215 Orotidine 5'-phosphate decarboxylase / HUMPS family

Protein sequence:

KIAKPTGKLFELMVQKESNLGLSADVATAEELLDADKVPKICMLKTHVDILPDFAPDFGSKLSADKHNFLFEDRKFADIGNVTVMQVEGGIFRLEWDADITNAHIIISGPGVLDGLKGLSRGRLLLLAEMSGAGNLATGAYTAAVKIAEDHSDFFVIGFISVDPAWPNPGDAPSLIHATPGVQLVKGDDALGQHYNTPSAVIADRGSDIIVGRGIKAANPMEAREYRLOGDWDVLYNCK

NbL07g11020.1 beta-glucosidase_BoGH3B-like [MW = 26.94 kDa]

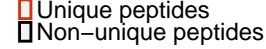
No. of times detected



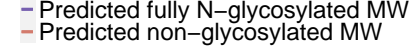
log(intensity)



Values from



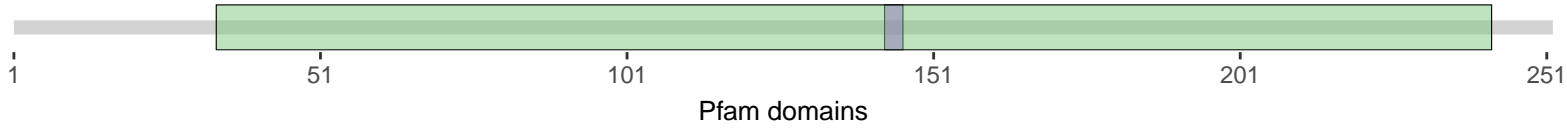
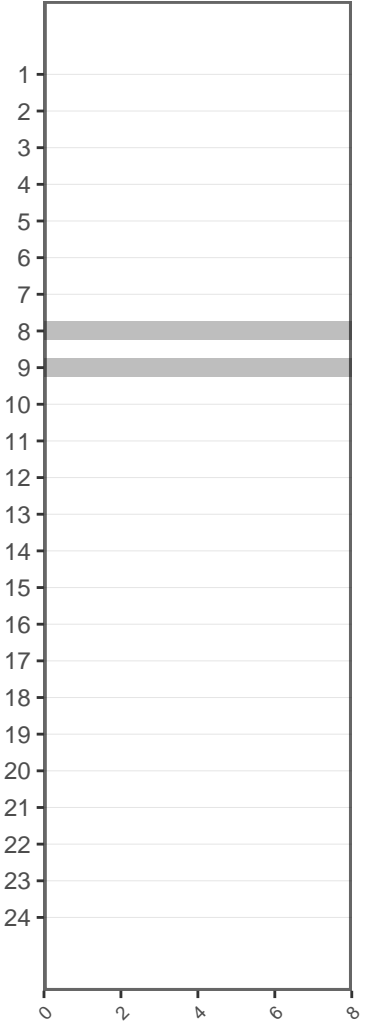
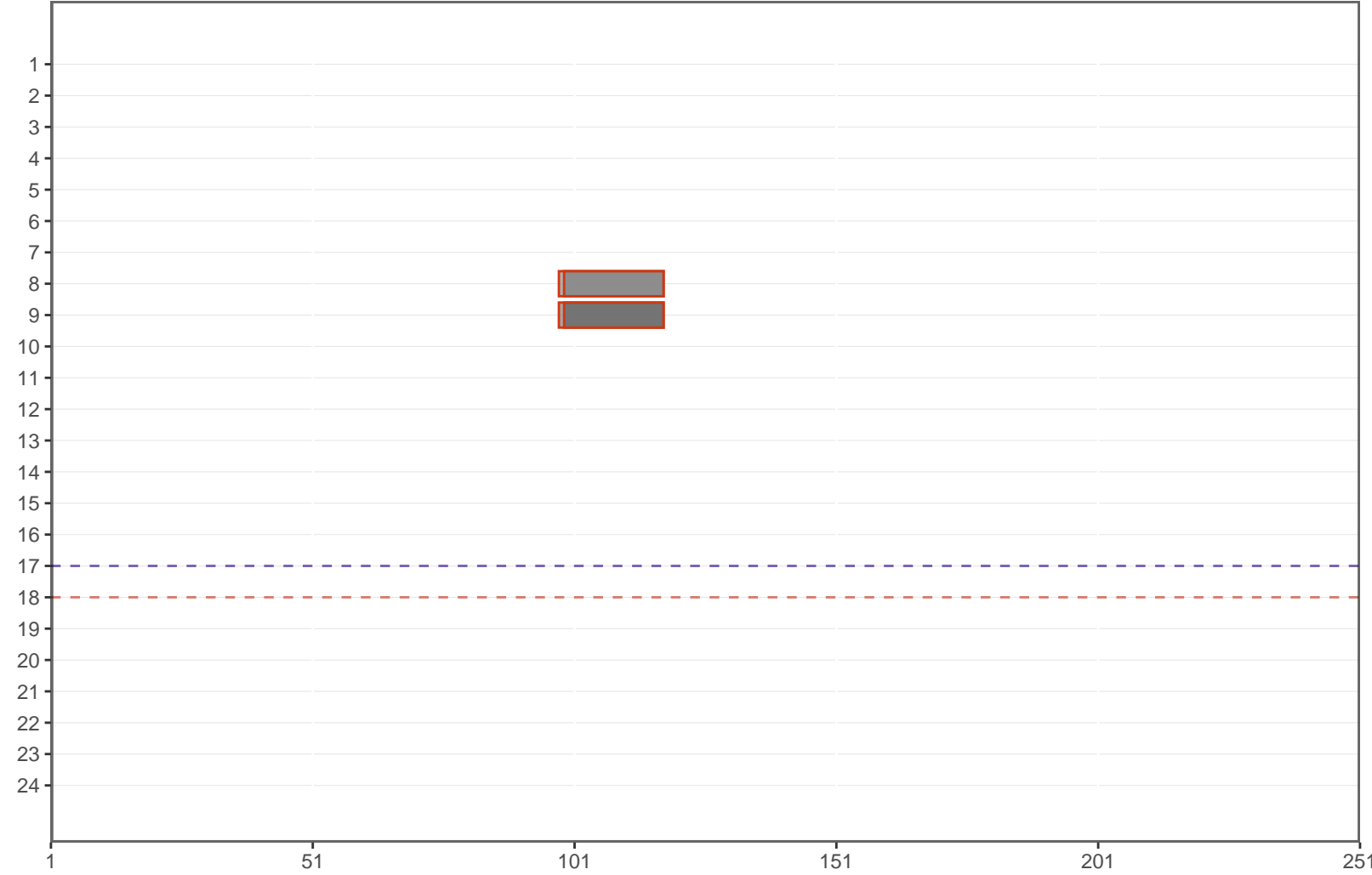
MW indication



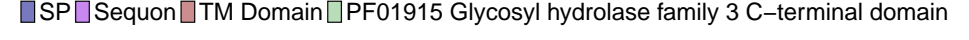
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

MDNFVSNKFSYAVVWVGEVPAEMFGDSENLTAEKRPETISHVGGAVKGVVVVSGRPRVLEPYVSKMDALVAWLPQTEGGVADALFGDYGFTGKGLARTWFKRVDGLPMGFDAHVDPLFFFGFTTRPKVGY

NbL07g10990.1 abscisic-aldehyde_oxidase-like [MW = 148.32 kDa]

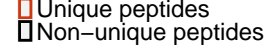
No. of times detected



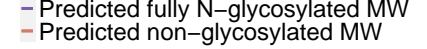
log(intensity)



Values from

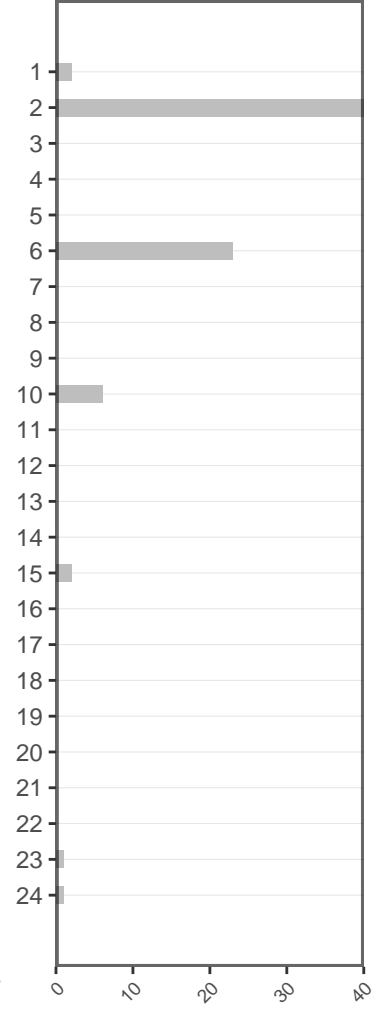
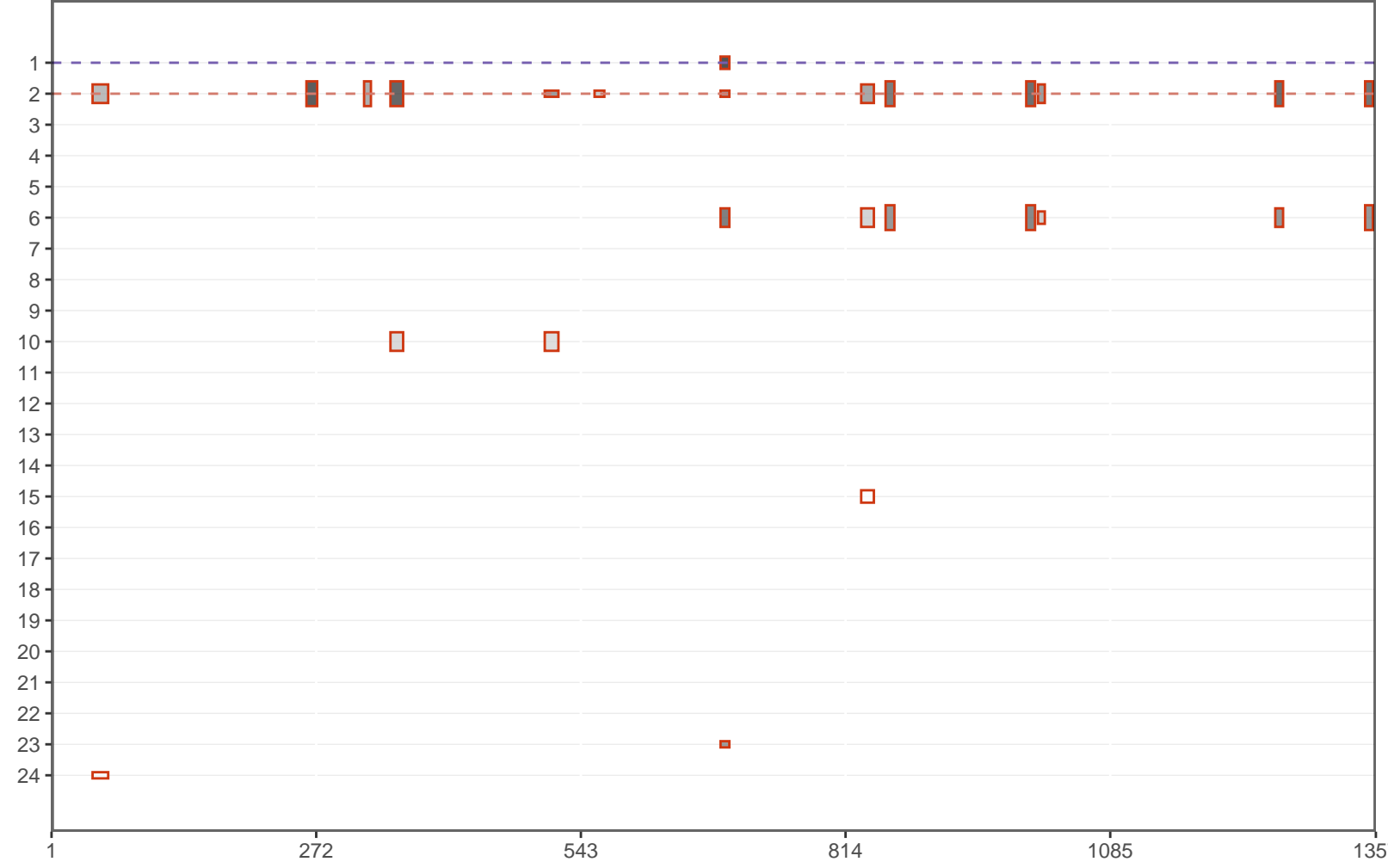
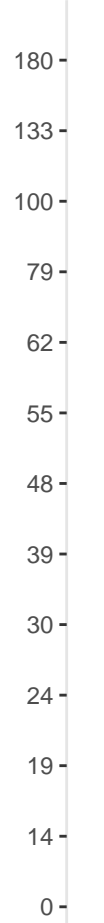


MW indication



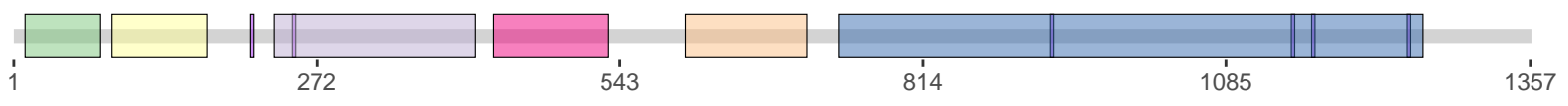
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



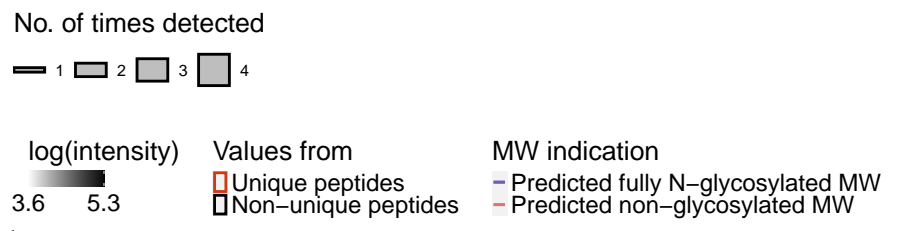
Pfam domains

- PF00941 FAD binding domain in molybdopterin dehydrogenase
- PF01799 [2Fe-2S] binding domain
- PF03450 CO dehydrogenase
- PF01315 Aldehyde oxidase and xanthine dehydrogenase, a/b hammerhead domain
- PF02738 Molybdopterin-binding domain of aldehyde dehydrogenase

Protein sequence:

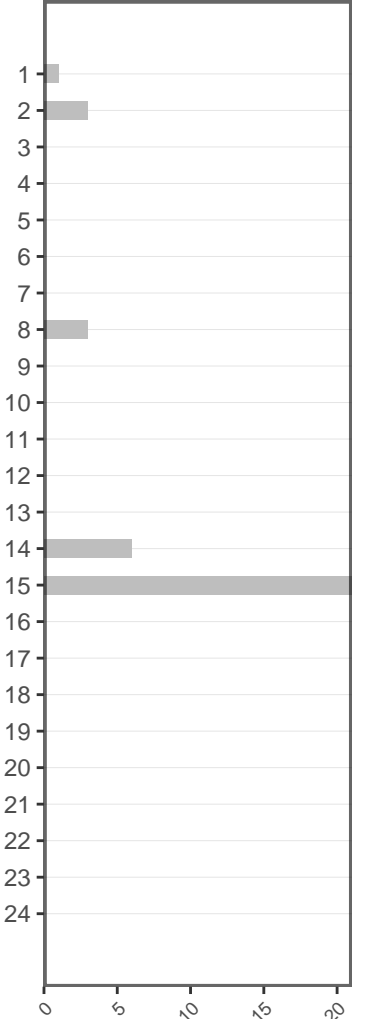
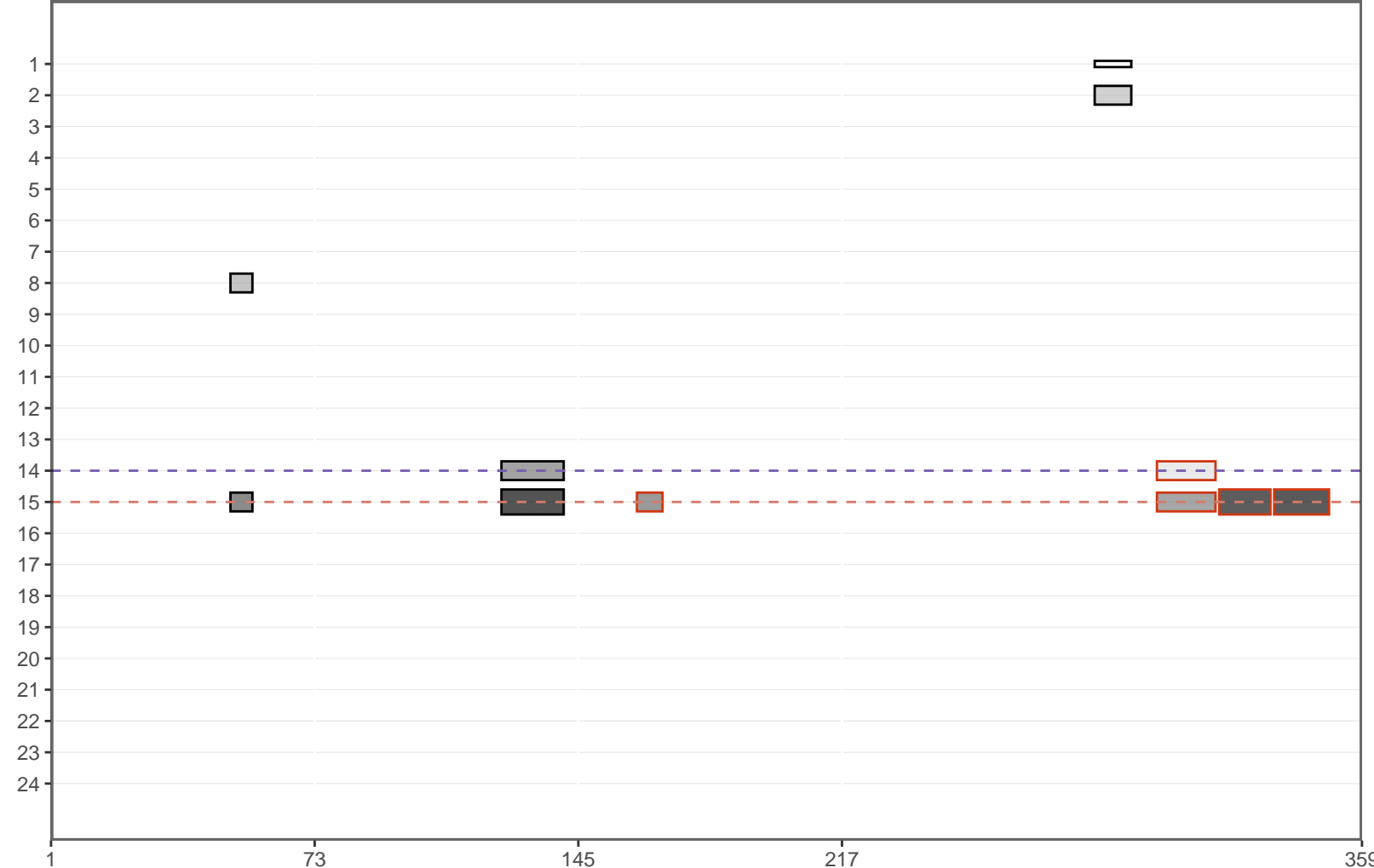
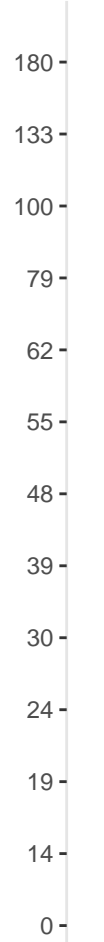
SITMFGPEPLFADDLVRCAGDRIAVAWDTQRGADVAATAALVEYDFTVNNNSPLTVEAEIKSSFFHPPFLYFKGVGDFEKGMAEADHKLSAEVRLGSAVYFYMETGATLAPDEDNGMVAVYTSGGQPEYAGNVAASCLGVPHNIRVITRRVGGFGGKAVRAMPVSTAGALAAKLRPRVIRVYRNNSDMMTGGRRHPMKVFTYVSVFKSGGKITALHLDILINAGISEDSPLLPSNVKAKKYDVGALSFDLKVQKTNLTKBAMRAPGEVGGVYAEIIEHVAISLLSKEVC

NbL07g10910.1 3-methyl-2-oxobutanoate_hydroxymethyltransferase_1_mitochondrial-like [MW = 37.84 kDa]

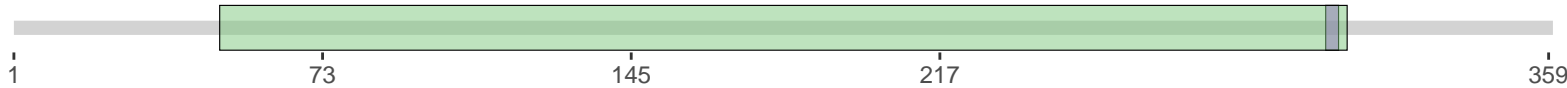


Molecular weight

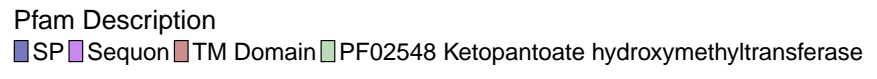
Gel Slice



Protein length



Pfam domains



Protein sequence:

PSRITAAKAVIAGIAVGHVHGLTPQASVILGGFRPQGRNVDIAKVVETAMALGEVGFSSVLEQVPPVAAATSAALGPTIGAGPFGSSGVLYHDLGMMQHPHAKVTPKFKGFGVGVGVNKAALVGVKVEVTNGSFPBSAHSPPYKIGAAADMGDFSELKLGFSDAASAAAAAAKIKGTANSPV

NbL07g10830.1 60S_ribosomal_protein_L30-like [MW = 12.43 kDa]

No. of times detected



log(intensity)



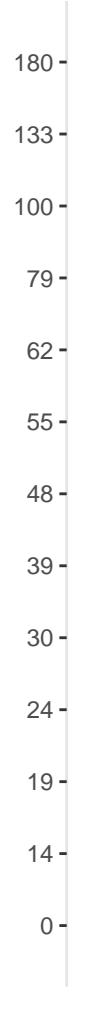
Values from



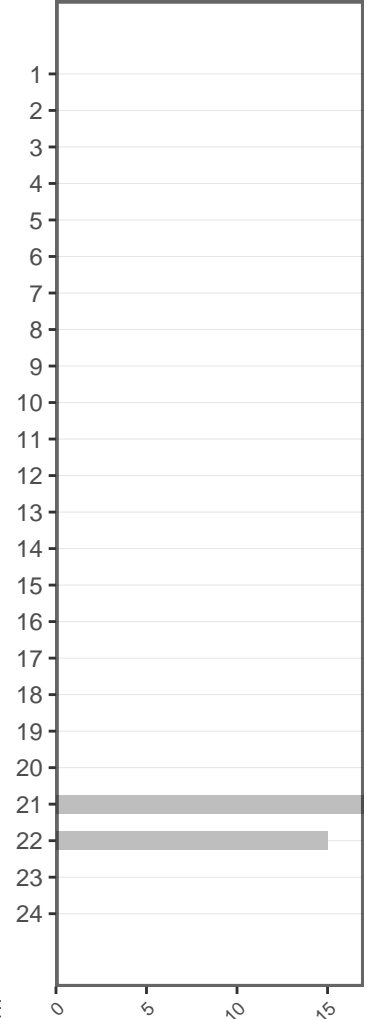
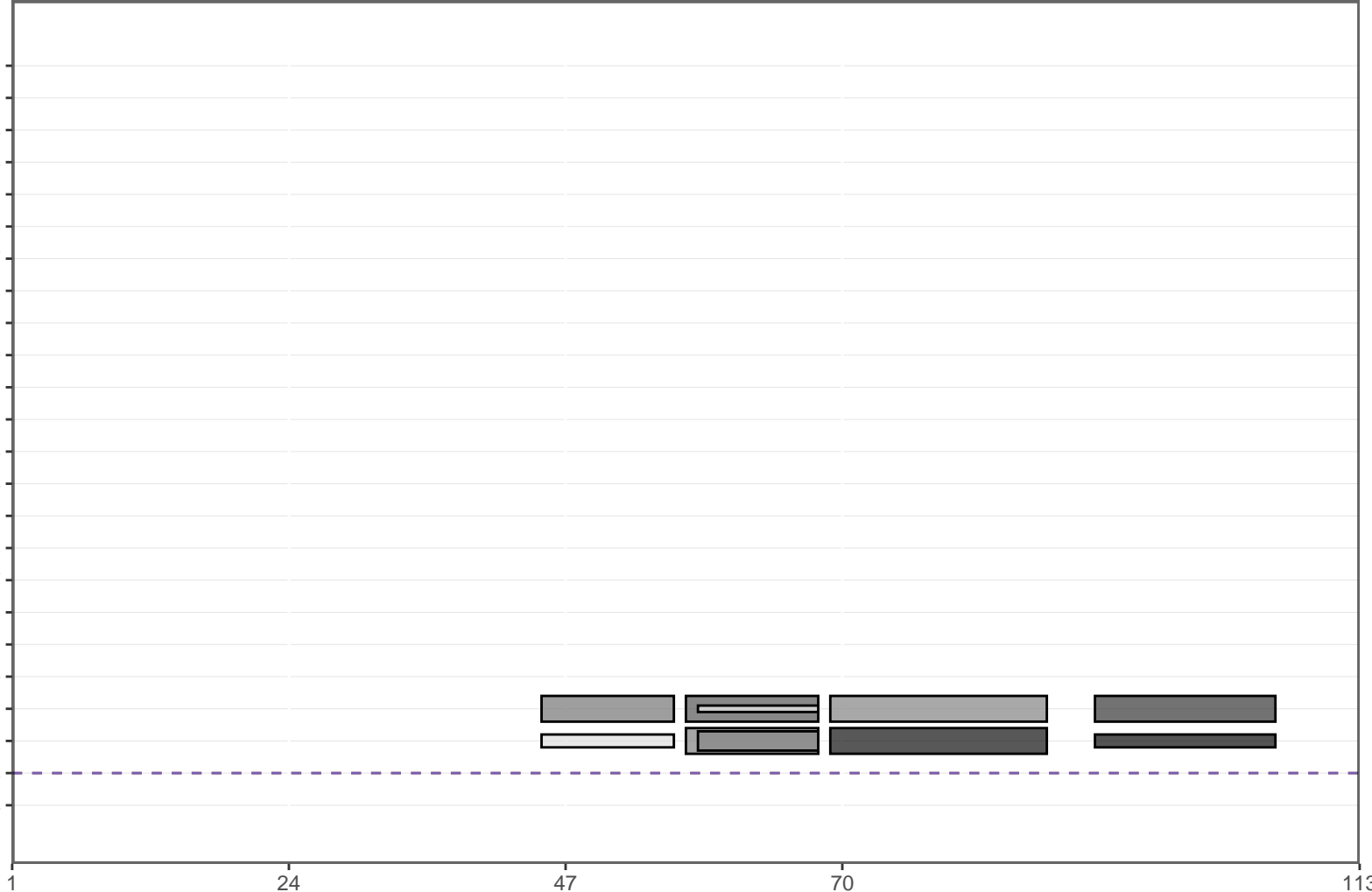
MW indication



Molecular weight



Gel Slice

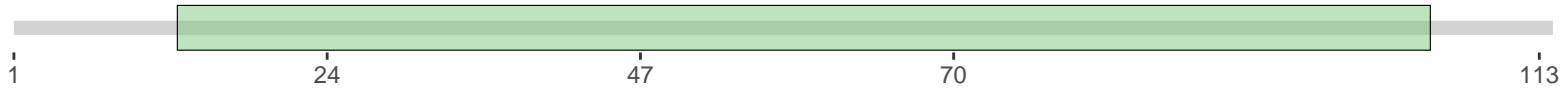


Protein length

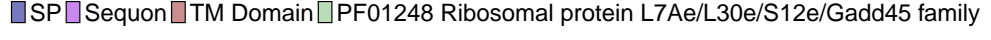


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

GKLIISANNCPPLRKSEEFYAMLAKVGVHHYNGNINVDLGTAGGKYFRVCGLSHPDGDSDIHKSPDQK*

NbL07g10810.1 agmatine_coumaroyltransferase-2-like [MW = 23.01 kDa]

No. of times detected



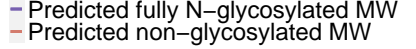
log(intensity)



Values from



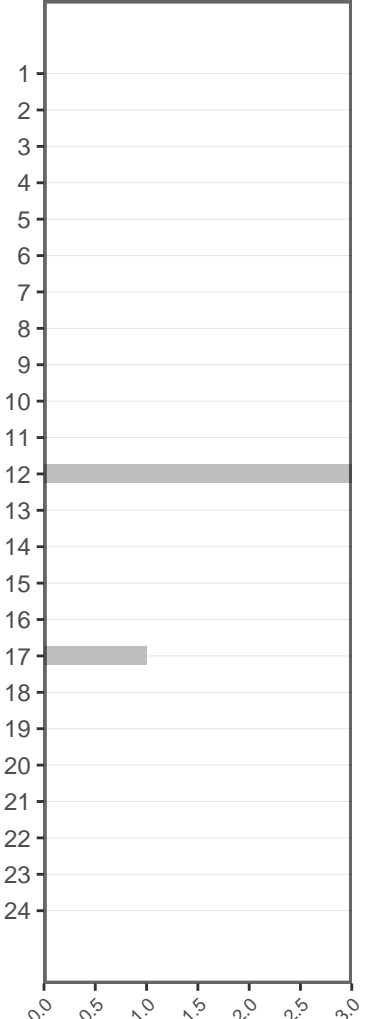
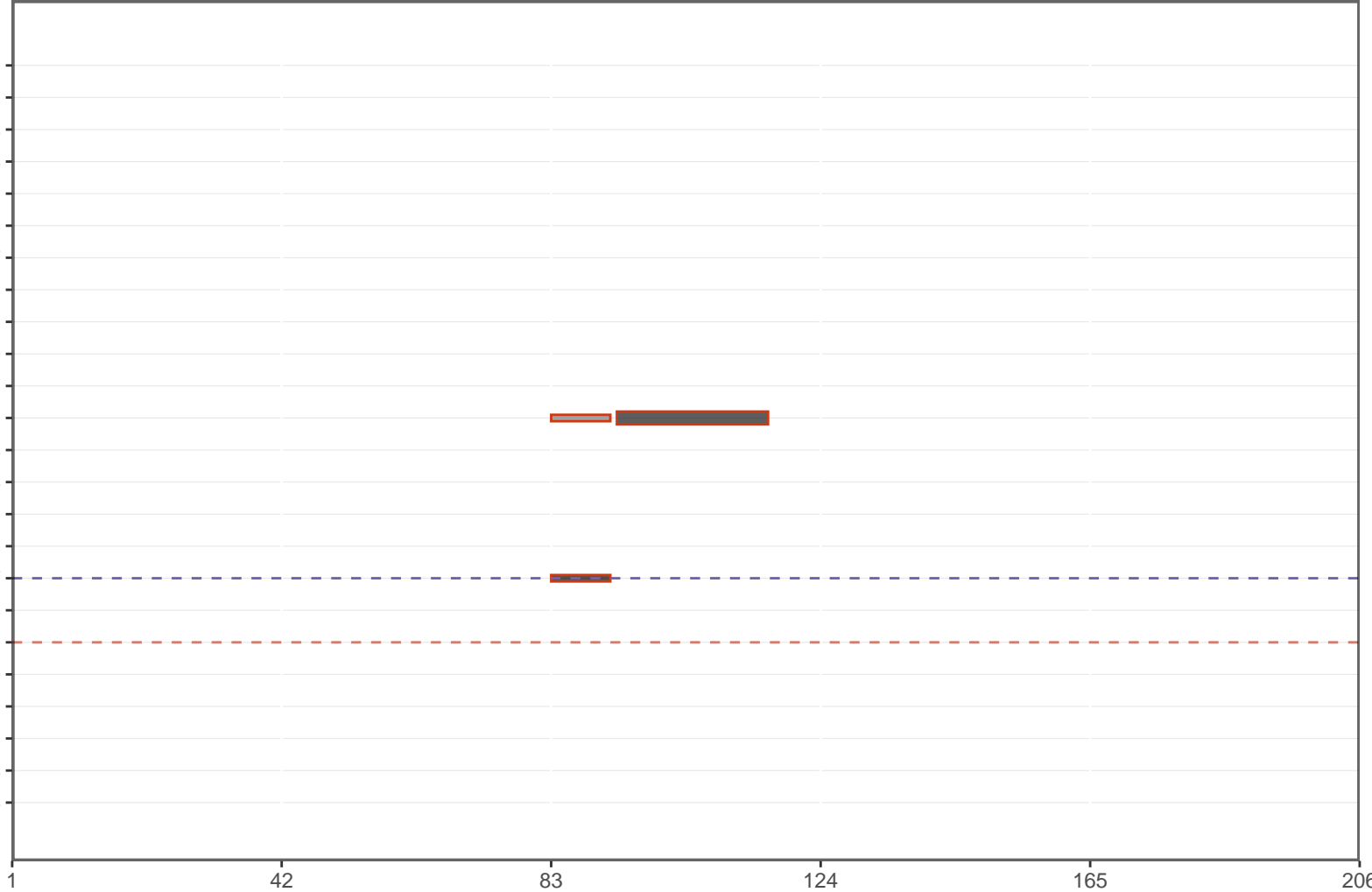
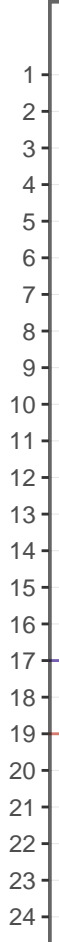
MW indication



Molecular weight

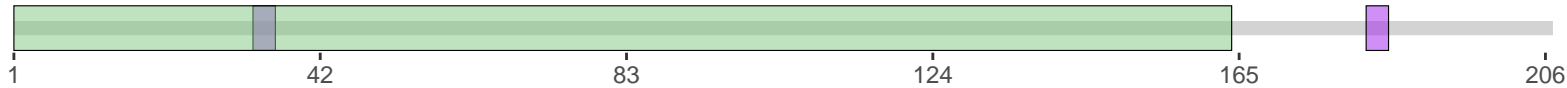


Gel Slice



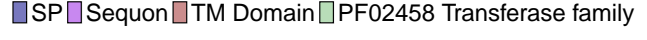
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

/RFIEASVDATLDELVLPKPSPLLKLHPSMKDVELIQQVQVTRFTGSGVWVFTGHHMADGHAASNFQYRLVFKATRNNKPVRRRDTNRTSGGTSNAVDFDELKFGNEITL

NbL07g10780.1 homoserine_dehydrogenase [MW = 44.38 kDa]

No. of times detected



log(intensity)



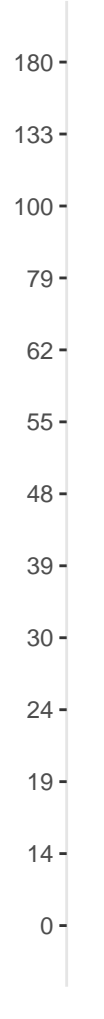
Values from



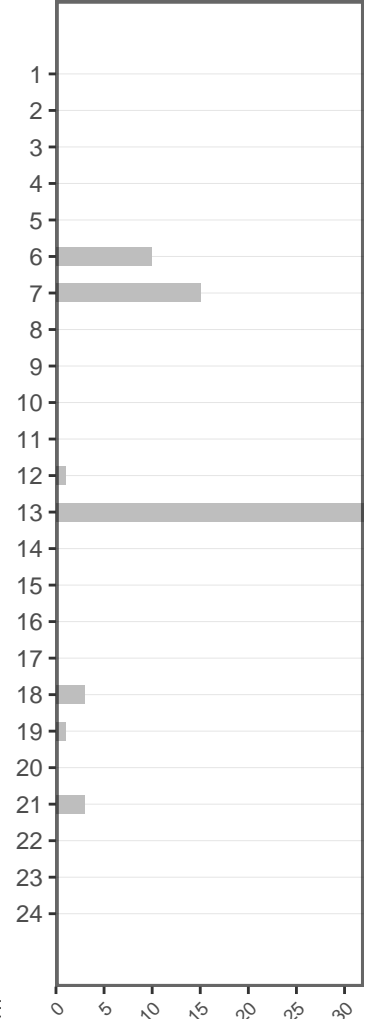
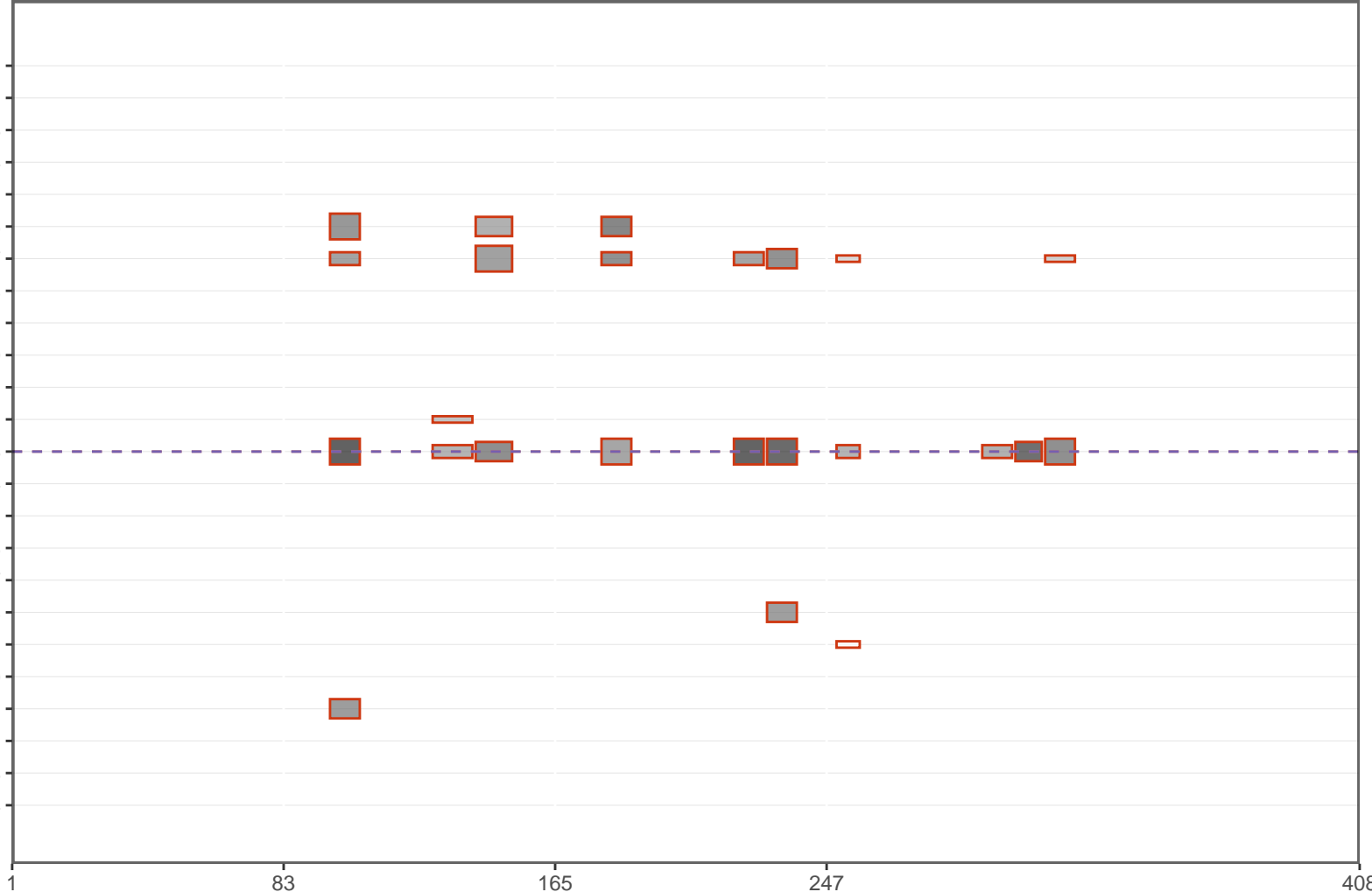
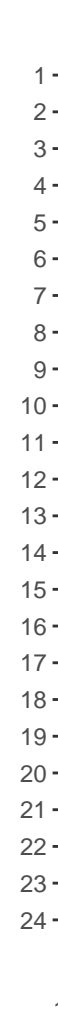
MW indication



Molecular weight

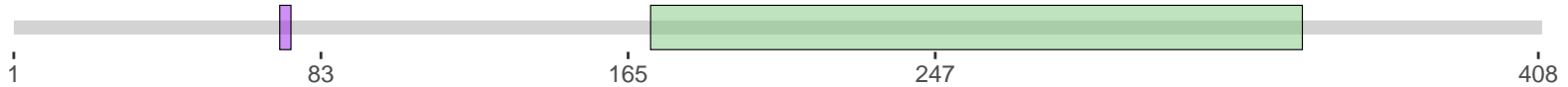


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LSLSGLGYVMSEVEDGKPFSGVSAAKSLGFTPEPRDDLGGMDVARKALILARLLGRHNLDDMKIEGLVPEEMGPDVMPLEDFLANGPLLDKNEIDRIKQASANGNLYRYVGLDDTRCEVIGEVPKDGLRLRAGSDNVVTWVSGHAESLFEQLLISVLRKPKFVITHLLSPCKTGLSLRWRYTAVVTRNRRWLSKVLGEMIPROLVS

NbL07g10690.1 feruloyl_CoA_ortho-hydroxylase_2-like [MW = 40.28 kDa]

No. of times detected



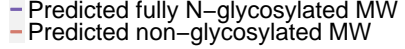
log(intensity)



Values from



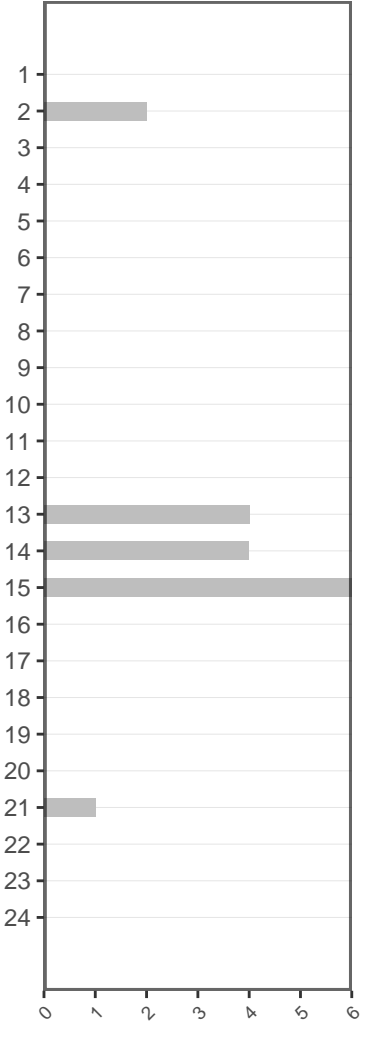
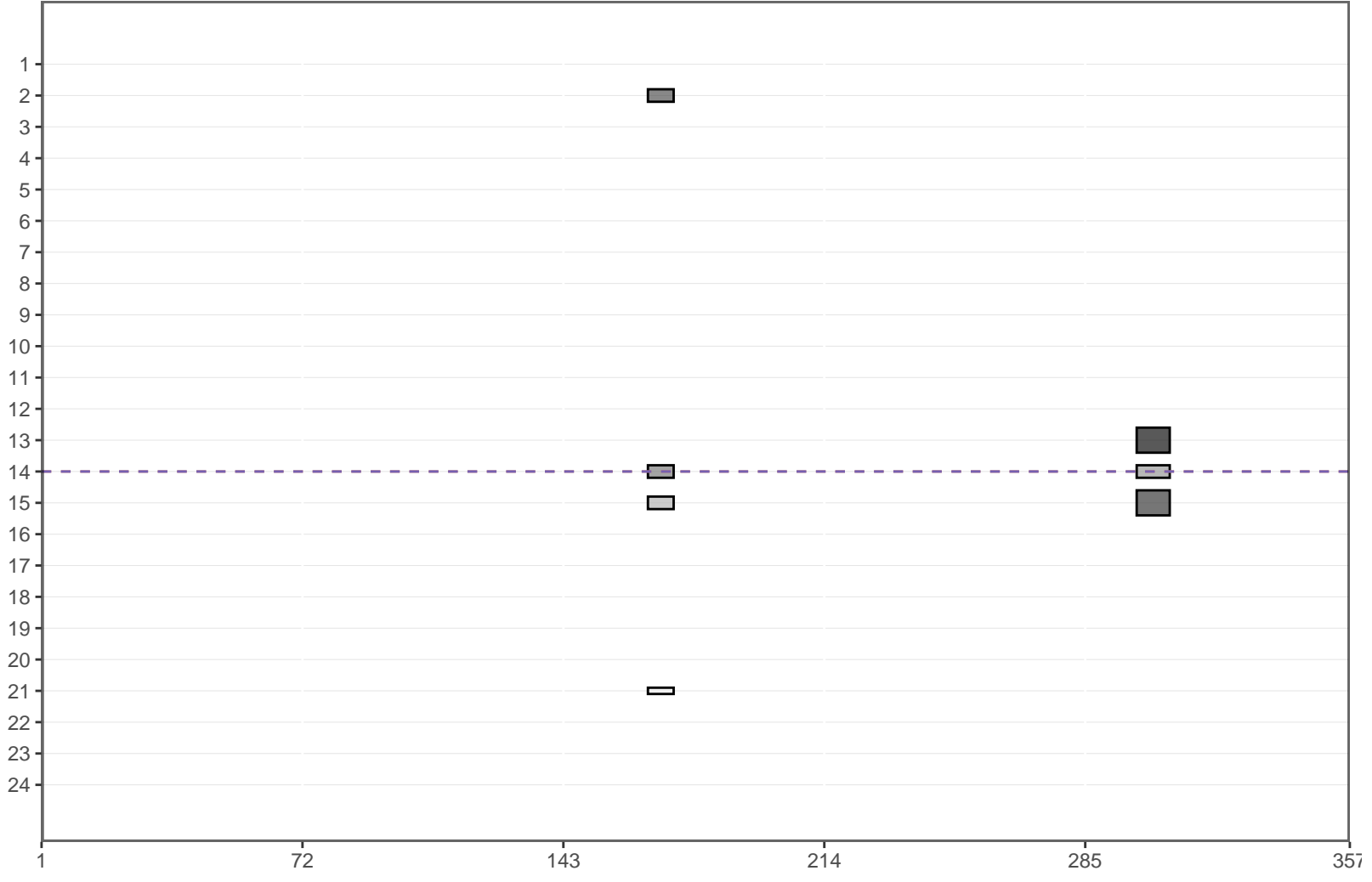
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF03171 2OG-Fe(II) oxygenase superfamily
- PF14226 non-haem dioxygenase in morphine synthesis N-terminal

Protein sequence:

RDQVLEYQKVAFLAKLLEIKLGLNVENIDSLKFLMLGTFMANNMYYGCPNPSLTIGRRHGDVSGITLLGDDTGLFLVROGTHDNNWVHTVPKGALAVNGDGLGMNDRYKVEHGAAVDSKARISPFVNRPLDTVIGFPFQVLENGEKPVYKVKVLFSDYWEYFFKRPSPGKASLDFAKI

NbL07g10600.1 elongation_factor_1-beta-like [MW = 24.81 kDa]

No. of times detected



log(intensity)



Values from



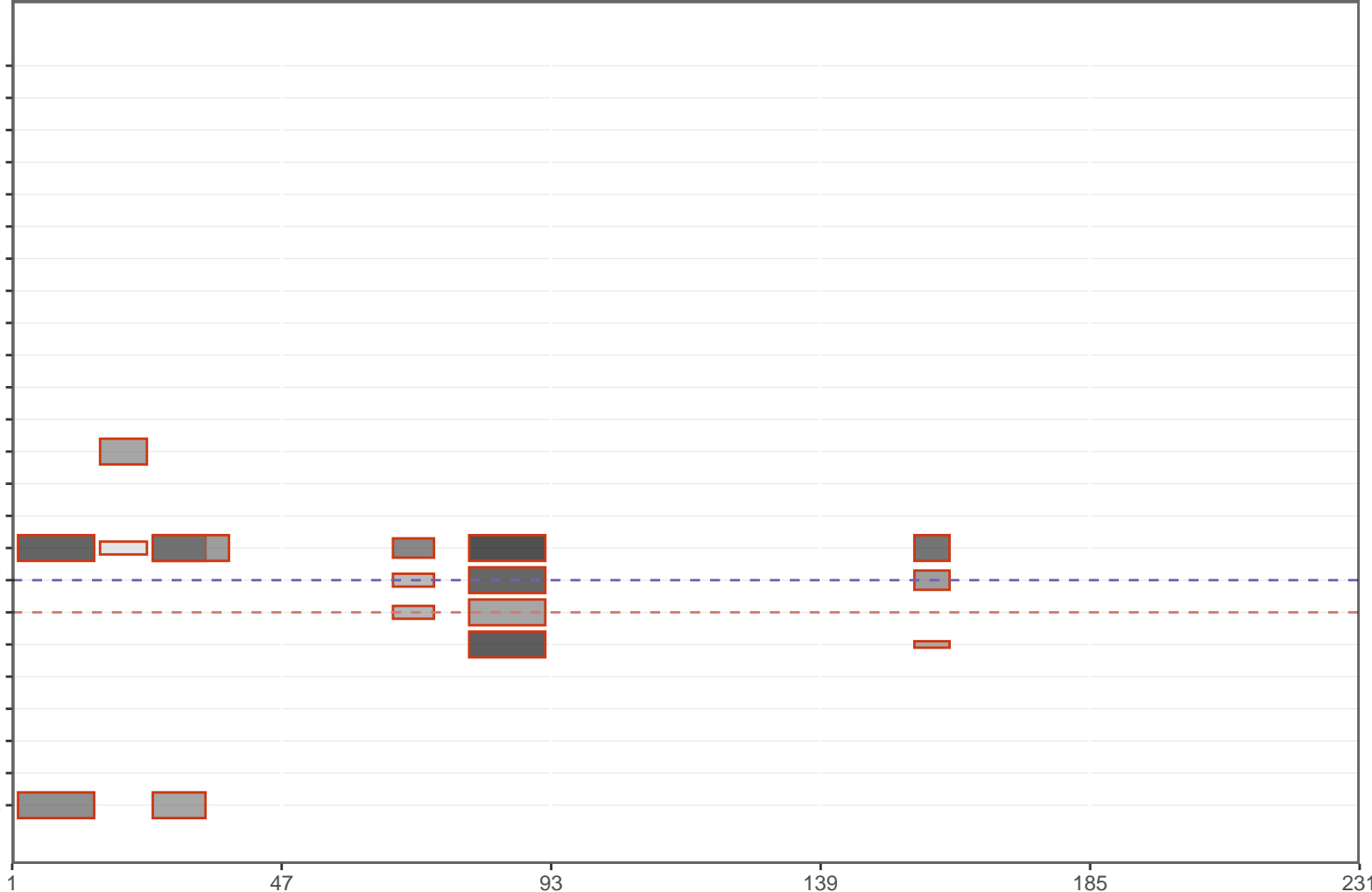
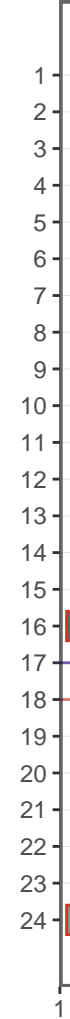
MW indication



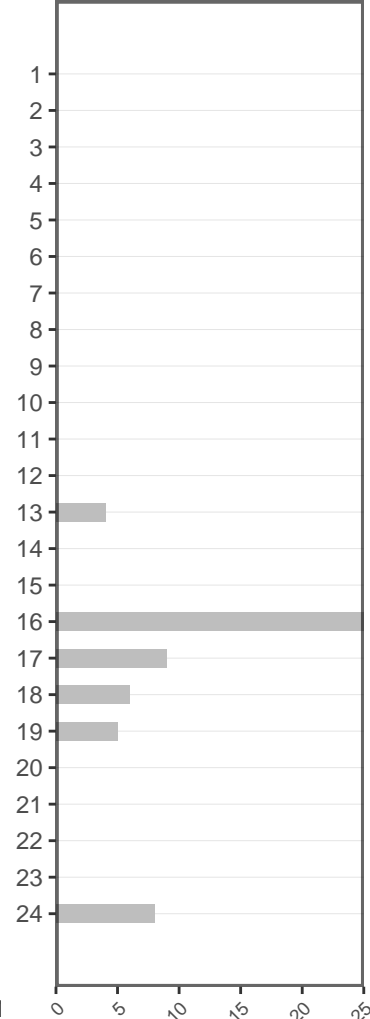
Molecular weight



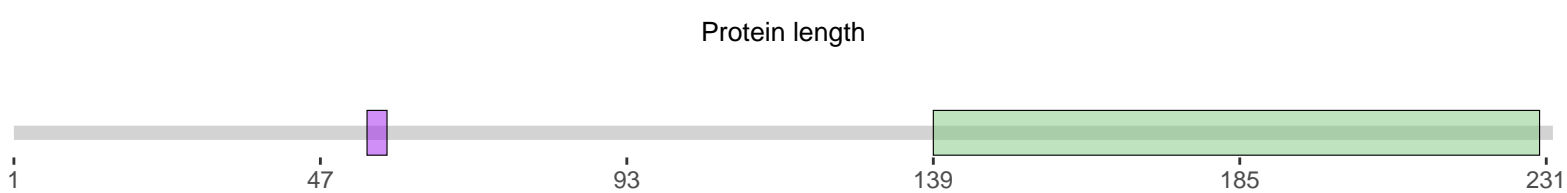
Gel Slice



Protein length

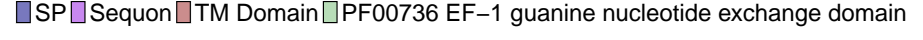


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DDDDDDLLFGEETEEENKAAEAREATKASTKKKGGKSSLLVNPVDDDETDMKLLLEAVRSVQGEGLTWGAFSLTAKLVFVGVGKIKLGMILTIQDOLVSDVTLVEEKLTVEPINEVYVQSCDVAFAKQ

NbL07g10590.1 calmodulin-7-like [MW = 20.77 kDa]

No. of times detected



log(intensity)



Values from



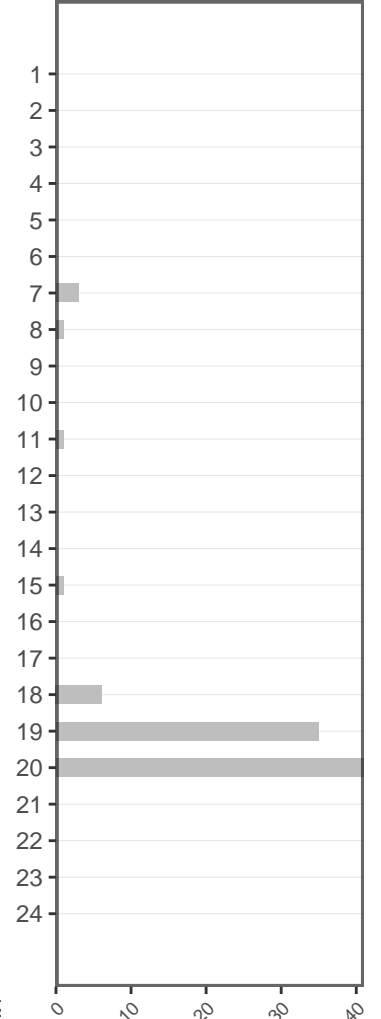
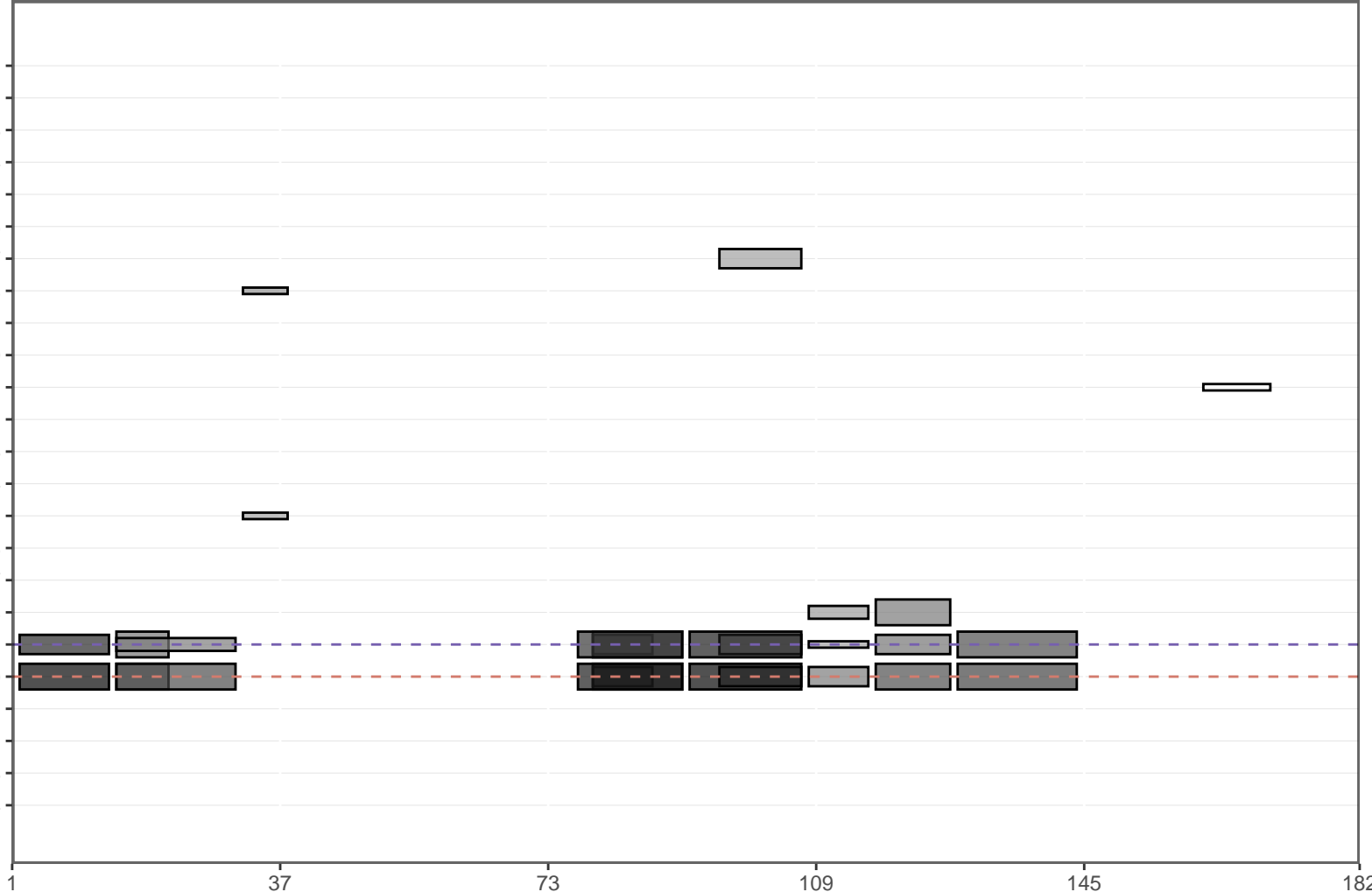
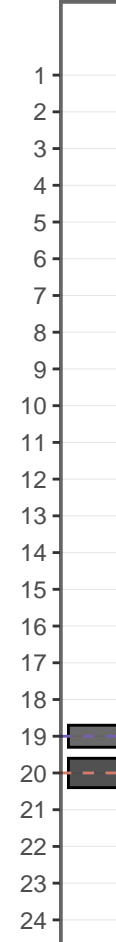
MW indication



Molecular weight

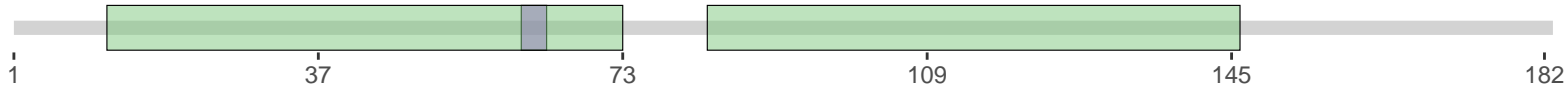


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

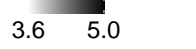
DTDSSEELKELAFRVFDKQNGFSAELRHVMTNLGKLTDEEVDDEMREADVDDGGQNYEEFVWVMANRRRRRIEESKRGYSHGSGNKRKRDRGRTLL

NbL07g10570.1 probable_calcium-binding_protein_CML13 [MW = 16.48 kDa]

No. of times detected



log(intensity)



Values from



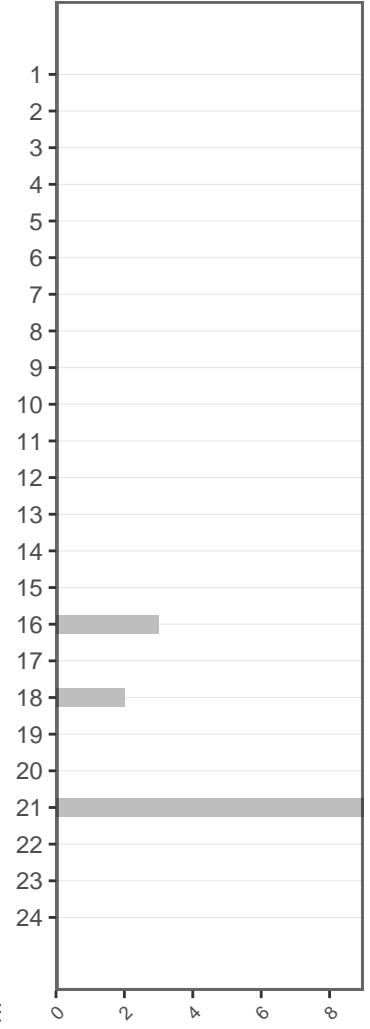
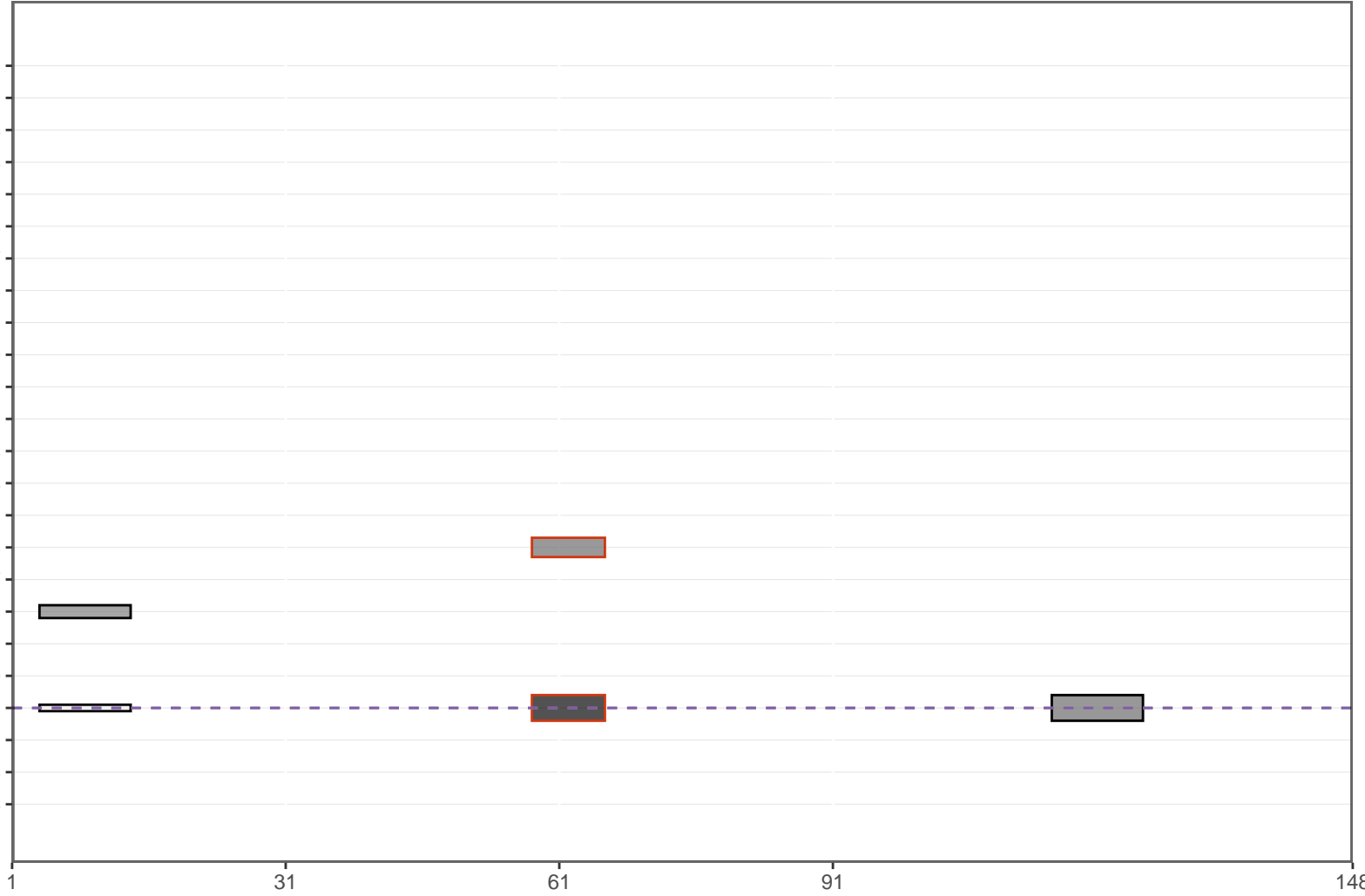
MW indication



Molecular weight



Gel Slice



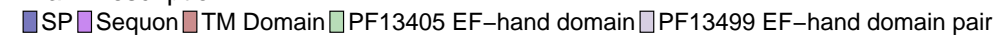
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

FDNRFLLMSKIKLPEPFDFRQLRGAFLKLDKDGTFVAVVSDLKHILTSIGKLEPFDFEWRREVVDSGDKIRYEDFIARMVAK

NbL07g10260.1 somatic_embryogenesis_receptor_kinase_2-like [MW - SP = 15.43 kDa]

No. of times detected



log(intensity)



Values from



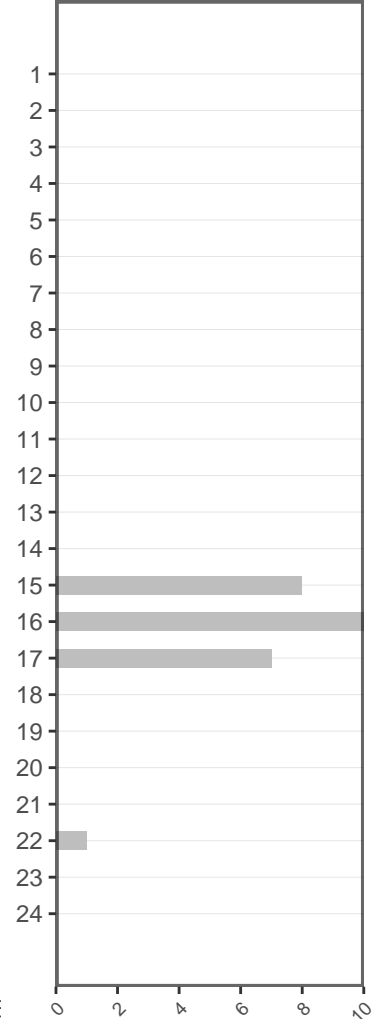
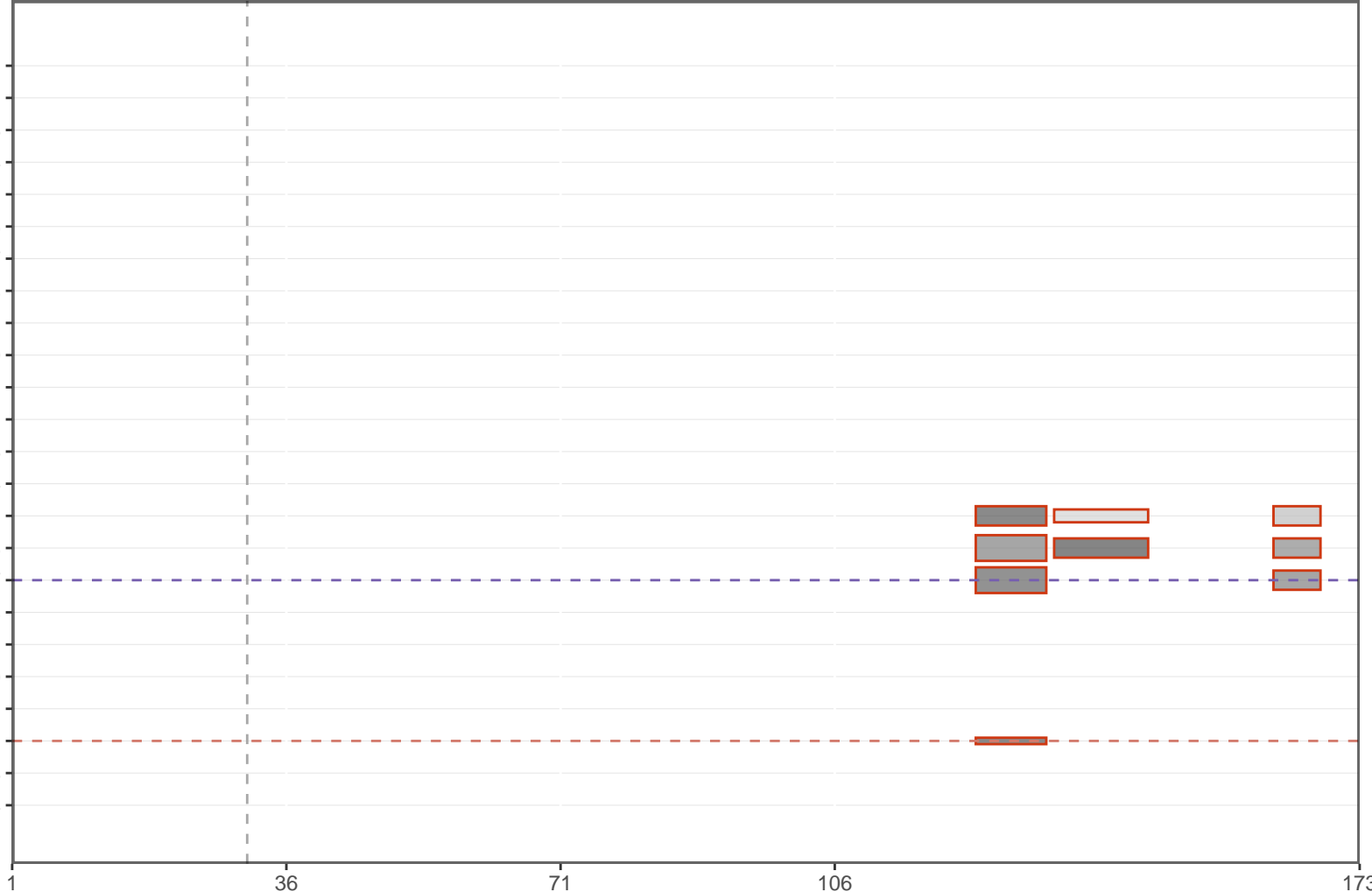
MW indication



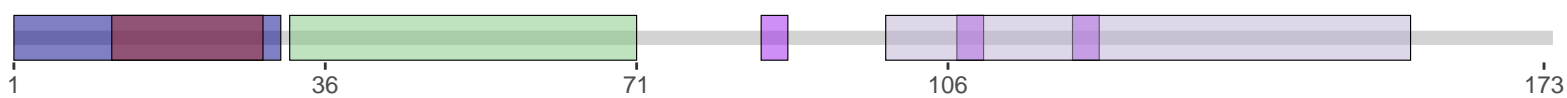
Molecular weight



Gel Slice

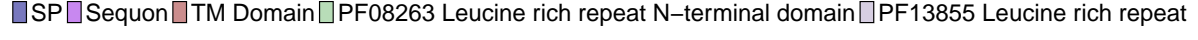


Protein length



Pfam domains

Pfam Description



Protein sequence:

NSVIRVLDLGAANLTGTLVPELGMLANLGHVGVENNFSGAIPFGLGNLTRLRLSLGLENNKLGSSPFLGKLNLSLRWMLRNLGNKLGKPIKIVLKLIVWG

NbL07g10160.1 photosynthetic_NDH_subunit_of_luminal_location_5_chloroplastic [MW = 27.38 kDa]

No. of times detected



log(intensity)



Values from



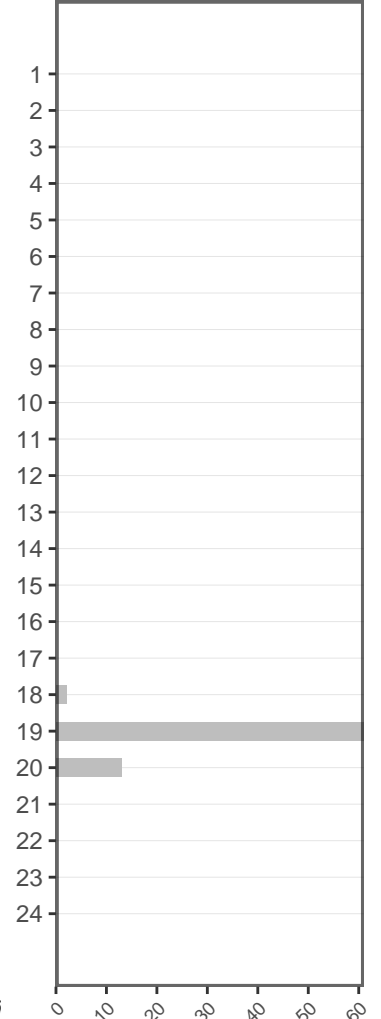
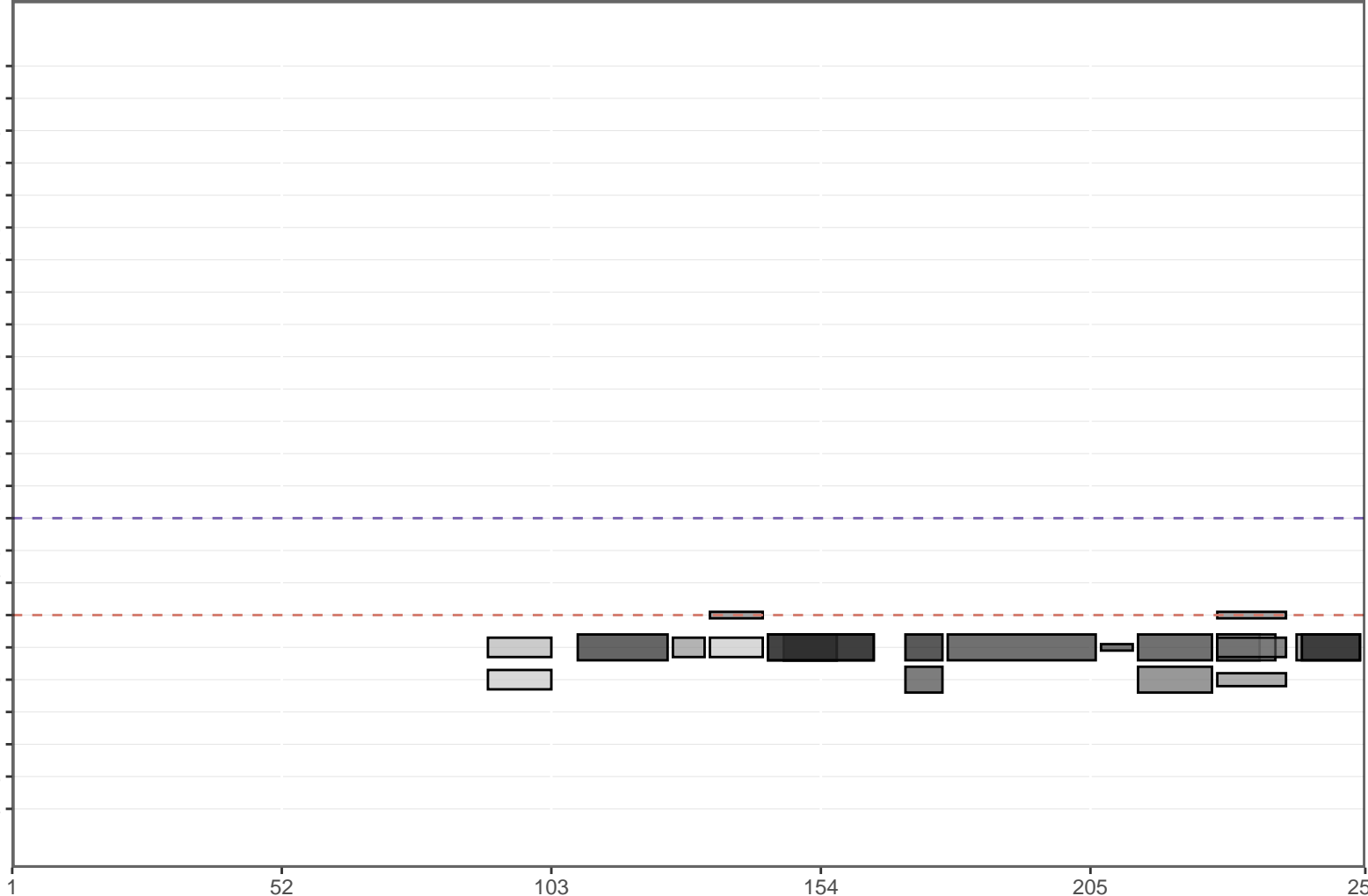
MW indication



Molecular weight



Gel Slice

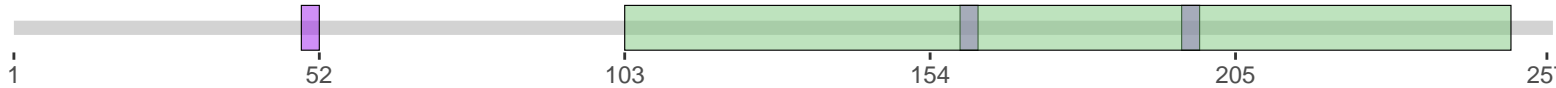


Peptide counts over 4 repeats

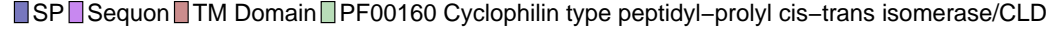
Protein length



Pfam domains



Pfam Description



Protein sequence:

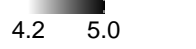
POTAENFRALCTGKGFYKDSAFHRVVKDFMIGGGDFDKGNGTGGKSYGRTRFKDENFKLTHFGPGVVSVMANAGPNTNGSFFICTVKTPLWDERHVVFGQVLEGMDVVKLEGGETDRGDRPRKRVVSDCCGELPVA

NbL07g10090.1 heat_shock_protein_90-1-like [MW = 94.64 kDa]

No. of times detected



log(intensity)



Values from



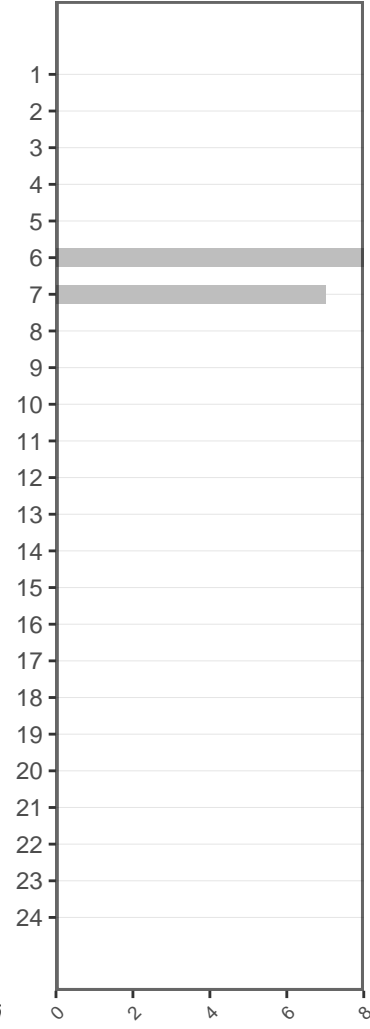
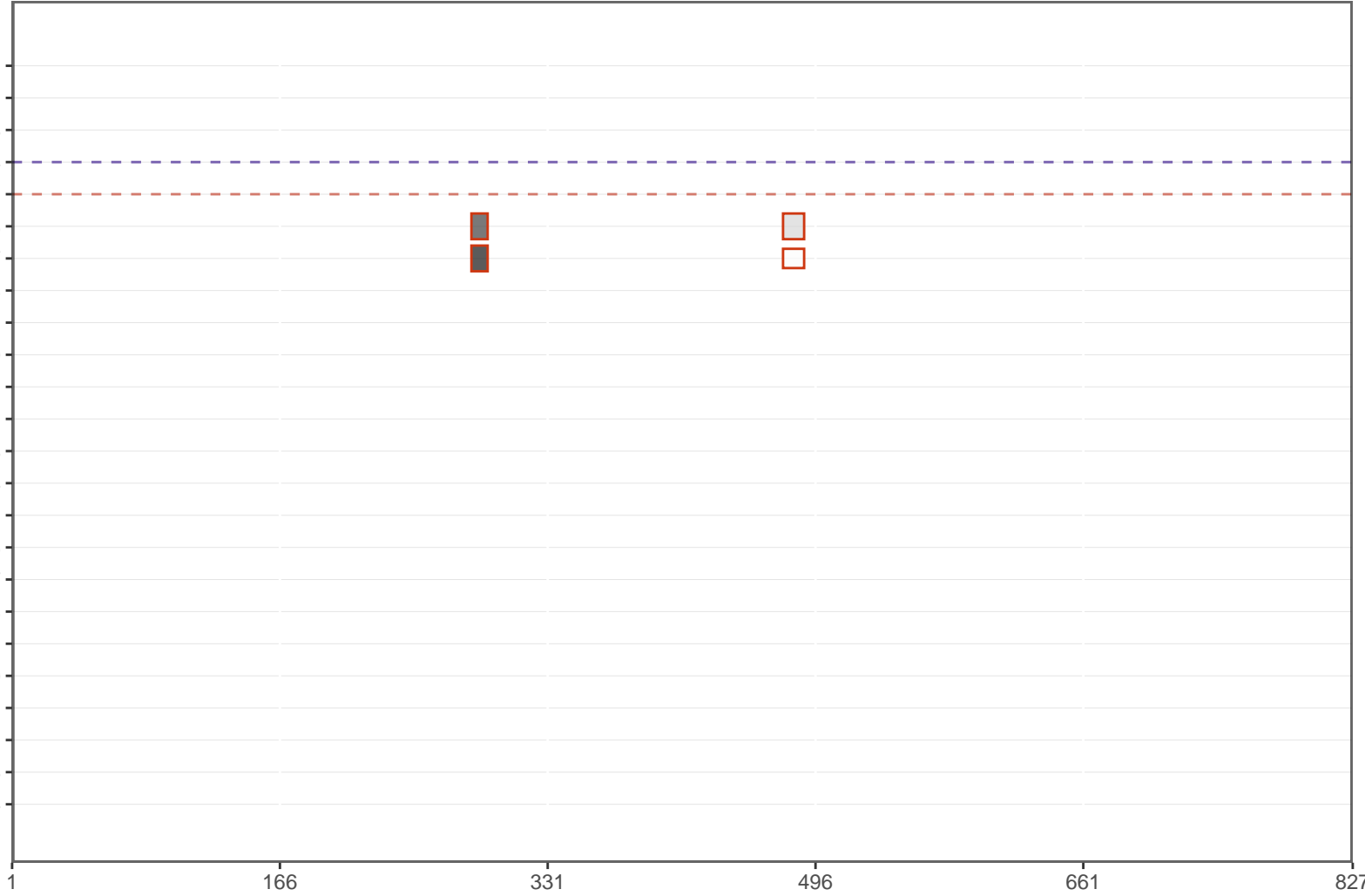
MW indication



Molecular weight

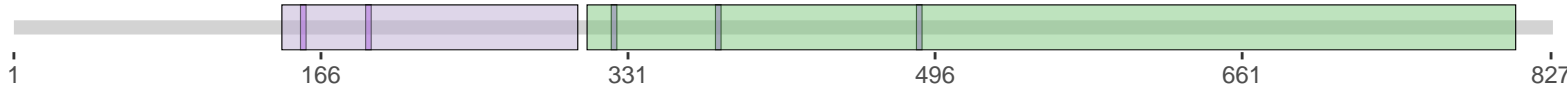


Gel Slice



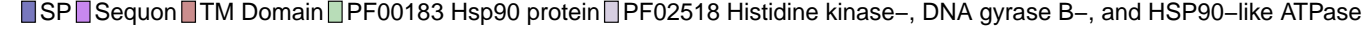
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YKKTSEFLDPLTYTHFTTEGEVEFRVLYIPGMFLNEDYTNPKTKNIRLYVWRVFSDDDFDGEFLFRVLSFVKGIVDNDLPLNVSREILQESRIVRMKRLVVKRTFDMQDLSEGENKEDYKFWENFGKFLKLGIEDTGNKRRITPLRFFFSKSEELSLDDVYENMGENKAVYVYATDLSGASAKTAPLEKLVQIGIEVLLVPEIDEVAIGNLQTYKFKVFDISKEDLELGDDEVEKERETKQEFNLLGDWIKQGLGEKAVKVVGNRLSSPCVLYVSGKFGVSAI

NbL07g09960.1 alpha-14-glucan-protein_synthase_[UDP-forming]_2-like [MW = 41.03 kDa]

No. of times detected



log(intensity)



Values from



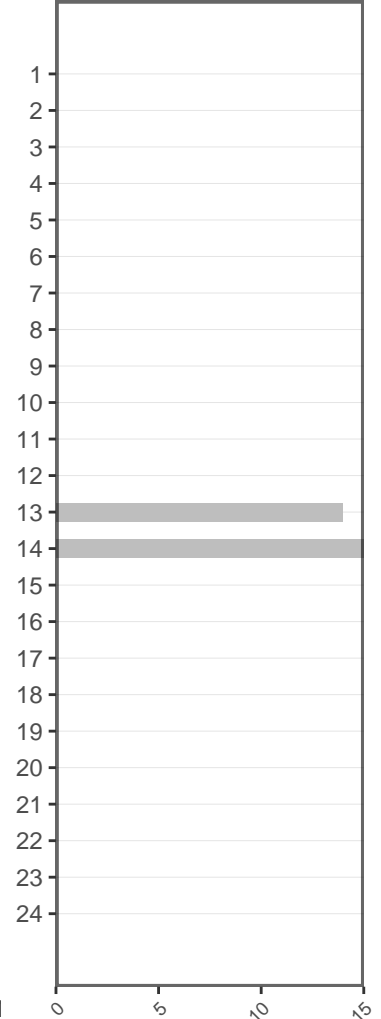
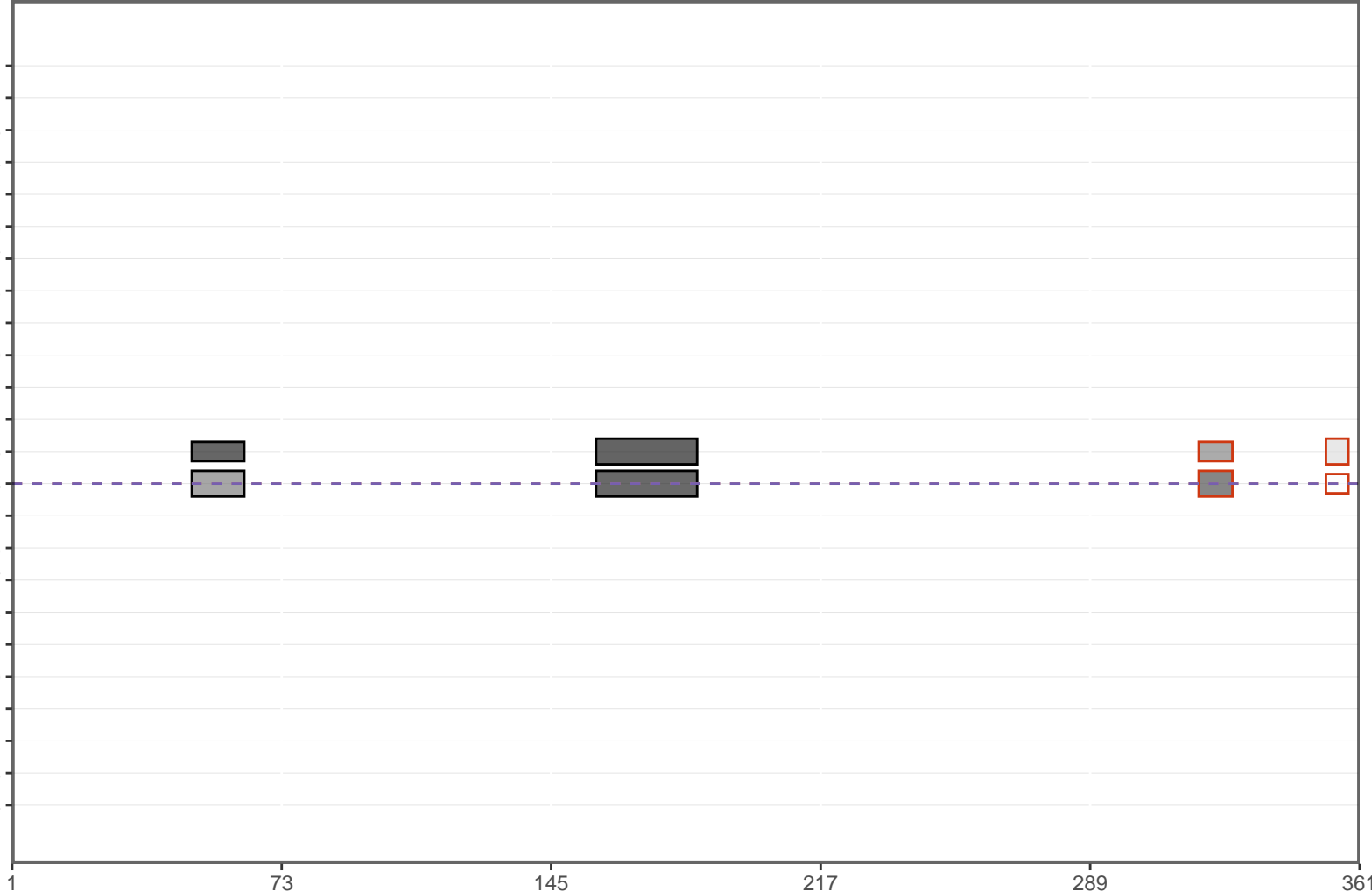
MW indication



Molecular weight

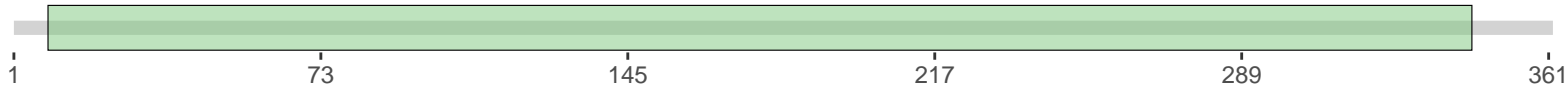


Gel Slice



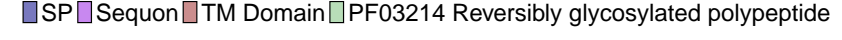
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

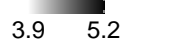
LNPDYDAFTQLYKFRRENTRYVDAWMTIRKGTLPFMGMNLAFLRELIGRAMYGLMDSGGPIGRYDDMWAGWCTKVICGHLGLGKGTGLPWIWHSKSNPFVNLKKEYKRYWDEEIFFFGAVTLPKECTTVGGCYHELAKGVKELSNIDPYFTKLAEAMATWIEAWDELNPTGENLAKLSISDQKAK

NbL07g09620.1 haloacid_dehalogenase-like_hydrolase_domain-containing_protein_3 [MW = 28.41 kDa]

No. of times detected



log(intensity)



Values from



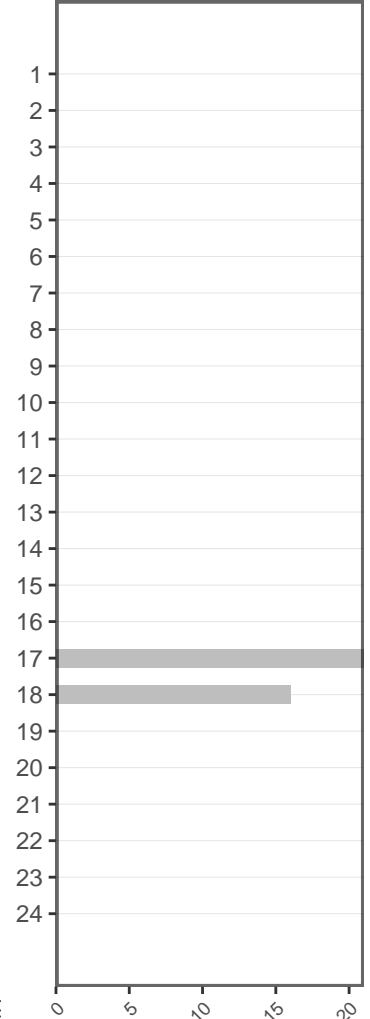
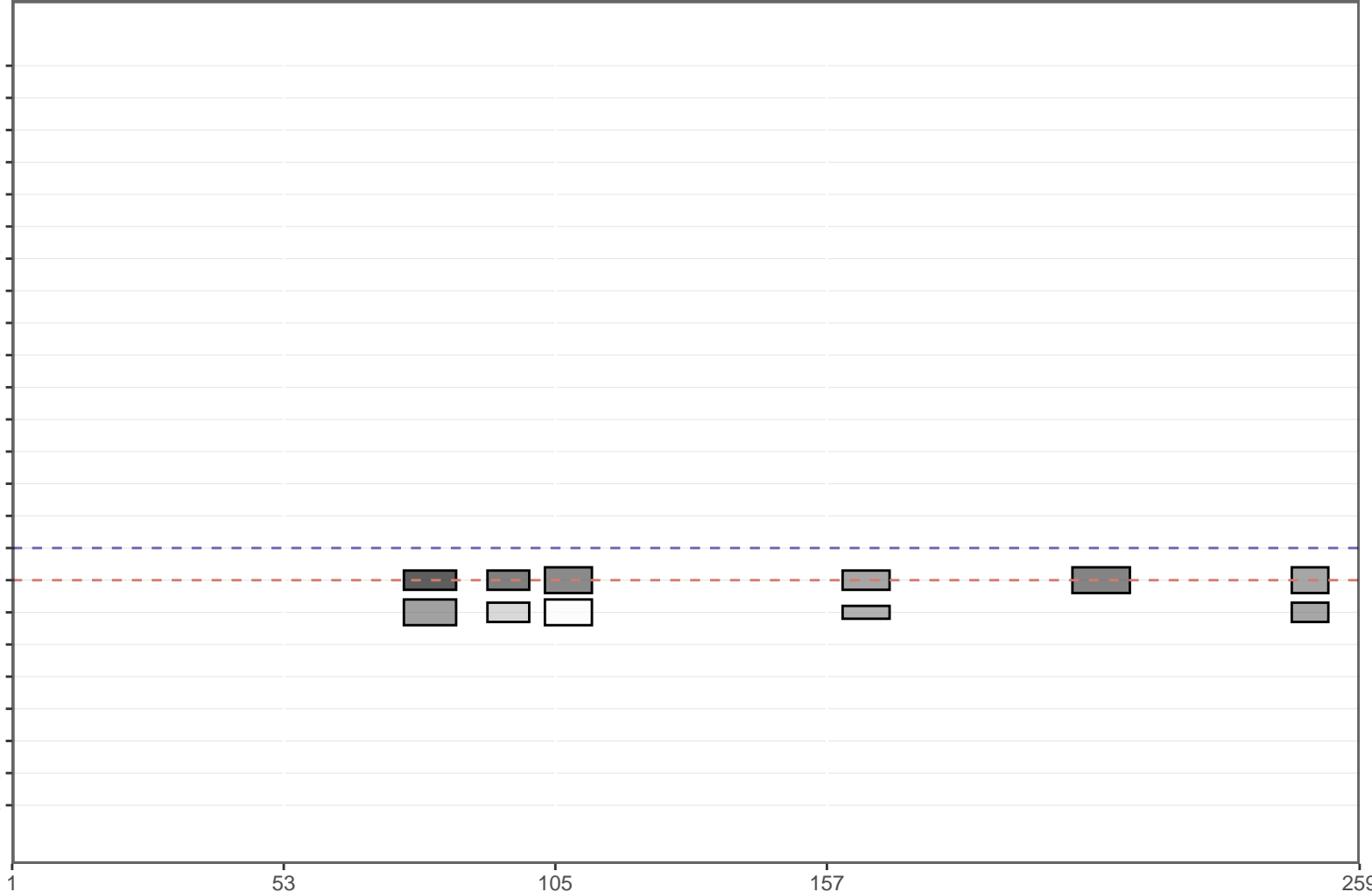
MW indication



Molecular weight

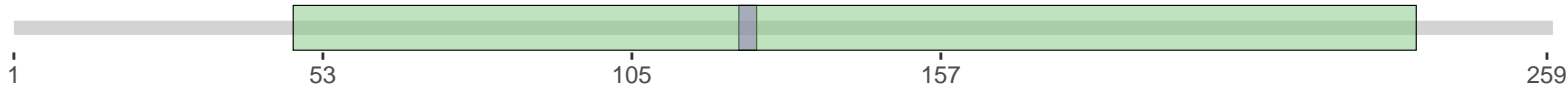


Gel Slice



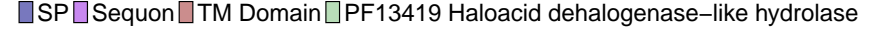
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VAEATGCSNNITYFEVYQGHASGGAWHLFGAYDTISLKHSGVNLAVSNFDFRLTRILKELKVLDFDAVISSEVGVYKPDIRFRALADGICVEAKTIVHVGDDKADKGGANAAGIDCVLWGVGVKSFADIGNRLLETA

NbL07g09410.1 26S_proteasome_non-ATPase_regulatory_subunit_7_homolog_A [MW = 34.95 kDa]

No. of times detected



log(intensity)



Values from



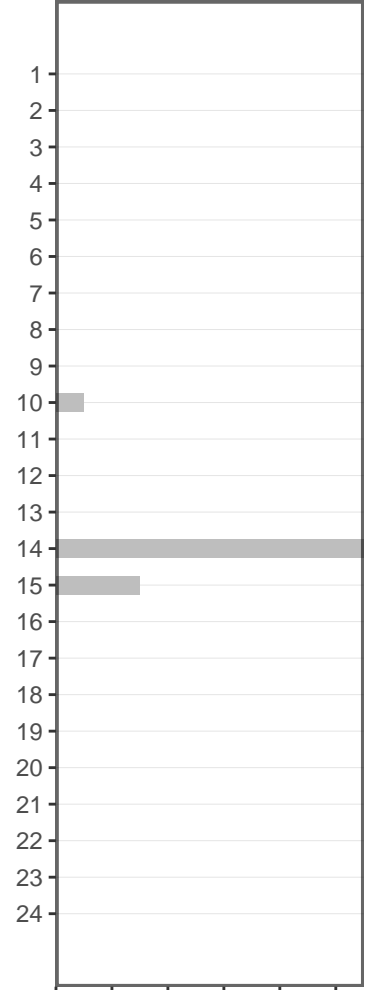
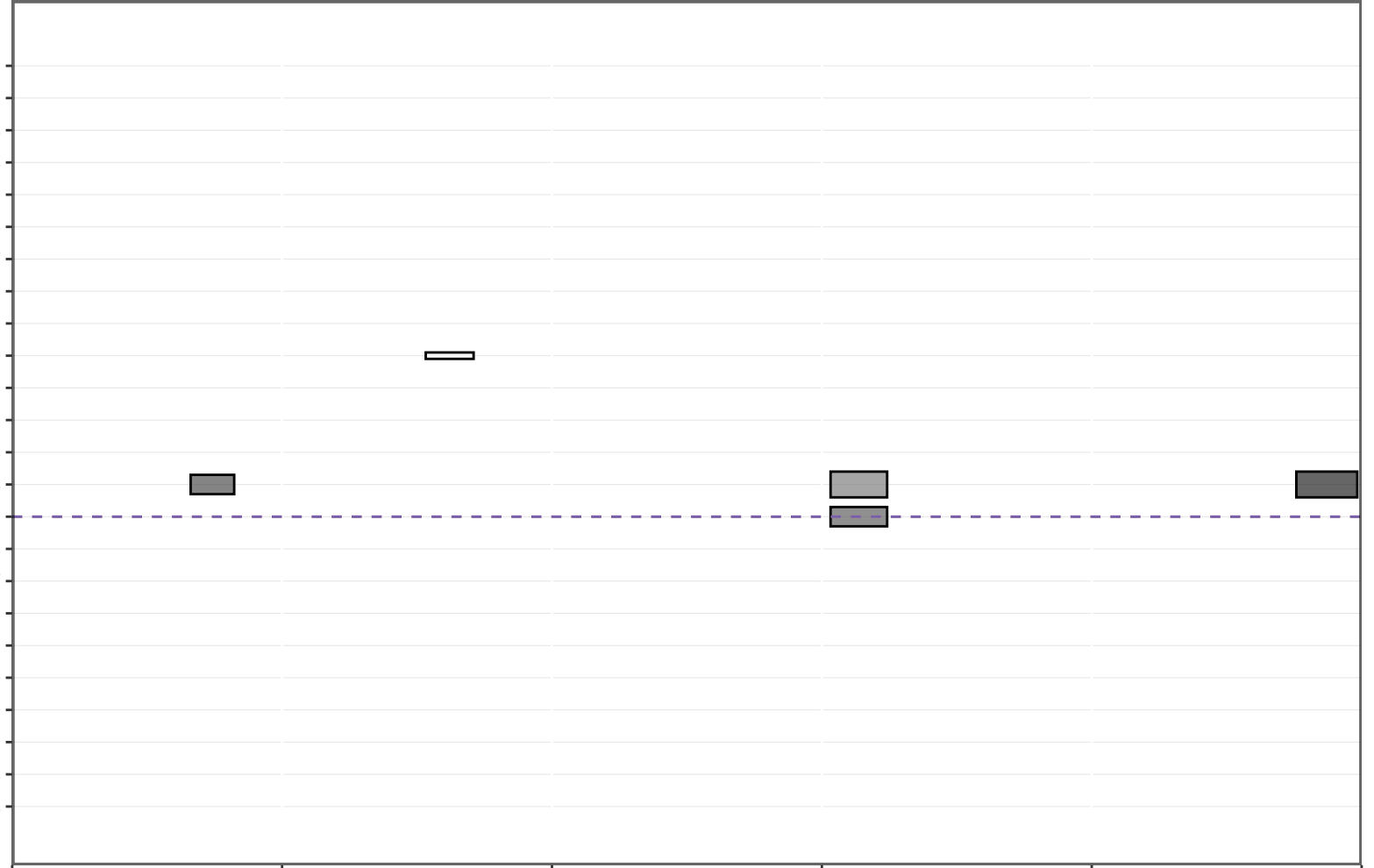
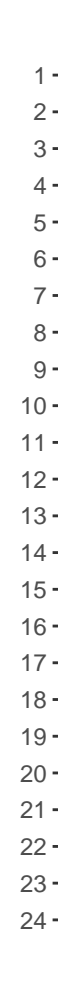
MW indication



Molecular weight



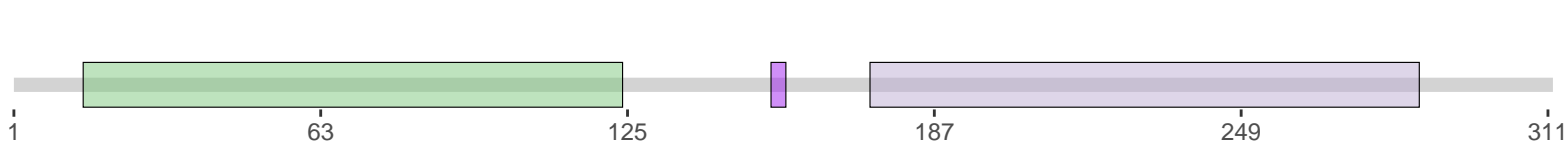
Gel Slice



Peptide counts over 4 repeats

Protein length

Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF01398 JAB1/Mov34/MPN/PAD-1 ubiquitin protease
- PF13012 Maintenance of mitochondrial structure and function

Protein sequence:

PTKAYAVEEVKENATQKSGKVFVHVPSEIAAHEVEEIGVEHLLRQVKDTTSTFLATEVYTGKLAALKGLDARLGEIRSYLDVDDGKPLNHEIYHGDVFNLLPNIINVAELVKAFSVKTNDDMMVYLSLRISVIALHNLINMKLKEHEKAEDSKPLAVPTAAGS

NbL07g09290.1 biotin_carboxylase_1_chloroplastic [MW = 58.44 kDa]

No. of times detected



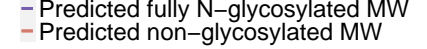
log(intensity)



Values from

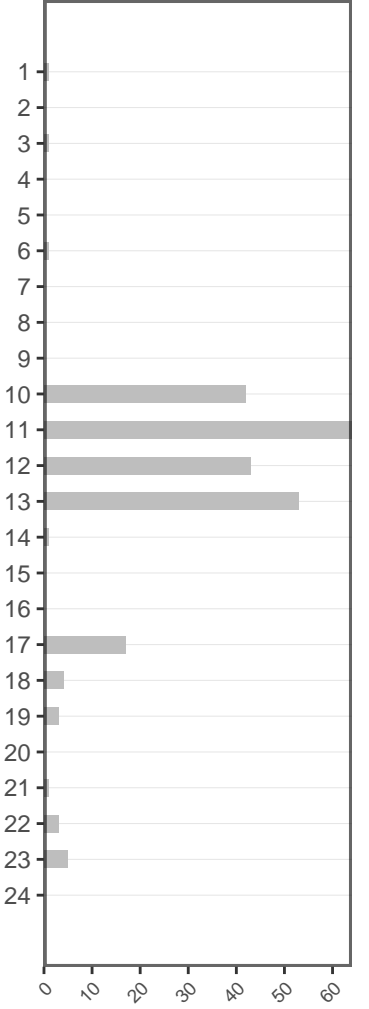
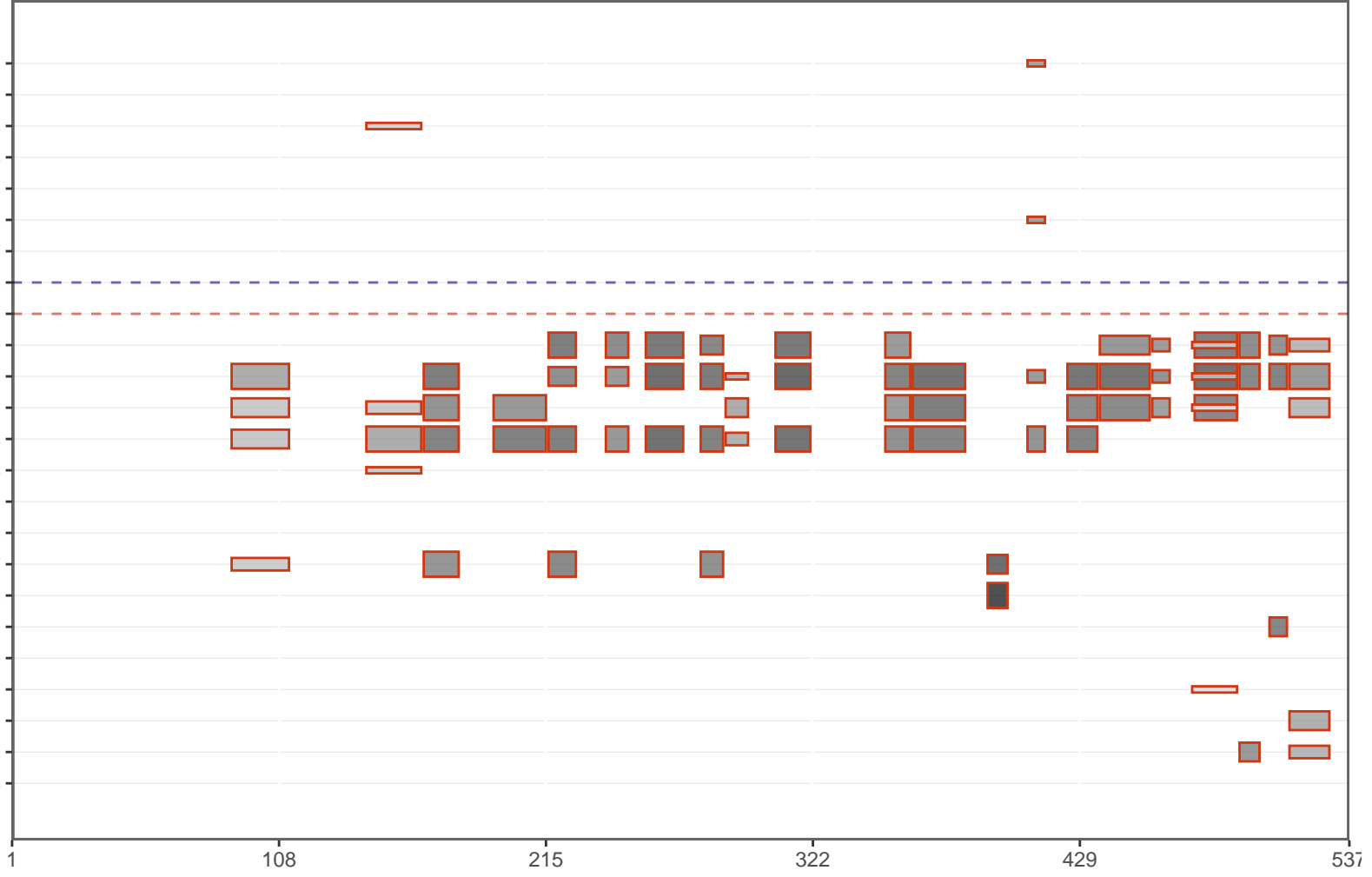
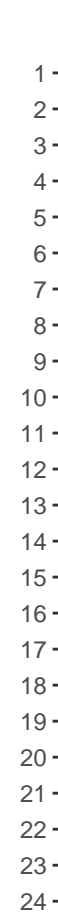
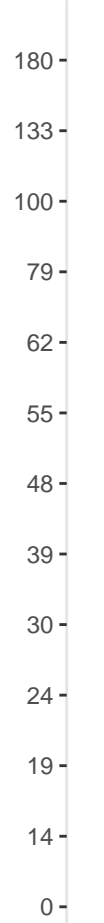


MW indication



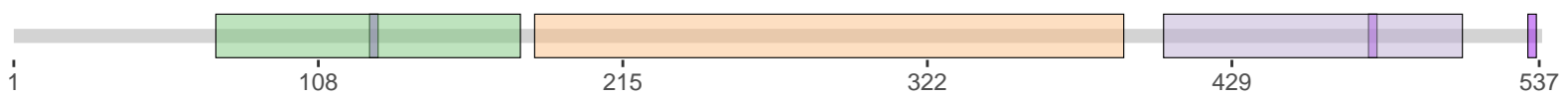
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- TM Domain
- PF02785 Biotin carboxylase C-terminal domain
- PF0289 Biotin carboxylase, N-terminal domain
- PF0286 Carbamoyl-phosphate synthase L chain, ATP binding domain
- Sequon

Protein sequence:

GSSEAAAFQNDGQVLEKYVGNPRHIEFQVLADKYGNVVFGERDGSQRRNKLEEFAPSPALTELRNAMGDAAVAAASGIVGVGTVEFLDERGSGFVEMENIRIQVHEHPTVEMISSEVDLIEEQIRVAMGEKLRVYQGEDVLRGHSIEGRNAEDAFKFRPGPGRITAVLPKSGPFVIMDGHVYFDVIVVPPPEVDSLLGLLIVAWPTREIERMKRALNDITIGVPTTIEYKQLDIEDFKNGKVDTAFIPKHEEELAPPQGMVPAATKEMVNASAI

NbL07g09270.1 thioredoxin_X_chloroplastic [MW = 24.31 kDa]

No. of times detected



log(intensity)



Values from



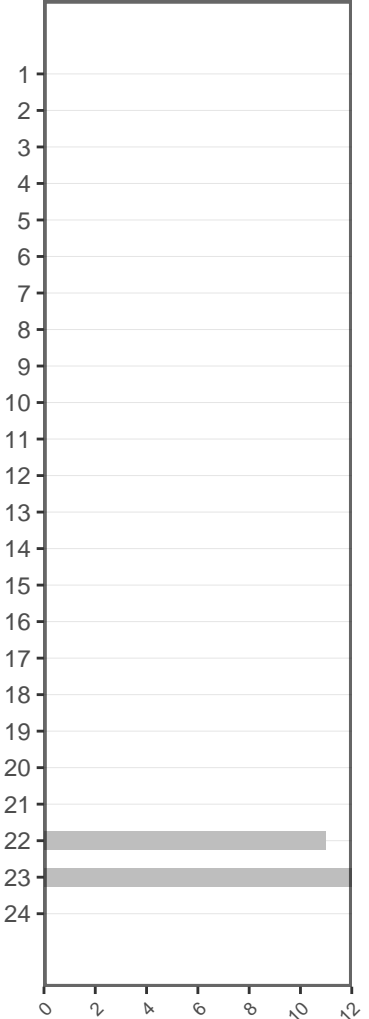
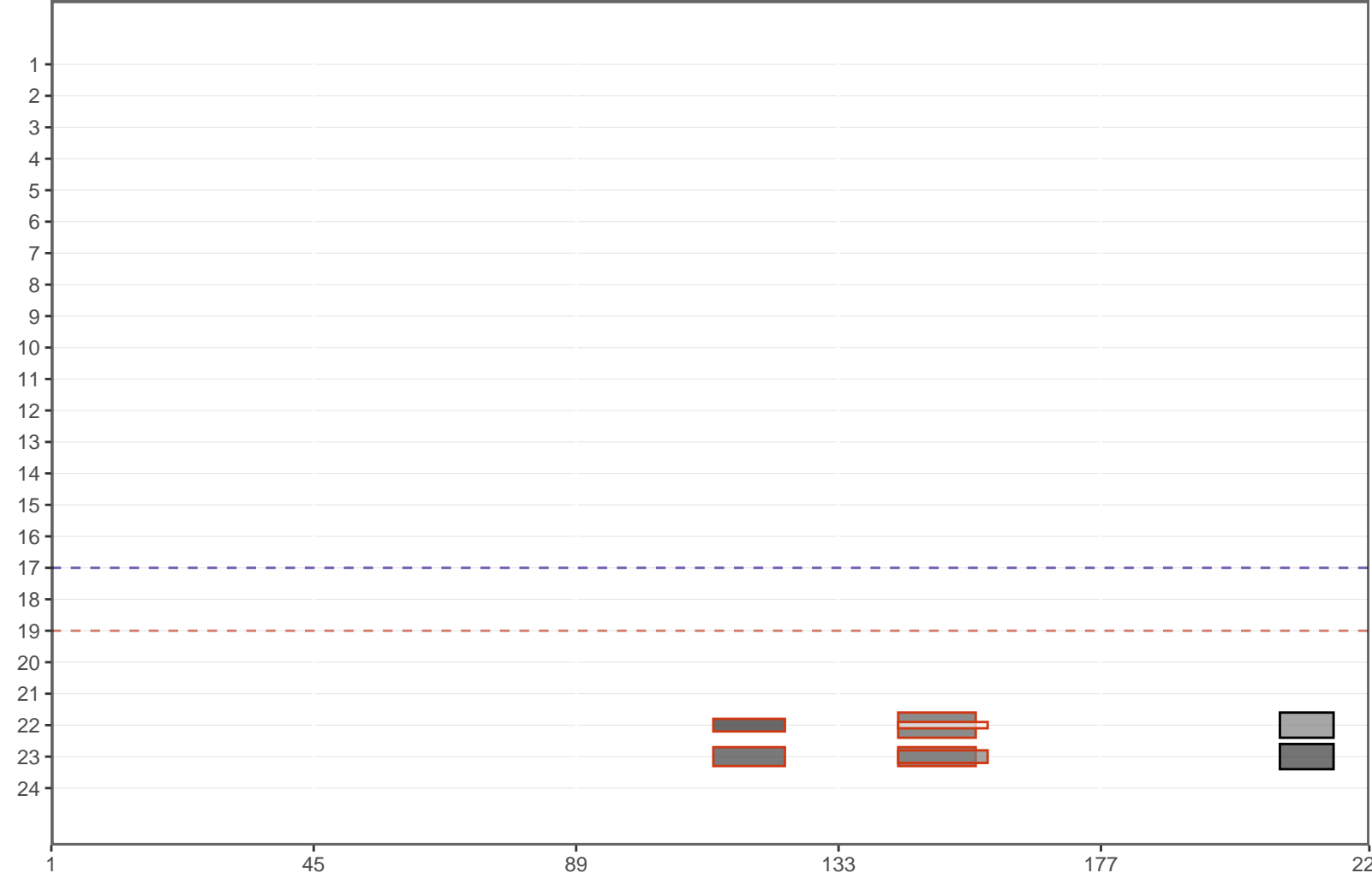
MW indication



Molecular weight

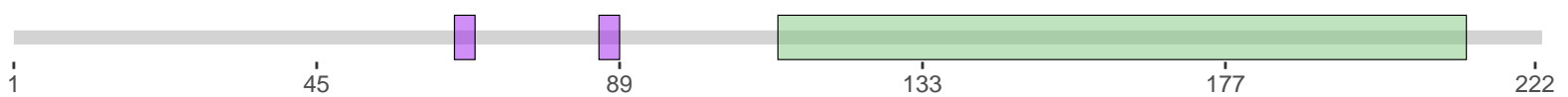


Gel Slice



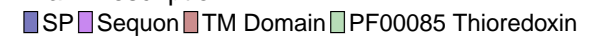
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SSSSTFRIRSGGLREIKEDDFSDVLLKSDRPLVLFVATWGGPCRLIGPAMEVSAEYKENTVYKIDHDANPKLIEFRVYGLPTLILFKDQKEVPDGRKREGATKWLKEYLDGLLTKTVSW*

NbL07g09170.1 glutamate--glyoxylate_aminotransferase_2-like [MW = 22.58 kDa]

No. of times detected



log(intensity)



Values from



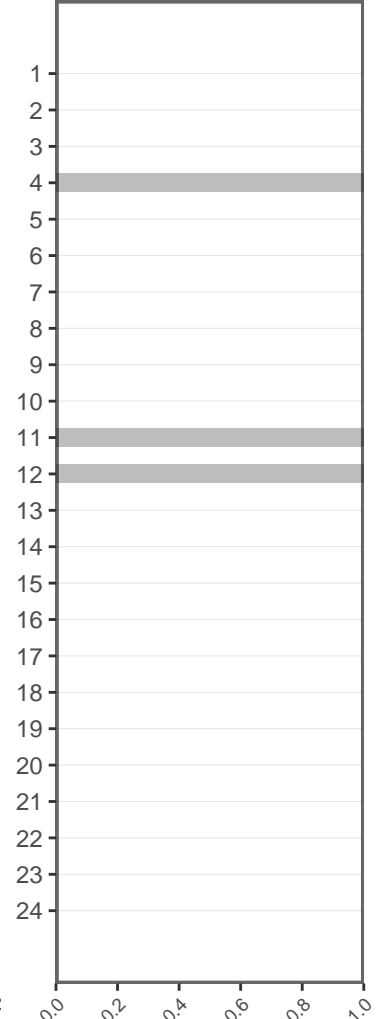
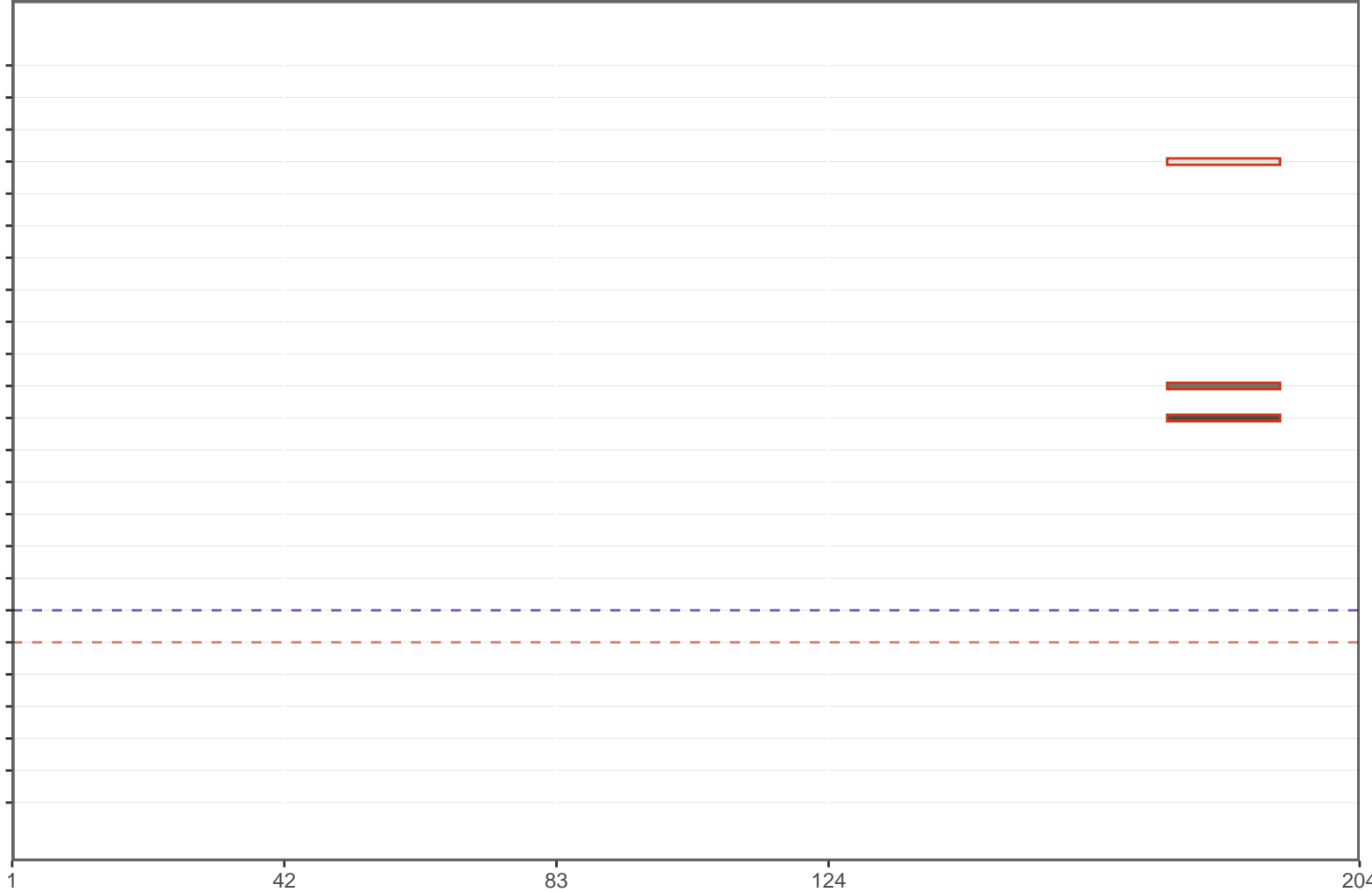
MW indication



Molecular weight



Gel Slice



Protein length

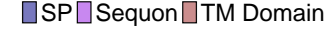


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ILESLRRRAHIMTDGFSNQRNIVYCNFTKGMVYFFQIQLPGDAIDANKLGGKAFNVAVGLKLEATGISTVPSGFGQKEGVFHLRTTLPAEEDGMPBMSBFRKFNDFMKQVE

NbL07g09080.1 uncharacterized_LOC107808191 [MW = 48.21 kDa]

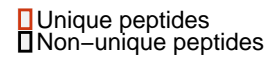
No. of times detected



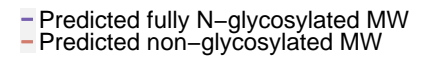
log(intensity)



Values from



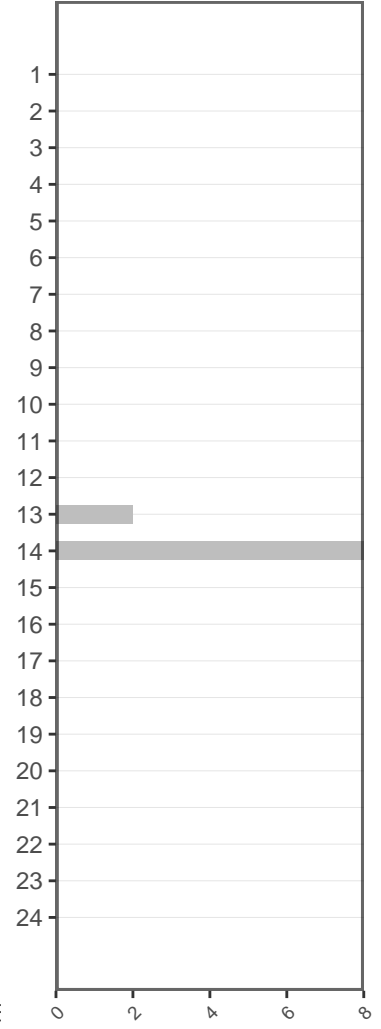
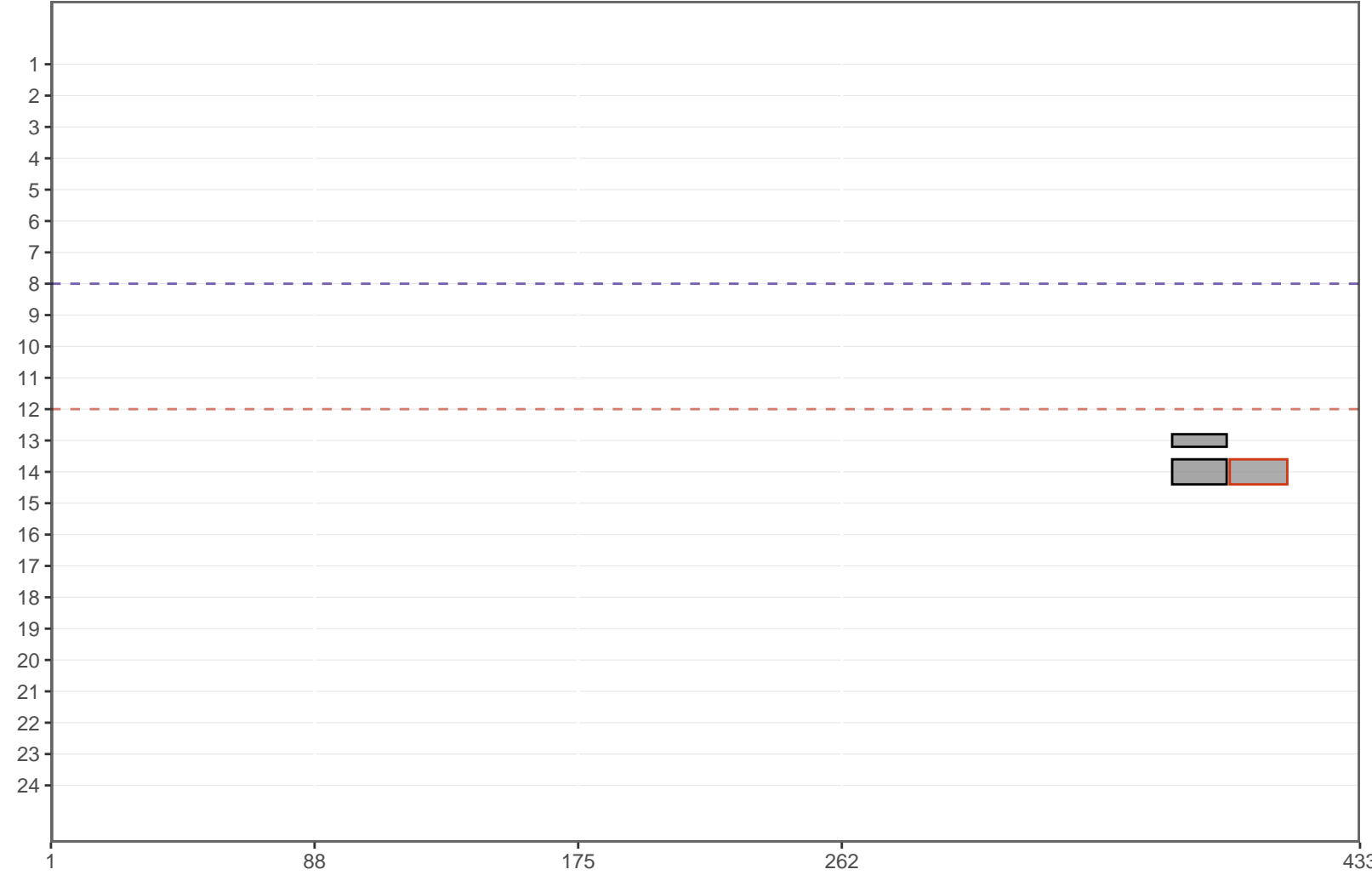
MW indication



Molecular weight



Gel Slice

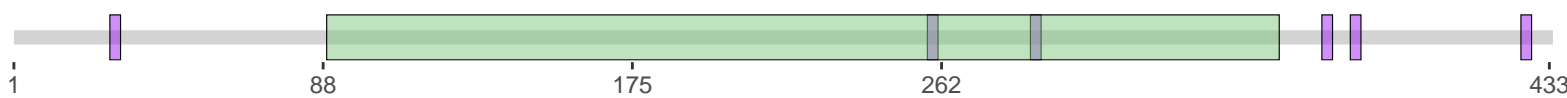


Protein length

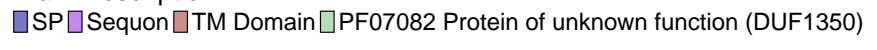


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

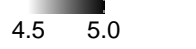
IGNVLMAFNKKDASLWPFSSVLAFLMMGNIGPVLSDIASPTIRLGAEMTKGQENLSPGVKGVFPLVLEGLPLVMDLKGKDNFTFRPEETGRRLRSVYIGIRNLKIKFKDDTIDETSLAQVLSGGSAISGMLDMSIRLPGDHALPLQGLPDVPPGMDAVNRSGELLANLTAGTPWESVANEVQNTLGNVDSHLLSGNGKDLDLVETITTSWMLNSGSPRLLG

NbL07g09040.1 protein_SLOW_GREEN_1_chloroplastic [MW = 40.19 kDa]

No. of times detected



log(intensity)



Values from



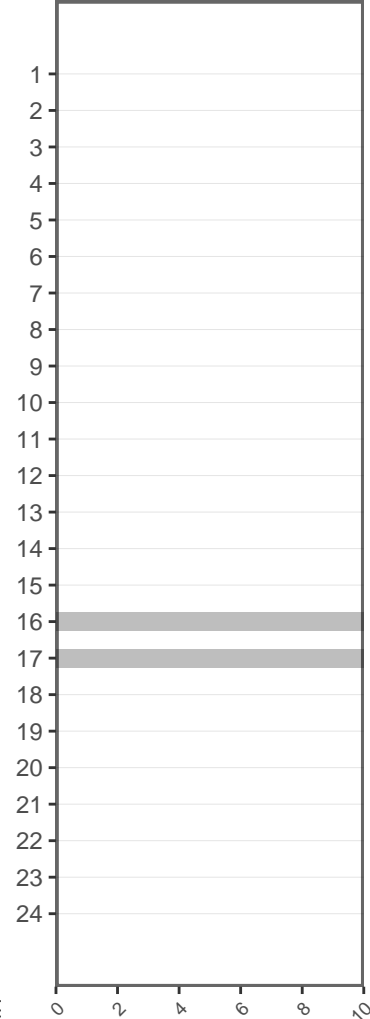
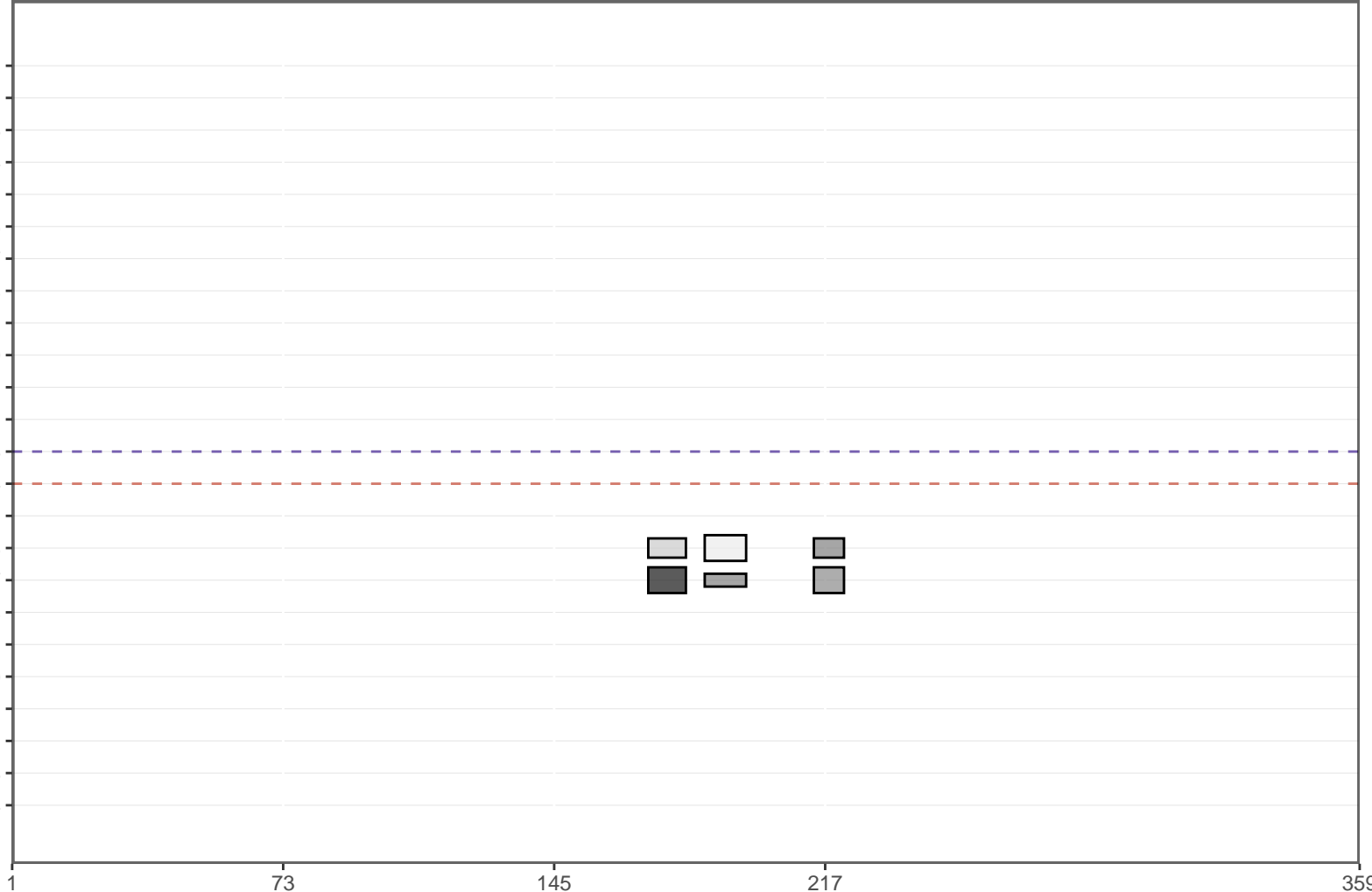
MW indication



Molecular weight



Gel Slice



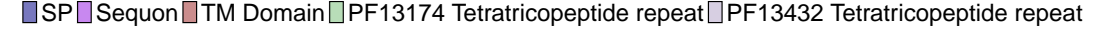
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKL EAGEDEESLKIWKLSAQPENTFWKFLTARLLNEMGKVGAEAREVFEELSKNPLSFEALFENALLMDSGEGVYVQRLLEEALIAEENKVKEGRDVRFIMAQVDFLQKNVEDALREYDELEKEKDFRPFYFGKGMVYSLDRNKEAREGFQAKYRELSPKPFVEGVYGLTFLSRMLFGTDKKER

NbL07g08920.1 glutamate_decarboxylase_4 [MW = 55.85 kDa]

No. of times detected



log(intensity)



Values from

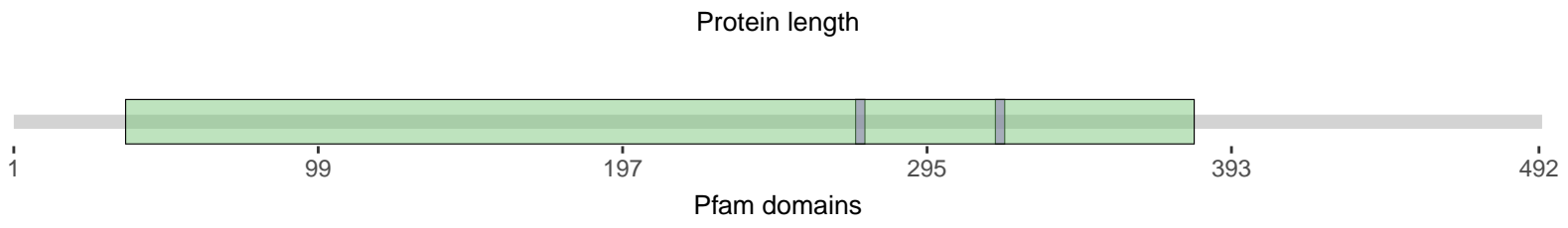
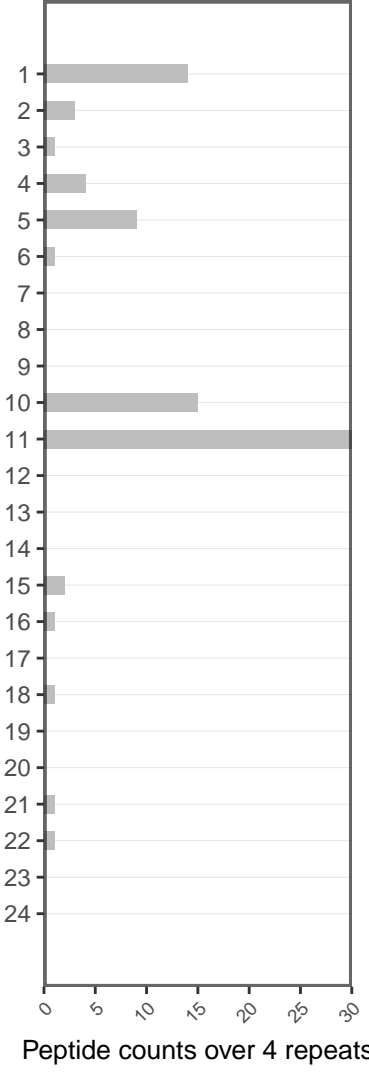
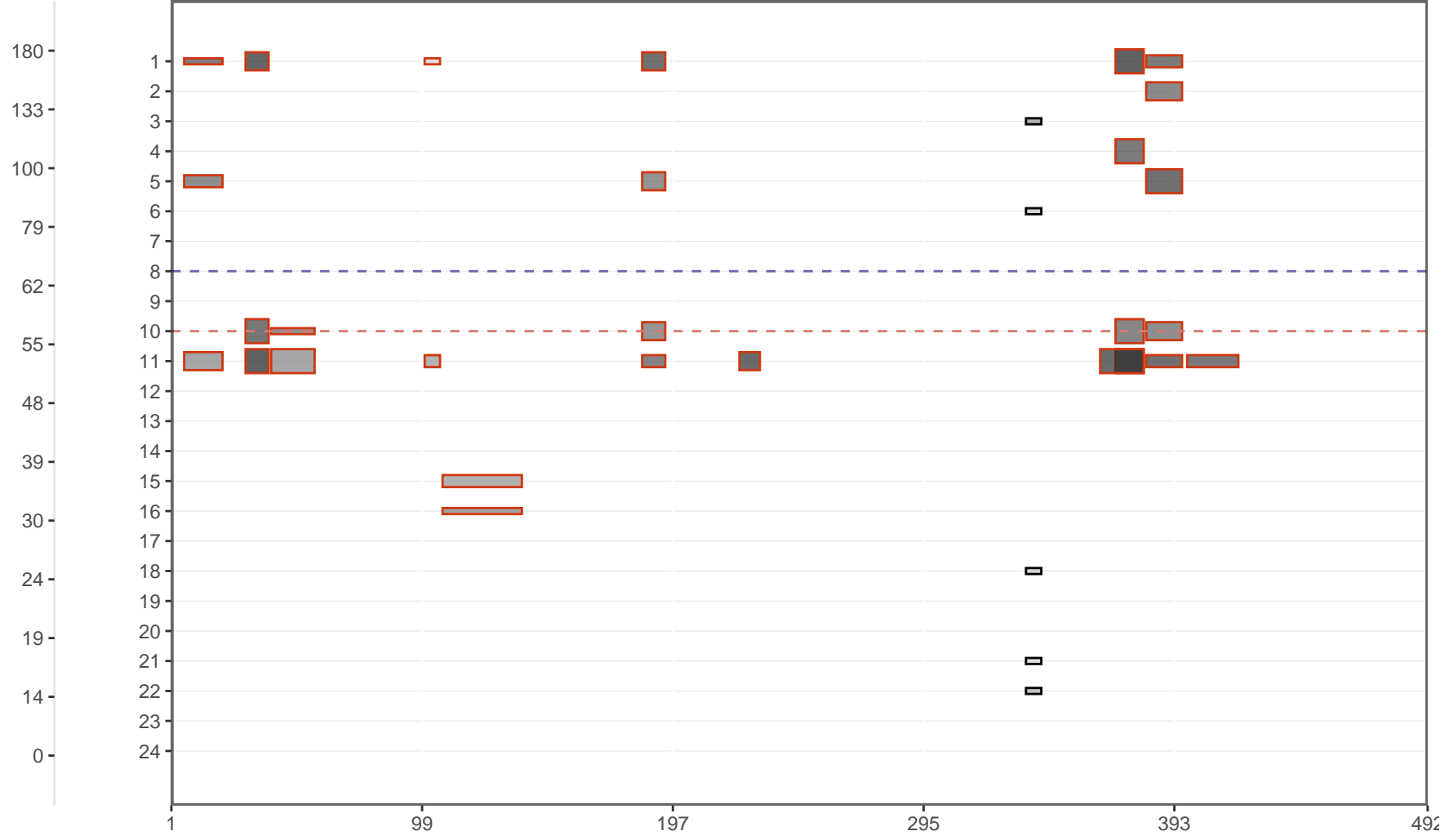


MW indication

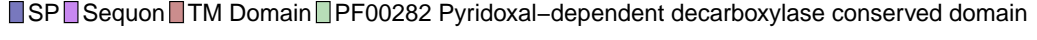


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

NKLTGWNTPIHVDASGGFAPFLYPELEWDFRFLPKGINVGGHKYGLVYAGIGWVWRTKQDLPELEFHNVLGADQPTFTLNFSGKSSQVIAGYQLRLGVEGVRNVMENGRENAVLREGLKTRFNKVDKDEGVPLVAFSLKDNSHINFEFEVSETLRRFGWVWPVYTMPADAGHVTYLRVAVREDFSRTLAERLVDIVKVLHELDLTPARLSAKLEEVKLVKNGKSEVEVQREVTVNWKPFVLRKAPVC

NbL07g08620.1 probable_S-adenosylmethionine-dependent_methyltransferase_At5g38100 [MW = 41.61 kDa]

No. of times detected



log(intensity)



Values from



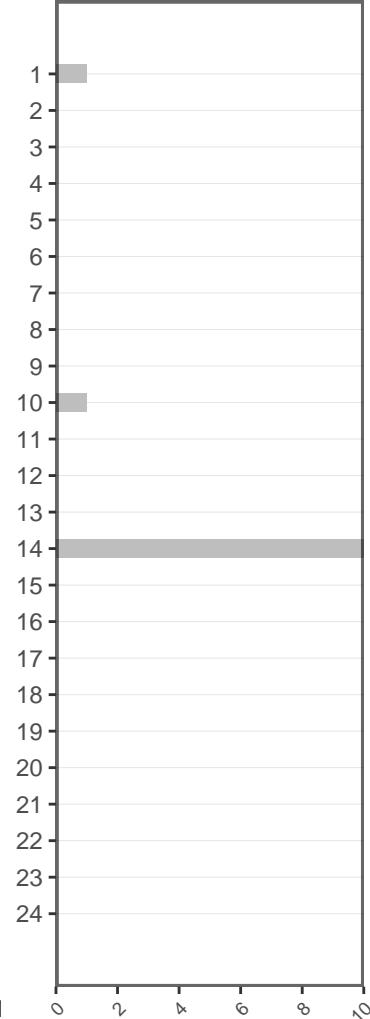
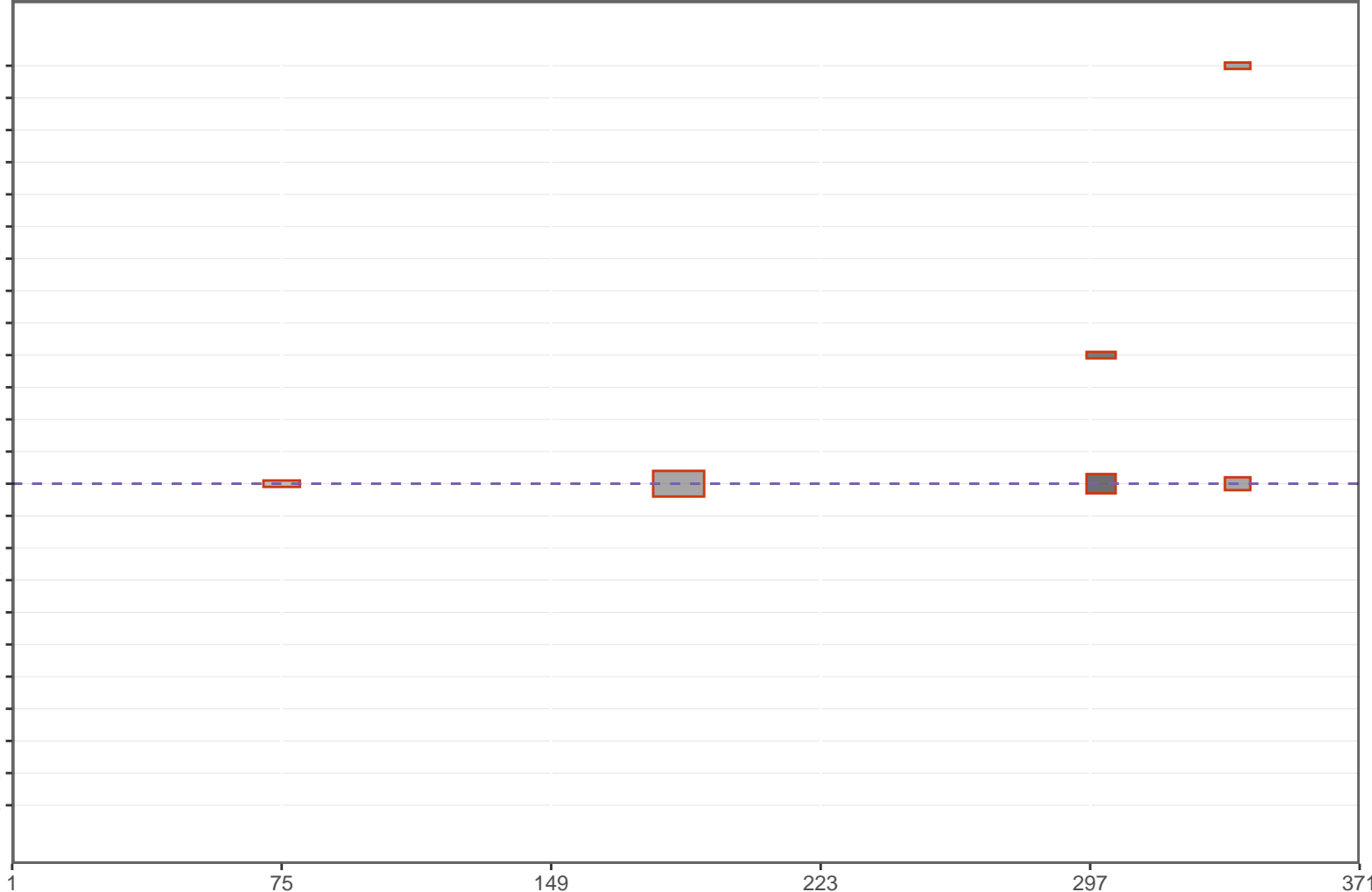
MW indication



Molecular weight

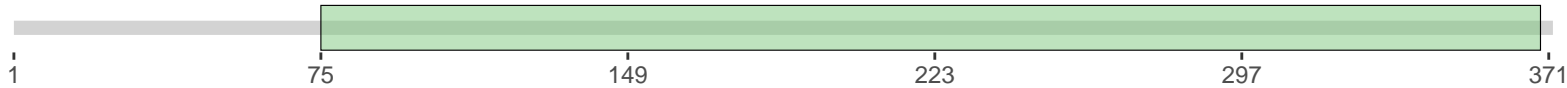


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

WLSKSPPELLDENSPWNGKHVYDAPNIAVNAVVGDFDKMEVFLNARAEIEVPGGIMVLVSPFGSYRLKFFGSSLDVAVNEGMIDESLVDVFNVLVYFSPFEDMTKIVVERNGCFSEIRIELAVPQDKLVNEADANSLMTNLRVLEGVFINIFGRKIADEAFGRITLKSEDSIAWAKAVYKPKQLFVALKRRK

NbL07g08610.1 aspartokinase_2_chloroplastic-like [MW = 61.31 kDa]

No. of times detected



log(intensity)



Values from



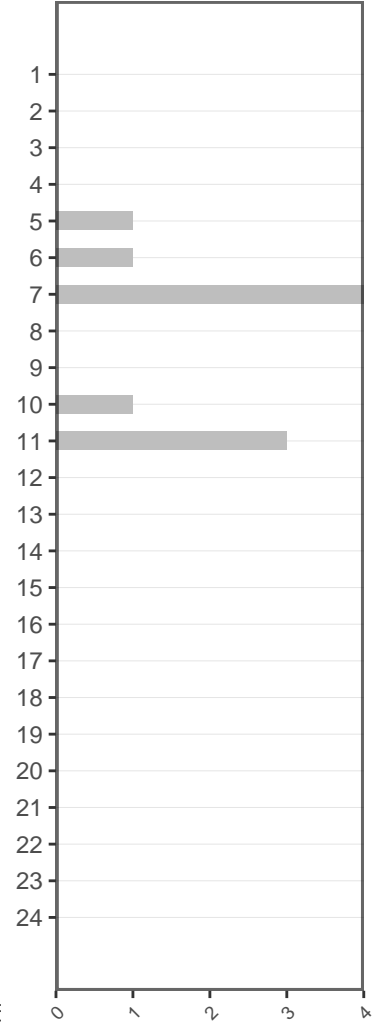
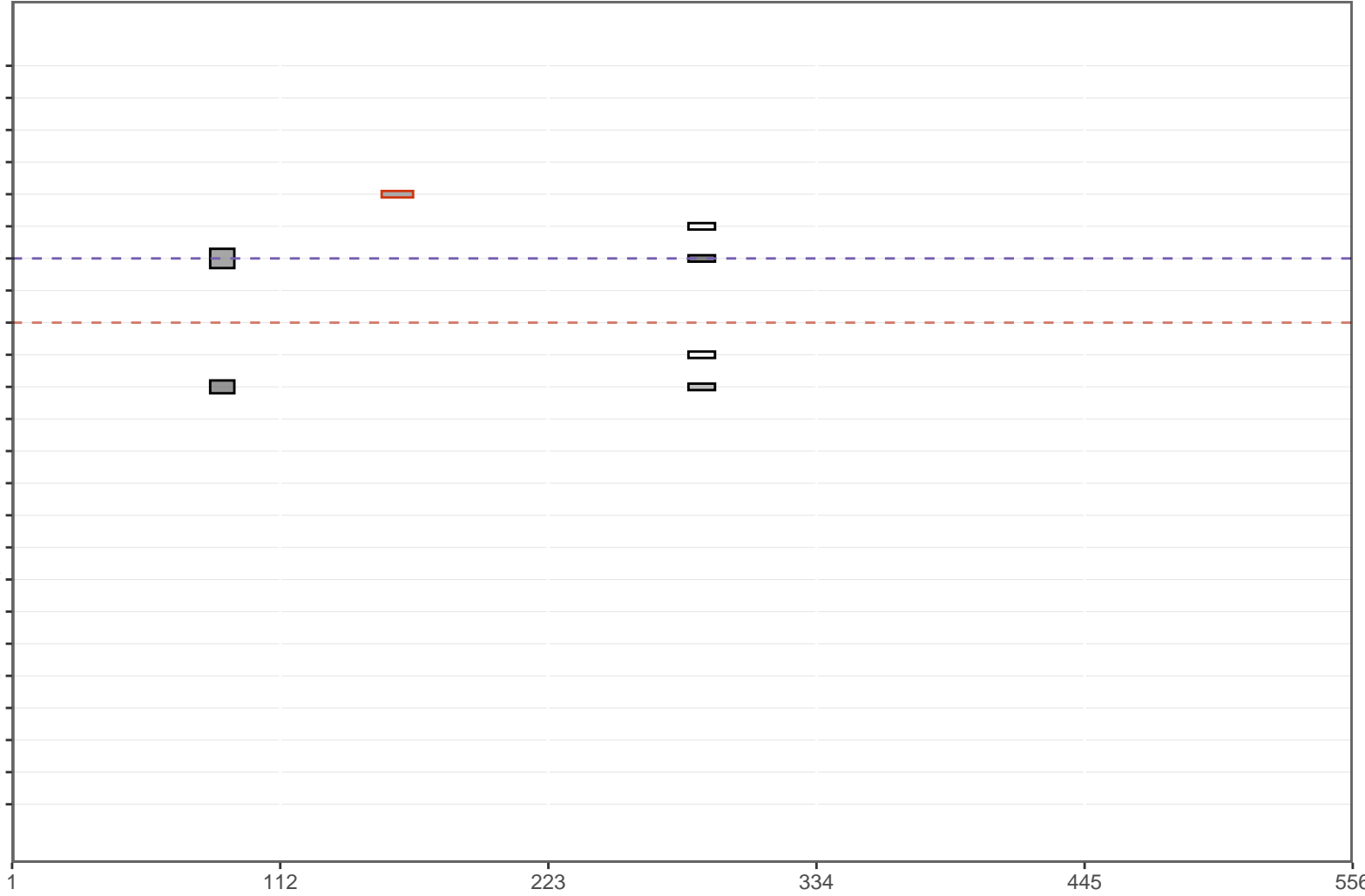
MW indication



Molecular weight

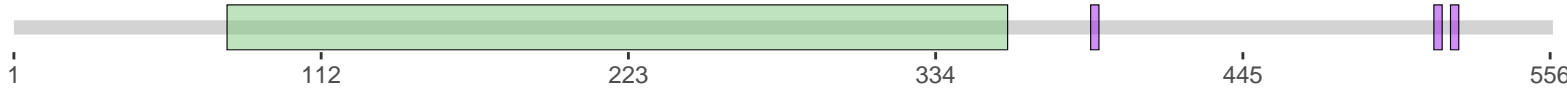


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GFLGGWRTCVAVFTLGRGGSDLTATTKGALGLREHQWVKDQGVLTGDPNIVPRAGPVVPLTFDEAAELAVFGAGVLPQEMRPARREGDIPVVKVNSVNRKAPGTLGRARRDMKAVLTVLKRNVMTLDNVTMLDQGFGLAKLLOVFSIFEDLGHVQVWATSEVSGILTLDPKLVSRRELJQOELDHNVVELEKIAIWNLLQHRHSISLGNVQRSSGLEKAFHVLRTNGINVMQSGQASKVINSLNNDSEAEQGVRAHKHTFFESDLSELWENGHVTPLST

NbL07g08590.1 aspartate-semialdehyde_dehydrogenase-like [MW = 44.53 kDa]

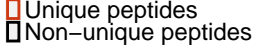
No. of times detected



log(intensity)



Values from

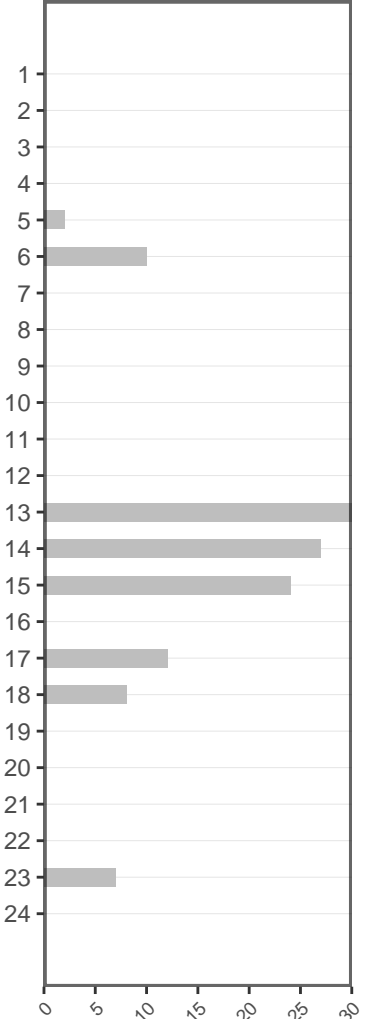
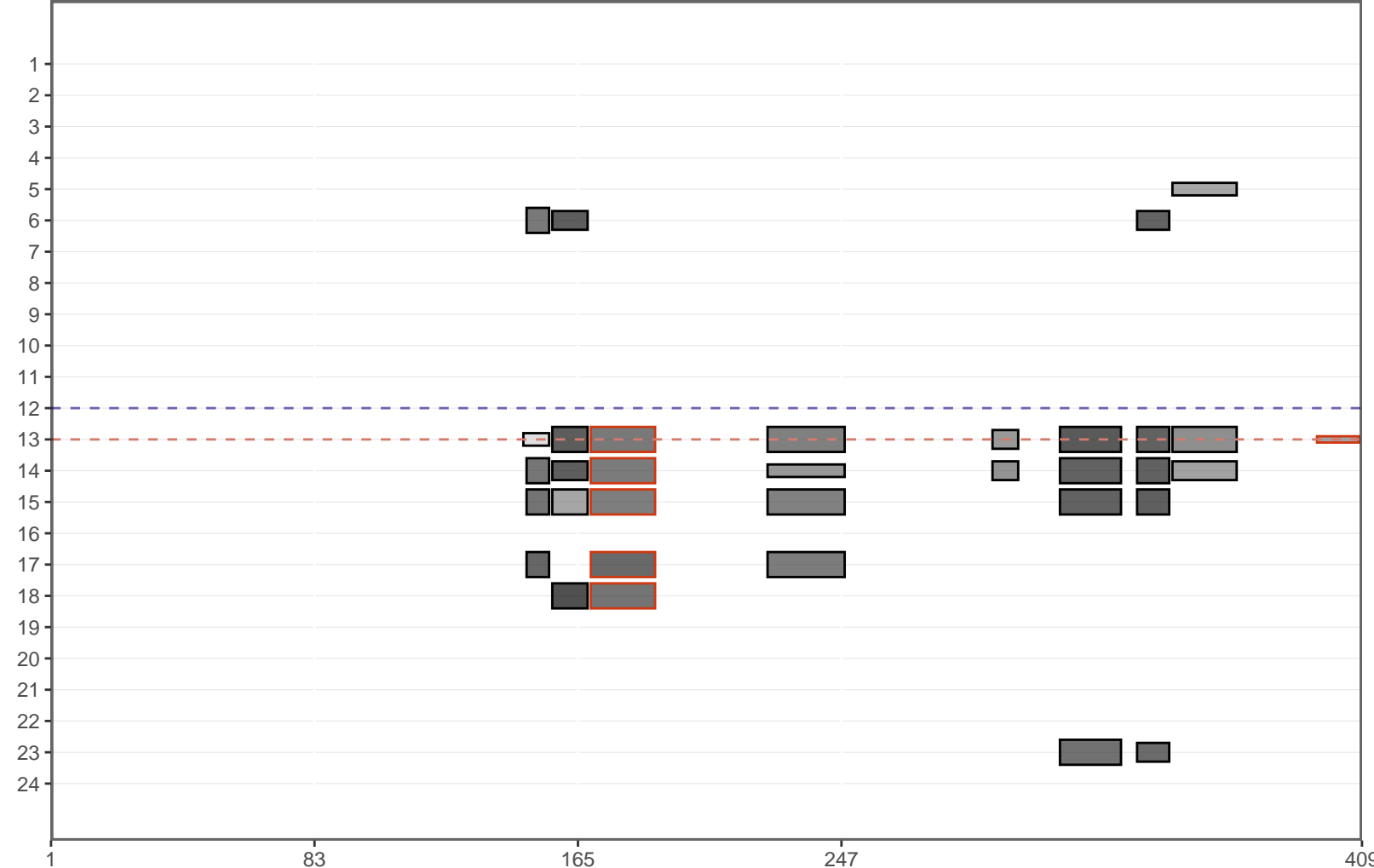
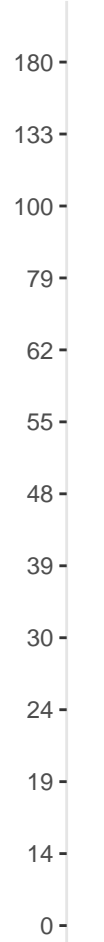


MW indication



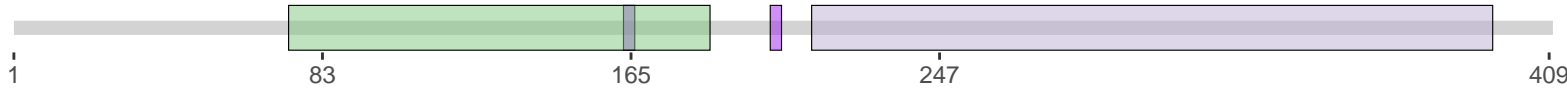
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfm domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01118 Semialdehyde dehydrogenase, NAD binding domain
- PF02774 Semialdehyde dehydrogenase, dimerisation domain

Protein sequence:

ISGKGLANPNCSTIKLMAVTPLRHRAKVKRMVSTYQAASGAGAAAMEELVQGTREVLGKKEPTGMFNQGVAFNLFNSHNPVQSGNGVNEEMKLYKTRKIKWDMDKVYATGIRVPMRAHAESVNLQFEKPLDEDTARDILKNAFGIHDHRSNRFFPTPLEVSNKDDVAVGVRVRRVSDGDDYGLDFVCGDQIRKGAALNAIQIEMLI

NbL07g08370.1 secoisolariciresinol_dehydrogenase-like [MW = 29.58 kDa]

No. of times detected



log(intensity)



Values from



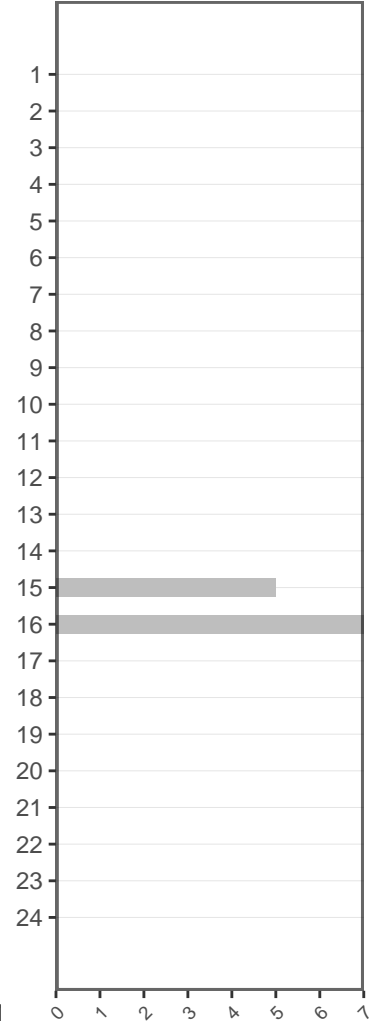
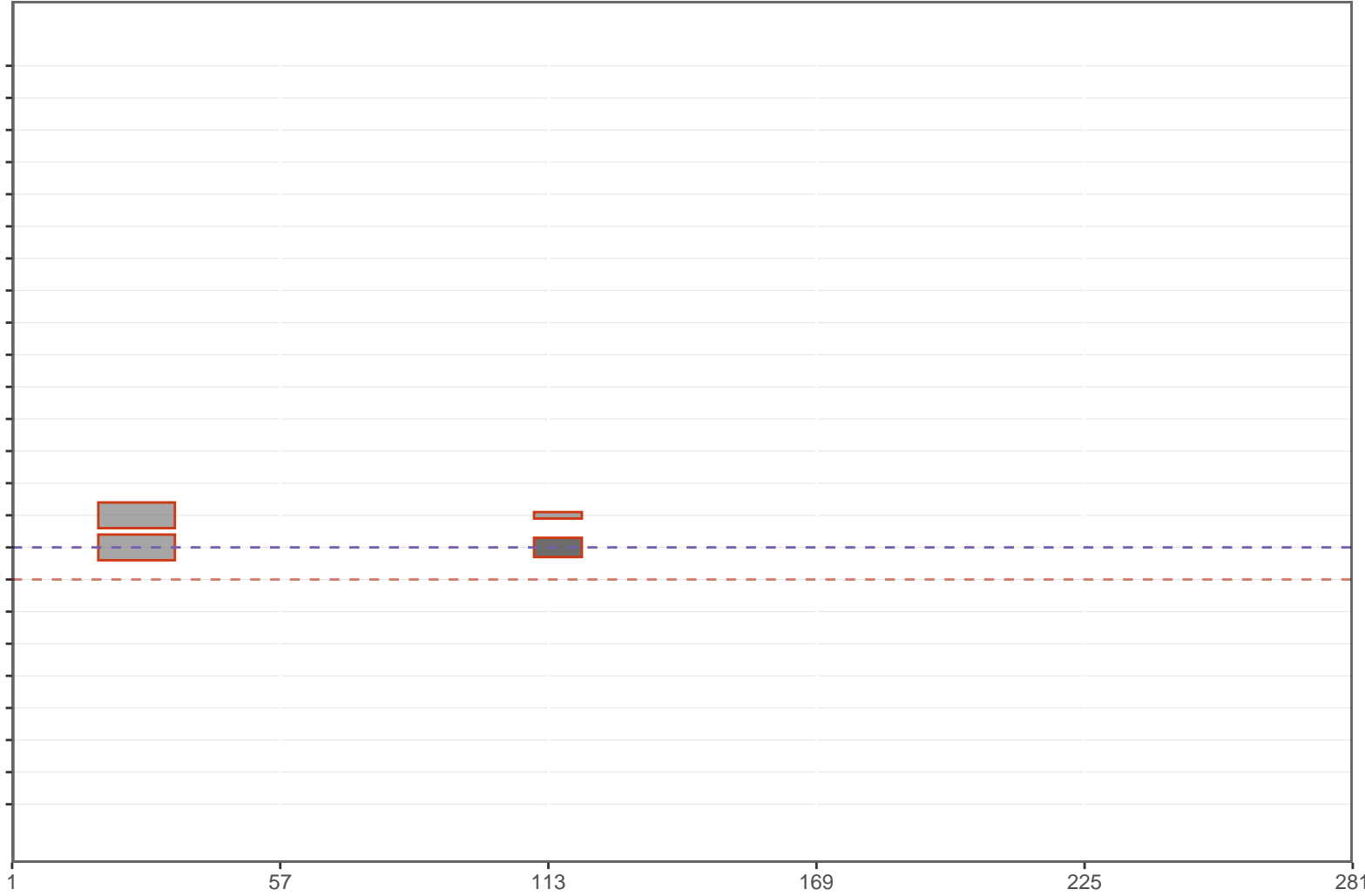
MW indication



Molecular weight

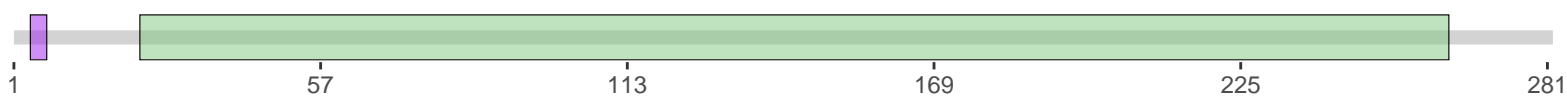


Gel Slice



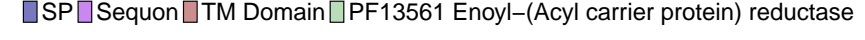
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AFLGAKHARVMSAKTGGILFTASVAVAGMSPHPYASBKHAIVGLANNLGAELGGQGRVNGITPSVWATPMVYKSKVWGDGSKVDEAVMKSANLKEAKLEVEDVAAMAVYLADESKYVSGLNLLIDGGYKTNPLFAMGIREILGDF

NbL07g08340.1 PHD_finger_protein_Alf1-like [MW = 28.16 kDa]

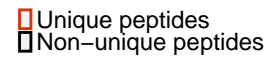
No. of times detected



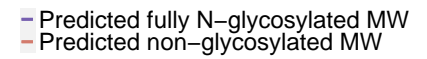
log(intensity)



Values from



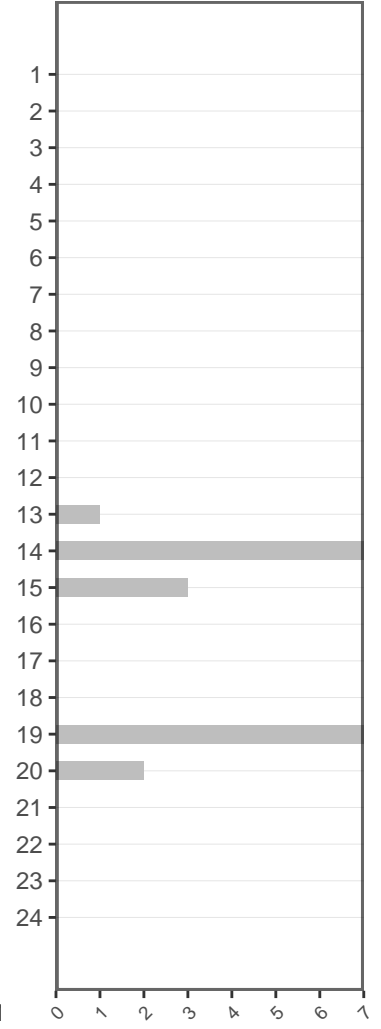
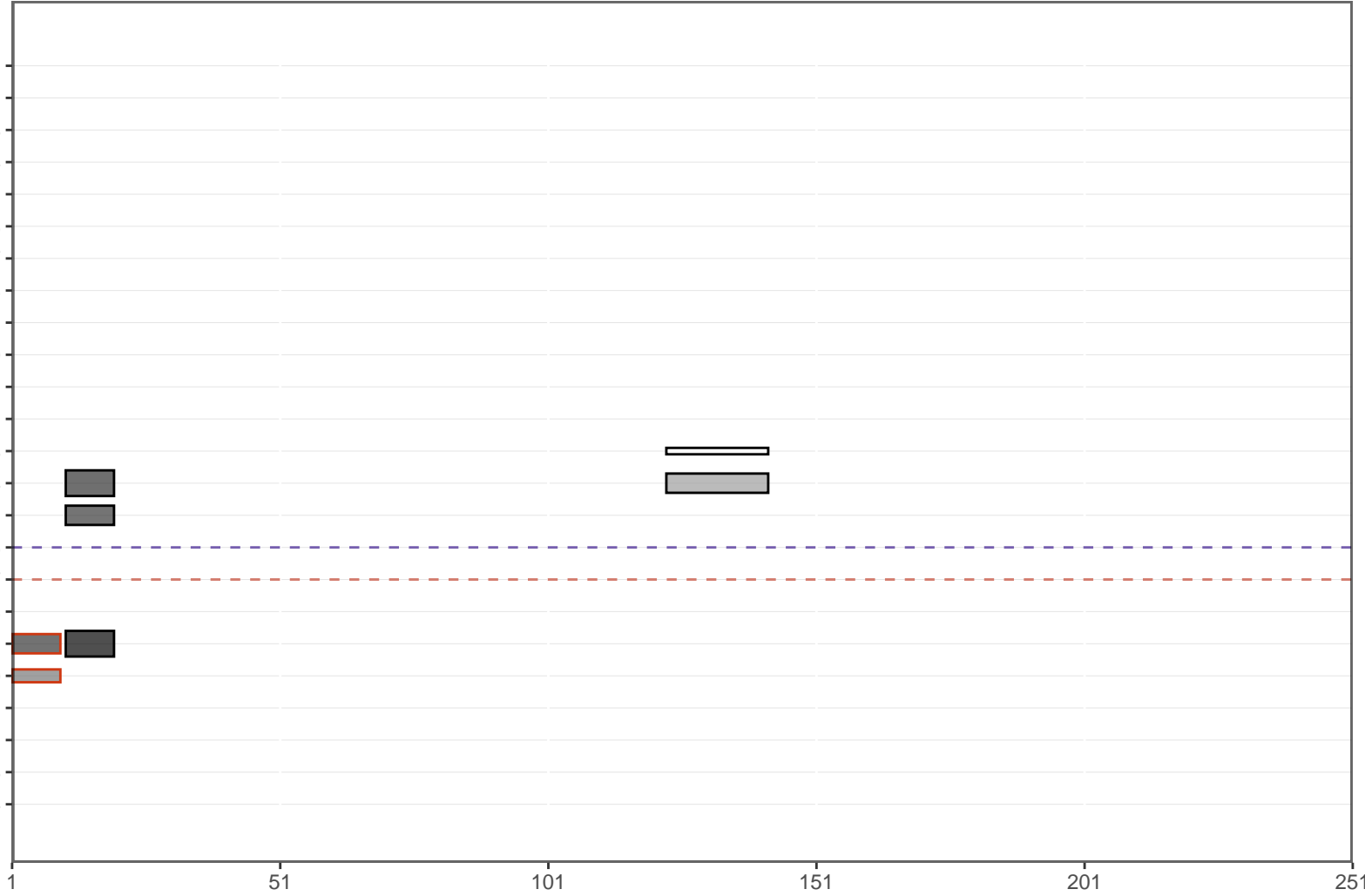
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FGKSERKRLFGMINDLPTVEVVTGAAGKARDAAHNSGKKS6GKFRG6EPQHGKGVKVFPPKKEE6GEEVEE6EGGATLGGAGGDNVGGDEFWDCGVCEKWFHKGKVKITPAEHNKGGKPGSGNKRARV

NbL07g08200.1 pectin_acetyltransferase_10-like [MW - SP = 43.79 kDa]

No. of times detected



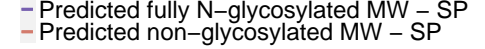
log(intensity)



Values from



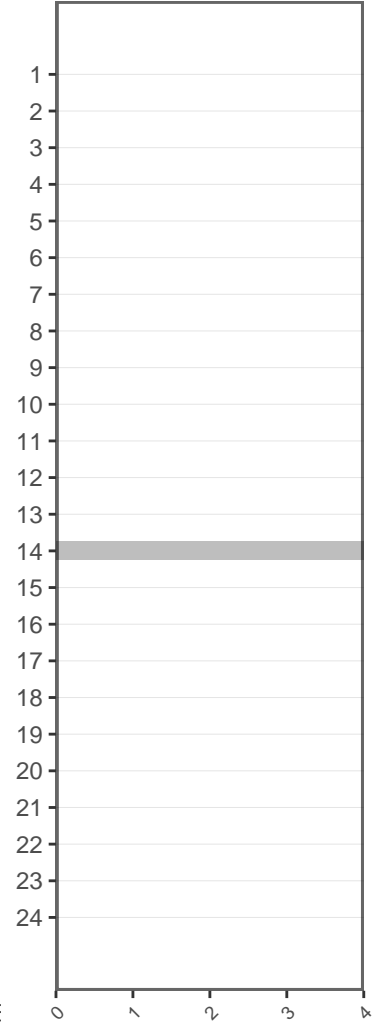
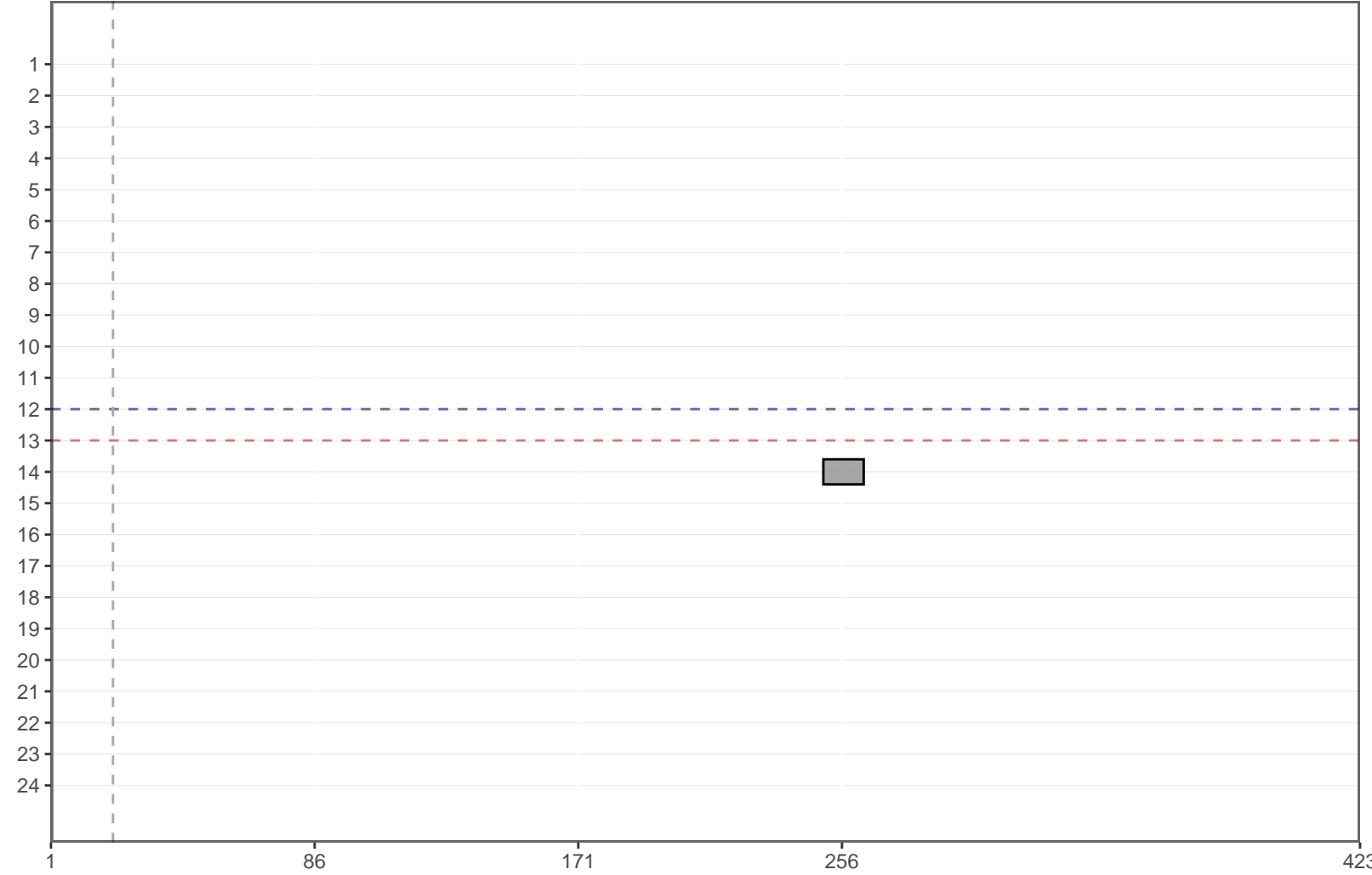
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

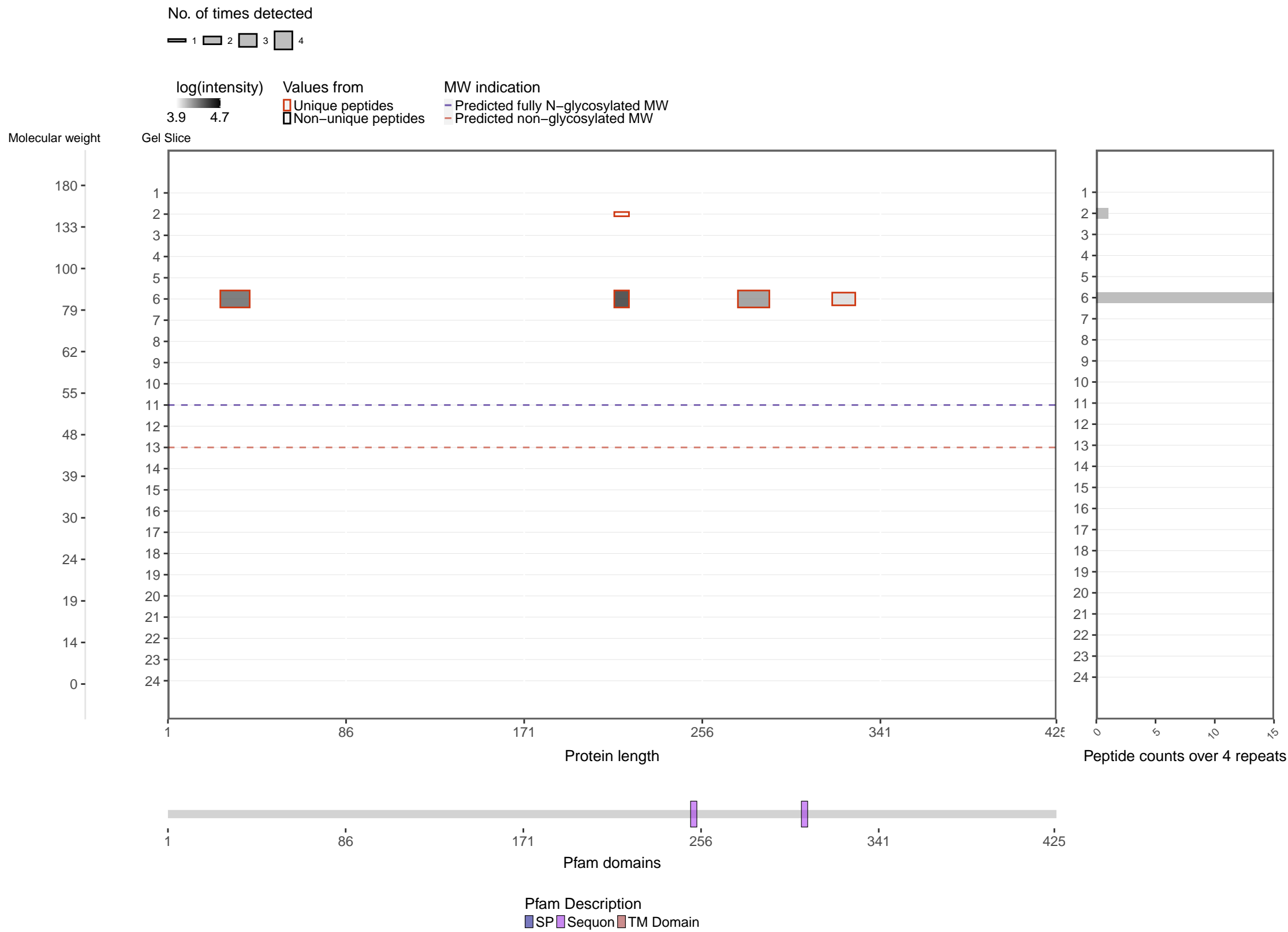
Pfam Description



Protein sequence:

ALLSGCSAGGLASLKHGDEFRTLFPSSKTKYKGLSDMGLFMDATVSGGHALRNLYGGVYVQDGLGKTLPTGTNKLDPSTGFFPNLIGNIKTFLFLNAYDQWVQVQSLAPPVADPKYKGLWHQCKLNEGGASQKGLGFRNDMLNAWKGFAASTQNGLFINSGFAHGGSEGGDTWFADDSPLNKNPVALAVGDWYFDRAGVKSIDGAYPCDKTKHNLVFKY

NbL07g08180.1 eukaryotic_translation_initiation_factor_5B-like [MW = 47.16 kDa]

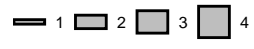


Protein sequence:

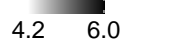
LEQNKETIYANVYEDKLAEGPEVRRKKKIDGEPNTEPKPENTPEAATEVPLKKEEVEENDTKDAKTNGEEDERKSVVTEAKETPEKAPVEIAGRISIELIANGNNKDEINVTTEANEATEAKKVVDEATATVTEKSGEESGKPKPETETKVEEETAGEVEPKLEGEAKADAAKDGGERKTLEEAFAKKEEVPAKPKGSDNLIISKMKGSLWAKKAIMKPKSPSKSETKNEVTA*

NbL07g08090.1 ATP-dependent_Clp_protease_proteolytic_subunit-related_protein_1_chloroplastic-like [MW = 42.52 kDa]

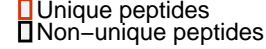
No. of times detected



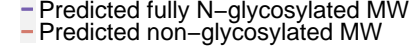
log(intensity)



Values from



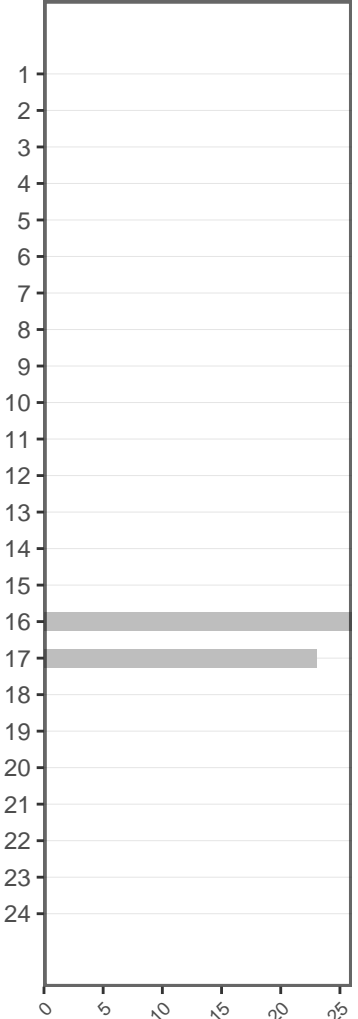
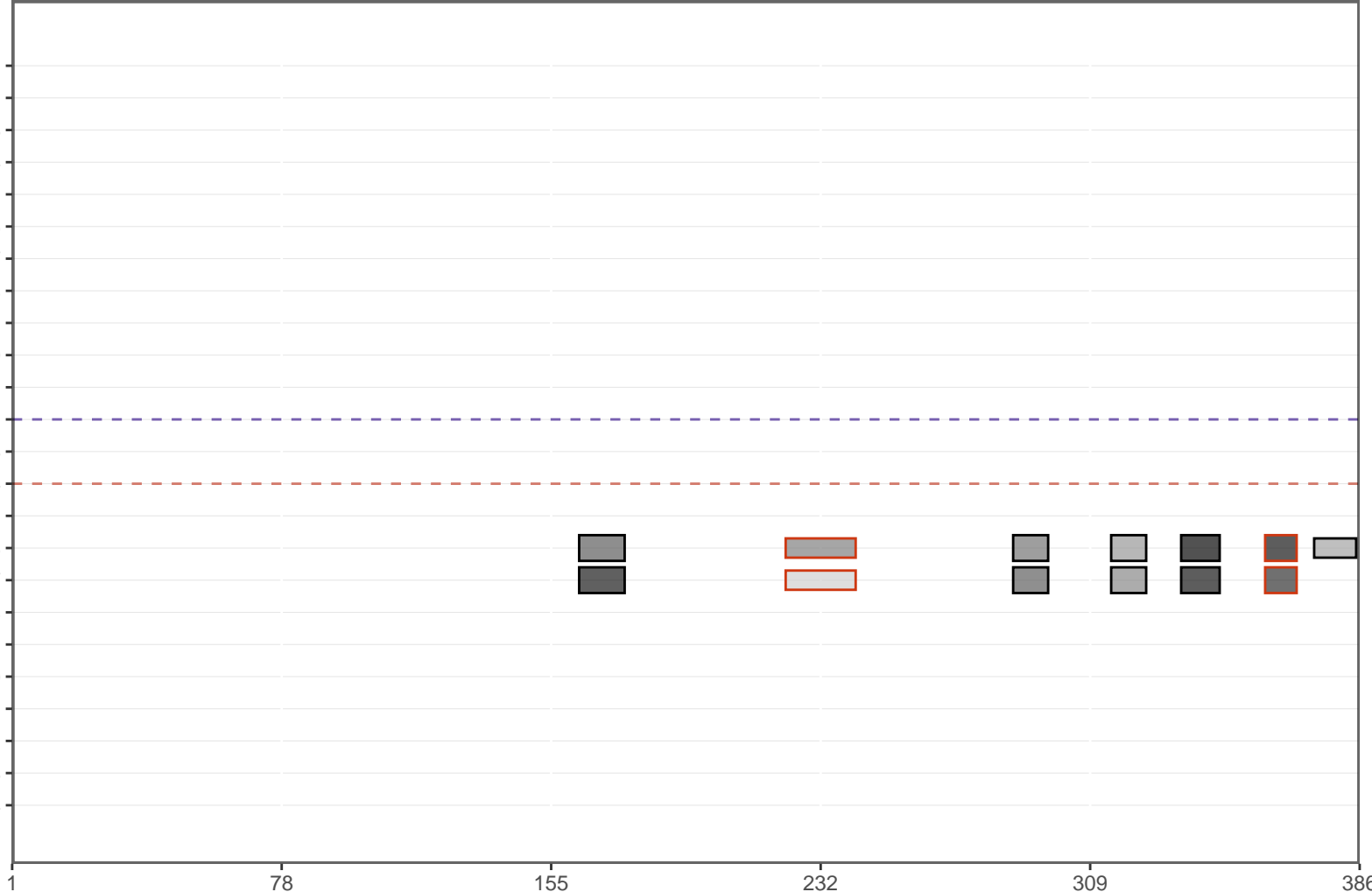
MW indication



Molecular weight

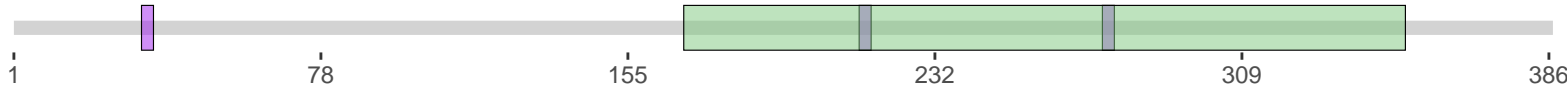


Gel Slice



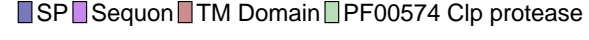
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IIVYLGMPIVAVITELLVAGFMWLDVYDNPSPKPYLYINSSGTGNEKMETVGSSETAVAVSDTMAVCKSDYTVNCGMAYGQAAMLLSLGLKGFAMQPNSTKLYLPKVYKSSGAVDMWIKAKELDANTEYVLELLAKGIGKPKKEIEKDGRPKYLRAGEANDYGIADKIDSRDNAFEKRNLYDEILAQSRAMRKAGPGQAAAPGFR

NbL07g08030.1 3-oxo-Delta(45)-steroid_5-beta-reductase-like [MW = 43.69 kDa]

No. of times detected



log(intensity)



Values from



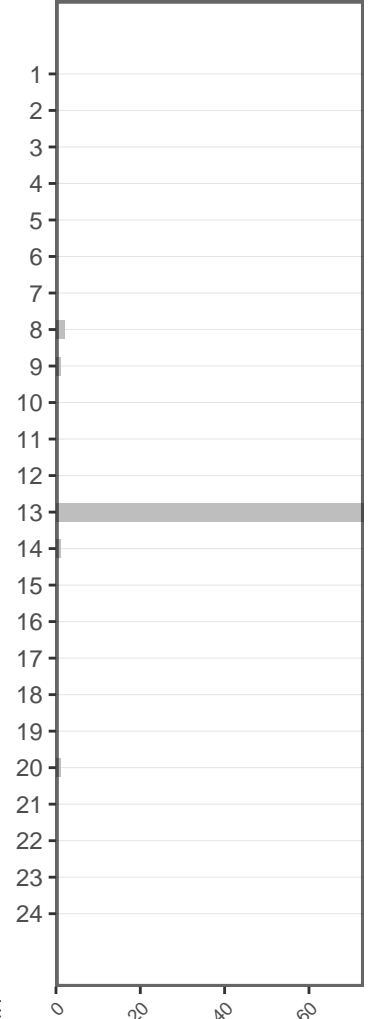
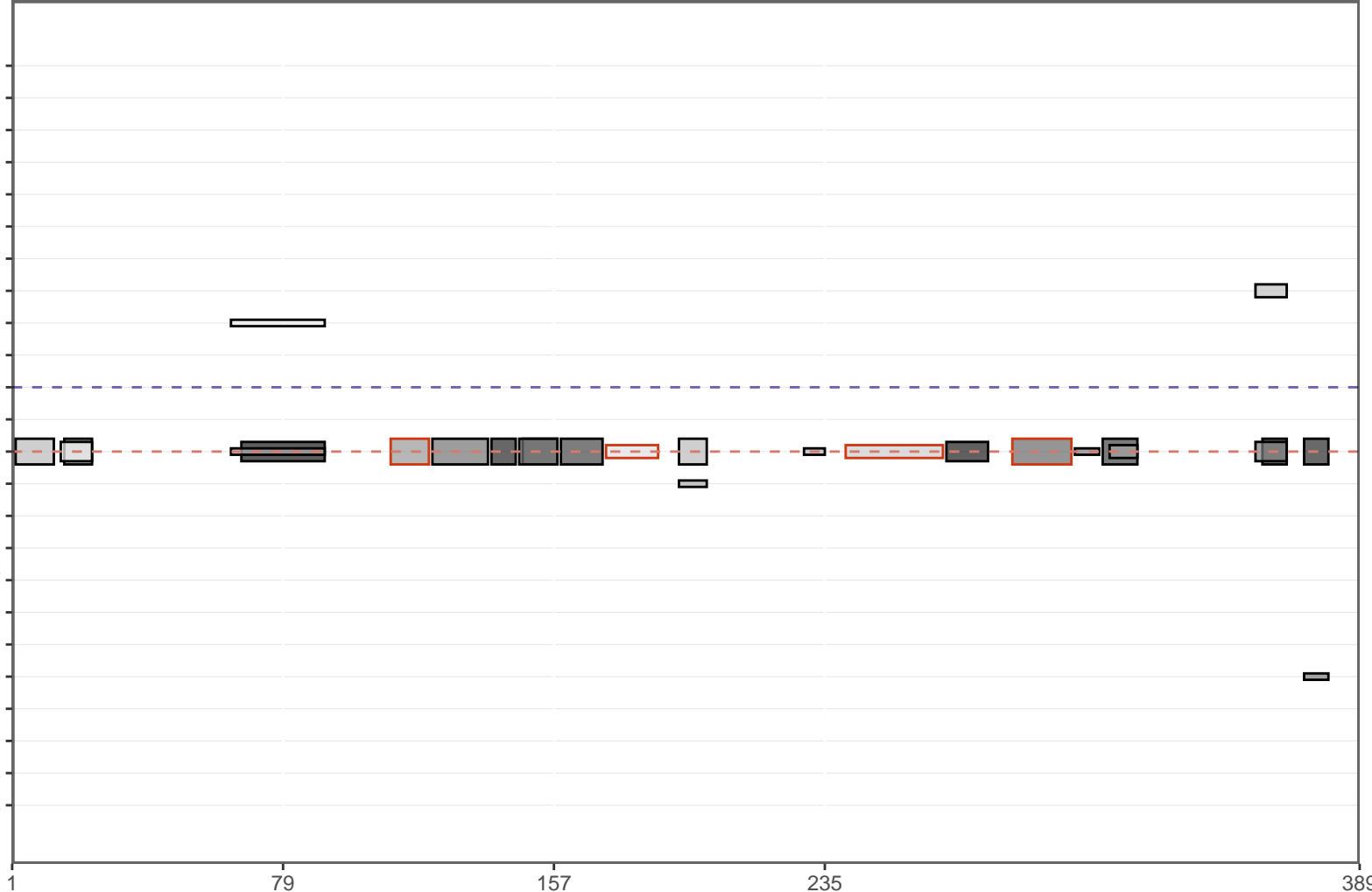
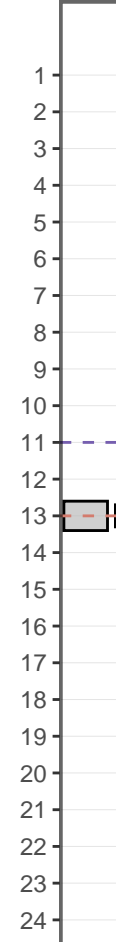
MW indication



Molecular weight

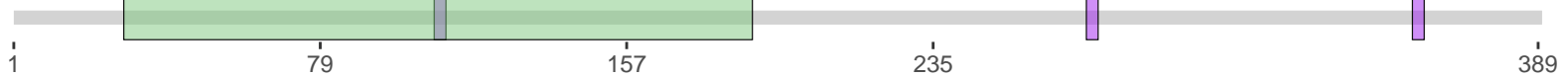


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

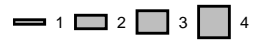


Protein sequence:

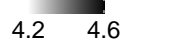
DVLFKEIEKGLTWSVHRPGTIFGFSPLMNVGTLGVAAIKHKEGLPKFPVKAAWDGVSDGSDADLAIEHQHAAVDPYAKNEAFNVSNQGVFKWVHFWKVAEGFGVAAAEFVNRCTLAEMMKDKGPVWDEIVKENGILPTTKLEDVGVWVFWDLILAGDGPLDTMKNKEHGLGFRNSQKAFISWIDKVKAKVVPV

NbL07g08010.1 omega-amidasechloroplastic-like [MW = 31.66 kDa]

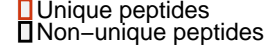
No. of times detected



log(intensity)



Values from



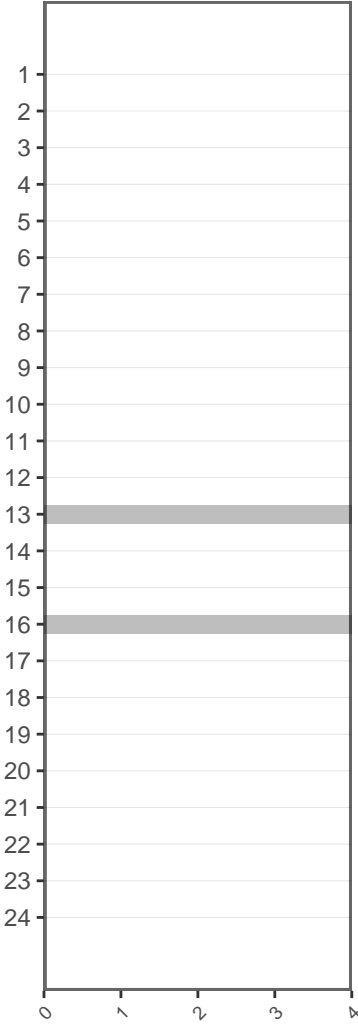
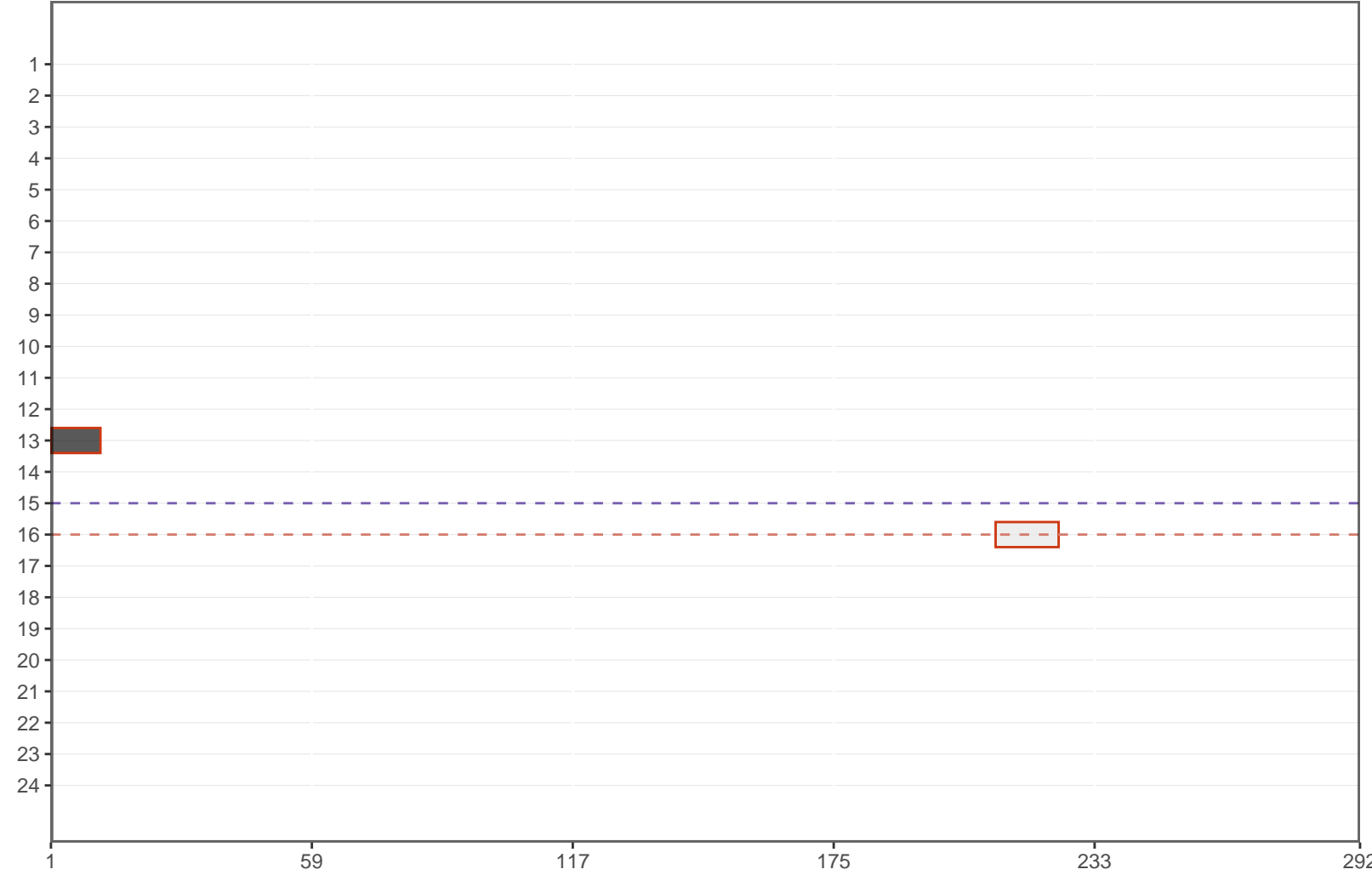
MW indication



Molecular weight



Gel Slice

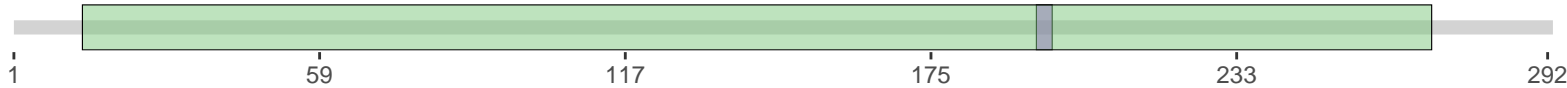


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

PLPLPEVDFKESDSHSAGDKPTVVDTFGGIGIGIGHDIRFAELAMYSARGAHLUCYPGAENMSTGAALWLEQRTRAVDNQLYVASCSPRDRSASGVYHGHSTVYGPMSGEIATTGHEEAVLIADIGVAAQLLARESPFLKSGRRDDHYQFVDLLG*

NbL07g08000.1 upstream_activation_factor_subunit_spp27-like [MW = 20.71 kDa]

No. of times detected



log(intensity)



Values from



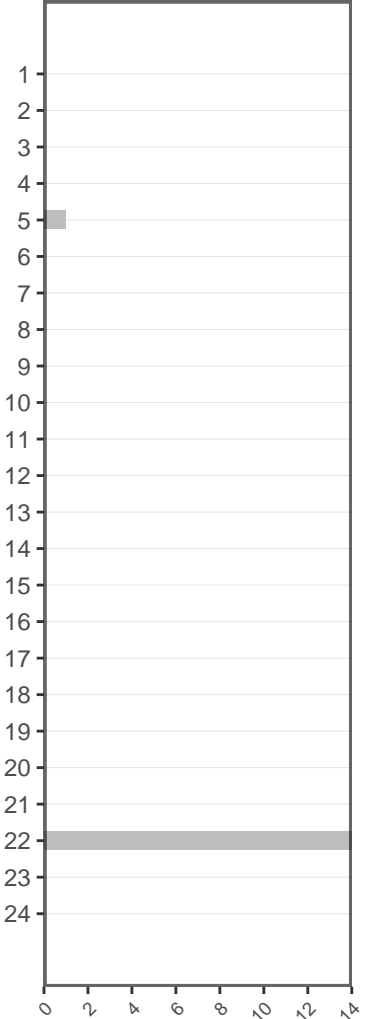
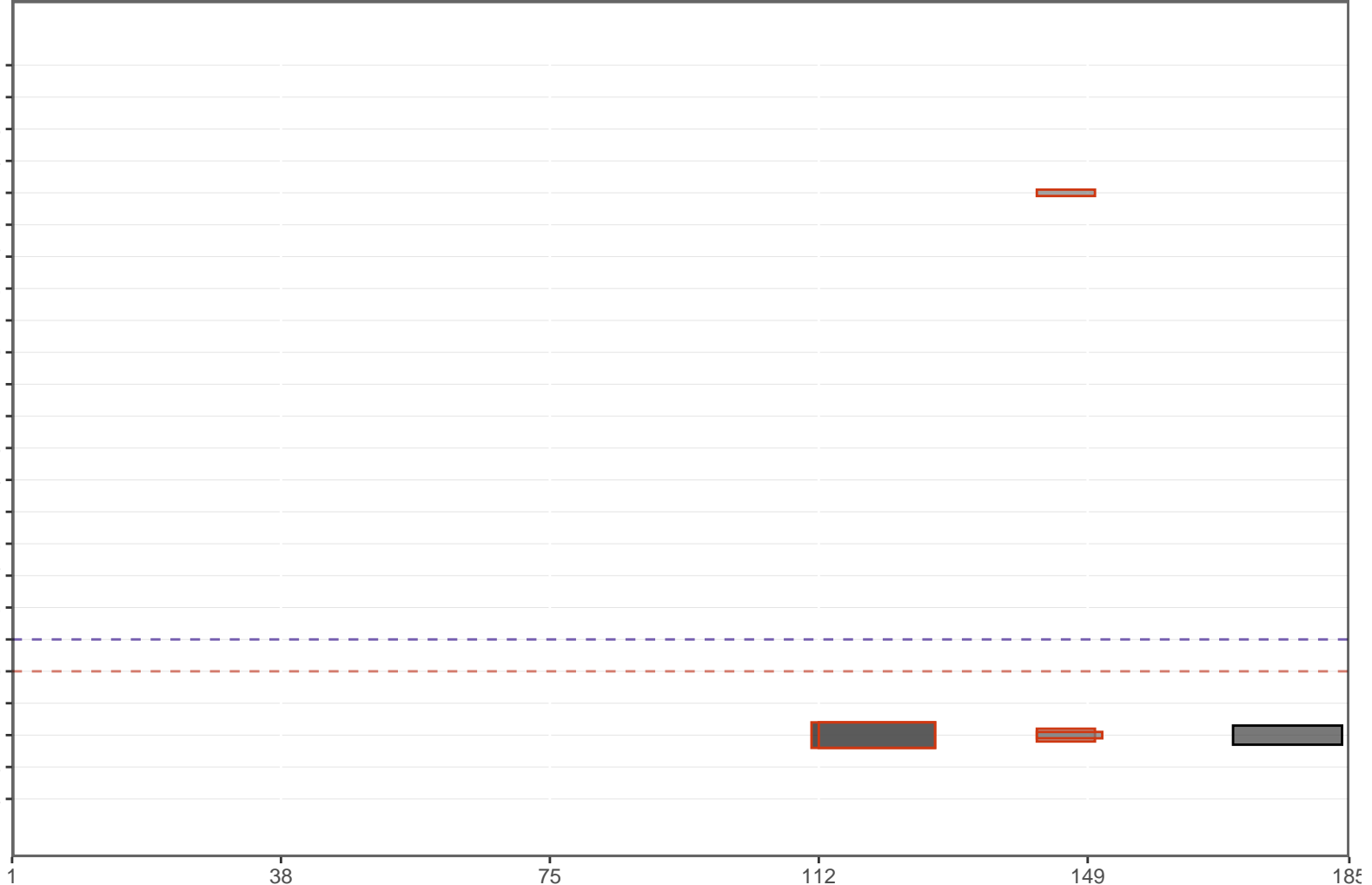
MW indication



Molecular weight

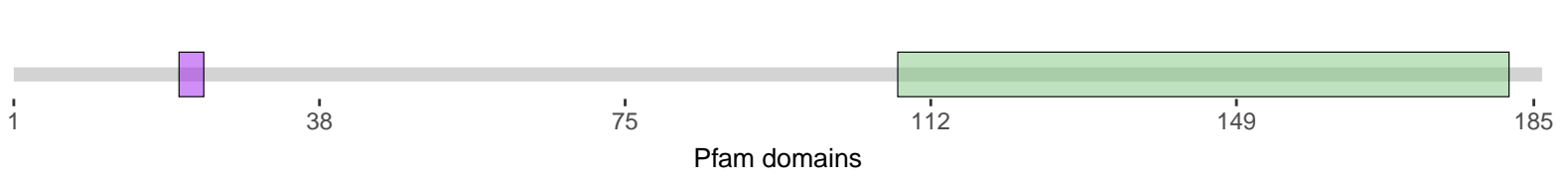


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LPRVRLMTFAASSKPKATTEPKRREPRGIMKRRVTPEDMDAFLGGLPKPRDQALKFWAHKKKLNQDPEDKQVWVQDEKLNIFGGRDRVGFLEIAGLISPHLKI

NbL07g07850.1 beta-ureidopropionase [MW = 46.63 kDa]

No. of times detected



log(intensity)



Values from



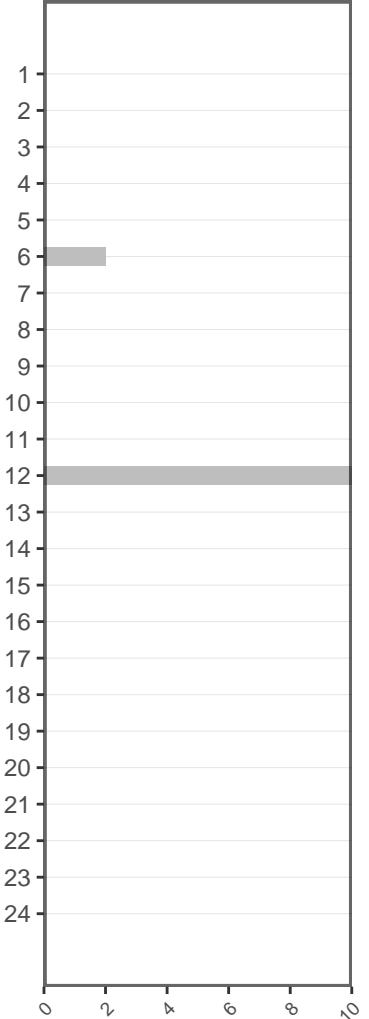
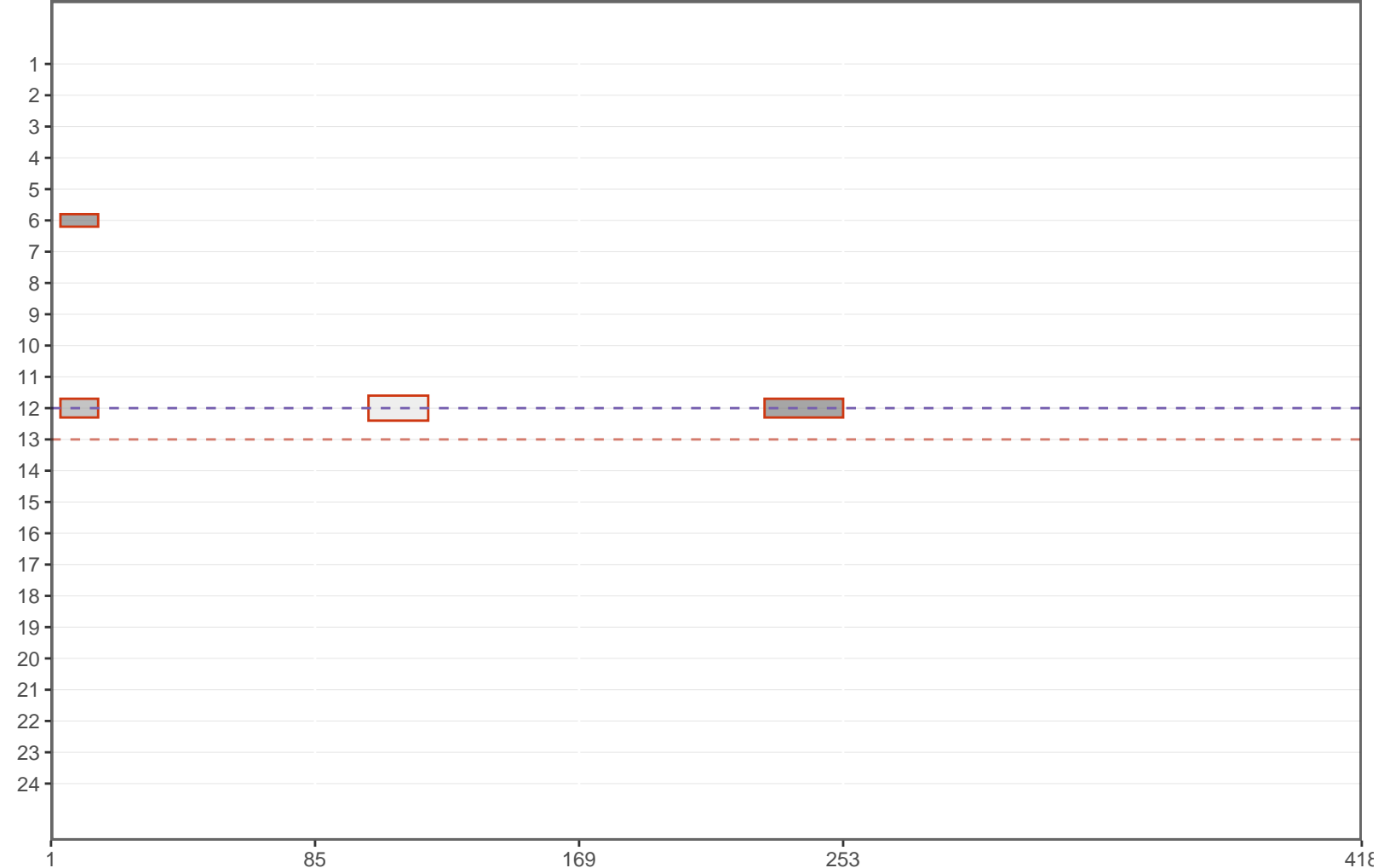
MW indication



Molecular weight



Gel Slice



Protein length

Pfam domains

Pfam Description



Protein sequence:

YHGELVNTAVIIGNNGNIKGRKHPRVGDFNESTYVMGENTGHVVFETAYGKAVNGYGRHHPLNWLAFLGNGAEIVFNSATVGLSEPMPIEARNAVAANSYFVGSINRVYGVTEVFNPFPSGDKPKQADFGHFYGSSEHFSAPDSGCTPBLSRHKDGLLISGMDLNLGRQLKEKWFGRMTARVYEVYADLLARYVWHDPEFGVIEDPLLYKNAI

NbL07g07720.1 porphobilinogen_deaminase_chloroplastic-like [MW = 39.35 kDa]

No. of times detected



log(intensity)



Values from



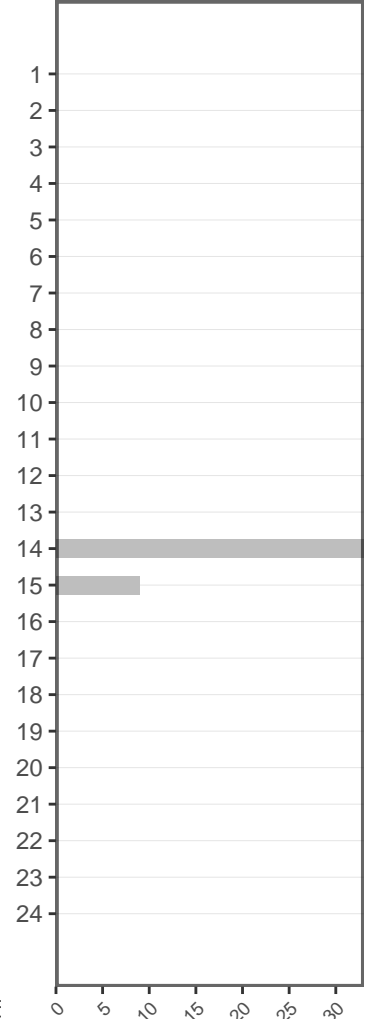
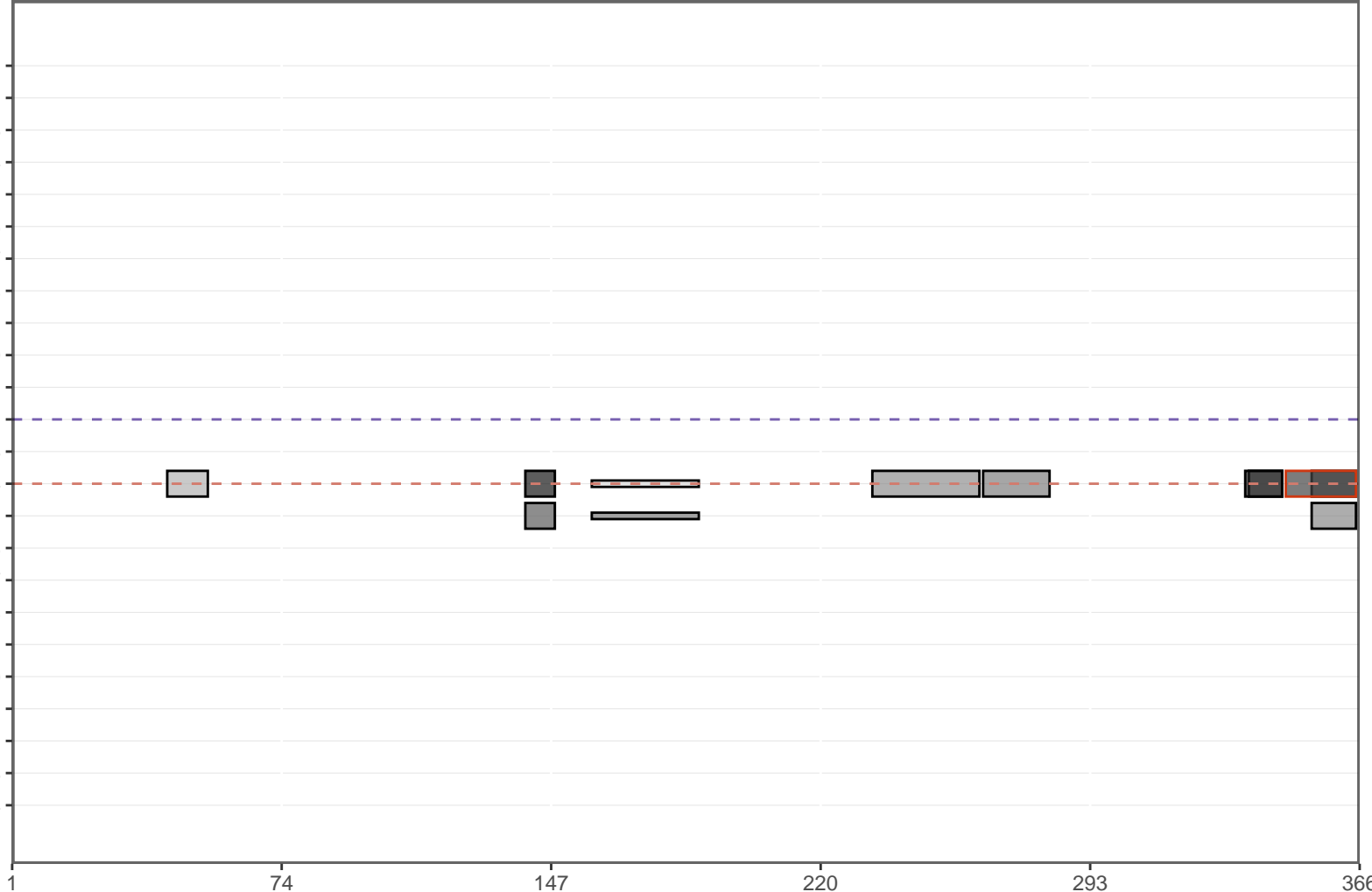
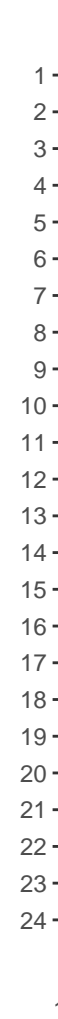
MW indication



Molecular weight

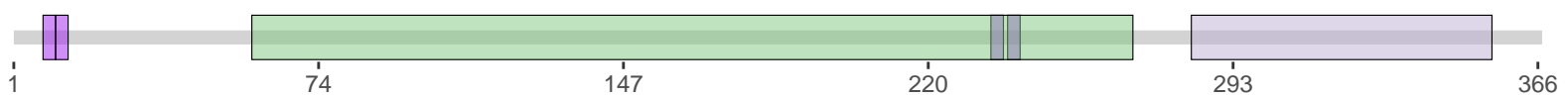


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01379 Porphobilinogen deaminase, dipyromethane cofactor binding domain
- PF03900 Porphobilinogen deaminase, C-terminal domain

Protein sequence:

IQLPSGSGTIGTASLRKRSQILHRYPBLNVLNFRNGVGRRLRKLNEGVGATLLALAGLKRMMTFENVTSLPFIEDMLPWAQGAAGAGRTDDETMANVYSLNHEETRLVACERAFKFLDSSGRTPIAGVACRGGEDGDFKGLVSPDGTTRVETSRKGPYTFEDMRMGEDAGKELLAEAGPFGFN

NbL07g07590.1 phosphoglycerate_kinase_cytosolic [MW = 42.32 kDa]

No. of times detected



log(intensity)



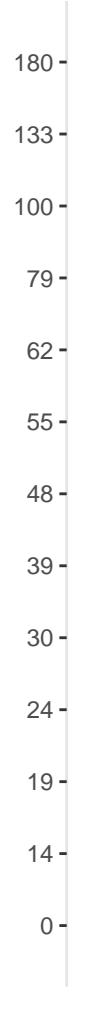
Values from



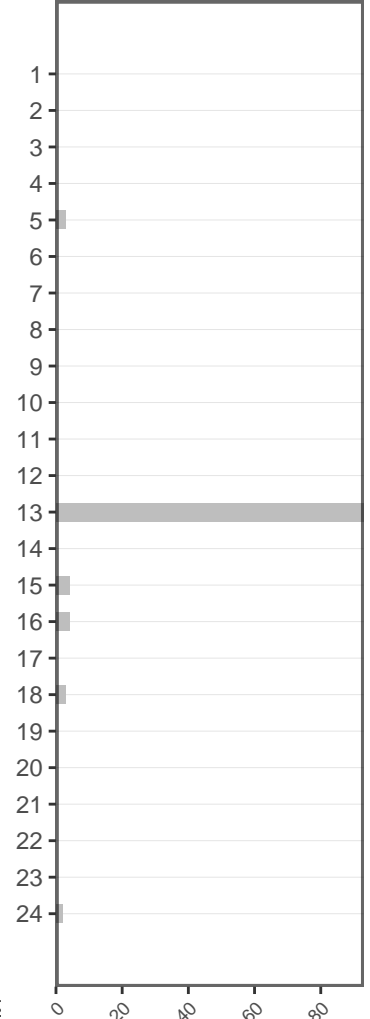
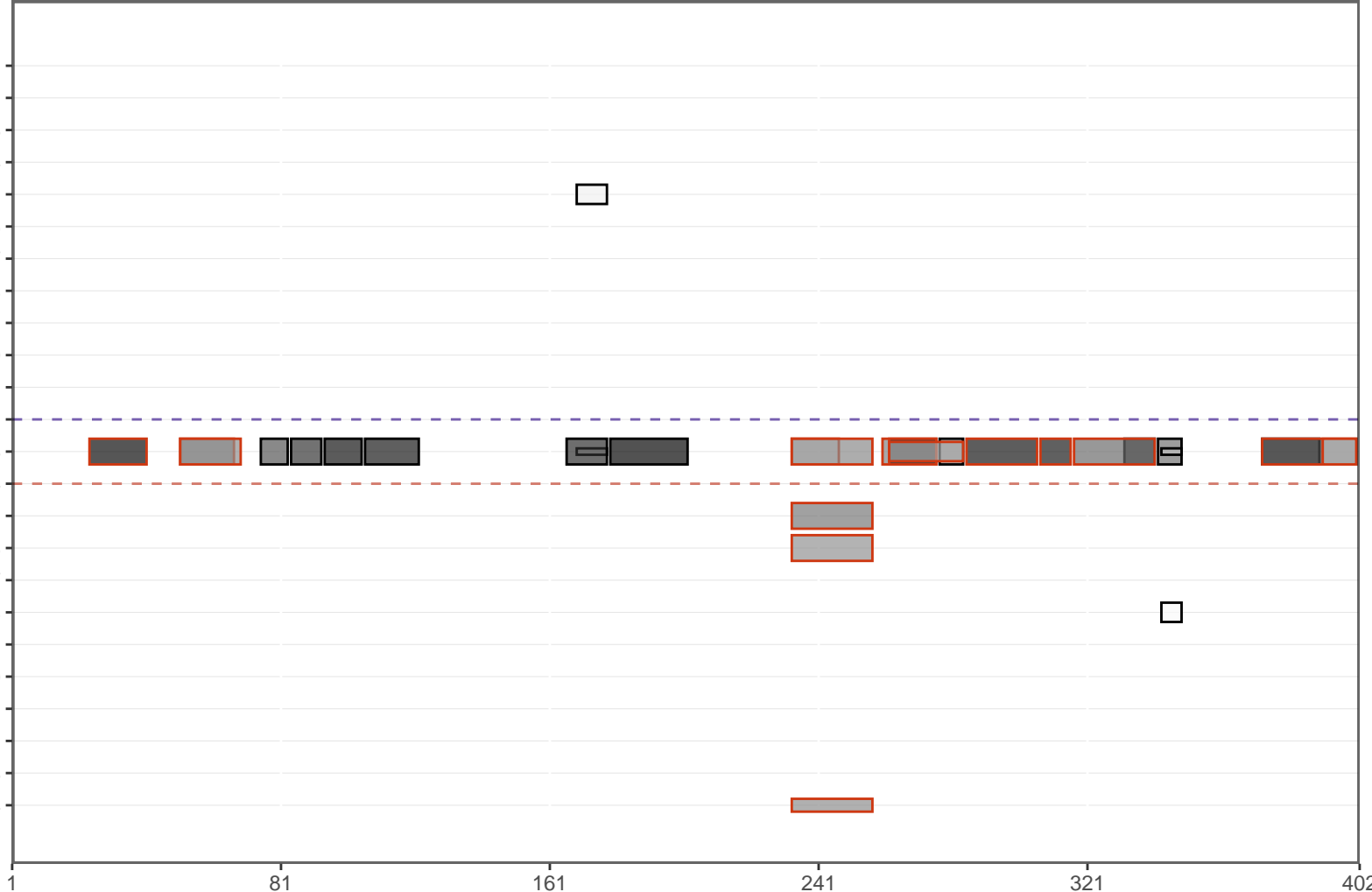
MW indication



Molecular weight

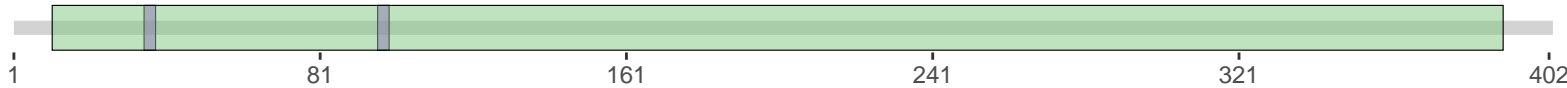


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

NPQKPFALVGGSKVSSKIGVIESLLEKVDKLLGGGMFTFYKAGGVAVGSSLVEEDKLDLATSLEKAKAKGVSLLPDVAADKFAADANKVWPAEIPDGVWMLDHPDAKFSFGSALDTRKTVWNGPMGVFEFDKFAAGTEAAKLAELSGKGVTRTIGGGDVAAVKVKVLAEKMSHSTGGGASLELEKPLPGVLAALDDA

NbL07g07580.1 phosphoglycerate_kinase_chloroplastic [MW = 51.12 kDa]

No. of times detected



log(intensity)



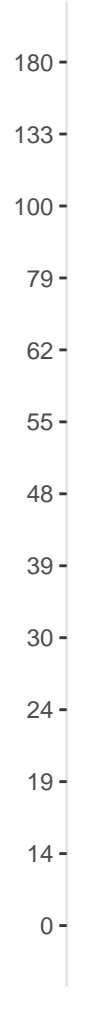
Values from



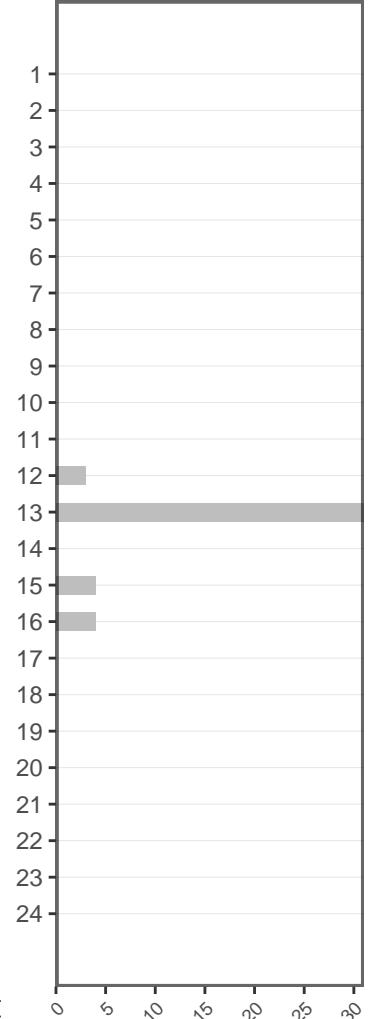
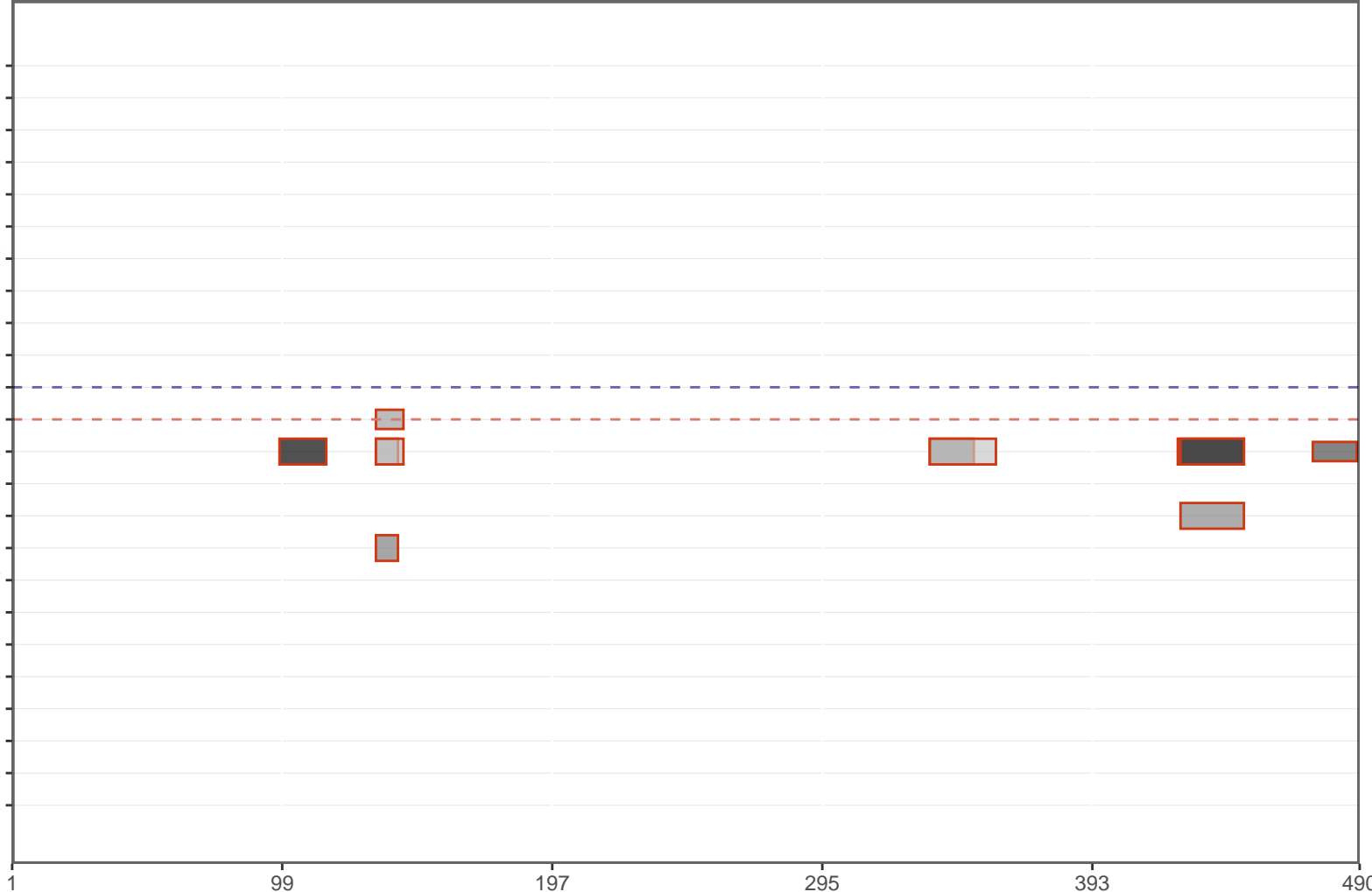
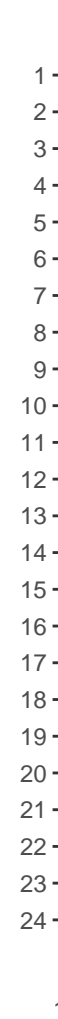
MW indication



Molecular weight

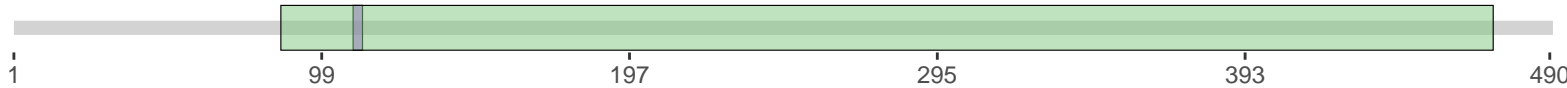


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ASTEGVTKFLKPSVAGLLQKELDLVGVSNPKRFFAAVGGGKVVSSKIGVIESLLEKGDLLGGGMFTFYKAGLSEVGSLSVEEDKLELATSLEKAKKGGVSLLLPGEVVIADKFAFDANRKMCMSEFSHIVPSAIPDGVWMLDGLDPSDKVKTNDALDTTKTVWNGPMGVFEFDKFAVGTAEANKLDLSEGEVTTTIGGGDSVAVERKGVAVSMVSHISTGGASLELEKGLVQVIALDEADAPVAV

NbL07g07200.1 glucose-1-phosphate_adenylyltransferase_large_subunit_2_chloroplastic/amyloplastic-like [MW = 61.7 kDa]

No. of times detected



log(intensity)



Values from



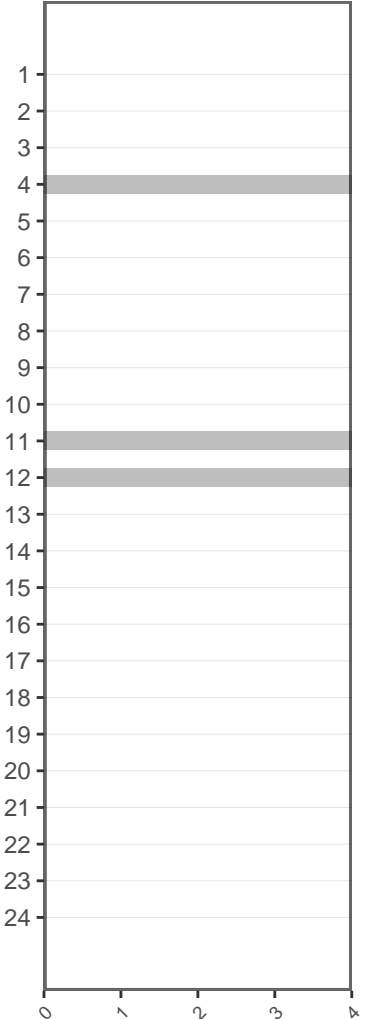
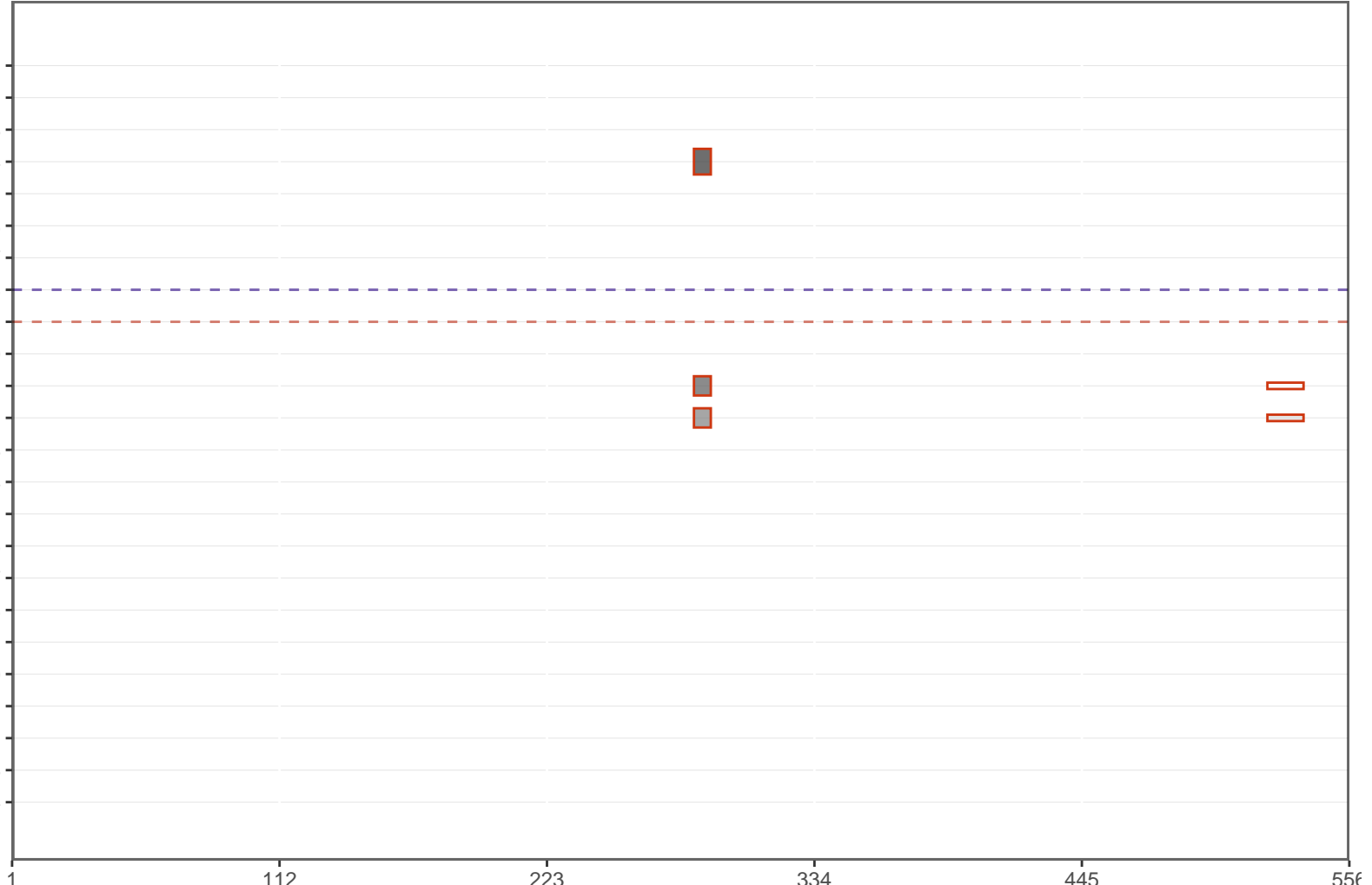
MW indication



Molecular weight



Gel Slice

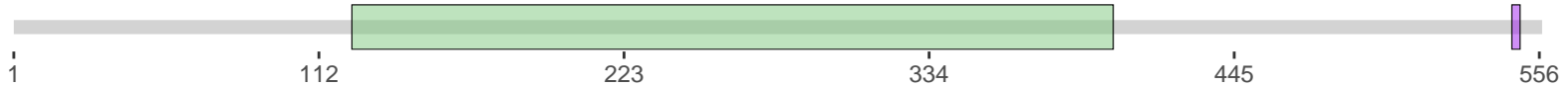


Protein length

Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

KXHNINADITYSCVPIVDGSRASDFGLVKEETGRIGFAEKPKGPKLAKMGVDTBLGLSEGEAAKSPYIASMGVYVRRTEVLLKLLKSGAYPSGNDGSEIHPISAVKDHNVGALVFSQYVEDIGTVKSFDDANLALTEGPPKFDNFDPKTRPFTSPRFLPPTKVKSRIVDAIHSHGCFMRREGSIGHSGVGRSLEDEYGVSKDTHMMMGADYYQTDSEIASLLAEGNVPMGVGSPNPKQNGKDKNANIGKDFRIGNKEGVVEEAERPNEGFEYRSGFTVMKNATKQGTI*

NbL07g06740.1 isoamylase_3_chloroplastic [MW = 86.88 kDa]

No. of times detected



log(intensity)



Values from



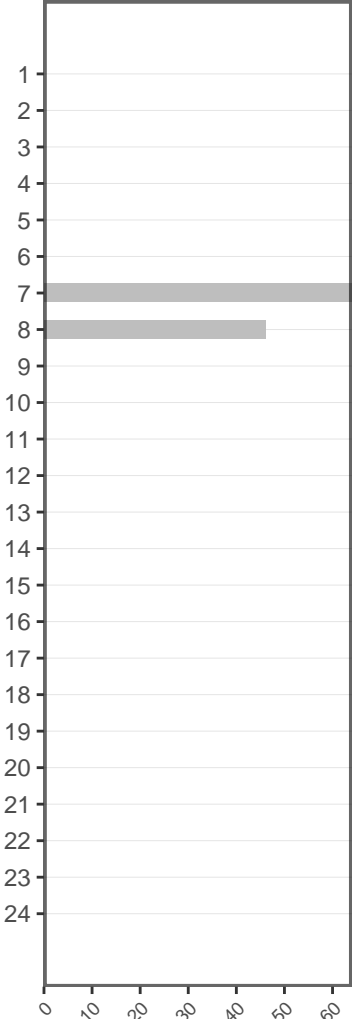
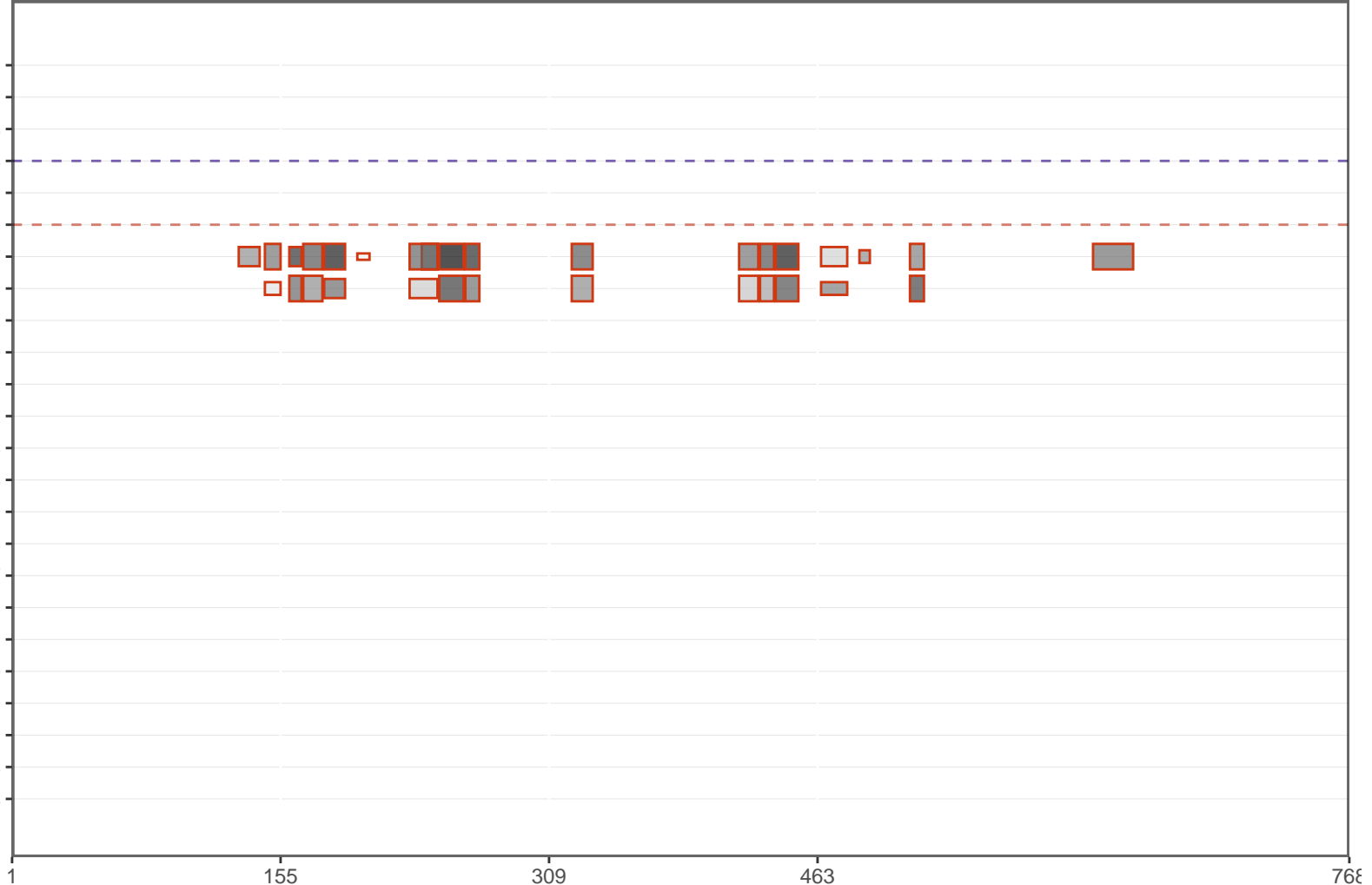
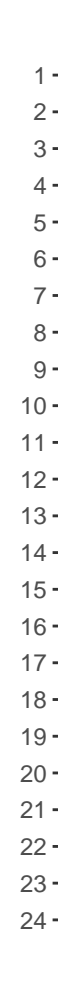
MW indication



Molecular weight

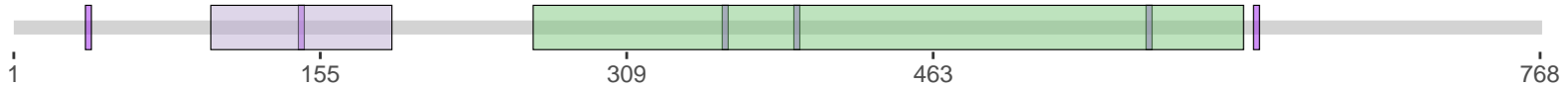


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IKVYYMVDLNNNGQLNFSGGGNTFNCRHPVMELESLRHVWTEYHYDGRFDLASVLRGTGDTPIINAPPLVKAIAKDSVLRGKIAIEPNDGGGLVKGKFNWDRWAEWNGKYRDDNRFRFKGDAGMKGNFATRWAGSADLYRVNKRKPKYHSVNFVIAHDGFTLVDLVSYNSKINDANGEGNDGGNDNFVSKNGGIEGETSDANIFALRSRQMKNFHIALMGGGTPMMLMGDEYGHTRHGNNSVYGHDTAINNFQWGLEAKNDHFRFFSKMIKFRQSHS

NbL07g06650.1 proline-rich_receptor-like_protein_kinase_PERK1 [MW = 69.69 kDa]

No. of times detected



log(intensity)



Values from



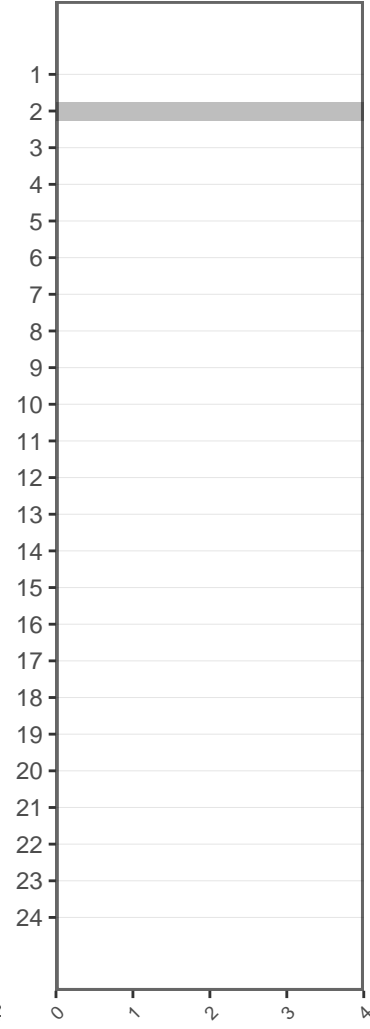
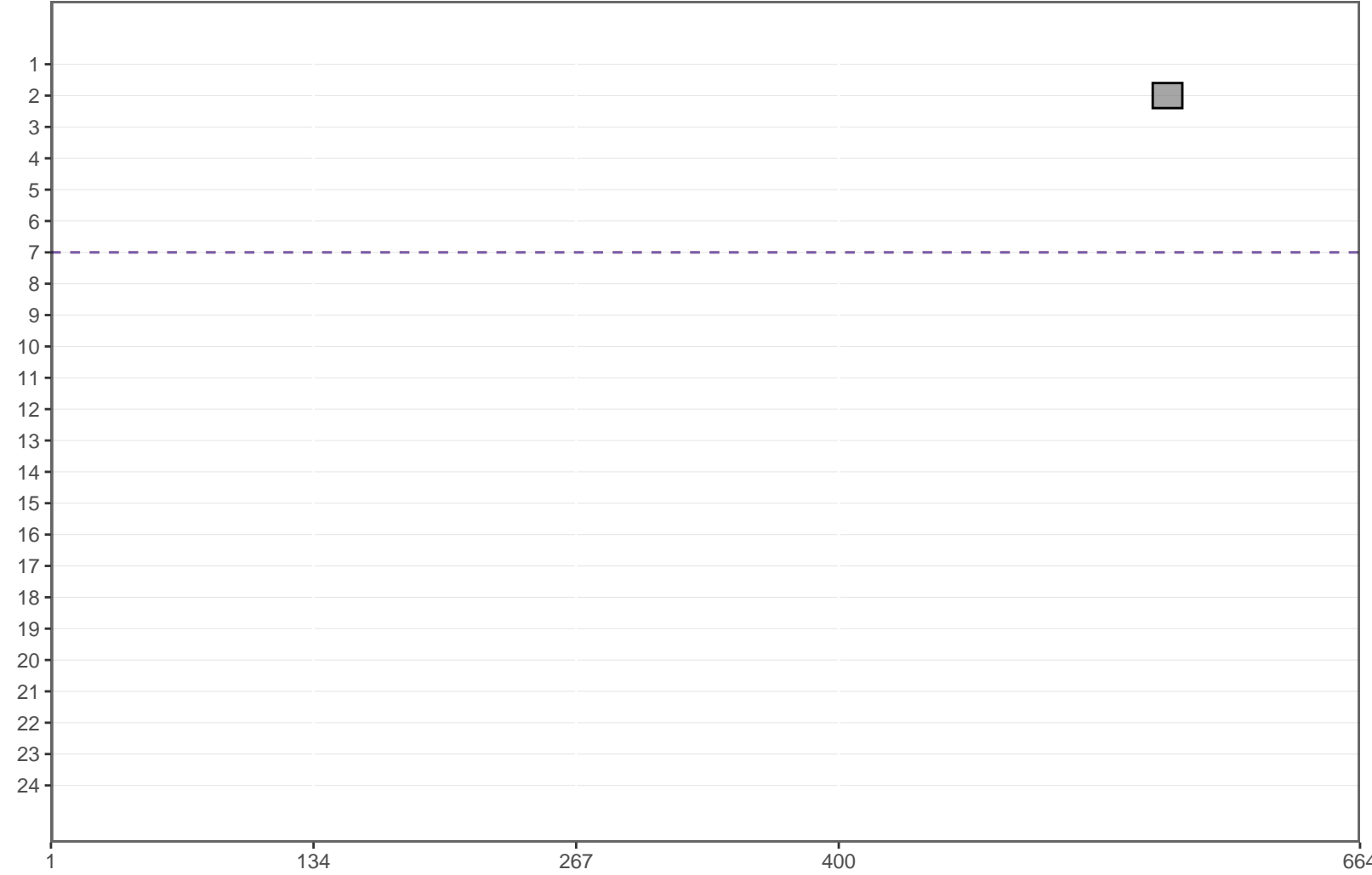
MW indication



Molecular weight

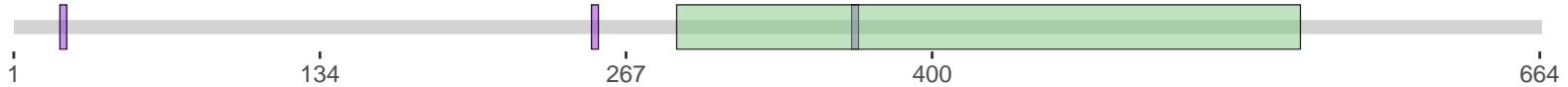


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGSGOGEREFQAEVEISRYVHKHLVSLVGVYGTGSRLLVYEFVFNNTLEFHLHGKGRPLDWPFRILKIALGEAKGLAVLHEDCGPKIHRDKAANKLIDFNFEAKVADFGLANLTSQVANTHVSSTRVMGTFGYLAPEVASGKLTENSDVFSYGMILLELTGRRPVDSGGTYMDDSLVDWARPQLTRALEDEKFDLSLDPRLGNVDYHNEVARMWCAACVRIHARRRRPRMSGVVRALEGDVLSLSDLNKGRPGHSTVYSHGSSDYDASQVNEEDMKFRKTALGSDQYIG

NbL07g06540.1 GEM-like_protein_1 [MW = 32.31 kDa]

No. of times detected



log(intensity)



Values from



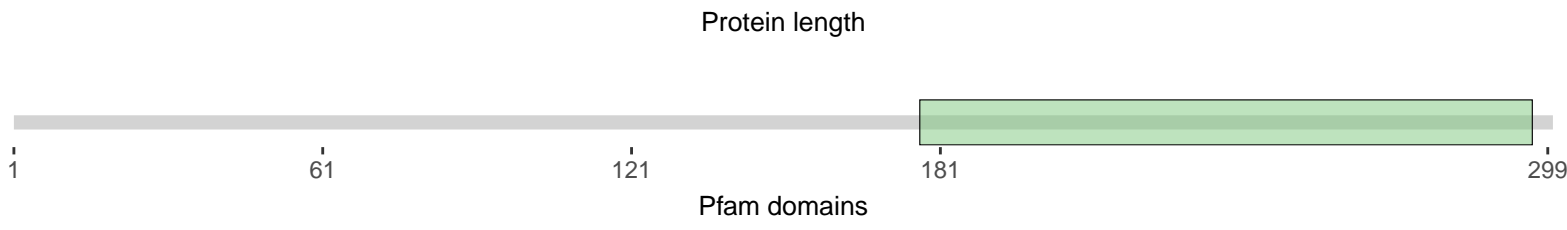
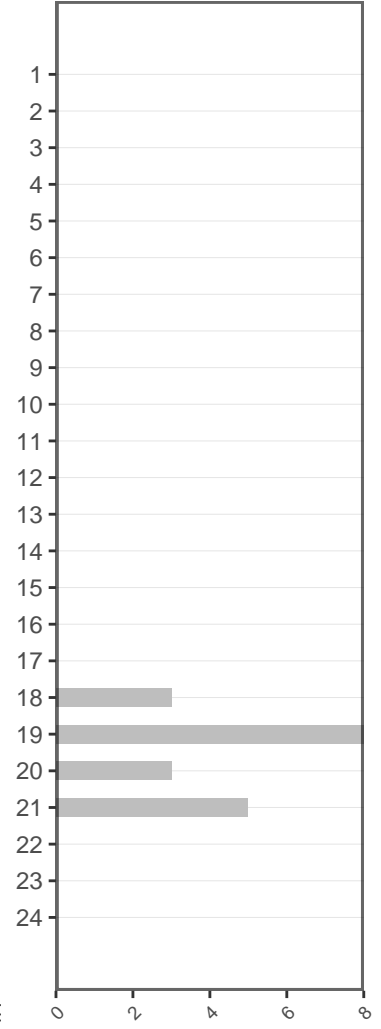
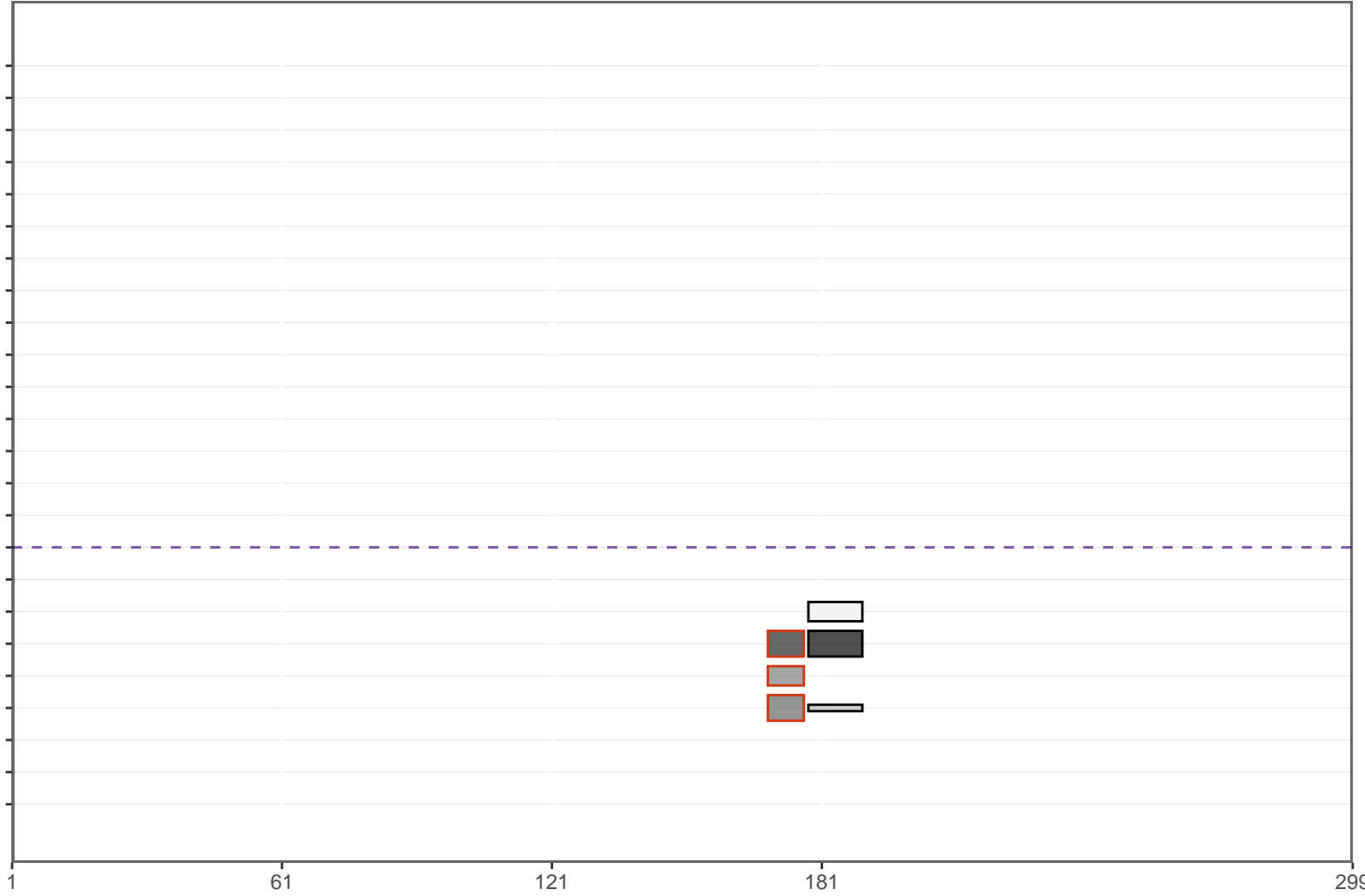
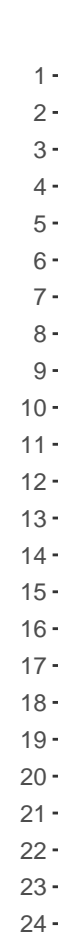
MW indication



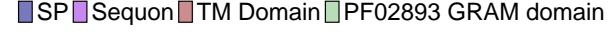
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

TKKAEDLAGNIMVGHKLTSPSLADAAAMSRIGAGTKVLAEGGVEKVFQGTFTETVPEEKLFKNSWADYLSSTAGPVMGVVLSLTKLAFGSNPLKYGDRTEYSSVYVWLPVLDGLKASPTSKNPKPKYQHSVDNHEFEWFMGFVNYDSAVKNLGGALLGHHS

NbL07g06500.1 3-hydroxyisobutyryl-CoA_hydrolase-like_protein_3_mitochondrial [MW = 41.64 kDa]

No. of times detected



log(intensity)



Values from



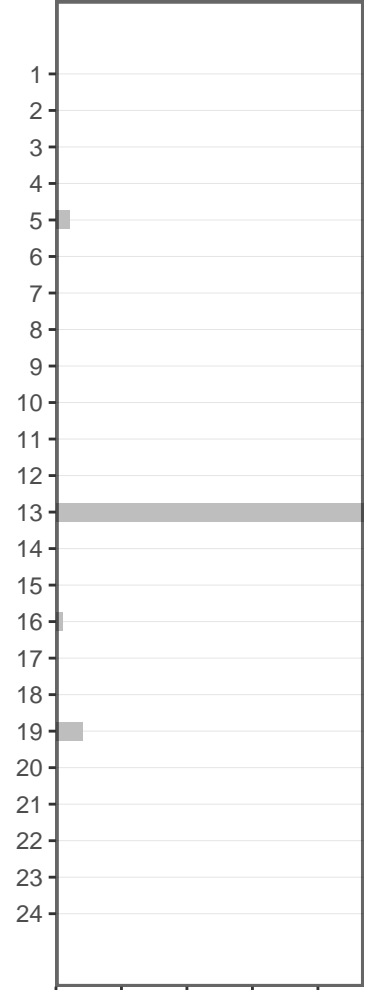
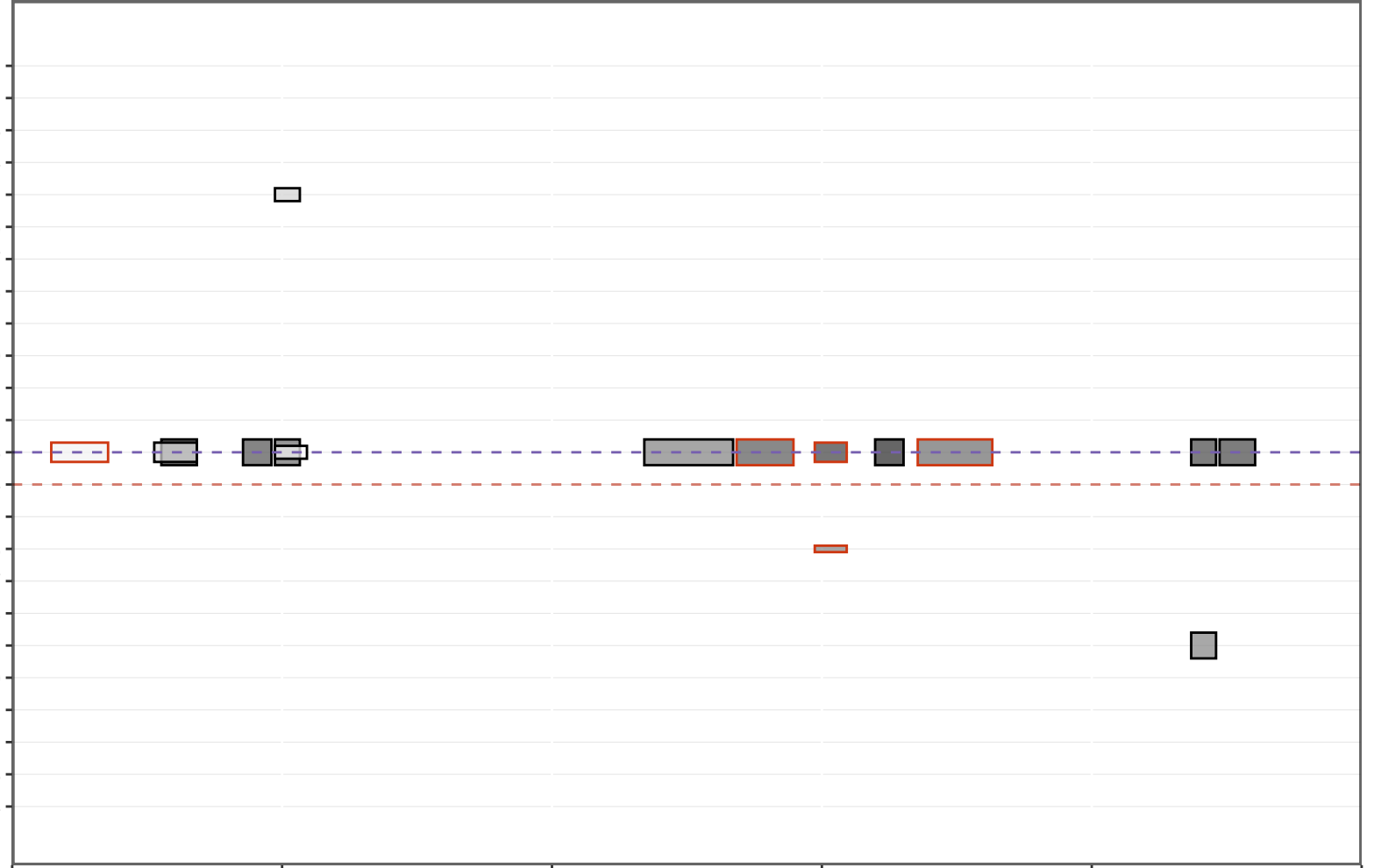
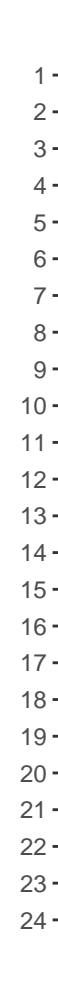
MW indication



Molecular weight



Gel Slice

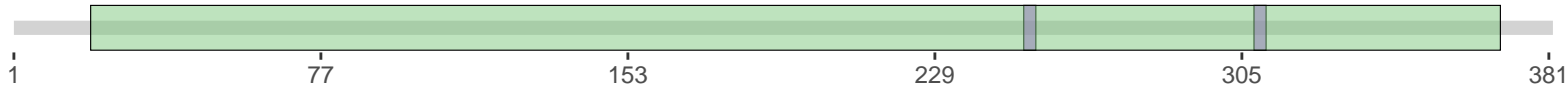


Peptide counts over 4 repeats

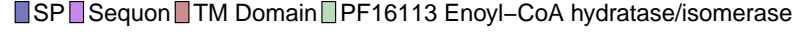
Protein length



Pfam domains



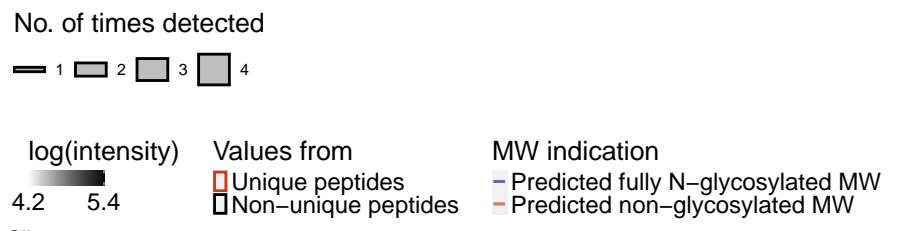
Pfam Description



Protein sequence:

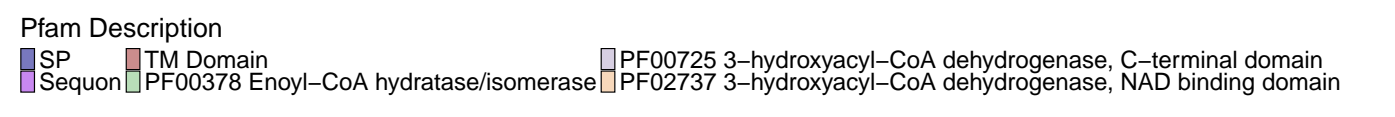
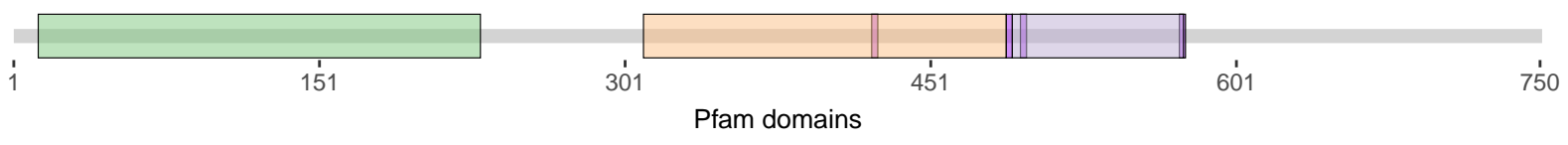
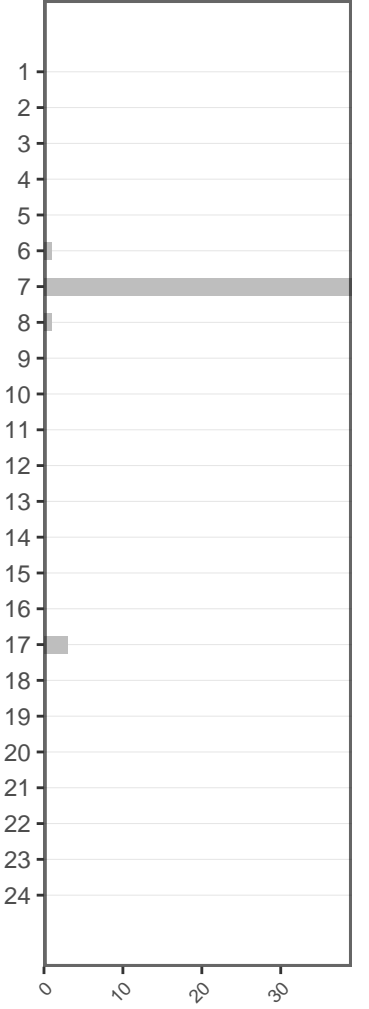
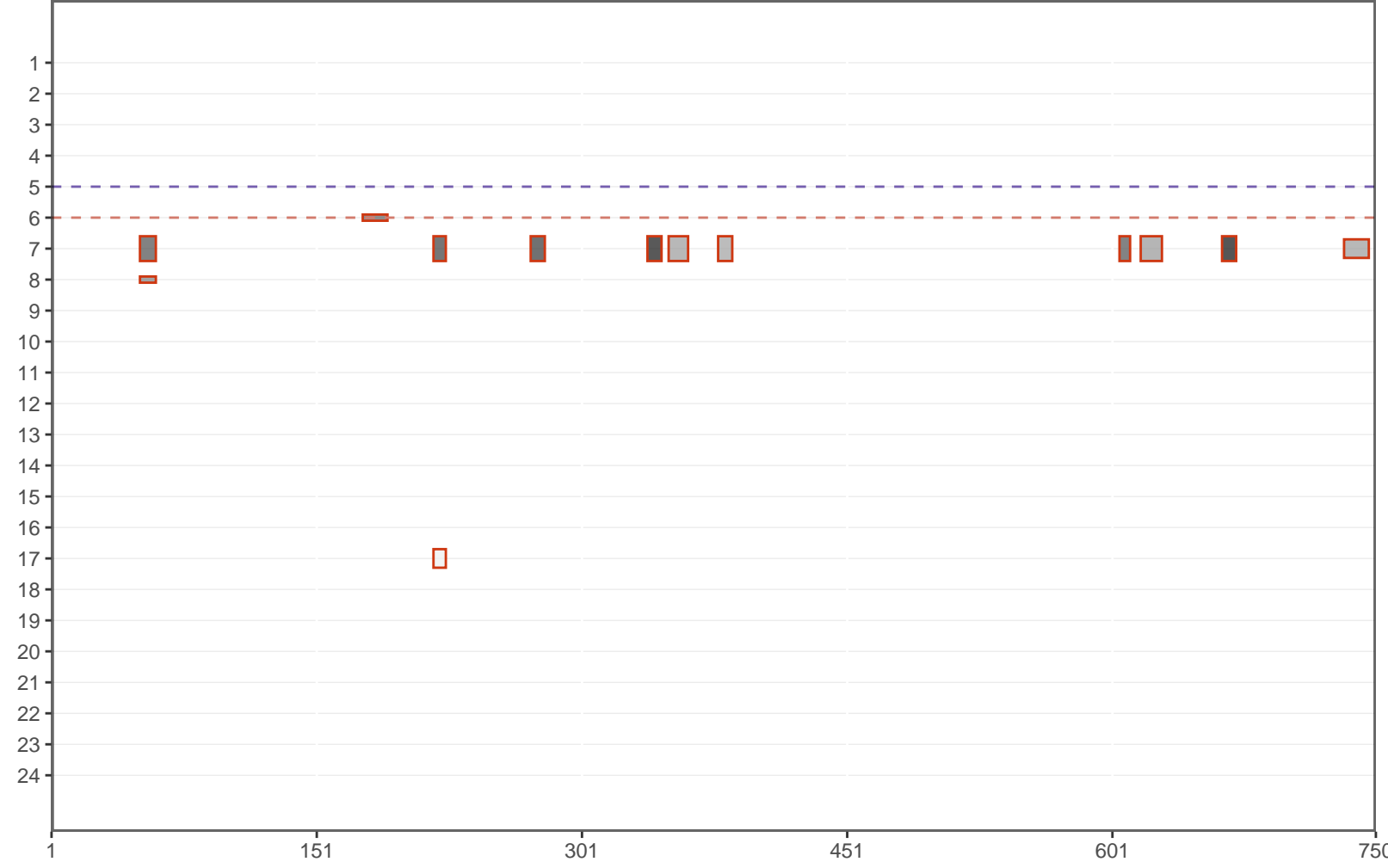
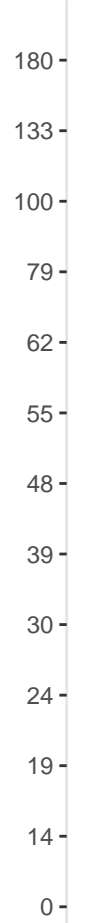
SRISTPADALYVGLGSHYVPSANLDTLKEAFLAATFSGDDPDEIKTLLEKYSDPDSERLKLPLRIISTFGNKSVMNIEELDNHGGSDTLVAEWAKDALGGLRKGAPFLGLTGGYVFSRIVASAGGNKNESTLKLPLVVMRTEYRIARBSALRNDFAEGVRAILVKGDNPRVWNPSSLEEVNNEVEVLFPELSPVELNV

NbL07g06420.1 peroxisomal_fatty_acid_beta-oxidation_multifunctional_protein_AIM1-like [MW = 80.69 kDa]



Molecular weight

Gel Slice



Protein sequence:
 .VARKLPGQKADKALSMKGLDYSDFKQDVAIEAVIENIPLKGIKIFSEIEKVGPPHDLASNTSTFDLNVIGENTRSKDRIGAHFFFSAHIMPLEIVRTEKTSAGAILNLMVAGKAKKVPVYVGNCTGFANRTFFPAQGAHILANLGVDIRBDAQITNFGLMGPFQDLDLTYGVAWWWGKEFRBAFSDRTFKSPLDILLKSGRNGSVAFFLWVAGSEVLLSTDTGFGAGNNGKGYIYKGRKRPDQFTVLPHEGRRLTNMPPGKPIVTDQEVEMLFPVNEAC

NbL07g06380.1 peroxiredoxin-2B-like [MW = 19.05 kDa]

No. of times detected



log(intensity)



Values from



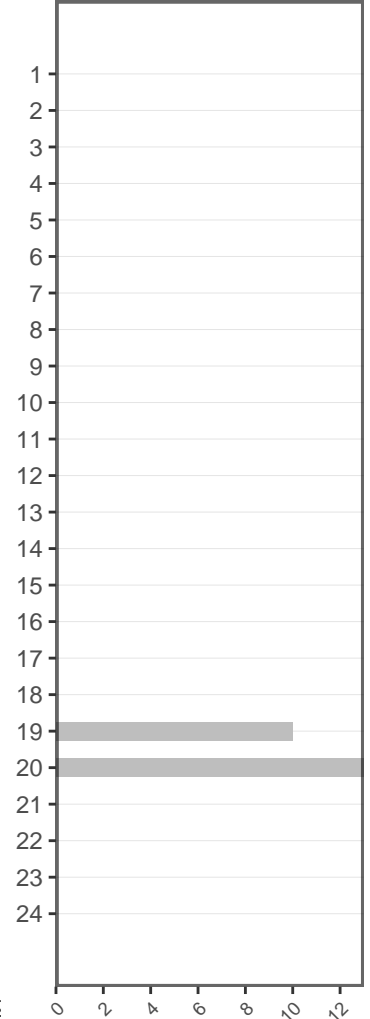
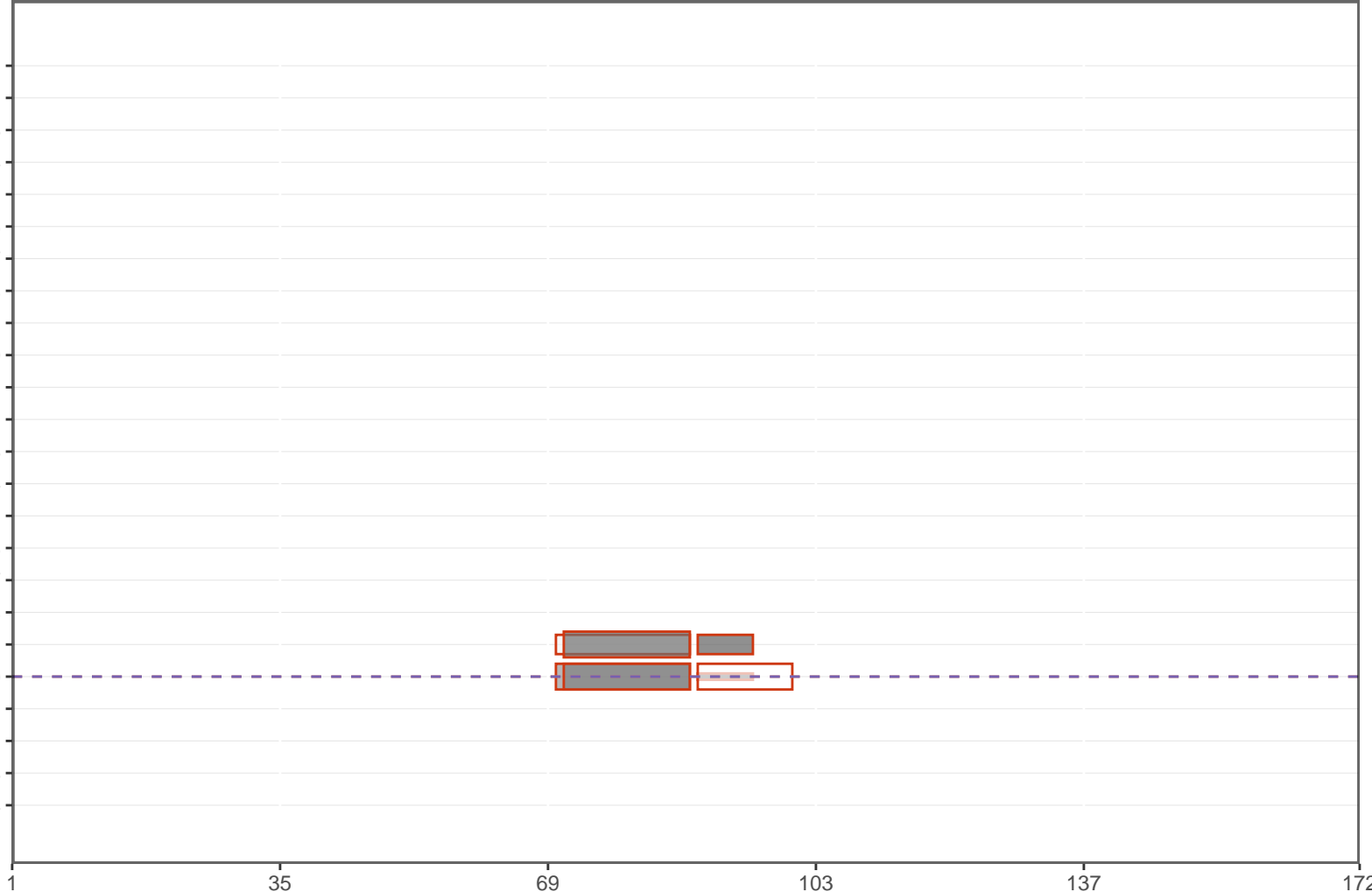
MW indication



Molecular weight

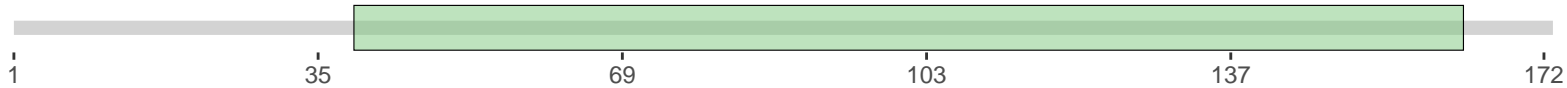


Gel Slice



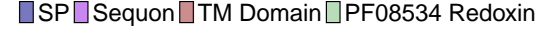
Protein length

Peptide counts over 4 repeats



Pfam domains

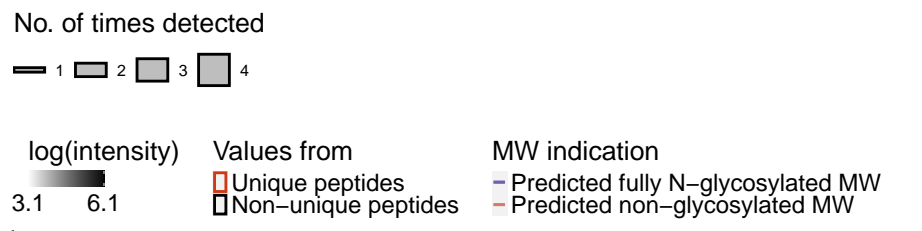
Pfam Description



Protein sequence:

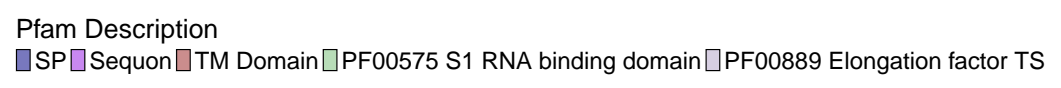
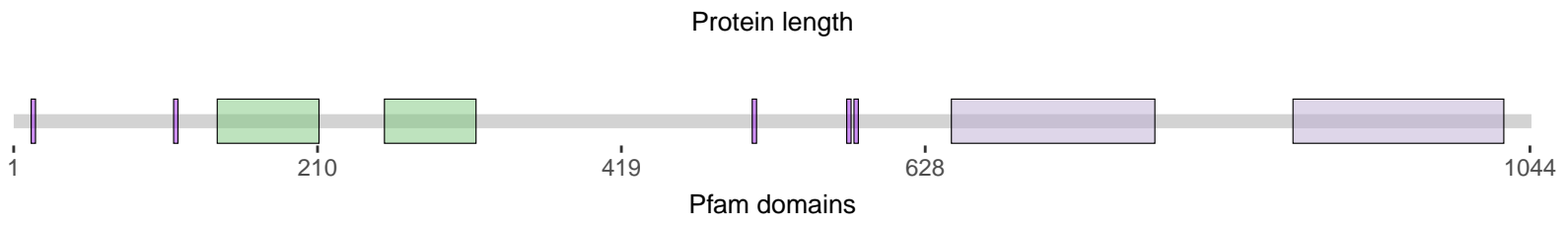
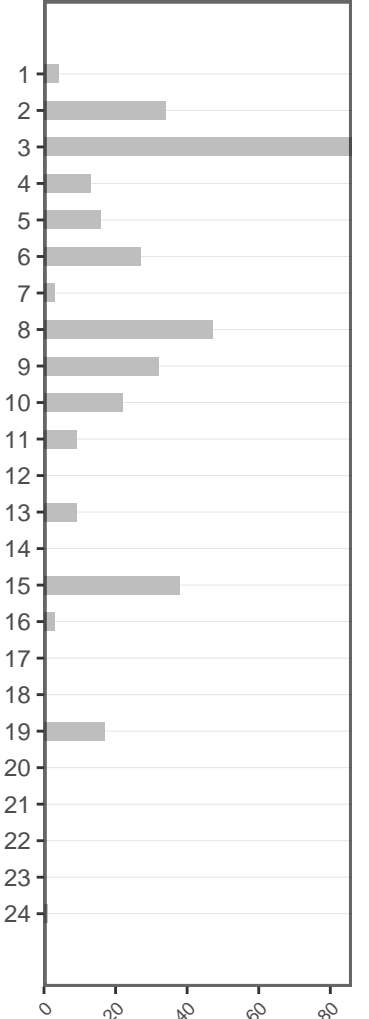
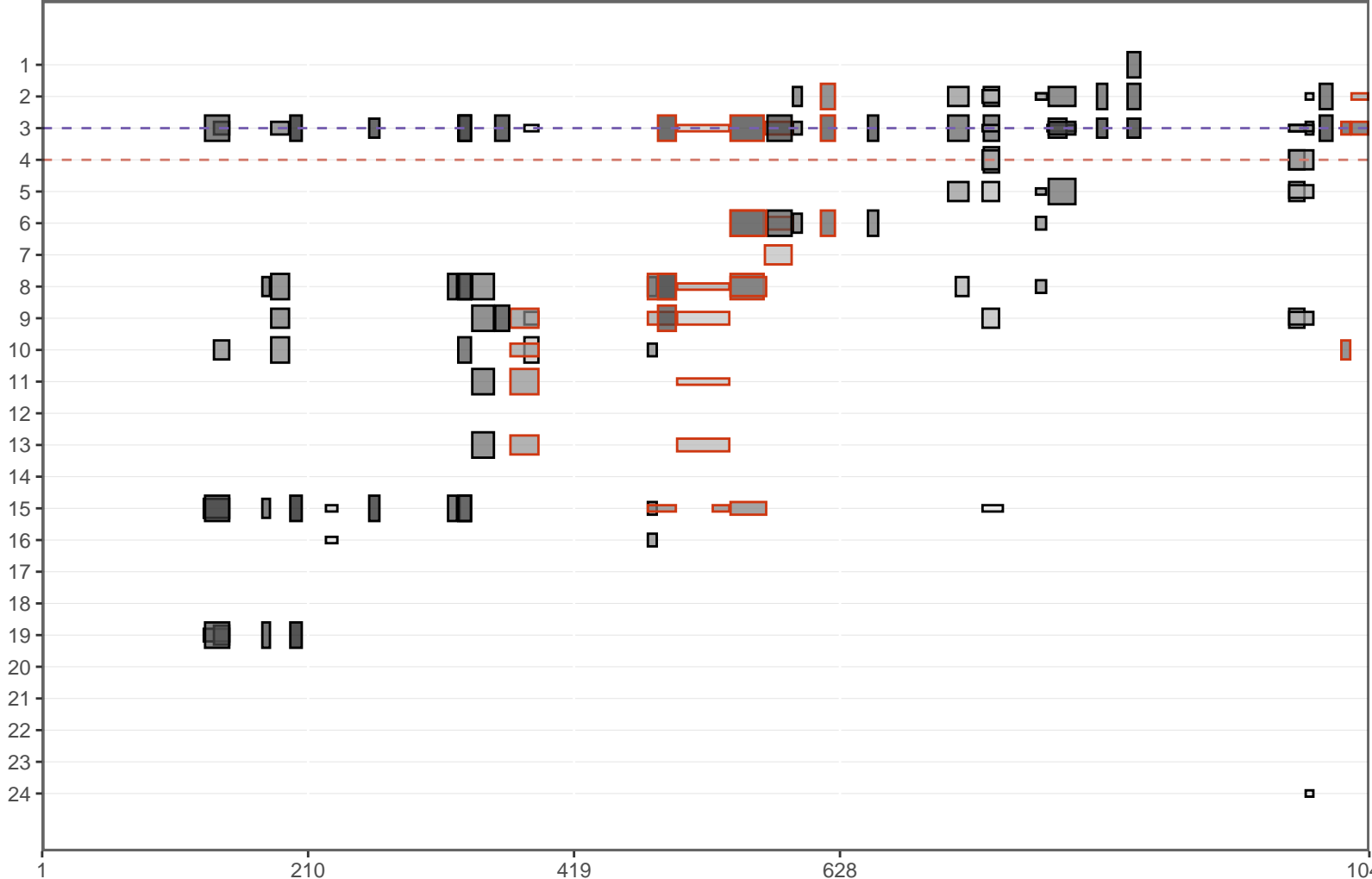
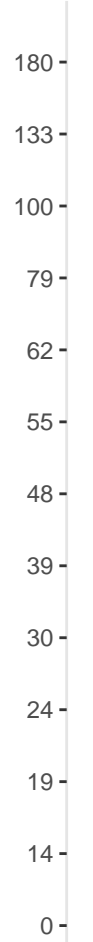
AVPGAFPTCTCKHVPGFIEKADELKBEKGVDEILGIEVNDPFVYMKAWKEKYPDNKHVKFLADGAGKYTHALGLELDLSEKGLVDFLEGLMFLWLRTR

NbL07g06340.1 uncharacterized_LOC104245598 [MW = 113.69 kDa]



Molecular weight

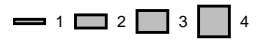
Gel Slice



Protein sequence:
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NbL07g06070.1 NADPH--cytochrome_P450_reductase-like [MW = 78.44 kDa]

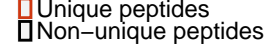
No. of times detected



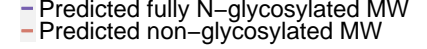
log(intensity)



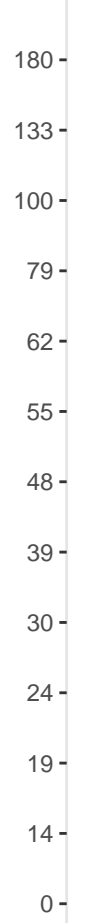
Values from



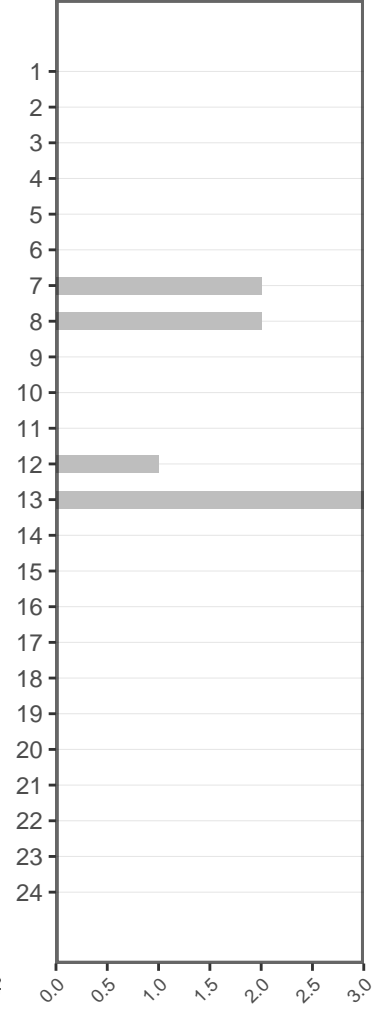
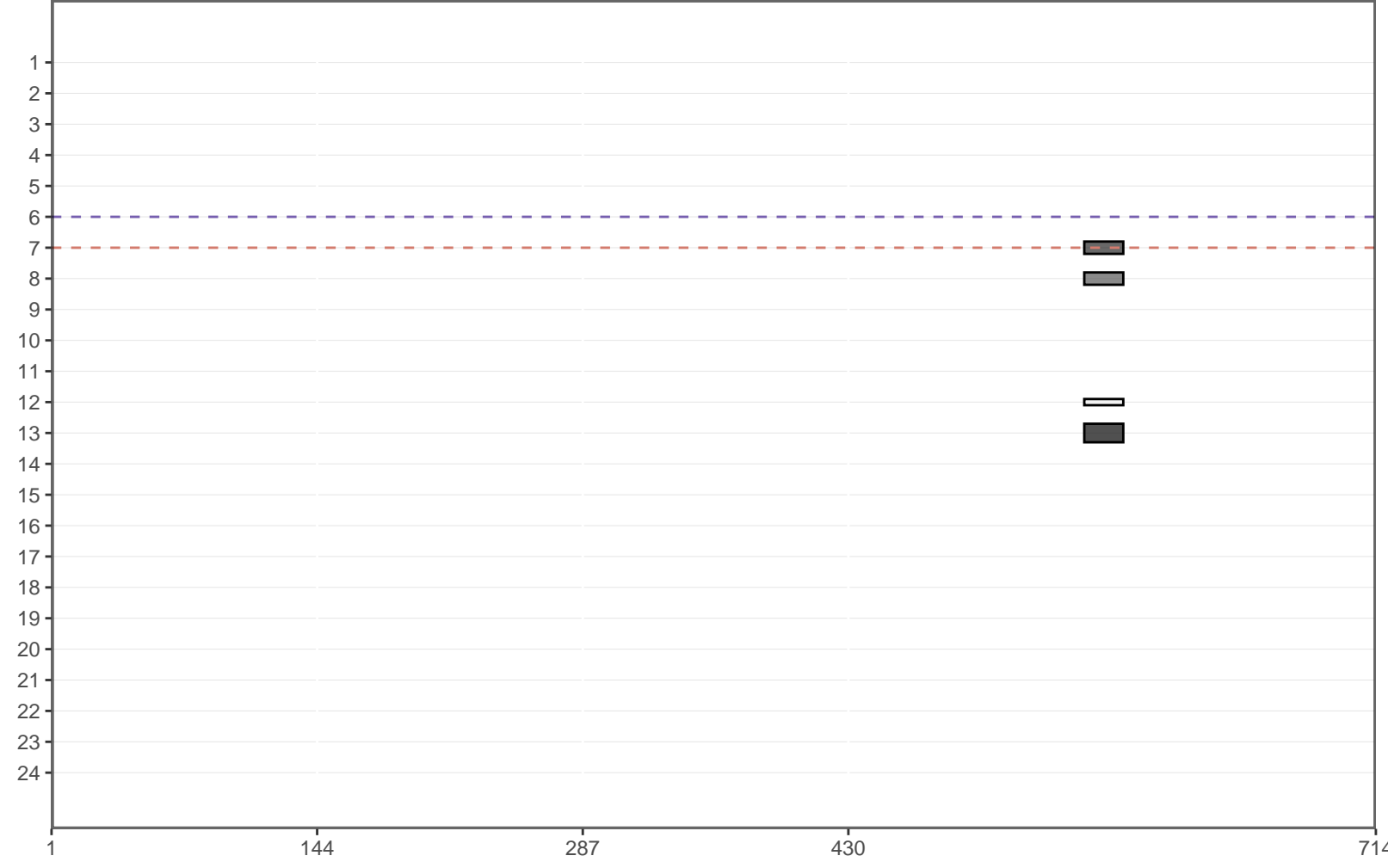
MW indication



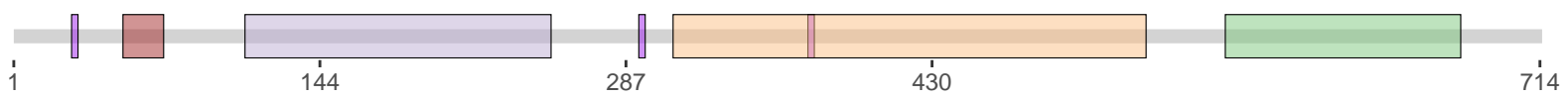
Molecular weight



Gel Slice

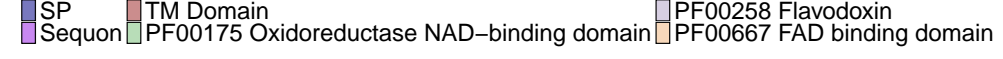


Protein length



Pfam domains

Pfam Description



Protein sequence:

LVYETGDHGVYCYENLIETVEEAERLLNISPDFFSHITDKVDGTPLEGSSLPSPFPFPGTLRTRALTRVADLLSSPKKALLAAGASDPNEADRLNLAAPKGEYQVWVASGRLLLEVMAEFSPAKPSLGVFFASVAPRLQPRFYSISGSHRMAPSRHVTGALVYDKMPTGRVHKGVGSTMKNVPLEEELSGSAAPFVROGNEKLPADNKVPIIMGPGTGLAFRRGFLGERLAKNEGAEIAPVLFSGRNRGMQVYQEEIINFLKANGAISELVAFSRREGPK

NbL07g06060.1 (DL)-glycerol-3-phosphatase_2 [MW = 27.26 kDa]

No. of times detected



log(intensity)



Values from



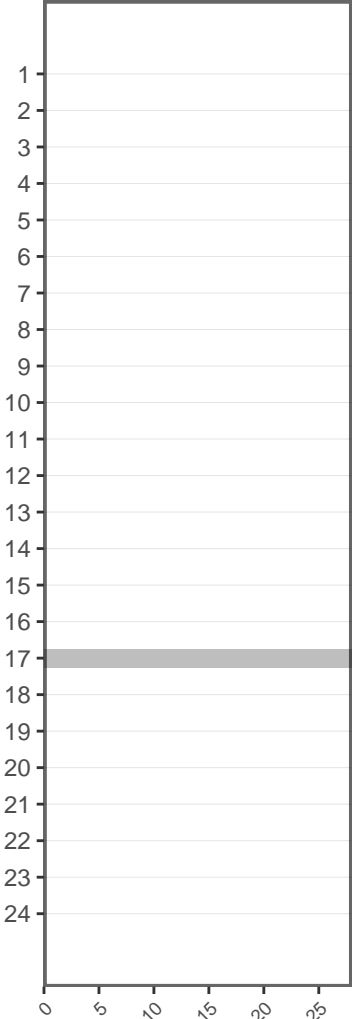
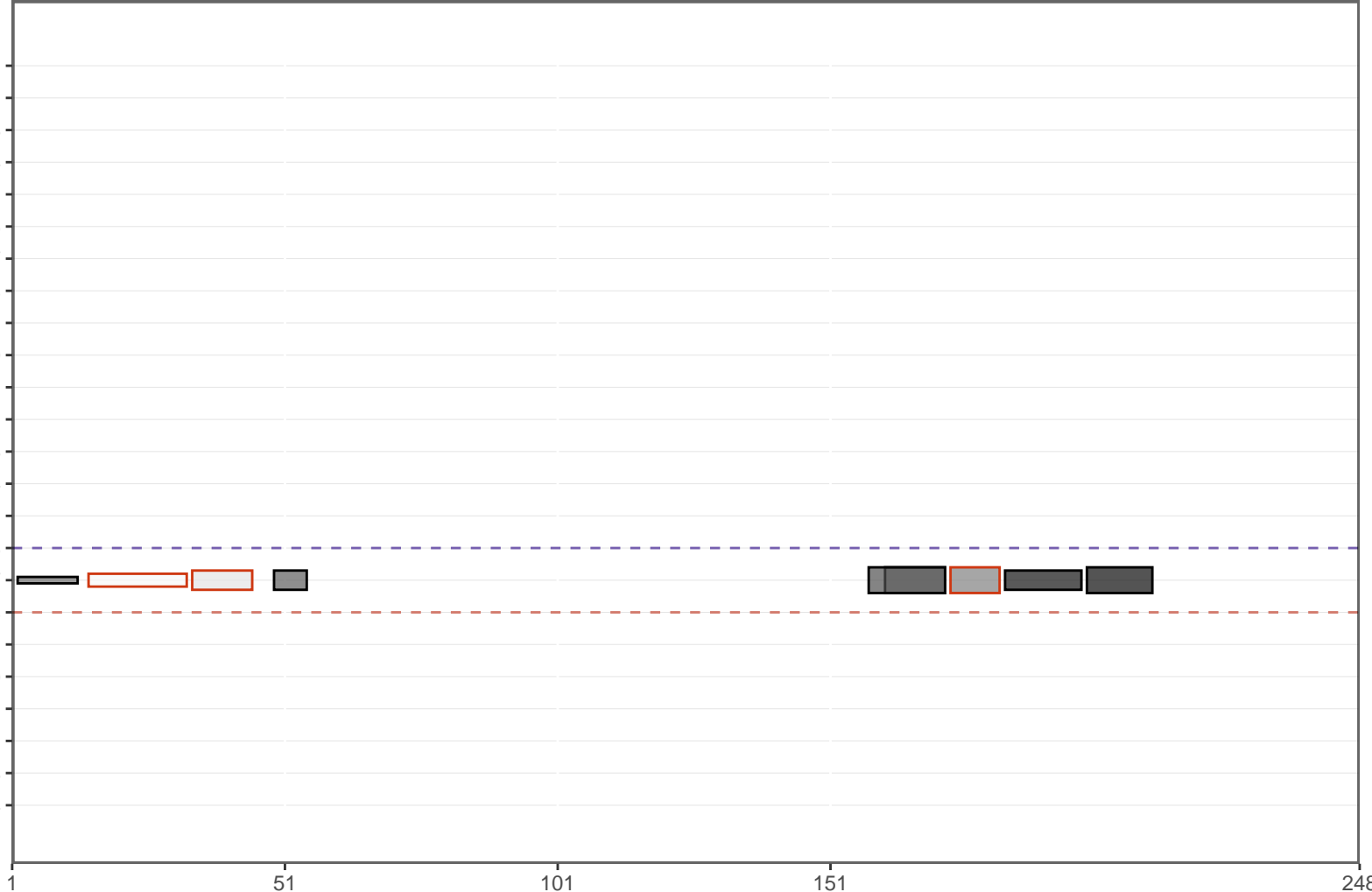
MW indication



Molecular weight

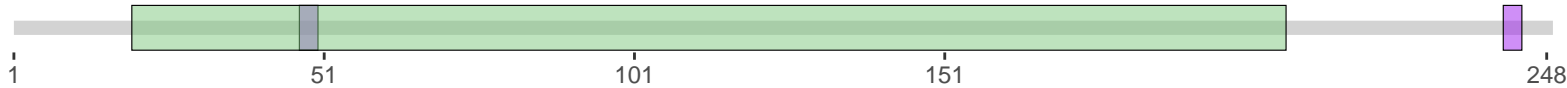


Gel Slice



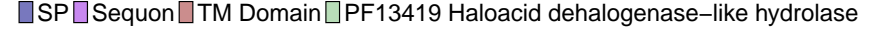
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

HLHANGIPICVATGTHTRHFDLKTQRHGEFLSLMHHIVRGDDPEVKGKPKSPDFLAAANRFEGGPFVDPQRILVFEDAPSGVLAANKNAGMVMVMPDARLDSSYHEVADGVLSLLDFNADWGLPFFENSSTKLD*

NbL07g06050.1 uncharacterized_LOC109234215 [MW = 68.88 kDa]

No. of times detected



log(intensity)



Values from



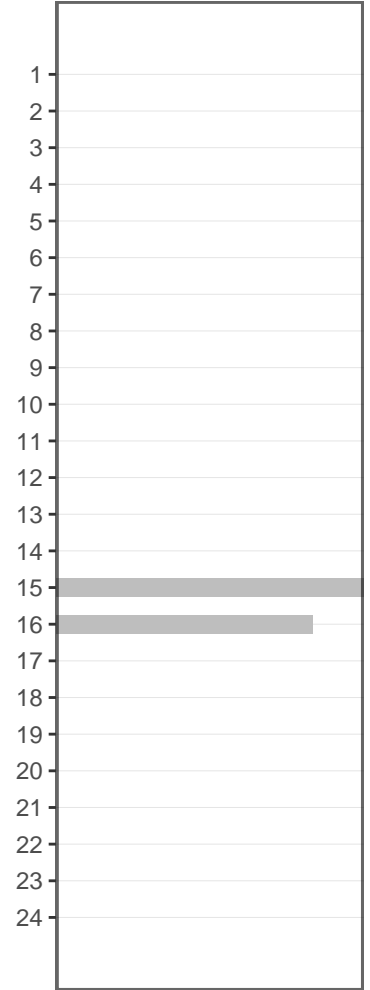
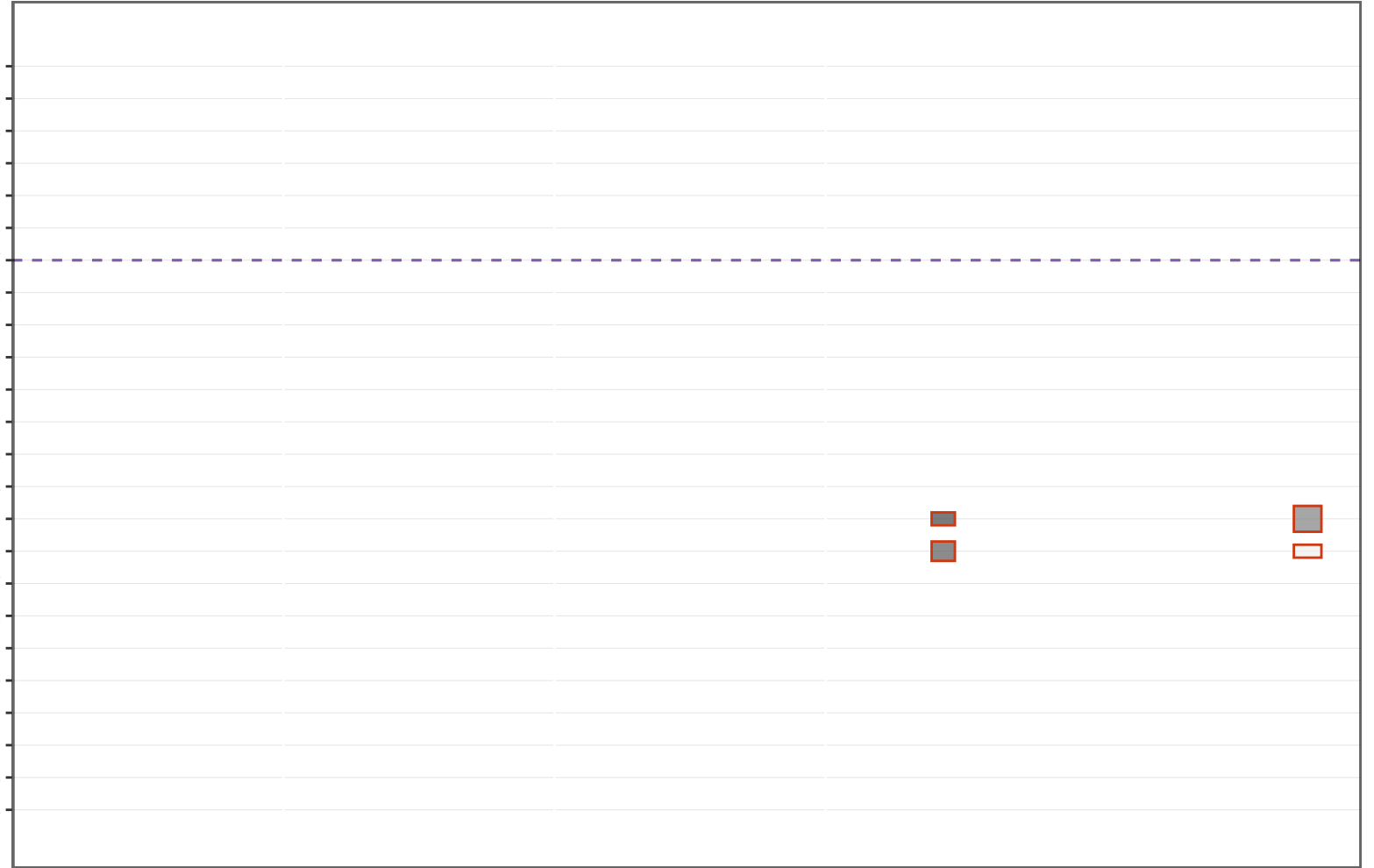
MW indication



Molecular weight



Gel Slice



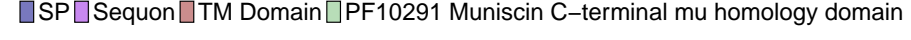
Protein length



Pfam domains



Pfam Description



Protein sequence:

1HGVEGFEGDYGGIEFSDGSLGGDFEGINDAWGGGLDASEYVYTKKWKDKDGLGELLELETSEPPKAAAGATDGGAGKKLELDLVKMMNGPEMIFTEIEBAEFRESLLARVGLMGVFLRFLFPKSSDDTETEFSPKVEGTGKWRFRVAMQNSHVBSLGNGLFHWKTAPEKPEPKYSLLPRLTFLRIRLVAKRLSGTLLSVMGLYVANPDLVPLRTNFTFVLLKLPVDPFTLLKVTPKAVLNRBERELKWHVDEIPLKGGHPGKLRARFPVINDDDGGSEELVLFQYVYKFS!

NbL07g06000.1 ribulose_bisphosphate_carboxylase_small_chain_clone_512-like [MW = 19.34 kDa]

No. of times detected



log(intensity)



Values from



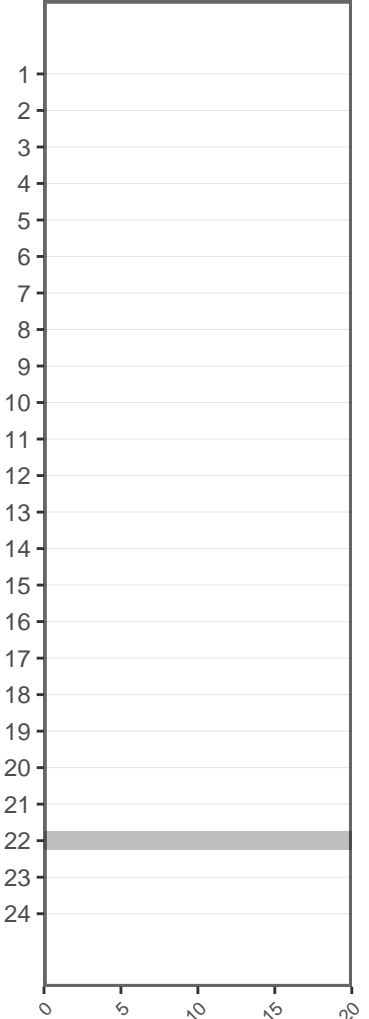
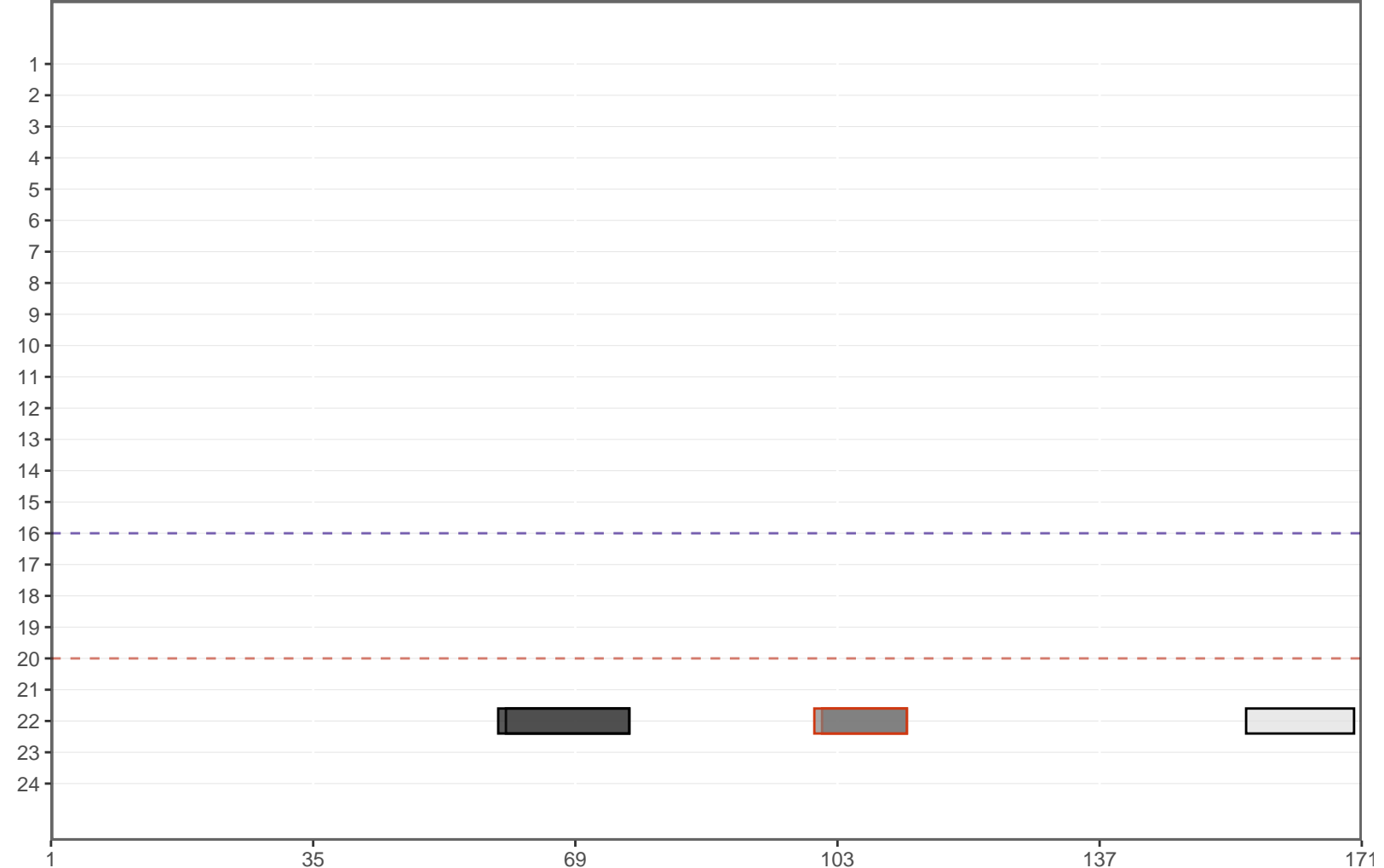
MW indication



Molecular weight

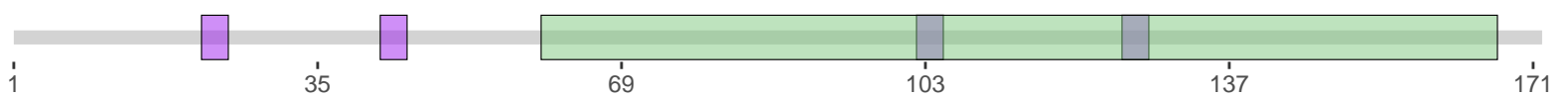


Gel Slice



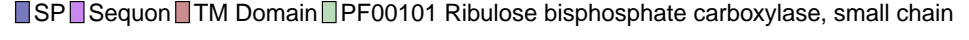
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL07g05970.1 putative_glucose-6-phosphate_1-epimerase [MW = 35.48 kDa]

No. of times detected



log(intensity)



Values from



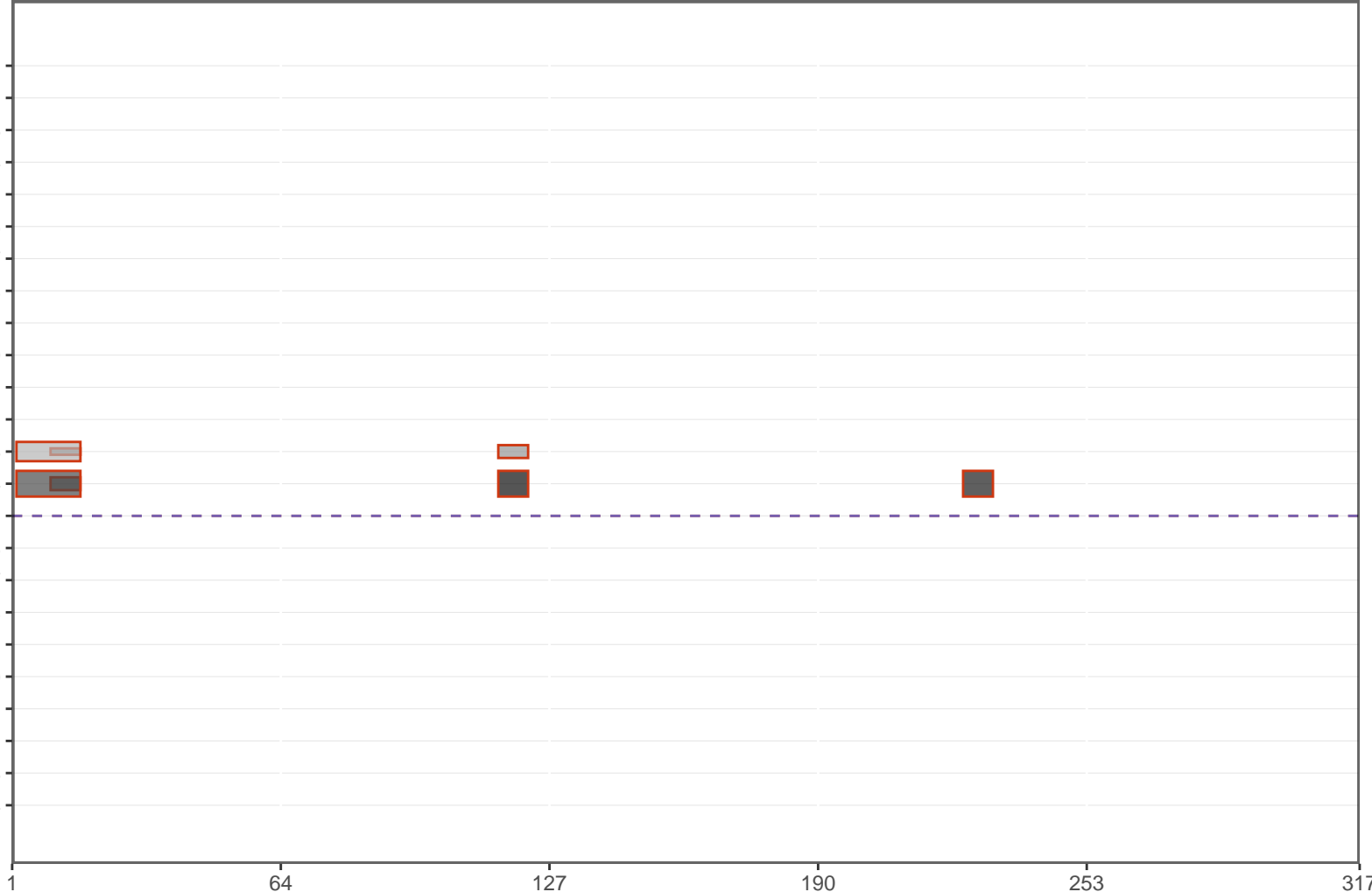
MW indication



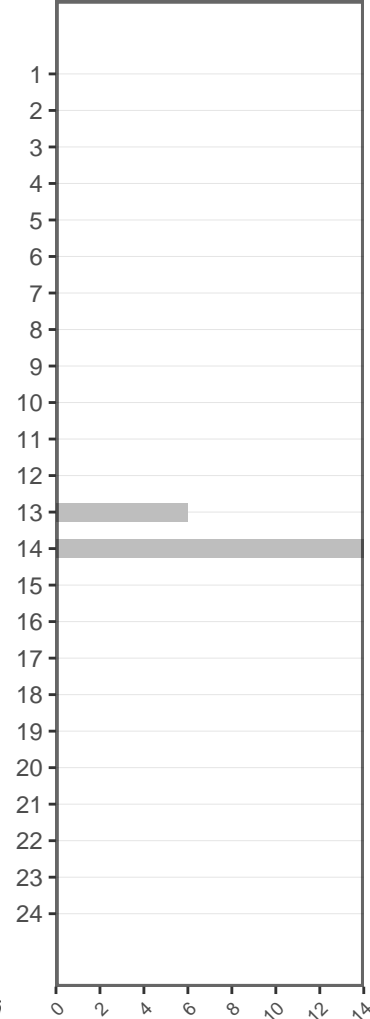
Molecular weight



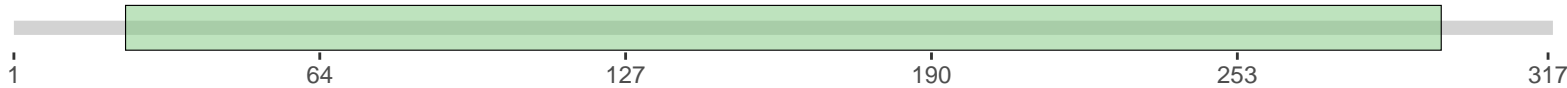
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

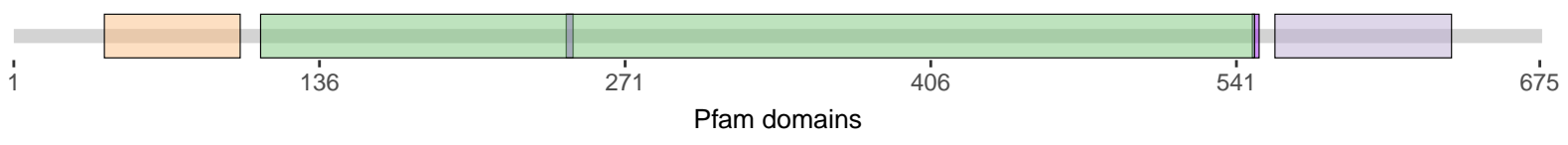
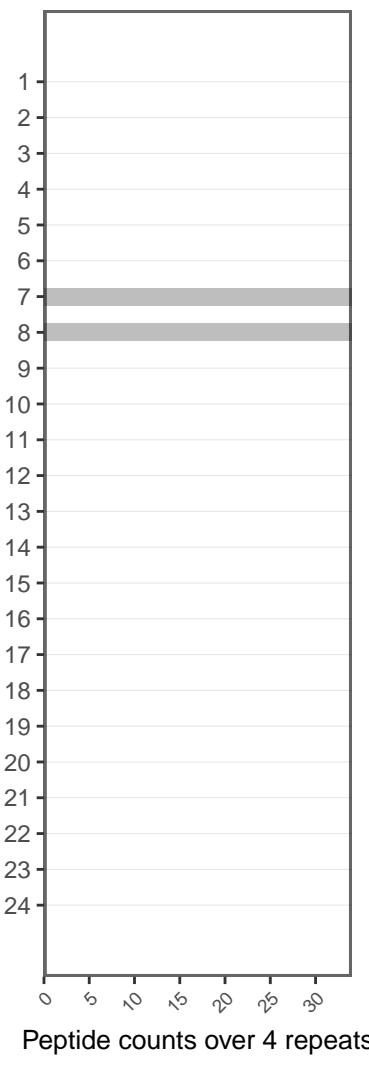
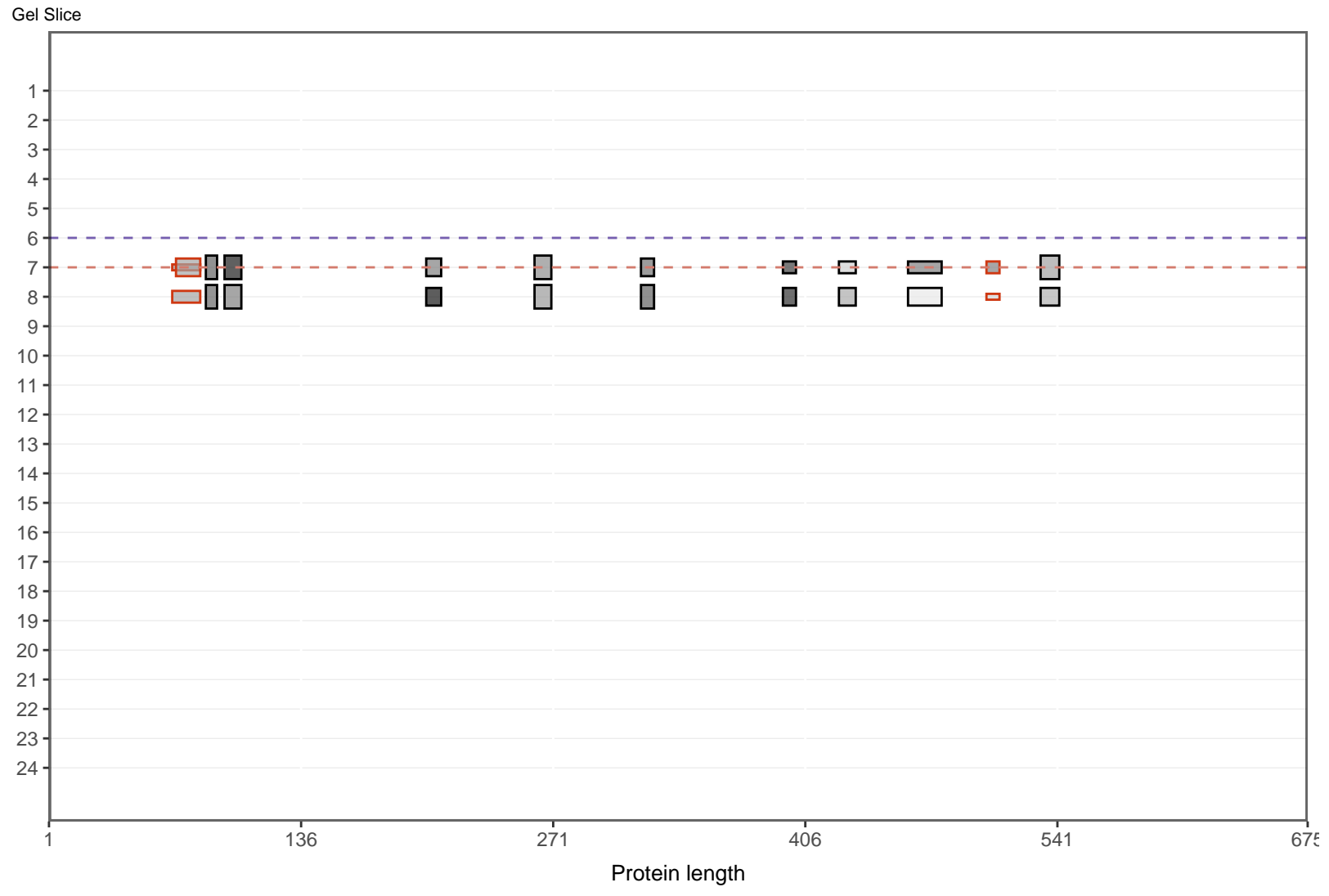
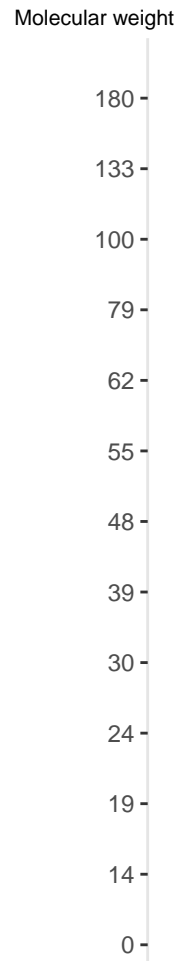
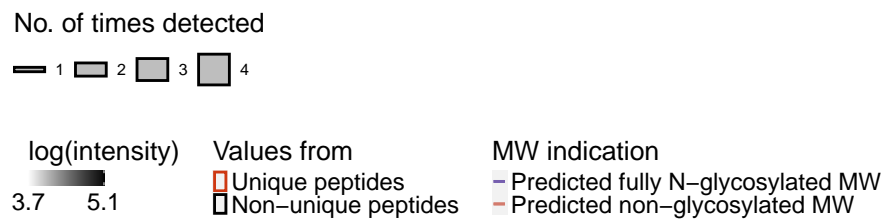
Pfam Description



Protein sequence:

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NbL07g05920.1 acetyl-coenzyme_A_synthetase_chloroplastic/glyoxysomal-like [MW = 75.03 kDa]



Pfam Description

- SP
- Sequon
- TM Domain
- PF00501 AMP-binding enzyme
- PF13193 AMP-binding enzyme C-terminal domain
- PF16177 Acetyl-coenzyme A synthetase N-terminus

Protein sequence:

IYWCADCGWITGHEKIVTYGPLLNGAINVVEFGVFNVPDAGRGWDVNDKYYKVFYETAPTLVRLMREGDEYVTRYSRKSLRVLGSGEPIPSAWRWFNFVYGDGRCPSDTHWQGTETGGMITLPSQAWPKQKGSATLFFFGVQVPIVDEKGVLEEGGGYLGVKSGWPSAFRTLVGDHVRVYGTTFYSAFPGYVFTGDDGNRDKDGYWLTGRVDDVINVSGHRIGTAEVESALVSHPKQCVAAAVGVHEVWGGHYAFVLAEGVPSSELRKSLKVVREKIG.

NbL07g05900.1 plasma_membrane_ATPase_4 [MW = 105.31 kDa]

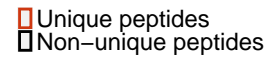
No. of times detected



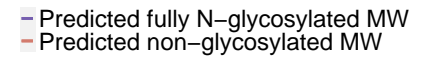
log(intensity)



Values from

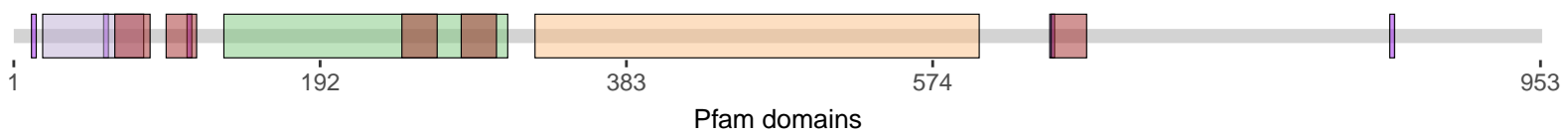
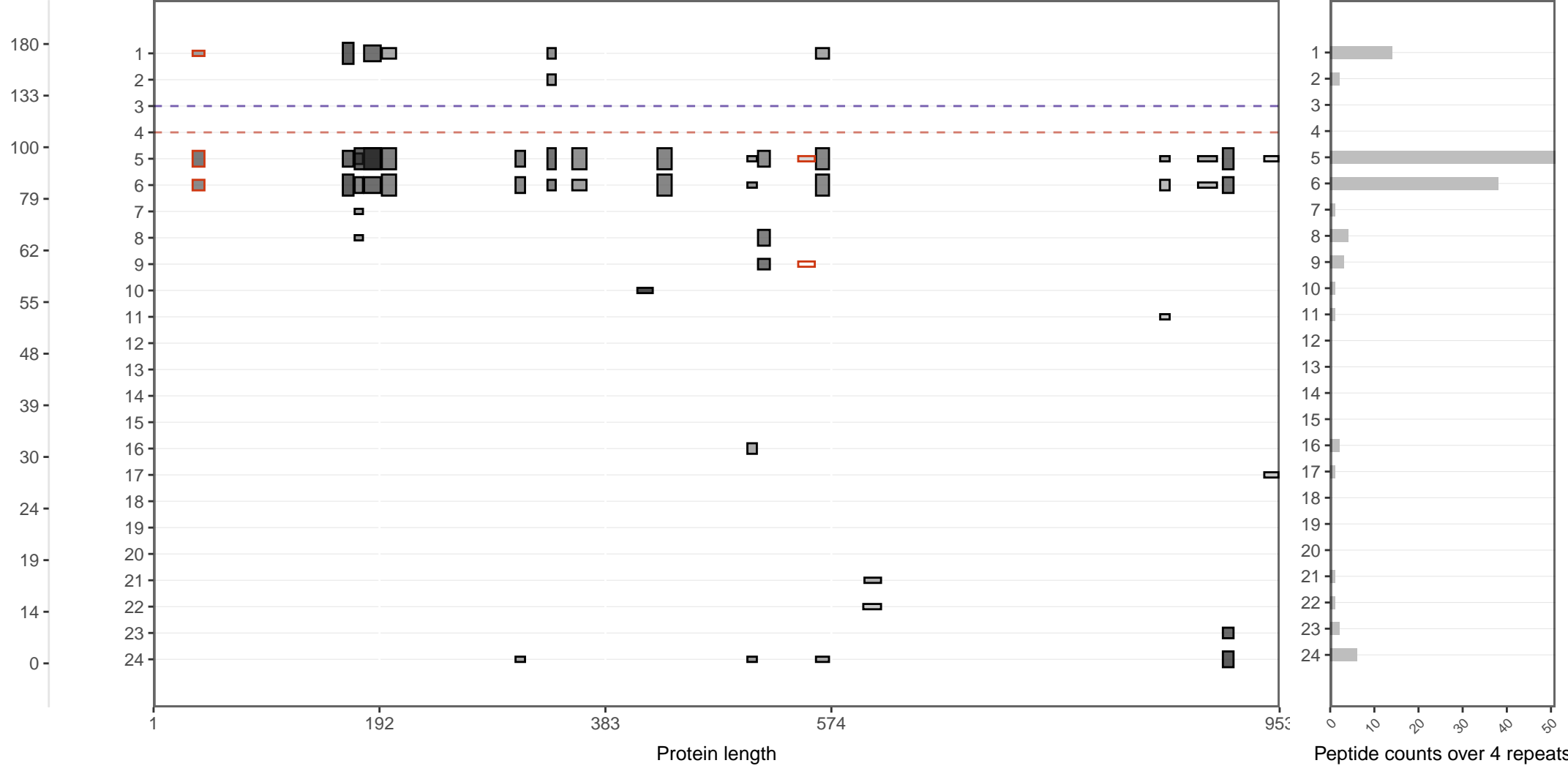


MW indication

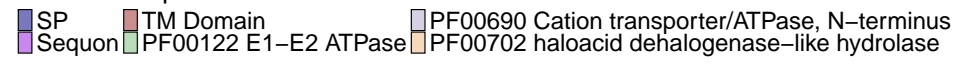


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

VAARQEVPEKSKESLSPGGRWEPVGVLPFDPPRRHDSAEITRRALNLGVNKKMTGDQLIAKETGRRLGMGTNMYPSASLLGGDDKDSAAIPLPEELIEKADGFVGFPEHKYEVNKKLGERKHVGMTEGGVNDAPALKKADGIAVADATDAARGASDVLTEPGLSVISALVTRAFQRMKNVTVAVSITRIVFGFMFIALWKVYDFSAFMVLIJIALNDGTMITSGDRVYKPSMPDGVKLEKFAFGVVLGGYQALMTVIFVWAMHDTDFSDKFGVKKLRNSDEEMISALYV

NbL07g05850.1 glucan_endo-13-beta-glucosidase_5-like [MW - SP = 52.51 kDa]

No. of times detected



log(intensity)



Values from



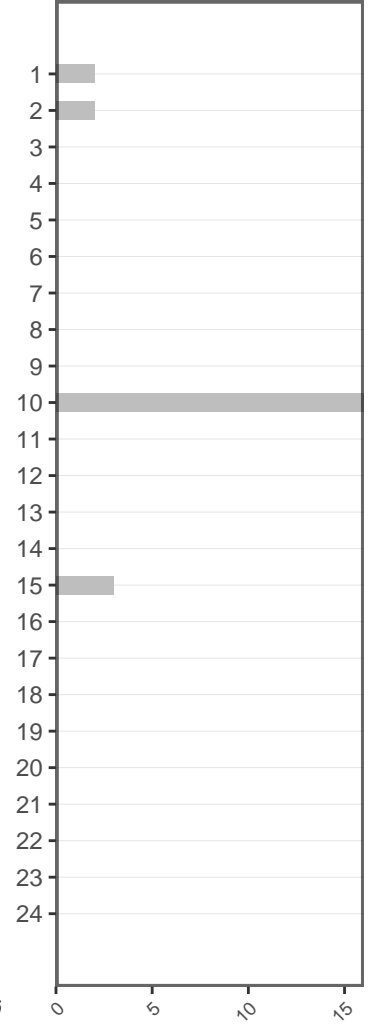
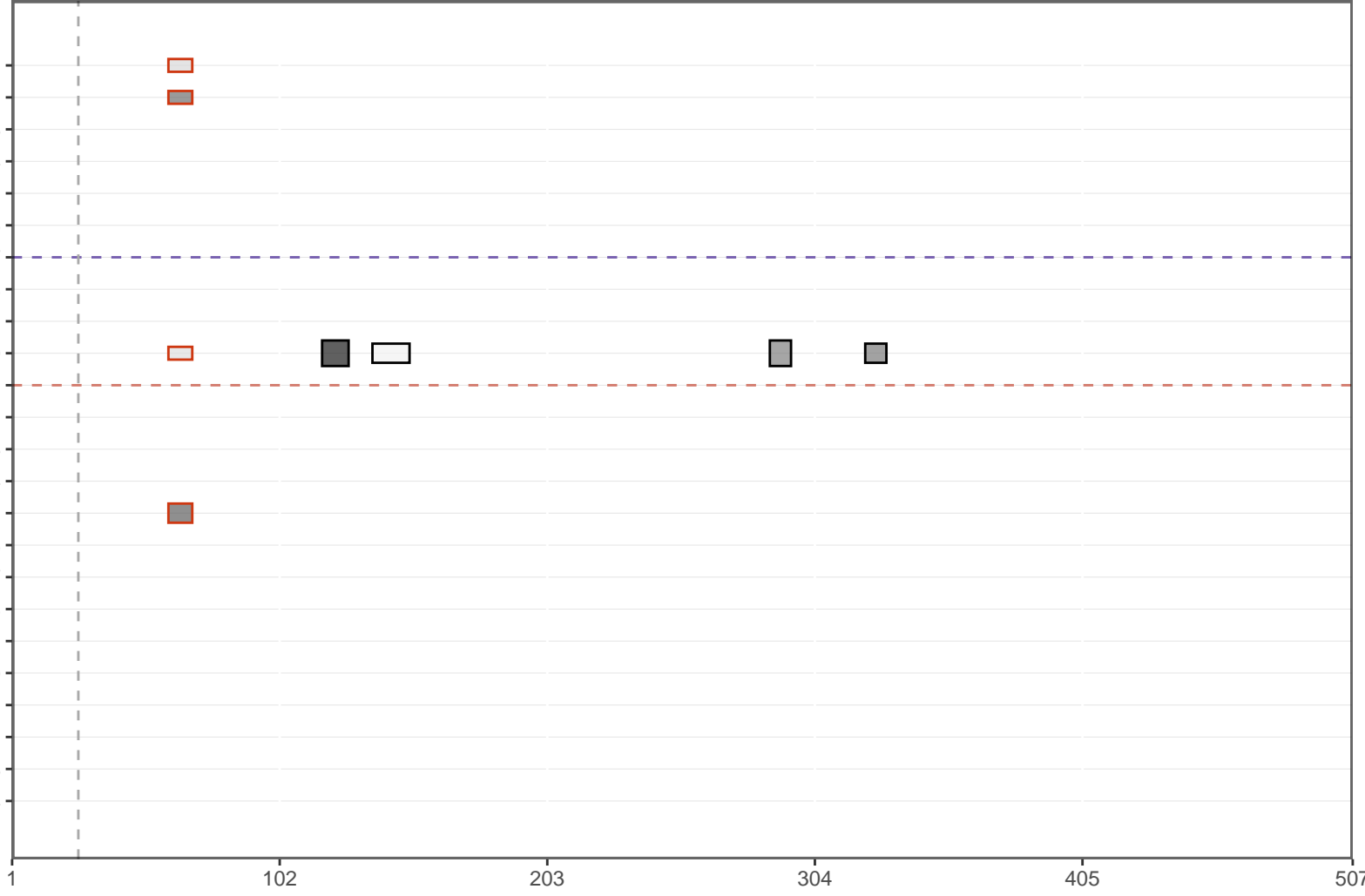
MW indication



Molecular weight

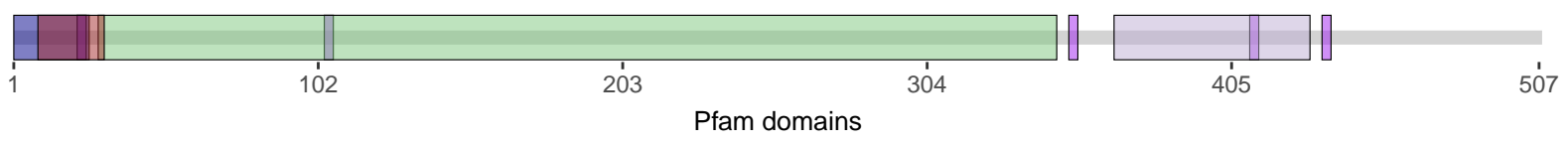


Gel Slice



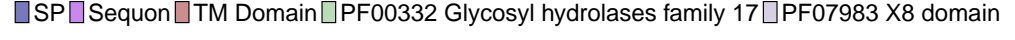
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

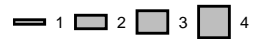


Protein sequence:

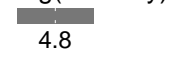
©NIFEANYDTLVYVALEKNGFGLSLPIVGEIGWPTDGDANANIEVARKFNQGLLDRISRGIGTPKRPPTDPIYFGLVDEDAKSIKPFGRHWGVVAFDGAIKYQLDLGNRRSLTPKGVYRILARKWICIMAFDANMDPSLAESNIVAGSYADCTSLGYGSGGGLDVKSMASVAFNMYQTMNGQKGGCCERFHLNLSVITTDIPSPSSSRGSSSSGGRFEMIDVGRHNSRANPQTSATKIKHFSLLFFLVLFVVDVYSLPWFPI

NbL07g05830.1 pectinesterase/pectinesterase_inhibitor_PPE8B-like [MW – SP = 56.17 kDa]

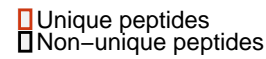
No. of times detected



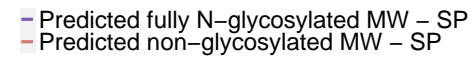
log(intensity)



Values from



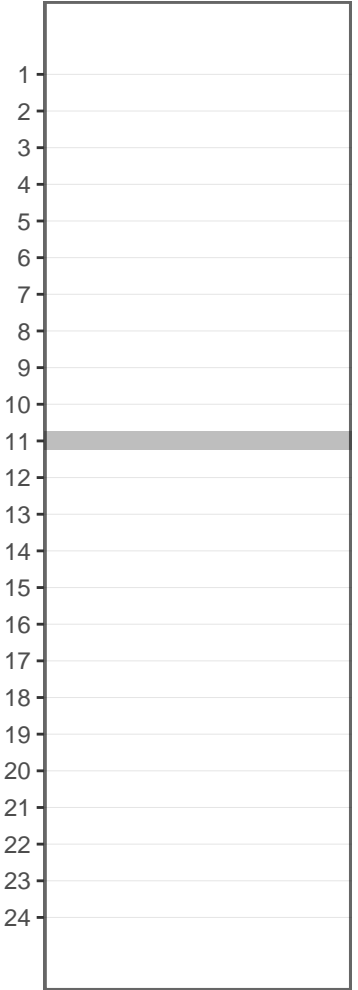
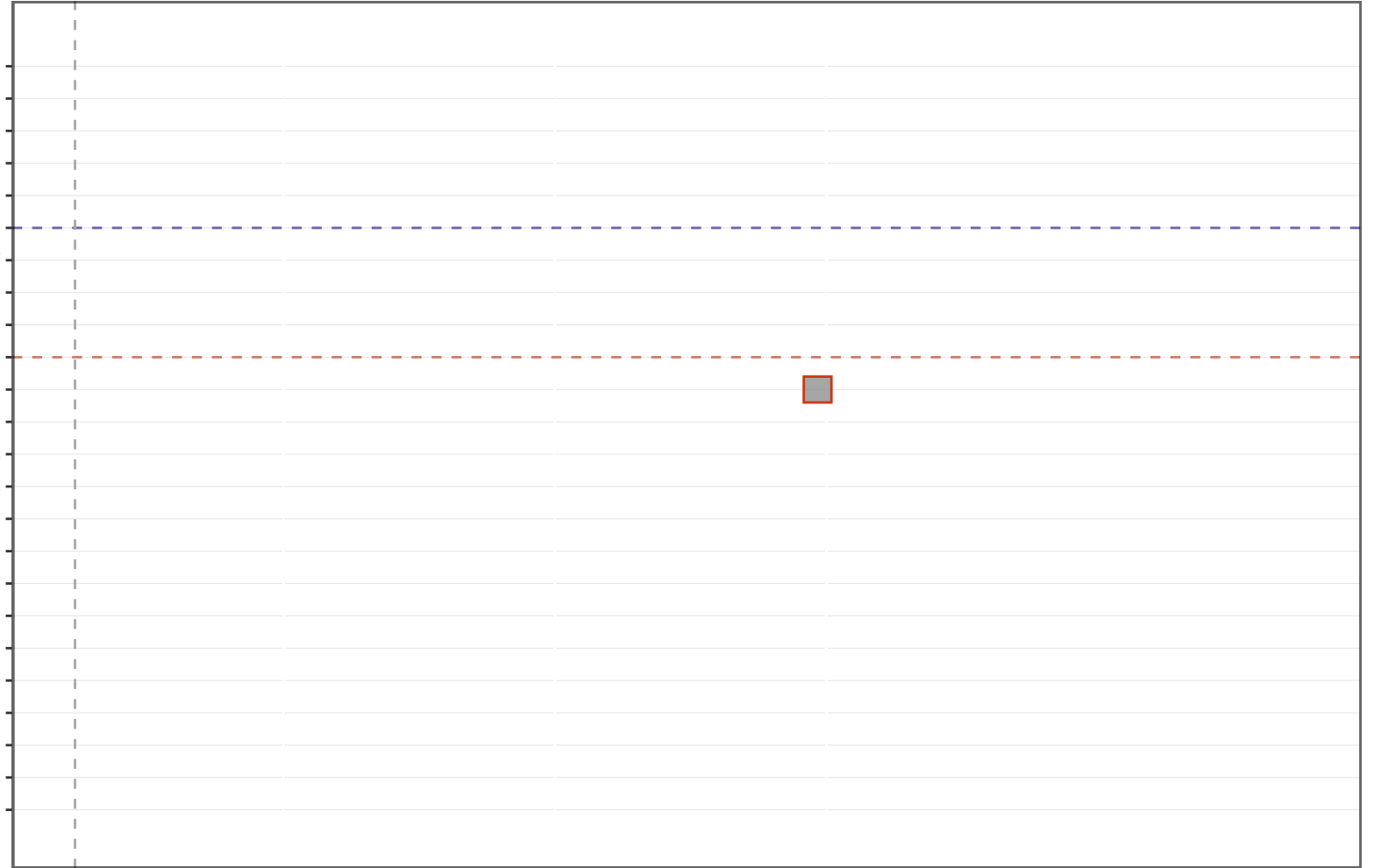
MW indication



Molecular weight



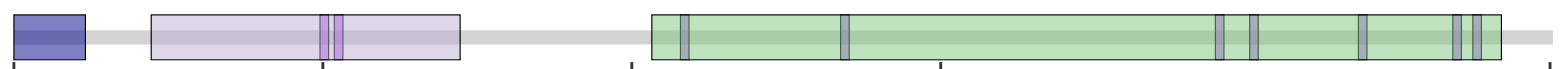
Gel Slice



Peptide counts over 4 repeats

1 109 217 325 538

Protein length



Pfam domains

Pfam Description

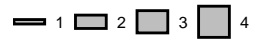


Protein sequence:

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NbL07g05700.1 lysine--tRNA_ligase-like [MW = 71.04 kDa]

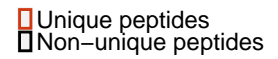
No. of times detected



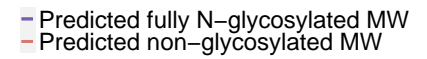
log(intensity)



Values from

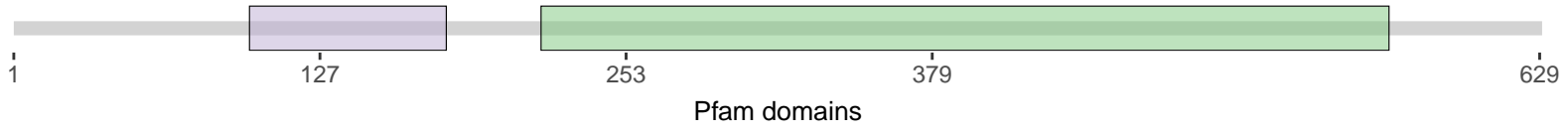
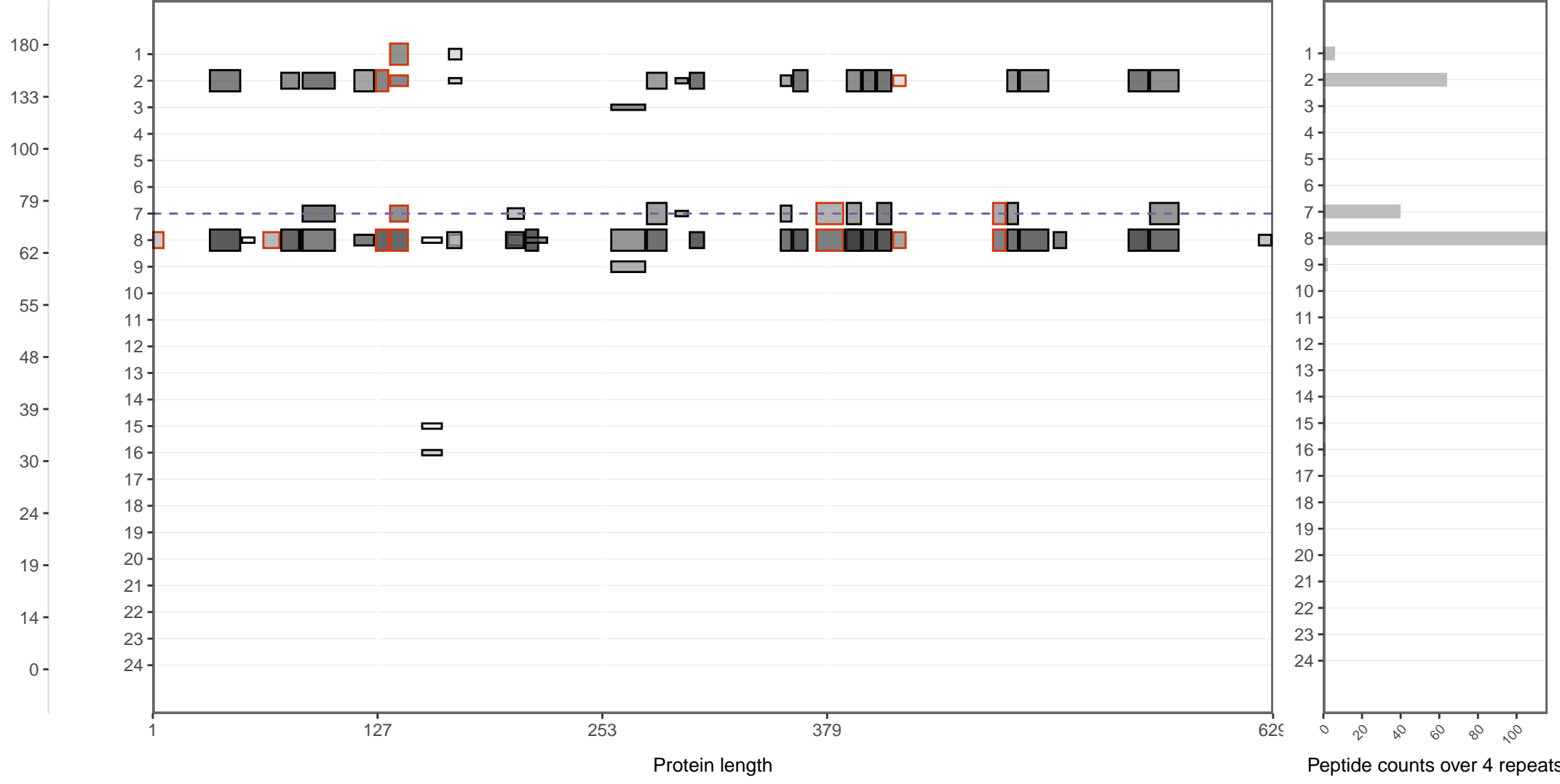


MW indication



Molecular weight

Gel Slice



Pfam Description

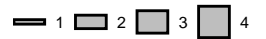
- SP
- Sequon
- TM Domain
- PF00152 tRNA synthetases class II (D, K and N)
- PF01336 OB-fold nucleic acid binding domain

Protein sequence:

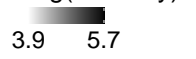
ILKELVGGLDRLVYKGGKGFNREGDITNINPEFTTCEFYMAVADYNDLMDLTKMLSGMVKELTGGYKHYHAKGLENDIEIDTFPRFRIDMVELEKLVANLNPKQLSSEVEANKYLDACAKLEKCPPTGGTARLLKDLKLGHFLEETGVNPFINHPKIMPEISPLAKVHRLKPLGTERFELFNKHELGNAYTELNDPVLVGRGRFADQLKDRSGDDEAMALDENFDTALEYGLPPTGGWGLGDRILAMLTDSGNKEVLKFPAMKPKQDEPPSKESNKKPQEESSAKLIDGQAK

NbL07g05520.1 peptide_deformylase_1A_chloroplastic [MW = 30.84 kDa]

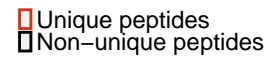
No. of times detected



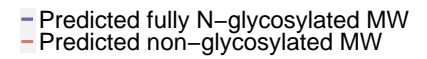
log(intensity)



Values from



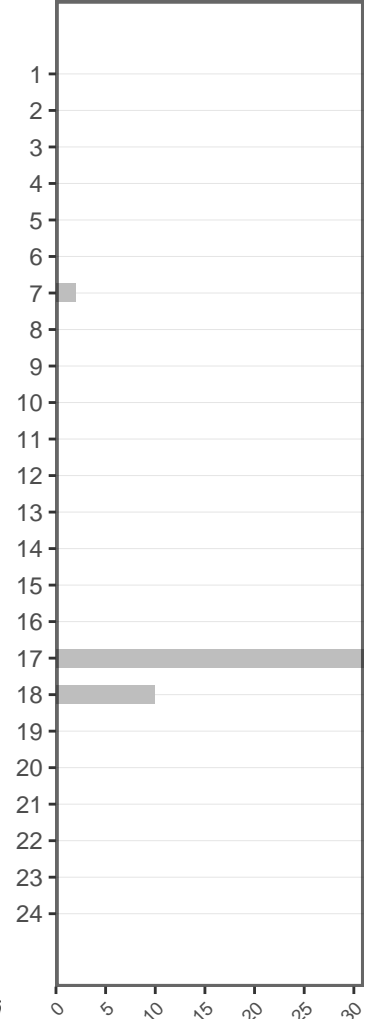
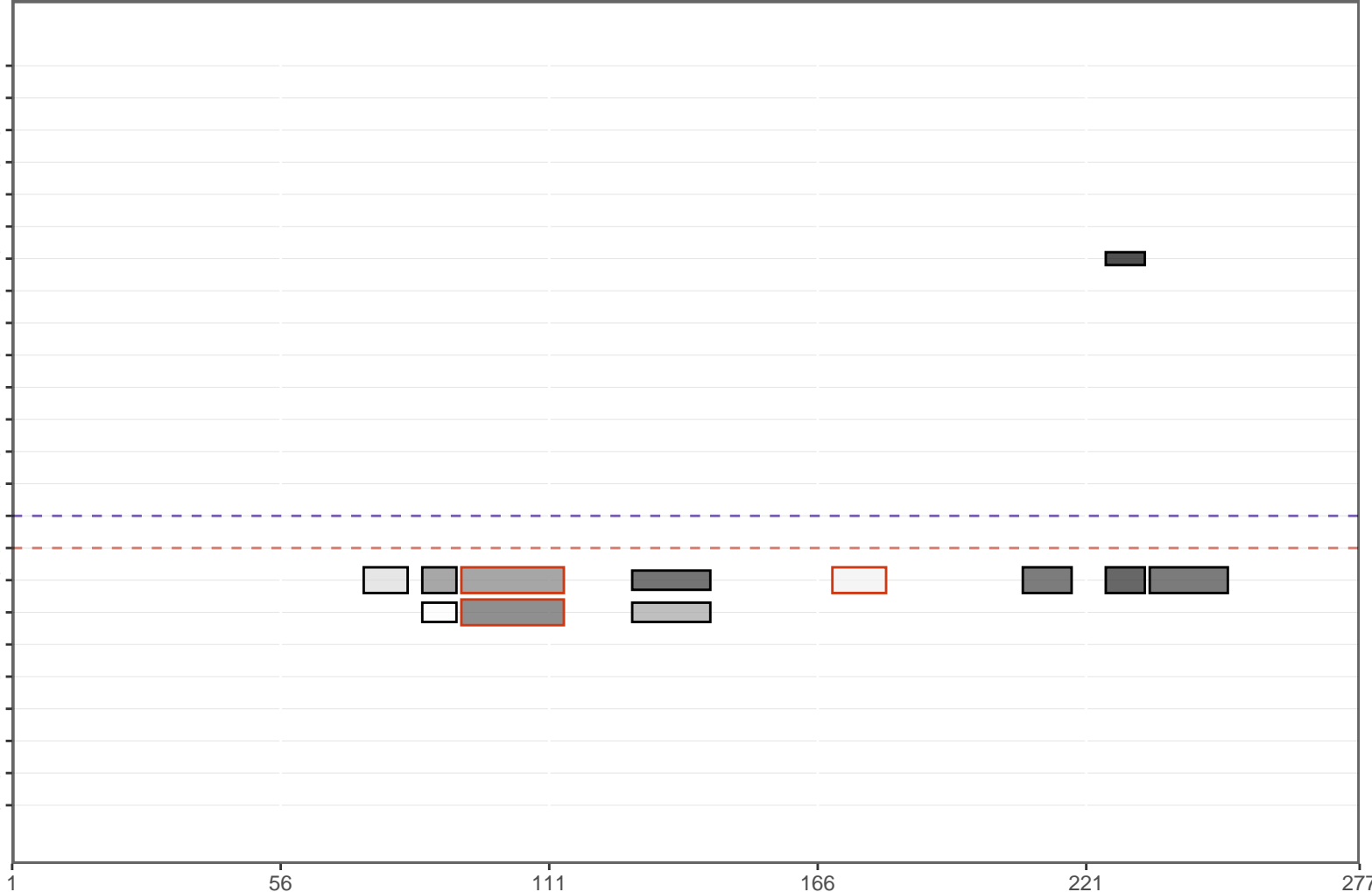
MW indication



Molecular weight

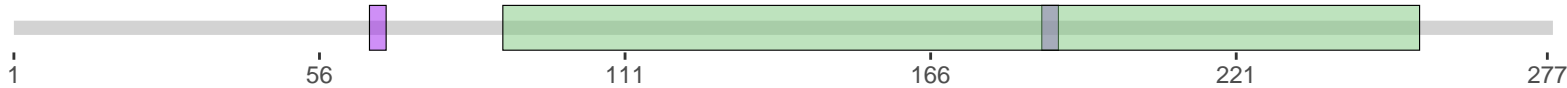


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

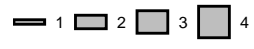


Protein sequence:

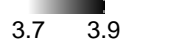
·MIRNAPGVGLAARQIGIPKIKVLEDTNEYSVAPKDETKAGDRRPFDLVIVNPKLKKGNKNTALFFEGCLSDGFRVAVERHLEVEVGGFDRNGKAIKVDASGWDARILQHEYDHLDTLVYDKMVPRTFRTEINLPLAAGPKLGVCI

NbL07g05420.1 ADP-ribosylation_factor-like_protein_2 [MW = 27.1 kDa]

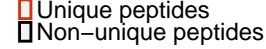
No. of times detected



log(intensity)



Values from



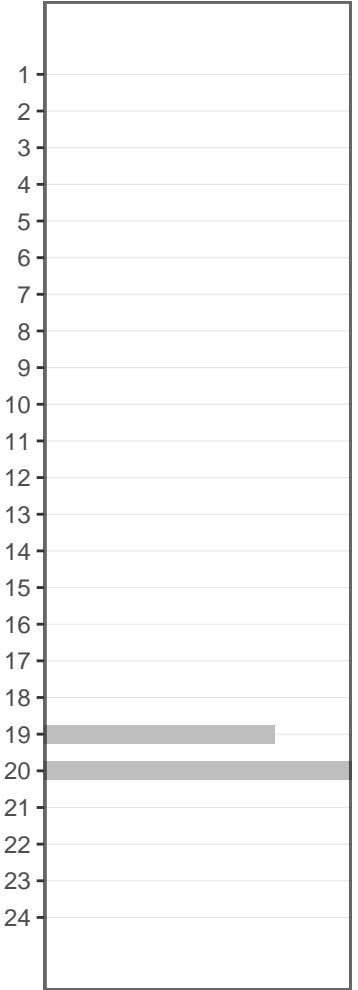
MW indication



Molecular weight



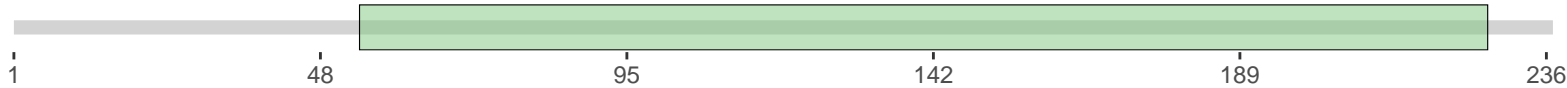
Gel Slice



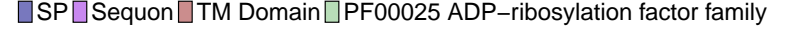
Protein length



Pfam domains



Pfam Description



Protein sequence:

YQKYTLNWDVGGGKTRSRWRYFEGTDLGWWVDSDDLRLDDCRVELHLLKEERLGGASLLIFANKDQDGLSPDEAKVNLLEAMDKSRHWRIWVGSAYTDGDLGDFWLVGGASRIYMLD*

NbL07g05400.1 isoamylase_1_chloroplastic [MW = 89.22 kDa]

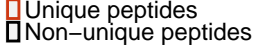
No. of times detected



log(intensity)



Values from

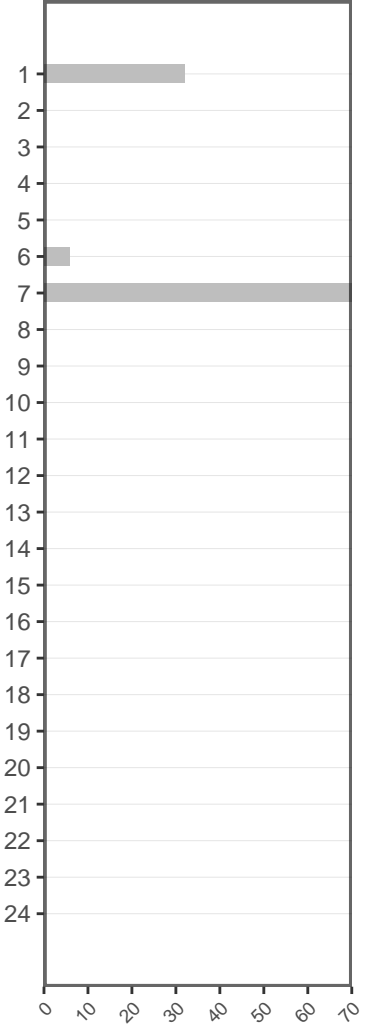
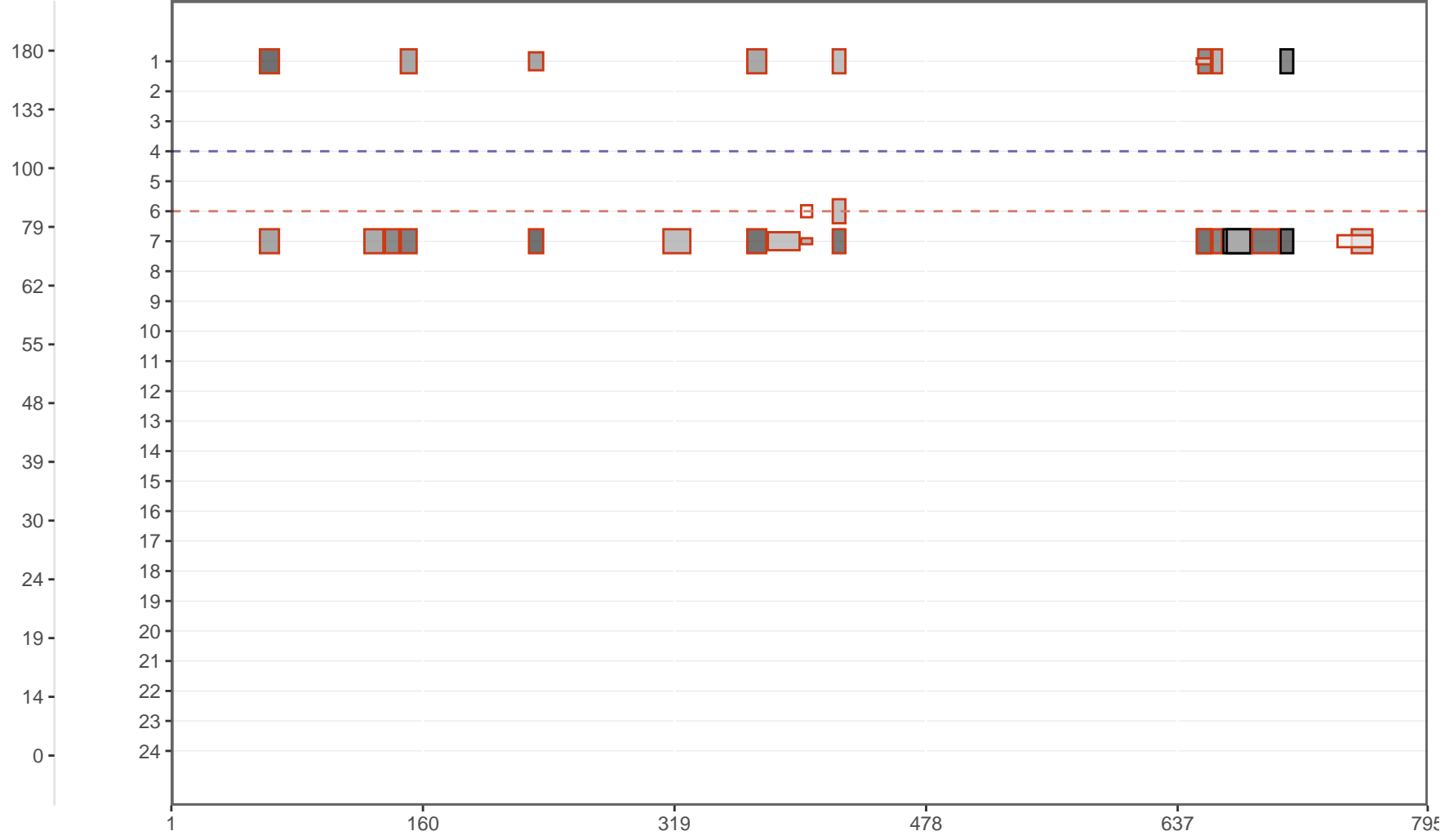


MW indication



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00128 Alpha amylase, catalytic domain
- PF02922 Carbohydrate-binding module 48 (Isoamylase N-terminal domain)

Protein sequence:

IGNTFTNCNHPYRQFMVQGLRYYWTEMHVDFRFDLAGILTRSSSLWDAVNYVGNSTVDVDTTGTPLTFPLMIDMNDPLRQVKLAEAWDDGGGLVQVGMFRHWVYSEVWNGKYRDRVGRFKGTDGFSGALAEGLGSPNHYEGEGRKPNWVNFVGAHDGFTLADLVTYNDKHNLANGEDNKGDNHNNWVNDGEEGEFAGISVKKLRKRMKRNFFLGLMVSQGVPMVMGDEYGHKGGNNNTYGHQNVNYFRWDKKDESSDFFRFCFVTKFRHECES

NbL07g05300.1 60S_acidic_ribosomal_protein_P3-like [MW = 12 kDa]

No. of times detected



log(intensity)



Values from



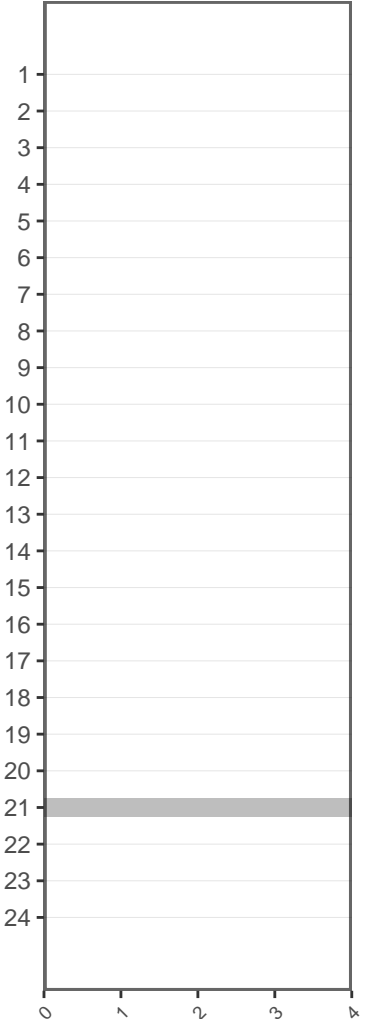
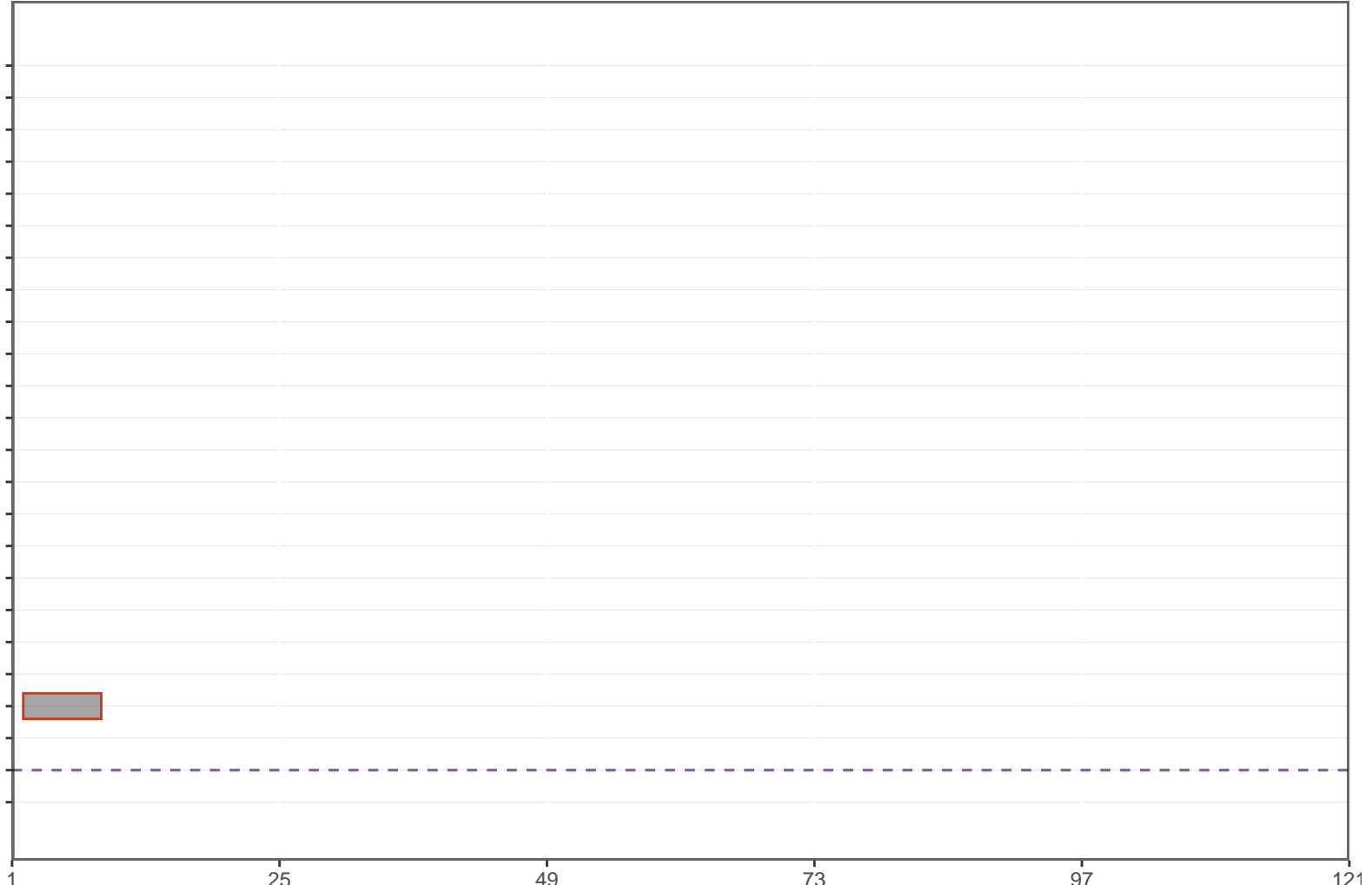
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISGVQSSFSYVTP6SAVFDVIGGGGGGIGGGGAAAAAP6GGAAAAEAPAAEKEEKEEEDDDMGFLFDI

NbL07g05130.1 26S_proteasome_non-ATPase_regulatory_subunit_6_homolog [MW = 44.29 kDa]

No. of times detected



log(intensity)



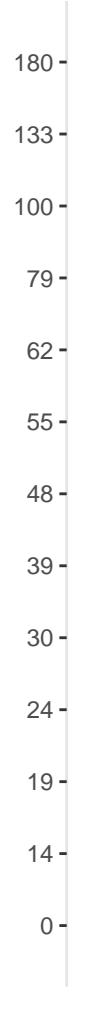
Values from



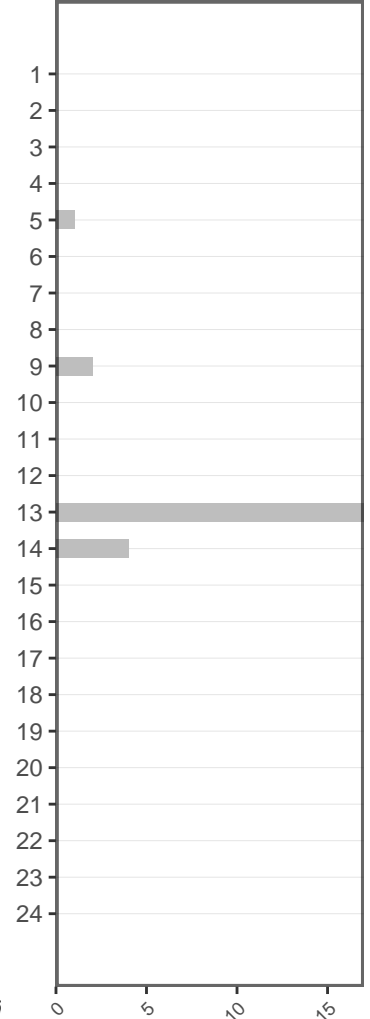
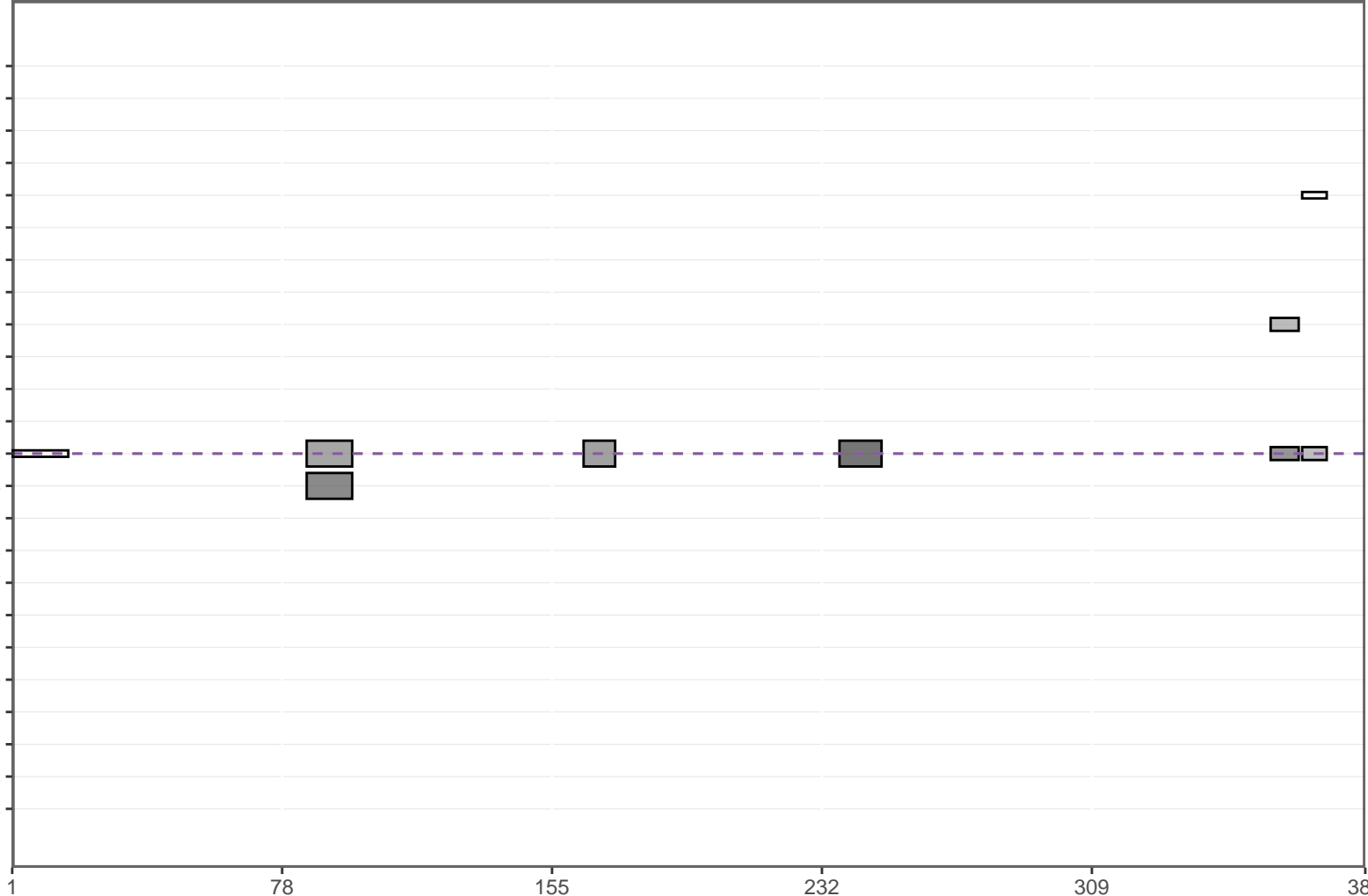
MW indication



Molecular weight

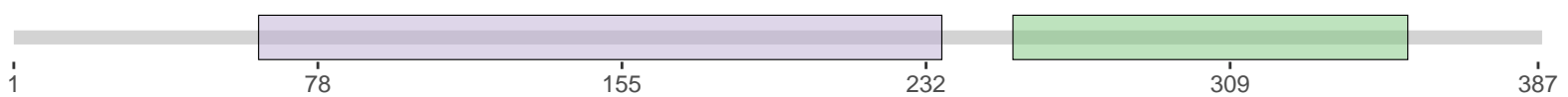


Gel Slice



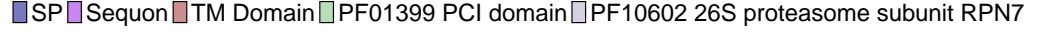
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILKYYEGLFCMSTRNFKKAAADLFLDGIETFTTYEIFFPYDFFIYTYLTSITFLDRVLSLQKQVVDAPFELTVGKIPYLSEFMNSLVEGQYKFFSAFAGLTHKILDRYLQPHFRYFMREVRIIVYSGQLESYKSVTIEAMAKAFQVSEDFDLLELRSFIAAGKLHCKIKQKVGVLLETNRFDANNAALYQATKGGDFLNRIGKLSRVIDL

NbL07g05110.1 ER_membrane_protein_complex_subunit_8/9_homolog [MW = 23.09 kDa]

No. of times detected



log(intensity)



Values from



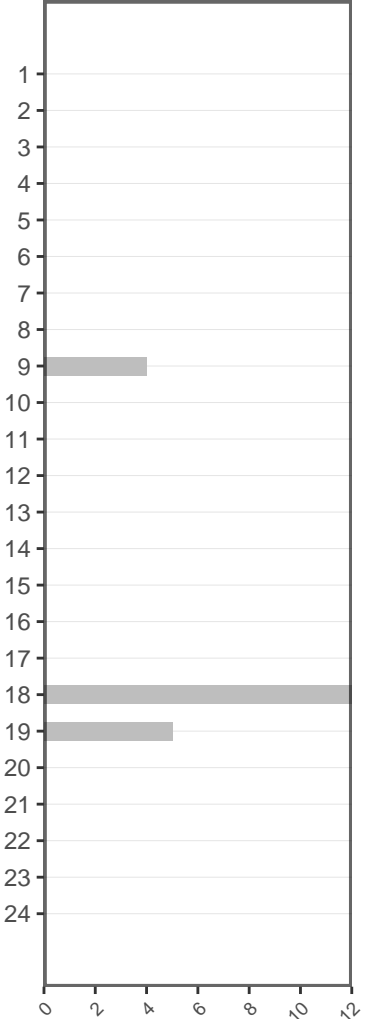
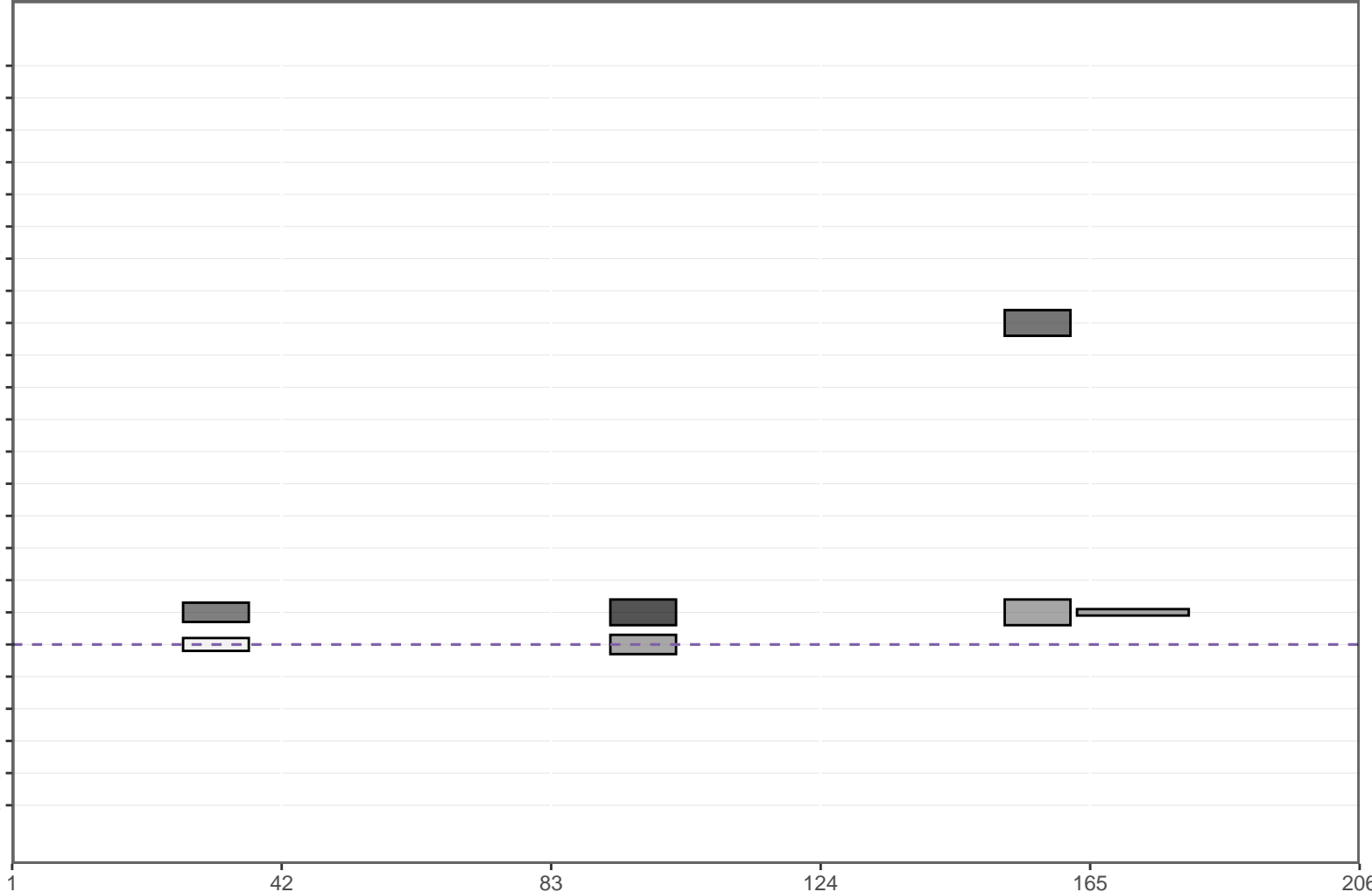
MW indication



Molecular weight



Gel Slice

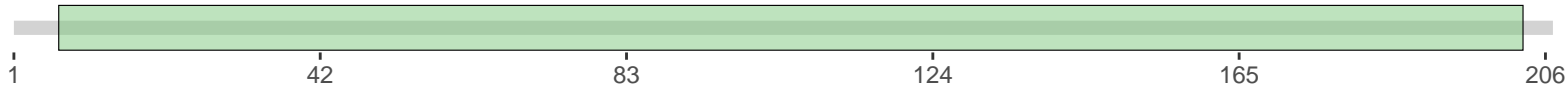


Protein length

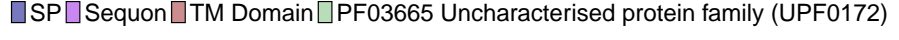


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

RFDDFEVGNVAKNADHFRKYFPGMALLLDNKKLEALKKEGDRSPVAMQLTKEVSRBWLVTGDASSPLKKEPSANVLLDHS6GKWKDIVDFDDHLDISGKDWLNPELFK

NbL07g05030.1 subtilisin-like_protease_SBT2.5 [MW - SP = 85.14 kDa]

No. of times detected



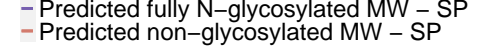
log(intensity)



Values from



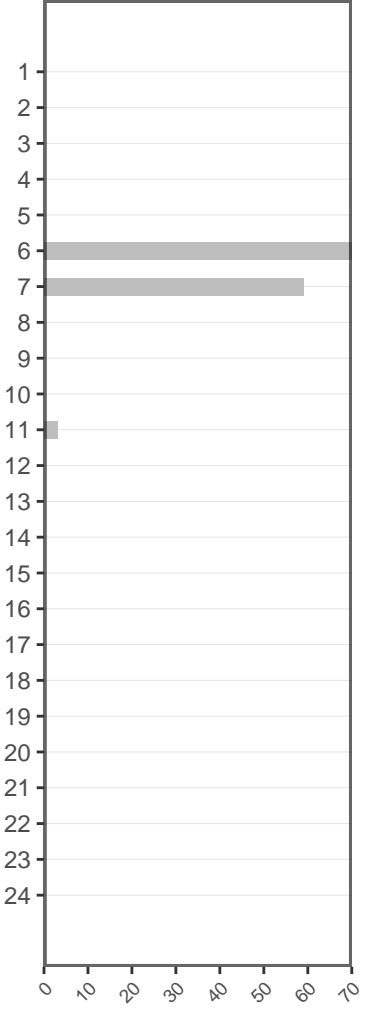
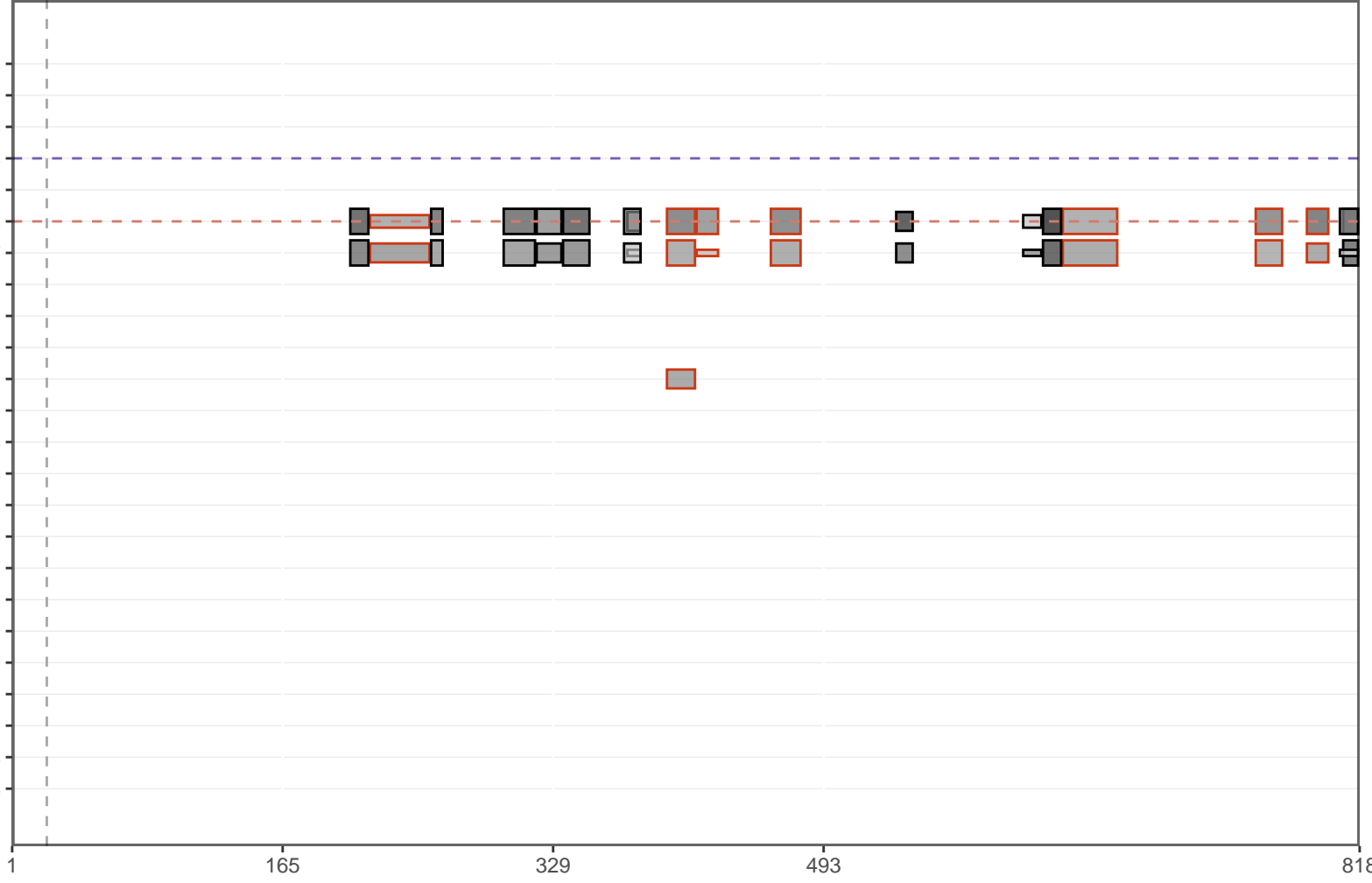
MW indication



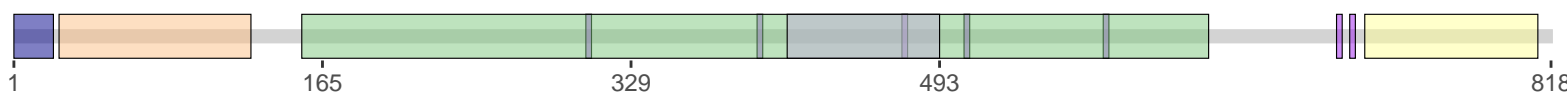
Molecular weight



Gel Slice

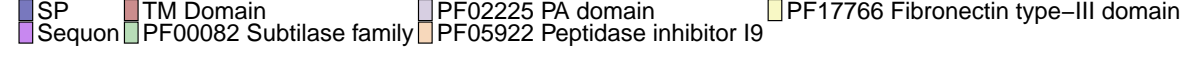


Protein length



Pfam domains

Pfam Description



Protein sequence:

IPNRTFTMLAANDVLLDSSVTKYSPADGDRPEVLNKNLVEGNLLGGFSNFVVGTAERKKVETAKALGAAGFVLAVENASPGAKFDPVPSIPQILTDVSGSMELVDYNYNFTSRDWTGRVYKFKSTGSGINLRPLHKSAQVWIFGARGPNKDYSGDADLLKPDILAPGLWAAWAFNGTDEANFGGEGFALISGTSMAAPFIAGISALIKQHHPHWSFPAKCALMTTS6TDRAERFLQAQGVSGSETMMLVPTPFVGGSHVNPRAALDPLFDAGYDYDGLFL

NbL07g04970.1 inosine-5'-monophosphate_dehydrogenase_2-like [MW = 53.27 kDa]

No. of times detected



log(intensity)



Values from



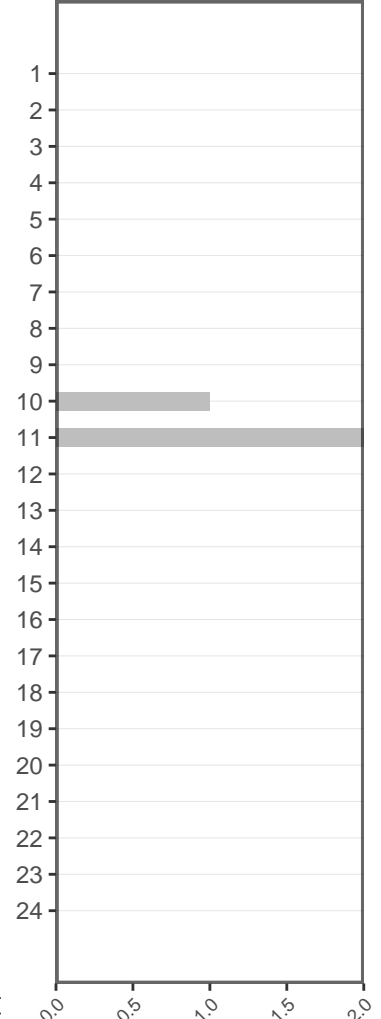
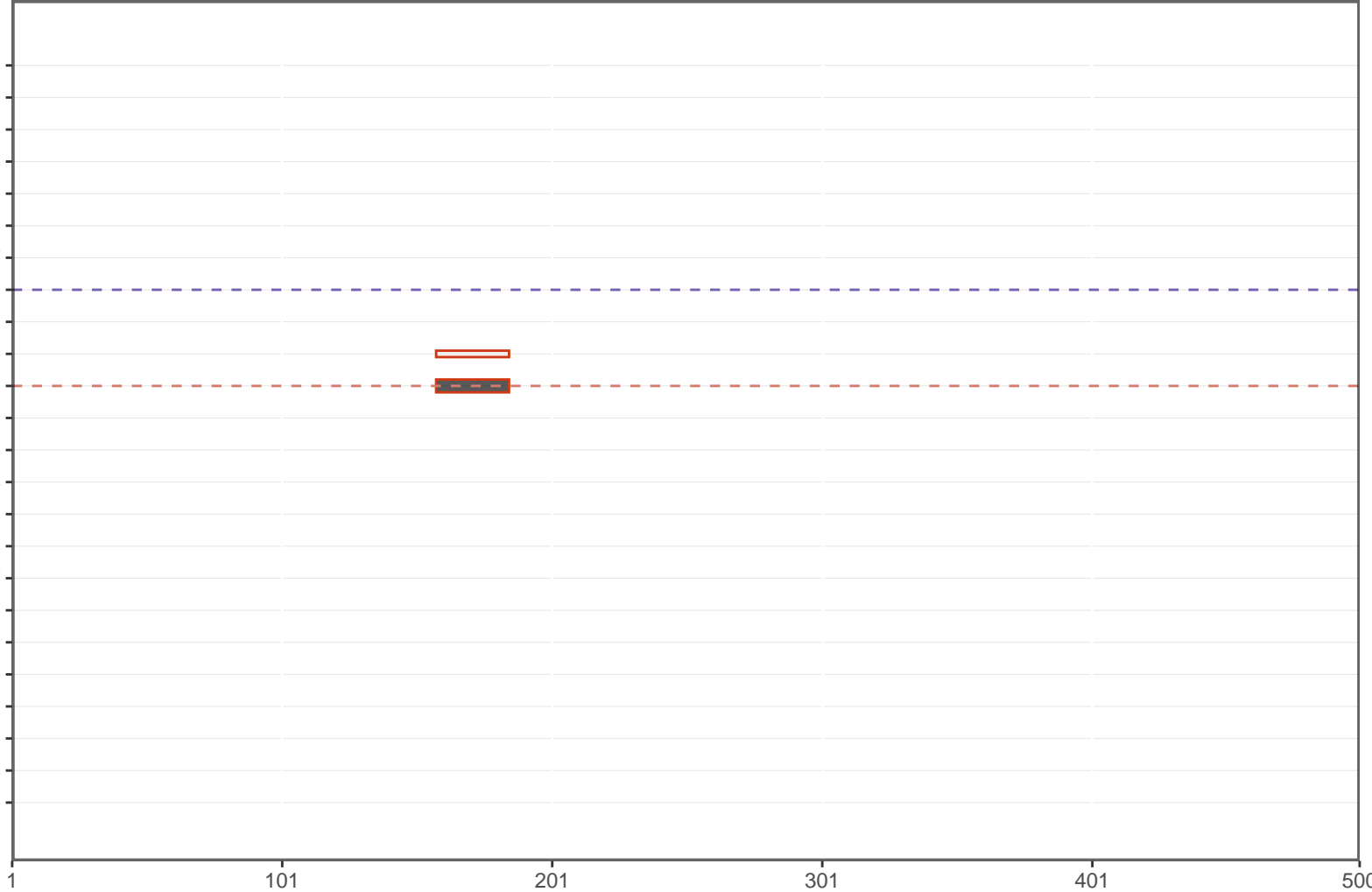
MW indication



Molecular weight

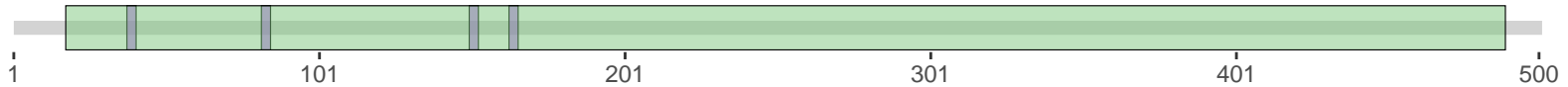


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TRSDSKERLERLLVKEGNAIVHDSGGNSLYGNMKHVKHHTYPHLEDVGGNVVTVYGAENLIKGGVDGLRVGMGGSSGCTTQEVCAVGRGATAVYKSVIAEGHQIPVADGGIENSGHVKALSLGASTVMMSGFLAGSNEAPGTVEYKNGLRVKKYRGMGLEAMTKGSDARYLGD TAKLIAGGVVGSVDKGGSLKFPVYTMQAVKGGFDGLGASLQSAHLLKSGKLRLEVRTGAAGVEGGVHGLVGEKIVE

NbL07g04880.1 transcription_factor_BTF3_homolog_4-like [MW = 17.34 kDa]

No. of times detected



log(intensity)



Values from



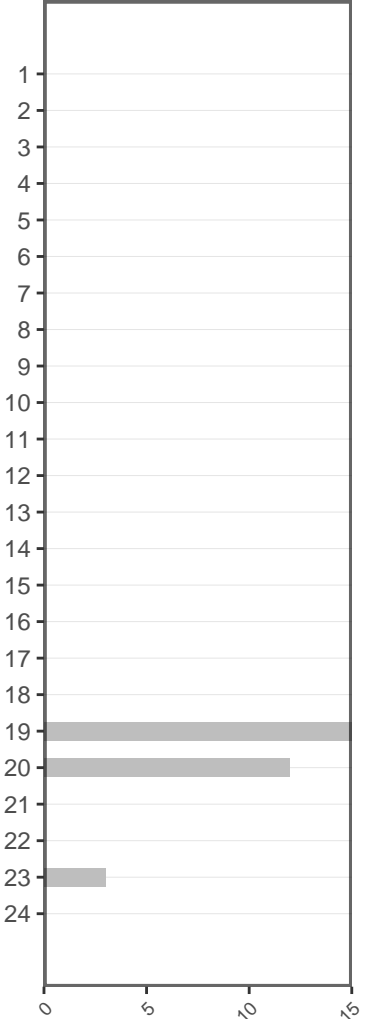
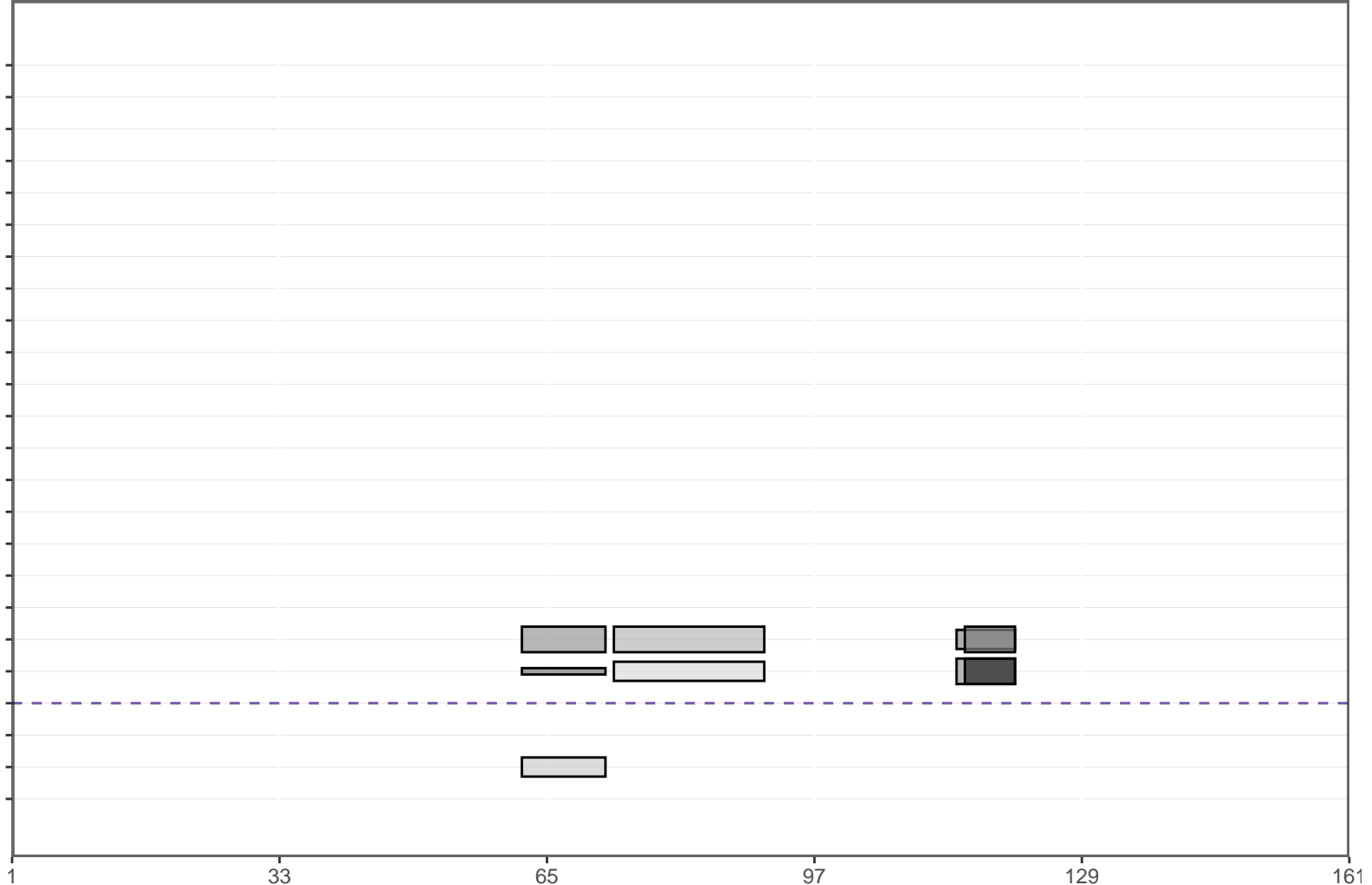
MW indication



Molecular weight



Gel Slice

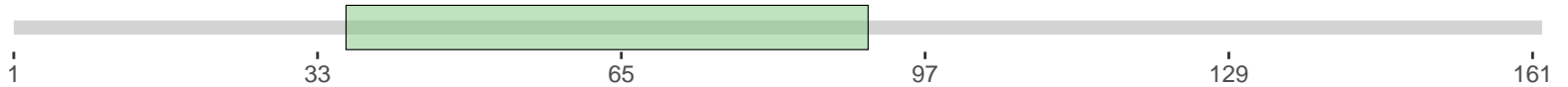


Protein length

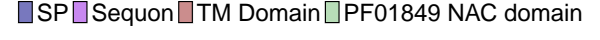


Peptide counts over 4 repeats

Pfam domains



Pfam Description

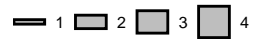


Protein sequence:

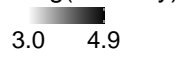
"NPKYQASIAANTWVSGSPQTKLGDLPQHHLGDPNLENLKLAEQFGKGGAAAGTGEAAAQEDDDDEVPLVAGTFEGAAEEGHTS"

NbL07g04800.1 ABC_transporter_F_family_member_4-like [MW = 84.86 kDa]

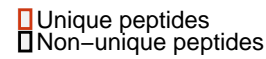
No. of times detected



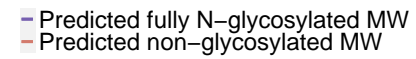
log(intensity)



Values from



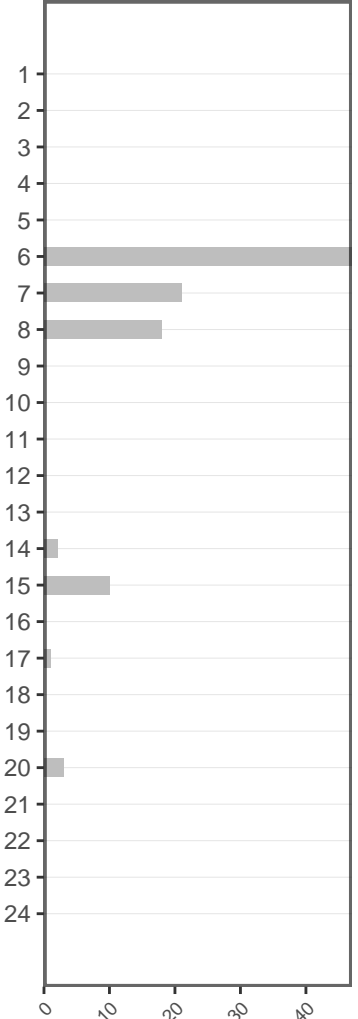
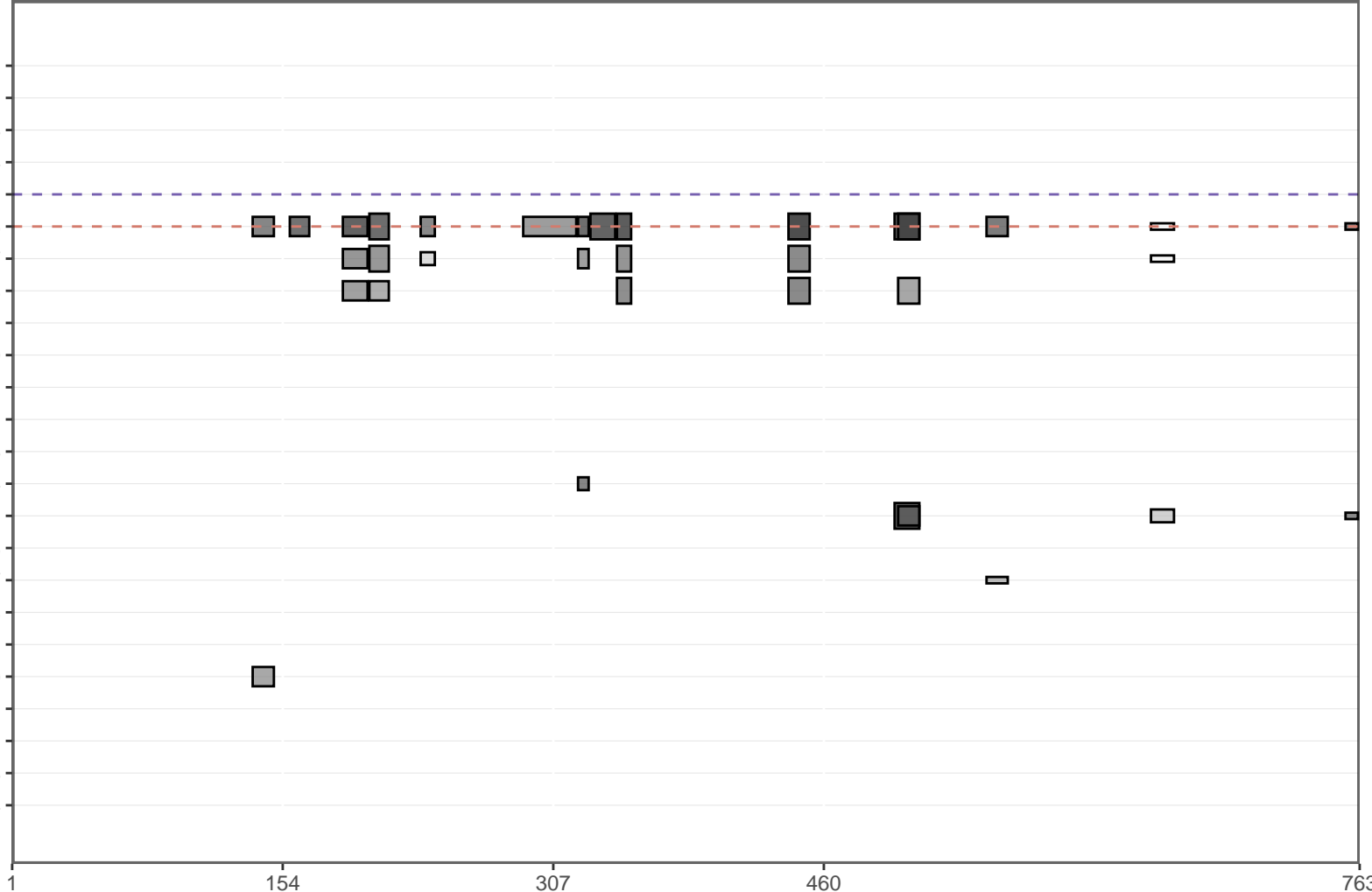
MW indication



Molecular weight

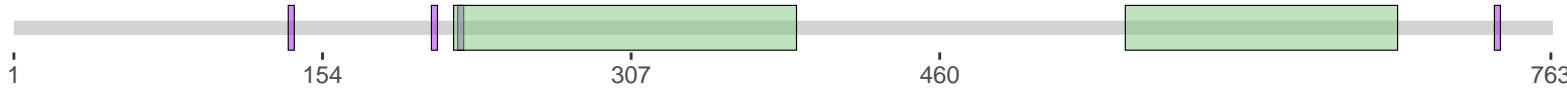


Gel Slice



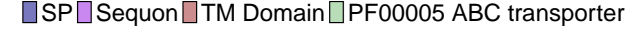
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IRISLARALFYOPTLALLDEPTNHLDRALVWLEELGRWKKTLVVVSHDRDFLNTVSEIHLHDMKLFYRGNFDGFEFGYEQRRKEMNKFEIYDQKGAARSGNRAQGERKVKRAKFAVAKEKKKGGKRRVDEDETPPEAPQKWRDYTVERHFFPEPTLTPLLQLEIVSFYFNRPDFRLSDVDVGGMGTRAVVSGPAGACKETLLNLLAGDLVPEGEVRRSGKLRIGRYSQHFVLLTMDETPVQVLLRHLPEGEQPSKGEAVRAKLGKGLPSINHLTPLKL

NbL07g04570.1 macrophage_migration_inhibitory_factor_homolog [MW = 14.34 kDa]

No. of times detected



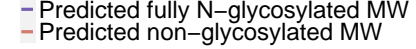
log(intensity)



Values from



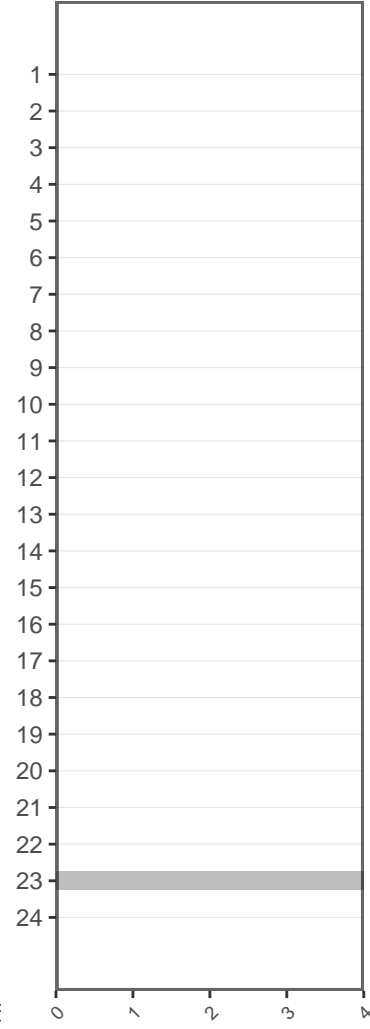
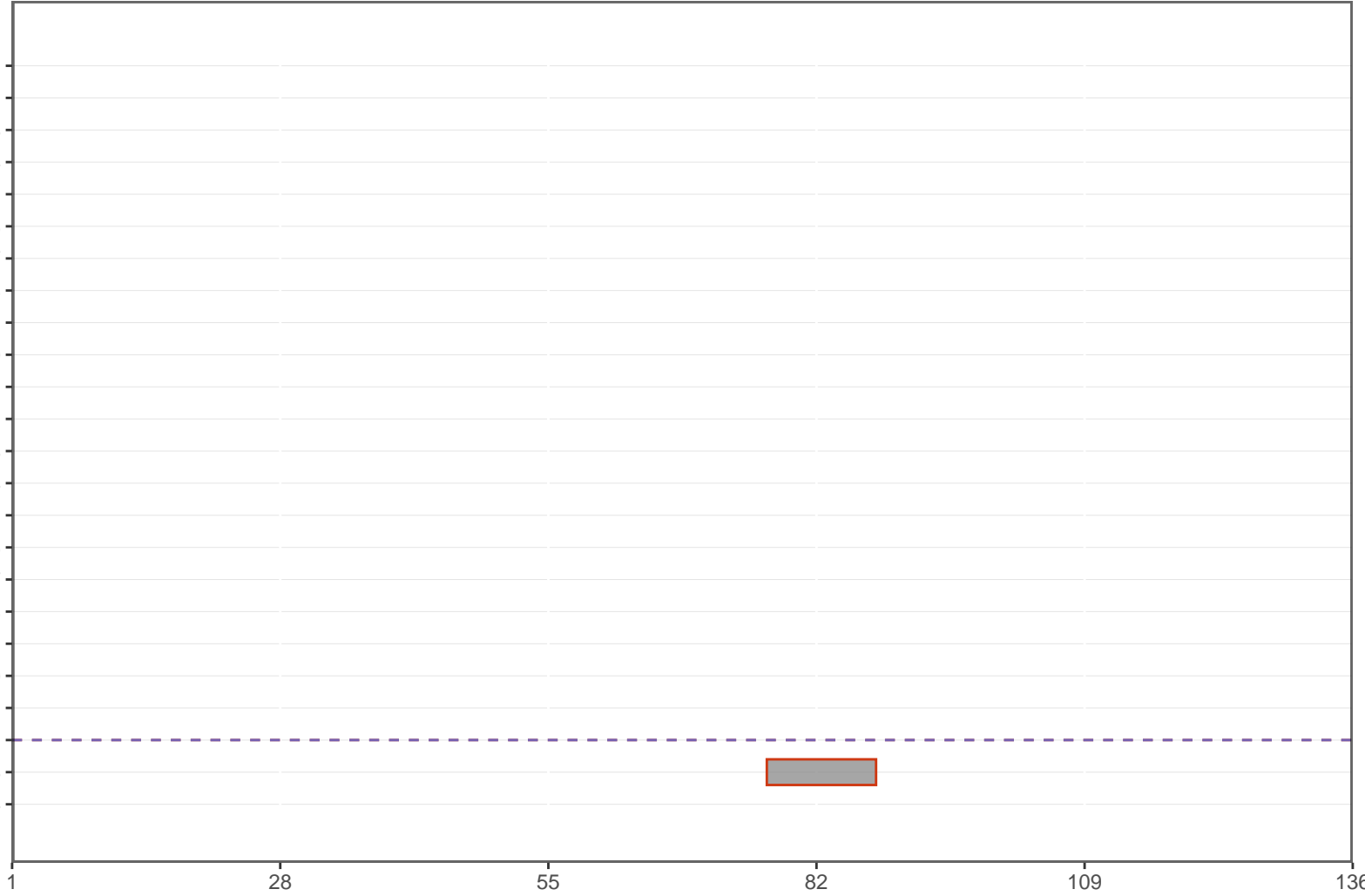
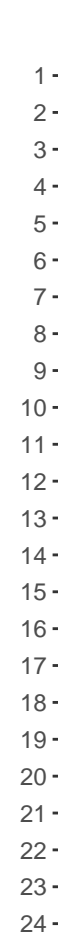
MW indication



Molecular weight



Gel Slice

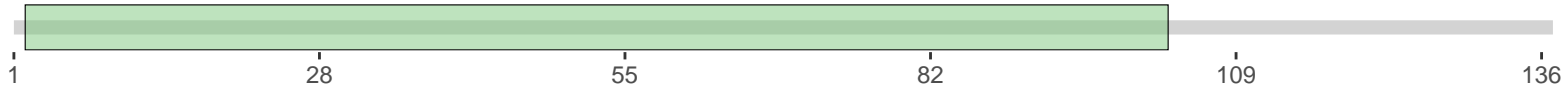


Protein length

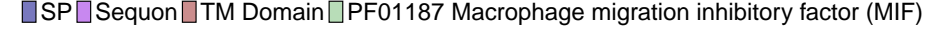


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

EAFLAYGELISICDLGPGVNGKLSSTIAELQTKLSDNRFRYKFDSPVSLYKREMSLSSLTPPPWATTGDRQGLN*

NbL07g04500.1 60S_ribosomal_protein_L7-4-like [MW = 28.09 kDa]

No. of times detected



log(intensity)



Values from



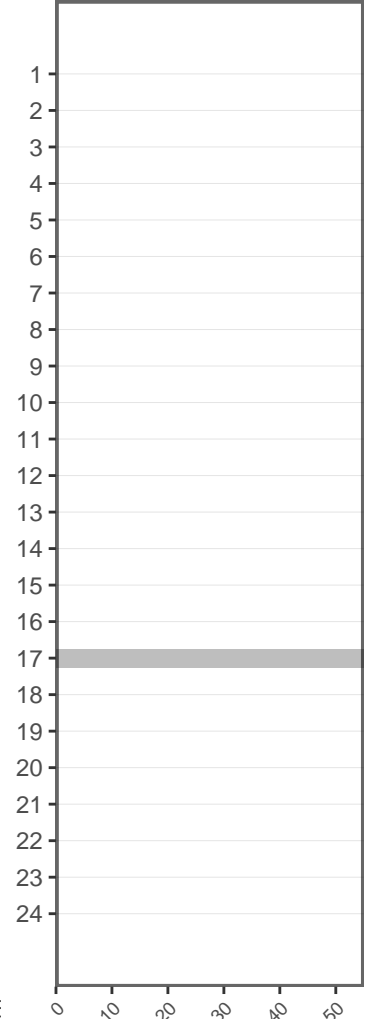
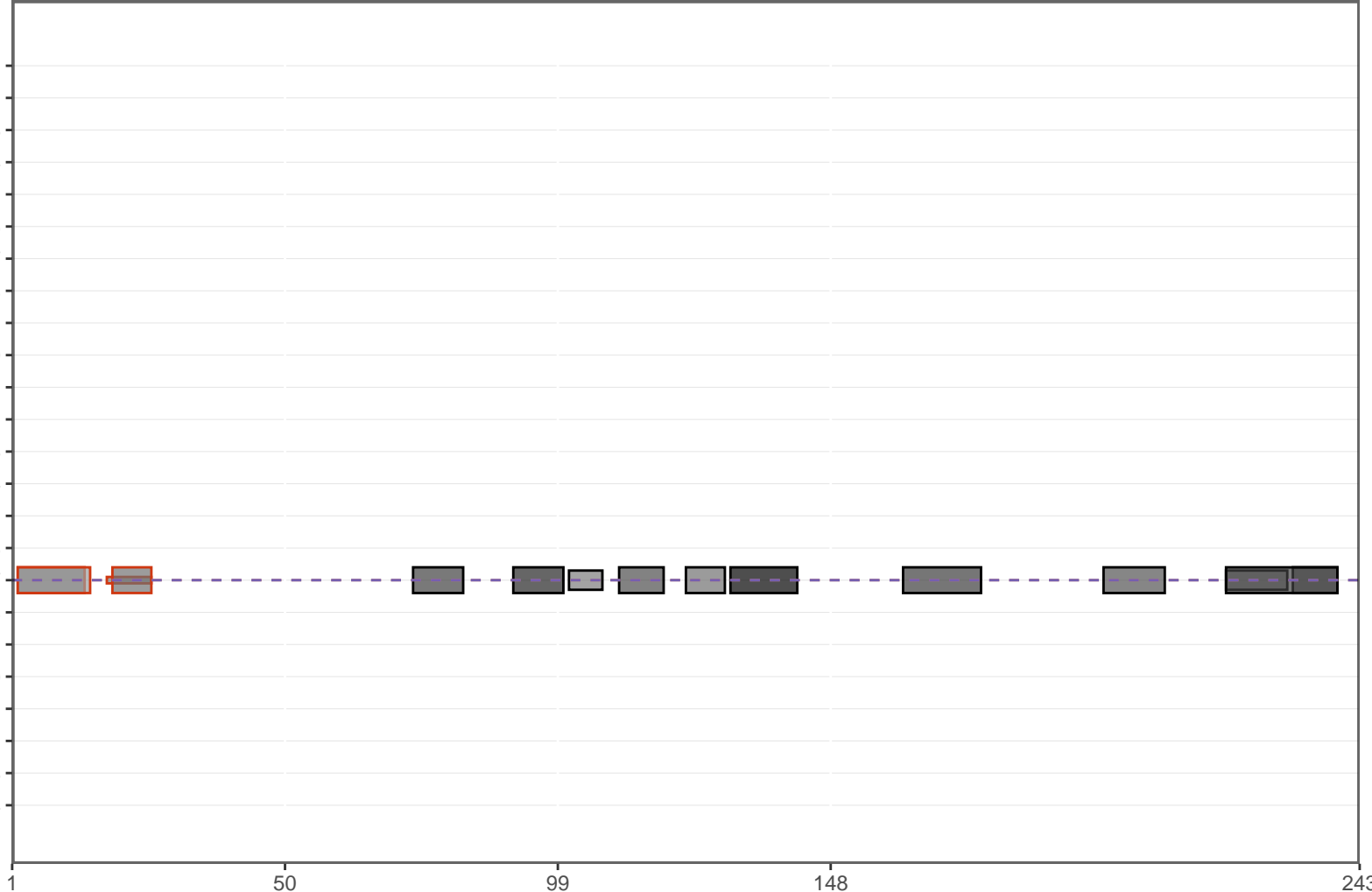
MW indication



Molecular weight

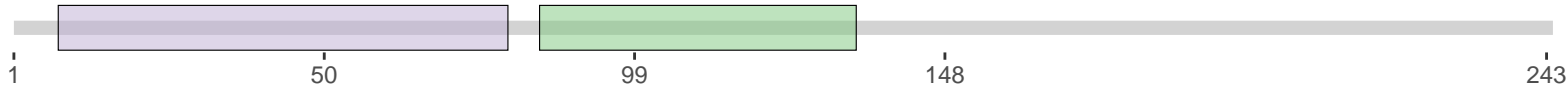


Gel Slice



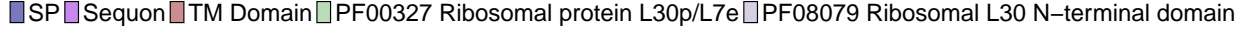
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

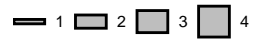


Protein sequence:

LRQIFNGVFLKYNKATVNMHLHREPEVYTYGPNLKRRELYKRGYKVDKQRALTONSVEIQVLGKKGICEDLWHEITVSPHFKKANNLWFFQLKAPLGLGKKRKHNYVEGGDAGNRENYNELIRRMN

NbL07g04460.1 calcium-transporting_ATPase_10_plasma_membrane-type [MW = 122.03 kDa]

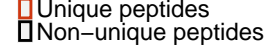
No. of times detected



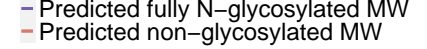
log(intensity)



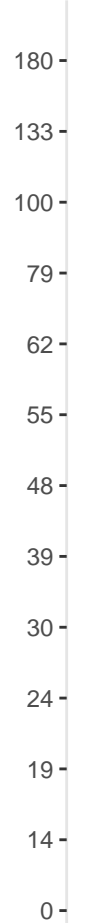
Values from



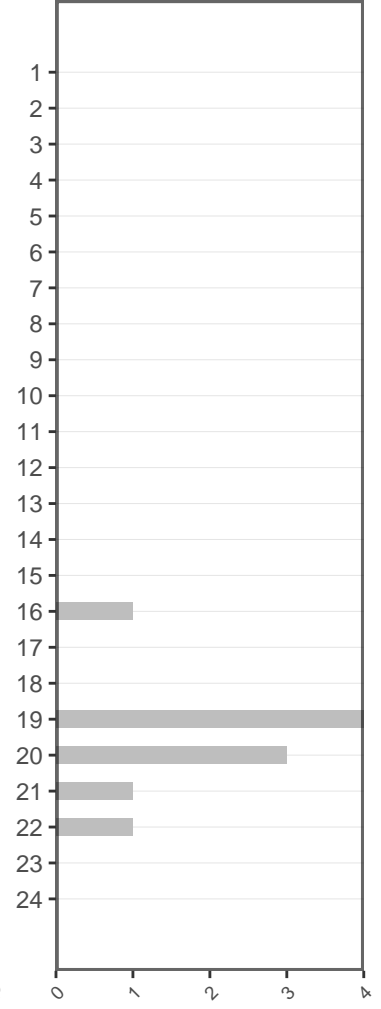
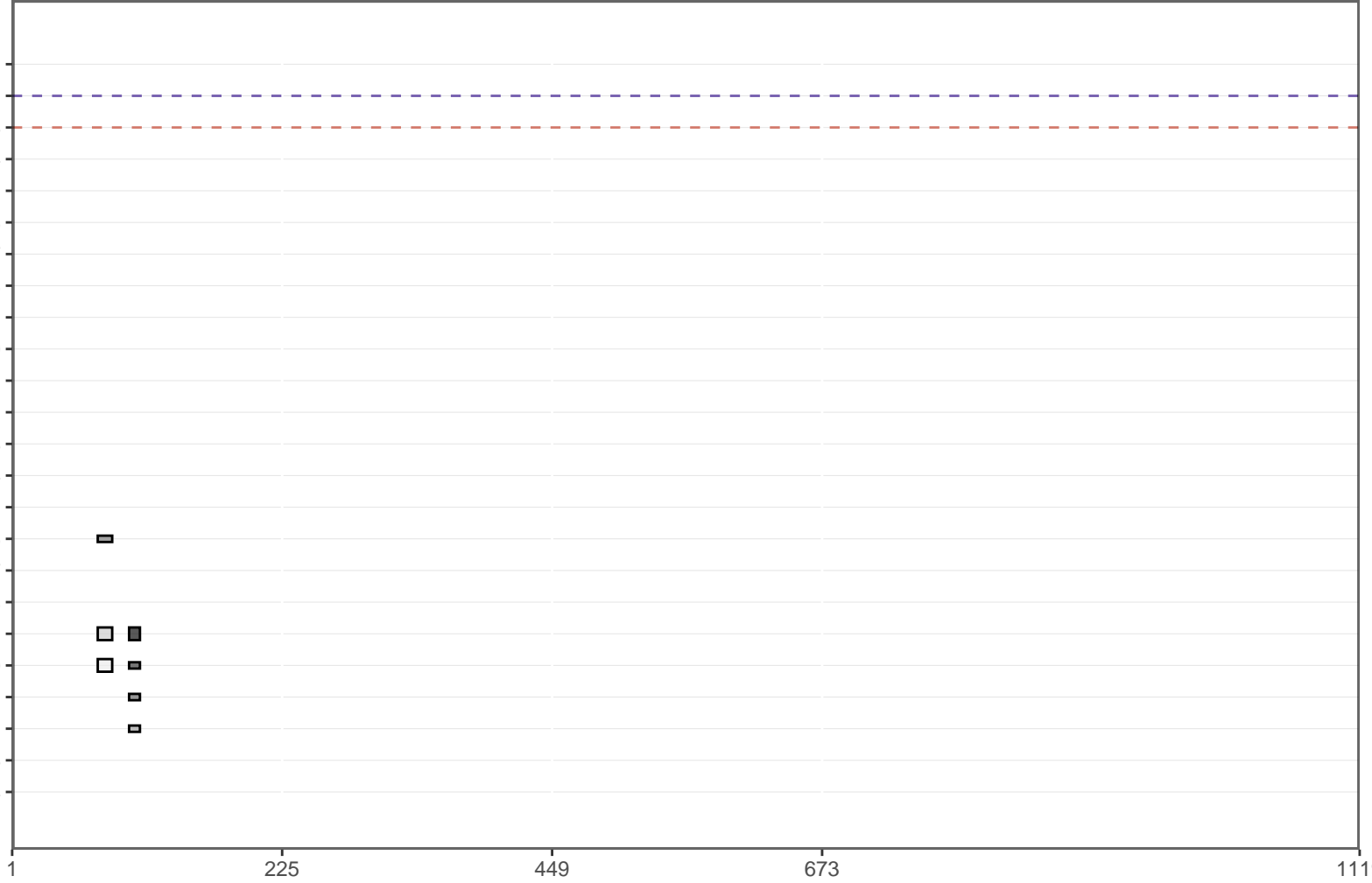
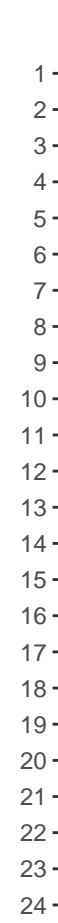
MW indication



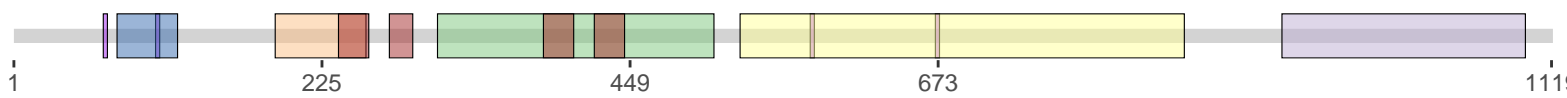
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

- SP
- TM Domain
- PF00689 Cation transporting ATPase, C-terminus
- PF00702 haloacid dehalogenase-like hydrolase
- Sequon
- PF00122 E1-E2 ATPase
- PF00690 Cation transporter/ATPase, N-terminus
- PF12515 Ca²⁺-ATPase N terminal autoinhibitory domain

Protein sequence:

ITVVEAYVCGIKINPPDRSAVPTFLSLLHEGVGLNTTGGIFVPGGGGAEISGSPTEKALQWAWNLGMNFDVQGEASIIHAFPNSEKRRGGWAALHDSVEVHLHWKGAAEVLSGGCTSFIDENGSVVPLGGDKVSHFKGQSDINMAASLRQVAAYRQFDKVEVNEEVEGWQPEGLVLLAVGKIDPCRPGRVDAVQLGSDAGVYKVRMVTGDNLGTAKAAIEGGKLSADATEPNLIEGKFRFALSEEDRKEVKEKISVMGRSFPNDKLLVQALRSKGHVAVT

NbL07g04430.1 uncharacterized_LOC107797264 [MW = 11.23 kDa]

No. of times detected



log(intensity)



Values from



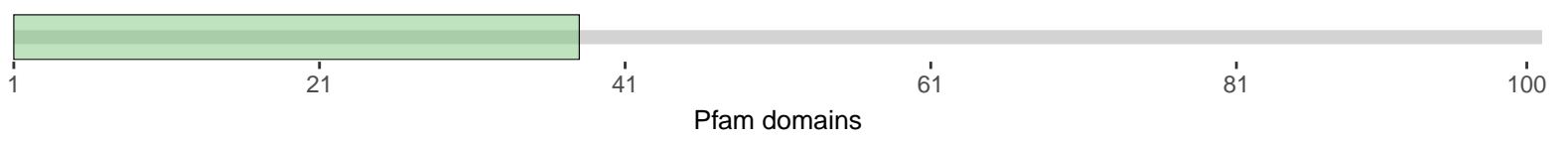
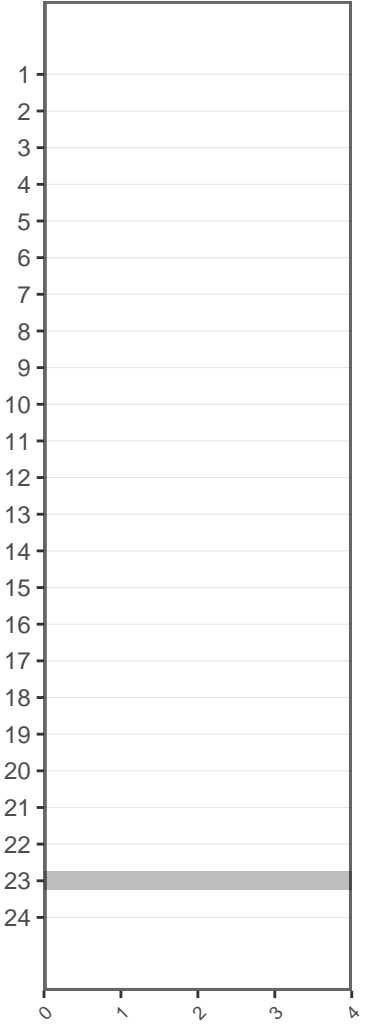
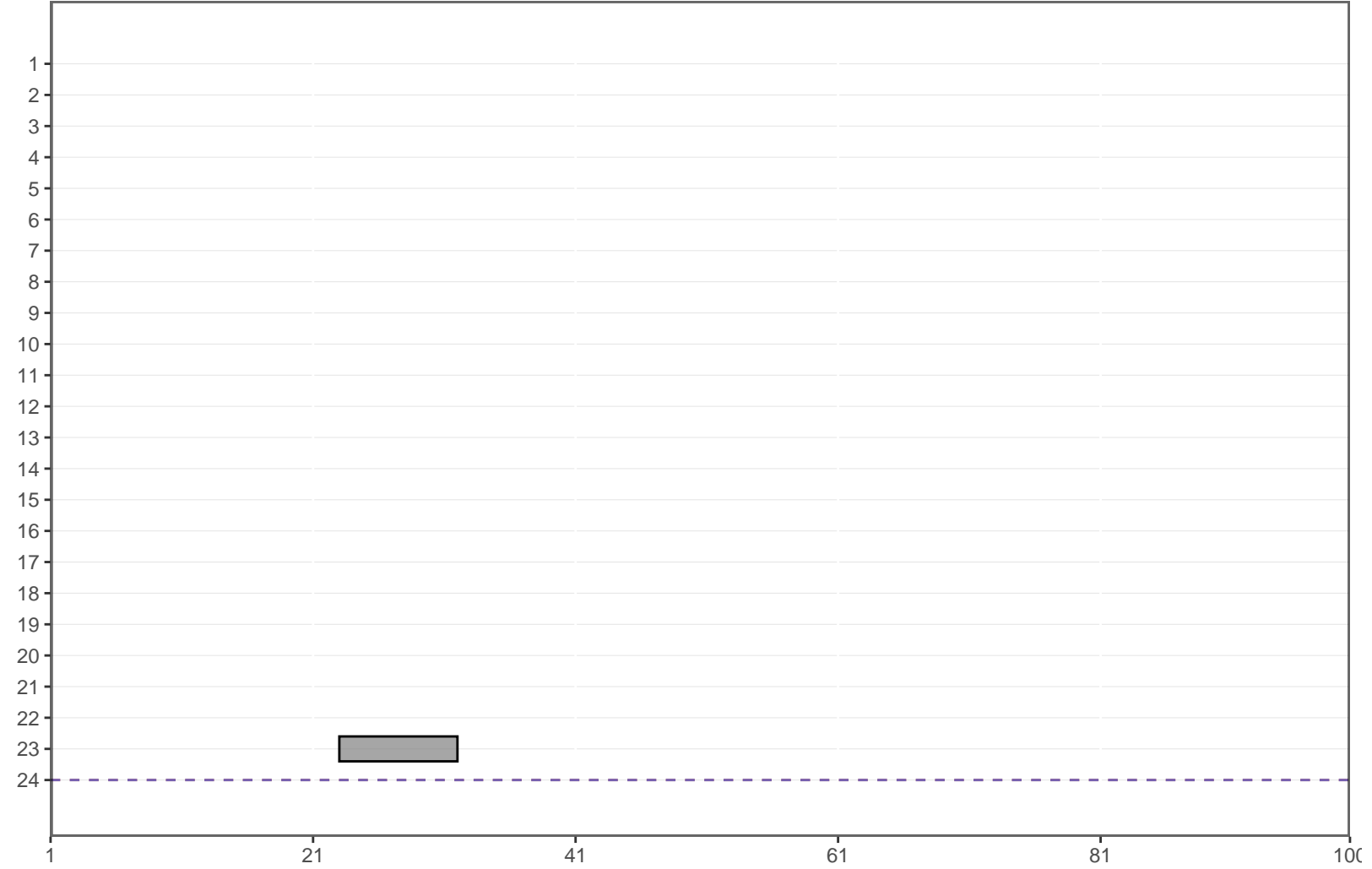
MW indication



Molecular weight



Gel Slice



Pfam Description



Protein sequence:

IQGYSTFASEGLSTTPVMTFRVTDGTSVTEGIRTGLEFLMPVKTEPTVTPWPKRGLVGLVFNISK

NbL07g04350.1 methyl-CpG-binding_domain-containing_protein_10-like [MW = 56.84 kDa]

No. of times detected



log(intensity)



Values from



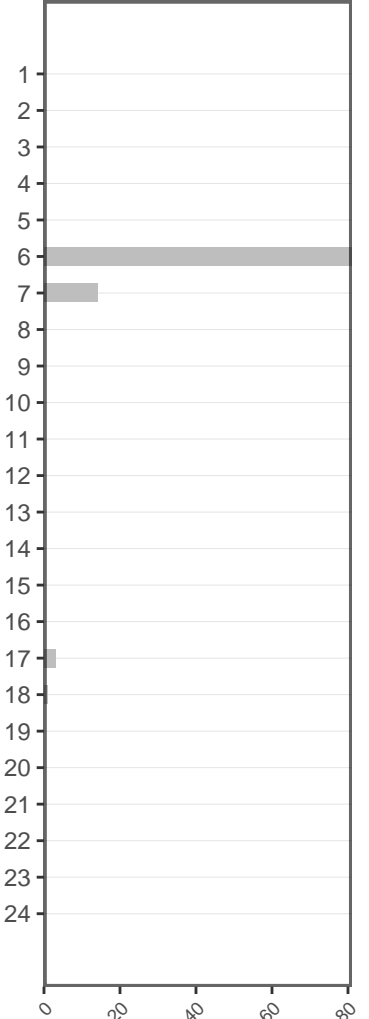
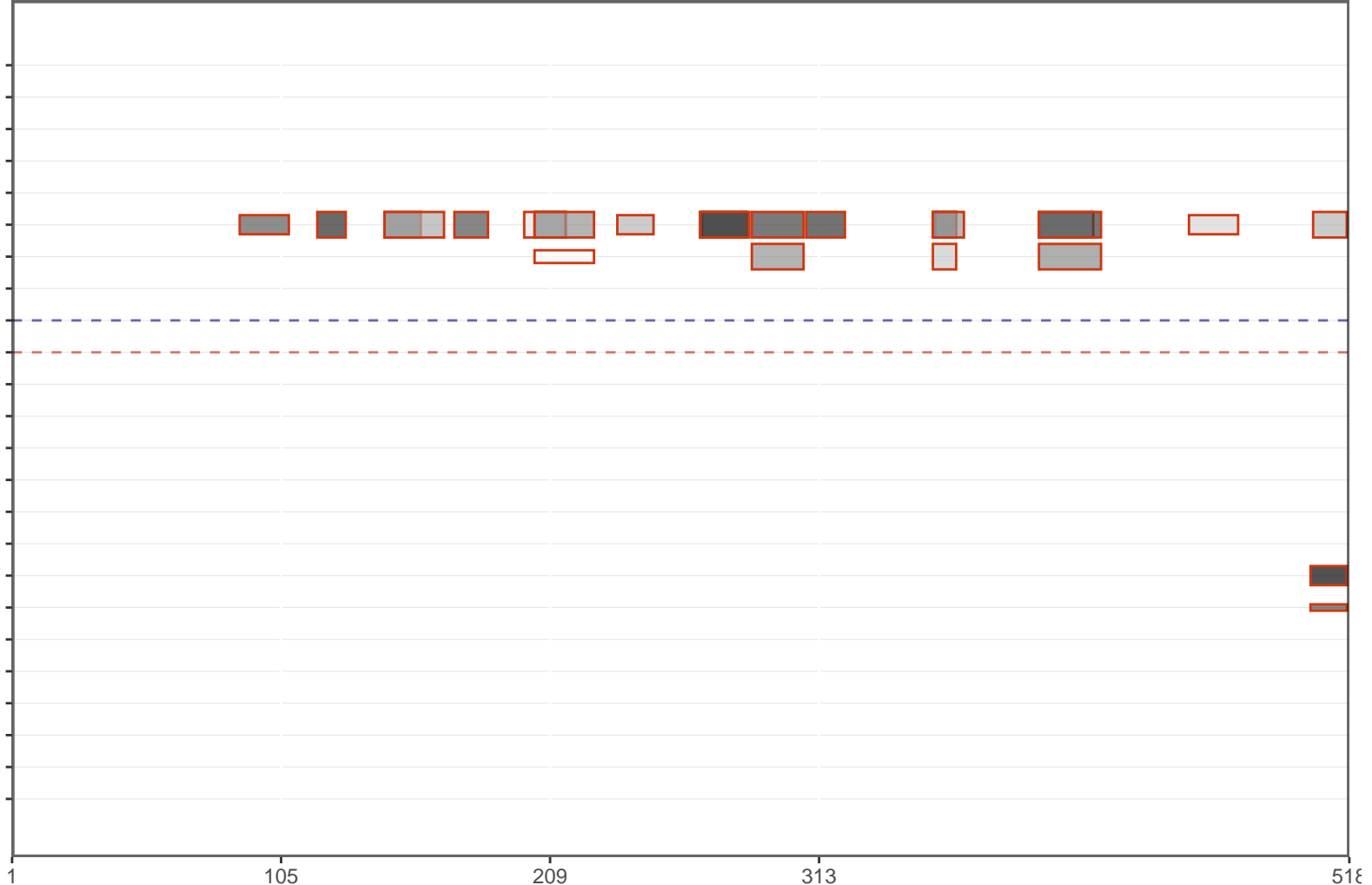
MW indication



Molecular weight



Gel Slice



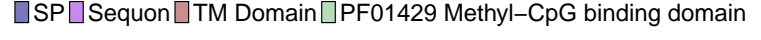
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

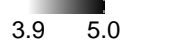
SKVLDVEKDVYKMGAGNAEKEMHSSNVDAVEENGADRKSDGGTDEGKAEEAAEGDKDKMADNVGHFVDEASVYKKAFLKFEATKDEEGKDVGVGSEVKEKLTETKEDPFAAVEKDKVMDADNAAEKKDEMHSNVDVAKENGADKKSEGGTDEGKAEDAPAAEAGDKDKVMDADNVGHFQHPEDVEASVYKKAFLKFEADVPEATRDDEEGKDVGVGSEVKEKFAEKKKEDLSAAEGKKHGFPEGEQRDENGAAARKSTGGDALMNSDN*

NbL07g04300.1 blue_copper_protein-like [MW - SP = 32.65 kDa]

No. of times detected



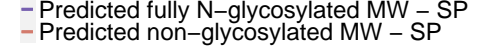
log(intensity)



Values from



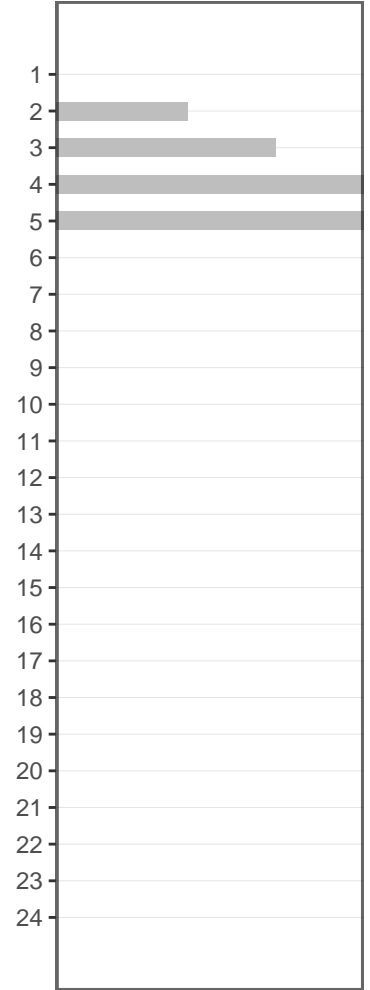
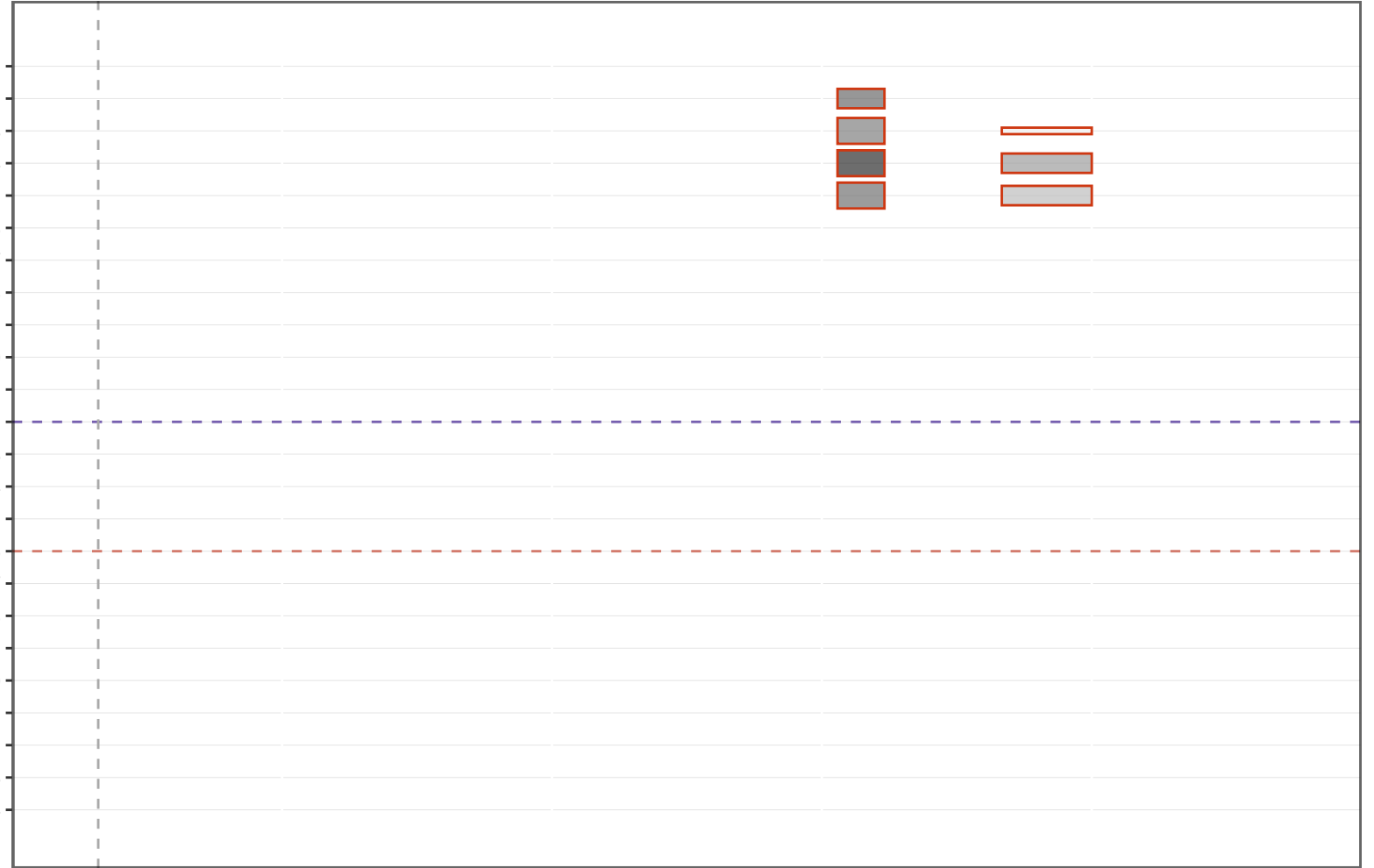
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

MFSLAATPSASAPKPEVAAGDTFVGGMMGWVFTTGGPNVAGTFWANGKSKFKVGDRLVFNFDGRHINAMNKAAYDGGNTTSPINTSTGPARHILNNGENYMGITFFNHSGLGKLIANVTGTSAAAPMPGIAATPDSGTVPEVPSGDSPTVSPPPPSASAPLVLAAALPTFLSLAFARLLN

NbL07g04180.1 uncharacterized_LOC109234414 [MW = 15.69 kDa]

No. of times detected



log(intensity)



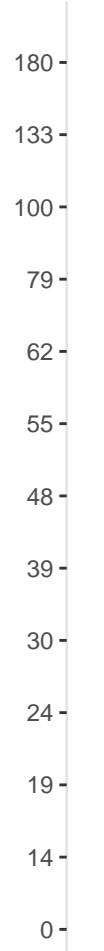
Values from



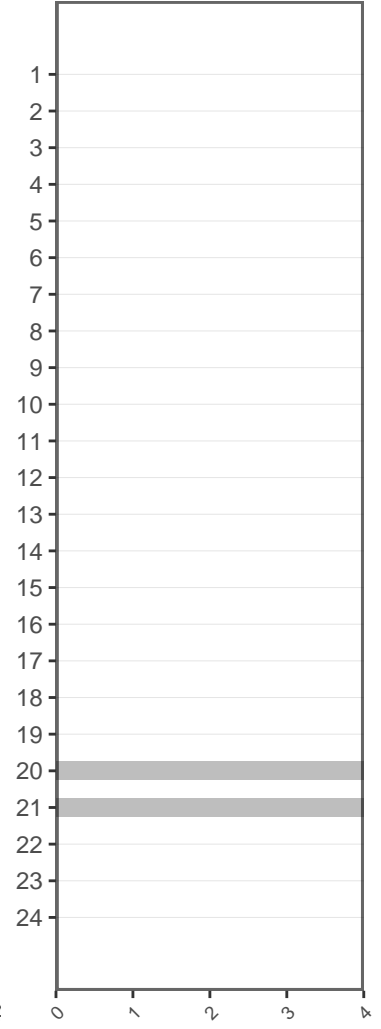
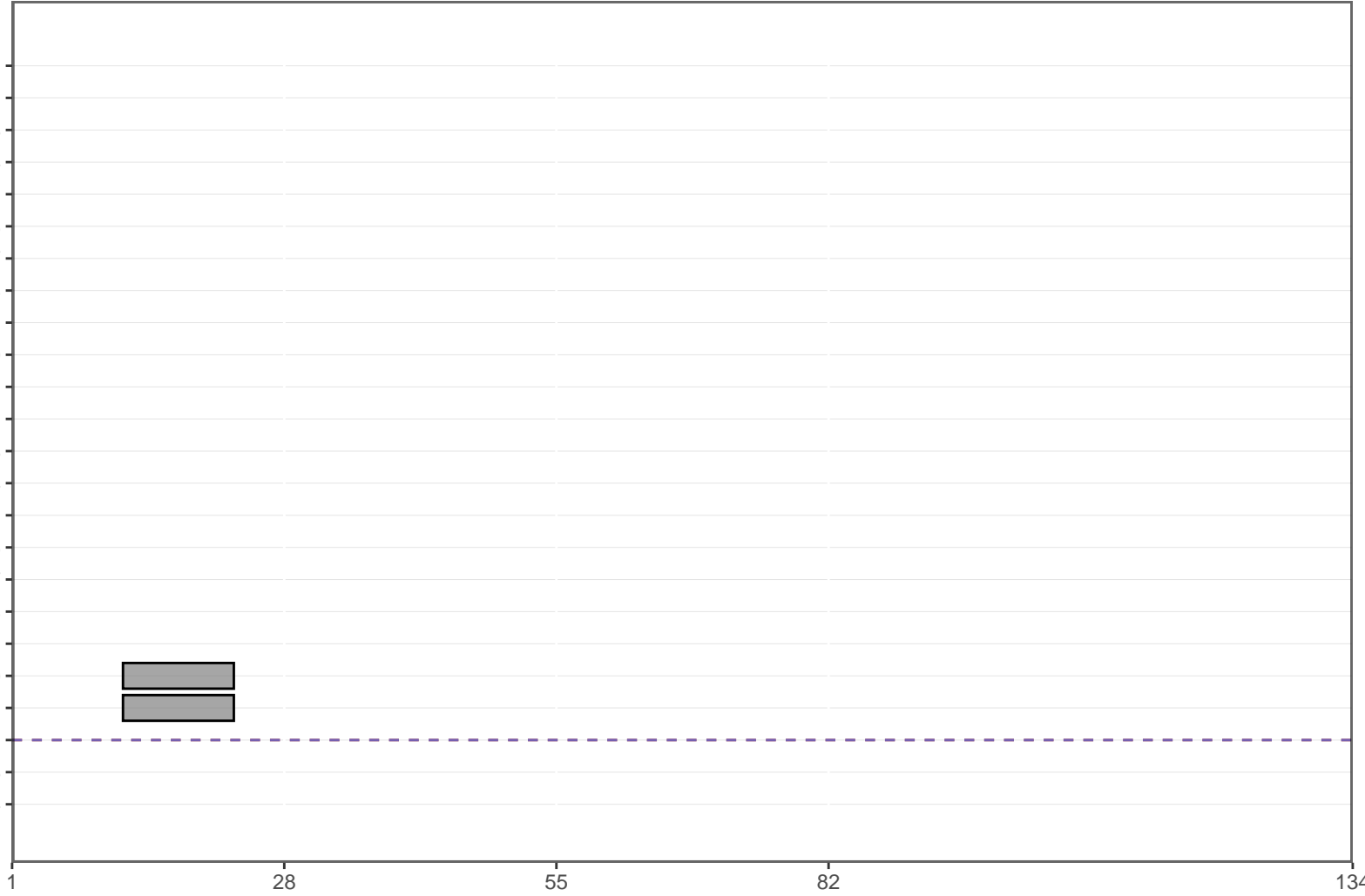
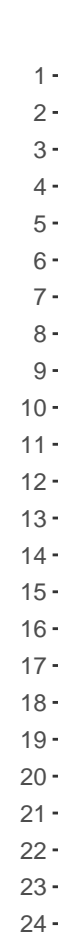
MW indication



Molecular weight



Gel Slice



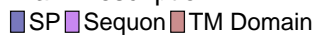
Protein length



Pfam domains



Pfam Description



Protein sequence:

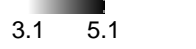
ARLRKEVLLAGQDWPYDPERKEMRTKQKGGKDRISAERKREKTAELMGMKMPDMLADYRKRIRWERIKMKAEEAARRAVGE

NbL07g04100.1 probable_galactinol--sucrose_galactosyltransferase_6 [MW = 100.53 kDa]

No. of times detected



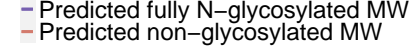
log(intensity)



Values from



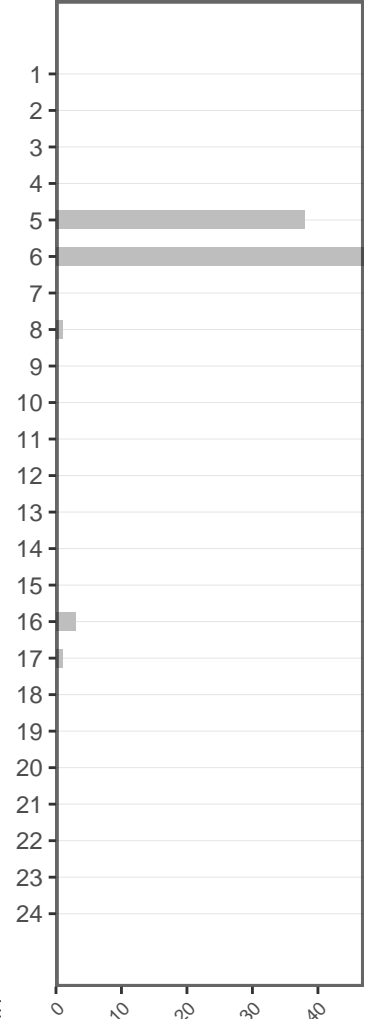
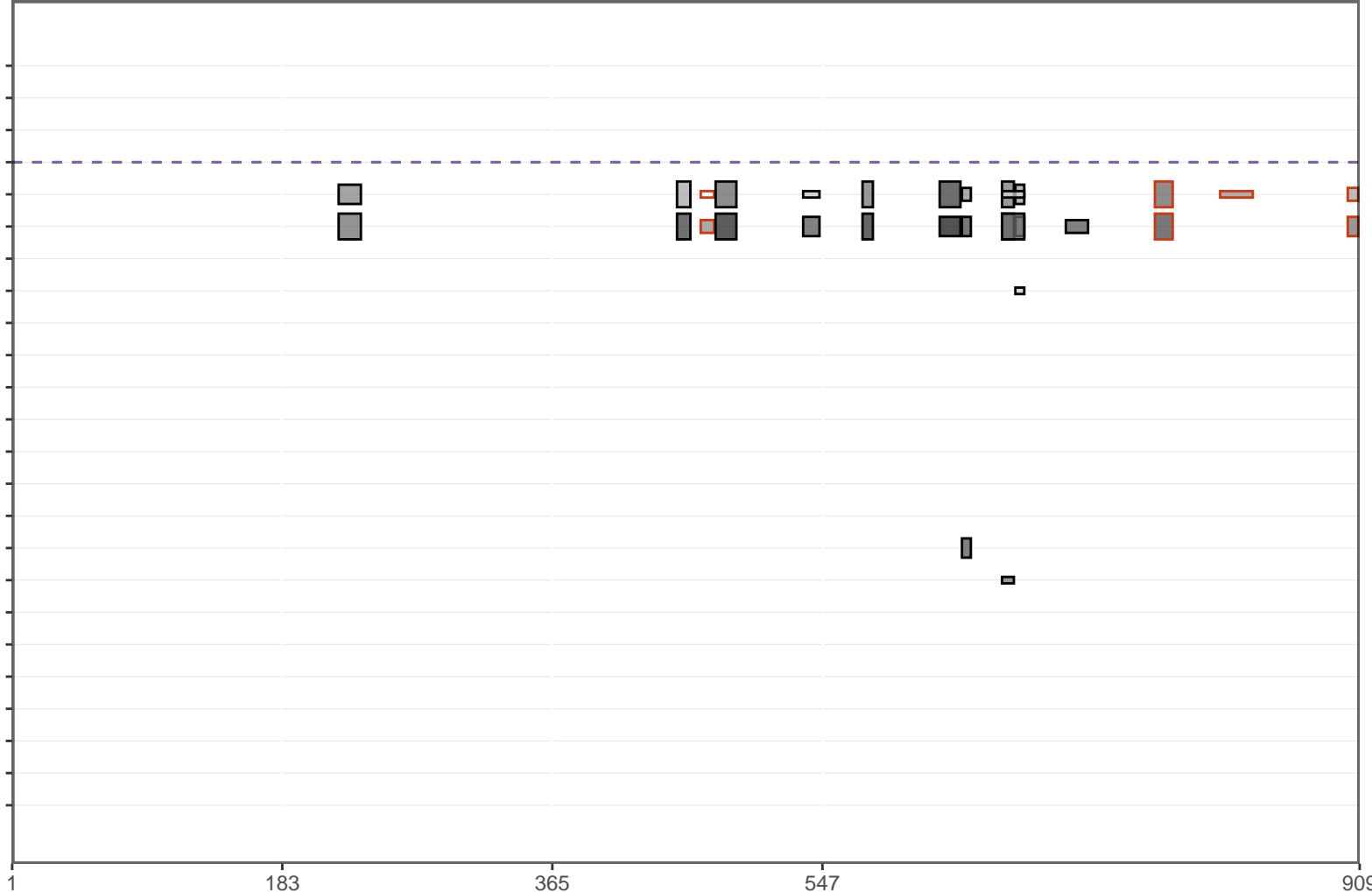
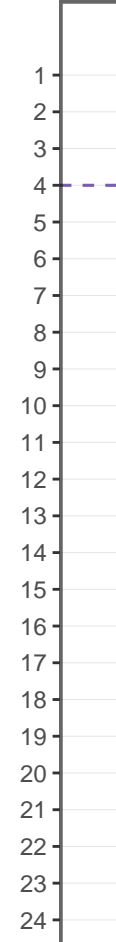
MW indication



Molecular weight

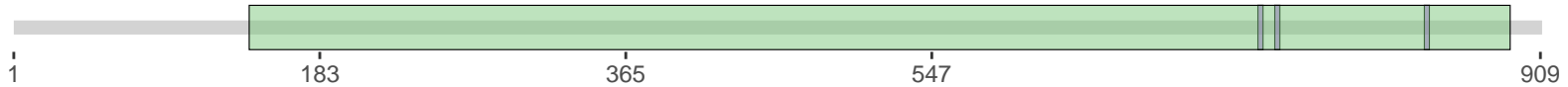


Gel Slice



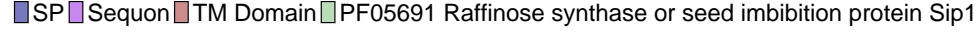
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IVKGMEEYGSVMKVPETKGMENEPGRWTDAAVQGLGLVNPKSAKFKYEMHSYLSAAGVDGLKVDVQGLLETLGDGLGRVELTKGYSQALDASVSKNFPDNGGACGMSHSTDAIYCGKGTAVVRASDDFYPRDPSHTIHAGVAVNSVFLGEIMVFDWDMFSLHFAEYHGSARALSGGPPVYVSDAPGKKNFDFVLRKLVLRDGSVLRARLPGRPTKDSLFSDFSRDGVSLKHWMMKYTGVLGVYNGGGAWNTVERKNTFHQTNSEATGYVRRGROVHFS

NbL07g04060.1 12-oxophytodienoate_reductase_3 [MW = 43.55 kDa]

No. of times detected



log(intensity)



Values from



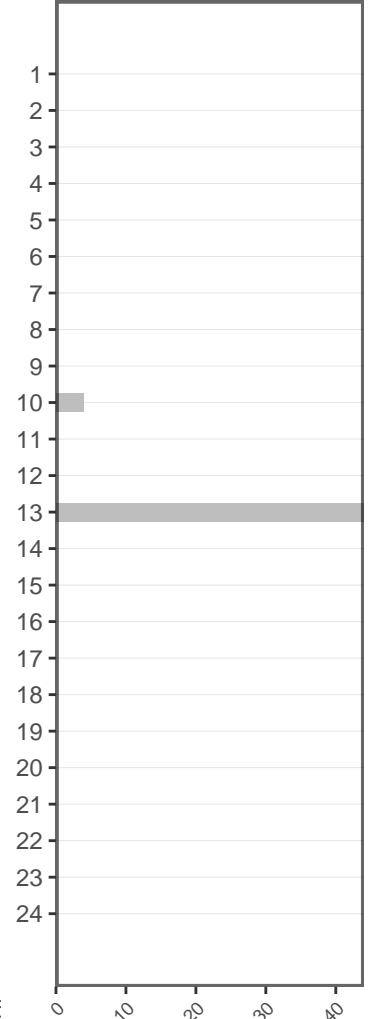
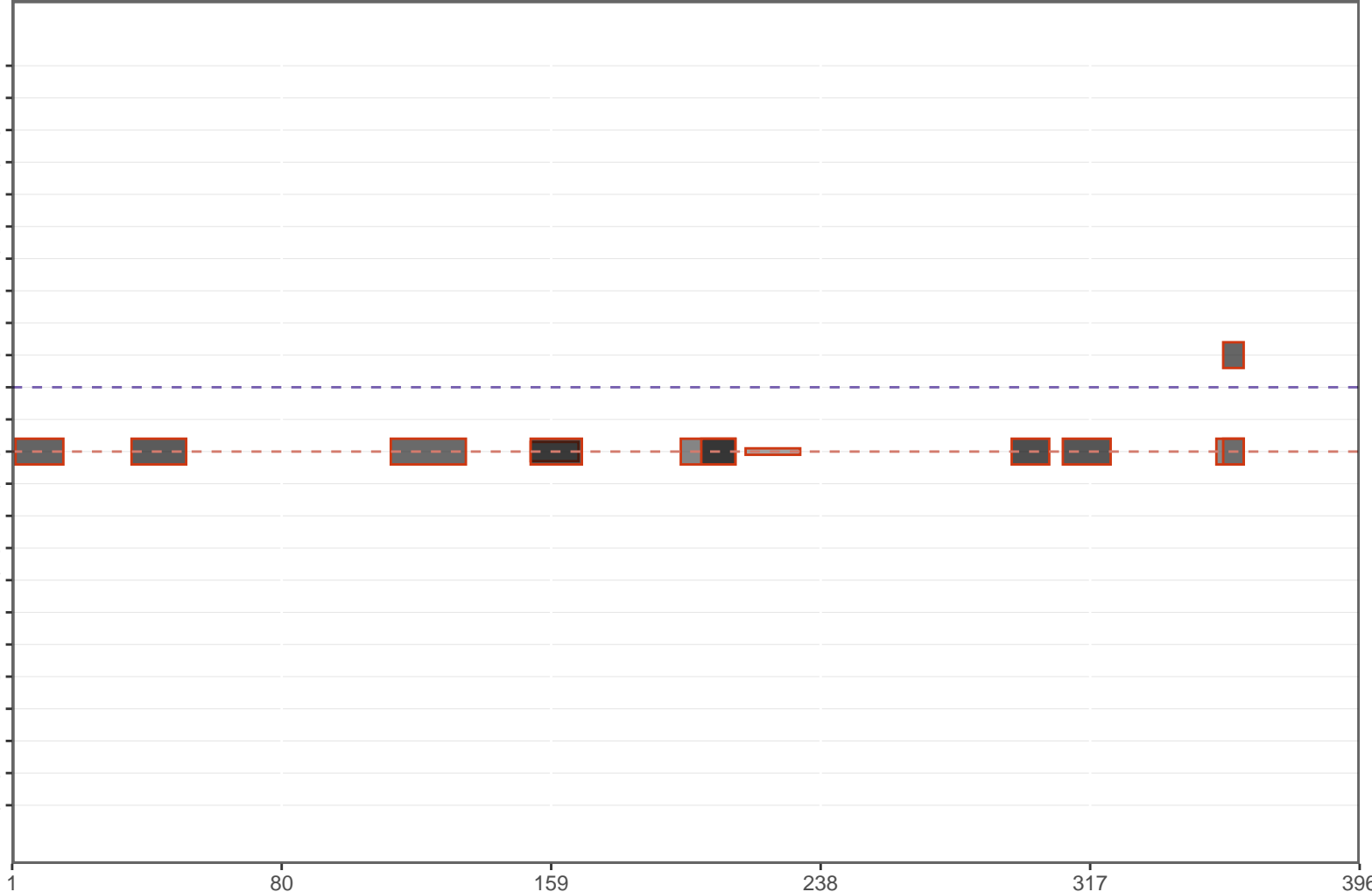
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

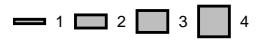


Protein sequence:

3AHGYLIDQFLKDGINDRTDEVAGSLNRCKFMGVVQAVVTAIGADRIVGVVMSPAIDHLDAMDENPLSLGLAVVERLNKLGHFQSKLAVLHVTQPRVYVYGTQTAGRLGSEEEALLMRTLRLNAYVGTIYIGSGGYTRELGIEAVAGGDADLVSYGRLEFNPDLMRLKVNAPLTKYIKRTFTYQDPVIGVYDYPFLGGNGNNVSLRL

NbL07g03960.1 probable_sucrose-phosphate_synthase [MW = 118.81 kDa]

No. of times detected



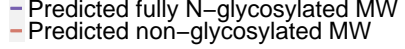
log(intensity)



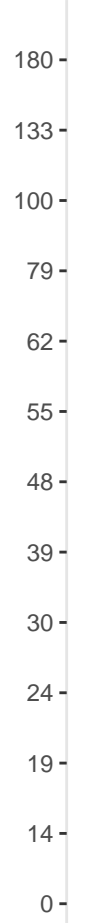
Values from



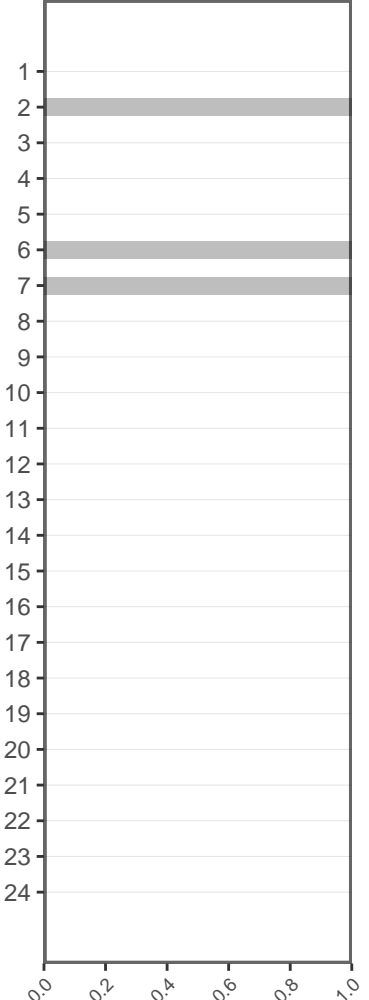
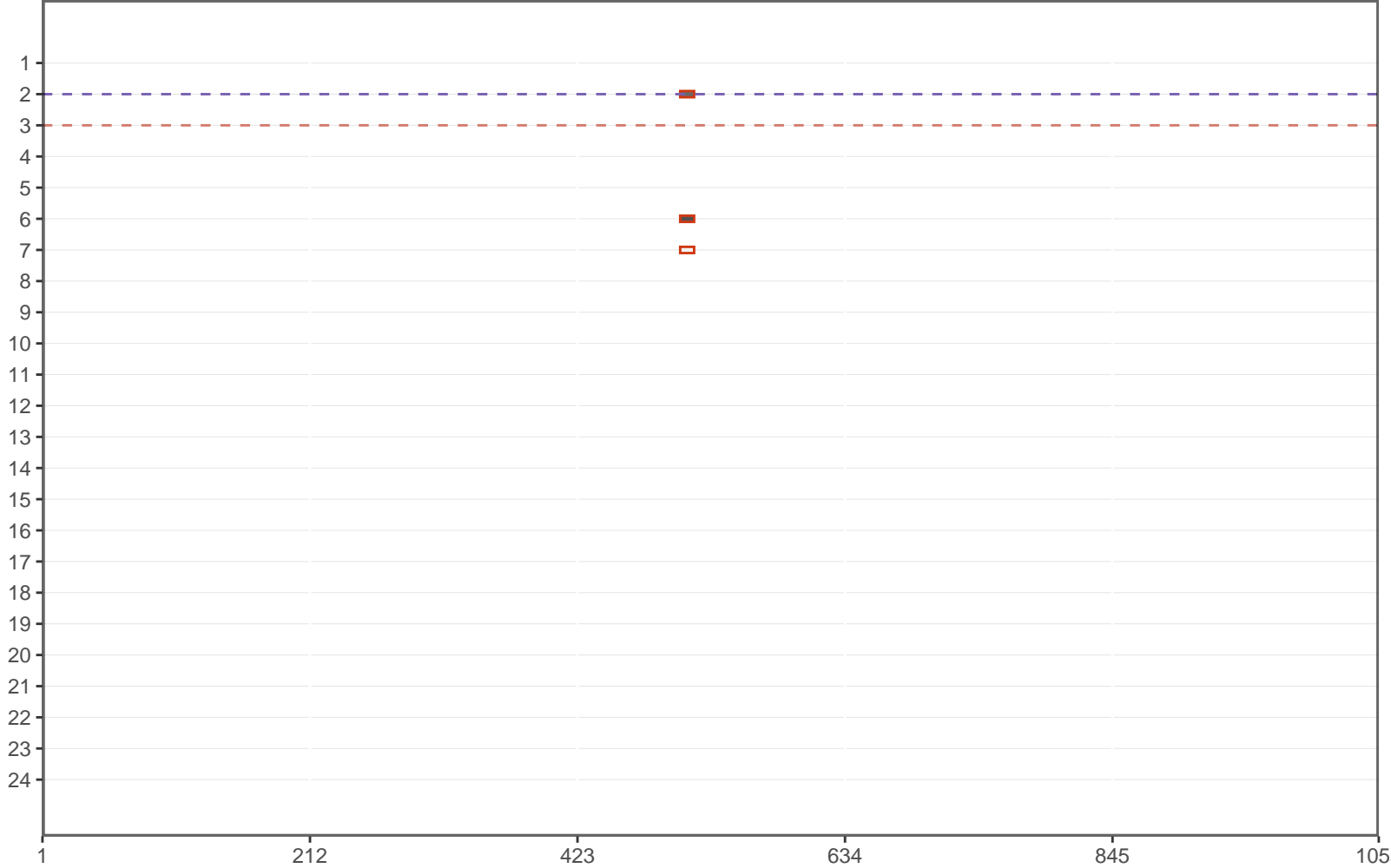
MW indication



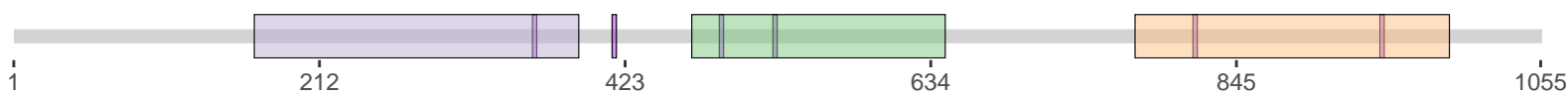
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

LMGSRDNDIDEMSTNSVLLSLKMDKVDLGGVWPKHKGADPDIYRLAAKTGVTNPFIEPFGLTLEAAAGLPMVATKNGGPPVDIHRVLDNGLLVDPHQQAADALLKLVADKHLWAKRANGLKNIHLFWPEHCKTFLERIASCKPRQPRVLRRTDDDDDENSETDPSDLSLRDHDHISLNLRFSLDGEKNDKNEADNTLDFEVRSKLENAVYLSWKGVLKSTPKAWSSDKDQDNGAGKFPARRRRHFVAVDGDTSGLSEVRFKFKVAKERAEQ

NbL07g03880.1 cytokinin_dehydrogenase_7 [MW = 57.94 kDa]

No. of times detected



log(intensity)



Values from



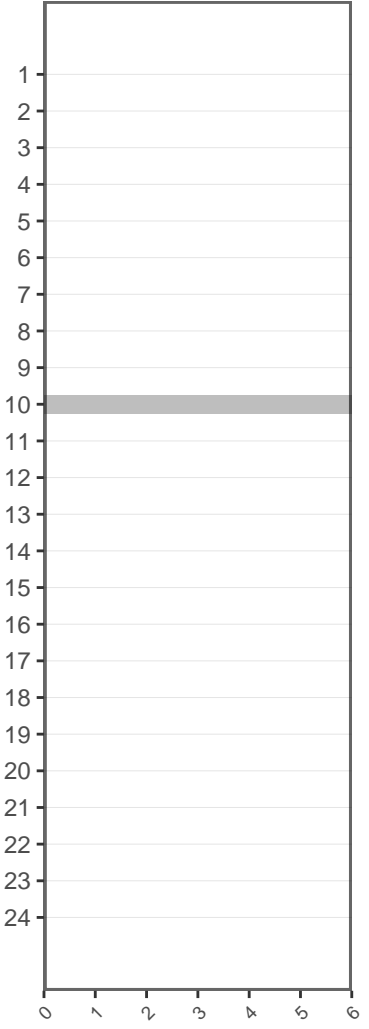
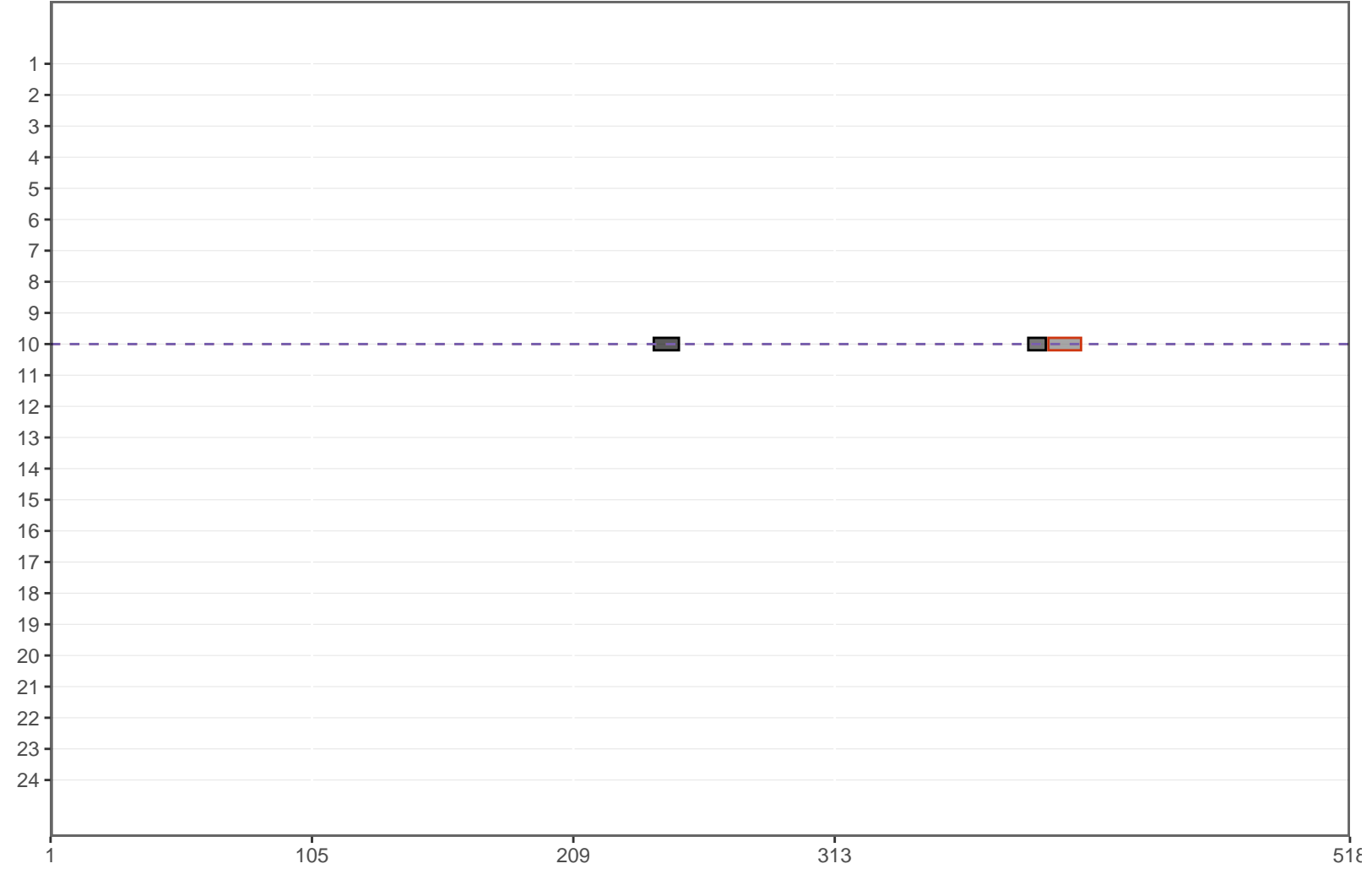
MW indication



Molecular weight

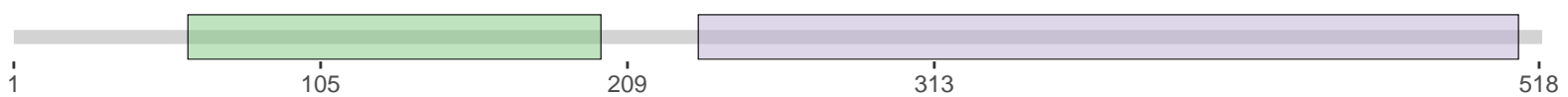


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01565 FAD binding domain
- PF09265 Cytokinin dehydrogenase 1, FAD and cytokinin binding

Protein sequence:

DEFTRDALLVMSPEFGDVFEGFVFNSSDDPVGWSPVLDNHPDFDPLPTNTGPAVLEVALHYHNDHPSTVNMVVEKLLGRLEFLEMFVYDLYMDLFLRVRKQVEGMARDGWDAPHPWLNMFVSKRDIAEFNRVIFGNILKDGINGPILTYPLIRSKWNRSSVLPKGEIFLVALLRFSHAHPKESIEINEMVAGNGEILGTCTNNGDFDKLPLPHYKSTEEWKKHFGDQWGRFVERKSGDFPKAVLAPGQKIFTRVGR

NbL07g03860.1 uncharacterized_LOC109237049 [MW = 26.65 kDa]

No. of times detected



log(intensity)



Values from



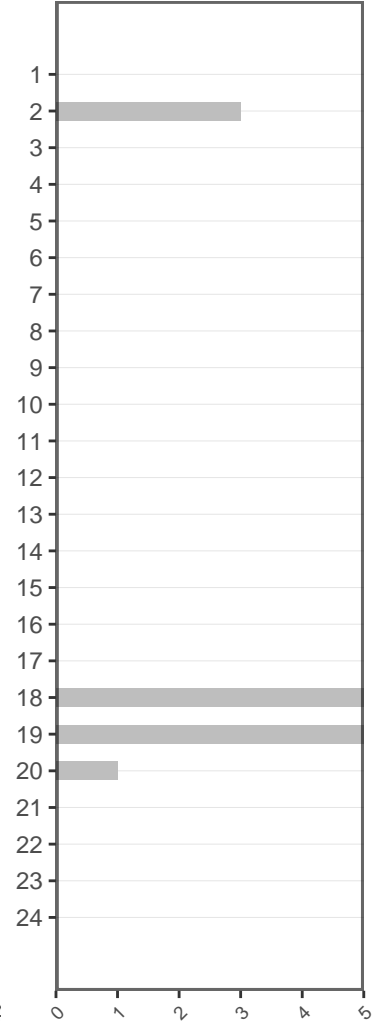
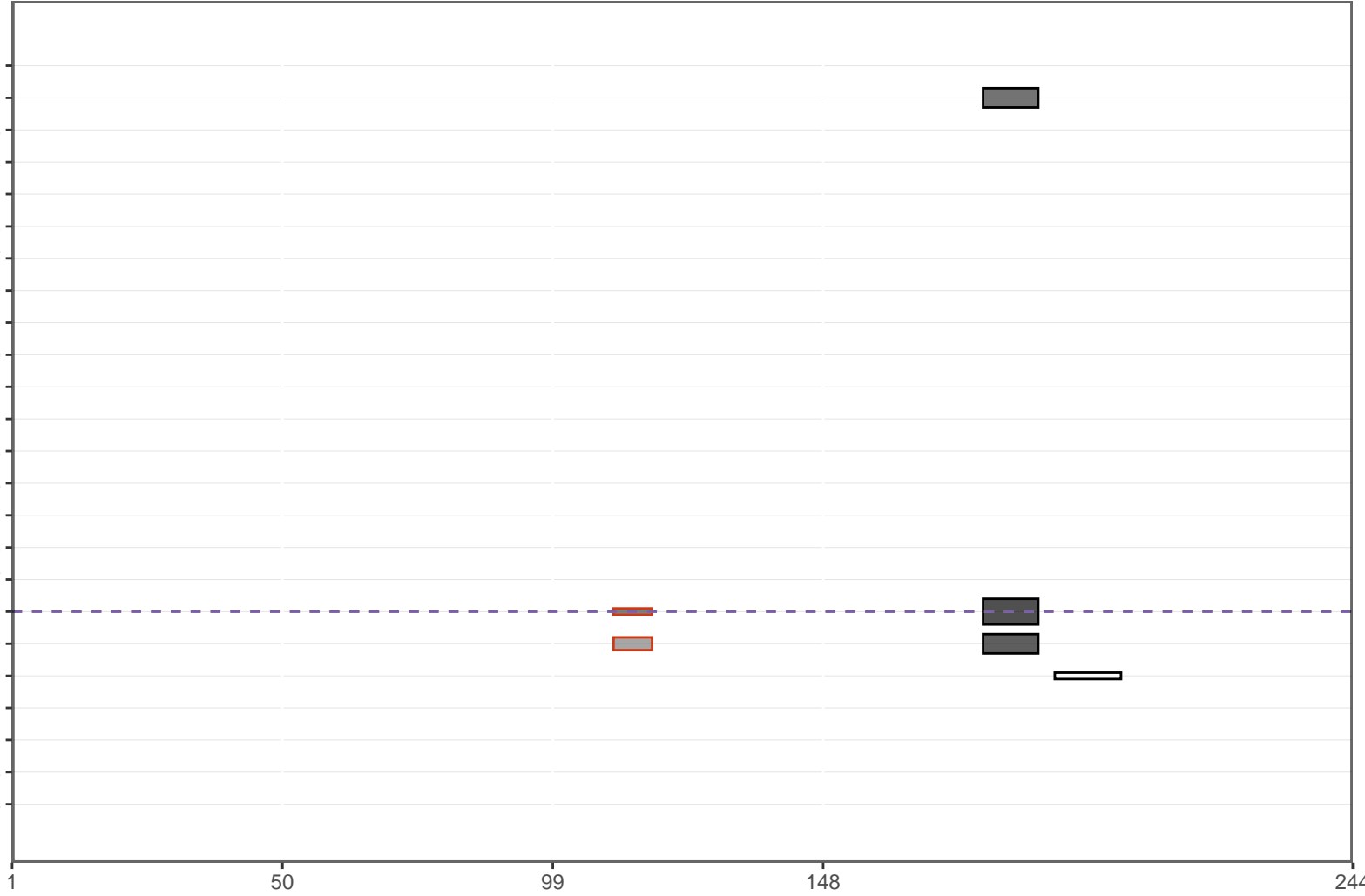
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



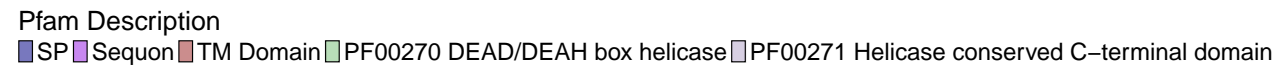
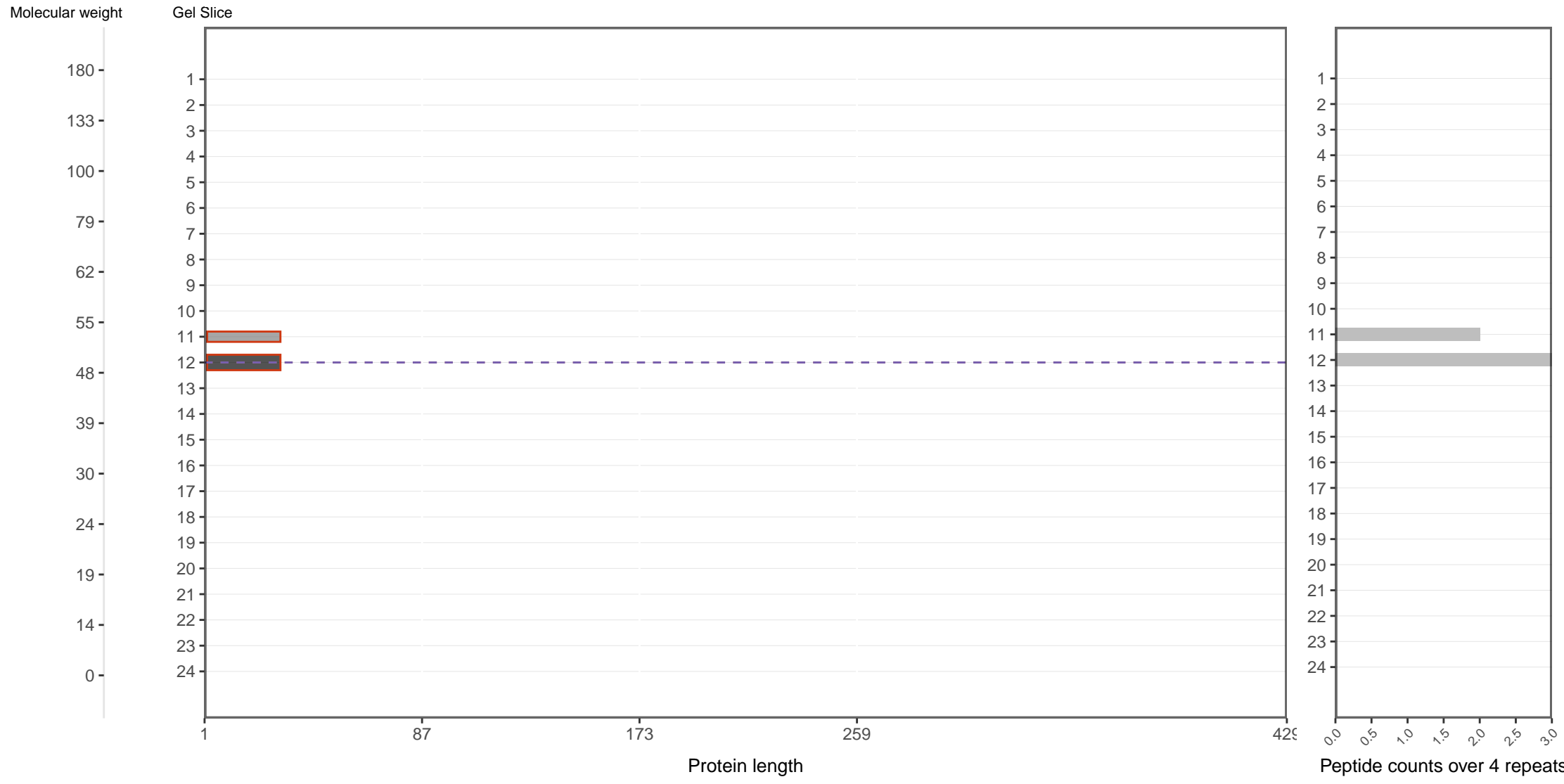
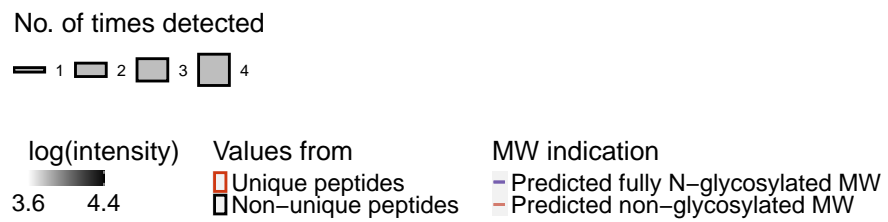
Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

SLEVDQPKYGDCCRNILRSGFASLRVNRWAGVASDDGNGESAENVDGGLSALEGLDLSLLLRASRNDPGASIDGMKAKITALNALDLSLLKTVPMMLDKGKIVADSYFFADEEDVTPKLDPLNKLQLESLL

NbL07g03630.1 DEAD-box_ATP-dependent_RNA_helicase_56-like [MW = 48.44 kDa]



Protein sequence:
 XXXLESLLDMRRDVGEIFRMTPHDKGVMMFSAFLSKERIPVGGKFMGDPMIEHYVDEEAKLTHGLVGHYKLSSETENRKLNLDLDFNGVYVFKVSRAAELNKLVECFNPFKIDHSGMTQEERLTRYKGFKEGHKRILVATDLVGRGIDIERVWVINYVMPDSADTYLHRVGRAGRFQTKGLATFFVSSASDSDLNQGQERFEVDIKELPEQIGTFTYMPD

NbL07g03500.1 protein_WVD2-like_5 [MW = 48.15 kDa]

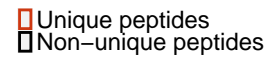
No. of times detected



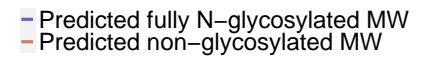
log(intensity)



Values from



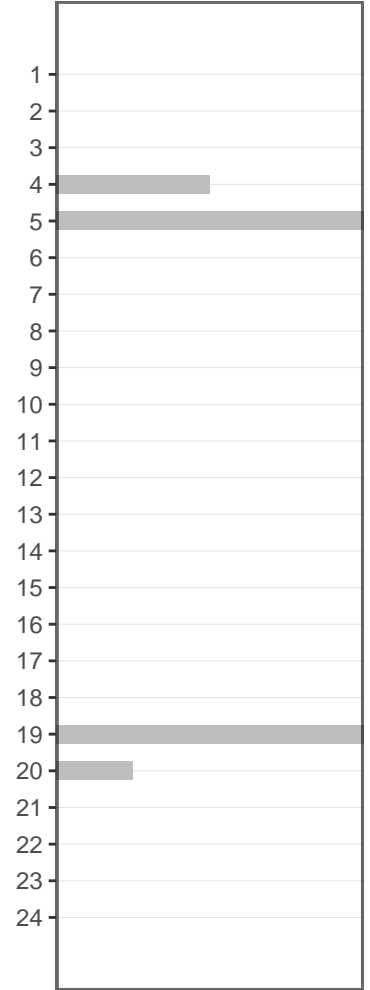
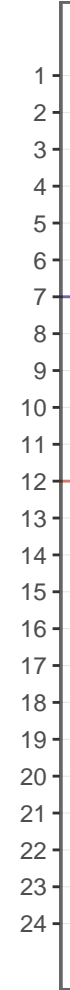
MW indication



Molecular weight



Gel Slice

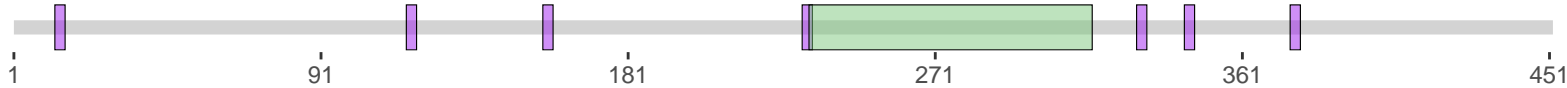


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

EEESPAAADAXPRKVGALPTYNMFSKGDERAERKREFYKLEEKHAKVEKENLQALSKADQEAIEKMLRSLKFKATMPFSGYDEPPPKVELKIPTRAKSKPLGRKKSPTTRVNDGTAMHTERLGLDENATGNFKVHAFDVKPKSRKSLPKLPKLP6GKVLKLSKSKPSELKTSIGKETNEAANNMNEVASGPNVLEGTNIEATGAVETSGSKTVEAGDAETNVVQGSIAWEI

NbL07g03330.1 ATP_synthase_subunit_b'_chloroplastic-like [MW = 24.05 kDa]

No. of times detected



log(intensity)



Values from



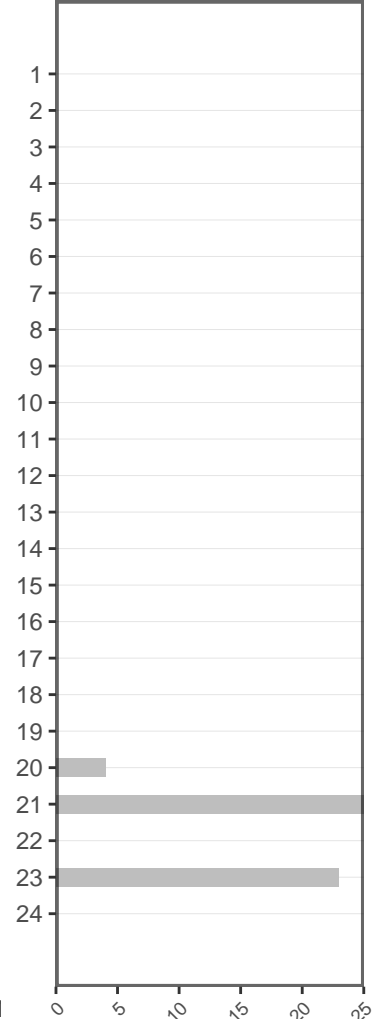
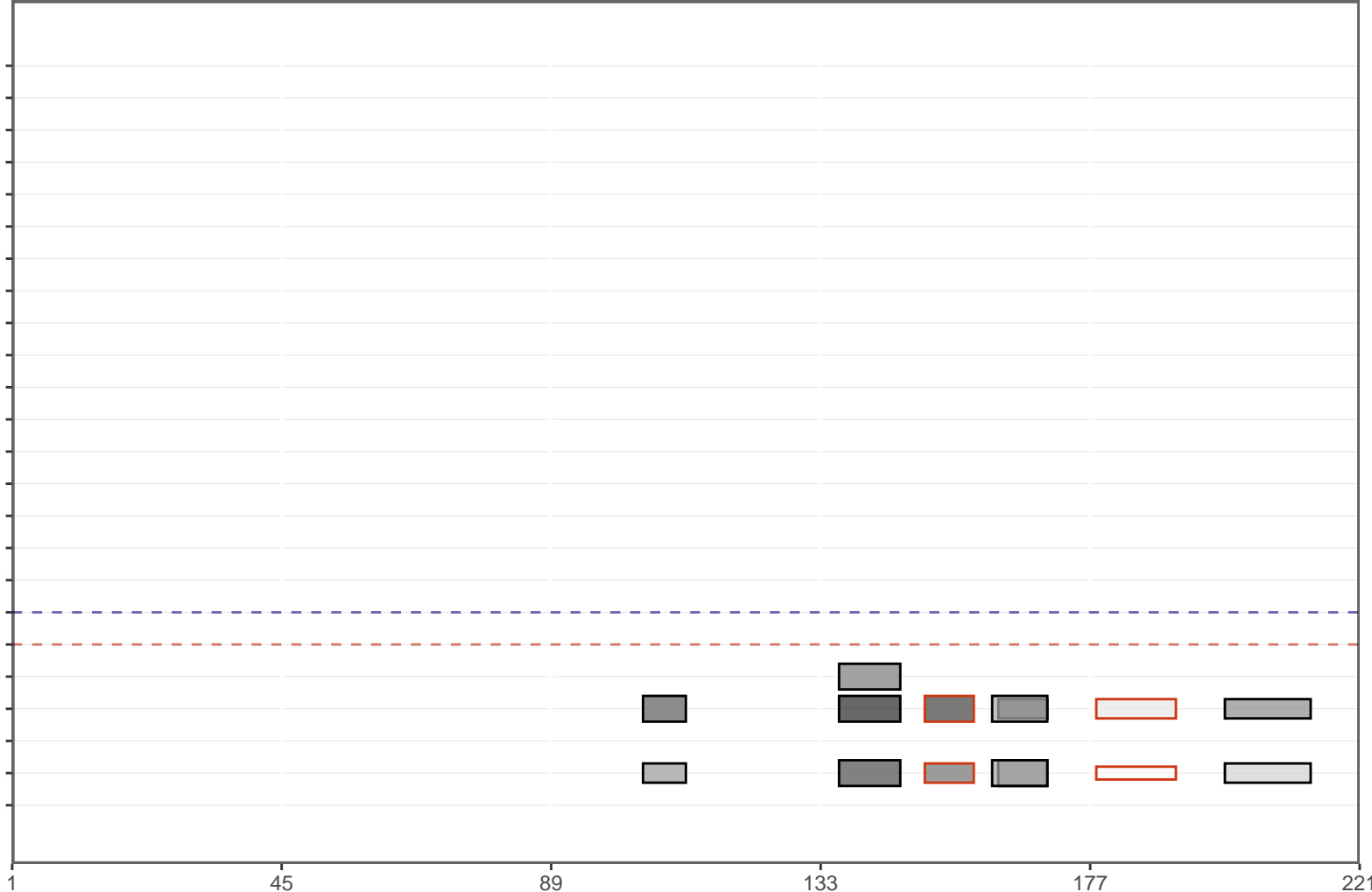
MW indication



Molecular weight

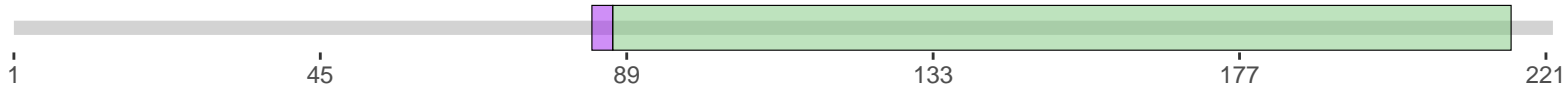


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LDKLYFSPLGKFMDERDSAIKELNSVKTSAEVKQLEDGAAAMKAAAEVSAALNKKMKETQLEVEGKIAEGRKKVVEVLDGALABLQKQKEETIKSLDSQAALSDIVKVKLPVSN

NbL07g03080.1 protein_MEMO1-like [MW = 19.57 kDa]

No. of times detected



log(intensity)



Values from



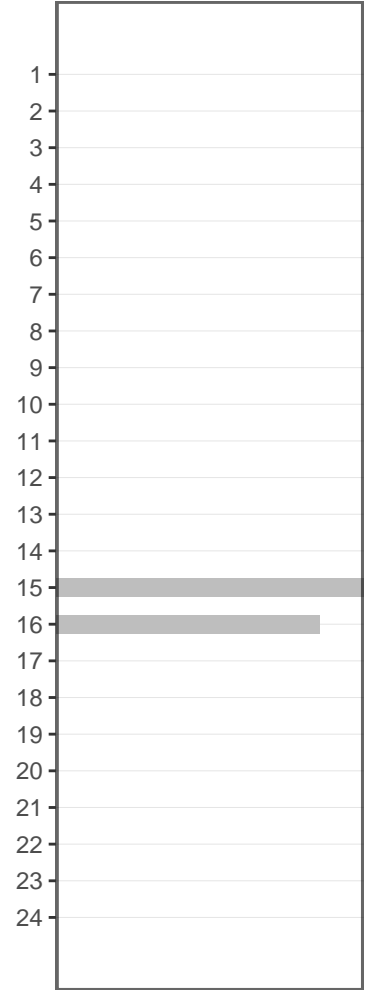
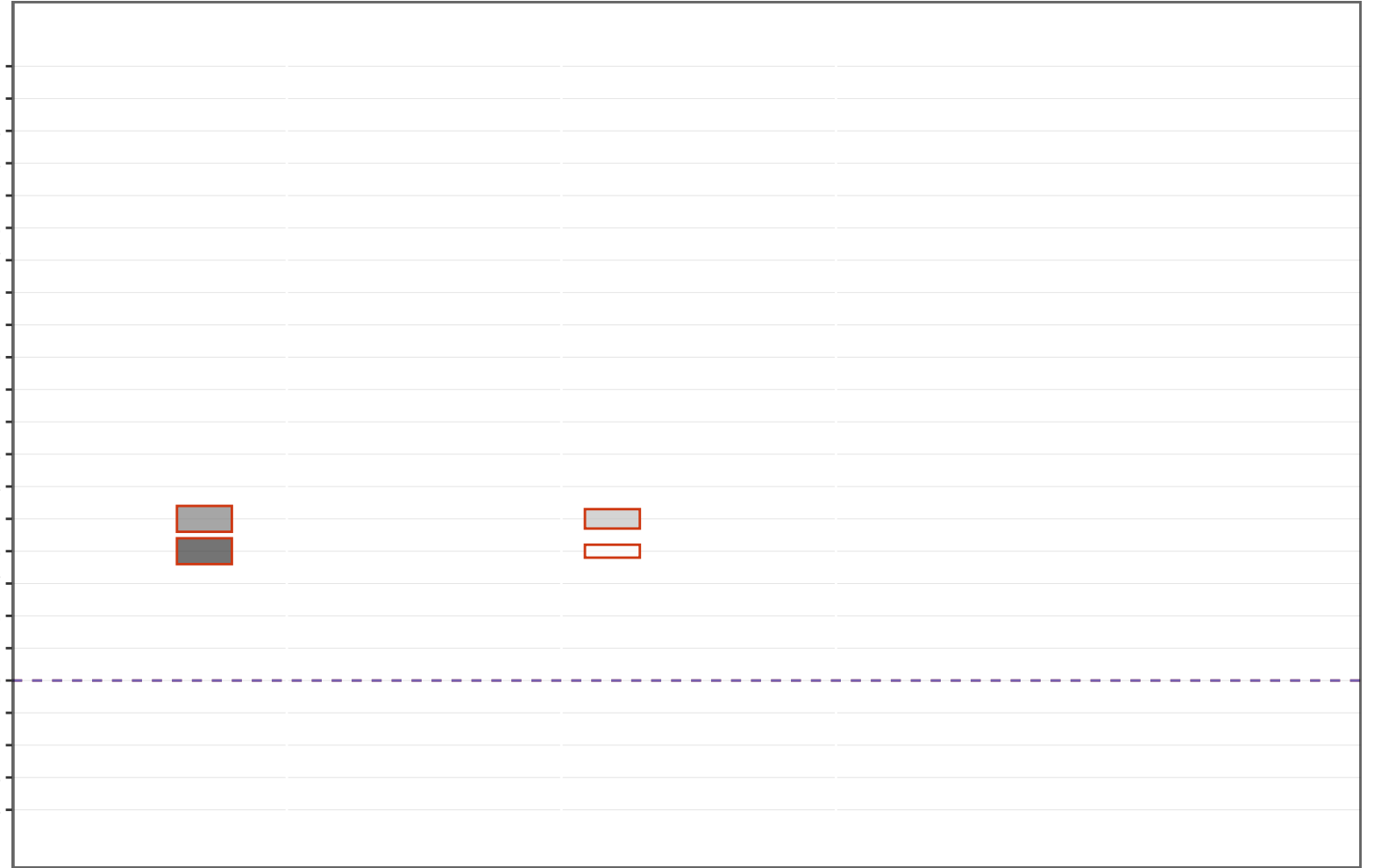
MW indication



Molecular weight



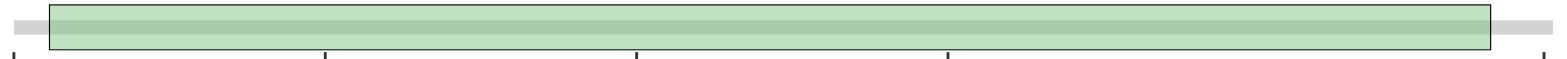
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

IRFNFMHYDKSHGANKKEIEALDKMGMDHETGDDPAKQKYLLETNTNTRGRHPISVFLHMLKH6STKIKRFLRYEG6SQCKEMRD66SVYASAVGKID*

NbL07g03000.1 40S_ribosomal_protein_S11 [MW = 17.7 kDa]

No. of times detected



log(intensity)



Values from



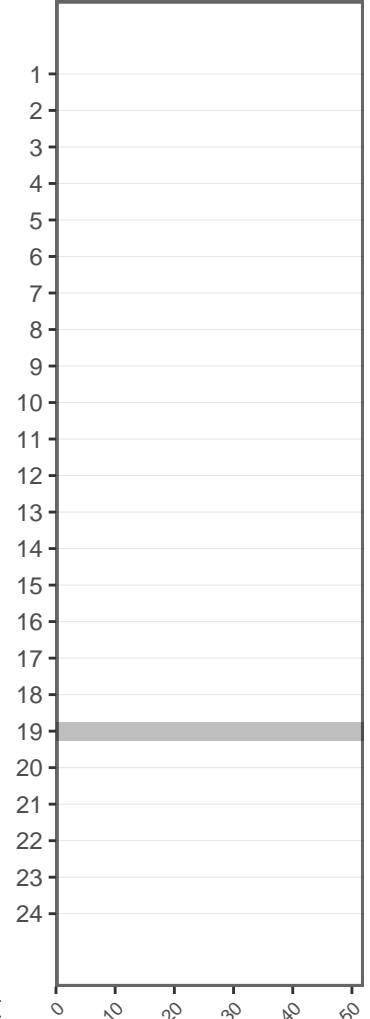
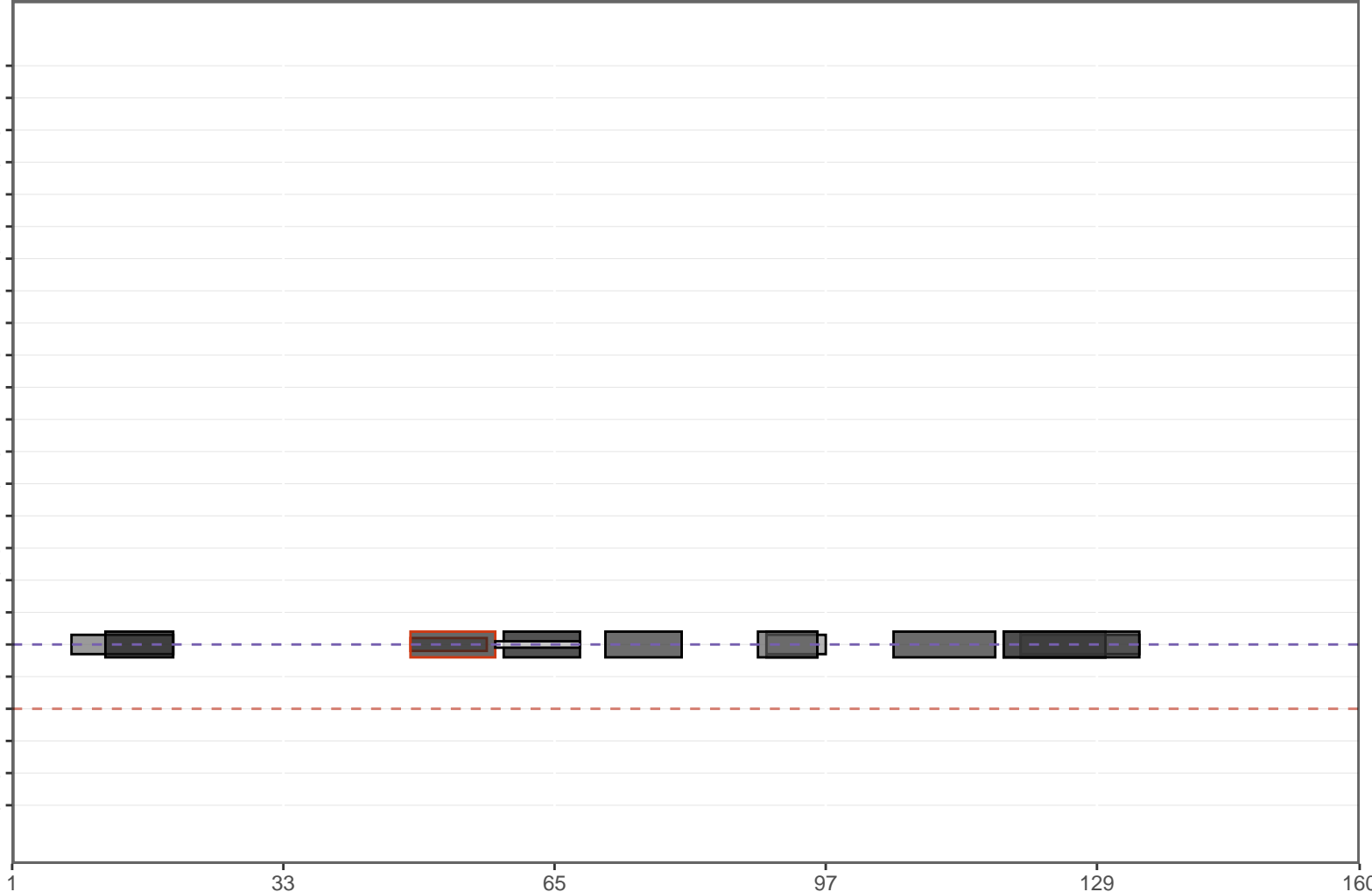
MW indication



Molecular weight

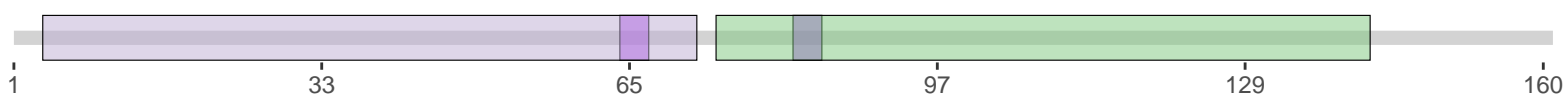


Gel Slice



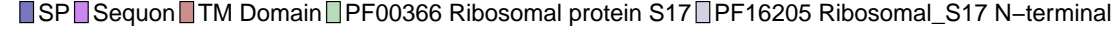
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

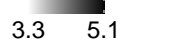
SIRGRILAGTCHSAXMNRITVRRNLYHYVKKYGRYEKRHSNPAHSGPFRVKEGDHVIIGDCRPLSKTVRFNLYKVIPIGSAAGGKKAFQGM

NbL07g02870.1 lignin-forming_anionic_peroxidase [MW - SP = 32.48 kDa]

No. of times detected



log(intensity)



Values from



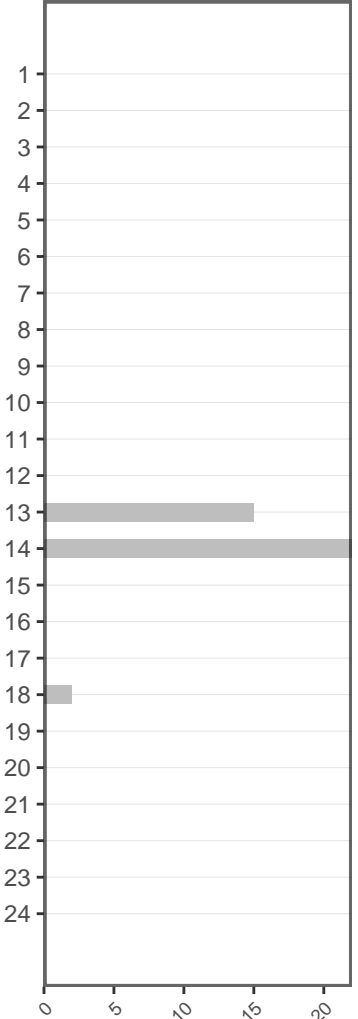
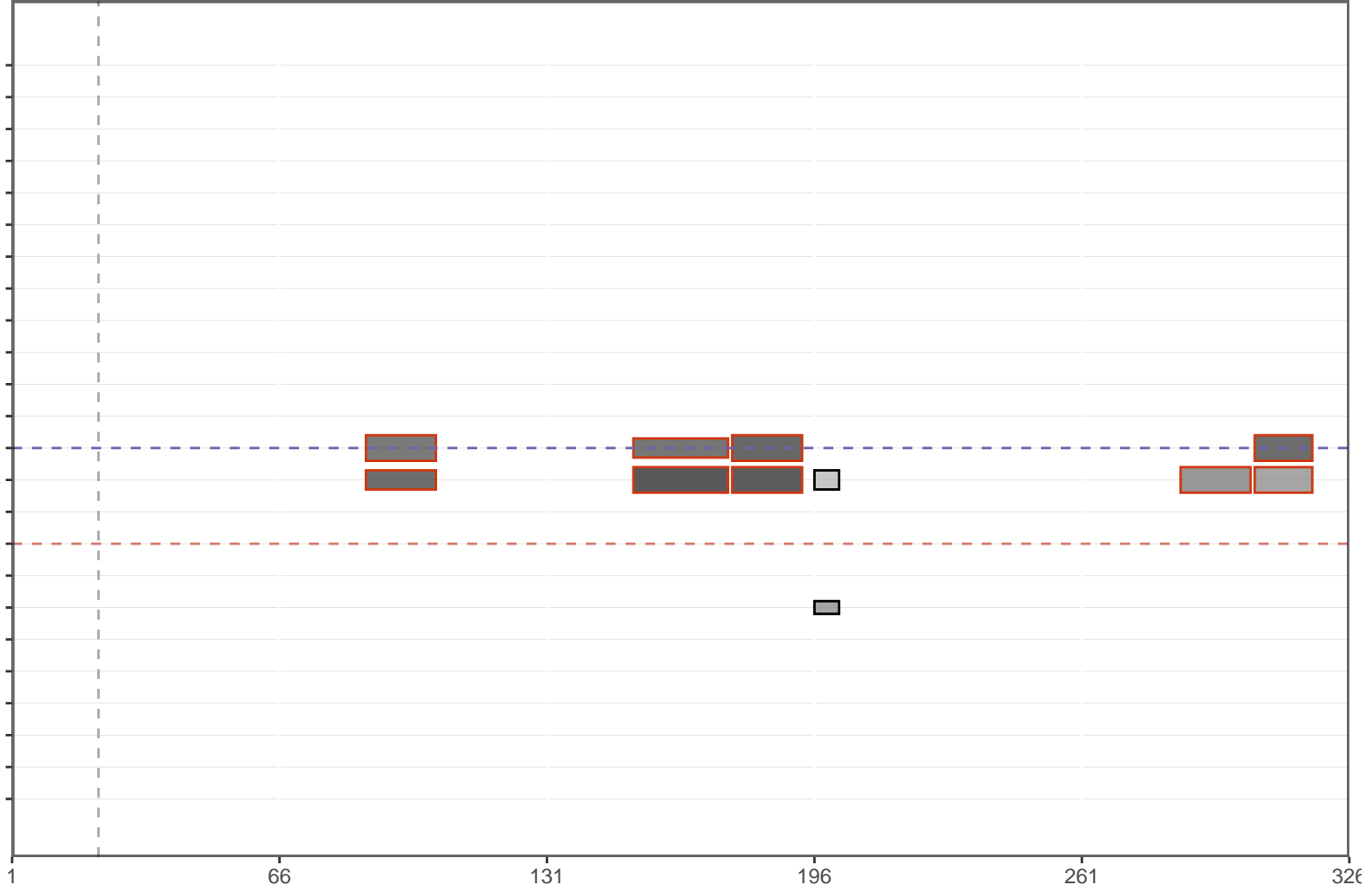
MW indication



Molecular weight



Gel Slice

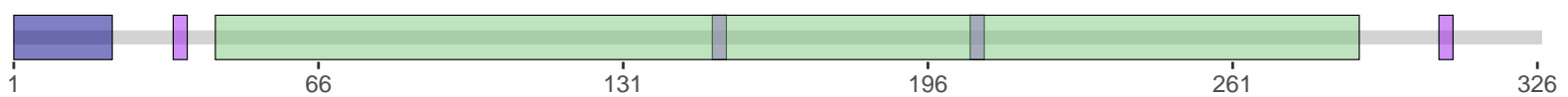


Protein length

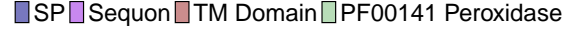


Peptide counts over 4 repeats

Pfam domains



Pfam Description

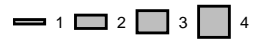


Protein sequence:

RSGAESDPSPFETLAVMTPTGFMKMDLTDLVALSGAHTFGARCGTFFQRLNFFSGSNPDPVDTATLQFLQGGPQGGNMGNTFTNLDSHTPNDPFDNDVFTNLQNNQGLLQTDGELFSFTTGSATAIANNRYA66GTQFFDFI68MKLGNISPLTGTNGEIRTDCKRVNS

NbL07g02850.1 formate--tetrahydrofolate_ligase [MW = 67.34 kDa]

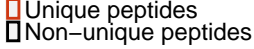
No. of times detected



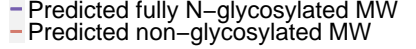
log(intensity)



Values from

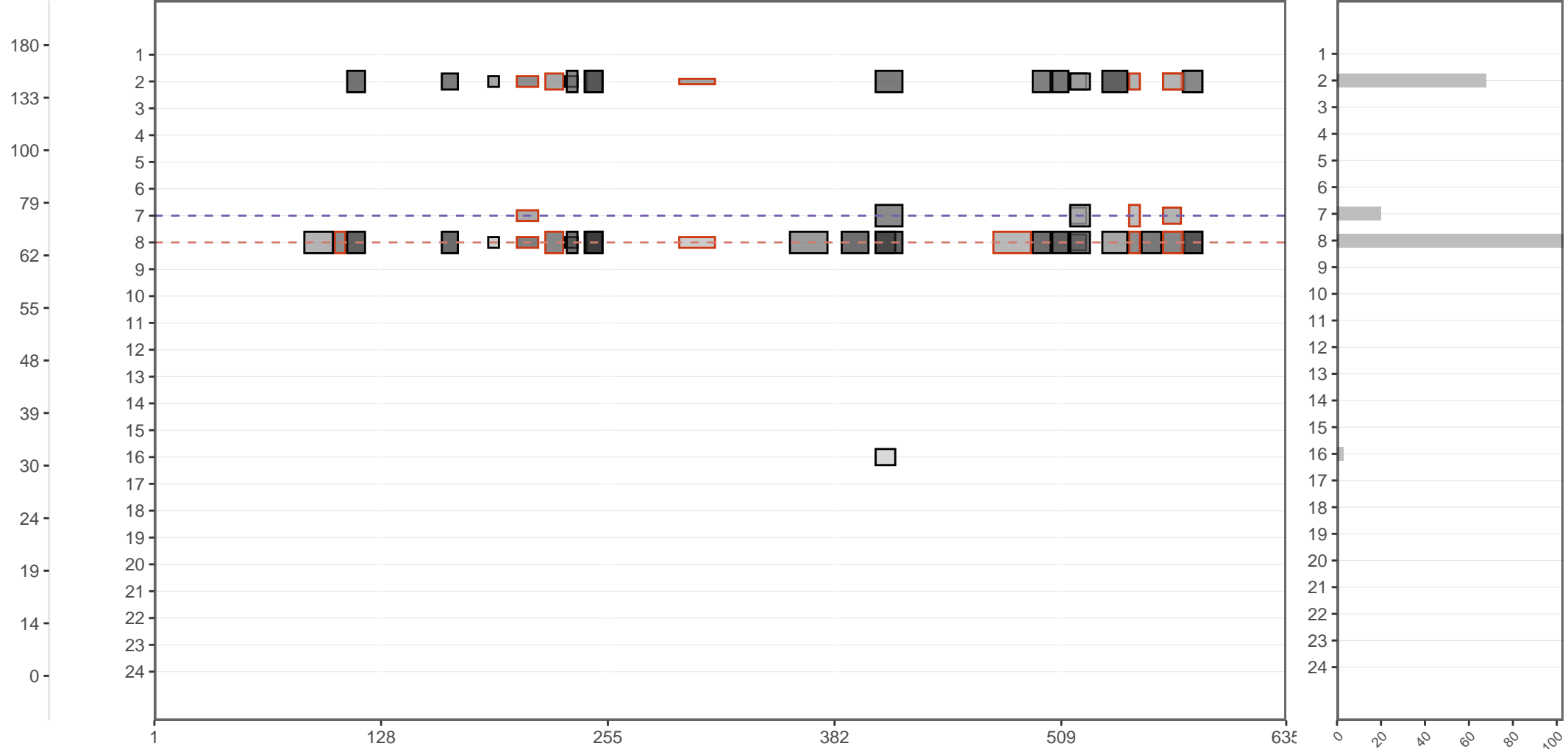


MW indication



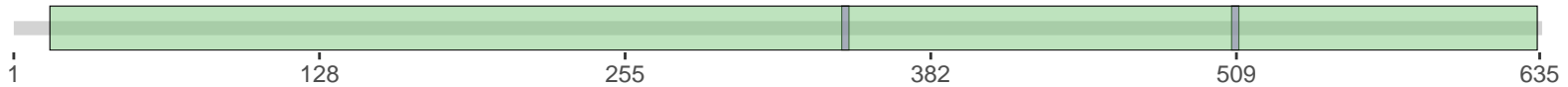
Molecular weight

Gel Slice



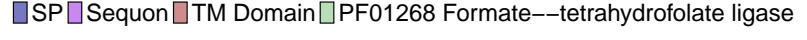
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LGVGSLTVLMKDAINPRLMQLTEGTPVLVHAGPFAIAHGH6SVADKIALKLVGPGGFVTEAGFGSDGTEKFMNKRYSGLKPQCAVWATVRLAKMHHGGGPDVTAGRLDRAYFENVALVEAGGVNLAHSHNTRKAYGANVVAWAFTTDTAEELNWKNAFAAGAFDAVGTTHHAHGGKGAVDLGIAMKAGENATGLRFLRFLPLDGIKDKIAIAAKSYGADGVVEYSEQAEGKEMVYKGGGFSLPFGMAKTYQYFSFHSESAKKGAPGGFLPIRDVRSASIGAGFY

NbL07g02630.1 arogenate_dehydrogenase_2_chloroplastic-like [MW = 42.77 kDa]

No. of times detected



log(intensity)



Values from



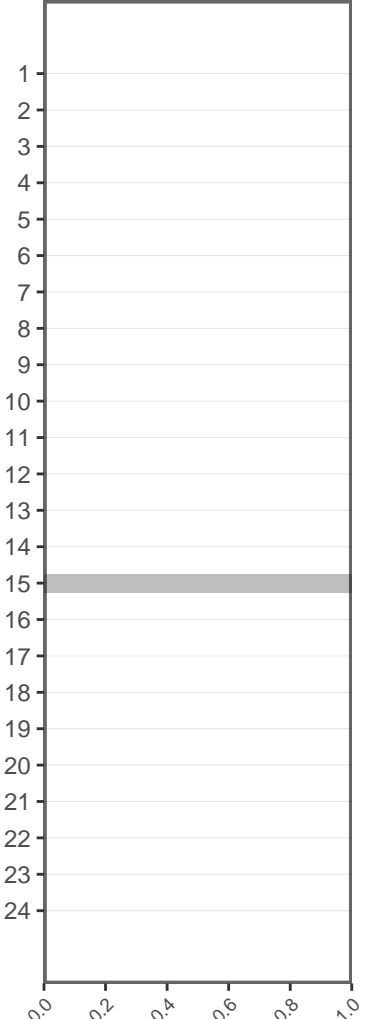
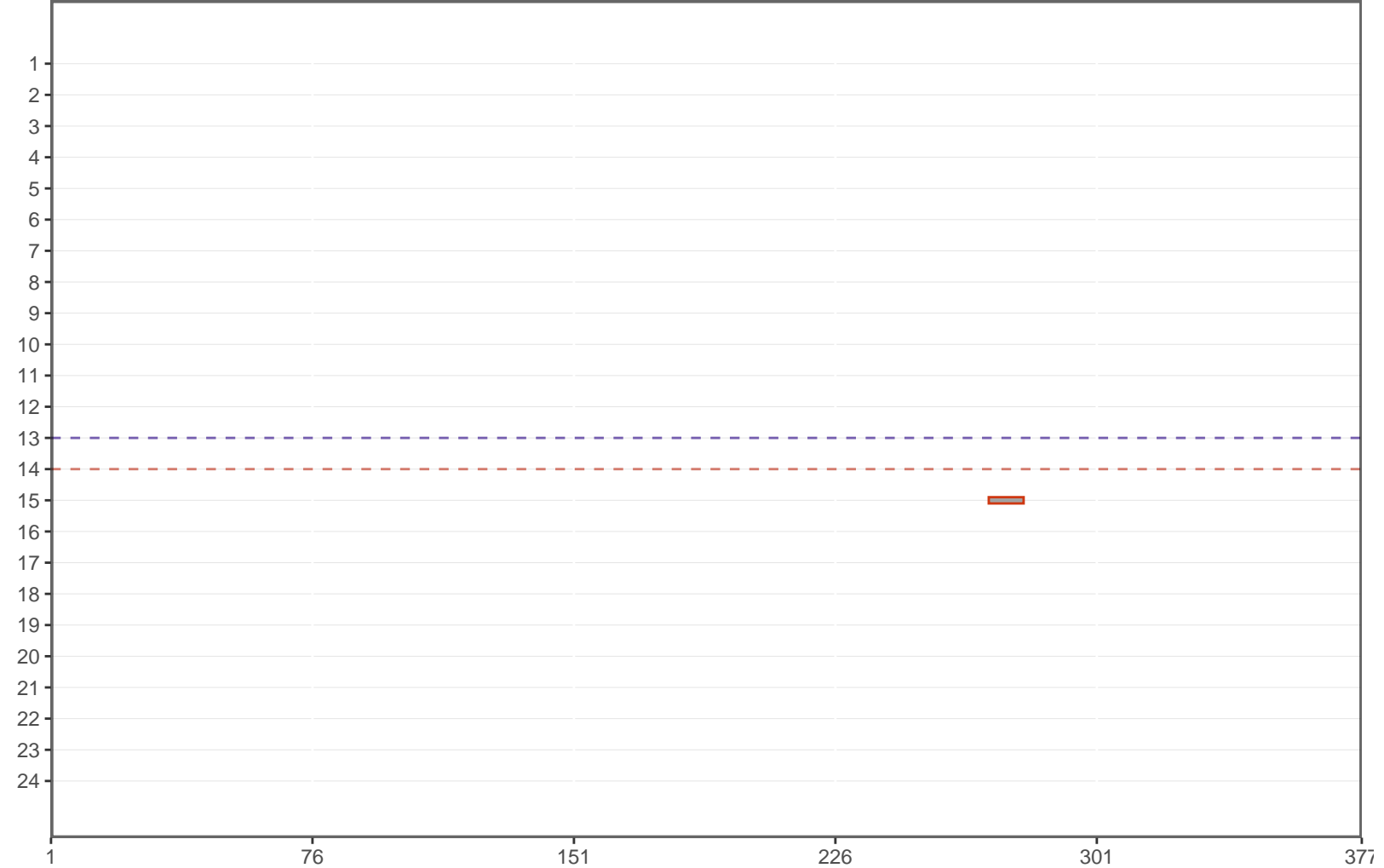
MW indication



Molecular weight



Gel Slice

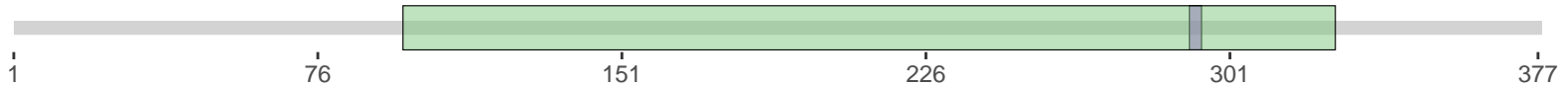


Protein length

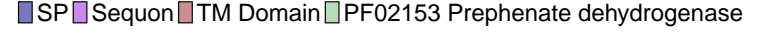


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IFLOVLPSPFDILCTHPMFQPESEGGKDWKDLAFVFDKVRIGEGDSRGRVDRFLDFEKEGGRMVPMTCAEHNRHAAGSQFTHMGRVLEKLDLETTPTNKGYETLLNIVENTSSDSFDLYYGLFMYNRNNAMEQLERLDLAFEALKKELFGHLHEVLRKGLFGKAEAGQRRLTKLPKNGYALFAPSEAVKGENI

NbL07g02590.1 actin-related_protein_2/3_complex_subunit_3 [MW = 19.55 kDa]

No. of times detected



log(intensity)



Values from



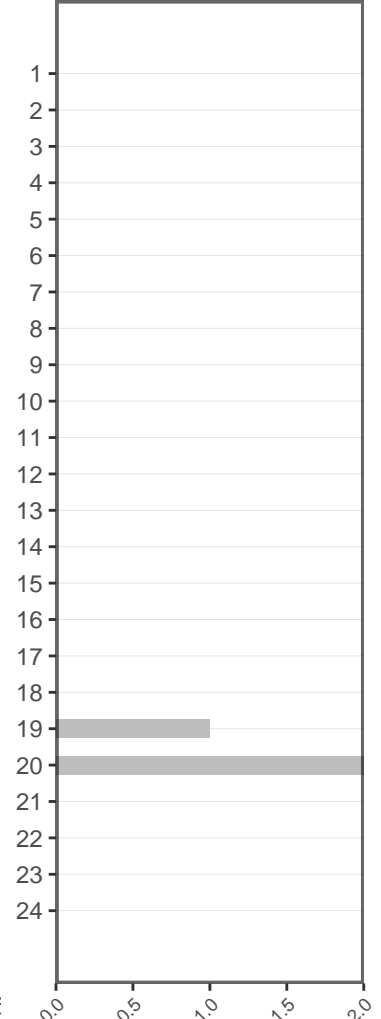
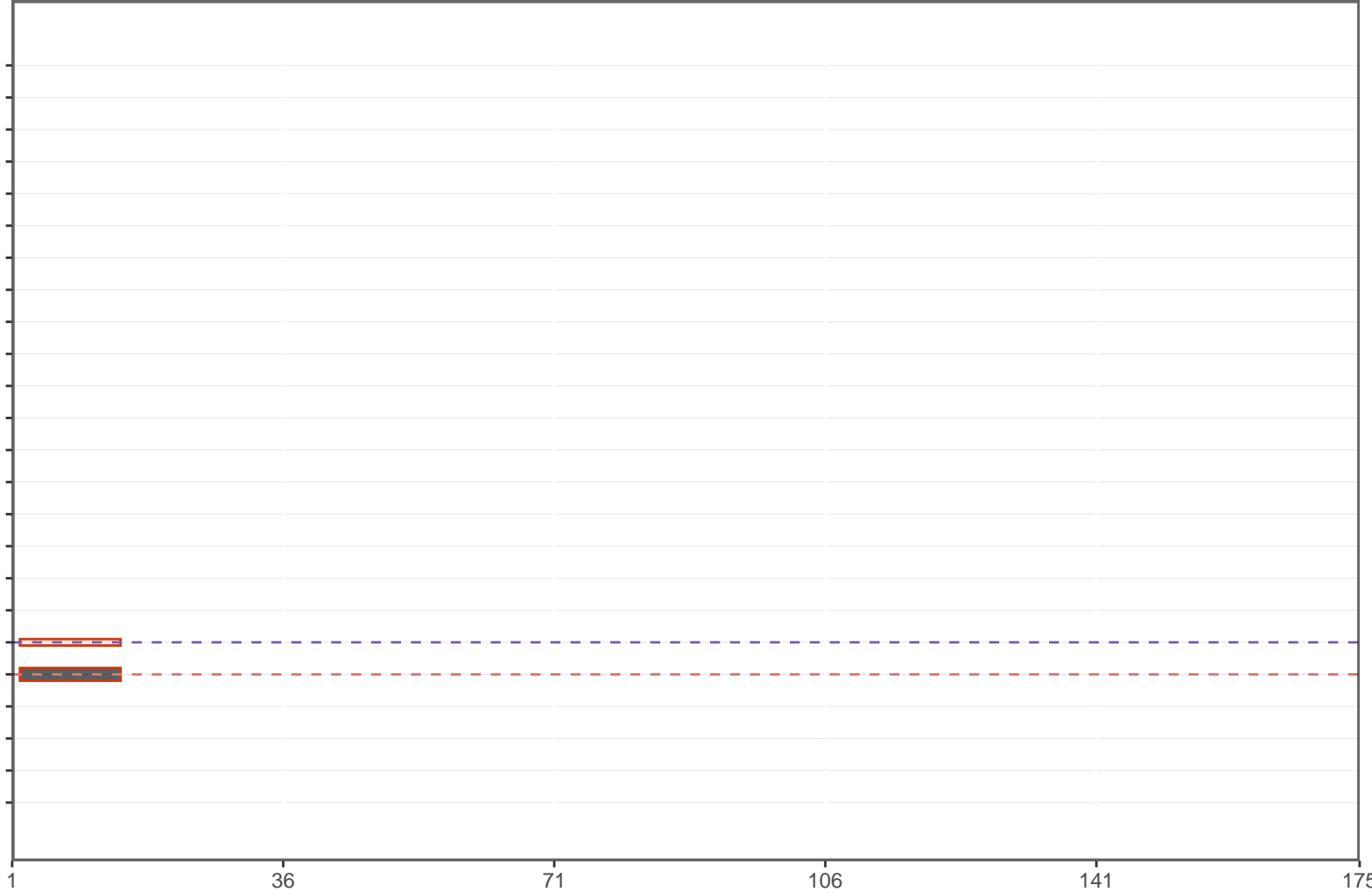
MW indication



Molecular weight

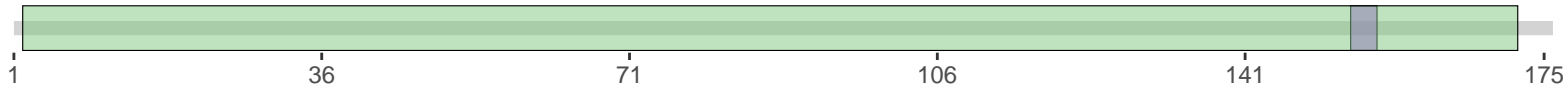


Gel Slice



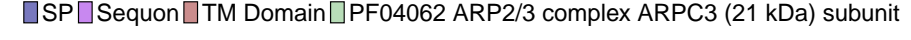
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

INALKRLEGCRITLAEGTKAINLGLKTVVPGESGPPFGLFTAQSKKEAEFRNLYLRQREETSGRLLVAVRHNGTPTKRWLLFAFKRKFMMNMLP

NbL07g02470.1 uncharacterized_LOC104229534 [MW = 27.08 kDa]

No. of times detected



log(intensity)



Values from



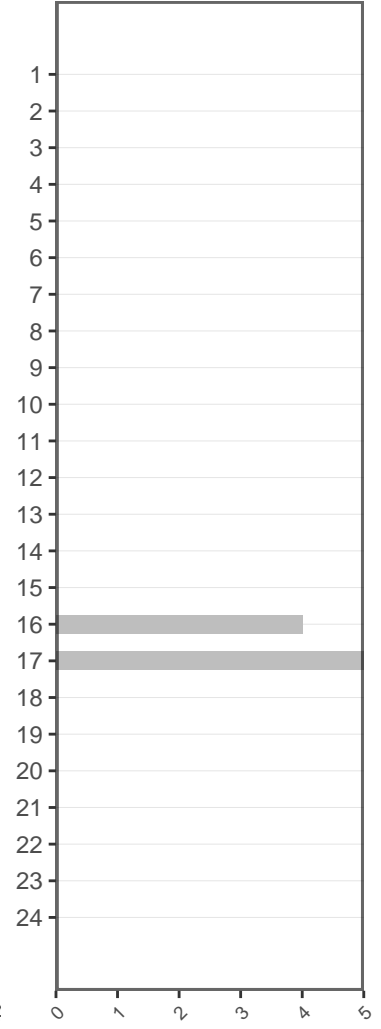
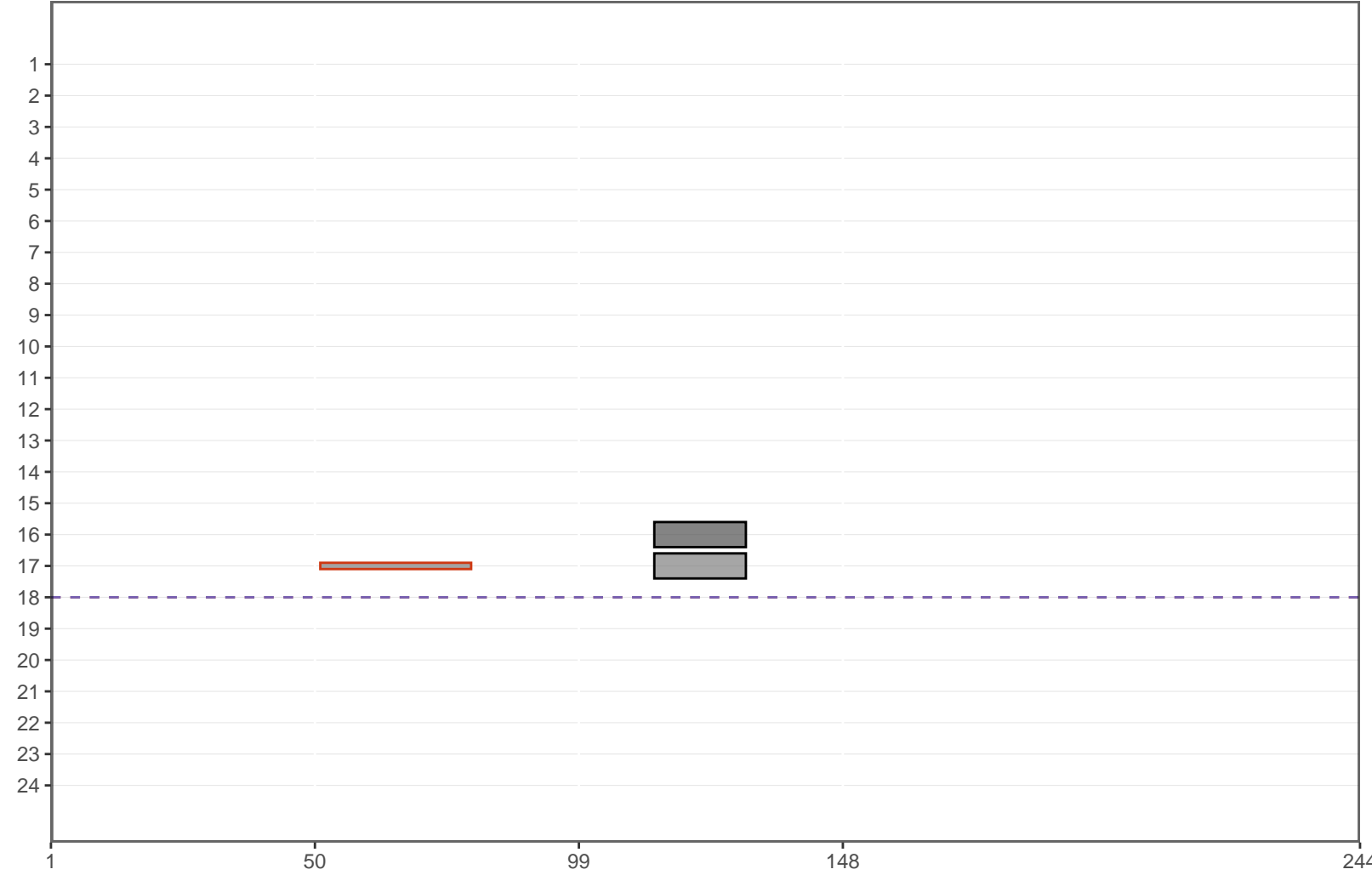
MW indication



Molecular weight

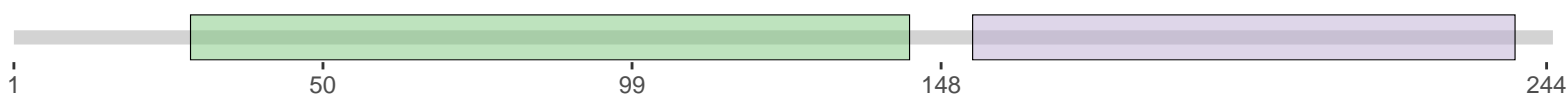


Gel Slice



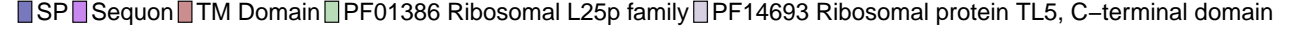
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PLQIRAGSGSSTLLEGGNVLFPKIHREDEETGKILNLVFWAEEGFKLVDPVVFVKGEEEGPGLKAGGSLNKRPTLRFVCPAEHFPQKIEVDASGLQVEDKVFVLDHDLHPAWKLLKNEAIPVCKIKATSDS

NbL07g02370.1 flagellar_radial_spoke_protein_5-like [MW = 49.44 kDa]

No. of times detected



log(intensity)



Values from



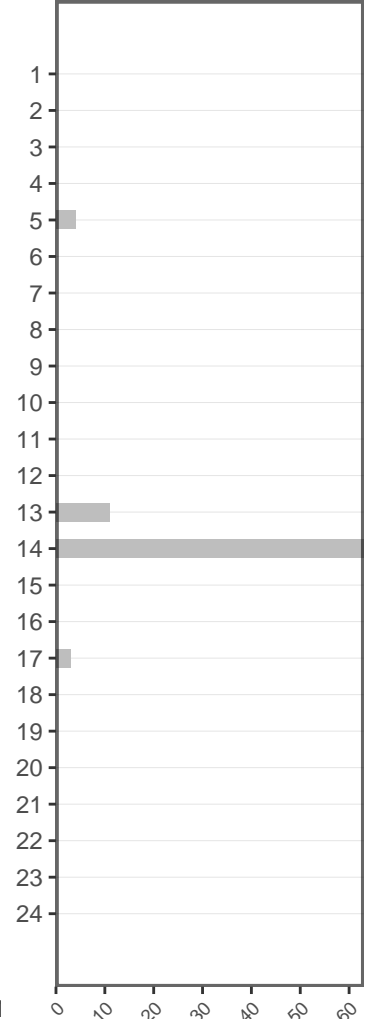
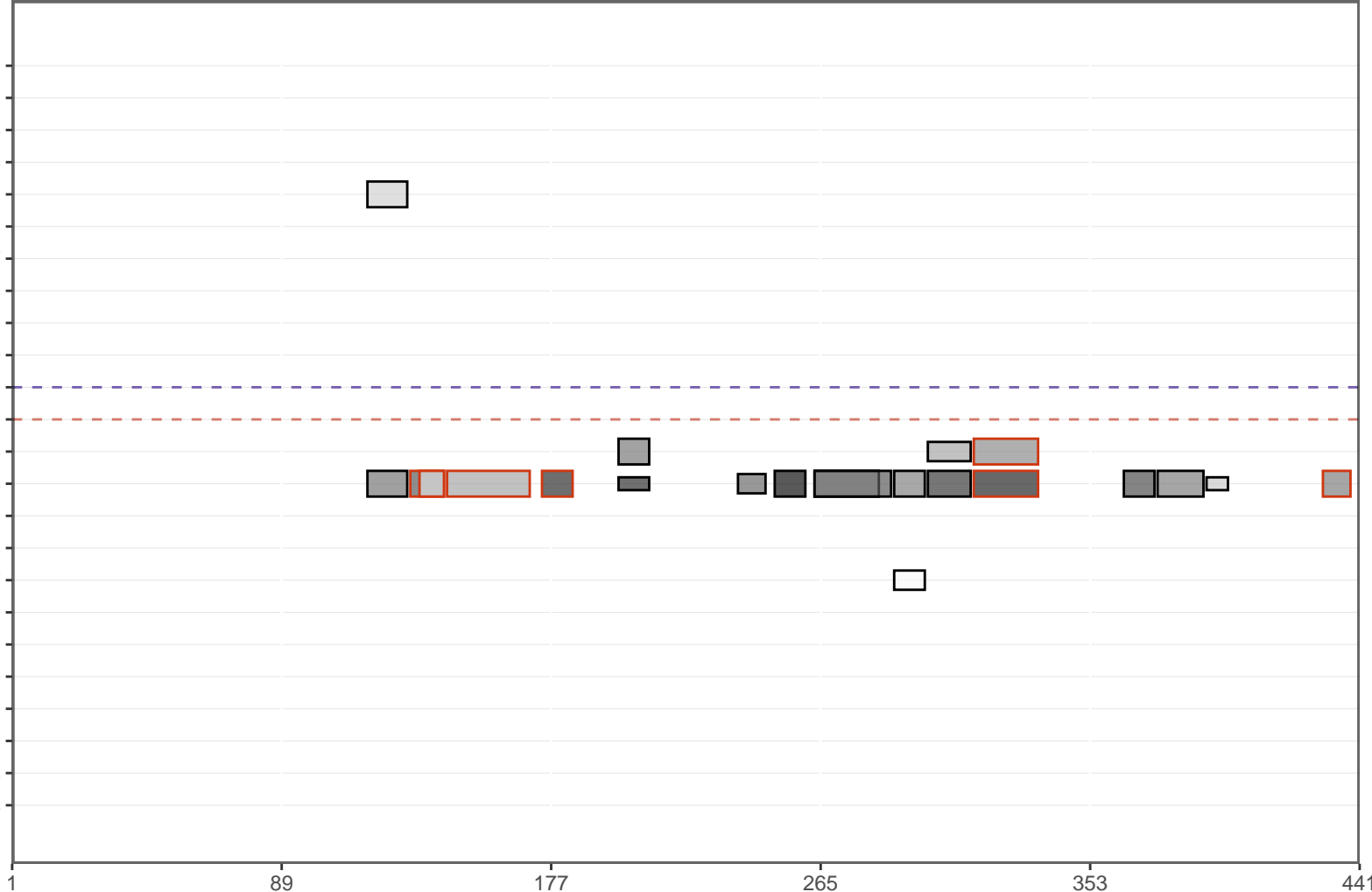
MW indication



Molecular weight

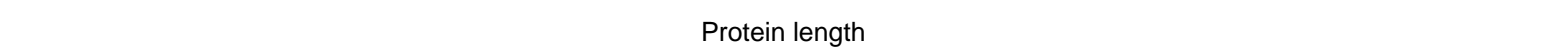


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

/SRKRMDVSLDMLGPHWWDVANSGLDALKHLTKKEGKIKTIALTFDFTERLRLILENGIPVVENGVQHSILDMRPGQMAELCOLTGVKLITYGTVMGSLSEKFLDTLNSIPFAAPLNTPLSLGKYKRMVDWVGWGSFQELFLRLKTVANKHGVSPTVWVKYILDQPTVAGSMGVRLGLSEHKIDVNAVFSVLDEEDKISLQVTNKGKDLGKVGDCDGEYRRA

NbL07g02360.1 uncharacterized_LOC104119615 [MW = 20.29 kDa]

No. of times detected



log(intensity)



Values from



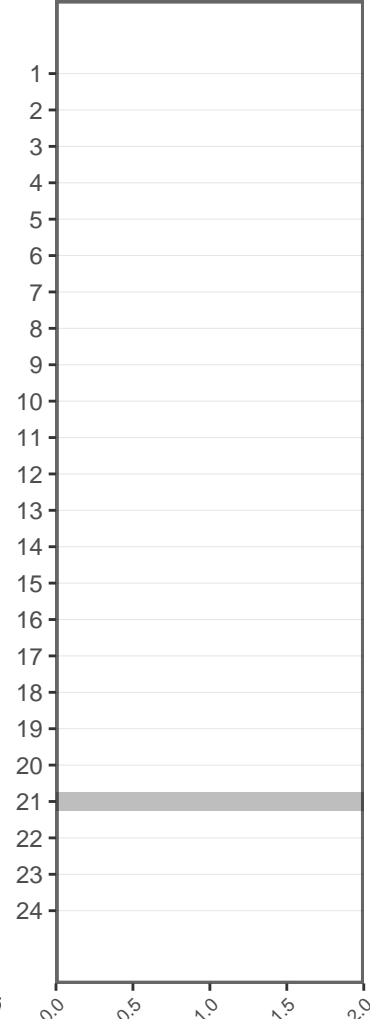
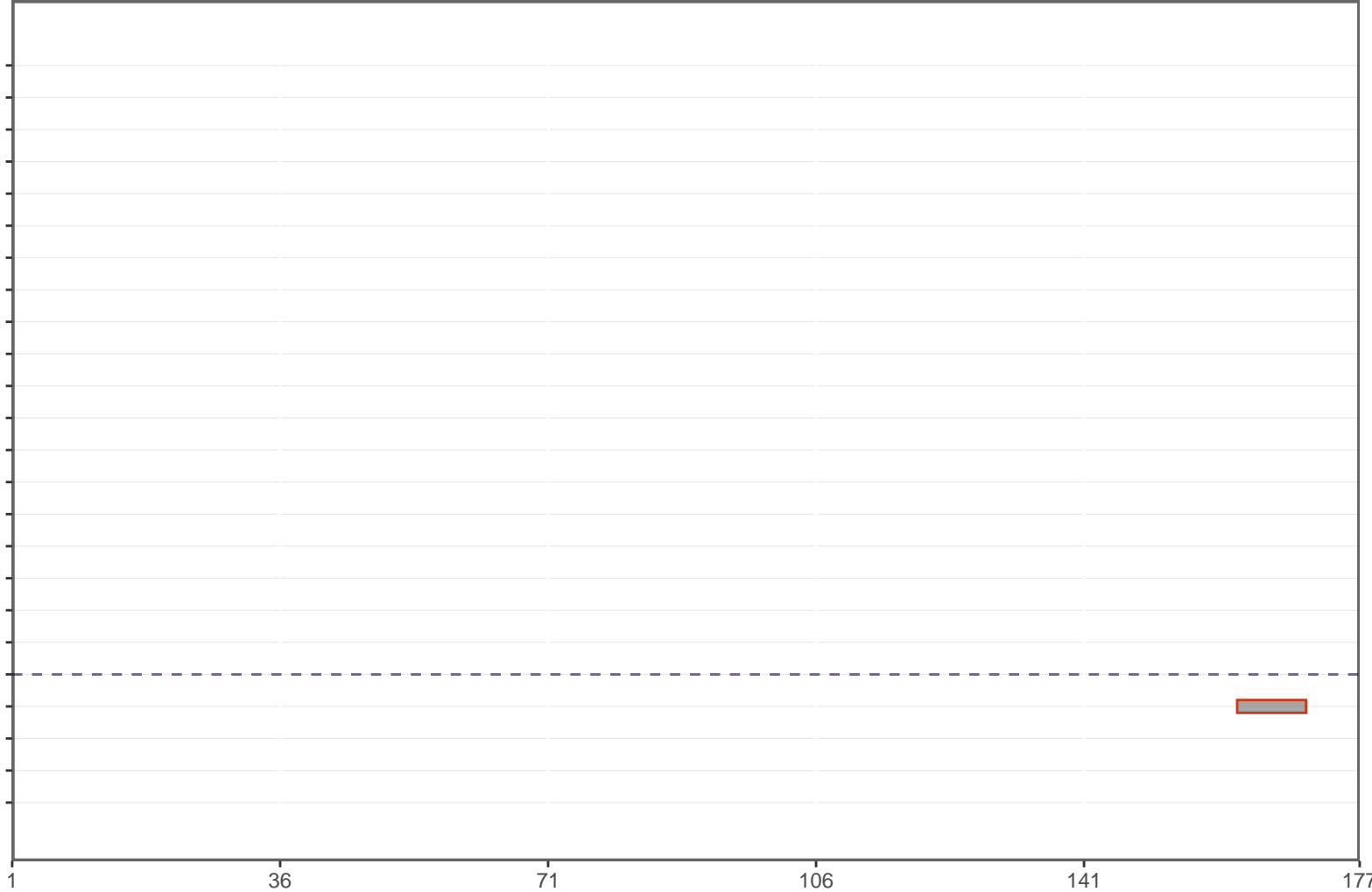
MW indication



Molecular weight



Gel Slice



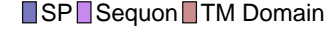
Protein length



Pfam domains



Pfam Description



Protein sequence:

DKELRRLQDSEQKLGSLPDLQAKERATQLESEVTLLELRLLIABGAEGMDGFRGRWELHGRITDTRKRLKLEALKGGMEKRRKDEPAESEPTKKRWFV

NbL07g02330.1 60S_acidic_ribosomal_protein_P2-1-like [MW - SP = 9.75 kDa]

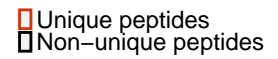
No. of times detected



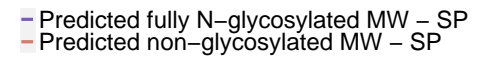
log(intensity)



Values from



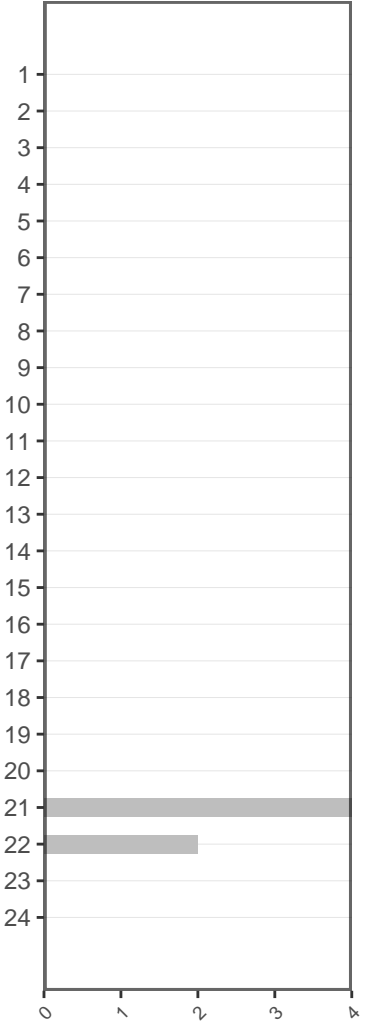
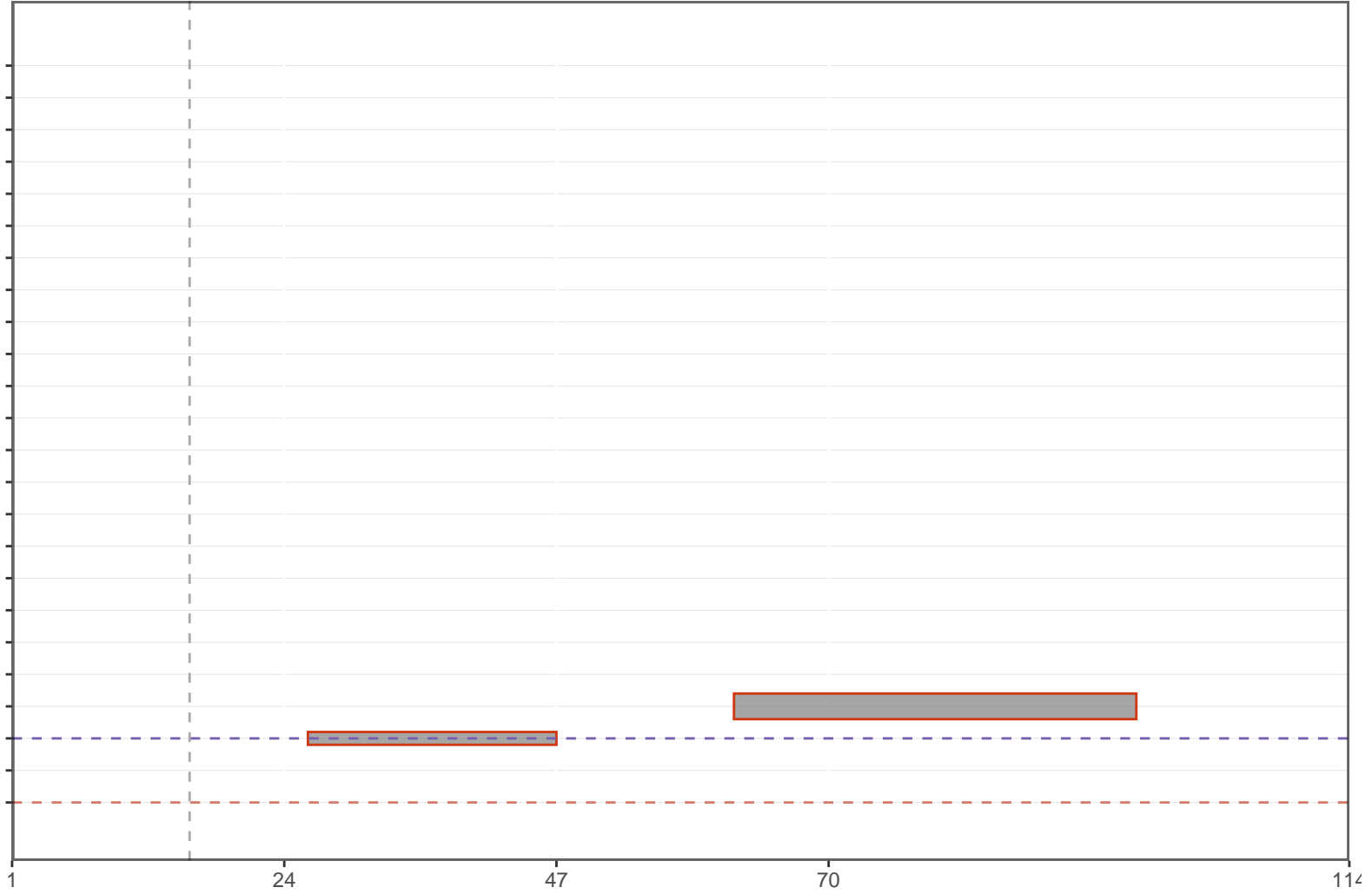
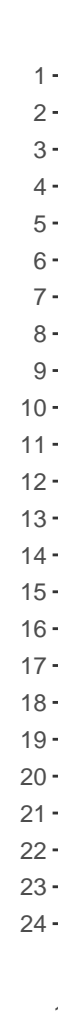
MW indication



Molecular weight

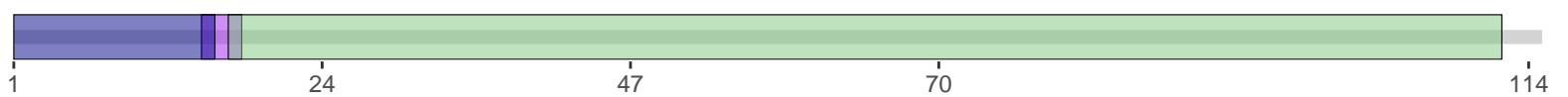


Gel Slice



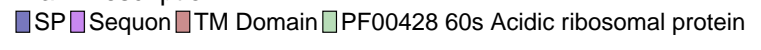
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DVKGKDTLLIANGREKIASVPGGGGGVWVAAPAGGSAAPAAEKKKEEKKEEESDDDMGSLFD*

NbL07g02260.1 putative_low_molecular_weight_protein-tyrosine-phosphatase_slr0328 [MW = 29.54 kDa]

No. of times detected



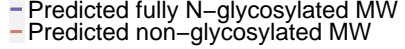
log(intensity)



Values from



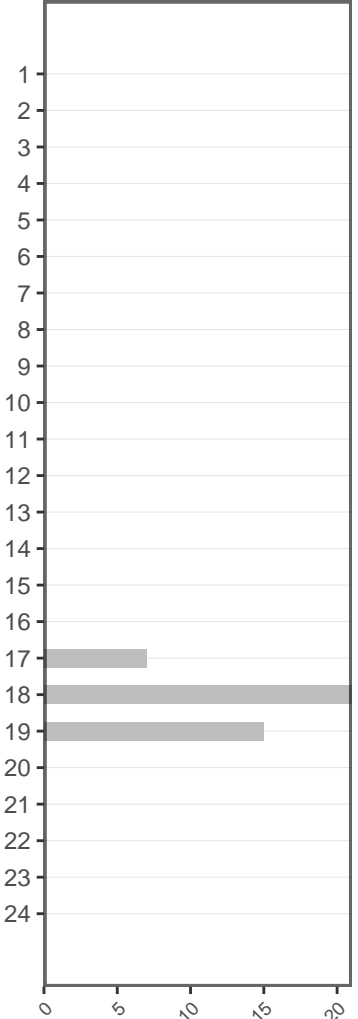
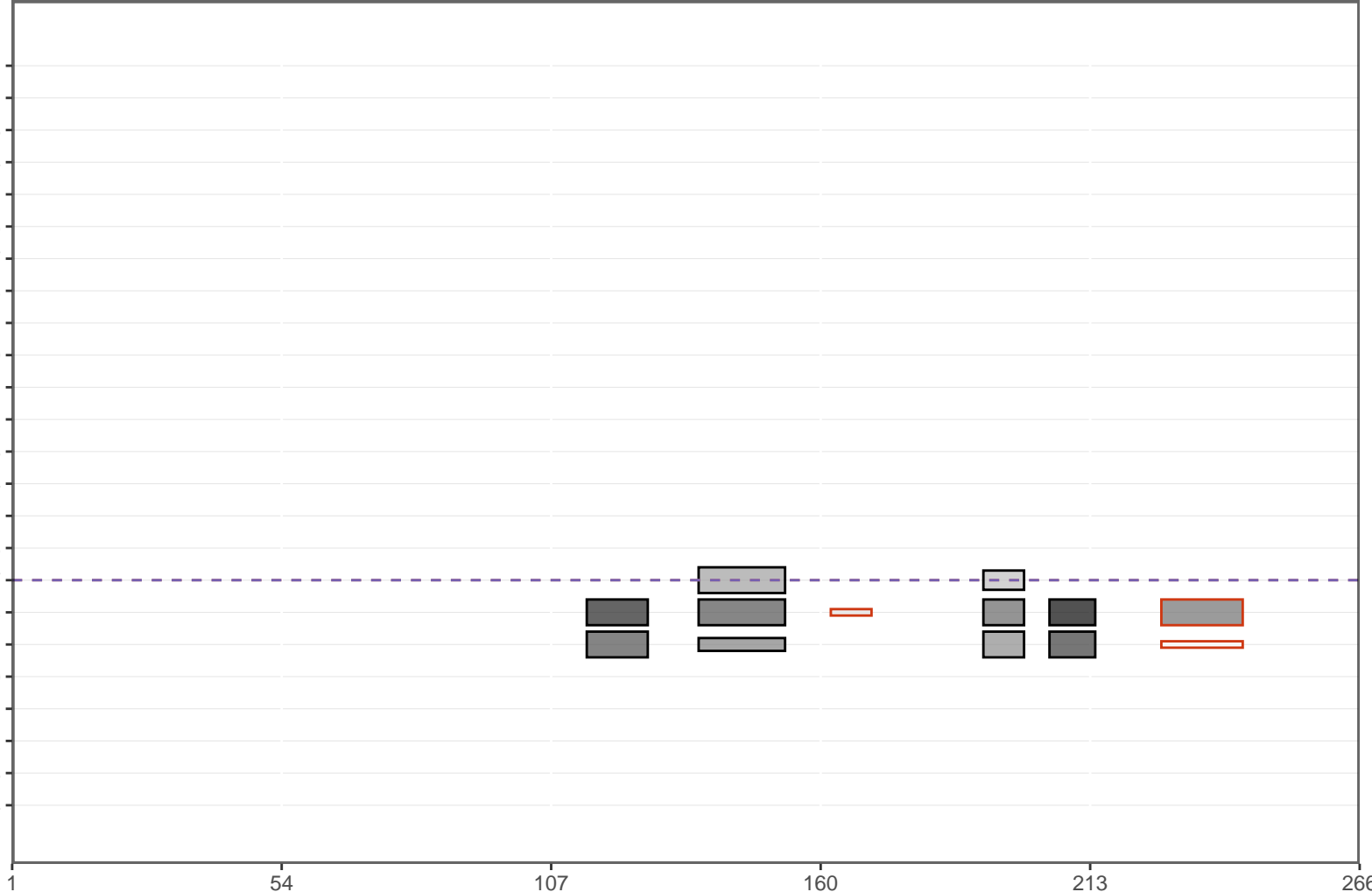
MW indication



Molecular weight



Gel Slice

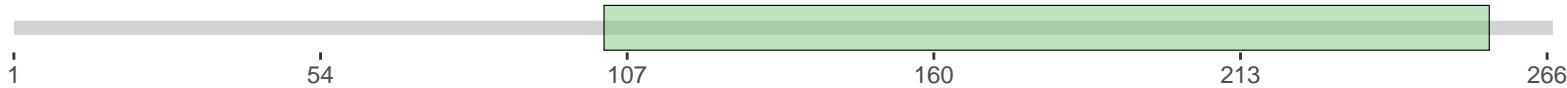


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SVFTDLVKKRGLDLSNFKIDISAGTINHYEGNEADPRMRAAAKRRGIATFSIRPIRPSDFKDFDLILAMDEGNKADLIGALERWVHRETLFADAPKRVLMCDYCKRHKETEVPDPYVGGAGGFENVLQLEDAGDSLLESIVAEKPI

NbL07g02230.1 photosystem_II_CP43_reaction_center_protein-like [MW = 46.54 kDa]

No. of times detected



log(intensity)



Values from



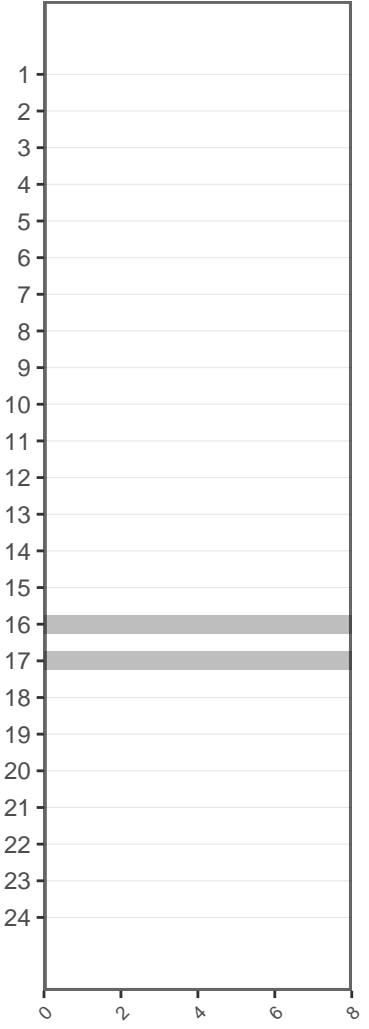
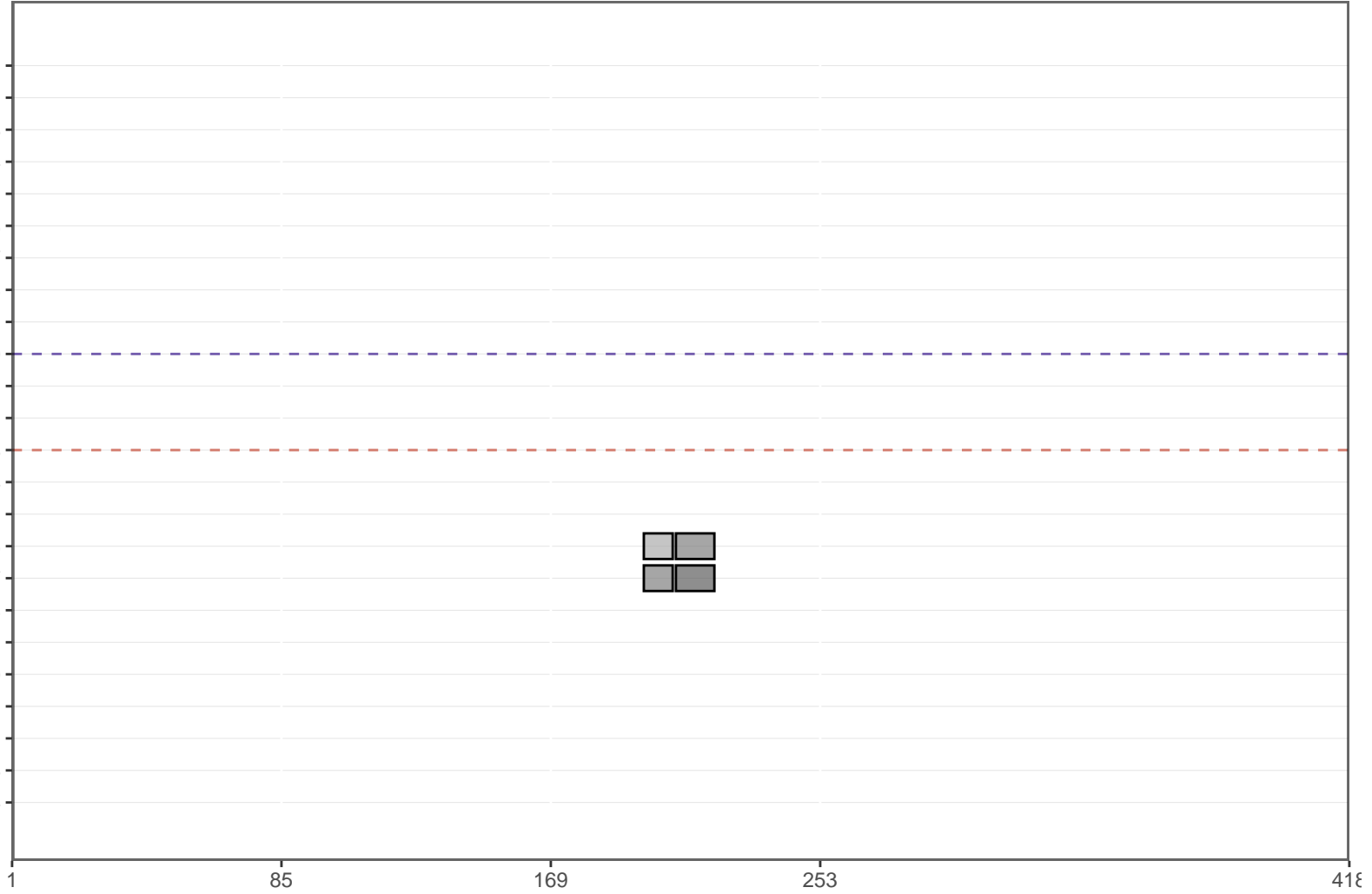
MW indication



Molecular weight

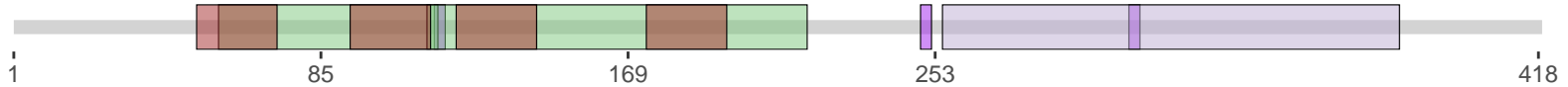


Gel Slice



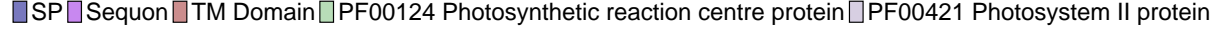
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SAVDYVSGEIRAAEDPEFETFYKNNLLNEALAGRDQETGFAWVWGNARLNLSVLFQGGYHALLGPETLEESFPFFGVWKRNRNMTRILGALSVFGRIAGCFVWFNNTAYPEFYGFTGPEASQADAFTELVRDQRLGANVSSAQGPTGLGKYLMRBRPEKSFLEERNYAFVWDLRAPVWLEPLRGPNGLDLGRITFEQKAFVMMKPFQALPFGRTTAI

NbL07g02170.1 bifunctional_protein_Fold_1_mitochondrial-like [MW = 42.17 kDa]

No. of times detected



log(intensity)



Values from



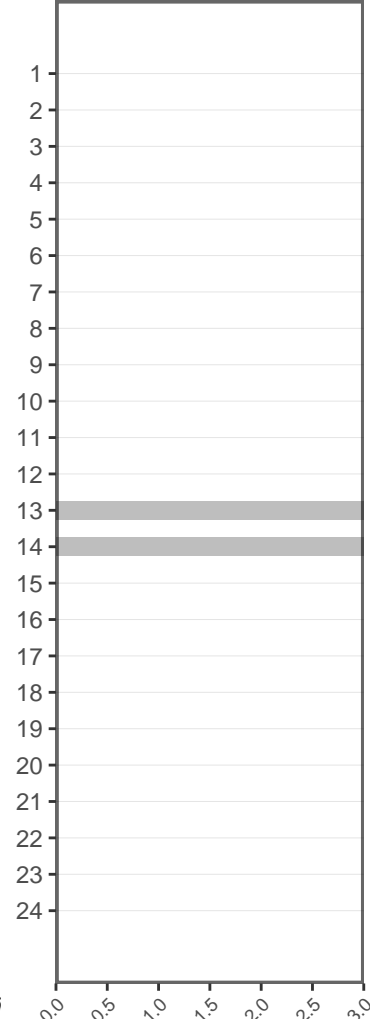
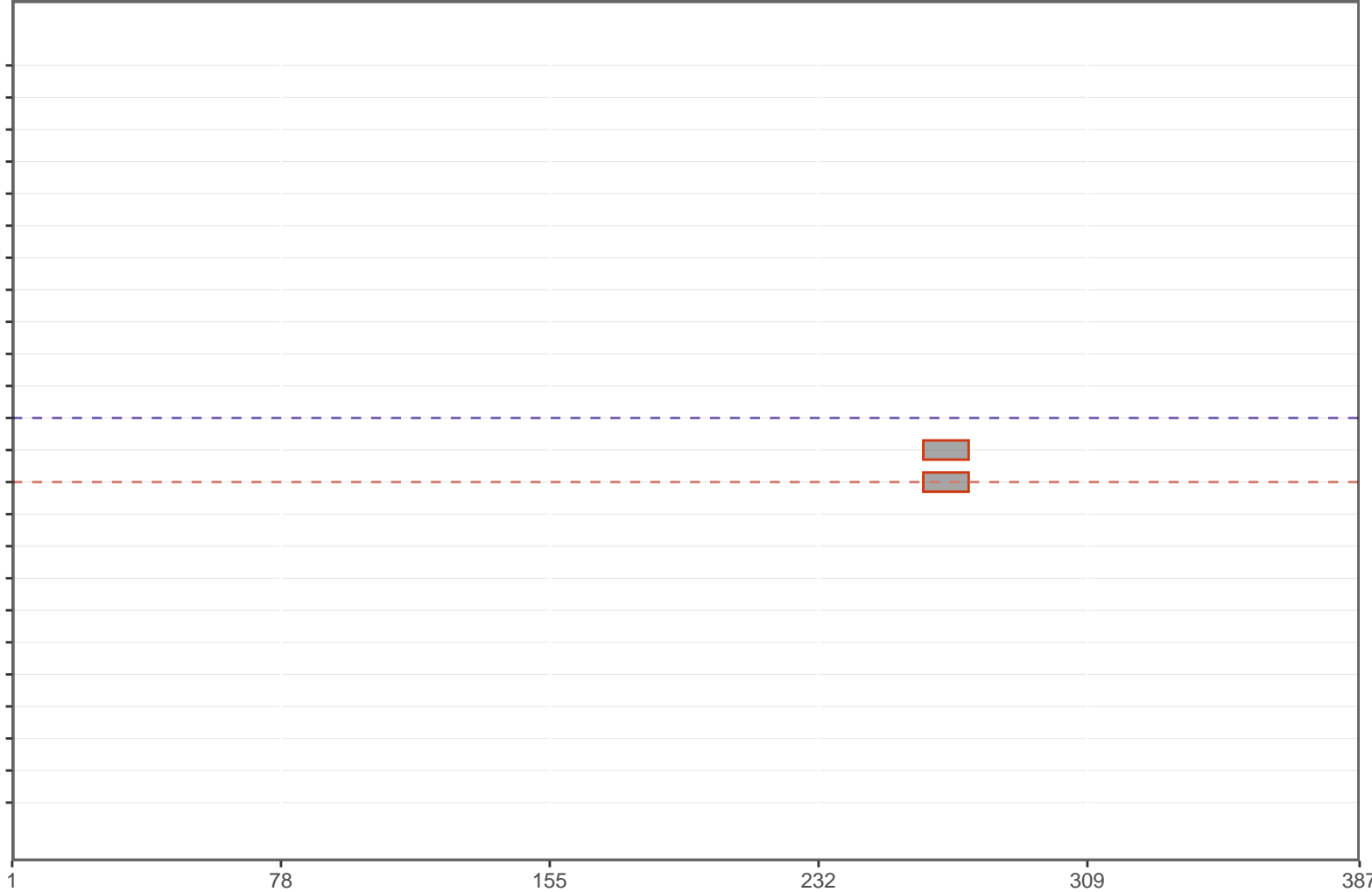
MW indication



Molecular weight

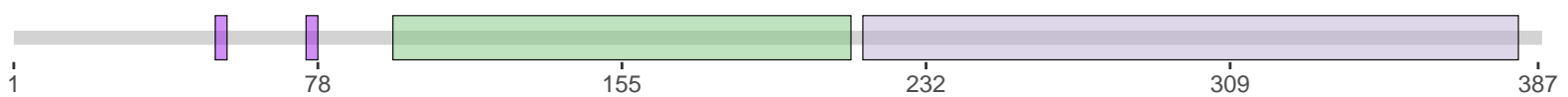


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00763 Tetrahydrofolate dehydrogenase/cyclohydrolase, catalytic domain
- PF02882 Tetrahydrofolate dehydrogenase/cyclohydrolase, NAD(P)-binding domain

Protein sequence:

/N/KDASHIG/LVQLPLPQHFEDEGKILNVLSEKVDGDFHPLNIGLADGREFLPIPTPKGCIPELLRSDVEVGRKRAVVGRRSNIWGLPTFLLQRHHATVSVIWHYSENPETMREADILWAAAGVFNLRGSGWLRKPAVAVLDGIRPESENGYRLIGDVGCFEEAVKASATPPVGGVGPMTVAMLLQNTLEAKRALHFT

NbL07g02150.1 uncharacterized_protein_At5g22580-like [MW = 12.26 kDa]

No. of times detected



log(intensity)



Values from



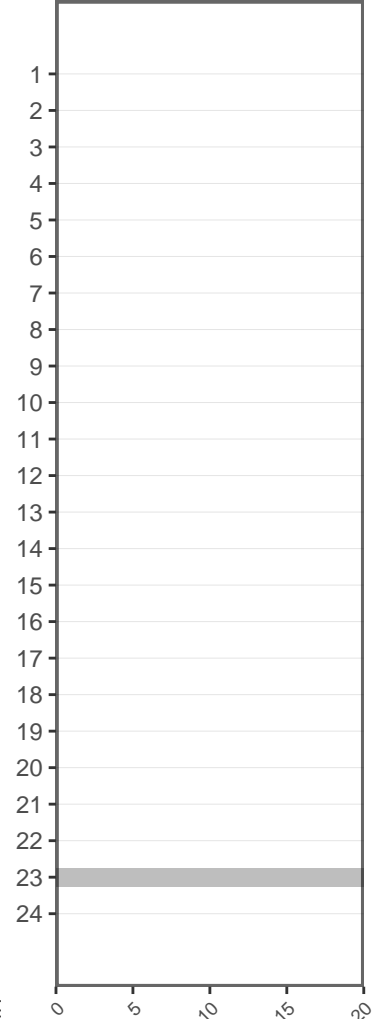
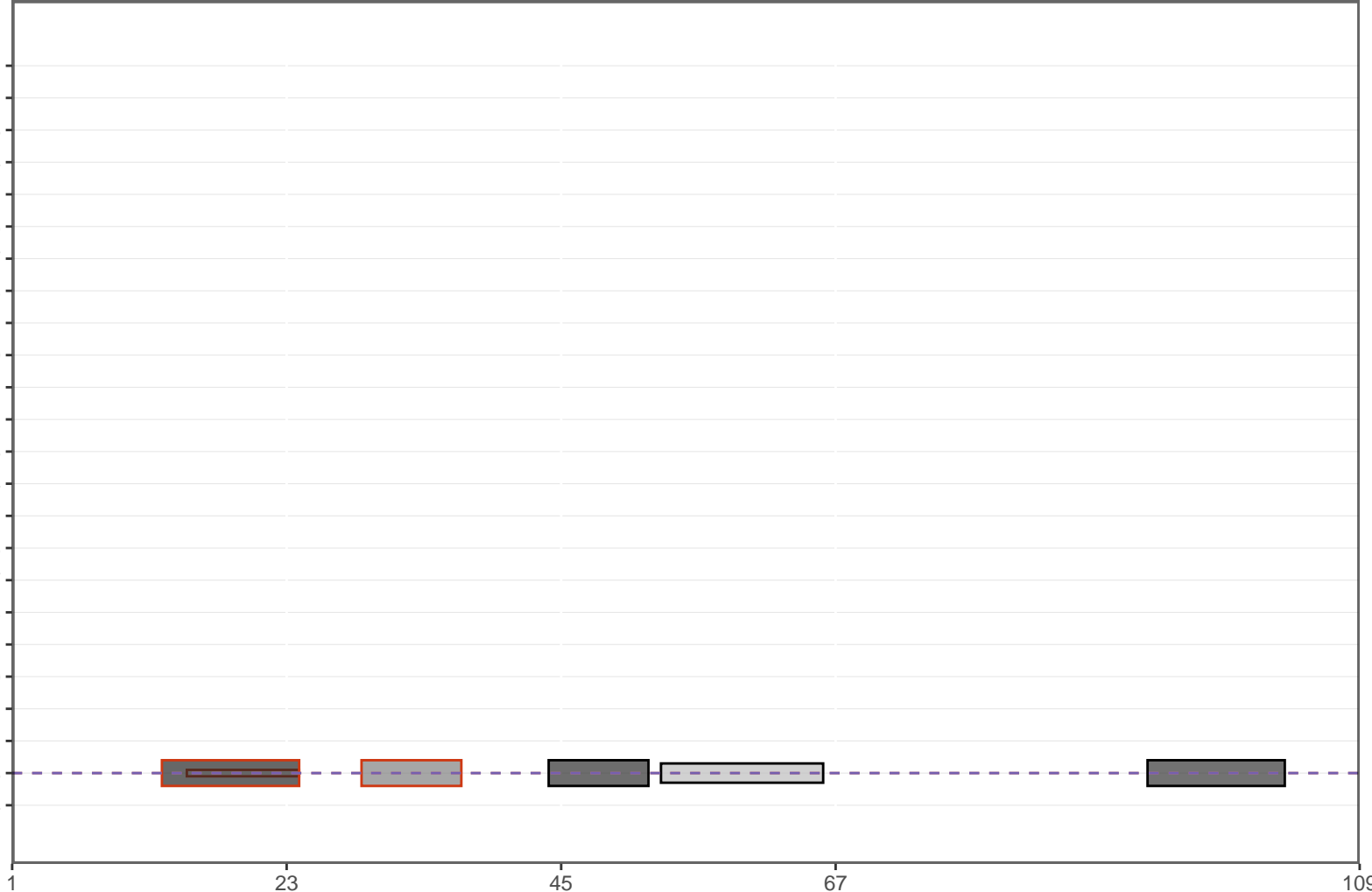
MW indication



Molecular weight

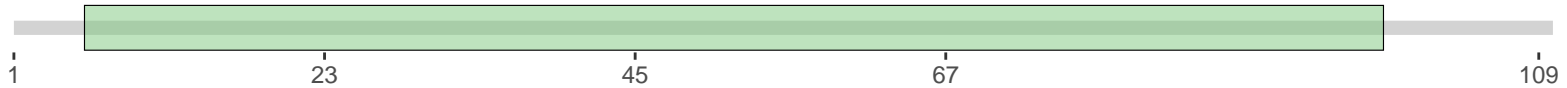


Gel Slice



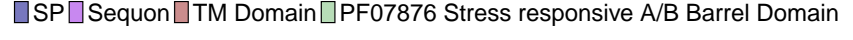
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGKDAEHEMLRGGFTNMFMLMFRNKKDDYTKFVSHPHNHFVSATFSTVIDKAVLLDFRMSVKKAPAV

NbL07g02110.1 arogenate_dehydratase/prephenate_dehydratase_6_chloroplastic-like [MW = 47.2 kDa]

No. of times detected



log(intensity)



Values from



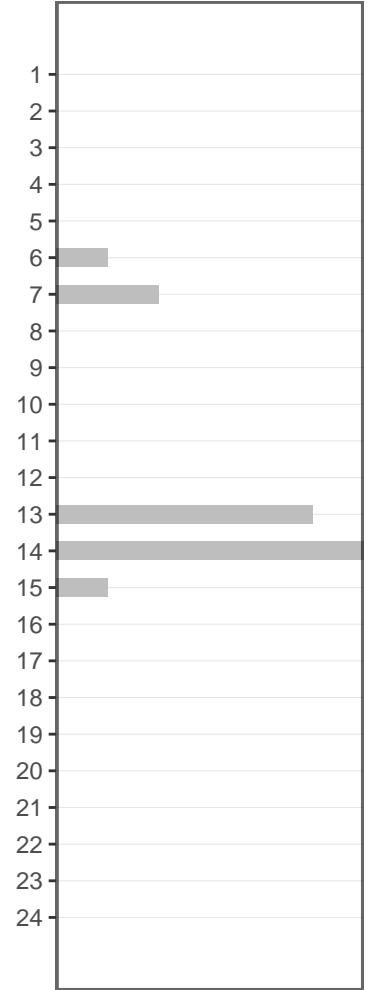
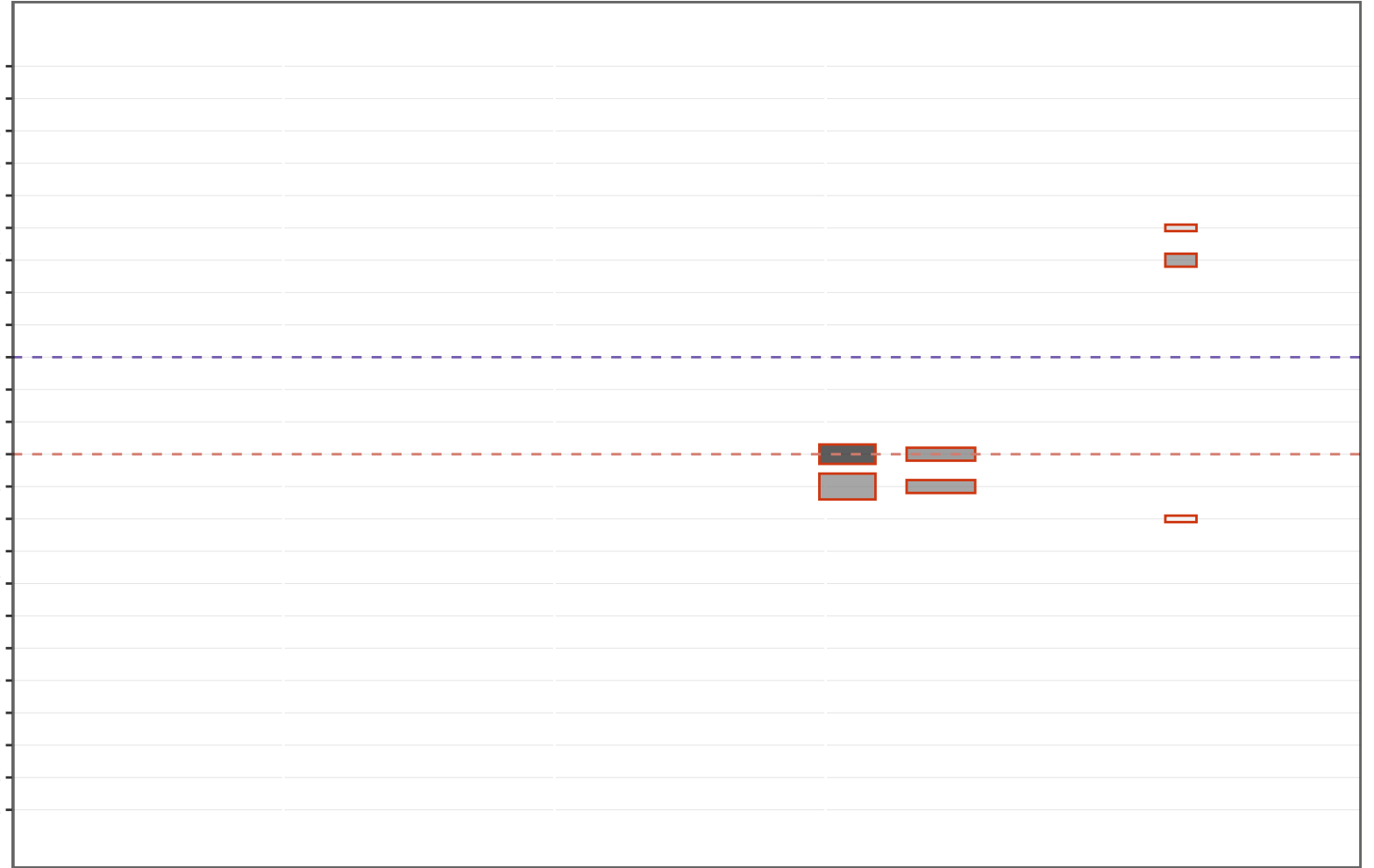
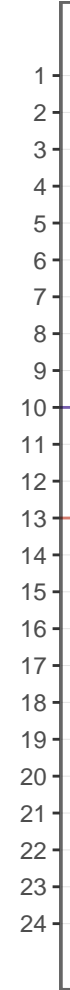
MW indication



Molecular weight

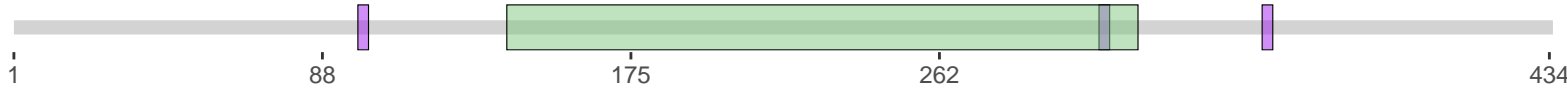


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

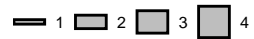


Protein sequence:

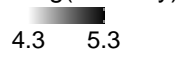
LLRRLRHLHYGEVQLPNNHLLLPQVRKEVLRVISHIQDALAGCELTFLKLGILNVAEAVDDTAGAAEYIAGNNLRDTAAIASARAADLVGLQLAEGHDDSSNVTRFVMLAREPIRTRDRPFKTSVFAHHEGTSVLFKVLKLSAFRNLTKESRPHRNRPIRVVDDANVGTAKHFEVYFVDFEASMDNRAQNALAEVGEFTSFLRVLGEVPMDMTPWCPREDS

NbL07g01930.1 UDP-D-apiose/UDP-D-xylose_synthase_2-like [MW = 43.26 kDa]

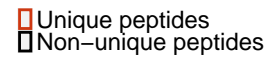
No. of times detected



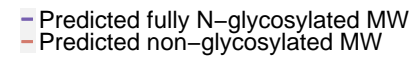
log(intensity)



Values from



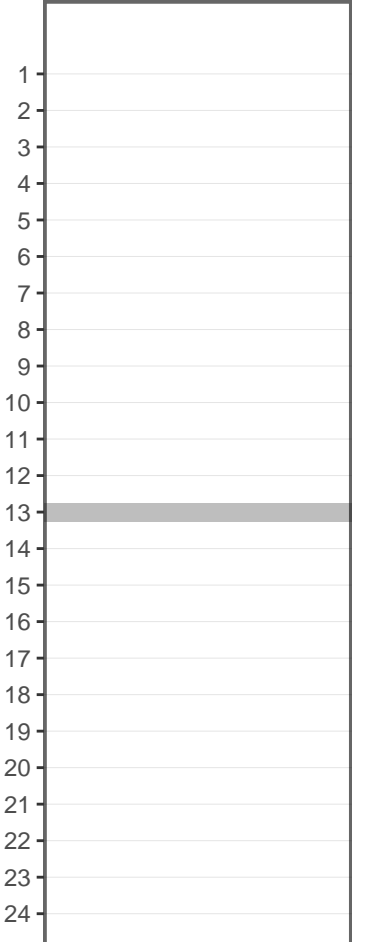
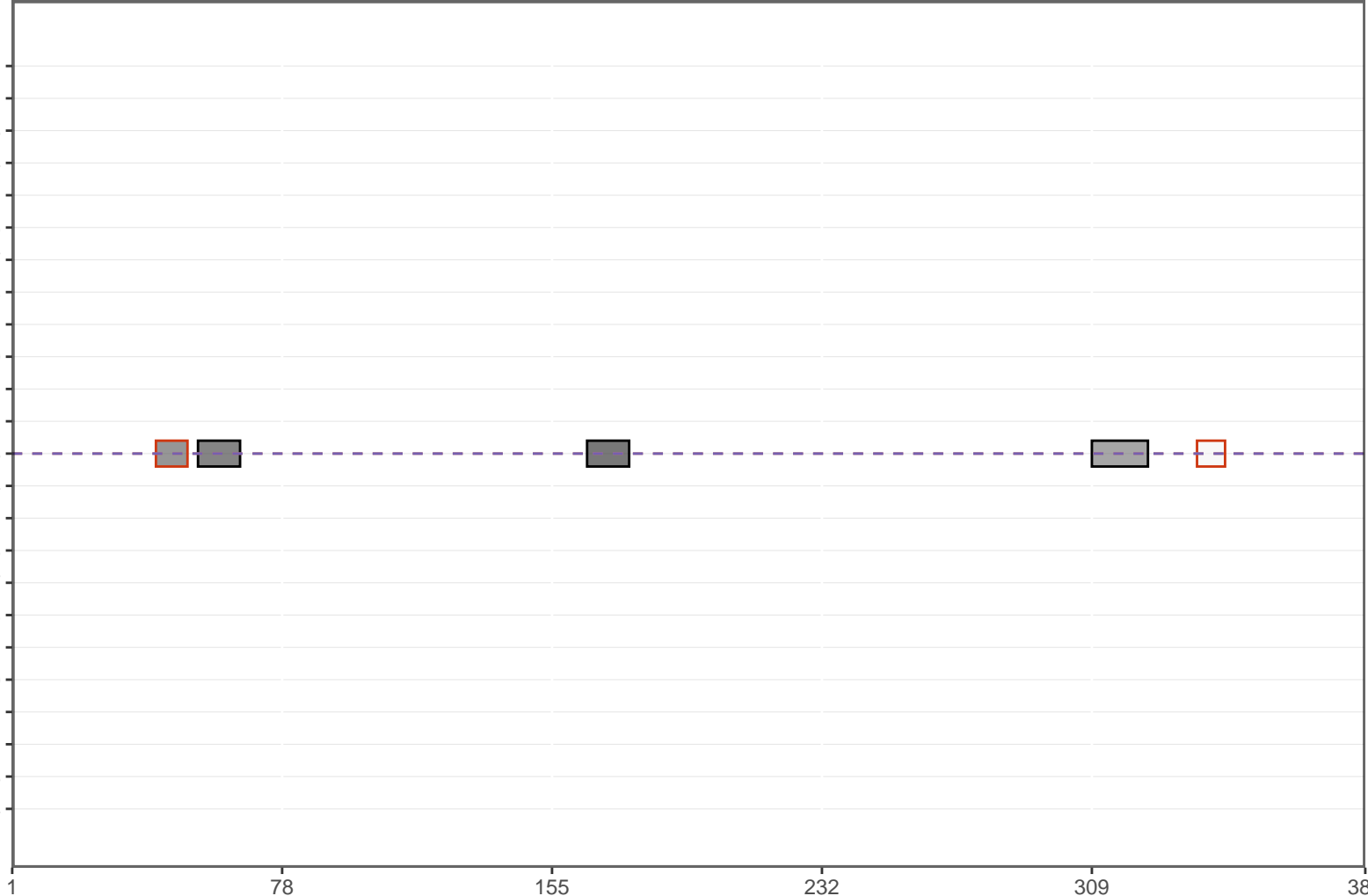
MW indication



Molecular weight

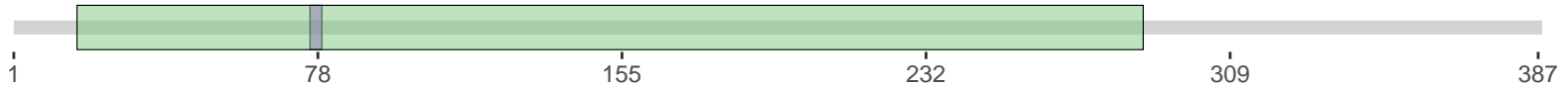


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ACAKQLIERLYAEGAEENGLEFTRVRFNWIWGRMDIFPIGDGSPSEGVPRVLACFSNLLRREPLKLVDDGESDRTFRYKDAIEAVLLMIENPARANGHFHNGNPNNEVTYVRLAEEMMTQVYSKVSSESSIEPTFDVSSKEFYGEGYDDSDKRIPDMTHIRQLGWNPKTSUWDLLESTLYGHRTYAEAVKQAMSKTTAN

NbL07g01840.1 VAMP-like_protein_YKT61 [MW = 22.61 kDa]

No. of times detected



log(intensity)



Values from



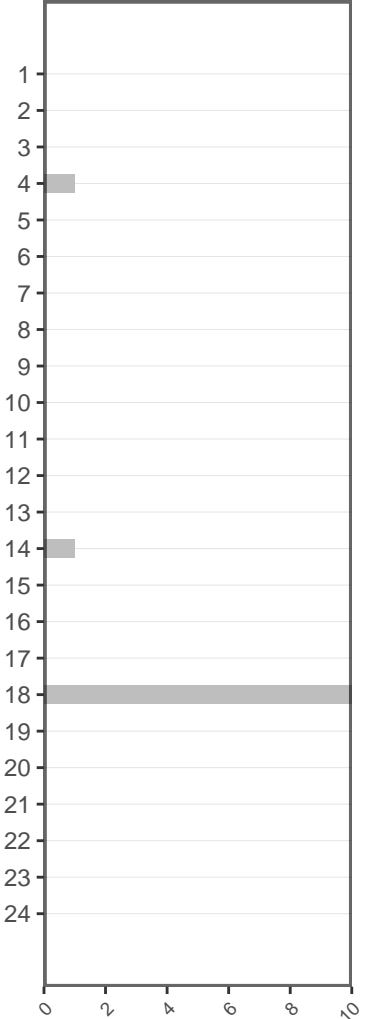
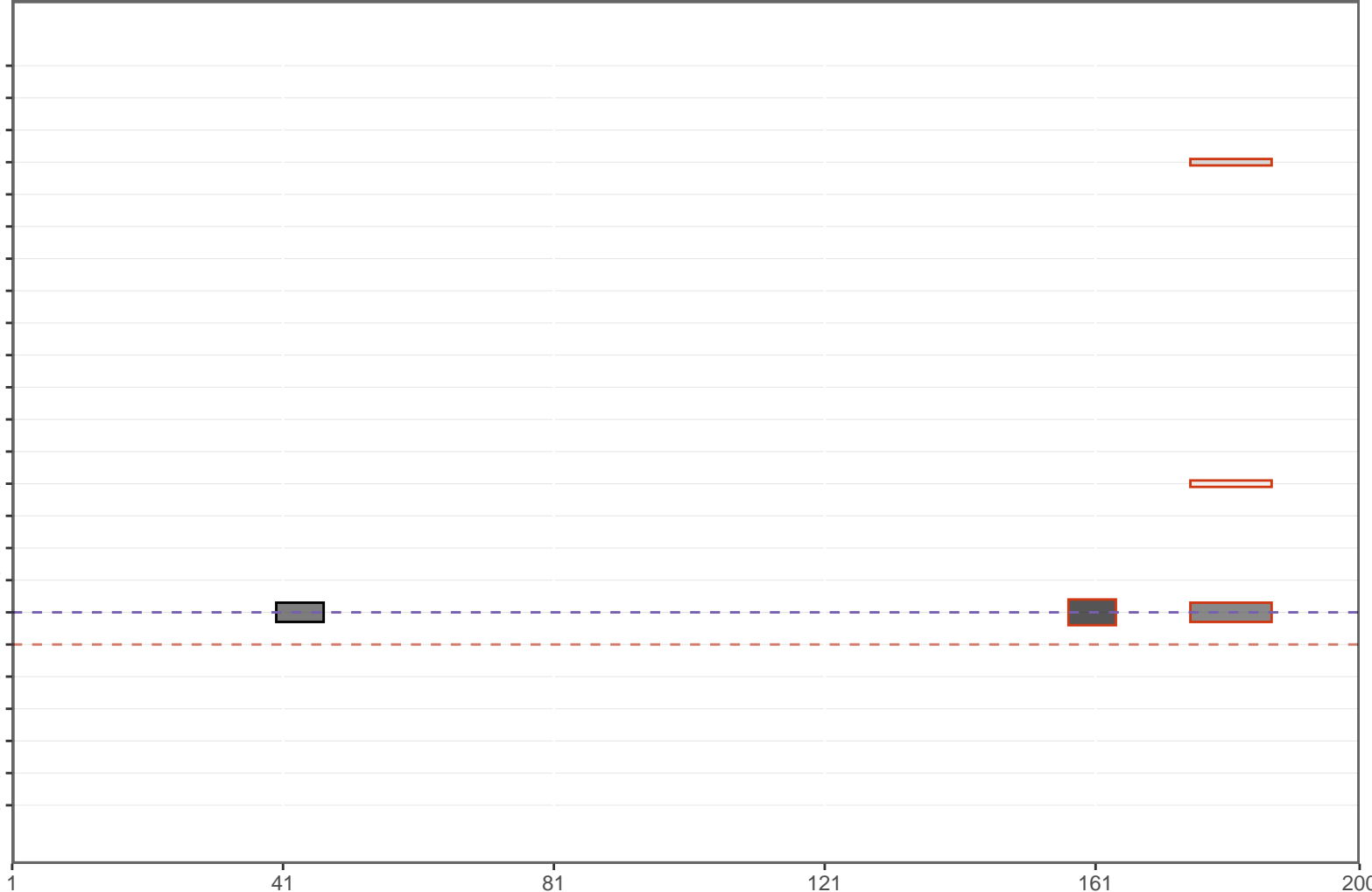
MW indication



Molecular weight



Gel Slice

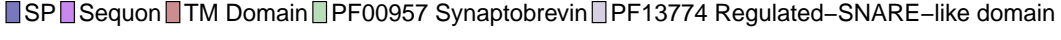


Peptide counts over 4 repeats

Protein length

Pfam domains

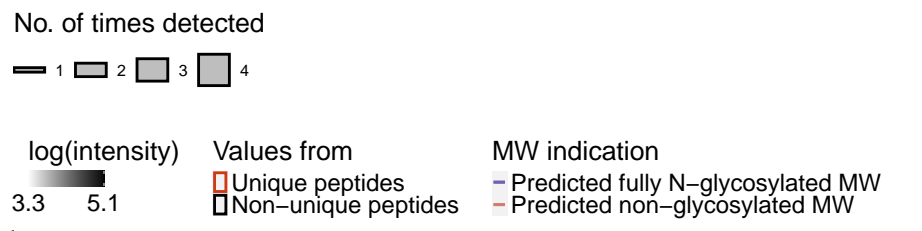
Pfam Description



Protein sequence:

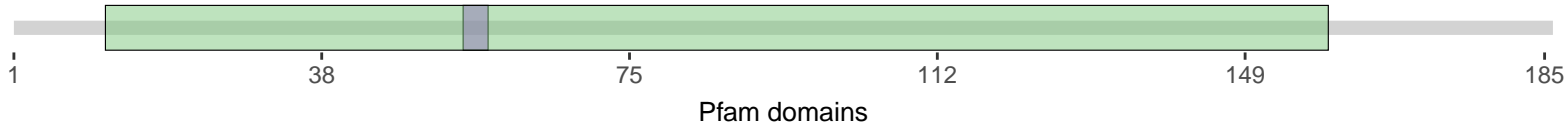
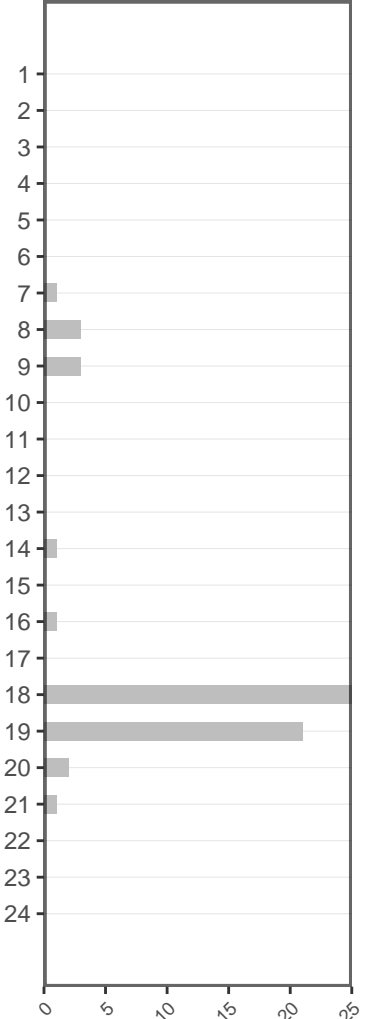
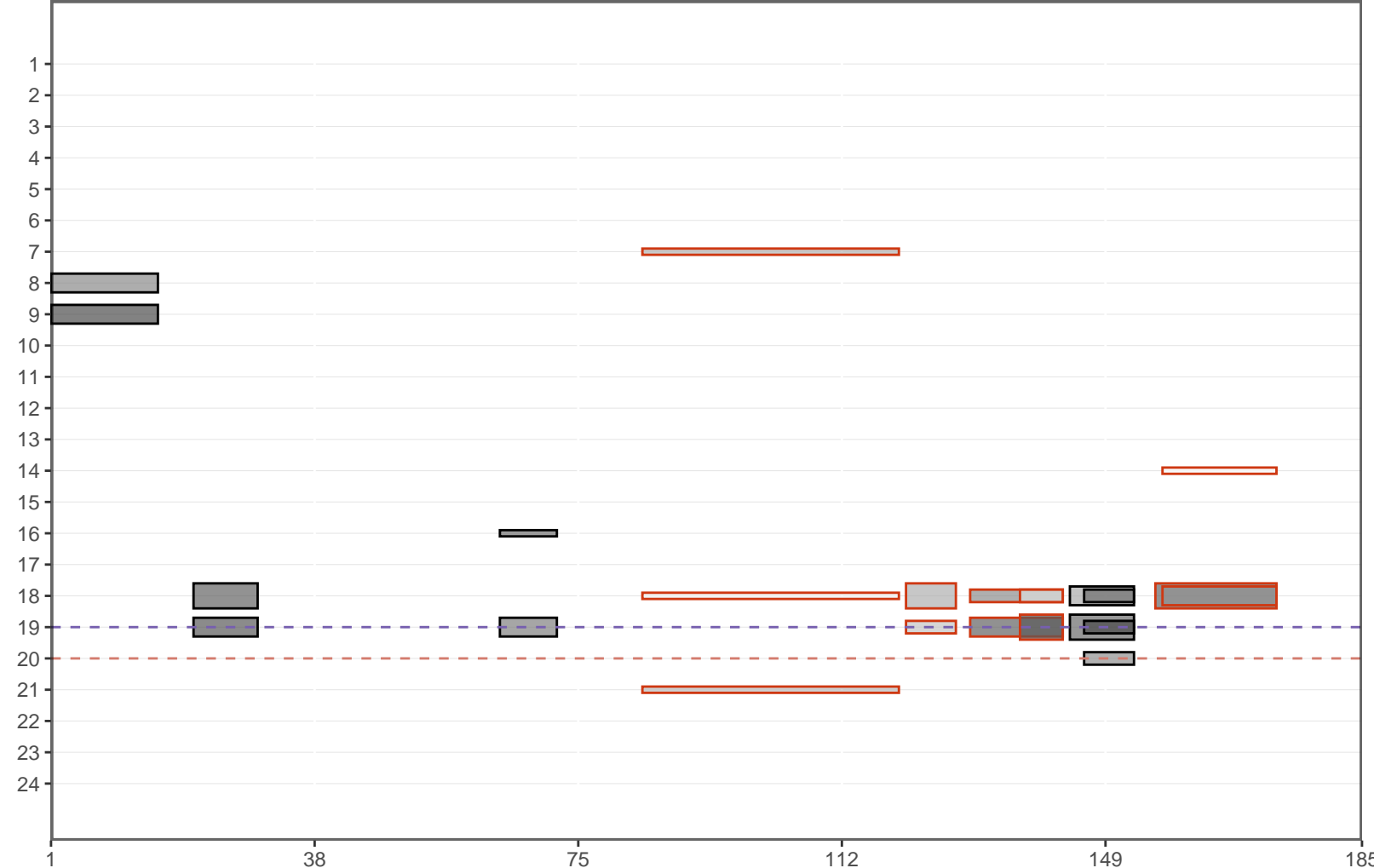
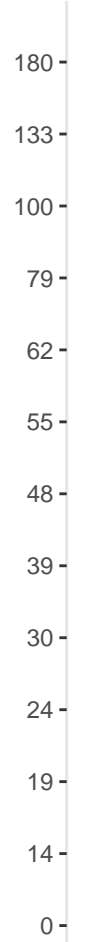
YPVRSAFSLNNOVLDVYLNKFGESWKTAGNDNAGDPWYLYNEALAKFQDPRAEADKLFKIQRELDKTIHLHKTIDVLERGENKLDLVEKSSDLAASGDMFYKGAKKTNSGCTIL*

NbL07g01830.1 temperature-induced_lipocalin-1-like [MW = 21.37 kDa]



Molecular weight

Gel Slice



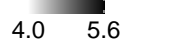
Protein sequence:
 IDEAKLVKFKYLPFLPIPIPTGDYWLHDDDKYALGQPSRNYLWLGRKTHLDEEKYMLIEKAKEVGVDEKLRKTPGSDPPPEGELPQDTKGAWLWIKSIFGR

NbL07g01690.1 S-norcochlorine_synthase_1-like [MW = 17.01 kDa]

No. of times detected



log(intensity)



Values from



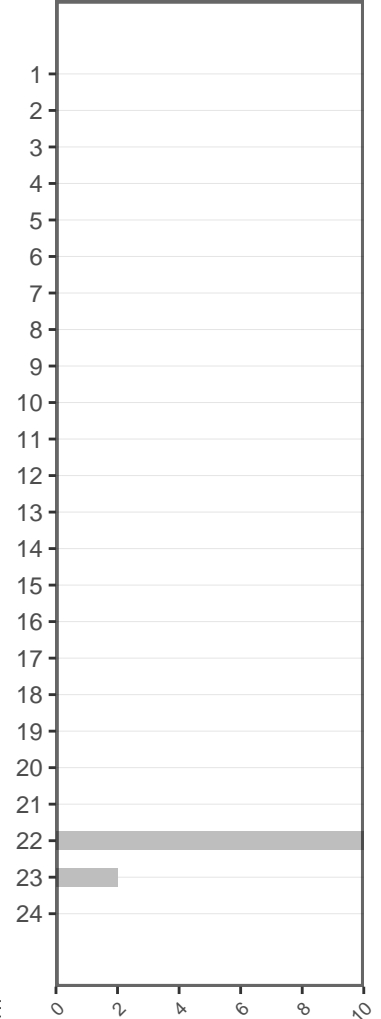
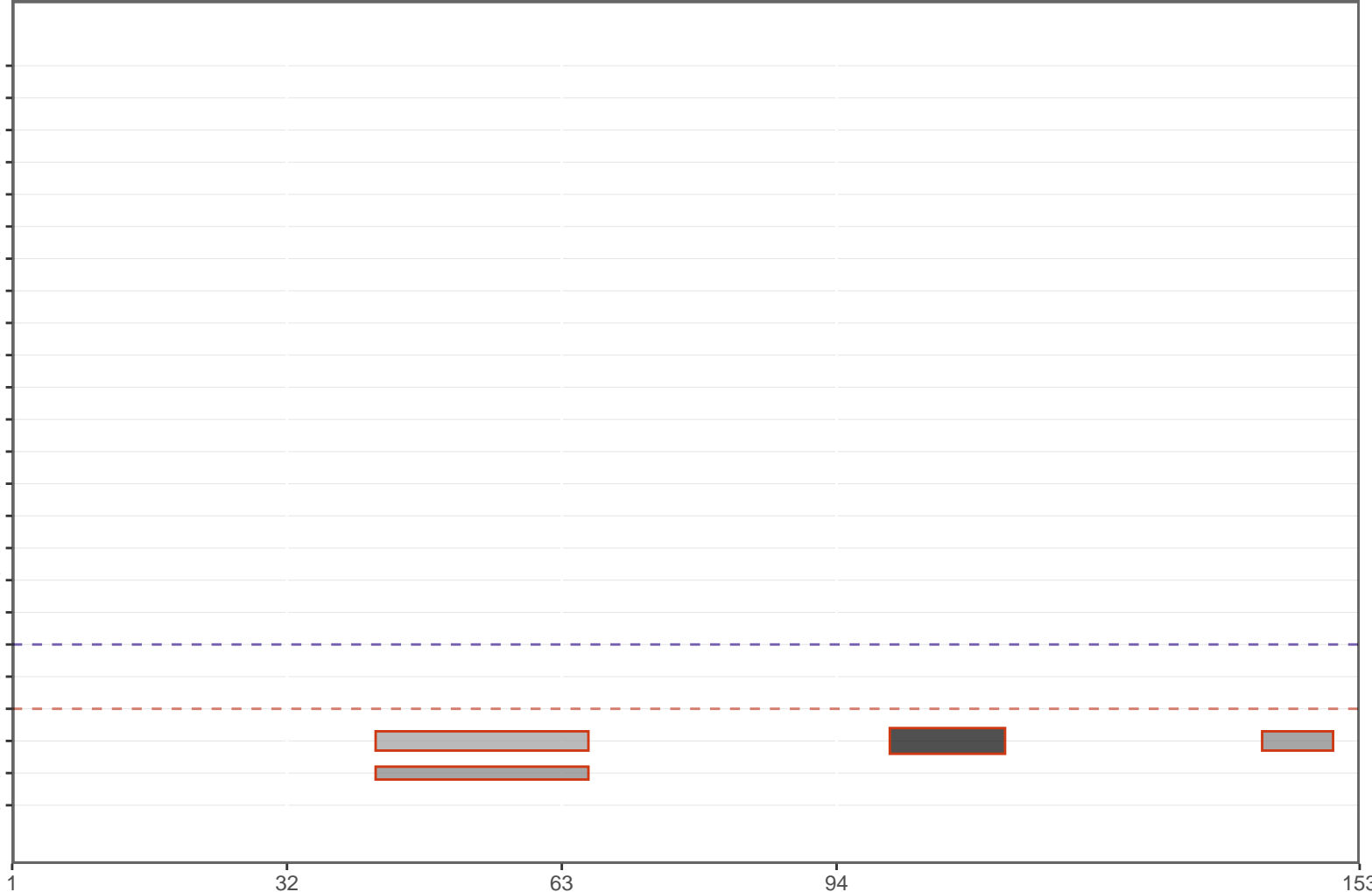
MW indication



Molecular weight

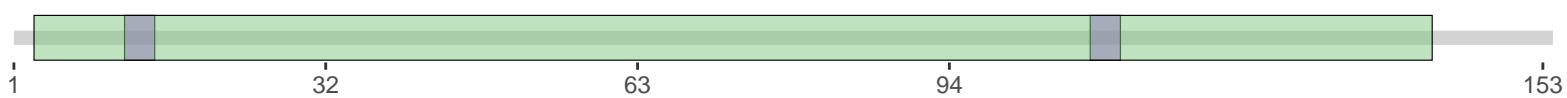


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

INAPYKXKPYSDIDKRWKEVEVEGGYLDLGFSPYGIKFEVIEKDENLGIKVTIDFETNDAENHLITGNGAFVAMKATVEYFSQKSK

NbL07g01670.1 NADP-dependent_glyceraldehyde-3-phosphate_dehydrogenase [MW = 25.97 kDa]

No. of times detected



log(intensity)



Values from



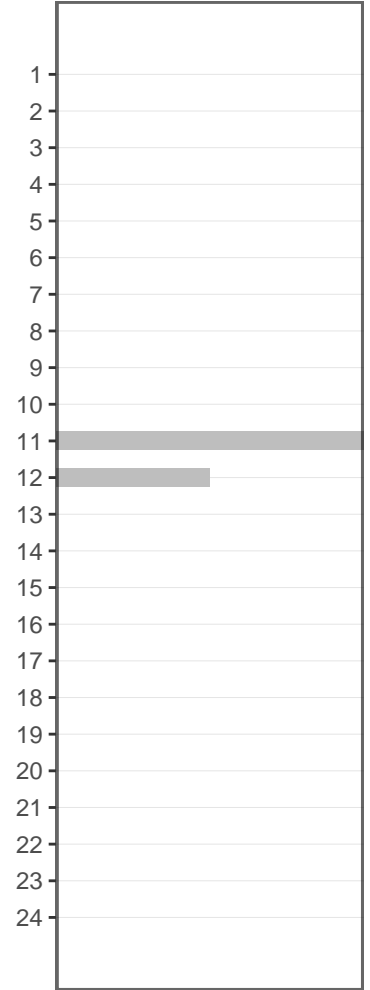
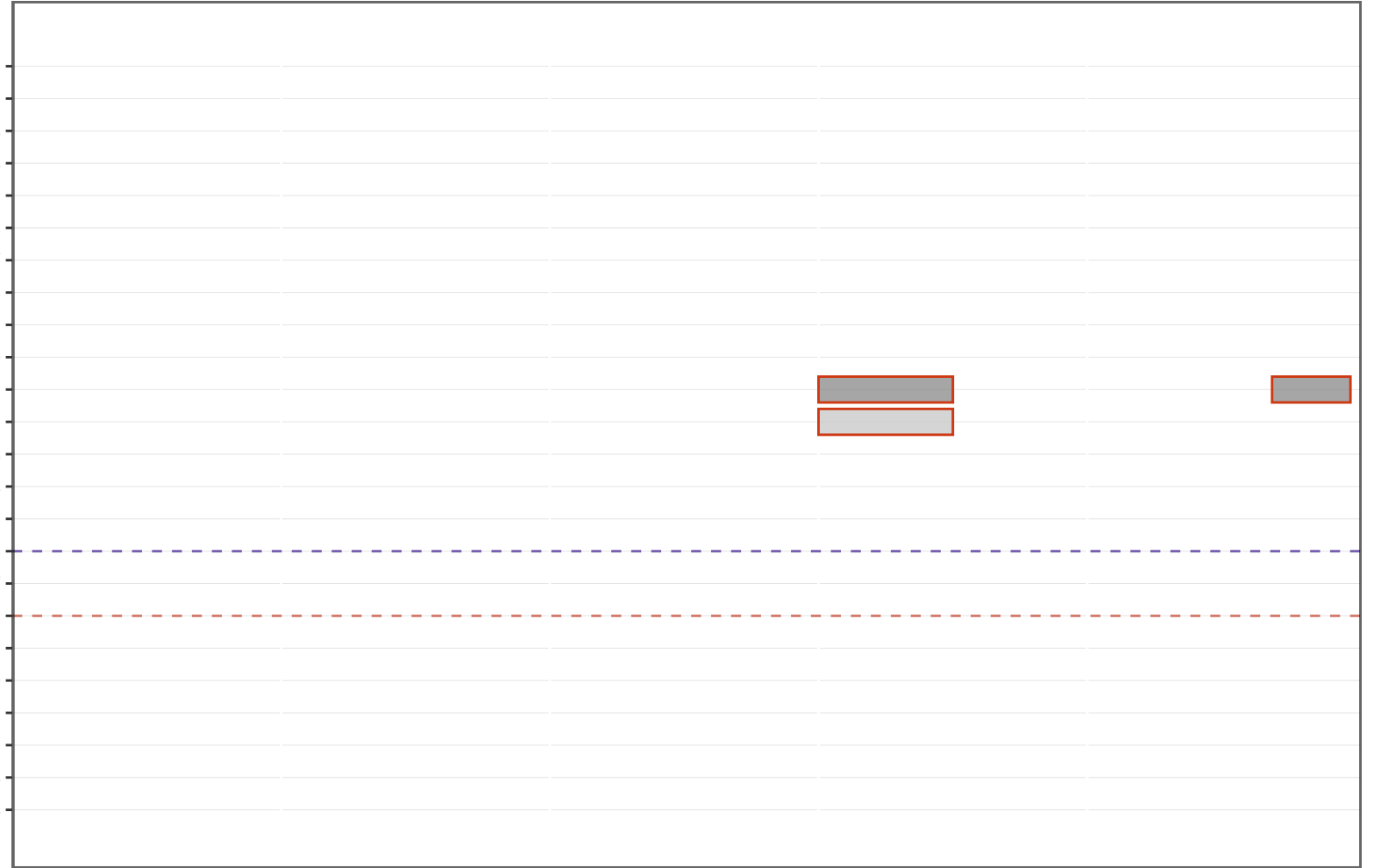
MW indication



Molecular weight



Gel Slice

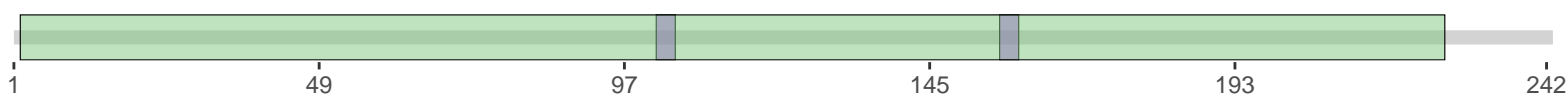


Peptide counts over 4 repeats

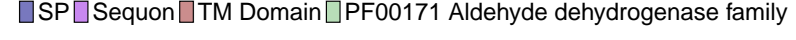
Protein length



Pfam domains



Pfam Description

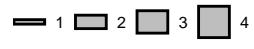


Protein sequence:

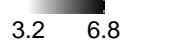
IQYKREGNLIVPLLDNVRPDMRIIAWEVFPQPLVPIRIRISVEEGHHGNASNFLGGGVFTRDNKALISDAMETGTVOINAPARQPHFFQGGKDSGGGGTNSINMMTKVKTIVNLPTPEVTMGLI

NbL07g01570.1 eukaryotic_translation_initiation_factor_5A-3 [MW = 17.54 kDa]

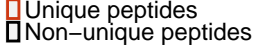
No. of times detected



log(intensity)



Values from



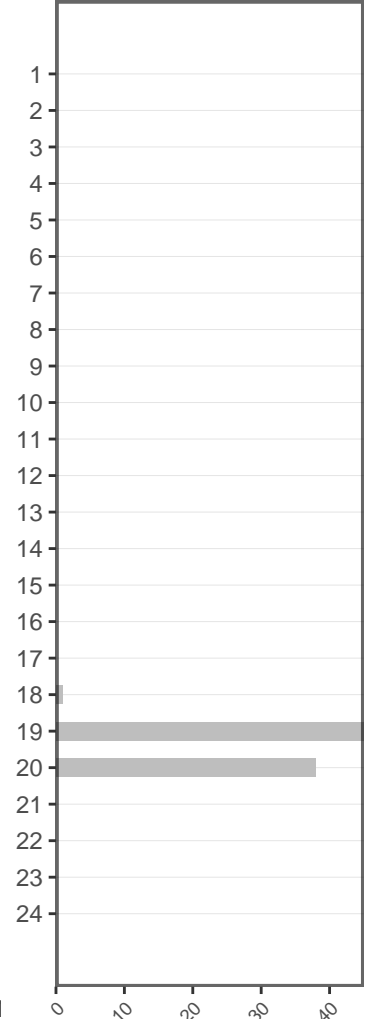
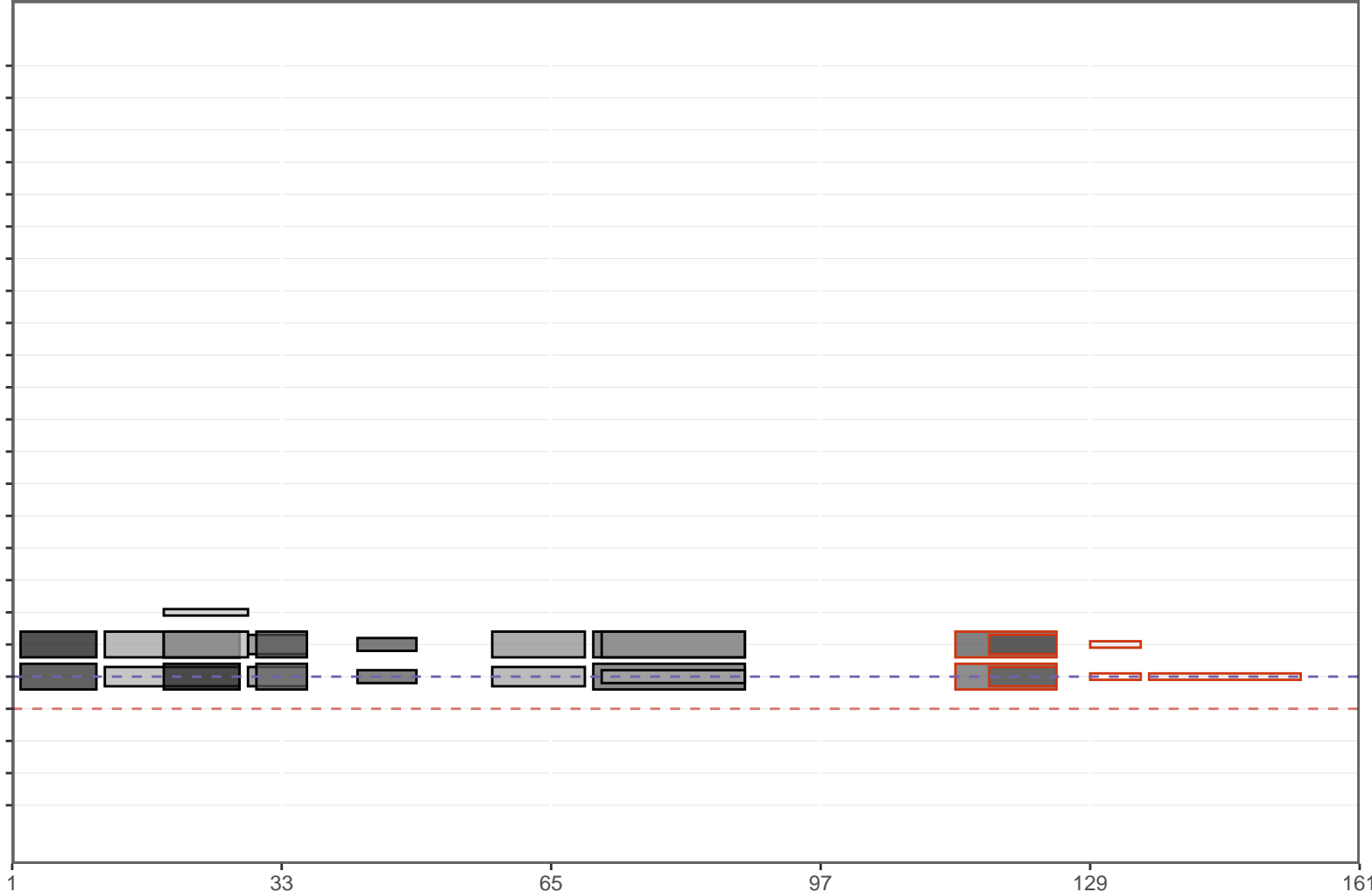
MW indication



Molecular weight



Gel Slice



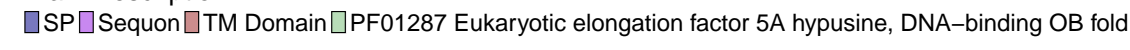
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGKKLEDIVPSSHNGDVFPHVNRITDVLQIDISEDFVSLTETSGNTKDDLRLLPTDEALLKQVNDGFGEGKDLVVEVMAMGEEGINVNDIGTKNY

NbL07g01330.1 shikimate_O-hydroxycinnamoyltransferase-like [MW = 48.45 kDa]

No. of times detected



log(intensity)



Values from



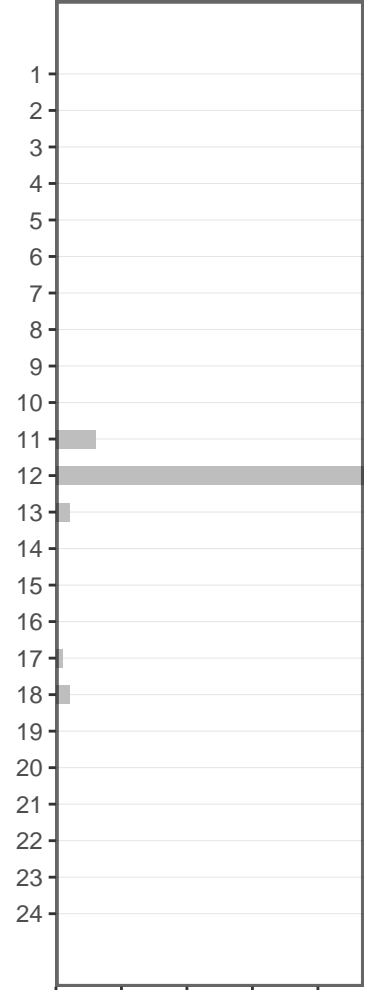
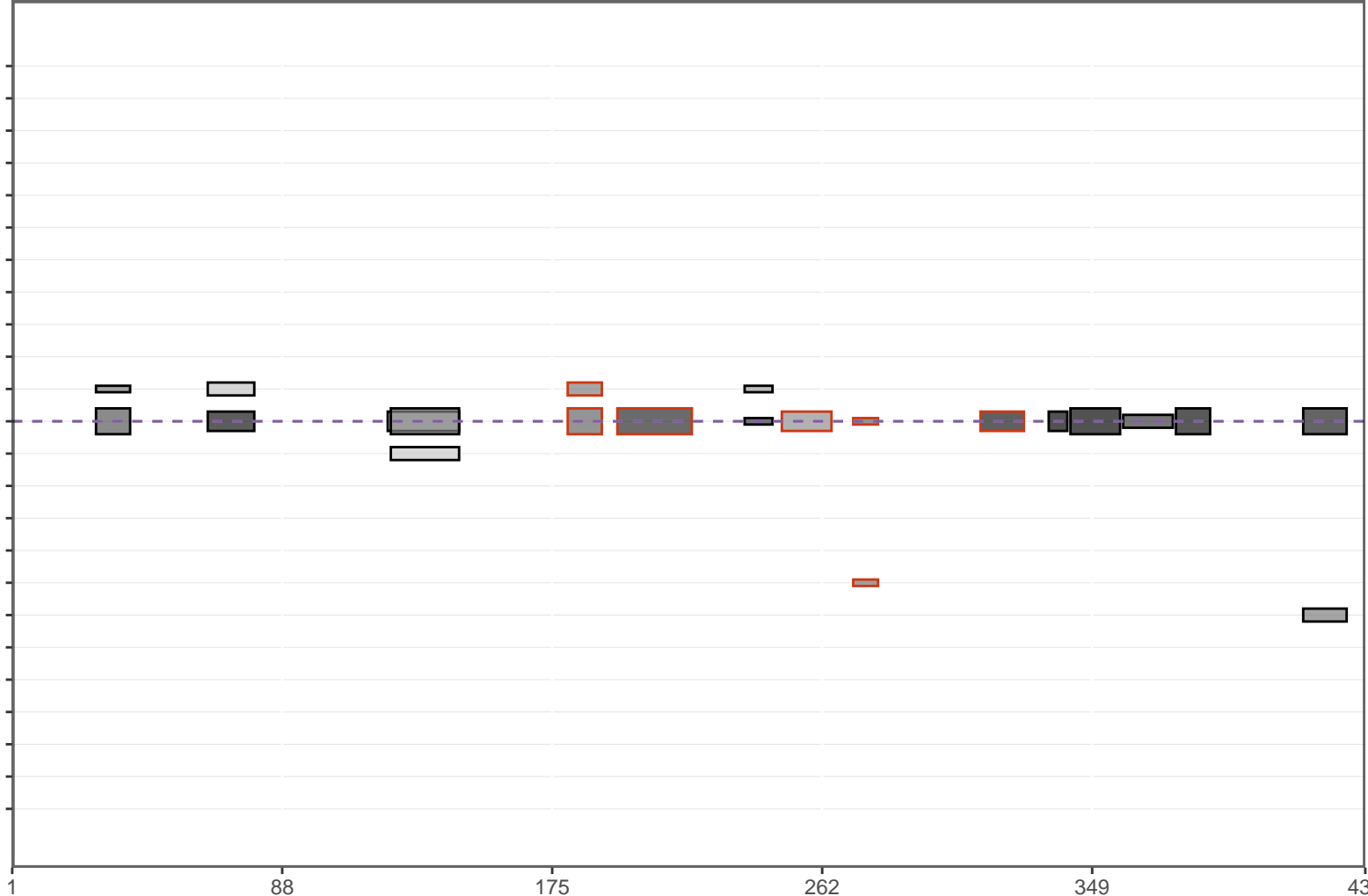
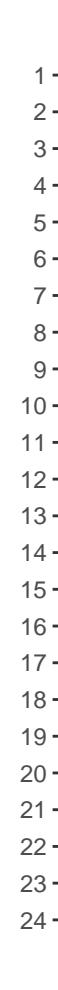
MW indication



Molecular weight



Gel Slice

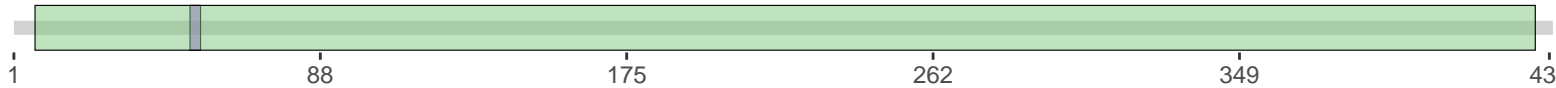


Peptide counts over 4 repeats

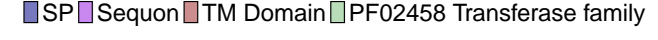
Protein length



Pfam domains



Pfam Description



Protein sequence:

IEYQSPPLSISSSKTKEGKSNPKPSTTTMLKFSDDQLGLLKKKHKEGFTYEILAAHWRCCTKARALADDQLTKLHWTDGRGRGLCPPLPGYLGWVFTATPMKSSSELLHEPLTNSANRHVLSKMDNDYLRSAIDYELGQDLSAURGPPTYPASPFLNINISWTRLPVHDSDFGWRGPRHMGPPAGLYEGTVYVLPSPNKKORNLRLAVGLDADHMLPEKYLEF

NbL07g01050.1 protein_disulfide_isomerase-like_1-4 [MW - SP = 62.13 kDa]

No. of times detected



log(intensity)



Values from



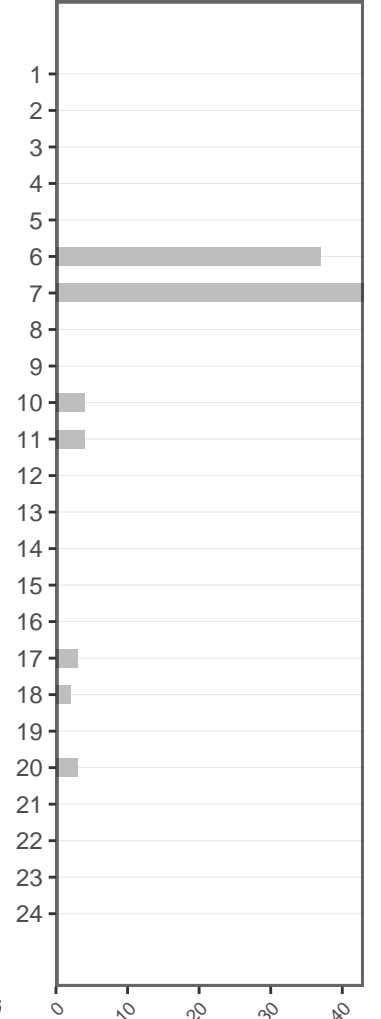
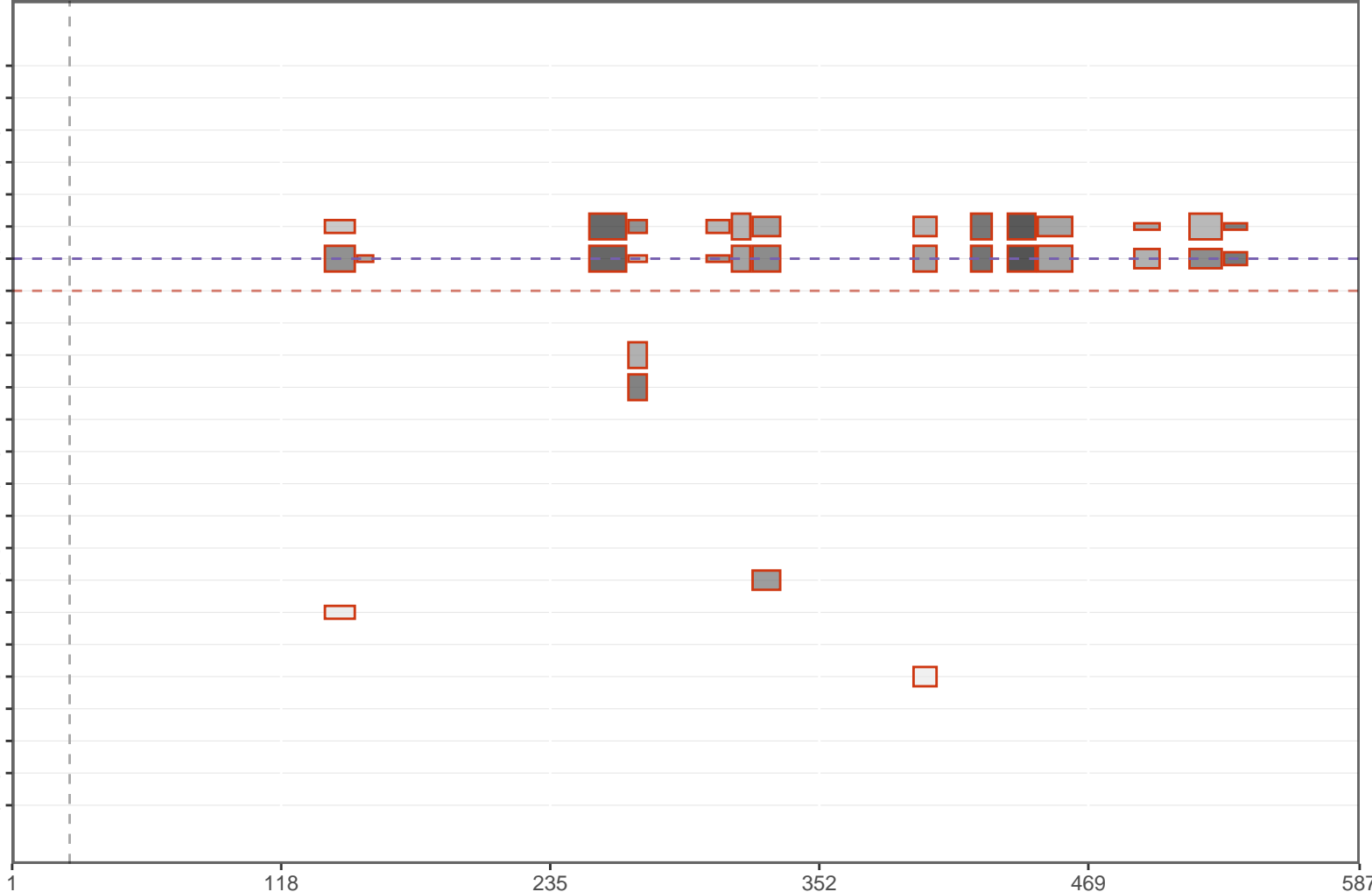
MW indication



Molecular weight

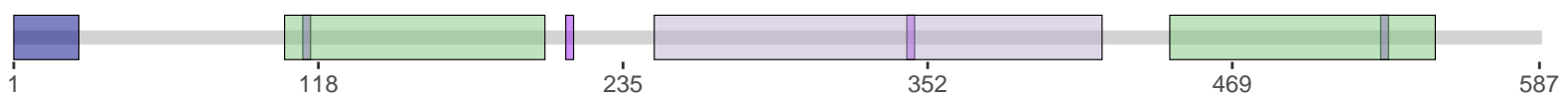


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ALLVFLKKEAEKVVHFAISDGGFTKSAIMEFVSAANKLFLVTTFTFRSGSPGFESPKKGVLLFATINDTKVFFPTFGAAKLFKGLIFVFNMDDEEVEGKPVSDVFGATGDSPKVIGYTGNEIDPRKVFDEGTEVEKLFKAFEGEFLGGKRAFYKSDPIPENNEGDKVIVVGNFDDVLDSEKDVILLEHVPWCGHQGLEPTYNKLAHLLHDESELVIAKMDGTNEHPQAKAEGFPTLLFFRPGAKSINIPVQADRTVVALYKFKKHABIPKLPKPKAS6TTSSESSEAKEDKVEI

NbL07g01040.1 4-hydroxy-3-methylbut-2-en-1-yl_diphosphate_synthase_(ferredoxin)_chloroplastic [MW = 82.2 kDa]

No. of times detected



log(intensity)



Values from



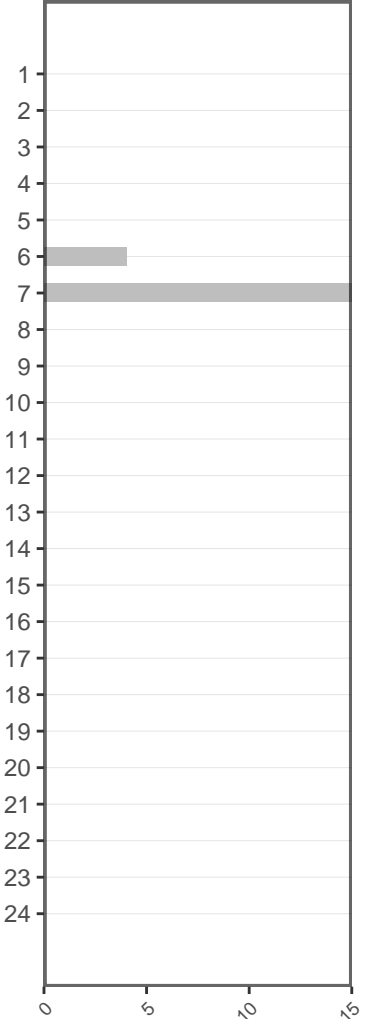
MW indication



Molecular weight

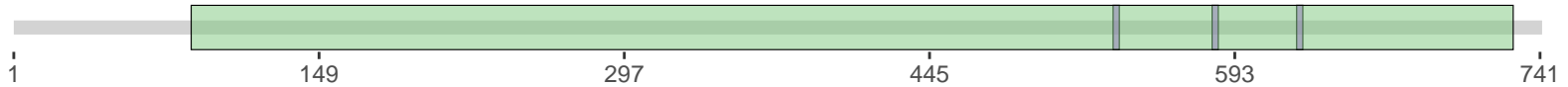


Gel Slice



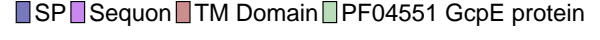
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RLANLGRRAELGGVWPFEEKNRVYDFDRRSGELPMRREGDEVYRGVLRHRDGSVLMSEVSLDQKTFELLYRSLAAKLVGMPEKDLATYDSGLLRLLPFRVDDKDRSLAKRILVDSIMGVITPLSEGLTKPLDAVLLVTLKELGGAGKLLPEGTRLVVSVRGGDESKDELETLSNSTVITMLKLNLPYTEEKIGRVHARRLFEYLSENLNFVPIHHHFSNDTHRDDLVGAGANAGALLVDGLGDLLEAPDQDFDLRNTSFNLLGGCRMRNTKTEYVSCSCGRTLF

NbL07g00850.1 beta-galactosidase_8 [MW - SP = 89.69 kDa]

No. of times detected



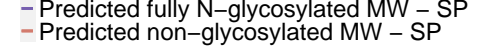
log(intensity)



Values from

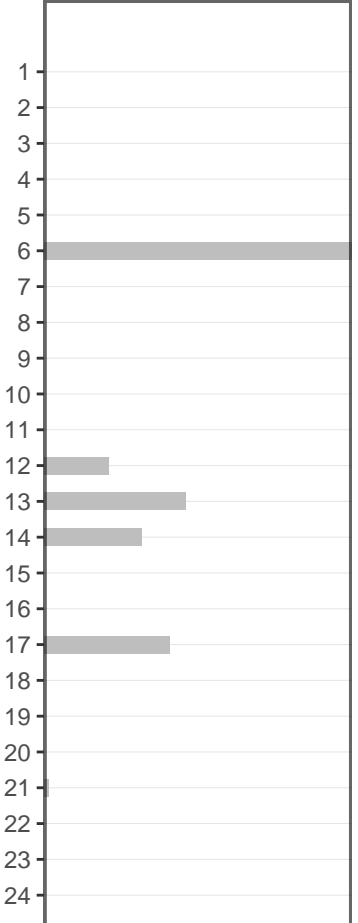
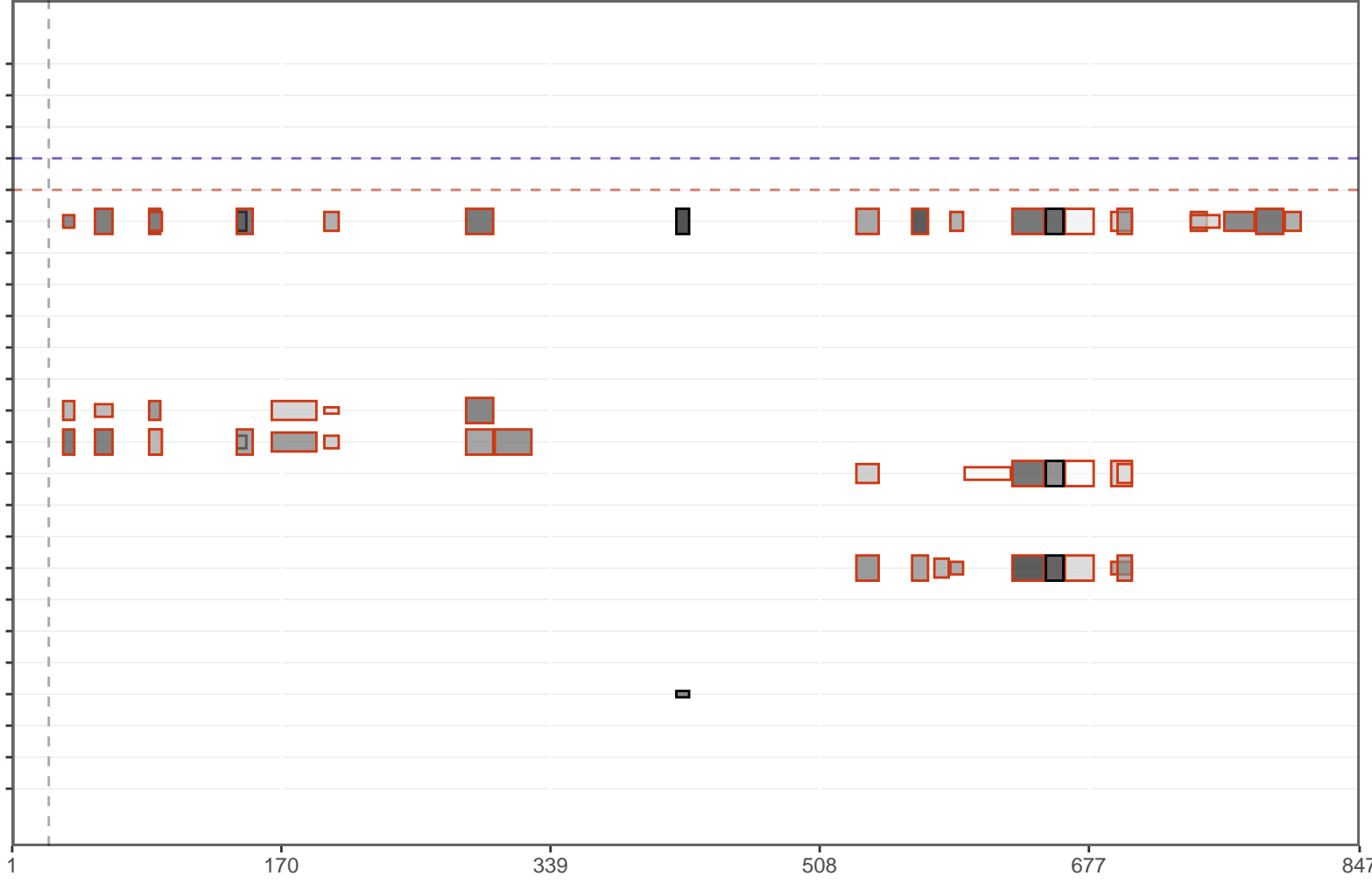
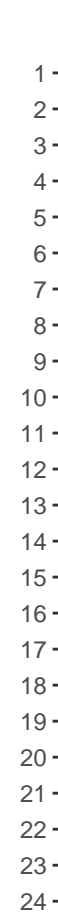
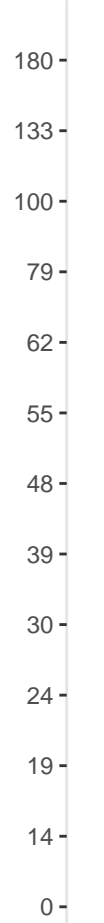


MW indication



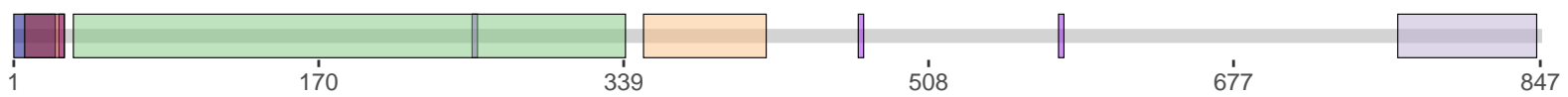
Molecular weight

Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IVAFSTAKNSMSTISKFTVQSTFADGSGAGLGGWTFWNEPVGISDPAFTKTLGMEQNTTADKSDHLYWYGLVNVNKNDEPFLGDDGSDTVLHVESLGHVLFHAFINGLKSGSGKNSGNSKVTDFVPTLVPGENKIDLLVNVGLQNYGAFFDLKAGITGTPVQLKGFNNGSTDLSSKQWTVYQVGLKGEELGLSDGSSLLWNSGSAALPTNGLIWKAFDPAAGDTPLELDFDTGMKGAEAWWNGSGHGRFVPTNTAFNGSGDSDGNVYRGEVNSKCKLKNCKPQSL

NbL07g00810.1 proteasome_subunit_beta_type-4-like [MW = 27.61 kDa]

No. of times detected



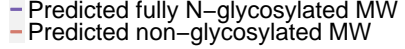
log(intensity)



Values from



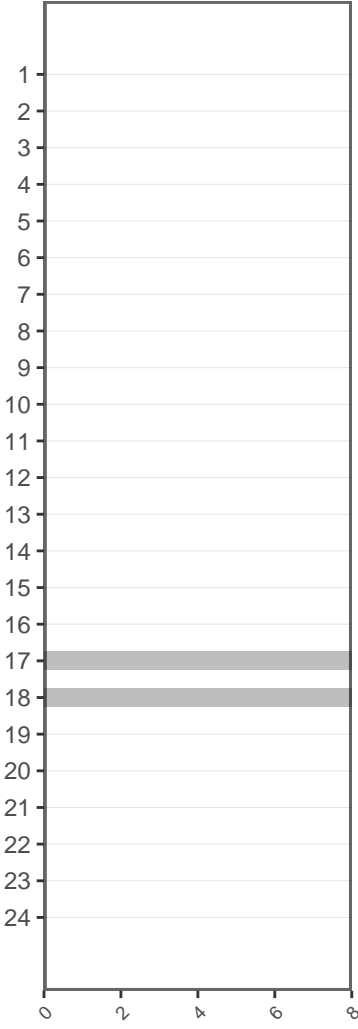
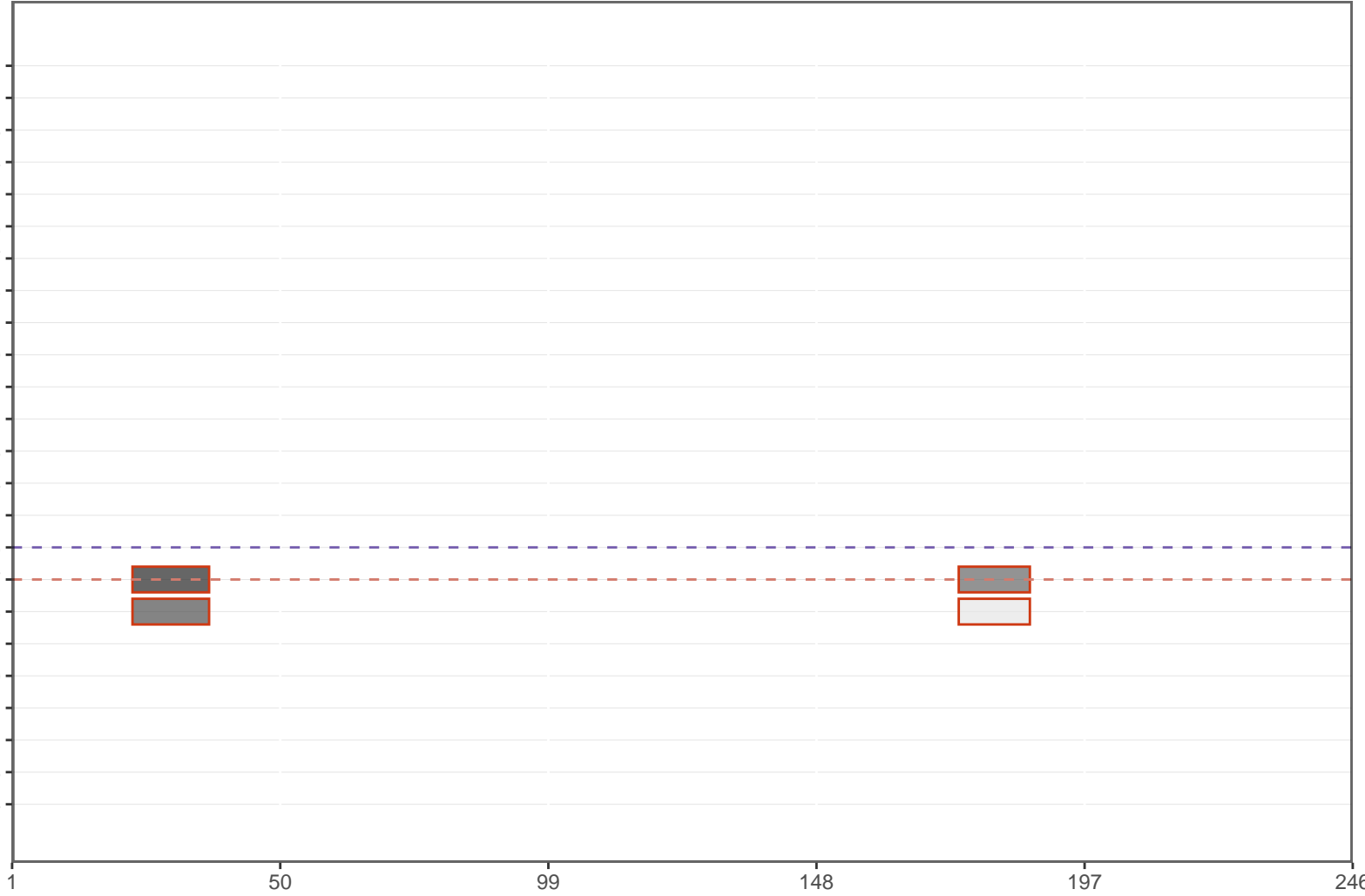
MW indication



Molecular weight

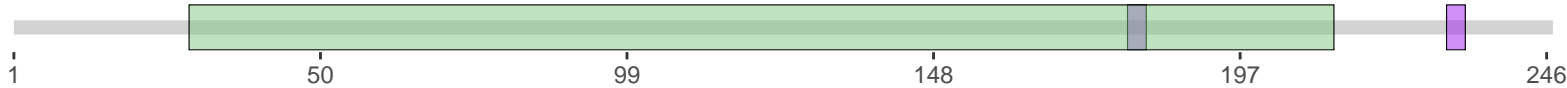


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NYLTRMNYNRNRNFKPLNSLVLGGVKNQKYLGMVGMIGVHYEDDHVATFGNHLARPLRDEWHENLSVEEGVLLLEKCMRVLVYRDRGAVNKLGIKITEEGVTVSGPYSLKTFVWFSAFQNPVTVAEGSSW

NbL07g00760.1 4-coumarate--CoA_ligase-like_7 [MW = 59.73 kDa]

No. of times detected



log(intensity)



Values from



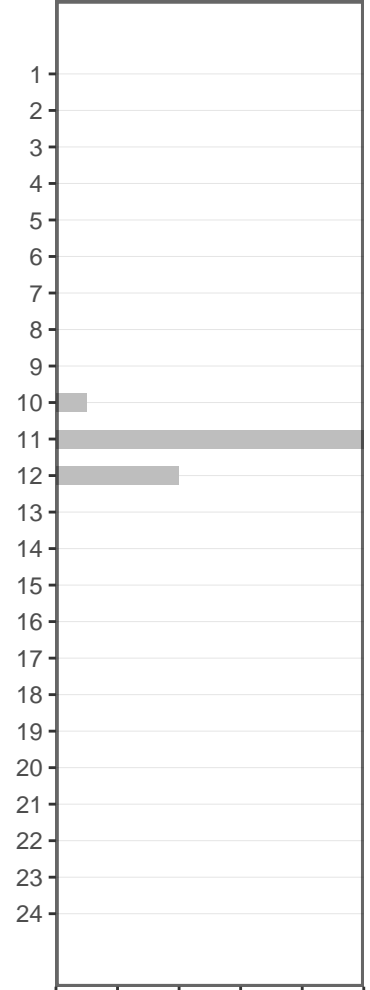
MW indication



Molecular weight



Gel Slice

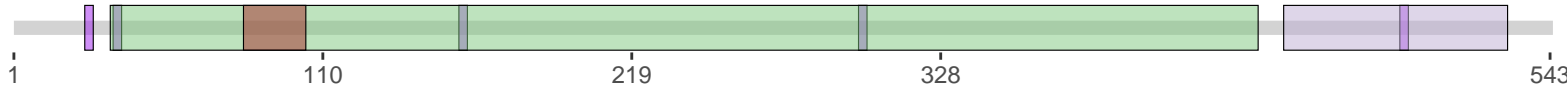


Protein length

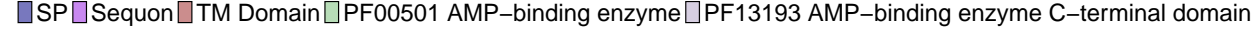


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KFDLEMLKTYDKYRVTHLWPPVLLAKIPVKKYKNTSLRNGSGAAPLQKELMECAKFPMAVFDGVMETETGGVAVESFVGRPRHTGSGAGTLVPGVEAQH6V9LKLPLPPGLGEVWRGPNMGGVFNPNQATHLTIQNGQVHTDGLGVFYEEGLVYVDRKELKYYKGFQVAPALEGLLVSHPEILDVWIPVQVYRFPDAEAGEVPIAVVVRPNSSLTTEEDVQKFIADQVAFPKRLRKYVTFVNSVPKSASGKILRRELIDKVRSLK

NbL07g00730.1 probable_inactive_purple_acid_phosphatase_29 [MW – SP = 40.34 kDa]

No. of times detected



log(intensity)



Values from



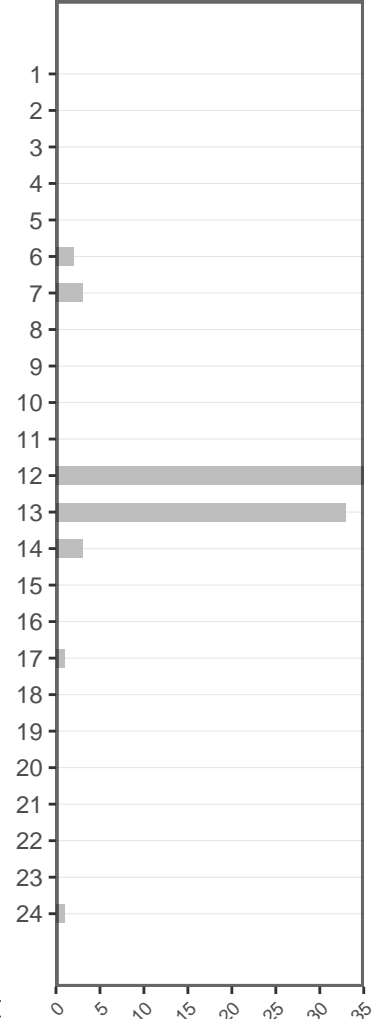
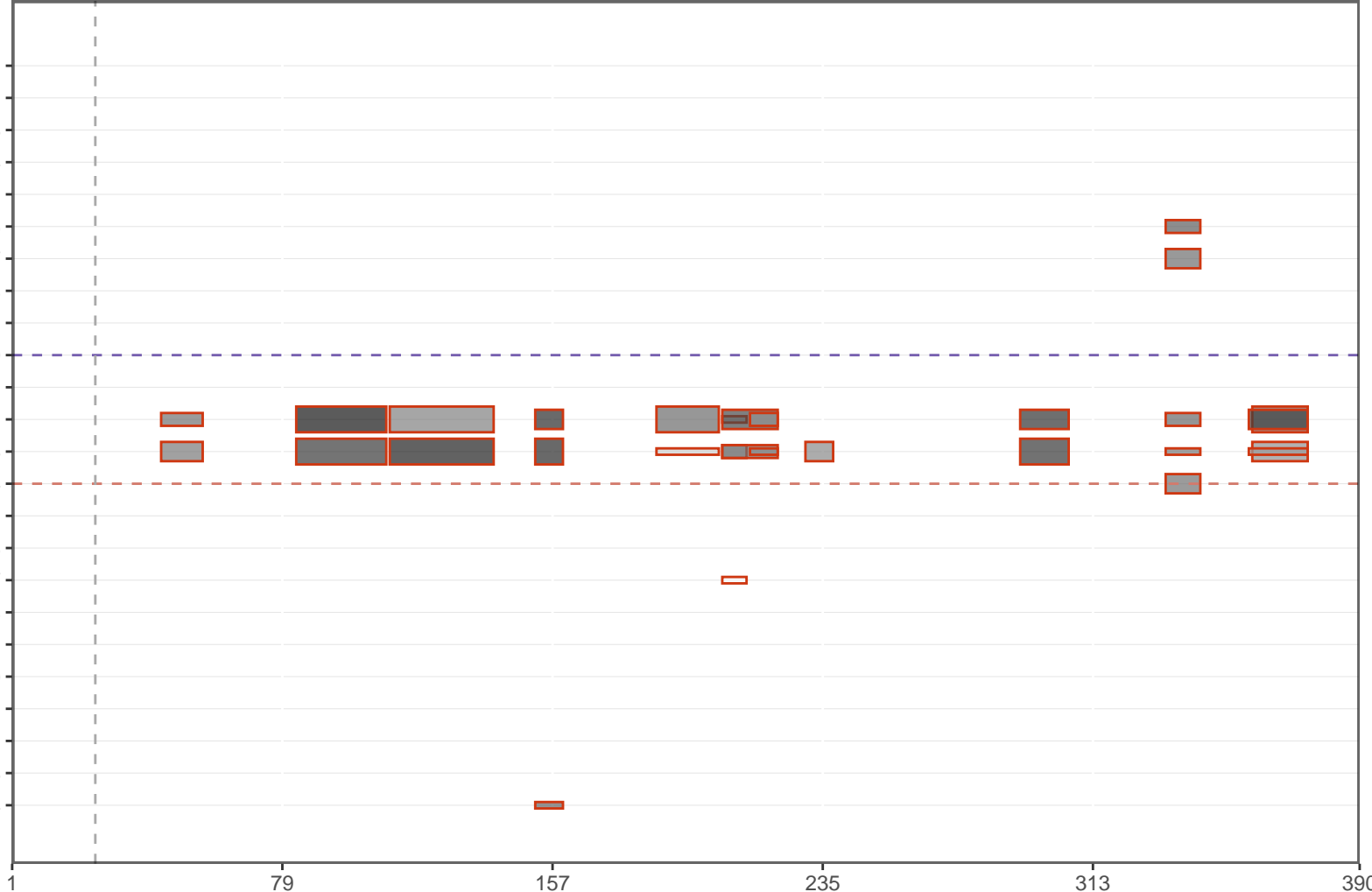
MW indication



Molecular weight

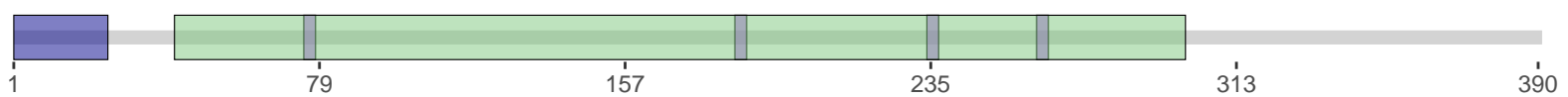


Gel Slice



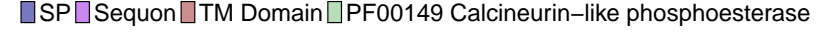
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

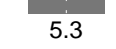
ANKSVLNLVFLDSDGKSTVPSRPVGVGKYSQQLWFGRTSKKIKKTYMNSAARKVPAKPLAVFHPLEPEVAFSDSNFTGVRRGEGISSASINSQFFTTMVEAGDKKAVFTGHQHNDFGQKLMNLCVAGGFGVHAYGKAGWRRARRMVAWLEETFGKGGVAVKSKRTWKRLLDDEHFTSDQVLSKRSAGTRRKKPKIGHQ

NbL07g00710.1 xyloglucan_endotransglucosylase/hydrolase_protein_31-like [MW - SP = 31.42 kDa]

No. of times detected



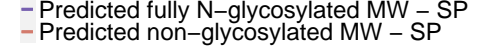
log(intensity)



Values from



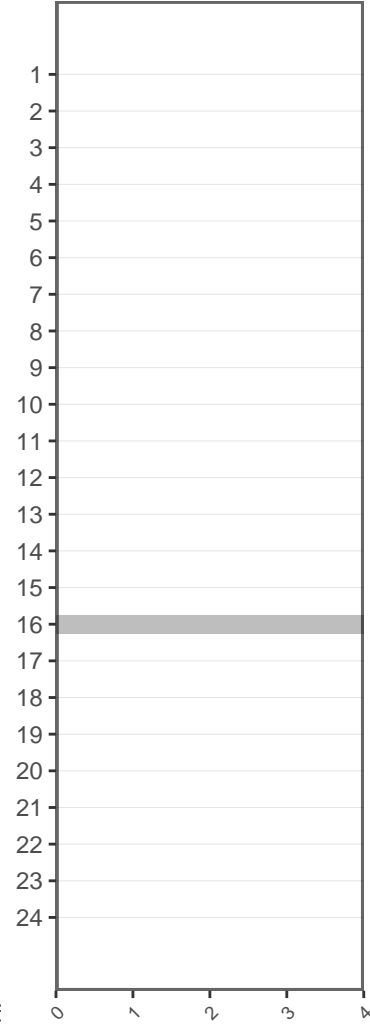
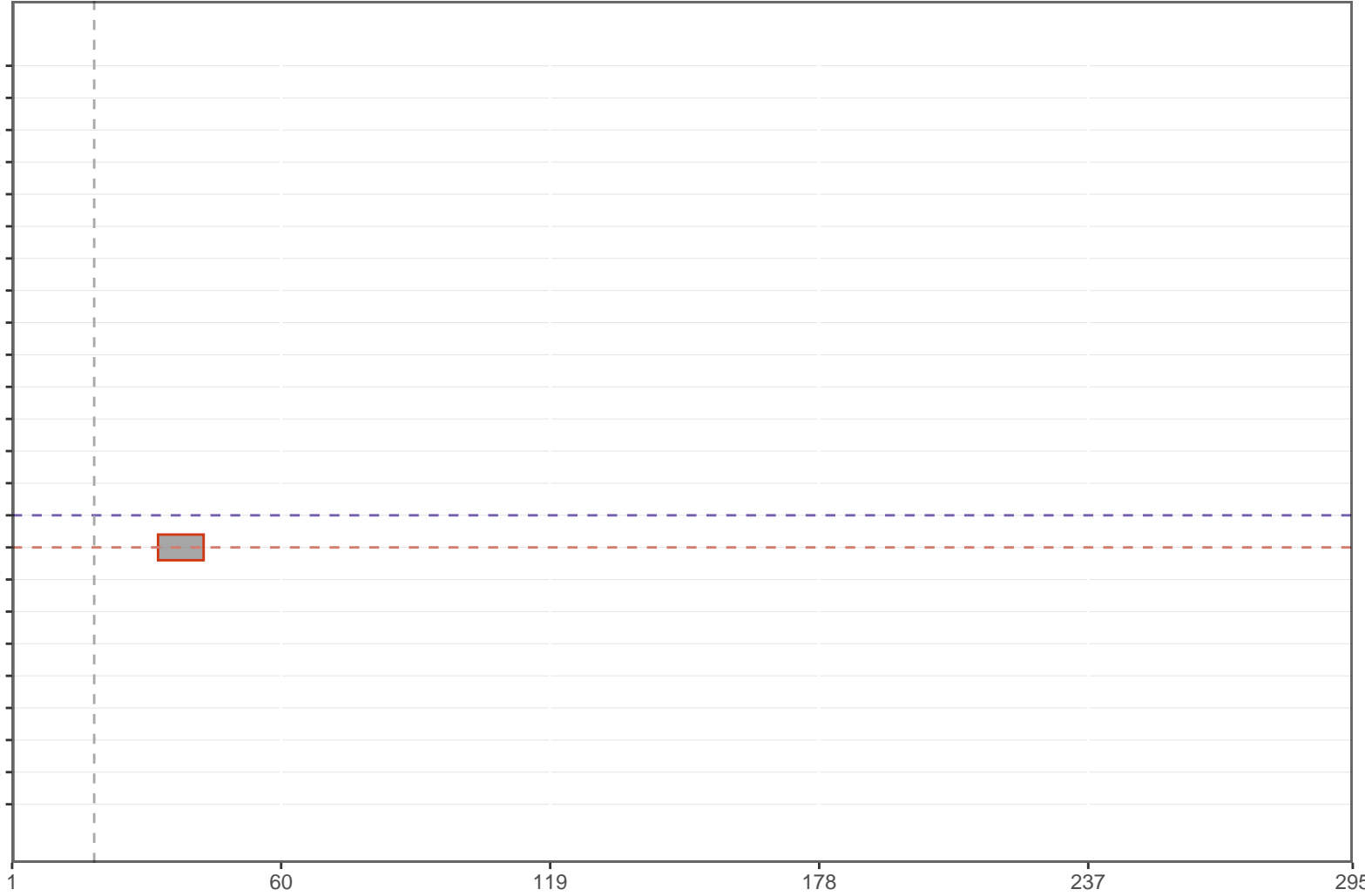
MW indication



Molecular weight

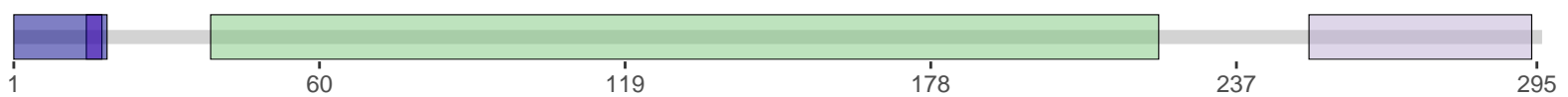


Gel Slice



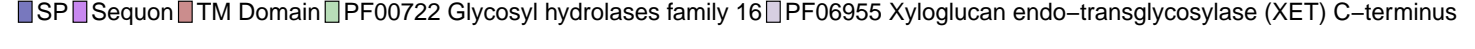
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IRGSGDGNIGREMKFLWFDPTGAVHNVALWDPNEIEFVDDVPIRRYPRKNDATFPQPMVYVGSWDSWATEEGRKADRYVDFVGVKYNFKIAGCTANENPWCGRSPSSPSRAGGLSRGQAAALWVGRNKKVYDGRDPRRDHHTPEE

NbL07g00700.1 vacuolar_protein_sorting-associated_protein_24_homolog_1-like [MW = 25.08 kDa]

No. of times detected



log(intensity)



Values from



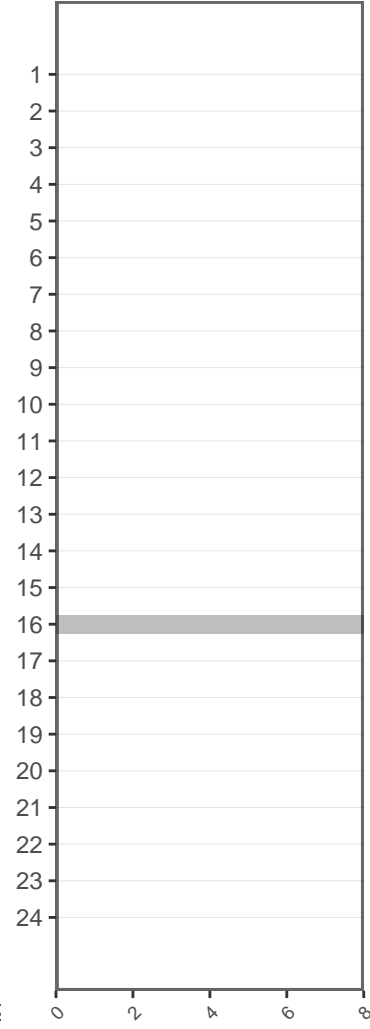
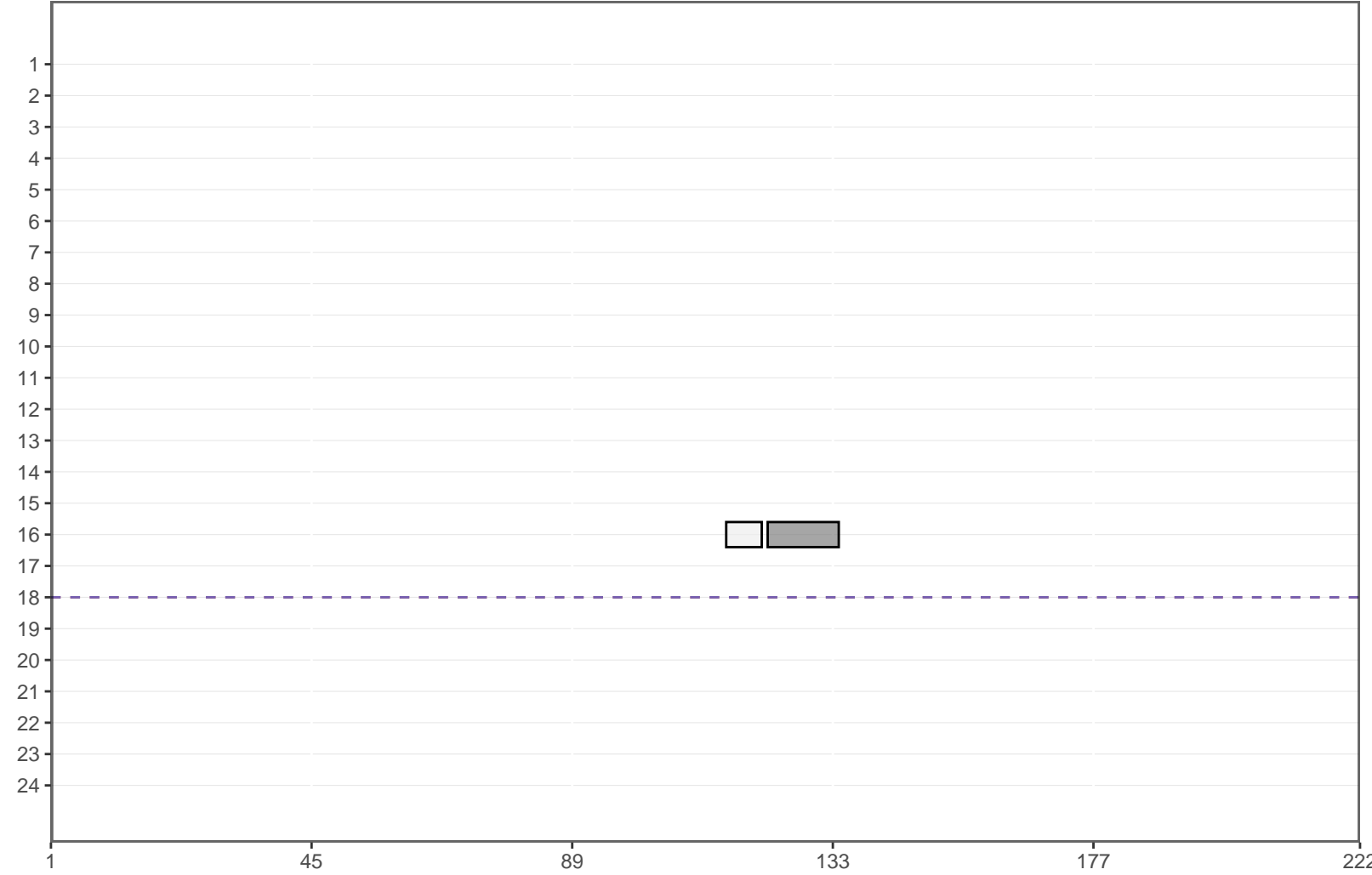
MW indication



Molecular weight



Gel Slice

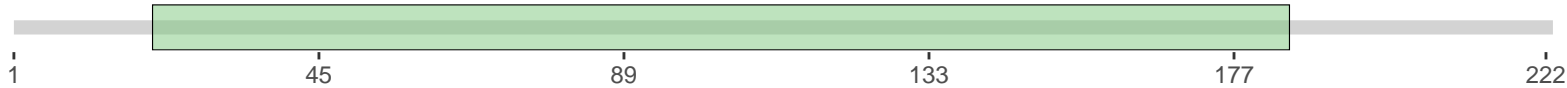


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

AAARTYGHLSKSAEVMKLVNLMKPEVAMTMOEFSKEMTKAGVMEEMVNDVDSALDSEDEDEEEEDVKVLTAAAGETTLPEAVRKKLKPQWAVEDAEGADEEEDLEELRRLAKVRD

NbL07g00690.1 serine_carboxypeptidase-like [MW - SP = 53.94 kDa]

No. of times detected



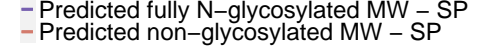
log(intensity)



Values from



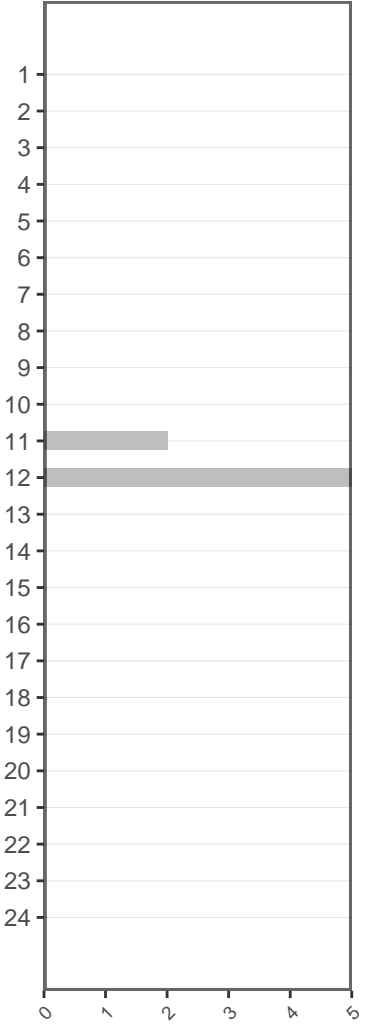
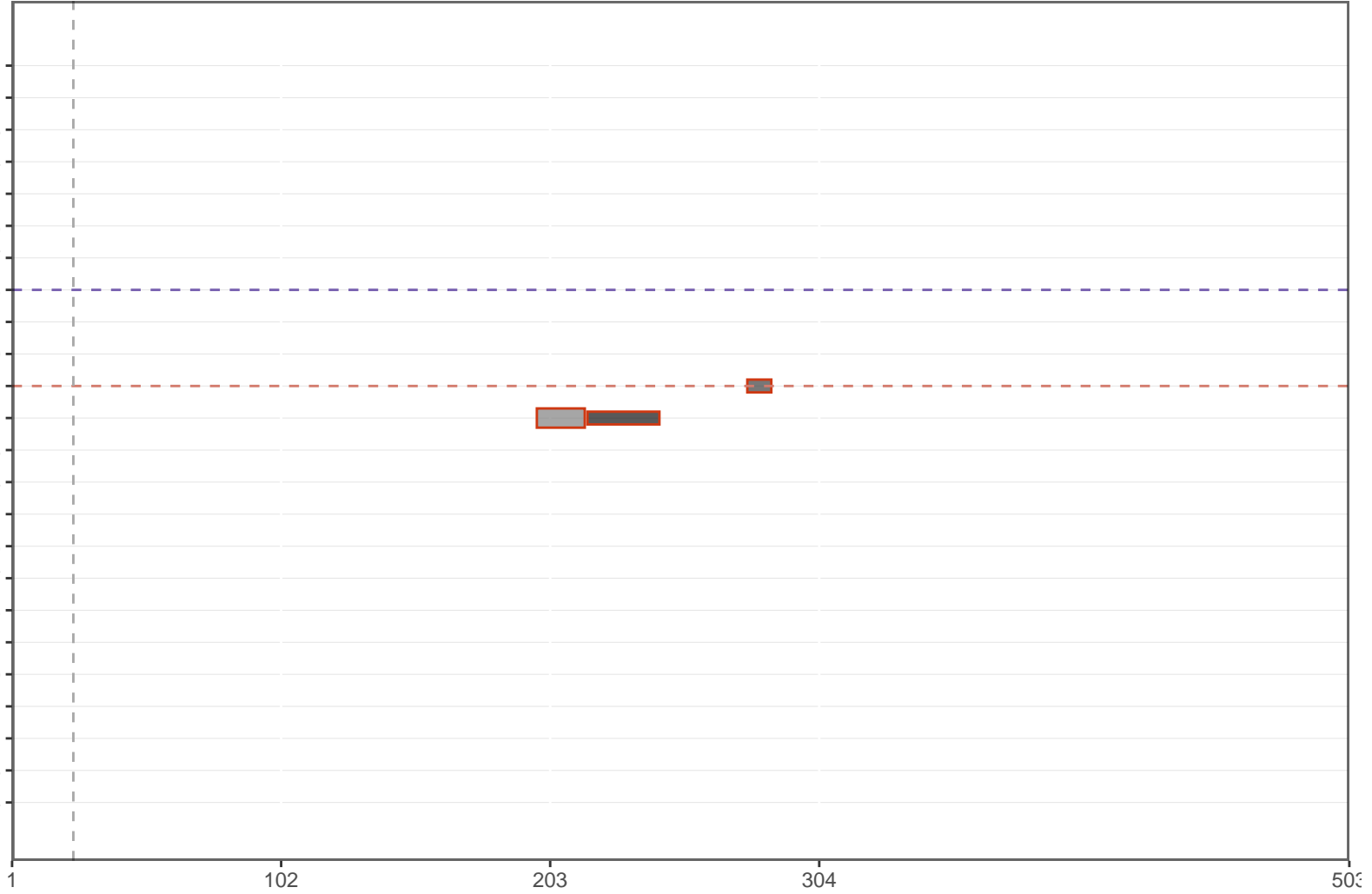
MW indication



Molecular weight

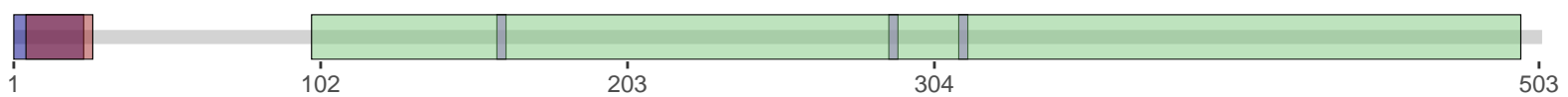


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

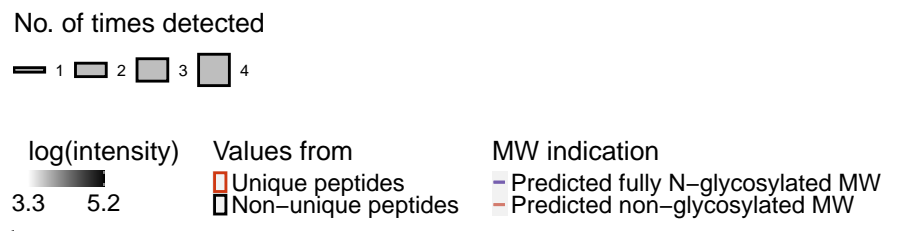
Pfam Description



Protein sequence:

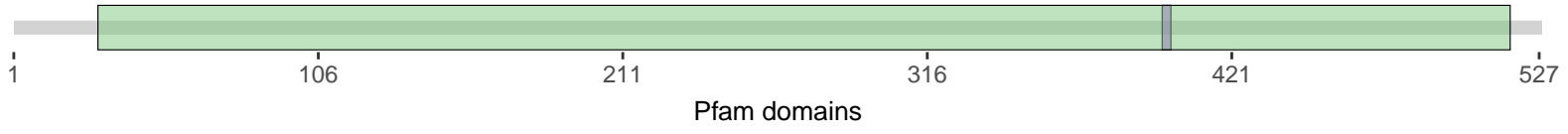
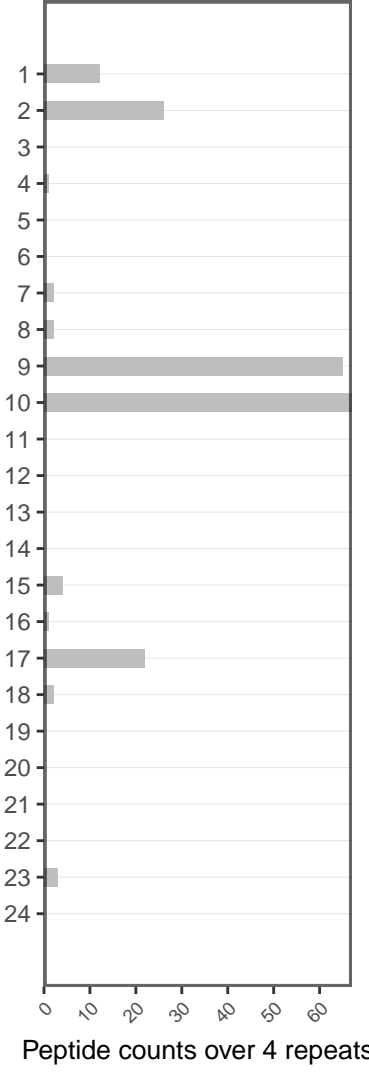
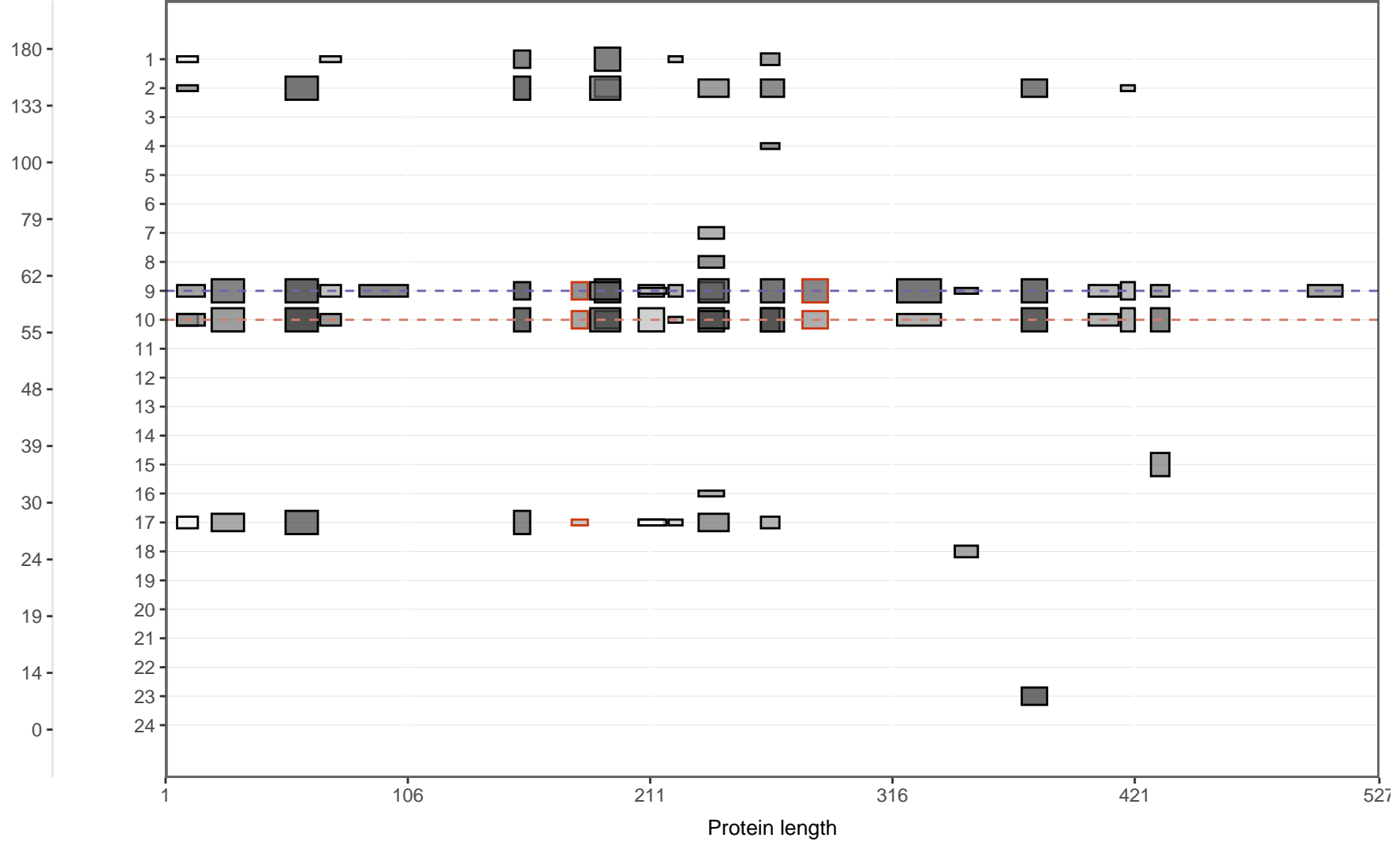
FASRVNCGNKXKEGINLKGFAHGSLTNPQIKYATDVALDMKLNQTDYDANKLYPQGGDEFTLGGNGSEDAQLDAFGRCTNIFSGIMDVSDKNYDIRKKEGNLCYDFSGMETYLNDDQVWRALGVPSNDFVSCGSETVYQAMETDMWIKNLEVDGIPSLLEDGILLIYAGEYDLICNGLNVDNWHAVEVSGGNDFAVPSVSTVDGEEKGKGNKGLPLFLKVDHAGHAFVPMDDQPKAALEMIGRWITQGLKLS

NbL07g00660.1 T-complex_protein_1_subunit_beta [MW = 57.01 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF00118 TCP-1/cpn60 chaperonin family

Protein sequence:

VRVDSMAKVALDELAEEKMKERVKVSHGNGVFNRLGLVNFPEELFDAGILAEHADFQGIERLGLVTGGGEASTFDNPESEVILGHCKLIEIMIGEDKLIHFSQVEMGGACTVLRGASPHVLDSEAERLHDGLVLSQTVNDRVLLGGGWPEMMAKAWDELAKKTPQKRHAEAFTRALLAIPTTADNAGLDSAEIAGLRAEHHKEESNAGIDVSGSVDMAELGISESFKVQVALLSATEAAEMLRVDIEITDAPRRREGM

NbL07g00650.1 alpha-L-fucosidase_1 [MW - SP = 55.91 kDa]

No. of times detected



log(intensity)



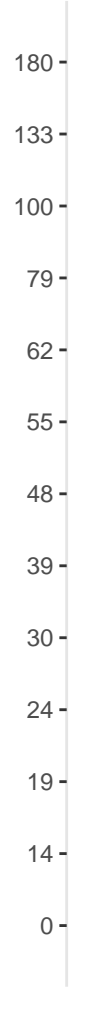
Values from



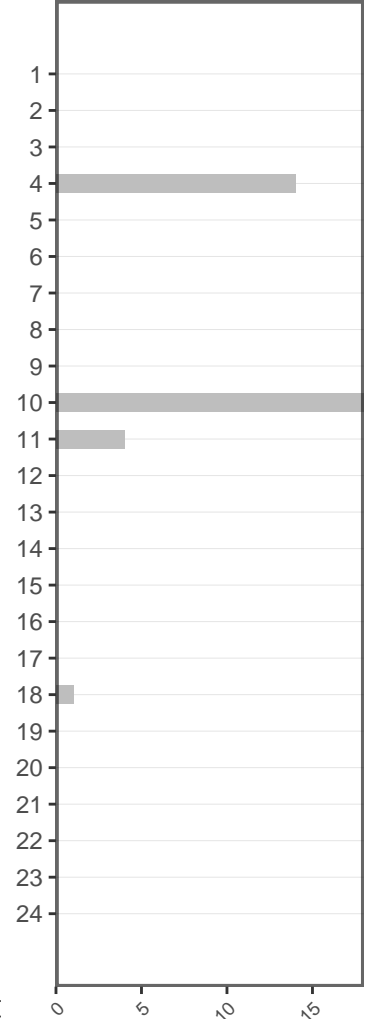
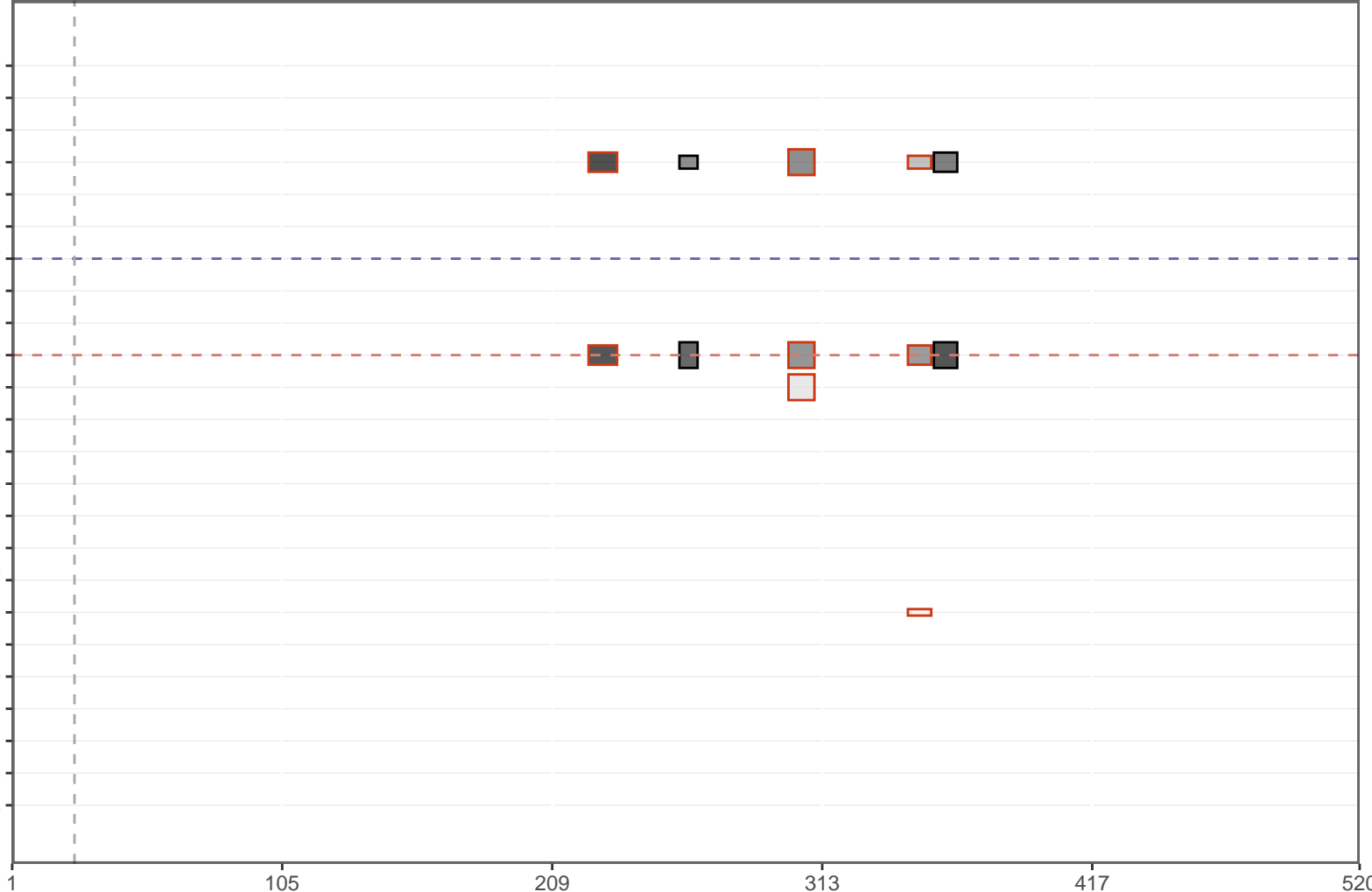
MW indication



Molecular weight

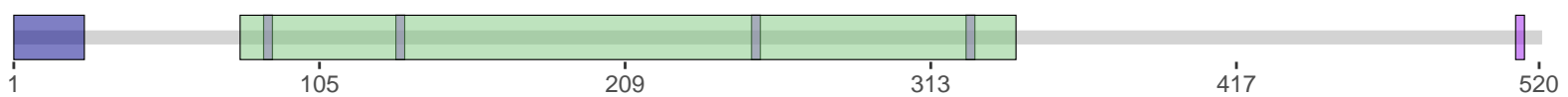


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CWLSLYNCSAVWIGGDNDFRYSRDGDPFGHDVWPAECGVSRPQWFWHPSEKPKSALTLLDNYKYSVSRNGLLLNVPNSGSLGIDEDLVKKEFSELRDSFISHNAKLSALLSASTRGGSKNSGFGPNIEEGLVTVWAPDEGSDWELVFEQGVAFNVLLELGEPIQMGRIEFLDLDLNDNGKWHQWVSGTTGYRRLVFFPTVNSHLRLVLDKSRVCPUSHLGYMDSVEVSRHVSQTRTKSKFINLVFRRTAYNRSGVSI

NbL07g00630.1 lactoylglutathione_lyase [MW = 26.03 kDa]

No. of times detected



log(intensity)



Values from



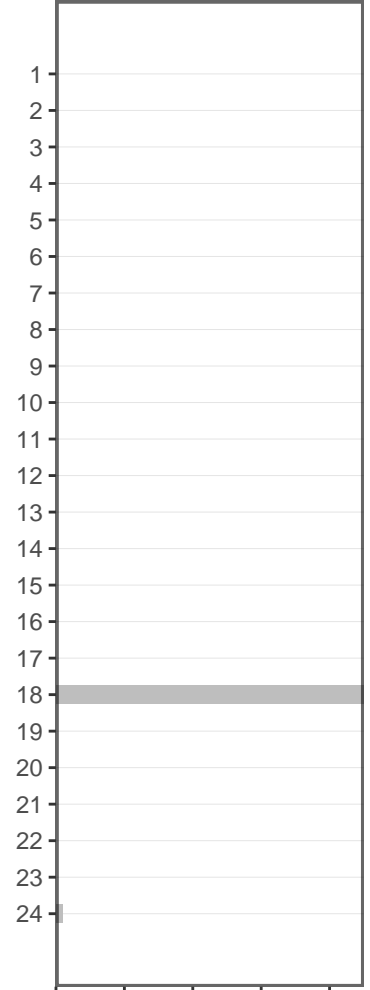
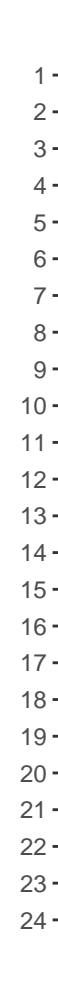
MW indication



Molecular weight



Gel Slice

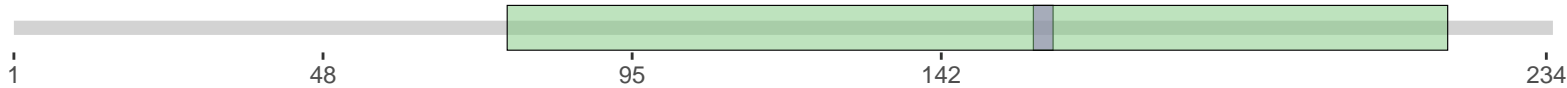


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

DFPEMKFSLYFMGVEDTSSAPSDAERTAWTFSGKATLELTHNWGTESDPNFTGYHNGNSEPRGFQHGIVTVDDVYKAGERFEQLGVFVKKPFQDGKMKGIAPVFKDPDGYWEIFDTKTIKEVAGAAI

NbL07g00510.1 superoxide_dismutase_[Cu-Zn]_chloroplastic [MW = 22.58 kDa]

No. of times detected



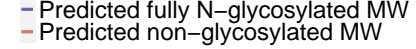
log(intensity)



Values from



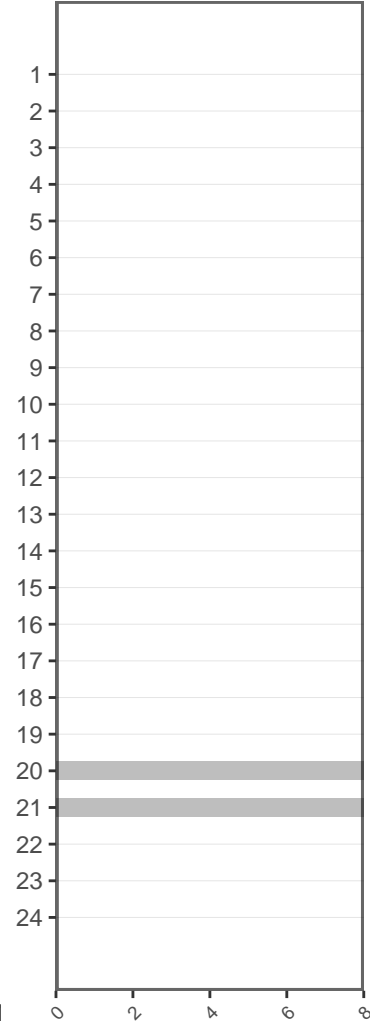
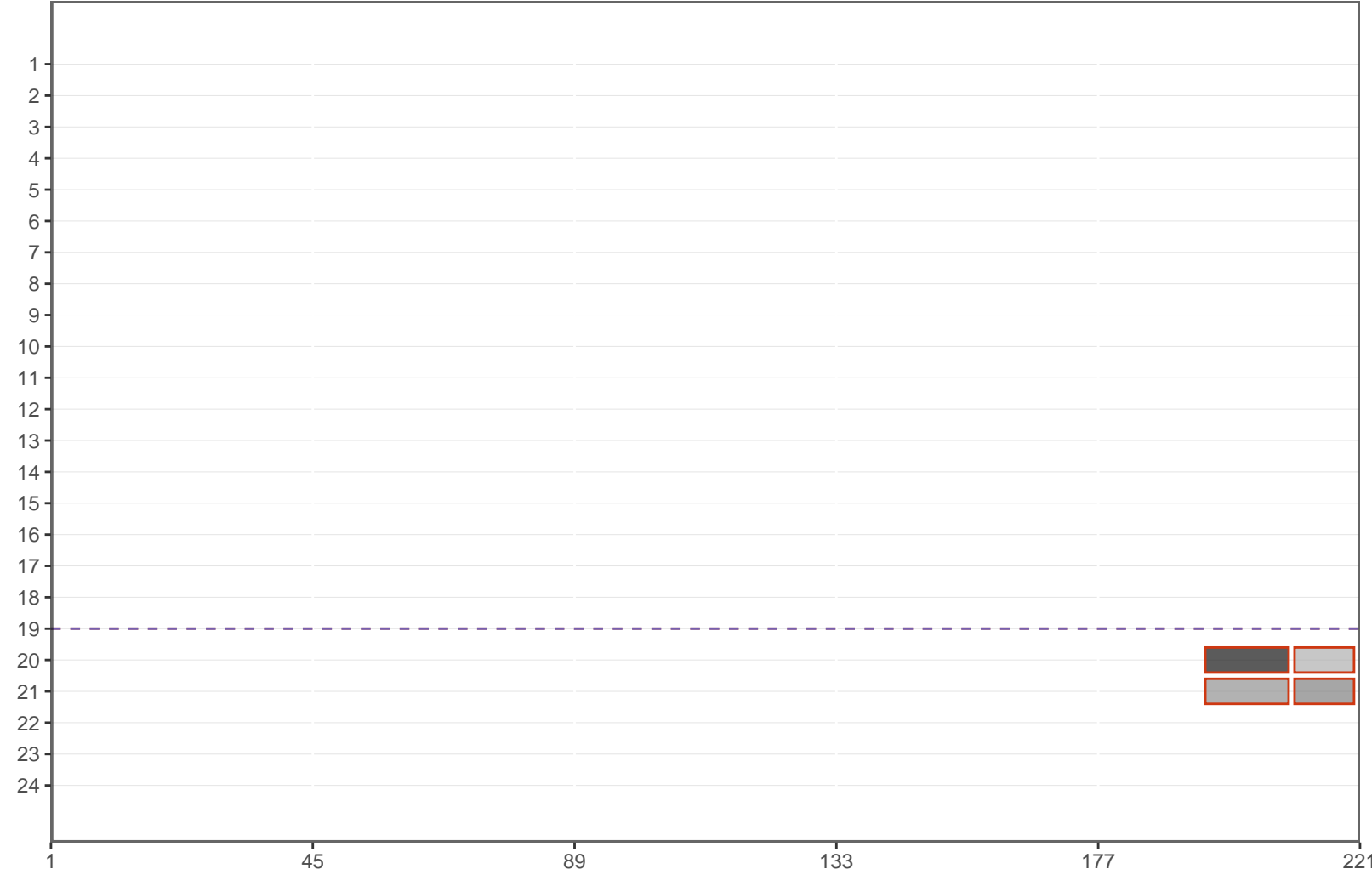
MW indication



Molecular weight



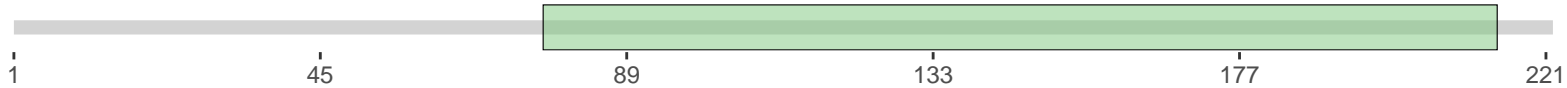
Gel Slice



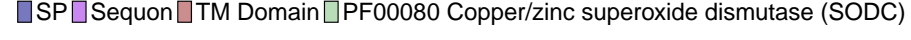
Protein length



Pfam domains



Pfam Description



Protein sequence:

KVIRITGLTGLHGFHLHEFGDFTNGMSTGPHFNPDGKTHGAPEDERIRHAGDLGNVANADGVAEATIDNIGNPLTGFNVIKRALVHLEEDDLKGGHSELGTTGAGGRLAGGVLGITPV

NbL07g00490.1 50S_ribosomal_protein_L9_chloroplastic-like [MW = 19.77 kDa]

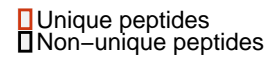
No. of times detected



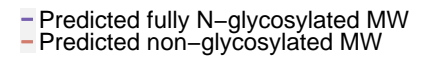
log(intensity)



Values from



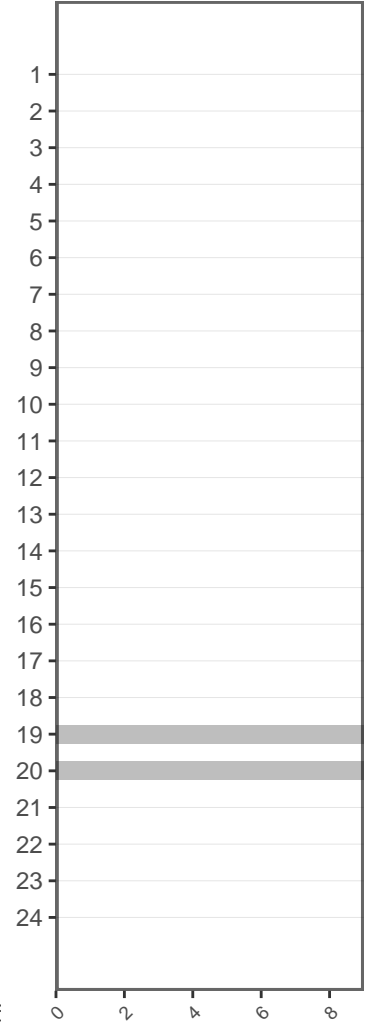
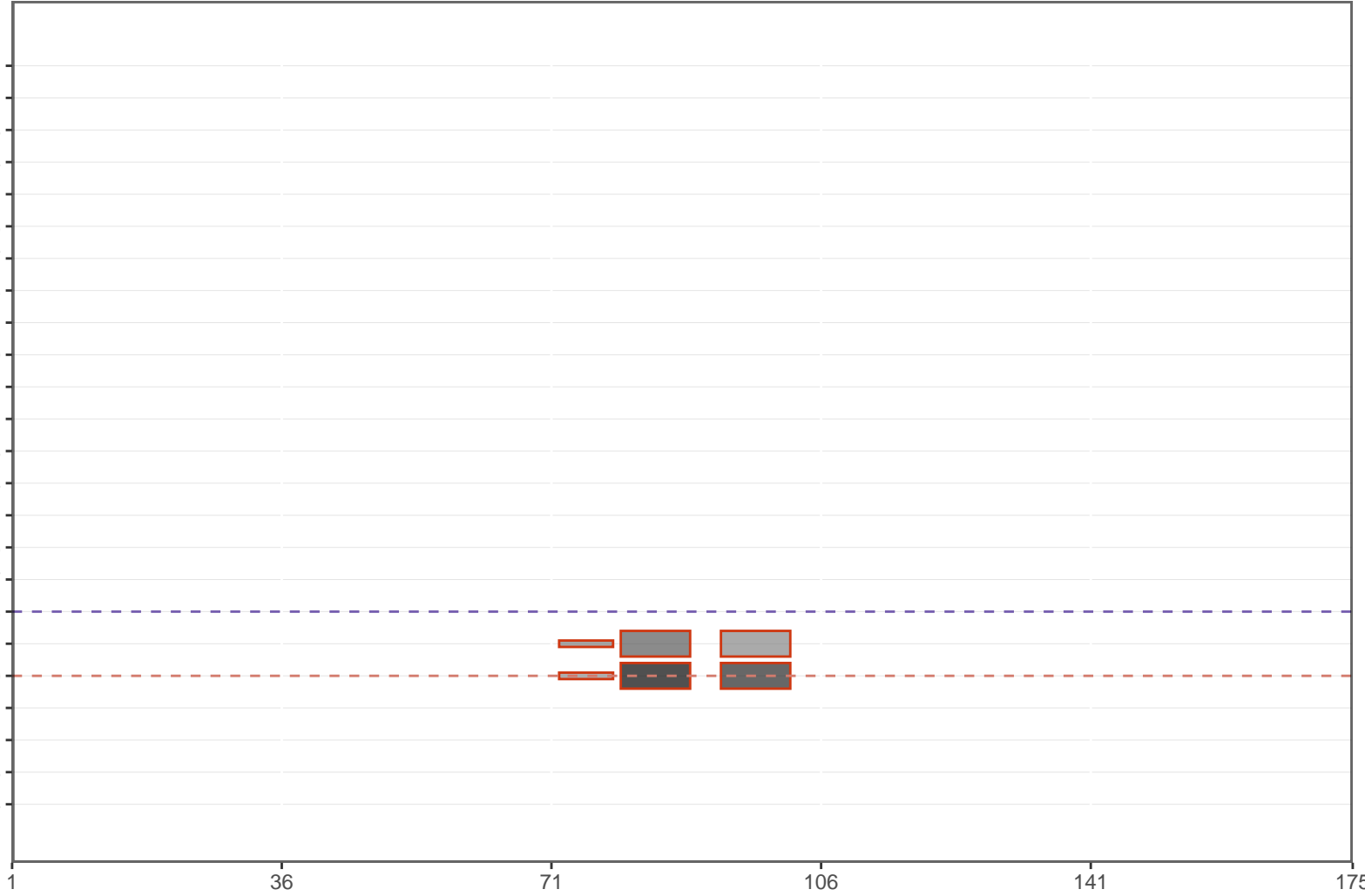
MW indication



Molecular weight

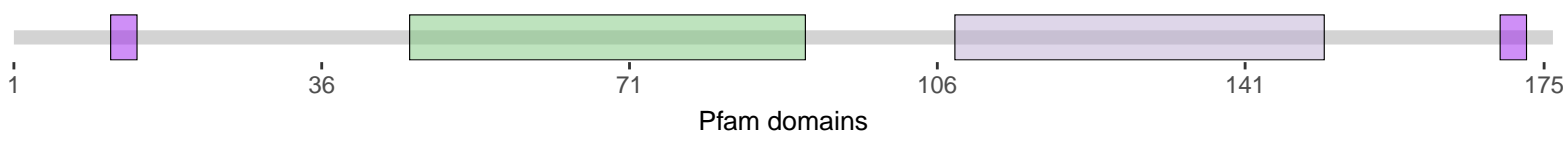


Gel Slice



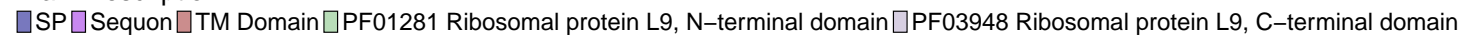
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PMGKIQIVPTLTKEMKEDERIEAEKGRVKEEALGLARFETVGAFKVRRKGGKQKIFGSGVTAQDLVDIKHBYRGRWTRKLCGLRFEKLENMLSL

NbL07g00400.1 serine_carboxypeptidase-like_51 [MW - SP = 47.24 kDa]

No. of times detected



log(intensity)



Values from



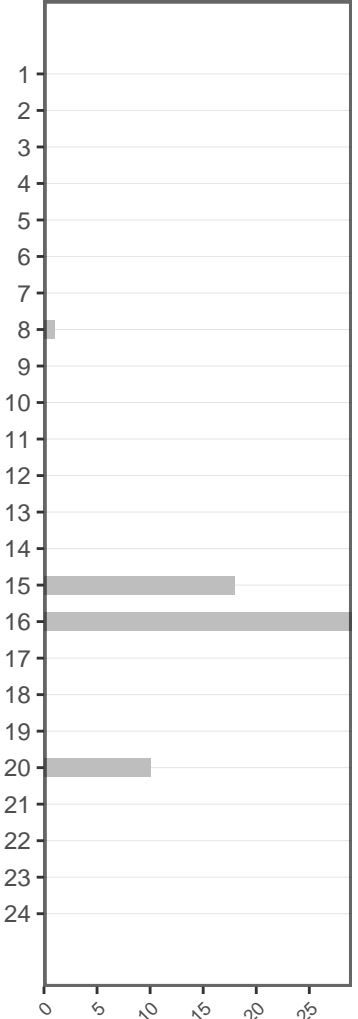
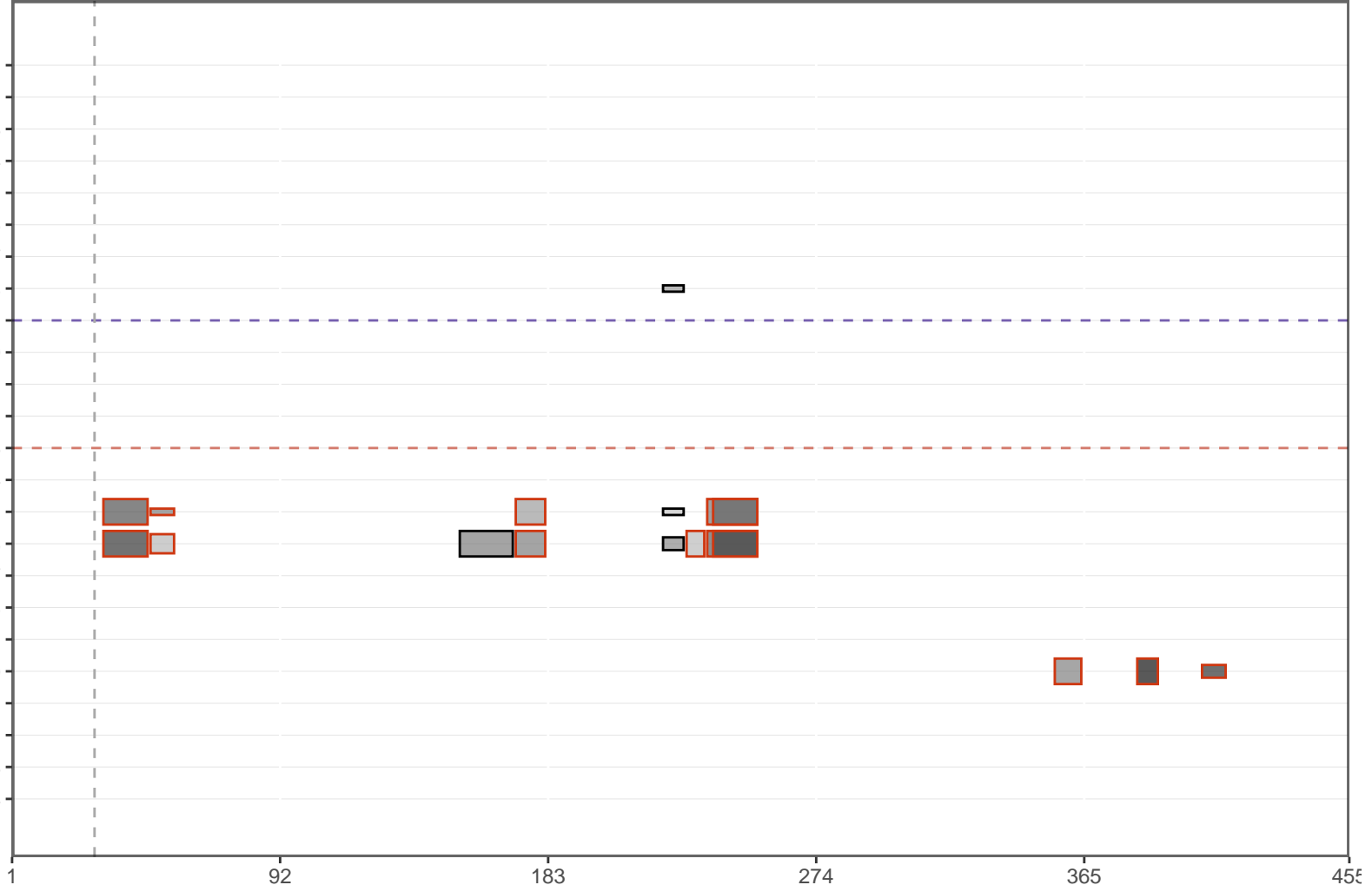
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

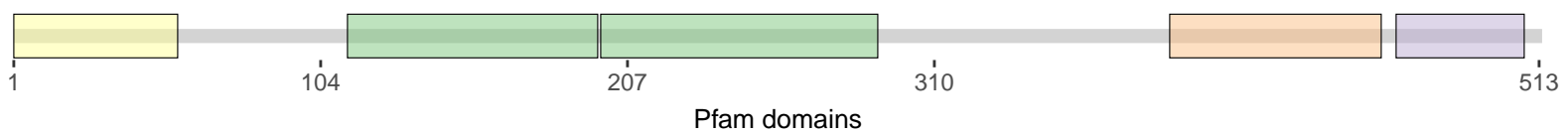
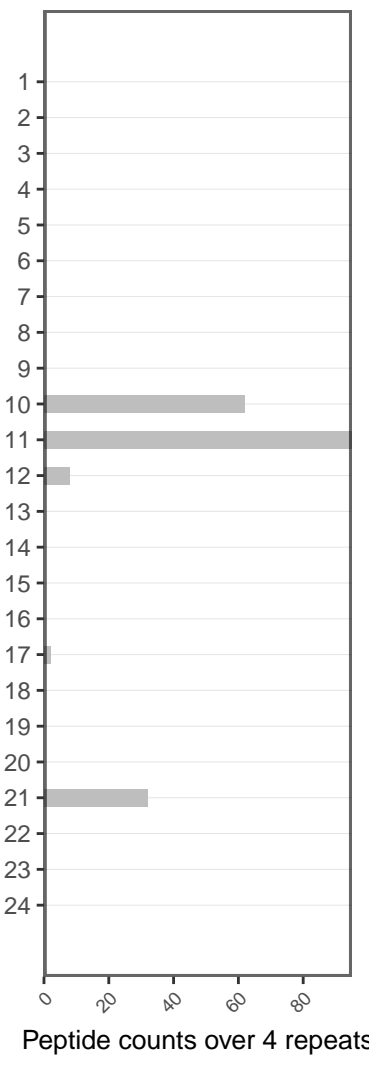
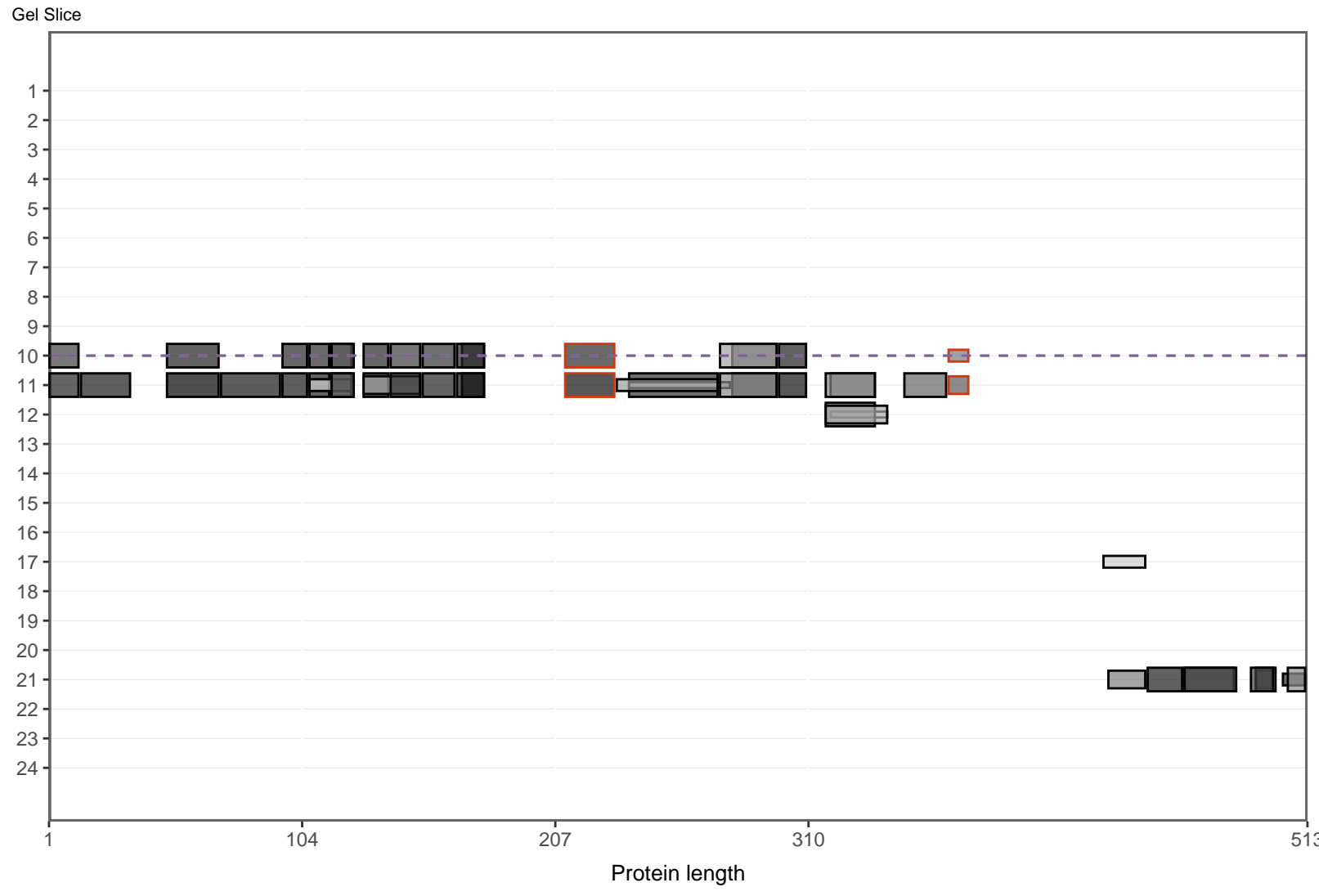
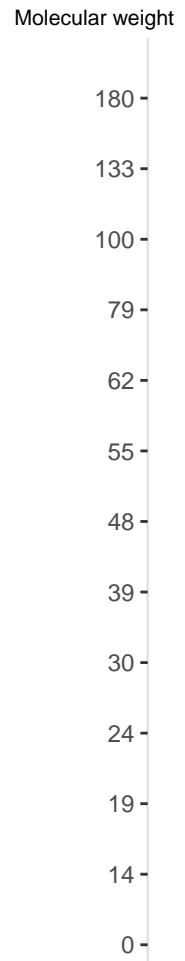
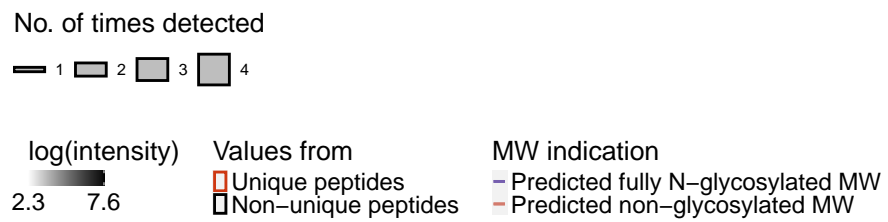
Pfam Description



Protein sequence:

.LKDYSRIDGYNGLQKNSVALKKGGKGGVYEAATNNSWRDLNENISDNNSVDFYNFMLDGGMDPLSLTASELGGGISMKRYSRVYLGSSRITPQSDVLDLDTLMNGAVKKKLIKIPQNVQWGGGSDSDYFNALFGDFMKPRIDEVELLAKGVNVTVYNGQLDLGKATGTEAWVEKIKWEGLEKTLFMDRBAHYGGGDKTKAFTKRYKNIHFVYVWLGAGHFVVDGQPCVALDMVAISRTK

NbL07g00230.1 ATP_synthase_subunit_beta_chloroplastic-like [MW = 55.16 kDa]



Pfam Description

SP TM Domain PF00401 ATP synthase, Delta/Epsilon chain, long alpha-helix domain PF02874 ATP synthase alpha/beta family, beta-barrel domain

Sequon PF00006 ATP synthase alpha/beta family, nucleotide-binding domain PF02823 ATP synthase, Delta/Epsilon chain, beta-sandwich domain

Protein sequence:

ITSIQAVYYPADDLTDPAKNTFFAHLDAITVLSRGLAAGKGYWVDPDLDSTMLGPRVIEEHEVETAGRVKQTLRKYKELQDIALGLDELSEEDRLWARKIERFLGSPFFVVEVFTGSPKYVGLAETRGQLLSEGLDLPQAFVLYVEVEIETNSGGIGLPHAPATAVDGLIRRLNDQWLTMLMGGFARIGNNEIFVUNDAEKGSDIDPQEAQDTLEAEANWKKAEGRQKIEANLARRARTRVEANPIS

NbL07g00220.1 chitinase-3-like_protein_1 [MW - SP = 39.81 kDa]

No. of times detected



log(intensity)



Values from



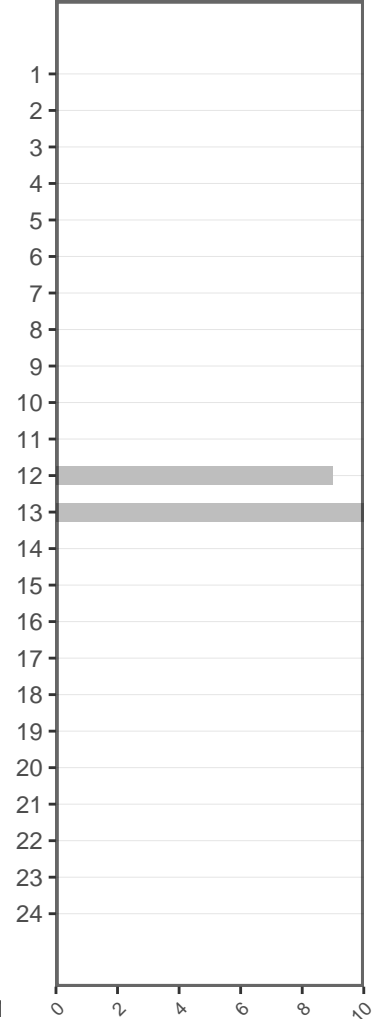
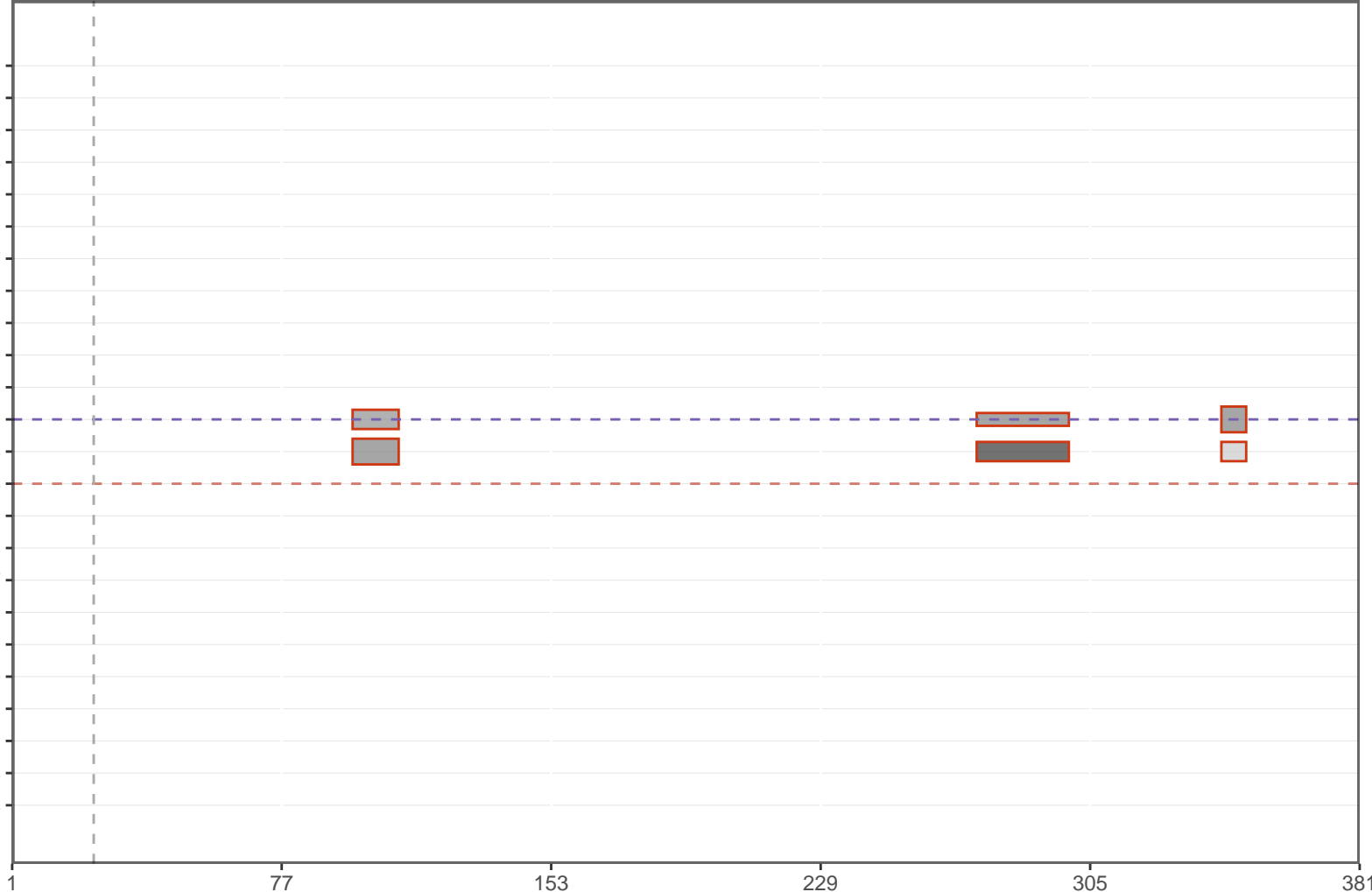
MW indication



Molecular weight

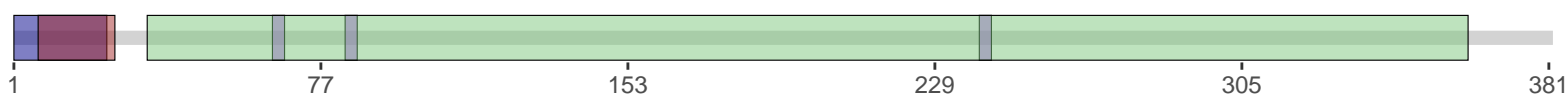


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PLLITAAVYFSVDFLSDEDFRYPVPSNKLNWLNLMCYVYRGSWDTSATGAPALFDTKNSISTSYGVRSWIKAGARSKLIMGLPLVGRTWLKDPPNVHGIGAPGIGVPGDEGTMTRYREVEKFNENNAKVVFDIATVSTYSVAGNSHWIGYDSSRSWMIKIGYAGRLRGYFFWVAGDLWISRTGPTPTAGAPIL

NbL06g21090.1 alcohol_dehydrogenase-like [MW = 41.25 kDa]

No. of times detected



log(intensity)



Values from



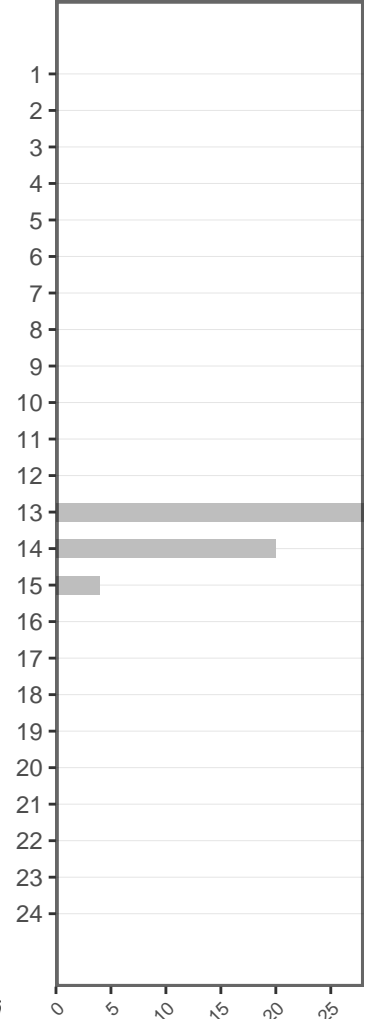
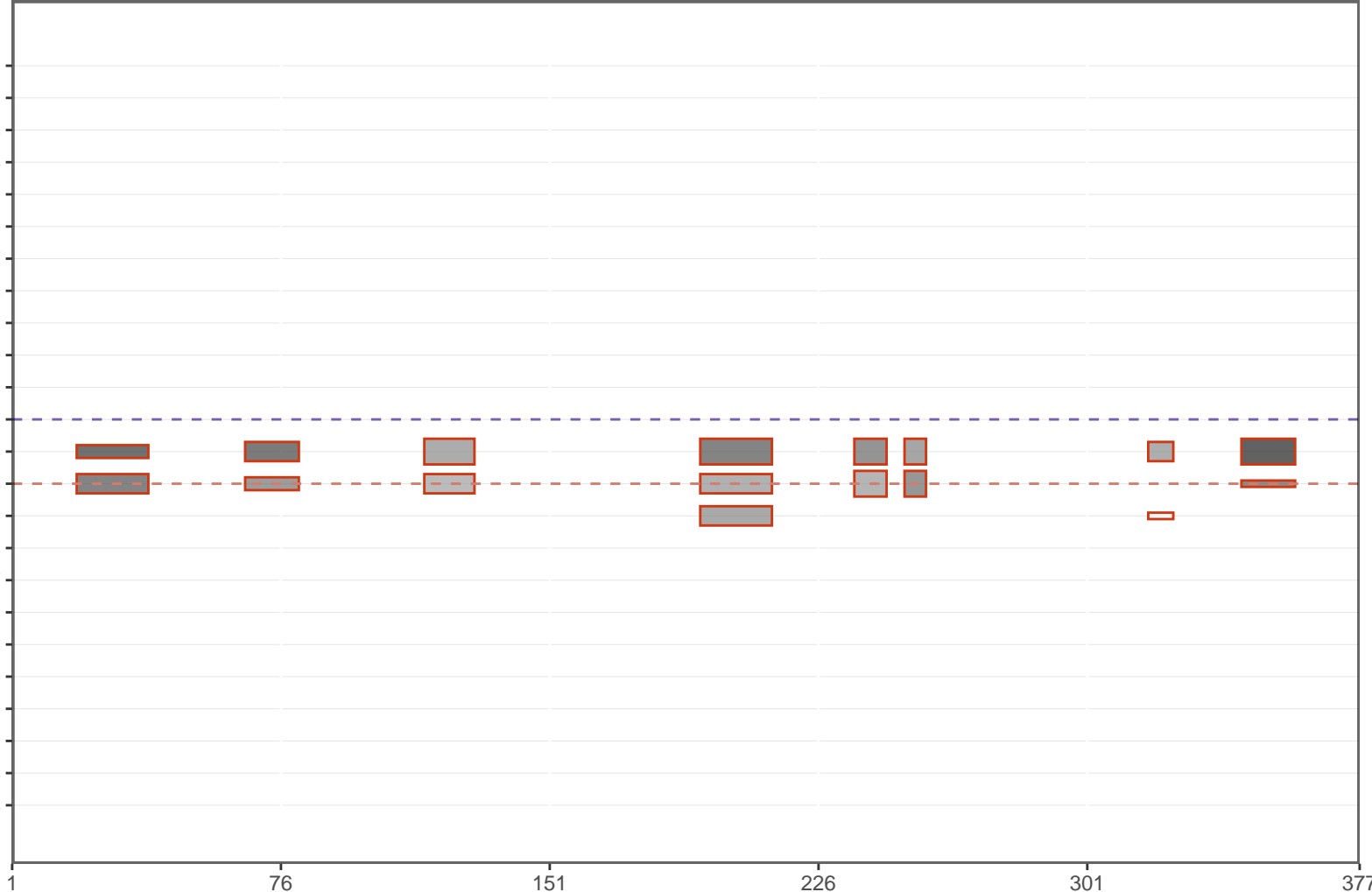
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CCAAFTTGGATFKDANIEKSGSTFWLGLGGVGLGVVEGAKGKEAAKIGIDHMKSEKANKFVTFDFINIKISEKISSELVKEATGGGLGVDFEFECTNVPHLMINNETOISTRMGVGTULLLAGLELDWQMSYVPLMLGRTLKGGISYGGIRTRTDLPSIFDKINKEIKLDELTHSEVSLNDVYKAFEYLYKEPNCVYVLYKIP

NbL06g21020.1 D-amino-acid_transaminase_chloroplastic-like [MW - SP = 44.73 kDa]

No. of times detected



log(intensity)



Values from



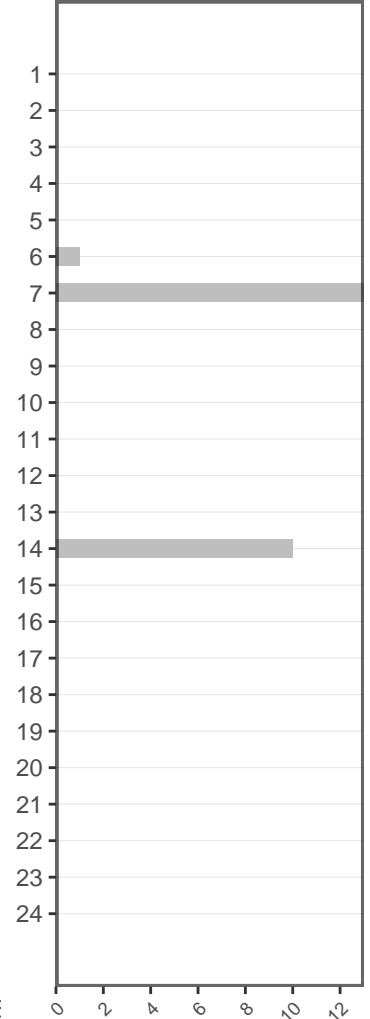
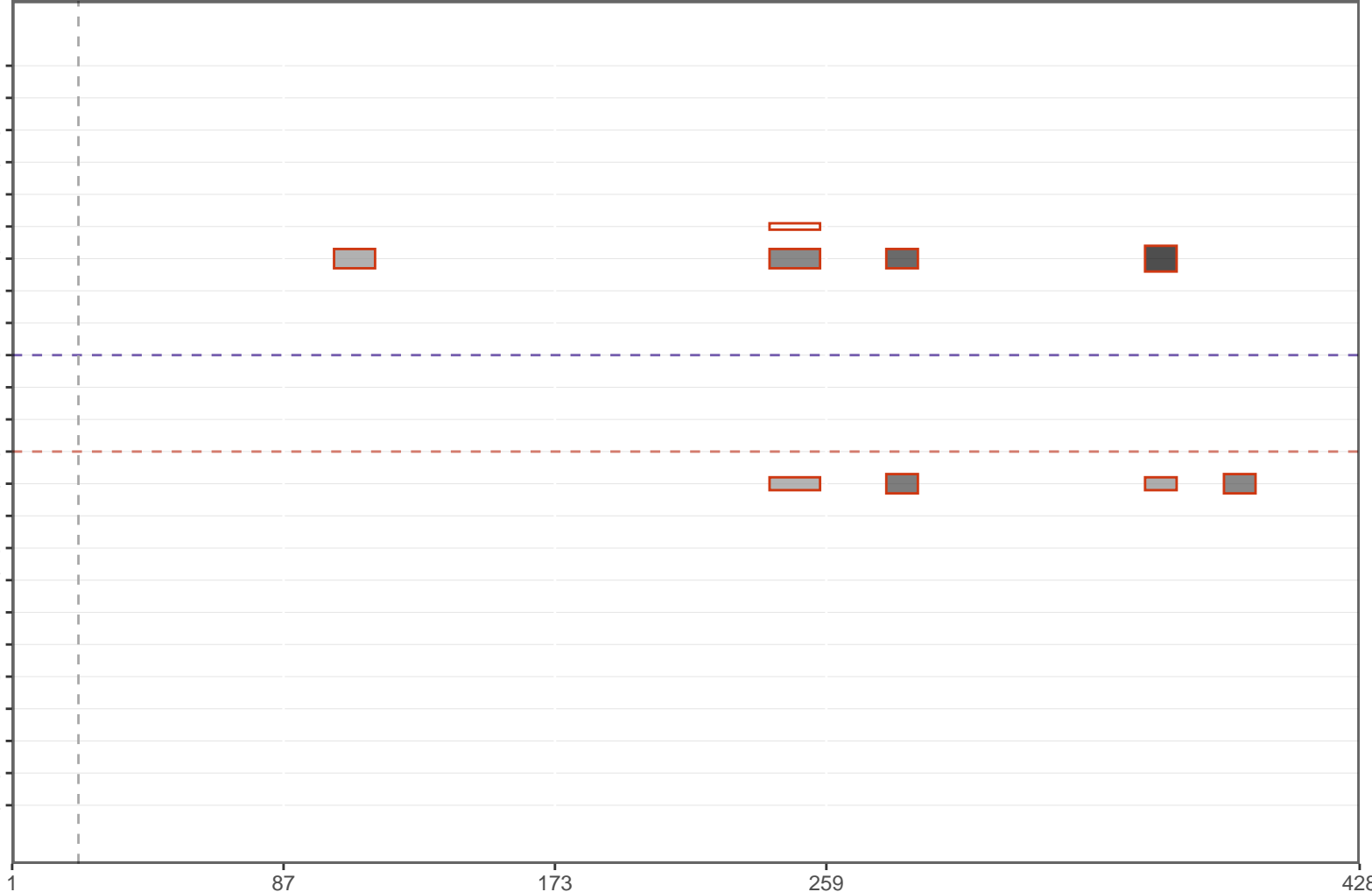
MW indication



Molecular weight



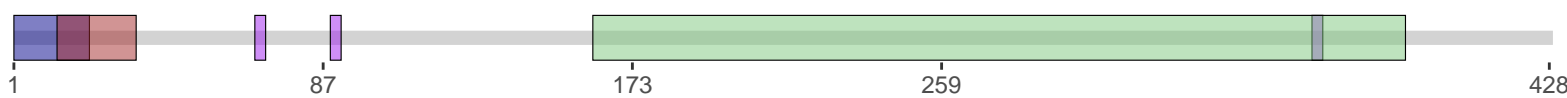
Gel Slice



Protein length

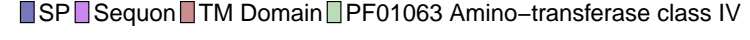


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RILRTYSVSDCRKSGELRYWLSAGPGDFQLSPGGPRAALYAVIGDGGPPDHRGRVVTSSIPKPPGFAMKESVNYLFPNALSKMEAEENDYAAWALDADGFAEGPNNMNFVYTKKELLMPFDKILSGGCTAKRVLVLAALVKEGKLRGVKIDNVVEDGKRADEMLLGGGLVLRVAVQWDEEIRDCREGPTQALLLLEDMKGGPAGVIRVFPVY

NbL06g20910.1 pectinesterase_31-like [MW = 35.58 kDa]

No. of times detected



log(intensity)



Values from



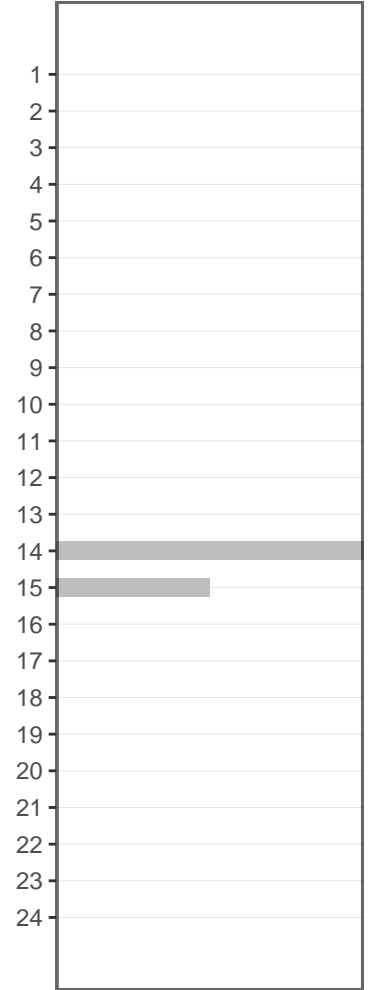
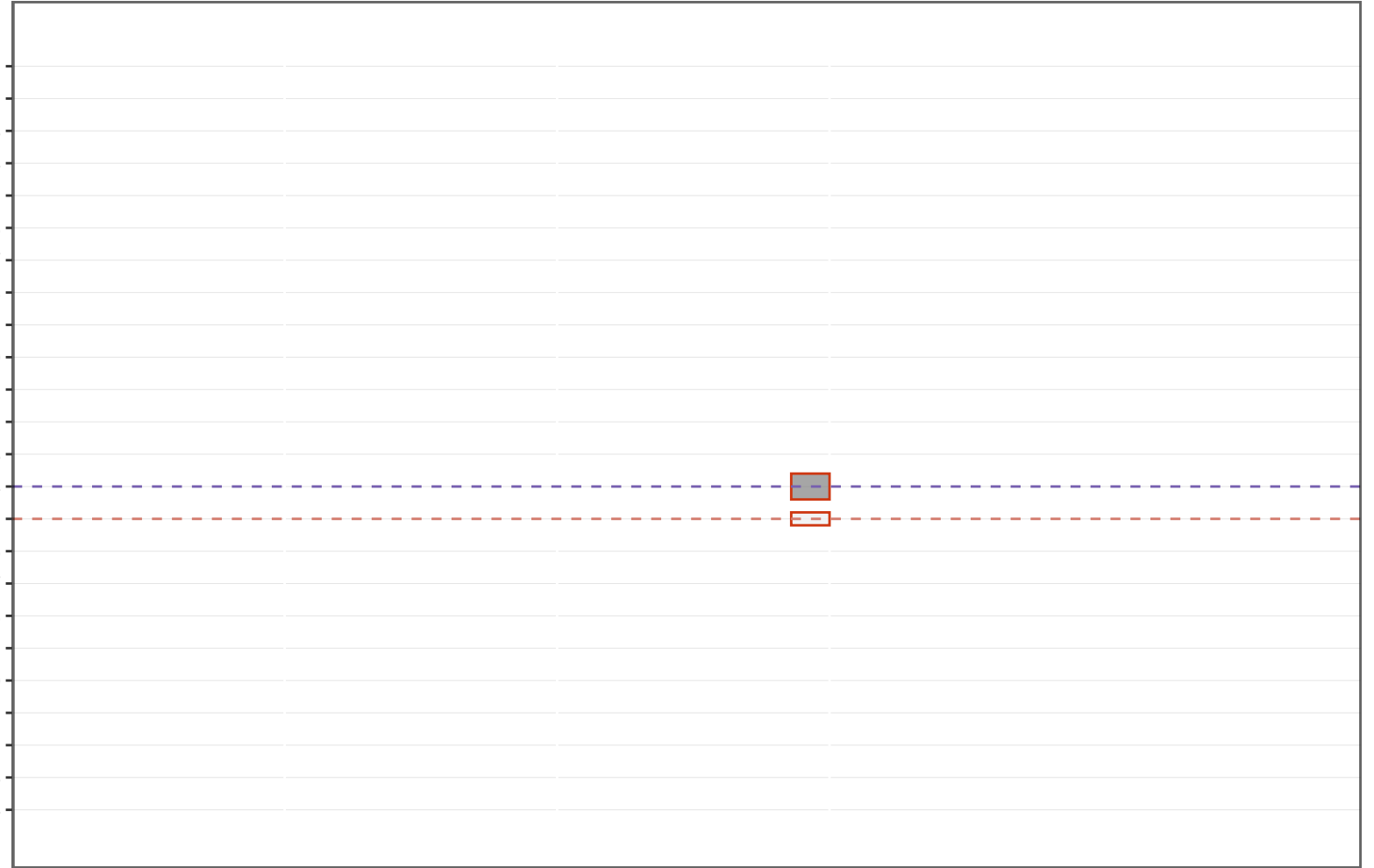
MW indication



Molecular weight



Gel Slice

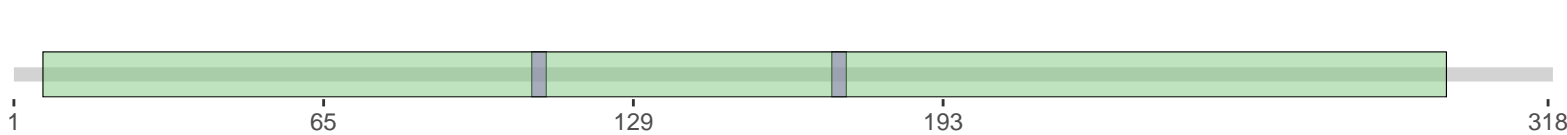


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IYGGKYLKDCYIEGSDVDFGNSALFEHGHKKSAGRTAGSRKSSQETTGYVFLRDVITGNGGSSVAHLGRPWGFGRRVVAVGHMDHCKHGDWNNWVKTENERTAGFYEVYRFGFGPGSGPSKRYTWARELMDDEAEQFLMHGFIDPDDGRPWLOGRMALRIPYSAY

NbL06g20870.1 clathrin_interactor_EPSIN_1-like [MW = 59.7 kDa]

No. of times detected



log(intensity)



Values from



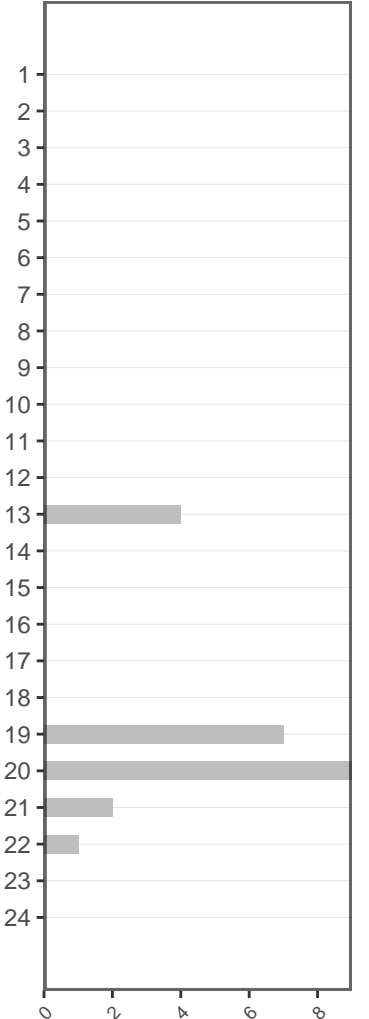
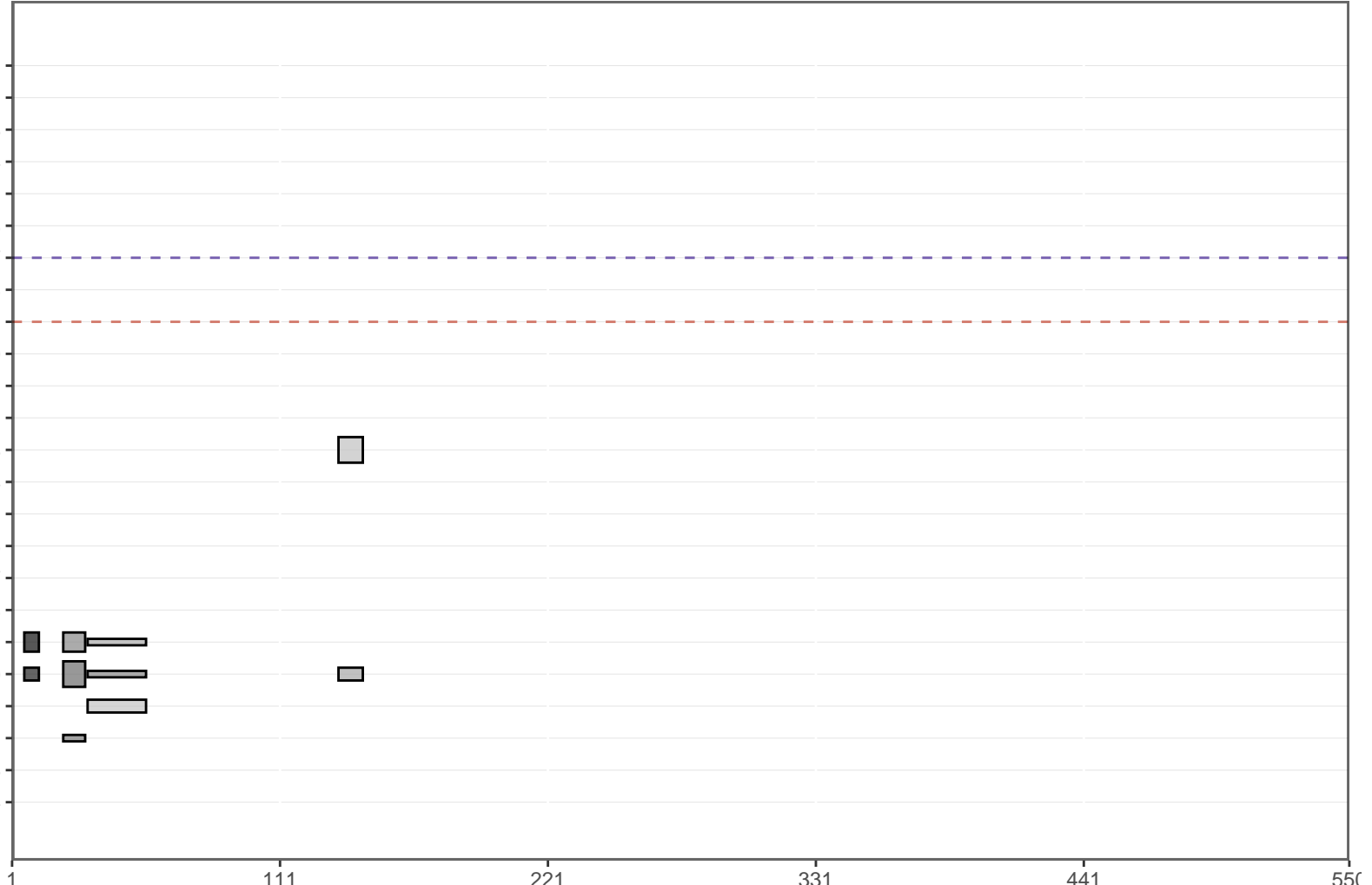
MW indication



Molecular weight



Gel Slice



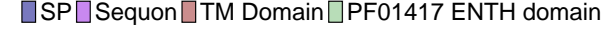
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

NPPHGAIVSSSKYEEEDFDPRGTSTKPKKGGQVDFLFGNLIQDLLVFTTPVADNNTVTSHPSEIDLFANFVSVKPKQSEINVDLFAQPKASSFAASSTIDFFSAPDPVVGSDRSGKSKKNTTVDPPFAVPLNTFDSDDFGKFNSHADPVSVASENANRGGNGEETPSKLDKSPVEANPAKPKKGFQVSGGHWADLSRGLDLNLSAFKKVNLADVGVGGLTGSSDQWKEKGPPTTEYMGRAMGGGTGLGGGGFTSTSGGGDDFFENHNYQFGSFOK

NbL06g20850.1 UPF0587_protein_C1orf123_homolog [MW = 18.51 kDa]

No. of times detected



log(intensity)



Values from



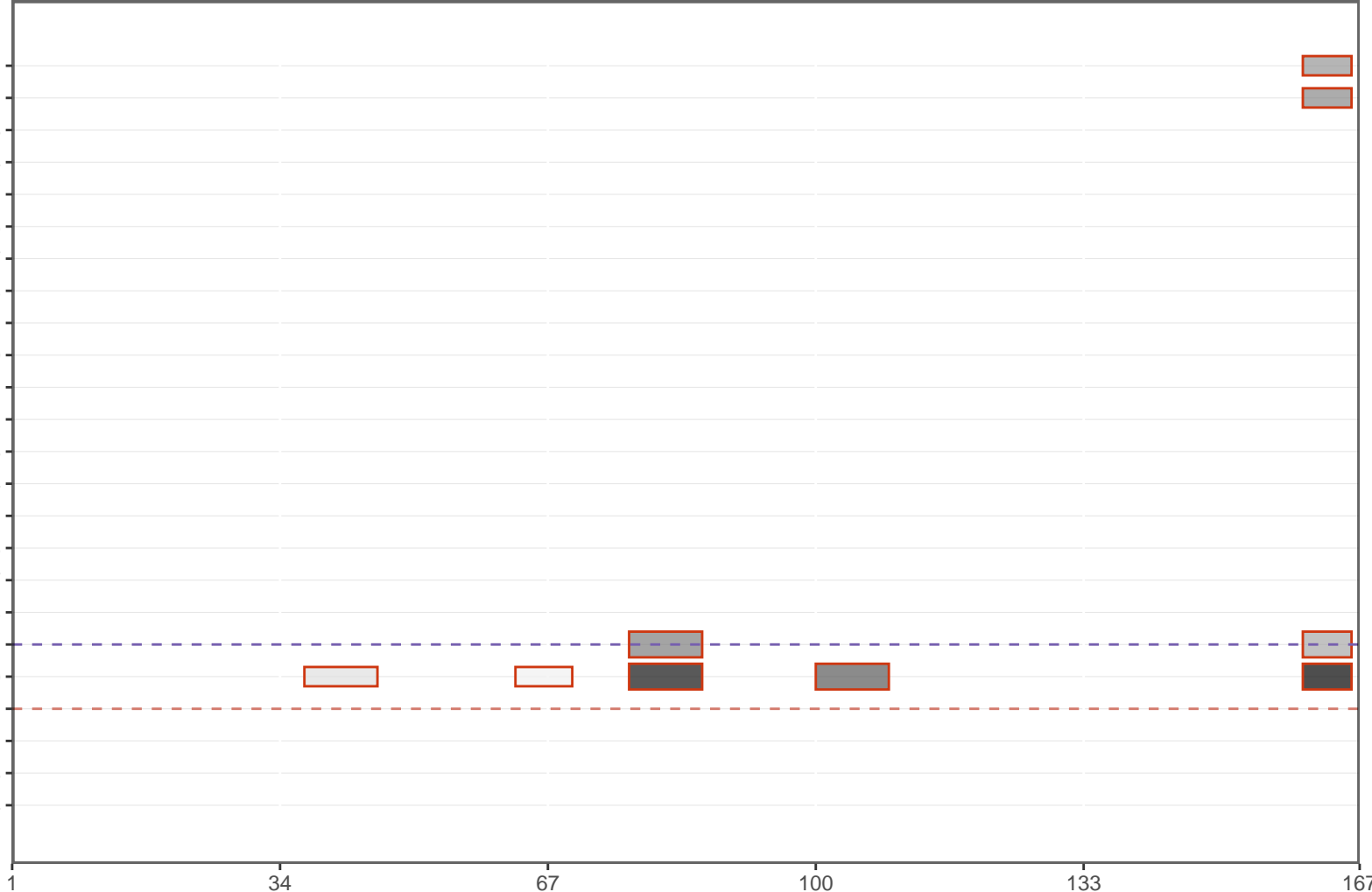
MW indication



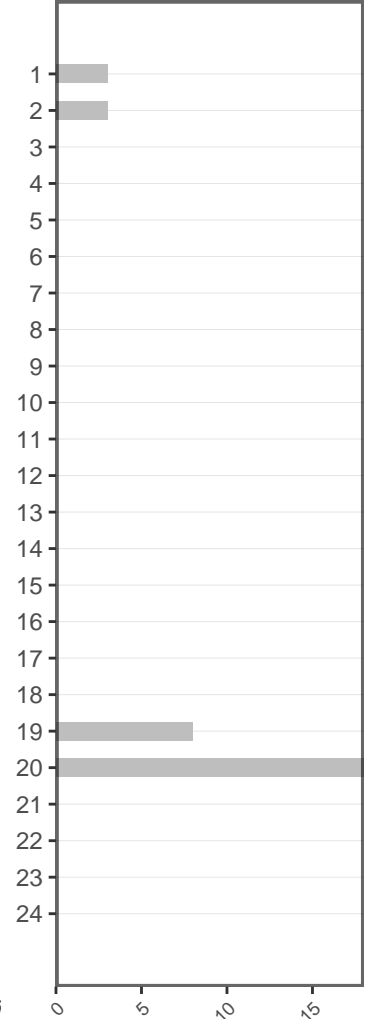
Molecular weight



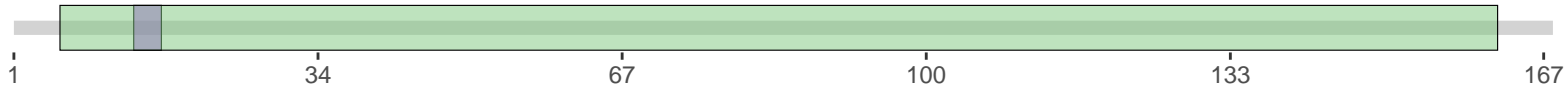
Gel Slice



Protein length

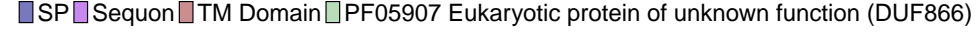


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KFCSRDGTVMITGRGRLTHGDGAGKYAPLMLFEGRGFEPLDFAFLGEWQAELEGTKFENYLSGDEFADYDEKGECPVMSINLRATFNVK

NbL06g20840.1 uncharacterized_LOC107809971 [MW = 35.11 kDa]

No. of times detected



log(intensity)



Values from



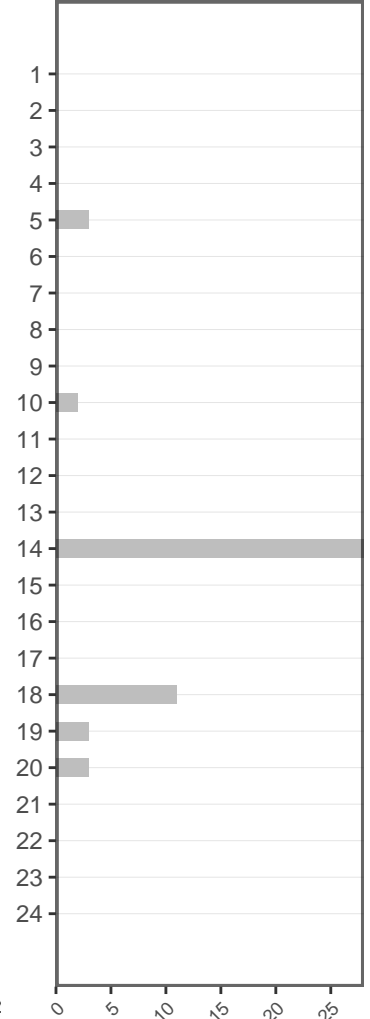
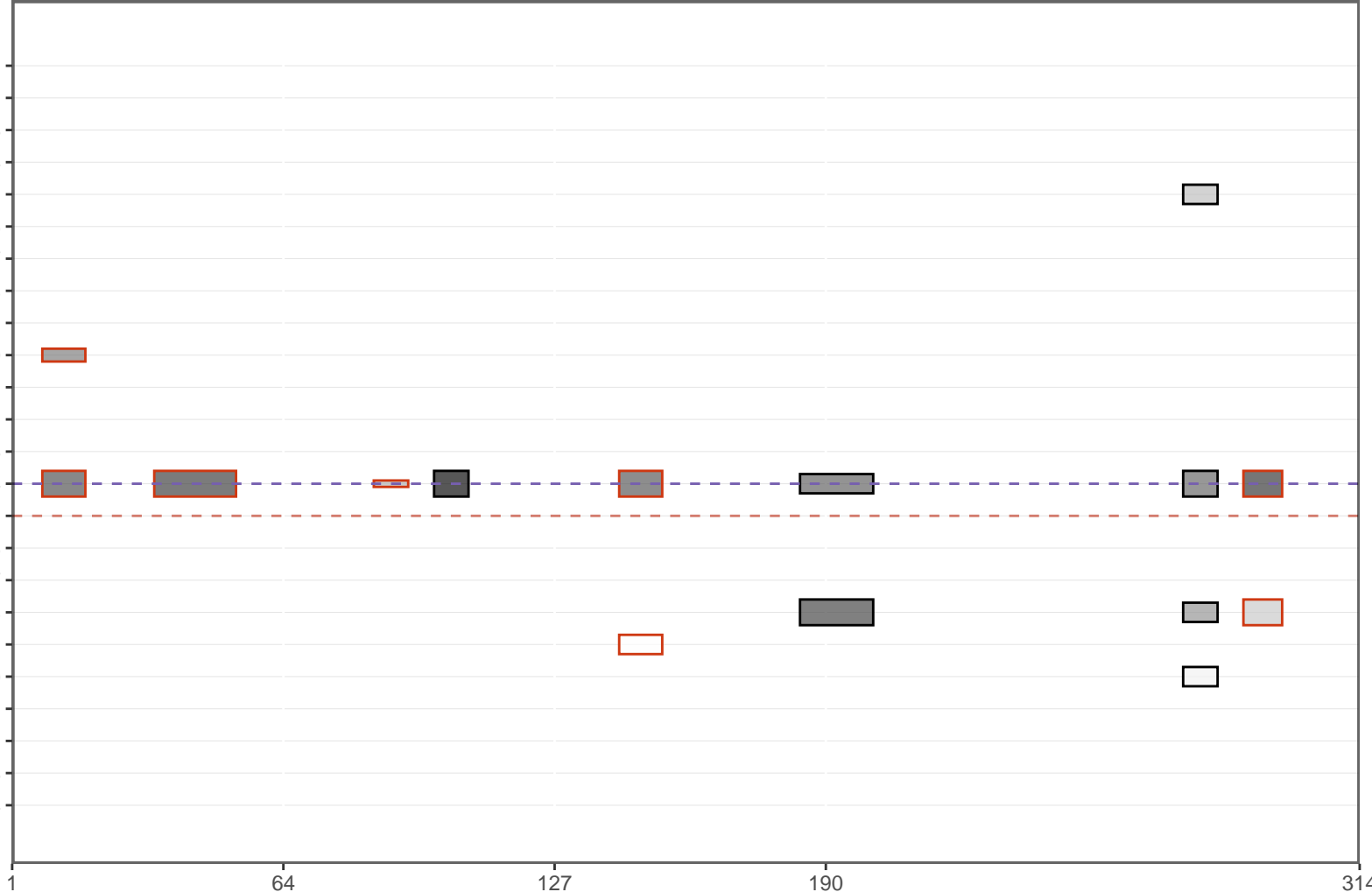
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



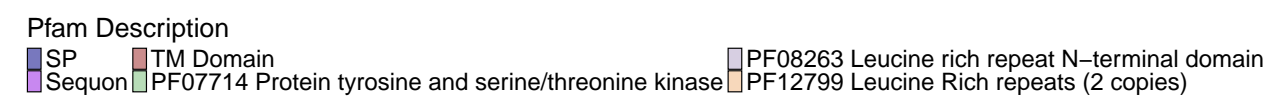
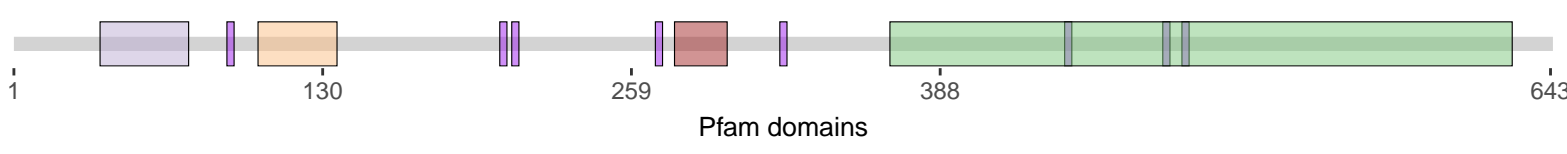
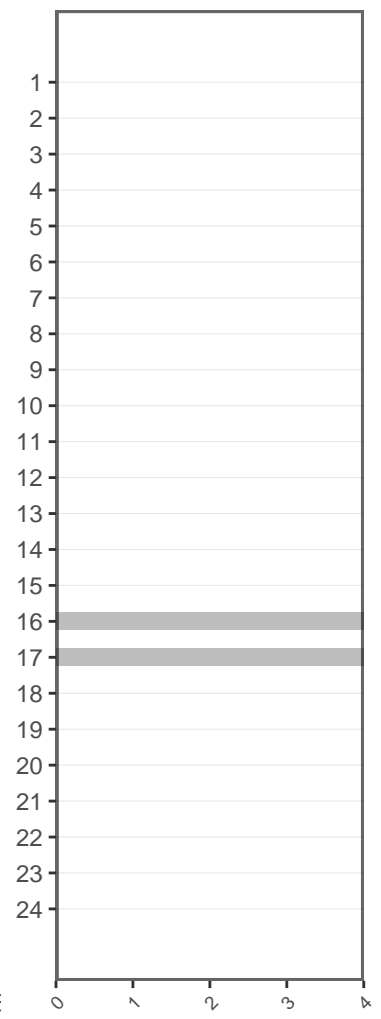
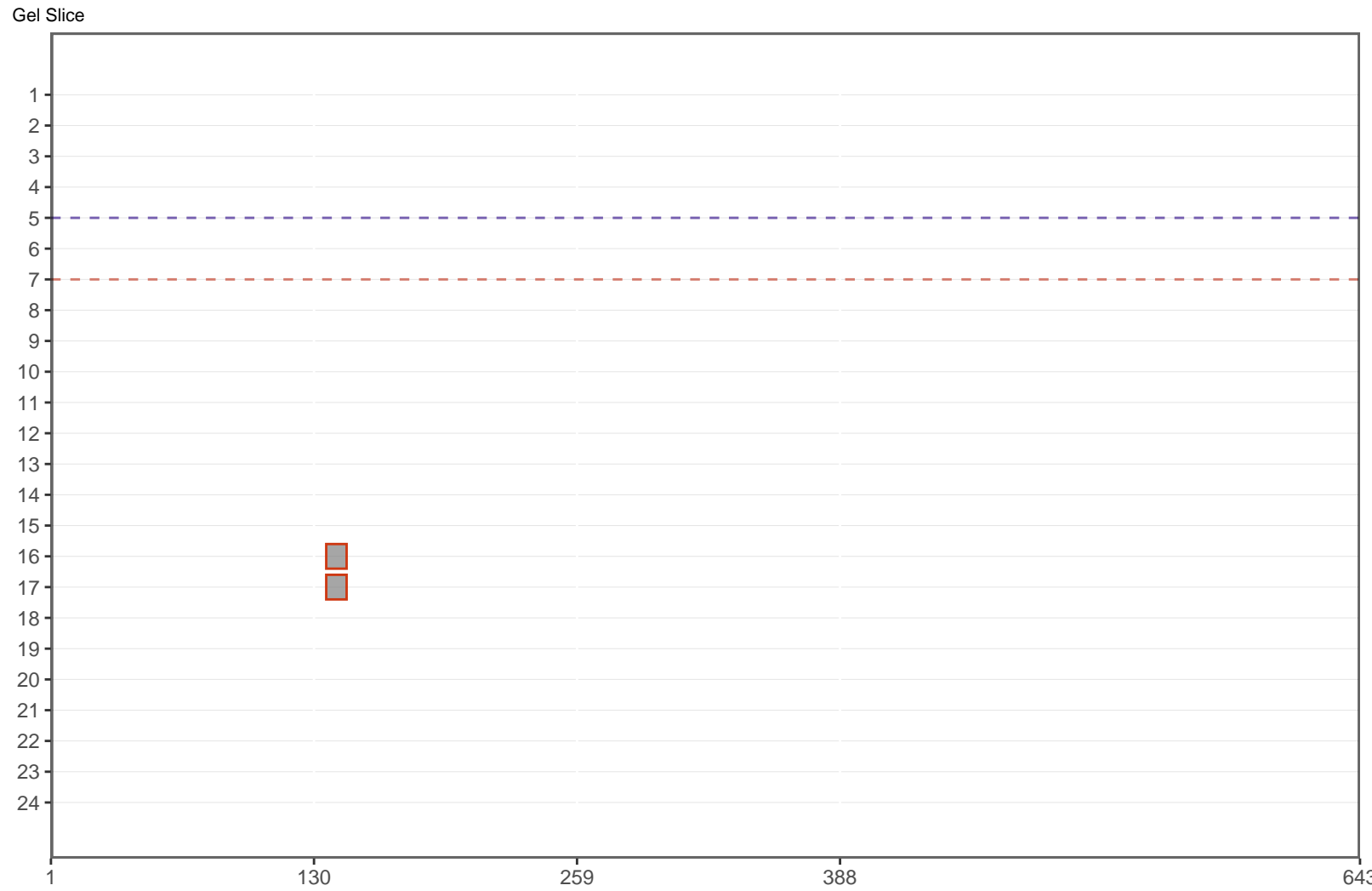
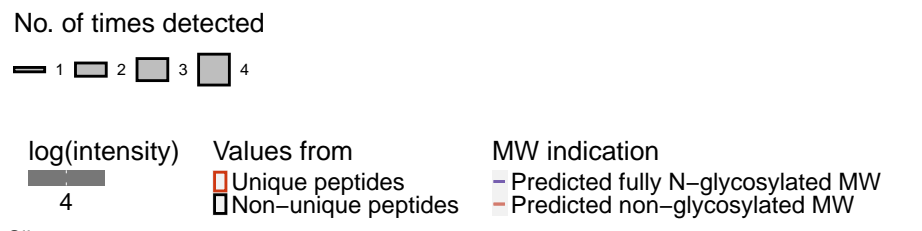
Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

IFQEGKLESSQFDLVHVGAGRTNGLDLGHVNRIVGDLMQMAHPGTEVGSRLHMSVLSYGVVREDDDSMYGTDTRPENKELGRIFPRGYSYTRKEGKPRPNVRFQFCMLVAGWQGNVTRKDMVEVSYKNFKERGANLIPADRFLHEVAFKMKWPKYGA

NbL06g20820.1 probable_leucine-rich_repeat_receptor-like_protein_kinase_At1g68400 [MW = 73.08 kDa]

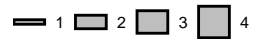


Protein sequence:

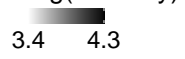
NKIVKYYIDISNSSSLVHSEFYGHILKDKKSDGFATMVFEGGKGFNKVEDLLKASAEMLGKGVSTSYKVAAMDCKDVKVVKRVIEKLLKMKDLGFLRLIGLRHQNIVSLRAYYSKKEELLYVDFLPLNGSLHLLHGRNGPGRTRFLDWSITLKYALGAAGLAFHSEYKTKGCHGNTSSNLLDHFQNAIGISDGLHLLLOMPISSNNGYKAEILLTGNMNTNINPRKFSQKCDVYSGVWLEILTKIATNEGEISLAKWQGRVWVKEWTWDFELARYKEMED

NbL06g20780.1 UDP-D-apiose/UDP-D-xylose_synthase_2-like [MW = 43.34 kDa]

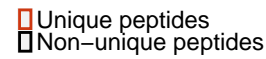
No. of times detected



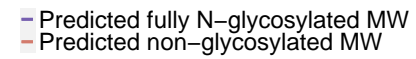
log(intensity)



Values from



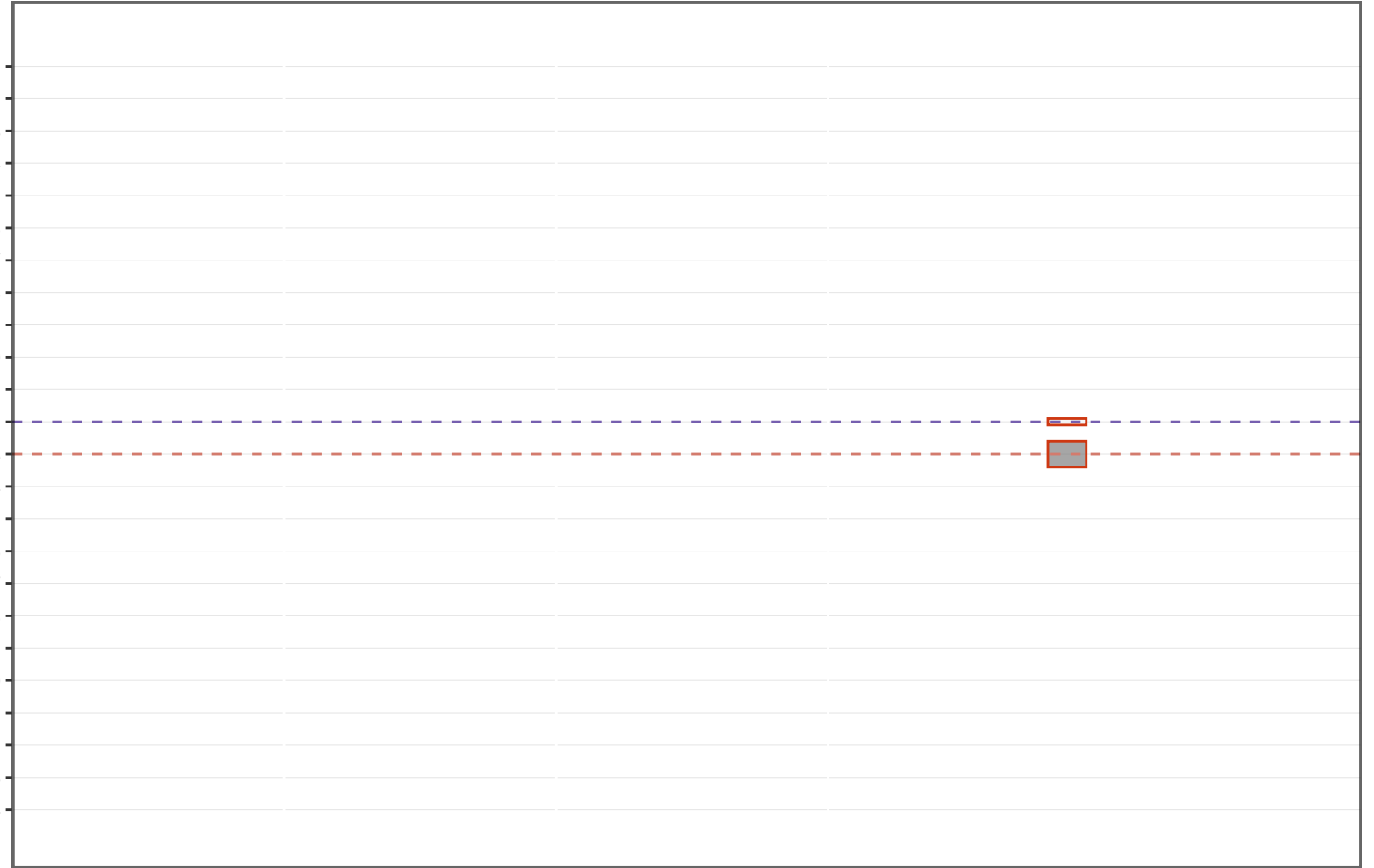
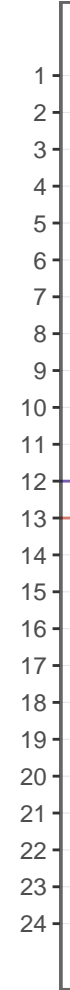
MW indication



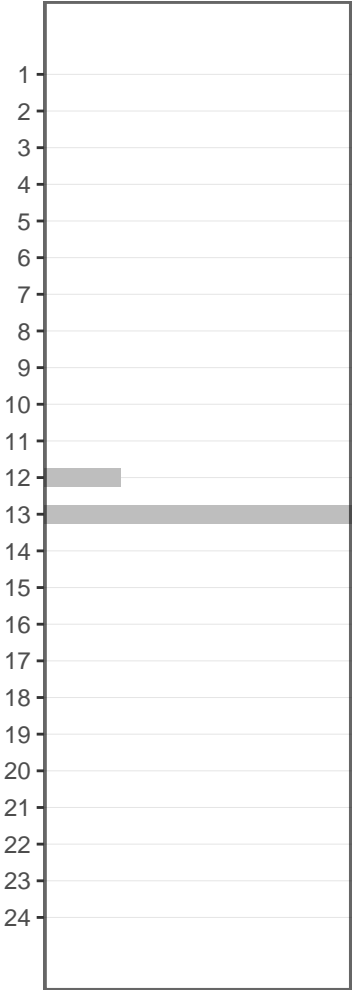
Molecular weight



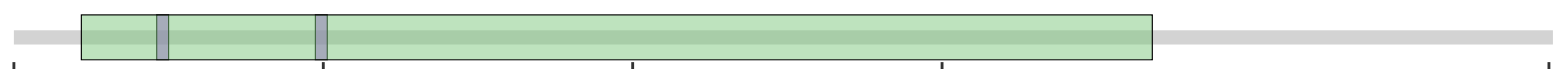
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

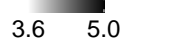
YACAKQLERLYAEGAEAGLEFIVRPFNWIGPRMDFPQIDGSPGEGVPRVLACFSNLLRHEPLKLVDDGHSQRTFFWKDAIEAVLLMIENPTRANGDFNVDNPNNEVTVRQLAEMMTGMFKYKVGESPEPTPTIDVSKSEFYVGGEGVDDSKRIPDMTINRDLGWNPKTSLWDLLESTLYQHRTYAEAVKQAMSKTTGN

NbL06g20500.1 indole-3-acetaldehyde_oxidase-like [MW = 151.08 kDa]

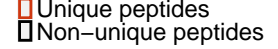
No. of times detected



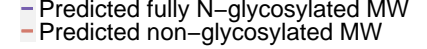
log(intensity)



Values from

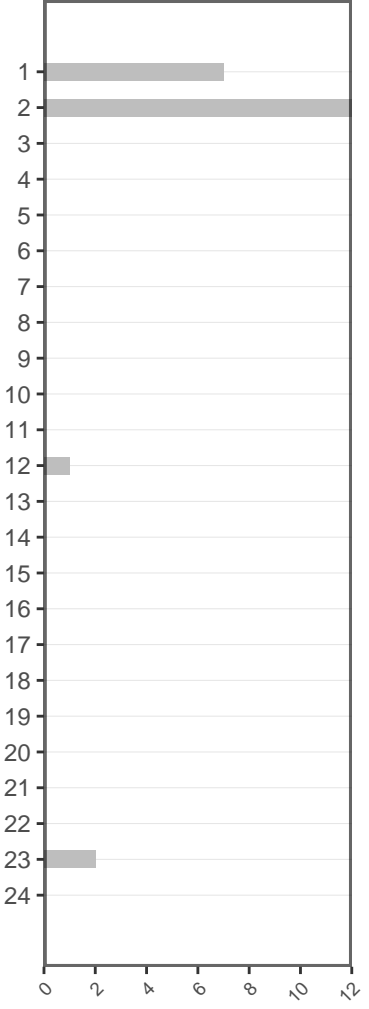
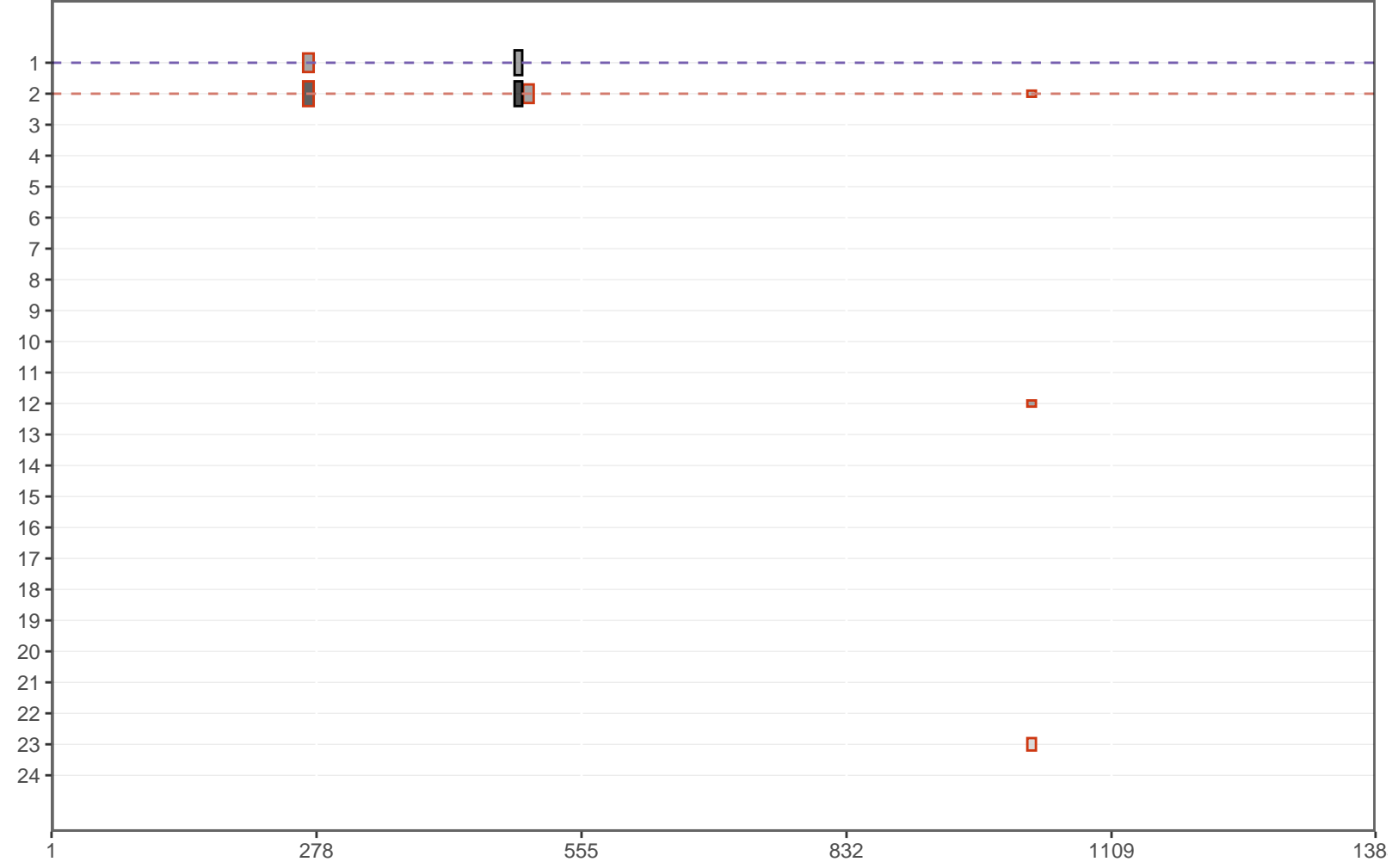
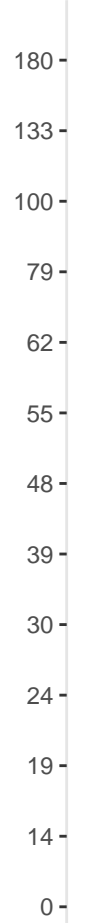


MW indication



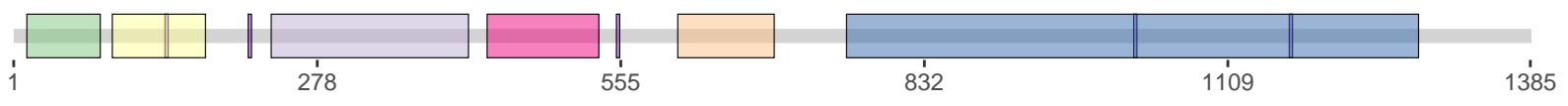
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

- PF00941 FAD binding domain in molybdopterin dehydrogenase
- PF01799 [2Fe-2S] binding domain
- PF01315 Aldehyde oxidase and xanthine dehydrogenase, a/b hammerhead domain
- PF02738 Molybdopterin-binding domain of aldehyde dehydrogenase
- PF03450 CO dehydrogenase

Protein sequence:

DDLARYAGDRIFVNPFLFRPFARRGGSGKWAESQRGADVAANMAVVEYDFENVDSPLTVEEAVGKSSFFQVPPFLYPKKIGDFSKGMAEADNKLSEMRLGGQYFYMETGTALAVPDEDNGMVAAYASGGGSEVAGSVAISGLGVPEHNIRVYTRRVGGGFGKAVRAMPVSTACALAEKLRPVRVRYVDKRTMMAGGRHPMKTYVGVGFKSNKITALHLENVANGIEDVSPILNFGALKKYDWAISLFDKVKYKTNVASKGAMRGPGEVGGSYIAEIMEP

NbL06g20430.1 5-methyltetrahydropteroyltriglutamate--homocysteine_methyltransferase-like [MW = 91.8 kDa]

No. of times detected



log(intensity)



Values from



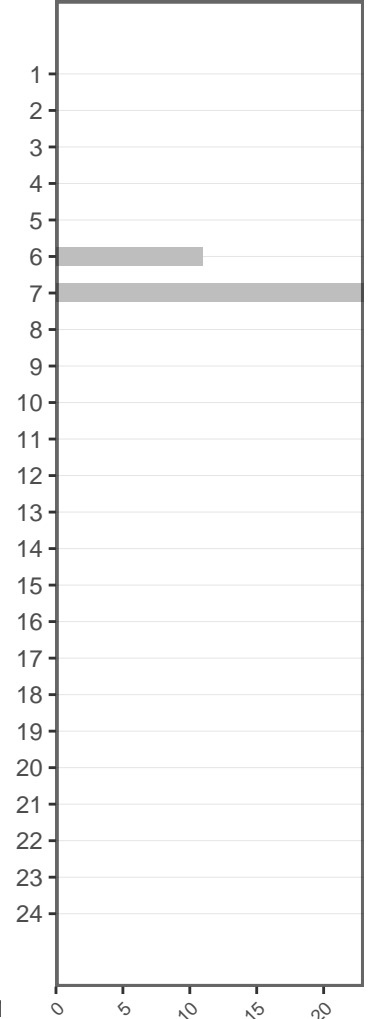
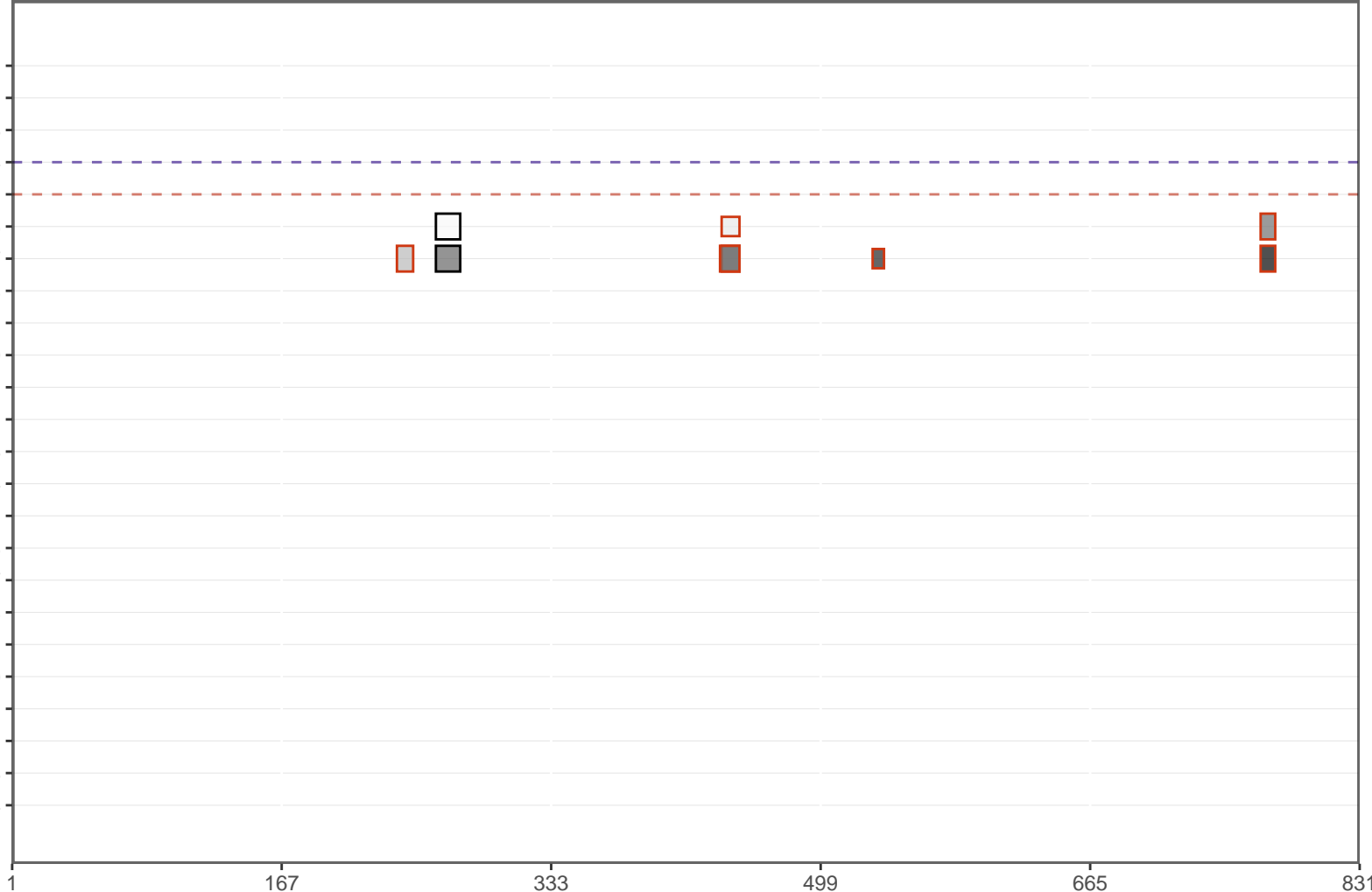
MW indication



Molecular weight

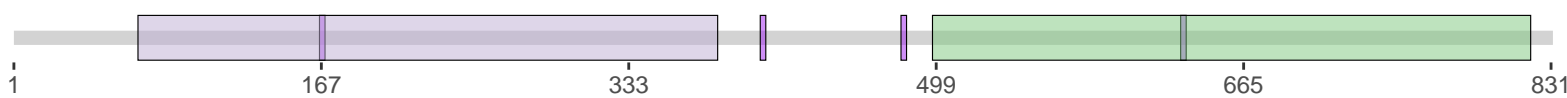


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

NETKLDDEIKSYLFAAGKLVENALAKLAGKRDEAFRSANAARTSRKGSPRVITNEAVQKAAALKSGSDHRRATNVSARLEAGQKKLNLPVLPFTTIGSPDQTELELRKVRREYKANKISGEGYVYHSEIEGKVKLQELDIDLVLHSEPERNDMVEYFGEOLSGFAFTANGWVQVYGSRCVKPPIYVGDVSRPKMTVFWVSSLAQSMKRPKMGVLTGPIVTLNWFVFRDDQPRFETOYQALAKDEVEDLEKAGINWQIDEAALREGPLRKSEAFYLVNVAWVHSF

NbL06g20350.1 uncharacterized_LOC104214226 [MW = 22.22 kDa]

No. of times detected



log(intensity)



Values from



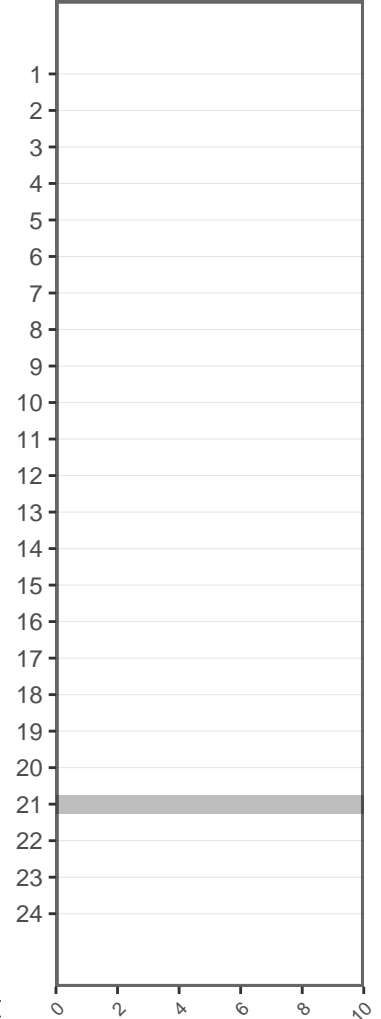
MW indication



Molecular weight



Gel Slice

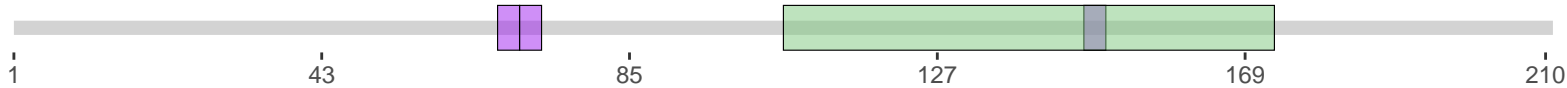


Protein length

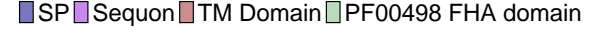


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

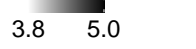
IAKPGSLKIPISAGAVTVSRVAEKADMPVPTVSAVHALLOSMEYLVVTDLDSTNGTFIDEKRLRPGVAAALPGSLTFGDTNLAIFRVALEKMETSSPEEEAEANTEEEEPSSP

NbL06g20340.1 molybdopterin_biosynthesis_protein_CNX1-like [MW = 70.39 kDa]

No. of times detected



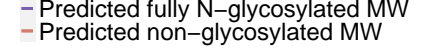
log(intensity)



Values from



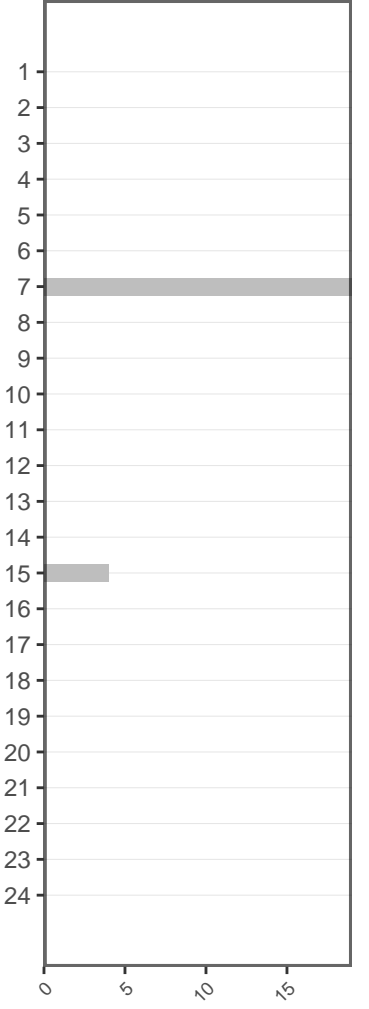
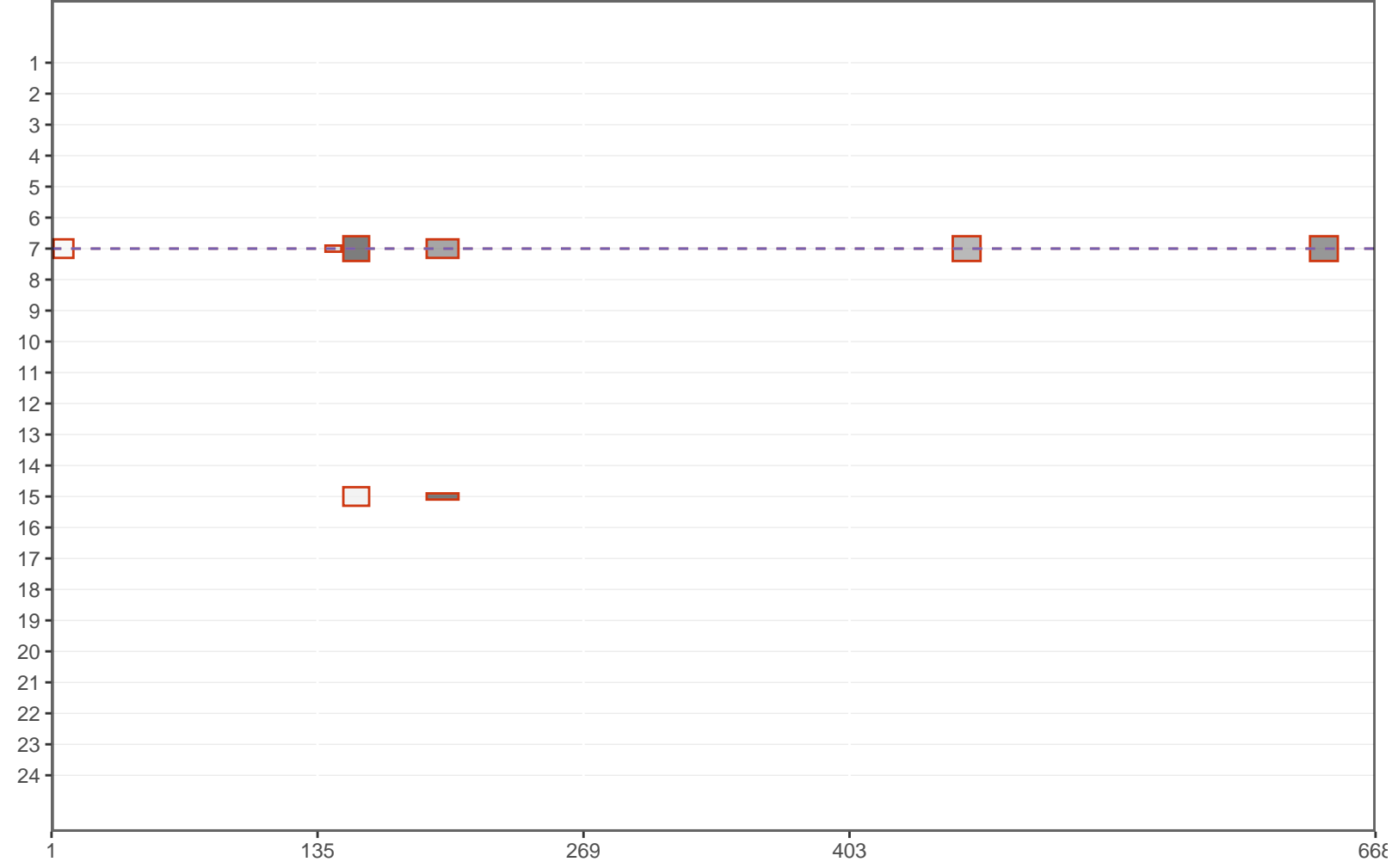
MW indication



Molecular weight

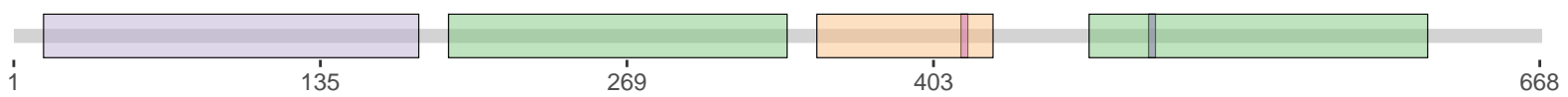


Gel Slice



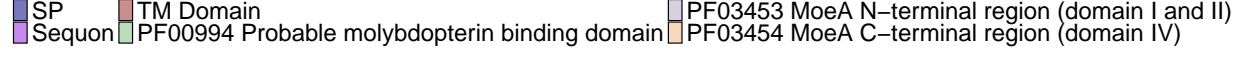
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SCLVCFHLTVAFAIRHISGAWANPHLPRVGAARVKHSHKTDFFRPEYHRAVHSWLNQSGSGFQGFMAESTGHQHSRLLSMKGANALLELPAHNSLPLAGALVALSILSDINSPGRRLQLPLDLSVQGEHKGAANTGSGGSEDFKVALTVSDTVAAGLGPDRSGPRAVSVVNSSSERLGGTSAWATAVVPDEMRRKIDMLQKWSVDKDKVLDLFLGGTGTTPRDVTPKATNSMKGKETPGLLYVMMREGLKVTGPSAMLGRAAAAGRGSTLIMPGRNVAIECEALLPAK

NbL06g20300.1 4-diphosphocytidyl-2-C-methyl-D-erythritol_kinase_chloroplastic/chromoplastic-like [MW = 45.21 kDa]

No. of times detected



log(intensity)



Values from



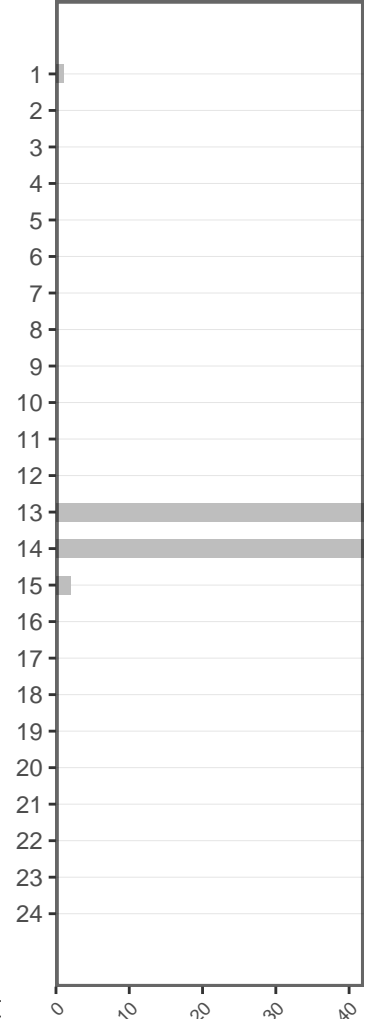
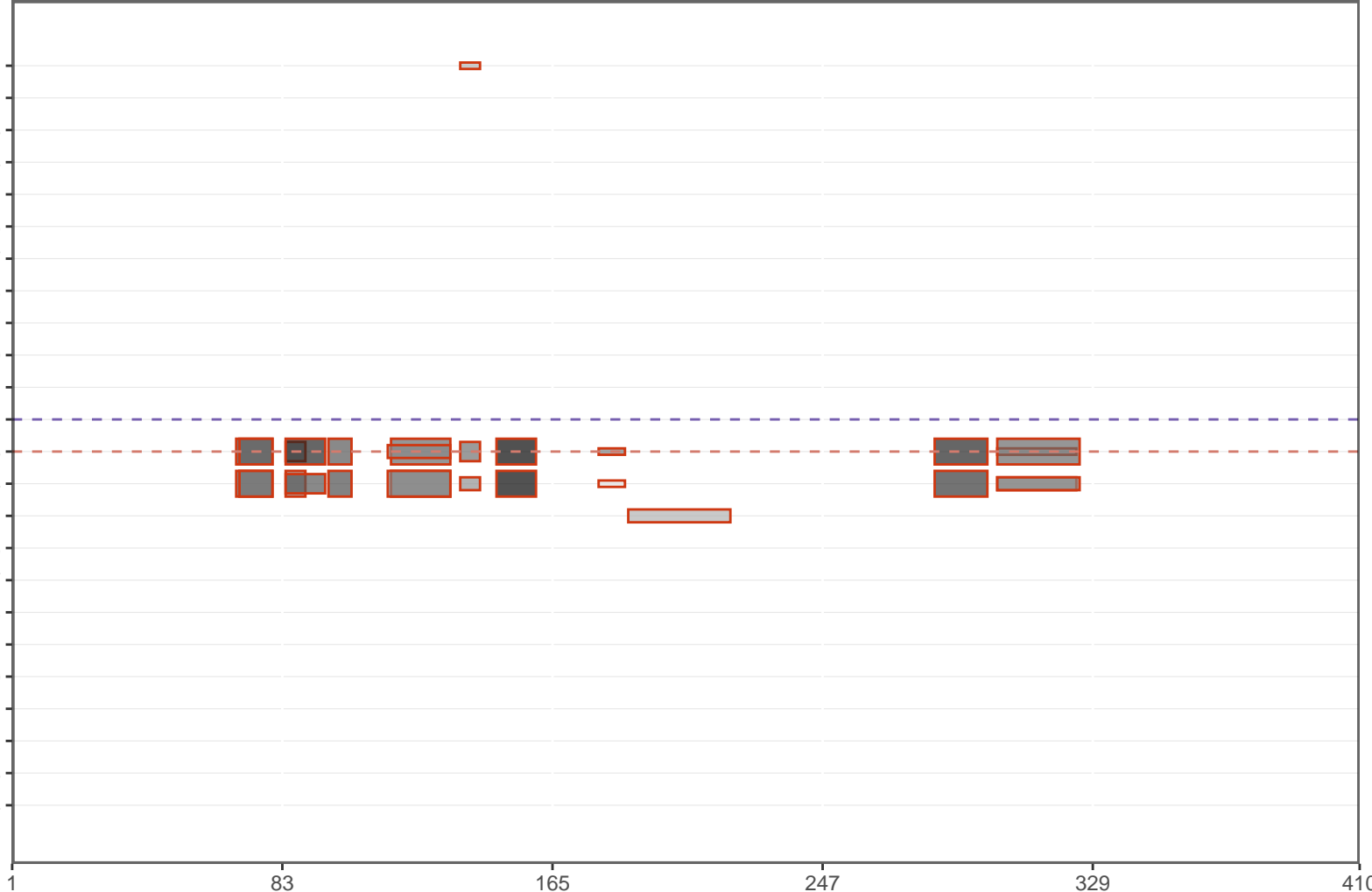
MW indication



Molecular weight

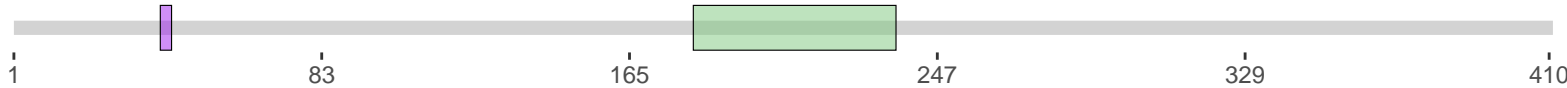


Gel Slice



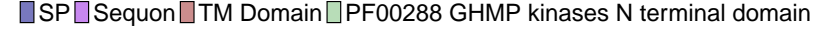
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GLGGSSNATLWAAANGFSGGLATEKLEQEWSEIGSDISFFFSHGAAVCTGRGGEVVDIPSPFPDIPMLIKPQEGSTAEVYKRFLLDQTSNDVPLLEKIKTSGSGQVGVNDLEPFAFEVLPKLRKQRIIAAGRGGYDAVFTMSGSGSTINGVSGPDPDPGFVYDDEEYKDVFLSEASFITRAANGWVEEPLSAGNYADQAEFGSDFNSI

NbL06g20260.1 UBP1-associated_protein_2B-like [MW = 52.41 kDa]

No. of times detected



log(intensity)



Values from



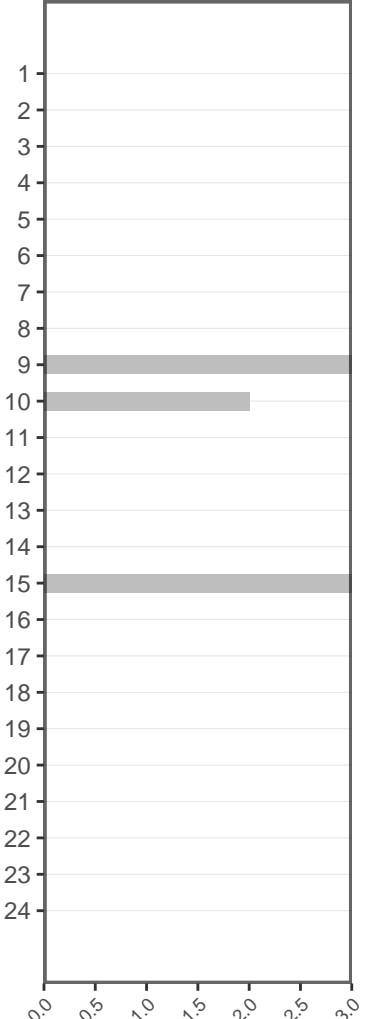
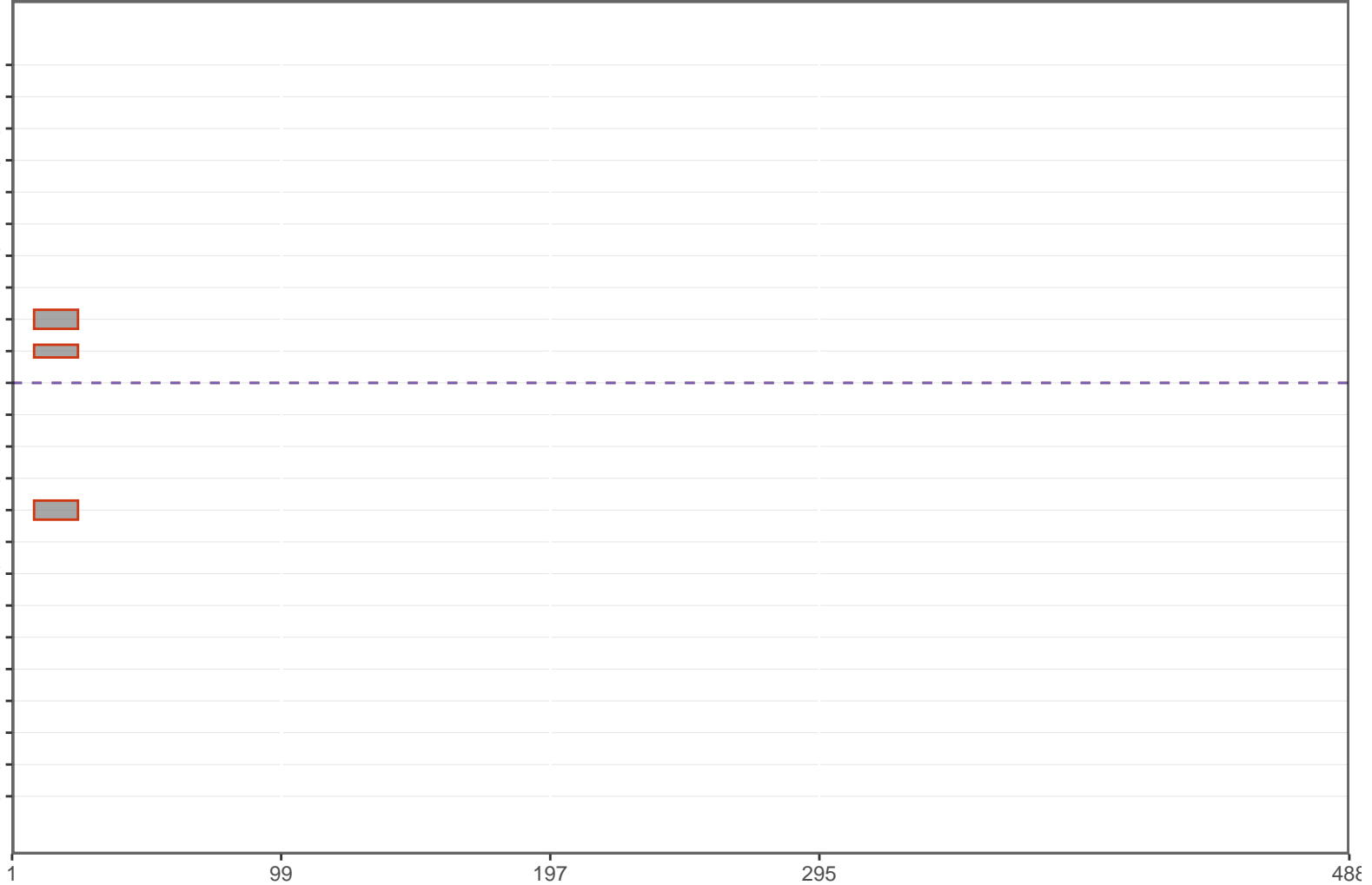
MW indication



Molecular weight



Gel Slice



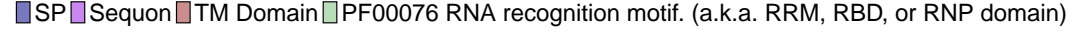
Protein length



Pfam domains



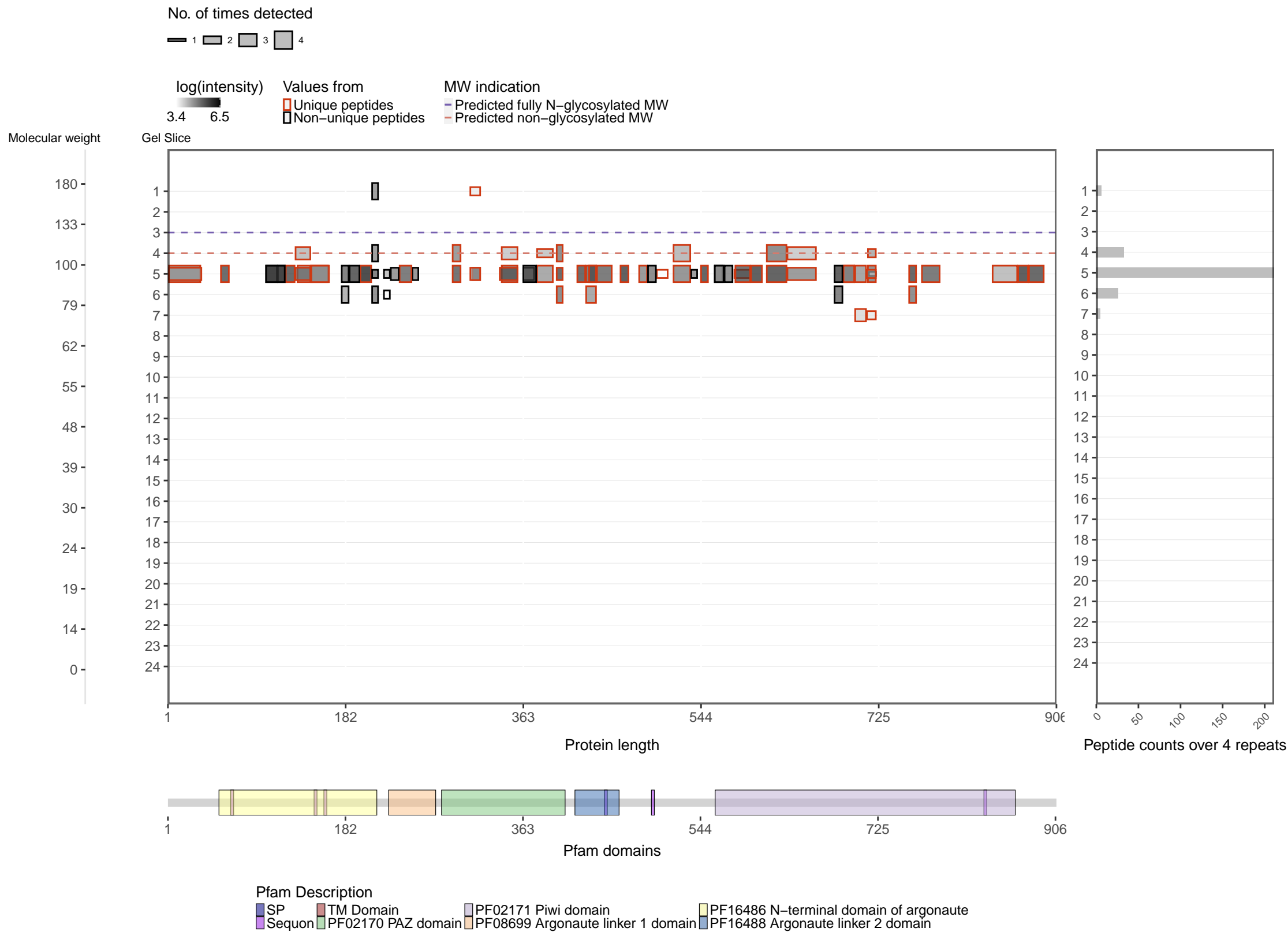
Pfam Description



Protein sequence:

GPVPPPPPTAAVPPVSEYTKRNFVSNVAADLPKLEFFSKFGEVEEGLDLDKGTGKPKGFDLFFVYKVEBARKALEEPHKFEGHTLHQGKAVDGRKNNNNYDGHQDQDGHYPQHQDQDGHVYQHPKAKGKYGGGSGSASASAGHLMAPSGFAPVGFNFWAPALGGALTALLTGGAGLGGNLLGGFSGPVPDQGVPPWNNAGGYGAGGAAAGGYGAGPMDQGNPQGGARPPGGGARPPVPGYGGH

NbL06g20250.1 protein_argonaute_4-like [MW = 101.42 kDa]



Protein sequence:

ICGISISSNFTQVEGRVLSPPKIKTGGDDFVPRNGRWFNFKRRLVDPFKIERWAVVNFSAKCNIGLISDLKDGKMKGMVEDPFDVFEESPGFRAPPLRVKEMKFEVQSKLPGAKFLGLLPERIKNGDIYGPWKRKMLAEFGIVTQCIAPFRVNDQVITNVLKINAKLGLNSMLTVEHAPAFMVKVPTILGMDVSHGSPGSDVPSIAAVVSSRQWPSISGRYRASVIRTQSPKVEIMDNLFRASDTEDEGMREALLDFVSSGKRKPEHIFRDGVSESQFNQI

NbL06g20210.1 phytochromobilin:ferredoxin_oxidoreductase_chloroplastic-like [MW = 39.86 kDa]

No. of times detected



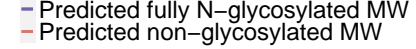
log(intensity)



Values from



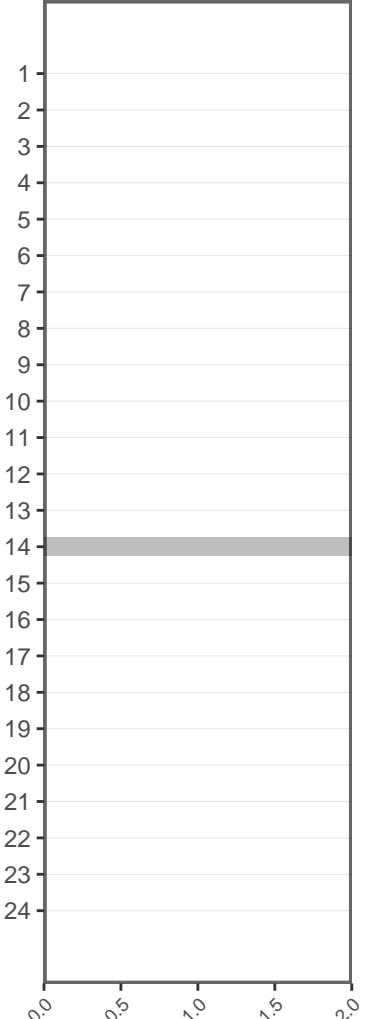
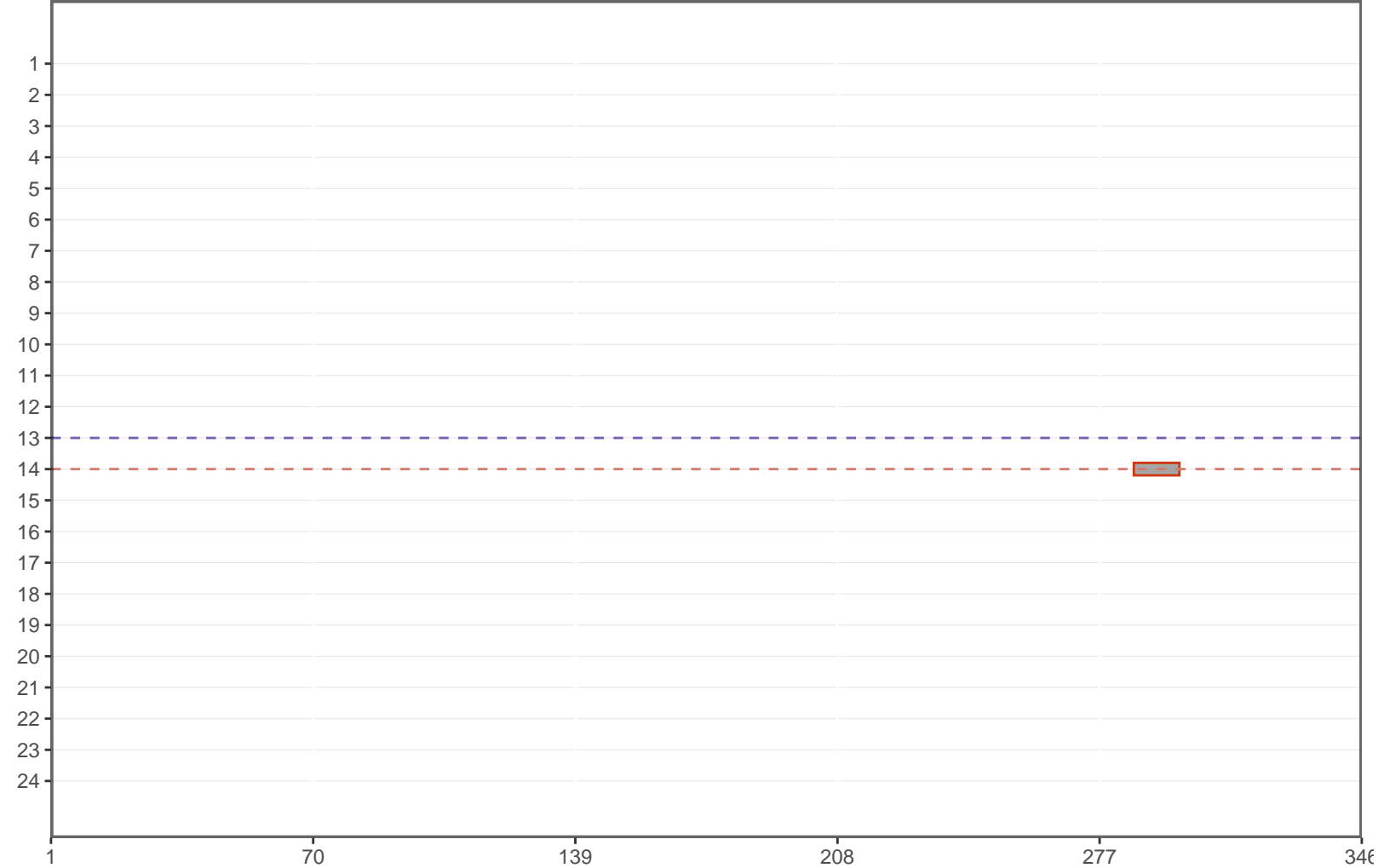
MW indication



Molecular weight

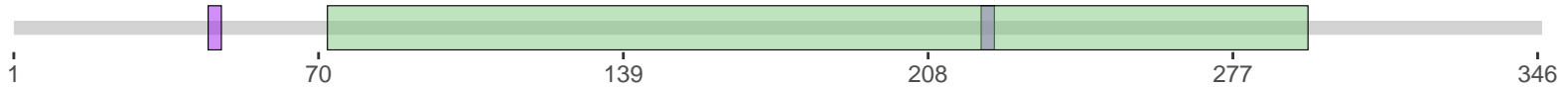


Gel Slice



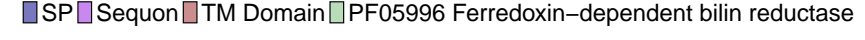
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NPLHDVDDQEDYKERYKYLKPLGLKYSDDLPLWGGKLTGSESLKFFSPWTRFSSSPNHSVLSFAKDYKAWLELTDKSEETDAFDVARNREAGHRYLTVRAEKDPGCHGVLKRLVGEALAKDISEFLFNGVNLKGGKTFLDYFPEYRGEEDGRVNEKRMIGKGFENRPWNRGEFGINP

NbL06g20200.1 uncharacterized_protein_At2g37660_chloroplastic-like [MW = 36.5 kDa]

No. of times detected



log(intensity)



Values from



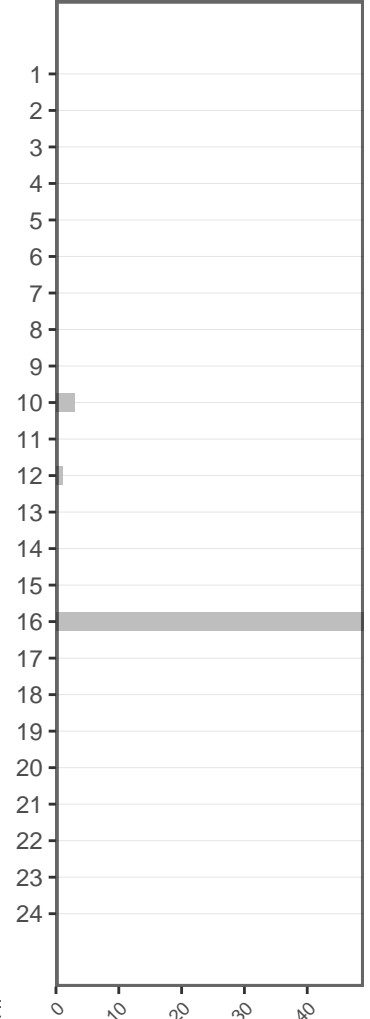
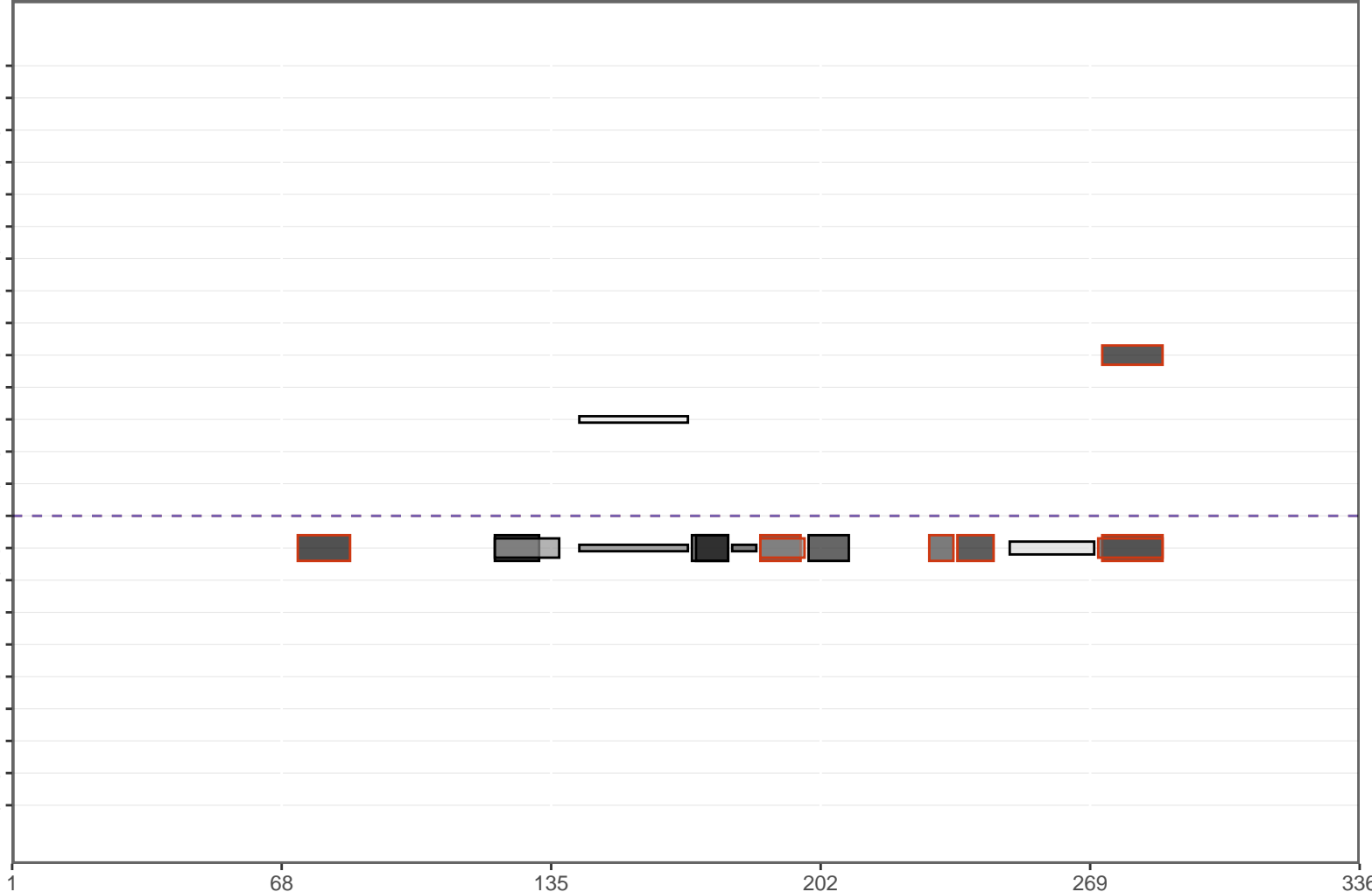
MW indication



Molecular weight



Gel Slice

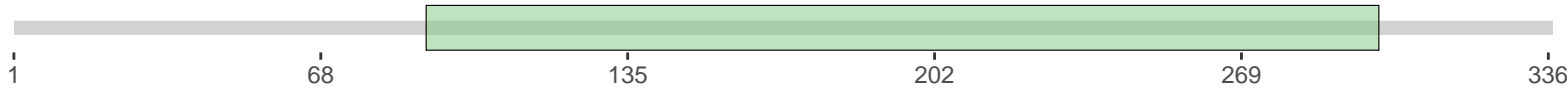


Peptide counts over 4 repeats

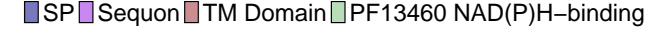
Protein length



Pfam domains



Pfam Description



Protein sequence:

THVICCTGTAIPSRRIWDGNTFERVWDGVEGRNLYSSLPQSLKRIVLVSSGIVTKFNEIPWISIMNLFQVLYKWKMGEDFVIRNSGLPFTIIRAGRLTDPQVTSYDLNLTLLQATAGERRAVALGGDGLVGEVSRLLVAEAGIALIDDFTEGGTYEINSPGGDQPSGDTLKWGELFRDSHNY

NbL06g19970.1 glucan_endo-13-beta-glucosidase_acidic_isoform_GL161 [MW - SP = 35.98 kDa]

No. of times detected



log(intensity)



Values from



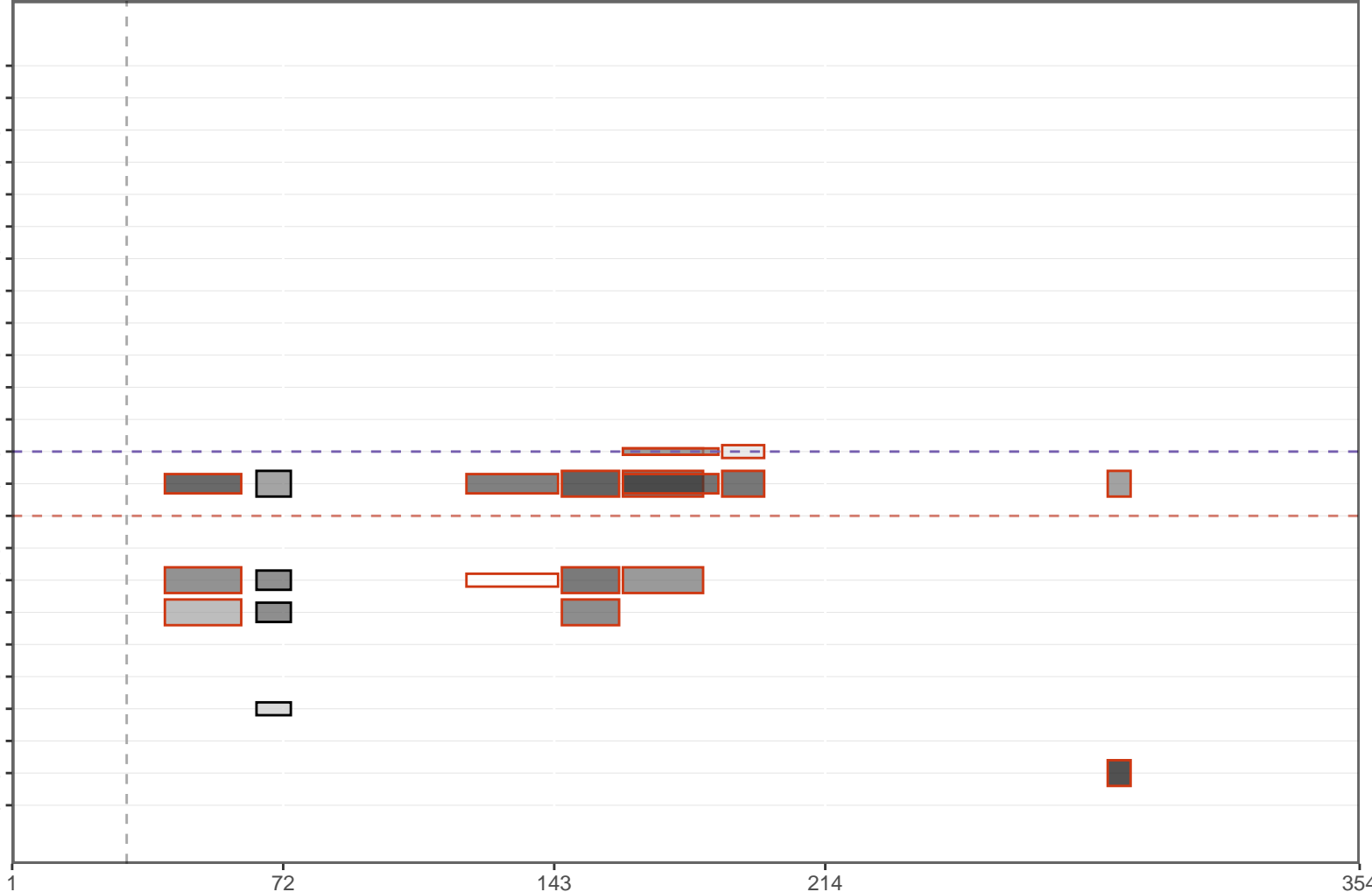
MW indication



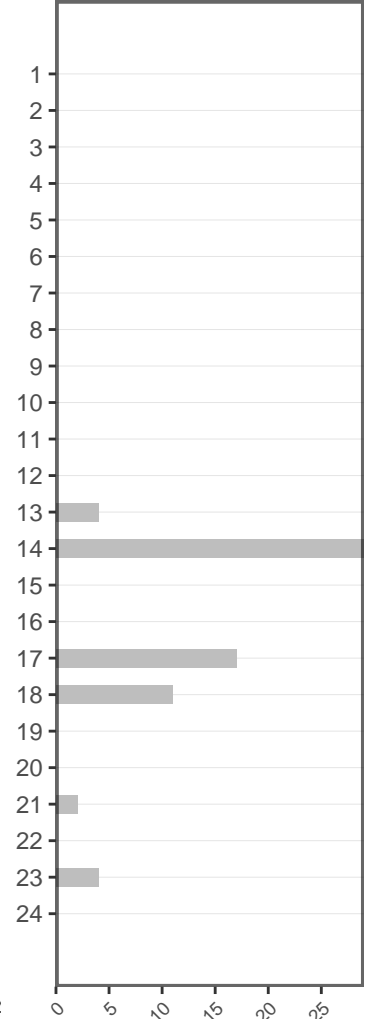
Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VYTSGLLNTYPPESSEIFREEFKSFIKFIKFLARNLPLLANVYPIYVHSNTVWALGYALFTQEEENSLGVGNLFDALLDSMYFAVEKAGGPNVEIVSESGWVPESSGVATIEIENAGTYRNLINHWSSGAGTRKPKPKTIETYLFAFDENDKIGIEIKHFGLFSPDGRKAYQLNFNLSLPWLP

NbL06g19940.1 cinnamoyl-CoA_reductase_1-like [MW = 35.7 kDa]

No. of times detected



log(intensity)



Values from



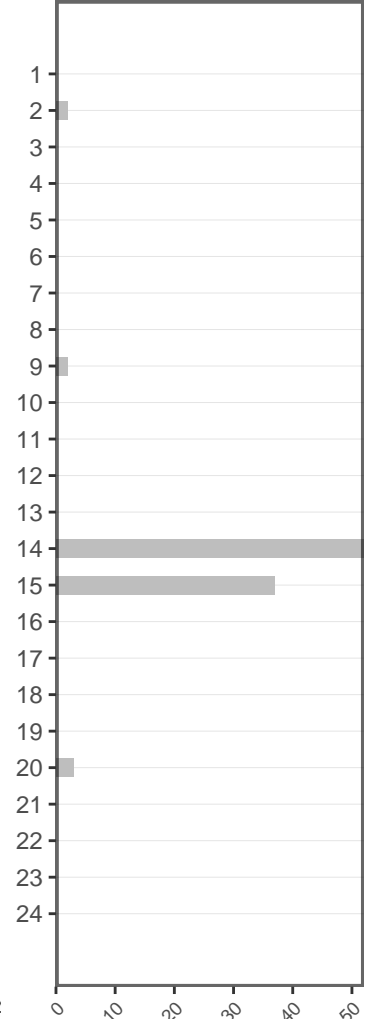
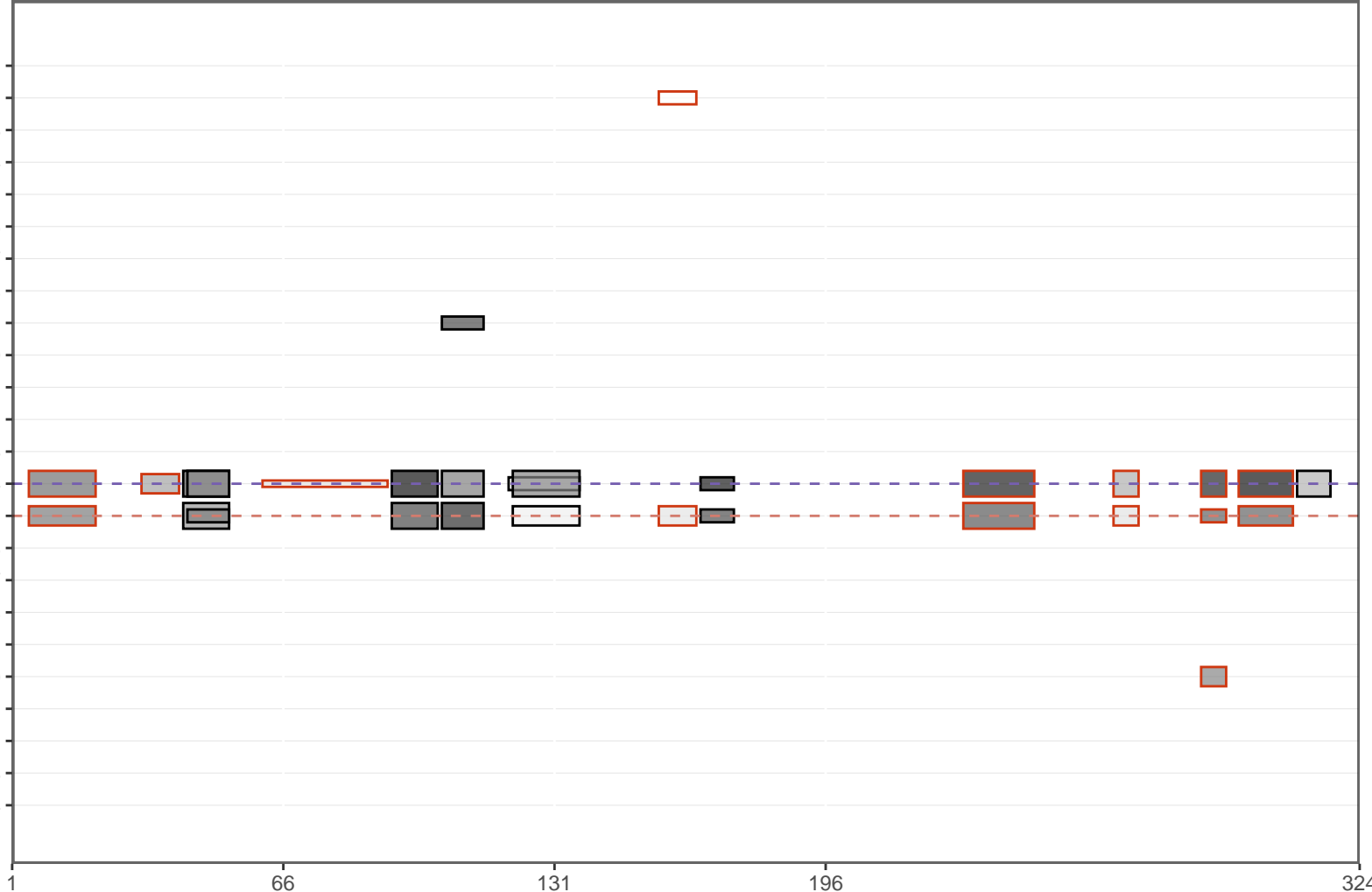
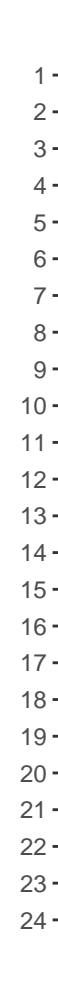
MW indication



Molecular weight

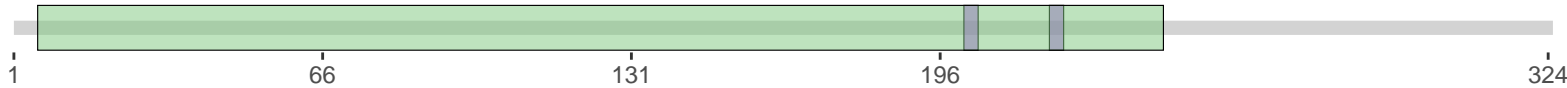


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISDPHLCRESDMYYVLEKTLAEDAAWKFVKEKADIMVTINPMMVIGSLIGPFLNTSGAAVQLGNGAVTYPNATLGGVWVKKVLAHLAFENPANGRYLMEVAWHYSELVKILREHYPTMKLPEKGVDDKPPFPKYGVNIERAKQLGVETPLAESKETVESLKEKPFYSDA*

NbL06g19920.1 cinnamoyl-CoA_reductase_1-like [MW = 43.22 kDa]

No. of times detected



log(intensity)



Values from



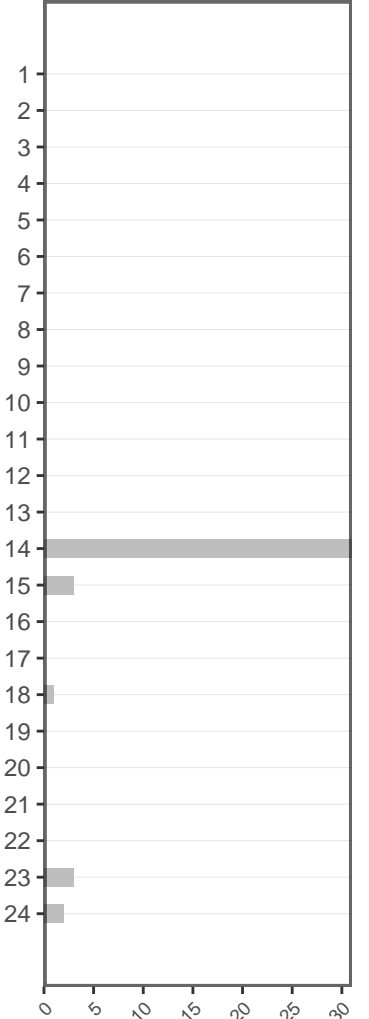
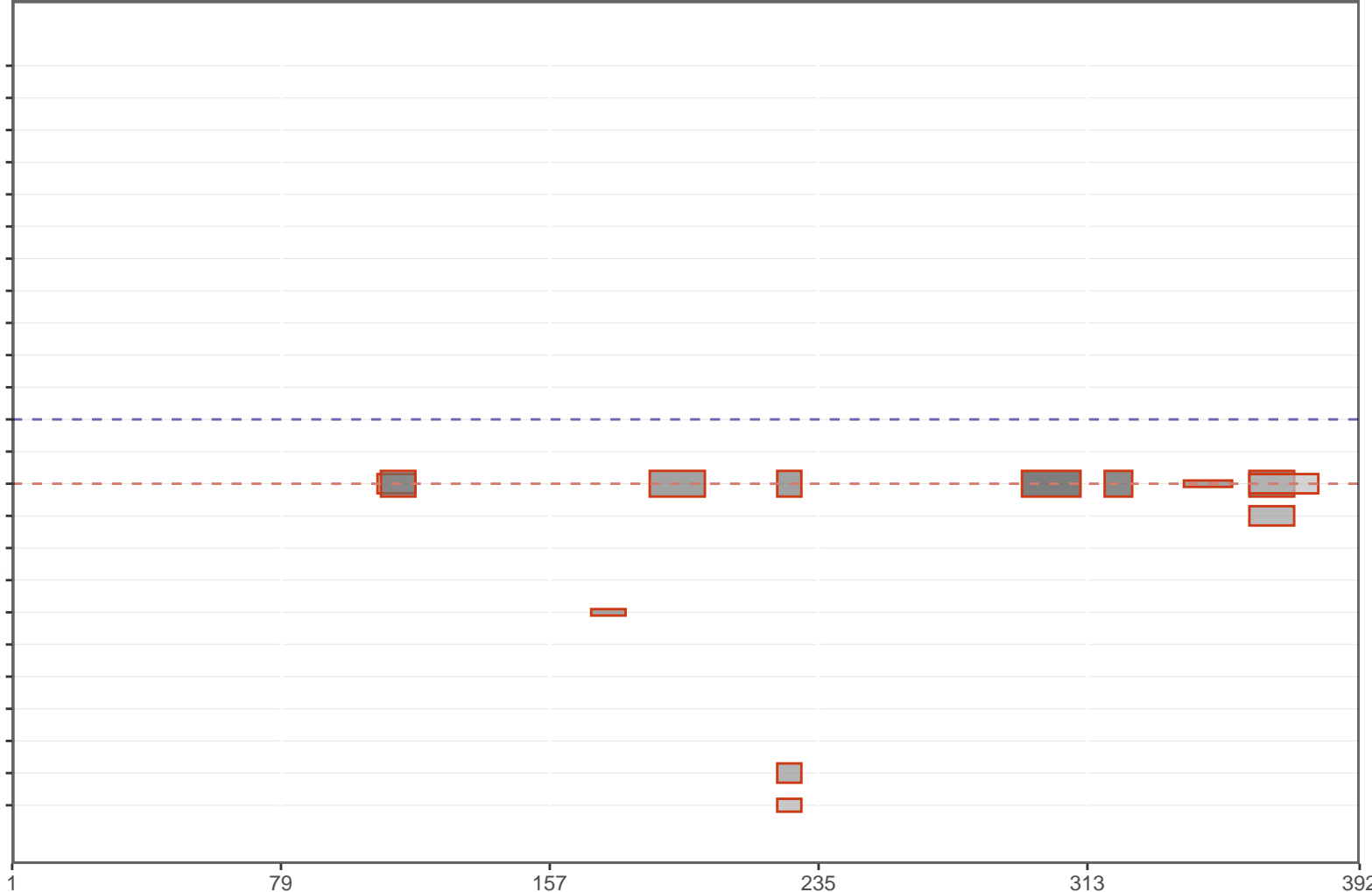
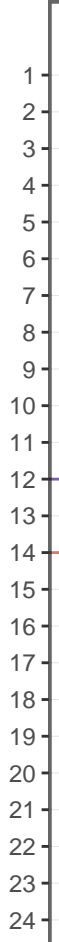
MW indication



Molecular weight

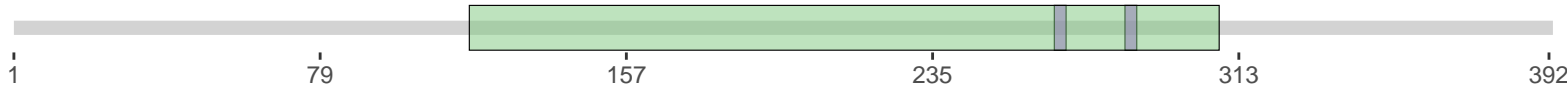


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

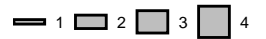


Protein sequence:

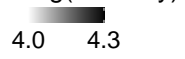
VLLTSSIAAVYSGGPRTPVVDVDEWVSDVSPDYGREKGLWVYLSKTLAEDAIAWFKVKEKGDIMVAANRPMVGPLLQPTLNTSSGAVLNLVNGAETYPNSTFGVWVWQVAVNAHLAFENPSANGRYLMVERVAHYSDIKLRDLYPTMRLPEKGAADNPLMGNVGVSKERAKSLGVFTPLLESIKETVESLKEKRRFGGSSAM

NbL06g19700.1 ADPATP_carrier_protein_mitochondrial [MW = 41.85 kDa]

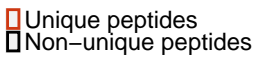
No. of times detected



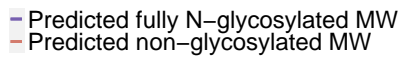
log(intensity)



Values from



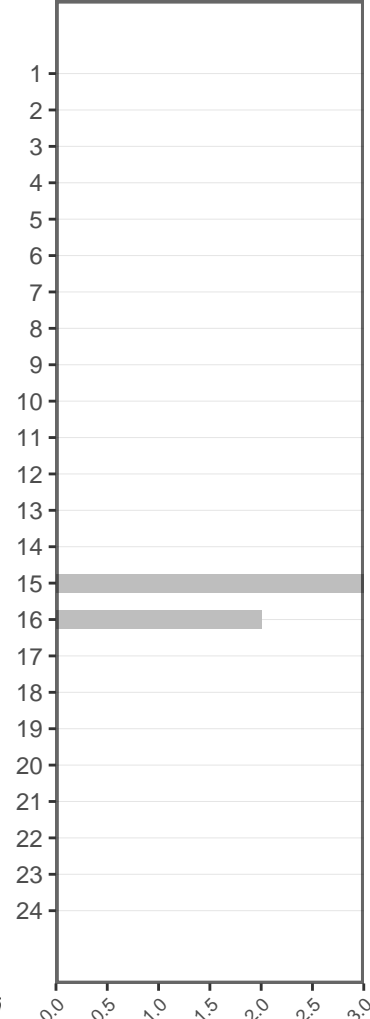
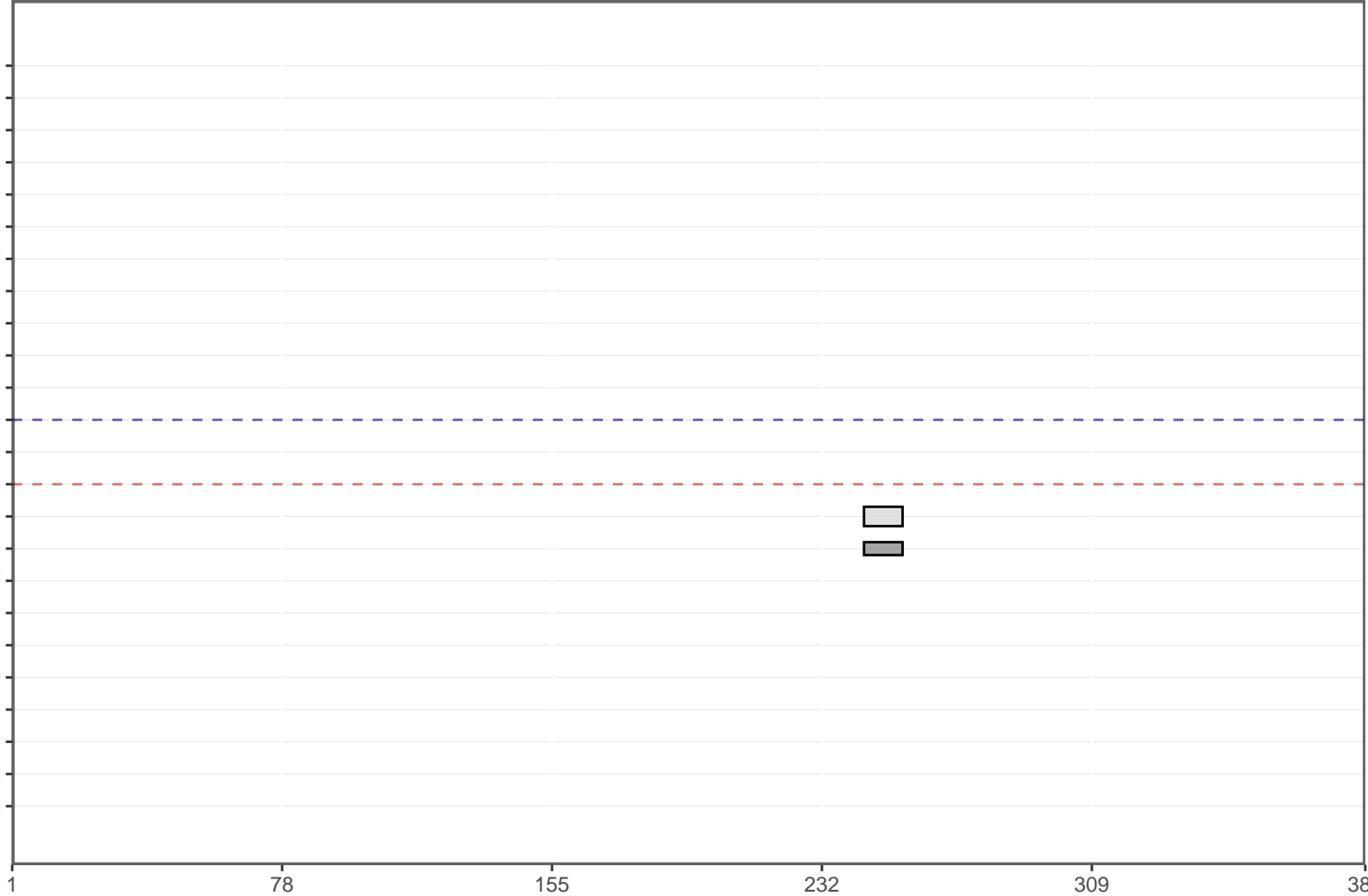
MW indication



Molecular weight



Gel Slice

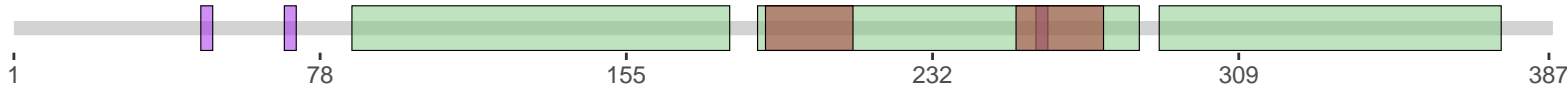


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description

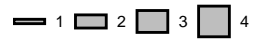


Protein sequence:

◊◊◊RDGYYWYFAGNLSGGAGASBLFFVYSLDWARTRLANDAKAAKGGGRGFNGLVYVYKTLASDGIAGLYRGFNISGVIIYVYRGLYFGMYDLSLKPVLITGNMGDFFFASFGALGWLTNAGLASYPIDTVRRRMMMTSGEAWYKSFDFSGILKNEGAKSLFKGAGANLRWAGAGVLAGYDKLGVVYFKYKYGSGGA

NbL06g19560.1 zinc_finger_CCCH_domain-containing_protein_14-like [MW = 35.68 kDa]

No. of times detected



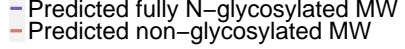
log(intensity)



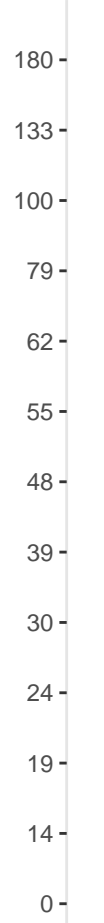
Values from



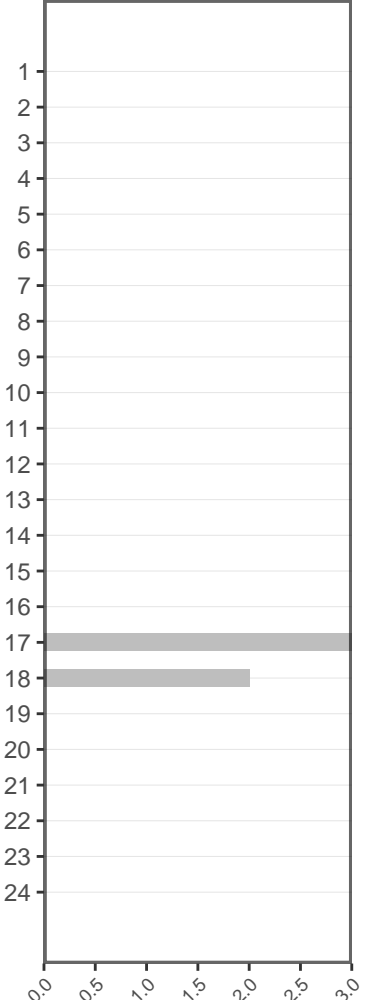
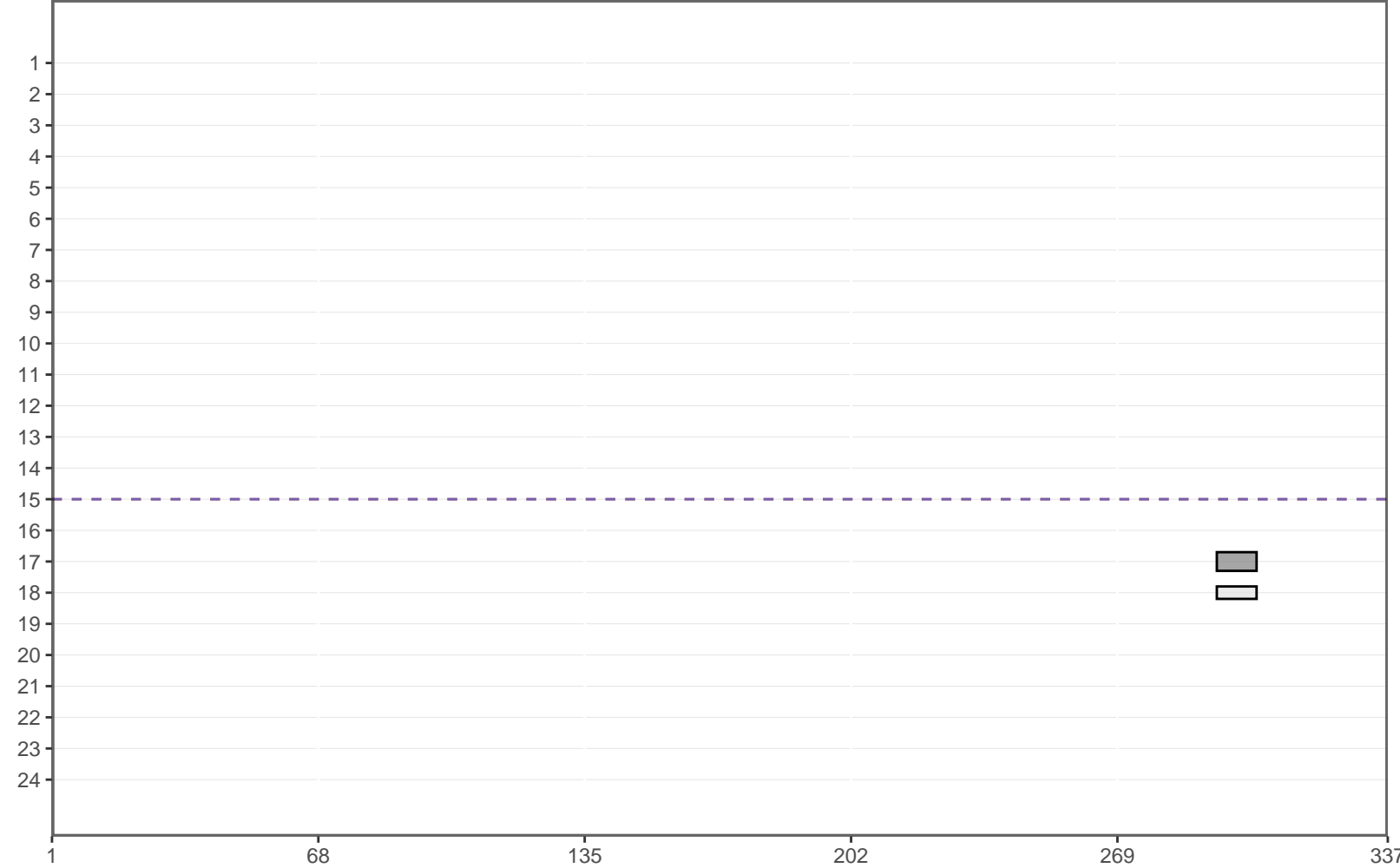
MW indication



Molecular weight

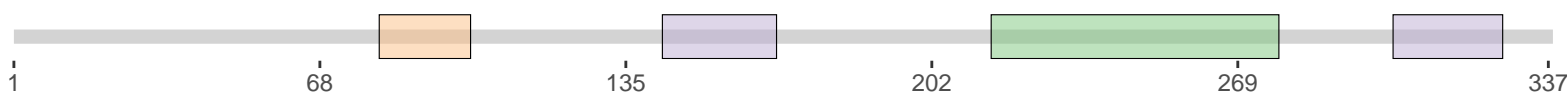


Gel Slice



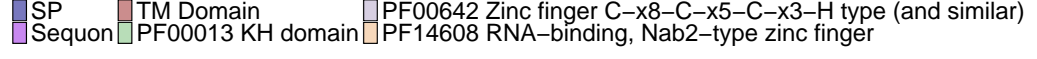
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

XFQDKNFAHGEWELGKMAPLHEEGRGMFQTHGWYGSRPETTPAGFAAASFSSATANISVDSLAGPFGKGGVNSKQISRVTGAQFSIRDHESDNLRINLELEGTQKGGASGMVRELQGVTAQSAAPLMKNPSSATSNFKTKLGDNFAGKSGCTTGERGCHFAHGAEEELRRSGP

NbL06g19430.1 vinorine_synthase-like [MW = 50.09 kDa]

No. of times detected



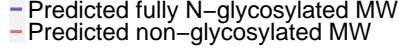
log(intensity)



Values from



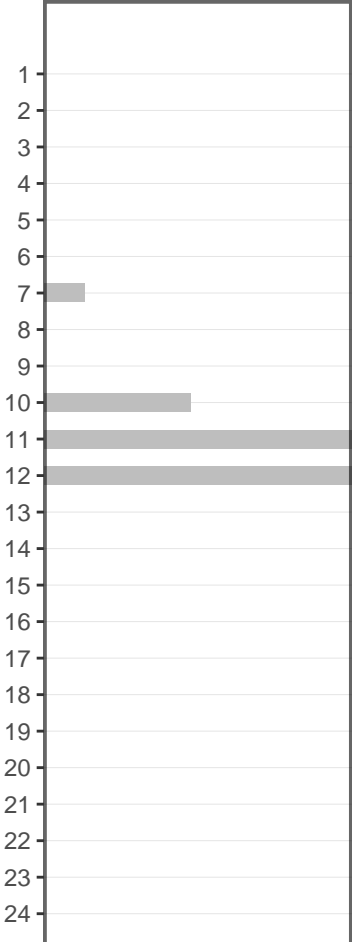
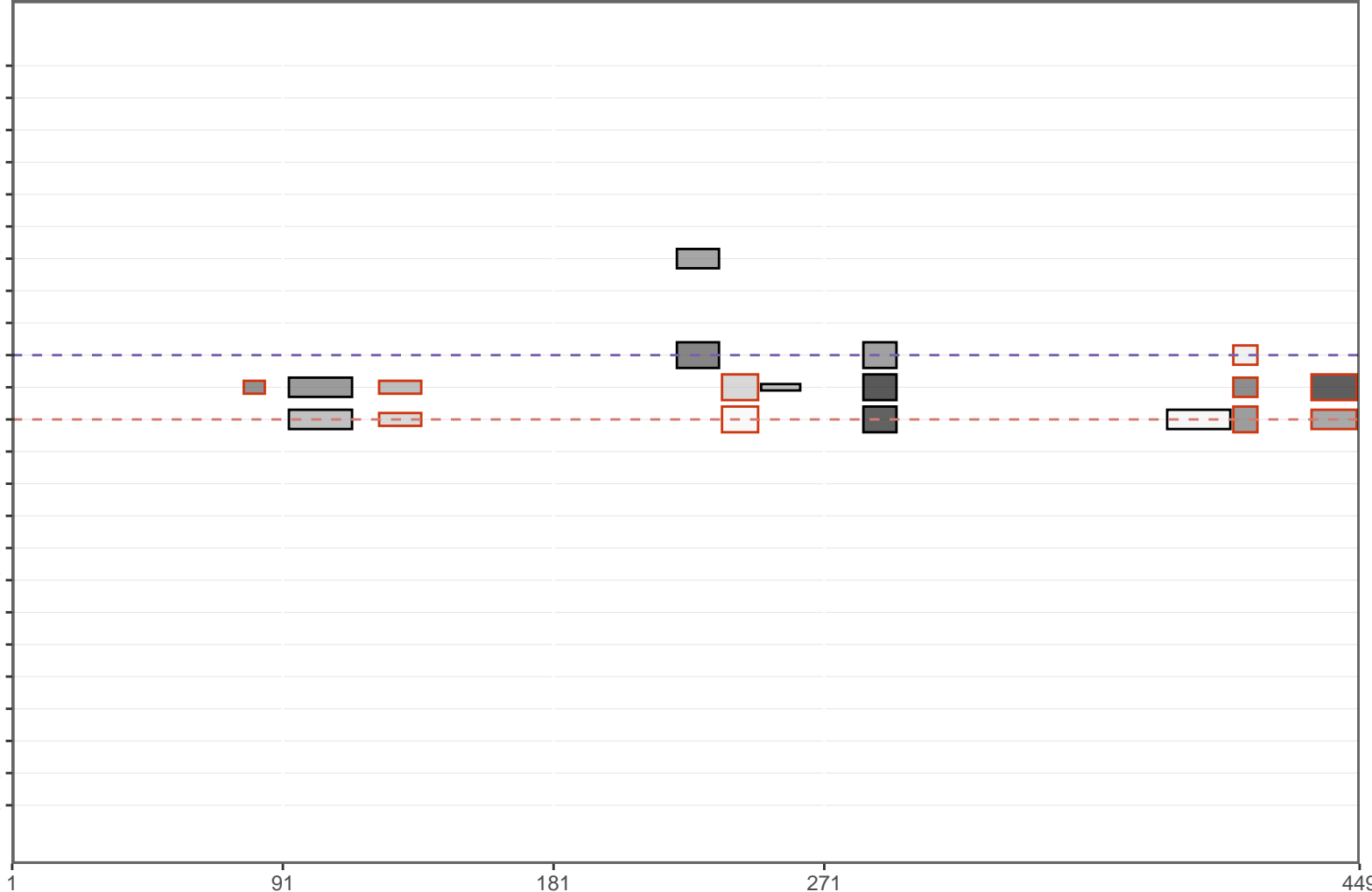
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

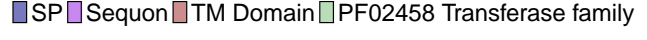
Protein length



Pfam domains



Pfam Description



Protein sequence:

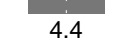
PHVSPNWSKIVEISIVSDNGHGTFKIFSDASTIASLKKANVSDDAVPKPRIVELVSAVMMKGFMTISTKTRTSBSQLMNVNIRKRLVPLFNNHGVGNVATRTTYKGGEDDGDLSLTVSGDKRIGSELGSKFVDKSRGDEALAPQDNLELGLAFNGGETLFINWGDGKFKYDVFDFGDKPLVWSDGLPKNFILLTDSRDSGGGNAAWNLKEGDMKAFEOELIDQAIQSAK

NbL06g19370.1 uncharacterized_LOC104215593 [MW - SP = 16.75 kDa]

No. of times detected



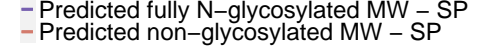
log(intensity)



Values from



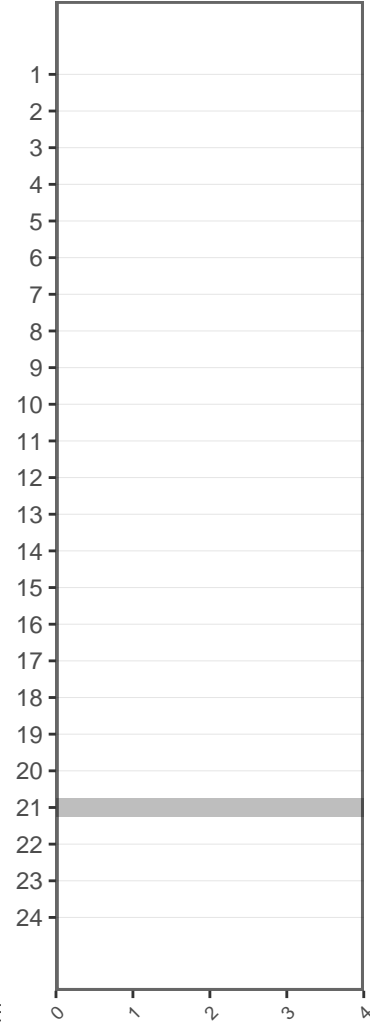
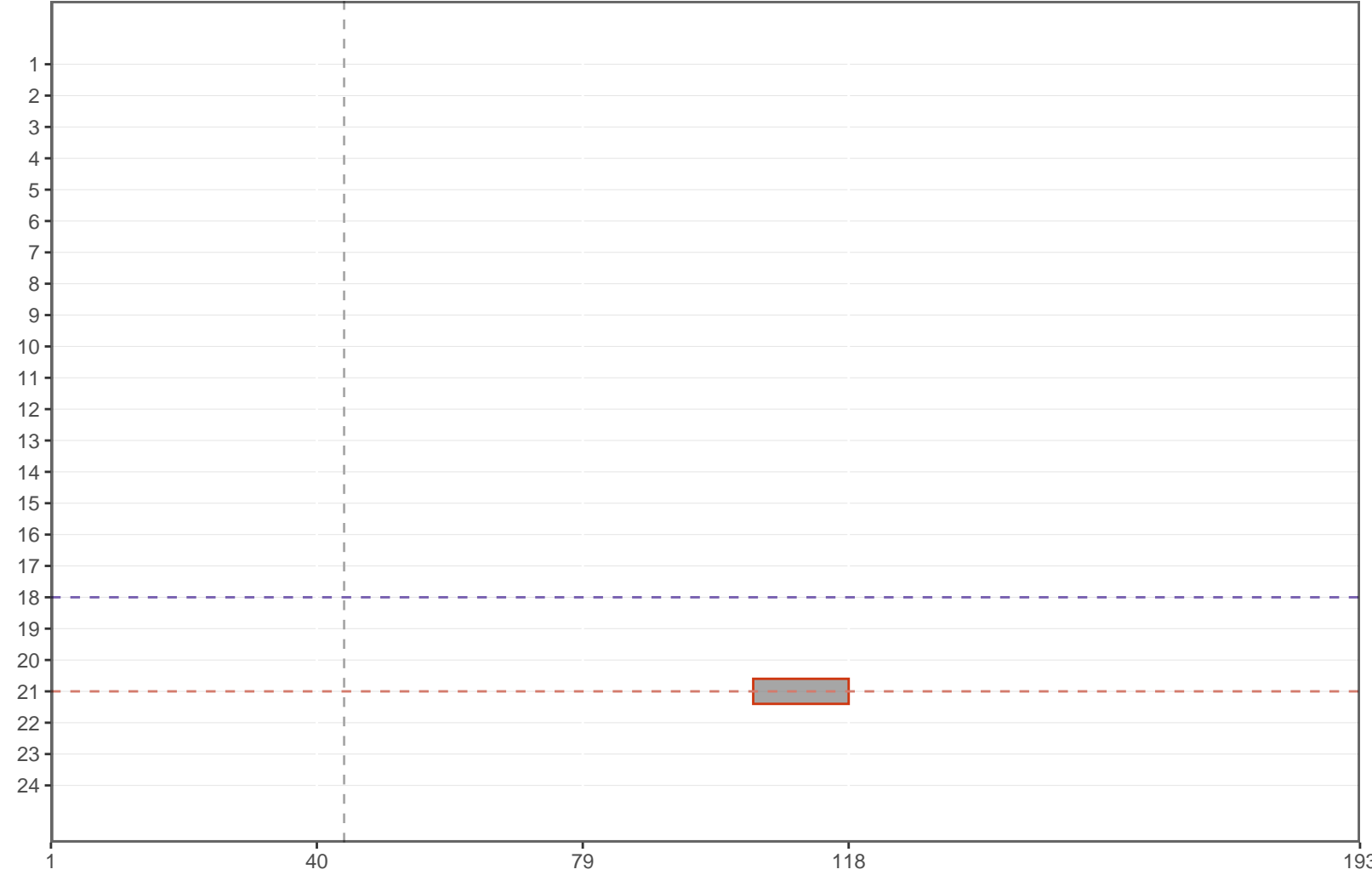
MW indication



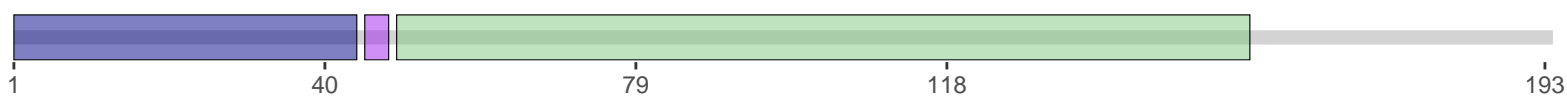
Molecular weight



Gel Slice

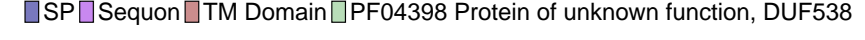


Protein length



Pfam domains

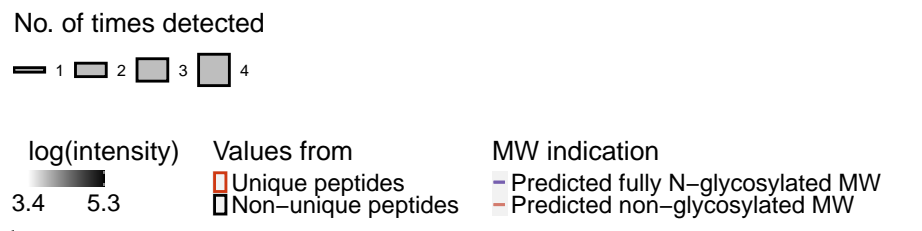
Pfam Description



Protein sequence:

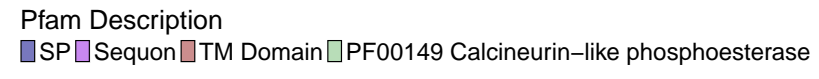
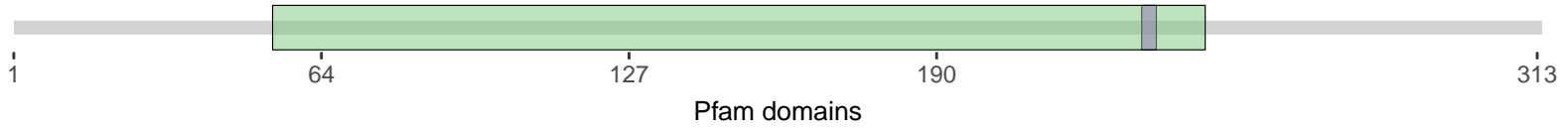
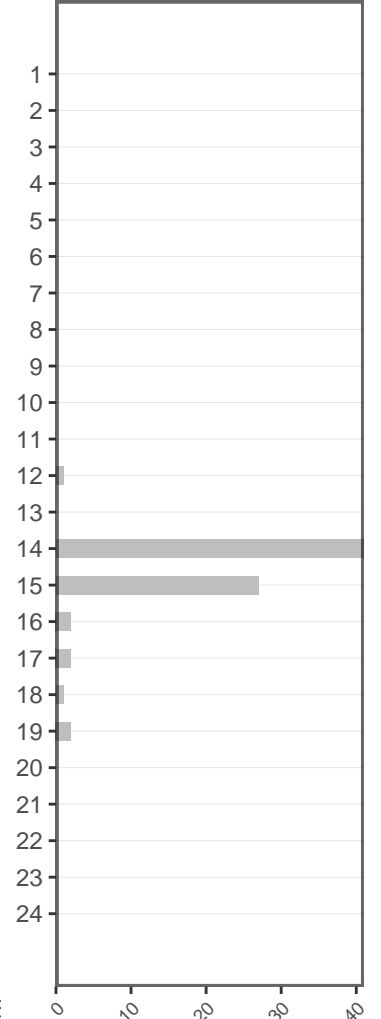
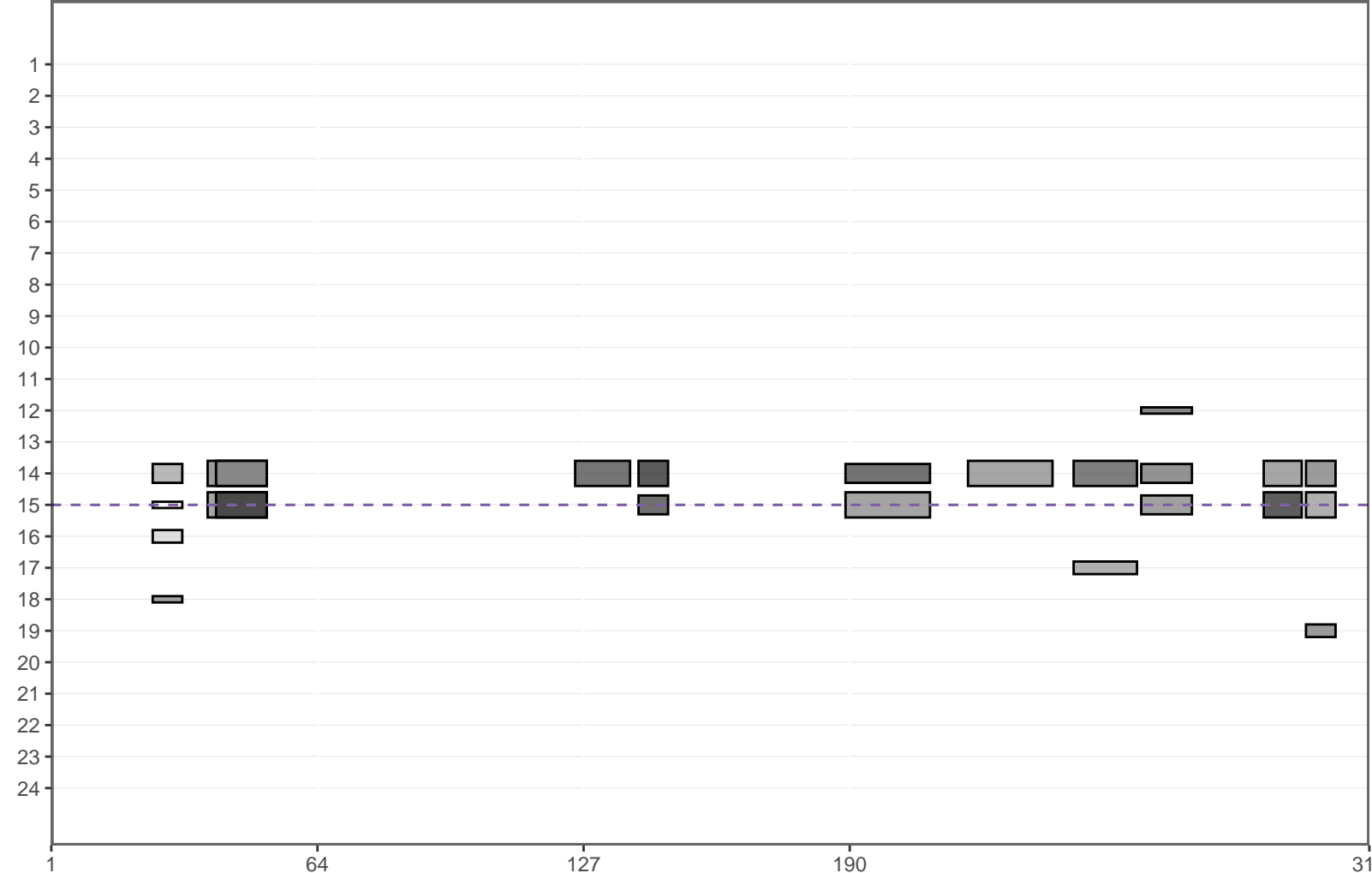
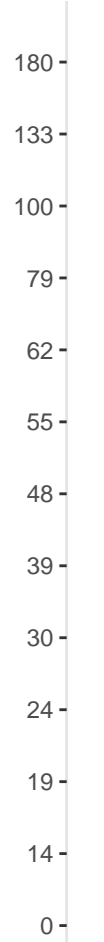
KPCYVEFELYLYAEKITGKLGSGTDLGDGQVWRFFLWLVNNEIRVDLPSGGSYFQVGHNKKLDMMNGFETVHSGRDNALCGGSLRQVLQLPDPVNDMPMLTE*

NbL06g19340.1 serine/threonine-protein_phosphatase_PP2A_catalytic_subunit [MW = 35.64 kDa]



Molecular weight

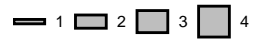
Gel Slice



Protein sequence:
 NVWKTFLDFDYFPLTALVESEIFGLHGLSPSIELDNINRFDVRVDEPHFEGAMGDLWSPDRDGGWGSPPRGAGYTFGGDSEGFNHTNKLKIHARAHQLVMEGFNWAHDQKVTTFSAFNYCYRGNMMSILEVDDERERTFQGFEPAPRRGEPDVTTRTPDFL*

NbL06g19240.1 importin-5-like [MW = 123.2 kDa]

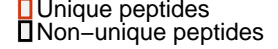
No. of times detected



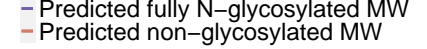
log(intensity)



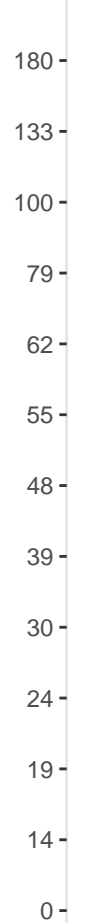
Values from



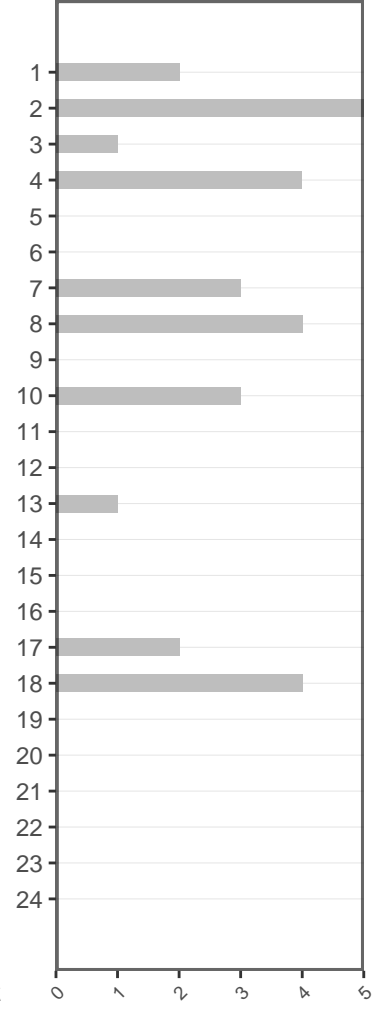
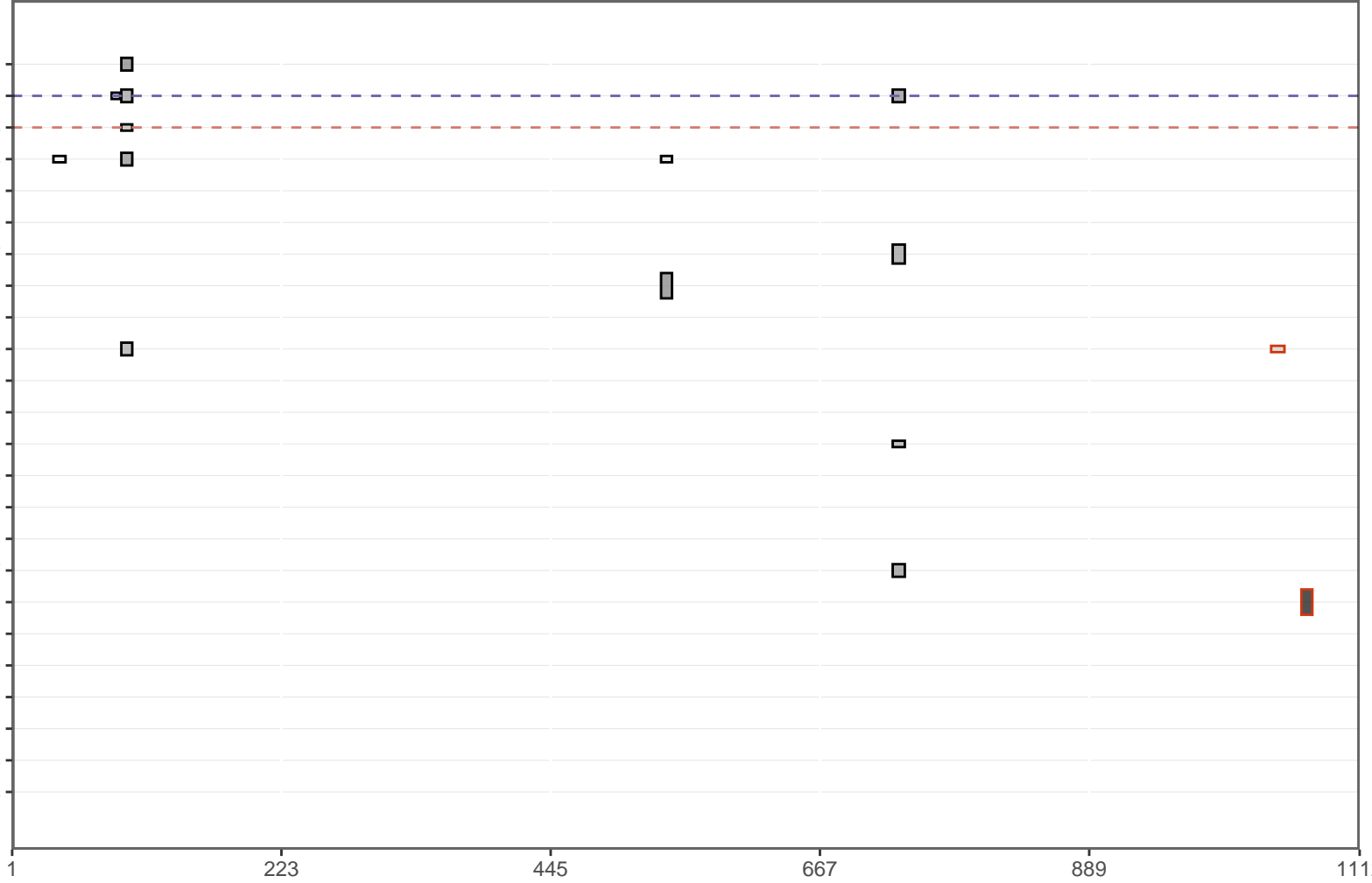
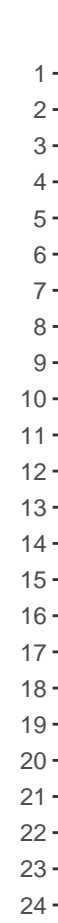
MW indication



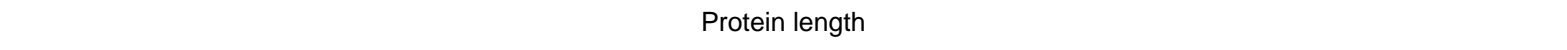
Molecular weight



Gel Slice



Protein length

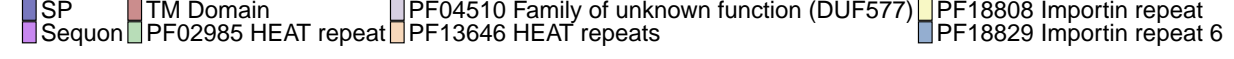


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KTILVNDKSNRMLRAKAMEGIGLVGMVAGKEKFRDDAKGVMEVLMISLGGSGMETDDPTFTSYMLGAWARLGGKLGDFLPMVSVVMPPLIQQSAQKPKDVTISGADSDNLEDESDDDMETITLGGDKRIGKTSVLEEKATACNMLGGVADELKEGFPYVWIDQVAPTLVPLKFFYHEVYRKAASAMPPELLRSAKLAVEKGIAGGRNESYVKQLSDVHIFALIEALHKEPDTFEGASMLDAINEGVQISGPLLDEGGVRSIVIEEIKGVITASSRRKRERARAKAEDFAEENE

NbL06g19230.1 uncharacterized_LOC104209961 [MW = 46.08 kDa]

No. of times detected



log(intensity)



Values from



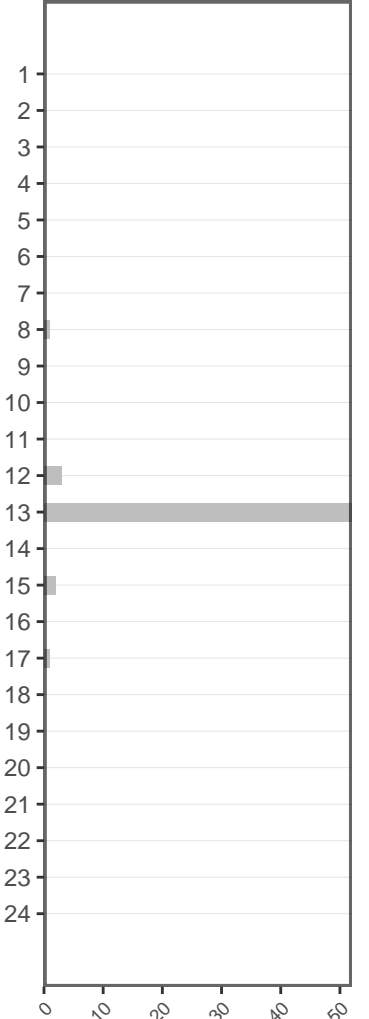
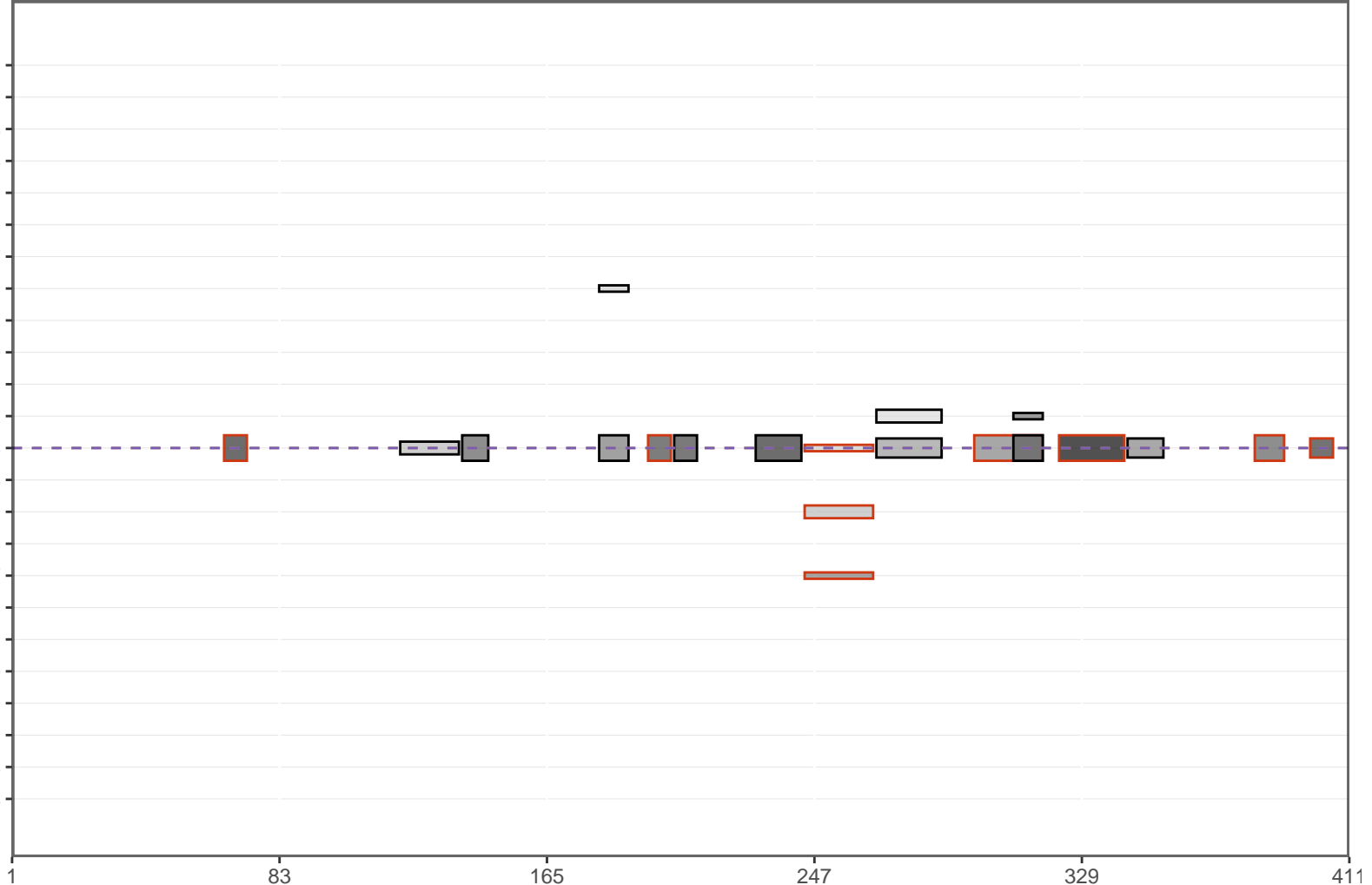
MW indication



Molecular weight

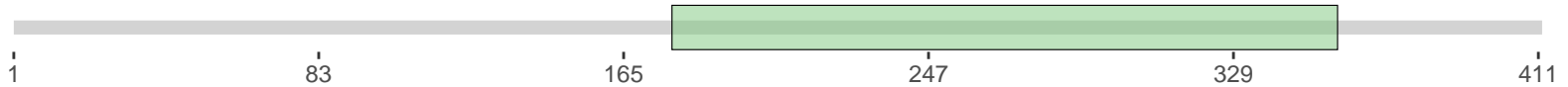


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

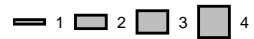


Protein sequence:

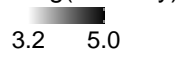
1HGERATSMTTYRDALISGWKGDMPFRFDVWDLKILADLTEREDDSSRIGITGSELGGMHWFAAFADSRWVVPPIGVGGFQWAEHDRWGRVDSKVFEEACADLGNKEIKEVVQKVVDRAPGLASQLDSPYTVFVAPRPLLLINGAEDPRCFIAGLDIPKSRTHKAGENAGCLPLFKVIAEAGGIGHKMTPLMVKESNWFDRFLKVV

NbL06g19210.1 mitochondrial_amidoxime_reducing_component_2-like [MW = 35.42 kDa]

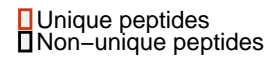
No. of times detected



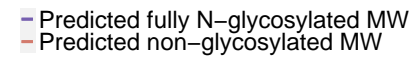
log(intensity)



Values from



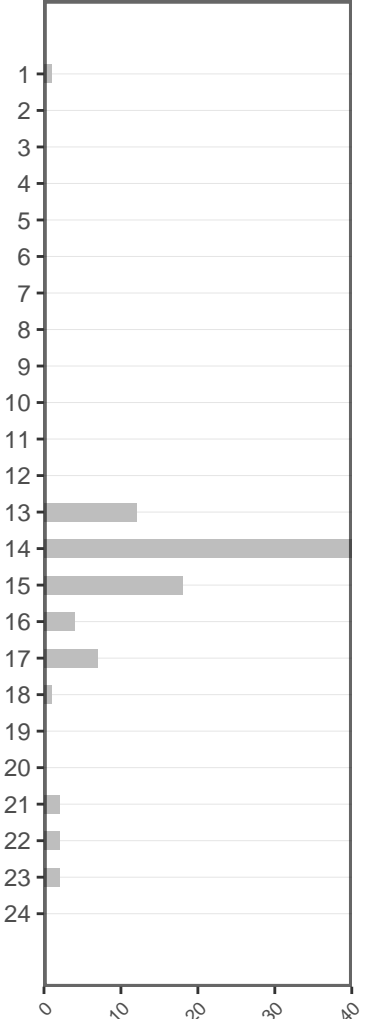
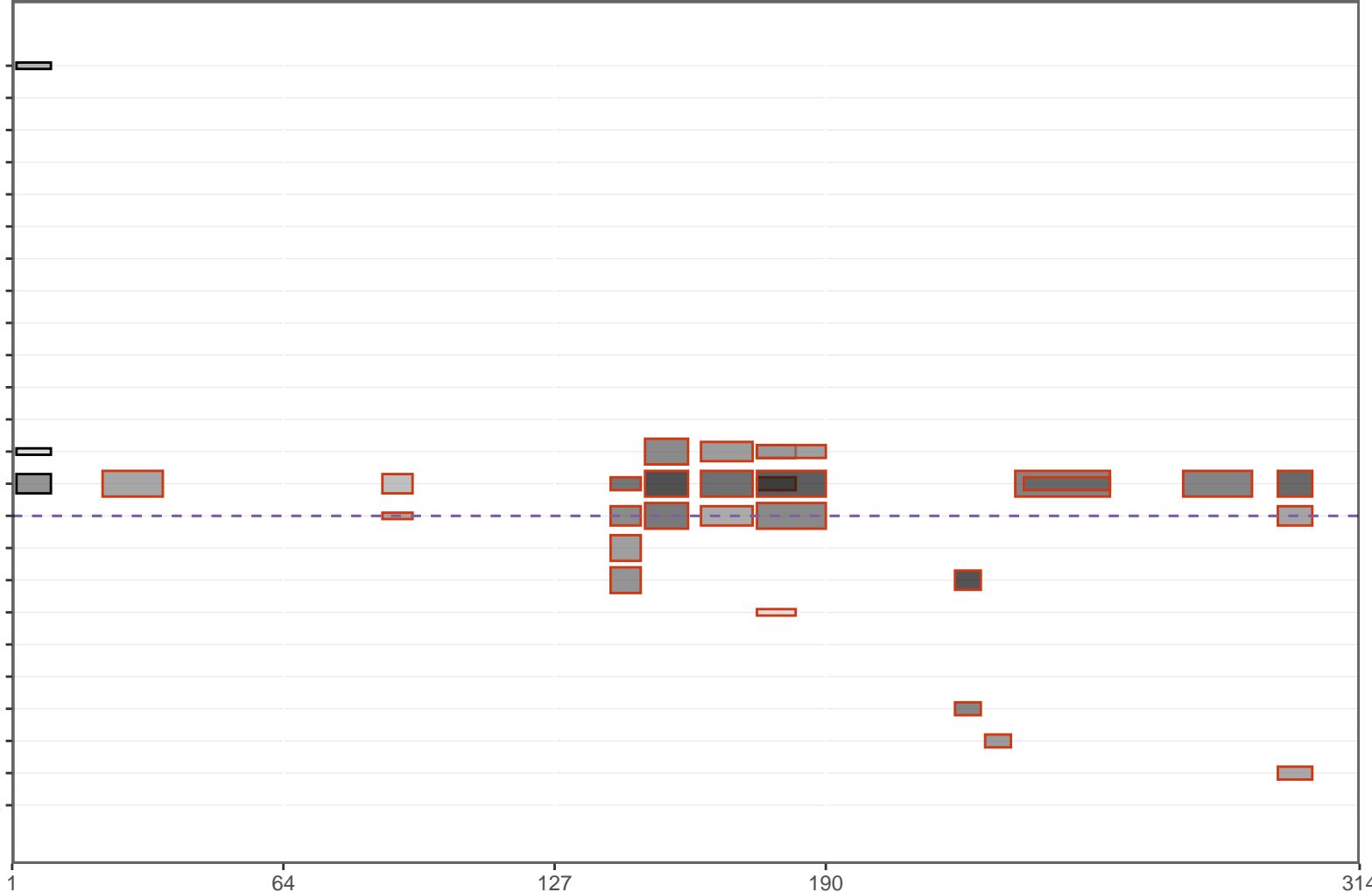
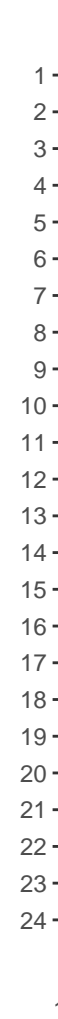
MW indication



Molecular weight

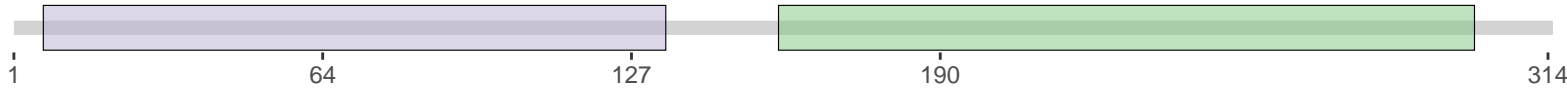


Gel Slice



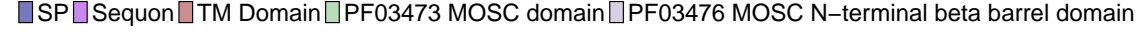
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEVSESLTDPNYAFQYKWKFSDFYFLLISGKSLDLVNEQLKPEFMSINFRFRGKWHAYGIVDQSEFFCEDLWKKIKGENTFRSTELCYRQKIPITNGETAEGPEPSETLWYKFRGDKLTKTKKPKQGRIFYGQNLVIGDLDQEKRTKTRVGGDPVYKIKVSSVVDVSV

NbL06g19120.1 chaperonin_60_subunit_beta_2_chloroplastic [MW = 65.26 kDa]

No. of times detected



log(intensity)



Values from



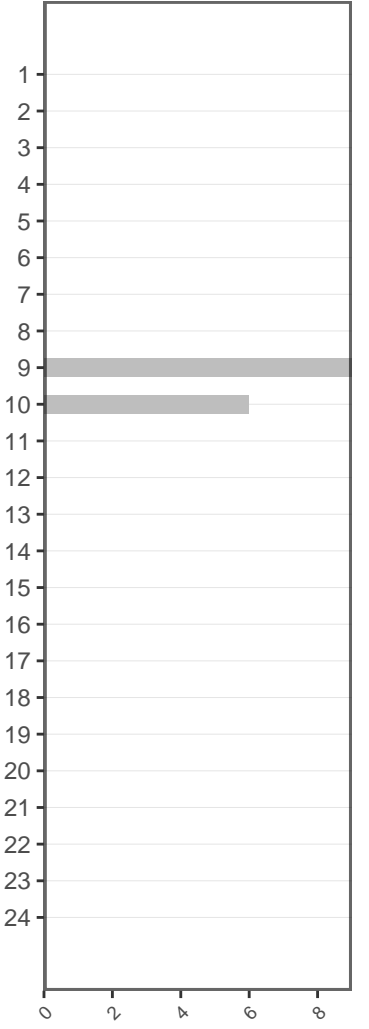
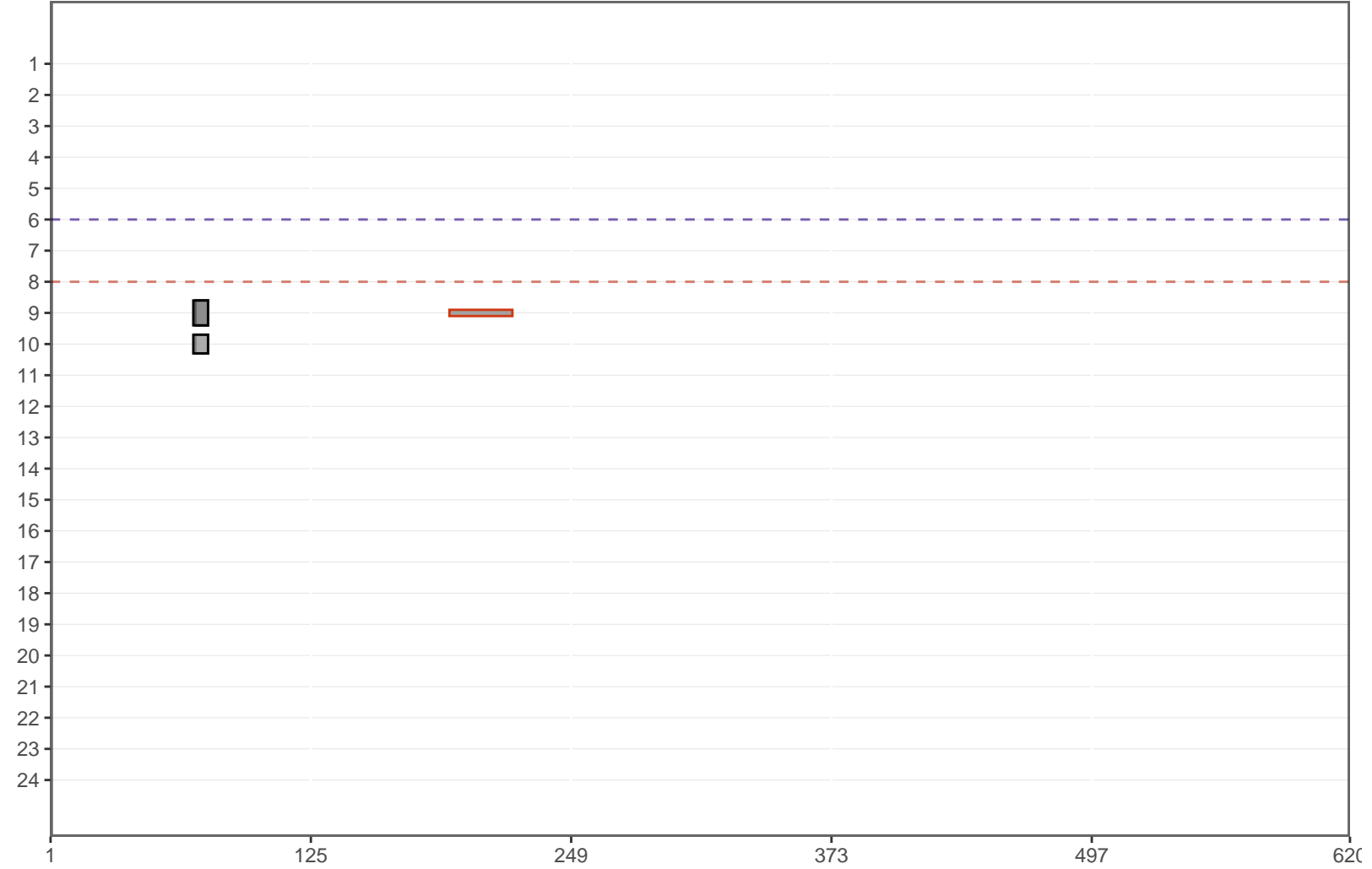
MW indication



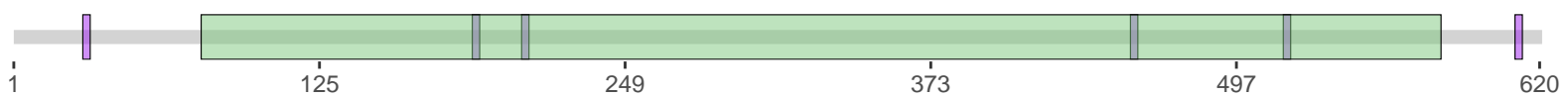
Molecular weight



Gel Slice

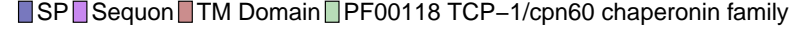


Protein length



Pfam domains

Pfam Description



Protein sequence:

IRNGYPLIIAEDIEGEALATLVNKLKRGALKVAALKAPGFRERKSGVLDIATLFGGTVRDELGLTLEKADKEVLGHASKVYLTQDATTIVGGSGTQDAVNRKVAQINKLIEAADDQVYEKELNERIAKISGGVWVQVAGTETELKEKIKRVEDALNATKAAVEEGIVGGGCTLLRLASKVDAKETLENDEEKVGDIVKRALSYPLKLAKNAGVNSVSEKVLSSDNPKFGYNATGNVYEDLMAAGIDPTKVRVROGLEHASSVAKTFLMSDDVWVEKEPEPVAAGSPMD

NbL06g19080.1 uncharacterized_LOC104245894 [MW = 76.08 kDa]

No. of times detected



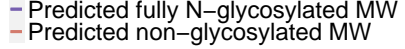
log(intensity)



Values from



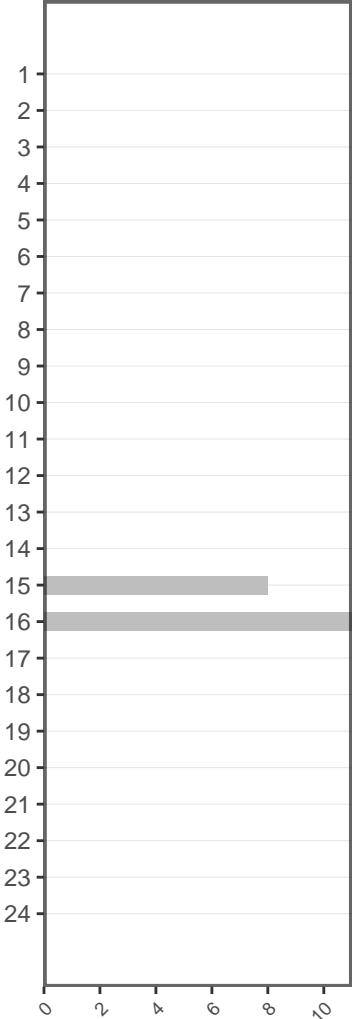
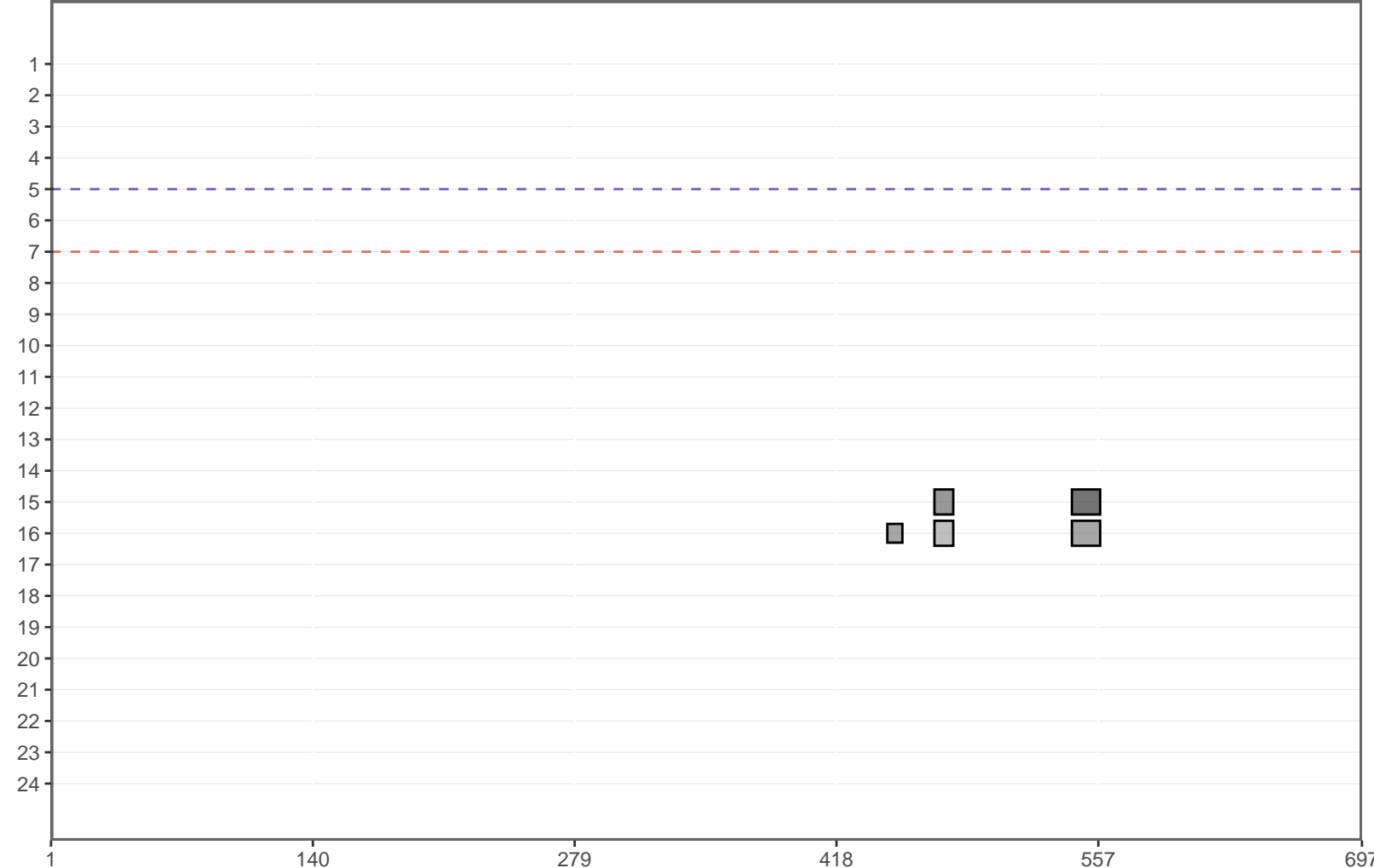
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GSNRYDSRATGRGWTFVDFNRFPRGRGNSFYGYGNENMDGLNELNRGPRGKSGKNGKGFPPALAVKGNPLFTVNDAEKDKGSLIPDKGQVNHDPDFVYTDKAFYKSYSEDDHKKIKYNYWASTPNGNKKLDAVGEAQKSGGGCPFLFFSVNTSGDFVGVVAEMGPVDKNSVEYWGQKWKGGDFVYKWHVHKVDFNSLLKHITLENNENKPVVTSNRDTGVEVMGGLGVKFKDHSKGGILDDFEFVEDRQKRIGERKAKQKQFQKQSOVVEEGKATE

NbL06g19060.1 2-oxoisovalerate_dehydrogenase_subunit_beta_1_mitochondrial-like [MW = 42.76 kDa]

No. of times detected



log(intensity)



Values from



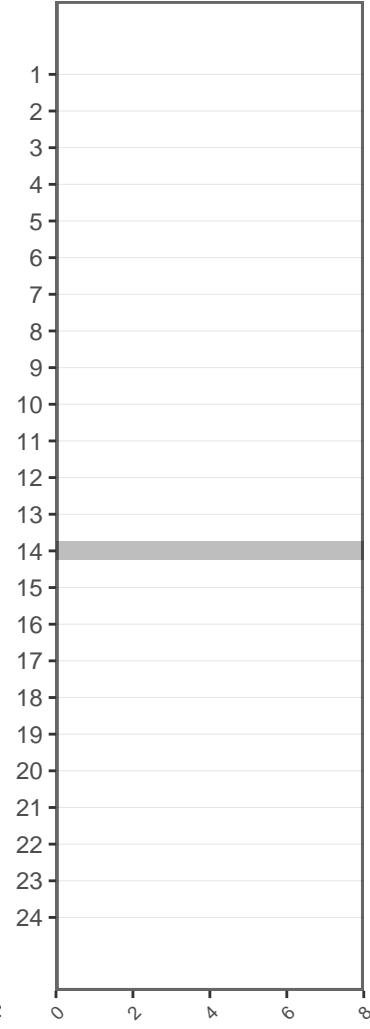
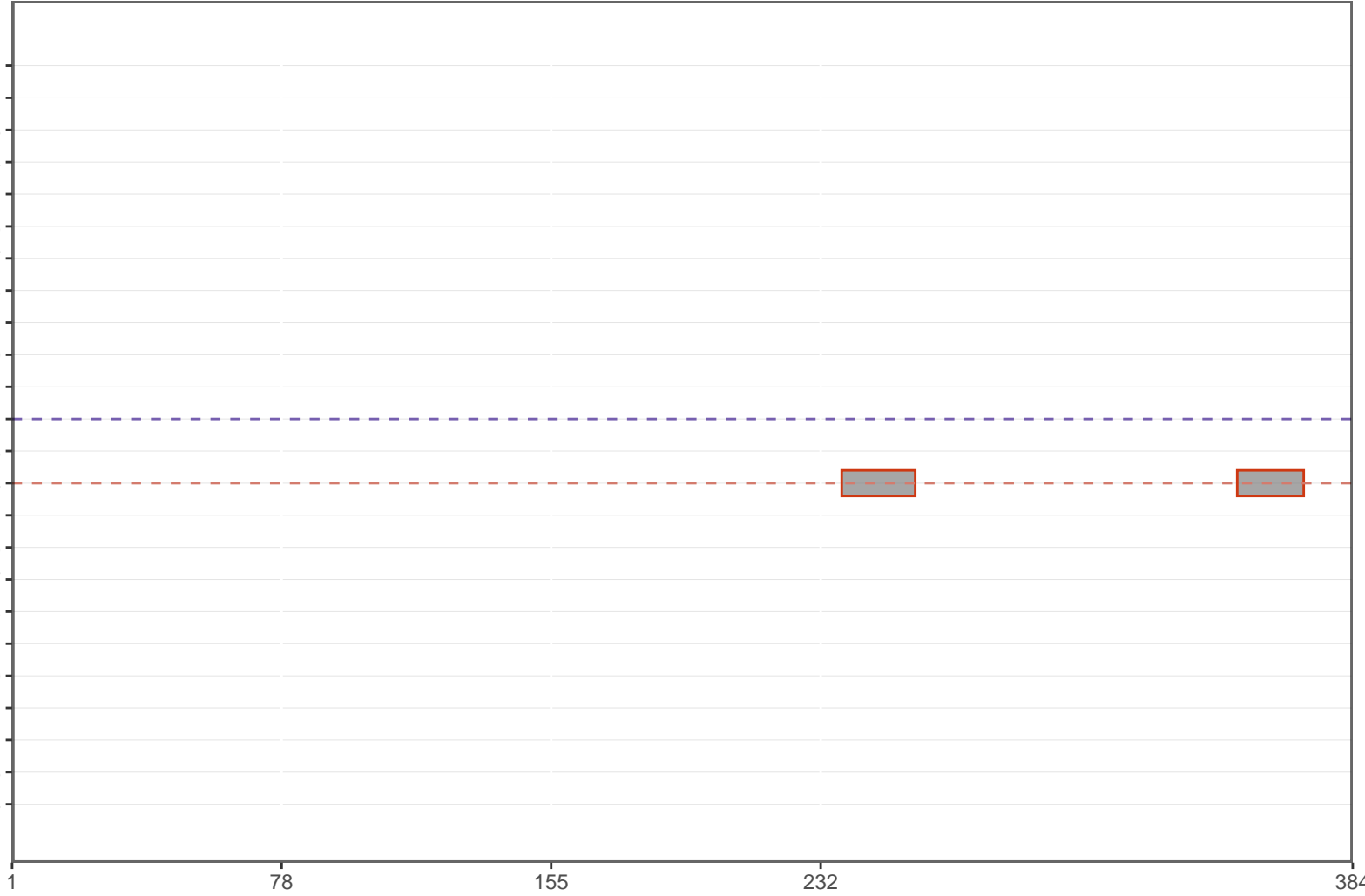
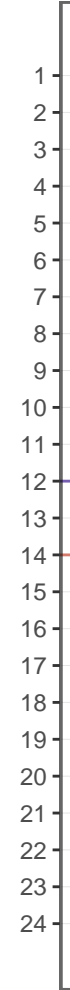
MW indication



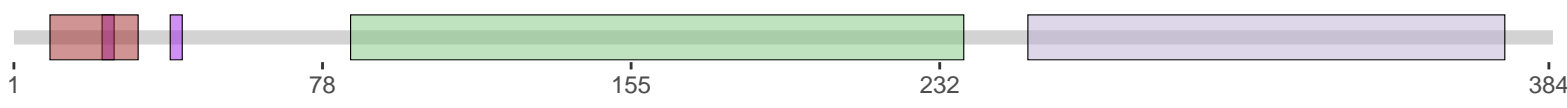
Molecular weight



Gel Slice

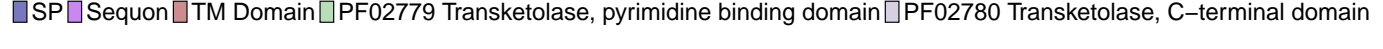


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VVGHGGIYHSQSPSEFFQHPGKVVVIRBPHQAKGLLSRRDNPVVFGEKMLYRMAVEEVEVDVMLPLSEAEVIREGSDTLVGVGAGLSTMEQACIEAAKEGISELIDKTLFVWDKETVEASVWKTGRLLVSHAPVTVGGFGAIEASIVERGFTREAPVAVVQGLDTPFLVFEFYMPTKNIKLDIAKSTVNY

NbL06g19040.1 sm-like_protein_LSM7 [MW = 10.71 kDa]

No. of times detected



log(intensity)



Values from



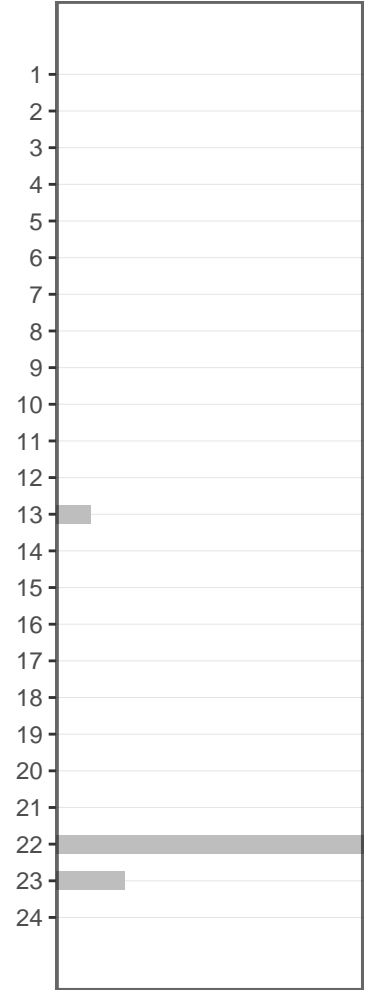
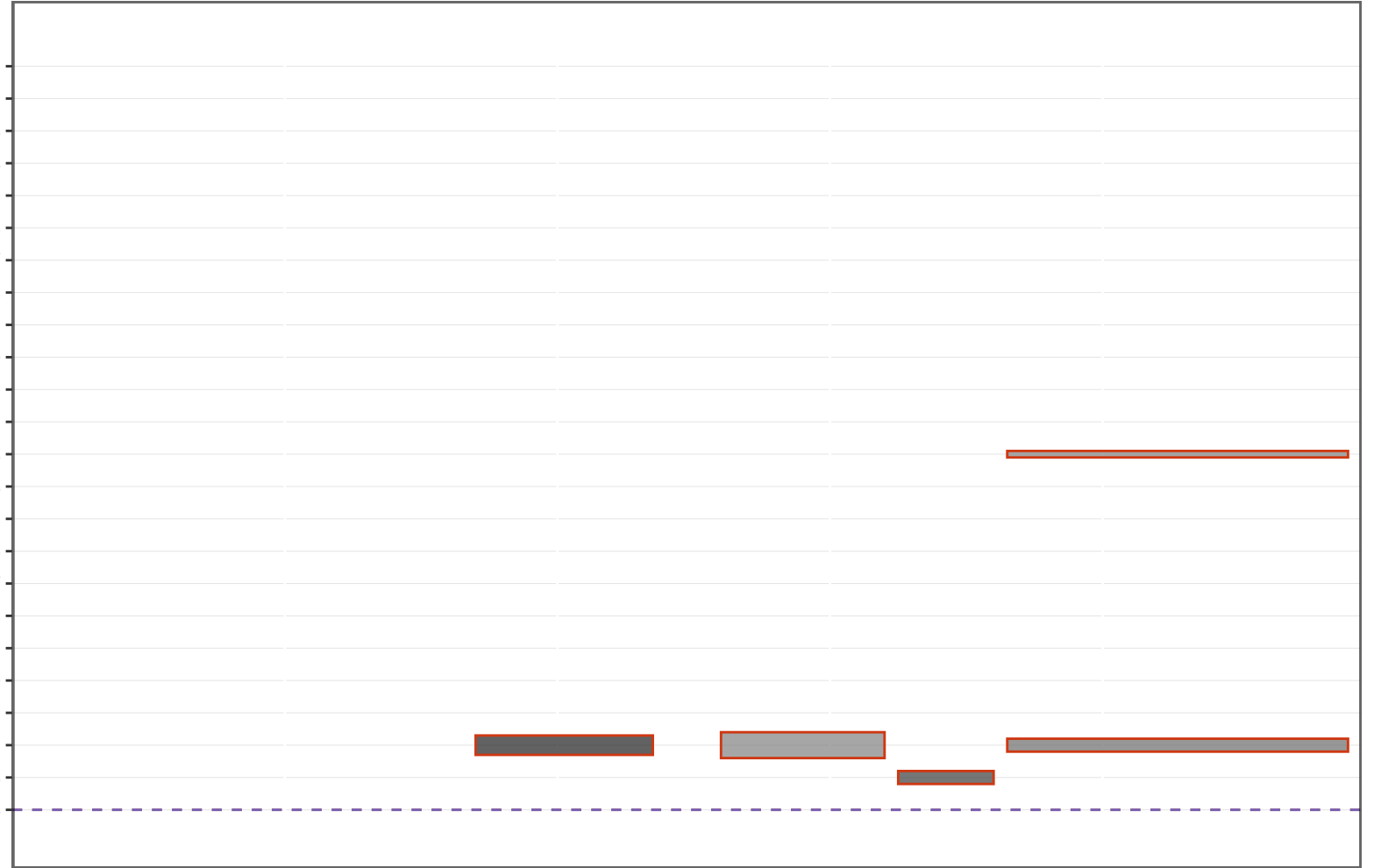
MW indication



Molecular weight



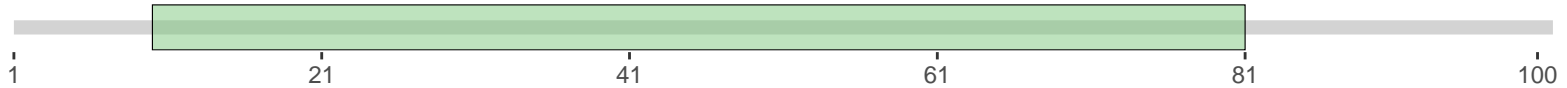
Gel Slice



Peptide counts over 4 repeats

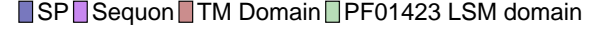
1 21 41 61 81 100

Protein length



Pfam domains

Pfam Description



Protein sequence:

FDQLLNLYLDEAKEVLRDADDPKLTFTGTRALGLVGRGTAVMLVAPTDGTDSEINPFVQPDGA

NbL06g18990.1 pyruvate_kinase_cytosolic_isozyyme [MW = 54.95 kDa]

No. of times detected



log(intensity)



Values from



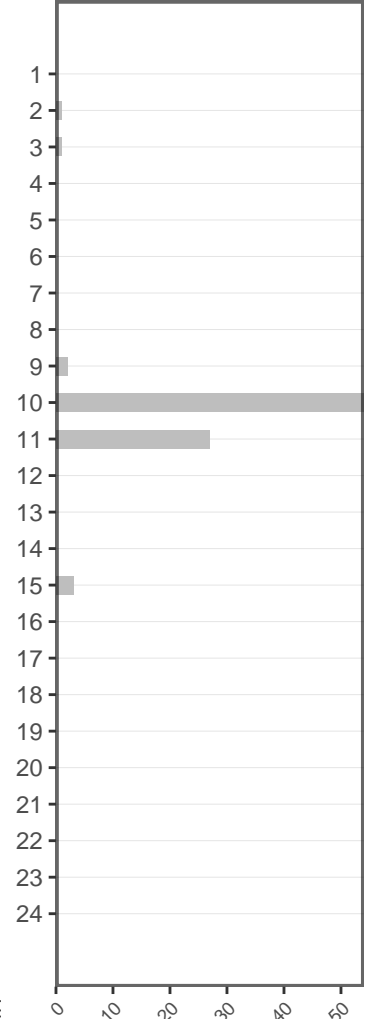
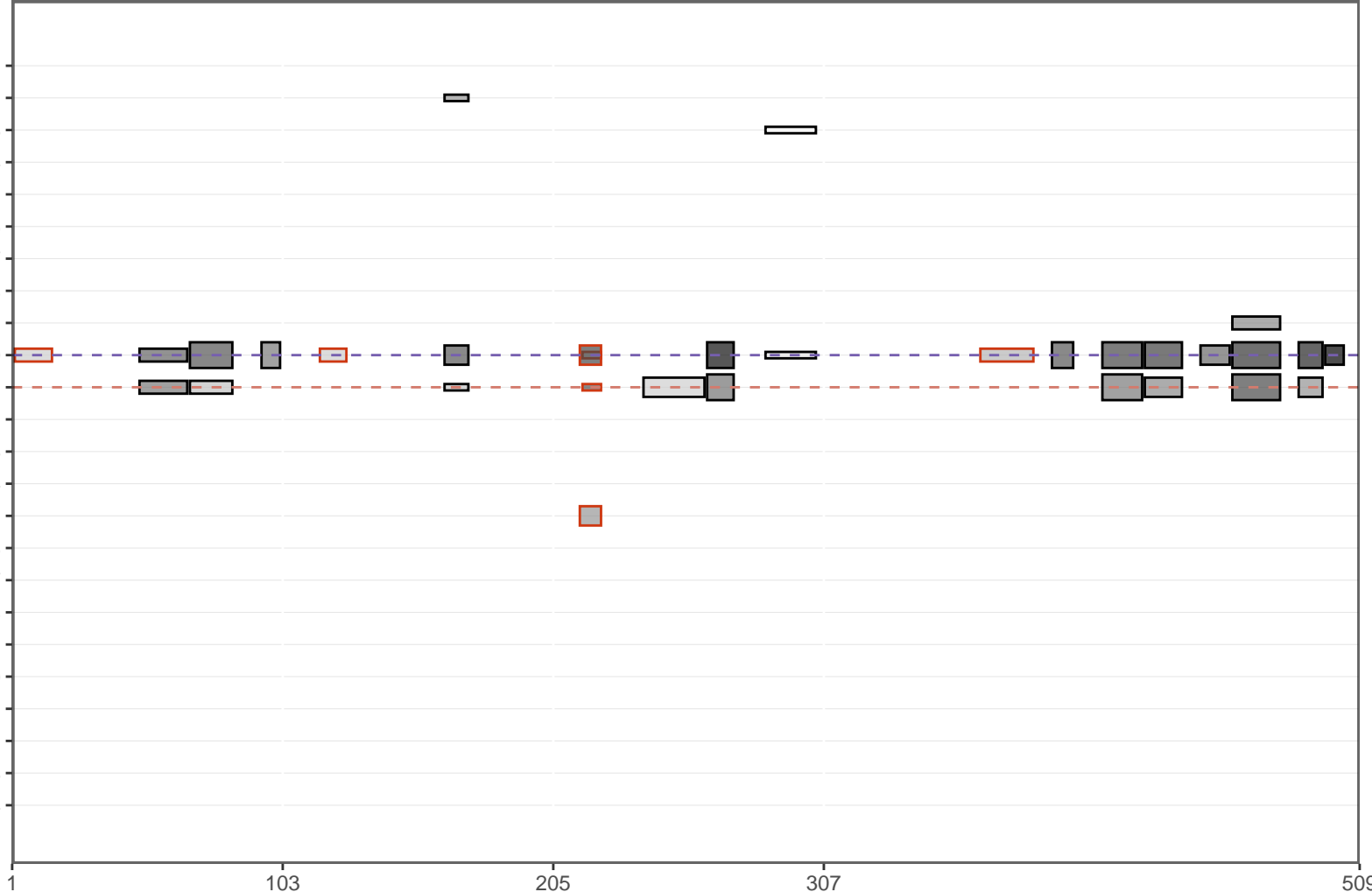
MW indication



Molecular weight

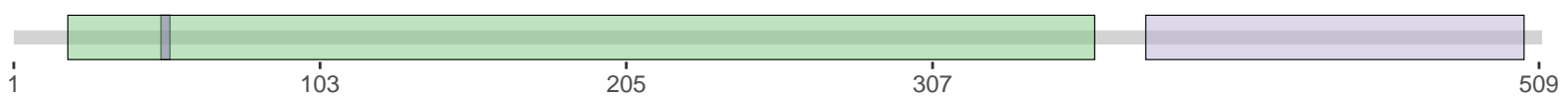


Gel Slice



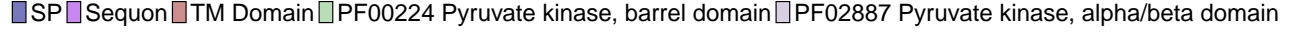
Protein length

Peptide counts over 4 repeats



Pfam domains

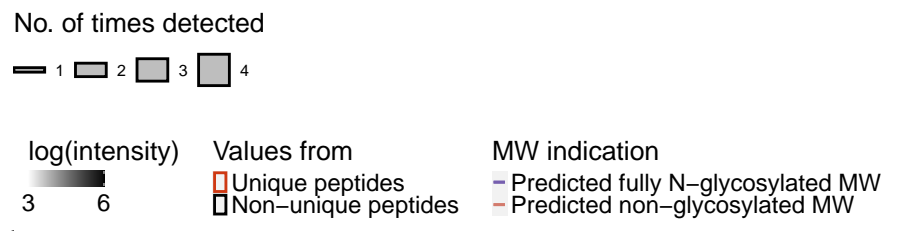
Pfam Description



Protein sequence:

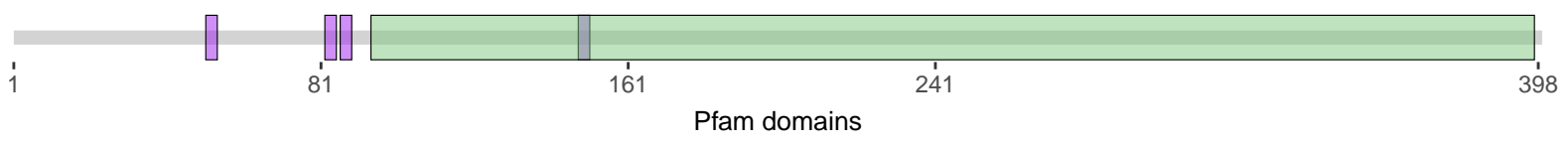
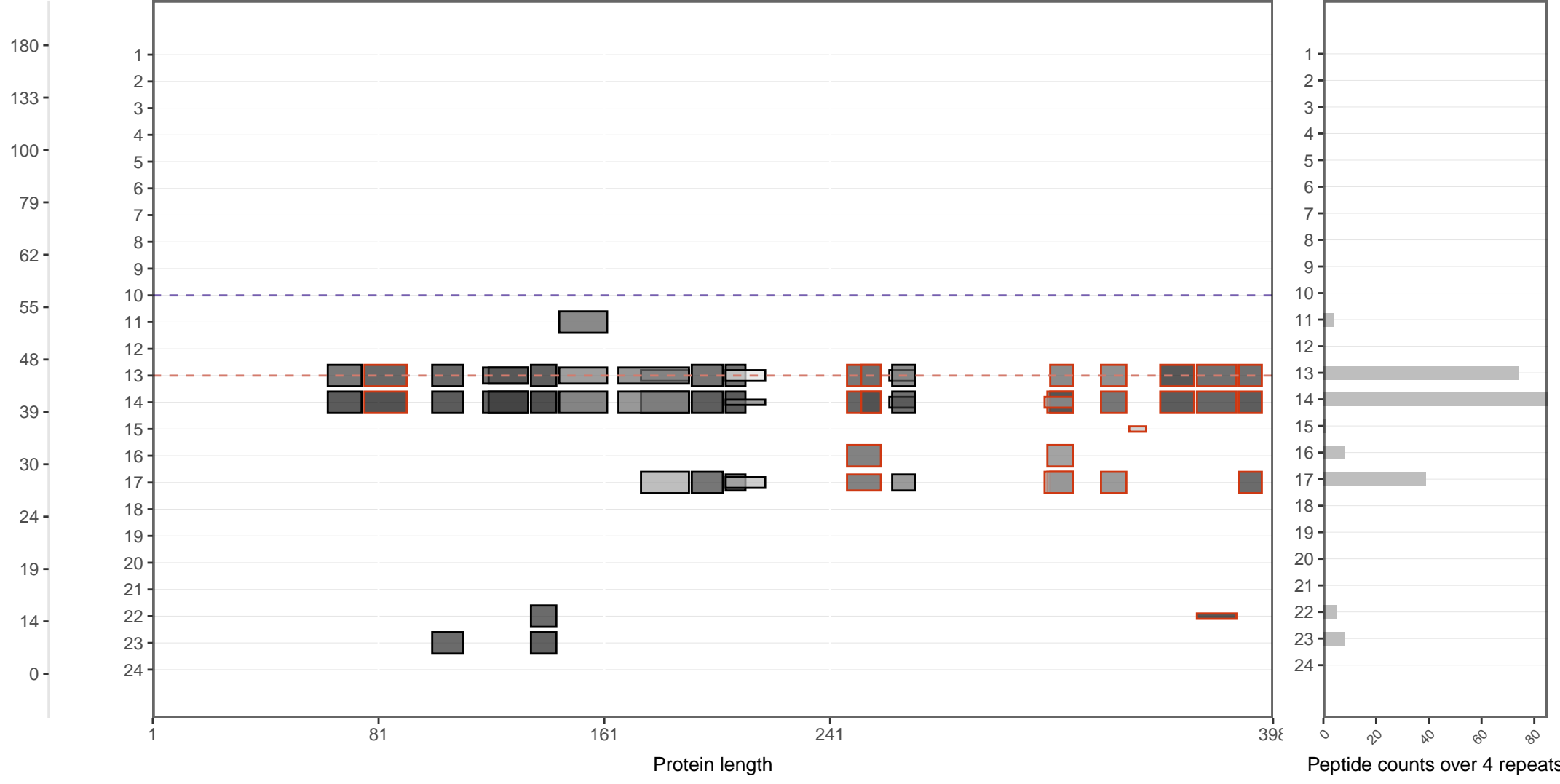
INDEGVAFDDLLNSDFMVARGDGLGMEIPKIFLAGKVMBSKNGGKPKVVTATQMLESMKSPRPTRAEATDVAANVLDGTDQVMSGETAGAYPLAVGTMAKIGIEAESTHYFDVFKRIMANAPVPMSPLELASSAVRTANSAKAAVILVTRGGSTAKLVAKYRPMPLSVVYPERKTDSDFTWTCGSDSPARHSLFRGLVPLVHAGSARASHEESTEEALDFALGHAKTKGLGKGGDSVALHRVGTAVKIKVTKI

NbL06g18830.1 oxygen-dependent_coproporphyrinogen-III_oxidase_chloroplastic [MW = 44.85 kDa]



Molecular weight

Gel Slice



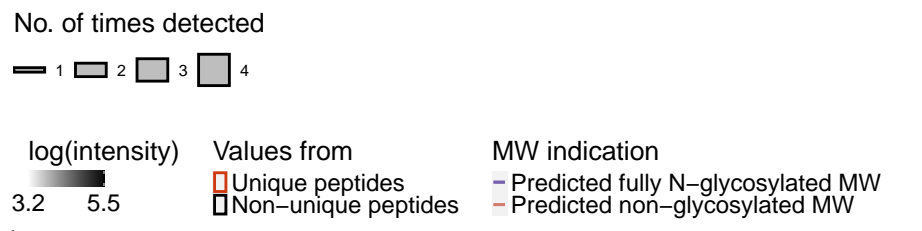
Pfam Description

- SP
- Sequon
- TM Domain
- PF01218 Coproporphyrinogen III oxidase

Protein sequence:

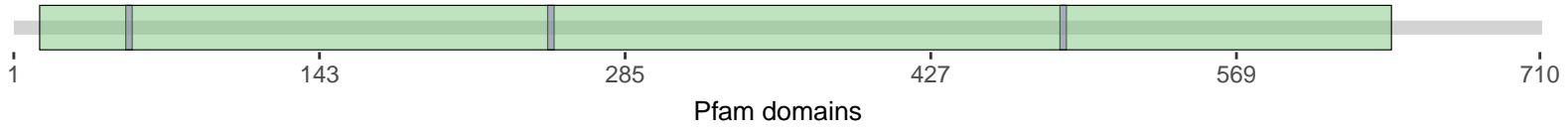
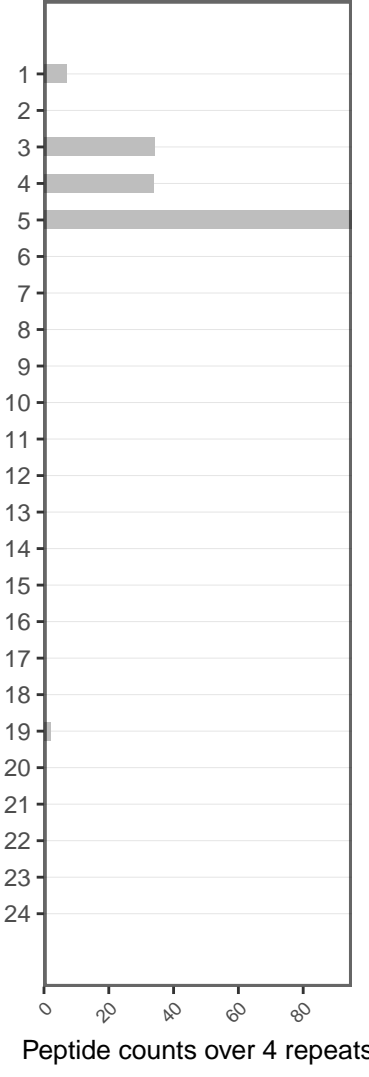
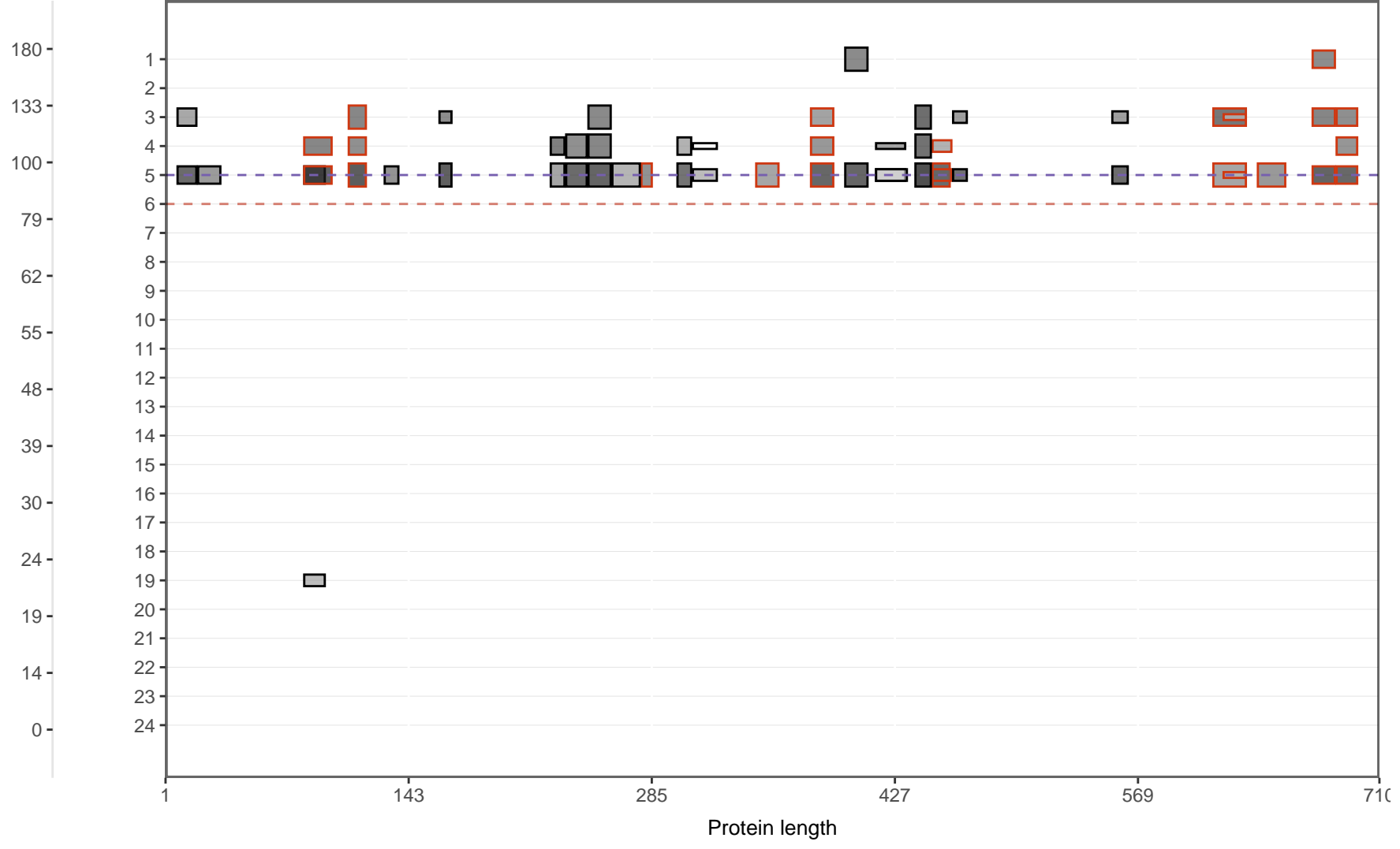
SSVLIHPKQNPFAPTLHFNRYRFETDAKIDAPKAPRQWVFGGGTDFTRWVFEEDVKHHSVQKAAAGDKFDFPSFYPRFKKWDQDFYKWRDERRRGLGGIFDDLNLDQEMLLSFGSTECANSVIYVPIEKRRKDDPTFDEHKAWQGLRRGRHYVEFNLYVDRTGTFGLKTTGGRIEELVSLPALTARWEYDHKPEEGTEEWKLLDAGINPKEWI

NbL06g18700.1 4-alpha-glucanotransferase_DPE2 [MW = 82.38 kDa]



Molecular weight

Gel Slice

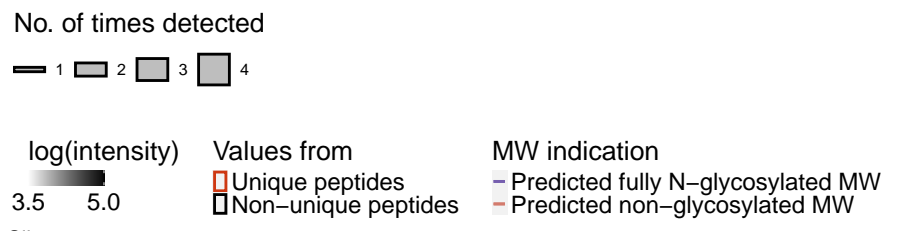


Pfam Description
 SP Sequon TM Domain PF02446 4-alpha-glucanotransferase

Protein sequence:

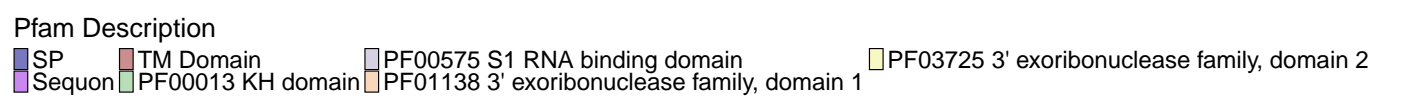
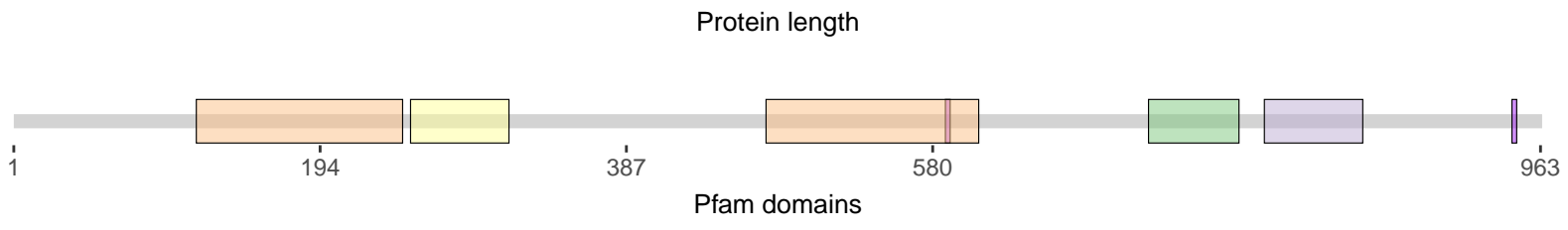
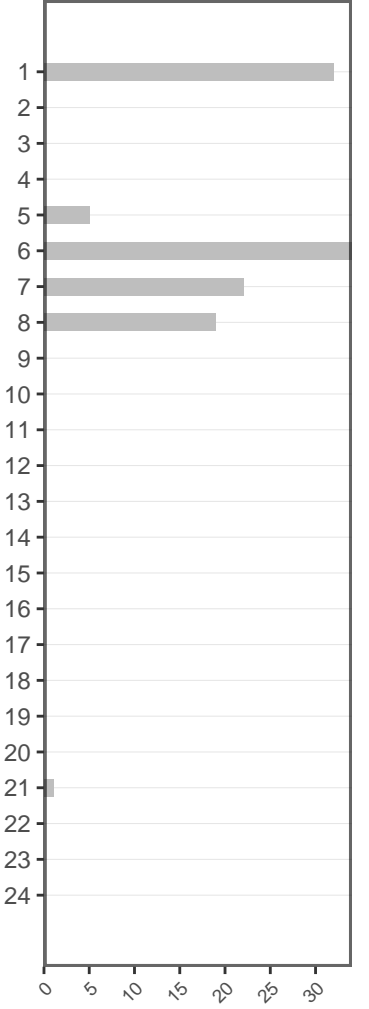
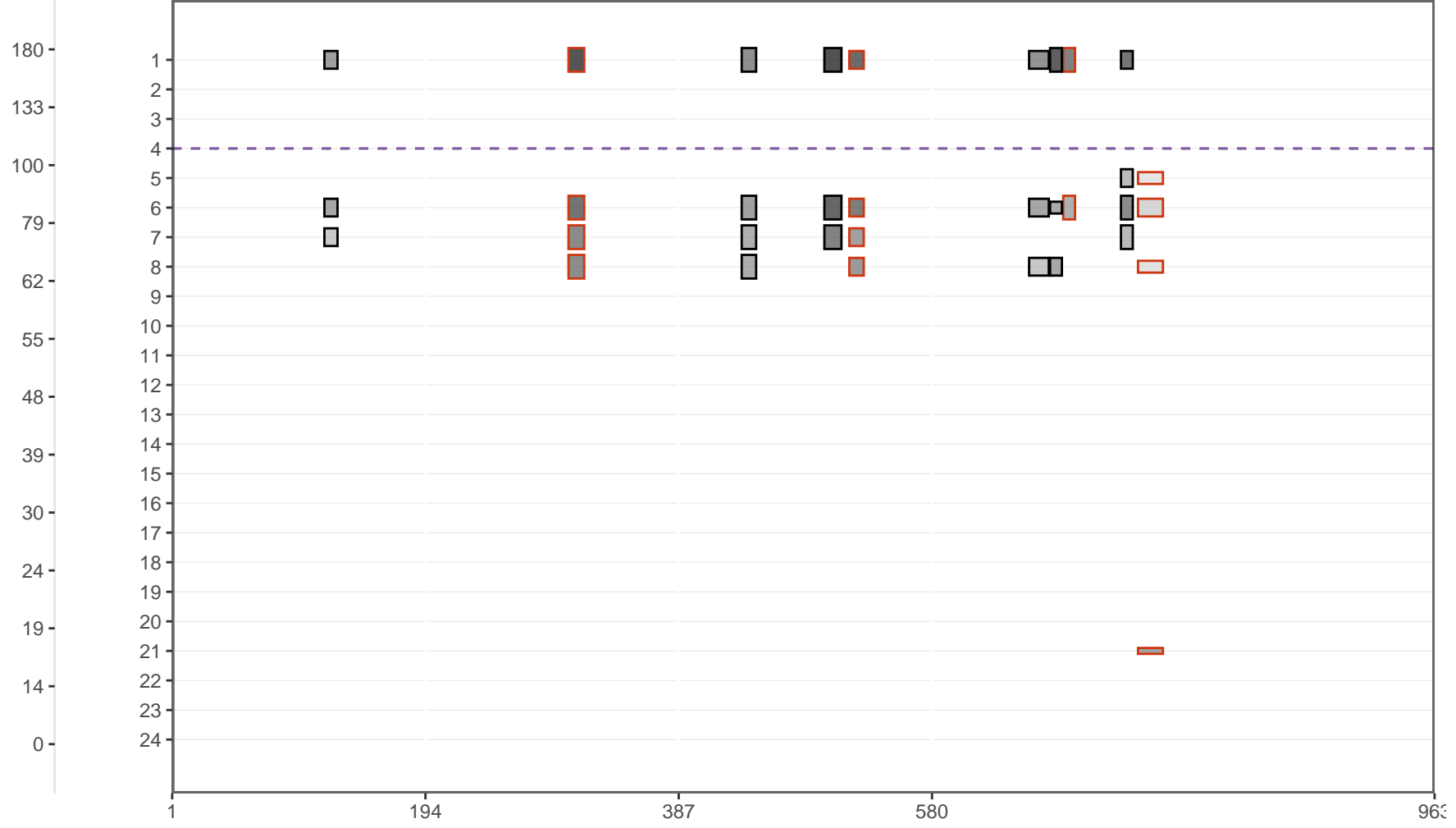
DFNRLTQPIYGQELLDENFGASWTHASTFLNEVQKGFYEFKKECNTTEEKIAVLSKSFLETSMVLESEKLRRLKFDLGNVALKDPEDLRKFRFRNIEDTTSFKDLQHSQVLRKRYDYDFYFRQEGELWRQNAKTLPLVLLNSNMLACGEDLGIPIQSVHPVMDGELGLVLRQRMNPEPGLFQIPGQYGYMTVQAPSDHDCGTLRAWVEEDEERRHRFFQAVVGSDELPPDQGSPEVHFVLRGHVEAPSMWISFPLGDLALAKEDKTRRPAEETINDPTNPKHY

NbL06g18610.1 probable_polyribonucleotide_nucleotidyltransferase_1_chloroplastic [MW = 104.22 kDa]



Molecular weight

Gel Slice



Protein sequence:
 RTLQERIVDARCGLLPRAHGSAFTFRGETGSLAVVTLGDKGMAGKIDNLDDEVEYKRFYLYGHSFFPSSVGEAGRVGAPSRREKIHGMIAERALRPLPFEDDFPYTVRVEGTTTESNGSSMSAVVGGGLALGDAGVPPVKDSIAGIAMGMVLDTKKEFGDGTPLHLSDLGSDASGDDMDPKVAGSDVGTAFQMDKDFGGFTLPMKQALLQANDGRKHLAEMSKGSPFPPGRKLSKHAFLIHHVMKVPKINLHGGGKRVKSHIETGVEADTGGDGVYKTKADLSLEK

NbL06g18570.1 39S_ribosomal_protein_L46_mitochondrial-like [MW = 26.98 kDa]

No. of times detected



log(intensity)



Values from



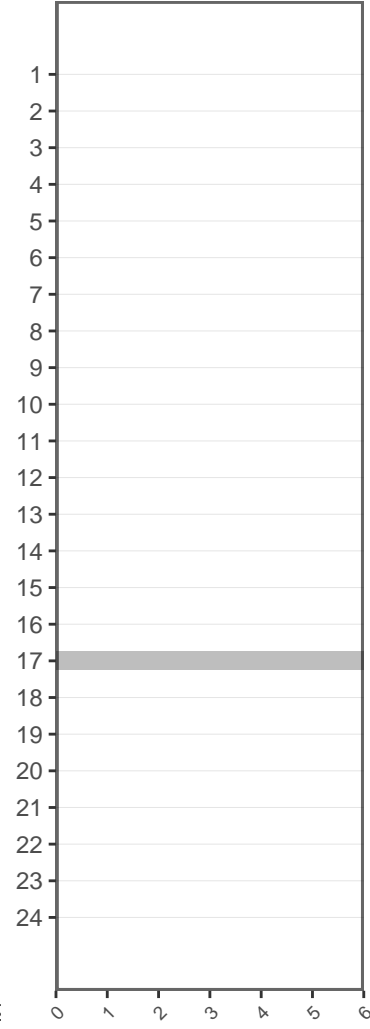
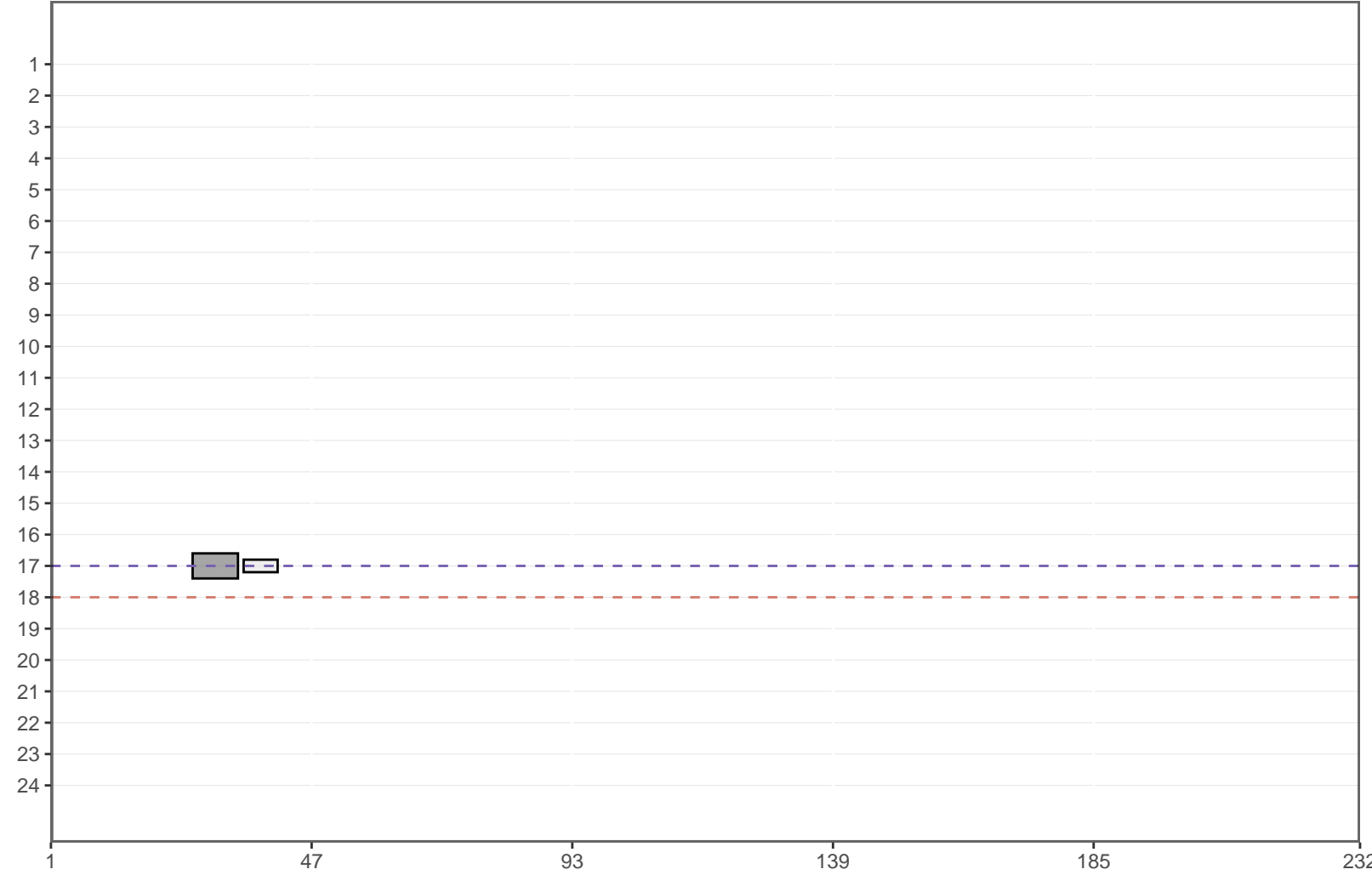
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ORALDKRLVLLVIGTTHGSPSEKPVWHFPEKVVYEEETLRKGAESALESVIGDLSHTFYVGNAPMGHVVQPTAEKENTSPKRRFFKSGVATNKFDIRKGDGFVWVTKDELLEYPEGAFLSKMIS

NbL06g18550.1 IAA-amino_acid_hydrolase_ILR1-like_3 [MW - SP = 45.5 kDa]

No. of times detected



log(intensity)



Values from



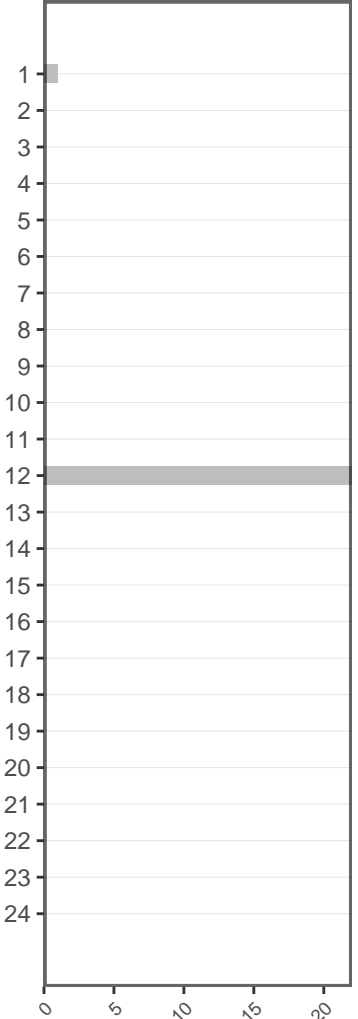
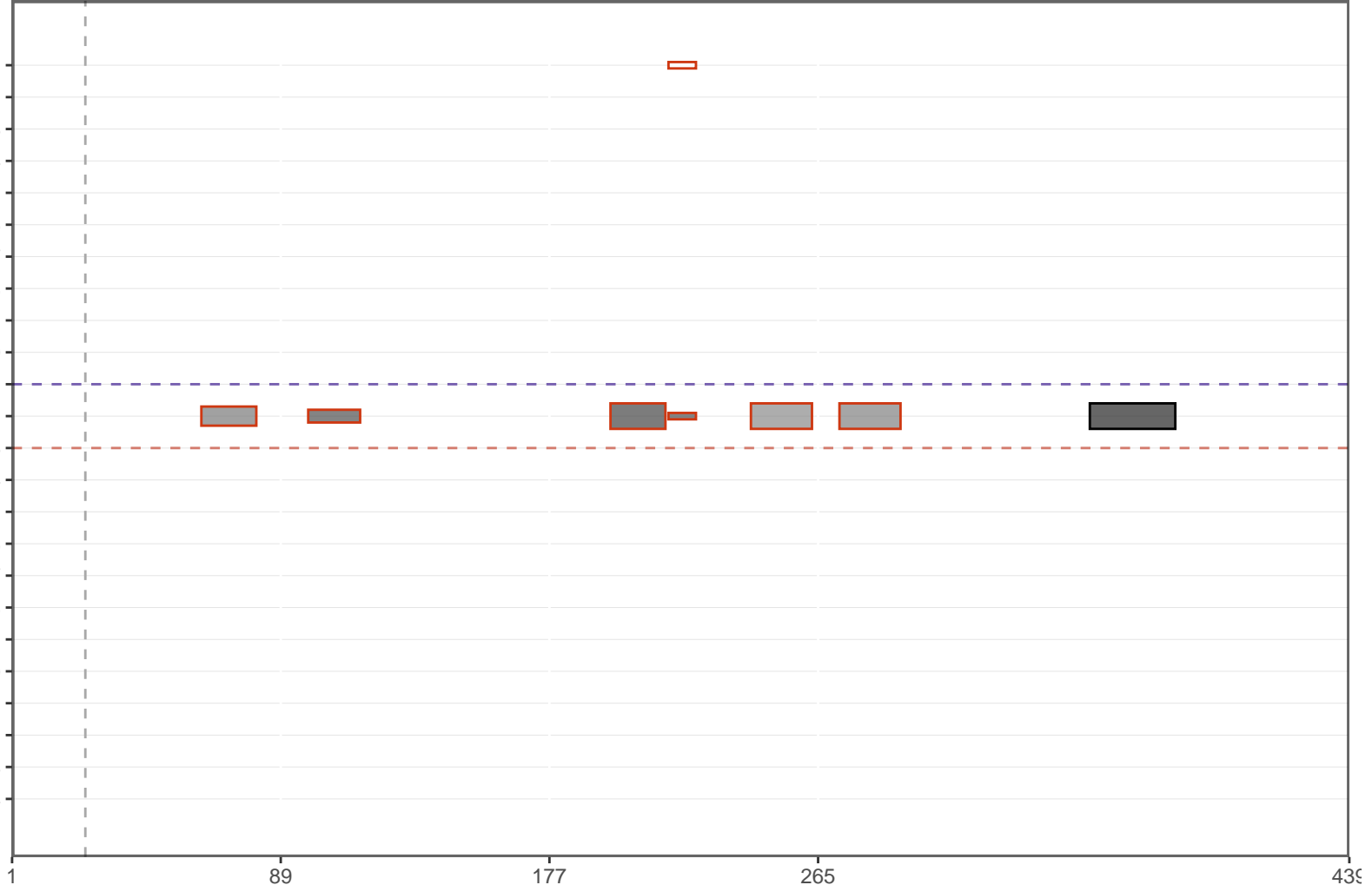
MW indication



Molecular weight

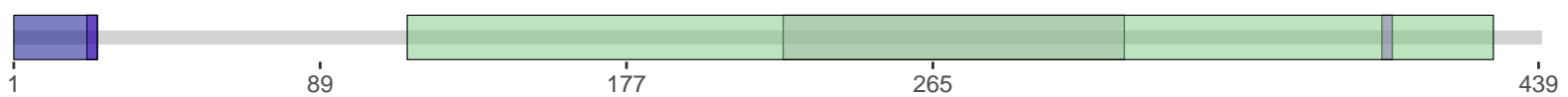


Gel Slice



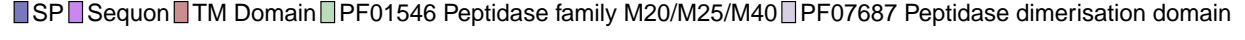
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

PFMPVGTGSKPGRMAGSSRFZAVVQKGGHAATPKIKTRDPLMAASMAVALLOGLISRETDPLFRVAVSVTFVDDGGAGNVPASVRFGGTRFRMTLEGYSYLKORIKETQAGVHQGSATDFMEEMRPYPPTINDPTVDHKKRIGELLGNNVGHSPALMAAEDFGFVSGKMAAAFFFGTGNKTDVSAIKGLHSPYFTIDEIVLPIGAALHAANVAVYLDTHSESE

NbL06g18400.1 DNA_ligase_1-like [MW = 41.94 kDa]

No. of times detected



log(intensity)



Values from



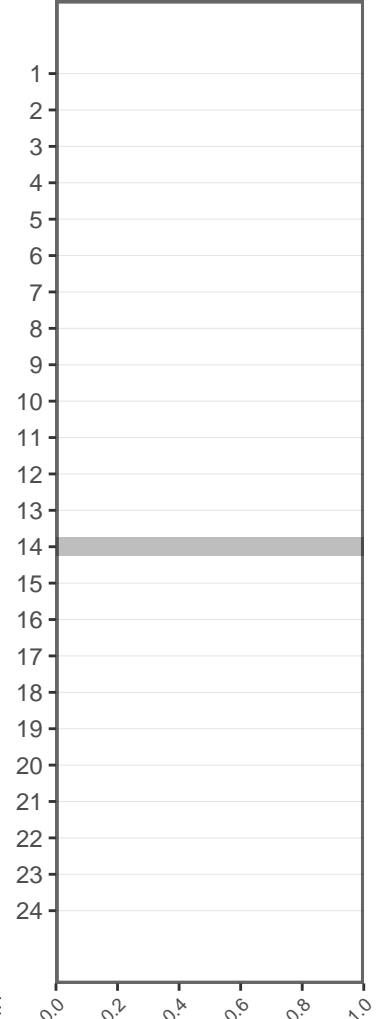
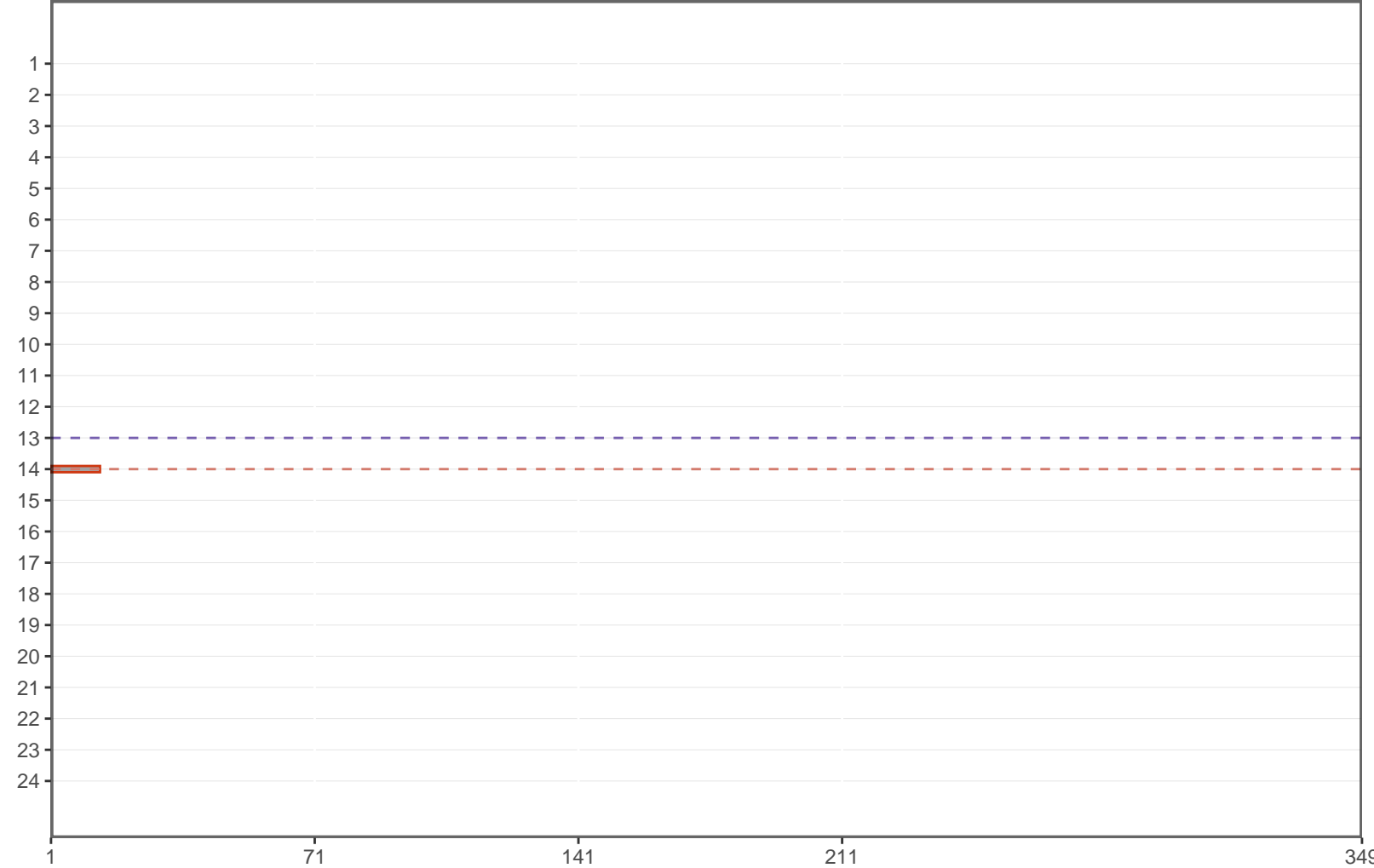
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

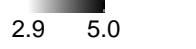
KKDKESKEKEDKSKGDLVEVEGEEEDDKNDKKADEKDKKGGKHKKDKDEEKKEKKEESLEETERKDKKDKKKKKKKEKDKDKKDKSGVLEEEEMEEKDDGKDKKKKKEKKKKEETKGNKTKNRRLEELADLEAHSRKEKETKDKKDKKDKKDKVDEKGRTEVTTREKIGGGENRMPDEEAH

NbL06g18340.1 ubiquitin_carboxyl-terminal_hydrolase_12-like [MW = 134.63 kDa]

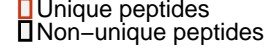
No. of times detected



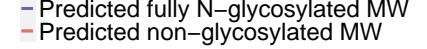
log(intensity)



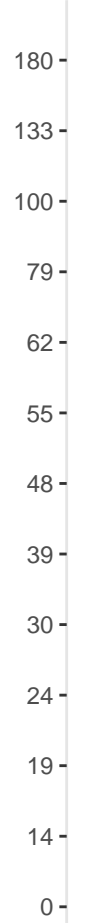
Values from



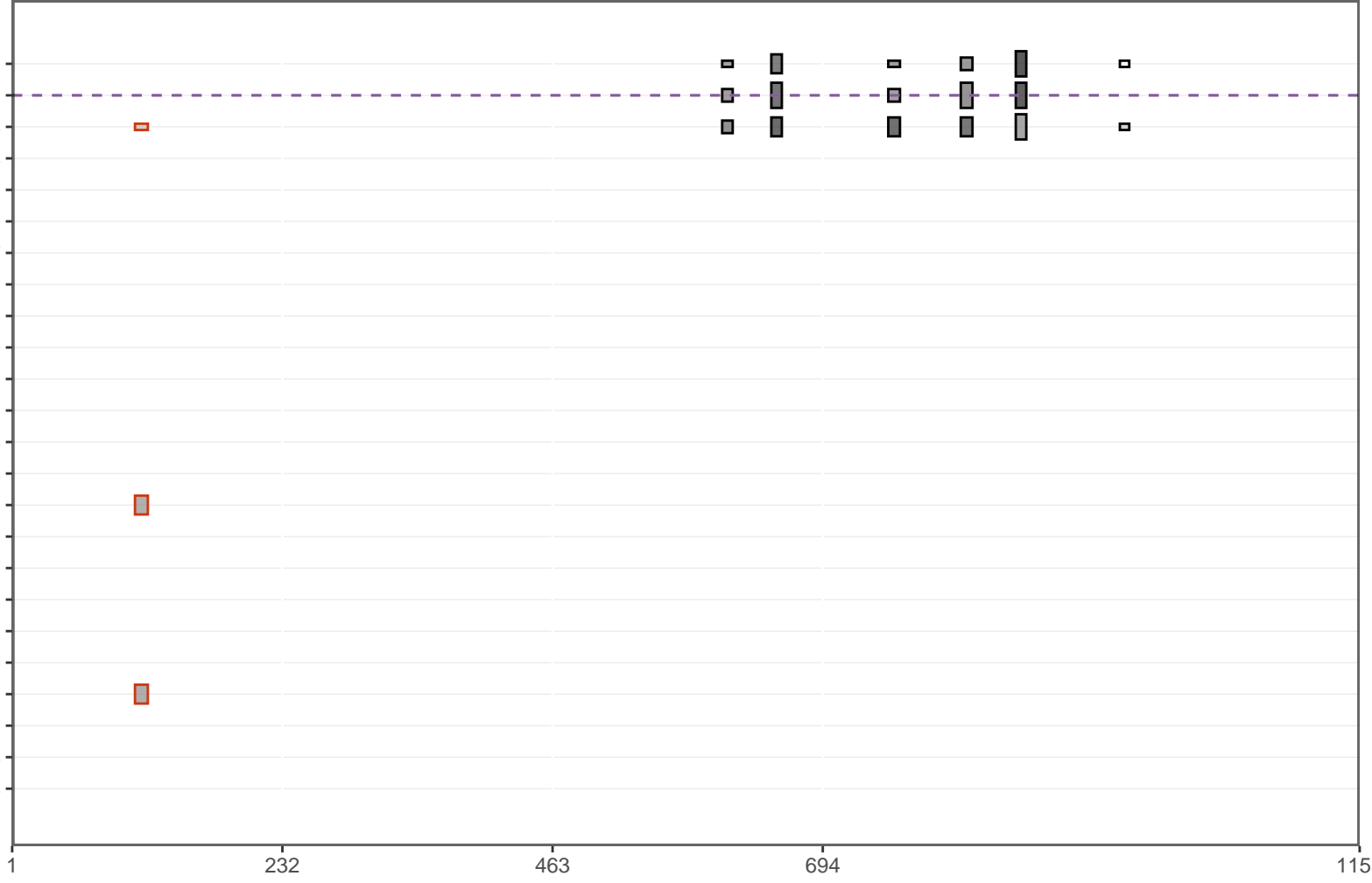
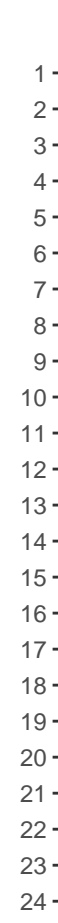
MW indication



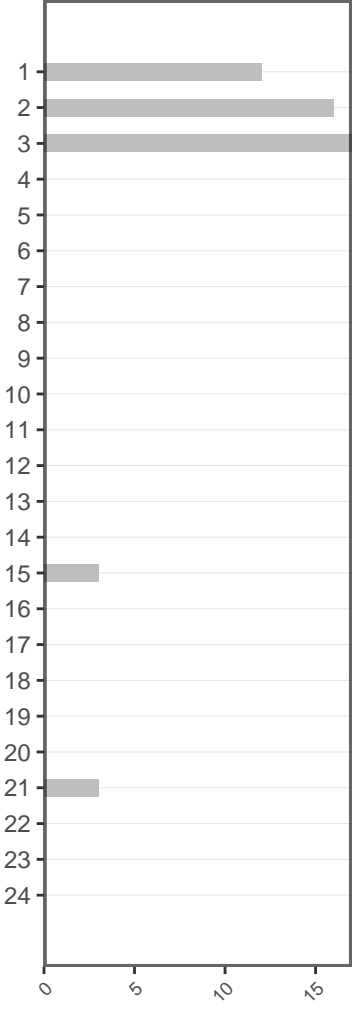
Molecular weight



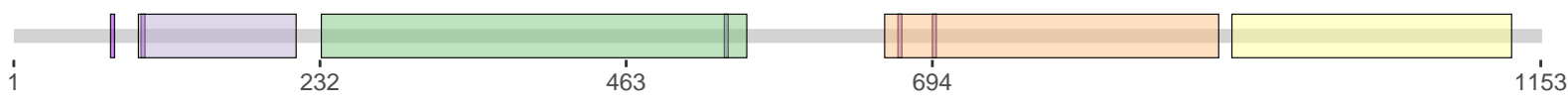
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00443 Ubiquitin carboxyl-terminal hydrolase
- PF00917 MATH domain
- PF12436 ICP0-binding domain of Ubiquitin-specific protease 7
- PF14533 Ubiquitin-specific protease C-terminal

Protein sequence:

1RESQKDKIICVDEKDAEHLRIPLKKEGEEKKRRYKAGAHLYTIKVARDEDEKIQGREYFDLVVHDKVHFSFRIQKQMPFNLFKEEVAKELGIFPQRFQRFVSWAKRGNHTYRPNPLSPQEELEQTVGQLREVSNKNTNTVELKLFLEVNHGPDLLPILPLLDKSKDDLLFFKLYDPAKEELRYGRLFVNSSSKPTDILGKLNELAGFAPDGDHLEFEEKFEPSPVMEHLDDKASFRSSGDEGDHGFQKPKSPREVEEQVRYPDVPSFLEYVKNRQVHFRALFKPKVEVDFC

NbL06g17860.1 probable_60S_ribosomal_protein_L14 [MW = 15.27 kDa]

No. of times detected



log(intensity)



Values from



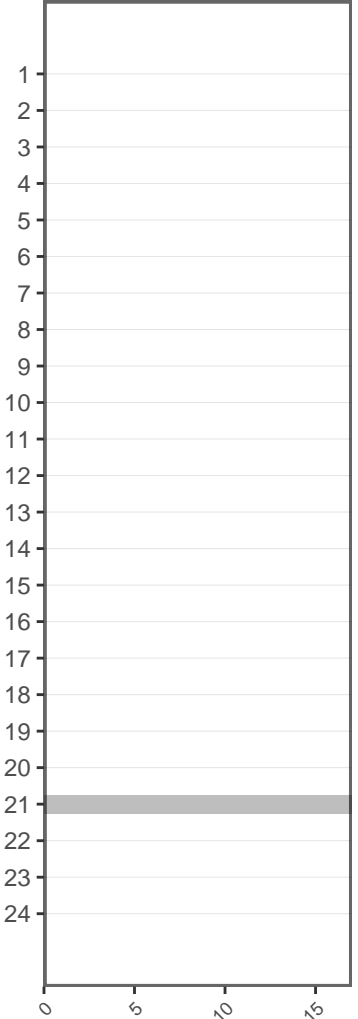
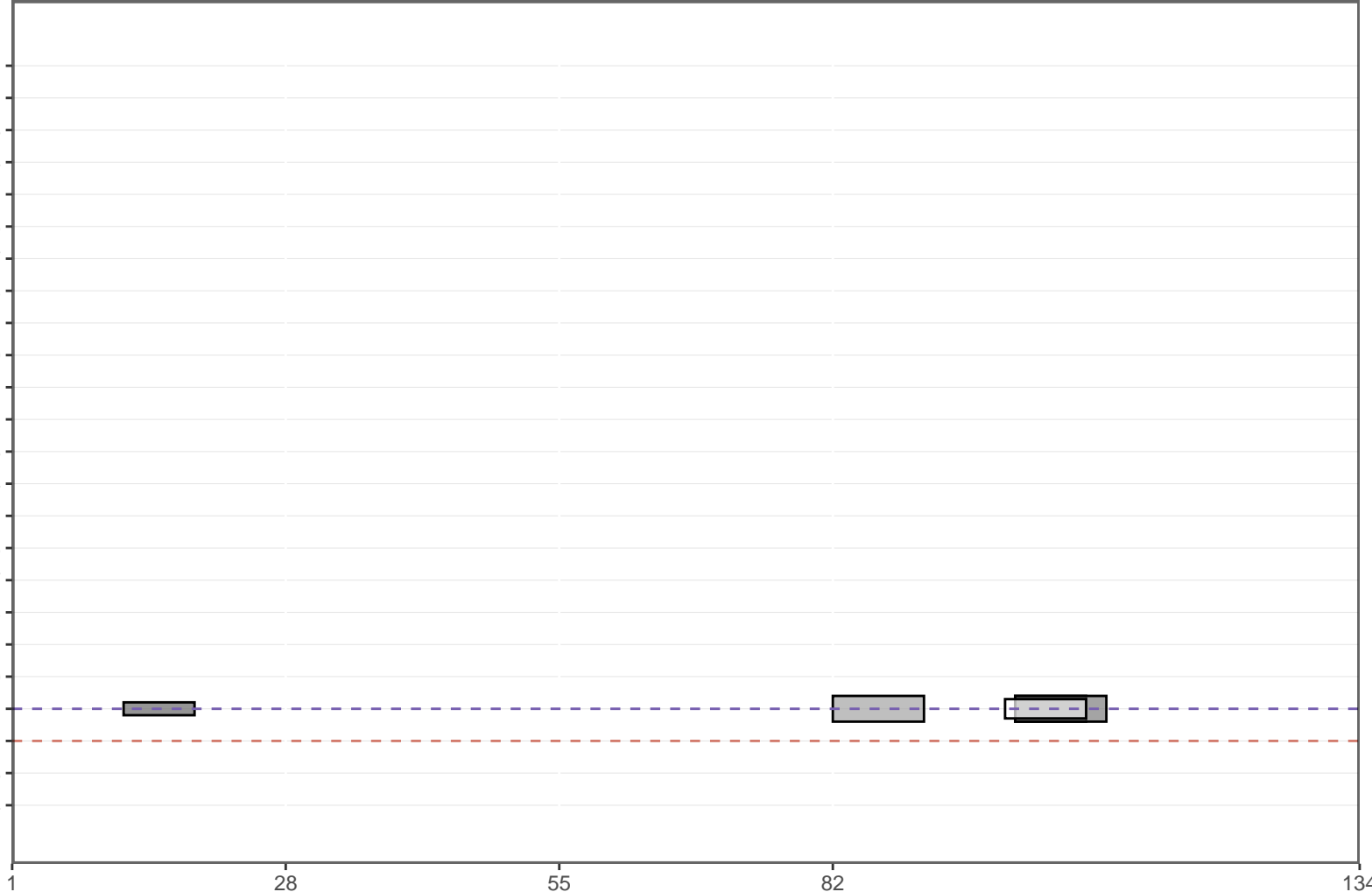
MW indication



Molecular weight

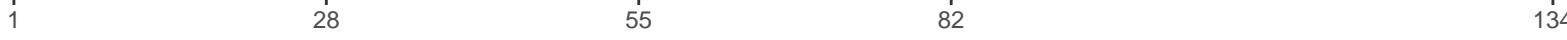


Gel Slice

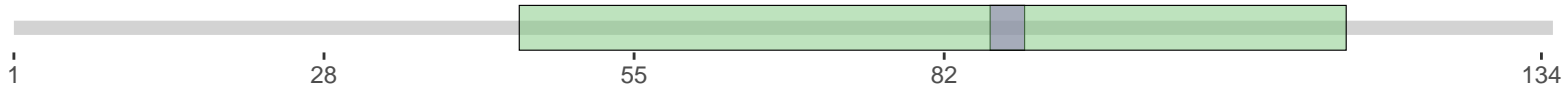


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

SLTDDKIDKRIIPKOKTFLVAMEAADVKTWENBSGWRKLVIGKRRALNDFDFKLLMLAKKIKRAGVVRQELAKLKKTA*

NbL06g17650.1 cysteine-rich_repeat_secretory_protein_3-like [MW - SP = 28.85 kDa]

No. of times detected



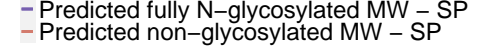
log(intensity)



Values from



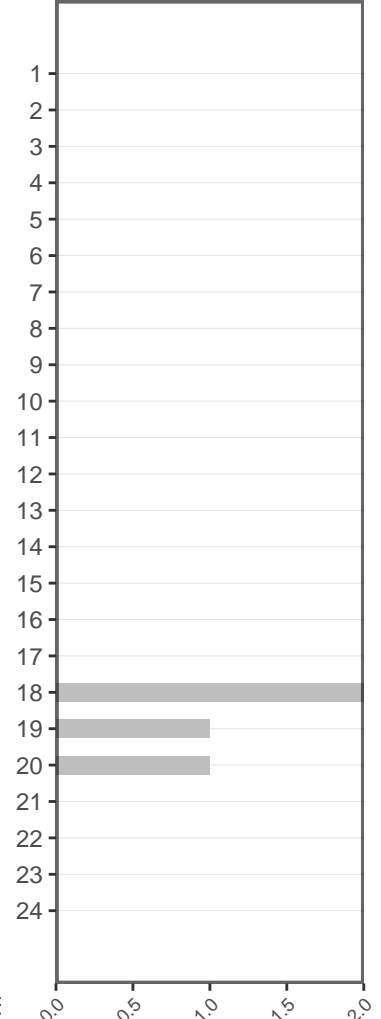
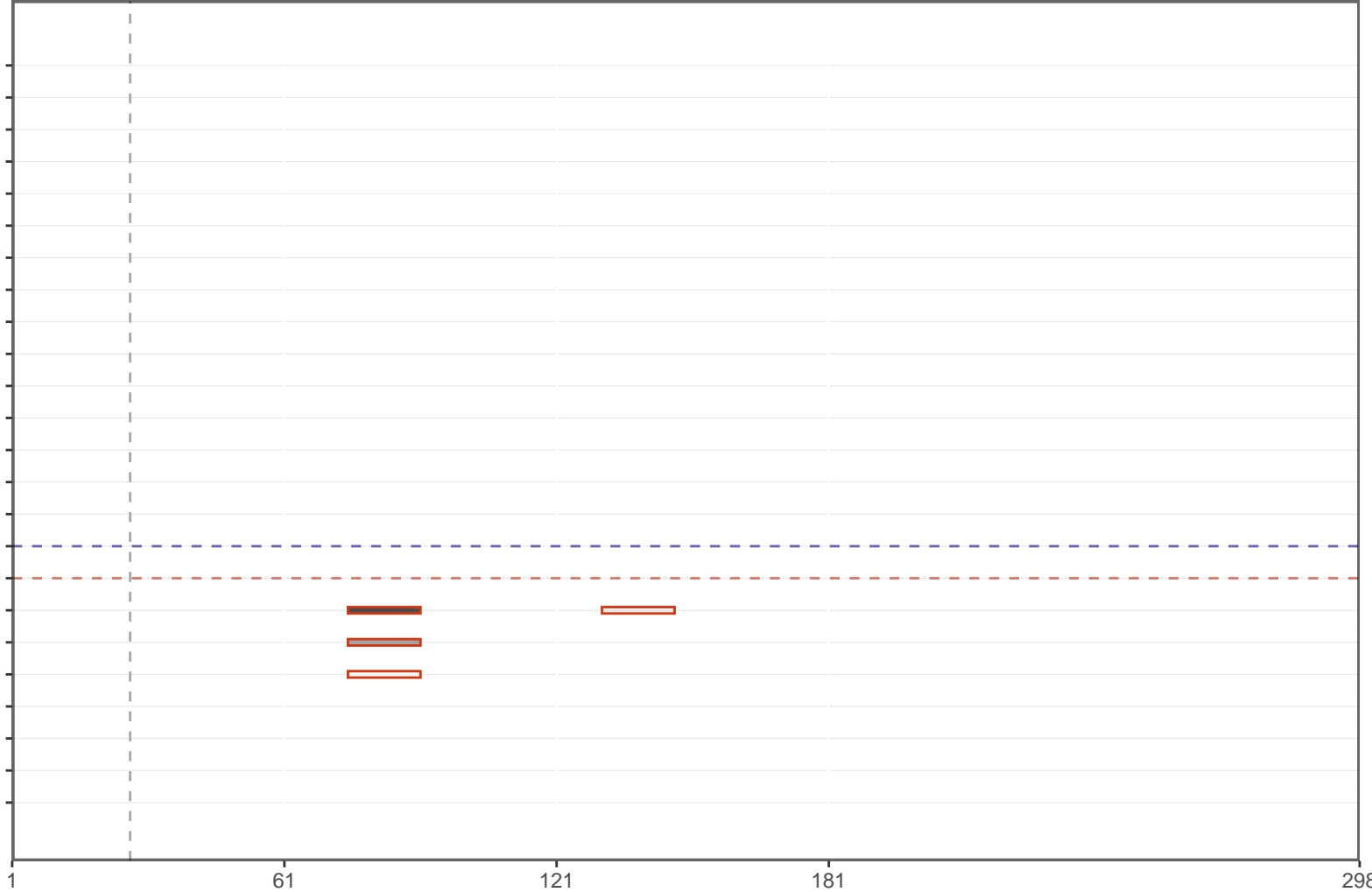
MW indication



Molecular weight



Gel Slice



Protein length

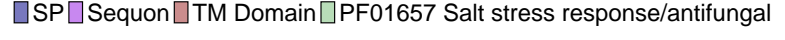


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

JTVGPTLLLYKCASTQASGGDFLRLETALGKAKGVFSSGNKGFYTGQYQSYVYLGQCEGLSEGGCVNCKVNAEAEAKNDGSSSIAQVLGQCYRIRYTPYSGVPTKSFSPSSGIRKSTQKTAVMLGGVLGVGLVLAQLLFTKSAFKKQVYVYGG

NbL06g17590.1 photosystem_II_reaction_center_Psb28_protein-like [MW = 19.96 kDa]

No. of times detected



log(intensity)



Values from



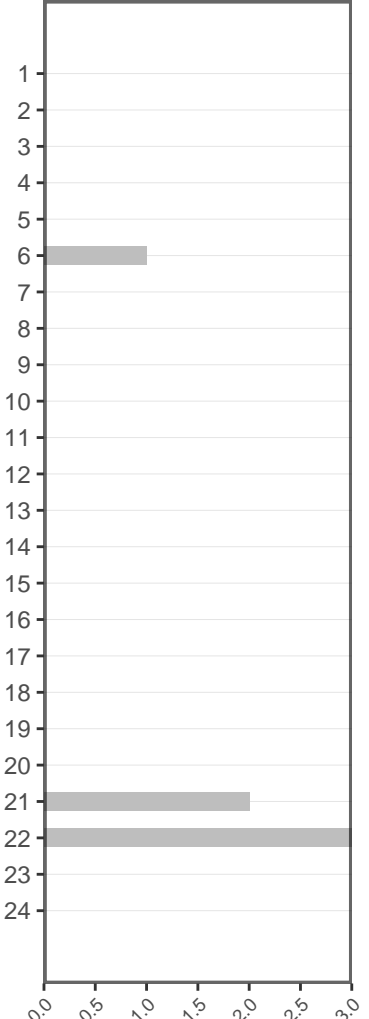
MW indication



Molecular weight

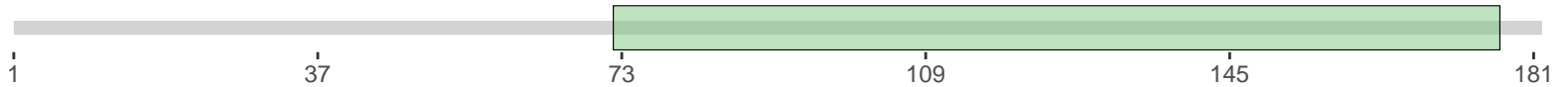


Gel Slice



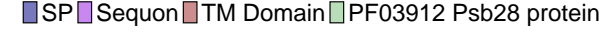
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

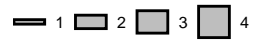


Protein sequence:

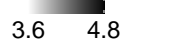
DEQTPDVKLTKSRDGTNGMAIFRFDPNSVFDSSGEGVDITGFYIMDEEGVLSGVNNAKFNKPKPGVEAKYIMRTPREWRDFRMRMERYANANGLOFVKP

NbL06g17540.1 tyrosine_decarboxylase_1-like [MW = 40.62 kDa]

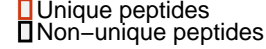
No. of times detected



log(intensity)



Values from



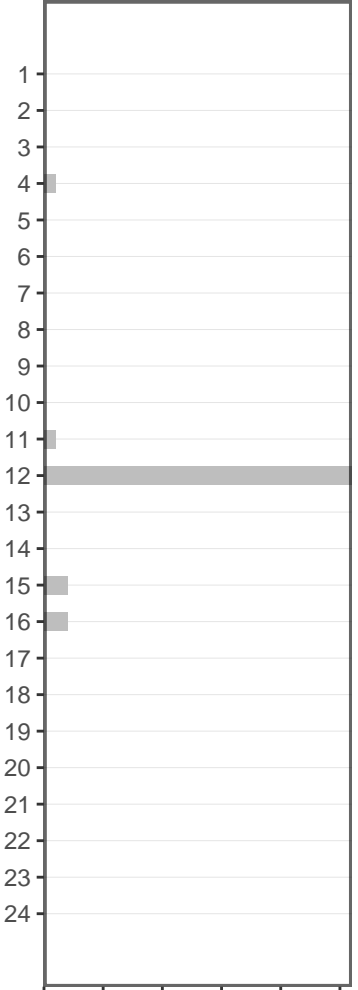
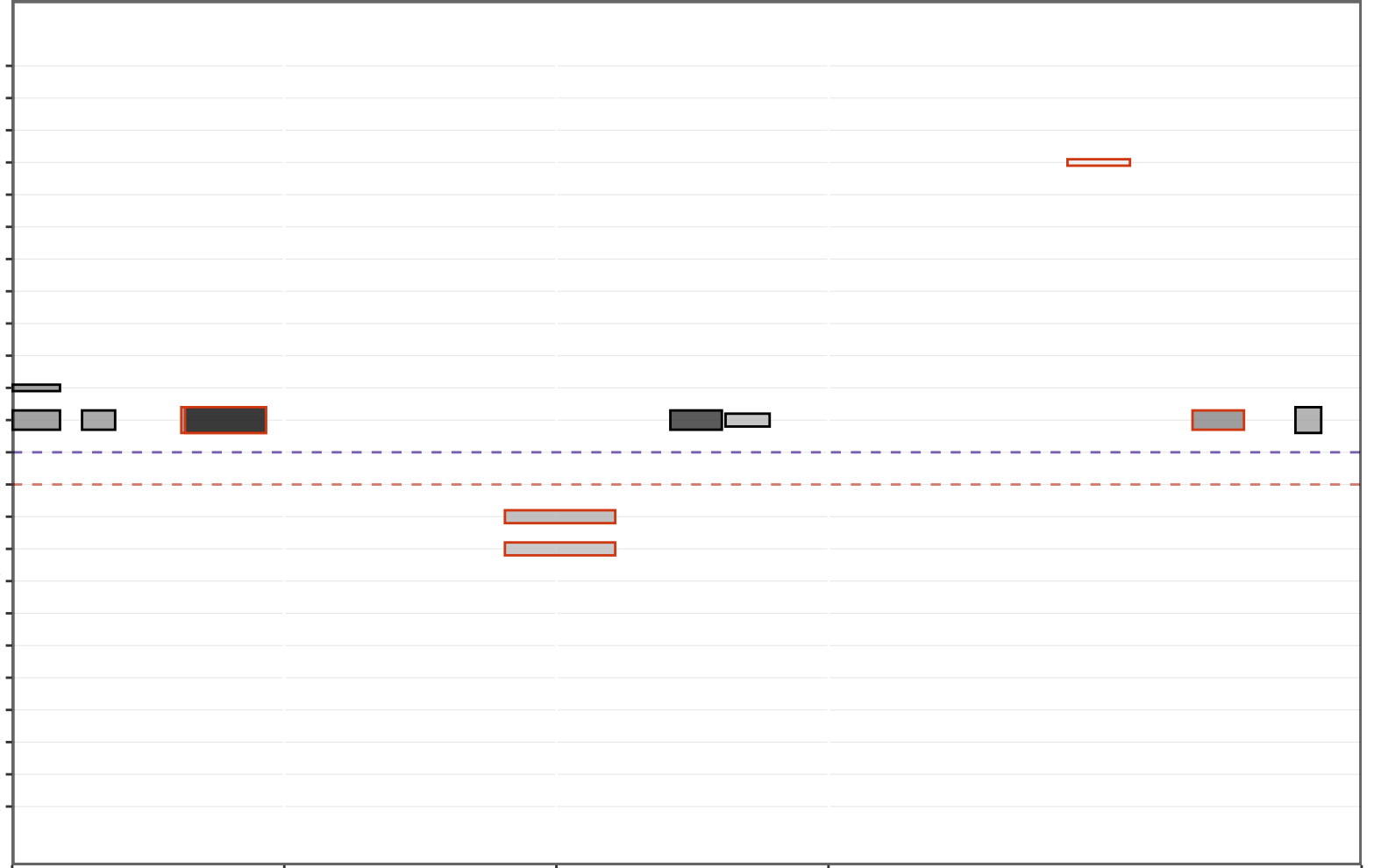
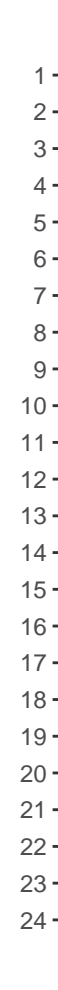
MW indication



Molecular weight

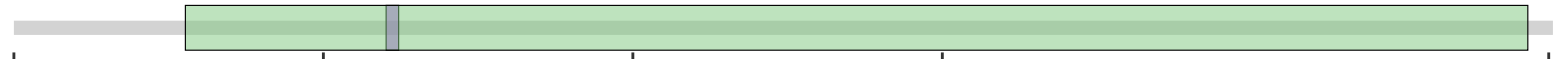


Gel Slice



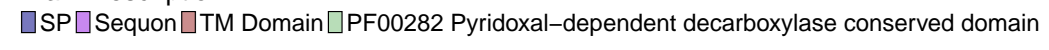
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RVGKDAIGKLVVYCSDDTHSALGKAGQGGHGFENFRMKAVSGRDVALSPDALSEAVSHDLATGLIPFFFGATIGTTSSTAVDPLLALGKIKNSNMWFHVDAAVAGSAGICPEFRHYIDGVEEADSFNNAHKWFLTFDCSALWVKDRSALIGSLSTPEFLFNKASGGNLVVDYKDWQPLGRFRSLKRGWY*

NbL06g17510.1 alcohol_dehydrogenase_class-3-like [MW = 40.71 kDa]

No. of times detected



log(intensity)



Values from



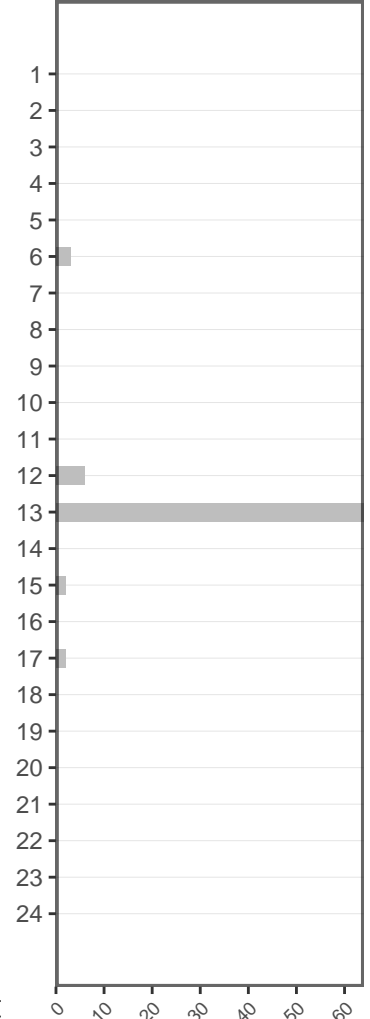
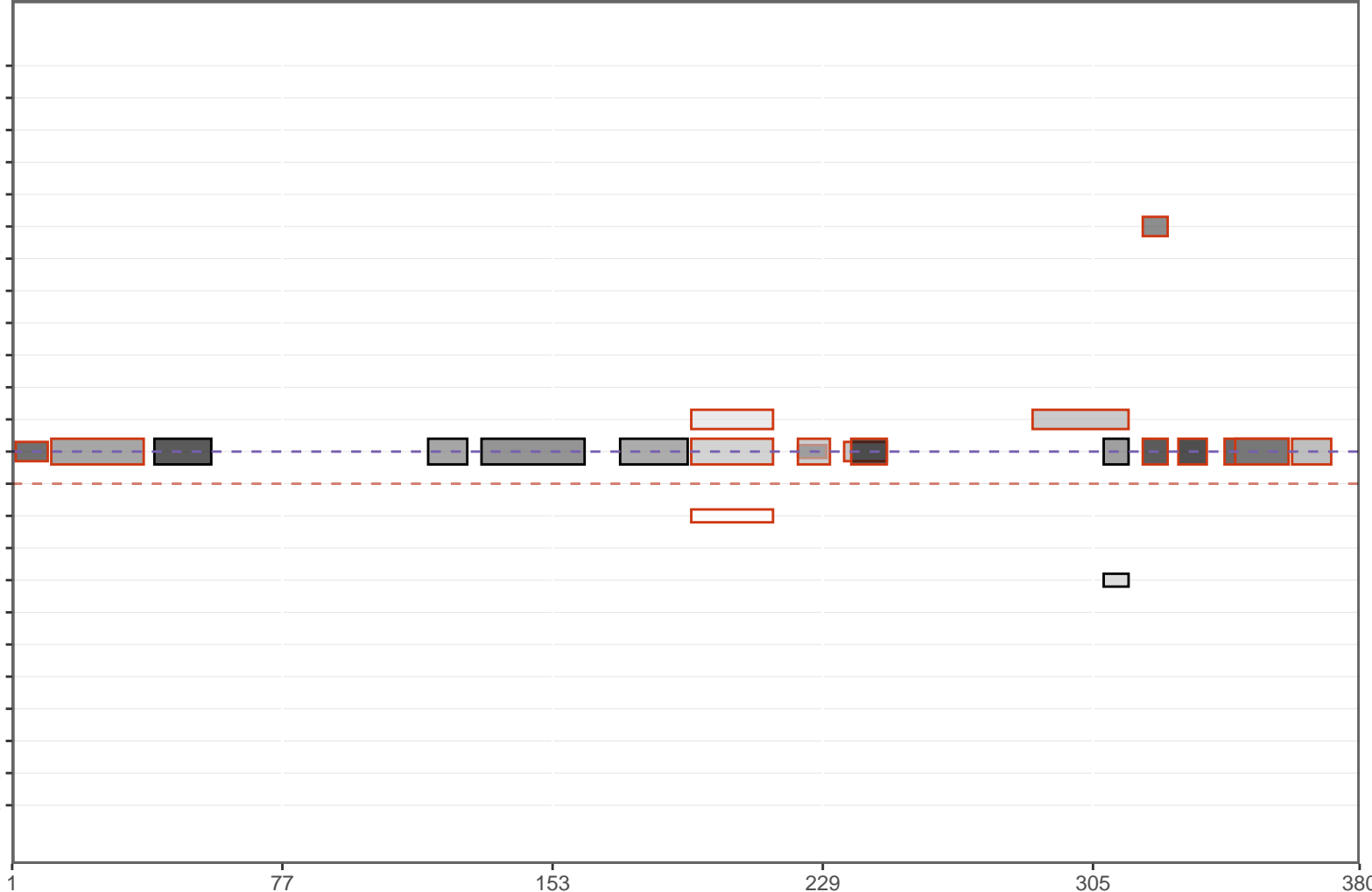
MW indication



Molecular weight



Gel Slice



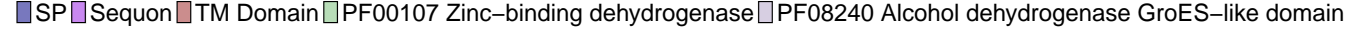
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

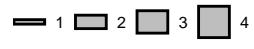


Protein sequence:

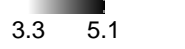
SCGVPTGLGAVWNTAKVEPGRVWVFLGLTGLVAEGAKAAGASRVIGIDIDSKKFRANKVGFTEFINPKKEKPKQGVVLDLTDGGVDYSFEGIGVSVMRAALECGHKGGWTSVIVGVAASGGEISTRPFQLTGRVWKGSTAFGGFKRSQVFWLVDKYLKKEIKVEYTHNMFLADINKAFDLMHDSGSLRVLDMPV

NbL06g17450.1 ribokinase-like [MW = 43.7 kDa]

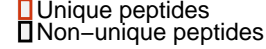
No. of times detected



log(intensity)



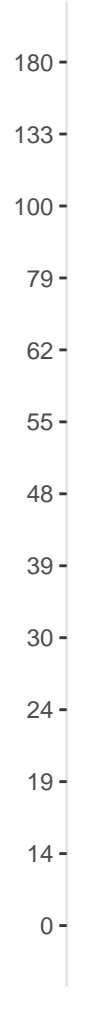
Values from



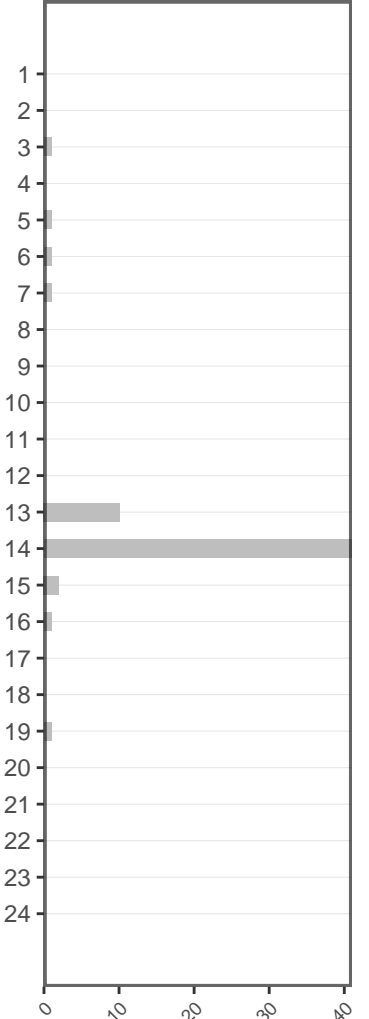
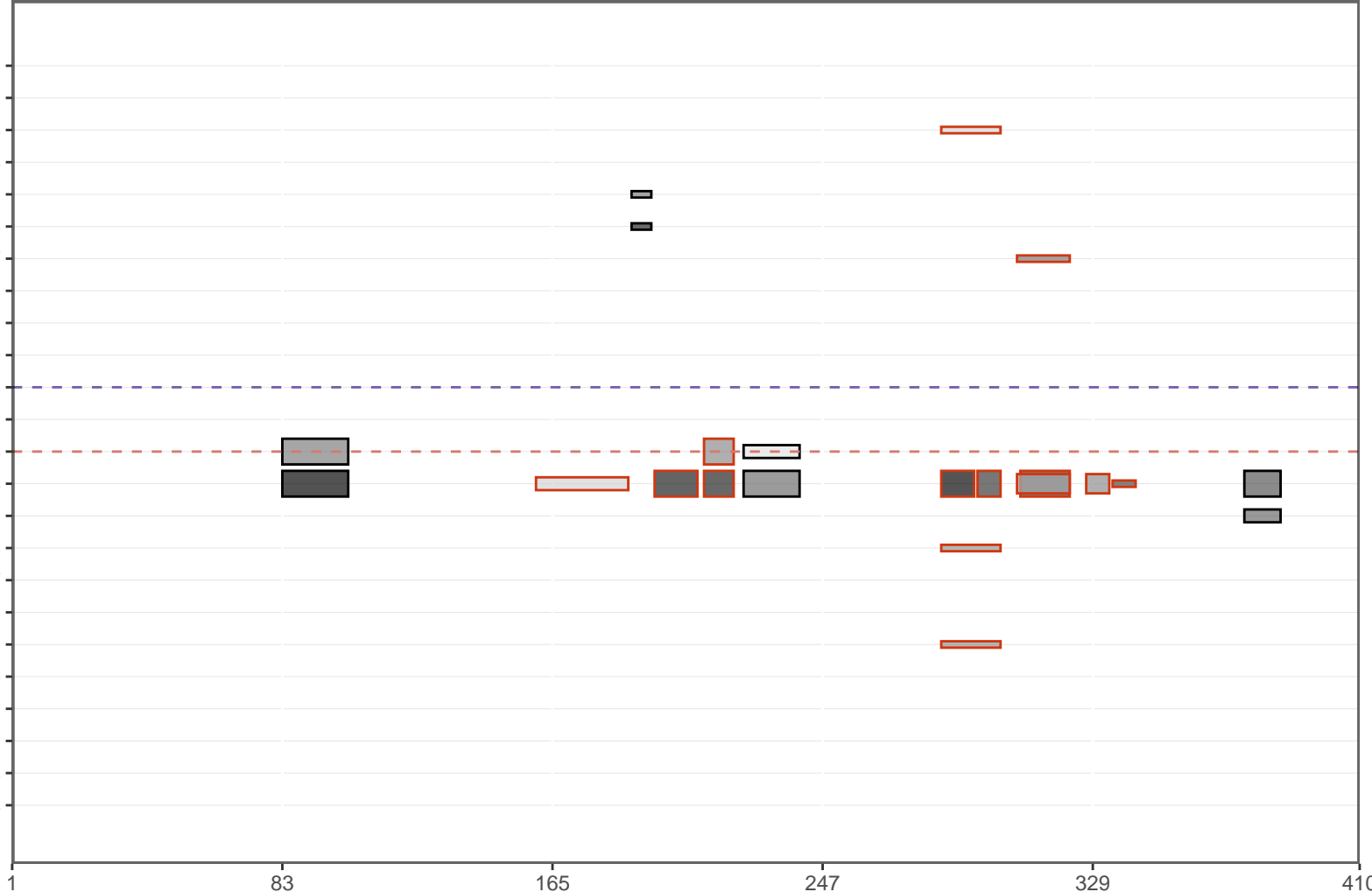
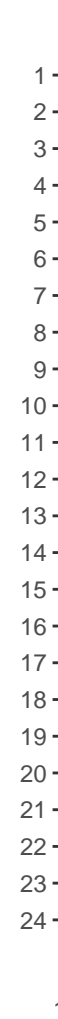
MW indication



Molecular weight

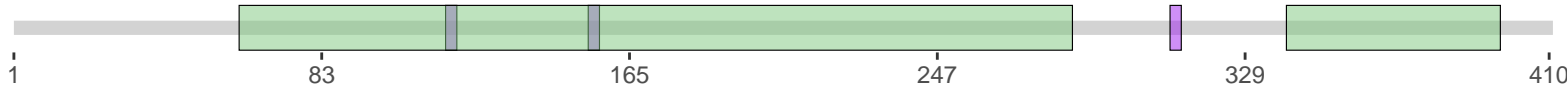


Gel Slice



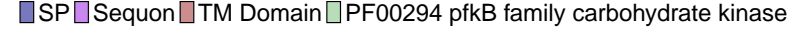
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

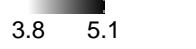
FDGR LHETAAVAASEANRRGIPILDAERKREGLDHLISFASVYVGGSTKFGDQWTEASSIPBALLSMLLRLLPKVYVITLGEDGGLMQRTEMONLDEPERDVEDDLFEKLNQKKTNTSPAGISSNVAKLHAKGIGTISGKLLVGTAEKIPQTELVDDTTGAGDAFAGVLYKICANMPKEMLPFAAQVAANKRAALGARAGLPHYDPRLRITFLV

NbL06g17350.1 GDSL_esterase/lipase_At4g28780-like [MW - SP = 37.22 kDa]

No. of times detected



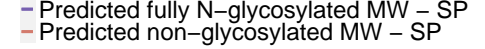
log(intensity)



Values from



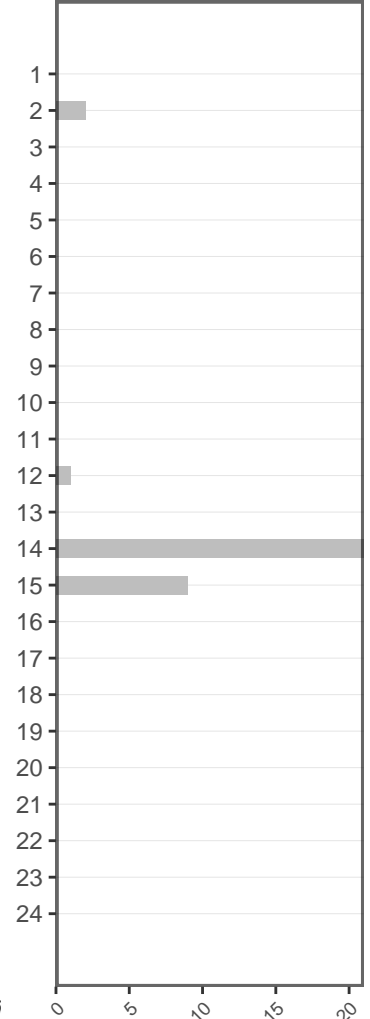
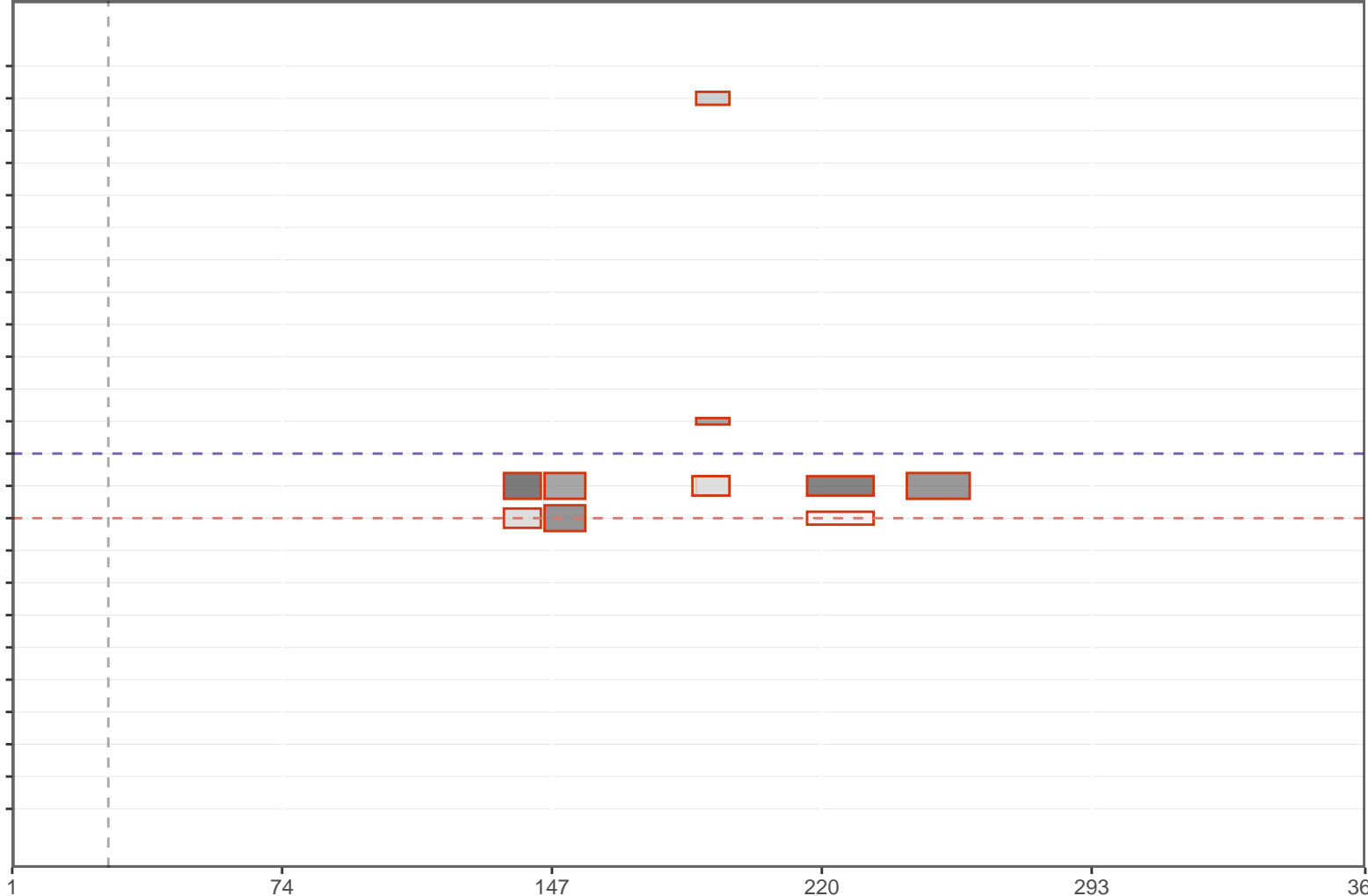
MW indication



Molecular weight

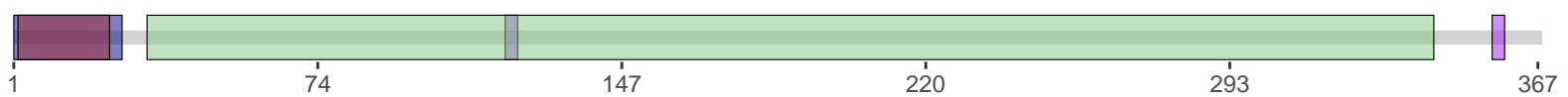


Gel Slice



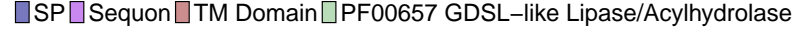
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YVNNYFLTPVSARRHQVNGDYSRRLVTEYRKLKRLHDLGGRRVLTGTGTPLGGVPELATRRSSNGEGCAKEPQAAAAFNPLVDMKRLNGELGDFVAVNMEMQNDFINNPKAFGFTVTSKIAQGGGPPYNGIGLCTAASNLCPNRDEYAFWDPHPSEKANKIKVITVSGGDKYTPMNLSTIMAEVY

NbL06g17180.1 3-ketoacyl-CoA_thiolase_2_peroxisomal-like [MW = 49.08 kDa]

No. of times detected



log(intensity)



Values from



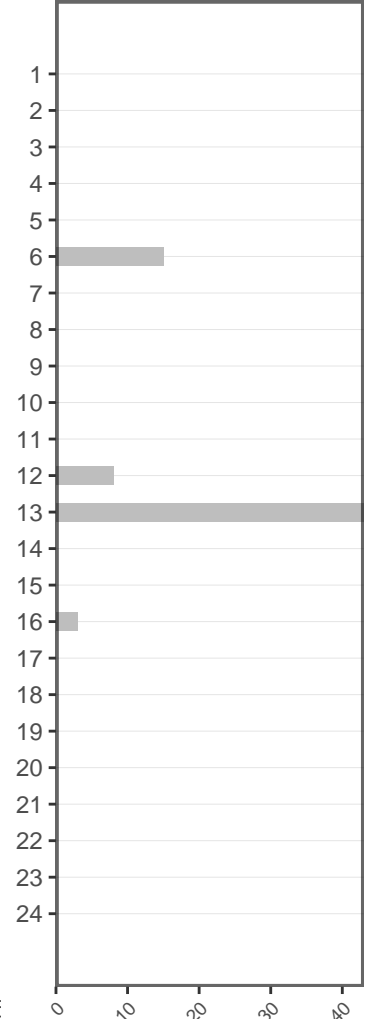
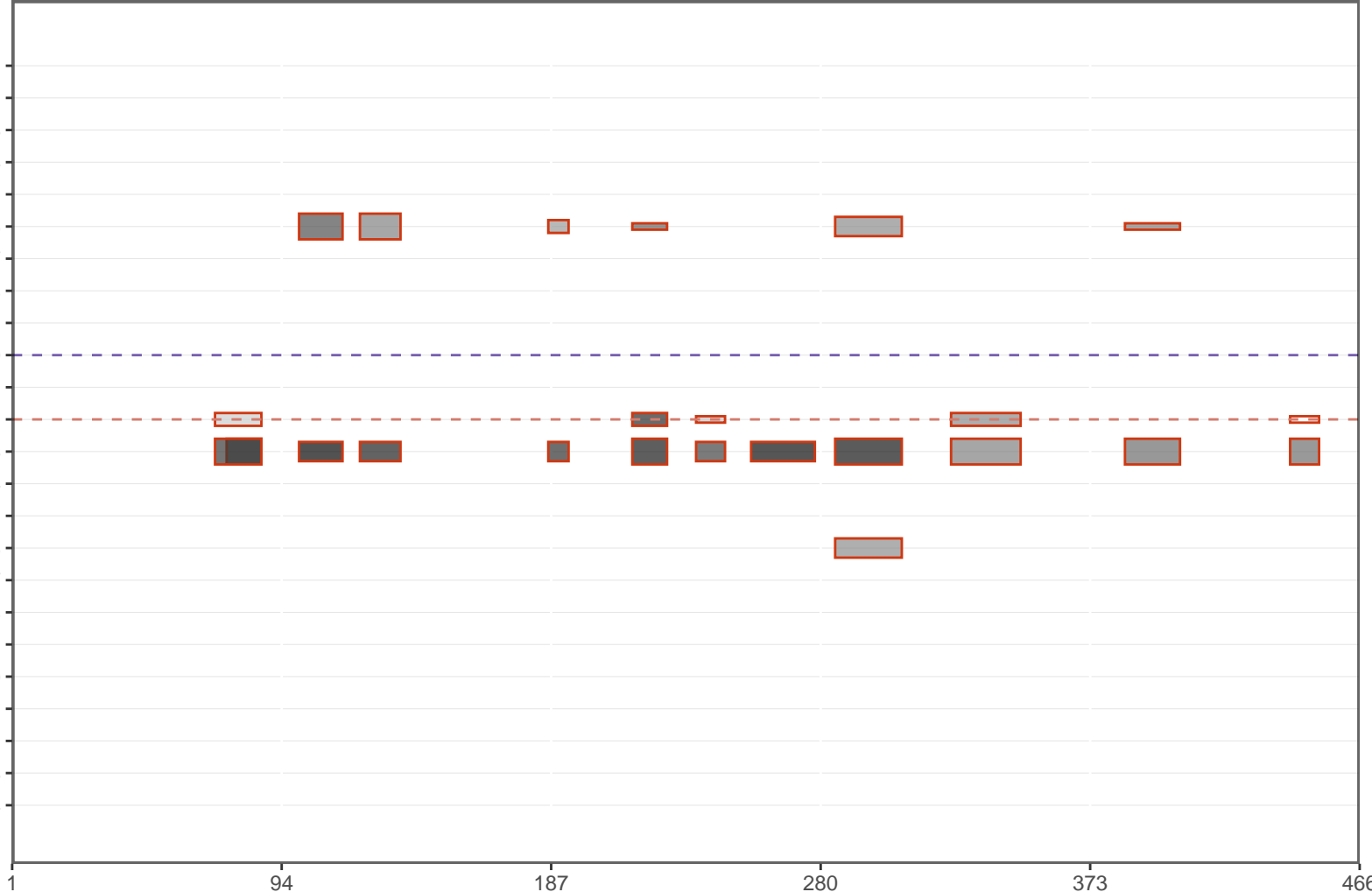
MW indication



Molecular weight

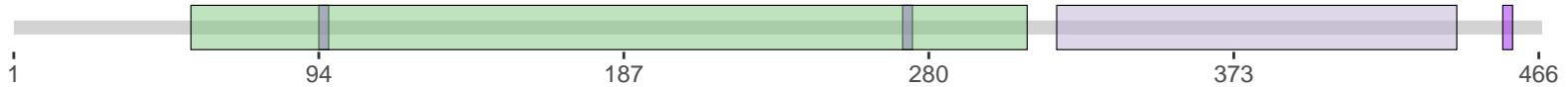


Gel Slice



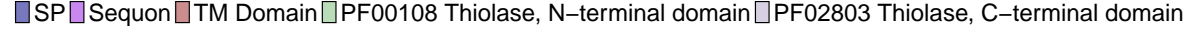
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

UVVSHQRAAAATASGKFKDEIFVLTQVDPQTRREKPIVSVDDGIRPNTNITLLEKLPKPFKSDGTTTGTAGTASGVSDGAAVLLMKRIVAMQKGLPLGVFRFAVGVDPVWVGIGRPAVPAVKSAGLELDNIDLFENEAFASGFVYGRKKNLIDSEKVVVNGGAMALGHPLGATGARGVATLLHEMKRRGKGRFGVISMCGSGMGAAVFERGDVDDLGARVNNNNFLSKDAK

NbL06g17110.1 pantoate--beta-alanine_ligase [MW = 34.92 kDa]

No. of times detected



log(intensity)



Values from



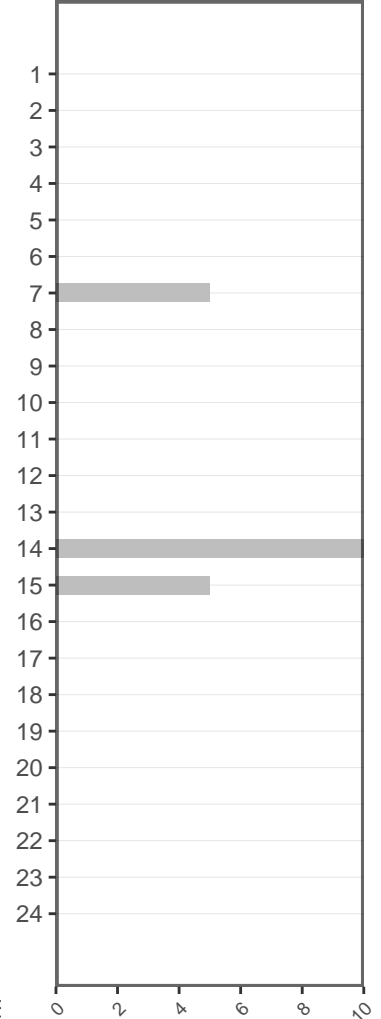
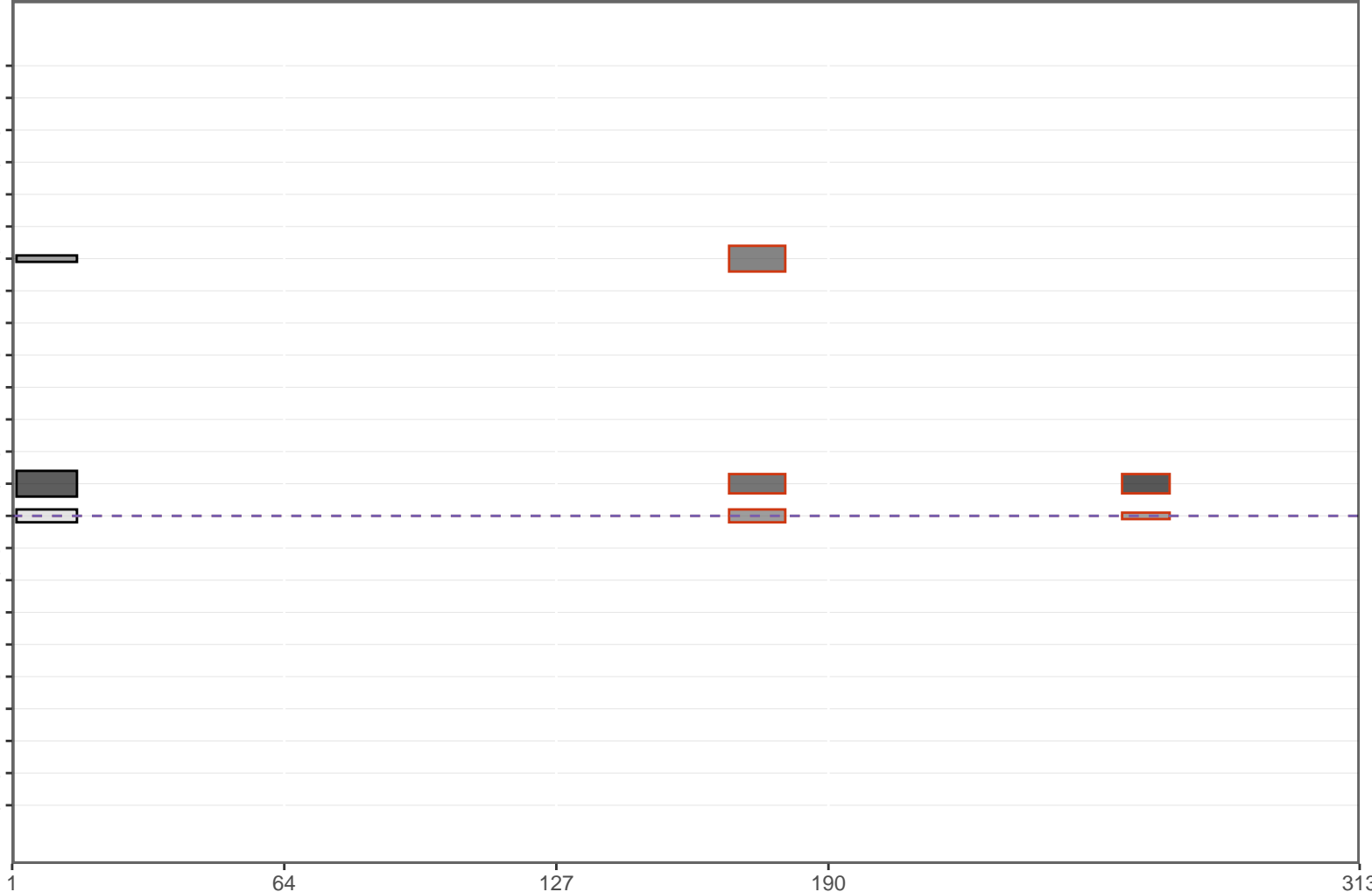
MW indication



Molecular weight



Gel Slice



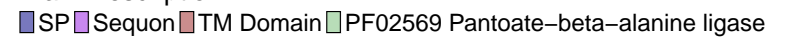
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

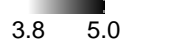
VENLEKLGCKSRPFVFRGVAIVTKLNFIVEPDAVAFGKHDKYQWRIRGRVRLDFGKIKVGSIVRIGHDGLMSSRNKVLSPEDRQKALISGRALSKAVAEKGGQVNGELIKSAIGTDEAGGKVDVAEIVEGESELPVETIKRPVVFQAAVFGKIVLVNMEIN

NbL06g17090.1 uncharacterized_protein_At4g13200_chloroplastic-like [MW = 24.09 kDa]

No. of times detected



log(intensity)



Values from



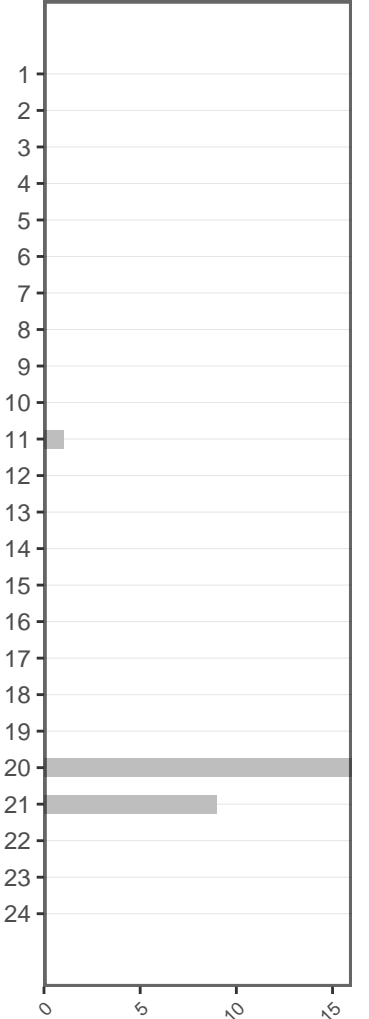
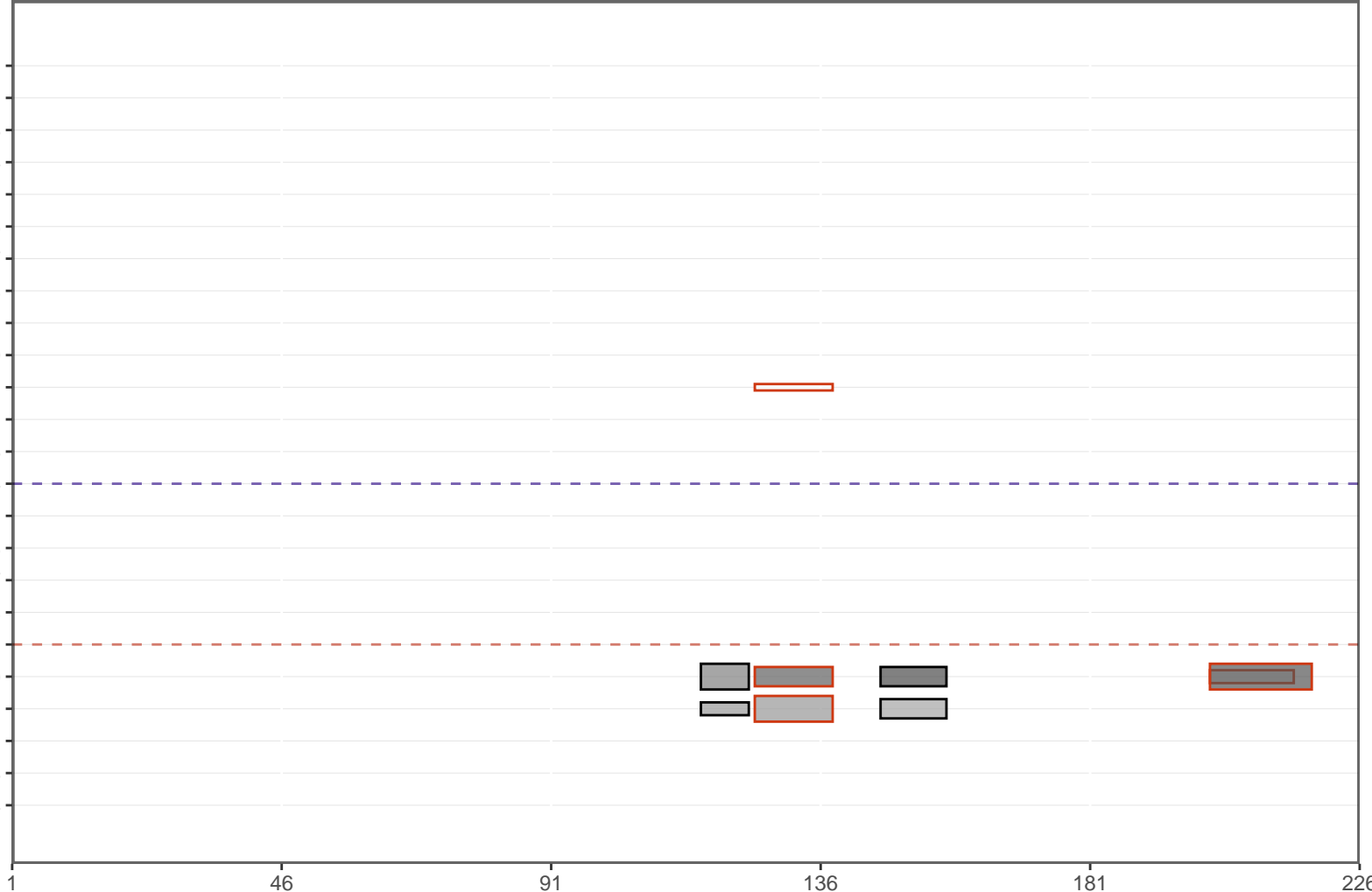
MW indication



Molecular weight



Gel Slice



Protein length

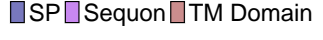


Peptide counts over 4 repeats

Pfam domains



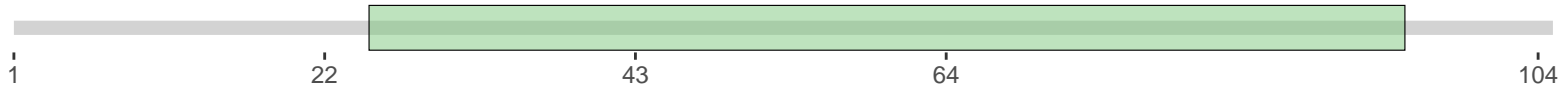
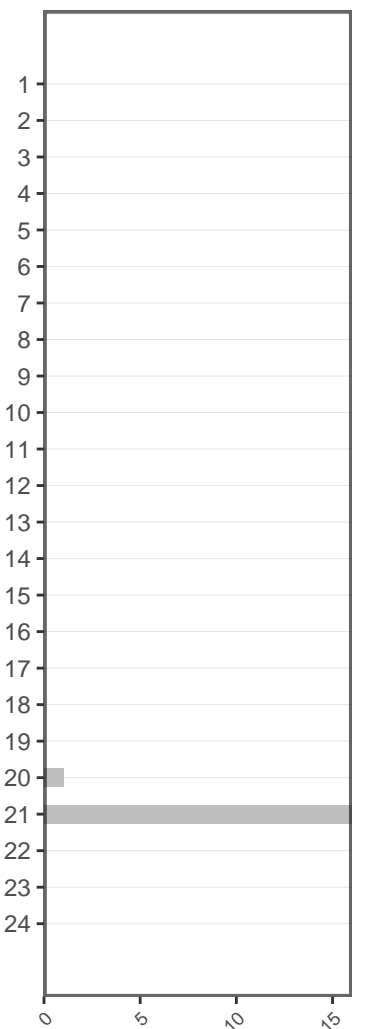
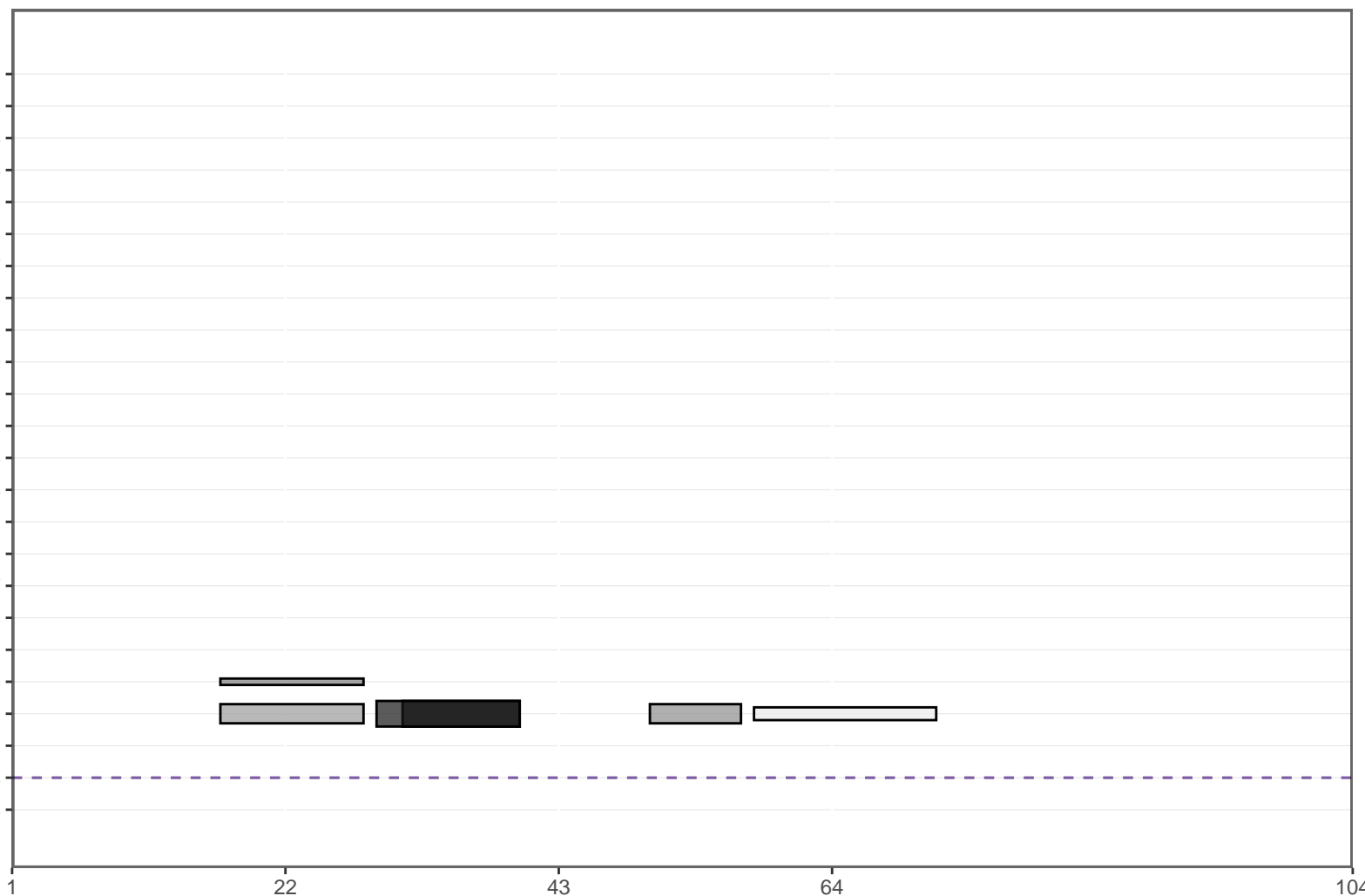
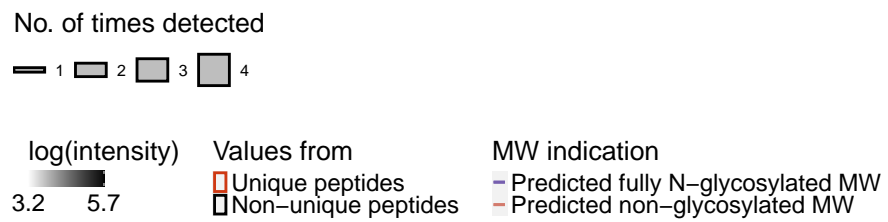
Pfam Description



Protein sequence:

INESKINLDAFFLGGKALAEAVTERNESTVGEFLGTGVRLLGAEQKQKQVDFGEEVLERAKGAKKEAAARETMDTQGLINFSFTADTSTAGTQVTSATSOQTRINSQPMMIDSEDKSKLGLSNGD*

NbL06g16870.1 small_ubiquitin-related_modifier_1-like [MW = 11.39 kDa]



Pfam Description

SP Sequon TM Domain PF11976 Ubiquitin-2 like Rad60 SUMO-like

Protein sequence:
FRKRNTQLRKLINAVGDRGQVDMNSIAFLFDGRRLLKGGGTPDELEMEEGDEIDAMLHGTTGNDV

NbL06g16860.1 uncharacterized_LOC109228095 [MW = 65.48 kDa]

No. of times detected



log(intensity)



Values from



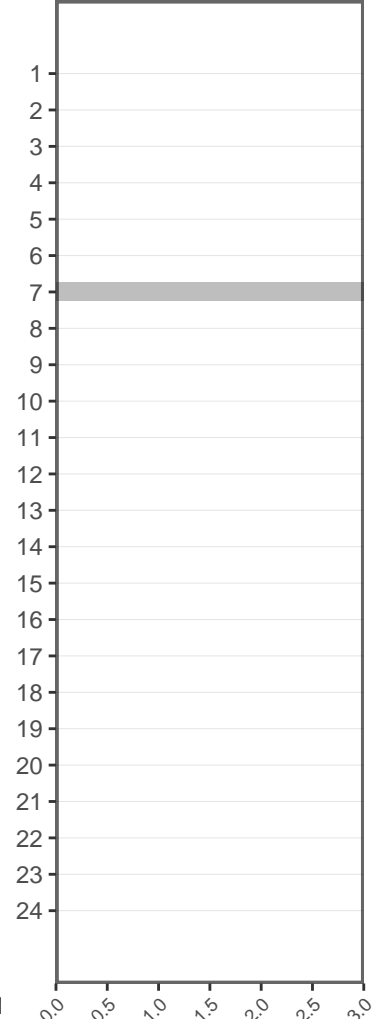
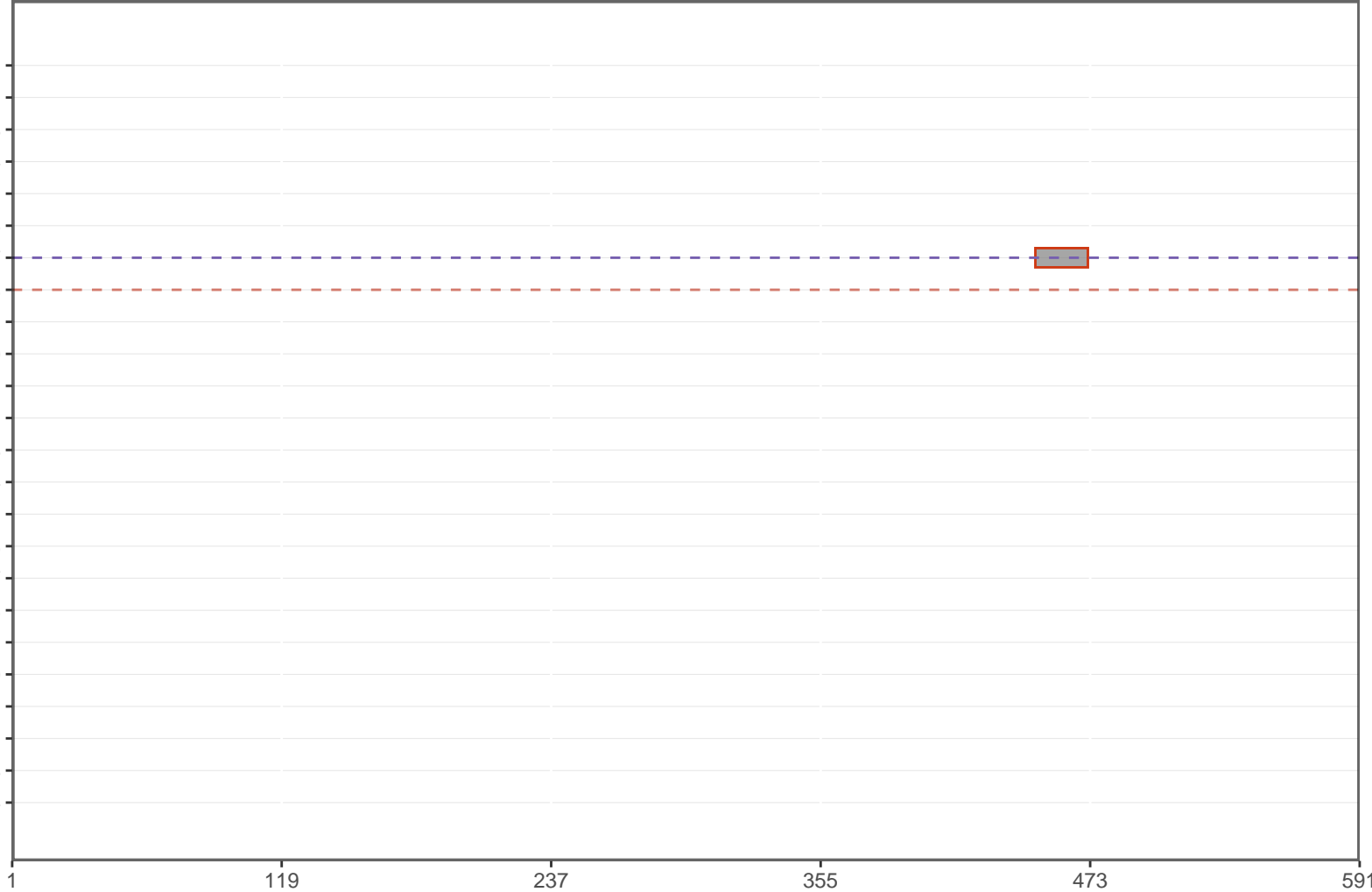
MW indication



Molecular weight



Gel Slice



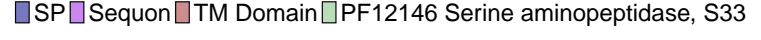
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

TRKSAVLTSDAGELSKLVNFEFGGRVSSPLFDLQERLFRIGDFQGLDLKLYDWFDFHYLEEDVPAAMEYKVGTRPKDKLLAIGHSMGGILYARLISWGGLEGREPLAAVTLASSLDYTSKSAKLLKLLPLADPMGLVNVPIPIRLLAAVPLSSRPVYLAWLNEMSATNMMIPDSLKKLVQNSFCNIPWLLQLQATAFQEGGLRDRBGGKYYKDKHLRKSSEVPMALAGLDQKIPPEAVYETWLPENLVYKVFGBADSPHYAHYDLVGGHIMATEQLYPC

NbL06g16850.1 SEC23-interacting_protein-like [MW = 24.62 kDa]

No. of times detected



log(intensity)



Values from



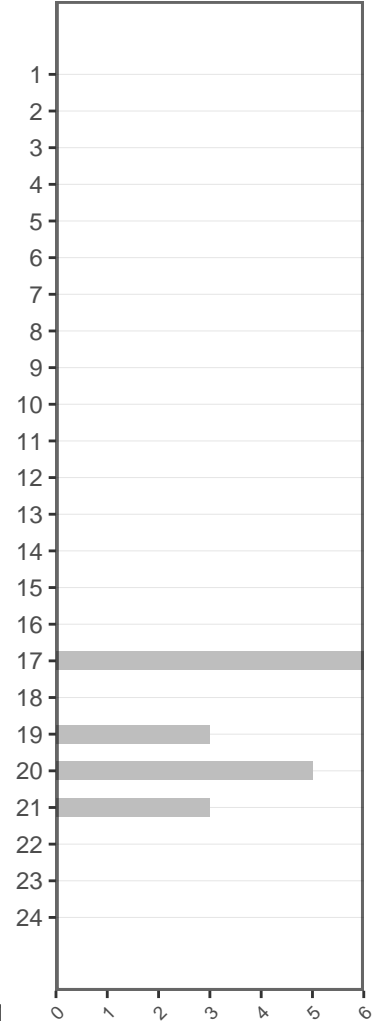
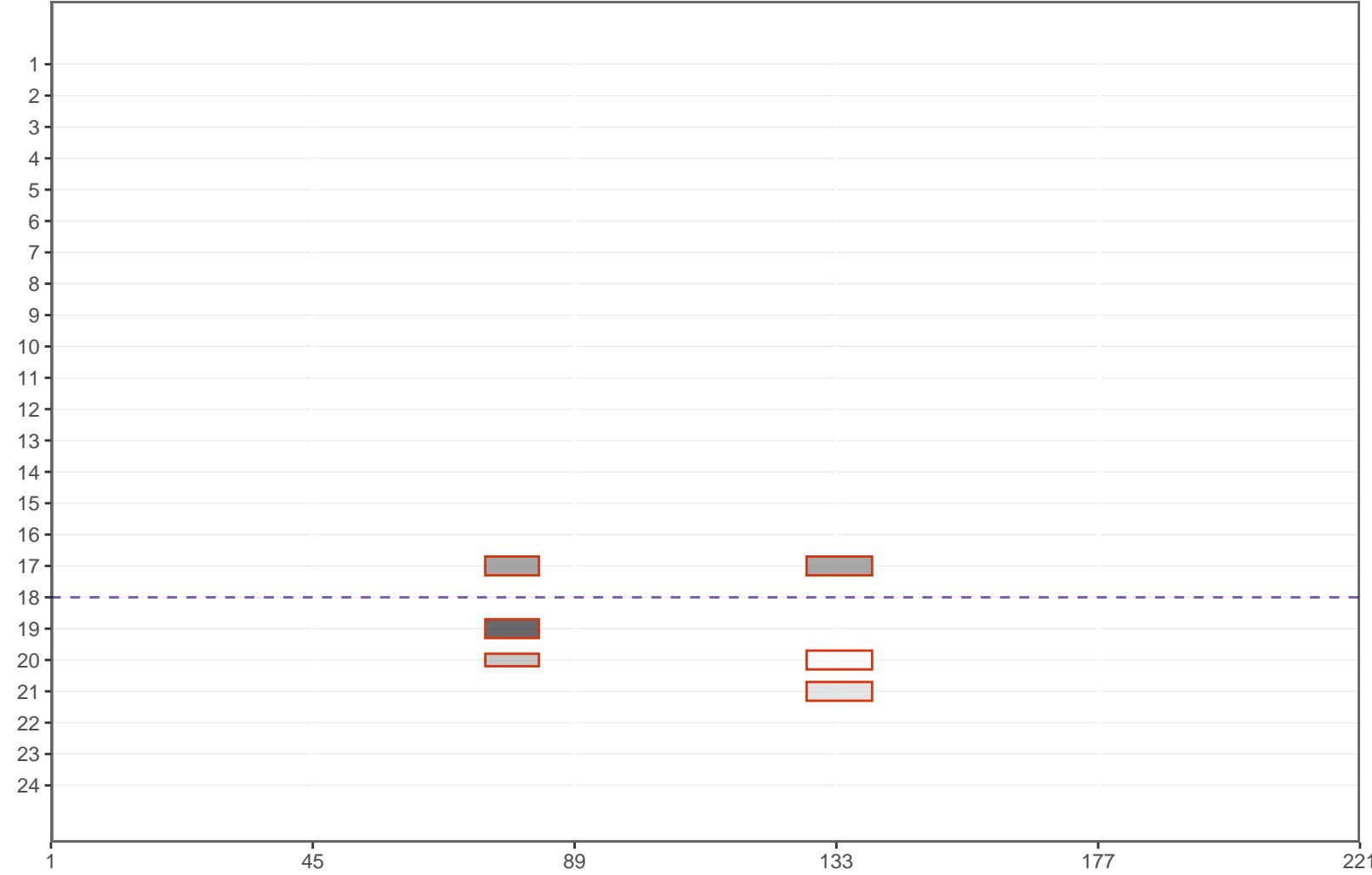
MW indication



Molecular weight



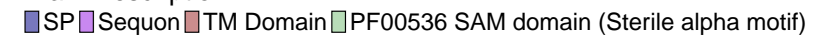
Gel Slice



Protein length

Pfam domains

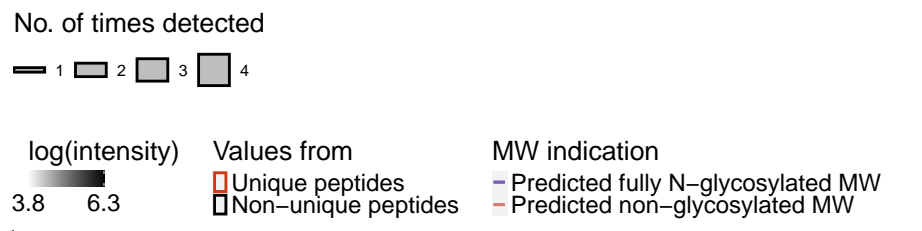
Pfam Description



Protein sequence:

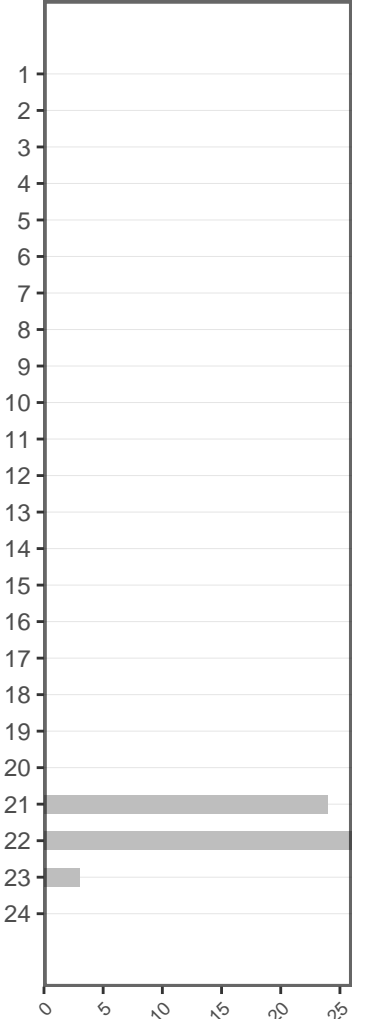
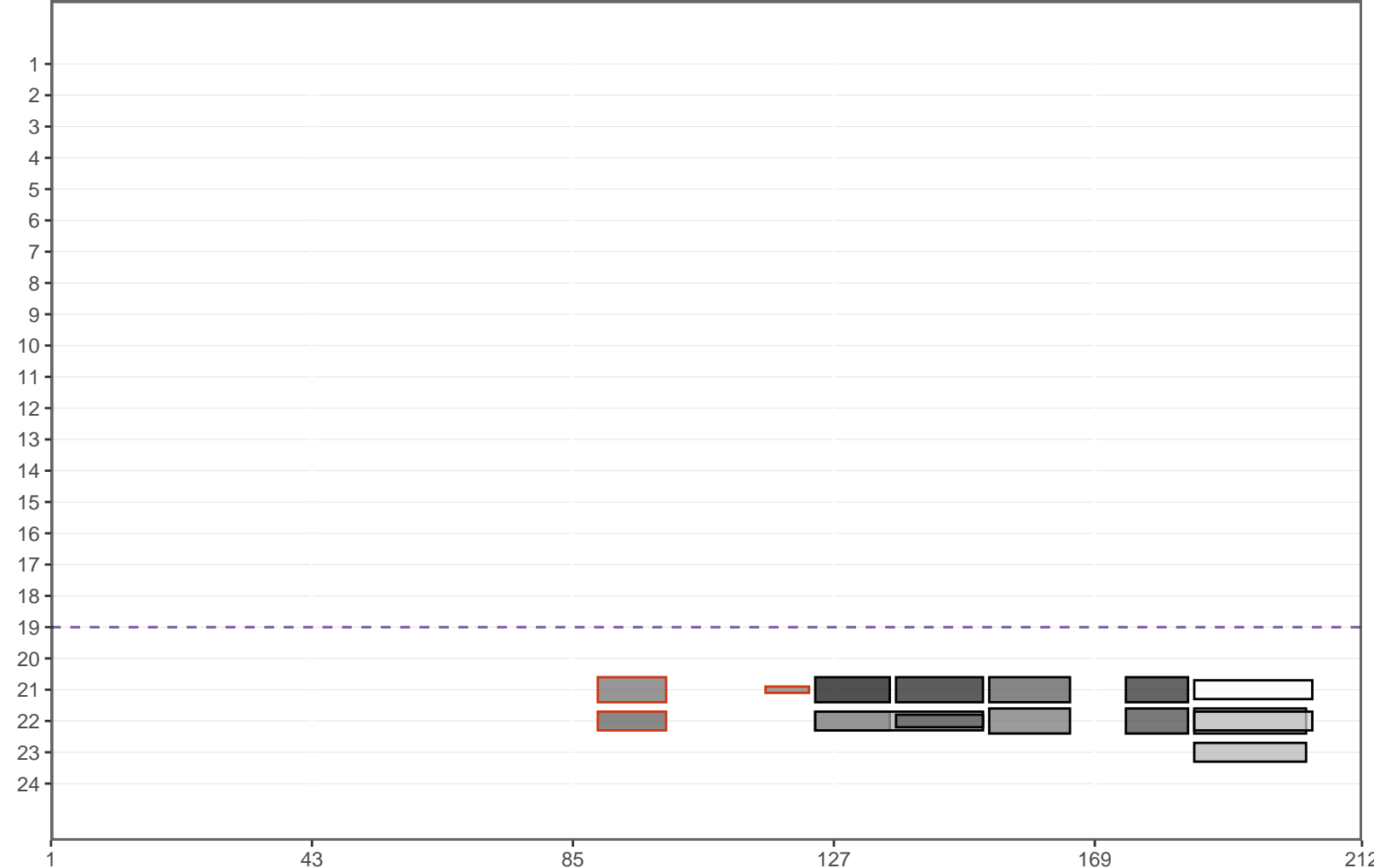
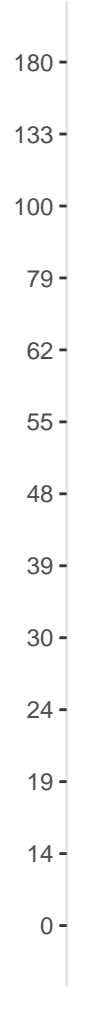
CLSGTYSQTYENVPPKAKLVAPEISKVRRRIVAAEAPMMETKKVASTVSKKKKGGKVGQVDFLQSLGKLYATFGAAEEVDMAALVHMTDEDLKAMGIPMVGIVMLYENSFEVTSQFSAF

NbL06g16510.1 peptidyl-prolyl_cis-trans_isomerase_FKBP15-1-like [MW = 23.15 kDa]



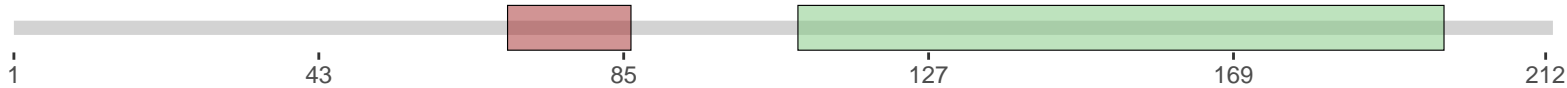
Molecular weight

Gel Slice

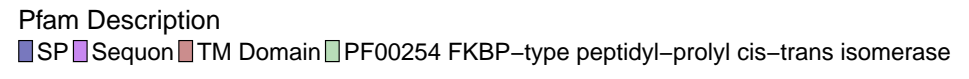


Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:
 ELQIQYKFKPKSCELKANKGDRVSVQYSGKLTGDTVFDSSVYERNDFEFELGSGGVHKGWDDGGLLGMVGEKRLKIPKALGYGESGSPPKIPGGATLVFDTELWVWNGKKAADSEL*

NbL06g16490.1 40S_ribosomal_protein_S8 [MW = 25.11 kDa]

No. of times detected



log(intensity)



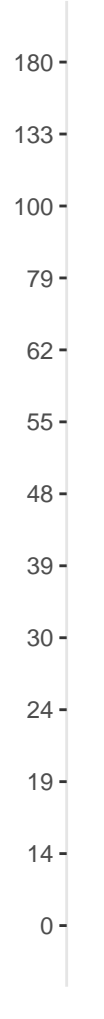
Values from



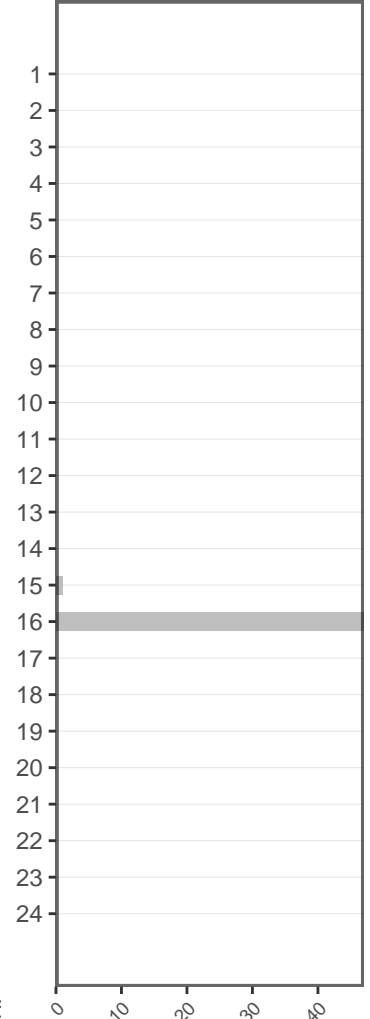
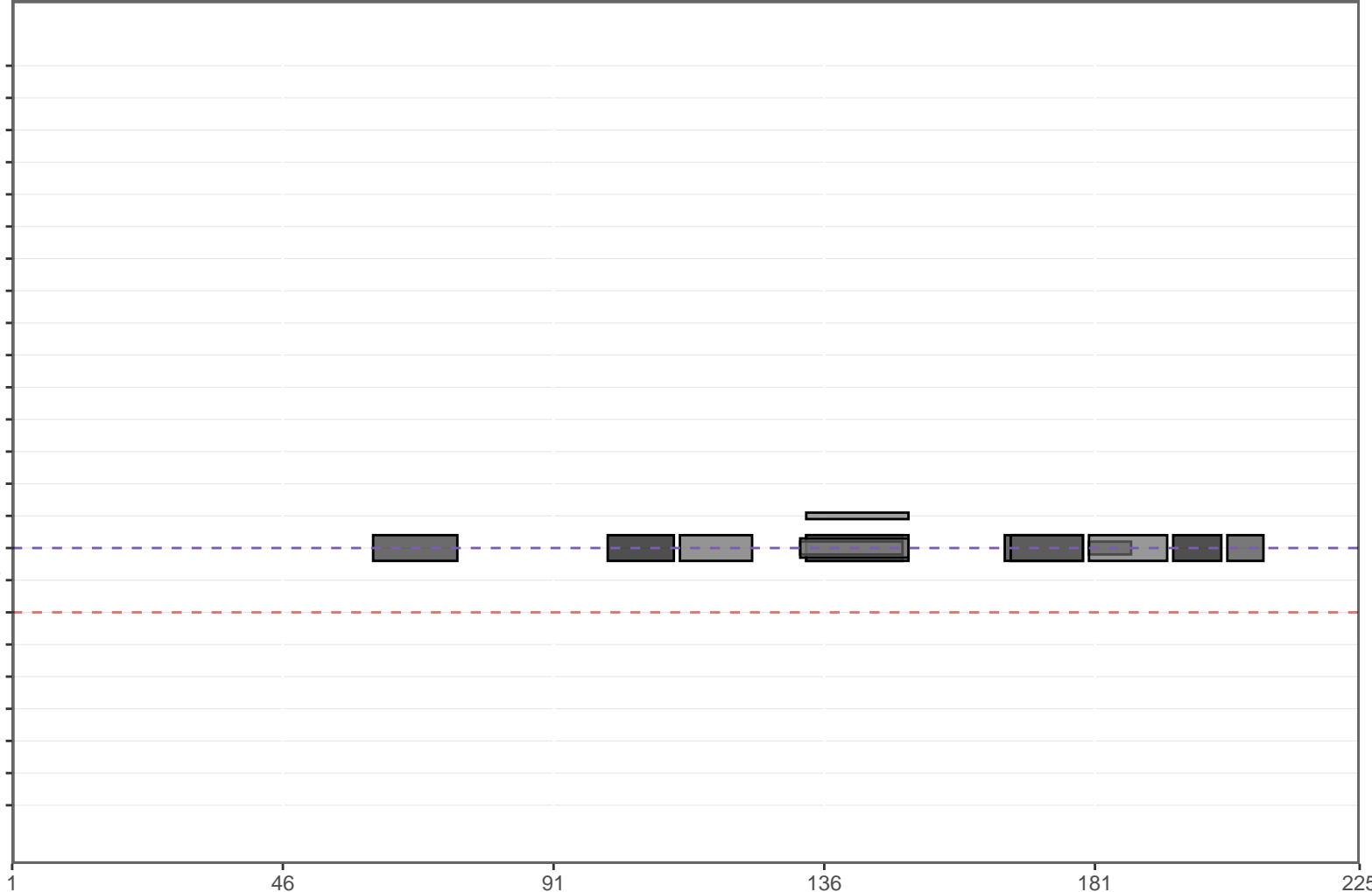
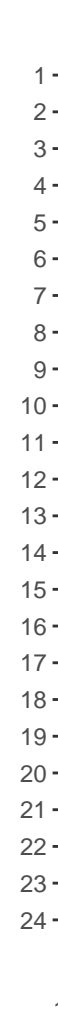
MW indication



Molecular weight

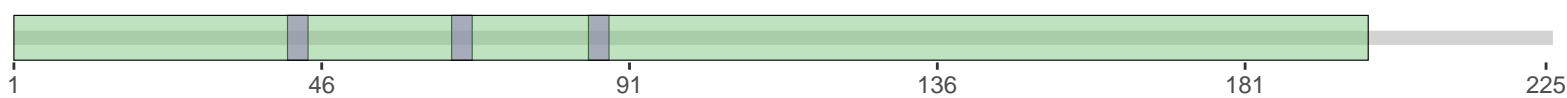


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

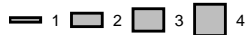


Protein sequence:

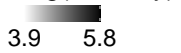
SAIVQVDAAPFKQWVLFQHYGVVDGRKHKGFANPKETEEEGEGAAAAAEEETKSNHLYLRKIETROKDRKLDPHIEEGFGGGRLLACISBSPGGGGGRADGVILEGKELEFYMKLGNKXKAGAGAA

NbL06g16380.1 cytochrome_b561_and_DOMON_domain-containing_protein_At3g25290-like [MW - SP = 23.16 kDa]

No. of times detected



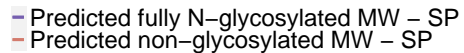
log(intensity)



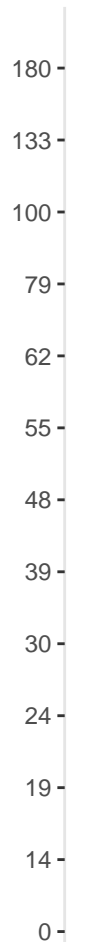
Values from



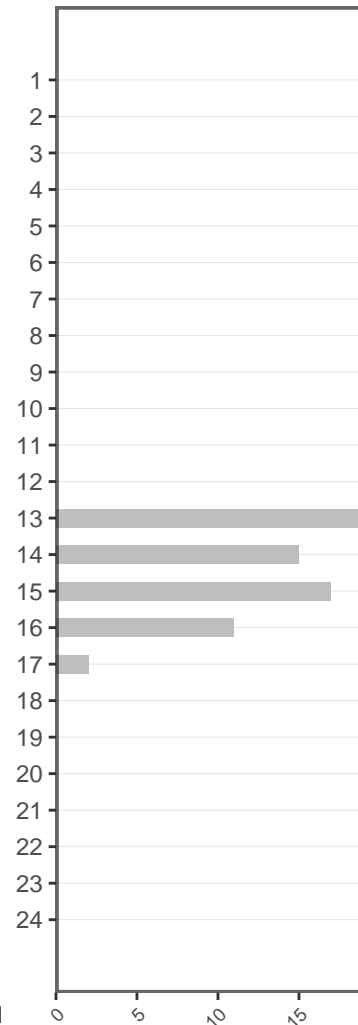
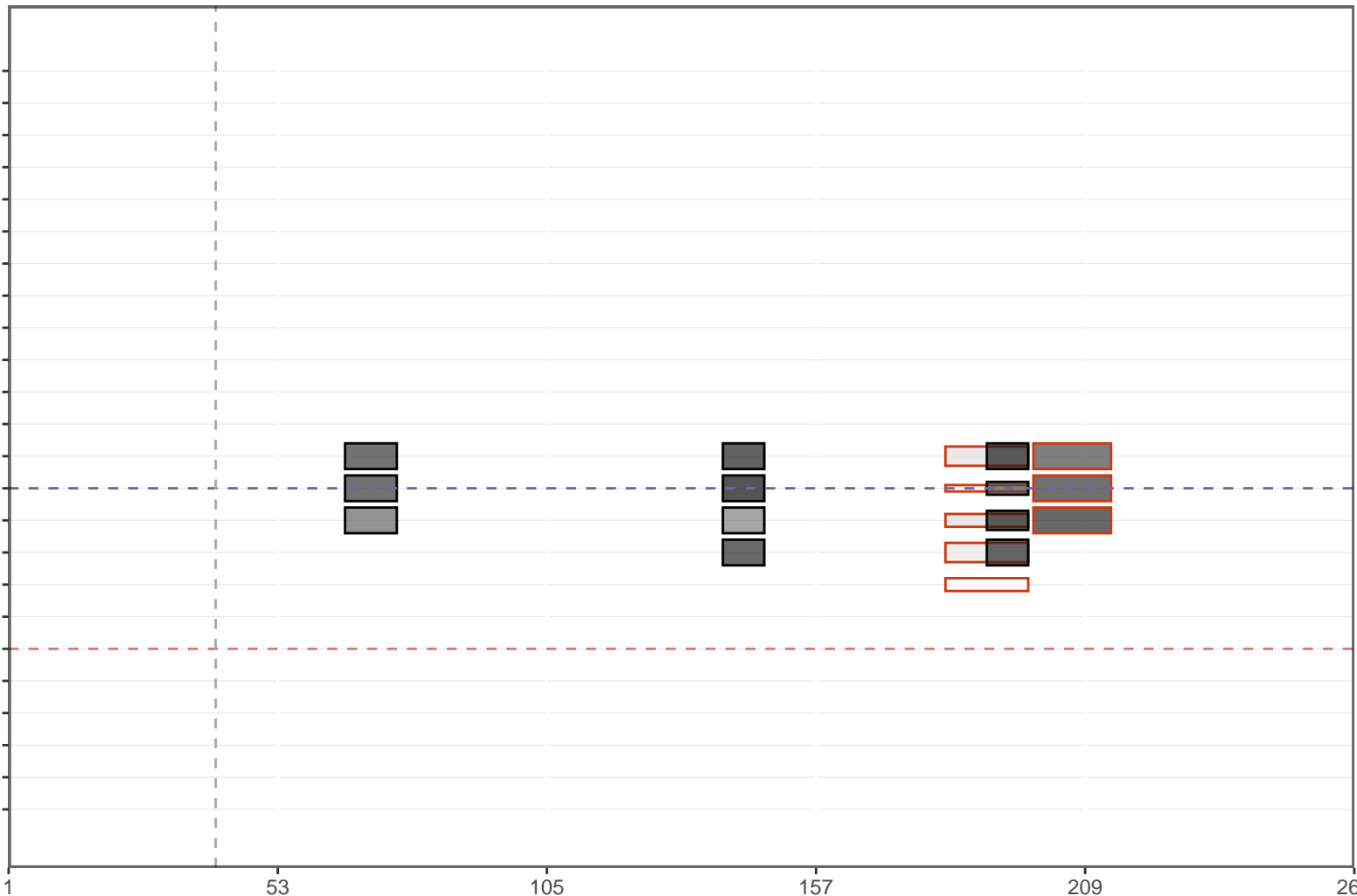
MW indication



Molecular weight



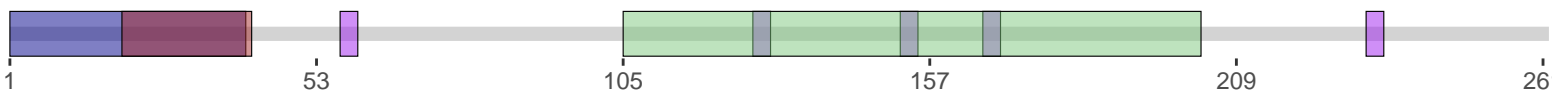
Gel Slice



Protein length

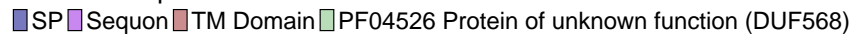


Peptide counts over 4 repeats



Pfam domains

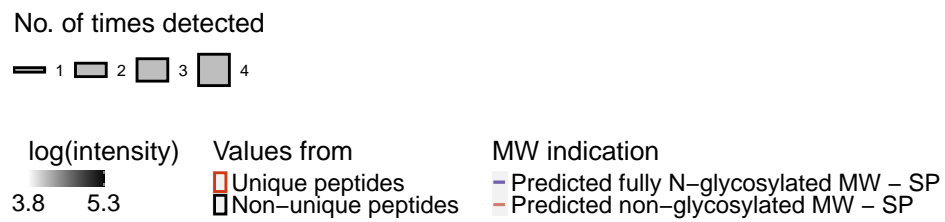
Pfam Description



Protein sequence:

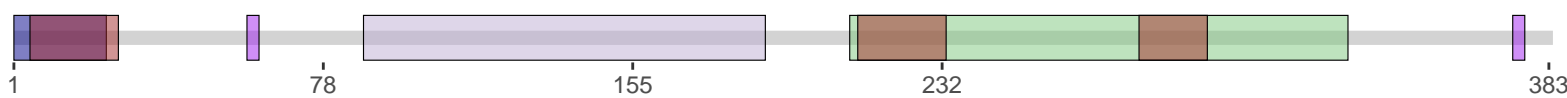
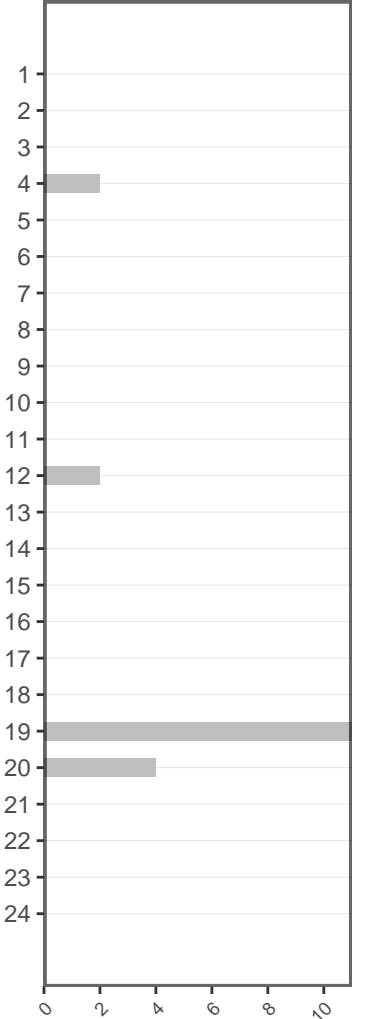
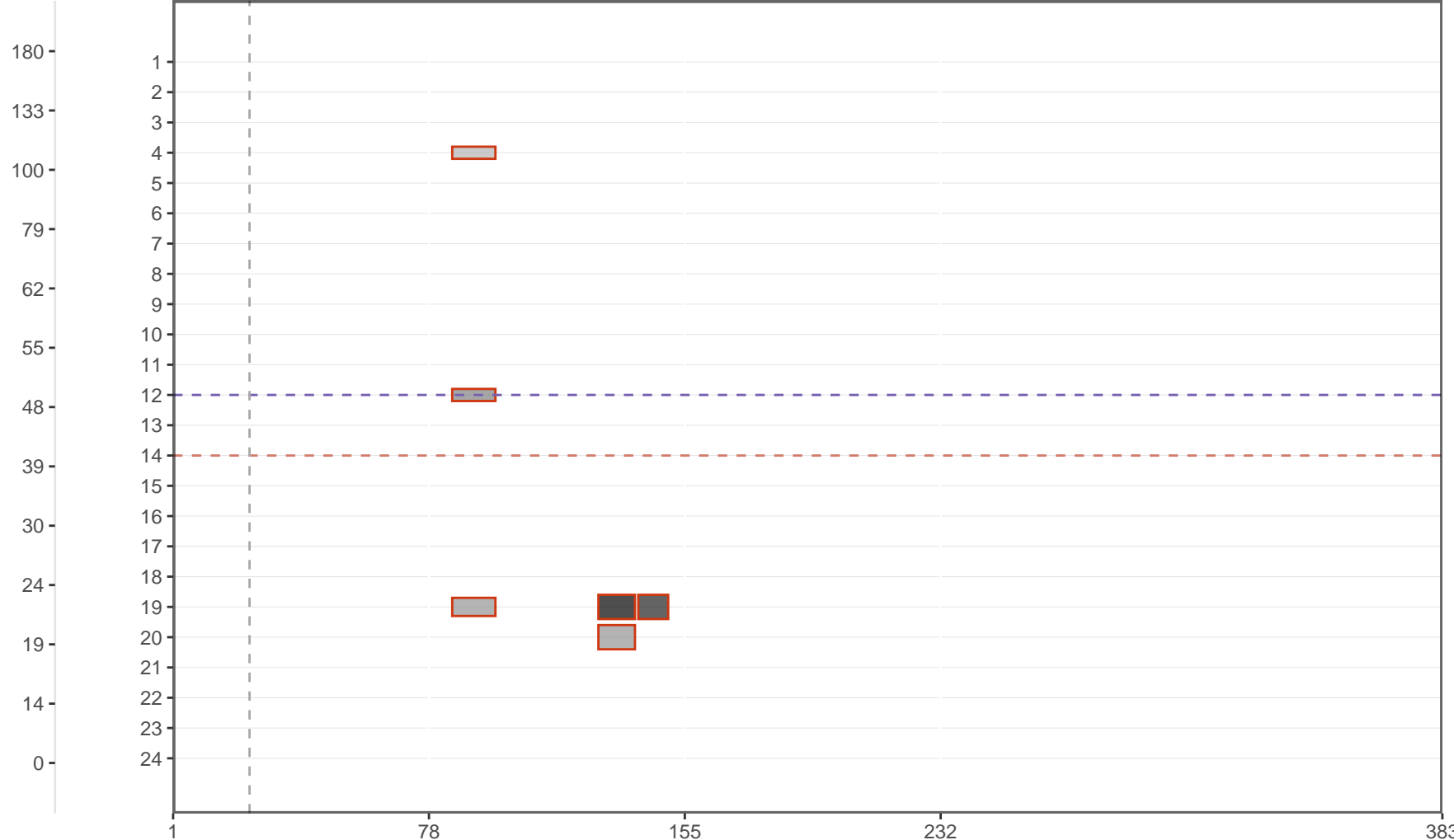
GAMVVKTYNLTSYKRFTEKLLNVLDSKAESSNGTMRKFALELPENTTTVNGVYQVGRWKGDKGKPVVHKFDTENLASKATLDLAATSSAGDGNKNAQSSVENSNSGGSGNETGSSSRILKSENGIFAFLLFLGVLLEQL

NbL06g16360.1 cytochrome_b561_and_DOMON_domain-containing_protein_At3g25290-like [MW - SP = 39.53 kDa]



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain PF03188 Eukaryotic cytochrome b561 PF04526 Protein of unknown function (DUF568)

Protein sequence:
QPNLNLSKGTLLDLGEGSKSGASGDEKWRKRNHGLNABWGLFPVGHIAHRYLRFSADPAWFLYHVSQCGSAVIGVAGWATGLKLGESKGFYDTRNHGIALFSLATLQVTFALLRPPKDKNYRFYWNHYHGVGVTMLVLELINVFKGLDILDPTKWRBAYGILVVGIAALLLEVTWVAVLKRKSNKSTKPYDG

NbL06g16230.1 uncharacterized_protein_At5g48480-like [MW = 16.86 kDa]

No. of times detected



log(intensity)



Values from



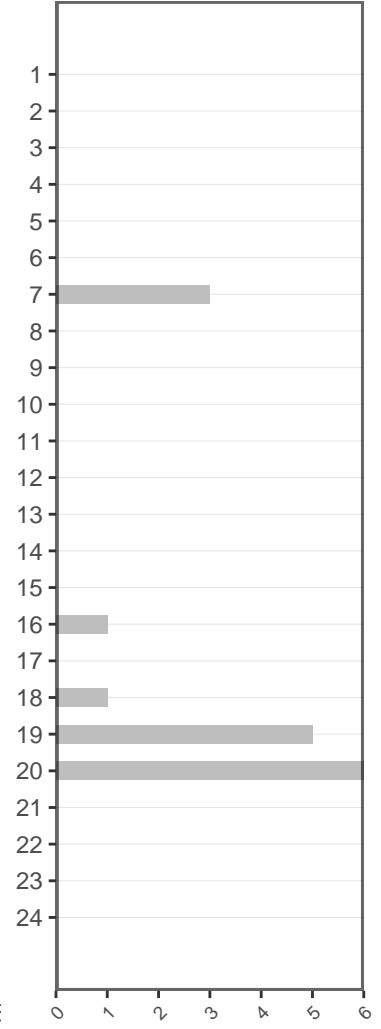
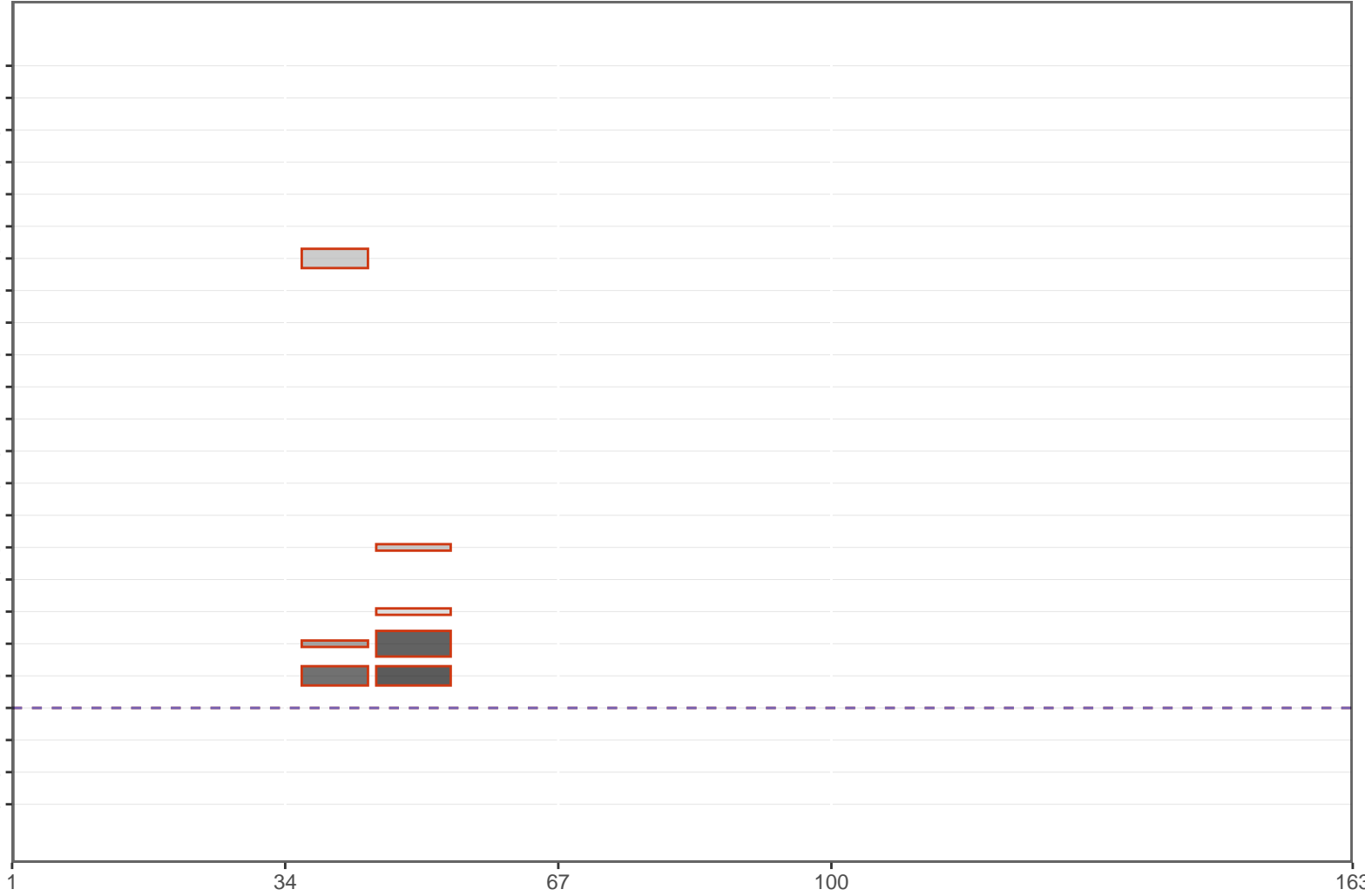
MW indication



Molecular weight

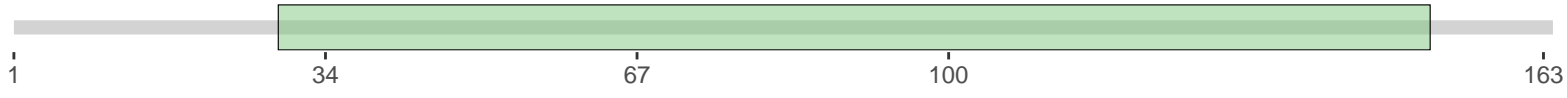


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MLLSAELKLGSTTFVSDSDLTDSDSAPVKTAGYVFLGLETEDEGAVAMAVTAGAVSEGEAEQDQACDGRVGLKDPYGNWLGSPKKGEE

NbL06g16190.1 LOC107783758 [MW - SP = 19.43 kDa]

No. of times detected



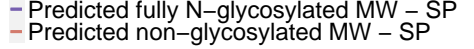
log(intensity)



Values from



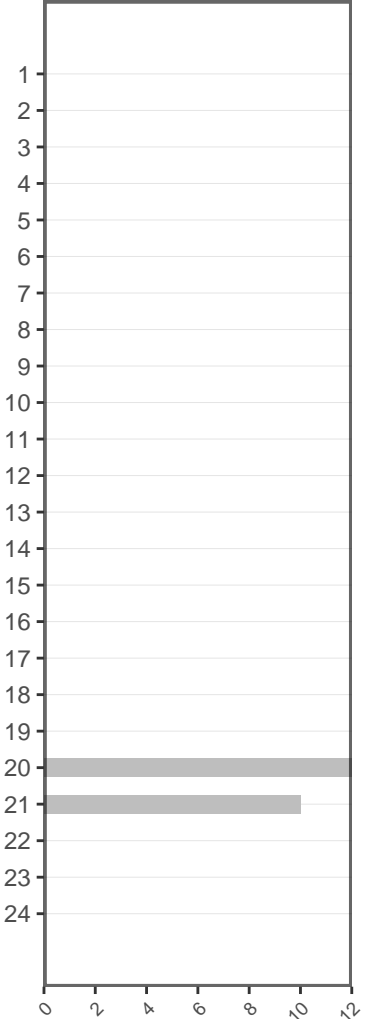
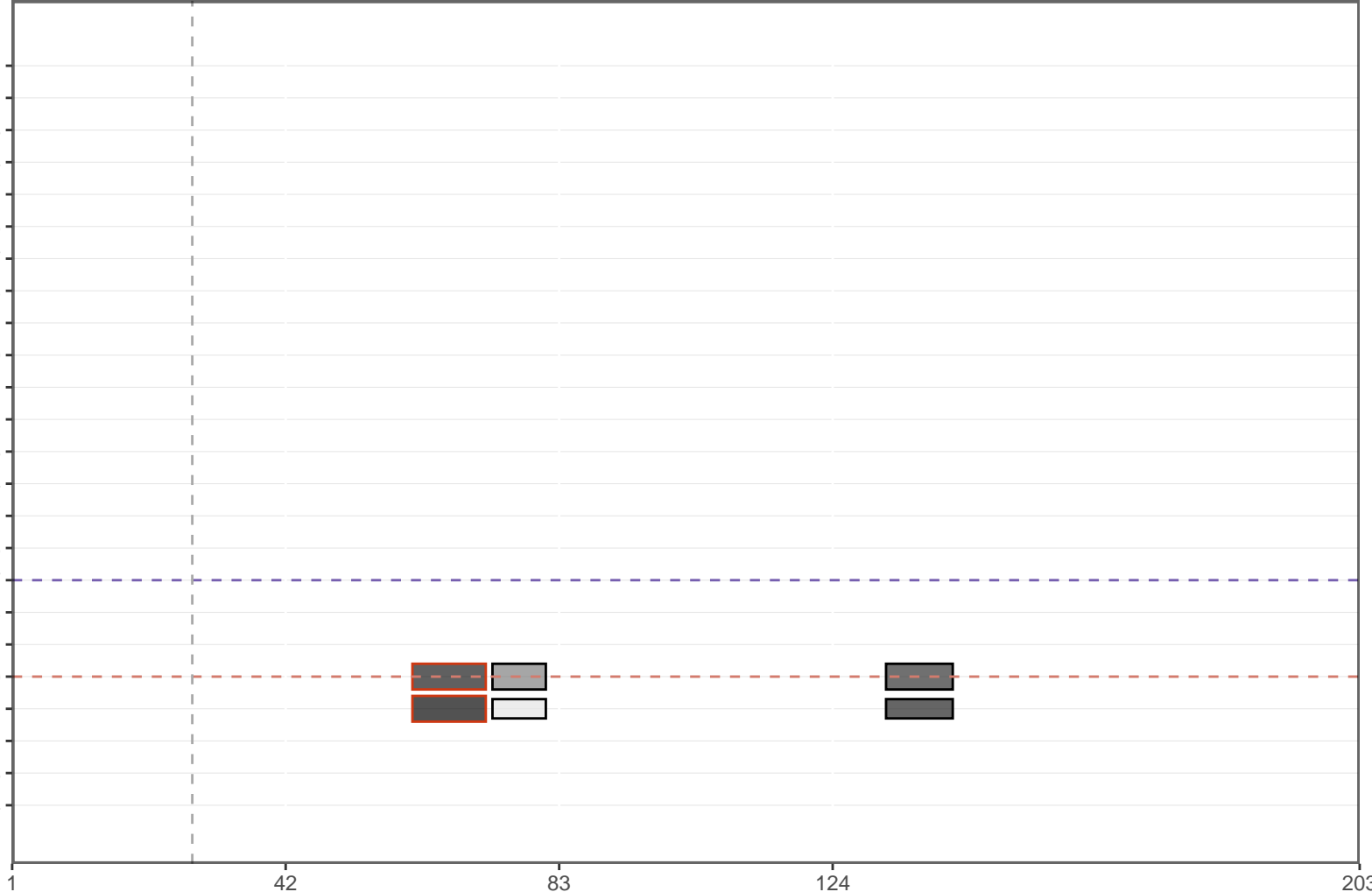
MW indication



Molecular weight



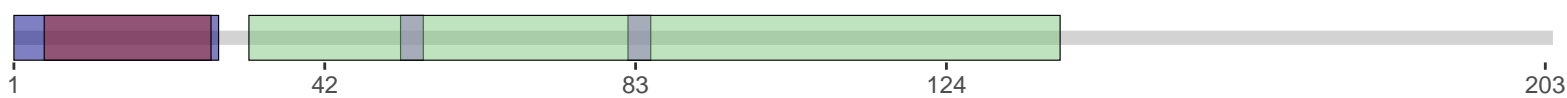
Gel Slice



Protein length

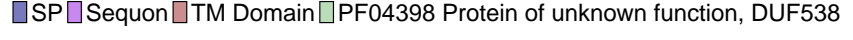


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

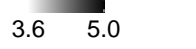
YQIHALSGIEAQDLFWFPVKDRVDPSSGLHYFNVGWVSKGFLSSFETPRDCTAVQLMLQDDMHADAASKTVRLHLVPCNSGTLAKSQSEELRYKFDGGNMGKRAL*

NbL06g16180.1 monocopper_oxidase-like_protein_SKU5 [MW – SP = 63.38 kDa]

No. of times detected



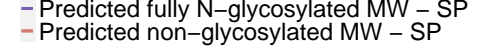
log(intensity)



Values from



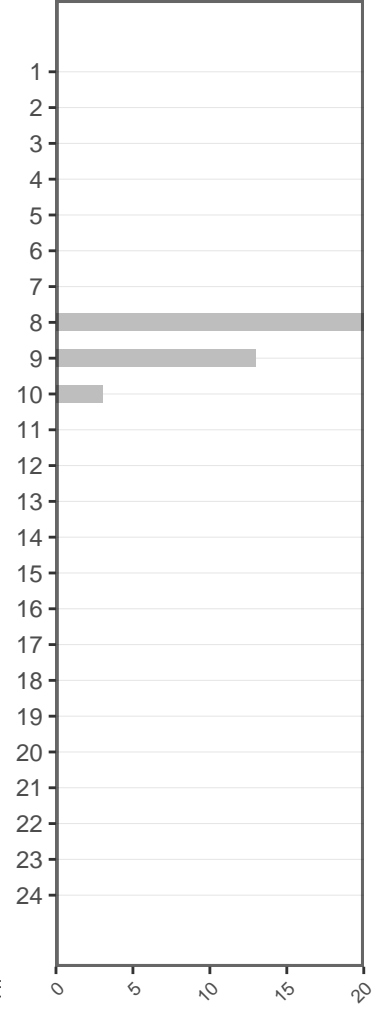
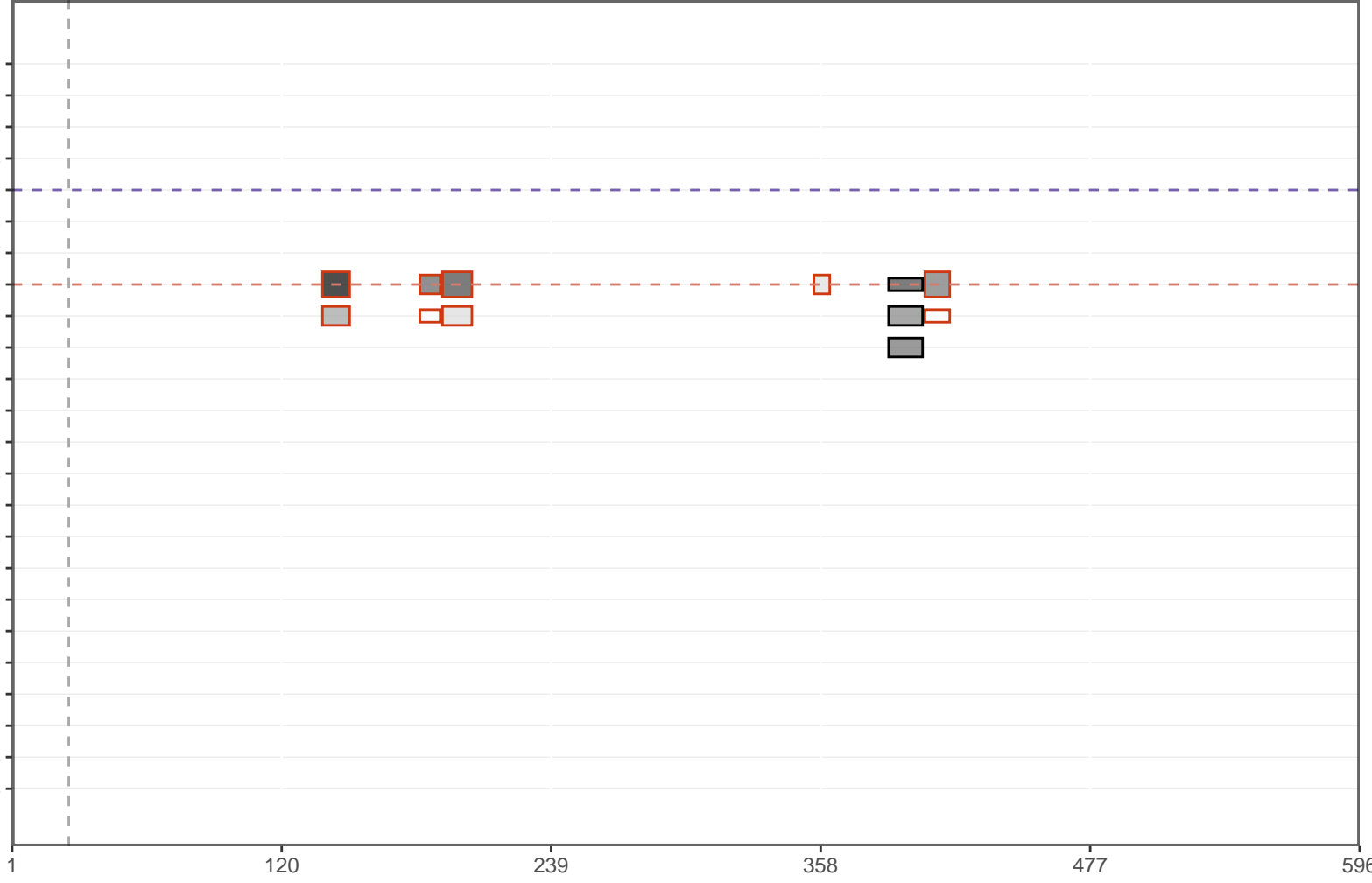
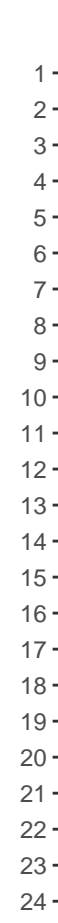
MW indication



Molecular weight

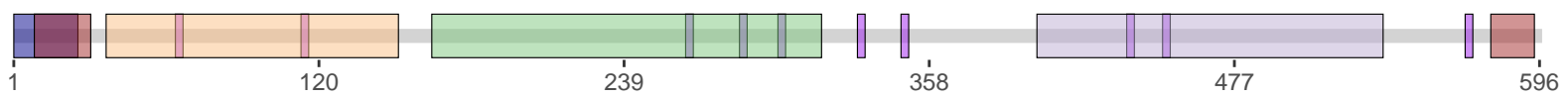


Gel Slice



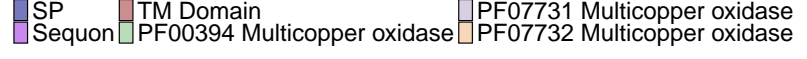
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISDYIYVSPRFVNSGGWSEKGVSVLHYENSQGPASGPLPPPPNESDFFSMGQARSRWVWSASAAARPKDGGFRVGETVTDVFLVLRPAELIEGKRRTTLEGGVLPASTPLKLAGGFNLGVFKLDFPKMMNRPAKVDTSHNGTYKAFVEIFGNDDTFVGSYHLDGVAFFVVGMDKGLWNTENSRTYKRWGQWARGTQVFRGAWTALLVFLDNDGWNLRAGMLDSWYLGQETVSEVWNPETTDKNDVLPANWYGGALSPLQKDAHRVNFSGAPSLQKT

NbL06g16060.1 ribulose_bisphosphate_carboxylase_large_chain [MW = 29.58 kDa]

No. of times detected



log(intensity)



Values from



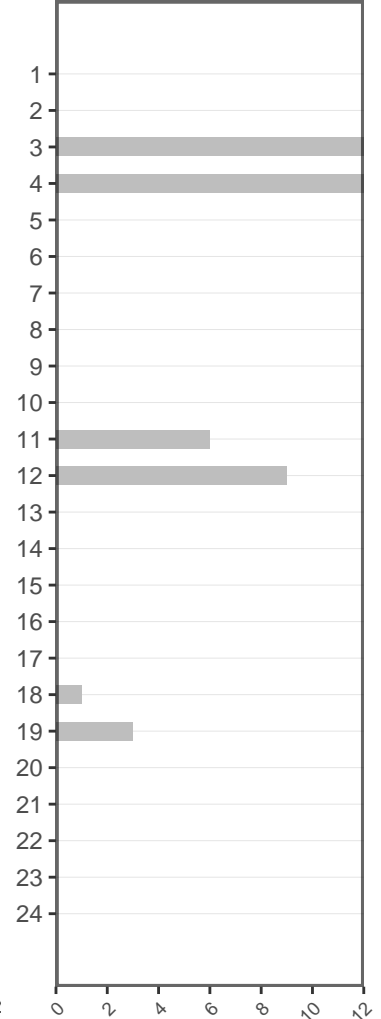
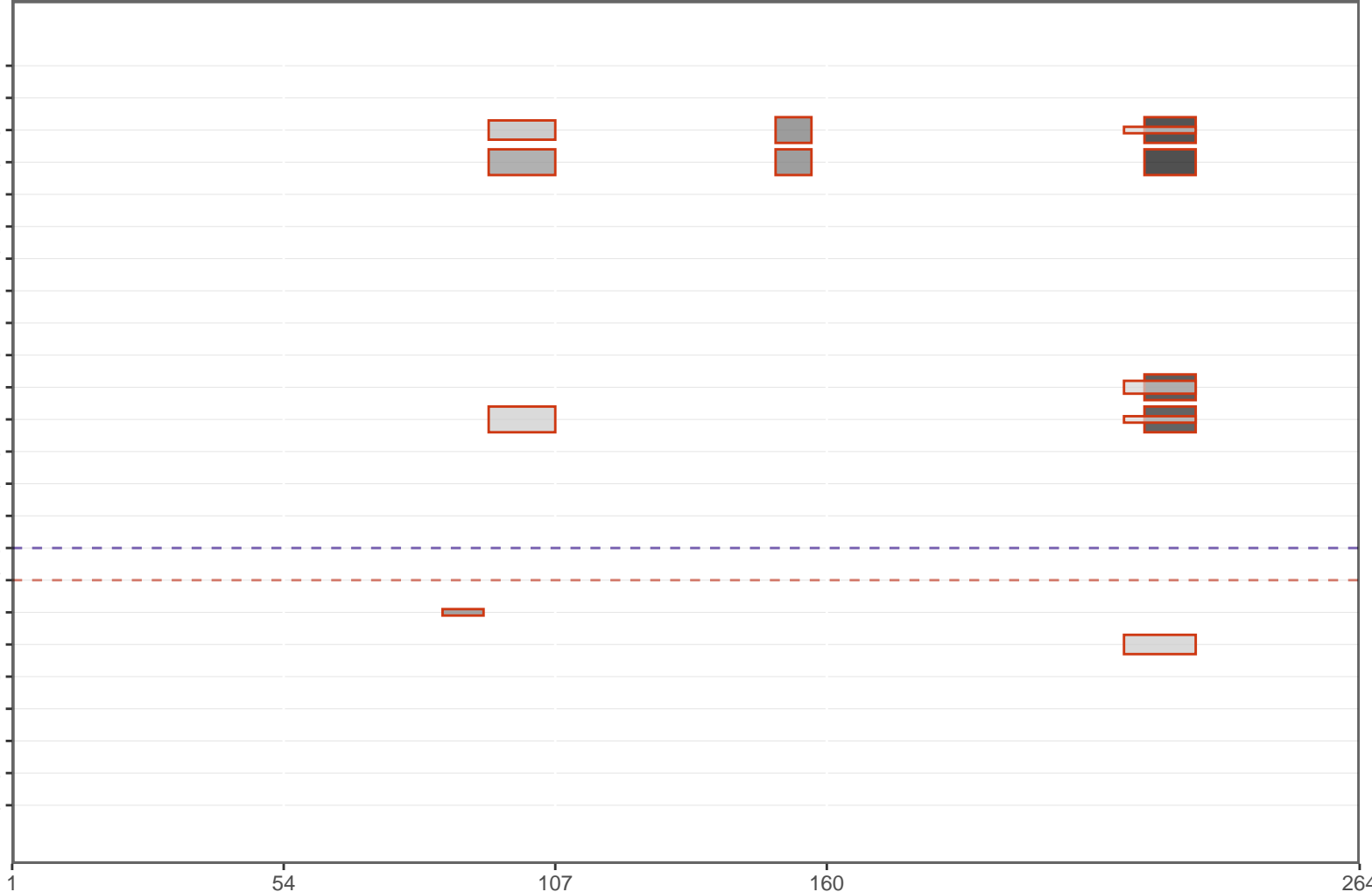
MW indication



Molecular weight



Gel Slice

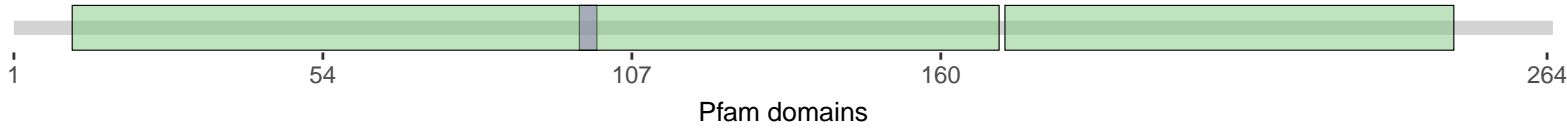
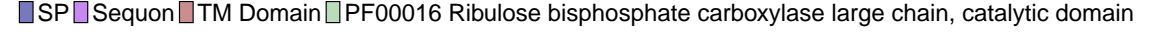


Protein length



Peptide counts over 4 repeats

Pfam Description



Protein sequence:

/MIDYLTGEFTANTGLAHYFGDNGLFFHHRAMHEVDKGNKHGHFRVSRLLALPALTEFGDDSVLHFGGGTLGHPWGNAPGAVANRVALEAGVKARNRGRDLAGEGNEIREDSEWPELDDMGCEVWKEIVFNFAASDVLDK

NbL06g15950.1 33_kDa_ribonucleoprotein_chloroplastic [MW = 35.34 kDa]

No. of times detected



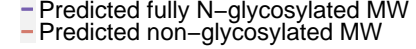
log(intensity)



Values from



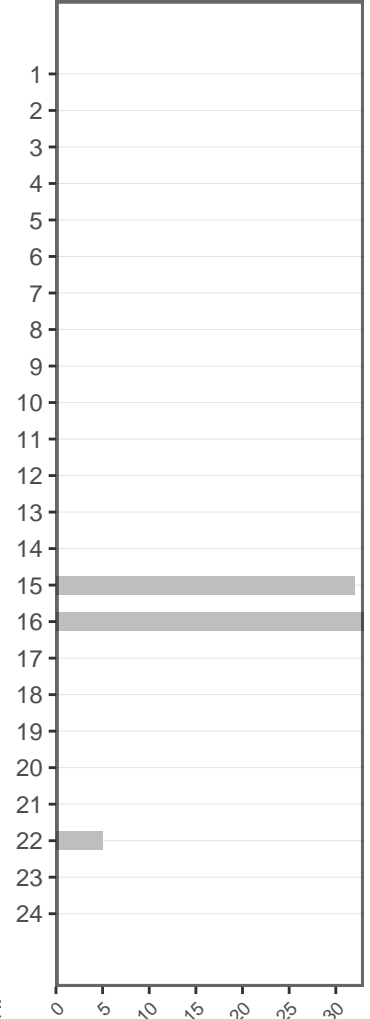
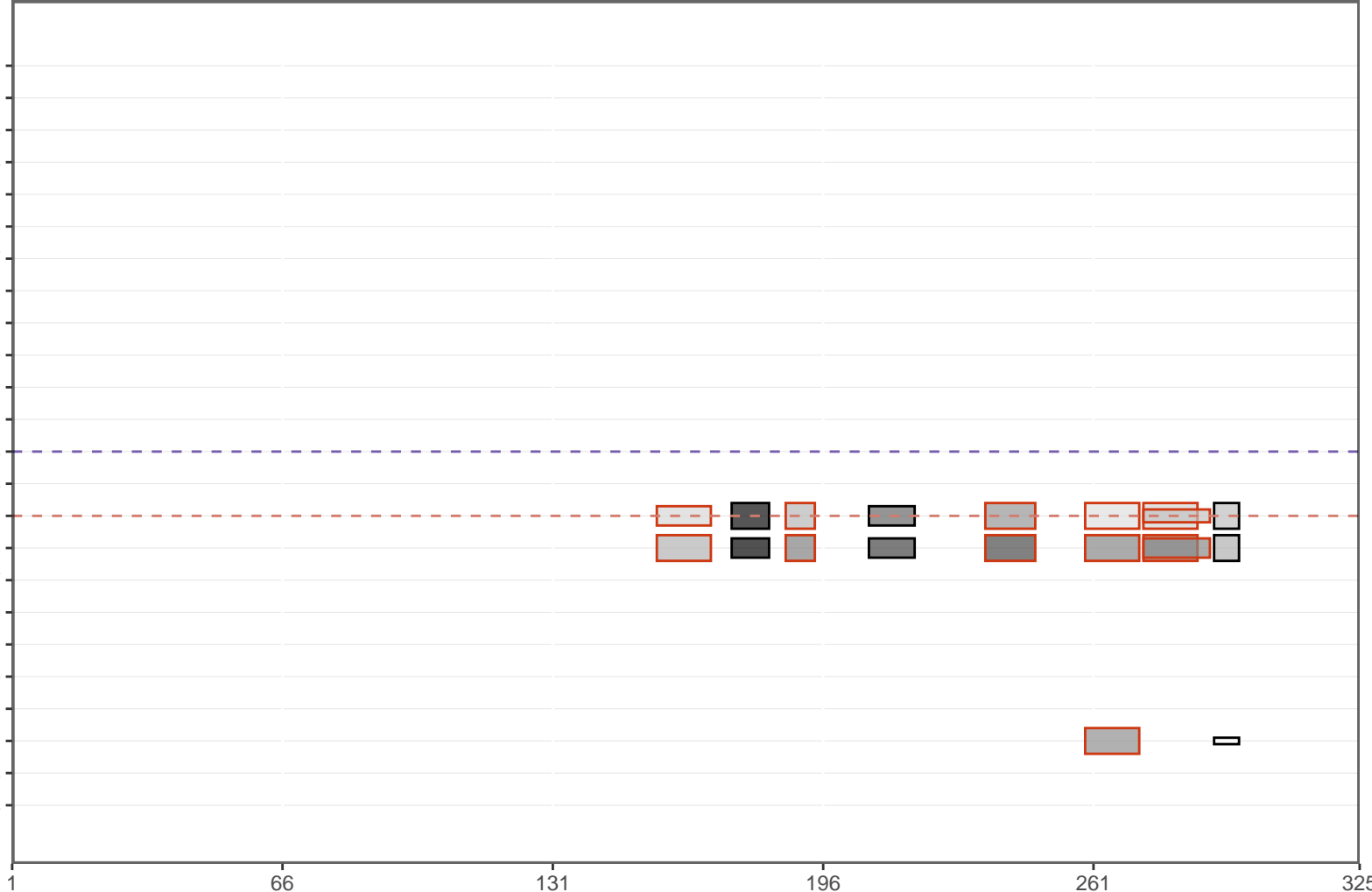
MW indication



Molecular weight

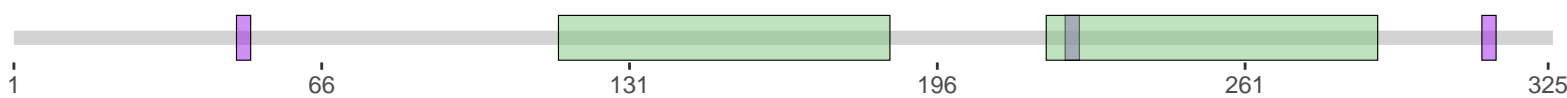


Gel Slice



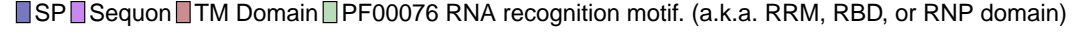
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IRSRGFVITMGSVEEAKAIRLFDGSGVGGRTVKVNFPEVPKGGEREVMSAKIRSTYGGFVDFPKHLYVNLISWALTSQGLRDAFVDQPGCFMSAKVYDRSGSGRSRGGFFITSSAEAMKSAIDTMNEVELEGRLRLNVAQKAKLSGPPLVETSPENDSENSELLSSLSG

No. of times detected



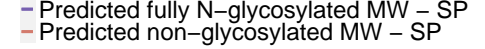
log(intensity)



Values from



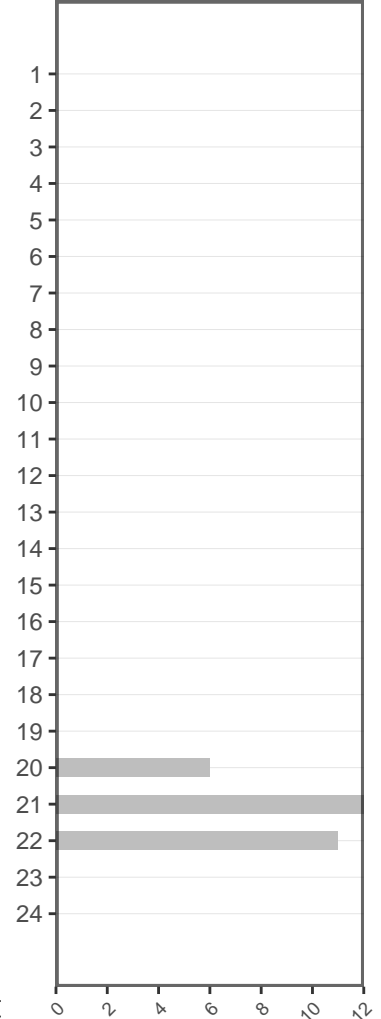
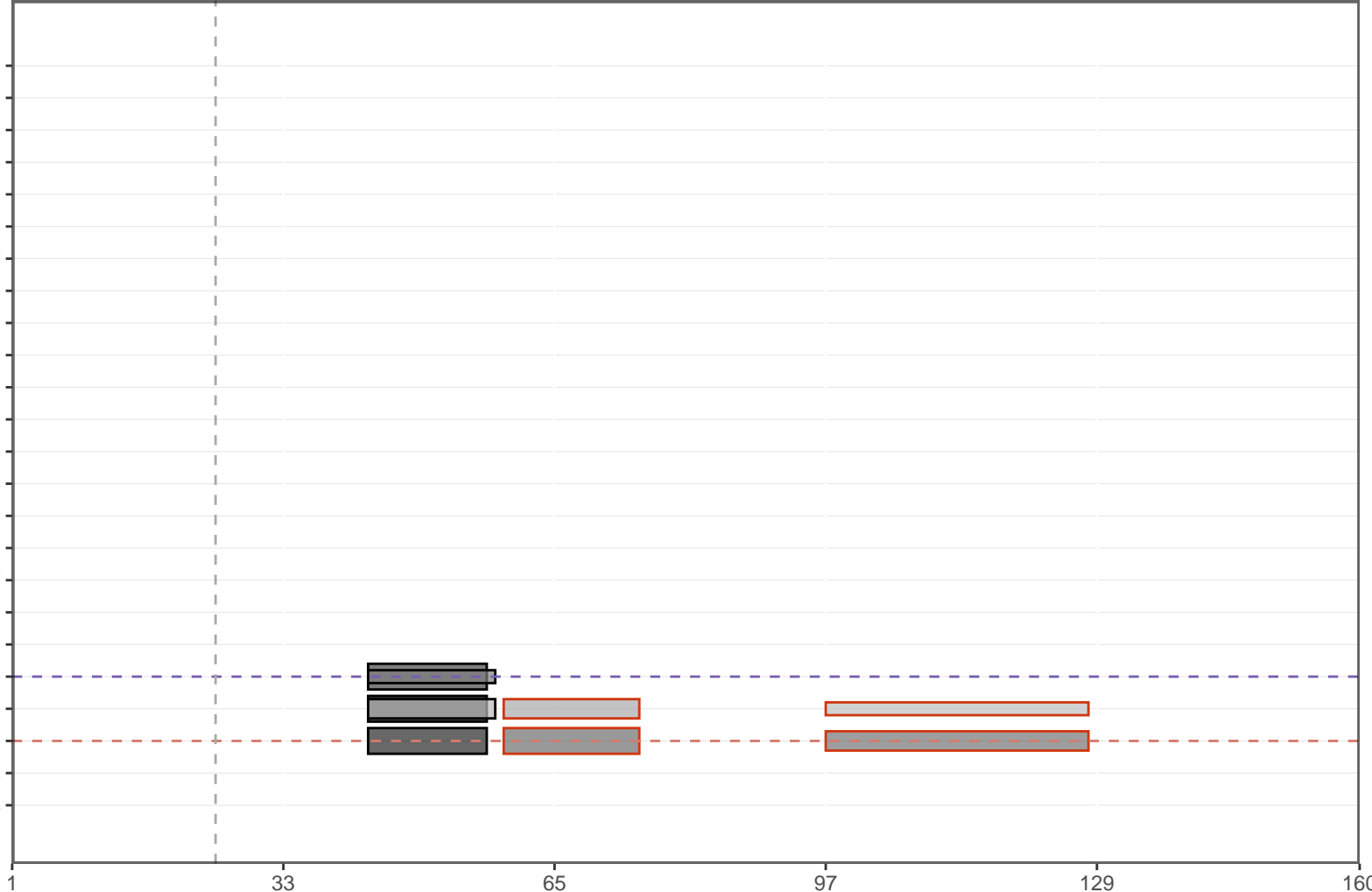
MW indication



Molecular weight



Gel Slice

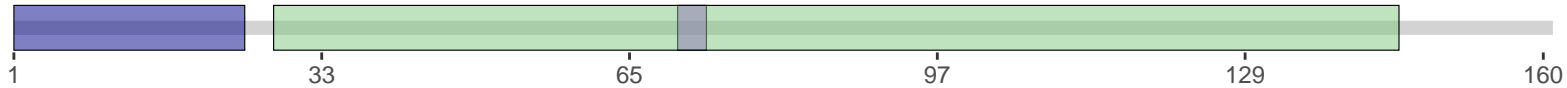


Protein length

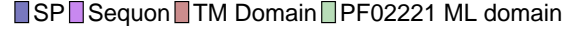


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

GQNLTGGKLVLDVNYLFFRVVHHEAIDLKETSQPAAGDFVISHGDELPGFTTTPGQVYLTMMVDDKKNHQLGGIGFGFSIGFIAESQALADS

NbL06g15810.1 fasciclin-like_arabinogalactan_protein_17 [MW - SP = 46.83 kDa]

No. of times detected



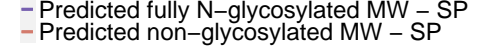
log(intensity)



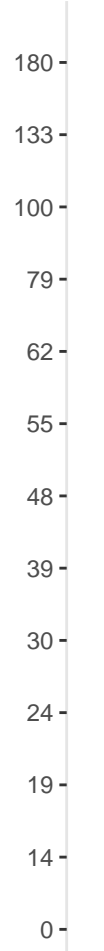
Values from



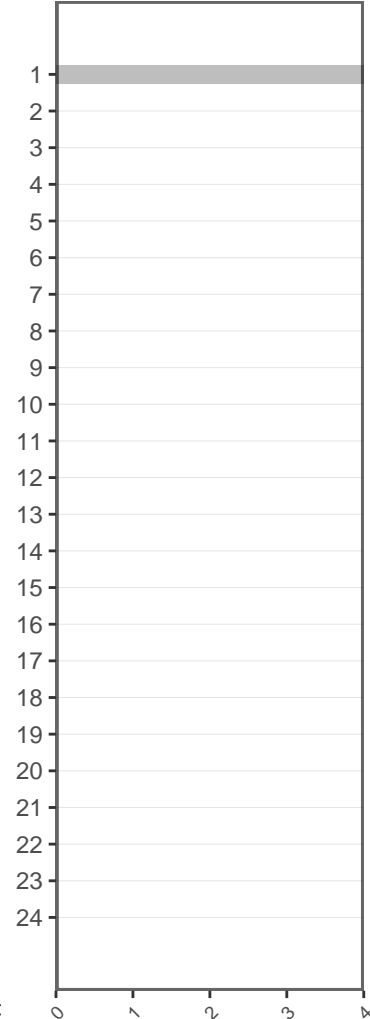
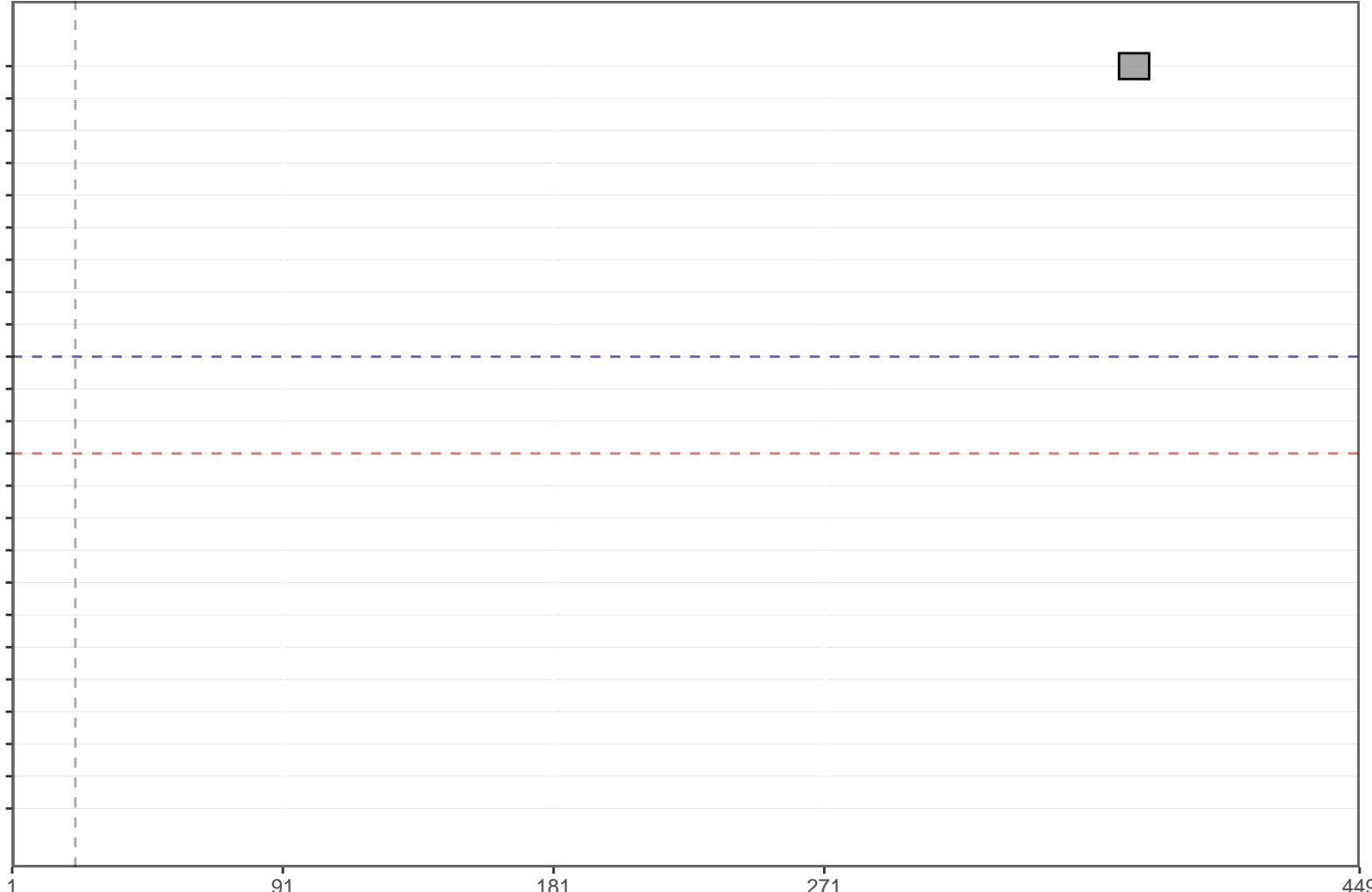
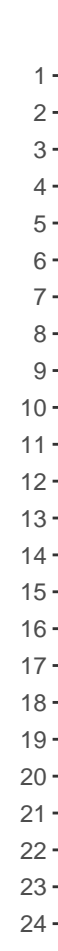
MW indication



Molecular weight



Gel Slice



Protein length

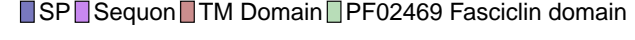


Peptide counts over 4 repeats

Pfam domains



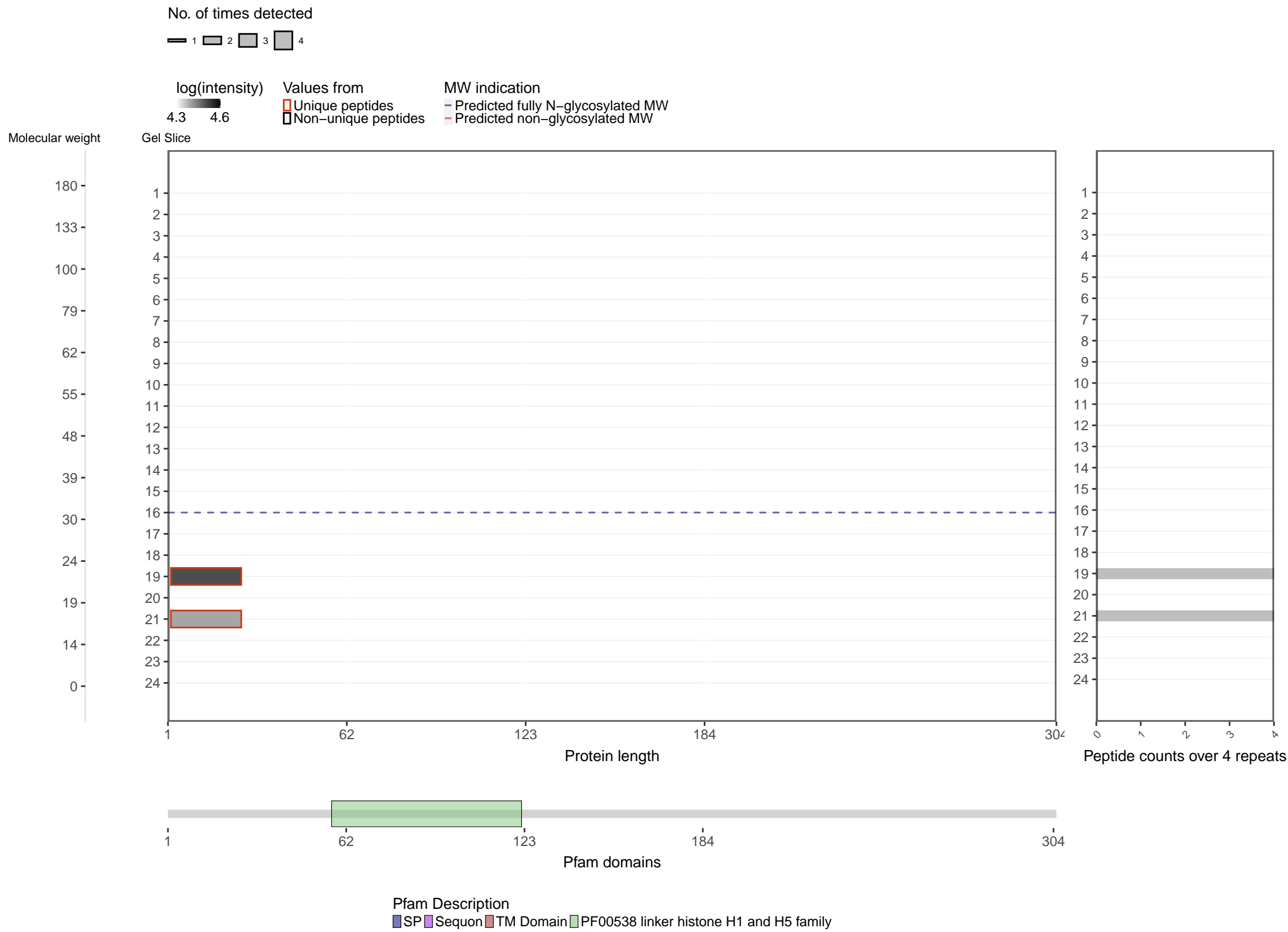
Pfam Description



Protein sequence:

TNRLKKKPTPTVYKGGAPNLPKYSAMAPGRELAFAPAPGPGGPHHFDGEGSKVDFQGLHYGGYNELADLVNLSLATEMGRVSEGVYLVLPNDKAMAKLTDQLSEPGAEGQIMYHLLPEYGTESMYNARRFRGKVKYDTRLFRHKVVAEEADGSKVFGVAEGSAVLFDPDYKTDGRISVGGIDGVLFPVEEKAAAPVAKVAKVAKPRRRLKMEVAGSVMSGFC

NbL06g15640.1 histone_H1-like [MW = 31.58 kDa]

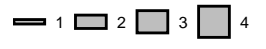


Protein sequence:

AAKPKAAAKAKPKAGKPKAKPKAGKPKAKPKAKPKAKPKAKPKAKPKAKPKAKPKAKPKAKPKAKPKAKPKAKPKAAVAPKPKATPVKAKAAKPKKAKETKPKAVRTTRTFTRKAAKPKATPKAKKEPKAKTTPAKSAKPKAKASTRRGGRK

NbL06g15610.1 glutathione_reductase_chloroplastic [MW = 60.28 kDa]

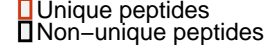
No. of times detected



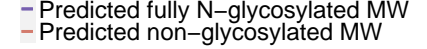
log(intensity)



Values from

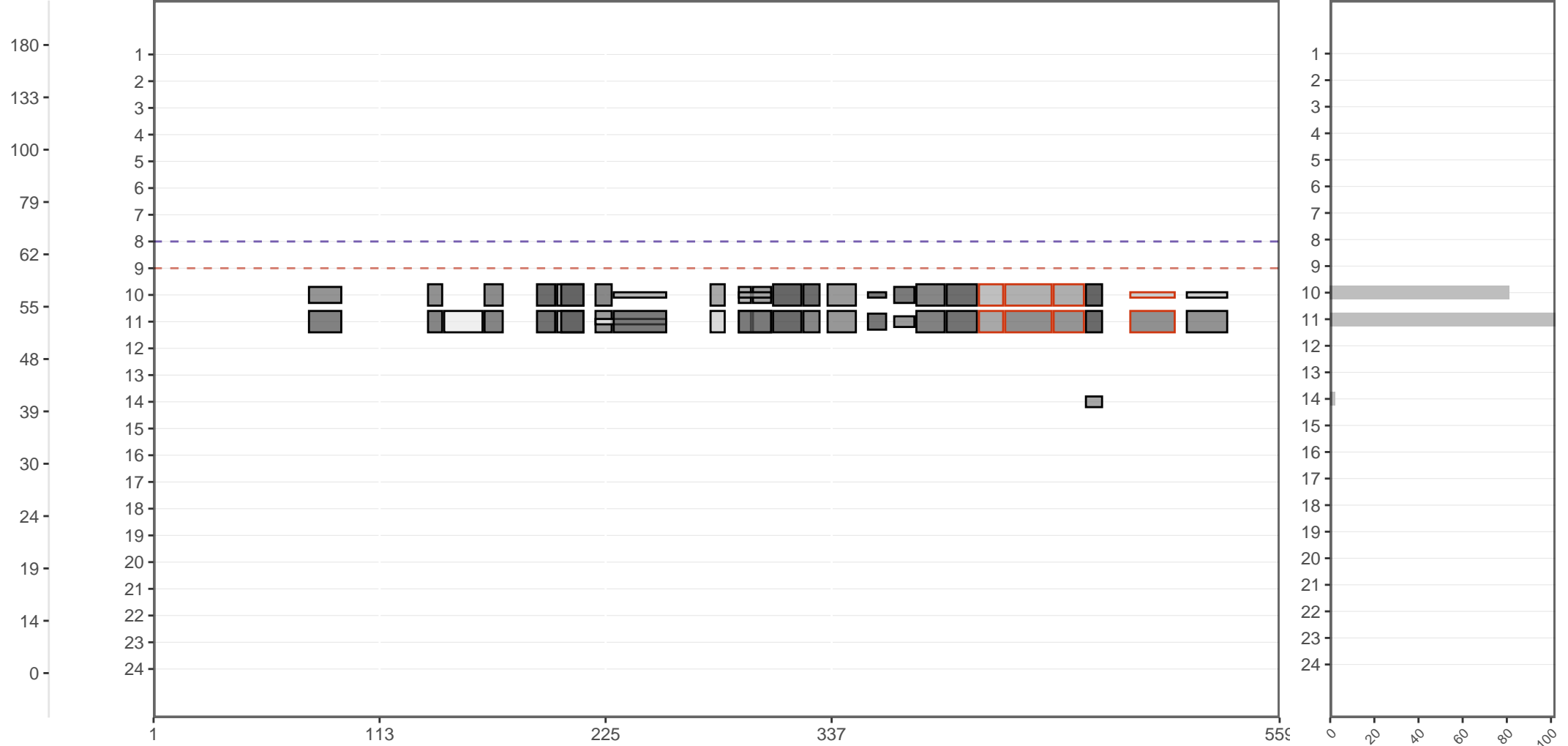


MW indication

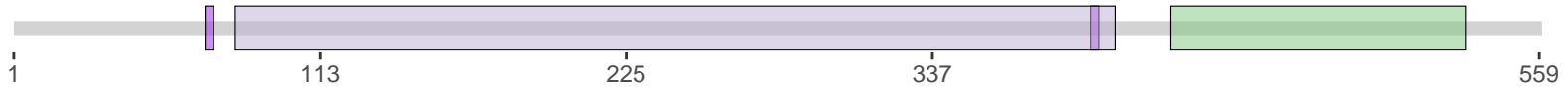


Molecular weight

Gel Slice



Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF02852 Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain
- PF07992 Pyridine nucleotide-disulphide oxidoreductase

Protein sequence:

IFAGIFNGLKSEVHYFRGKVKLRGFDIEIRDFVGEQMSLRGIEFHTEESPAIVKSDGSLKTSRGTVEGFSHMFATGRPNKTLGLETGVNMTKNGAEVDEYRSTVPSWVAGDFTDRINLTPALMMEGGALAKTFADERTKPDVIRNPAVAFSGPPIGGVSLMEQAIKEFGDDVYTNFRPLKATISGLPDRVFMKLVGAKTSKVLGLHMGDDAPEVWQGFAMVWAGLTKADFDTVGHPTSAEEFVTRMRTPTKRVKRSRPEEGKAEDIKAAAGV

NbL06g15110.1 acyl-CoA_dehydrogenase_family_member_10 [MW = 92.74 kDa]

No. of times detected



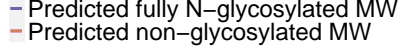
log(intensity)



Values from



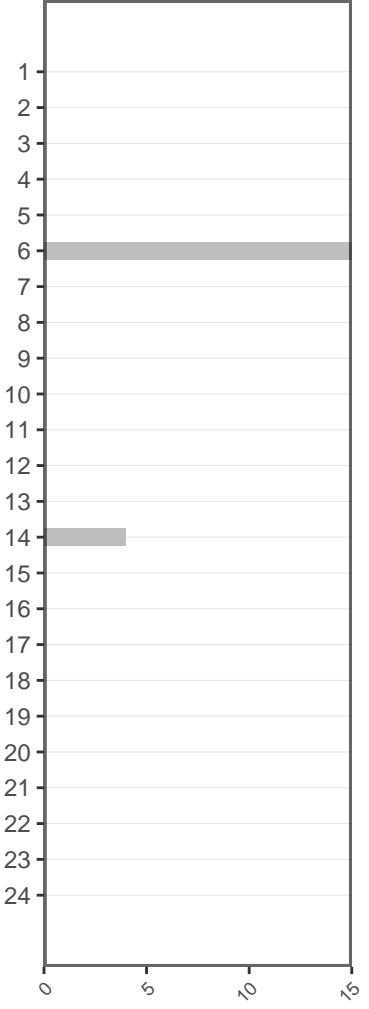
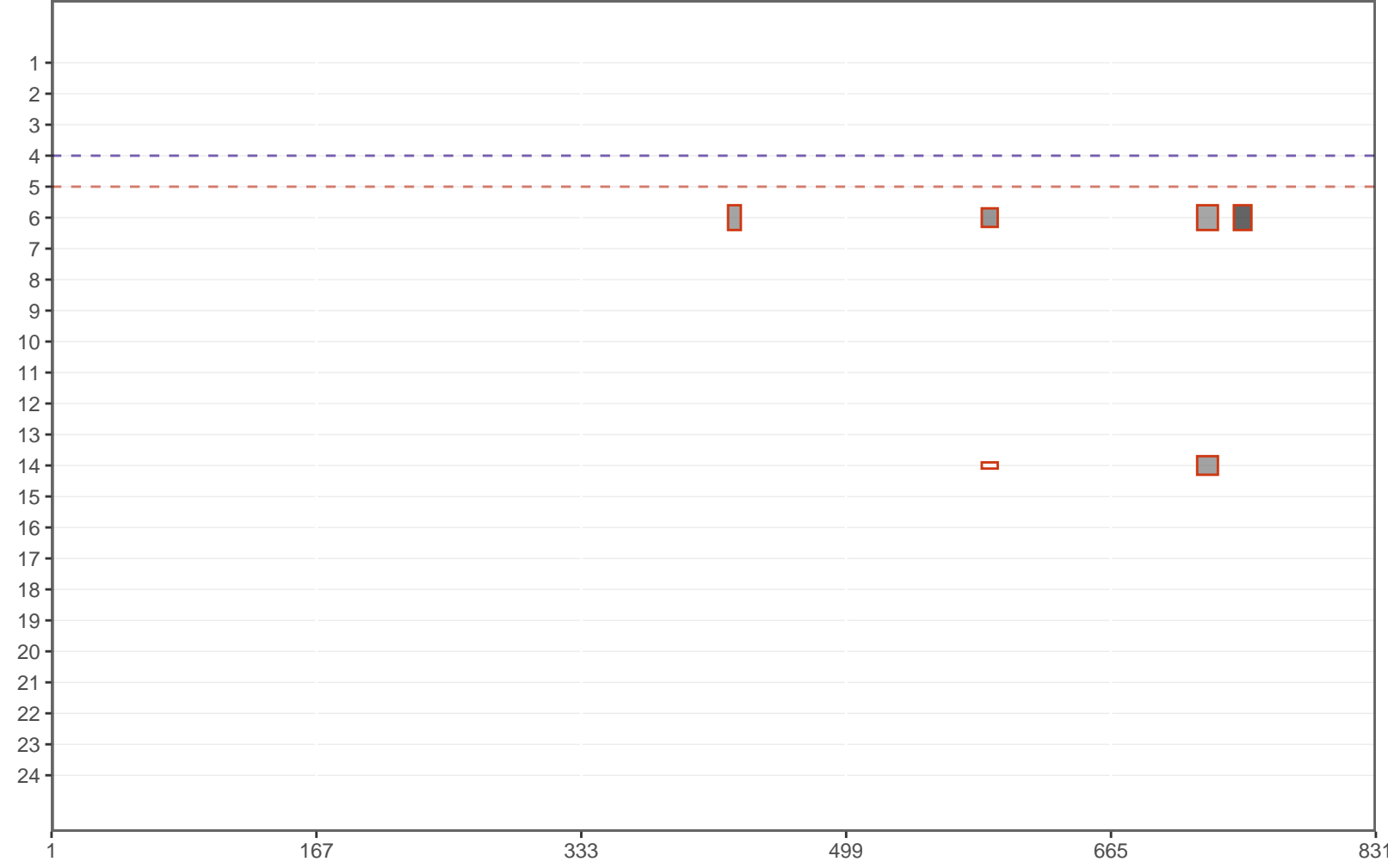
MW indication



Molecular weight

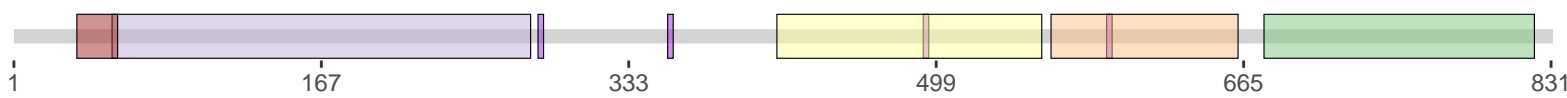


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

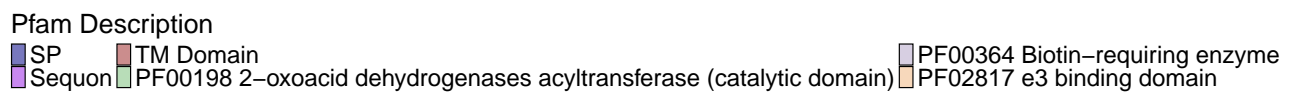
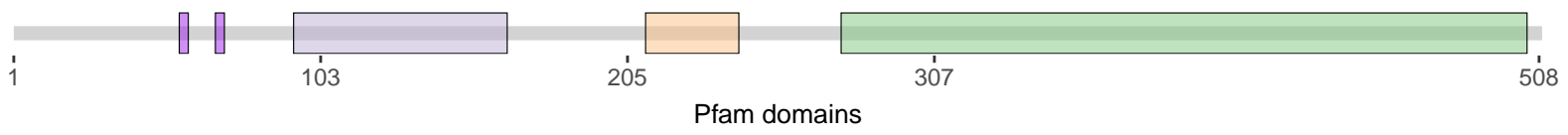
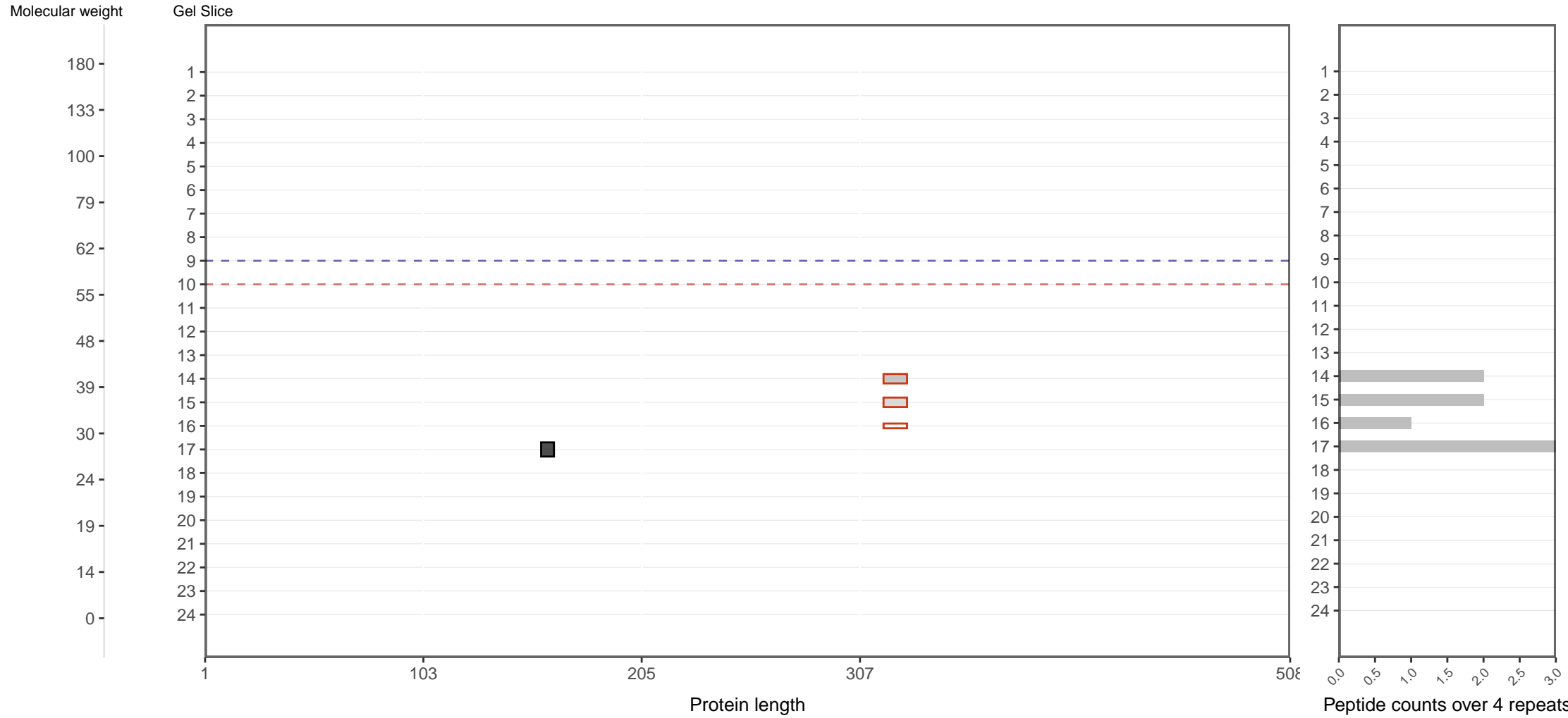
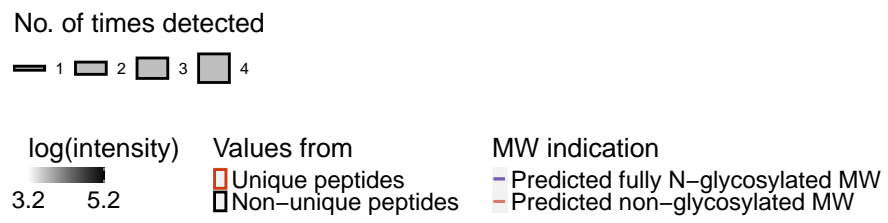
Pfam Description

- SP
- Sequon
- TM Domain
- PF00441 Acyl-CoA dehydrogenase, C-terminal domain
- PF01636 Phosphotransferase enzyme family
- PF02770 Acyl-CoA dehydrogenase, middle domain
- PF02771 Acyl-CoA dehydrogenase, N-terminal domain

Protein sequence:

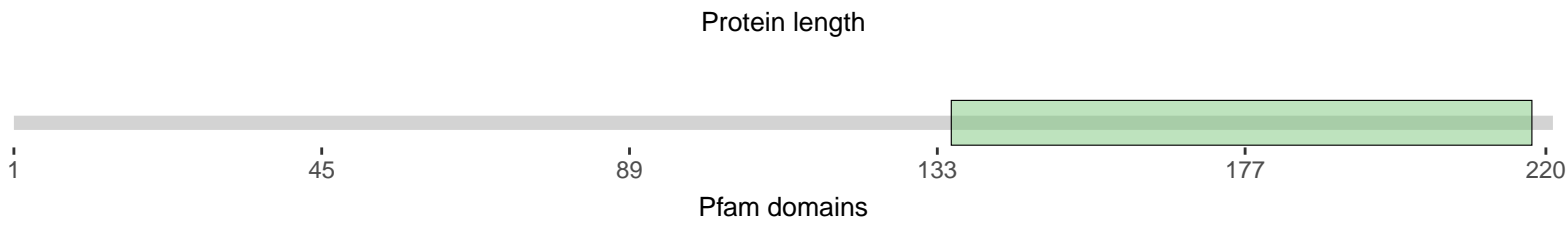
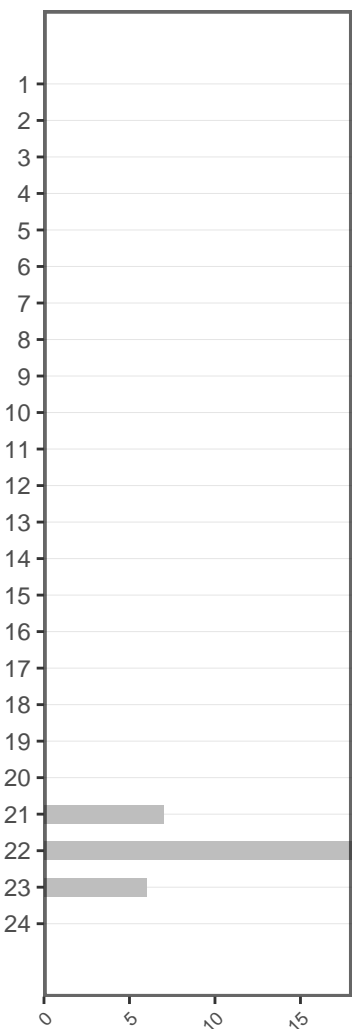
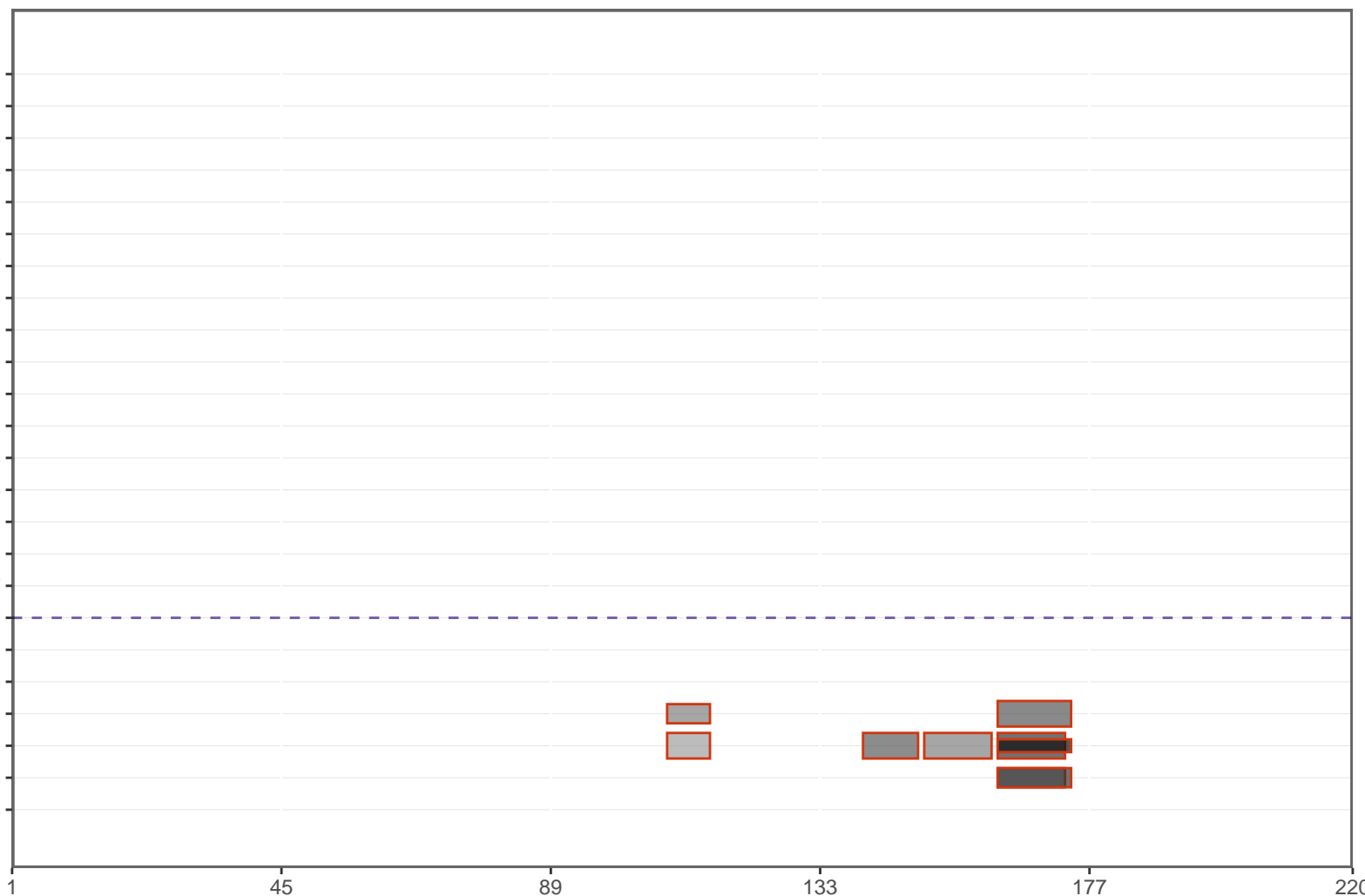
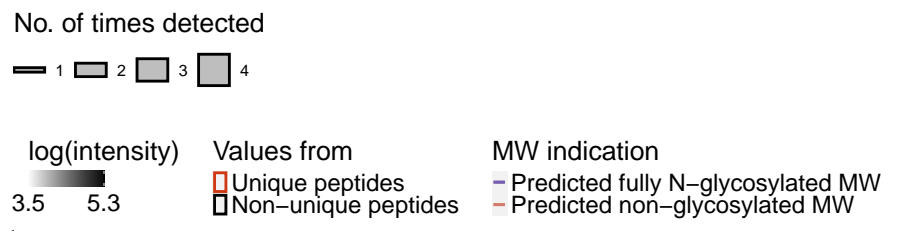
SGRFVPSSEKVKLRKLRKLFKMEHIVPRENEFSKLAGSNMRWTHPDEEKLEKELAKKEGLVNLWPFDDAARARELYVGRNGLSNDSDRLLAGLNLGVGLGCEIMSRGVAWPAQFNGAPDGTGMVEVLLRFGNEVGMKEVLPLEKGRISGFAMTEPQVASSDATNEGSKIRHGDGVYVNGTKWVTSFGAMDPRGKILVMGKTDLAAPHKGGSMMLVDNISRGITVWRPLTFVGFDDAPHGHAEILFENVRVPAANNLLEGCGGFEIAGGRKLPQRLHHCMLRIG

NbL06g15030.1
 lipoamide_acyltransferase_component_of_branched-chain_alpha-keto_acid_dehydrogenase_complex_mitochondrial-like [MW = 55.26 kDa]



Protein sequence:
 IEDVTNVAIQKGLINEALECAQDRHSEVSLIGGGYEDKTLGLRGVQRMYKSMFLAAKHPFYFIEEMNVCNVALVELKQKFNENSDPEIHTFLPLVLIKSLMALTHPMLNLSRFSEESYEVLKQSHNGIMAMATPNGLVVPNKNVQSLSEITKELTRLQKAKINIKLSPDDKGGITLNSNGHGKGFGLPLNSPEVAHSLGRHQKIAQFGEDGDVYPASVMTINGADHRVLDGATVAFKFCNDWKKFVEKPDLLLLLHTR

NbL06g15000.1 dynein_light_chain_1_cytoplasmic-like [MW = 24.65 kDa]



Protein sequence:
 IFEDMSEDAKRTGGVPAKFTSDRRRTSSGGVPSFGKIKITKISADMKPDKVQKEAVDIAAFEKYNEKQVAEGKQKFEFDKIKYGPRTWHGIVGKRFDSVYTHETNHKVEYELDQKAVLLFKSG*

NbL06g14840.1 CAP-Gly_domain-containing_linker_protein_1-like [MW = 16.47 kDa]

No. of times detected



log(intensity)



Values from



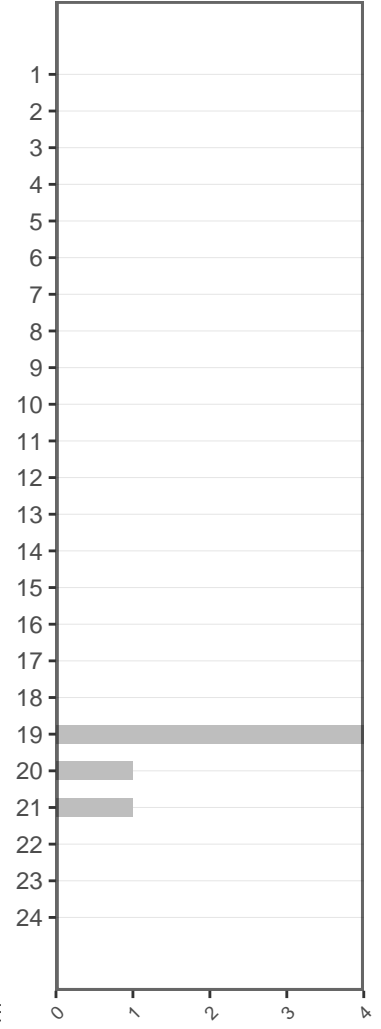
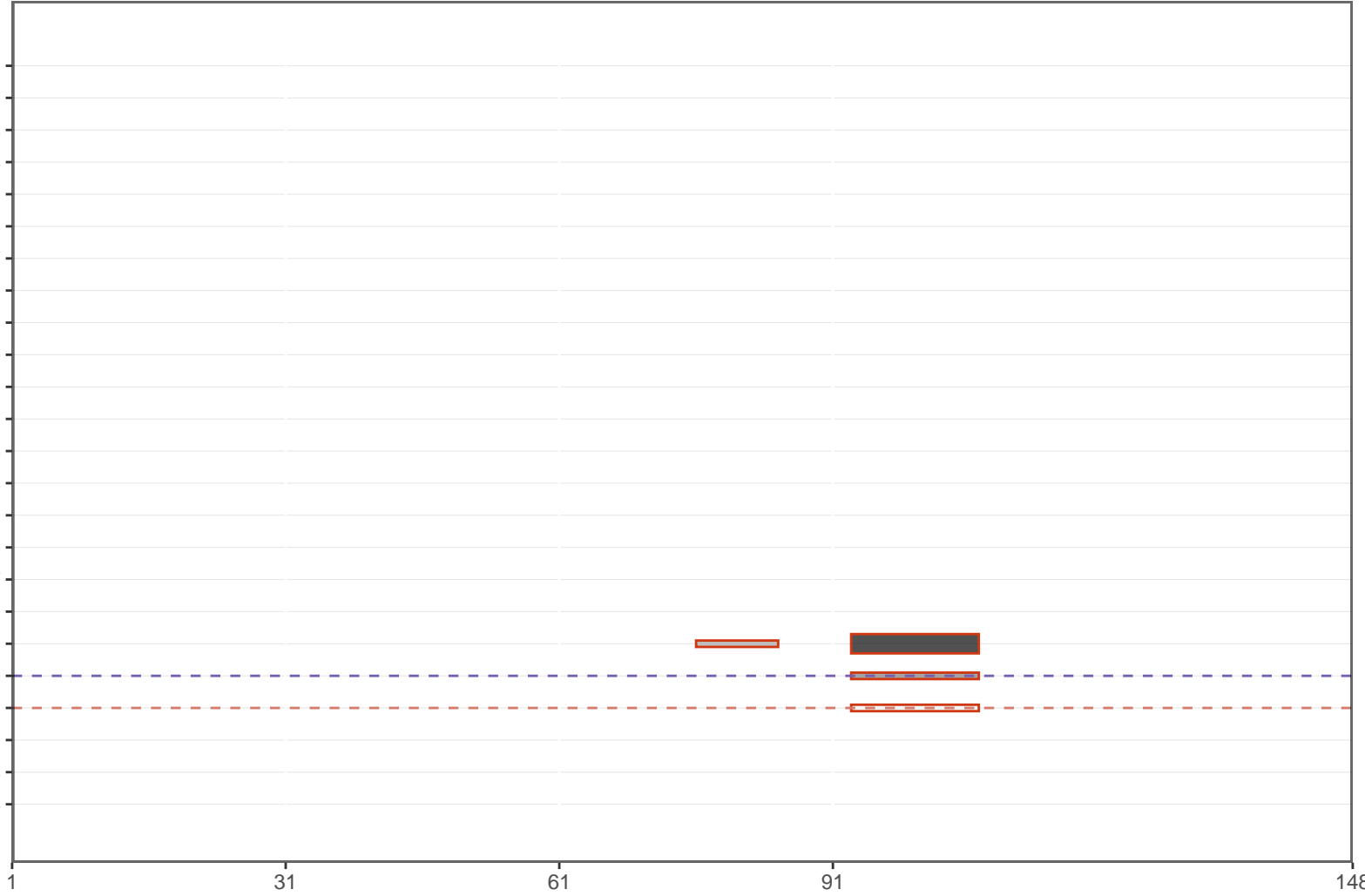
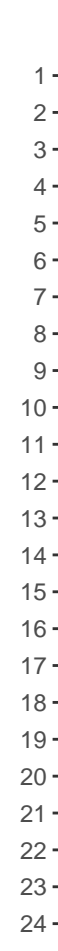
MW indication



Molecular weight



Gel Slice



Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

SVKYYRDELSELKXSLNVEVDGLRSEFQELKTRLGGQGEDVTASLRINLGLGDVSEETKEAEDAKPKNDEEKSGEELPKDGGKDTDQ

NbL06g14640.1 branched-chain-amino-acid_aminotransferase_3_chloroplastic-like [MW = 45.22 kDa]

No. of times detected



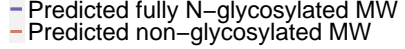
log(intensity)



Values from



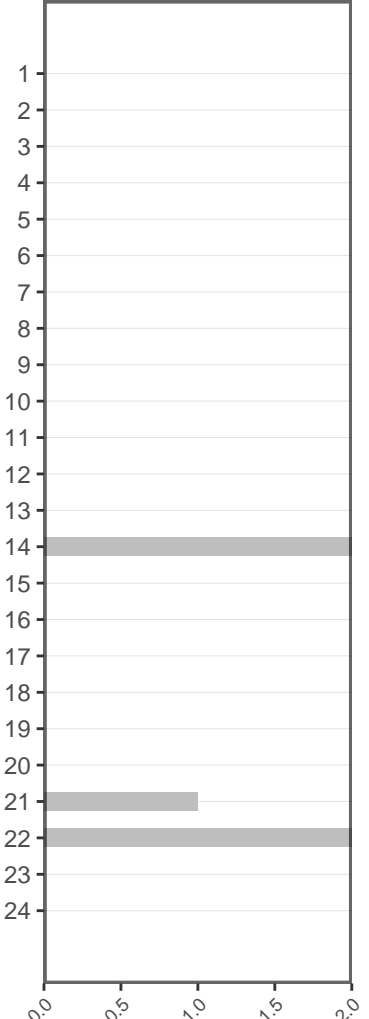
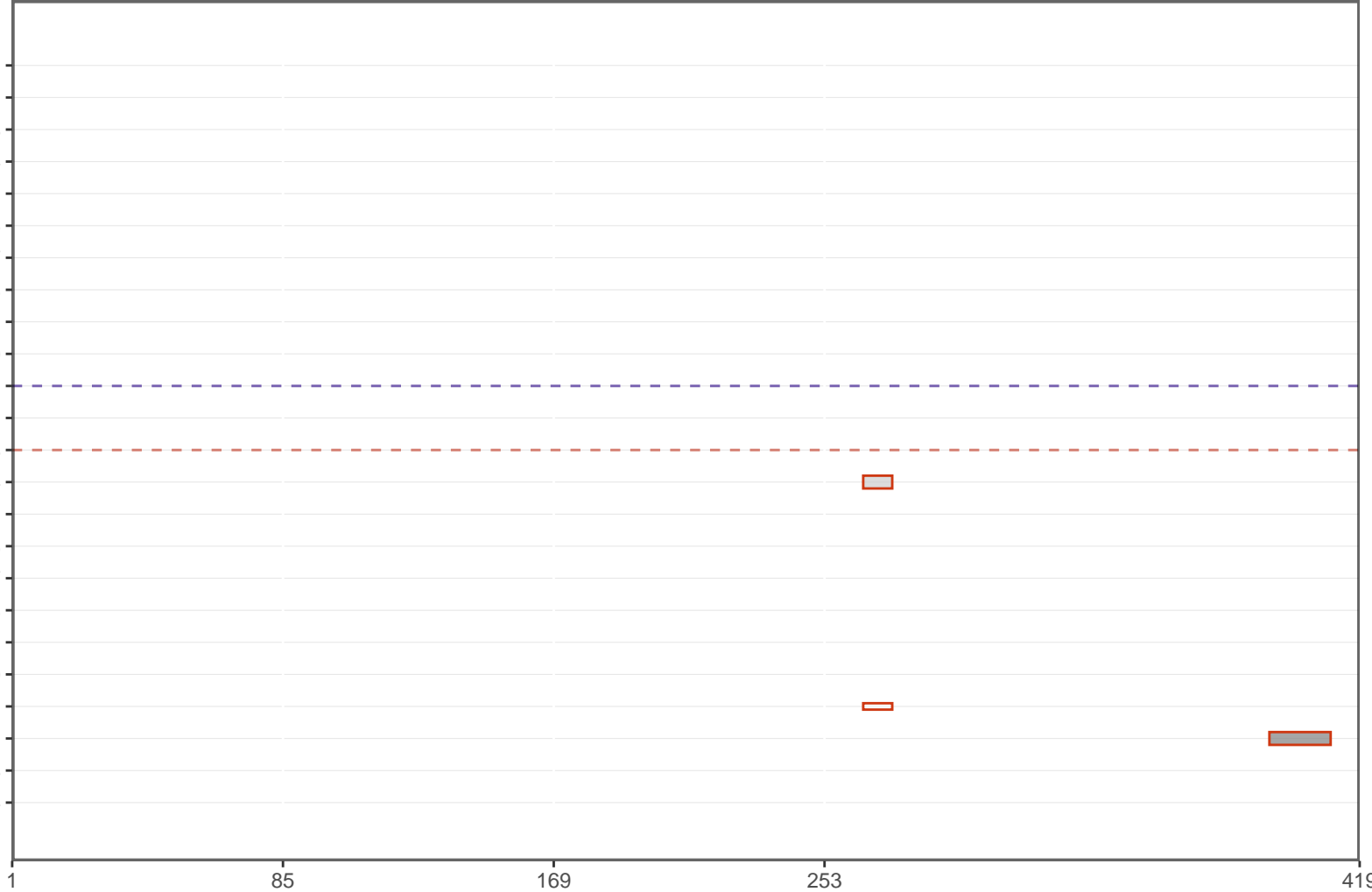
MW indication



Molecular weight

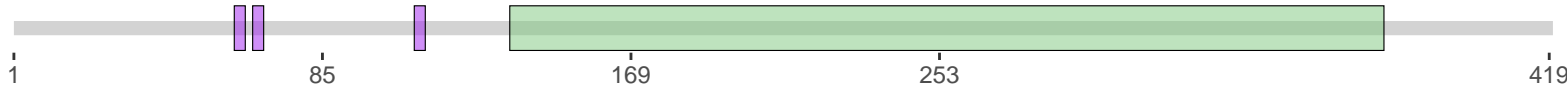


Gel Slice



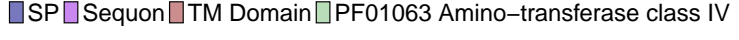
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MPPPGKGLYRPLMLMSSGAVLGVAFAPETFLVYSPVGNVFKEGMAPINLVETEMHRATPGGTGGVKTIGNVAALKAGSAANKAGVSDVLLDENVKRYLVEVSSGNFVIVGNLITFAIKGTLPLGTRIKEDVAVSDGFGVVEERHVSVDLLGAEDEVFGTAVVSPVGSITHMKKRIFYGSDGVRVSDGQVLSALTSGLQMLGLEDKMGWVLEK

NbL06g14540.1 60S_ribosomal_protein_L26-1-like [MW = 16.77 kDa]

No. of times detected



log(intensity)



Values from



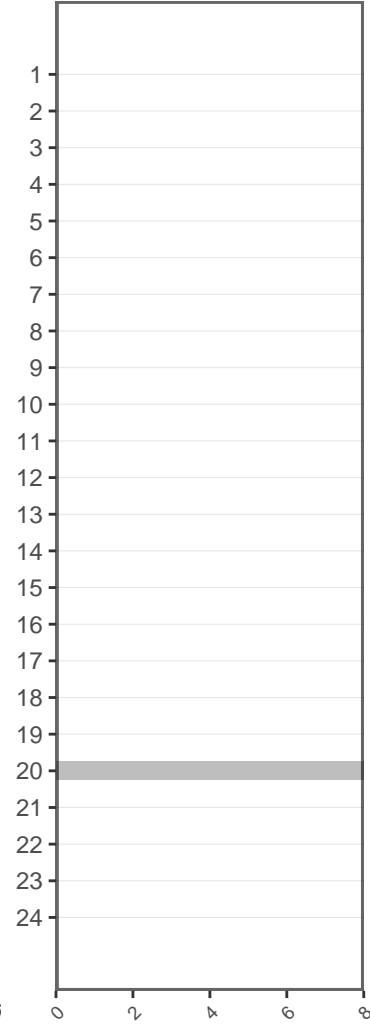
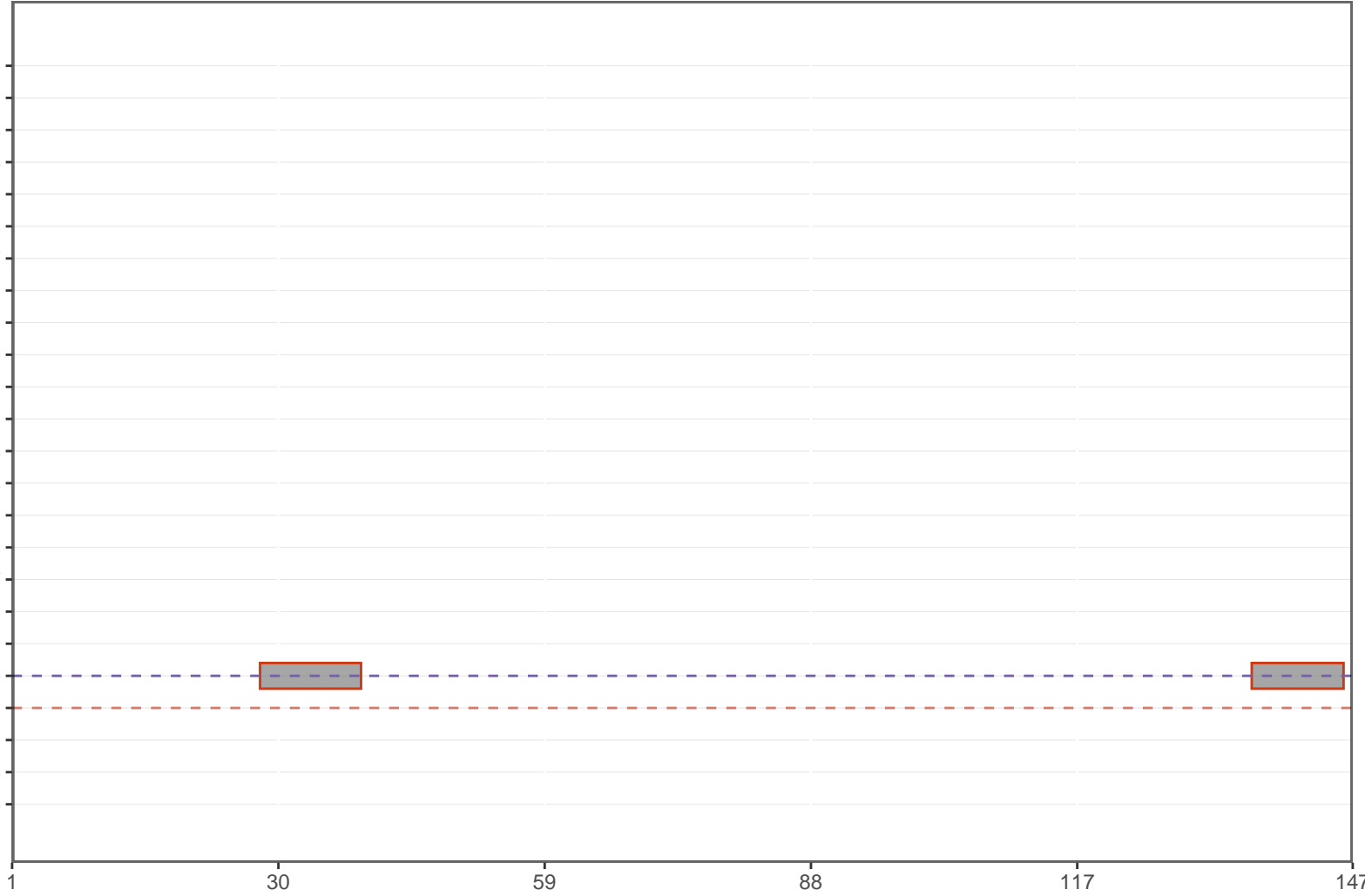
MW indication



Molecular weight



Gel Slice



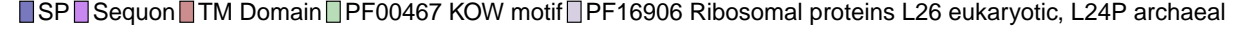
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISTYKGRGKVVQYRKKWVHERITREKVNSTVNVGHPKTVITRLRLDKRKLIDRKAAGRAAADKDKGTFKFTEDIMQTVDF

NbL06g14490.1 subtilisin-like_protease [MW - SP = 82.64 kDa]

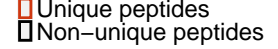
No. of times detected



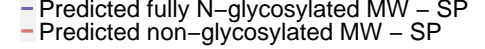
log(intensity)



Values from

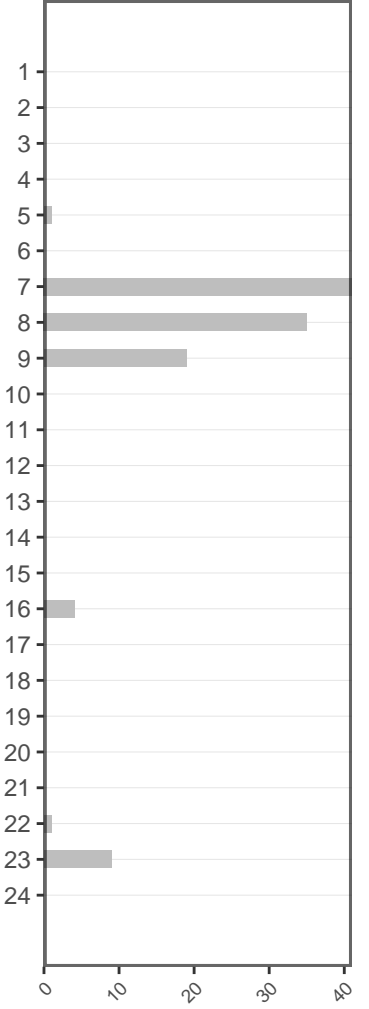
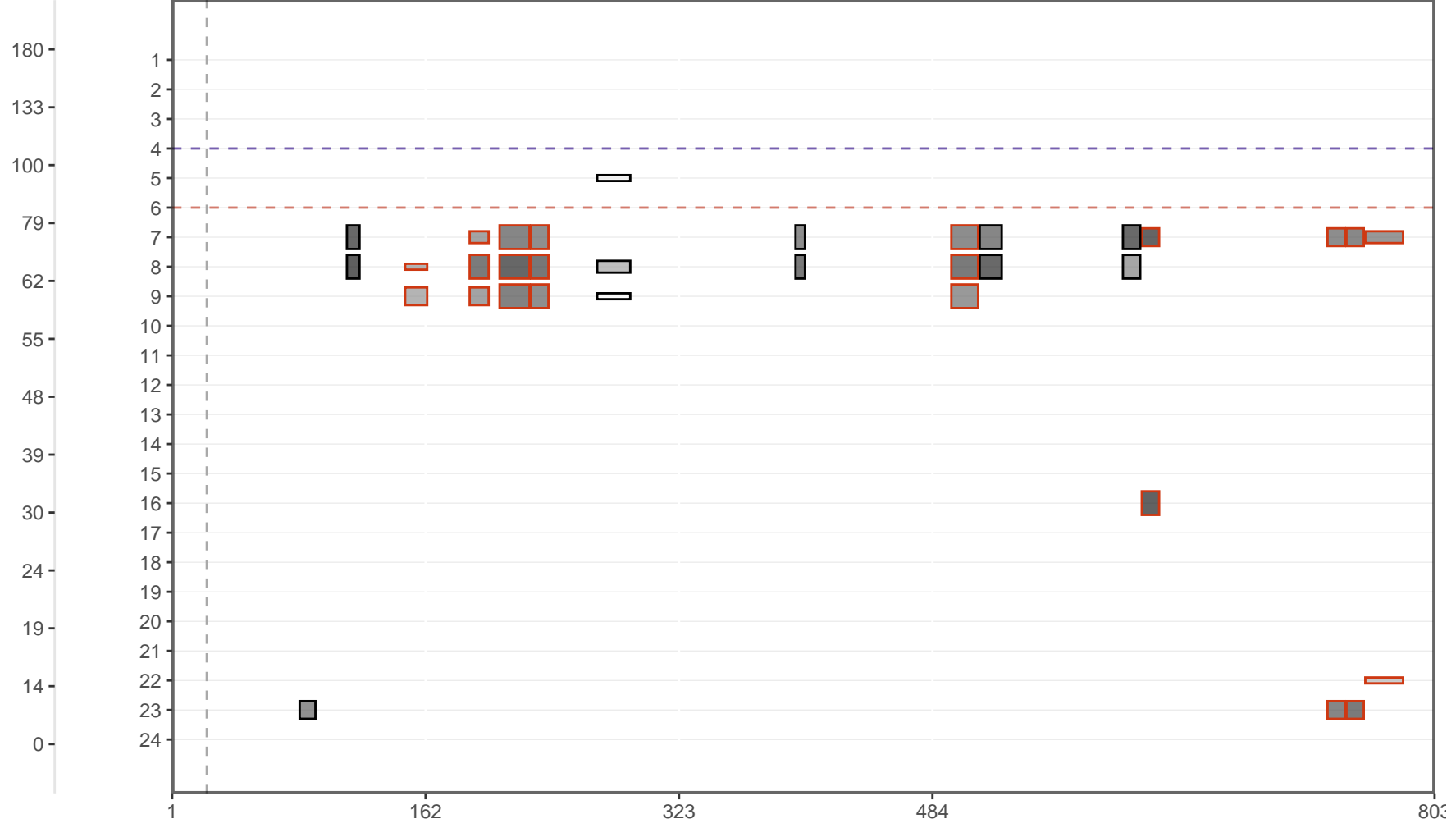


MW indication



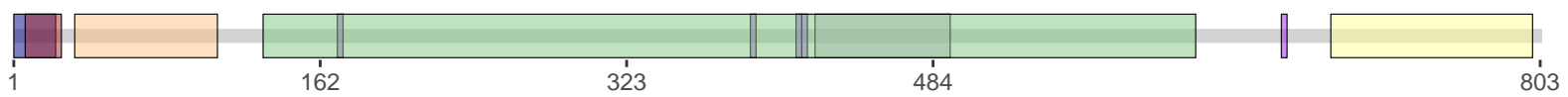
Molecular weight

Gel Slice



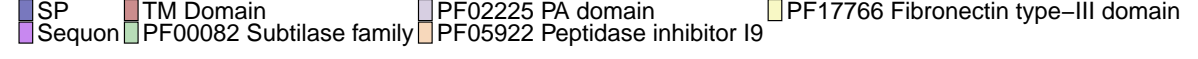
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKNFSGVSLYKGDLELKMILPEVYAGNASNTTNGNLGNTGTGLIPEKVGKIVLGDGGINPRVQKGSVYKEAGGVGMVLANTRANGDELVADAHLLDATTVGGTTEGAIKKYLTSDDNPITATLFEGRKVGKIPSPVAAFSSRGNPSITQELKPDHAPGVNLAGWTGAVGPTGLAEDTRRVGFINISGTSMSGPHVSGLAALLKGAHPEWSPAIRSALMTAVTVYKNGGALGDVSTGKPTPEFDHGAGHVDPAALNPGLVYDLRADDVNLFLGALNYTSIQINSIARRNYN

NbL06g14470.1 tRNA-dihydrouridine(16/17)_synthase_[NAD(P)(+)]-like [MW = 49 kDa]

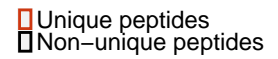
No. of times detected



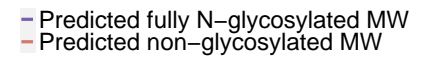
log(intensity)



Values from



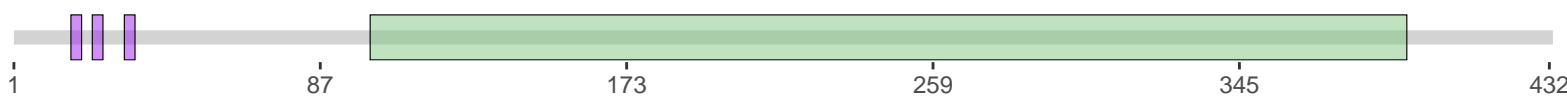
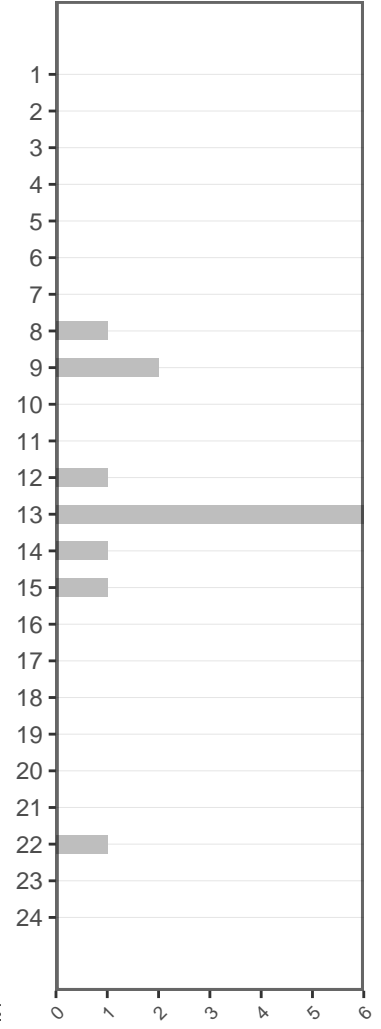
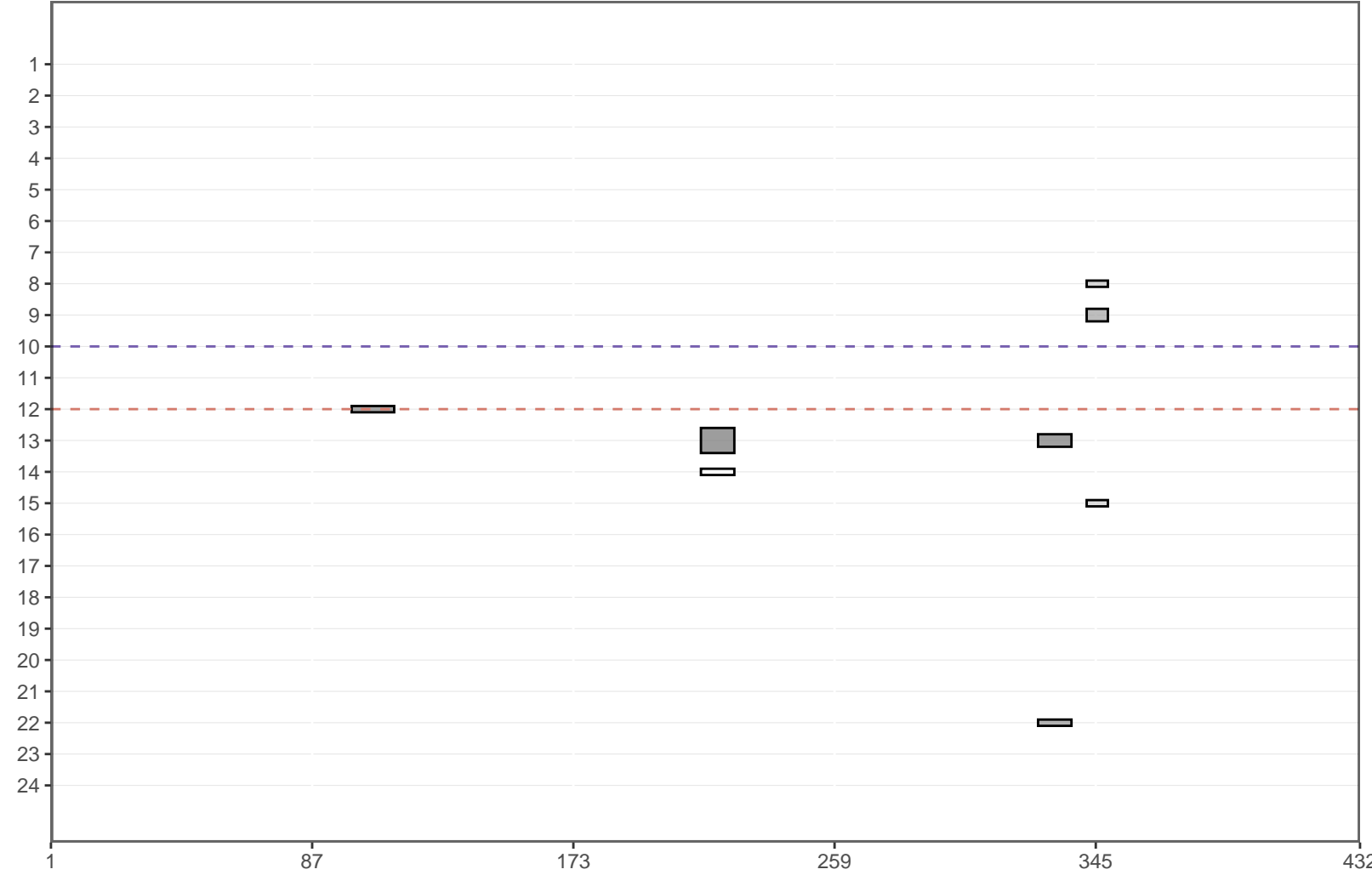
MW indication



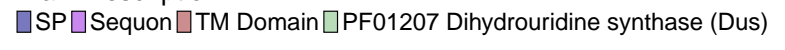
Molecular weight



Gel Slice



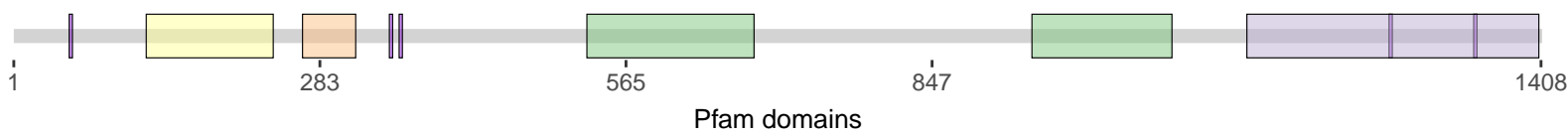
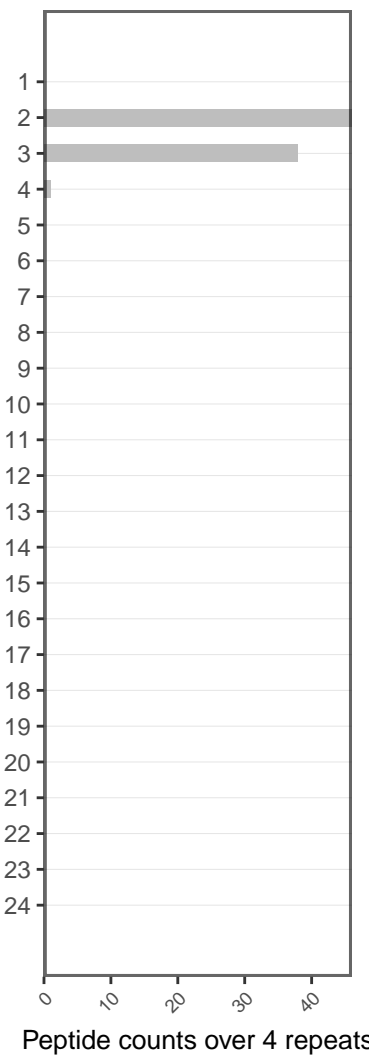
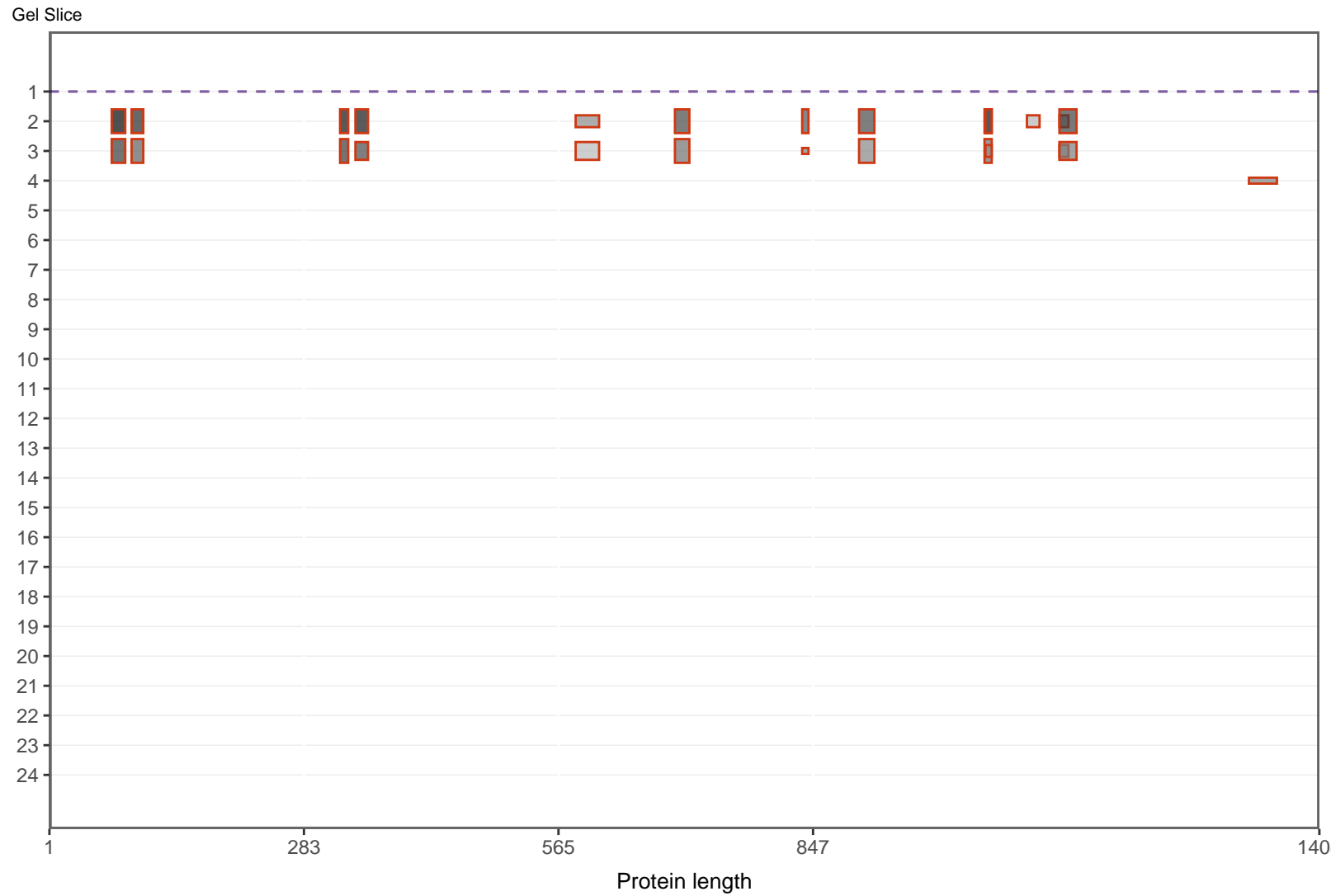
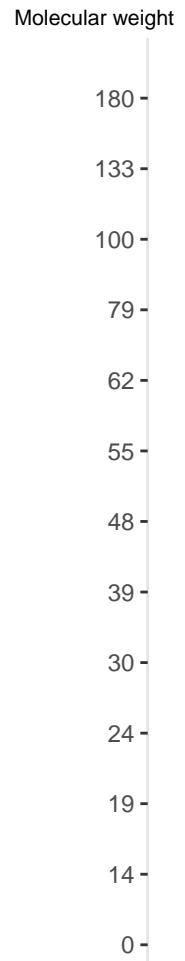
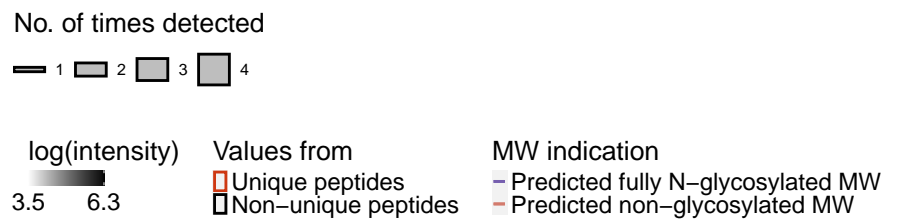
Pfam Description



Protein sequence:

IDNLPVLSLVKLANLNINPVSGKIRVFPNIGDLSVAKMLEEAGGSLAVHGRTRDEKDKKFRADWEAKAVRNFVRIPVLANGDIRHMDVDVQNLDETGDGVLSAEGLLENPALFAGVYRTAEWGLSGAGIREGKLDQAEKLEKLEKPKVPPWRMRIRSHVHKMLGEVFKGPSVREDFNKQSKLTFEFLVDVTLGRELGVSPVWVETRDEAASNGHWI

NbL06g14360.1 probable_phosphoribosylformylglycinamide_synthase_chloroplastic/mitochondrial [MW = 154.1 kDa]



- Description
- TM Domain
 - PF02769 AIR synthase related protein, C-terminal domain
 - PF13507 CobB/CobQ-like glutamine amidotransferase domain
 - PF18072 Formylglycinamide ribonucleotide amidotransferase linker domain
 - PF18076 Formylglycinamide ribonucleotide amidotransferase N-terminal domain

Protein sequence:

PPPPPAVDLELEKVA.GDMPKTKTEFFRRMNNLR.EPLDIAPIFTVLDLKRVLRLPVGSKRFLFTKVDRCVTLGVAQQGTVGLPGLPLADVAWAGTYDLDLGSAGSISGEPKIGLLDPKAMARLVAEALTNLWAKVYSLGDKWASGNWMMWAKLDGEGAAWYDAVAALSEAMIELGIAIDGGKDELSSAAHSSGELVAKAPNLVSTVYTCPIKTYVTPDLKLGDDGVLHLDLAKGRRLGGGSAIAGAFDQIGDESPDLDDVYKTVFNEVQNLISDELISAGHIDSDGGL

NbL06g14330.1 red_chlorophyll_catabolite_reductase_chloroplastic [MW = 36.47 kDa]

No. of times detected



log(intensity)



Values from



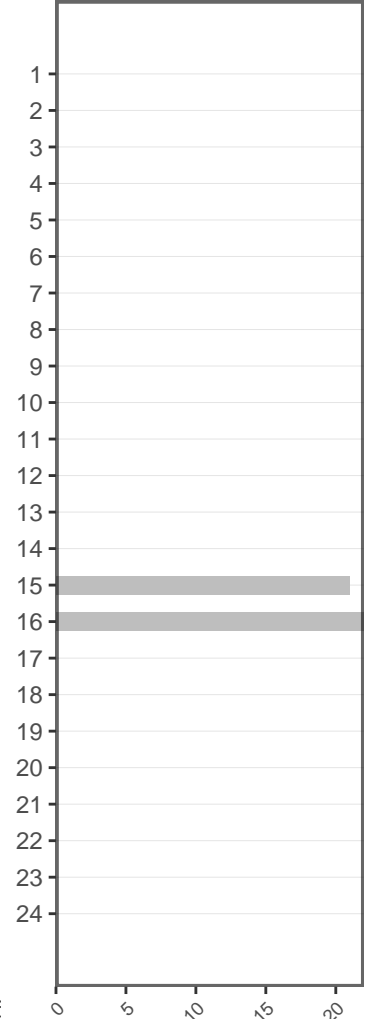
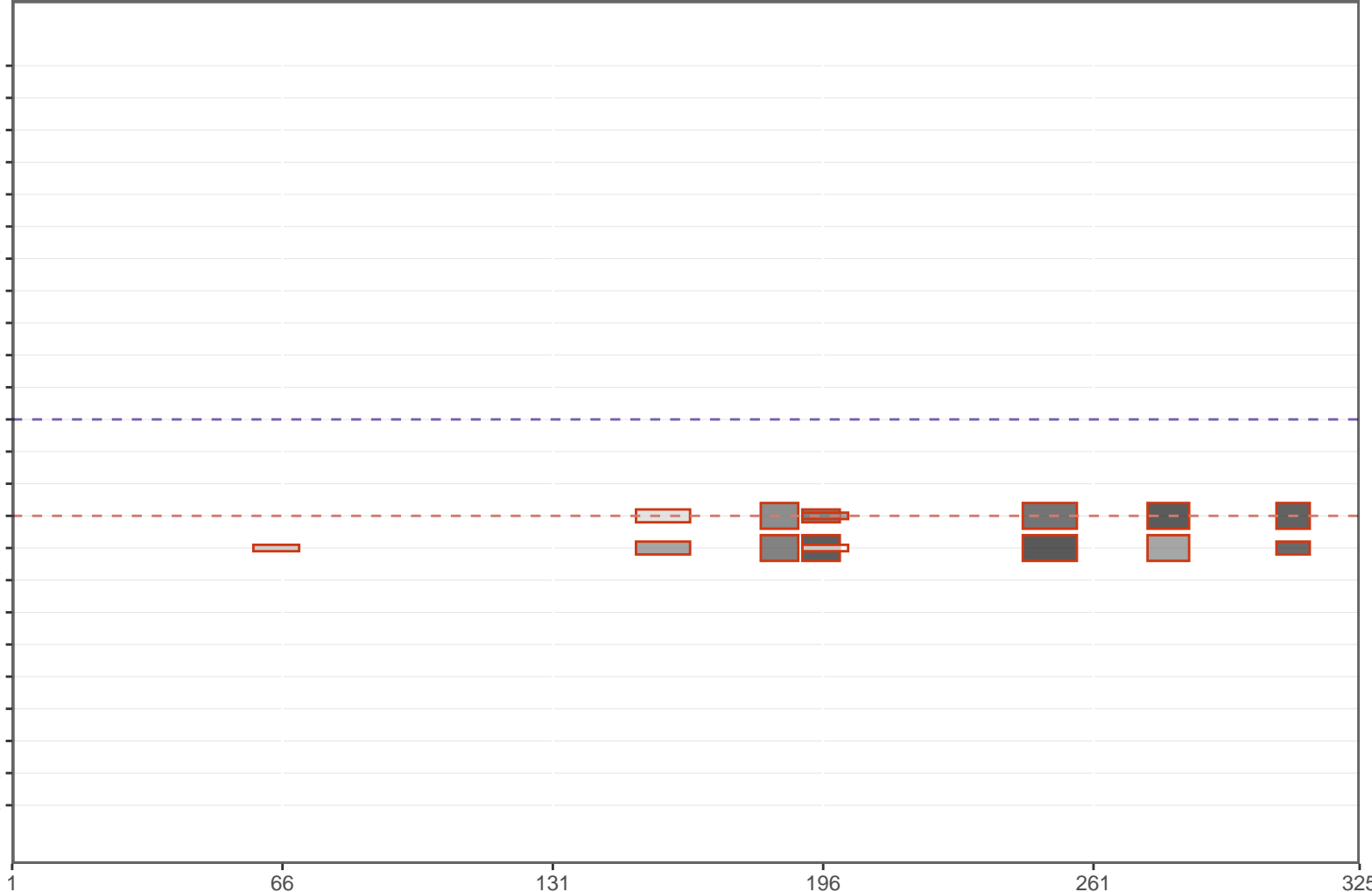
MW indication



Molecular weight



Gel Slice

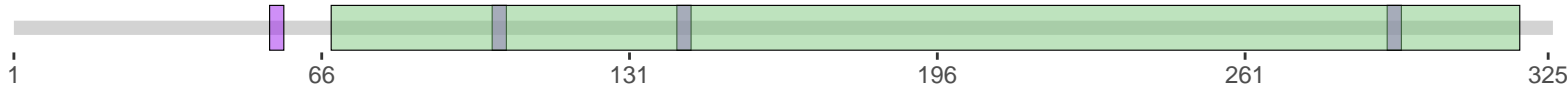


Peptide counts over 4 repeats

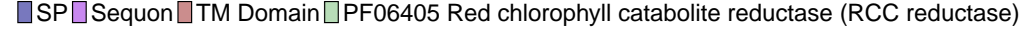
Protein length



Pfam domains



Pfam Description



Protein sequence:

IAYLRPSTDAFNFLMEVRSRSPSTLSLLLDLPPRKDLVGHHPDVLNKFYEETQLDKGRLLLEKLEPKVYFSSSLYRAVVSPSAILVSIETASGAVRIDEHGQHSIPAAVVALETWLDLGDACPERRLTDESTALAKRDKFNKNTIEDLSESSFRILFGQEVANKVLGVLRKNNAA

NbL06g14260.1 patatin-like_protein_3 [MW - SP = 42.86 kDa]

No. of times detected



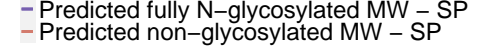
log(intensity)



Values from



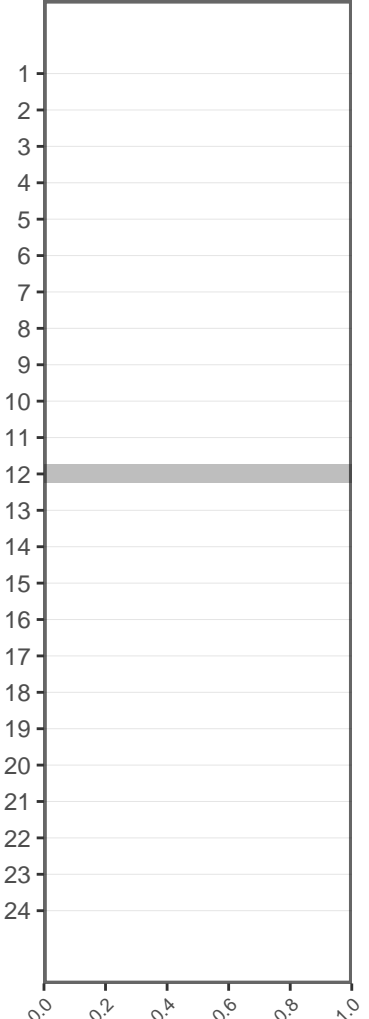
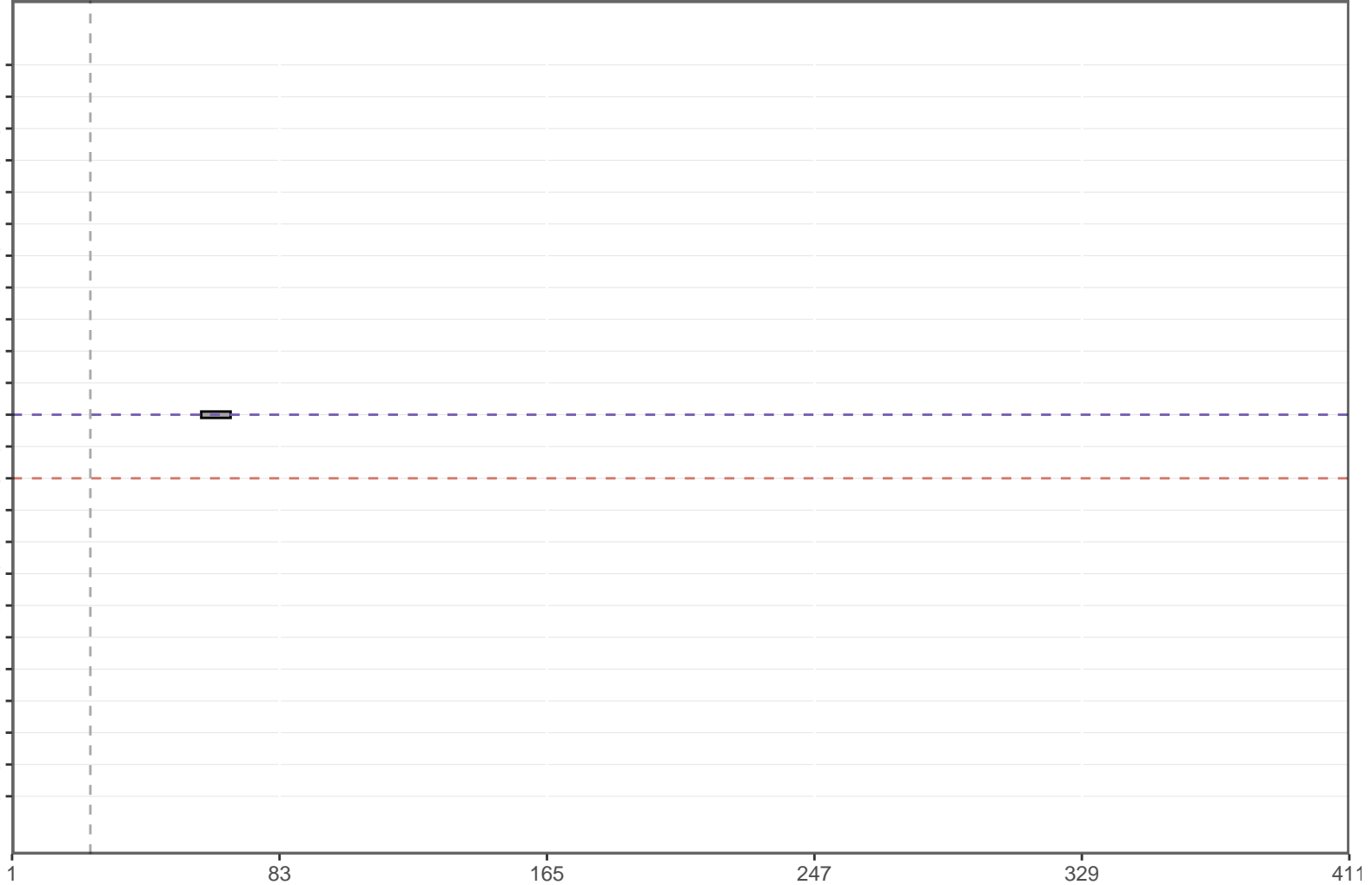
MW indication



Molecular weight

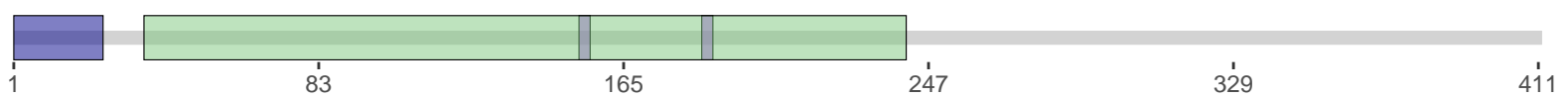


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL06g13790.1 alpha-14_glucan_phosphorylase_L-1_isozyme_chloroplastic/amyloplastic [MW = 110.32 kDa]

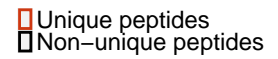
No. of times detected



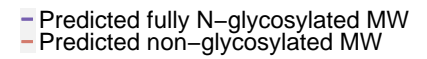
log(intensity)



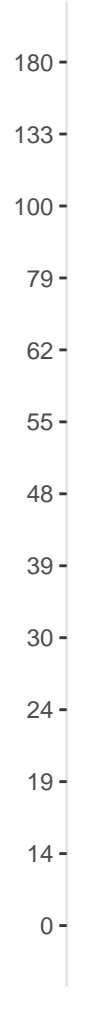
Values from



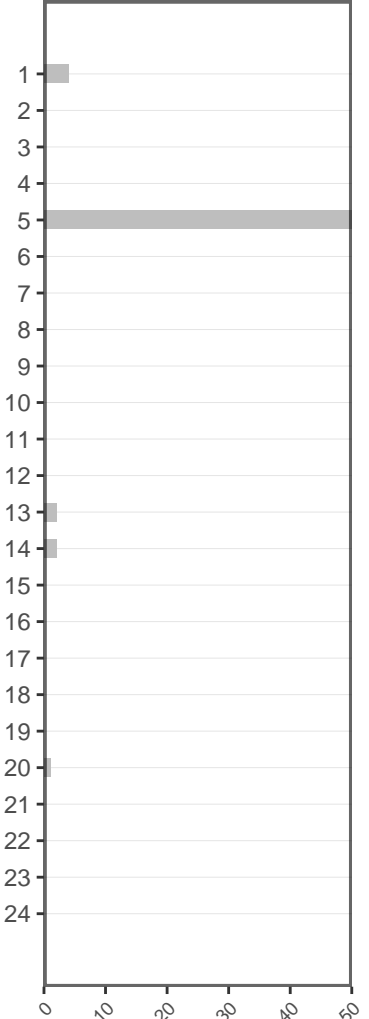
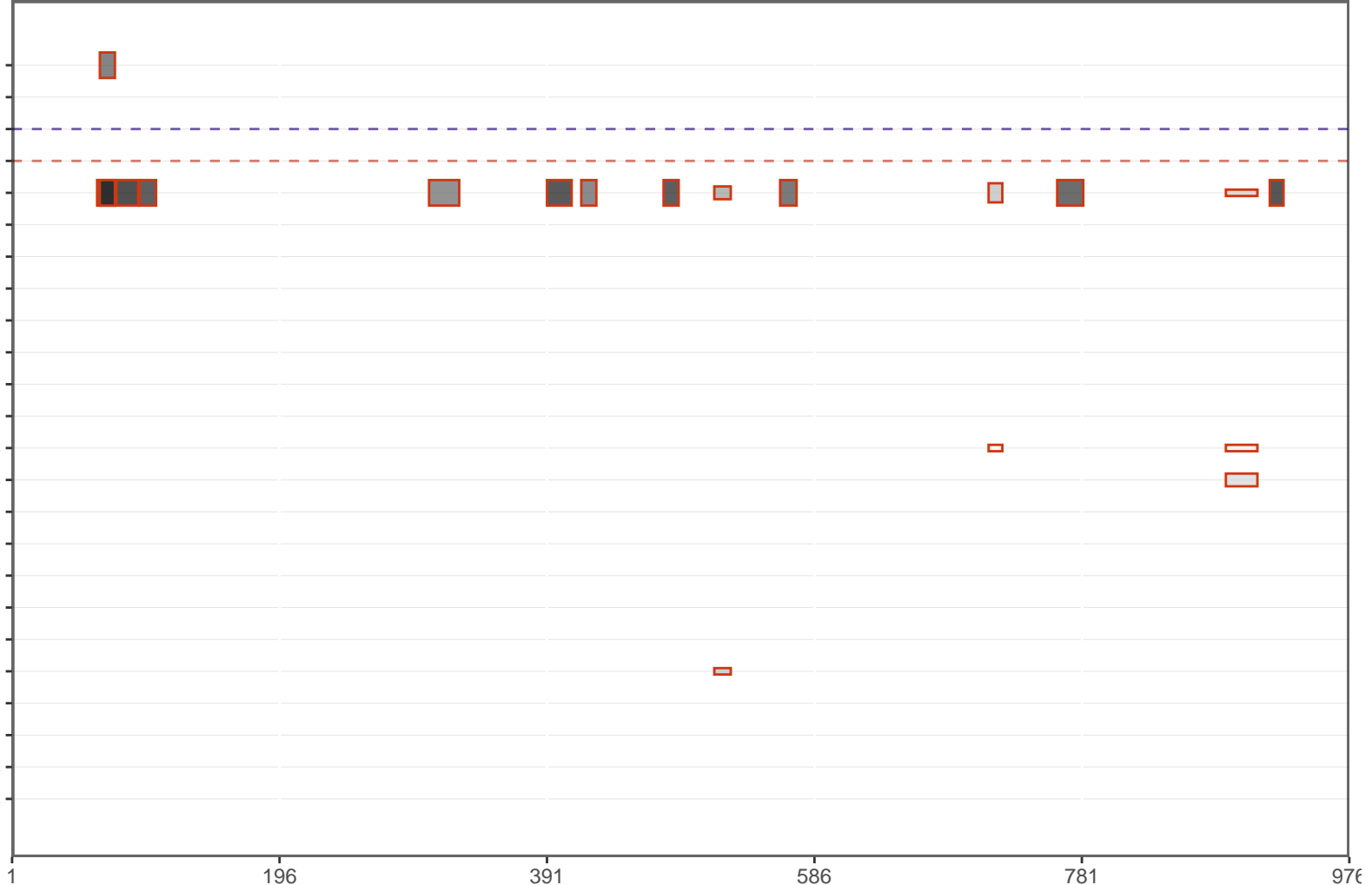
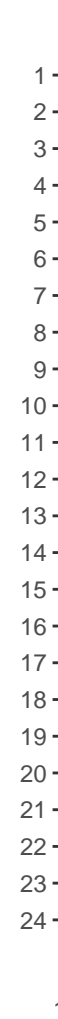
MW indication



Molecular weight

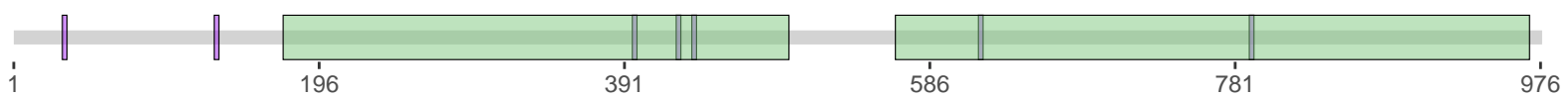


Gel Slice



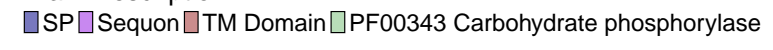
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

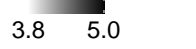
IKYGSLELDKLEEKAAAMRILENFDLPSWADLFTKPERLVDADTETVEVDKVEVVTNDEEDKNEEDDTGKKTGSKPEPGAKDIDKTTLVPDPAVPPKMRMANLGVVGHAVNGVNAEHSERKEEVNEFYELVPEKFNKNTNGVTPRRWRFGNPNPLSGITKVTGTEGVVLTETKLAELQGFADNEDLQIEWREAKRINKKAVSFLKEKGTGYSVIPDAMFDIQVKRHEKROLLNFGVFRYKMKKEMTAERKAKAYPRVQIFGGKAFATVQAKRIVKFTDVGATI

NbL06g13670.1 cystathionine_gamma-synthase_1_chloroplastic-like [MW = 59 kDa]

No. of times detected



log(intensity)



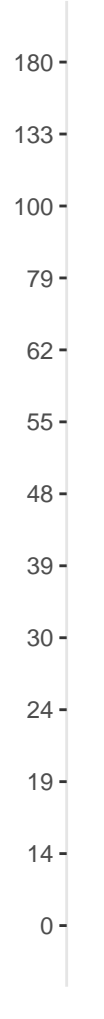
Values from



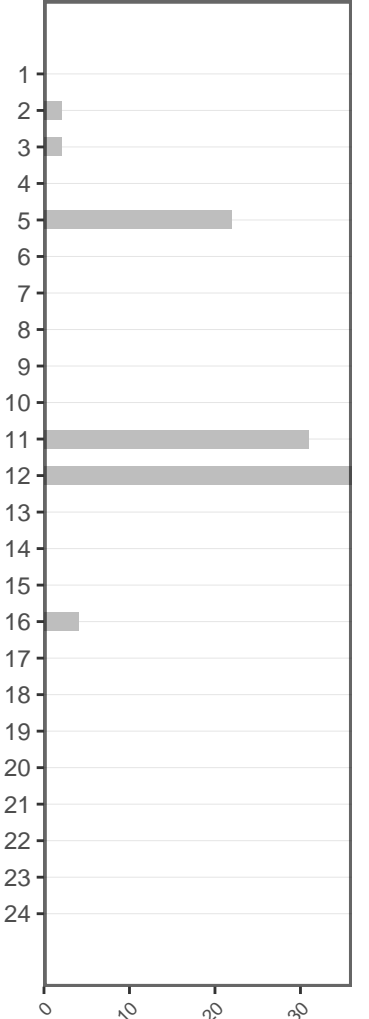
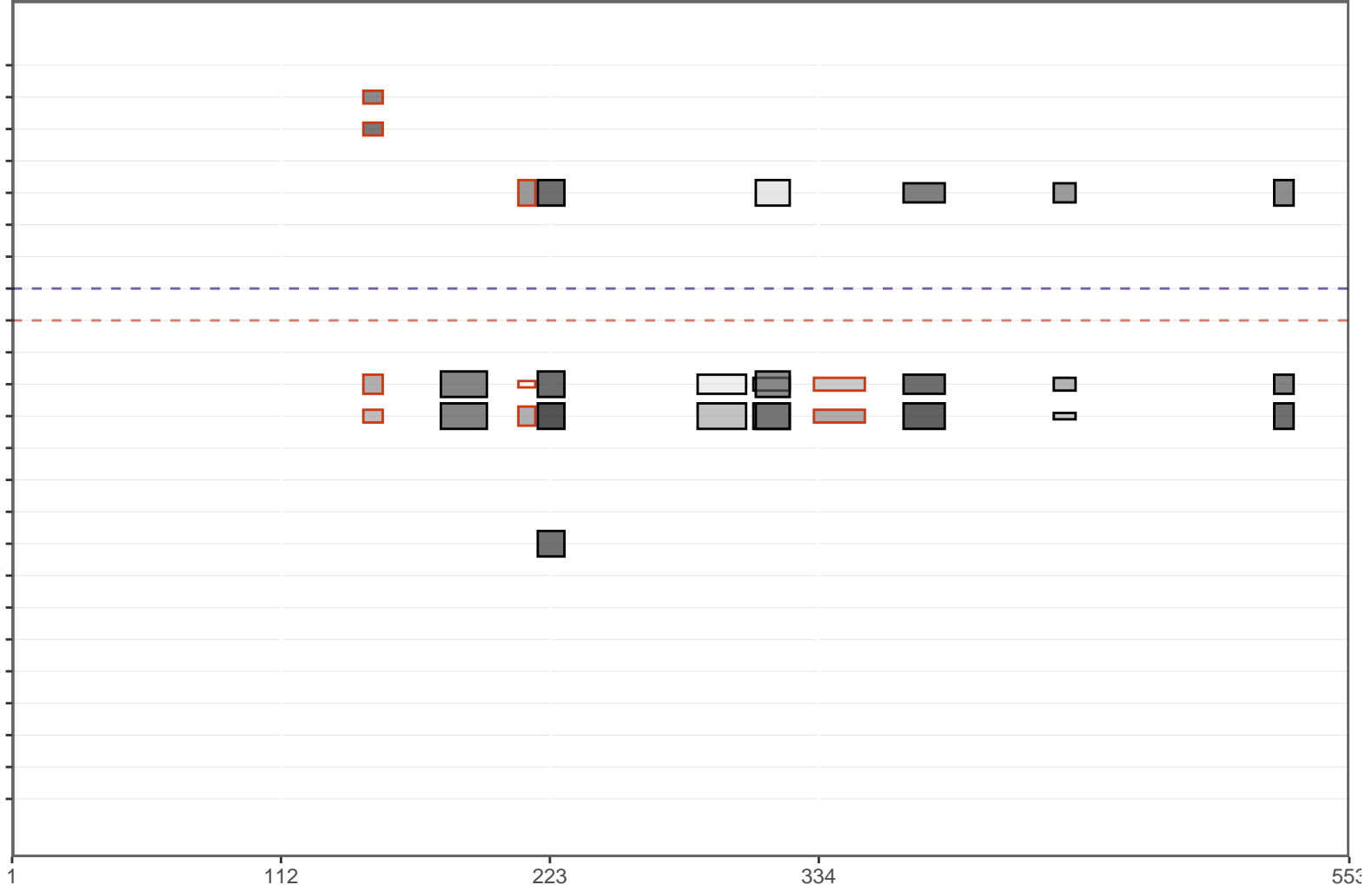
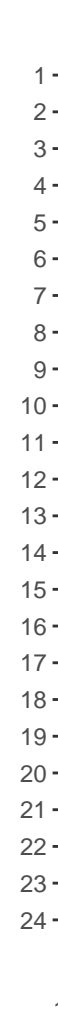
MW indication



Molecular weight



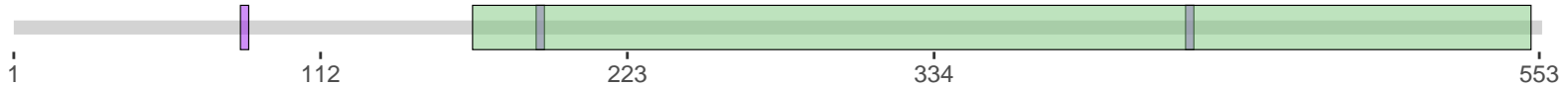
Gel Slice



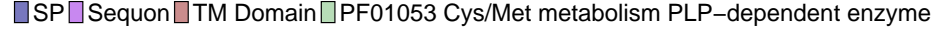
Protein length



Pfam domains



Pfam Description



Protein sequence:

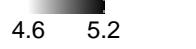
PAGGHIVTTTDCYRKRTRIFRIETLPMAGTATVDVADIGALESVLKKKVTLFFTESPTNPLFRVQDIELVSKLCHENGALVQDGTATPLNGKALGADLVVHSATKYGGKNDVLAGGIGSPEKLVSVVRNHLGGAINPNAAYLIIRGMKTLHLRVQDQNSTAGRIAELEAHPKVRGCVVYPLGPHPEHGLAKIGMAGFGVGVSEFVDGDLLETKAFIDALKIPYIAPFSGGGSISVDGFRNIMSVYDL6SDRAKYGILENLVRFSGVEDFDKADLQALEA*

NbL06g13570.1 transcription_factor_PRE1-like [MW = 10.16 kDa]

No. of times detected



log(intensity)



Values from



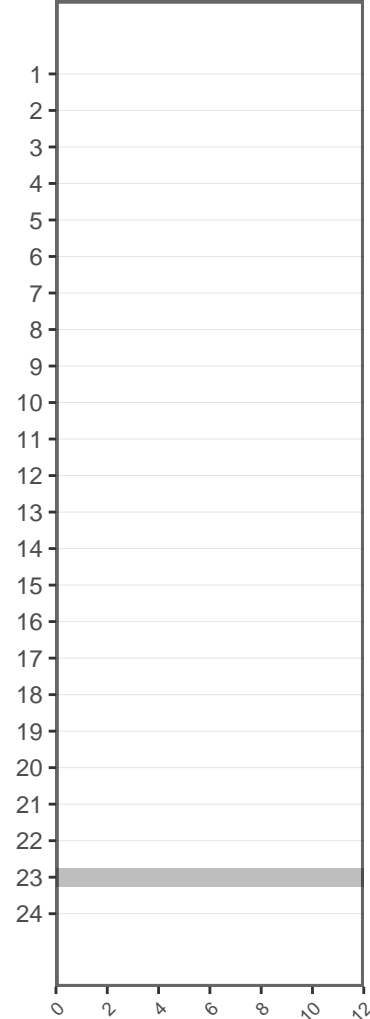
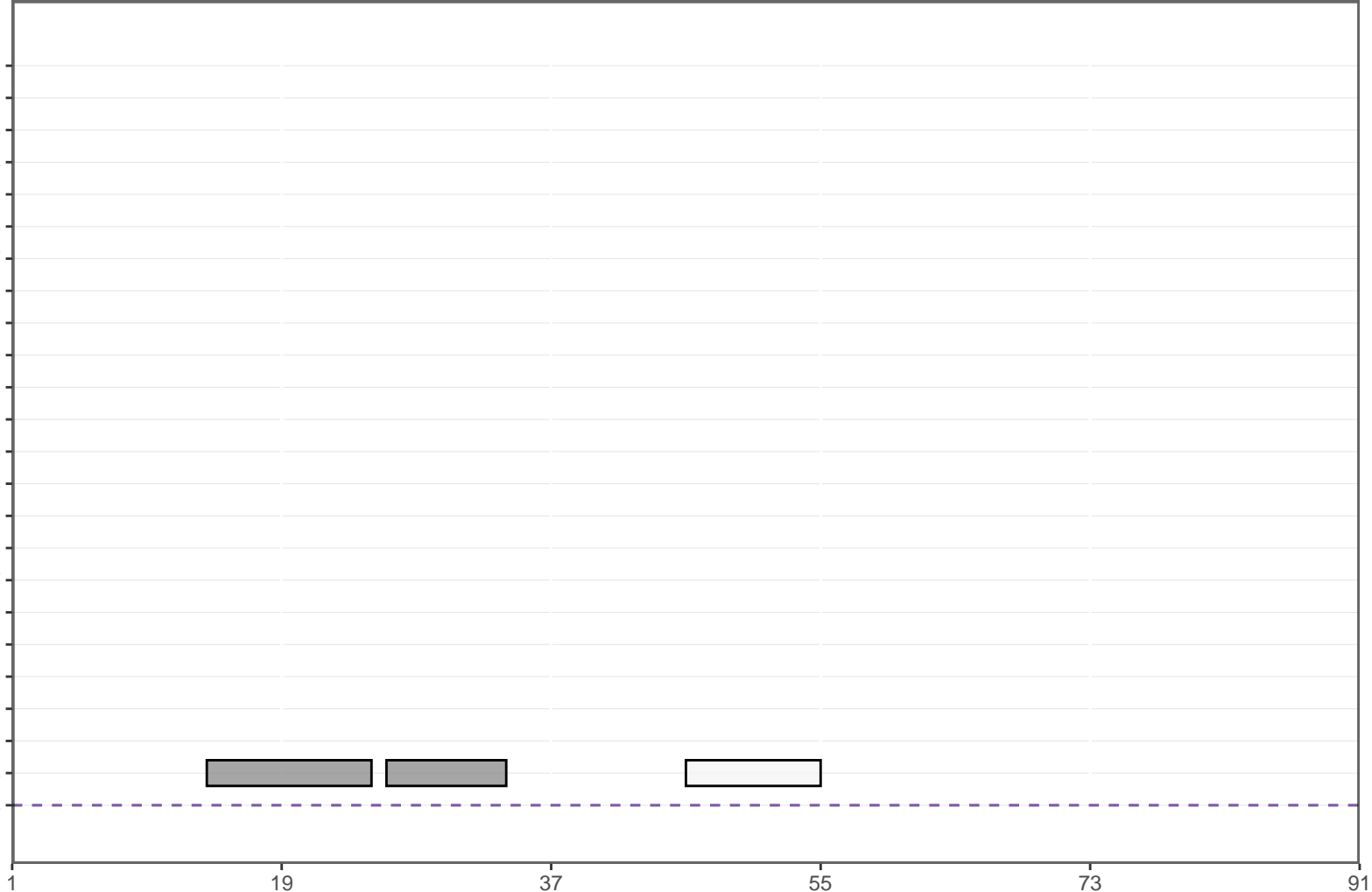
MW indication



Molecular weight



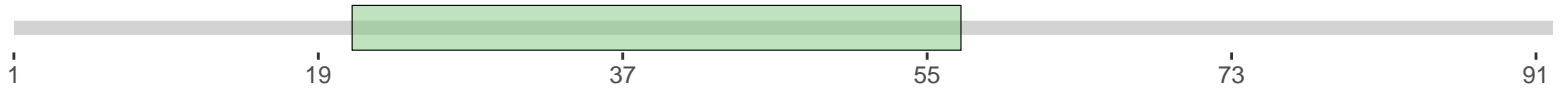
Gel Slice



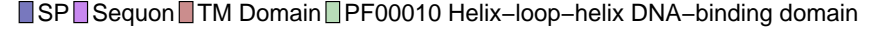
Protein length



Pfam domains



Pfam Description



Protein sequence:

EIRTRSSKASASKVLGETGNYIRSLNREMDLSDRLGQLLSTVDADEPEAMIRSLF

NbL06g13480.1 hypersensitive-induced_response_protein_2 [MW = 15.96 kDa]

No. of times detected



log(intensity)



Values from



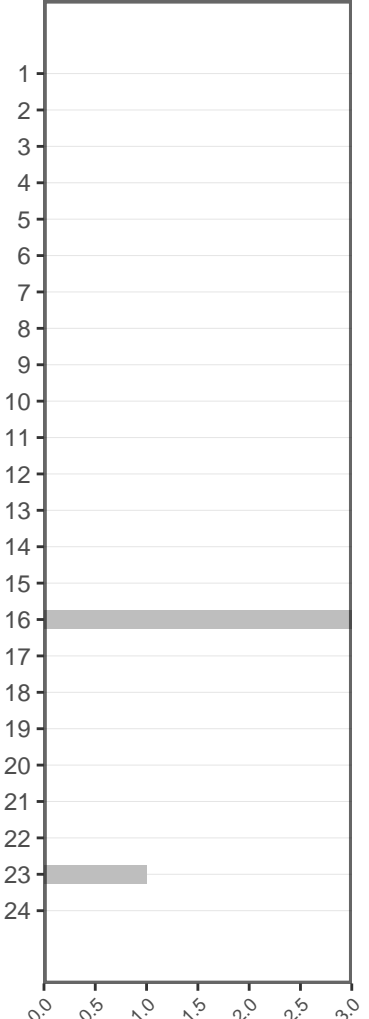
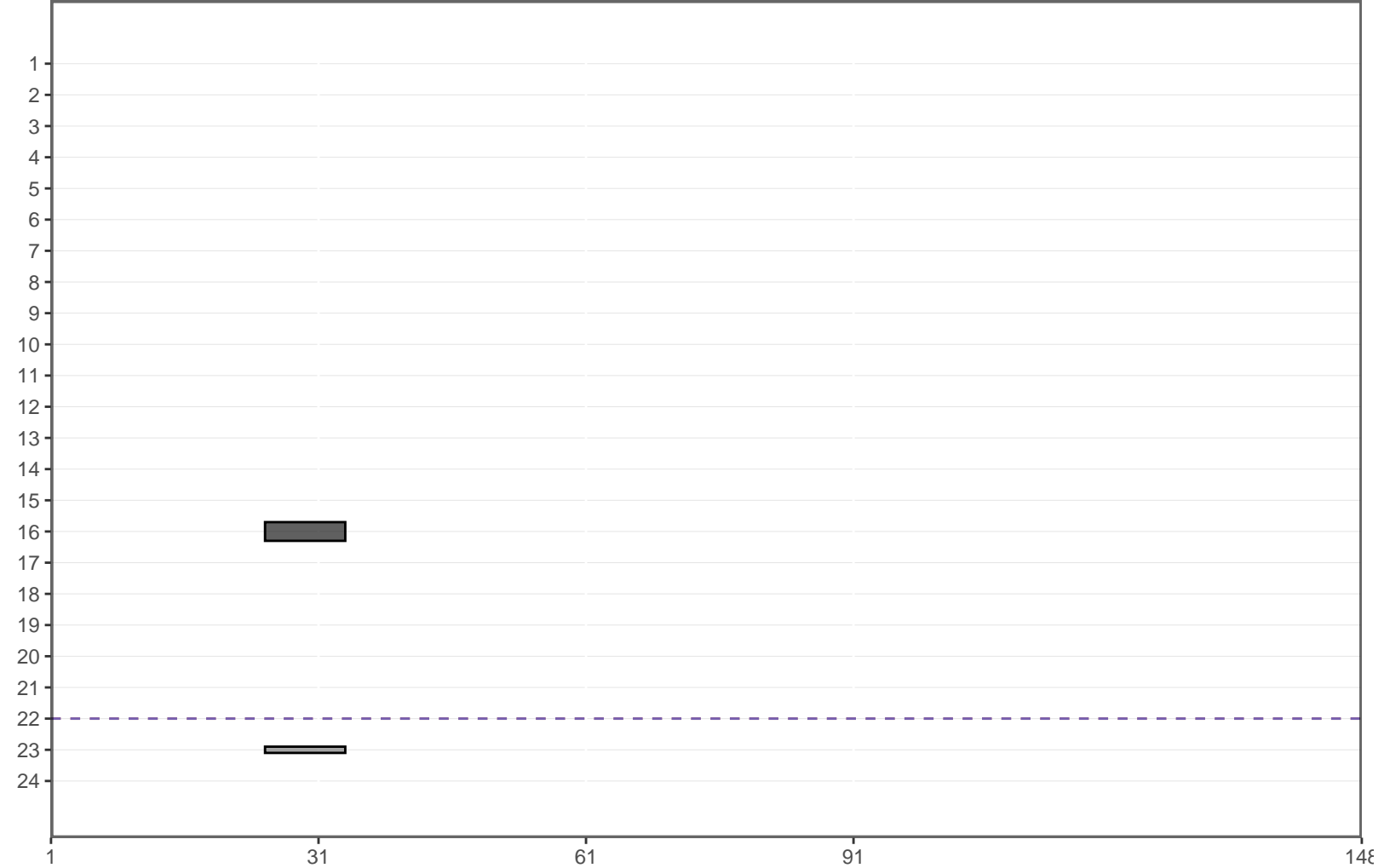
MW indication



Molecular weight



Gel Slice



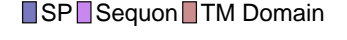
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

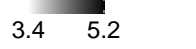
KYSSQLGIARQRCAIVDGLRDSVLAFAEENVPQTAKMDLDTMKEIGATSKSYAVFPHGPGAWKDVVRFSLKVFSELTKTKDS*

NbL06g13430.1 protein_transport_protein_SEC13_homolog_B-like [MW = 32.65 kDa]

No. of times detected



log(intensity)



Values from



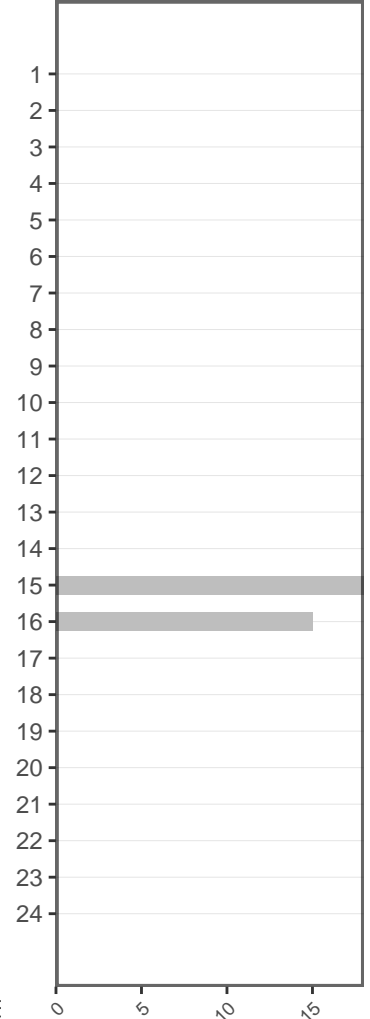
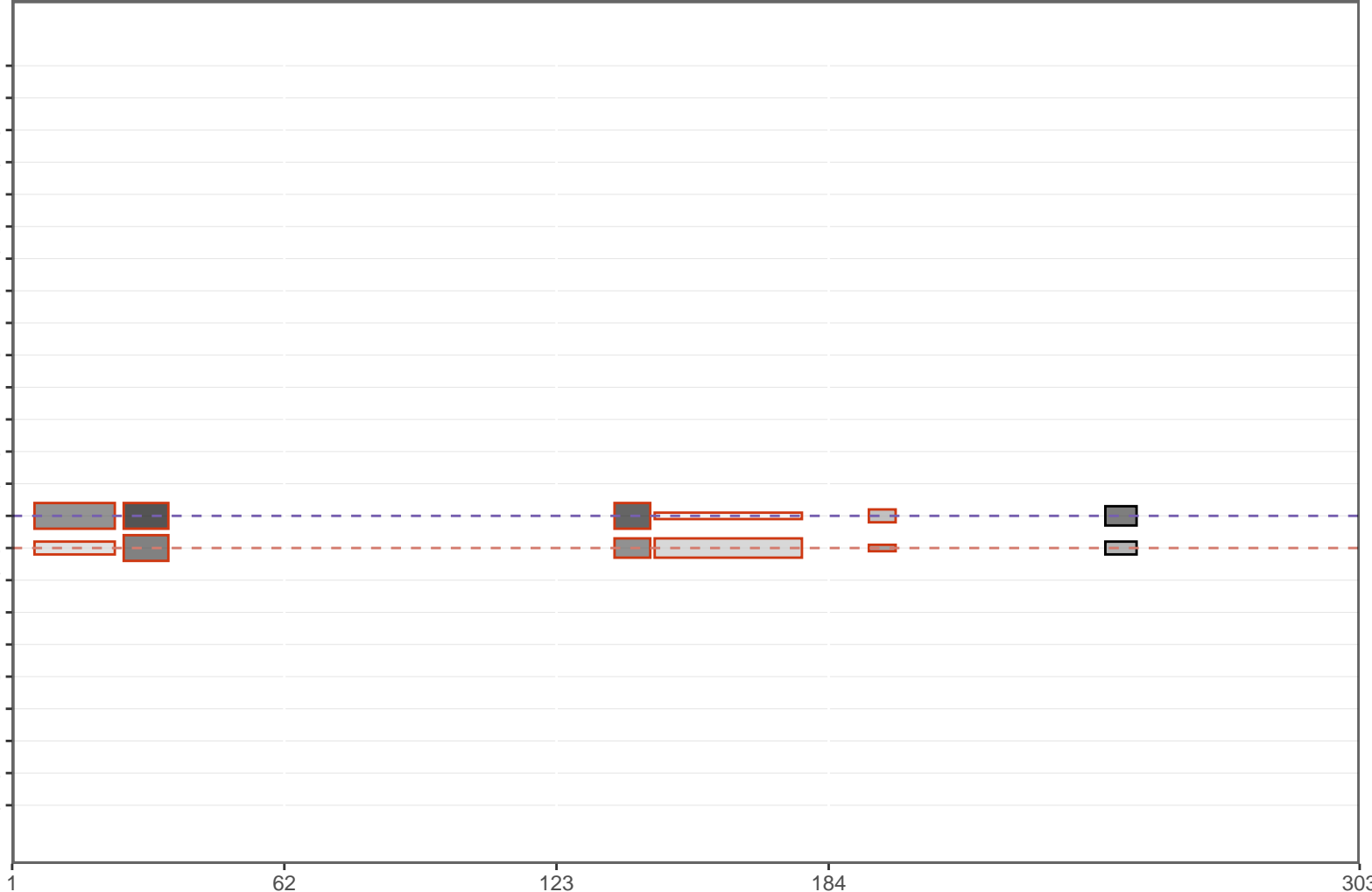
MW indication



Molecular weight

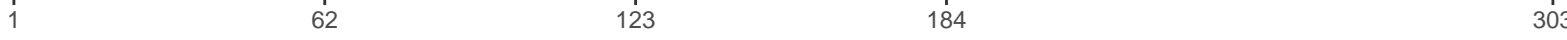


Gel Slice

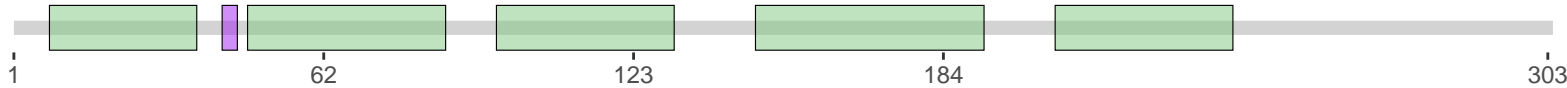


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

DTTKIDQAIHPVGVYAVSWAPEMAPGALVGGVLEFPVQKLAGGGGNTVKKWKLNGVWMDCFPLGKHTNWRDVAWAPNLGLPKGTIASASEGDTVWVWTVAKEGGDQWEGKVKDKFKTPVWRVBSVSLTGALLAAAGENDVTLWKEAVDGEWGGVTSVDQ*

NbL06g13360.1 phosphoglucan_phosphatase_LSF1_chloroplastic-like [MW = 66.9 kDa]

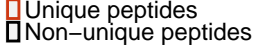
No. of times detected



log(intensity)



Values from

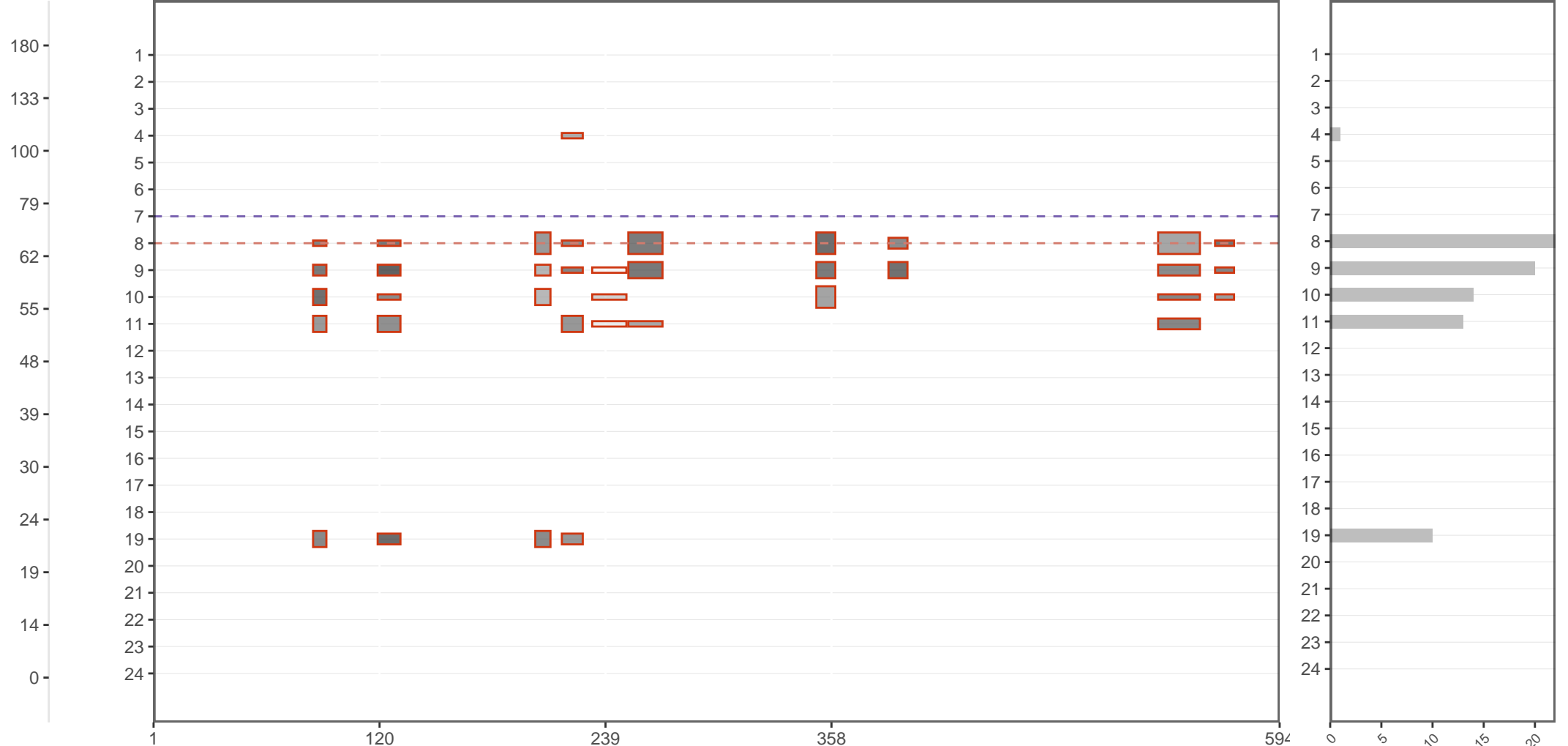


MW indication



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00782 Dual specificity phosphatase, catalytic domain
- PF16561 Glycogen recognition site of AMP-activated protein kinase

Protein sequence:

DLGIRYSKITEGIYVGGSHQKEADVEMLSNVVEVYHGHGTAIVLNFQRGIEAENWGSVAININEGSCORFNLMINYPREGDSDFMRKQLPFCVGLLLRLKKNHRVYVTCITGDFDRSPGCVIAYLHMMTDTSLHAAYNFVTLGHSGKPRDRAIAWATWDLVAMVESGAHGDGPATHAVTFVWNGHEGEDVYLVGDFDTGNHKEPKAWKGGQRGFEAEVRLGGQKLYKHYHNGDWRHSTGSPFTEPDERAGNLTNIVVYGDVASVRFPTVGLQKKBANMKVIERPLTENEFMLAKAA

NbL06g13350.1 50S_ribosomal_protein_L12_chloroplastic-like [MW = 19.66 kDa]

No. of times detected



log(intensity)



Values from



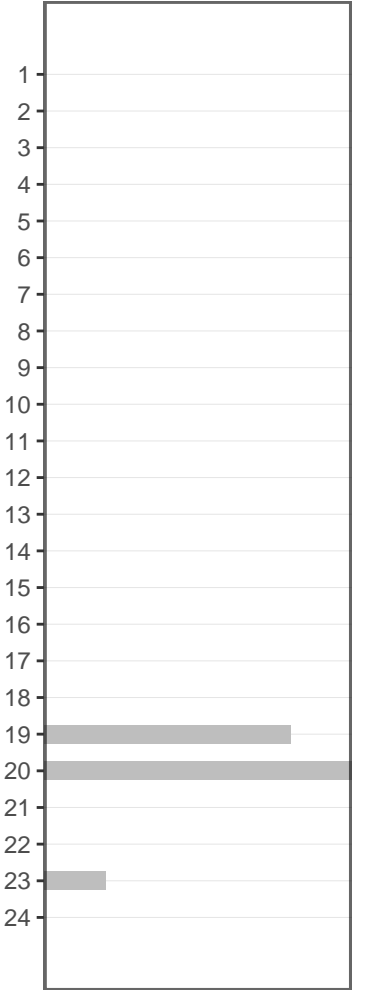
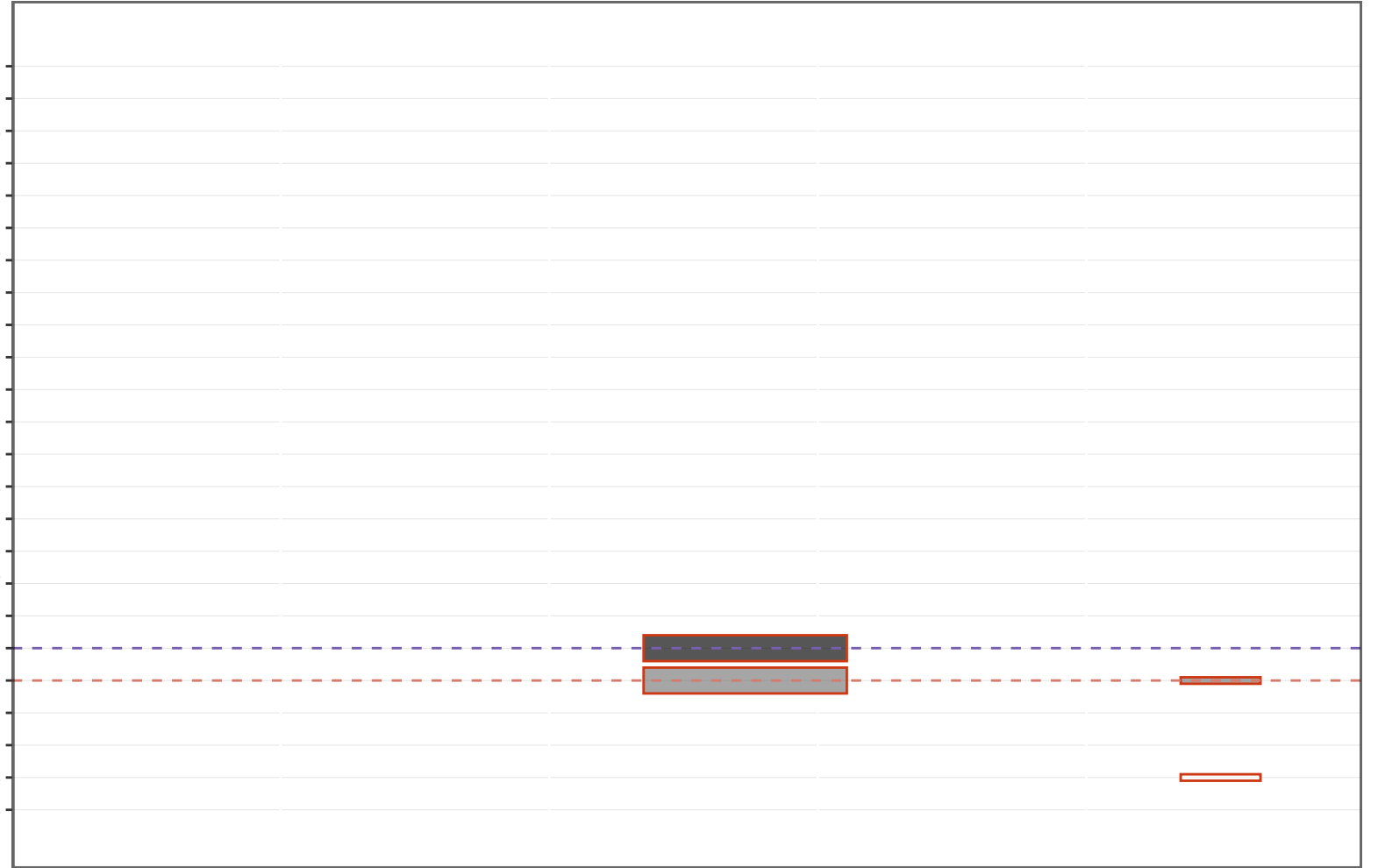
MW indication



Molecular weight



Gel Slice

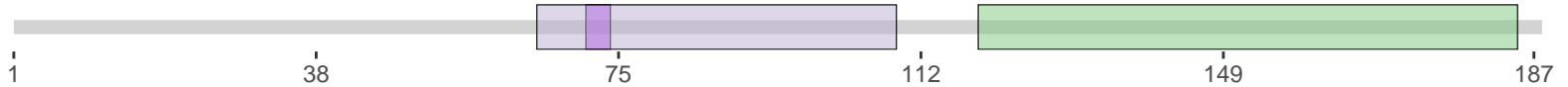


Peptide counts over 4 repeats

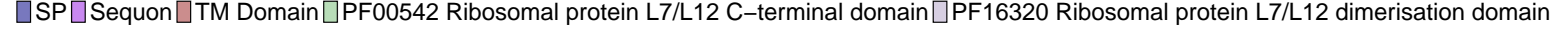
Protein length



Pfam domains



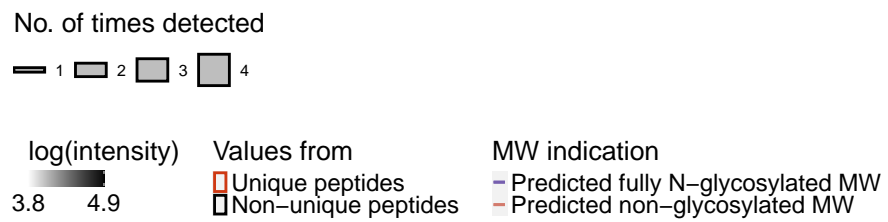
Pfam Description



Protein sequence:

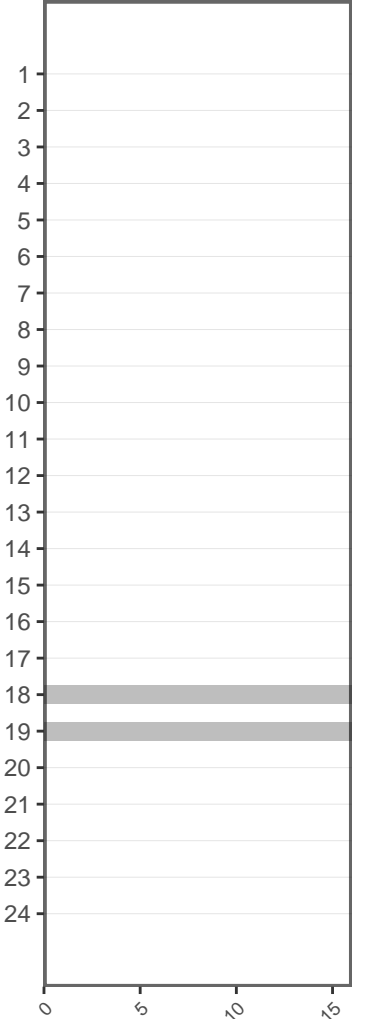
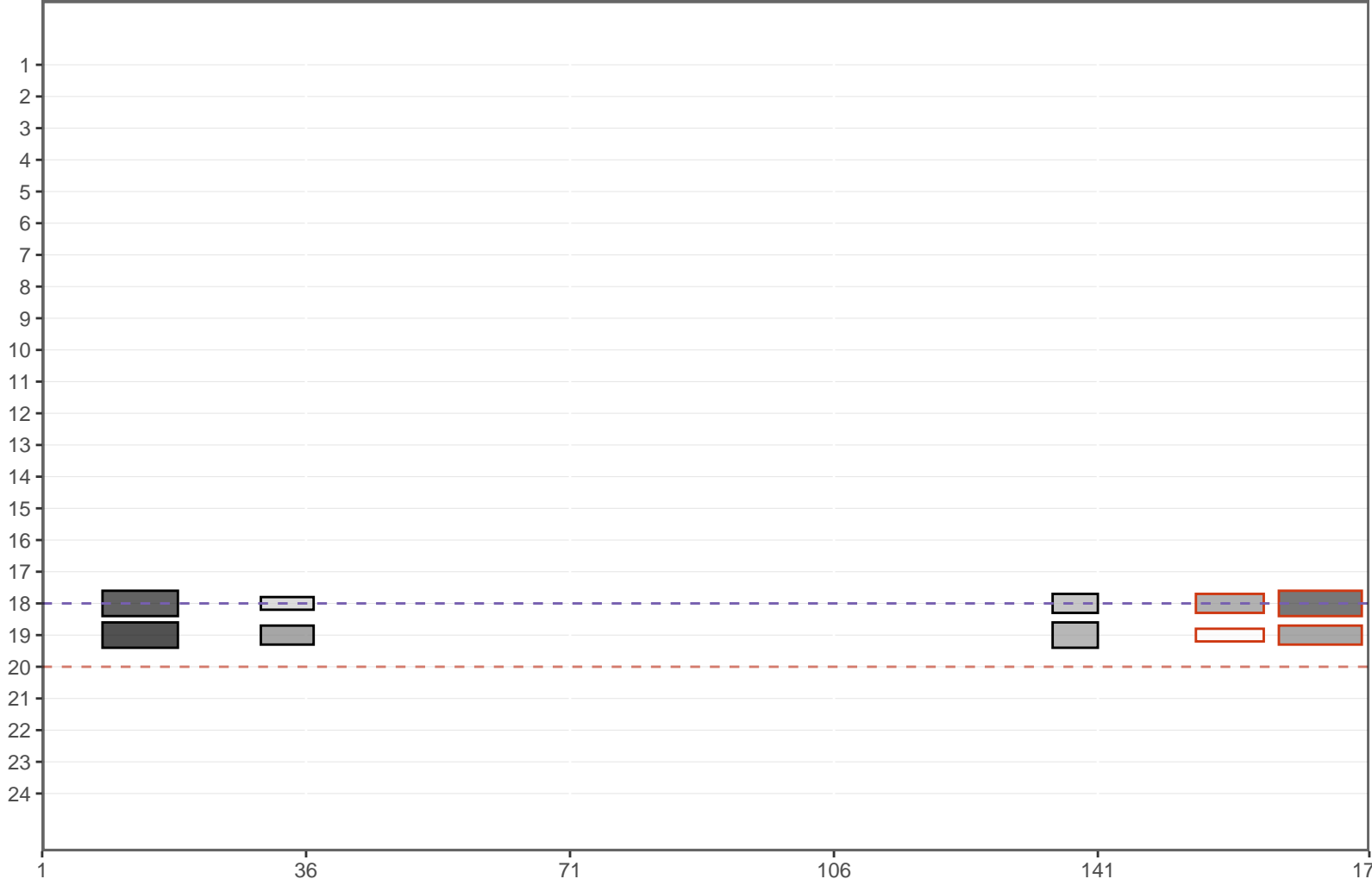
LVEYLODKLGYTAAAFAPAVSAAAPAAAEAPVWVEEKTEFDVHIEVPSNRIAAKAVRALTNLALKEAKELEIQLPKFKFEGIGKDEAEAAKQGLEAGAKVSI

NbL06g13340.1 universal_stress_protein_A-like_protein [MW = 19.79 kDa]



Molecular weight

Gel Slice

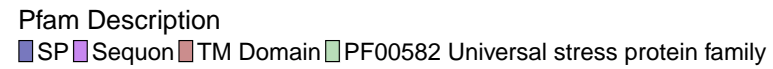


Peptide counts over 4 repeats

Protein length



Pfam domains

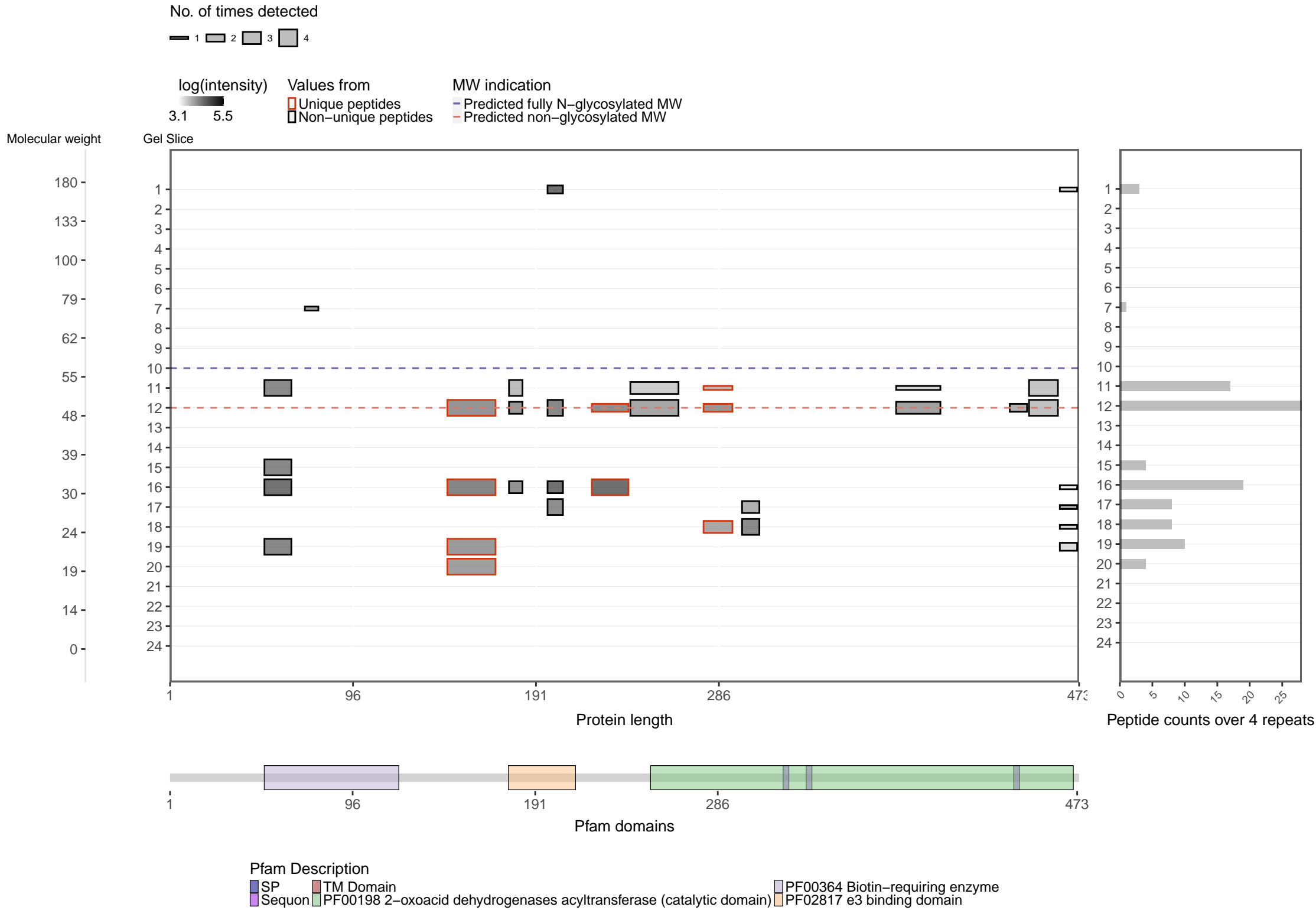


Protein sequence:

VLLKRDKIRGLHLELYFVNRGHEIGVPEAWIKGGDRKEVYCHEVRRVGPDLVVSGRGLGFFQRVFNQTVSEFDVWHAEGPVVTKRSAETPQDPIDP

NbL06g13100.1

dihydrolipoyllysine-residue_acetyltransferase_component_4_of_pyruvate_dehydrogenase_complex_chloroplastic-like [MW = 49.25 kDa]



Protein sequence:

TAVAAAPDAALAAAKASPTSFDPDIPGISTVYPPFTFMQAVSNKMMESLSVPTFRVGYVPYSTNADLALYKVKPKGVMTALLAKAAATLADHPVYNATOKDKGKSYFNSSINAWAWANGGLTPVLDGDKLQVLLSKWKEVYDKARAKQLQPHQVYNSGTFITLSNLGFMFGVDRFDALPPGOGAIMAVGASKPTVYSDSEGFPSWIKMLVYVYADHRIYVYADLAFLQTFKIVENPELTM

NbL06g13030.1 actin-like [MW = 41.68 kDa]

No. of times detected



log(intensity)



Values from



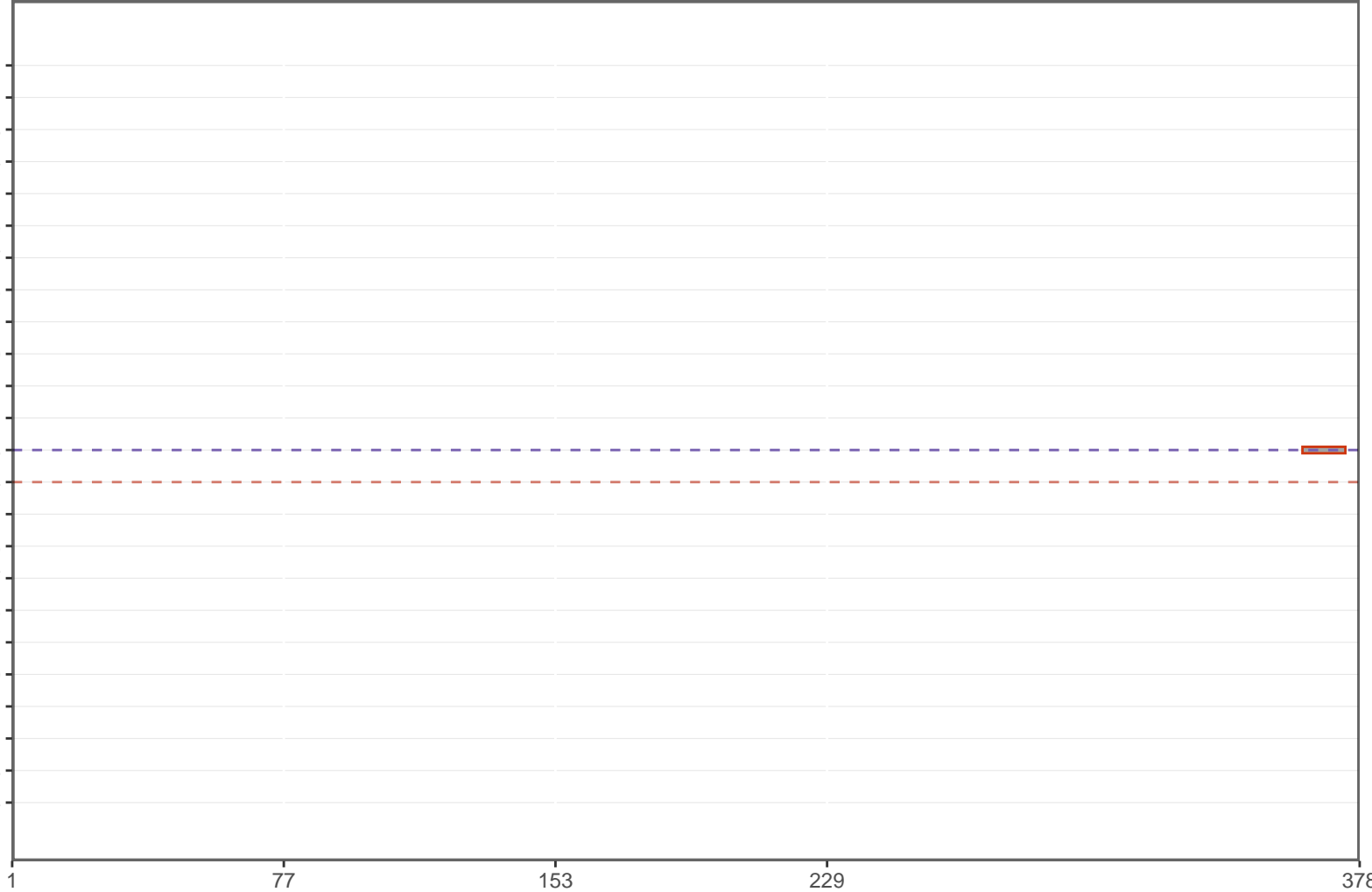
MW indication



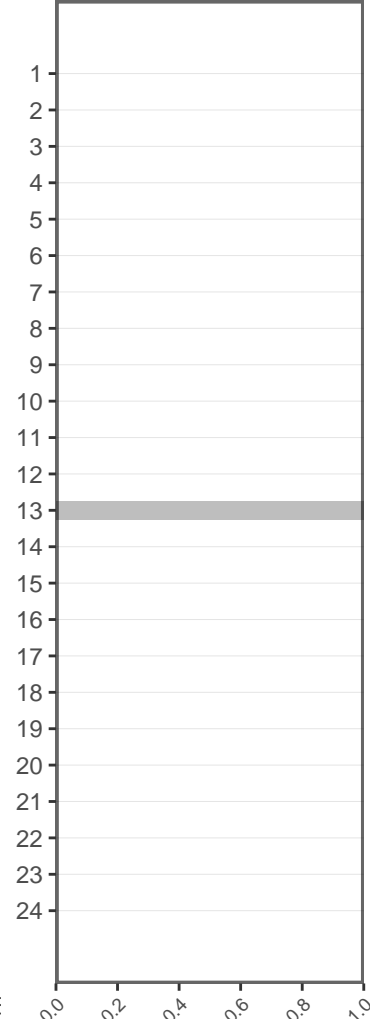
Molecular weight



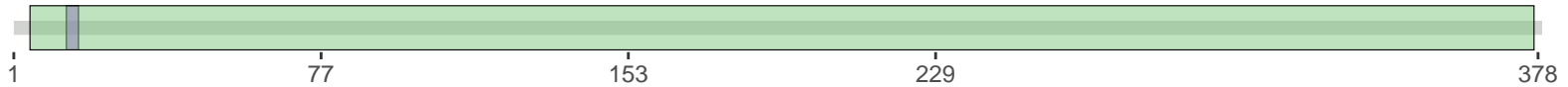
Gel Slice



Protein length

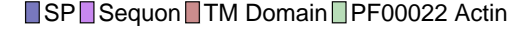


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PHAILRLDLAQRDLTDNLMKILTERGVYFTTAEIREIVRWKKEKLSYALDYEQELETSSKSGSSVEKTYELPDGGVITIGAEFRRCPEVLFPQPMIGMEAAAGIHETTYNSIMKGDVDRKDLGYNVLSGGSTMPFGIADRMSKEITALAPNSMKIKVVAAPPERKYVYVWGGSLASLSTFGQMMWAKAEYDEAGSPVHRKGF

NbL06g13010.1 photosynthetic_NDH_subunit_of_luminal_location_1_chloroplastic [MW = 25.66 kDa]

No. of times detected



log(intensity)



Values from



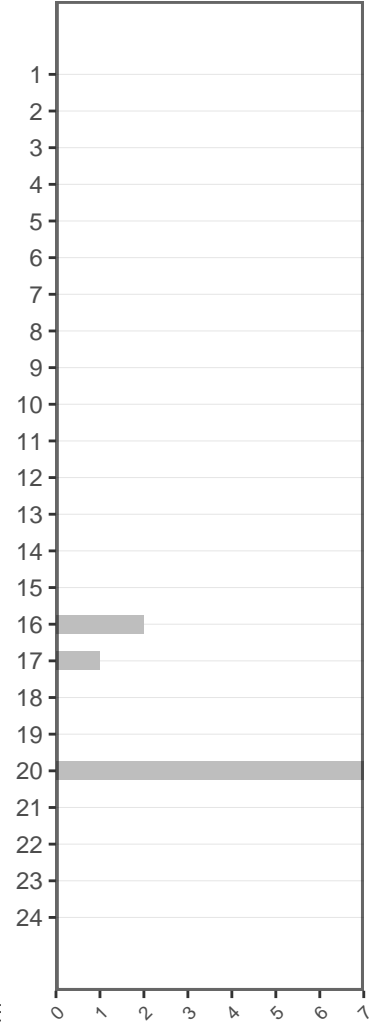
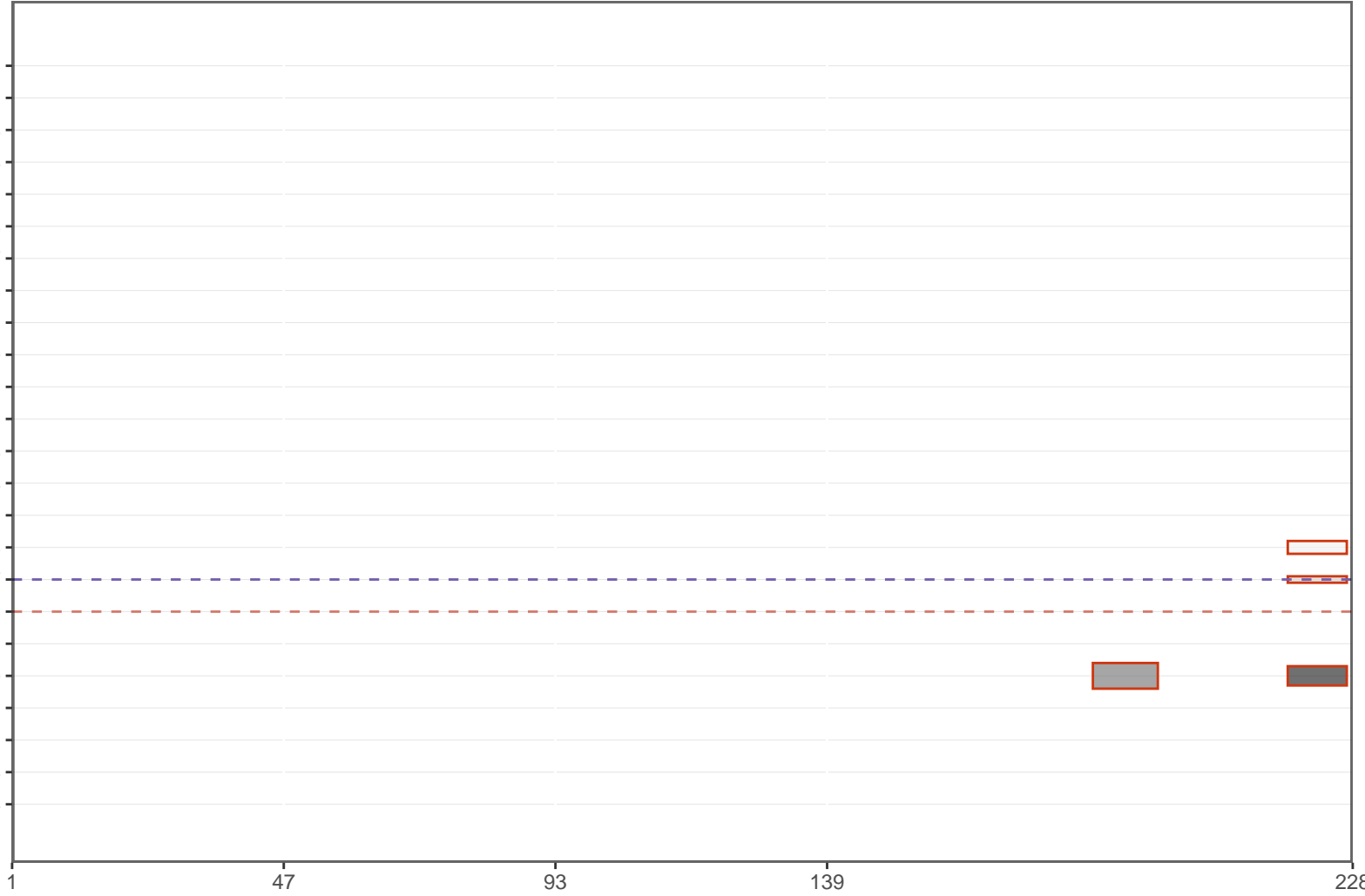
MW indication



Molecular weight

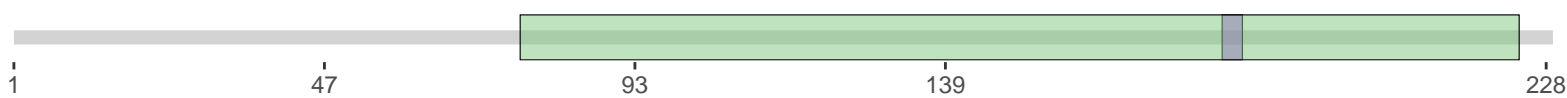


Gel Slice



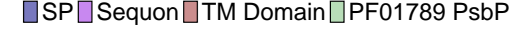
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RGHDSAFKDRYLQIGNVRLSFIPTDKSDHDLGPMEEVAVNLVHKVYSAFNQVNMIMEMREBTDGKNYCTFEYVLTSPNFSRAAFABIAIINGRYYTLVGANERRWRKFRNKLVVADDFQVLDI

NbL06g12960.1 transcriptional_corepressor_LEUNIG-like [MW = 76 kDa]

No. of times detected



log(intensity)



Values from



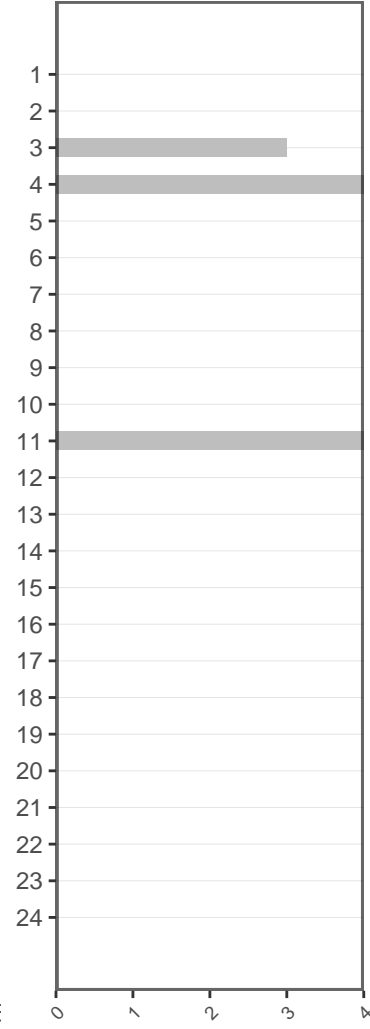
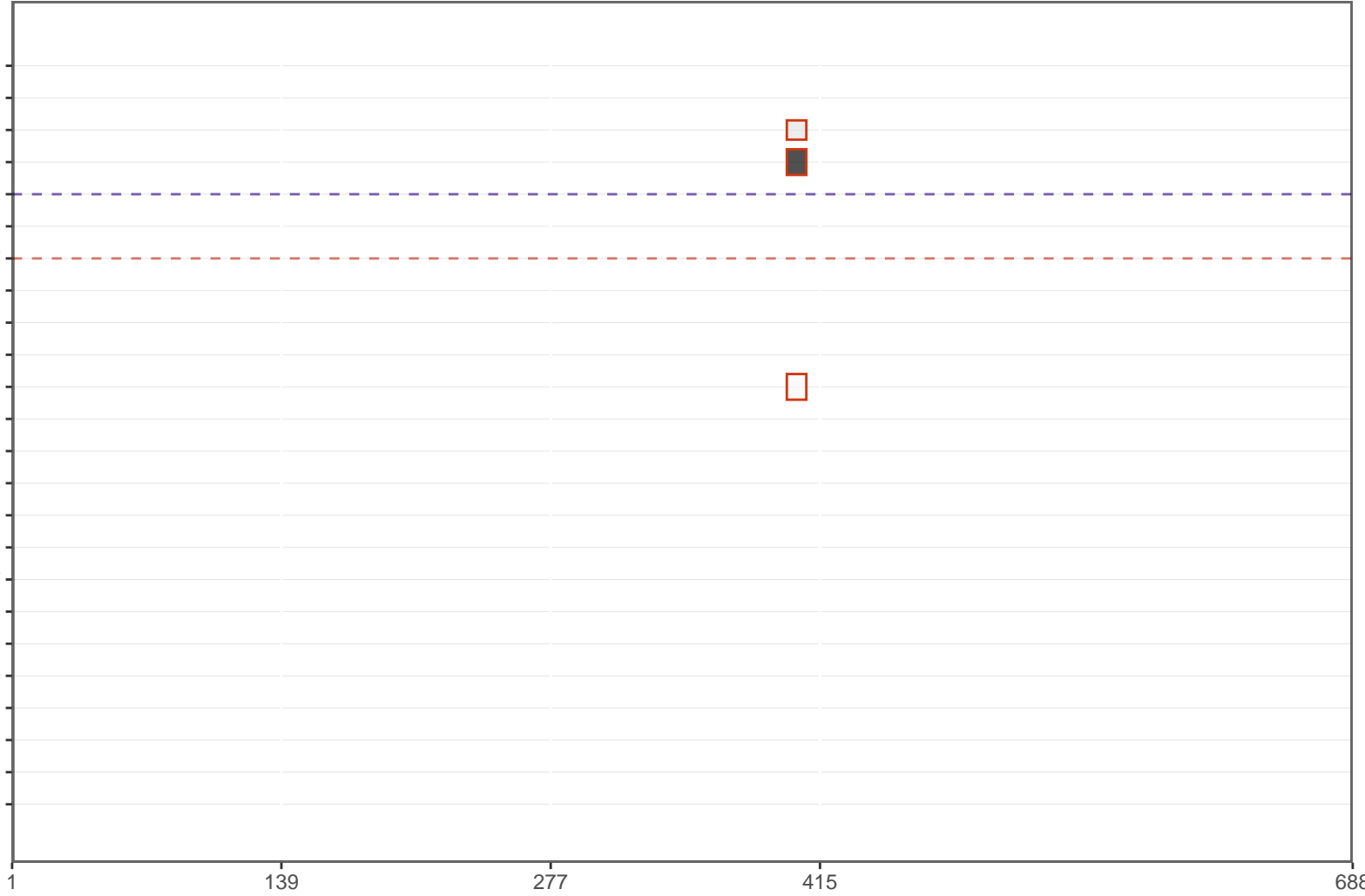
MW indication



Molecular weight

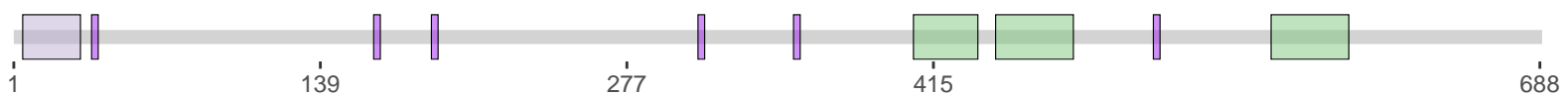


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

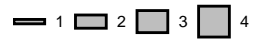


Protein sequence:

PSSIQOQDKRYVTSGSSTMEVSLNITSGGDDQADVPLINHGSDSSEVEFFLSDNADTESSSRGGSTKDKDTLLEIGTFRSSSVNDGDLSSDDGLIANGEDKKYVWGTDSGQKYLKEHSDMFDVRFSPRLPLRSLA66SLDKRKKWVHNPGHSGIRGFTGHSASVMSLDFPTKEDLIGCDNVTIRYVWIKNGGGAGVSKVGTATVRFQFNRGKYLAAMVANGVSLIDVETTTGTRVPLKGHSHKGAQVSS66SEYLA66LSEDMVQVWIKGSSGEOCCMHERSVK

NbL06g12900.1 beta-D-xylosidase_1 [MW - SP = 81.3 kDa]

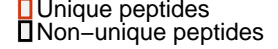
No. of times detected



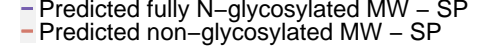
log(intensity)



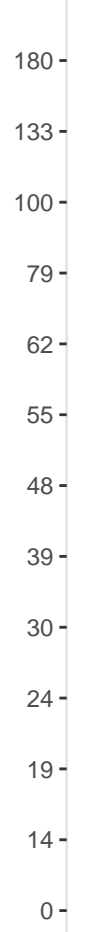
Values from



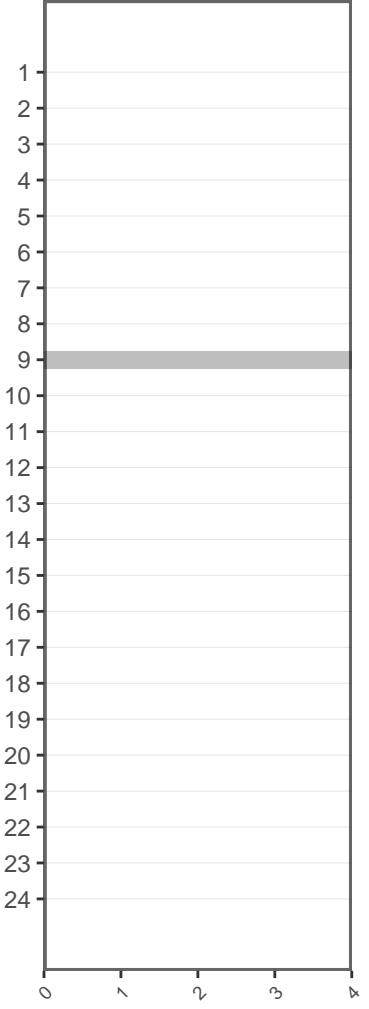
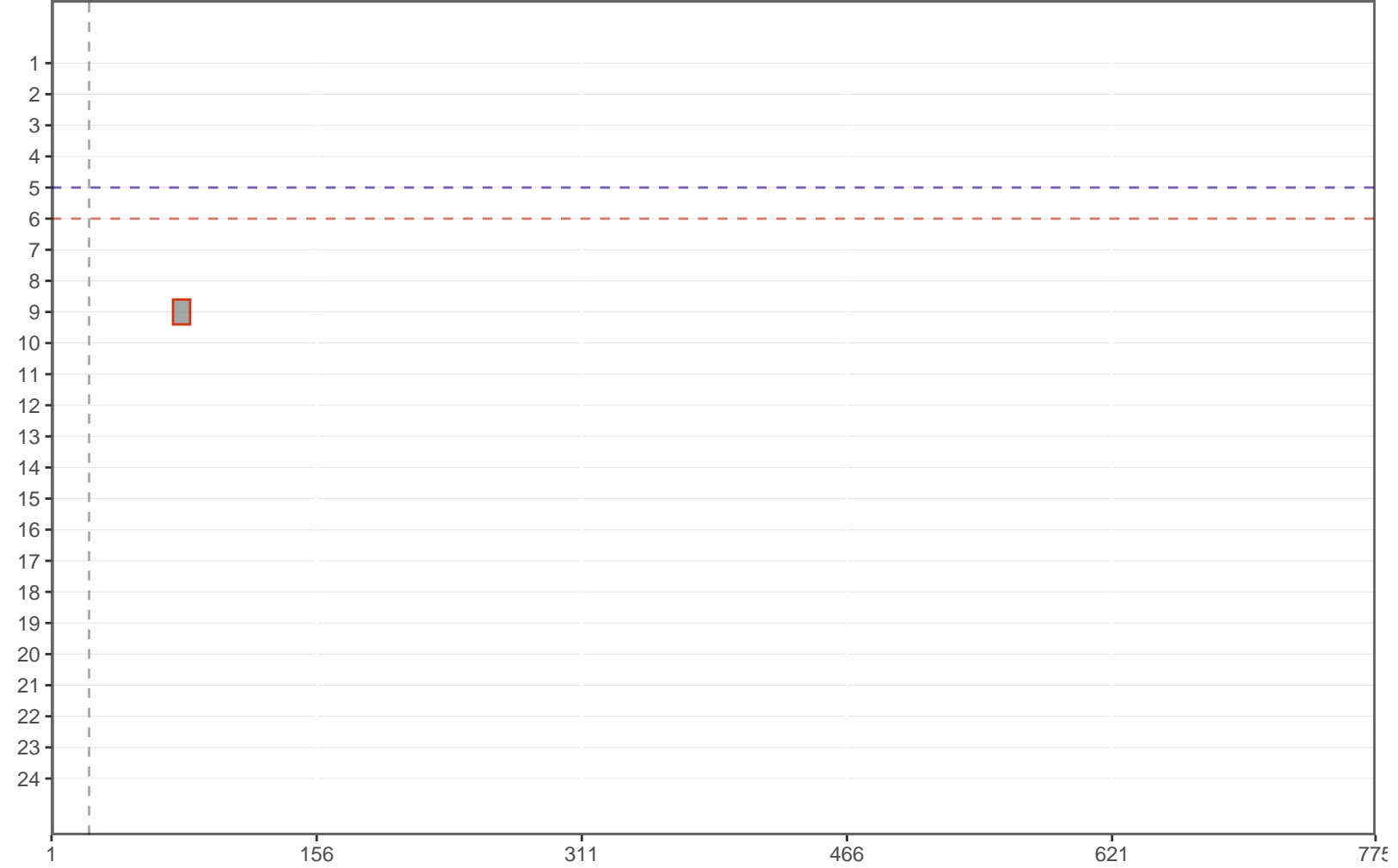
MW indication



Molecular weight

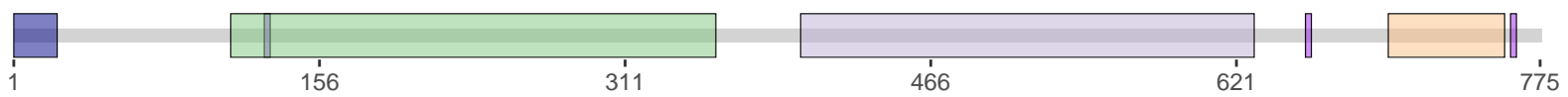


Gel Slice



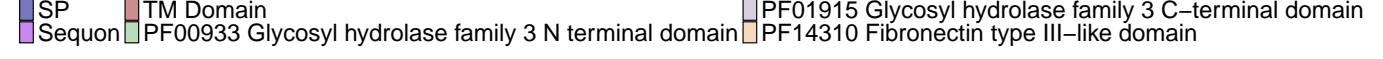
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

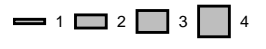


Protein sequence:

NGPYANLGRDVCERNHGGALGAAREGIVLLKNIQRGLPLSPQRHRTIAVIGPNSDQVITMIGNVAGVPGVYISPLGGIARVARTVHQHGCMGAGCPNQGFVAEVAARHADATVLMAGLDQTEAEARDVLSLLPQVGGELIKVAMARGPVWLVLMBSGSDVTFKANDRVSAILWGGYPGAGGAAADLVFGAANPQGGKLPMTWVPGQYAKVAMTNMDMRADPARGYPGRTRYREYKGPVWFFPGAGFSYTRFSQIVSAPNIVSPTLHSLDGNSTRKXFA

NbL06g12840.1 uncharacterized_LOC109232177 [MW = 389.76 kDa]

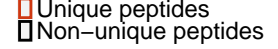
No. of times detected



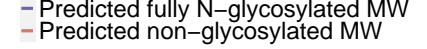
log(intensity)



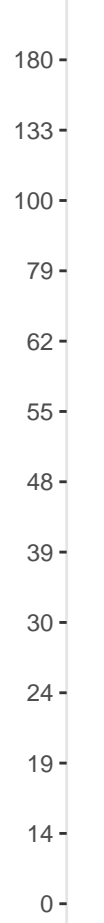
Values from



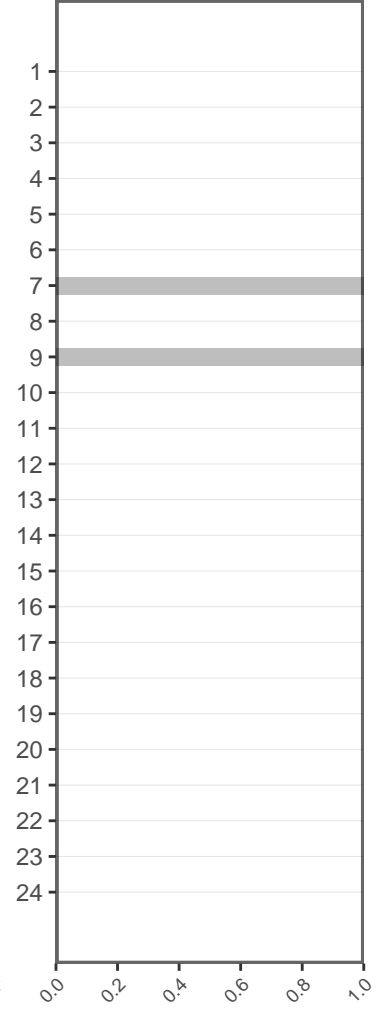
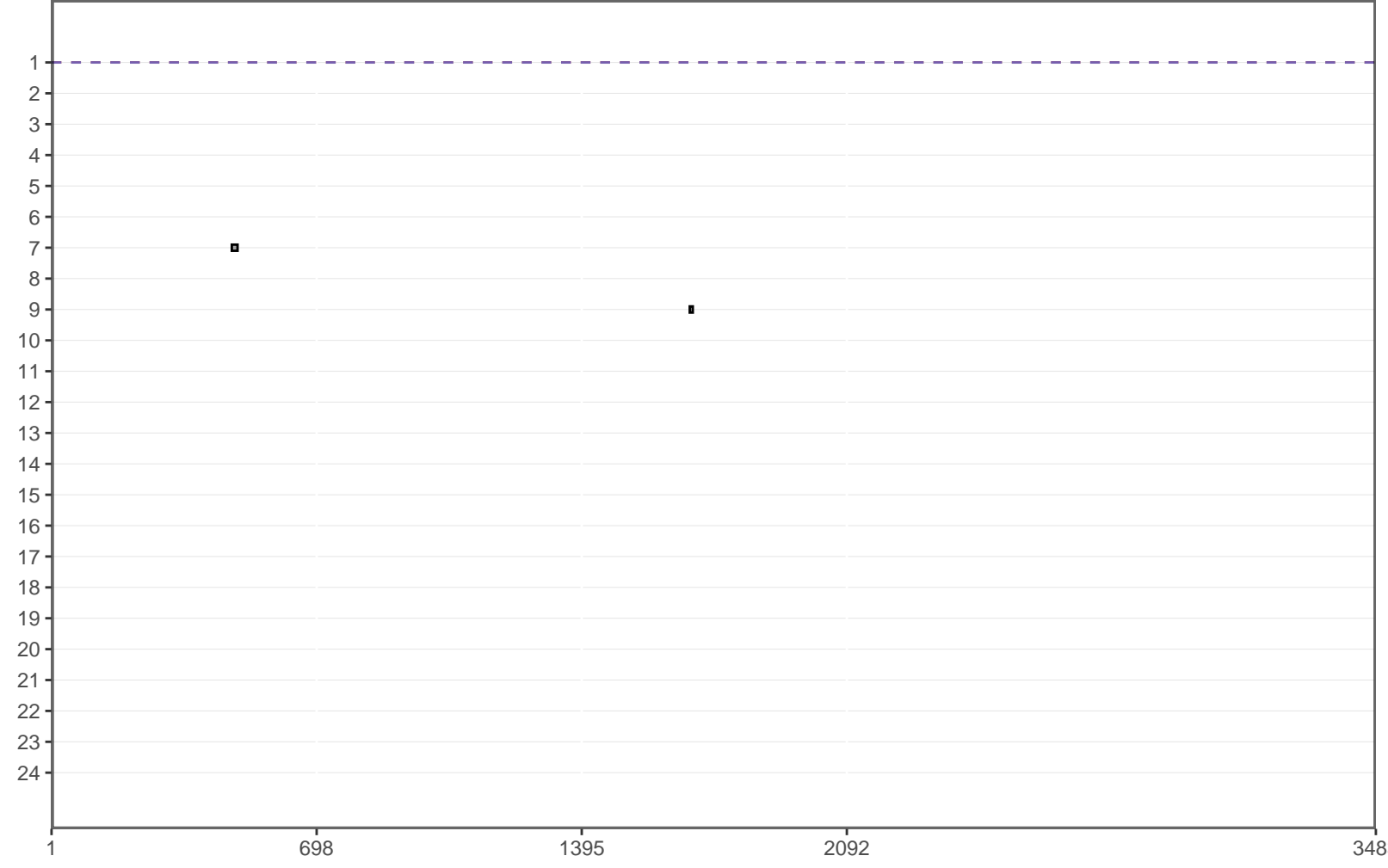
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF06650 SHR-binding domain of vacuolar-sorting associated protein 13
- PF12624 N-terminal region of Chorein or VPS13
- PF16908 Vacuolar sorting-associated protein 13, N-terminal
- PF16909 Vacuolar-sorting-associated 13 protein C-terminal
- PF16910 Repeating coiled region of VPS13

Protein sequence:

LSDHLYFVQFVDFECRAAGPSGFSVQVFKFQRLKFBLLADGKWSBSGPLELLMTNLLGSEINAGNEMEGLVKGEVQVYNNIDKALWEPLFHWVQLSIRRHDDHLLSSDVTSNLHESTTQNLNLTESLIEVSRAIEMTKNAWDLVQLTANSEIPFLKQISENLDRSSPPVILQNLTSPLPEHWYQQGQSGYGLVPSMKGKGYLGPQSSIPVYVSESLDQLRYRFRAGSGDQLGDKKGVKPHHYLVQLEGTSPFRAPISMVLGIRYFVDFSKSSRK

NbL06g12820.1 pyruvate_dehydrogenase_(acetyl-transferring)_kinase_mitochondrial-like [MW = 42.22 kDa]

No. of times detected



log(intensity)



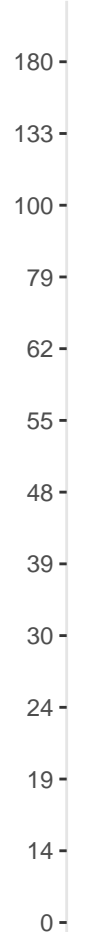
Values from



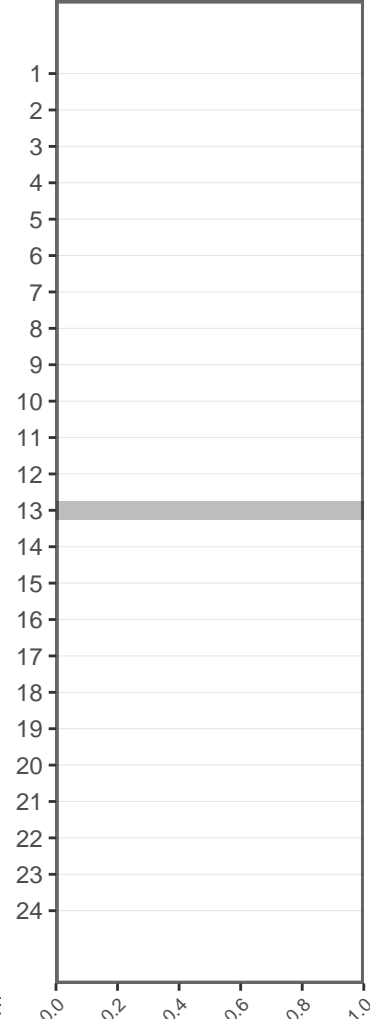
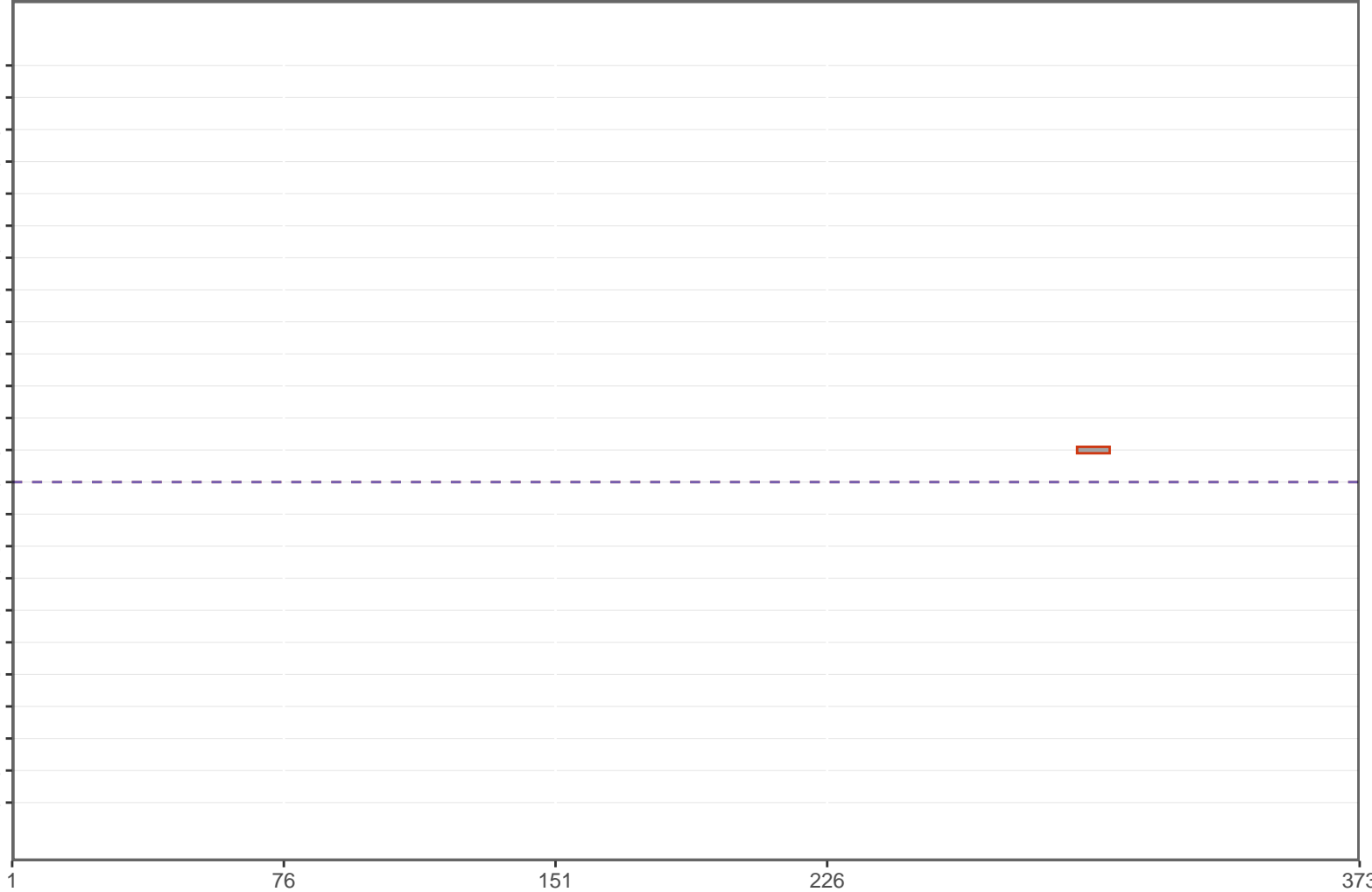
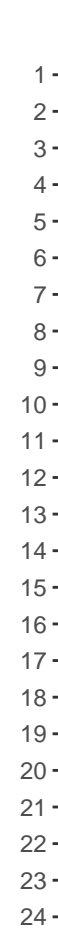
MW indication



Molecular weight

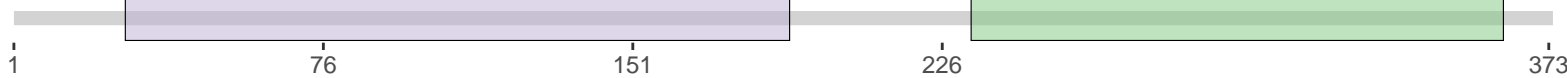


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF02518 Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase
- PF10436 Mitochondrial branched-chain alpha-ketoacid dehydrogenase kinase

Protein sequence:

IVALLIDPNNPPPCVGVYHTKMSPLEVARSASEDARGICAREVGSAPDNHYGDPDFTFFVYPTHLGLMVFELMKNLRAVEERFMDSDKVARRIRIVAGLEEDVTRKVDDEGGGPRISGLPKIFITLYLSTANNPLDEHSDLETTDVAWLSLAGYGVYGLPISRLVARYFGDGLQHEMEGVGTDVAHLHSLRIGDGGDEPLP

NbL06g12690.1 galactokinase [MW = 54.62 kDa]

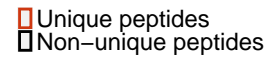
No. of times detected



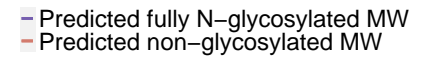
log(intensity)



Values from



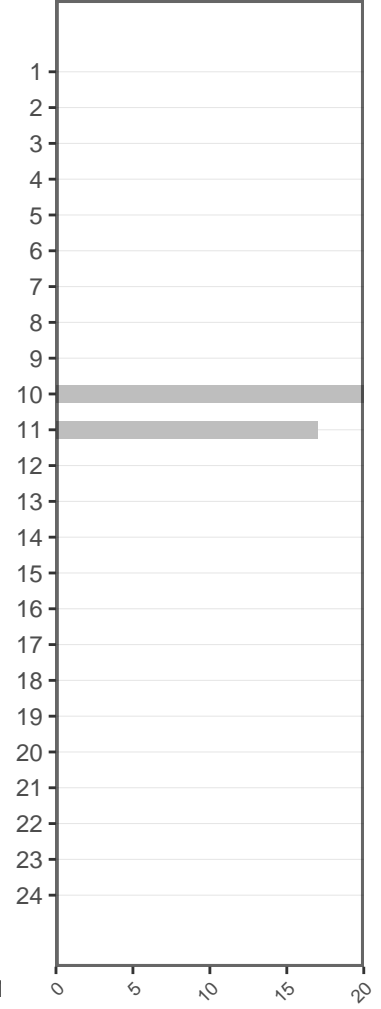
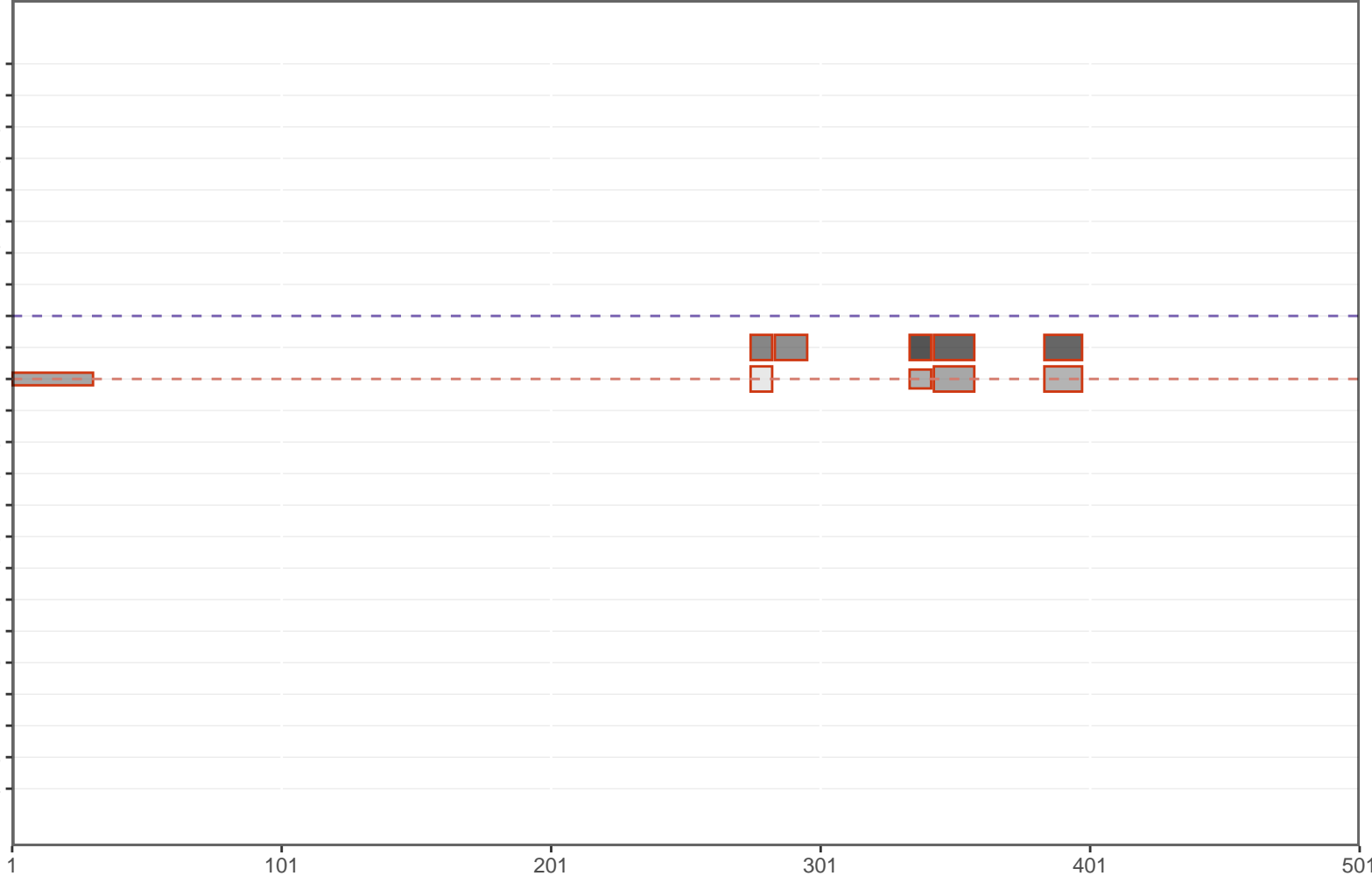
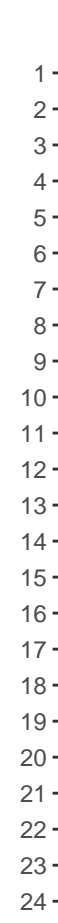
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DVQLPAGGTFYIAHSLAESGKAVTAAVNNRNVVEGLRAAVLGIKLGMEPEHAIFNKTLSDEVEGLGISFAGSHGSDSDPLAVKELHEEPVTSKIDENITQKLETYVFAASPTSLDVLRAAKGKYLHQRAAHVYSEAKRWHAFKDTVSSSELSDEDMITKLGDLINESHGSCVLYEGSCPELEELKIKGRDNGALGARLGTGAGWGGCAVALVKESLVDPFLNLKEQFYQSRIDKGTINKNDLGLYFASKPSSGAAIKF

NbL06g12520.1 uncharacterized_LOC104235511 [MW = 35.45 kDa]

No. of times detected



log(intensity)



Values from



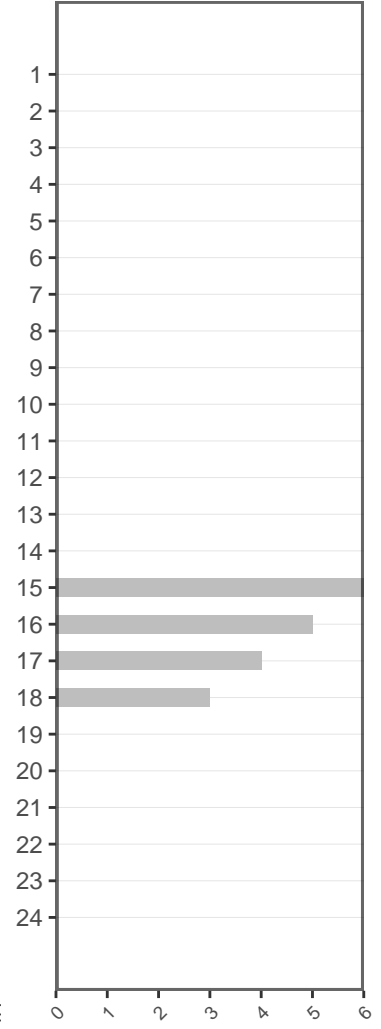
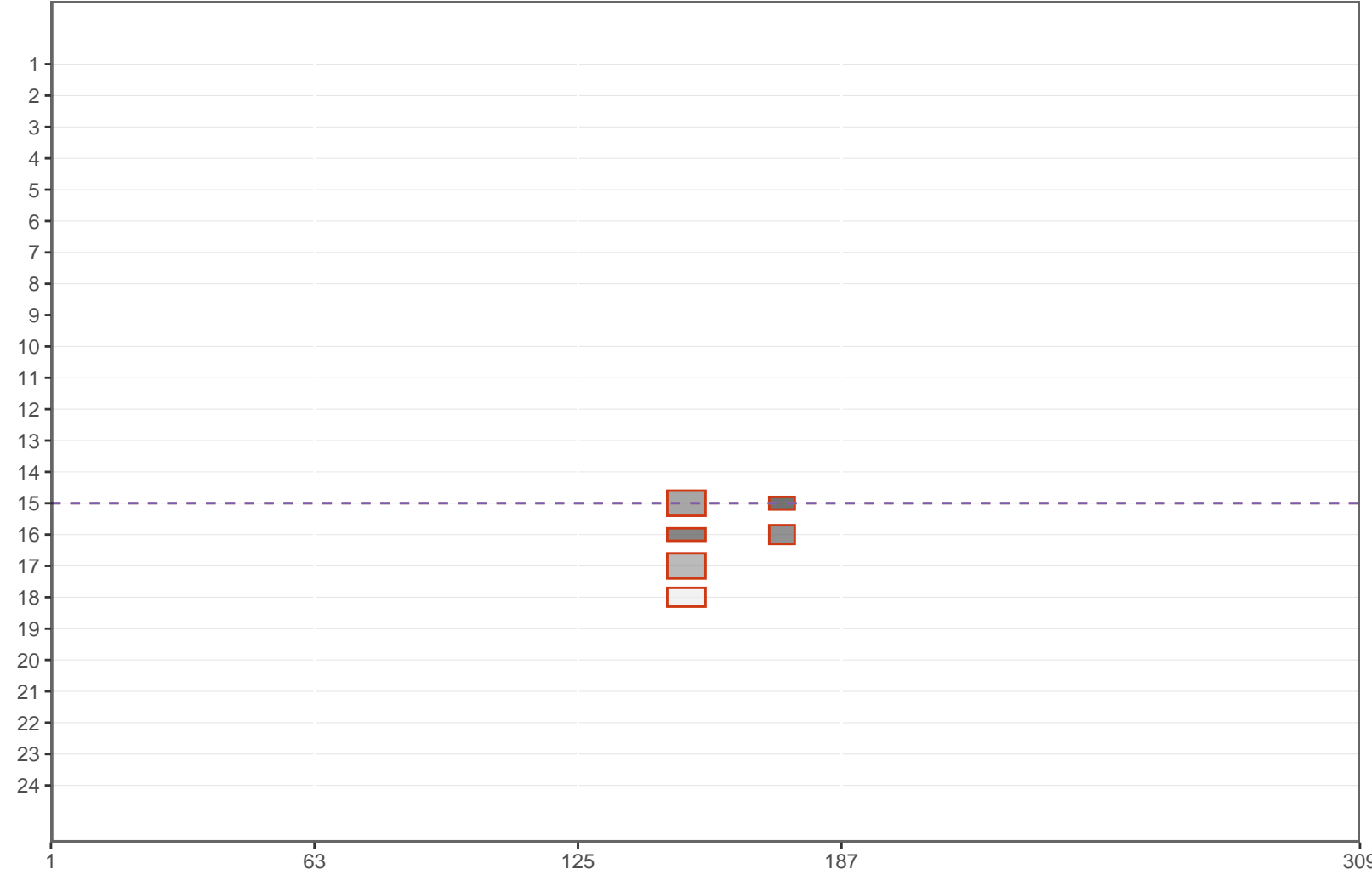
MW indication



Molecular weight

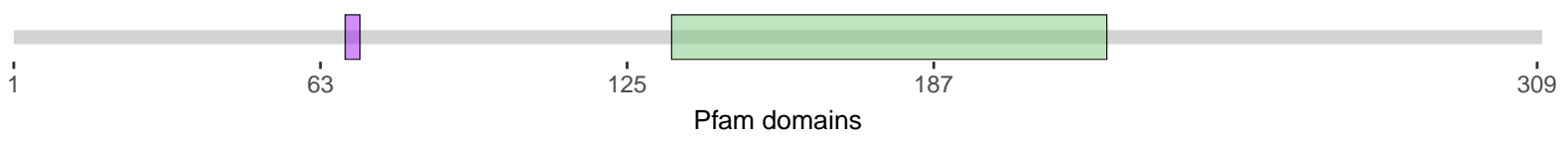


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

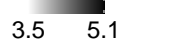
EDRADEVESYNTKVDQFLKFKKGGKLRFSDDGMRRLAVKIKQKASRAHYLLMNFLEAKVWDFKSMLEKDERVRRHLMKQDKAETEDGPPPPFHTLRAGTDDNEEDMDDDFDYEEEDLLEGGDDDDDDTGGVILVDVDDNVDGRDSRNIGQISTHKGIGRQKVEV

NbL06g12480.1 probable_enoyl-CoA_hydratase_1_peroxisomal [MW = 29.26 kDa]

No. of times detected



log(intensity)



Values from



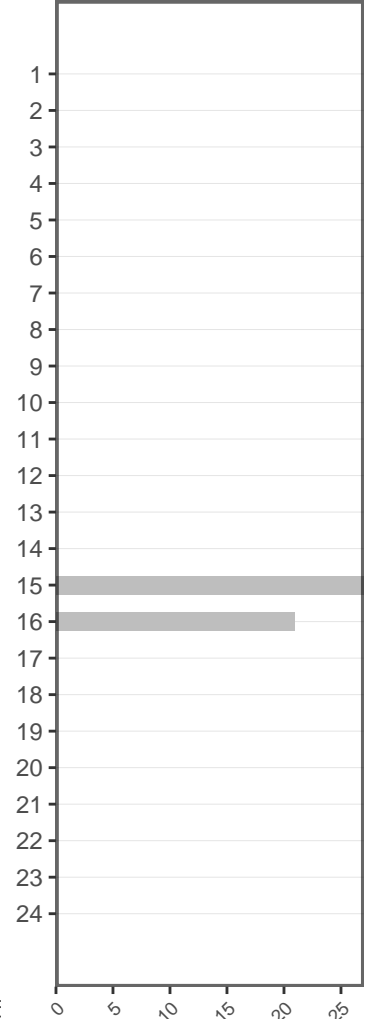
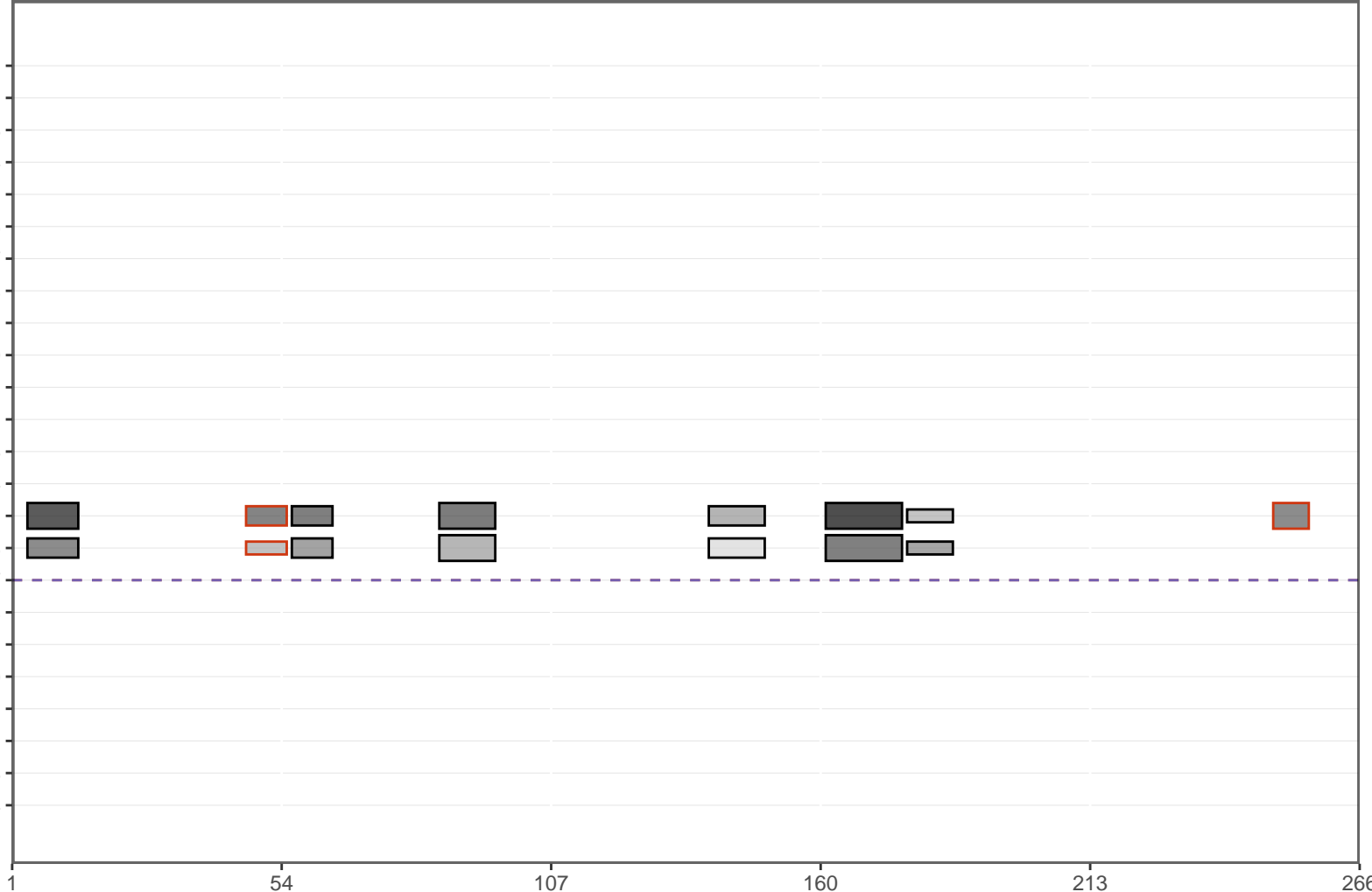
MW indication



Molecular weight

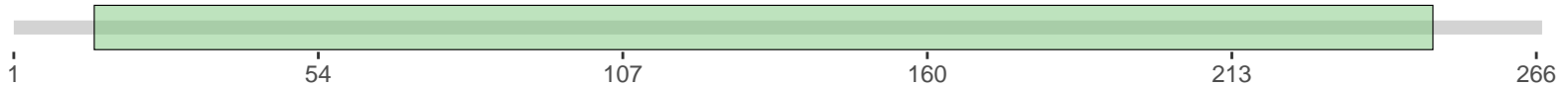


Gel Slice



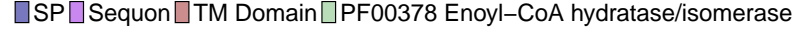
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DLLVASNDKFLDTHARFGFPPWGLGKLSRVIGPSRAREABLTPMSIAEQAERWGLVNYVDRSELLKKARQAEAIKNNHDLVLYKAVINDGFKGDLARALALEKERAHVYVDGMSKDFKRLGEFIADRSSSKPSSKLL

NbL06g12430.1 ATP-citrate_synthase_beta_chain_protein_2 [MW = 65.58 kDa]

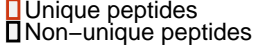
No. of times detected



log(intensity)



Values from

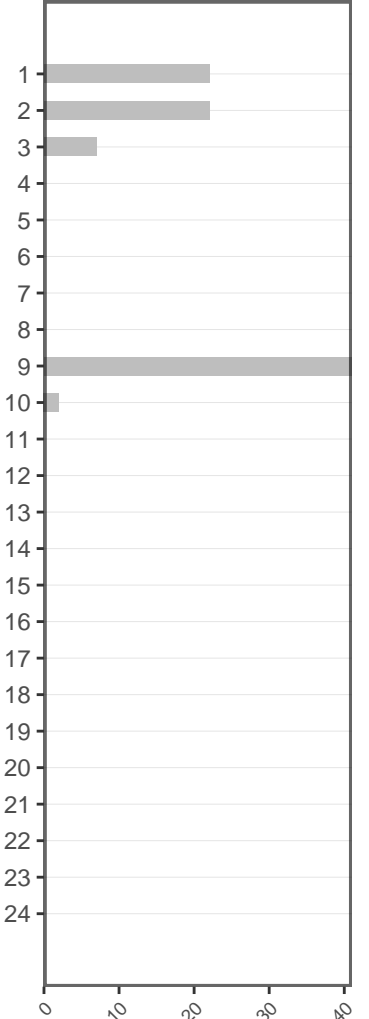
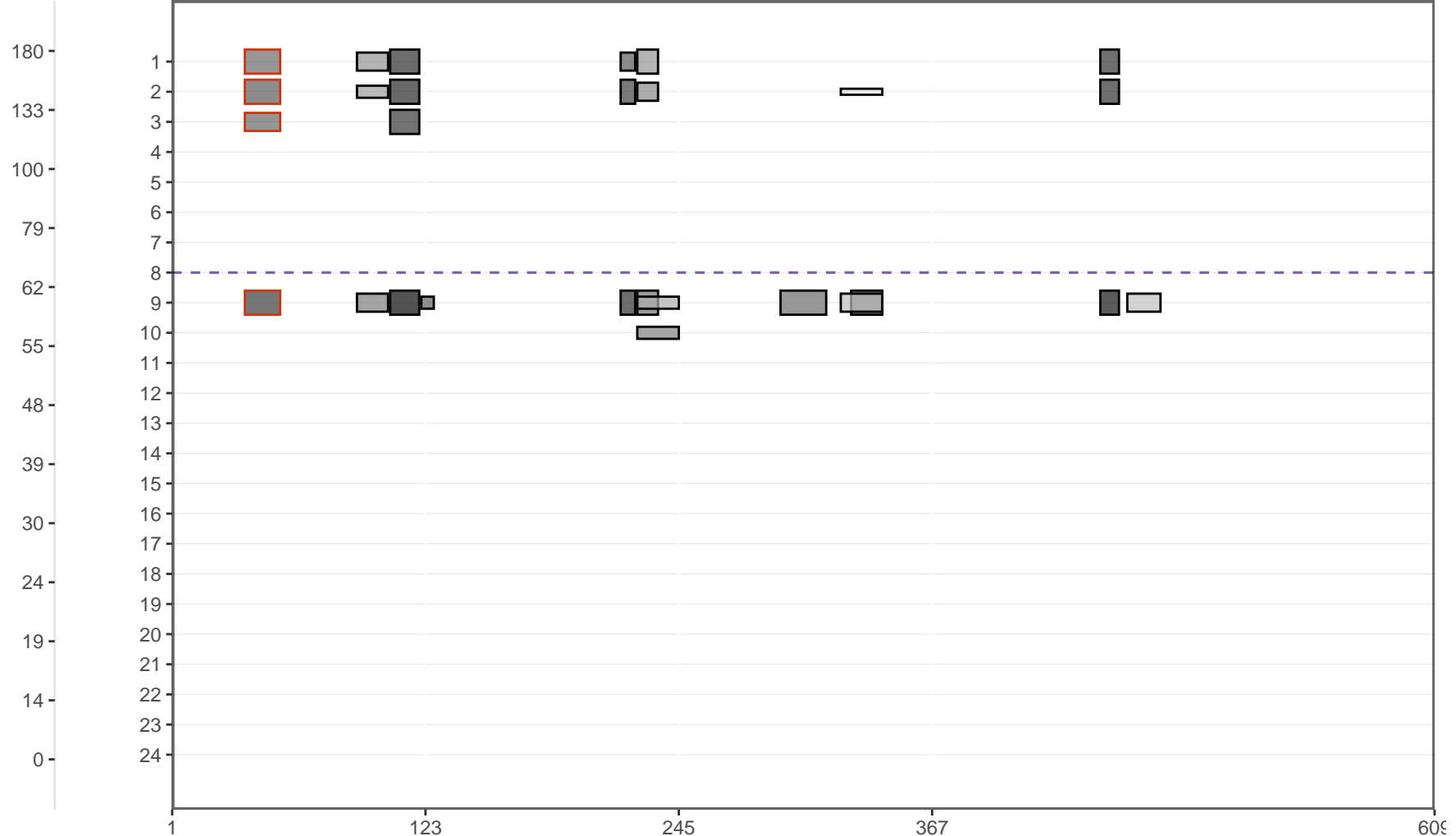


MW indication



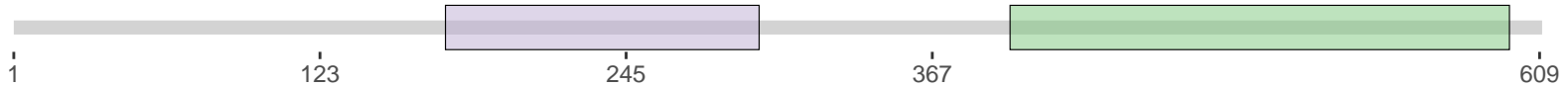
Molecular weight

Gel Slice



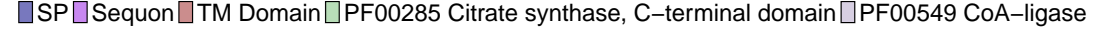
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ALRDAGAVPTSYSAFEGAKNDTFEKIVEAGKTPPKVEVSRPPQPELSTAKKGGKVRAPTHISTISDGRGEEPCVAGVPMSSVEOGLGVGDVSLWFKRSLPRVCTRFIEICVMLCADHGPCVSGAHNSVITARAGKDLVSLVSGLLTIGPRFGAIDDAARYFKDVKGLTPYEFVEMKKKGGIRVPGIGHKRRKRDNRKRVELLQVARENFPEVKYMEVAVGVETVTLKANNVAVDGAIGSLFLDLLAGSGMFKPEIDVEIEGVYNGLFLVARSIGLIHTFDCK

NbL06g12380.1 glucan_endo-13-beta-glucosidase_basic_vacuolar [MW - SP = 37.23 kDa]

No. of times detected



log(intensity)



Values from



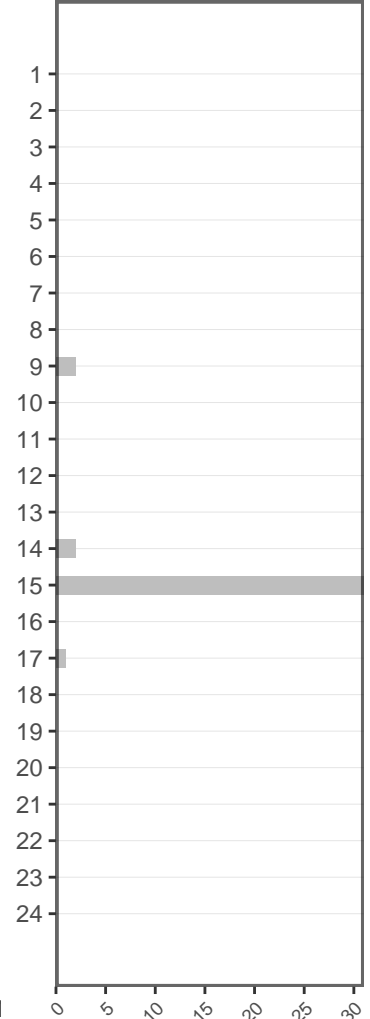
MW indication



Molecular weight

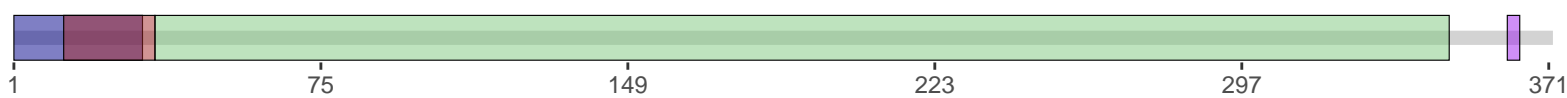


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISYPPSOGSFRINDARWVFDVWVGLRDTAPLNVVYFVSGNPDGDISLPSVSLTAPNVVVDGSRGQYRNLFDMLDVEVAALERGGGABVGVVSEGGWPSAGAFGATYDNGTYLRNLQHAKEGSRPKPGIETVIFAMFDENKPKPELEKHFGFLFSFNKQPKYVNLNFGVSGGVWDSSEVETNATASISEM

NbL06g12330.1 endoplasmin_homolog [MW = 101.65 kDa]

No. of times detected



log(intensity)



Values from



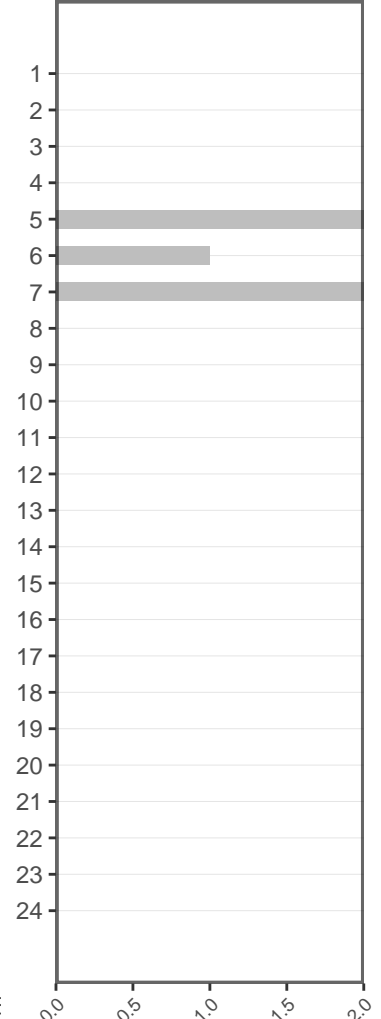
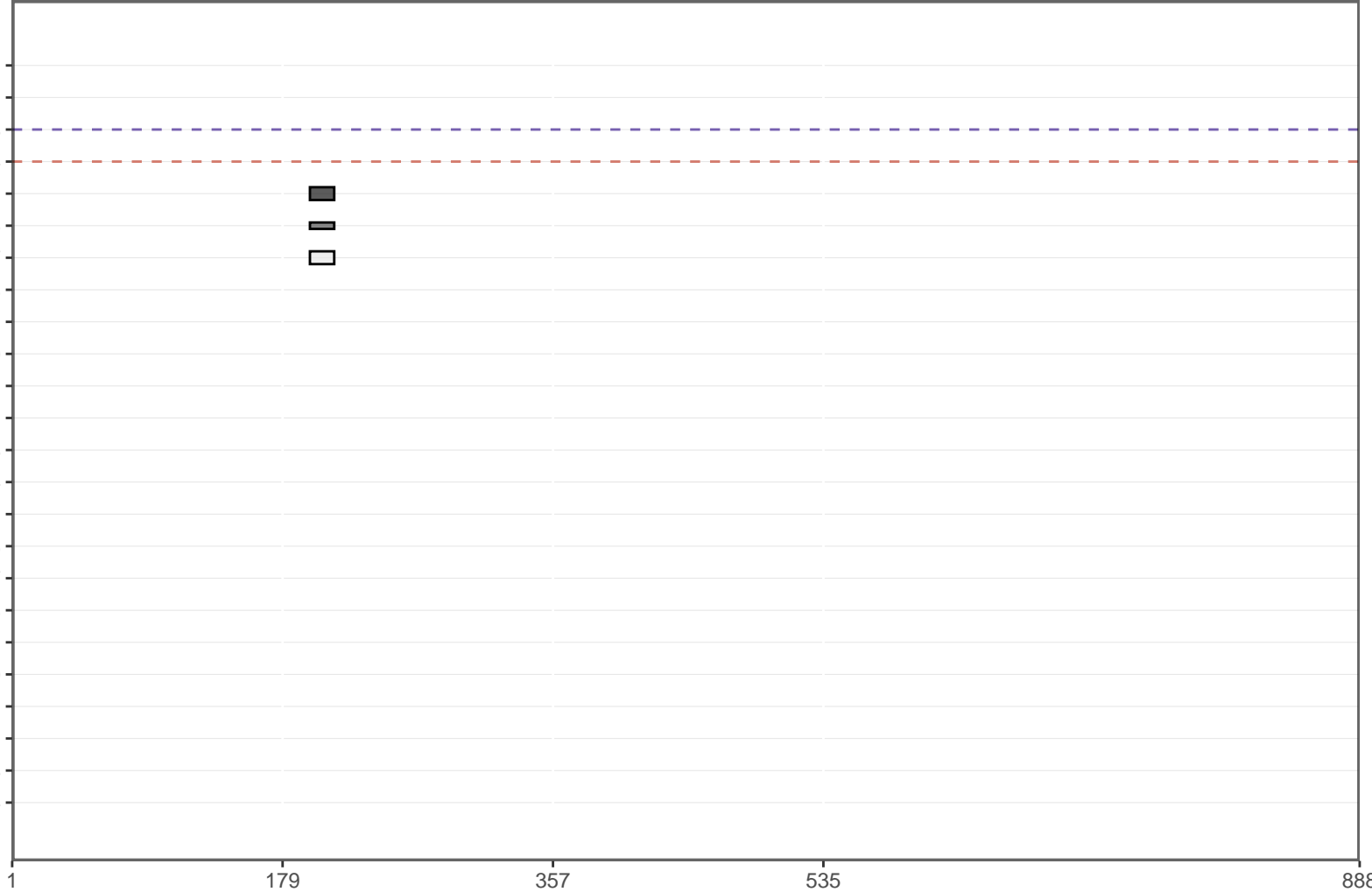
MW indication



Molecular weight



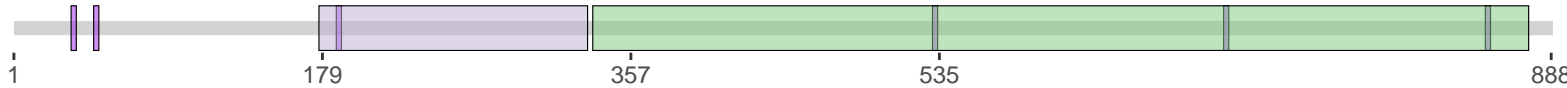
Gel Slice



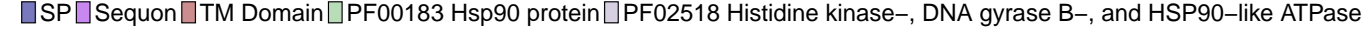
Protein length



Pfam domains



Pfam Description



Protein sequence:

VTTEETKPYHSLAKDFSDKPLAWSHFNAEGDVEFKAVLFPKAPHDYEGYVNSKKNLKLIVRRVRSDFDEFDLPPKLSFLMGLVDSDTLPLNVRERMLQGHSLKTKKLRKALDMRKIADEDPDESNDKDKDIEESADNEKGGVAKFWNEFGKVKVGLGIEDATNRNRLAKLLRFETSKDGGKLTSLDQVHSRMKAGQKDFVYTGASKEQLGEGSPFLERLTKKNYVEFFTFDPVDEVLGMQVLMQVYEDKFKQVSKVKEGLKLGKDKAKELKESFKELTKWV

NbL06g12200.1 12-dihydroxy-3-keto-5-methylthiopentene_dioxygenase_1 [MW = 22.26 kDa]

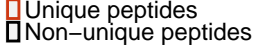
No. of times detected



log(intensity)



Values from



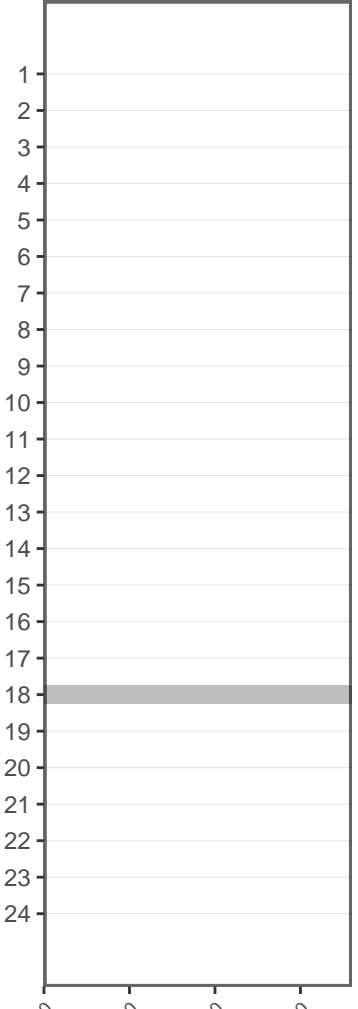
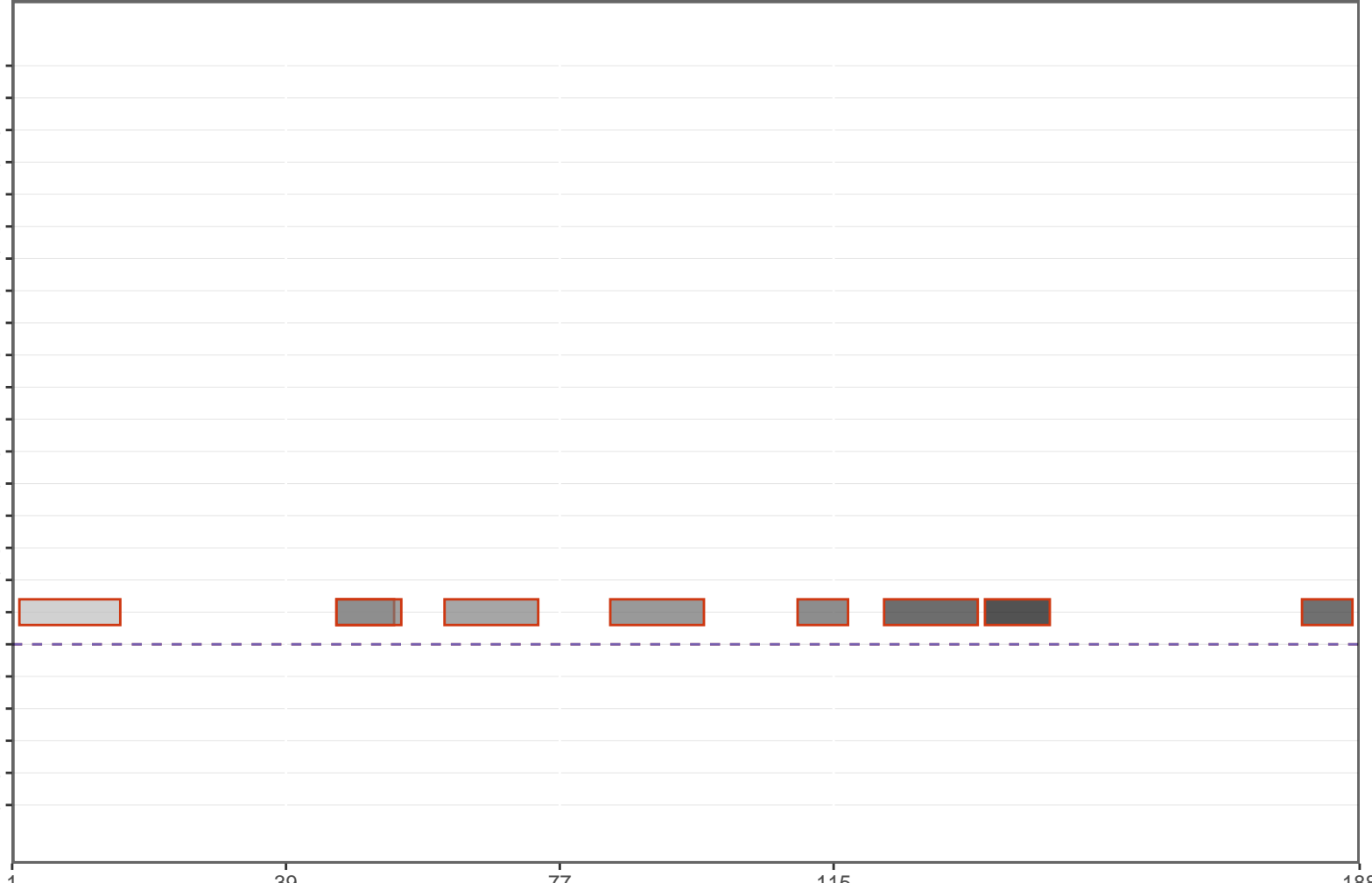
MW indication



Molecular weight

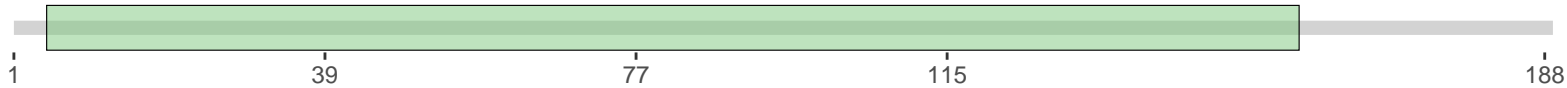


Gel Slice



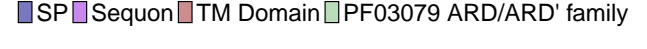
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

QKLNFTYEHIADEERYGLEGGYFDVRDNEHDHWIRWIKAGDLILFAGYHRFLDTGNVYKMLRFLVGEPLWTAHNRPOEDHPARREYKSVTERVGVPLAAH

NbL06g12160.1 probable_histone_H2AXb [MW = 14.65 kDa]

No. of times detected



log(intensity)



Values from



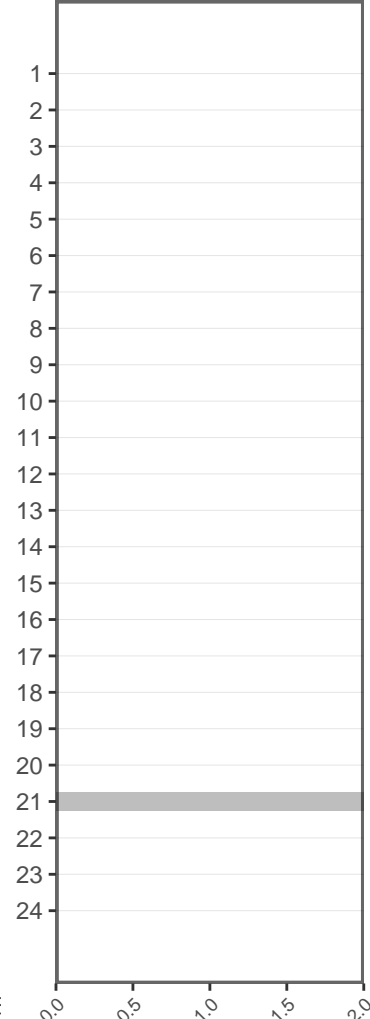
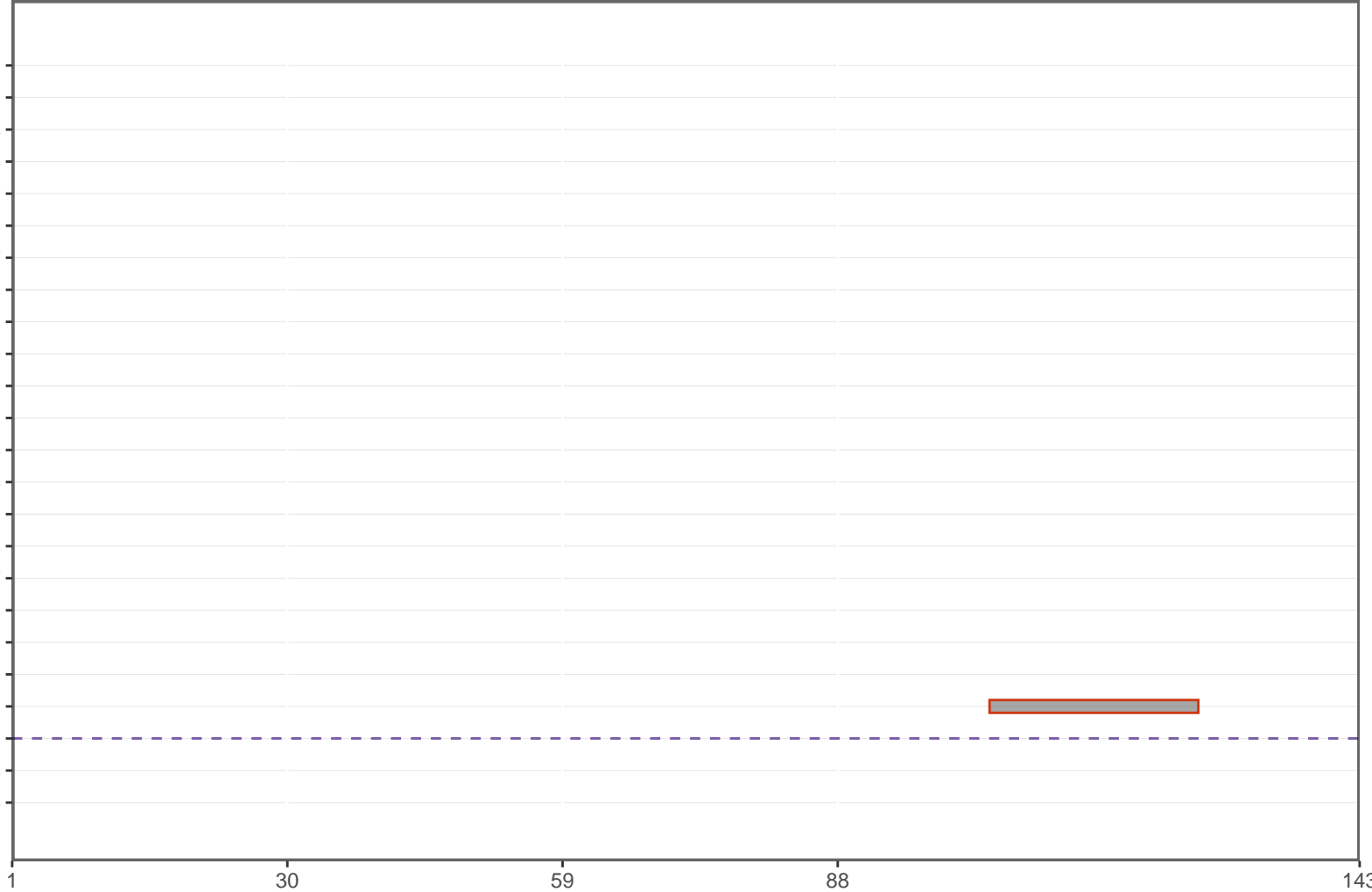
MW indication



Molecular weight



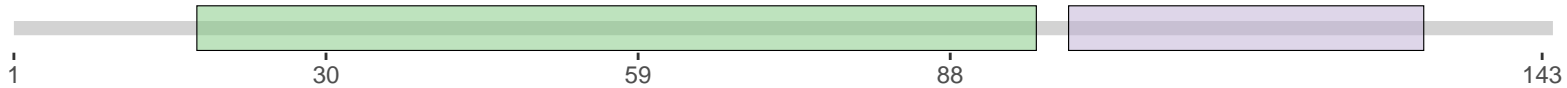
Gel Slice



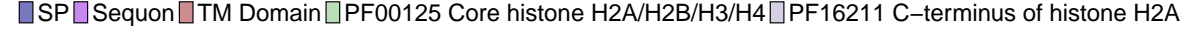
Protein length



Pfam domains



Pfam Description



Protein sequence:

YLSAVLEYLAEEVLELAGNAARDNKNRIVPRHQAVRNDEELSKLGGVTIANGVLPNHNQNLPPKAGSGKGGDGSAGDEP

NbL06g12030.1 peroxidase_2-like [MW = 32.36 kDa]

No. of times detected



log(intensity)



Values from



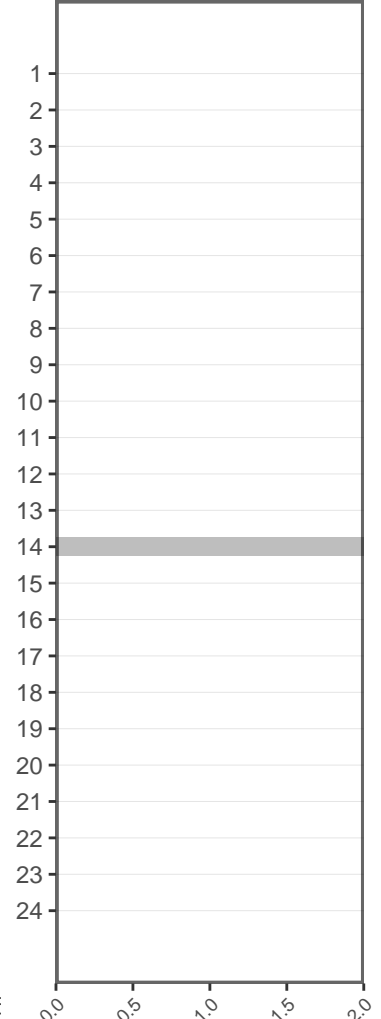
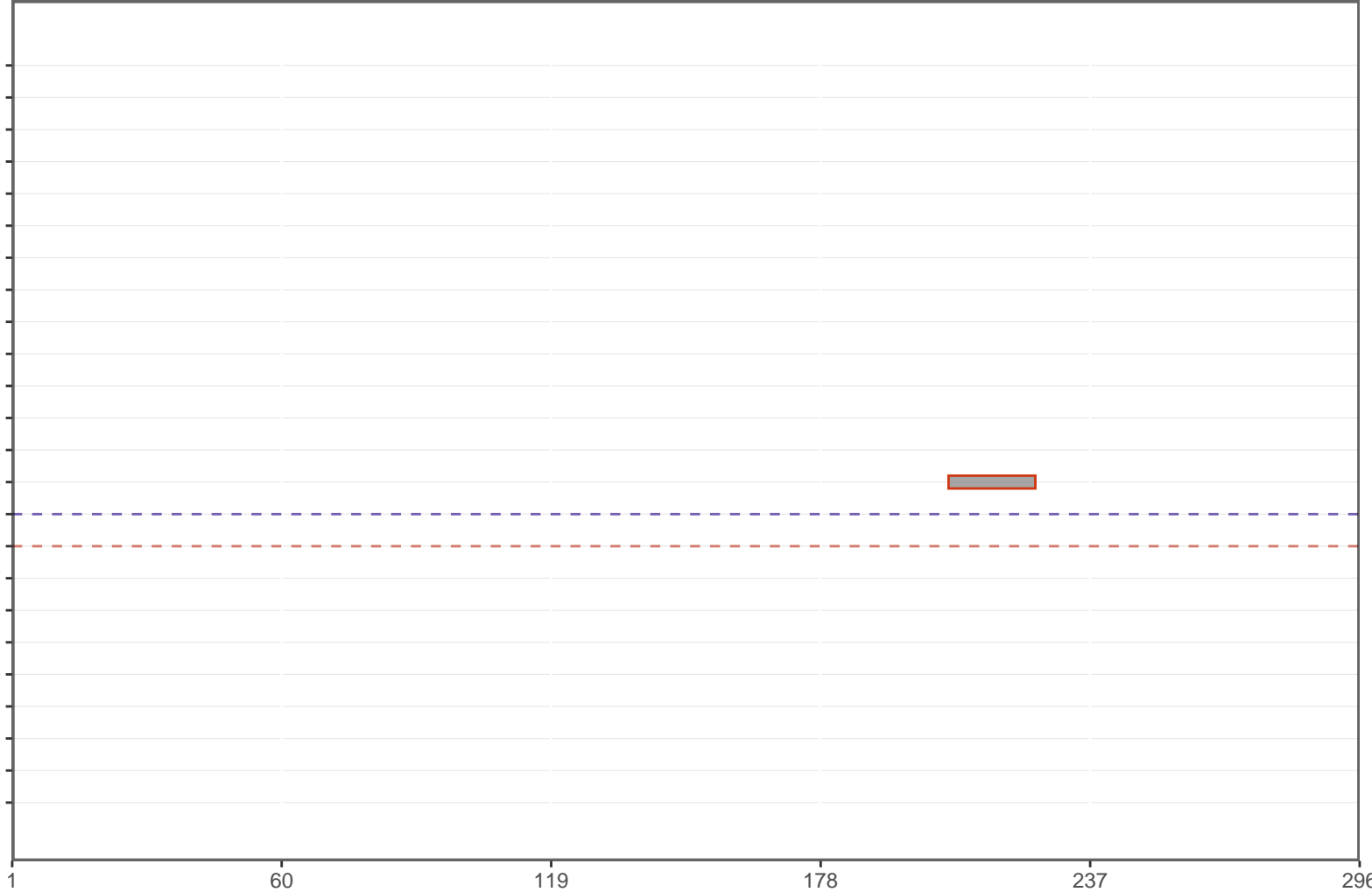
MW indication



Molecular weight



Gel Slice

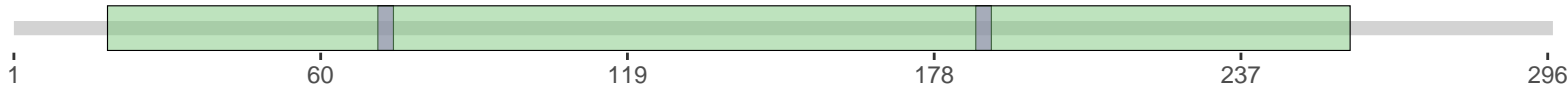


Peptide counts over 4 repeats

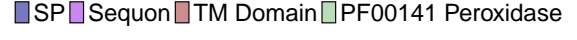
Protein length



Pfam domains



Pfam Description



Protein sequence:

VNDIPSPFTMDLPAHNSFKNOGLKEDLWALGGHITLGFAGQCFTRRNRYNETNNDSTFAAGQAGNCPFRGGGDNLASLDPTAALFDGKYFQNLVSKKGLLHSDQALFSGGTTDGLVKTYSFNLGTFKDFAEEMKMGKPKLPTGNQGGIRVNRKRVN

NbL06g11920.1 COBRA-like_protein_7 [MW - SP = 68.86 kDa]

No. of times detected



log(intensity)



Values from



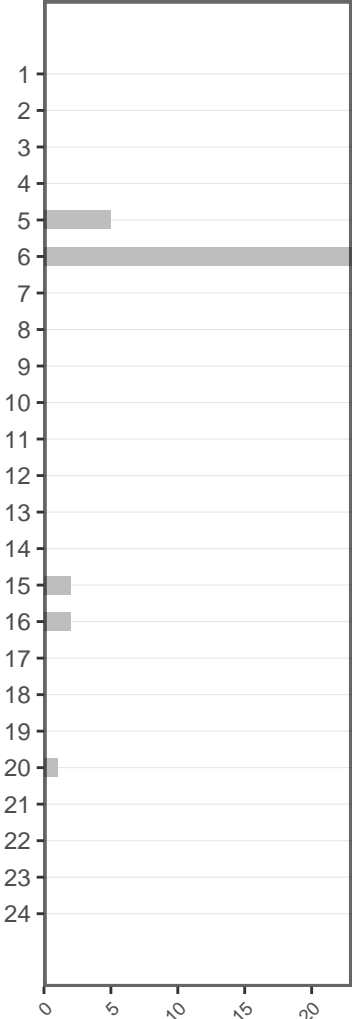
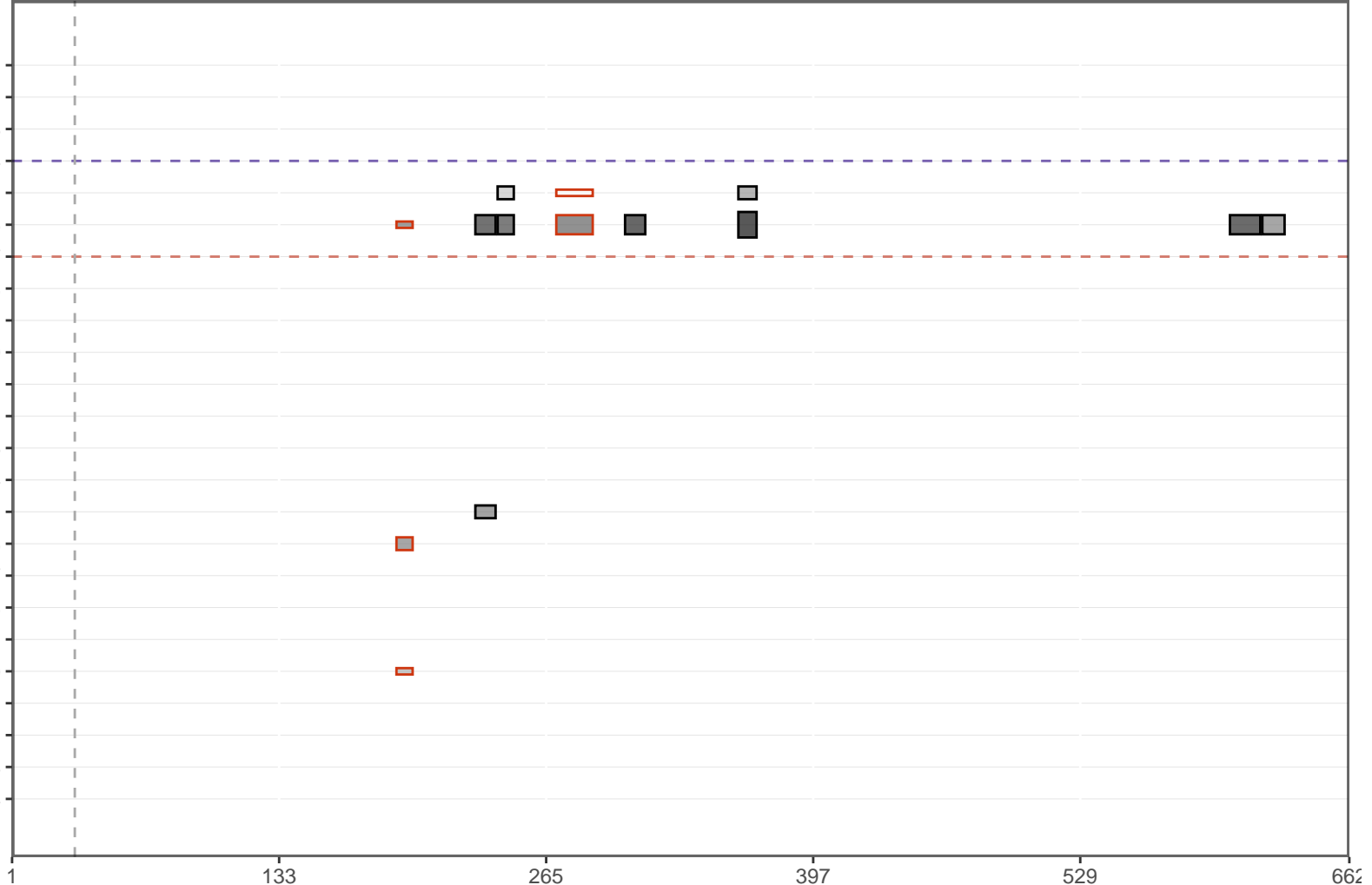
MW indication



Molecular weight

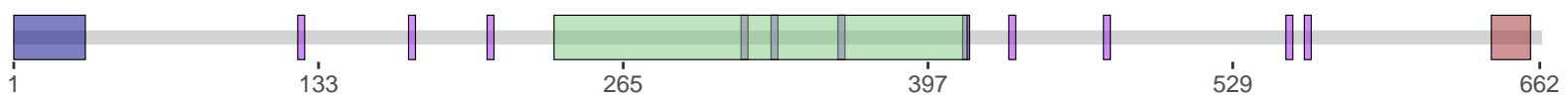


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KLGMIPFCRNGTILPRMMDPKKASAFQINVFKMPPDLNRSGFTTPQNWIEGRILNFDYKGGPPRVRVSPSGQFDPSPGSLPNTAFASWVWVGNITDQKGSAPRRCVYSFSAFYNEIIPCPPTGGCGGCPENTARTGSAKAPALLPQGLALVPEFNRTKMLAWADNHLPLVSNPLPGGDNDGVSINWHLFTDQYRGGWSARITLFWDDTSEFDWFTAVQLDKAALGFDAVYSEFNGTLDGWNNTLFGMOGLEGLNLYVAETDGANPEKDRPRVPGKGGVYSFTKXNSPQNP

NbL06g11810.1 acetate/butyrate--CoA_ligase_AAE7_peroxisomal-like [MW = 62.55 kDa]

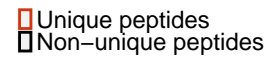
No. of times detected



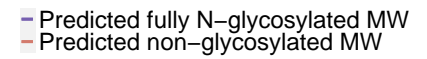
log(intensity)



Values from



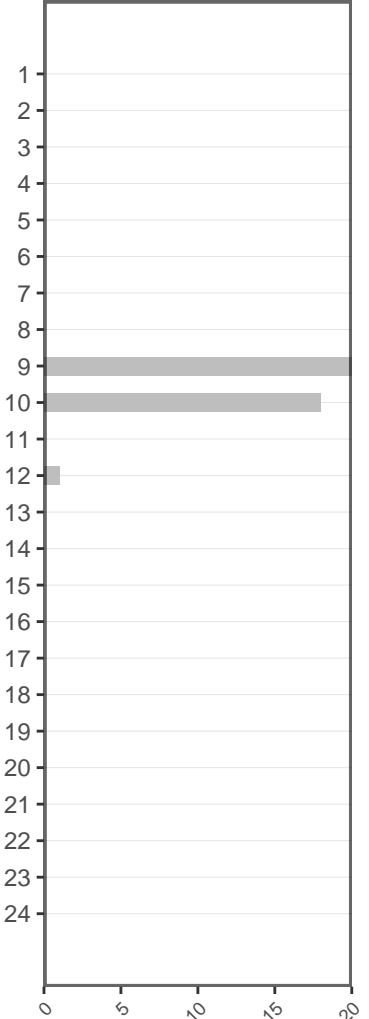
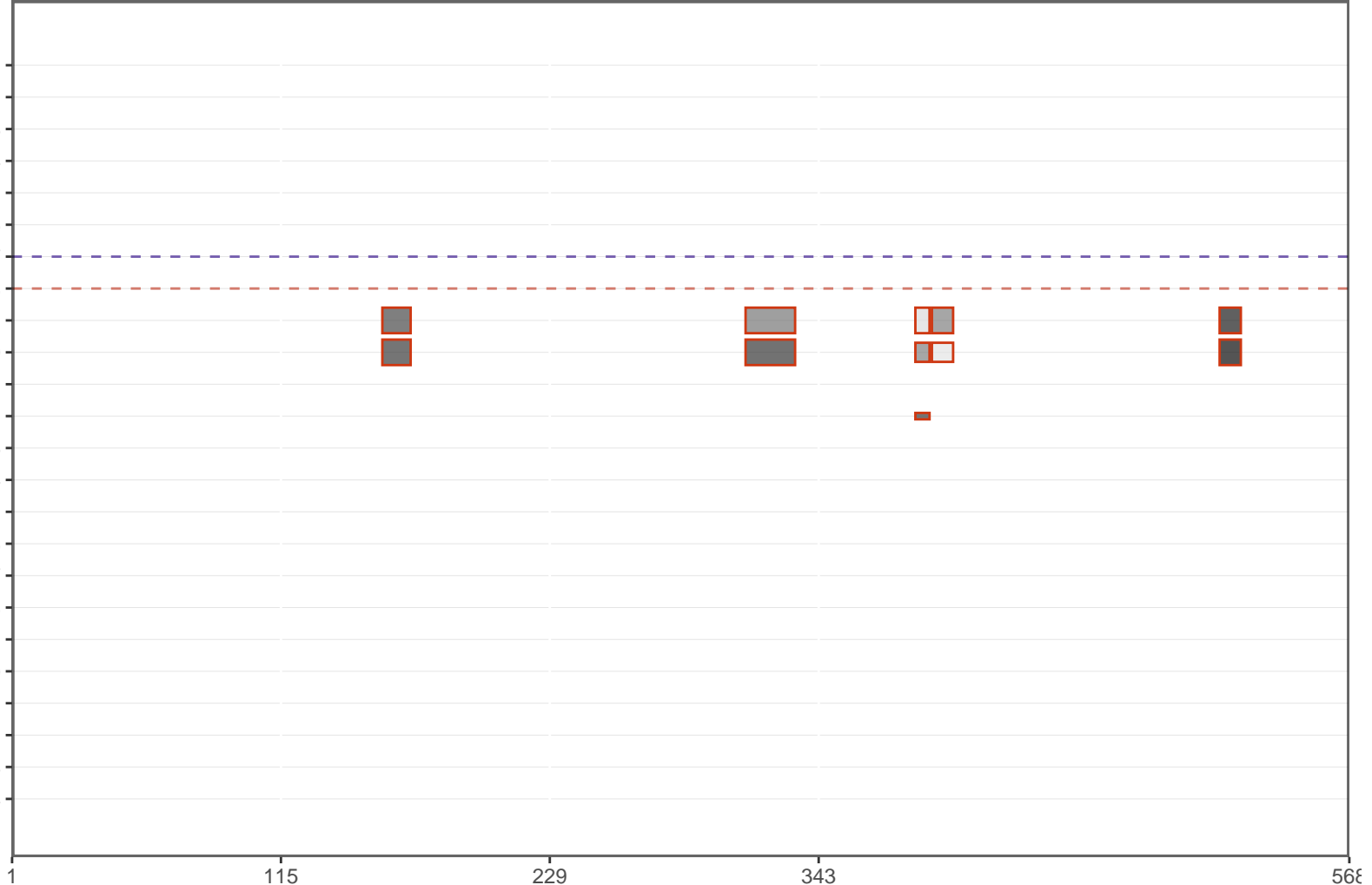
MW indication



Molecular weight

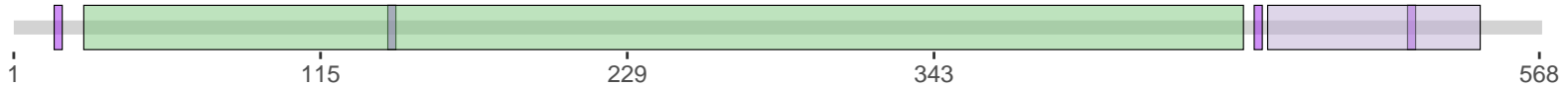


Gel Slice



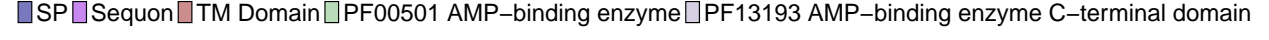
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VTKAVYSAITHLGVTHFSAMPVAVLNTINAPKEETLPLRLVHVSTAGASPPPSVLAAMTQRFGRVRLHYGLSETYGPSTGCTWKPEDWLLPTDQARLNARNGVRYVLSLEKLVNPKDMTPVPAKNGKTMGEIVFKGNVVMKGVLPKPKANEAFAFGWVYHSGDLAVKHPDGYIEKDRKDIHSGGENISSEVENILYQHPALEVSVVARDPDEGWGESPCAFVTLKPNVKETDQGLAEDIMNFSRKMRRVWVPKSVVFGPLPKTATGKQKHLRAKAKEMQPMG

NbL06g11790.1 GTP-binding_protein_SAR2 [MW = 21.96 kDa]

No. of times detected



log(intensity)



Values from



MW indication



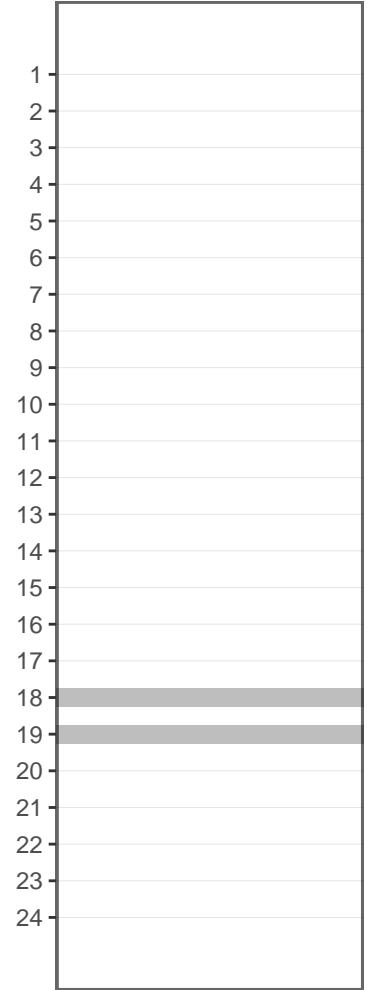
Molecular weight



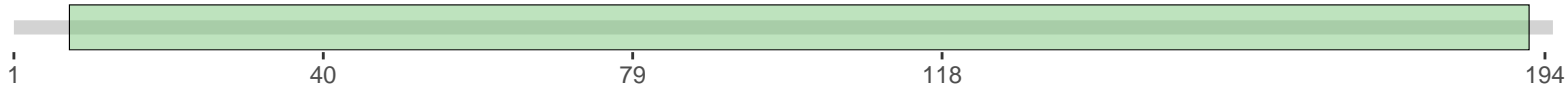
Gel Slice



Protein length

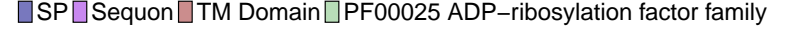


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YYAKVDAVYLYLDVDRERFPEGKELDGLLSDSLANVFLILGNKIDIPVAASEDELRHYLGLTGVTGKGNVNLGNTNVRPIEVFMGSRKRMKGYGEGFRKMSGYK

NbL06g11660.1 proteasome_subunit_beta_type-2-A [MW = 22.59 kDa]

No. of times detected



log(intensity)



Values from



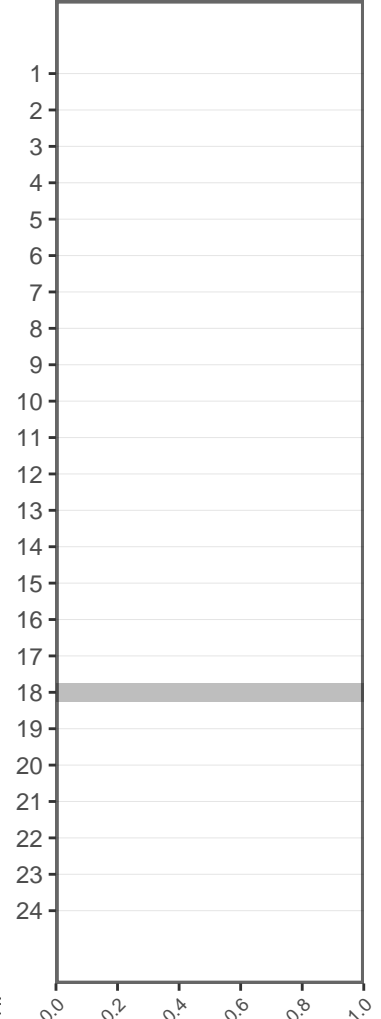
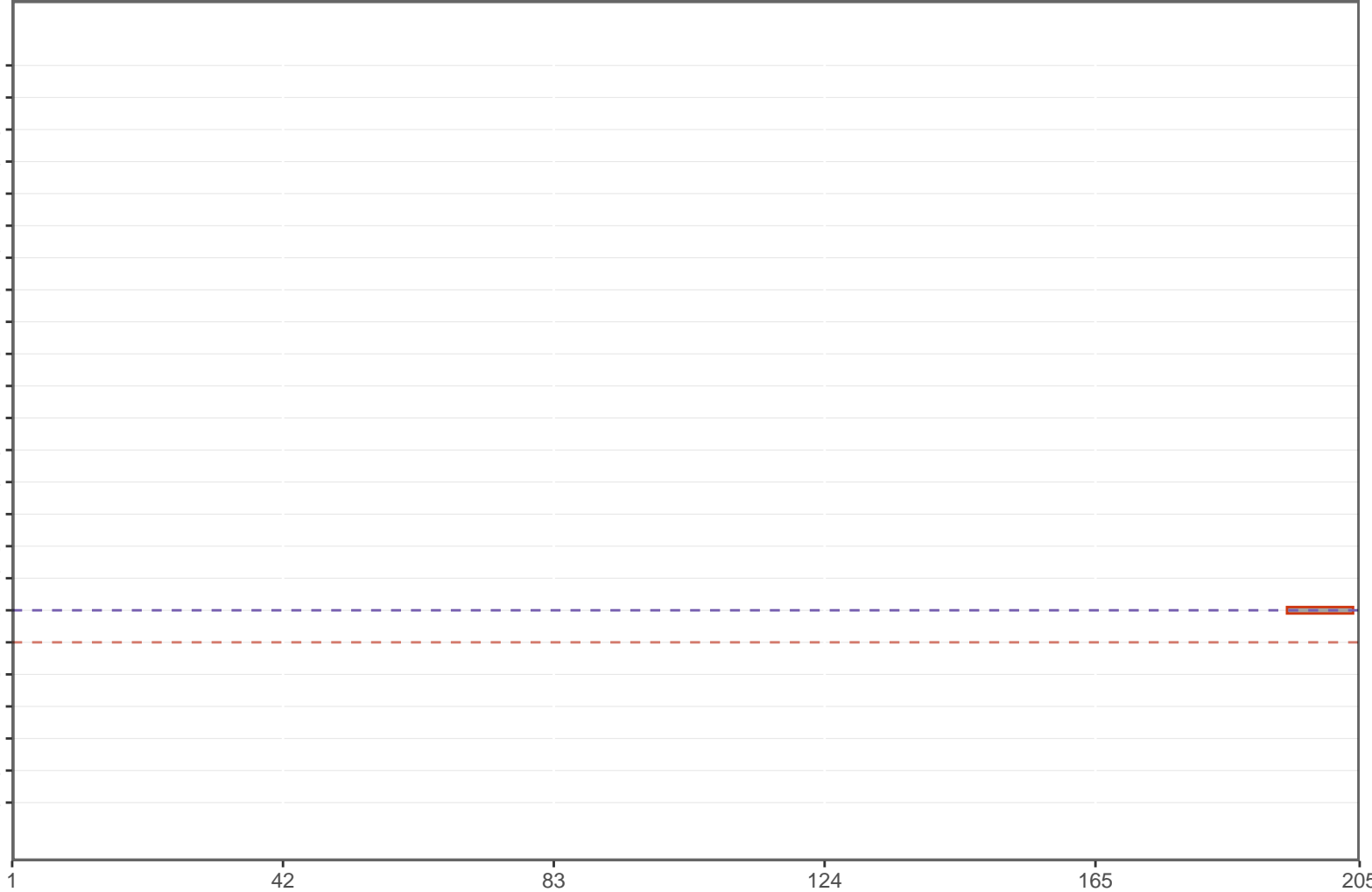
MW indication



Molecular weight



Gel Slice

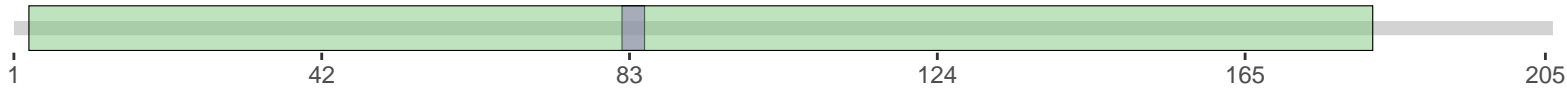


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ITALRKNPYM/NILAGYDKETGPELKYVDHATLHKVDKAAFGYGSYFSLAMMDRHYRKDMTVEEAVDLADKGLERIRLWAPPNFVKIKVDDKDGAREYVWRGSKDAPVSDS

NbL06g11420.1 synthase [MW = 34.22 kDa]

No. of times detected



log(intensity)



Values from



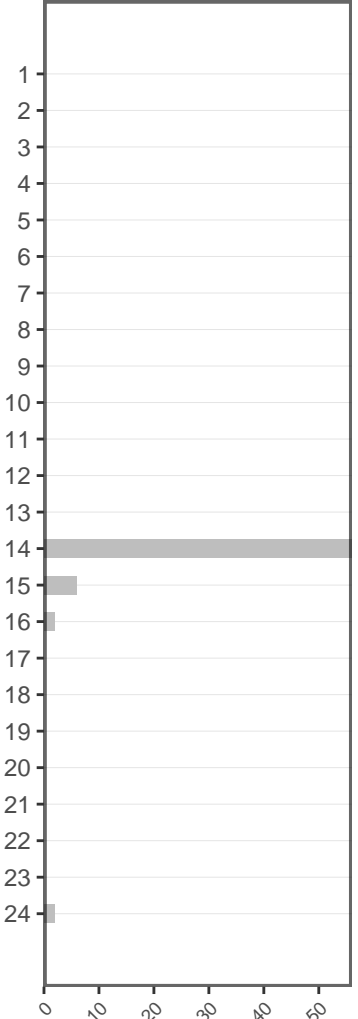
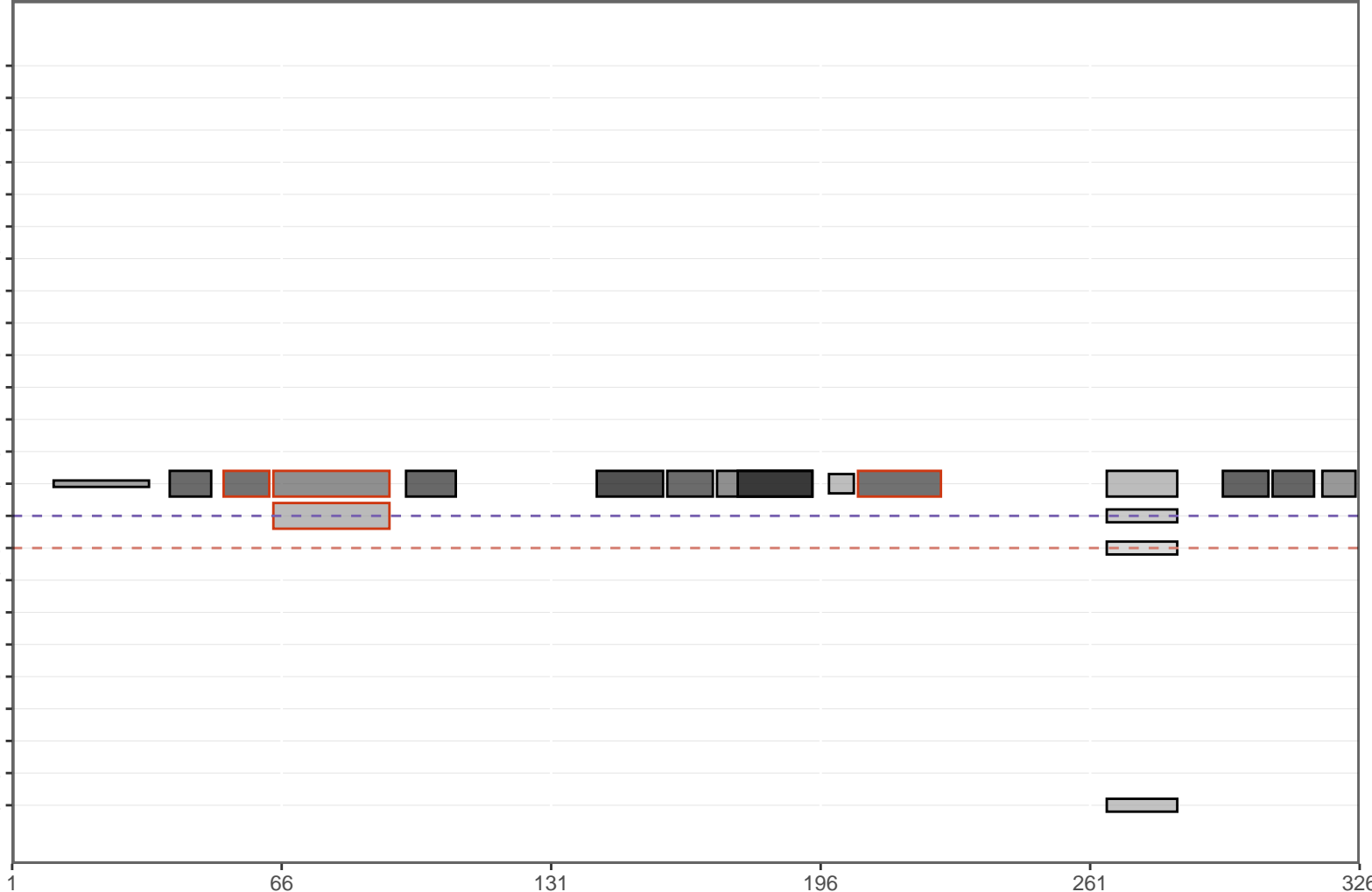
MW indication



Molecular weight



Gel Slice

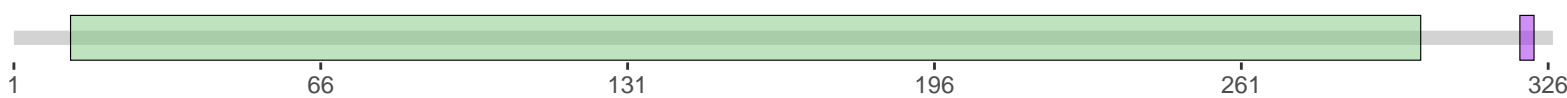


Protein length

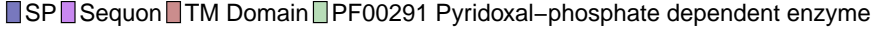


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

JFENPANPKYHYETTPGEIWKSGNGKVDALVSGIGTGGTIGSGKYLREQNPDKLYGVEPVEASLGGNGPDKKQGGIGAGFIPGVLEVLIDEVQVSSSEANETAKLLALEGLLVGSSGASAAAALKLRPENAGKLVAVVFRPFGERYLGSVLFESVRRREANMTVEP

NbL06g11280.1 heat_shock_70_kDa_protein_8 [MW = 62.51 kDa]

No. of times detected



log(intensity)



Values from



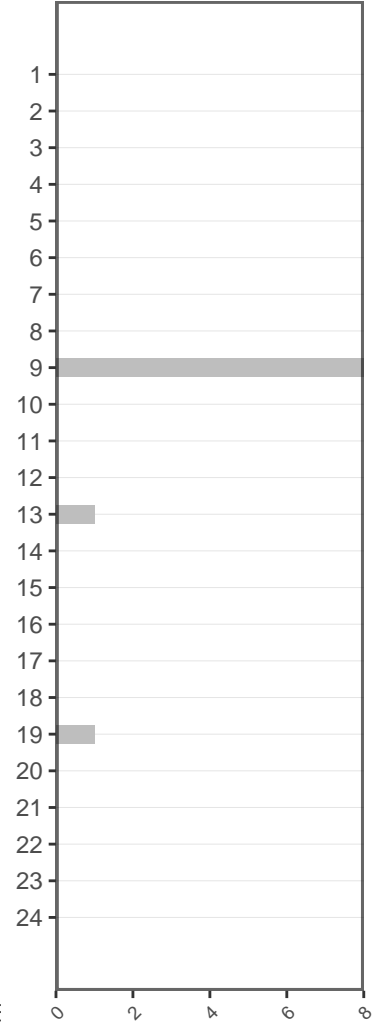
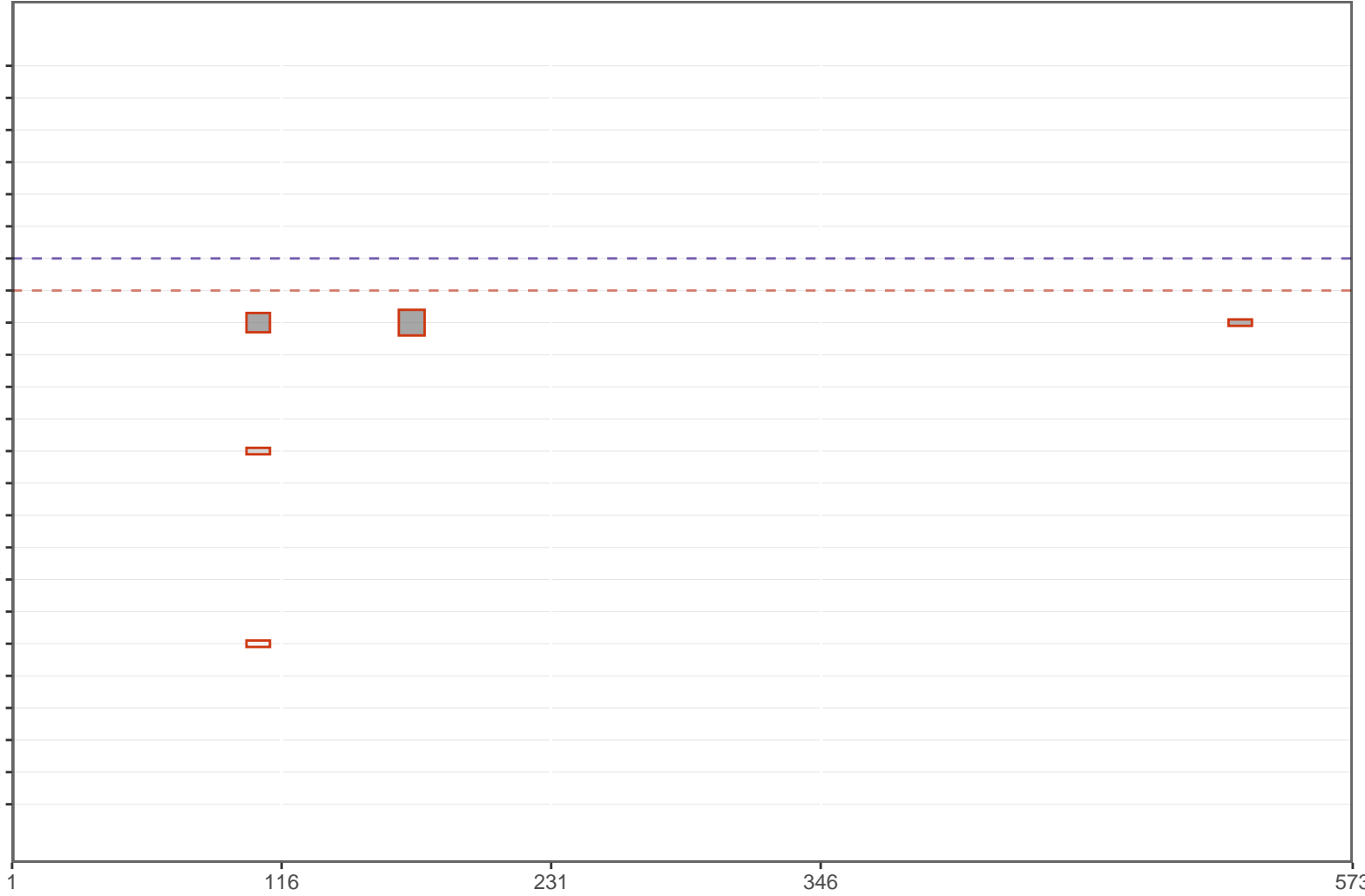
MW indication



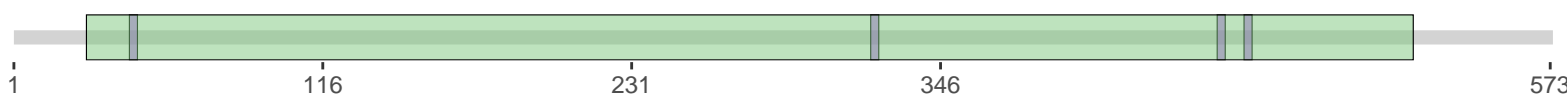
Molecular weight



Gel Slice

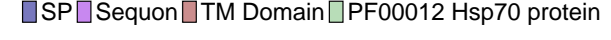


Protein length



Pfam domains

Pfam Description



Protein sequence:

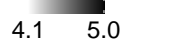
MLLPSMDHIFSSHSIEENRMQLLRVATQDAHRLSSEMSPVDPVVLNGTKIKFLERAEFEVYNKEVFGKDETLERGLRDAKLEAEDVDHVIIVGGSGVYKPKRINVMISIKREELYSGMNPLEAAVIRGAALGAWASGSDPFGDLDLITGATPLSISGQADGSGNFVPIYQNTTTPVRKEGNFTTVHDNGAEALIFVYEGDEKTVKDNHLGYFKTGIPVYKGVPEINVMDHDSANLRFVAGVIIPGAKGPPFMEVIRMPVDDGHWASAGTLHRTYGLDLDVTVKXKGC

NbL06g11160.1 mavicyanin [MW – SP = 16.4 kDa]

No. of times detected



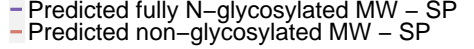
log(intensity)



Values from



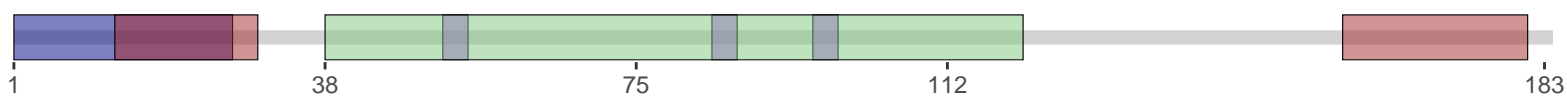
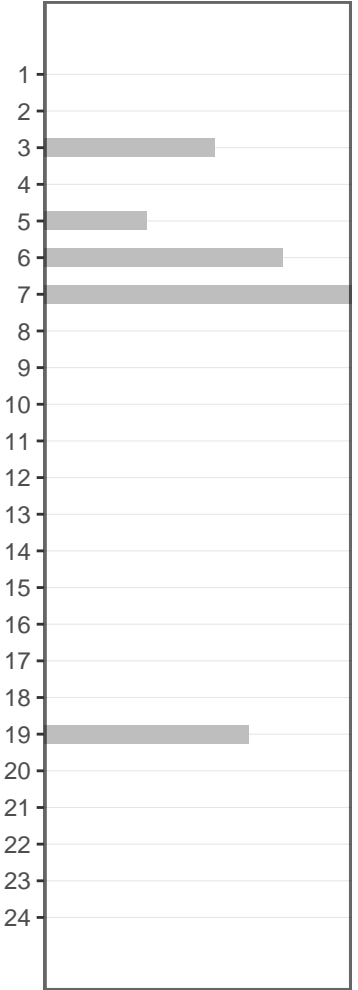
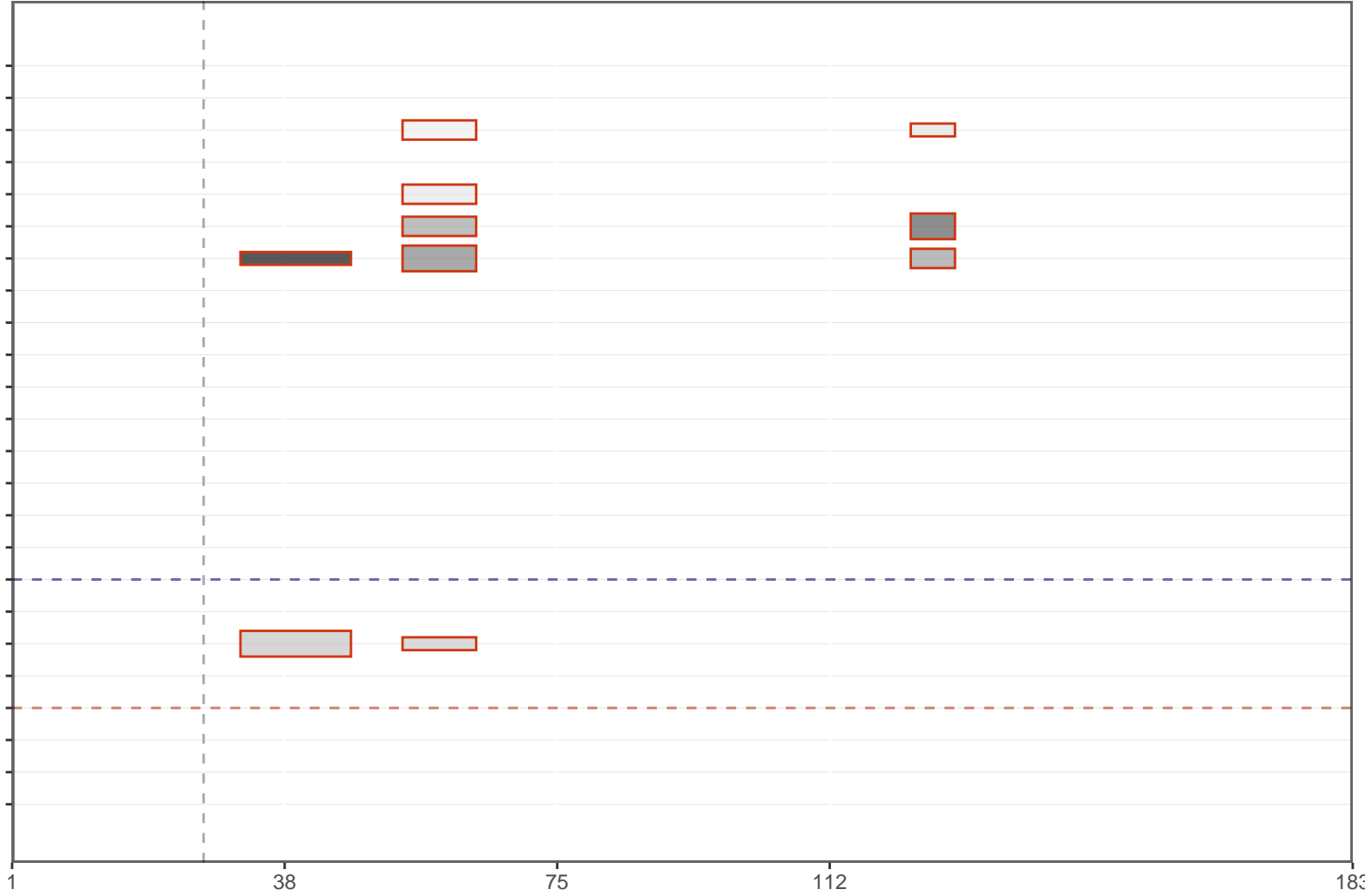
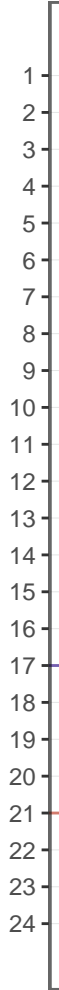
MW indication



Molecular weight



Gel Slice



Pfam domains

Pfam Description



Protein sequence:

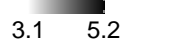
IAEYQSCNASSPAAHTTGNDSIAITTHGHFFFLGGVPGHGAGGKVDINLRA66SASPNPSTSESPVAITEVPAKPSPHASVWLPEKIGIAMAVSVLLNFNA

NbL06g11080.1 RAN_GTPase-activating_protein_2-like [MW = 61.24 kDa]

No. of times detected



log(intensity)



Values from



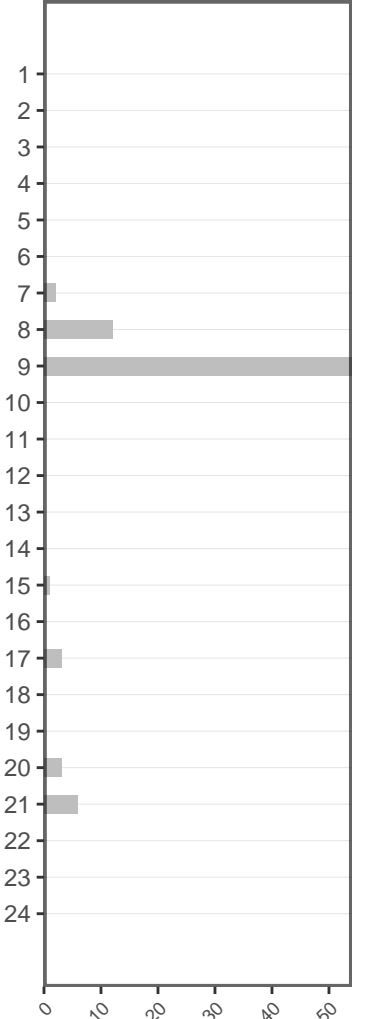
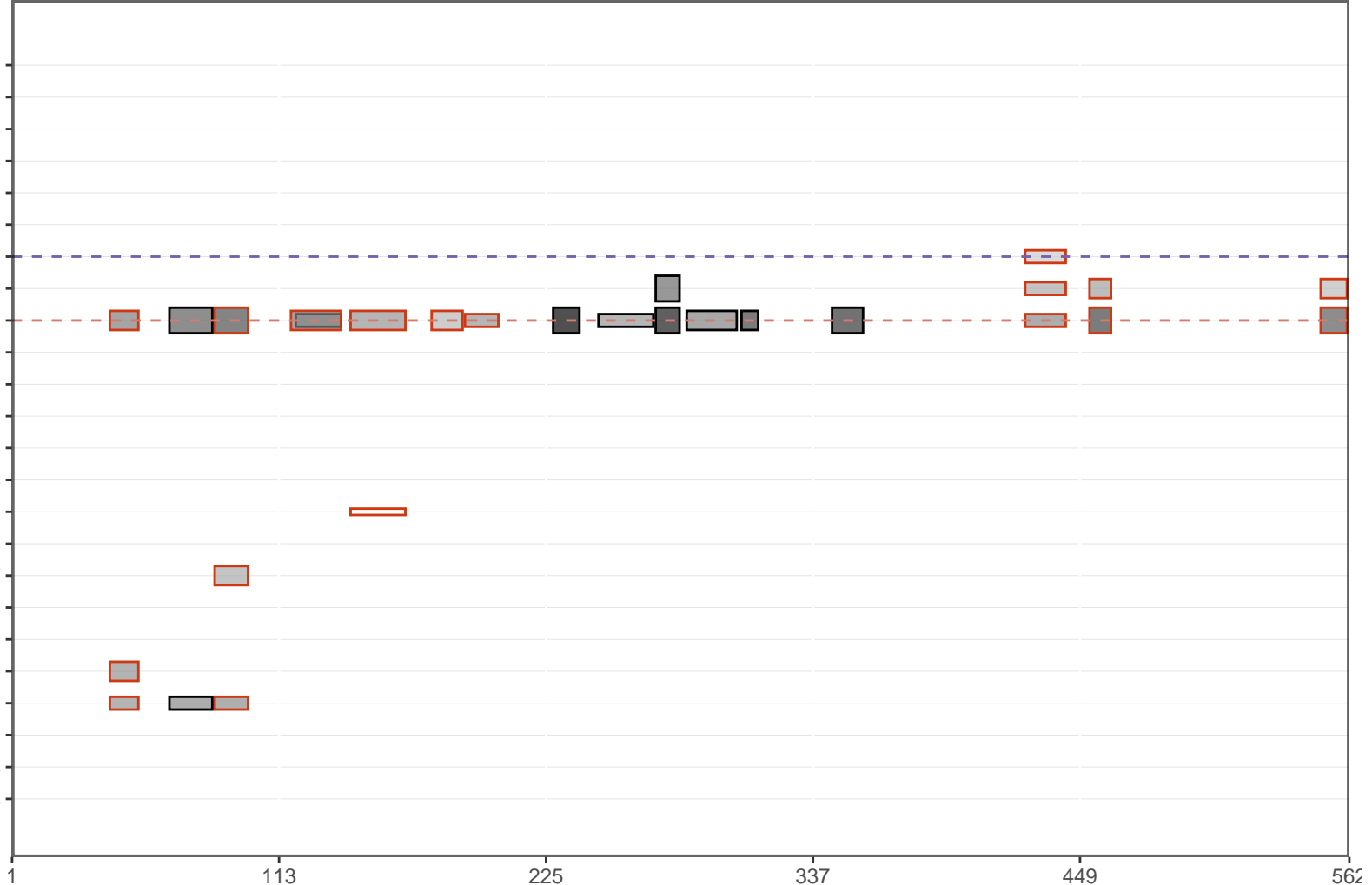
MW indication



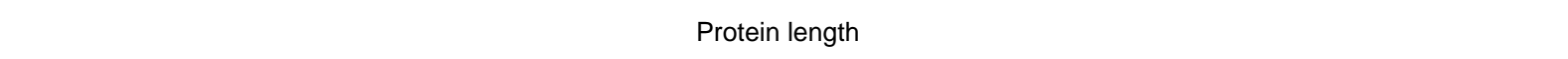
Molecular weight



Gel Slice

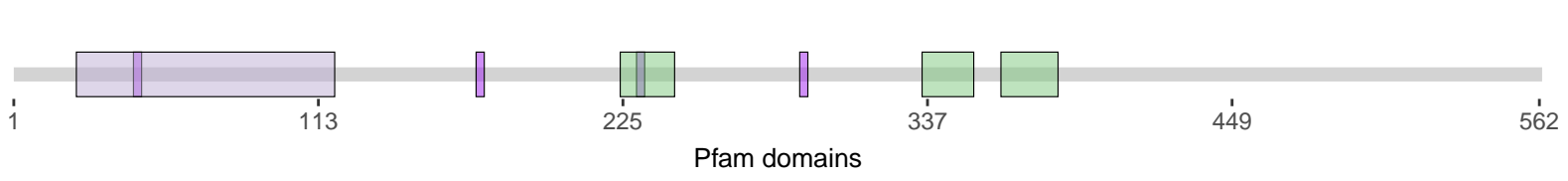


Protein length

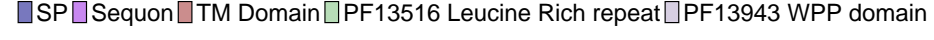


Peptide counts over 4 repeats

Pfam domains



Pfam Description

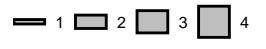


Protein sequence:

IAVSELPSTKLVVHFFHNMITGDEGAWAIEIKR8PLLEDFR66STRV6SEGG8ALCEALGMCSHLKLLDLRDMFGPEAGLVLSKALKSHKEKTEVYVLSVLEDEGATAIANNALKDSAPLSVLEMGNDITGEAAPMASGIAAKQPLKLSLGENELMDEGADQAKALRGNHLEKVDMMNTLRRAGAVLARTVLHKDFEKLNNVNGNFRSEEGVDELKDFKFKSPFEMLASLENDPLGEVNEEEKEKESGDEGKDGDELESLKLNLEKGGESLDAPSN

NbL06g11000.1 glucose-1-phosphate_adenylyltransferase_large_subunit_3_chloroplastic/amyloplastic-like [MW = 57.28 kDa]

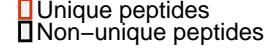
No. of times detected



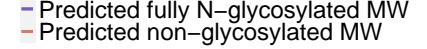
log(intensity)



Values from

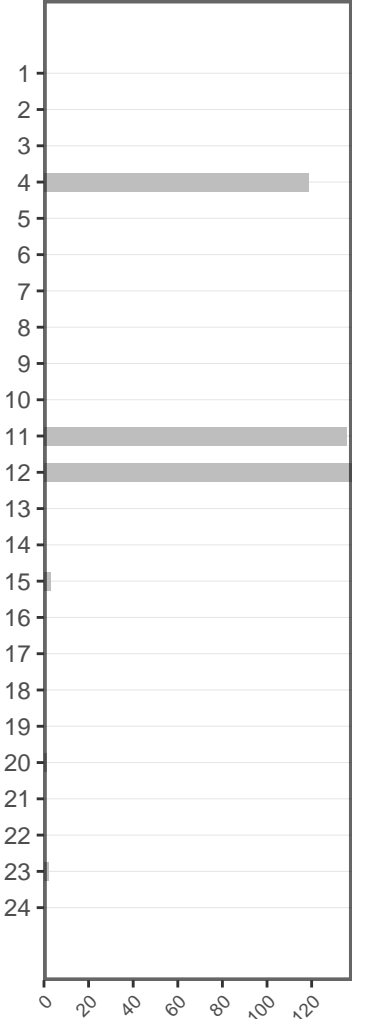
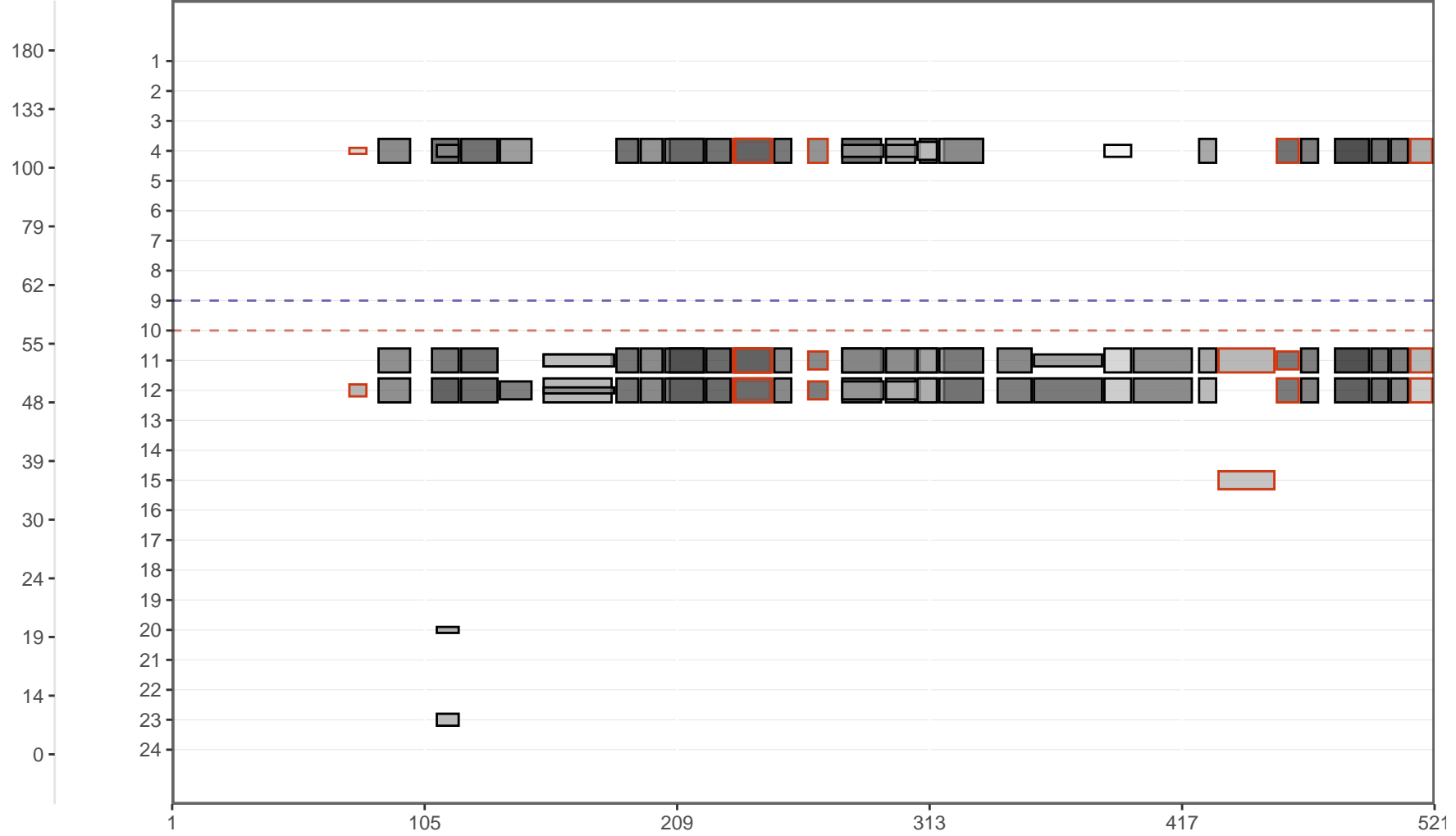


MW indication



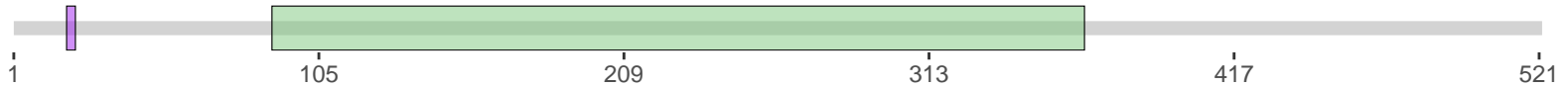
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IDDRRASDFGLMKIDDTGRVLSFSEKPKGDDLLKAMAVDTSVLSGLSPPEAKKKPKYASMGVYVFKKELLNLRLWRFFPTANDFGSEIIPASANEFGKAVLFNDYWDIGITRISFFEANLALTEHPKPSFSDATKPKVTSRRNLPPSAINDKPKIVDSVHSGFLTNGFVEHVVGRSRIGSNVHLKDTVMLGADYVETDAEIASGLAEGKVFPMGIGENTRIKEGIDKNAKGNVYVIANSEGVQEAADRBSSEGFYRSGITVILKNSHSDGLV

NbL06g10970.1 peroxiredoxin-2F_mitochondrial-like [MW = 20.96 kDa]

No. of times detected



log(intensity)



Values from



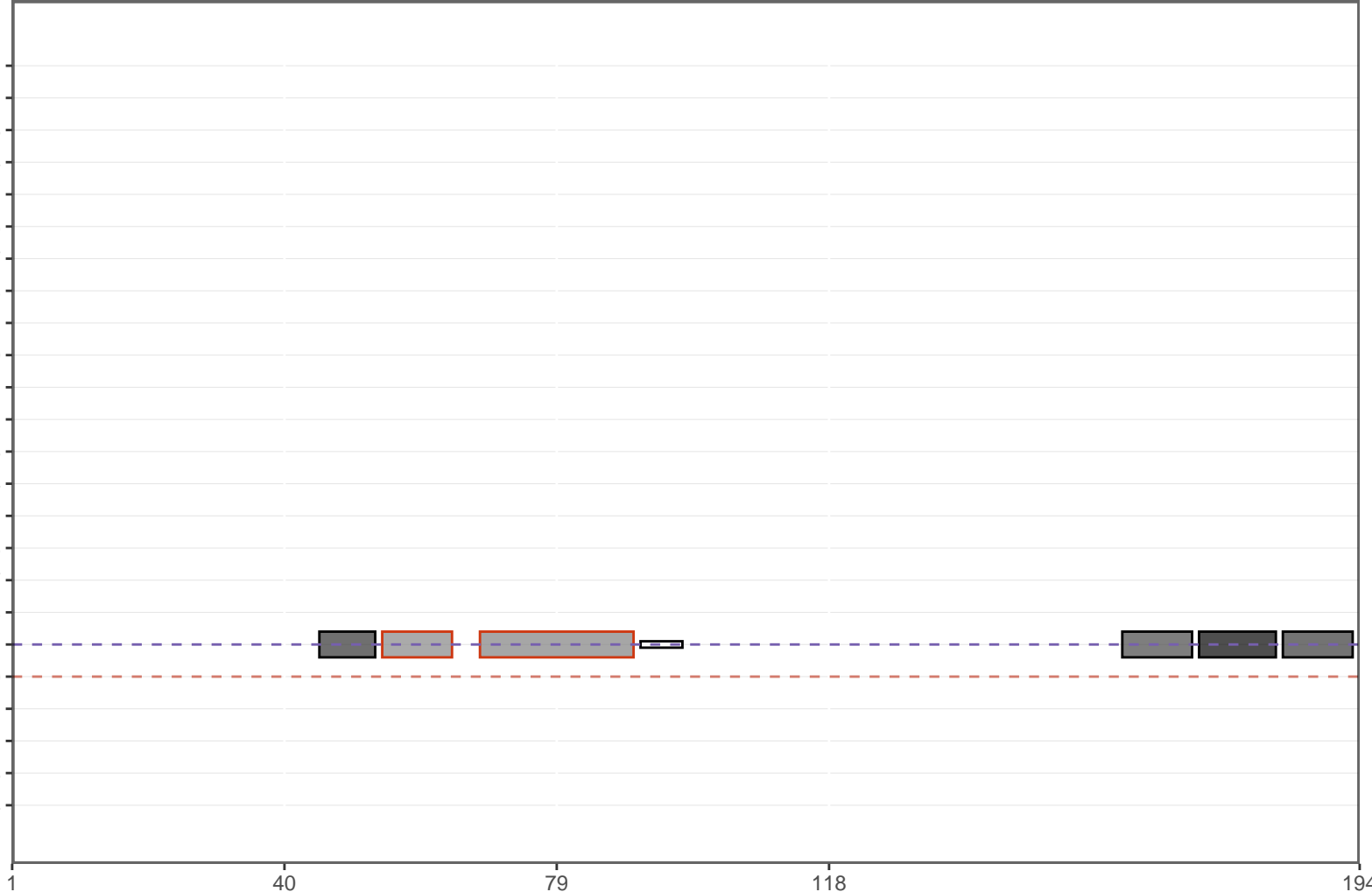
MW indication



Molecular weight

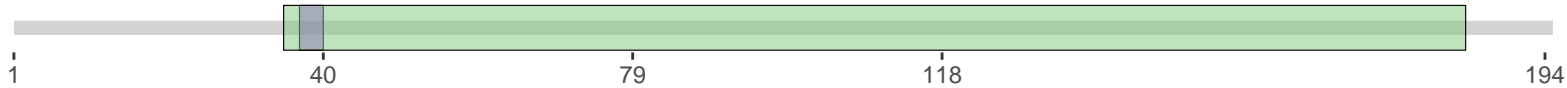


Gel Slice



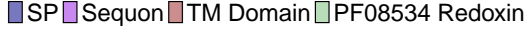
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

QHVPSTYKINIDKFKAKGIDSDVGVWNPYVMNGWAEKLGAKAEFYDGFDSFHKSLDITDLCALLGPRSHRWSAVYDDGNVWLVNVEEAPDFKVSGGDVLGGP

NbL06g10940.1 NEDD8-activating_enzyme_E1_catalytic_subunit [MW = 49.57 kDa]

No. of times detected



log(intensity)



Values from

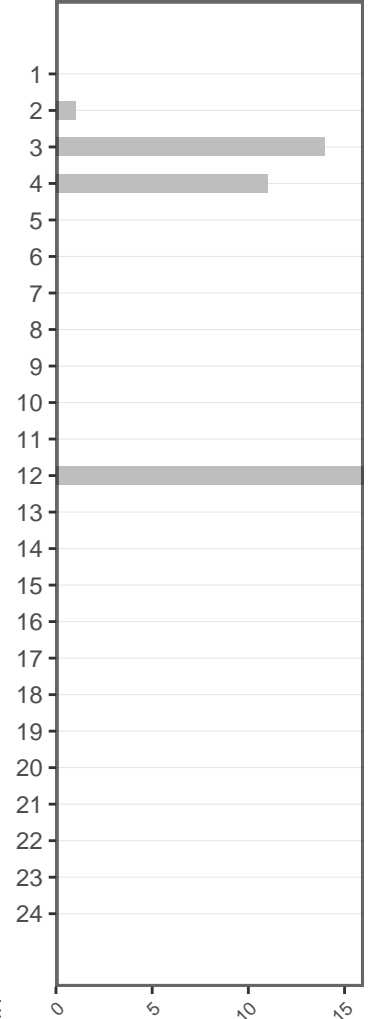
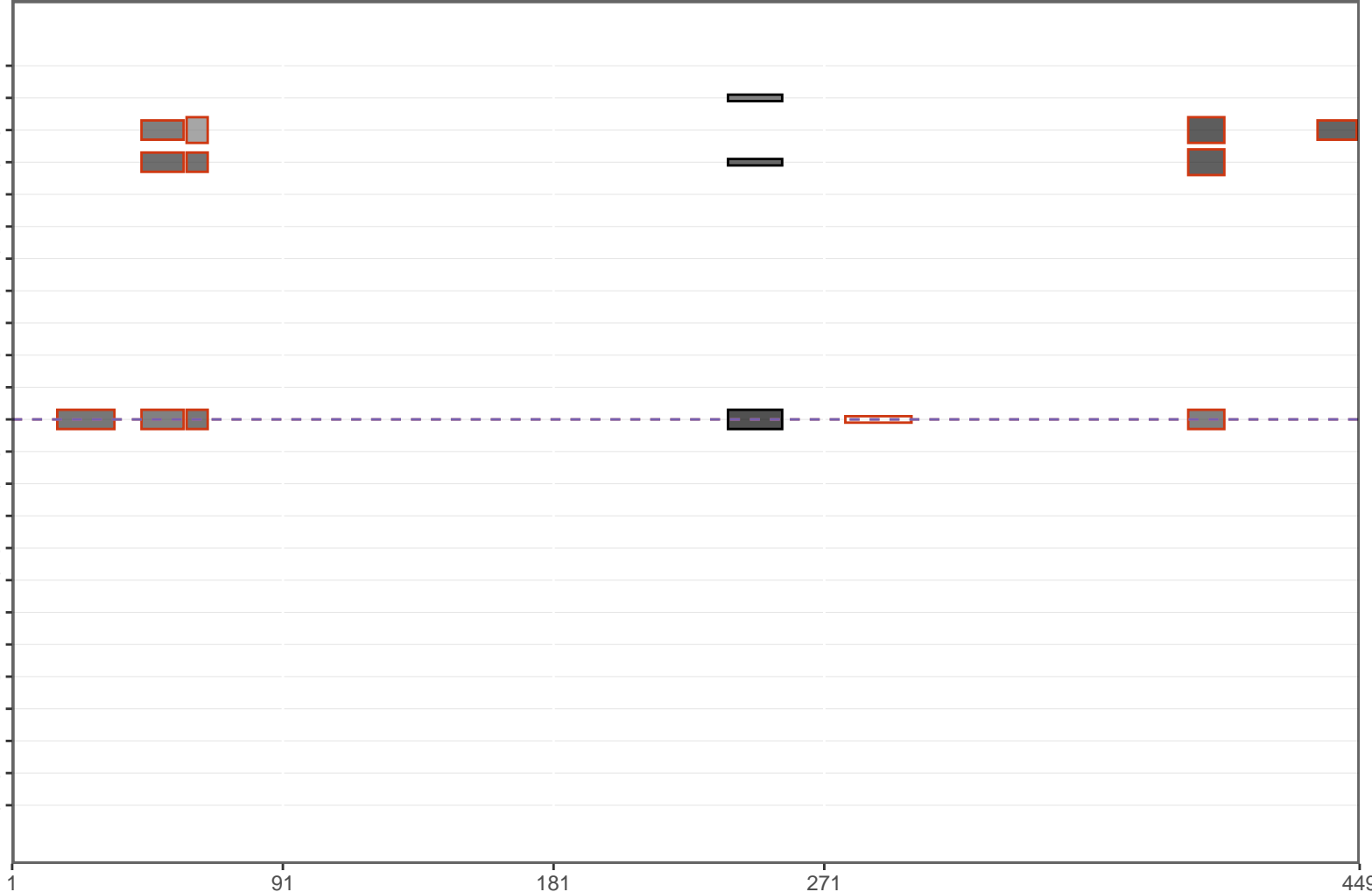
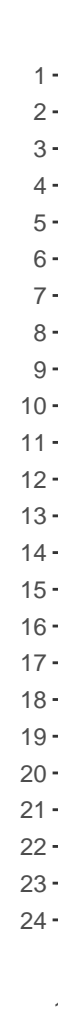
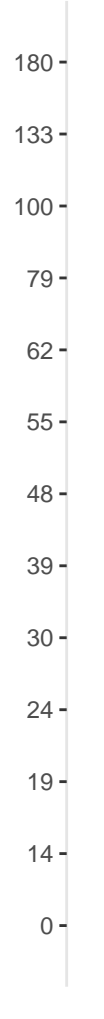


MW indication



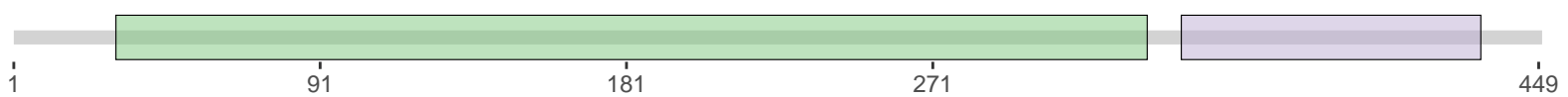
Molecular weight

Gel Slice



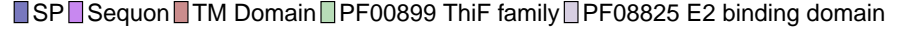
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TLAETPTAAHCIEVHLIKWDEVHGSKTFDPDPEHMQWVYSEAVKRAELFGILGVTYSLTQGVVKNIPMASTNAISGACALETLKLVSGGSKTLSENLYTYNGVEGLHTRVTEFVRDKEGLVSPGQLELEASVTLKKFGLLEDHPKLLLTRVGVTYRGNLVMQAPVLEEMTRSNLDLPLFELMSEKTRDVIHYGTAGKGDTKGSGSRKLRVVFYKGDGVTDMDMAGGA

NbL06g10920.1 ATP-dependent_(S)-NAD(P)H-hydrate_dehydratase [MW = 22.38 kDa]

No. of times detected



log(intensity)



Values from



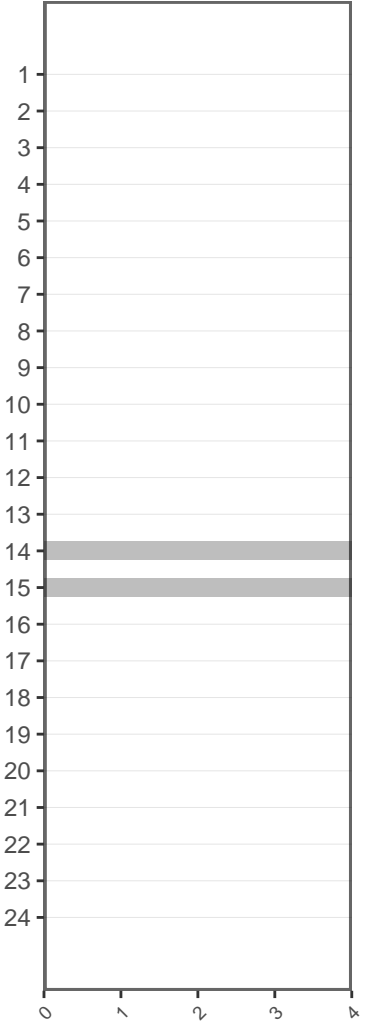
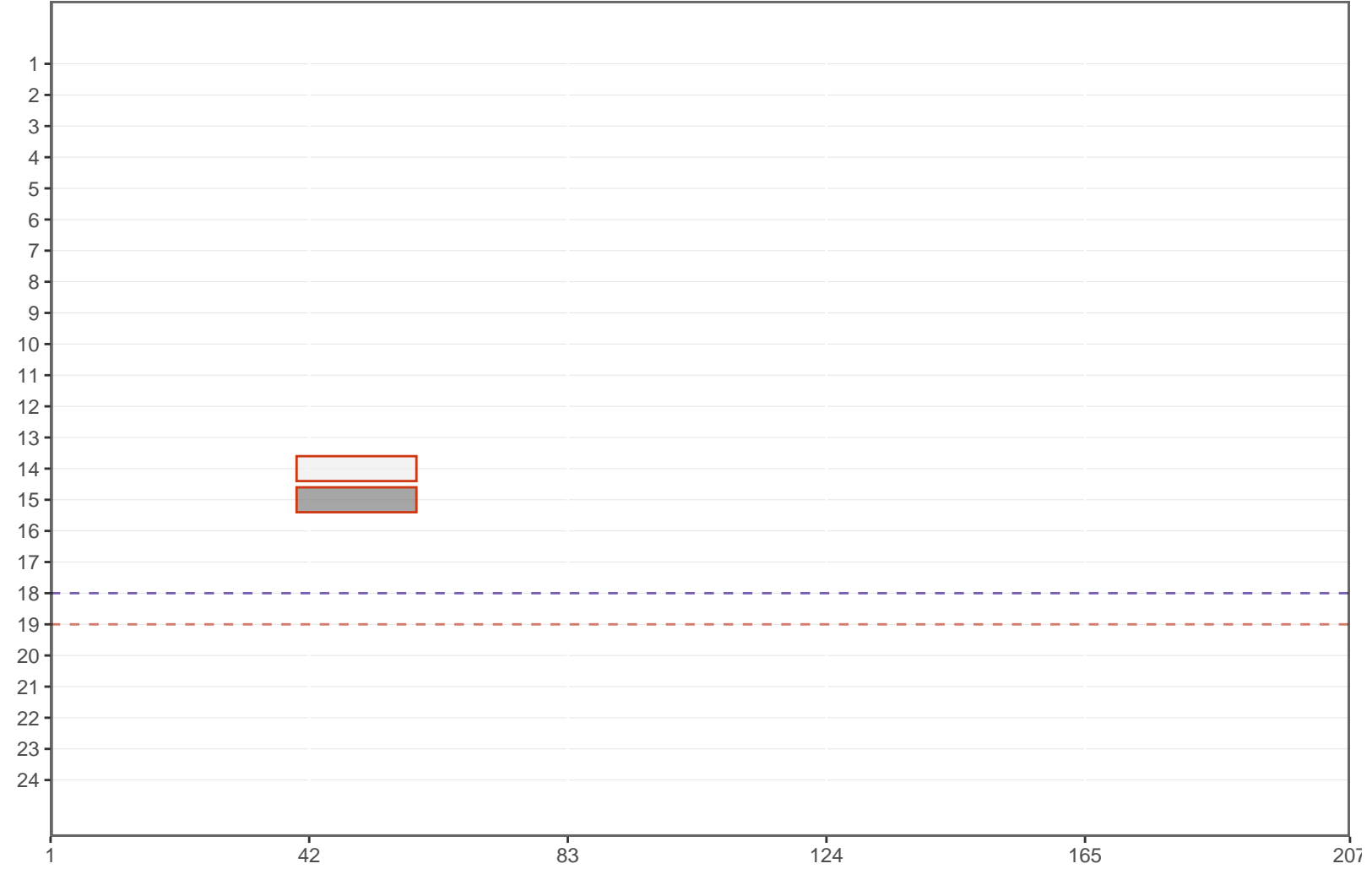
MW indication



Molecular weight



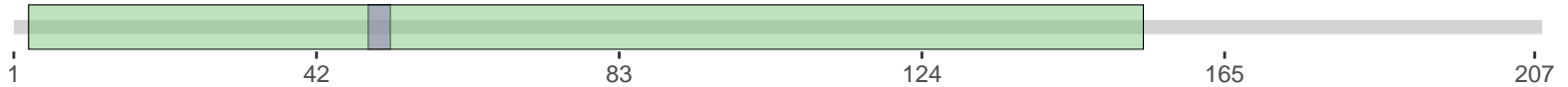
Gel Slice



1 42 83 124 165 207

Protein length

Peptide counts over 4 repeats



Pfam domains

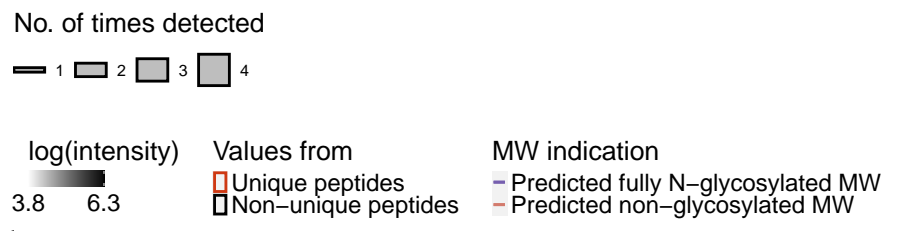
Pfam Description



Protein sequence:

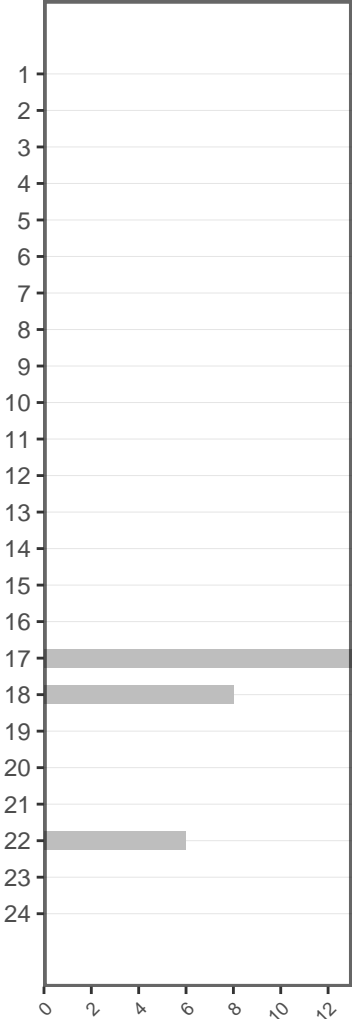
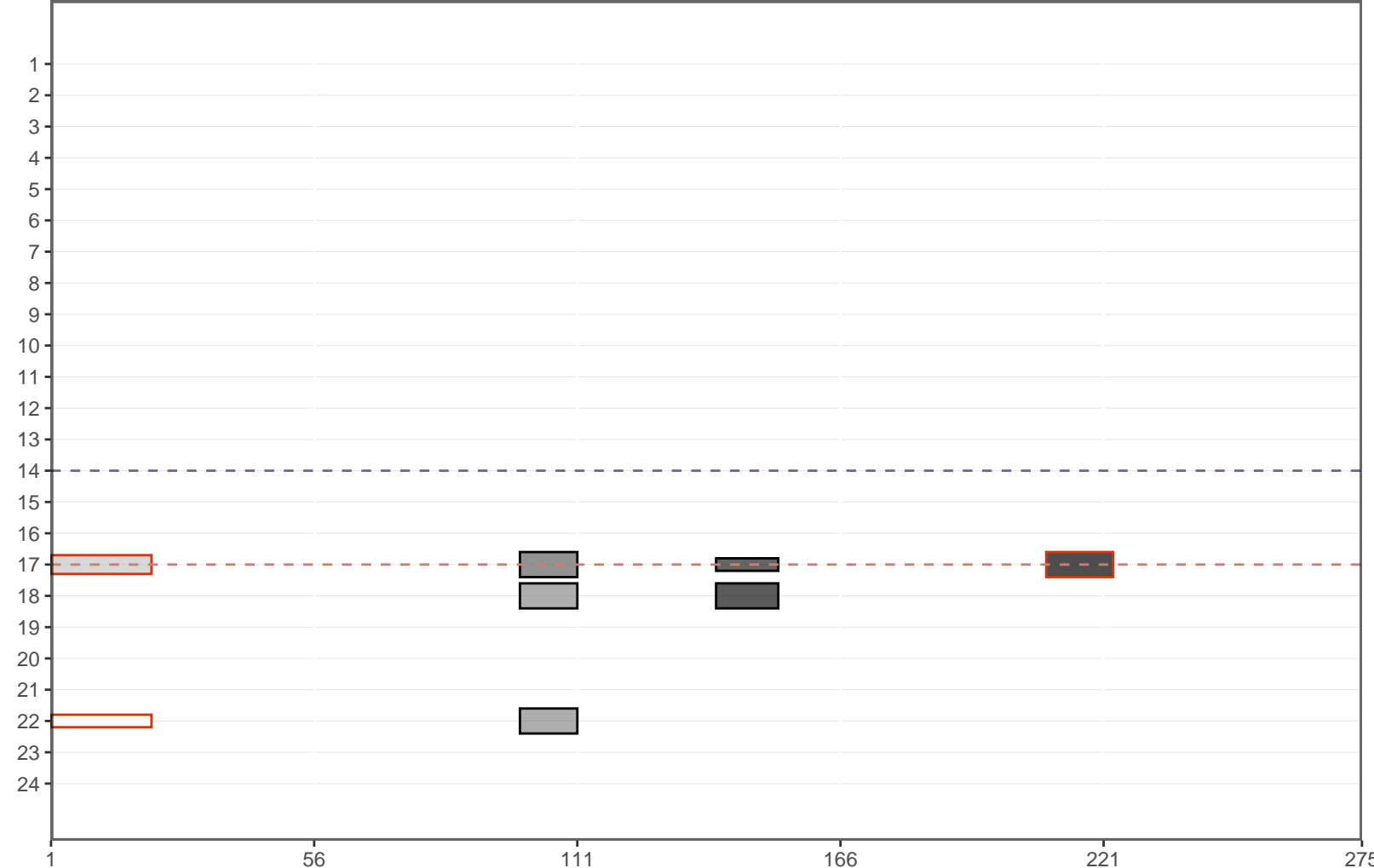
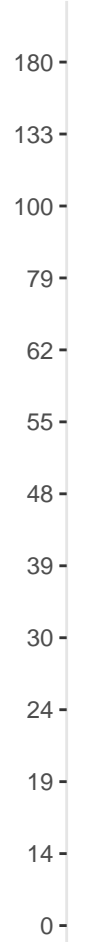
ICGGGDDLSGSIWFLGWARQHWAKGEVEMNPTLGGVGSALLRRAASLAFETKKRSTLGVIEGLGRKKYQDENRNFMEGFMGAQHMYSKLEEFLWGRANGKRRKNNK

NbL06g10900.1 stem-specific_protein_TSJT1-like [MW = 30.04 kDa]



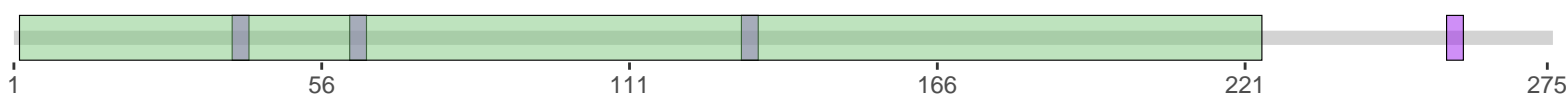
Molecular weight

Gel Slice

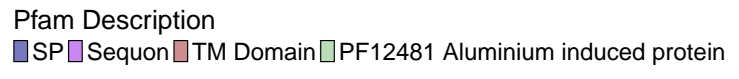


Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:

IGHLEGNFTTIVFDKSTFLVATDQGVKPLVWGTADGYVAFANDADLLKAGGKSLASFPQGCYFSTVSGELRGLYENPKNKITAVPATEEEHWGTYKMDPVEISGGFRGRCGSGSHIEDLFLBELGLWVNESEREWQKMGGRALVGM

NbL06g10770.1 UPF0613_protein_PB24D3.06c [MW = 37.06 kDa]

No. of times detected



log(intensity)



Values from



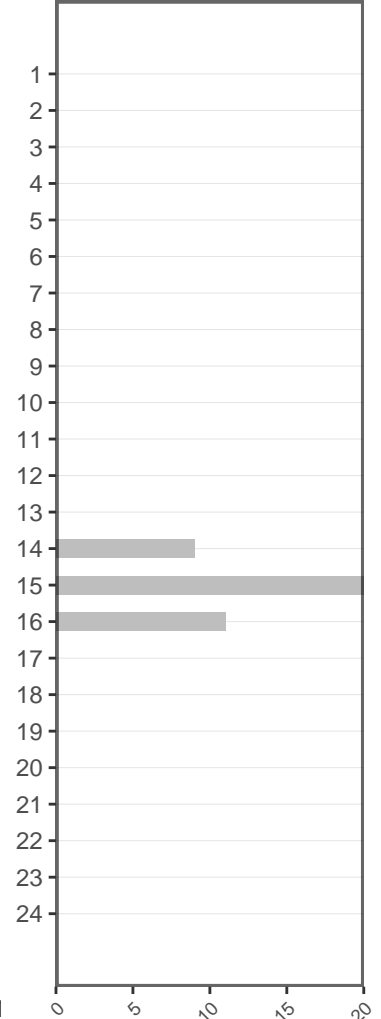
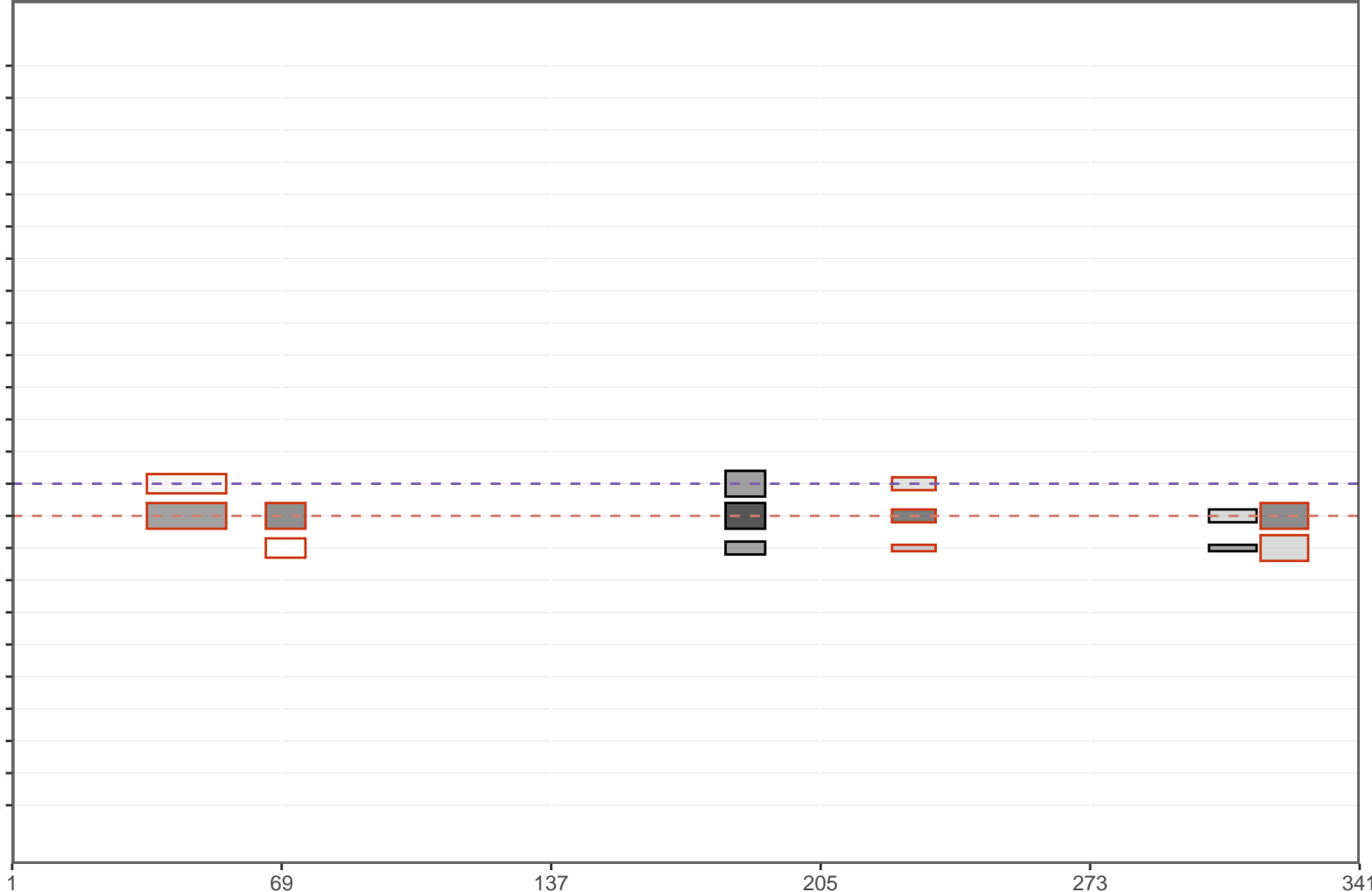
MW indication



Molecular weight



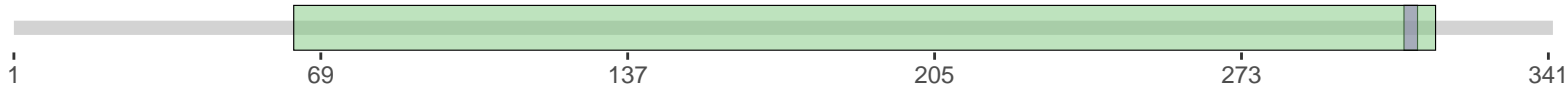
Gel Slice



Peptide counts over 4 repeats

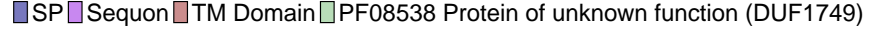


Protein length



Pfam domains

Pfam Description

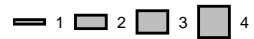


Protein sequence:

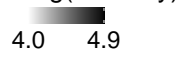
STGCCDYYMRTNAAGSRAVRAALGAPVSDREYKATLPDTASMDLANSMISEGRESELMPREANPDAPTFRRYHSLGAYNGEDLFSDDFSDDLKQRLGHMSNTPCGVVFMSGDEYVPEVYDKKALVDRLGRAMGGAERKVEIEHGNHLSNRVAEAVESMSFVKREGPSGWDPPWV

NbL06g10700.1 NA [MW = 29.94 kDa]

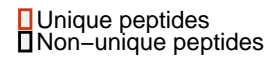
No. of times detected



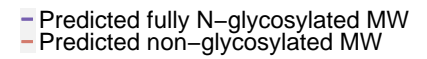
log(intensity)



Values from



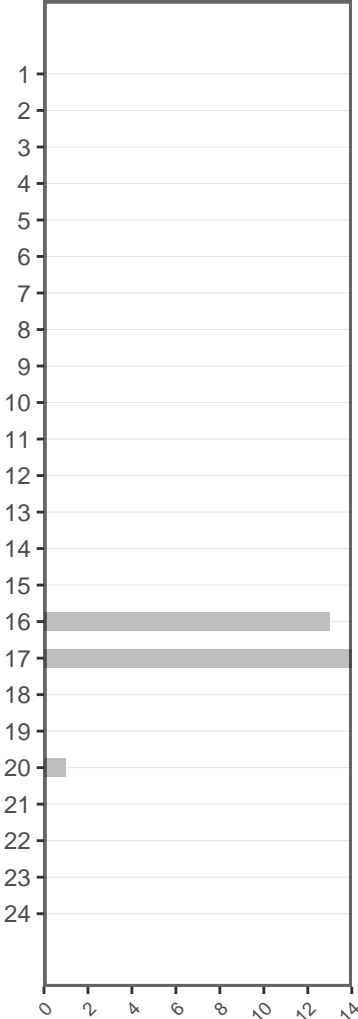
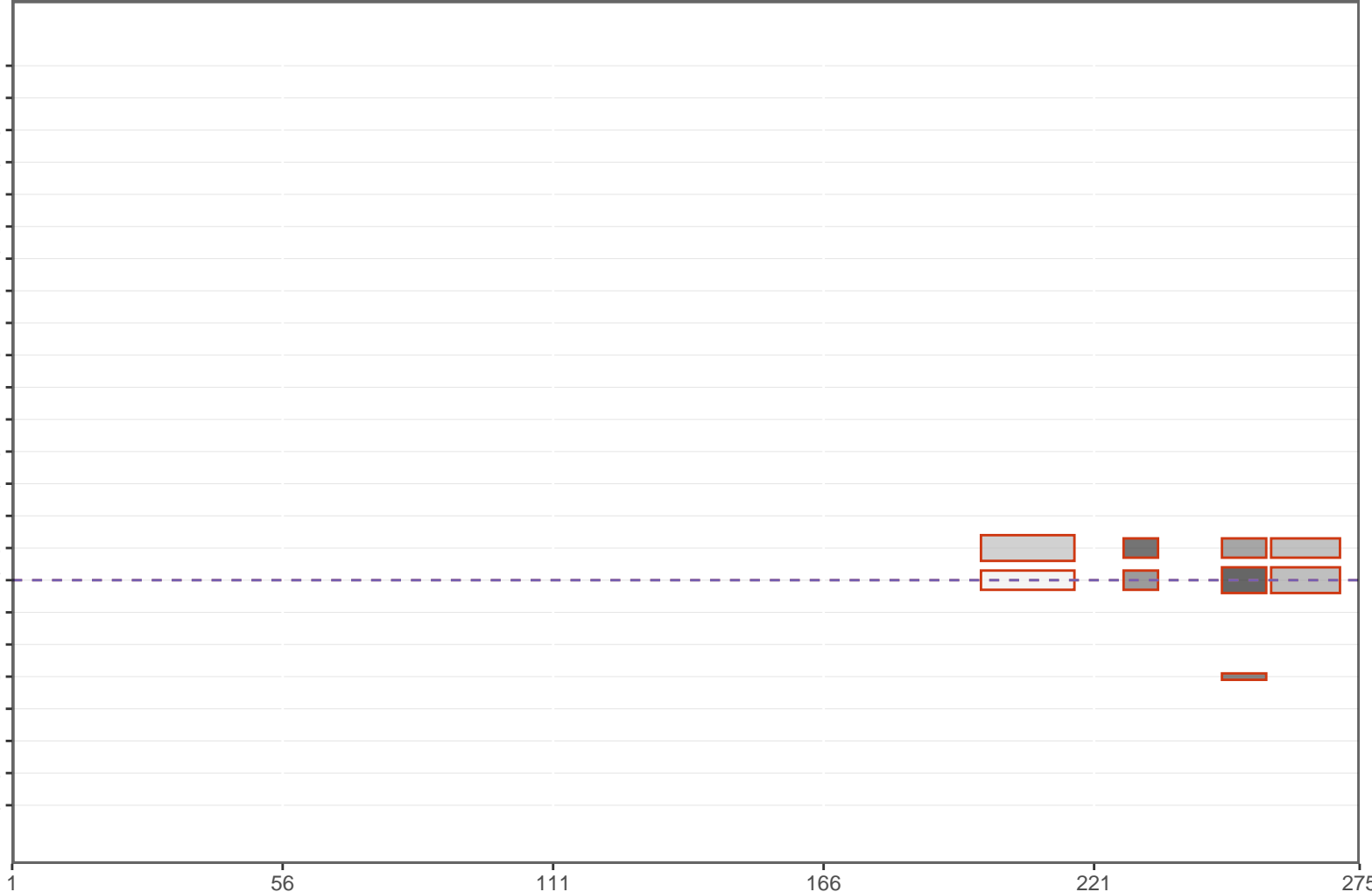
MW indication



Molecular weight

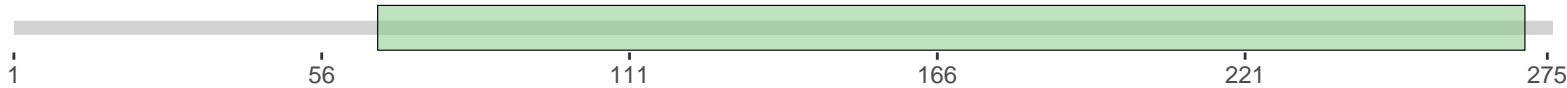


Gel Slice



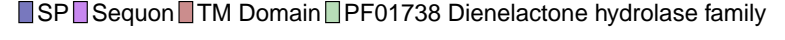
Protein length

Peptide counts over 4 repeats



Pfam domains

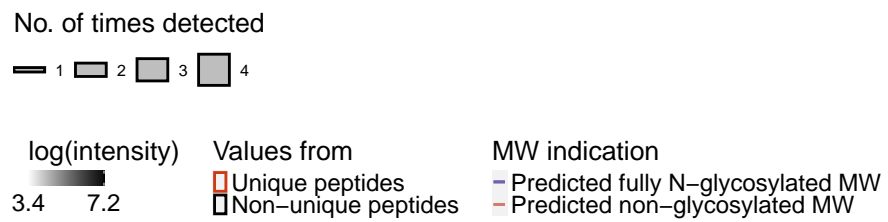
Pfam Description



Protein sequence:

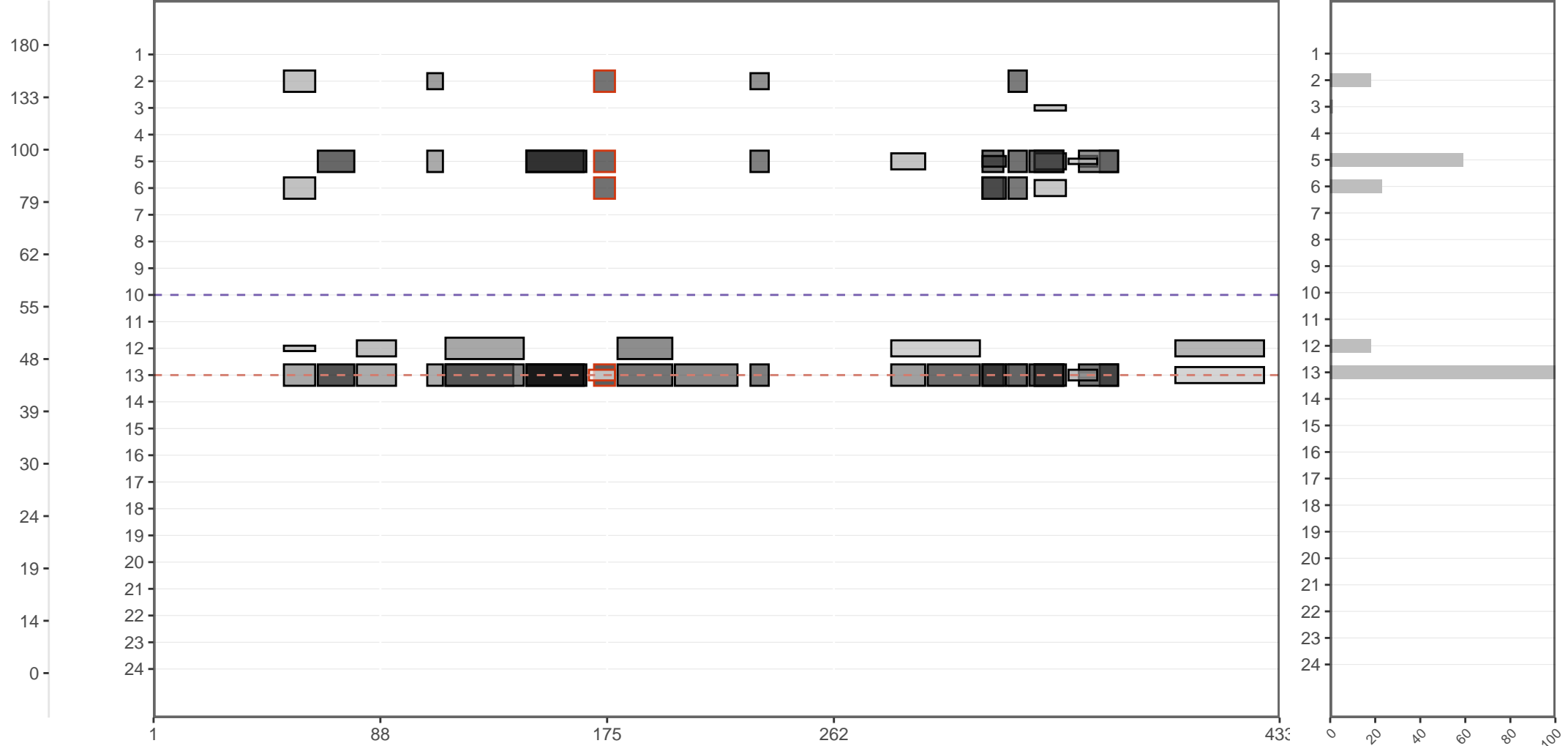
QTVLIDHGVKGGCEBAAKAVESLKSNGVBAAGAFDQWGMVSKLAKYETSIGAVILHPGRTVDEINEVKVPTALAAEHDHFLPDQAKLGDALSAKSEIEEIVNIFPGVHGWTVRYNVEDESAVAAAEESHSDMLNWFKFIN

NbL06g10590.1 glutamine_synthetase_chloroplastic-like [MW = 47.53 kDa]



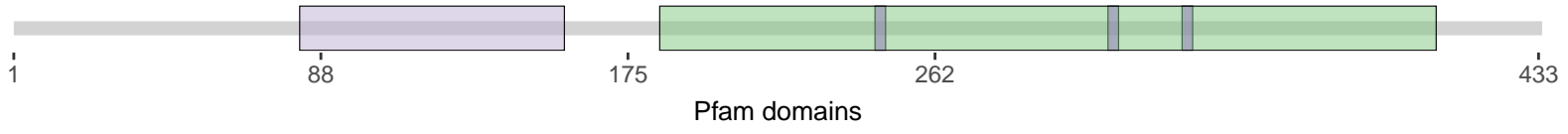
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

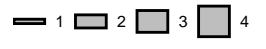
Pfam Description
 SP Sequon TM Domain PF00120 Glutamine synthetase, catalytic domain PF03951 Glutamine synthetase, beta-Grasp domain

Protein sequence:

MPVGGYPGDGRYYDGGADKSGFRDIBDAHYKALYVAGINISGTNGEVMPSGQWFEQVQSPVSEAGDHWGARYLERITEGAGVLSLDPKPIEGDWNAGDCHTNYSTLSMRREGGFEVKKKALNLSLRKHEHISAVGEGNERLTFQKHETASIDKFSWGVANRGASIRVSRDTEKGGKGLLEDRRPAENMDPVYVTGLLAETRLWEPTLEAEALAAQKALN*

NbL06g10410.1 pyruvate_phosphate_dikinase_chloroplastic [MW = 105.82 kDa]

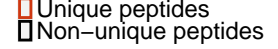
No. of times detected



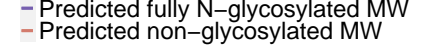
log(intensity)



Values from

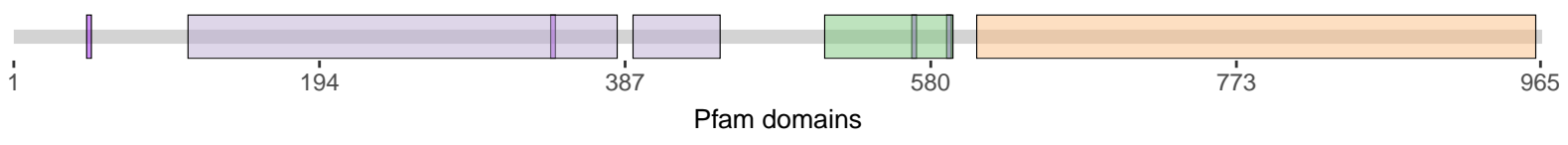
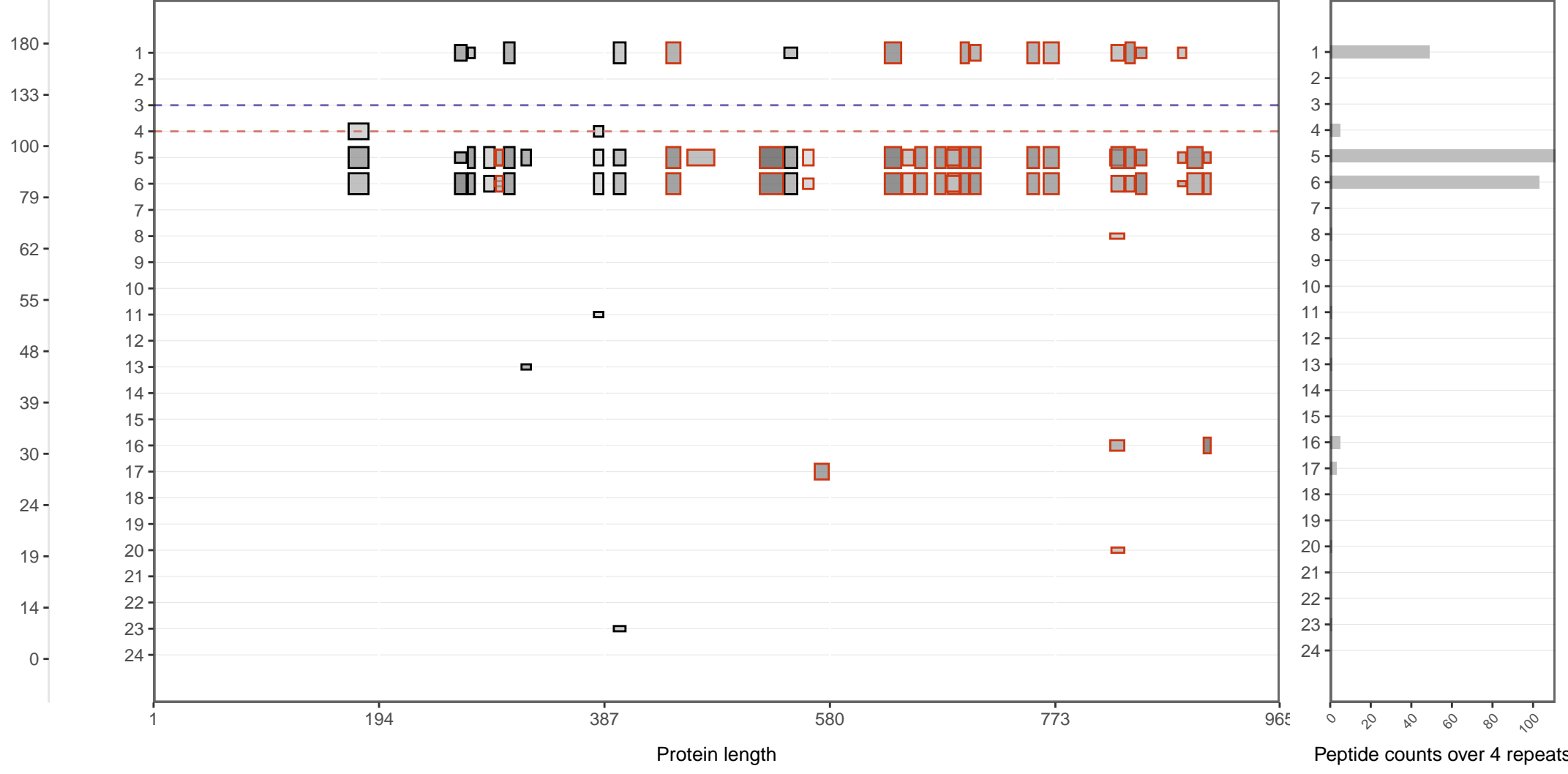


MW indication



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00391 PEP-utilising enzyme, mobile domain
- PF01326 Pyruvate phosphate dikinase, AMP/ATP-binding domain
- PF02896 PEP-utilising enzyme, PEP-binding domain

Protein sequence:

IQLLHPQFEDPSAYKDKVATGLPASPFGAIVGGVIFCAEDAIAHWAGGKSAIVRTSPEDVGGMHAAGLITARGDMTSHAIVVARGWGKCCVSGGNDIRVNESDKVVIIGDKMHEGEWLSLNGSTGVEVLSGKQPLAPRMATGNLEIFMWDKRRKRVMAANADTPEDALTRNNGAGDGLGRTEHMFASDERLKAIVRRMIMVTPRGRKEALDSLLPVRGSDFEFGFRAMDGFVYTRILLDPPLHEFLPEGNLEEVNLTDDIGMREEDVYSRIEKLSEVNPMLGFF

NbL06g10370.1 uncharacterized_protein_At4g15545-like [MW = 36.06 kDa]

No. of times detected



log(intensity)



Values from



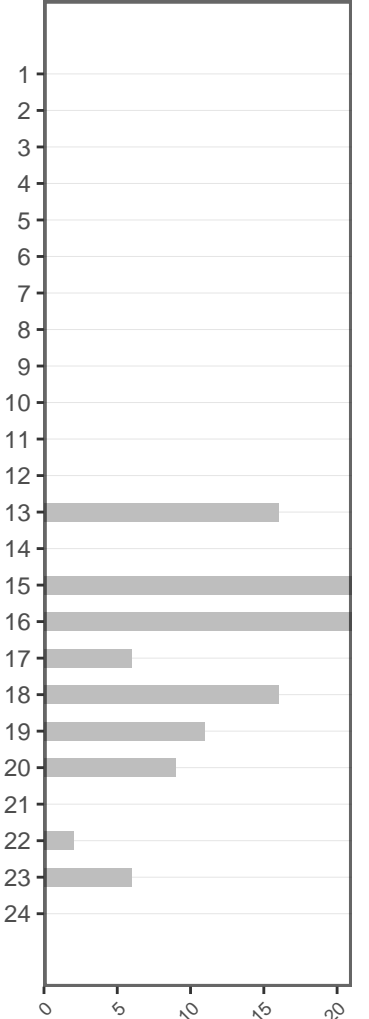
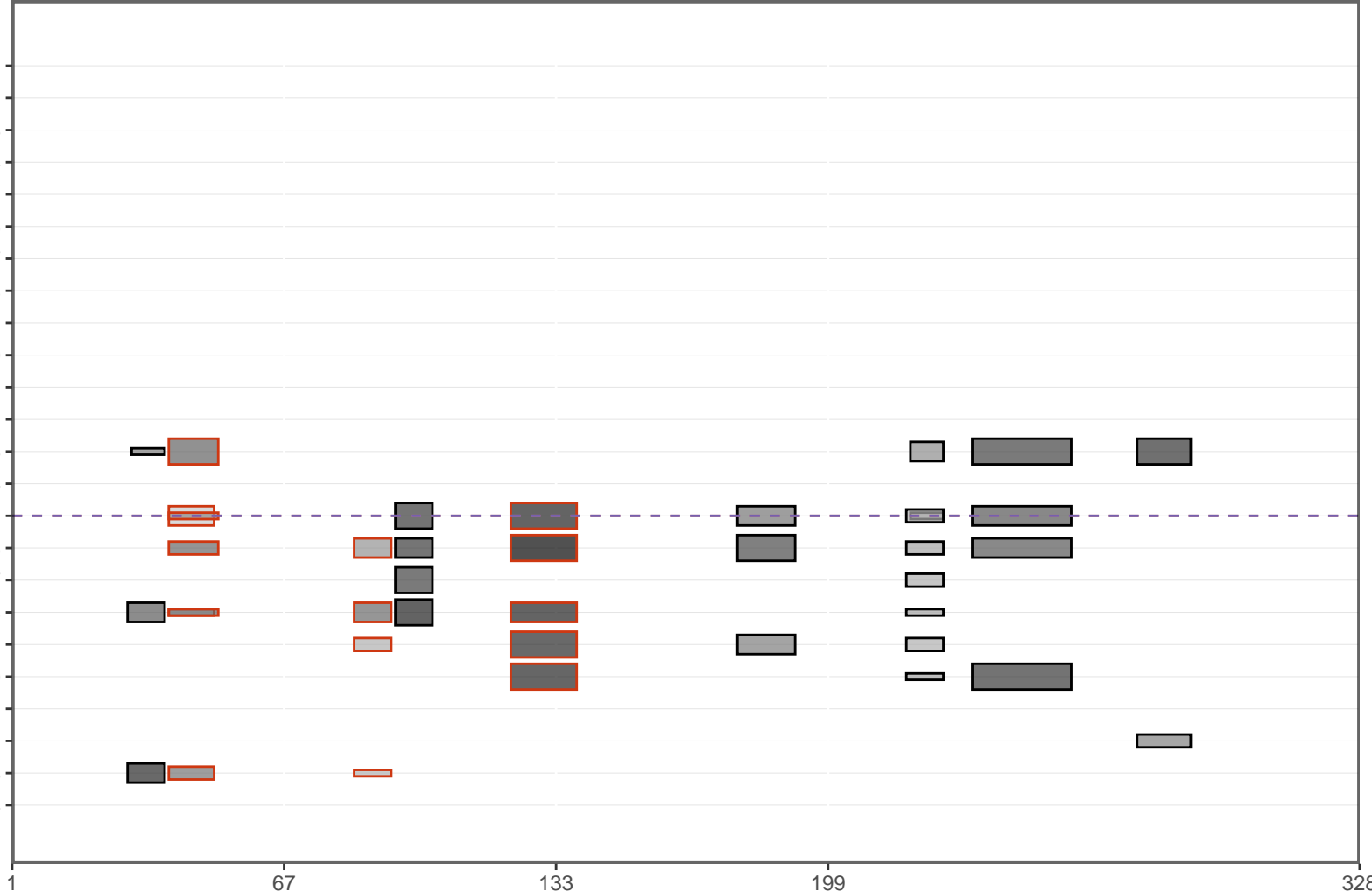
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

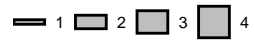
Pfam Description
 SP Sequon TM Domain

Protein sequence:

MQTOSTSGHSYSEDASETSRPRRSPGILLLAGDTSTPLTPGSPPLSASVSPSRPRPLSPRRHSISFSTTRCFMFDDRSSVYSSTSSQVGMGLETGGGTARARVDQKEFFRQVRSRLSYEGQGFALTNVKELNSHKGTKEIDLRKAAEIFSDENKDLTYFEGLITRNAQ

NbL06g10350.1 probable_prolyl_4-hydroxylase_4 [MW - SP = 29.96 kDa]

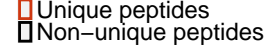
No. of times detected



log(intensity)



Values from



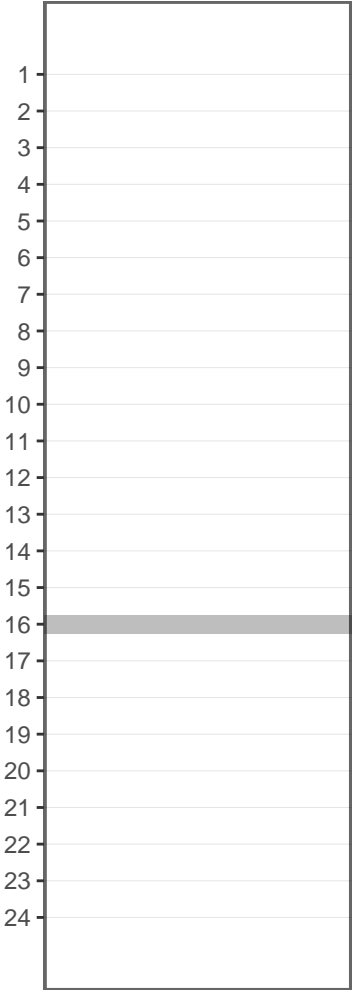
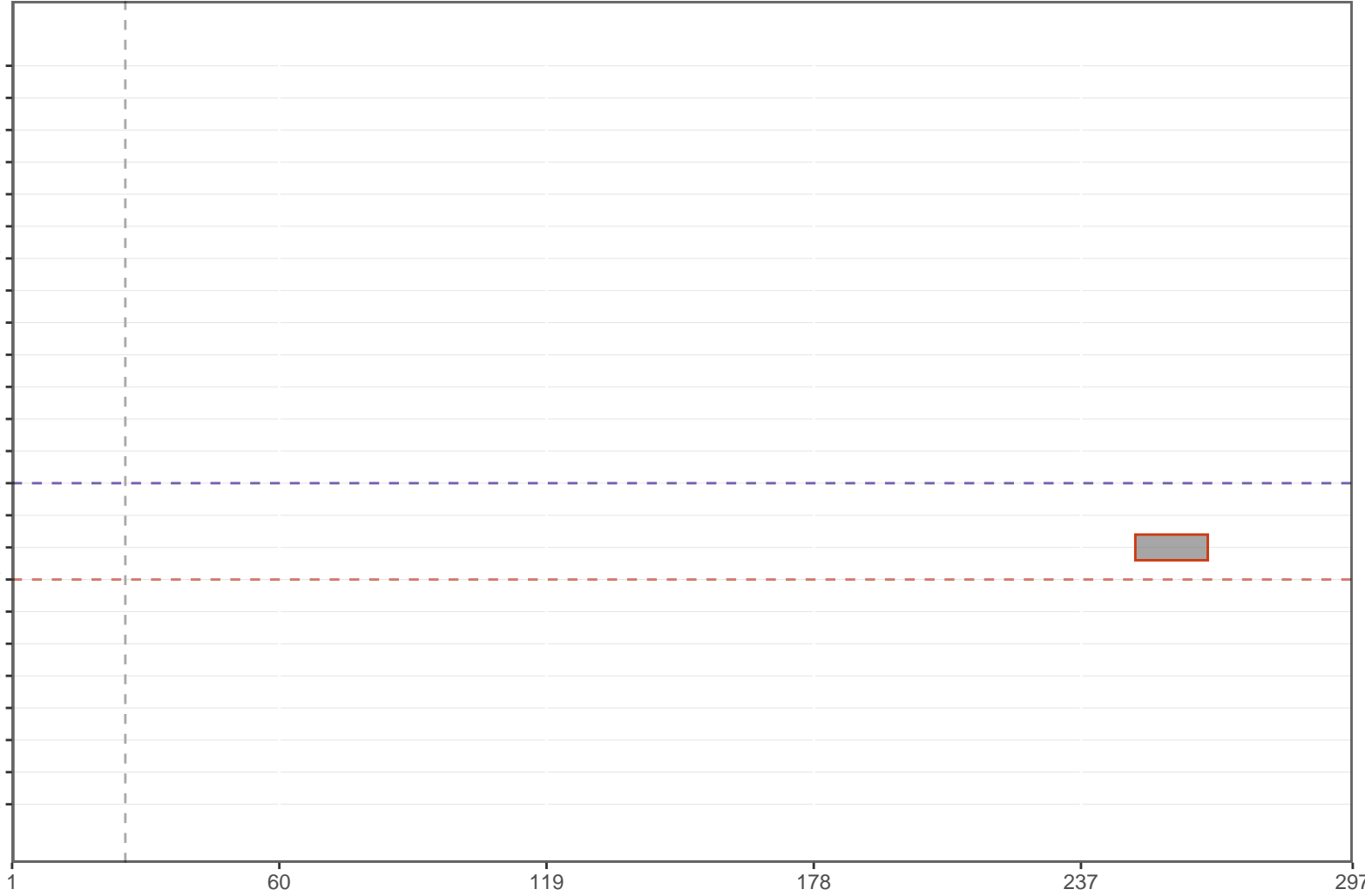
MW indication



Molecular weight

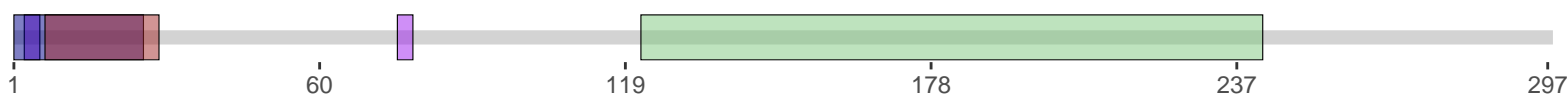


Gel Slice



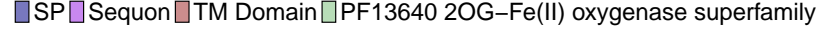
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

FSDKINVRGQHRRLATVMVLDGVEKGETVFPPEAEESTRRRSMADNLSGCRKGIKPKRKGDALLFFSLHPNAVDPMLHGCGPVEIEKWSATKWHVDFDKIVSGEESGADGNENDEERVAALGECTKNPEYVMGSSDLPGGCRKSKKAC

NbL06g10330.1 uncharacterized_LOC109225403 [MW = 100.08 kDa]

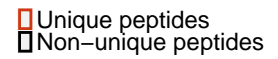
No. of times detected



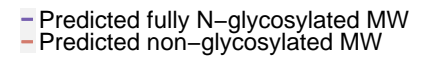
log(intensity)



Values from



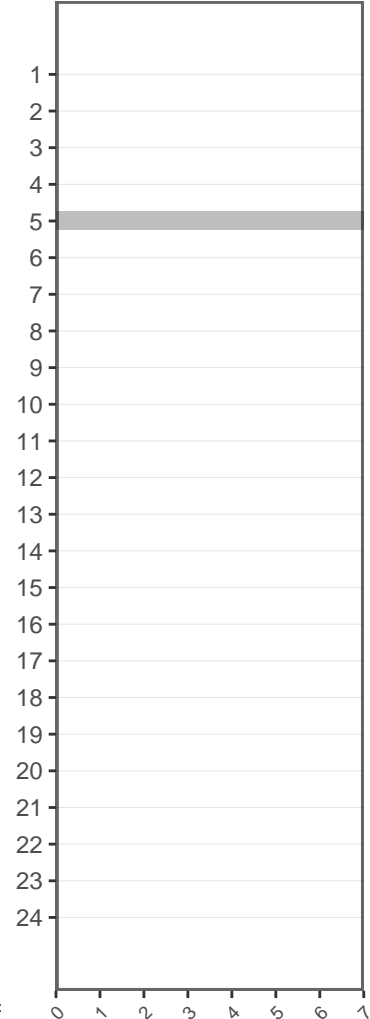
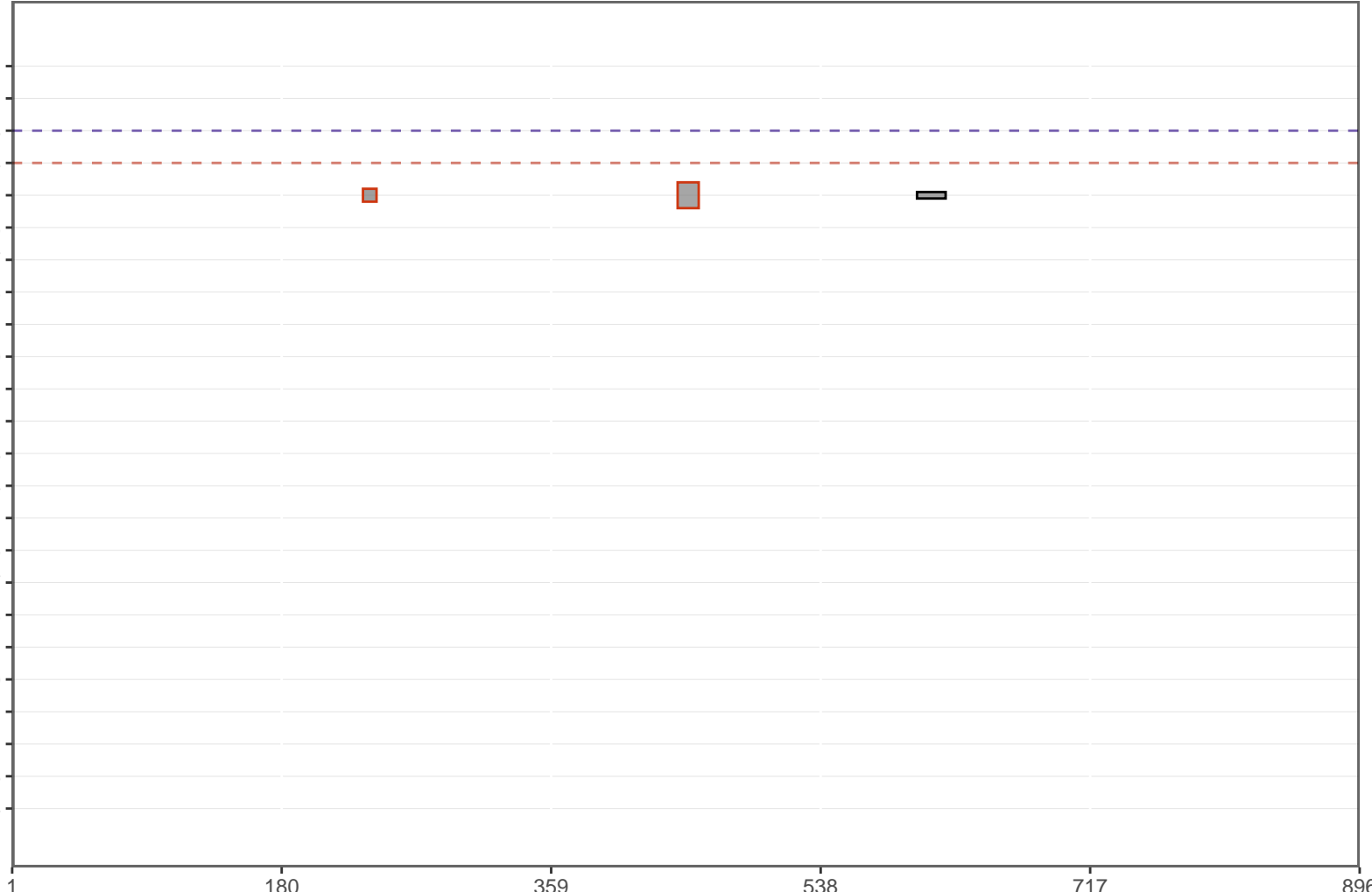
MW indication



Molecular weight



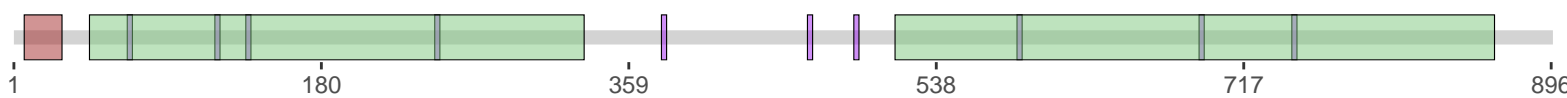
Gel Slice



Protein length

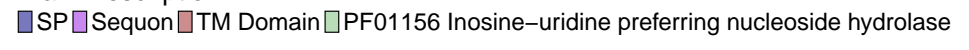


Peptide counts over 4 repeats



Pfam domains

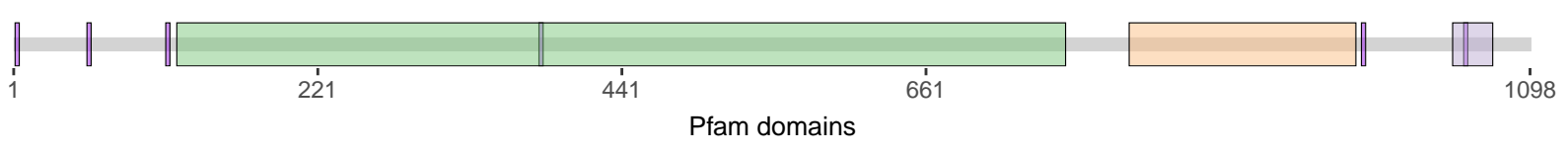
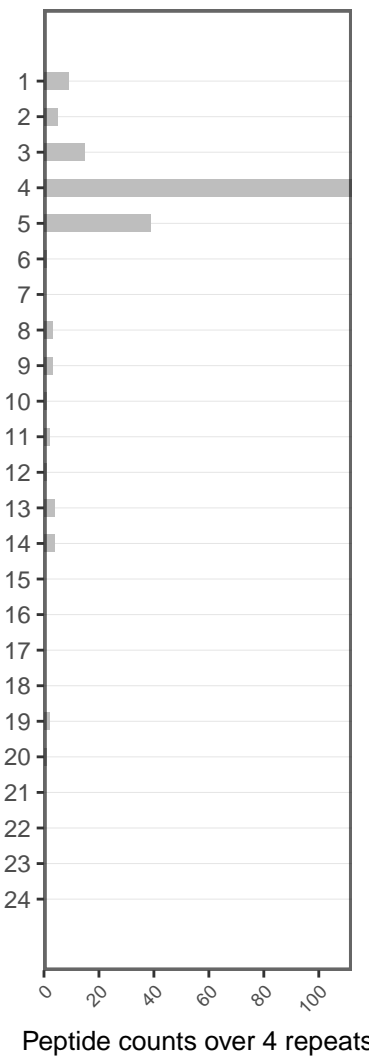
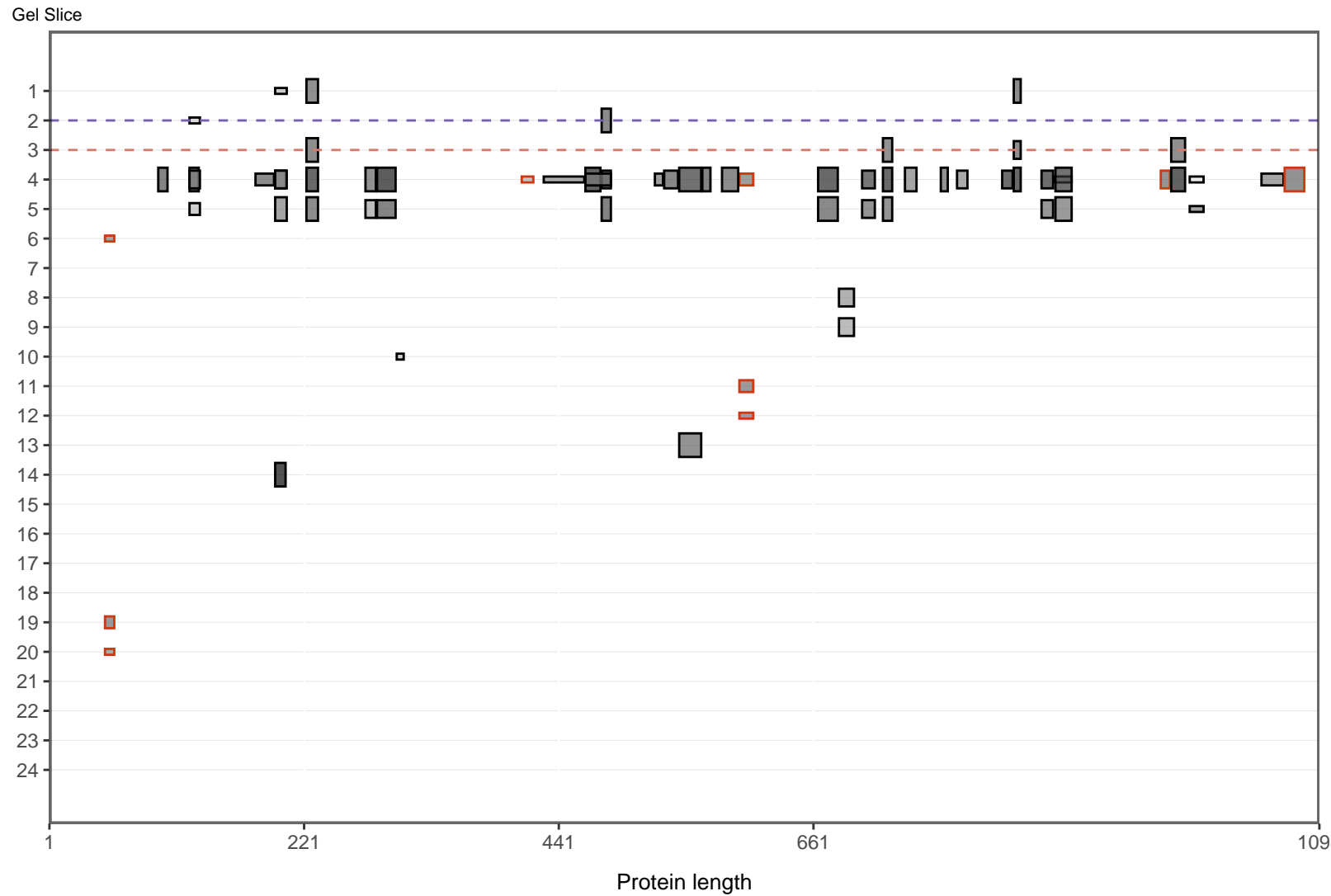
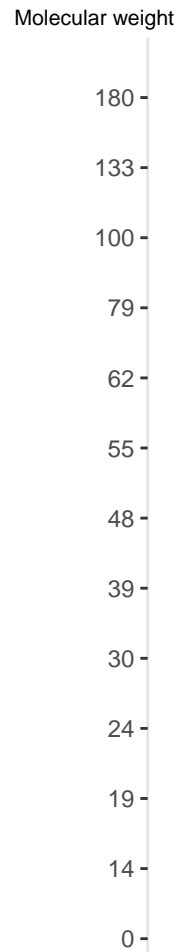
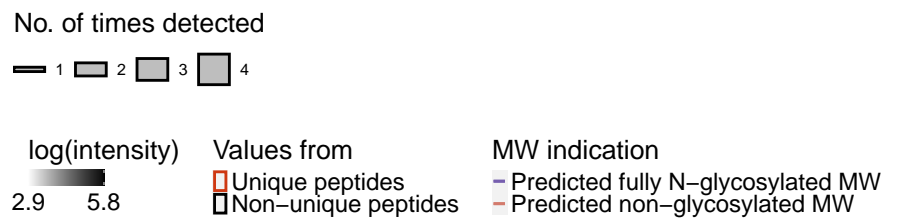
Pfam Description



Protein sequence:

IGRCDDGYTKEVYGGSGVPVAVRAKPNRINASSVLDREFYVGFLELVNQRKNSGKFNFTSTGFPYKELKPKDFRQKHLGKVVFDMDMSAGDFLALFYLLKLPVEINKAIVSPTGWANATDSVYDLLHMMGRDDIPVGLGDMFAMNNGSDPVFSAVGECKYKVPDGGSGFLDSDTLYGLSRSLPRSPRYTAENSVKFGAPRDTDHPELRQPLALEVWESVYKSLDGGKVTILNGLTNMAKLLAGKNTKAGGILVGGHINYDTEKGNVINVPSNRFQ

NbL06g10190.1 isoleucine--tRNA_ligase_chloroplastic/mitochondrial [MW = 123.75 kDa]



Pfam Description

- SP
- Sequon
- TM Domain
- PF00133 tRNA synthetases class I (I, L, M and V)
- PF06827 Zinc finger found in FPG and IleRS
- PF08264 Anticodon-binding domain of tRNA ligase

Protein sequence:

WFAVSEGFDAAMDANQVYTWPTGAVNRIASMTSGRSDDWIGSRGRVYVPHFYHSEKELPMNAETVDHKSISGKGSDAWWWYMSVEELLPEKYRDKASNYEKGTDTMDVWFDS6SS6AAWLLDKREGLNYPADLVLEGGTDQHRGWFQSGSLLSIATKGMAPYRQVITHGFLVDERGLMKSLGNVVDPRMVEEGKQKESPPYSADVLRLLWVSSVDYTGDLVLPQVLRQMDIYRKLKGLRFLFLANLHWKADCAVPSSELPMDIGVLFQLANVYNNIR

NbL06g10160.1 heat_shock_factor-binding_protein_1-like [MW - SP = 10.83 kDa]

No. of times detected



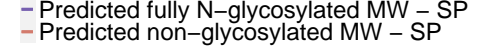
log(intensity)



Values from



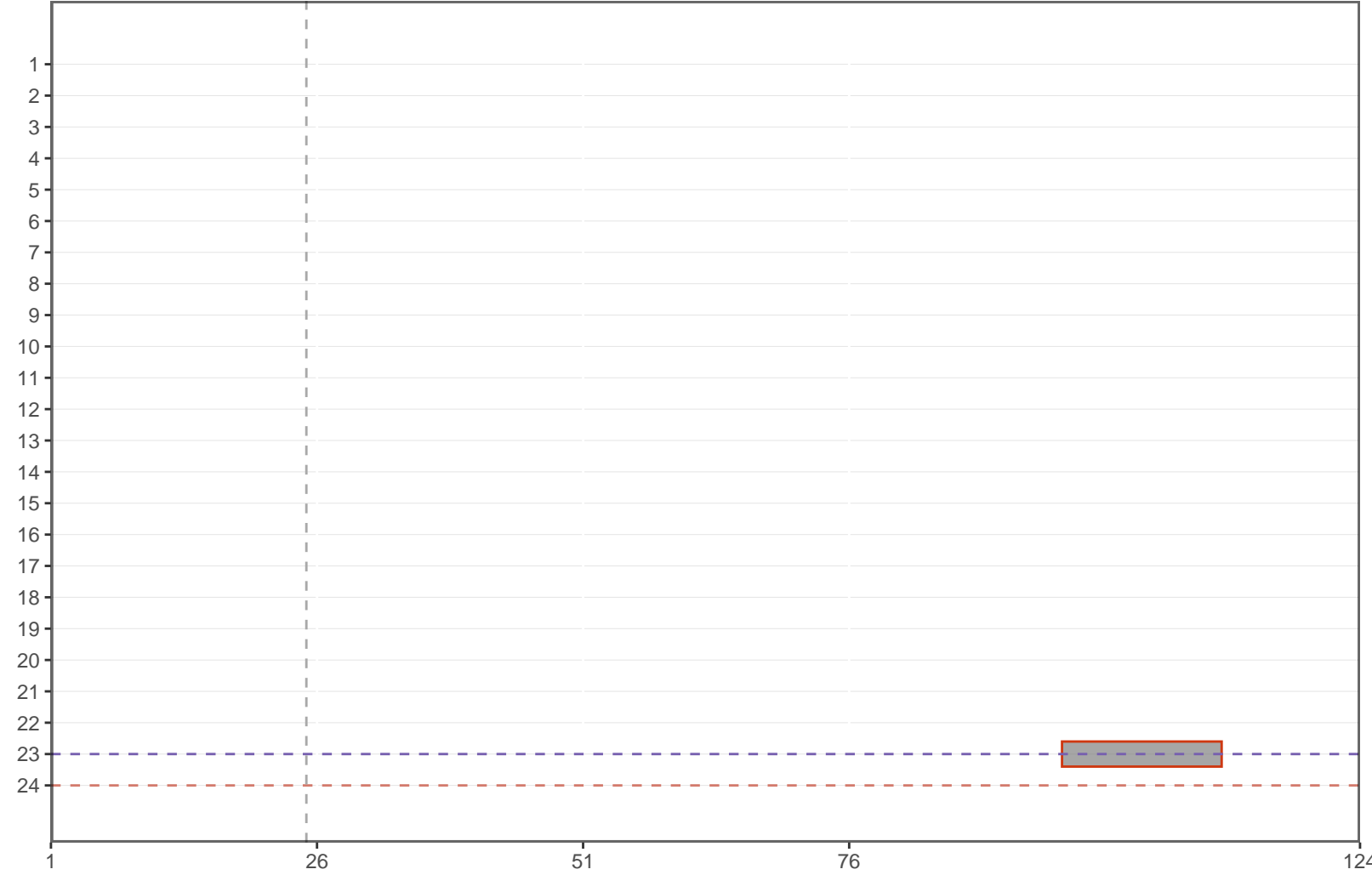
MW indication



Molecular weight



Gel Slice



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

CMQTSLYIASIFCEINLEKVLGVLEVAALDEMGHRIDELQGSINDLRITEMGGEGPSPSAALKSKDEPKSAEDST

NbL06g10050.1 acyl_carrier_protein_1_chloroplastic-like [MW = 14.05 kDa]

No. of times detected



log(intensity)



Values from



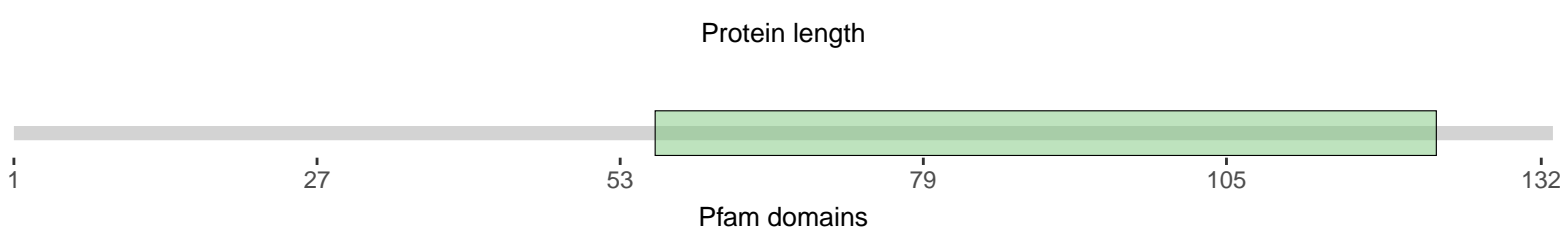
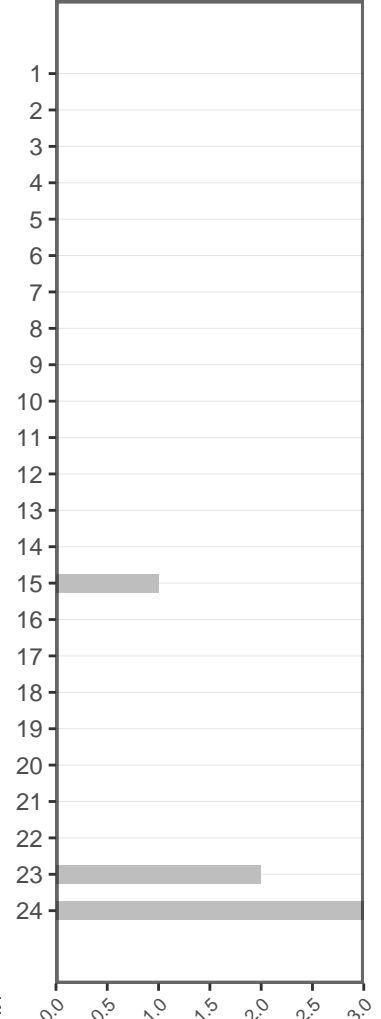
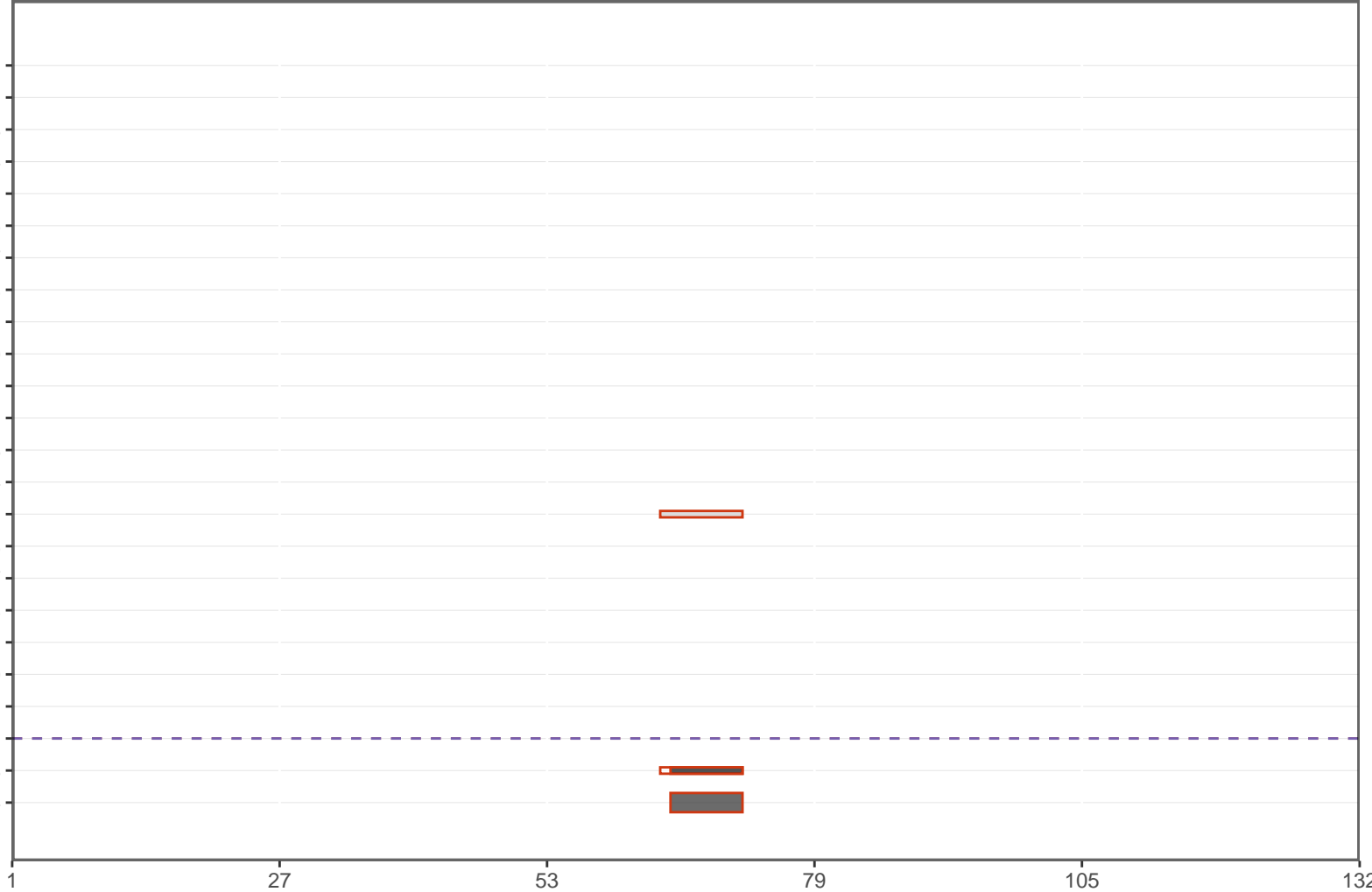
MW indication



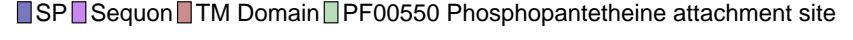
Molecular weight



Gel Slice



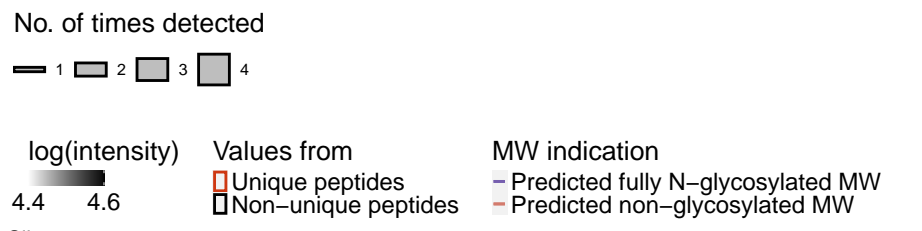
Pfam Description



Protein sequence:

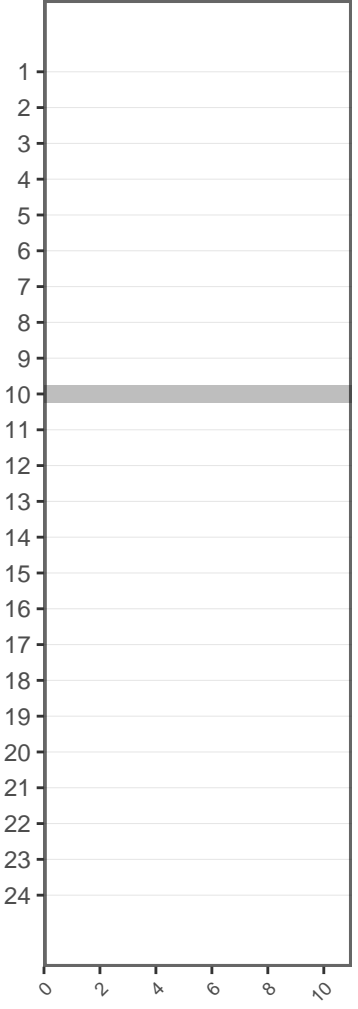
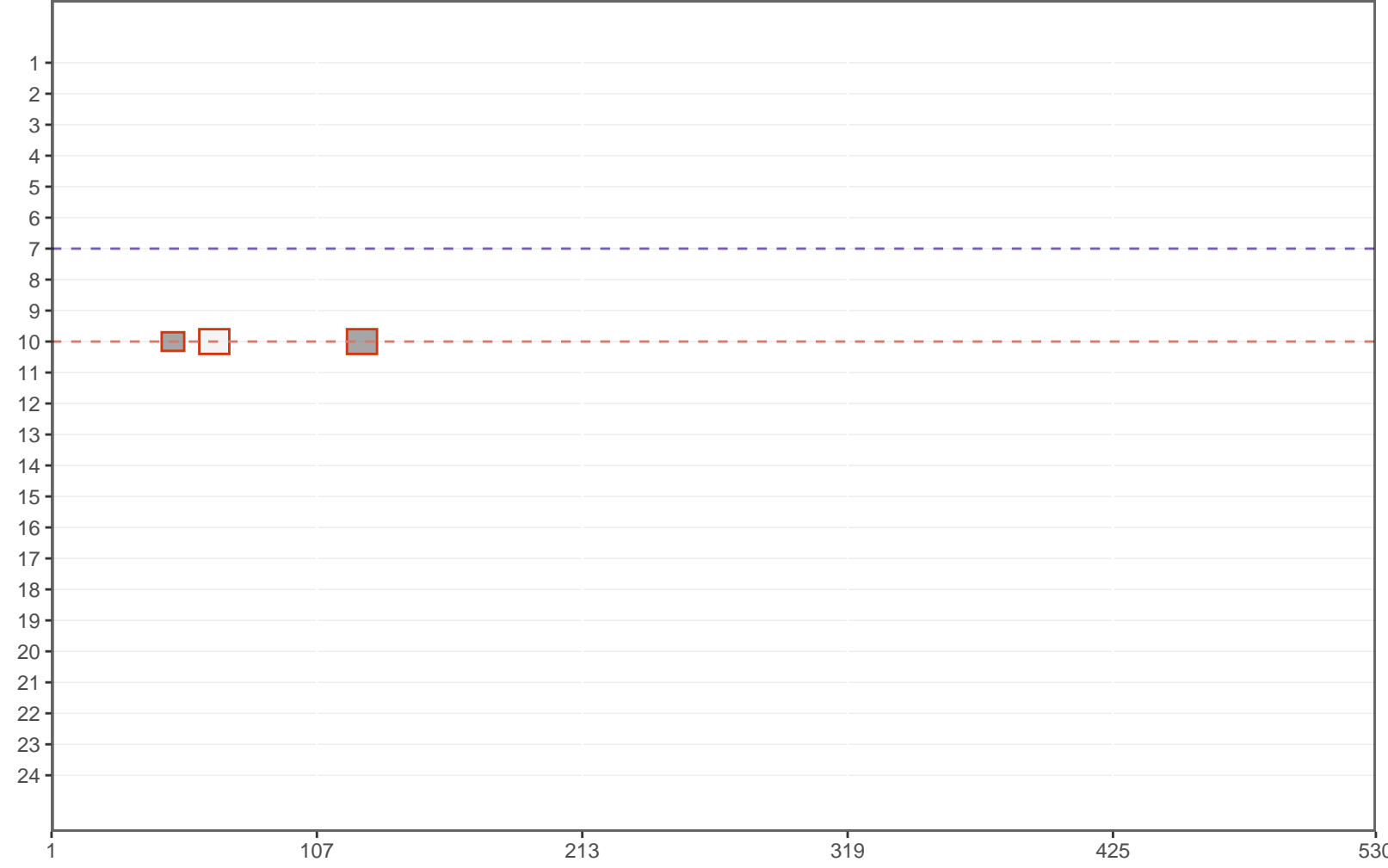
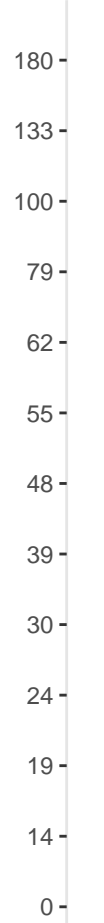
ETVDKYCEIVKXKQALTDKRVNNGESKFTALGADSLDTVEIVMGLLEAFGRIVVEENAGTATVGDAAADJEDUSKKA

NbL06g10040.1 bifunctional_3-dehydroquinase_dehydratase/shikimate_dehydrogenase_chloroplastic-like [MW = 57.51 kDa]



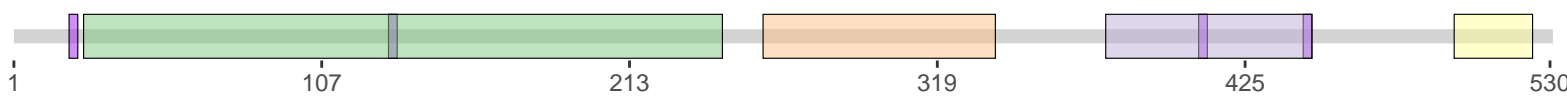
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01487 Type I 3-dehydroquinase
- PF01488 Shikimate / quinate 5-dehydrogenase
- PF08501 Shikimate dehydrogenase substrate binding domain
- PF18317 Shikimate 5'-dehydrogenase C-terminal domain

Protein sequence:

PQTRVFGIGKIPVSHKSEPLLYNEAFREVGFGNGVYMLPLVDDVANNFRRTYSGLDIAFGSCTPHKEAVDDGDEIDPTAKLIGAVNGVYRRPDKLFGCNTQVIGASIAIEELQSSQPSMSRPLAGKLFVWIGAGGAGKALYGAKEKGRVIANRTYERARELADVGGGALSLELGNHPENDMLANTTSIGMSPKVDPTNRKEALRYSLVFDVYTPKTKLLREAGESEGKWTGVEMFIGGAYEGYERFTGLPKELFKKIMAGY

NbL06g09910.1 probable_xyloglucan_endotransglucosylase/hydrolase_protein_8 [MW - SP = 32.04 kDa]

No. of times detected



log(intensity)



Values from



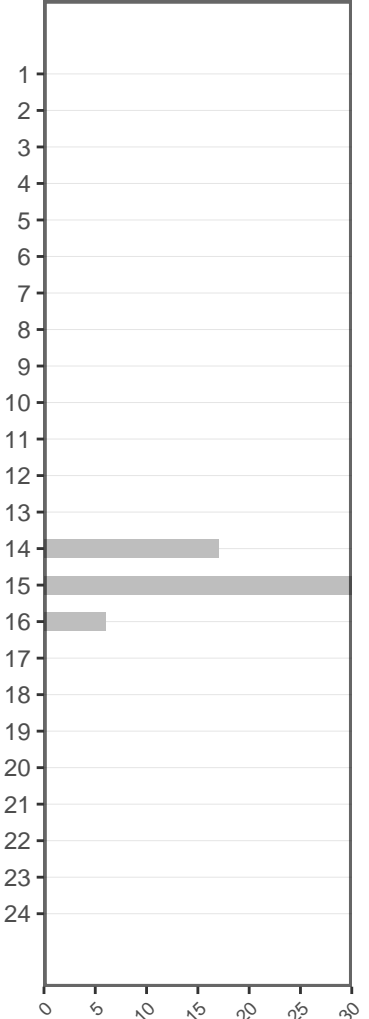
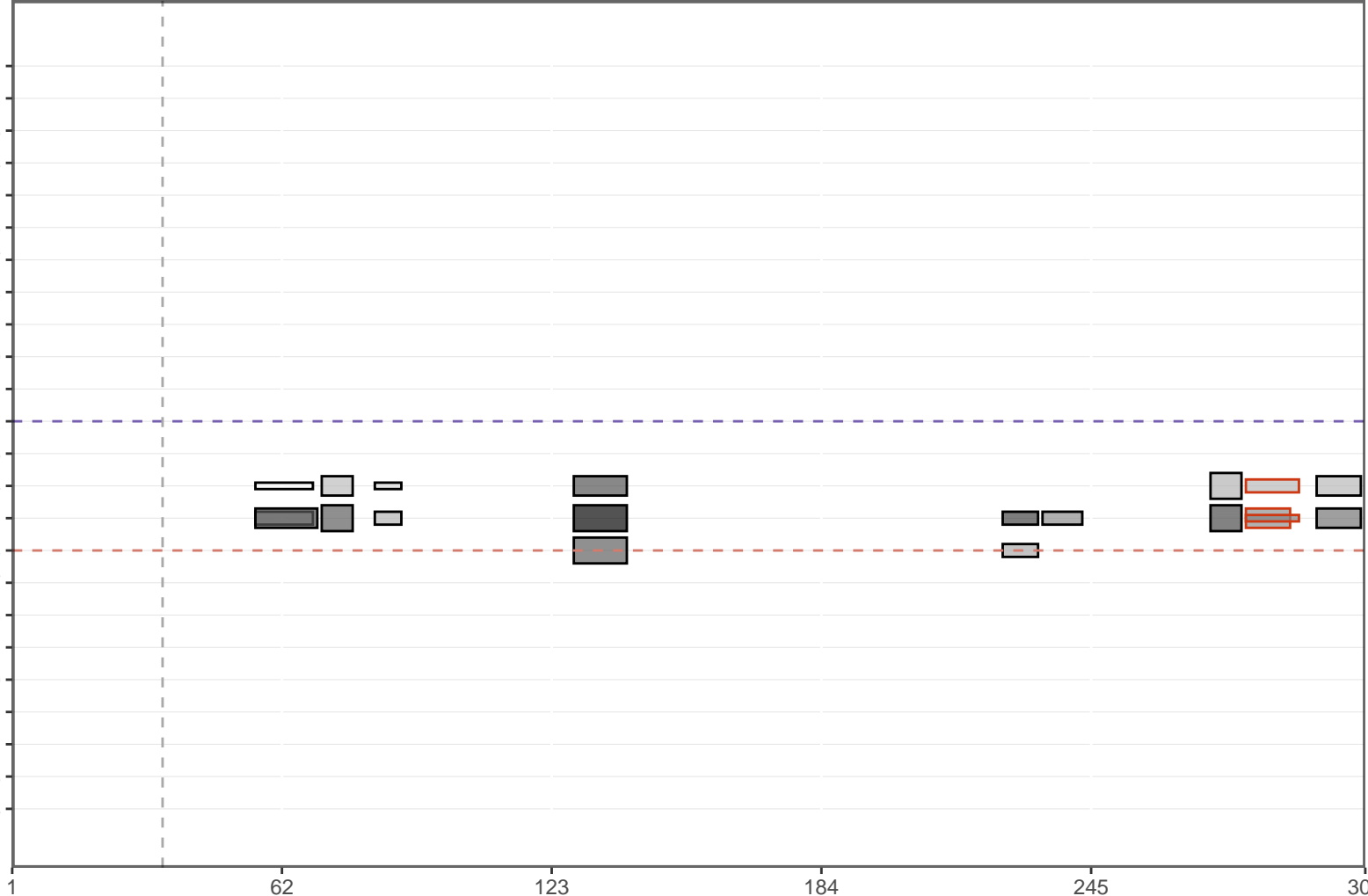
MW indication



Molecular weight



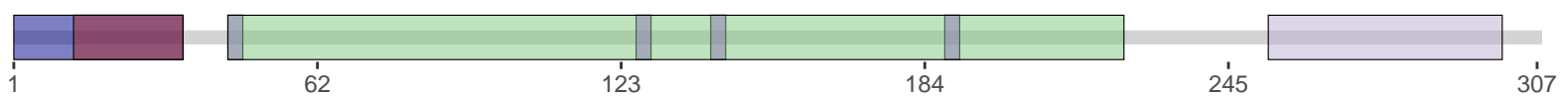
Gel Slice



Protein length

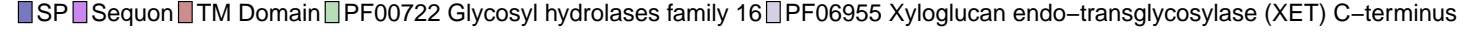


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GNREMRHNLVDFTEGPHYSLNHTHGIVFVDRIPRVYKNNYTNFFPNEKPMYLFSSGWNADDAWTRGGLEKTNWKNQPFVSSYKDFSDVGGQWKPDPKACVSTTTNWWDDQVNSWHLSNDQKMDYAWVGRNLTVDYGDQKERFFKPKKEEGWLNPEE

NbL06g09730.1 probable_acyl-activating_enzyme_6 [MW = 68.46 kDa]

No. of times detected



log(intensity)



Values from



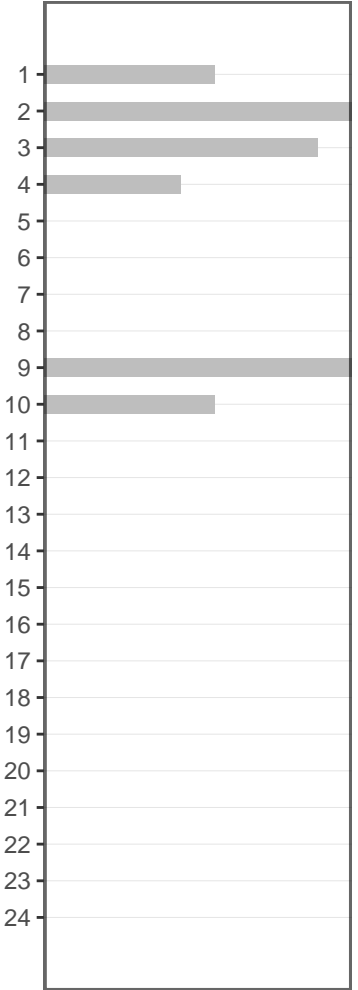
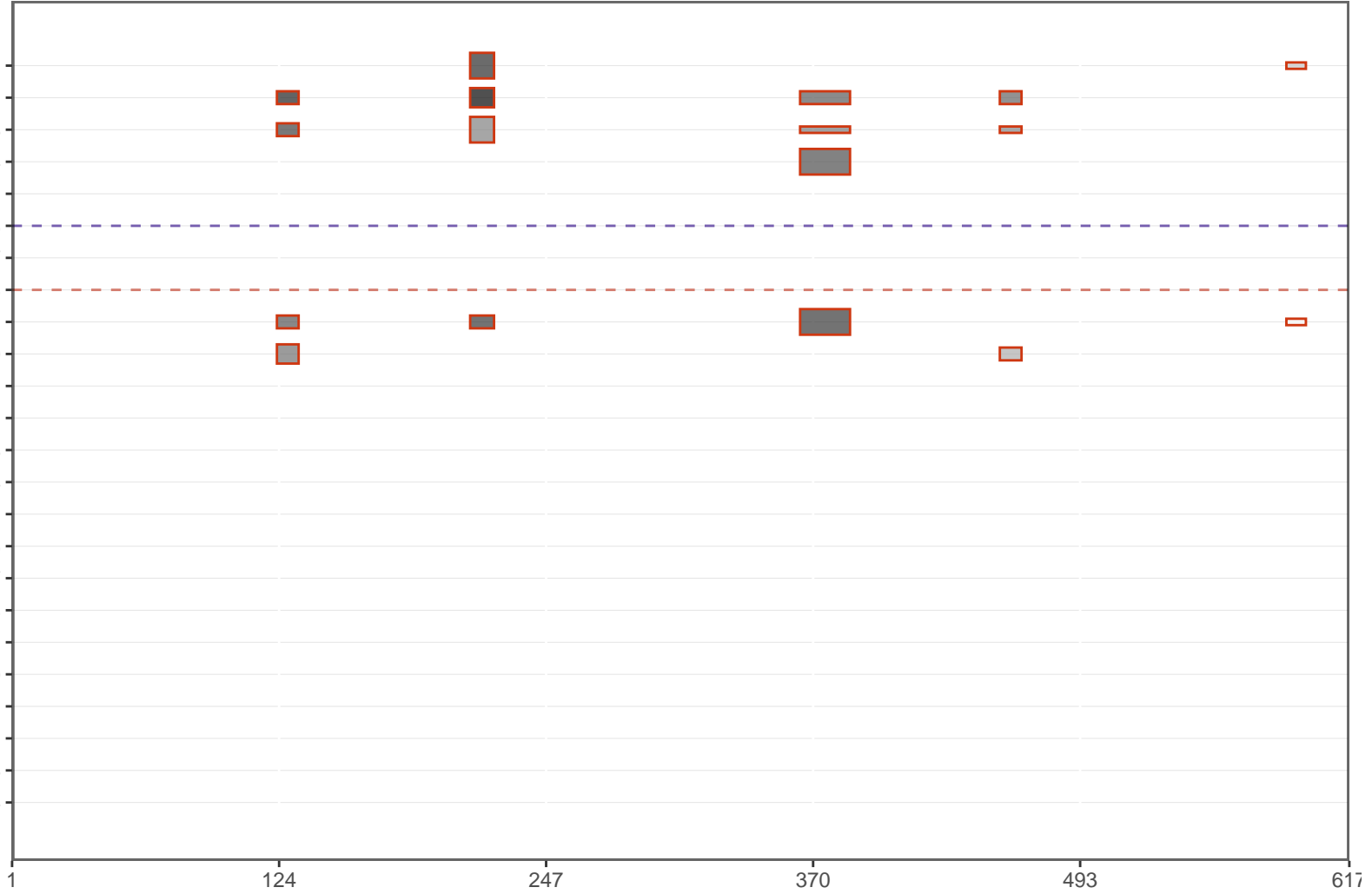
MW indication



Molecular weight

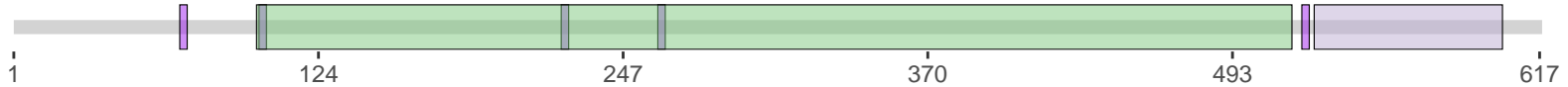


Gel Slice



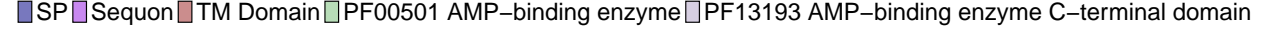
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LWTLPIFIANGWGFQWGMMAVGGTNVQLRRGHDASSIVEAIHQHKVTHMCGAPVAVNMLSTYPRKQPLDSPVWYTAGAPPPVLRRTESLGFVISHVYGLTETGGPVTGAWKGEWDLPGSERAKLKRGGVIRMVGFTEVDVDFETGISIERNGIAGEVLRGGSVMLGLYLNKDEGTSKGMKNDGWVYFGDGVGMHSDGYLEVKDRLKVHICGGENISSEVESEILYKHPWNEAAVWAKPQNVWGETPCAFISLKTDAEKMTFEKLRDFGKQKPLLYM/PRTV

NbL06g09640.1 thioredoxin_reductase_2 [MW = 35.16 kDa]

No. of times detected



log(intensity)



Values from



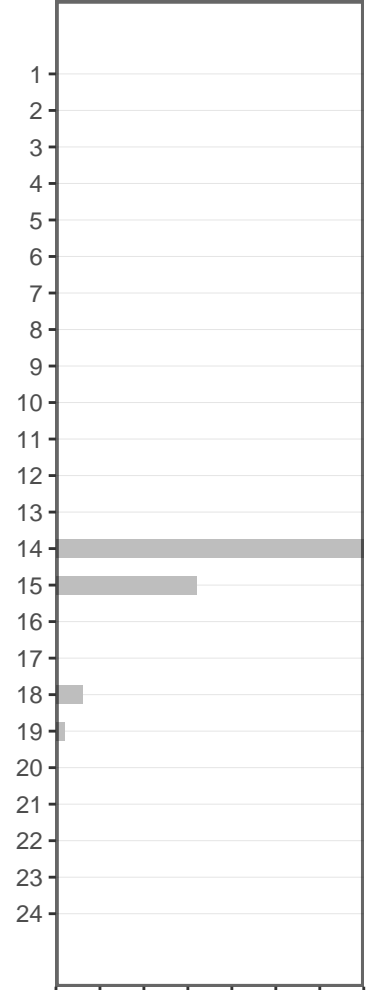
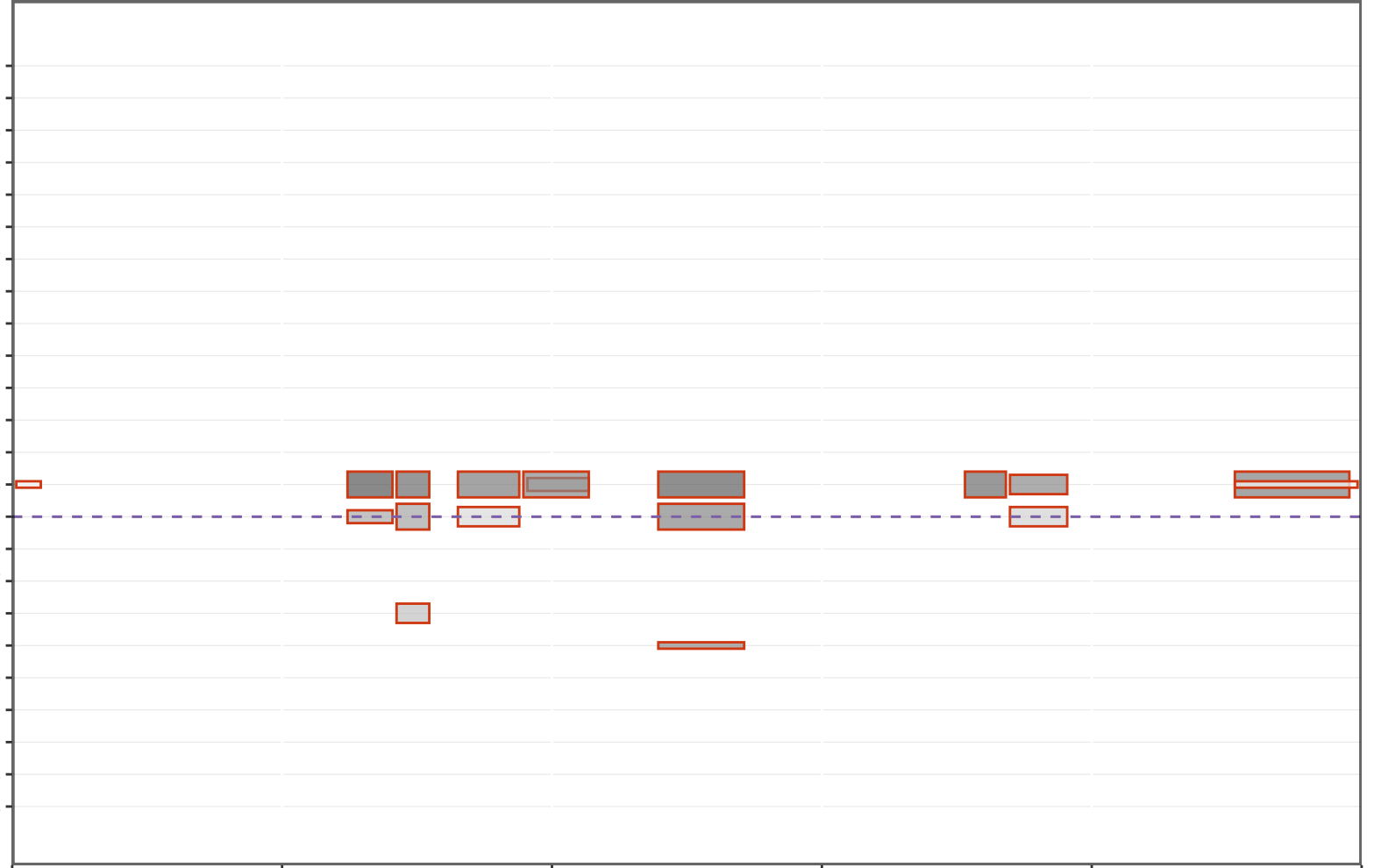
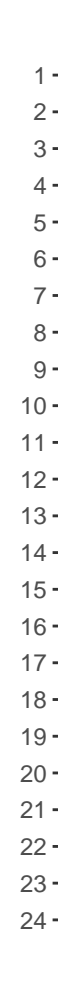
MW indication



Molecular weight



Gel Slice

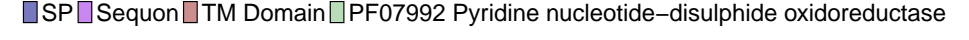


Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

MAPIFRNLFLAVIGGGDSAMEEATFLTKYGEKVIHRRDEFKSKIMRNRALENPKIEVWNSAVVEAYGEKVLGGLKWNVWNGEVSDLKVGSLFFAIGHETMTRFLDGOLELSDGCVVTEPGTTKTSVIRGVFAAGDNGDKNRQNTAAGGGGMAALDAEHVLEIGAGEGKSDI

NbL06g09550.1 nucleoside-triphosphatase_THEP1 [MW = 21.87 kDa]

No. of times detected



log(intensity)



Values from



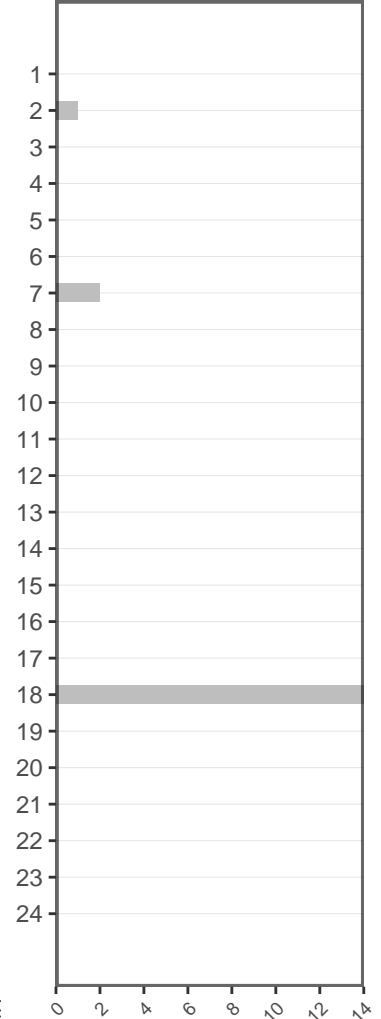
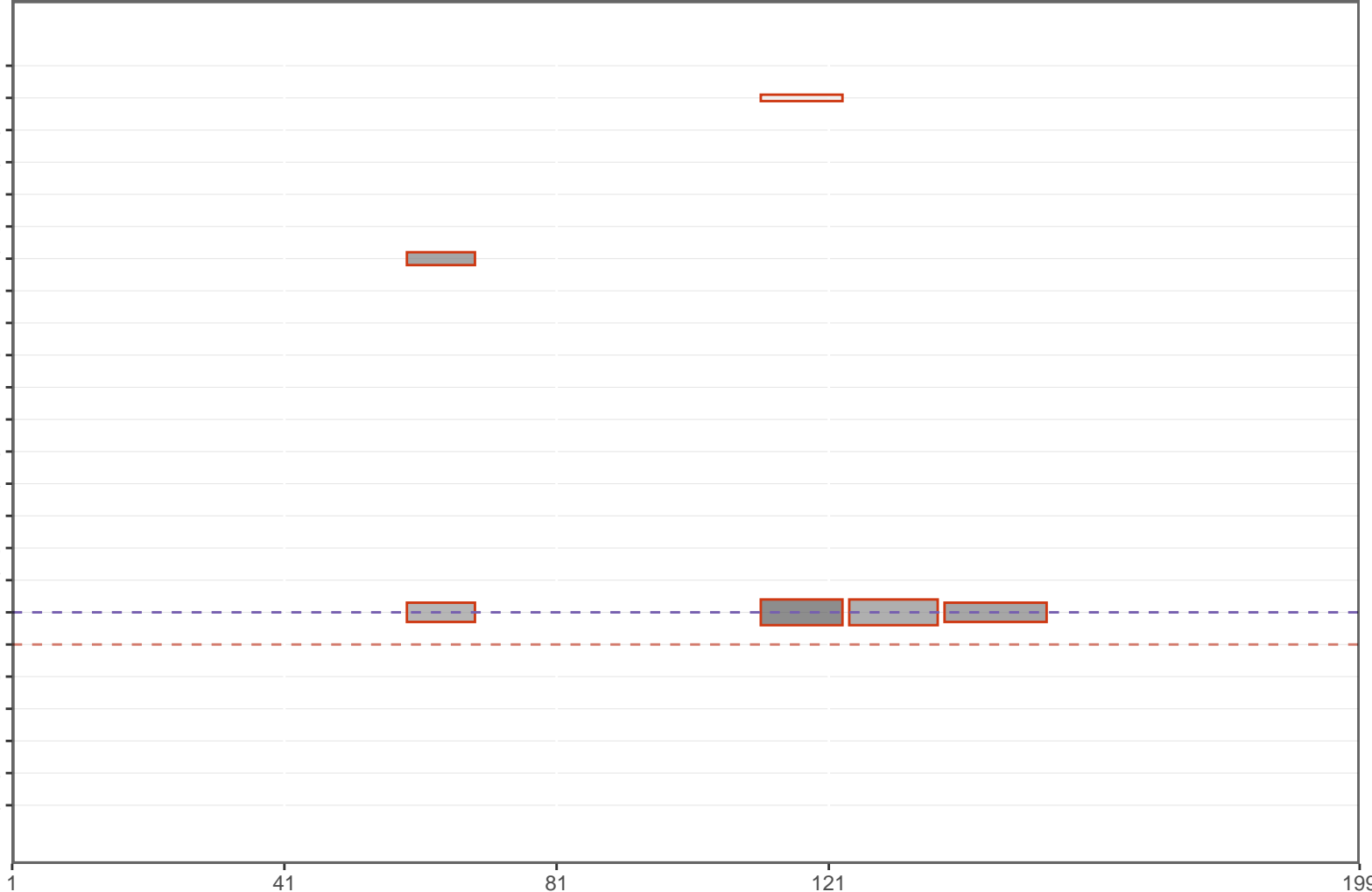
MW indication



Molecular weight



Gel Slice

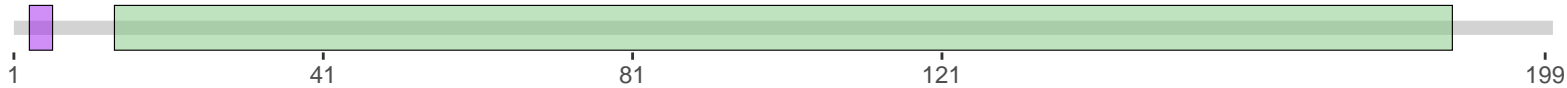


Protein length

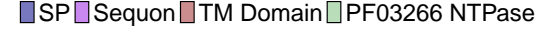


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

MPVTGIRYRVDAVAFSEELALPELQVREDTDLFIIDEVGMELYS66SFFPWLVKVLGENIFLASIPKAGRIDPGVARMRNHPGAEVFTLNANNRDR6MREGQ6STLADMLQKP

NbL06g09510.1 ubiquitin_domain-containing_protein_DSK2b-like [MW = 59.16 kDa]

No. of times detected



log(intensity)



Values from



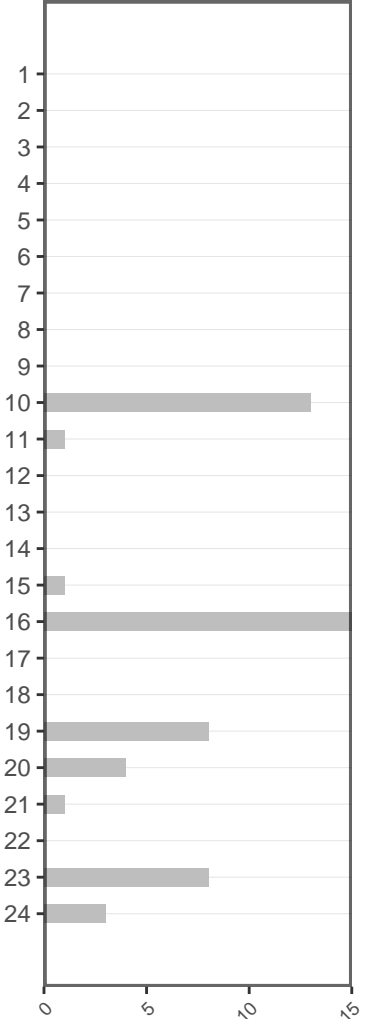
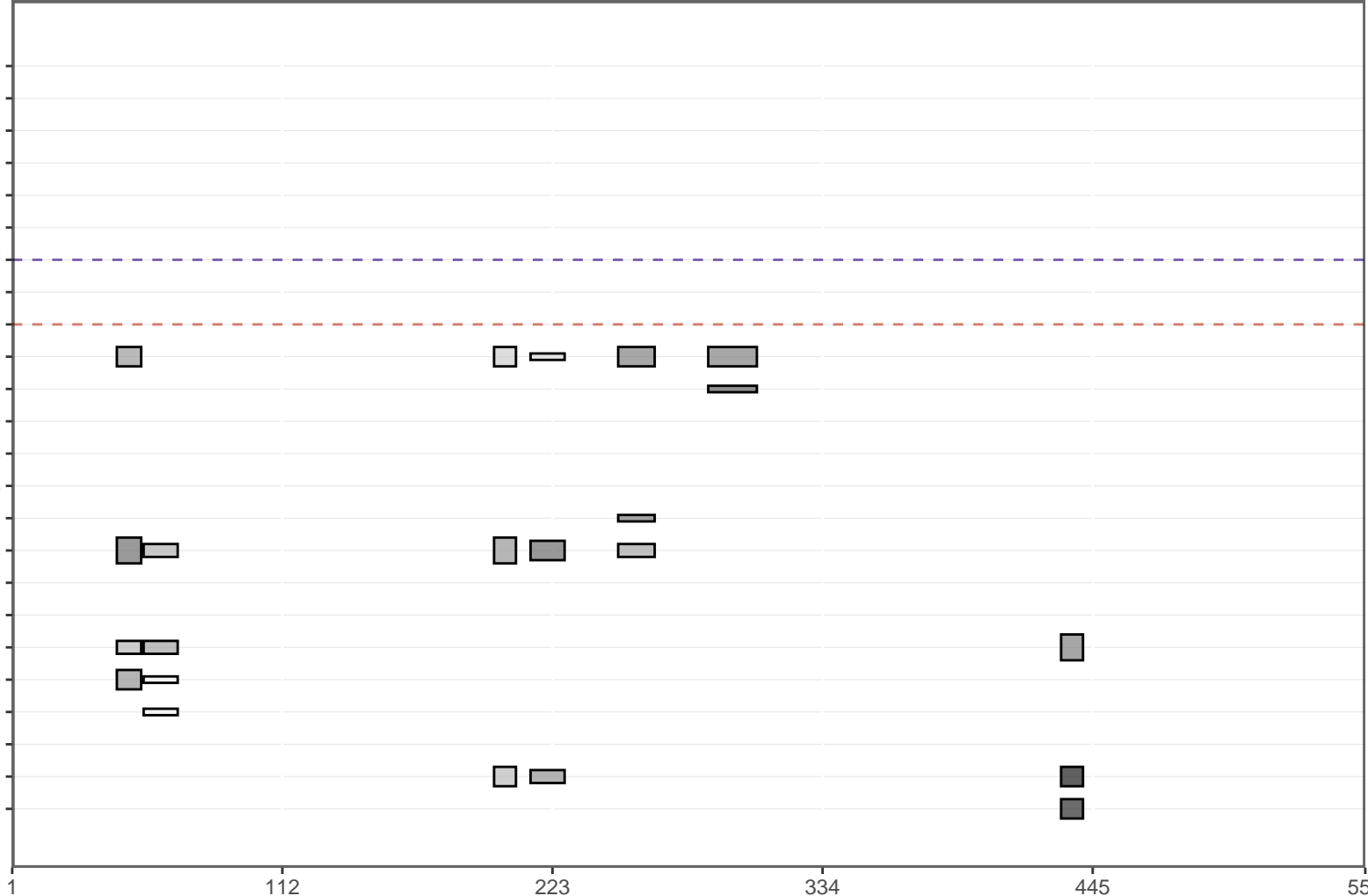
MW indication



Molecular weight



Gel Slice

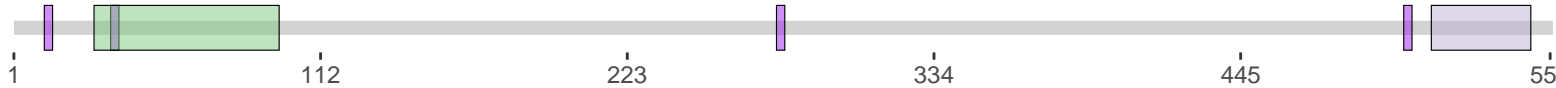


Protein length

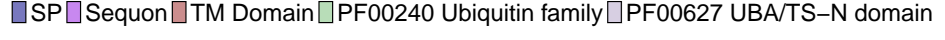


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

AYENVQEPFLNATLSGGDRTRNDVSNPFAALLGADGGGGGRHQSNPPPTSGSETTDNPPAPNTNPLPNPFWASAGTGAAGANTPARBNTAADTRAAPLGGGLGSLGMLSGMPDITSLNGMGNPAISGMQSLLENPQYMNQVLLGNLPQLRMLDNSHLEMMGNPEFIRQLTSPETMQQLMTFGHGLLGGAVRQGTNGQVGNAGGAAGDNGMEMLMNMFQGLETGGLVNRSNVPPEELVATQLTQLGEMGFFDTGENIRALLATAGNVAVEF

NbL06g09140.1 probable_serine_protease_EDA2 [MW - SP = 52.01 kDa]

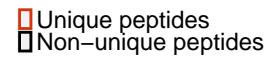
No. of times detected



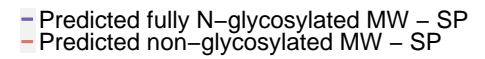
log(intensity)



Values from



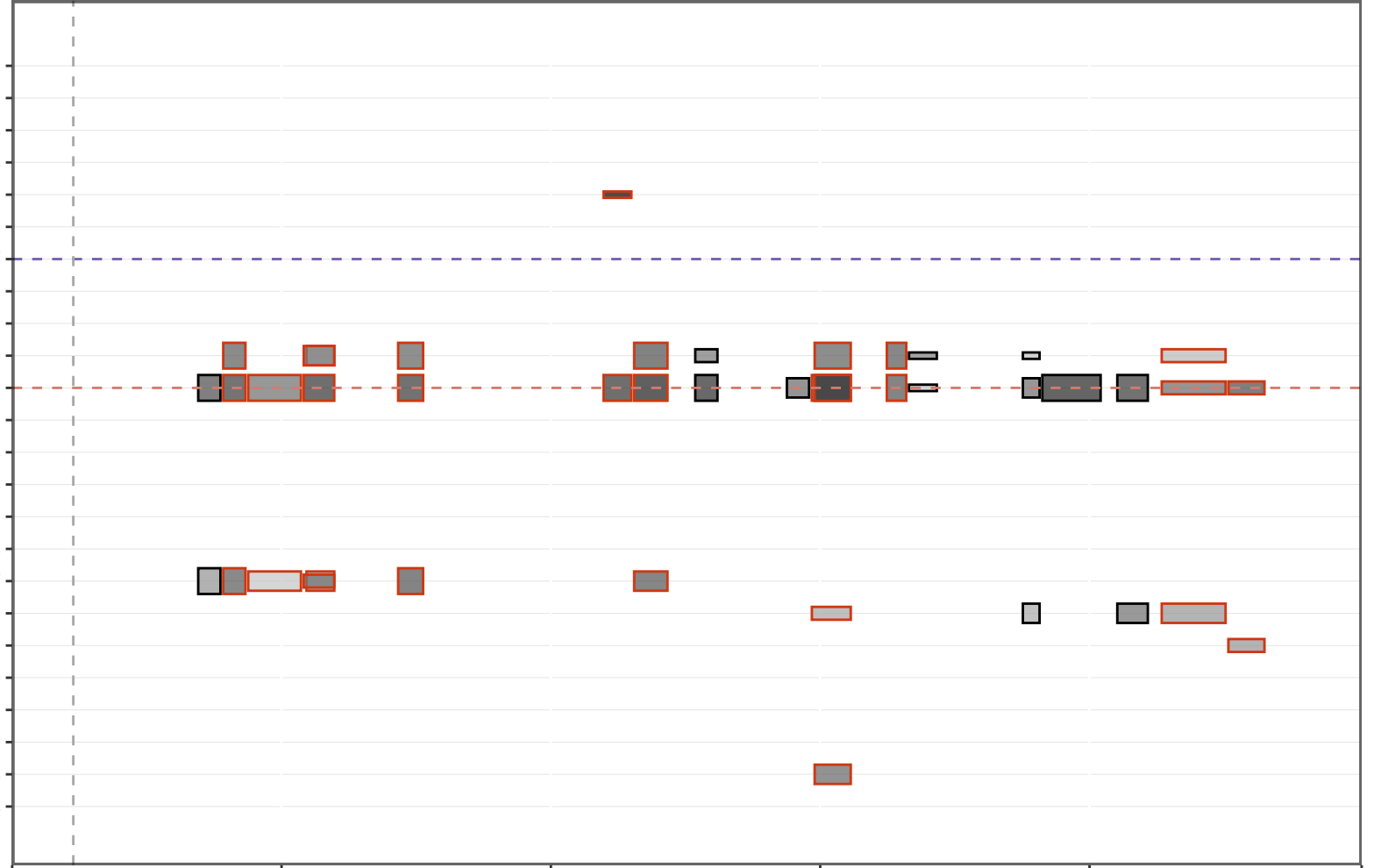
MW indication



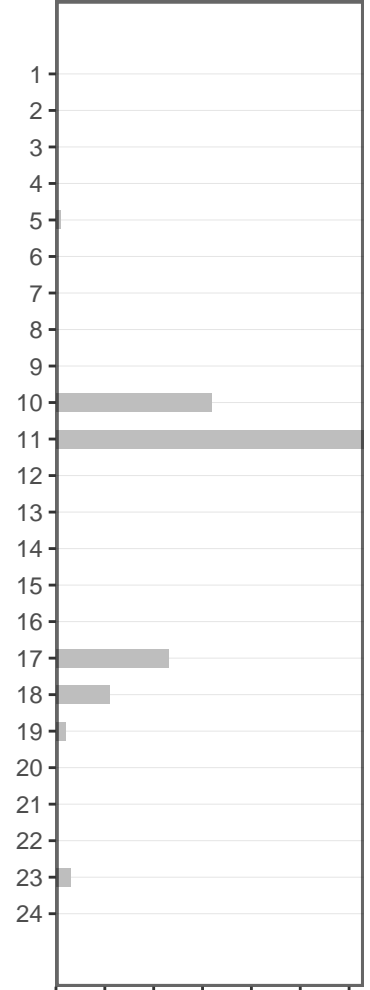
Molecular weight



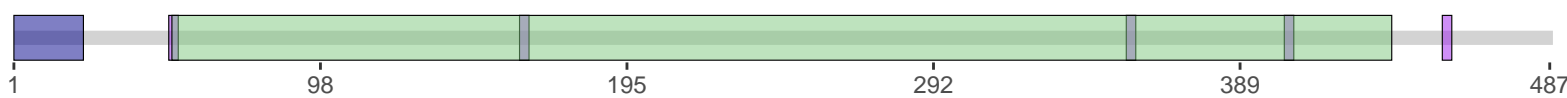
Gel Slice



Protein length

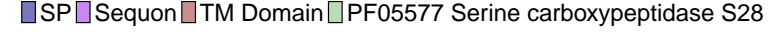


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

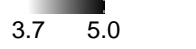
LVETRLASNRKDKLALFQADELRIDGDFLVFLADAAVAVSIVGSPDKLGIPLLEAKSGEDLVNAYAVVKEYYKTLGVSVKTYNGENLNTAVNSDTSRDLWVFGVQVTEVAVFQVAPRNDGIRRSKVDTRYHLDLGRNVFGAGIYPEVDATLNYGGTKIAGSKIFITNSGDDPVRHASKQTSPEMPYEVVYVSGCHNGHGTDLRGCPQGFVLPVPEGDANKNSGSDPAVRKVRREKVEYIDLWLSGGQVSGRSWV

NbL06g09080.1 thioredoxin_H-type [MW = 15.27 kDa]

No. of times detected



log(intensity)



Values from



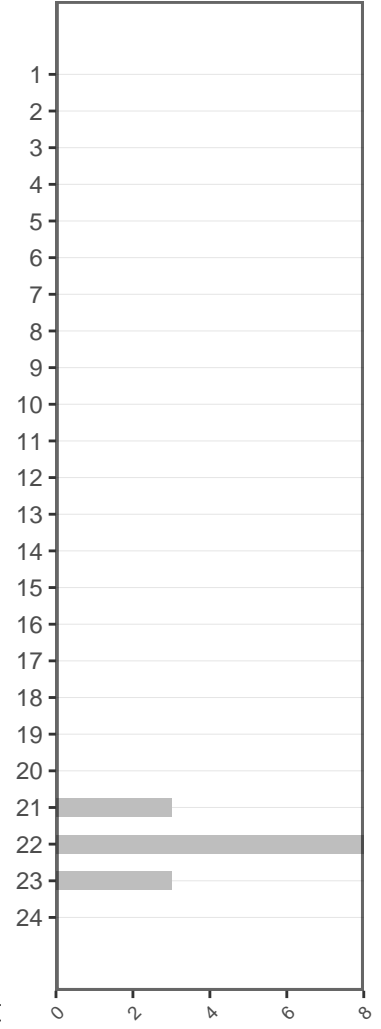
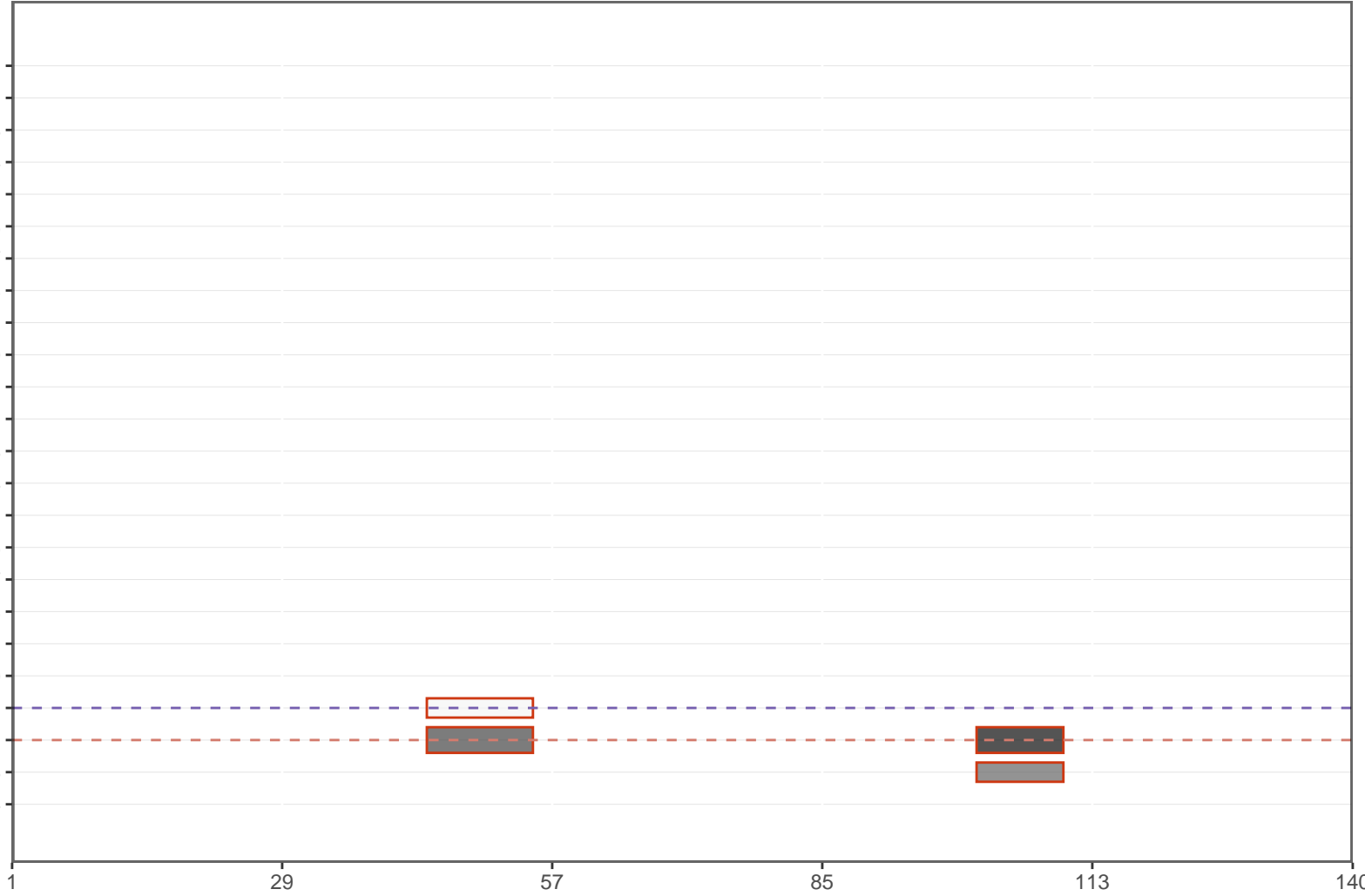
MW indication



Molecular weight

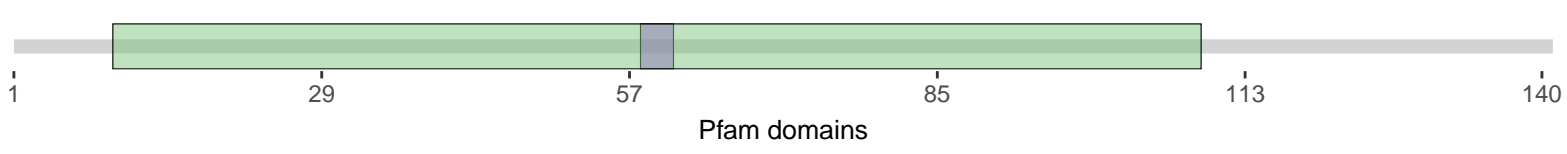


Gel Slice



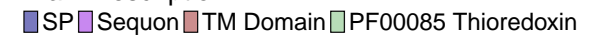
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

PNVFLKVDVDELKSGWTDWAVEAMPFTFMFLKEGNVDKVVGAKKEELQQAIAKHMEYFGLNKGCGKGAELAVGSTTAFD

NbL06g08750.1 thylakoid_membrane_protein_slr0575-like [MW = 31.08 kDa]

No. of times detected



log(intensity)



Values from



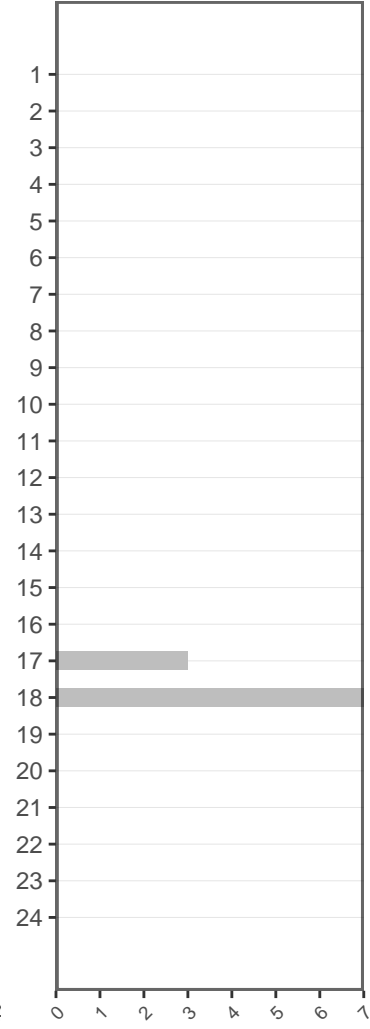
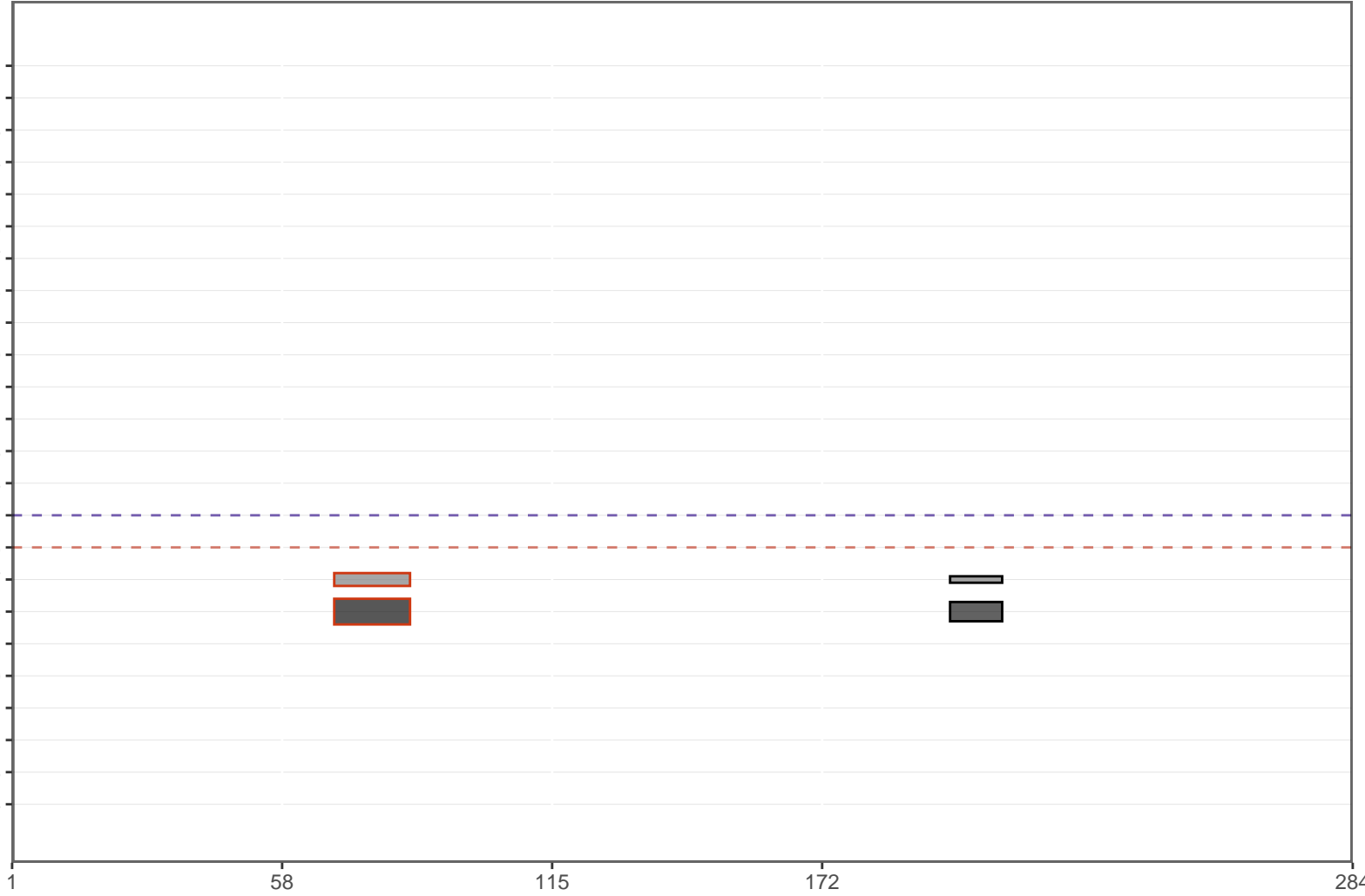
MW indication



Molecular weight

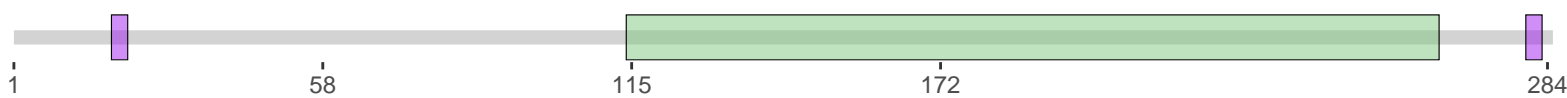


Gel Slice



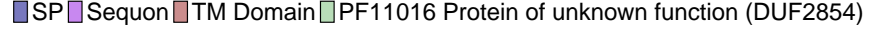
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

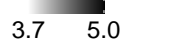
MSALMLTYGFLTIGMALKYAEIKPVPQIFYSDAQLLREKCATPKLQVRSQVIRVRYGDEQHLDESLKRIFQFGLGGIPRRSAPVLMIREEVTEDDKYGLVLFVEAKALGLSDLEKRAKAFSFFGPGISAEIAKGEKDALYEVRLISNTLV

NbL06g08740.1 14-3-3_protein_4-like [MW = 29.38 kDa]

No. of times detected



log(intensity)



Values from



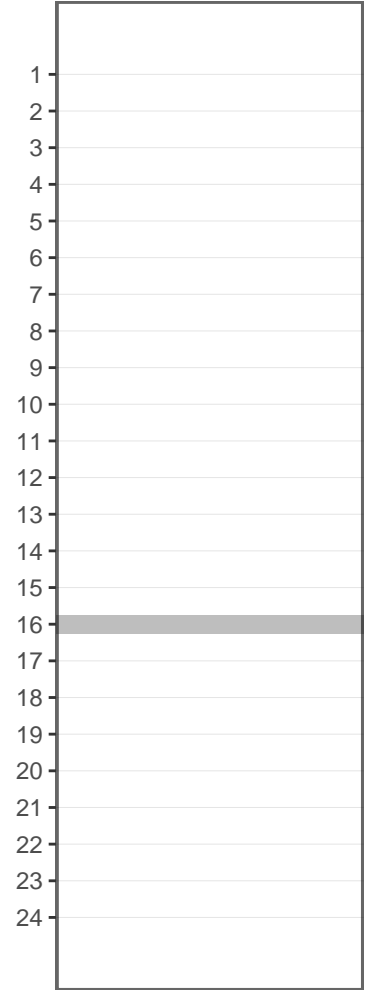
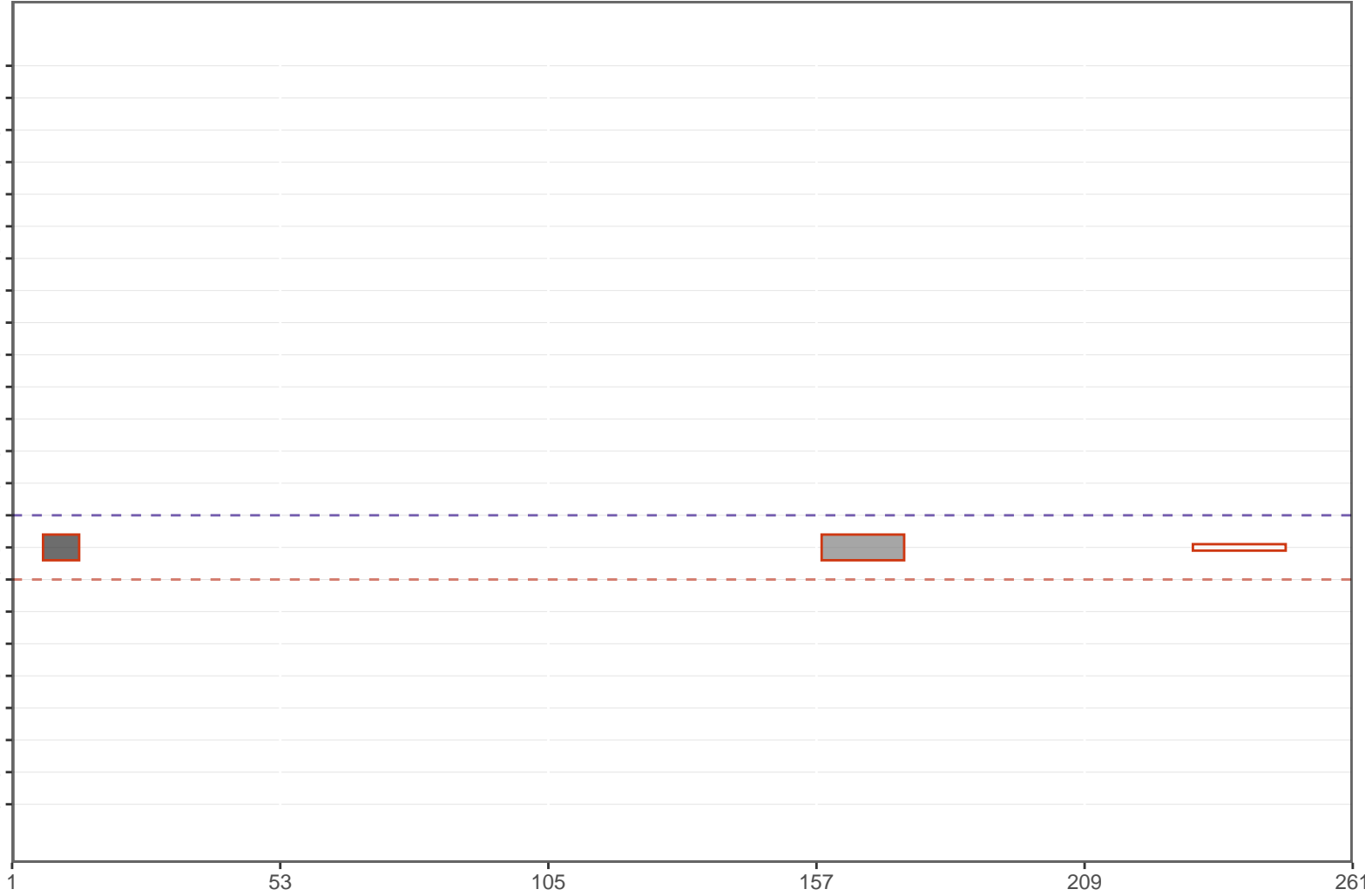
MW indication



Molecular weight



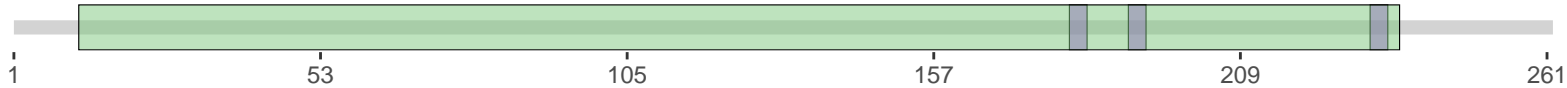
Gel Slice



Peptide counts over 4 repeats

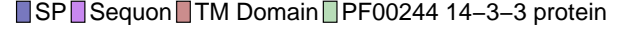
1 53 105 157 209 261

Protein length



Pfam domains

Pfam Description



Protein sequence:

TAEISKVFLKMKGGWHRVLAEFKTAERKEAENTLLAVKSAQDDALDELAPHPIRLGLALNFVFFYEILNSEDRAKLANAKAFDDAAELDTLGEESYKSDTLMOLLRDDNLTLWTFSDTDDAGDEKEAKRESGGDGEQ*

NbL06g08680.1 ribulose_bisphosphate_carboxylase_small_chain_chloroplastic [MW = 20.34 kDa]

No. of times detected



log(intensity)



Values from



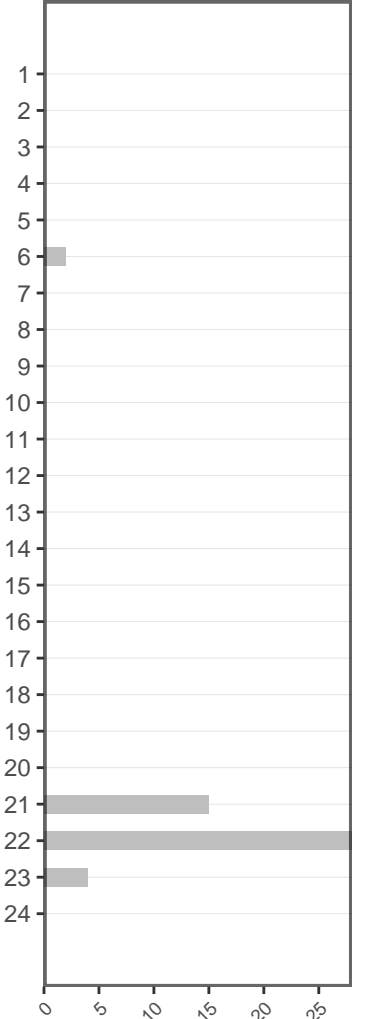
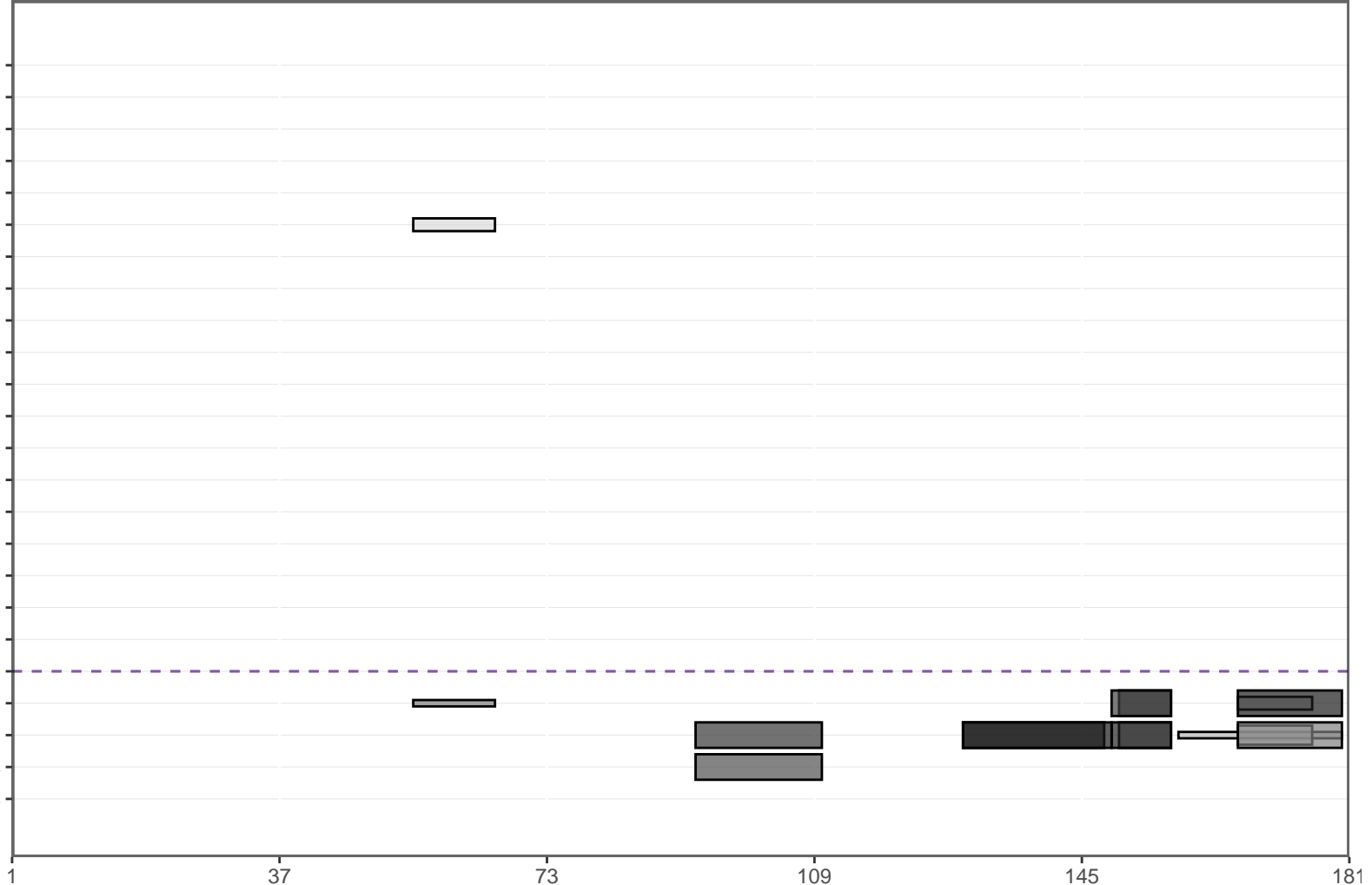
MW indication



Molecular weight



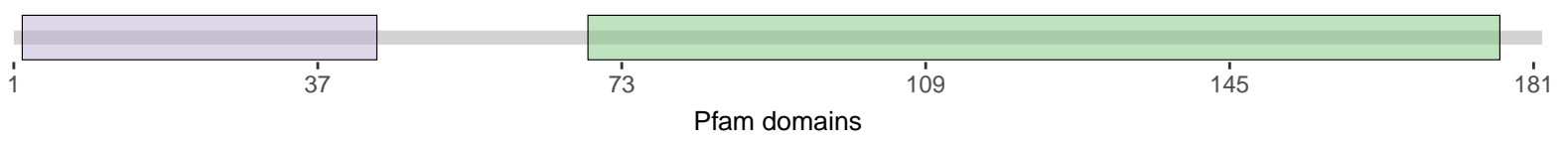
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00101 Ribulose bisphosphate carboxylase, small chain
- PF12338 Ribulose-1,5-bisphosphate carboxylase small subunit

Protein sequence:

LSVEQLLSEIYLLKNGWVPLGEFETEHGEVYREHHKSPGYDGRVYTMWKLPMFGGTDATQVLAEEAEAKKAYPGAWRIRIGFDNVRQVGGISFIAYKPEGY

NbL06g08590.1 non-specific_lipid-transfer_protein_2-like [MW = 16.55 kDa]

No. of times detected



log(intensity)



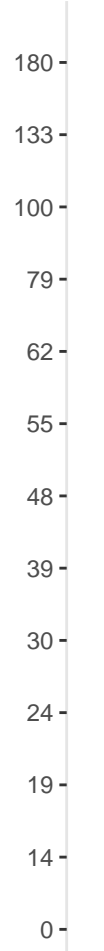
Values from



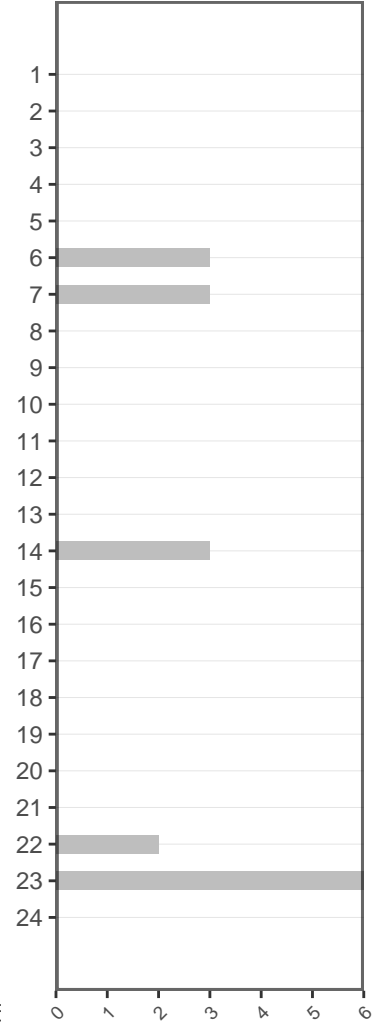
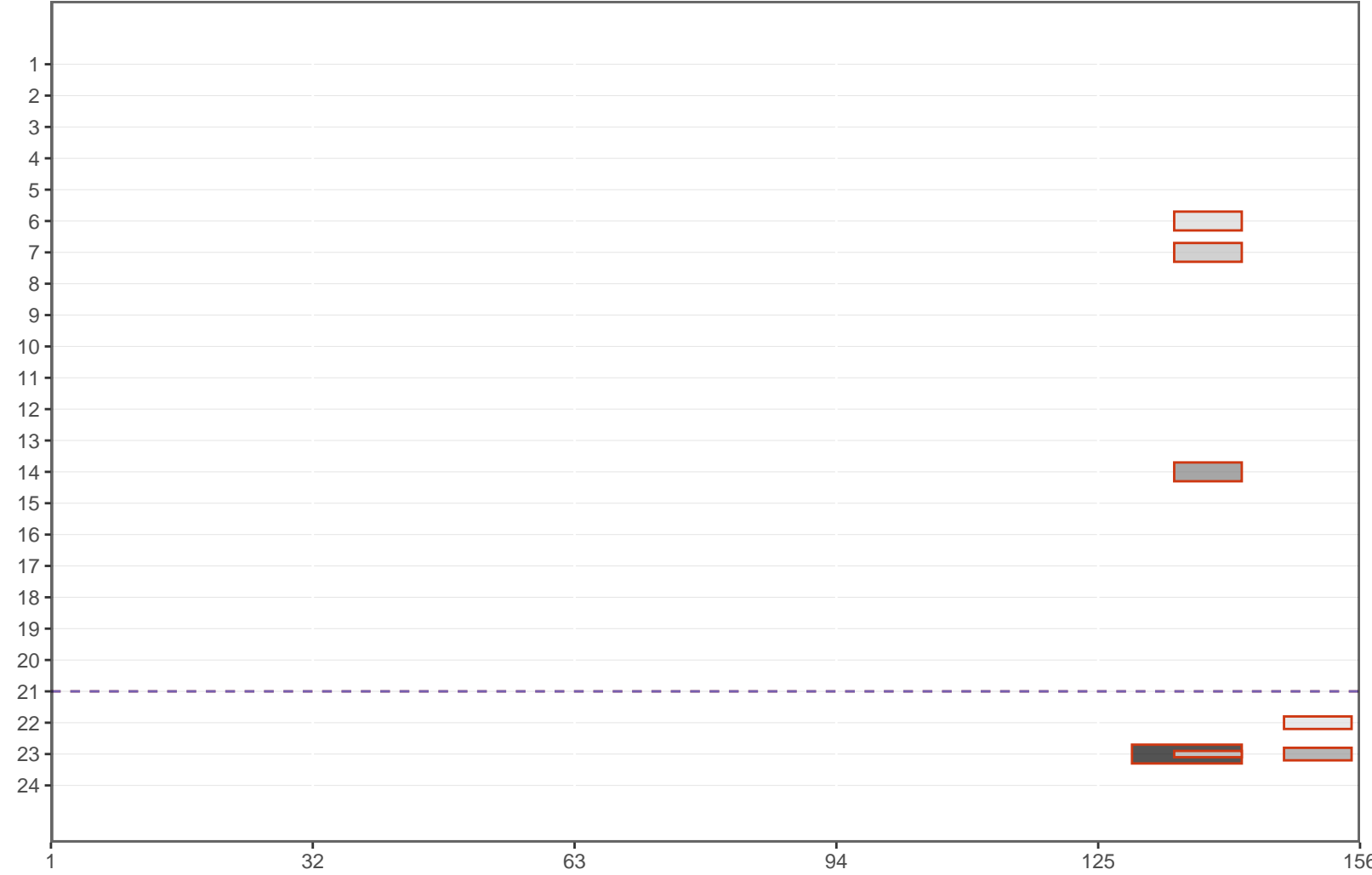
MW indication



Molecular weight

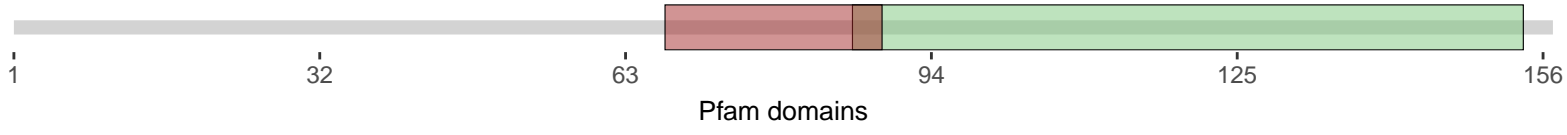


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SCAAFLVLTLLFLGFLVTEAVTGSAVELSPCAGATSPRRPSSGGSAALREGKPKLGGYLDKPNLRPIVNSPNAKRVAKSGGVPTPSC

NbL06g08370.1 GDSL_esterase/lipase_At1g29670-like [MW - SP = 37.24 kDa]

No. of times detected



log(intensity)



Values from



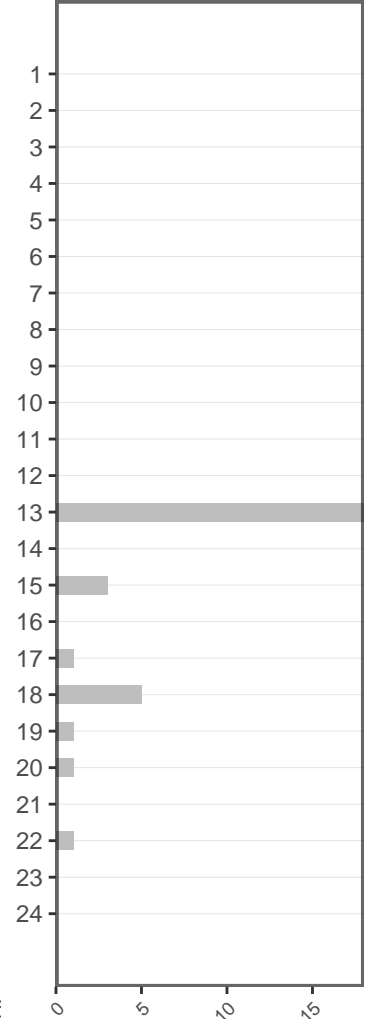
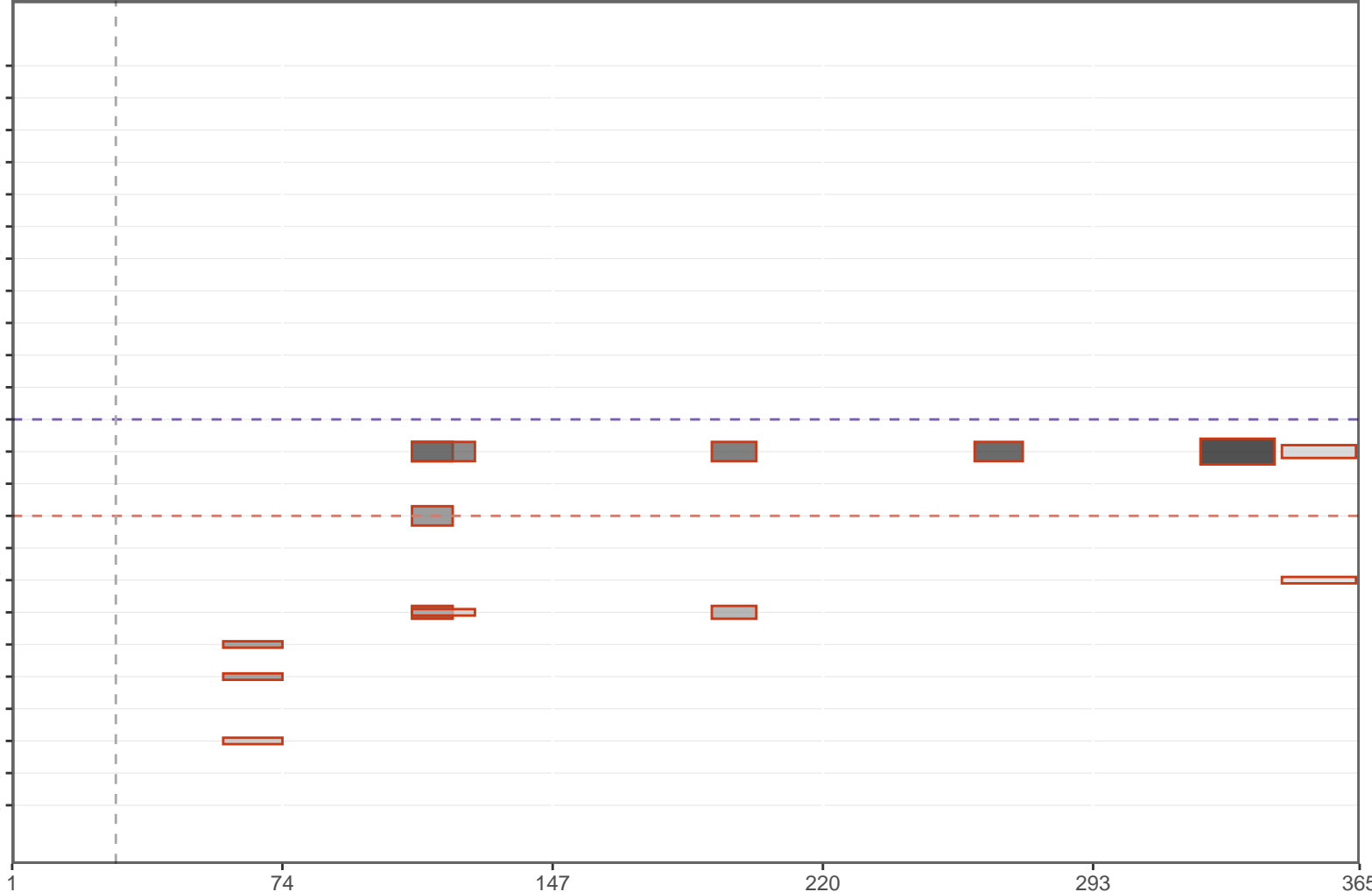
MW indication



Molecular weight

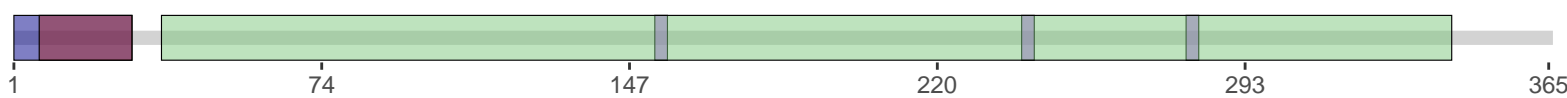


Gel Slice



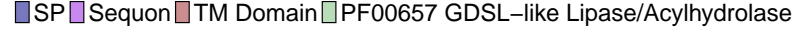
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MGNDYLNLYKPGFYLSRNLVTPDGFATVLRQFSEQLRTLVSYGARKWWSNIGLGGLPPELEEFGGNAGGCVDFNNYAKLFNDKLLKLLDNLNLPNARFIYKQTSISGGGPTPVGFTVDSSGGTSETAEGGGRIGEPGNSNRDGYIFFDNYHPTVEANMATARRSFNALLPSDAYPTDSDQLVDT

NbL06g08190.1 GDSL_esterase/lipase_At5g45910 [MW - SP = 38.42 kDa]

No. of times detected



log(intensity)



Values from



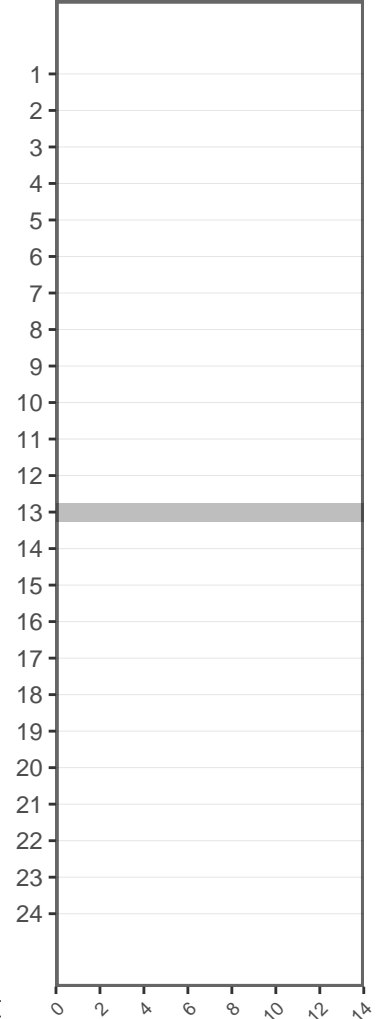
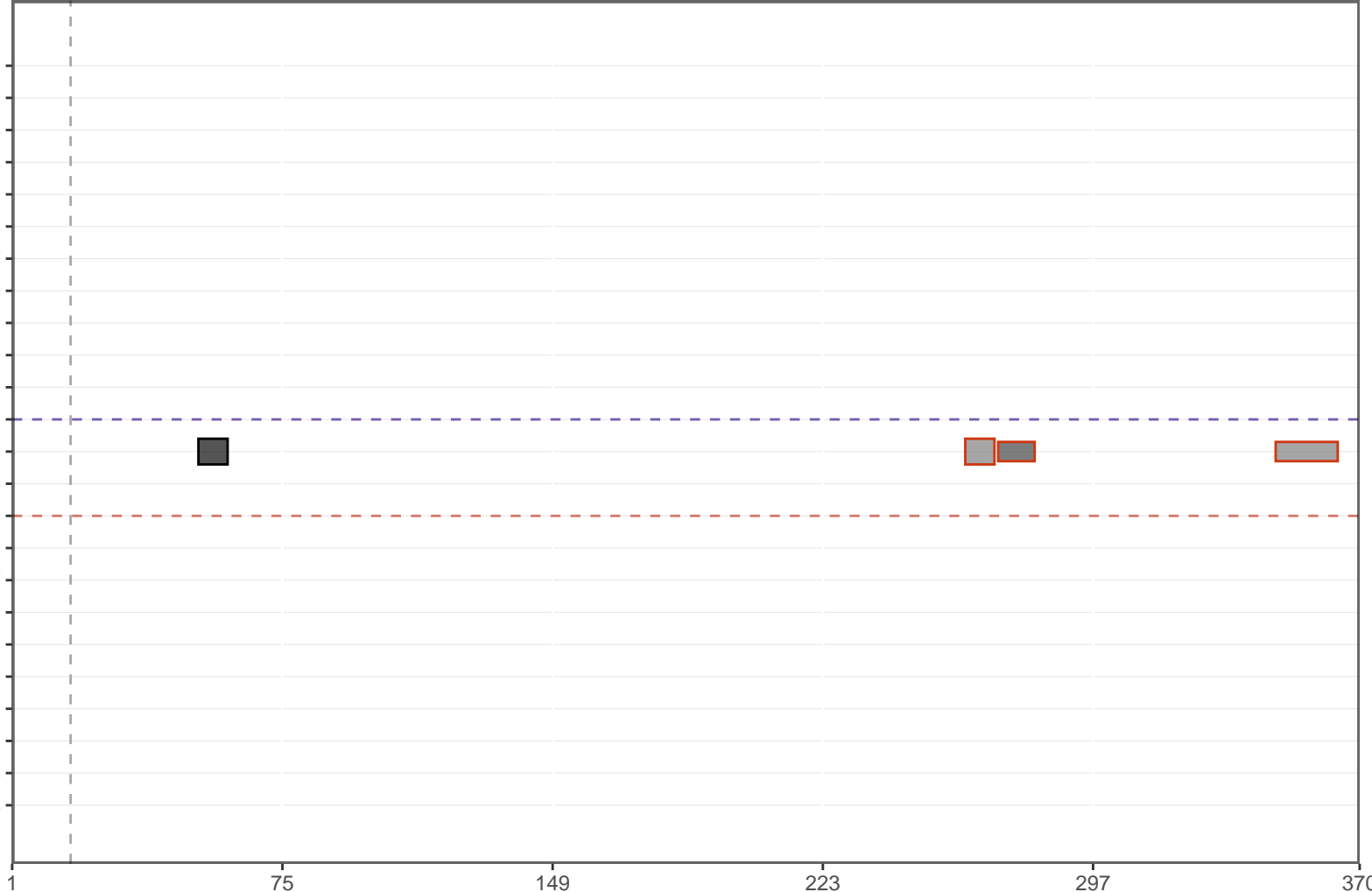
MW indication



Molecular weight

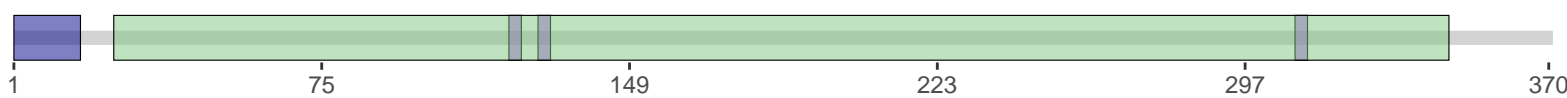


Gel Slice



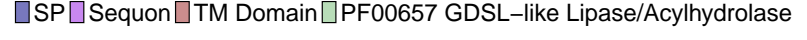
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

/P/YFVGGSIKLLKAVPRVIVETIEATSVLIEEGAVELVPGNLPGCBAYLTLFGTQNKAAVQKNGGLKTYNAFSKYHNAQLKLSLEKLEEVYHAKIIVADYVGAAKRFFHAPKHYGFSNTLVAGCGGGSPYFNFNNSARGHGGKAGLDTSKLANVWDGHLTEAVYHIAKGLLNGPFTSPPLTFSPKQKLT

NbL06g07940.1 epoxide_hydrolase_A-like [MW = 35.77 kDa]

No. of times detected



log(intensity)



Values from



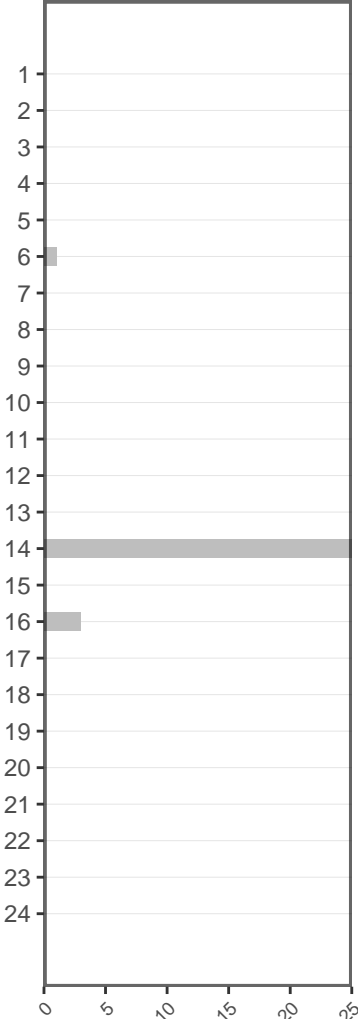
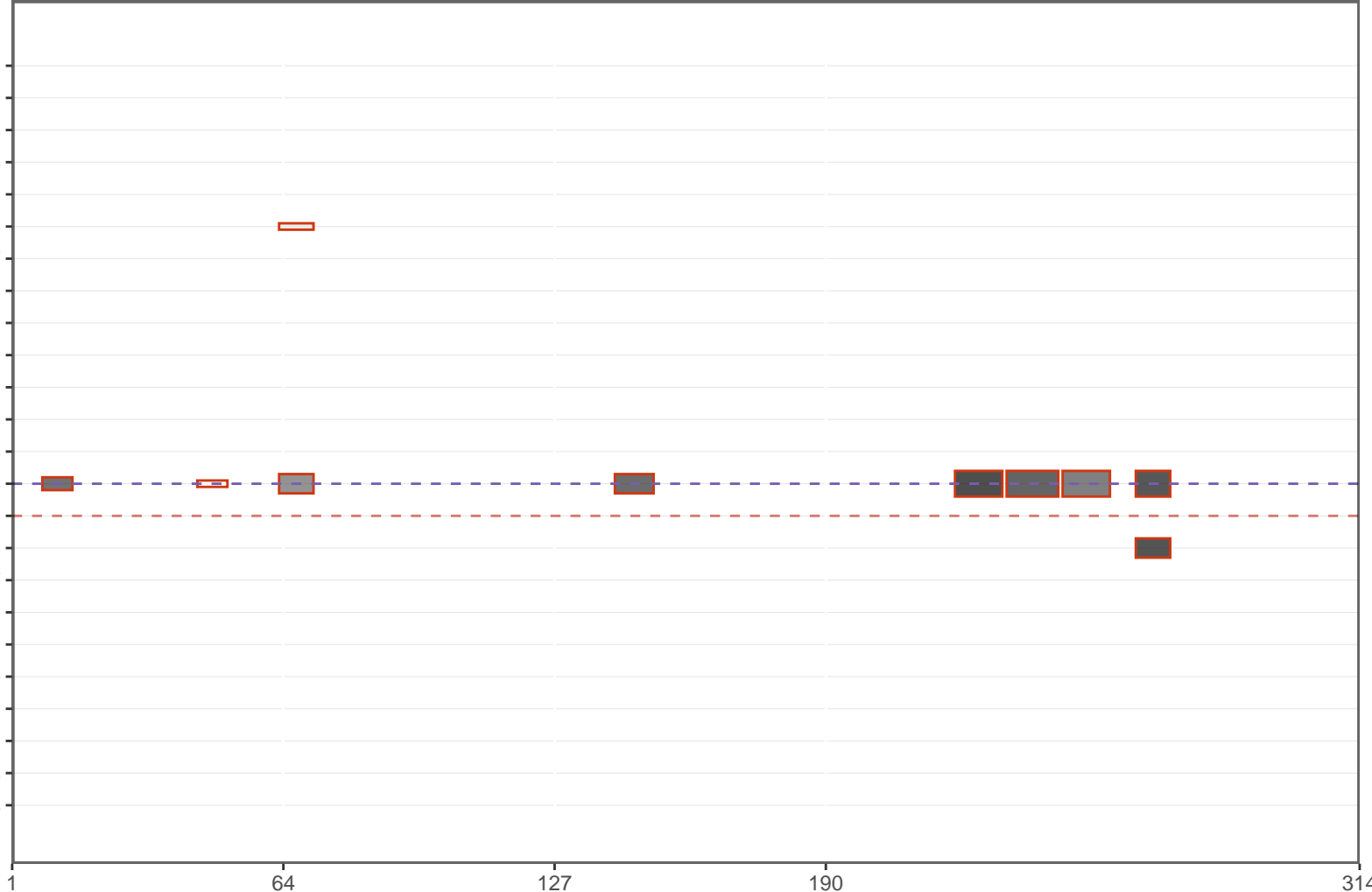
MW indication



Molecular weight

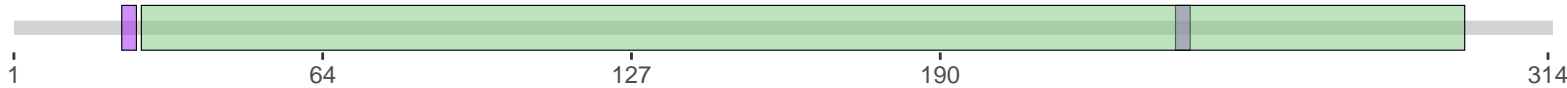


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

EGFYSRWRPQRAEADFGFRFDTKTKVIRKVIYLFRRSEIPIADENGEILDVEPSTLFFWFSEKDLAFYGLYKESGFLTALQVPIYRAMGEQLNLTADPKQVFPALLMGEKDVYKFFDIEGVTRSEKIKRFPNVEIIFMPEGTHFVDEGSPDEVNGQLLNFLHENS'

NbL06g07810.1 acylsugar_acyltransferase_3-like [MW = 36.87 kDa]

No. of times detected



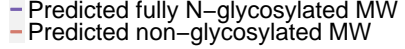
log(intensity)



Values from



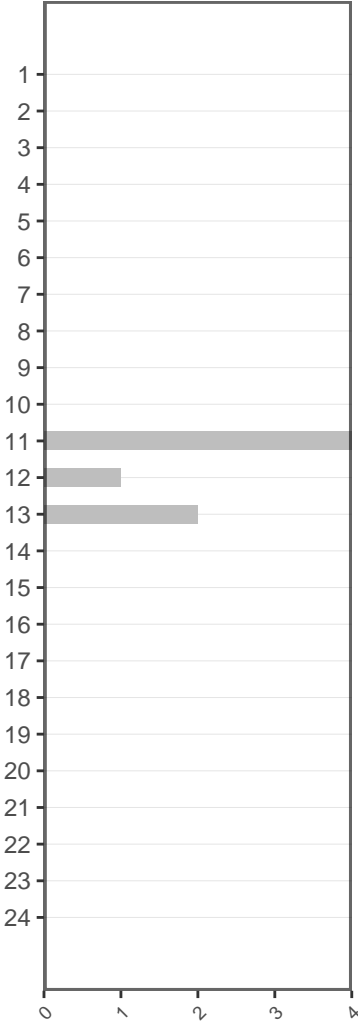
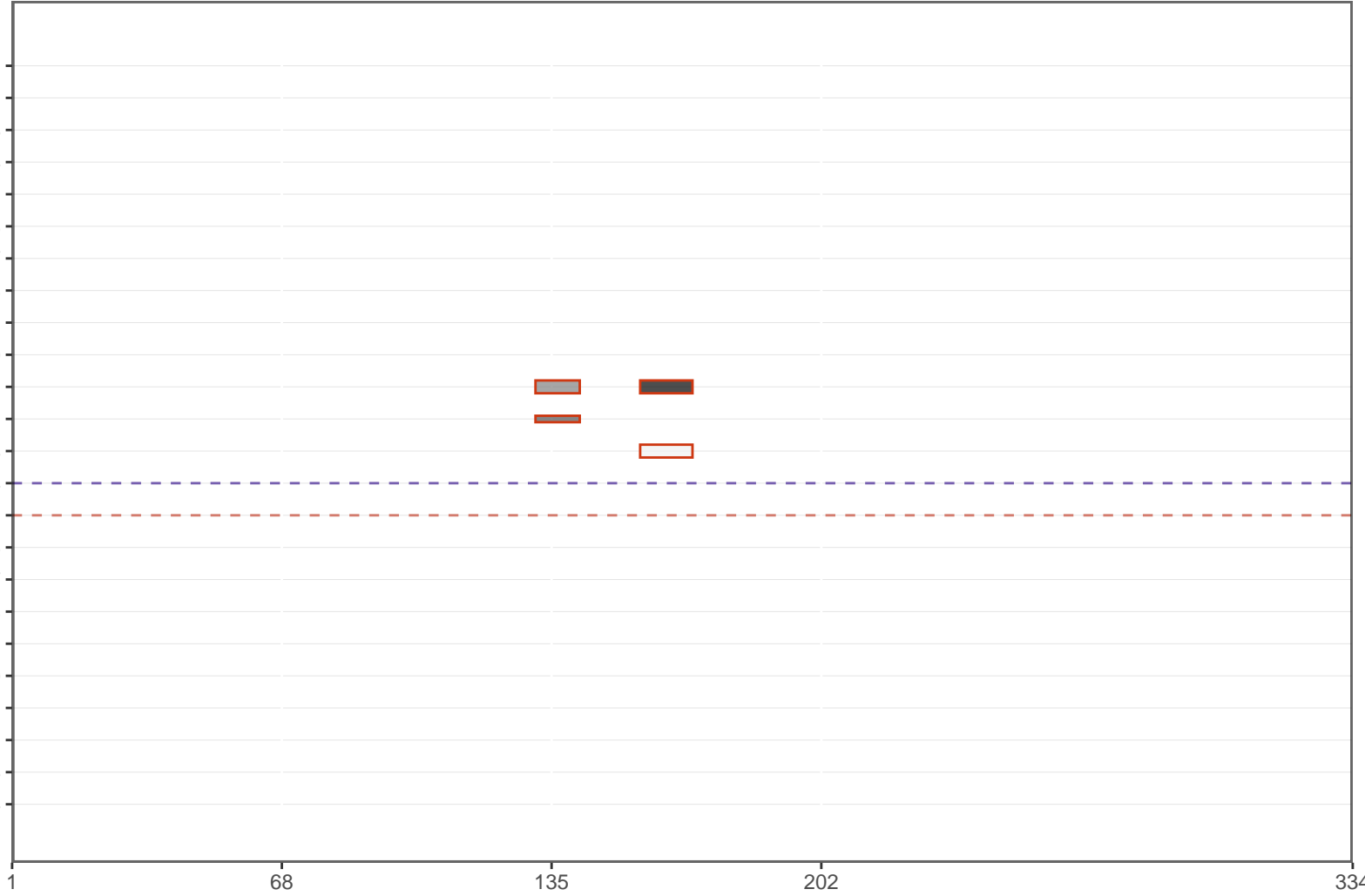
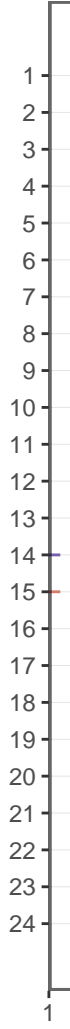
MW indication



Molecular weight

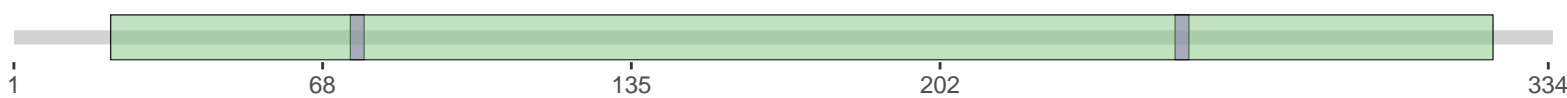


Gel Slice



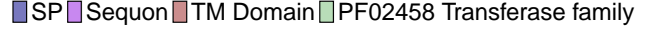
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

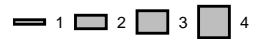


Protein sequence:

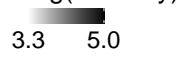
KAIAASSANIQPSKLVHFLNVRTMTKPRLRIRBAGNLSVFTTEATGDIELRPLVQNLKEVEVAYKKDGVNENELVLETVDGMKKGKLPFEKKAENSTMVFCGNVGGFPLVSVDFDVGKPERVCLANGPSKNIYFLKDYKSGGGVEARVMLEKHMSAFEGDEELLQFTS66VPL*

NbL06g07480.1 uncharacterized_GPI-anchored_protein_At1g61900-like [MW - SP = 45.73 kDa]

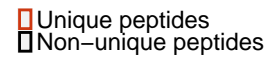
No. of times detected



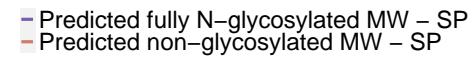
log(intensity)



Values from



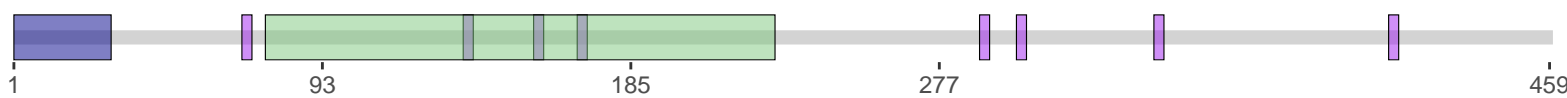
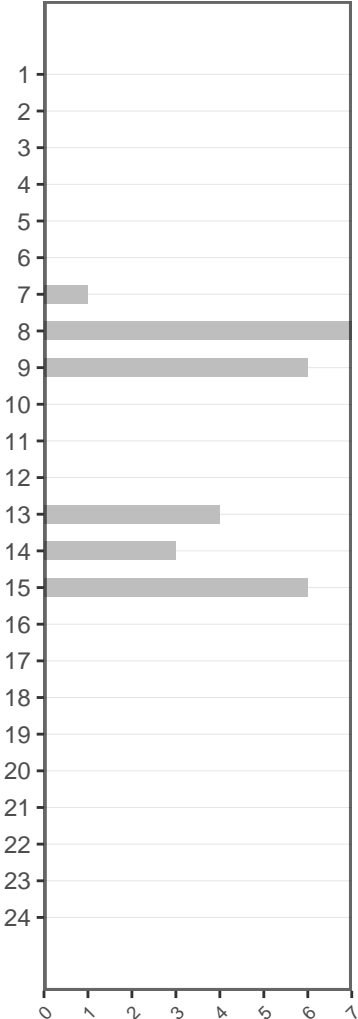
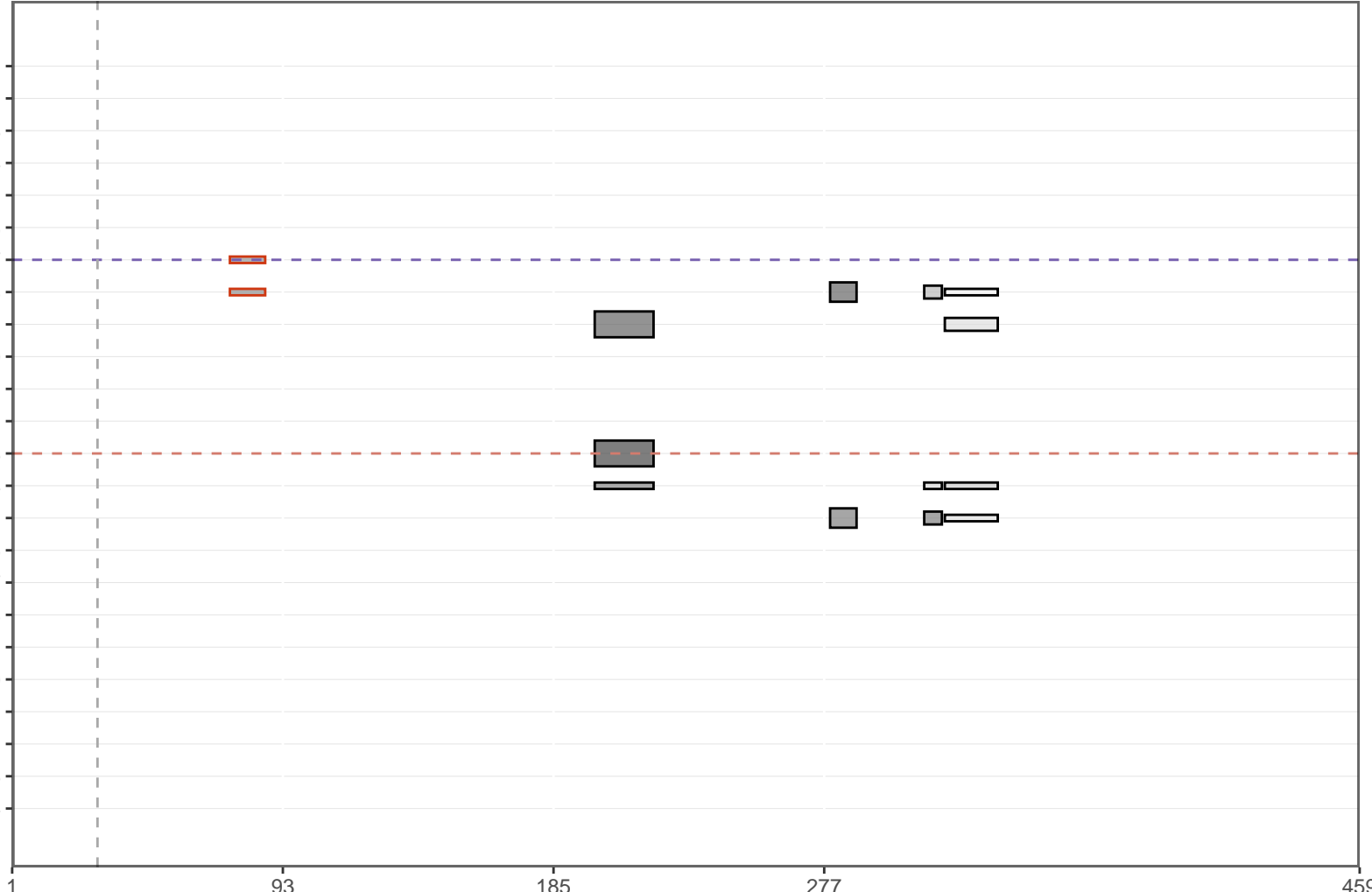
MW indication



Molecular weight



Gel Slice



Pfam Description
 SP Sequon TM Domain PF19160 SPARK

Protein sequence:

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NbL06g07470.1 UPF0051_protein_ABCI8_chloroplastic-like [MW = 61.18 kDa]

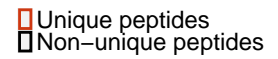
No. of times detected



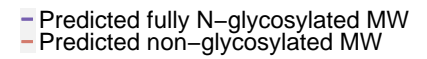
log(intensity)



Values from



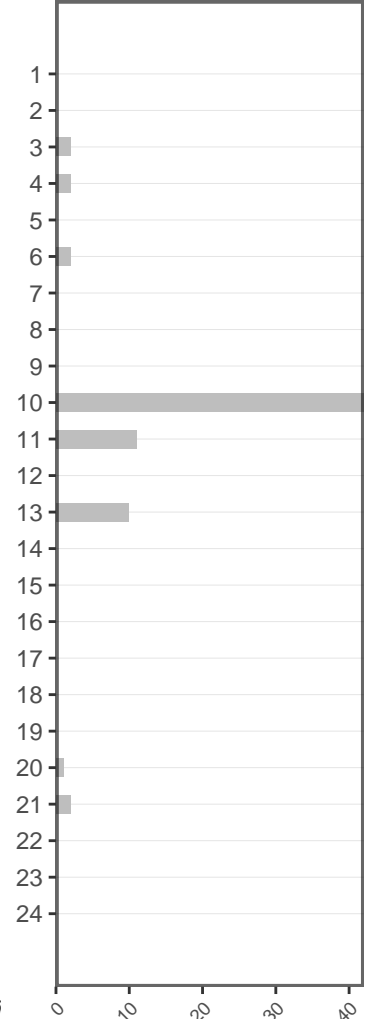
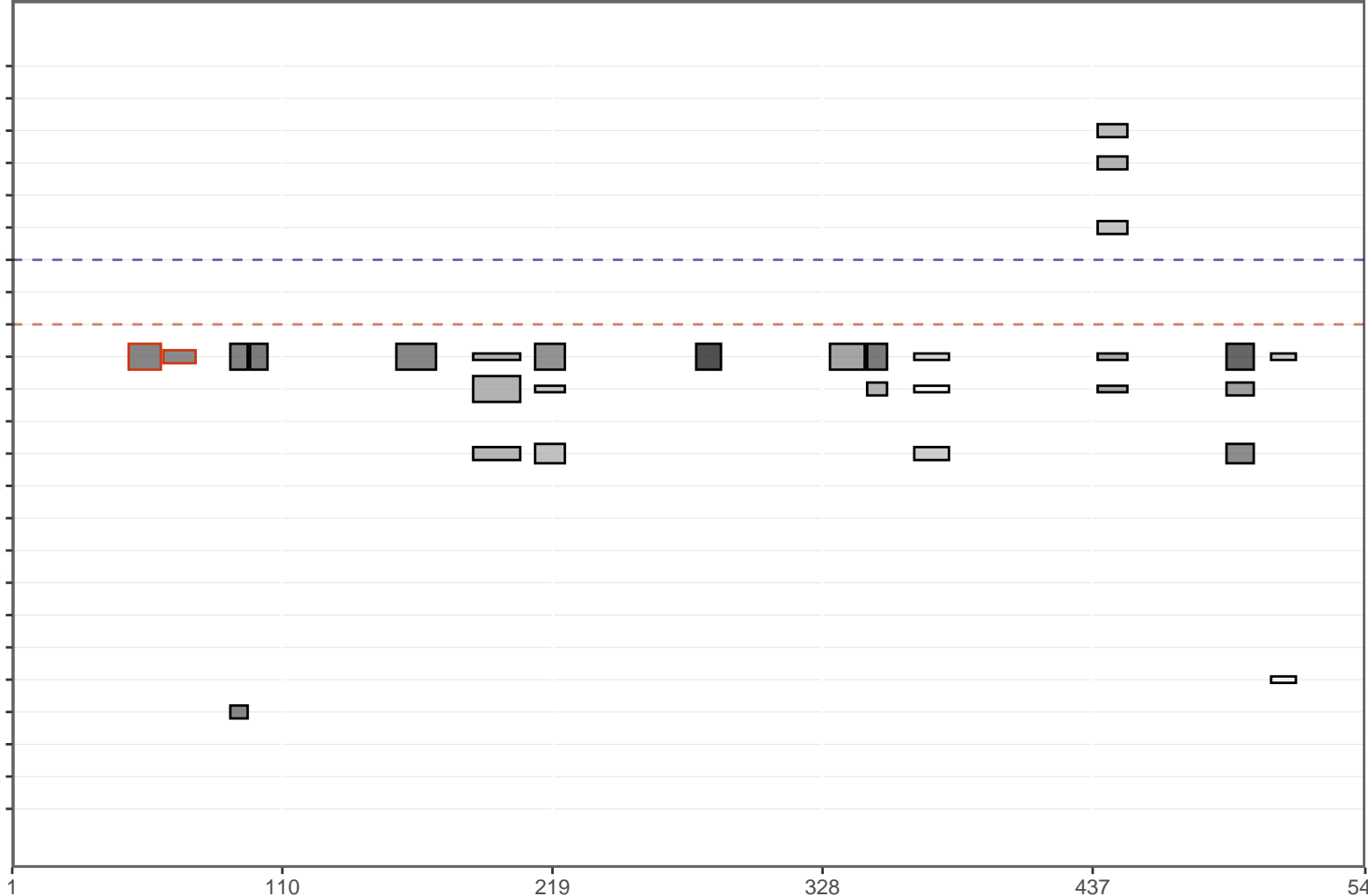
MW indication



Molecular weight



Gel Slice



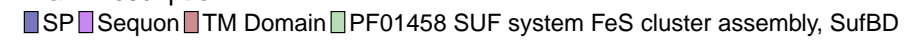
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

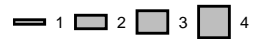


Protein sequence:

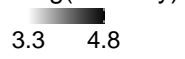
KNTRCPMQISTYFRINAMETGGFERTLIHAEESGFEVLEGGTAPVDNQLHAAVVELVCEEGEAERIKYSTVQNVYAGDEEGKGGHNFVTKRGLGAGARSKISWTSQVETGSAITWYKPSVLEEGDESVGFYSLVNTNNGQADTGMHMKGNKTRSRISKIGSAGHSRNCYRGLVGLNENAKNNS60GDSMLIGDSAAANTYPPVIGSKNPTARIEHATTSKIGEDGLFYDQGRGIEYKMAAMMSGFGDRDVFNELPDEFGEAEVNGMLSKLEGSVQ*

NbL06g07450.1 polyadenylate-binding_protein_RBP45-like [MW = 46.33 kDa]

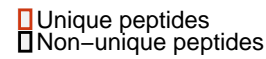
No. of times detected



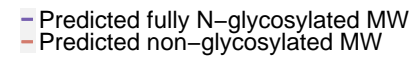
log(intensity)



Values from

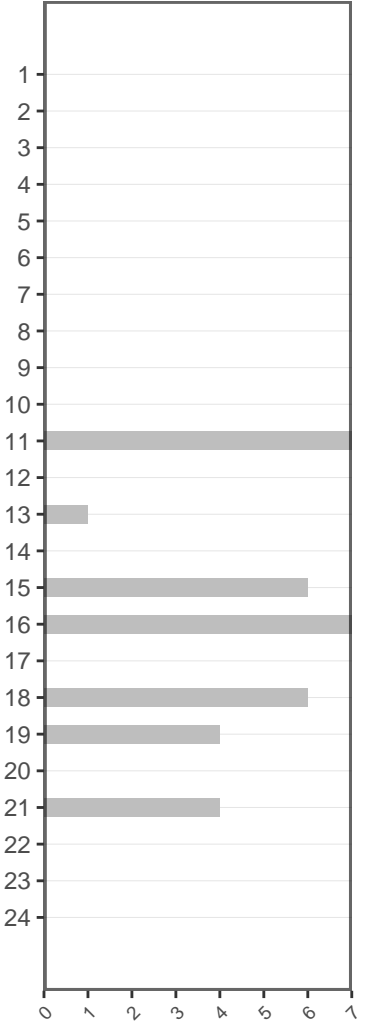
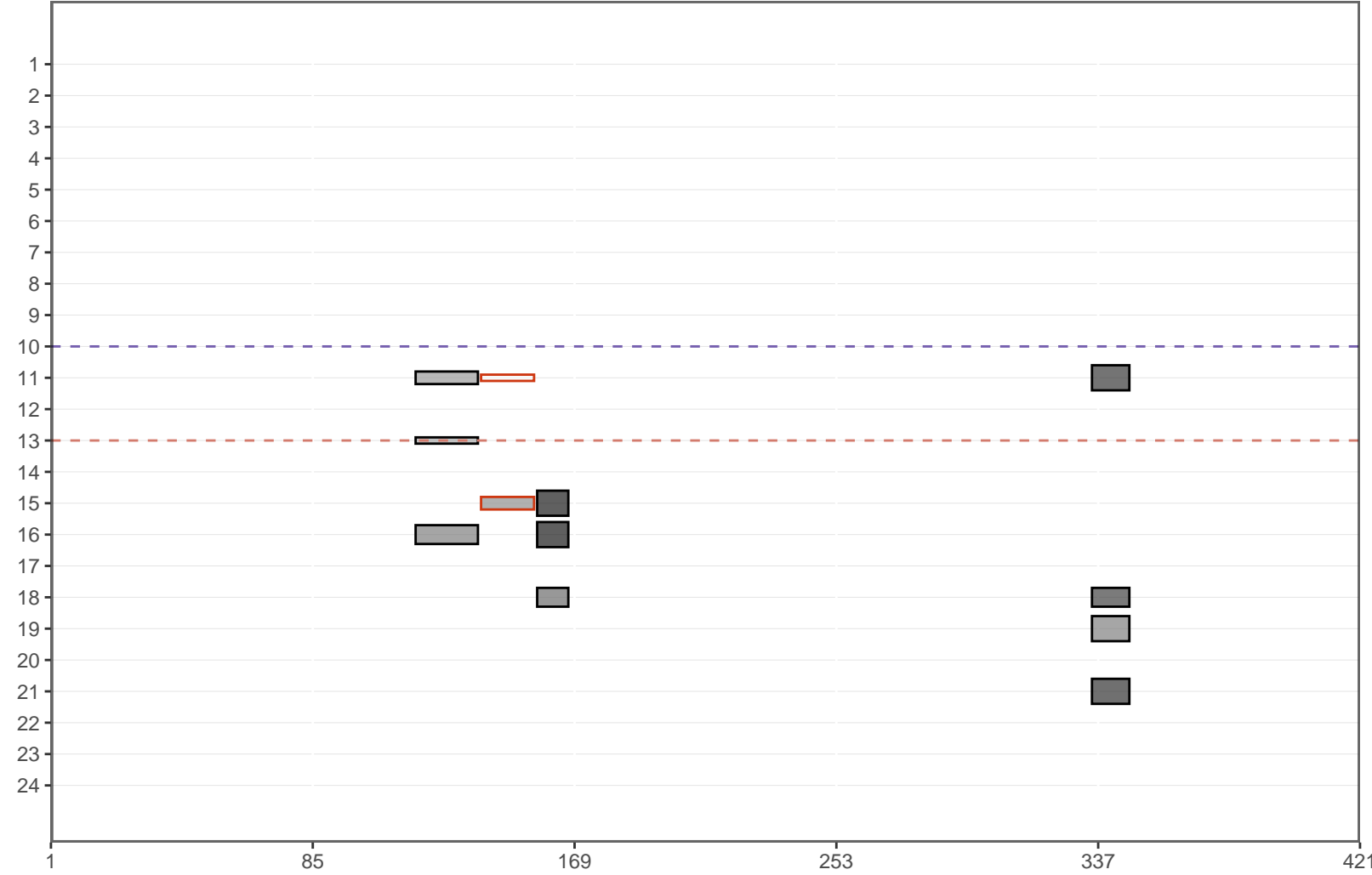


MW indication



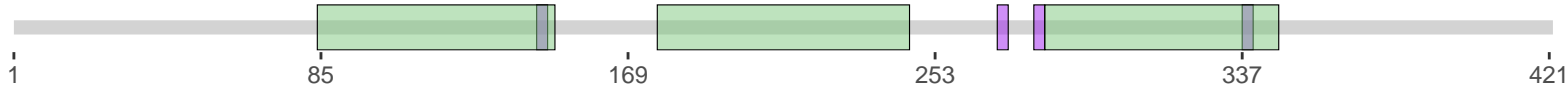
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SYPSPVKGAKVYTDVITGRTKGYGFVFKGDESEGLRAMTEMNKGKFGSTRFMRIGPANKNNSVAGGVDASVIGSTNGTQNEDDPNTTFIVGNLDSQVTDHILRQVFGVHLDLHVPVQKRCGFVDFADRSCAEAEALRVLNGTQLGGQIRLSWGRSPSNKQVYQPGADFNQWNSGGYFYGTAGYDAAAAVGAQAGDPNLYVWAGVGNYPFGQGGQGPQ

NbL06g07410.1 vacuolar_protein_sorting-associated_protein_28_homolog_2-like [MW = 23.36 kDa]

No. of times detected



log(intensity)



Values from



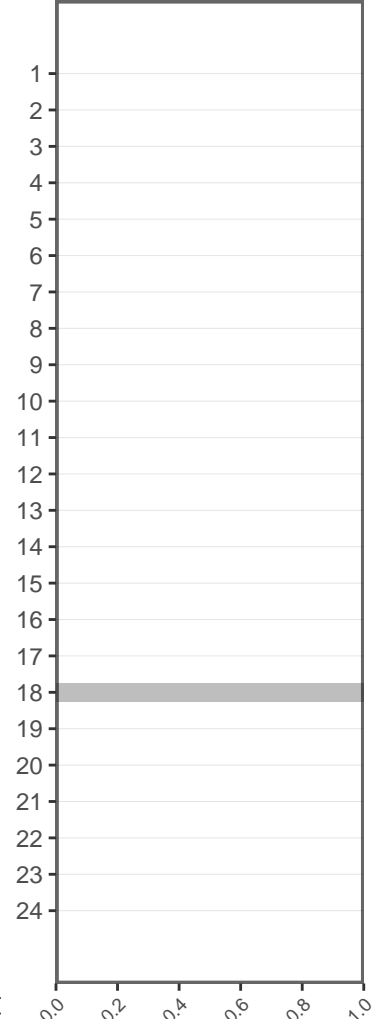
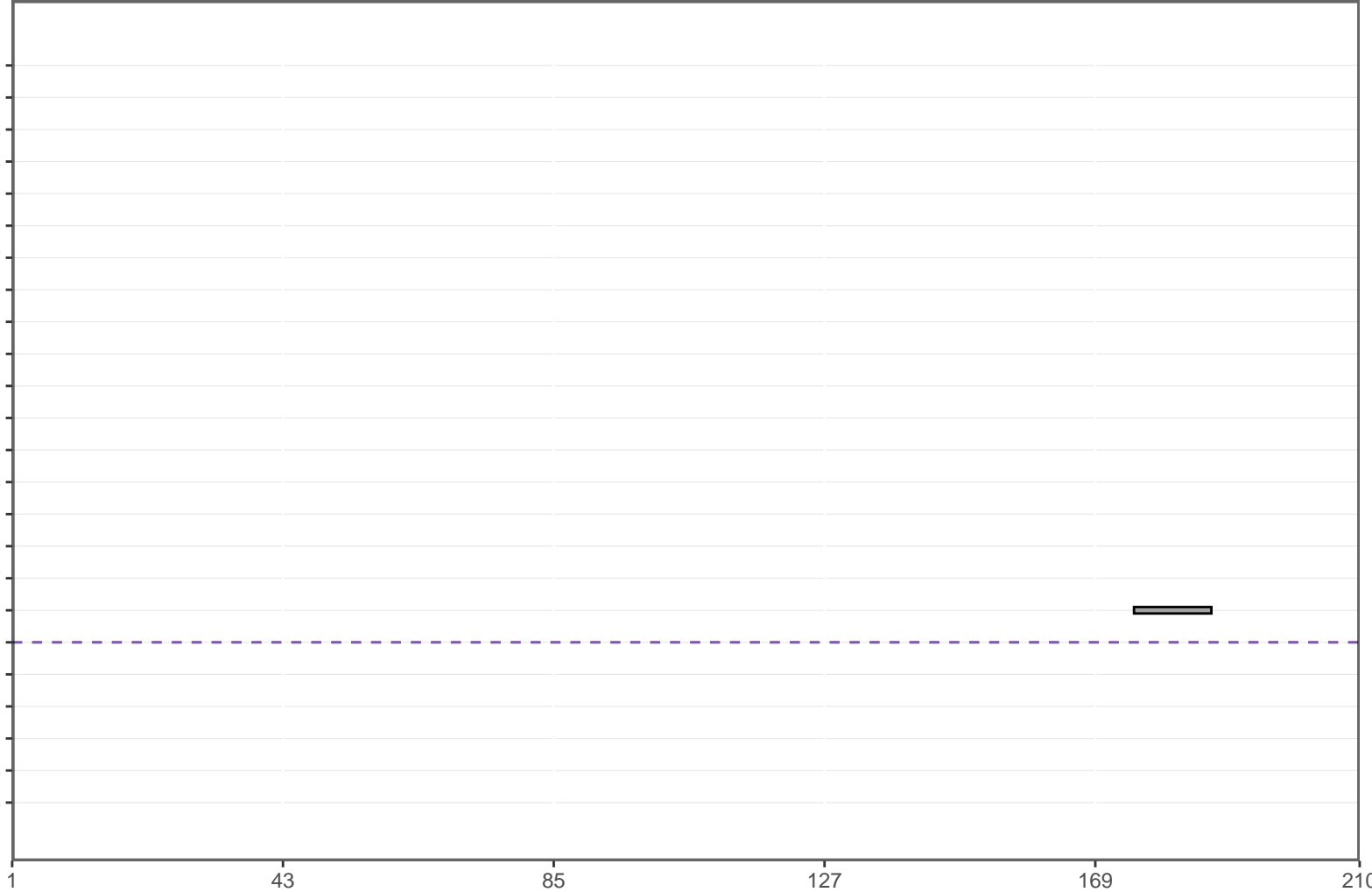
MW indication



Molecular weight

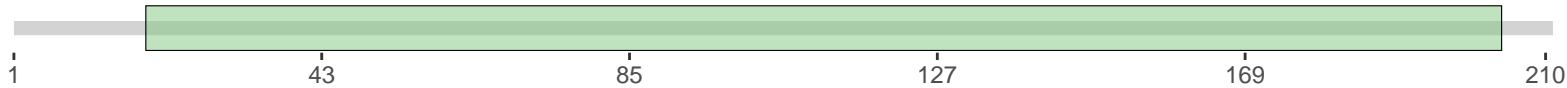


Gel Slice



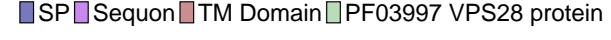
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

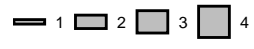


Protein sequence:

/P/ATVEHRAAASMSAITSAAVAECVGNFTAMDGLKLNMAVDGWHPLLELGGSLNKLKSLPVDFFGKTRMREWL SRLSKMGAADELTEGGARGLHFDLEGGVNSFMAALPTDGT*

NbL06g07300.1 eukaryotic_translation_initiation_factor_4E-1-like [MW = 24.79 kDa]

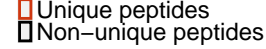
No. of times detected



log(intensity)



Values from



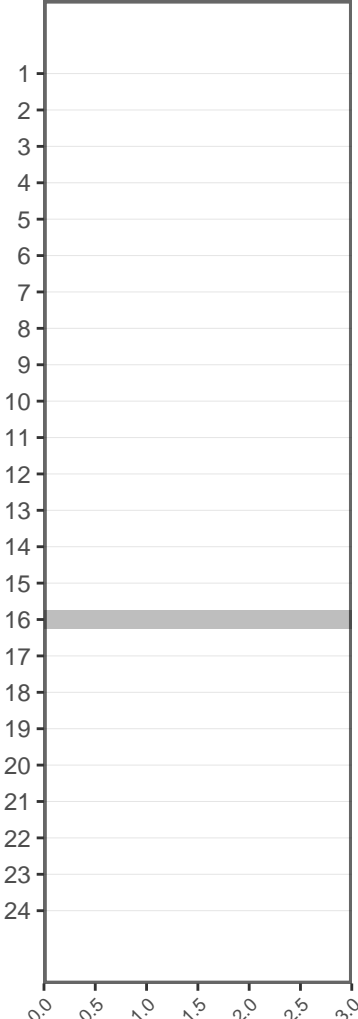
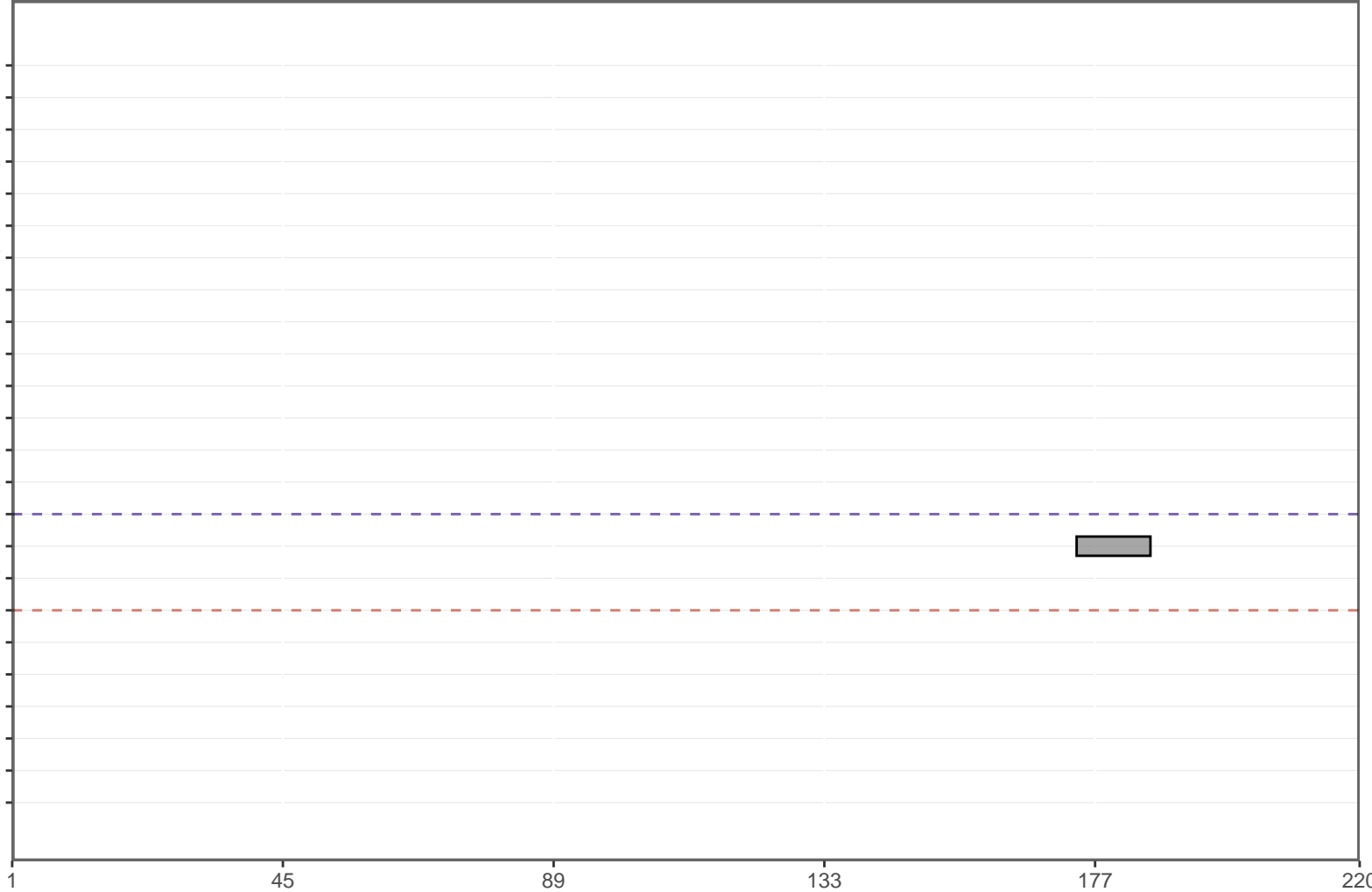
MW indication



Molecular weight



Gel Slice

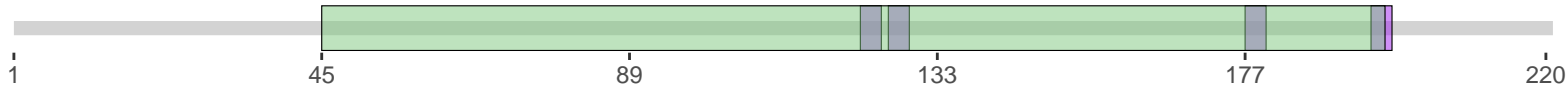


Peptide counts over 4 repeats

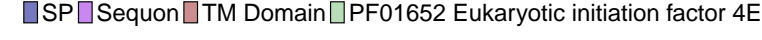
Protein length



Pfam domains



Pfam Description



Protein sequence:

IGADHCFKHTPEPKWEDPVCADGGNWTMNFSGKGSQTSWLYFLAMIGHQFDHHEEEKGGAVVSVIRNKGDKIALWTKNAANETAGVSGKQWKEFLDYNSSIGFTFHVDSMRLRGRGAKNSYTV

NbL06g06640.1 polyphenol_oxidase_E_chloroplastic-like [MW = 67.04 kDa]

No. of times detected



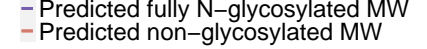
log(intensity)



Values from



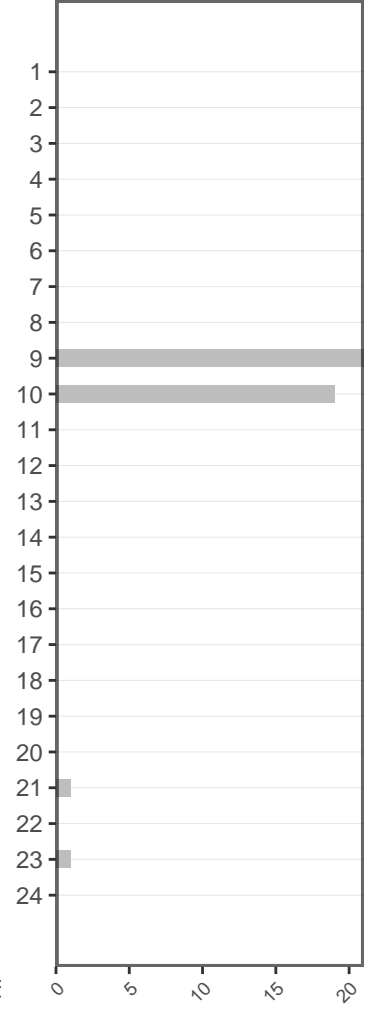
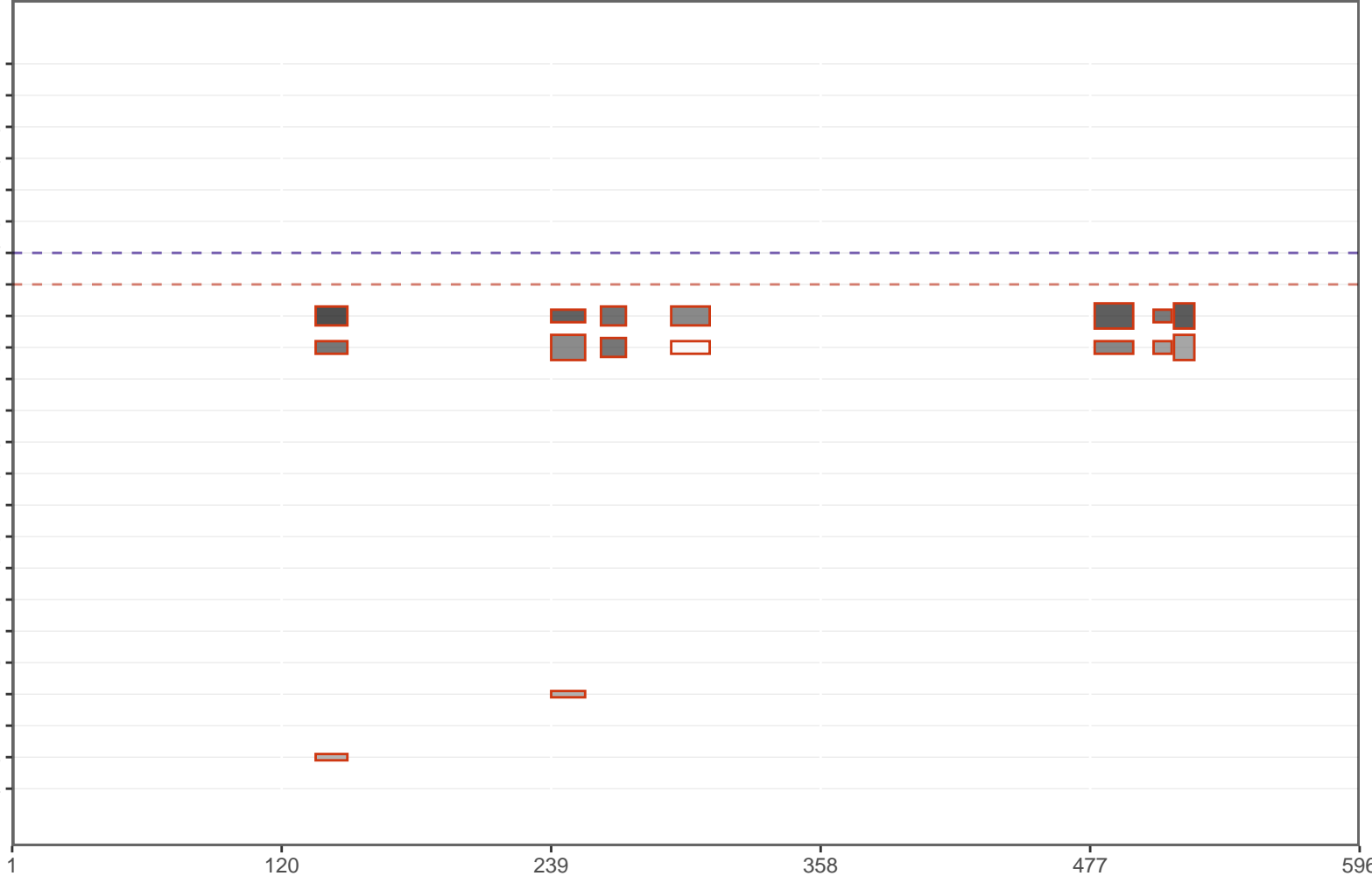
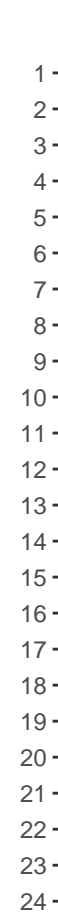
MW indication



Molecular weight

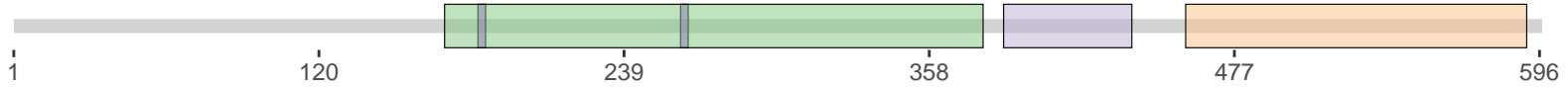


Gel Slice



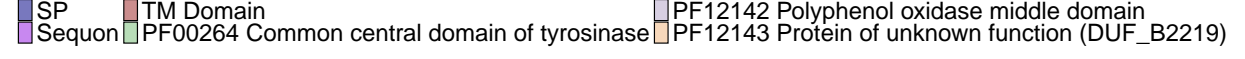
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

JLMYROMITNAPCLLFFGEPYRFGSKPNPGGGTIEHPHTFVHHWTGTVOGTDLGNQVYKSGEDMGNFYKAGLDPVFYSHMANVDRMWNKWKGLGGRKRDLDKDWLNSEFFFYDENRDPWRVYKVRDCLDKRKMGGVYDKPKATPWRFKPKGKTTDPGKYNLRGKVPKSKVPLSNLDRACFSIERPATSRRGGQDKDFEEVLTNNLKYDDSKYKFDVFINADKTVNAGDQDQKEVAGSSTLPHVHGPNATASHAVEVEKFLATELLEDGLEDITIAVTVPI

NbL06g06540.1 branched-chain-amino-acid_aminotransferase_2_chloroplastic-like [MW = 35.11 kDa]

No. of times detected



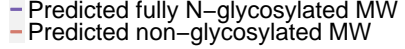
log(intensity)



Values from

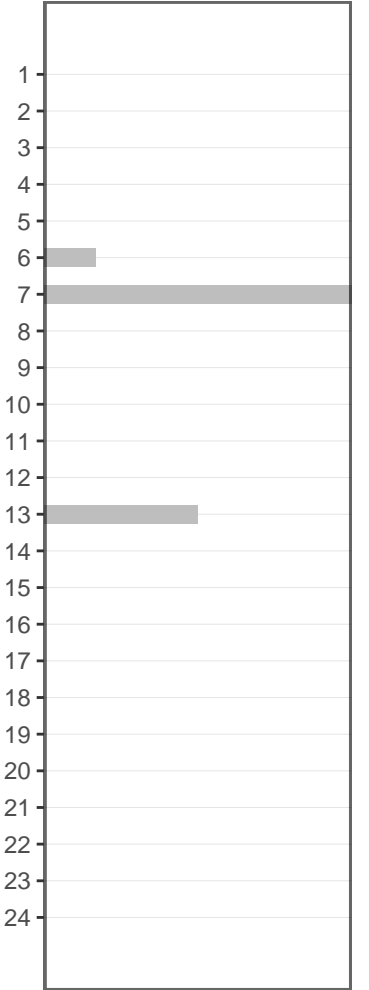
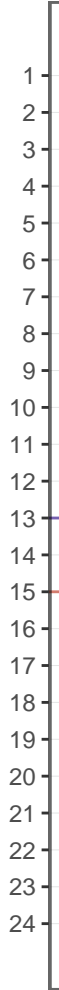


MW indication



Molecular weight

Gel Slice



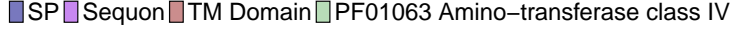
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

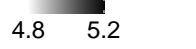
PTLVYEEHHRRASQEGAGGVKBITNYGPKLKAIRAKRERGVSDVLYLDVNNRYIEEVSAAANFLVGRVATPIPGDTLEGITRKSDDIAHDLGVQVEERLIEAEELTADVEVFGTGTALGWPIGSDTKNKRREKYSSELISEQVNTFLVAGKGIIEKDRDWVLEIK

NbL06g06470.1 tubulin_alpha-3_chain [MW = 49.74 kDa]

No. of times detected



log(intensity)



Values from



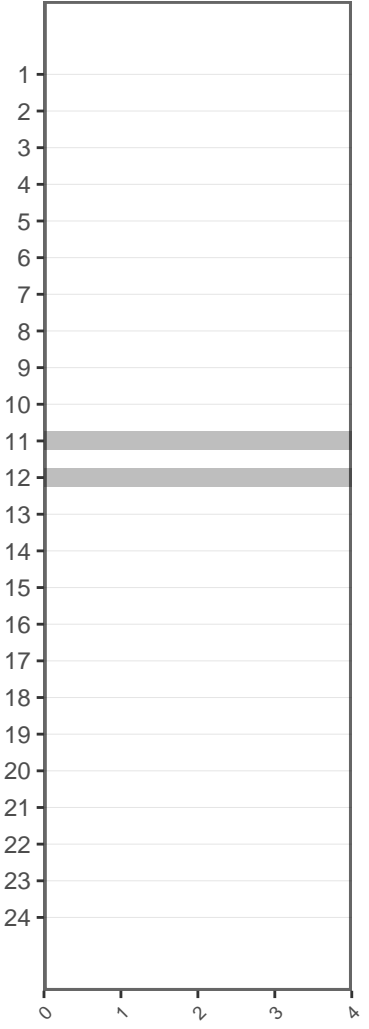
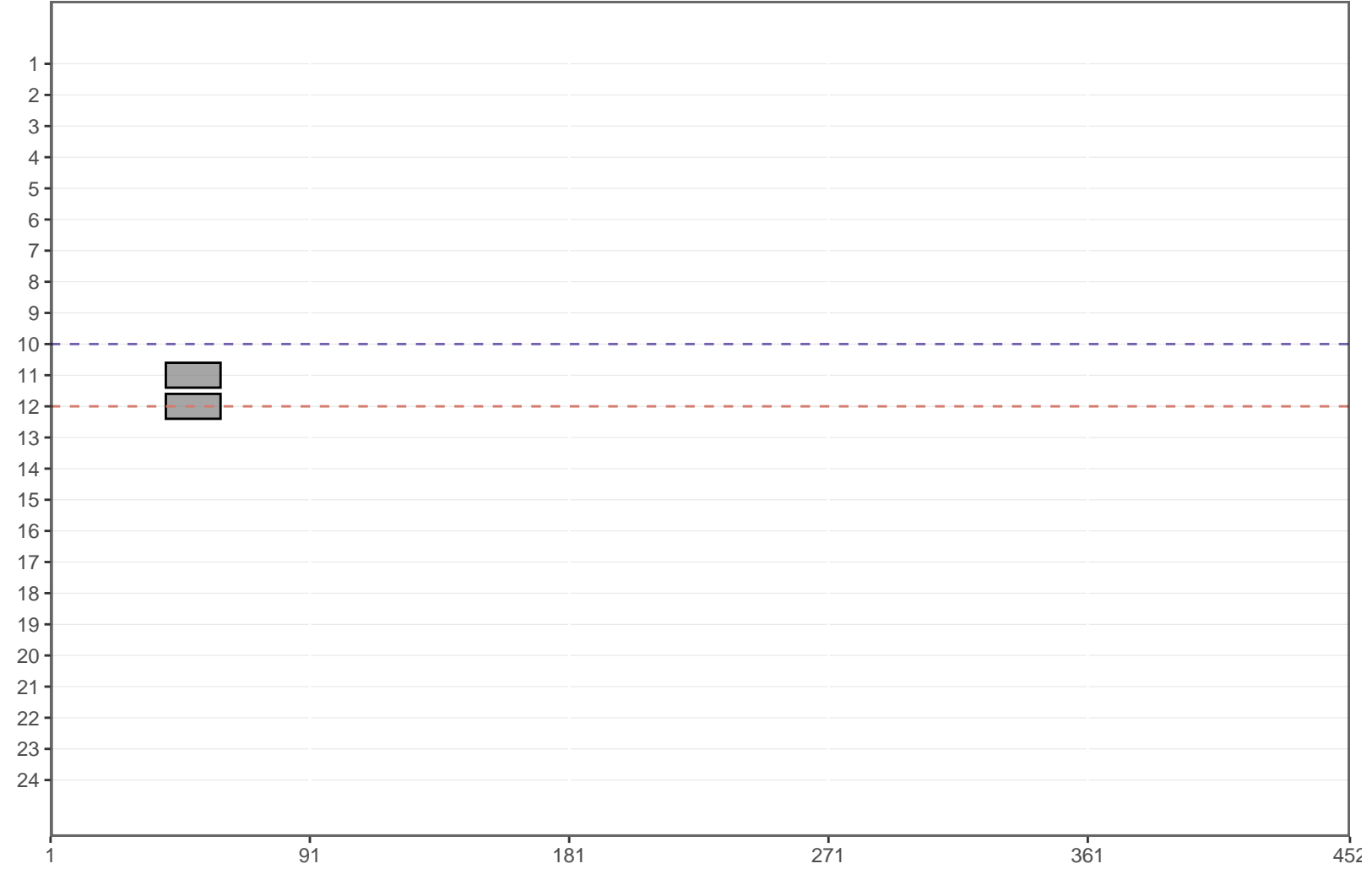
MW indication



Molecular weight

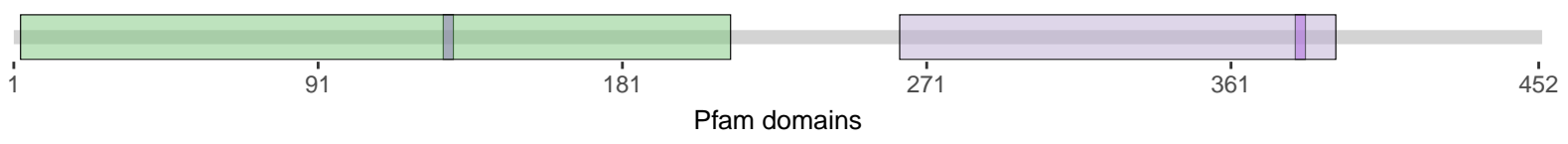


Gel Slice

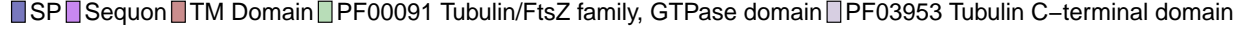


Protein length

Peptide counts over 4 repeats



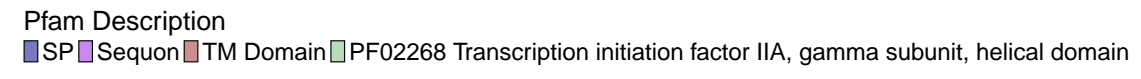
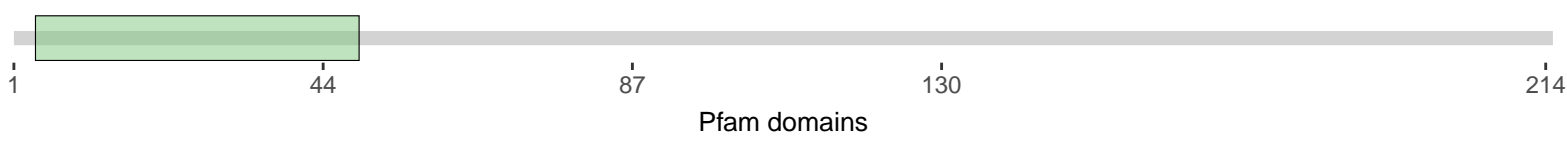
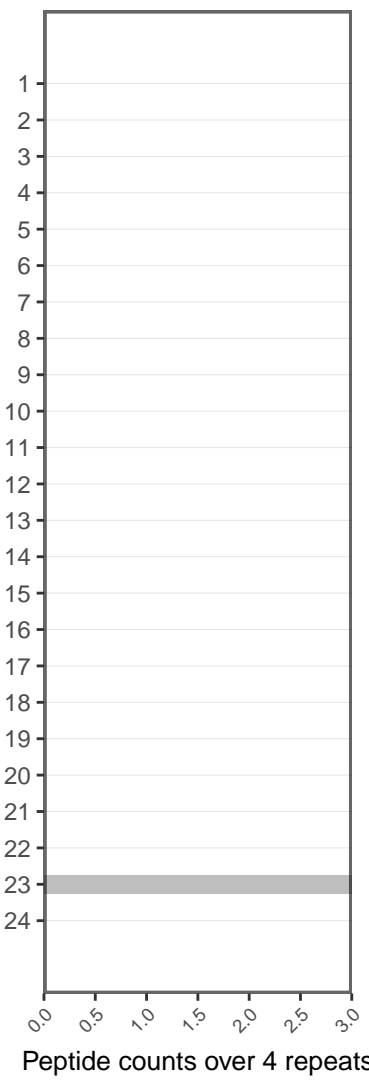
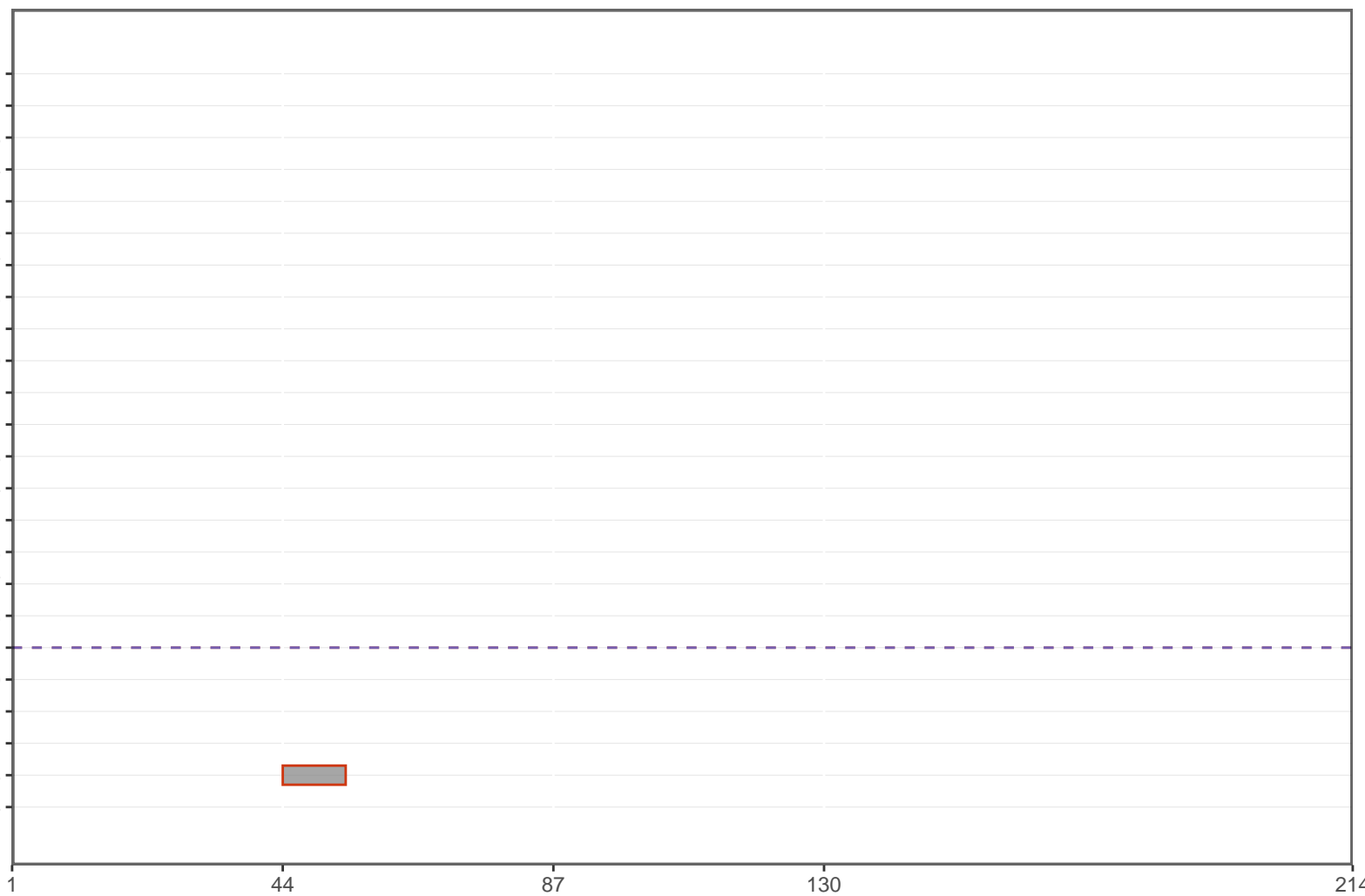
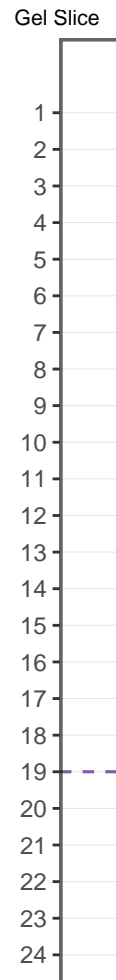
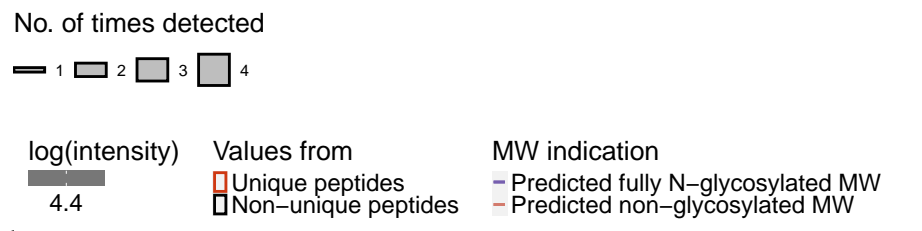
Pfam Description



Protein sequence:

RSLDIERPTYTLNRLISQVHSLTASLRFDGALNVDVNEFGNLVPPRIHFMLSSYAPVBEAKYHEQLSVAEFTNSAFEPSSMMVXGDRPHKGYMAGGLMFRGDVAPKQVNAVAATKTRTQFDVDCPTGFKDGINVGPPTVPGGDLAKVQRAVCMISNSTSVAEFTSRIDHKFDLMYAKRAEVHVVYEGEGMEEGEFSEARDLAALEKDIIEEVGAEVDDEEGGDEGDEV

NbL06g06400.1 transcription_initiation_factor_IIA_subunit_2 [MW = 24.11 kDa]



Protein sequence:
 MSVRDIFPTDSVYTMCGPLSYKMLGSRANKRRLAALRLWHVYFGSGHSEKAADGGNLFQIGISFNEIDVREIWEQRMGGKGDYHSGVSRQPFTEFVYFQSKHLQLSVKLLYL

NbL06g06340.1 aspartyl_protease_AED3-like [MW - SP = 44.55 kDa]

No. of times detected



log(intensity)



Values from



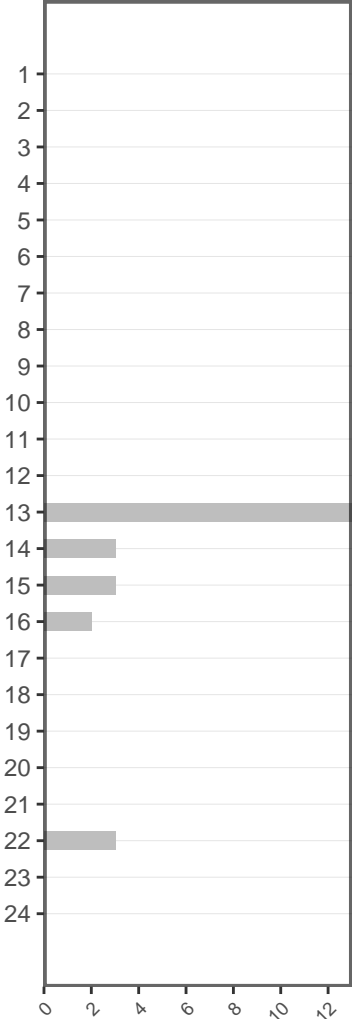
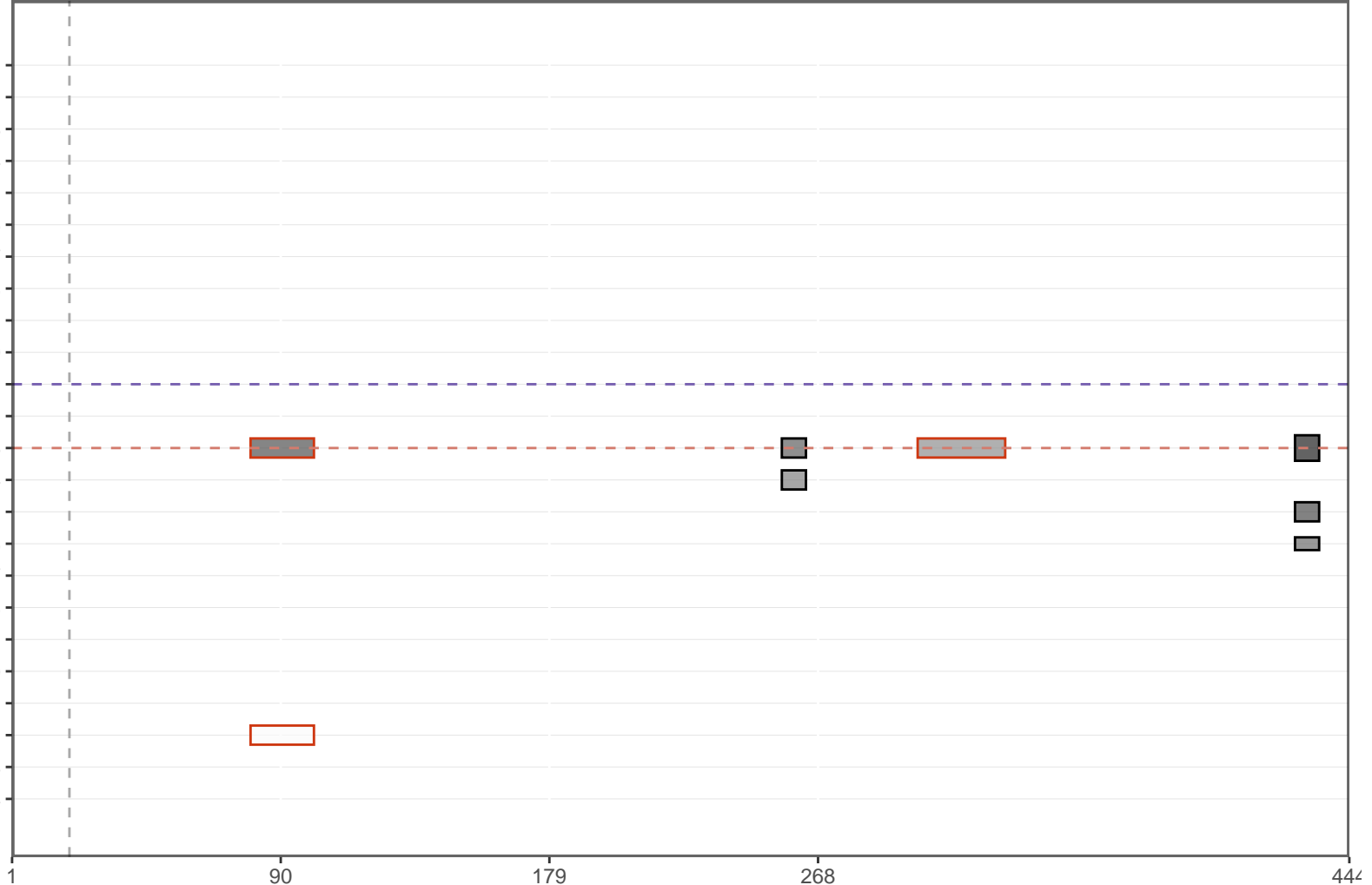
MW indication



Molecular weight



Gel Slice

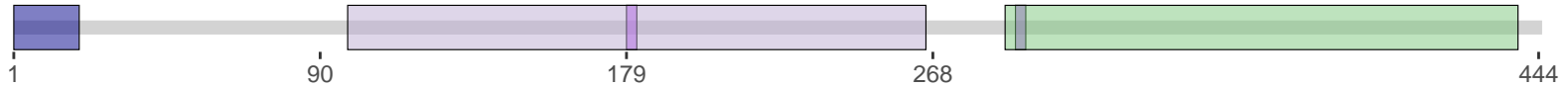


Protein length

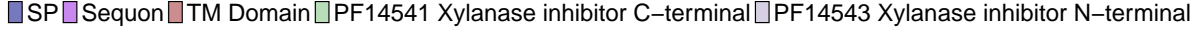


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

AFGCISAVSGNAIPFQGLLGLGRGTMLM9GSGSLYSVGVFSLPFSKSYVYFSGSLKLGPLGPKKTTPLLNPRRPSLYVYVNLTSVGVGRILVPAEPLGDFDNTGAGTIDGGTITRFVPPWNAIRDEFKQVKGKPFSSLGAFDTGFAFASNEAGAPKILTFEGMDLKLPMENTLHBSATPLACLAMAAAPSNVNEVLNVAIANLQGGNLRILFDTANRVIAREVEN

NbL06g06090.1 14-3-3-like_protein_B [MW = 30.88 kDa]

No. of times detected



log(intensity)



Values from



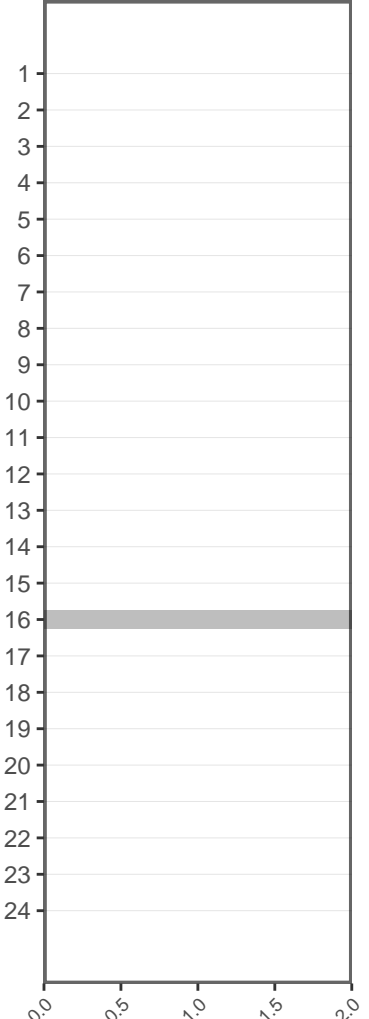
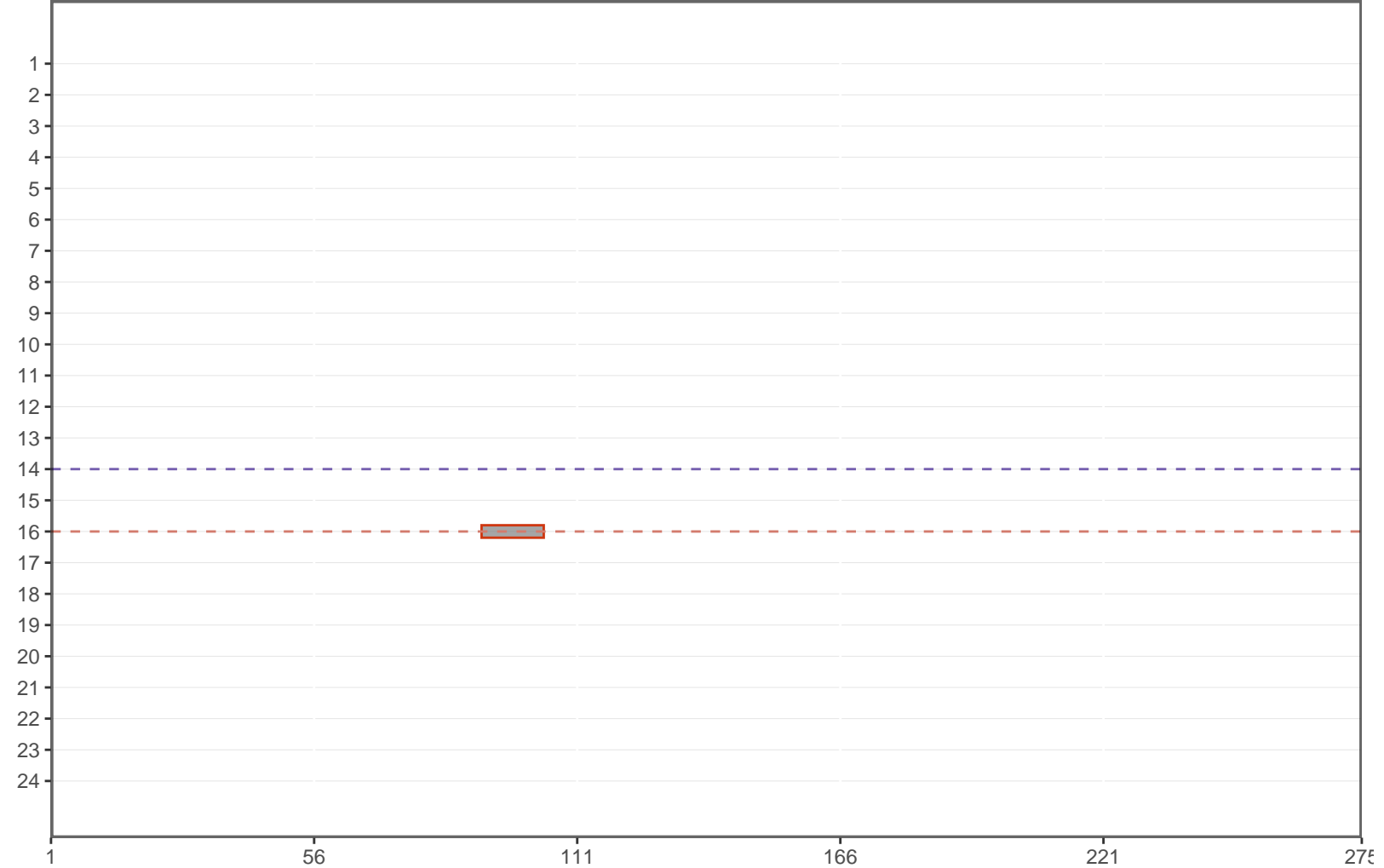
MW indication



Molecular weight

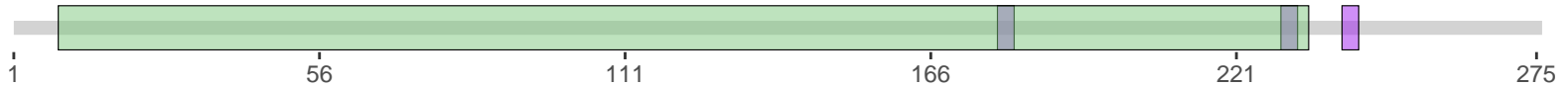


Gel Slice



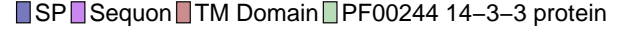
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL06g05820.1 fructose-16-bisphosphatase_cytosolic-like [MW = 34.22 kDa]

No. of times detected



log(intensity)



Values from



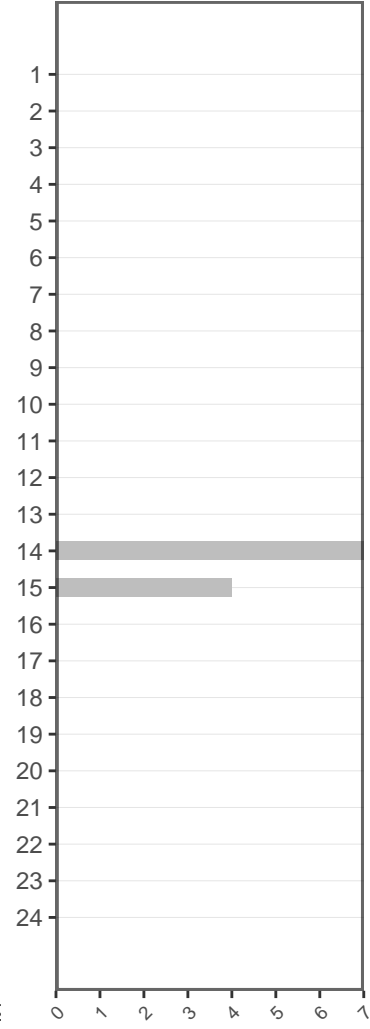
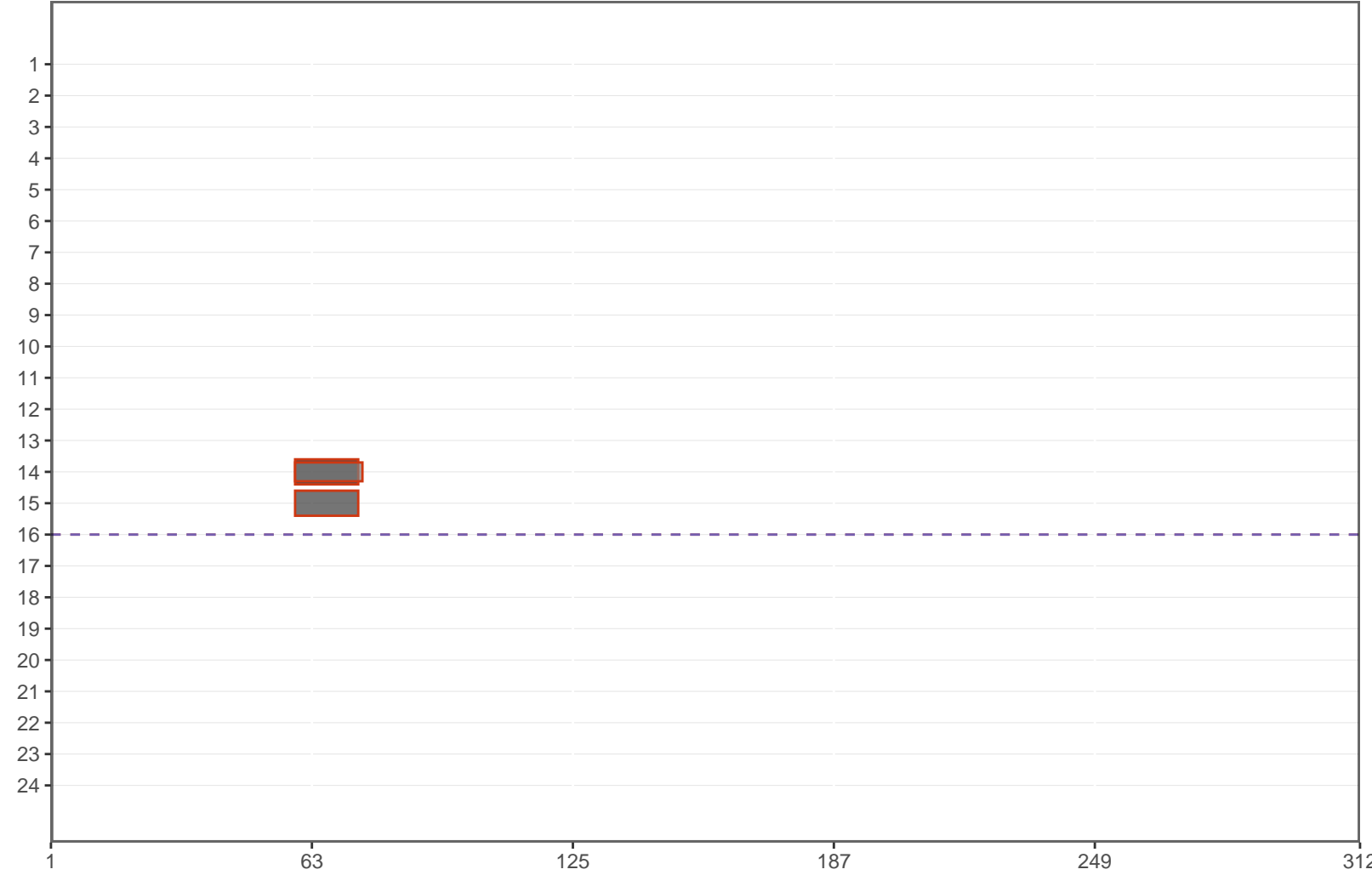
MW indication



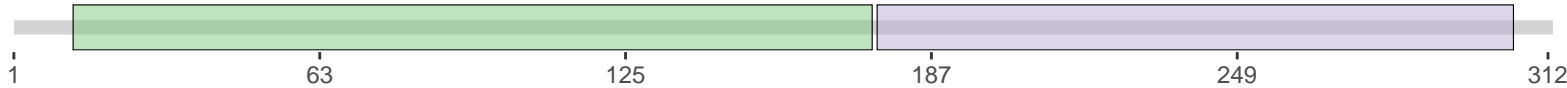
Molecular weight



Gel Slice

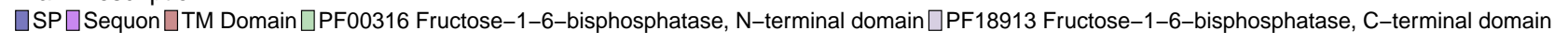


Protein length



Pfam domains

Pfam Description



Protein sequence:

IKDAHEPTLDDVLPQGNMLAAGYCMYGS66TIPKKGKIVSANEGNAKHWDPSTSKYVENCKFPNDG66SPKSLRVIGSMADVHRTLLVGGIFLYPADKIKFNGKLRVLYEVFMSFLMEQAGGGAFTGKGRALDLPKKIHERAPFLGSDVDEEIKRLVAEENK

NbL06g05710.1 secoisolariciresinol_dehydrogenase-like [MW = 29.62 kDa]

No. of times detected



log(intensity)



Values from



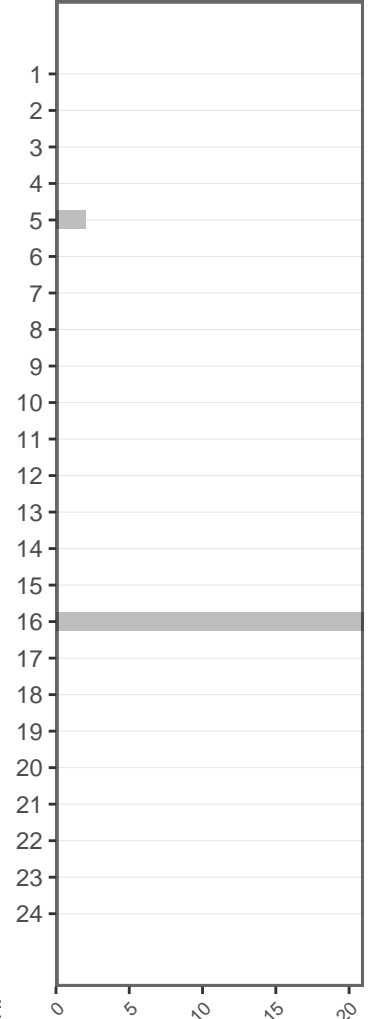
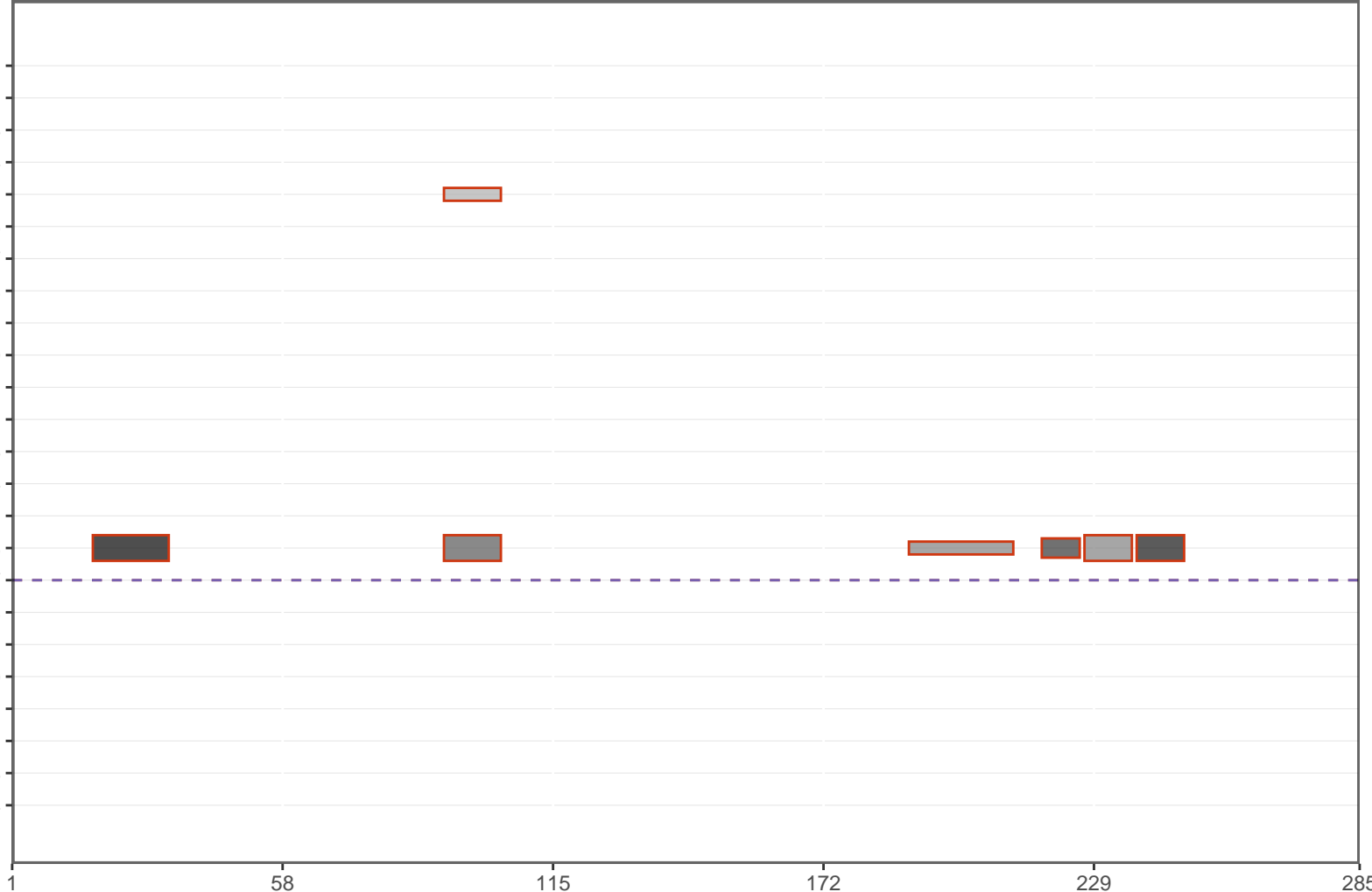
MW indication



Molecular weight

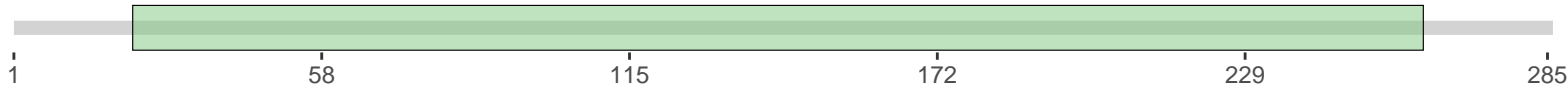


Gel Slice



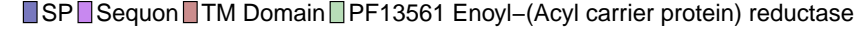
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FCAKHAAARYMPNKKGGSHFASAAVTVGLVPHVYSASKGAVALGLEKNQVELGKYGKIVNVSPLVHSTPLVLAIVGIADRGIADKWFVFAEGGNLKGALLDDEEVKAVLYLADSDSKYVSGMNLVLDGGFSTTNVLTAAVNLKLPSESTHQLV

NbL06g05620.1 secoisolariciresinol_dehydrogenase-like [MW = 29.75 kDa]

No. of times detected



log(intensity)



Values from



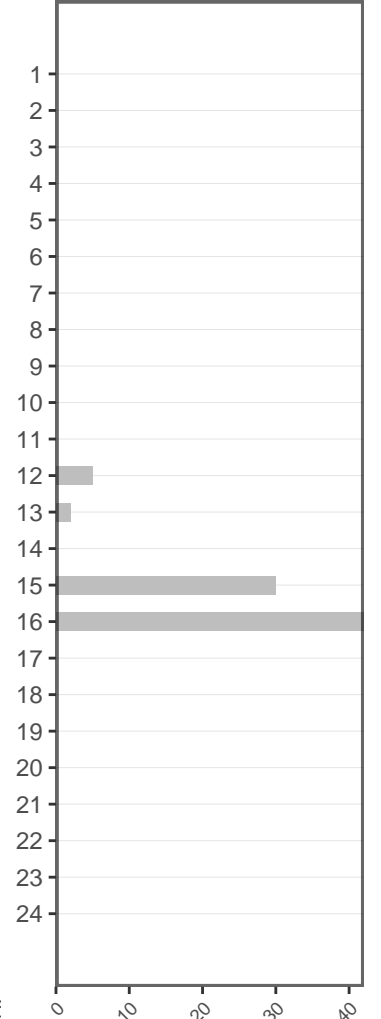
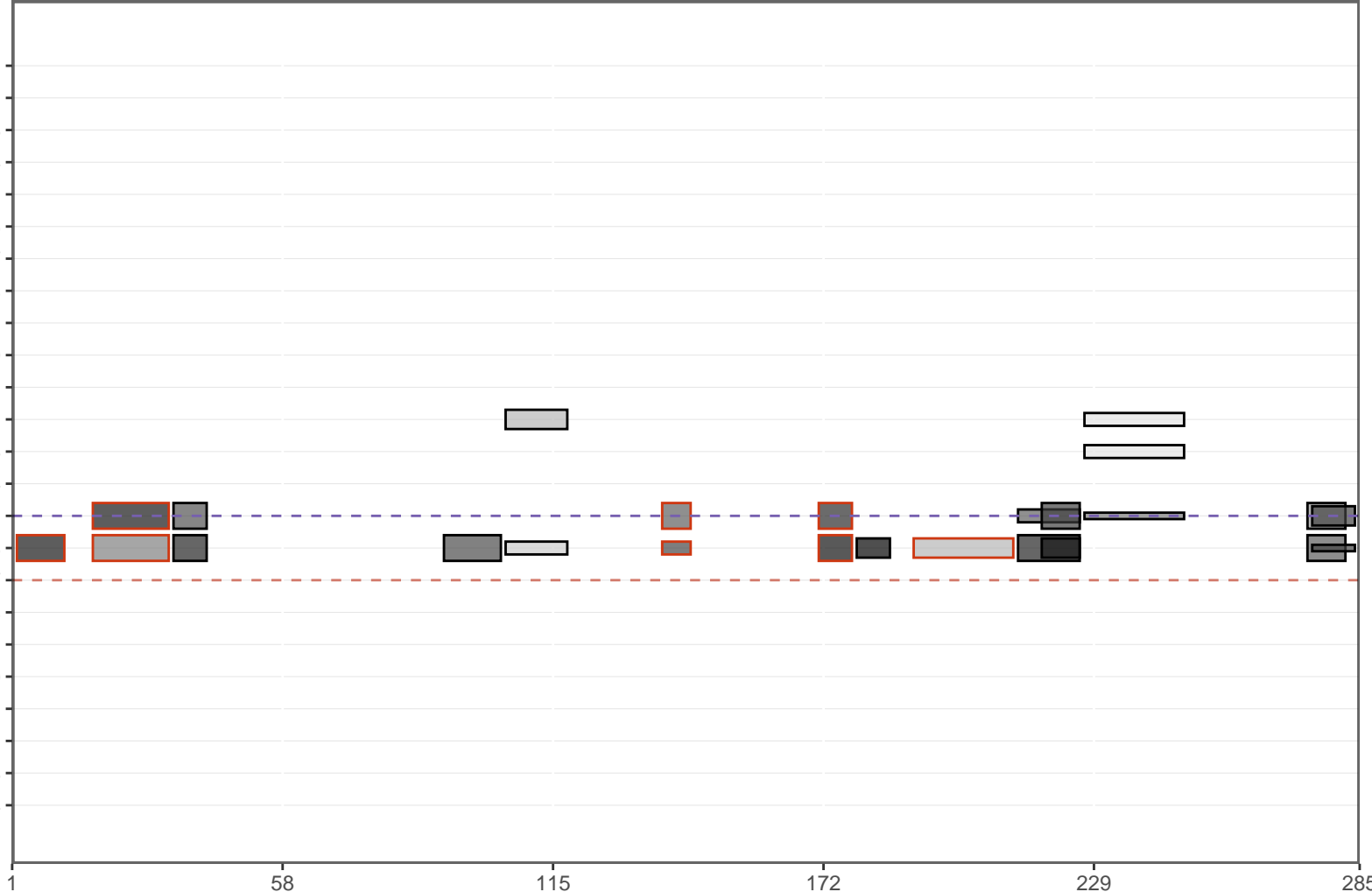
MW indication



Molecular weight

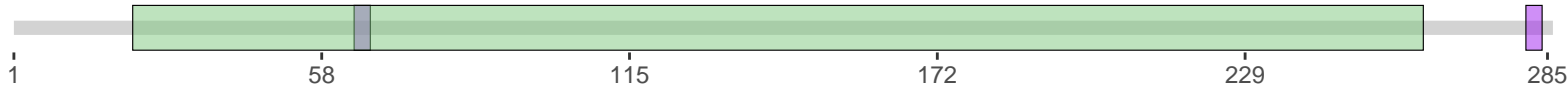


Gel Slice



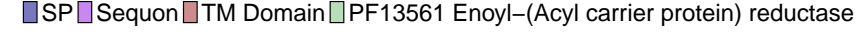
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CAKHAAARVMIPAMKGVIFETASASTEVVGTAPHTLAKNALVGLKNNVDELGKYGIRVNDVSPFYHETPRLNGFGIDKGTADKWFAEAGNLKCALLGVEDWANAVLYLASDSSKYASGMNLVLDGGFSTINVAITEAYKKLFPSTTKTEI

NbL06g05610.1 secoisolariciresinol_dehydrogenase-like [MW = 30 kDa]

No. of times detected



log(intensity)



Values from



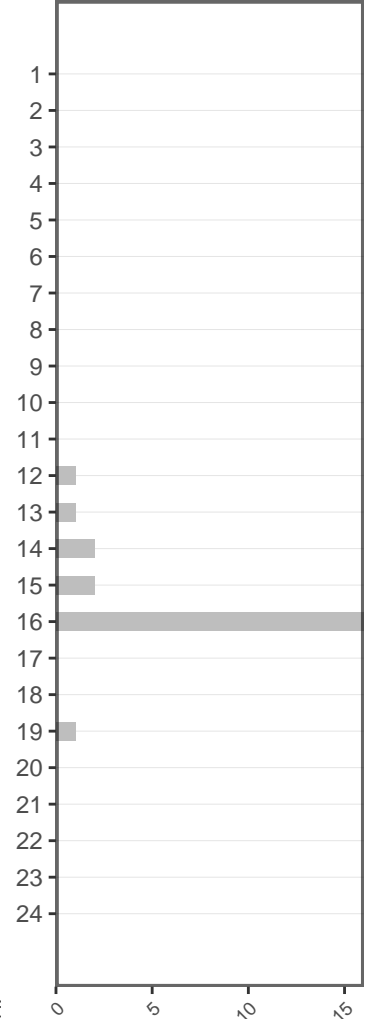
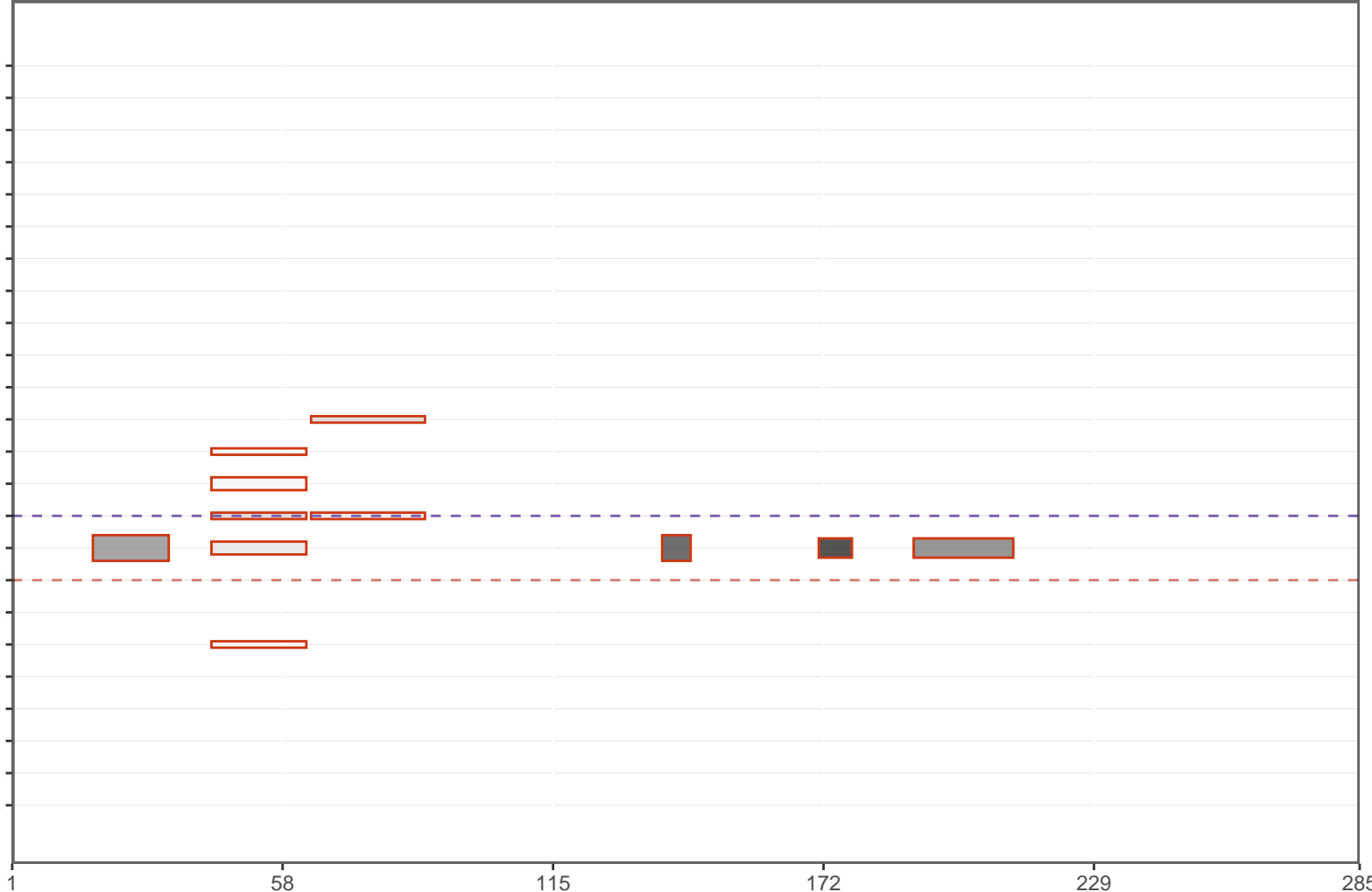
MW indication



Molecular weight

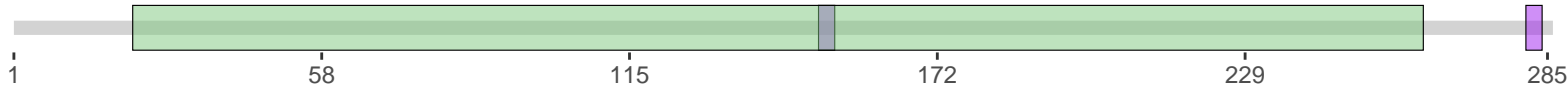


Gel Slice



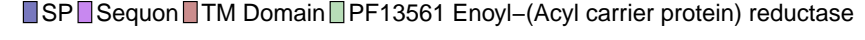
Protein length

Peptide counts over 4 repeats



Pfam domains

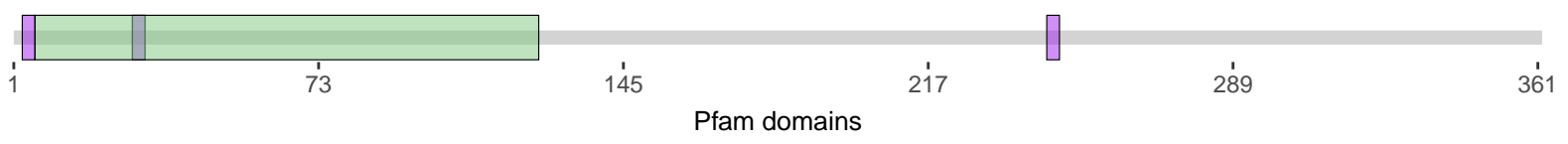
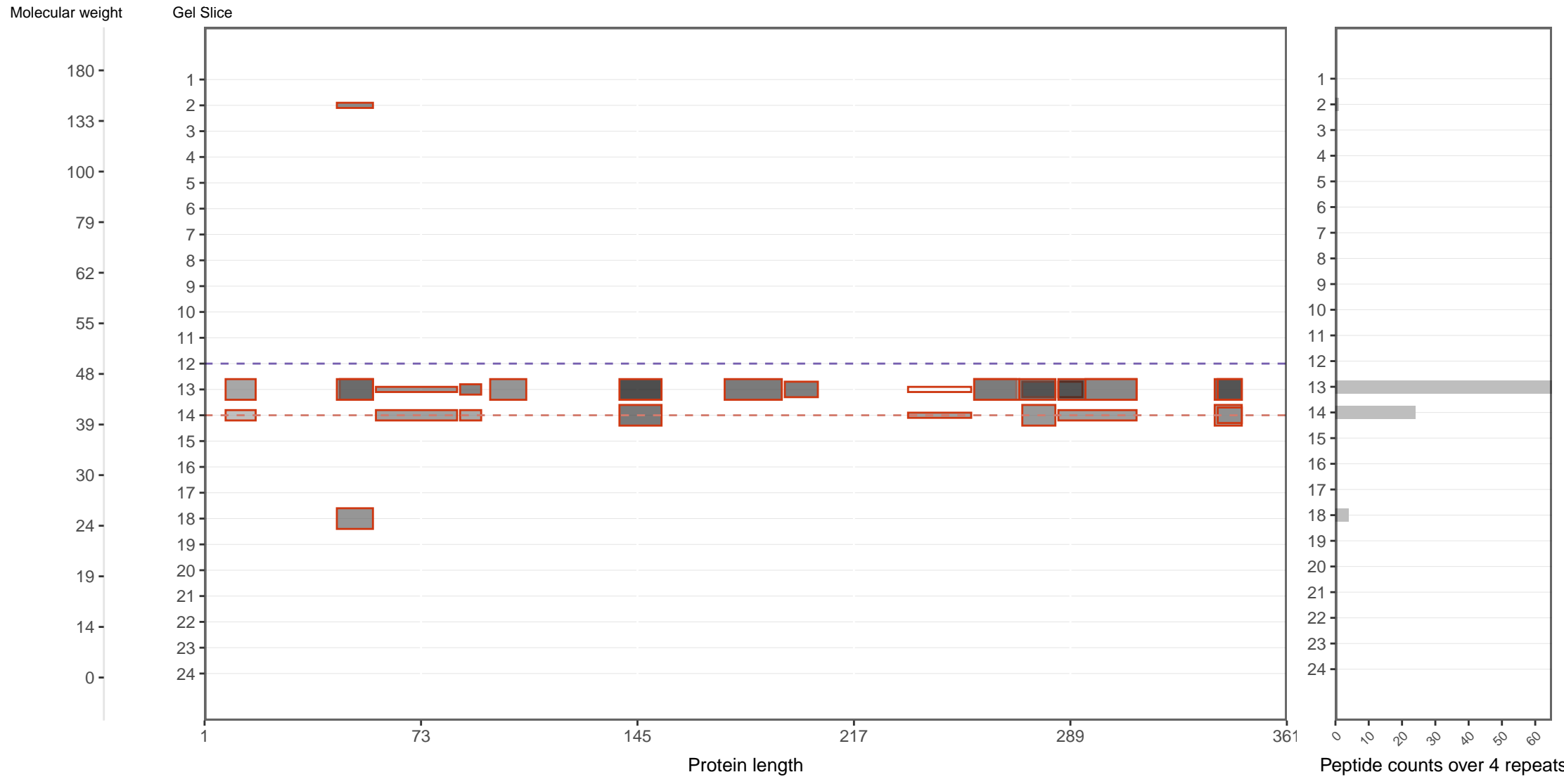
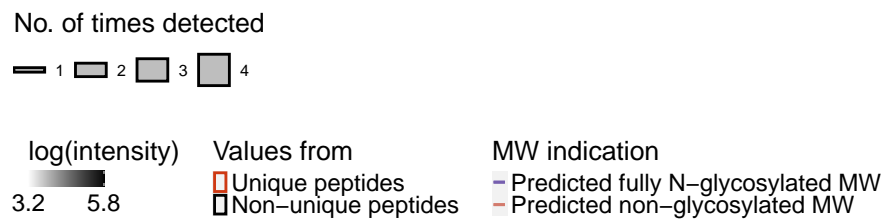
Pfam Description



Protein sequence:

AKHAARVMPFNKGSIFNASASTEVGVSAIMHTSLASKNAVGLGKNNVGLGKGRIRVNDVSPFYHETPLILNGYGDKGTADKWFAEAGNLKCALLGVEDVAVANLVLYLADSDSKYASGMNLVLDGGFSTINVAITEAYKKLFPSTTKTEI

NbL06g05510.1 uncharacterized_oxidoreductase_At4g09670 [MW = 39.72 kDa]



Pfam Description

- SP
- Sequon
- TM Domain
- PF01408 Oxidoreductase family, NAD-binding Rossmann fold

Protein sequence:

I F L E N D I R V K P D L D A G A L G D V G W Y R G L W A D F E L P K S V A L R N P V F N K A G V V I S G A S L S W E D G K V A S F H C S F L S A L T M D L T A V G T G T L H I H D V I P F E E K K A S F V S A V E S G F K E L T G W E P K P S E H T V M T D F P D E A L M V K F S R L V A S I K E G S K P E K K W P T L S R K T T L L D W K A S E K G F E A V E I S

NbL06g05470.1 ATP_synthase_delta_chain_chloroplastic-like [MW = 26.76 kDa]

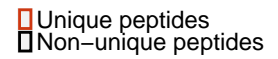
No. of times detected



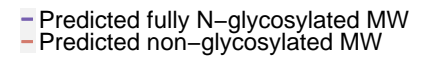
log(intensity)



Values from



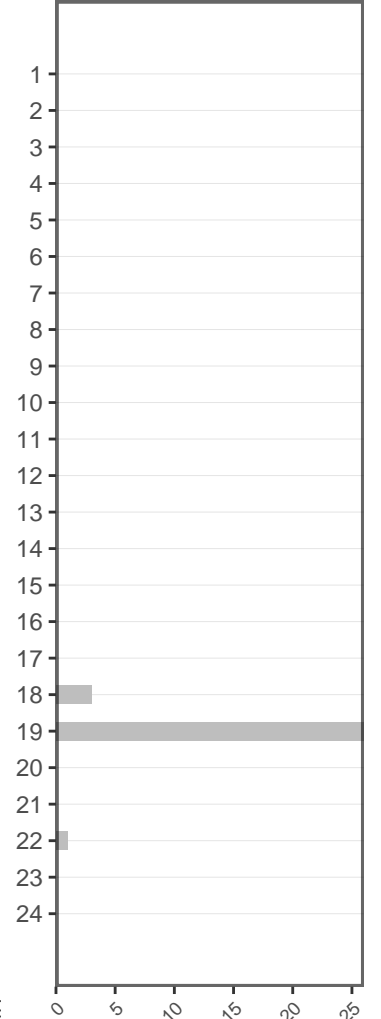
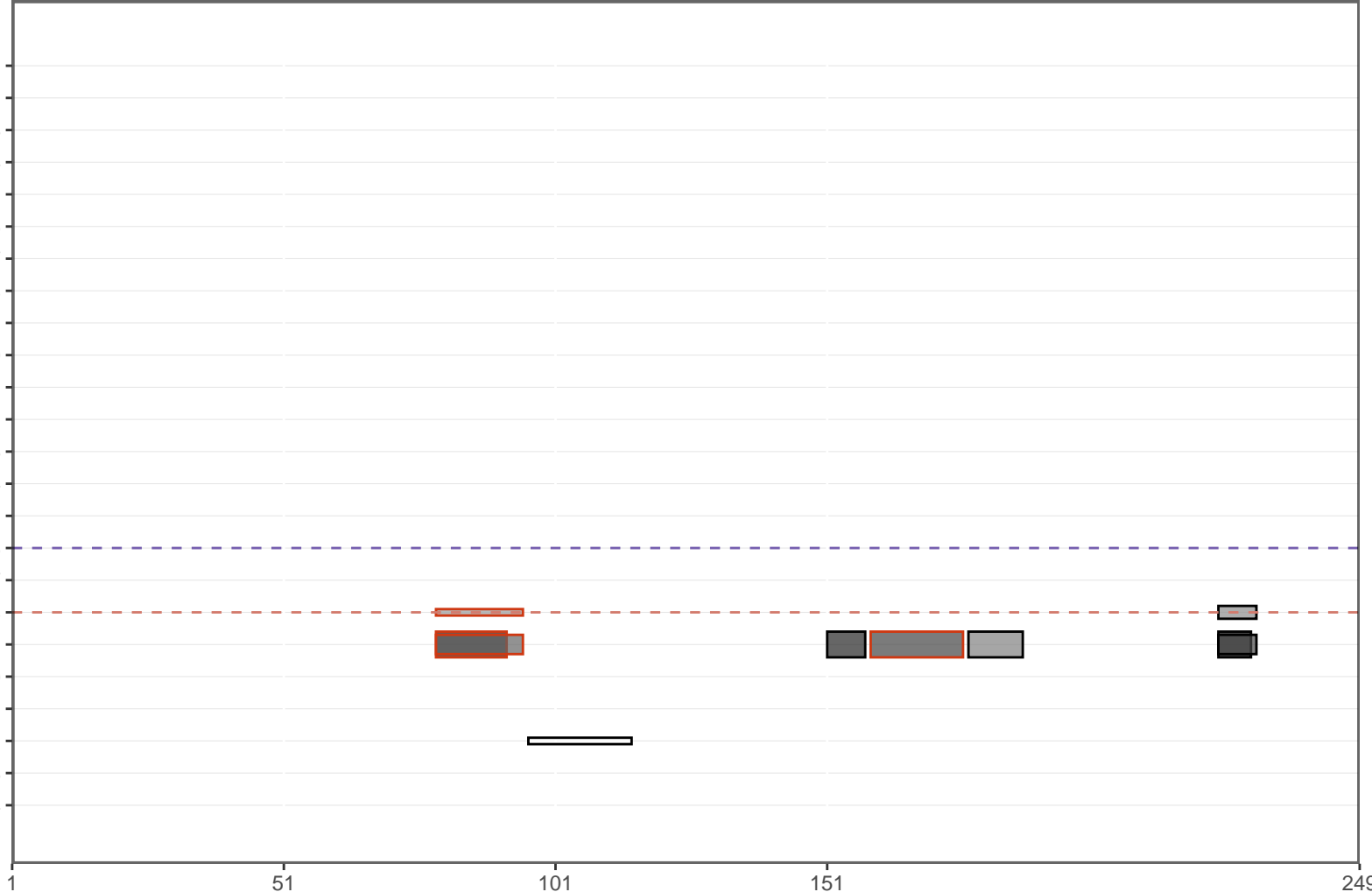
MW indication



Molecular weight



Gel Slice

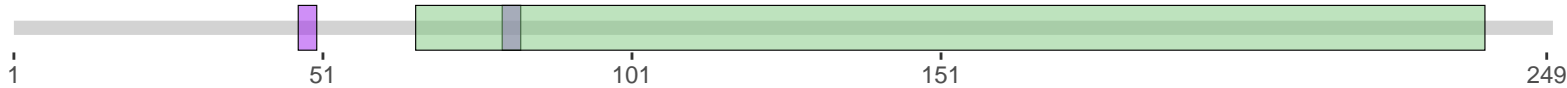


Peptide counts over 4 repeats

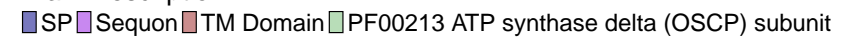
Protein length



Pfam domains



Pfam Description



Protein sequence:

YVGEKKRELVDENFSSSSGPHYANFLNLDMKRVELKEIKVFEKFKVYNTLDTDELAVVTSVVKLESGHLAQAKGVGRLTGSKNVRKTAIDELVAGFTIRYVNGSGSKLIDMSVVKLEDAAGLEIGDQLAV

NbL06g05160.1 glutathione_S-transferase_T1-like [MW = 29.72 kDa]

No. of times detected



log(intensity)



Values from



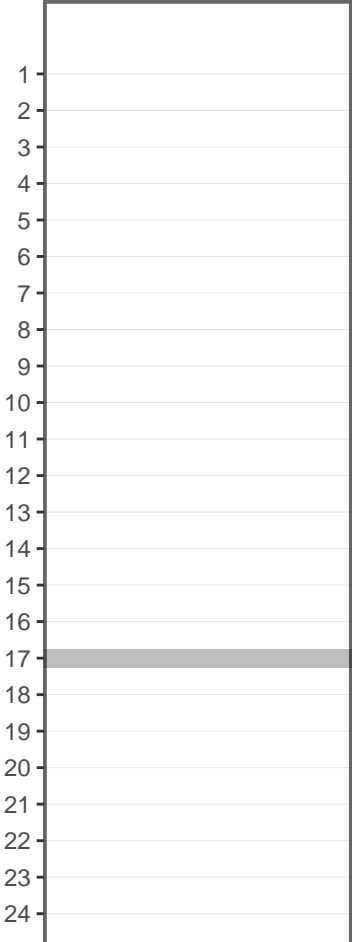
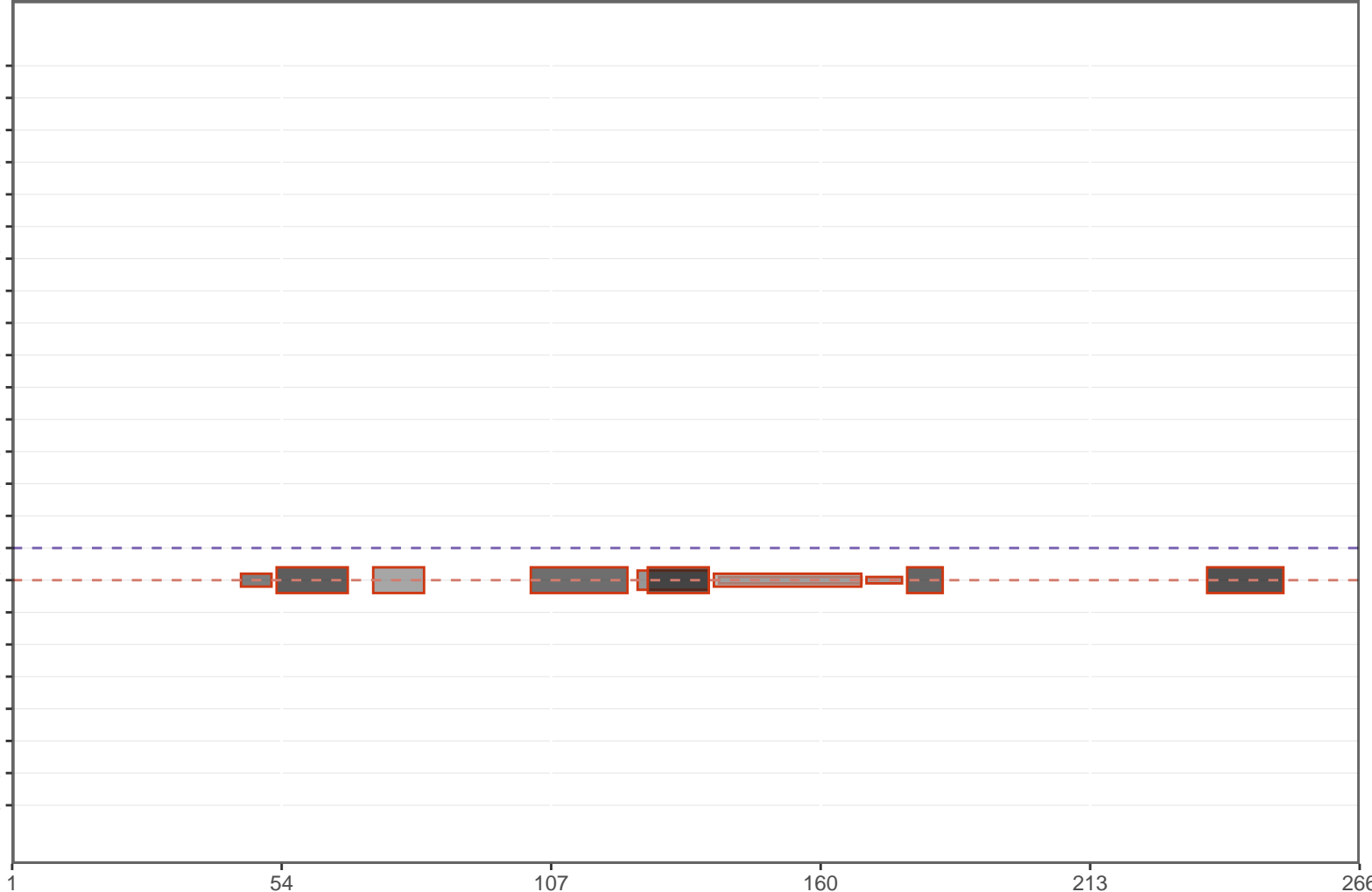
MW indication



Molecular weight



Gel Slice



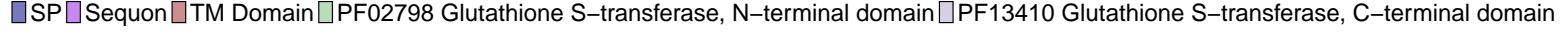
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

QKRAKTESVLDWVHNSLRGSDVGVYVLSNPLAFALGLPLNPQAAAEQEKVLSASLANIDTYWLGKDGDFLLGNSSPSADLANLVCEIMOLEVWDEKDRHRLSAHKVNLKWDVSKSATASHFDEIATLFLKVKEIFQKGRSAGAS*

NbL06g05150.1 probable_glutathione_peroxidase_8 [MW = 19.4 kDa]

No. of times detected



log(intensity)



Values from

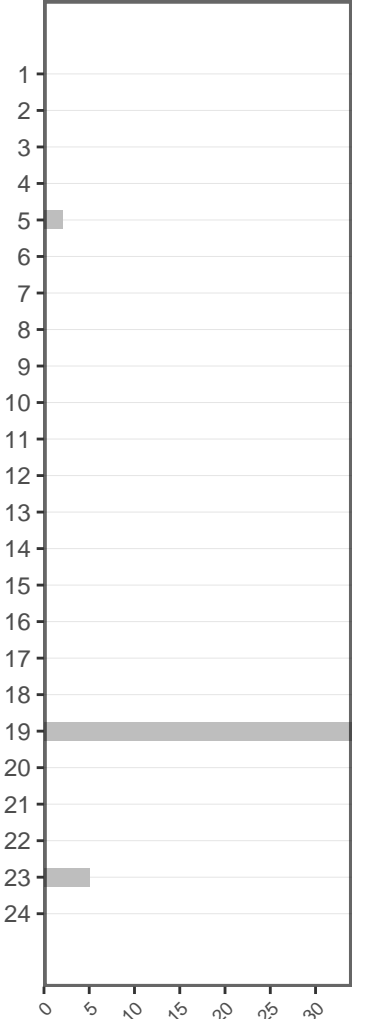
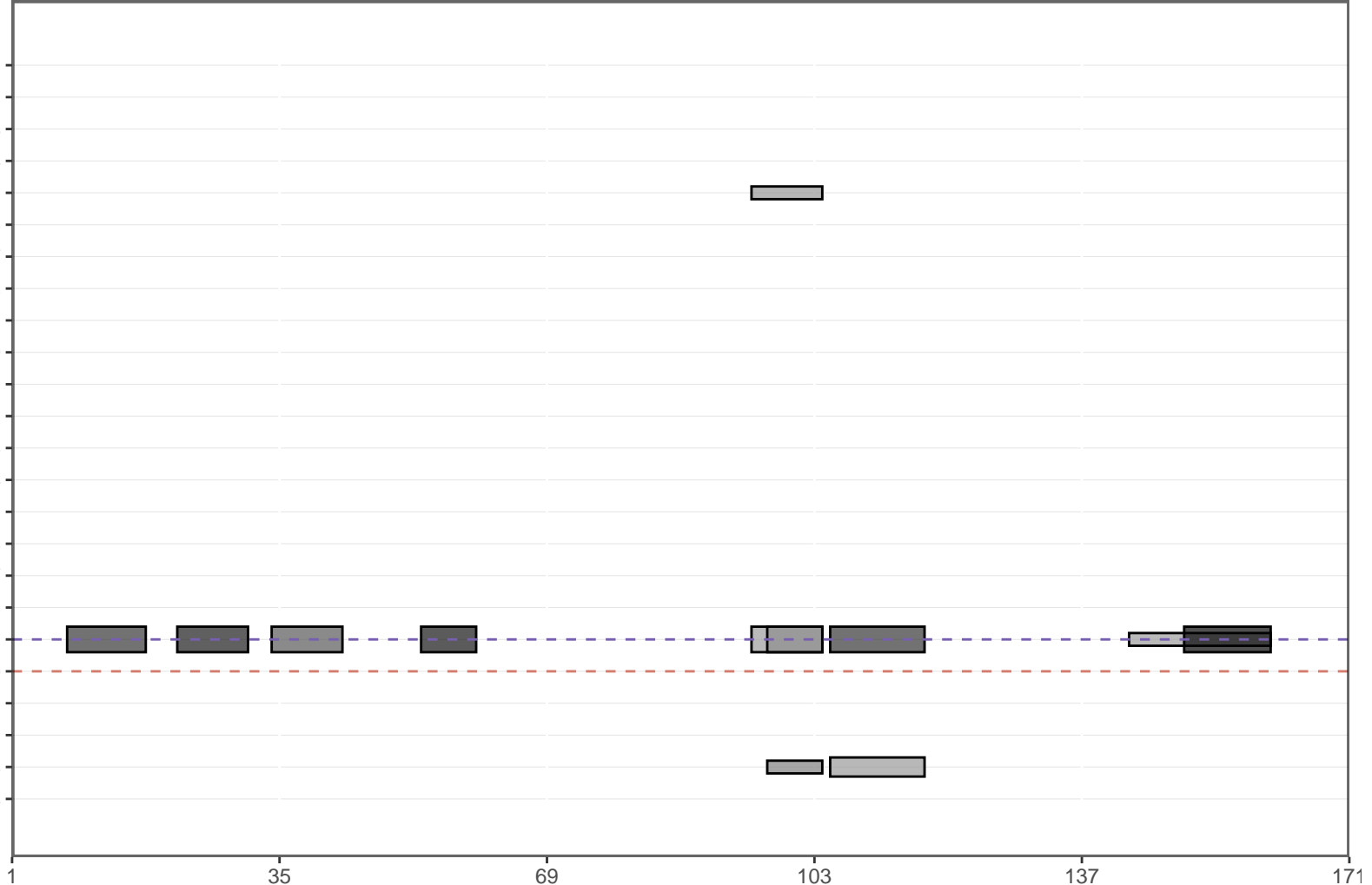
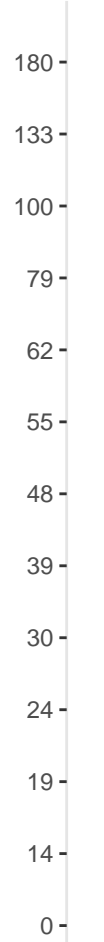


MW indication



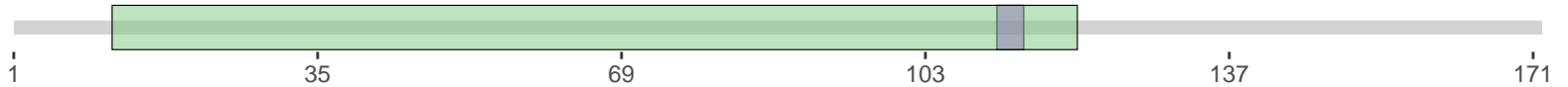
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

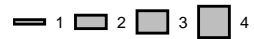


Protein sequence:

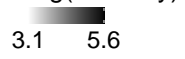
PCNCFGEELPSSNDGLDFVCTRFRKBEFFRFDKIEVINGENASRLYLLKSGKGVIFGDDQWNAFLVLDKNGGAADRYVPTFSPLTERDKKLELV

NbL06g05030.1 V-type_proton_ATPase_subunit_E-like [MW = 32.94 kDa]

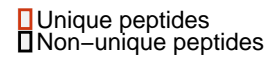
No. of times detected



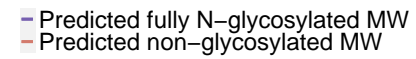
log(intensity)



Values from



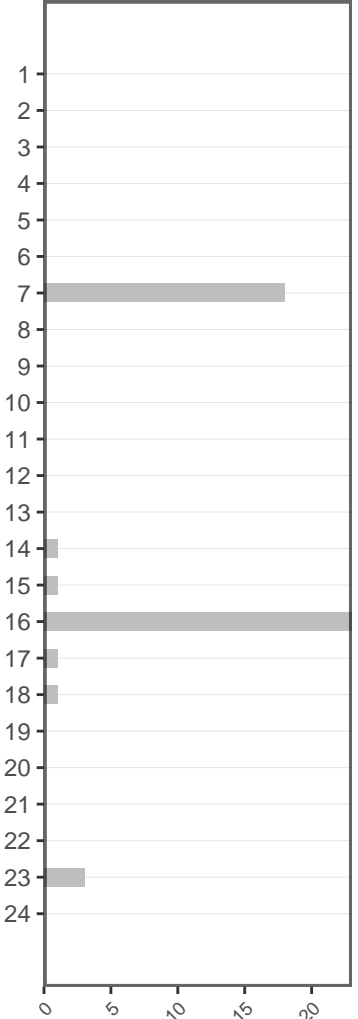
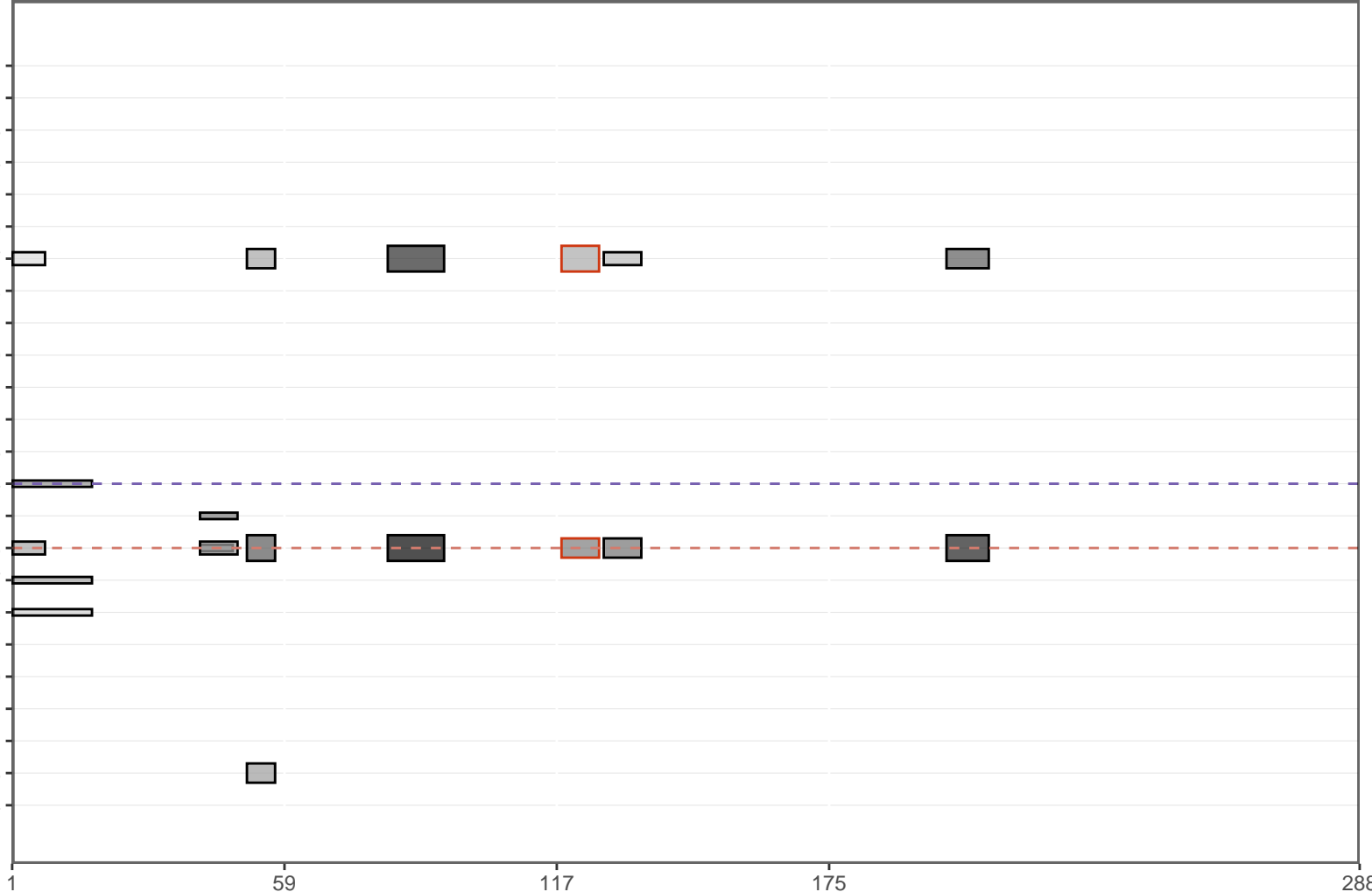
MW indication



Molecular weight

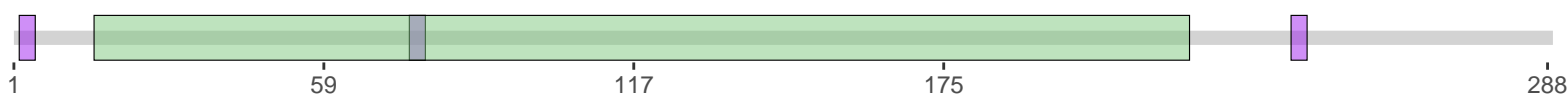


Gel Slice



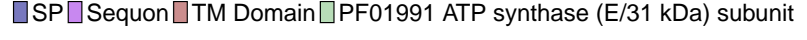
Protein length

Peptide counts over 4 repeats



Pfam domains

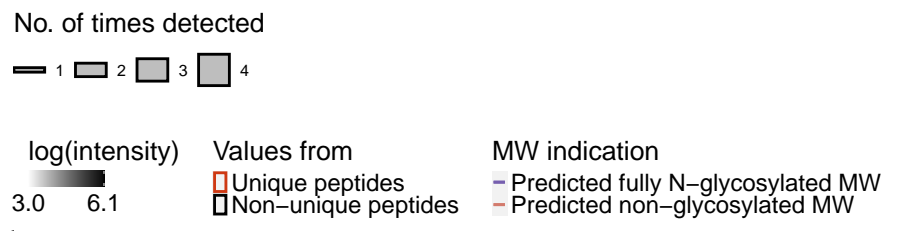
Pfam Description



Protein sequence:

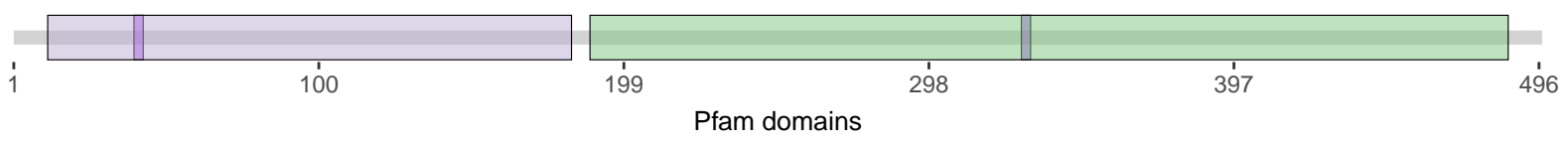
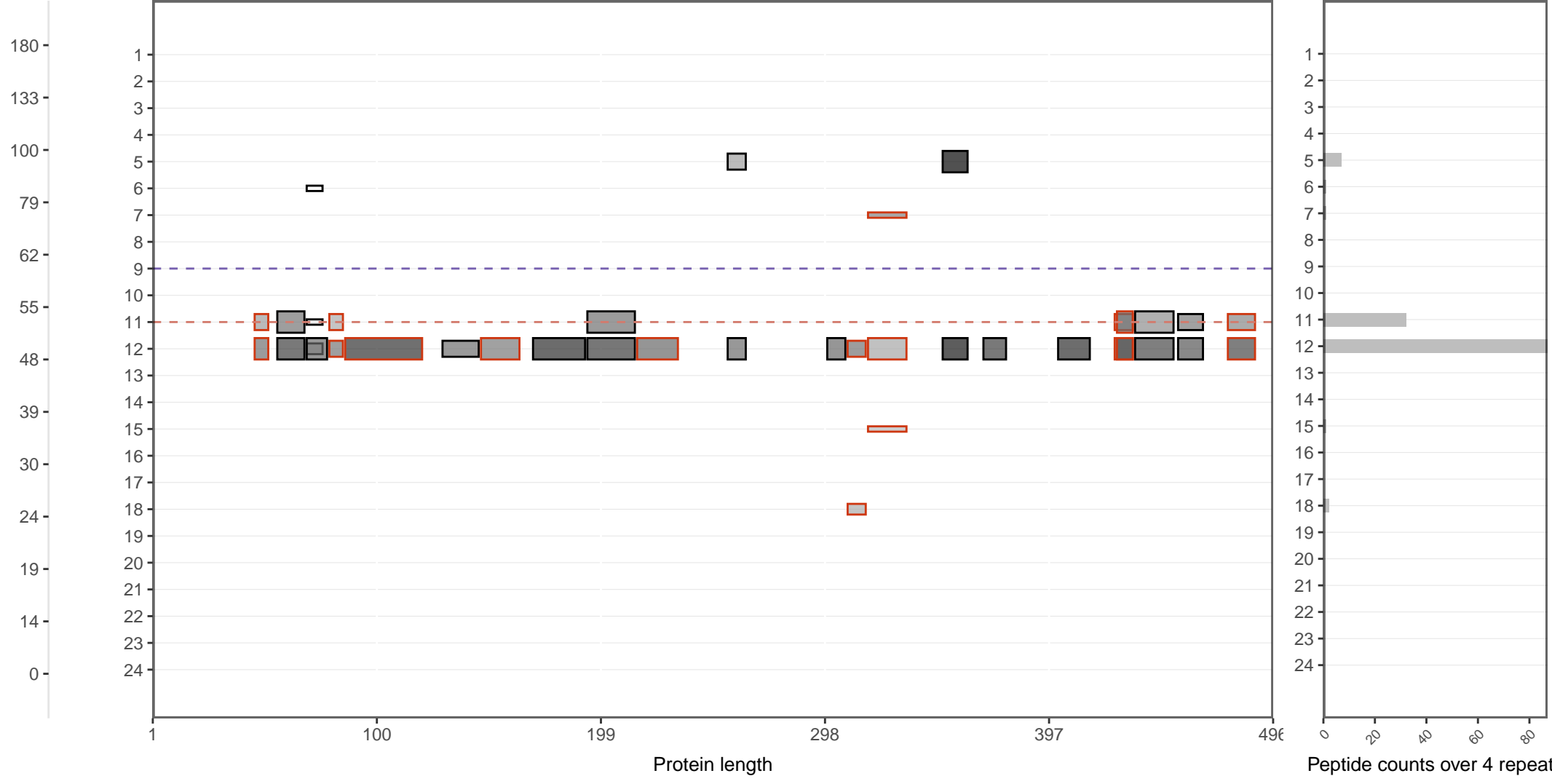
PSVLLRCRKDDVHSEVDLDAKKEEYAEKAMVHSPREIVDHIHLPAPGSHNAHGPSGSGGVVLSRDGKIVCENTLDARLEVVFRKKLPEVLALVLSVLLVLSGGLANFSSFPSTGYTFVWLPVSHYLLQMHPLFFRCHVDLISLHDHYL

NbL06g05000.1 6-phosphogluconate_dehydrogenase_decarboxylating_2_chloroplasic-like [MW = 54.17 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00393 6-phosphogluconate dehydrogenase, C-terminal domain
- PF03446 NAD binding domain of 6-phosphogluconate dehydrogenase

Protein sequence:

LESFLVETADIFNWKDEKTSGGSELVDKLDKTKGKWTGVGGAELSAAPTAAELSDRYMGLKEEREDAAIGFKKEGLKEEINFVNSGSDVKRLLIDVRLGALYASIKSGSYAGQAMNLRKSAEKGGWNLNGEMARIWGGGIRAVFLDRKKYAGRNPLGLANLMDPEFAEMVGRGAAWRRVYGGAGDRGSEVFGMSASLGYFDYTRRSLPAILVGAQRDFGGAHTYERIDMPCGAYHTEWKLARKARY

NbL06g04800.1 30S_ribosomal_protein_S6_alpha_chloroplastic-like [MW = 24.76 kDa]

No. of times detected



log(intensity)



Values from



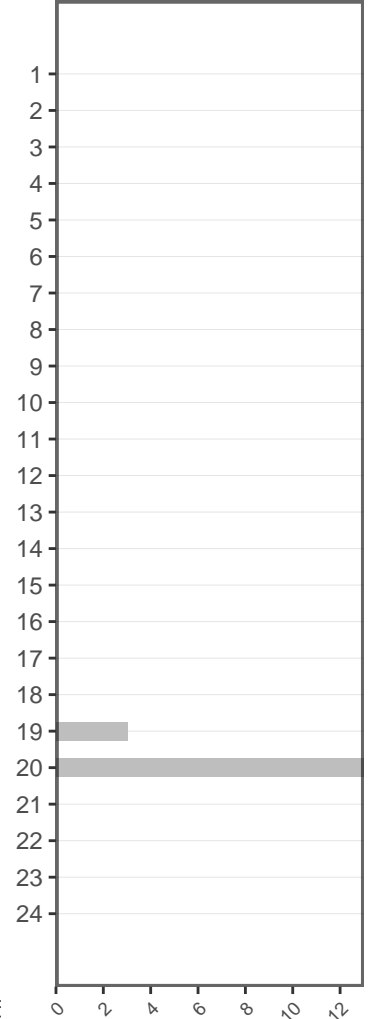
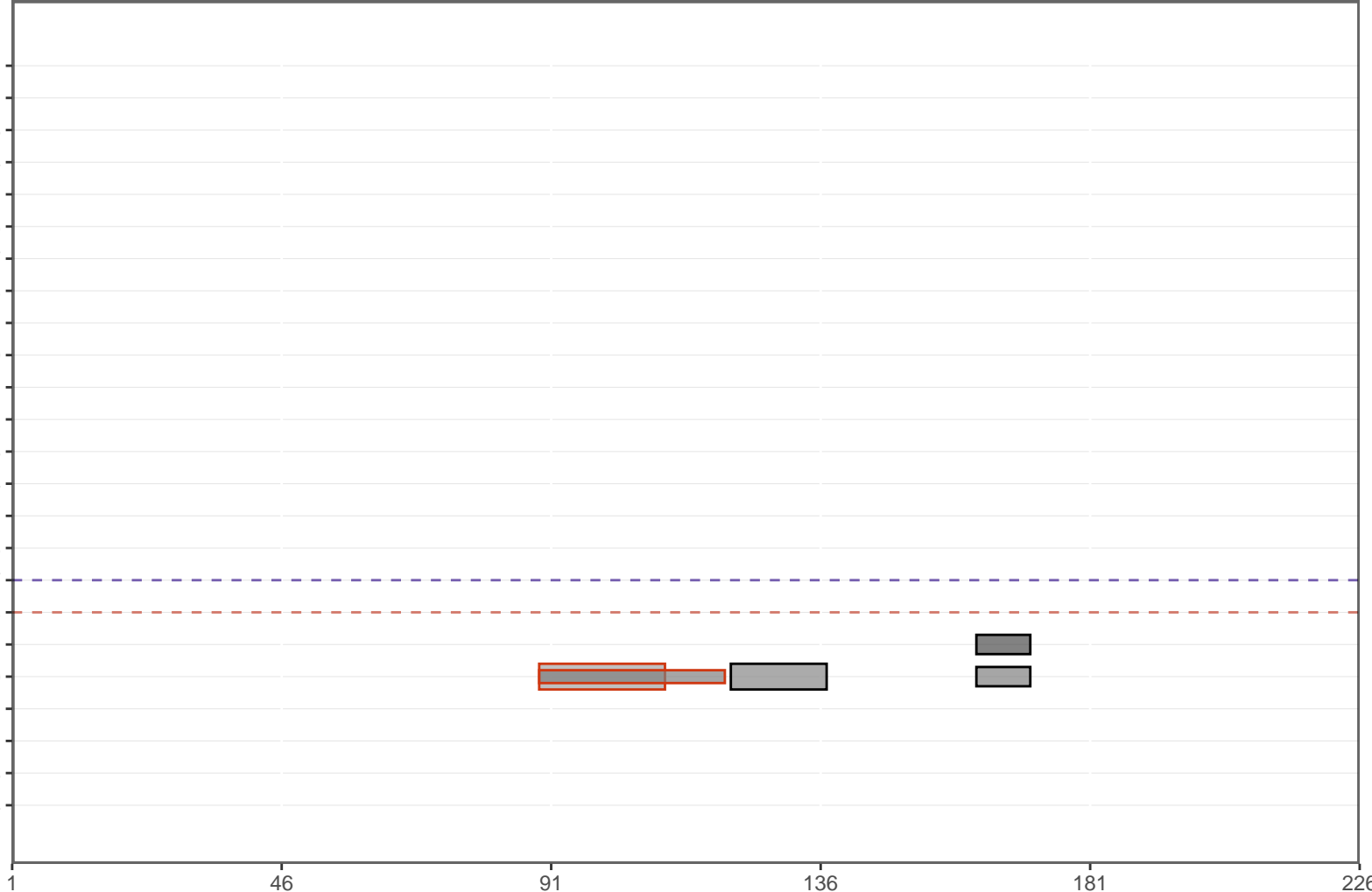
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

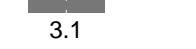
SSGIAAVEDKEEPPGPPGMPVETMAVLRPDMSEDERLALTKYKVELLVAGGGMYVEVFNKRGVPLAYSIRRNKKAQETNTYLDGIVLFTFYFKPQSMTAEATLNTDDVHRSSSFKIRKRYK

NbL06g04750.1 glucan_endo-13-beta-glucosidase_11-like [MW - SP = 43.02 kDa]

No. of times detected



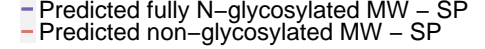
log(intensity)



Values from



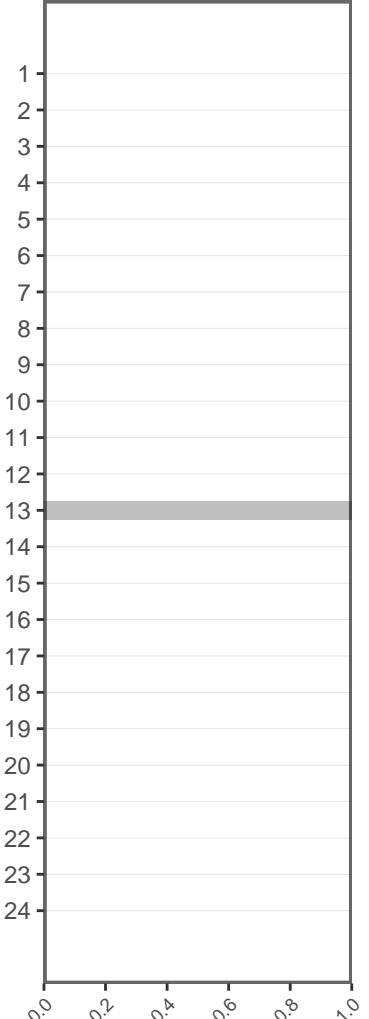
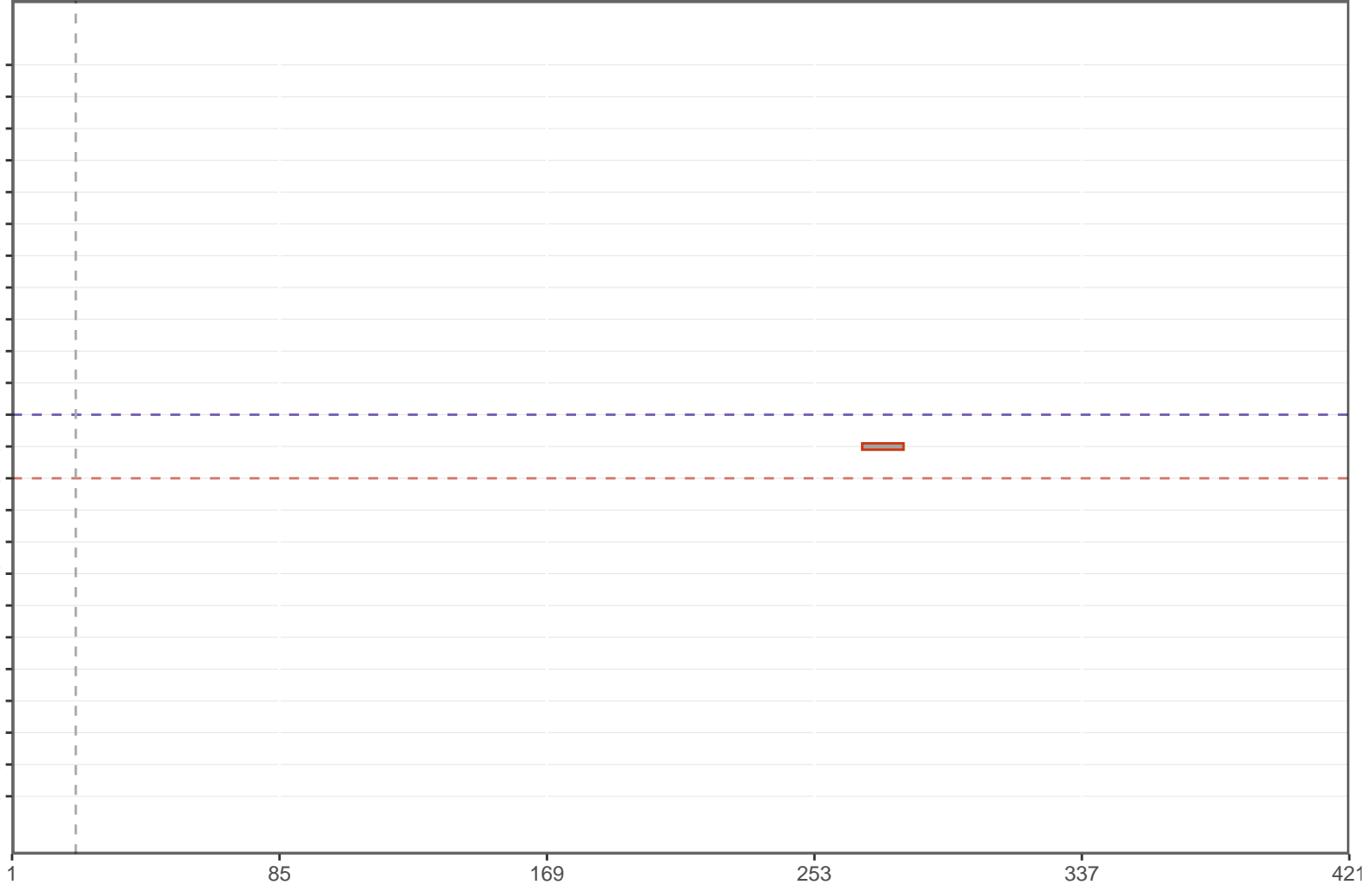
MW indication



Molecular weight

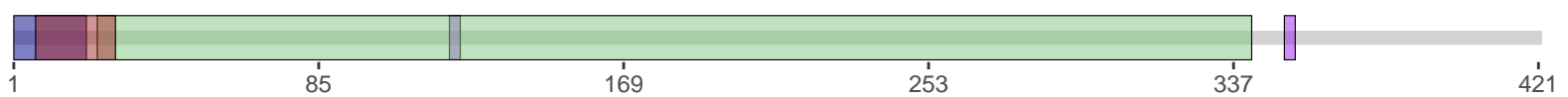


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

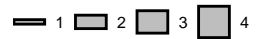


Protein sequence:

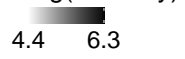
FAYKANPKHIVFLDYVLFQNPNGVDFVTLNHYDNMLYAGIDAVHSLALASIGYKNVCVQISEGWPFGKGDGDEVGATPDAARKYKCNLIKUVSGKKGKTPLRPNTLNIVYFALFNENLKPFTSERNYGLFKPDGSPVPLGFGAGINAVGTN656565PATGTG656565TS656565TPWNSPDGVL6TSD6GRVQFCWIBAILGLLGLGFSTARNDMSCHLR*

NbL06g04740.1 lysosomal_beta_glucosidase-like [MW - SP = 65.91 kDa]

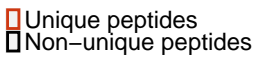
No. of times detected



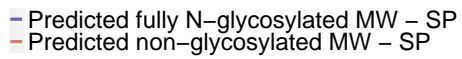
log(intensity)



Values from

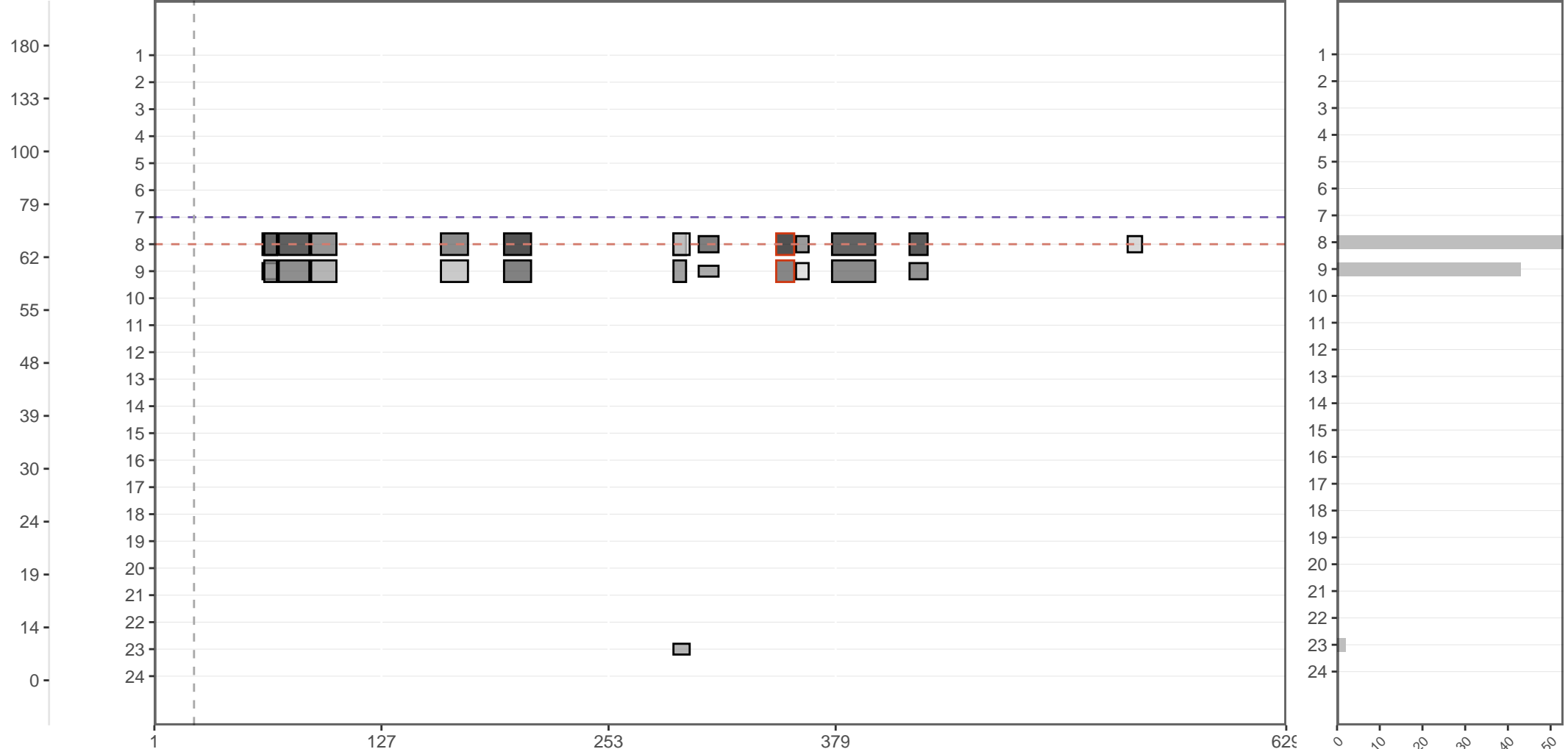


MW indication



Molecular weight

Gel Slice



Protein length



Pfam domains

Pfam Description

SP Sequon TM Domain PF00933 Glycosyl hydrolase family 3 N terminal domain PF01915 Glycosyl hydrolase family 3 C-terminal domain

Protein sequence:

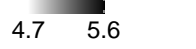
KFRGFVSDVCGIDRITDPPHANNYSYSGDAGMAGIDMMVPEHYREFIDTSTGQVKANIPMSRIDDAVKRLRKFVAGLFENPMSDPLANQLGSGEHRLELAVRKRLLKLNKPTSPGRLLLPLPKAKPKILVAGTHADNLGYGGGVTEWGGVAGNDLGTITLTAIKTKTVPSTQVYVQGNPDANFVSKNKFSAVAVVGGVPAEMFGDSSNVTIVEPQPTISNVCGAWKGVVVVSGRPPVLEPYIKIKDLWAWLPSTEGGGVADALFGDYGTQKLRITWFI

NbL06g04730.1 soluble_inorganic_pyrophosphatase_PPA1 [MW = 24.27 kDa]

No. of times detected



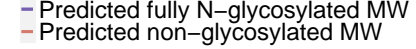
log(intensity)



Values from



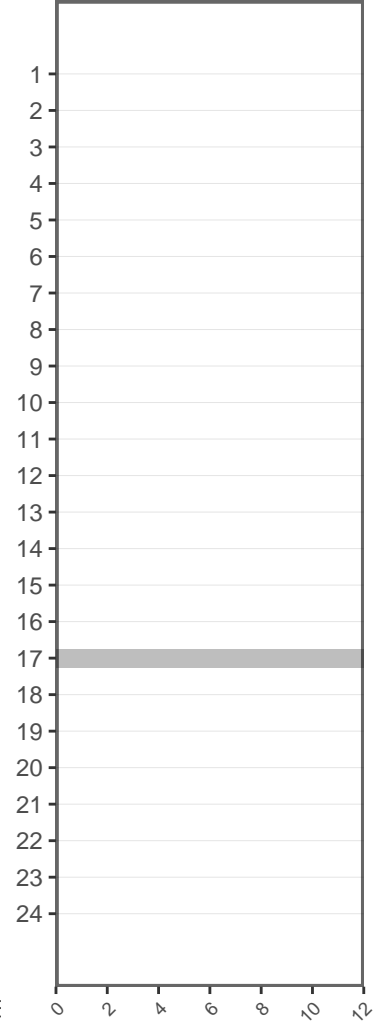
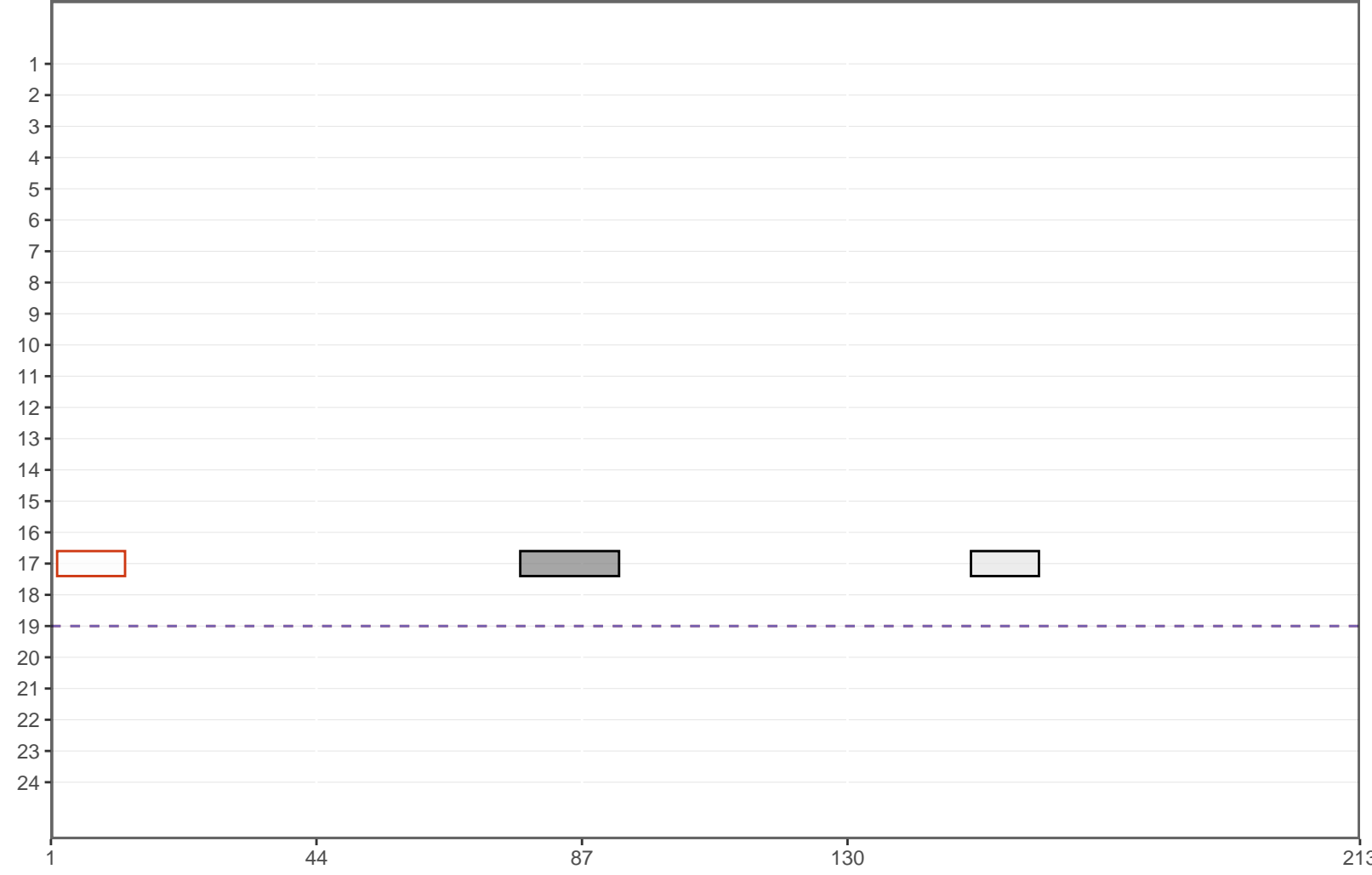
MW indication



Molecular weight



Gel Slice

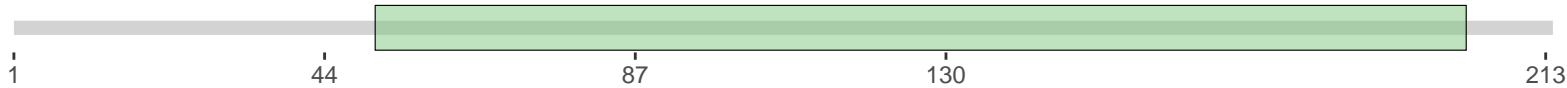


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

RTLCEEDNPMQVLLVMGEPVLPQGFRRARAIGLMPMDIDGEGKDKKIAVGADDPFVRRHYTNINQLPPHRLAEIRFFEDYKKNENKEVAVDFLPPSTVAIDIGYSMDLVAEYIHLRK

NbL06g04700.1 probable_cinnamyl_alcohol_dehydrogenase_1 [MW = 38.58 kDa]

No. of times detected



log(intensity)



Values from



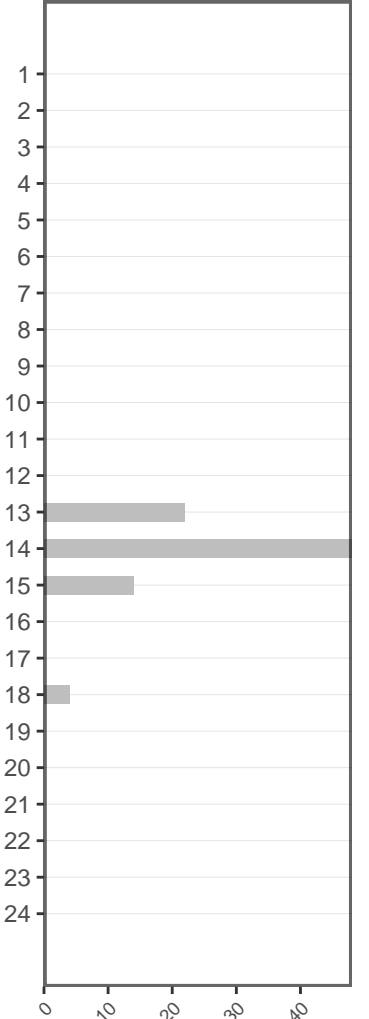
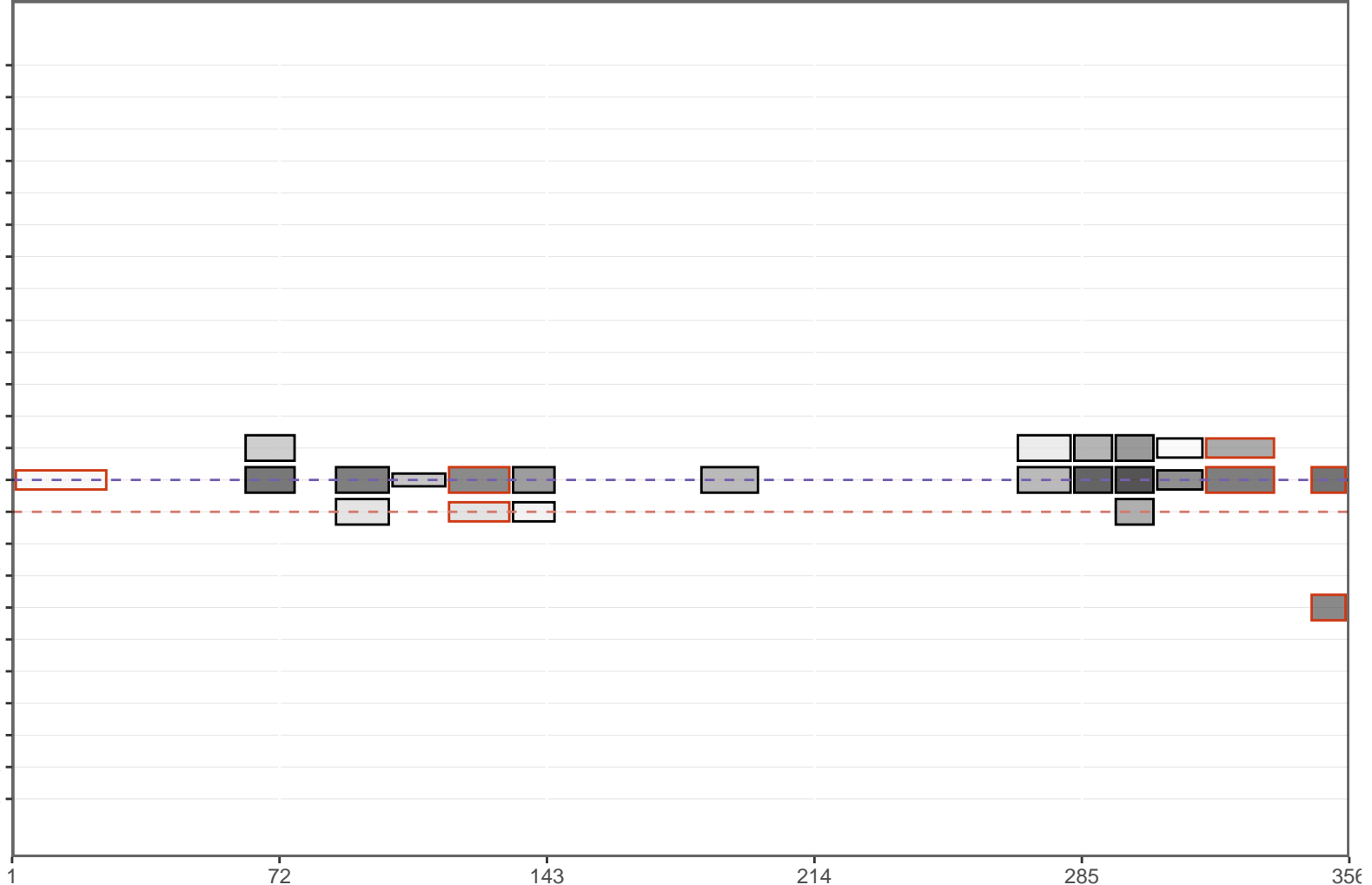
MW indication



Molecular weight



Gel Slice



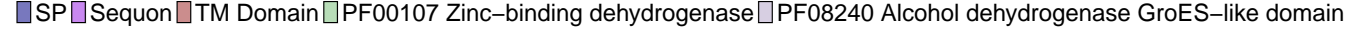
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LCAGITVYTPMRHNMNPGKSLGVLGGGLGLAVKFKAFGLNVTYFSTSEKREAAKLLGADNFVVSDEQGMALGMSDFMINTASGDFPFLVLSLKTAGLVLVGGFFTEYKFGPCNLVLGMMKIVGVTGGTKGTGEMLDFCDASHKHYPEIEIVPIQVANEALERLUKKNVYRFVIVDGNLK

NbL06g04280.1 uncharacterized_LOC107769601 [MW = 33.74 kDa]

No. of times detected



log(intensity)



Values from



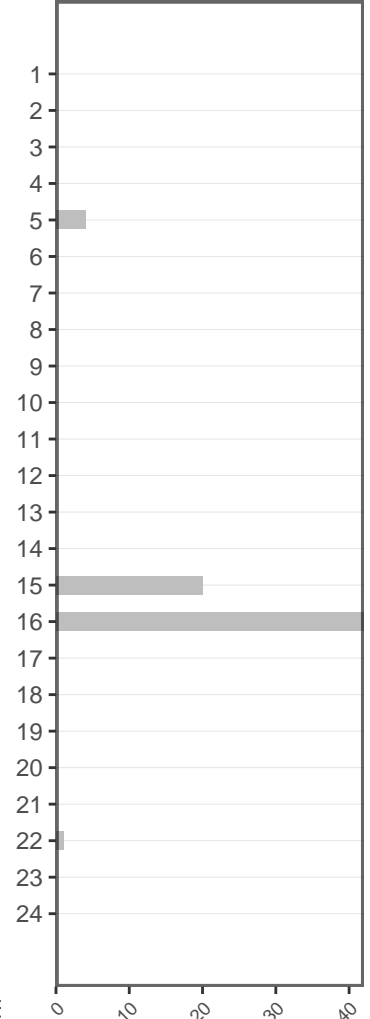
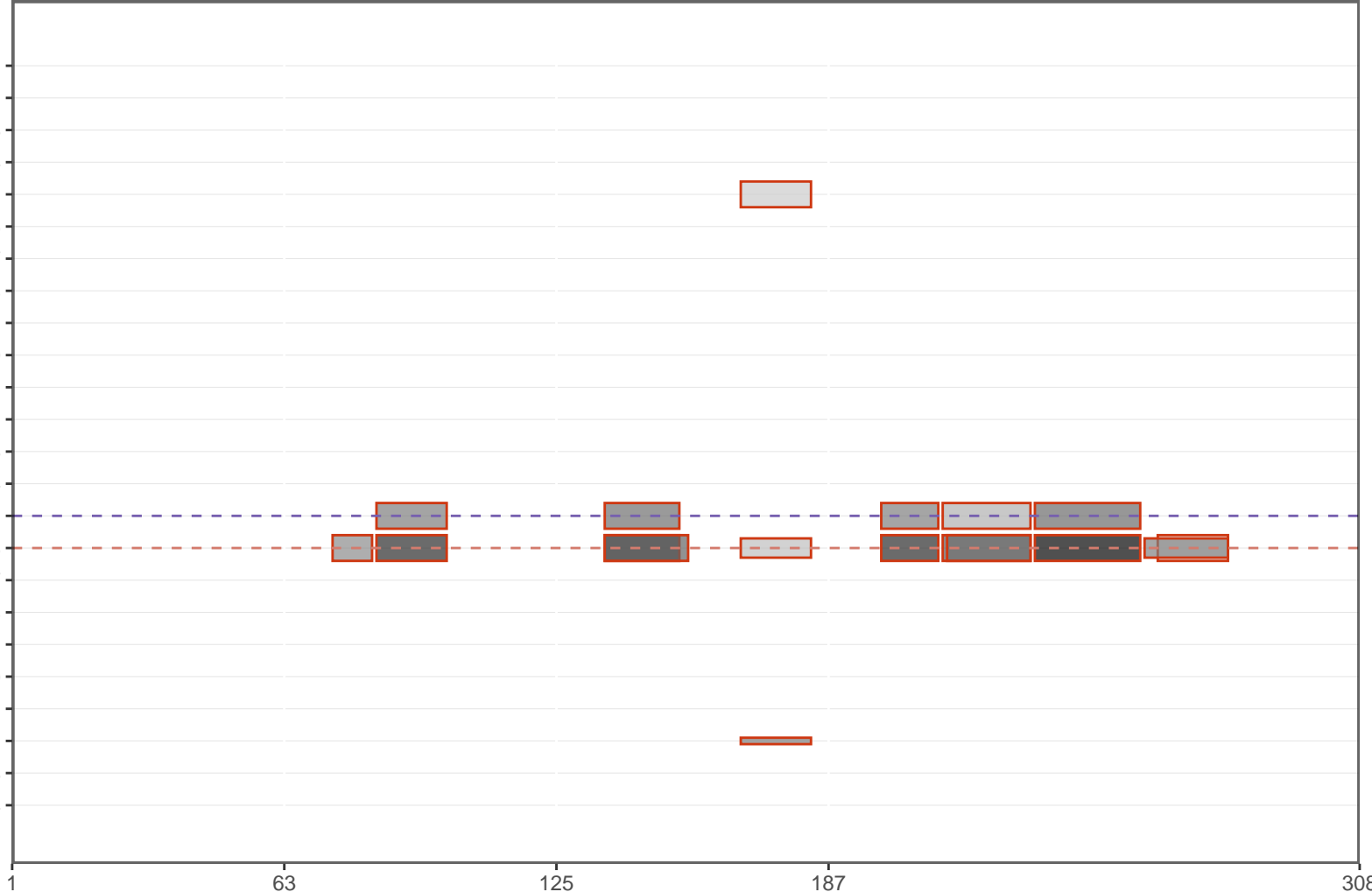
MW indication



Molecular weight

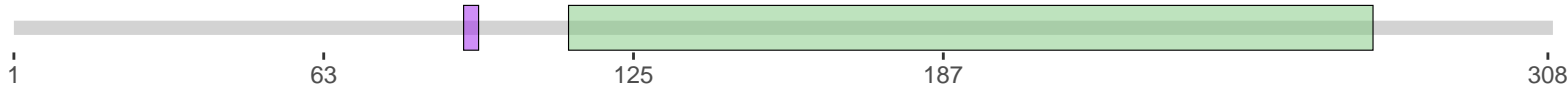


Gel Slice



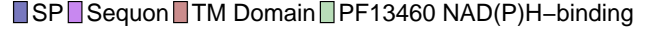
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

"GTYVEPIAGDAKDRBLKALRGRVRAICPNEGFSINIESWKLGHVILLGSLVYRGGSSGVAIVTANARKMAEGDESLVMSGVPYTRIRAGLLVNPAGNGDGFNFNEGSAISQKLSKEDAFICVEALDTPKQGLIFEVWNGEDVMDWKGQFATLKESEL"

NbL06g04270.1 uncharacterized_LOC104210585 [MW = 89.55 kDa]

No. of times detected



log(intensity)



Values from



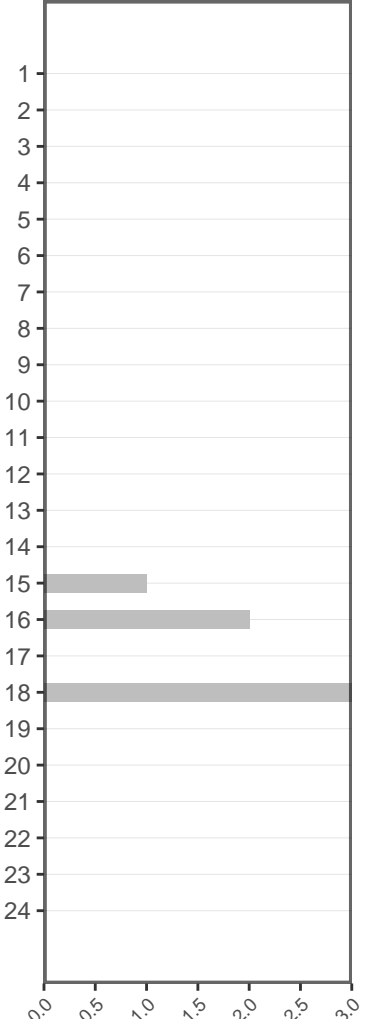
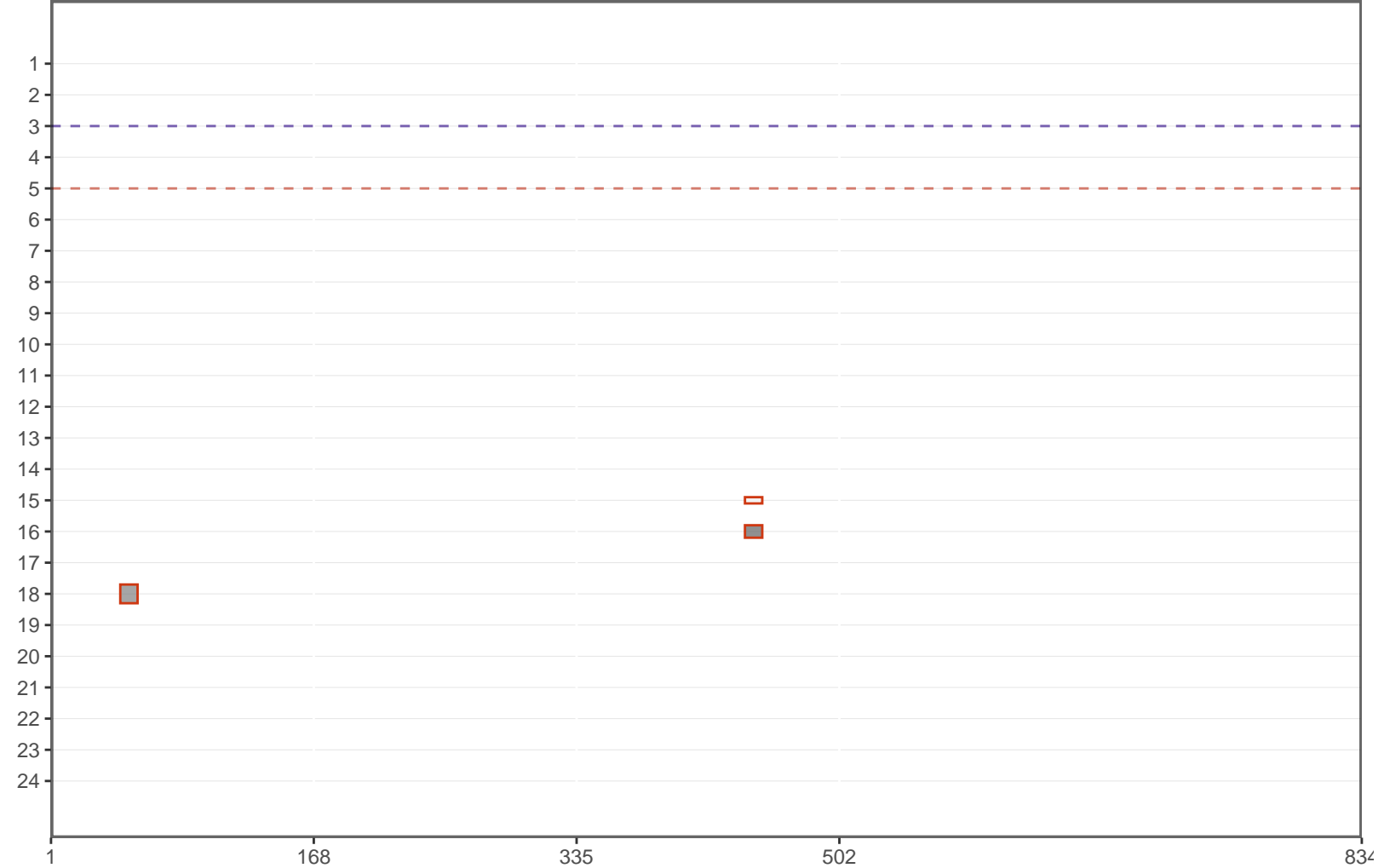
MW indication



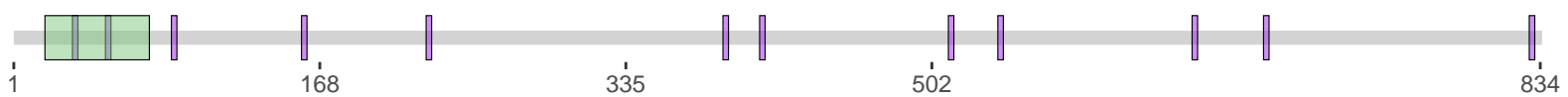
Molecular weight



Gel Slice

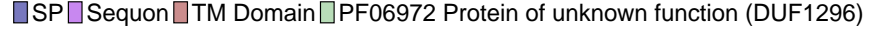


Protein length



Pfam domains

Pfam Description

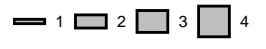


Protein sequence:

ASRLNIDNVVIAEHRVSETRDRGLTFGFGAELPKDLDEESGTESSRLSLVLESEPTDEPVGSKQLDLADDRVQNPGLTSPGSGVLDLQKLDLADRRESSPELDLQVTDVGLVQDNRASVTFPEGGGGGASNLSSFSYDPTGTGYDIPYFRPAWDEALHGGGAGDEALSSHAANSMPASTIPMVGQVGHQHPQAGMYPQVHVSHFANLMPVRYHFSFVYVPPMAMPQVSSNRPVHPFPNGSNYLLMPGGGSHLSANGLKYGIGGQKPVPTGSAEGFNFTSPTGYAI

NbL06g04210.1 beta-galactosidase [MW = 94.38 kDa]

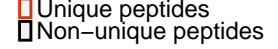
No. of times detected



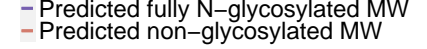
log(intensity)



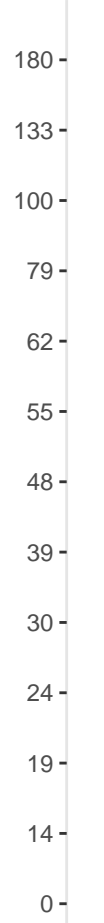
Values from



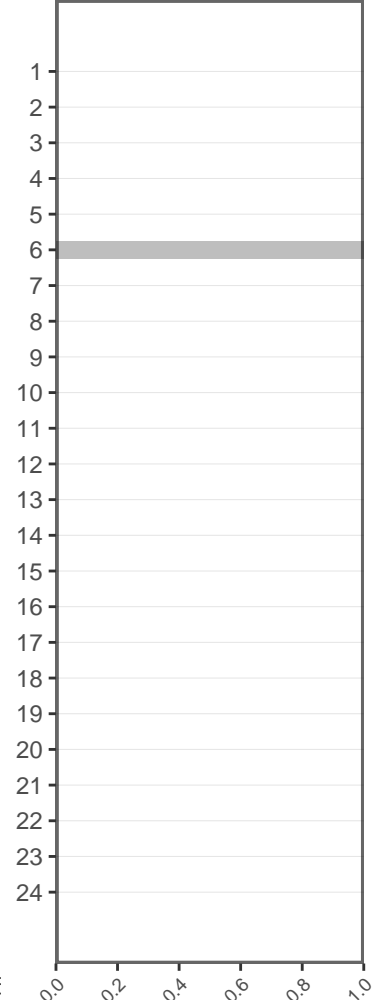
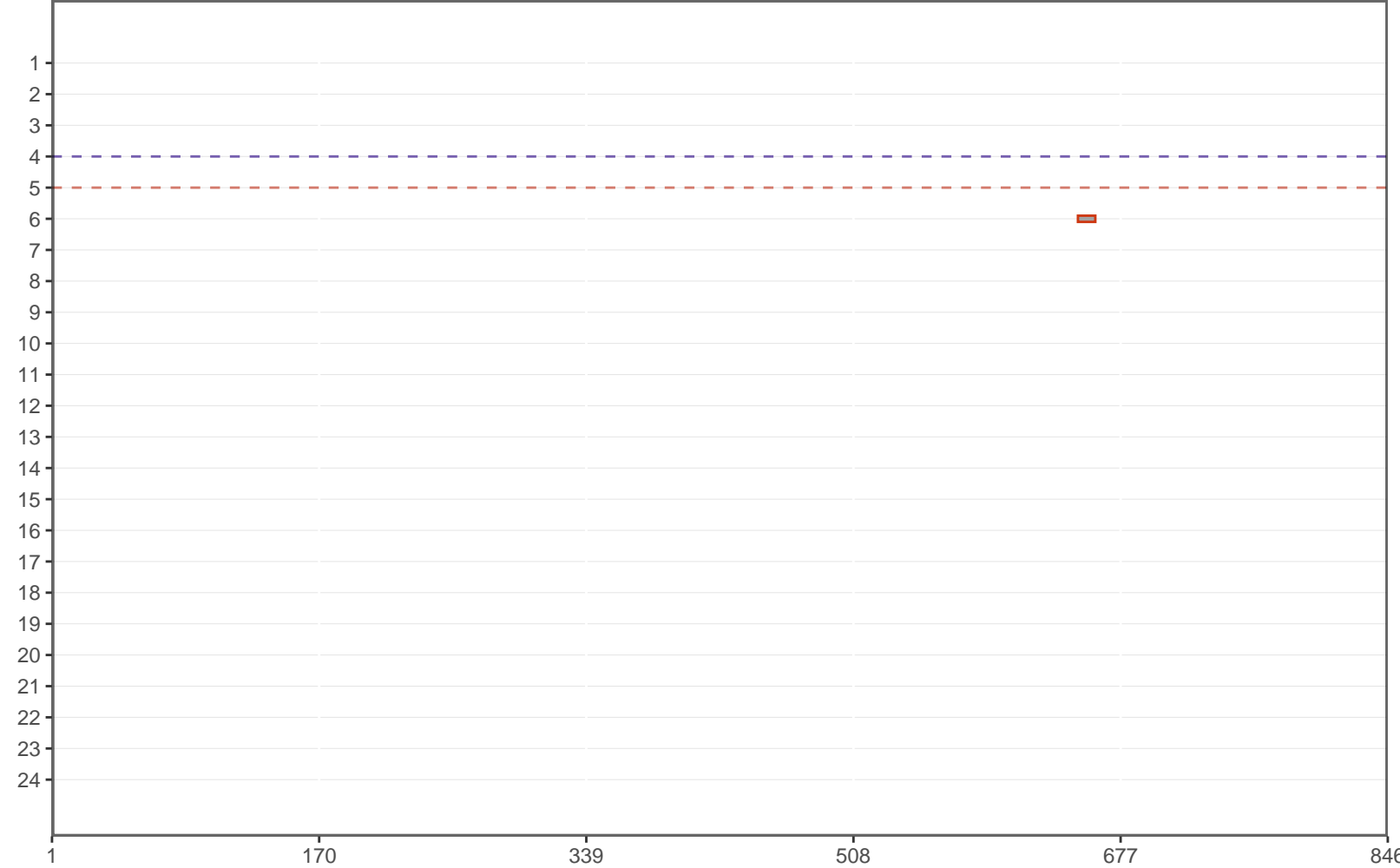
MW indication



Molecular weight



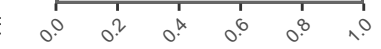
Gel Slice



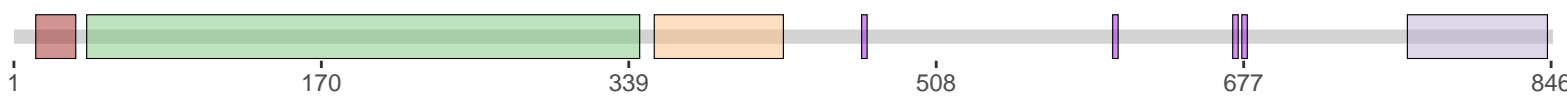
Protein length



Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

XNTVYNTARVCAQSAQGMKMPVNRGFEWGSYNEDAALHEEDNTVTVVGLLEGINTRDVSQHLWYMTDVEIDPTEGLNSGNWPLVTFVSAGAHLVFVNGDLAGTVYGLLENPKLTFENGINLRAGINKELLSIAVGLPNTVGRPHFETWAGVLPVSLSGLENGTRDLTWGKVFYKVLKGEALSLHSLNGSPSEVVEEGLVAGKPLSWYKTTFNAPAGNEPLALDMNTMGKGGVWINGGELGRHWPGYKSGSNGTADNTYDGFDEKGLSLNCGEGSORWYI

NbL06g04170.1 ubiquitin_carboxyl-terminal_hydrolase_6-like [MW = 54.66 kDa]

No. of times detected



log(intensity)



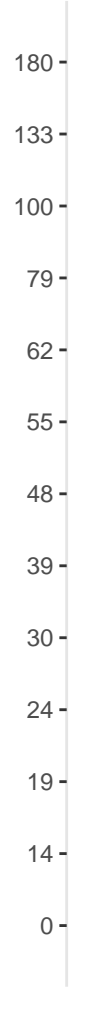
Values from



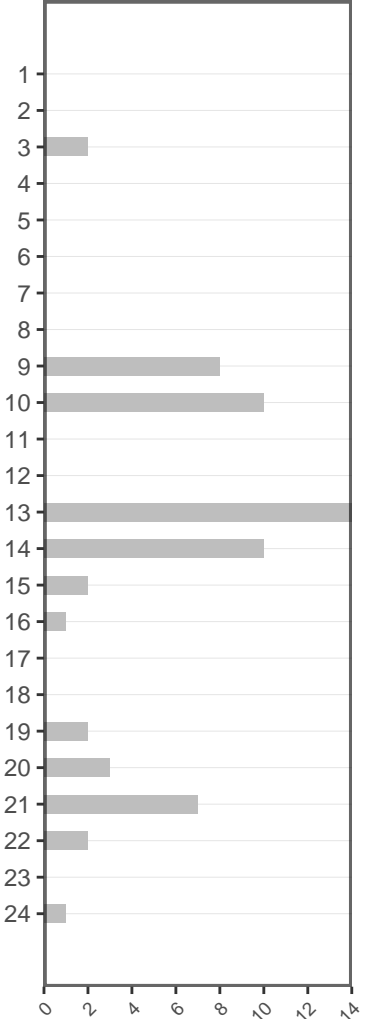
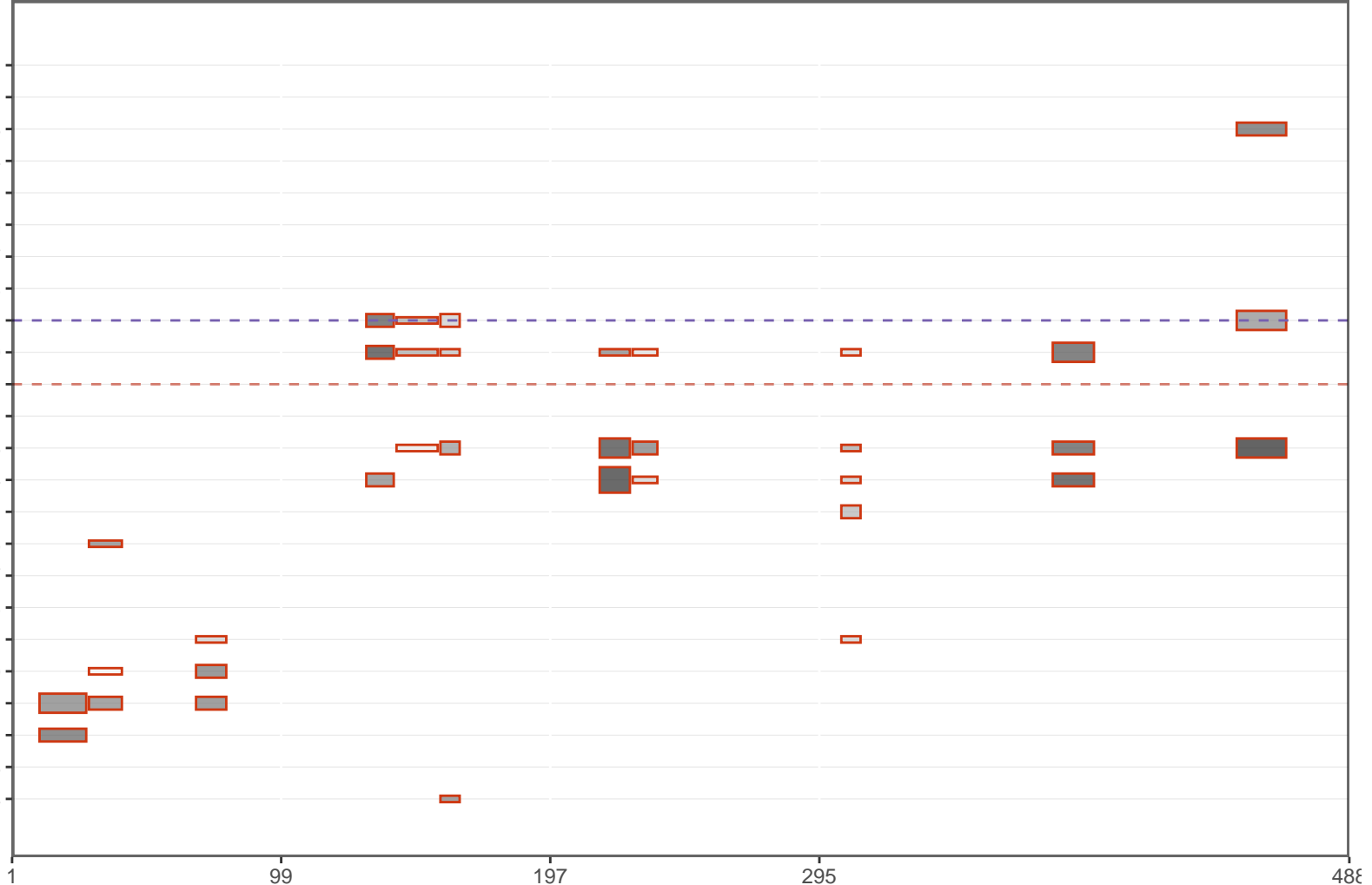
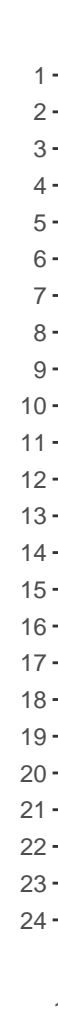
MW indication



Molecular weight

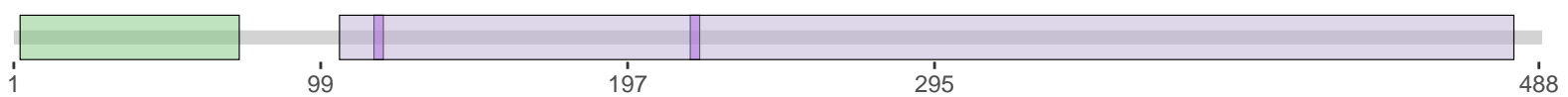


Gel Slice



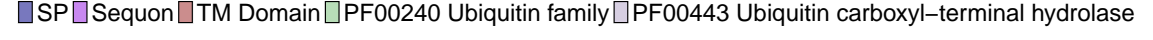
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEFDNRHICAEESGSESTERETVYSLKCHISDEVNHLEGLKRLKSELEKASPELGRSAVYVNDGRNGLPRYLTFQVFRFFVKRESNGKAKILRKYDVPFLSDVYDFGSEDLRKLKLEGRPRQVLRDAEGKAKGLKTSKTKTSSTDDGVMTEAEESSSGGSGEASKTKTQEVNSISGVLPKEKHFTFGINDLVAVLTHKGRADSDGHYAWKQENGVWVGFDDNPFQREEDPILGGGGDWMVHGMKARVPM

NbL06g04130.1 60S_ribosomal_protein_L28-1-like [MW = 15.84 kDa]

No. of times detected



log(intensity)



Values from



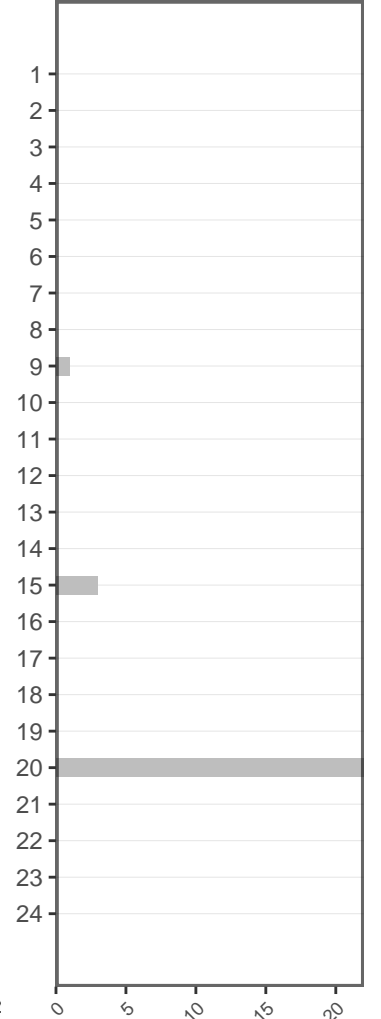
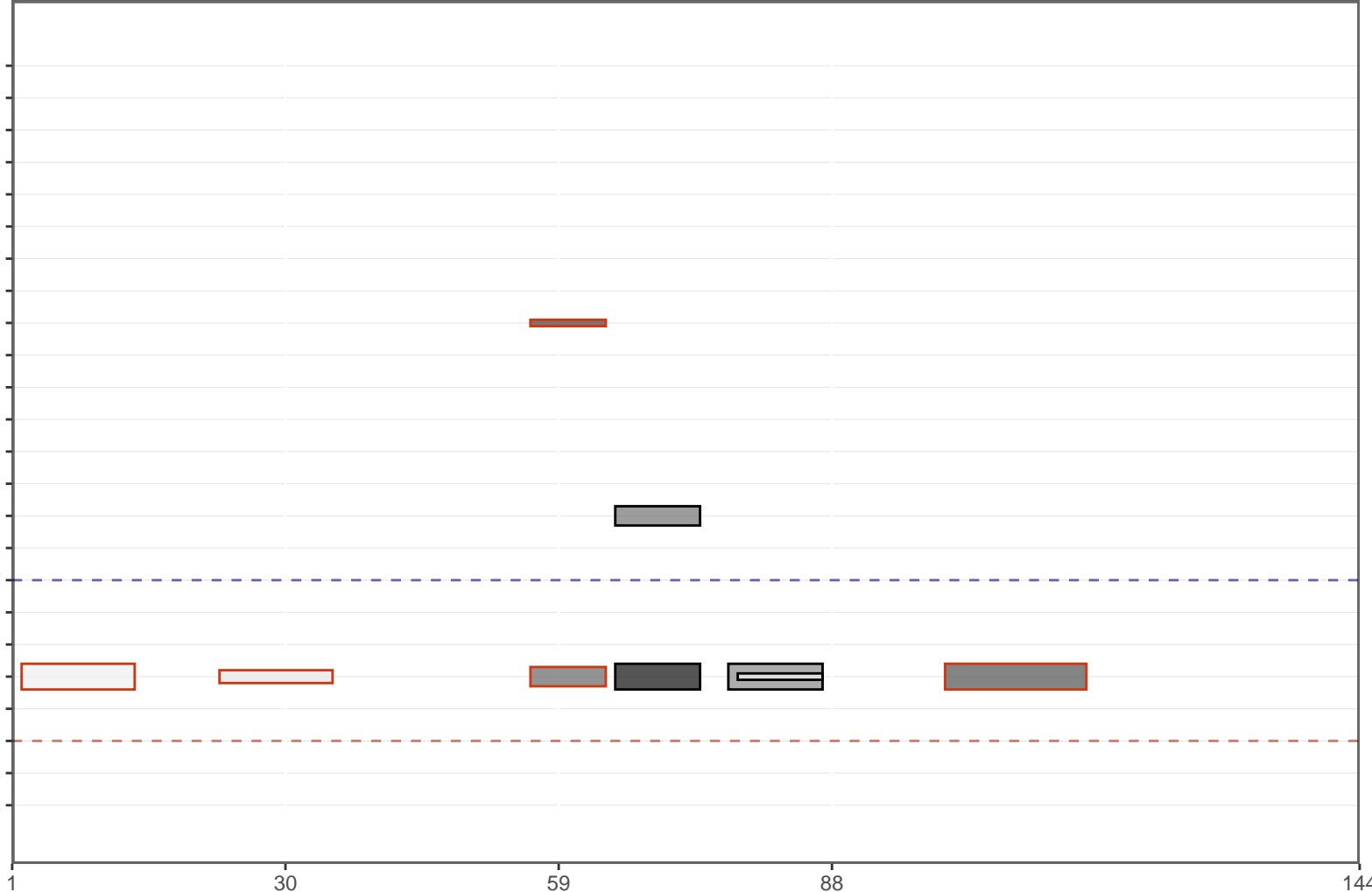
MW indication



Molecular weight



Gel Slice



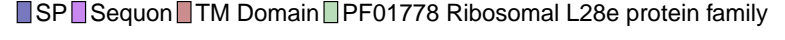
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

QAVGKDDQSVLLATFKTKGKGNPKPSLLNKSGAMKKEFRMAKAVSNGWADNYRDPDKKAAALRLSAVNRSLKAVNSGVKKRNRGA*

NbL06g04050.1 NADP-dependent_malic_enzyme_chloroplastic [MW = 70.38 kDa]

No. of times detected



log(intensity)



Values from



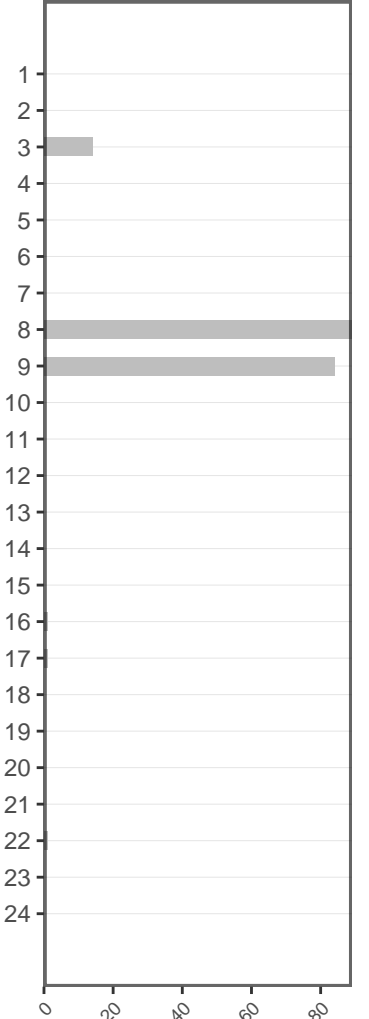
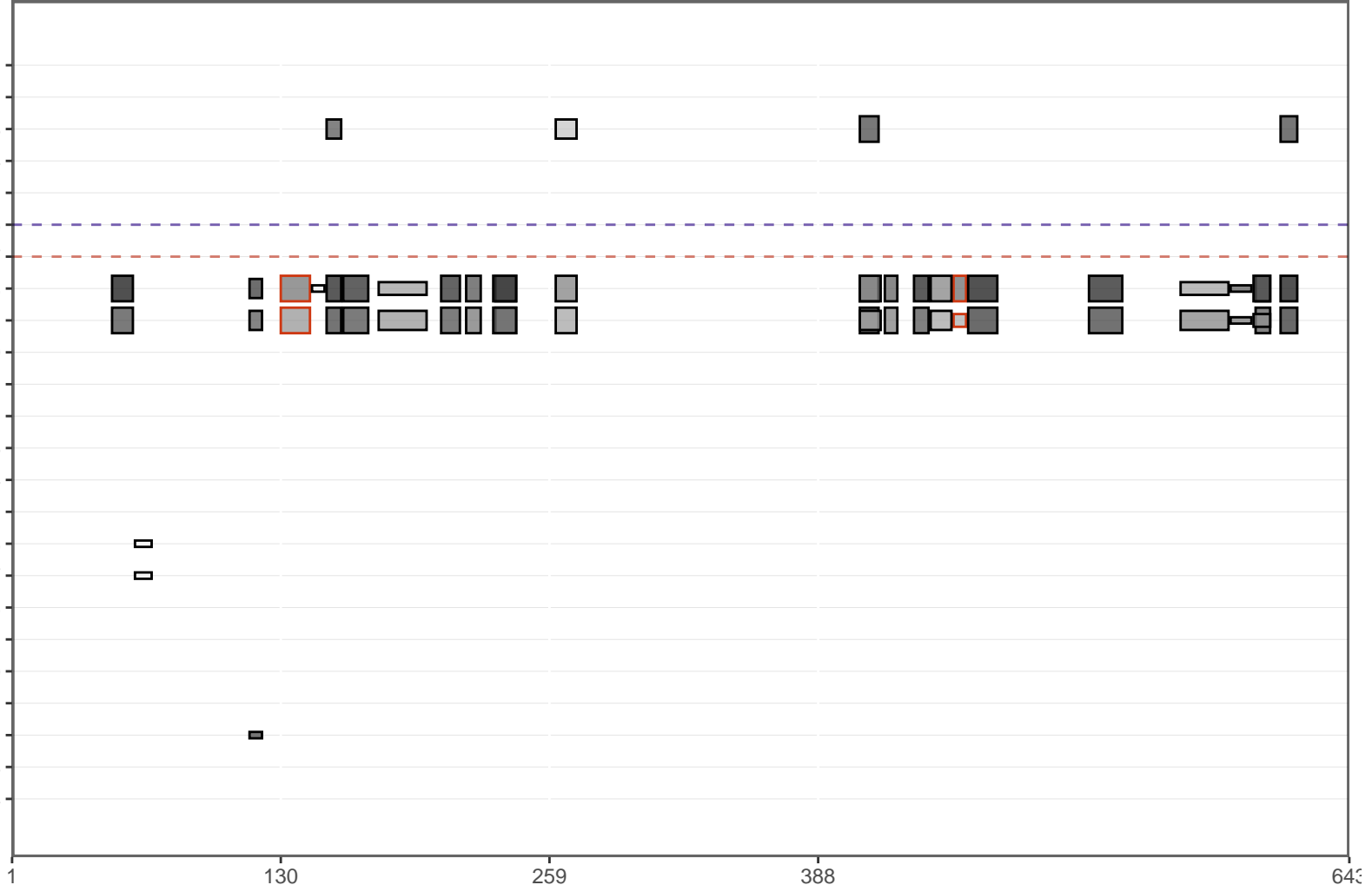
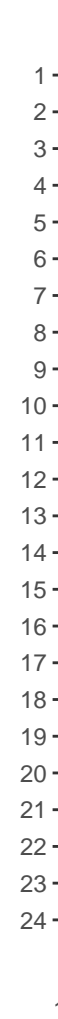
MW indication



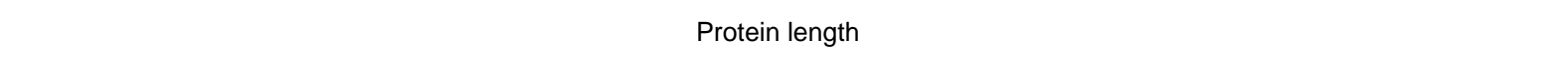
Molecular weight



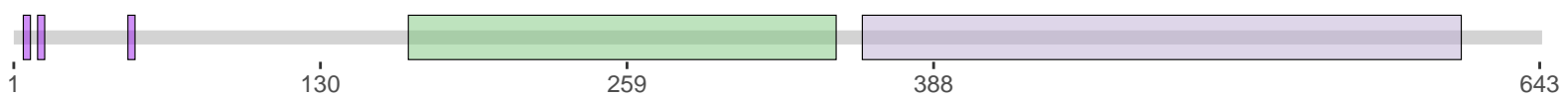
Gel Slice



Protein length

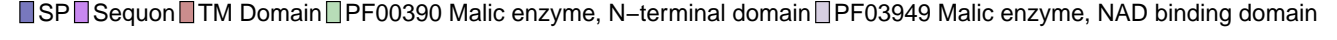


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGQEYAELEDFELMVAWKGNYGKVLQGFEDFANHNFDLLAKYGGSHLVFNDDIGGTASVVLAGVMAALQGLVGGTLEHTFLFGAGEAGTGIAELIALEVGGKGTGPLEETRRKKWMLDQKGLVNSRMEISLQHFKRFPWAHDHDFPKDLVNAVSKKPTVLIGSSGAGRFTTEKVVQAMATFNEKQIFALSNPTGSGSECTAEAAVTVSEGRAFASGGFFAPVEYNGKVYASGGANNVYFPFGGLGHSGAIRVHDDMLLAASEALAEQVSGENFEKGLYPPFTNRKISANJ

NbL06g03900.1 cytochrome_b6 [MW = 24.15 kDa]

No. of times detected



log(intensity)



Values from



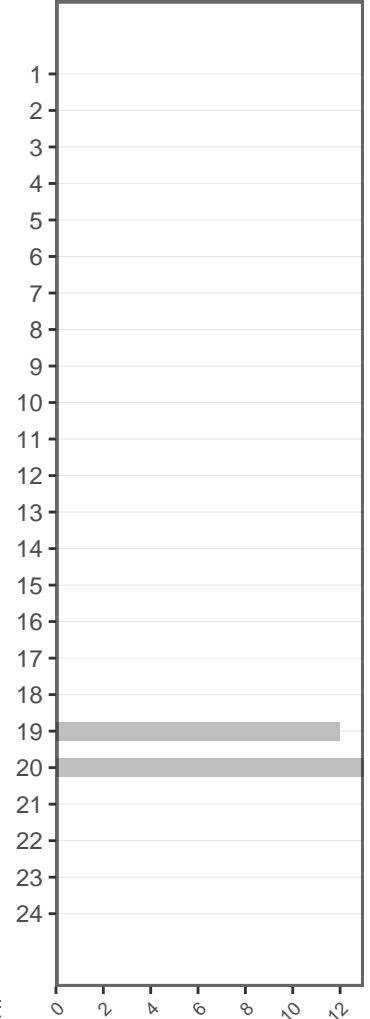
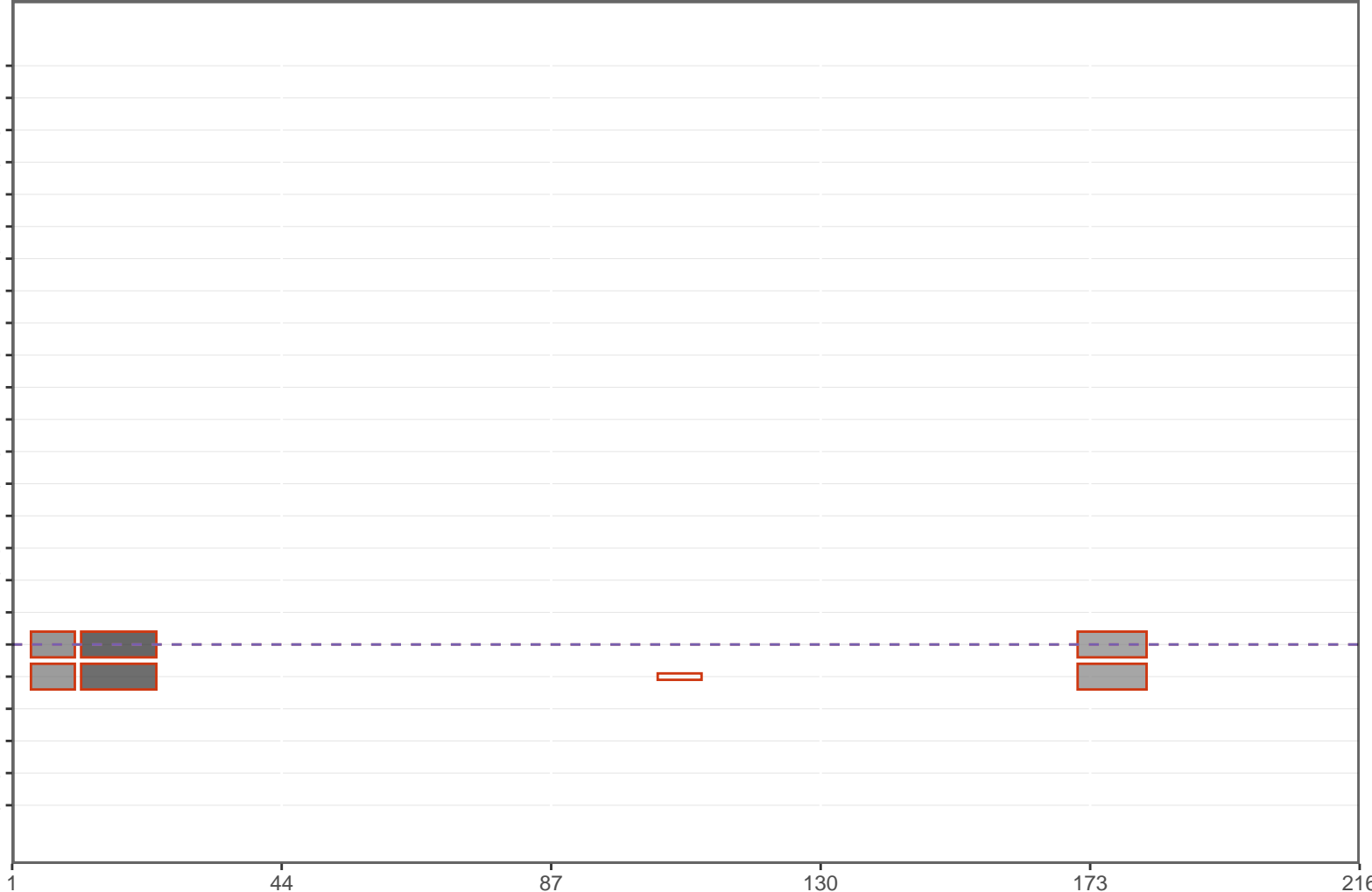
MW indication



Molecular weight

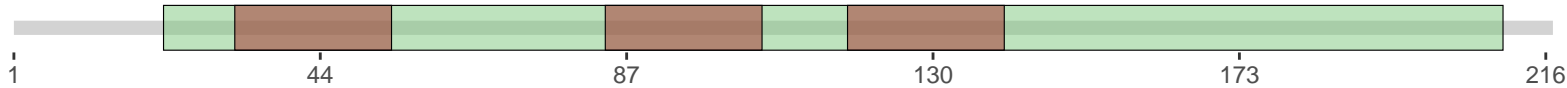


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

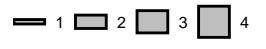


Protein sequence:

LMMLHFRYYLTGGFKKPRELFWTGVVLAVLTASFGVYGLPFDQDQGYWAKKVTGVPDMPVIGSPLVELLRGSASVGGSTLRFYSLHTFVPLPLTAVFMLMFLMIRKGGISGL*

NbL06g03810.1 heat_shock_70_kDa_protein_15-like [MW = 94.07 kDa]

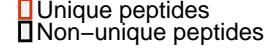
No. of times detected



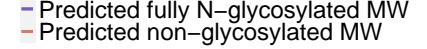
log(intensity)



Values from

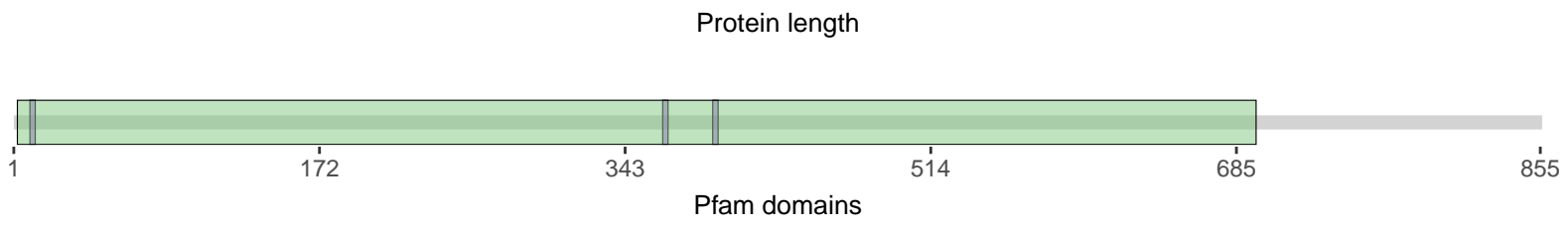
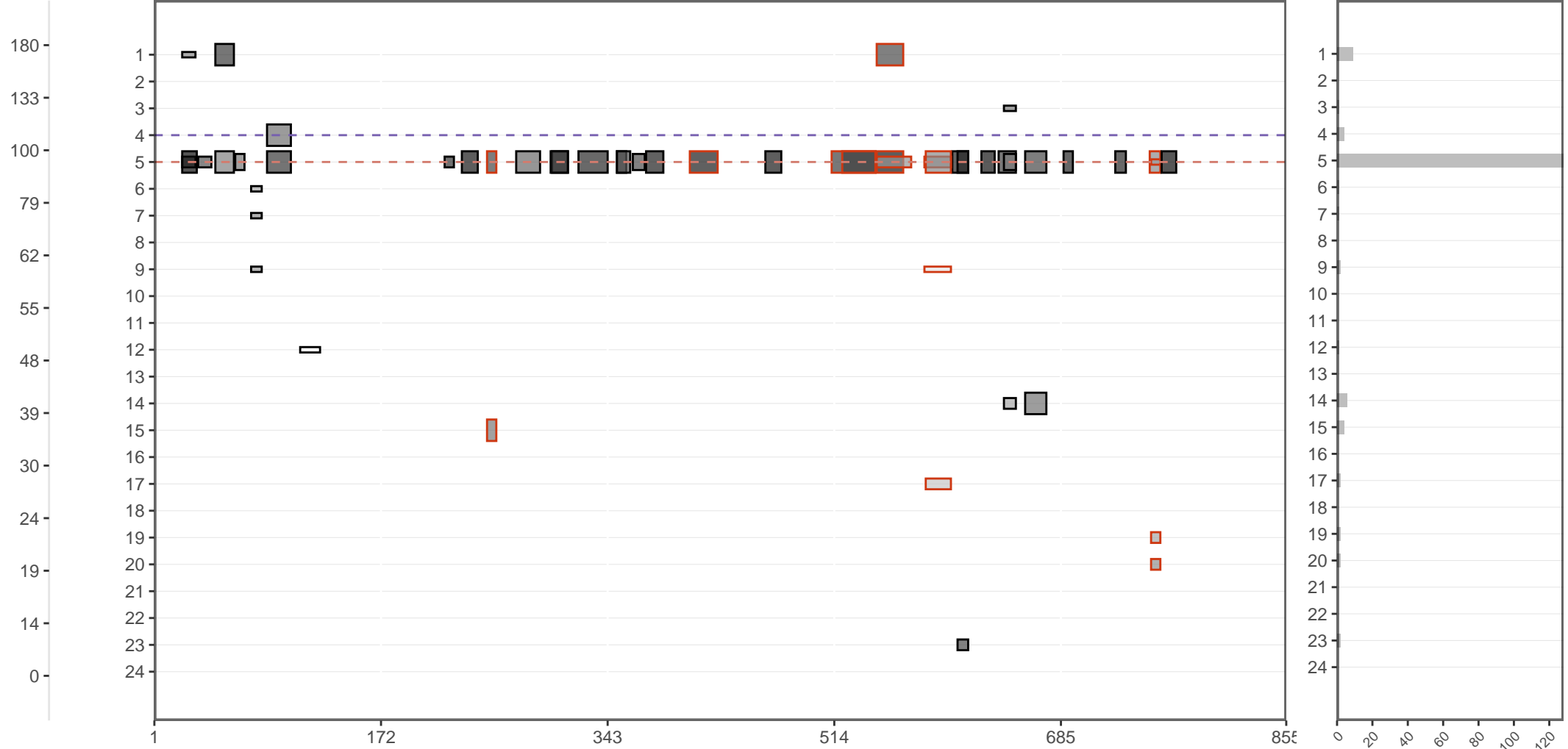


MW indication

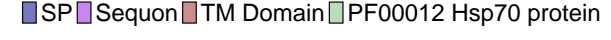


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

ITVFFKGNPISVYKALTFYRSGTFTDVGVAIDSELGAPAWISTYTHGPFQSAKGERAKLKVWRNLHGVIVDFATLLEEEVEVPIVKEAVKFAKMETDEASGDAPSTTSSESDVNMAGDAKAGDASGTENGVPESGDKPKVKMETDAKVEAPKPKVKTKTSVPIVTEIVYGAMAAADVQKVEKEMALGDRVMEETKDKKNVAEAYVDMRNKLSGKYGEFVDSEREGFMALGVEVDLWYEDGEDETKGVYIAHLEELKKGGDPIQRWKEGEMERGSDYIDQFYCI

NbL06g03640.1 pyrophosphate-energized_vacuolar_membrane_proton_pump-like [MW = 80.23 kDa]

No. of times detected



log(intensity)



Values from



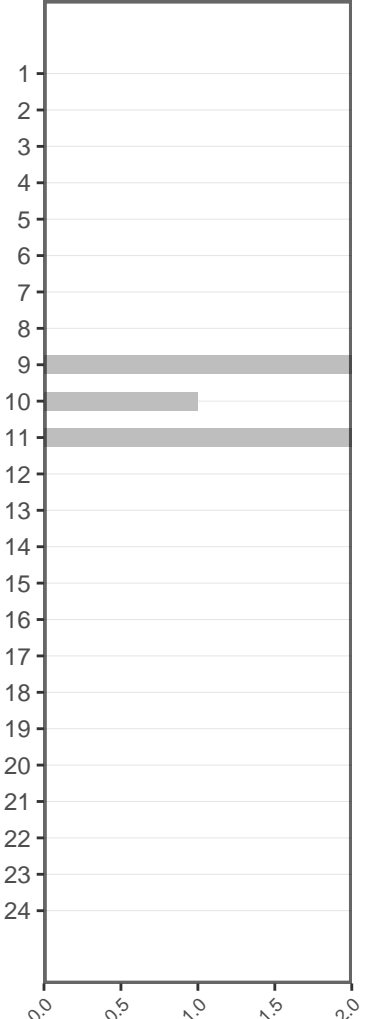
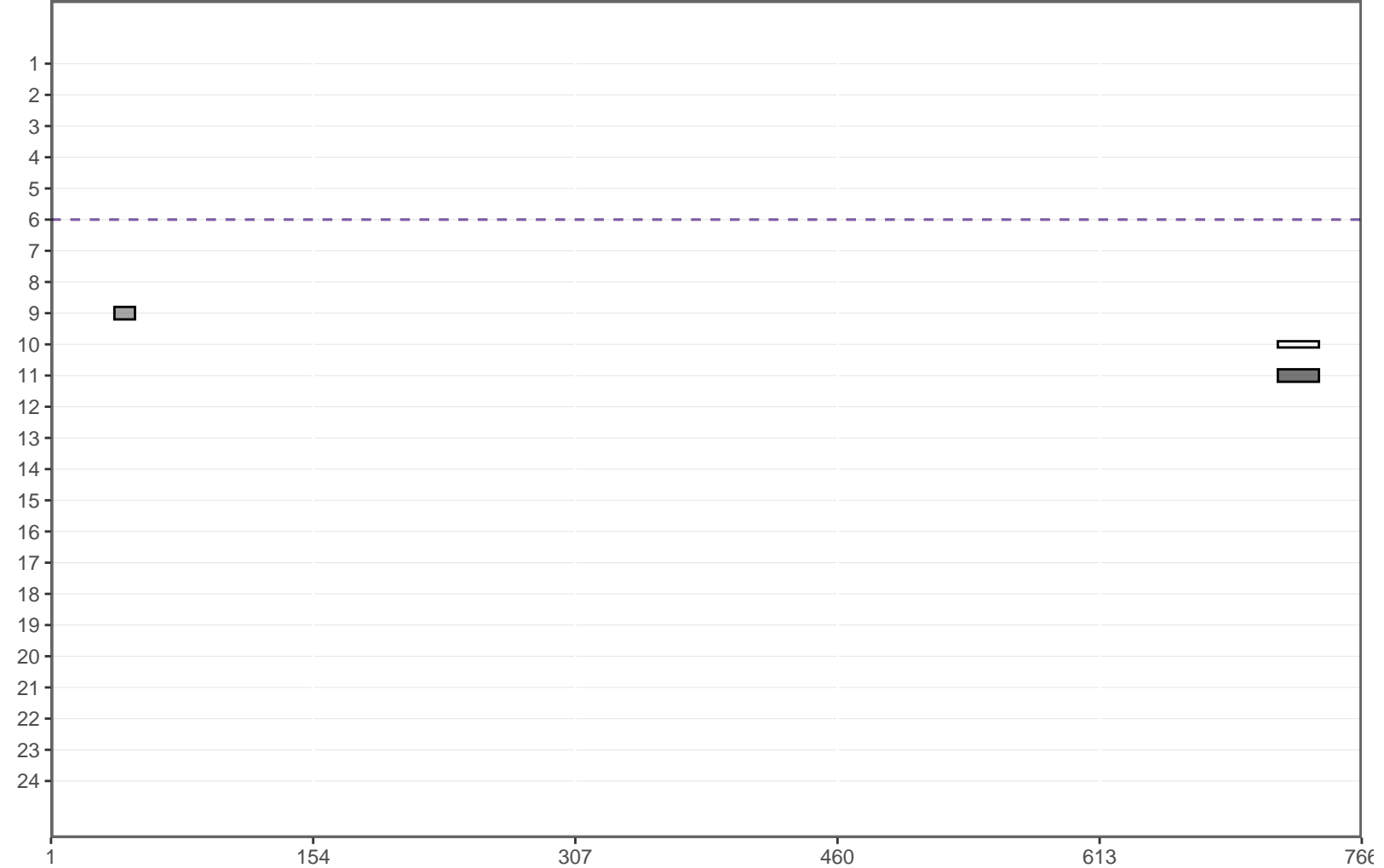
MW indication



Molecular weight

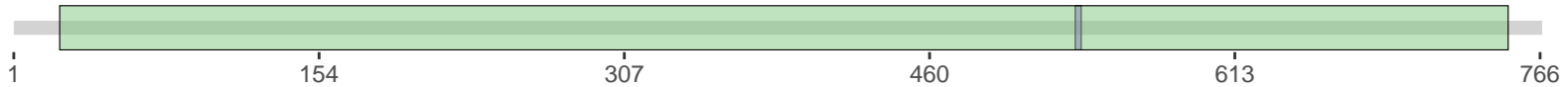


Gel Slice



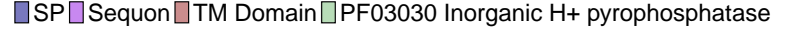
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

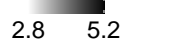
MTVGIAVITWTCLEPSFTIFRFGAGKVKNNWQLFLGVAVGLWAGLHGFVTEYFENAYSPVGDVDSGRGTGAATNVIFLGLAGYKRVIPFAIAIAIVSFQFSAAMYGVAALGMLSTATGLADAVGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTAAIGKGFAGSAALVSLALFGAFVSRAAITVDVLPQVFIGLVGAMLPWFSAATMKSQVSAALKMVEEVRROFNTPDGLMEGTAKPDVATGVWISTDASIKEMIPRGAALMLTFLVGFVETLSGVLAGALVSG

NbL06g03590.1 uncharacterized_LOC107791394 [MW = 29.7 kDa]

No. of times detected



log(intensity)



Values from



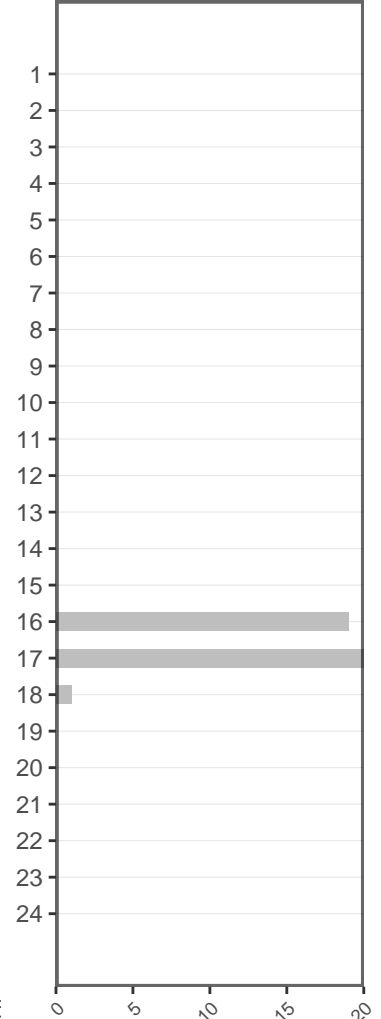
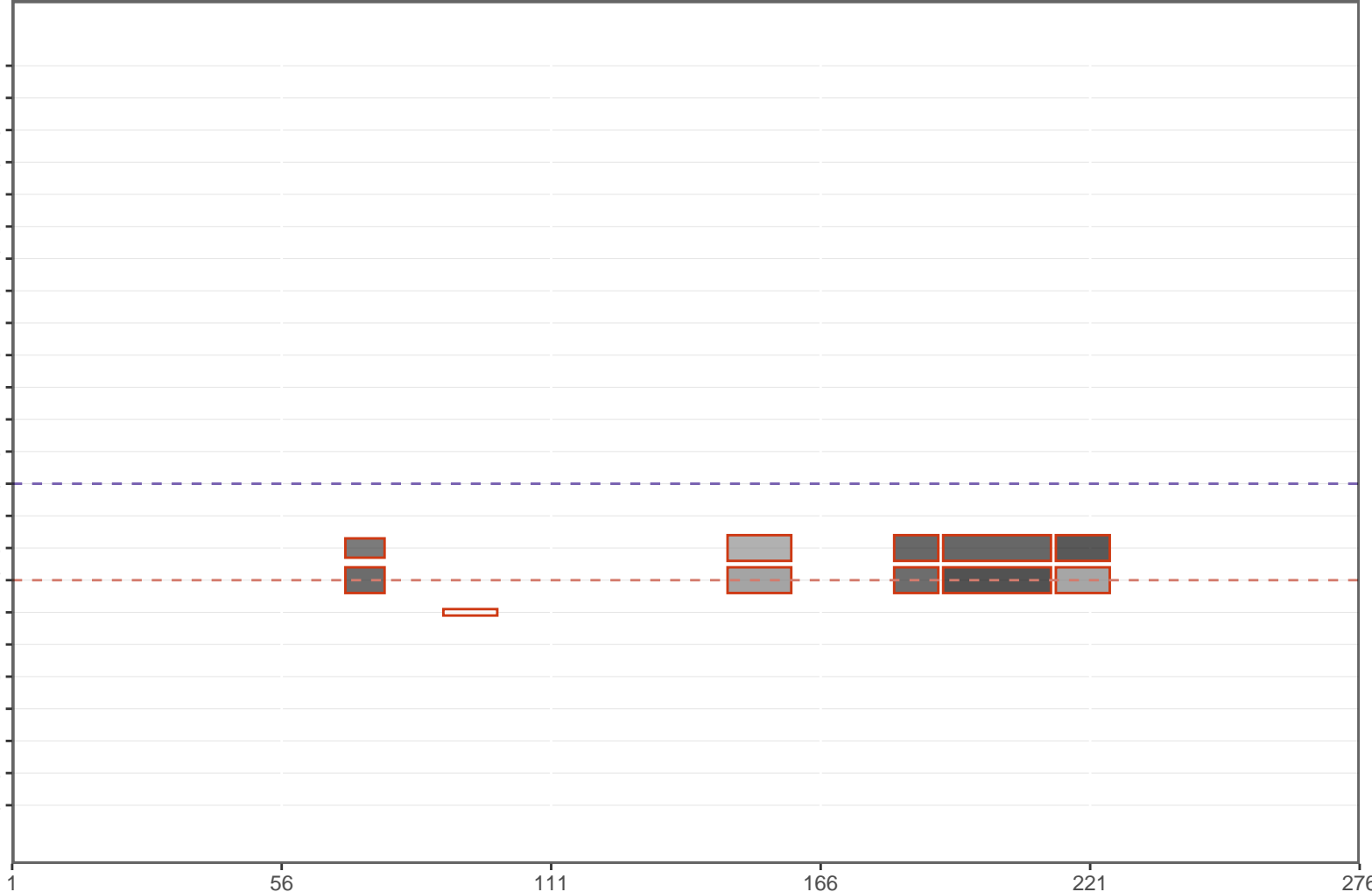
MW indication



Molecular weight



Gel Slice



Protein length

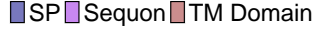


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IFNQPIMCGEPRAMLMKTRGKADPPYTHQIGPKHALGLIFETNGTEWDGPPYRLGFQVFNWIRNKPTEFEFTEGLAGELSGEGAGDKAIFPDITNIVITRQAMVGNLSVEGGDRGDLDIVPGGIDFSGSPHFNPLANVDDGSGPPVSDAED

NbL06g03340.1 guanine_nucleotide-binding_protein_subunit_beta-like_protein [MW = 37.69 kDa]

No. of times detected



log(intensity)



Values from



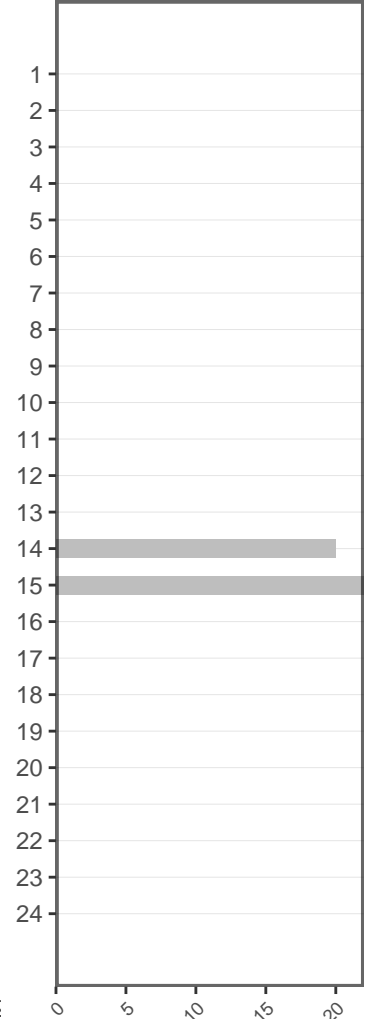
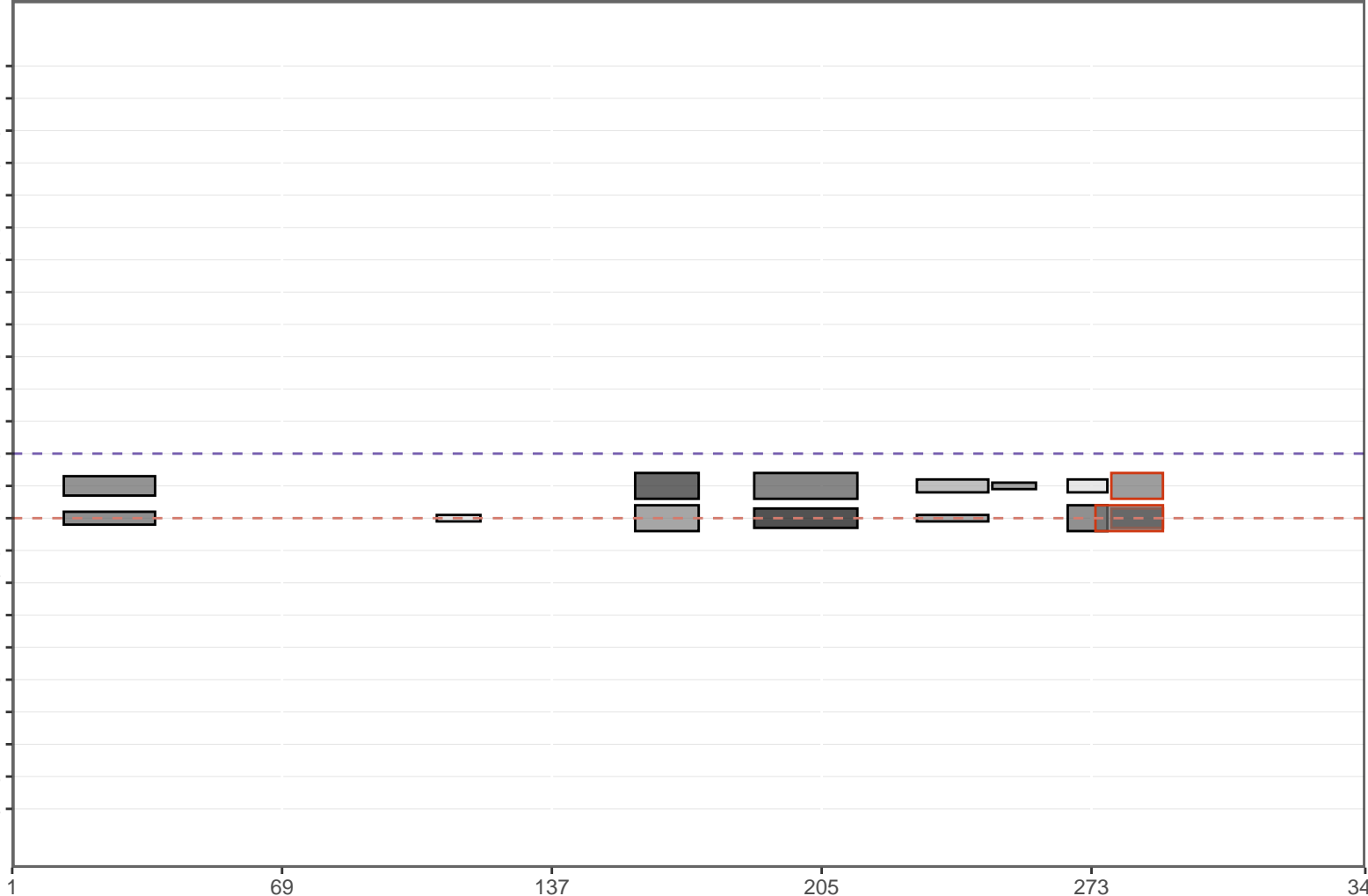
MW indication



Molecular weight



Gel Slice

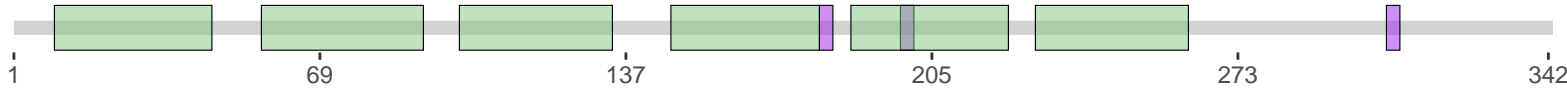


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

CVRFSPNLFQPTIVGGSDWRTVKNWLNKLRATLGHFTGVYNTAVSPDGLGASGGKDGIVLLWDLAEGKIKYLSLEGGIHLGFSFNRWVLAATSESSIKWDLKSTIVDQKVDLKHGESEMAEGTAGKQKVDLFFVIFDFPKNVTFFGLLDGVFVSENEVIGLNWVYHISFGGCVLLP

NbL06g03220.1 psbP-like_protein_1_chloroplastic [MW = 26.71 kDa]

No. of times detected



log(intensity)



Values from



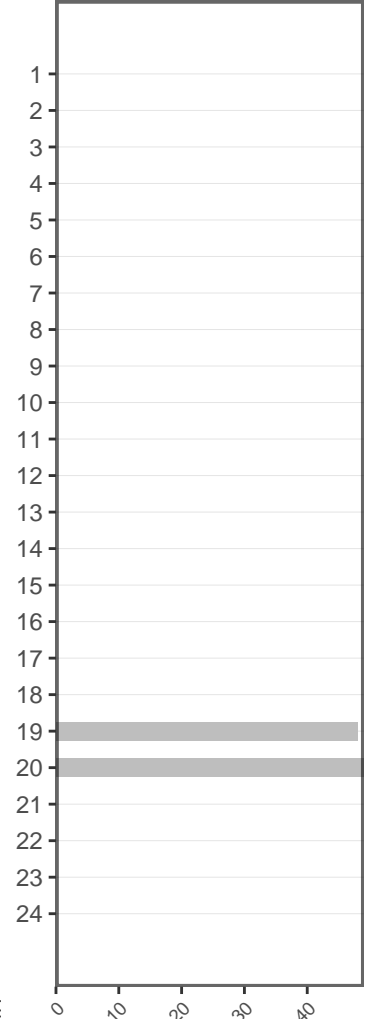
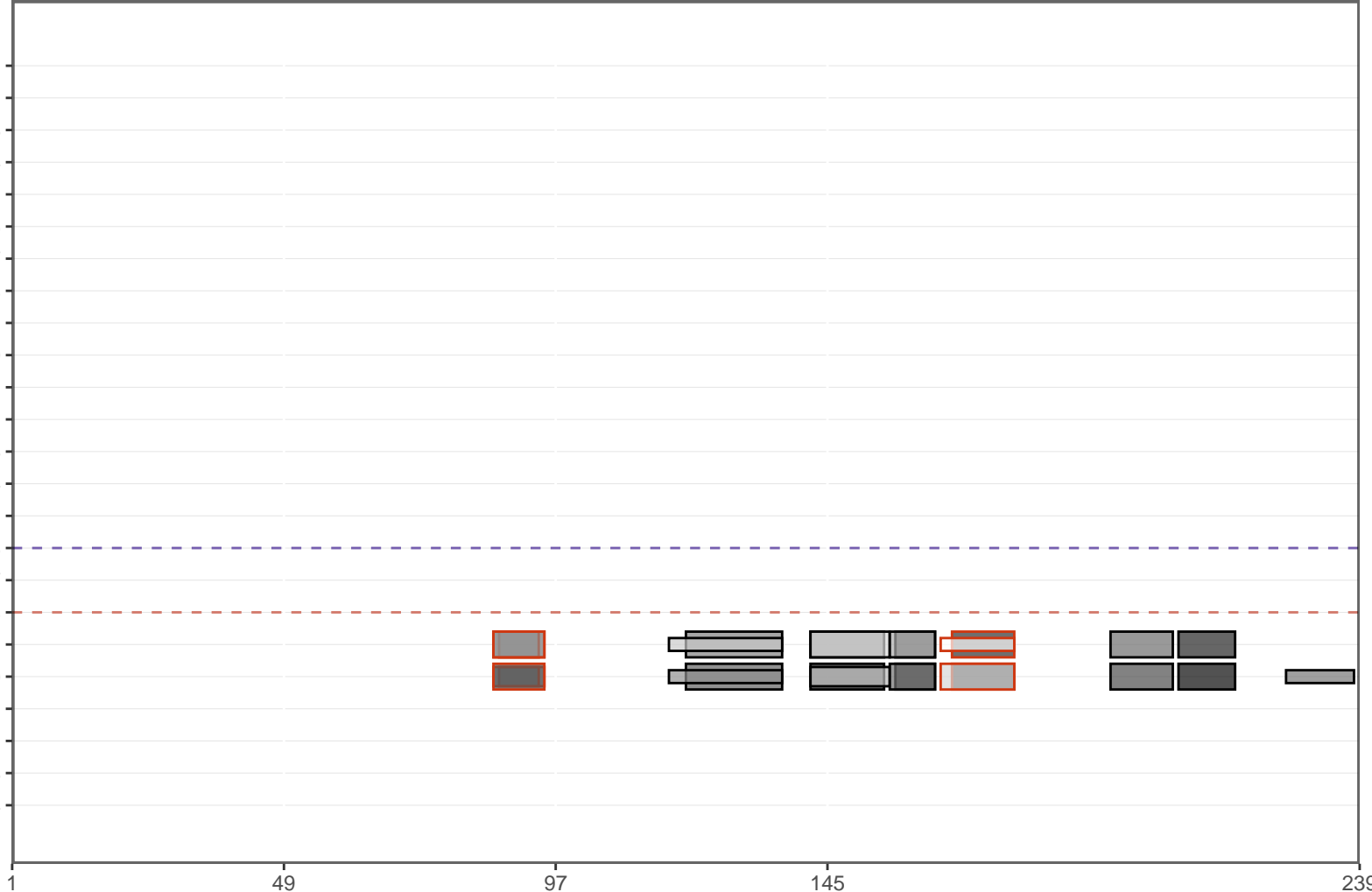
MW indication



Molecular weight

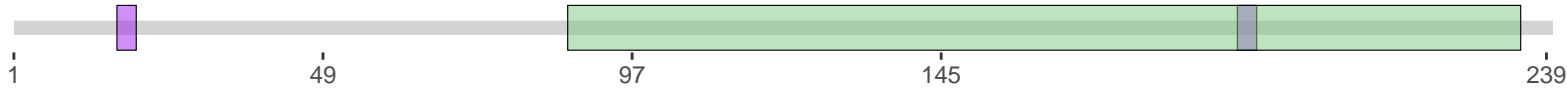


Gel Slice



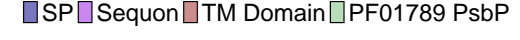
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SWQEVVVEGGDKVFKDVEFLFESGVNVIPTSKGDRDFGSPQEVAEETLKKFLFSSPQKTKLEASQYDVEGKAYTFEFWQAPNFRHGLTAVGIGNGKFKYTLTGANERRWEKMDRLHTVVDSEDFQVY

NbL06g03050.1 serine/threonine-protein_kinase_16-like [MW = 38.69 kDa]

No. of times detected



log(intensity)



Values from



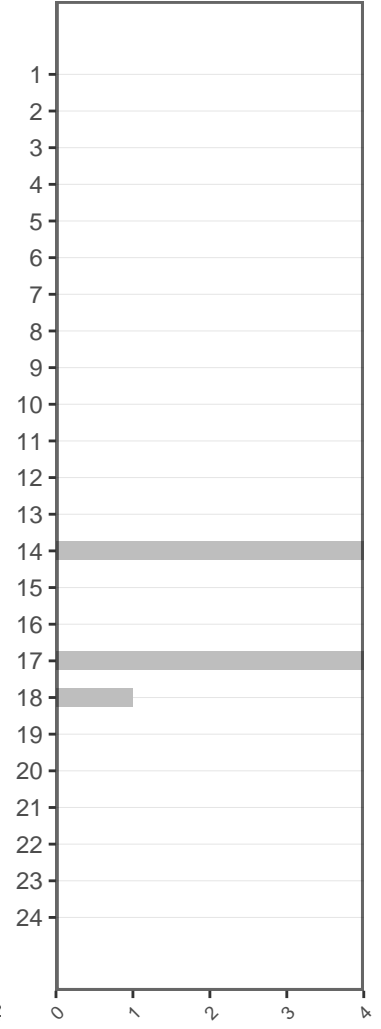
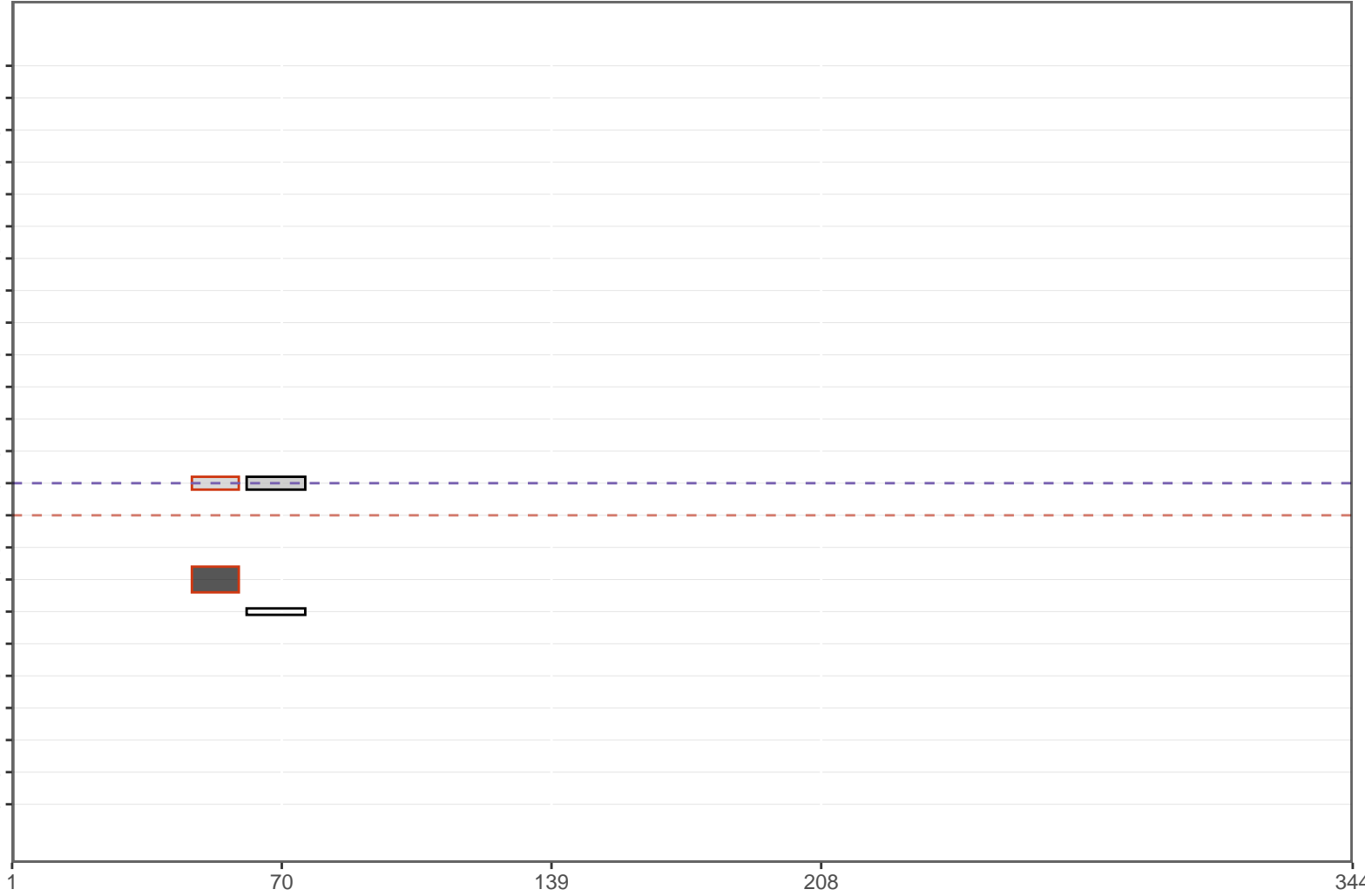
MW indication



Molecular weight

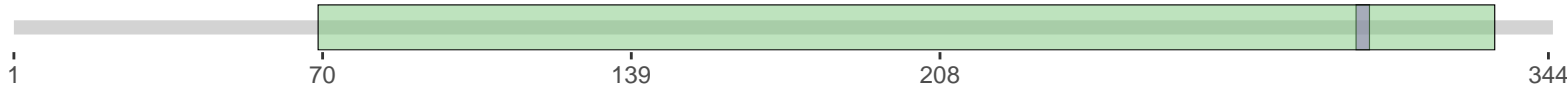


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

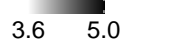
DIFRQLCAGLQIMHNFDPPIAHNDVKRANLLTHKKGQTPKTKLMDFGNARPARRGRISPEALQLQIEWASEHWAPFRAPELWDGPGSGCIDDERTDIWSLGGTFLFAMYGVSFFEFYAFEESESPQLAVNAQIKWTEPNTSYPDALHGFVTWMLGPGATVRRPRIDDIKVDKLSKYSTN

NbL06g03040.1 agmatine_deiminase [MW = 41.91 kDa]

No. of times detected



log(intensity)



Values from



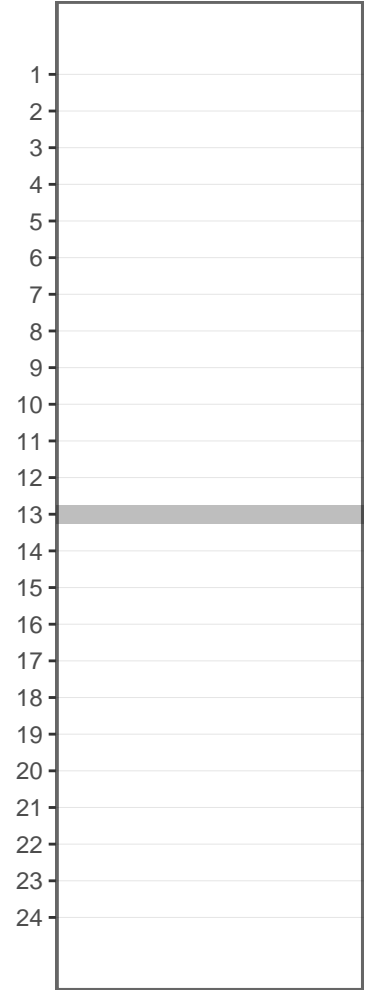
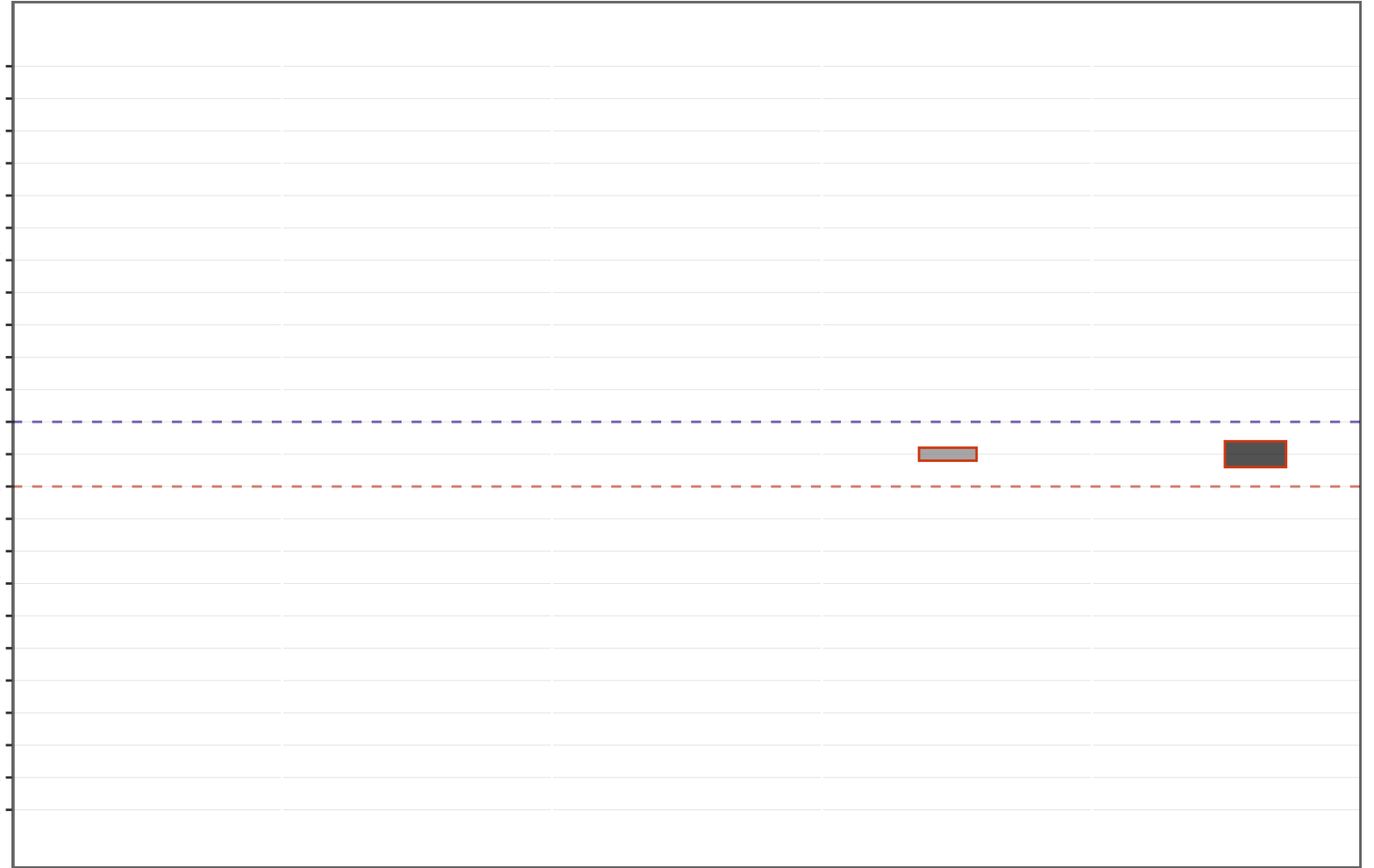
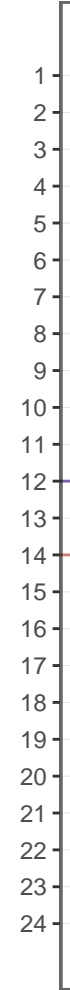
MW indication



Molecular weight



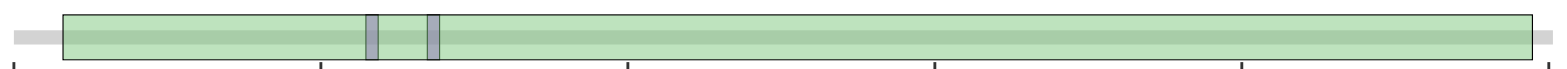
Gel Slice



Peptide counts over 4 repeats

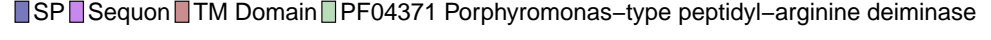


Protein length



Pfam domains

Pfam Description



Protein sequence:

IGTCLTTECLLNKRNPHLSKEGIEHELKAVLGVVKIIVLPRGLFGDDDTNGHIDMCGCFKPGVLLLSVTDQDSDPQYERSEALSILETTFFDANGRIKLVKLVHPCLMTDEEADGFQDGDAAKPRTSGLRLAASVYVNFYIANGAITPFGDKKWDDEANIRVLSLAFDPHEVVGEGAREVLLGGGNHGTGGQPSGP

NbL06g03020.1 H/ACA_ribonucleoprotein_complex_subunit_2-like_protein [MW = 16.97 kDa]

No. of times detected



log(intensity)



Values from



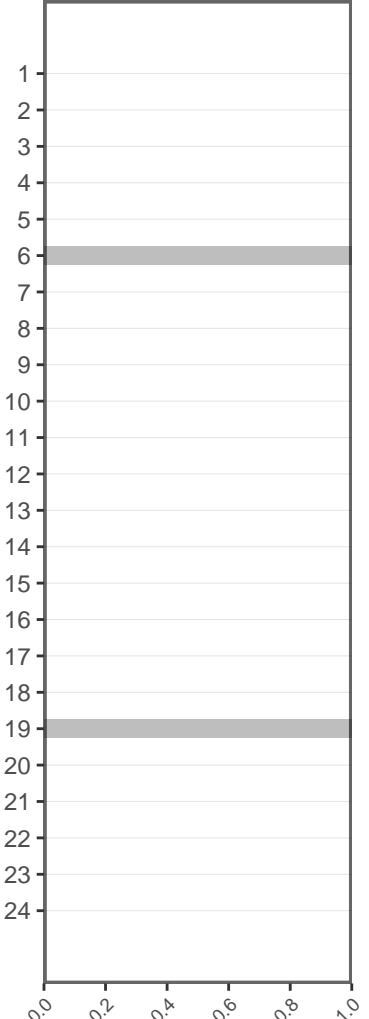
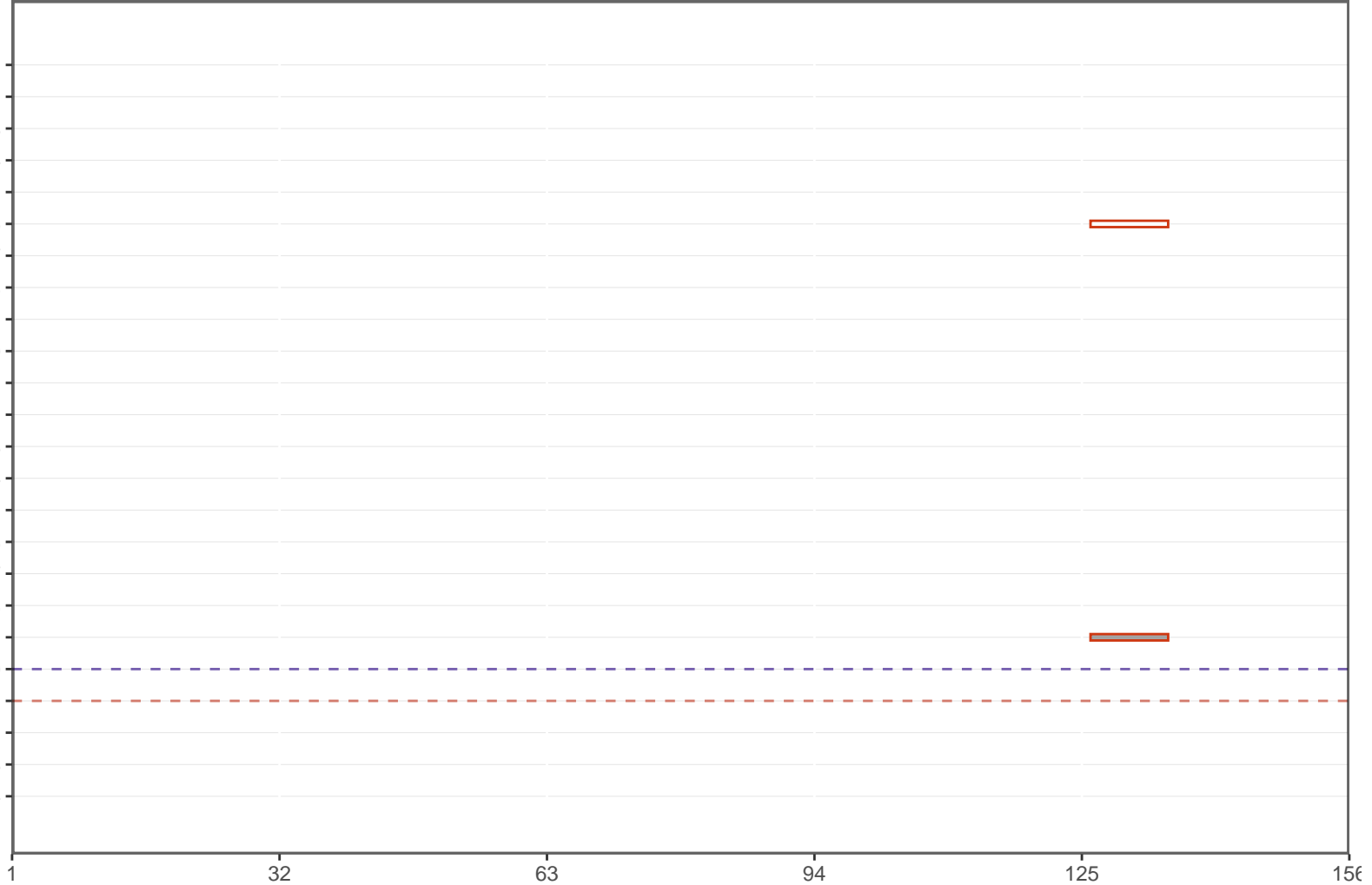
MW indication



Molecular weight



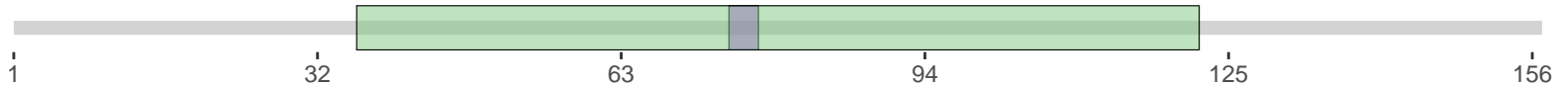
Gel Slice



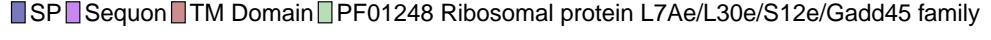
Protein length



Pfam domains



Pfam Description



Protein sequence:

QKGVVIAQNSPIDWTHVPLGEEAEPVYVSSKEELANAGATKRPTGCVLQTKRAGELSGEDGKPKADYDQVYVSEVGEASSEMF

NbL06g02670.1 ATP_synthase_subunit_gamma_mitochondrial-like [MW = 35.28 kDa]

No. of times detected



log(intensity)



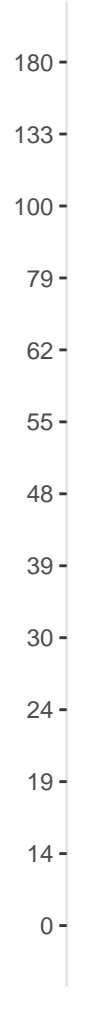
Values from



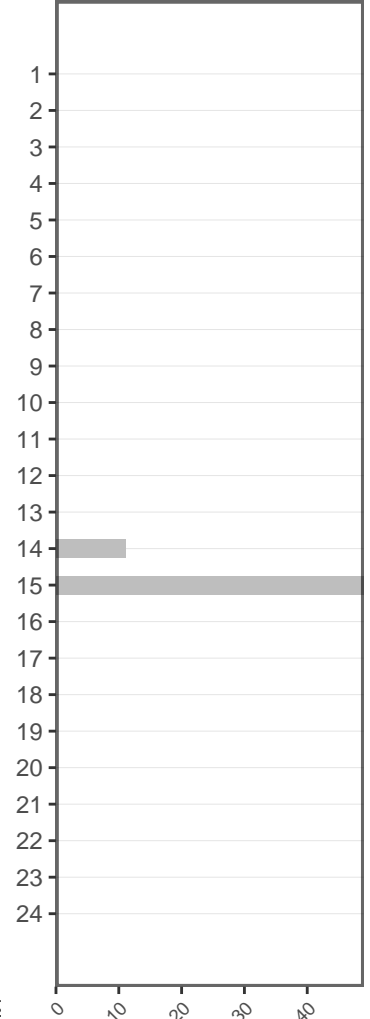
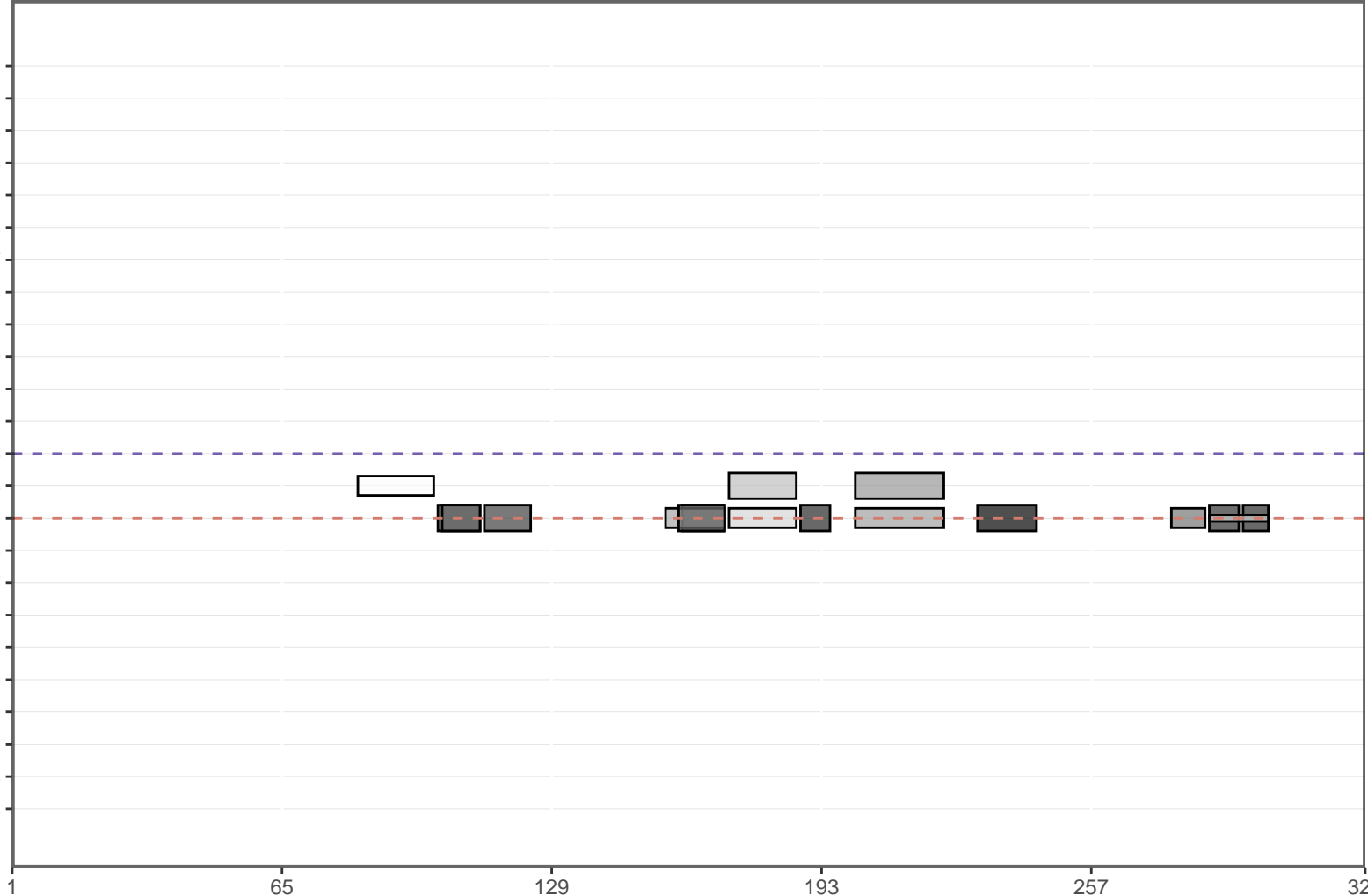
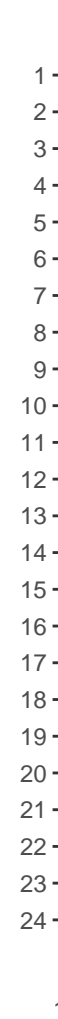
MW indication



Molecular weight



Gel Slice

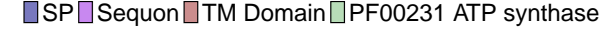


Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

KAQAQLVRSKXKDELIMTELGKPLNVTGQVSVWADDLKNVFEFDALRIYKFGVAVFLPTMSTVLSPEVVEREESGGKLGELDSYVEVEGAETKSEVLQNLAEFGFQVFLNALLEENATGEQGARMSAMDGSSRNAGDMLDRLTLTYNRRTRQASITTELEIHSASALEG*

NbL06g02600.1 40S_ribosomal_protein_S19-3-like [MW = 16.04 kDa]

No. of times detected



log(intensity)



Values from



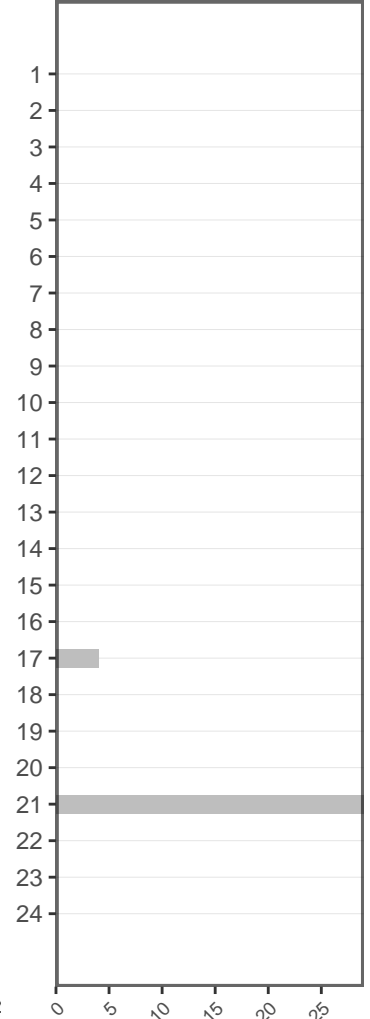
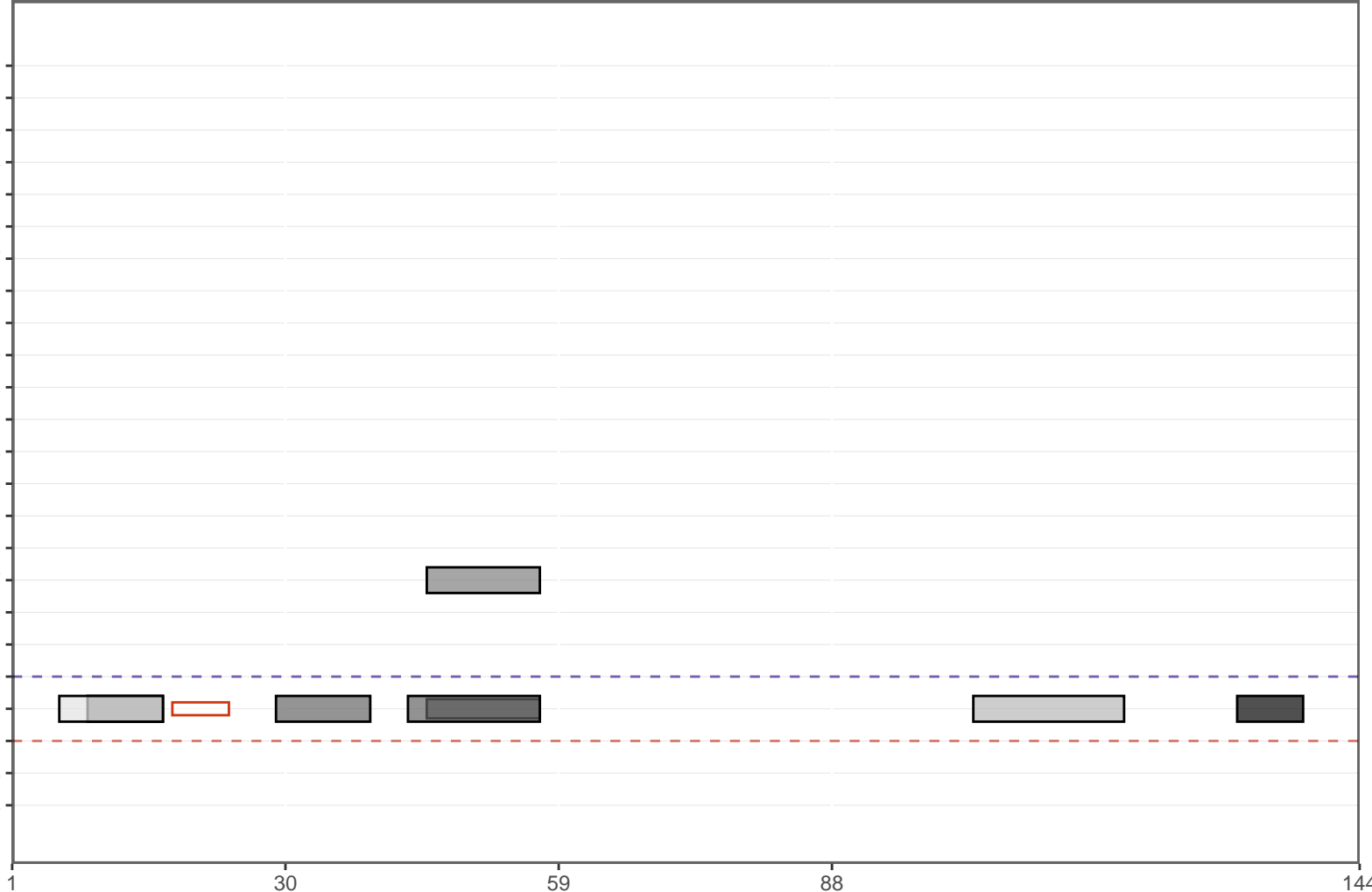
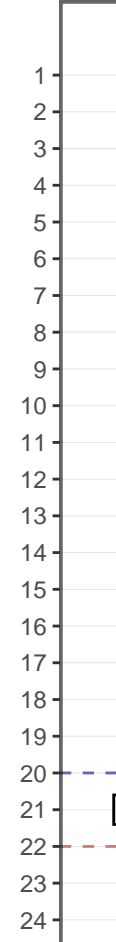
MW indication



Molecular weight

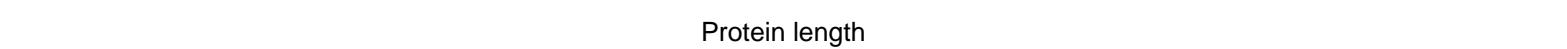


Gel Slice

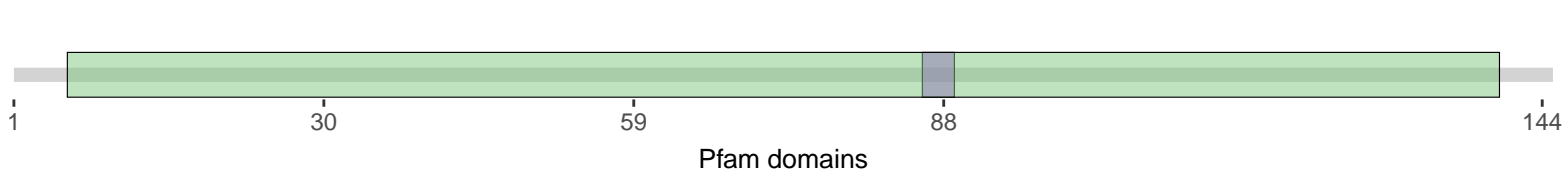


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

ISMARKYLRGGIGVGFRRIRYGGNGRNGRNGRPRHFCKSGSGVARNLQQLGMNIVDFDPKGGRRITFNGGRDLQVAGRIAAAL

NbL06g02190.1 probable_voltage-gated_potassium_channel_subunit_beta [MW = 44.68 kDa]

No. of times detected



log(intensity)



Values from



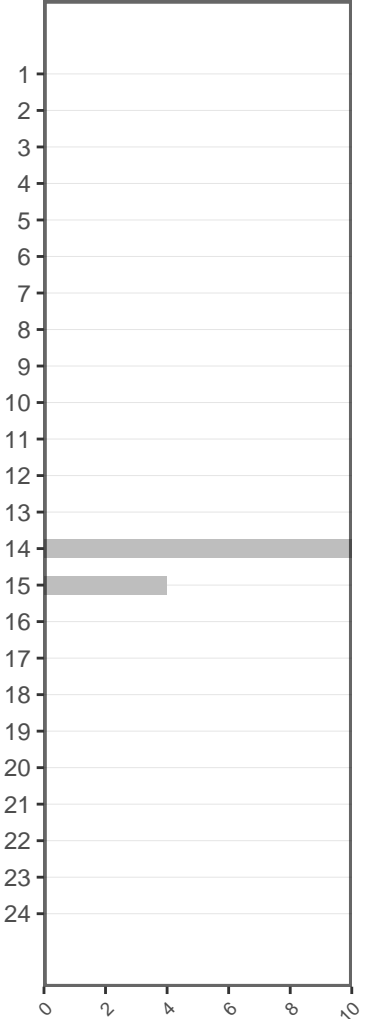
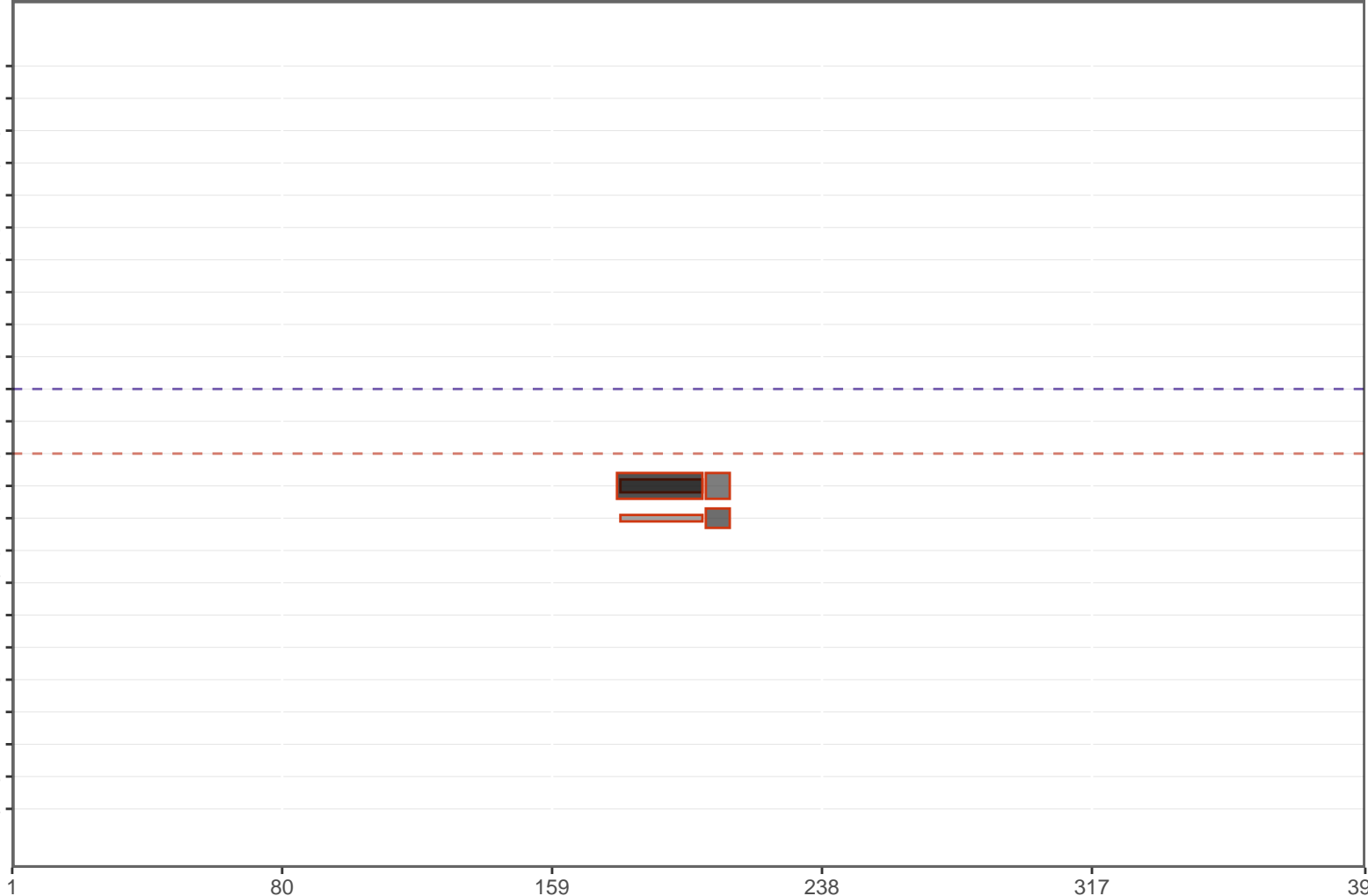
MW indication



Molecular weight



Gel Slice

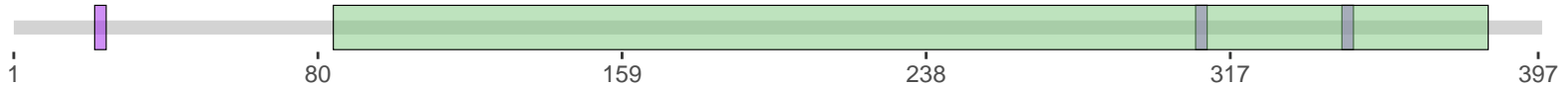


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

XLVYHRPDASTPIEETVRAMNYYVQKGFVAFYVGTSEWBAQQITEAWGVQRLDVLGPIVEGDFENLLSRHKVSEYLPVLYNVDGLTFTWSPVLAAGVLTGKYVAGNIPADSRFALENYKLNANRSLVDDLRKRVDDGKPIAESLGVPLPQLAAWGAANPNVSSVITGATKEYQIEENMKAINVPIMLTRVAMERIEAVVSGKPKRGGDSYR

NbL06g02000.1 PLASMODESMATA_CALLOSE-BINDING_PROTEIN_3-like [MW - SP = 17.13 kDa]

No. of times detected



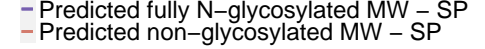
log(intensity)



Values from



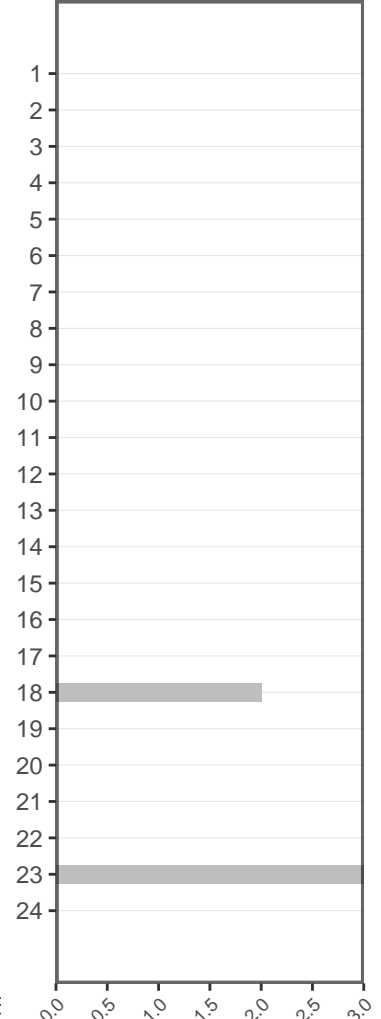
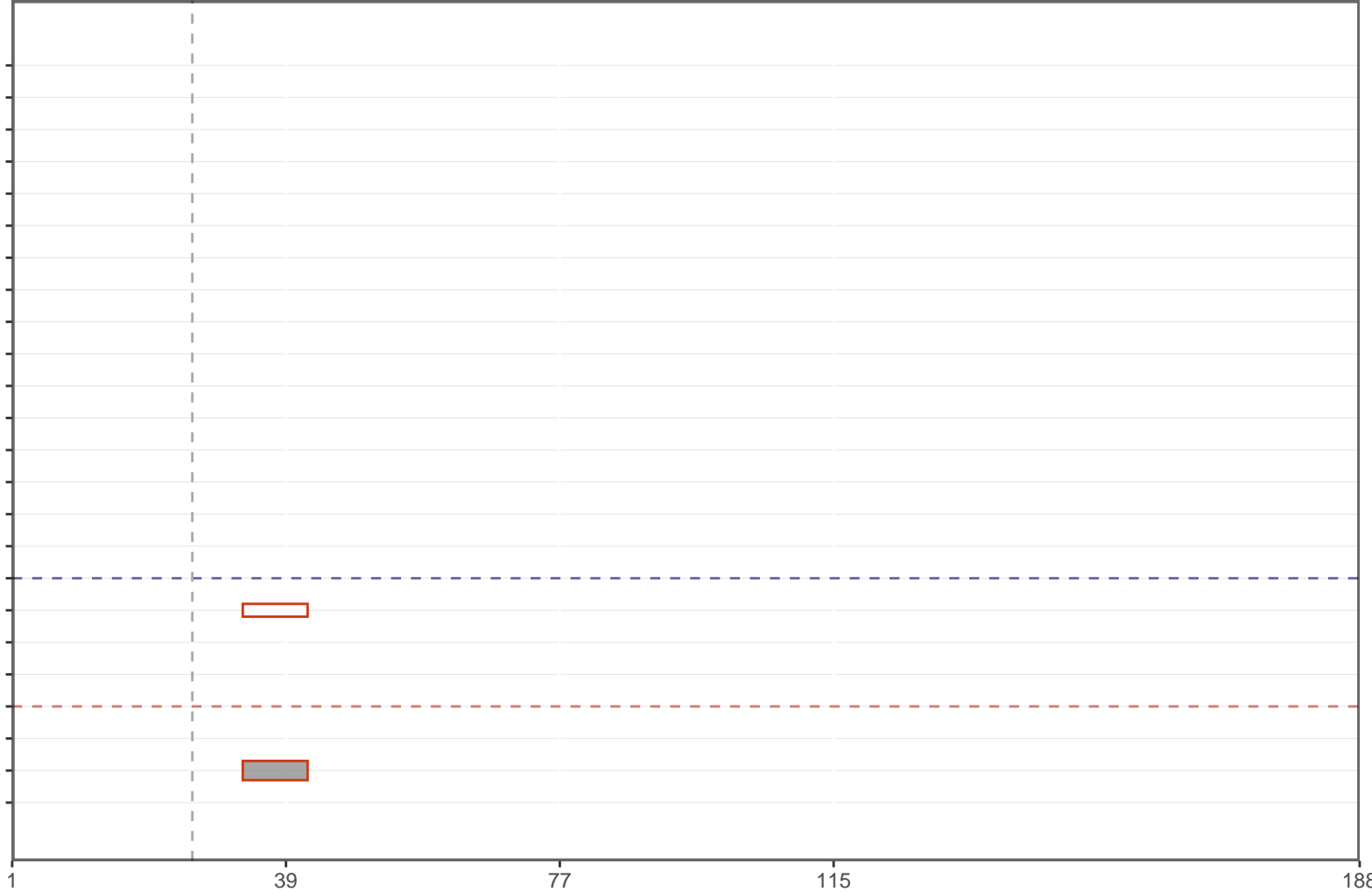
MW indication



Molecular weight



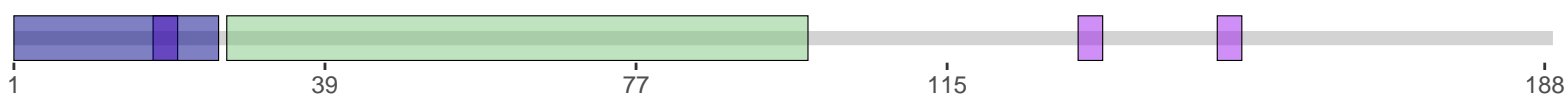
Gel Slice



Protein length

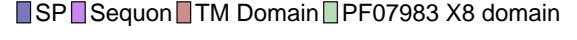


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SRKNEAPGSCFESGTATFAKTDPEYGGCVYAPRAAGGLPFAEAGHKNTSGGISTPNNNAVYGNQSDIPNQGHSKATSPKFWTVAVLPGHMLLFLHIFGHL*

NbL06g01990.1 stress_response_protein_NST1-like [MW = 46.51 kDa]

No. of times detected



log(intensity)



Values from



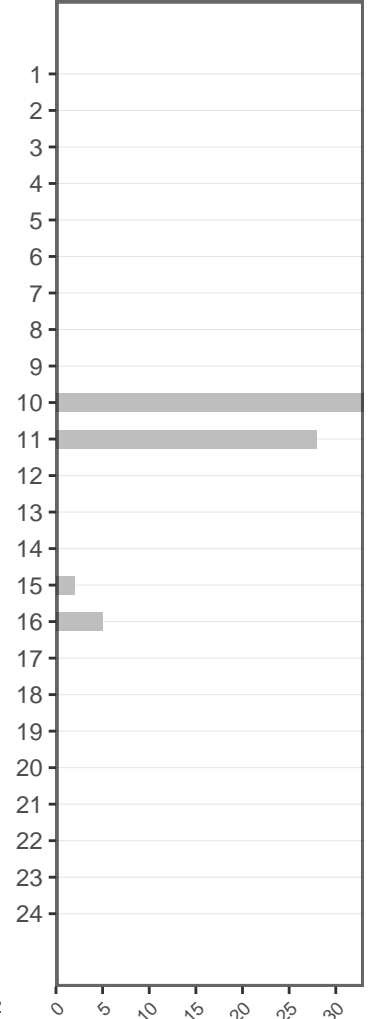
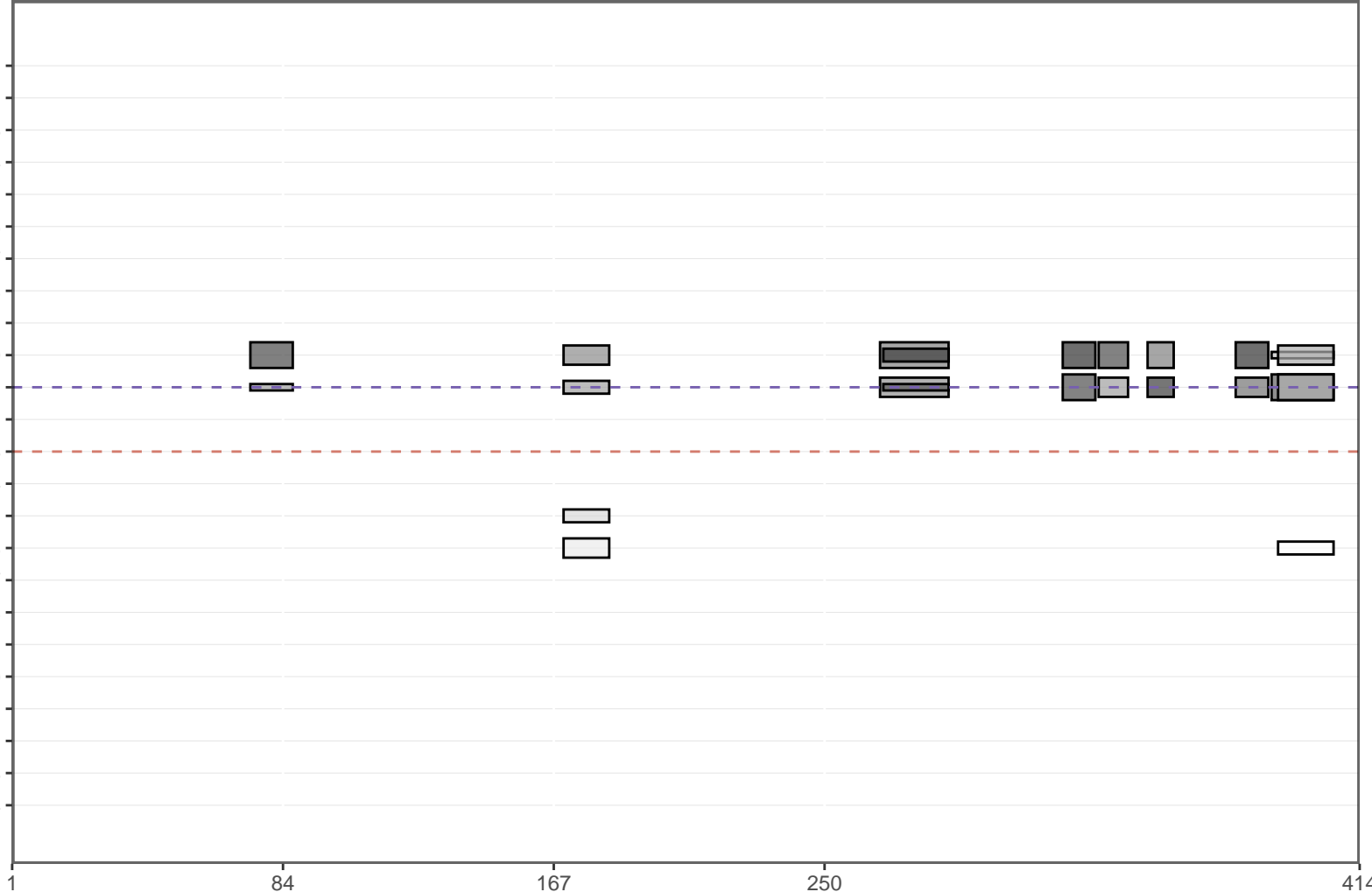
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ERARXXXXEEERORERERERERERIRIGKELLEAKRMEEENERKRRIALRKAENKAEQGRAREKIRKQLEEDKAEERRRKLGLPAEDPAWPKSTPVVEENKITLPIVRRPATKAERMREGLRLTKGTHKDDKAAKVTAFNTLLTYAKNVAIWPNEEKYRKRILSNAAFQDRIGKLGGEFLEHCGFENEGGEFLVLPREKVDMAVINTAGTELNAIKNPFQVL

NbL06g01960.1 glutamic_acid-rich_protein-like [MW = 65.82 kDa]

No. of times detected



log(intensity)



Values from



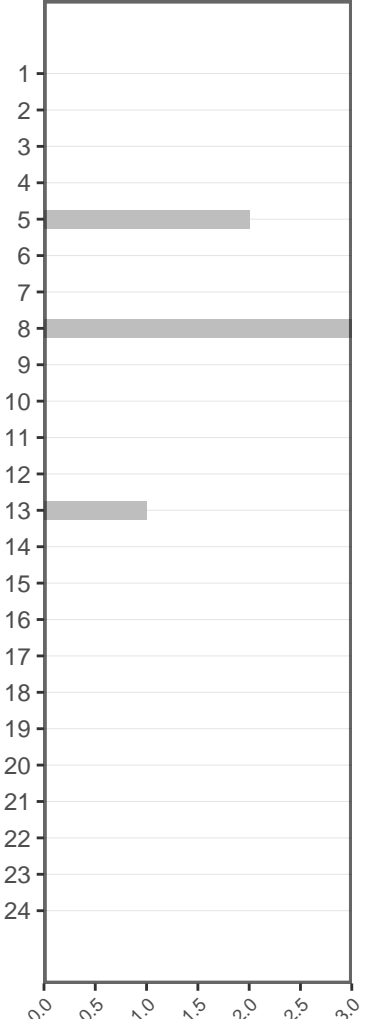
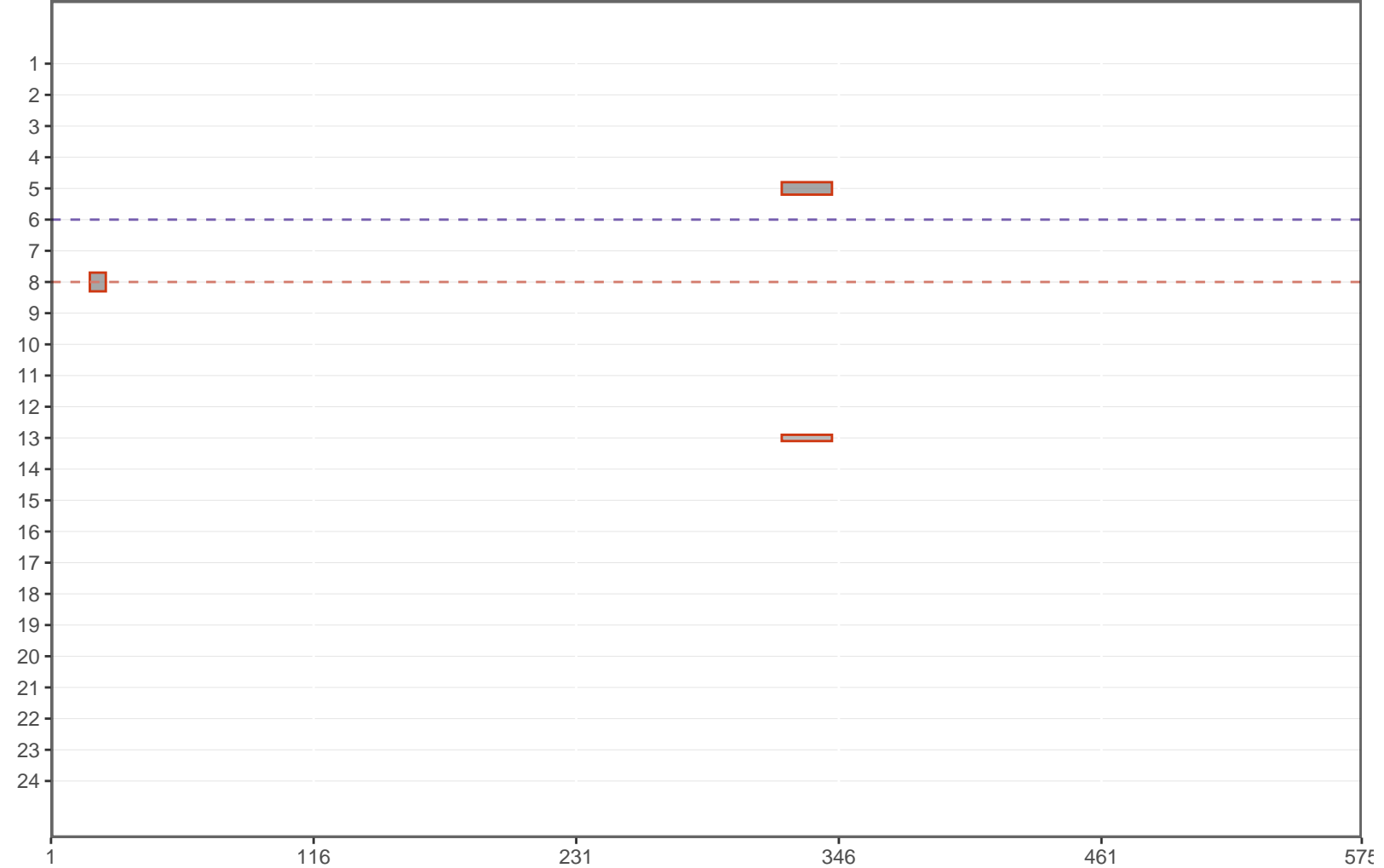
MW indication



Molecular weight



Gel Slice



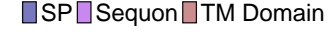
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KPREKDKKDKDAKSHAKKDKREKDKKMEKKAADKSAHRKSEPKDKRDINNKSDFFNVSNTHNQVPLVFKDNAGVTEGIRKRIKIEINFLHSEVIRPAKLRPPSSSHPTGNGKISDTHGKAEMLSSNKGGVTADVGVVVKERSVNGTNGKGGVTADVGVVVKERSVNGTKLENKQHGVDNGLANKENRVDGTVKGGPLAMKPKAGSMSPGADQFAEASRRPPHPDSKYLNGILVPMKDEWSGIDDQEVLFGSKSTLWPKFMGLDEVNDSRVVSEALQI

NbL06g01850.1 probable_receptor_protein_kinase_TMK1 [MW – SP = 97.44 kDa]

No. of times detected



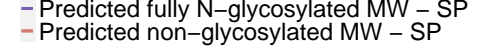
log(intensity)



Values from



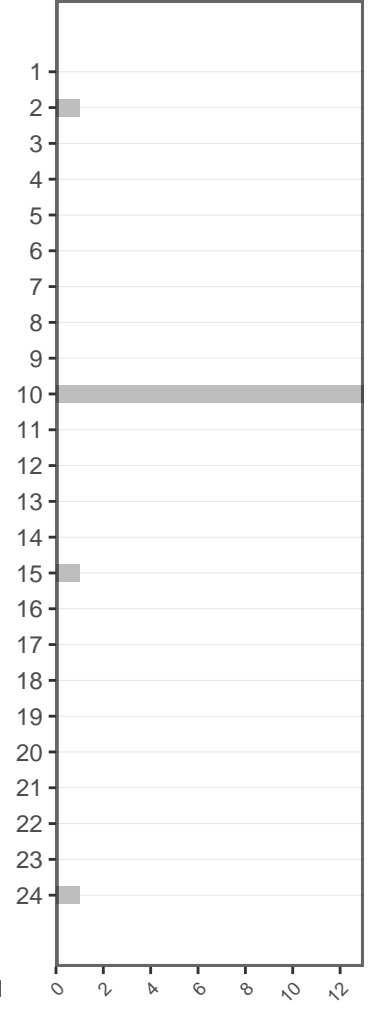
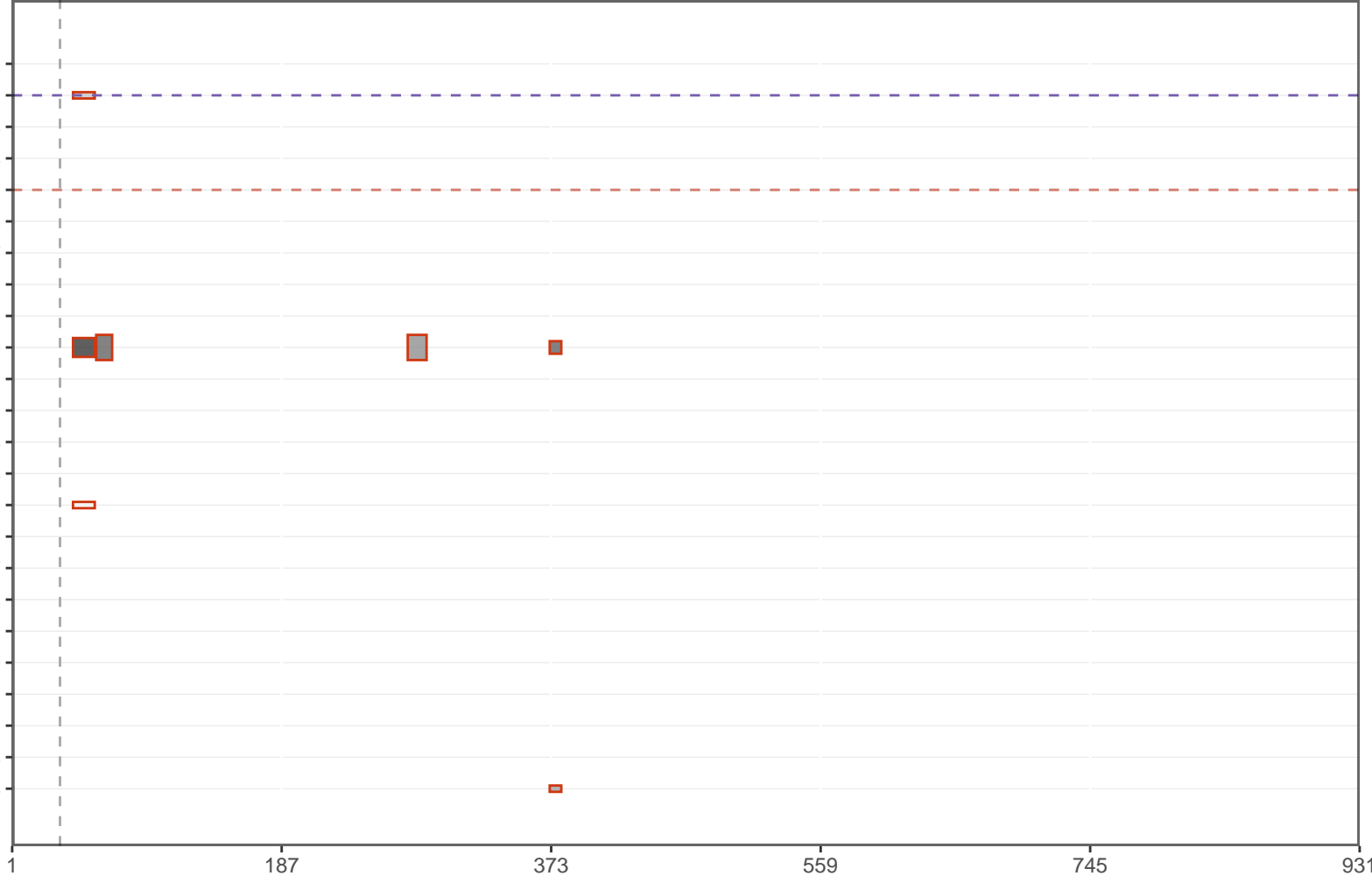
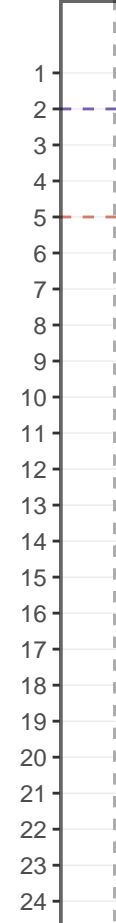
MW indication



Molecular weight

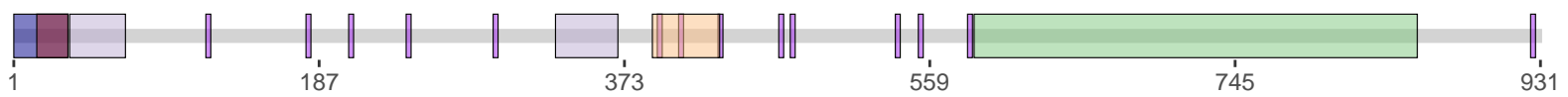


Gel Slice



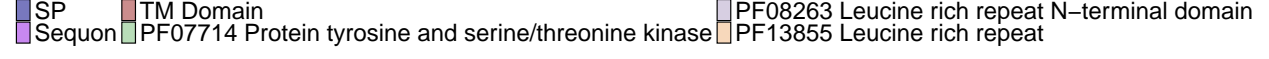
Protein length

Peptide counts over 4 repeats



Pfam domains

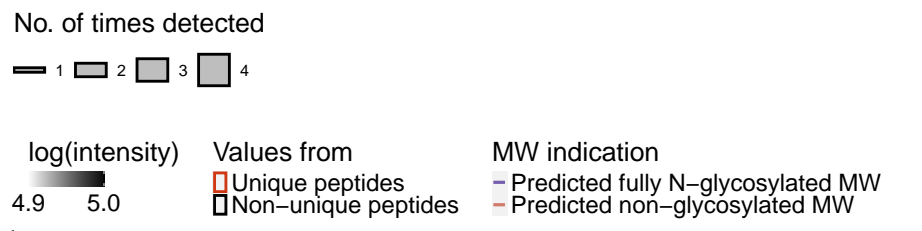
Pfam Description



Protein sequence:

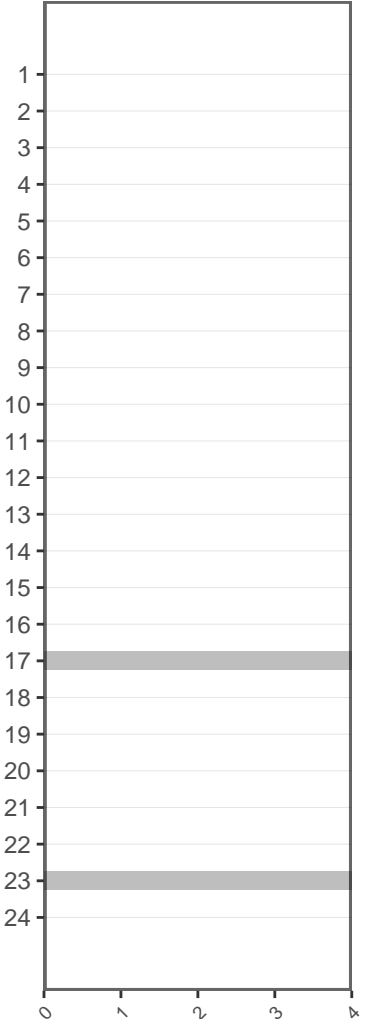
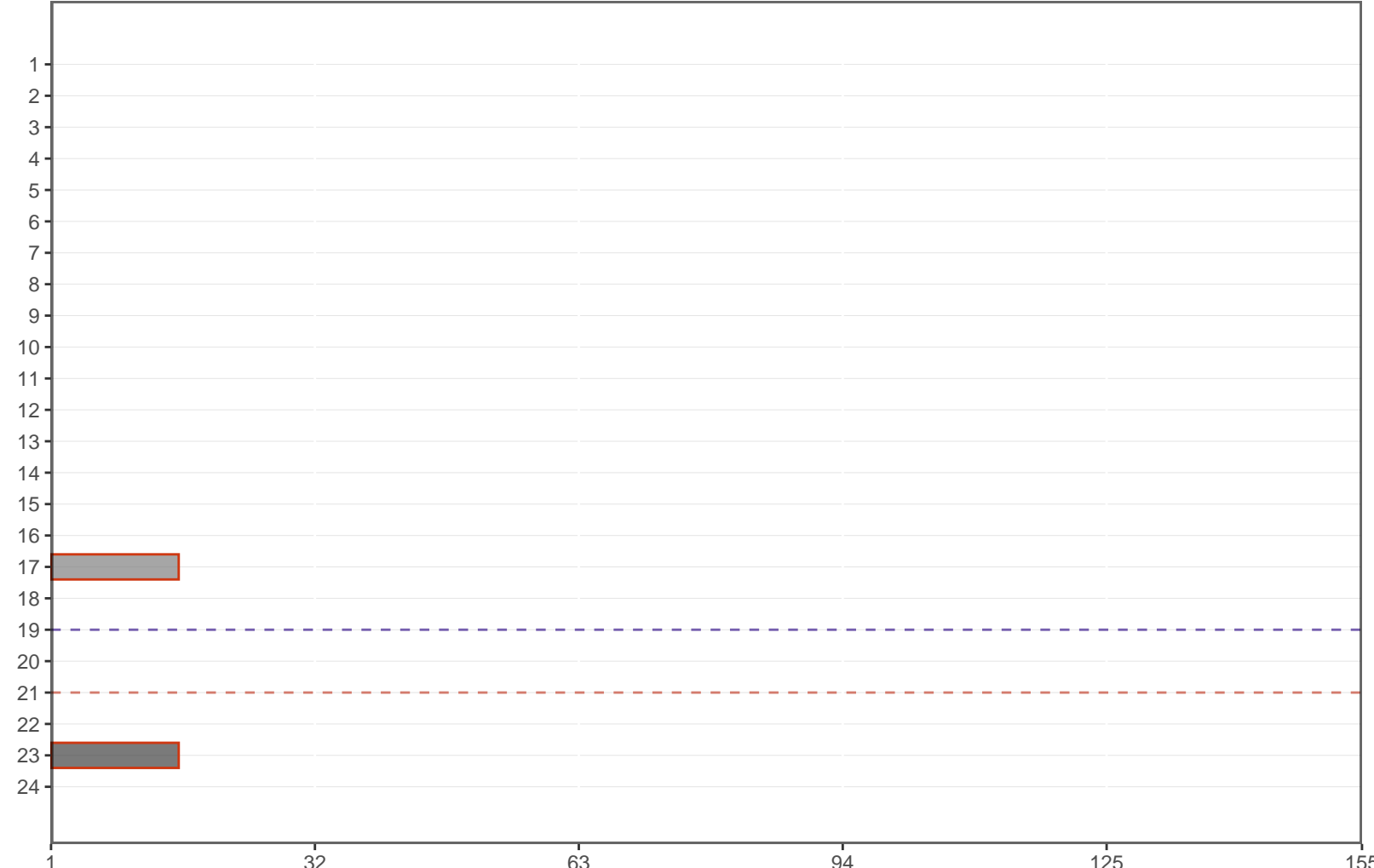
SDGSGGLPQPNSSSDGNTSGGGKSTVSGAGMVGIVHVVFLVLLVFLVYKQYKRRIRKRFGRVETPEGGNGMVKPSPVINGTNGYAGVITELQNGS66DHEMPEVFEFGNAISQILRQVITNFEENLGRGGFVAVYKGLHDGTRIAVKRMESGAMGTGKMGNEFQAEAVLTKVRRHRHLVALLGFGVNGNERLLVYEMPGQGLSQHLFEWDELGYPLLTWKGRTIALDVARGVKHLHSLAQDSFIHRDLKPSNILLGDDMRKAVADFGLLRNAPDQKYSVE

NbL06g01770.1 serine/threonine-protein_phosphatase_4_regulatory_subunit_3 [MW = 17.87 kDa]



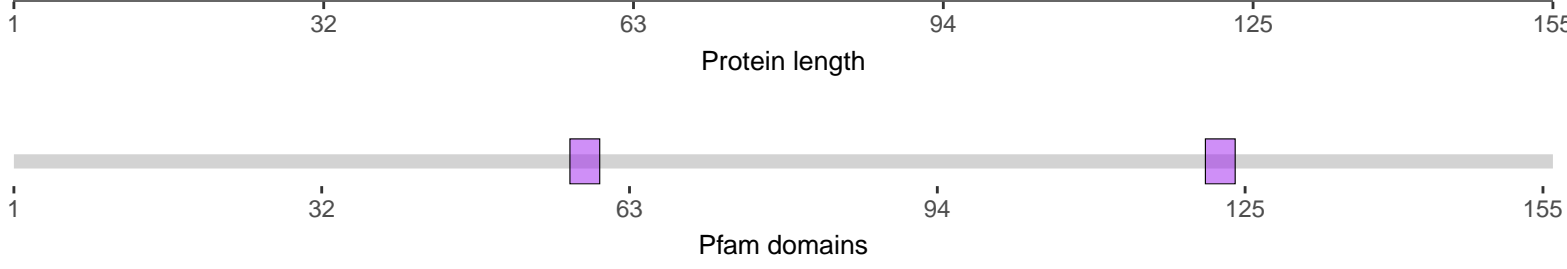
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

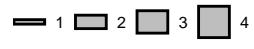
SP Sequon TM Domain

Protein sequence:

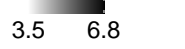
RSIAEDYRKQEDTHWRDPEYETALSPQETTGSGYHWQNGVGRNMFSSLNNETHSVNSQLRELPPVGFLLRFPDTKDGGEWHQ

NbL06g01720.1 major_allergen_Pru_ar_1-like [MW = 17.65 kDa]

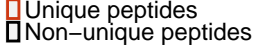
No. of times detected



log(intensity)



Values from



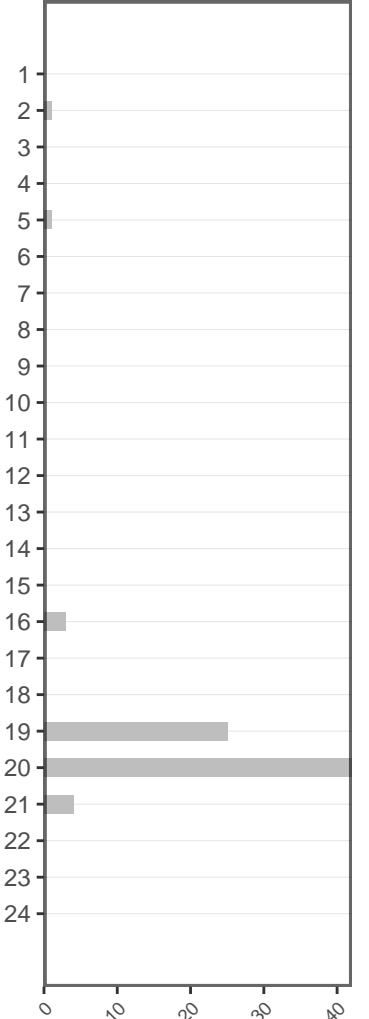
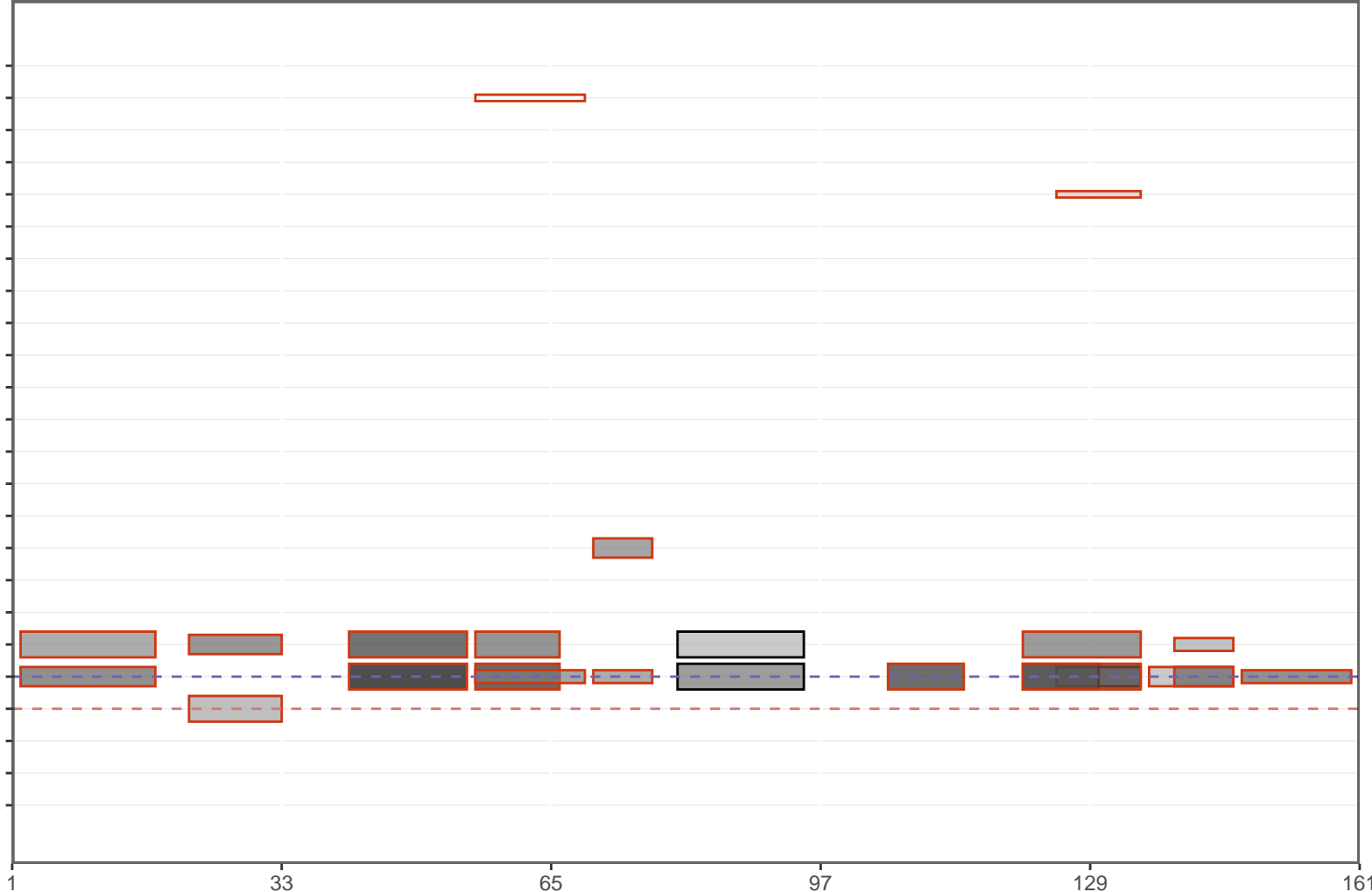
MW indication



Molecular weight



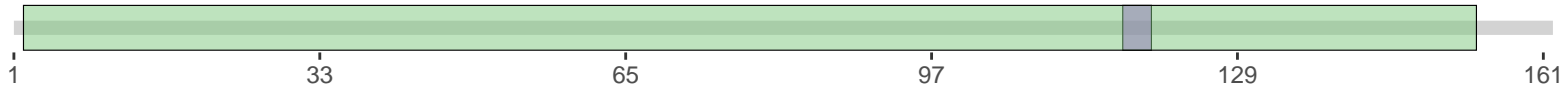
Gel Slice



Protein length

Peptide counts over 4 repeats

Pfam Description



Pfam domains

Protein sequence:

/KHIVDAIEKEMTVAITLIEGDTLMDIKDIBIEYKVFESMPDGGGKGNFKYNTKPGVEKEEIKAGKEMAGIVKVAEALWNPNEV*

NbL06g01640.1 glyoxysomal_fatty_acid_beta-oxidation_multifunctional_protein_MFP-a [MW = 79 kDa]

No. of times detected



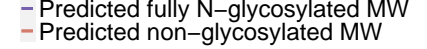
log(intensity)



Values from



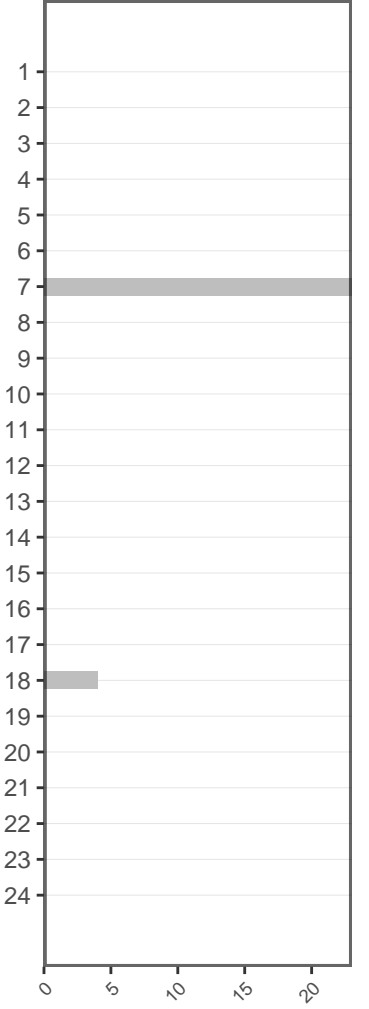
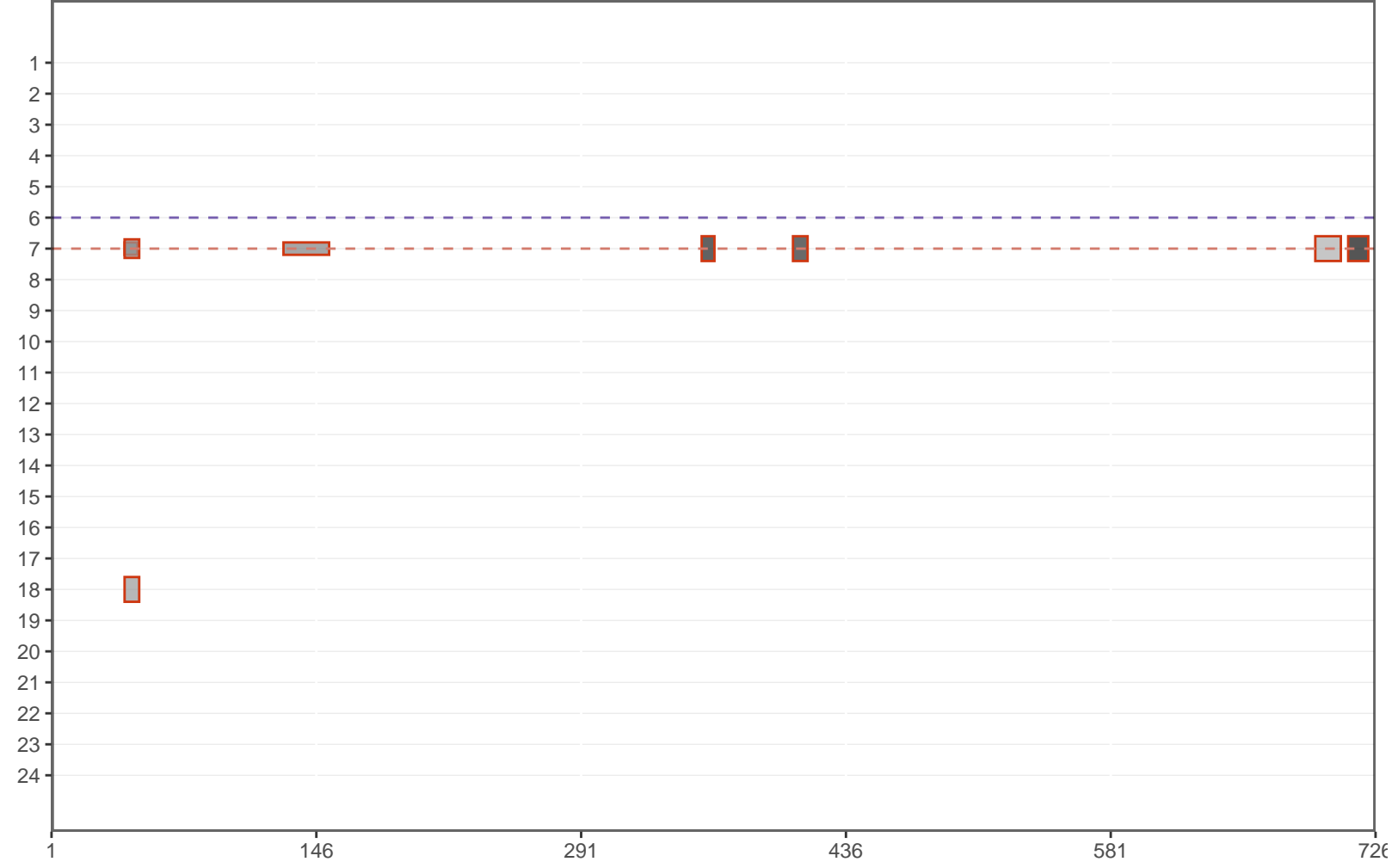
MW indication



Molecular weight

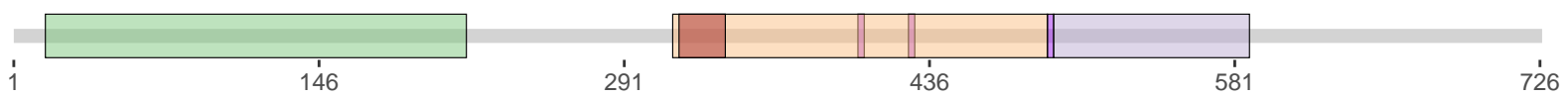


Gel Slice



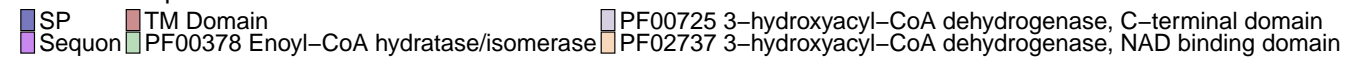
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SMGRYKANIQSSVWKGKMSPEKFEKTLISLKGSLVYEFGRVDMVIEAVIENVSLKQGFADLEKYGPSHCLASNTSTIDLNLGSEKTRSGDRIGAHFFSPNHWMLLEIVRTQKTSPOVIVDLIDVSKKIRKTPVAAGNCTGFVNRIMFFPYTQAALLVERGTDVYRIDKATKFGMPMSPFRLLGDVGFQVAATGGGFVMMFPERTYKSMILPLMGEDKRAGETTRKGFYVYDORRKASPDPEIKKYIEKAREMSGVTDPKLAKHSKDIEMIFFFVINEACRYLAEGLIA

NbL06g01620.1 5'-nucleotidase_domain-containing_protein_4-like [MW = 70.63 kDa]

No. of times detected



log(intensity)



Values from



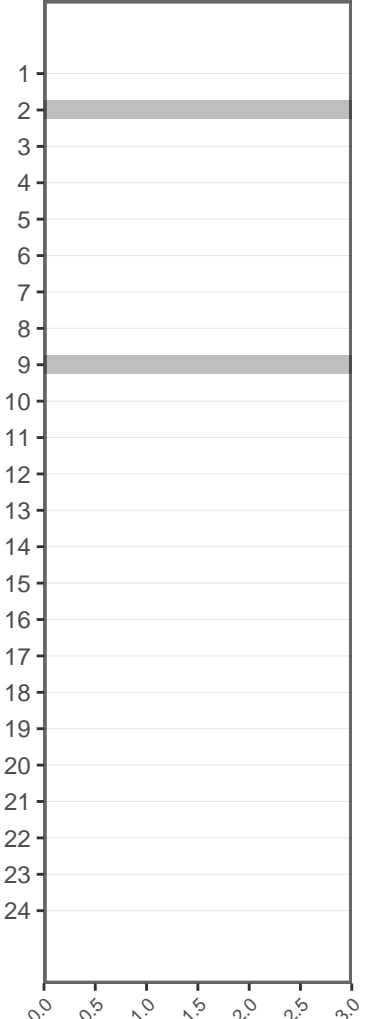
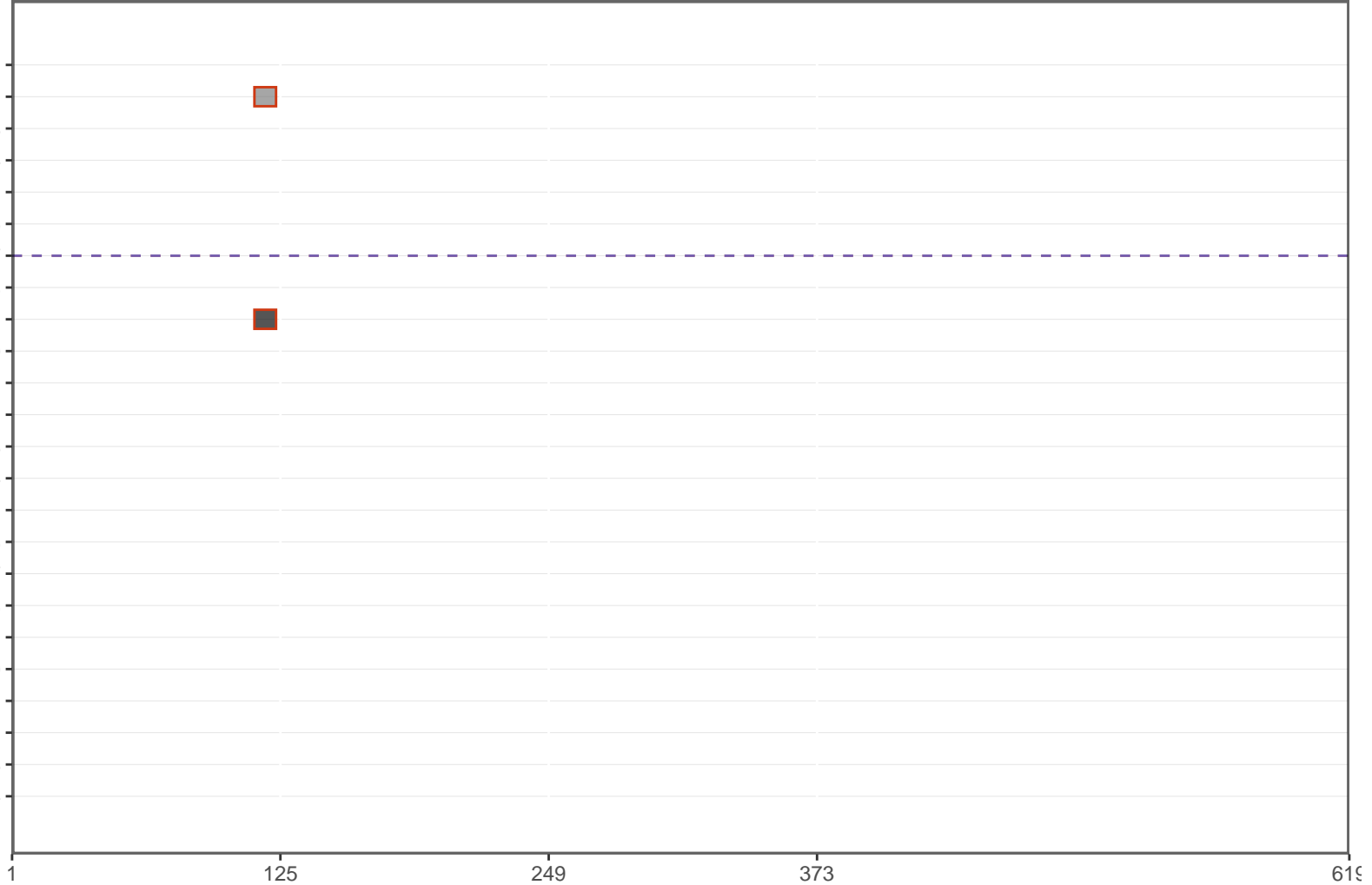
MW indication



Molecular weight

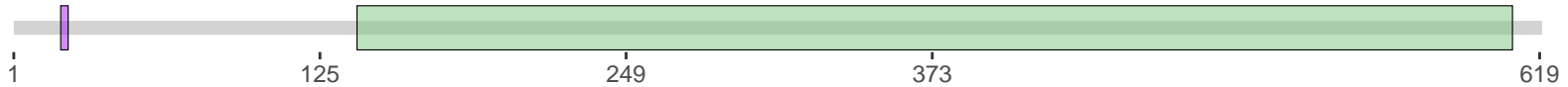


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

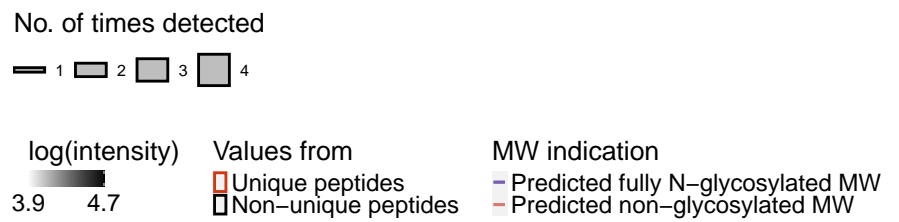
Pfam Description



Protein sequence:

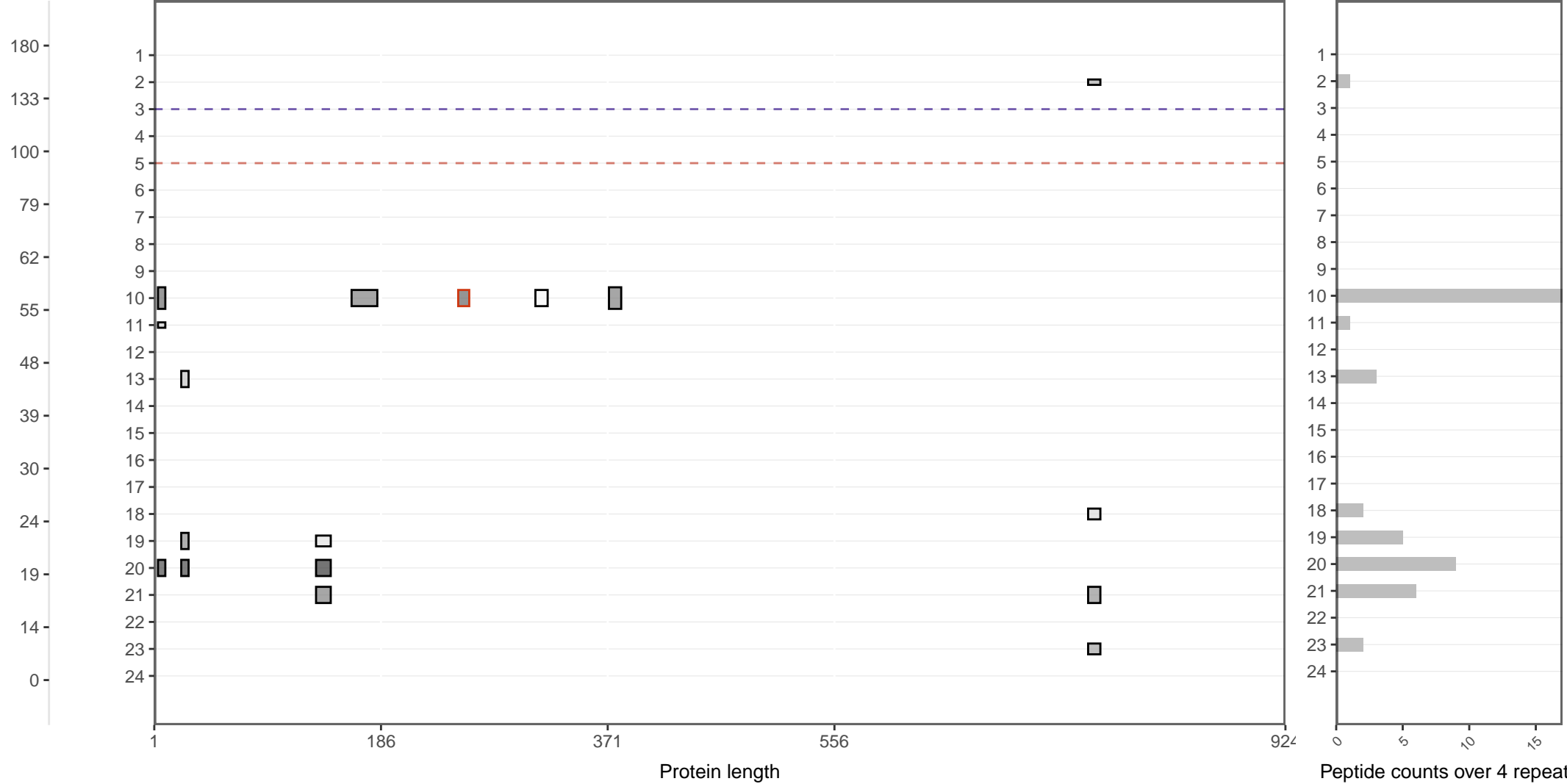
SKALFRAHVEGQLKSEMKPELFEVDPDELPLALLDQKAEAGKRLLLFTNSDHYTDKMMQHSFNRYLPNDMSWRDLFEMVIVSRRKPEFFQMGHPMVEVTSGLMPCFKARPGKARPGVSGGSAQMISSSLNHYGDELIVGDHYTDVSVKVIHLRWRRTALICRELEEEYNALHSGQHRATLIDLNKVEVLDGDFNGLRLSLGRRRTMGRPAQTLAATHMEDNELTSGMQLLWVWQRLDQKIGPMLHEDGELFNKRWGYLSRAGLWDKSHLMRQIEKYADITYSRVSNF

NbL06g01580.1 clathrin_interactor_EPSIN_2-like [MW = 97.44 kDa]



Molecular weight

Gel Slice



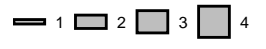
Pfam Description
 SP Sequon TM Domain PF01417 ENTH domain

Protein sequence:

ISNQMFEDPFGDCGFRAMTFENSHQTYLGNSTSFHPNINGSPELPGVPGGAIEGGATGSGVTPPTNMQYAGGELSTSNQIEIDLADILFPPGGPPPSVQATQAGFESHGGSETTQHTGHLALTGRWVPTTGFAAQPGGGSPHTFSPGGGSTRPAGFSGGANNSPFPGGFFPAGGASGDTGFGPGGGGPAFLAGFHSATGFYPGGFGGPGGSSMNNANAGGYNTGLGATGPFPGMGGTSGGGPFVLSGPTAASHMPGMPLQVSGTQTSNALLVIQTTPASTAPIS

NbL06g01370.1 ATP-citrate_synthase_beta_chain_protein_2 [MW = 65.66 kDa]

No. of times detected



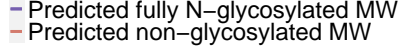
log(intensity)



Values from

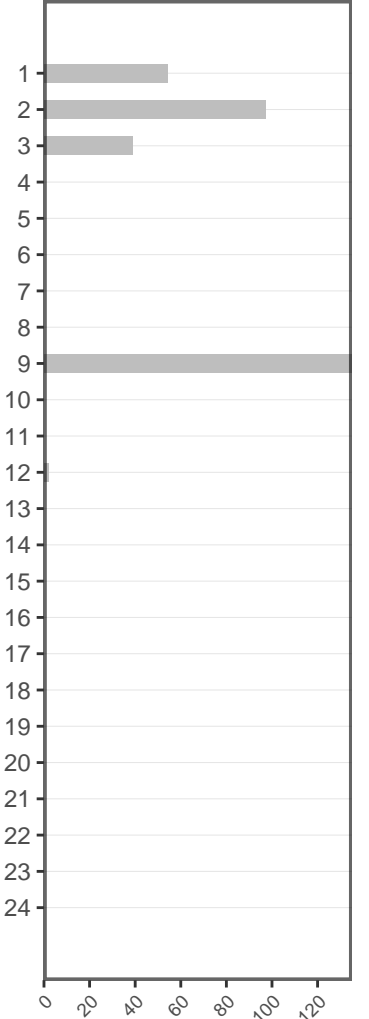
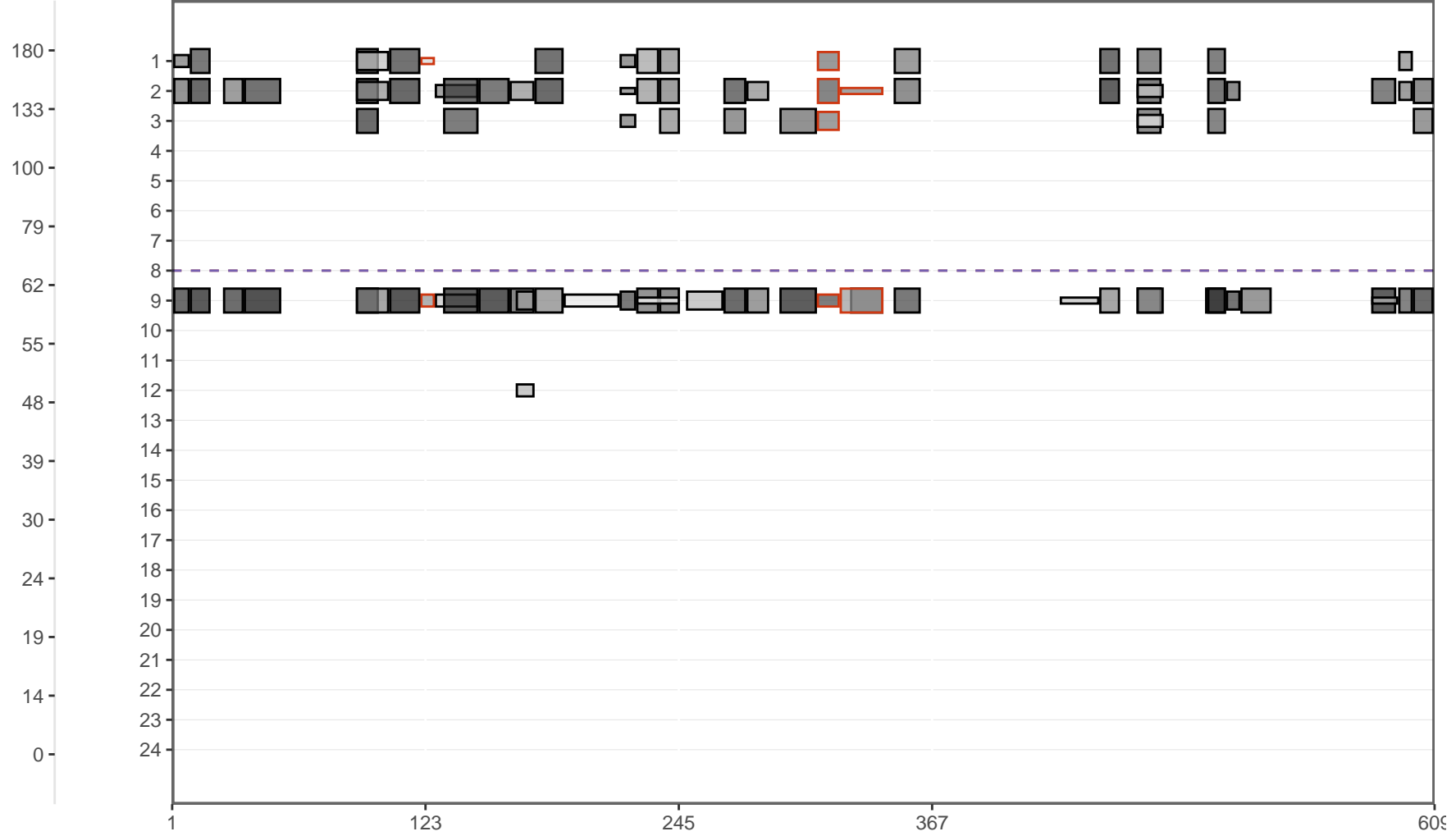


MW indication



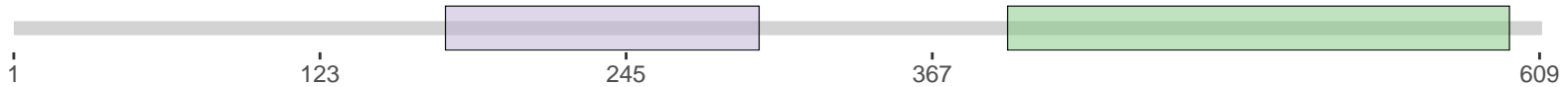
Molecular weight

Gel Slice



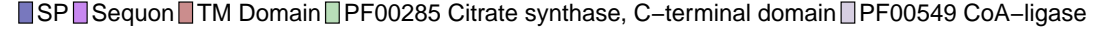
Protein length

Peptide counts over 4 repeats



Pfm domains

Pfam Description



Protein sequence:

JALKDAGAVPTSYEAFEGAKAEAFEGQLVSDGKSTTPVKEITPPQIPEDLNTAKSGKVRAPTHHISTISDDRGEPCVAGVPMSSIVEOGLGVSDGILLWFKRSLPRYCARFIEILLCADHGPCVGSAAHNSIVTARAGKDLVSGLVGLTIGPRFGGAVDDAARYFKDAYDRGLTPYEFVSMKKKGRVPGIGHKRGDRKRVIELLQVARENFPSVKYMEVAVGVETFTLAKANNLNVDSGAIGSLFLDLLAGSGMFTKPEIDEIVEIGYLNGLFVARSIGLIHTFDOK

NbL06g01320.1 huntingtin-interacting_protein_K-like [MW = 12.17 kDa]

No. of times detected



log(intensity)



Values from



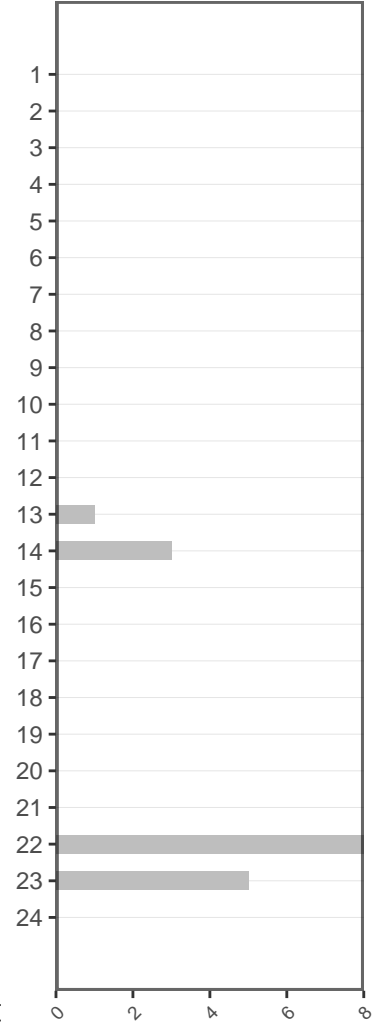
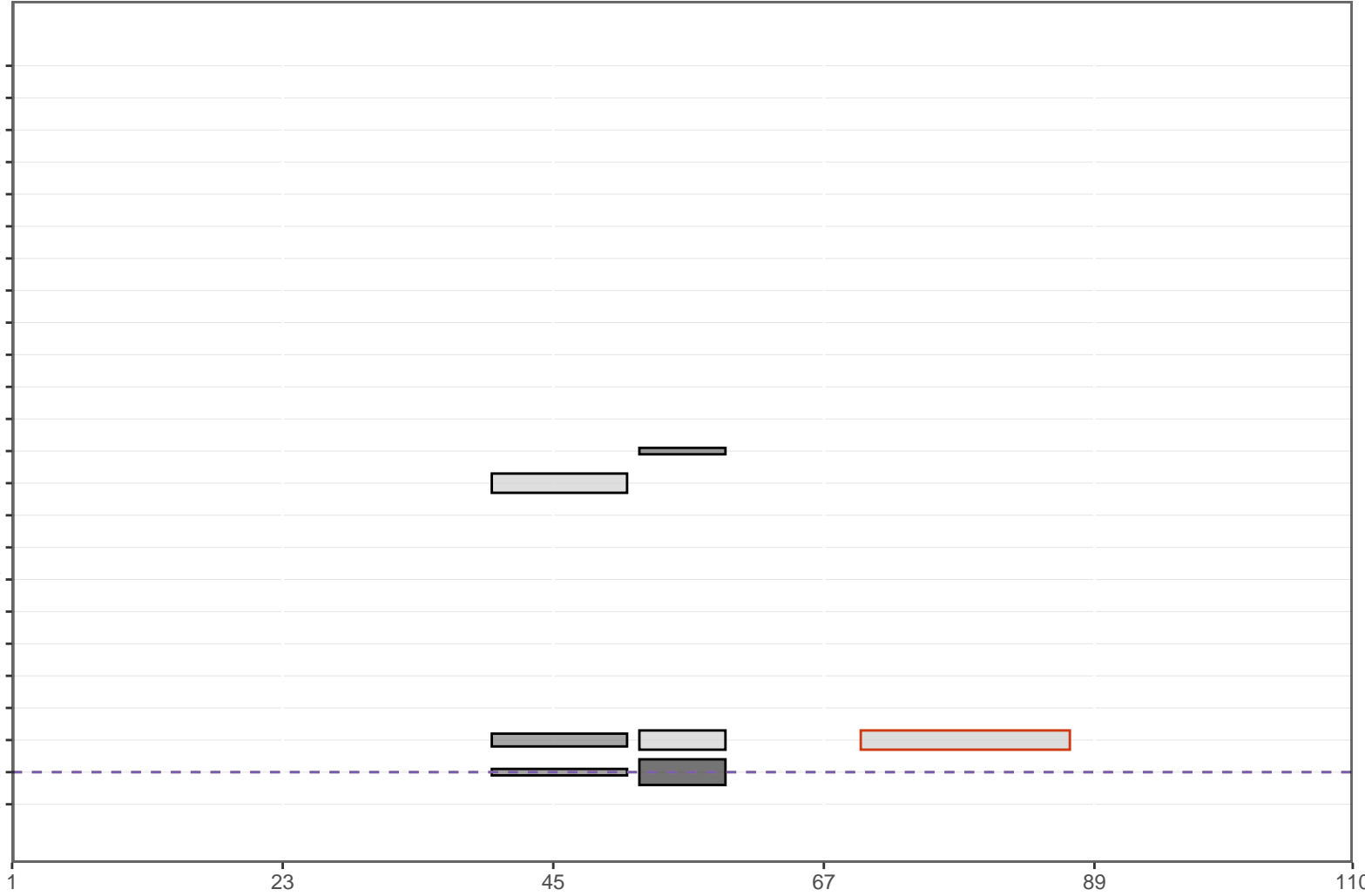
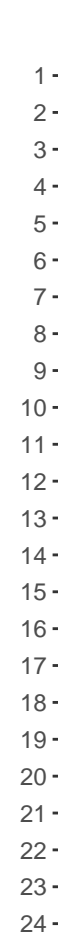
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

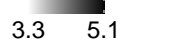
IQTAMASIVASKEADLQAGMRREKELAAVKNADIDIANELEVDKKAVERFLREHKGDAAARHLEN

NbL06g01290.1 cell_wall/_vacuolar_inhibitor_of_fructosidase_1-like [MW - SP = 15.7 kDa]

No. of times detected



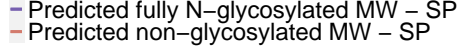
log(intensity)



Values from



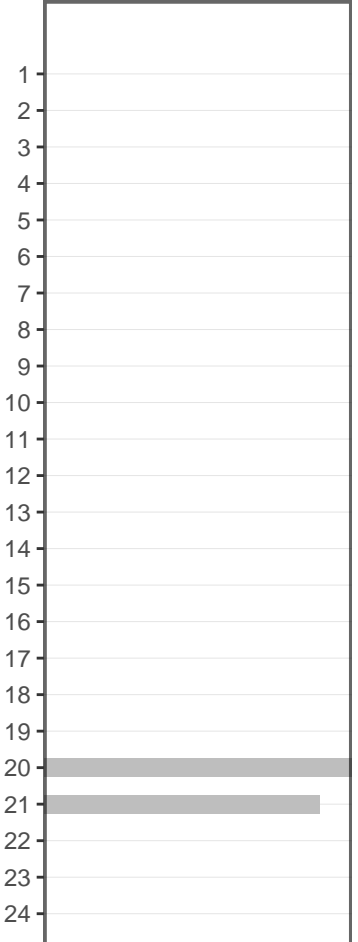
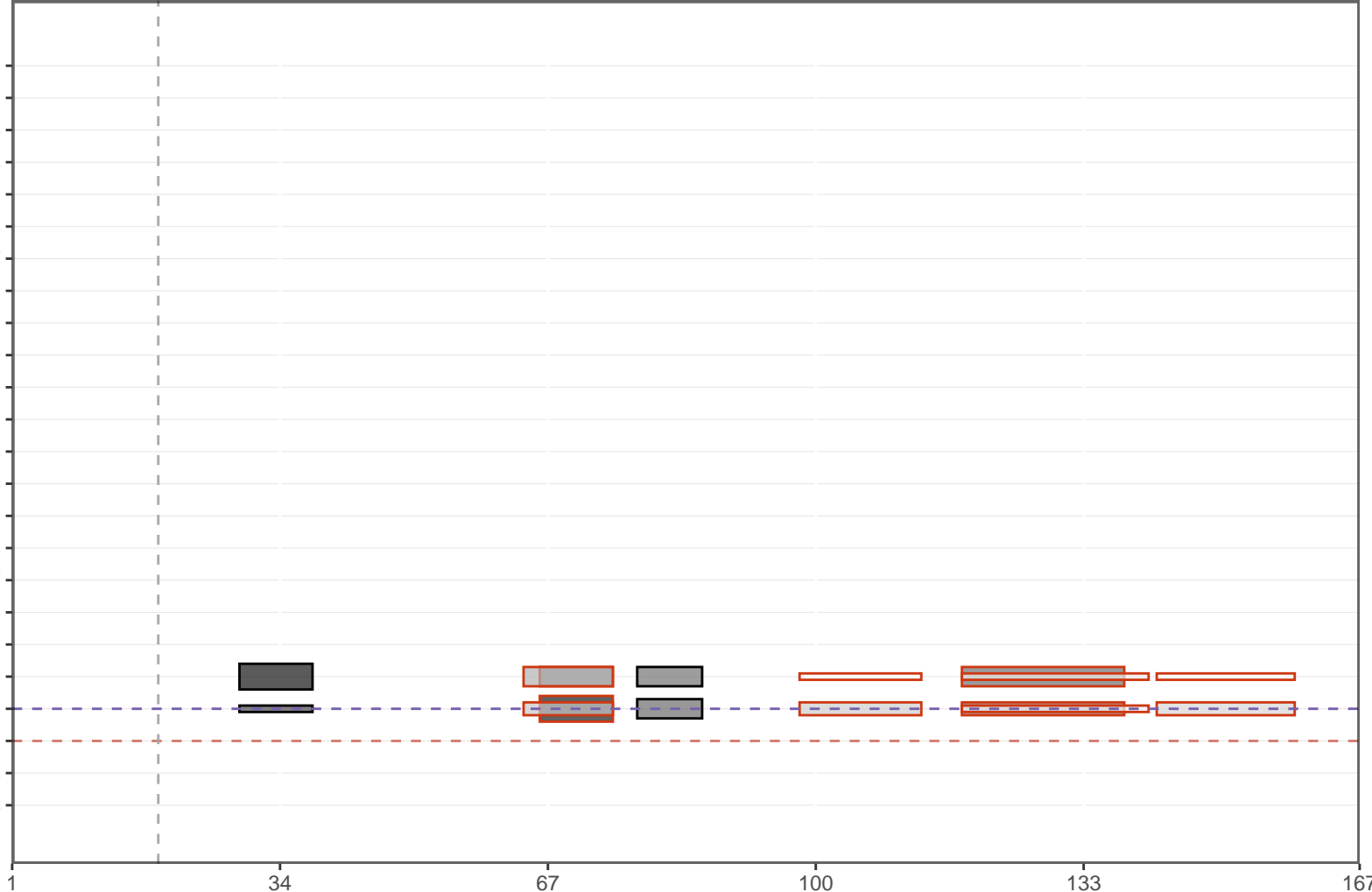
MW indication



Molecular weight

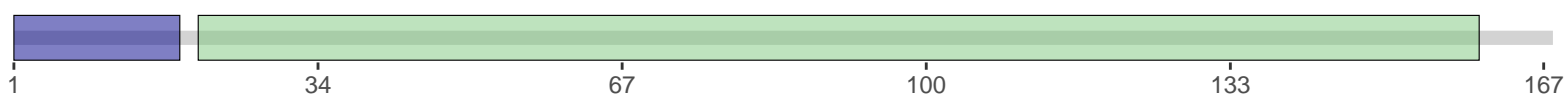


Gel Slice



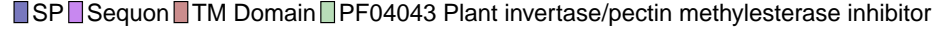
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TTSKLRHISNPPAAVWVWGLNKAFAFYKYLTAALPEAIEALTKGDPKFAEDGMVSGSGDAGEEENFKGSKPFPSALNVAHWQLSDVGRAIVRNLL

NbL06g01240.1 serine_carboxypeptidase-like_33 [MW - SP = 51.62 kDa]

No. of times detected



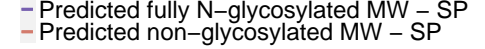
log(intensity)



Values from



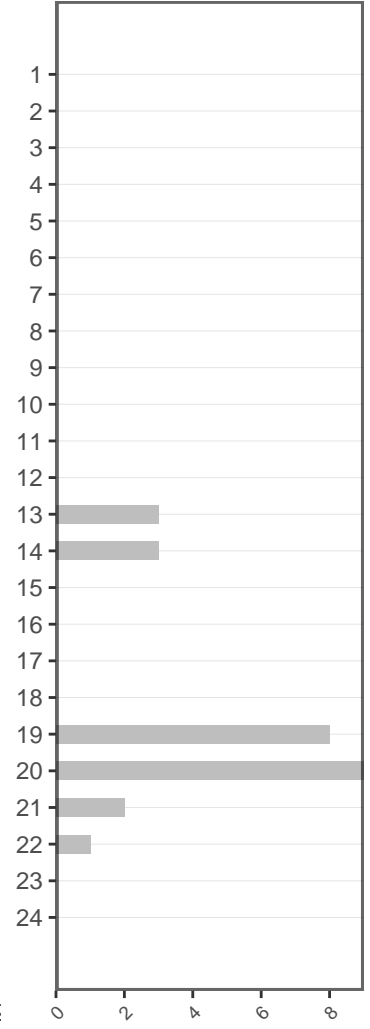
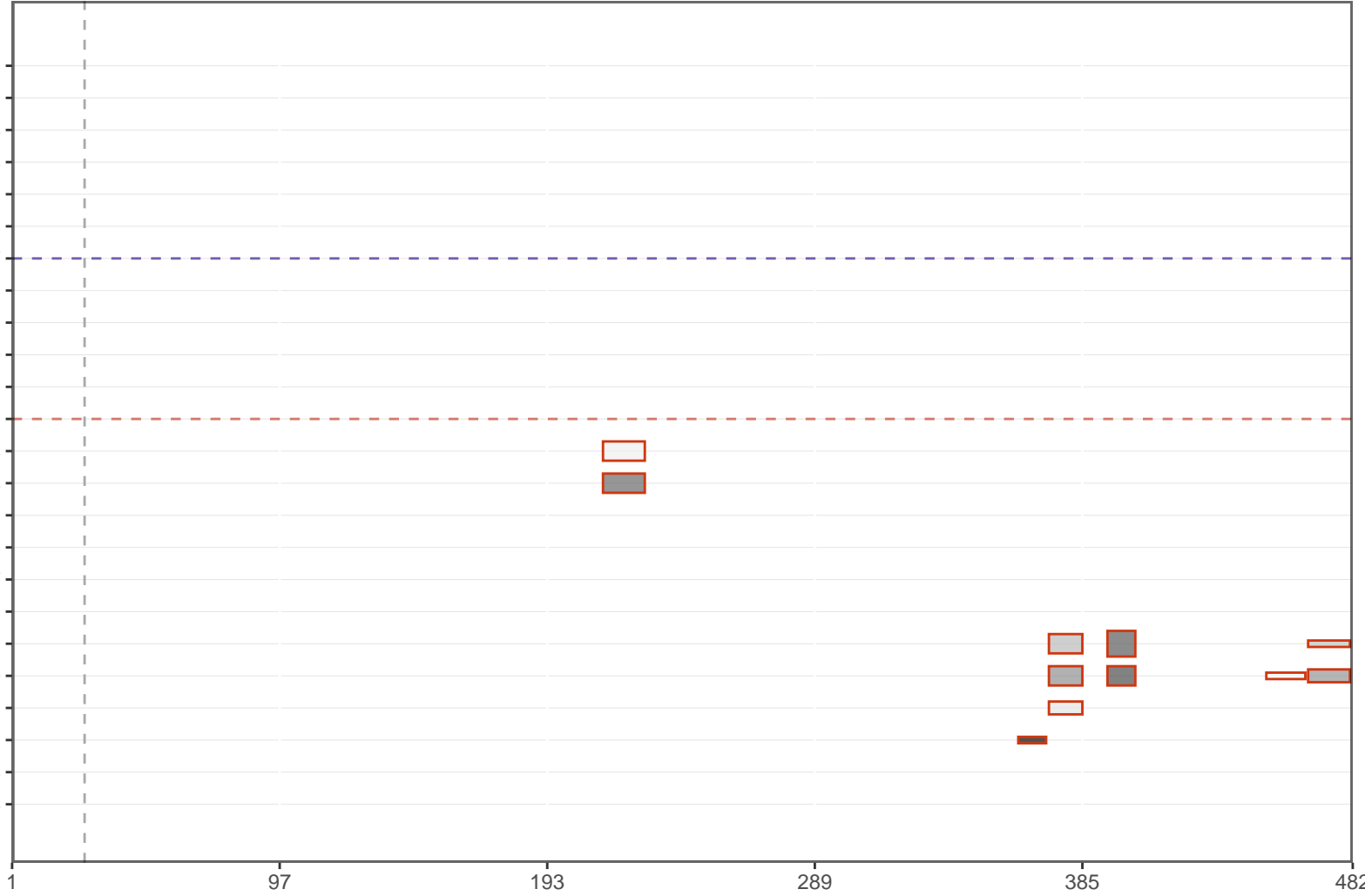
MW indication



Molecular weight

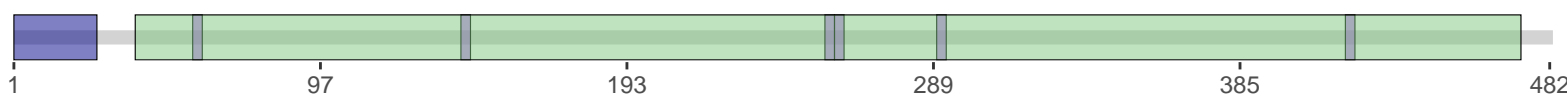


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

KGILEYAWSHAVIYDGGYEKAKGVGDFENLGNWSDACNDAMKVVVDKYEEDYNYVAPKGLRNTS6555ASLTVSGHESKLGALNHPKRMQRIPGGYDPCYAFTEEYFNRLDVGSLHNSEGRHTRVWVWGS6DFVLQKYNVYFVLPYKLIQGGKLIWFGDADGRVPIGTRYGQALNLTLSKSEWHSWFHNNQVAGRIVEEGLTFVTRGAGHLVPLKPSPEARALHSLTGEELPAHR

NbL06g01210.1 dihydrolipoyl_dehydrogenase_mitochondrial [MW = 53.49 kDa]

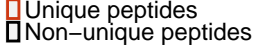
No. of times detected



log(intensity)



Values from



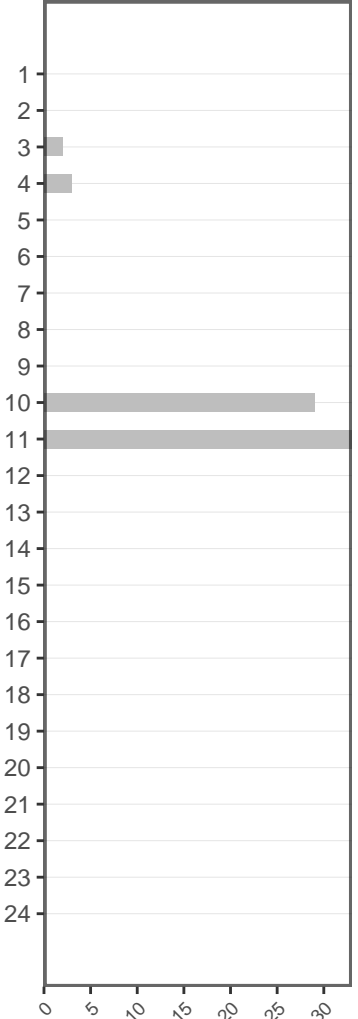
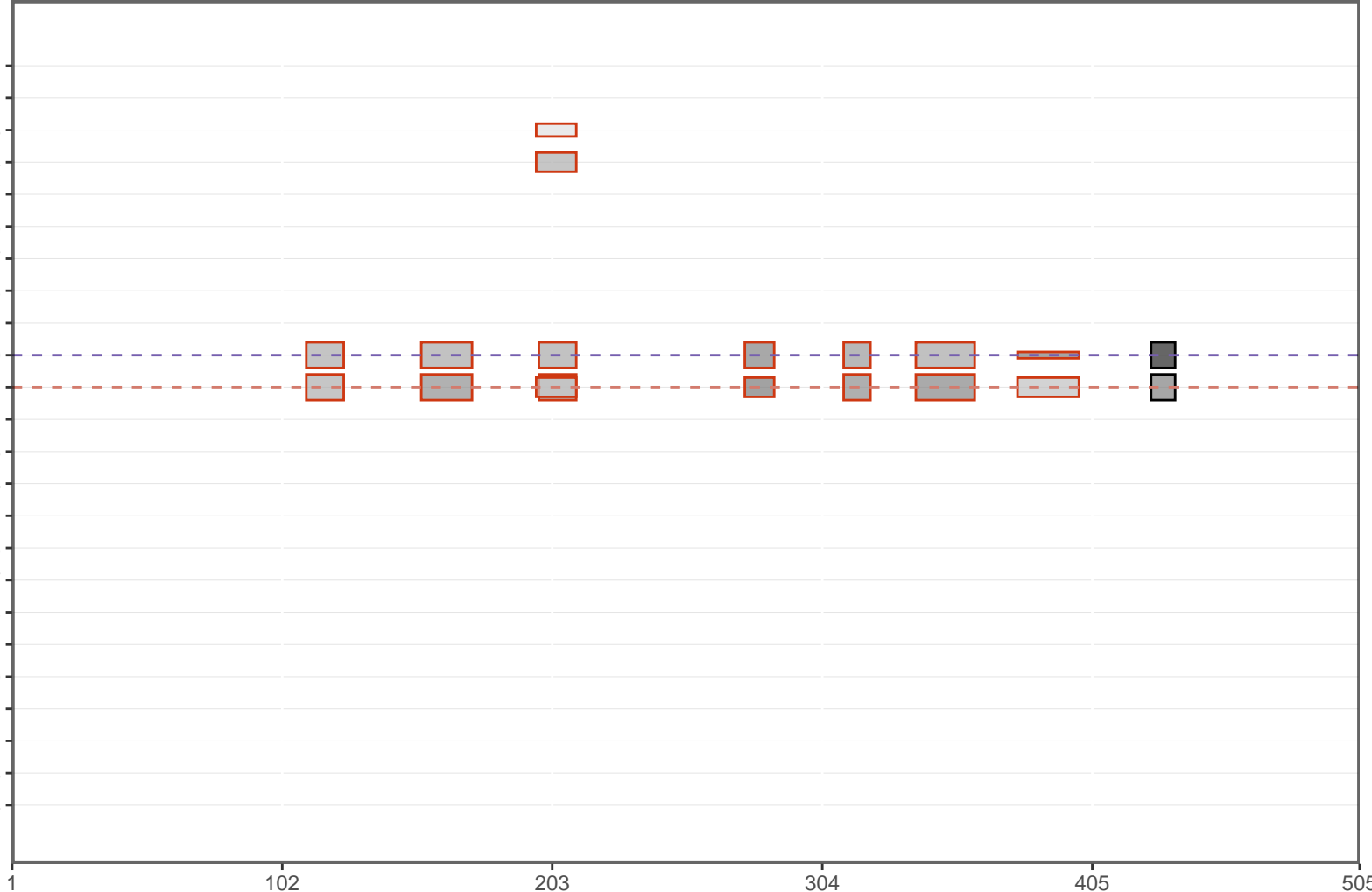
MW indication



Molecular weight

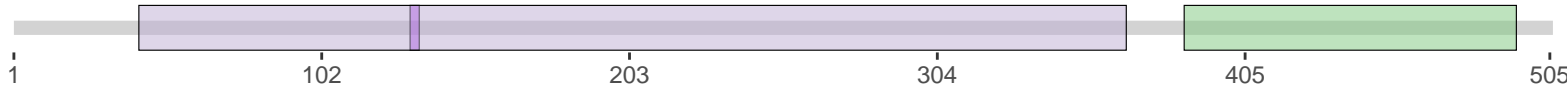


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF02852 Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain
- PF07992 Pyridine nucleotide-disulphide oxidoreductase

Protein sequence:

IFAAADIVPTMDCGEVRRKGFQRALENGKMKFKMLKTKVSVSDTAGDGVKLTLEPASGGDQDTLEADVLLVSSAGRVPTFSGLGLGKLVETDKAGRILMVKRFASNPVGVGIVIPGPMALAKAEEDGVACVFEIACKEGHVYVDMVPGVVYTHPEVAVGKTEEGVKRGGVDRVYGVKFFFLANRRAKAIIDMEGLVKLAKEESKILGVHMSPNAGELHSEAVLALQVGSSEDIARTDHAHPTMSEALKEAAMATYDKPHM

NbL06g01180.1 ubiquitin-40S_ribosomal_protein_S27a-like [MW = 17.7 kDa]

No. of times detected



log(intensity)



Values from



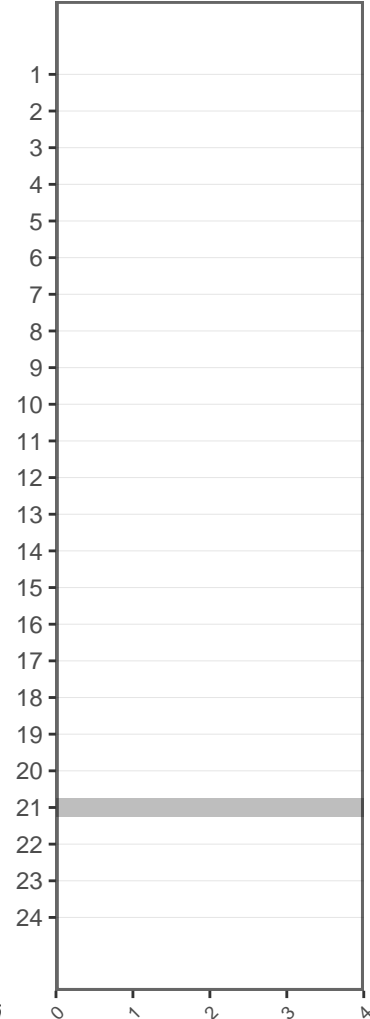
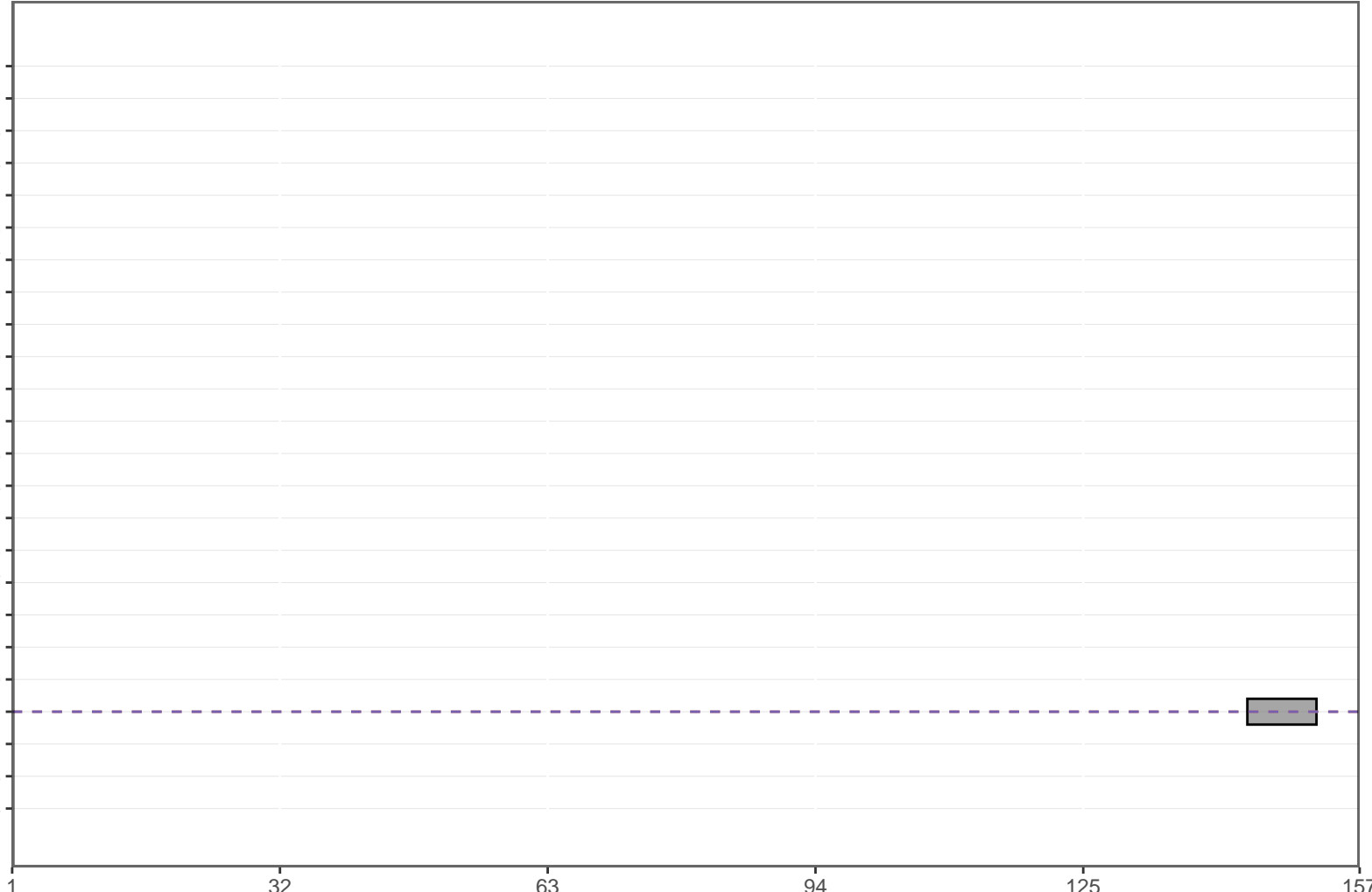
MW indication



Molecular weight

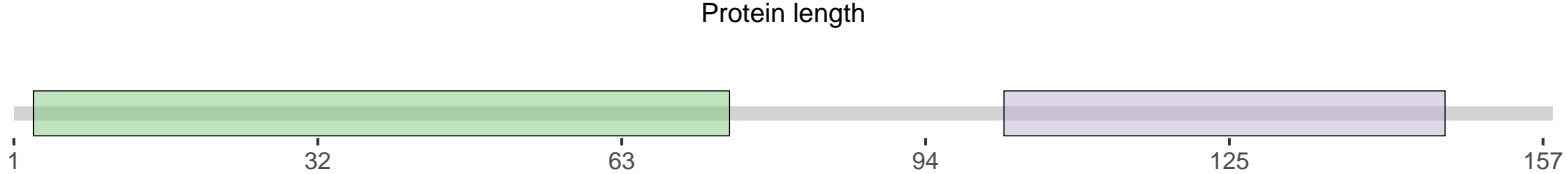


Gel Slice



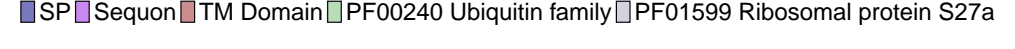
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

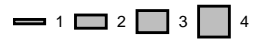


Protein sequence:

LVLRRLRGGAXKRKKTKYTRPKKKKKKKKKLAVLGFYKVDSDGKVGRLRKEGPNAECCAGTFMANNHFRHYCGKGLTYYVQKAGGD

NbL06g01150.1 S-adenosylmethionine_synthase_2 [MW = 48.13 kDa]

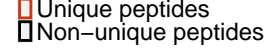
No. of times detected



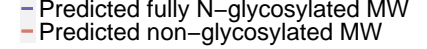
log(intensity)



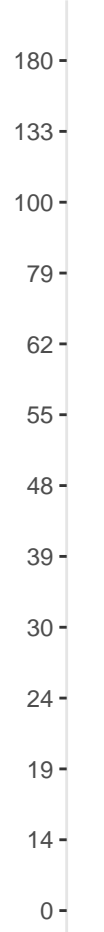
Values from



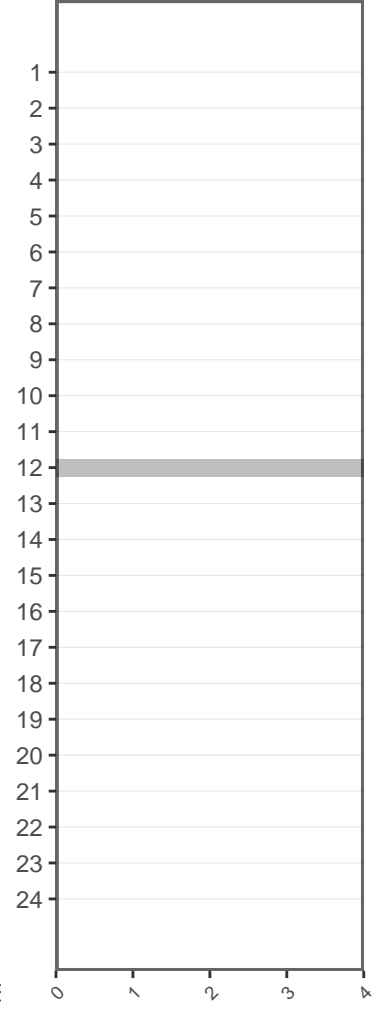
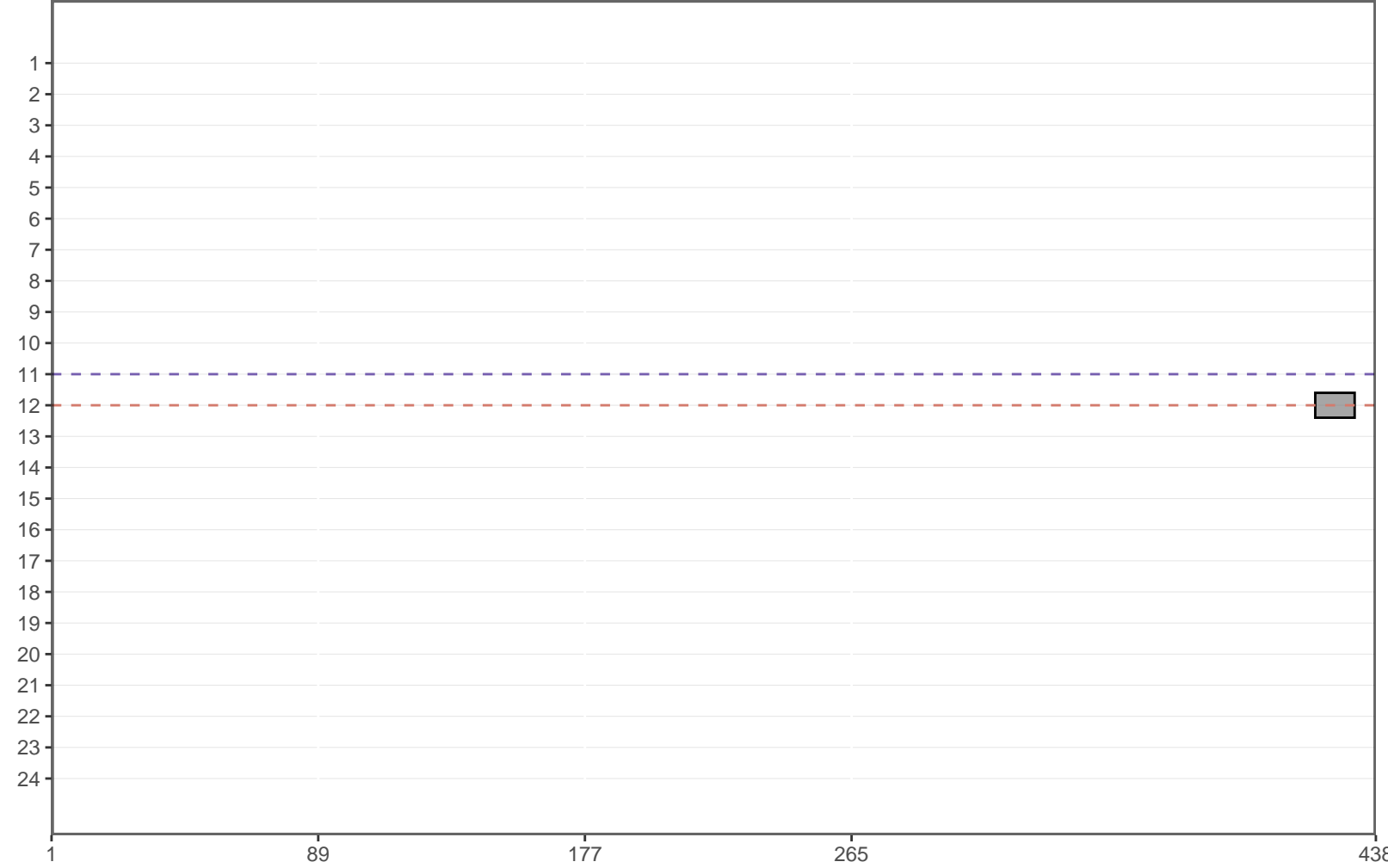
MW indication



Molecular weight

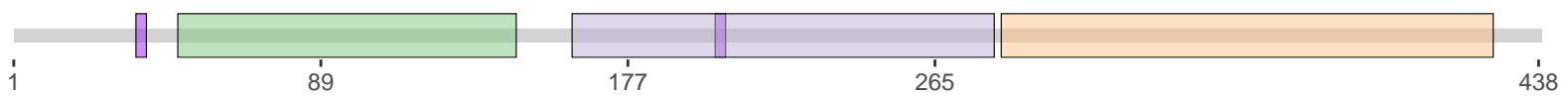


Gel Slice



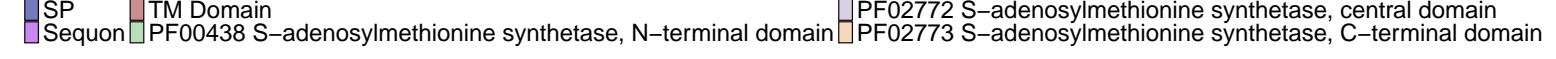
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

WLRPDKTQTYVEYHNDNGAMNPLRVHTVLISTQHDVTFNDEIARDLKEHVKIPPEKYLDEKTFIHLNPSGRFVGGPHDAGLGTGRHIIDTYGGWGAHGSGGAFSGKDKPTKVDREGAVYRGAAKSIVANGLARRGVGVSYAIGVPEPLSEVFDYGTGKIPDKEILNWKENFDRPGMISINLILLGGNGRFLKTAAYGHFGRDSDSFTWEVWVPLKWKPKDA

NbL06g01090.1 [Pyruvate_dehydrogenase_(acetyl-transferring)]_kinase_mitochondrial-like [MW = 41.82 kDa]

No. of times detected



log(intensity)



Values from



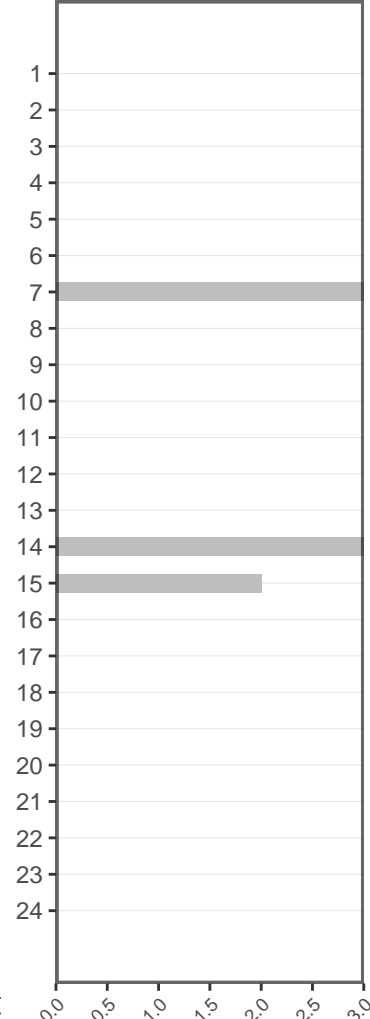
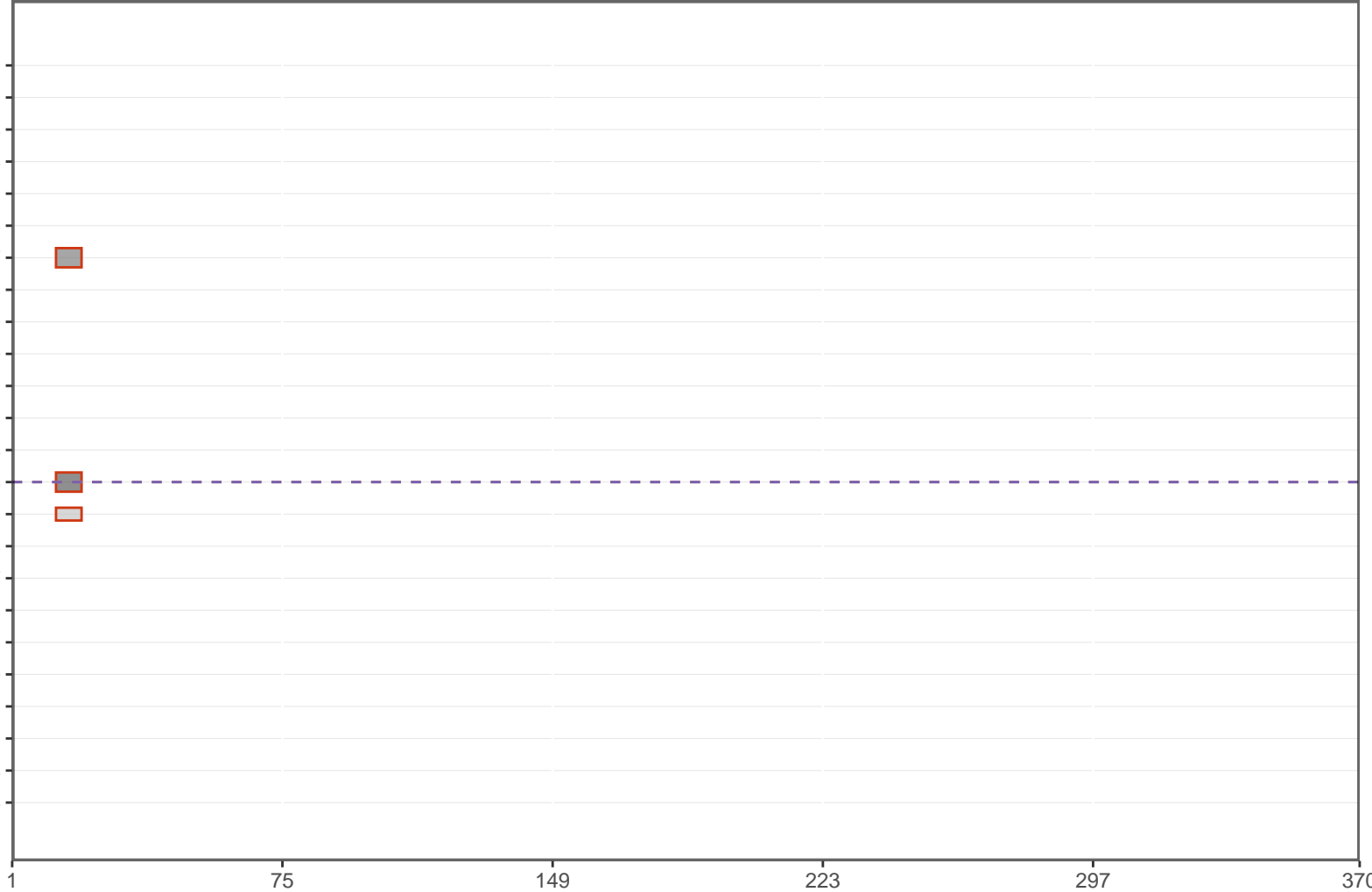
MW indication



Molecular weight

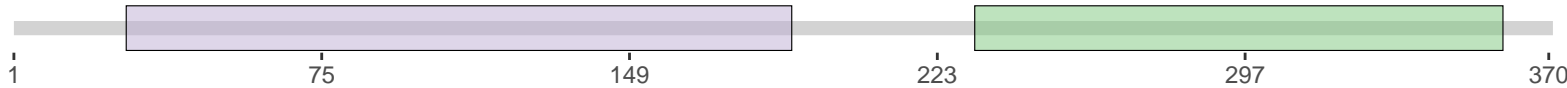


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF02518 Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase
- PF10436 Mitochondrial branched-chain alpha-ketoacid dehydrogenase kinase

Protein sequence:

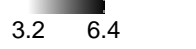
IQHVALHIDPNPPNKGVGHFKMSPLEVARTASEDARGIGLREYGSAPDNVYGGDFDFFPVPTHLHMMFELVKNNSVRAVGERFMDSDKVAPIIRIVADGLDEDYTKVSDDEGGGIPRSGLPKFTYLYSTARNFLNEHFTTTDVAWTSFLAGYGYGIPISRLIARYFGGDLQHSMEGYGTDALHLSRLGDGSGEPLS

NbL06g01060.1 50S_ribosomal_protein_L18_chloroplastic-like [MW = 18.43 kDa]

No. of times detected



log(intensity)



Values from



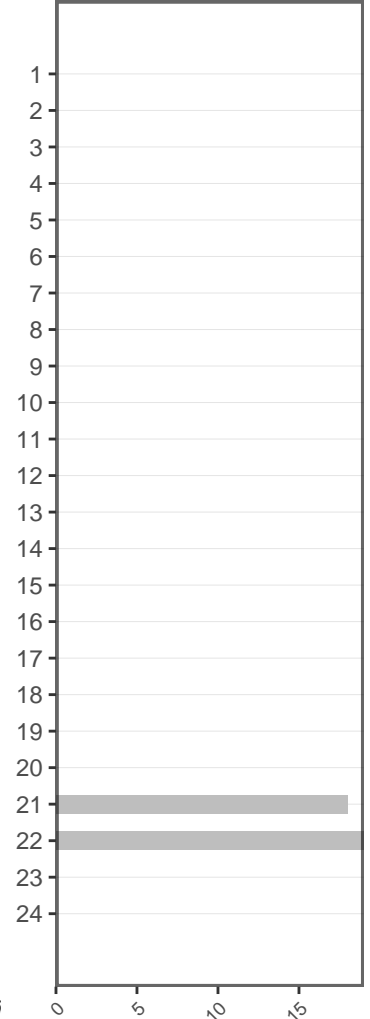
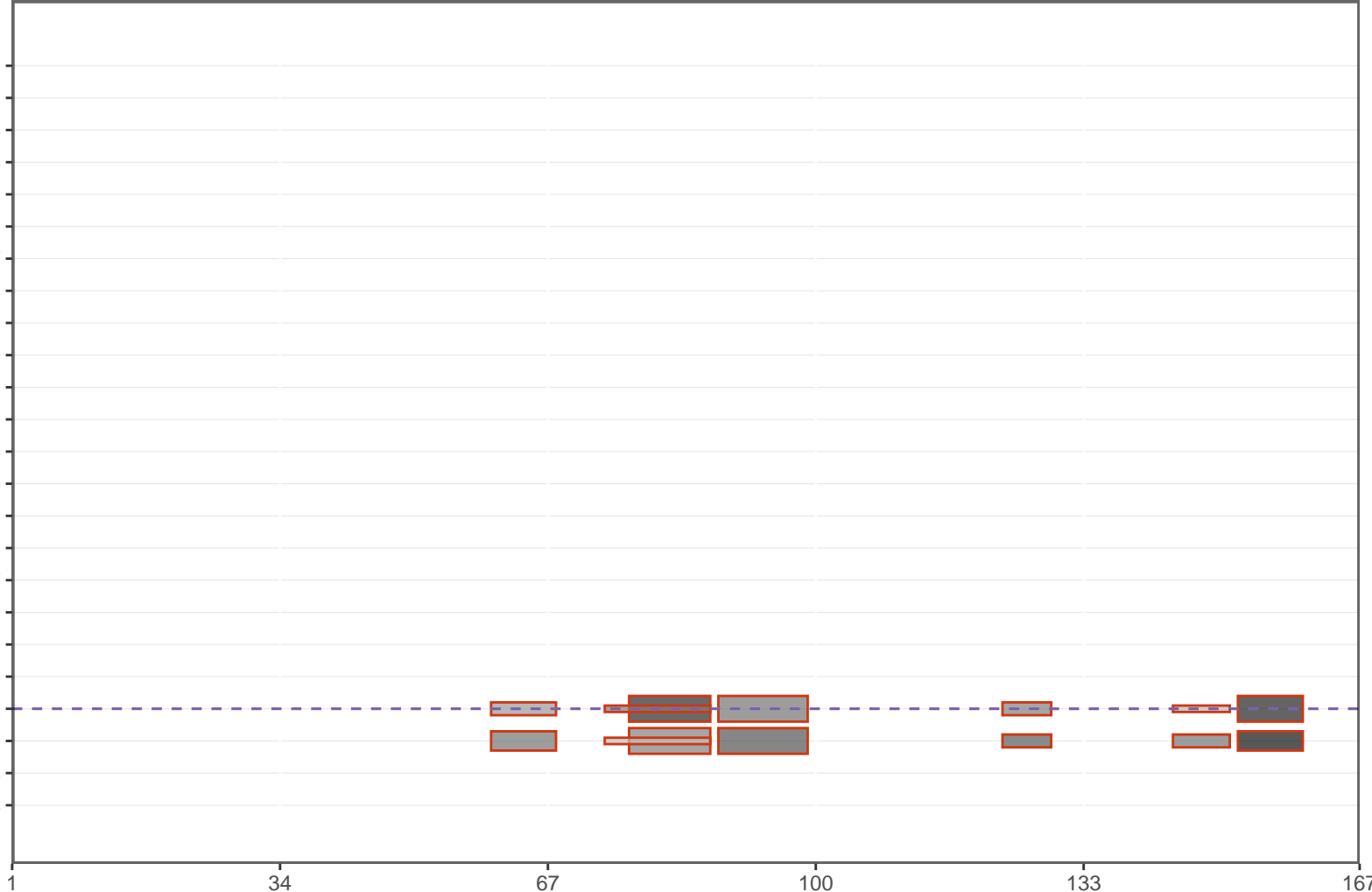
MW indication



Molecular weight

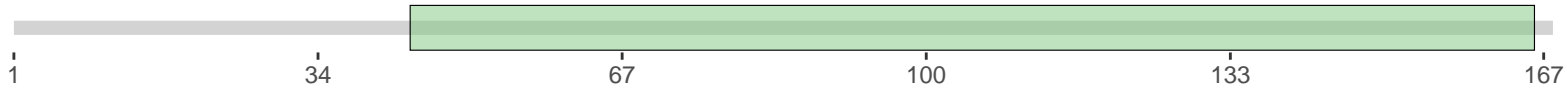


Gel Slice



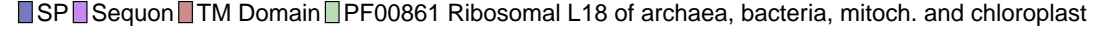
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VFRSNKHYYVQVDDSKMHTLASASTMKNKPIAEFFDYAGPTTVSSGGVANKVGEVIAKALEKNGITKVFDRGGYYPYHGRIEALADAAREHGLOF

NbL06g00970.1 protein_FAM32A [MW = 16.28 kDa]

No. of times detected



log(intensity)



Values from



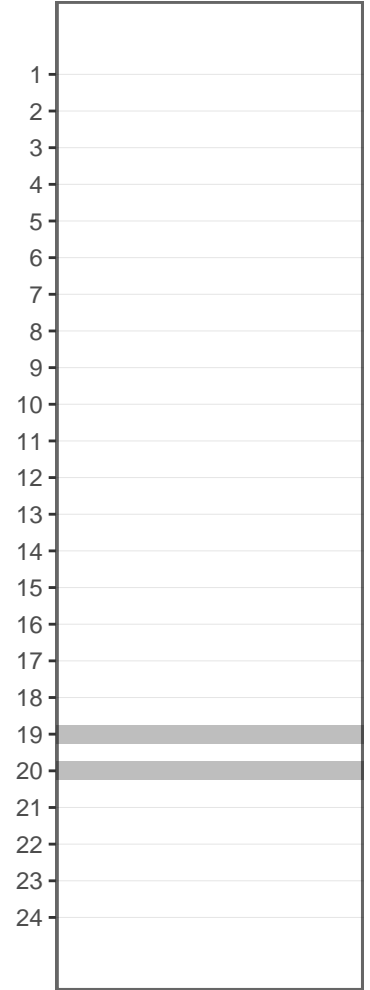
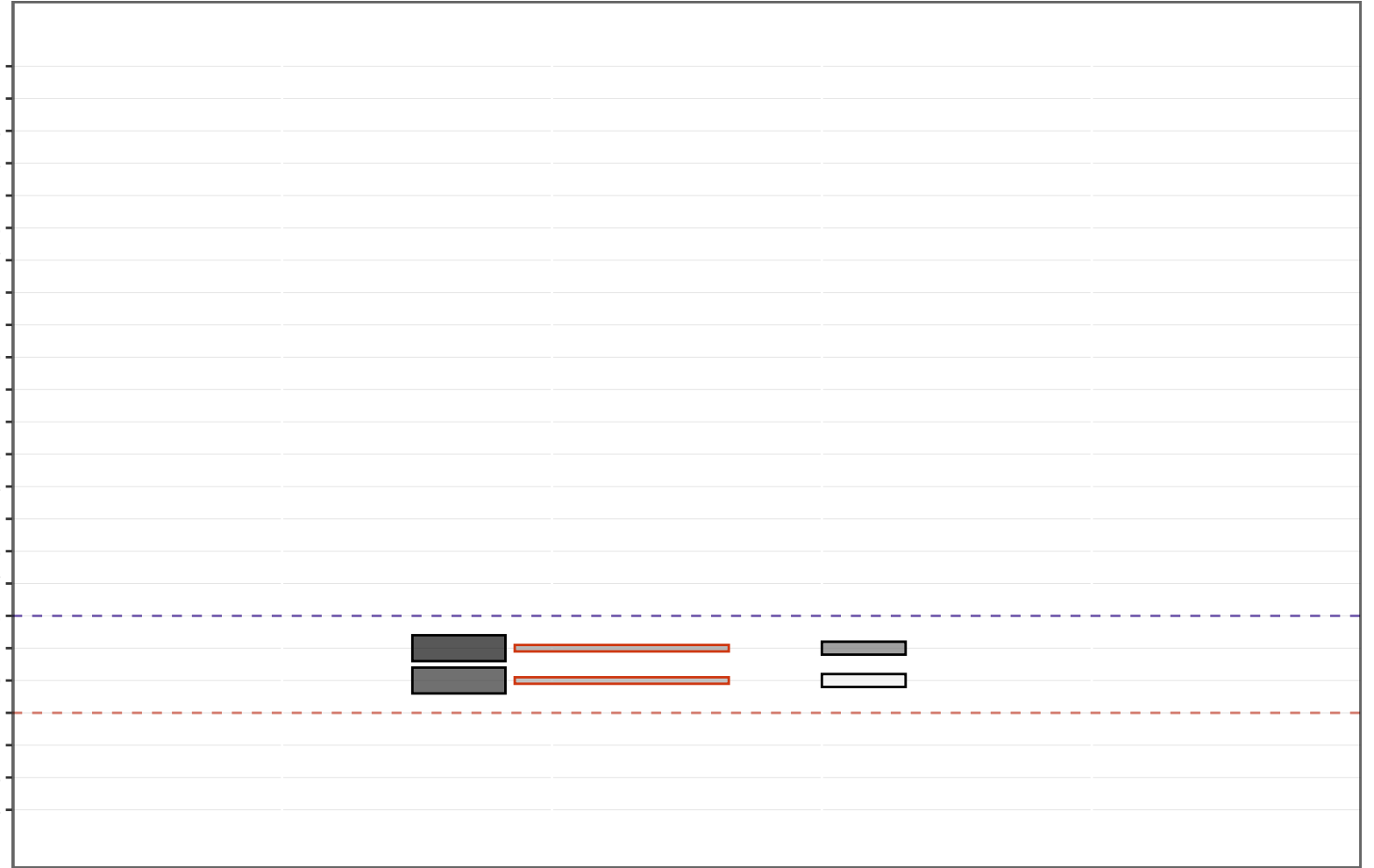
MW indication



Molecular weight



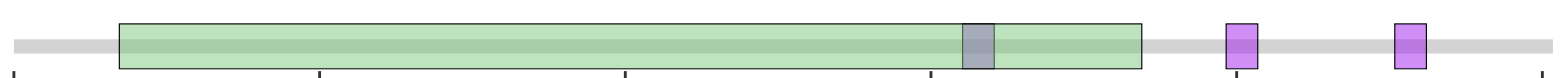
Gel Slice



Peptide counts over 4 repeats

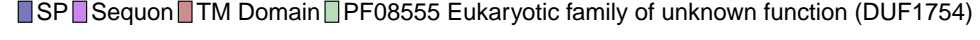


Protein length



Pfam domains

Pfam Description



Protein sequence:

GGSLDDPTKEESTDATKSVGEENAGRWDNLTFAERRYIEGRERIDMVKMAKTANKSHRDIEDFNGLANMSEHYDIPKVGSP

NbL06g00900.1 probable_histone-arginine_methyltransferase_1.3 [MW = 59.12 kDa]

No. of times detected



log(intensity)



Values from



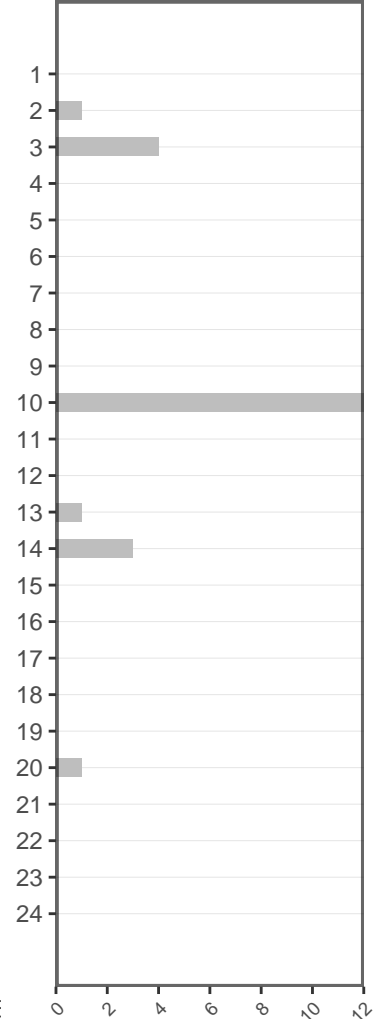
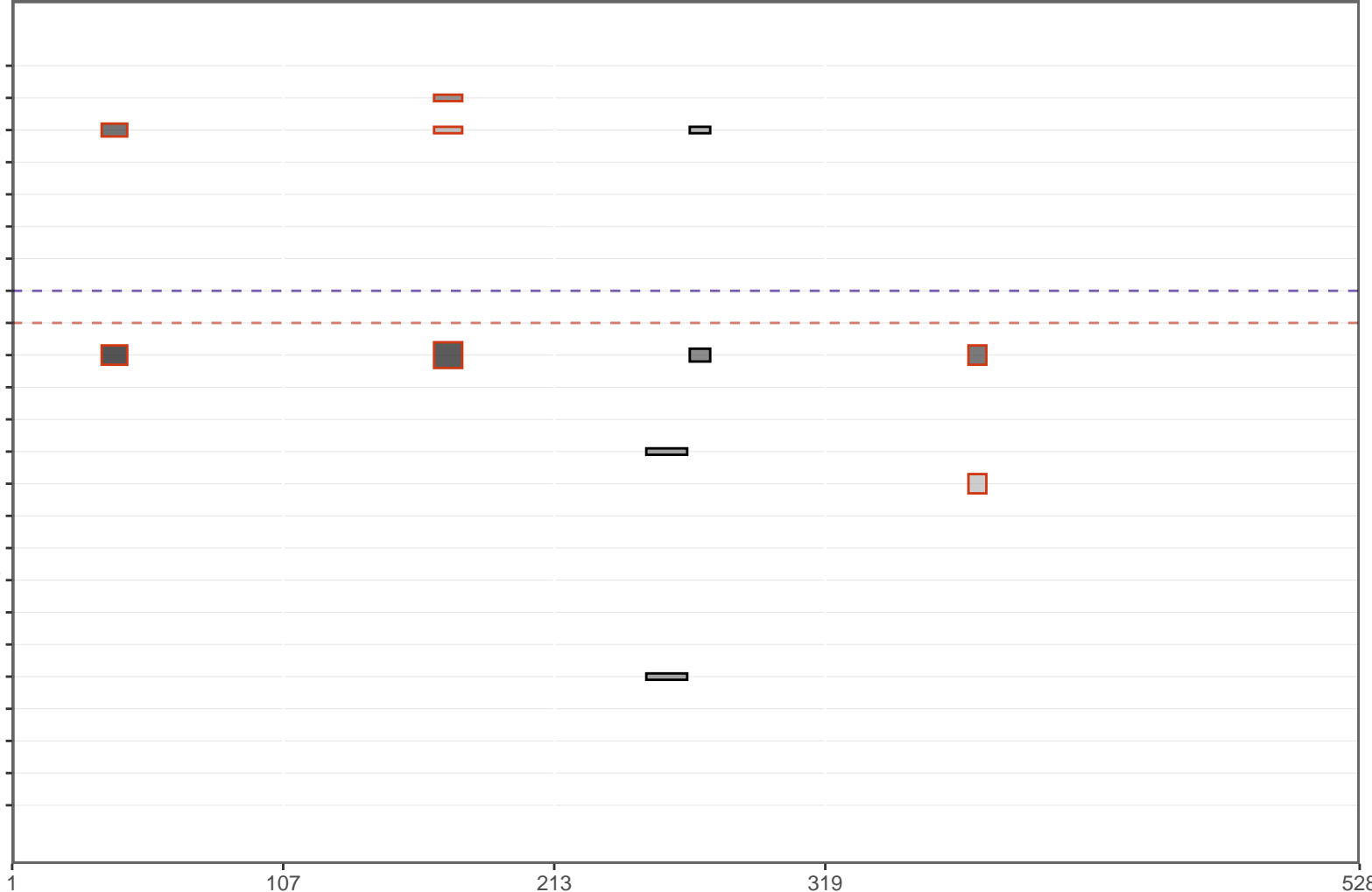
MW indication



Molecular weight



Gel Slice



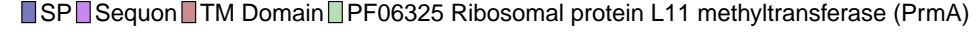
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILISEPMGTLVNEIRMLEEYVARDRFLVNGKMFPGVGRHMAPPFSDSEYLYMEANKATFVQDQNYFGVDLPLHSGAVGGYFSGPVDVADFRPLLVAPEVSHVNFNSKEEDLYEIDPLRFLEESVSTRHGLAGWFDVLFNGSTVGRWLTAPGAATTHVYQLRQVLPQLVYMPGQGEIFGRLLHWKAGSFTVYFLSALVSDMLGTSSVKLDLKEPYPRMSPQAVSLAGDDGPNQLLGTODELPERDEEDGSLMOPFPNSGAELHSL*

NbL06g00820.1 glucosidase_2_subunit_beta-like [MW - SP = 65.35 kDa]

No. of times detected



log(intensity)



Values from



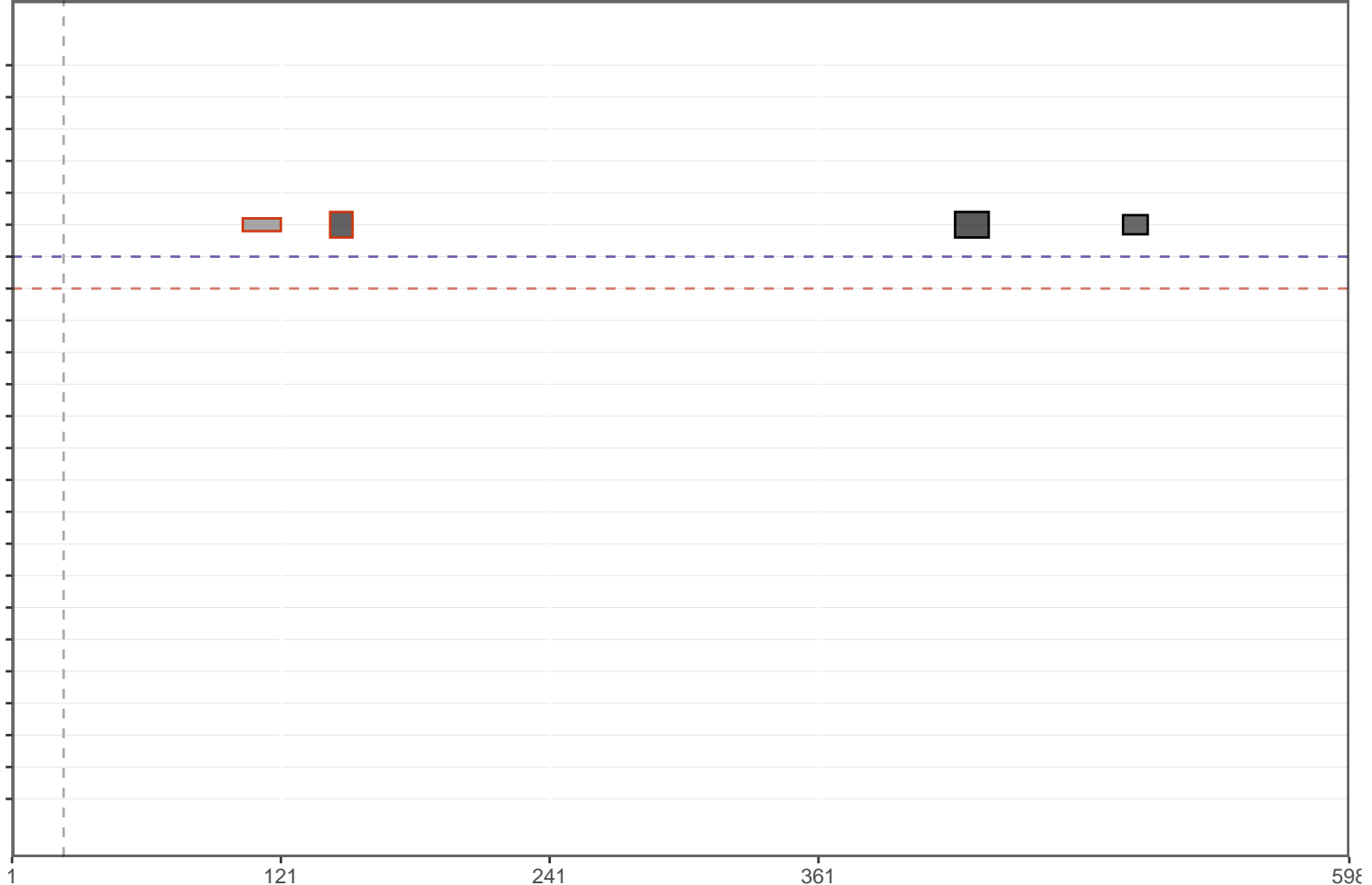
MW indication



Molecular weight



Gel Slice



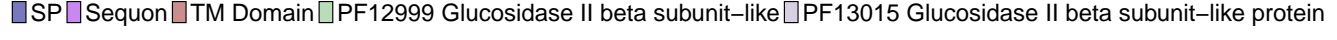
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

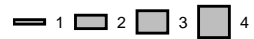


Protein sequence:

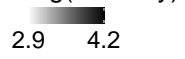
DSSQEKDANTEILSLKKEELGRVYSGRWLGGKKGSEGELEEVGAGTDYHNDHDEVLFDPTHEEEVNGYDSEEDHKYDDGDKDQVEDFYGEDHDS66SLHKSE6DDDD6DFADTTTSSPSWMEKIQGAWKSFRAVNLFGTPTVNSDADRIRKEYDESSVWLTNGSRISGLTEKLGDFGPEKEFYGFHDGDFESKENVYTKICFFKFA6GVGEGVSTTRLGNWIKFED6VYKTMGFSNGDHWINGFNRBLKWKVLRGLNKLTFVDEPSRQDEYLAFLSTPALCREELKEI

NbL06g00690.1 rhodanese-like/PpiC_domain-containing_protein_12_chloroplastic [MW = 33.91 kDa]

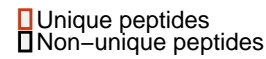
No. of times detected



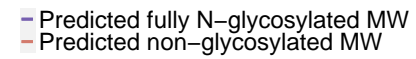
log(intensity)



Values from



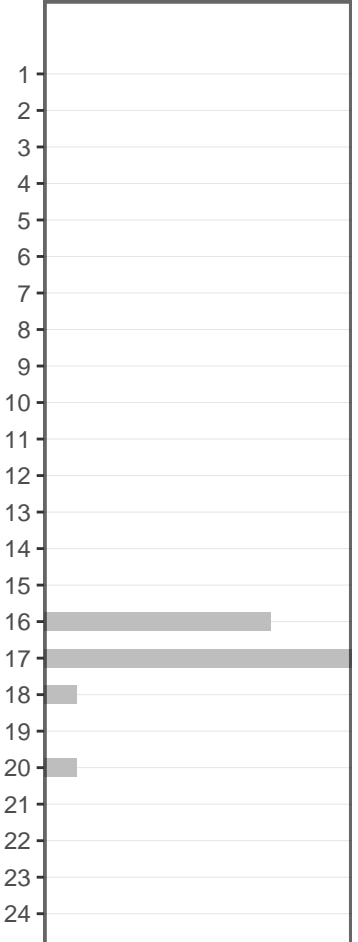
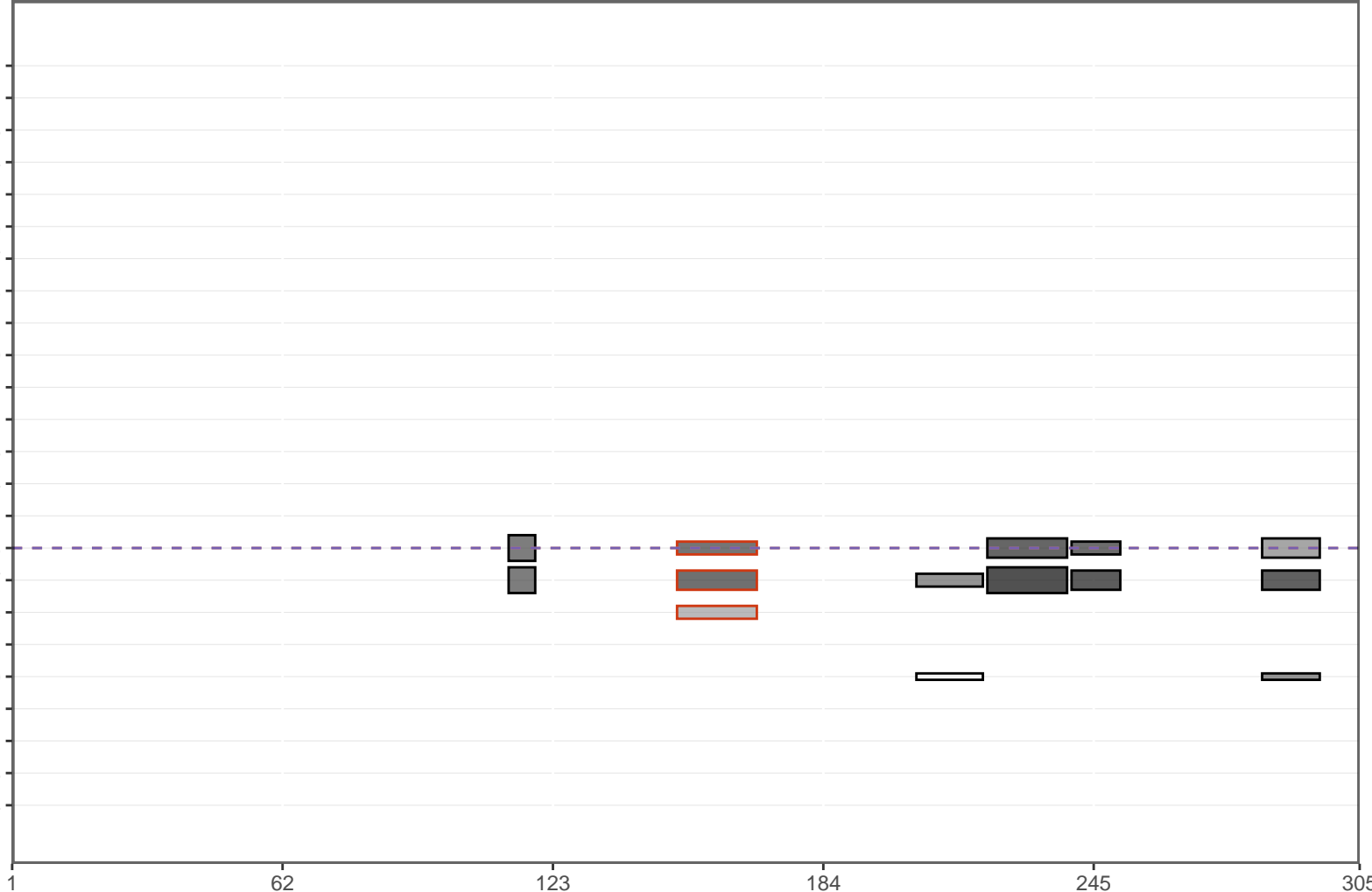
MW indication



Molecular weight



Gel Slice

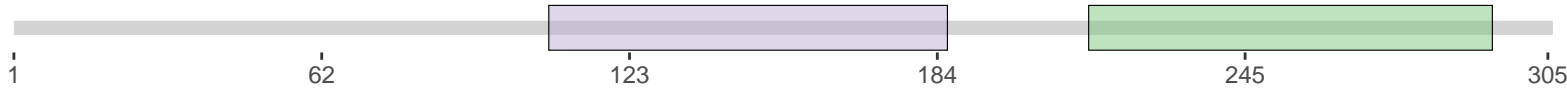


Peptide counts over 4 repeats

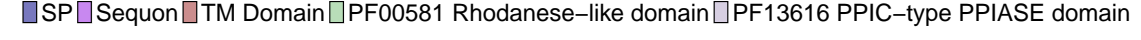
Protein length



Pfam domains



Pfam Description



Protein sequence:

IGQMLGIVYRKGQMVPEFEEAFAVPLNKVKKKTKFGWHLGVLGEREEVLEHQPNEFHVKGDPFLEEAQIIVREPEEVAQASLPGFVLPRLRFGSGWGPETITKFDPKDITYVLGHHGMRSLQVAVWLGTFGRKVFNIAGGNEVAVKVDPSPTVY

NbL06g00670.1 signal_recognition_particle_9_kDa_protein [MW = 17.72 kDa]

No. of times detected



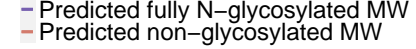
log(intensity)



Values from



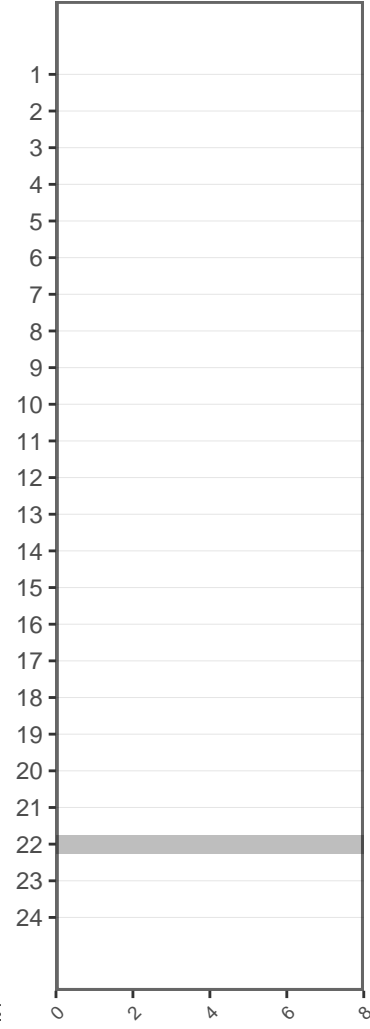
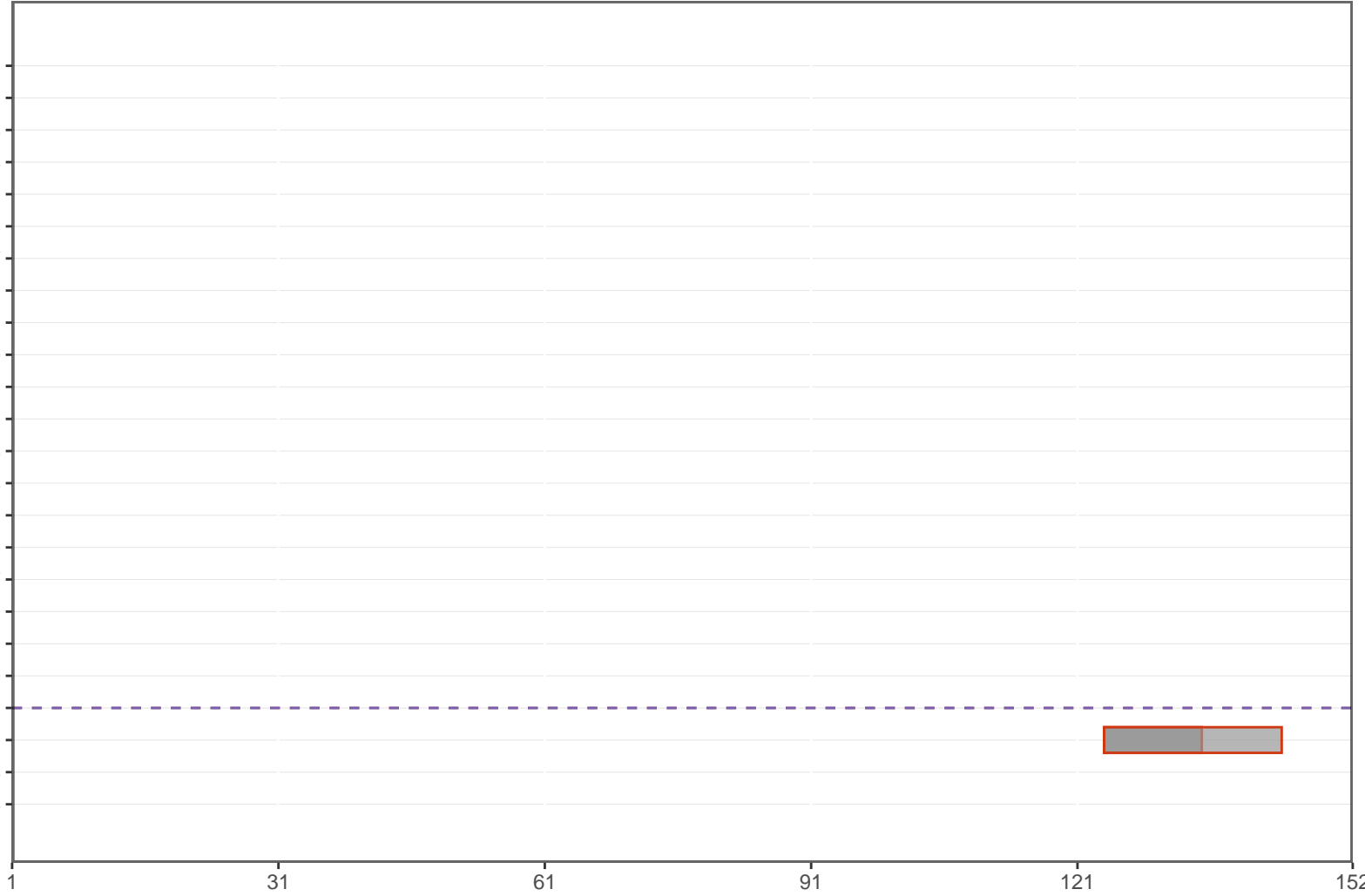
MW indication



Molecular weight

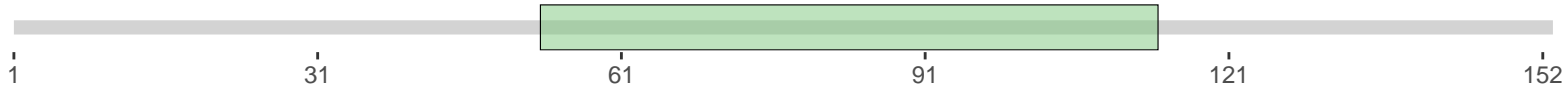


Gel Slice



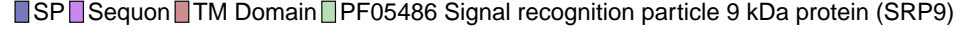
Protein length

Peptide counts over 4 repeats



Pfam domains

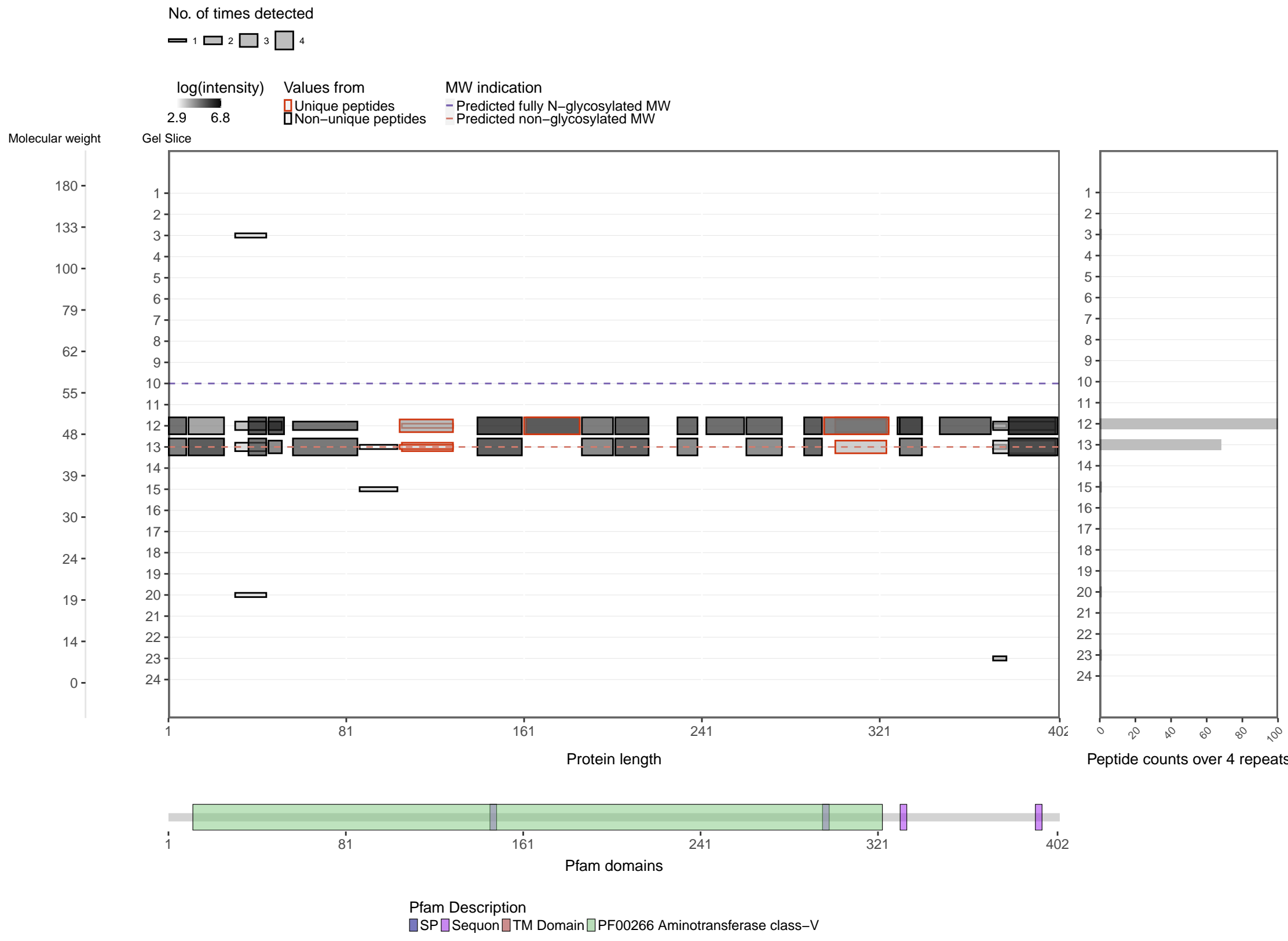
Pfam Description



Protein sequence:

ILFRADPEKTRYVIMKYRHSEGKLVKVTDDTEGKIFRTDQAGDANKMEKLNIFFTLMARGPDADISEVGGKGEAGAPKKGRGRKQ*

NbL06g00500.1 serine--glyoxylate_aminotransferase-like [MW = 43.92 kDa]



Protein sequence:

WGVDAVLTGSSQKALSLPTGLGIVDASPKALEAAKAKSVIRVFFDWSVYLKFKYKMGTYWYFTRPSIQLLYGLRAALDLFEELLENVIAHRAHLGKATRLAVAWLGNLTKQKEEWFSDTVAWVAPPYIDGAEVVKRAWRVYVNLISLGLGNKVGKVFRIHGLGNLNEGLQLGLGAGVEMVLDKDYVYVFKFGSGVAAASTFLGNSTPLIPRI

NbL06g00460.1 calmodulin-7 [MW = 22.62 kDa]

No. of times detected



log(intensity)



Values from



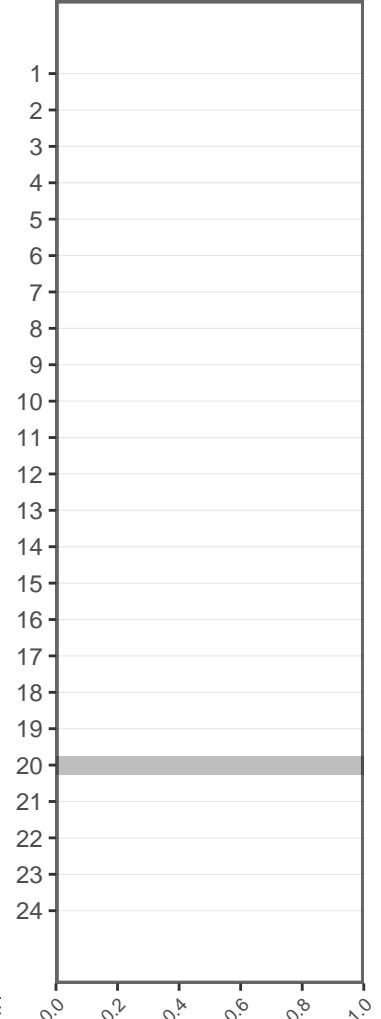
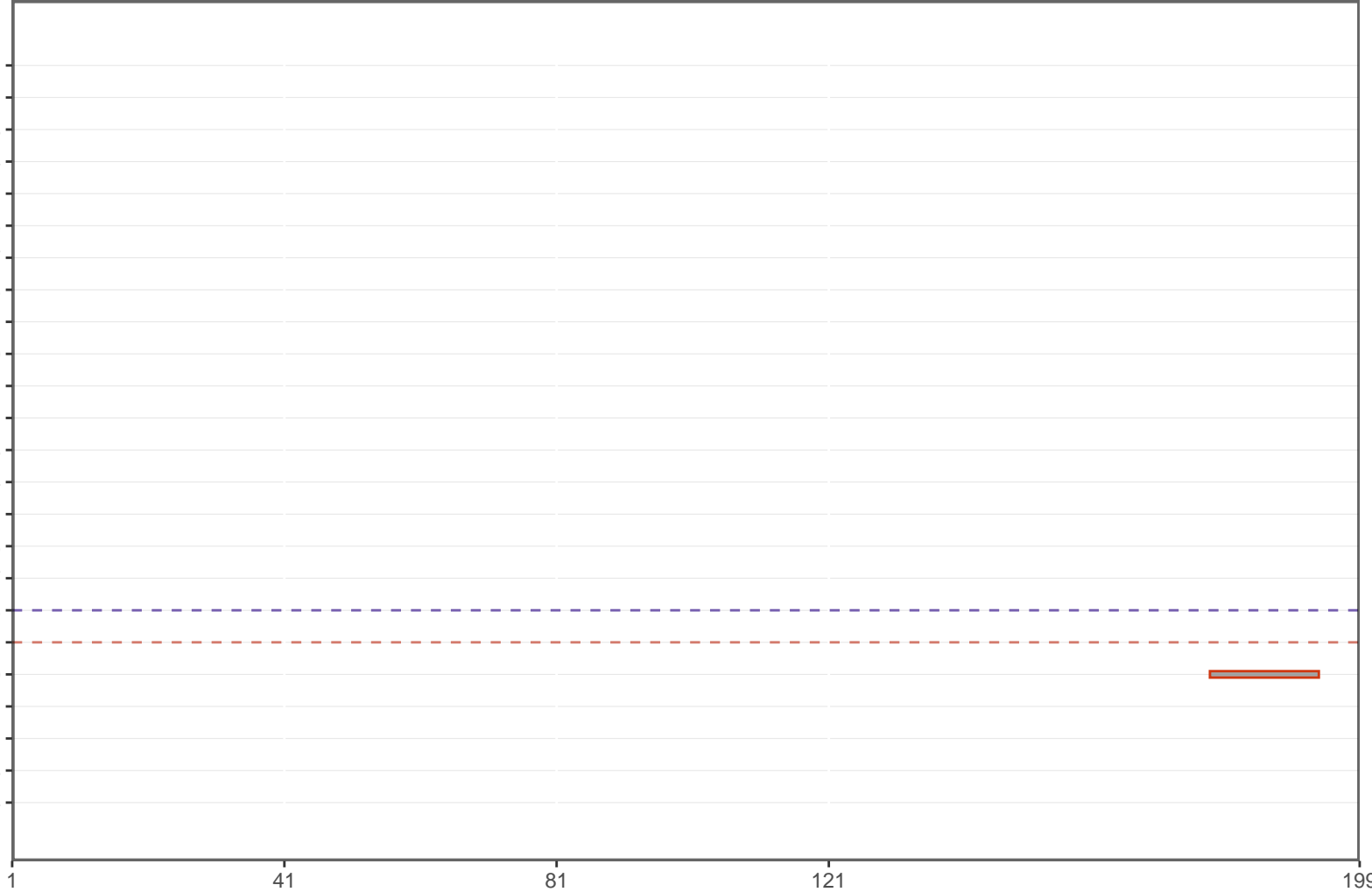
MW indication



Molecular weight



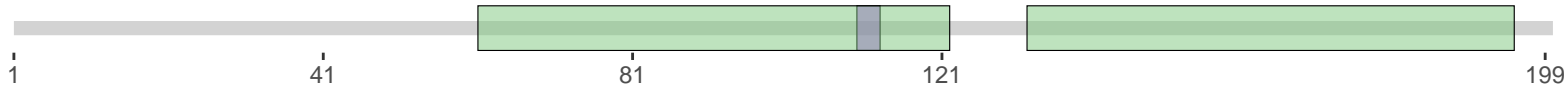
Gel Slice



Protein length



Pfam domains



Pfam Description

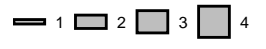


Protein sequence:

LGQNPTEALELQDMNEVDADGNGTDFPFELNMARKMKDTSSEELKEAFRVFDKDGNGFSAEELRHVMTNLGKELTDEEVDEMIREADVDDGQHNYEEFVWMMAK

NbL06g00340.1 uncharacterized_LOC107818673 [MW - SP = 94.01 kDa]

No. of times detected



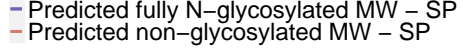
log(intensity)



Values from

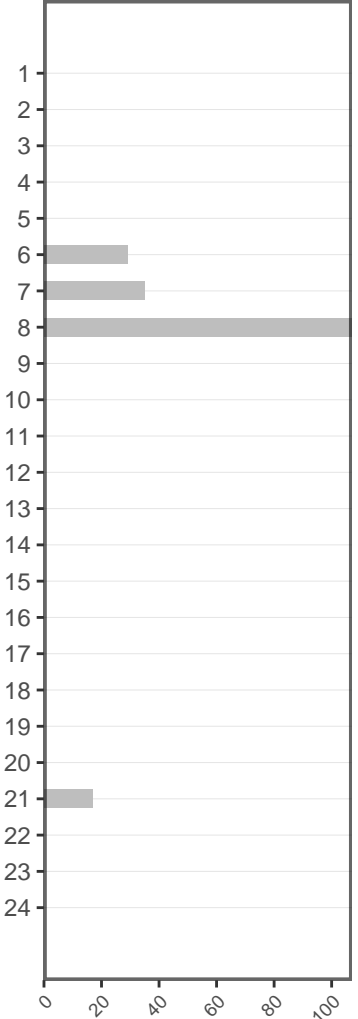
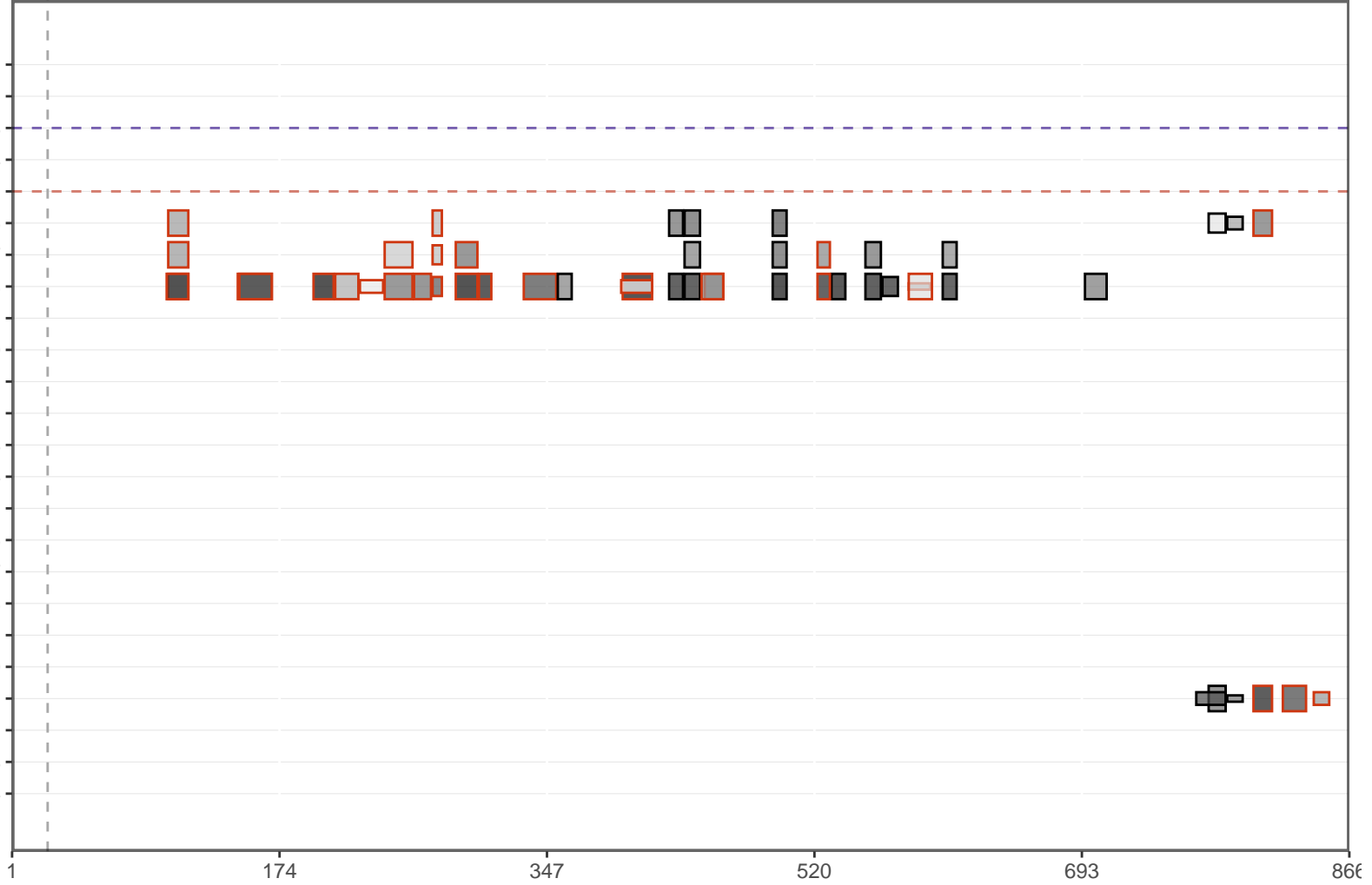
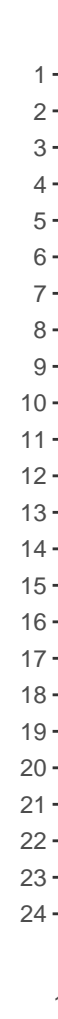


MW indication



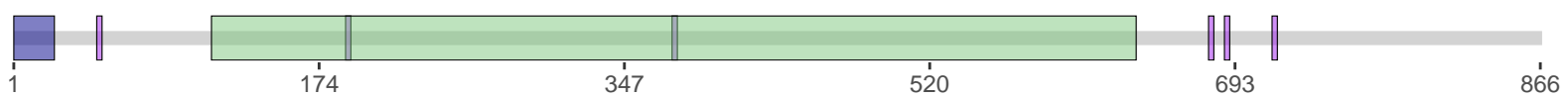
Molecular weight

Gel Slice



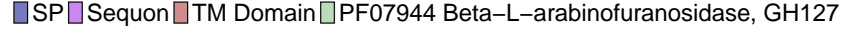
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

/SRILFRVYTKEMAWADYERALTNGVLSIGRGRDPGVMMFLRLRGGKKAHSYHGWTGDFDFWCCYGTGIESFSLGDSVYFEKGNTPFLVYIPSTLDDWKSQGLVSGKIEPVSWIDNRLLVTTTISGNGKATGVLSSTLNLRFPSWYTSGGAKATLNGKDLGLPTPGNLSITKHWQGGKNTLELPLMSLRTEAKDDRPEVASVQALYGPVLLAGHS66GDVETNSSTDLSDVITYPADVNSGLISLMQESGNATEVLTNSGSHQMEKFFPAGTDAU/SATFRLSLA

NbL06g00290.1 50S_ribosomal_protein_L6_chloroplastic [MW = 25.15 kDa]

No. of times detected



log(intensity)



Values from



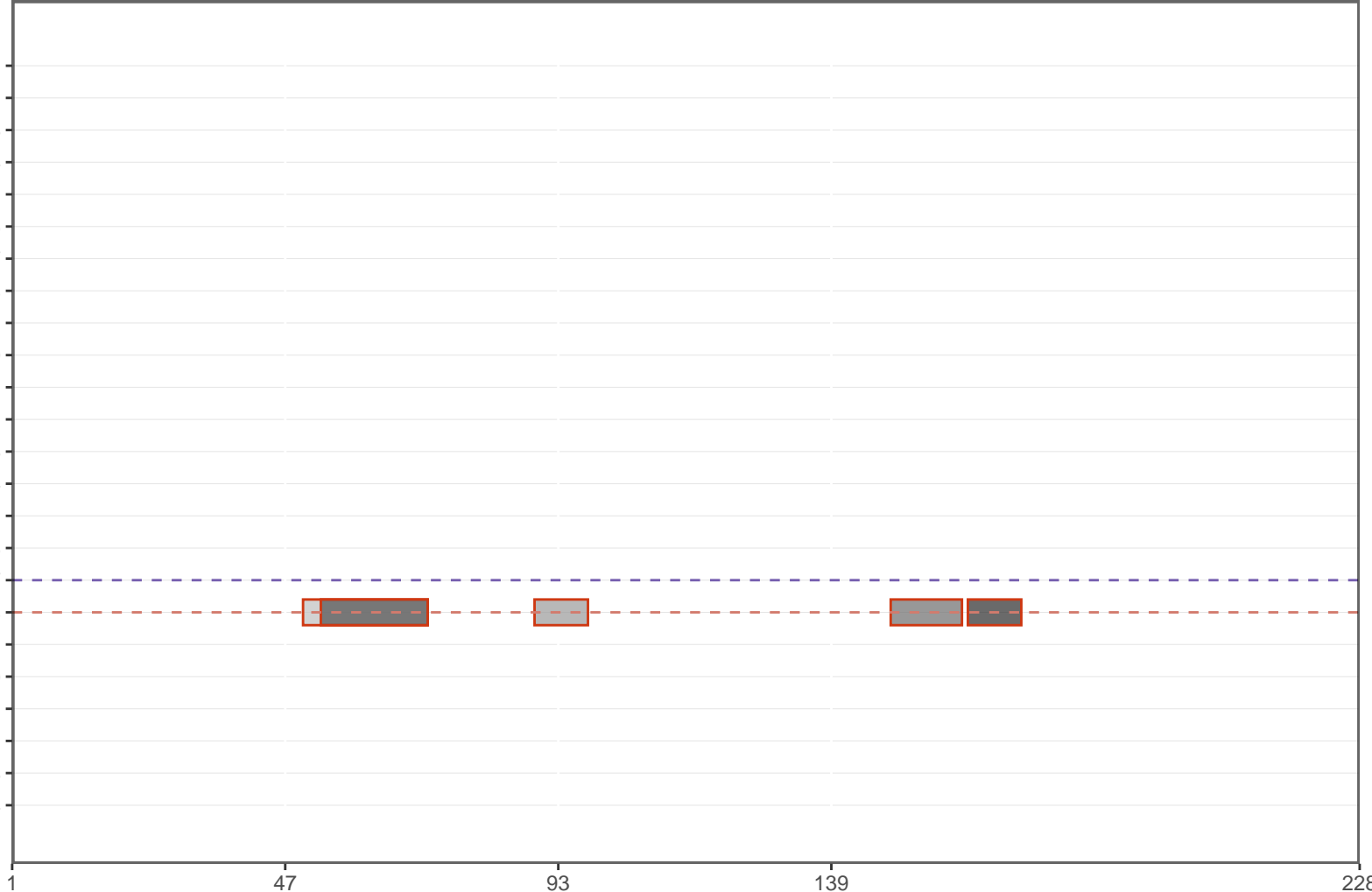
MW indication



Molecular weight



Gel Slice

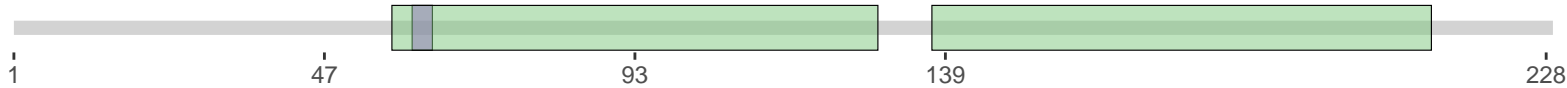


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description

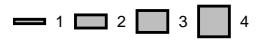


Protein sequence:

AVETRRANDQMHGLFRITLTDNMVAAGVSGKFEKLLQLVGVGYRATVEGKEIVLNLGFSHPWMEIPNGLGVVYENTRITVSGVDKSEHGQFAASIRKWRPPEPYKGGKGVYADEIVRRKEGKAGKKK

NbL06g00270.1 pleiotropic_drug_resistance_protein_1-like [MW = 162.13 kDa]

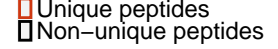
No. of times detected



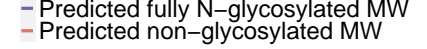
log(intensity)



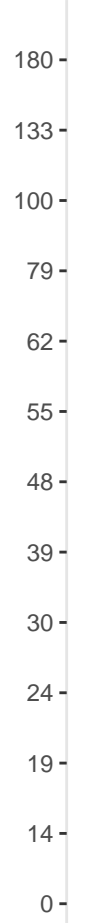
Values from



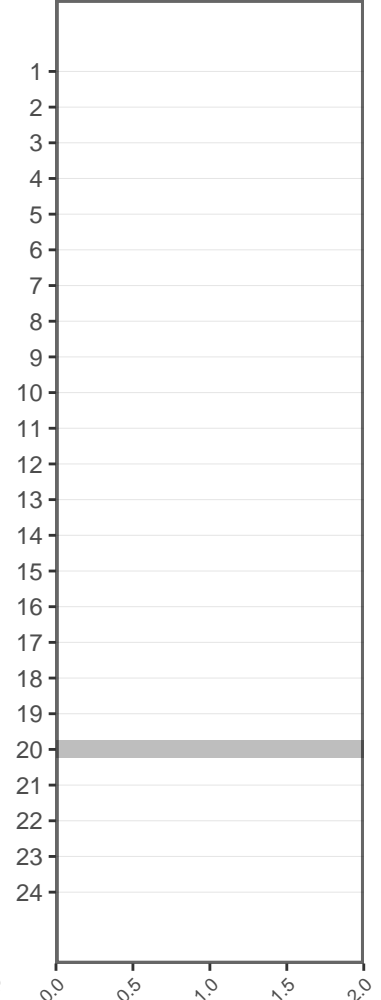
MW indication



Molecular weight



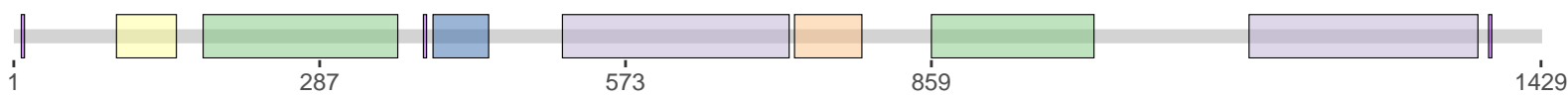
Gel Slice



Protein length



Pfam domains



Pfam Description

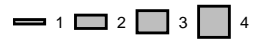


Protein sequence:

WVWGYWTSPLMYSINSIFVNEFDGKRWKHAFNPIEPLGDVAVRBRGFFPDVFFWIGGALIGFTLFGNCFNLALAYLNPFGKPPVMPKDNEDVKTFTDEKEGNSSEDDGSKKGMVLFPEFHSTFDFEIVYSDVDPGEMKDDGATEDRILVLLKGVSGAFRPLVLTALMDVSGAKTTLMDVLAGRKTGGVHEGKIKGGYFKPKQETFARISGVYEGQNDHSPVFTVYVESLVYSAWLRLLPHDVEDERTKMFVDVAMVELVETFLRSLALGVDPGVNGLSTEQKRLTAIVELVA

NbL06g00260.1 selenoprotein_O-like [MW = 72.31 kDa]

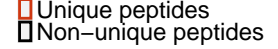
No. of times detected



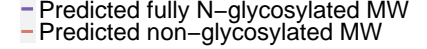
log(intensity)



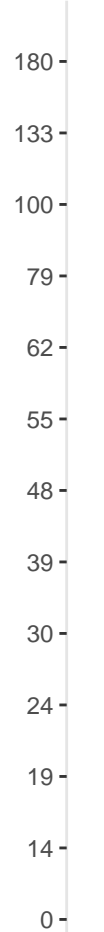
Values from



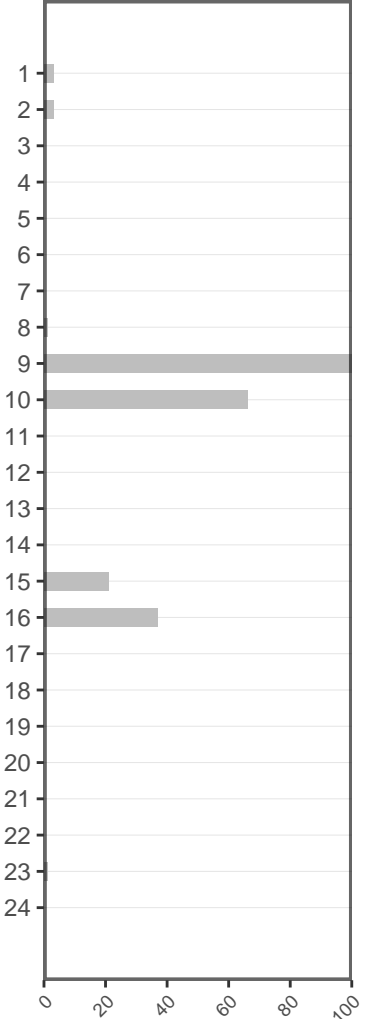
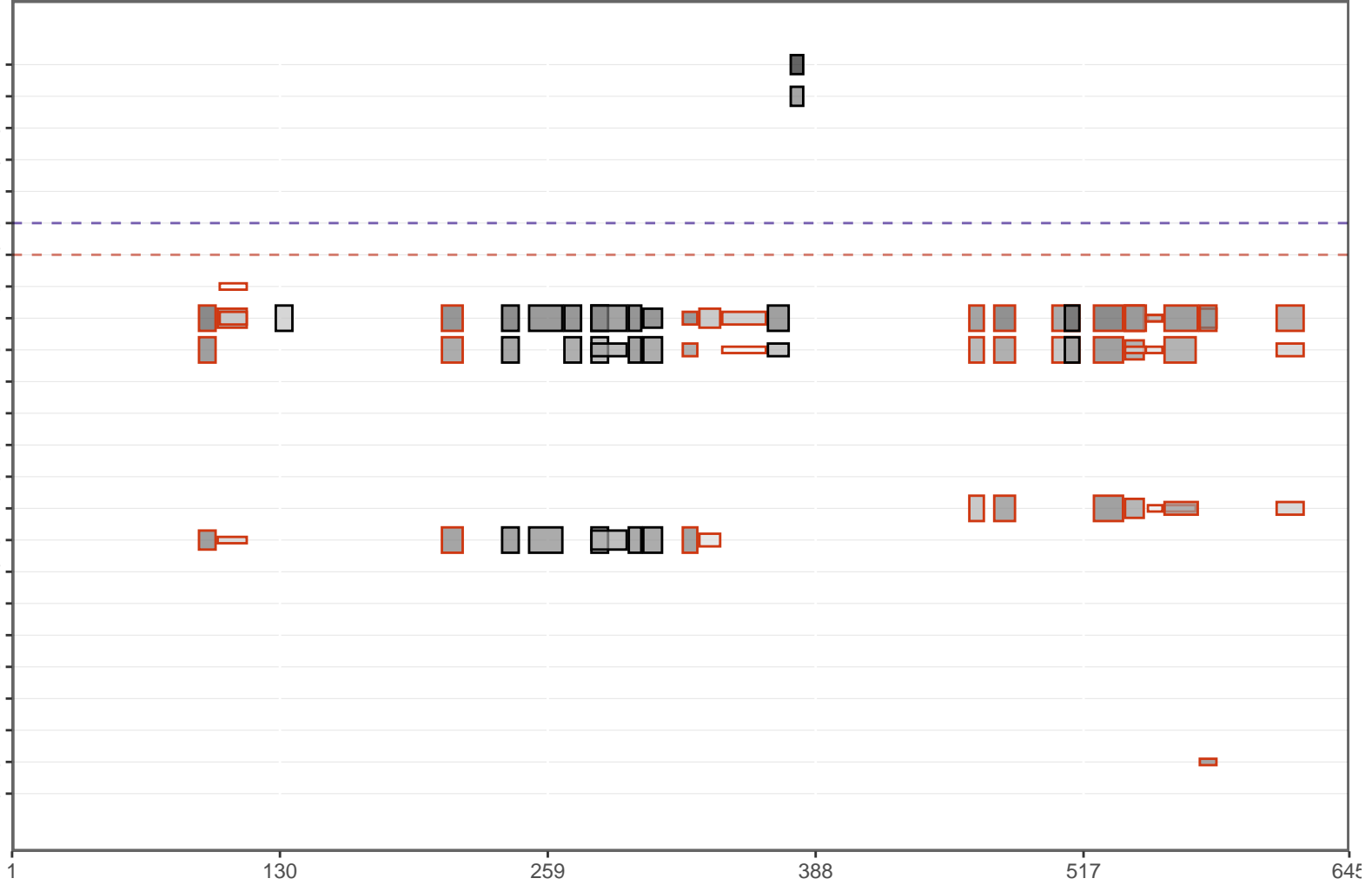
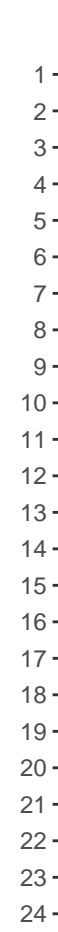
MW indication



Molecular weight

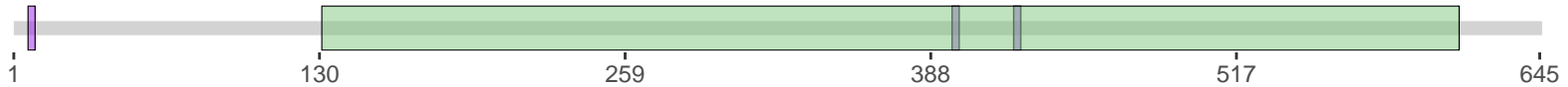


Gel Slice



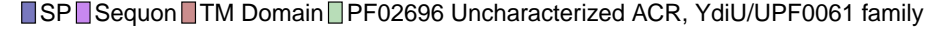
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

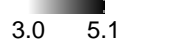
ILHASRGGKDFEIVRALADYAIRYHFPLENMRNNGGGISFNTGEEEDNSAVDL6SNKYAAWVAERTASMIARWGGVGFTHGVNNTDNMSVLGLTHDYGPFGLDFDFFSFTNTTDLPGRRYGFANGPQVGLWVIAQFTSALGTAELLNDKEDAVMERYGNKFMDDVGVIMTRKLGKAYHKKLISELLKNMAIDKVDYTNFRLLSNKANKPTGQEDQLIPLKGLVLDIGERKEAWTTWYKGVGELSTTGVSDDEERKVMNSVNPKYLRNLVGGTADDAEQQDFGE

NbL06g00220.1 dehydrodolichyl_diphosphate_synthase_2-like [MW = 30.87 kDa]

No. of times detected



log(intensity)



Values from



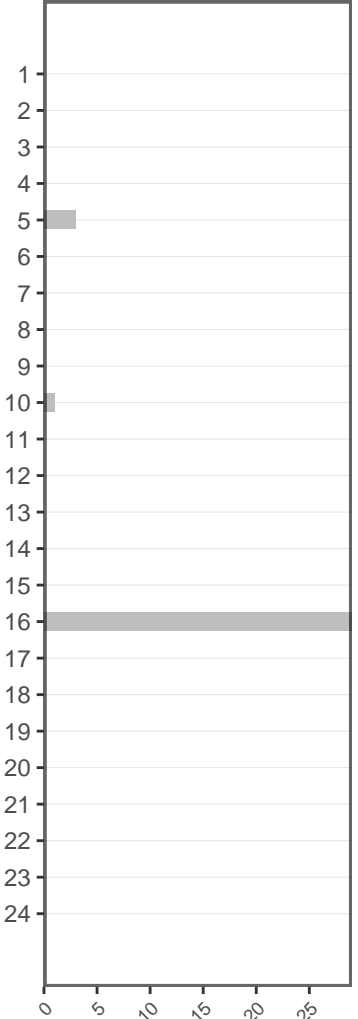
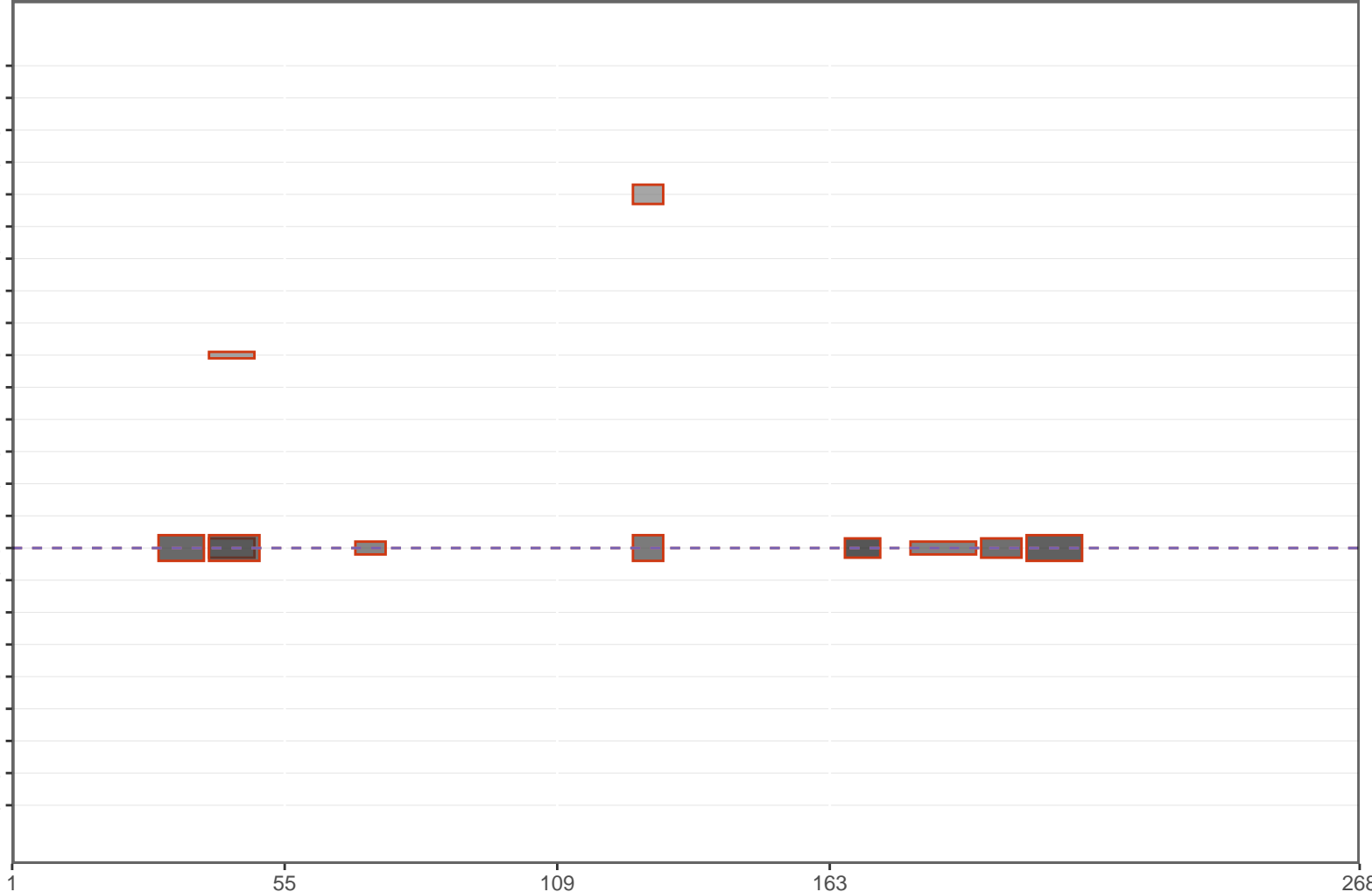
MW indication



Molecular weight

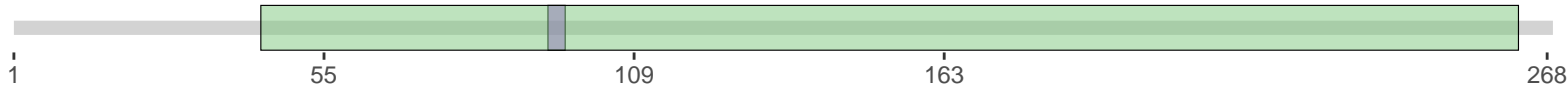


Gel Slice



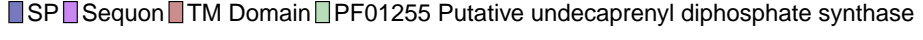
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

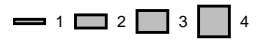


Protein sequence:

YGMKMSVIGDKSNLPSNLKEAINHAEETFDKNGLHFVAALNYGGRYDITGATKNTATKVDGVDGFEDINDKLDIGLETKNLEYPNDLLIRTSGELRISNMYLWGLAYSEFCFVKKLFFDLDEADFAALRSFORRRQRYYGGHKP

NbL06g00150.1 DNA_(cytosine-5)-methyltransferase_CMT3-like [MW = 101.77 kDa]

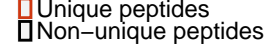
No. of times detected



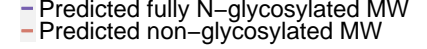
log(intensity)



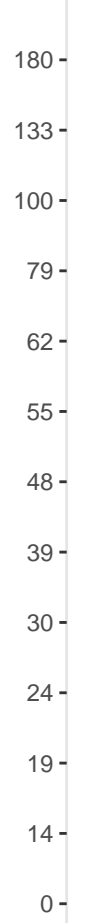
Values from



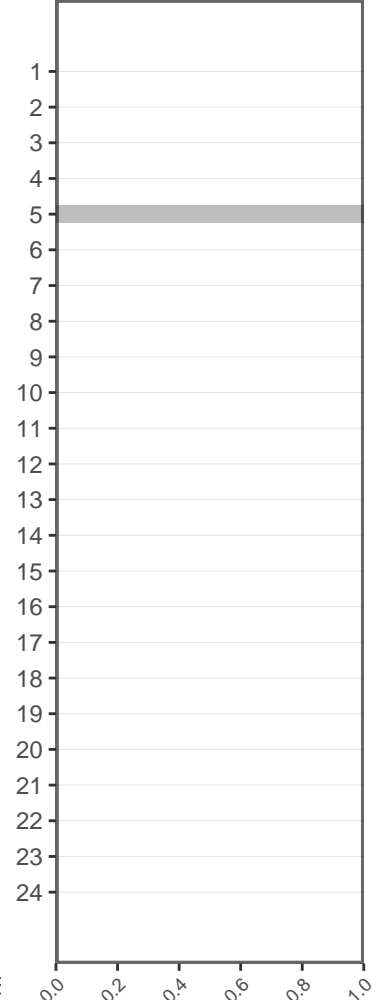
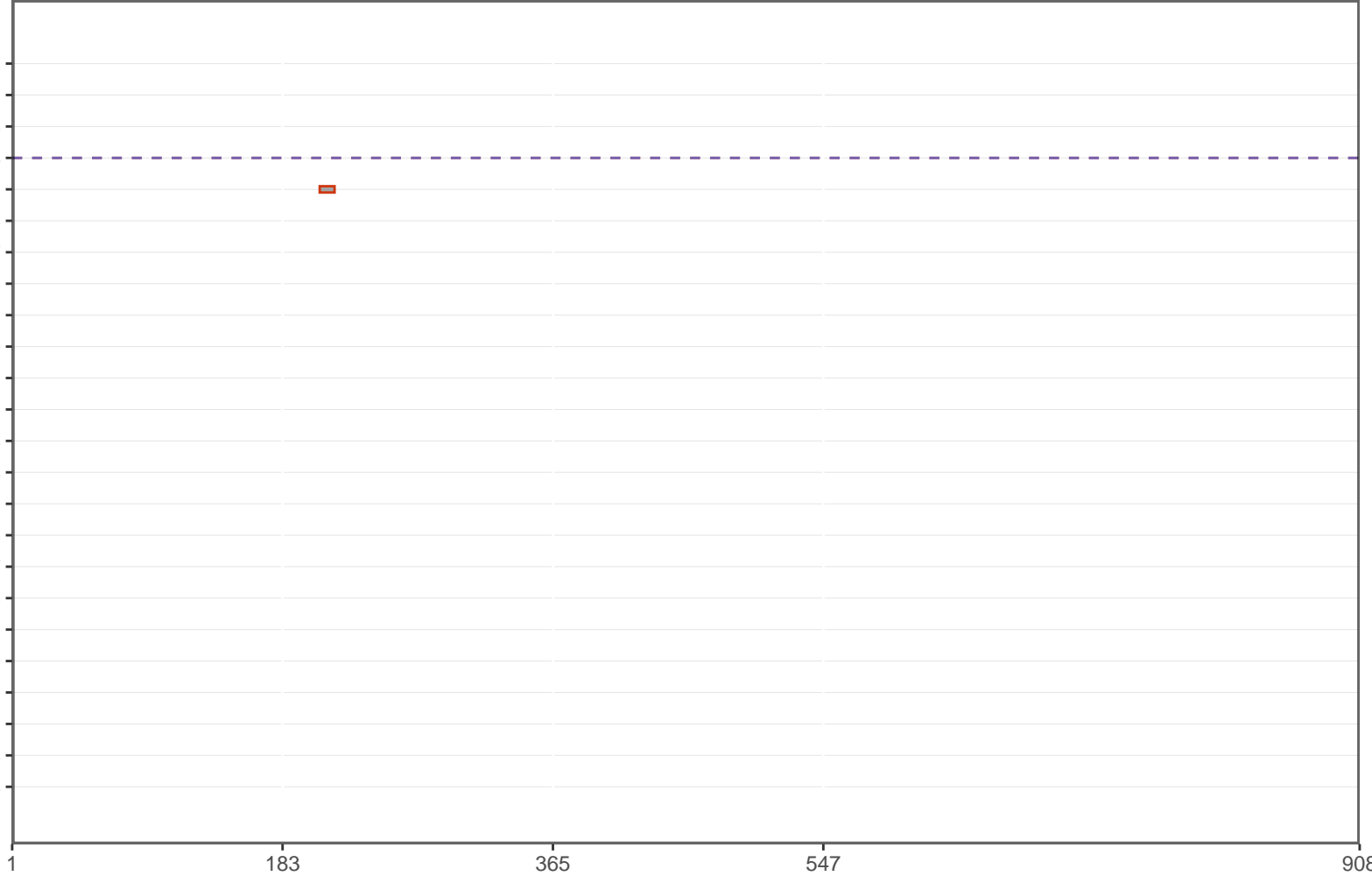
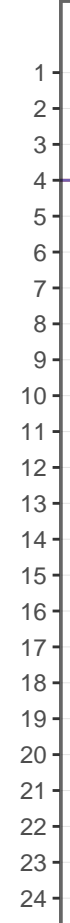
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

DDSEDSDDDKKGEFEVEERLELVYGGDPNVRKPGLYFKVWVGWYGGPEEDTWERPDGLSECPKRIREFVTKGFKANLLPLPGDVIWVGGPPGGISGIFNFRNKENPLGDPKNGDLEVFMDIVDFLKPREFLMENVVDLKIFSNGLFGRYALGRLVGMNYYQARMGMMMAAGAYGLPQFRMRVFMVWVAGLSSEKLPQVPLPTHKVIVRQVIRTEFESENTAFDEGMELELNKEVFLGDALSDLPVYENNEQRDEMAYTNEPTSDPFQHFIRLGRDGLGSVLYDHRPLQLA

NbL06g00110.1 spermidine_coumaroyl-CoA_acyltransferase [MW = 49.93 kDa]

No. of times detected



log(intensity)



Values from



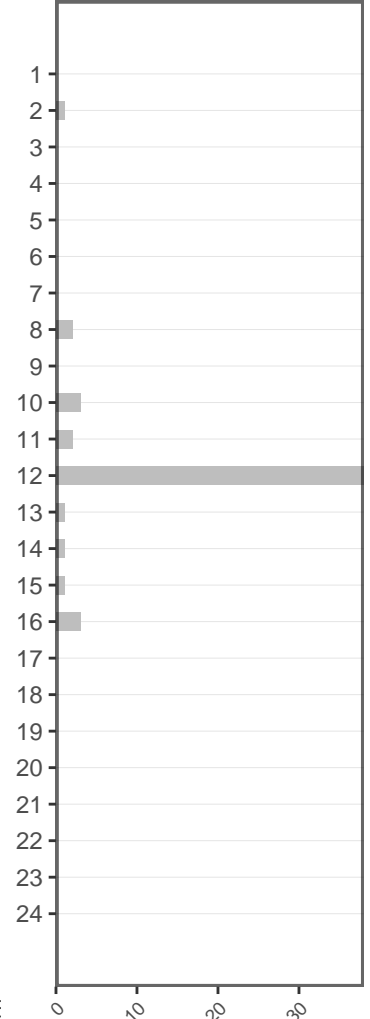
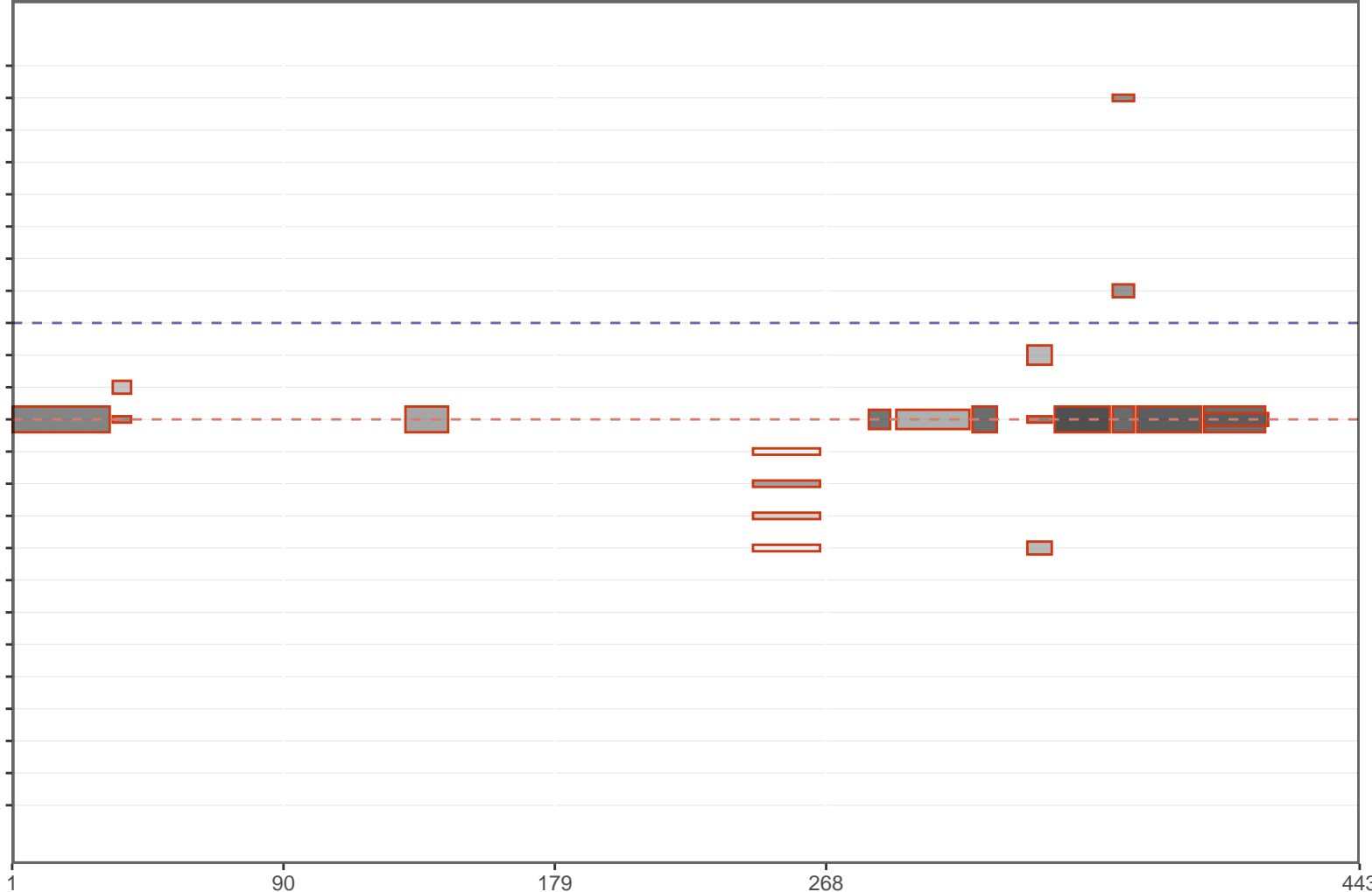
MW indication



Molecular weight



Gel Slice



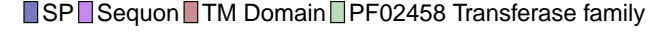
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEFFSLAKDSVPLYGGGKPIWRKQFEVYKDEWLDRLKGLFHEGSGLNFTTFEALGAFIWRAKAKASKIPGDEMVKYWLTRRTRVYKALPMGYWNGGCVPIYVOLLAKDLNPIWKTADAKKSKSHITDEYVRSLIDFQELHYDEGITAGNRVSAFTDWRHVHSHETVDFGWWGGPVTVFPLSRHLVGSVEPQFFLPSGATEGKKDKGFRVVLVGLGEEAMPVFKKEEMKQLEHLS

NbL05g22310.1 cysteine_proteinase_inhibitor_1-like [MW – SP = 9.97 kDa]

No. of times detected



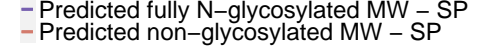
log(intensity)



Values from

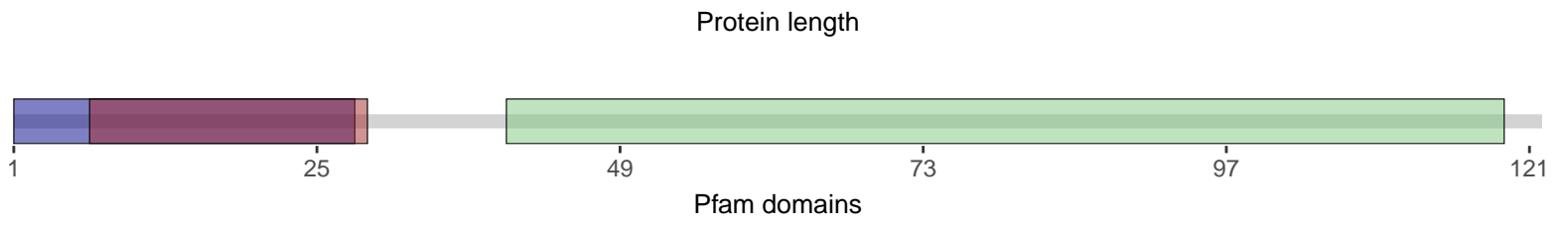
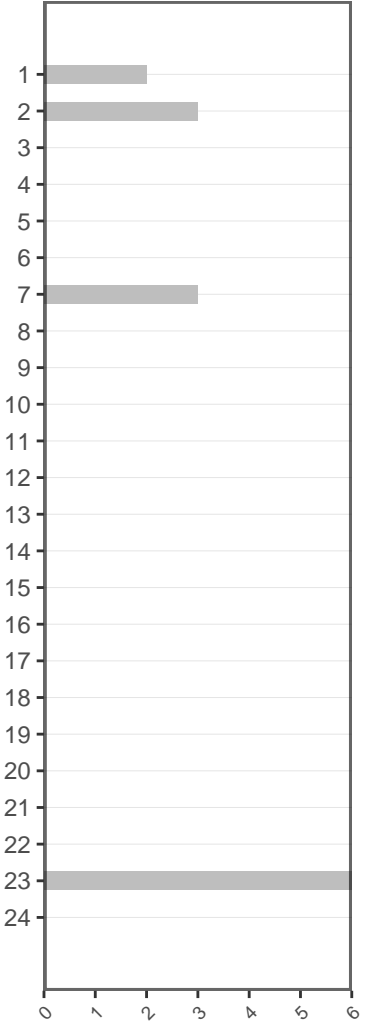


MW indication

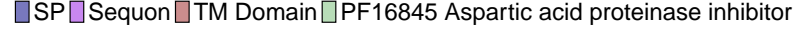


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

IGQFAVNEHFKKAGTKLEYGQNAKGETGVWAGTNYRLVINAKDGGGVHKYLAIVWDPKPEKWKRTSRKQK

NbL05g22270.1 induced_stolen_tip_protein_TUB8-like [MW = 16.18 kDa]

No. of times detected



log(intensity)



Values from



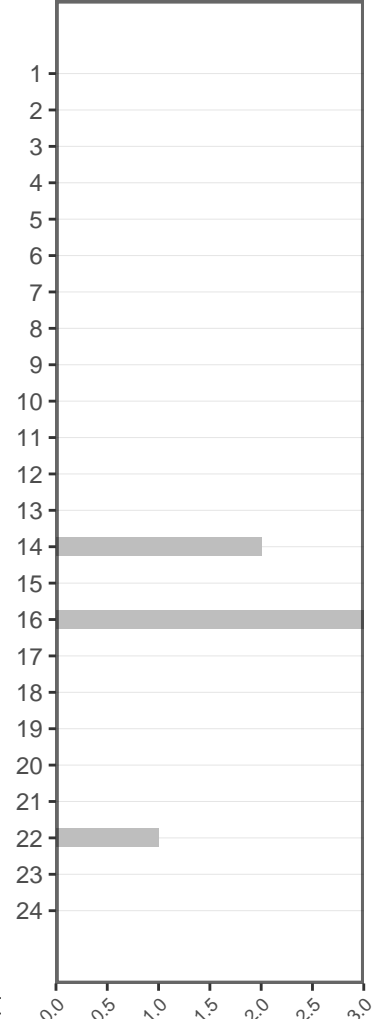
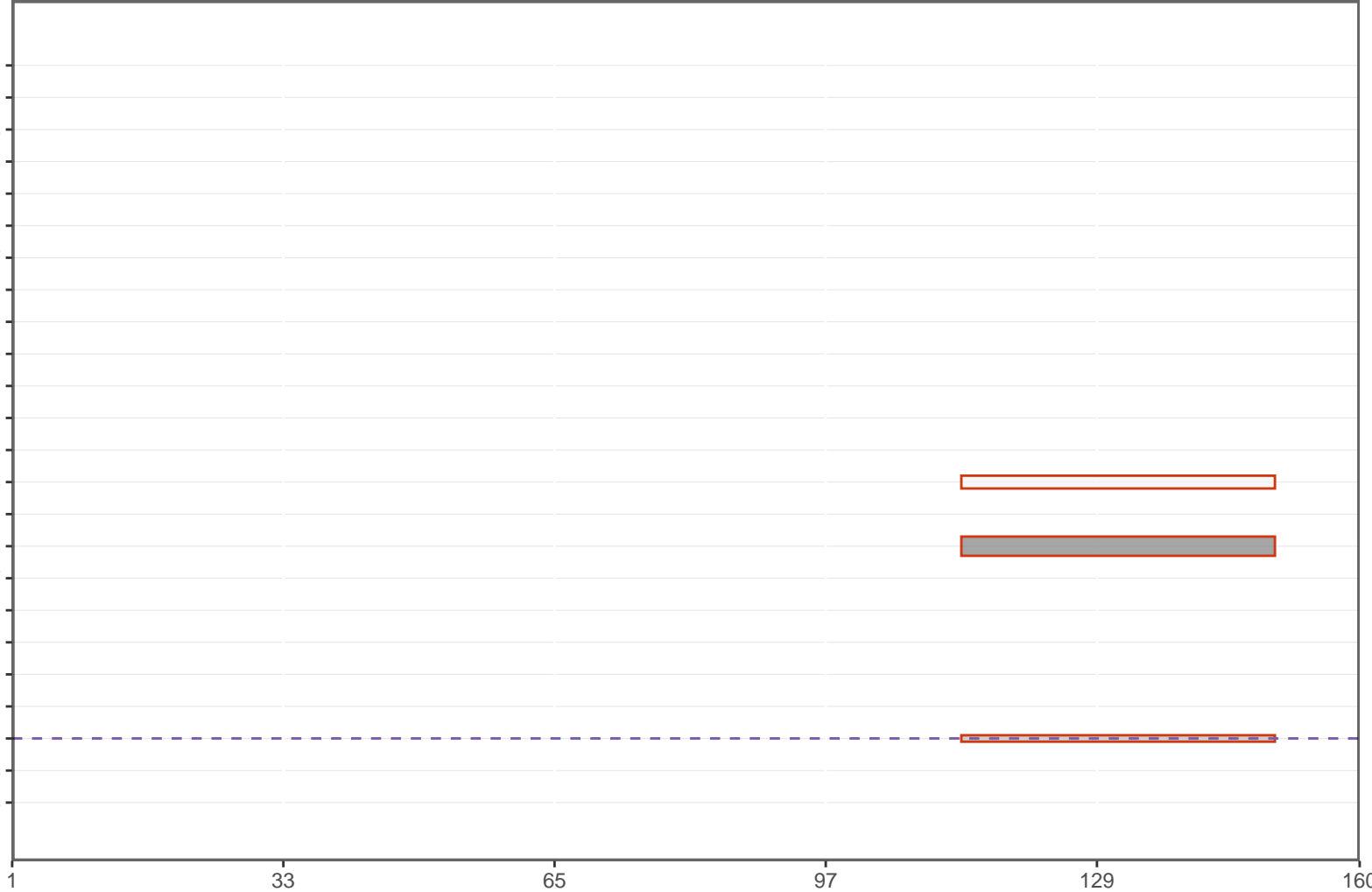
MW indication



Molecular weight



Gel Slice



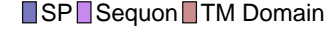
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IPVAAAEPIKTTETGEPSTVGFVEEVAAPVDEVELEAAPVEEPETEKAVPVAEESAPVTEAAAEETINAPAEEPVAAAEVEEKAVPVEKAEI

NbL05g22200.1 fumarylacetoacetase [MW = 50.04 kDa]

No. of times detected



log(intensity)



Values from



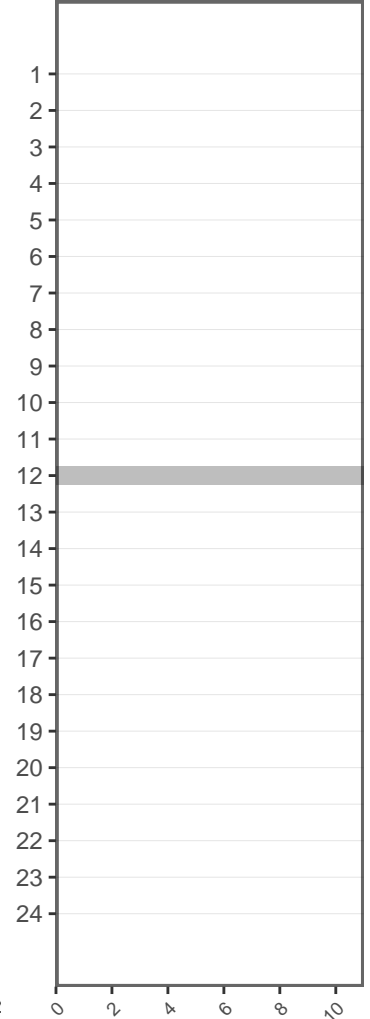
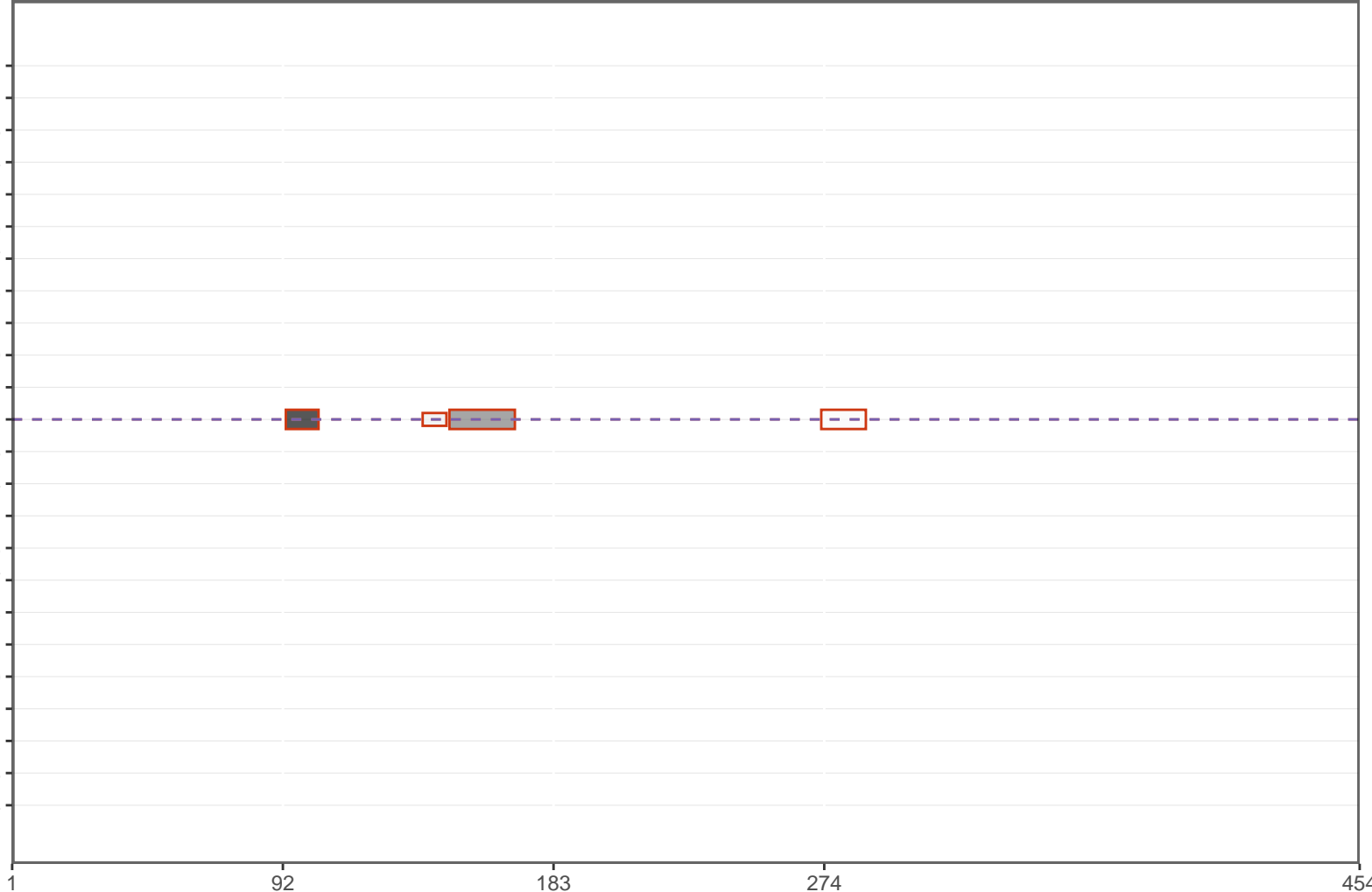
MW indication



Molecular weight



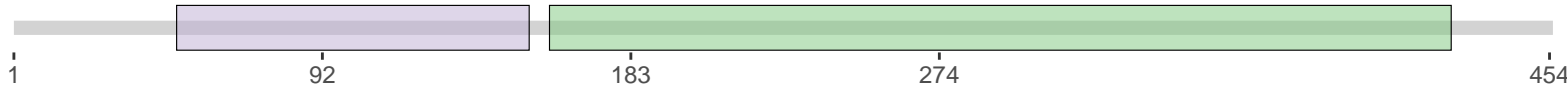
Gel Slice



Peptide counts over 4 repeats

1 92 183 274 454

Protein length



Pfam domains

Pfam Description



Protein sequence:

MPTGNSAPYFGSRKLDLELEMAAVVPGNELGTTVDVNEAADHIFGLVLMNDWSARDIQAWVEYMLGFFLGGKSGFTTSPWVTLDALEFPAGEAPKQNPSPLETLMKETSRYNDISLEVLKPKSGRADSCVTRSNFNHLVWITQGLAHTINGGNLRPGDLFGTGTGSGPEPEYGGLELWNGKPLSLGGTTRTRFLEDGDEVTFYGGYVWFWLWLLFFPLPHEVLVQWL*

NbL05g22170.1 malate_dehydrogenase_[NADP]_chloroplastic [MW = 48.4 kDa]

No. of times detected



log(intensity)



Values from



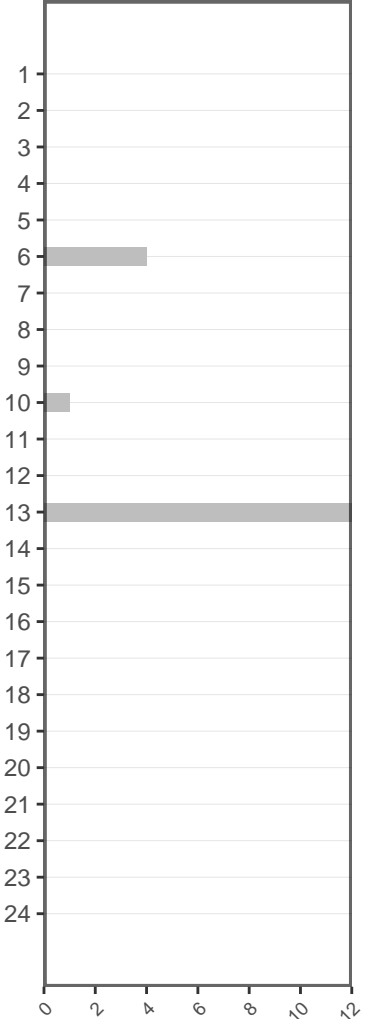
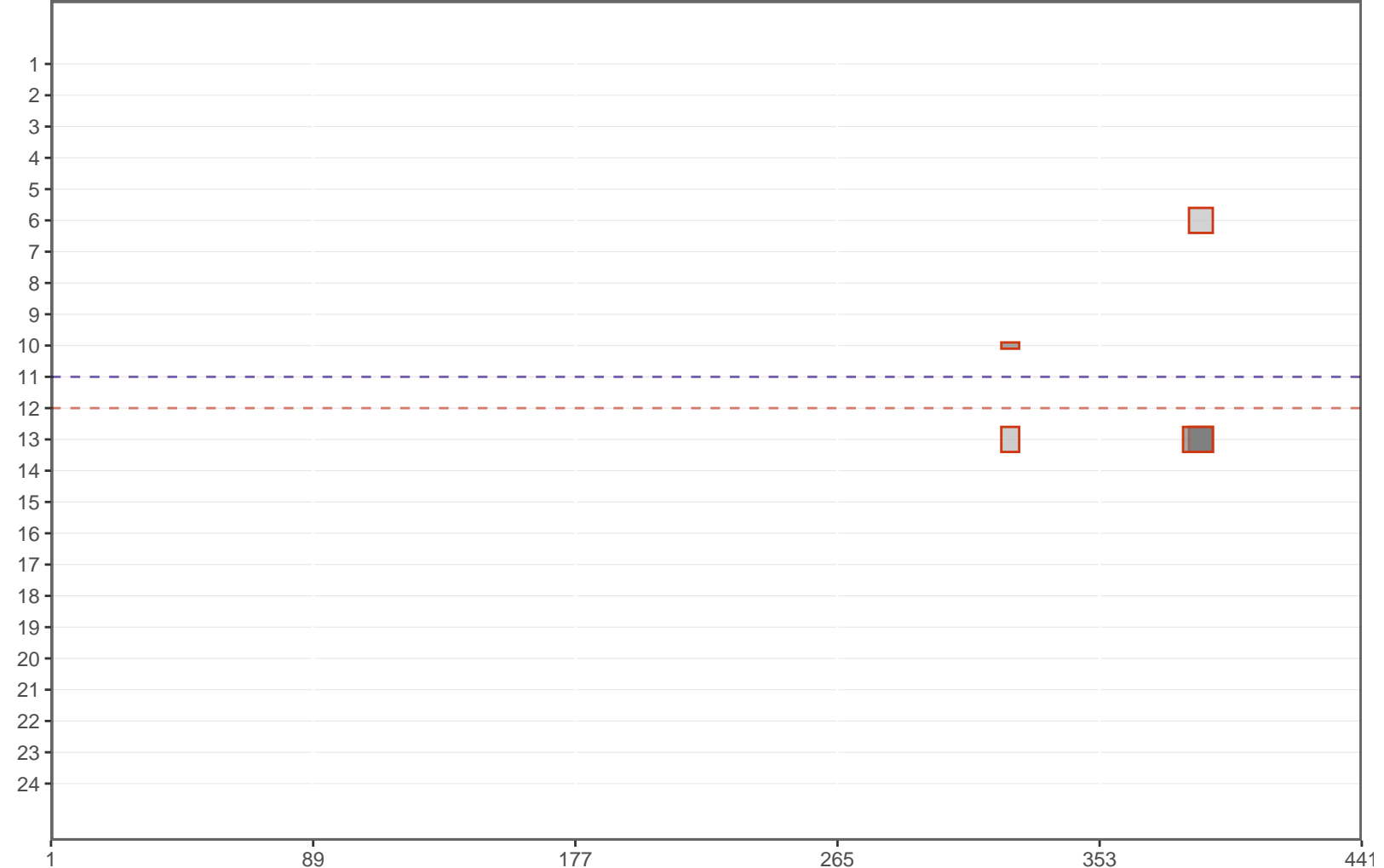
MW indication



Molecular weight

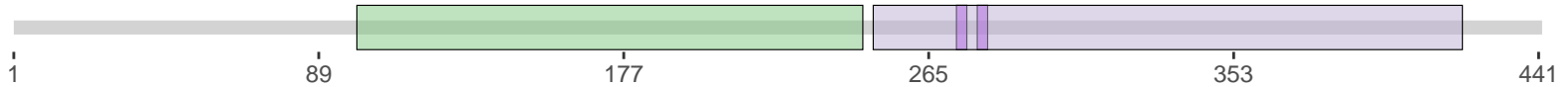


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF00056 lactate/malate dehydrogenase, NAD binding domain
- PF02866 lactate/malate dehydrogenase, alpha/beta C-terminal domain

Protein sequence:

ALNAVASRNKYIVYGNPCNTNALGLKNAIPNAKFNHAIKTRLDENRAKGLKAGVYDKVSNVTVWGNHSTGTQVDFLNAKINGLPVKEVYKDKVLEEFTEKVKRKGALIKQKWRISAAASTAVSIVDAIRSLVTPPTPEGDWFFSTGVVTSGNPVGAEIDIVFMPKRSKGGDFELVKEVDFDYLWSRKKSEDELLAEKRWALHTGEGIAWGDLPDGLPGEI

NbL05g22140.1 pullulanase_1_chloroplastic-like [MW = 105.99 kDa]

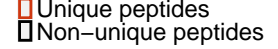
No. of times detected



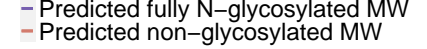
log(intensity)



Values from



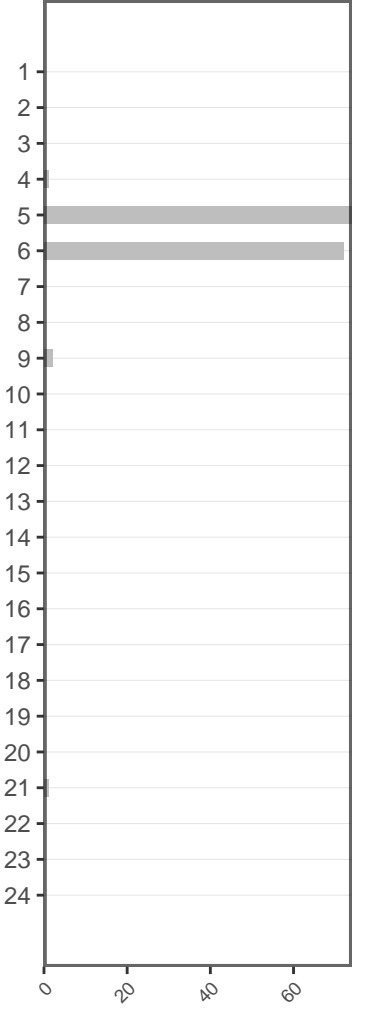
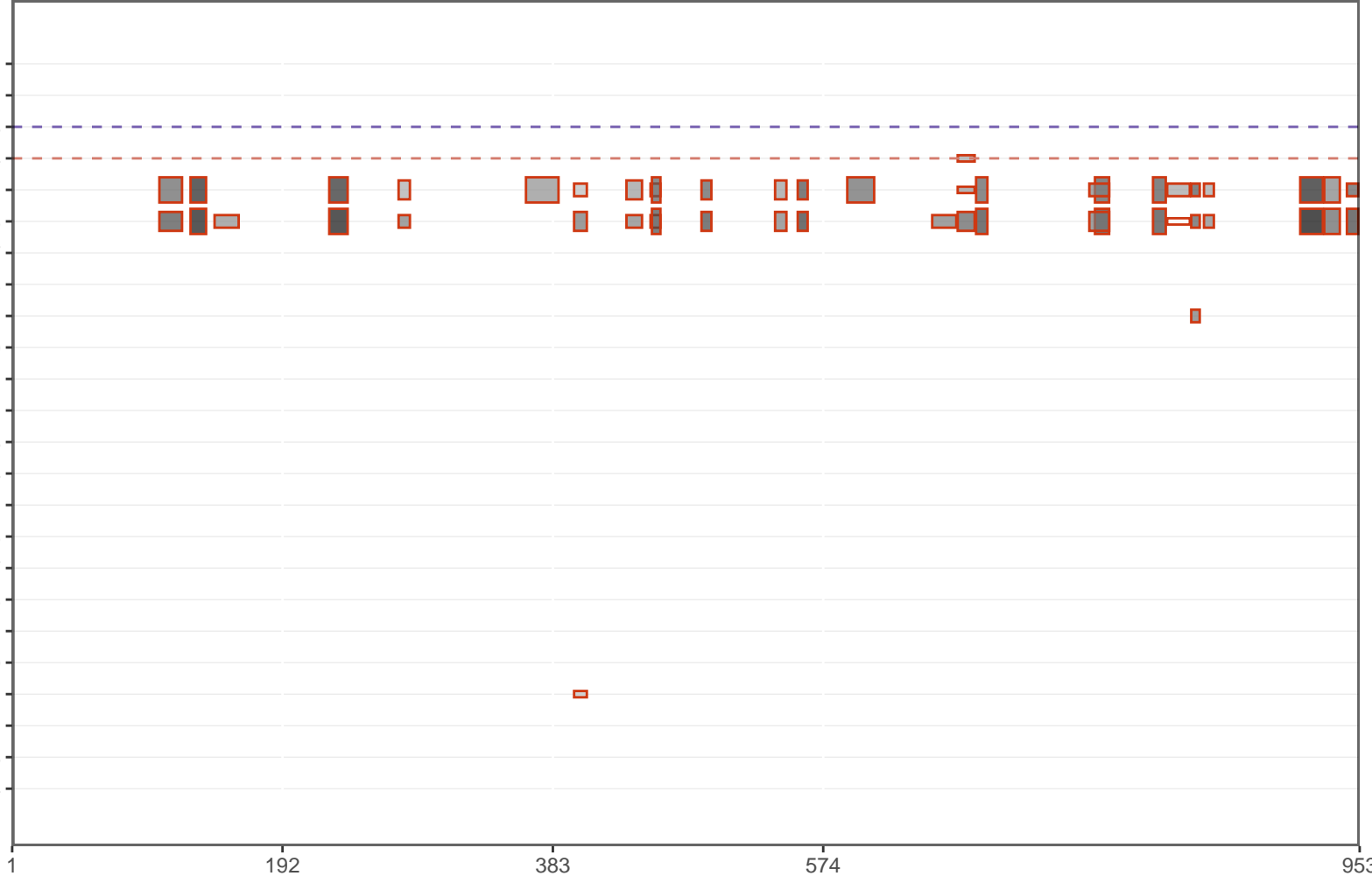
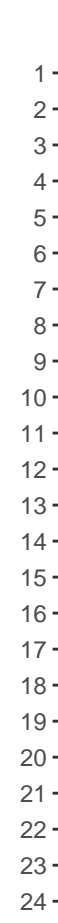
MW indication



Molecular weight

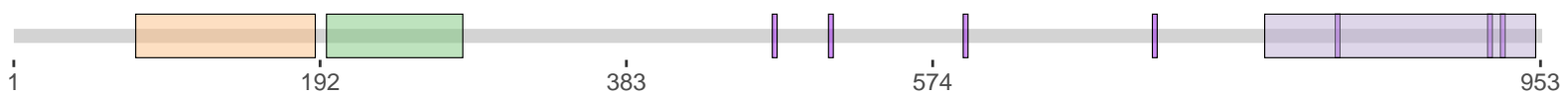


Gel Slice



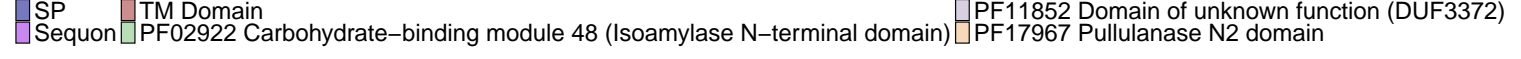
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

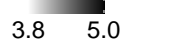
VLLDVYNIINASGHFDFFSALDKIVPGYLLRRNADGGIEHSTGVNNTSSEHFVERLILDDLKCWVAHYKIDGRFDLPMGHMKRTMVAKSLINSLSKDKNGVDCGRSHYGEWDFGEVANNRGRINSGGFNLFGGGGISFNDRIKDALGGSPFGHLPHGQGITGLYLEPNGHDLGDKANVERMLAVSMDHQGVGMANKDKFVLTNGDGEVKGSEVLLHDKRKPVGYSASPETVNVVSAHDNETLFDHISLKTPKDISEVEERGRMHLATSVHLSOGPPFFHSGDE

NbL05g22050.1 serine_carboxypeptidase-like [MW - SP = 53.21 kDa]

No. of times detected



log(intensity)



Values from

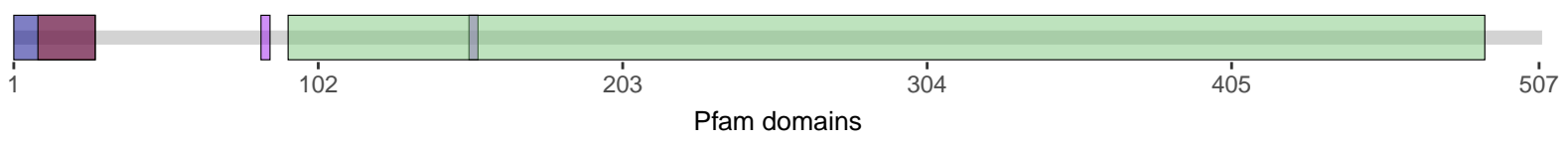
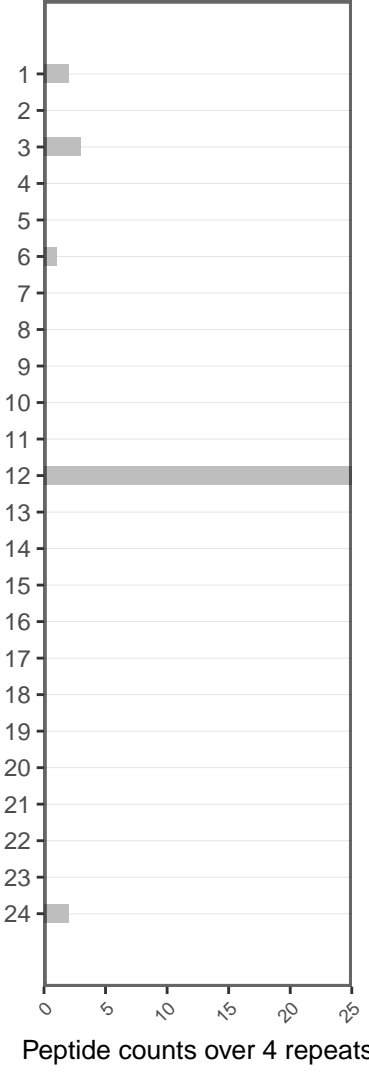
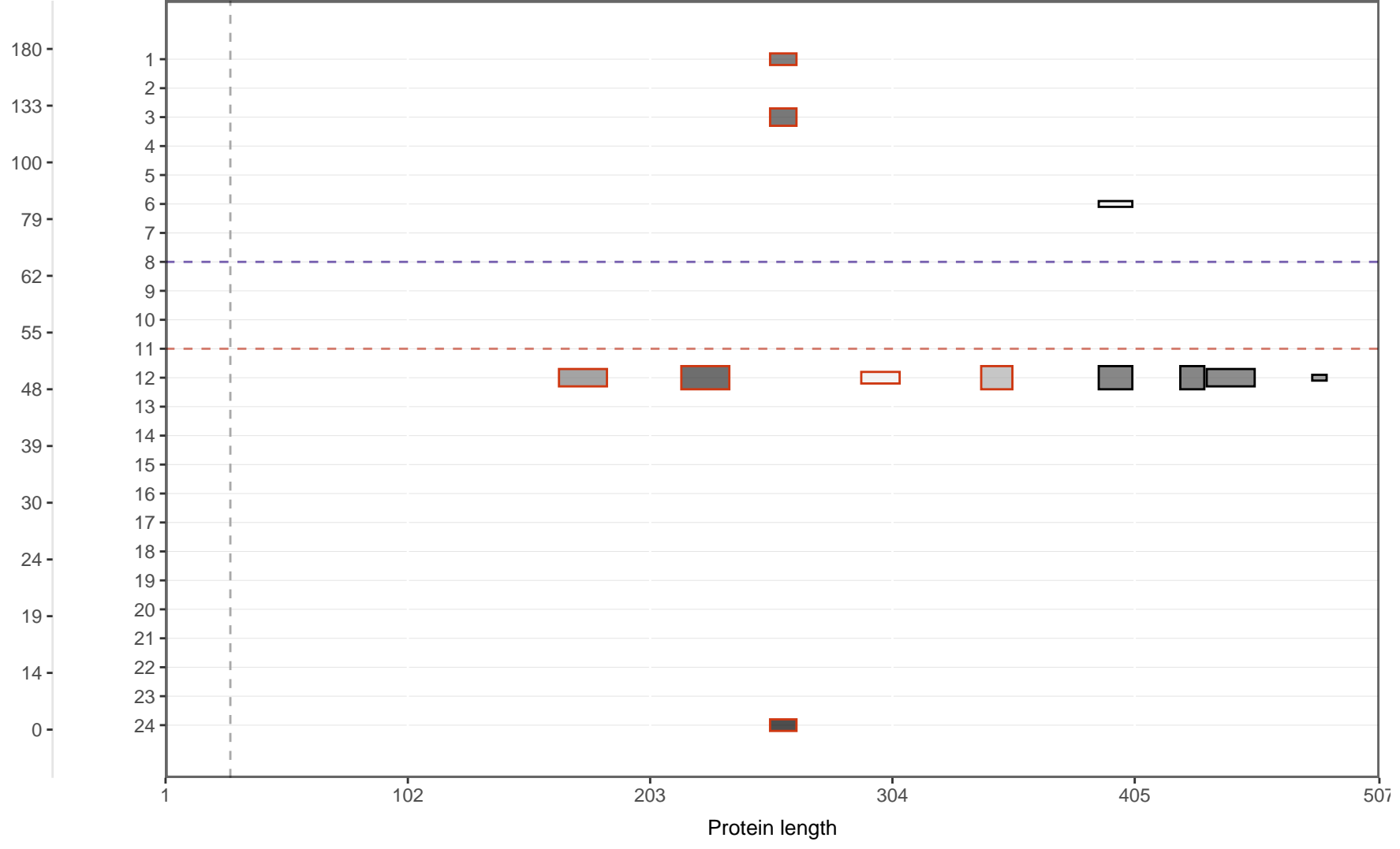


MW indication



Molecular weight

Gel Slice



Pfam Description



Protein sequence:

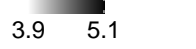
IKGKEGHINLKGFMANGLTDPKIGVAYTEVALDMLGISKSDHNRINKLPVCEVANLIGCTDGRISGLAAFYVCSNIFSAVRARAGADINHYDIRKKGVGALGYDFSNMELKLNHSHVKGLALGVEDIEFVSGSTTVYQAMLDWMRNLKAGIPTLLEDGKLLVYAGEYDLKHWLGNRRVVGQMEVSGKKEFVASPDVDFEYVDSSEAGLLKSHGSLPLFKVHDAGHMVPMDDQPKALEMLKRWGTLGGQTTGTDKLVASL

NbL05g21990.1 kinesin-like_protein_KIN-UA [MW = 121.11 kDa]

No. of times detected



log(intensity)



Values from

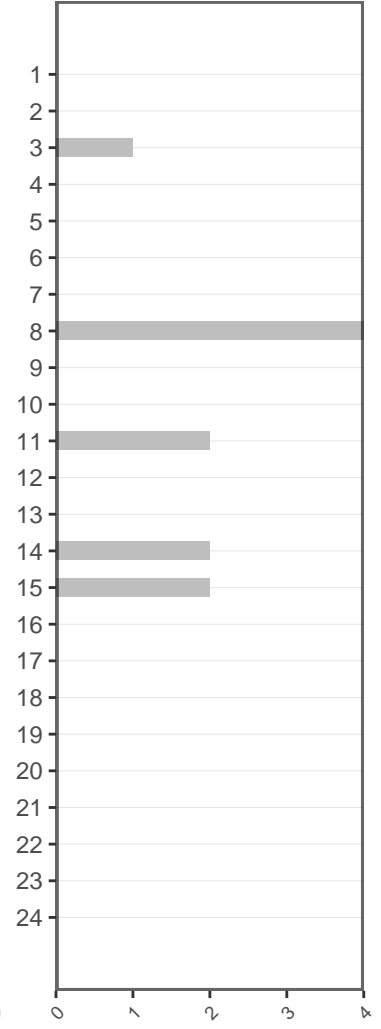
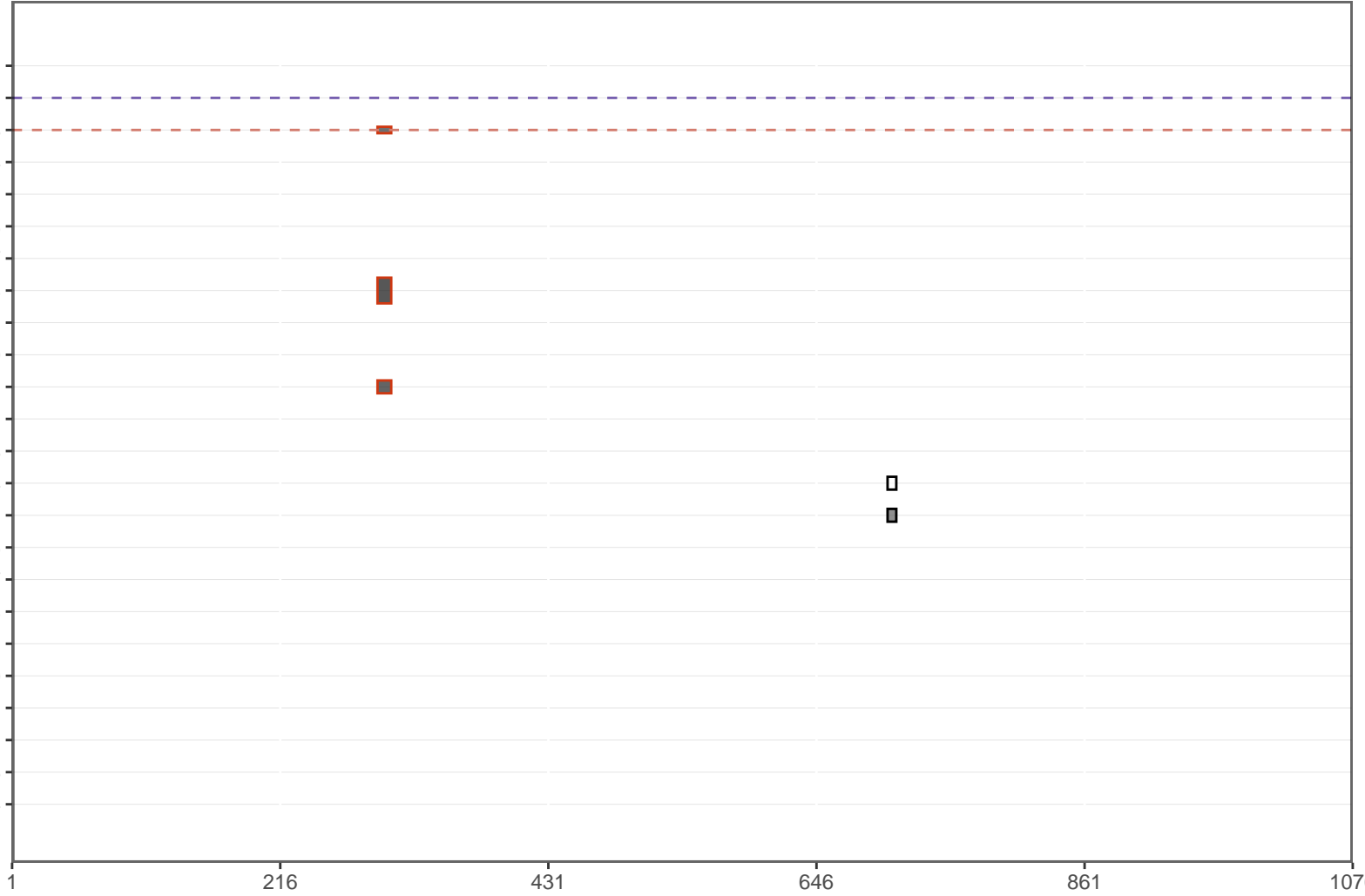


MW indication



Molecular weight

Gel Slice



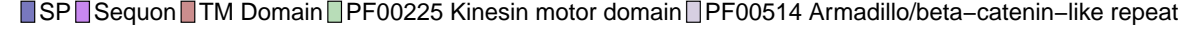
Protein length

Peptide counts over 4 repeats



Pfam domains

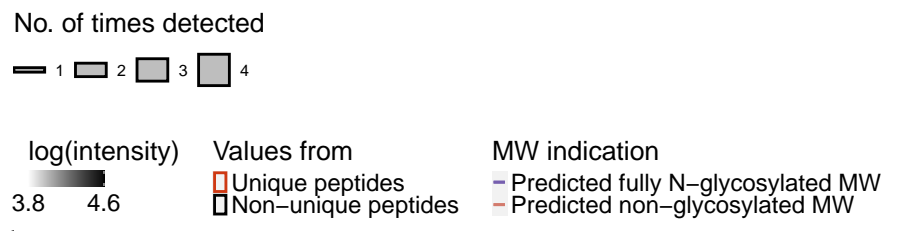
Pfam Description



Protein sequence:

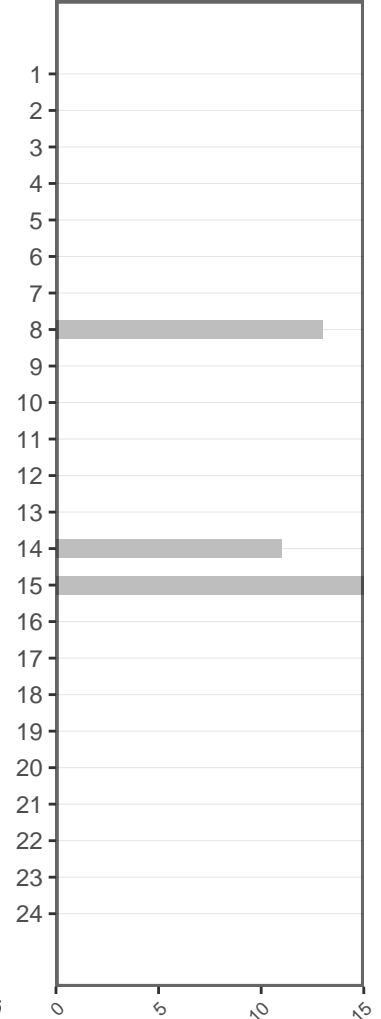
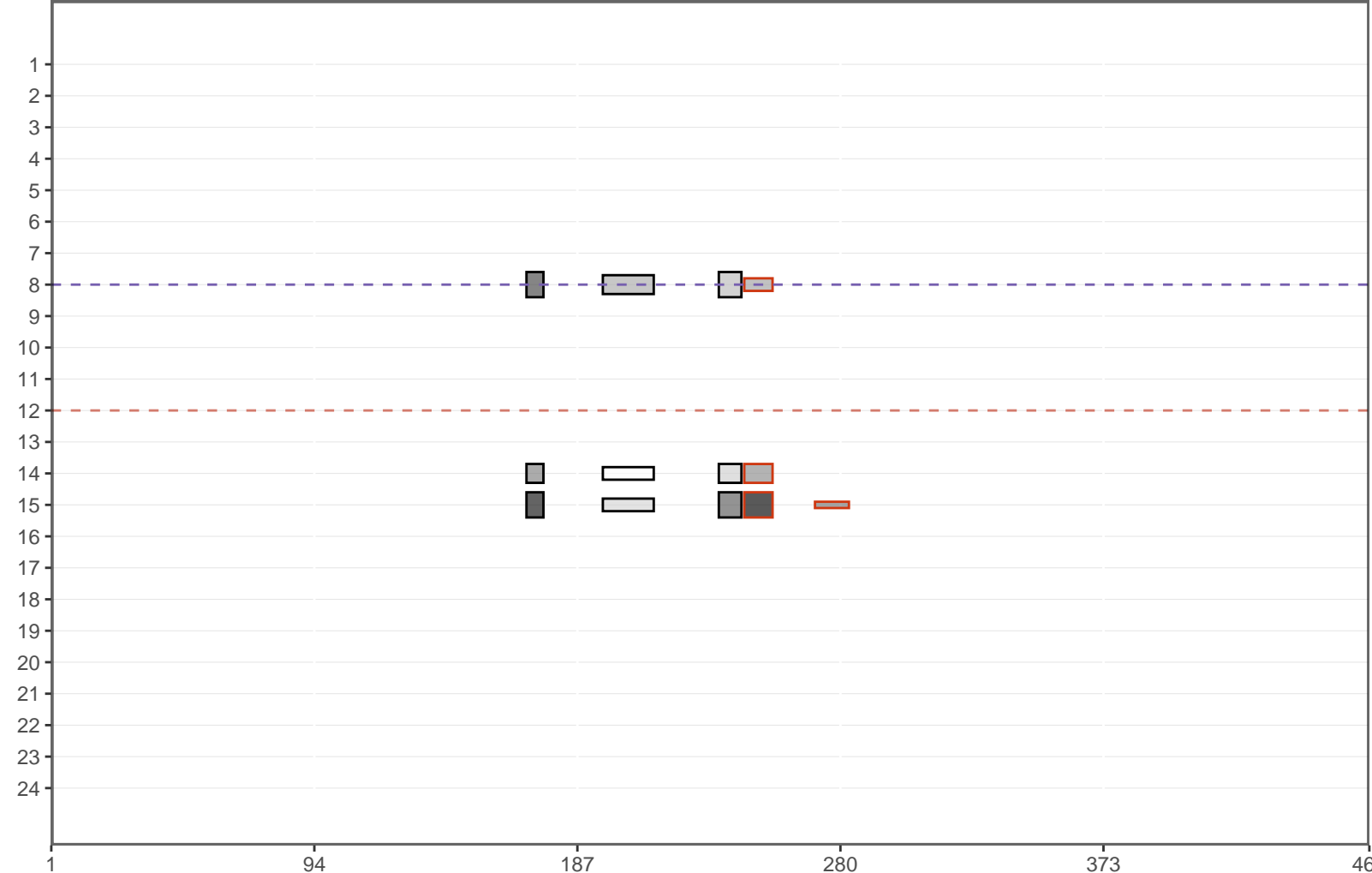
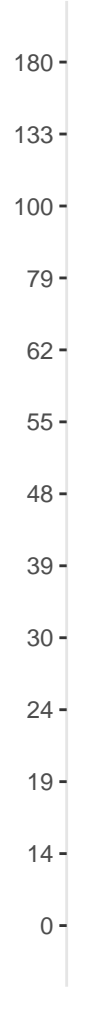
IVKLESDFNNSKLLKEMGGLKVELENVLDKDFNRKIKHNLLQDEVAHLEKRLNDSKGGQLENSYKILAEINQSDYKIKIADLMKGLIEDERAGSENGDQGLLELMKKEGLTGVVEELMGGHSHKQKTSFYKQKELADTTLVYEKIKLQLEQLLNDESHVENVKEQLHAEIQGFTDHTSVKQKREKIDALRSLRLEDMHGLVEPTVEELQTLKTEYGVLYSKKKAHDELHEVRRGTLLEEKQKKAENELFNMKKLVPESEDDGFEDKDKSYMKGYTTGGGFNMRSTESRERFAHC

NbL05g21970.1 hydroxymethylglutaryl-CoA_lyase_mitochondrial-like [MW = 50.25 kDa]



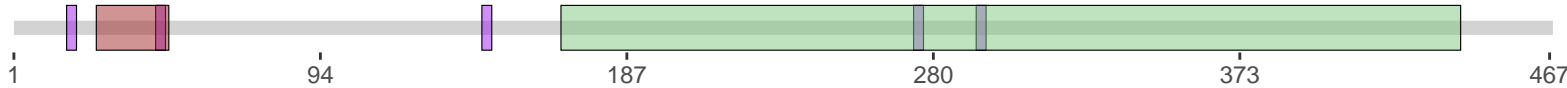
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00682 HMGL-like

Protein sequence:

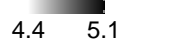
ADAKDVEAVRSLTGVRLPALTNLKGFETVAAGAKEVFAAASEFRRSNNGSIEDSLARYRDLAAAKNNSPRIGYSGVGGPVEGAVSPKVVVAKELDMGCFEISLGGTGTGTPVPMLEAVTQVVFVERLAWHFHDTYGGALSNIIVSLGMGISTVDSVSGLGGCPVAKGASGNVATEDVYMLNGLGVKTNVDMRKLISAGDFICKLGRP66SKAAVALRRKSTASKL

NbL05g21760.1 thioredoxin-like_3-2_chloroplastic [MW = 21.96 kDa]

No. of times detected



log(intensity)



Values from



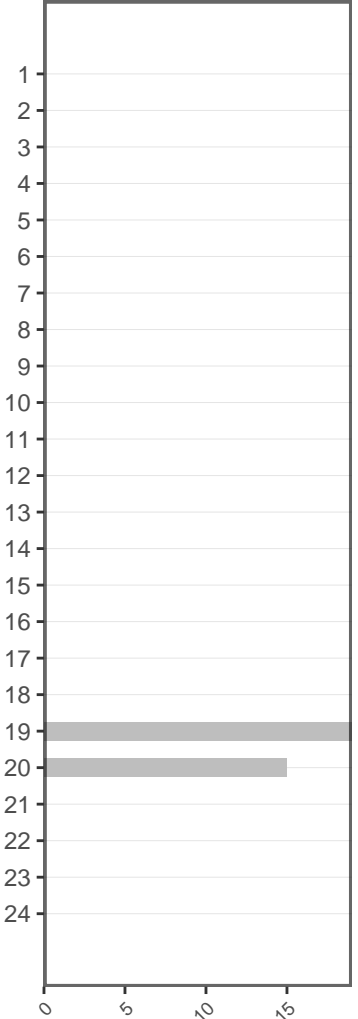
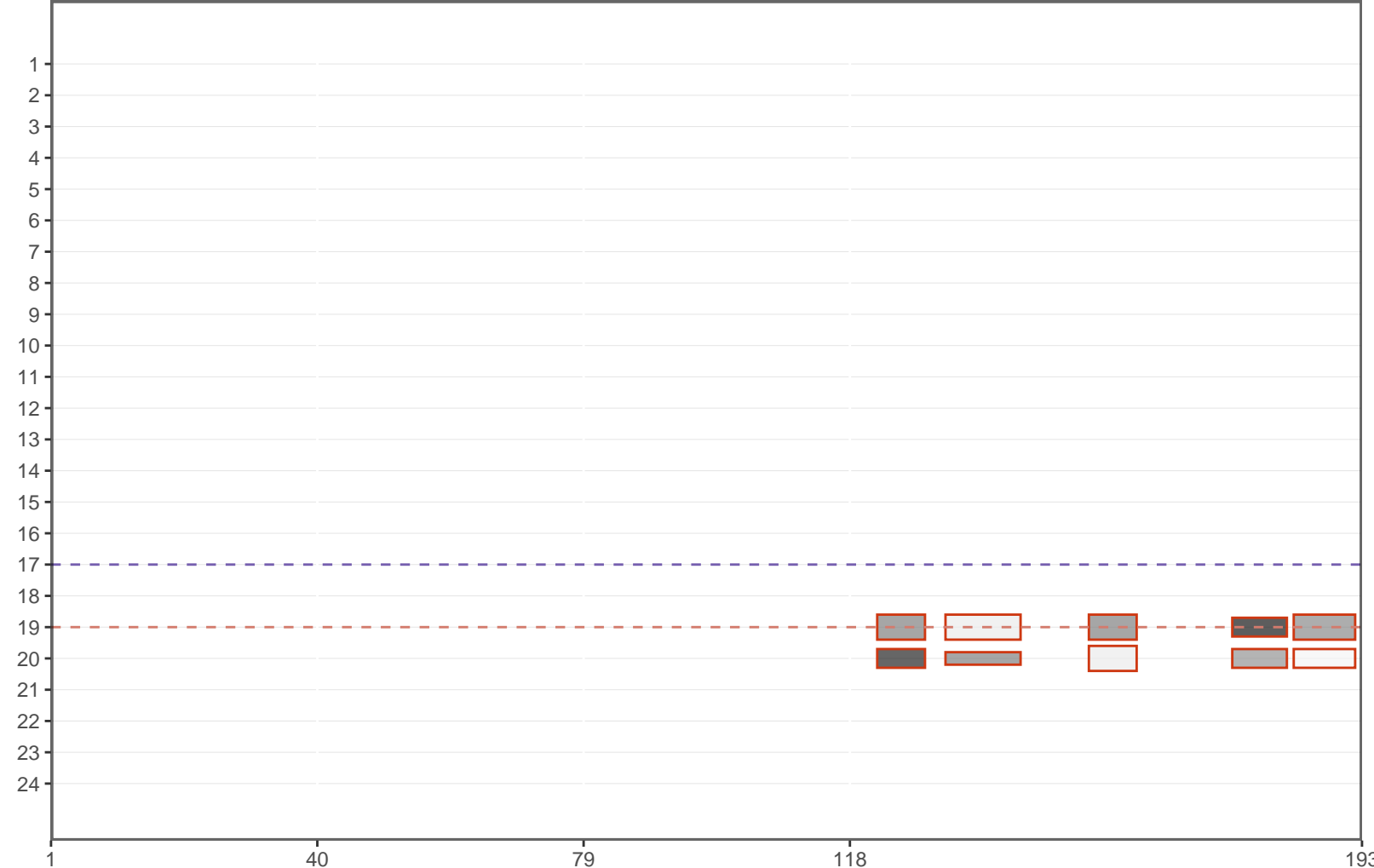
MW indication



Molecular weight

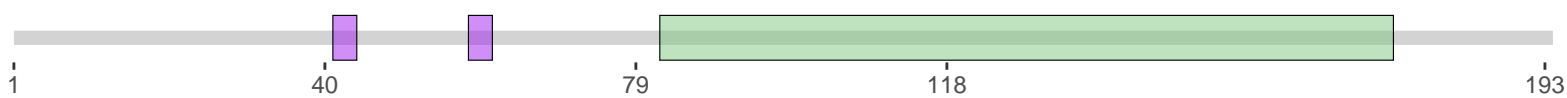


Gel Slice



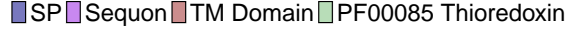
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IQFDRVISEAQQIDSEVVLWMTWCRKGNLKRKLEKLAADYFRFRFYGVNANNVFKLIVRAGITKMPITGLWRDGNKGAEVGGHKAVLVTEVRDMEIENENNL

NbL05g21730.1 actin-related_protein_7-like [MW = 39.68 kDa]

No. of times detected



log(intensity)



Values from



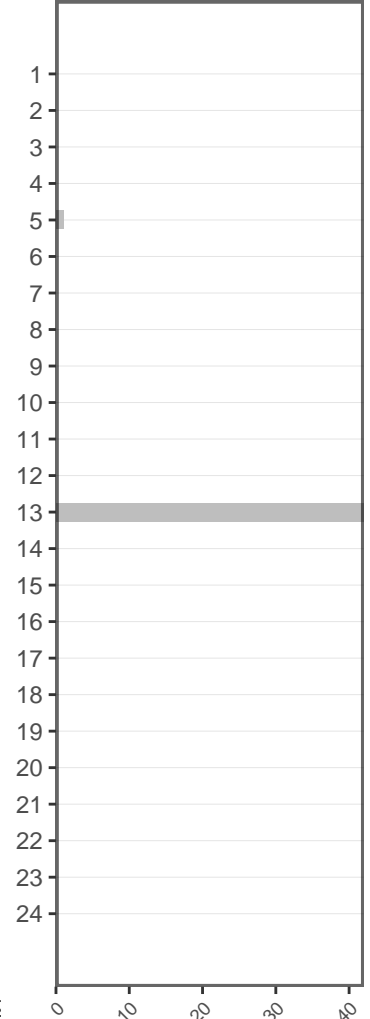
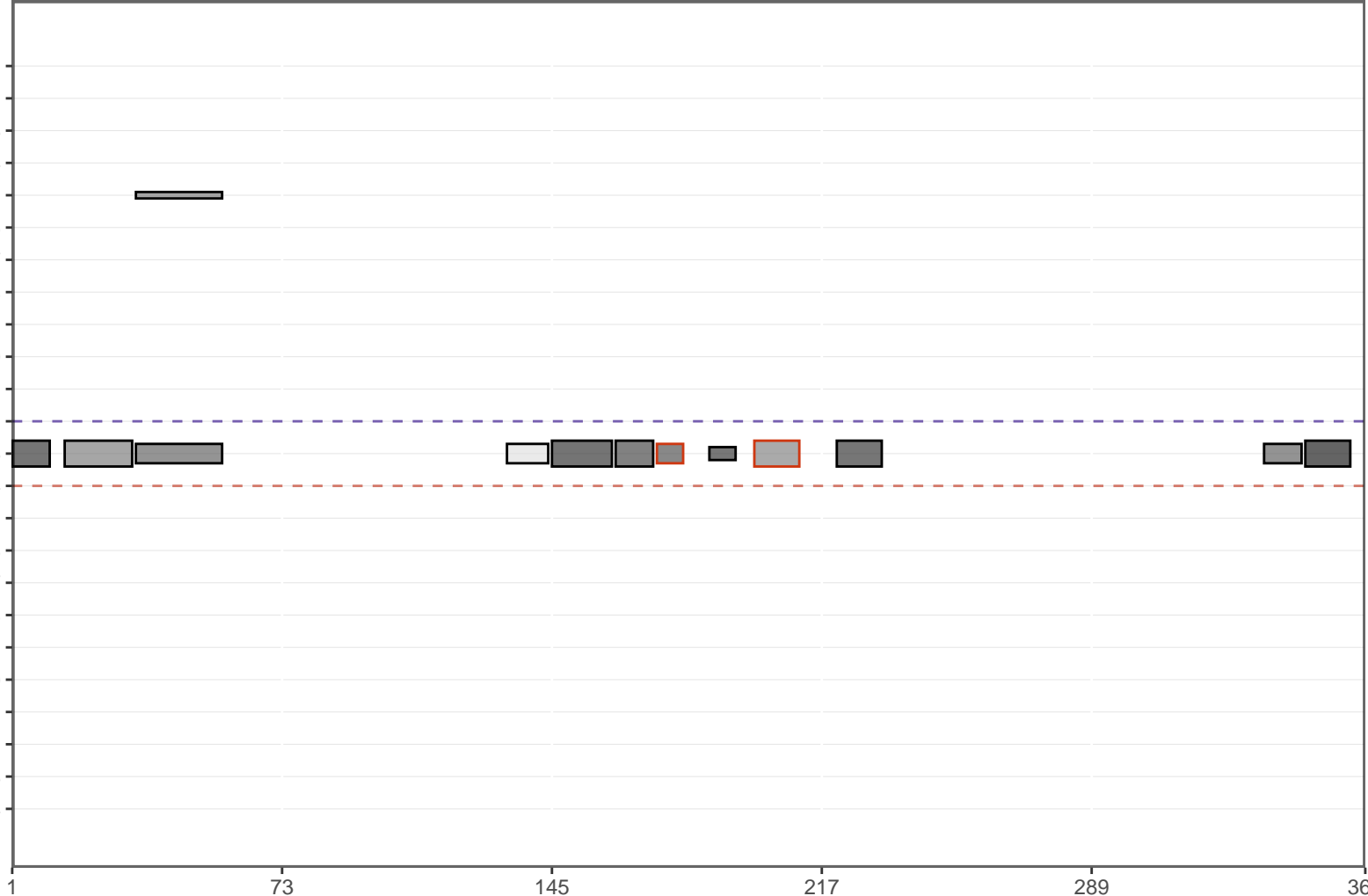
MW indication



Molecular weight



Gel Slice

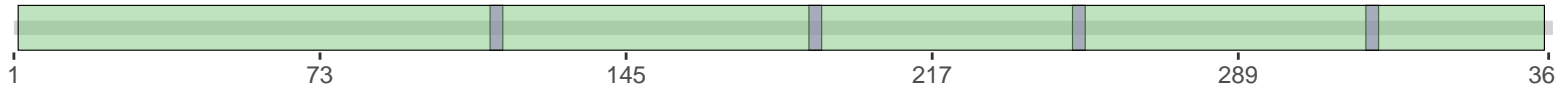


Peptide counts over 4 repeats

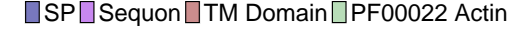
Protein length



Pfam domains



Pfam Description



Protein sequence:

.DLTKLADLTKSNPTVALNSDVEKLERVACGAAADDAIWEKLGSGLEENHTLPDGGVITGKERVTVGEALFQPSILGNDTHGVEQLVHSISVSSENHRQLLENTVLGGGTATITGFEDRFQREAMLGSSAVRPLVYKPEYMPENLTSVSAWIGGAILKVVFPQNGHTKADYDESGPVAHRKGF

NbL05g21620.1 phosphoglycolate_phosphatase_1B_chloroplastic-like [MW = 40.92 kDa]

No. of times detected



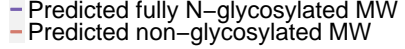
log(intensity)



Values from



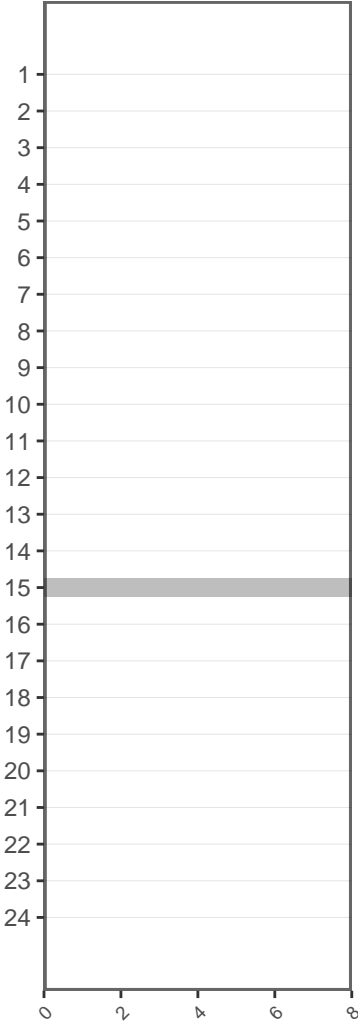
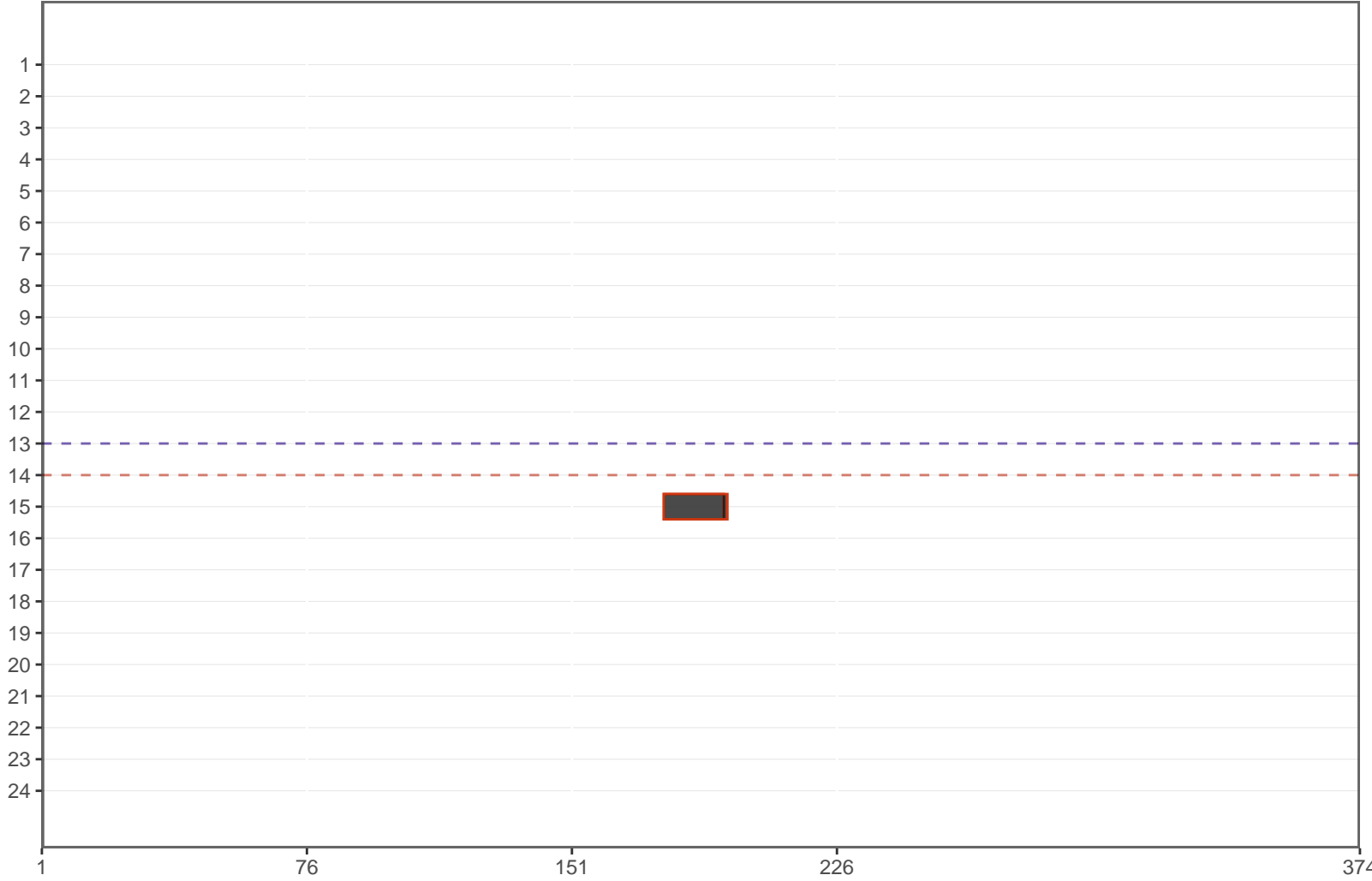
MW indication



Molecular weight



Gel Slice

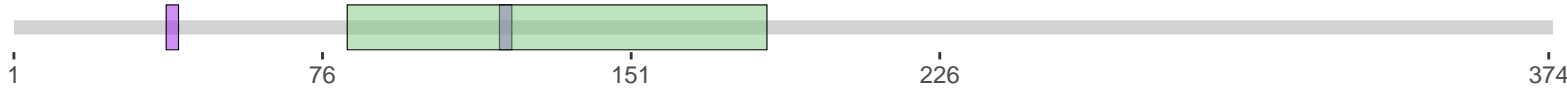


Protein length

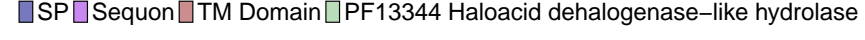


Peptide counts over 4 repeats

Pfam domains



Pfam Description

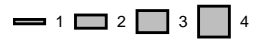


Protein sequence:

KELELAGQHGPPEDGDKKELKPGYVMEQDKDVGAVVGFDRYFNHKKQYATLGIENPCDLFATNRDAWTHLTDQDEWAGGGGMVGAIGLSTKREPLVQKPKSTFMMQVLANEYGTLSITISVILGLLFLLSGGSSSAPFFLSLGGSSSFADSLVTTGFQVGNMGAQSFHQGFCKLVNVMGNQNMGMVIMFDLI

NbL05g21550.1 protein_transport_protein_Sec24-like_At4g32640 [MW = 117.58 kDa]

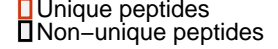
No. of times detected



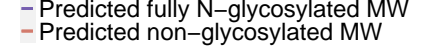
log(intensity)



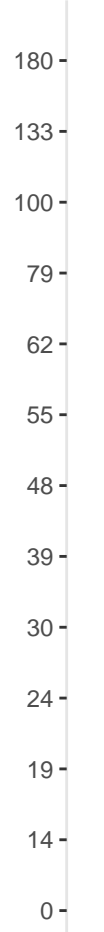
Values from



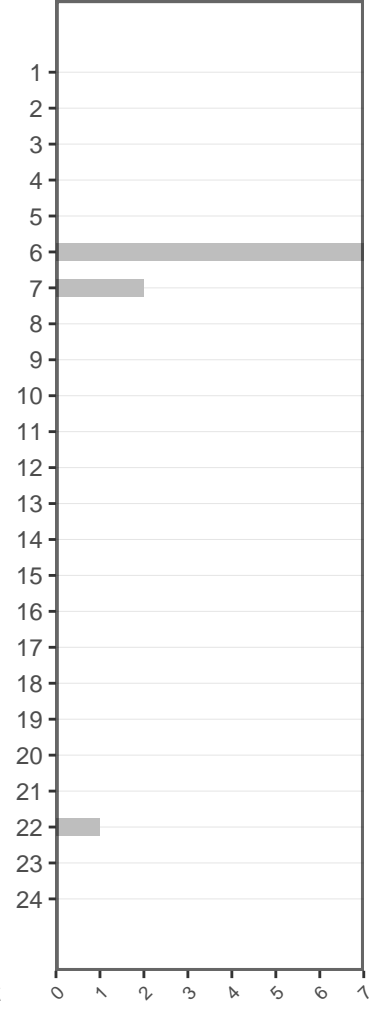
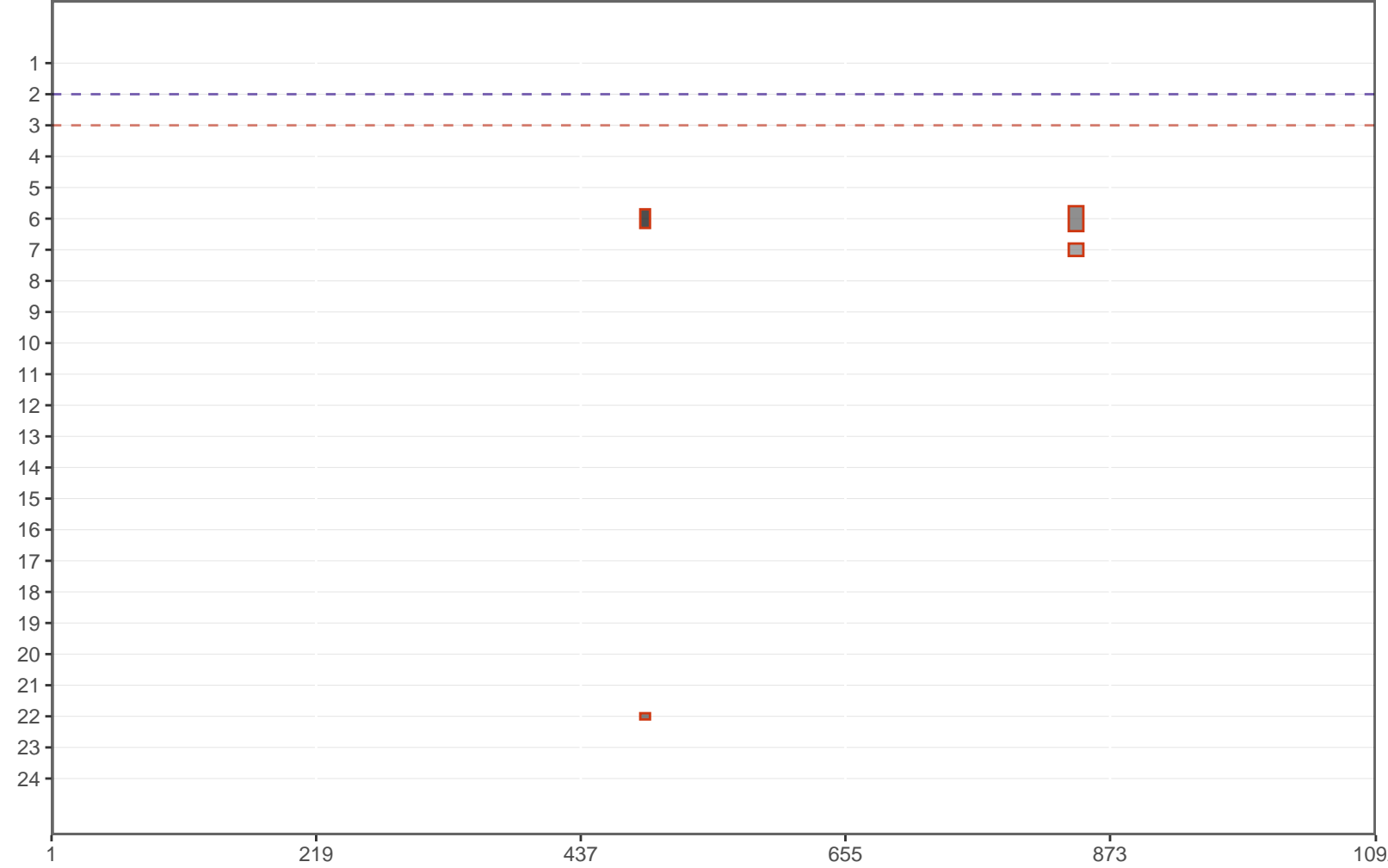
MW indication



Molecular weight



Gel Slice

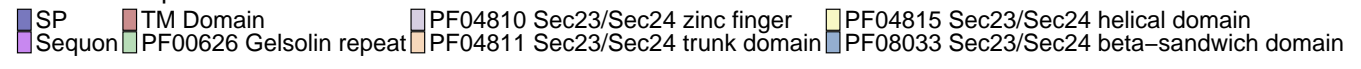


Protein length



Pfam domains

Pfam Description



Protein sequence:

GATAACSAISQVITDLPEGRRLVGVWTFDSTHFYLNKRALGGRLMLVDPVQGVYTPLGTDVYVQLSEGRQMLELLEESPTMFGNNRTADSAFGAAKAAFLAMKSTGGKLLVFGVLPSTGGALSAREAEGRNLGAAEKAHKLGGADKTKTMAEFAEVGVGVYVFLTTGSVYDASISVPIKTTGGGVVYFFPSALADSAKLVNDRWNRTRPGGFVAMRVKSGGGVGVGVSEVGNVYKRIPTVLDLPAIDGDKTIMVTLKHDDKLDGSGE6FSQAVLYTTDGG

NbL05g21480.1 NADH_dehydrogenase_[ubiquinone]_iron-sulfur_protein_2-like [MW = 25.91 kDa]

No. of times detected



log(intensity)



Values from



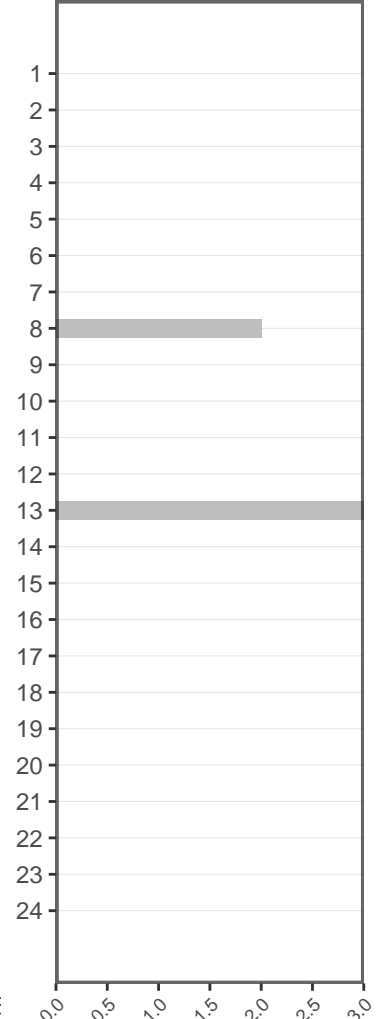
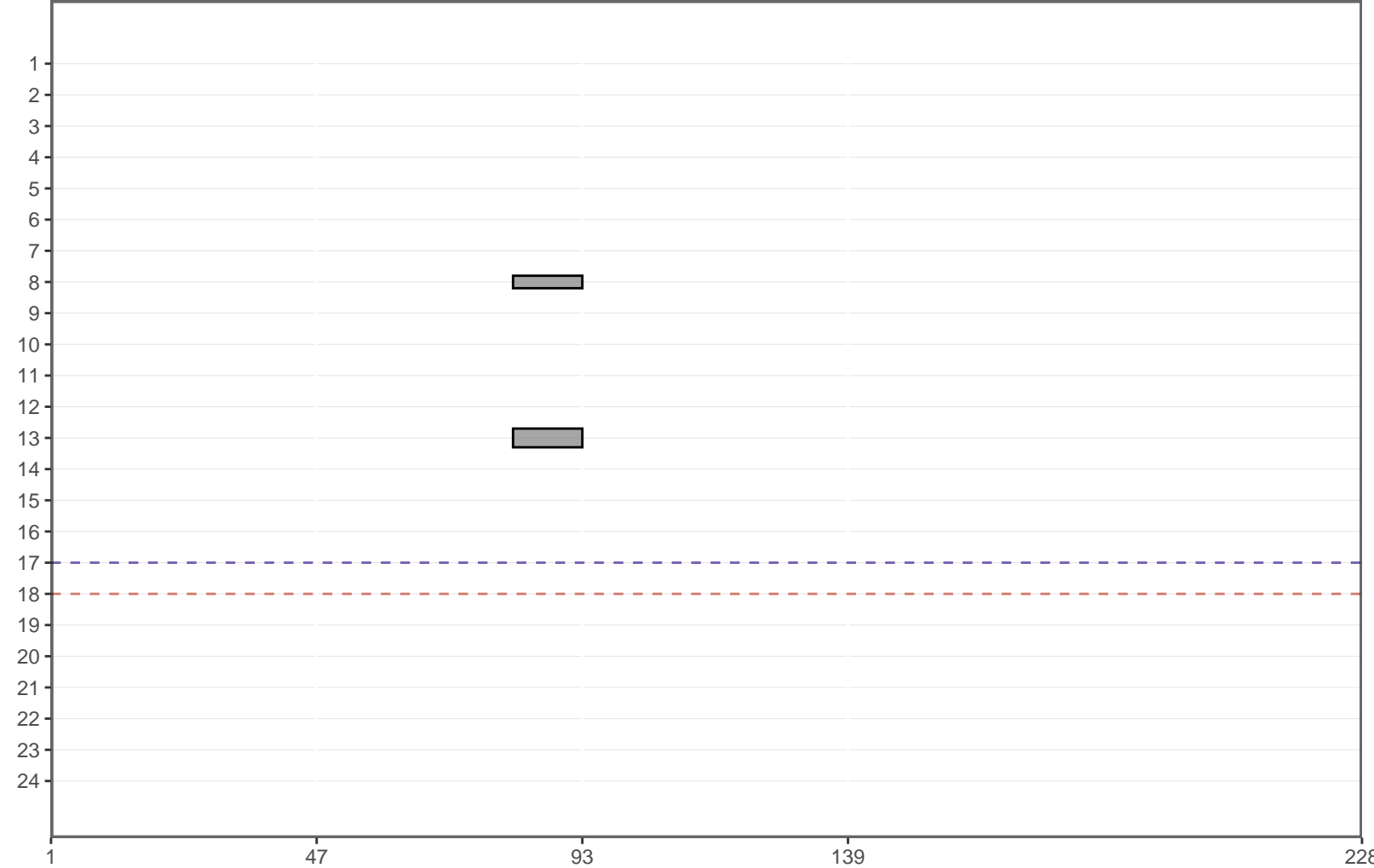
MW indication



Molecular weight

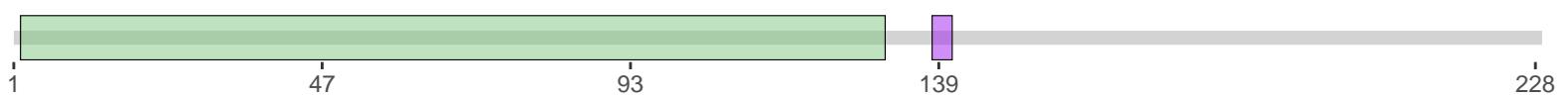


Gel Slice



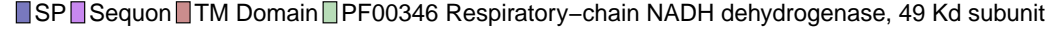
Protein length

Peptide counts over 4 repeats



Pfam domains

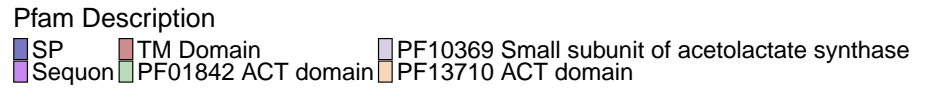
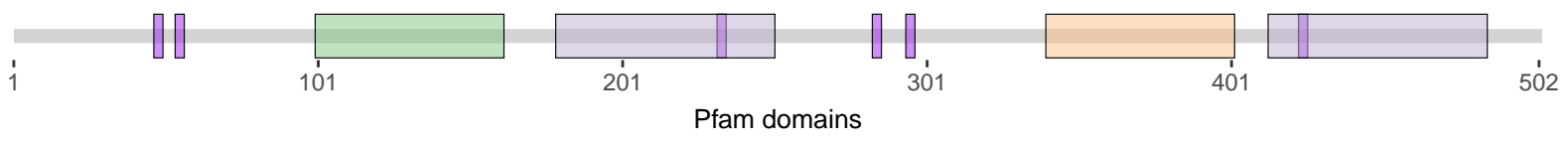
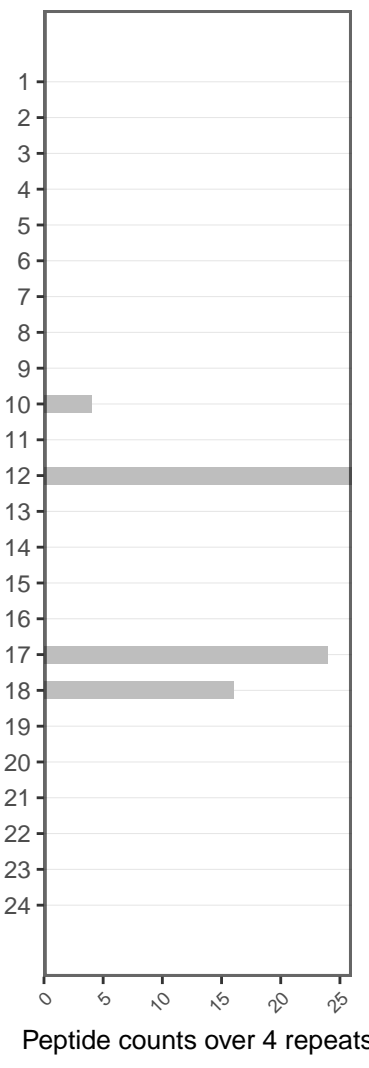
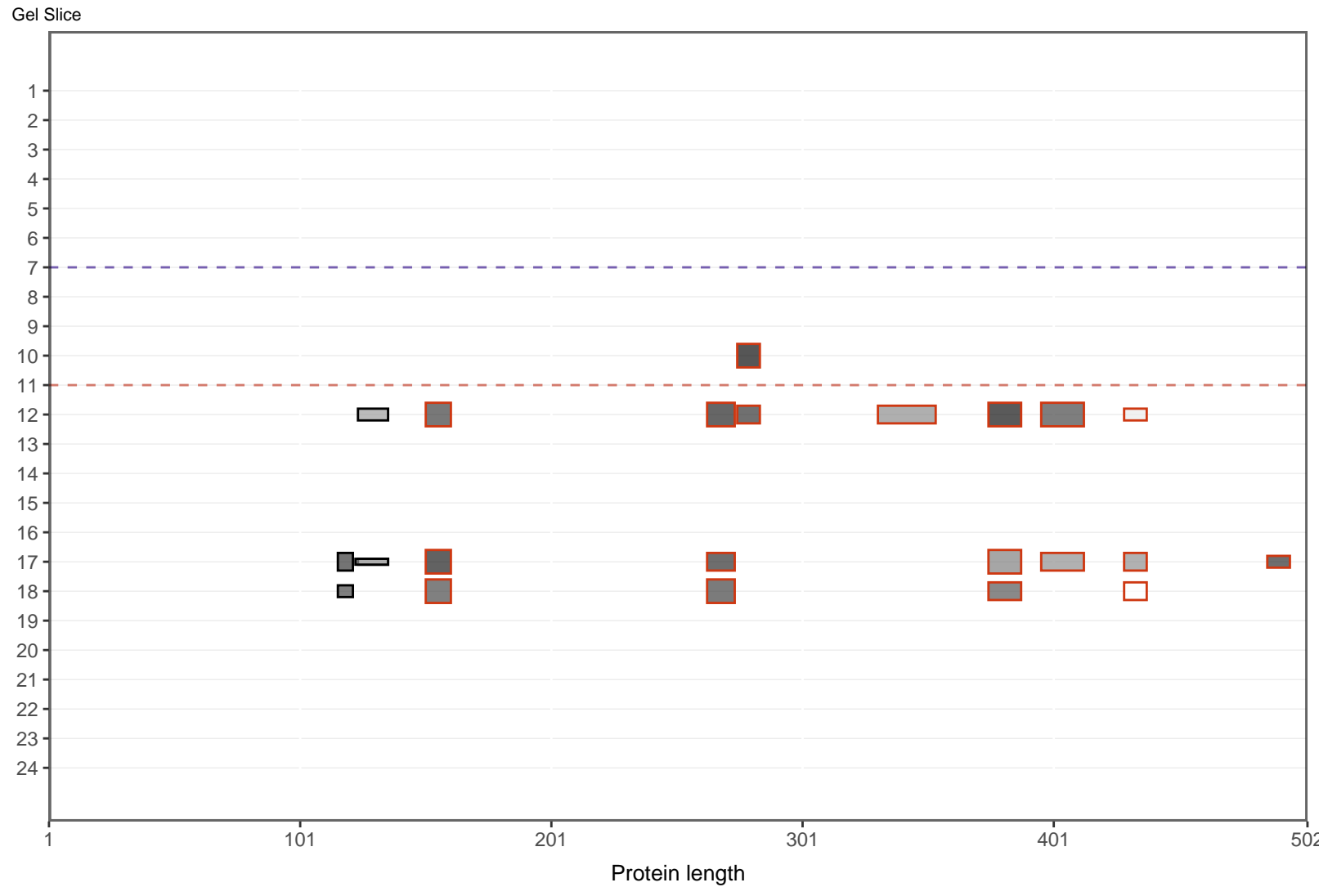
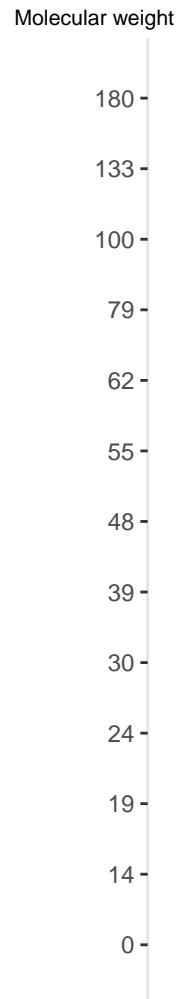
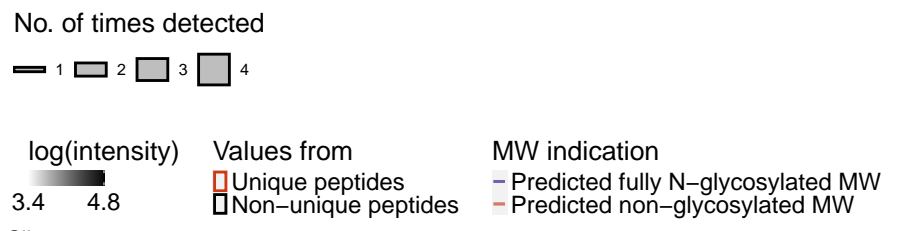
Pfam Description



Protein sequence:

/MLKGSRCYDLRKAAPYDVHNGLDLDPVAMBSSTINETHIGVIRWRRIELPFLTETQVLRILGLTLVYGDWHNRVVPYRTAGGRAAFVVAAGDNLVLRPRSERAYRWTVAVPLSELEHNNLH

NbL05g21230.1 acetolactate_synthase_small_subunit_1_chloroplastic [MW = 54.43 kDa]



Protein sequence:

IKELARTGKALRRENKMGEDAPFWRFSAASVPLEEKIPSVILNKNKSRIPNEASNDGRGVYFVSSDDSHVQVLDHAWGVLYDGLSGLRGHTSMILVNNAPGVNLITGVISRRGVYVQSLAVGPAESKGLSRITFTVPGTDETIKGLVKGFKLVNHDVEVDGTHLPEAERELMKVVAANATARRDLDAISIFRAKPVQVSDHTVLTLETGDFNKLALQRLLEFPYGEVARTGRVALRESGVDSTSLRGVPLP

NbL05g21060.1 membrane-associated_protein_VIPP1_chloroplastic [MW = 35.56 kDa]

No. of times detected



log(intensity)



Values from



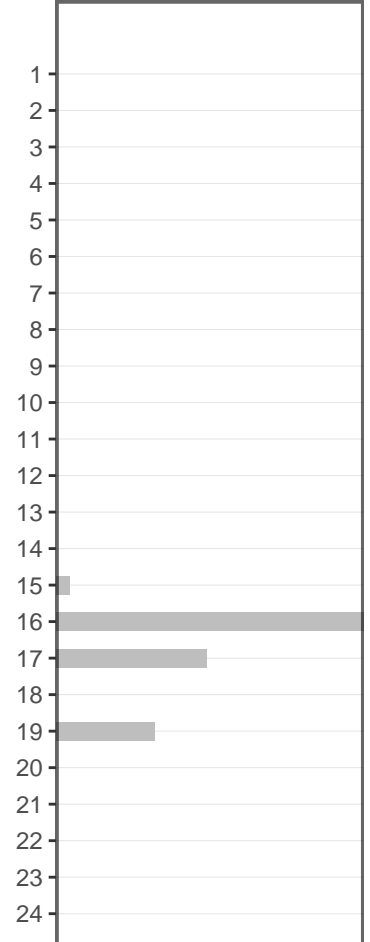
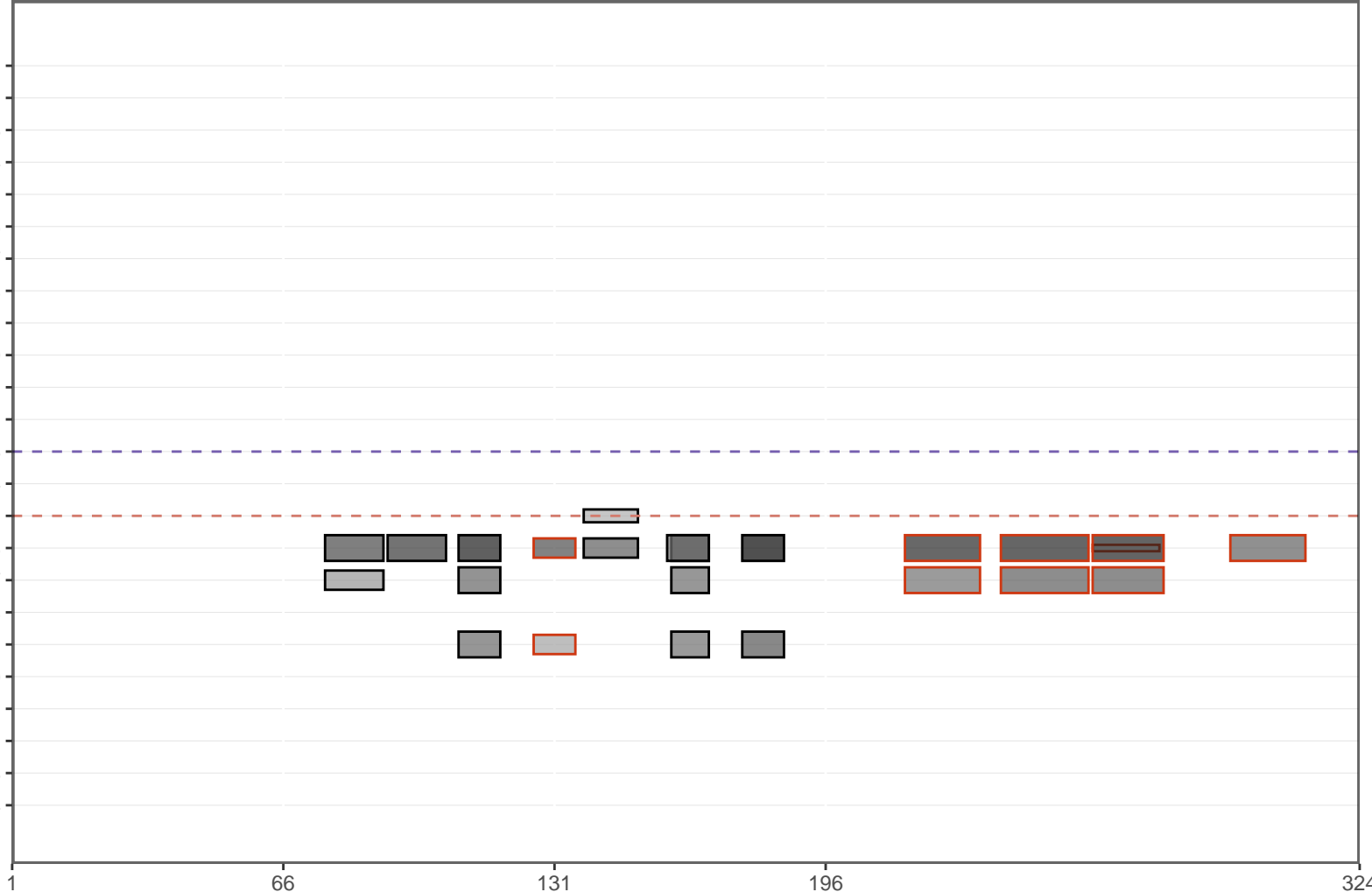
MW indication



Molecular weight



Gel Slice

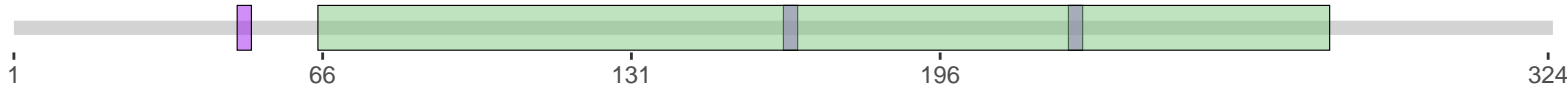


Protein length

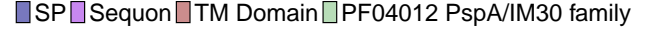


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ILAREALKRRKAYADNASALKAGLDGQKGVVENLVENTLLEESKIGEAANKKDTLAKARAGAEAKTATKIVSEMLGNVNTSEALSFAFERMEEKVLTMESQADALNQLTDFDELEGKFMLETSSVDDDLASLKKELTGSSEKKGELPPGRITTVASSSSTLGFQDSEIEKELNELRRANDI

NbL05g20990.1 haloacid_dehalogenase-like_hydrolase_domain-containing_protein_At4g39970 [MW = 34.41 kDa]

No. of times detected



log(intensity)



Values from



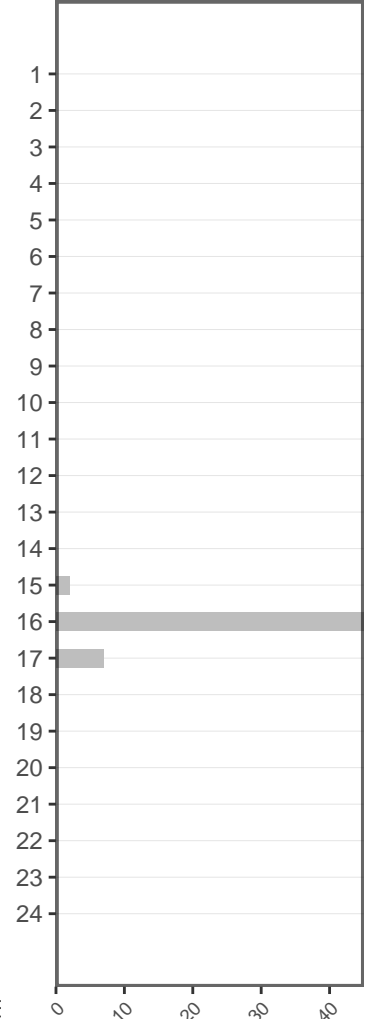
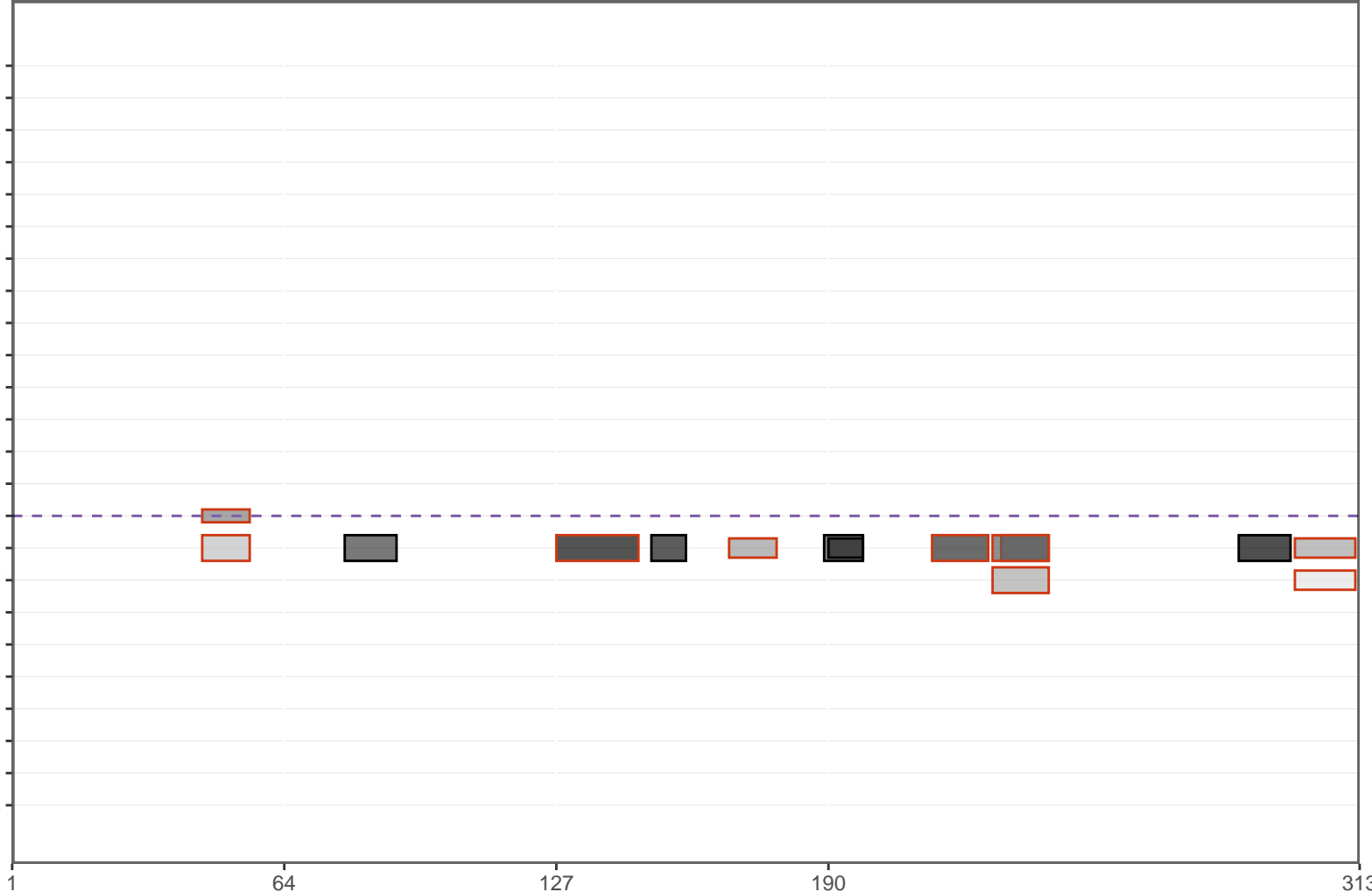
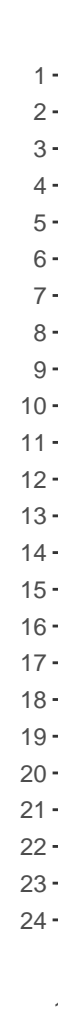
MW indication



Molecular weight



Gel Slice

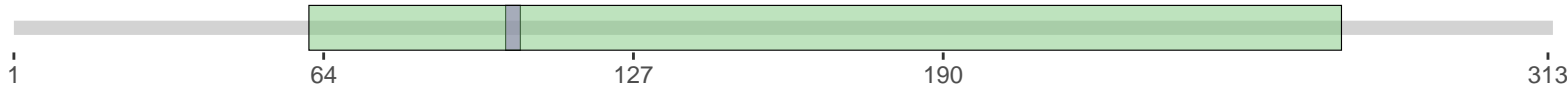


Protein length

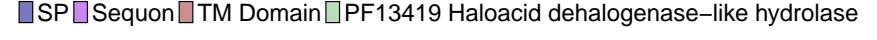


Peptide counts over 4 repeats

Pfam domains



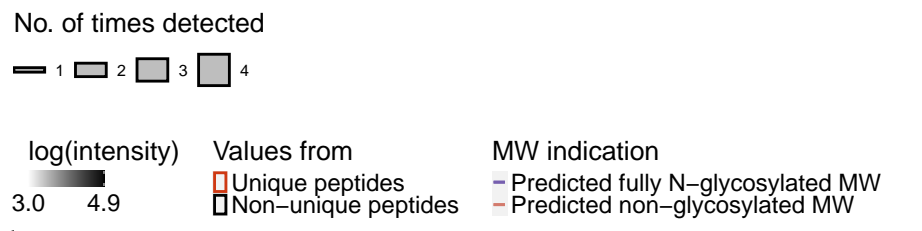
Pfam Description



Protein sequence:

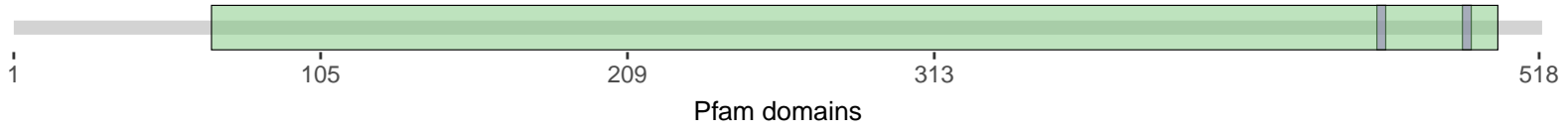
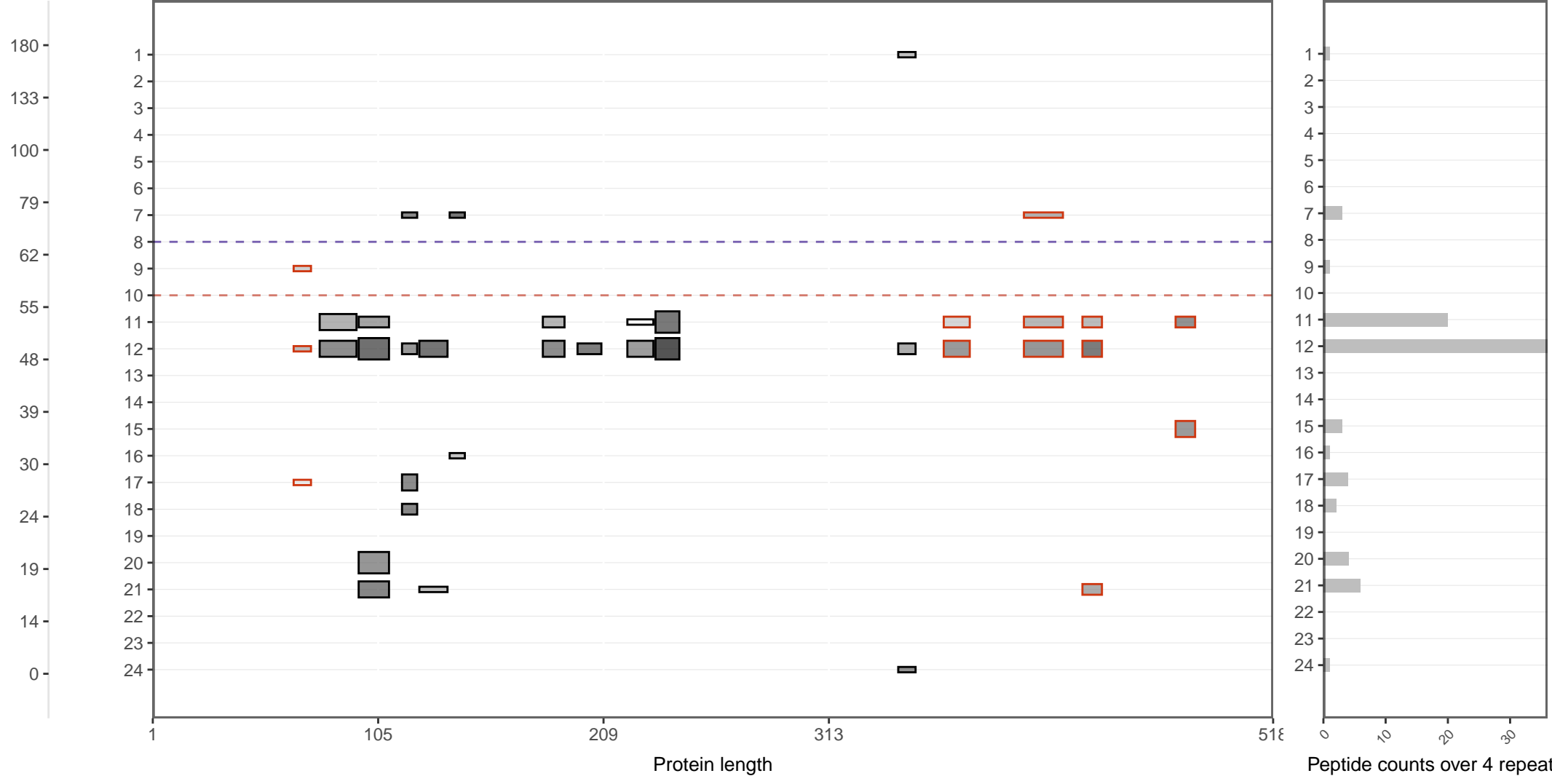
DDSNRAKLDITLQDWKTERYKQIKSGTVKPRPGVLRLLMDEARAAGKHLAVGSAATKSSVIMGLNLLGLDRFHGLDFLAGDDVKKPKPDSIYTAAKKLVGSESNGLVVEDEVLQATGAGMSQVITVTSSTADGGDFKEAIAIYPLSDVRFNDLESLIGDQVITK

NbL05g20920.1 phospho-2-dehydro-3-deoxyheptonate_aldolase_2_chloroplasic [MW = 57.49 kDa]



Molecular weight

Gel Slice



Protein sequence:

IWNLDFVENSECGRYGELAHRYVDEALGMAAGLTVQHPIMATTFDFWTSHEGLLLPYEQALTRDSTGSLFYDGSAMHWVGERTRQLDCAHVEFLKGVANPLKQKVSQKMPNELVKLIDLNFTNKPGRITVIRMGAEINMRVKLGHUHRVARGAGGIVTVWVQDPMHGNTKAPCGLTKRAFDSILAEVRAFFDVHEQEGSHPGGHIEMTGQNVTECIGGSRITVYDGLGRVHTHGDPRLNAQSGLELSFVIERLKRKRMSQRL

NbL05g20870.1 tRNA_(cytosine(34)-C(5))-methyltransferase-like [MW = 100.42 kDa]

No. of times detected



log(intensity)



Values from



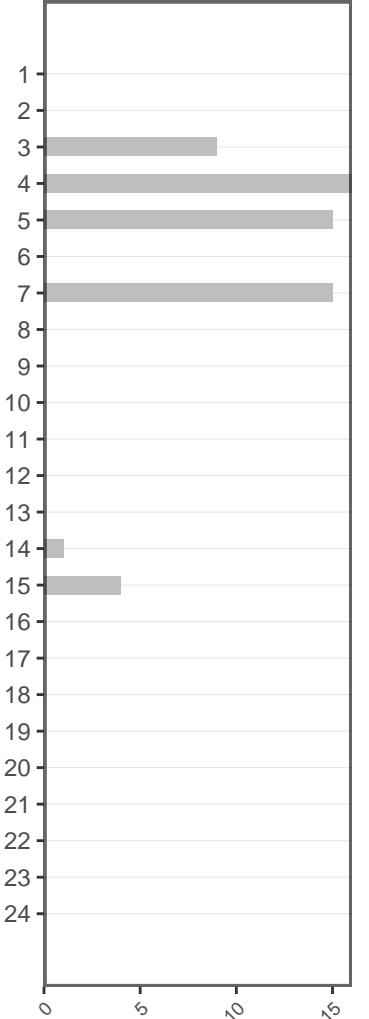
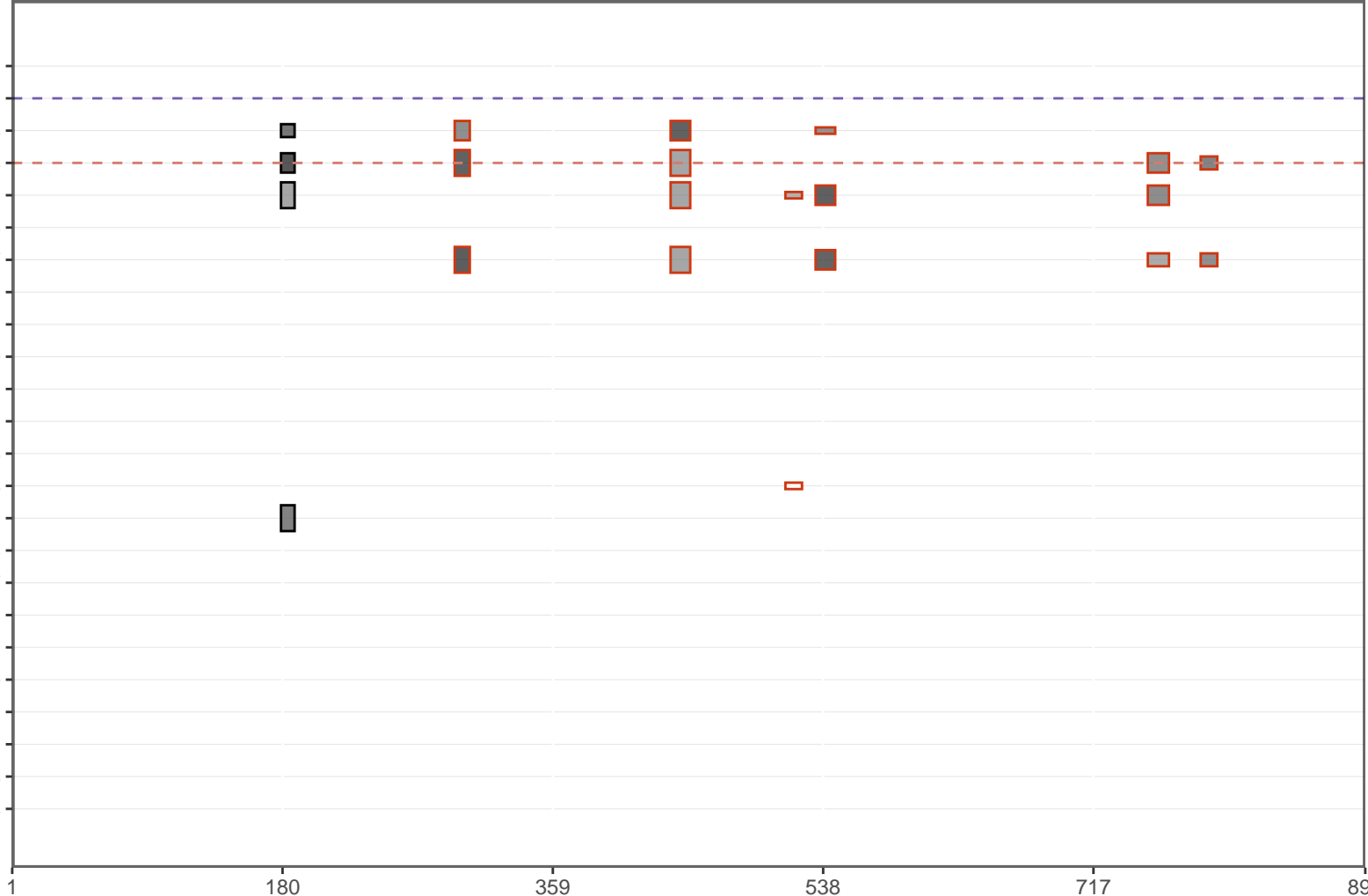
MW indication



Molecular weight

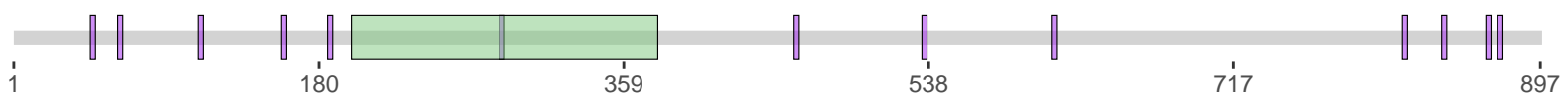


Gel Slice



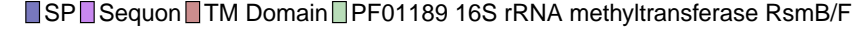
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

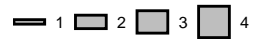


Protein sequence:

VFPSGKTYDASEGNDATRAQLGSDNGNNDTSENDMPLVEDSAAATILDDEEVESTLPLKRGMRIRVPHDQNSGAFFIAFHKLSPMPASAFQKKKPVSLQKLNLSNGAELSTTKVKEDENEEDVNPVDSVANEQVITMDDTDQAEGLTTEVKEYVWADVKPKVDSVGSSEETTTVDGNGTDETLDAEFPSETLEKKEKDETSSTYTRAEPEGNRGRKLGMDGKWRGVDVWFVYKEEAAVGKIKDFYGGKDSFFFEGLHTRNSGDMNHKRVKYYKSKVEVLIHLFLA

NbL05g20860.1 peroxidase_17 [MW – SP = 35.31 kDa]

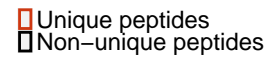
No. of times detected



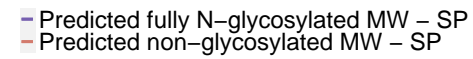
log(intensity)



Values from



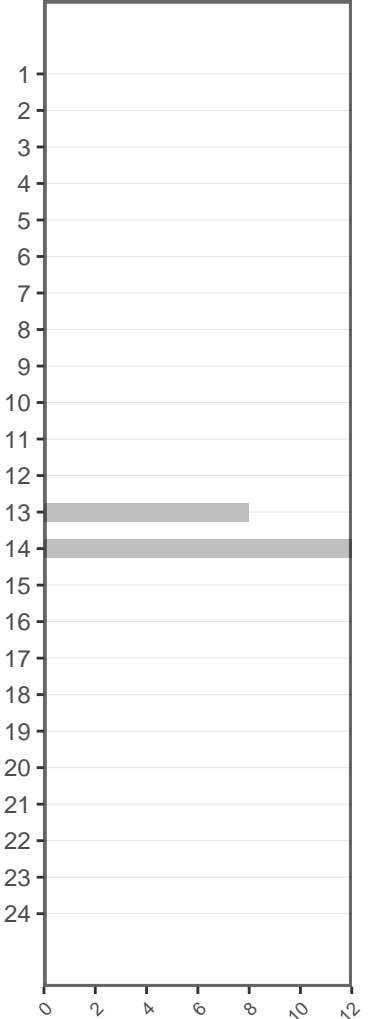
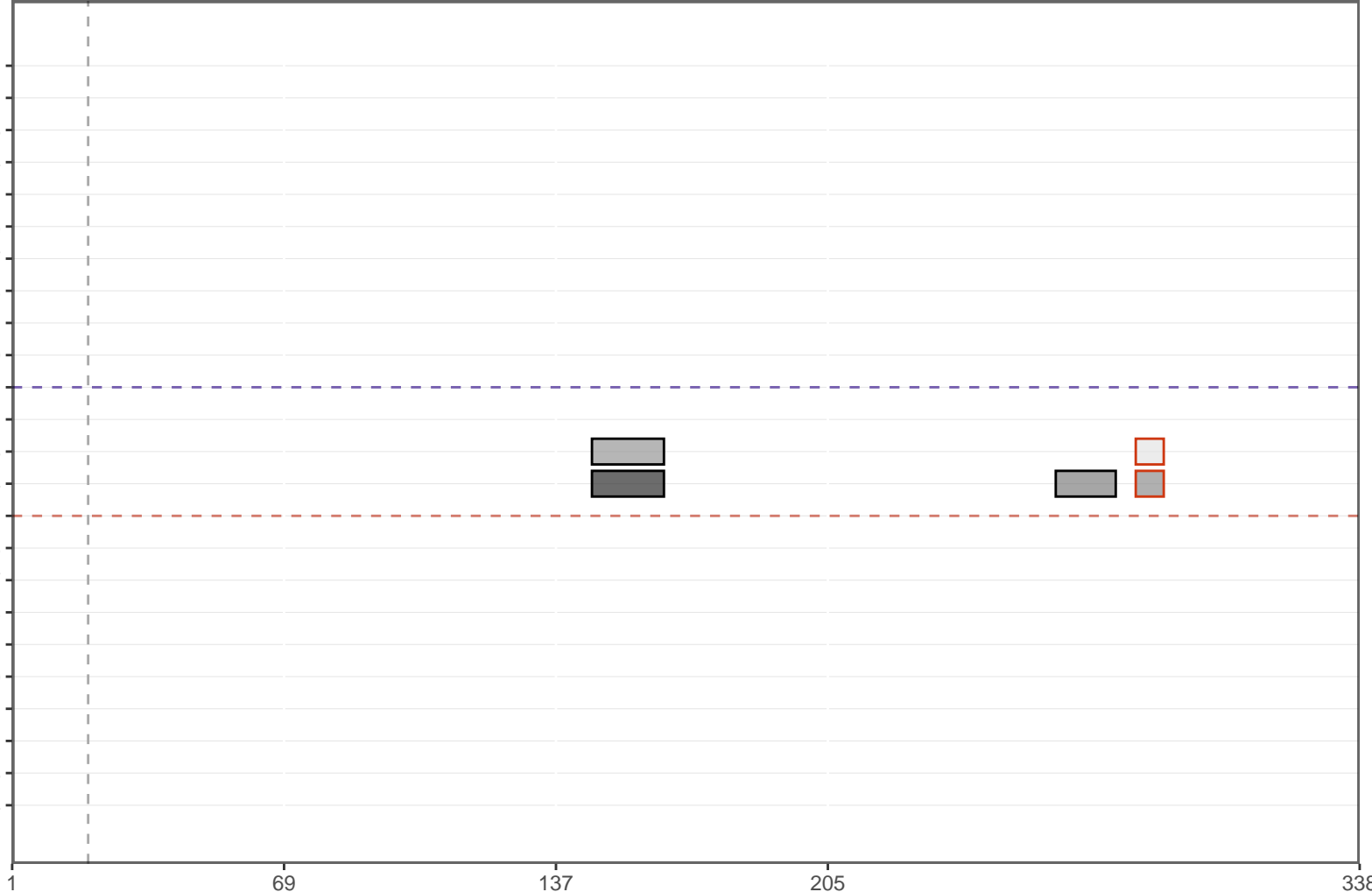
MW indication



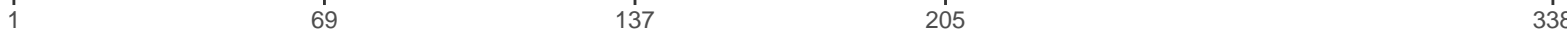
Molecular weight



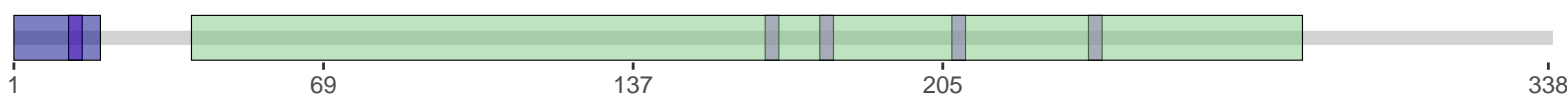
Gel Slice



Protein length

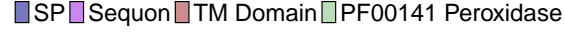


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

INQIMPSPRSNATYLDLFRYLNLSKDLVALGGSHSGKGRCFVFRILYNGGSSGRPDPTIEPRFREKLDKLPLOGGDNVTDGLDQPEVFDNGYKDLVNGRGLNDDGLFTNPLTRVYRFEVDSQEKFKAFVEGMITMGDLGSGRPGEIRRDGRVNVNHRPRVEVLFETSNGGE

NbL05g20800.1 lanC-like_protein_GCL1 [MW = 50.23 kDa]

No. of times detected



log(intensity)



Values from



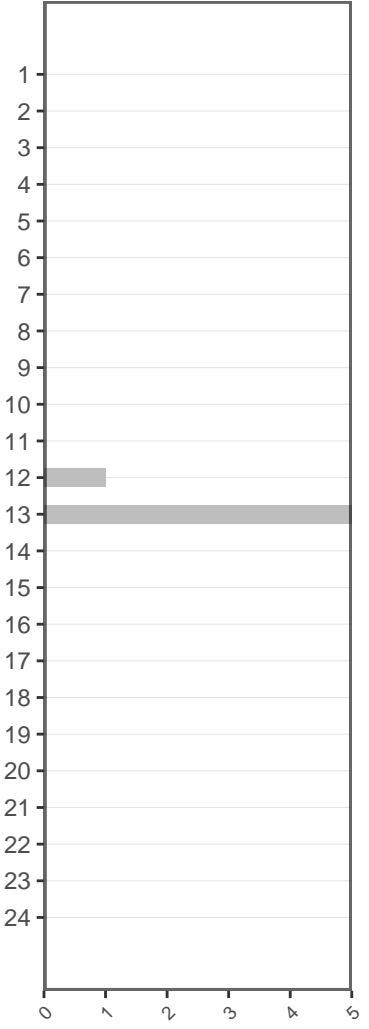
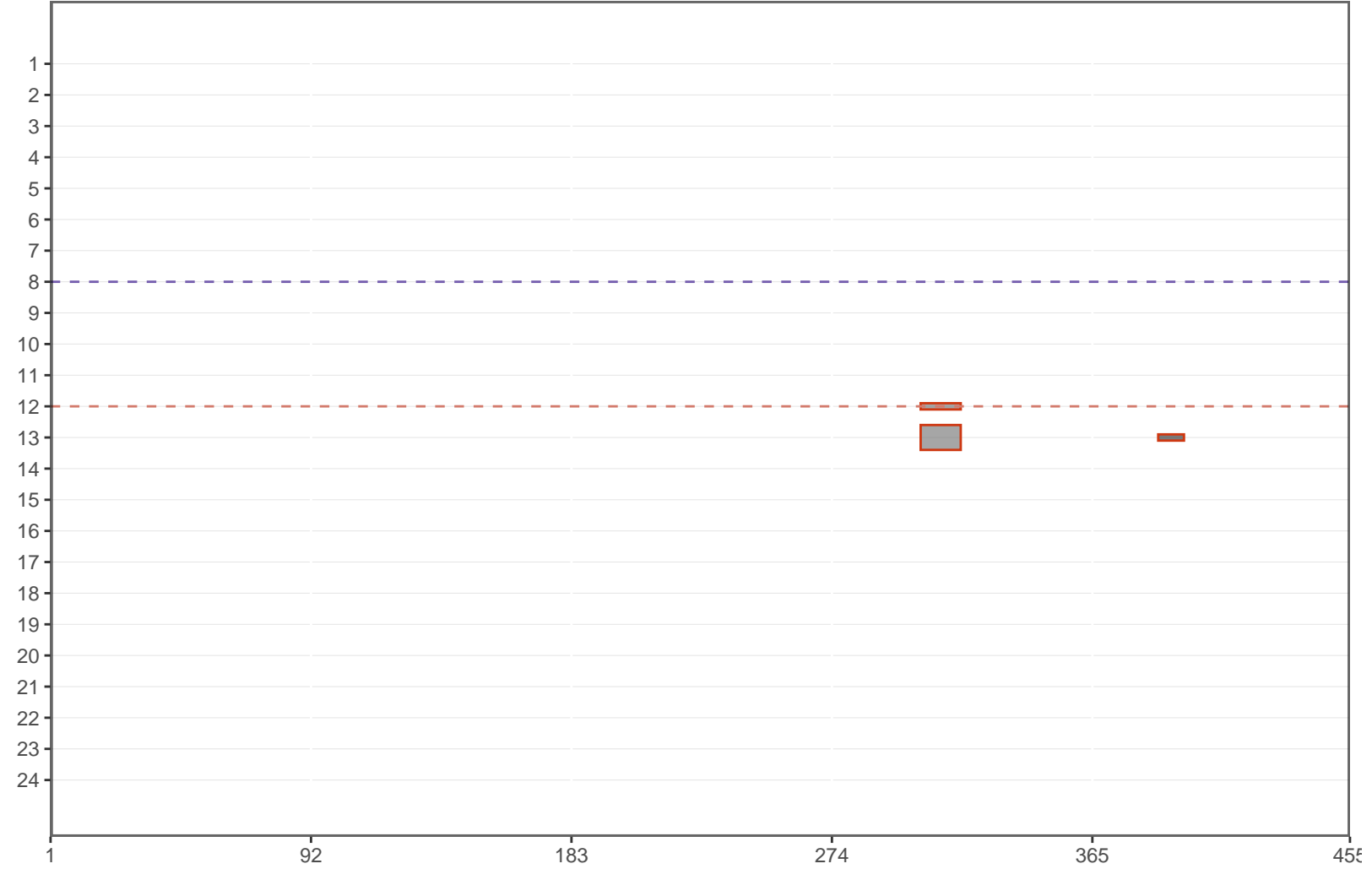
MW indication



Molecular weight



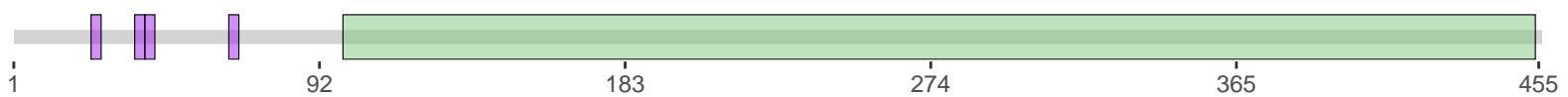
Gel Slice



Protein length

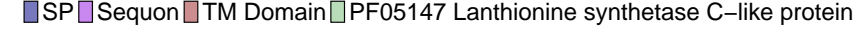


Peptide counts over 4 repeats



Pfam domains

Pfam Description

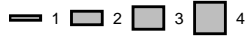


Protein sequence:

LWALPIRKYIGAEIVPDEIVMPVVEALAGGRAGATENPAGPLMYRWHGTRVWGAAGHLAGLHLLHFLPLPDEIKDKVETLRYMMSNRFLHSGNIPVSEGNPRDKLVQVSHGATGATMCKKASEVLSNDRFRDAAVEGGEVWKNGLVKKVGLADGASGNVWFLSLFRITGEEIYEERARAFASGLYHNARTIVNARHNEADHSGYFQGLGGVAFLEFLDITPVSRRFPGFELV

NbL05g20720.1 nicotinamidase_1-like [MW = 27.01 kDa]

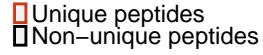
No. of times detected



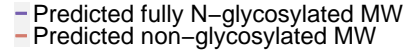
log(intensity)



Values from



MW indication

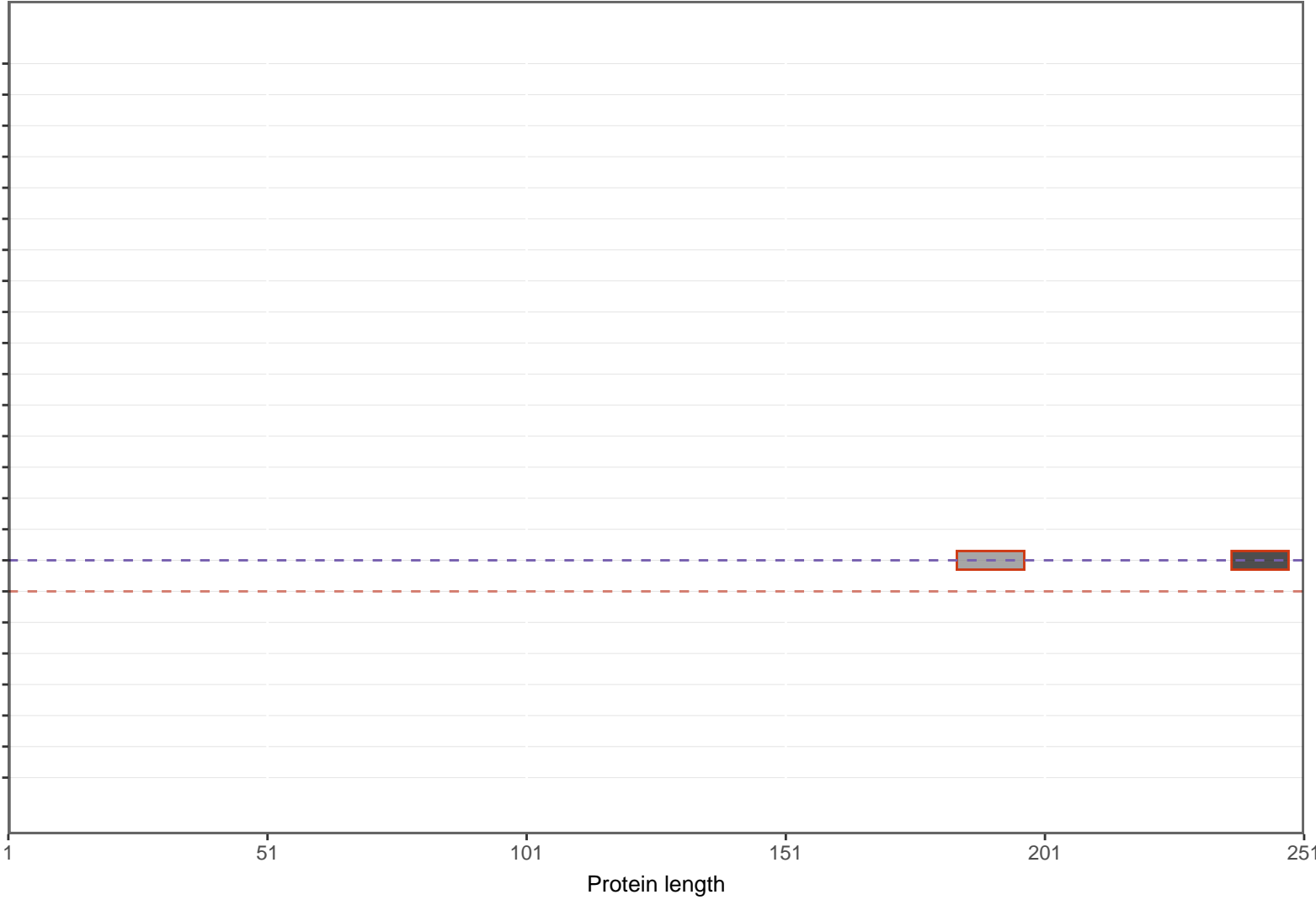


Molecular weight

180
133
100
79
62
55
48
39
30
24
19
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24
0

Gel Slice

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22
23
24

Peptide counts over 4 repeats



Pfam Description



Protein sequence:

YPALQWLESEPNVFLRCKDDIDGFLGSEIKDGENVYVDWVKAHEKALVVDICTDGLVDFVGSVLEARNRNGFLSPLLEDVIVYSRGCTFDLPAQIANIKGALPHPGQELMHHLGLYMAKGRGAKVYVEVFDTSAAKAT

NbL05g20680.1 uncharacterized_protein_At1g04910-like [MW - SP = 53.29 kDa]

No. of times detected



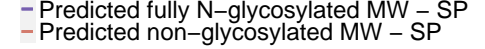
log(intensity)



Values from



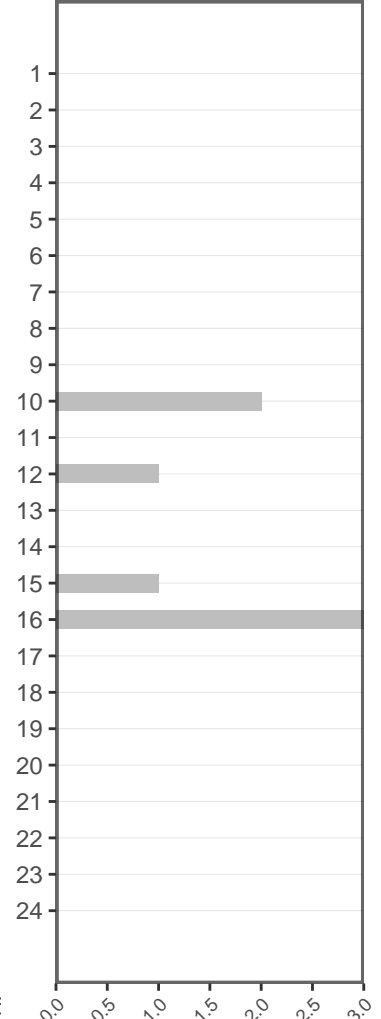
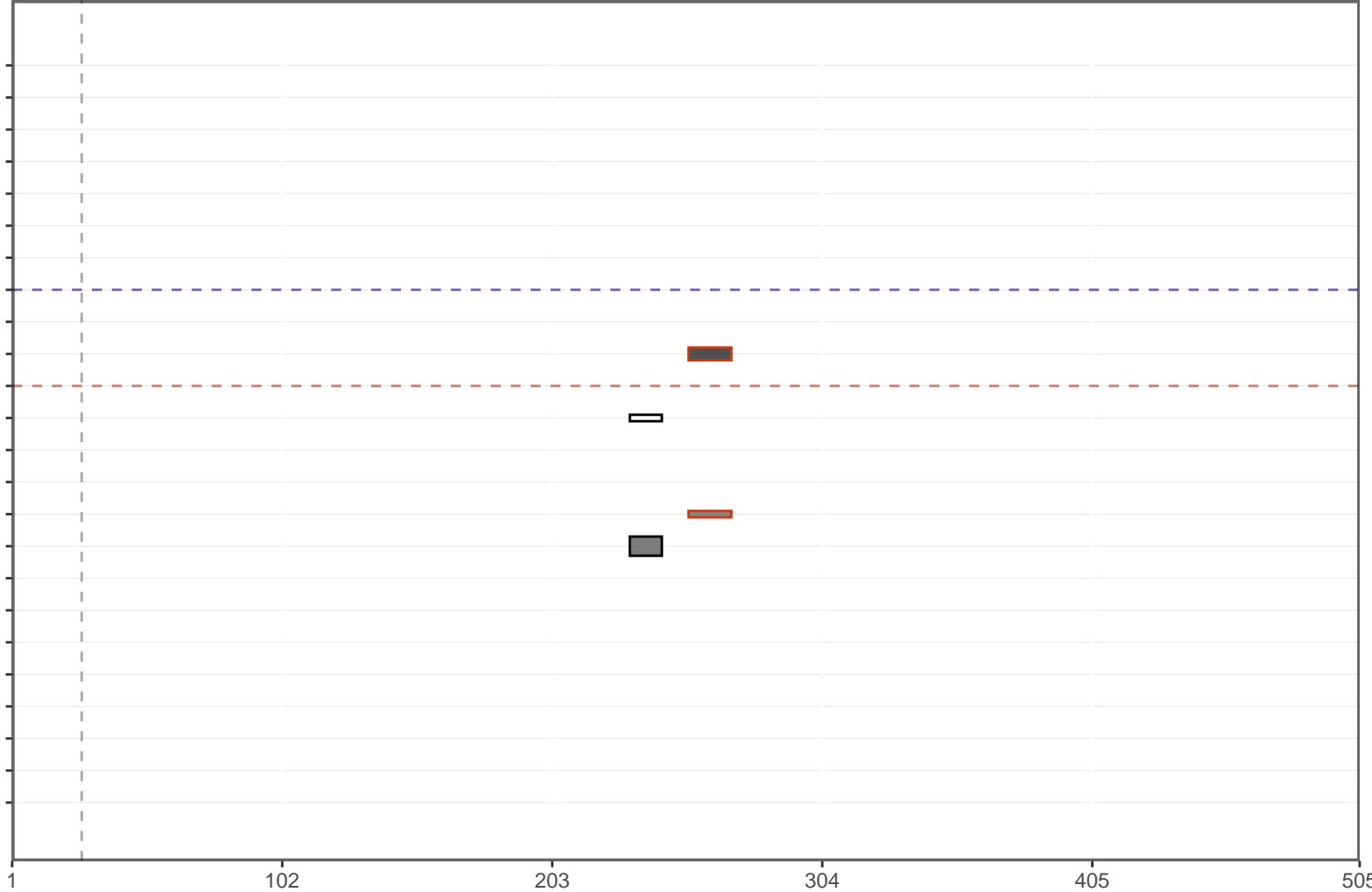
MW indication



Molecular weight

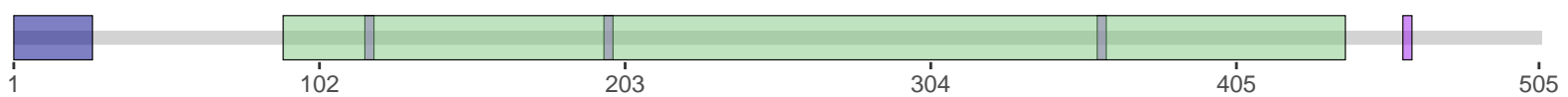


Gel Slice



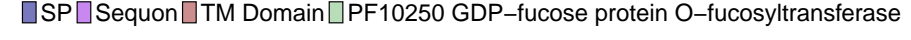
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IVRIHGLDALINLRIDPPPEEGMIVSNLYREVIDPKPKGGAGKFAVHLHFRDKDMAAHSACDFGGGKAENLAKYRQVWQGRVINGQFTDEELRSGGRCPLTFEEVGLLLAALGFDNSTRFLASHKIVYGGERRISALRNLFLFMEDKKSLSASSEERALIKGKAEKLLAVDYYVGMHSDIFVSASPGNHNHNMVGHRTYNNMKTIRPNMALLGGFLFNKLTITWPEFDQESVEGHKNRGGQIRLRKPKGSLTYTPADQCMGQA

NbL05g20560.1 14-3-3-like_protein_D [MW = 28.27 kDa]

No. of times detected



log(intensity)



Values from



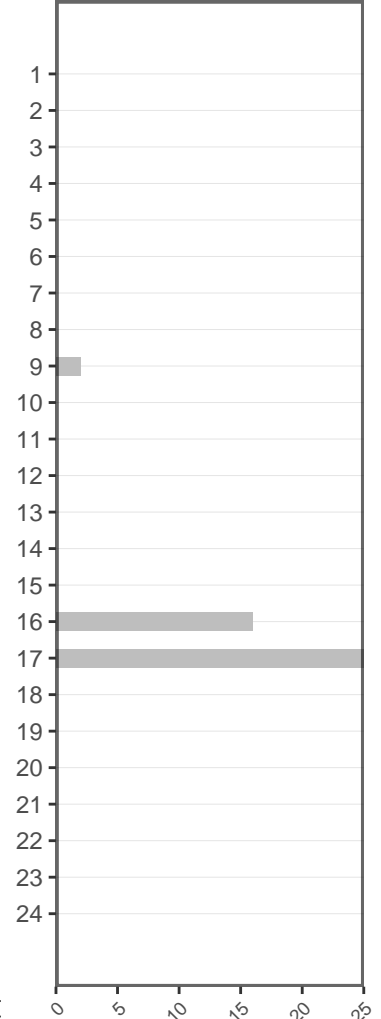
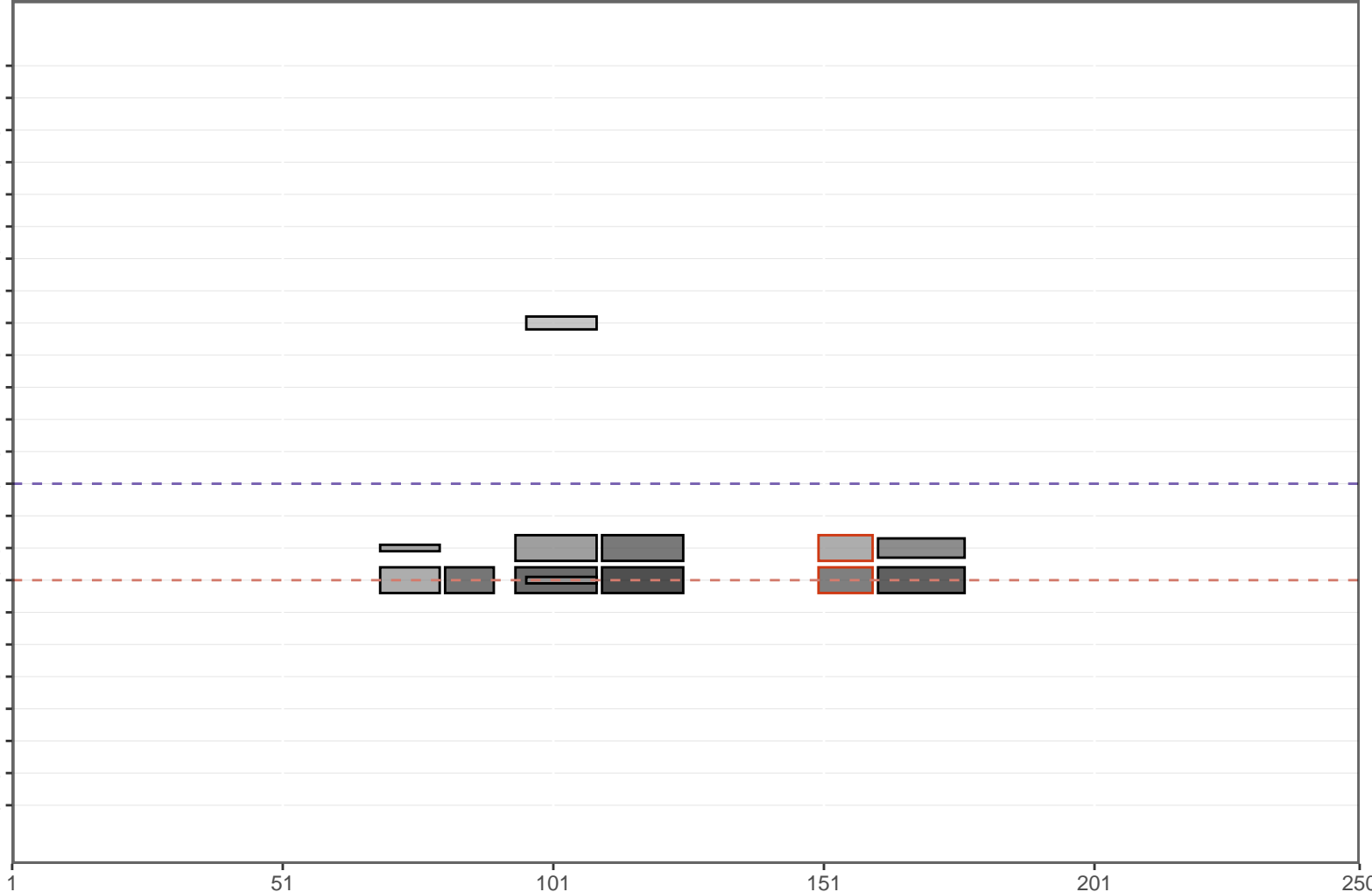
MW indication



Molecular weight

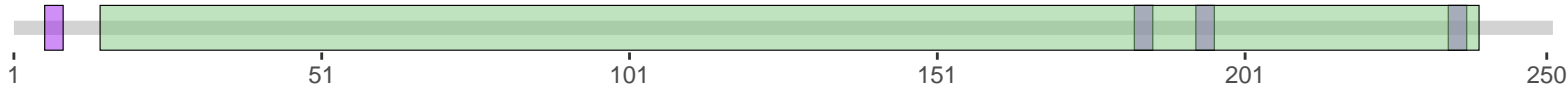


Gel Slice



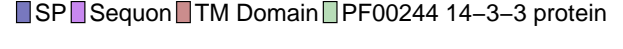
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IQYLIPASAGEKVFYLNKMGDYRYVLAEPKVKVNERKEAAEATMLAVKAGDDIAELAPTRHRLGLALNYSVFYIELNASEKAKSMKQAFEEAAEIDLTGEEESYKDSITLMQLLRDNLTLWTGSDMQEIQDEA*

NbL05g20430.1 14-3-3-like_protein_16R [MW = 30.56 kDa]

No. of times detected



log(intensity)



Values from



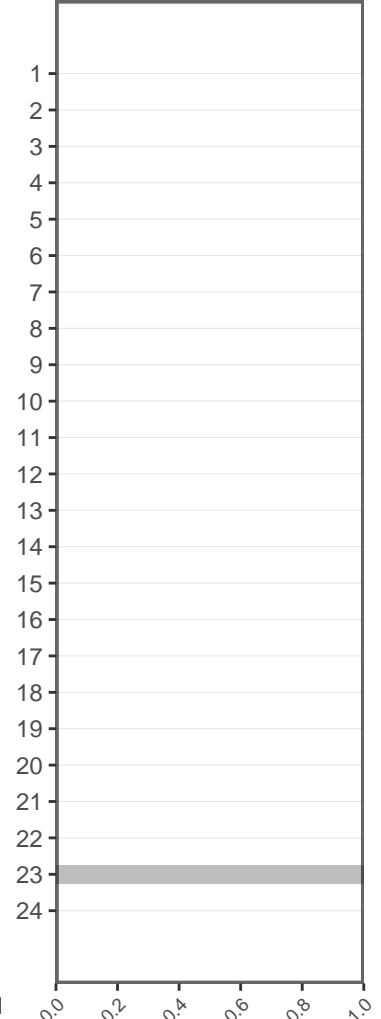
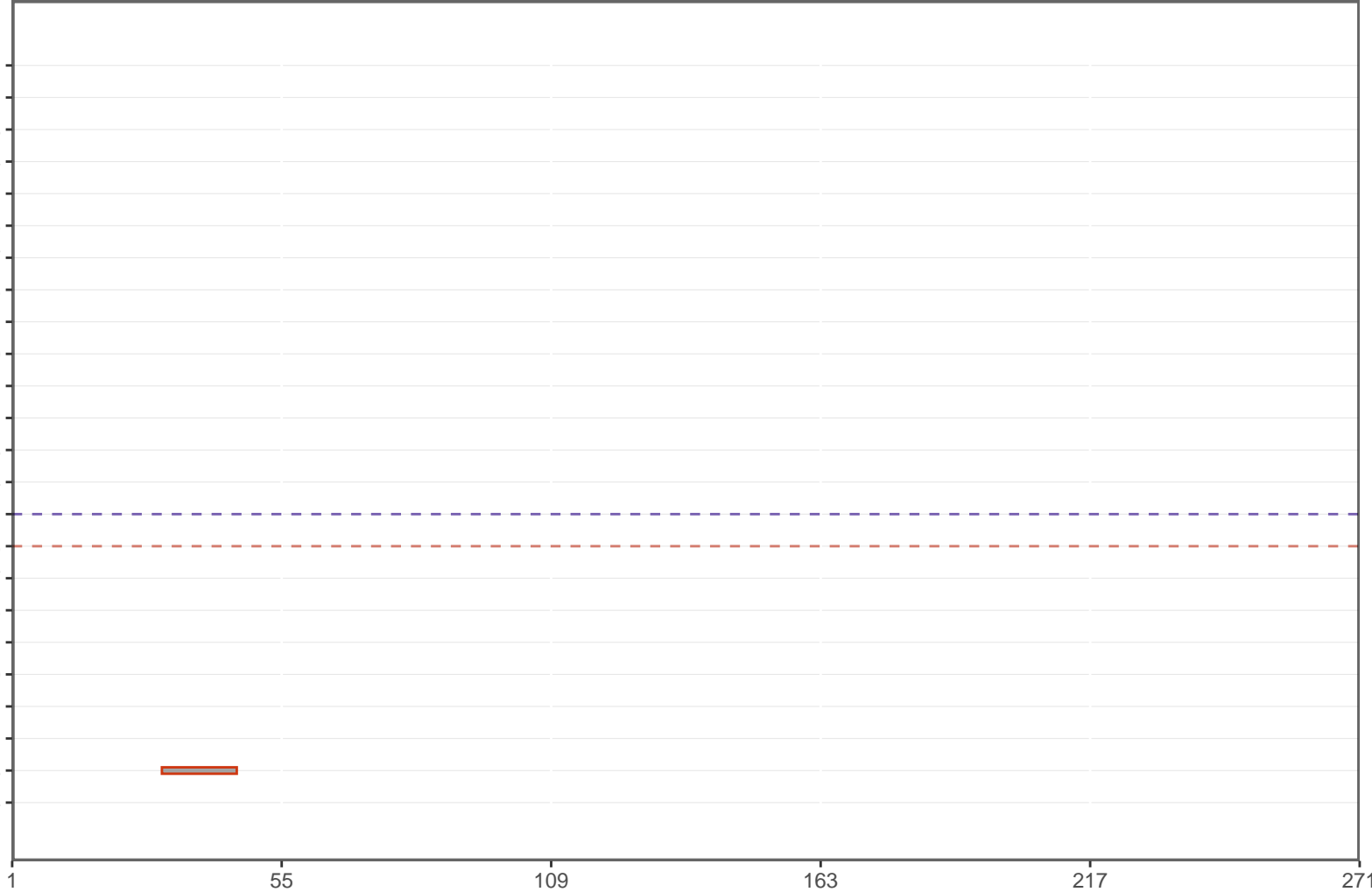
MW indication



Molecular weight

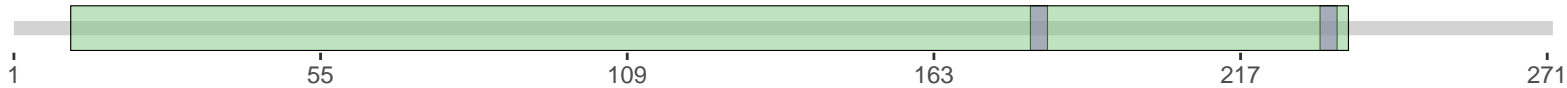


Gel Slice



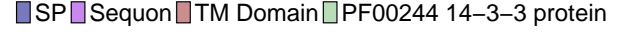
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

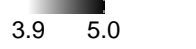
LVFLVMKGDYHRYLAEFKTGAERKEAENTLSAYKSAQDIANTELAPTRHRLGLALNFSVYFYELNSPDRACNLAKGAFDEAAIELDTLGEESYKDSITLMQLLRDNLTLWTSMDQVDSIFLLENKIKVSSPFSYDFINLGVLLNLF

NbL05g20050.1 uncharacterized_LOC109208398 [MW = 12.05 kDa]

No. of times detected



log(intensity)



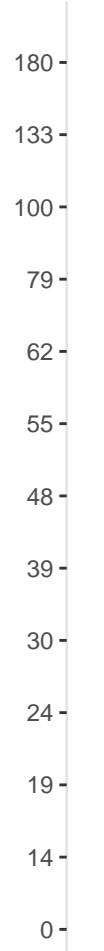
Values from



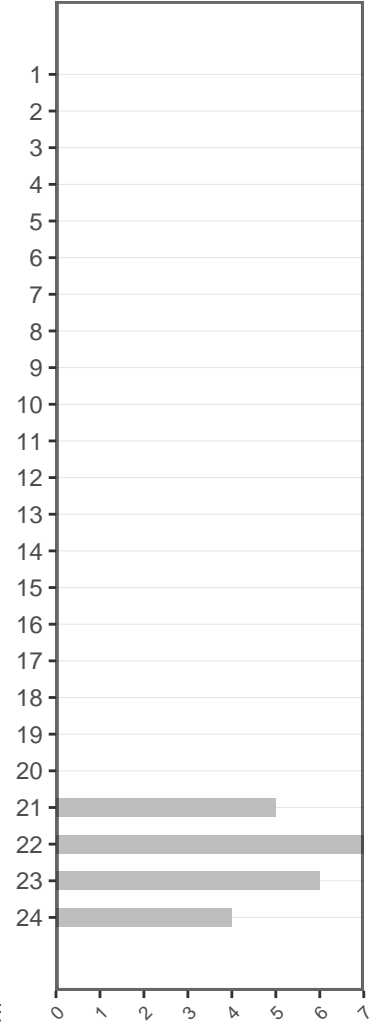
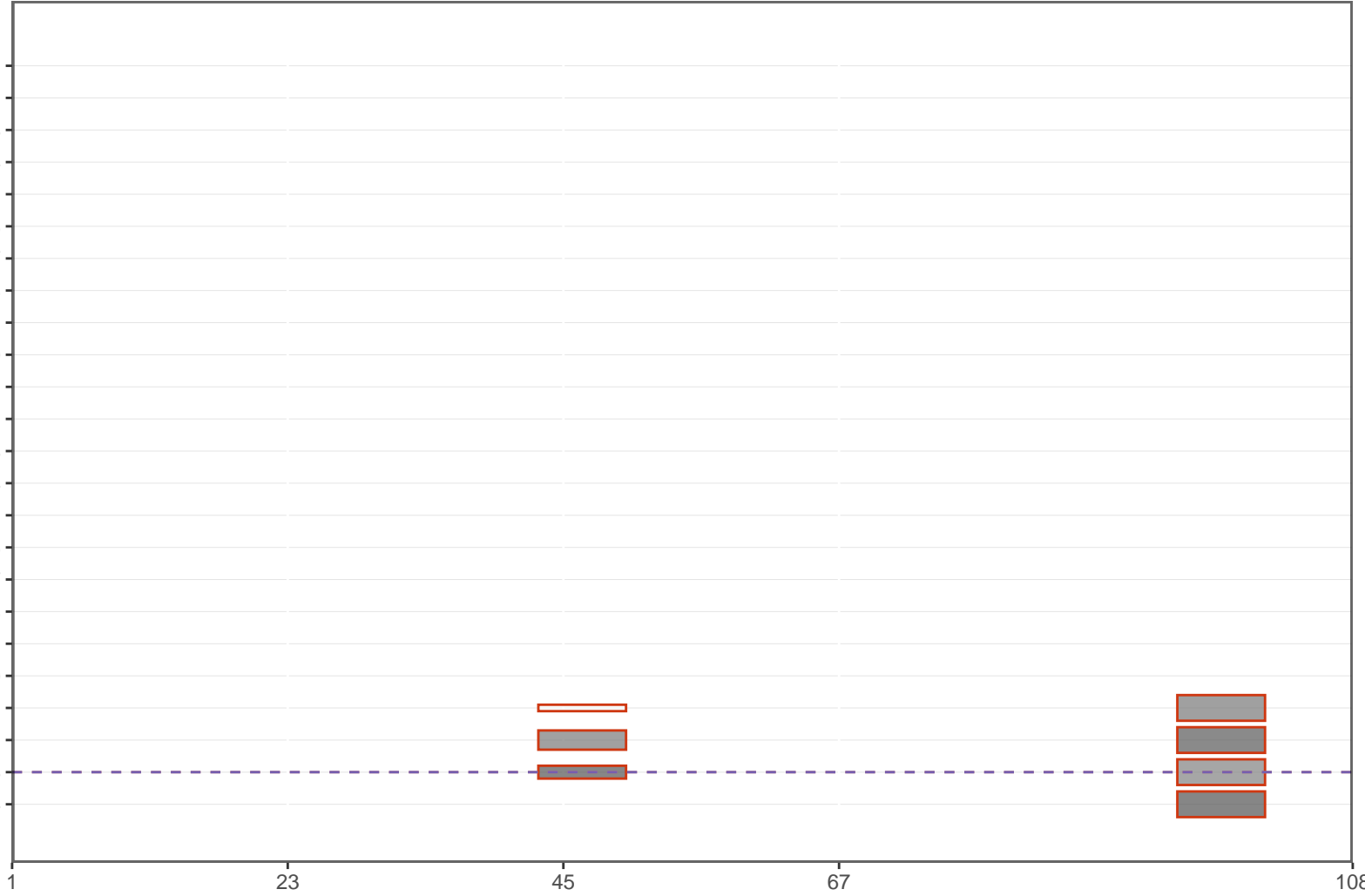
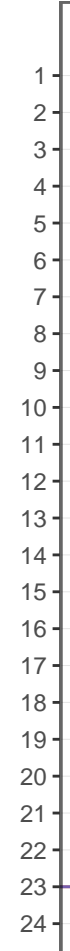
MW indication



Molecular weight



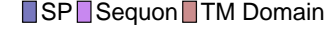
Gel Slice



Protein length

Pfam domains

Pfam Description



Protein sequence:

VFKDPSLLKLLLEKSKGNKKNKKSIEDKYGLRGAEWGIDGSGTAGMTPFEERDSFIAMKGRVAE*

NbL05g19980.1 8-hydroxygeraniol_dehydrogenase-like [MW = 38.73 kDa]

No. of times detected



log(intensity)



Values from



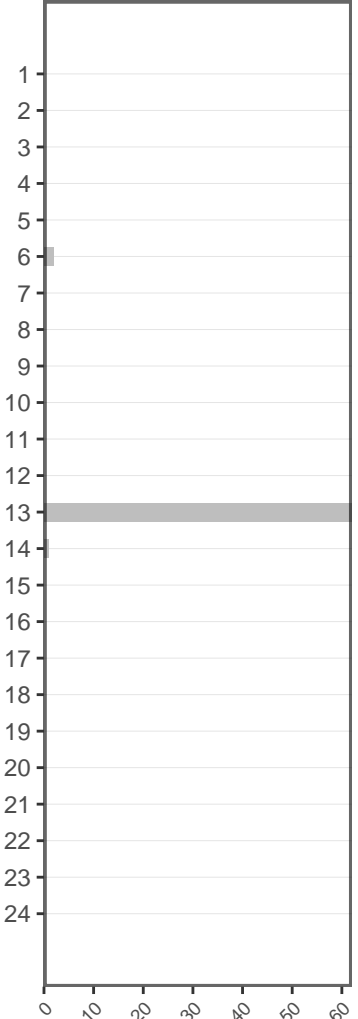
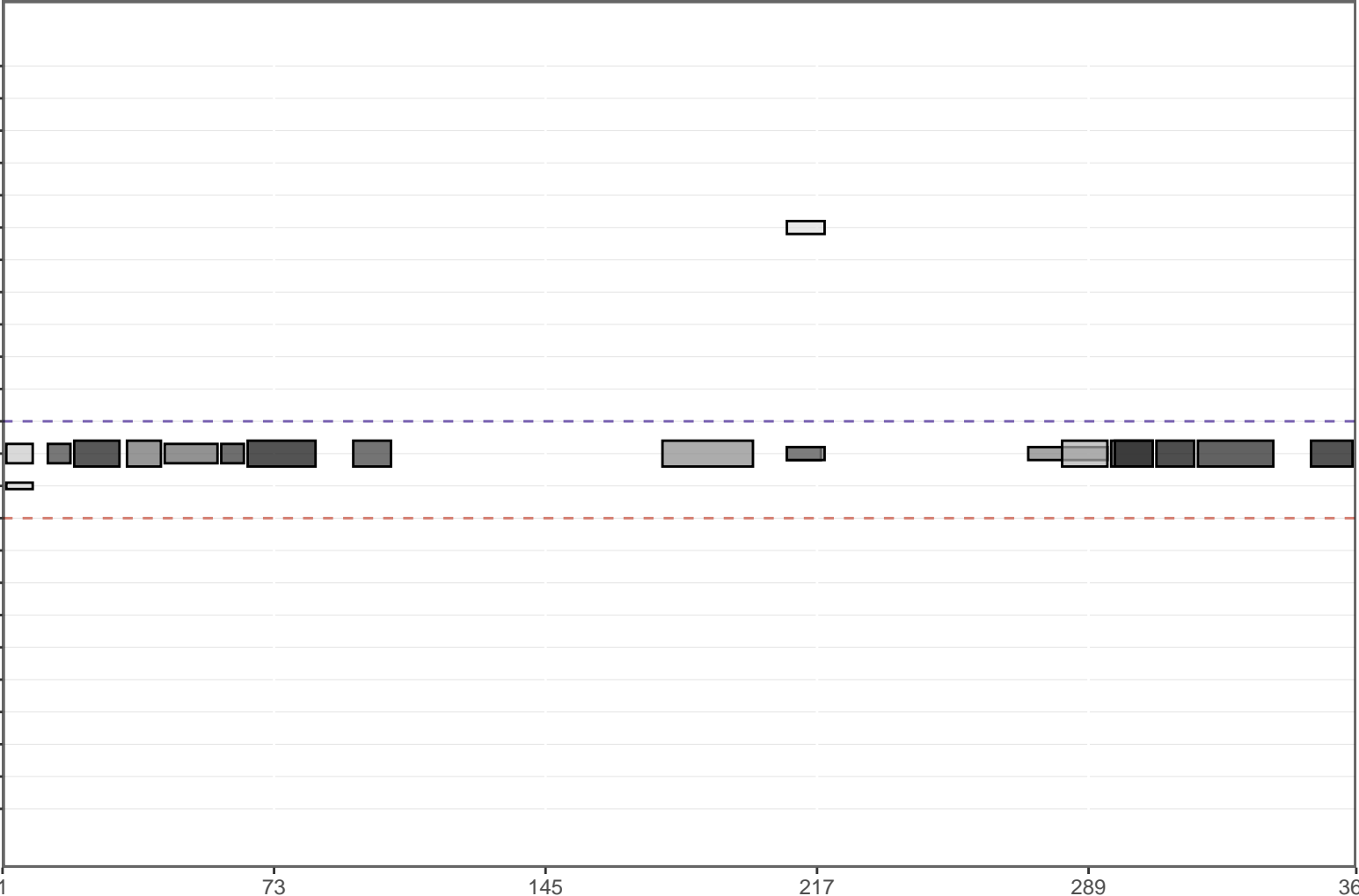
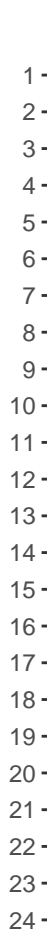
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length

1 73 145 217 289 360



Pfam domains

Pfam Description



Protein sequence:

CAIGITTYSPLYYFGLDKPMHGVGLGLGHMAVFAKAFGAKVTVISTGKQKDEALGHLGADLFLVLSGSPGEGGALNTMDGDIHDSADHPLLLGLMLKPKHKLMMVAYYKPLGLPVPFPLGLGRKLVAGSAAGVYKETOEMLDFASKNITPDVEVPMVDVNTAWHRLKSDVYKRFVLDGKHSNSA

NbL05g19970.1 8-hydroxygeraniol_dehydrogenase-like [MW = 38.9 kDa]

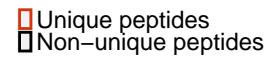
No. of times detected



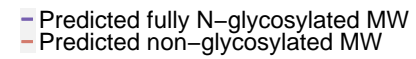
log(intensity)



Values from



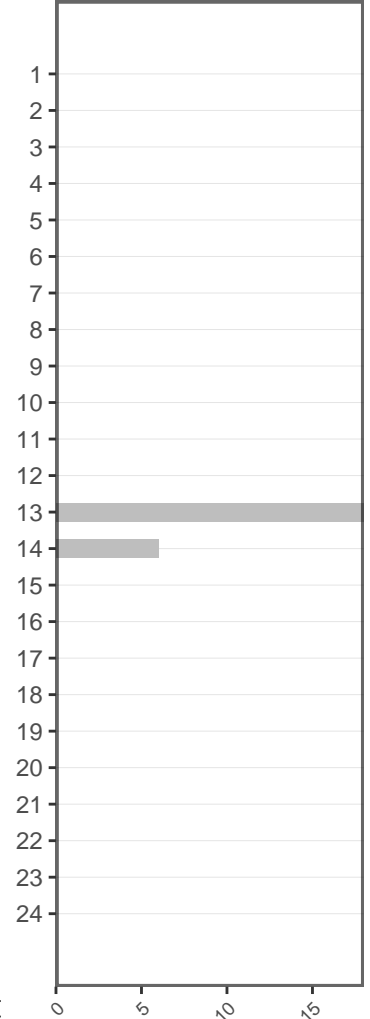
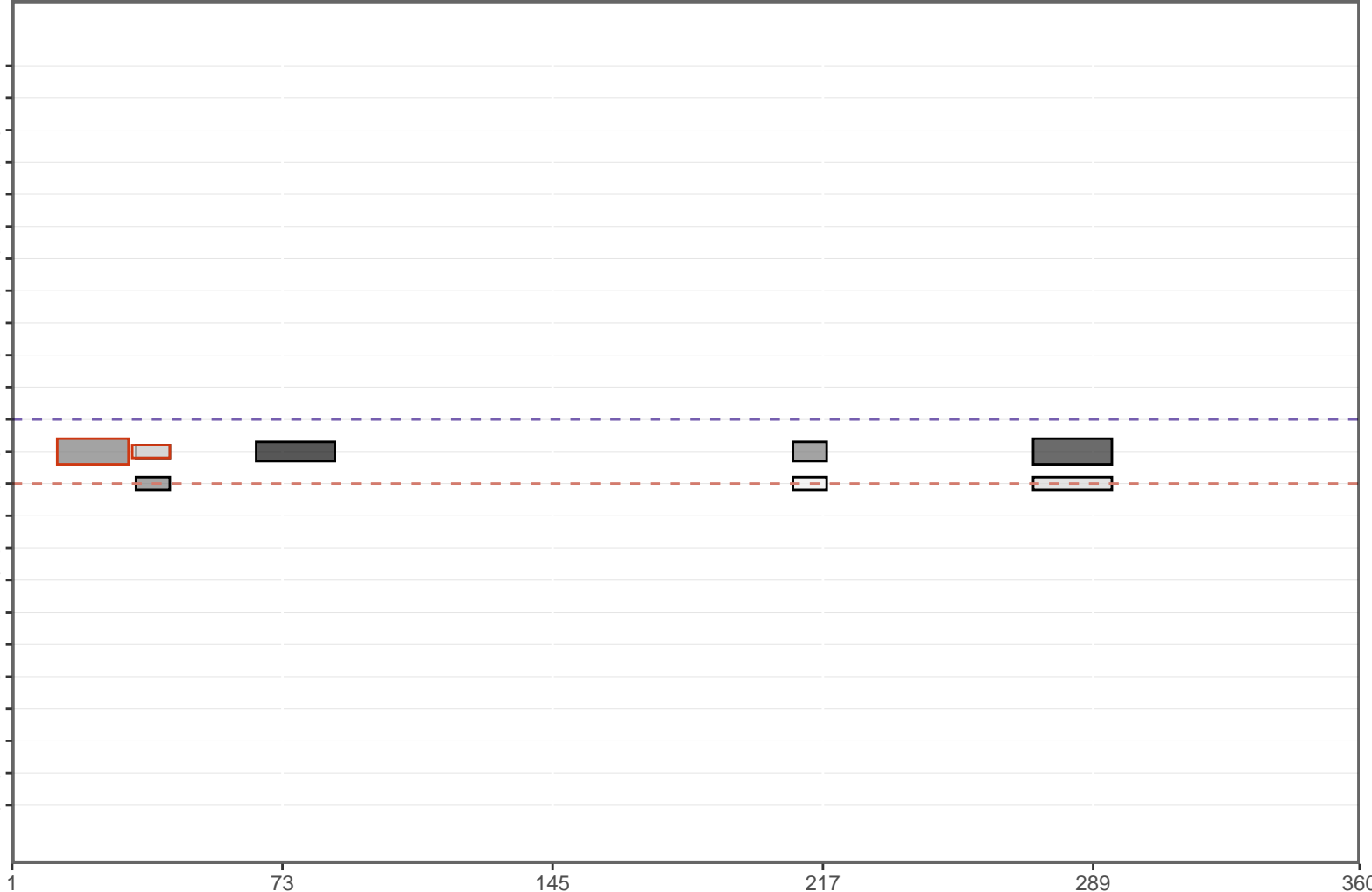
MW indication



Molecular weight



Gel Slice



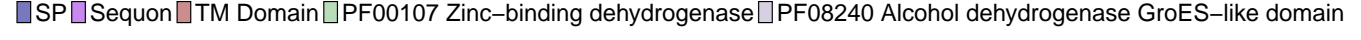
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

.LCAGITTYSPLYKFEFDKPLNGVVLGGLGHMAVFAKAFQKGVTVISTVNNKDEAERLIGADEFLLSGDPPEQLGAASFLDGHDTVADHPILPLLNLRPHGKLVVGGAPKPLELPVFRIMGRKIVGSGISGGMKTEGEMLDFAAKHTIPDVEVVAAMDYVNTALERLLKSDKRYRFLVDVGETLKAD

NbL05g19960.1 8-hydroxygeraniol_dehydrogenase-like [MW = 27.54 kDa]

No. of times detected



log(intensity)



Values from



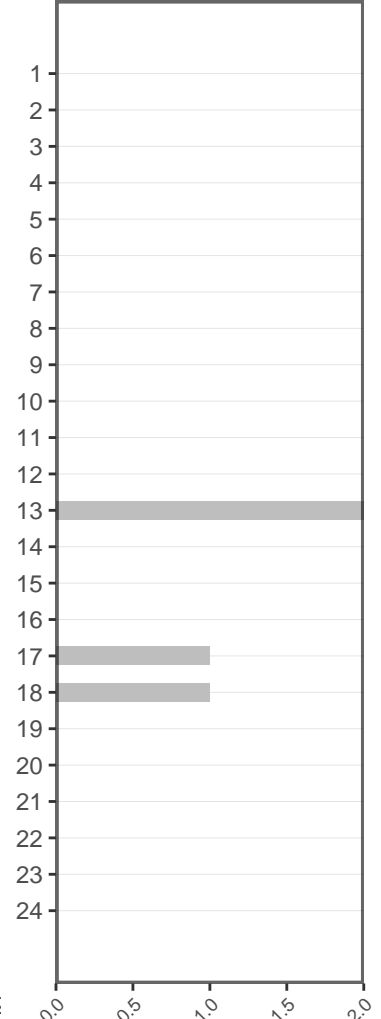
MW indication



Molecular weight



Gel Slice



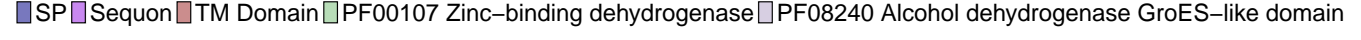
Protein length



Pfam domains



Pfam Description



Protein sequence:

ILPMEAPLLRAGITFTYSPKLYFGLDKPMHIGVFLGGGLGHMAVFKAFQTKVTVISTSAKKKGEAERLGDADFLEIRDTQGMQAMETLDGHDTVSAVHPILPLLELLNLMVSLWLVHDKNGWVSCQFLYFVWGGP

NbL05g19940.1 8-hydroxygeraniol_dehydrogenase-like [MW = 39.15 kDa]

No. of times detected



log(intensity)



Values from



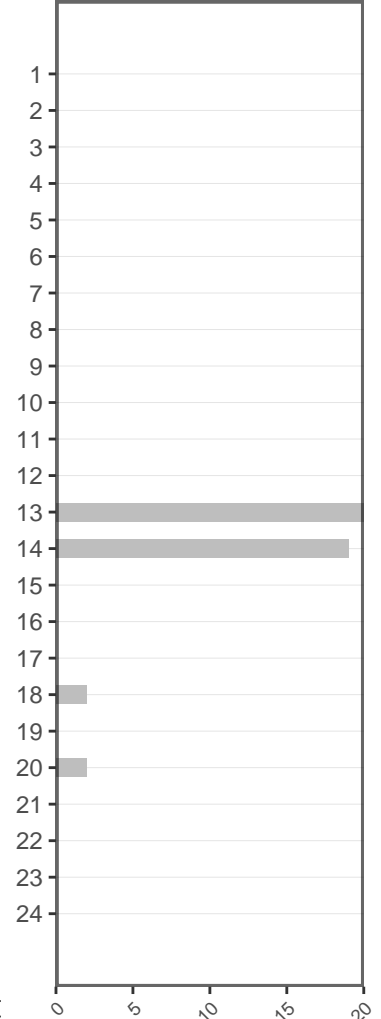
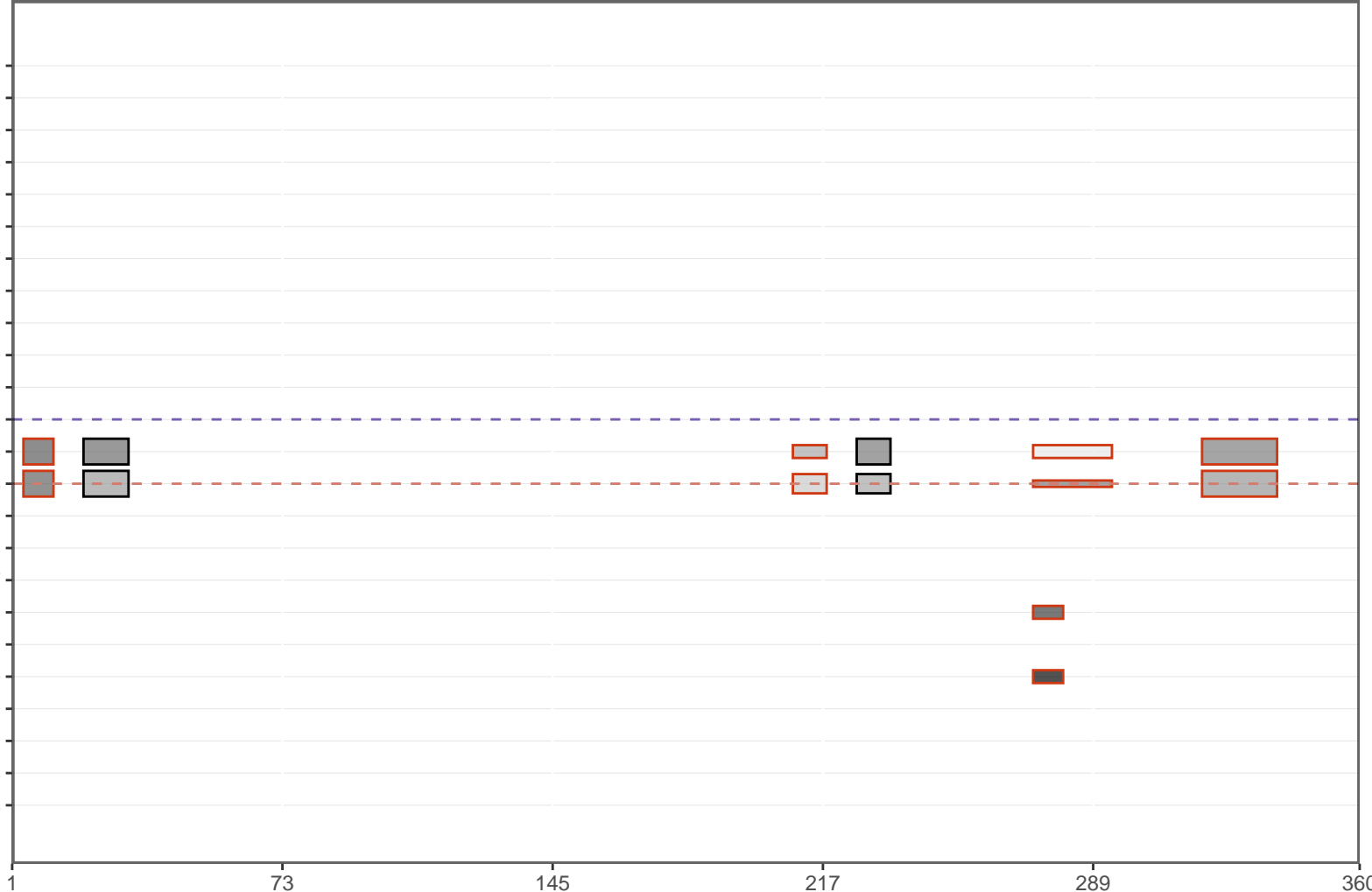
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

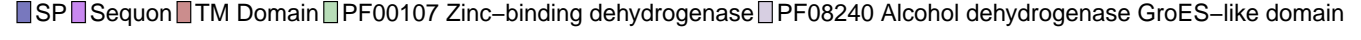
Protein length



Pfam domains



Pfam Description



Protein sequence:

LNAGITTSPLKYLFGLEKPCAMHGVVGLGGLGHMAVFKAFKAGTGVTVISTVSVSKKGEAERLIGADSFLLGRDPDQMGAAATGSLGDHDTVAHVPALLPLLNLLKTHGKLVILGAPKPLPLVPLLLGRKLVAGSGCIGGMMKETGEMVDFAAKHINTPQVEVPMKVVNTAERLAKSDVRYRFLDIGSTLNKPS

NbL05g19850.1 glutathione_S-transferase_DHAR3_chloroplastic [MW = 28.55 kDa]

No. of times detected



log(intensity)



Values from



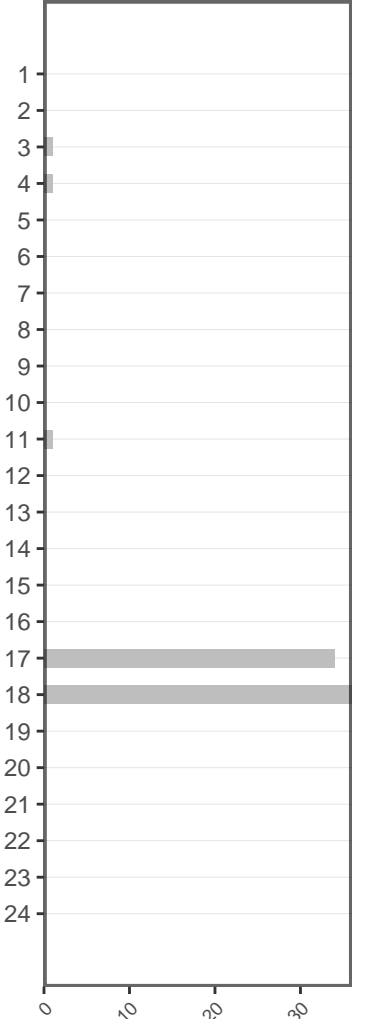
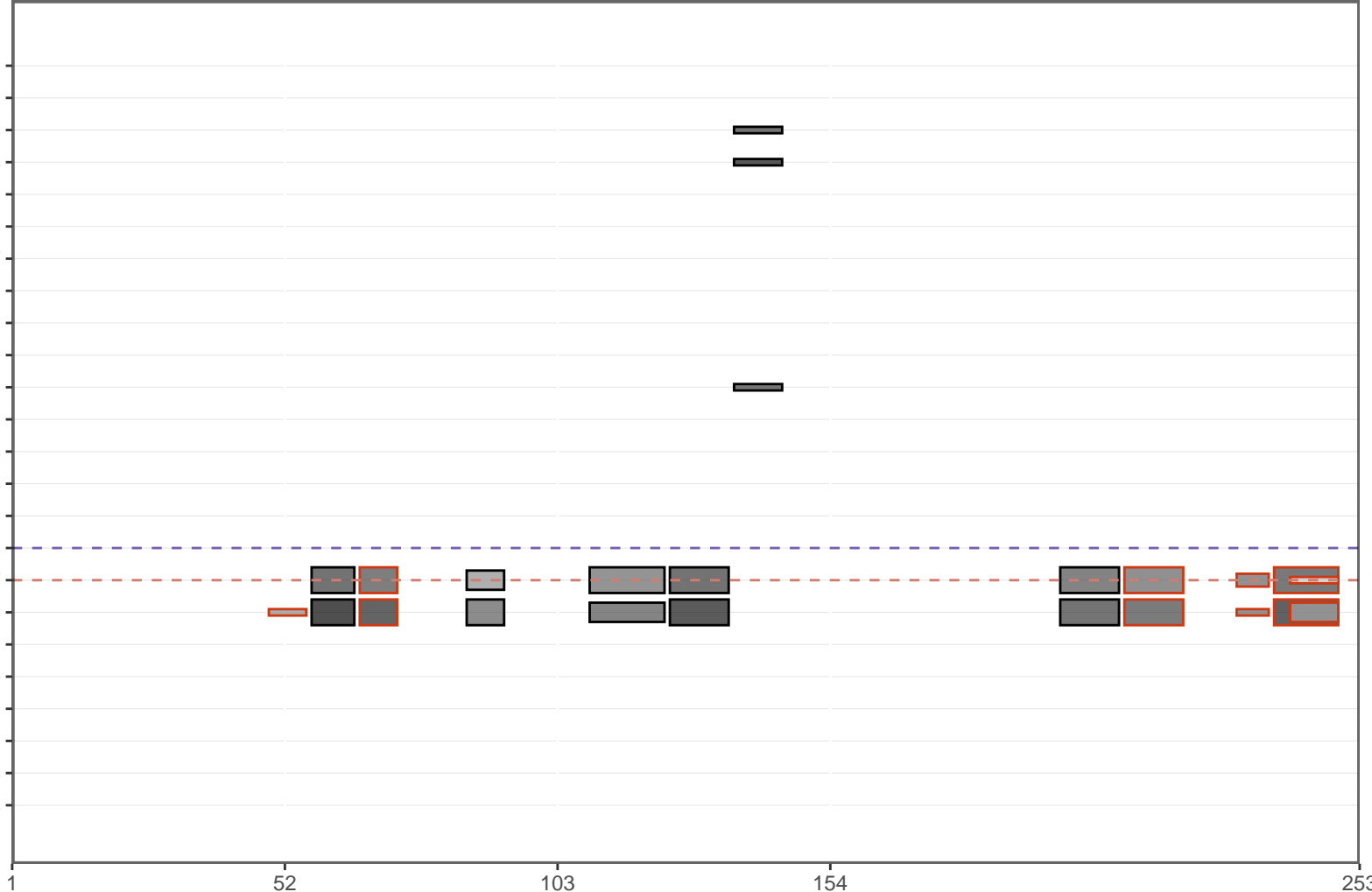
MW indication



Molecular weight

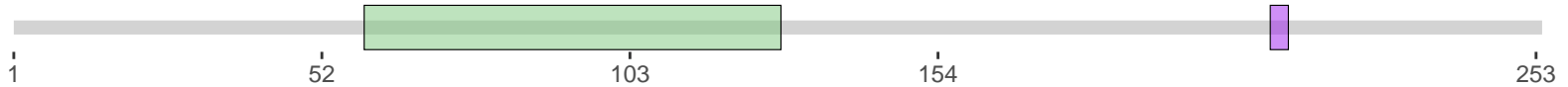


Gel Slice



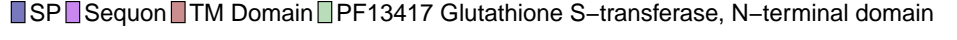
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VITQALEEKFPQPPNFTTPEKASVGSKIFPKFVFLKSKDPDGTGEGELLDLTAFDYKENGPFINANEVSAADLGLGPKLYHLEALGHYKWNVSPDSEFYKSKVYKMSIFRSRESFINTRALKEDVLEGWPKVMG

NbL05g19790.1 NADH_dehydrogenase_[ubiquinone]_iron-sulfur_protein_1_mitochondrial [MW = 84.82 kDa]

No. of times detected



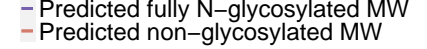
log(intensity)



Values from



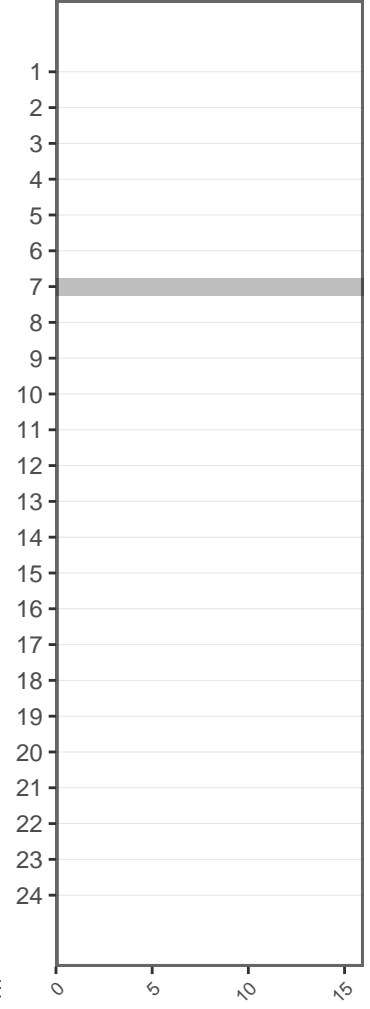
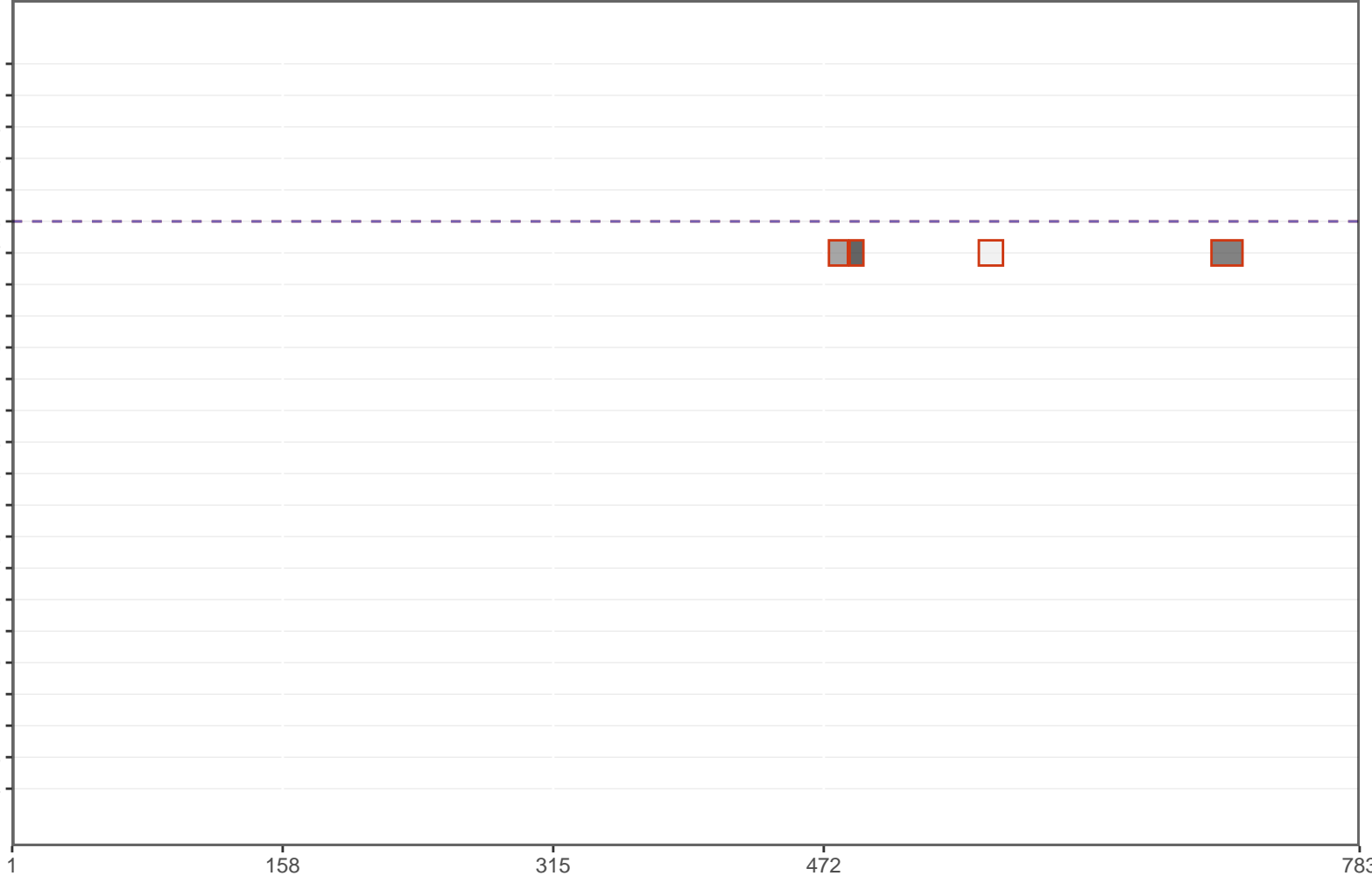
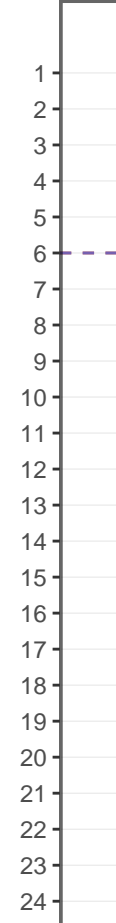
MW indication



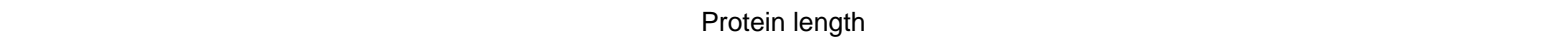
Molecular weight



Gel Slice

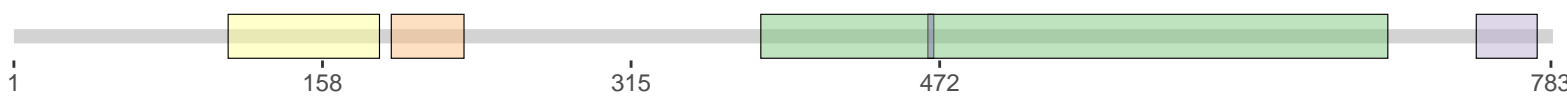


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

- SP
- TM Domain
- PF09326 NADH-ubiquinone oxidoreductase subunit G, C-terminal
- PF13510 2Fe-2S iron-sulfur cluster binding domain
- Sequon
- PF00384 Molybdopterin oxidoreductase
- PF10588 NADH-ubiquinone oxidoreductase-G iron-sulfur binding region

Protein sequence:

RQRLNDPMIRGADGRFKAVSWRDALAIWAEVMHQKPEEIVGVAGKLSDAESMMALKDLELNKMGSGNPFCEGNGMPPNADLRGVMNTSISGLEKADAFLLVGTQPRVEAAMNARIRKTVRANNAKGVYGAADFNVDHQHLGTDPTGLVEIAEGRIHFSSALKNAKNPVIVGAGVDFREKIDVFAAIDTAKNNNVVRSDWNGNLLNLLNAAGAAALDLGLVPESEKIDSAKFIYLMGADDVLSLKLKPDPAFVYVQGHGDRGVYRANVLRPSAFTEKEGIYNT

NbL05g19760.1 NADH-cytochrome_b5_reductase-like_protein [MW = 36.15 kDa]

No. of times detected



log(intensity)



Values from



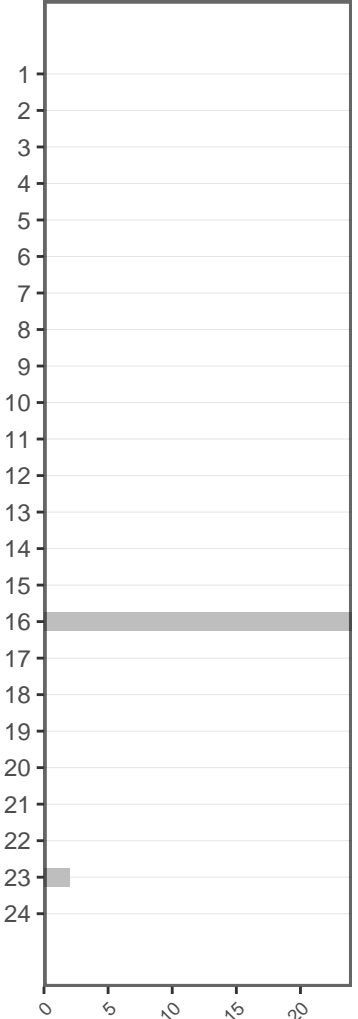
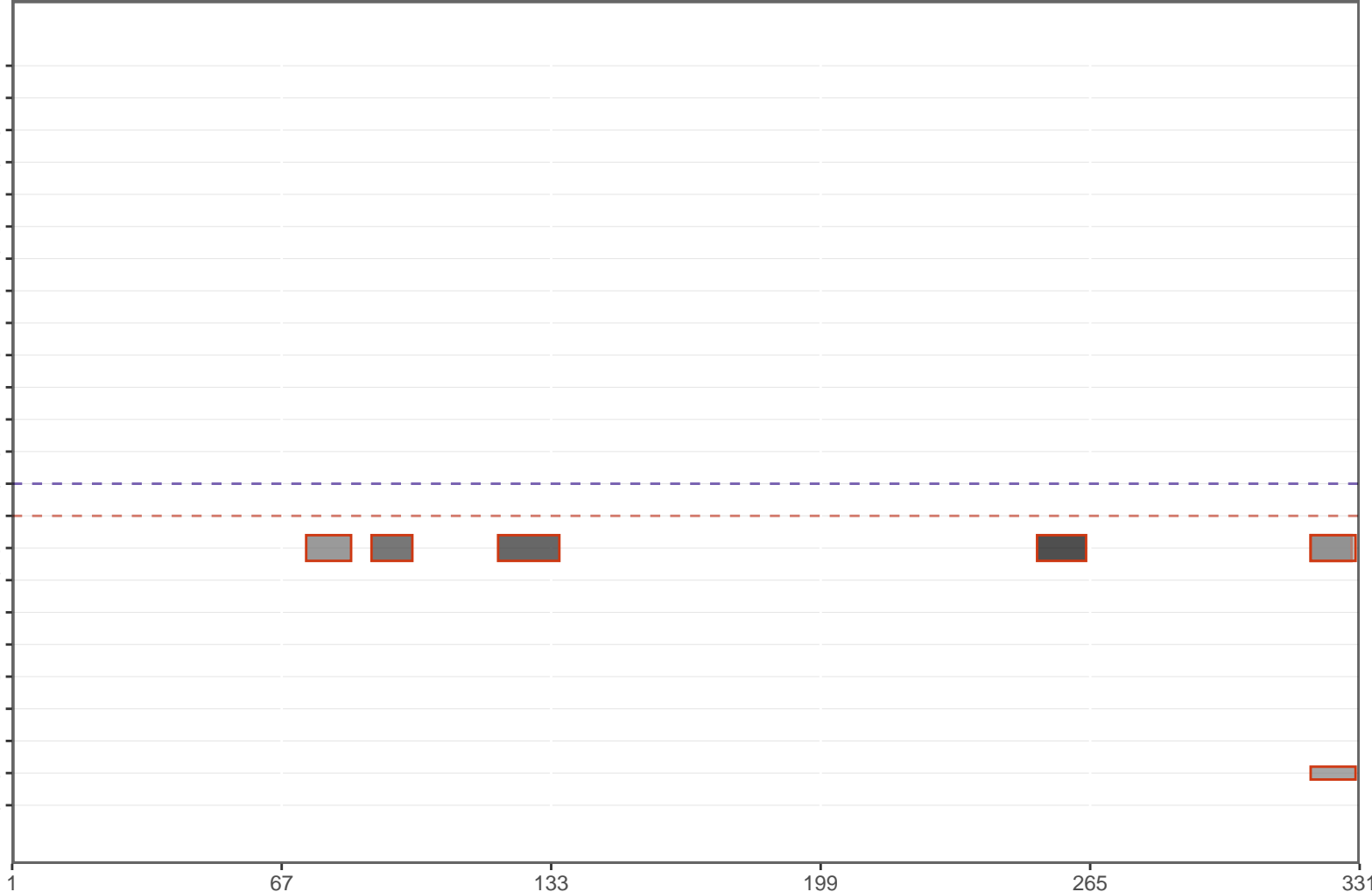
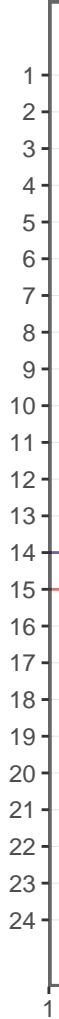
MW indication



Molecular weight



Gel Slice

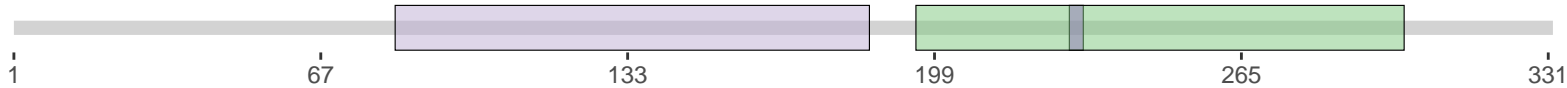


Peptide counts over 4 repeats

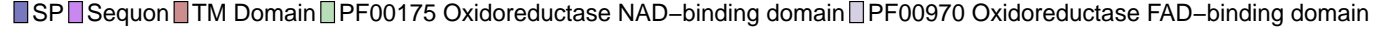
Protein length



Pfam domains



Pfam Description



Protein sequence:

LKIVYFEGKMSQHFASLKPQGVLEKVGPIEKLRYSSTNMKKHGMAGSGGFTPLMGVHEALKNFDDNTQVSLVWVNSPDDLLKKKLDVLAATHPLKVFYTVDSPTNDWRGGIGYVSKDMIKGLPPSSDSTLILVCGPPMMKHLSGEKPKPREGGELTGLLKDVGFTENMVKF-

NbL05g19660.1 UPF0678_fatty_acid-binding_protein-like_protein_At1g79260 [MW = 18.46 kDa]

No. of times detected



log(intensity)



Values from



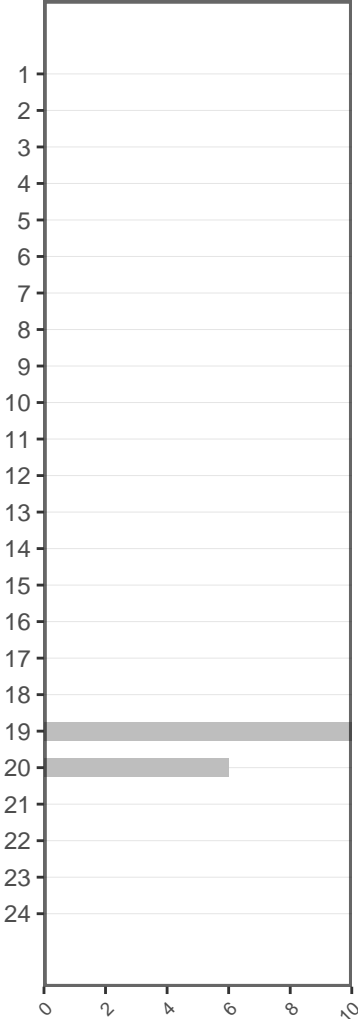
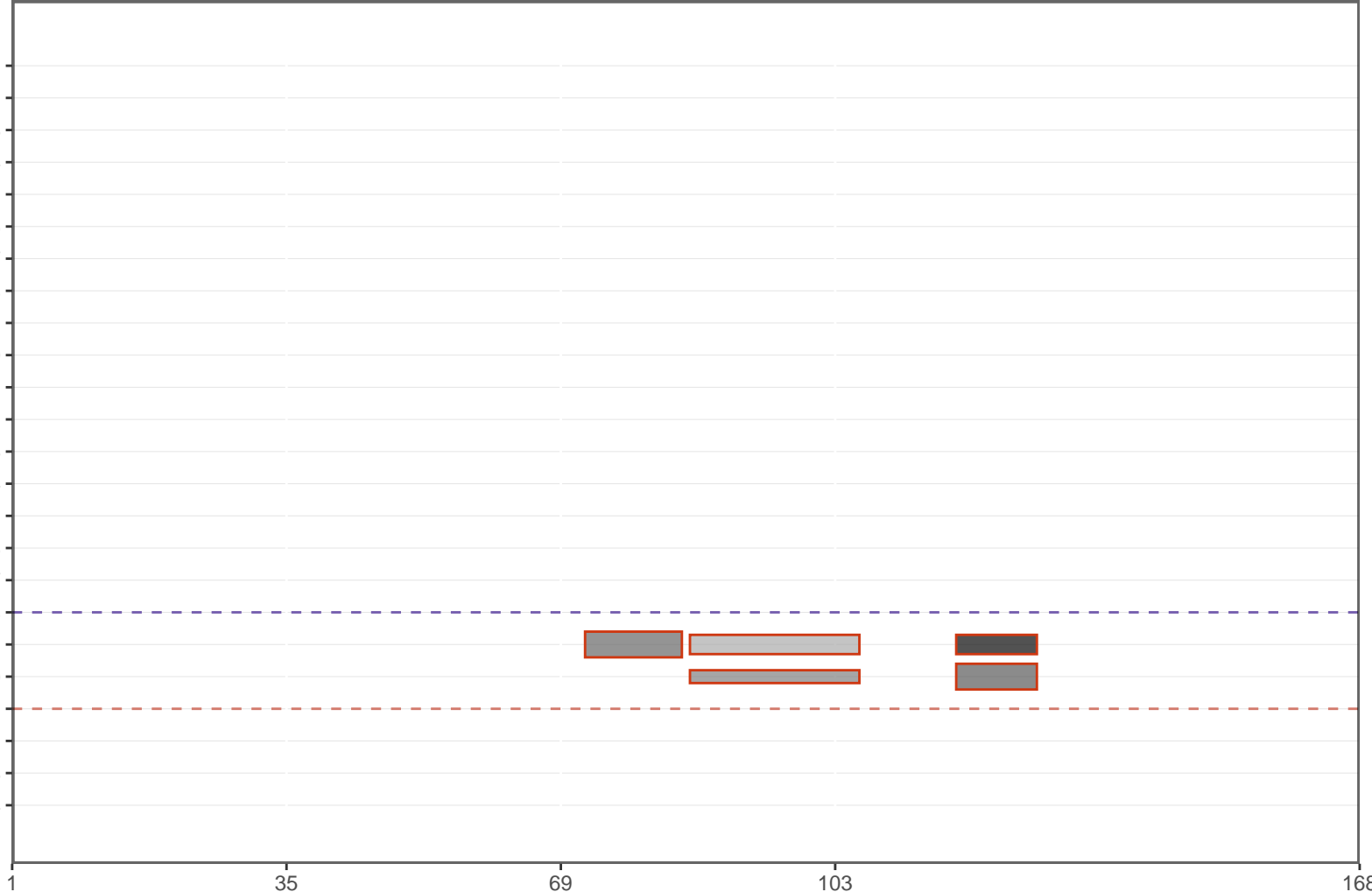
MW indication



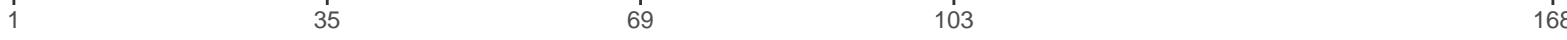
Molecular weight



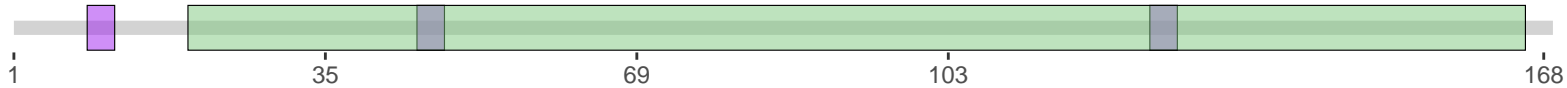
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

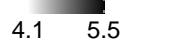
MSGGPMMISESGYWRPKPDGTIEAVADSTGLVEVGKGTVDMKEGVVKLSBELVGNASKVKEISRFVKVENSLSYVVEMATSLGLGPHLAKSLKL*

NbL05g19610.1 glutamine_synthetase [MW = 39.08 kDa]

No. of times detected



log(intensity)



Values from



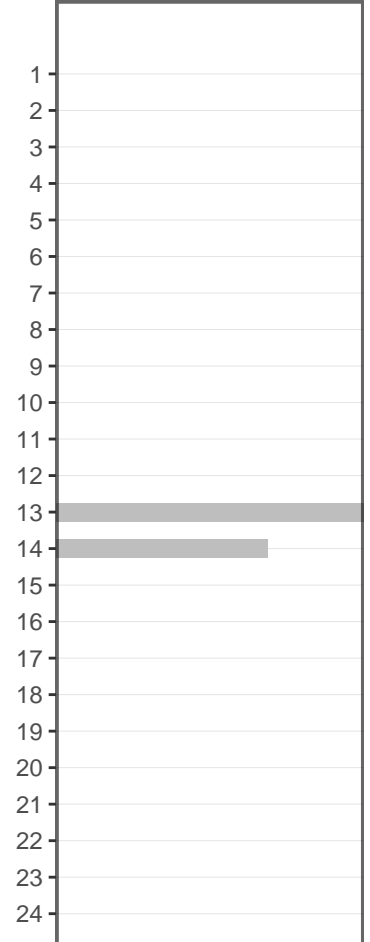
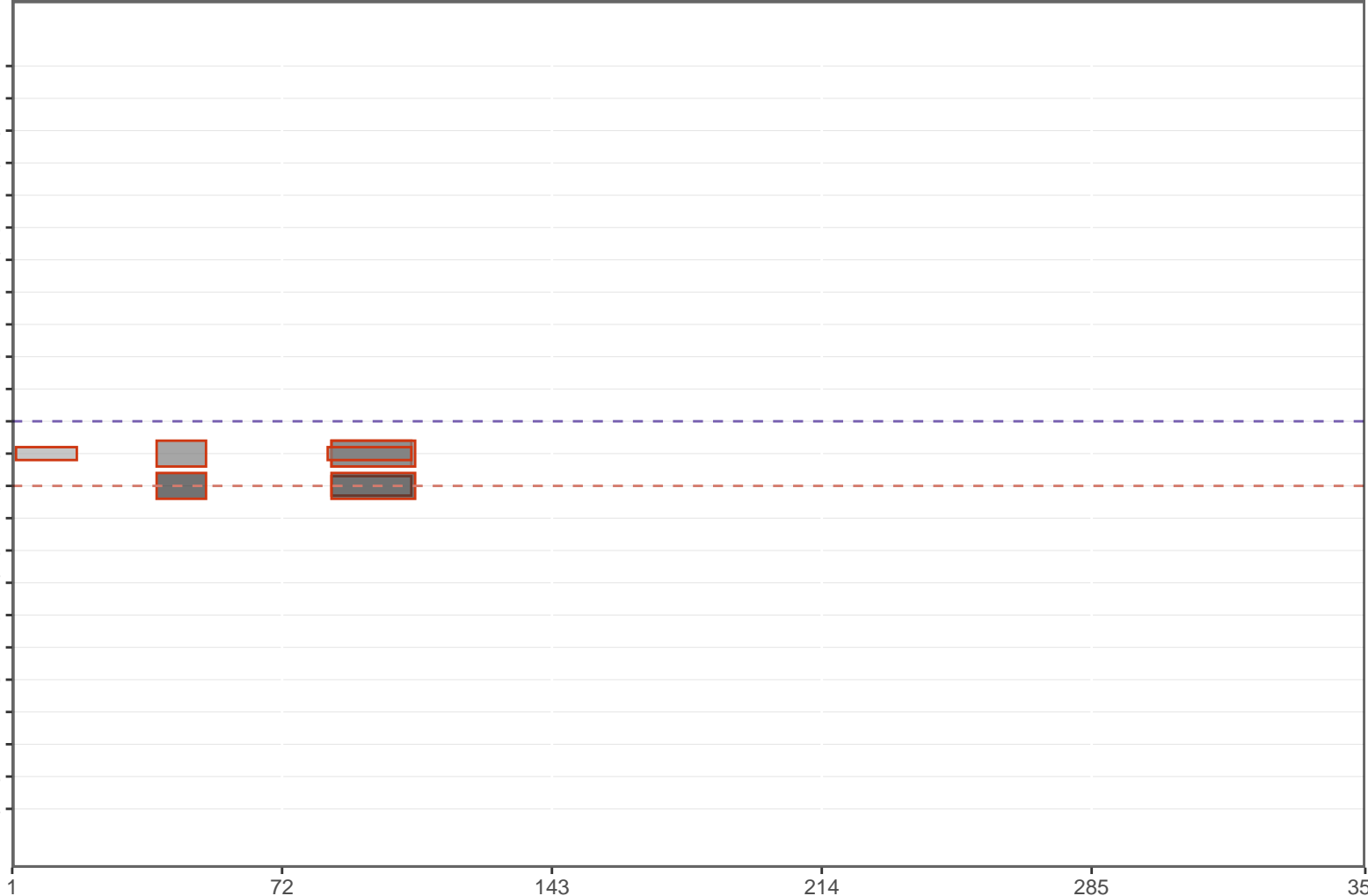
MW indication



Molecular weight

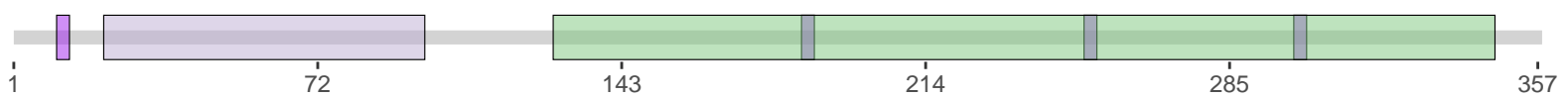


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

MFGRDIDSHYKAGLVAGINSGINGEVMFGQWFEFGVSPVSGISAGDEWVWRYVLERITEAGVVVFDPKPIPDQWNGAGAHNTNYSTKEMREDGGVEVLKAEKLGKHKHEAAVYEGEENRRLTGKHETANISTFKWGWANRGAASVRYVGRDTEKAGKGYFEDRRRASNMDPFWVTAMIAETTRWKP

NbL05g19390.1 peptidyl-prolyl_cis-trans_isomerase_CYP19-3-like [MW = 18.82 kDa]

No. of times detected



log(intensity)



Values from



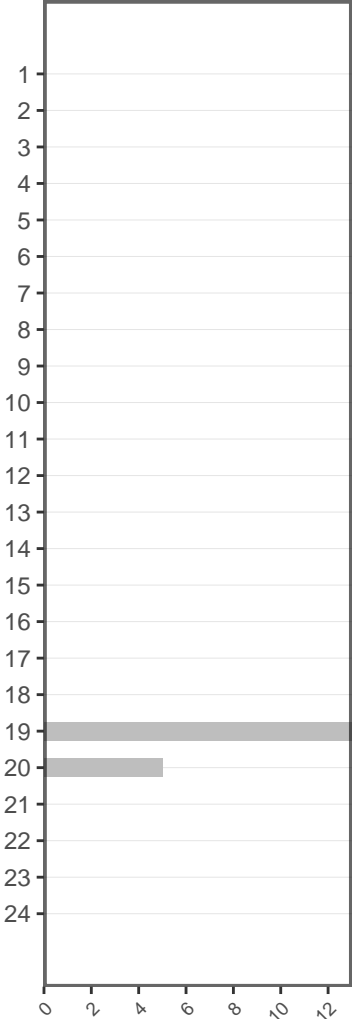
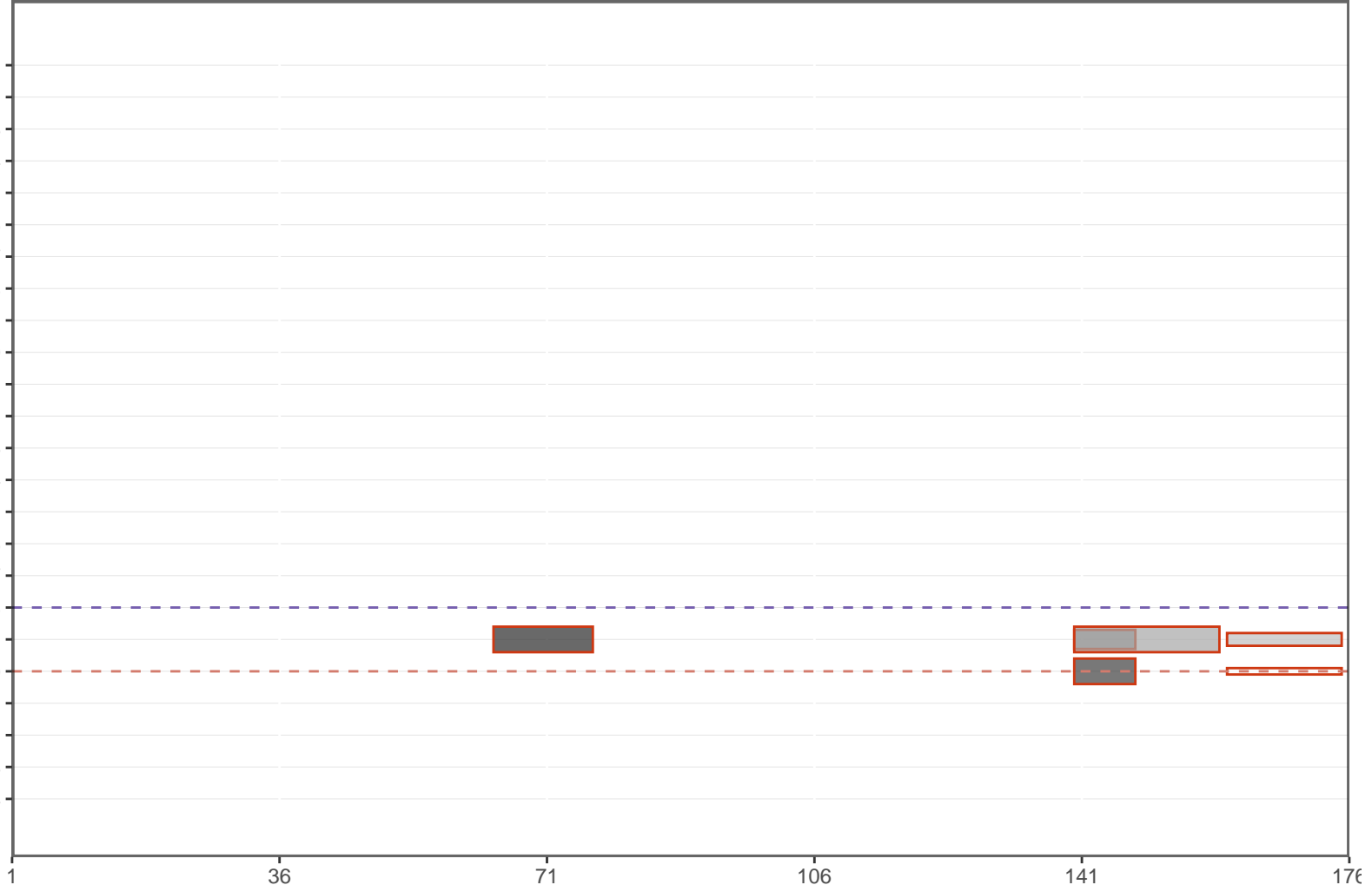
MW indication



Molecular weight

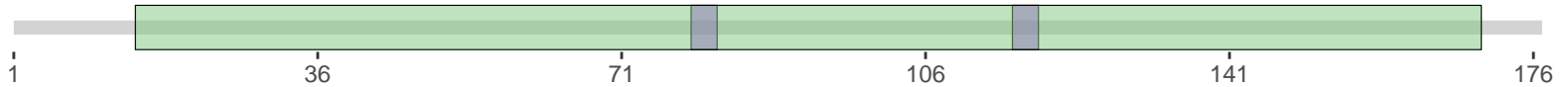


Gel Slice



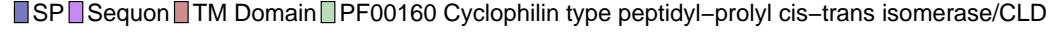
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKNGTGGESISYGAKFAEDFSVHITPGLLSMANAGPNTNGSOFITTPWLDGKHVFGKVDGYSVVKEMENVGSDSGKTSCTVSEIDCGELKEN

NbL05g19120.1 probable_pectinesterase/pectinesterase_inhibitor_51 [MW = 63.84 kDa]

No. of times detected



log(intensity)



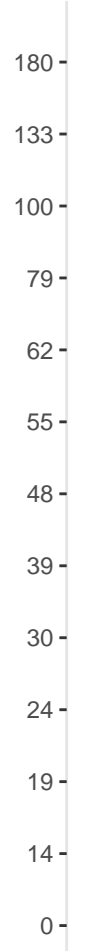
Values from



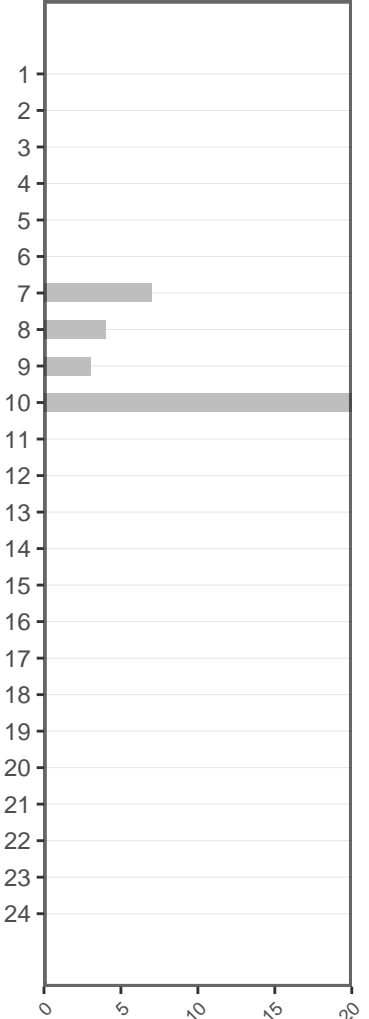
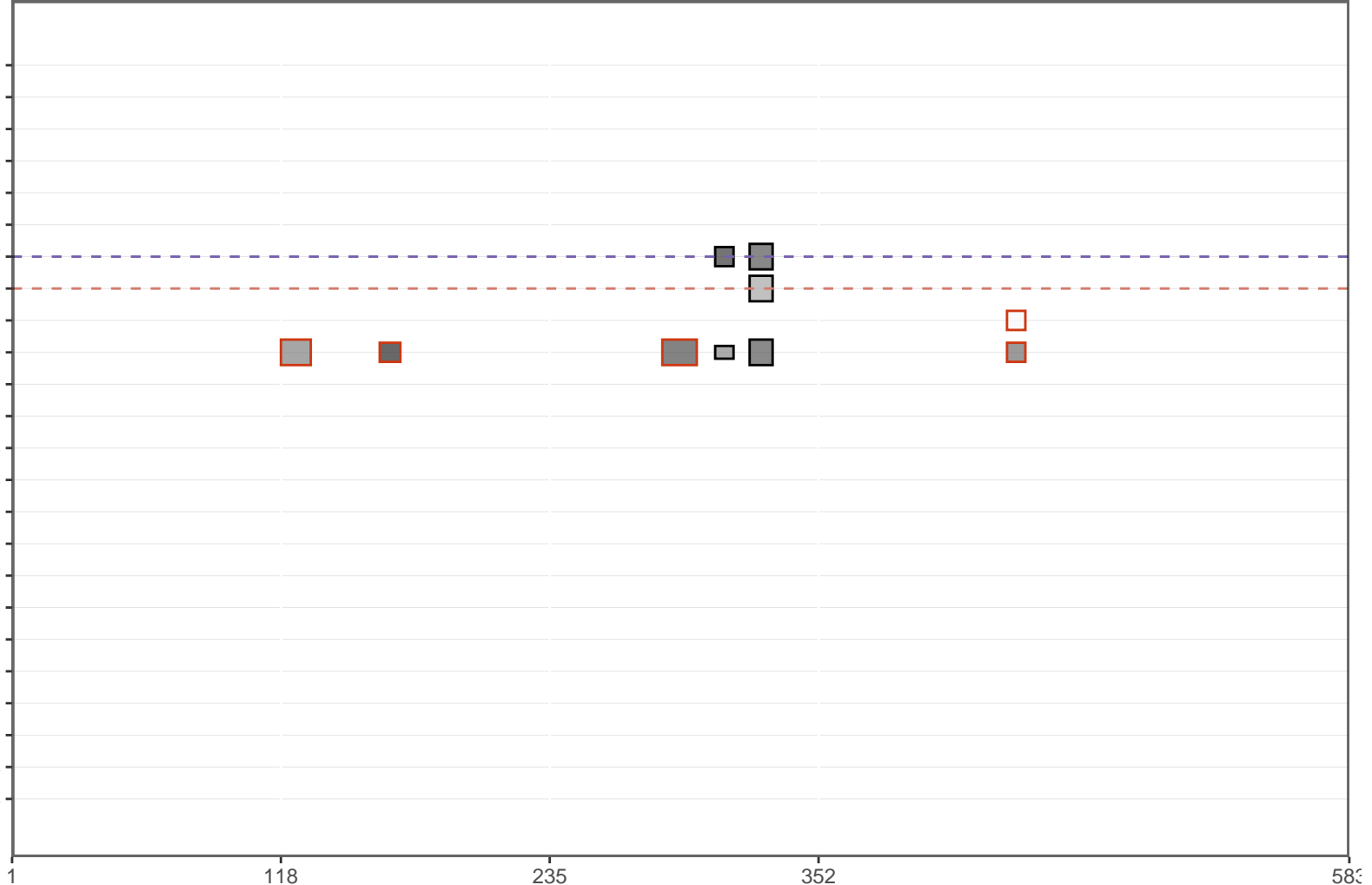
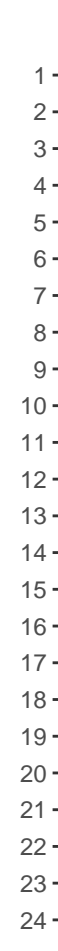
MW indication



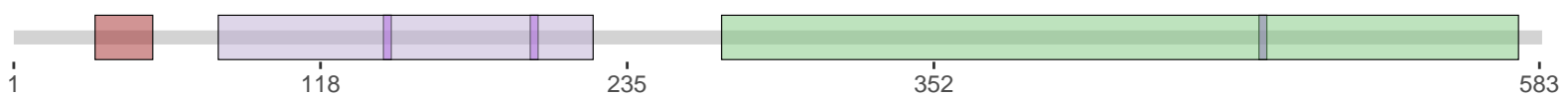
Molecular weight



Gel Slice

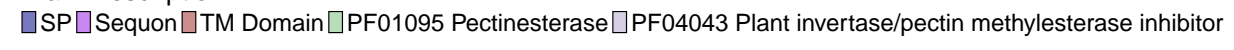


1 118 235 352 583



Pfam domains

Pfam Description



Protein sequence:

DDYKIVQEA/N/A/AFDNGLTRKRFVWIKAGLYDEIVRVPPEKKNV/VFLDGMGKTYITGSLVSGINGINTYETATVGVAGDGFMASGMTFQNTAGANANQAVAFRSDSDLSIENCFEMGNGDTYVHTLRGVYKSGRIQGNVDFIFGNSAFAFRDGDILAPRQLLPEEGETNPVTAHGRIGDAGTGFVFGNGLNGTDKYMALYKKNPEVHKNYLGRPWKEYSRTVFRQCTLDALVSADGWLFWVNGDFALSTLYVGEVYRNTGAGANTAGRVPWSSQIPGEIYVNSYSLQNFQI

NbL05g19110.1 probable_pectinesterase/pectinesterase_inhibitor_51 [MW = 61.51 kDa]

No. of times detected



log(intensity)



Values from



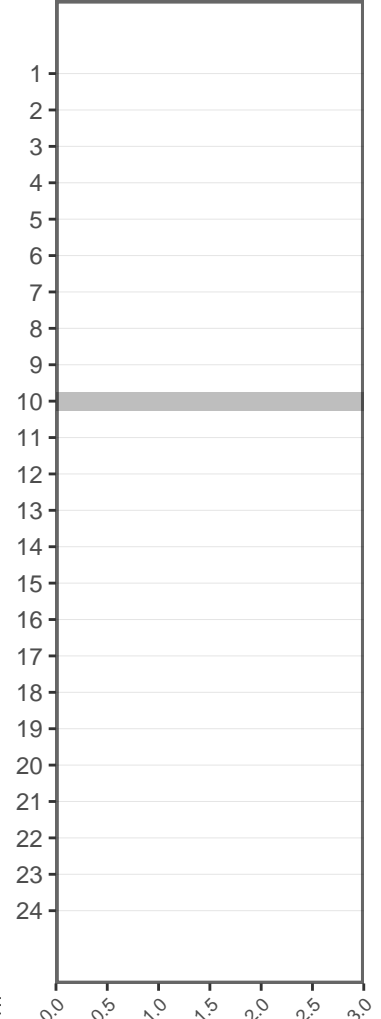
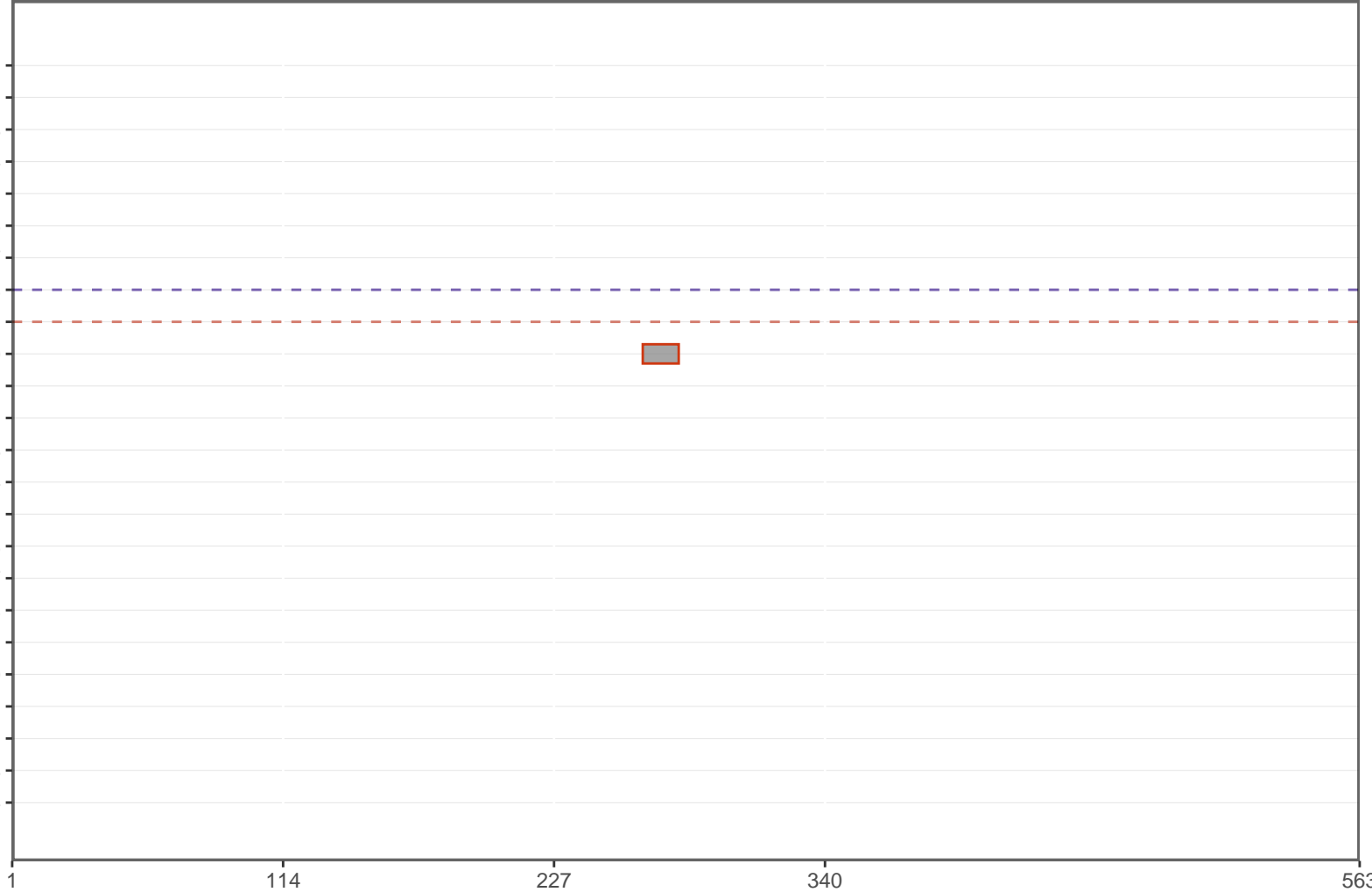
MW indication



Molecular weight

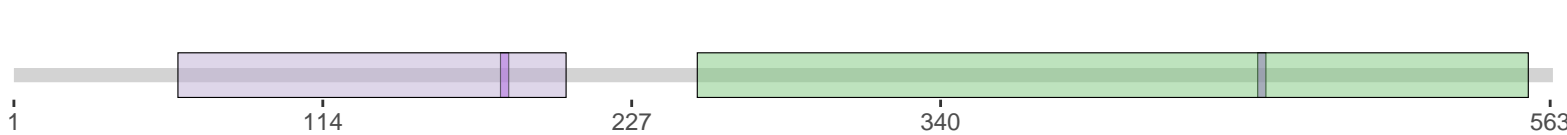


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IAVNAAPDNQVTRKPEVWIKAGLYEEKLVLPLEKNNVFLGDDGDKTFTVGBLNVGMAGVITYTETATVGVVGDGFMASGTFONTGFPVAHQAWAFR6SDLSLVIEGEEFIGNDITVAHALRQVYFKSCRIGSNVDFIFGNSAAFFQEGEDIFAPRQVNPKEGKKNVATHGRIDPAQ6TGFVFNQNLNGTEQYMALYYKPKVHKVNLGRPWKEYSRITVFECTLEALVLDGWLFWISGDFALKTLVYGEYRNTFGAGANTAGRQW6SQIPAEHNSYKSNFQSDQWTT

NbL05g19090.1 probable_pectinesterase/pectinesterase_inhibitor_51 [MW – SP = 55.98 kDa]

No. of times detected



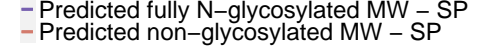
log(intensity)



Values from



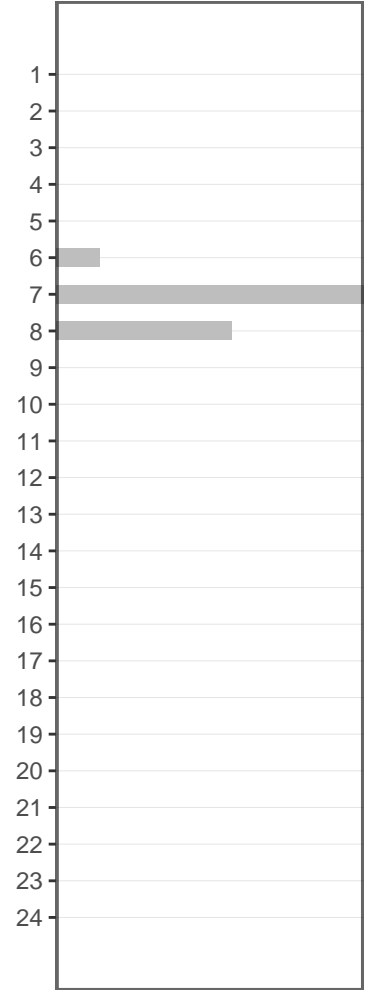
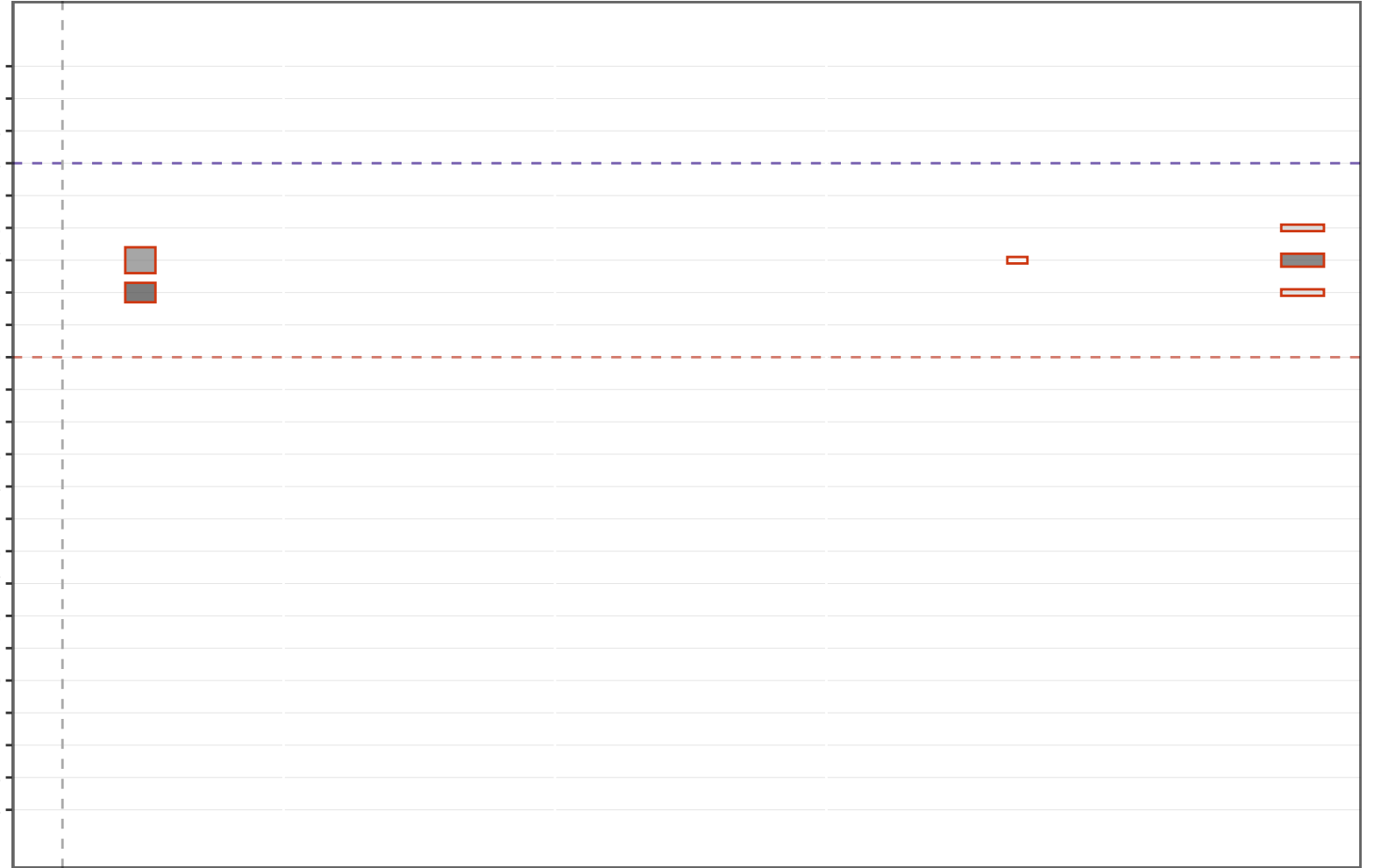
MW indication



Molecular weight



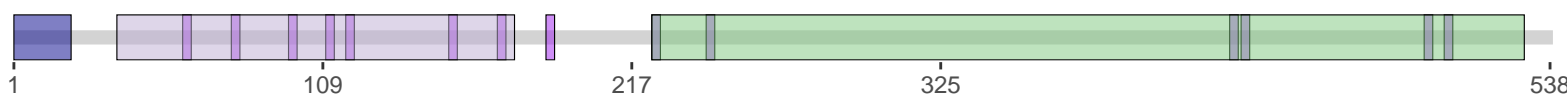
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKAGLYDEIVRYVPLEKRNIVFLGDGDKTKVTIGSLVGLVPLGMMTTEYEGATVGVSGDGFMASGLTKQNTAGIDAGDAVAFRSDGDLSEIQNCEFLSNGDITLYTQSLRQYVKSCKRIGNVDFIFGNAAAFQDGNLVAPELLNPEKGEKNAVTAHGRLDIPGGSTGVYFQNGSINGTEEYMTLHFNPKVHRSFLGRPKWEYGRVYFINSLELVNISEGVMPPWNGEFALATLVYGFENITGGGANITGRVTVSSGQPAEHNYSYKVNFIQGGKWPFPSCV

NbL05g18670.1 50S_ribosomal_protein_L15 [MW = 31.86 kDa]

No. of times detected



log(intensity)



Values from



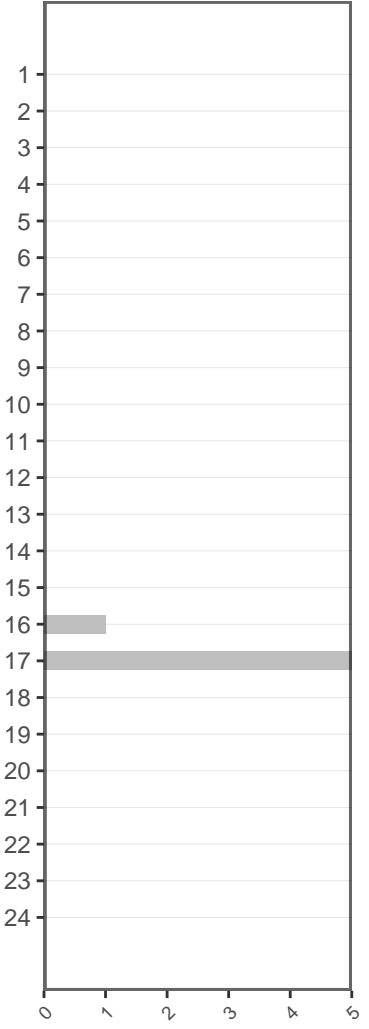
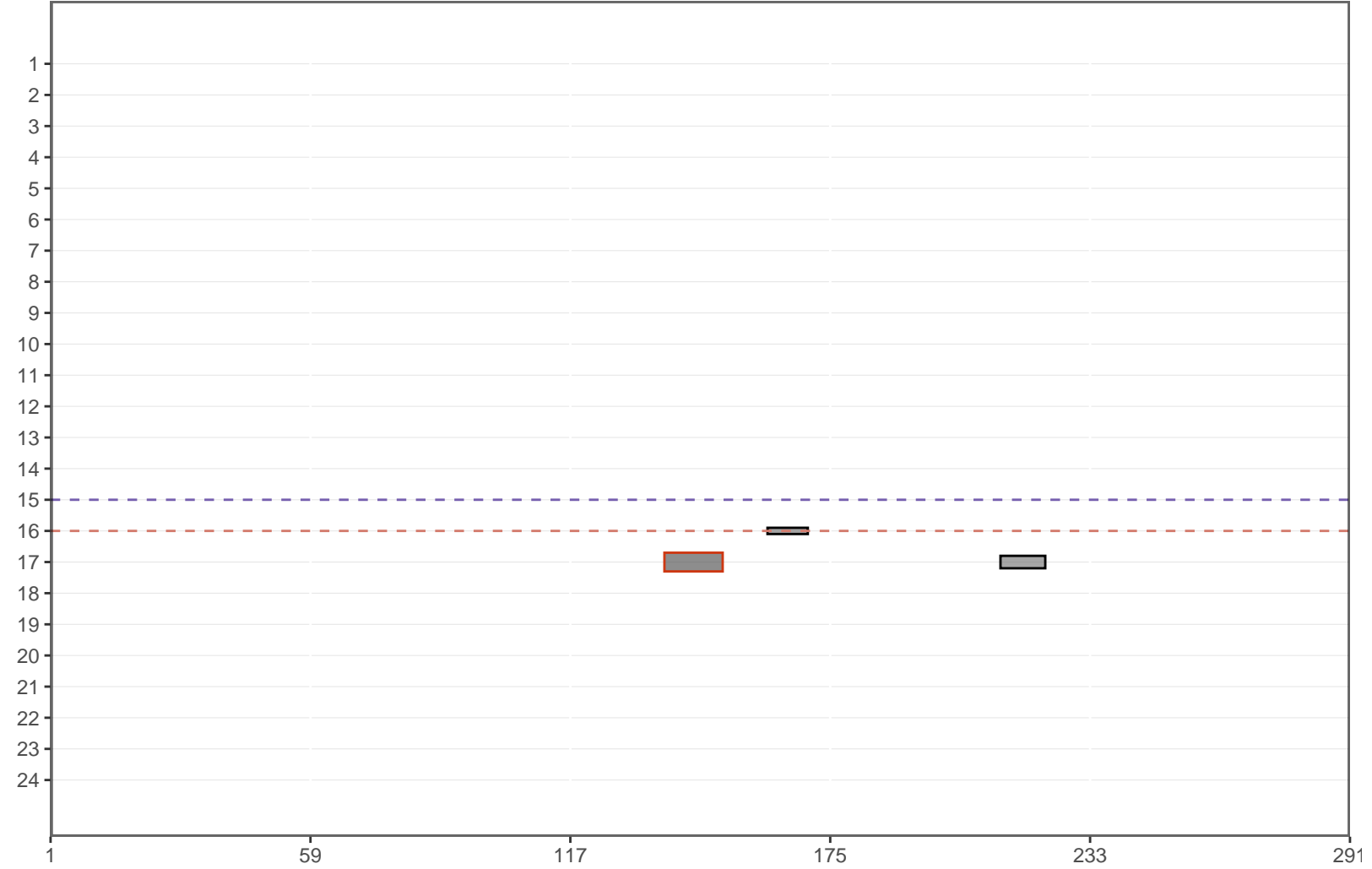
MW indication



Molecular weight

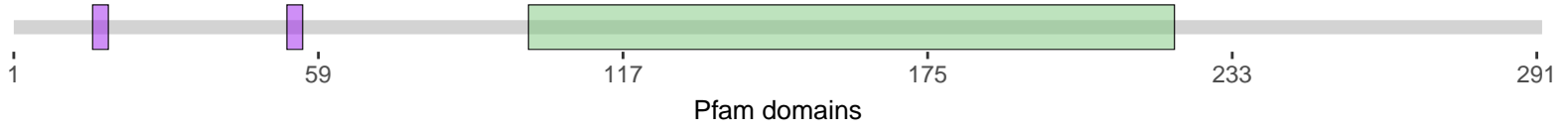


Gel Slice



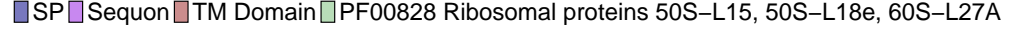
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PKRGRKQNFSLTGPVGLGKAKLNGKIDSSSEIFMKTLDKSAANGKGGDGVRLMGRGAEHQWPHLEVERVTVRAKAAVEAAGGSVRRVHYNKLGRLALKPEWFEKGRLLRPRAPPPKPKKEKVDGSLRPAFTKPIFAAEETEAMSAAPV

NbL05g18320.1 ycf3-interacting_protein_1_chloroplastic [MW = 33.92 kDa]

No. of times detected



log(intensity)



Values from



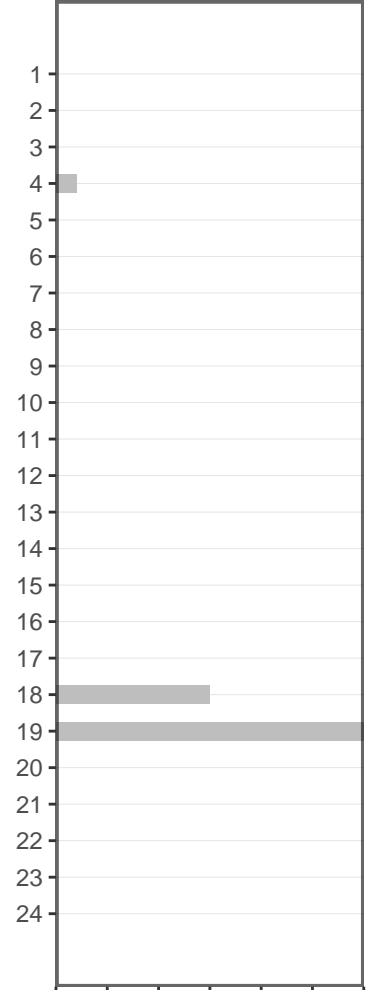
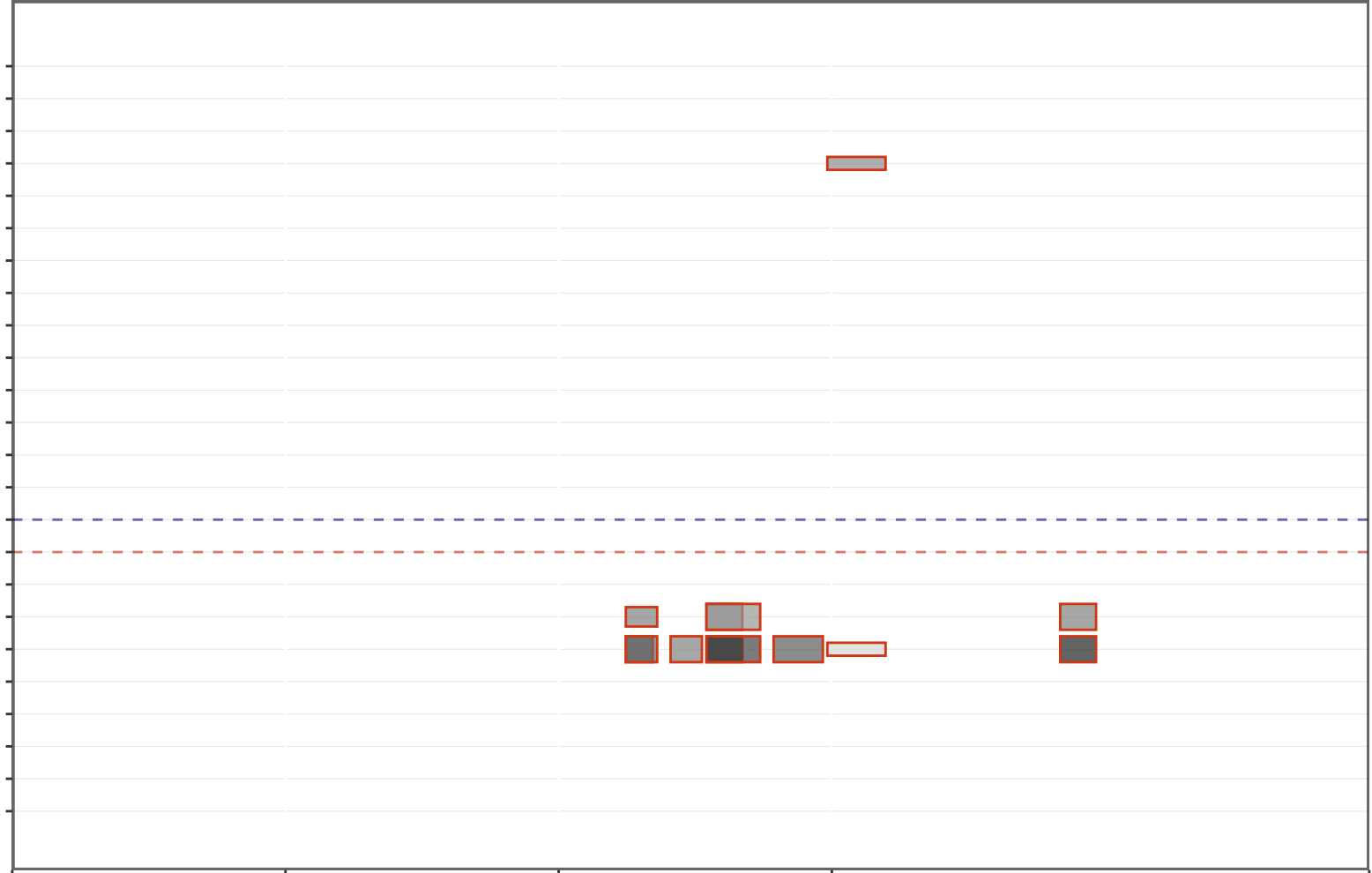
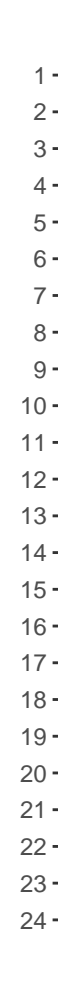
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

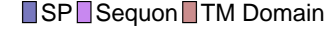
Protein length



Pfam domains



Pfam Description



Protein sequence:

ISVLELLKRNDRDMLFGEVKLTIMIEDPRDVERRRLLGIDDENAPTRDDLAALAEINEGKPKDFDALQMLAEEMNSWPNLEVEATKGNKGRBLVAKATDTGIDPKAAKRUKIDWDGAAEIDDSAGSDPEVPPALGYGALVLEAFPHIGIVVILFYNSLQ*

NbL05g18270.1 plasma_membrane-associated_cation-binding_protein_1-like [MW = 28.57 kDa]

No. of times detected



log(intensity)



Values from



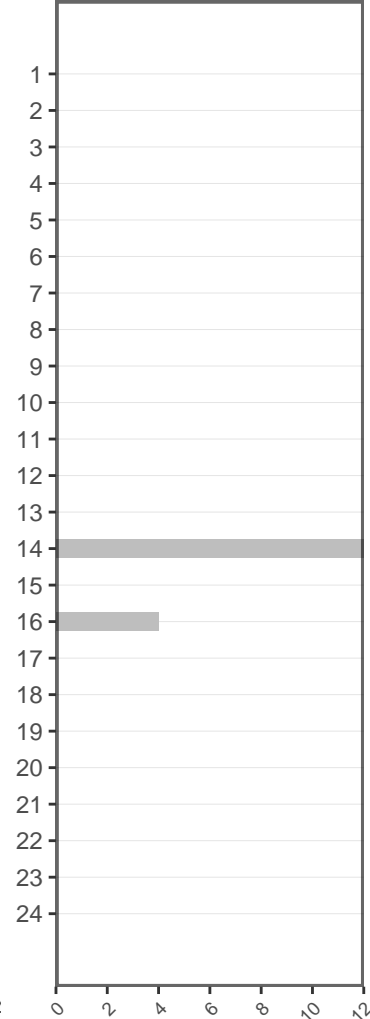
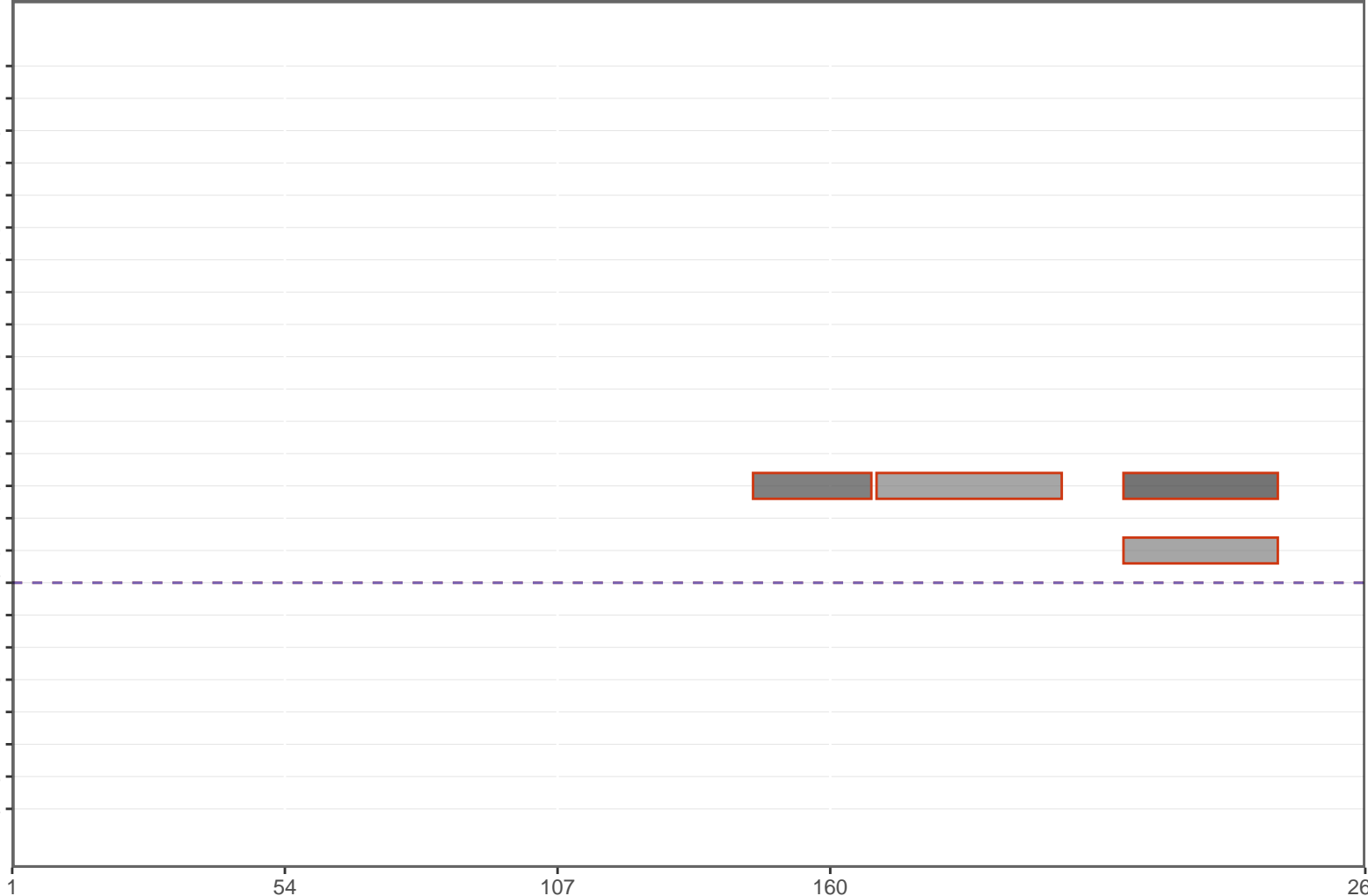
MW indication



Molecular weight



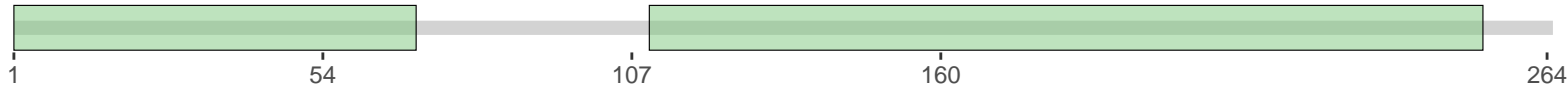
Gel Slice



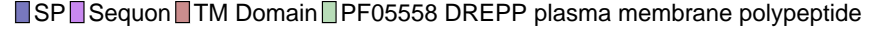
Protein length



Pfam domains



Pfam Description

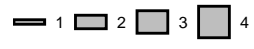


Protein sequence:

SLKXKSTGVQKFLDELWKEFPFGKAVSEASNFGRVYSGPFFVFEKSTFTVTEQKKEEAAAAAASASDAEATVTPVEVKEKEIVVEAEAKKKEEPAPAPAPAPAPAPAAAEVATAADAPAKVVEEAPAAVAAPEPKA

NbL05g18240.1 polyadenylate-binding_protein_RBP45-like [MW = 46.09 kDa]

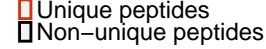
No. of times detected



log(intensity)



Values from



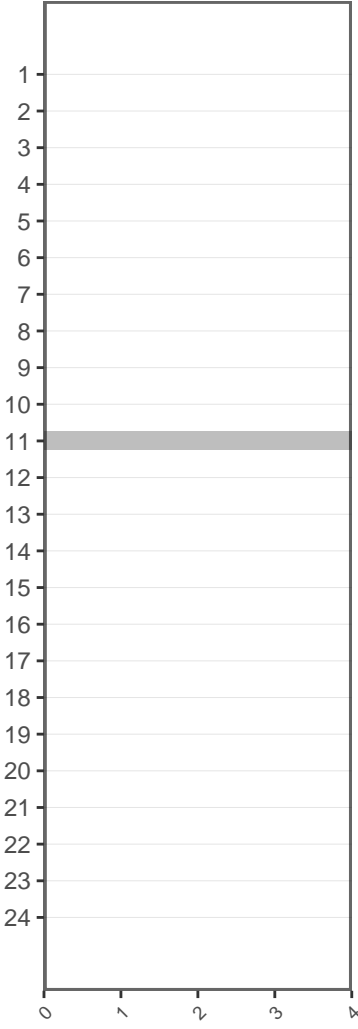
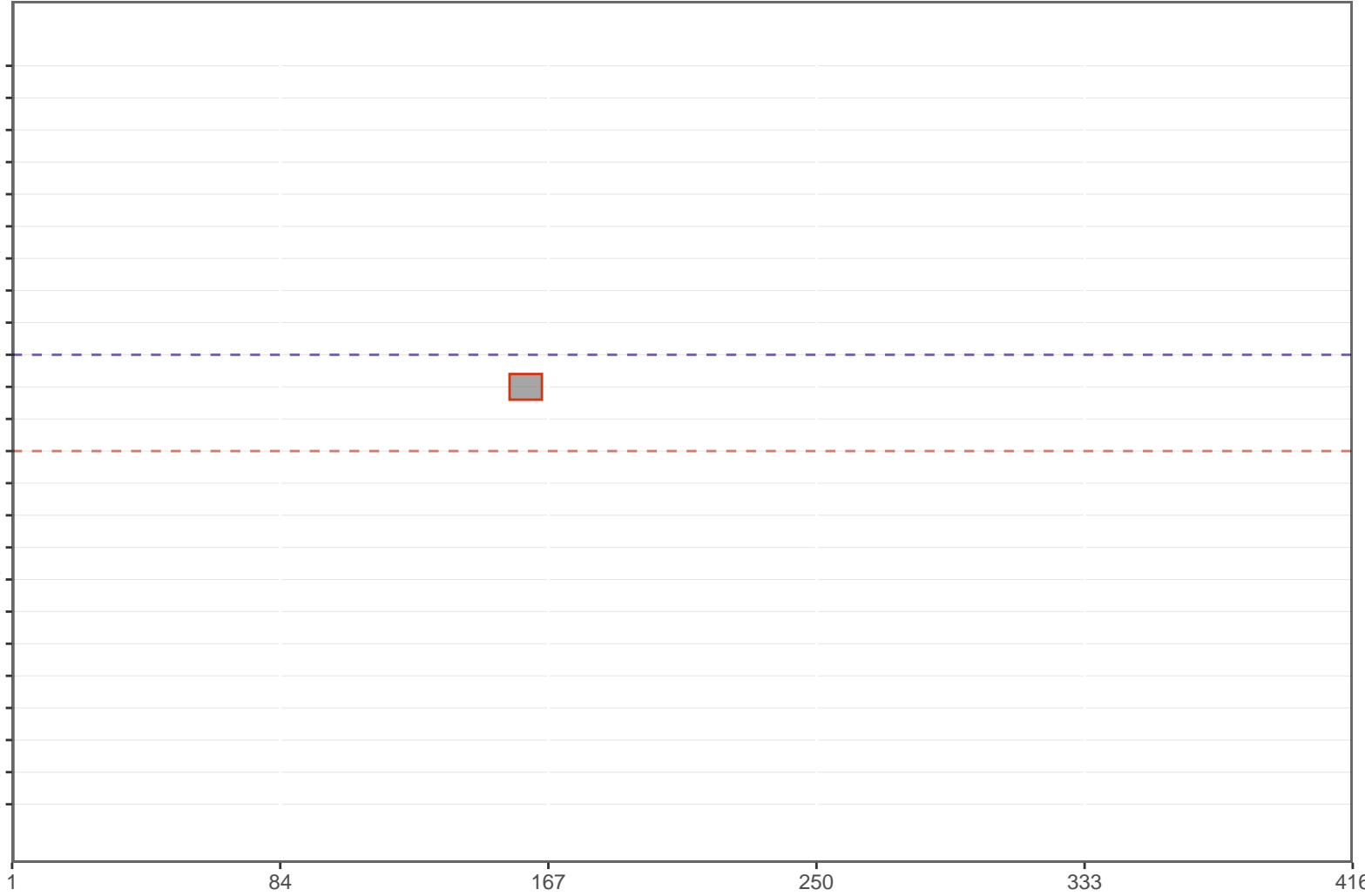
MW indication



Molecular weight

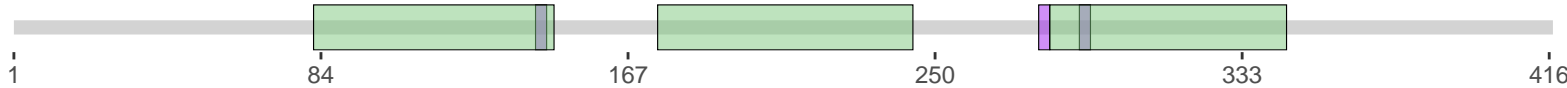


Gel Slice



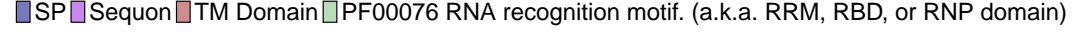
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LVNPSYKGAQYDTRATGHTKGYGFVRFQDESEQLRAIAEMNGKFGSTRPMRIGPANKKSGGGMDASVGTSLGTQNEDDPTNTTFVGNLDSNVTDDHLRQVGFHGGQLLHKVPIGKRCGFVGFSDRSCAEELRALSGTQLGGQSRILSWRSPNKKGGPQVDFNHYGGDYGYTTPGYEAYGWPPAGDPNMYAGYAGYGNVWAPPQQGGQMSGGPQ*

NbL05g18210.1 adenosine_deaminase-like_protein [MW = 40.69 kDa]

No. of times detected



log(intensity)



Values from



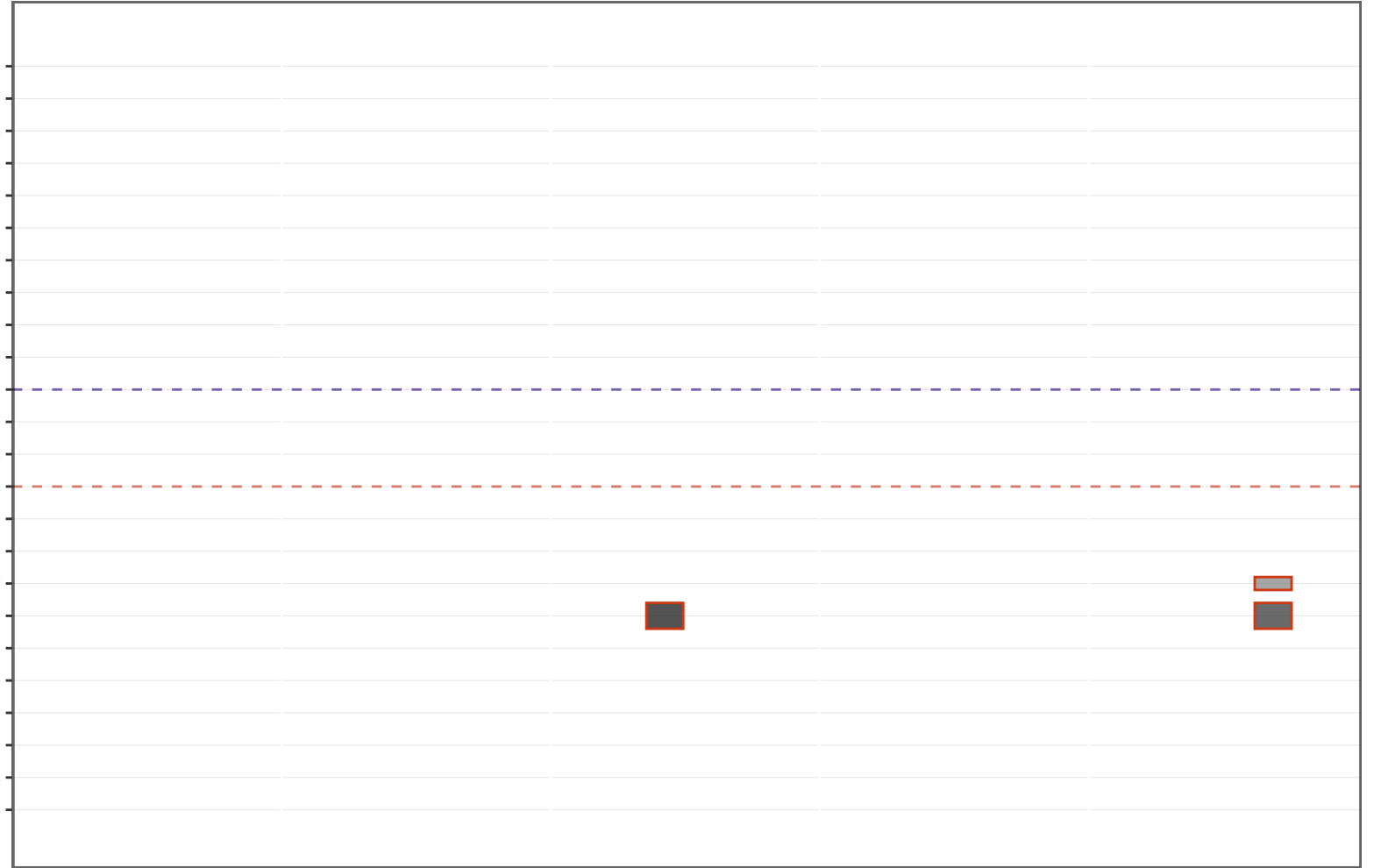
MW indication



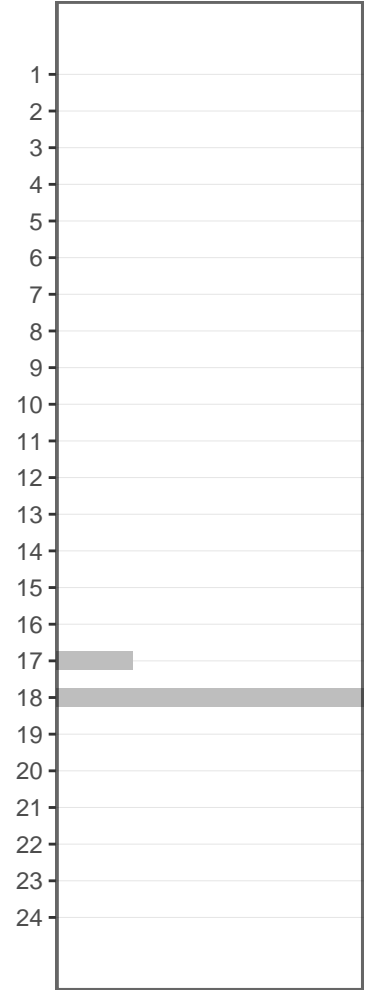
Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RRRESTESAMETVNLALEMRHKGVGIDLSGNPIGGEWITFLPFLFAFEKGGLLFLRHGQEVNPNPVEIHAMLSFLPMRIGHADCGFEEEWANKLGLKIPVEIGLTSNIRRTETSSLDIHFADLYNSGHPVVLCTDDSDGVTFTSVSGEYSLAASAFGQIKREMFQIARSGINFIAGDKVYKQEELEGFLDLAAKGLFP

NbL05g18030.1 uncharacterized_LOC109207523 [MW = 15.6 kDa]

No. of times detected



log(intensity)



Values from



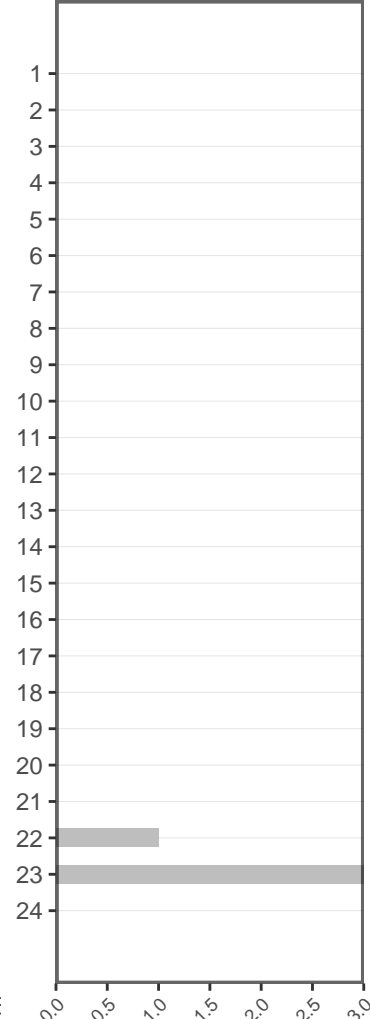
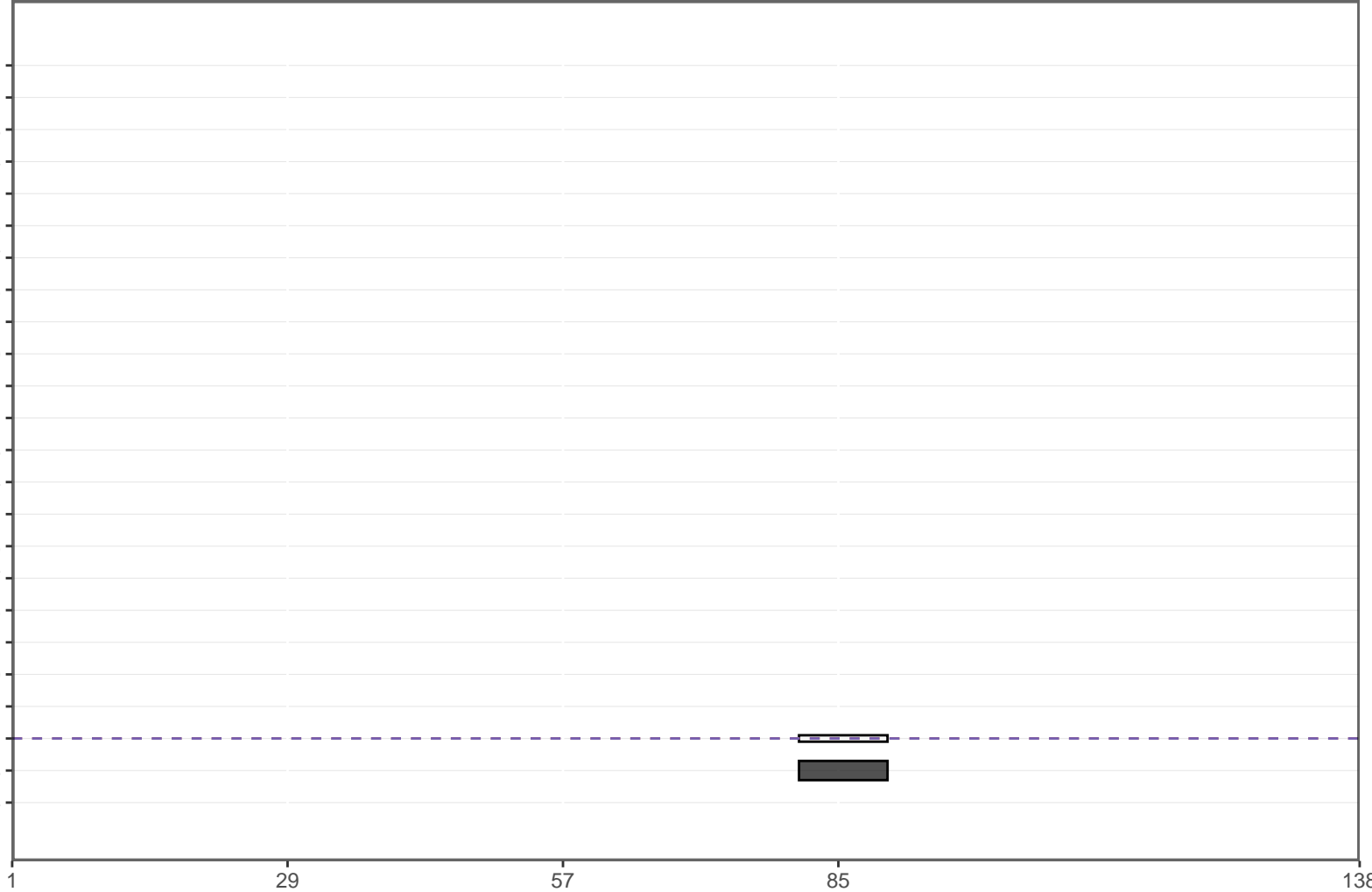
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

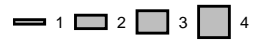


Protein sequence:

RSFLTLEAGLVEVSGLSTHERFLQRTISGLNLRVAEQEGCSIEELNAGRVCDFLKDILKREQNLSEAVLQWDEGDFLL

NbL05g17590.1 nudix_hydrolase_15_mitochondrial [MW = 33.98 kDa]

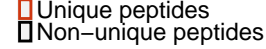
No. of times detected



log(intensity)



Values from



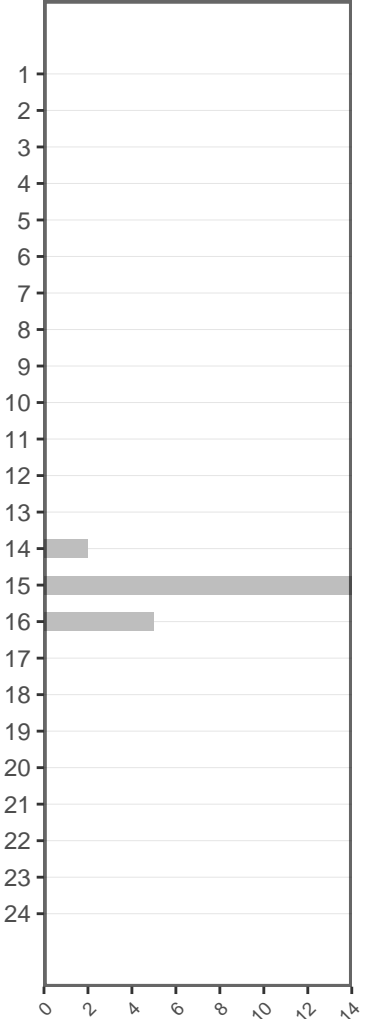
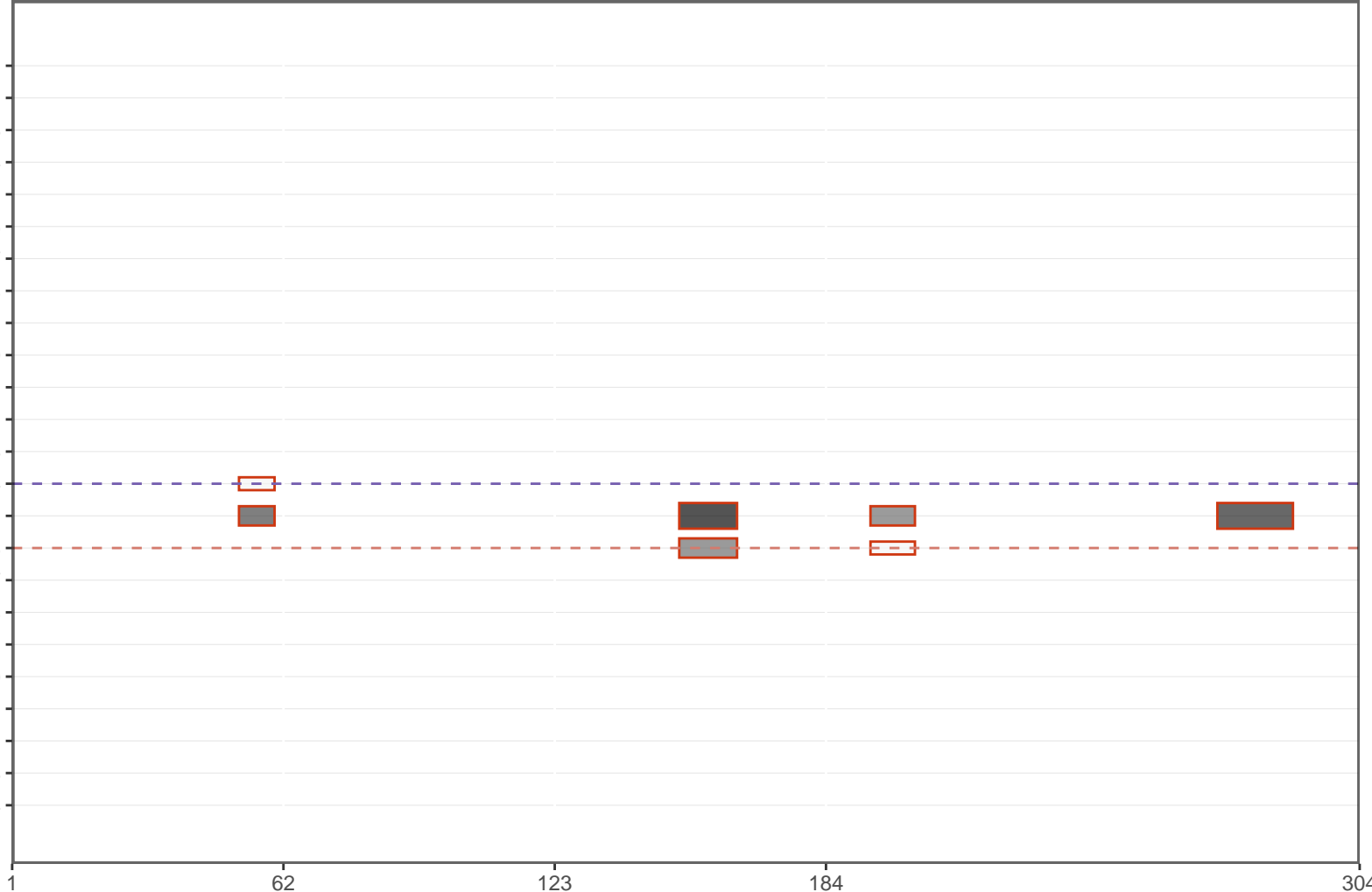
MW indication



Molecular weight

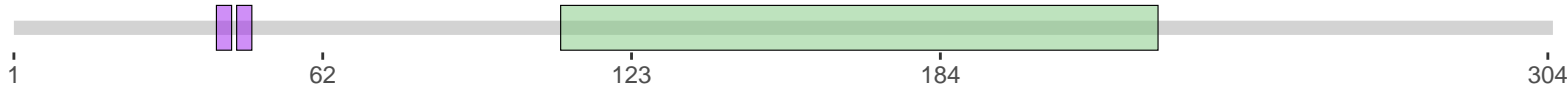


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

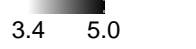
THSGEVALPGGKAEEGGASDADTATREAKEIEGLDPSLNVITOLEPFLSKHLRVPVIGLSEKFKFNPTPIAIEVEAVFDVPLAMFLKDNRRBEEREMWGEKYLHLFDYELDNKKYLWGLTAGLIRAAASVYQRRPAFLGQPKFKLPKVVQKDTTMS

NbL05g17570.1 magnesium-chelatase_subunit_ChII_chloroplastic [MW = 46.43 kDa]

No. of times detected



log(intensity)



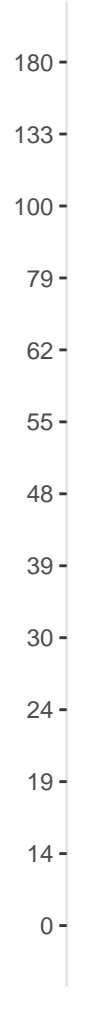
Values from



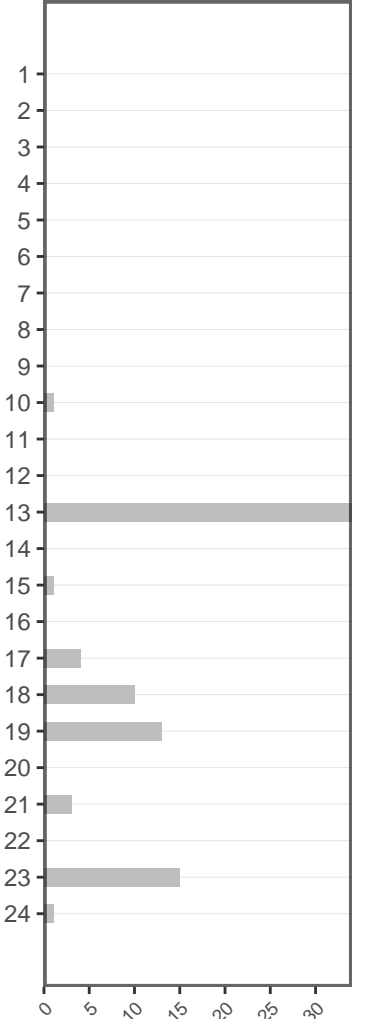
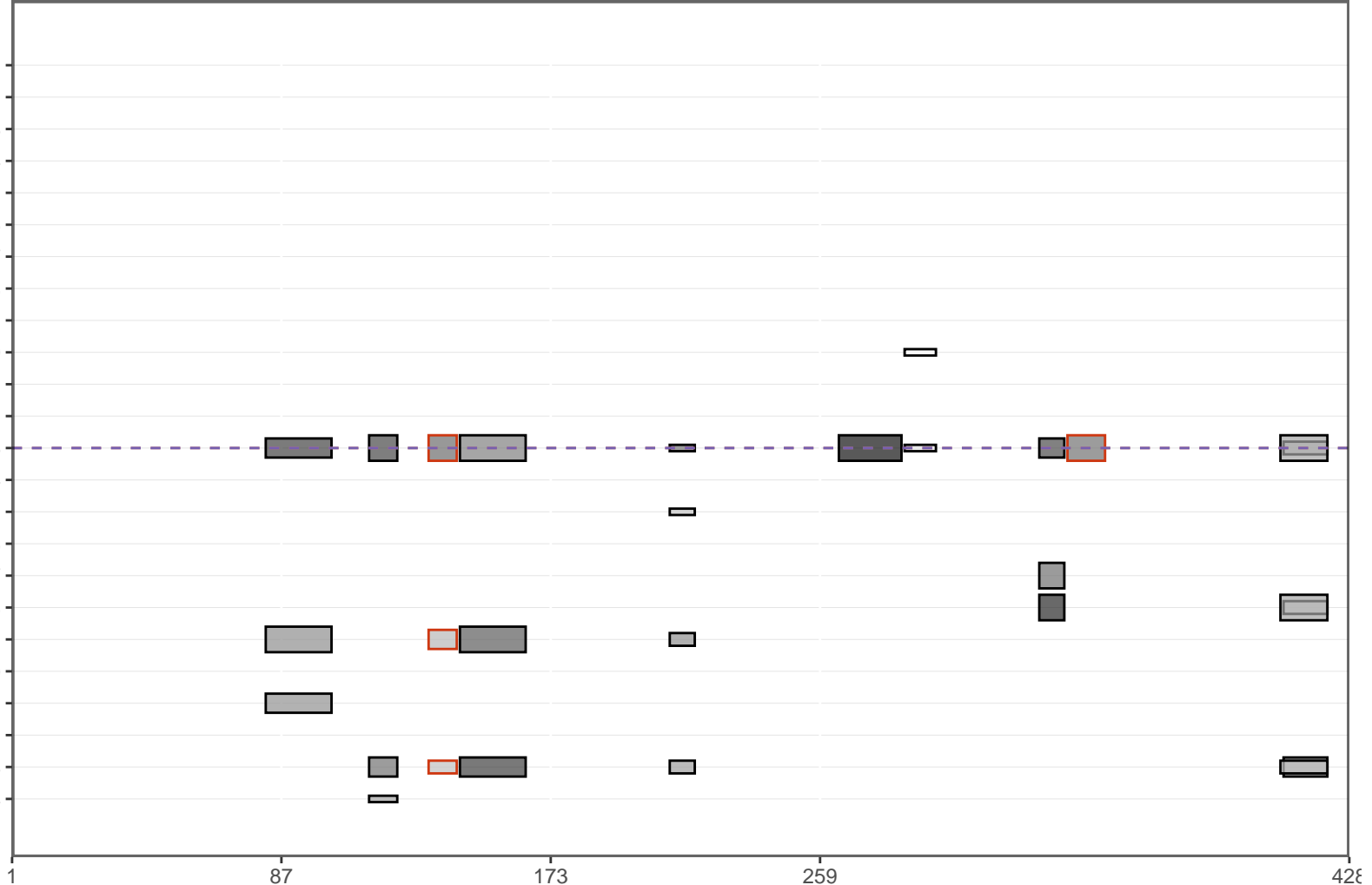
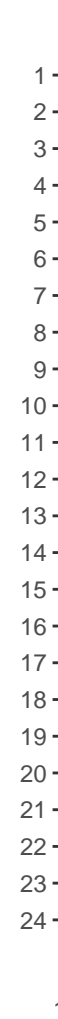
MW indication



Molecular weight

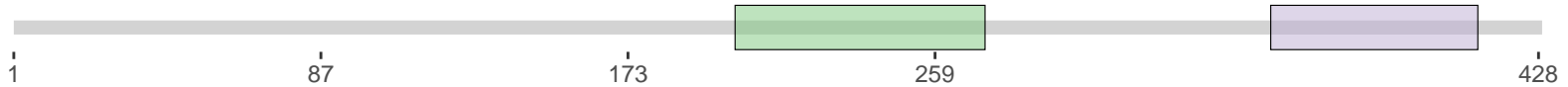


Gel Slice



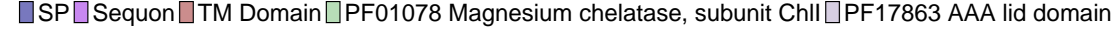
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEKALTEGVKAFEPGLLAKANRGLVYDEVLLDDHIVDALLDSAAAGWNTVEREGISHPARFLIGSGNPEEGLRPOLLDRFGMHAGVGTVDALRVRKIVVEERARFDKPKKFRFESYKAEQELGNQIDSRNALSAVTTAHLRVRKIKVKCAELNVDGLRGDVTNRRAARALAAKGRDKVTPREDATVFNGLRHLRKRKPLRESIDGGVLLVEKFEYVFAI

NbL05g17520.1 malonyl-coenzyme:anthocyanin_5-O-glucoside-6"-O-malonyltransferase-like [MW = 50.68 kDa]

No. of times detected



log(intensity)



Values from



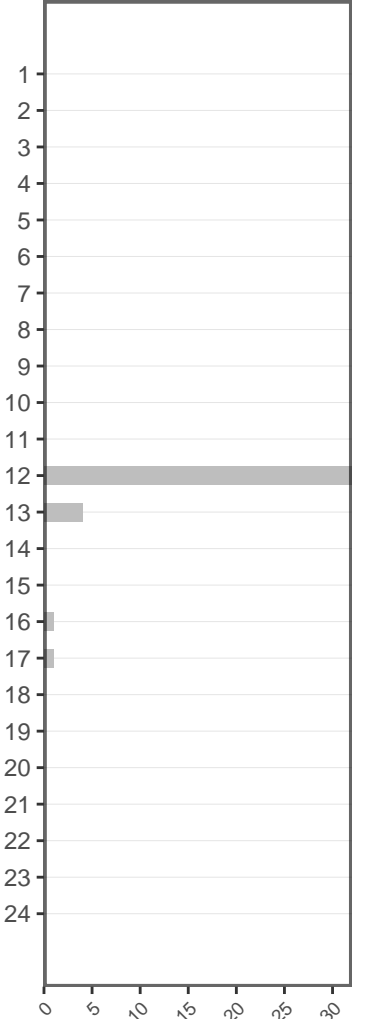
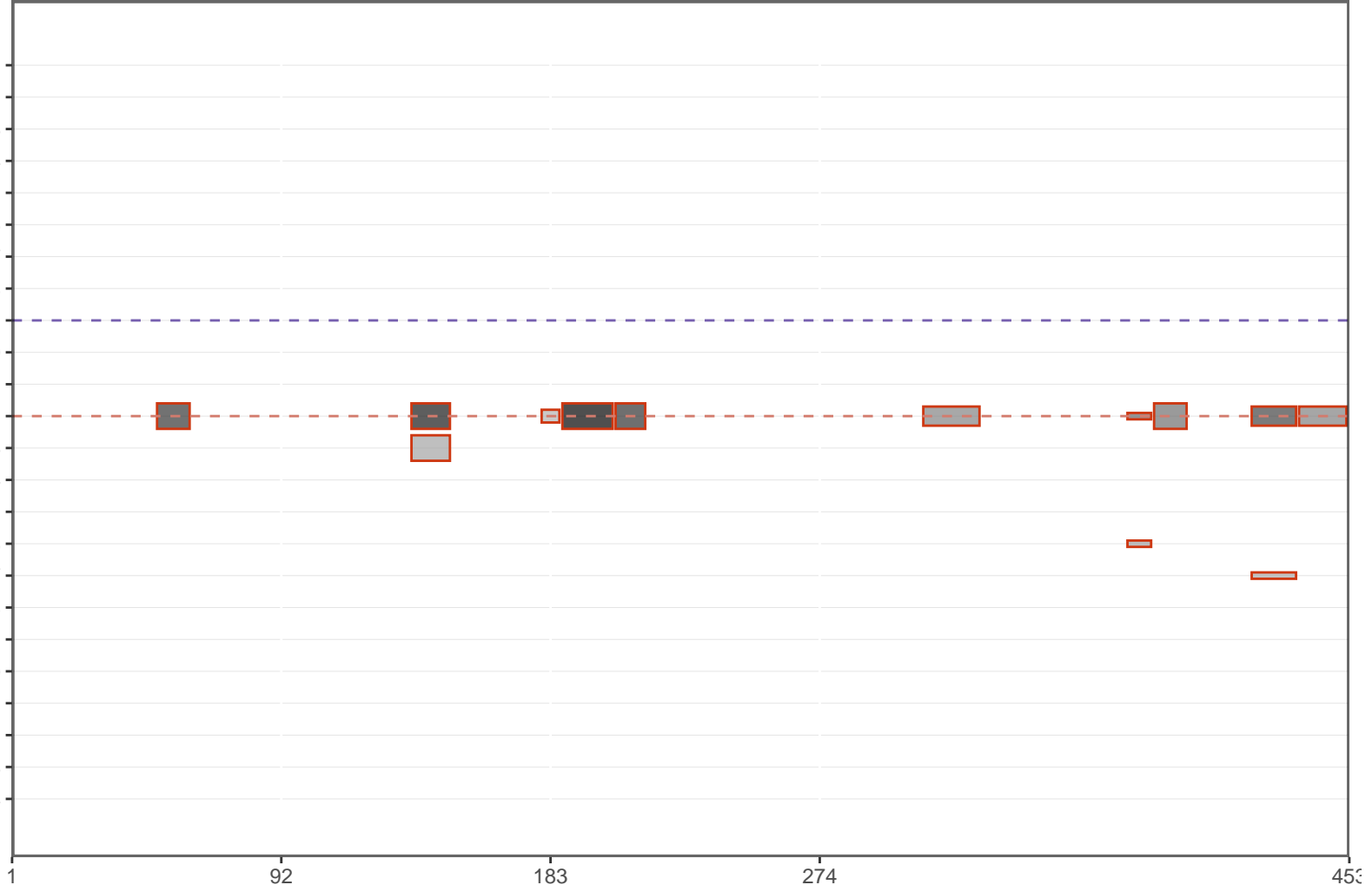
MW indication



Molecular weight

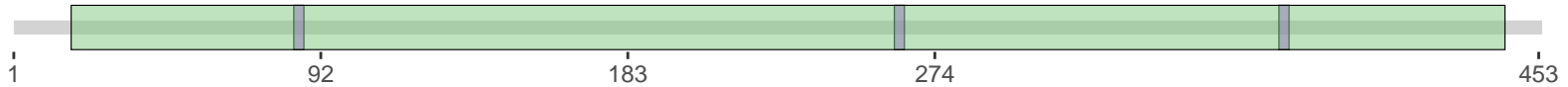


Gel Slice



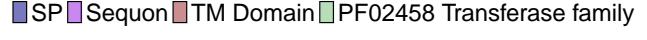
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KSLVLDGKXKHSSMGDTMAPPDNIRGTFVSRDDLKPKNLISRRPNLHVTSTFTVCGAYWTLGLKEAAMKGERDENGMVFFGCAADRARLNRRPQTYVFGNGVGVVTRTRHADLAGKEGFTIWEELGETIQKRMKDENVLITGEWFKVKGTDGKRTLSITGSPKFDLYAADFGWGRLEKLEFVSNINDQVTFMLSLKGKSDGDLVGLSLPKTQMNAFAAETHGLSFL*

NbL05g17490.1 diacylglycerol_kinase_5-like [MW - SP = 53.96 kDa]

No. of times detected



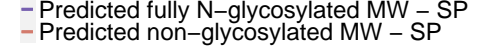
log(intensity)



Values from



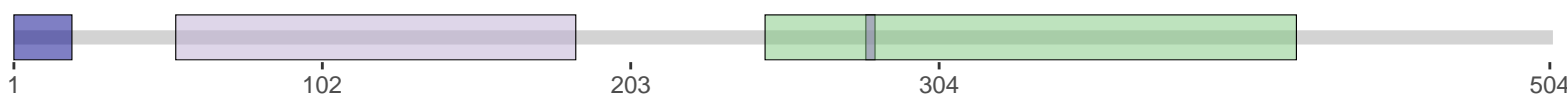
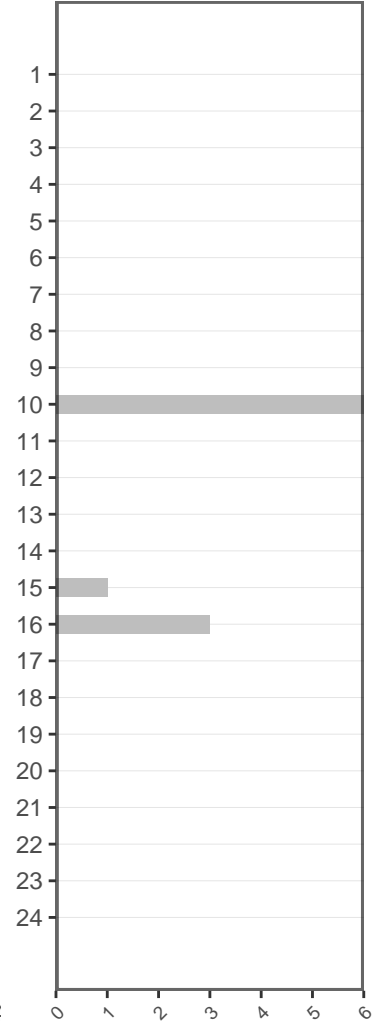
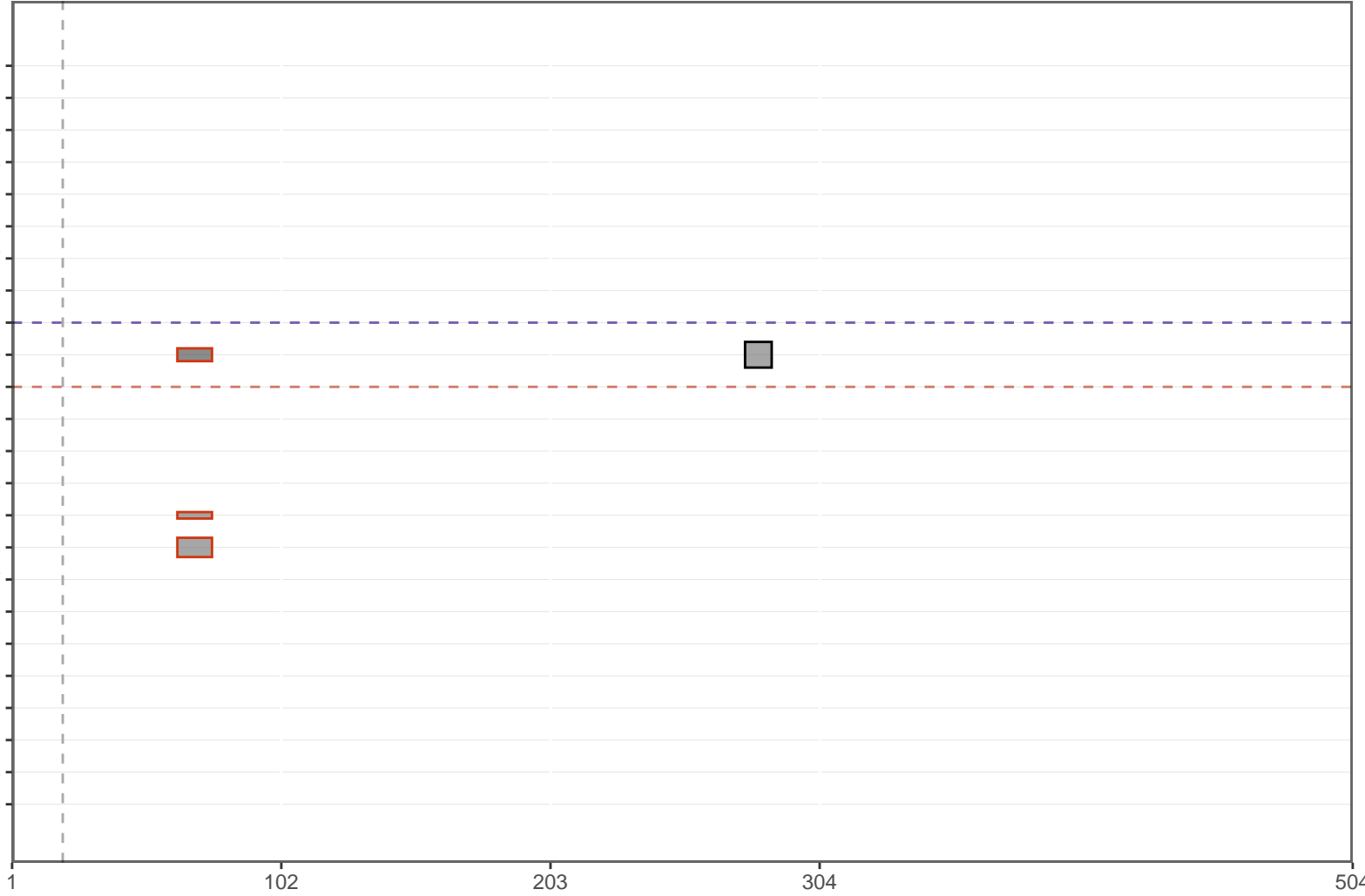
MW indication



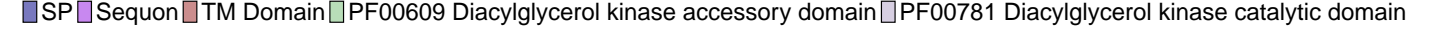
Molecular weight



Gel Slice



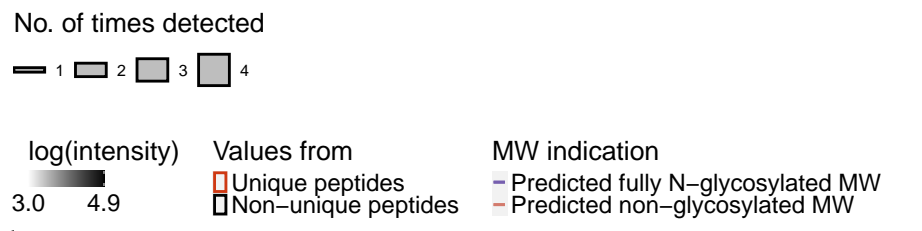
Pfam Description



Protein sequence:

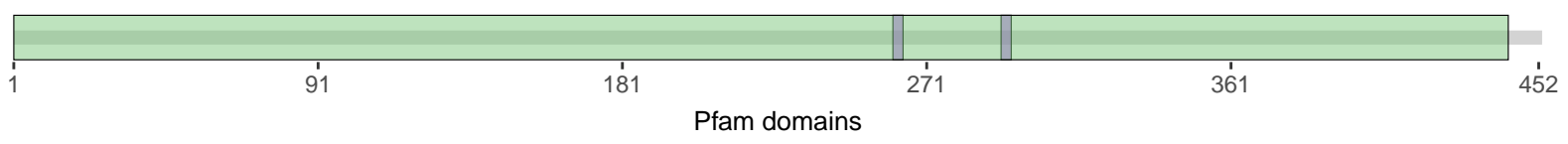
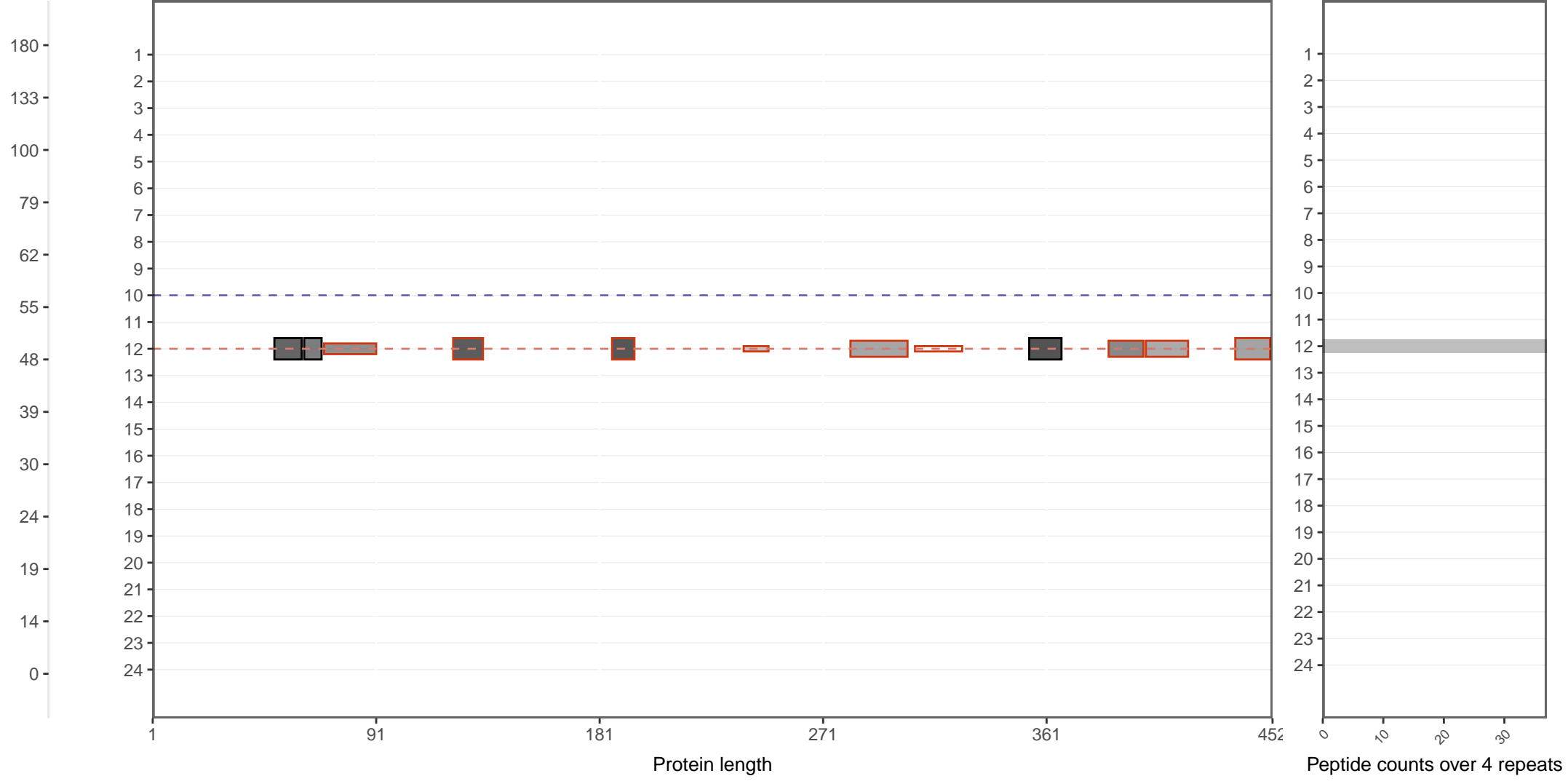
FRGGFVNYTSMGMDAGVSYAFHSERKMNPEKFKNGLVNGSTYARLGGTGGWFFASLFRHPSGRNIAQLAKVIMKMRGGEWDDLHPHSRISVGLNLPSFSGGLNLPWGTFTNSNKRDRDLTPFFVDDGHLEVVGFREAWHGMVLLAPNGHGRTRLAGAHRIRFEFHKAADHTFMRIDGEPWKGPLVDDDTVVEIAHGGVKKMLATHGGRGSKMHPDPSGHVNHGDDGDDGSEEDSVVEEQRFKAADTFKIPDEVSHLS

NbL05g17420.1 malonyl-coenzyme:anthocyanin_5-O-glucoside-6"-O-malonyltransferase-like [MW = 50.17 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF02458 Transferase family

Protein sequence:

GMISVDETKXXKLEMDQVTPPKVRCFTFTVTDGVRKLNKLMSSRRPNLTHVTSFTVTDGAVVWTLGKSEDAIREEEIENVTELFQGVADGRSRLNPLPPVYGNCLVJARASHVGLVQKGEFTVAVEVIGETQKRMKNDENVLTGEVFEFGGDKRSLGSDGPKLQVDFGVEKPEKLEFVSDNGDGVEMSLTKSKDSDGDLGLSLKTRINAFAMFTHGLSFL*

NbL05g17320.1 jasmonic_acid-amido_synthetase_JAR1-like [MW = 68.18 kDa]

No. of times detected



log(intensity)



Values from



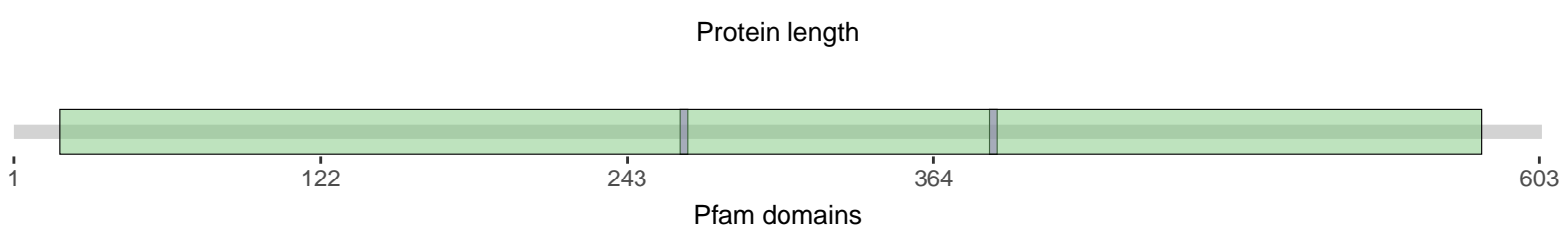
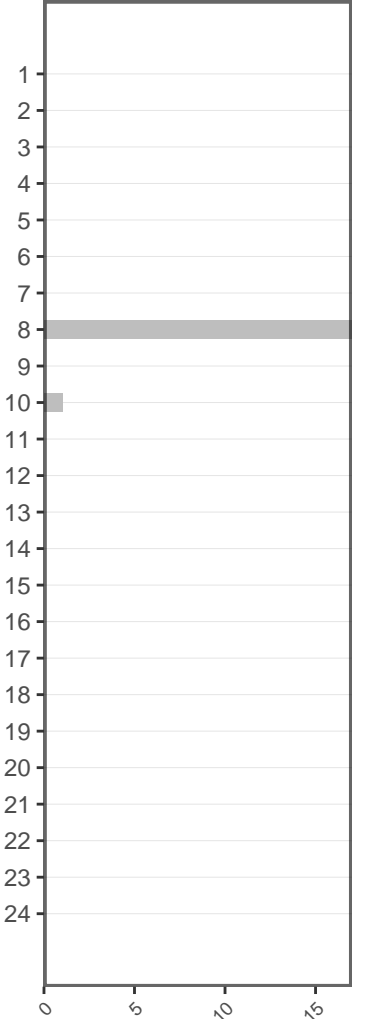
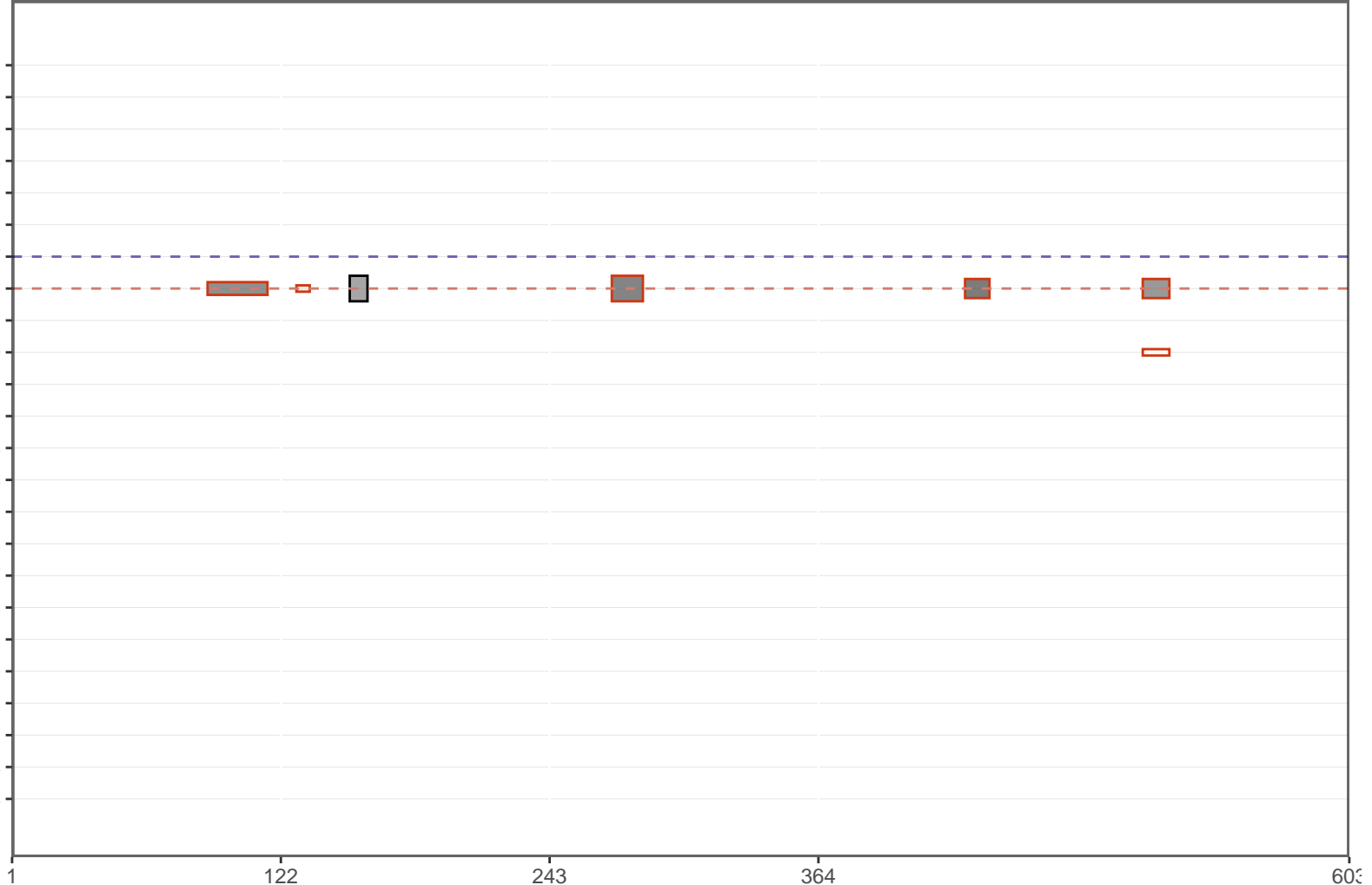
MW indication



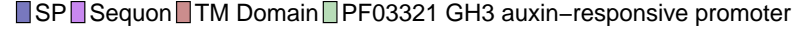
Molecular weight



Gel Slice



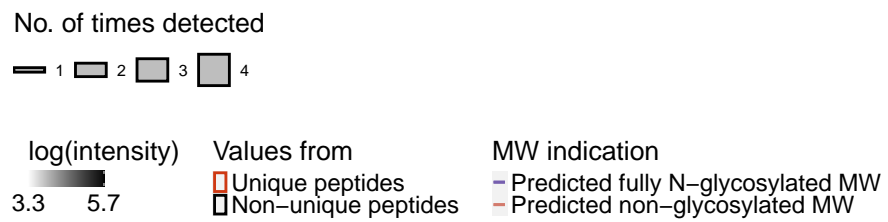
Pfam Description



Protein sequence:

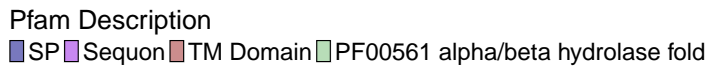
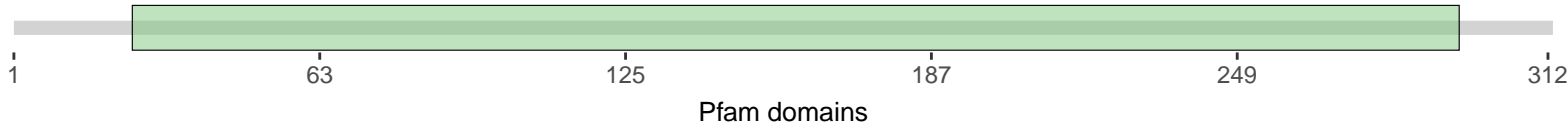
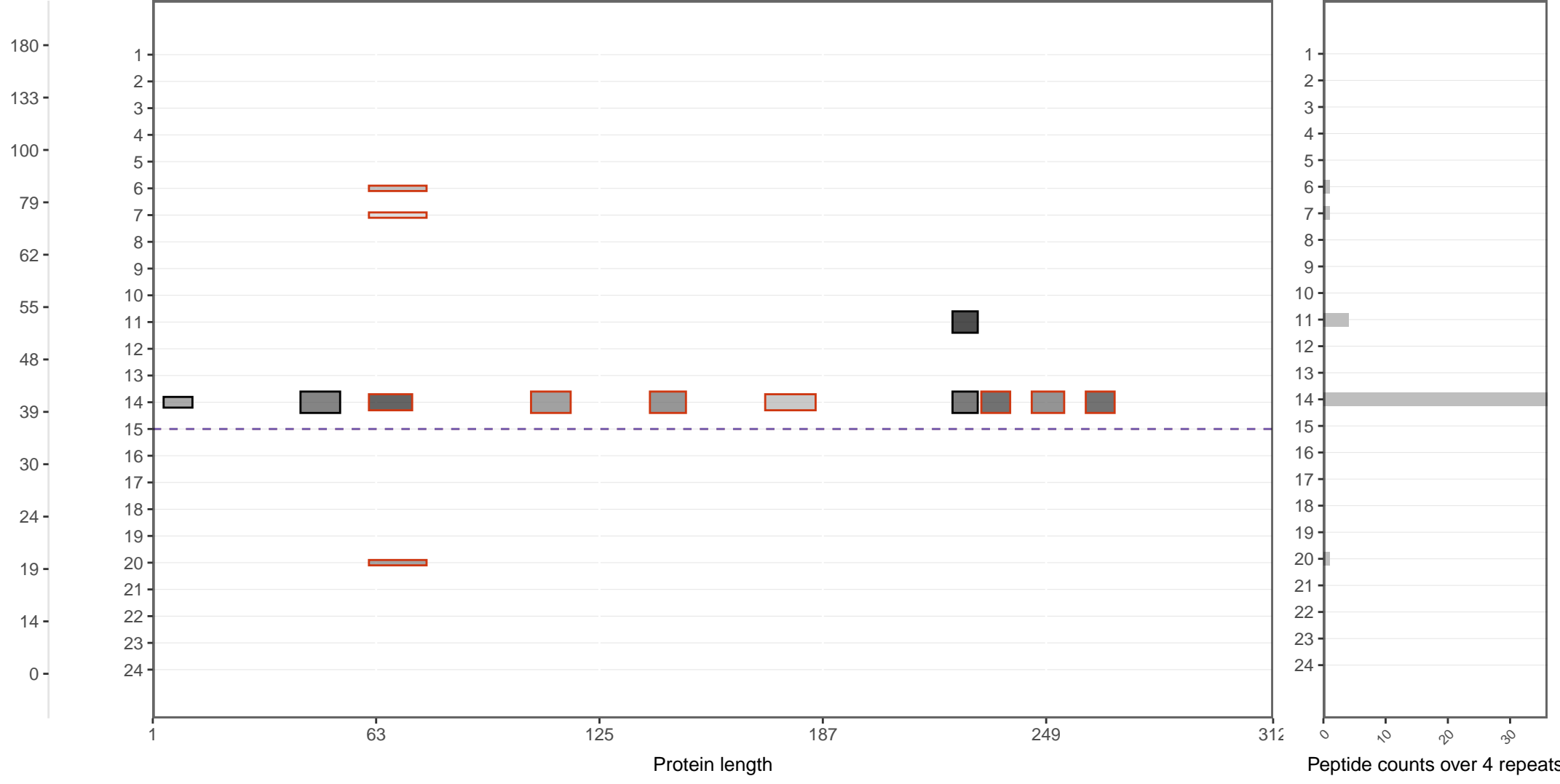
ICEVEKEDWFSIPRLWPNAAKYYVIMTGMGPYLTKLRHYAGKPLVADYGSTESWIGVNVPESSPPEKVTFAVPTFFAVFEPLHRTKSGNCHNSDGNLADDFIEDDPVFLGGVKGGEYEVLTFTTGLRYRLGDVVEVAGFHKNTPKLNFGRRLKLTVNDKNTKDKLQLVVERGSDLQKSRALVDFTSANAAKRPDGHVYVYWEIKGGEVENLVGEGCREMDASFVHDHGVYVSRKTNBSIGPLELQVIGERTFKKILEYFIGNSAALGDFKTRPCTSNQVLLTIL

NbL05g17240.1 bifunctional_epoxide_hydrolase_2-like [MW = 35.39 kDa]



Molecular weight

Gel Slice



Protein sequence:

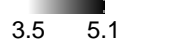
SFYMLRIVQEGRAEKDFGRFDTKTVKNIYMFSGSELPVAKDDEEIMDLVDRPAPLPDWFTEGDLANYSLSVEKSSFRITLQVPPYRAWLEEVGVDKIKVYPCLLVMGEKDYSLKFGGLEGVYKSGMKEYVPALETILPEGSHFVQEGQFEGVNGLIITLKKLP

NbL05g17230.1 lanC-like_protein_GCL2 [MW = 46.95 kDa]

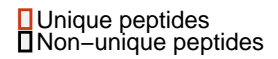
No. of times detected



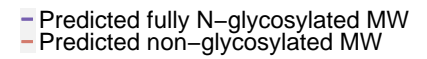
log(intensity)



Values from



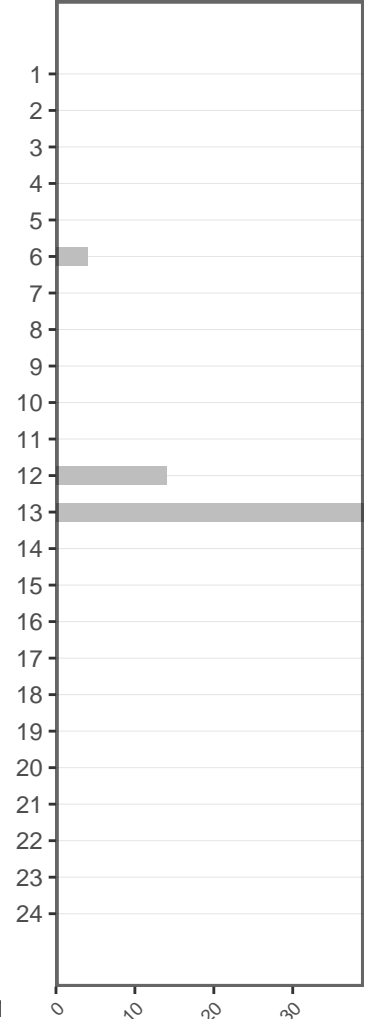
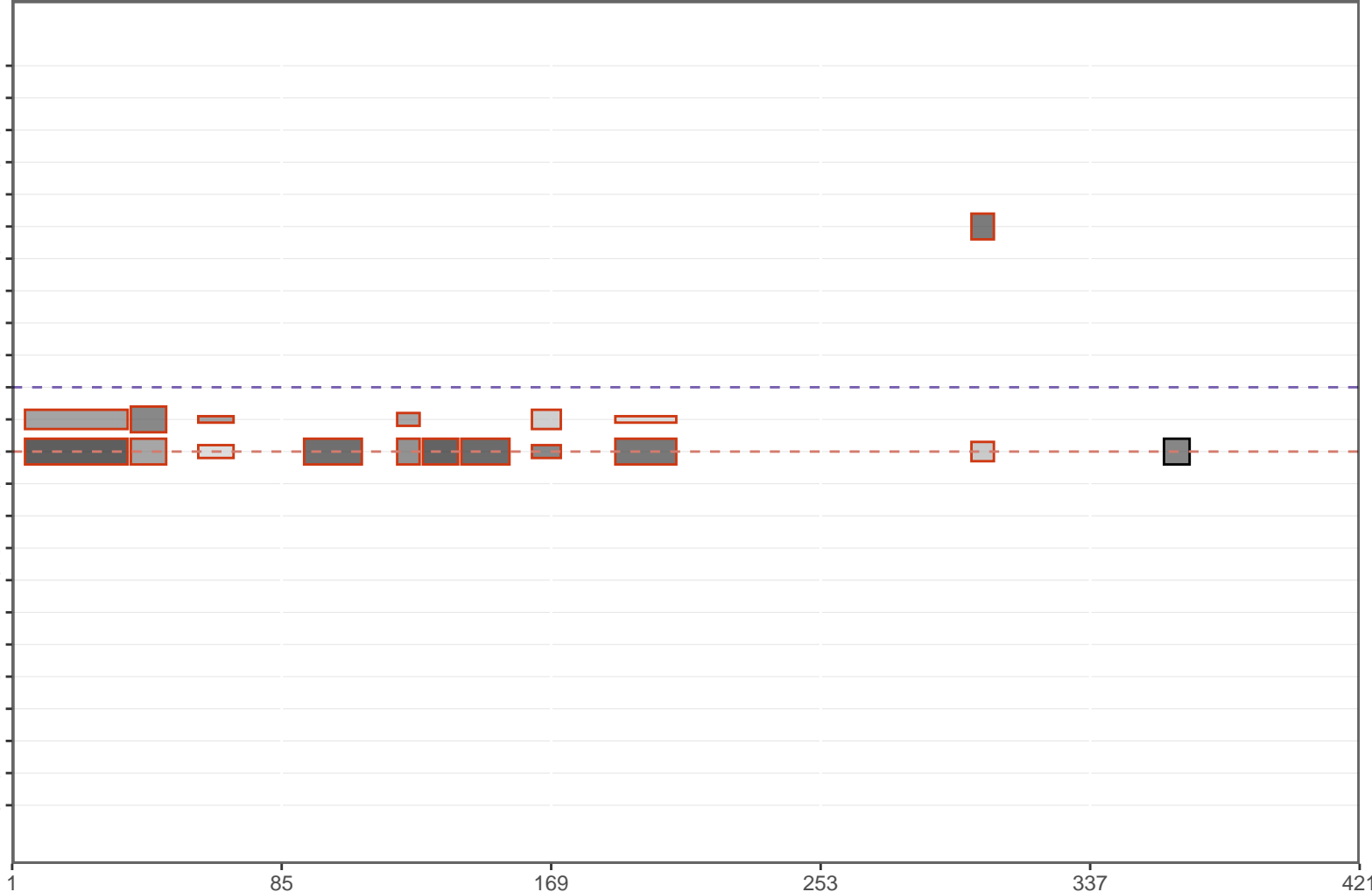
MW indication



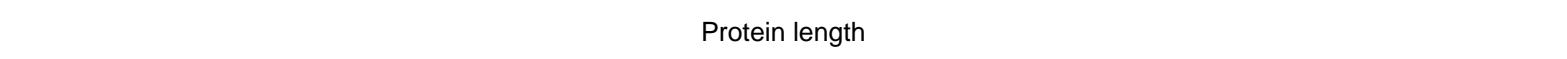
Molecular weight



Gel Slice

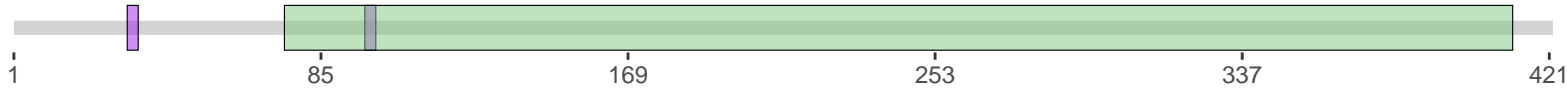


Protein length

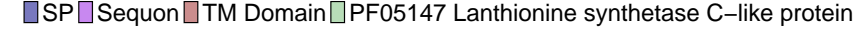


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

YNELIENRRRLGGKGSPLMVEWYEMVGAHSLGAGIMVYLMDFELKPDLELDVYKELRYMVAANRFPDGNVPTSEEDKRROVLVHWCHGAPGIALTVKAAELFGDRFLNAVAAGAEVVAWNRGLLKHGMCHGIGSNVYVFLSLYQLTGNVEYLYRAKAFAGFLLDRAHKLIJAKGEMHGGDNPYSLFEGIGGMAYFLDMTEPKEARFPWGGKVKHAT

NbL05g17130.1 uroporphyrinogen_decarboxylase_1_chloroplastic [MW = 46.01 kDa]

No. of times detected



log(intensity)



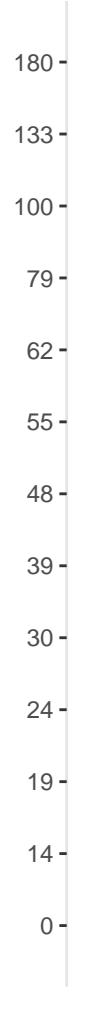
Values from



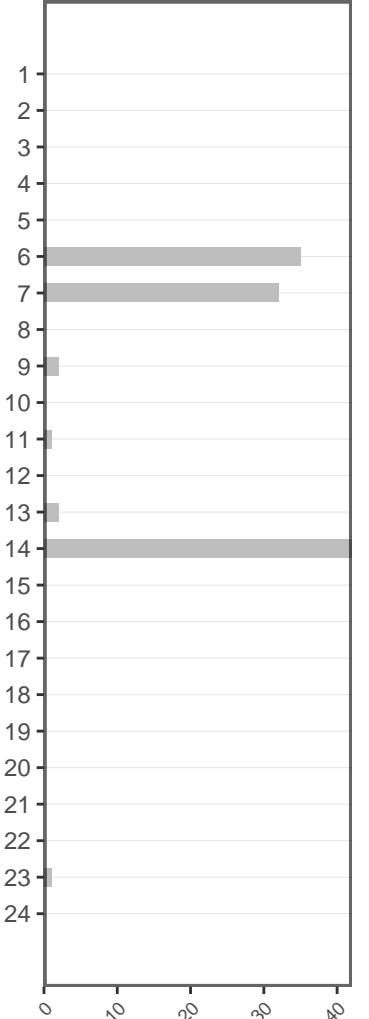
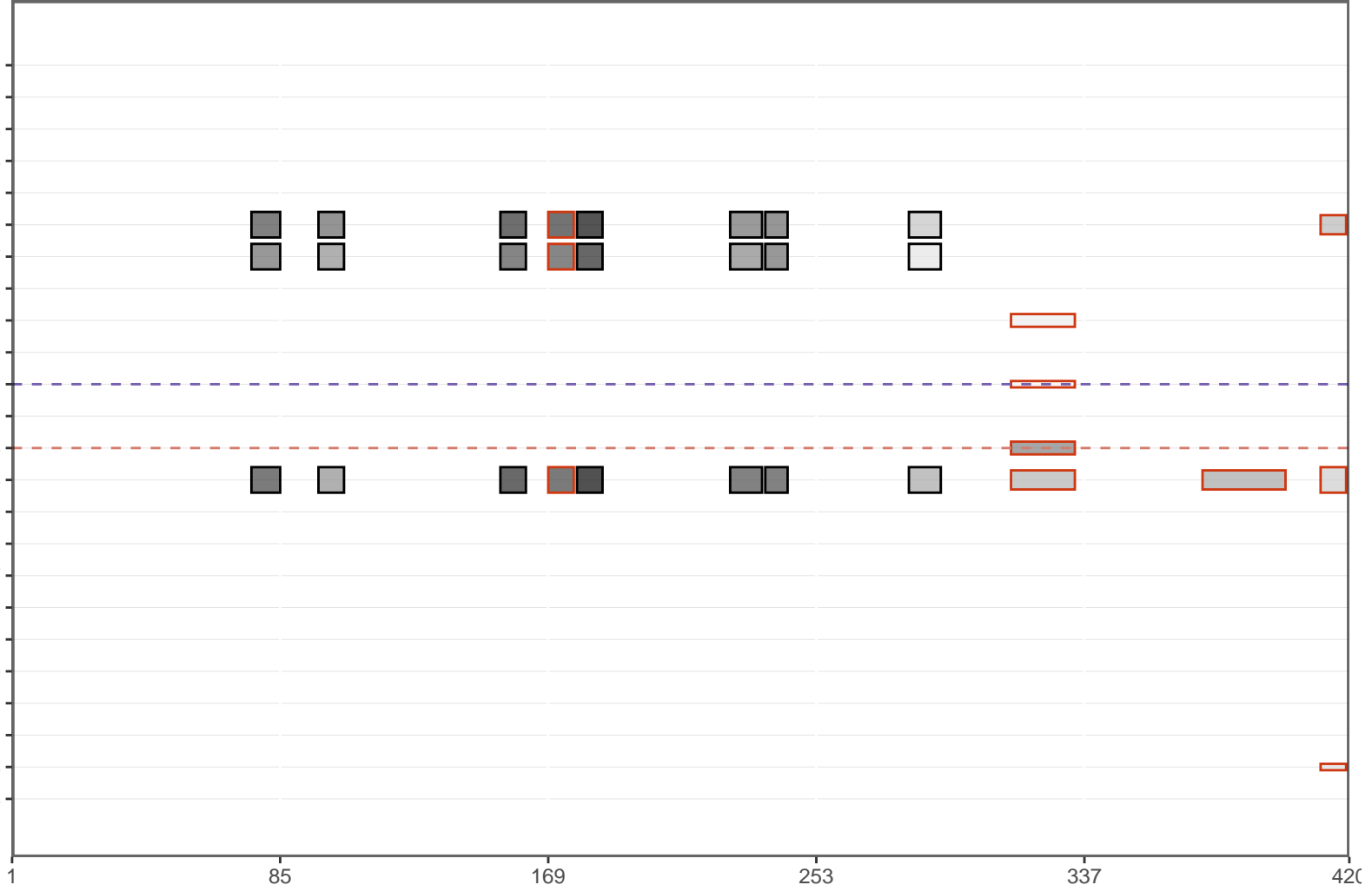
MW indication



Molecular weight

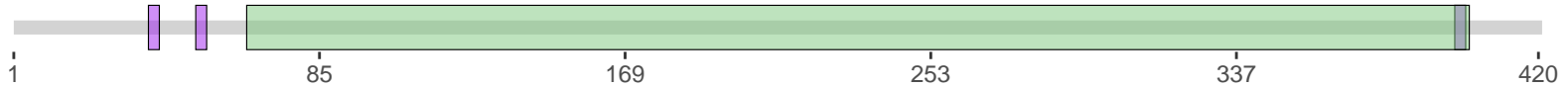


Gel Slice



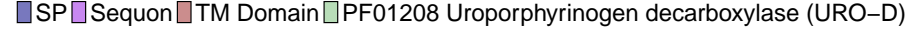
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

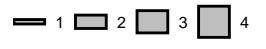


Protein sequence:

AAVLGFVQAPVTLATVYVEGGTTRFTYTRIKDMGHTAPKIVLRALLSHLSKAAAEVYVQVSEGAHQDFDEWGGQLPPIHMWDQWSEKPYDEIVATIKRKGQPTPLVYVINGNGLLERMKMETGVNDVGLQWTVDMADGRKRLGTDIGIQGNVDPASLFGPLPALTDEIERVYKASAGTRGHNLGHDVLVGTPEEAAWHFFNLYSKSDFDKVDRLESEANTVAAL

NbL05g17110.1 phosphoenolpyruvate_carboxylase [MW = 110.41 kDa]

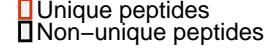
No. of times detected



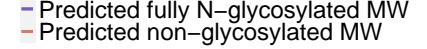
log(intensity)



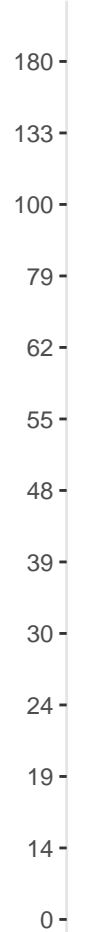
Values from



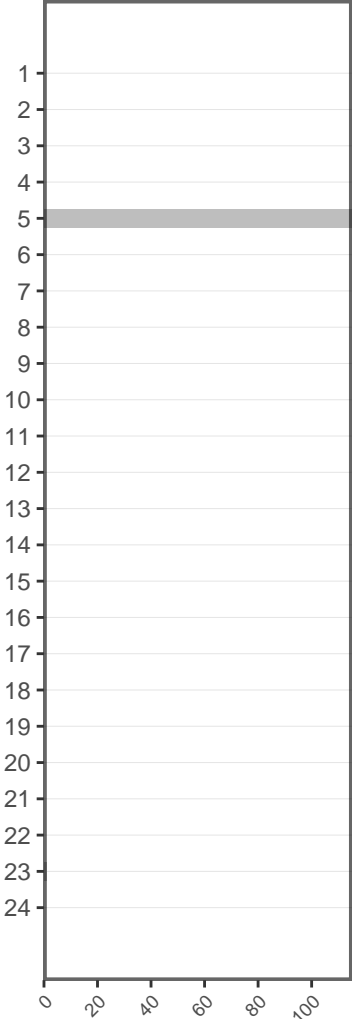
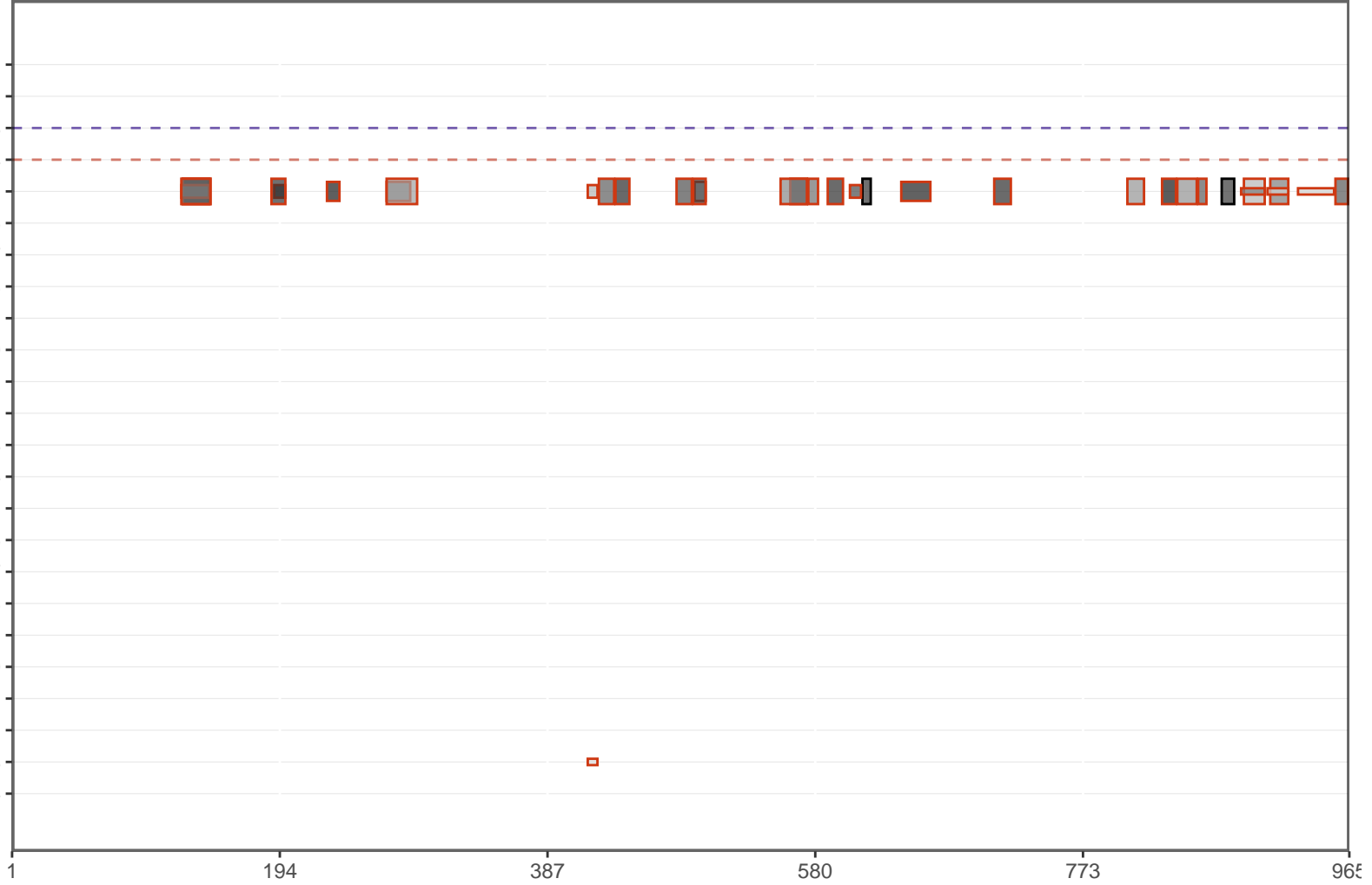
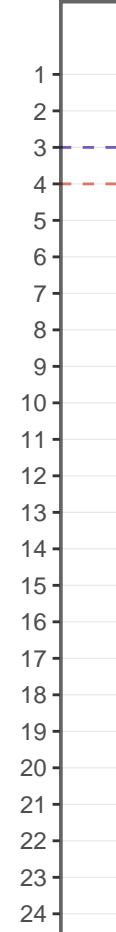
MW indication



Molecular weight

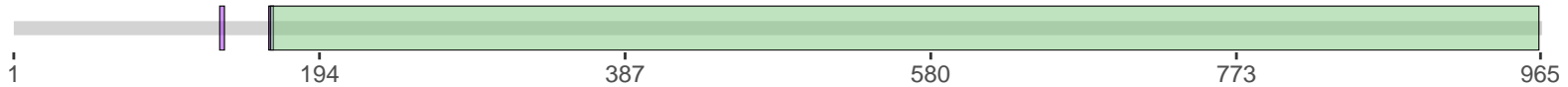


Gel Slice



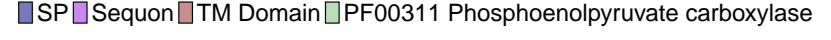
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGSYREYSEERRGWELSELGGKRFPGDLPRTTEIADVLDTHVIAELPQDFGAIHSMATPSQDLAVELLGRCHVKGPLRVPLFEKLDLQESAPVAWRLFSEIYWRNRIRNGKGEVMMVGYSDGKMGKRFSAWVQLKAGDELKVAKEHGKVKITMFGHGGTVGRGGGPTLAILGPPDPTGGSLRVTVGGEVIEGSGFGEHLQFRTLGRFTAATLEHGMMPPVSPKPEWRALMDEIWAATEKYRSIVFKFRPVEYFRLATPELYGRMNGSRPSKRPKSGC

NbL05g17070.1 ubiquitin-conjugating_enzyme_E2_36 [MW = 17.22 kDa]

No. of times detected



log(intensity)



Values from



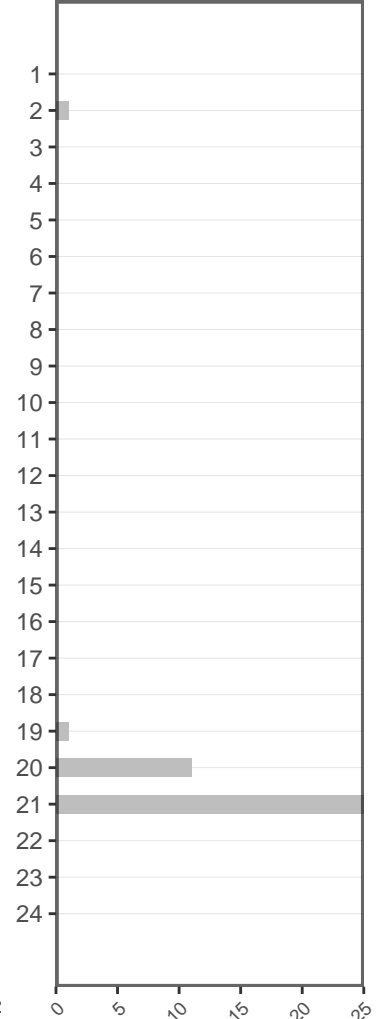
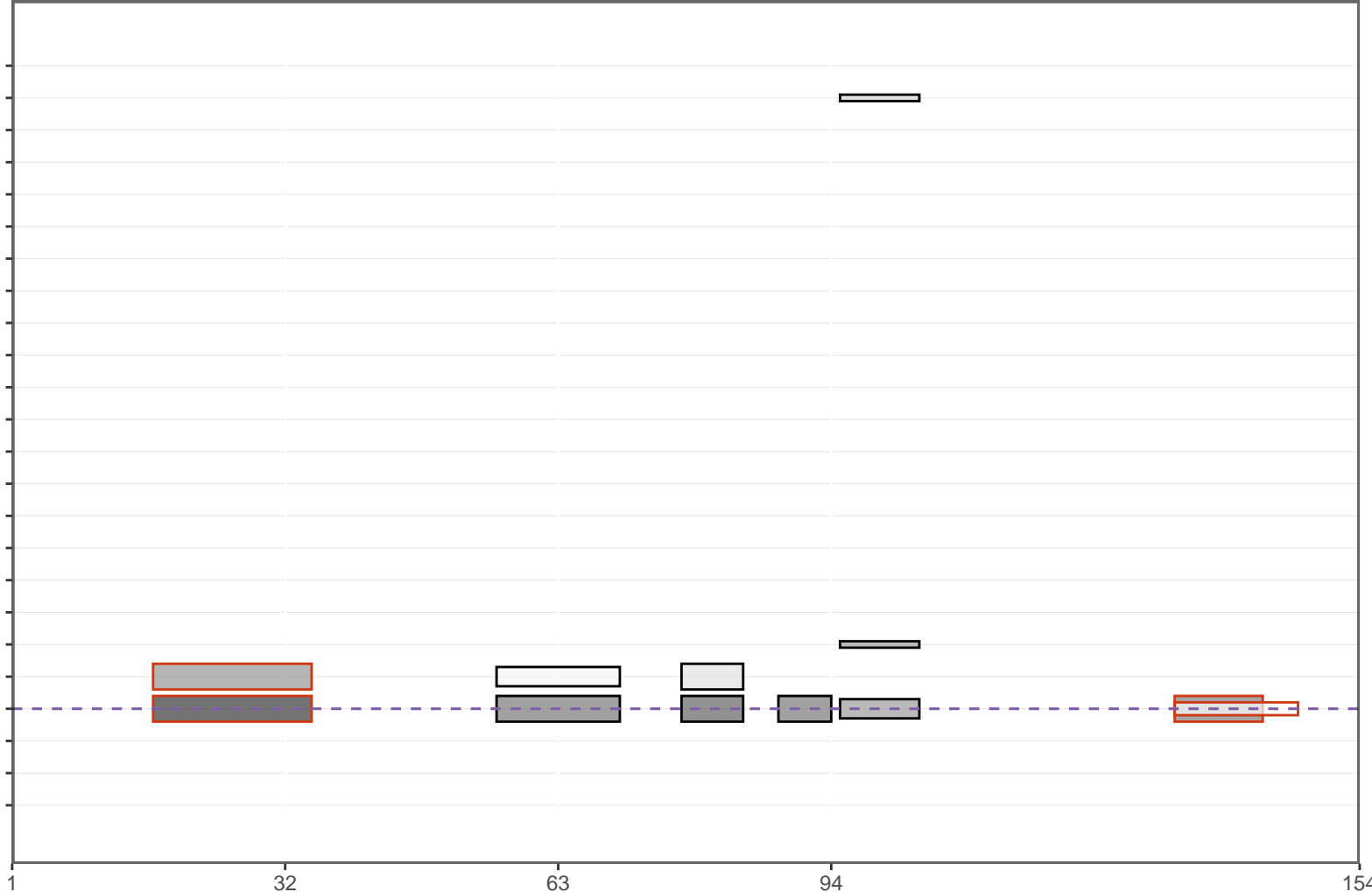
MW indication



Molecular weight

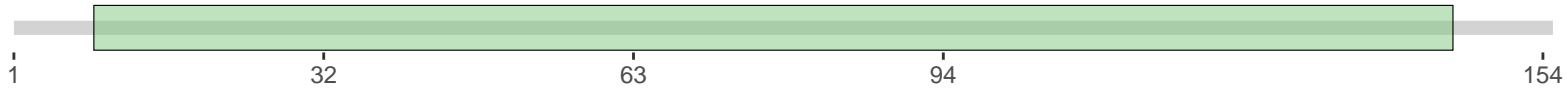


Gel Slice



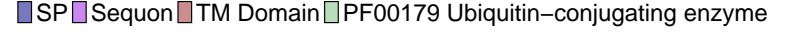
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

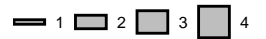


Protein sequence:

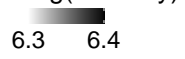
LYPMAAPKVRFLTKYHFNIDKLGRIQLDLNDKWPALQIRTVLLSHGALLSAPNPDPLSENAIHWKNEAEAVETAKEWTRLYASGA

NbL05g17020.1 malate_dehydrogenase_mitochondrial [MW = 41.53 kDa]

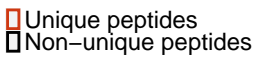
No. of times detected



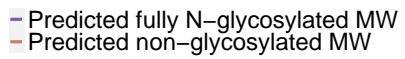
log(intensity)



Values from



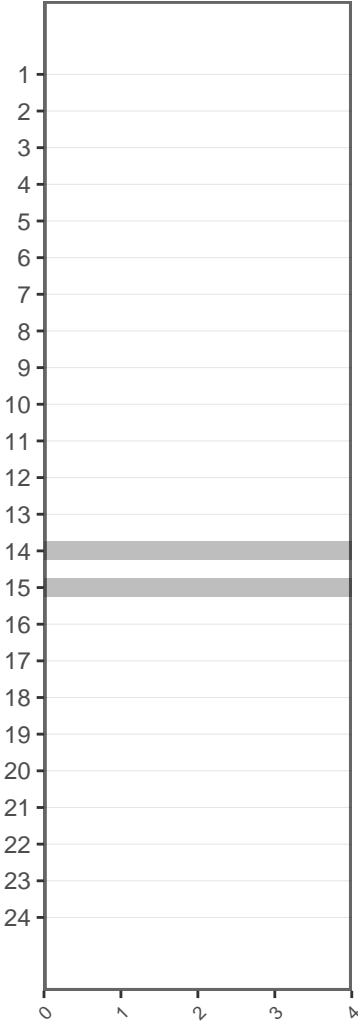
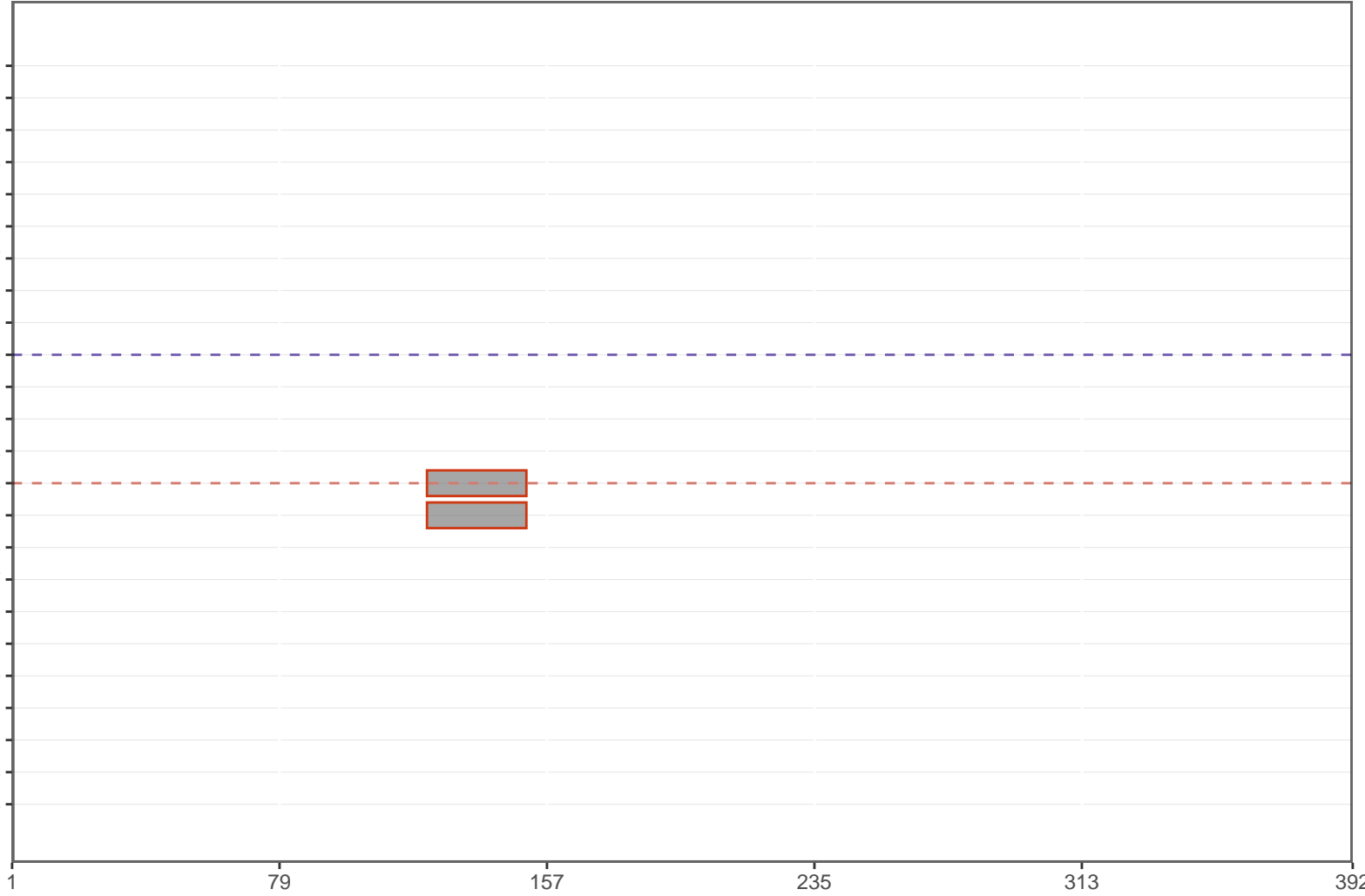
MW indication



Molecular weight



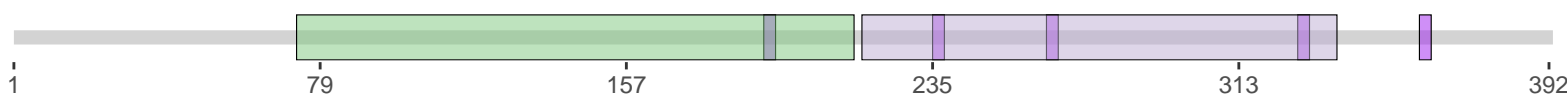
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF00056 lactate/malate dehydrogenase, NAD binding domain
- PF02866 lactate/malate dehydrogenase, alpha/beta C-terminal domain

Protein sequence:

MSINPYNSTVPIAAEVEFNKAGTYDEKRLFGVTLDDVRAKTEVAGKAKNNSVDNVPVVGSHAGITLPLLSGATPKANLSDEEINLTKRTDGGCTEVVKAAGKGGSATLSMAYAGAFADAKLGLNGVFDVVEGDFVGSNVTETLPPFASKYVTHIGALPNMPSGSSPTPIHFSALKKNTTELMNAKHGGSKIVGDKLGRKKE

NbL05g16840.1 glutamyl-tRNA(Gln)_amidotransferase_subunit_A_chloroplastic/mitochondrial [MW = 57.18 kDa]

No. of times detected



log(intensity)



Values from



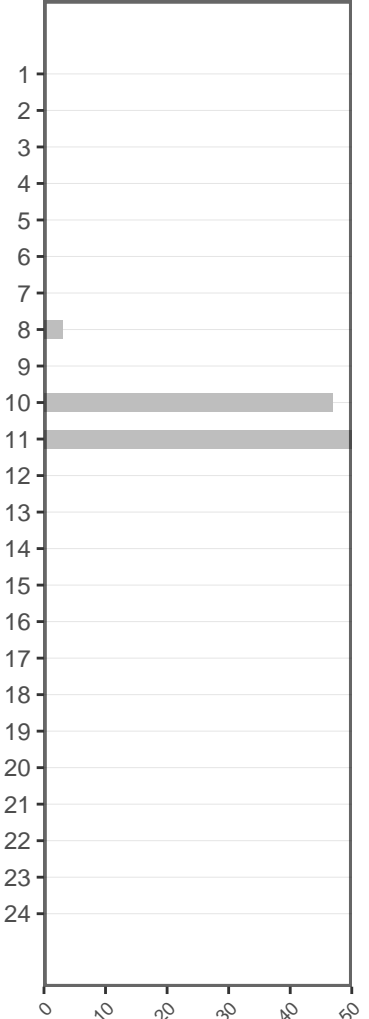
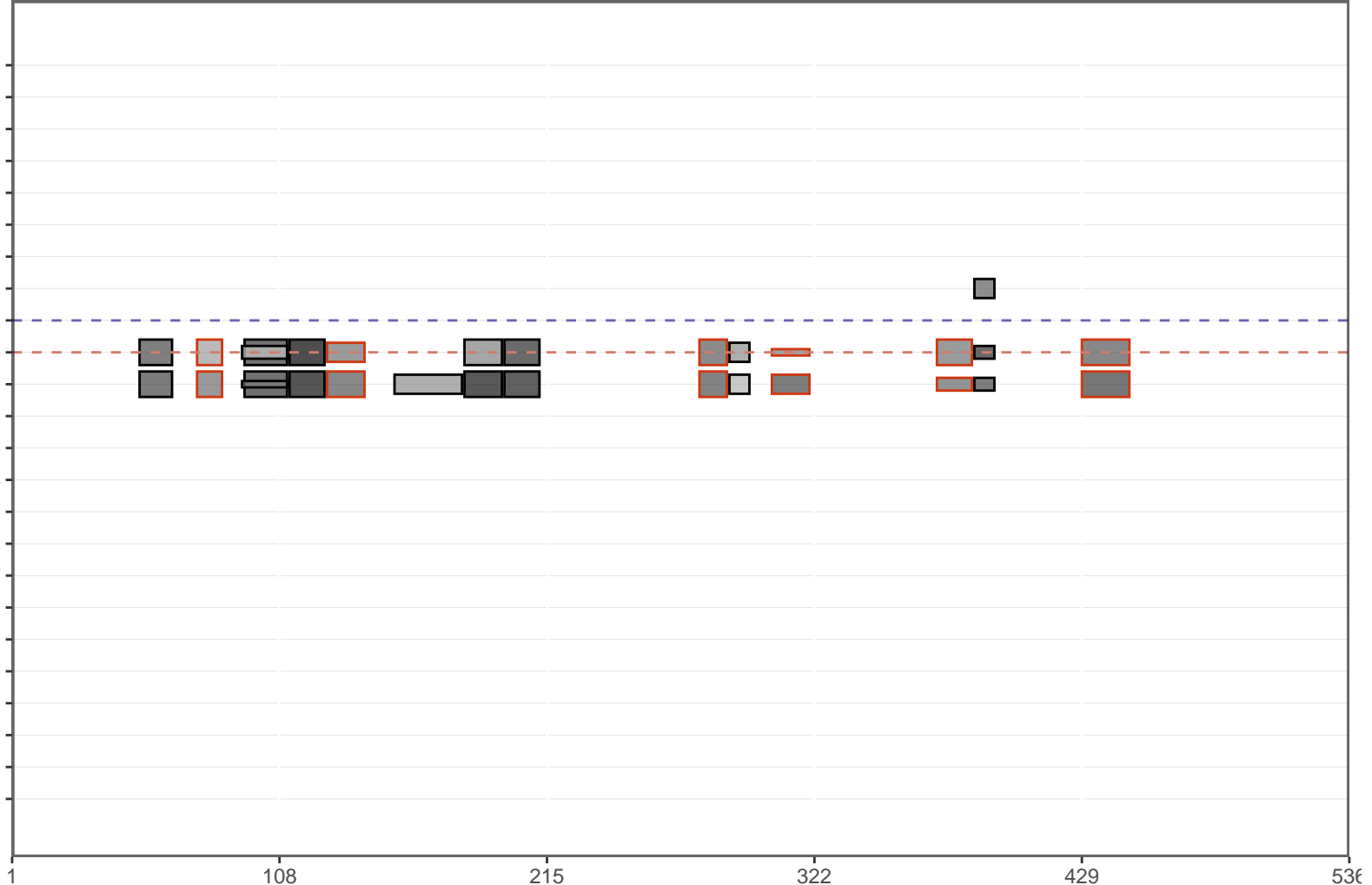
MW indication



Molecular weight

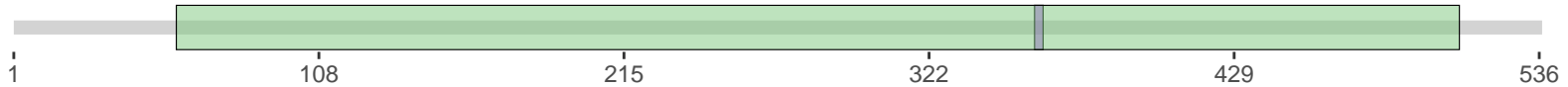


Gel Slice



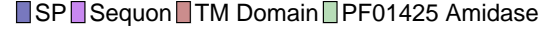
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ADAGILHAISSGHDKYDATTSSKREVPNFASQFIARDHLDGKPLKGLRVGLURETIEDGVDPEVITGIRGAASHLEELGCTVTEVSLPFSLLGFPVYILASSESSSNIISRVDGIRYKGVQFADELNSLYGSRAGFGGSEVKMRILMGTVALSAGYVDAYYKRAGQVRLVRENFRAALENDILSPAPSAAYKIGEKNDPLSMVGDIMTVVNLNLAGLPAVLPCGFGVDSSAALPVGIMIGAFEEKLLKVGHFEGTLGGCFIPVVADELADG

NbL05g16630.1 proteasome_subunit_alpha_type-2-A-like [MW = 25.65 kDa]

No. of times detected



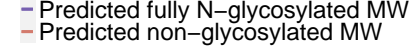
log(intensity)



Values from



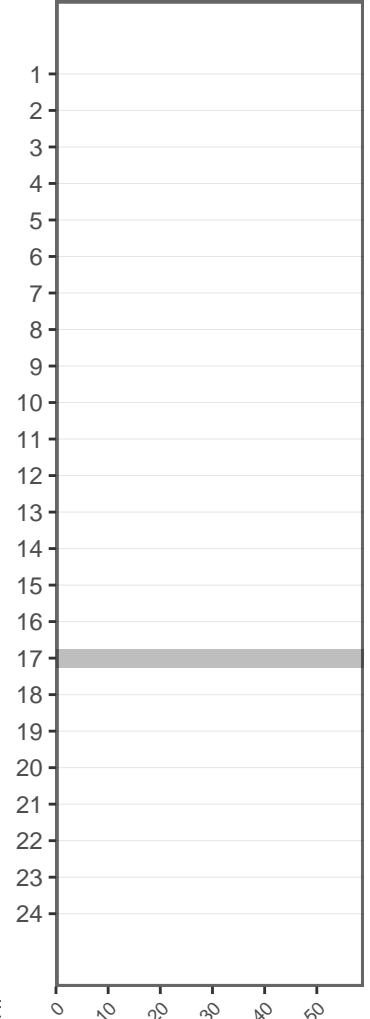
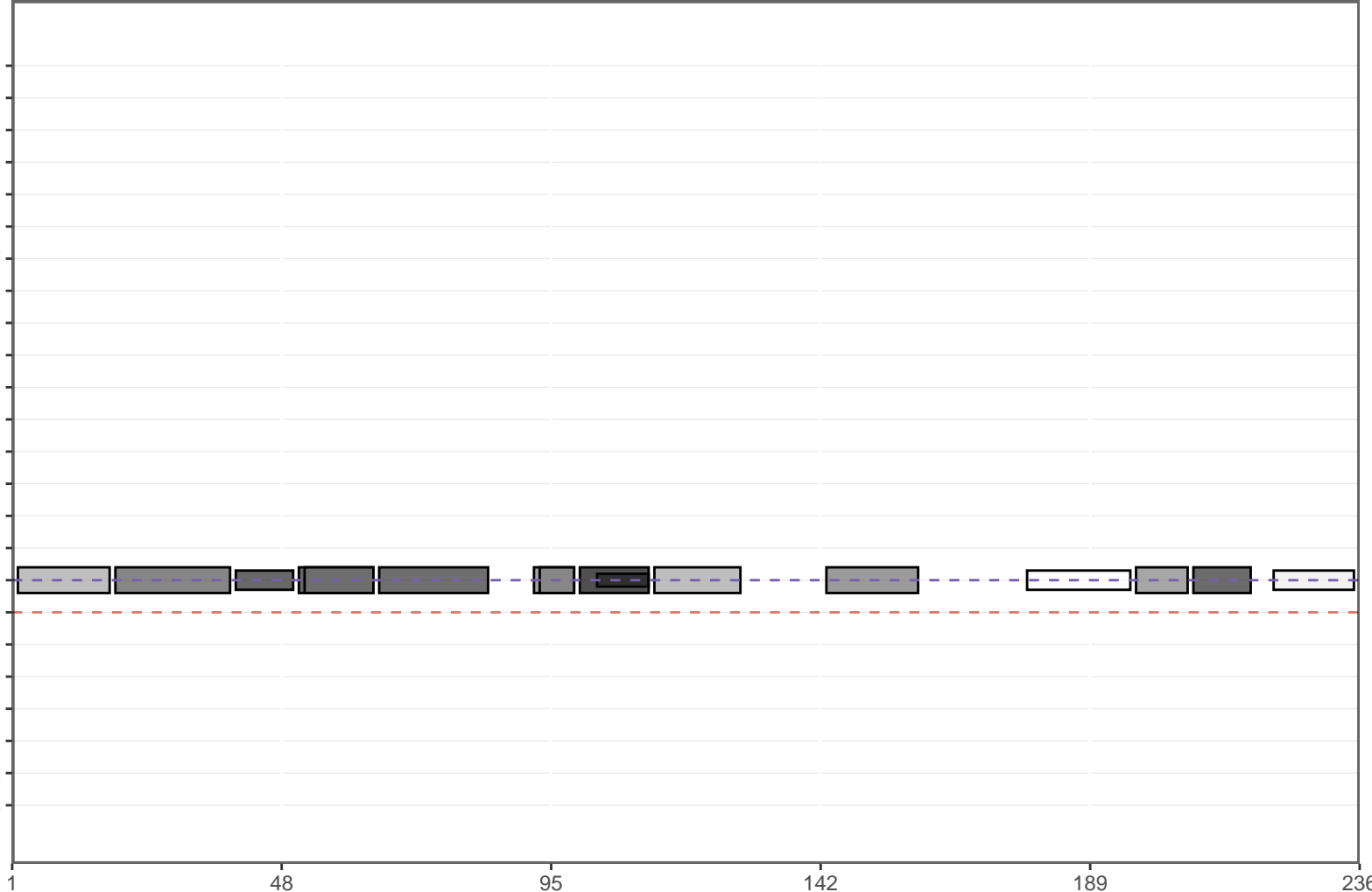
MW indication



Molecular weight



Gel Slice



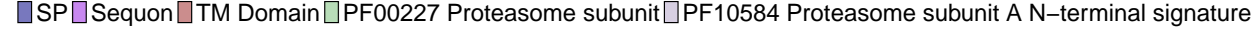
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

"IPVITQLVREIAVAIMGEFTQSGGVRPFGVLLWAGYDDKGGPLQVQVDPGSGYFSAWKASAMGKQVSNAKTFLEKRYTEDIELDDAWHTAILFLKEGFGGSGKNEIGKNDKVKILTPTIEDDYLQEV"

NbL05g16610.1 14-3-3_protein_9-like [MW = 21.44 kDa]

No. of times detected



log(intensity)



Values from



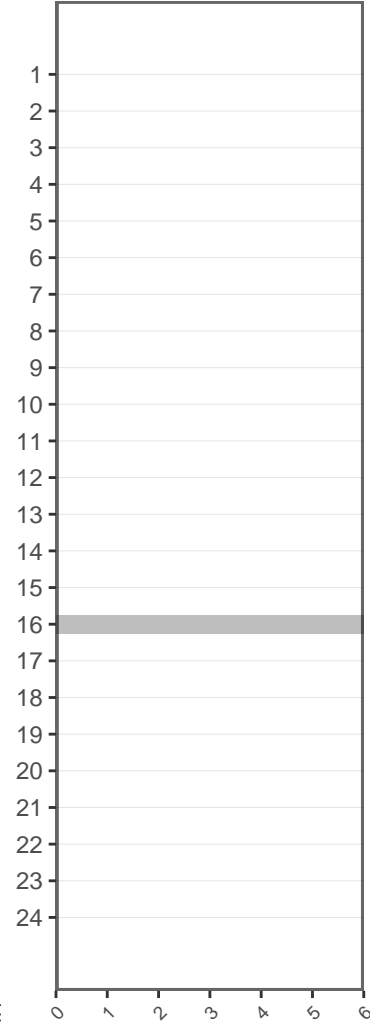
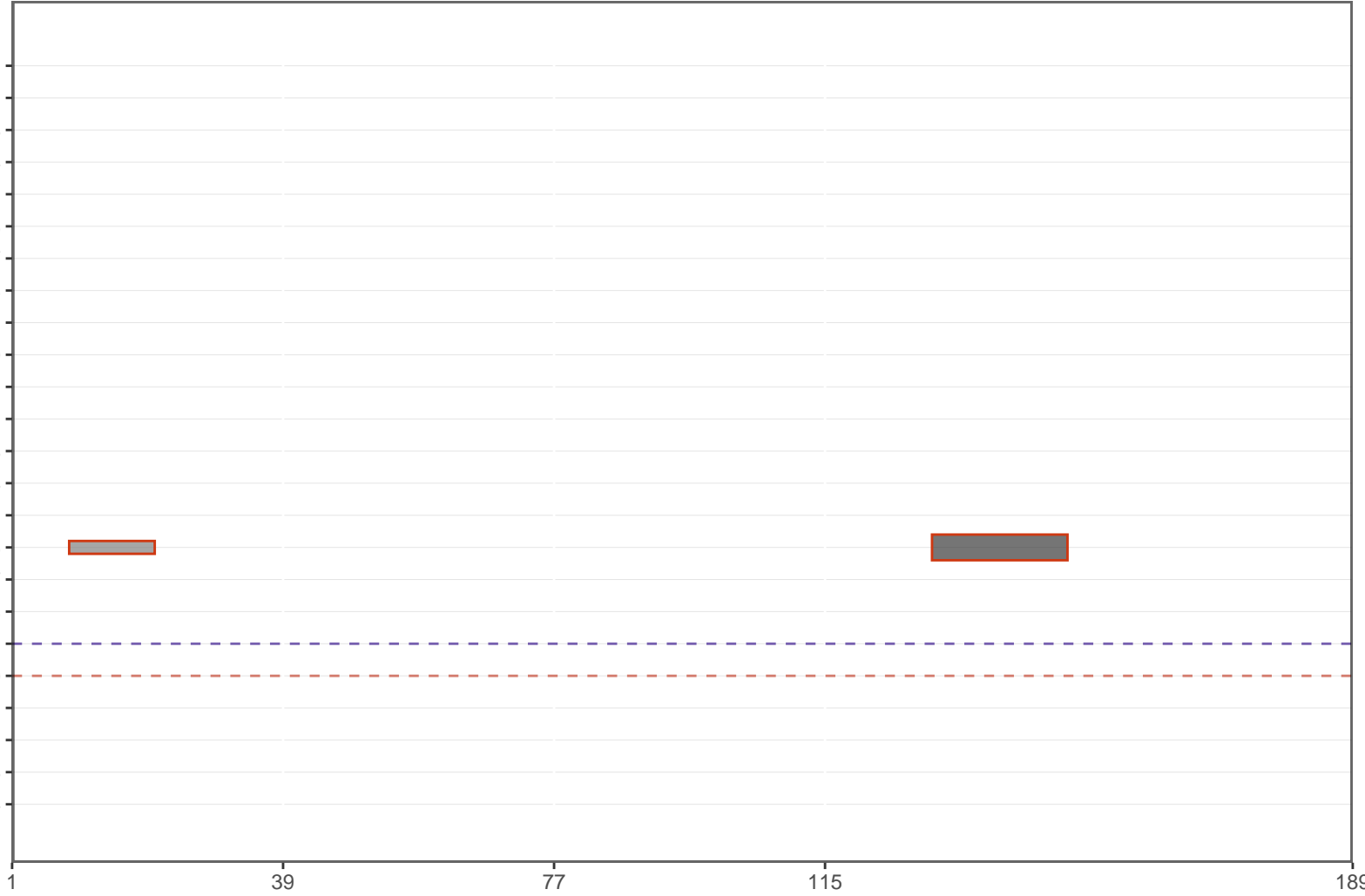
MW indication



Molecular weight



Gel Slice

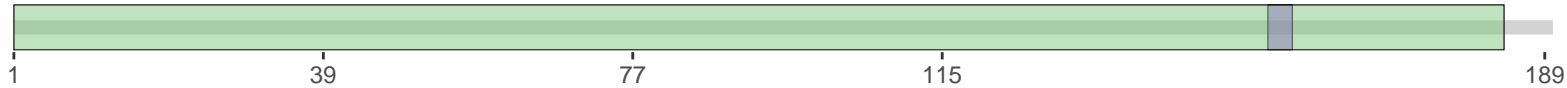


Peptide counts over 4 repeats

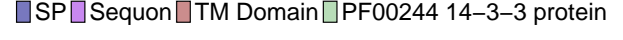
Protein length



Pfam domains



Pfam Description



Protein sequence:

ITVIDEHLPSCPAGESEVFFYKSEGDPYRYLAERKFTOTDKKEVSDLSKAYGSAITTAETELFPPTHPIRLGLALNFSVFYIYELNSPERAGHLAKQAFDEANSEWAEI

NbL05g16530.1 60S_ribosomal_protein_L19-3-like [MW = 24.82 kDa]

No. of times detected



log(intensity)



Values from



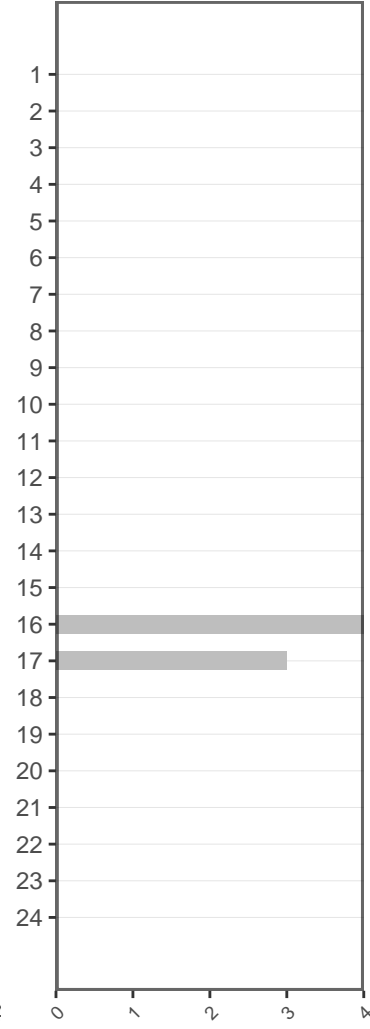
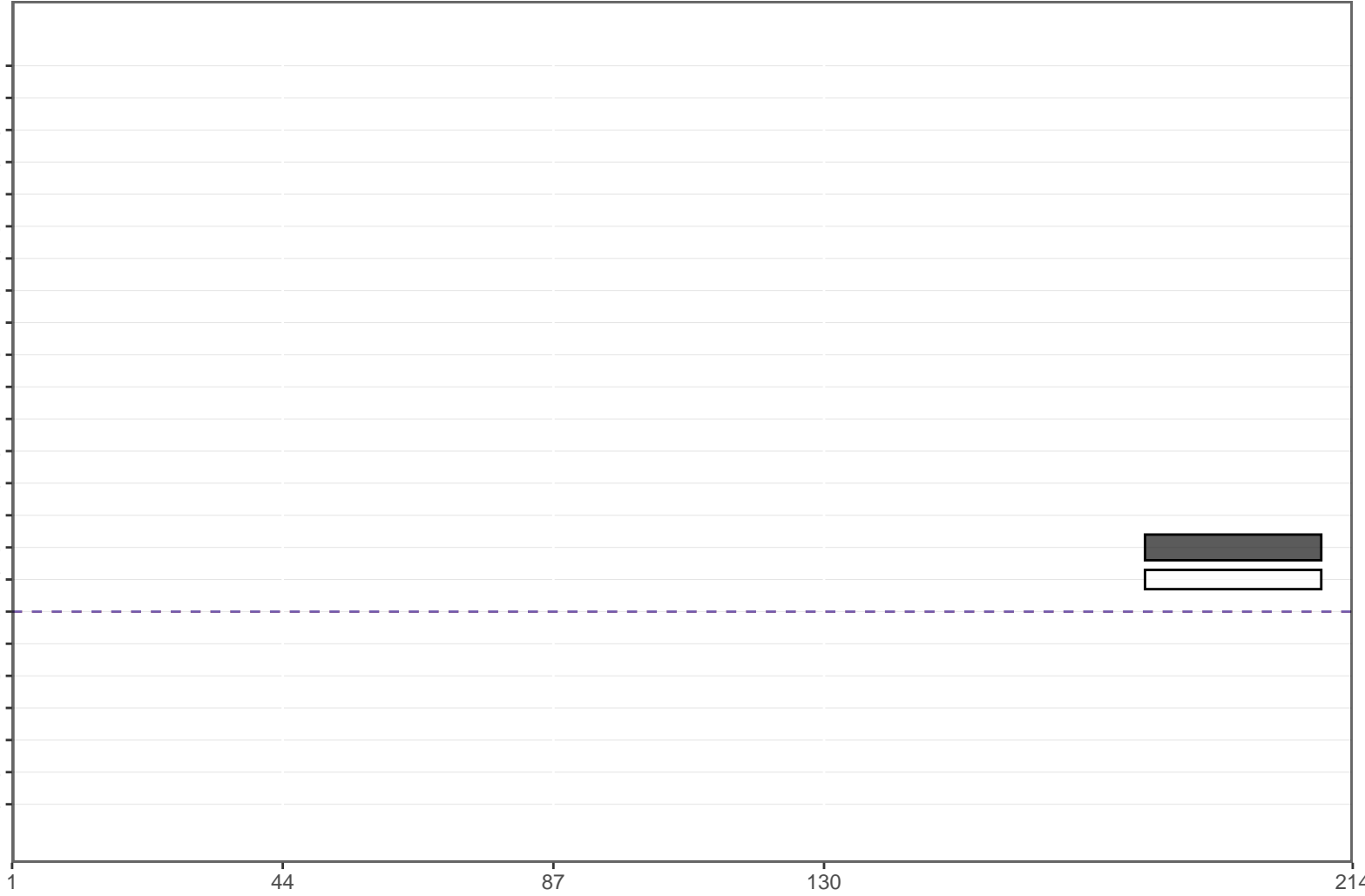
MW indication



Molecular weight



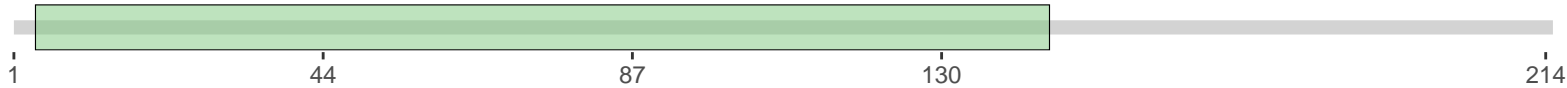
Gel Slice



Protein length



Pfam domains



Pfam Description

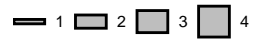


Protein sequence:

MMRSMRYLRRLLRKRVREKQIDRHMHYDMVMKVGKGVFNKRVLMENIHKTAEKAREKTLSDGFARRAKKASREKRFARREERLADGPGERPVQPAAPAAAPKQALGSKSKK

NbL05g16470.1 importin_subunit_alpha [MW = 59.01 kDa]

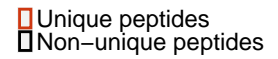
No. of times detected



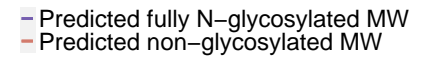
log(intensity)



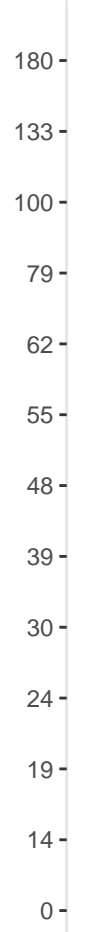
Values from



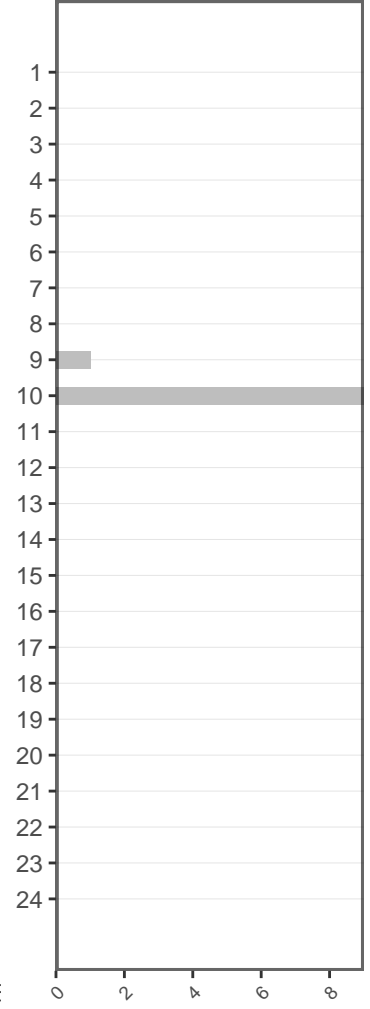
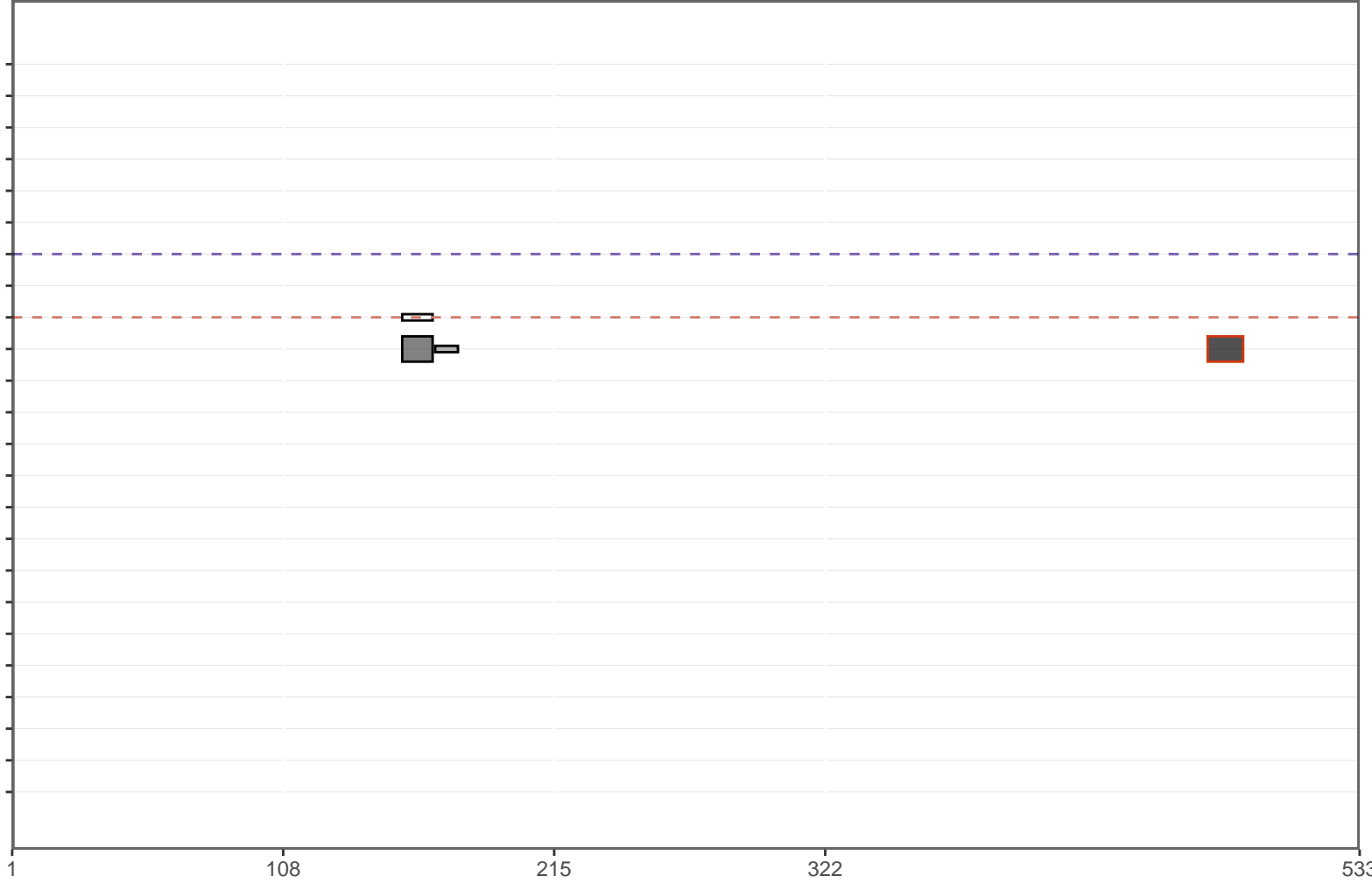
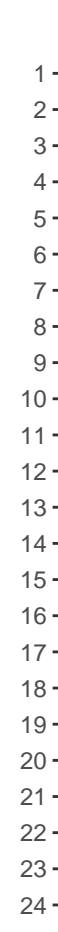
MW indication



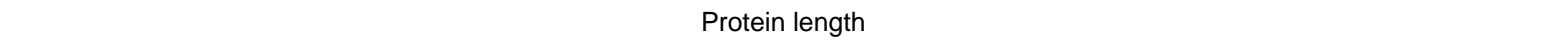
Molecular weight



Gel Slice

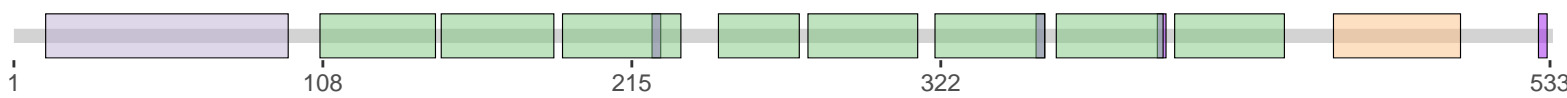


Protein length

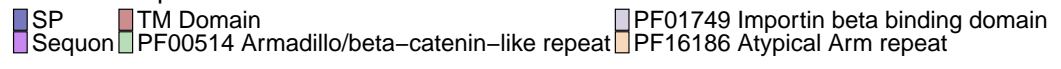


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

TLARLHSDNEEVLTDAAGWALBYLSDGTNDKIGAVIEAGVGRPRLELLHSPSPVLPALRTVGNVYTGDDQGTQVIDHHLPCLLNLLTGNVYKSKIKKACWVTSINATAGSRNGIGAVIEAGIAPLVHLLGNVAEIEKKEAAWAINSNATSGGNHDDQIKFLVSGGKIKPLGDLVCPDRPRVTVGLGLENLKIGKADKDLGNTFGVNVYAQIIDEAEGLEKENLQSHDNTFYEKAVKILETFWLEEDDEQLPSADAGHSQGNFNGGGELPLP6GGFNFS*

NbL05g16350.1 calvin_cycle_protein_CP12-1_chloroplastic-like [MW = 14.35 kDa]

No. of times detected



log(intensity)



Values from



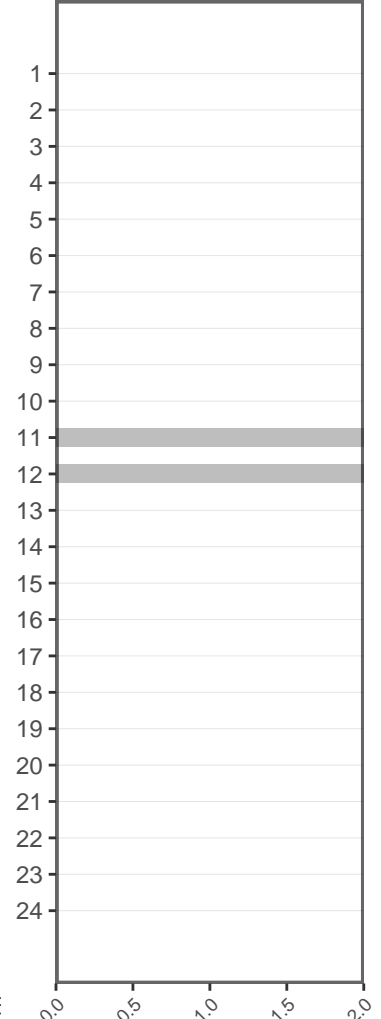
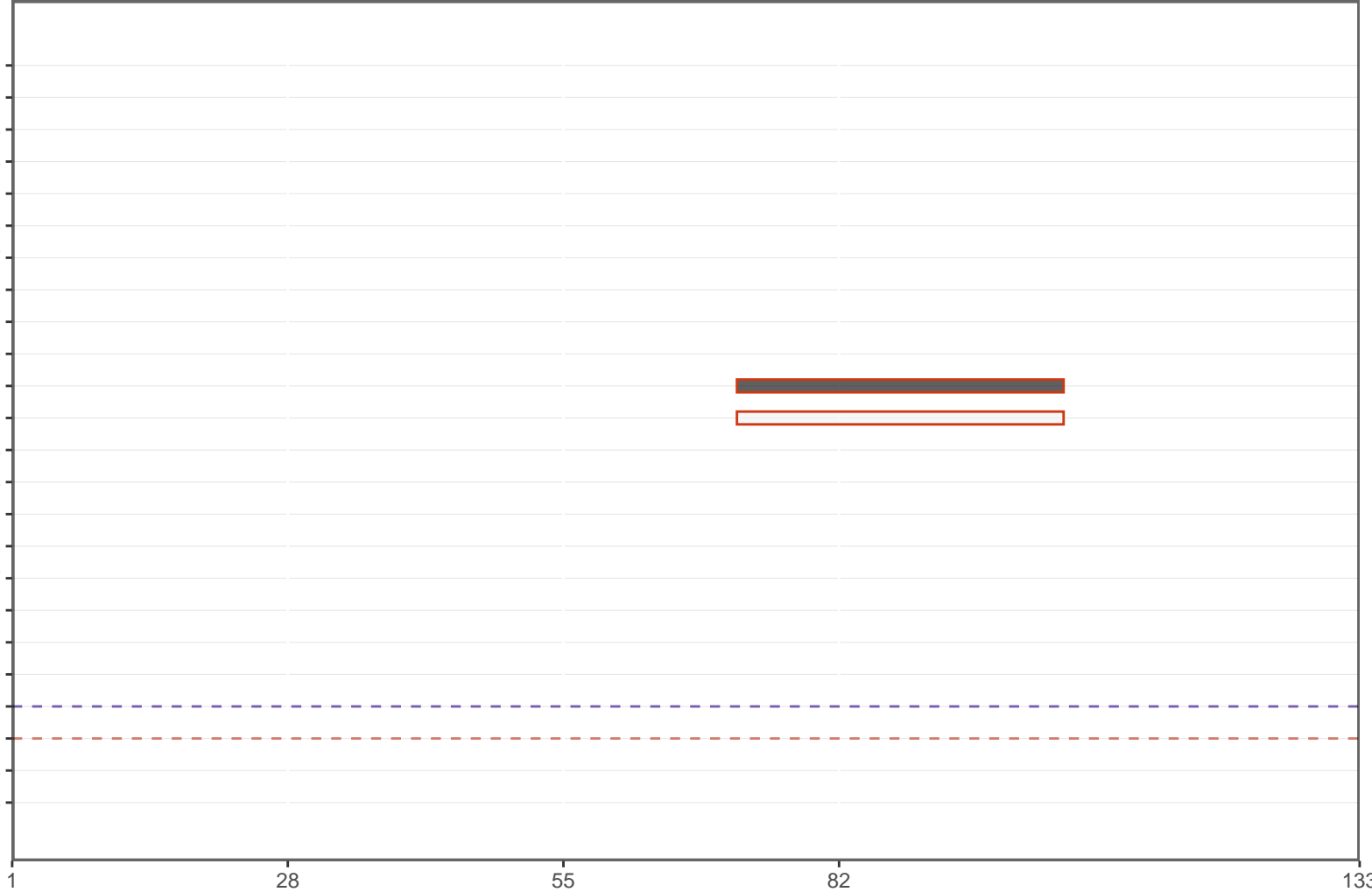
MW indication



Molecular weight



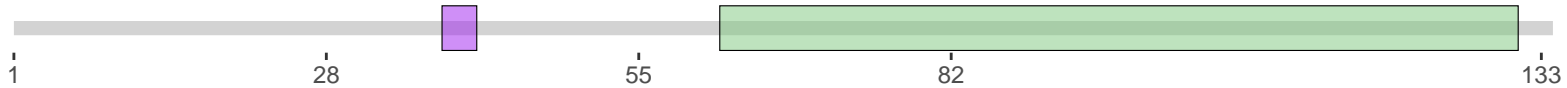
Gel Slice



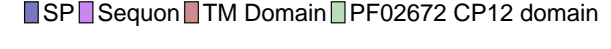
Protein length



Pfam domains



Pfam Description

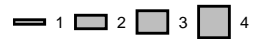


Protein sequence:

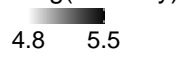
SATPDNKLSDLVAEGVKEAEAGAEAFVSGEGAAAWDVVEETSAASHARDKKKESDFLENYKDNFETDECRITYDN

NbL05g16240.1 V-type_proton_ATPase_16_kDa_proteolipid_subunit [MW = 11.42 kDa]

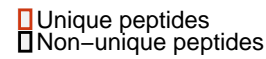
No. of times detected



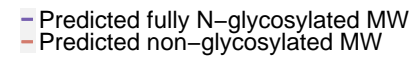
log(intensity)



Values from



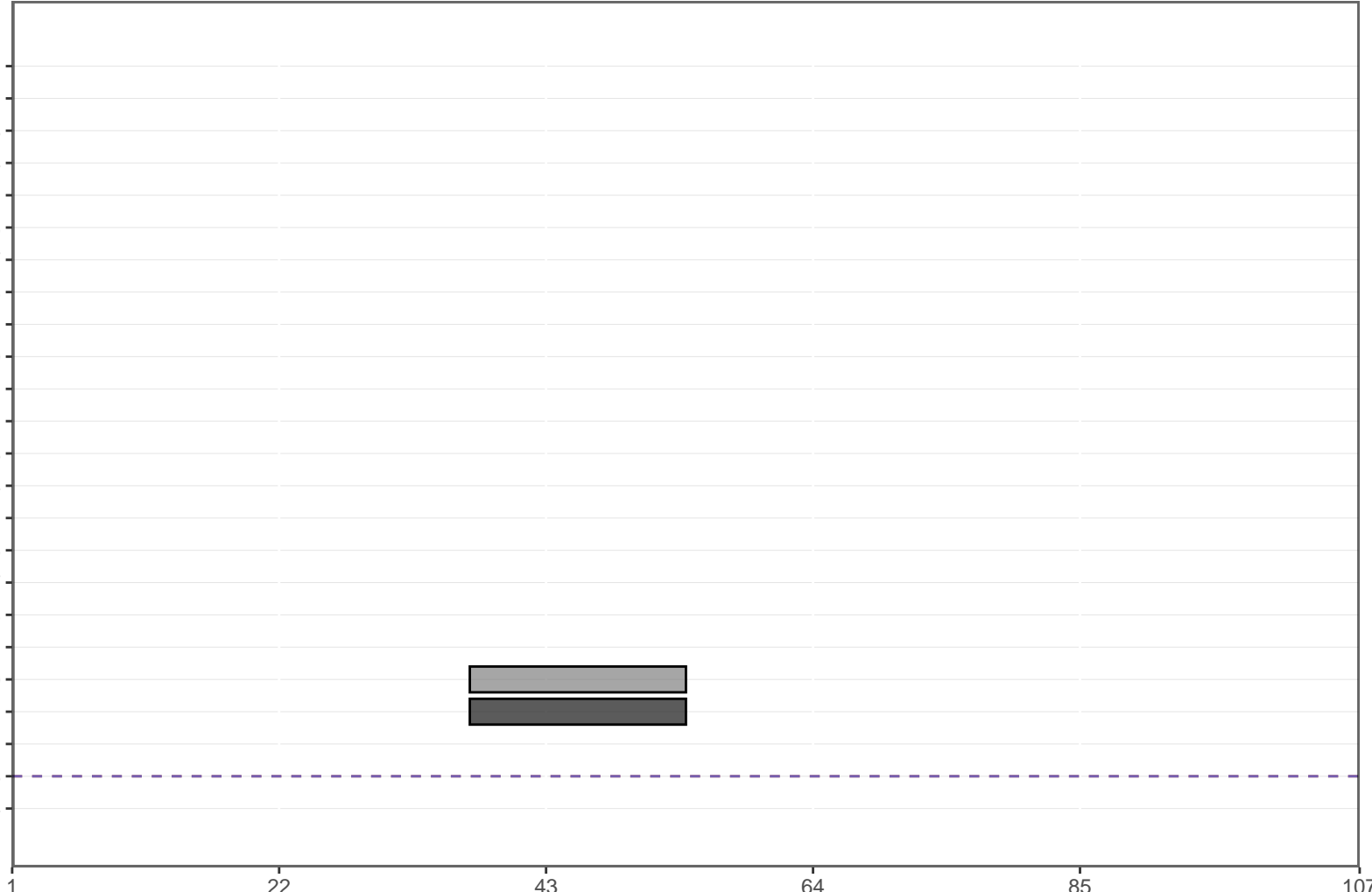
MW indication



Molecular weight



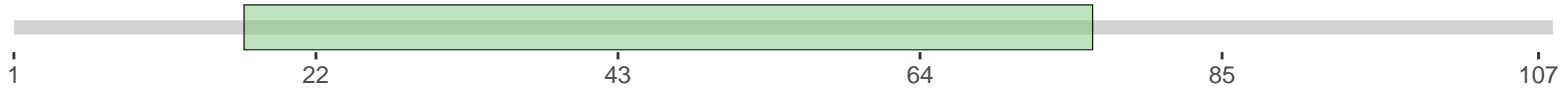
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

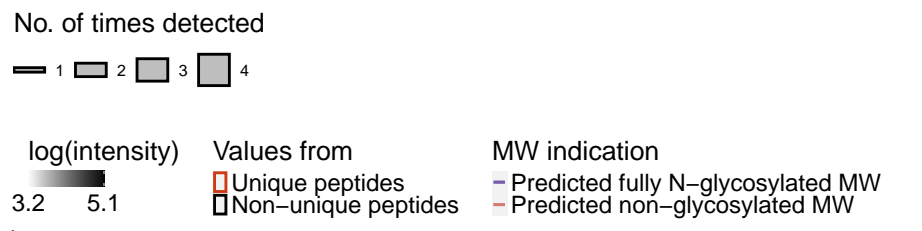
Pfam Description



Protein sequence:

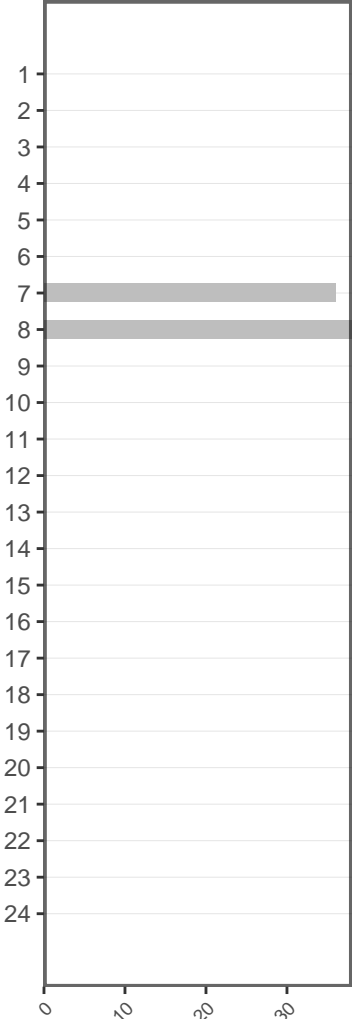
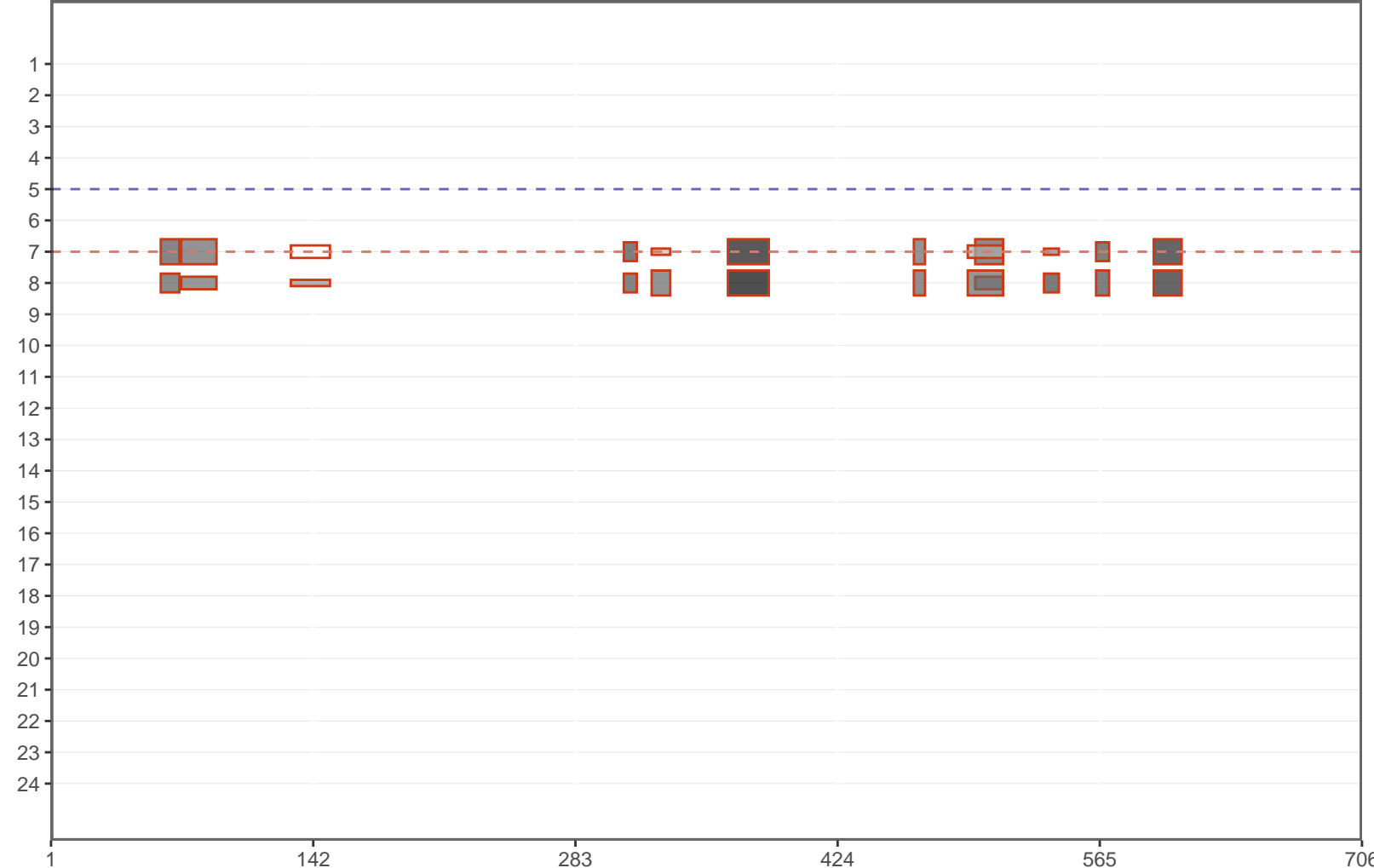
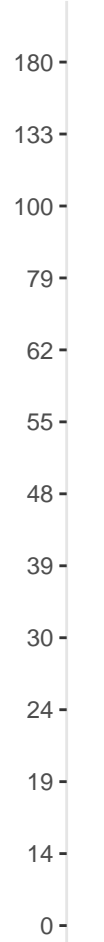
VGVASMGVIRPELVAKGSLVAMPGLVGHYGMIVVISTGINKTLHVFVRLGLFETVHFLNV*

NbL05g16220.1 uncharacterized_LOC109215494 [MW = 79.01 kDa]



Molecular weight

Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF07676 WD40-like Beta Propeller Repeat

Protein sequence:

LNPPTHYNYFFSPEATFLSYRFRGESSPGDGFNLDVVSPTKGLRMLRLNGSFPSPGDFIAFNGDFANSLKIVKSDGSKRWTLFKGRITTFGNSWFAEPNVLTSVGPVDFSVKATVQIARVSEFLDNLNEDGAGEIPLEIKVLTKEETGNNAFFSGSPDGKHMVFRSGRSGKNLVMDAMKGELEGSEIRQLTEGPDWIDTMPFVSPDGLIAFSSNRHNPDNISGFSYVHPDGTGLRRVYAGPFGSEEDKERLNHVFGRKDEWLLFTANLGGVTAEF

NbL05g16150.1 nitrogen_regulatory_protein_P-II_homolog [MW = 23.6 kDa]

No. of times detected



log(intensity)



Values from



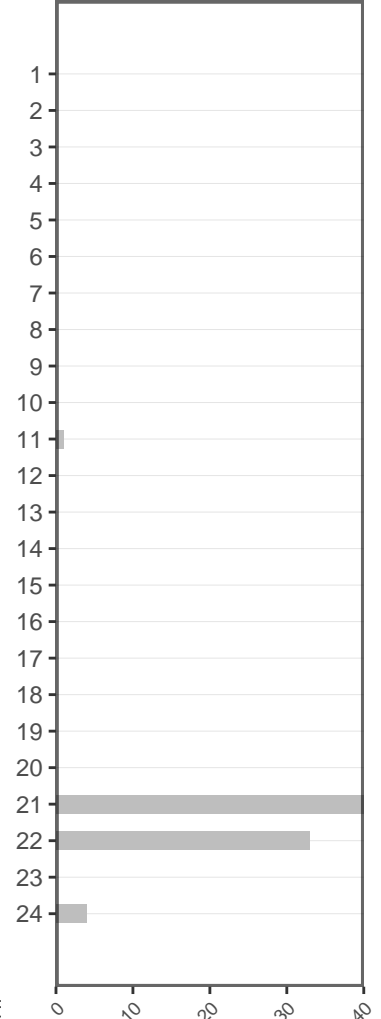
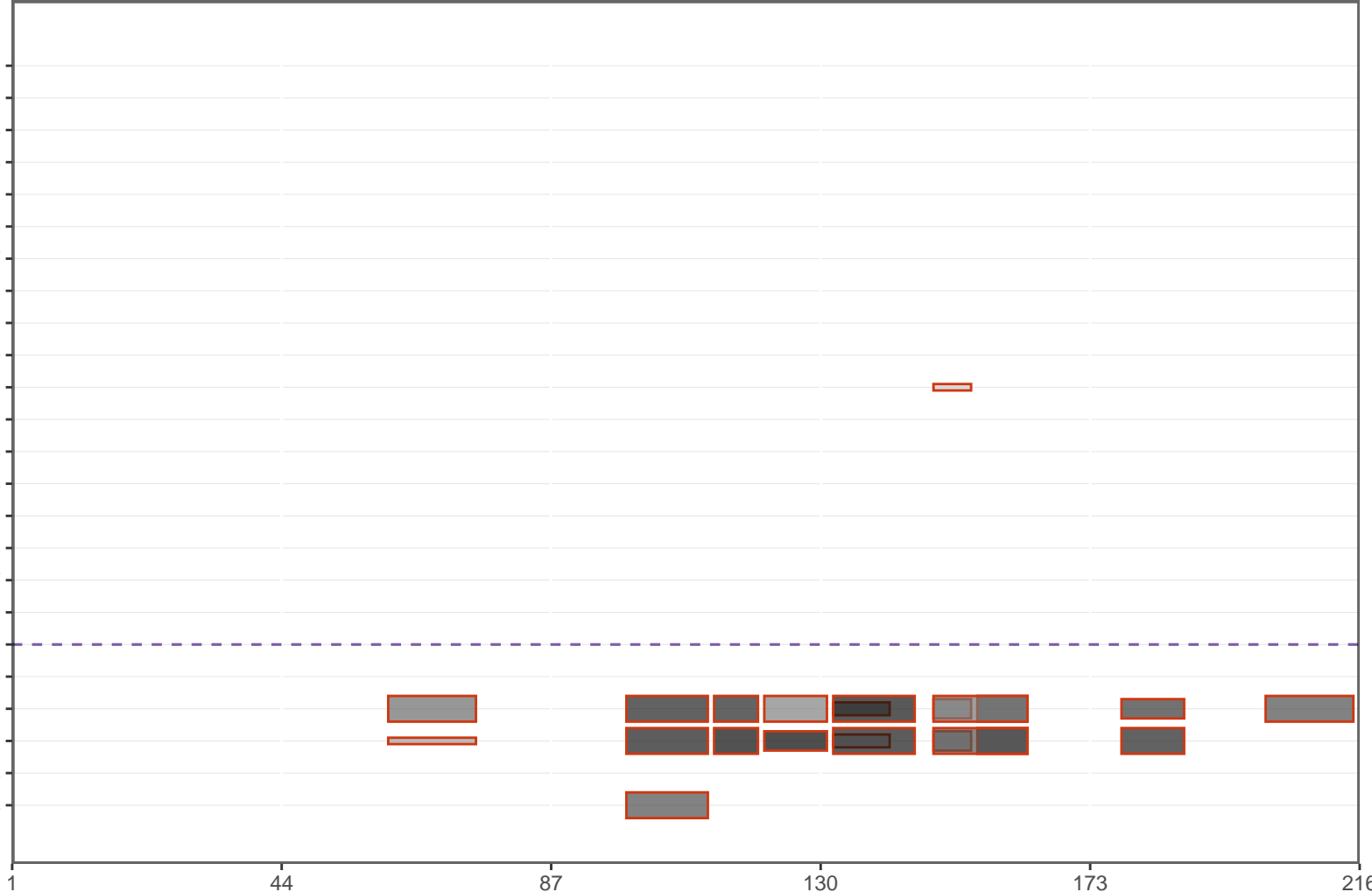
MW indication



Molecular weight



Gel Slice

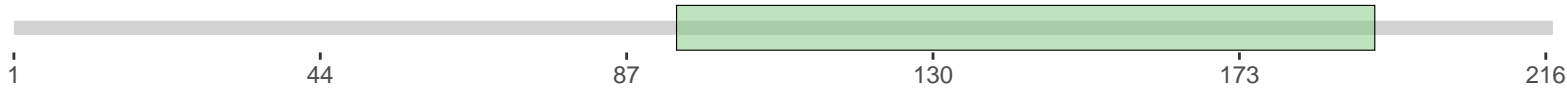


Peptide counts over 4 repeats

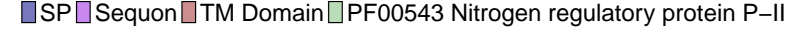
Protein length



Pfam domains



Pfam Description



Protein sequence:

RIQQVSSALLGMGRGVTVSDVRFGRGAGGLTERDAGGSEFSEDFKFAKWKMEIVVKKDQVEGVAKIIEEARTGEGDGGKFLIPEDVIRVIRTGERGEKAERMVGGHADMSALETSP

NbL05g15890.1 GDSL_esterase/lipase_At2g23540-like [MW - SP = 38.27 kDa]

No. of times detected



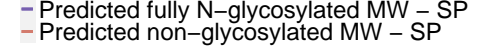
log(intensity)



Values from



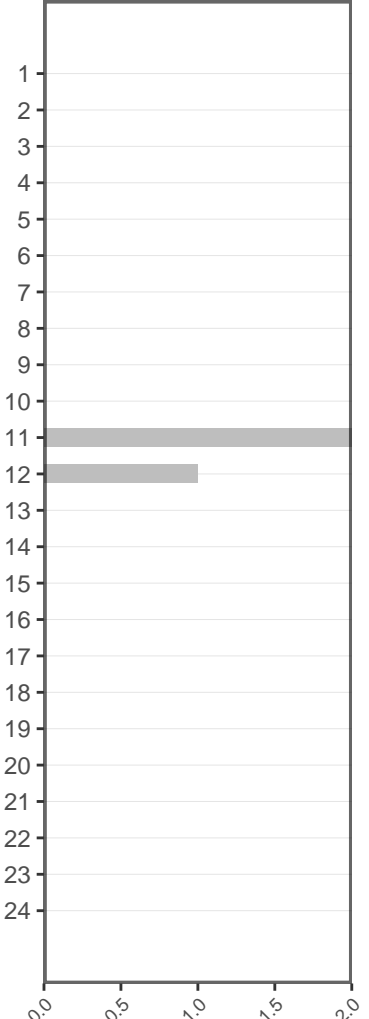
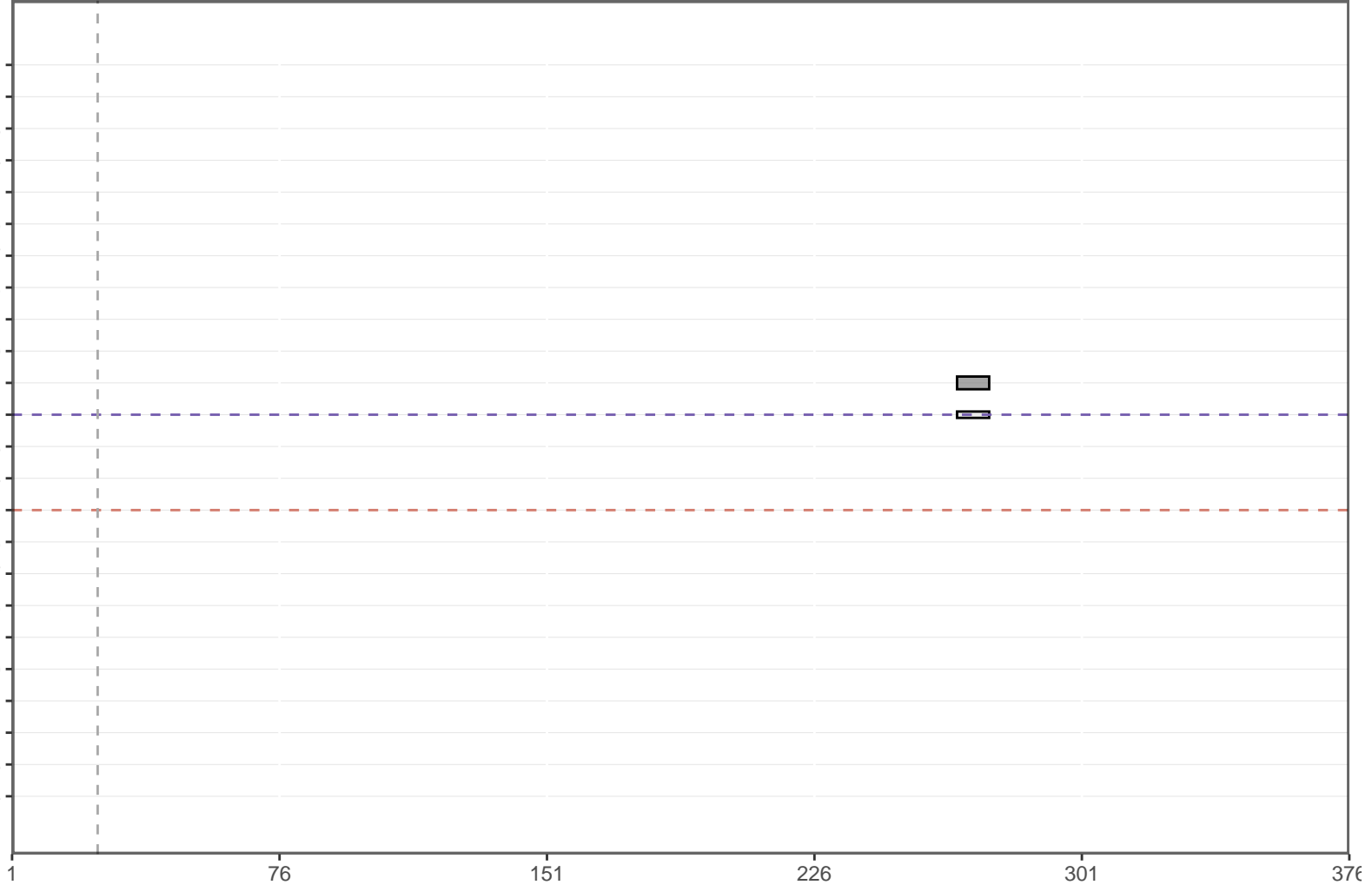
MW indication



Molecular weight



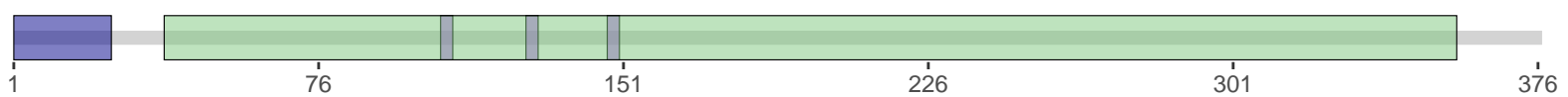
Gel Slice



Protein length

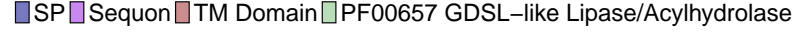


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGSNDFLNYYLLLVLSIGTRITRESFDIDLLHKAQLTRLYKLDARKFIGNVPSPGGIPYKTIKNGLKENEGVELANIKALQGNARLKDMLSEMKNKLDGATFLHANNVDLVMELTNYDKYGFATATKADGENSGGFAGVPCGPTSGMCGSDGDKHVFWDPPYHPTFEANLIJAKLLEGDPTYSFMNLKQLRDLI

NbL05g15840.1 40S_ribosomal_protein_S11-like [MW = 20.79 kDa]

No. of times detected



log(intensity)



Values from



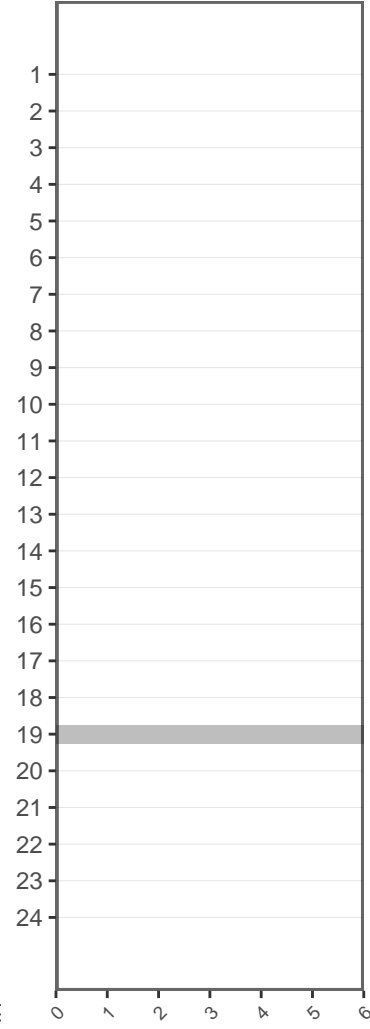
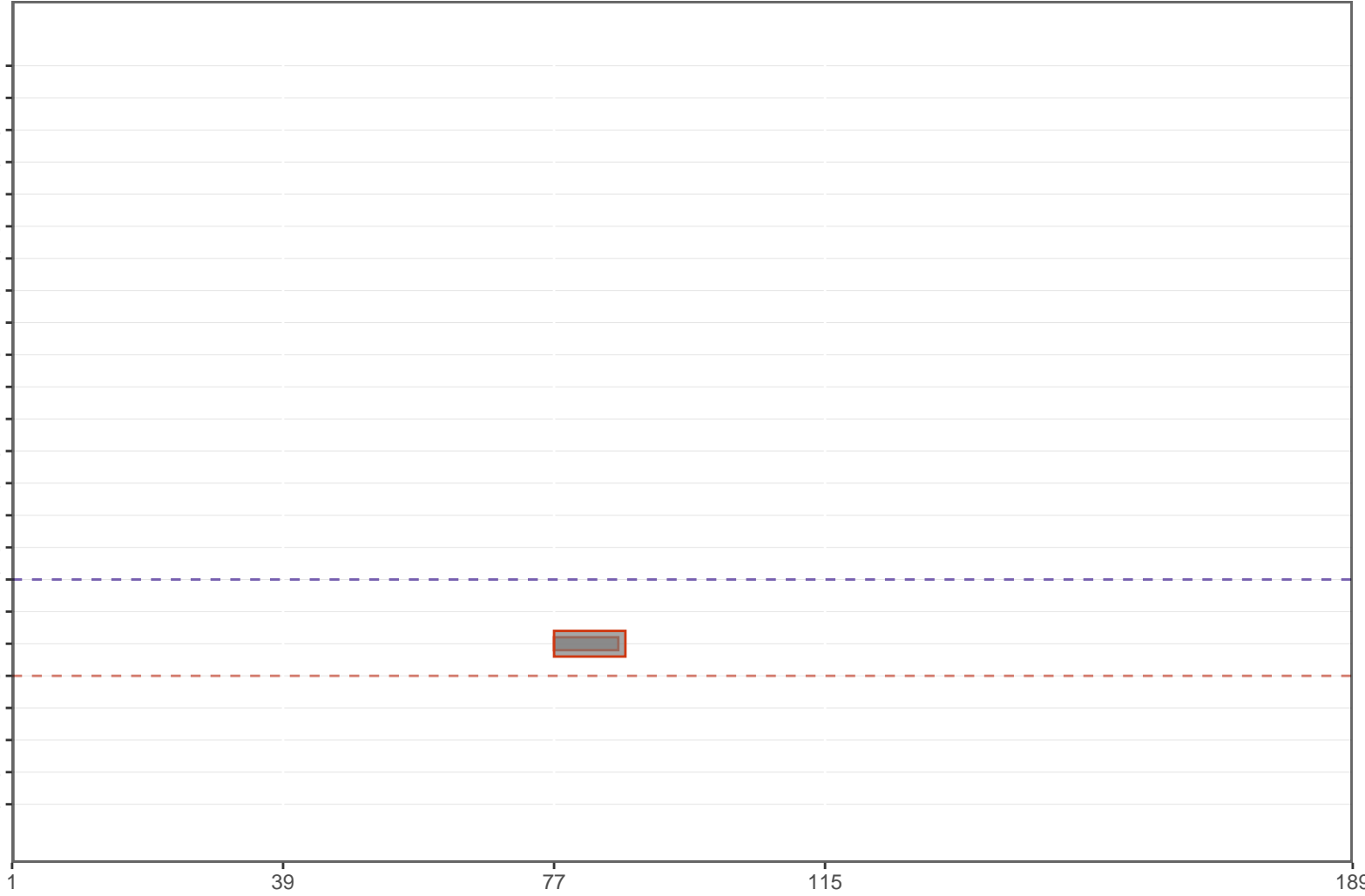
MW indication



Molecular weight



Gel Slice



Protein length

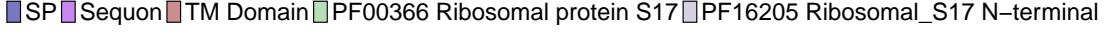


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

GFYIDKKCPFTGNVSRGRLAGTCHSAKMRTHIVRRNVLHVKYQRYEKRHNFAHISPCFRVKEGDHWGGCRPLSKTVRFNVLKVPAGSAGGGKKAFTGM

NbL05g15650.1 60S_acidic_ribosomal_protein_P3-like [MW = 15.95 kDa]

No. of times detected



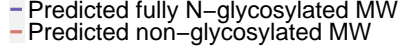
log(intensity)



Values from



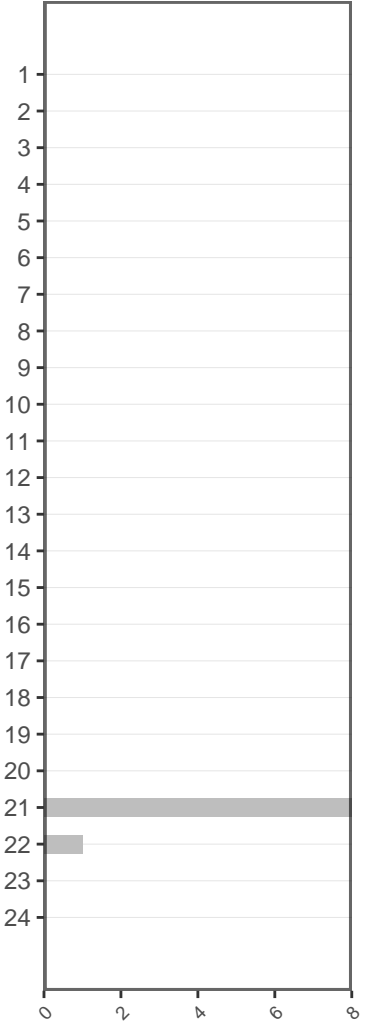
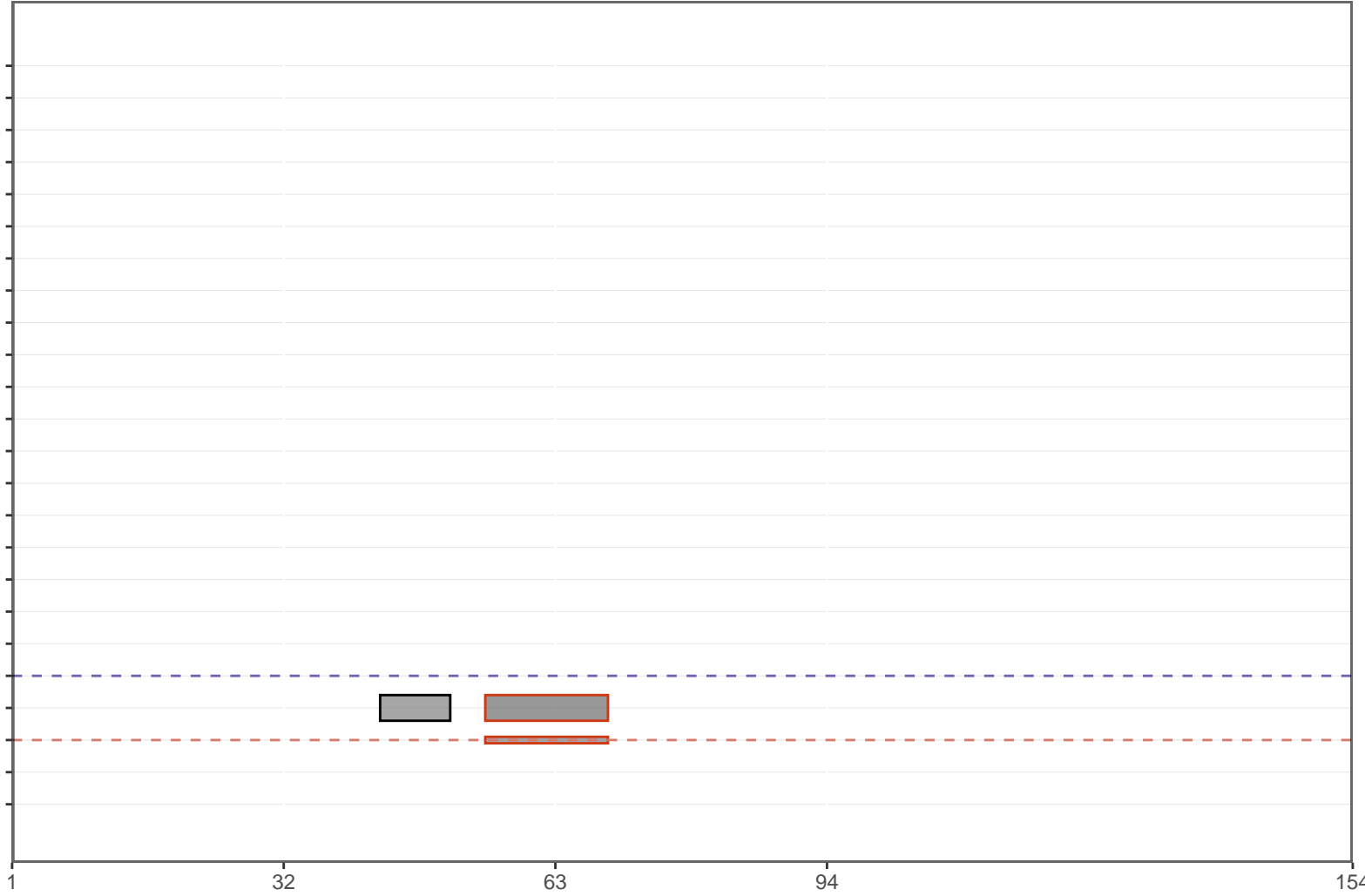
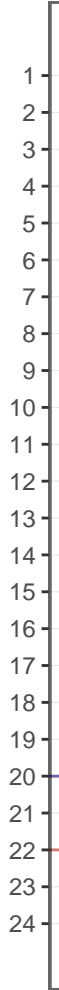
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

YDLORLKVQALSTDSGGVGSFVYTPSSAVFQVHGGGGGGFGGAAAAAPSGGAAAAEAPAAEKKKEEESDDDMGFLFD*

NbL05g15520.1 phospholipase_A2-alpha [MW = 27.22 kDa]

No. of times detected



log(intensity)



Values from



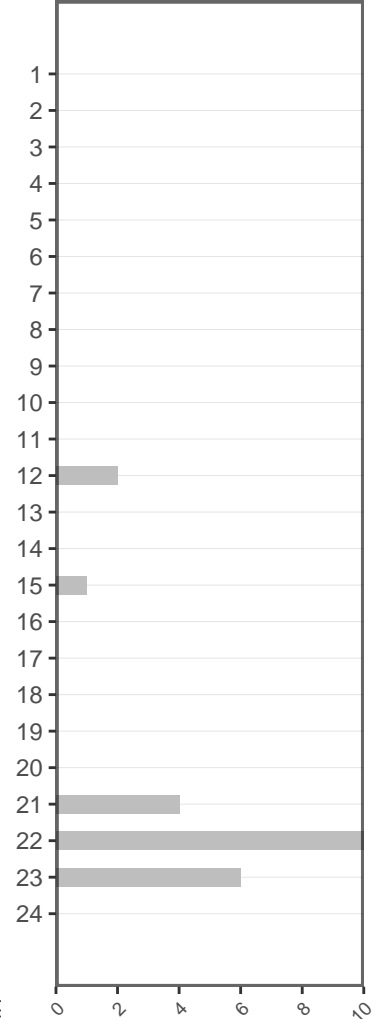
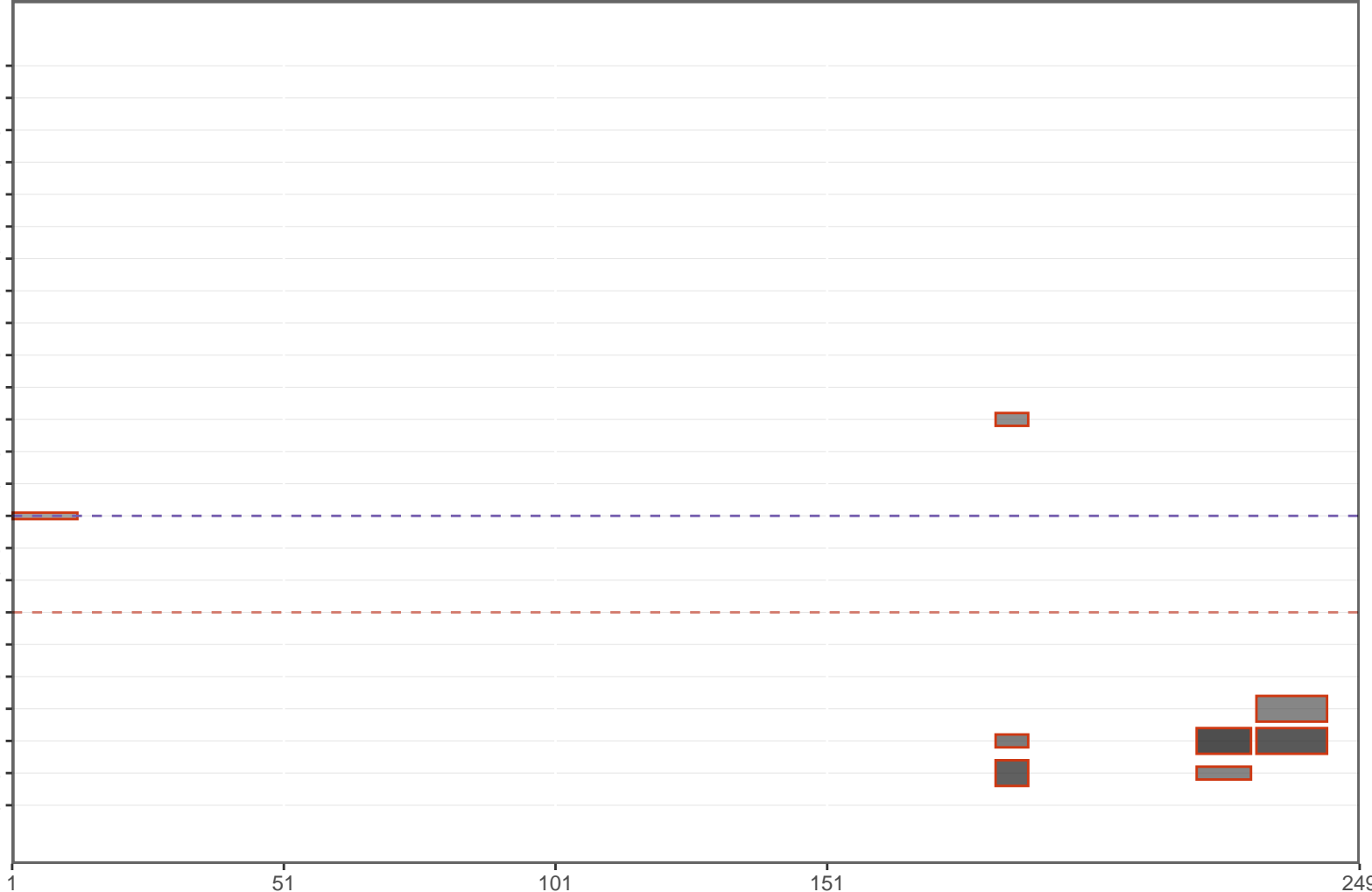
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

FSPTSYHALNGIETNAGISLEKEGSRTEGSEKFGAVPPLLRVYGYGGVLYSGSGPEQPDGLDTCGMKHDLGIQRKGNVYLNLECGNSFLNCVATFTKSGAPSKNGNSGVGTVYRVITDVIDAWVAKGFKKPK

NbL05g15510.1 peptide_deformylase_1A_chloroplastic [MW = 30.83 kDa]

No. of times detected



log(intensity)



Values from



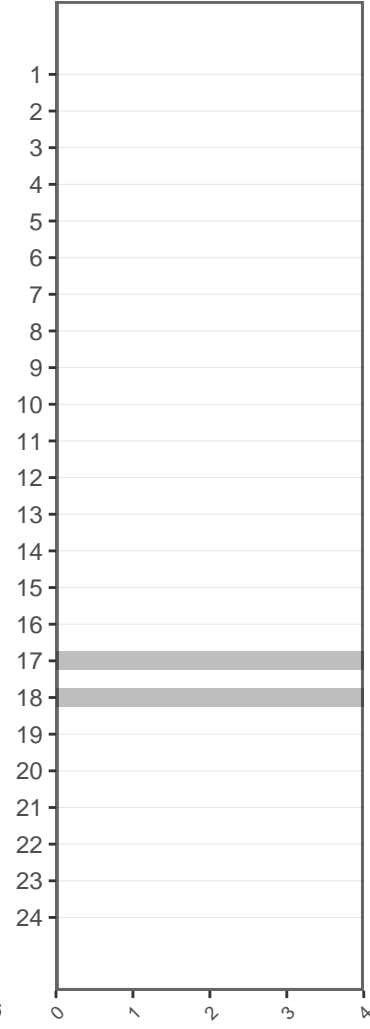
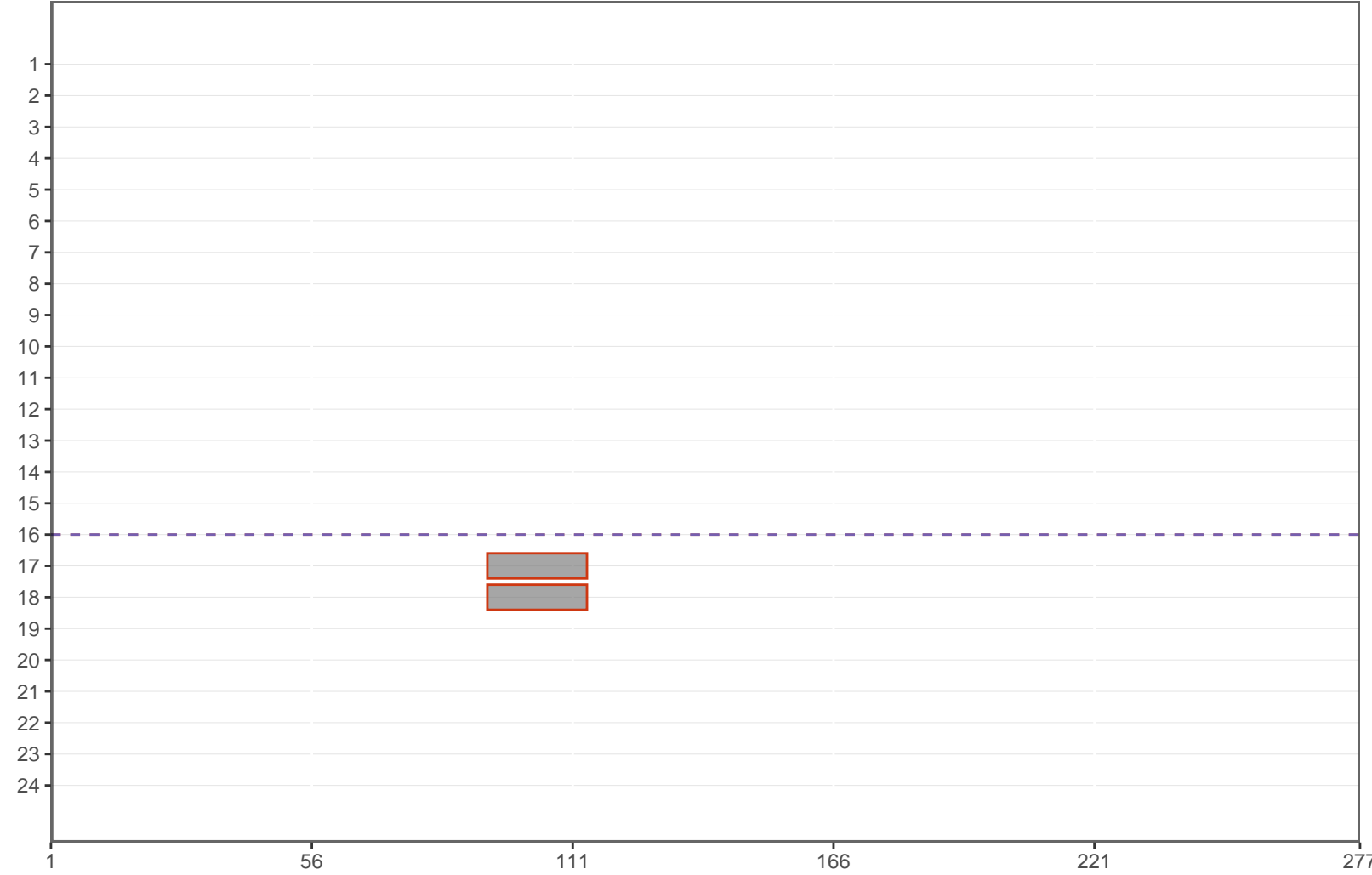
MW indication



Molecular weight



Gel Slice

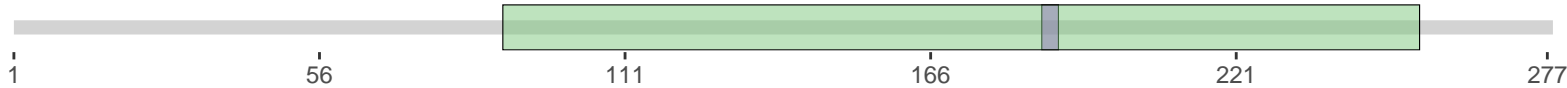


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

/MRNAPGVGLAAPGIGPLKIVLEDTNEVSYAFKDETKAGDRGPFDLVINPKLKKKDKNTLFFEGGLSVDGFRAYVERHLEVEVGGFDRNGKAHKVDASGSGARLQHEYDHLDDTLVYDKMVPRTFRFRVENLDFLAAGGPNLGVRI

NbL05g15410.1 proteasome_subunit_beta_type-6-like [MW = 17.29 kDa]

No. of times detected



log(intensity)



Values from



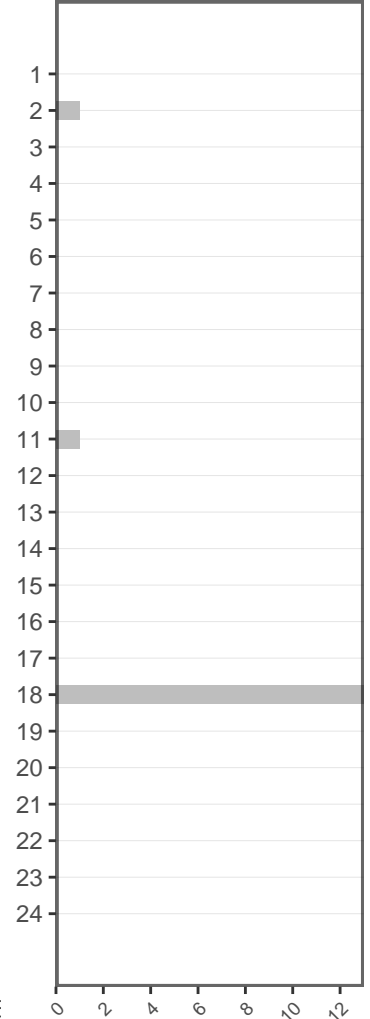
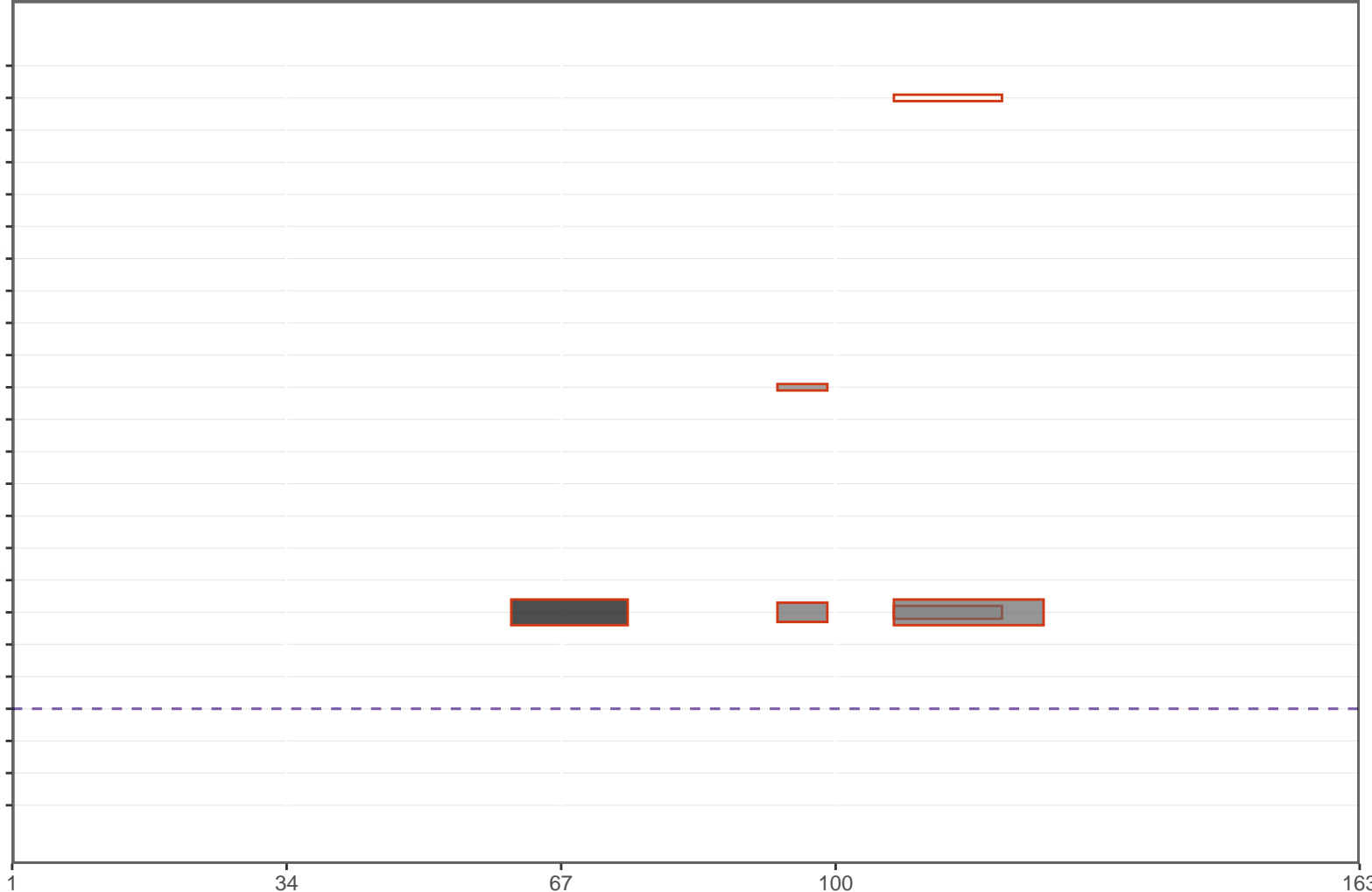
MW indication



Molecular weight

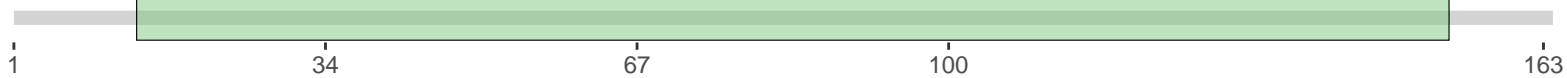


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YVSDYRYFLHCHTDLGGPRFVVAANLRLLEBYNNKAMLQTMIGGWDKYEKGGKYGVPLGGTLEQPFPAIGGGSSVLYGFSTKHOGKE

NbL05g15350.1 lysine--tRNA_ligase-like [MW = 69.81 kDa]

No. of times detected



log(intensity)



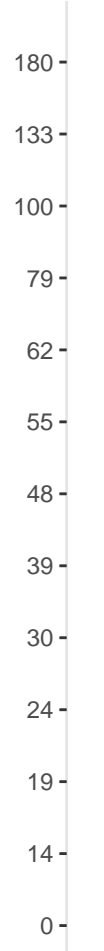
Values from



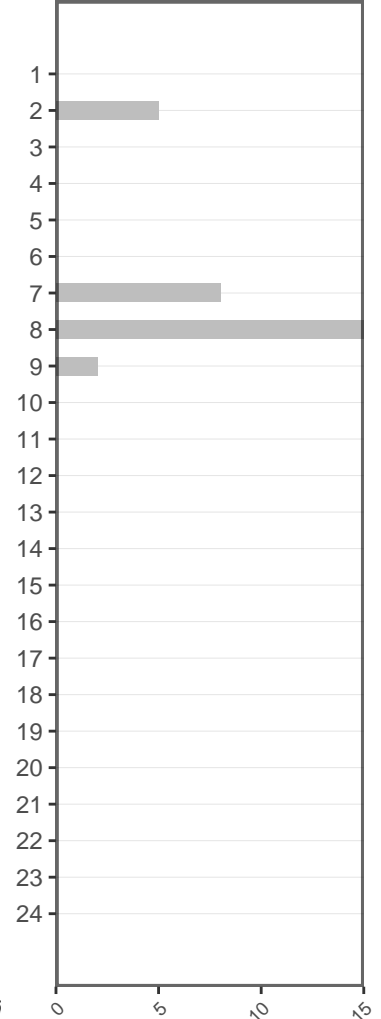
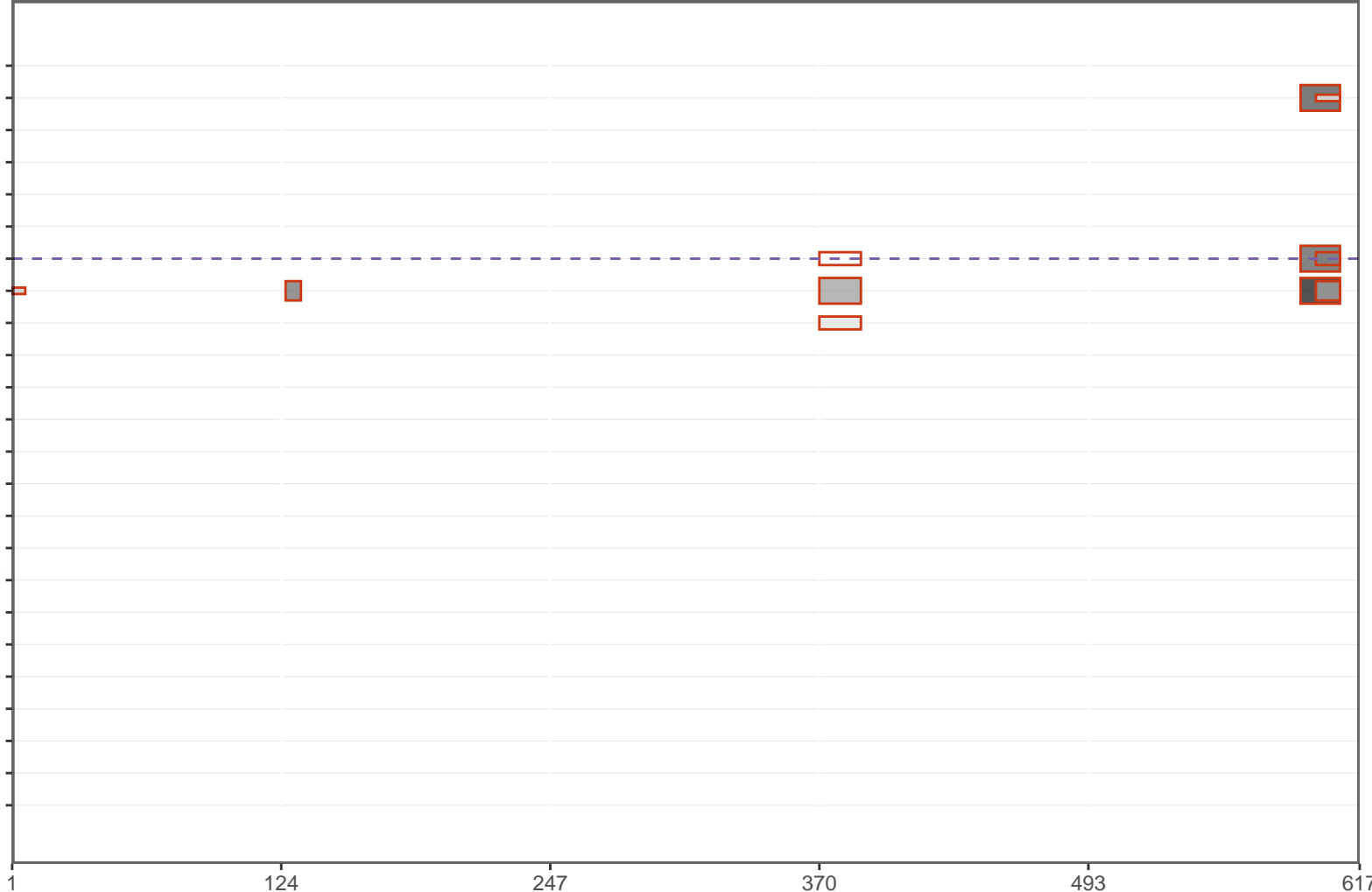
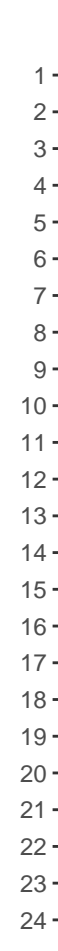
MW indication



Molecular weight



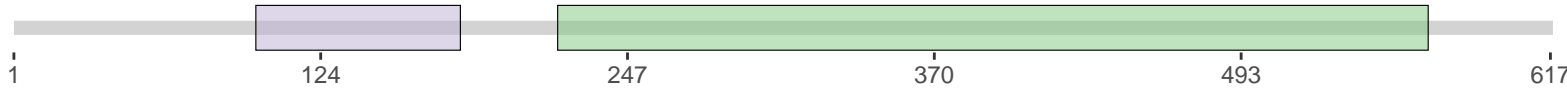
Gel Slice



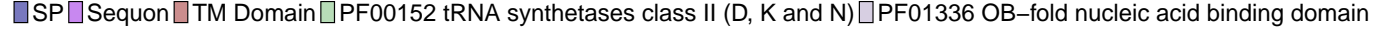
Protein length



Pfam domains



Pfam Description

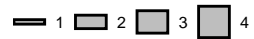


Protein sequence:

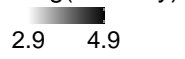
'MRIAPELLYLYKELVYVGLDRLVVEIGKGFNRNEGIDLTHNPEFTTGFYMAVDYNDLMDLTKMLSGMVKELTGGYKYHANGLENDRPEIDFTPPRRDMVEELEKVNANLNPKDLSSVEANKYLDAGARLEKGFPPDGTARLLDKLVGHLEETGVNPFANINPEIMSPKAKWHREKPGLTERFELFNKHELGNAYTELENDPVVQGRQRFADQLKDRGSGDDEAMALDENFTALEYGLPPTGGWGLGIDRLMLLTFDSQNIKEVLLFPAMKPPQDEPRKESNKKQPEESA'

NbL05g15200.1 pectinesterase/pectinesterase_inhibitor_PPE8B-like [MW - SP = 56.68 kDa]

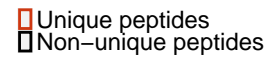
No. of times detected



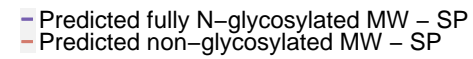
log(intensity)



Values from



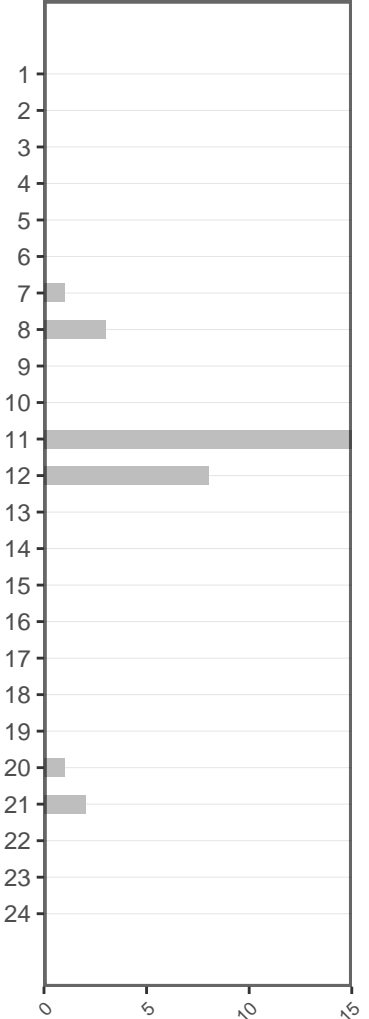
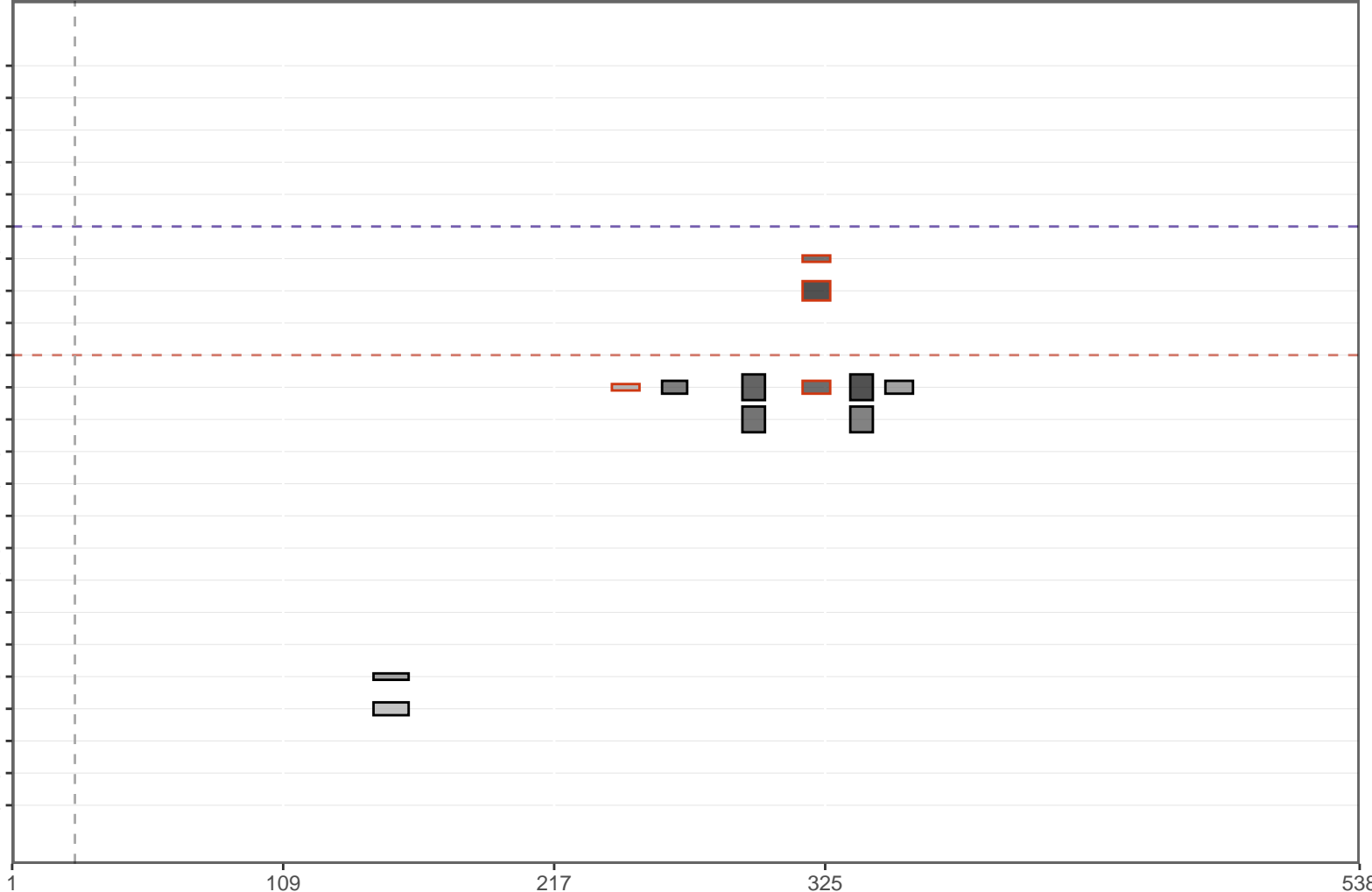
MW indication



Molecular weight

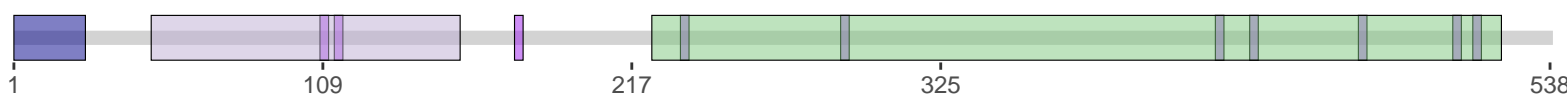


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

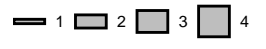


Protein sequence:

IKKGYNEYEISKKWNLMDGGDEVTVEBGNRSPFDGWTTFYRSATFAVKGQGFARMTFFENAGPQKHQAVAFRSDSDLEVLFRGAFRGYQDTLWHSMDQFYRNCVITGTVDYDFDGDGTLYFQNGQILARKLPEQKNITTAGGRKEAETTFGFSIQFNSGEPDLLASLNSGTQFLGRPAKAYSRVTVMDSYMSNVKPKQGWLEWNGNBLDTLYVAEYQNYGPGAGLSARVNWPGYHLLNDSGGANNFTVAGFILGNWLPSTGWYTAGLAW*

NbL05g15120.1 plasma_membrane_ATPase_4 [MW = 105.24 kDa]

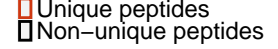
No. of times detected



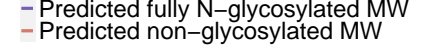
log(intensity)



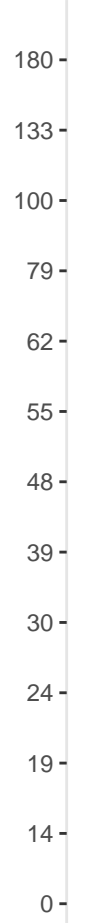
Values from



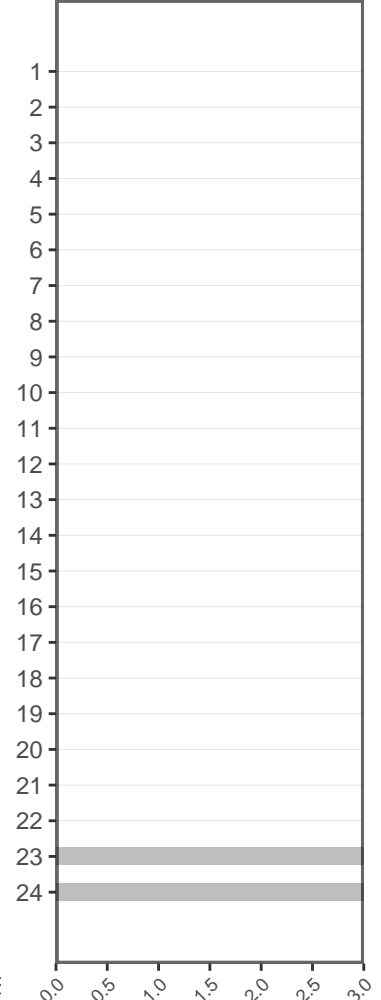
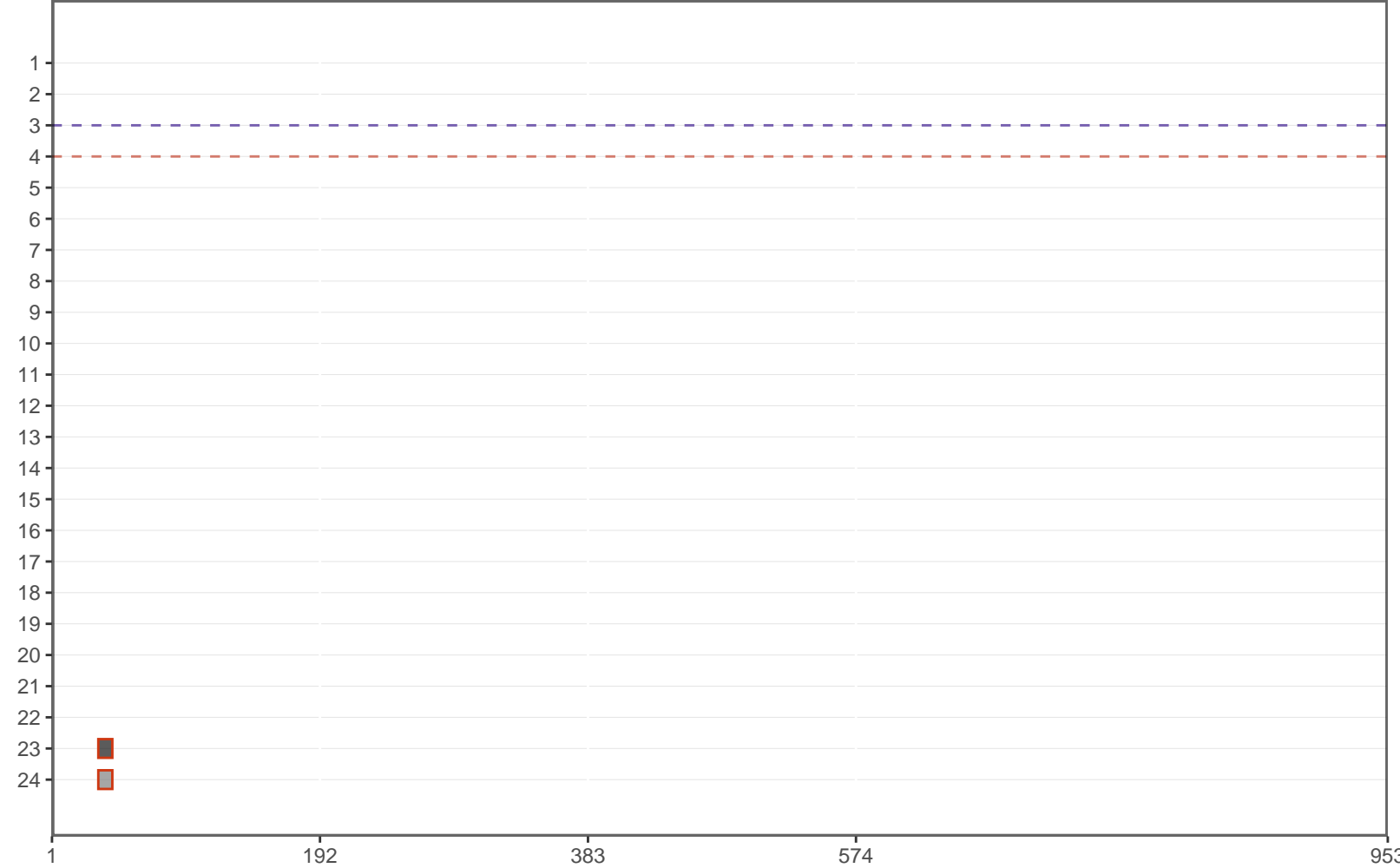
MW indication



Molecular weight



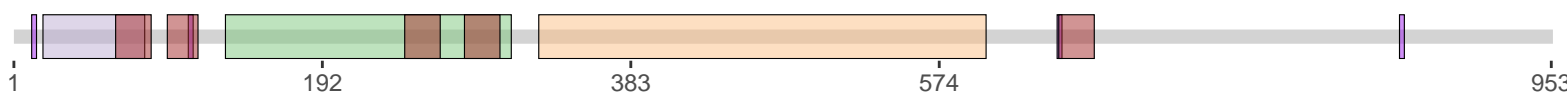
Gel Slice



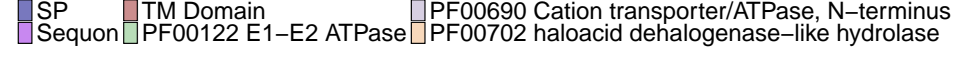
Protein length



Pfam domains



Pfam Description

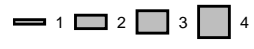


Protein sequence:

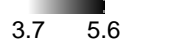
ARQEVPEKSKESFGGRWFEVFDVLPFDPRPHDSAEITRRALNLGVNVMKMTGDQLAAKETGRRLMGNTNMYPEASLLGDDKDSASLPLVEELIEKADGFAGVFPPEHYEYKVLGERKHIVGMITGGVNDAPALKKADIGIADATDAARGASDIVLTFEPLGVISAVLTSRAIFQRMKNYTHAVSITRIVFGFMFALIWQYDFSAFMVLIHAIINDGTMITISKDRVYKPEFMPDGSWKLKEIFATGVVLGGYQALMTVIFFWAMHDTDFDFKFGVKSLRNSDEEMSAALYLI

NbL05g15070.1 putative_glucose-6-phosphate_1-epimerase [MW = 35.54 kDa]

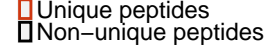
No. of times detected



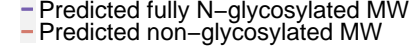
log(intensity)



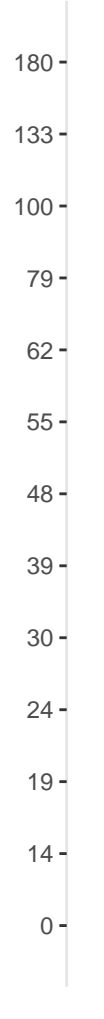
Values from



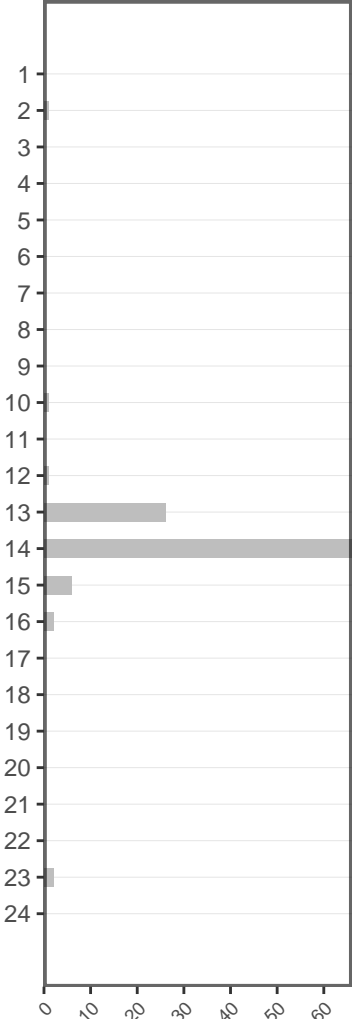
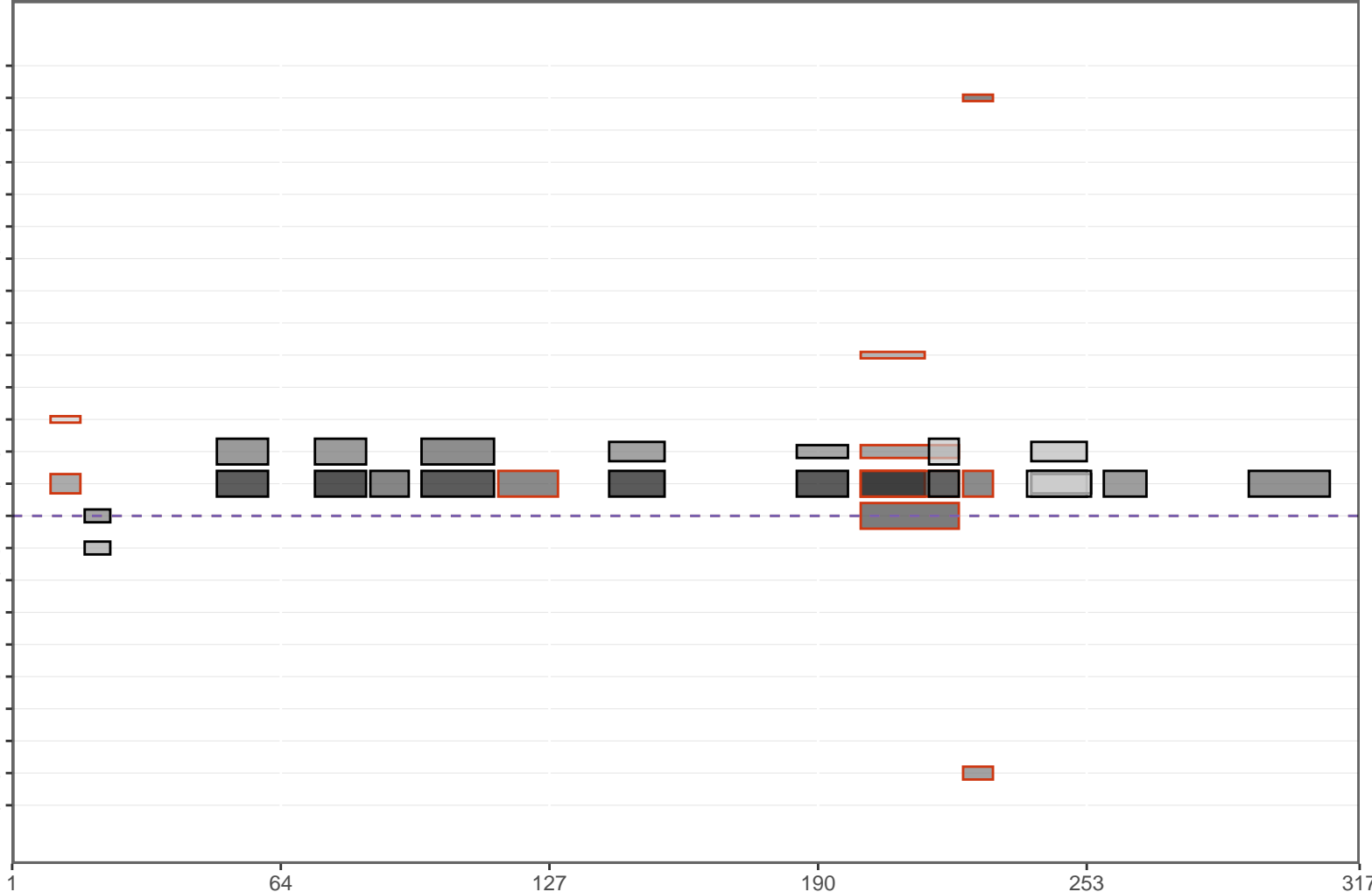
MW indication



Molecular weight



Gel Slice

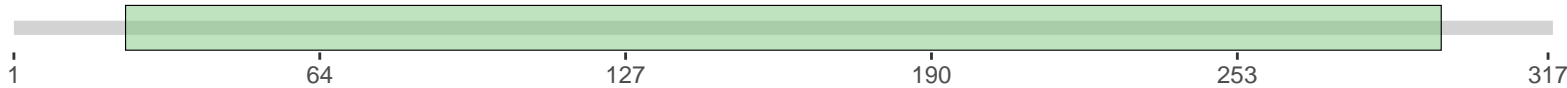


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

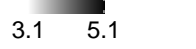
IGDLMLTSRIRNTYTDGKPFSTFAVHTFYFSDISEVRVEGLETLQYLENKRERFTEGGDAITFESEVDKYLSTPTKIALDHEKRRFTVLRKDGLPDVAWNPWDKKAAMADFGDEEYKMLGVEAAAEKPTLKPGEVWRGRGELSAVPSYSGGGLDKRVLGGP

NbL05g14960.1 uncharacterized_LOC104245598 [MW = 115.33 kDa]

No. of times detected



log(intensity)



Values from

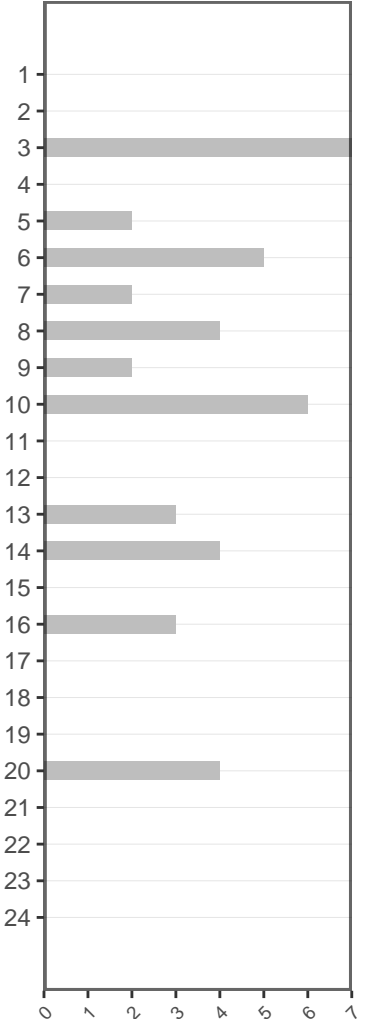
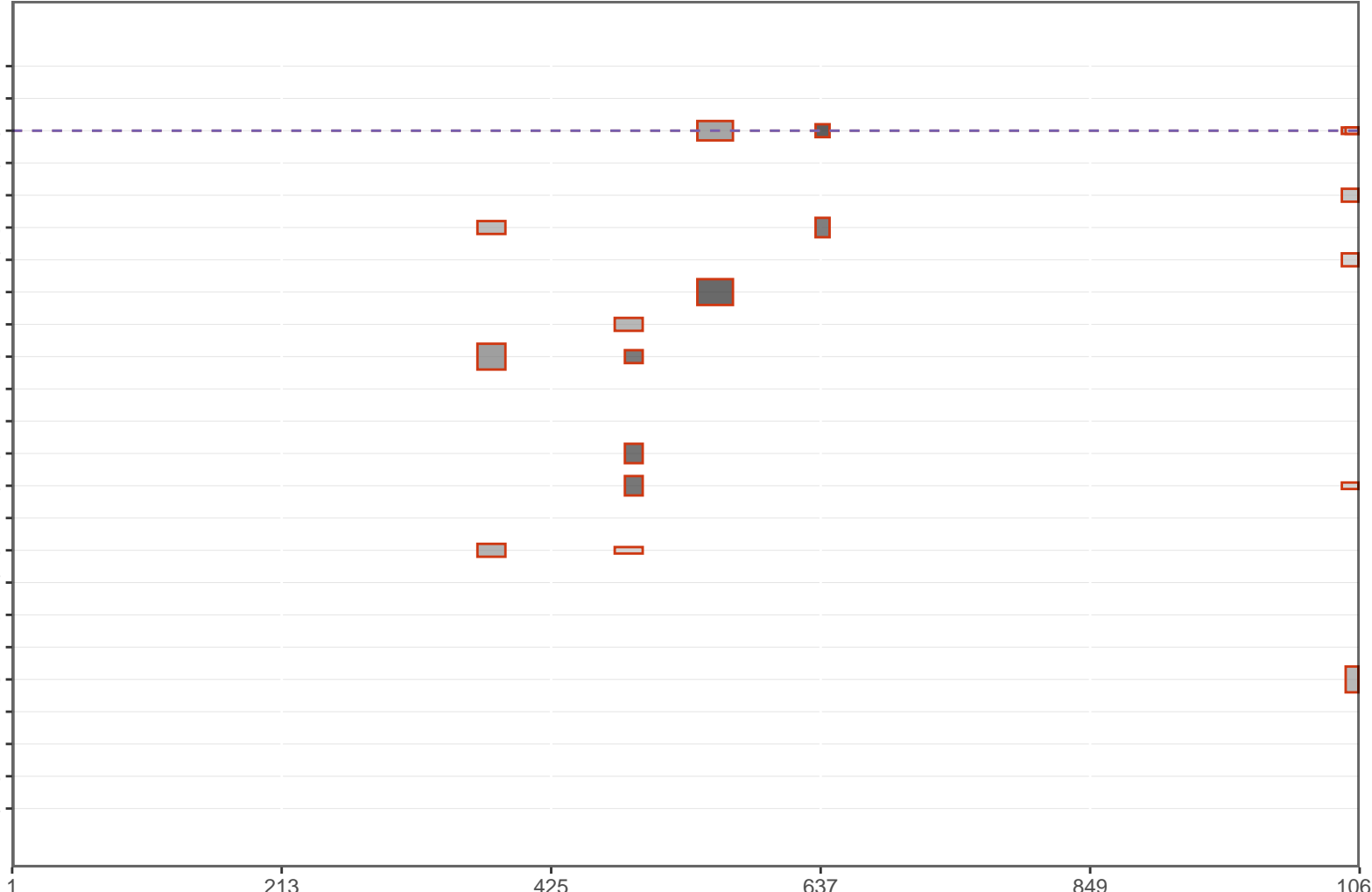
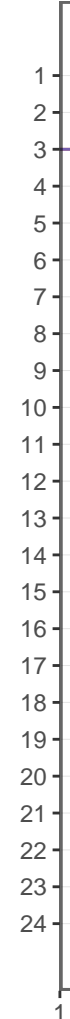


MW indication



Molecular weight

Gel Slice



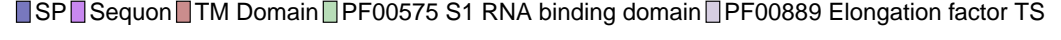
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

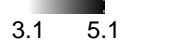
IQSEAPLENISKDEVGGEGAEVVEKRVENTPSIEDQSSDTAAGQEEVATAEODRNVANSSEQNGTASSNEAAAKDRNVAKSSERNGTALNEAAAKAISPALVGLREETGAGMDDCKNALSETGGDIKAGEYLRKKGLASADKKSSRATTEGRIGSYHIDSRIGVLIENVGETDFVSRGDFIKELVDLAKMGAAYPQVGVLYPEVDVPEEINKEREIEMQKEDLLSKPEQIRSKVDRNKRLEELALLEGPYIKNDKLVKDWVKGDTATIGENKVKRFYRYNLGEGLEK

NbL05g14930.1 uncharacterized_LOC109234215 [MW = 71.67 kDa]

No. of times detected



log(intensity)



Values from



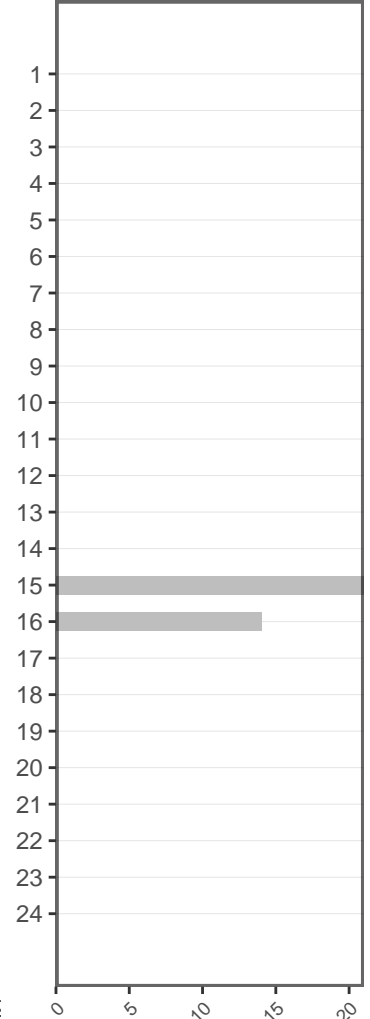
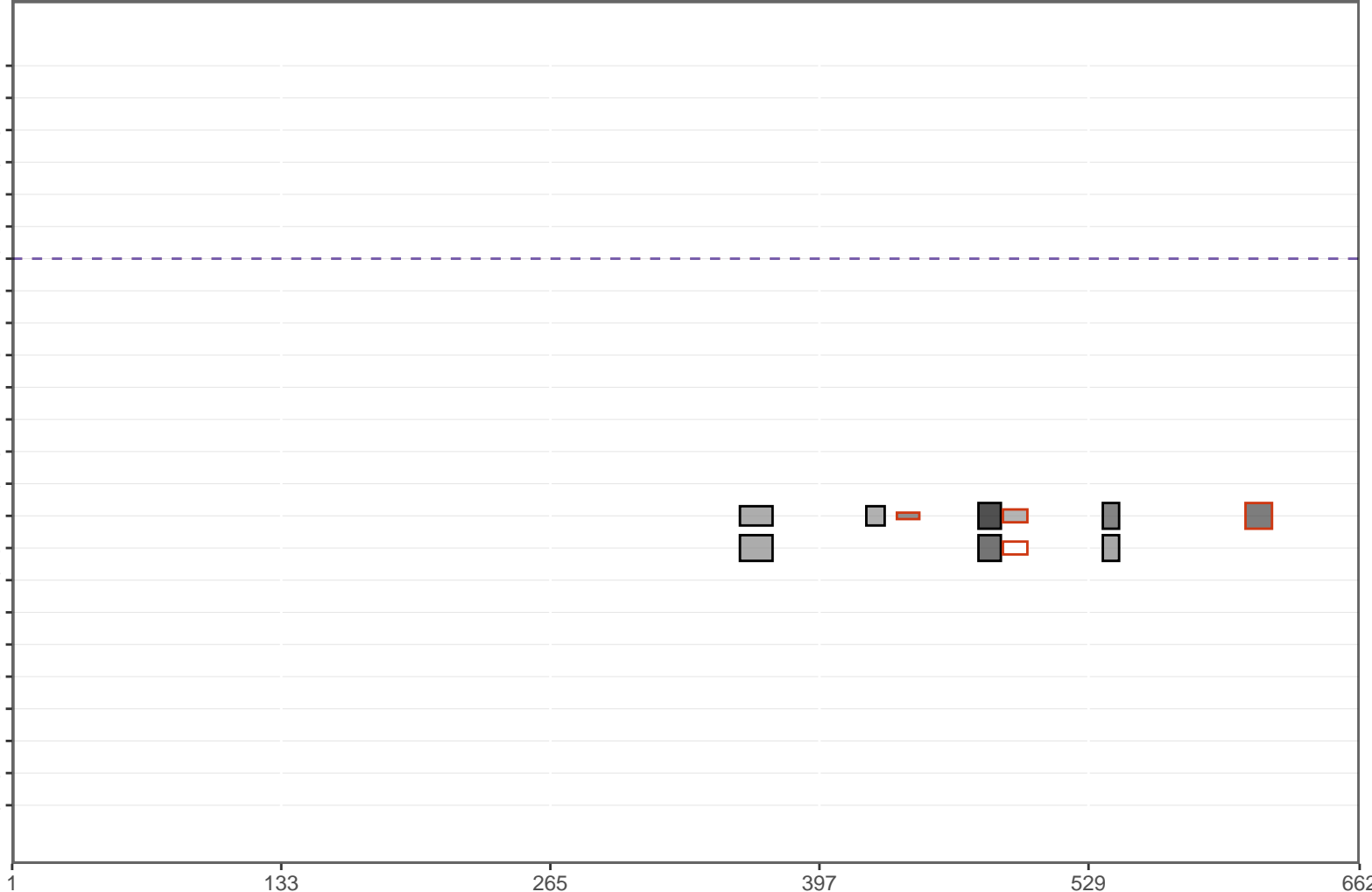
MW indication



Molecular weight



Gel Slice



Protein length

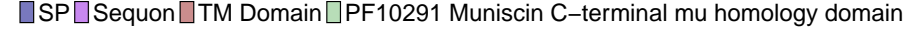


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

GIEFSNDGSLTQQDFEGINDAWGGGLDASEYVGTTHKVKDKDGLGGLLELETSEPPKAAAGAAATDGGAGKLEDLVKKMNGPEMFTTEINAERFRESLLARVGLMGVFLRFLSPKSSDDKETEFSFKVEGTAGVWRKRFVMMQNSHVBSLGNGLFHWKATAPSNKPIKYSLLPLPLPLRIRLVKRLSGTLLSVMGLVYANPDLVPLTNTVTEVHLKLPVDPFLKVTPKAVLNREBELKWHVDEIPLKHPGKLRARFPVINDDDGGSEELVLFQVYKRSOGPRLLSGSLC

NbL05g14920.1 (DL)-glycerol-3-phosphatase_2 [MW = 27.28 kDa]

No. of times detected



log(intensity)



Values from



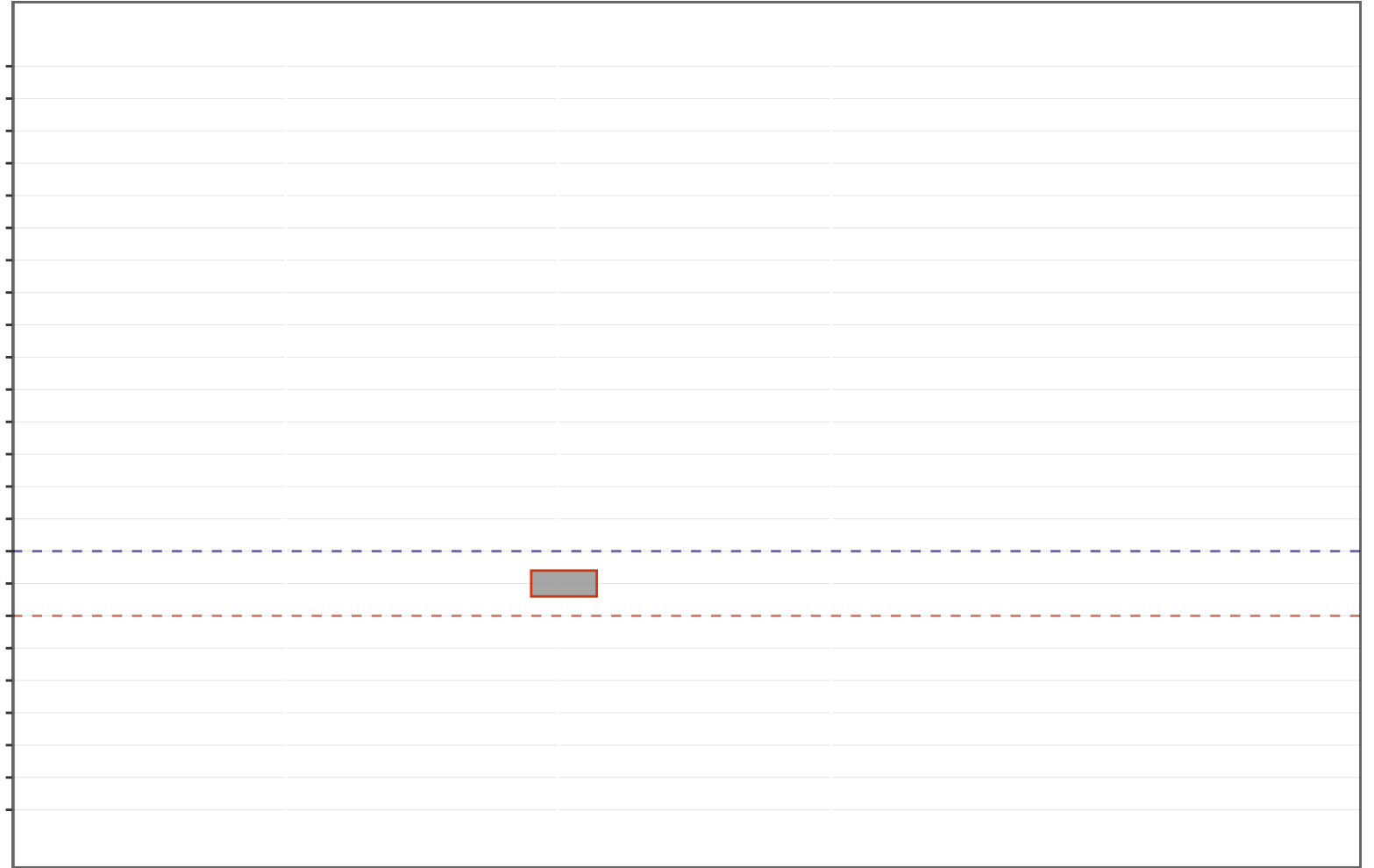
MW indication



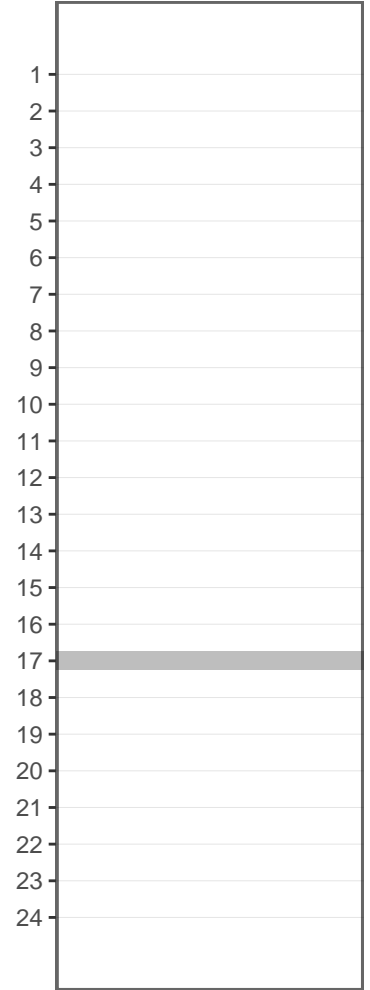
Molecular weight



Gel Slice



Protein length

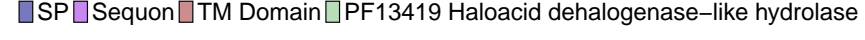


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILHANGIPICVATGTRHFDLTKRHHGELFSLMHHVRRGDDPEVWGGKSPDFLAAANRLKGGPVDQRRLVFEDAFSGVLAANKAGMEVVMVQDARLDSSHYEVAADGVLSGLLDFNPAWGLPPFENSSTKLD*

NbL05g14860.1 replication_protein_A_32_kDa_subunit_A-like [MW = 27.14 kDa]

No. of times detected



log(intensity)



Values from



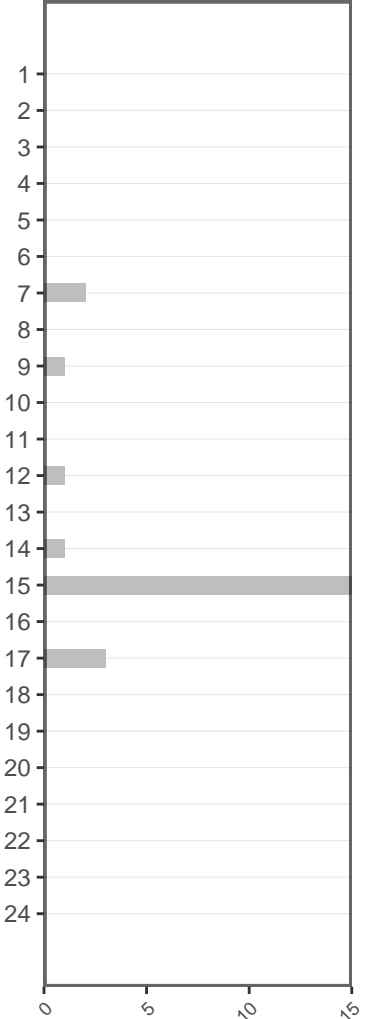
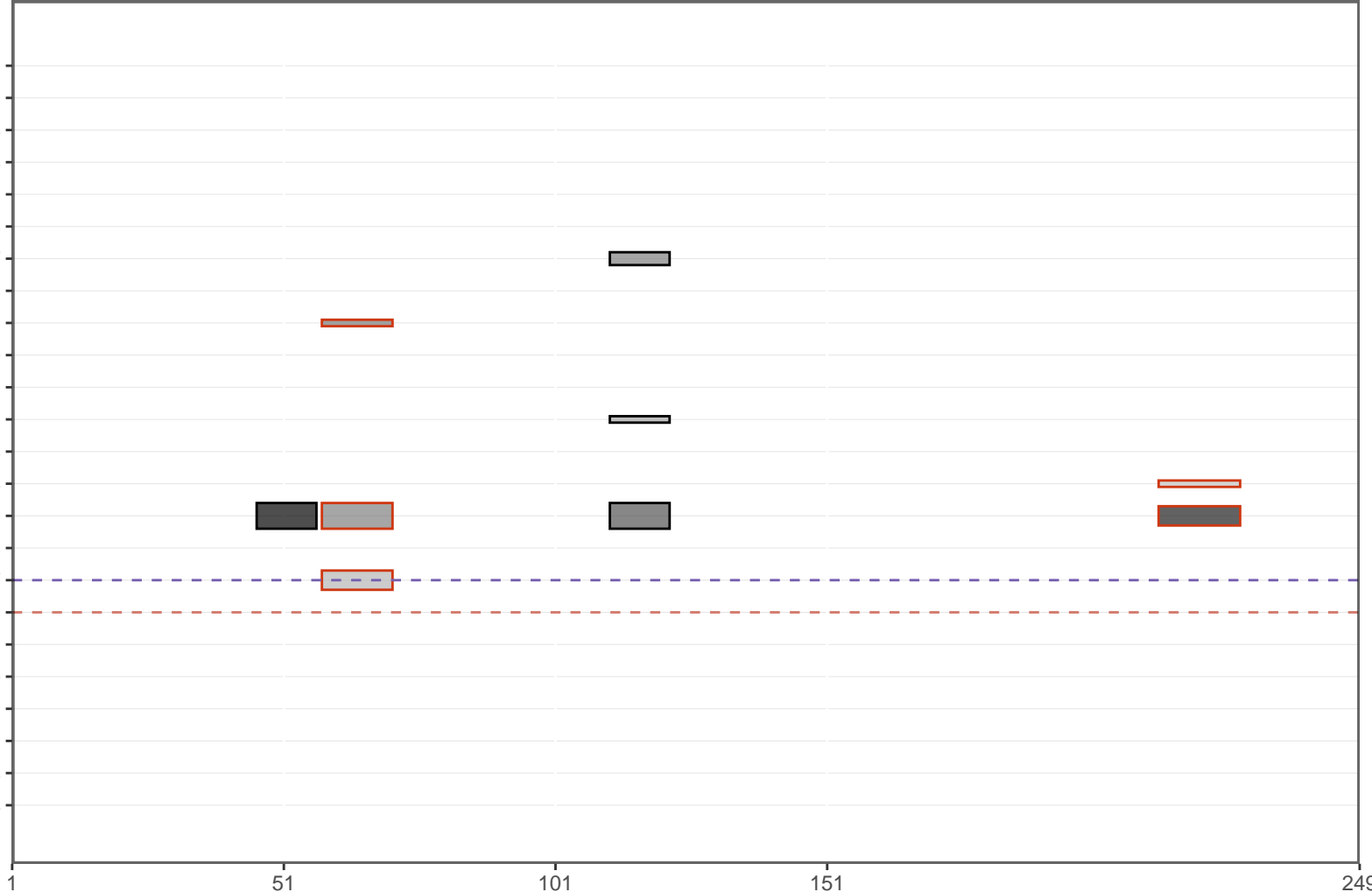
MW indication



Molecular weight



Gel Slice



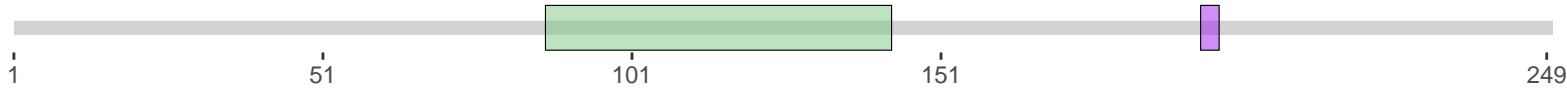
Protein length



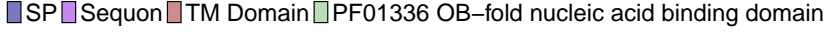
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

CEVEVSDGMYYRVHGHKGFQKTLQVFAIRPITDNEVATHFLECHVYHHCNRPQSGSIVAPDGTDSAAVAAPSSGFNSQLSGHLSIDGLKGIKAWIDYLEQPSLSGDEKGIHWNELLNKFLWRKRGRQ

NbL05g14730.1 3-hydroxyisobutyryl-CoA_hydrolase-like_protein_3_mitochondrial [MW = 41.77 kDa]

No. of times detected



log(intensity)



Values from



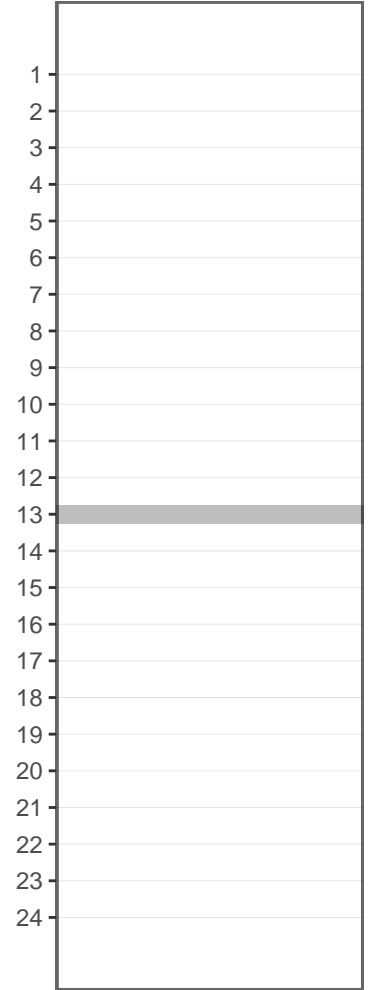
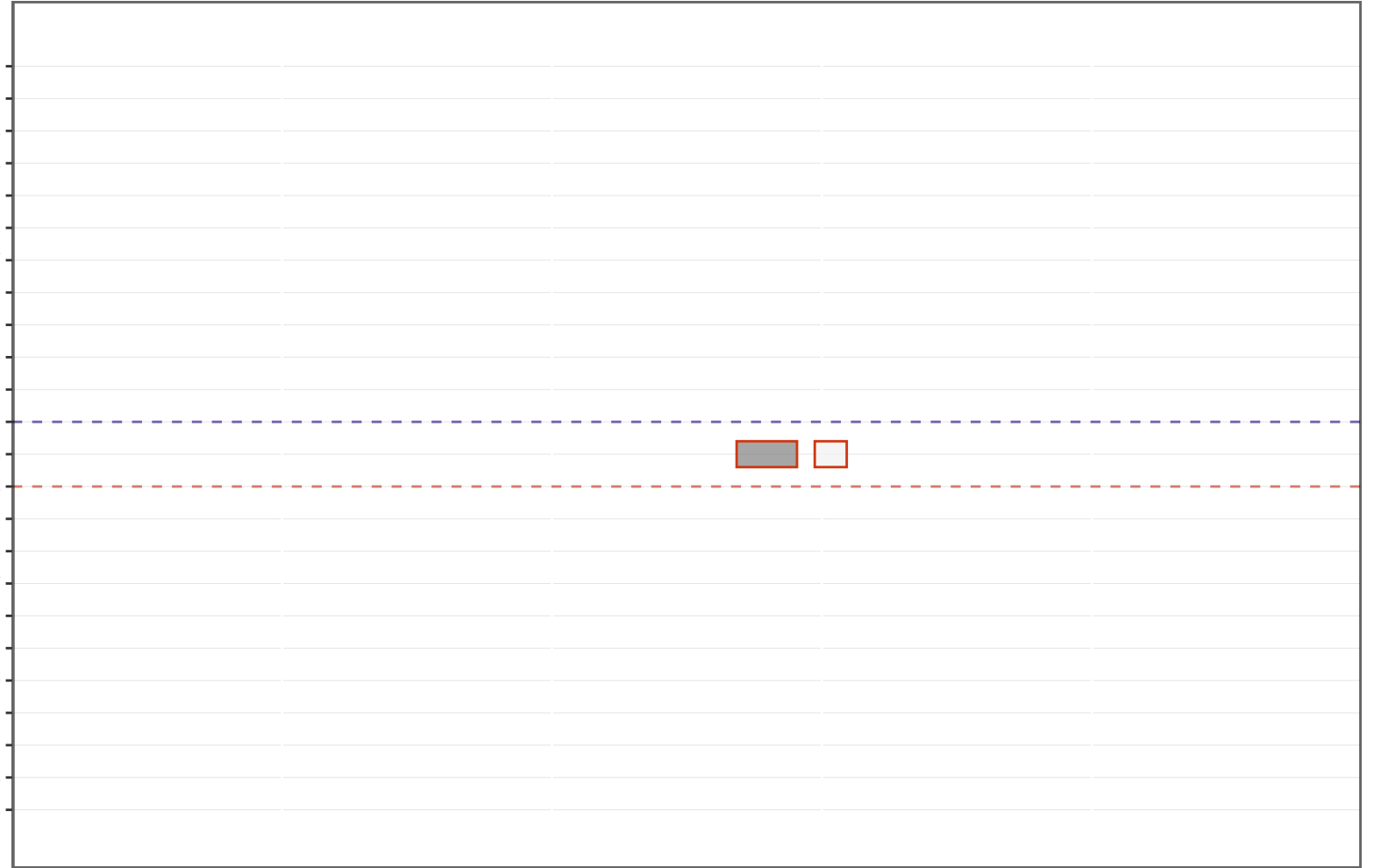
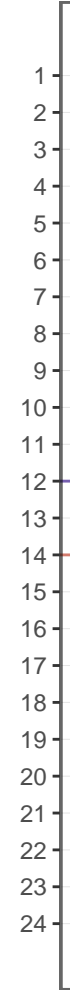
MW indication



Molecular weight



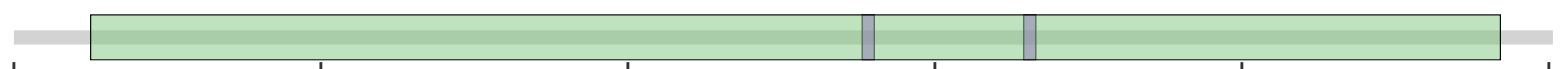
Gel Slice



Peptide counts over 4 repeats

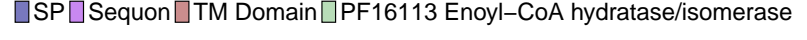
Protein length: 1, 77, 153, 229, 305, 381

Protein length



Pfam domains

Pfam Description



Protein sequence:

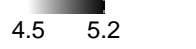
RISTPDAALYGLGSHYVPSANLDTLKEAFLAANFSQDPDDEIKRLLEKYSTDPDSESRLLKSLPRISSTFGNKFTWNEELENHGGGADTLVAEWAKDALGGLRGAFFSLQLTGHYFSRVASACGKNENTLSKLPQVMRTEYRIAIRSALRNDFAEGVRAILVDKDKGNPRVWPSLEDVNLNNEVEALFEPLEPELVN

NbL05g14580.1 40S_ribosomal_protein_S14-2 [MW = 16.37 kDa]

No. of times detected



log(intensity)



Values from



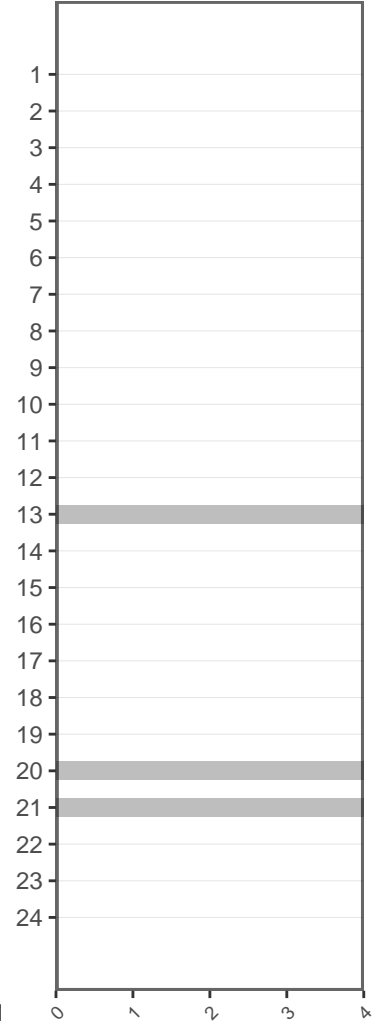
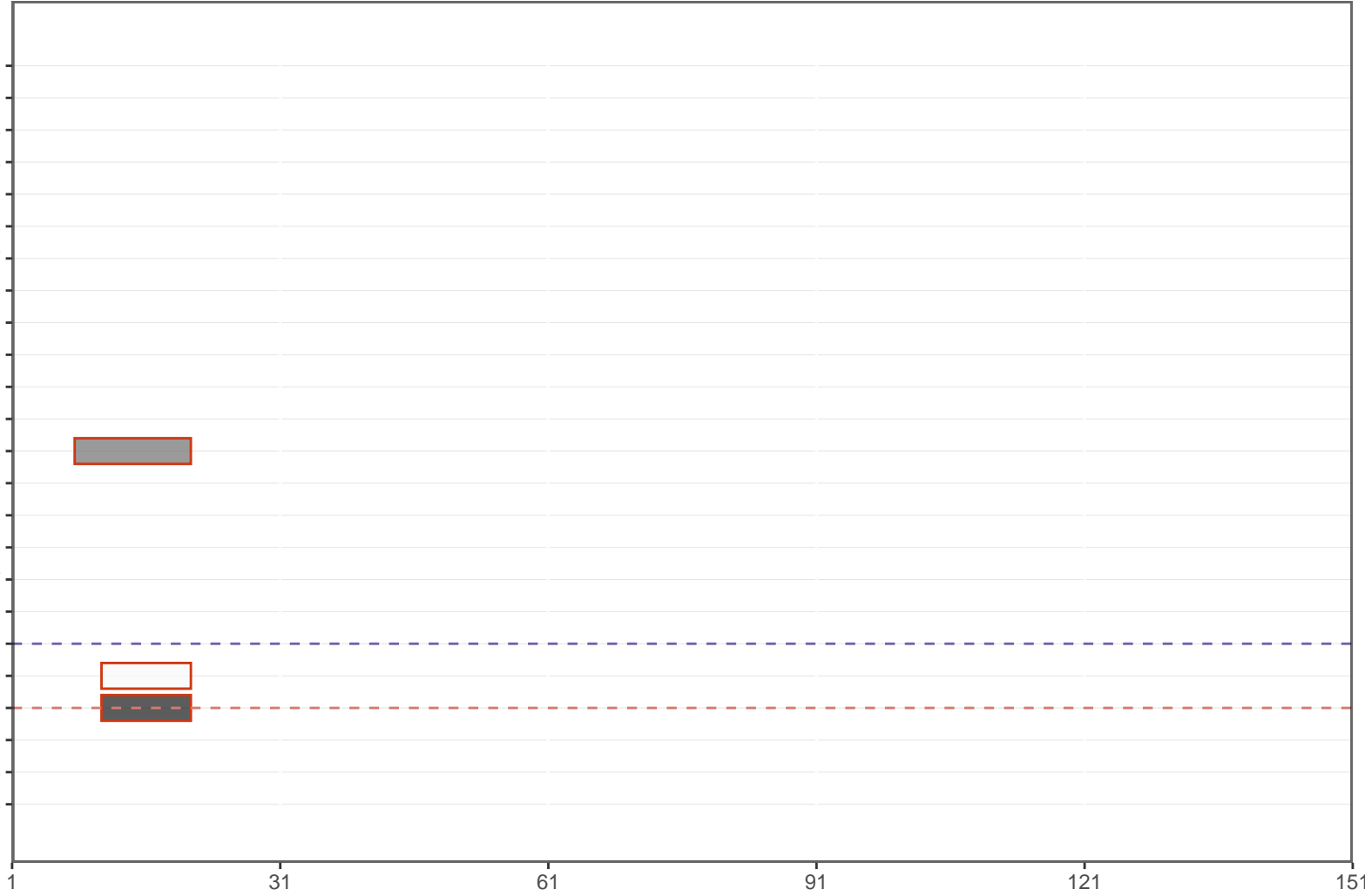
MW indication



Molecular weight

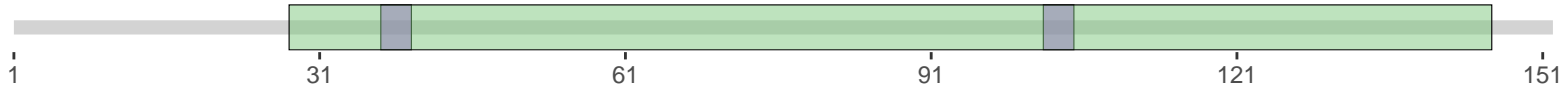


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

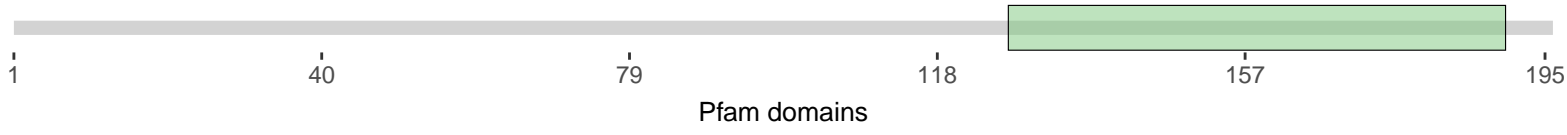
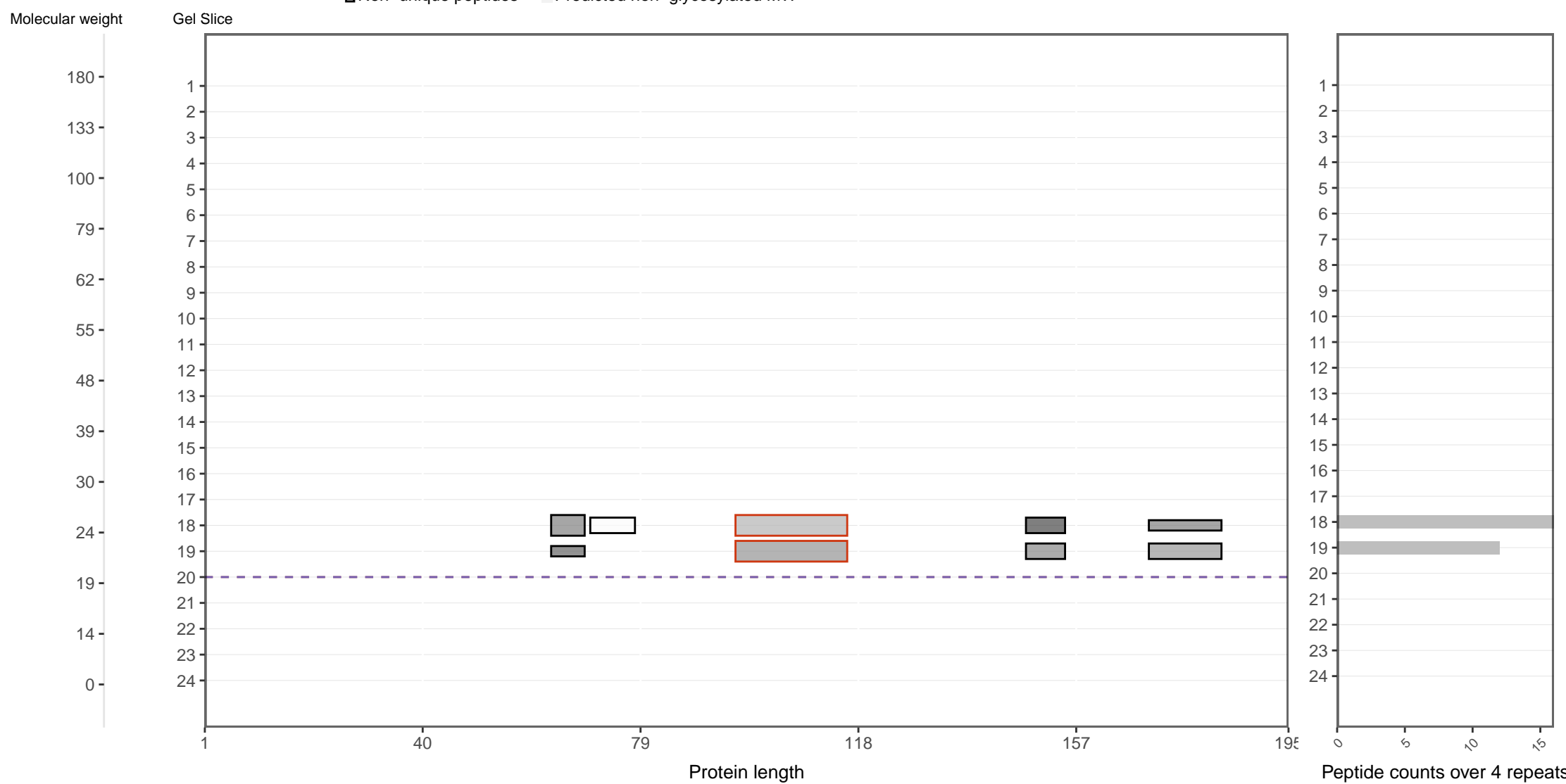
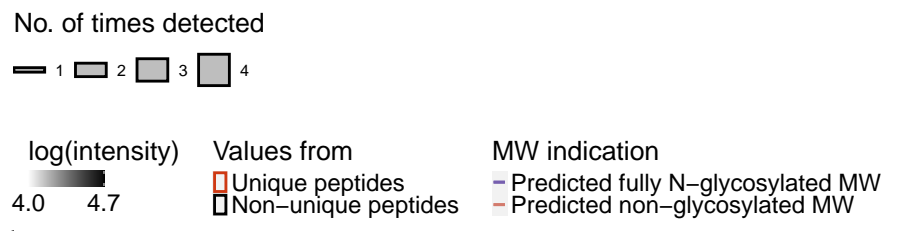
Pfam Description



Protein sequence:

ADRDSSPYAAMLAAGDVGSRCKELGNAHKLRLATGKTKTRPGGQGBALRALRSGMKIGREDVTPPTDSTRKGGRRGRRL

NbL05g14540.1 50S_ribosomal_protein_L7/L12-like [MW = 21.26 kDa]



Pfam Description

- SP Sequon
- TM Domain
- PF00542 Ribosomal protein L7/L12 C-terminal domain

Protein sequence:
 ILRILRIPNLKQISVEGIDLGAMGGAGGGPKAEKKAETKTSFDVKLEKFDAAAKIKKIKKIKVEKRFSTLGLKEAKDLVEKVPMLKGGVTKKEANEIEKIKAAAGGVAWME

NbL05g14510.1 1-aminocyclopropane-1-carboxylate_oxidase_homolog_1-like [MW = 41.63 kDa]

No. of times detected



log(intensity)



Values from



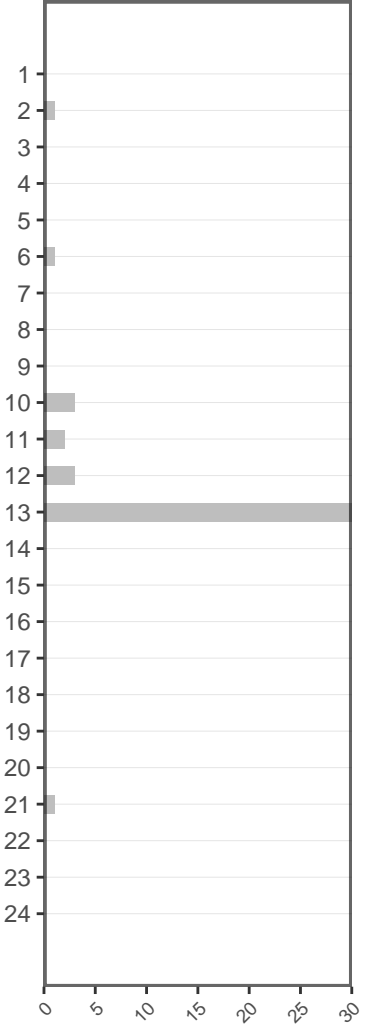
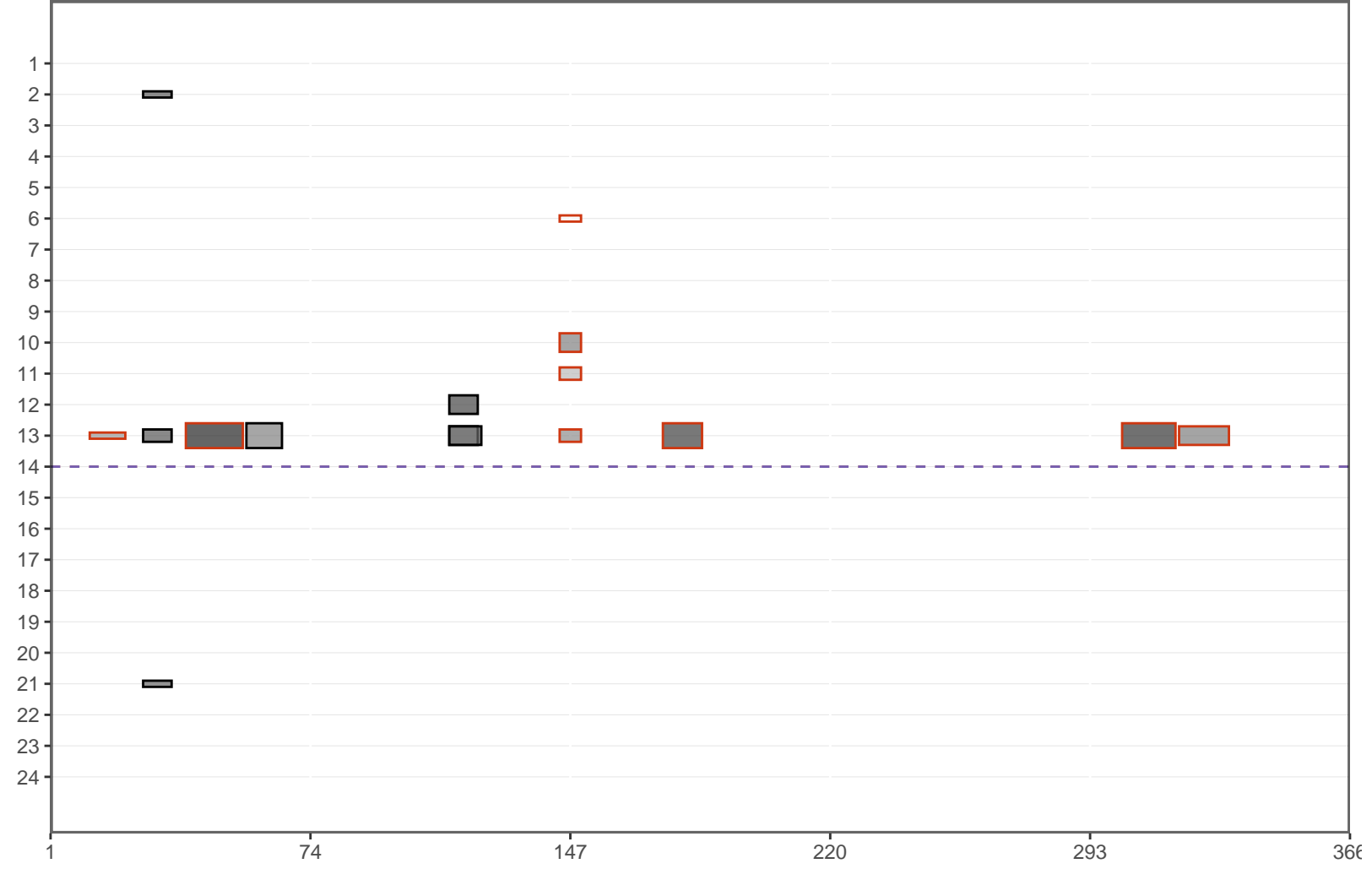
MW indication



Molecular weight

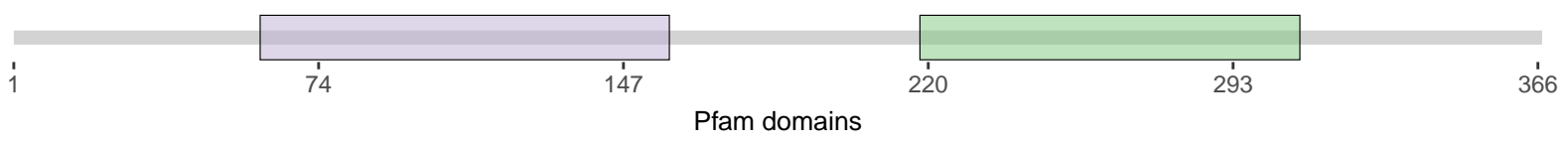


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF03171 2OG-Fe(II) oxygenase superfamily
- PF14226 non-haem dioxygenase in morphine synthesis N-terminal

Protein sequence:

SVCRDILFEYTNQVAMKLAITIFELLSEALGLKPKSHLNDMMGSGELGALGHYYAGCPQELTLAGAKHADENFLTLVLDGNGGLQLVHGNHWVDPPTPGALVWNGDLLQLHENDKFKVEHRVLANKVGSPRIEMAGFGTTSFLPTERLYGPIQELISEHNPRIKYEKTTVEYENKGLDQTSALLHFRUKTY

NbL05g14450.1 heterogeneous_nuclear_ribonucleoprotein_R [MW = 53.64 kDa]

No. of times detected



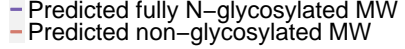
log(intensity)



Values from



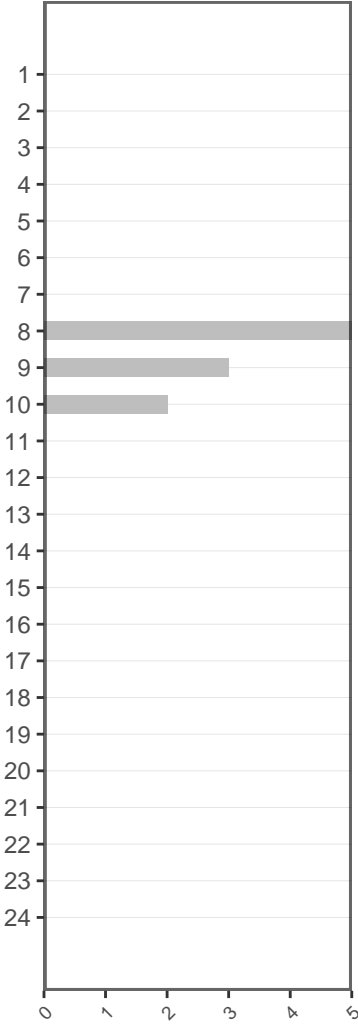
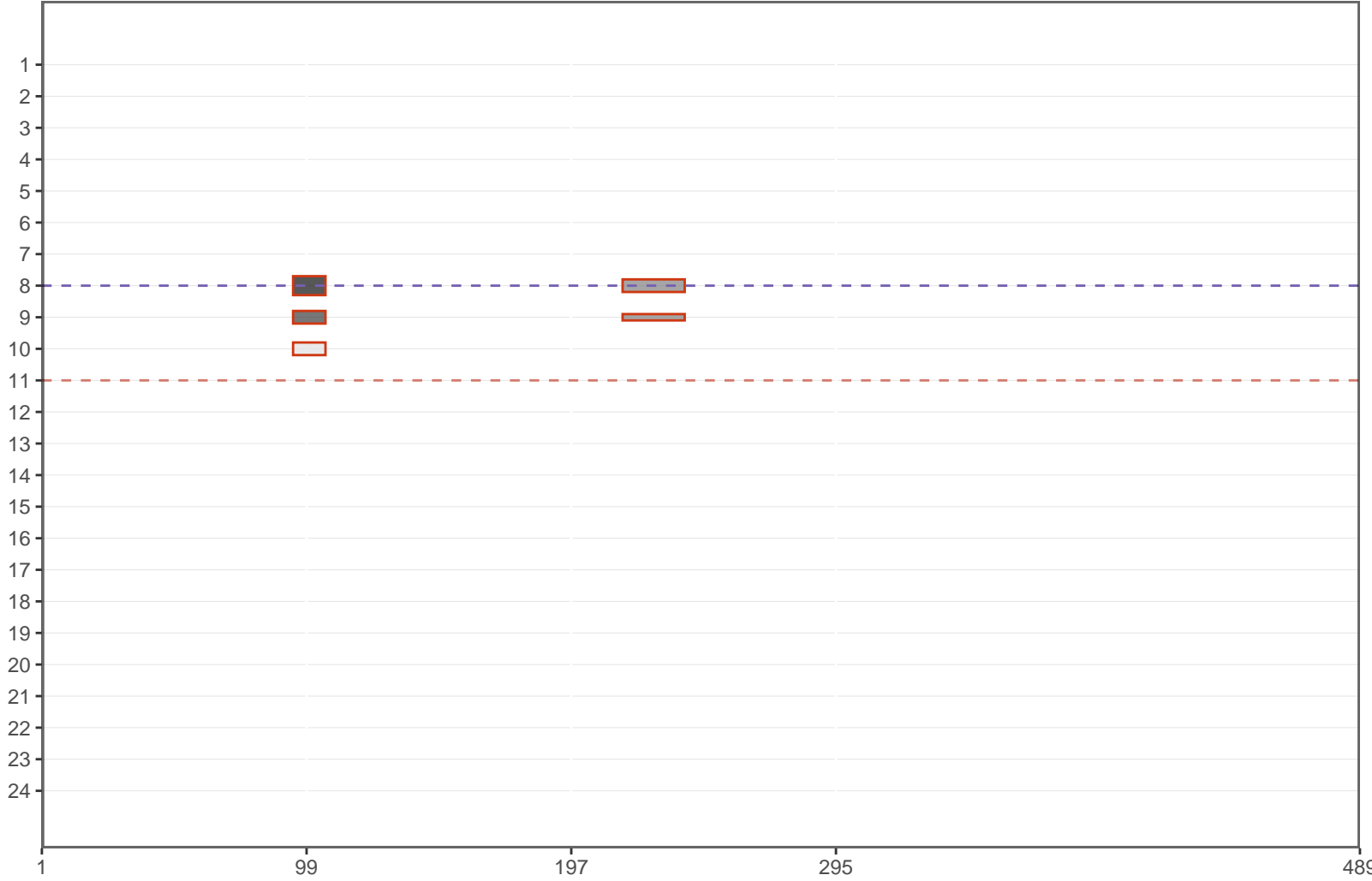
MW indication



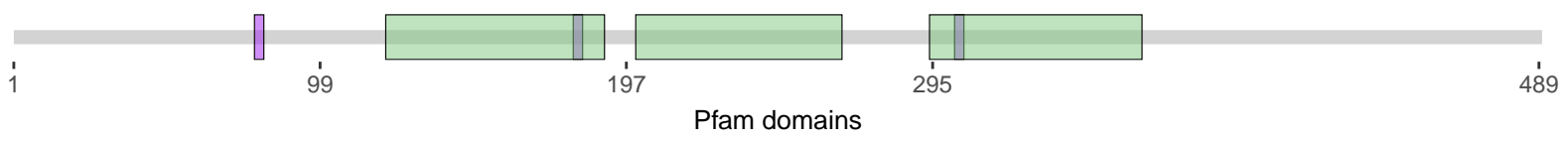
Molecular weight



Gel Slice

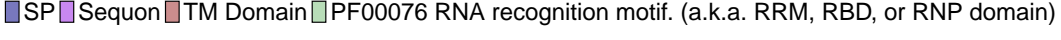


Protein length



Pfam domains

Pfam Description



Protein sequence:

QNSGRNRGFATFEYNNADAEYSRQKMSNSDFKLDNAPTIVSWADPKNAETAASAGVAVYVKNLKNITGDKLKELFHGHGKIMKVVLPKAPQGEGRYGFVHFAERSSAMKALKNTERYEIDCKILEGSLAKPQADQKSGSGSSQKPTLPTVPRRIGYGMVGPYKALSAQYGAAGVGGPLVYGRGATPAGLAMMPMLLPDGRIGVVLGGPQVMTPTPPKRRGGRSSGGSSGRRGDSGRGRSRNPV

NbL05g14140.1 glucose-6-phosphate_1-dehydrogenase_chloroplastic [MW = 66.95 kDa]

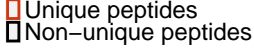
No. of times detected



log(intensity)



Values from

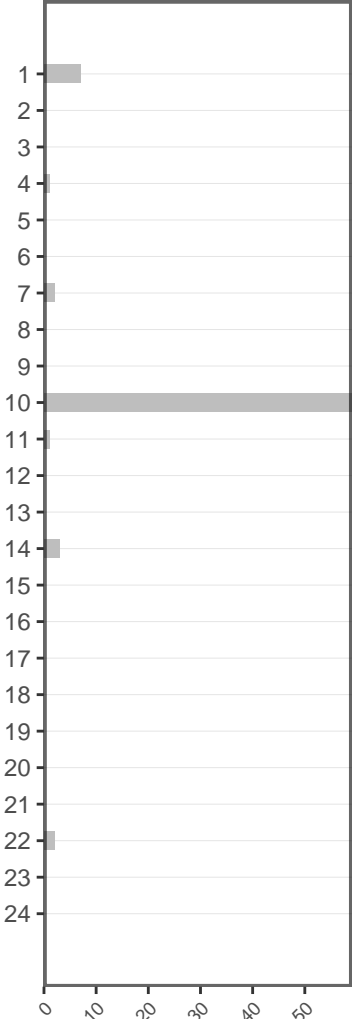
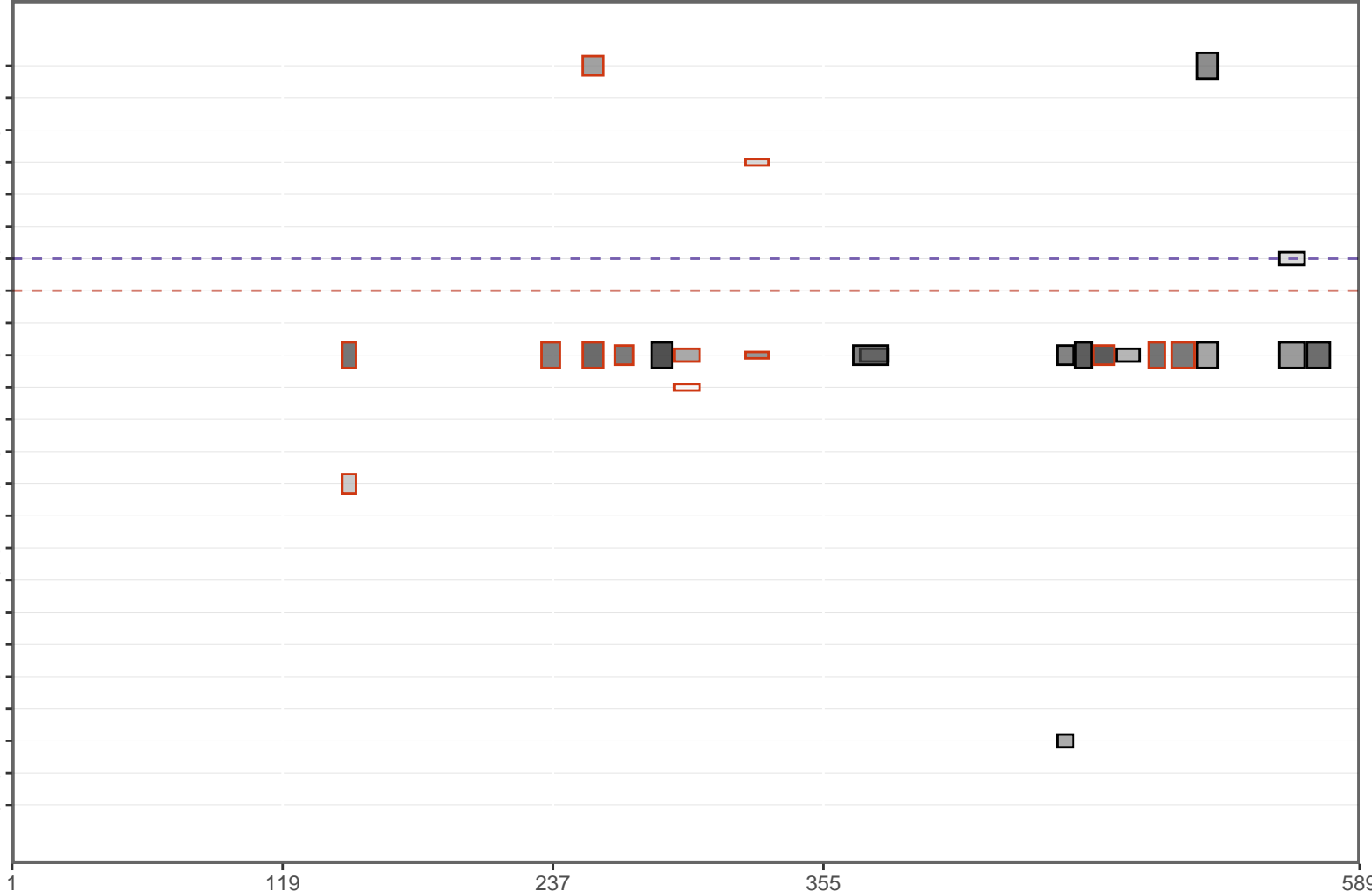
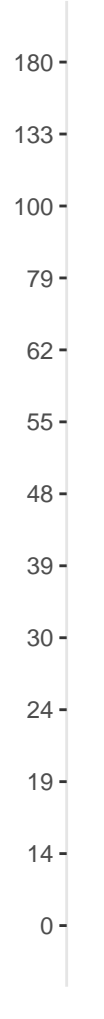


MW indication



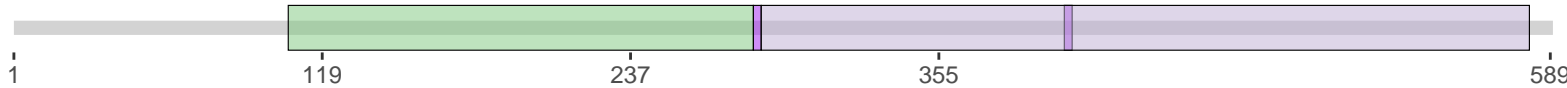
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF00479 Glucose-6-phosphate dehydrogenase, NAD binding domain
- PF02781 Glucose-6-phosphate dehydrogenase, C-terminal domain

Protein sequence:

VEVLSVLRFSNLYFEPVWSRNYRNVQFFSEDFGTGEGGGYFDNYGIRDMQNHLLQHALFAMETPVSMADAEGRNEKVKVLRSMRPLQLEDVYVGGYKHSKGGKLYPVYTDPTVPSGIFPTFSAALFINNARWDDGVPFLMKAGKALHTRAEIRVGRFRHVPGLNLYKKNFGLDKATNEVLVRLGPDGAYLKNKVPGLGMLRDRDNLNLYKAYRGEIPDAYERLLDMEGERRLIRBDELDAWALFTLLKELEEKKAPELYPYGRGPPVGAHYLAAKH

NbL05g14040.1 fasciclin-like_arabinogalactan_protein_2 [MW - SP = 41.23 kDa]

No. of times detected



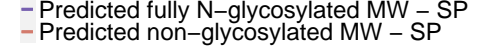
log(intensity)



Values from



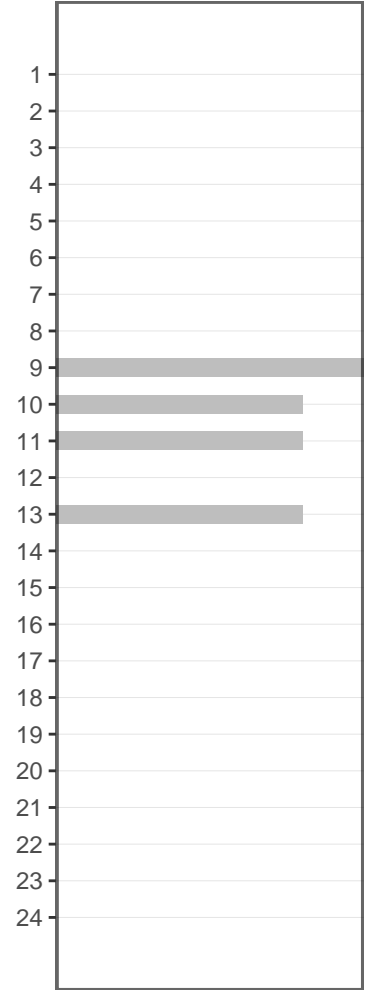
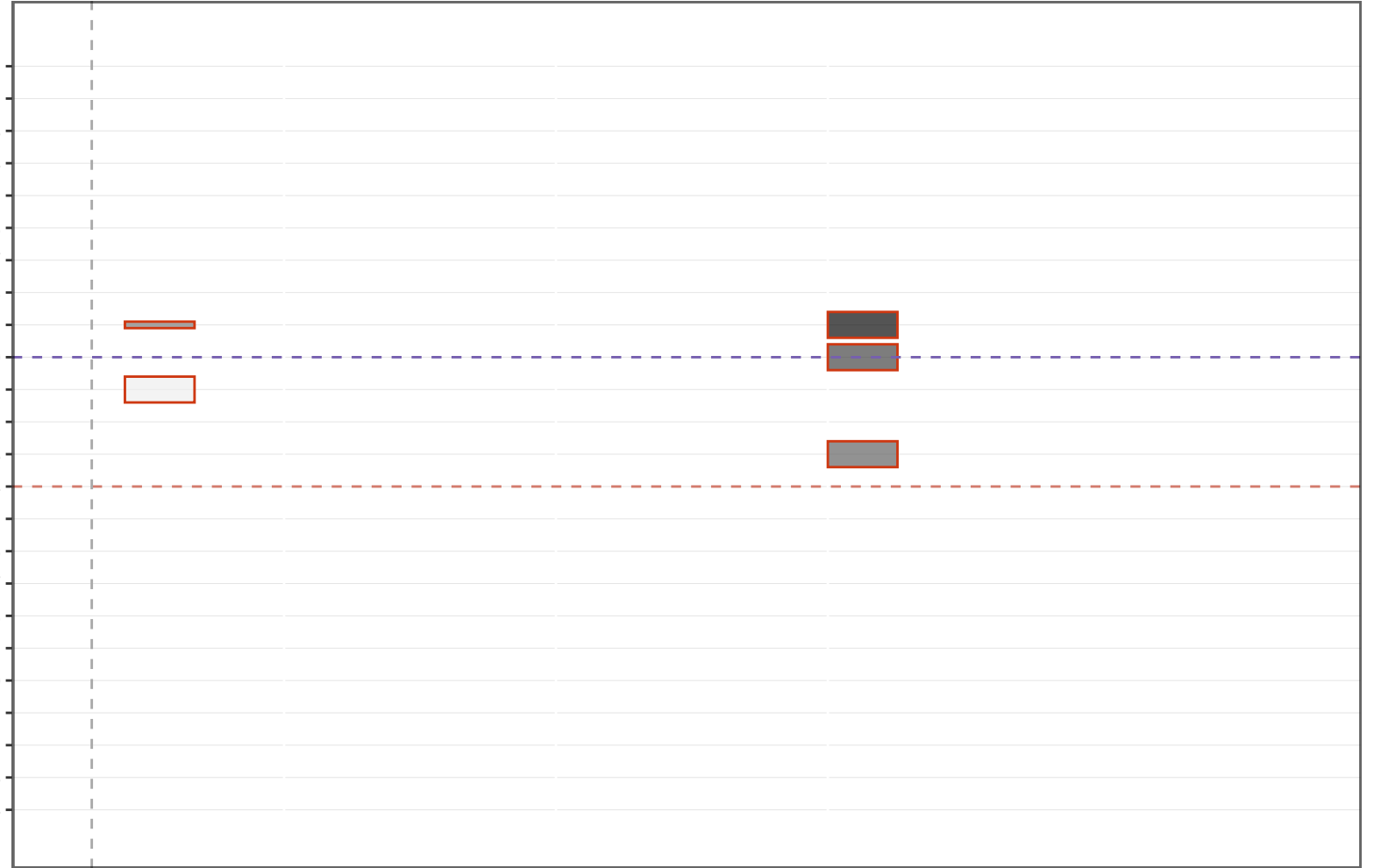
MW indication



Molecular weight



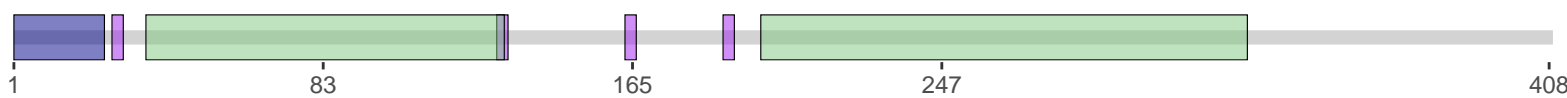
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

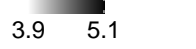
ISEGGCKAFSDLLKSHFDVSKTFAENVEGSLTFVCFPTDGVLNGFMFKPKKLTQDQASLLLYHGIPVYNSLGMKJENGLMNTLATEGKNKYDFTVQNDGGDVMKTKVYVTTATSGTLYDEEPLVYVYDKVLLPRELFRKAWAEFPAPKPGGKHKHKGGGGDVEDDQAFEPGLEEDDAPAESENLNAGISVKGGWLVTVLGVQVAFI

NbL05g13960.1 acetyl-CoA_acetyltransferase_cytosolic_1-like [MW = 41.3 kDa]

No. of times detected



log(intensity)



Values from



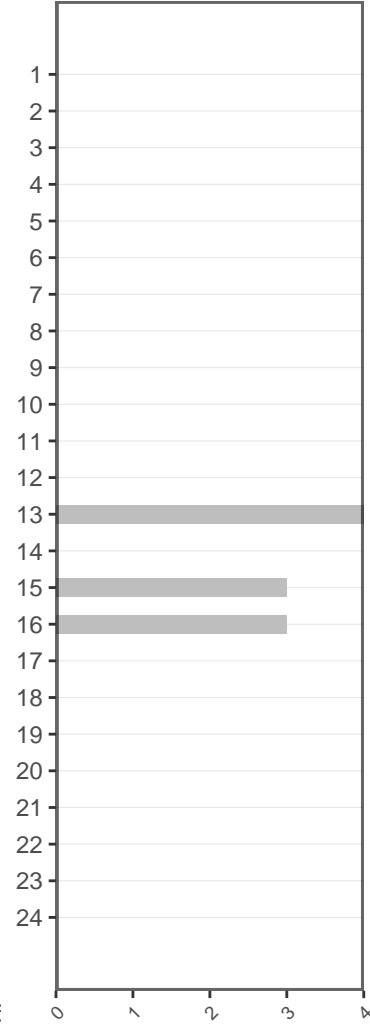
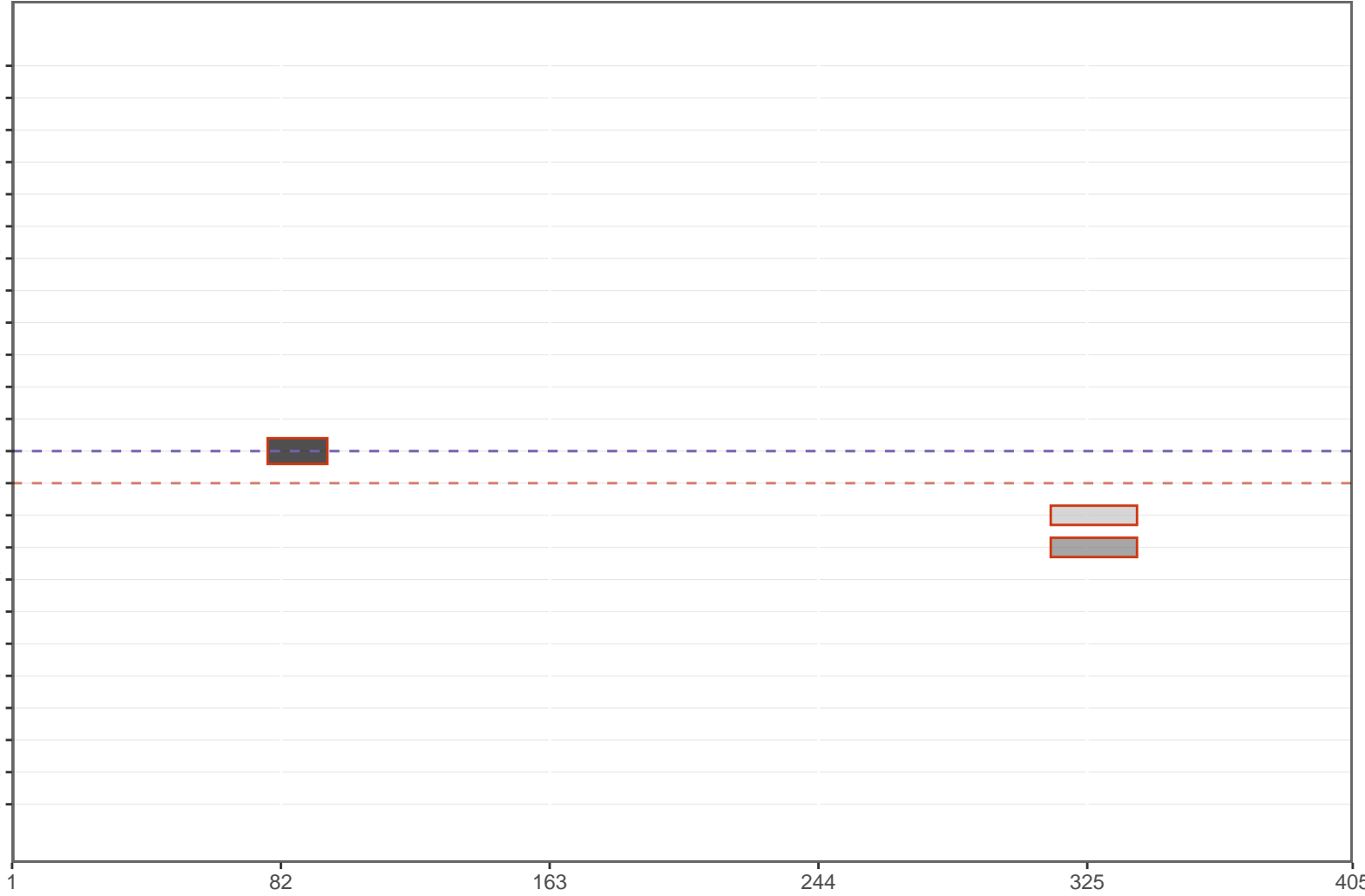
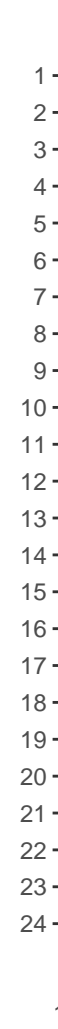
MW indication



Molecular weight

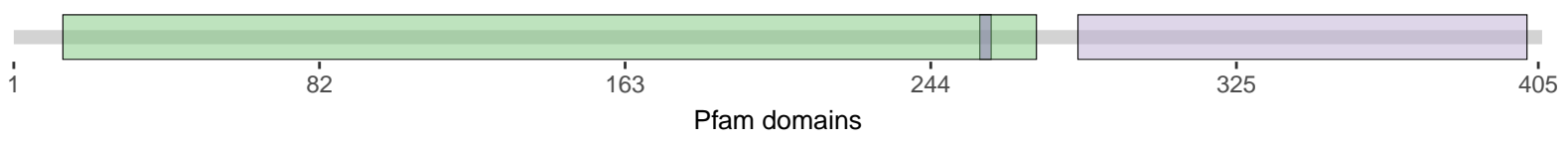


Gel Slice



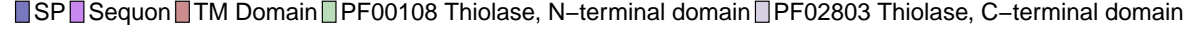
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



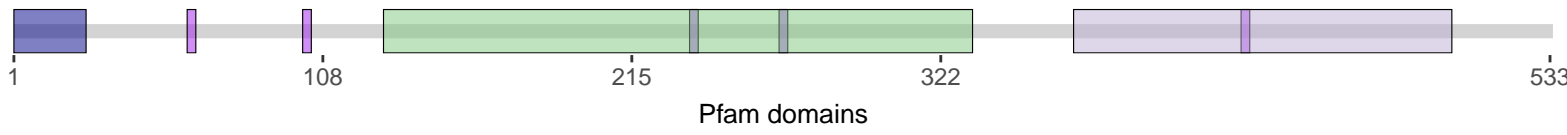
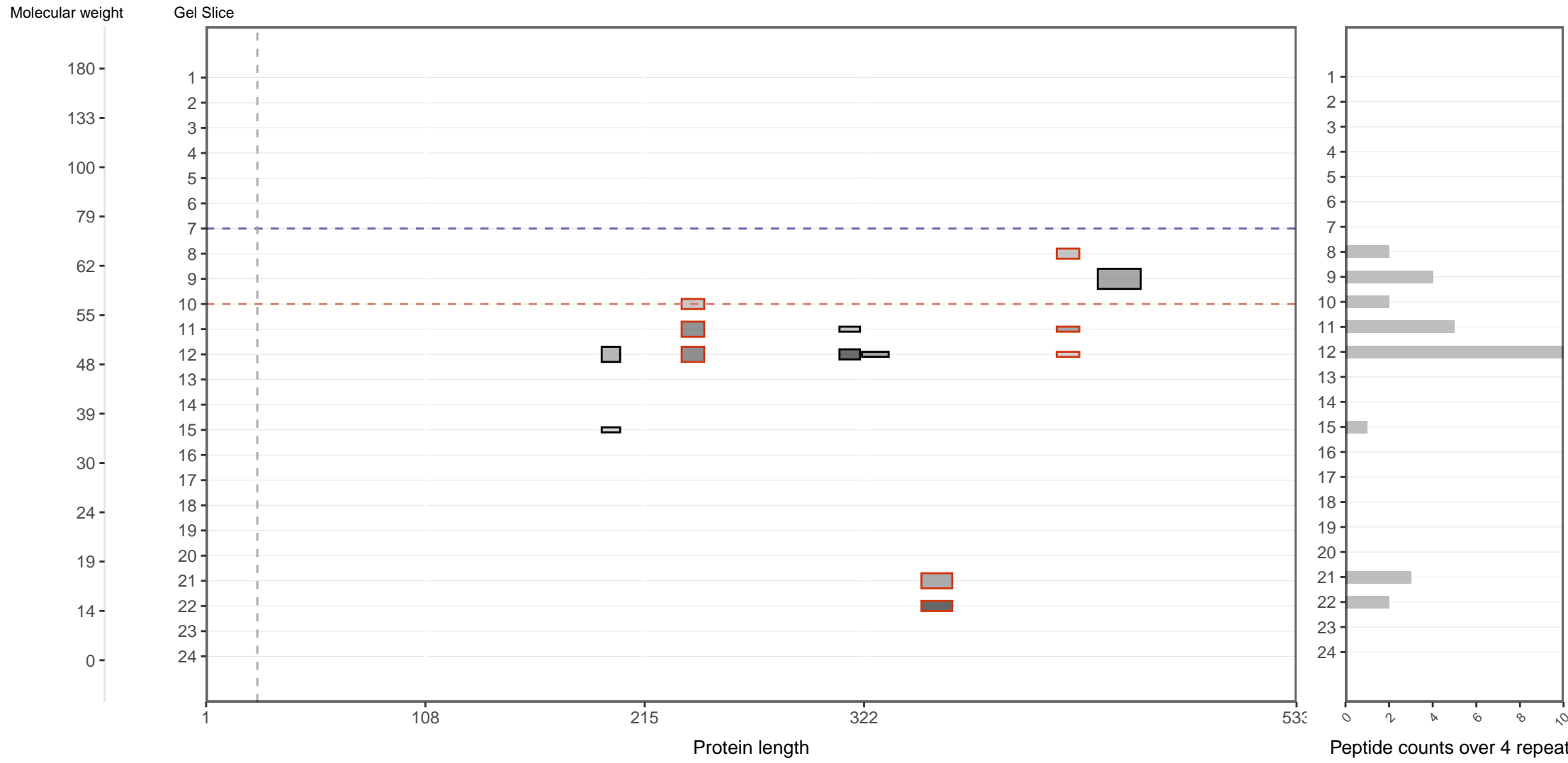
Protein sequence:

YAVQSFERGAIAQDEAGFAWEIVFVEVPGGRGKPSHVDKDDGLGKFDGANLRLRPSFKEDGTVTAGNASSISDGAALVLSGEEKAKLGLNVIGKISGYADAAGAPELFTTAPALAPKAIKASALEASQIDFYENEAFVYVSLANGKLLGLNPKKWNVHGGAVSLGHPFGGSGARIVTLGLVLRQNKSGAAGVCAAGGGGASALVLELV

NbL05g13930.1 ribulose-15_bisphosphate_carboxylase/oxygenase_large_subunit_N-methyltransferase_chloroplastic-like [MW – SP = 57.77 kDa]

No. of times detected
 1 2 3 4

log(intensity) 3.2 4.9
 Values from Unique peptides Non-unique peptides
 MW indication Predicted fully N-glycosylated MW – SP Predicted non-glycosylated MW – SP

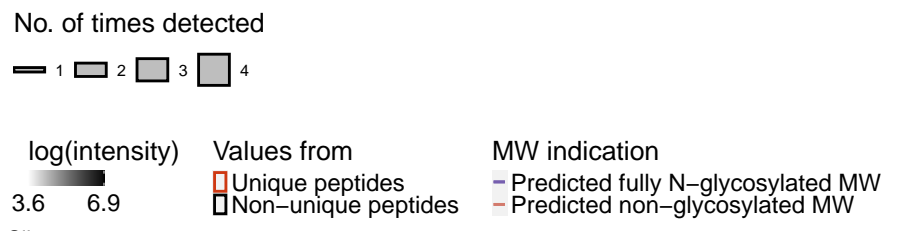


Pfam Description
 SP Sequon TM Domain PF00856 SET domain PF09273 Rubisco LSMT substrate-binding

Protein sequence:

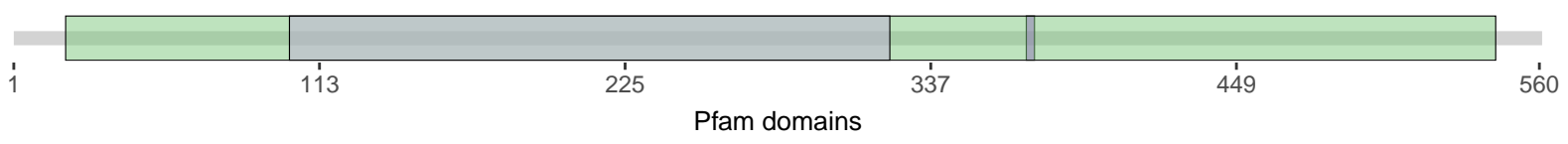
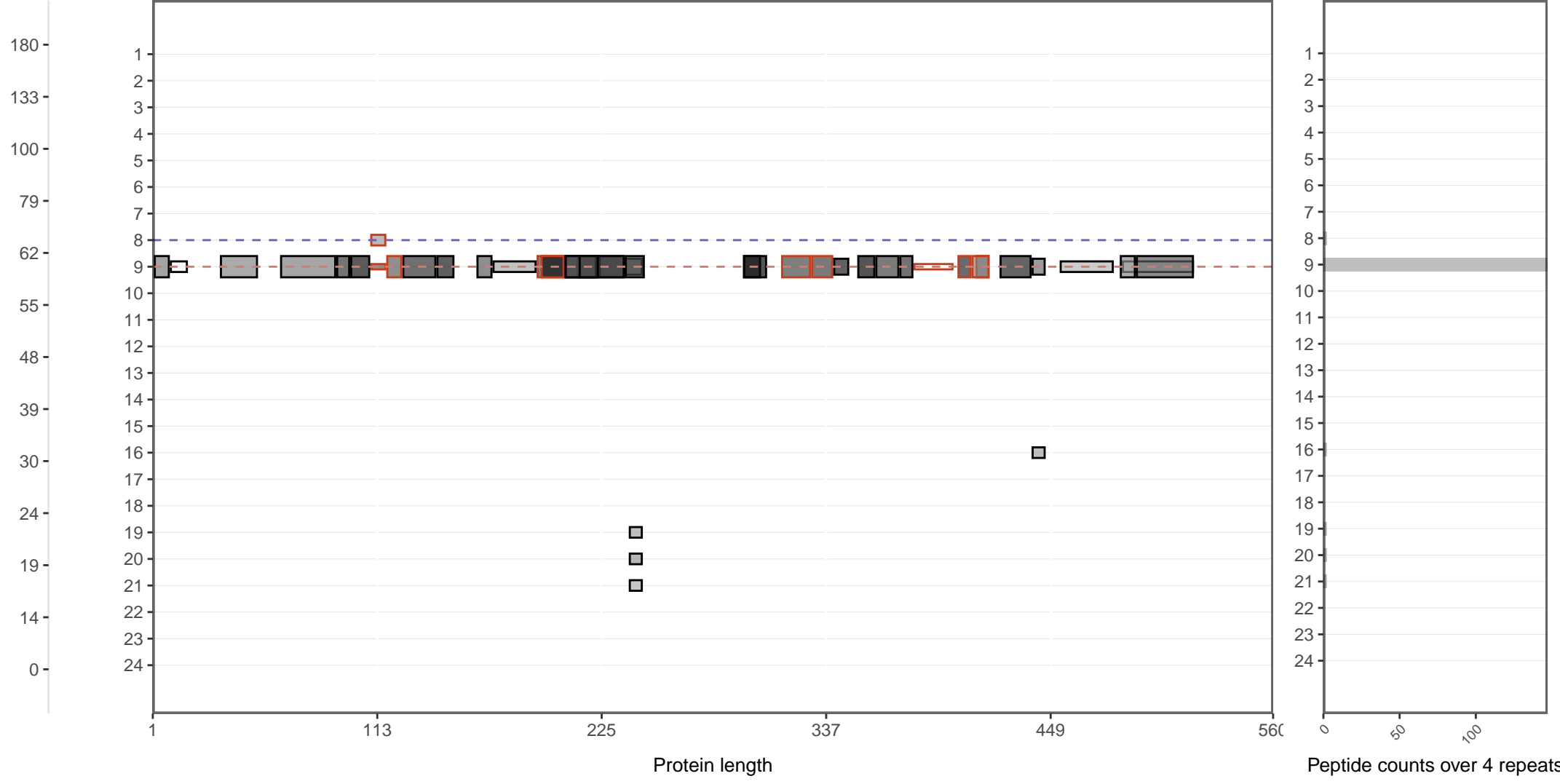
FFEEIFNIETFNWYFGLFRLRLPMDGRVALVPWADMLNHNGEVETFLDYDKSSGGVFTTDRAYGPGEGVYFVGRKNGELLVYGFVREGTNPDSIELSFLKLYDKCYKEKVEALKKHLSASECFNVTGWPLELMAFAYLVVSPPMRSGFGEMAAASNNKSTKXKDMKYPFEIEEALQFLDGGESISKYSKFLQASGEMDLVDVTPKGLNRRVFLKQLAVDLCTSEIRLFRSGYLRRRLRDRSGELKALKLFDGLRNLFK---

NbL05g13540.1 23-bisphosphoglycerate-independent_phosphoglycerate_mutase [MW = 61.19 kDa]



Molecular weight

Gel Slice



Protein sequence:
 /DDNGKPYGPIIDGDAVTFNFRADRMMLAKALEYENFDKFDVRVYKIRVAGMLQDGELOLPRHYLVSPPEIDRTSGEYLVKRVGRTVFAGETVYKFGHYTFVWNGNRGIVYFNKLEEVYFIPSDVGIITFNVDPKMALEIAERTDAILSGKFDQVRVNLPNGDMVGHGTGDKATEACKSADAEAVKMLDMEIQVGGYLVYADHGAEDMKRKNKGEPAIDKNGHGLTSHTCPEVPIAIGGPGIAPGVRFRODLPTGGLANVAATFMNLHGVEAPSDYEPSLIEVVC

NbL05g13420.1 probable_polyamine_oxidase_2 [MW = 54.5 kDa]

No. of times detected



log(intensity)



Values from



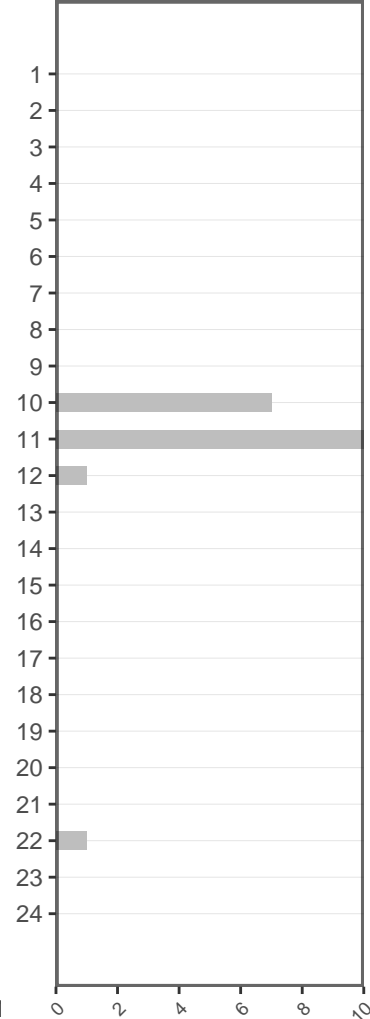
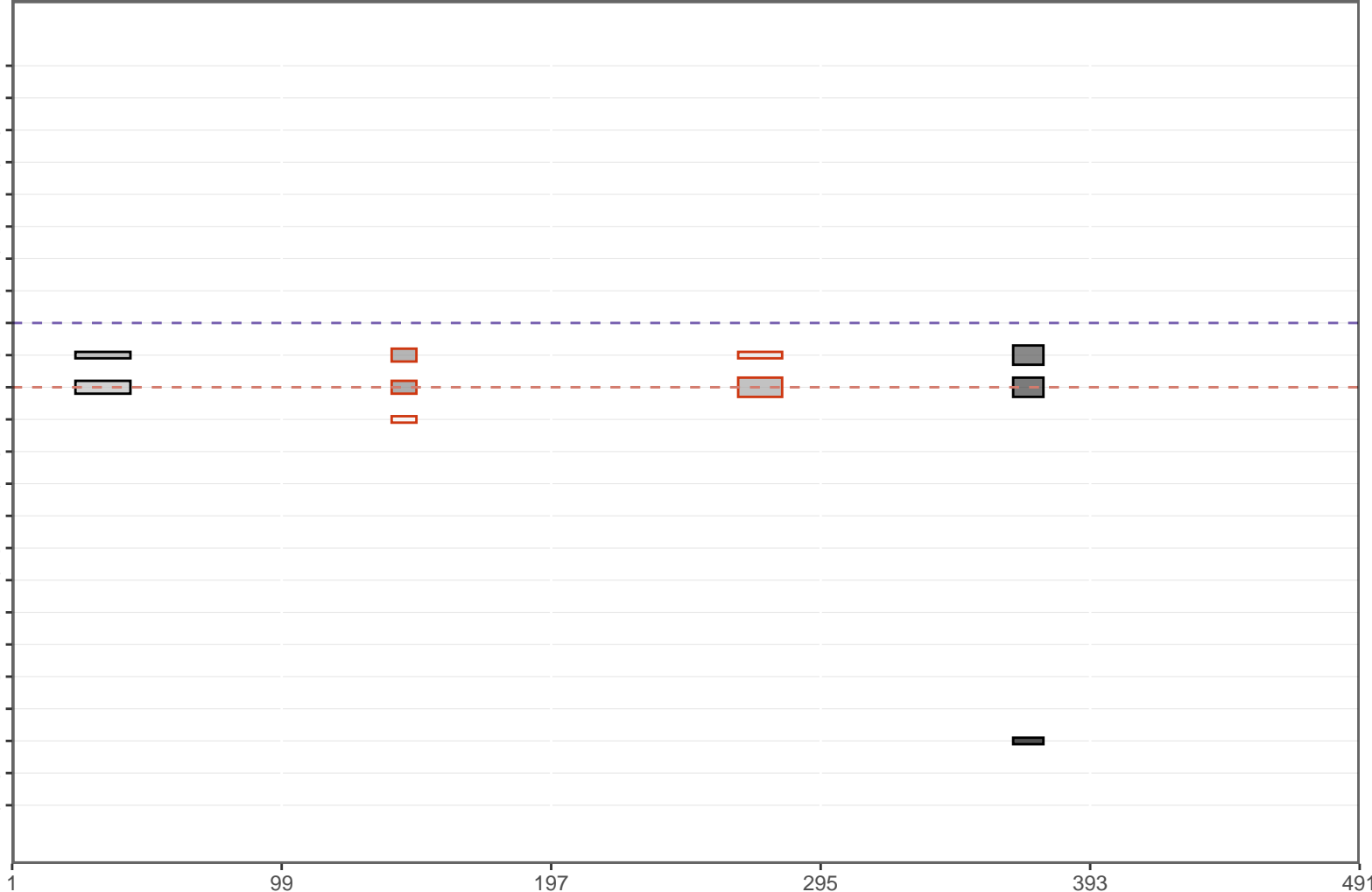
MW indication



Molecular weight

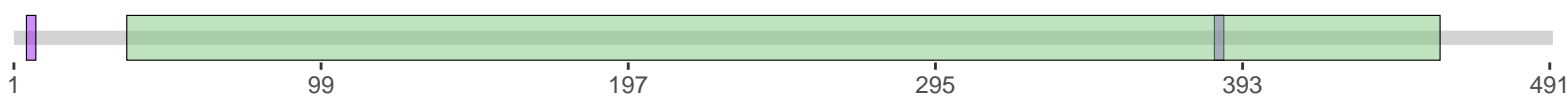


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VNLTAKGLDIRLGHRAQVVRIRYNGVKVTEVDGRTFVADAAVWPLGVLKSRKIFEPRLPEWKEAANELGIVGIEKILHFKVFWPNIYVERLGIWAEGSYEGSYFLNLHKATGHPVLVYMPKQGLARIDIEKLESDAAAFAPKQLGRILPNSTTRIGVLSHWGTQNLGSGVSYDTYKPFHEFYERLRIPVDNLFYAGEATGMDYPGSHVGYSTGLMAAEDCRMVLERYGELDFQPMAGEDTPVWPLLSRM

NbL05g13400.1 uncharacterized_oxidoreductase_At1g06690_chloroplastic [MW = 39.81 kDa]

No. of times detected



log(intensity)



Values from



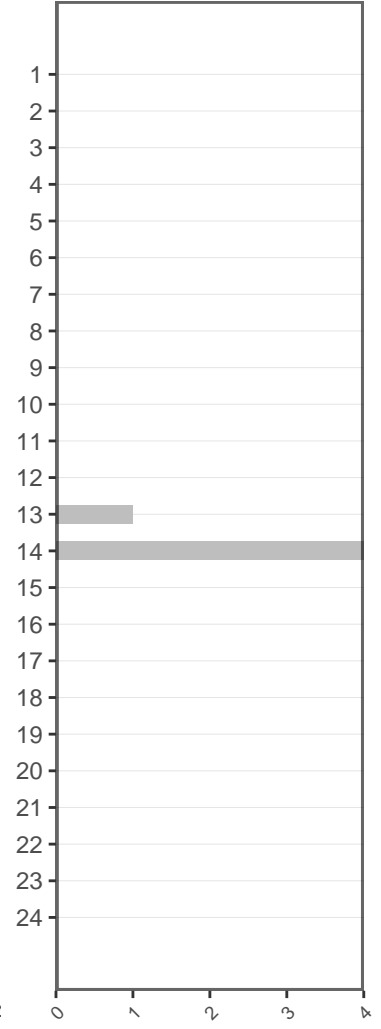
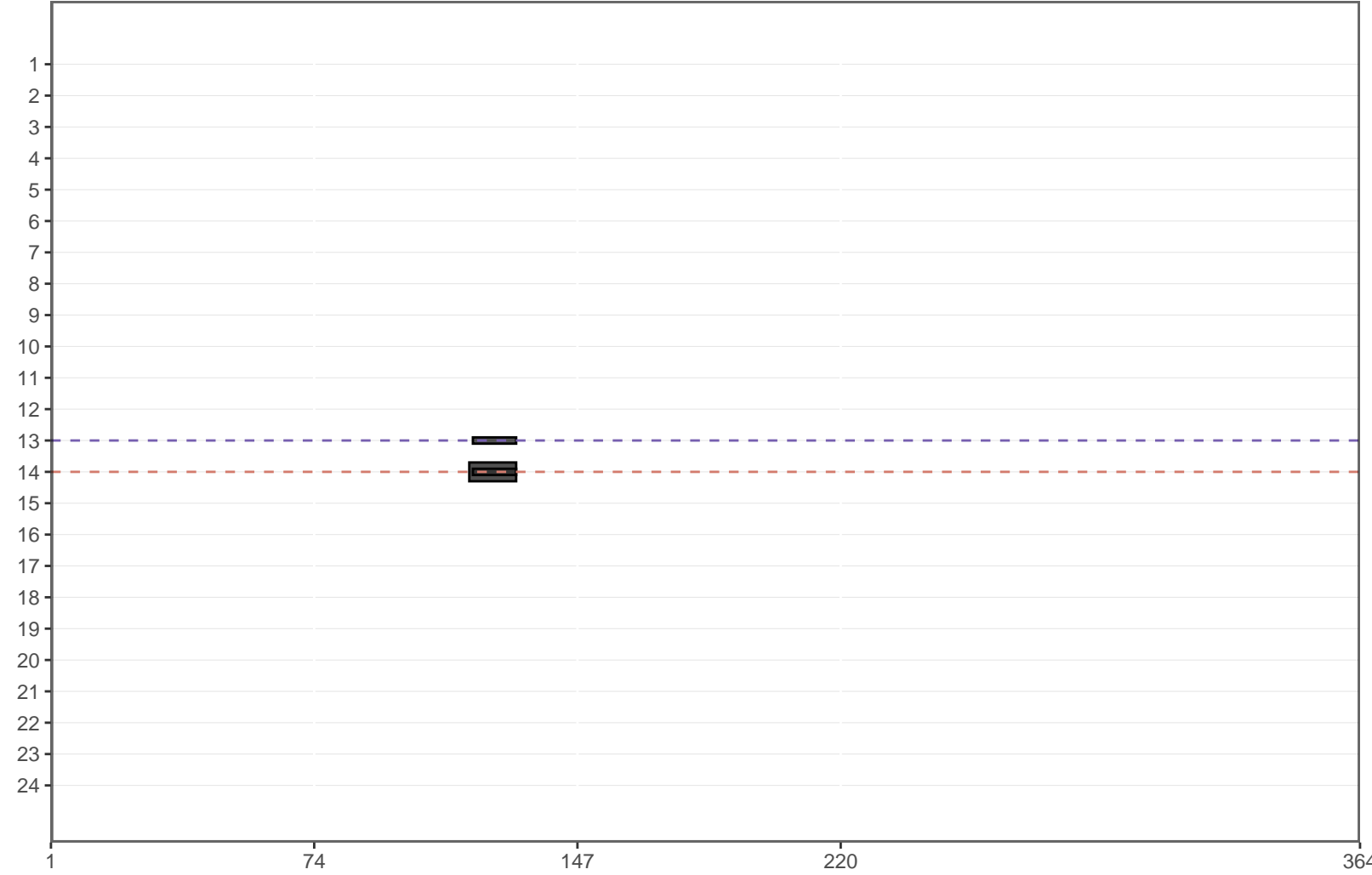
MW indication



Molecular weight



Gel Slice

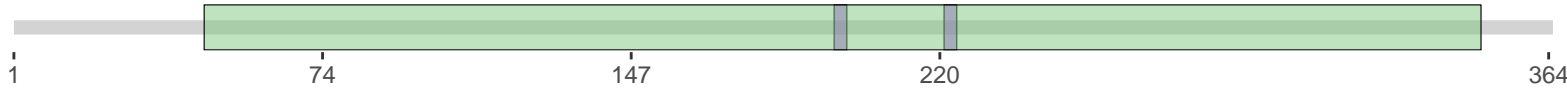


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SIWNGEYIDGLGVAIEGGLKAVGVNYSSEKRLRAAVEGLKRRGIPLASNGVYSLYRPFPEQNGVKAAGDELGVTLIAYSPIAGDGLTGKYPENPPRSGPRGHYTPFLTKLGLPLNRKEIGESYKKTPTQVVLNWLHAGENLPIPGAKNADQAKEFAGALGWRLTGDDEVDELRSALADKPKVTFGFPVEKLI

NbL05g13380.1 heat_shock_70_kDa_protein_17 [MW – SP = 97.08 kDa]

No. of times detected



log(intensity)



Values from



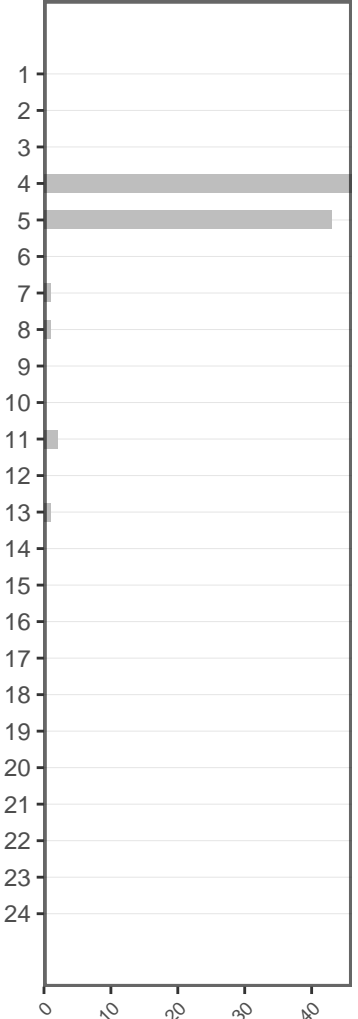
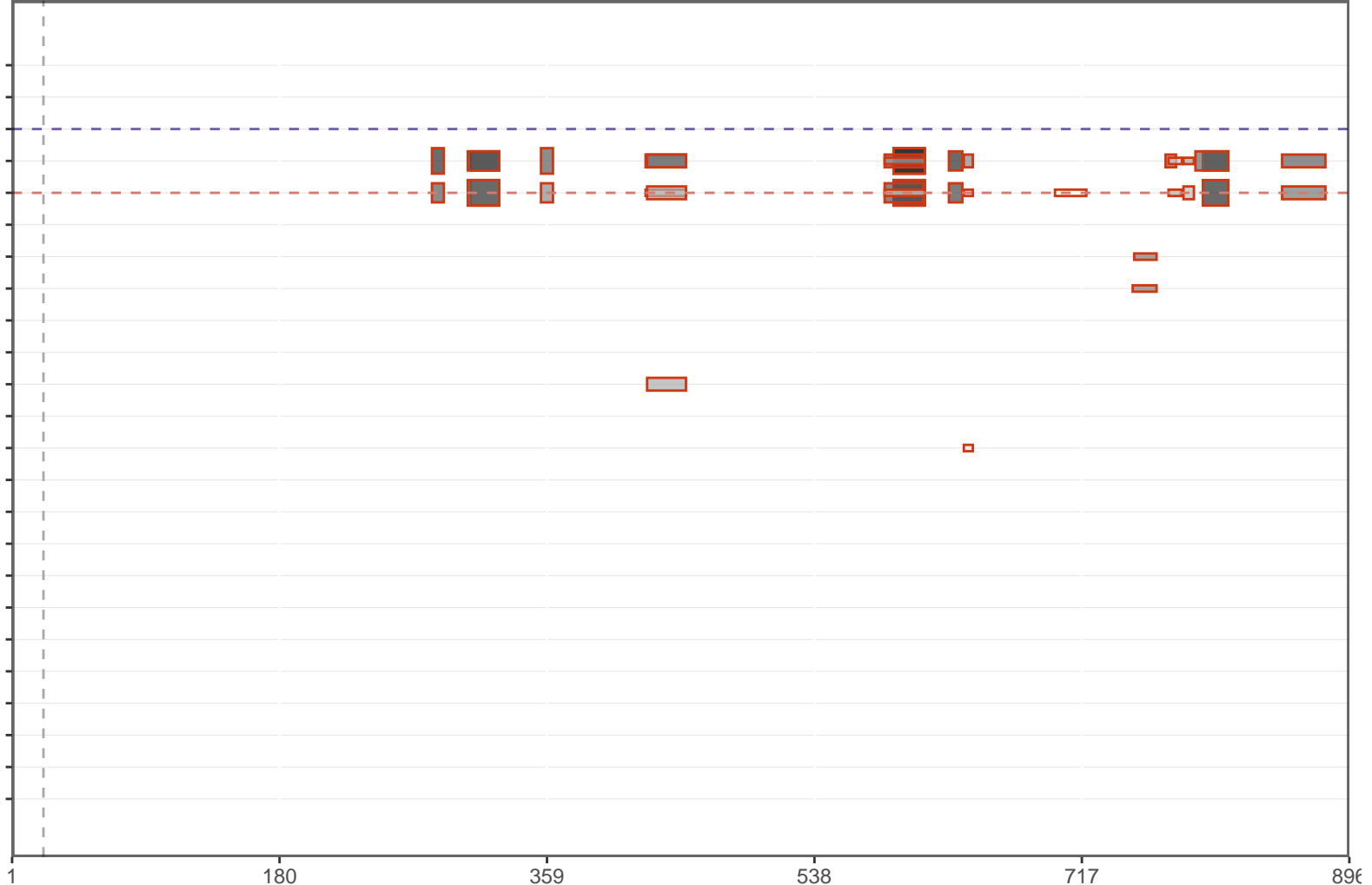
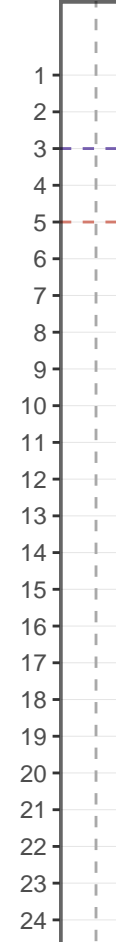
MW indication



Molecular weight



Gel Slice



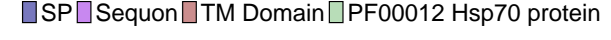
Peptide counts over 4 repeats

Protein length



Pfam domains

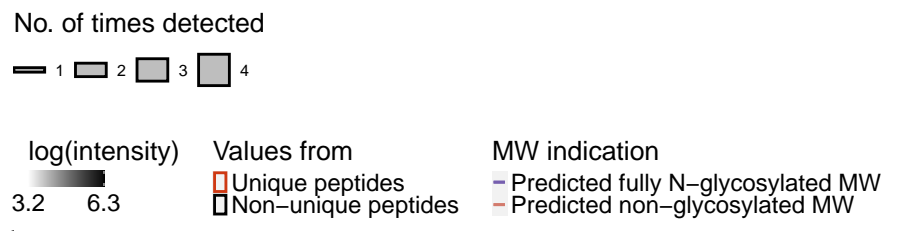
Pfam Description



Protein sequence:

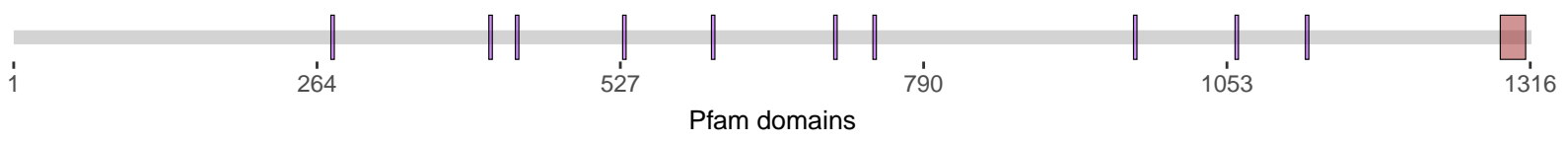
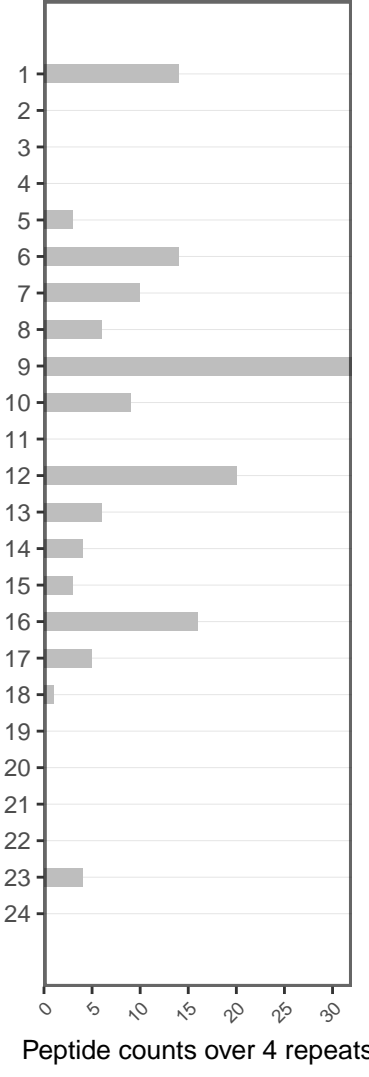
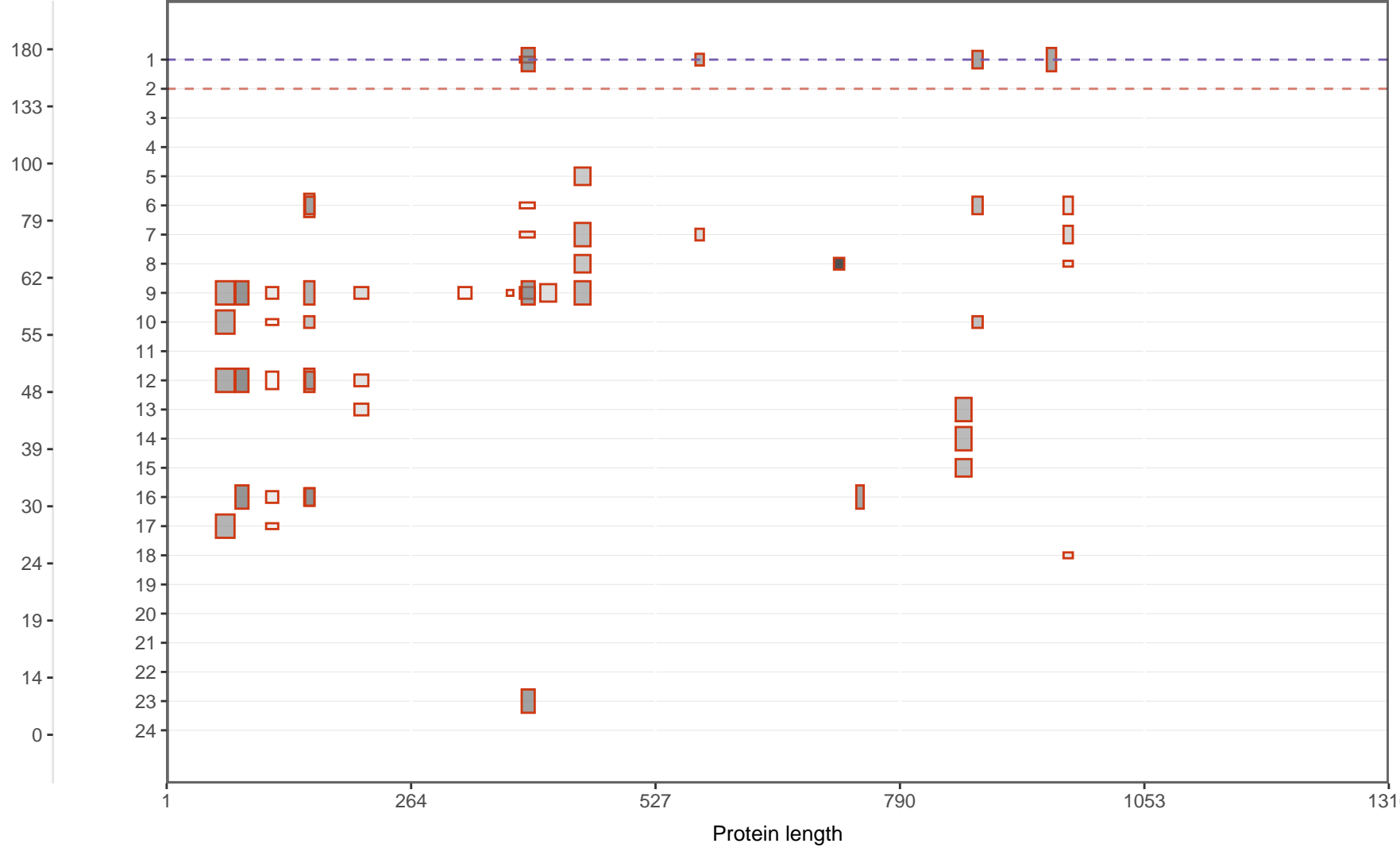
IYDGPDLPKDESTKQLIPRMKKLPSKMFBSIVHNKDFEVLAVESDEFLLPPTSLFTAGYAVSGLADASEKYASRNLSAPKANKLHFLSLSRSGIFSLDRADAVHEIEIVVEYPRKNTLVDSNSTSASTNTSNENSPNPEESSEKVNADDRINSNNDGPNENSDSSTLSLSTKLLKRTFRVPLKIDKTAGPGLSKESFNEAKSKLEALDKKDEERRRTAELKNSLEGYNDTRKLESEDFAKISTGDRGQSFIEKLEDEVQEWLTYDGEDASATQPKRLDELKAGDPIFR

NbL05g13320.1 myosin_heavy_chain_cardiac_muscle_isoform-like [MW = 147.83 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain

Protein sequence:

KYRIQLEEEQISTLEKKGVAEEVSKKHADRADELEAEVEAFQMKSSSLEVALEETKEKEKELNGGLNNVTEKNEKLEQVYVTSIEKLAETENLLEVRNELNATQQRLEGENDLNAAGLKESEVMEKLNKSAEEQLEGGGRVLEQATARSIELESKLDHFLKRRSELKIGETAKGFYVTRDSEADITLNEKLNKALEDQLKSYEEQIAKSTESBSAKEELDQVLVKLASSETDNEVLKPKKILEAEKKAADLSENGQLAETNMLKNGKNGVSDLEEQLNBAHAEKASVYQQLVSHMNTTI

NbL05g13310.1 gamma_aminobutyrate_transaminase_1_mitochondrial [MW = 56.9 kDa]

No. of times detected



log(intensity)



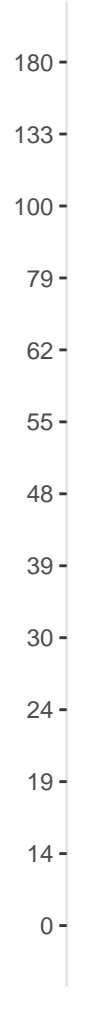
Values from



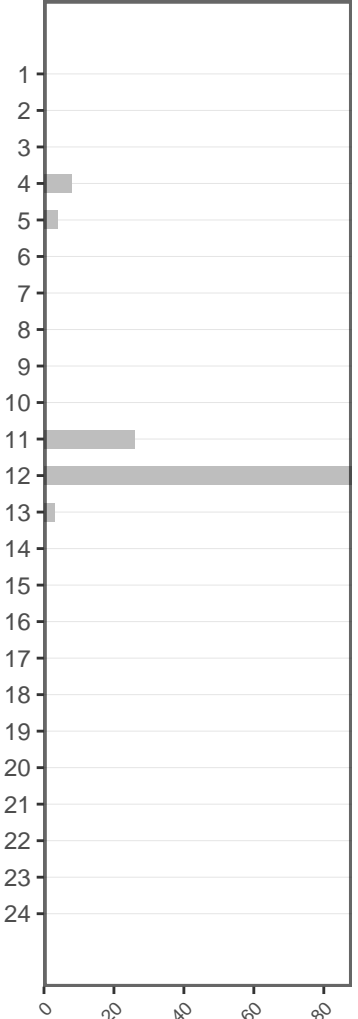
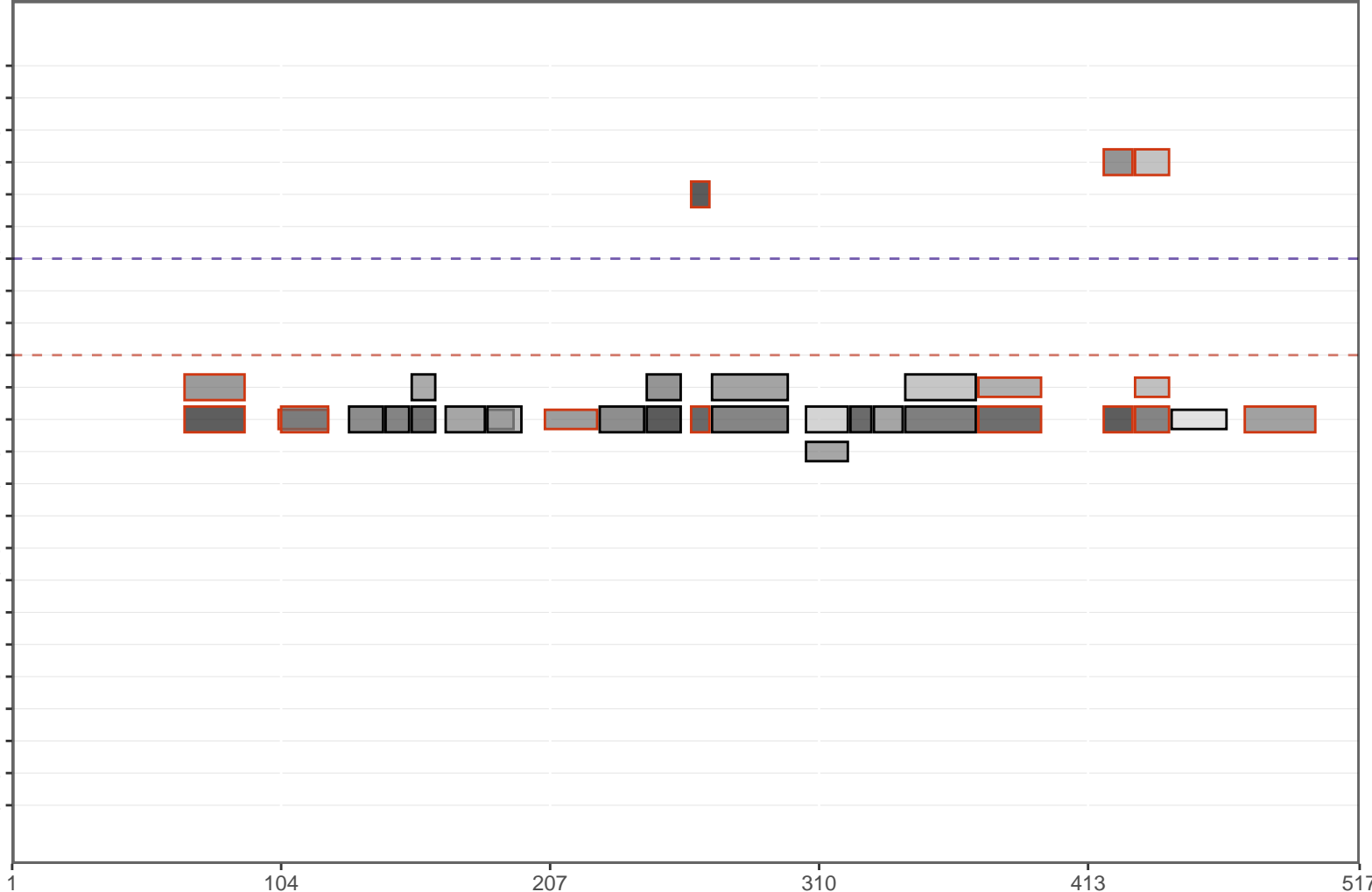
MW indication



Molecular weight

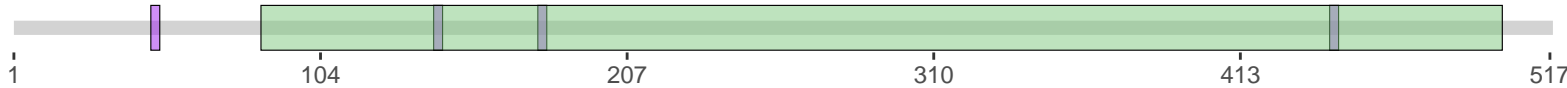


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RYVHLPQETEETEFSTRLLAKNLEDLKEGPEVIAAFIAEPVMGAGGVIPPTATYFDKIQAVVKKYDILFIADVEVDAFGRLLGTFMFGGDKYNIKPOLVSLAKALSSAYMPVIGAVLVSPVEVSDVHYSGENKLGFSHGFTYSGHPVSGAVALEALKYKERMMVEKVRNRSKPFQEGKKAFFSDSPVGEIRGTGLLATEFADNKNPNDPFPPEWGGVAYFGAOCENKMLVRYAGDTIMSPRPVTPPEEVDLISYKALKETEKREVEELKSGK

NbL05g13250.1 UDP-glycosyltransferase_71E1-like [MW = 54.33 kDa]

No. of times detected



log(intensity)



Values from



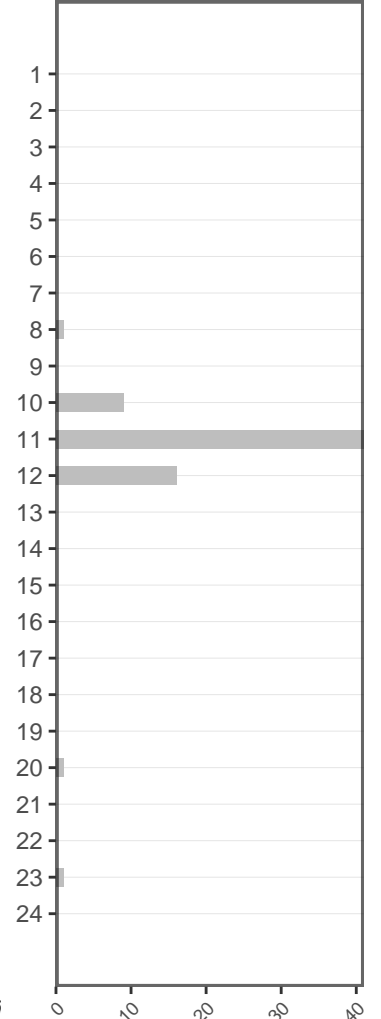
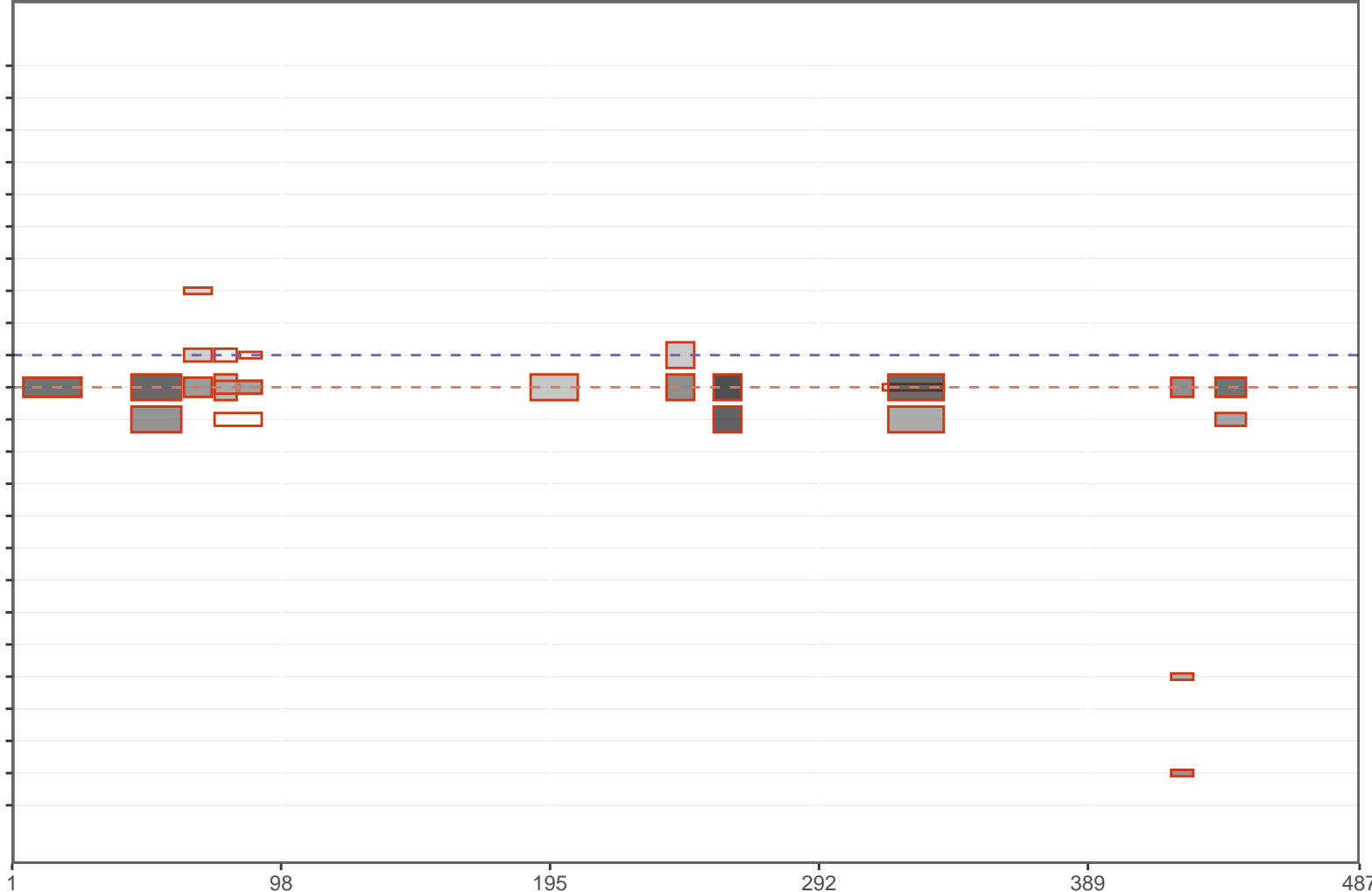
MW indication



Molecular weight

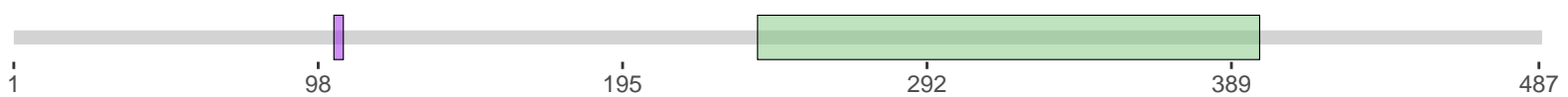


Gel Slice



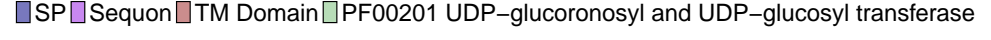
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VLPKHPVGPVYVNIKGGHGRNSQGETESIKWLDKPESSVWFLQFGSMGSFEPQKKEIALEGGSHRFLWLSLRPPPKGKMLPKNYENLEEVLPQGIERTNGVGVKVGWAPQVTVLHSPWVGFVSHQGWNSILEGFCFGVFMATVPHYAEQGMNAPALVKELELVAEIRMDYVKDIEGKNPVDVTAKEESGRQLMADGEEESGRKVKVKEIKSSAAMKGGFGKELKAKRGLTHVFTYTR

NbL05g13240.1 anthocyanidin_3-O-glucosyltransferase_6-like [MW = 53.58 kDa]

No. of times detected



log(intensity)



Values from



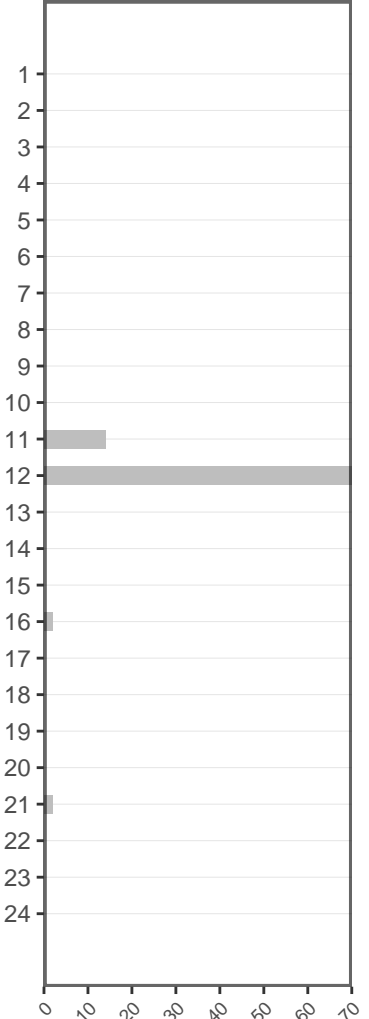
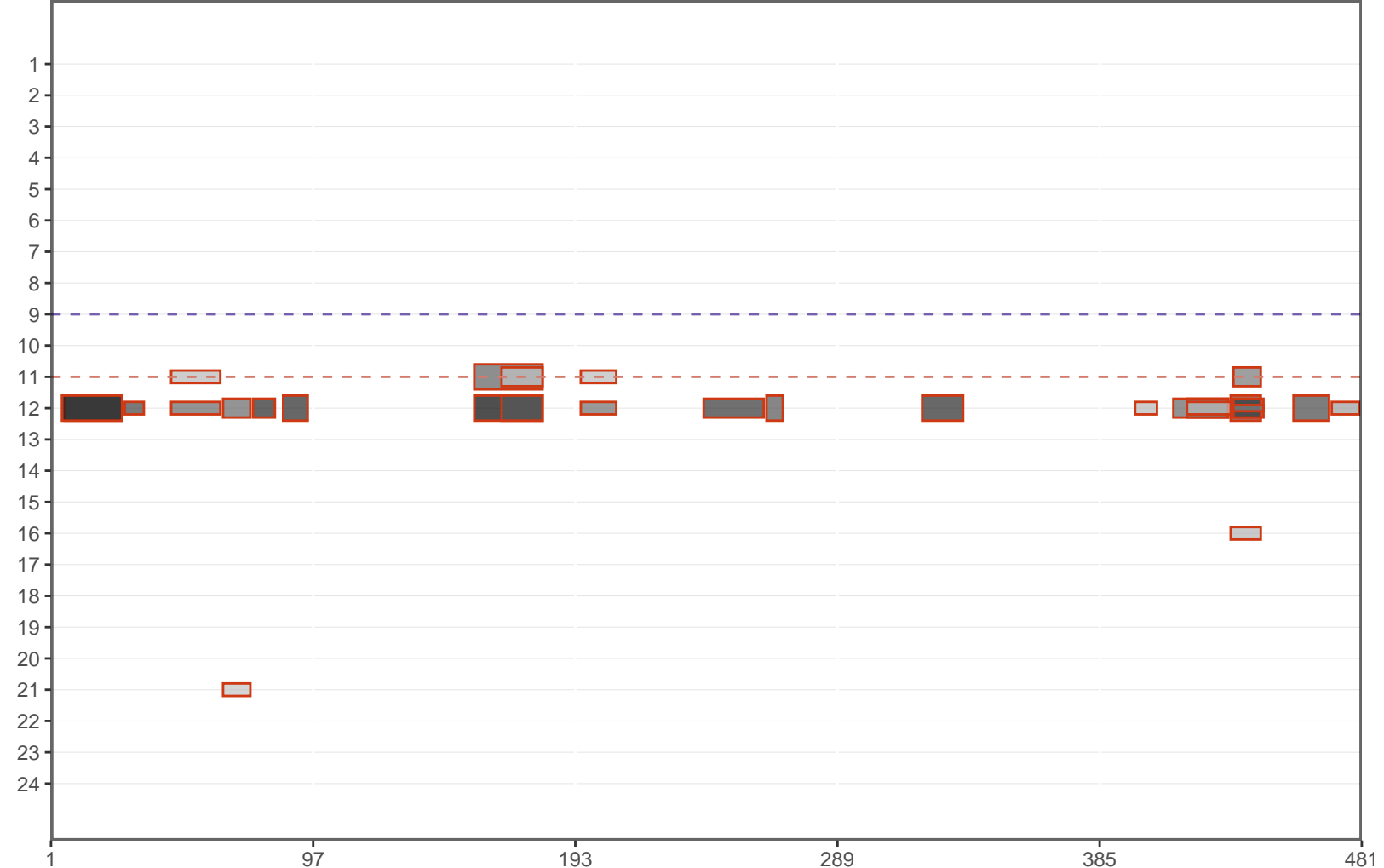
MW indication



Molecular weight

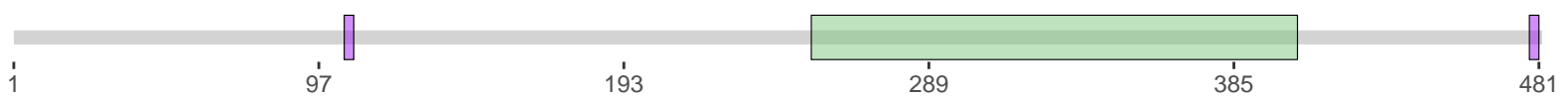


Gel Slice



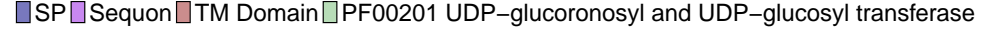
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILSDARIVKQIYPIPIPIAYSEDNKPEIESIKWLDGQPKSGLFLGFTLGSFEPEQVREIMALERSGHRLFLSLRPPPKGKVMKPKNYDSEEVLPFGFLDRNGIKGKVGWAPQVTVLSEHPWGGFVSHCGQWNSVLESGCGGVPIAAWPLVAEQGMNFFLLKVELGLAVERMDVYKDFEGKPNVDIVGAGEIEGAIKKLMADGEEENRKKVKEMGEKSRVAMEEGSSVYSLRLKDFISNI*

NbL05g13180.1 pyruvate_dehydrogenase_E1_component_subunit_alpha-3_chloroplastic-like [MW = 47.75 kDa]

No. of times detected



log(intensity)



Values from



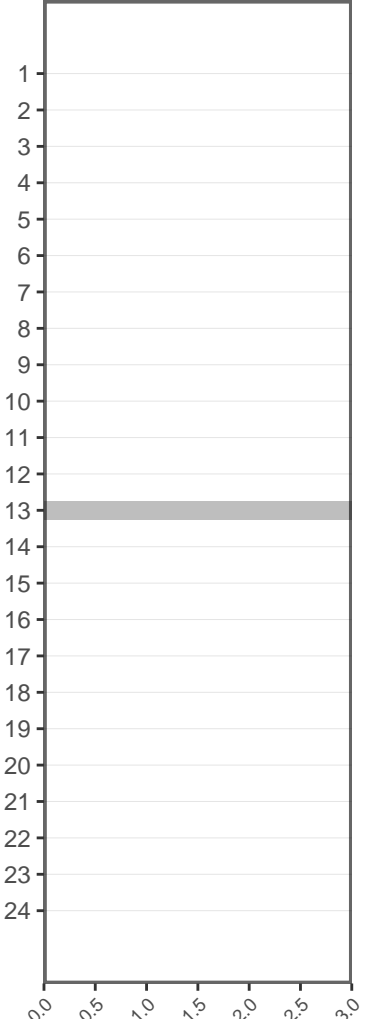
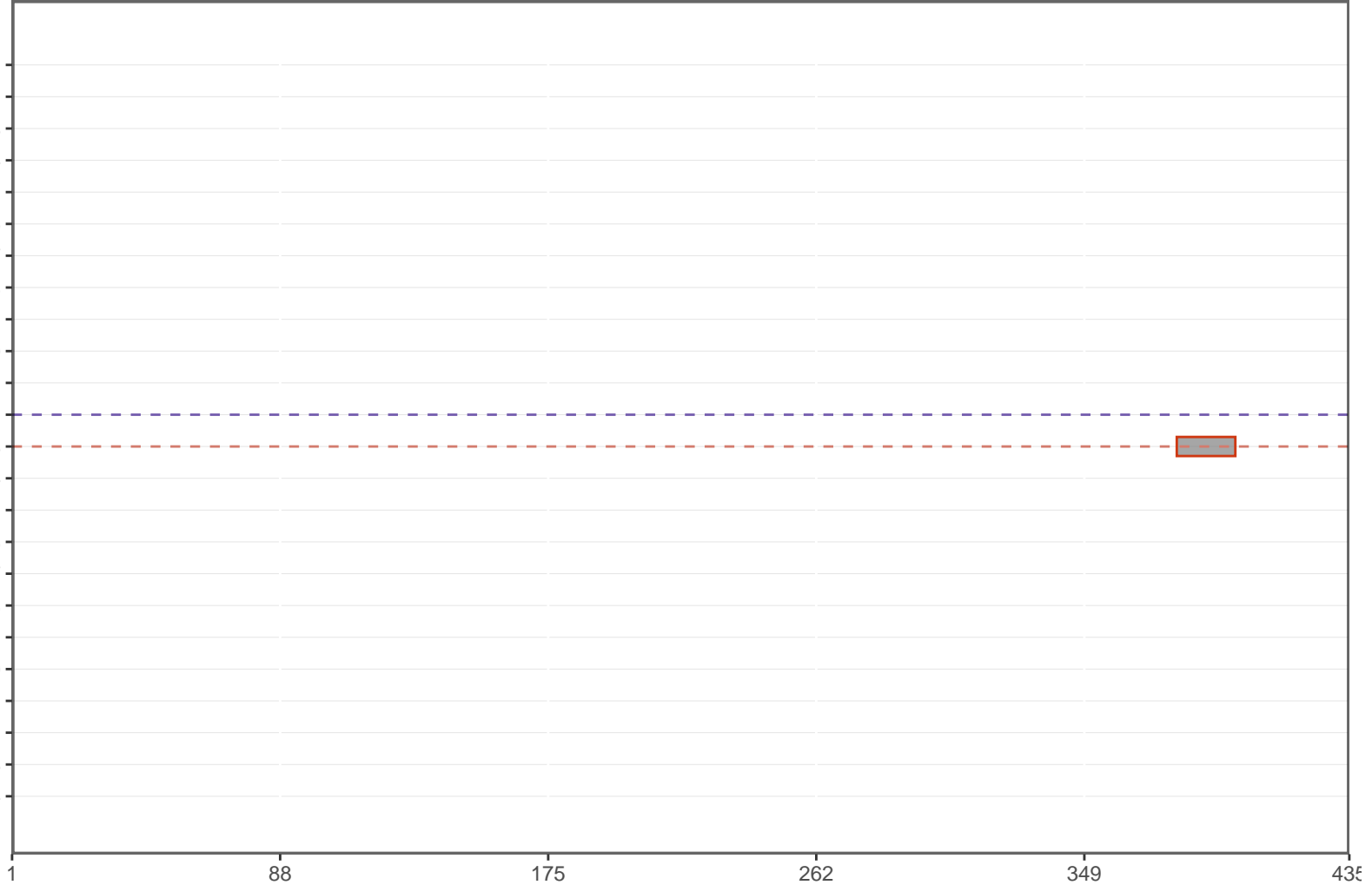
MW indication



Molecular weight



Gel Slice

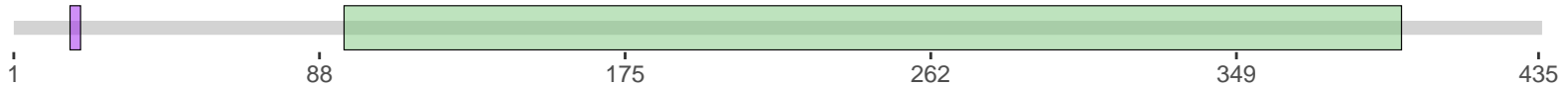


Peptide counts over 4 repeats

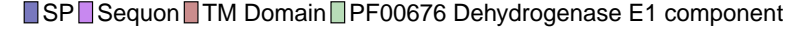
Protein length



Pfam domains



Pfam Description



Protein sequence:

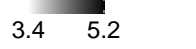
ITGAFTSKYRKEVKGAECDHVTLAFFDGTGNGDFYEGLNMAAIWKLPIIFVFNLLWAGMSHLRSTSDPEIWKKGPAFGMPGVHYDGMVLRKREVAKEAGARRGEGPTLVEGETYRFRGHSLADPDELDRPAEKNHVATRDPTALKKVMFENNLVSEELKADKKDEVVEESVDFADASPVPARSGLLENVADPKRFGIGDGRVRCEDPKFTEGTAMV

NbL05g13080.1 glycogen_synthase-like [MW = 61.76 kDa]

No. of times detected



log(intensity)



Values from



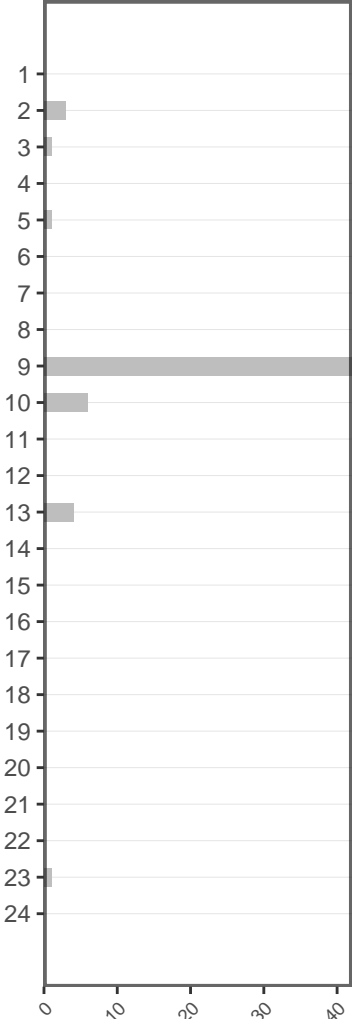
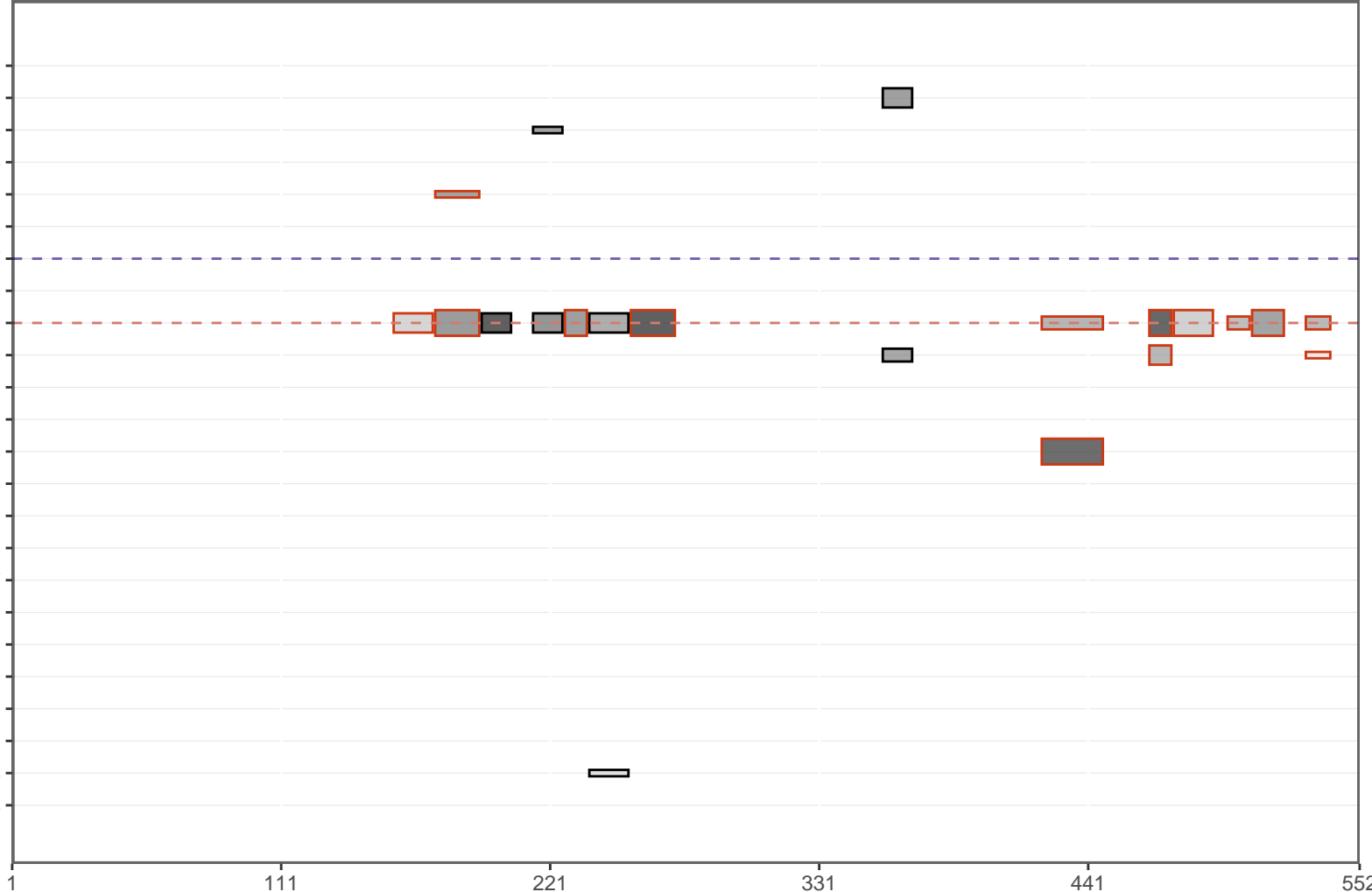
MW indication



Molecular weight

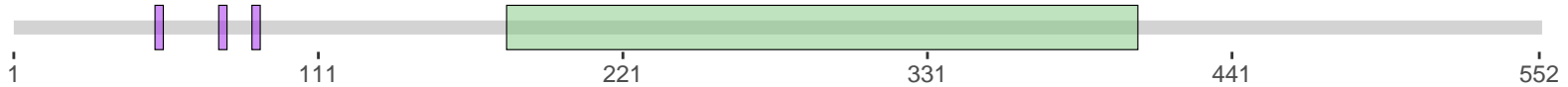


Gel Slice



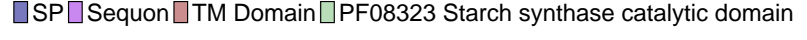
Protein length

Peptide counts over 4 repeats



Pfam domains

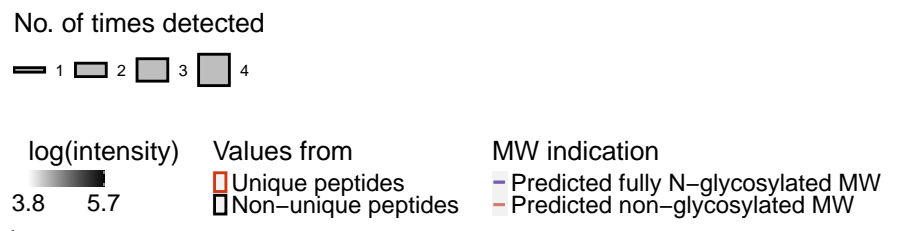
Pfam Description



Protein sequence:

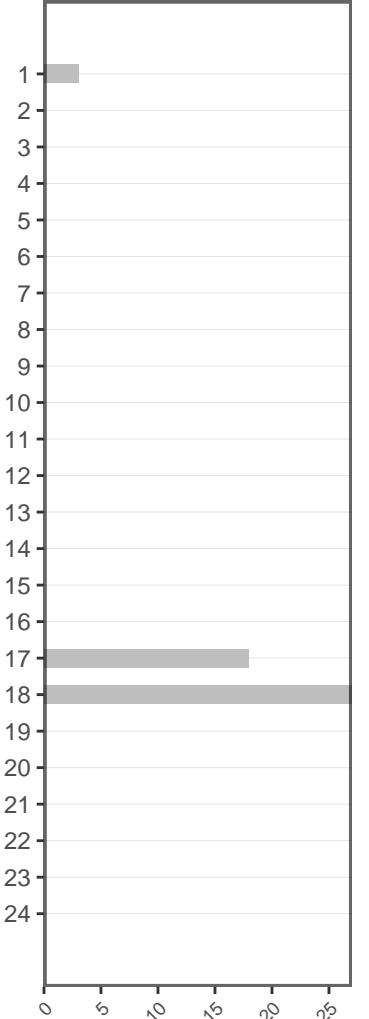
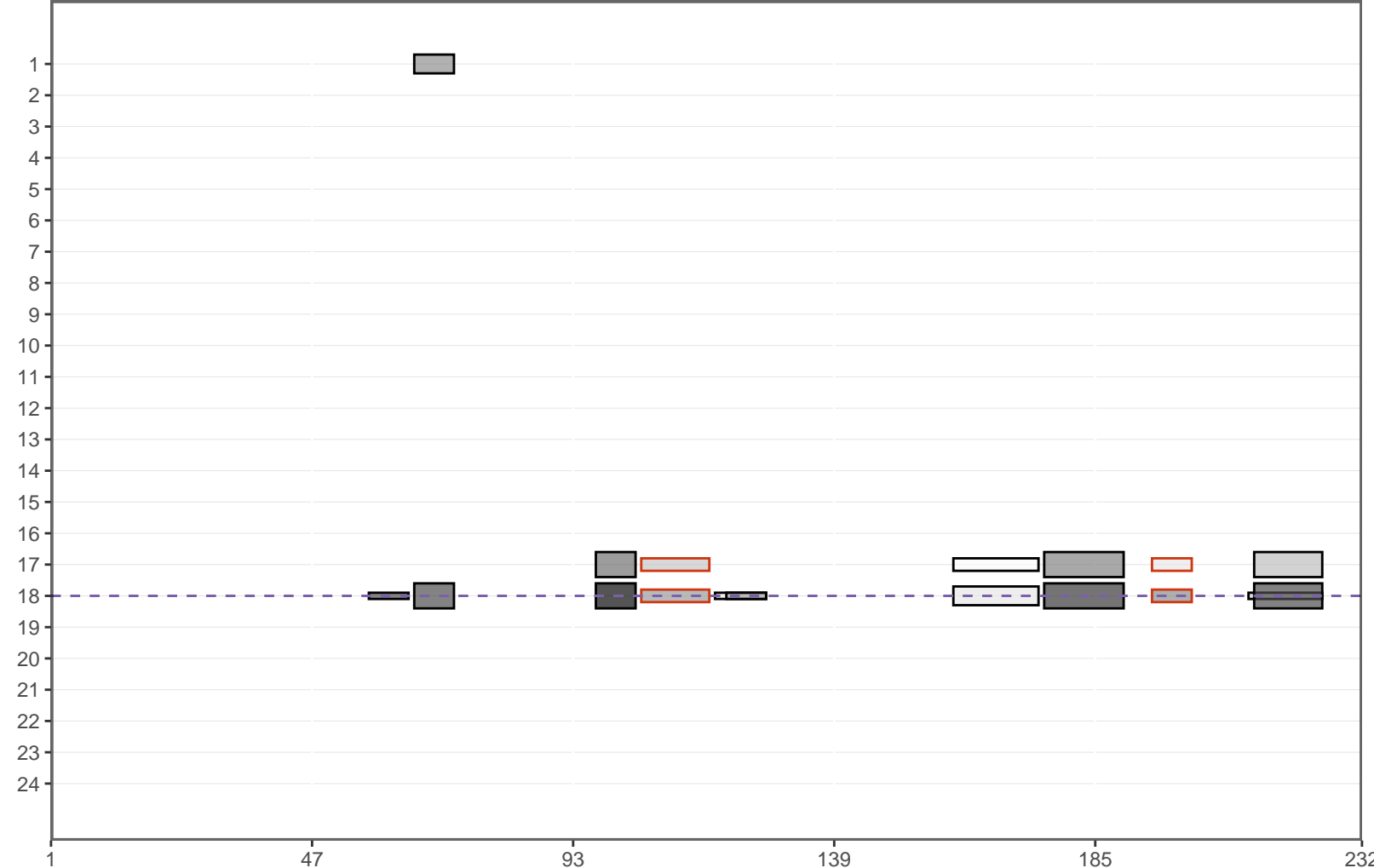
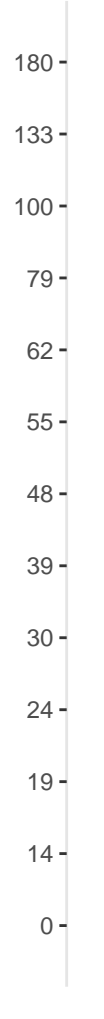
ILIEPSNIIFFKGTNIVGGSSYLEEAVLFFSRAGLELMQVDTGTGPDHIVHEWQTSALPLFYWDMYGFLEGLKPRIVLTHINMEHYGECRQEQLSKFLDGSVATEDKADDDRTVGHNFERLRLSKGGIVYNAVTVSPTVLYKELTLCGGWLSGALMRNRDXYSGILNGIDTEMNRPATDVLPAKFDASKIEGRKCKQFVGRGLGLPFESIKGGTQVADGVPLVQITRLVAQKGLHETHAKHVEELGGQVLGRASDGRVVEREFEGLAELHNKGNIRLLMYR*

NbL05g13000.1 eukaryotic_translation_initiation_factor_3_subunit_K-like [MW = 26.3 kDa]



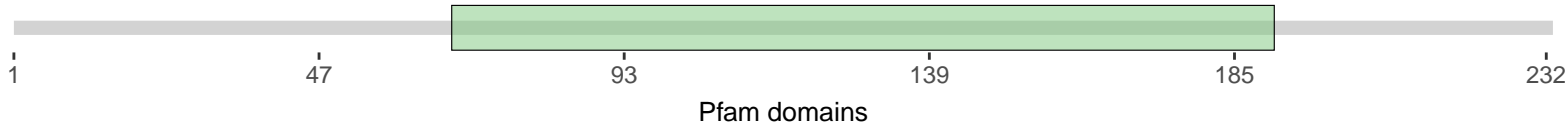
Molecular weight

Gel Slice

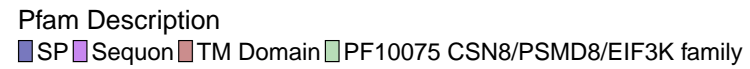


Protein length

Peptide counts over 4 repeats



Pfam domains

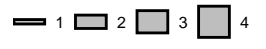


Protein sequence:

DFKTLILLSHYLETARFRGFVDEAAKSRHIVEVVPGFQAIQAVVHVLISFYQKVPRAVAEAINEGLSDKFLFHQVSNQVWVIEKGGKQGLFLPRTEFNHPELKKNTADSVPLEHVTFRIFLIG*

NbL05g12990.1 sucrose_synthase [MW = 92.63 kDa]

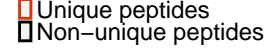
No. of times detected



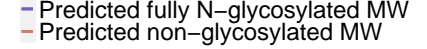
log(intensity)



Values from

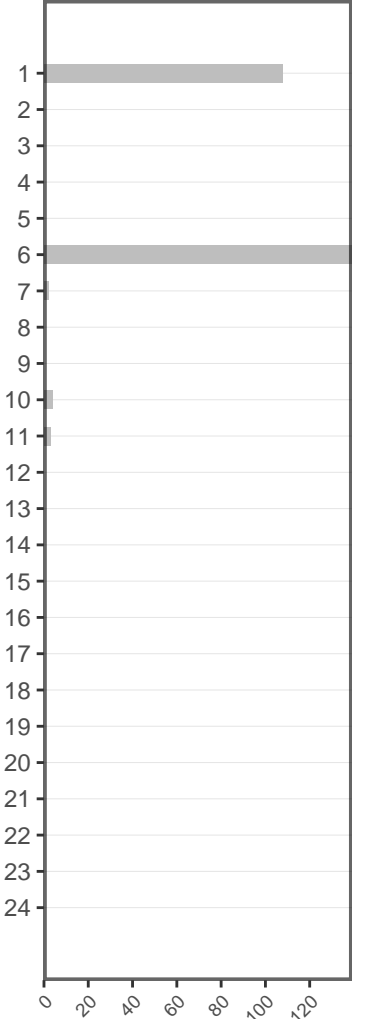
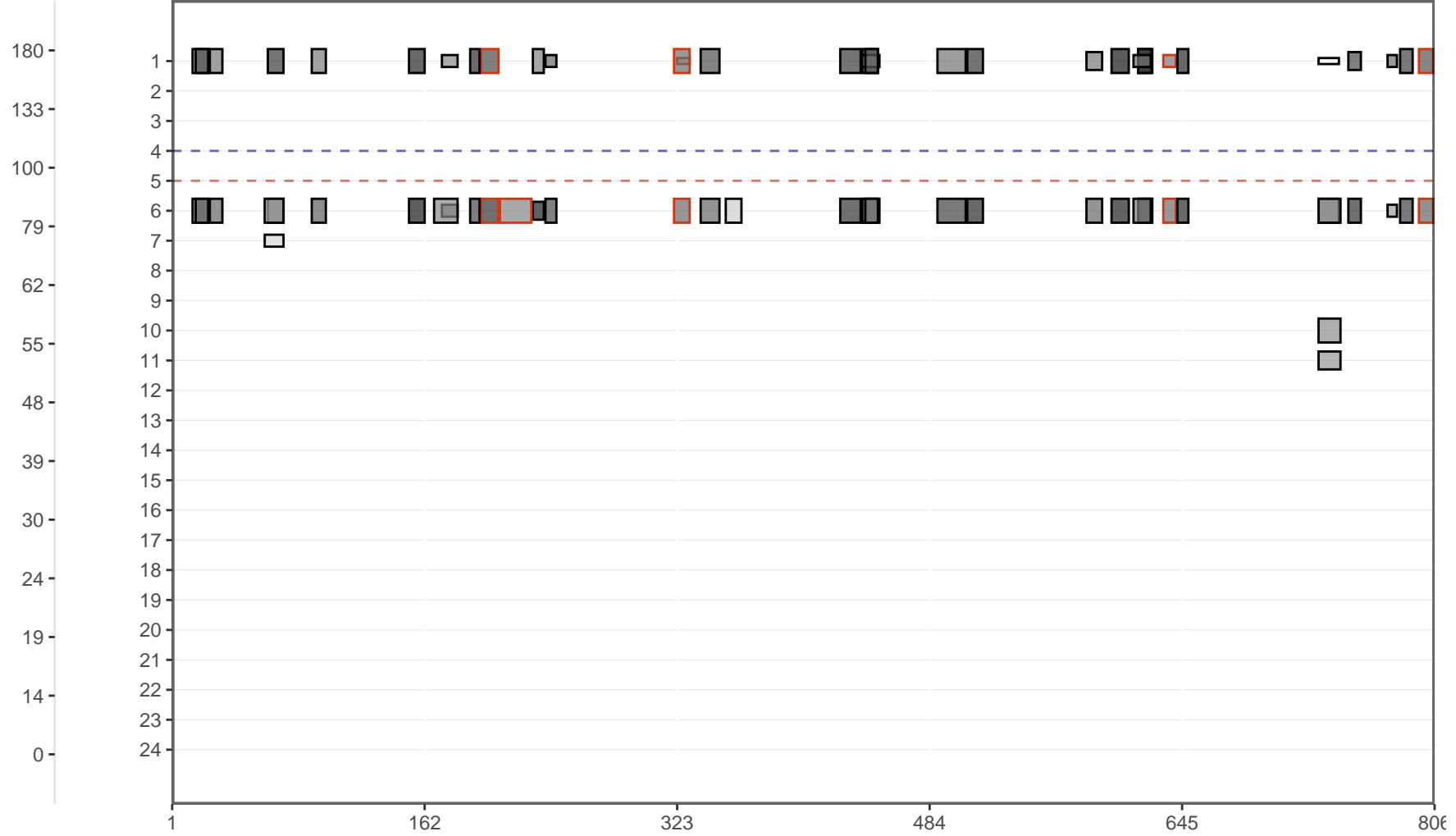


MW indication



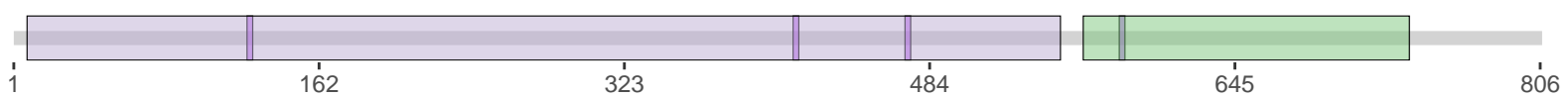
Molecular weight

Gel Slice



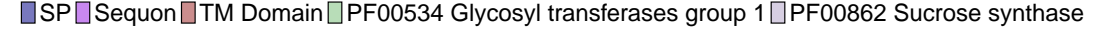
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FTTEDVAKEIAEELGAKPDLKGNVSEGNLAASLLAHKLGVTQGTIAHALEKTKYFDSYILKXFKDEKYHFSAGFTADLIAMNHTDFITSTFQEIAGSKDTVGGYEHSMFTMPLGIVYVHGISVDFDKFNINISPGADMNLYFPYVEKEKRLTARHTEIEELLFSDVENDEHMDVLDKDRKPIFTMRLDRVKNLTGLVELVAKNPRRLRELNLVYVGGDRRKESKDLDEGAEMKMYELIKHNLNGDFRWISSGMNVRVNSGELYRWADTRGAFVQPMFYEAFLQTVVEAMTCGL

NbL05g12970.1 sucrose_synthase-like [MW = 91.19 kDa]

No. of times detected



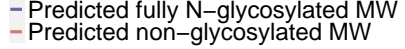
log(intensity)



Values from



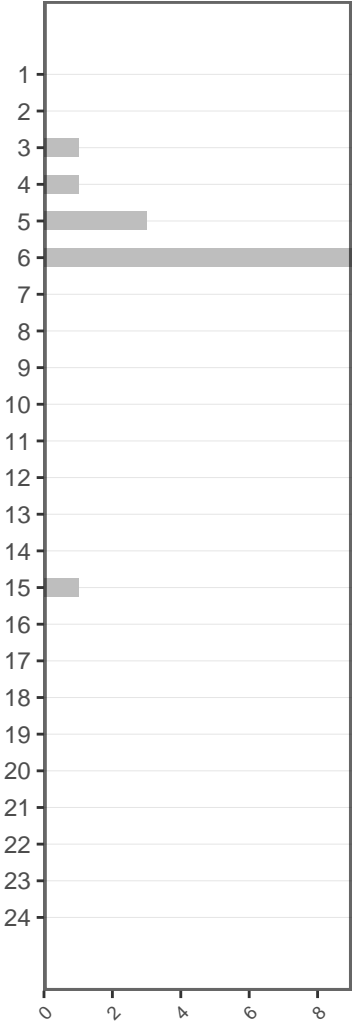
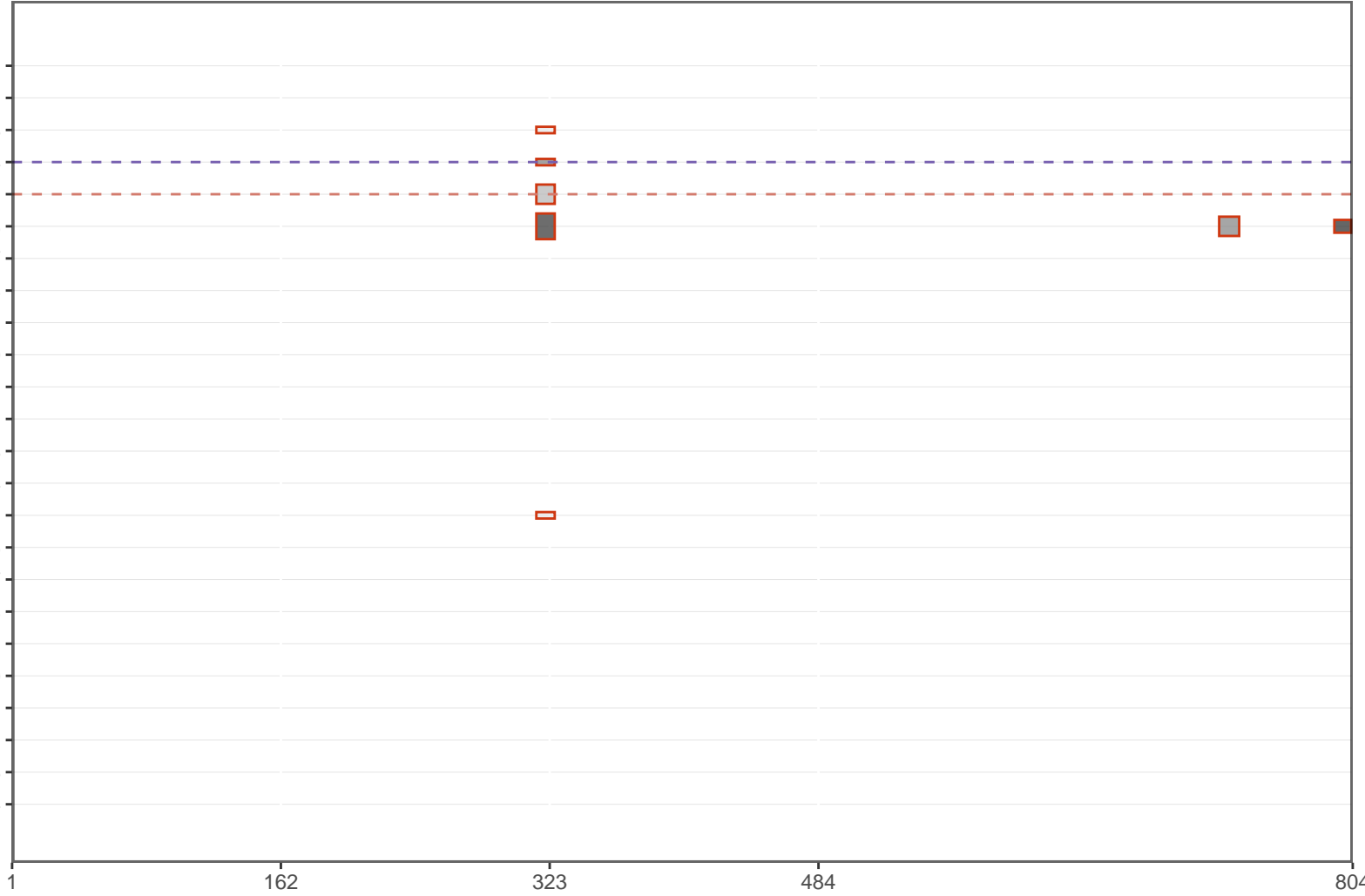
MW indication



Molecular weight

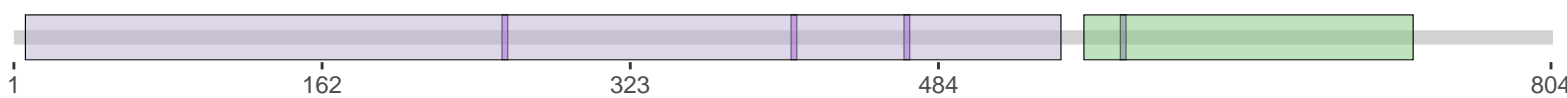


Gel Slice



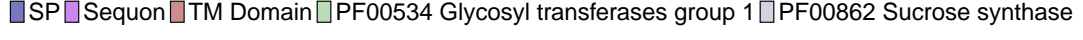
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IELLKELOQKPOLIGNYBEGNLAASLLAKKFGATGCTIAHALEKTKYNSNLSLWKKFDKDYHFSSGFTADLFAMNHTDFITSTFQEIAGSKNTVGVQYESHAFETMPLGYYRVVHGGIDFDPKFNIVSPGADMSHVPYFTEKTKRNLNPHPEIEELLYSPVENKDHLOVLDKRNKILFTMARLDRVKNLGLVQWYAKNARLRELNLVYVGGDRRKEKDLDEEQAEMKMYDLIETYNLNGDFRWISSGMNRVNRNGELRYVIADTRGAFVQPAFYEAFGLPVVESMTCOLPTFA

NbL05g12930.1 peroxiredoxin_Q_chloroplastic-like [MW = 23.7 kDa]

No. of times detected



log(intensity)



Values from



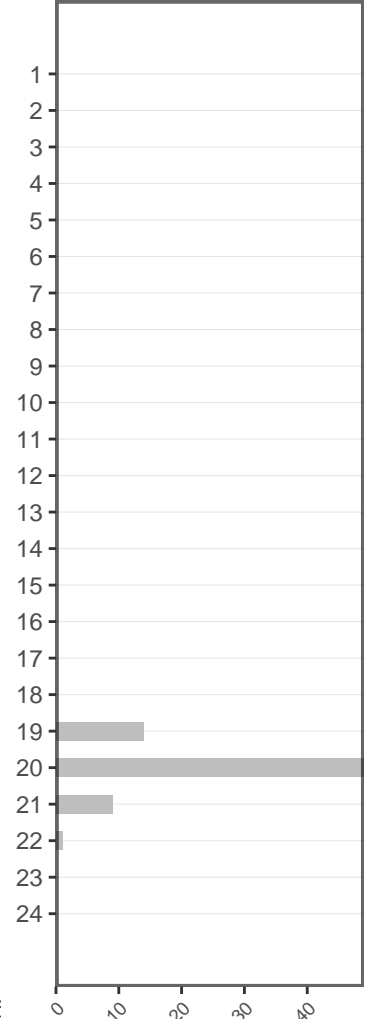
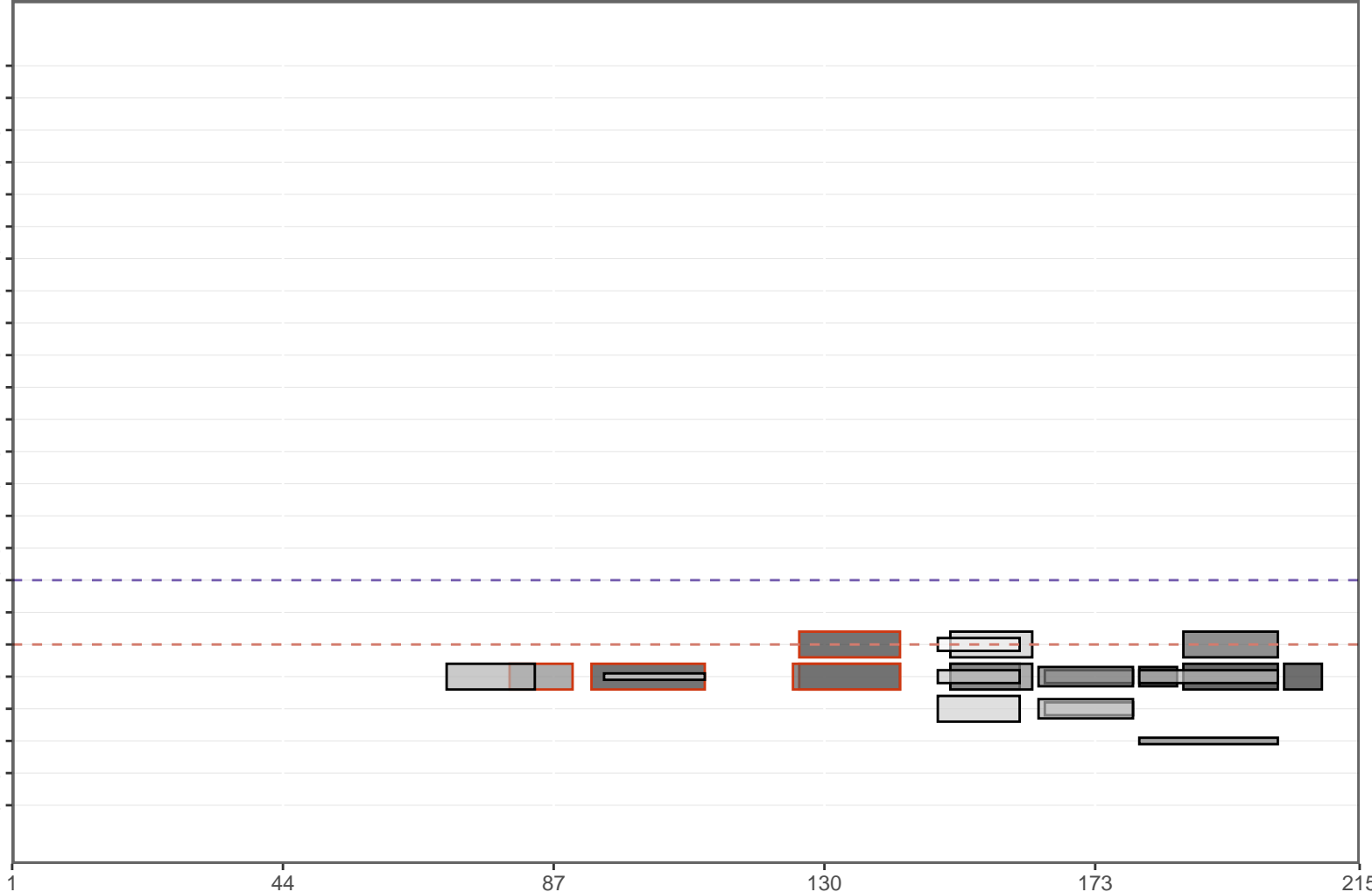
MW indication



Molecular weight

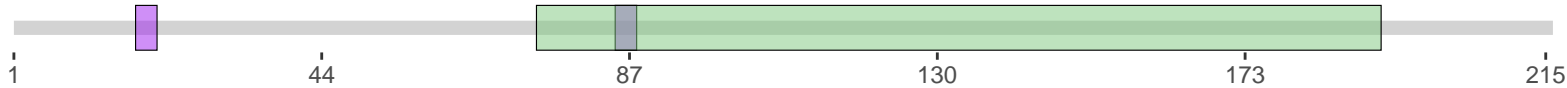


Gel Slice



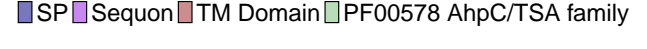
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

***VYFYPAIDETPGCTKQAGAFRDSVEKFKAGAEVVGISGDDPASHKAFKAKYRFPFTLLDDEGNKVRKEWGFQDLFGTLPGRGTVALDKNGVQLIYNNOFQPERKHIDETKLLGSL*

NbL05g12850.1 20_kDa_chaperonin_chloroplastic-like [MW = 26.47 kDa]

No. of times detected



log(intensity)



Values from



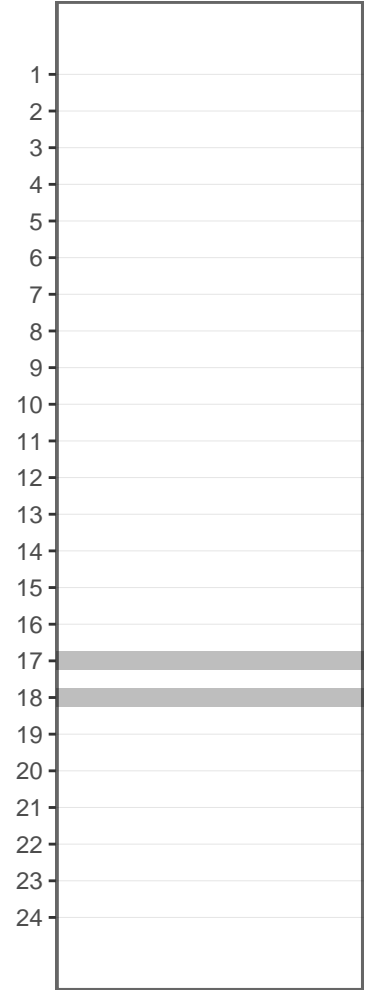
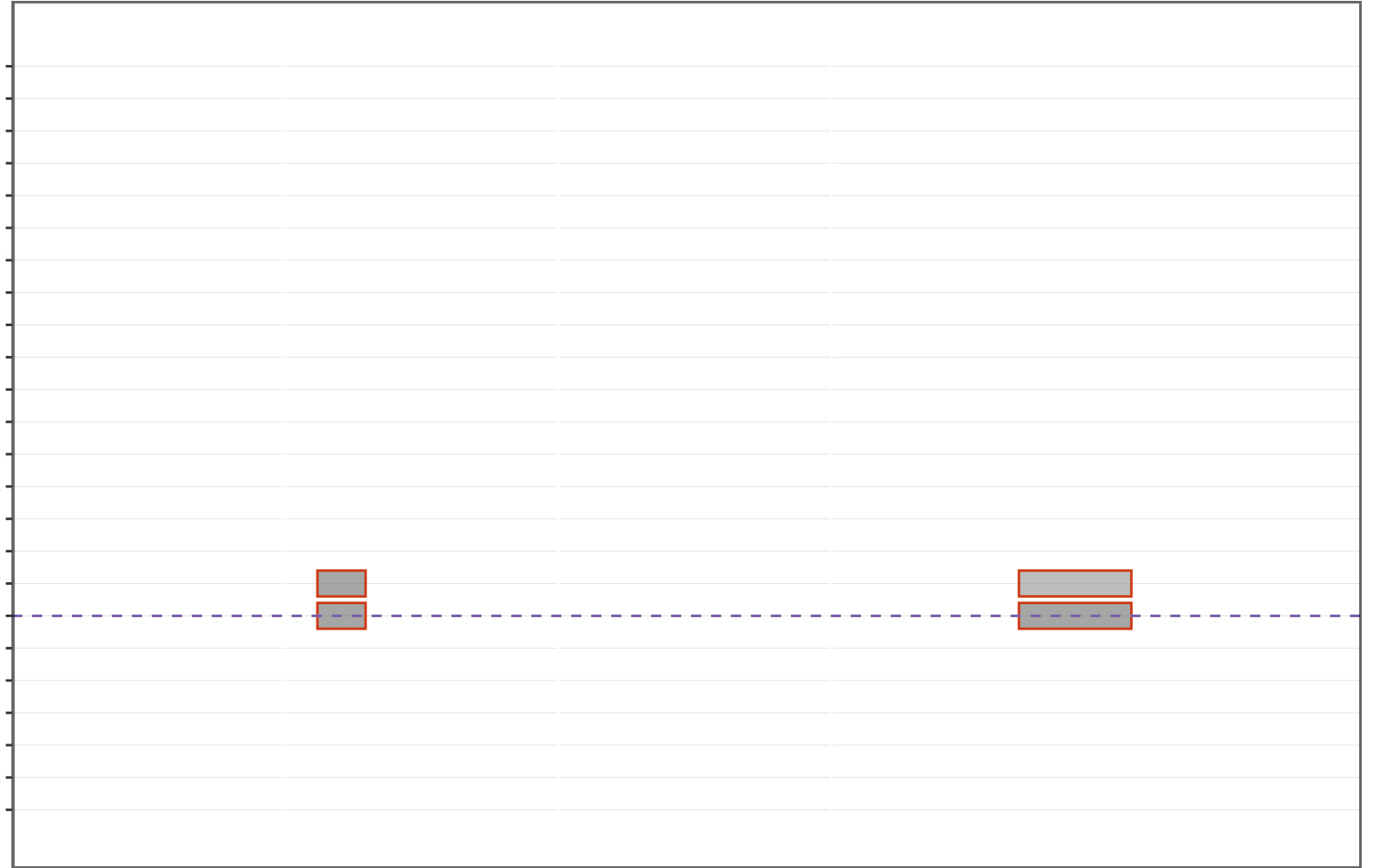
MW indication



Molecular weight

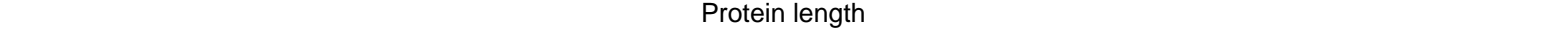


Gel Slice



Peptide counts over 4 repeats

Protein length



Protein length



Pfam domains

Pfam Description



Protein sequence:

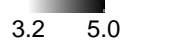
DISVKTGAQVVYYSKYGTEVEFDGSKHLKEDDVGVLVLETDKIKLQPLNDRVLIKVAEAEKTAGGLLLEAAKEXPISGAVAVGPGPLDEEGNRKPLSVSPGNTVLYSKYAGSEFKADGSDVTLRASDVMAVLS*

NbL05g12650.1 subtilisin-like_protease_SBT1.8 [MW - SP = 79.19 kDa]

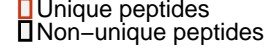
No. of times detected



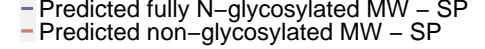
log(intensity)



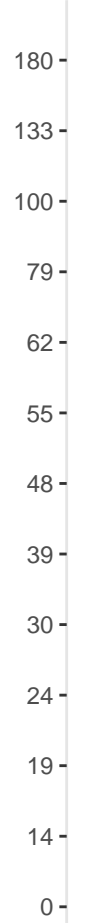
Values from



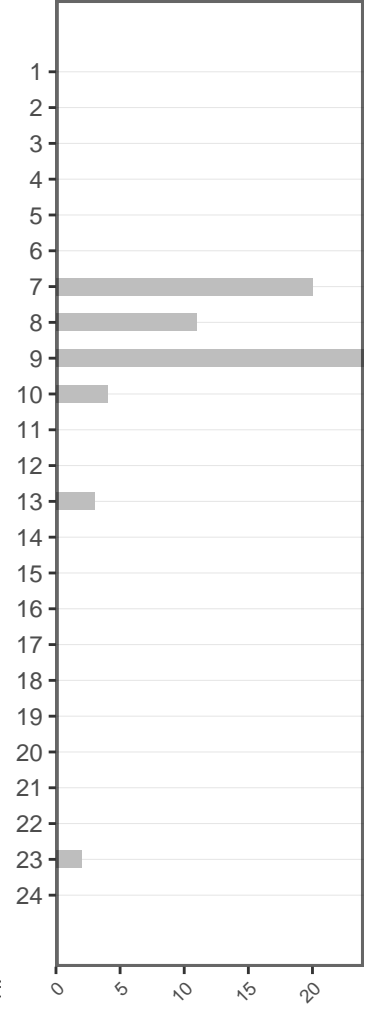
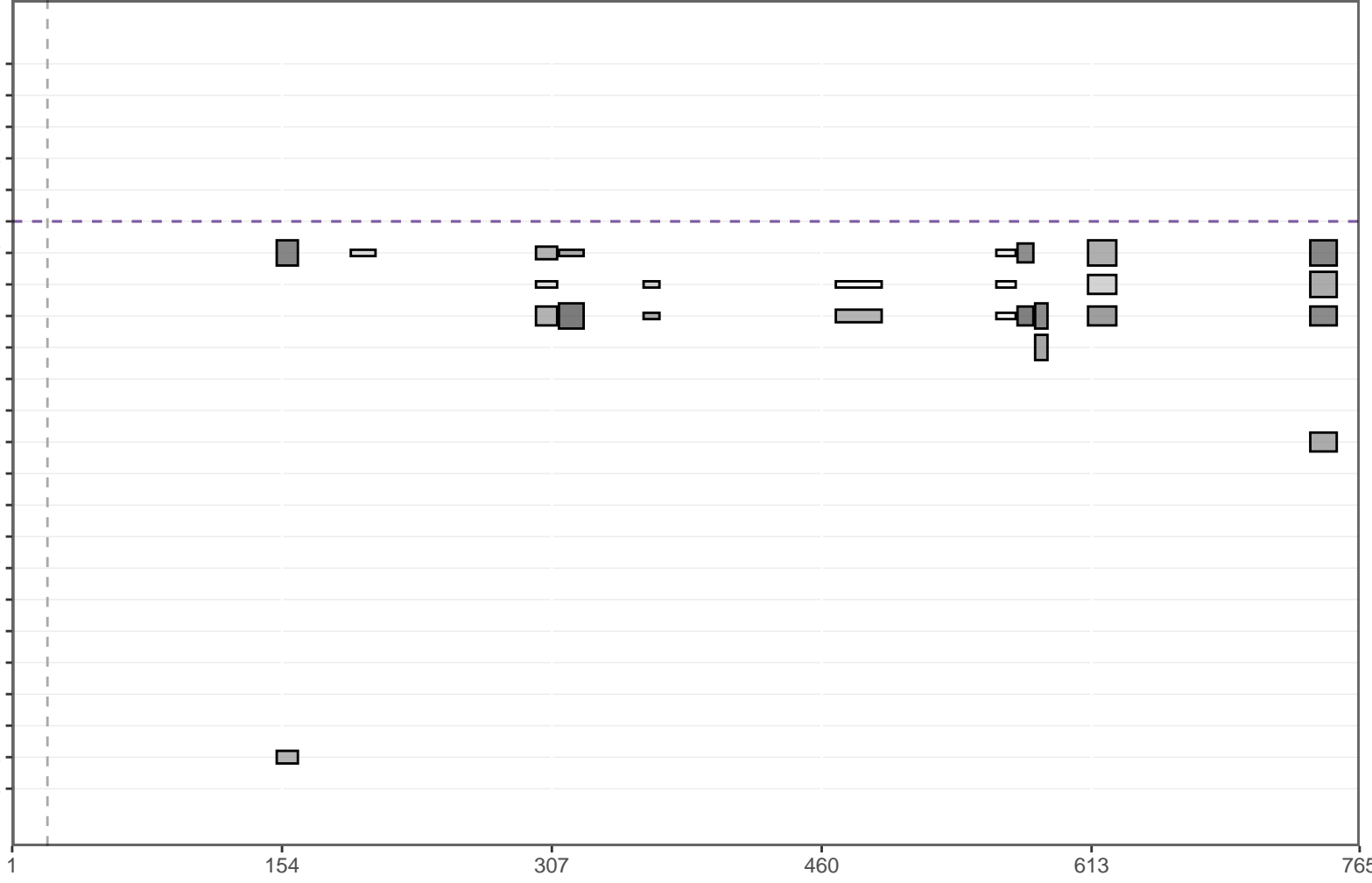
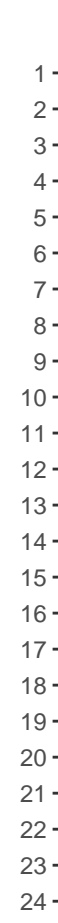
MW indication



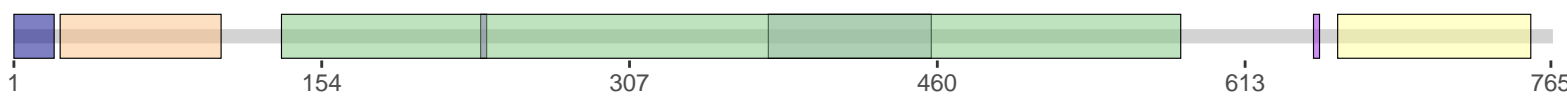
Molecular weight



Gel Slice

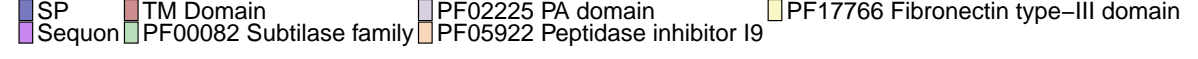


Protein length



Pfam domains

Pfam Description



Protein sequence:

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NbL05g12610.1 cysteine_proteinase_3 [MW – SP = 37.02 kDa]

No. of times detected



log(intensity)



Values from

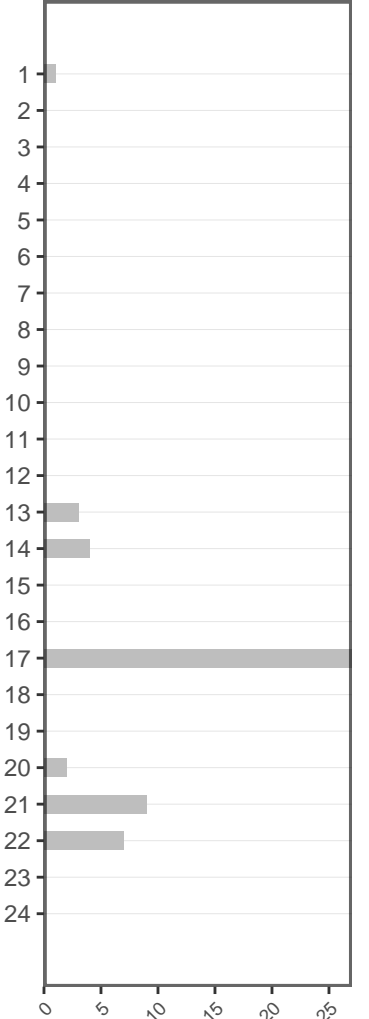
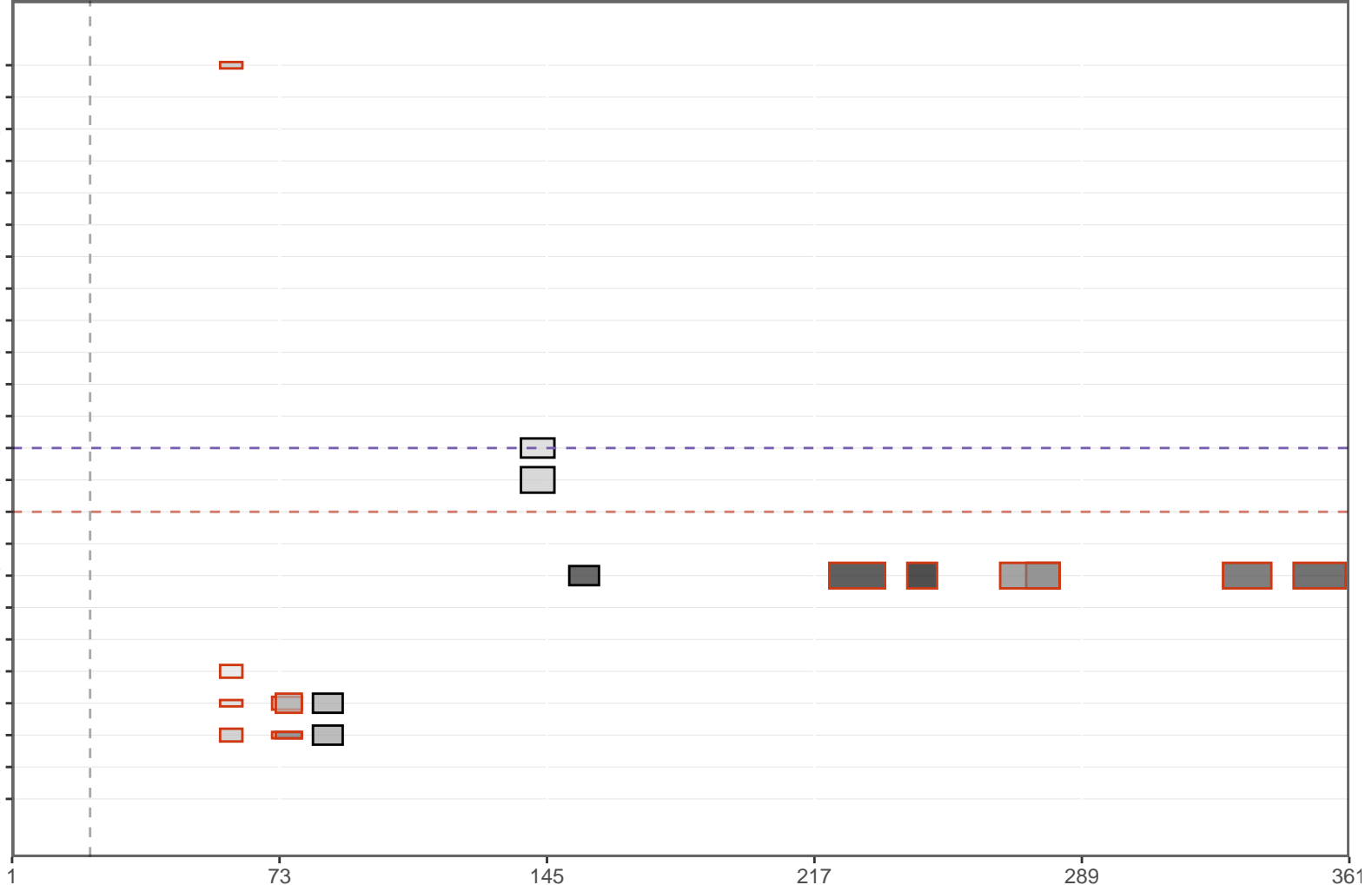
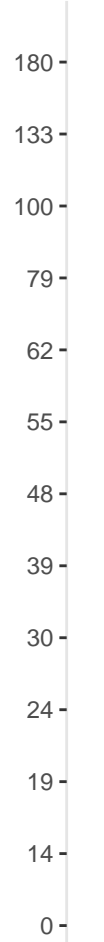


MW indication



Molecular weight

Gel Slice



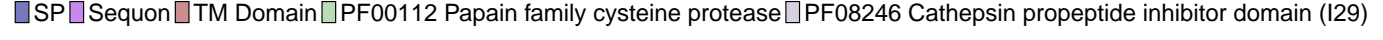
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

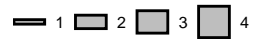


Protein sequence:

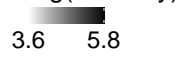
FFSTTGALAAAYGQAFGKIGLSEGLVDGAGAFNFGGNGGLP6QAFYKIKSNGSLDTEEAAYPTGKNGSLKFSSENVGVKVIDEWNITLGAEDLKYAAVALRVPVSAFEVKGKFKYKSGVYVYVSTEGCGNTFMDNHNHAAVLAAGVYGVKNGVPPWLRKNSWGAADWNGVYFKMEMGKNMGGATGASVYVVA

NbL05g12600.1 tubulin--tyrosine_ligase-like_protein_12 [MW = 100.24 kDa]

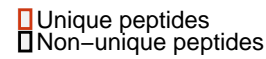
No. of times detected



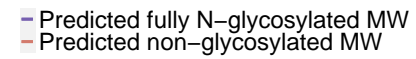
log(intensity)



Values from



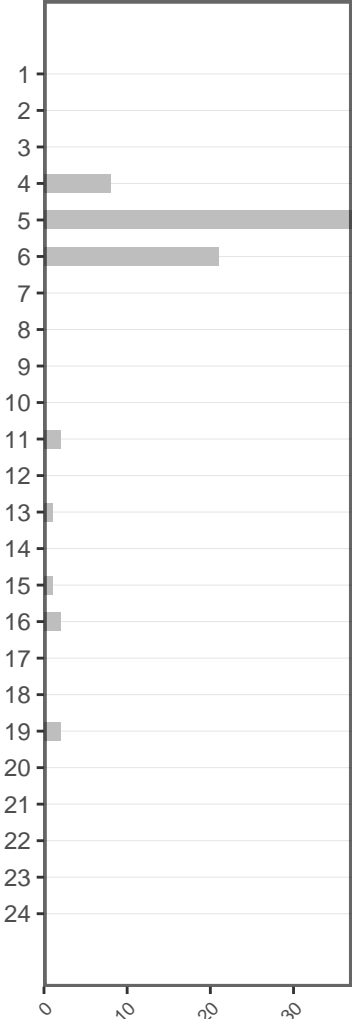
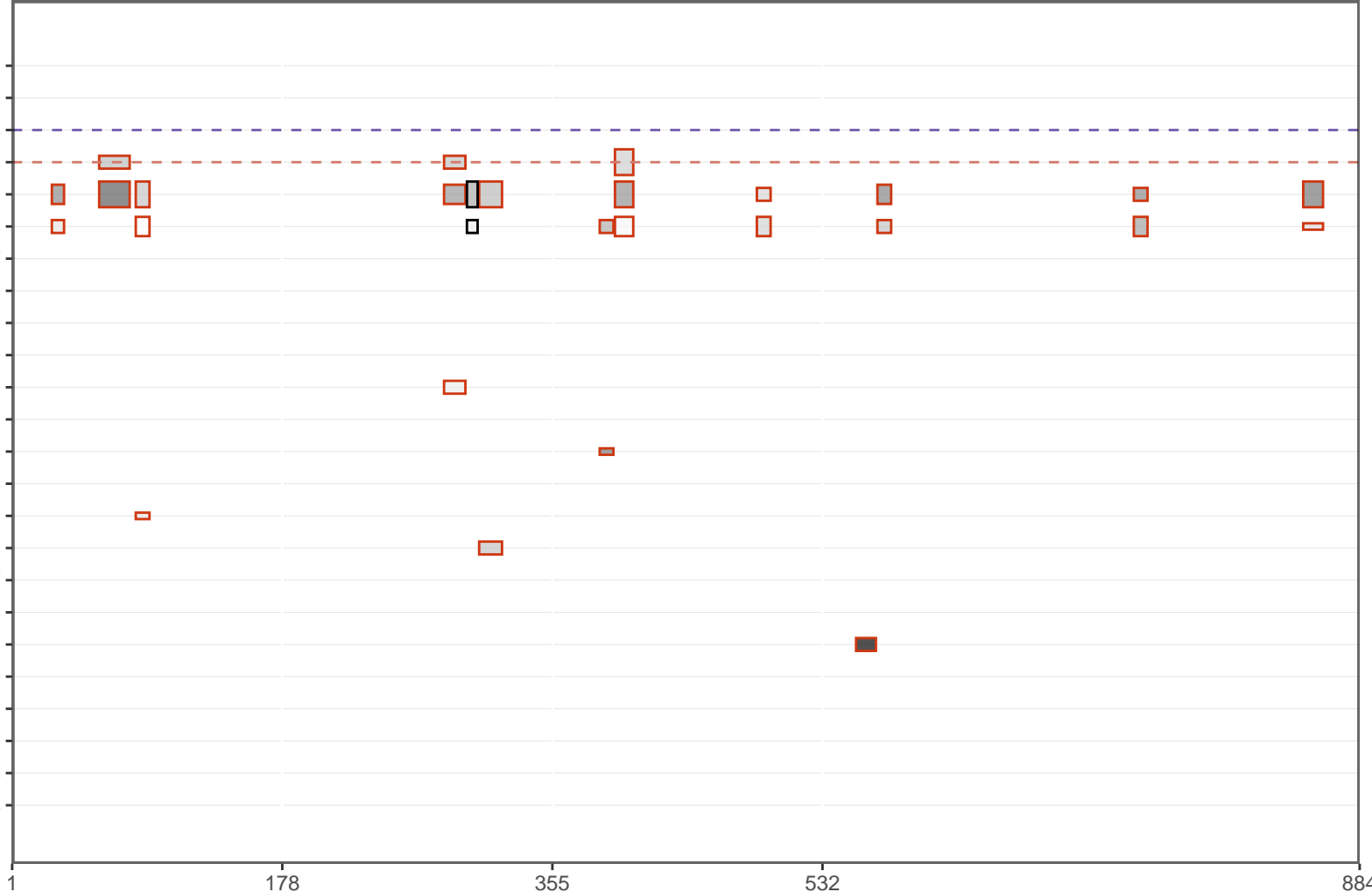
MW indication



Molecular weight



Gel Slice



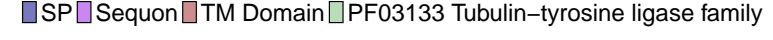
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IETSYVYYMDELGALRHSDKPNRFLRPFLLMPEGNLAVAVSYSLVWIDDVREGDETRDHLFGIGEEKRGRSARLTAWHFTRPNYFRKEVEKYKNGKGNKVFSPVGGSSVTSNLSHSDGSSALRVFTDPPVEEYLTRNEFVITTEPKDADIWTSMDKDEETKKAAGLNDEQYINQFFFEAFLVLMKHLEAETQKAKHGLVEWLGFTYNYLETQTLQIGDFQDREREKLDNLWIKPFWNMARTDITTTISNLSAIRLMEETGPKIGQKYEHPLFKGAKFDLRYILVYRSMNPLEI

NbL05g12510.1 auxin-binding_protein_ABP19a-like [MW - SP = 19.89 kDa]

No. of times detected



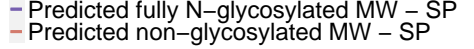
log(intensity)



Values from



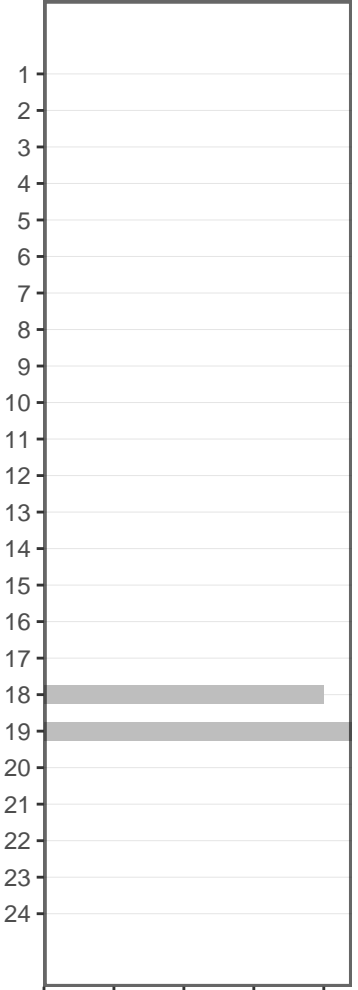
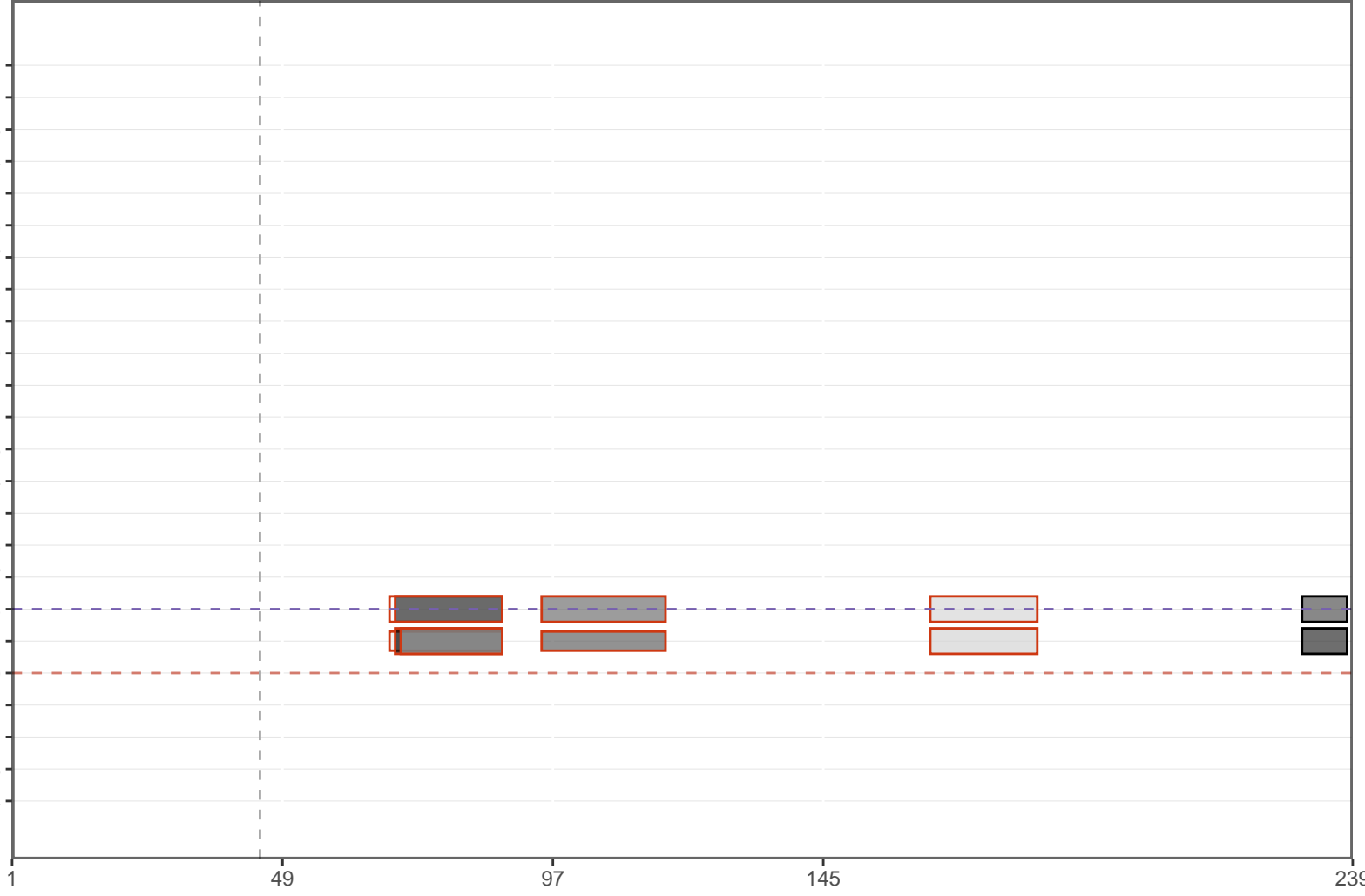
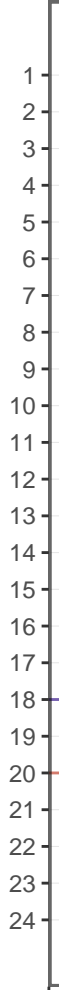
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

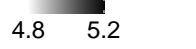
PGLNGLGISMARLDLAIAGGVIPMHTHPGASEVLYVSGGEICAGFI66SDNKVFFKNLKGQDMVFPQGLLHFQINSKTAALAVVFSPTPLGIFDFALFANDLATEIVQATFLDAATIKRKLKGLVGGTIN

NbL05g12500.1 40S_ribosomal_protein_S27-2-like [MW = 12.23 kDa]

No. of times detected



log(intensity)



Values from



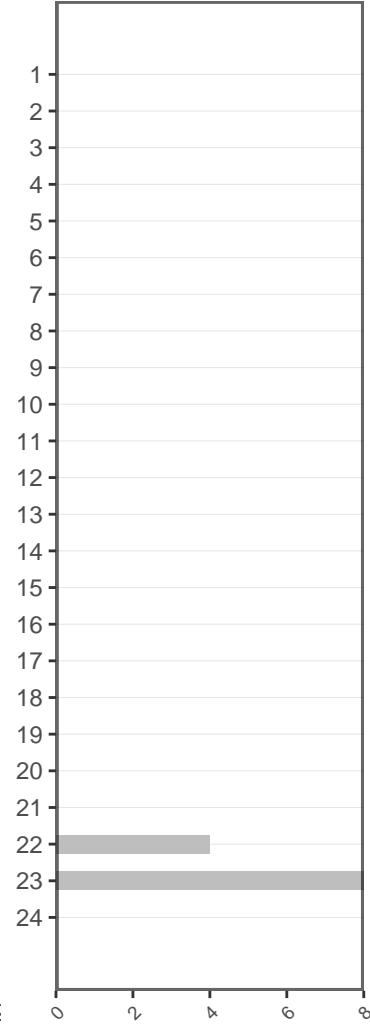
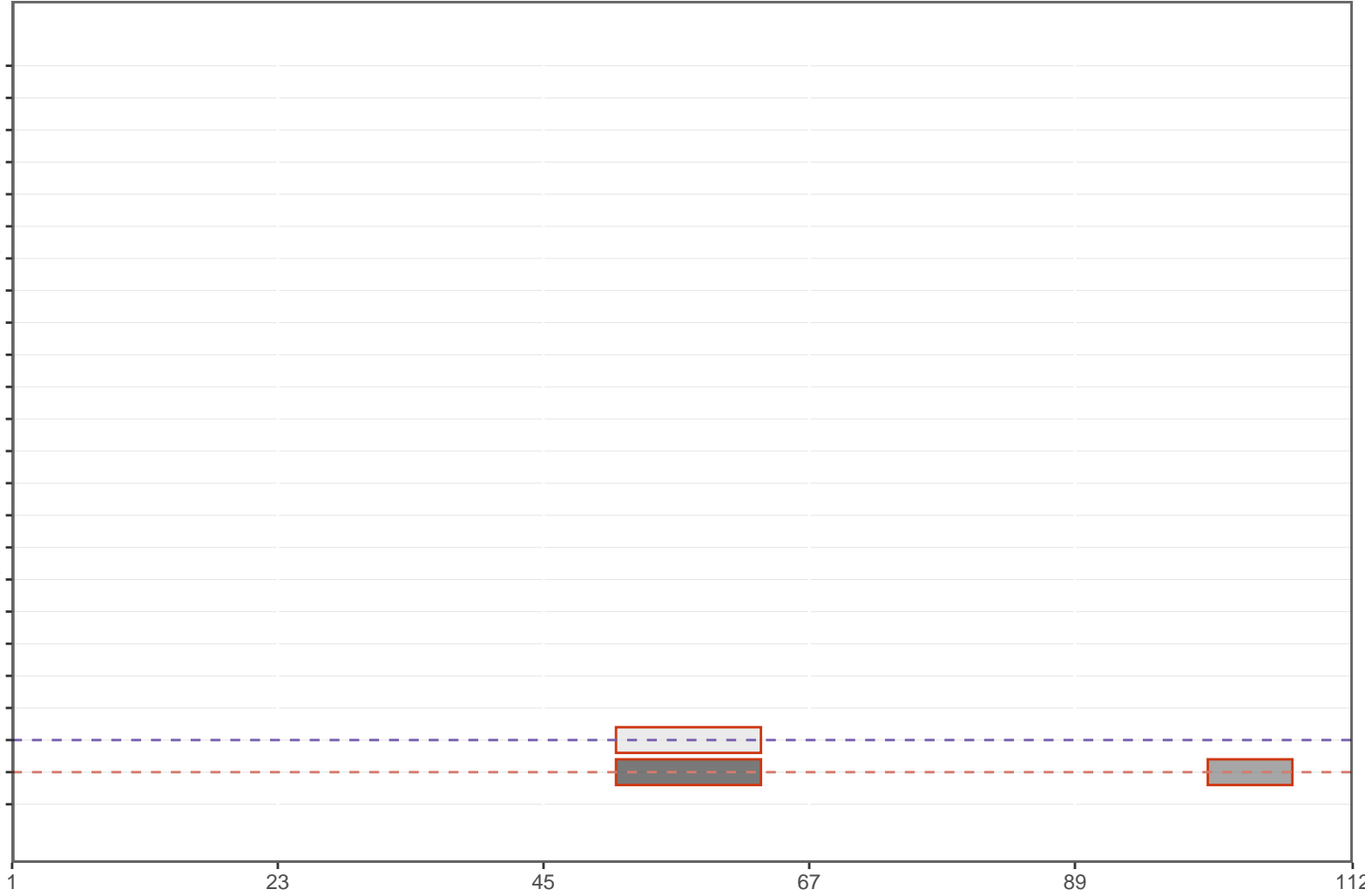
MW indication



Molecular weight

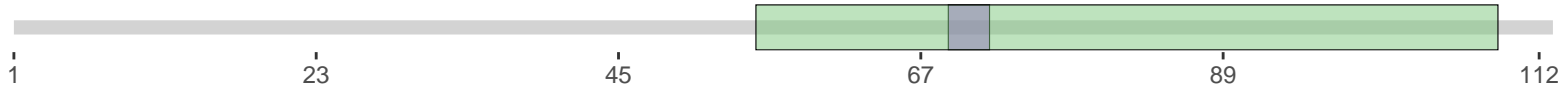


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KHKLRLLVQSPYFFMVKKGGGNTTFVSHSGTVAWCGNGQTVLGGPTGGRAALTEGGGFRKGD

NbL05g12440.1 stress-response_A/B_barrel_domain-containing_protein_UP3 [MW = 33.43 kDa]

No. of times detected



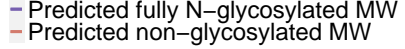
log(intensity)



Values from



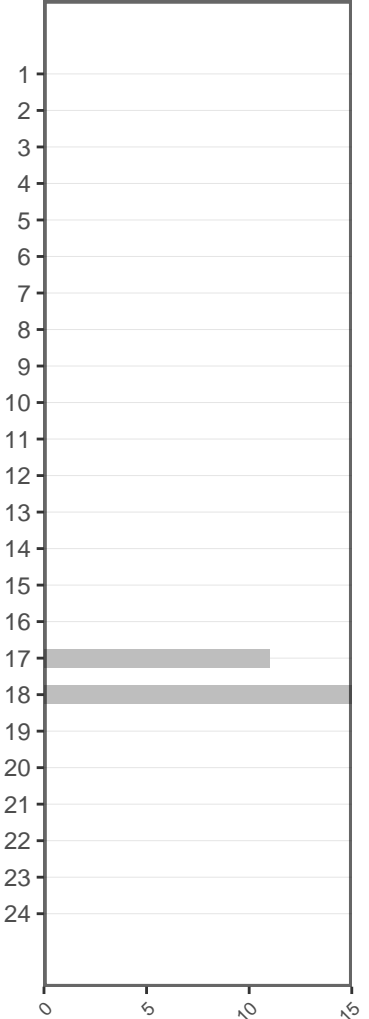
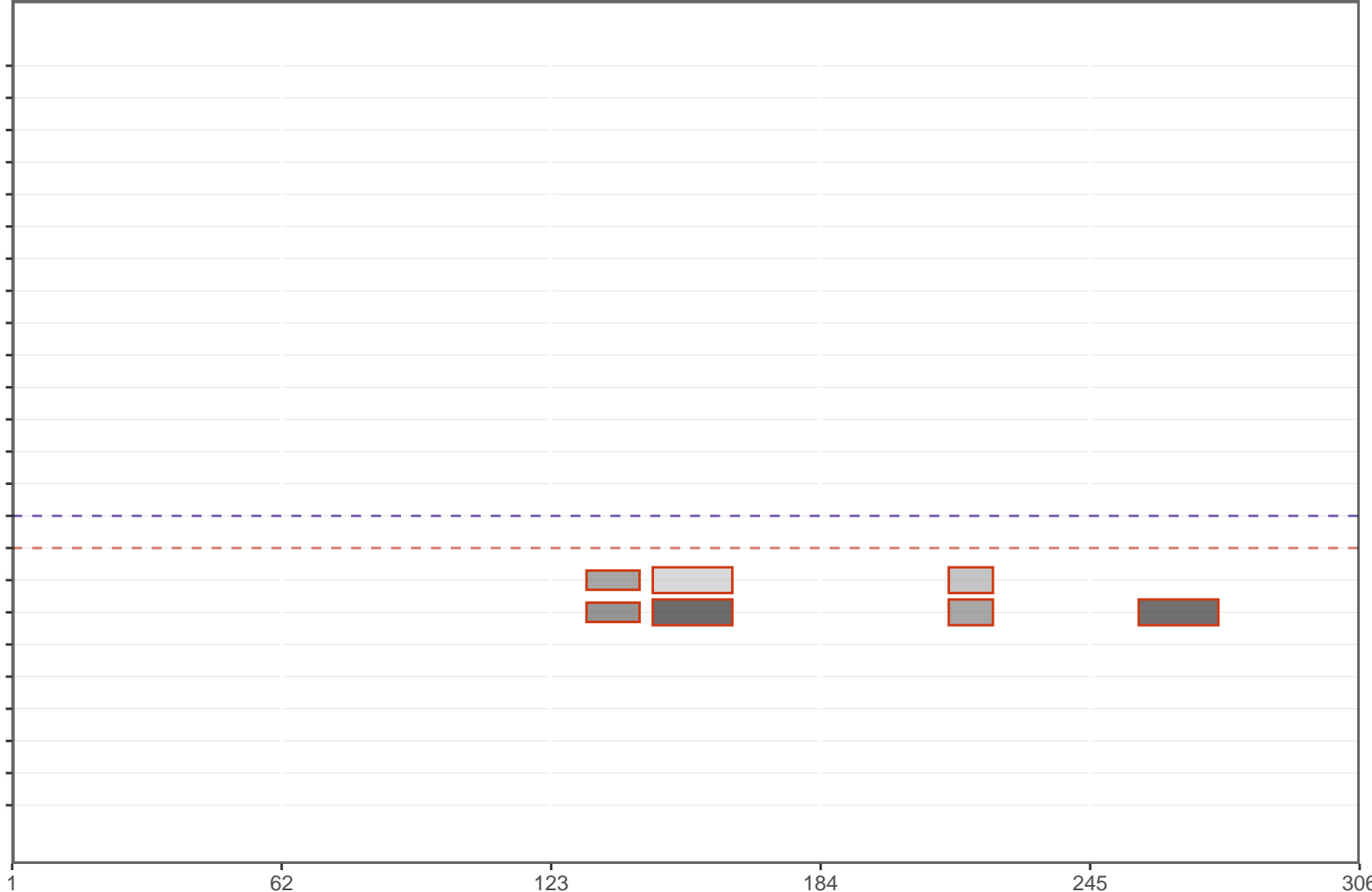
MW indication



Molecular weight



Gel Slice

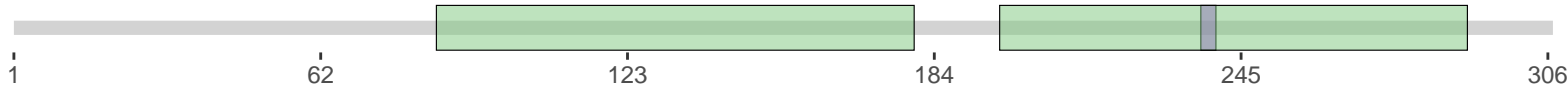


Protein length

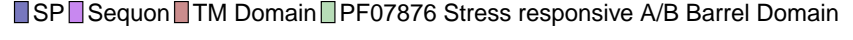


Peptide counts over 4 repeats

Pfam domains



Pfam Description

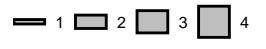


Protein sequence:

HSRYKISLDLADYSAHPDQVIVVKEVLPVVDIMAVDWIPTDFGPRSEVPPQGSALRVTFKLIKENLGENEKSGVLSAVGGKEKFPDIEQLTVGENFSPGRAKGFSIASIAVFKGVNLEALESGOTELANEQEKVRFDDGWWWVWVWLPDQSPSLVWIKI

NbL05g12300.1 glucose-1-phosphate_adenylyltransferase_small_subunit_chloroplastic/amyloplastic [MW = 57.24 kDa]

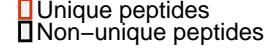
No. of times detected



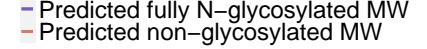
log(intensity)



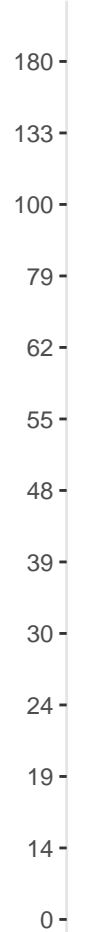
Values from



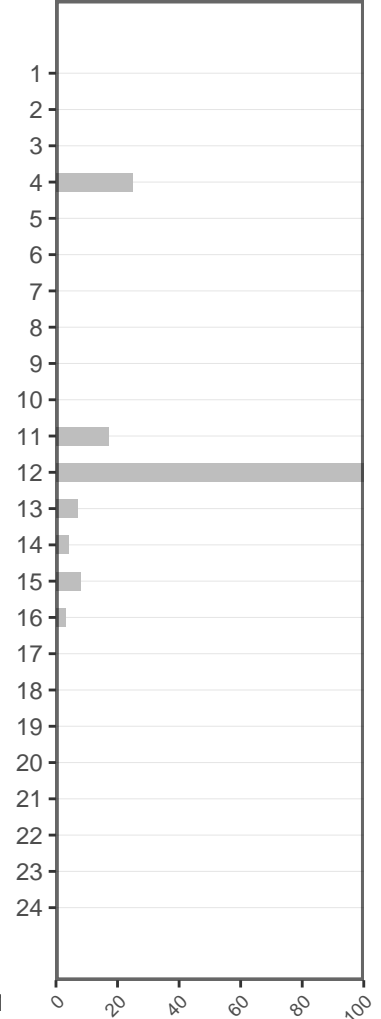
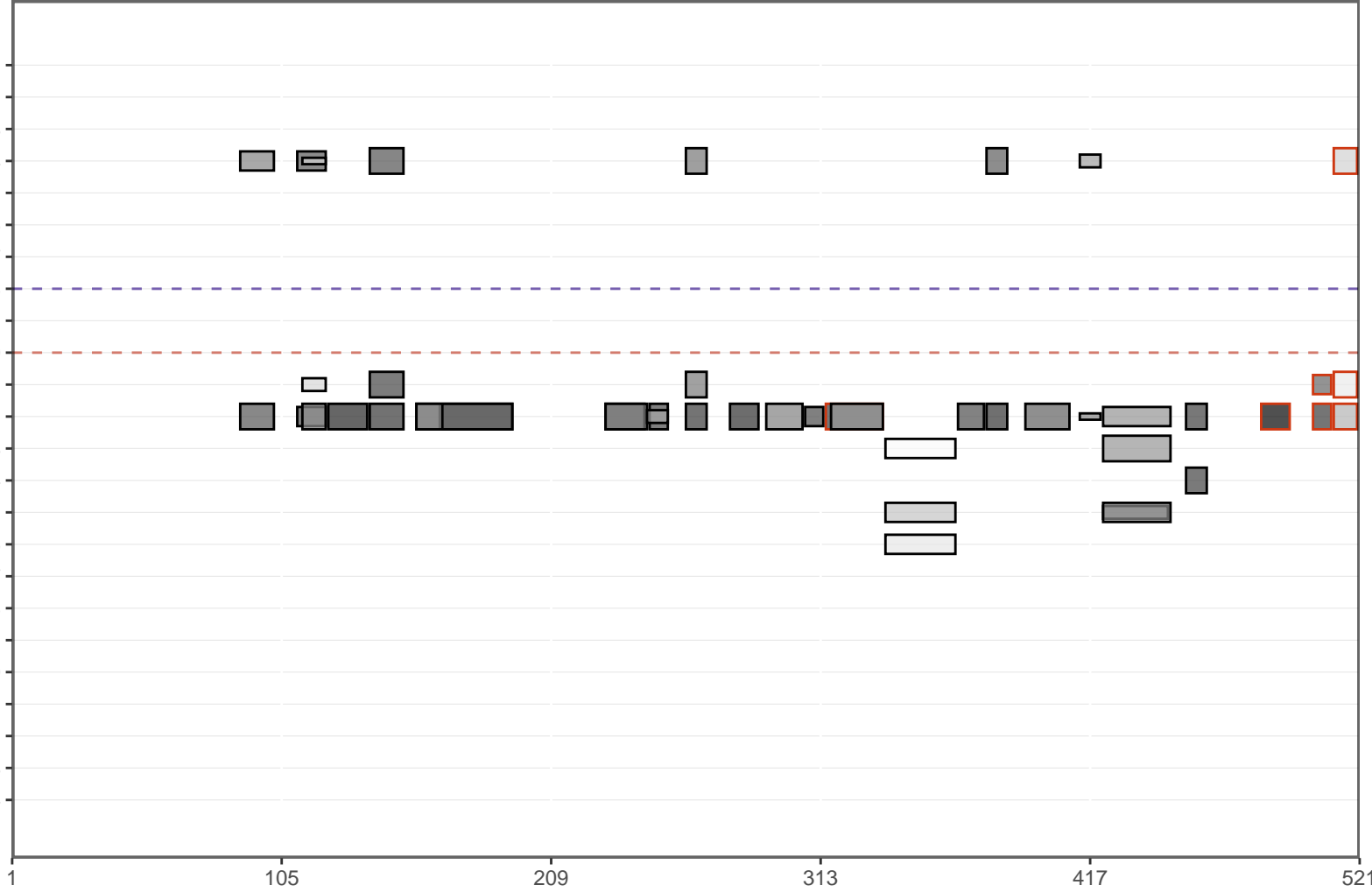
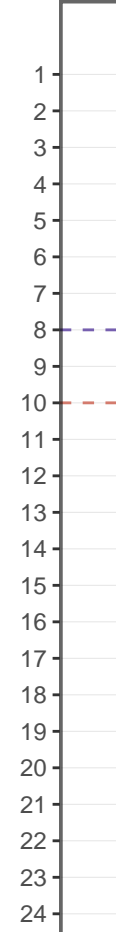
MW indication



Molecular weight

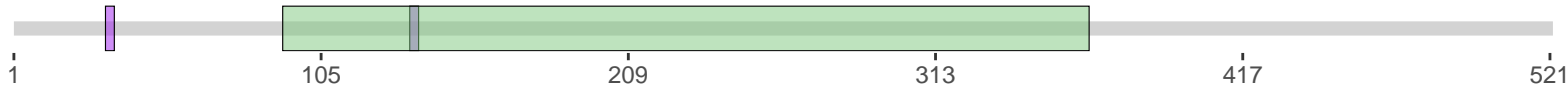


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

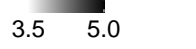
DEKRTAFGLMKIDEGRIIEFAEKPKGEGQLKAMKVDTTLGLGDDERAKEMPFIAEMGIVYIKDVMNLNLRDRFPGANDFGSEVPGATSLGMRVGAVLYDGVWEDIGTEAFYANLGITKPKVPPDFSFYDRSAPVYTPRYLPPSKMLDADVTDEVIKGGVVKIKKHHVVLGRSGEGSAGIEDSLLMGADVYETDADRFLAAKGSVPIGIGKNSHKIKRAIDKNRARGDNVWINDENVGEAARETDGVYFKSGIVTVIKDALPQGIH

NbL05g12260.1 subtilisin-like_protease_SBT5.3 [MW - SP = 79.89 kDa]

No. of times detected



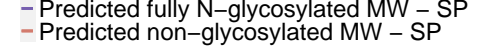
log(intensity)



Values from



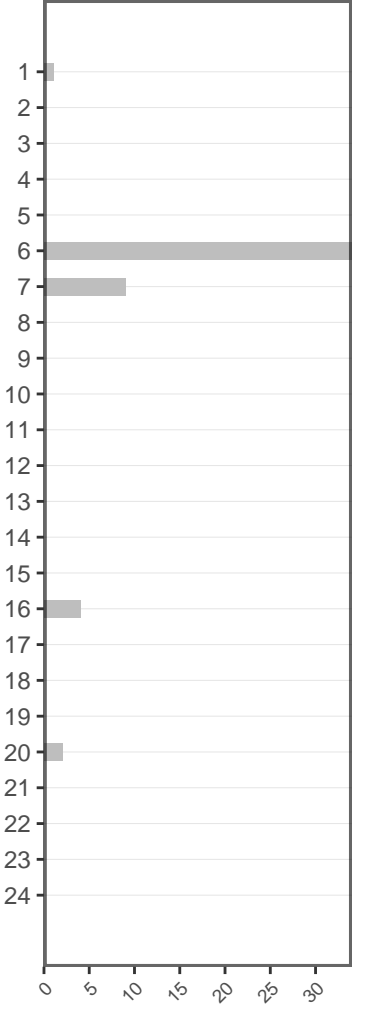
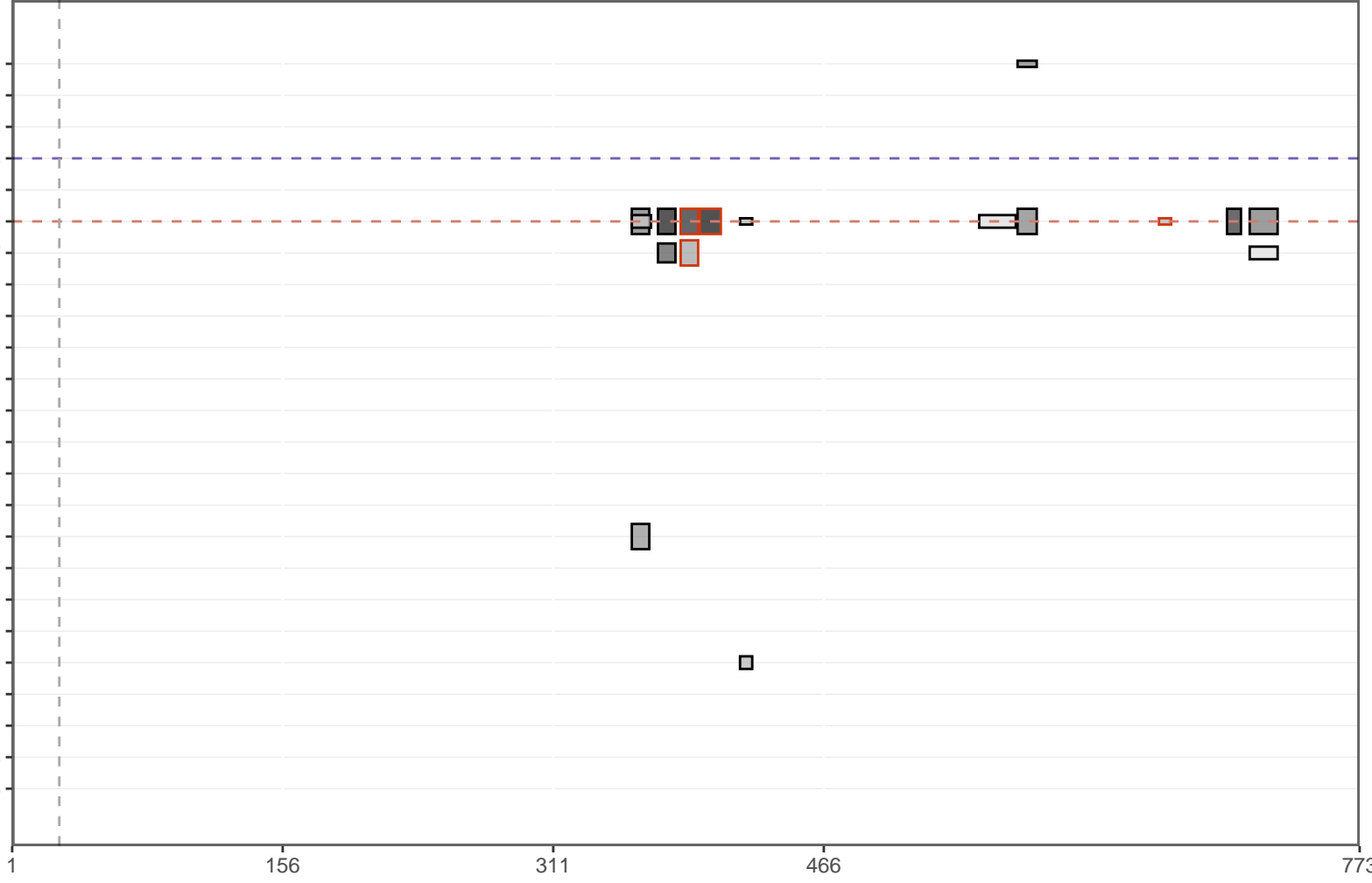
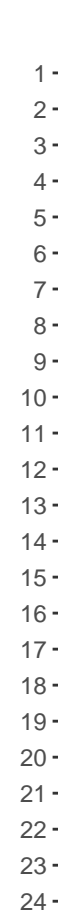
MW indication



Molecular weight

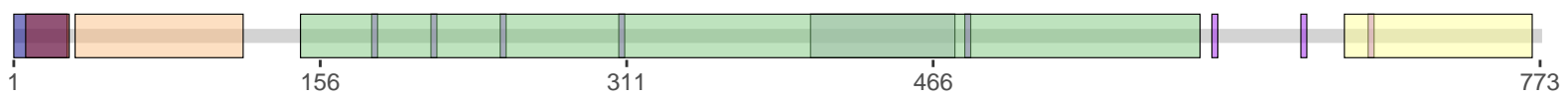


Gel Slice



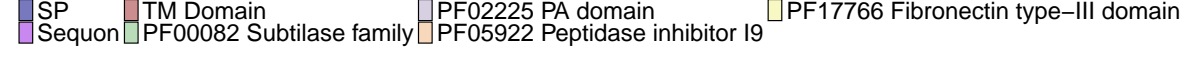
Protein length

Peptide counts over 4 repeats



Pfam domains

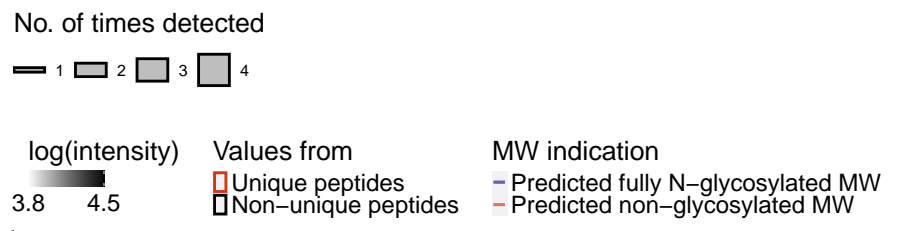
Pfam Description



Protein sequence:

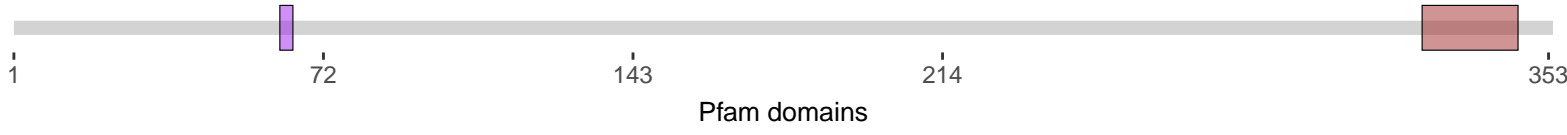
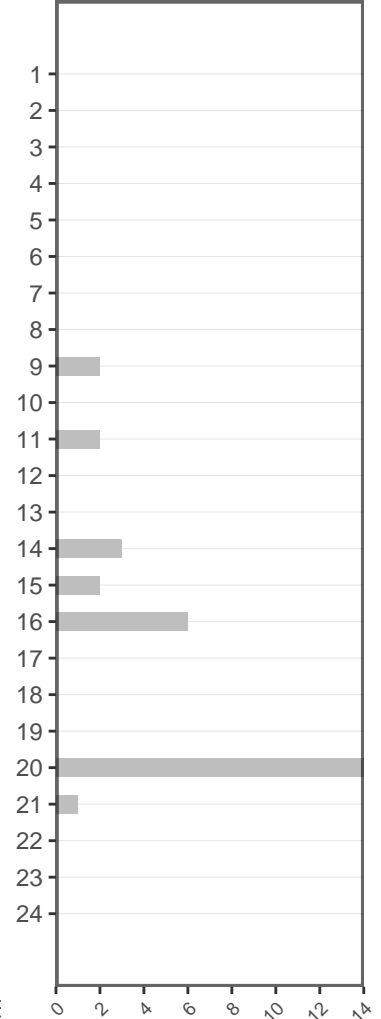
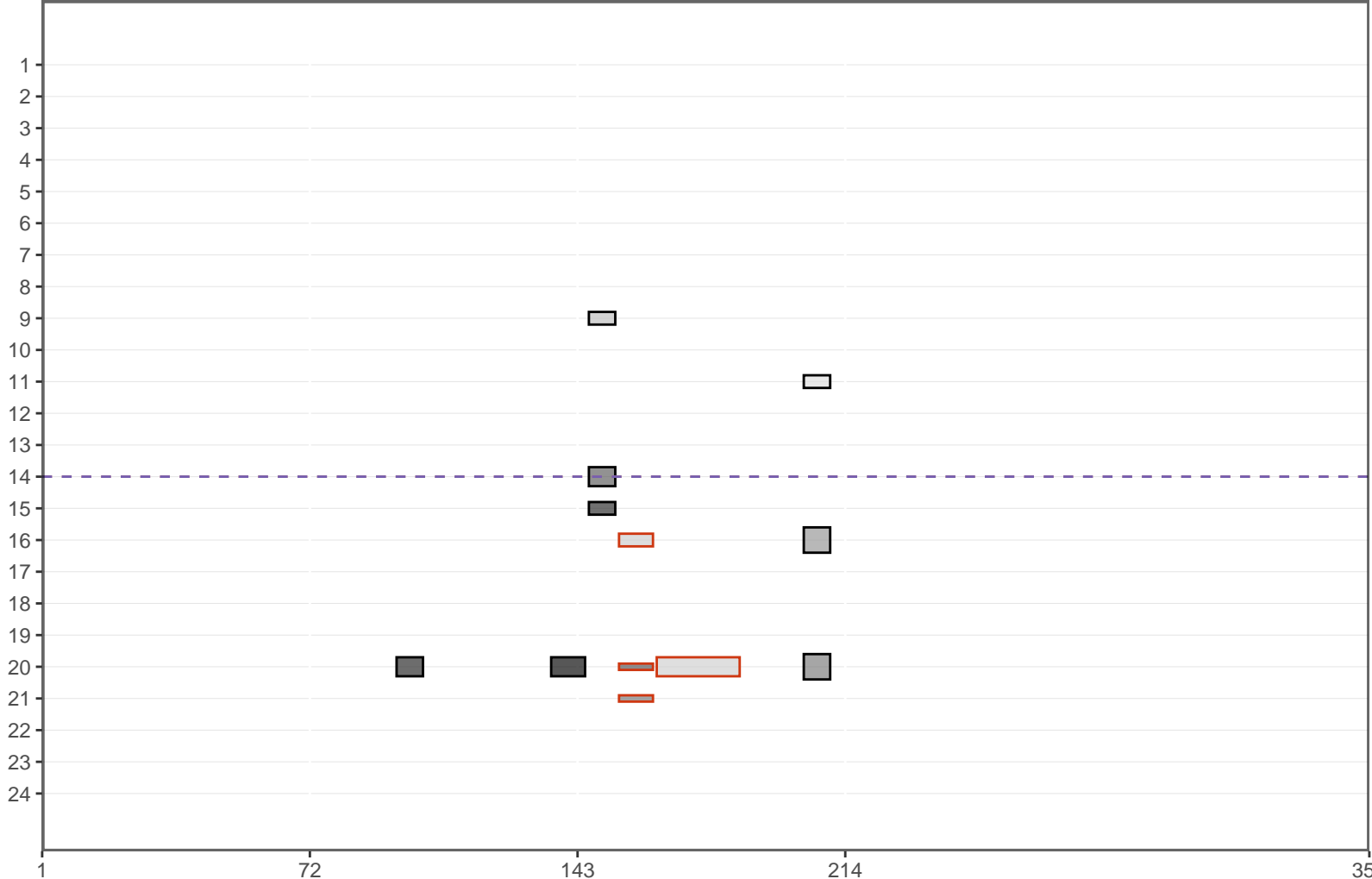
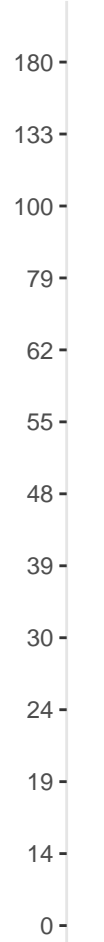
KGESLSVELPKGKFFPHSAASAKPHASTDDMLGKAGSLDPKVKGTSLVQLRGNARVDKGGQAAAGAVGMVLANDVASGNEVIADPHLPATQI@VYTDGLLELFTFYVNSTSTPTASITHPTFQLGTRKPKVMAAFSSIGINTVTFELFKPKDITAPGVGIIAAVTGAEQPTMGDFDKRRVWFNFSVSGTSMGSPHVSQGLVLLKTLVPTVWSPSAKSAIMFTARTRDNAIEPMLNASYKTEPLAYGAGHVRFRNRAMPGLVYDLTDDYLSFLGADGYNETOIKTTTQGFKCI

NbL05g12070.1 peroxisomal_and_mitochondrial_division_factor_2-like [MW = 39.41 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain

Protein sequence:

QHLITAMNDLEGSNSELGGVKSTLEGLKSSSENMFTVLDLAEISERNLLLSKLERLEASGNNGRGEVVEKKEEIRGLKKHIELEGTVVNNEEWEKEKTELHMVVEELEKRVKEMARAAALEKLEKEKVKITERLVAGNNGIPFGDVKVGVFGDAEVLNLPVVAASVVWAVIGVVDYLYKGRKA

NbL05g12030.1 ribose-phosphate_pyrophosphokinase_4 [MW = 35.74 kDa]

No. of times detected



log(intensity)



Values from



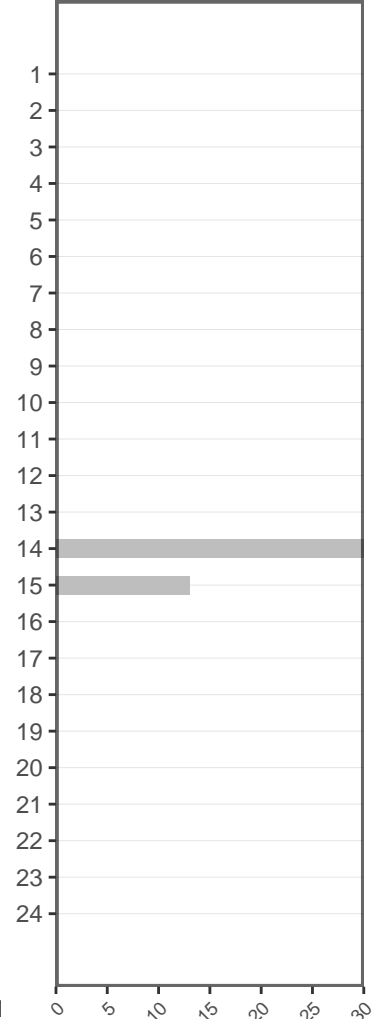
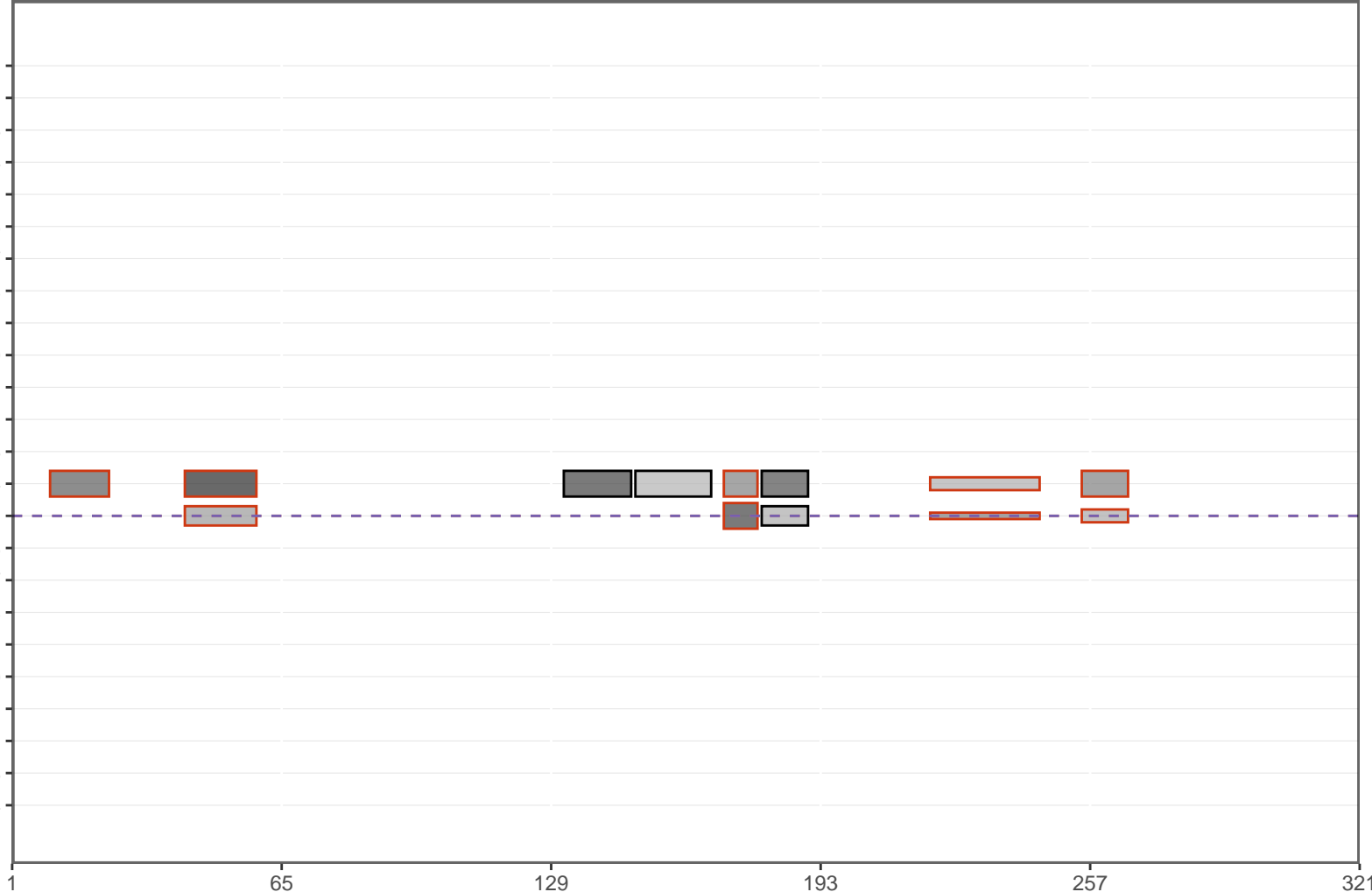
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

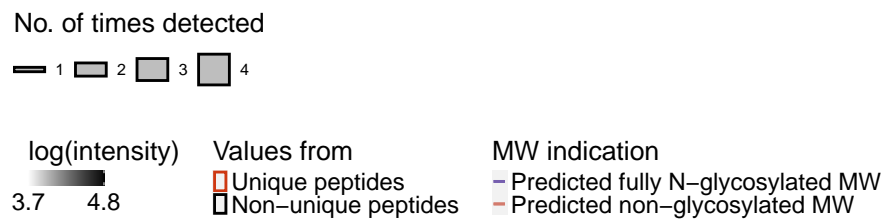
Pfam Description

- SP
- Sequon
- TM Domain
- PF00156 Phosphoribosyl transferase domain
- PF13793 N-terminal domain of ribose phosphate pyrophosphokinase

Protein sequence:

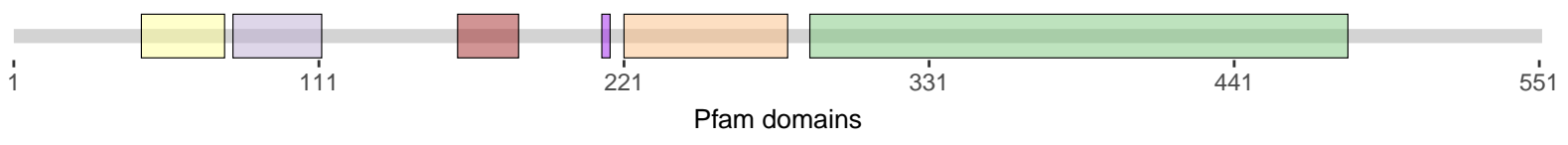
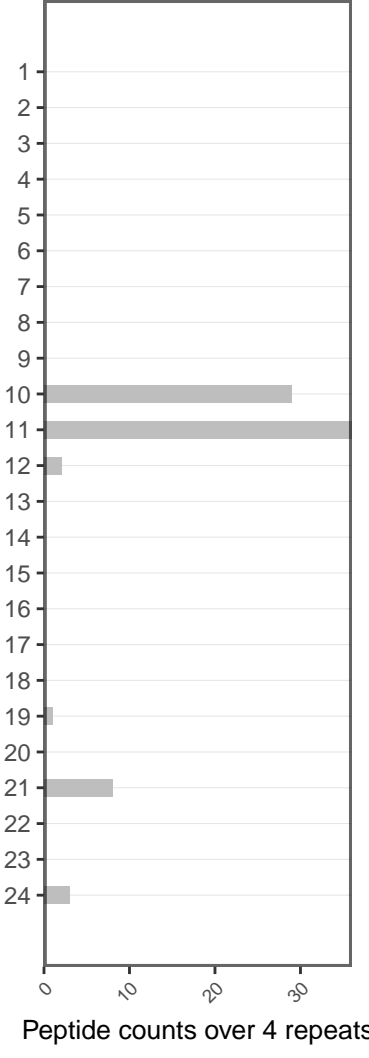
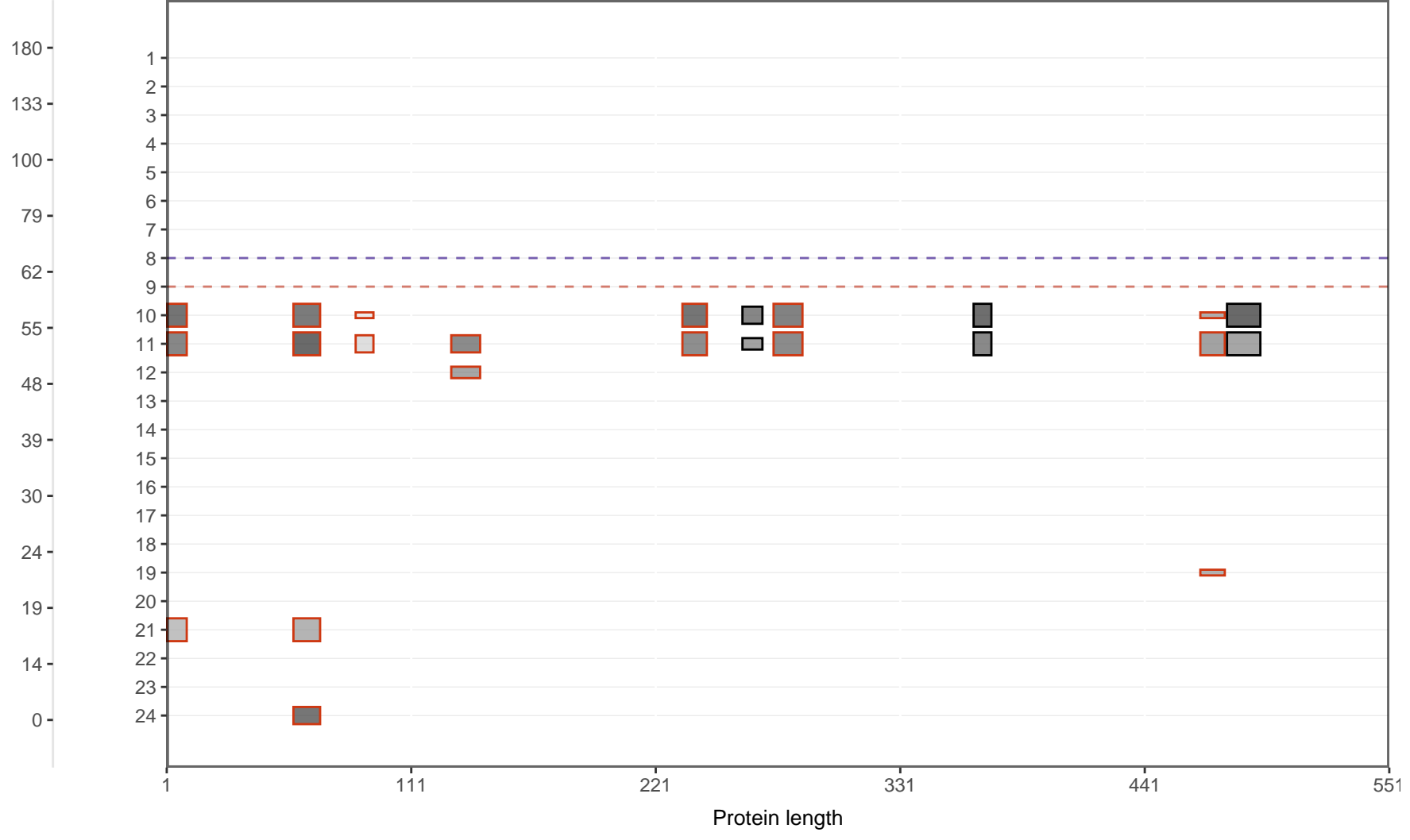
FYFGDHYLPLFETGIPLLKGRLLGQLPQTEKIVAFPDGAWKRFYKGLGHYPAWGTQVREGRKRVRLKEGNPAGCHVIVDDLVQSGGTLIEGKVLAAHGAAKVSAVTHGVFPKRQWERFIKDDGSEKAFYFWITDSDGLPTVNIADKAPFEVSLAGSIADALGT

NbL05g11920.1 serine/threonine-protein_phosphatase_5 [MW = 61.32 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- TM Domain
- PF00515 Tetratricopeptide repeat
- PF13181 Tetratricopeptide repeat
- Sequon
- PF00149 Calcineurin-like phosphoesterase
- PF08321 PPP5 TPR repeat region

Protein sequence:

"QVLTREMLRALPLSLVDIVPEGKFTVCGDHHGQFYDLNFDLNLGSPEDNPLFNGDFVDRGFSLEIVLTLFAFKMGCPGAYLARGNHESKMNKIVYFEGEVRKLSSETVELFAEYFQGLPLAHVINGEYLVHGGFLFSDVGVKLSDIRADRFCPEPPEEGLMCELLWSDPQPPQGRGPKRGVGLSFGADTKRFLGNNLDLVVRSHEVKDEGYEIEHDKLTFVFGAPNYCDQMGKGAIRFEAPDMKPNVTFSAVPHDPVKPMAWANFLRMFS"

NbL05g11900.1 malonyl_CoA-acyl_carrier_protein_transacylase [MW = 39.78 kDa]

No. of times detected



log(intensity)



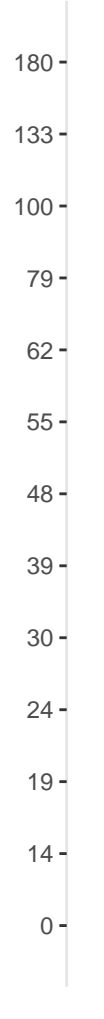
Values from



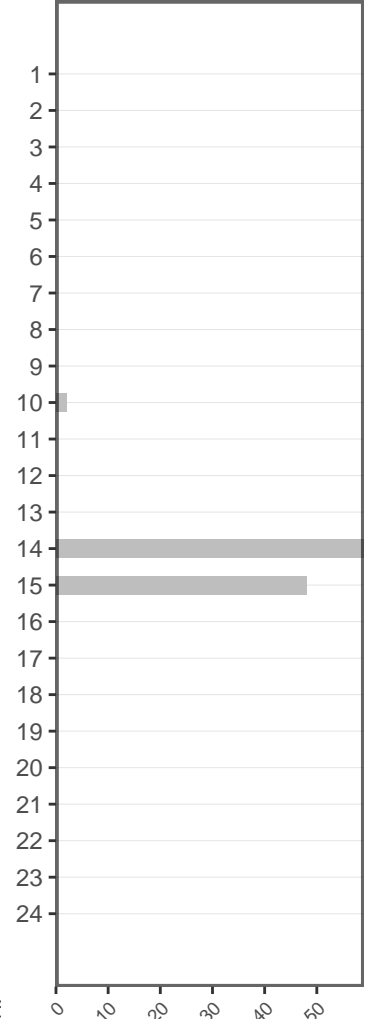
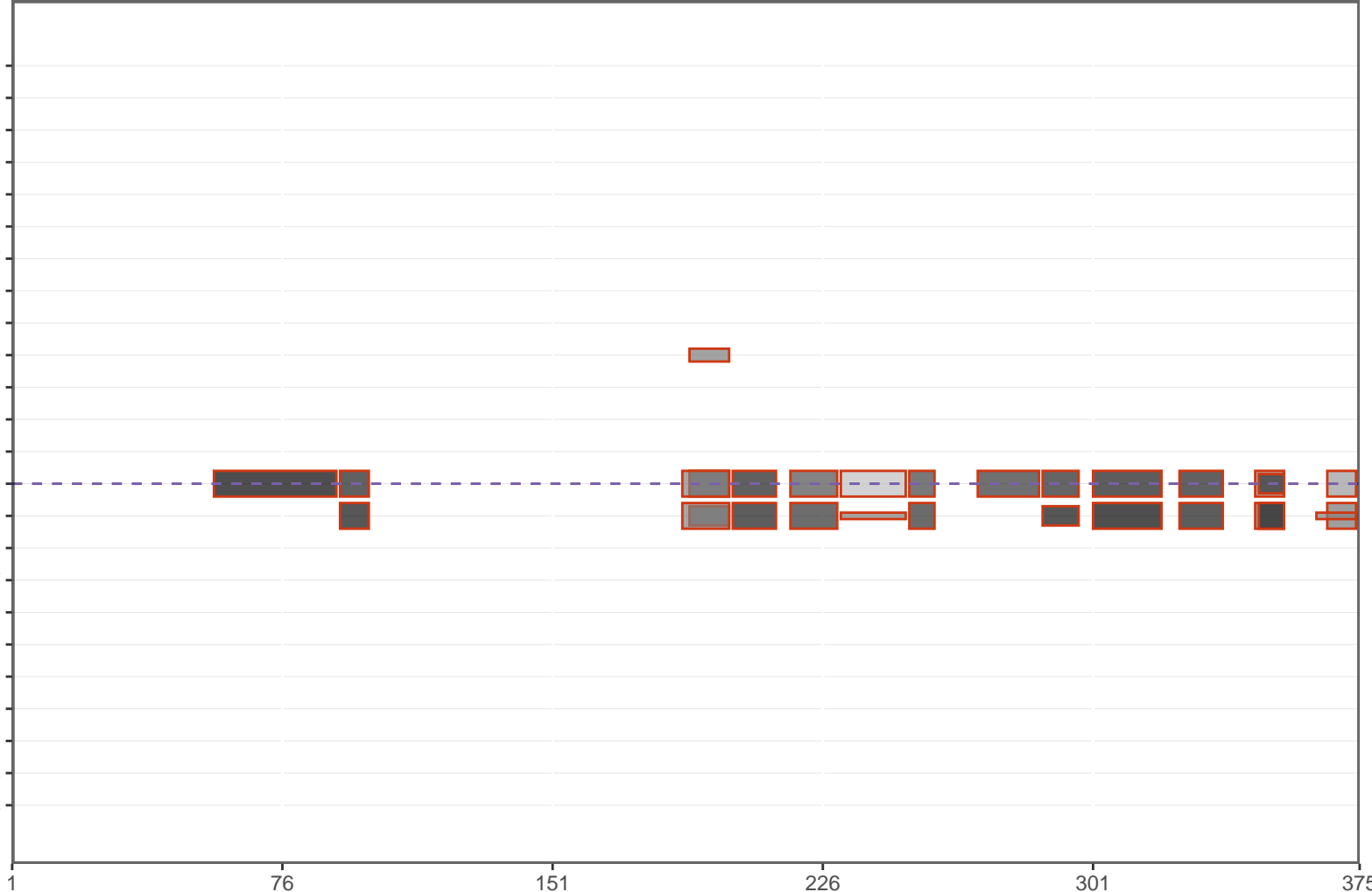
MW indication



Molecular weight

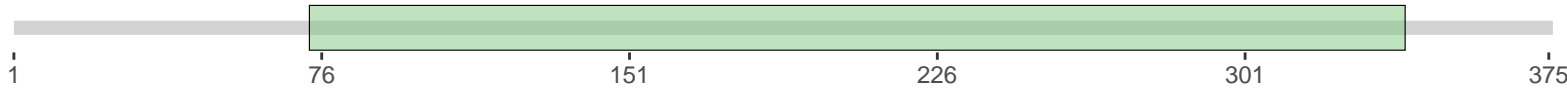


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

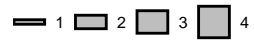


Protein sequence:

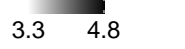
AFSFDGLKLVLRGEAMGDAADAAKAMVIVIGLDSKVKLGDAAANEEVDEANRVDQANFLCTGNVAVSGGLKGVVEVKAQKFKARMTVRLVAGAFHTSFMNFWSRLELDALGATEIRTPRIPIVSNVDAGPHADPDINKILARQVTSPIVQWETTVKTLTKGLKIKYELGPGKVIAGVIRMDKGAIVENIGAV

NbL05g11840.1 protein_trichome_birefringence-like_43 [MW - SP = 37.79 kDa]

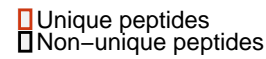
No. of times detected



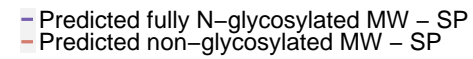
log(intensity)



Values from



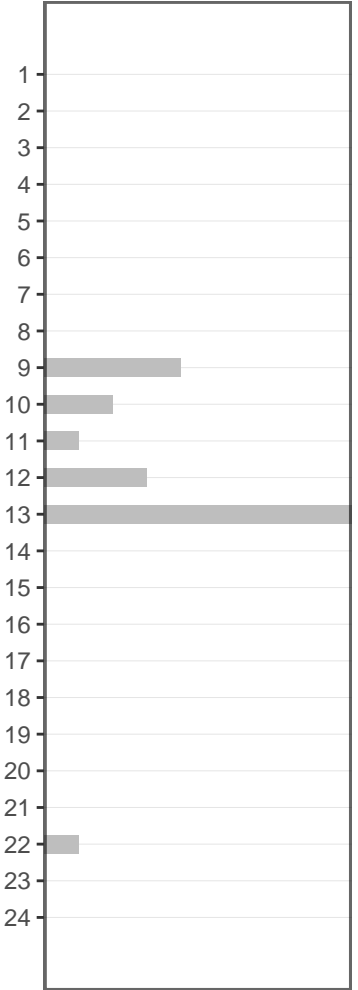
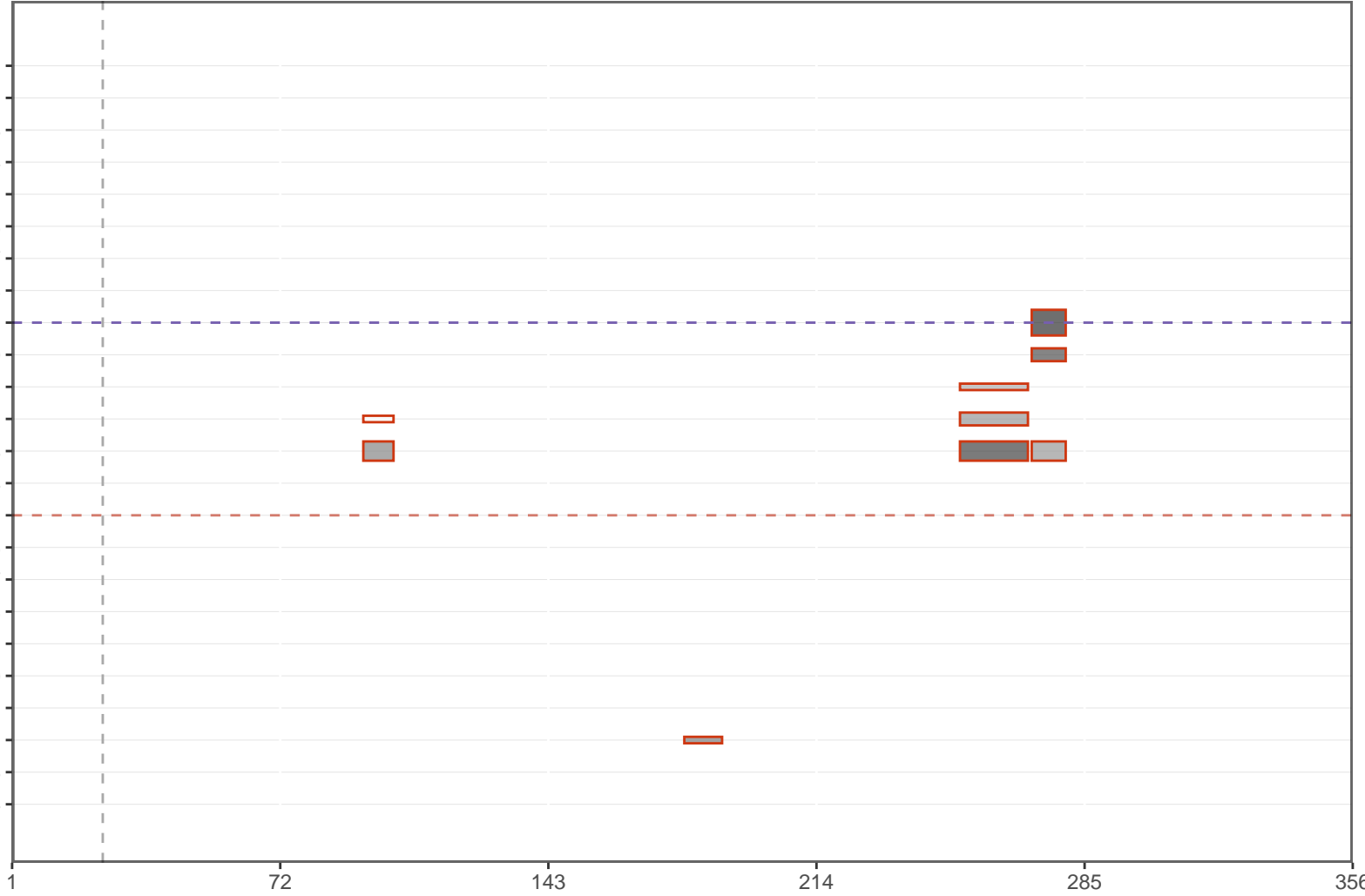
MW indication



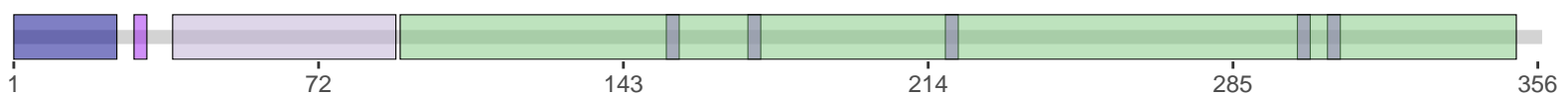
Molecular weight



Gel Slice

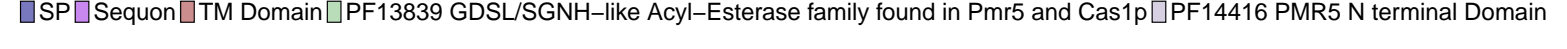


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TENNQTRYLKLDLSSAAGWQKMDVLFDSWVWHLHFGRRKQPDVLDGGNFTYDGRPLTLVEKALNTWAKWVWDEVDITKTVFFDQVSPDHNFTS6SGSKTCEGVTPRLKSTEEVHQDEELVLEKVLKRGMMKSVLLNITKLSQYRADGHPVTVGHGGRDLDGTHWGLAGVVDTWLFLNALLGL*

NbL05g11690.1 probable_alphaalpha-trehalose-phosphate_synthase_[UDP-forming]_7 [MW = 97.34 kDa]

No. of times detected



log(intensity)



Values from



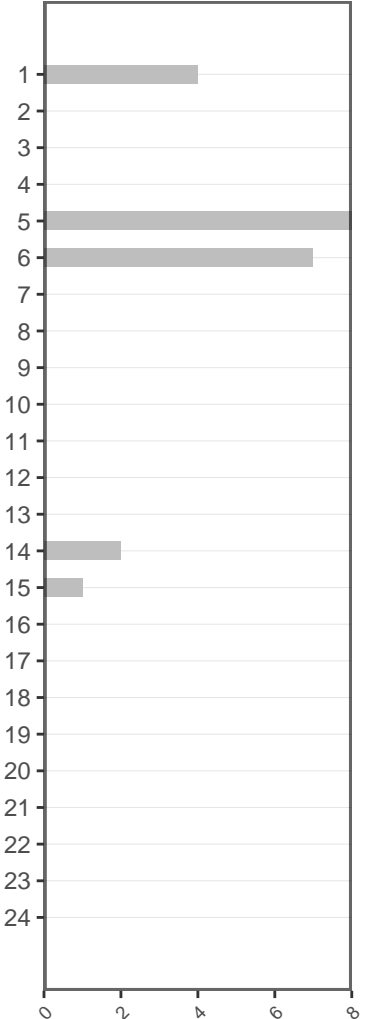
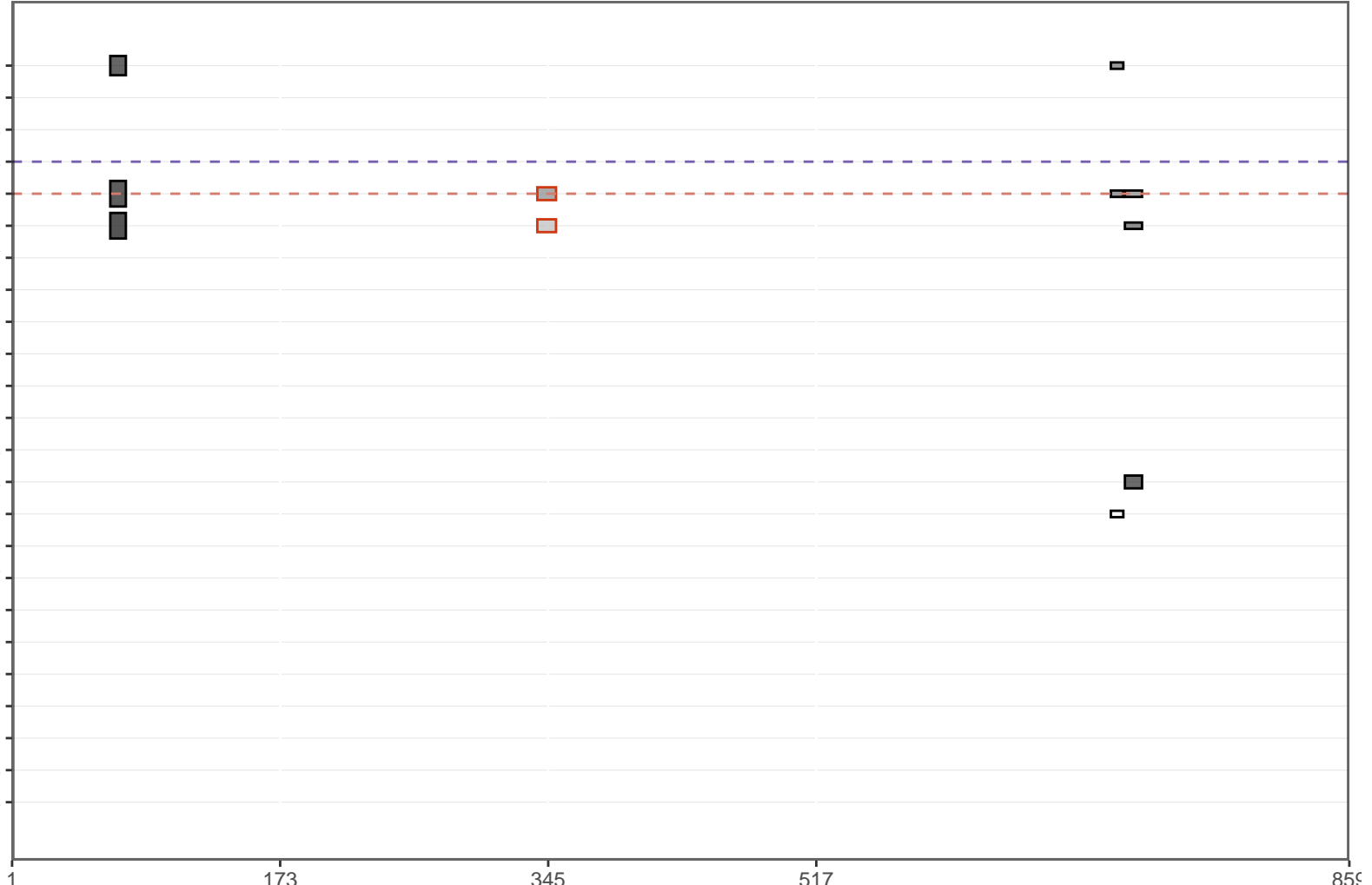
MW indication



Molecular weight



Gel Slice

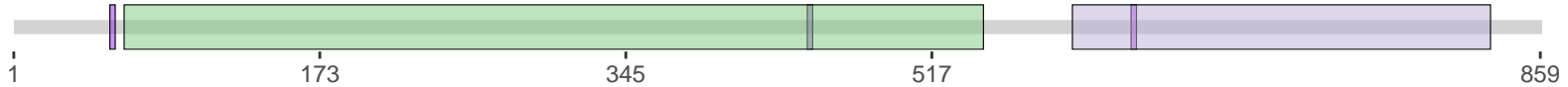


Protein length

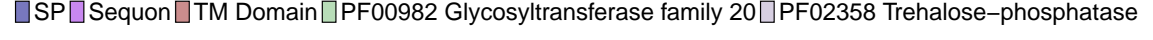


Peptide counts over 4 repeats

Pfam domains



Pfam Description

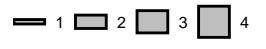


Protein sequence:

YIDKPYSSSERMAYVLAEGVAVAVRDRGMNLTPEYIVGRHGVSGETDGGVGLDKMLVVSSEFVIGGSPDLSGARIPNPNVEATAEAMNEAVSMAEGEKQLRHEKHYRFVSTHDVAWVSRGFLQDMERTCADHFRKRCYVIGLGFGRVVALDIPNFRHLSDDVNAVHKSRAFLDQDGTVMQNSIKKSPSEVISLNRIGDDNNTVFIVSRGRGRLSKVWFSPGRKRLGLAEHGVFLRVAEDGEWEVGGTSDGFQWMLAEPVMDGYTDATDSCIERKES

NbL05g11580.1 aspartate_aminotransferase_mitochondrial [MW = 46.91 kDa]

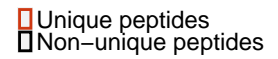
No. of times detected



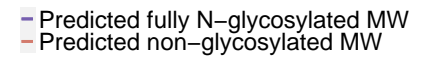
log(intensity)



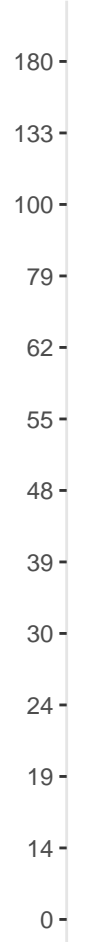
Values from



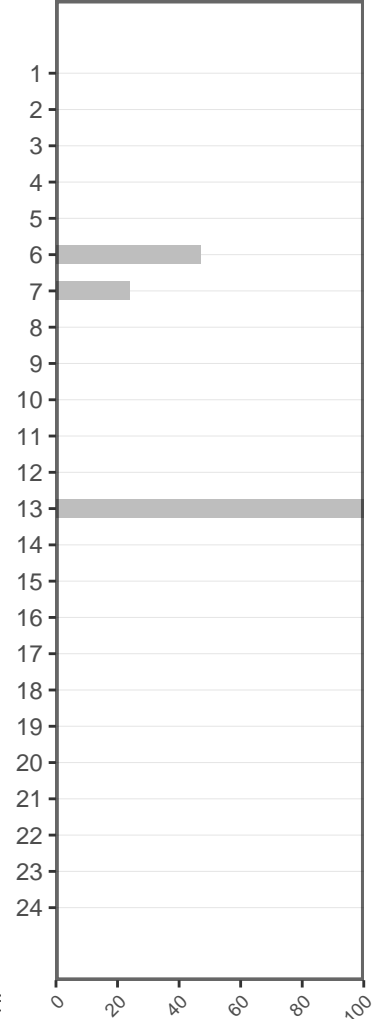
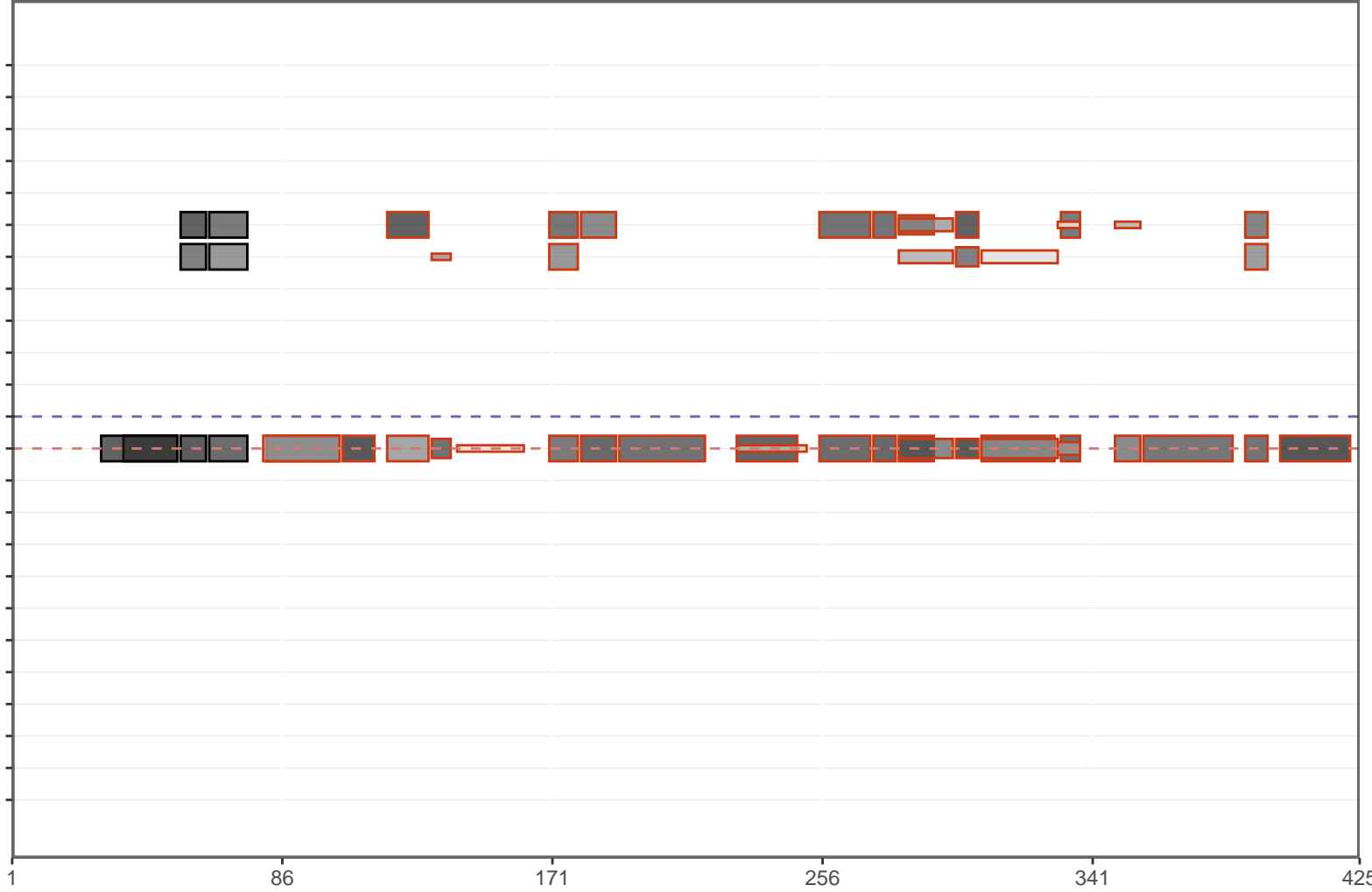
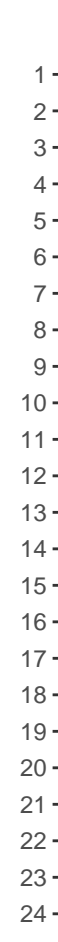
MW indication



Molecular weight

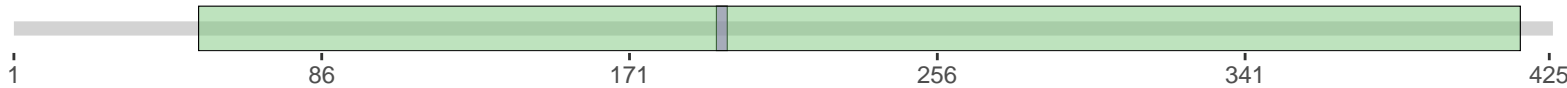


Gel Slice



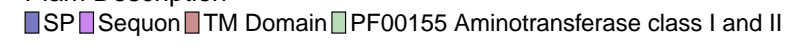
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL05g11560.1 peroxidase_P7-like [MW = 35.66 kDa]

No. of times detected



log(intensity)



Values from



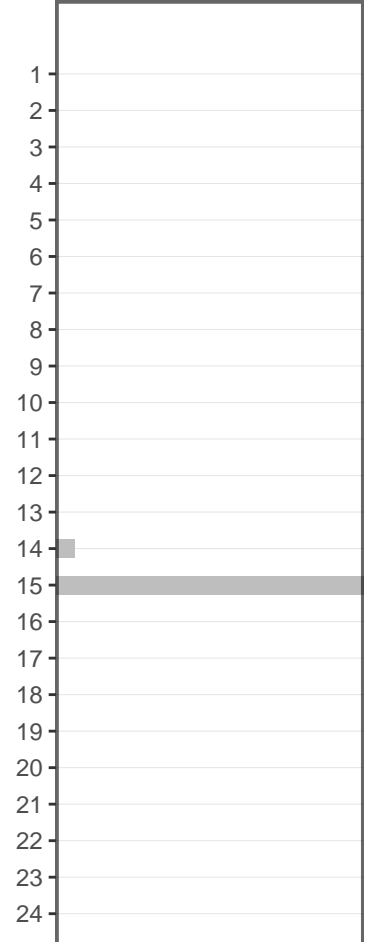
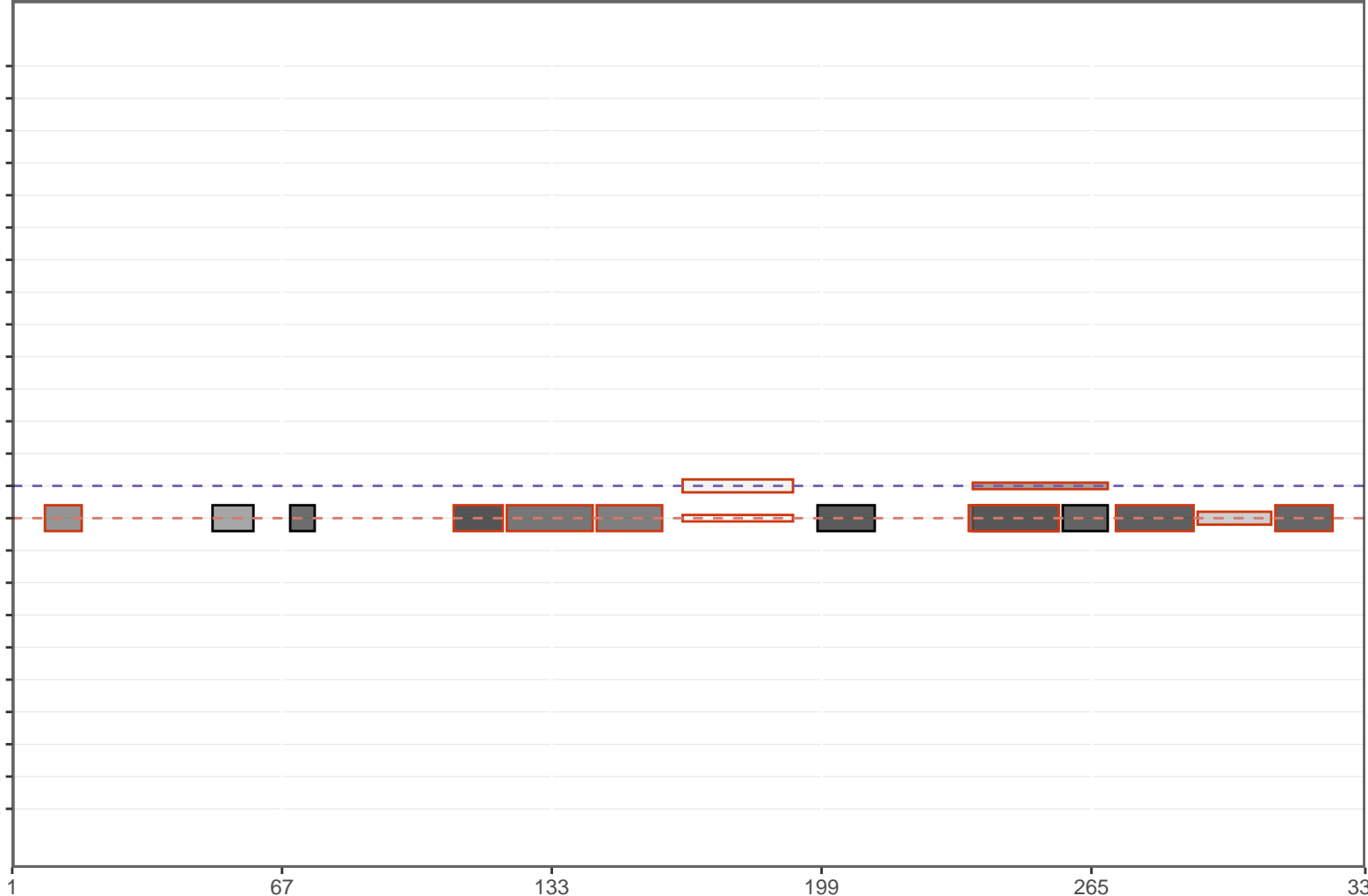
MW indication



Molecular weight

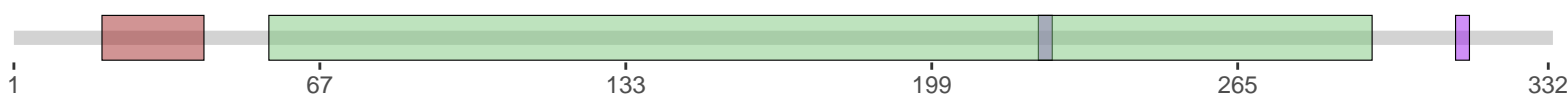


Gel Slice



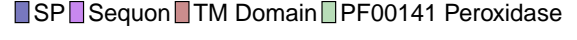
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

AVPLGRDARTASGSAANAGPAPTSELSTLLGMFSAKGLNARDMTALSGGHTHGQARCTFFRTRHYNDTNDGQFATRRATCPSSGGSDNLAFLDHTNRFDFNDYQNLVARRGLLHSDGELFNGSGSDALVREYSTNVAFTSDFAAAMVVMGNSPLTGTNGEIRRRGRAIN

NbL05g11230.1 uncharacterized_LOC107832338 [MW = 24.48 kDa]

No. of times detected



log(intensity)



Values from



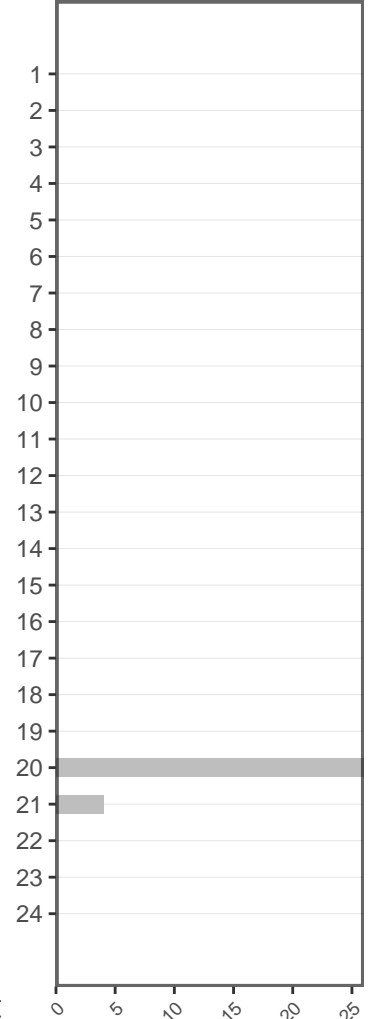
MW indication



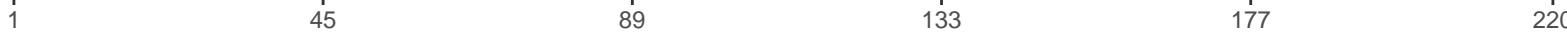
Molecular weight



Gel Slice

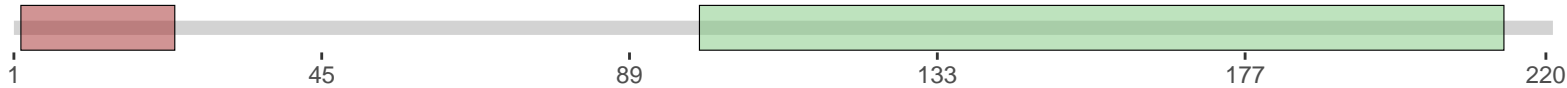


Protein length



Peptide counts over 4 repeats

Pfam domains



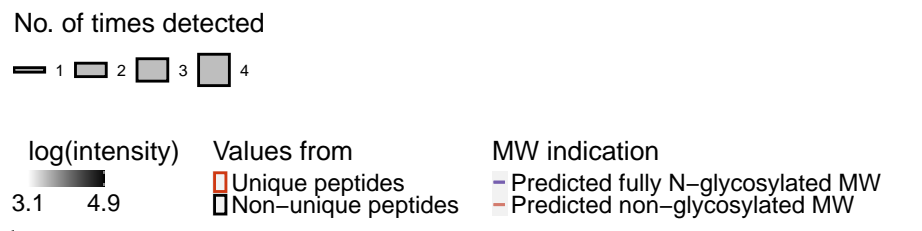
Pfam Description



Protein sequence:

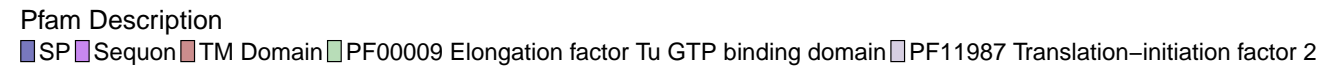
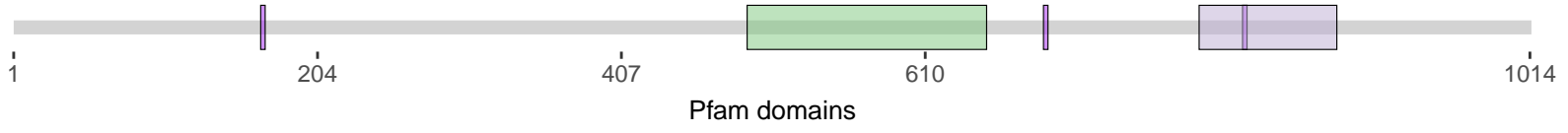
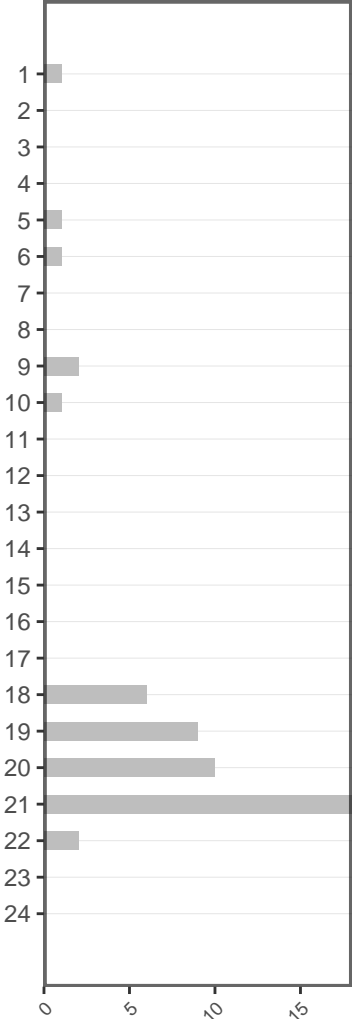
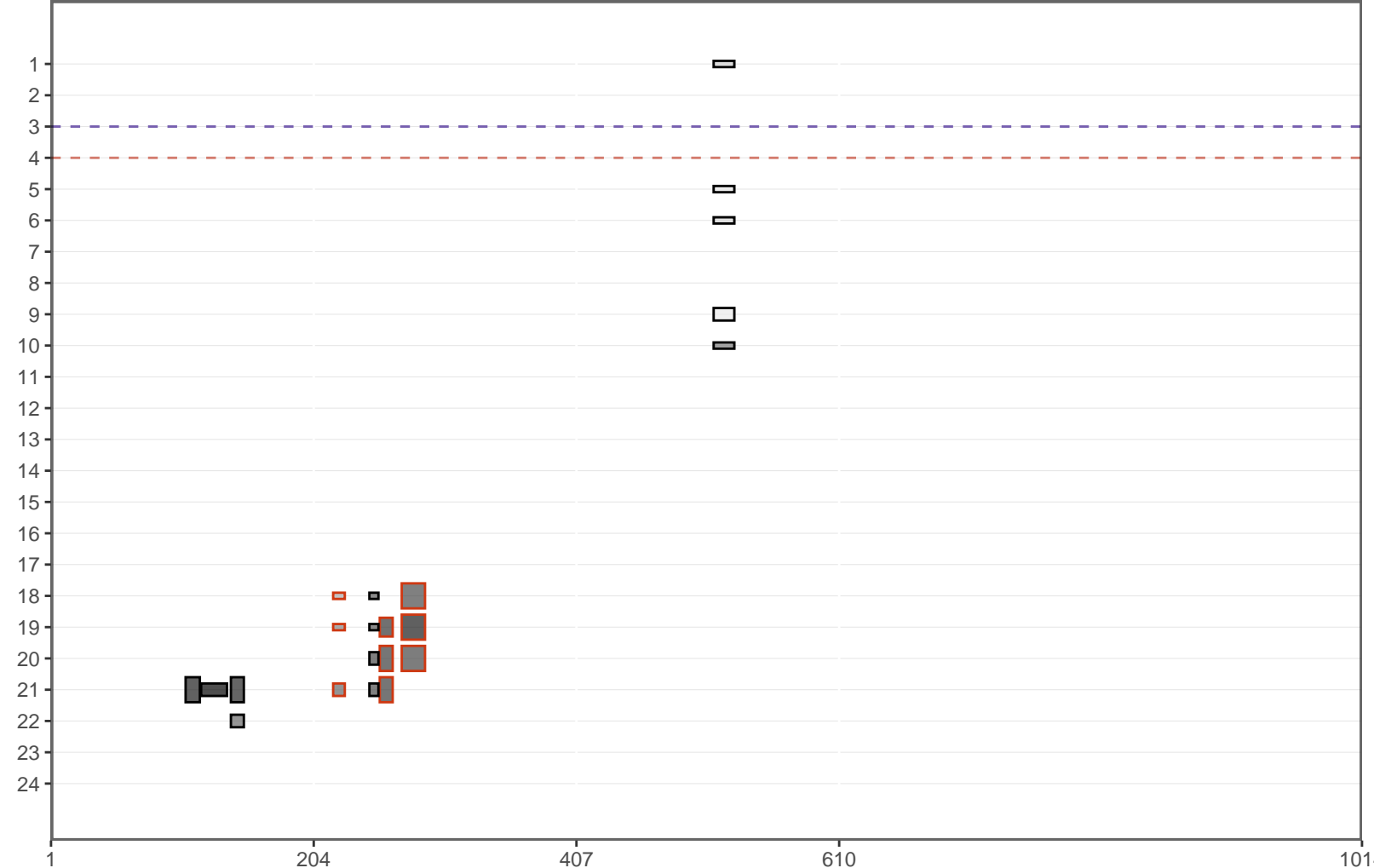
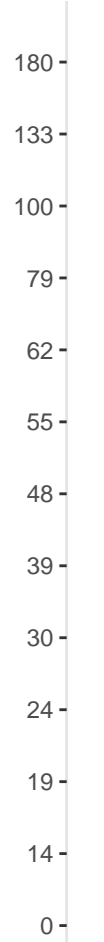
/SMHIVGLCEILERLDFYQNLGLEINEARPHDKLPIYRGAWLWVGEEMHLMELPNPDLTRPEHGGDRRHGTGAIRDVSKLKVLDGAGIPVTLRSRGRPFDFTRPDANALEFTQVDA

NbL05g11050.1 translation_initiation_factor_IF-2_chloroplastic-like [MW = 108.29 kDa]



Molecular weight

Gel Slice



Protein sequence:
 *PVTIMGHV D H G K T F L L D H R K T K V A A S E A G G T G G I G A Y K V Q V P D T K P G I C V F L D T P H E A F G M R A R G A R V T D A I R V A A D D G R P O T N E A I H A K A A G V P V I A N K I D K D G A N P E R V M G E L S S I G L M P E D W G G V P M V Q I S A L K G E N I D L L E T V M L V A E L G E L K A N P Q R N A K G T V E A G L D N S K G P W A T F V I N G T L K G D V V C G E A Y K V R A L F D K G K R V D E A G P S I P V Q V I G L N N V P V A G D E F E V W G L D V A R E K A K T R E E G L R T E R L E A K A G D G K V T L S S F A S A *

NbL05g10980.1 probable_glutathione_S-transferase [MW = 25.71 kDa]

No. of times detected



log(intensity)



Values from



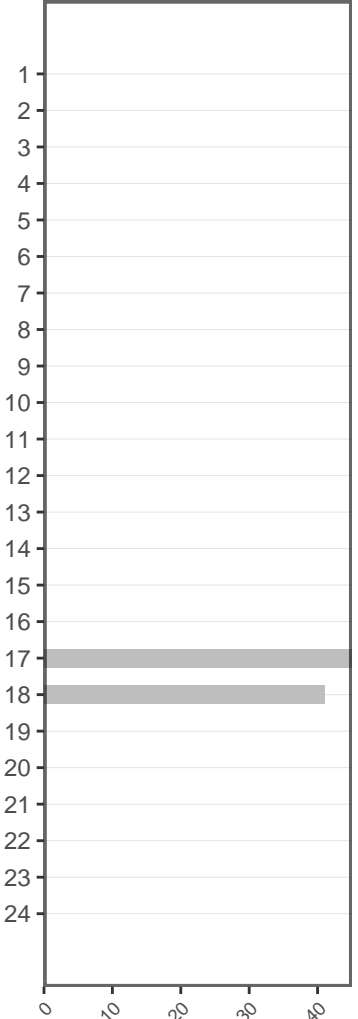
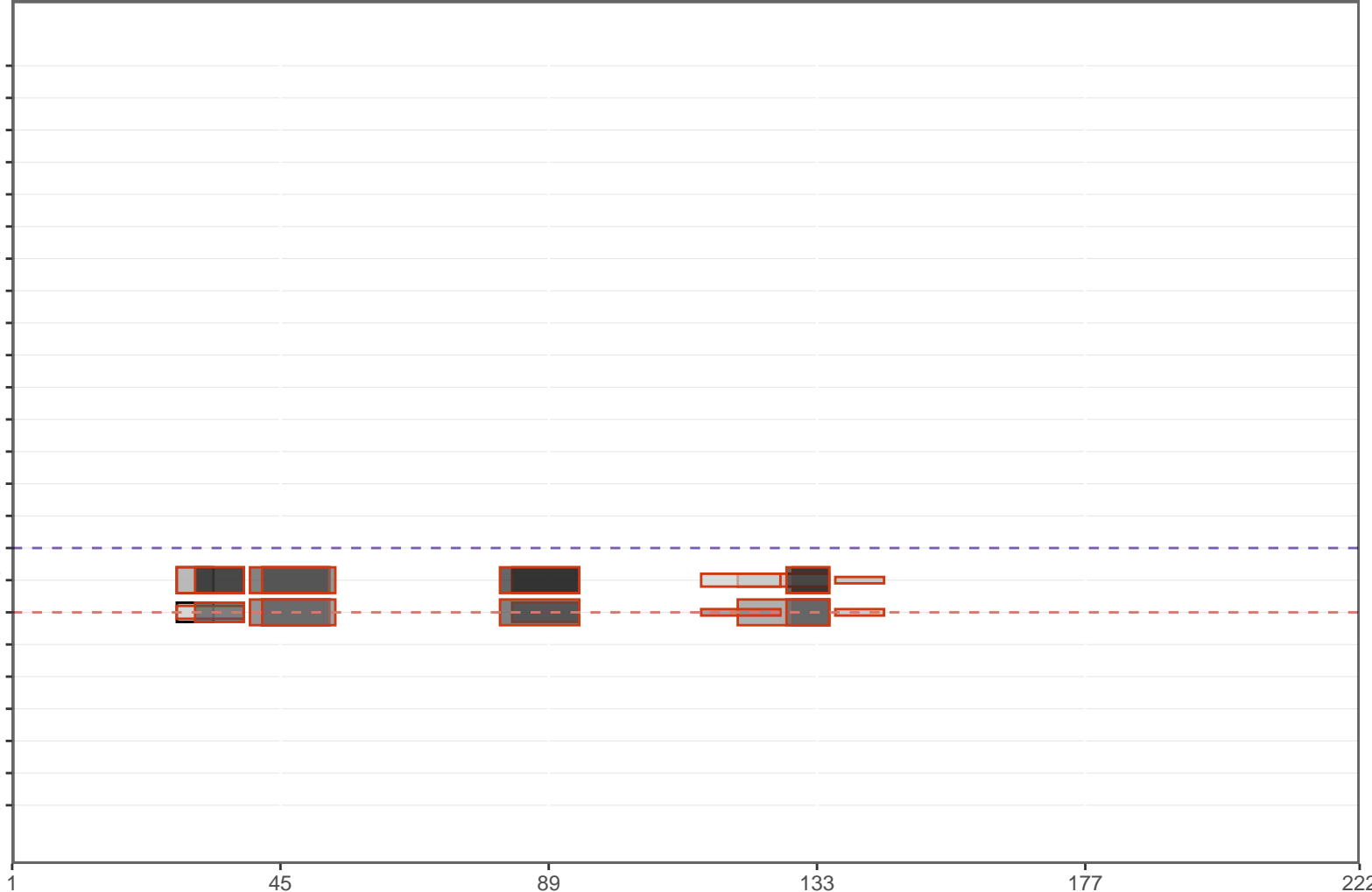
MW indication



Molecular weight

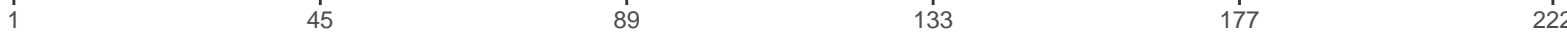


Gel Slice



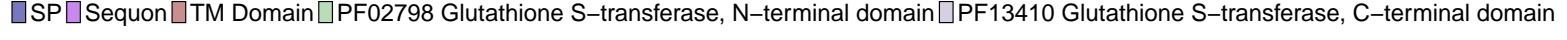
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

WADYIDKLLYDGRKRLWATKGEDEAANKDFIEGLKVLLEGALGDKPYFGGSEFGFVDAIAGYYWFWYVETFGNFSTEAEQPKFVAWAKRGMGRSVAKSLPDPKVLFEVYKLRGKGFLE

NbL05g10970.1 probable_glutathione_S-transferase [MW = 16.3 kDa]

No. of times detected



log(intensity)



Values from



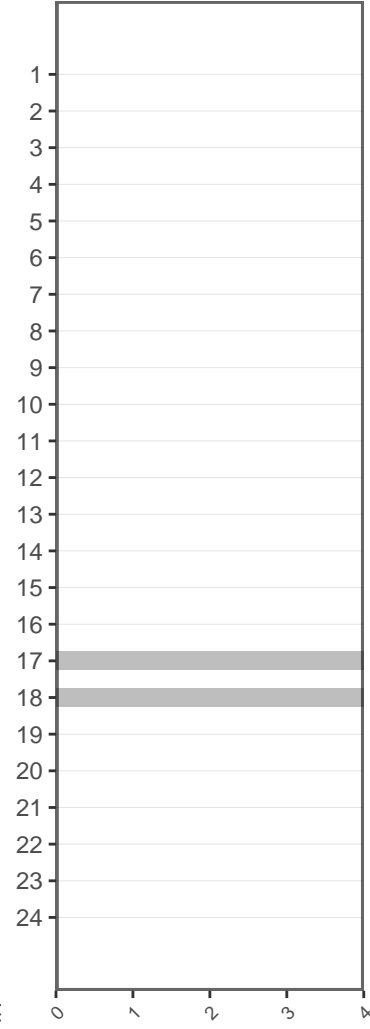
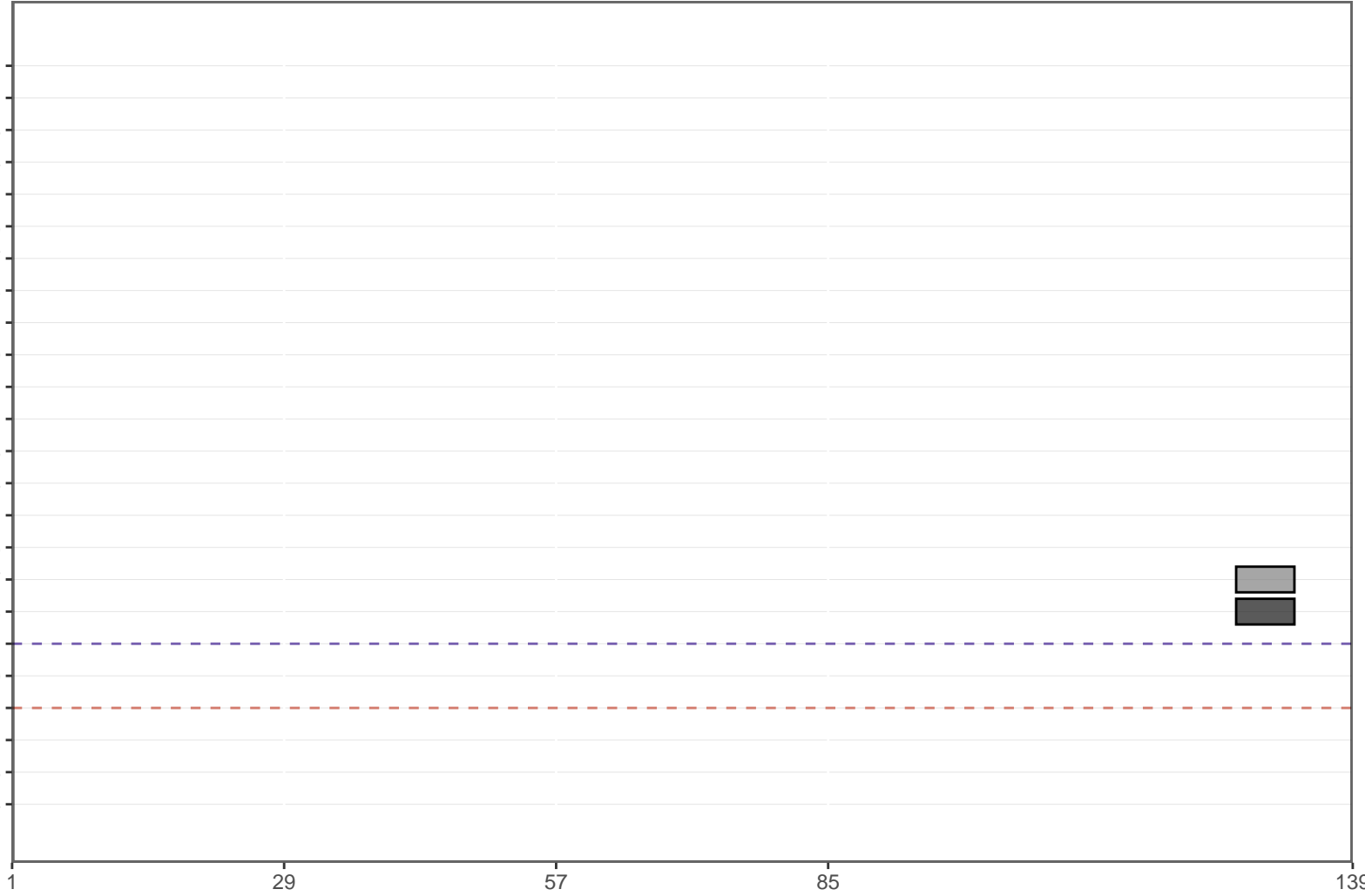
MW indication



Molecular weight



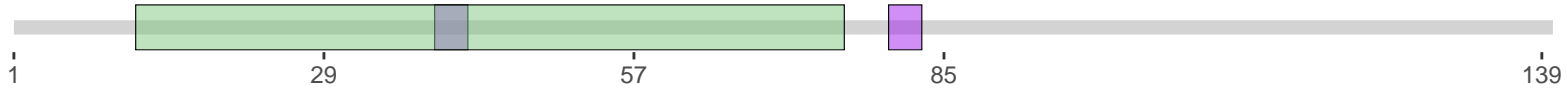
Gel Slice



Peptide counts over 4 repeats

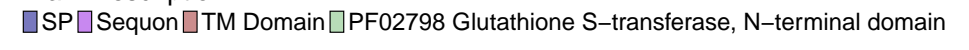
1 29 57 85 139

Protein length



Pfam domains

Pfam Description



Protein sequence:

JHNGKPCESLIIVYEIVWNNKTFPMSDPYMRAGARFWADYHKKIVESGKKMMVTSKVEDDEAANKFIECLKHWKGN

NbL05g10960.1 probable_glutathione_S-transferase [MW = 29.88 kDa]

No. of times detected



log(intensity)



Values from



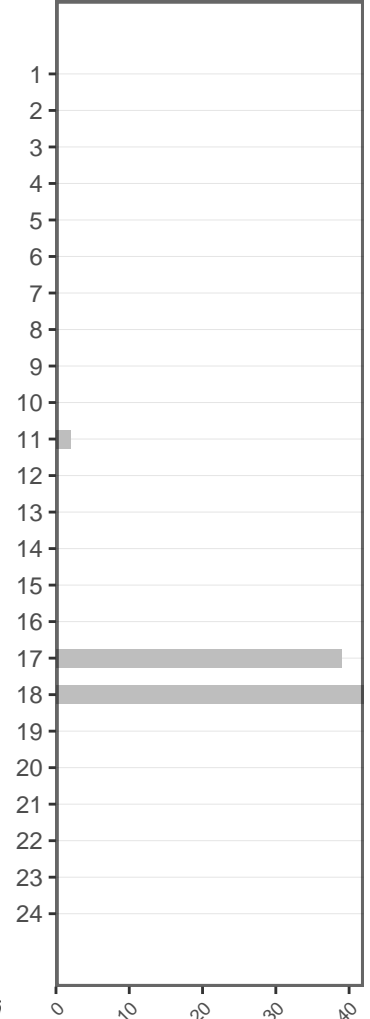
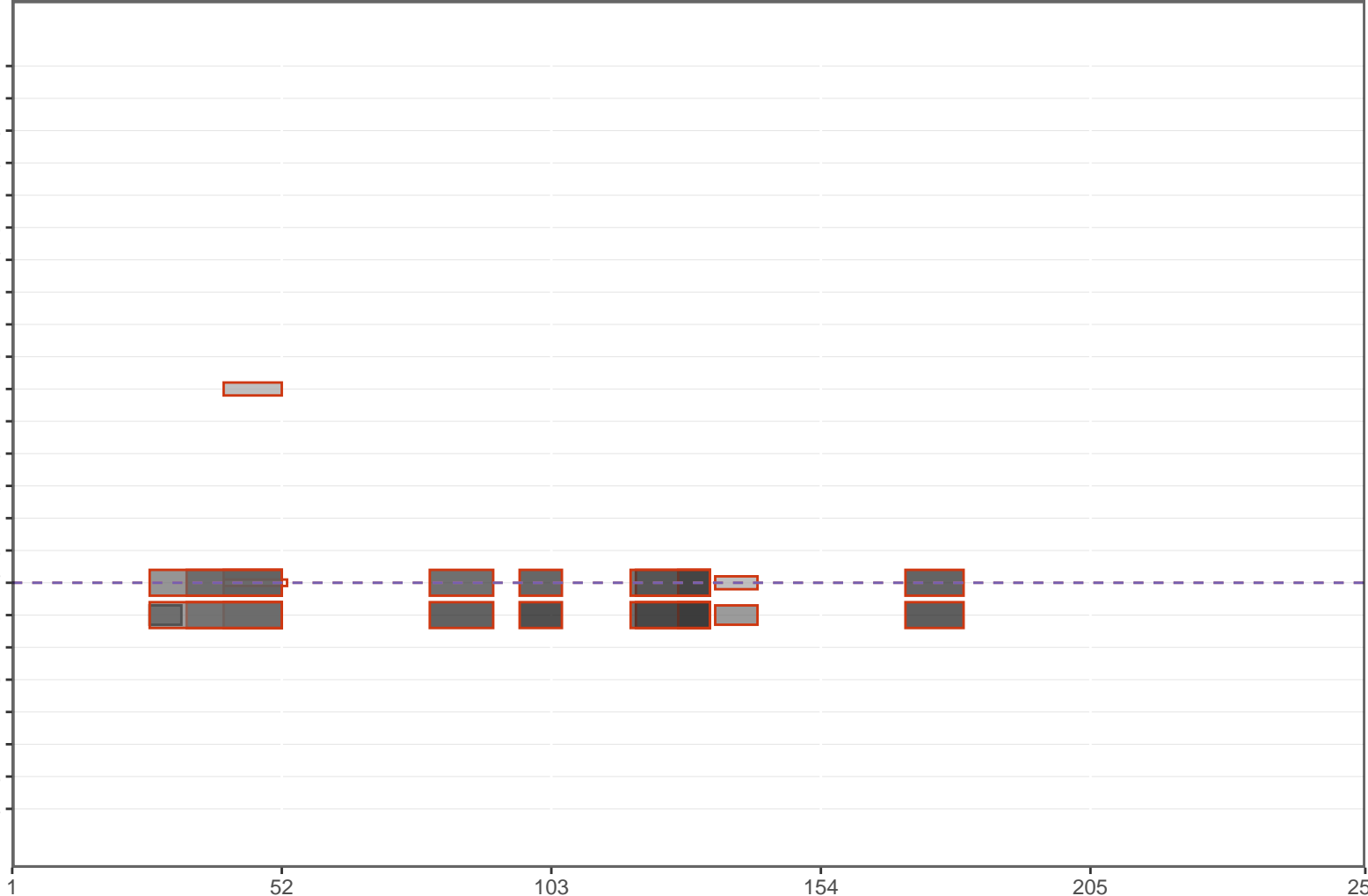
MW indication



Molecular weight

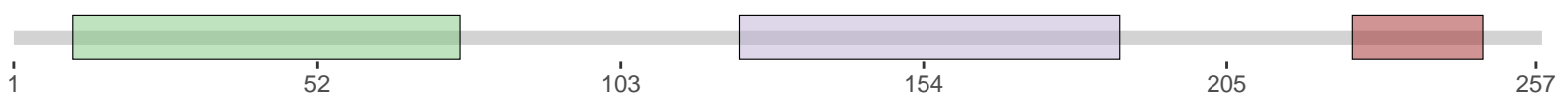


Gel Slice



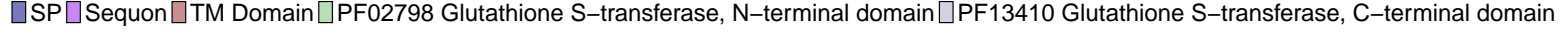
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

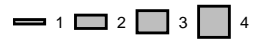


Protein sequence:

SKKEDQEAANKFEKFKLLEELGDKPYFGGEGFGFVDMALIPYITWFRWKEKFNFNIEAEGPKVVEWAKKGMKKEVSKSLADPKVYVFMVGHYKHSPRIRIGQVFWMGRVMMMPFLGLVSWSSKGRVIA

NbL05g10930.1 peroxisomal_(S)-2-hydroxy-acid_oxidase-like [MW = 40.61 kDa]

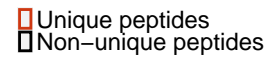
No. of times detected



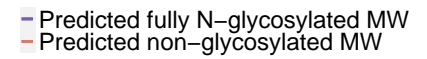
log(intensity)



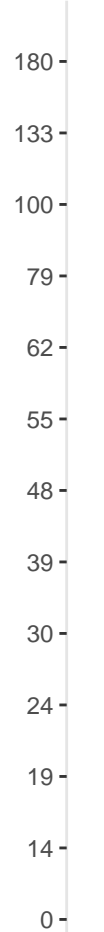
Values from



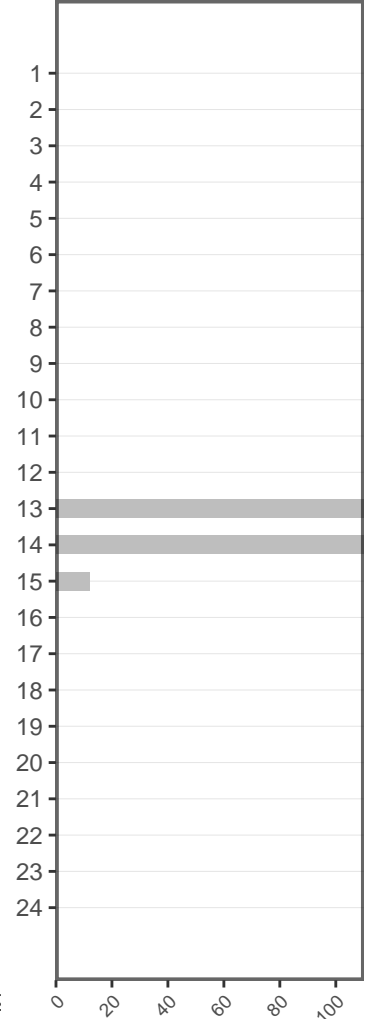
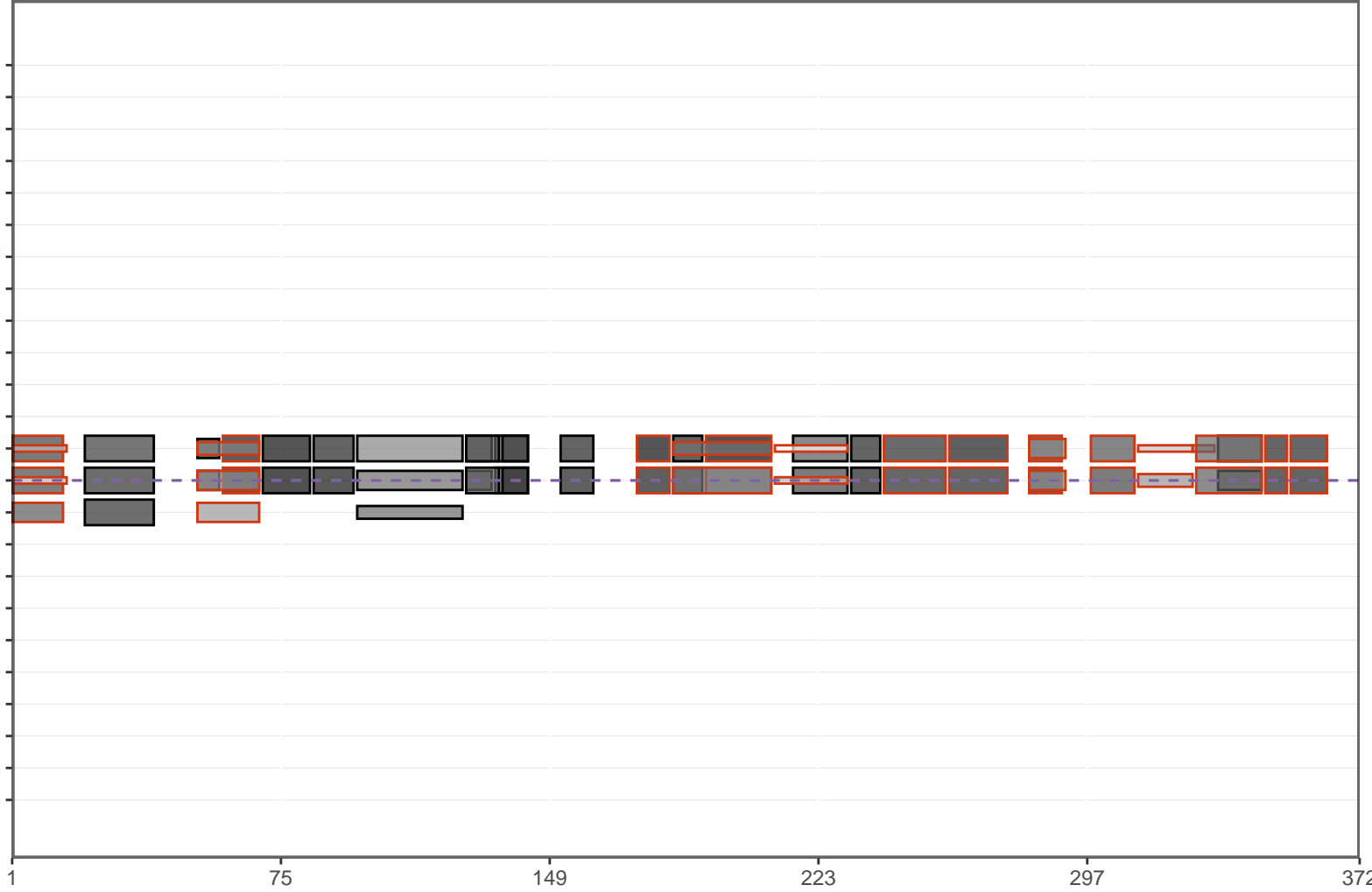
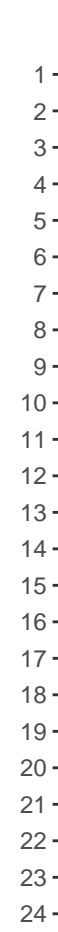
MW indication



Molecular weight

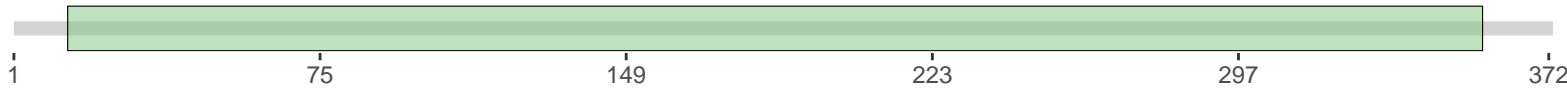


Gel Slice



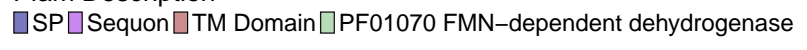
Protein length

Peptide counts over 4 repeats



Pfam domains

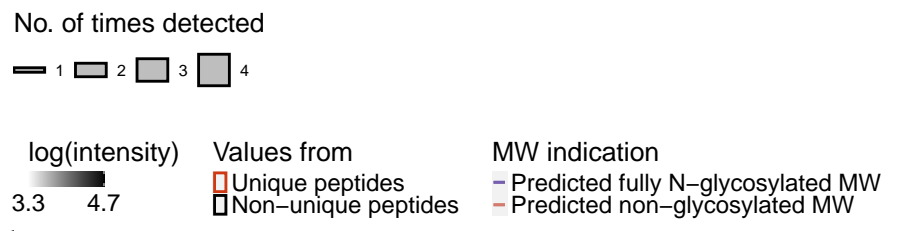
Pfam Description



Protein sequence:

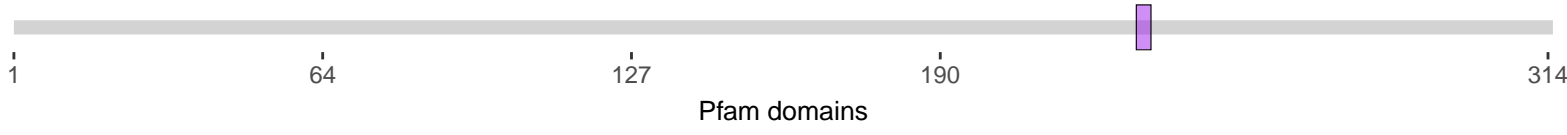
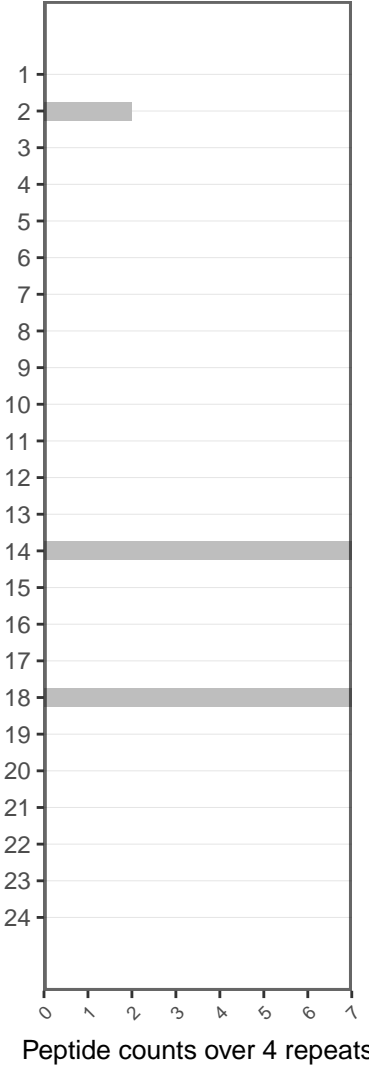
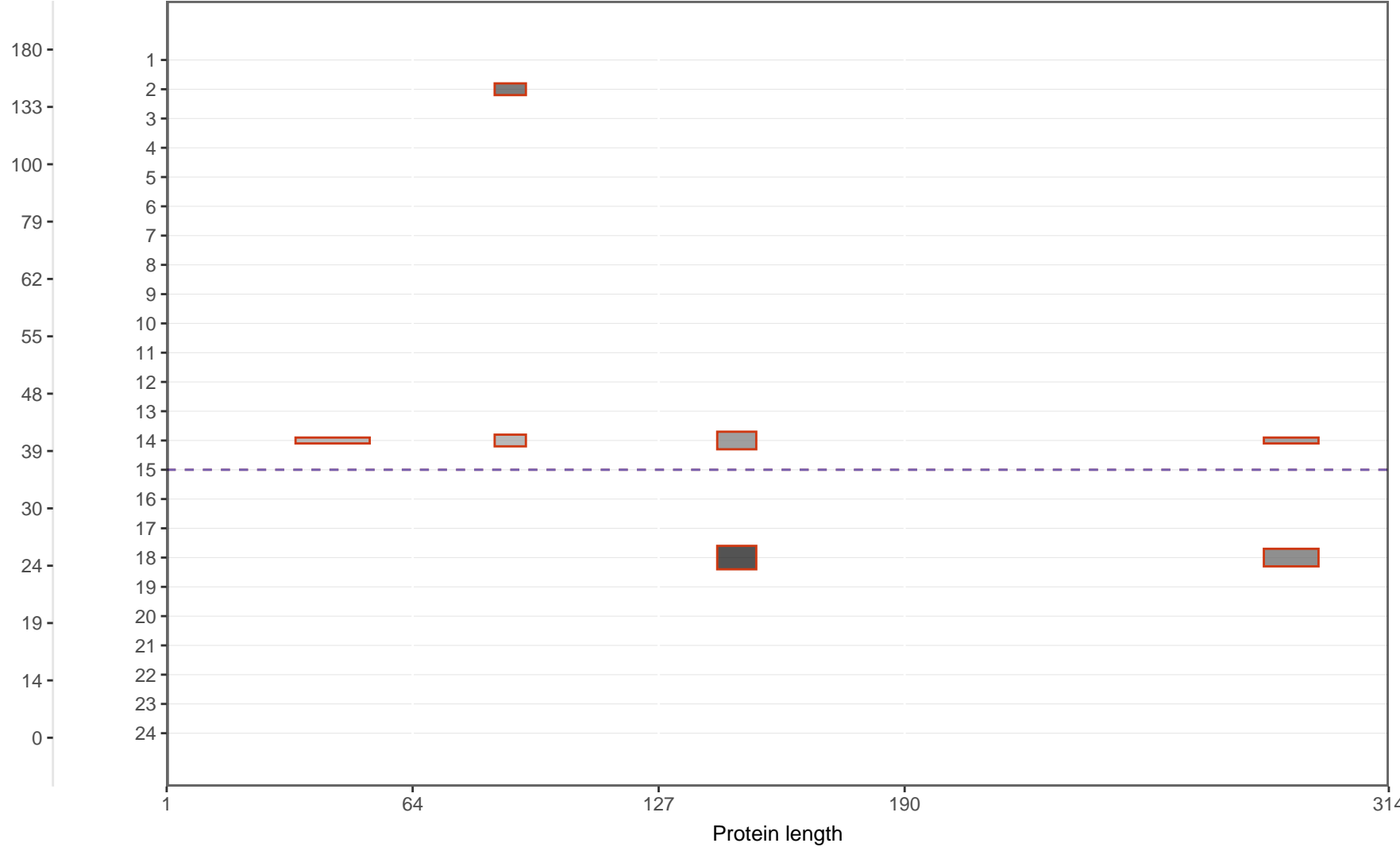
YLPFLLTKNFEGLDLGKMDGSDGSLASVAGQIDRTLSWKDQWLGQTTSPLPKLVGVLTAEDARLAWQAGAAAGVSNHGARQLDYVPTFMALVEEVKAAQGRIPVFLDGGVRRGTDFKALALGASGIFGRPVVFSLAEEGAGIKKLVGMRLDEFELTALMSGGGRSLNETRNIVTEWDAPRAALPAPRL

NbL05g10850.1 uncharacterized_LOC107809971 [MW = 35.03 kDa]



Molecular weight

Gel Slice



Pfam Description SP Sequon TM Domain

Protein sequence:

SFOGKTLSSQFDLVILHVGAGRRNVLKDLHVNRLVGDLMQMAHPGTEVGRUHMSVVFSGYVREDDDSMYSIADTRPENNKLSRIFFRSGYTIKEGKPRNRFQFCPLVAGWGNVTRKDMVEAYSQYDFKEHGANLVPADRLLEHVAFKMVKPKYGA

NbL05g10830.1 vacuolar_protein_sorting-associated_protein_32_homolog_2-like [MW = 24.39 kDa]

No. of times detected



log(intensity)



Values from



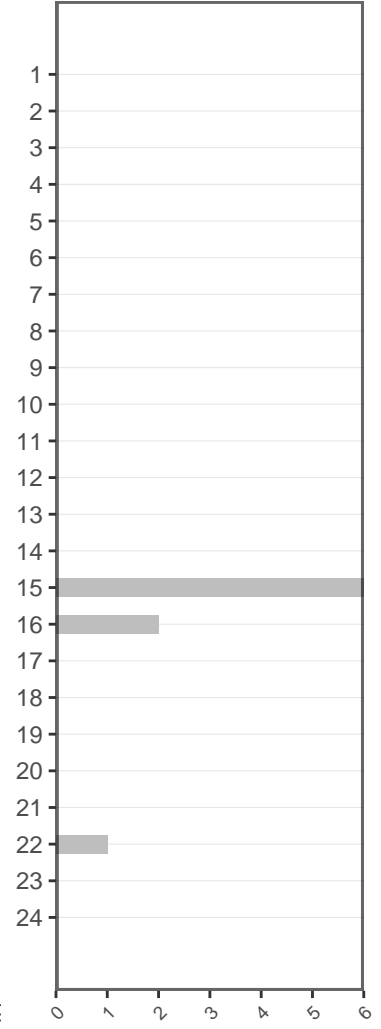
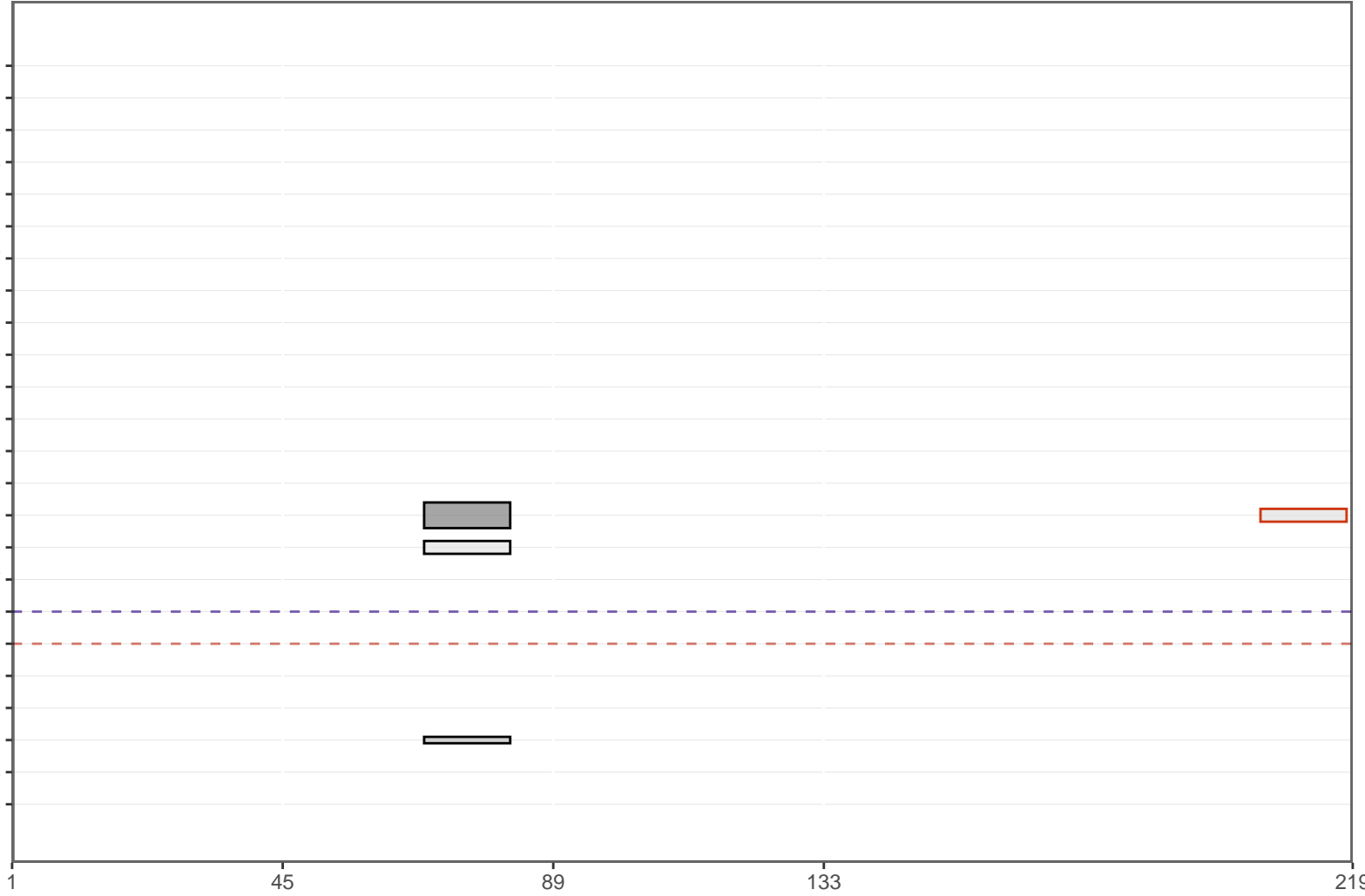
MW indication



Molecular weight

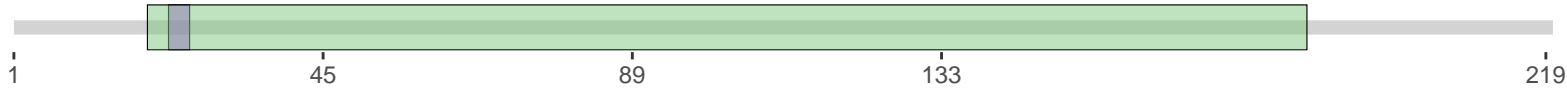


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FETV¹DALRTGAA¹¹AKMK¹⁶KATND²⁰V²¹DKTMD²⁵INE²⁶QGTEN³¹MK³²IQEAL³⁷ST³⁸PG⁴¹AA⁴²DFDE⁴⁵LELE⁴⁶LELE⁴⁷GALE⁴⁸EE⁴⁹QL⁵⁰LP⁵¹WT⁵²AP⁵³SI⁵⁴PI⁵⁵PT⁵⁶GR⁵⁷QQ⁵⁸VR⁵⁹PT⁶⁰AG⁶¹GN⁶²RA⁶³EDEL⁶⁴AAL⁶⁵GAEMAL⁶⁶

NbL05g10660.1 50S_ribosomal_protein_L24_chloroplastic [MW = 20.63 kDa]

No. of times detected



log(intensity)



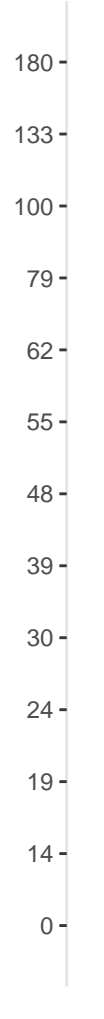
Values from



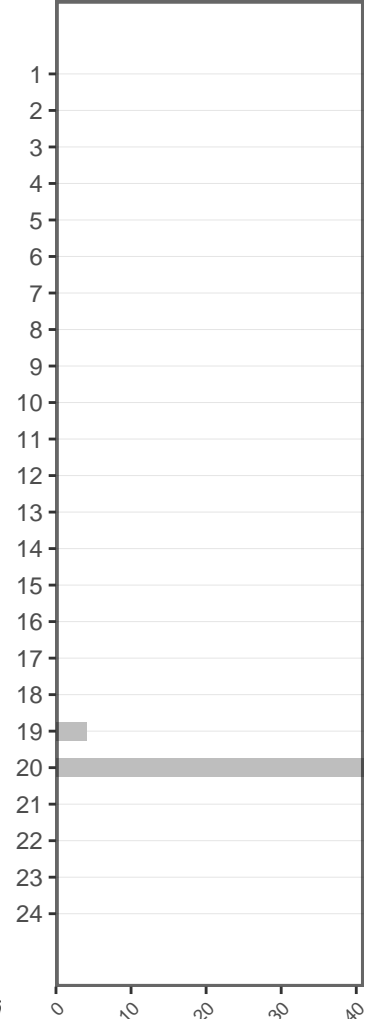
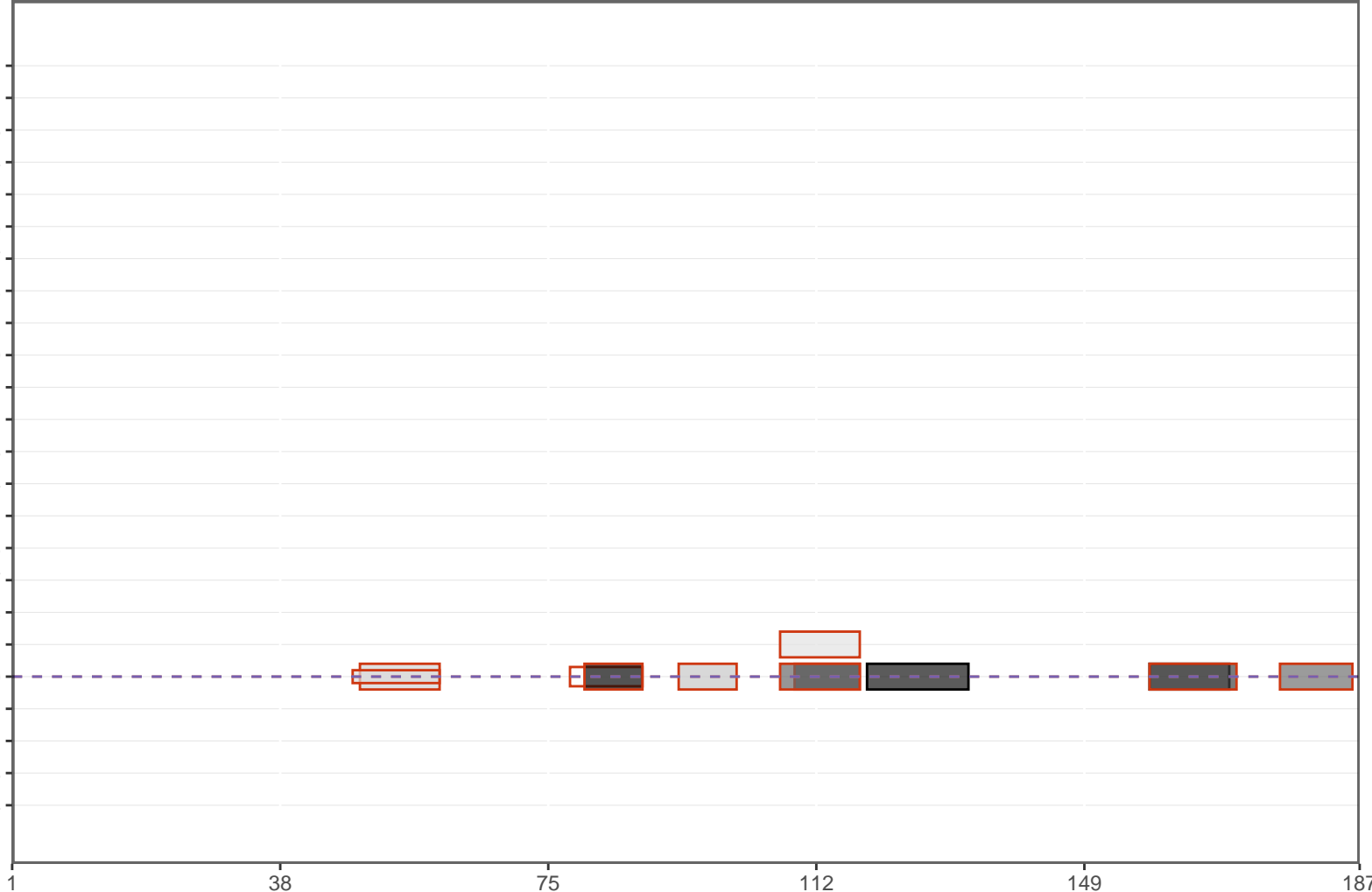
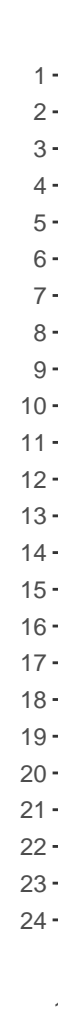
MW indication



Molecular weight

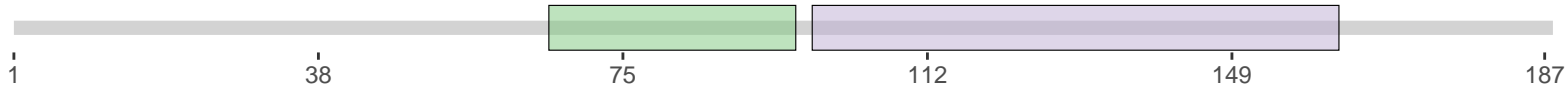


Gel Slice



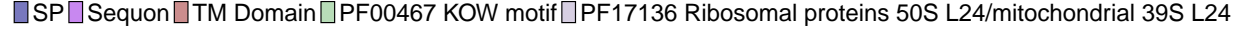
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

VVGEITLIRIKNSKVVYKDVNLKTRHVKRSRSEDEPGGIVKKEAFPHGSHSNVLYSKEGKVASRVGHKFLDNGKRVRYLTKTGEIHSIAENWKKAVKEKEKTEAAVAAAS

NbL05g10610.1 60S_ribosomal_protein_L8-like [MW = 30.94 kDa]

No. of times detected



log(intensity)



Values from



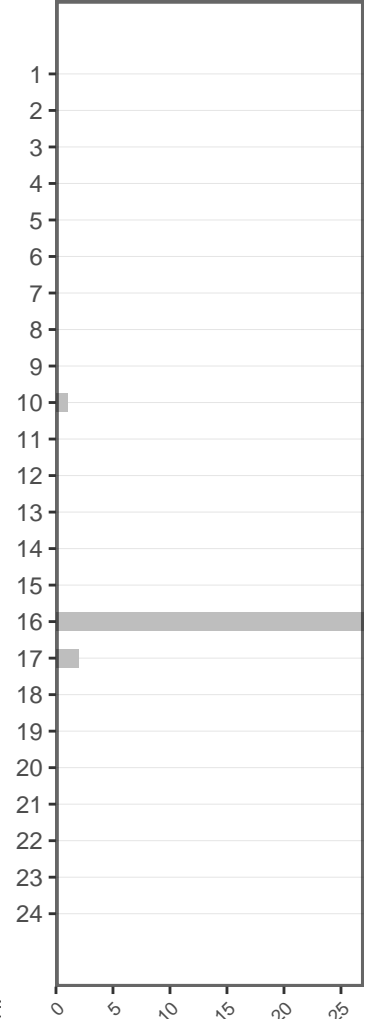
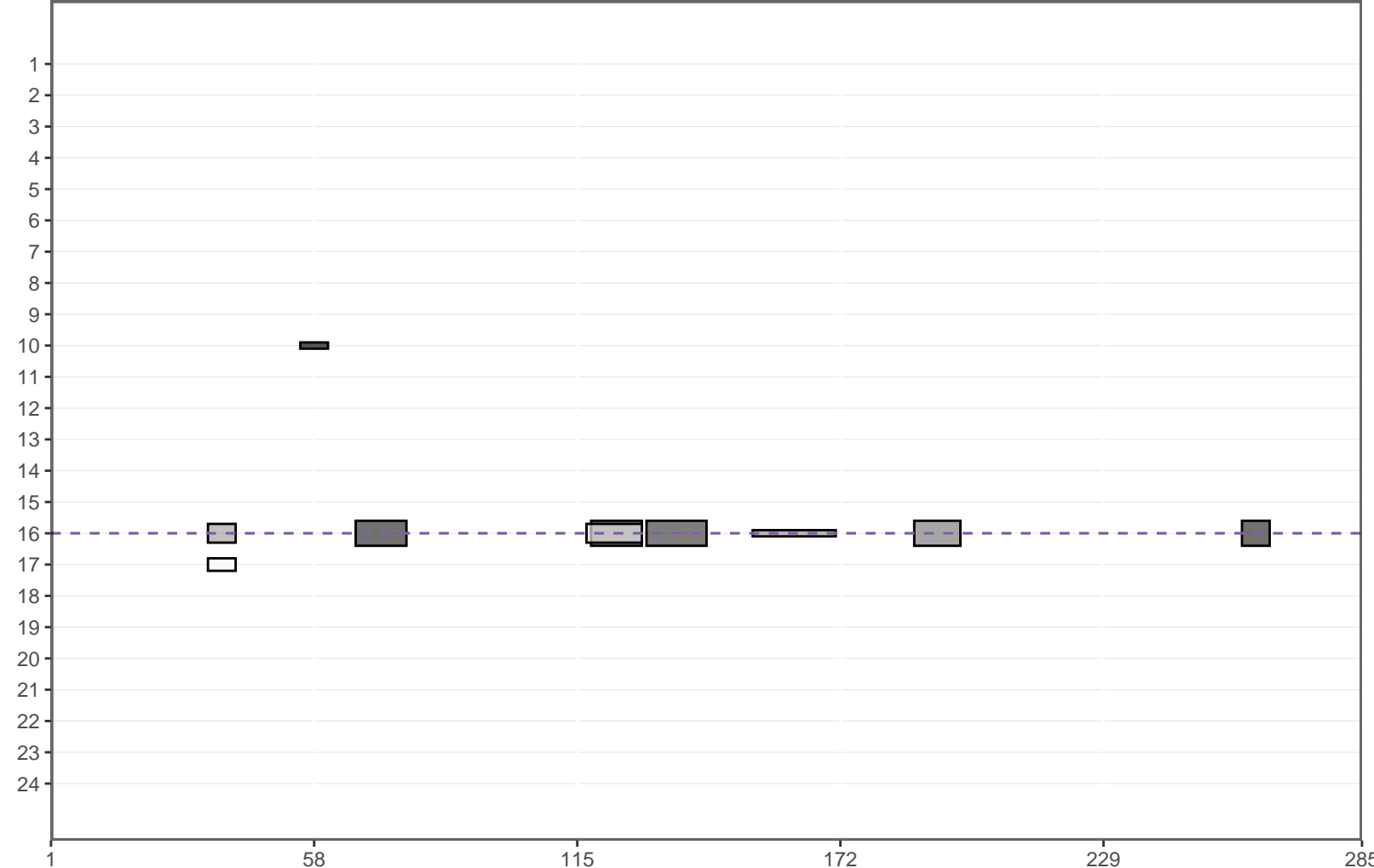
MW indication



Molecular weight



Gel Slice

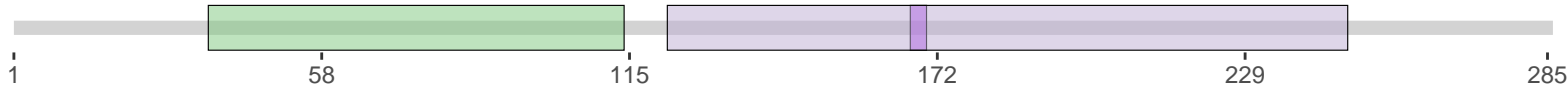


Protein length

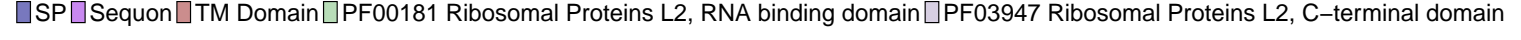


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

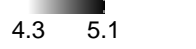
IPEGAVVCNVEHKVGDGRGVFARGSGDVAIVSHINPQNGTTRIKLPSGSKKVPSPGGRAMIGDVAAGGRTEKPKMKAGNAYHKYRKRKNGWPKVRGVAMNPFVEHPHGGGNHQHGHASTVRRDAPPQGVLLAARRTGRLRGAAATAKAKDKV

NbL05g10490.1 uncharacterized_LOC107827684 [MW = 26.45 kDa]

No. of times detected



log(intensity)



Values from



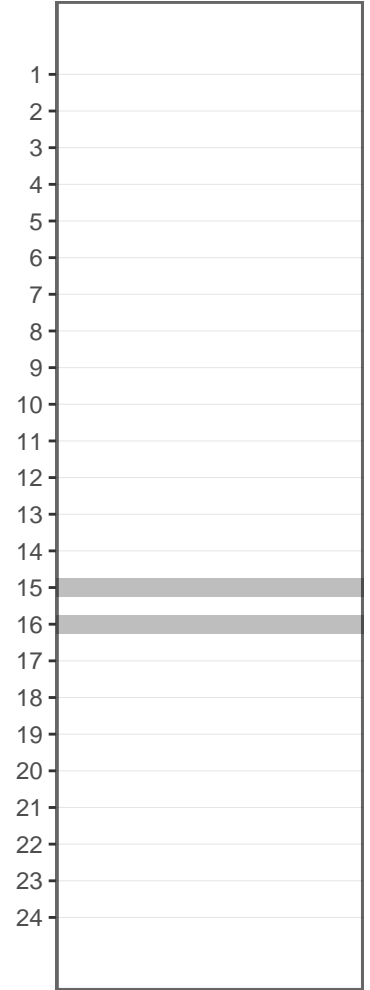
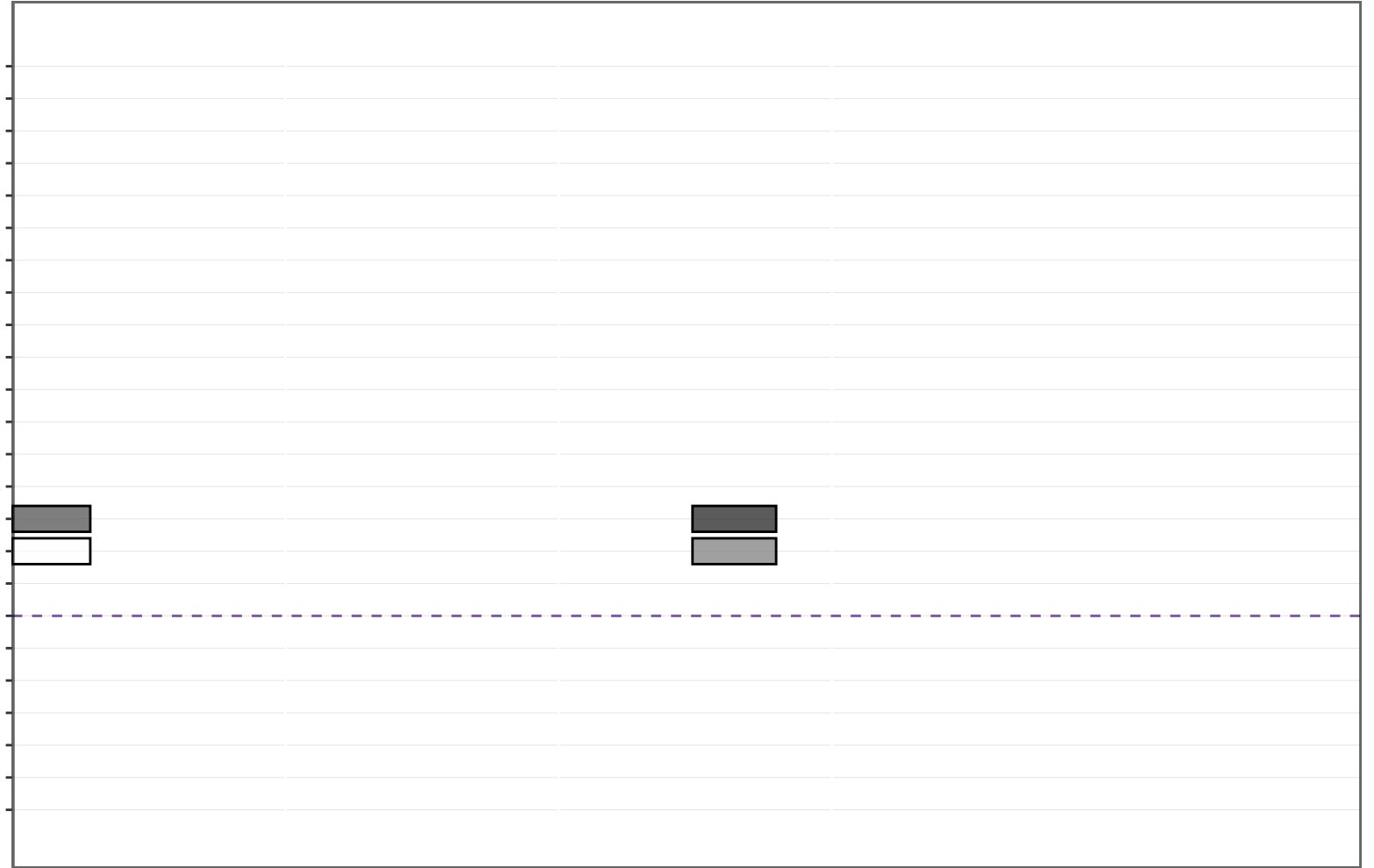
MW indication



Molecular weight



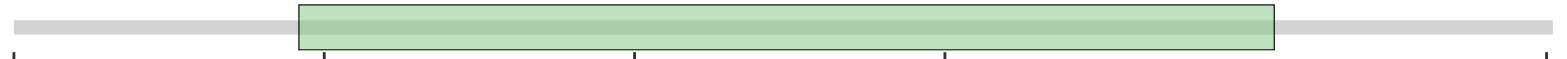
Gel Slice



Peptide counts over 4 repeats

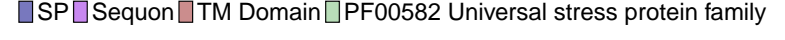


Protein length



Pfam domains

Pfam Description

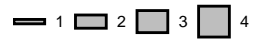


Protein sequence:

KLEDDFDFTTTTKASDSDQPLVDQDFPKIHVKDHDMRERLGLVERLGLSAVIMGSRGFGATKRGDRGLGSDVYGVRHGVCPVWVRRYPDDKDGSGANAAVEPVVSVASAAEEDDEDAEYHDAADHRKDS*

NbL05g10460.1 ubiquitin_carboxyl-terminal_hydrolase_14-like [MW = 88.88 kDa]

No. of times detected



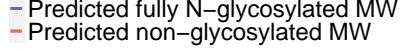
log(intensity)



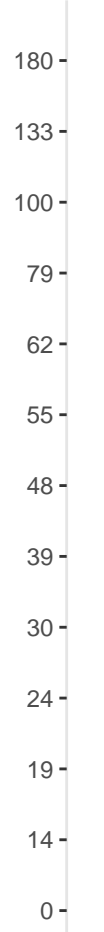
Values from



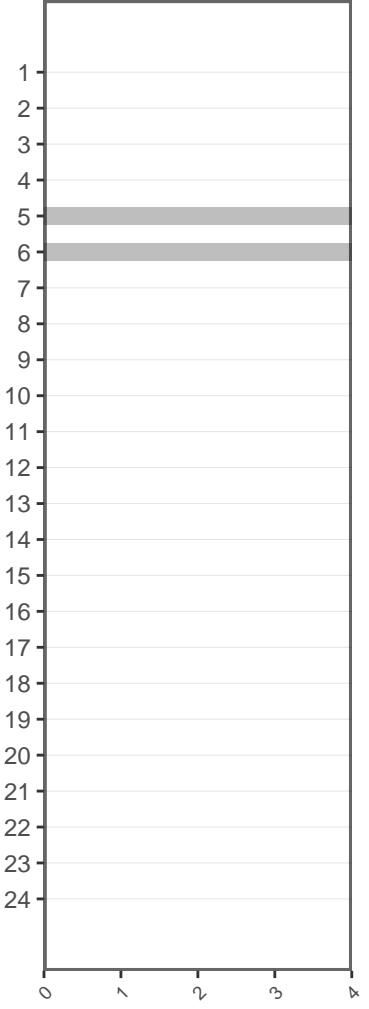
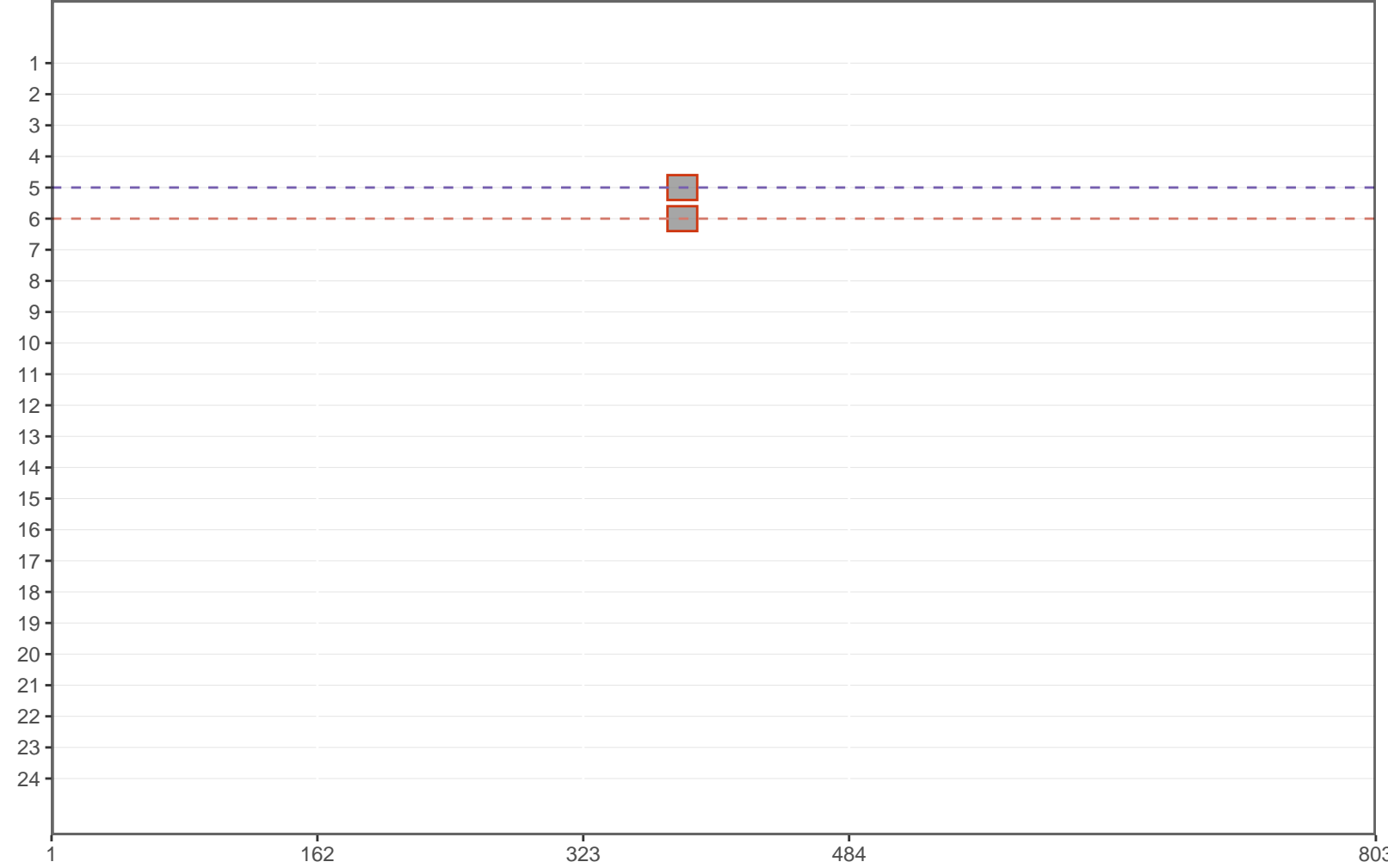
MW indication



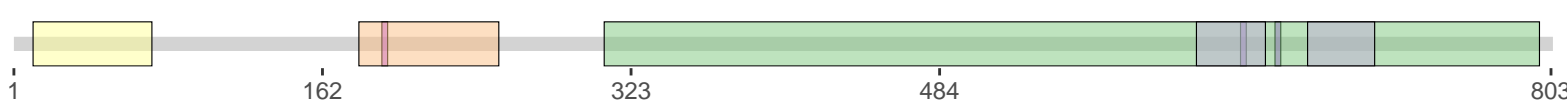
Molecular weight



Gel Slice

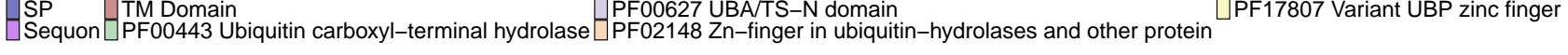


Protein length



Pfam domains

Pfam Description



Protein sequence:

AAASSPKQDESISPRMFKSVAASHPEFSTMRGGDALEFFLHFIDQVERMNSGKPDFDPSRSKFGIEERLQCPGKVAAYNRRNDVILSLNIFLEKAINKELAEFGNLIKSKAAEGKELGADEIVRPRVLSNDLQDFSPAEVEHFEYSTALKARTTAKTGLTSPDYLVLHMRKFMEEGWPKKLDVYDVPETIDSGMRTNGKPGEEELFDSDAGDGGEGSTKLLANEDVVAQLVEMGFNLLHGKKAINTSNKGVFAAMWLLLEHVNDSDIAPISQVQNPDDQSDSDT

NbL05g10200.1 beta-glucosidase_18-like [MW - SP = 58.12 kDa]

No. of times detected



log(intensity)



Values from



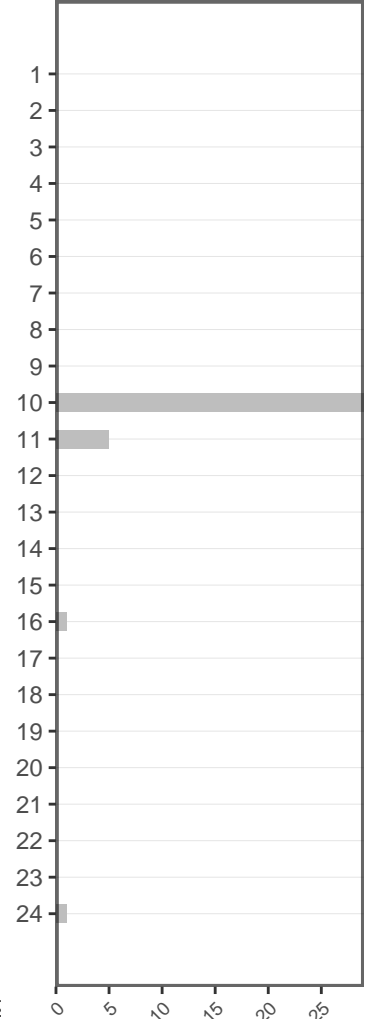
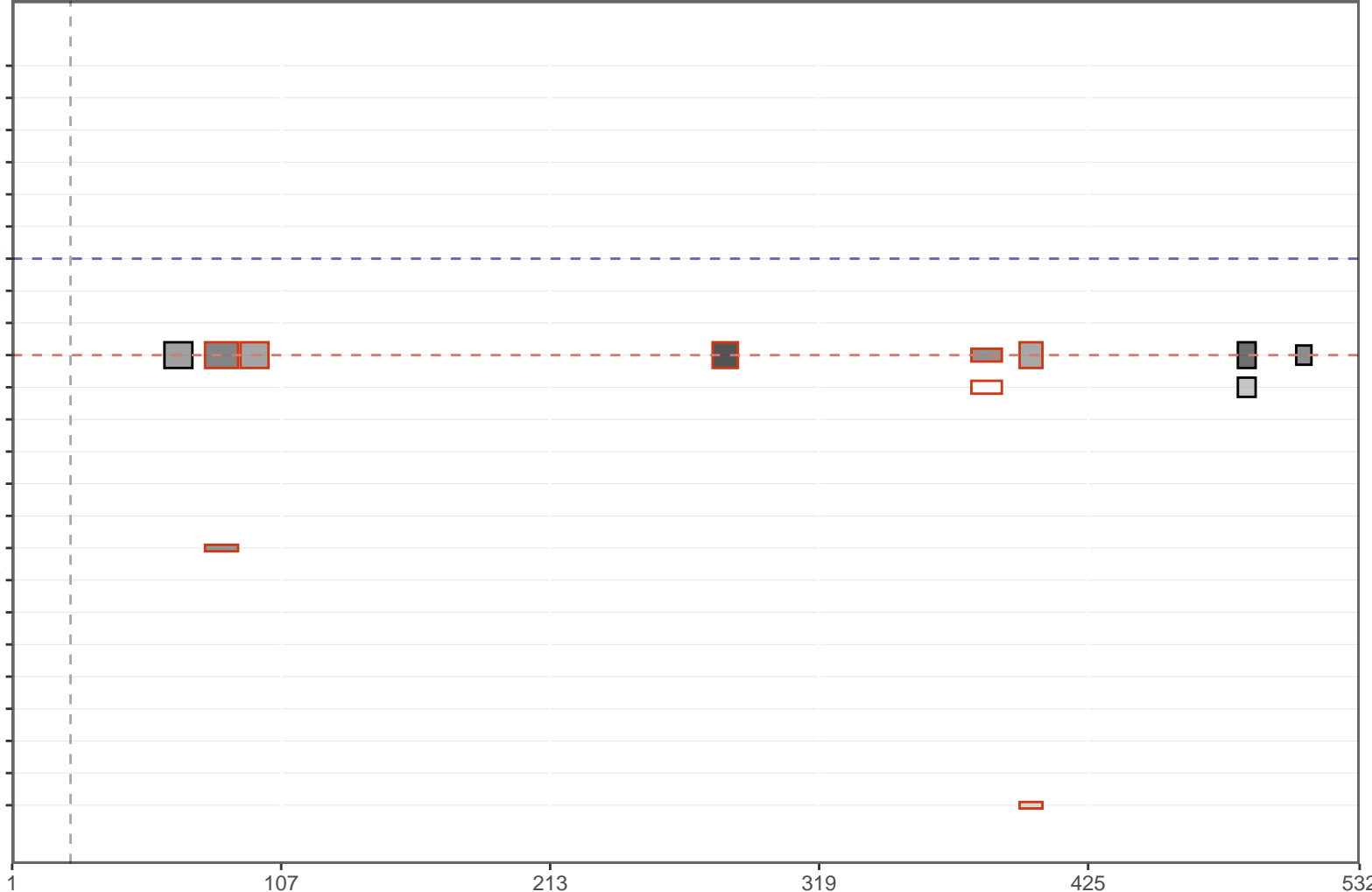
MW indication



Molecular weight

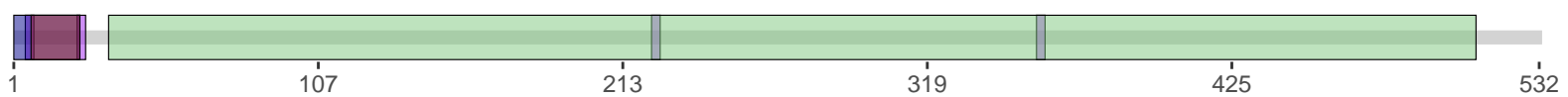


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SEHFGOSKIDCLGIVVHAFMYKPLRNDDFLDAANRALVFTAAWIDPLVYGYVPRMRYGLESSELPFTSDEKRLKDSIDFIGVNHVGTLVAKDCHSSVCGNSGCAAGDHPHGVLFTLGEKDGVPVGEPTGMSRFVVRPGMEEIVDYIKKRYPNKPMFVTEFNGYSELNPTTGAALQHDIKRVEFHKSYLALGLARMRKMGADVRGYFVWLSLMDNFEWASGYELKFGLYVDRSTLNRVPLKSAKYYRDFLTGKARTALFRHTGADHVEHK-

NbL05g09870.1 probable_bifunctional_methylthioribulose-1-phosphate_dehydratase/enolase-phosphatase_E1_1 [MW = 56.55 kDa]

No. of times detected



log(intensity)



Values from



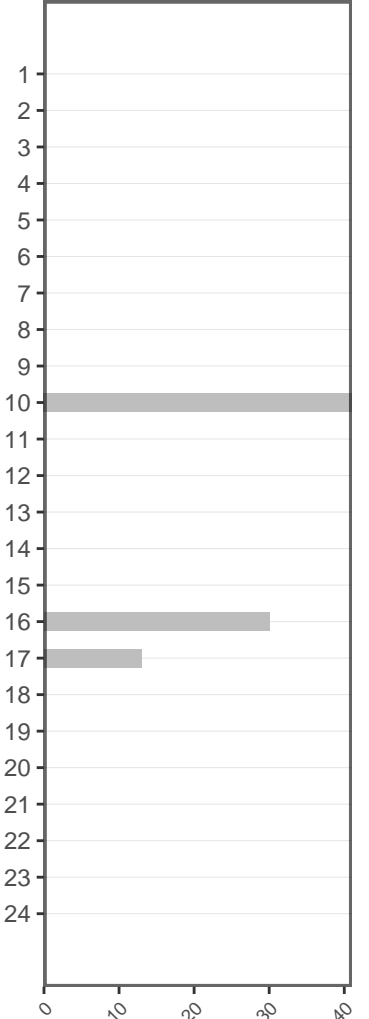
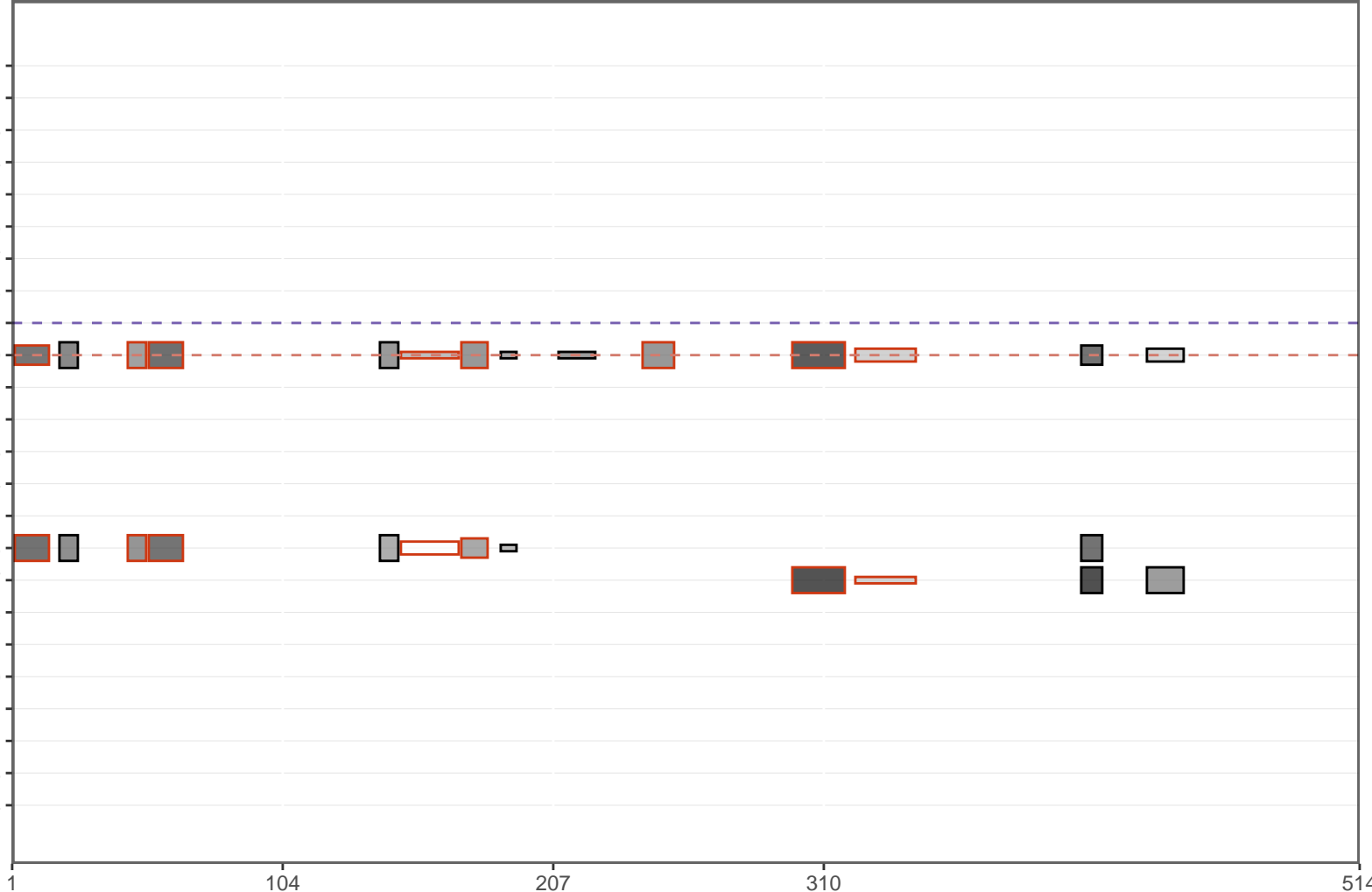
MW indication



Molecular weight



Gel Slice



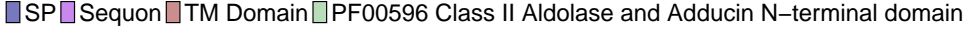
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NGHFAGIQNAKASAMGGTLAENGSKPERRRIGVLDIEGTTPTTFVTDVLPFYARDNVGSHEDATYSGAETGDDKLLRAGMOODLENGVAGAVYIPSDDAGKMEVAALVANVEAMKADRKITALKELGHWGTGFENNELEGLVFDVDPQALEKWTSLGFKVYVYSSGSRLAGRLFGHTKHGDLRNLYLGGFFDTTVGNKRETKSYQETASLGLVDNPSEILFDVYQEATAKAAAGLEVISVIRPQNGRLPNDHGFRTRHSFSEI

NbL05g09830.1 3-hydroxybutyryl-CoA dehydrogenase [MW = 32.1 kDa]

No. of times detected



log(intensity)



Values from



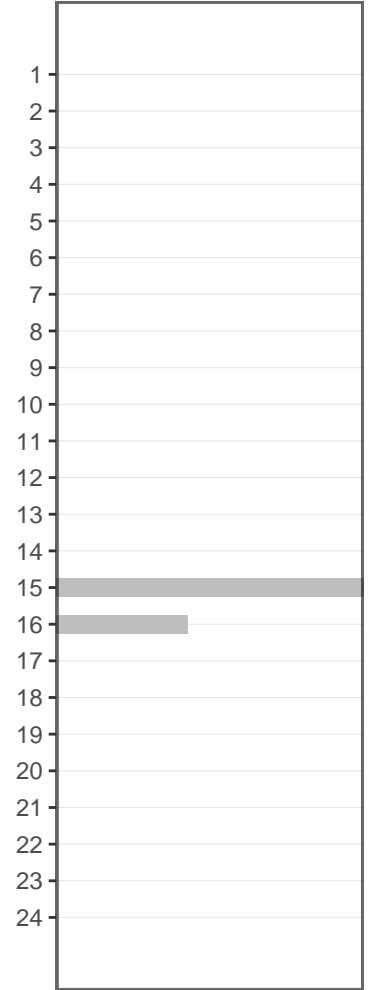
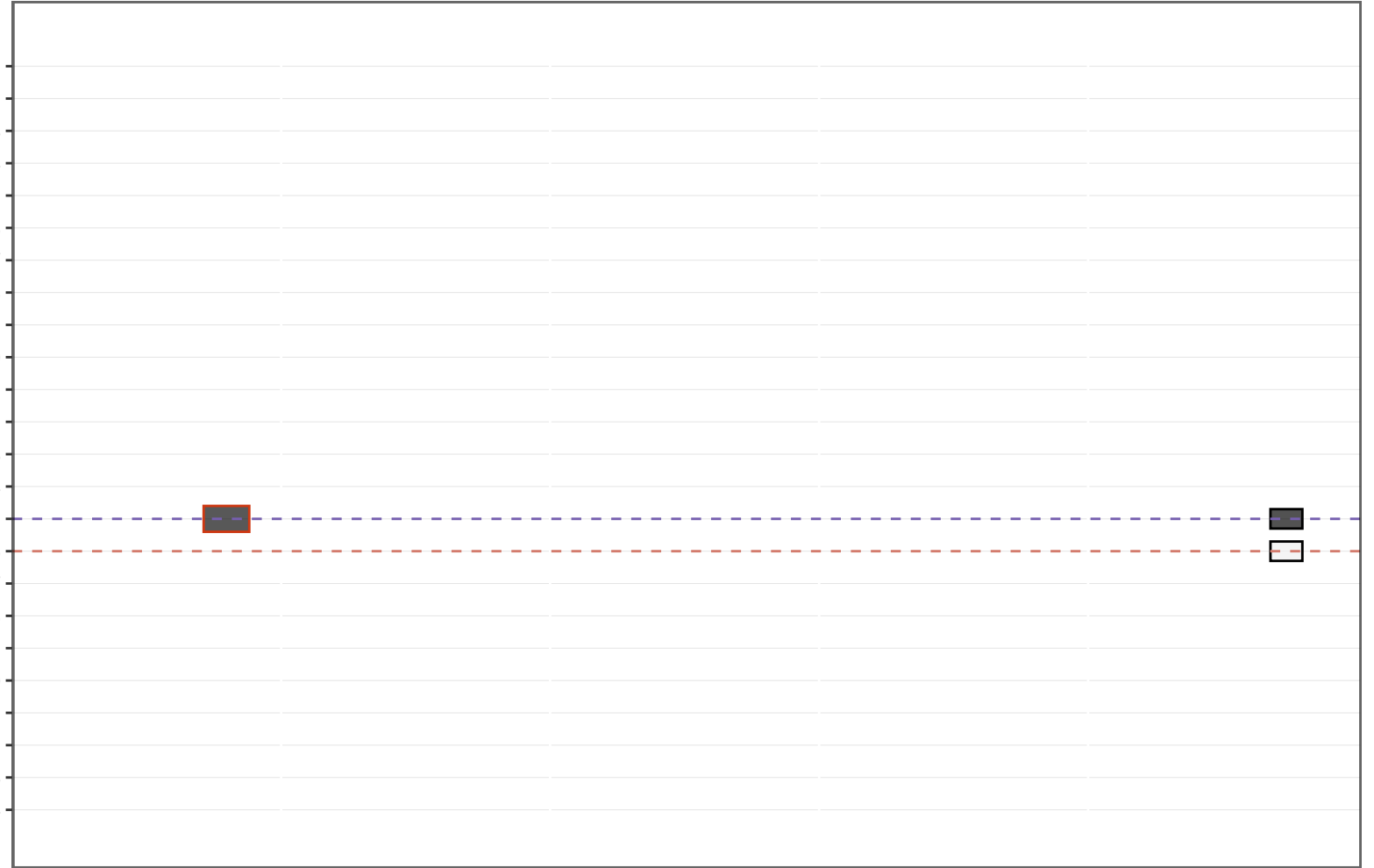
MW indication



Molecular weight



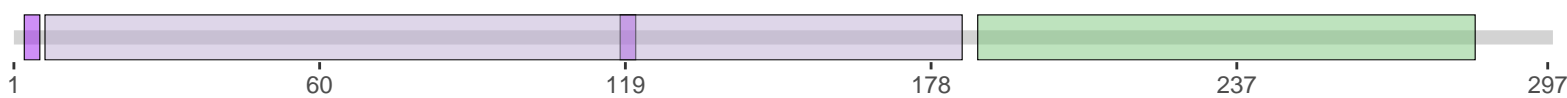
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00725 3-hydroxyacyl-CoA dehydrogenase, C-terminal domain
- PF02737 3-hydroxyacyl-CoA dehydrogenase, NAD binding domain

Protein sequence:

VIGMFMNPPMIMKLVHHRGADTSEDYFATKLAERFGKTVICGDDYDFIVNRIIMPVMEAFHLYTGVATKEDIDTGMILGTDHFMGPLELADFIGLDVLSMKVLAHVLGDDKYPAPCLLVGVYDGDRLGKRRGIVDYRGAADYKGPRL*

NbL05g09540.1 protein_DJ-1_homolog_B-like [MW = 47.03 kDa]

No. of times detected



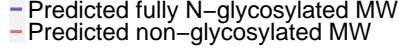
log(intensity)



Values from



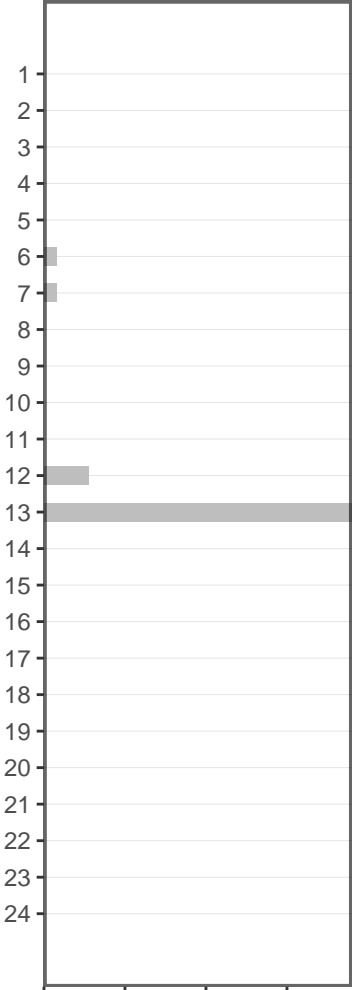
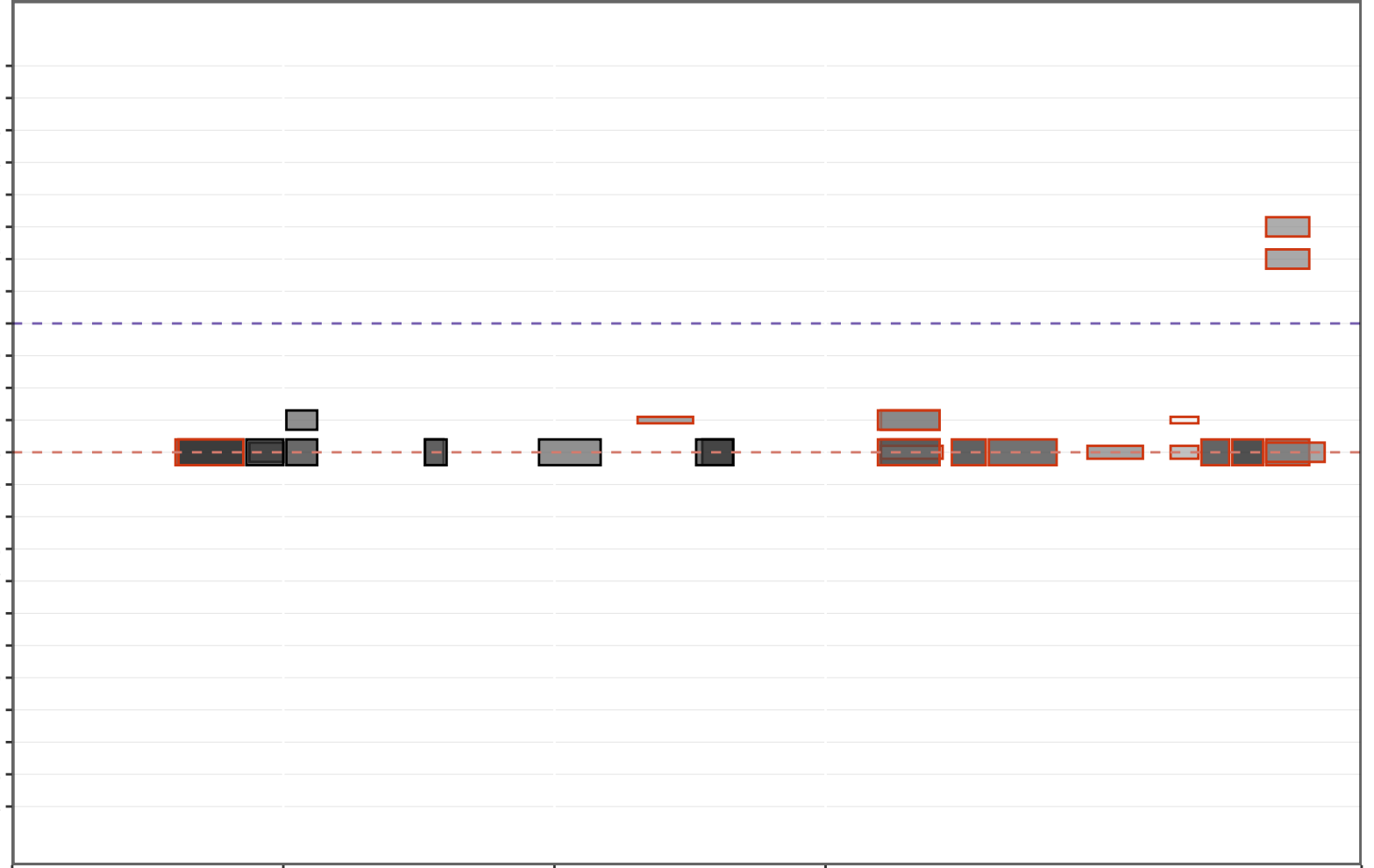
MW indication



Molecular weight

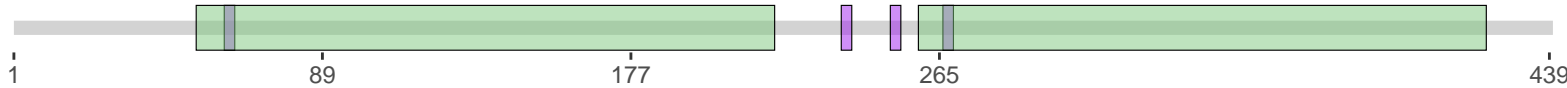


Gel Slice



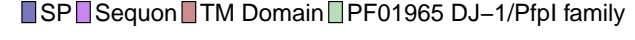
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

AIEYAVLVLEQLYGKEKADKDEVSGPLVLRNENHSEEFVFAELNKNVWNTFTSKPQLVPIANGSSEIEAATIDVLRANAGLVASLEDTLETVASGRKVKLVADVLDDEAAKQSGYDLVLPGLGGAGAFANSEKLVDMUKKQRESSPKYGMDCASPLVLERHGLLKGKKTAFPMQNKLSQPSSEANRVLVDGNLVTSRGPGTTFEFLAIADKFRGRKEVLELAKKMFV

NbL05g09490.1 ubiquitin-conjugating_enzyme_E2_35 [MW = 19.29 kDa]

No. of times detected



log(intensity)



Values from



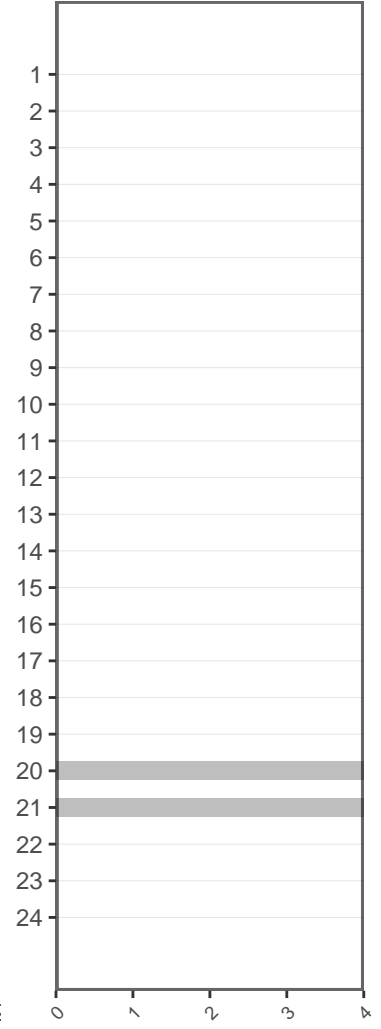
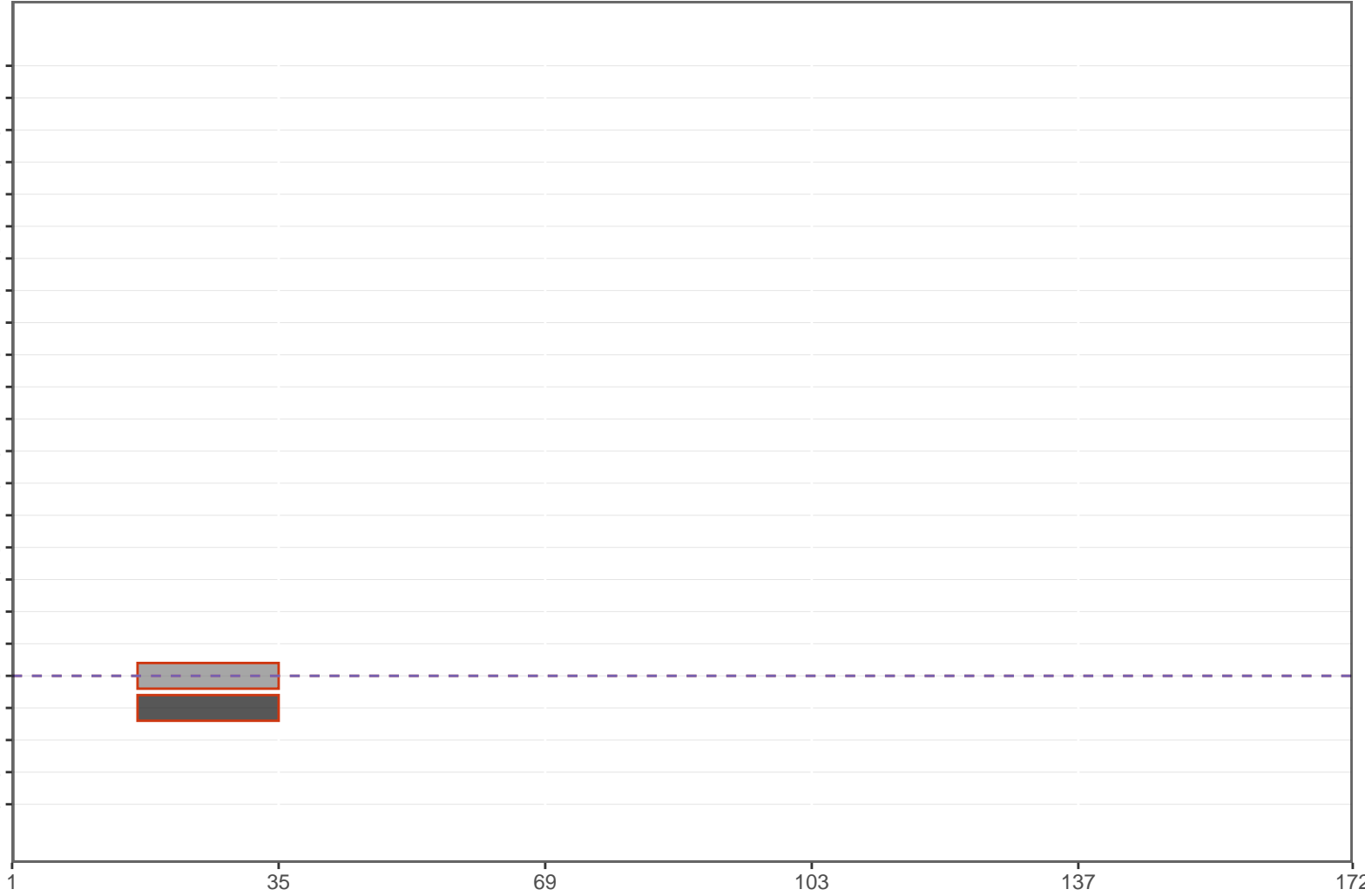
MW indication



Molecular weight



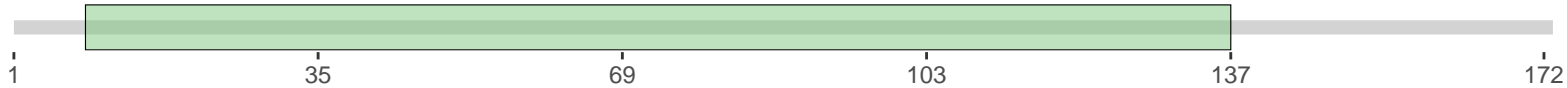
Gel Slice



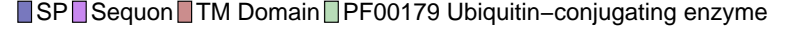
Protein length



Pfam domains



Pfam Description



Protein sequence:

VRFLTKYHPNDKLGKGLDLDKDKWSPALQRTVLLKIGALLGAPNDDPLSENAKHWKSNKAEAVETGSLYSGLSYGLGTSPDQWNRVYTFEFTFLI

NbL05g09440.1 phosphoenolpyruvate_carboxylase-like [MW = 36.72 kDa]

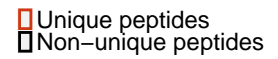
No. of times detected



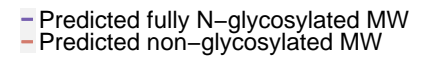
log(intensity)



Values from



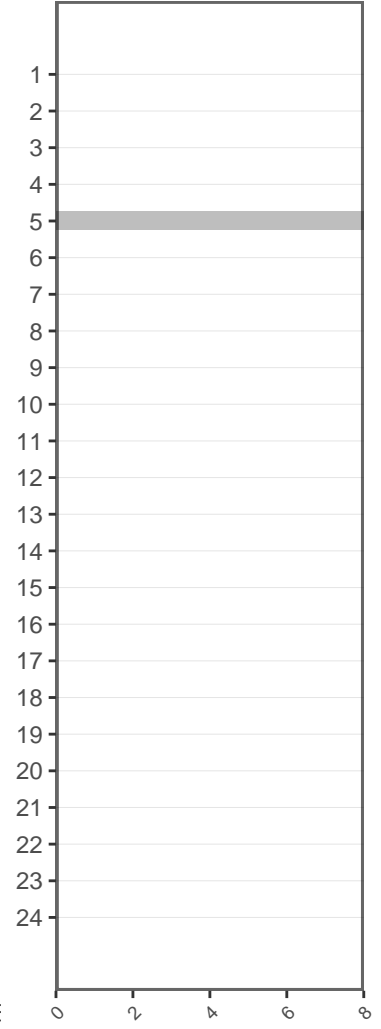
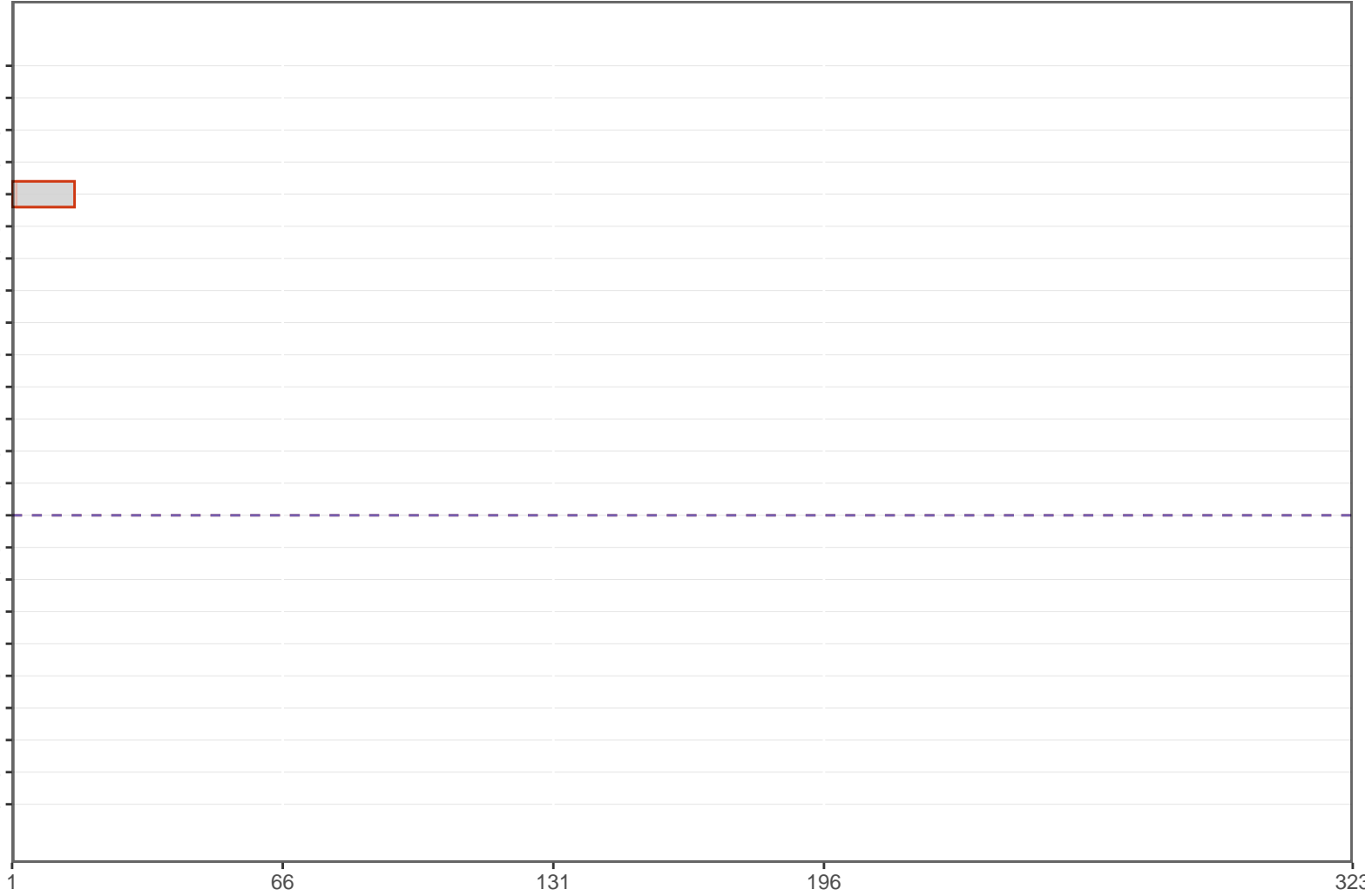
MW indication



Molecular weight



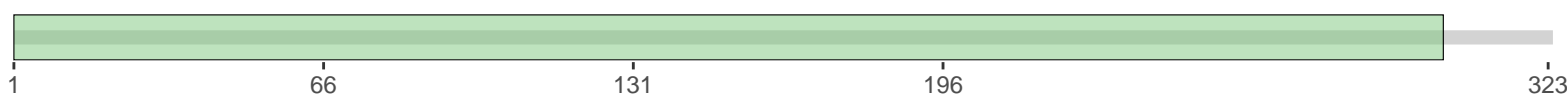
Gel Slice



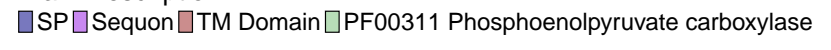
Protein length



Pfam domains



Pfam Description



Protein sequence:

EEHLCFRTLQRFSTSALEHGSMNPLPSPKPEWRRLDEIWAIEKYSRIVFKPEPPVEYFRLATPELEYGRMNGSRPSKRKPSGGIEPLRAIPWFAWTQTRFHLPLVWLGFGAAFKYALNKDKNLHLDGMVYKWPFFRVTDLVEMVFAKGRPRRHGCFRQASGFRFRVLR*

NbL05g09420.1 epidermis-specific_secreted_glycoprotein_EP1-like [MW - SP = 26.05 kDa]

No. of times detected



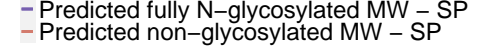
log(intensity)



Values from



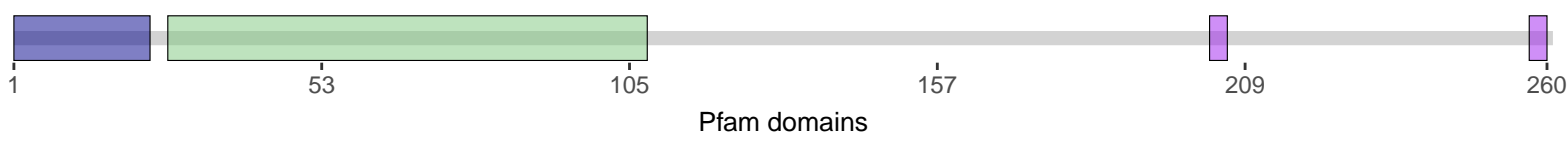
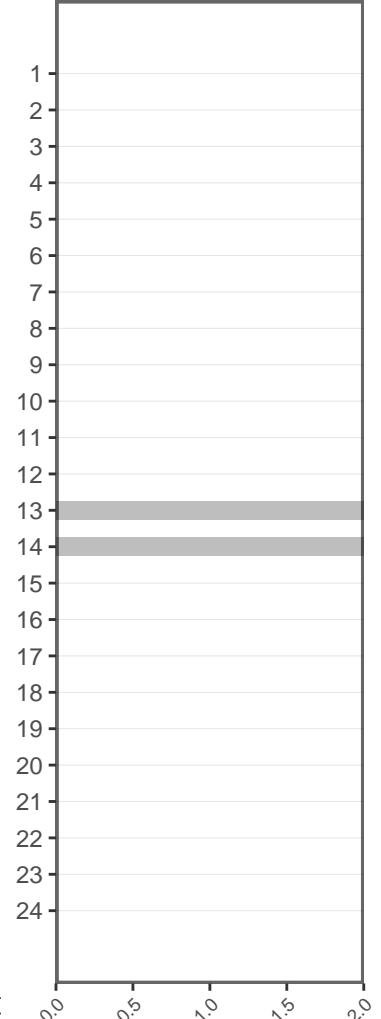
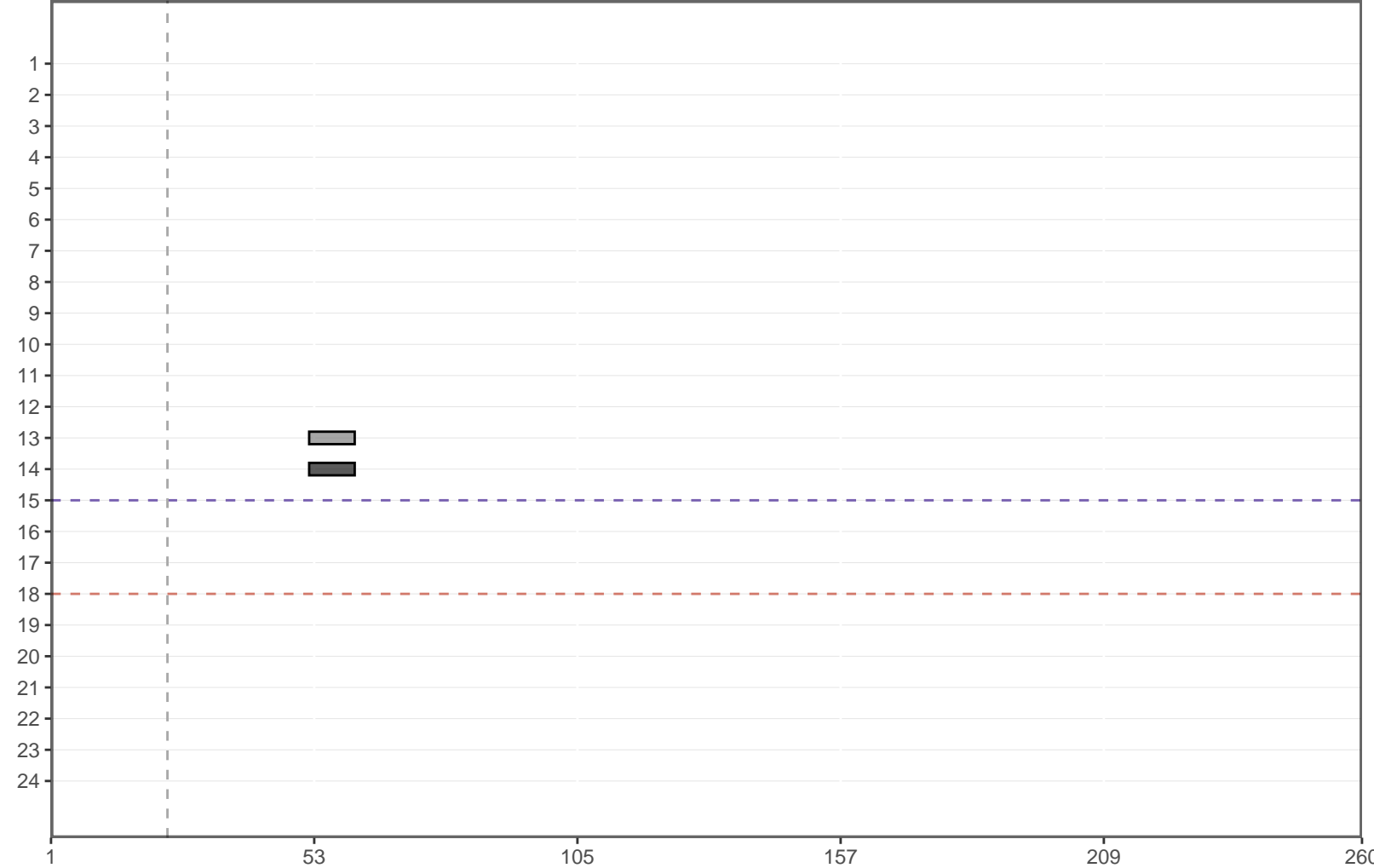
MW indication



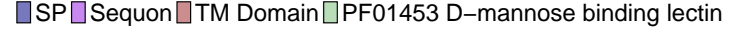
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

VANGPYSLVYKPKFGCEFE66GGGKFLGRMPGVLETA6LPLKGRDKFVALEIGKNNMTWVLDAEIHLDMGPGDAIKDRNNASTDDGAKALIFLRHRLDEVDKPLUUNGLKERYDNLKLVLPQARDDENPKANS

NbL05g09390.1 polynucleotide_3'-phosphatase_ZDP [MW = 46.52 kDa]

No. of times detected



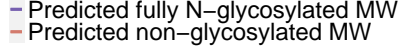
log(intensity)



Values from

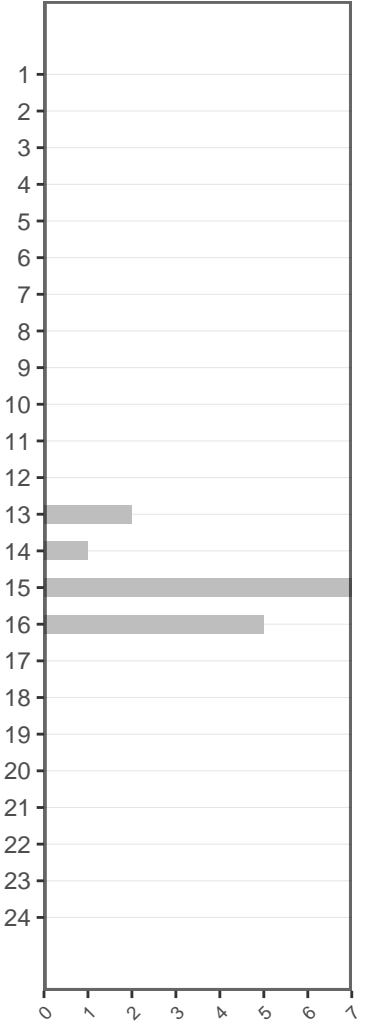
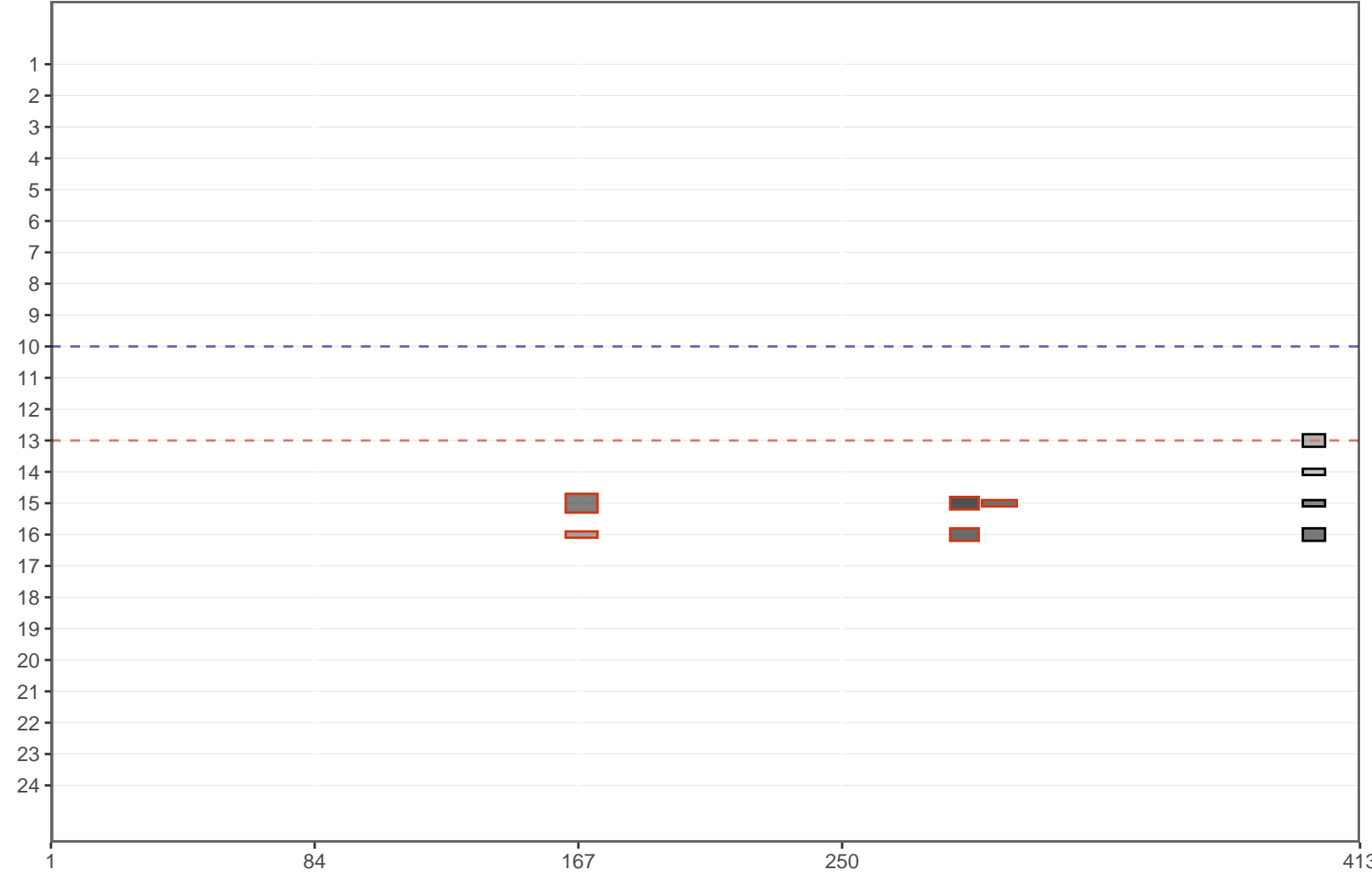


MW indication



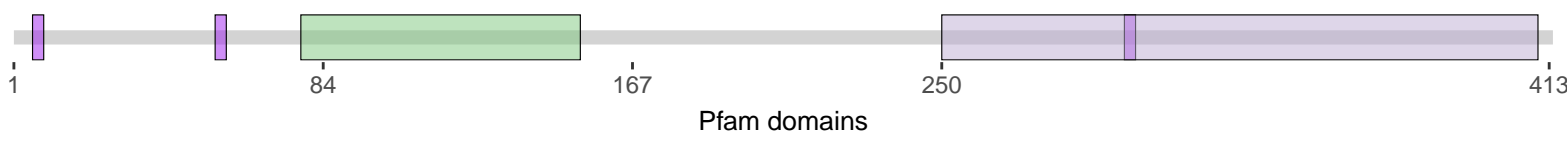
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00645 Poly(ADP-ribose) polymerase and DNA-Ligase Zn-finger region
- PF08645 Polynucleotide kinase 3 phosphatase

Protein sequence:

QKRLKLSATDEGAELEAFSTSDVKTTPKDAKLPKWRAPFTIYLEKDDVLAHGHKAAAFDFDGLAKTGVKRVGADAWLSLWYSPPEKMGSLVNDGXYLVIETNESNERWKKRQAAVDSKGRLEGFRLAGVFPQVFIACGLSNKPKEDFRKPKIGMAVNMKMGFNFGISFEMDKGFVVGDAAGRGGDHSADIRFAQAGLKFVPEEFFGK

NbL05g09370.1 multiprotein-bridging_factor_1b-like [MW = 15.33 kDa]

No. of times detected



log(intensity)



Values from



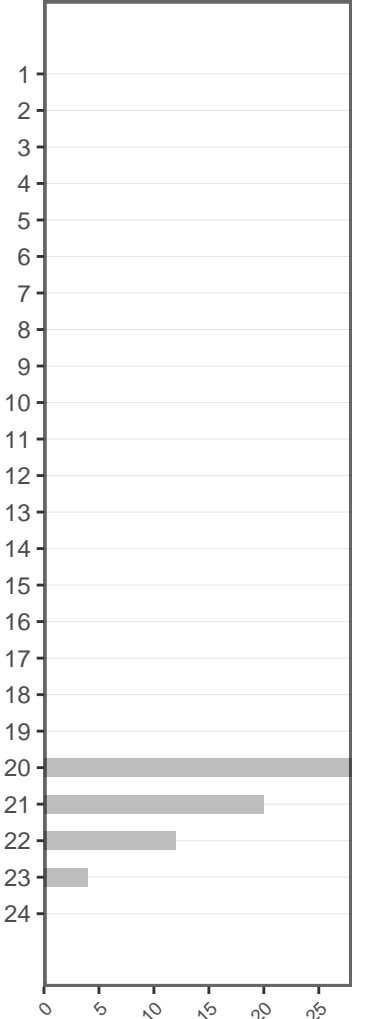
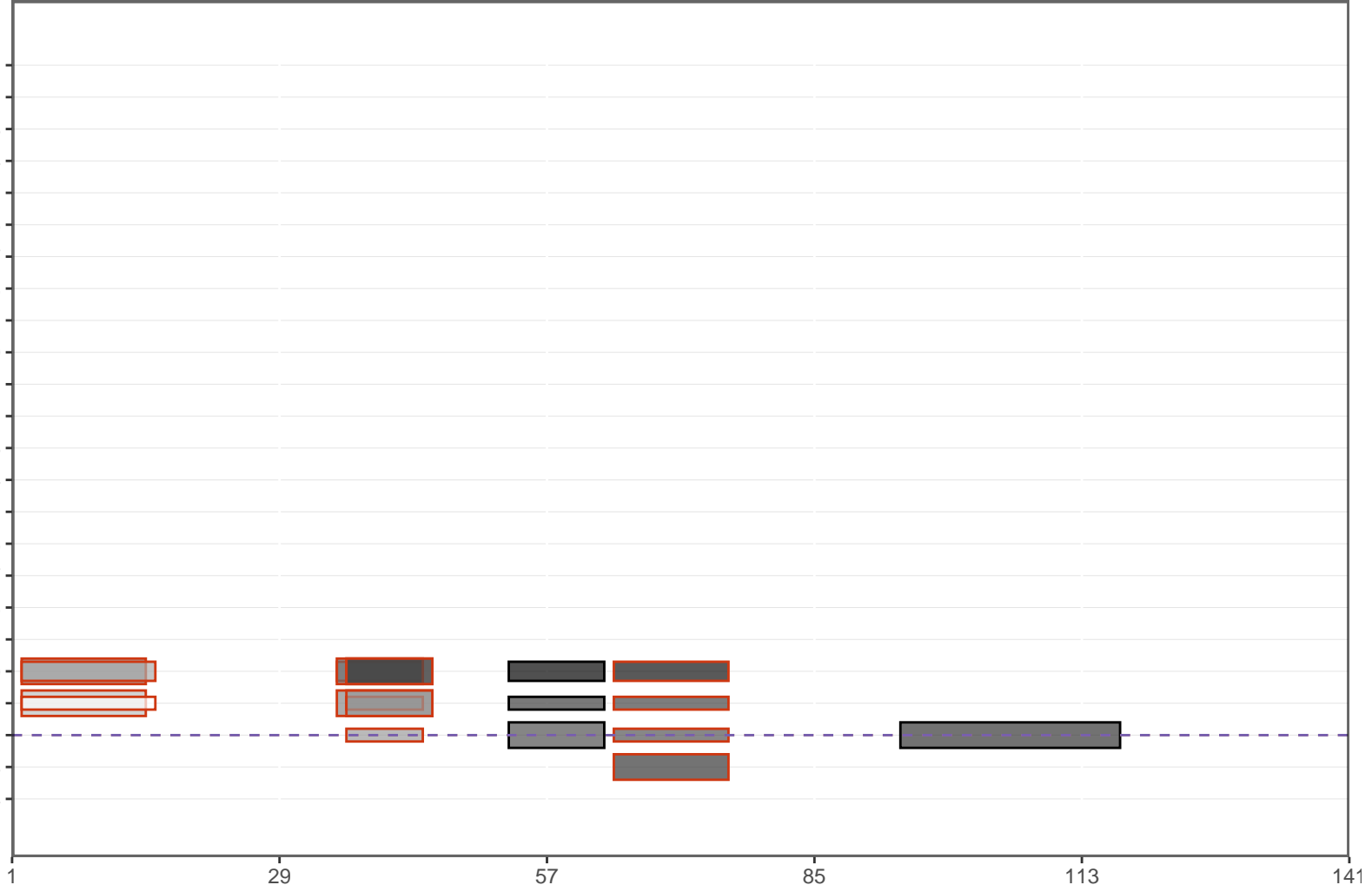
MW indication



Molecular weight



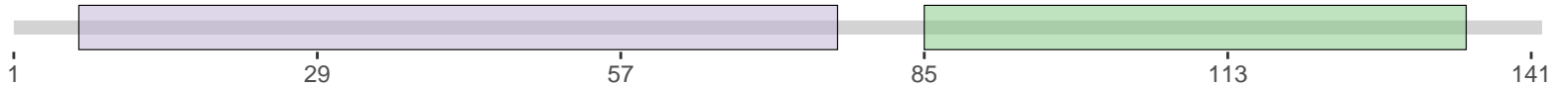
Gel Slice



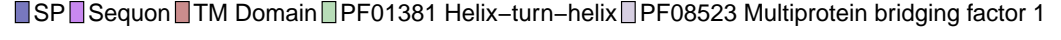
Protein length



Pfam domains



Pfam Description



Protein sequence:

STTLNTRKLDDETFENLAHQKVPTELKKAIMQARGDKKLTGAQLAQLNEKPKQIQEYESGKAIPNGGHSKLERALGAKLRGKK

NbL05g09160.1 peptide_methionine_sulfoxide_reductase_B1_chloroplastic-like [MW = 24.46 kDa]

No. of times detected



log(intensity)



Values from



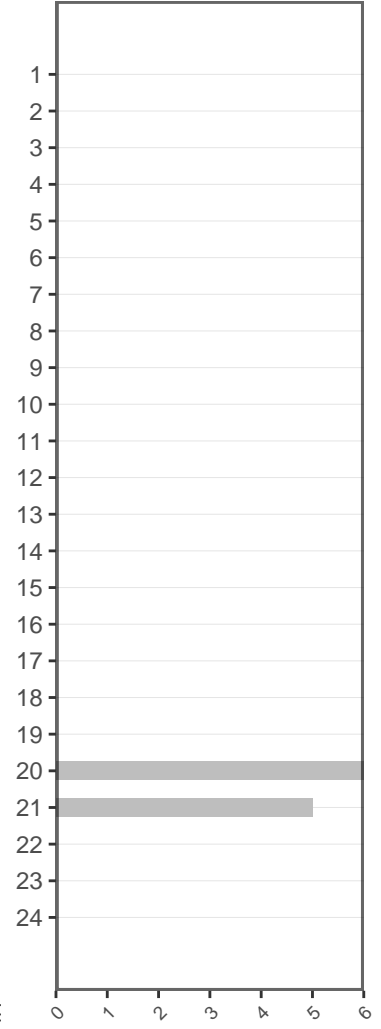
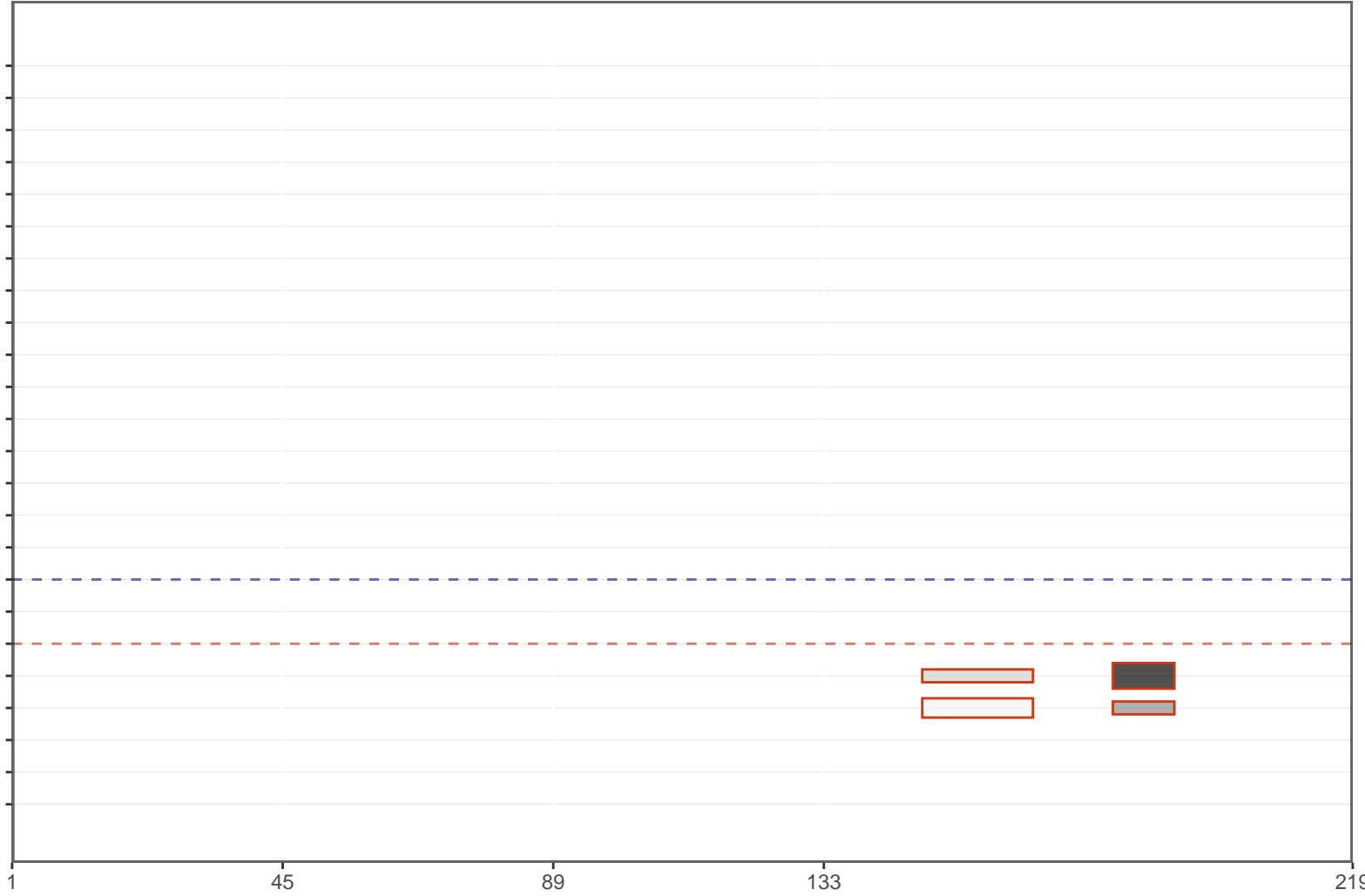
MW indication



Molecular weight



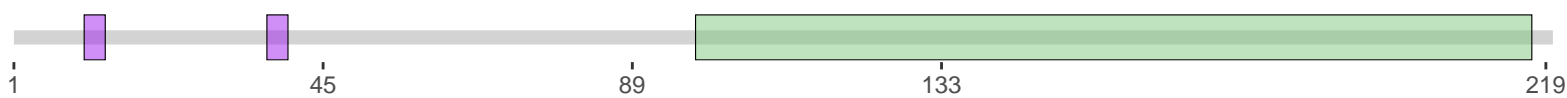
Gel Slice



Peptide counts over 4 repeats

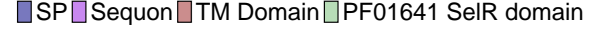


Protein length



Pfam domains

Pfam Description



Protein sequence:

EWKQLTNEQFYTRKQKGTERTAFTEYWNKIKGTYHGVCGDTPLFE66TKFD66GMWPEYVQFVDMNVKSKMDSIFMPRQEVLGAVGDARLGHVFDGPPPTGKRYGINSAAALKLKP*

NbL05g09100.1 persulfide_dioxygenase_ETHE1_homolog_mitochondrial-like [MW = 32.71 kDa]

No. of times detected



log(intensity)



Values from



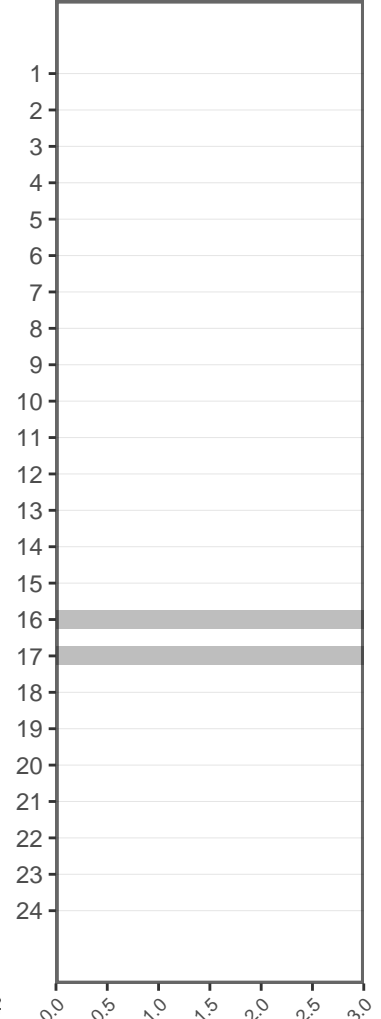
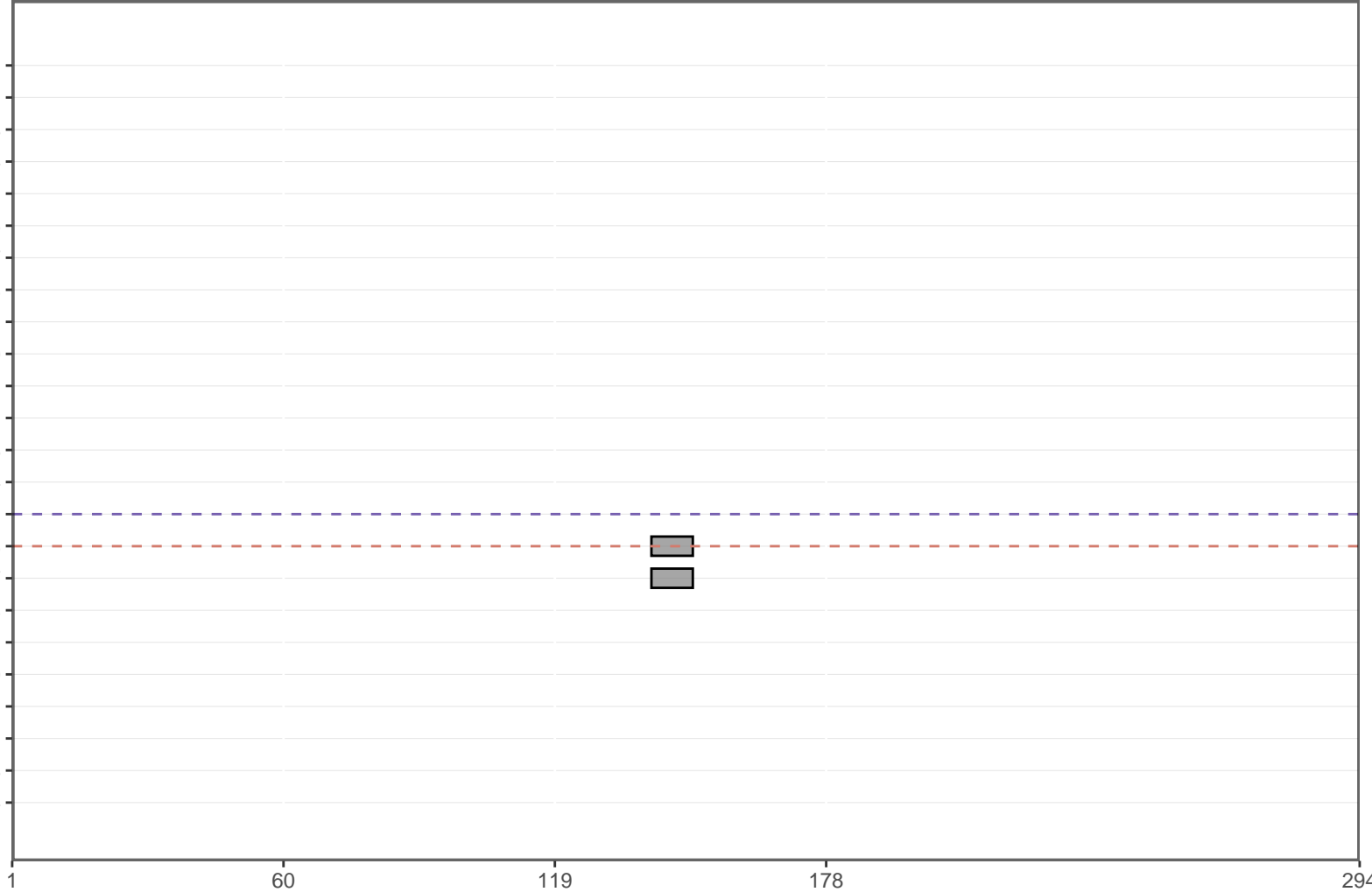
MW indication



Molecular weight



Gel Slice



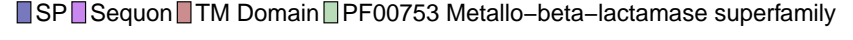
Protein length



Pfam domains



Pfam Description



Protein sequence:

IAKADLVPEPGDKHFQDFLEFRATPGHTLGGVTVYTGEGPNSQPPRMAFTGDALLRGGCRATDFGGSSSEKLYDEVYGGIFLPKDTLVVPAHDYKGFVSTVGEEMQYHNRLLSKDKETFKNMGNLNLSEYFKMMDVAVPRNMVCGLGQETKSEAY

NbL05g08970.1 heme-binding_protein_2-like [MW - SP = 23.45 kDa]

No. of times detected



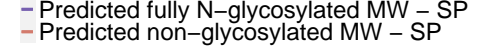
log(intensity)



Values from



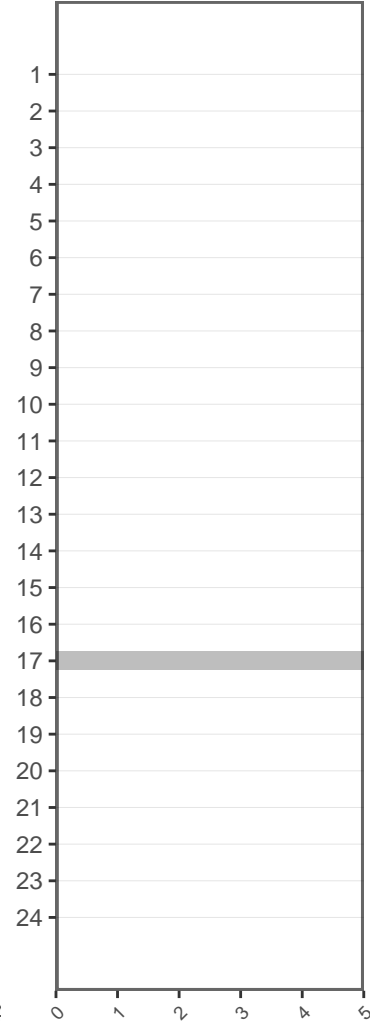
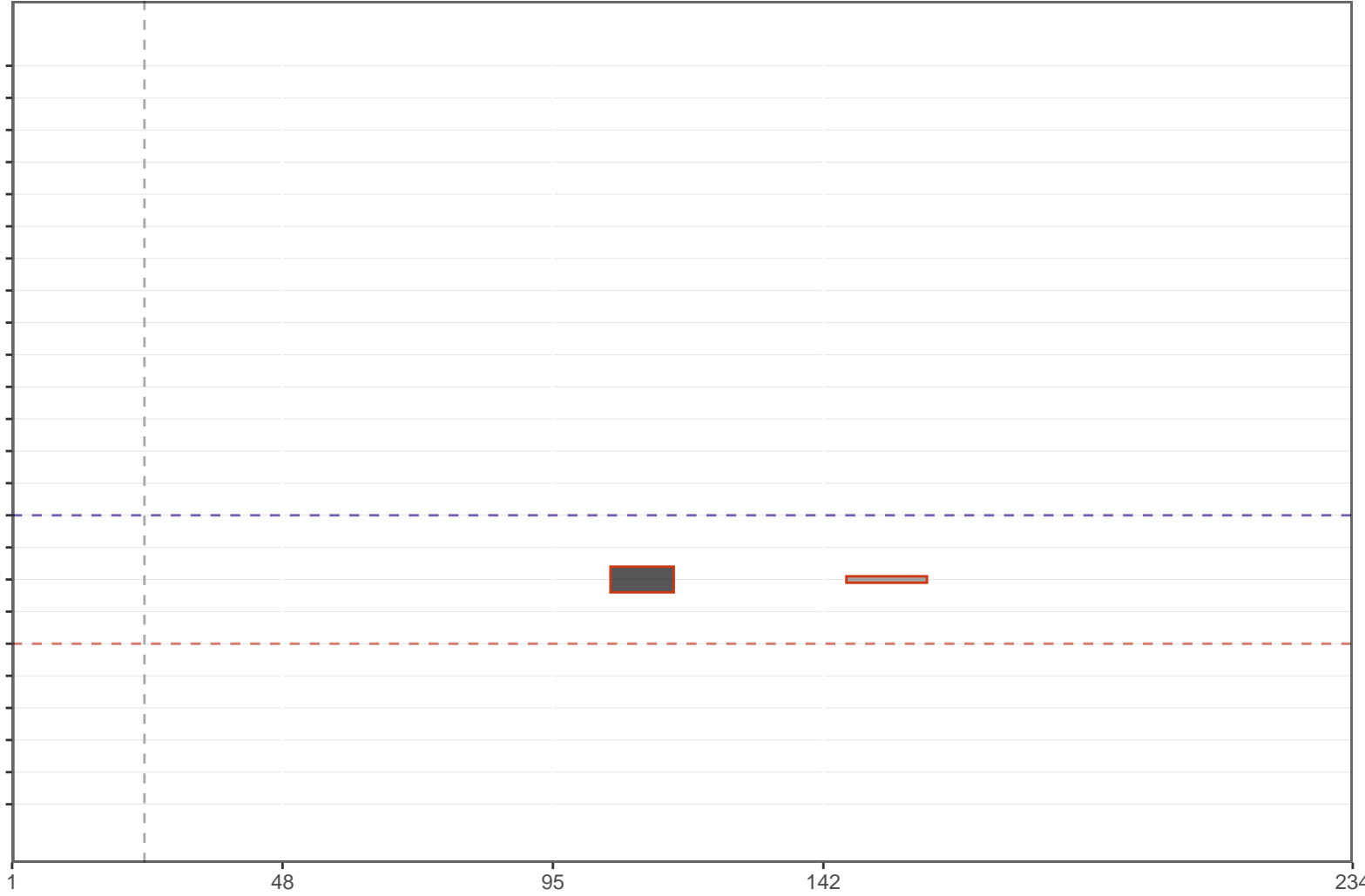
MW indication



Molecular weight

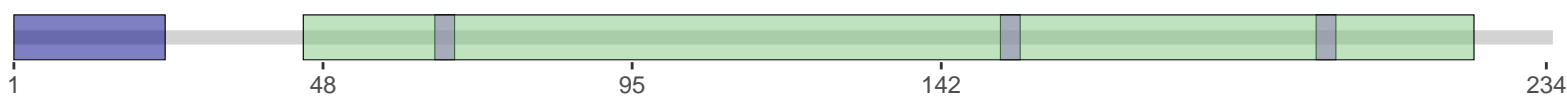


Gel Slice



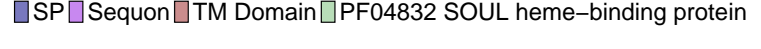
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EMTAPVITQVKPSDGFDCASFSVFSYPRKKNPNPPAKGLHVGHWNTYVWRQDFGVADVDWAKEAAALASIAIDTKWAAWVEKSHAADNTMTYVAGYNSPFKDRVNEWFTFDLQKASAI

NbL05g08850.1 thiamine_thiazole_synthase_chloroplastic [MW = 38.06 kDa]

No. of times detected



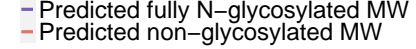
log(intensity)



Values from



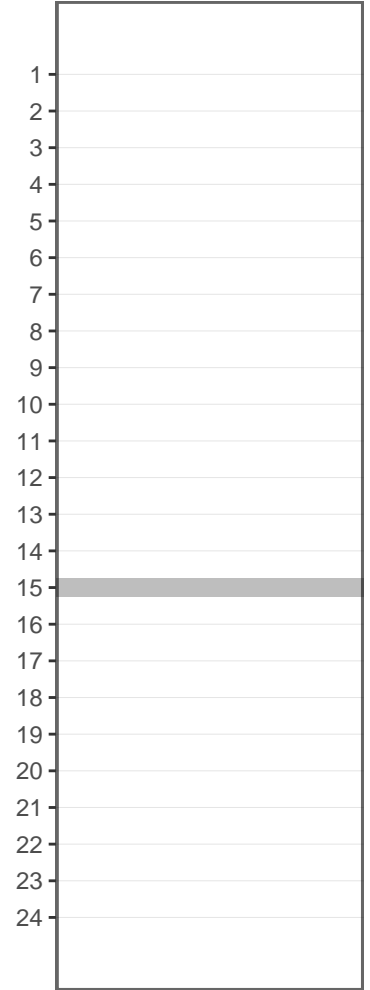
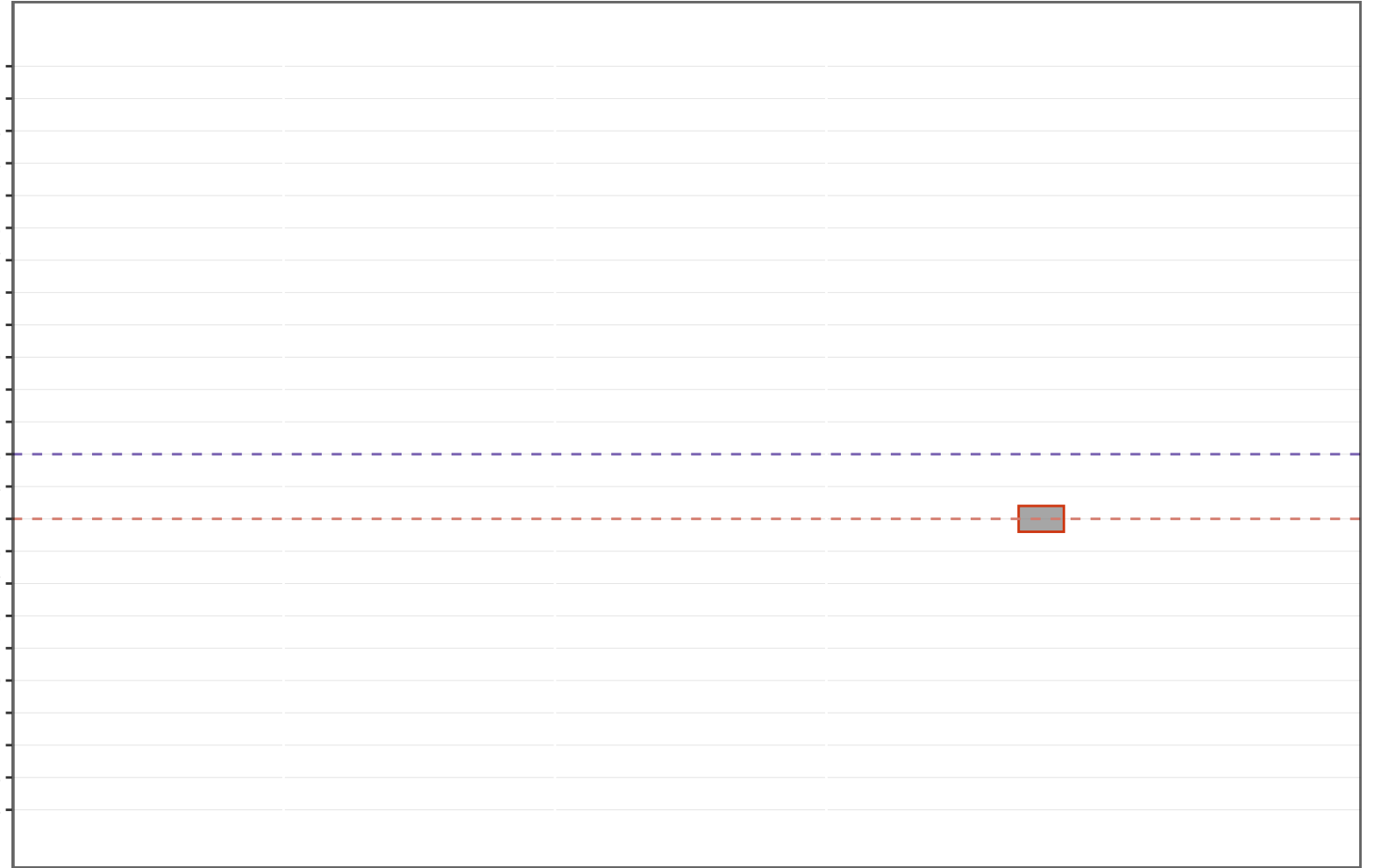
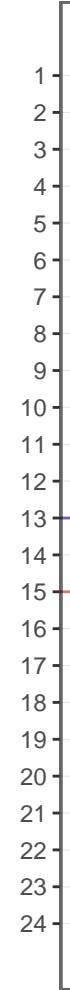
MW indication



Molecular weight



Gel Slice

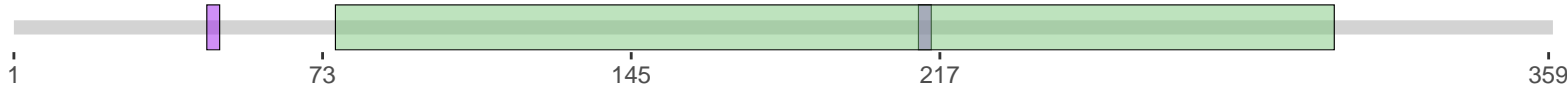


Protein length

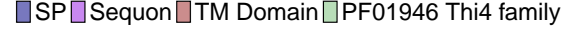


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VKIQHAAFTSTMSKLLARPNVKLFNAWATEDLVKNGRIVGGVWTFNWSLVSGNHDTGSGMDPNVMEAKRVVSSCGHIDGPMGATGKKRLKIGIMNHVPGMKALDINAEDAVRLTRREVVPSMIVTGMVEAIEDGAPRMGPTFGAMMISGQKAAHLALRALGLPINALDGTAESTHPELILAAADNAETADA

NbL05g08840.1 pectinesterase_2.1-like [MW = 61.88 kDa]

No. of times detected



log(intensity)



Values from



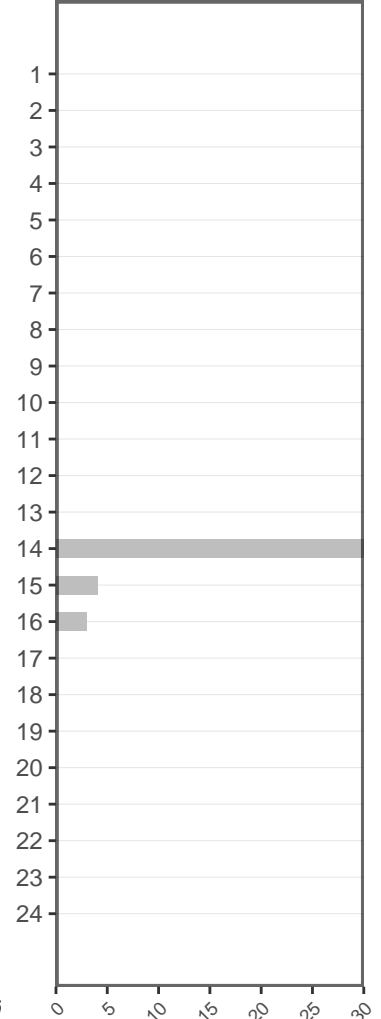
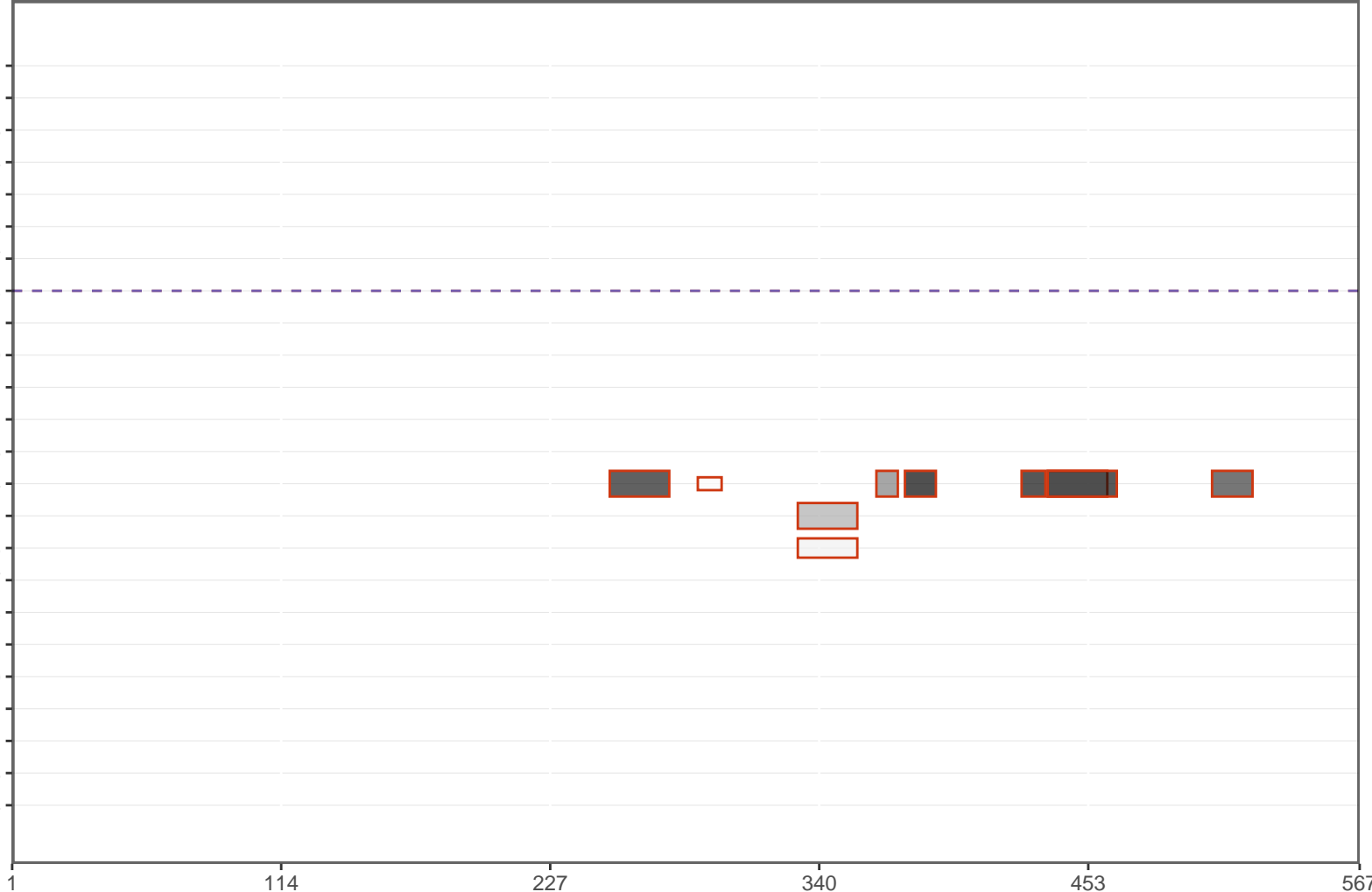
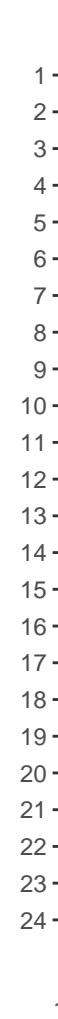
MW indication



Molecular weight

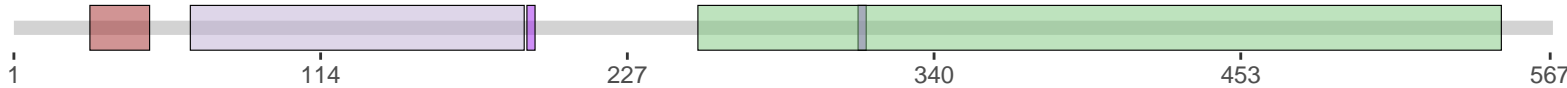


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

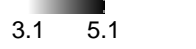
FDKSKTRYVYVYKGGYKKEVEVTKKKMNLMIYVGGDGMNSTFTGSLNVDGSGFTFRSATLAAVGGGFLGDICGNTAGPEKHQAWALRVGADLGVNRRGRDAYGDTLVVHSLRQFYRDEYVYTGTVDFIFGNAVVLKGDQVLRPKPKQKGNQNMVYTAGGRDTPNAGTGTGHLGDIASDLEFPKSEYKTYLGRPKVEYGRVTVVMSYLGDDIDPAGWSEWGGDFALKTLVYGEVMNNGPGAGTSKRVKWPQGHVHTEAAEARPFTVAELIQQGGBWLSGTVTFVEGLDE*

NbL05g08740.1 probable_protein_phosphatase_2C_55 [MW = 40.07 kDa]

No. of times detected



log(intensity)



Values from



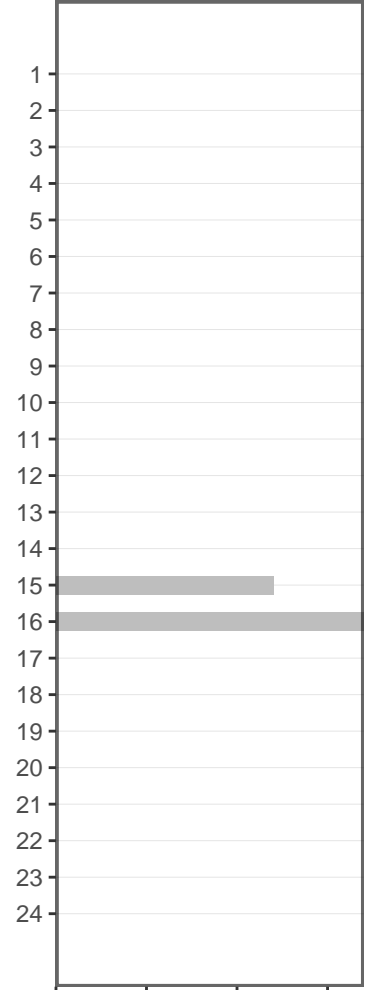
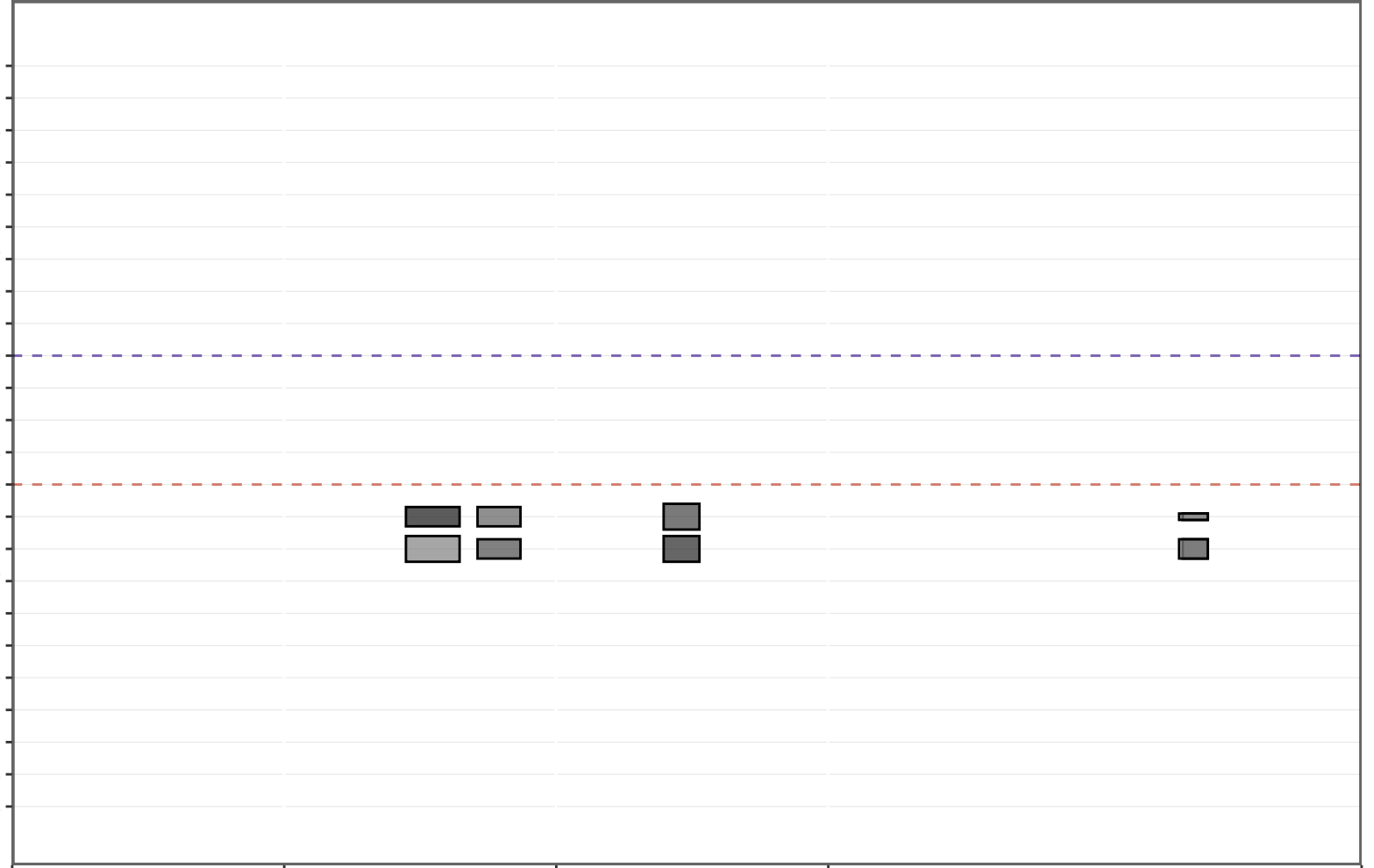
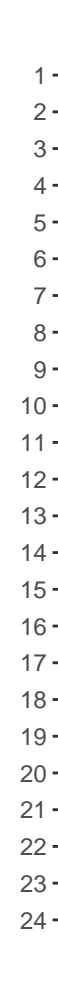
MW indication



Molecular weight



Gel Slice

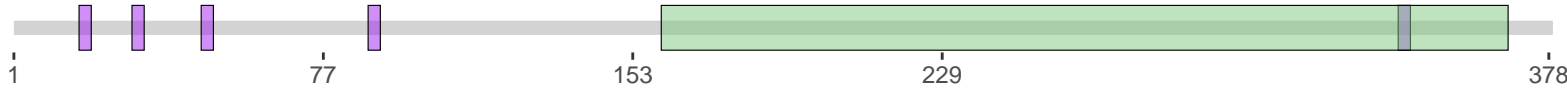


Peptide counts over 4 repeats

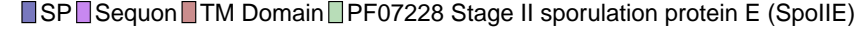
Protein length



Pfam domains



Pfam Description



Protein sequence:

GIDAGLYARELMSNLAAREEPKGGIDRALDKAYMETKAKGSGTAGIATTEEGLYAVNLGDSGFMVIRHGVAAFKSPAGQHGFPYQLDGNNAAGDPSSEAMFKVAVAPGVDLJAGTDLDFNLYDEDKGVVAGSVEAGLGPQMTARRIAELAAGRRAKDPINSSFFSDGADGAGFEHHGGKLDRTVVVGVYIMNENS

NbL05g08670.1 DNA_polymerase_I_B_chloroplastic/mitochondrial-like [MW = 91.9 kDa]

No. of times detected



log(intensity)



Values from



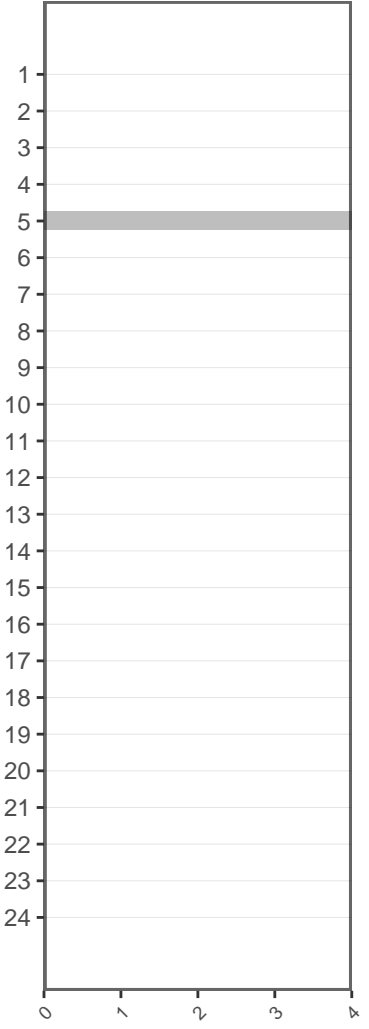
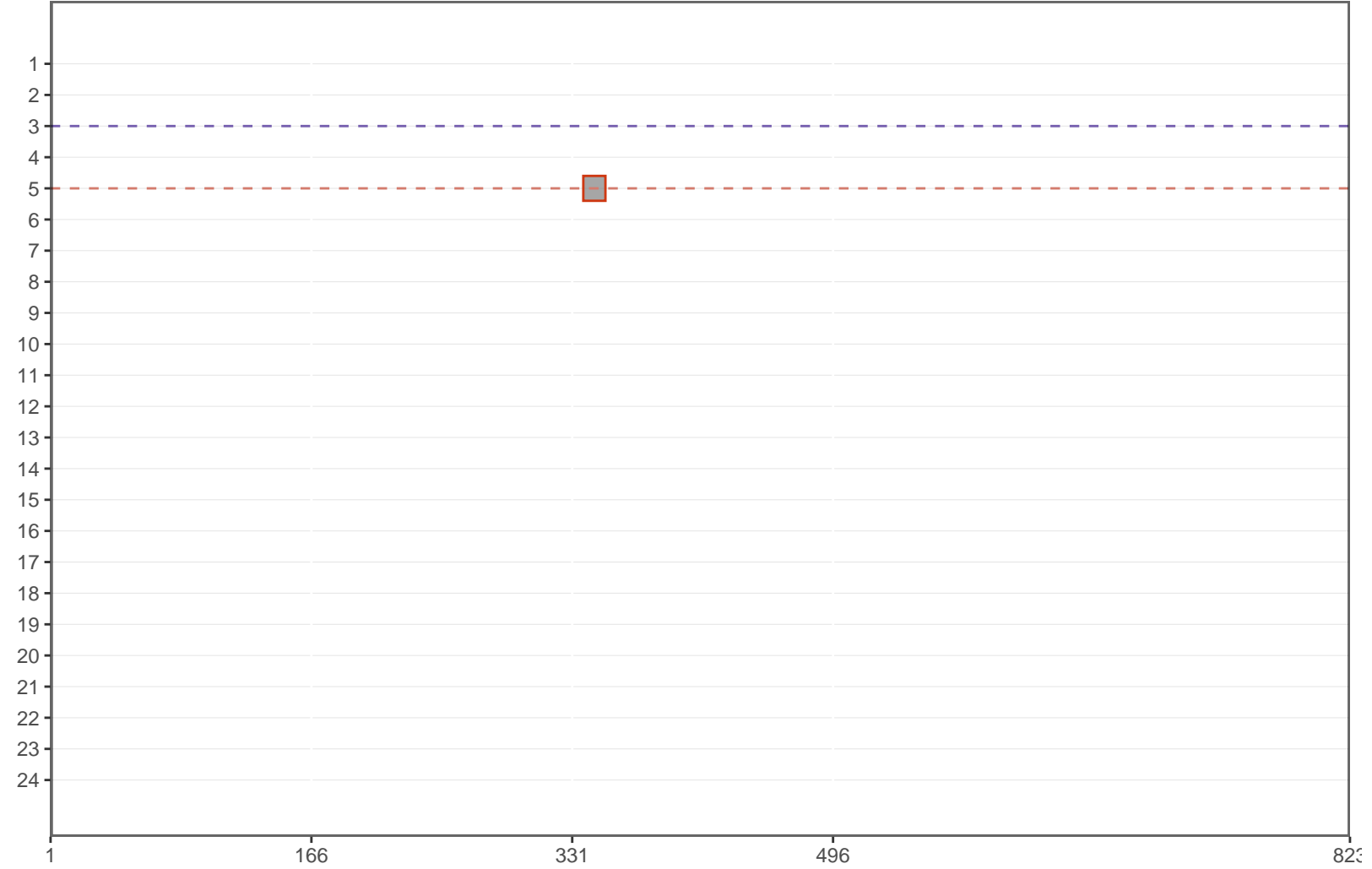
MW indication



Molecular weight



Gel Slice



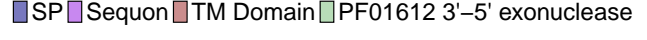
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

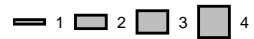


Protein sequence:

VKQQTPTVDTGDIICFSGSGPEADFGDGKSGHWVDLDDGGKLNLLVEFAFFGQSPSRKWWHNYSPDNHVIENYGFKVSFGHADTMHMARLWDSRRSTGGYSLEALTGGSTVMRDARPHVAERLHFGSEGLFGKISMKTFGRNKLKDKGTEGKVTVPISVEELQKTERELWCGYVLDGISTLMLVESLKNLKRKVVTFDGVKSGMVEFYEKYWRPFGLLWQMETEGVLVDRALAEIKVANSSEGGQVAANFRFRNWAQYKPDQKYMNVNGSDTLRQLRFGGIGNI

NbL05g08540.1 polyadenylate-binding_protein_RBP45 [MW = 45.29 kDa]

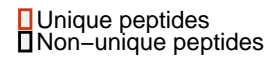
No. of times detected



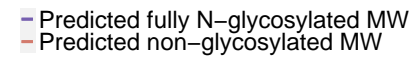
log(intensity)



Values from



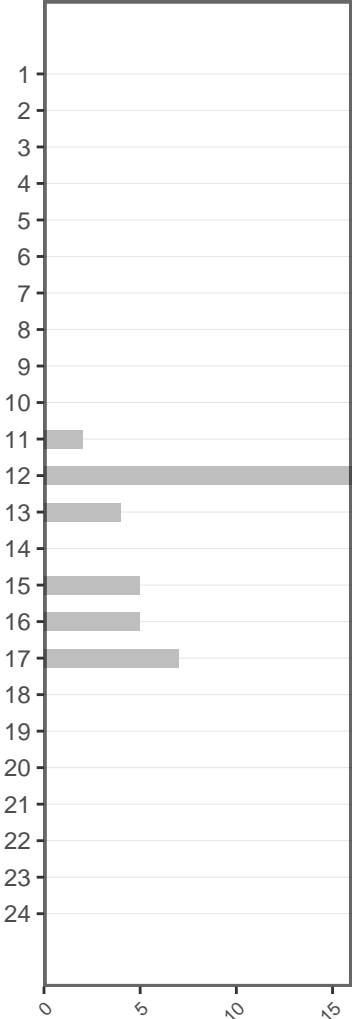
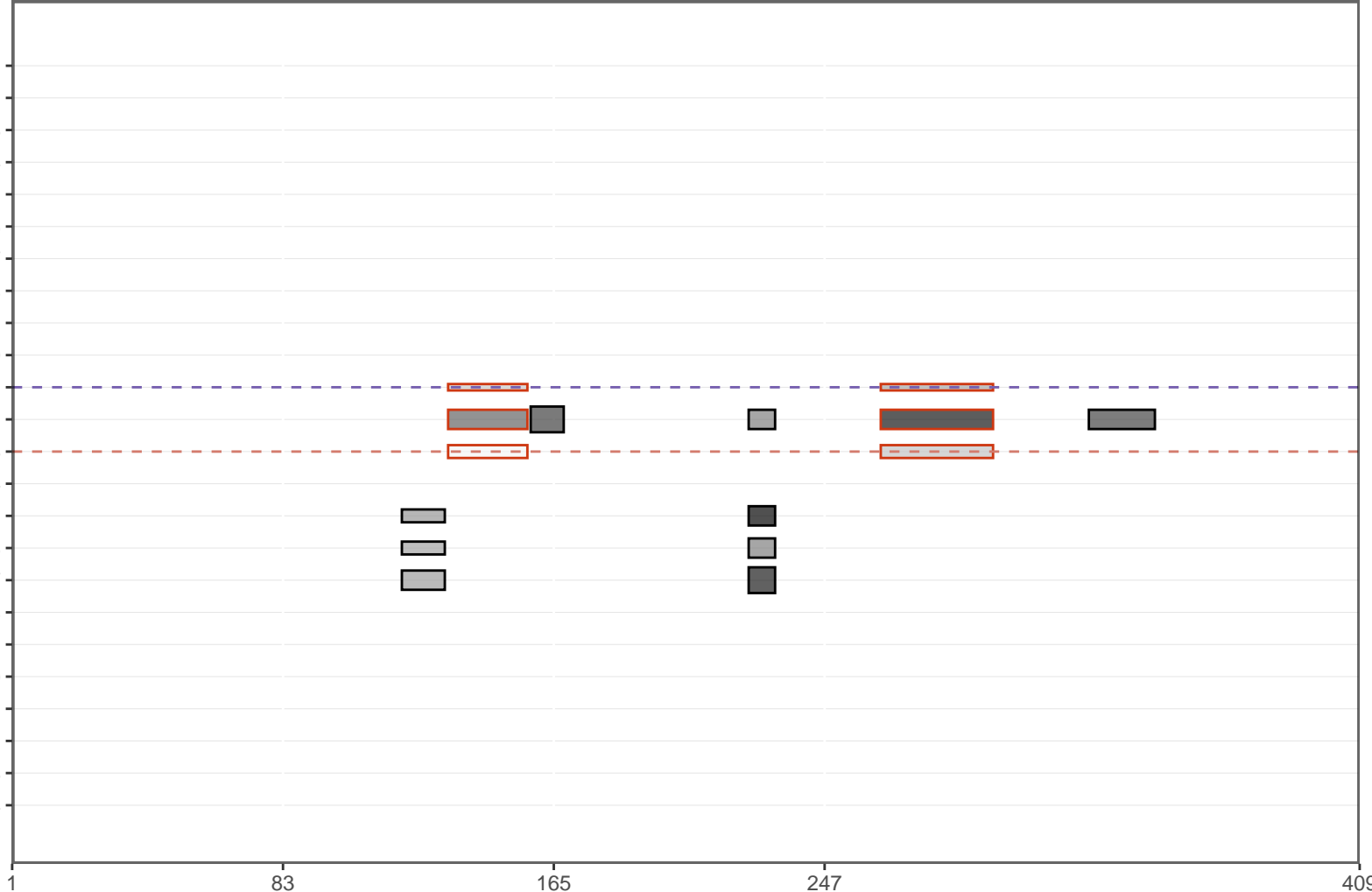
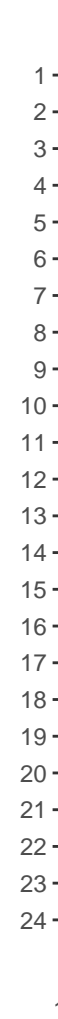
MW indication



Molecular weight



Gel Slice

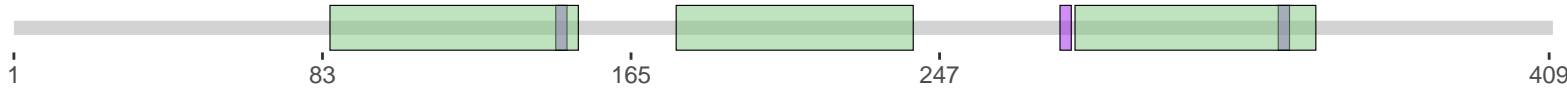


Protein length

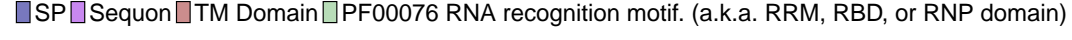


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ILQETFKSYVSSVYRGAQVTDRIYGRKGGYGFVKFADESEGLRAMTEFMNGLGSTRPMRIGRANAKKPVGTPQKVTYQNPQATGGESDPNNTTFVGGLDPTVAEEHLRQVFSPIYDELVHWVAGKRCDFVDFGTRASAEQALSELNGTQLGGQSRILSWGRSPSKQTDGTDQWGGGGGAAYGYGGGGYEAQYAPPPQDPNMYGNYGYPYTYNGGPGQ*

NbL05g08490.1 ubiquitin_thioesterase_OTU1 [MW = 23.32 kDa]

No. of times detected



log(intensity)



Values from



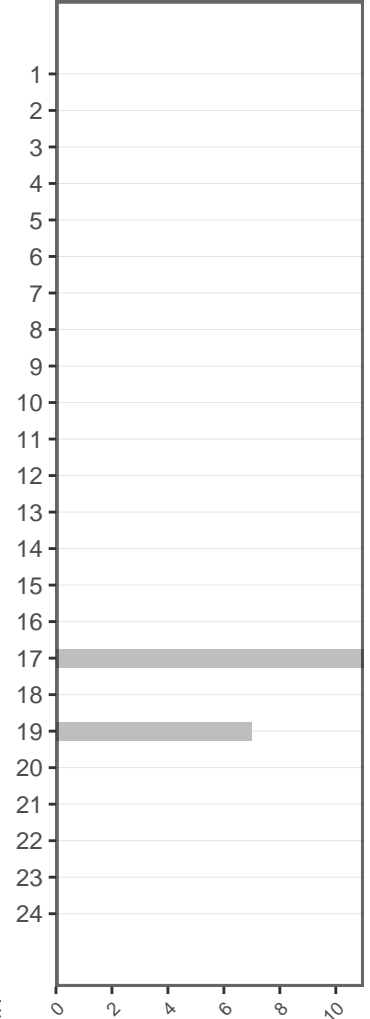
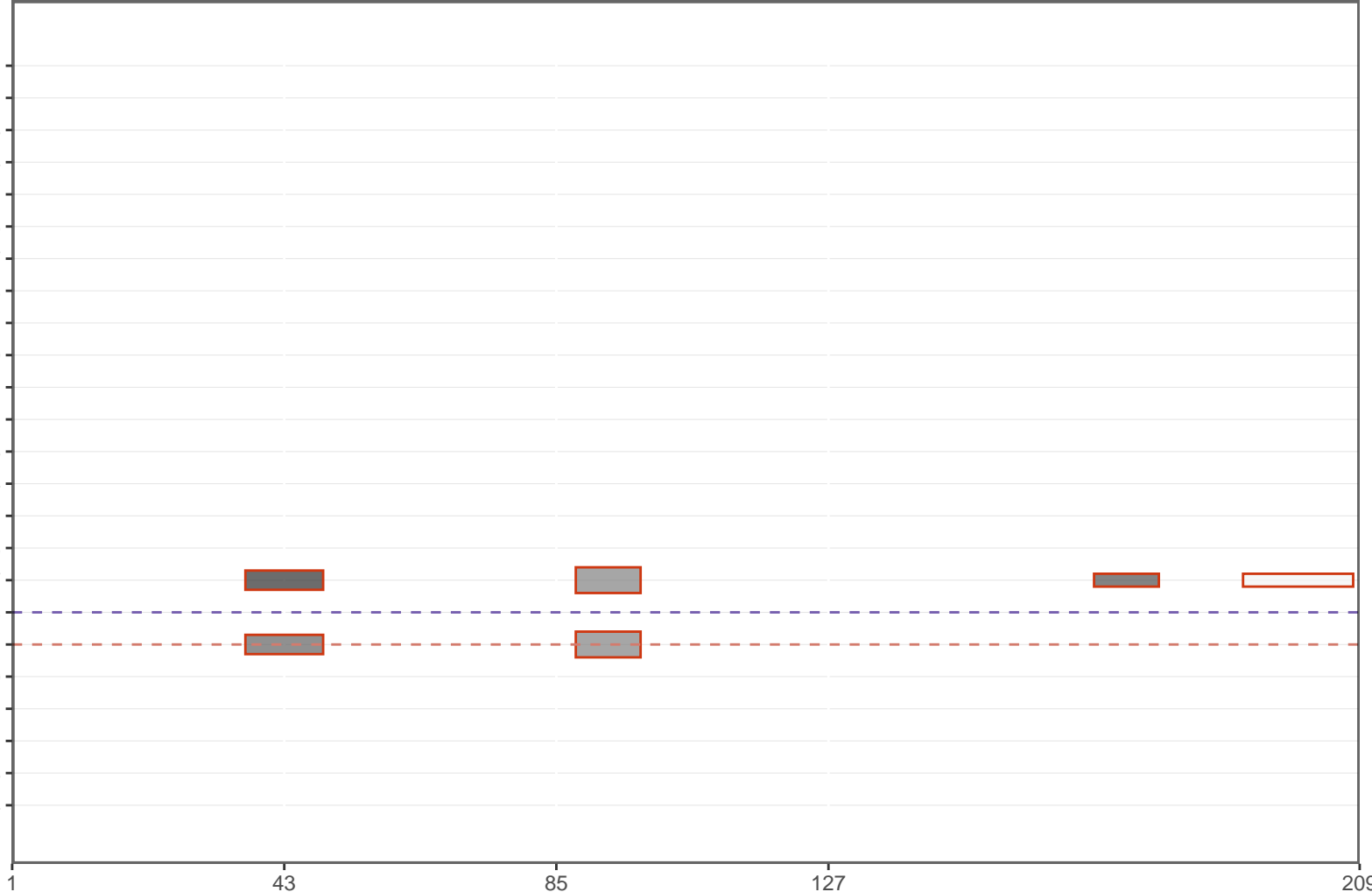
MW indication



Molecular weight

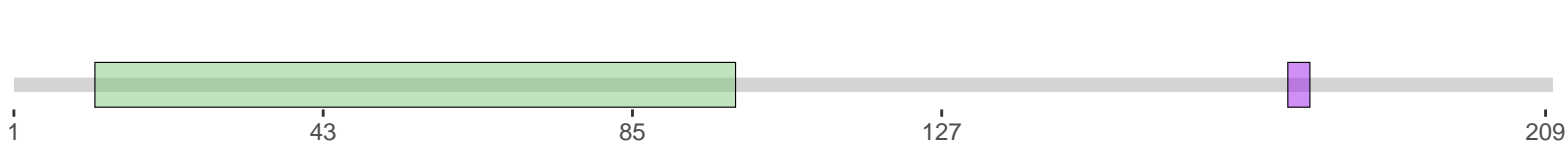


Gel Slice



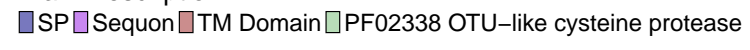
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DIQTRCDLYGQGNKNGERVMILYDGLHYDALAMSPAGEAPEEFDGTFITVQRDGTVGPALRLALDLVKEGQKRKRYTDTANFTLRGGVGGVGGVGGKEAVEHAQATGHVNFGEFYK

NbL05g08430.1 aconitate_hydratase_cytoplasmic-like [MW = 51.01 kDa]

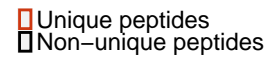
No. of times detected



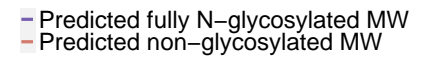
log(intensity)



Values from



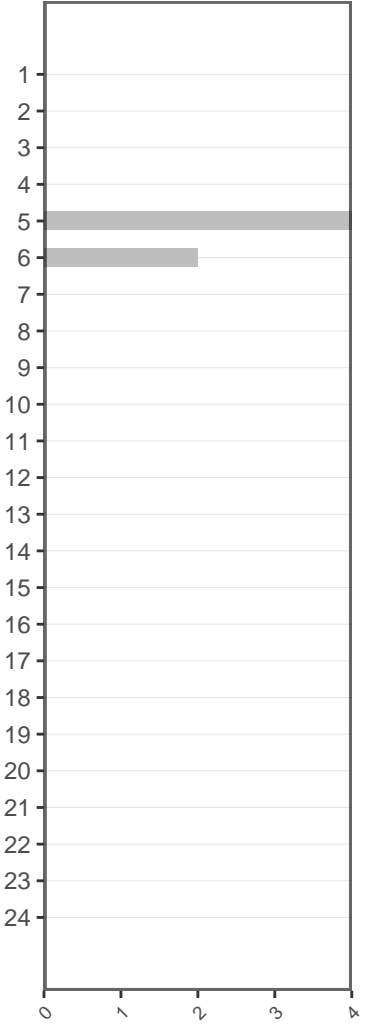
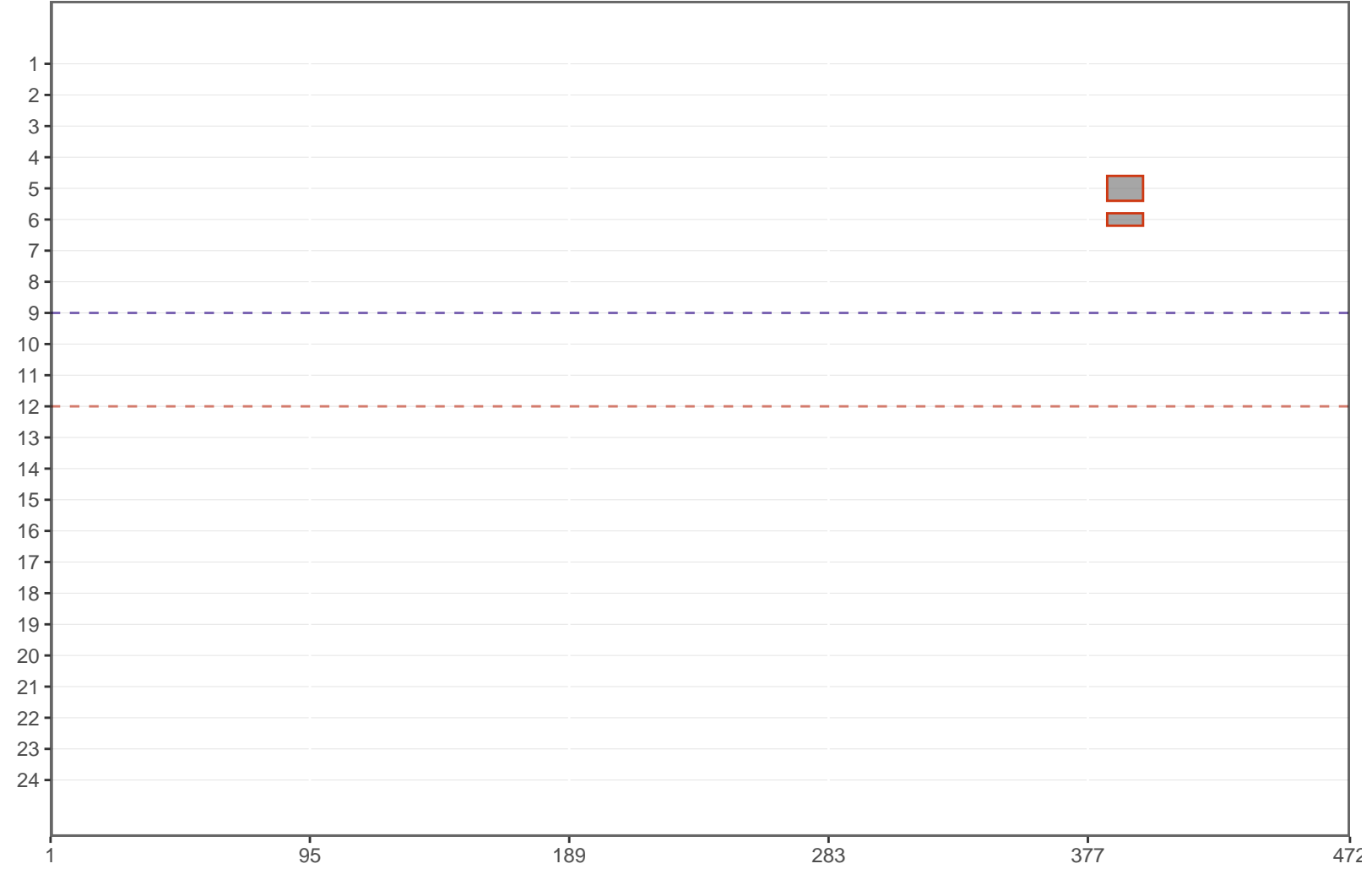
MW indication



Molecular weight



Gel Slice

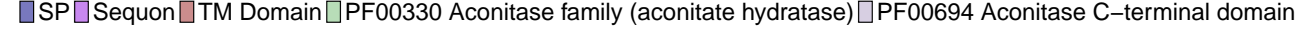


Protein length



Pfam domains

Pfam Description



Protein sequence:

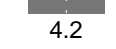
3PYPYKDMISVDPFGPHGKDAVGLLNFQDSBITDHSFMSGSHKDSPPAMVLMERGVQRKDFNSYGSRRGNDVEMARGTFTANIRINKLLNGEVSPKTHIPSGEKLIVYDAMRYKSTGHDTHVAGAEVYSGSSSRDWAAKGPKMLLGVKVAIAKFERIHRNSLNVGMGHPLGFKPGEDAEALGLTGHERYTIDLQRIISGRPGDQLTVTFDSGKGFCTCLRFDFTEIELAVFDHGGILPVIRNLKQ*

NbL05g08410.1 mimitin_mitochondrial [MW = 21.49 kDa]

No. of times detected



log(intensity)



Values from



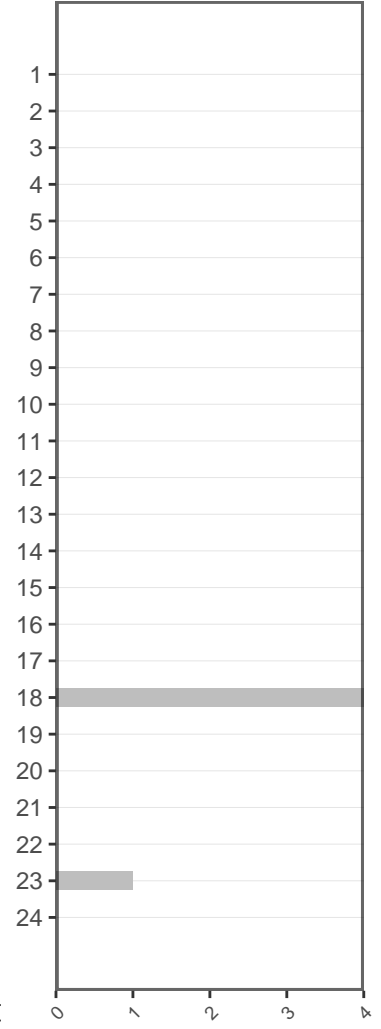
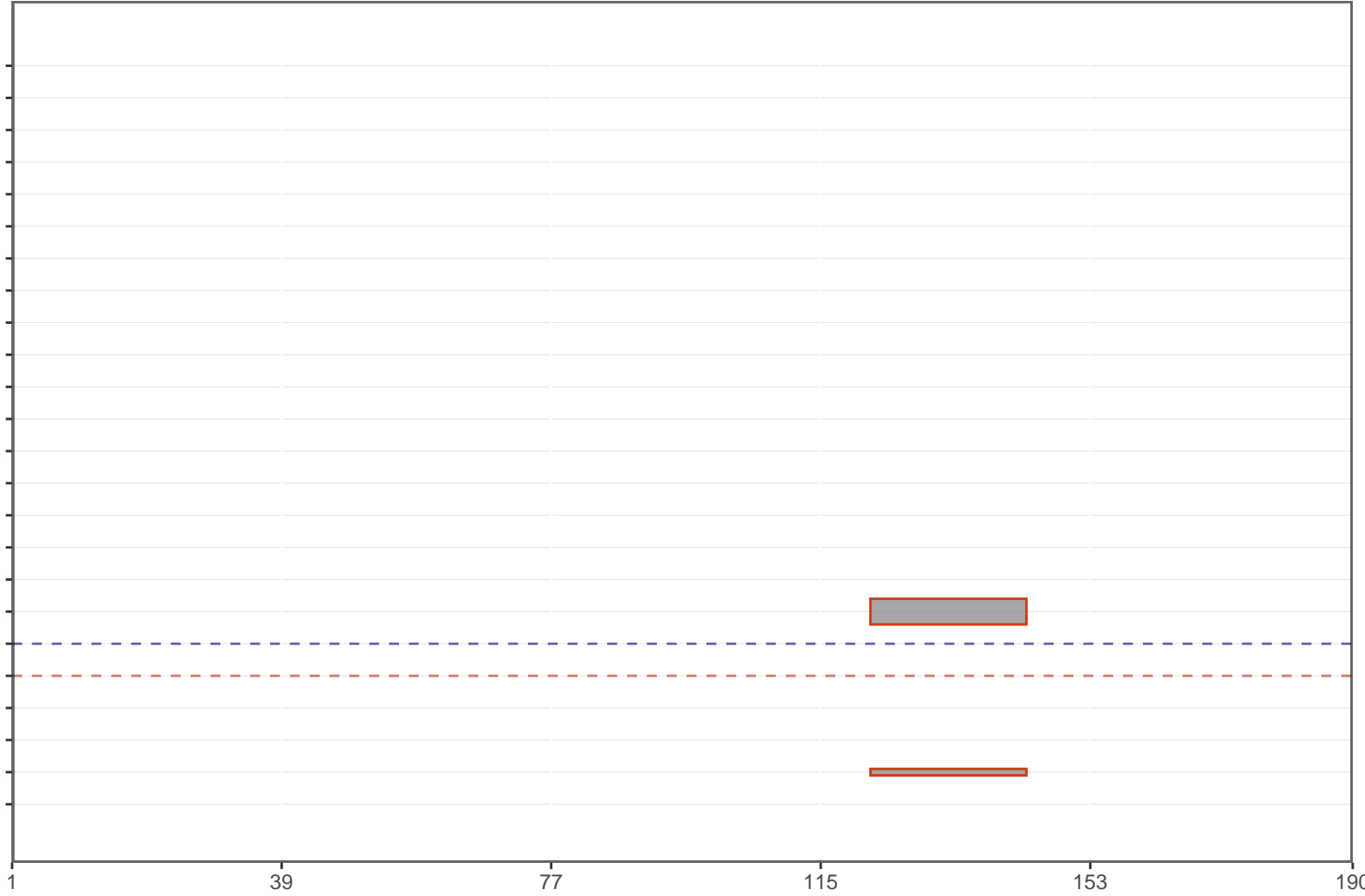
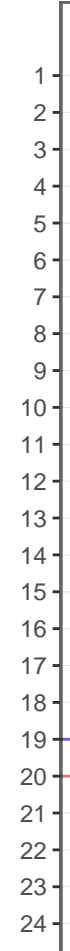
MW indication



Molecular weight

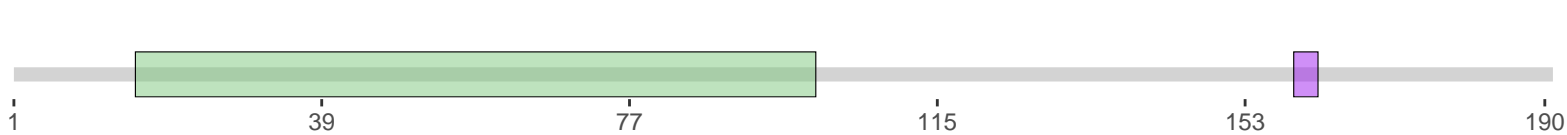


Gel Slice



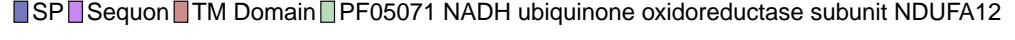
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

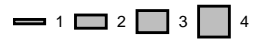


Protein sequence:

RRFVFLNARLRKKEEERKAKEGKNNKATGIGKADGPDLSKSFVGGFPDASEGDIPEASDTQKGVRRHARKETAEKNMRYLKGQPLSSEPTGSGESFRPDTWQPP*

NbL05g08130.1 nardilysin [MW = 118.64 kDa]

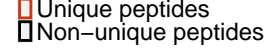
No. of times detected



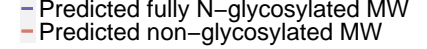
log(intensity)



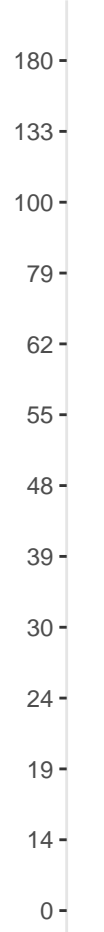
Values from



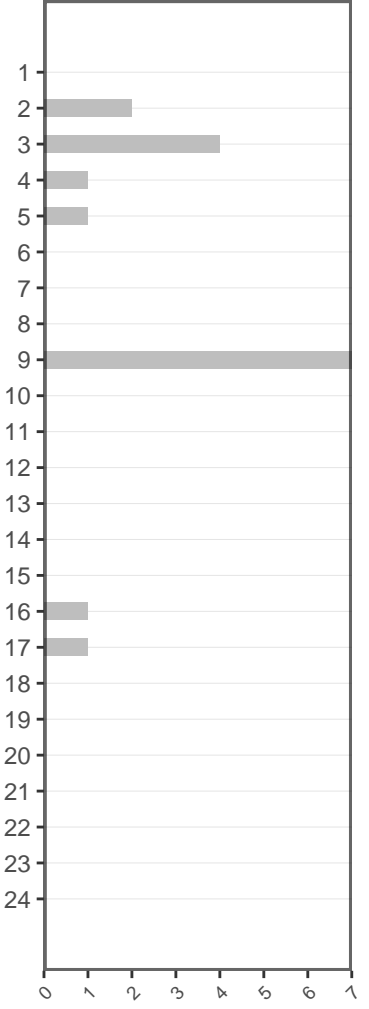
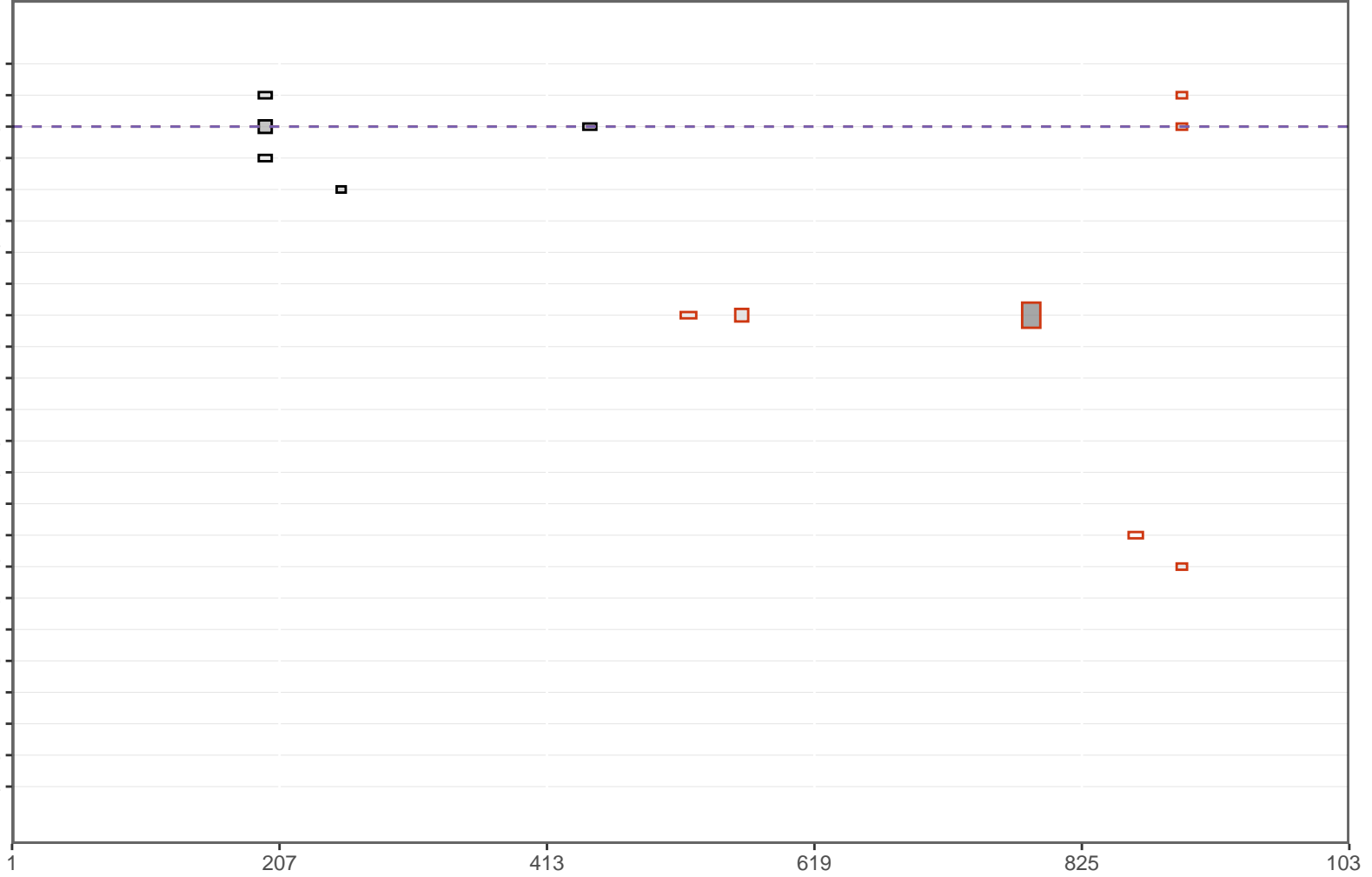
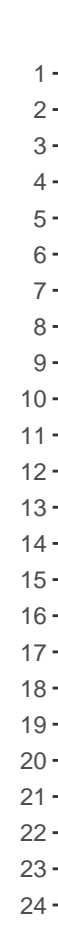
MW indication



Molecular weight



Gel Slice

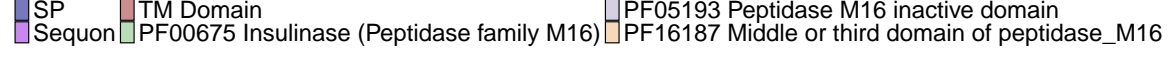


Protein length



Pfam domains

Pfam Description



Protein sequence:

DFRRFENMRDVTYKFGKEDDDGEPWFQSRVYVEEDPISLFEIWKDPEISVGLHLPKAKNEFIPDFSRRAEKVNDGSKNAKPRGILEEPLMKIWKYKDKTEKLPKPRANTYFRISLGRGGYGNKLNALLTELFHLLKDELNEIYQAGVAKLETSVLVLGDKLELKYVGFNDKLPVLLSKVLAATKISFLPRDDRFRVWIKEDMERTLKNNTMKPLNHSYLRLLGLVGGDFWVVEEKLLLLNDLTLAEKAFPELLSGVLEGLGHGNLLEEEALNSIFRNFSAQPLPSEMTHKEI

NbL05g07950.1 glucan_endo-13-beta-glucosidase_9 [MW - SP = 50.41 kDa]

No. of times detected



log(intensity)



Values from



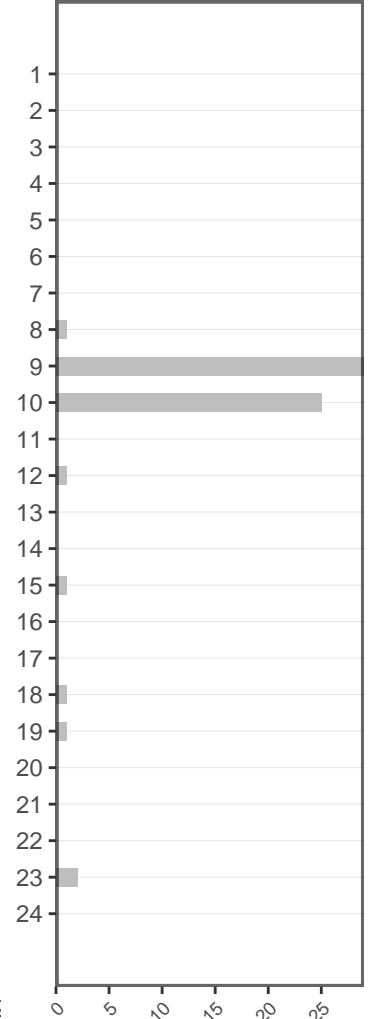
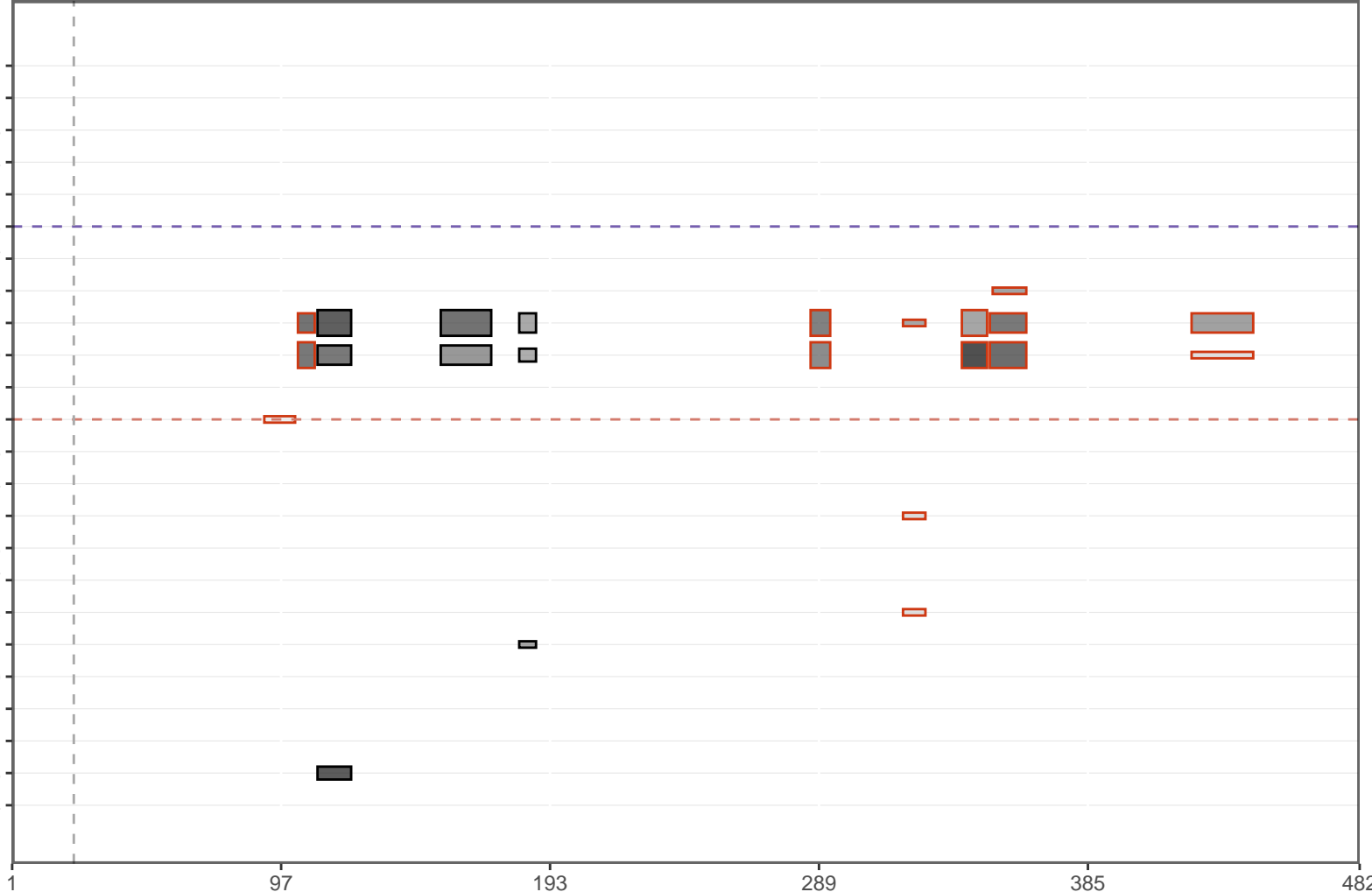
MW indication



Molecular weight



Gel Slice



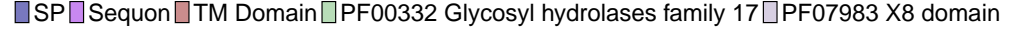
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RRITYKNSFDLSYDILVSALESAGSGDKMDIVIGIGWPTDGAASATSSNAGVFMKFLKLEHHSRREGTFLRPKEPIEAYLLELDEENRSIATGNFERYWGVTFDDGAAKYQLDLGGGSRKLVNMQNVGHLSKRWCVVNNKQNLNATTRALEAGSSADGSALEPGAGCFNLEWPGNLSVALNSVYGGQHDRADSGDFDGLGLFTTVDPEVGTGRFIVQLRTSSASFFISHWRITASTILWLWVGGGFGWT

NbL05g07930.1 40S_ribosomal_protein_S4-like [MW = 29.85 kDa]

No. of times detected



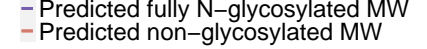
log(intensity)



Values from



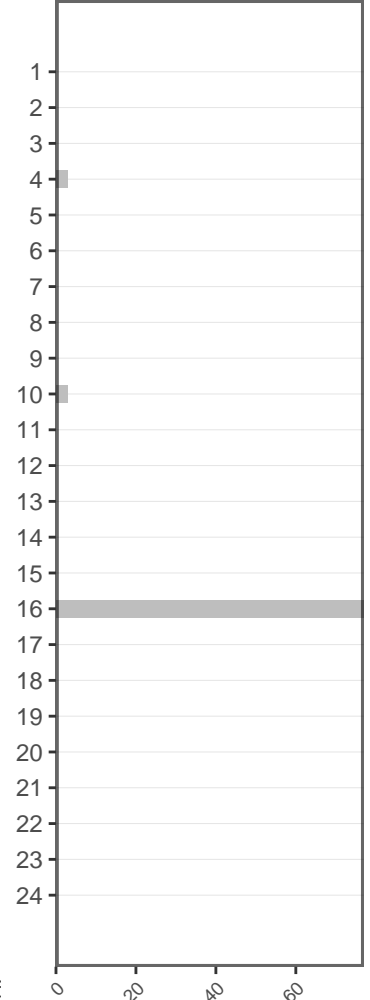
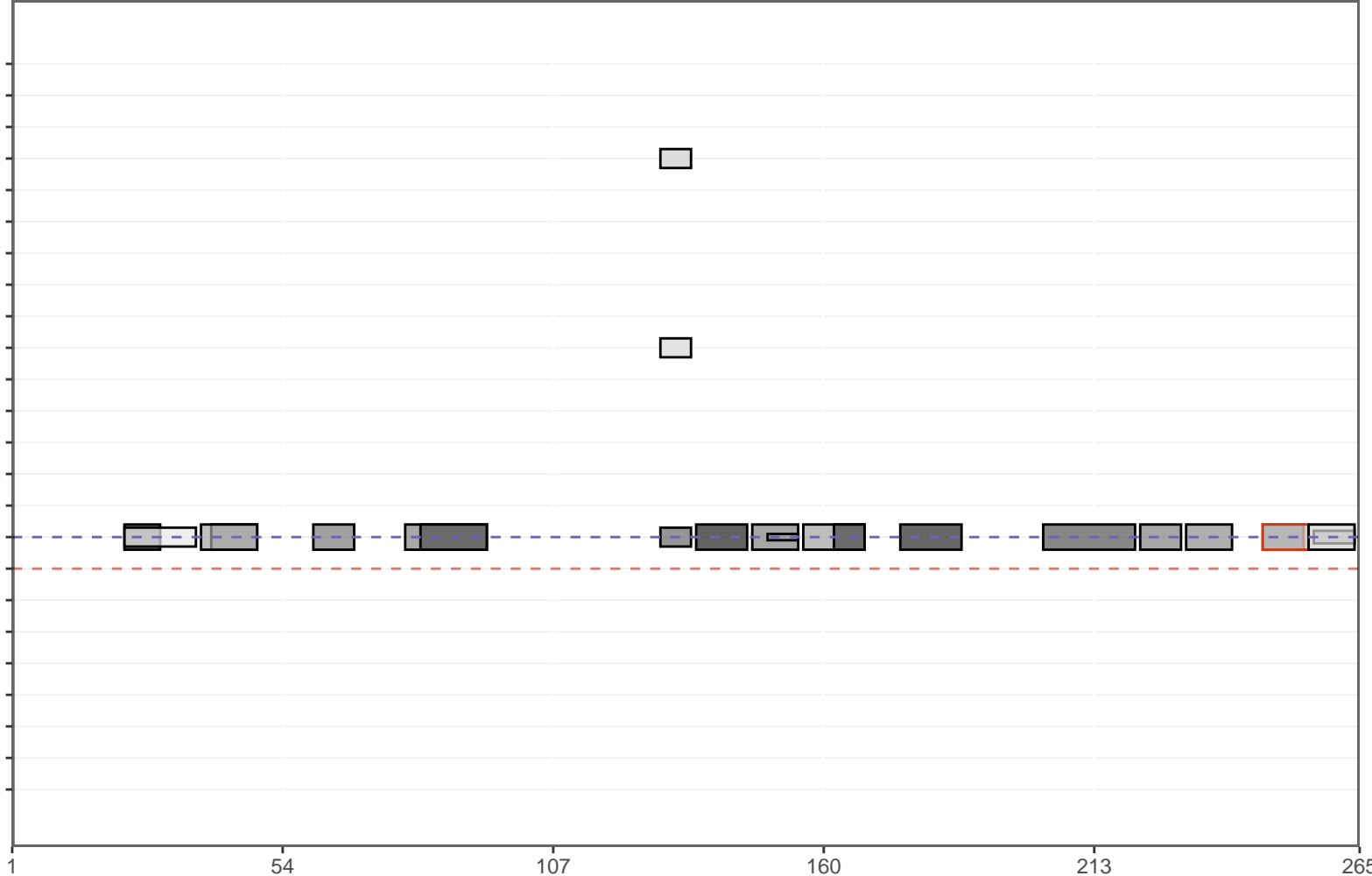
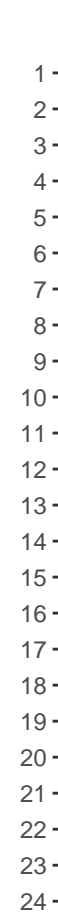
MW indication



Molecular weight

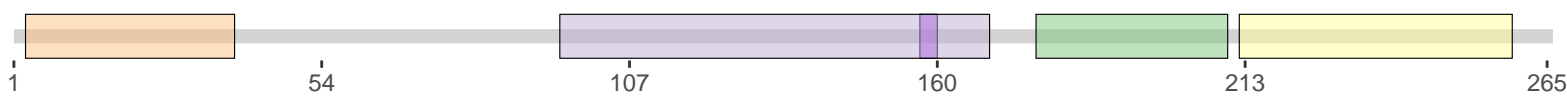


Gel Slice



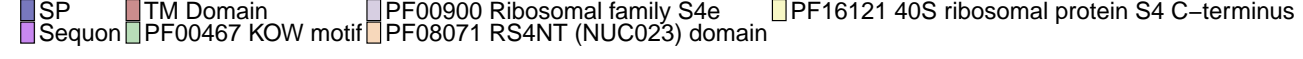
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

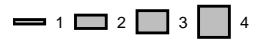


Protein sequence:

AKFKLCKVRSIQFGTGGIPYLNTYDGRTRRYPPLKANDTKLDELGNKVDKRFKFDVGNVAVMTGGRNRGRVGVKVRKREKHKGSFETVHGDALGHEFATRLGNVFTLGGKTKPWWSLPKGKGLKLSIEEAGKRLAAGSATA

NbL05g07750.1 alpha-glucan_phosphorylase_H_isozyme [MW = 100.46 kDa]

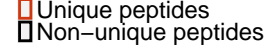
No. of times detected



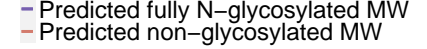
log(intensity)



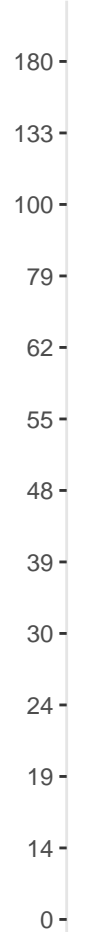
Values from



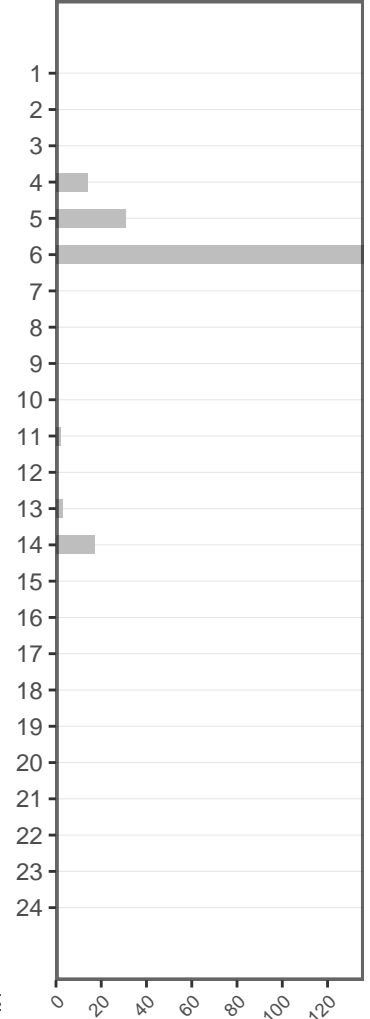
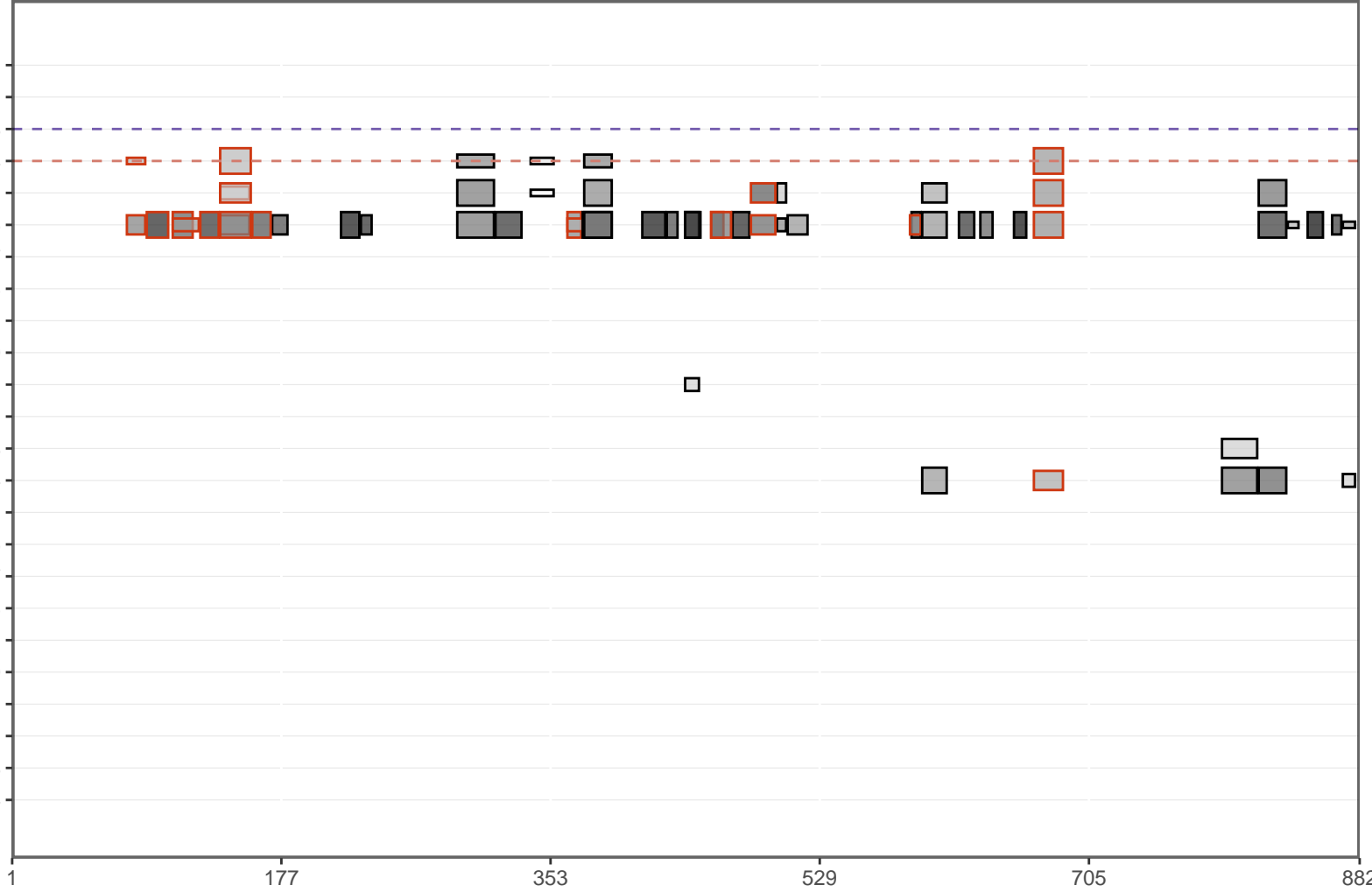
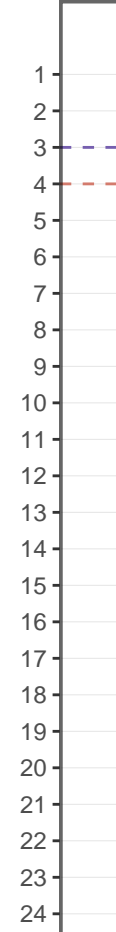
MW indication



Molecular weight

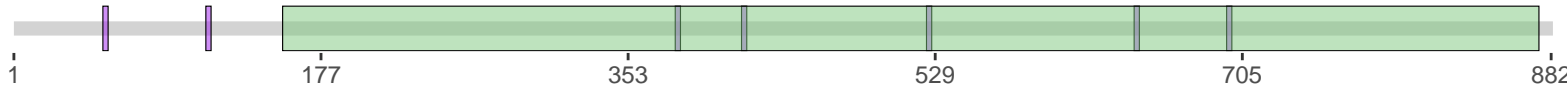


Gel Slice



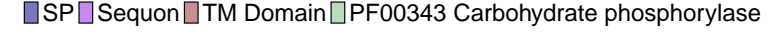
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EKWVSAVMVLLPRHMEIEIDRRFVAVKSERPDLNPKPSMRLDHNAGKPVVRMANLGVVSGHTVNGVAKLHSDLKAELFADVGVWPTKFNKNTGTPRRWVFCGTFPELSDITKWLKTDQWVTLNLELLANREFADNAELHAEVESAKMANKRRLAGVYLRVTGVSIDPDTLFDIGVWRHEYKRLNVLGVVYRKYKLEKEMSPQERNNTTPTVAMGGKAFATYNAKRKVLTDVGDVNSDPRDNNVYKWFVFNVNVVGAEMLPGSELQIHSTAGMEAS

NbL05g07740.1 neutral_ceramidase-like [MW - SP = 82.2 kDa]

No. of times detected



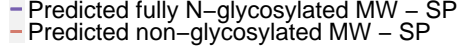
log(intensity)



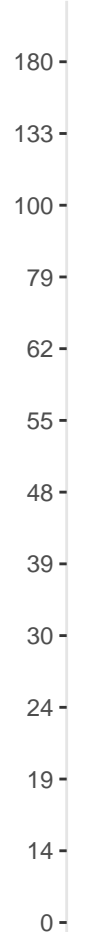
Values from



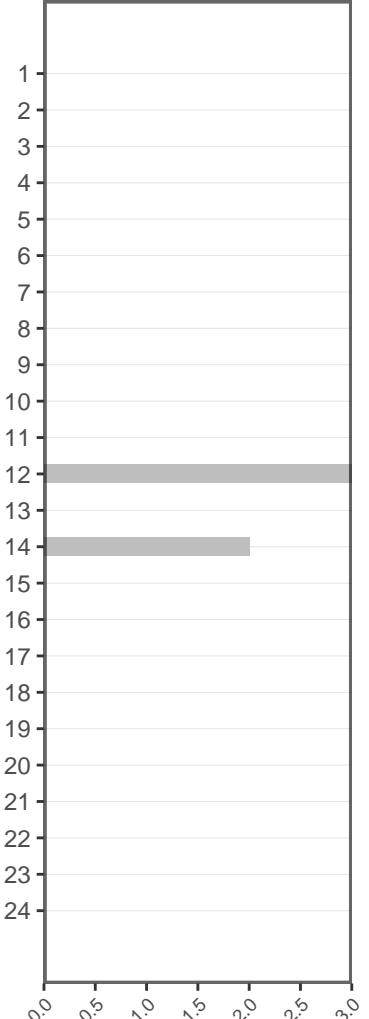
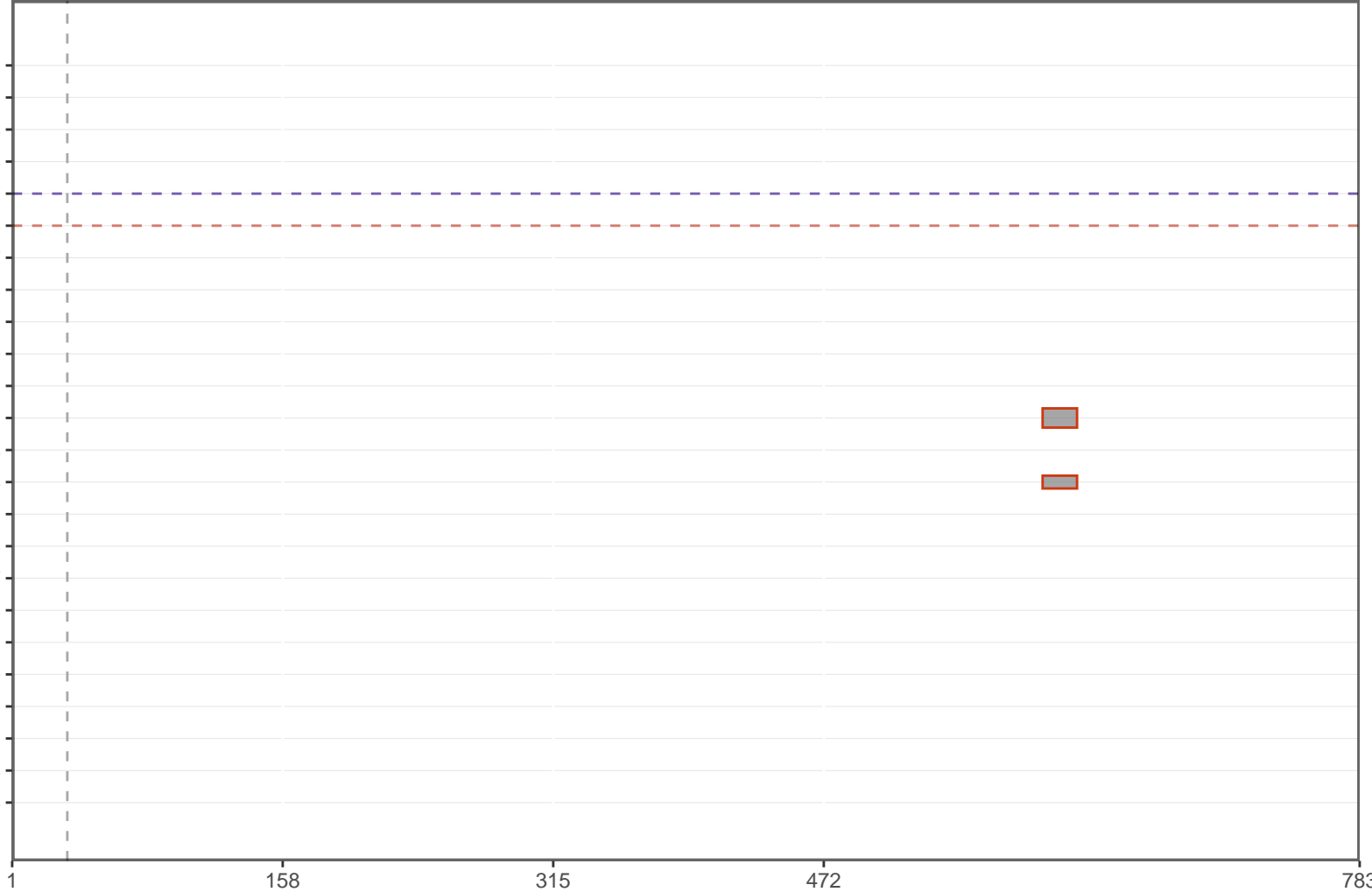
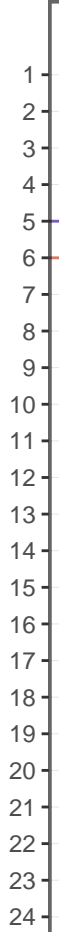
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

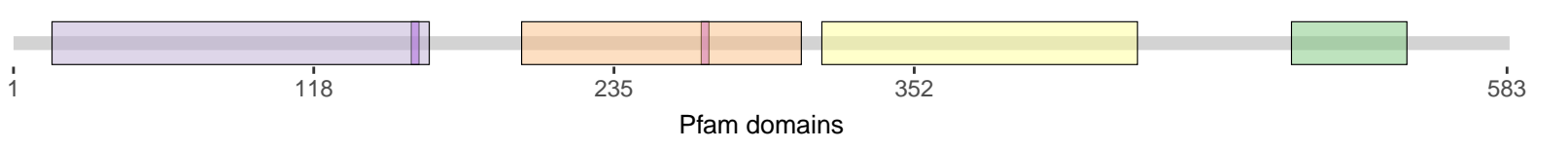
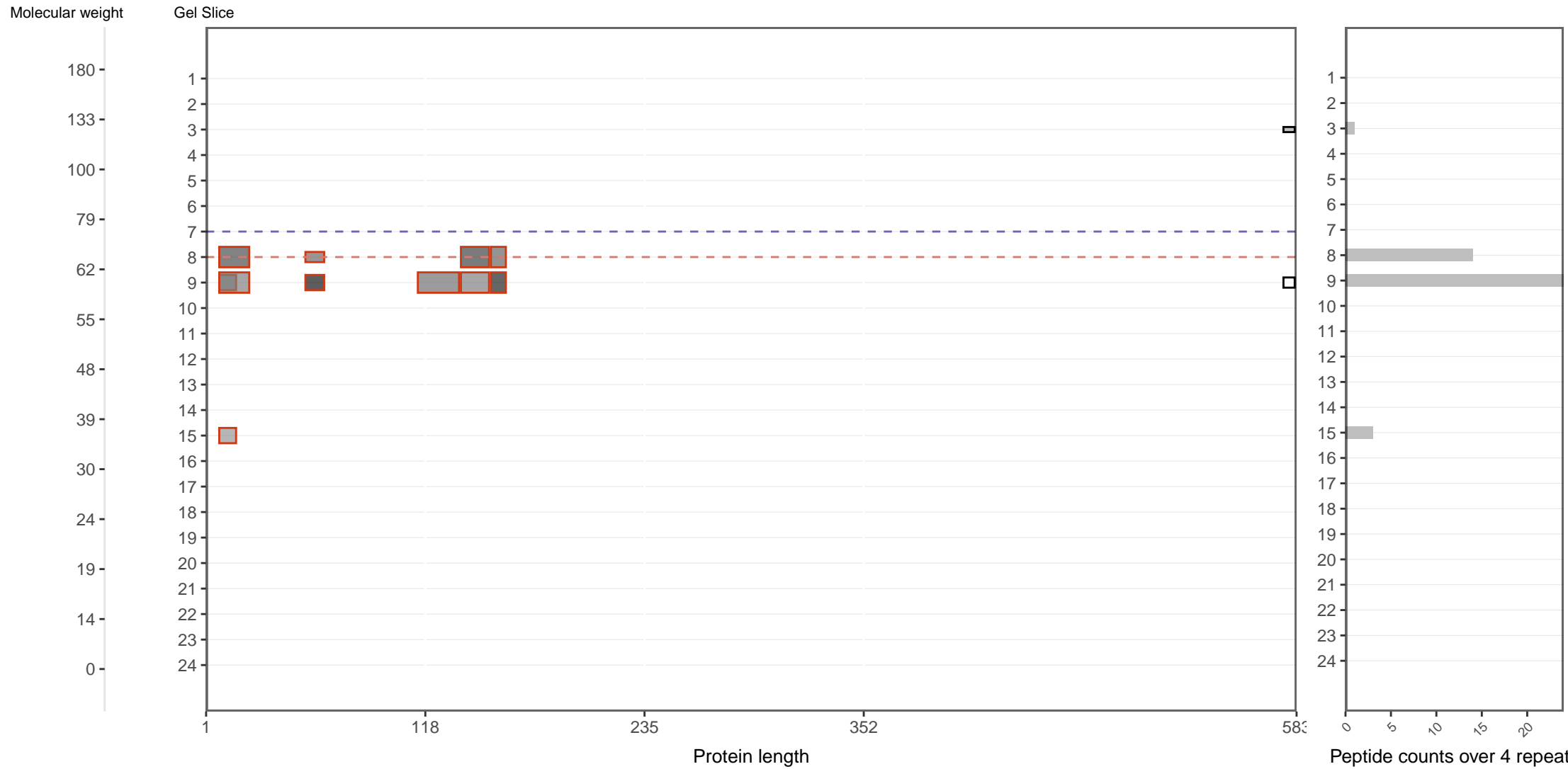
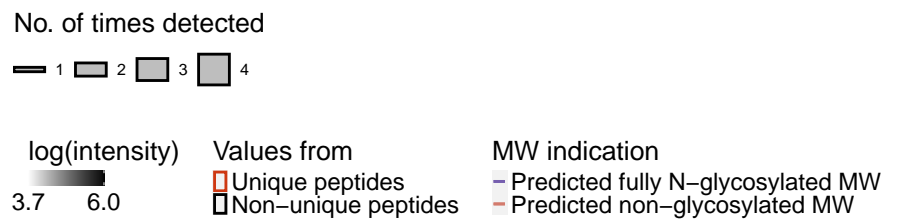
Pfam Description

- SP
- Sequon
- TM Domain
- PF04734 Neutral/alkaline non-lysosomal ceramidase, N-terminal
- PF17048 Neutral/alkaline non-lysosomal ceramidase, C-terminal

Protein sequence:

TCGGKNELCYGRGPGYDFEFSTRIGERQFKKAVLFFNKATEQVKGKVDFRHTYVDFSNLEVTIPKVEGAGIETAKTCPKAMGFAPAAAGTTDGGPAGDFDGGDDKGNAPVLRVLRNLLKPKSSEQKQKQKHPKLLDTEGEMKEPYDWPASILPVQILRGGQVLEVPGEFETMAGRRLRDVAKMLVTSGGTKEFDGSIHVVIAGLNTYSDYITTFEYQIQIRVEGASTLVGPHLTSANVQKFTLAAALFTGGTLGVGQPPNLLGKQIGLLPPVMDATPLGSKFGDLTDDPQ

NbL05g07700.1 phosphoglucomutase_cytoplasmic-like [MW = 63.3 kDa]



PF02878 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain I PF02880 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain II
 Phosphoglucomutase/phosphomannomutase, C-terminal domain PF02879 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain II

Protein sequence:
 RMGLSKSHSEPNPEFGAAADGADRNMILGKRFFVTPSDSVAIAANAVEAIPVFSGLGKVAEMPTSAALDVAKSLNLFVEVPTGWNKFFGNLMDAGMCGIGGEEFGTGSDFHREKDGIVAVLWLSLADKNKDTLGGKLVSVEDVGRQHWATYGRHYTRYDYENDAAGAKELMAHLVKLQSLDENVKIKGHSQVSNVYHSDFEYKDPVDSSEKHHGRRVLFEDGGRLVFRILSGTGSSEGATIRVYIEQYKPKIKGRDSDGALAPLVEVAKLSKMQEY

NbL05g07580.1 probable_LRR_receptor-like_serine/threonine-protein_kinase_At1g06840 [MW - SP = 103.14 kDa]

No. of times detected



log(intensity)



Values from



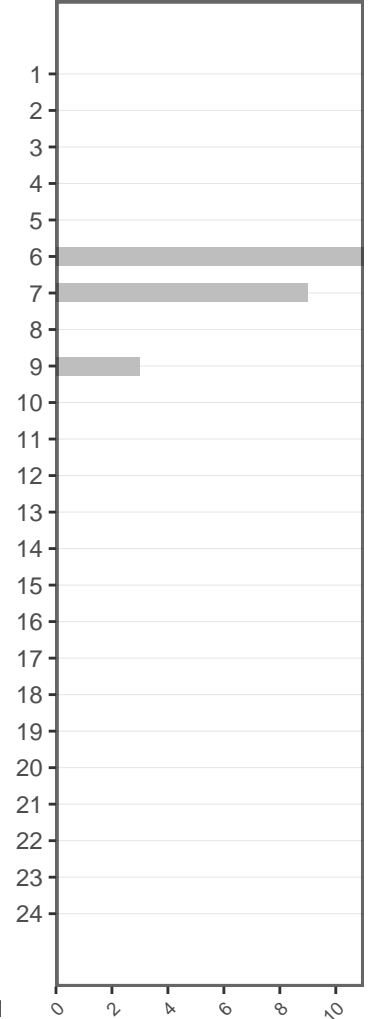
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

VTSSLDDLDLYQLWIDVYFWEKGRRLRMHLKLPVAVGVSTFNESEVLRSEIFASWVEFGDGLFGPYELLNFTLLGPKYSYLNPEIQSKRKSQVLIAGVAAVFAANSTVTLISRRRAKYKSMRKRLLSTKLSKIDGVRSFTTREMALATNYFDG6STQVGGGGYGVFKGLADKKYVAIKRAKESGLGGKFEFLTEIILSRHLHRLNVLVLLGYCDEEGOMLVYEFMPNGTLRDWLSAKSKGNLKFGARLRALGAANKGLVYLHTEADPPHFRDKAKNILLDSKLTAKVAD

NbL05g07500.1 receptor-like_protein_kinase_FERONIA [MW - SP = 93.8 kDa]

No. of times detected



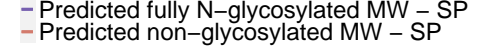
log(intensity)



Values from



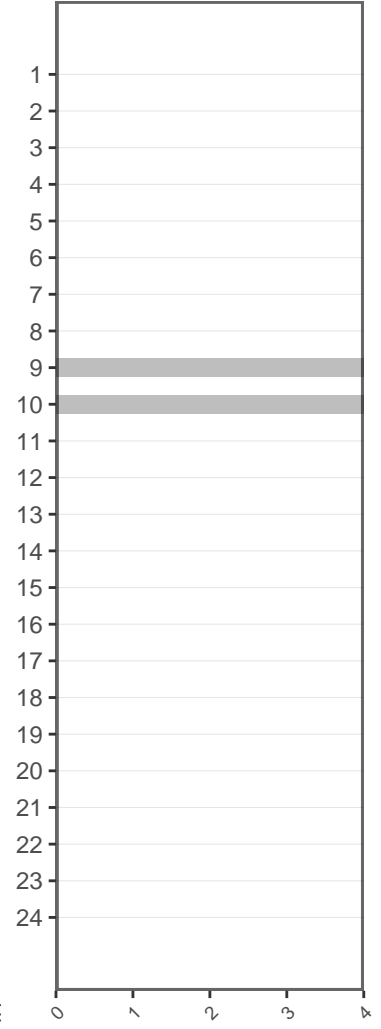
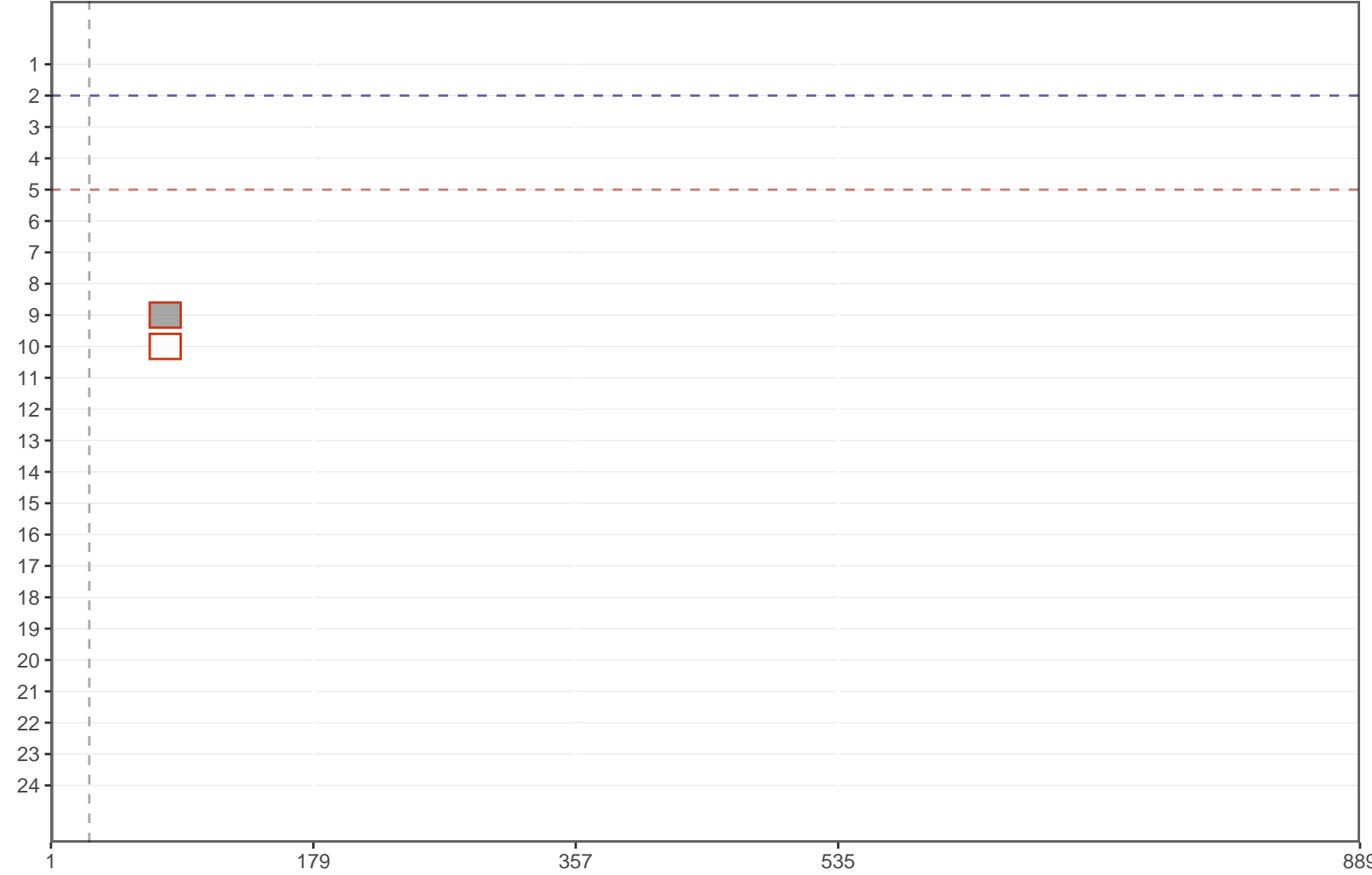
MW indication



Molecular weight



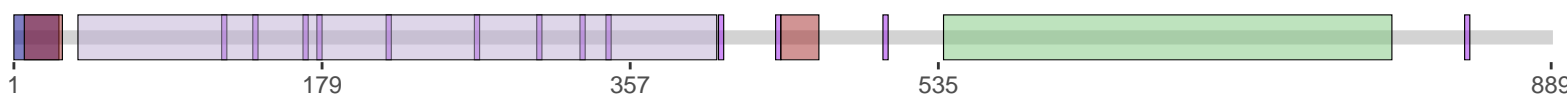
Gel Slice



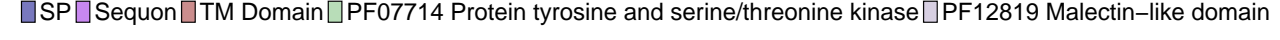
Protein length



Pfam domains



Pfam Description



Protein sequence:

SKKGGSKNSKSAIGGGVGGGAWVILGLAVGLVTRRRKHGKGVSPDGPSSGWLPLSLVGNHSHTGGAKNTTGGVASSLFPNLCRHFSAEKAAATNFDSELLLVGGFGKYYKGEIDGGTVAIKRGNPLSEGGVHEFGTEHELLSKLRHRHVLVSLIGVGEENGEMILVDDYMAHGTLREHLVYKQKPLPFWKGRLLDGGGAARGLHYLHTGAKNIHHRVKTNNLLDEKWWAVVSDFLKLTGPTLDHTVSTWVKGSFGVLDPEYFRROGLTKSDVYSFGVYVLFELL

NbL05g07470.1 vacuolar-sorting_receptor_1-like [MW - SP = 66.98 kDa]

No. of times detected



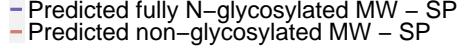
log(intensity)



Values from



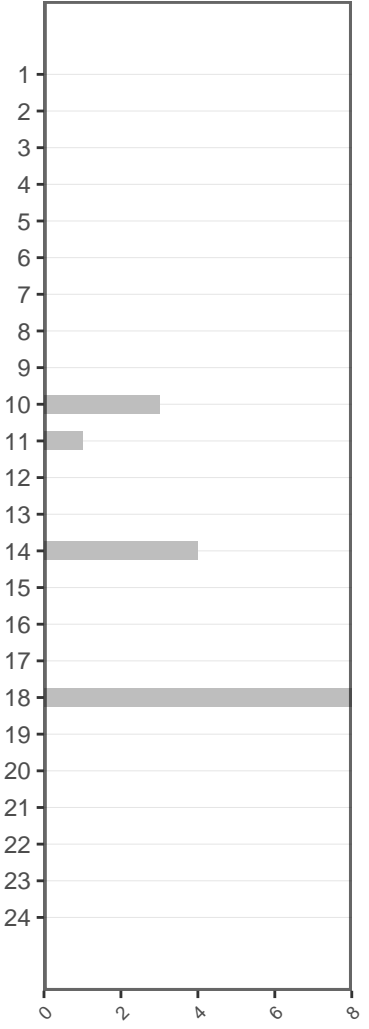
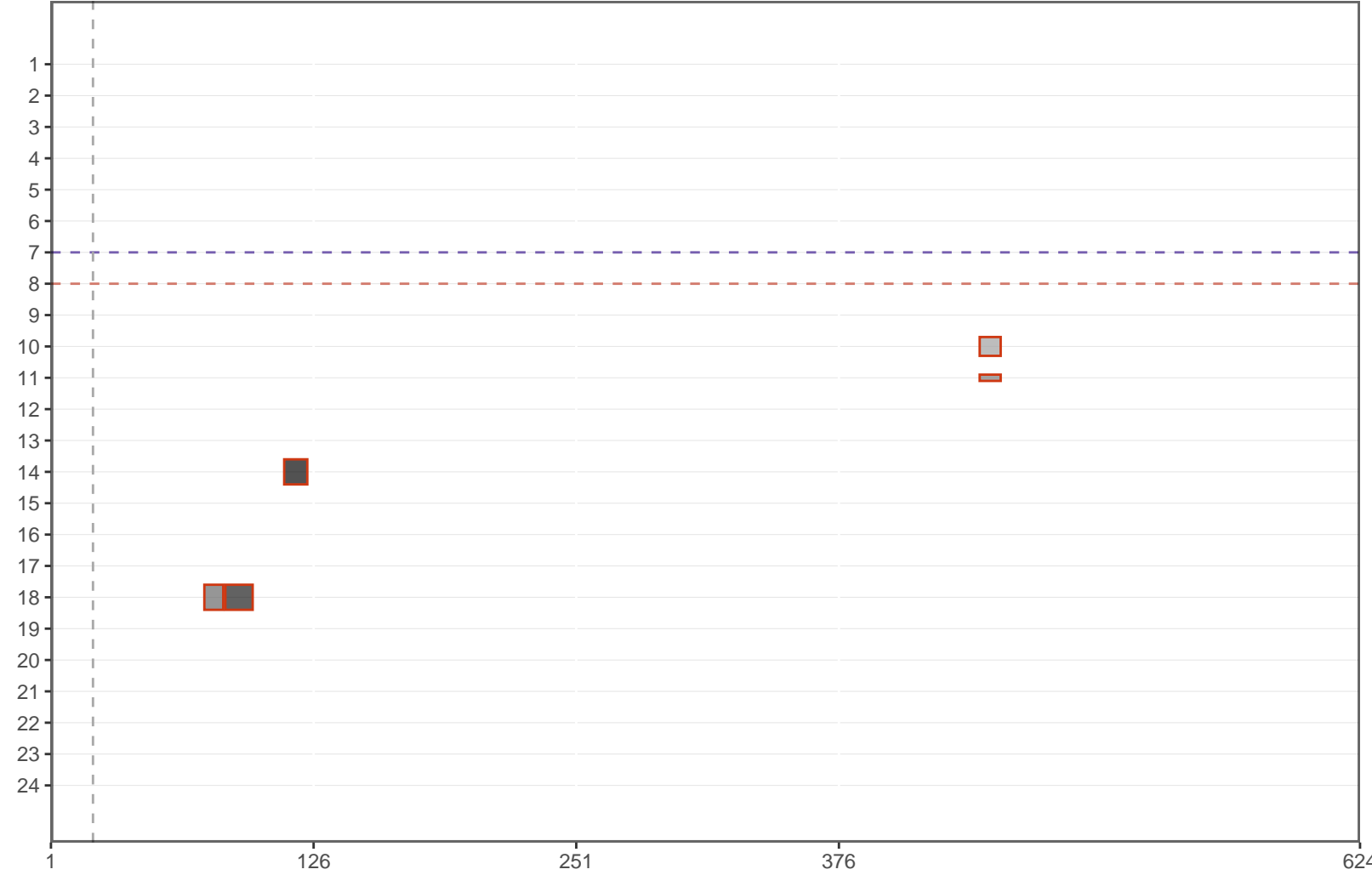
MW indication



Molecular weight



Gel Slice



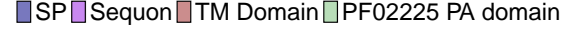
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

WDVYTDFAIRCPMKKKYTKEGADVKSIGFDVKKQEKGVGDPEDATDNPVLKAEQDSGSGKARGDVTLPFLVNNRQVYRGKLEKGAALKKSGSFFETEPALCTEEIETNEGLSNGGQWGGKAAANTACRDTRFRGRVCEPVPVGGKFKVGGYTRCEASGALRCEIENSGGKWKGGQDGSAYSAGIDHTKGGKPPGPKGGVNSCEDIDEGKEKLACQCFEKGKNTWGSFDDSGGGLMMHEHDTQISGDSKSEFSGWGLWVTWILGLAAVAVAVVYKYRI

NbL05g07380.1 non-specific_lipid-transfer_protein_1-like [MW - SP = 9.46 kDa]

No. of times detected



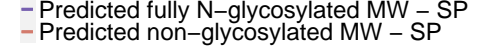
log(intensity)



Values from



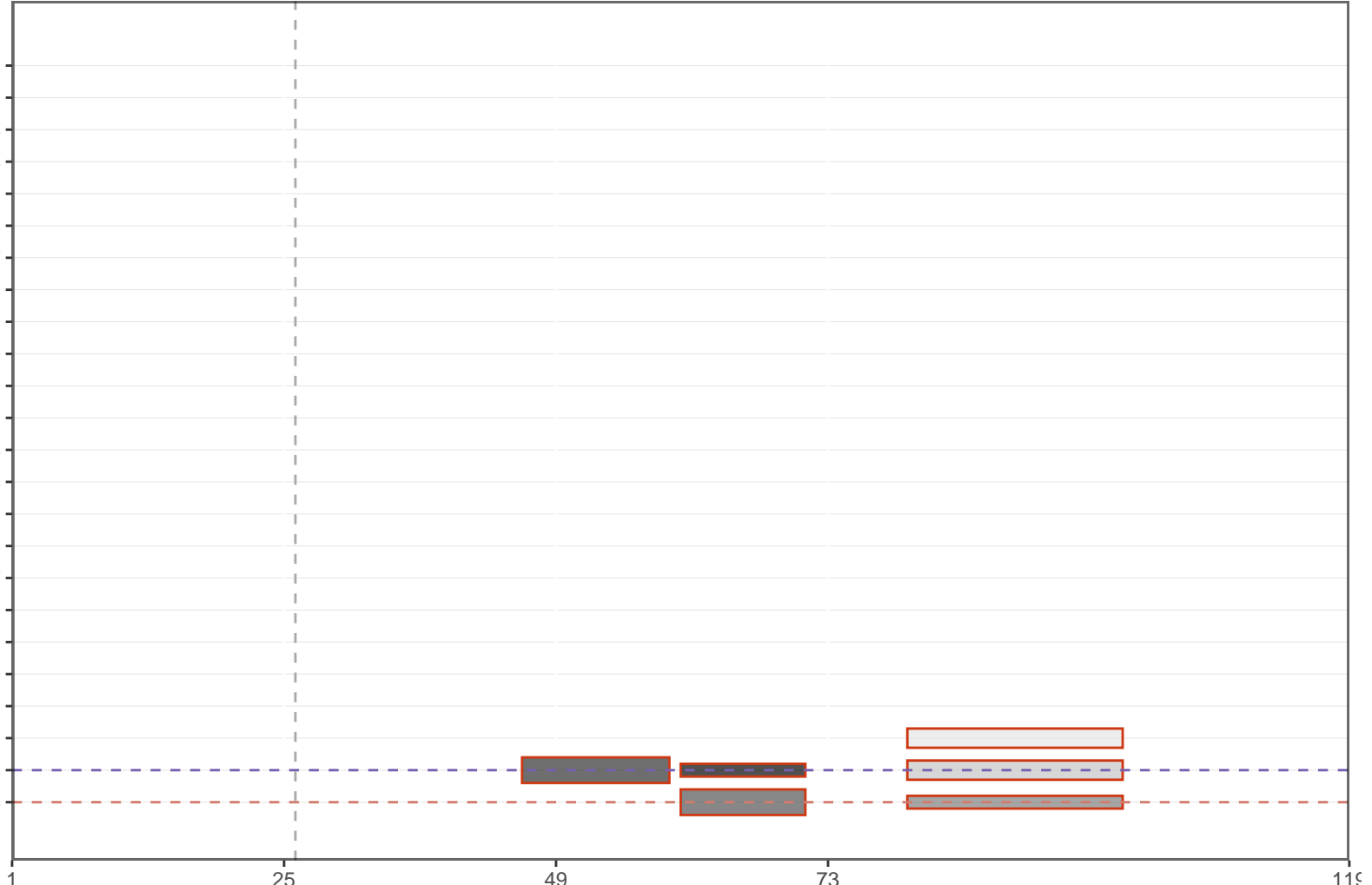
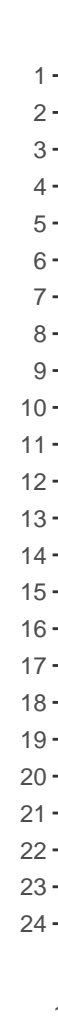
MW indication



Molecular weight



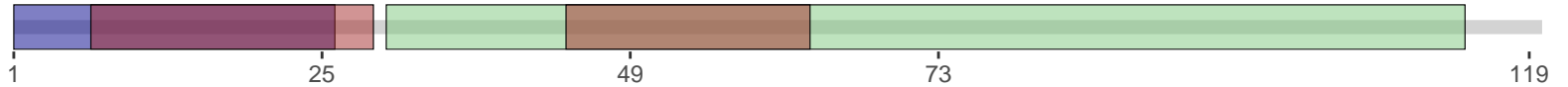
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

SGVPTMCCNGIRSLFSAASTFGDRFTVGNMGKSAAGVSGVNLNLAALPKGGVWIPYKISPSIDCAKQI

NbL05g06990.1 ubiquitin-activating_enzyme_E1_1-like [MW - SP = 124.19 kDa]

No. of times detected



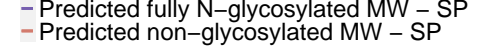
log(intensity)



Values from



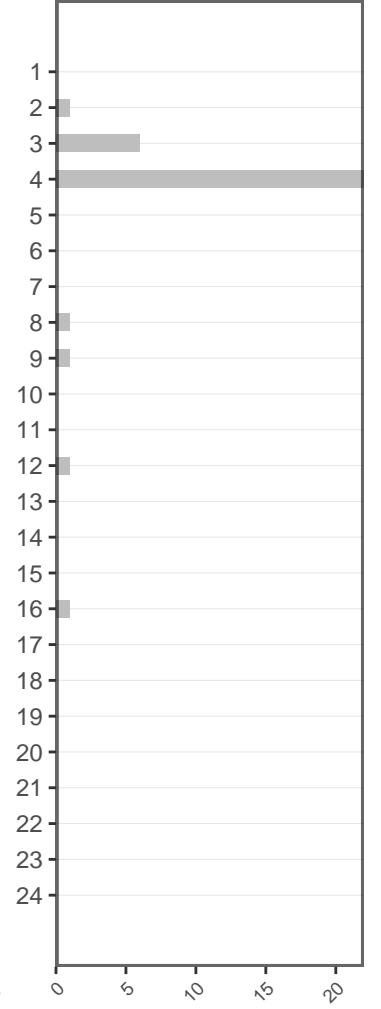
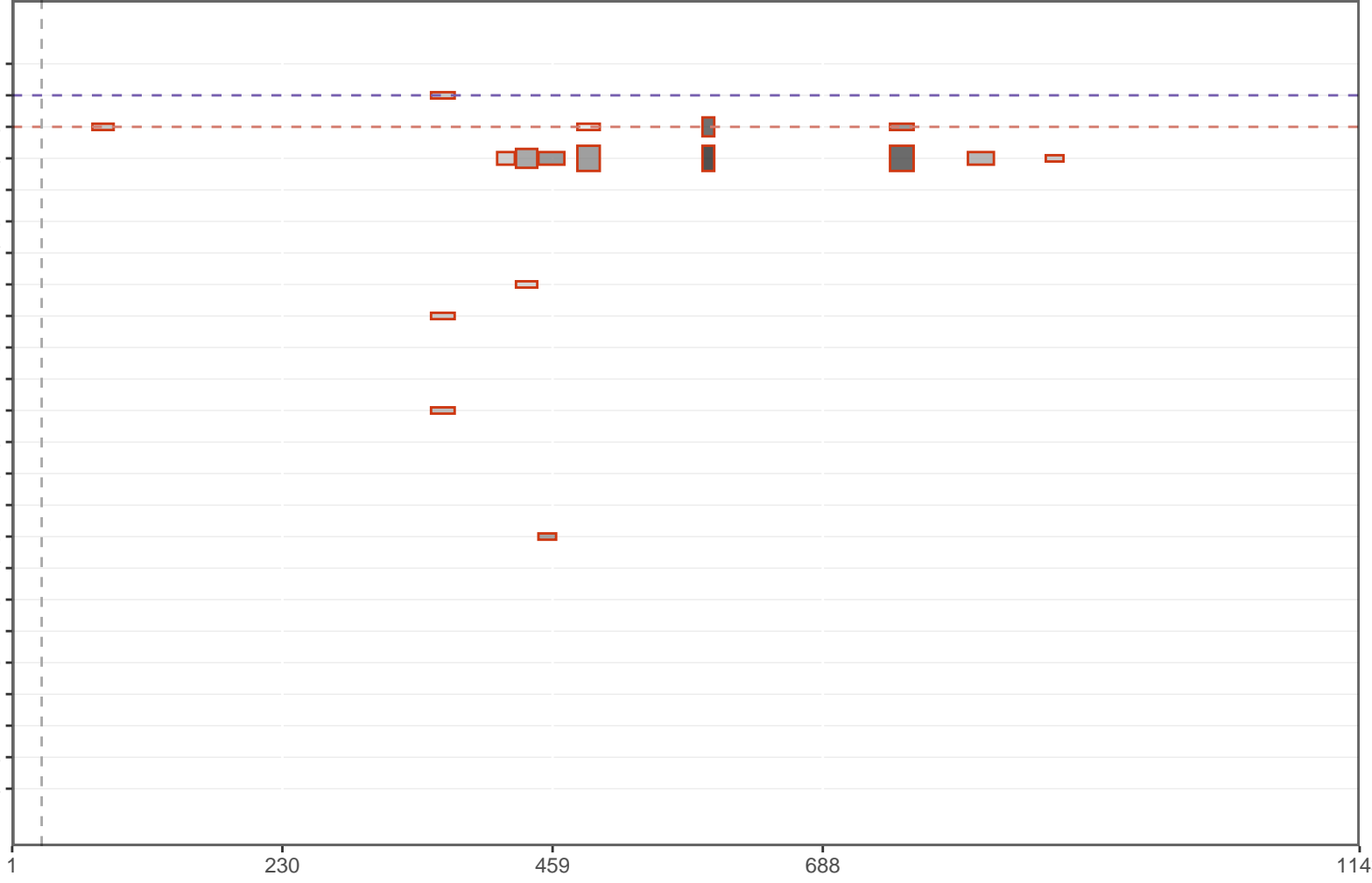
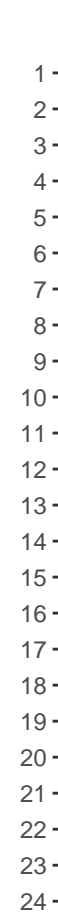
MW indication



Molecular weight

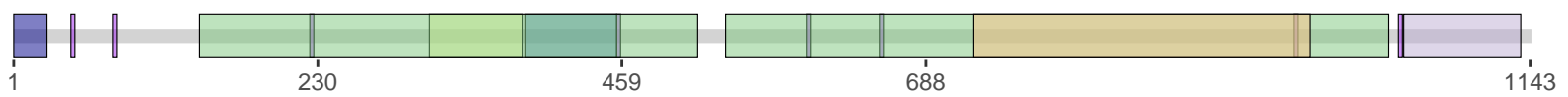


Gel Slice



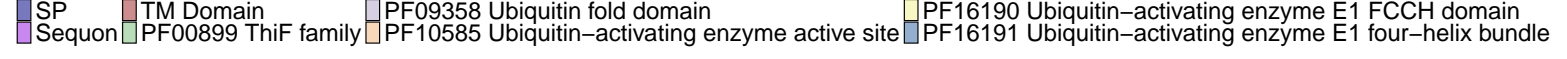
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISSGALGCEFLKLNALMGVCGGDKGKLNIFDDDDVIEKINLGRQFLFRDWNIGGAKSTVAAAAALNPFCHIEALGNRASPETESVFDQTFWENLKVNALDINVARLYHDGRGLYFQKPLLESGLGAKNGTGMVPHLTENYGASRDPPKGAQPMCTVHGFHNDHGLTWARSEFEGLEKTPTEVNAFLINPDSVISAMQKAGDAGARDLDRVLEGLDKERCQDTFGDQGITWARLRFEDYFADRKWLQITFTFPEEATTS6GAPFW6SKRFRPLQFSYDDASHLQFLJ

NbL05g06630.1 GDSL_esterase/lipase_CPRD49-like [MW = 28.31 kDa]

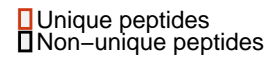
No. of times detected



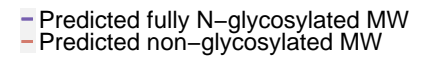
log(intensity)



Values from



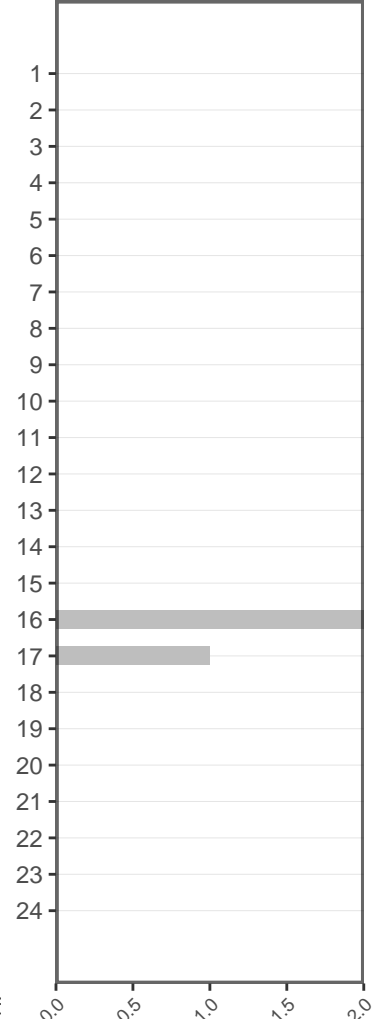
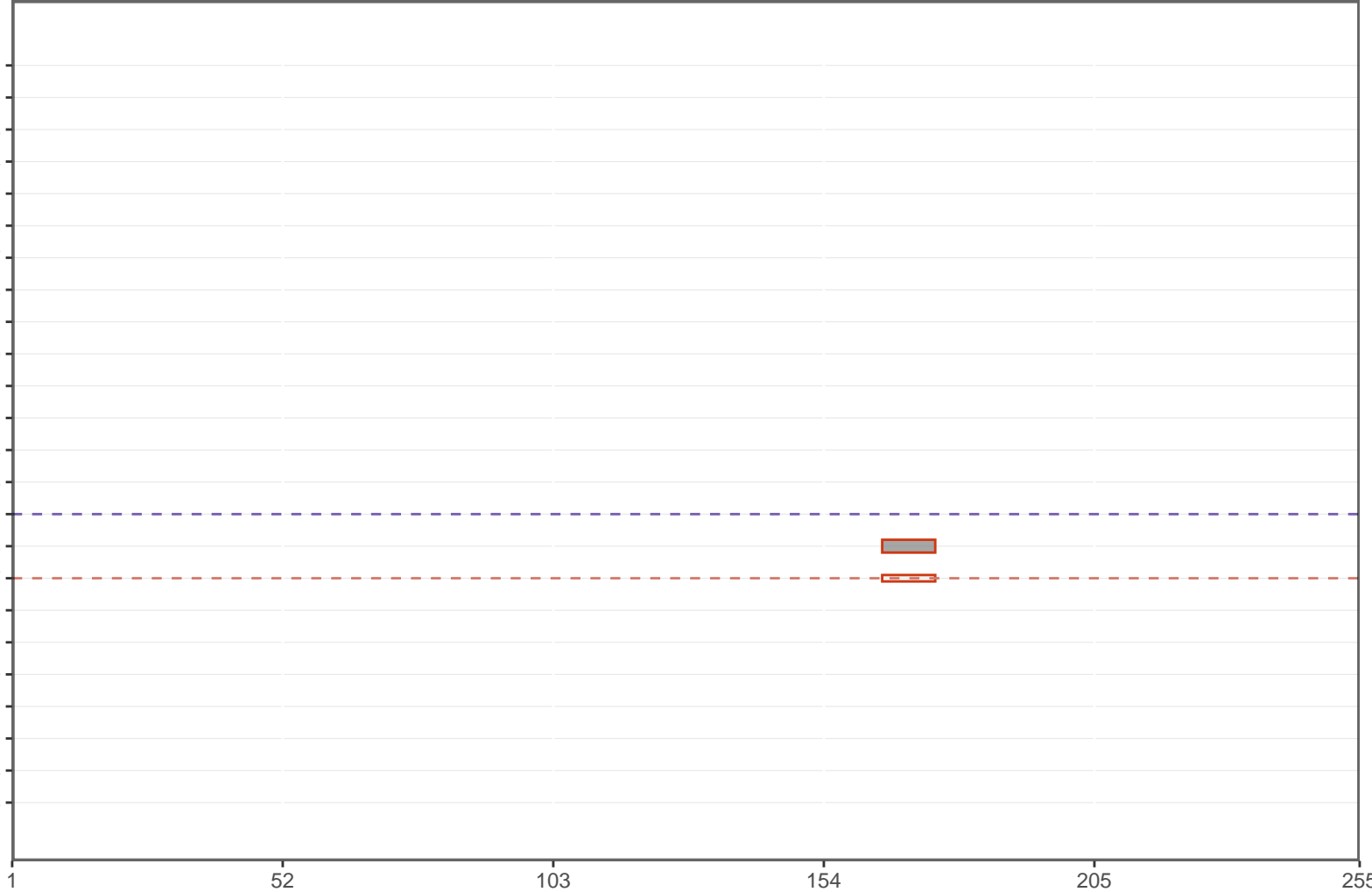
MW indication



Molecular weight



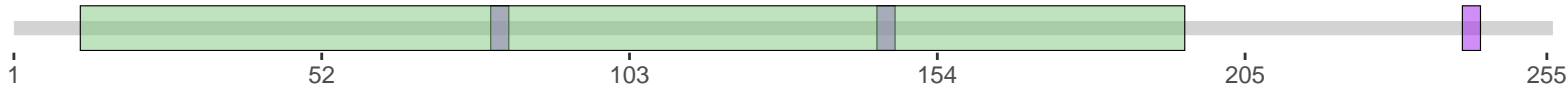
Gel Slice



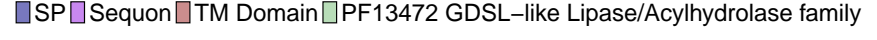
Protein length



Pfam domains



Pfam Description



Protein sequence:

SDKTHILLSAPWNEADITVEFGNGLGRSNGSCKRYSEACIGLGGELGVKVIDLWTTLGGRRDWAACGFTDGRHLSSEGSQVAKELKYLKAEAEWEPNLHWRSLFIEFFPEISPIYFVDFKGETAWNVSGLDLEWGTQWYH

NbL05g06480.1 uncharacterized_LOC104227496 [MW = 53.13 kDa]

No. of times detected



log(intensity)



Values from



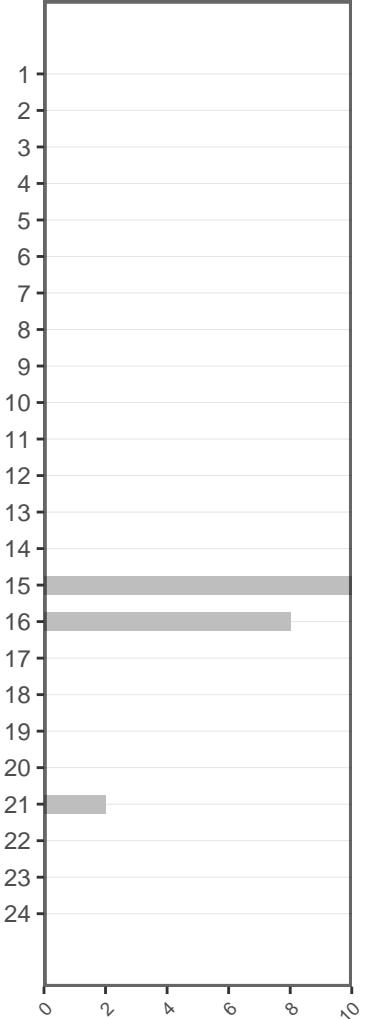
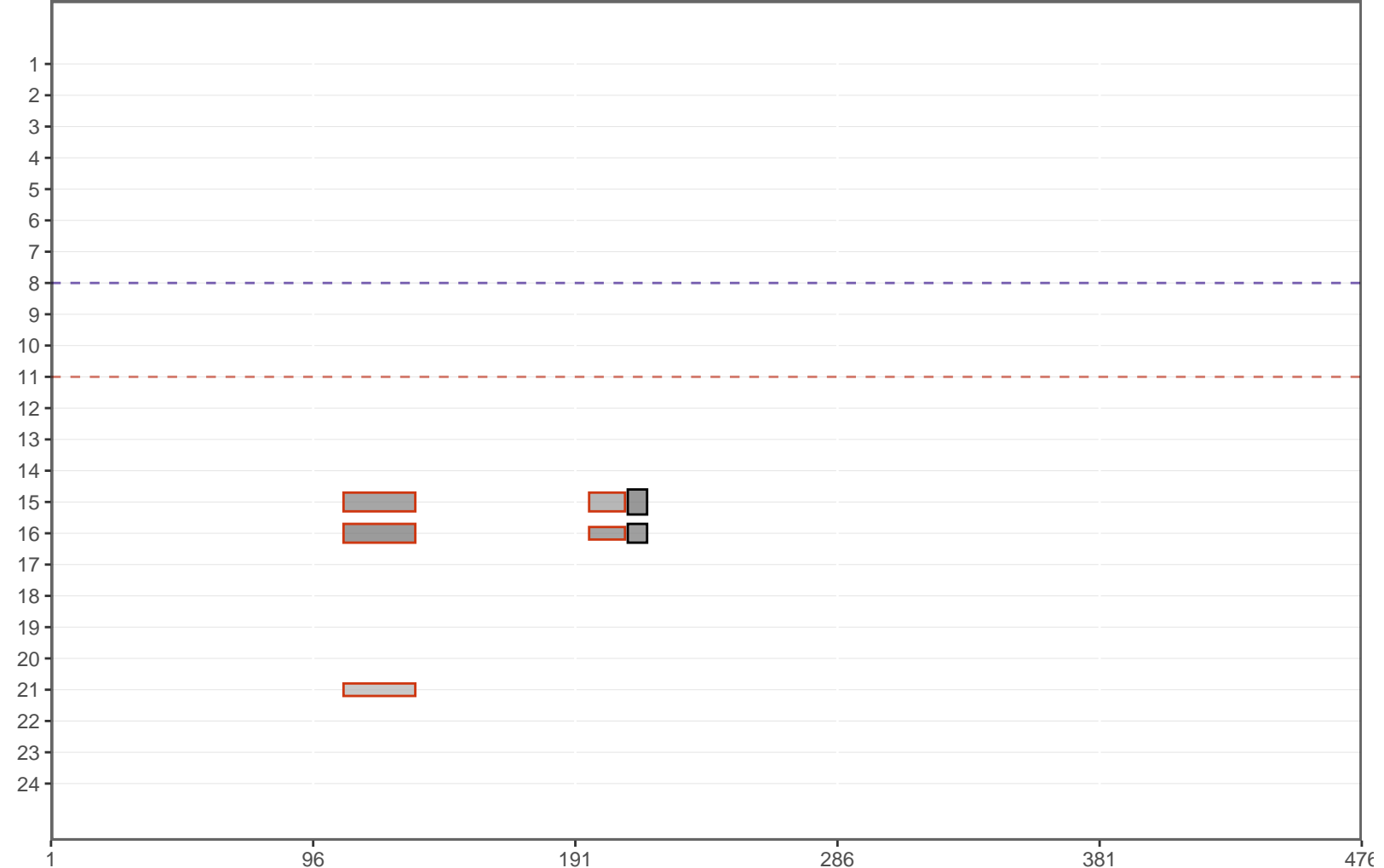
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

WDNAELQTVIEQEPAAEGSESAVNPFEILAEINLVPTPTVAVDEDDINEKKSNEVLAMVAENITEVKEEDVNTNLNEDTHETKVGKNGMVFNDEVLSSKKEFLVARETPVPLVPLGLTQVLDMDKVAIEISVSGNGEELNVLDDKVMGNKYVTEGSLGKKEEFNVPELSSNNEVATDTHPRETPEMMLNWKGEVGRNEDIEKSEFVEGGDWPBGKPVVEIFDSDMKVWKRRLGKFFANLGFRRVLEGL

NbL05g06350.1 proteasome_subunit_alpha_type-4 [MW - SP = 27.04 kDa]

No. of times detected



log(intensity)



Values from



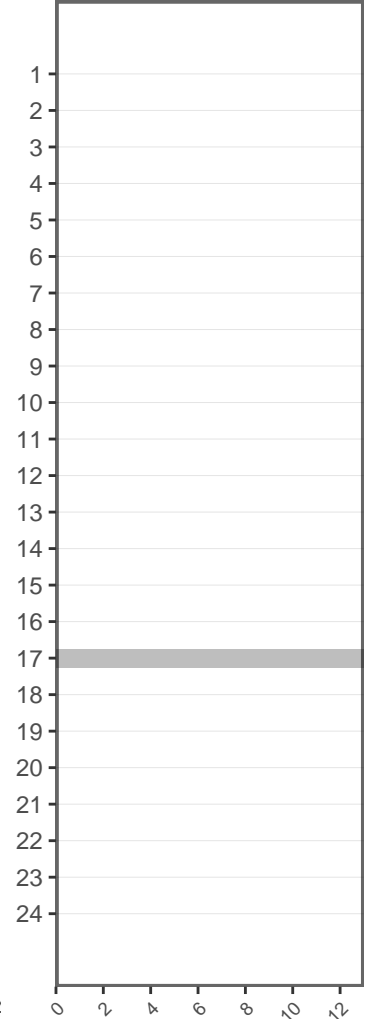
MW indication



Molecular weight

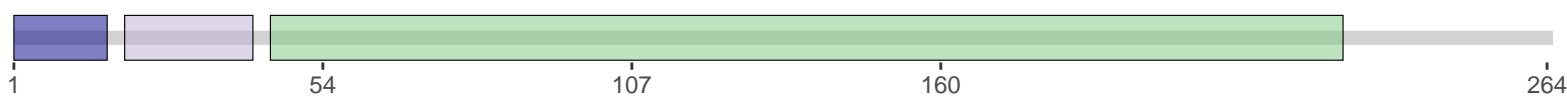


Gel Slice



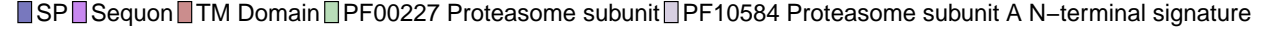
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

VEQLVQLSLCDTKDGGVYTFQFGLRPFQVSLFAGWIKNYVGLYMDPFGNYGGWKAAGANNGAAGEMLKGGVKGDETRREAAKLVKLVLSKTMDSITLSEKLELAIEVFLFNKWKYVGVHSESELNLLVGGSLTQPAAD*

NbL05g06140.1 fructose-16-bisphosphatase_chloroplastic-like [MW = 44.84 kDa]

No. of times detected



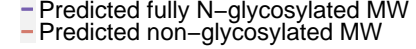
log(intensity)



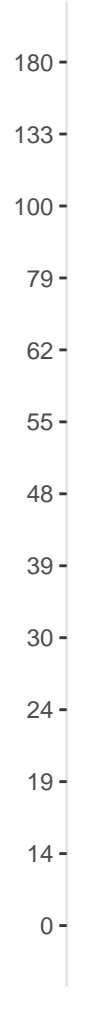
Values from



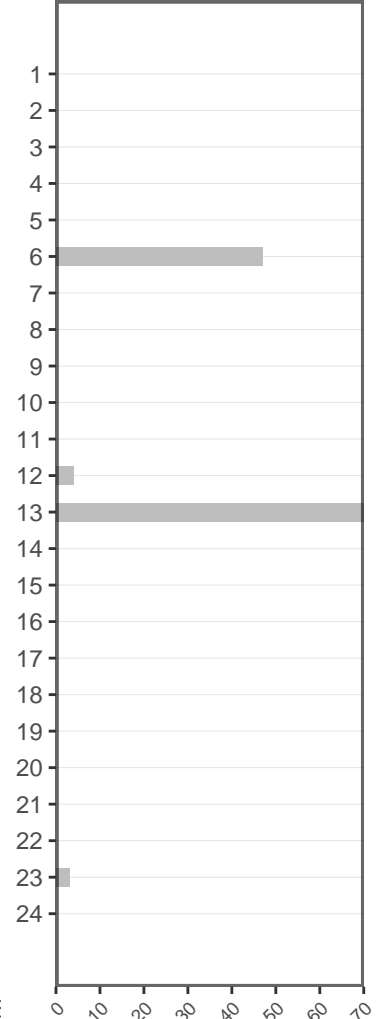
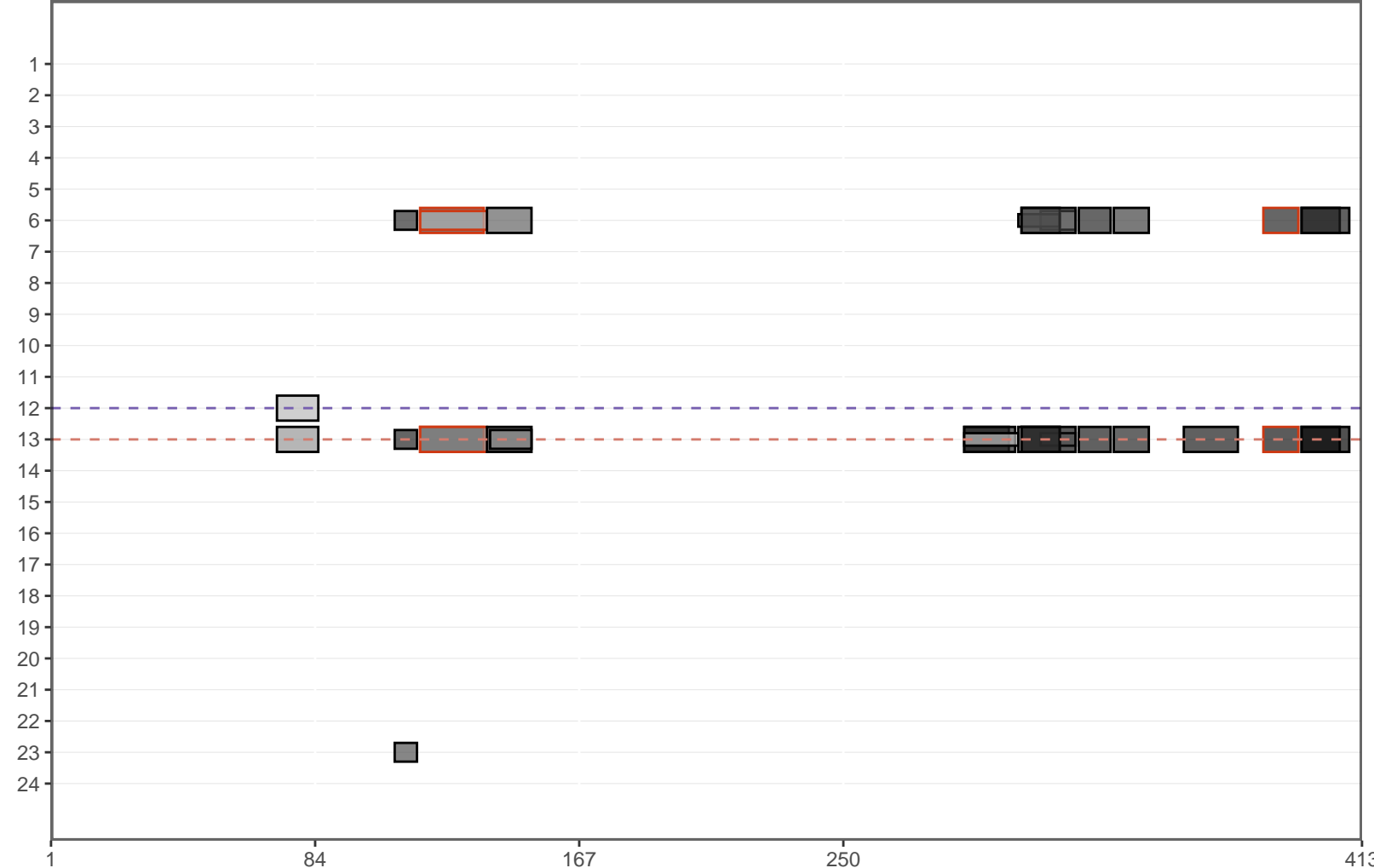
MW indication



Molecular weight

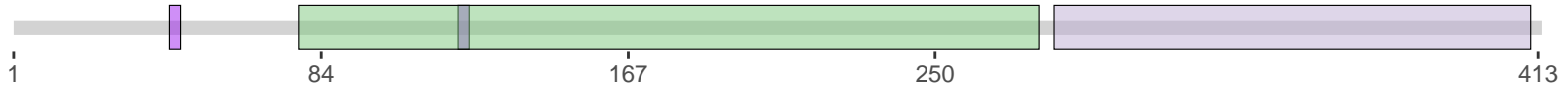


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00316 Fructose-1-6-bisphosphatase, N-terminal domain
- PF18913 Fructose-1-6-bisphosphatase, C-terminal domain

Protein sequence:

LVSTGIFGIYSPNDEGLADLGGDSTLDNVEGRGIVNVDQPGSNLLAAGVGMYS65SIFVFTLGNQVFANLDFMVEFVLTQENIQIPK6GKIYFNEGNGYLDWDLKKYKVIDDKDPCFSGKPYEARHYIGSLVGFHRTLHYGGYGYPRDKKKNKGLRLLYEGAPMFLVEGAGGKGGDGHQRVLQDQPTENQRVPLVIGSTEEVEKLEKLYL6*

NbL05g06090.1 probable_glutathione_S-transferase [MW = 24.99 kDa]

No. of times detected



log(intensity)



Values from



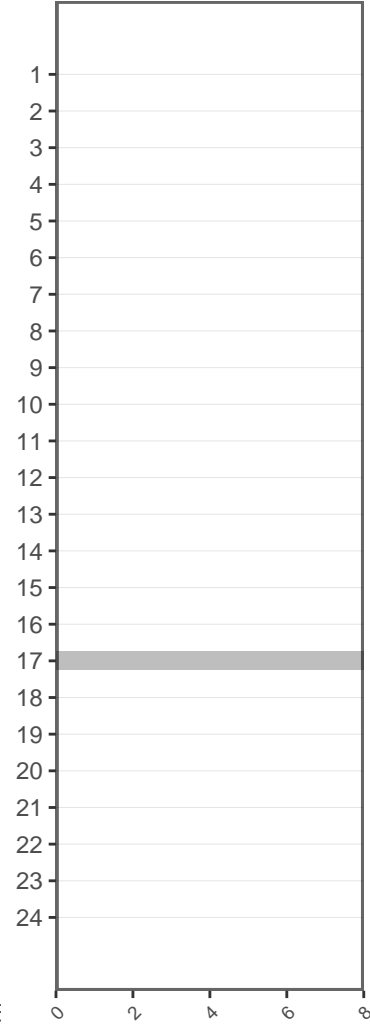
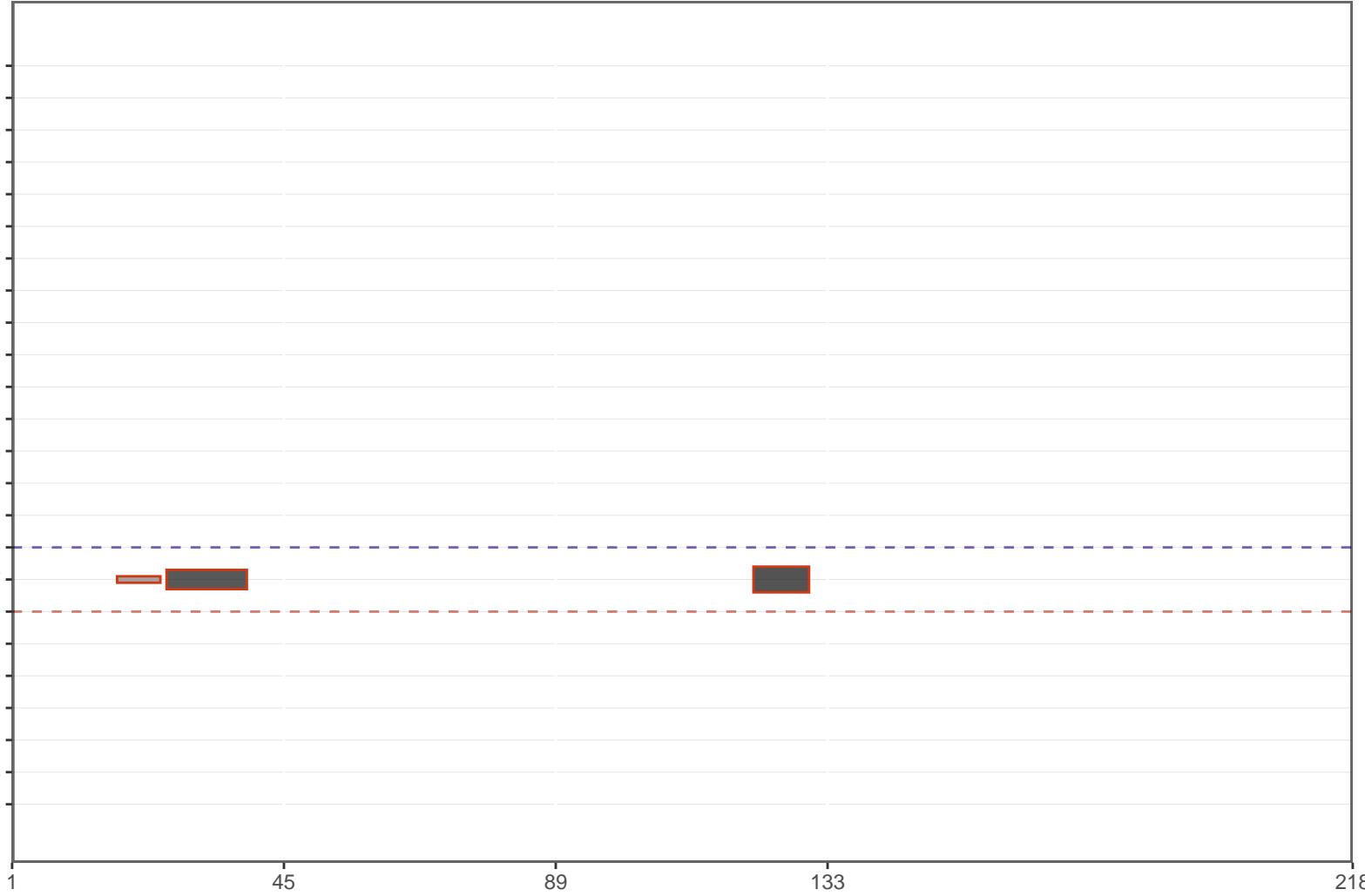
MW indication



Molecular weight

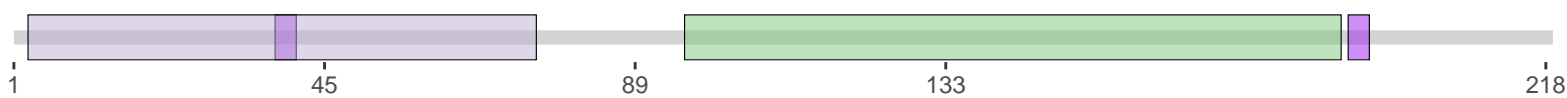


Gel Slice



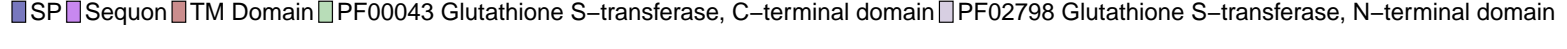
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IAKFLLEDKVPVAVGKSFFLKGEEGAKGKEEAFEVLLKILDELKDKKFFFTGDKIGFADAAANFVGLWLVGFEEASGILVTRKFFNFNGAWRDEYINYSQNKVLPFRDELLAHFKARQAAAPK

NbL05g05910.1 probable_proteasome_inhibitor [MW = 31.91 kDa]

No. of times detected



log(intensity)



Values from



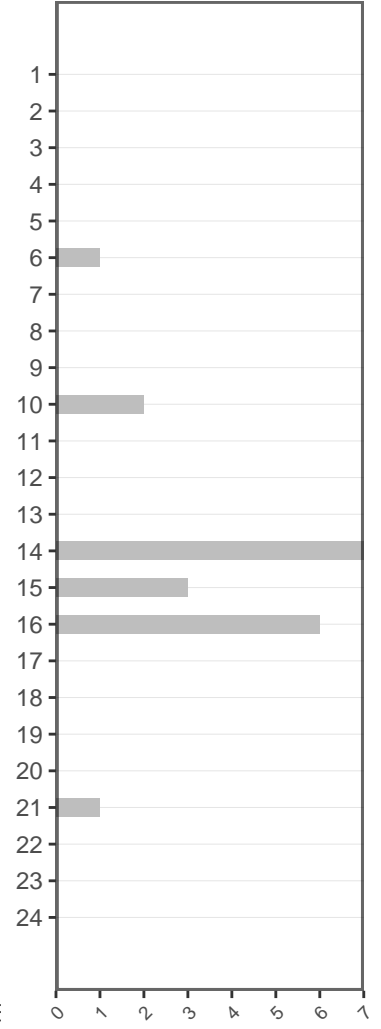
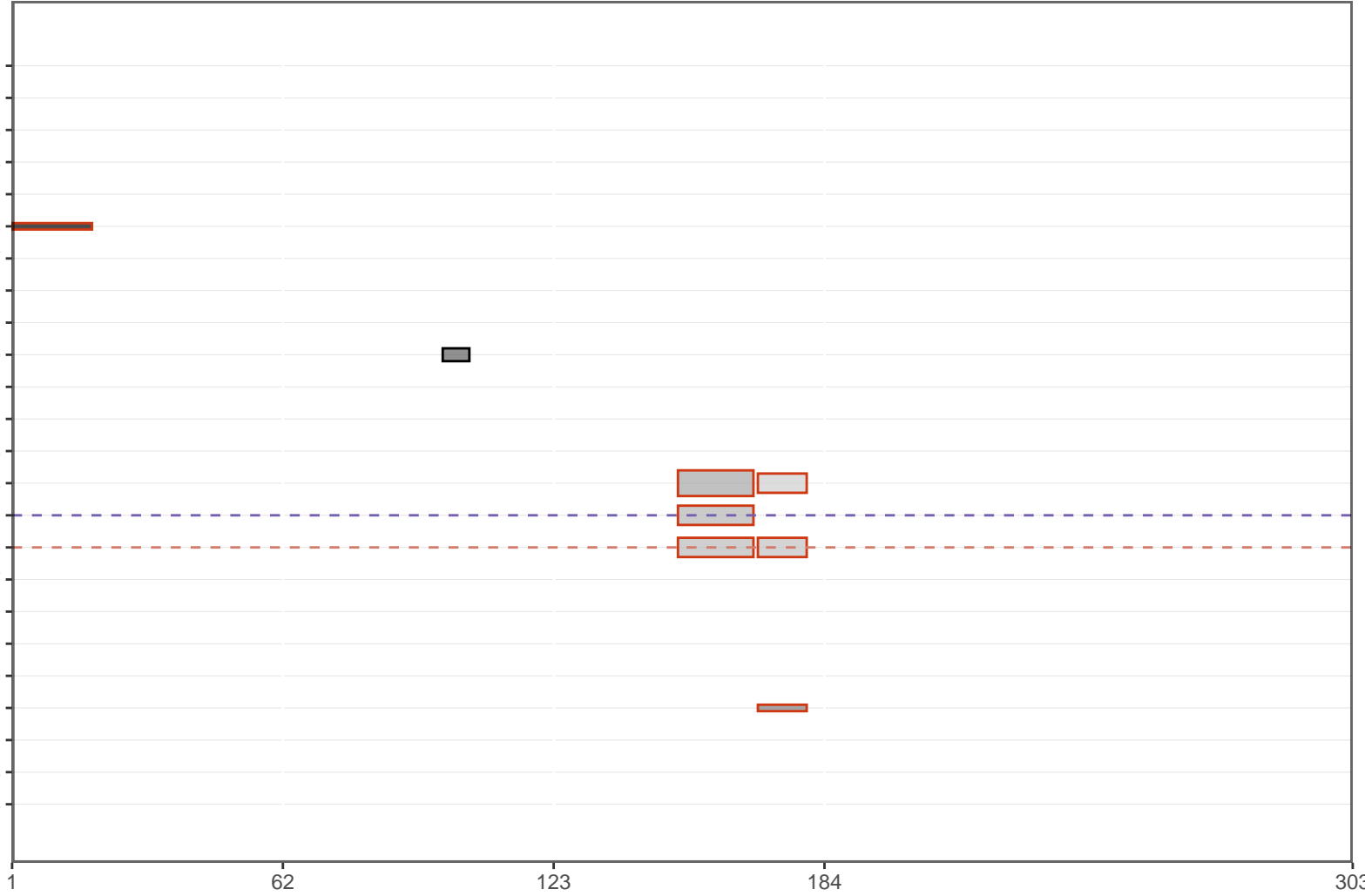
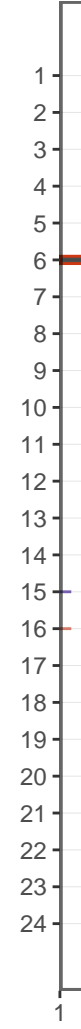
MW indication



Molecular weight

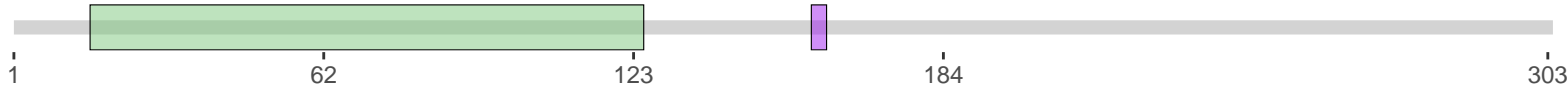


Gel Slice



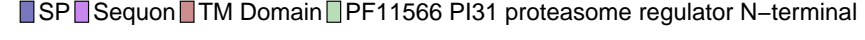
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IELNKEVLSKYSGSEVANSTGTSFGKGGLEDQPSAELRSQVYQPSGSSFPSSVYVPPICGGGGDLFPSPGAGVYPTROGSPGGGSMVGPNDPRFFGGMGGDPRLPGLPGLVLPGARFDVYGPSQVPGFEGFRFRDPRRPGGGRPHDLPHPFGGSDDFY

NbL05g05840.1 uracil_phosphoribosyltransferase [MW = 30.85 kDa]

No. of times detected



log(intensity)



Values from



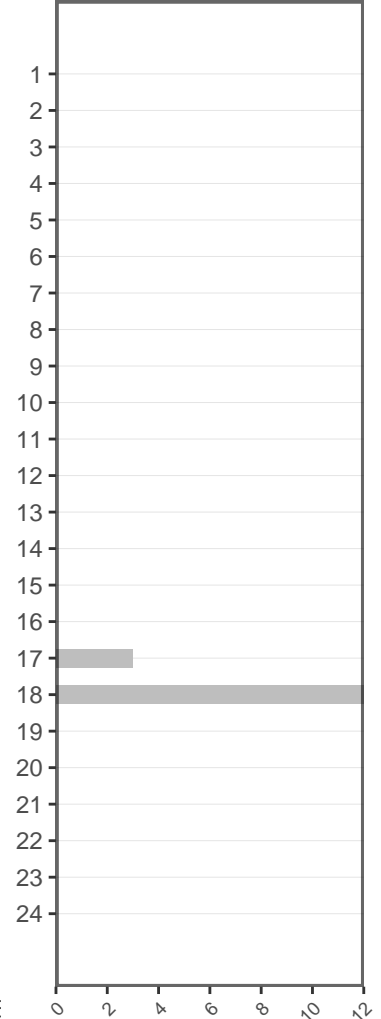
MW indication



Molecular weight

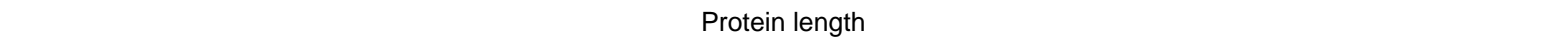


Gel Slice

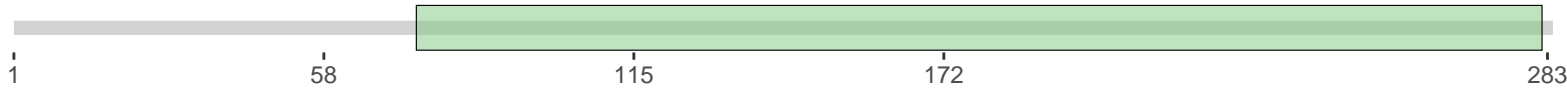


Peptide counts over 4 repeats

Protein length



Protein length



Pfam domains

Pfam Description



Protein sequence:

ISPMGVASVEFYDREPFVAVPIIRAGLVLAEHASSLPATKTYHLGIRNEETLQPSVYLNKLPDKFPEGSRVFFVDFMLATGGTVAANDLKEHGVDSNGIKVCAVAFAPLQKLEKFPGLHYVAGILDPTVNDKGFIRPOLGAGDREFGT

NbL05g05670.1 ribulose_bisphosphate_carboxylase/oxygenase_activase_1_chloroplastic [MW = 52.67 kDa]

No. of times detected



log(intensity)



Values from



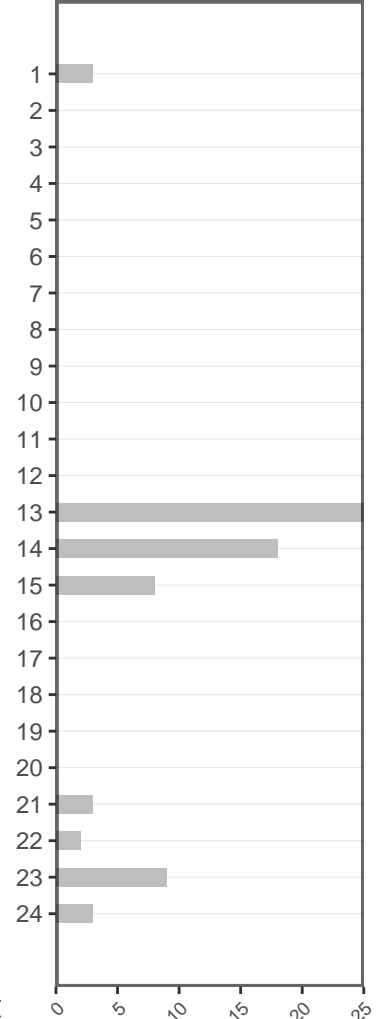
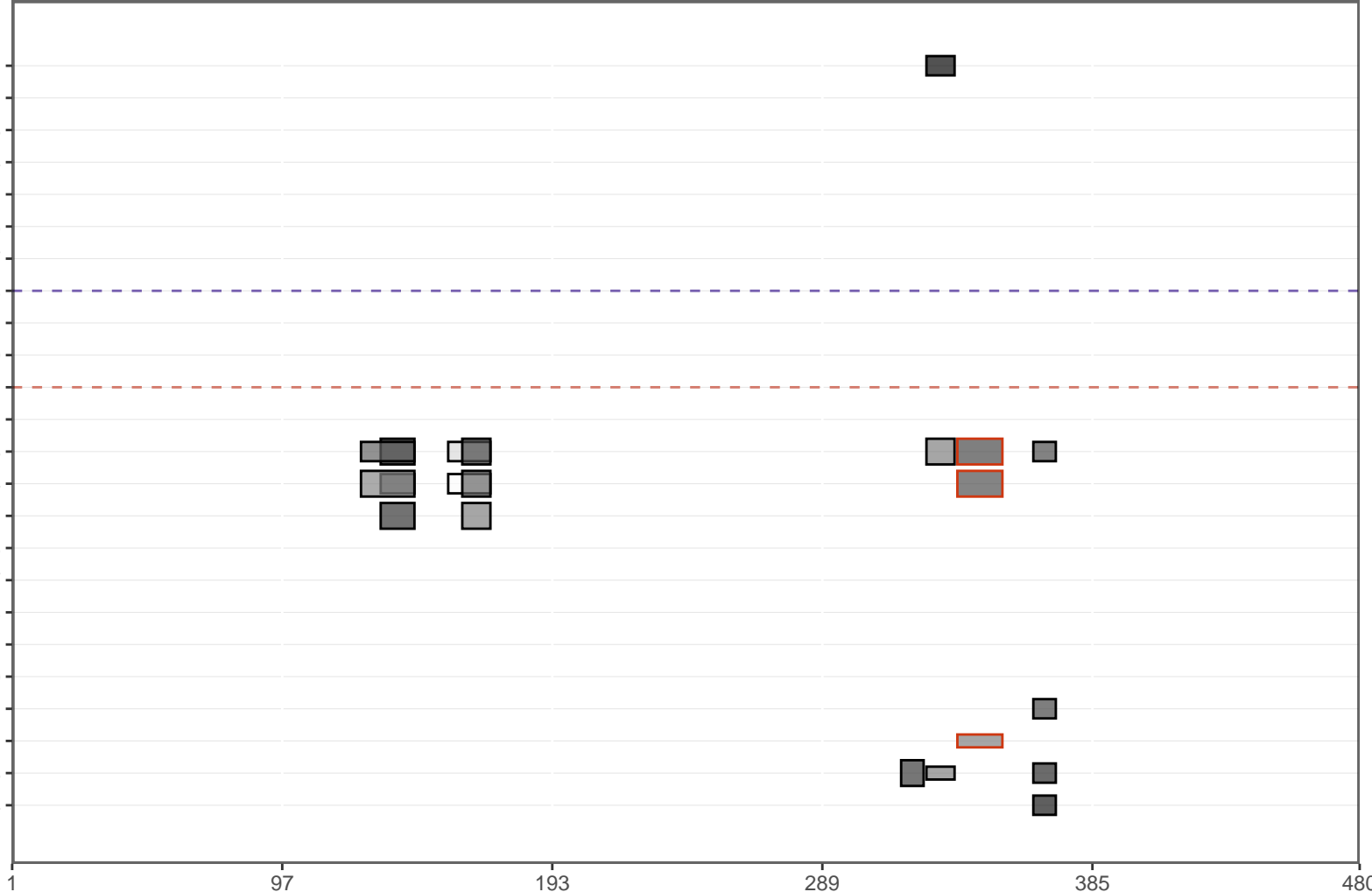
MW indication



Molecular weight

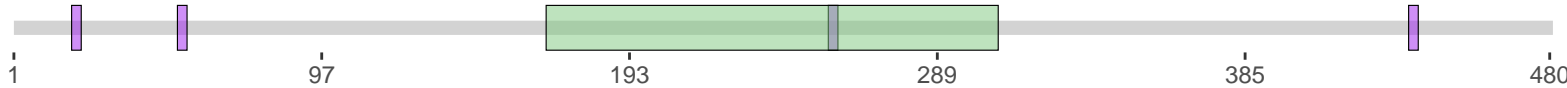


Gel Slice



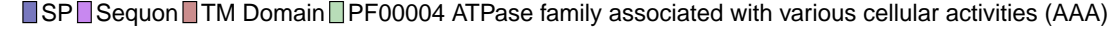
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CLFINDLDGAGRMGGTTFQYTVNNGMVFATLMLNADNPTNVLQPLGMYNKGENARVPIVTDGDFSTLYALURDGRMEKFYWAPTRDRIGVCTGFRDNDVPAEDVYVWVDSFFQGSDFFGALRARVYDDEVKRVWVSGTGIERKIDKLLNSFDGPPFEGQPKMTDKLLEYQNLMLVQGENWKRVLADKYLKEAALGDANADAINNGSFFTRTEAAGHADVPVGEGETHSIATKLDSTSRADGGSYLFKPF

NbL05g05510.1 uncharacterized_protein_At5g02240-like [MW = 32.25 kDa]

No. of times detected



log(intensity)



Values from



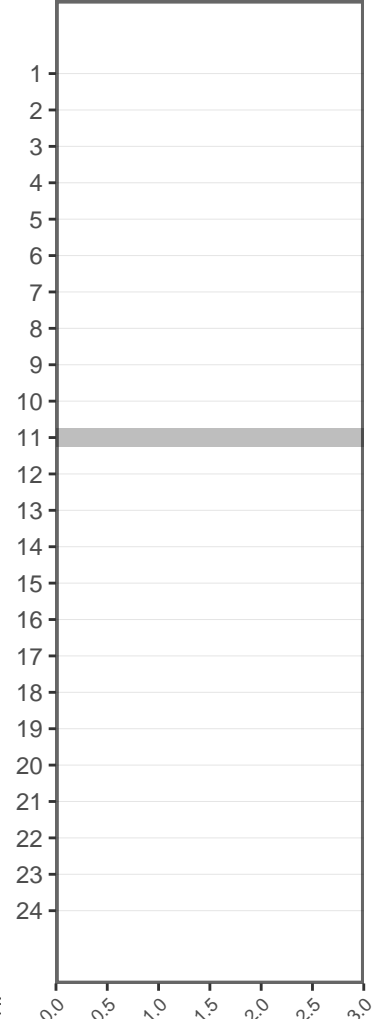
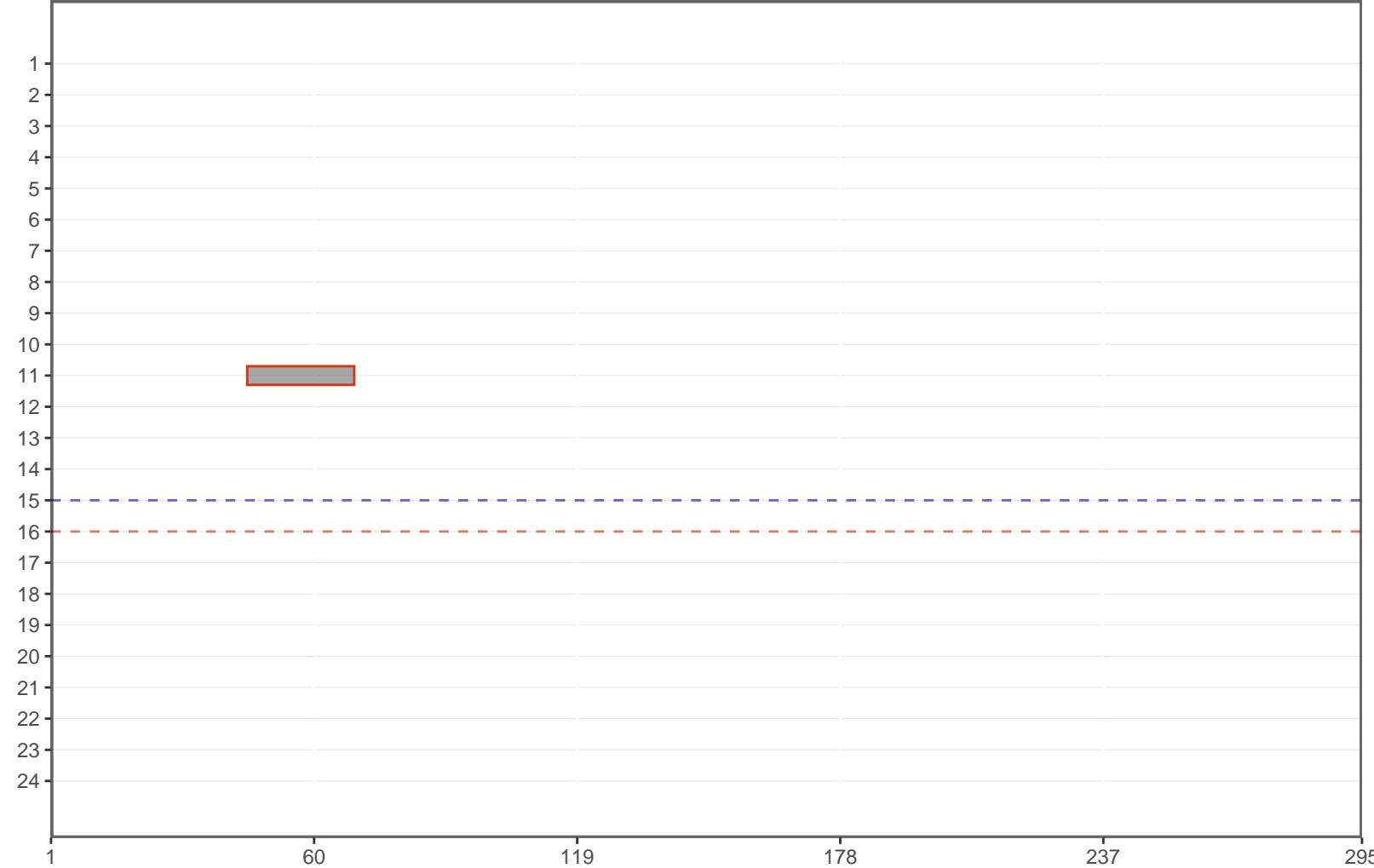
MW indication



Molecular weight

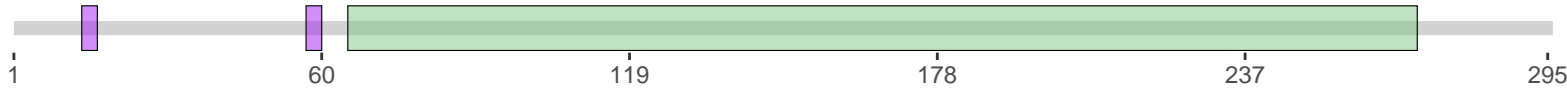


Gel Slice



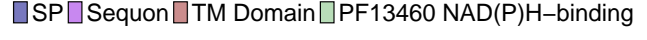
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

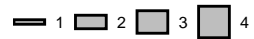


Protein sequence:

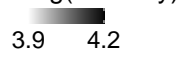
LMKPGFDPTGGGRPEFYFEDGAVPEQVDWIGKNGIDAKAAGVKGQVLVSGMSGTNPNNPLNSIGNGNLWKRKAQYLADSGIPYTHRAGSLQDKEGIRELLVGGKDELLOTETRTRADVAEIVGQILLFVLRVDVCGGFFDQLOGFTPTTHFLV

NbL05g05450.1 ribonuclease_II_chloroplastic/mitochondrial [MW = 92.73 kDa]

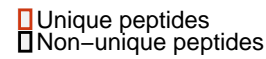
No. of times detected



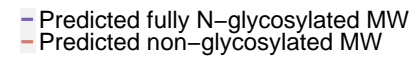
log(intensity)



Values from



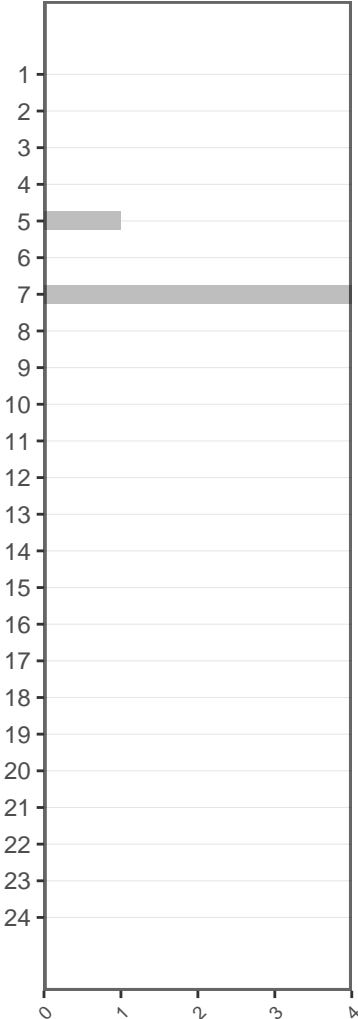
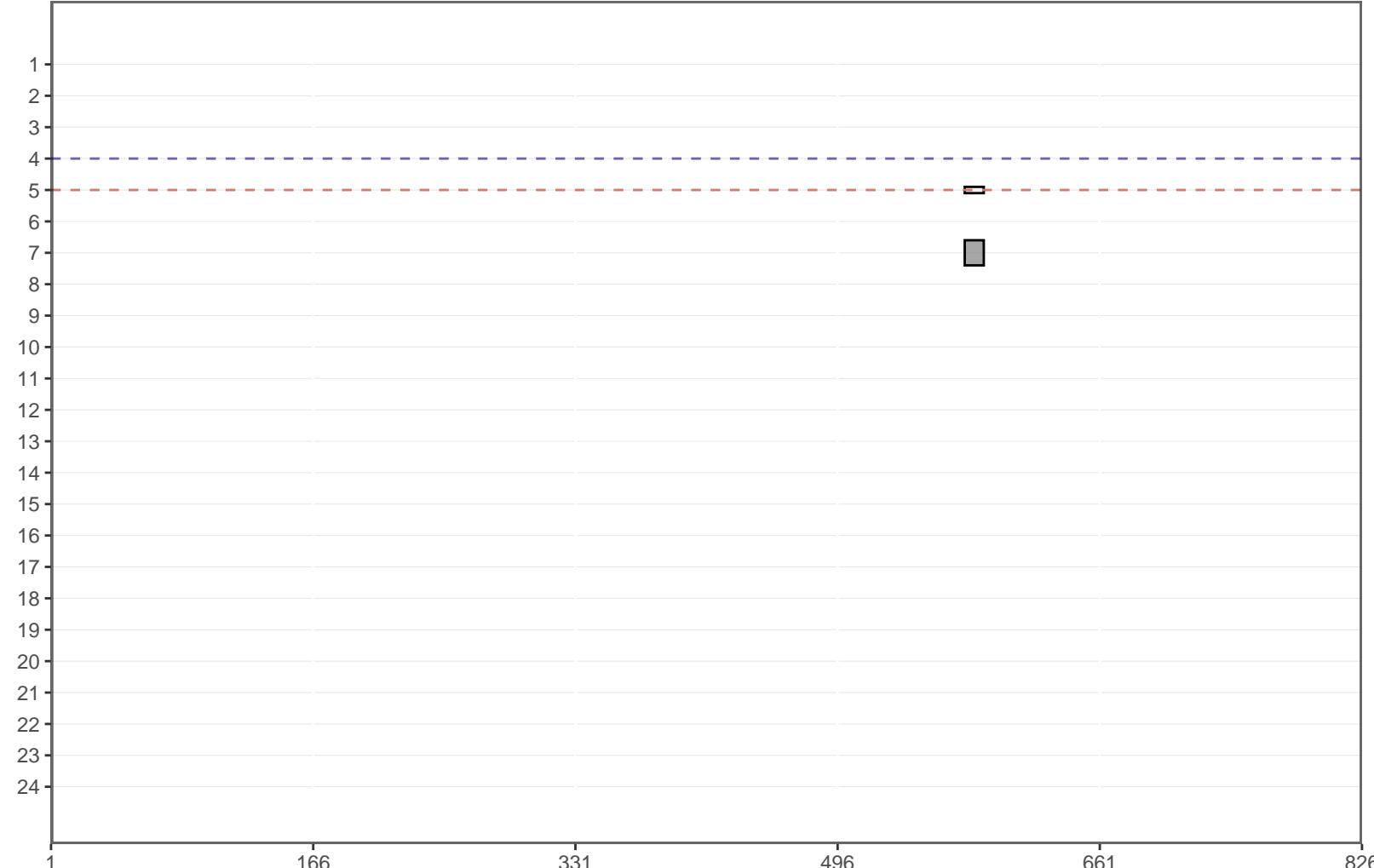
MW indication



Molecular weight



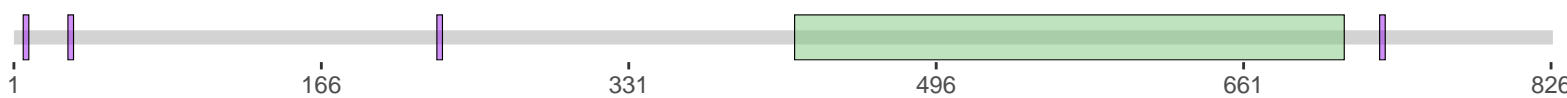
Gel Slice



Protein length

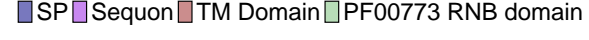


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RDEILVAEISLSSPTDLDEADRVLTDLKVAIDVDEDELDDALSATRLGGGRKVVHVVADPTSLQPGSHDKDARRRGTSLFPLTATYPMFPERLAMEGMLKGGRLGNVTVSVLVRDGGDAEYVSVNSIKPTVMALTYEATLHLLNEEEIEIKVLSAAAALRLRWRREGGADTGTLETIRKVTNFDHPPEPKLVVENGADAAARLVSEMMVVGGEVATYGSHPNPLPYRGGPQENIDTSAFEHLPEGPVRSAAVIRIMRAAEMDFRNPVRHGVLGLPGYVQFTI

NbL05g05440.1 expansin-A3-like [MW - SP = 25.59 kDa]

No. of times detected



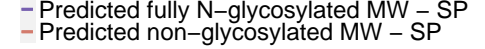
log(intensity)



Values from



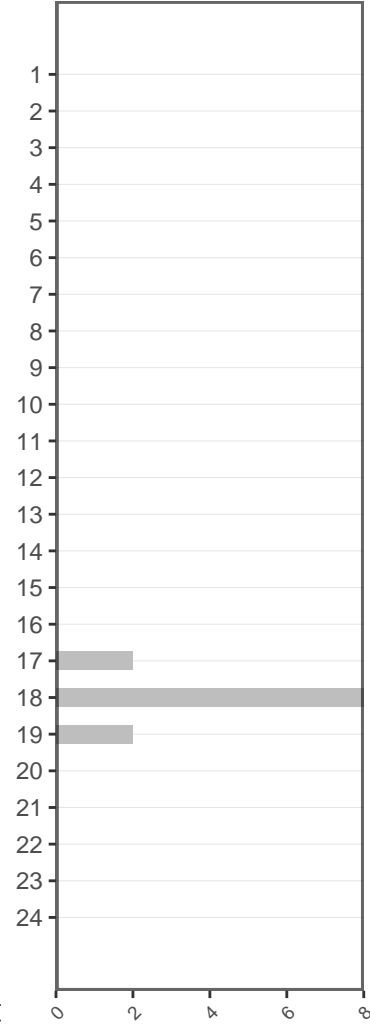
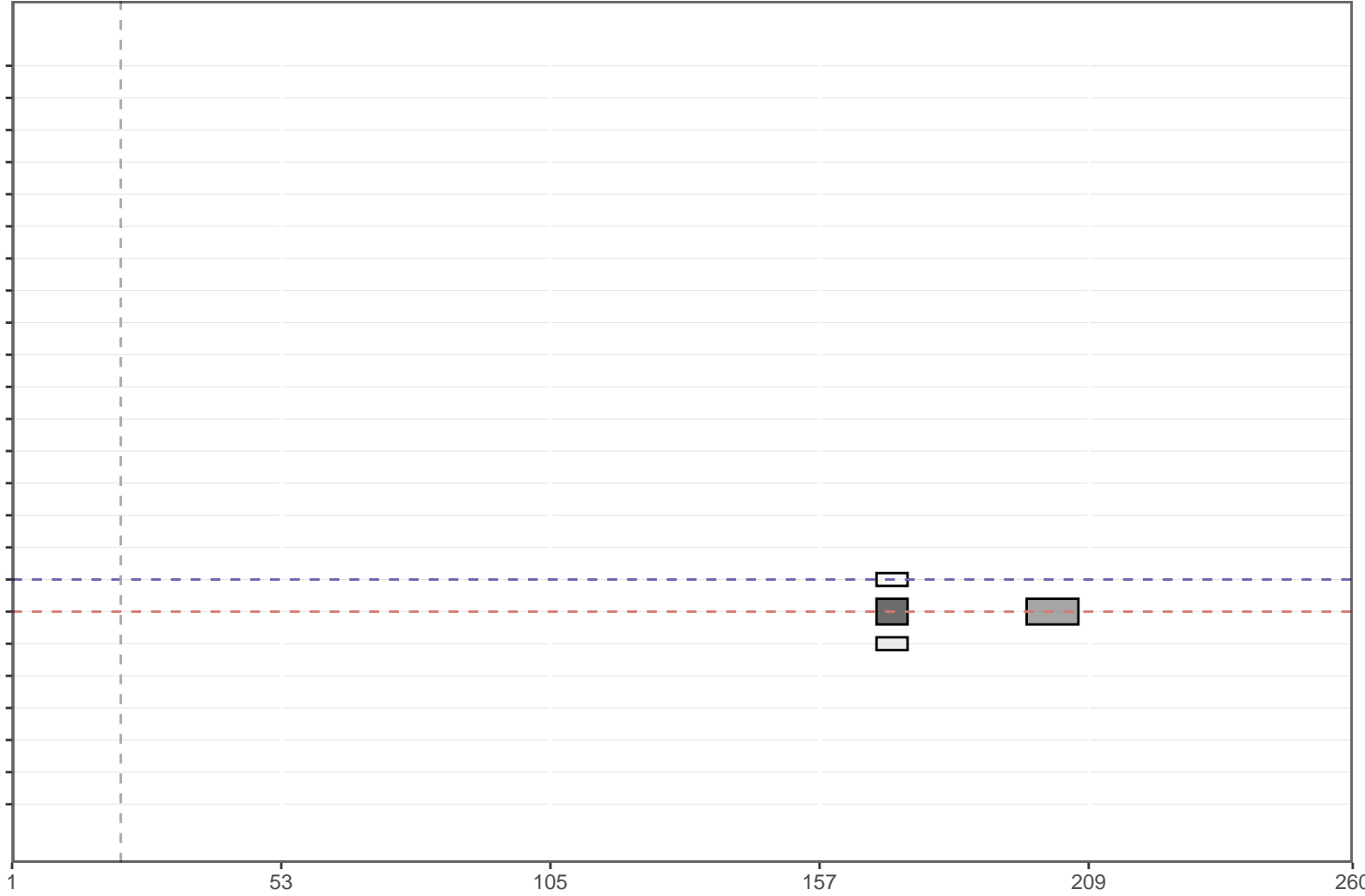
MW indication



Molecular weight



Gel Slice



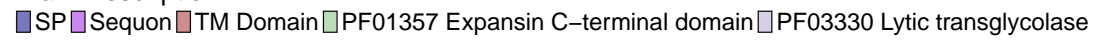
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

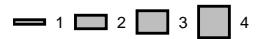


Protein sequence:

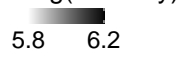
PNDDGGWCNPPRPKFDLAMPFLKGGYRAGIVFVYRVRPCRKAGGRFTNGFRVFNLLLVNAGAGDQKVLKGTNTQWAMBRNWSGNWGTNVLVGGALSIRWASDRPVTSTNVAFPNWFQGGTFEGKFRV

NbL05g05270.1 shock_cognate_70_kDa_protein_2-like [MW = 71.1 kDa]

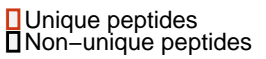
No. of times detected



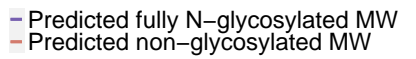
log(intensity)



Values from



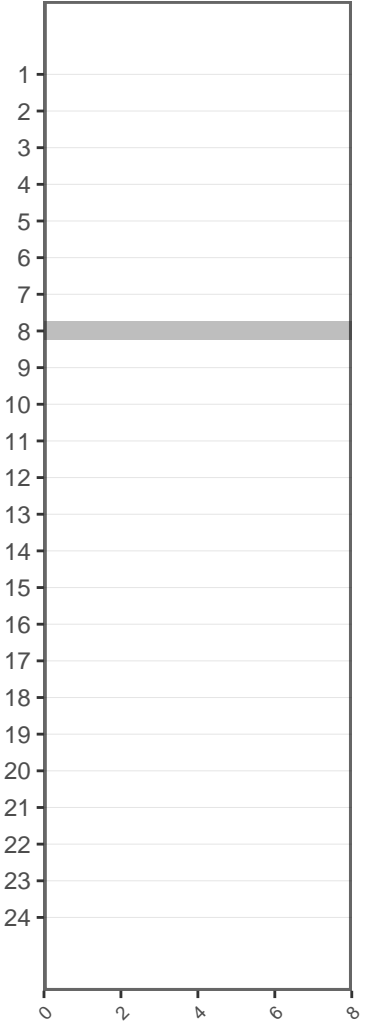
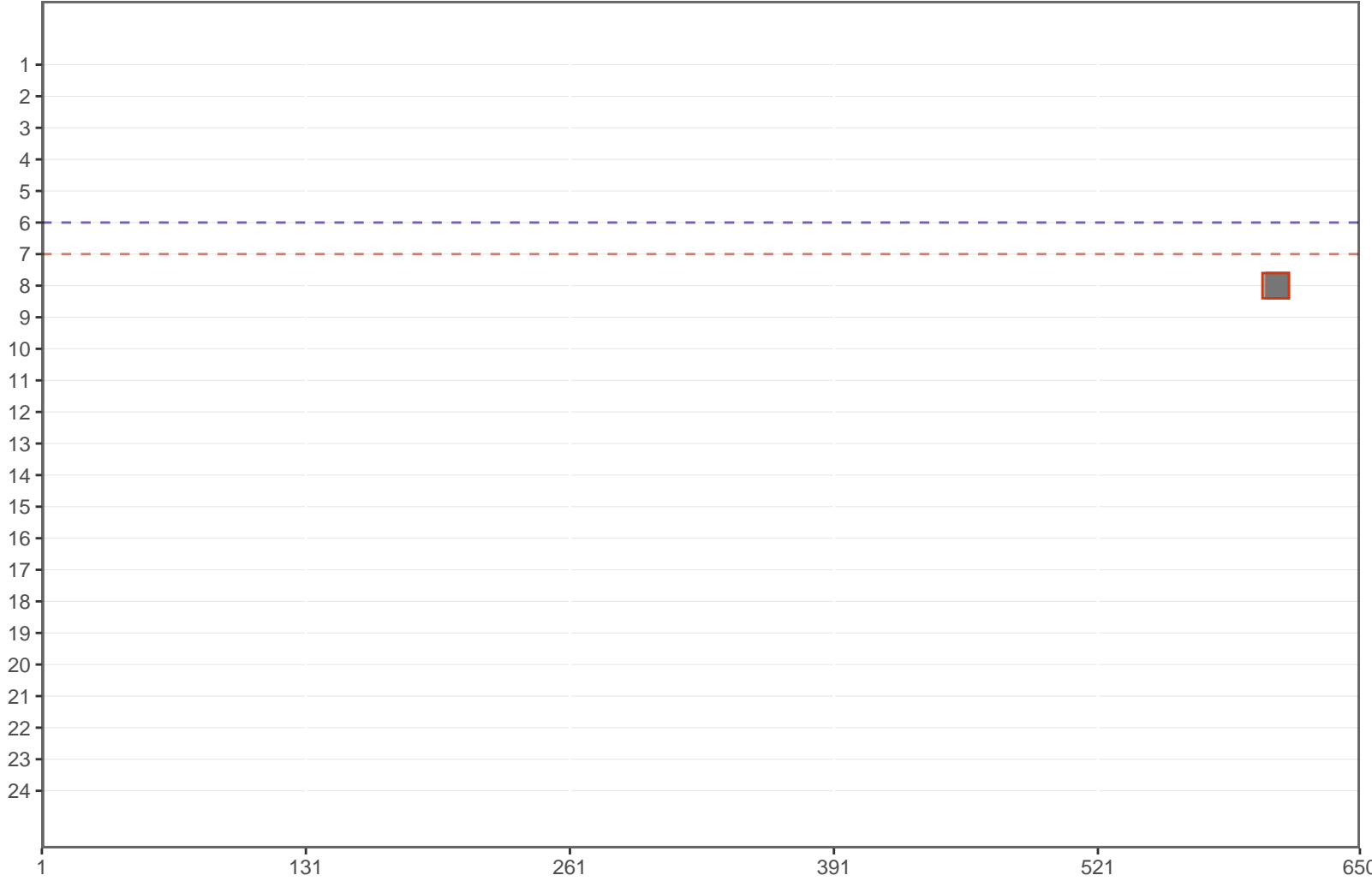
MW indication



Molecular weight



Gel Slice

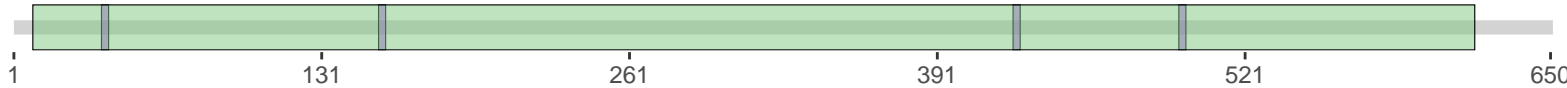


Protein length

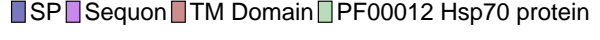


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LFRRKCMPEVKEKLRDAMDKSTHEDVLLVGGSTRIPIKVDGLLDGDFNFKELGKSNPDEAVVYGAIVQAAALSGEGNEKVGDLILLDVTPLSLGLETAGGVMTVLIPIRNTTIPFKKEGVFSTYSQNGPVLQVYEGGERTRTRDNNLKGKELGSPAPRPGVPGITVCFDIDANGLNVAEDKTTGQNKTTITNDKGRLSKEEIEKMWGEAEKYKSEDEHKKKVEAKNLENVWMMRNTVYKDEKIASKLPKADKKKIEDIEAAIGWLDANGLAESDEFEDMKKELESVCA

NbL05g05150.1 5-oxoprolinase-like [MW = 137.99 kDa]

No. of times detected



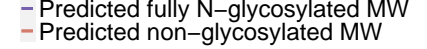
log(intensity)



Values from



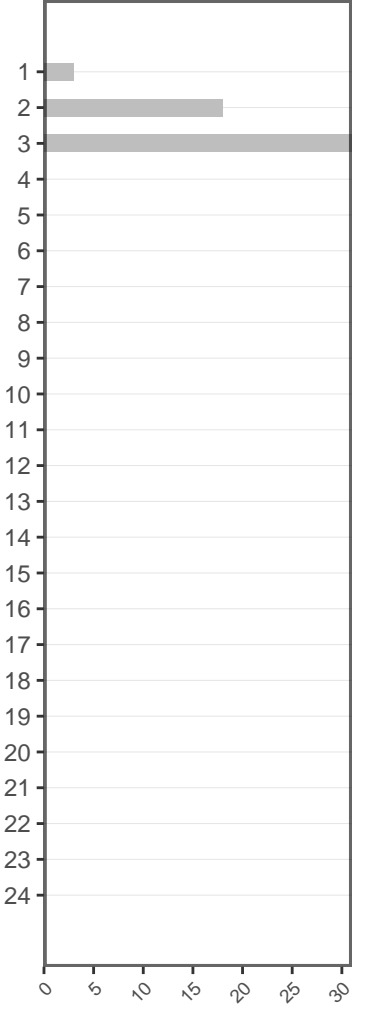
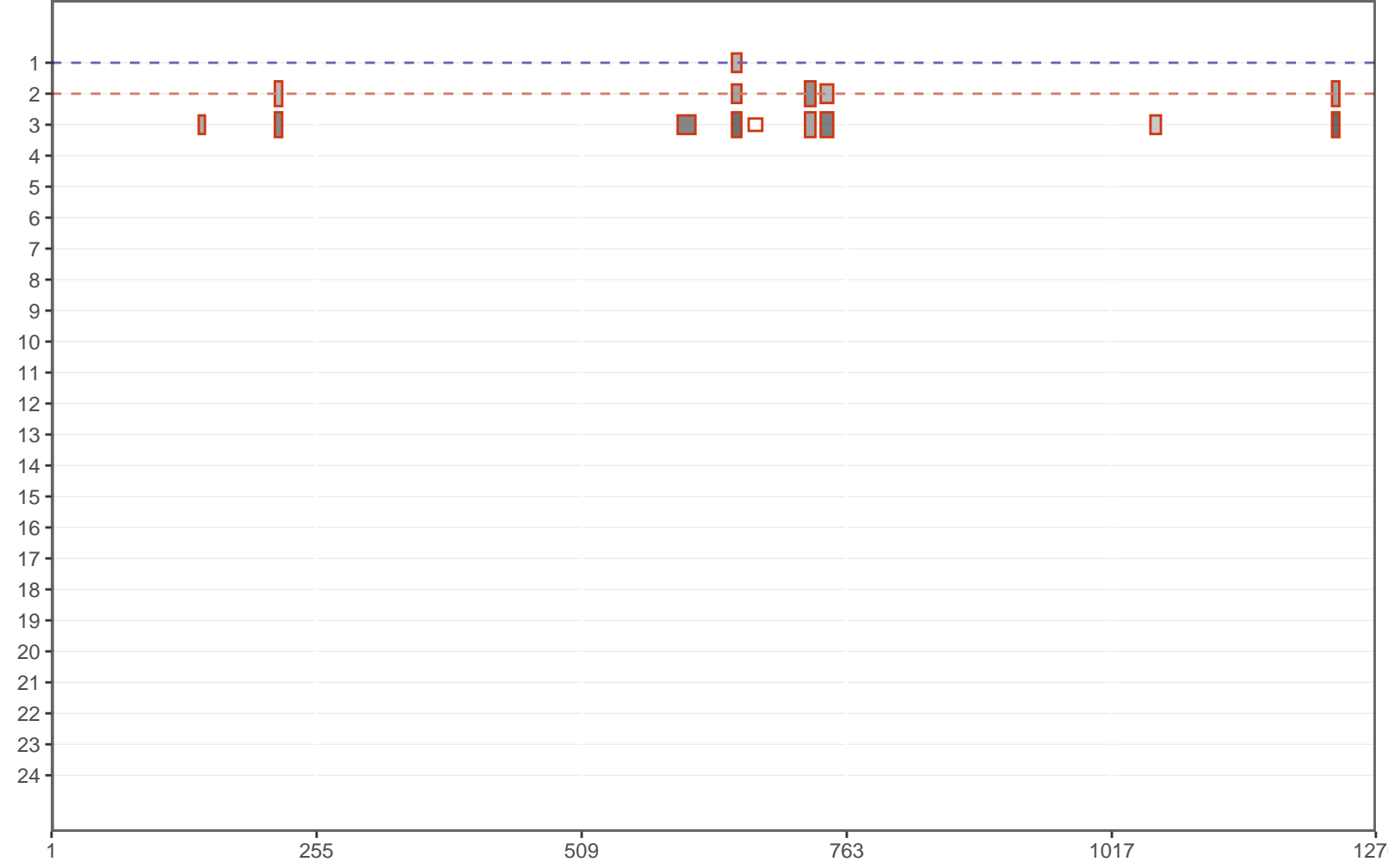
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01968 Hydantoinase/oxoprolinase
- PF02538 Hydantoinase B/oxoprolinase
- PF05378 Hydantoinase/oxoprolinase N-terminal region

Protein sequence:

IEYGFKLQNRNVIGDVRVRGVGVYTNLKPRLDSEFPAPKIEHYSKVVYFNGWNETPLFKLENLAVGNVYVPGRIIMNGNSTVIVEPNKASITKYGNKIEEGASNTAKLDEKVAHYVQLSEFNFRFMGIAEQMGRTLQRTSISITNKERLDFSCALFGPDGLVNAFHPYVHLGAMSSVTRWQLGHVWGDNLNEGDLVANHPSAGGSHLPDITVTPVFNKGRLEFFVSRGHMAEIGGITPQSMPPFSKFIWEEGAIAKAFKLVKGTPTQEEGTKLRYPCSEESTHNIPG

NbL05g05030.1 eukaryotic_translation_initiation_factor_3_subunit_A [MW = 111.63 kDa]

No. of times detected



log(intensity)



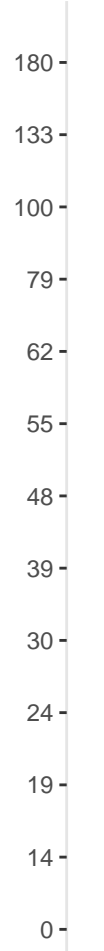
Values from



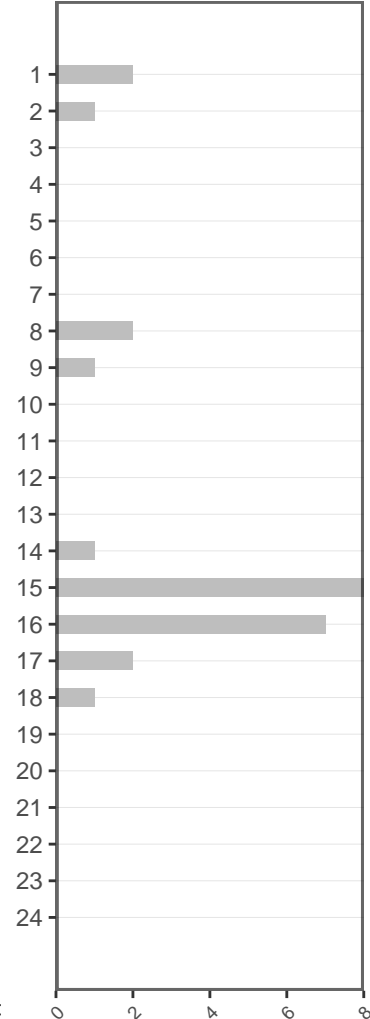
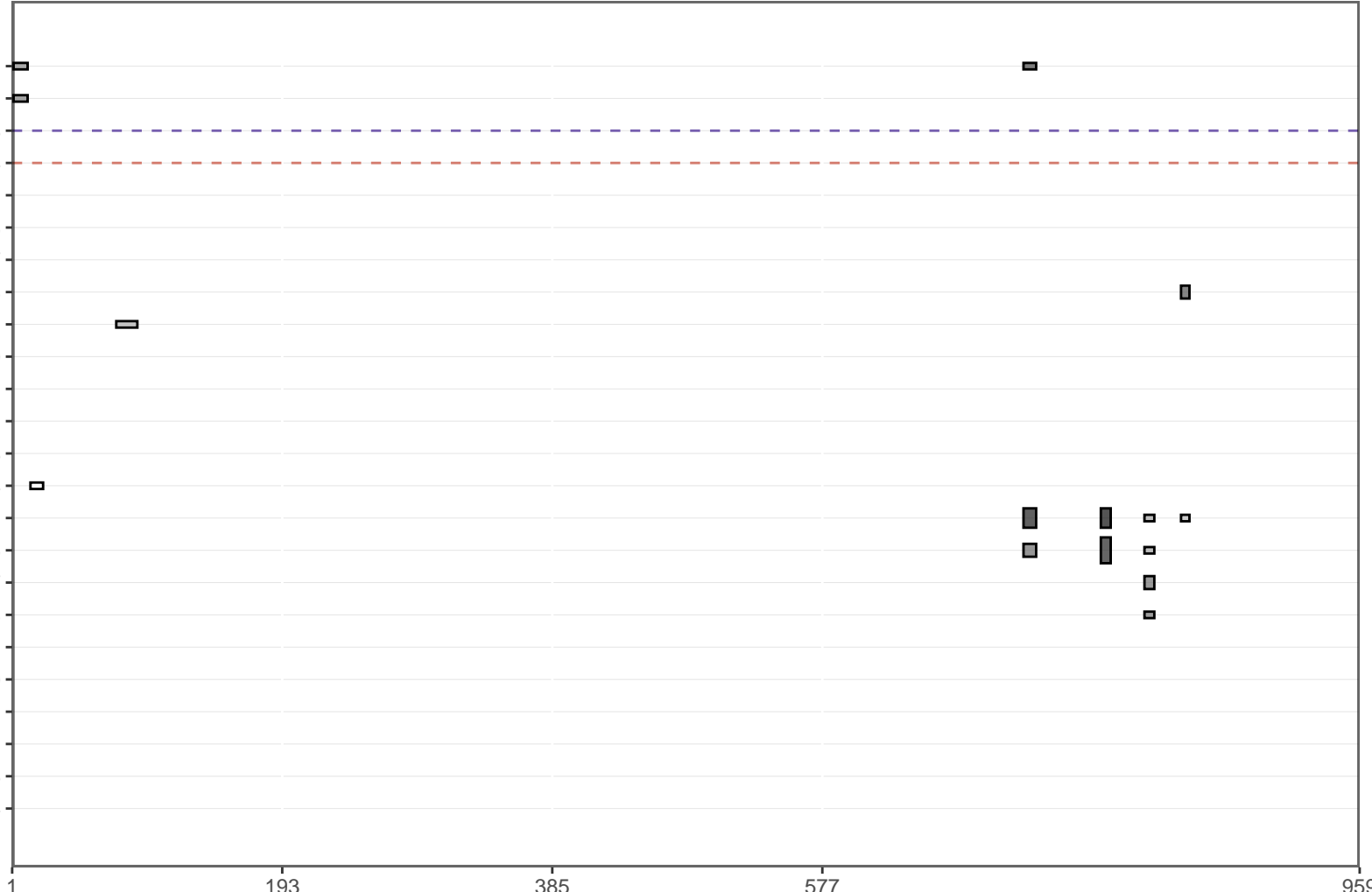
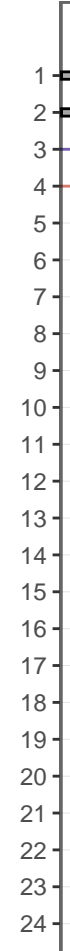
MW indication



Molecular weight

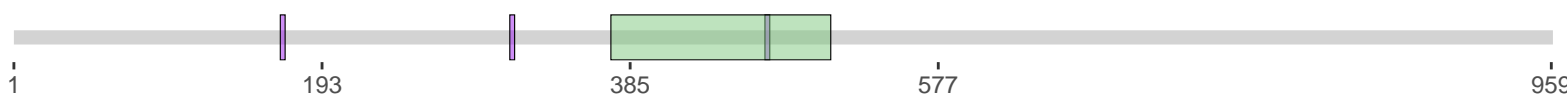


Gel Slice



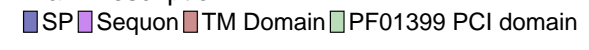
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NISKMIPFFDFTYIEKIVSDAVRRNFLAKVVDHMKGVAFVFGKGSIEAEGLRDHLSLLAEELSKARTMYPYPAKKAALKEALSNAIEVEKEHKRLARKSHIEKRKEEGEQLLLEMERVEETKRRRELQKMTTEEAEGKRIAVEVEGRRRNRILKHEIDRELEEAGALLHEAEKRKRKKKPVLEGEKMTKGVIMELALNEQLREGEEMKLLKFAKTMHLEERAKREEAAPLIESAFKGLRAEEAALHEREGQDIEELSRGRHAGDLEEKRLGRMLENKRLOEKVYSREAEF

NbL05g05010.1 actin-depolymerizing_factor_1 [MW = 15.95 kDa]

No. of times detected



log(intensity)



Values from



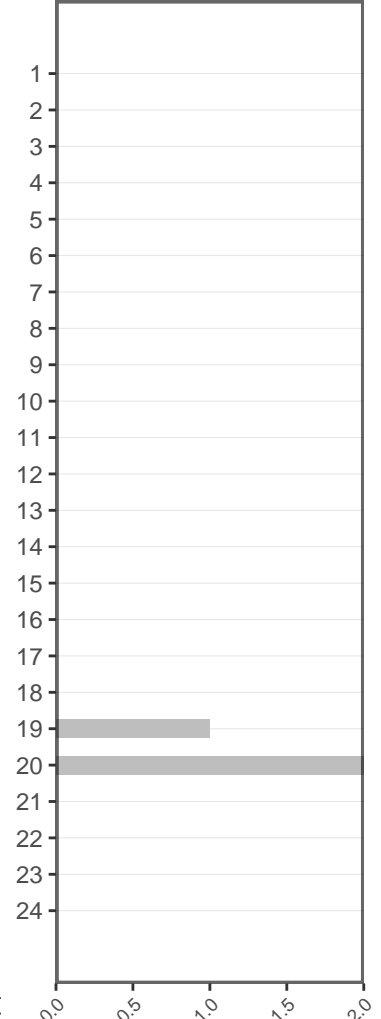
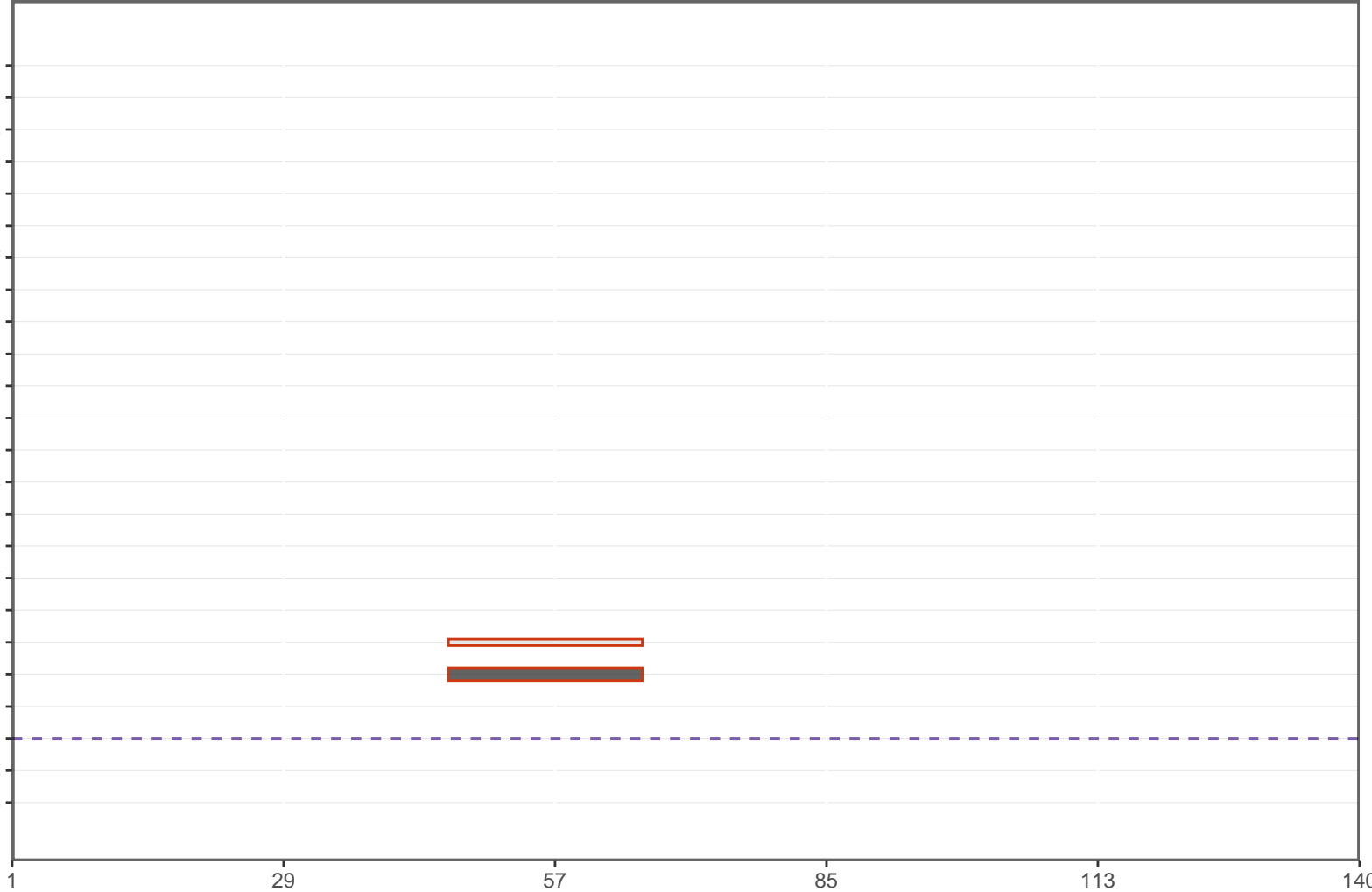
MW indication



Molecular weight



Gel Slice

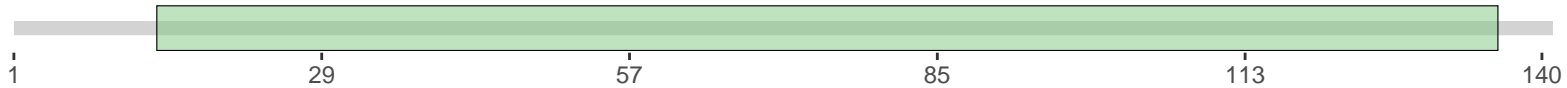


Protein length

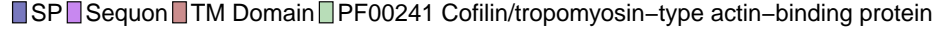


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

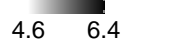
MAASLPDNECRYAVVDFDFVTAENQKSRIFIAWSPDTERVRKMKVYASKDKRFRKRELDGQVLEQATDPTKEMGLGVKSRAN

NbL05g04990.1 arginine_biosynthesis_bifunctional_protein_ArgJ_chloroplastic [MW = 49.27 kDa]

No. of times detected



log(intensity)



Values from



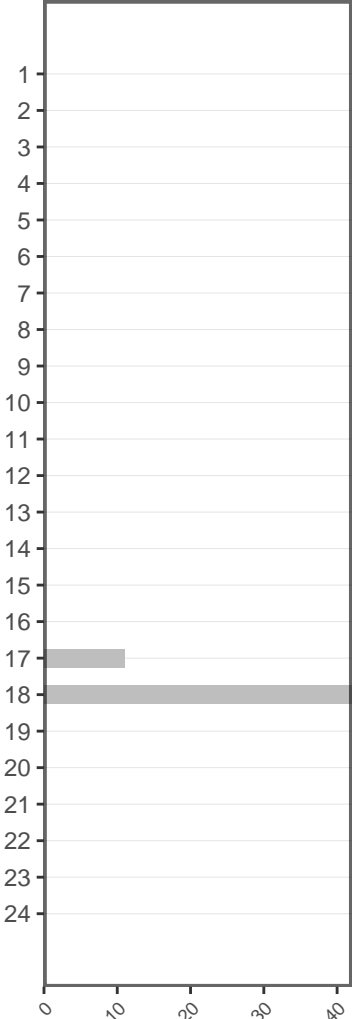
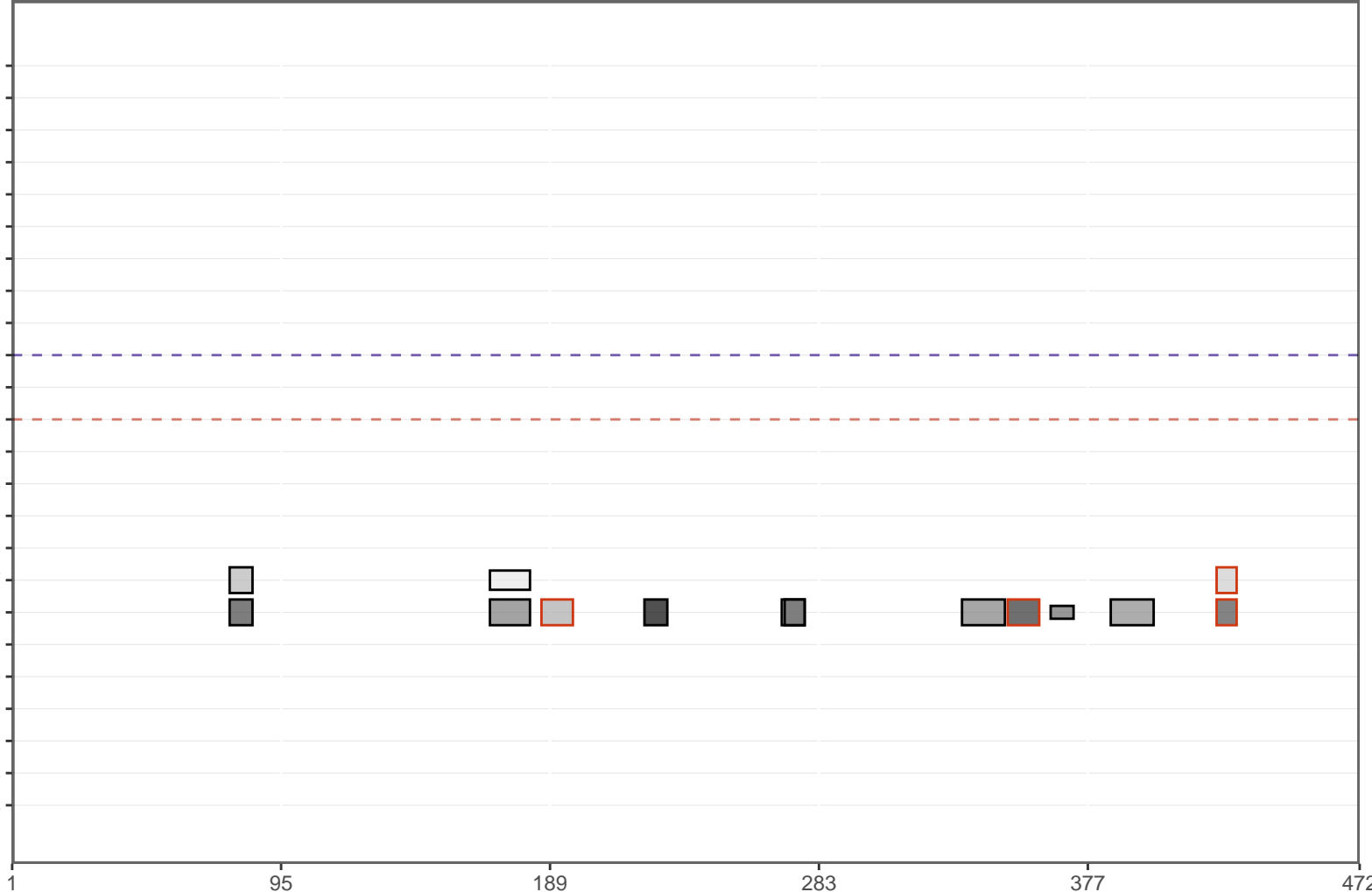
MW indication



Molecular weight

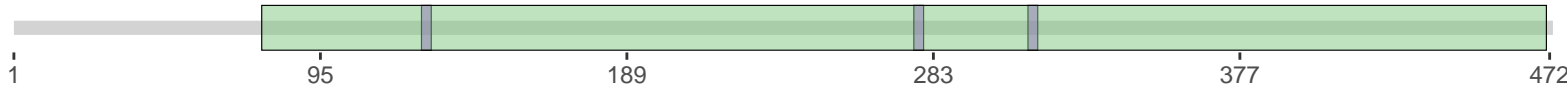


Gel Slice



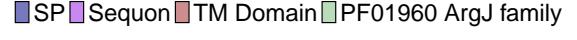
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ETEVKTRIRIVGGMAKGGSMHPNMTMLGVVTTDASVTSQVSRKMGVAVVRSFGITVGGDTSTNDVAIALAGLSESEYELSLNCEAEHLGNLGDVWMLGKLSKSIWVDEGEGATGLIEVRRVAGADNEADAAKIARVSAASLKVAAVYGRDPNWRGRIAGAAAGYAGIPFNDSKLRISLGDVLMKAGDLPFFDRIAAASNYLRKAGDVHGTVEIQISTGDCGPGSSGLAWGCDLSDYDVKINAEYTT

NbL05g04950.1 soluble_inorganic_pyrophosphatase-like [MW = 24.46 kDa]

No. of times detected



log(intensity)



Values from



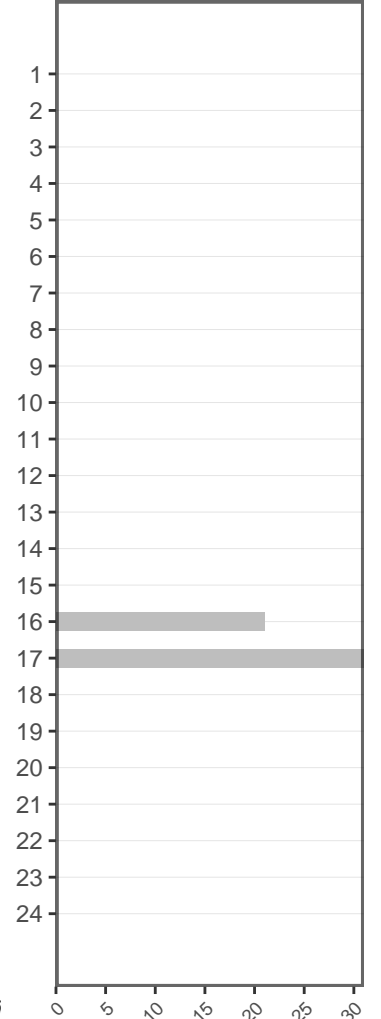
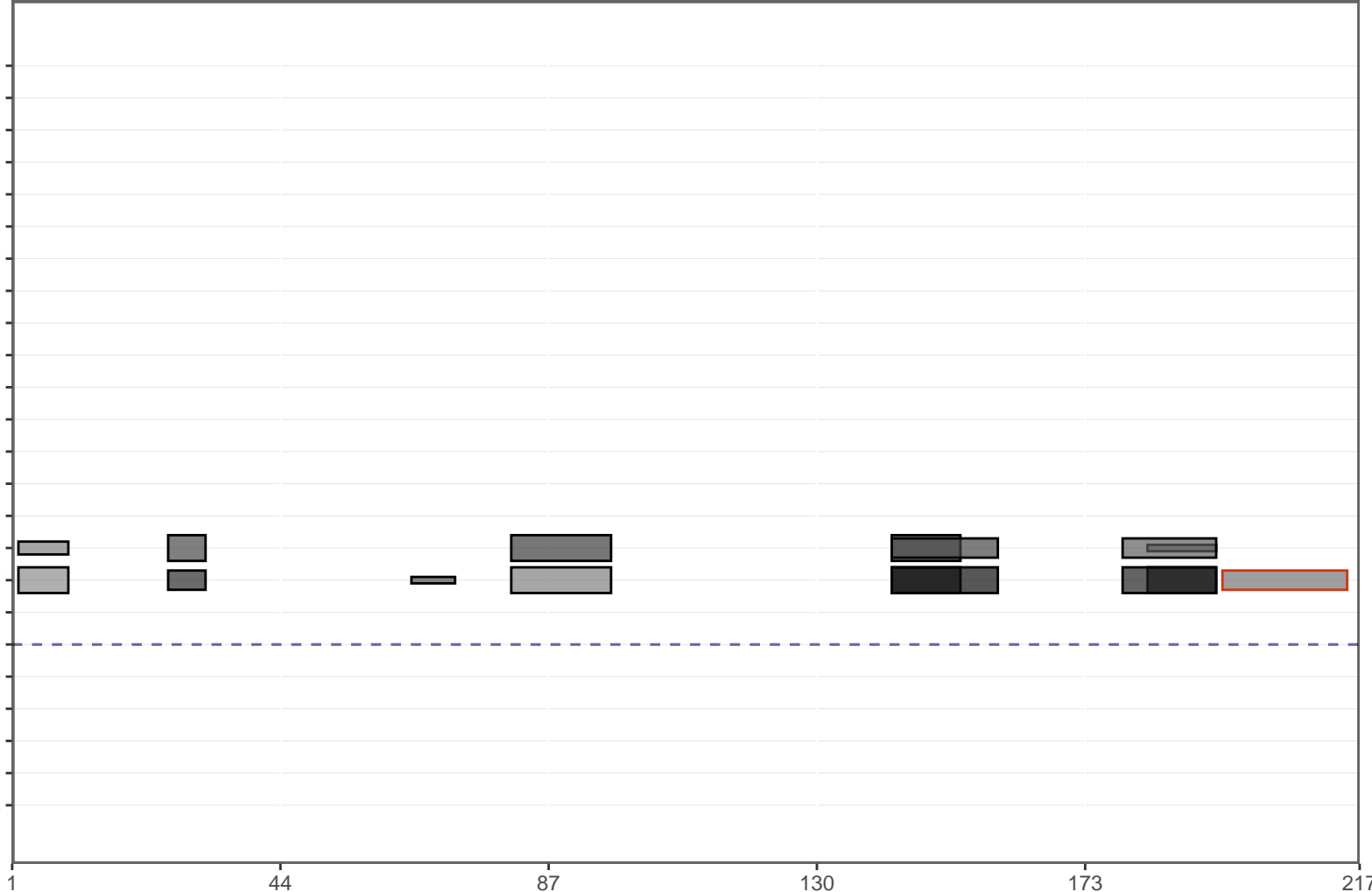
MW indication



Molecular weight

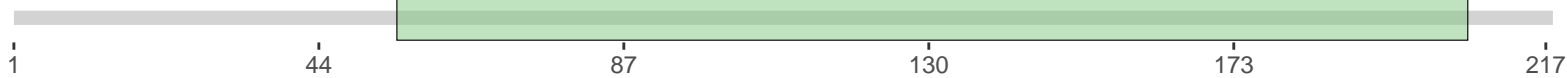


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IPRTLCEDSPLDVAVMQEPVLPNGFLRAKAGLMPMDGGEKDKIIVAGADDPPEYKDYDKMLPPHRLAEIRRFEDYKKNENKEVAVNDFLPATKAFEAVGHSDYADYVVEELRR*

NbL05g04920.1 ras-related_protein_RABE1c-like [MW = 23.99 kDa]

No. of times detected



log(intensity)



Values from



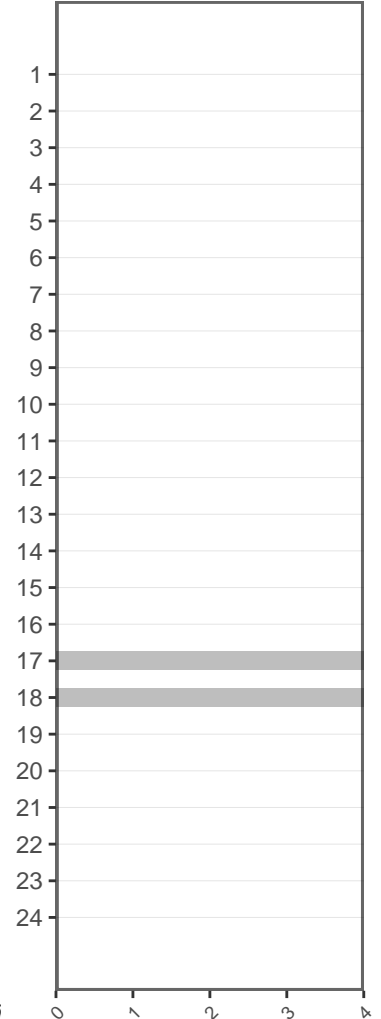
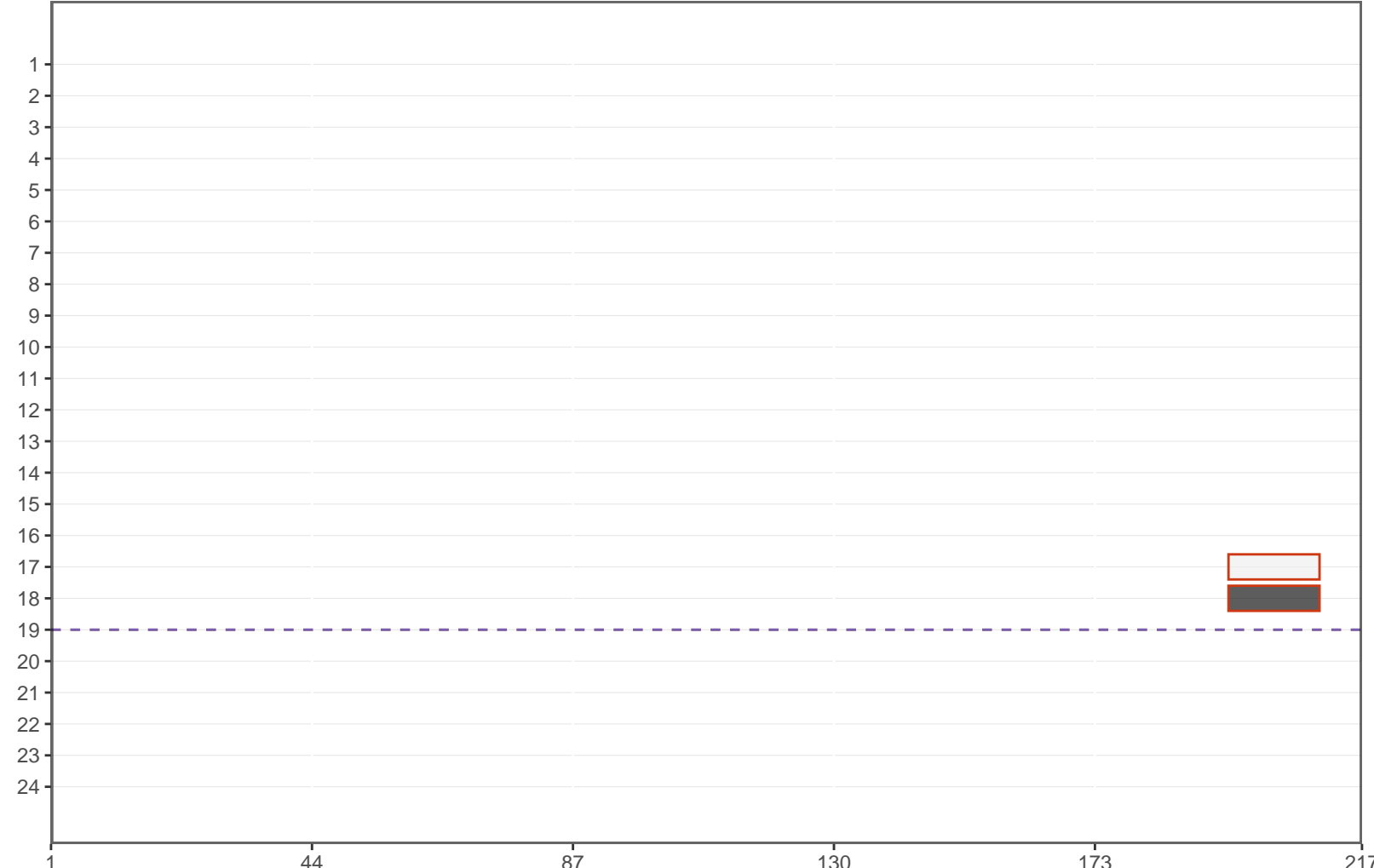
MW indication



Molecular weight



Gel Slice

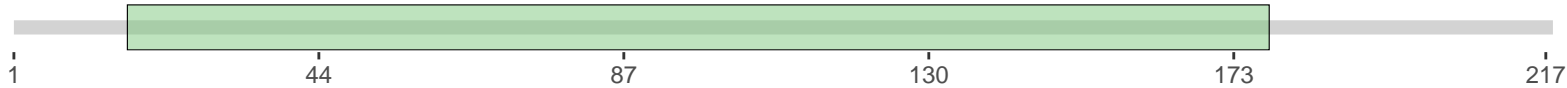


Protein length

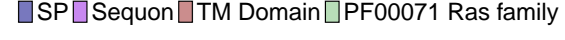


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

DESSFNIRNRYWRNEQHASDNNKILVGNKADMDSEKRAVPTTSKGGALAEYGIKFFETSAKTNMNVVEVFFSARDIKRGLAEESDSEKAEPTQIRINQPDGAGAGAGKSAAGGS

NbL05g04890.1 diaminopimelate_epimerase_chloroplastic-like [MW = 39.77 kDa]

No. of times detected



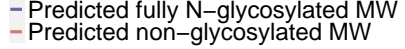
log(intensity)



Values from



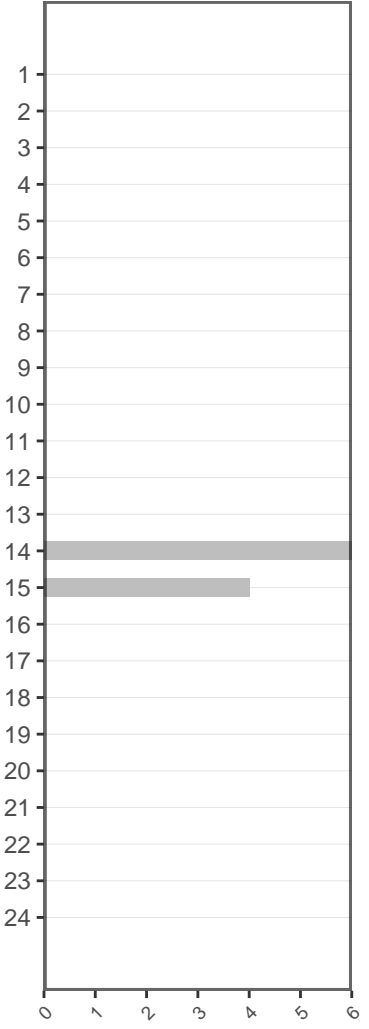
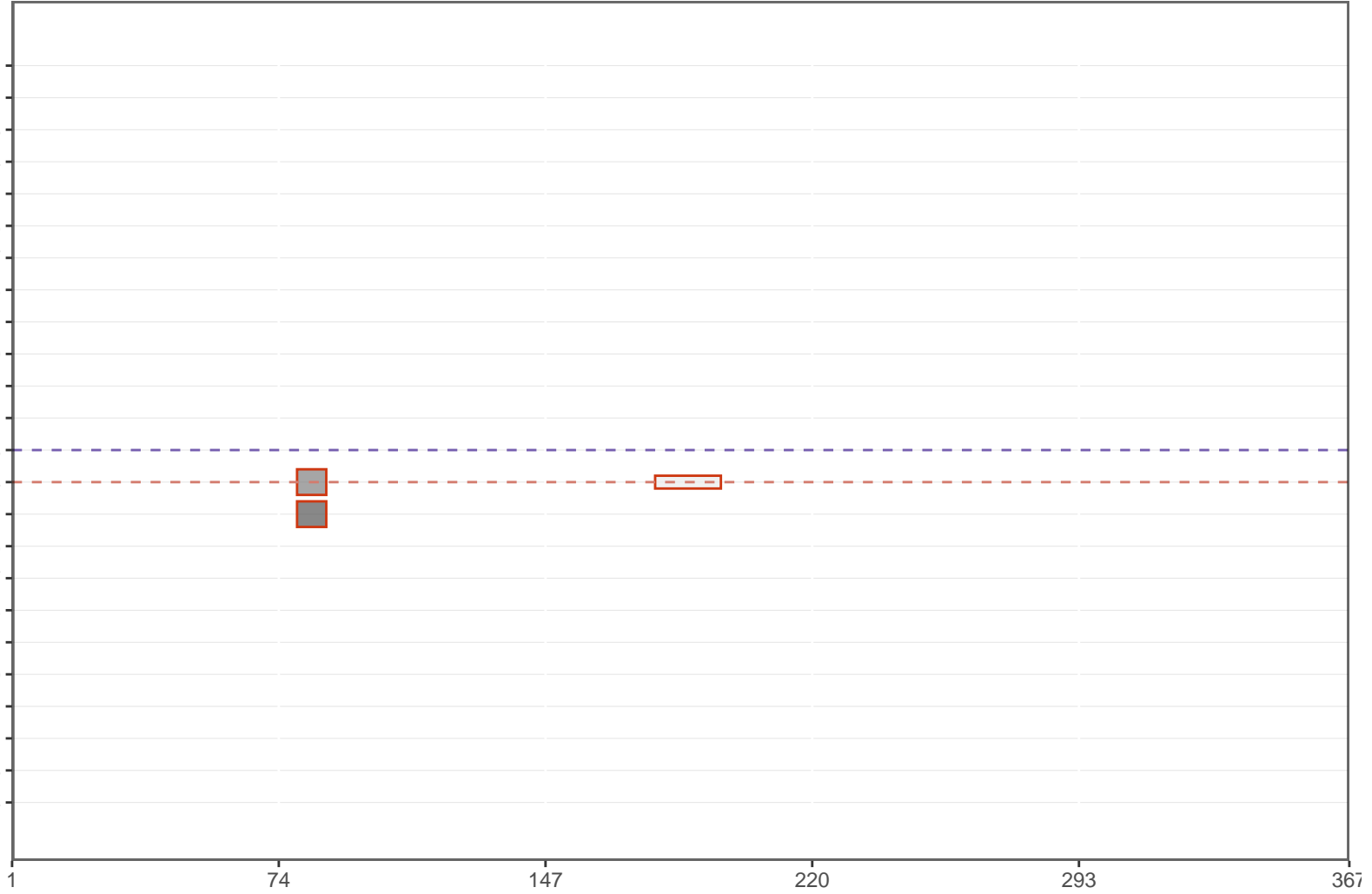
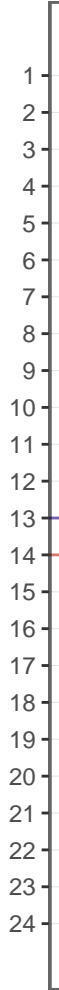
MW indication



Molecular weight



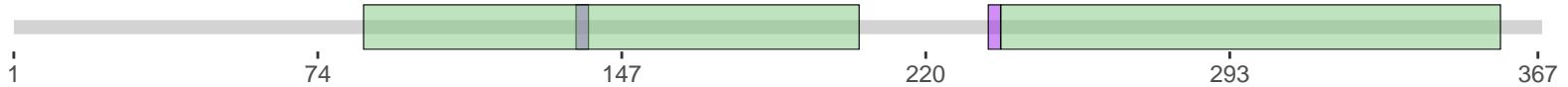
Gel Slice



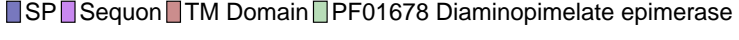
Protein length



Pfam domains



Pfam Description



Protein sequence:

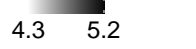
IGKRSFTHTGGGLVPEIQEENKVRVDMGEPLKASDVPFKLFPNRDQKVVAKRLVDGTAWNVTGVSMGNPHCVTFGTGGSDLVDELNLADIGKFEHHVMEFARTNTEFVGVFSPHLKMRVWERGAGVTLAGGTGACAVAAVALEDRARRCTVLDLPGPLDIEWSEKDNHHYMTGPAEVVFFYGVPLV

NbL05g04860.1 protein_SLOW_GREEN_1_chloroplastic-like [MW = 40.07 kDa]

No. of times detected



log(intensity)



Values from



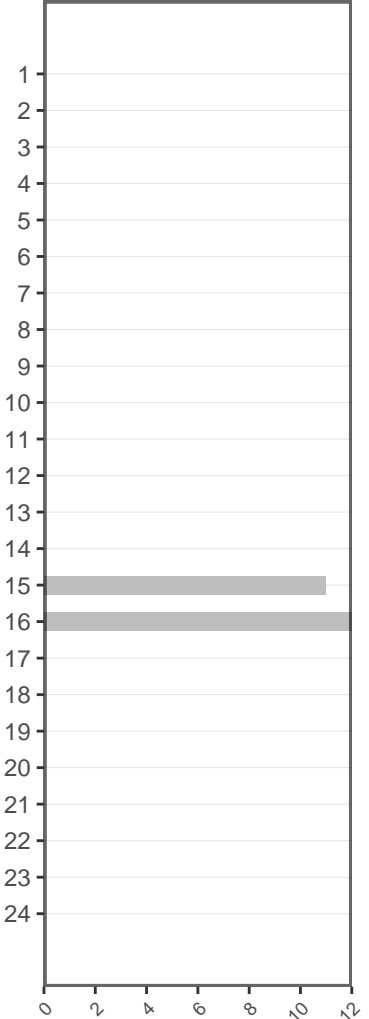
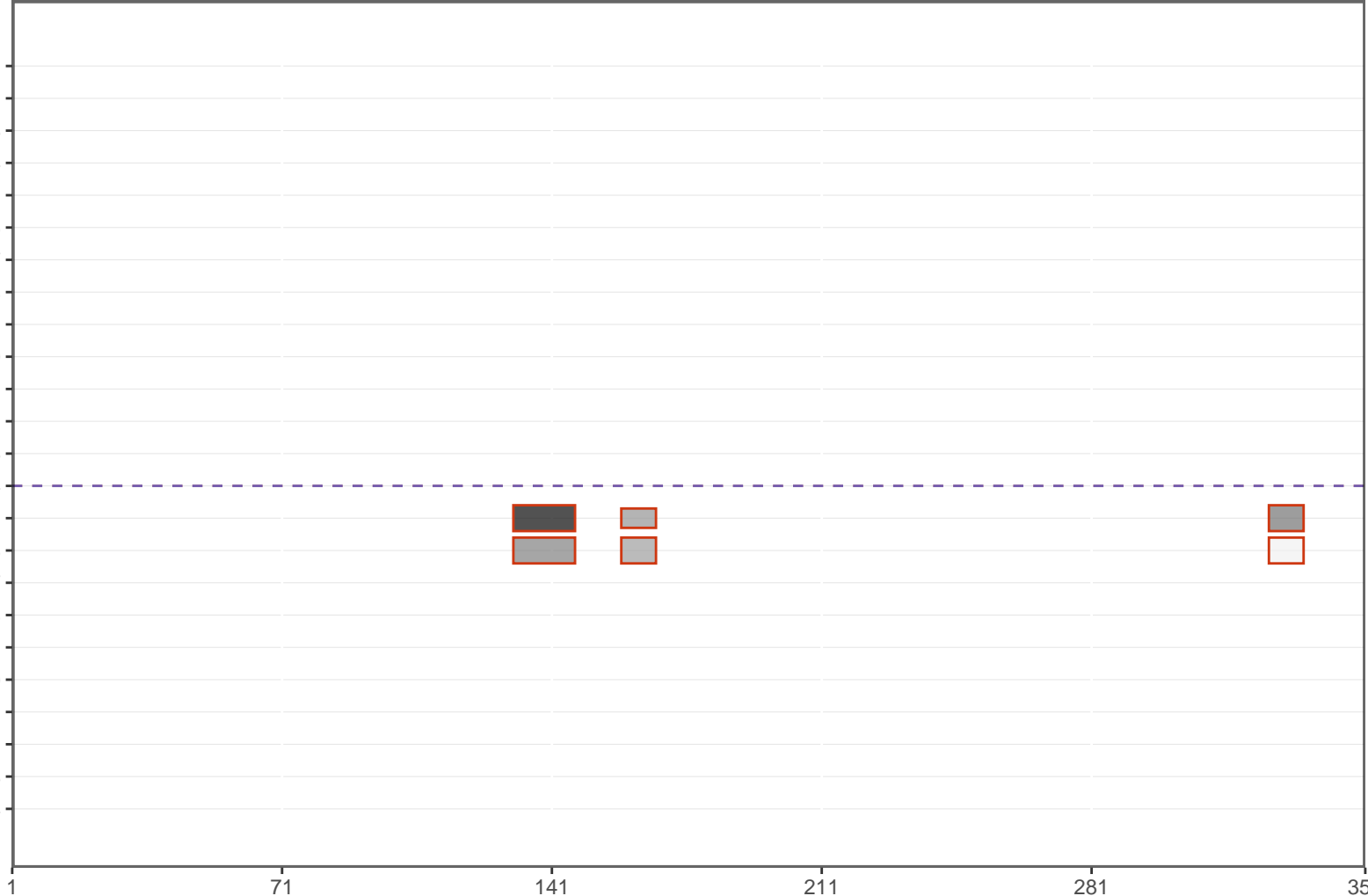
MW indication



Molecular weight



Gel Slice

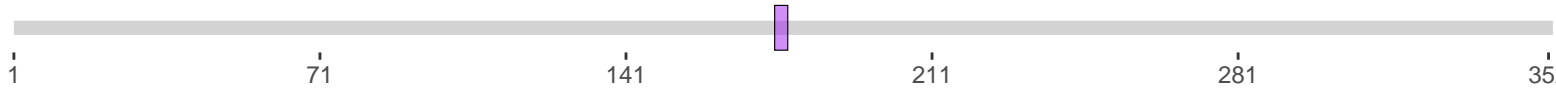


Protein length

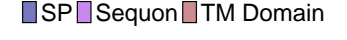


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

MDKLEVEPNESEWPLMKSHLYVNGEVELAKVGFNEIHKKDFRVEAYHGLVMAASQDEEDLKGIEKMEEGMGLGKKNKKTDLRDFRLLLAGRIVIEGKYEDALKVYVELNKEPRDFRPVLOGGIYTLRKSSDAEKGFERYRLVPGQHPVARYFDENMATHKVFQKVENERAGSKS

NbL05g04800.1 UDP-glucuronic_acid_decarboxylase_1-like [MW = 48.72 kDa]

No. of times detected



log(intensity)



Values from



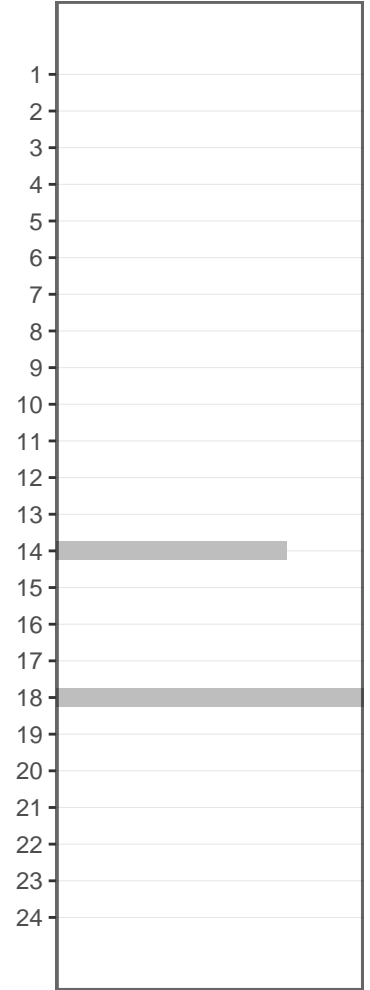
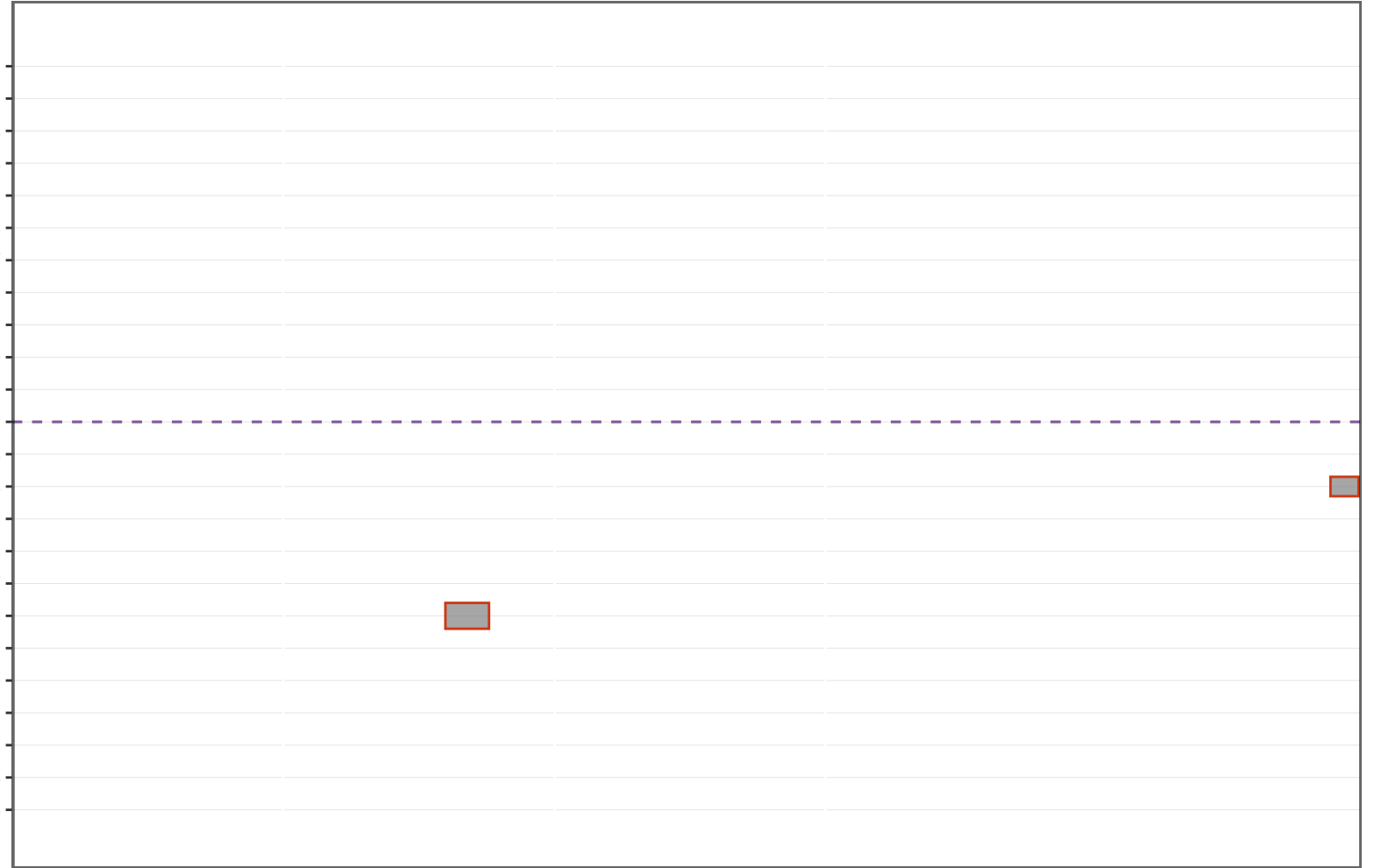
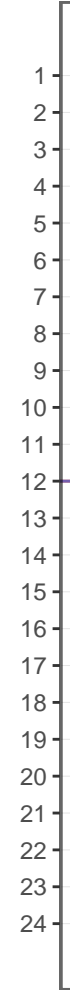
MW indication



Molecular weight



Gel Slice



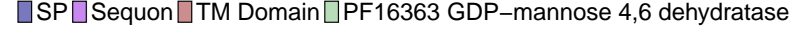
Peptide counts over 4 repeats

Protein length

Pfam domains



Pfam Description

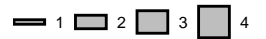


Protein sequence:

IVMSTLMLGLAKRIGARFLTSTSEVYGDPLEHPQKETVWGHVNPIGVRSQYDEGKRTAETLMDVHRGAGVEVRIARFNTYGRIMCLDDGRVSNVFAQIRNQPMTVYGDGKQTRSFQVSDLVLDGLVLMGEHIGIPFNLGNPGEFTMLELAEVVKVEIDPSAKIEFRANTADDPKRRKPDISKAKELLNWEKRVPLREGLPLMVNDFRIRLNDEDEGEN

NbL05g04580.1 protein_MODIFIER_OF_SNC1_11-like [MW = 21.42 kDa]

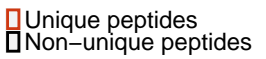
No. of times detected



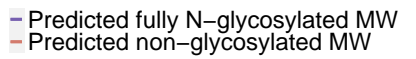
log(intensity)



Values from



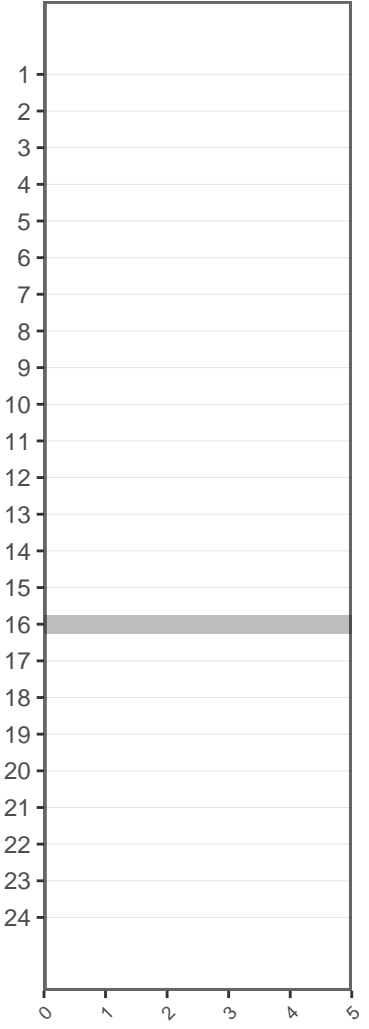
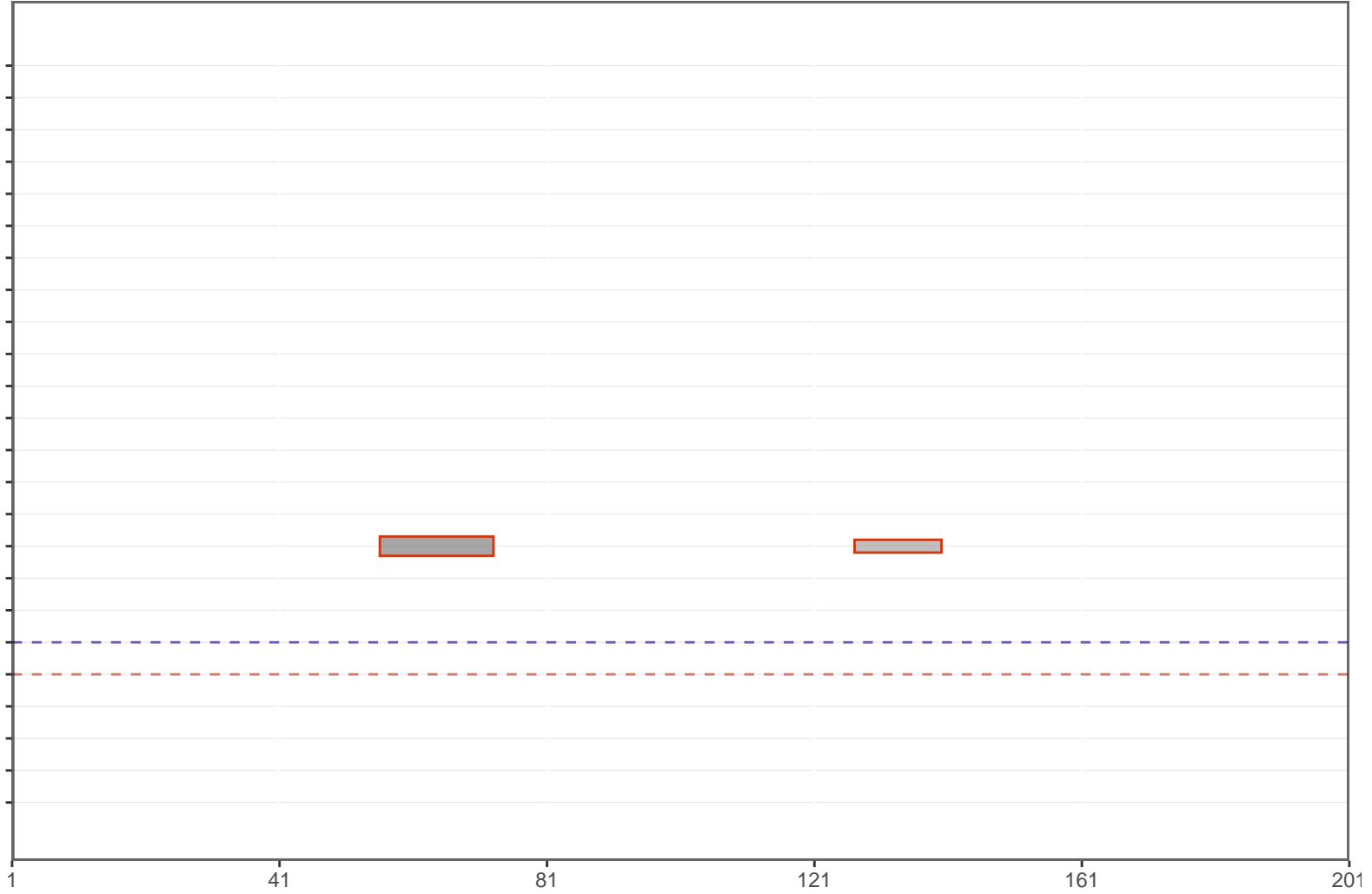
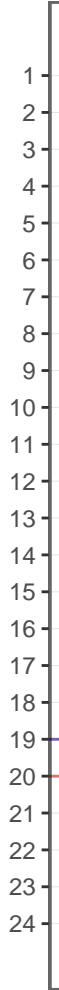
MW indication



Molecular weight

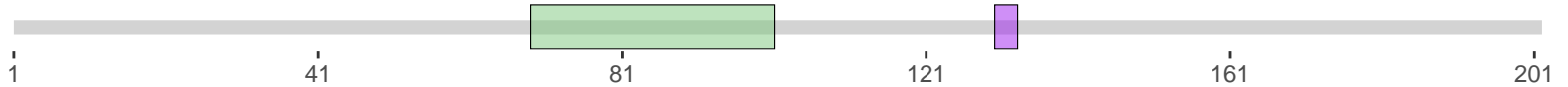


Gel Slice



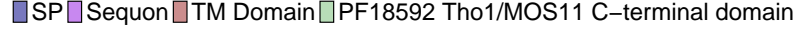
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IQEKRNTSRERFGTASAGGSDMLKKSEEGKRKRAERFQINGSDSADEEAKKKARLFRFTSTVKADPVEEDKRRKARALRFSGSGSGSGSENGKNGKIEQDTVVEKAGGGT

NbL05g04470.1 60S_ribosomal_protein_L4-like [MW = 48.06 kDa]

No. of times detected



log(intensity)



Values from



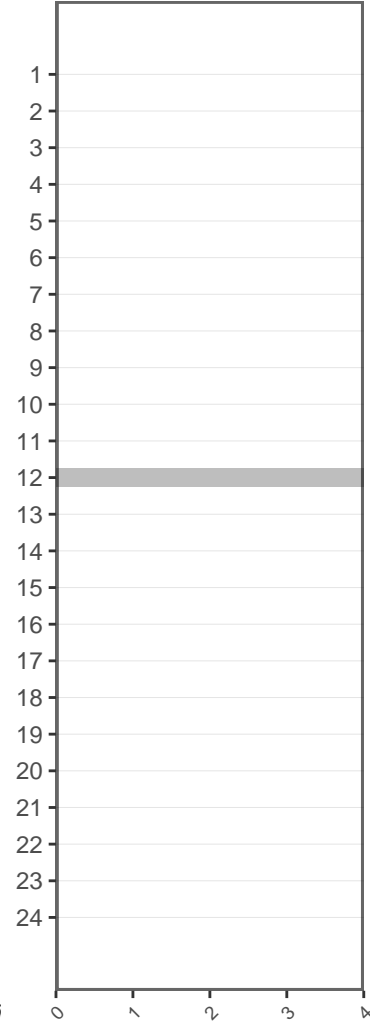
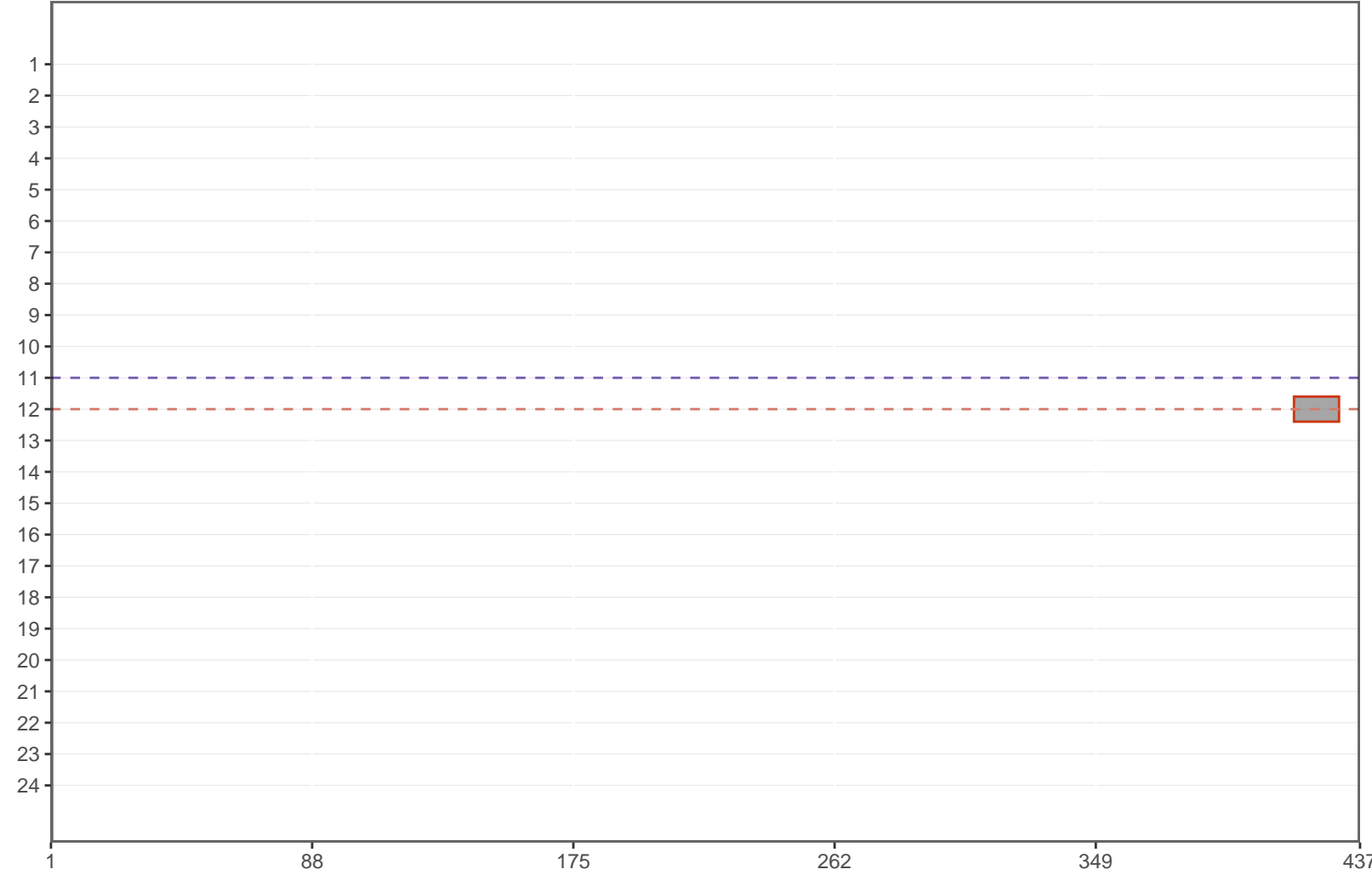
MW indication



Molecular weight

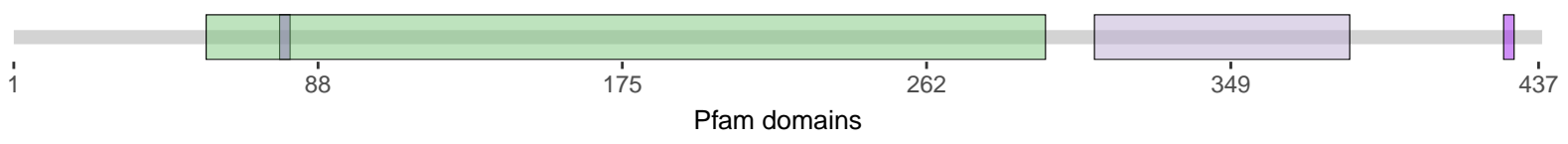


Gel Slice



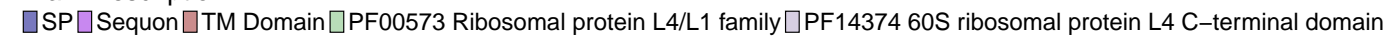
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CGVAYPDAEKAKNSHAIKPGKGMNRNRRVYSKGPLVYVGTGAKLWKAFRNIPGVEICHVDRLNLLKLPAGGHLGRFVWTKSAVEKLDSDSYGDFKPEKIKGKYLFRPRMVAADLARINSDEVSIVRPIKQVNRATLKKRNLNLLKLPVAKTARRMSSLAEADRIVKAKKEKLDKRRHQITKEEASAIRSASHWYKTMIDSDSYTEFDNFKWLVGSD

NbL05g04450.1 L-ascorbate_peroxidase_2_cytosolic [MW = 27.6 kDa]

No. of times detected



log(intensity)



Values from



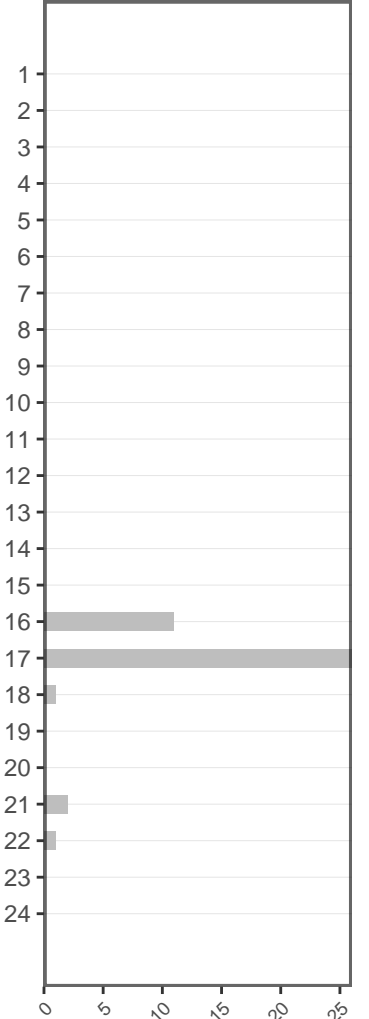
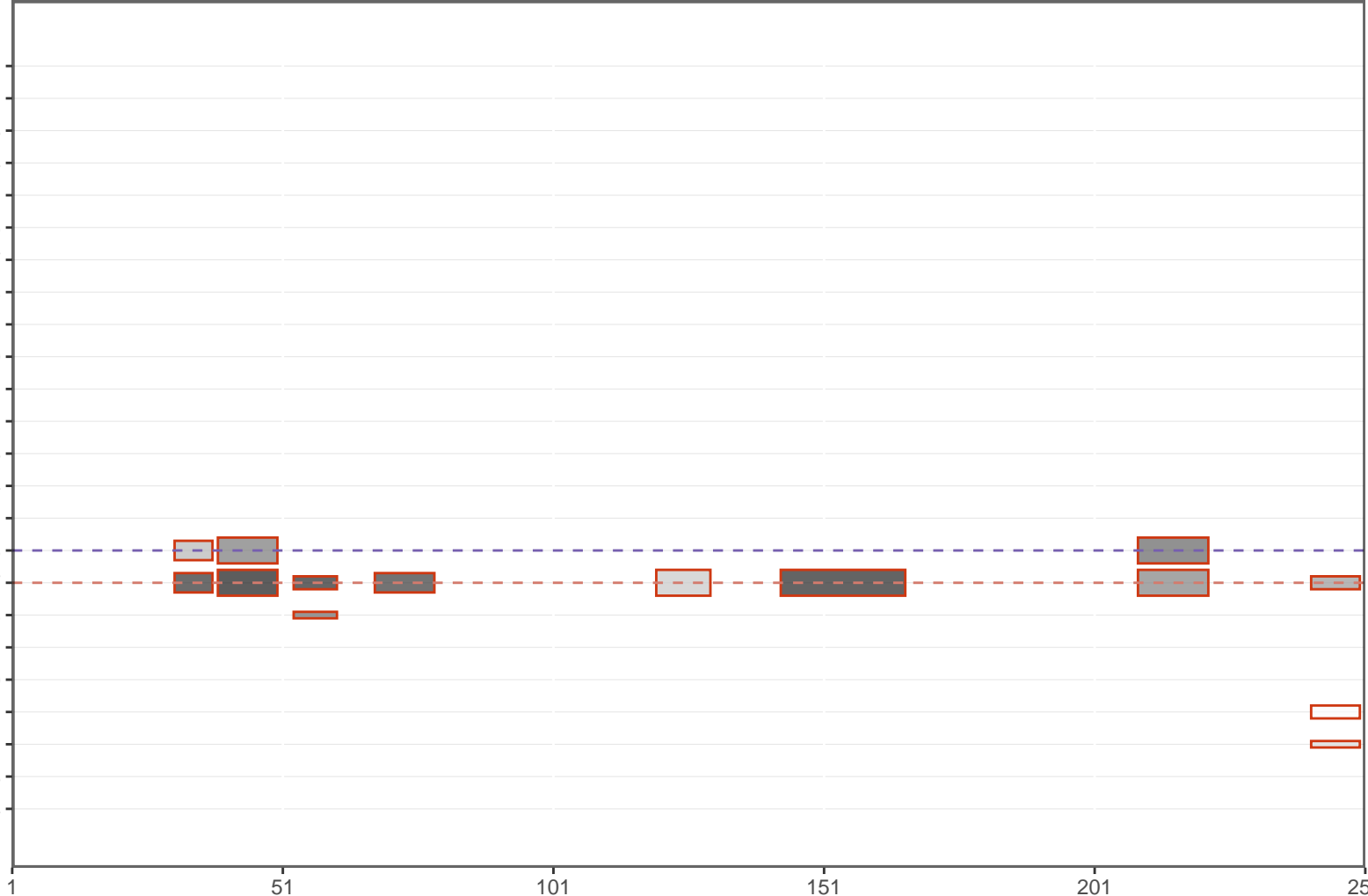
MW indication



Molecular weight

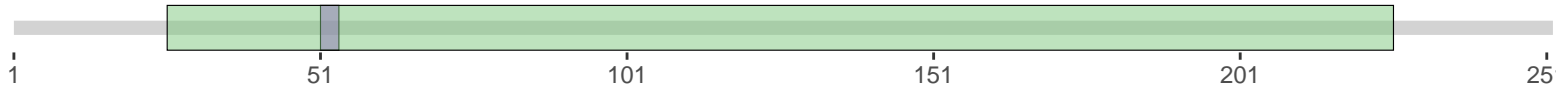


Gel Slice



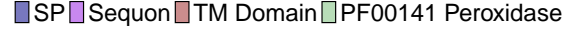
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FHPGRDCKTEPPPEGRLPDNTKGGSDHLREVFQGHMGLSKDKVALSGGHTLGRCHKRSDGFEGAWTNNPLIFDMSYFRLELLSGEKEGLLQLPDQKALLEDVFRPLVKEKYADEDAFFADVAEAHKLSELGFADAE

NbL05g04420.1 probable_LRR_receptor-like_serine/threonine-protein_kinase_At1g67720 [MW - SP = 100.33 kDa]

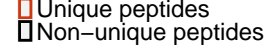
No. of times detected



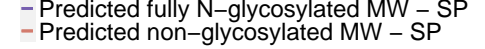
log(intensity)



Values from



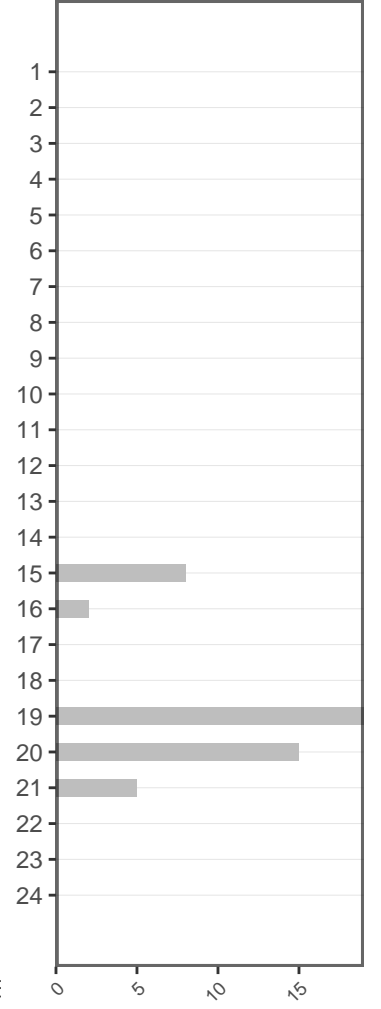
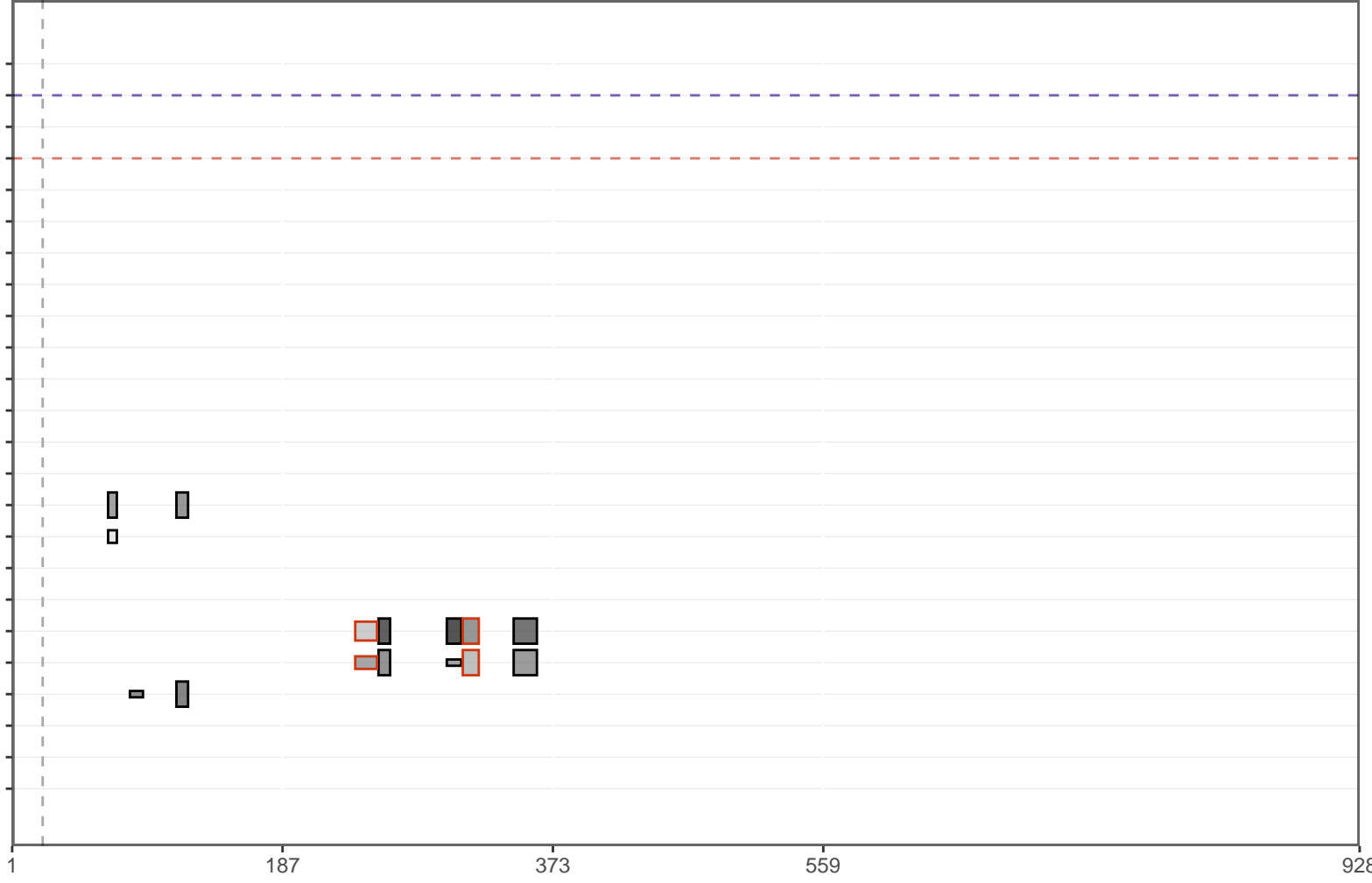
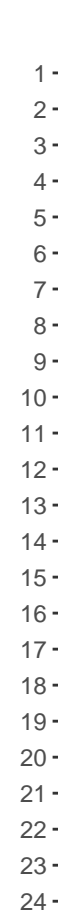
MW indication



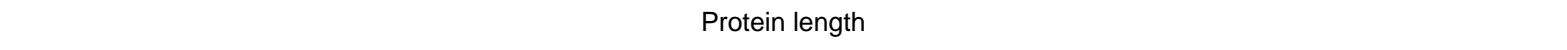
Molecular weight



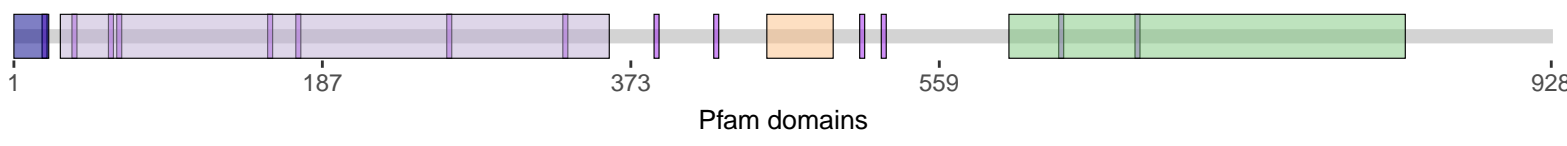
Gel Slice



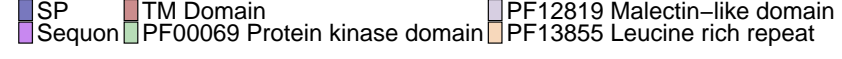
Protein length



Pfam domains



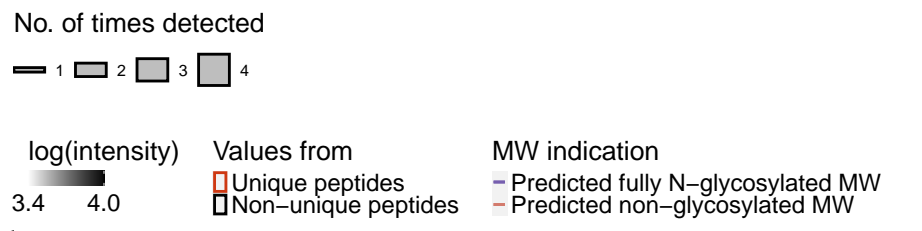
Pfam Description



Protein sequence:

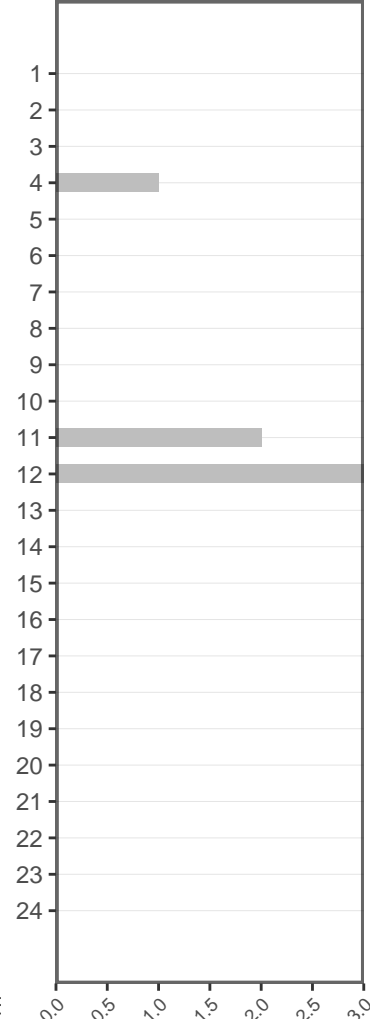
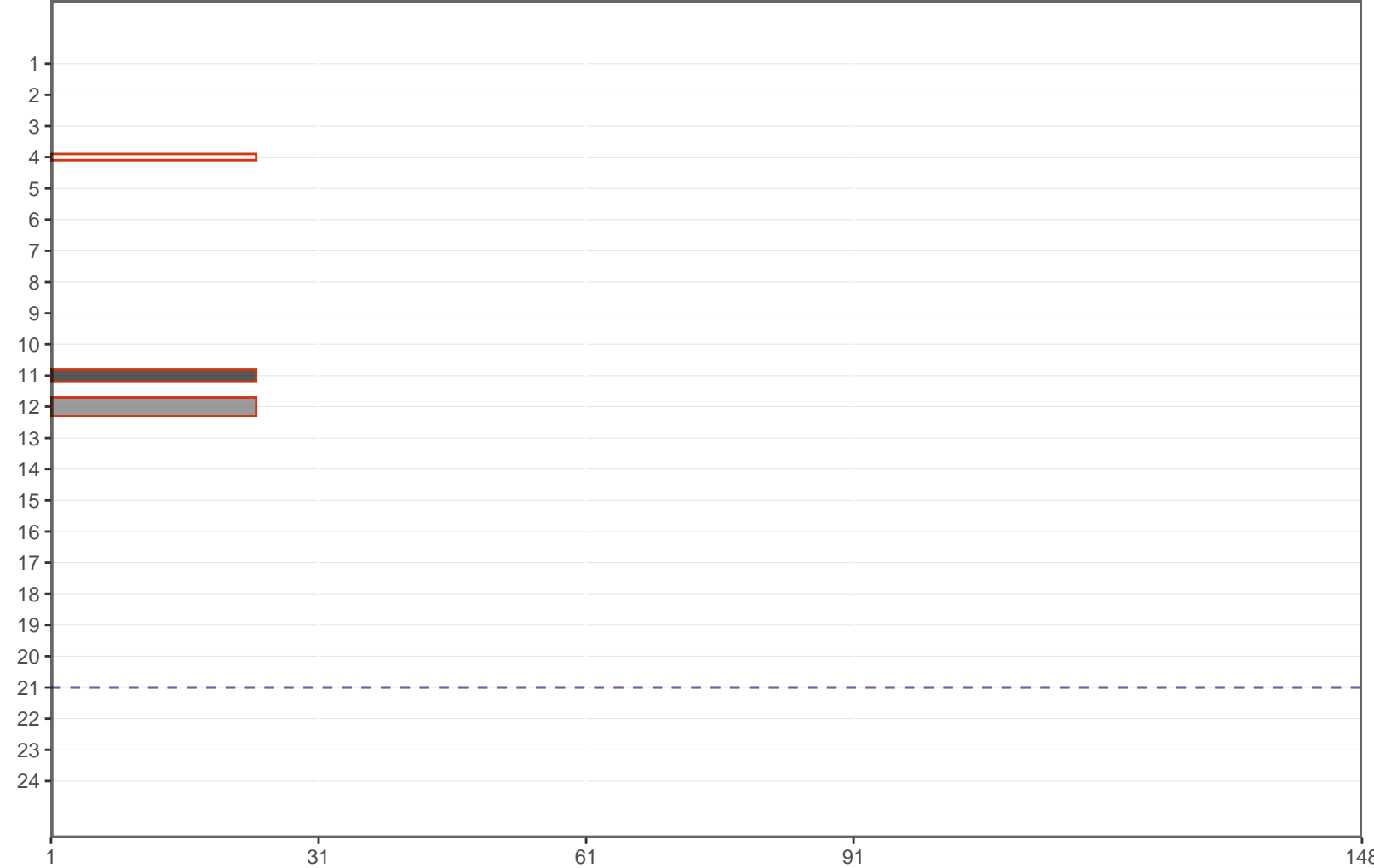
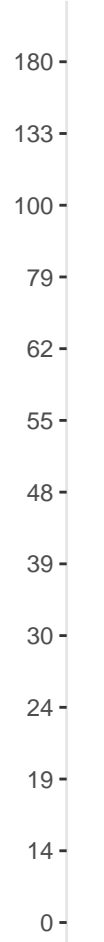
TGPPDFSGCPNLGIHLENNQLSGELPSSLEGLTSLKEIYVQNNRILTGSVTSGLLNGVILNYTGNLREGDGNHGRKKIIGSTVGSALLATVAGSILLQKGGKSPKGGLEQLPQRVYSSFGDAAEAHDFLELEEAATRNFEKRVGGGGFVYYGKLDGKEIAVWLTNNSFGGKREFSVEVALLGRHHRNLVDFMGFGGEGDGKISILYEFMNGTLKEHLYGQLPDRSINWRRLKLEAEDAAGKIEYLMGGVPSIHRDVKTSNILLDKMRAKVLDFGL

NbL05g04310.1 thioredoxin_domain-containing_protein_PLP3B-like [MW = 16.78 kDa]



Molecular weight

Gel Slice

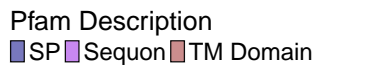


Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:
MAADRIASLKKKEAEKREALKRQGHGSEYREIGEGDFLGEVYTGGEKVFHFVYHREFYRCMMMDKHLSLAPRHVDTKFLKLDVEEGNRF

NbL05g04150.1 valine--tRNA_ligase_mitochondrial_1-like [MW = 128.48 kDa]

No. of times detected



log(intensity)



Values from



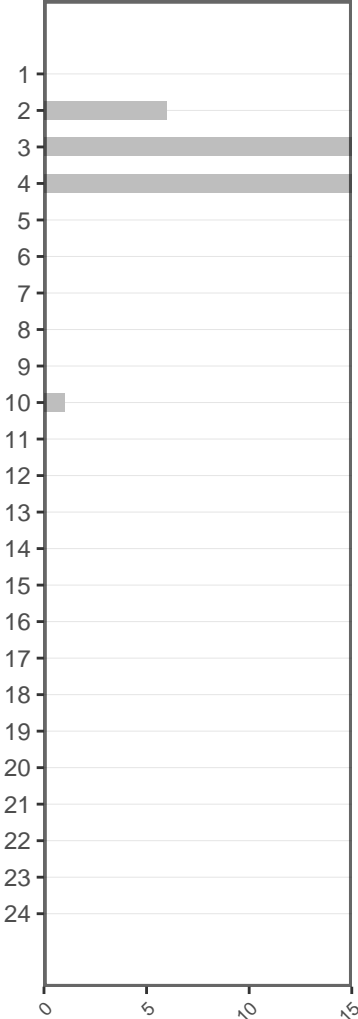
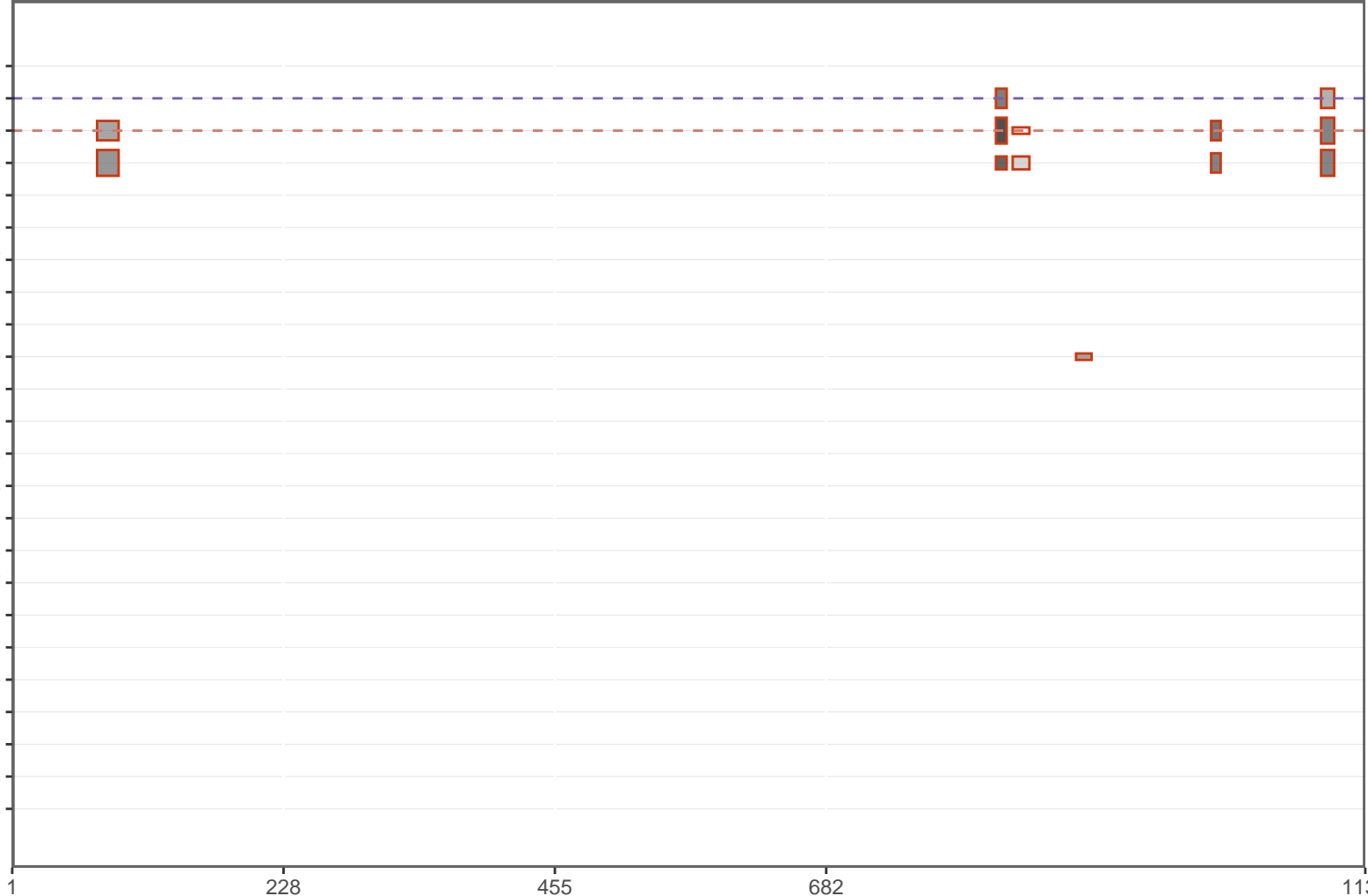
MW indication



Molecular weight

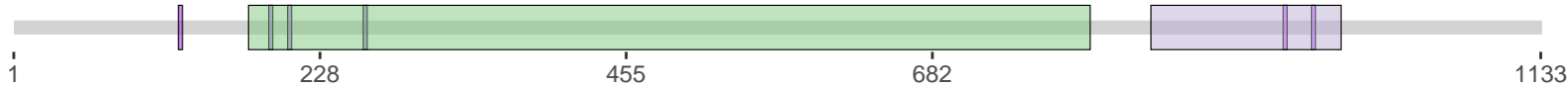


Gel Slice



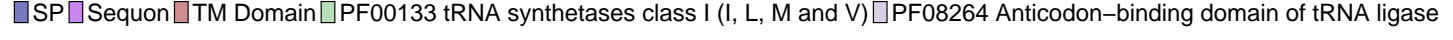
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DDNRKMEIPKQYAEWKRWLENIRDWGIRGLWVGHRIFAWVYVTLHDDKGEFGVGDHVVWIRNEEAGRLAGRFSGKEIVGLTQDPDVLDTWFSBGLFPLVGLWPDQADFKTFYPTFSVLETGHDLFFWARMVMLGKLGDPVFTKIVLHPMIRDAHGRKMSKLGNDVPLEVINGIELAGLHKRLKEGLDAKEFERAKEGGAKDFPSGIEGGADALRFALVSYTAGSDKNLIDGRVVGVRQWQNKLVNIRFAMKLGDEDTPTTKIVPREMPFSQI

NbL05g04020.1 PIP2-1-like [MW = 31.18 kDa]

No. of times detected



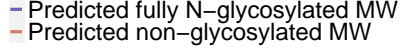
log(intensity)



Values from



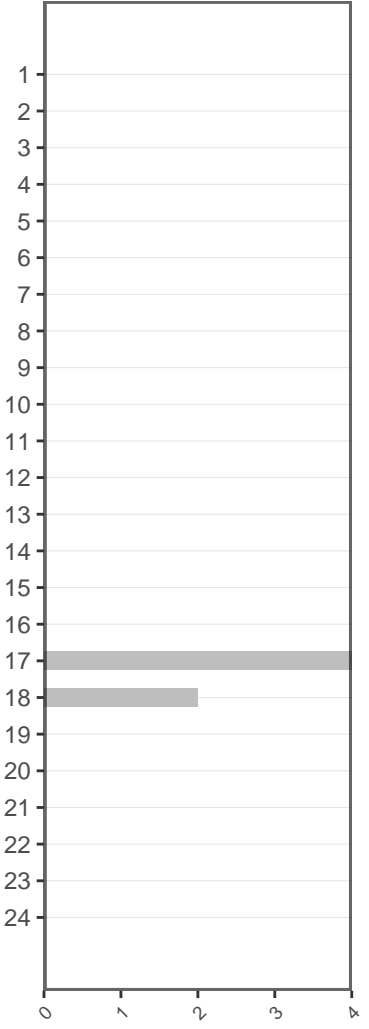
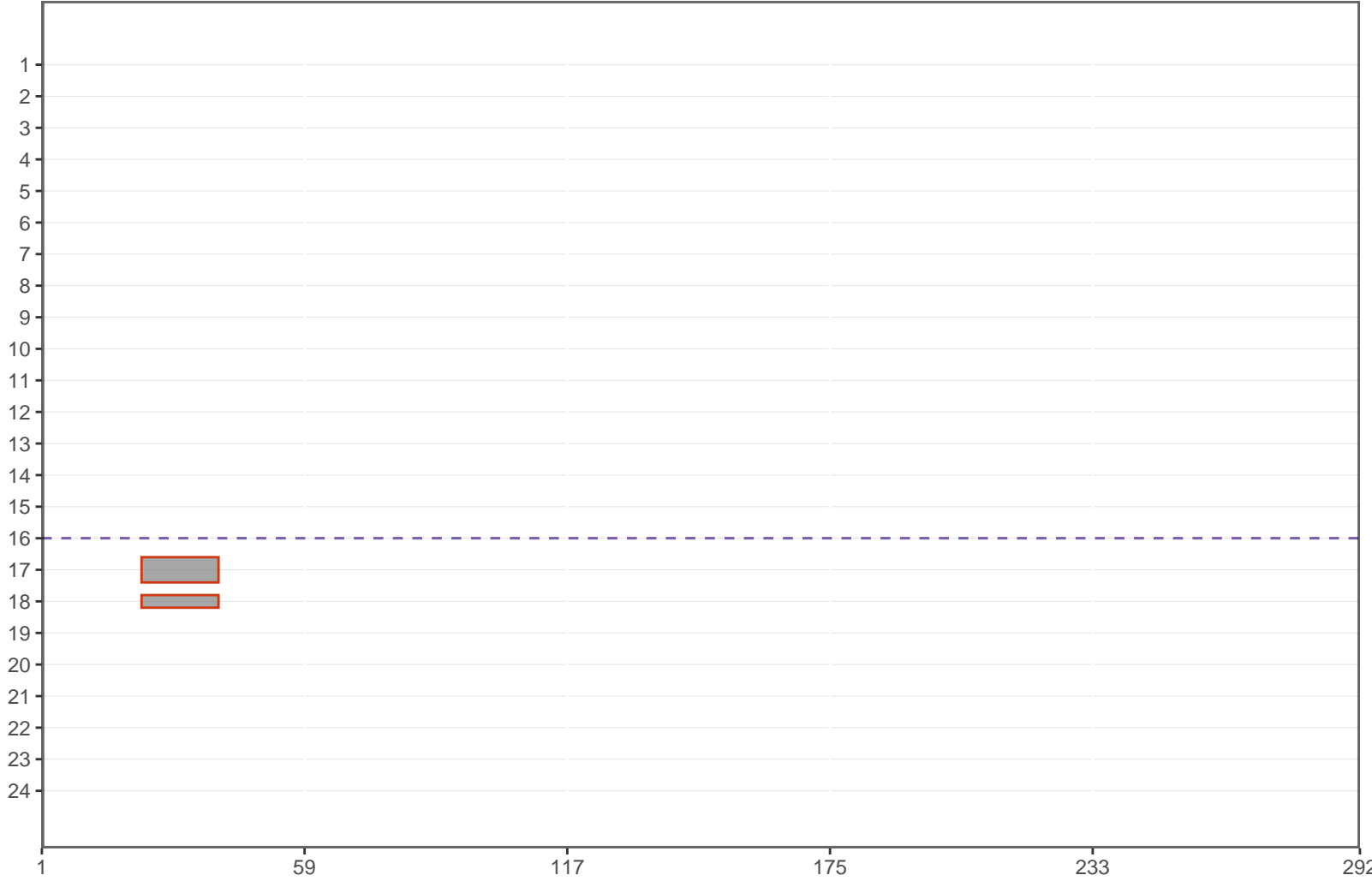
MW indication



Molecular weight

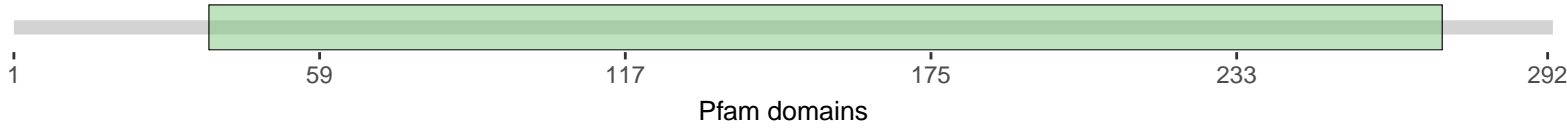


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILAACLGACGCGSLKAFKAYKYYKGGANTLNDGYETGTGLGAEHGTFLVYTVFAATDPKRNARDEHVPVLAFLPFGFAVFMHLLATPVTGTGINPASFGAAYVYKKNKAWDDQVFWGFFFGAAMAFYHQLRAGAVKLGFRSNV

NbL05g03930.1 29_kDa_ribonucleoprotein_A_chloroplastic [MW = 29.67 kDa]

No. of times detected



log(intensity)



Values from



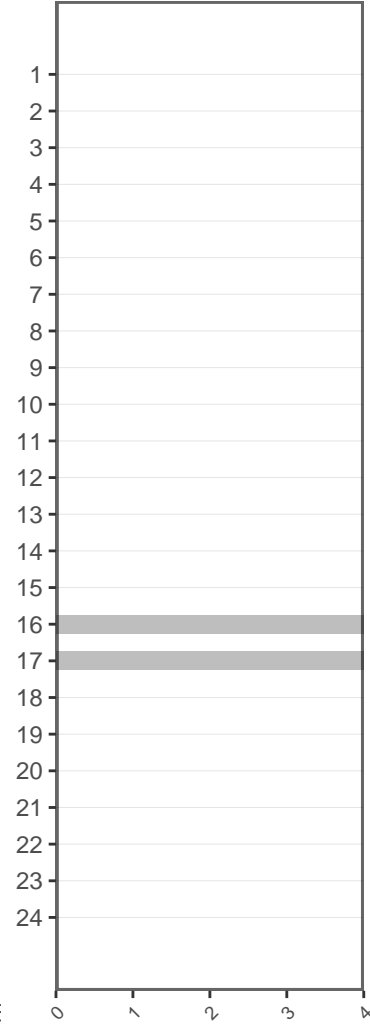
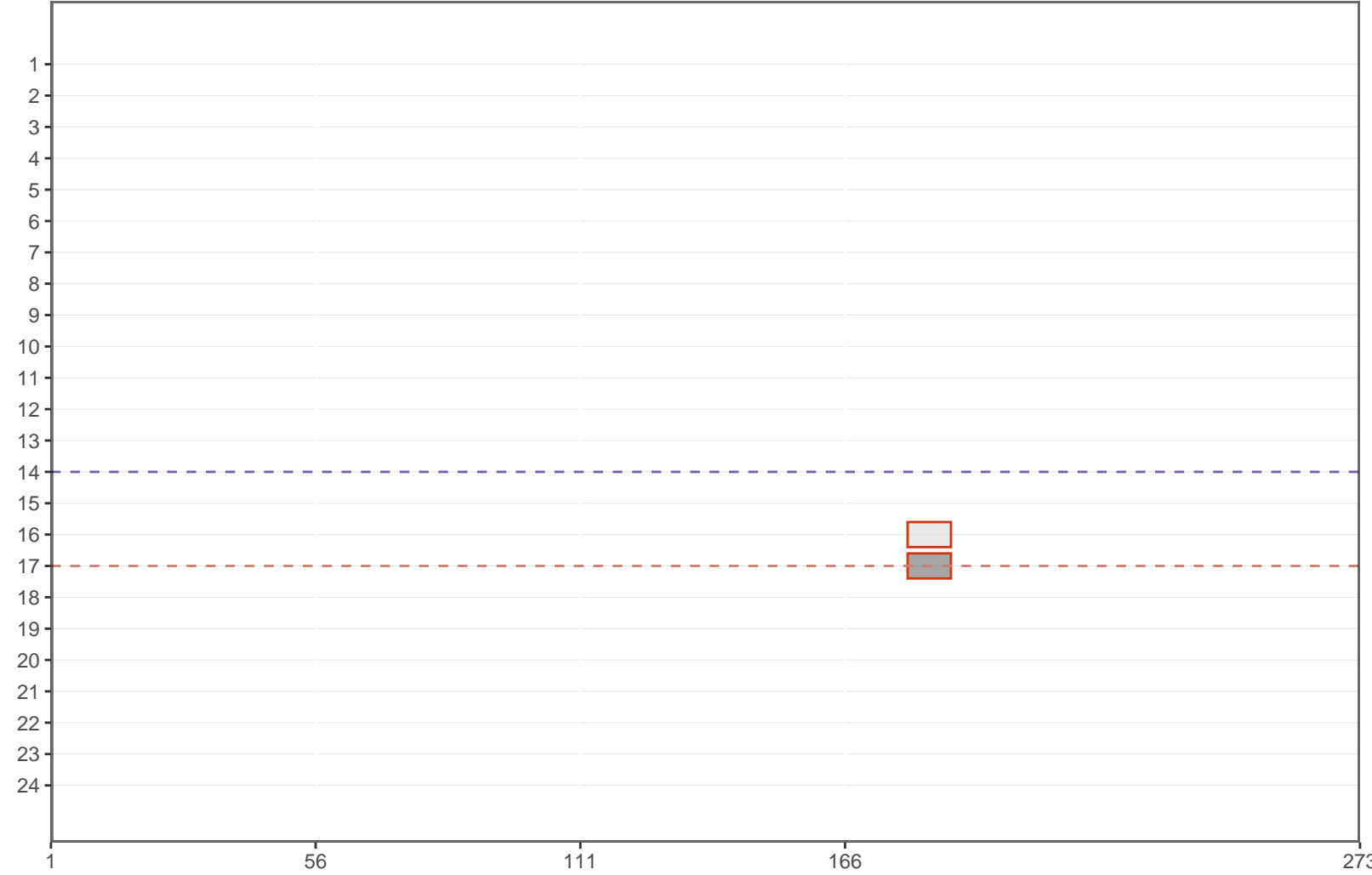
MW indication



Molecular weight



Gel Slice

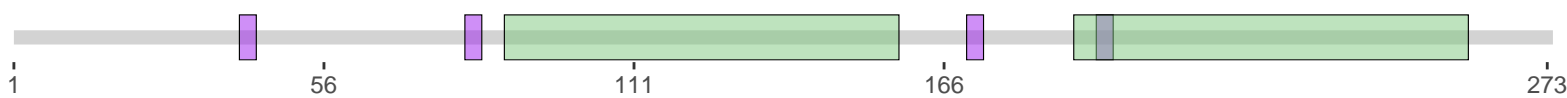


Protein length

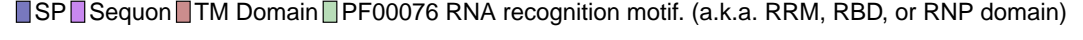


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

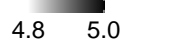
RGFGVVTMSKKEEVAADGGFNGYELDGRRLRNVSGPPPKRENSDFRGNRRGGGFFDSSNRVYVGNLWVGVDDALETLFSEQKVVDAKVVVDRDGGRRGRGFGVTVYSAAEENNAEELDGVDLNRRARVSLAEARPPRRGF

NbL05g03910.1 ethylene-insensitive_protein_2 [MW = 143.76 kDa]

No. of times detected



log(intensity)



Values from

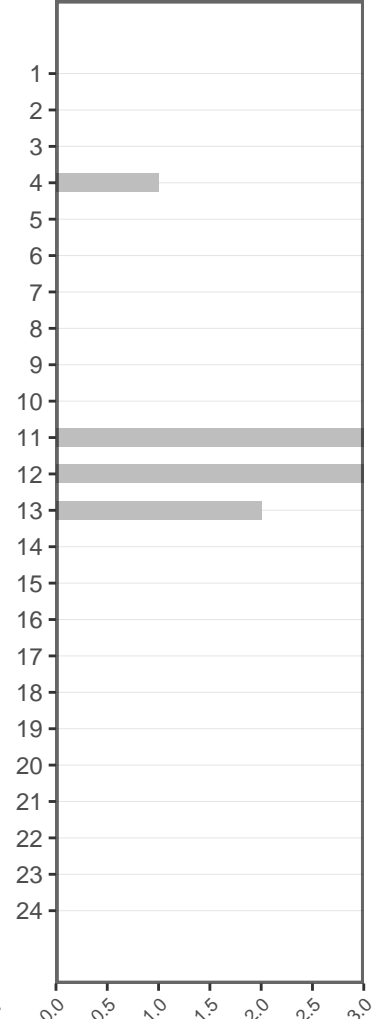
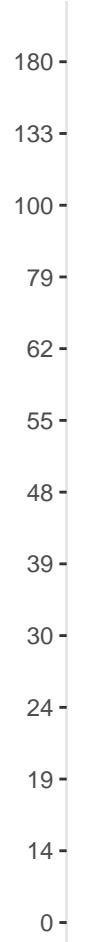


MW indication



Molecular weight

Gel Slice



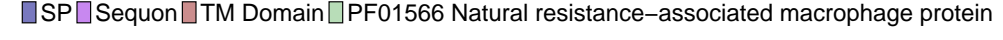
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGSLRLAGLGRAARRGLTIVNEFVGGFLFDYHGAATPEAKKGLDVLGLDQKVDPKPAFASLKMESRRDFNNAVIPGSGAKVPEGLINENYSPKGGVVGCTVDSITYRVFKFESVSSSHMKLLDHYMGSSNSNILDGERRRYSMRIPTSSAGYDGGPATVHGQYGTAVLNGIAKERGSDKLNGLQLESPPRRVSVSSMSNVAEPPARALGKPKGSGVSRAPPFGFNVPVARNNSMQPNTLTDLSSFTETAEVAGAAANKKYKLLPDIGRVIIPRODSALSDGRAVI

NbL05g03880.1 ammonia-lyase-like [MW = 78.01 kDa]

No. of times detected



log(intensity)



Values from



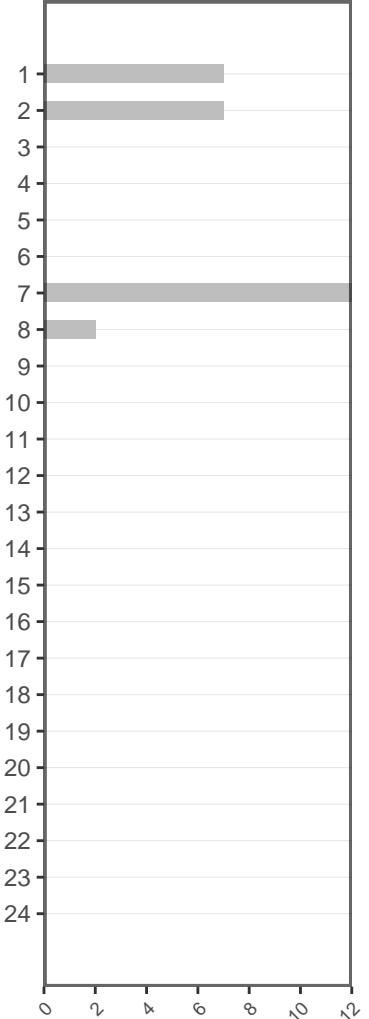
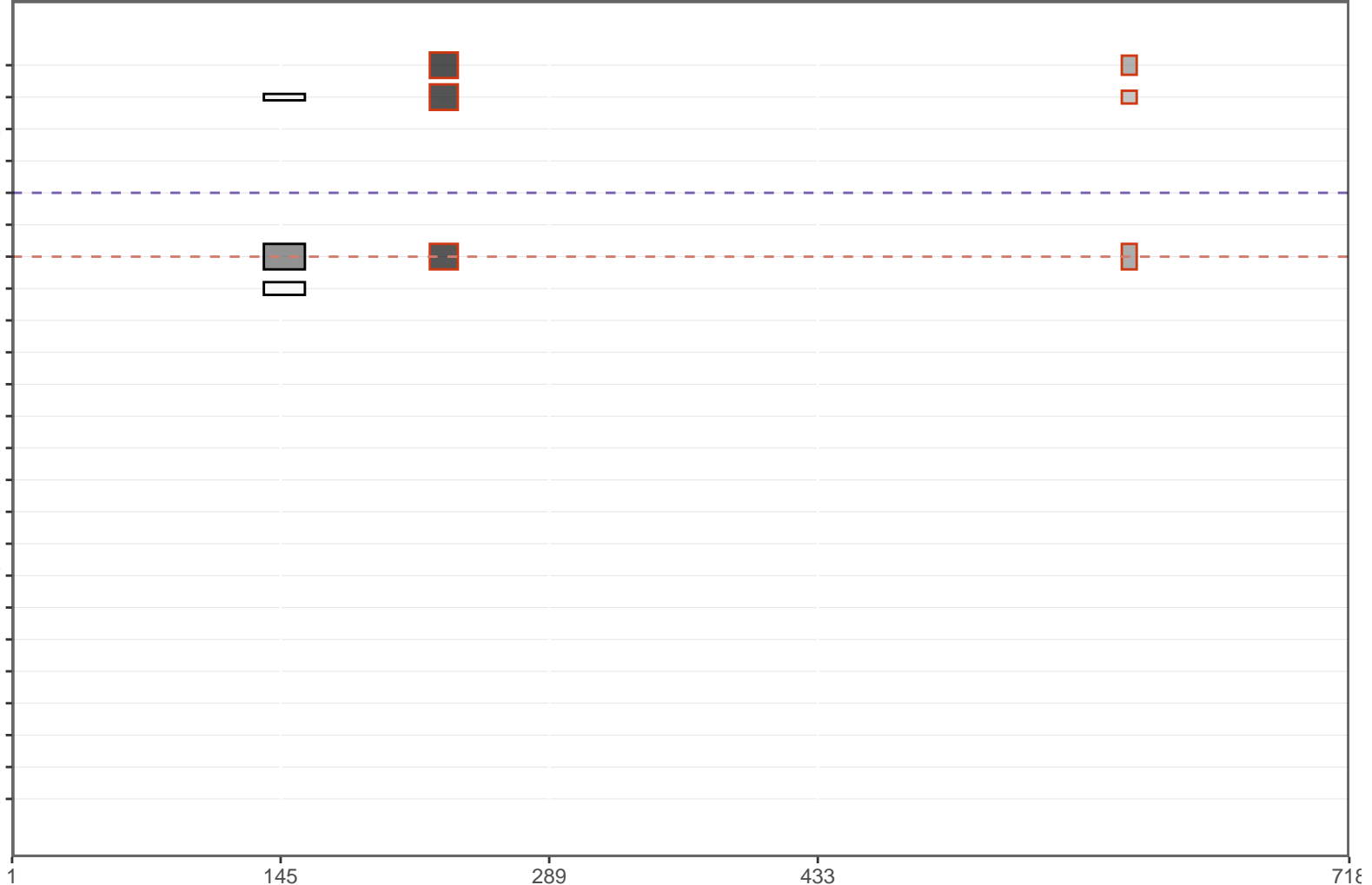
MW indication



Molecular weight

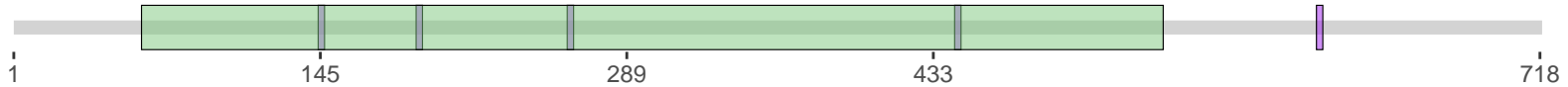


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KPKCDRYALRTSPQWLGPOEIVRSATKMIEREINIVNDNPLDVRNKAHLHGGNFQGTPTGVMQDARLALASIGKLMFAQFSELVNDYNNGLPNTASRNPFLDYGFKAEMAMASYCELGFLANPVTNHYGSAEQHNQDYNLSGLISARKTAEAVDHLKLMSTYLVAALCGAIDLRHLEENLKNVAVNTVSGVAKRFLITMGANGELHPRFCEKELLRVVREYLFAYADDFQSGNYPMLGKLRQVLVDHAMKNGESEKNVNSBIFQKIGAFEDLKA/LPKVEVSAF

NbL05g03850.1 kinase_2-like [MW = 37.55 kDa]

No. of times detected



log(intensity)



Values from



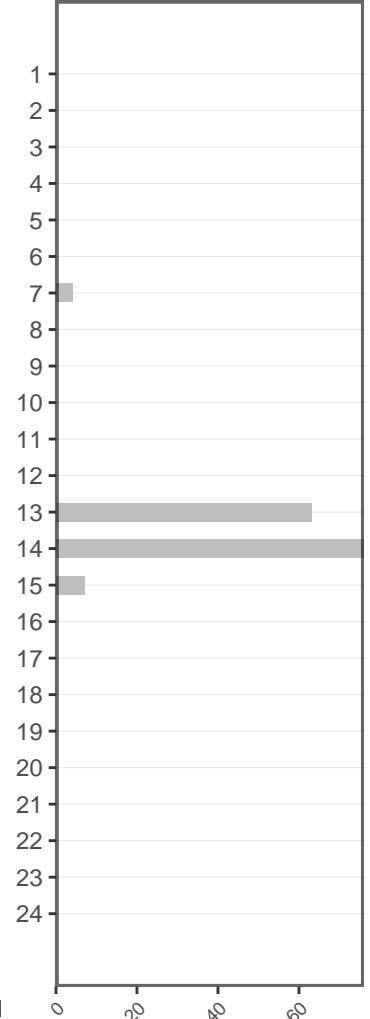
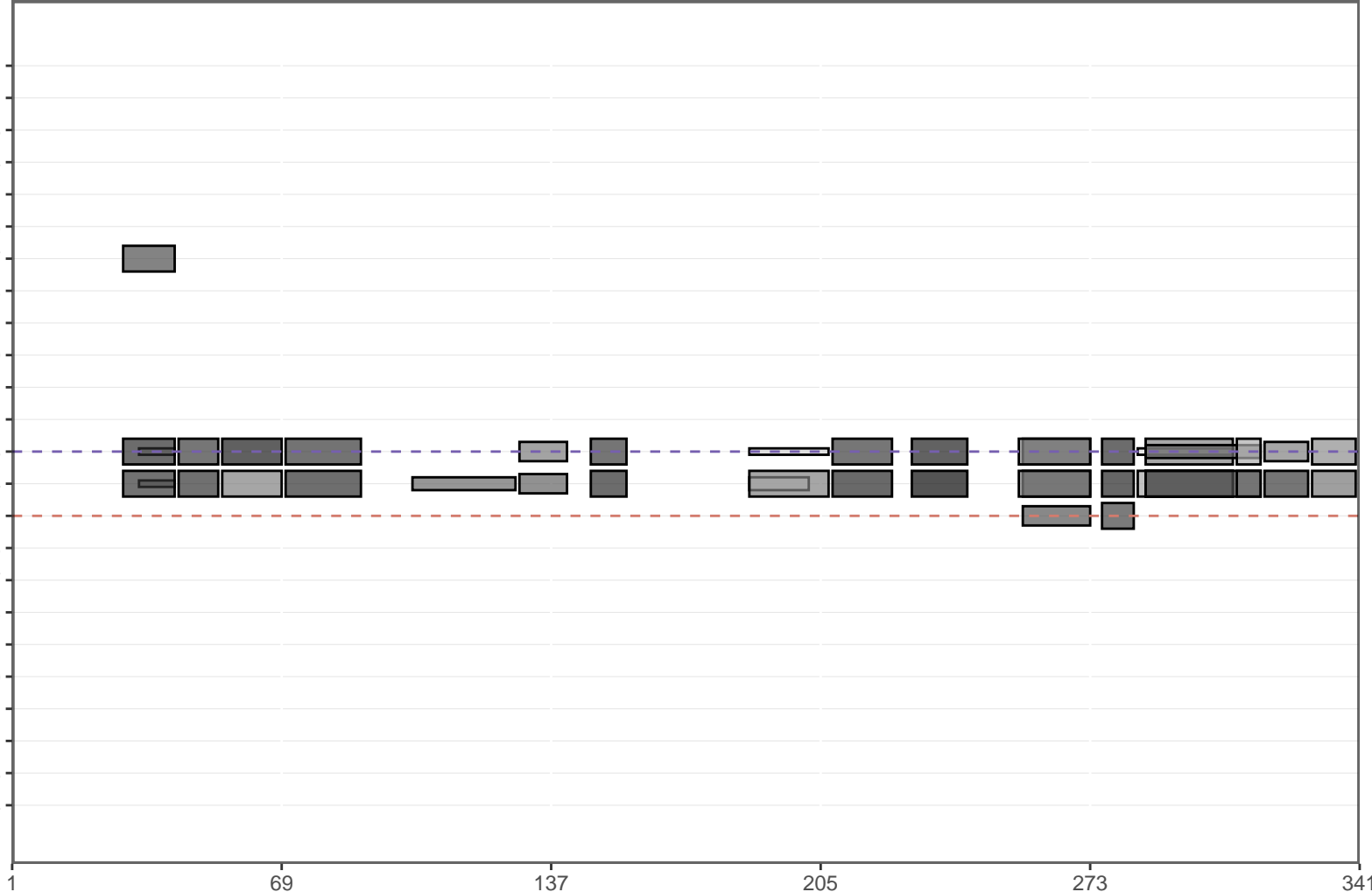
MW indication



Molecular weight

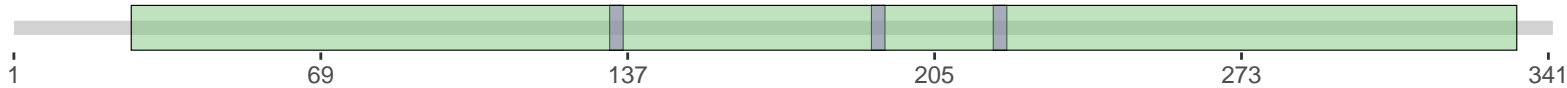


Gel Slice



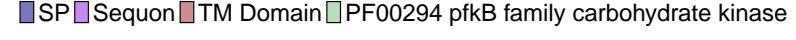
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

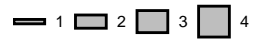


Protein sequence:

KAKFYYAGFLLTYSPEHQMAEHAANNKIFSMNLBAPFCIGFFRDPGEKALPYMDFVCGNETEARTFSKVHWETDNEEIALKISEWPKASETHKRITVITQGDAPVVAENQKALFFVPLPKELVDITNGAGDAFVGGFLSGLVQKPIVEDGVRAGCYASNVIGRSGGCTYPEKPDFV

NbL05g03730.1 cell_division_cycle_protein_48_homolog [MW = 89.69 kDa]

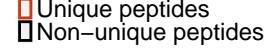
No. of times detected



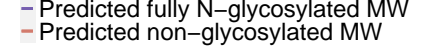
log(intensity)



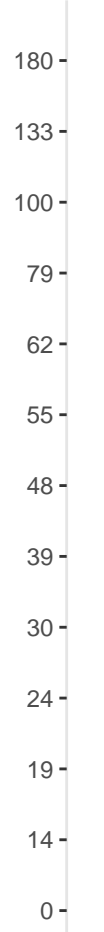
Values from



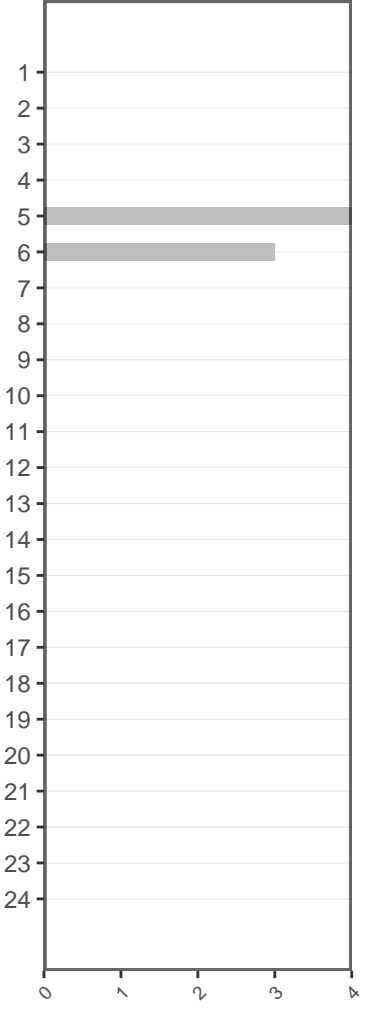
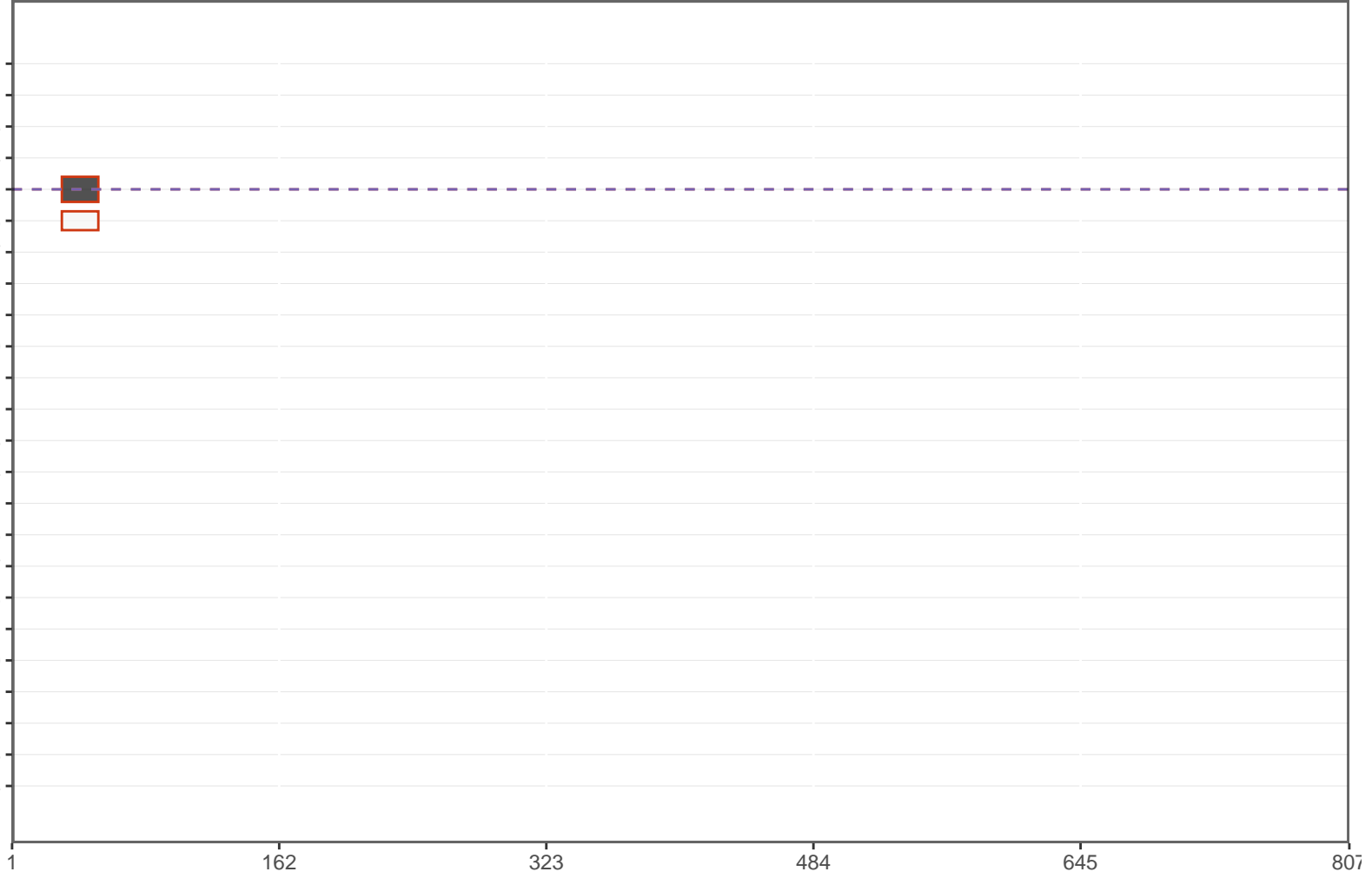
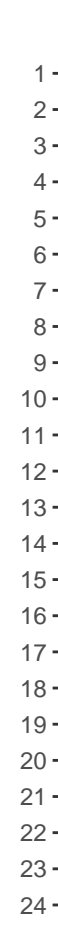
MW indication



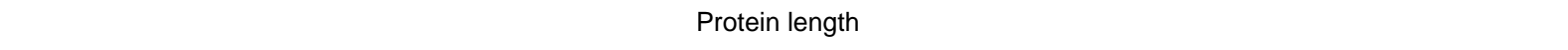
Molecular weight



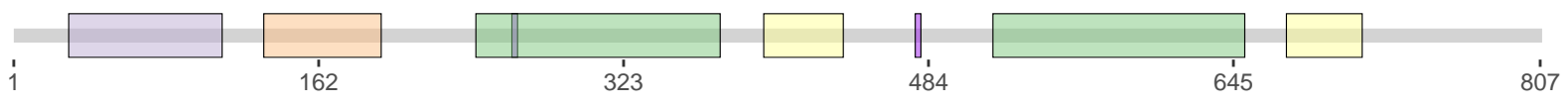
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- TM Domain
- PF02359 Cell division protein 48 (CDC48), N-terminal domain
- PF17862 AAA+ lid domain
- Sequon
- PF00004 ATPase family associated with various cellular activities (AAA)
- PF02933 Cell division protein 48 (CDC48), domain 2

Protein sequence:

IKLAEDVLDLERIGKDTGHGVVADLAALGTEAALGQREKMKMDVIDLEDETIDAEILNBMVATNEHFSTALGTENPSALRETFVEVFNVSWEIDKGLLENKRELQGETVGVVPEHPEKFKFGMSPKSGVLYFGPPGCGKTLAKAIANEQGNFISVKGPELLTAMWFGSEANREIFDKARGSAPOVFFDELDGATGRGSSGGDAGGADRVLNQLLTEMDSMNAKKTVFVIGATNRPDIDALLRPGRLDGLVHPLPDEDSRHGHFKAGLRKPLSKDILRALAKYTGFS

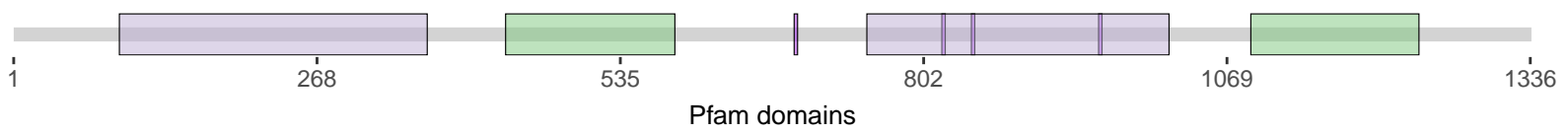
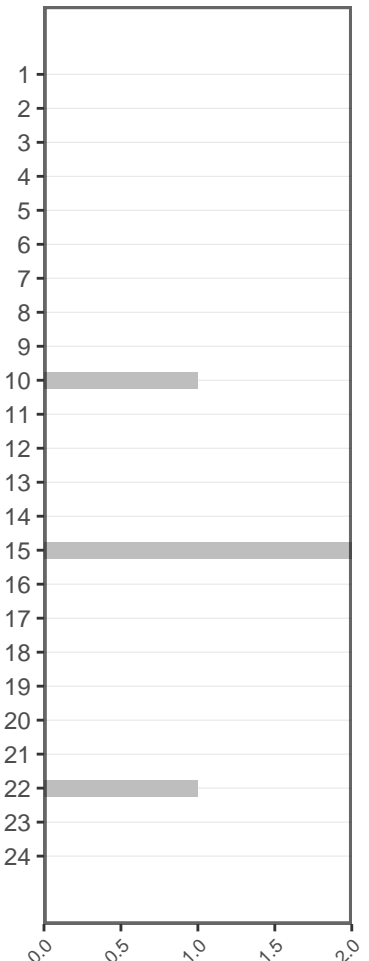
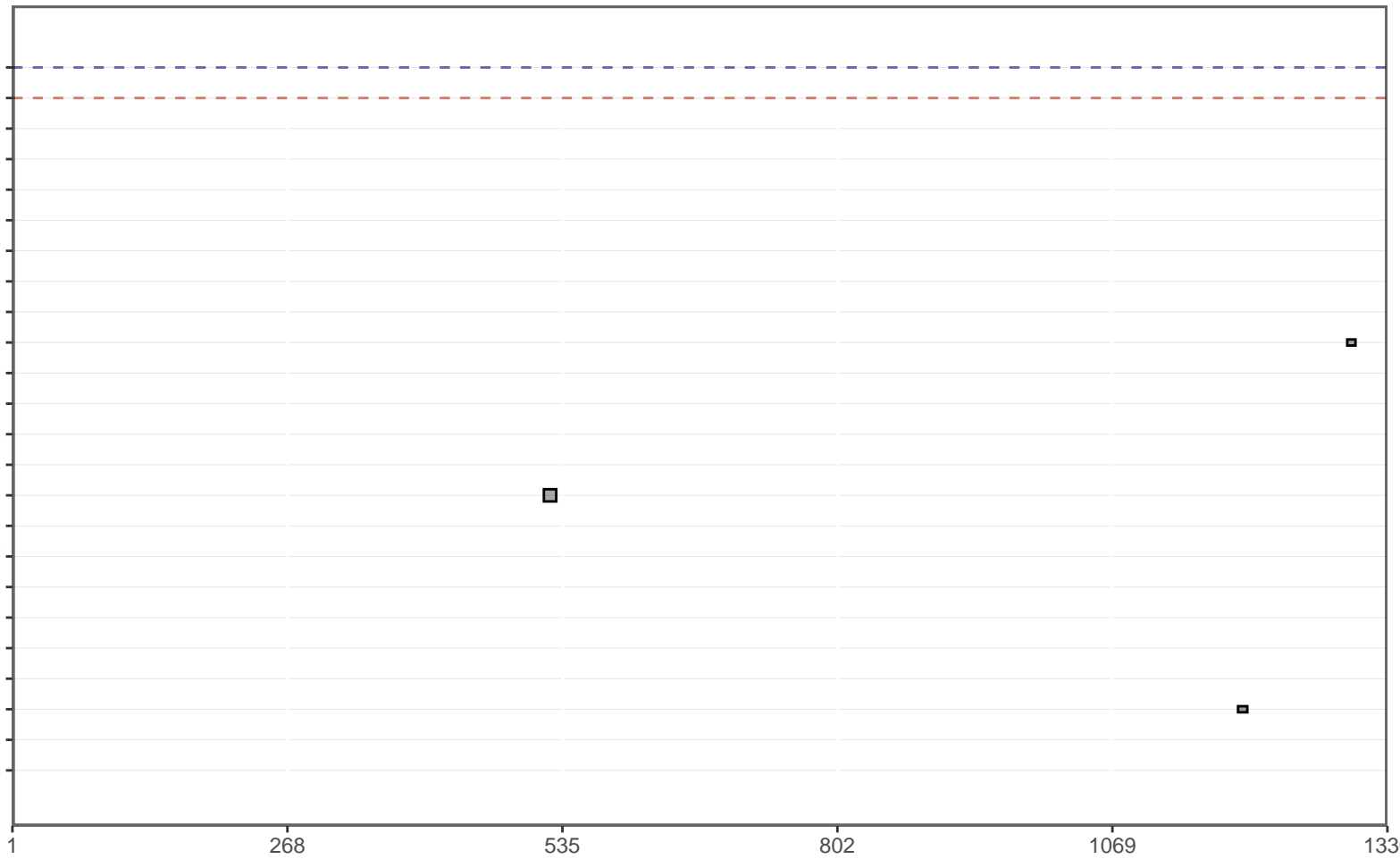
NbL05g03610.1
 ABC_transporter_B_family_member_1_(LOC104237401)_transcript_variant_X1_mRNA_XM_009791552.1_PREDICTED:_Nicotiana_sylvestris_ABC
 [MW = 146.58 kDa]

No. of times detected
 1 2 3 4

log(intensity) 3.8 4.7
 Values from Unique peptides Non-unique peptides
 MW indication Predicted fully N-glycosylated MW Predicted non-glycosylated MW

Molecular weight
 180
 133
 100
 79
 62
 48
 39
 30
 24
 19
 19
 21
 22
 23
 24

Gel Slice
 1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
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 18
 19
 20
 21
 22
 23
 24



Pfam Description
 SP Sequon TM Domain PF00005 ABC transporter PF00664 ABC transporter transmembrane region

Protein sequence:
 EAAHETLSNARKSSARPPSSARNVSSPIFRNRSYGRSPYGRRLSDPFTSDFLSLEDAVSSYRHEKLFKIDGASSPFLAKMMSPEVSYLVGSGVGGVCSLSAFFAVVLSAVLSVYYPDHAVMKQIAKCYLLIGVSSAALIFNLTGHFFWDVYGENLTKRVRKEMLDVLMKMEWFDQEEENDSSRIARLADANNVRSAGIDRSVIMONSALMLVAGTAGFYLOWRLAEVLLWFFVVAATVLEKMFMTGFSQDLEAAHARATQAGEAWANRITVTAFNSETKI

NbL05g03540.1 S-adenosylmethionine_synthase_3 [MW = 42.62 kDa]

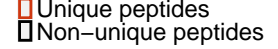
No. of times detected



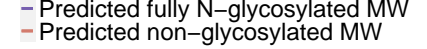
log(intensity)



Values from



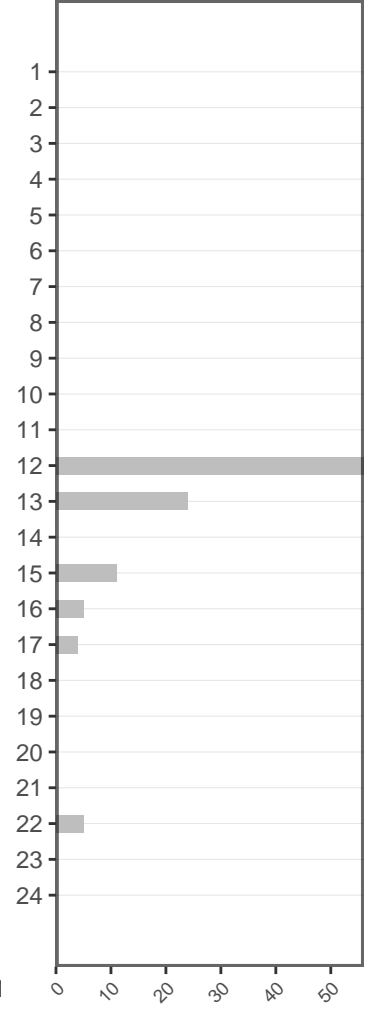
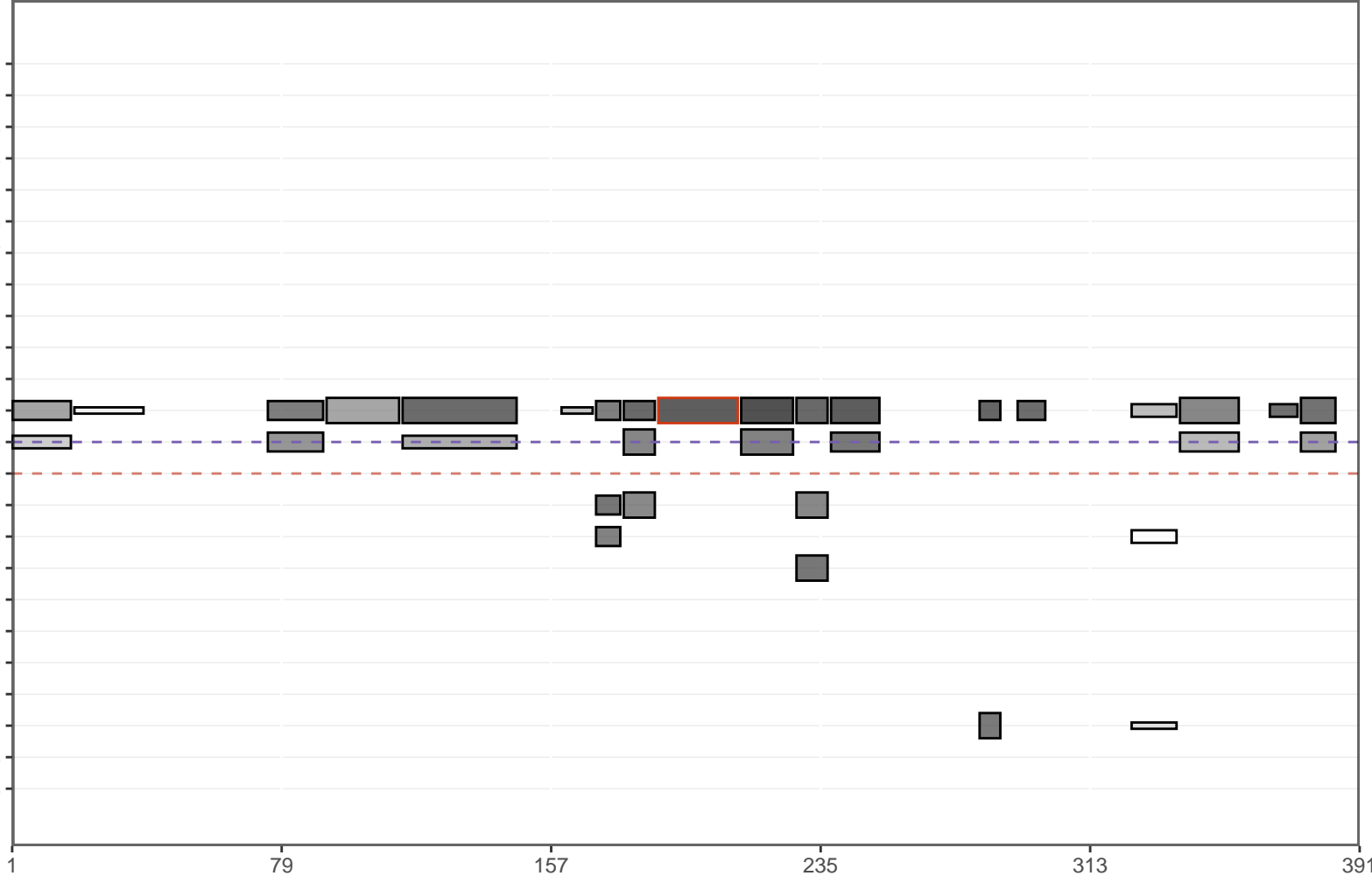
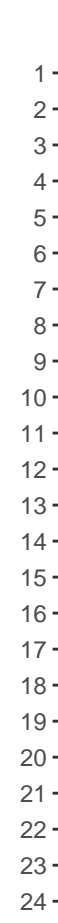
MW indication



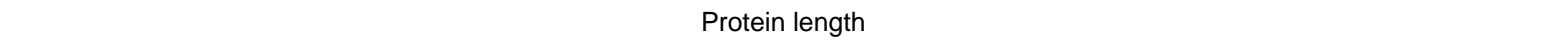
Molecular weight



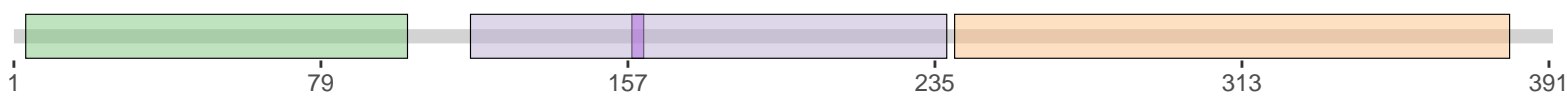
Gel Slice



Protein length

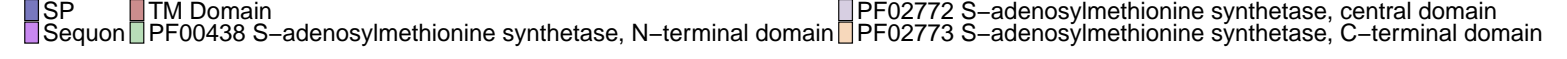


Peptide counts over 4 repeats



Pfam domains

Pfam Description

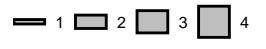


Protein sequence:

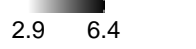
SAMVPIRIVHTYLSIQHDEIVTNDQIMQDLKEHVKFIPVPAHLYDEKTFHLPNSGRFVGGPHGDAGLTKRKHIDTYGGWGAHGGGAFSGKDKPTKVDKRSQAYVIRQAASVVAISGLARRGIVQVSYANGVAEPLSVFVDTYKTKTQTPDKDLAIKENDFDRPQMMSINLDLLRGNFRYKQTAAYGHFGRDDPQFTWETVYKLPKVA

NbL05g03090.1 threonine_dehydratase_biosynthetic-like [MW = 65.61 kDa]

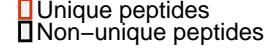
No. of times detected



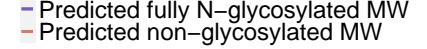
log(intensity)



Values from

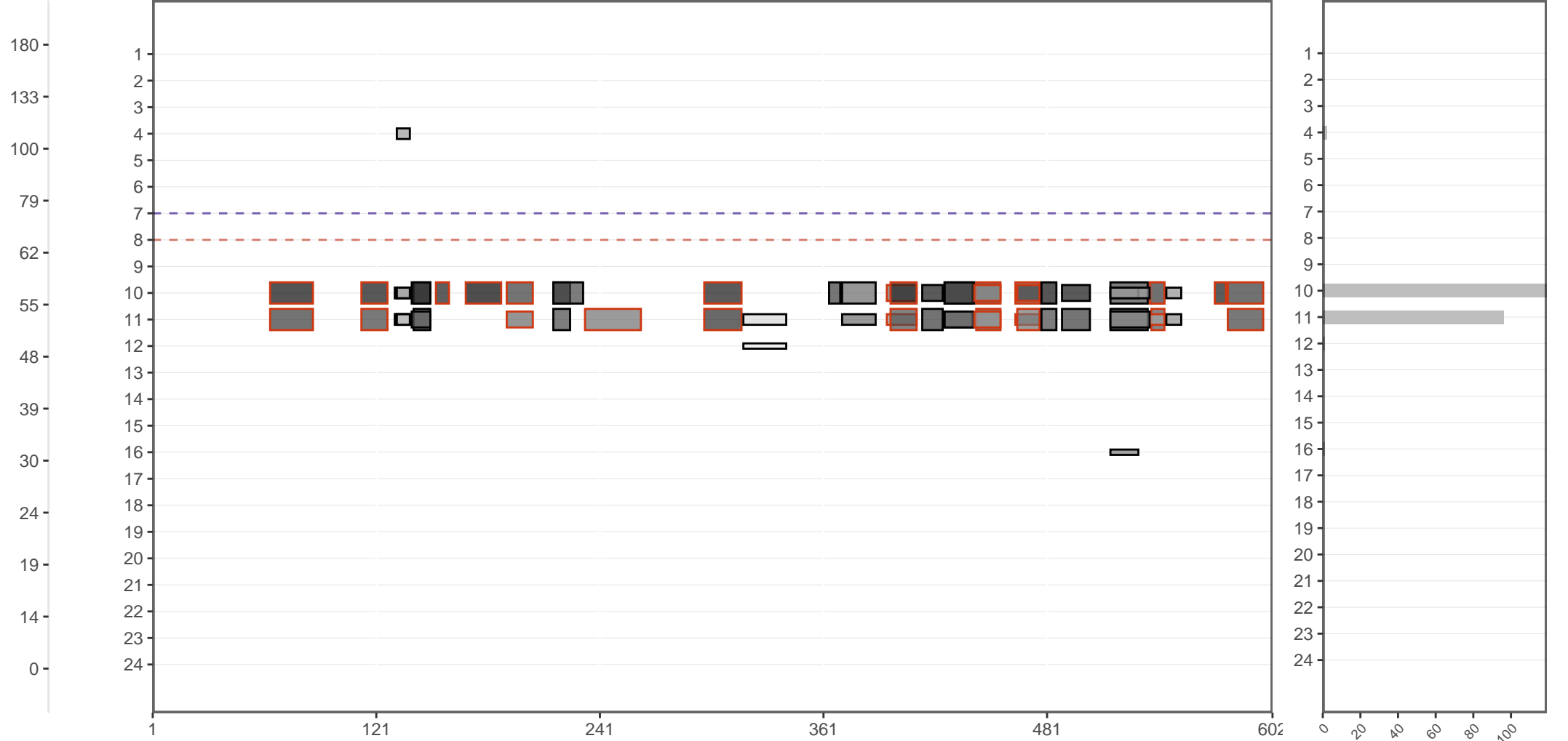


MW indication

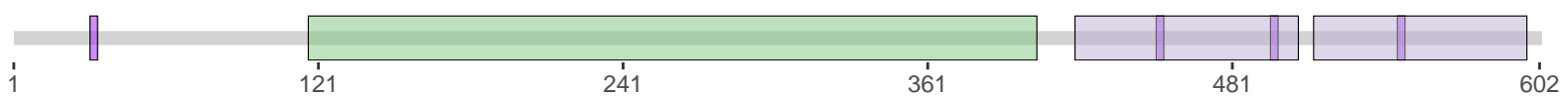


Molecular weight

Gel Slice



Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00291 Pyridoxal-phosphate dependent enzyme
- PF00585 C-terminal regulatory domain of Threonine dehydratase

Protein sequence:

RVAPHTKIGVEPFGASSMTGSLYHGERVLEGVDFADGVAWLVGEEFRLLCKDLIDGMVLYSNDASIAVAWVYDEGRNLETSGALAIAGAEVCKYVNIKGNVVAASGANMDFSKLKVLDLADIGDGRREALLATFMPFEFQSKFKFDELVSPMNTFKYRYNSGRKGLVLYVGVNTRKSDLESLELERNKMSGLNTVNLNINLVKHLRHLMSGRSEPSNEIFQGFIFFEKPGALRKLFLVDFSPRWNSLFRHYREGGELDASLVVGFQVPKGEIEEFVQANNLQ

NbL05g02960.1 uncharacterized_protein_DDB_G0284311 [MW = 54.42 kDa]

No. of times detected



log(intensity)



Values from



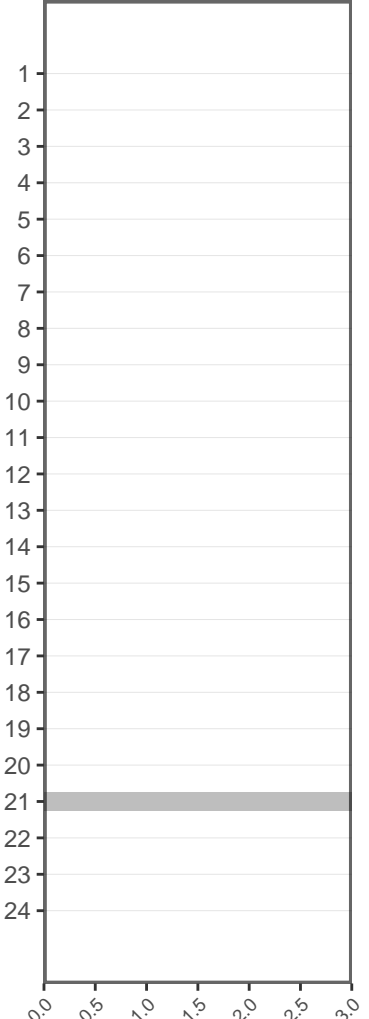
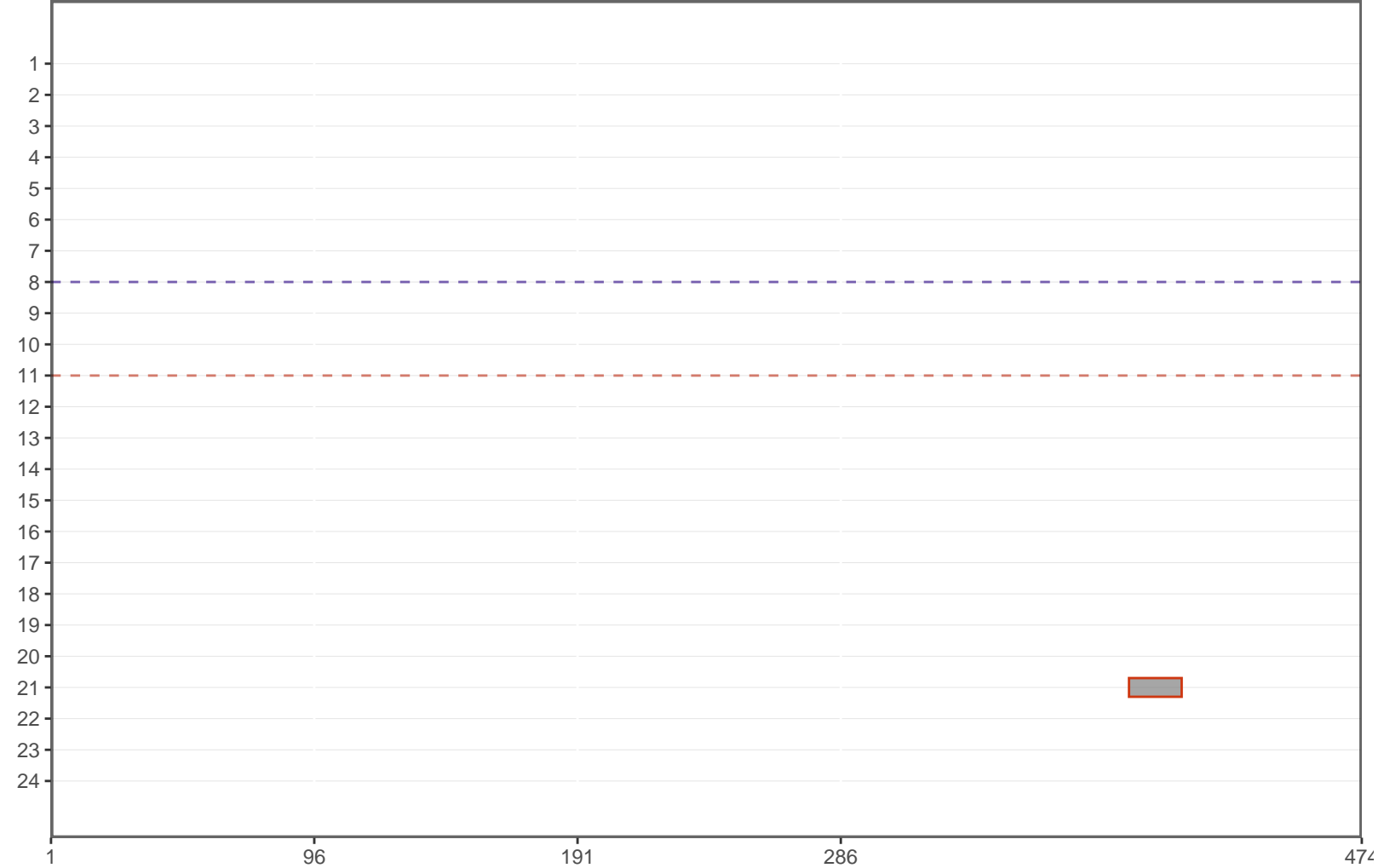
MW indication



Molecular weight



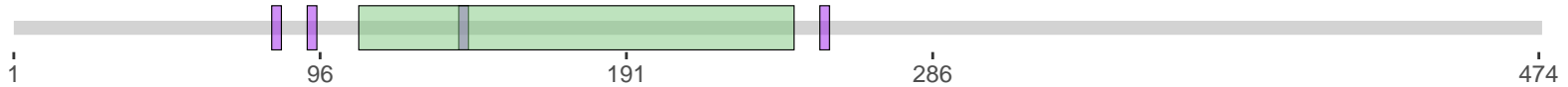
Gel Slice



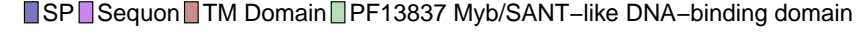
Protein length



Pfam domains



Pfam Description



Protein sequence:

KEEVKLLNSQHLFFREMCAYHNSCGHNNTSTGGSGSNVQLSTEVAEVNNQAQRCLHSSENARIEVHLEEGTKMAGKSVDDDDDEDDDDDEEMSGARGGCHHHSHGHNEVDDMDERSKRPRKRGKGLSPMVQQLSSEVANVIGDGRSSIEKRWLKTRMVOLEEGHGVYLCQAFELQKQRUKWEKFTSKKEREMEKELINERKKLENERMALLLRQKELELLDFHQHQNHRNSDP66VTD*

NbL05g02840.1 peroxiredoxin-2E-2_chloroplastic [MW = 24.82 kDa]

No. of times detected



log(intensity)



Values from



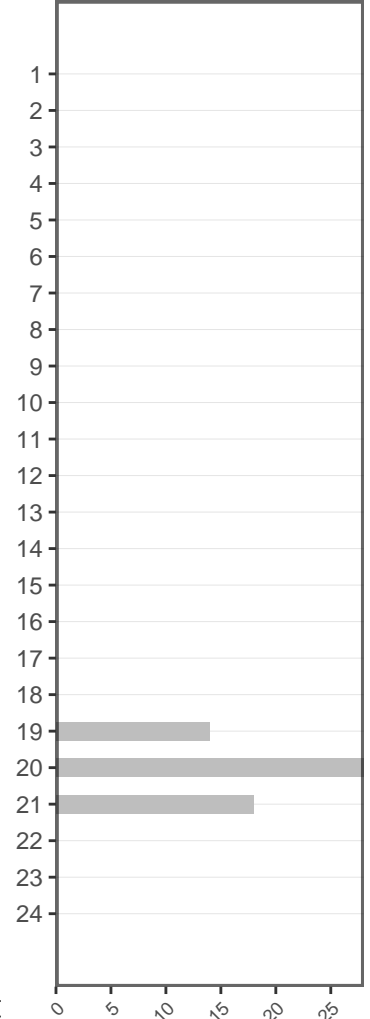
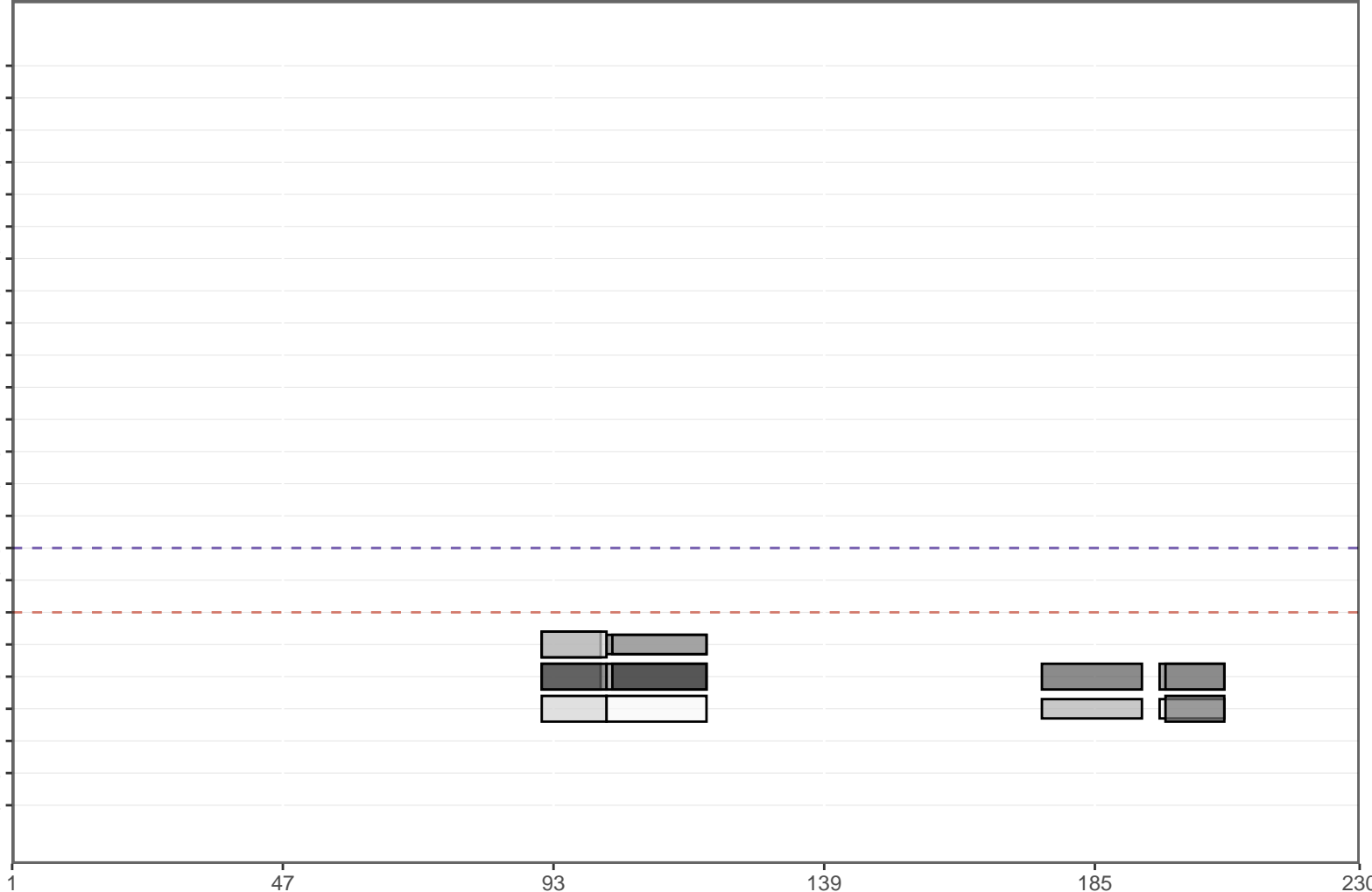
MW indication



Molecular weight



Gel Slice

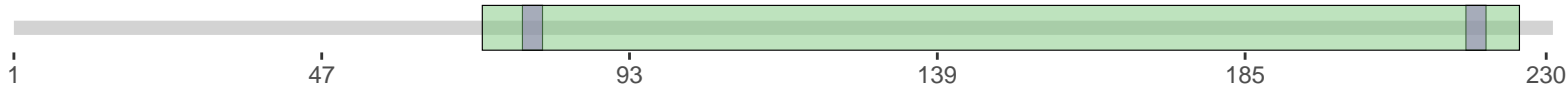


Protein length

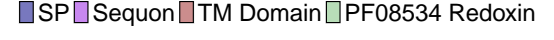


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VLLAVPGATPTTC5QKHLPGFVENSKEKKBKGDVDTACIGVNDAFVMKYKVENLGINDEVMMLSDGNLEFTKAGCELDLSQKPVGLGIRRRYSMLVEDGVAKILNLEEGAFNVSSADDILKAL*

NbL05g02830.1 enolase-like [MW = 58.33 kDa]

No. of times detected



log(intensity)



Values from



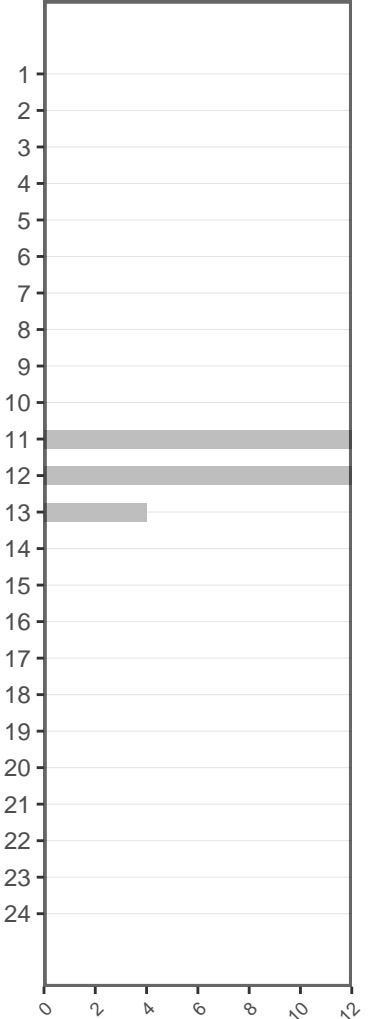
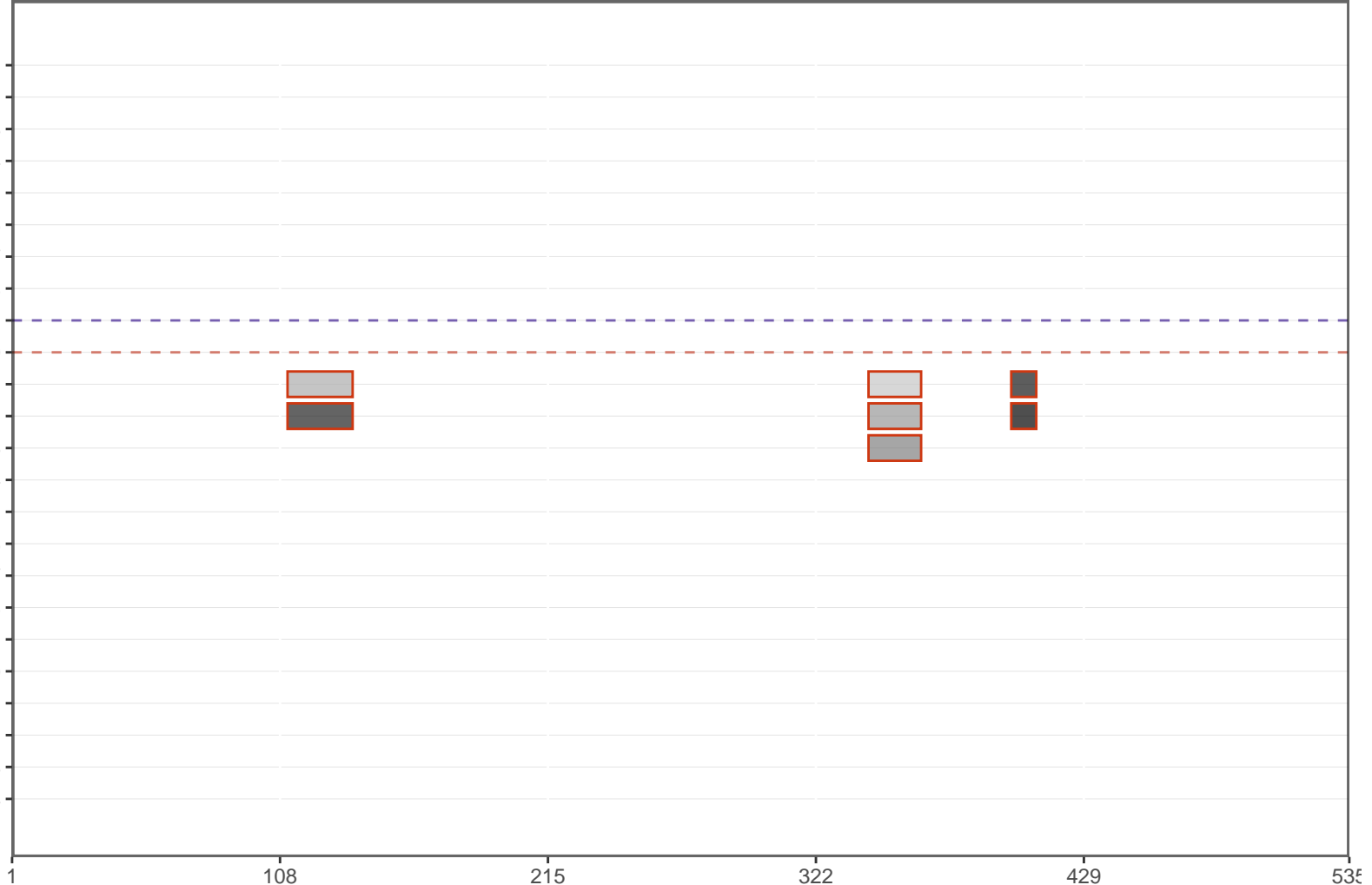
MW indication



Molecular weight

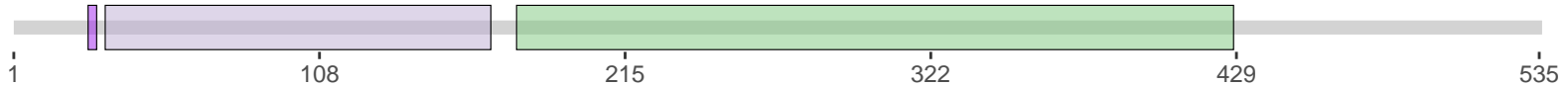


Gel Slice



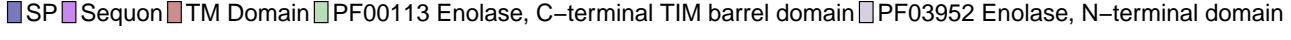
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKEGLELLKTAIEKAGYTGKVVIGMDVAEFLFKDKSVDLNFKEENNGSGKISGDDQKDKLYKTFVSEYKPVSEIDPPFDGDDWETVAHLTTEIGEQQVQVGGDDLLNPKRVAKAAEKTONALLKLVNKGISVTESEIAVKMSKAGAGVMTSHRSGEETEDTFIADLAVGLSTVILFLGLGHNDGRYLWLFIPVSGVNEFSRKLGGTNGDWSSLGVRASRGVQDPQNPSPSGLPLASLLOQKMYSLNKNKMWFRFLEVTSRALSTVLNFYSFVPSGS-

NbL05g02790.1 protein_Ycf2 [MW = 73.26 kDa]

No. of times detected



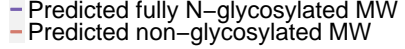
log(intensity)



Values from



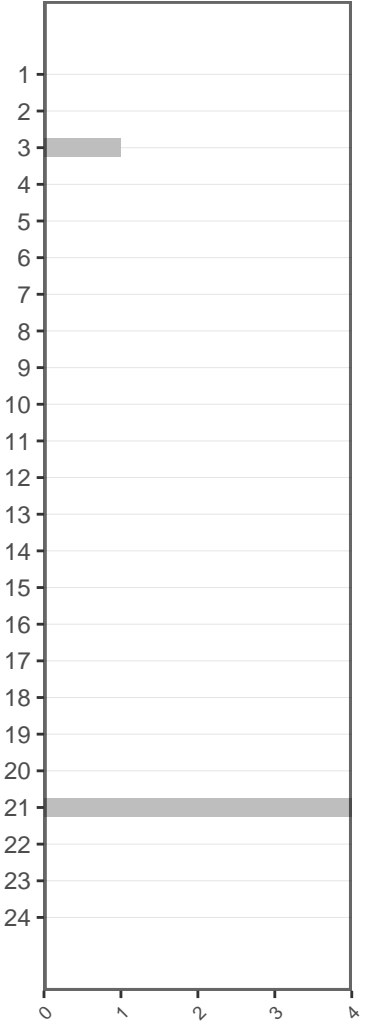
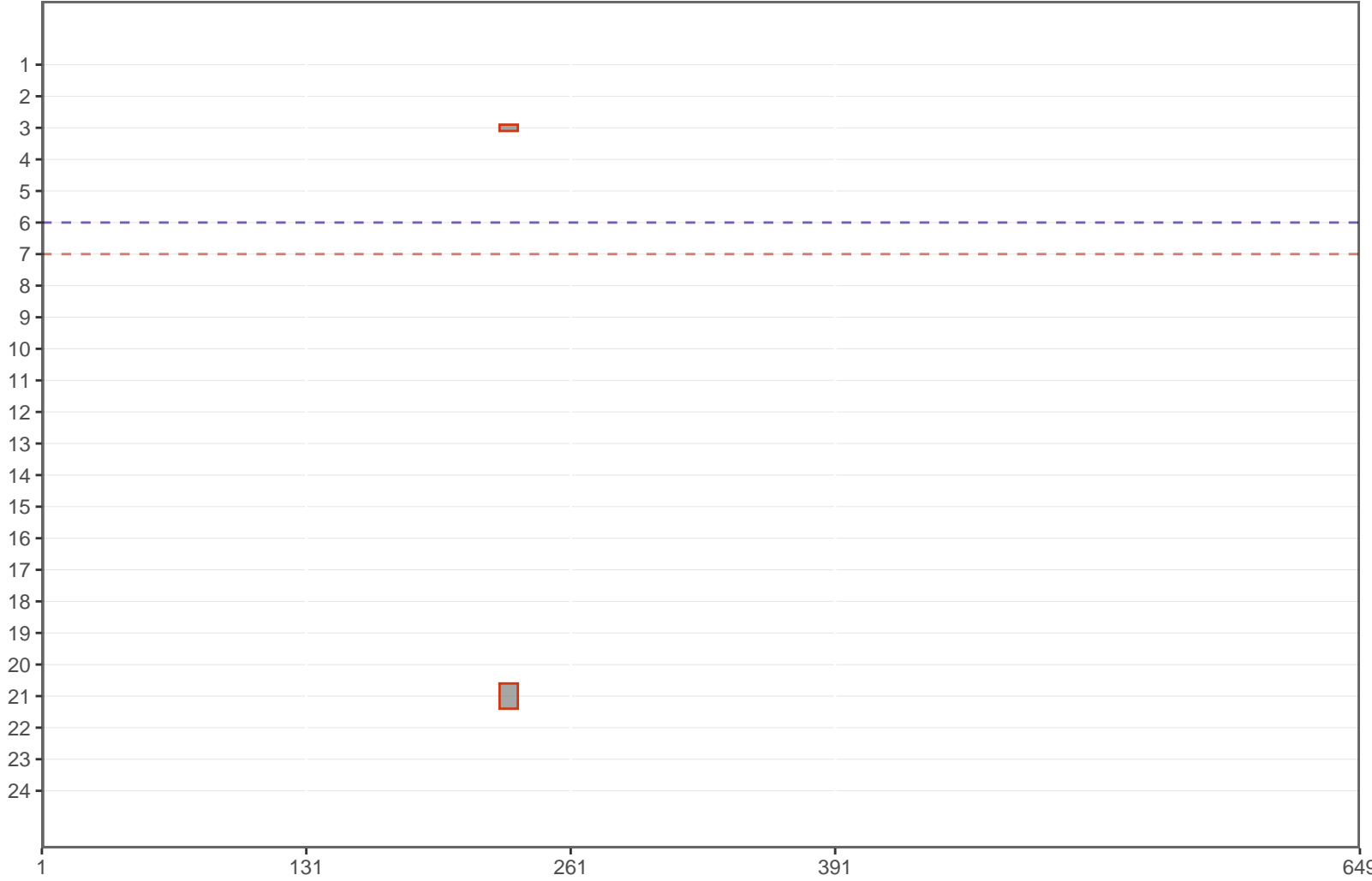
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

SQFDNDRYTLLLRPEPRNPLDMQNSGSLDQRFLYKYESEFEFEGEREGALDQGEDLNFHIIWAPRIWRPWFGLFDCIERPNELGFPYWSRFRKRIKRYDEEDELQENDEFLQSGTMOYQTRDRSKEQGLFRISGFIWDPADPLFLFKDQPPGVSFHSRHLFADEEMSKGLTSGQDLEPRRFLKGTDFLTFINFWAGSRGDIWFFSFSFYTGPMDHGLNGHQLKGLGPGDRRPDKVHLAPMGRVNYPRRHSKLEGETNPPGGLPSGKSYDTGAGFSKQPR

NbL05g02730.1 photosystem_I_P700_chlorophyll_a_apoprotein_A2 [MW = 12.55 kDa]

No. of times detected



log(intensity)



Values from



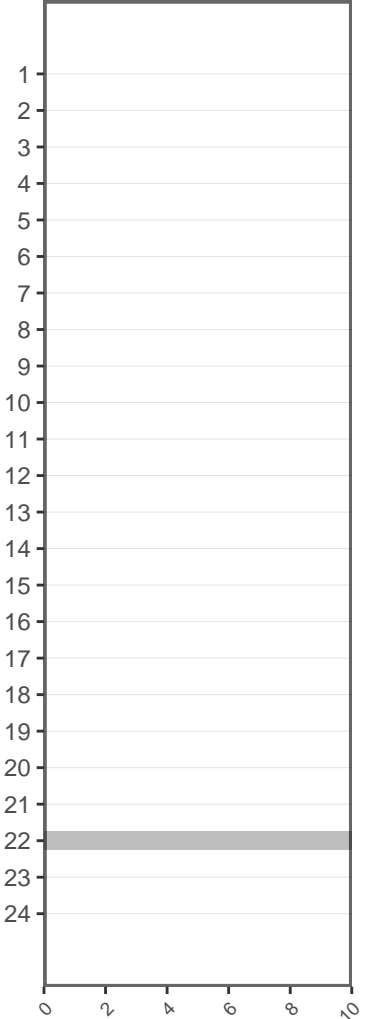
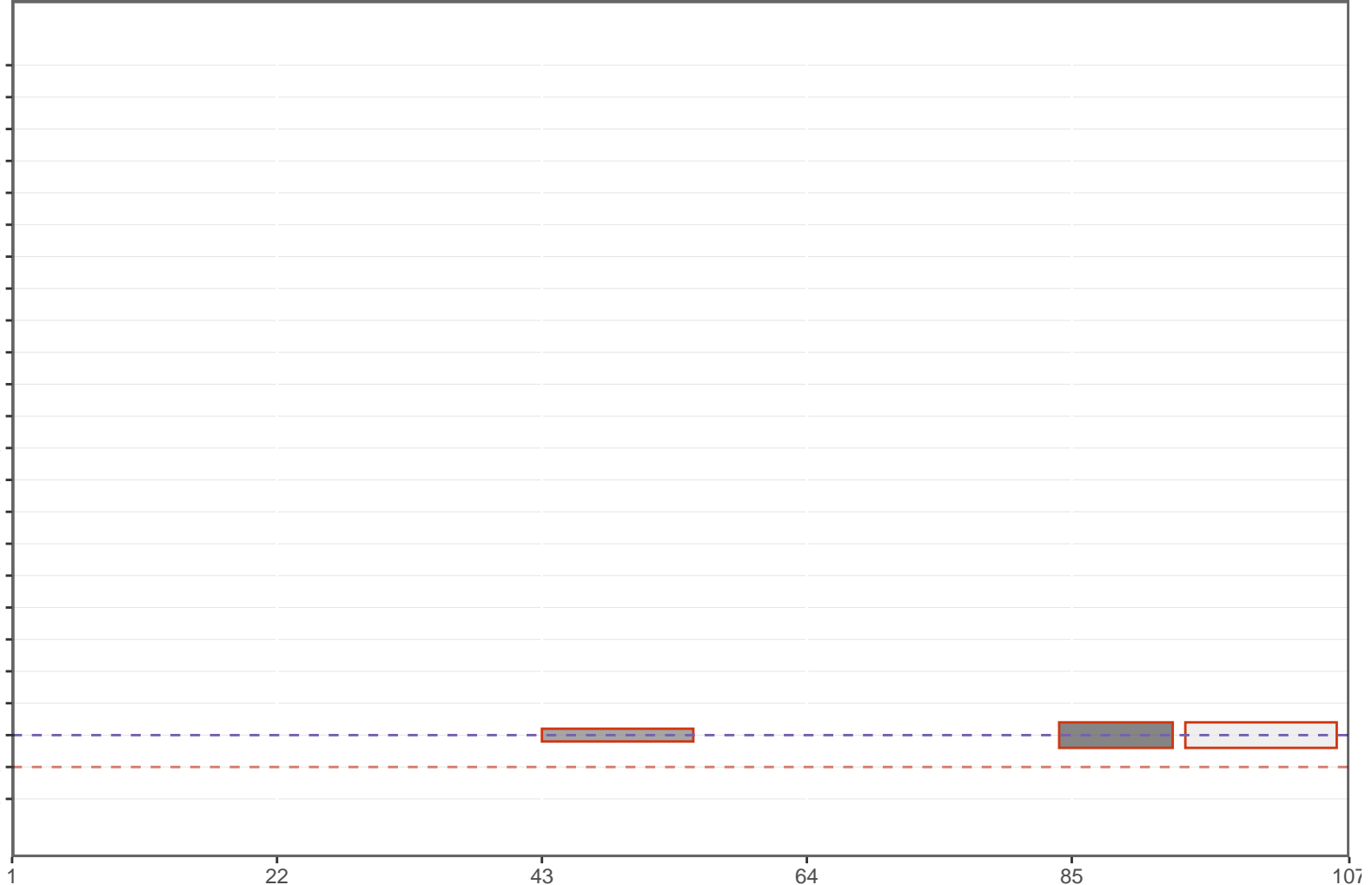
MW indication



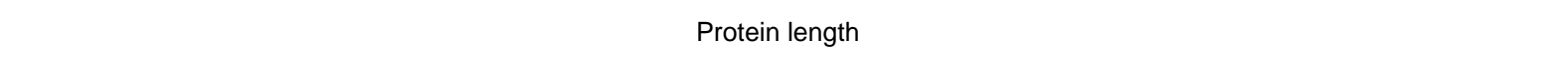
Molecular weight



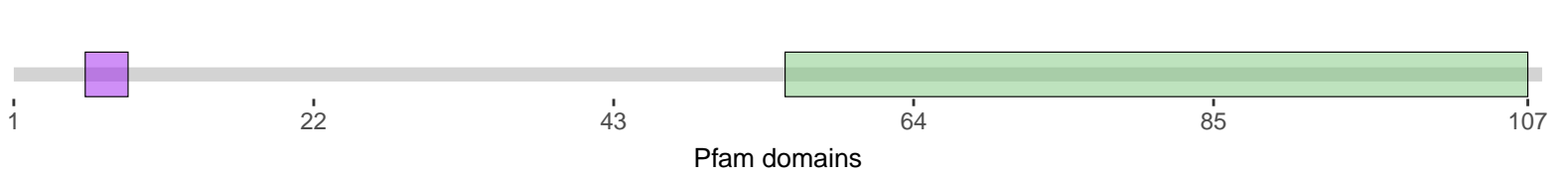
Gel Slice



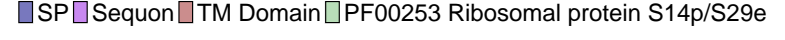
Protein length



Pfam domains



Pfam Description



Protein sequence:

IKVPSLSKDKWEIYGHGLGFLPNSAPTRLHRRGFLTGRPRANYRDFGLSGHLREMYHACLPGATRS

NbL05g02710.1 30S_ribosomal_protein_S7_chloroplastic [MW = 17.37 kDa]

No. of times detected



log(intensity)



Values from



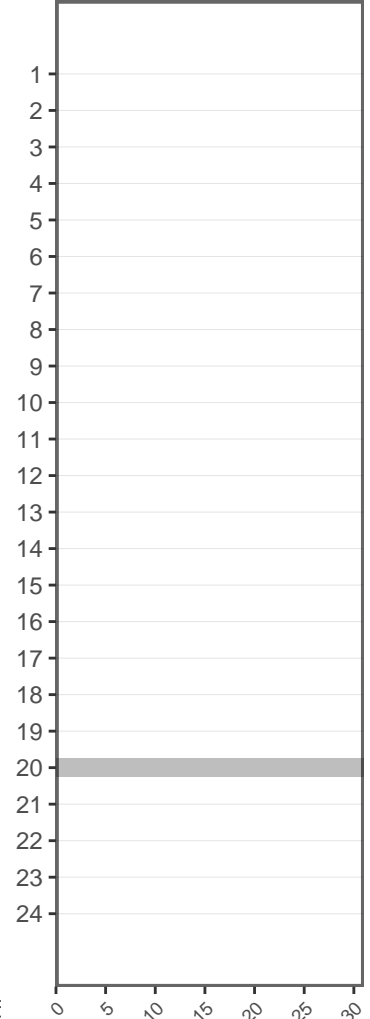
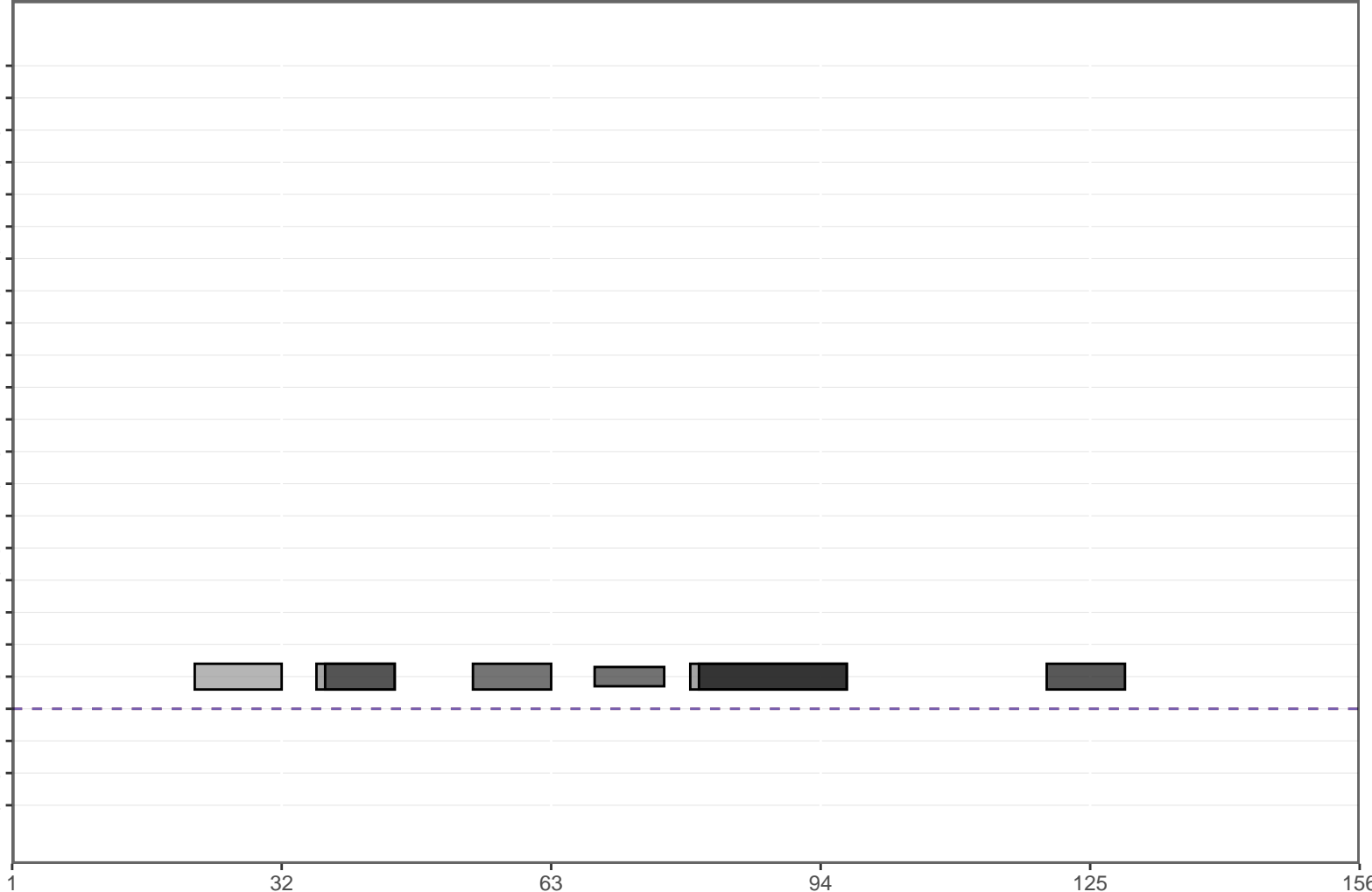
MW indication



Molecular weight



Gel Slice

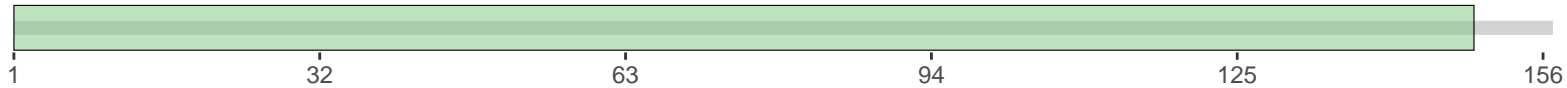


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IRGVTPDITYKARRVGGSTHQVPEIGSTQKALAIRWLLAASRKPRGRNMAFKLSSELVDAANGSGDARKKEETHRMAEANRAFAHRI

NbL05g02620.1 fructose-bisphosphate_aldolase_cytoplasmic_isozyme [MW = 41.49 kDa]

No. of times detected



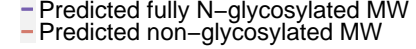
log(intensity)



Values from



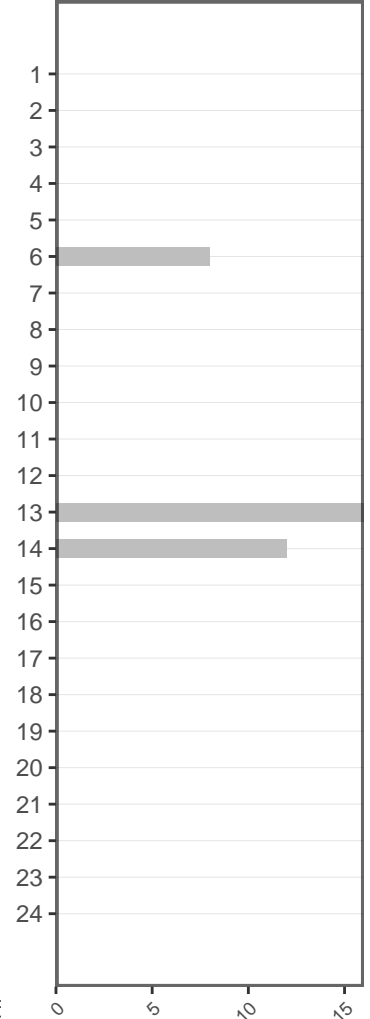
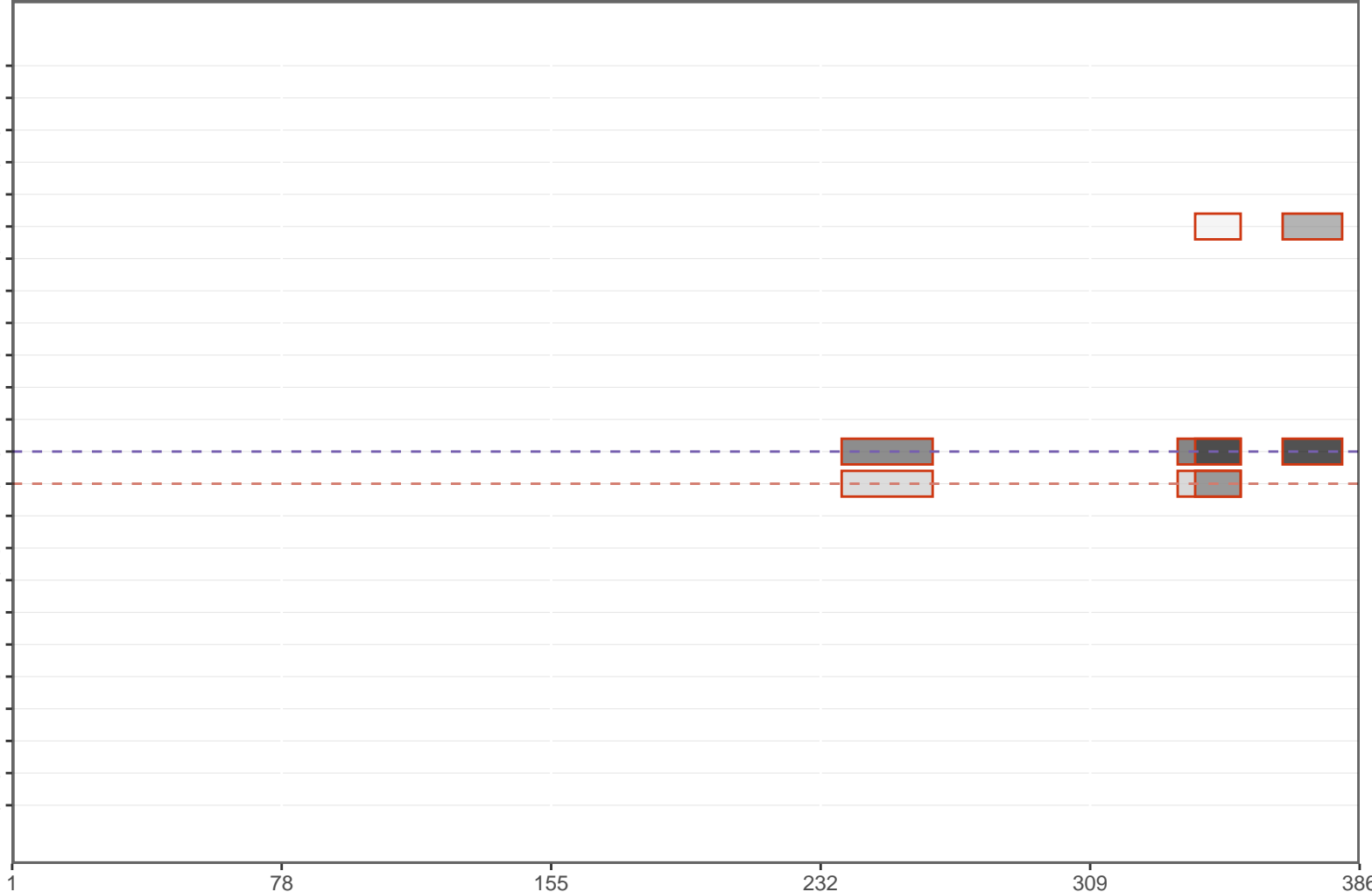
MW indication



Molecular weight

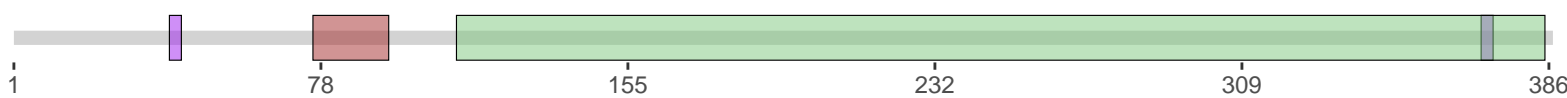


Gel Slice



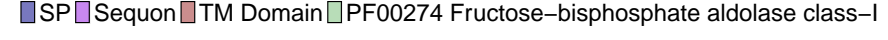
Peptide counts over 4 repeats

Protein length



Pfam domains

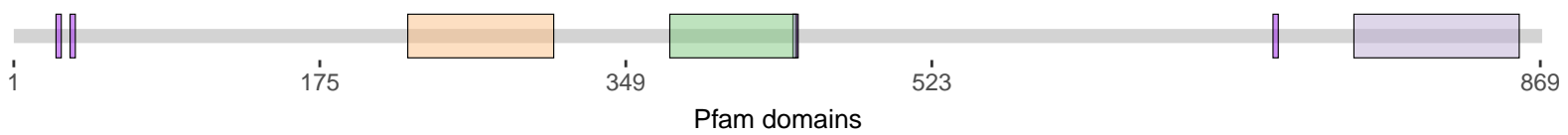
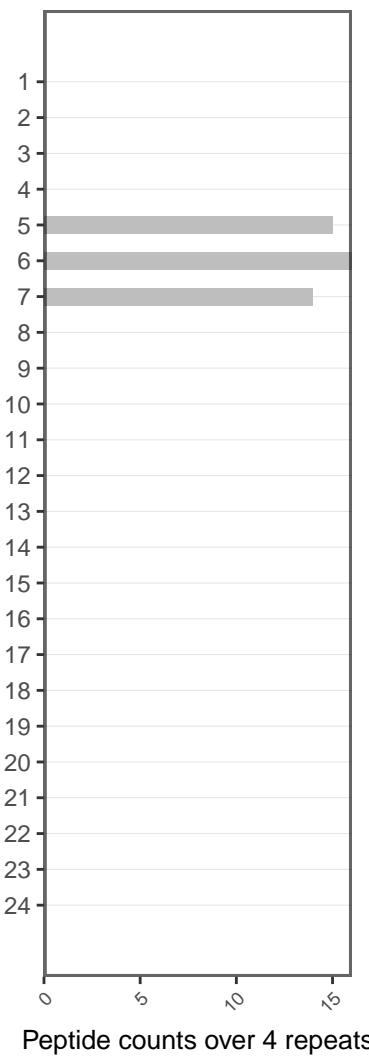
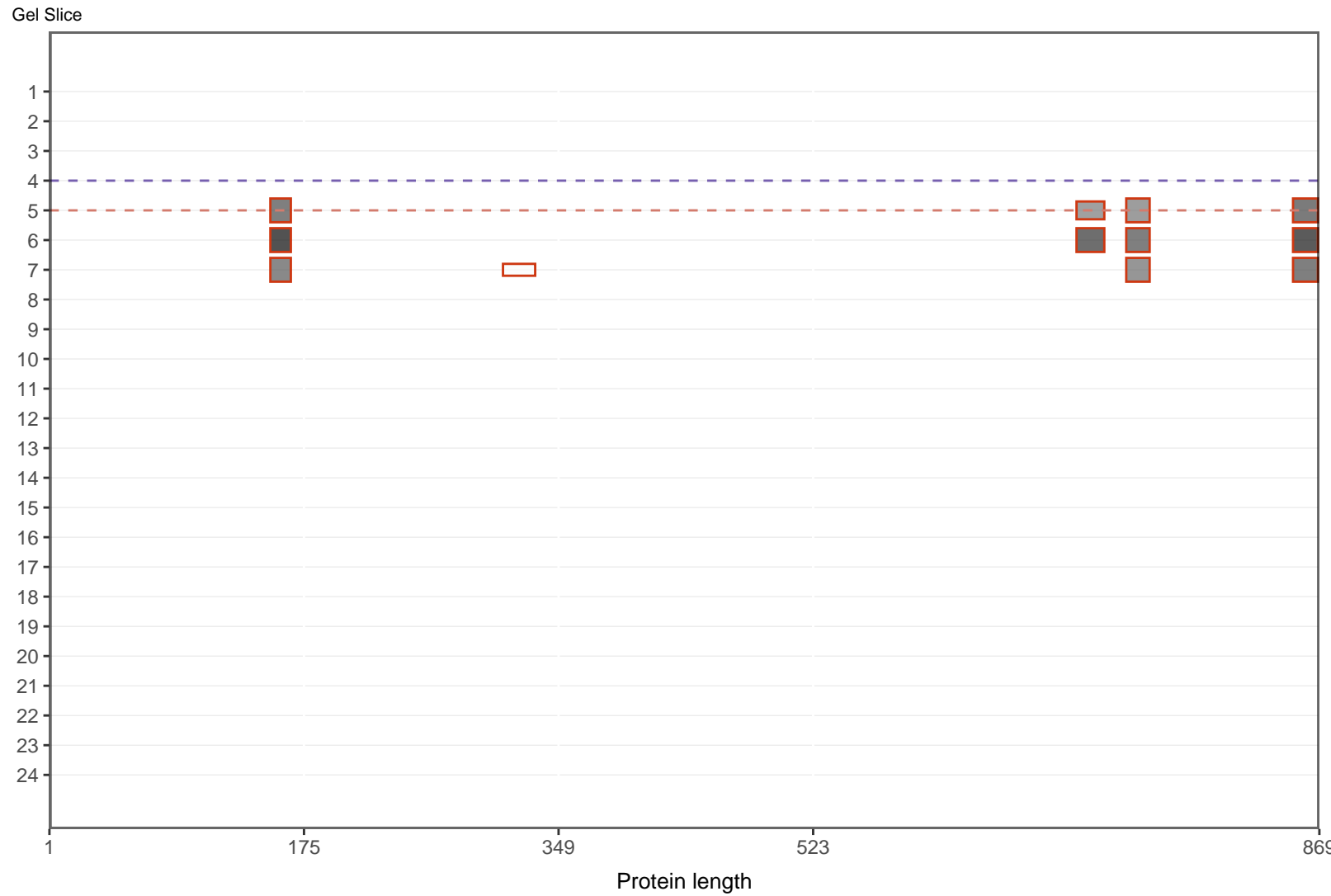
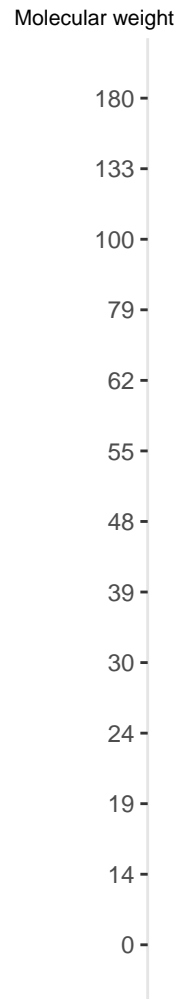
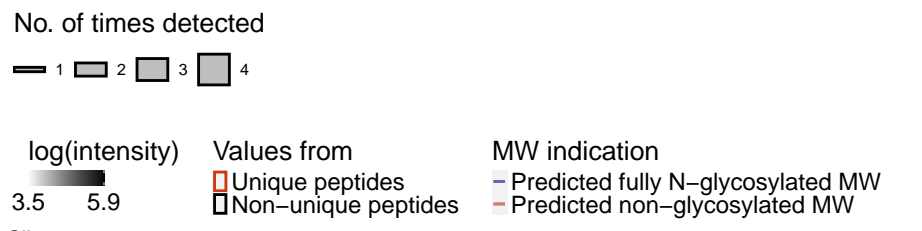
Pfam Description



Protein sequence:

IPSQLAINENANGLARYAIHGGNGLVPIVEPELVGGSHDINKGADVTERVLAACYKALNDHIVLLEGLTKPFNMITPGSEAAKVAPEVIAEYTRIALGRTPMVAWVWVFLSGGGSEEEATVNLNMINLQTKKPKWLSFSFGRALGGSTLKAWGKEENVGMGAAFLTRCKANSEATLGVKAGATNLSEGAESLHVNDKYV

NbL05g02530.1 14-alpha-glucan-branching_enzyme_1_chloroplastic/amyloplastic-like [MW = 99.21 kDa]



- Pfam Description**
- SP
 - Sequon
 - TM Domain
 - PF00128 Alpha amylase, catalytic domain
 - PF02922 Carbohydrate-binding module 48 (Isoamylase N-terminal domain)
 - PF02806 Alpha amylase, C-terminal all-beta domain

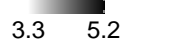
Protein sequence:
 AHLEGIYVLMIDIVHSHASNTLDGLNMFDDGTDSDGYHSGSRGYYHMMWDSRLFNHYGHWELVRLYLLSNARWLDDEFKDFGRFRFDGVTSMYYTHHGLGVTFITGNYNEVFGFATDVAAYVLLMNDLHGLFDPDAITGDEVSGMPTFRIPVQDGGVGFDFVRLHMAADKWIELLKKRDEQWRVQDVIHTLNRRIWSEKGVSAEESHDDGALVSKTAFVLLMNDKDMYDFMALDRPPTPLIDRGALHKMIRLFTMGLGEGYLFNFMGNEFGHPPEWDFPRAEQHLPGDGVF

NbL05g02520.1 uncharacterized_LOC109207925 [MW = 35.31 kDa]

No. of times detected



log(intensity)



Values from



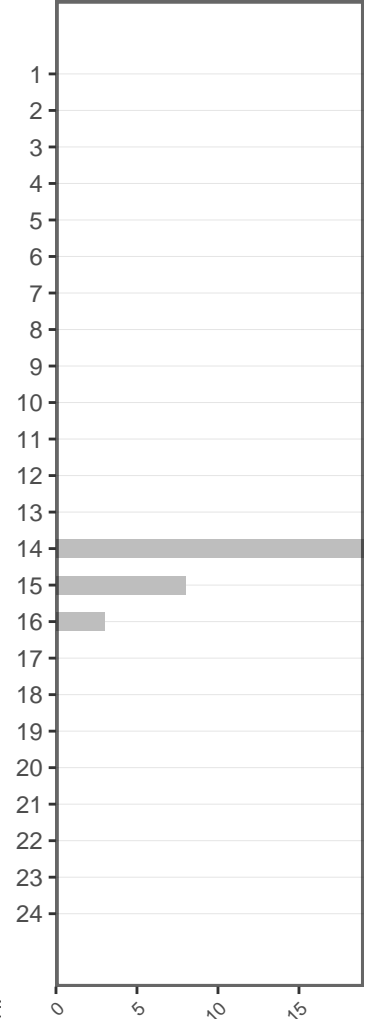
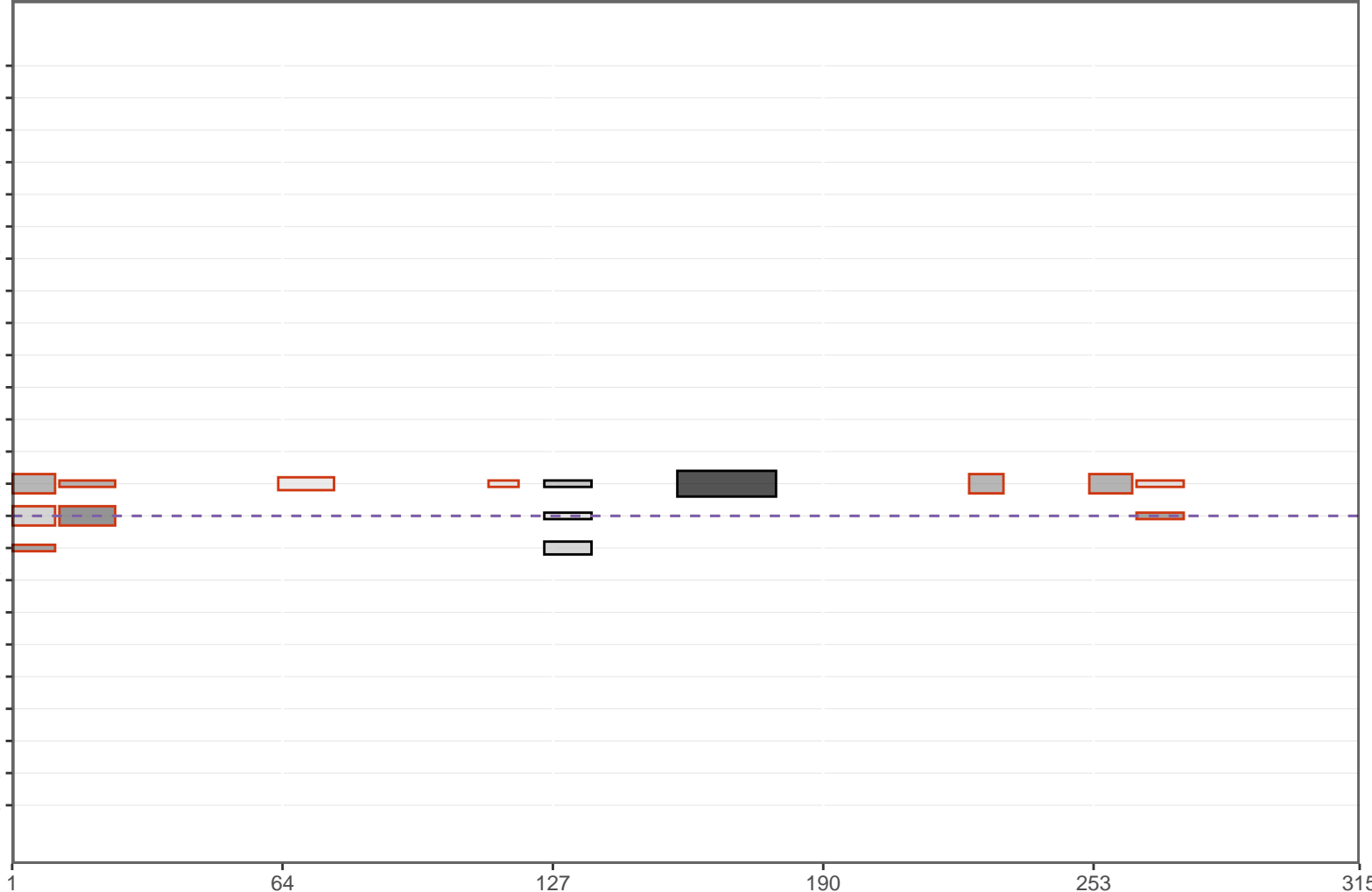
MW indication



Molecular weight

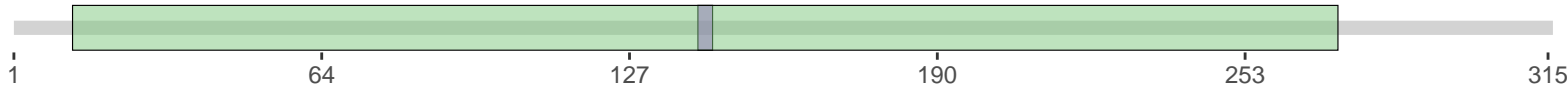


Gel Slice



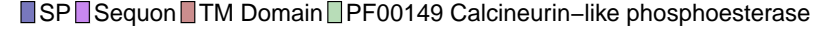
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ITVYKNTYKGIYKGSYDAAPTFESYGVPHGSADLMKAVPDEHKKFLADLVWHEEDDVCKADEGKSKCLMVAHGLEKNDVVEGKTLKAKDTRISKVYEAISGRKNWWEIPQELRTPAVVSGHHGKGFHEGLRLVIDEGGGLEGNPVAVVLPMEVWRDTHLVK

NbL05g02460.1 monodehydroascorbate_reductase [MW = 47.09 kDa]

No. of times detected



log(intensity)



Values from



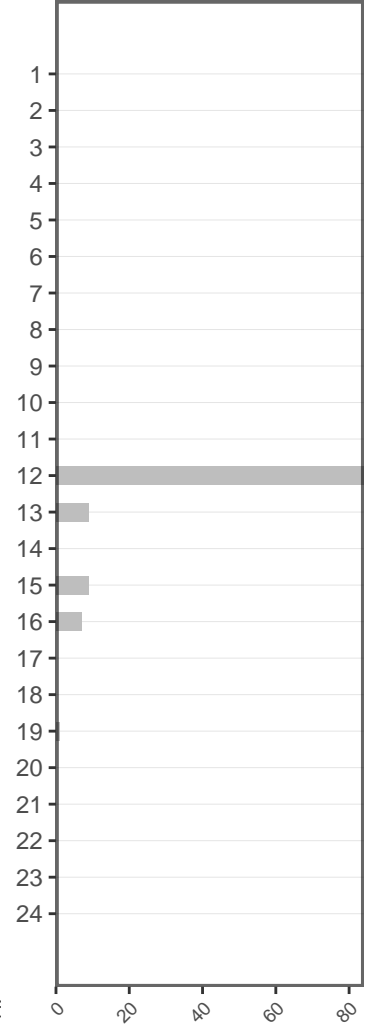
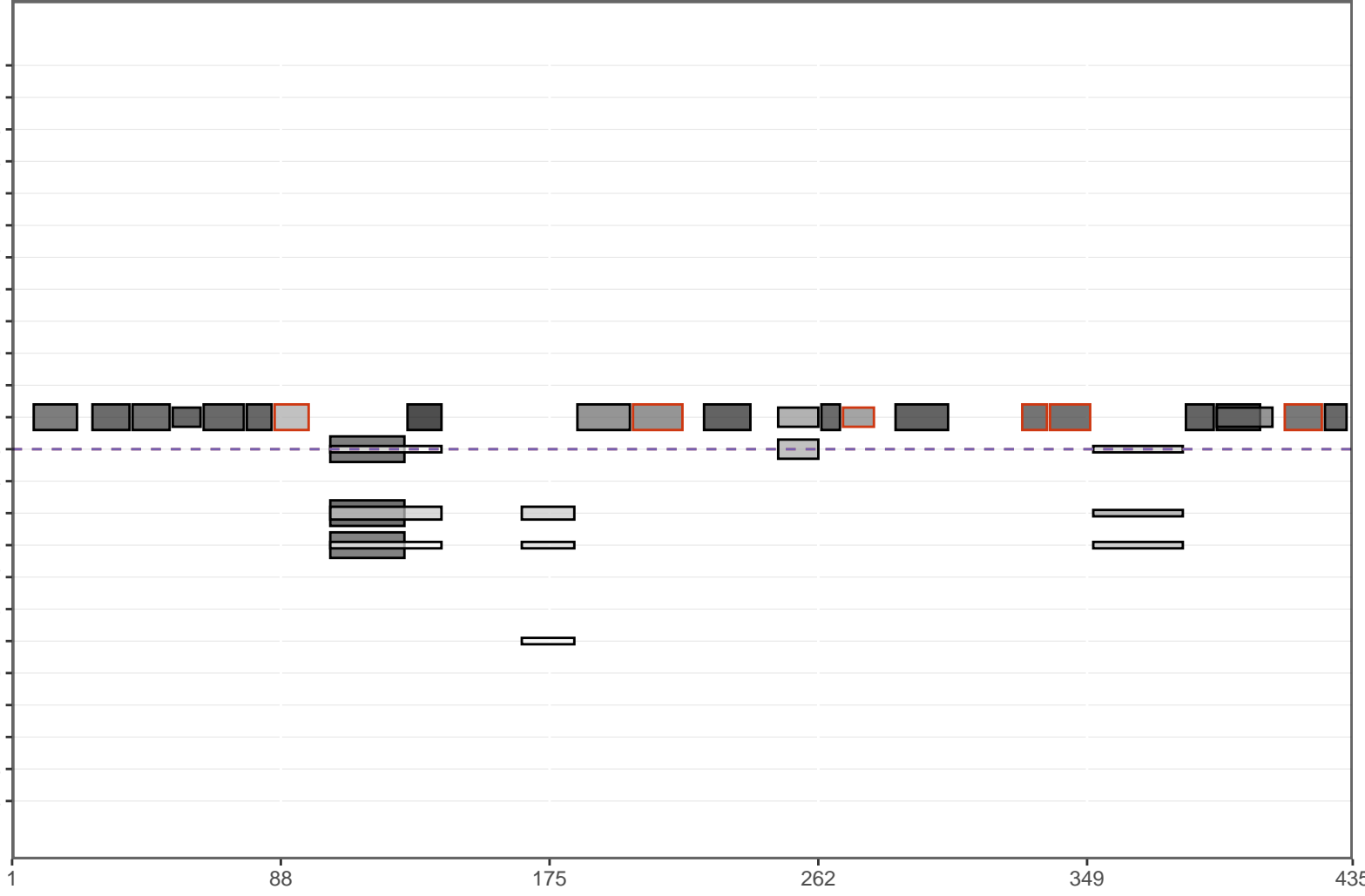
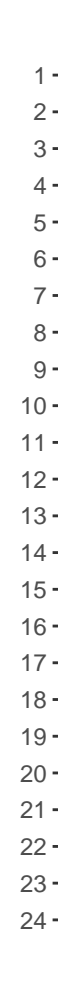
MW indication



Molecular weight

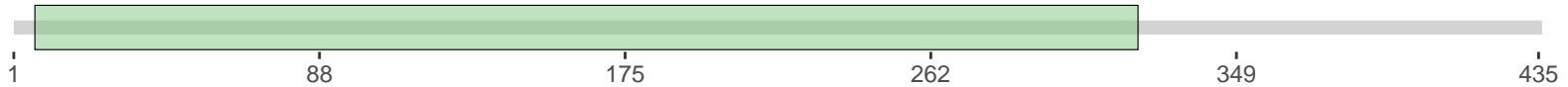


Gel Slice



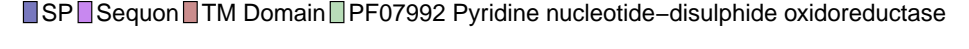
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MAAFYEGYQNKGNKGTVAWGFDRPNSEKVEKLVKDRVLEADIVAVGVGRPLTFLFKGGVVEEGGDKTDAFFKTSVDPVAVAGDVAFFPKMVDNRIRVHVHDSRKSAGAVKAIFASEGGKVEDEYDLPIVYGRAFDLVWQFYGDVNGETVLFEGDADPNATHKFGGVYWGDKVYVGFLESGTPEENKAIKAVKVGPLVSLDGLAKEGLSFASKP

NbL05g02020.1 syntaxin-51-like [MW = 25.87 kDa]

No. of times detected



log(intensity)



Values from



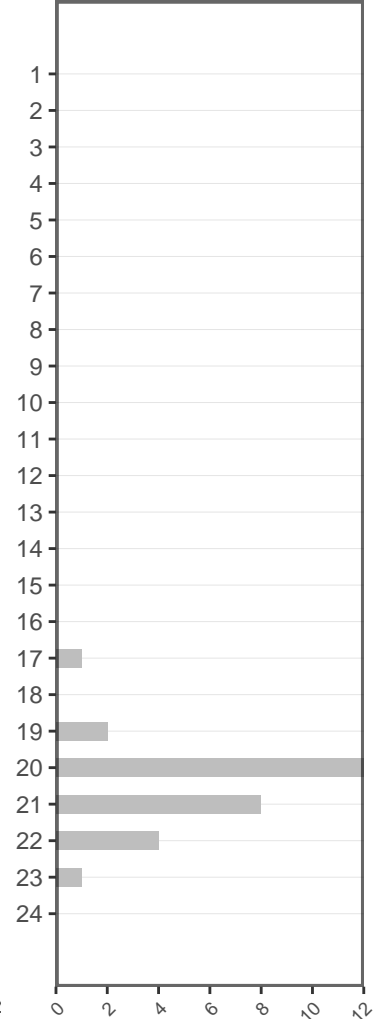
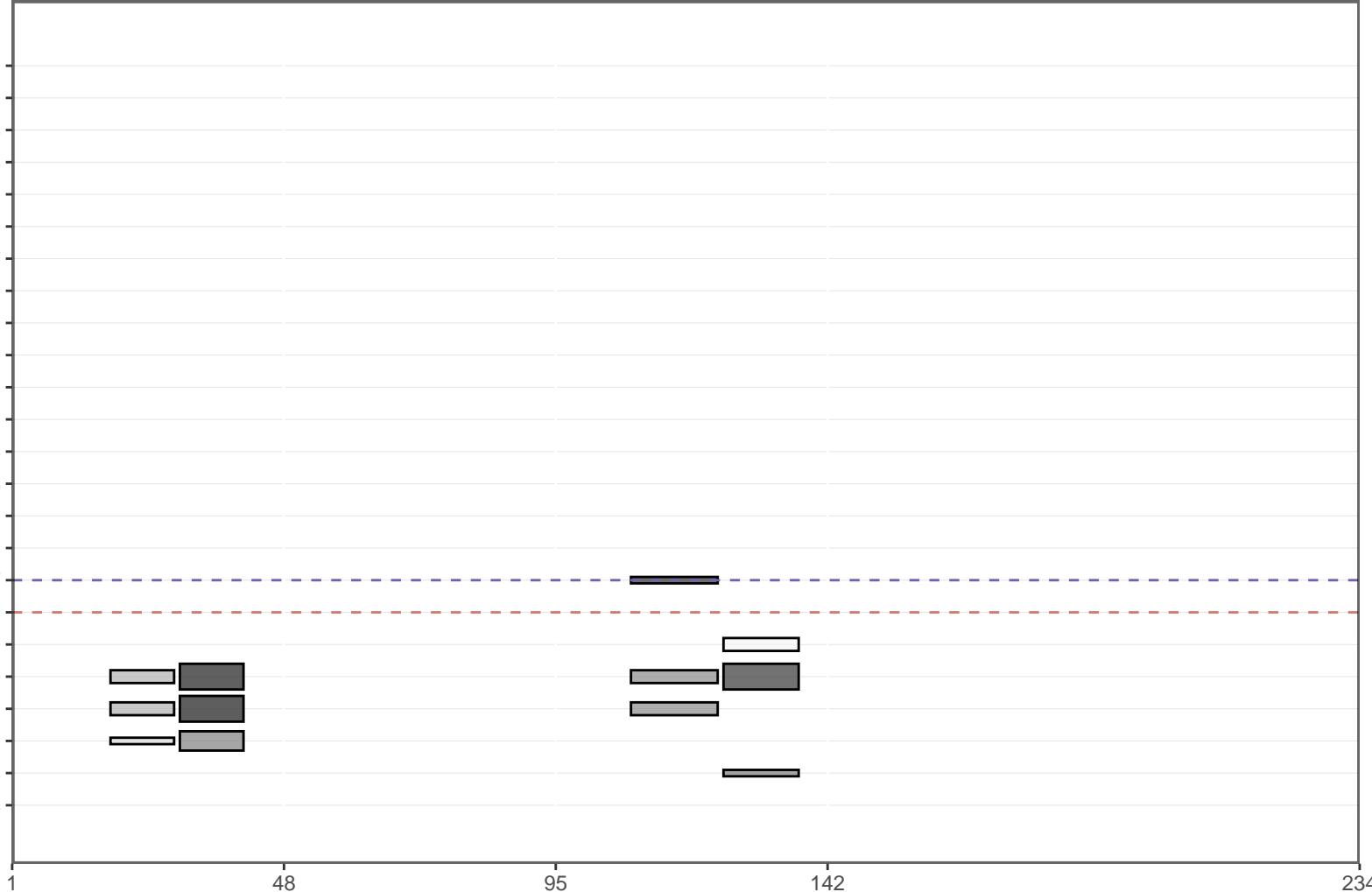
MW indication



Molecular weight



Gel Slice



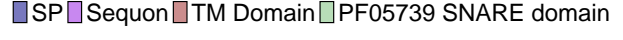
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SPANRDSLLGPEKPVDMASRATGLDNYGVVGLQRQIMKEQDEGLENEETVMSTKHIALAVNEELGLQTRLDNLDHVDVDFDRLRQVQKKAALNKRKTGGCGCMOLLLEVLGVVAVVWLLKVL*

NbL05g02000.1 serine/threonine-protein_phosphatase_PP-X_isozyme_2 [MW = 35.72 kDa]

No. of times detected



log(intensity)



Values from



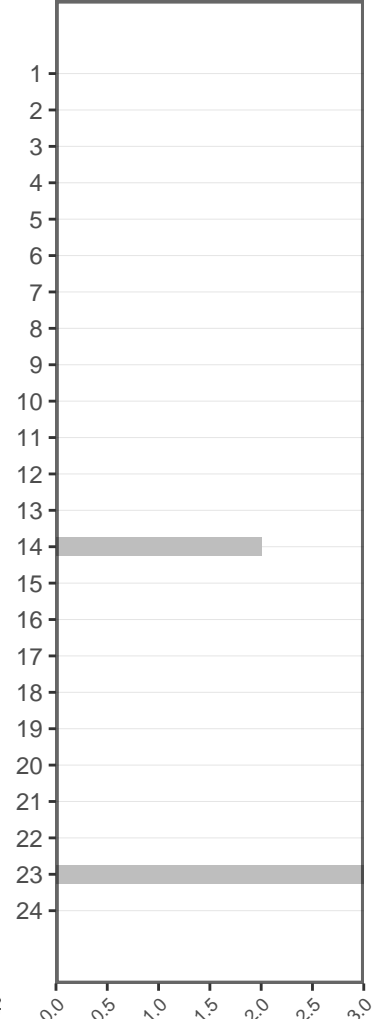
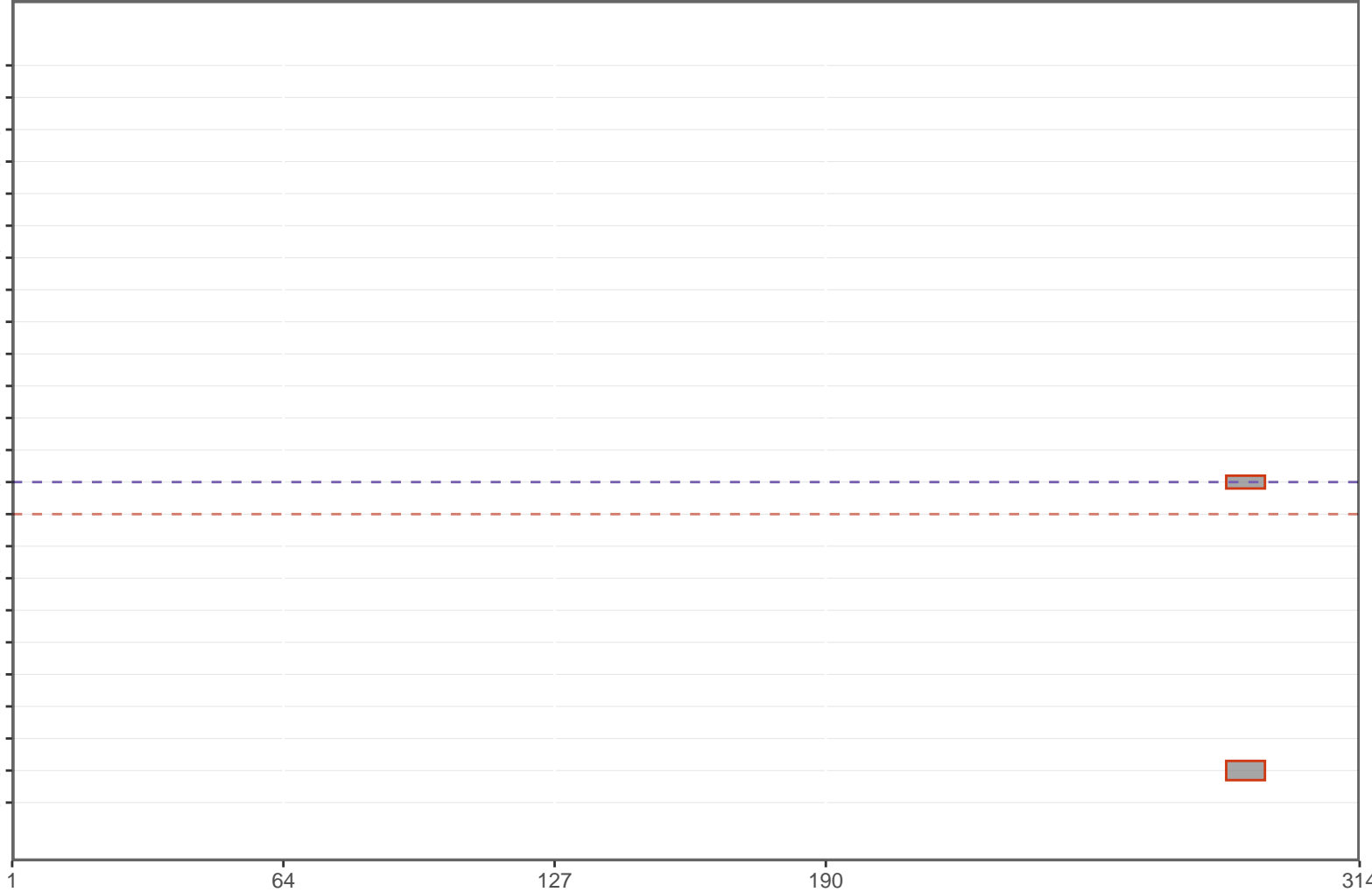
MW indication



Molecular weight



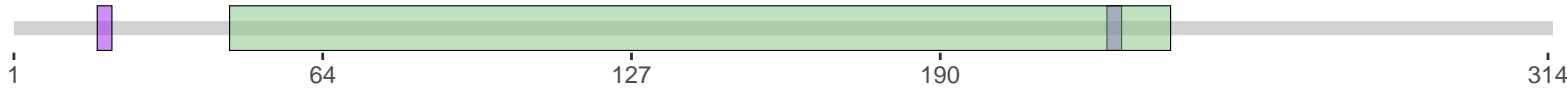
Gel Slice



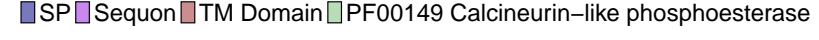
Protein length



Pfam domains



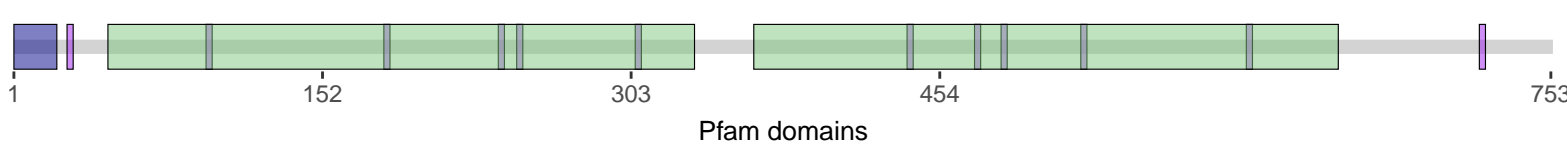
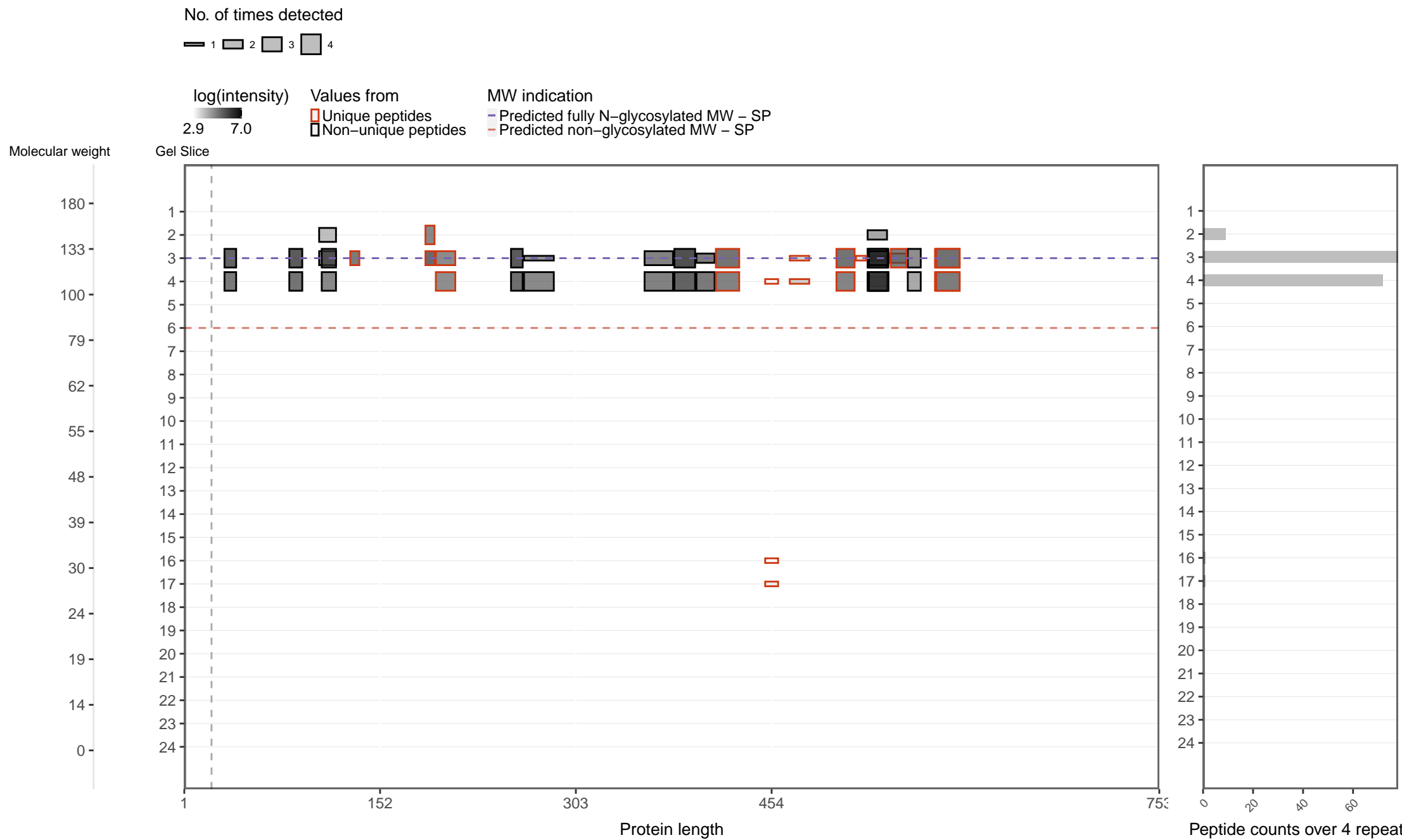
Pfam Description



Protein sequence:

DYLSLSALEIKFVSHGGLSPRTISLDQRTDRKDEVPHEGAMCDLLWSDPEDIVDQWLSLPRGAGFLFGGSVYTSFNITNNDVYGRAHQLMVEGRKVMFNNGIVTVWSAPNYCYRDCNVAALLELDENLNKGRFRVFAAPQESRGTAKRLSGPPAKRPPDYFL

NbL05g01940.1 glycerophosphodiester_phosphodiesterase_GDPDL3-like [MW - SP = 79.67 kDa]



Pfam Description
 ■ SP ■ Sequon ■ TM Domain ■ PF03009 Glycerophosphoryl diester phosphodiesterase family

Protein sequence:
 ISEGASDYPGCTBLAYTKAASDGDALDGPVMTKDGIPFLGSLINIDKTTAAGSPFSNATVPELKITNGILNLTWAEKQSLKPAENQWVDFRFRNPKARNDGNFTSLADFLAFKKNATSVGVMSIENAAVYLAGKGLGVTSVAIDLAKSKGYDNGTAKKVLHGSTDSVLEEFKPKREYELVGVGDDIRNIEG6TLEKTFKSVITKKSVPFSEGAFAIAGTNNVQKLG6SNLTVVYQLFDMEFVSGQAWDFFS6SLELNNVAGAGIDGVTGYPTAARYRNRCLG

NbL05g01900.1 40S_ribosomal_protein_S8-like [MW = 28.87 kDa]

No. of times detected



log(intensity)



Values from



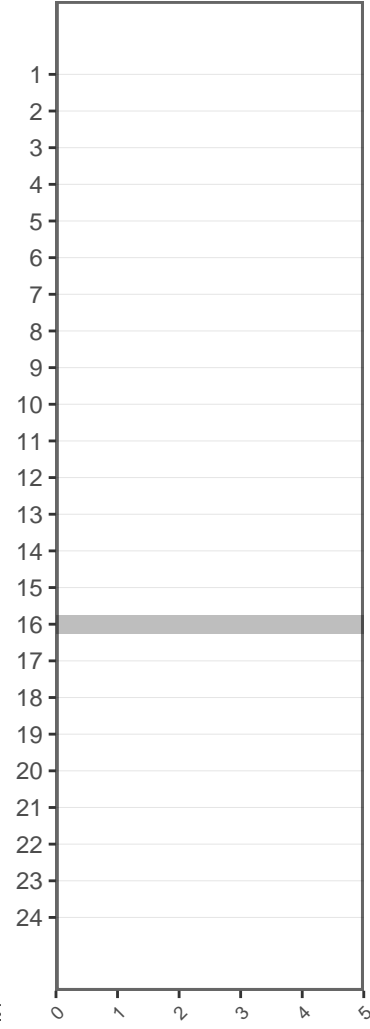
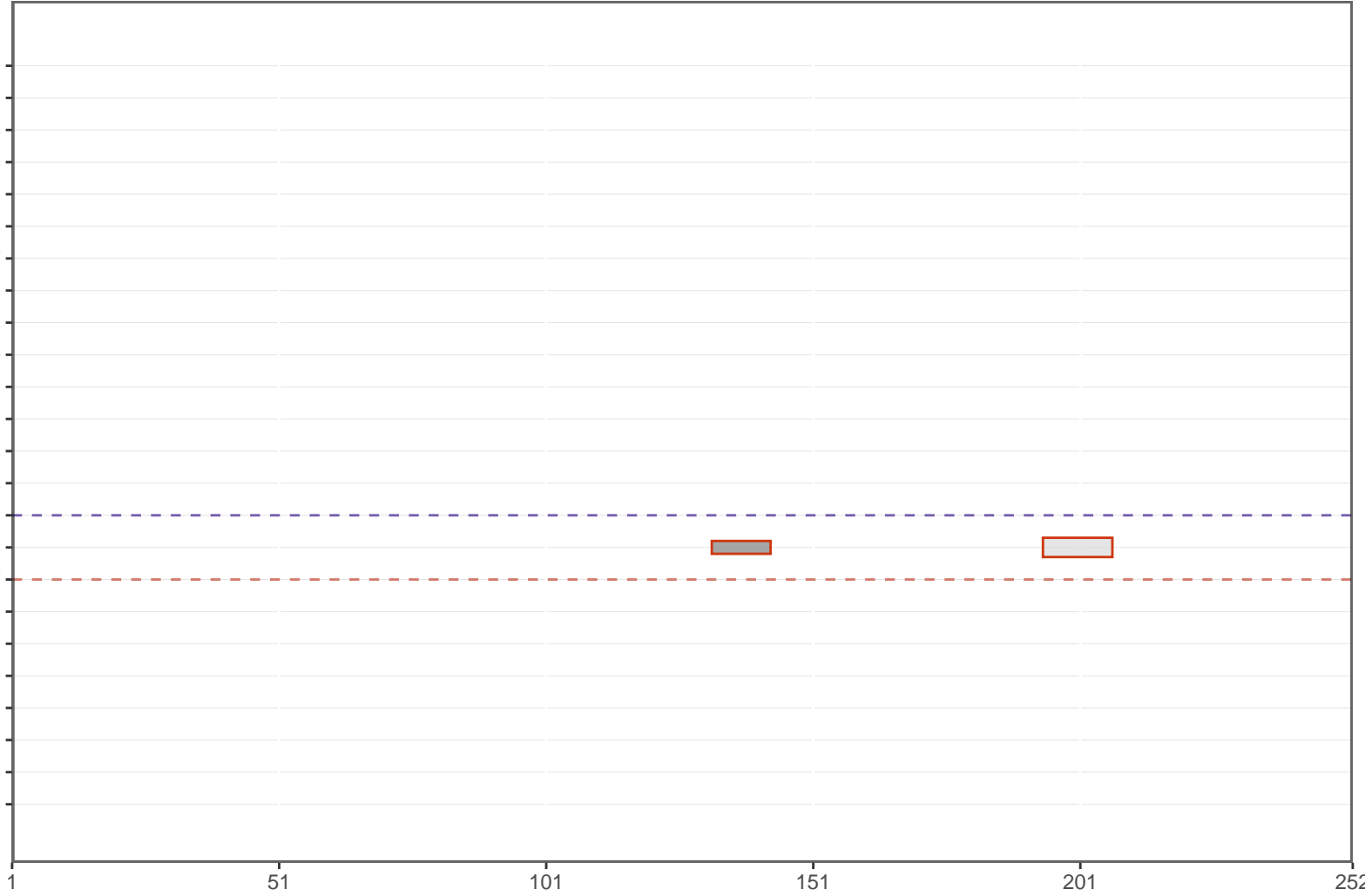
MW indication



Molecular weight

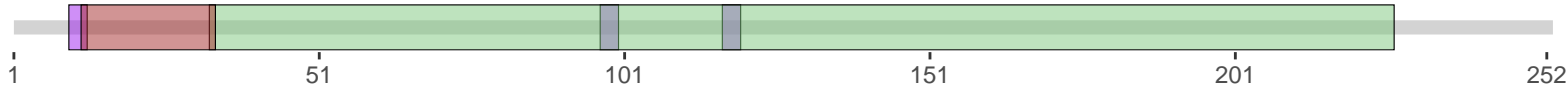


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

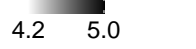
***YNASNEIURTGTFLWGAIVQVDAAPFKQWVLRGHYGVDIRRKKTAASKKEGEAEAVPEEKKNHVDRLKLRGGDRKIDPHIEEGFSSGRLLAASRPDGGCRADGYILEGKELEFYVKKLGRKKGKASGAA*

NbL05g01890.1 uncharacterized_LOC107809878 [MW = 35.24 kDa]

No. of times detected



log(intensity)



Values from



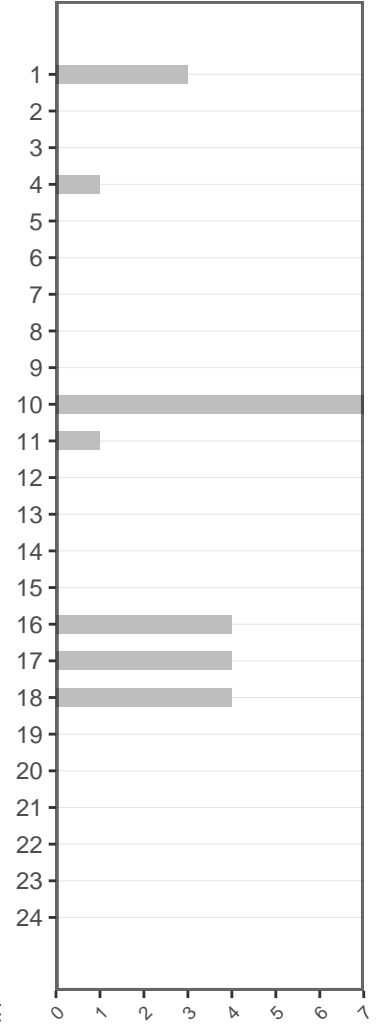
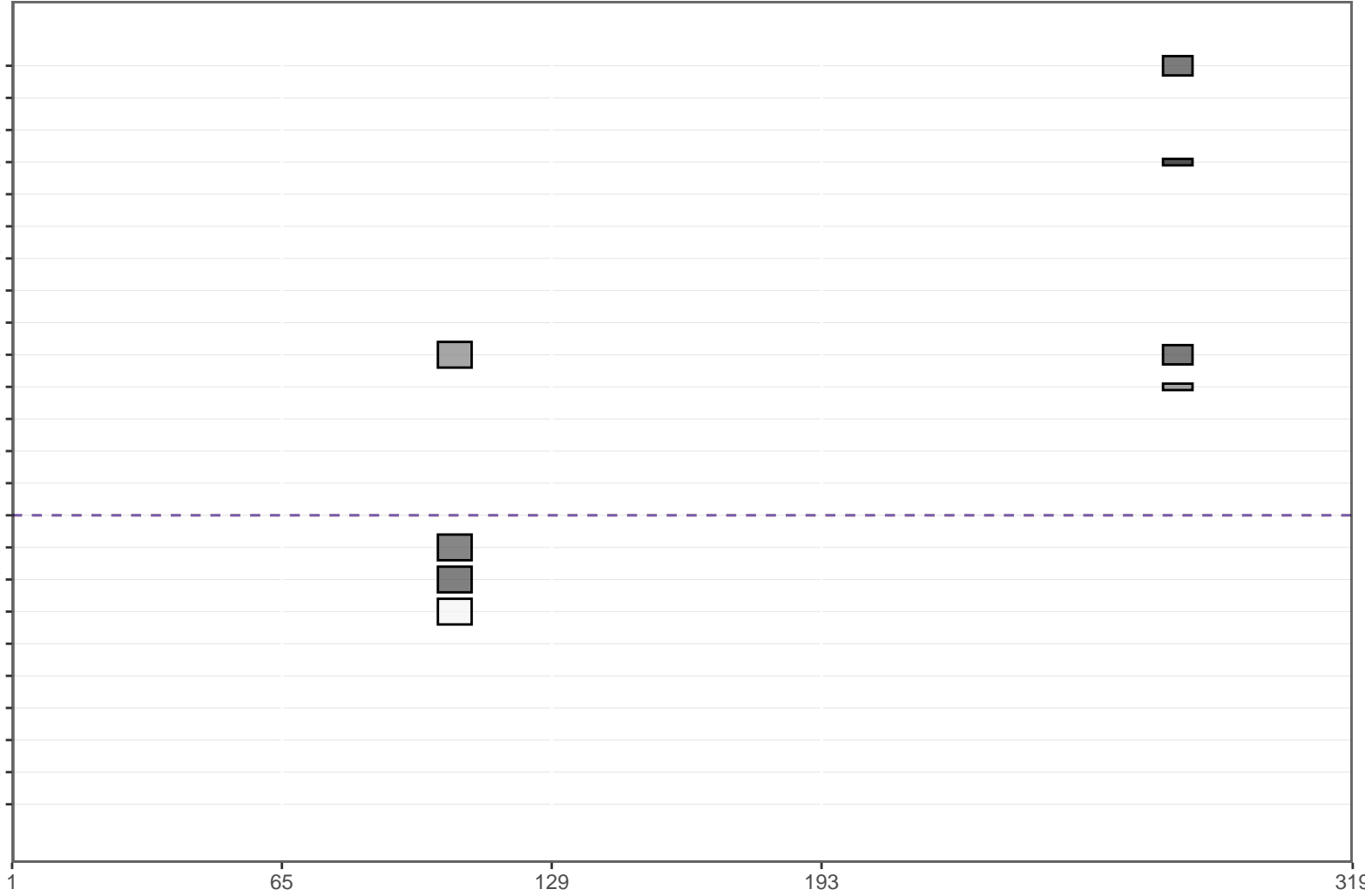
MW indication



Molecular weight



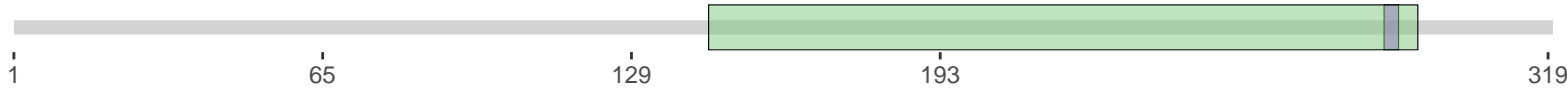
Gel Slice



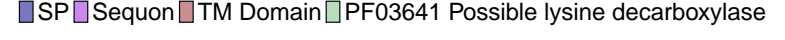
Protein length



Pfam domains



Pfam Description



Protein sequence:

DAATGGALQAGKRVGFGFKIGREAGEWTAENFHPYLPSESYLGRFFSARKHGSLVDAAVVRCKSSERTAVAVLPGDGLTDEIFEVMAKQLERIGSGLPVPFLMNYDSFYNNLEFLNDCERKWTGTVSNKNEVASLWVQNNNSEALAYLTFYVGLSPVETGRKDPESSEGRSSP

NbL05g01760.1 imidazole_glycerol_phosphate_synthase_hisHF_chloroplastic [MW = 65.05 kDa]

No. of times detected



log(intensity)



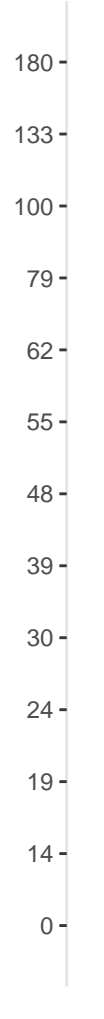
Values from



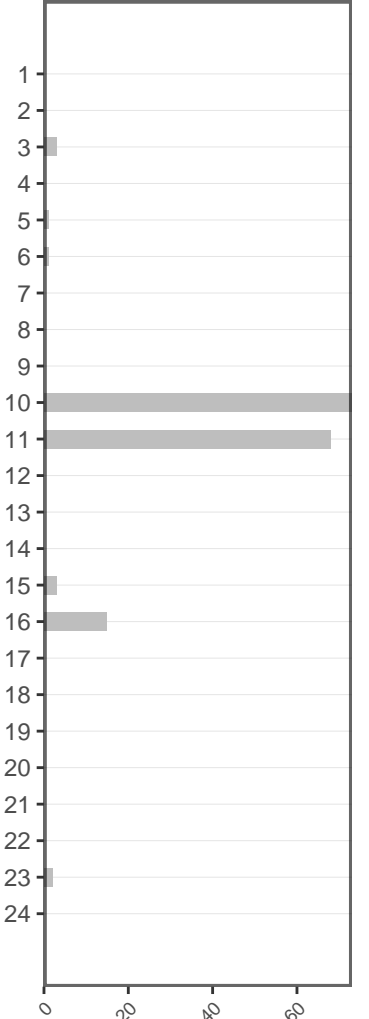
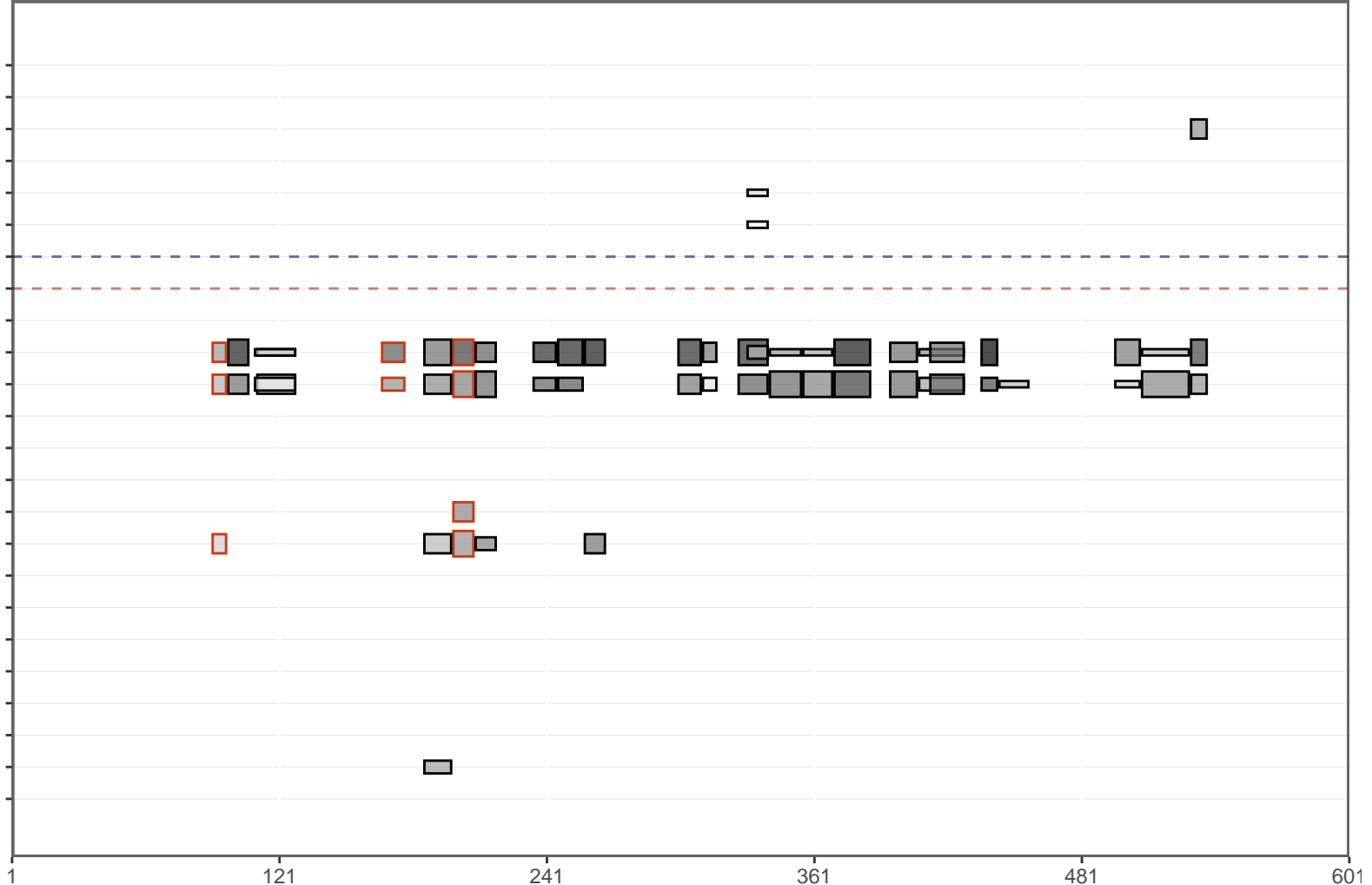
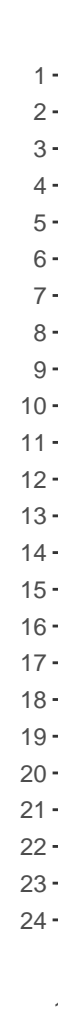
MW indication



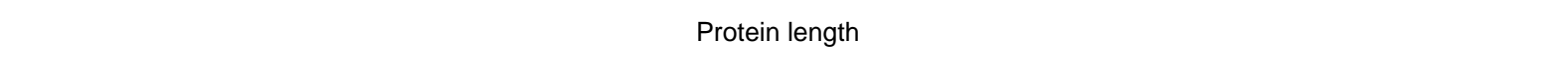
Molecular weight



Gel Slice

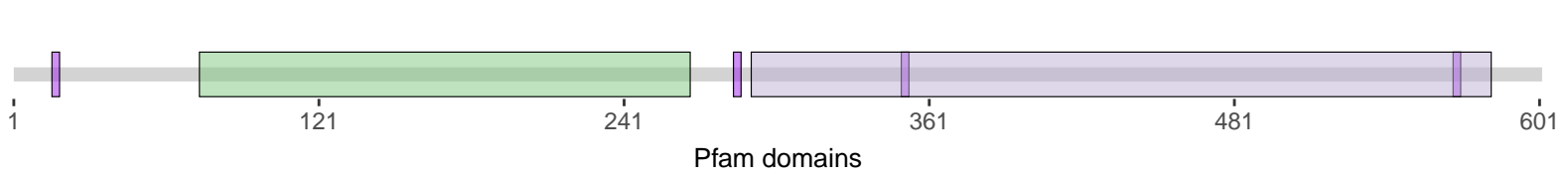


Protein length

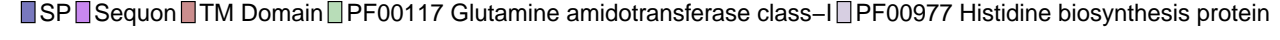


Peptide counts over 4 repeats

Pfam domains



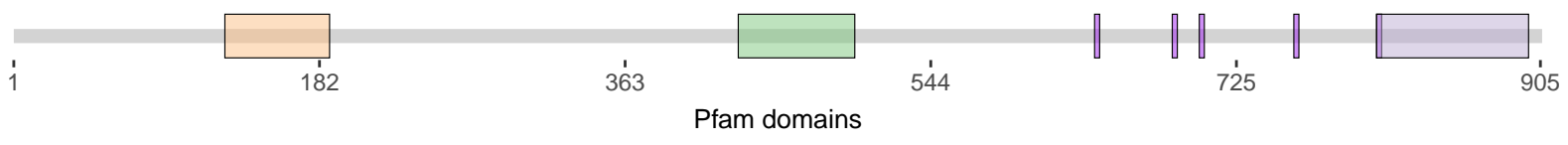
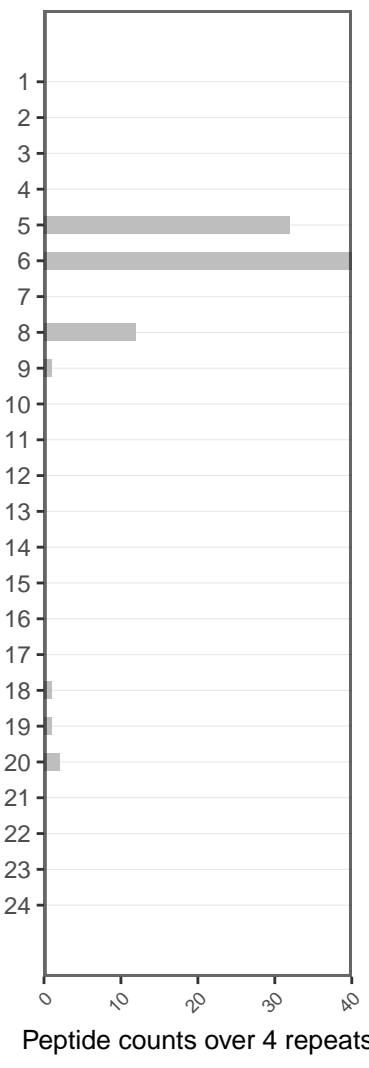
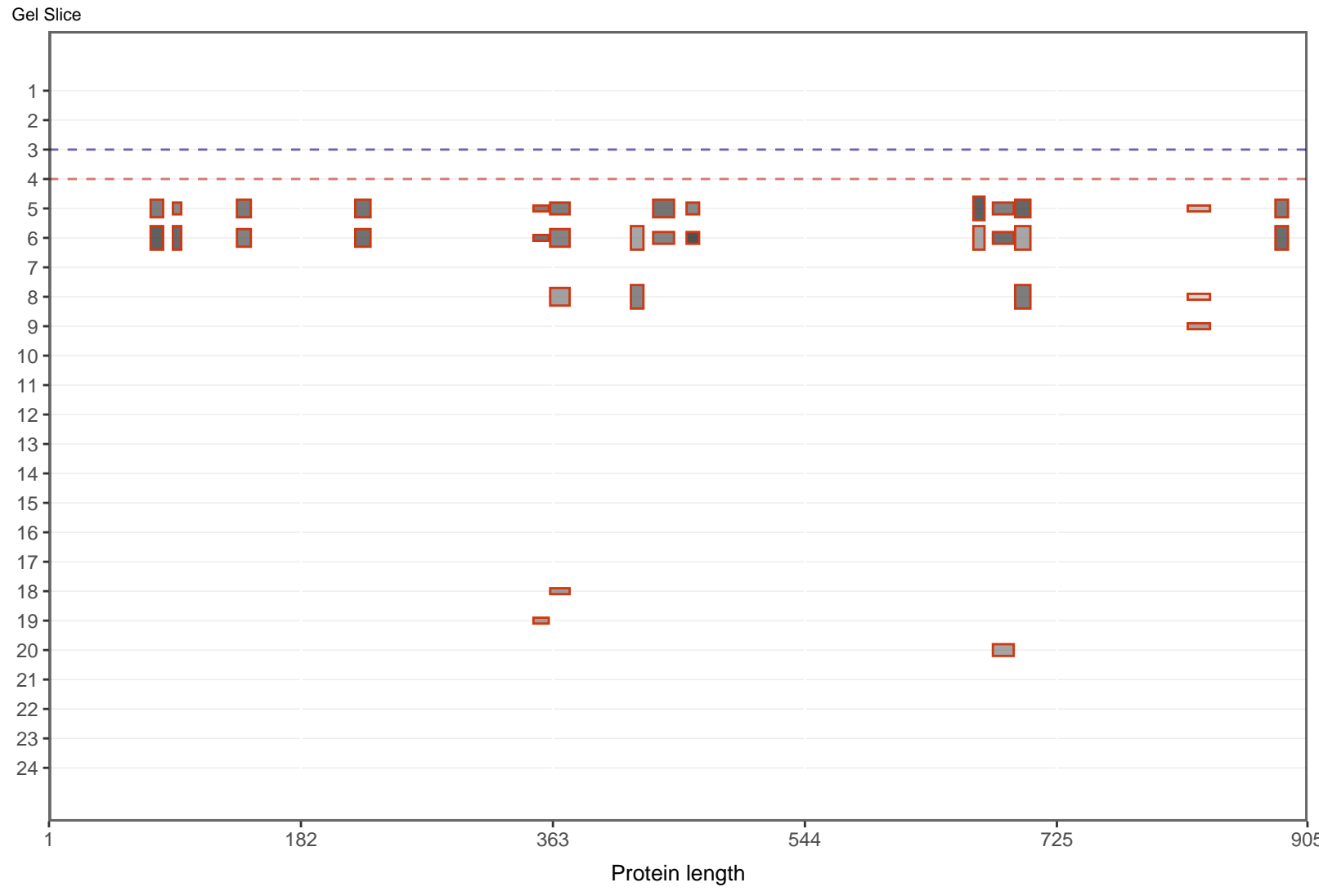
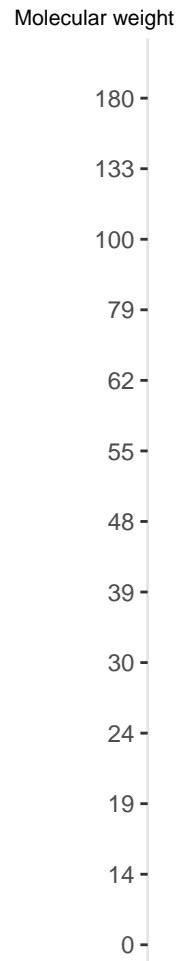
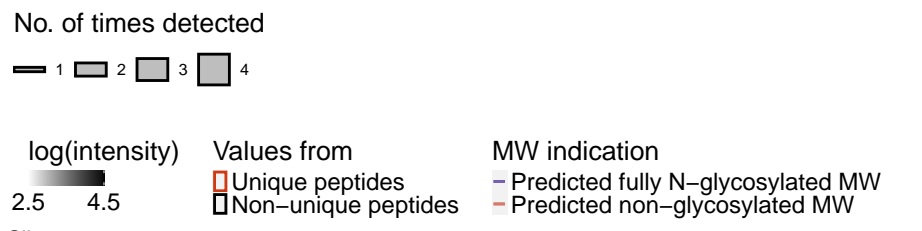
Pfam Description



Protein sequence:

LAKRIVACLDVRTNDKGDGLVYTKGGYDVRHETKENEVRLNLGPKVLDLAGYKDGDAEVSFLNTAFRDFPLGDLPLMLQVLRVAEENFVPLTVGGIRDFKNGRGRYVSSLEVAEYFRGADKVSIGSDAVVAEEYLRKGGVTKGKSLGEGISRVYGNDAVAVSDIPRRVYVKDKPAVEFRVYKVRSPGPNGEVAVWYQGTVSGGREGRPAGVLAELAKVAEELGAGELLNGIDGDDGGKGFDDILKLIHSDAVSIPVAISSGGAGTVHFSEVFTETNASALAGFTRKEI

NbL05g01750.1 14-alpha-glucan-branching_enzyme_3_chloroplastic/amyloplastic [MW = 103.76 kDa]



Protein sequence:

YNAIGLVVEIKDYFTVGRVTFVWISRFQTPDPRKRLVDEAHGLGILLVLEIVHSHYAAADEMVLGSLFDGDTNDYFHTGKRNKIKFVGRTRMPKYGDLDLHLHLLSNLNNWWWEEYQVDFHFHSLSSMLYTHNGFASFTGDMDAVYGNQYVDEKALLYLALNEVLHAIHPWITAEADTFPLGDPDPSGGGLGDFVFNLSASEMVALLENTPDHEWMSKIKVTLVGGRGHVDKMLLVAENHNSHSGGRSFAEILIGNSKIKFNSGSEFRGCSLHKMLRLTS1

NbL05g01690.1 GDSL_esterase/lipase_At5g55050-like [MW - SP = 36.68 kDa]

No. of times detected



log(intensity)



Values from



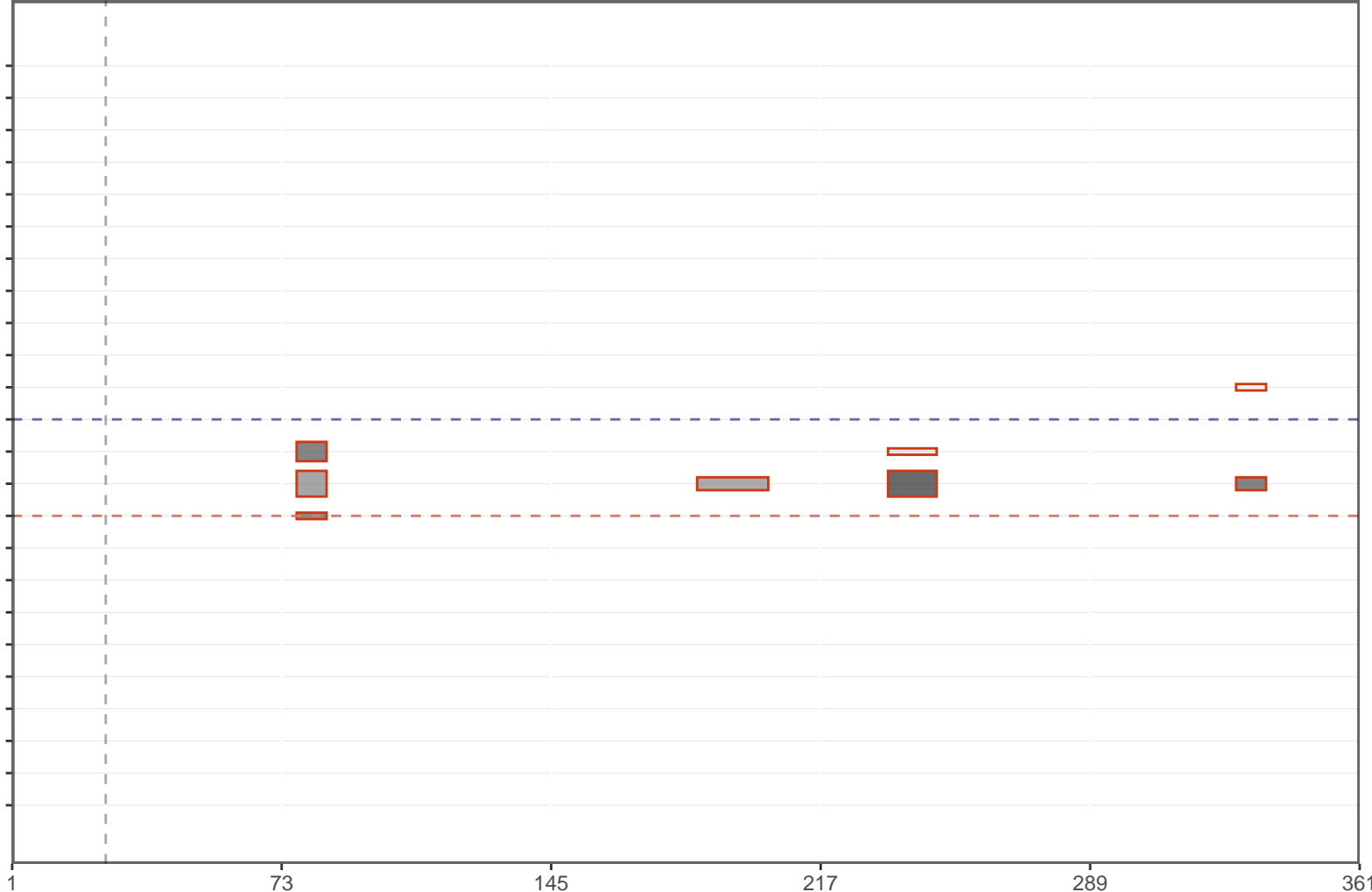
MW indication



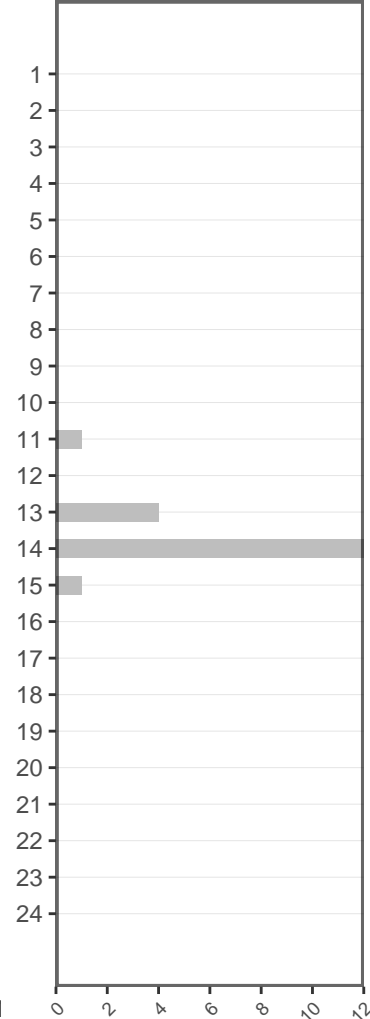
Molecular weight



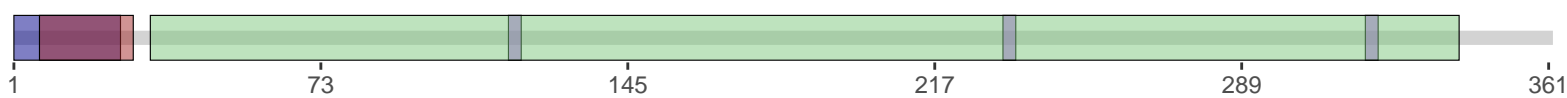
Gel Slice



Protein length

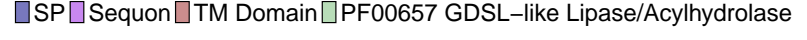


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISNDINIFYKSDSKLPKTIIPDQYNGMVSGLGGGKGLKGLGARKFVVGVSIGGIPLLRVGSANKSGECGGQANWYTNKYNGFGVSLGGLSELKDFYSYFDFTNLLLDVIGNPMYGFSEVKAACGGLGLNAHLPTPISTFCSNRSDHVFVDRYHPTTEVANRIRDSAFHSGKGYVFLNWKGLTL*

NbL05g01640.1 bifunctional_bis(5'-adenosyl)-triphosphatase/adenylylsulfatase_FHIT [MW = 24.35 kDa]

No. of times detected



log(intensity)



Values from



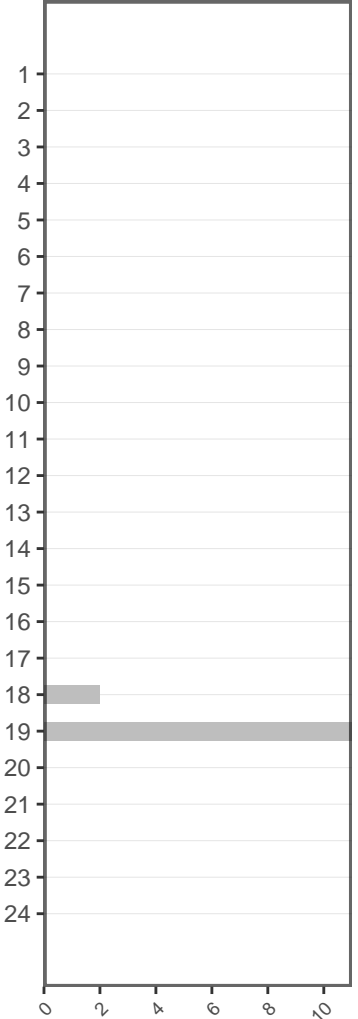
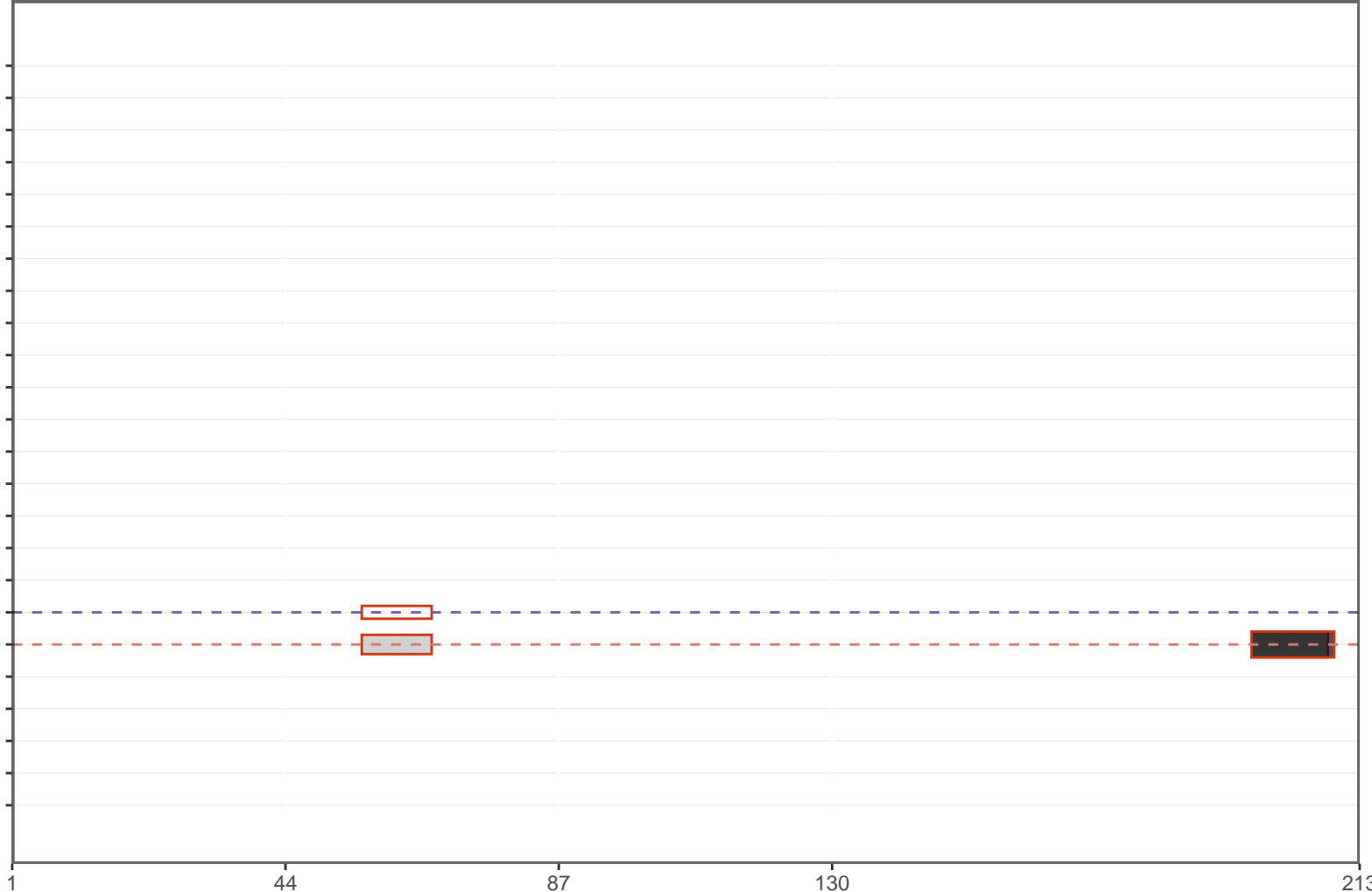
MW indication



Molecular weight

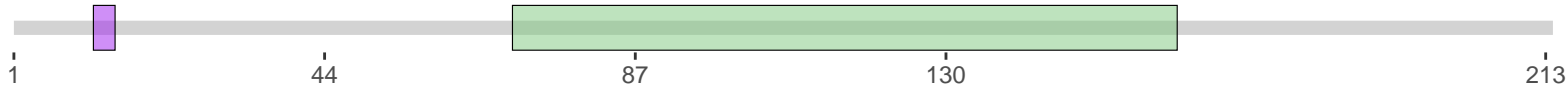


Gel Slice

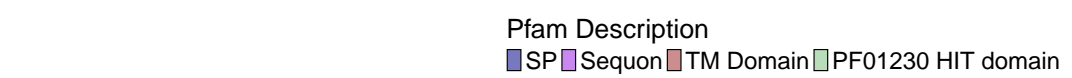


Protein length

Peptide counts over 4 repeats



Pfam domains



Pfam Description

SP Sequon TM Domain PF01230 HIT domain

Protein sequence:

/LVCPRRQVKKRFVQLTADETSGLWLTAGKVGKGLSEYHKASLTFAGDGPQAGQTVPHVHHIPRKGDFEKNDIYDALVKEKEMKGLDLNDRKDRSIEEMAEAEYRKLFG

NbL05g01590.1 CBS_domain-containing_protein_CBSX3_mitochondrial [MW = 22.6 kDa]

No. of times detected



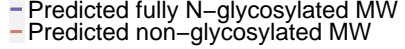
log(intensity)



Values from



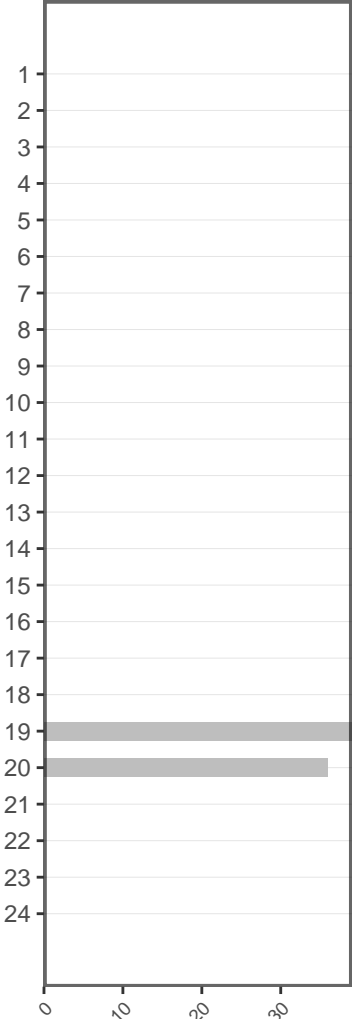
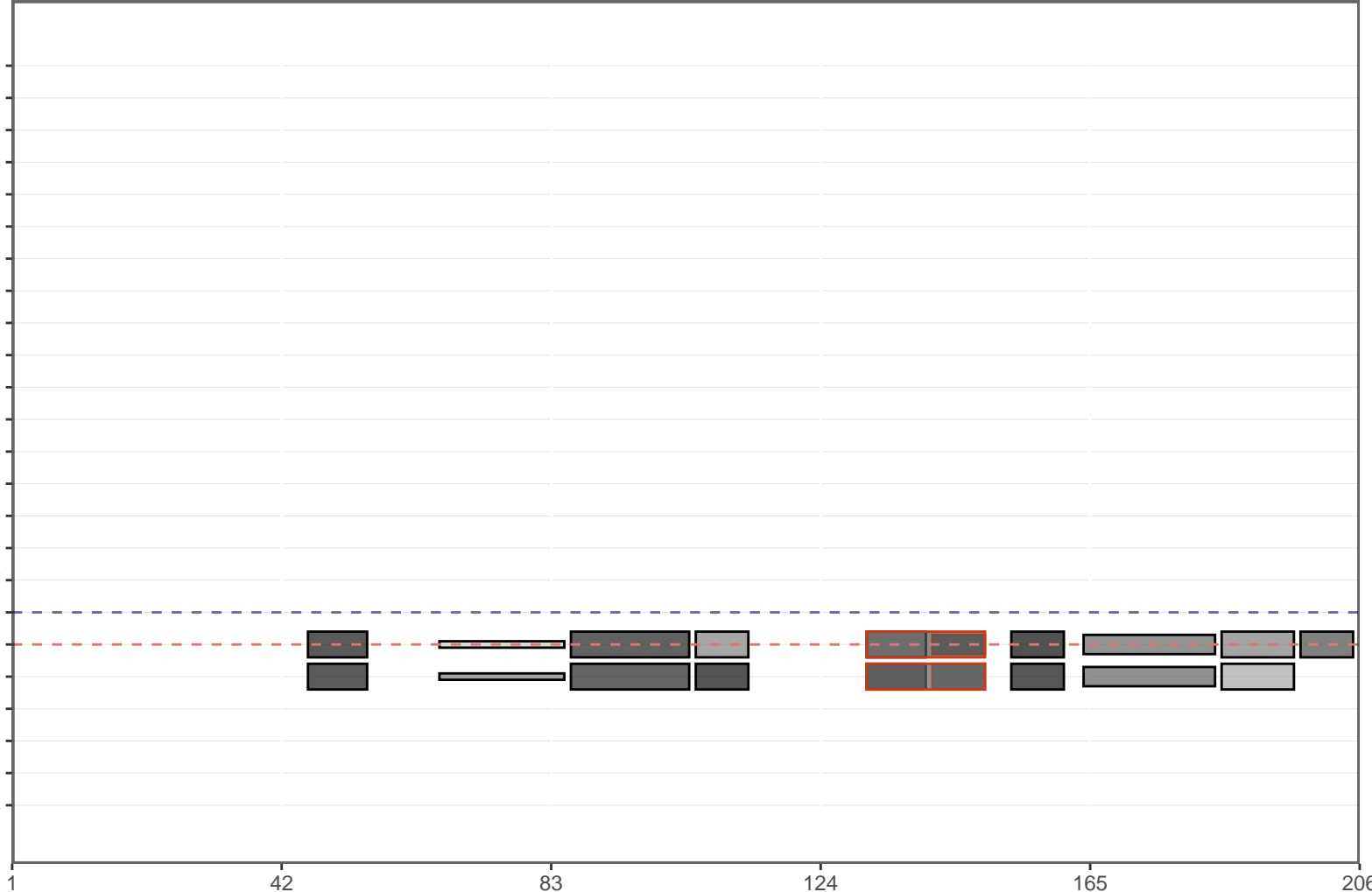
MW indication



Molecular weight

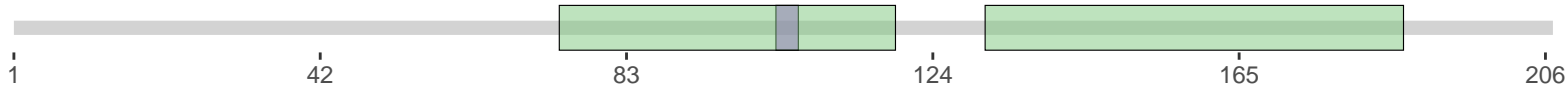


Gel Slice



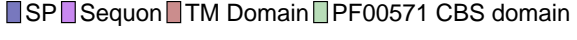
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DIHNVGALVVKPKGENKSIAGHIFERDYLKRIKIVGGRSEKSTKVGDMTEENKLIIVYFDTKVAKAMQLMTDNRIHFVVDQGTGMGMVSIQGDVRAVVEHREELNRLNAPFIGGGY*

NbL05g01570.1 oligoribonuclease-like [MW = 28.23 kDa]

No. of times detected



log(intensity)



Values from



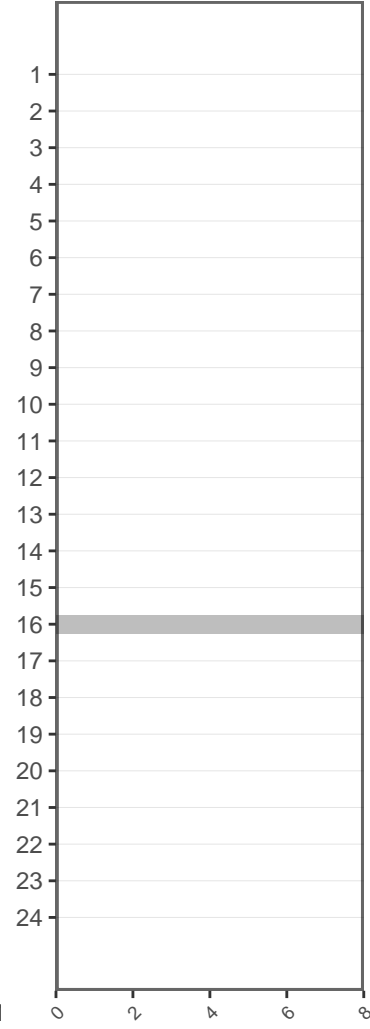
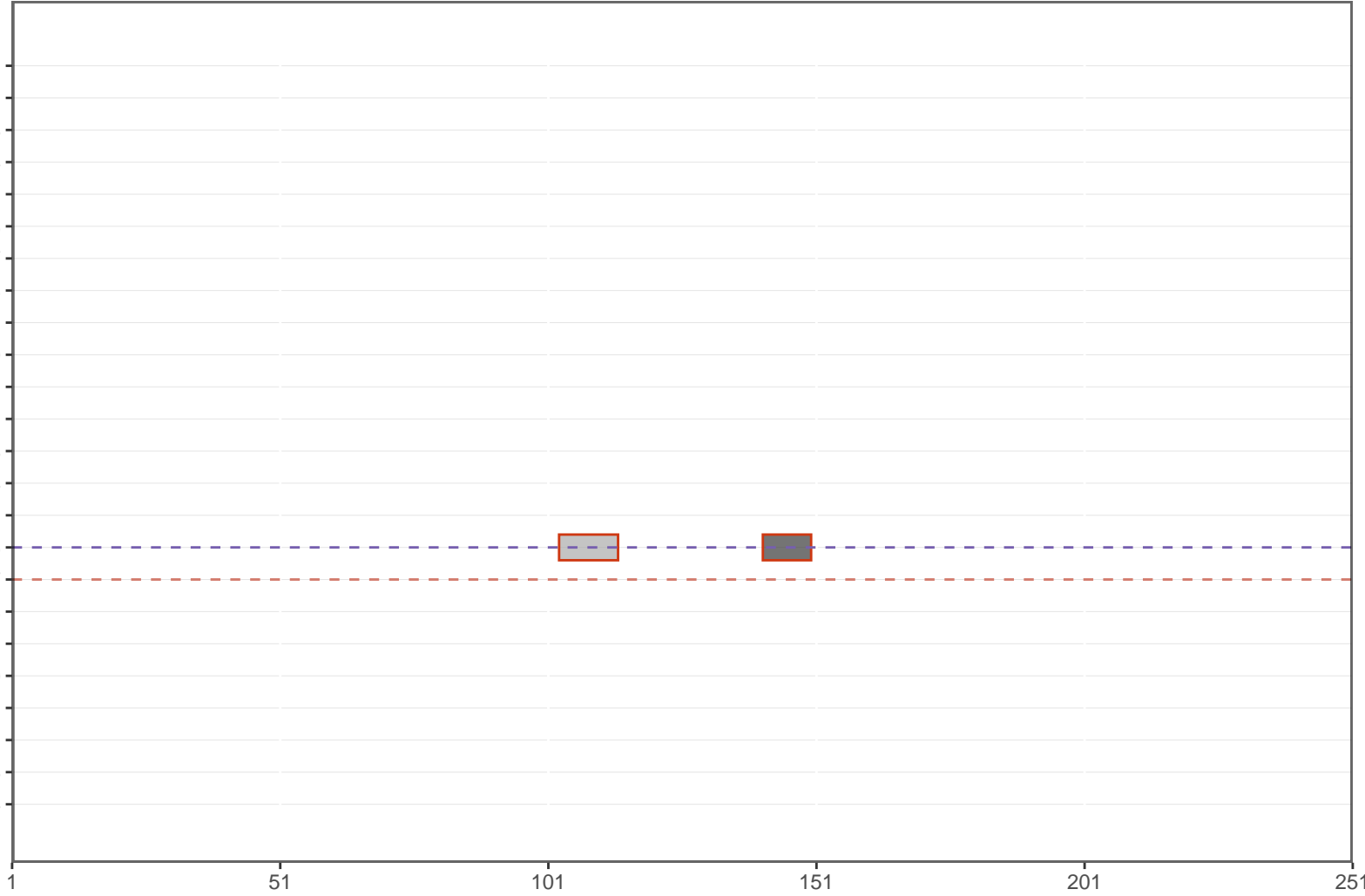
MW indication



Molecular weight

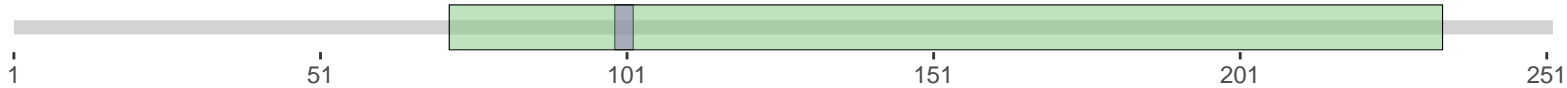


Gel Slice



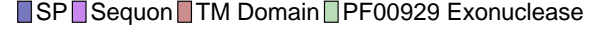
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SRKECLDKMGEVGGQEHAAAGSLTGRVLKSTVTEEEAEKGVDFVKRNIGTYTPLLAGNSVYVDFGLKQKMPNLAFLSHLVLDVSVKALGVRFPRDSKAPKPKESKSRAMDDEKESIAELKVFKEHIFKASKEKNI

NbL05g01530.1 uncharacterized_LOC107809774 [MW = 22.76 kDa]

No. of times detected



log(intensity)



Values from



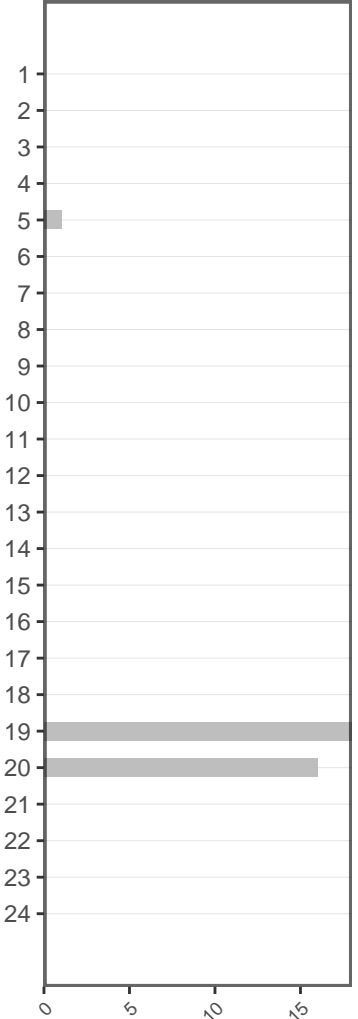
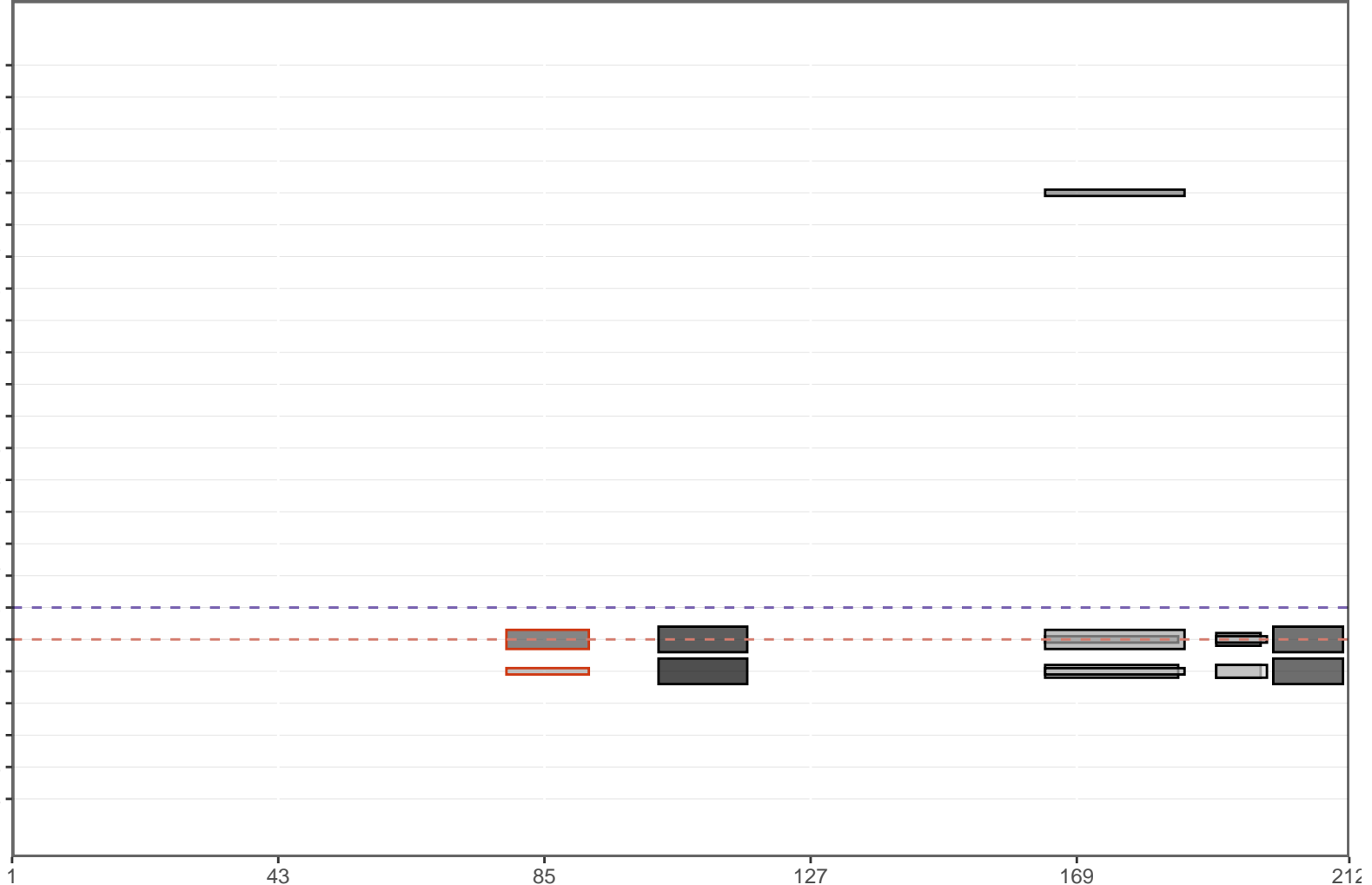
MW indication



Molecular weight



Gel Slice

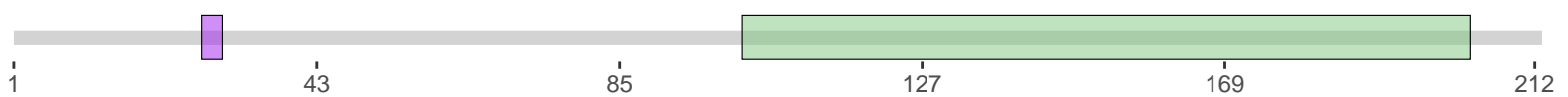


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

QAAKAPAKSLPQIMMEEDVPSLKTILEAGDDISLELMFNDNKLLEGFSSKGNFYGFVAFPPDLTGANGFSLSSVGGSPSTVEFLVDEKKTAKHVVVVVEKRLAAGDHPVWNE

NbL05g01440.1 60S_ribosomal_protein_L5 [MW = 37.44 kDa]

No. of times detected



log(intensity)



Values from



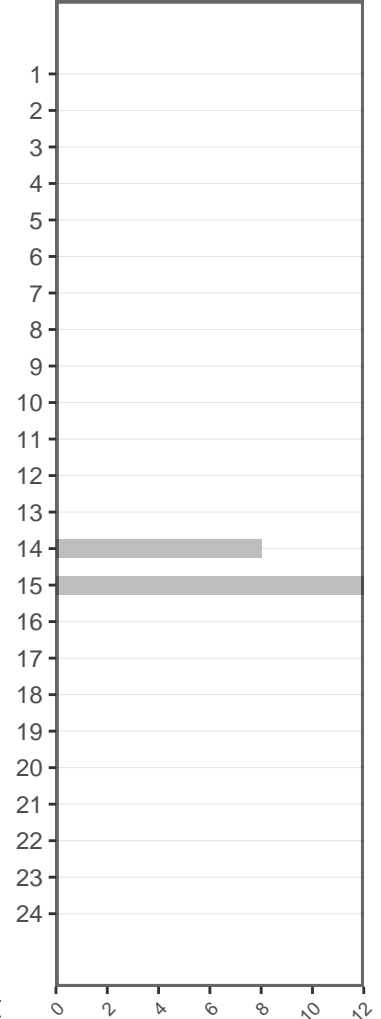
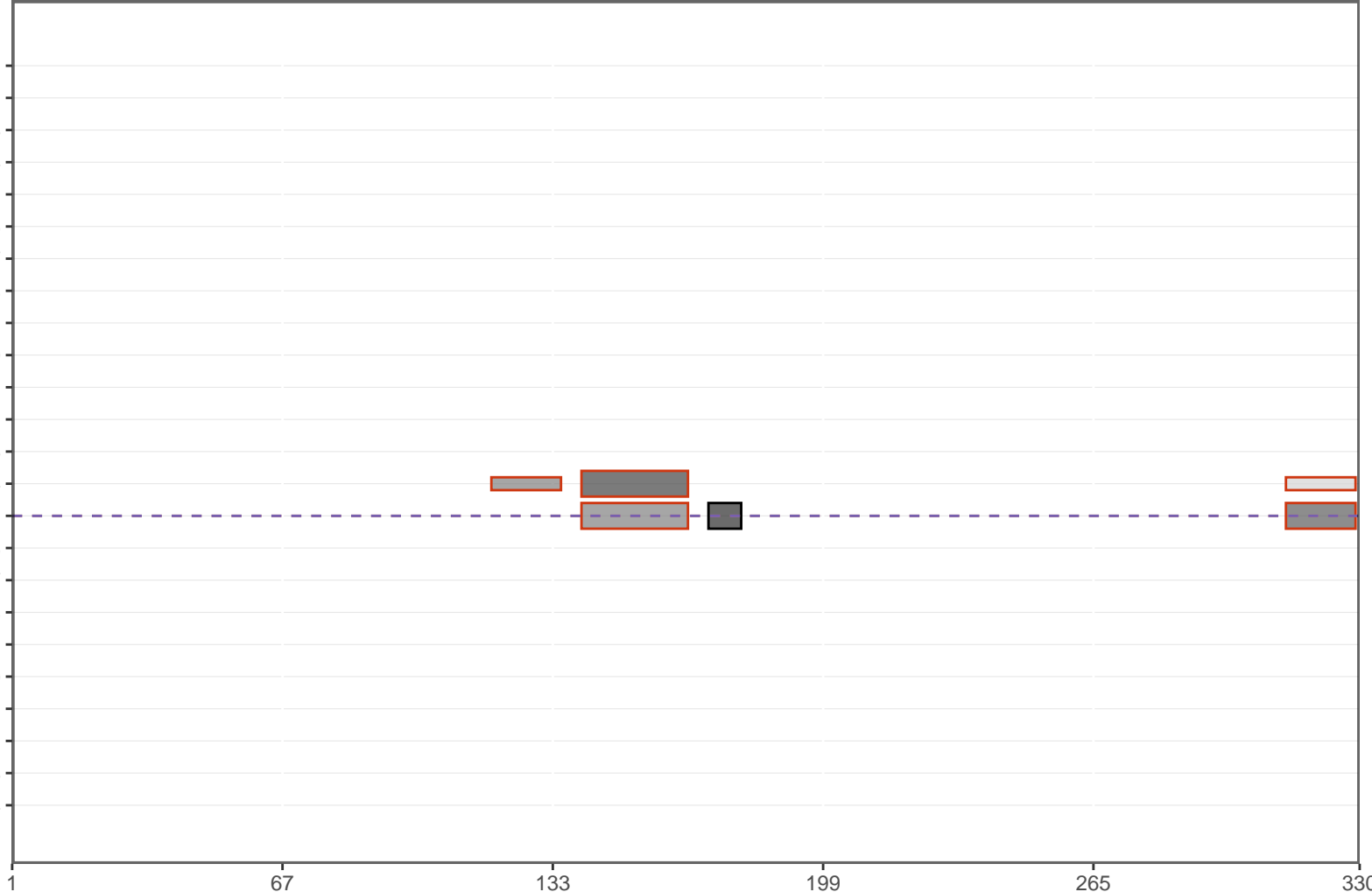
MW indication



Molecular weight

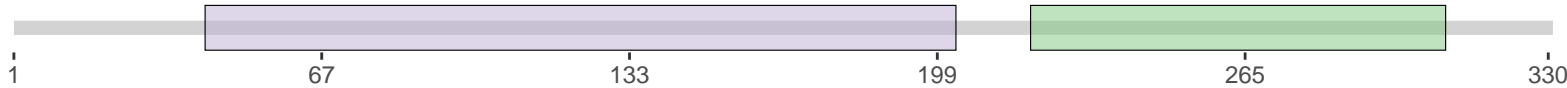


Gel Slice



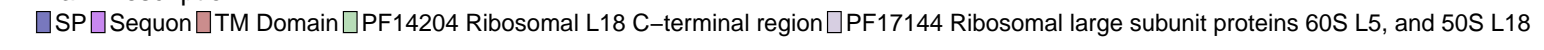
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ATGEDYVVEPAESRRPFRALLDGLVIRFTTGNRIFGALKGALDGLDHPHSEKRFAGFSKDSKQLDADVHRKRYVYGGHWATYMKTLTDEDEPKFQSHFSEYKIKGLEADLEEMKKYKVAARADSPKPKSEKQPPKQHKRYLKKLTYEERKAKLERLMAALNSAAGNDEEEEDD

NbL05g01240.1 leucine--tRNA_ligase_cytoplasmic-like [MW = 123 kDa]

No. of times detected



log(intensity)



Values from



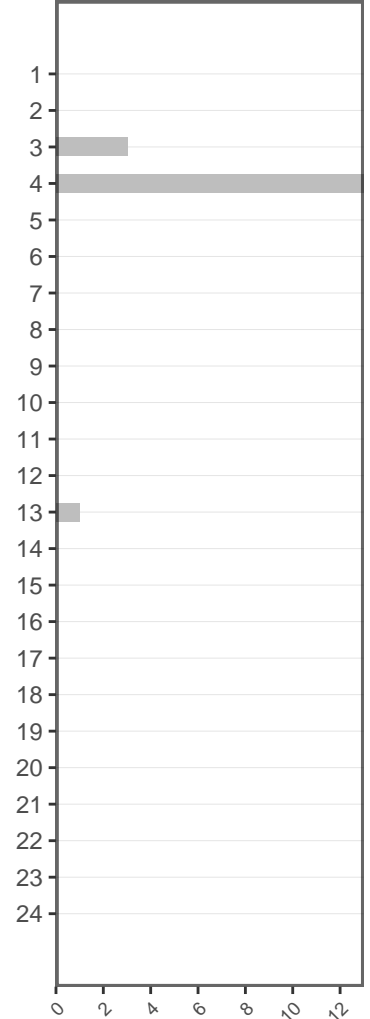
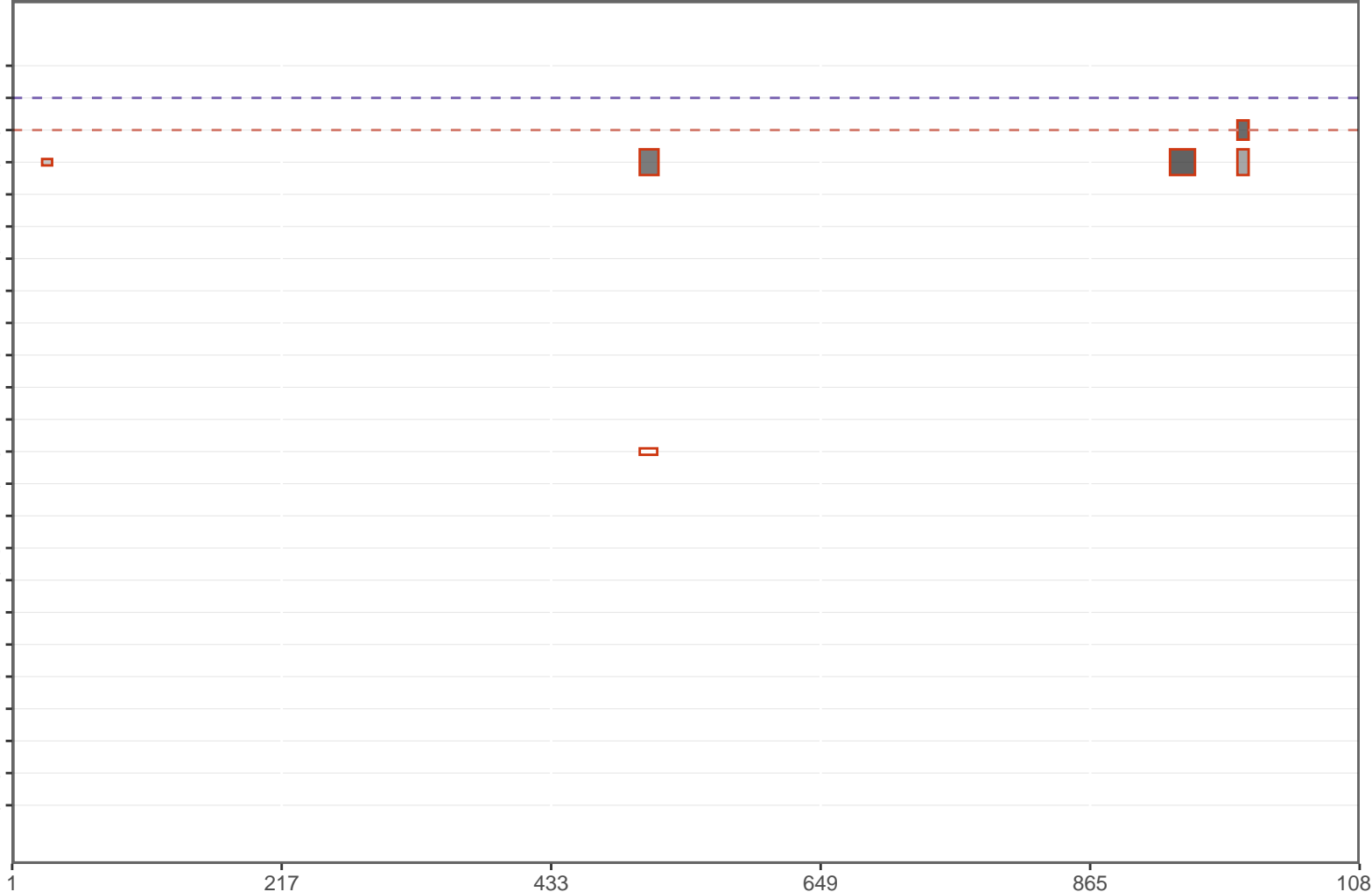
MW indication



Molecular weight

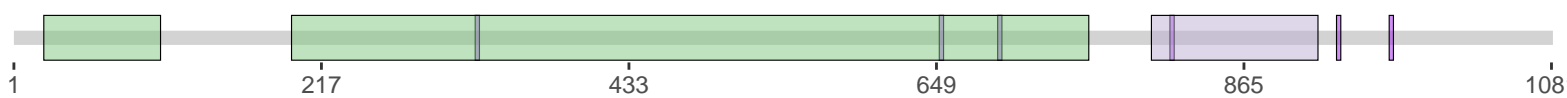


Gel Slice



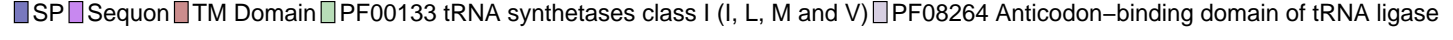
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

CVVLTLDQWYLYTGELEWRKAAEDCLAMNLYSDETHRGFEHTLRLWLNQWAGSRNFGLGTRPFWDEDFLVEESLSDSTHYMAYKTVAILLQKGDVYGTGHSVKPEQLTDEWVEFLFGNGPYPENSGSBSLLKEMQDEFWYYPDLRVSGKDIQNHILTFQIYVHTAFKPHHWPRFRGRNGHMLNSEKMSKSTGNFRTLRQAEIEFSADATRFALADAGDCMDDANFVETANAAILRLKELIWWMEVLAAESLRSRGGPPSTYADCVFANEINFAVRRTEKNYSEYMI

NbL05g01220.1 2-Cys_peroxiredoxin_BAS1_chloroplastic-like [MW = 34 kDa]

No. of times detected



log(intensity)



Values from



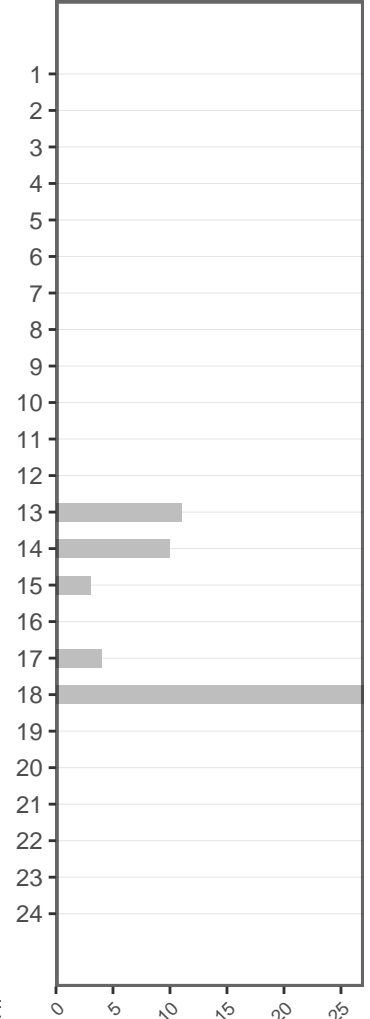
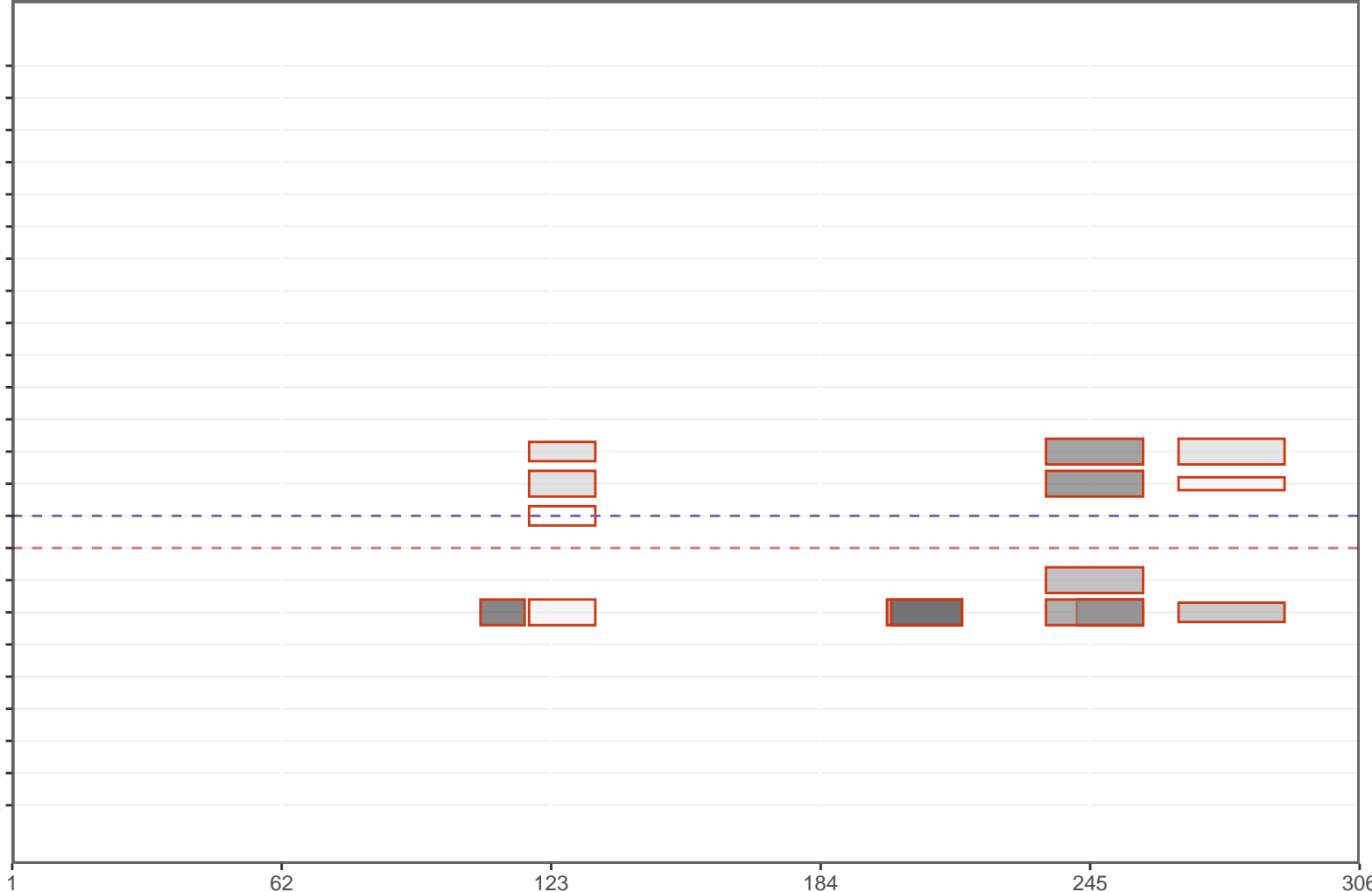
MW indication



Molecular weight

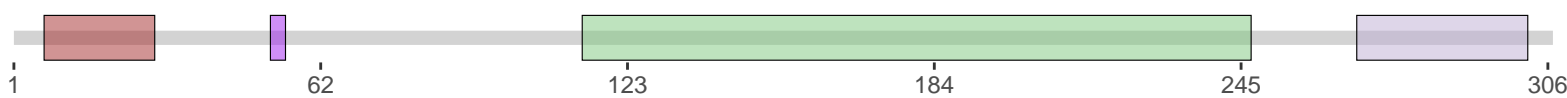


Gel Slice



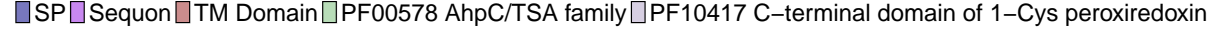
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IGKYYILFFYPLDFTFFVGPTEITAFSDRYEEFQKYNTEILGVSVDGVSFSLAWVGTDRKSGGLGVLYNPLISDVTKSIKSYNVLIPDGGIALRGLFIDKEGVIGHSTINLNAIGRVDETLRTLGAALGYVDENPDEVGPGAGWKPDKSMKPPKSGKEYFASIP

NbL05g01120.1 ubiquitin-conjugating_enzyme_E2_variant_1D-like [MW = 16.71 kDa]

No. of times detected



log(intensity)



Values from



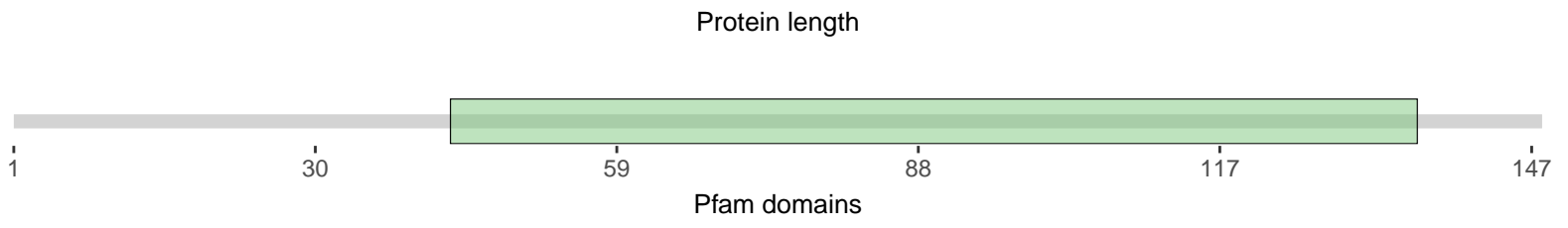
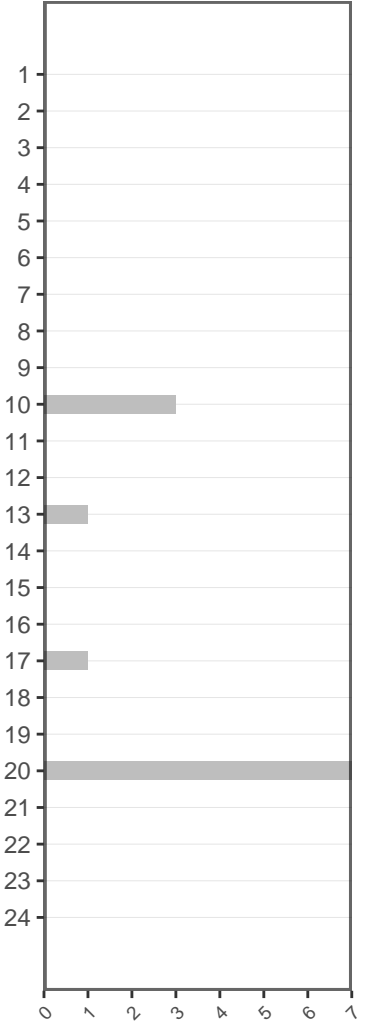
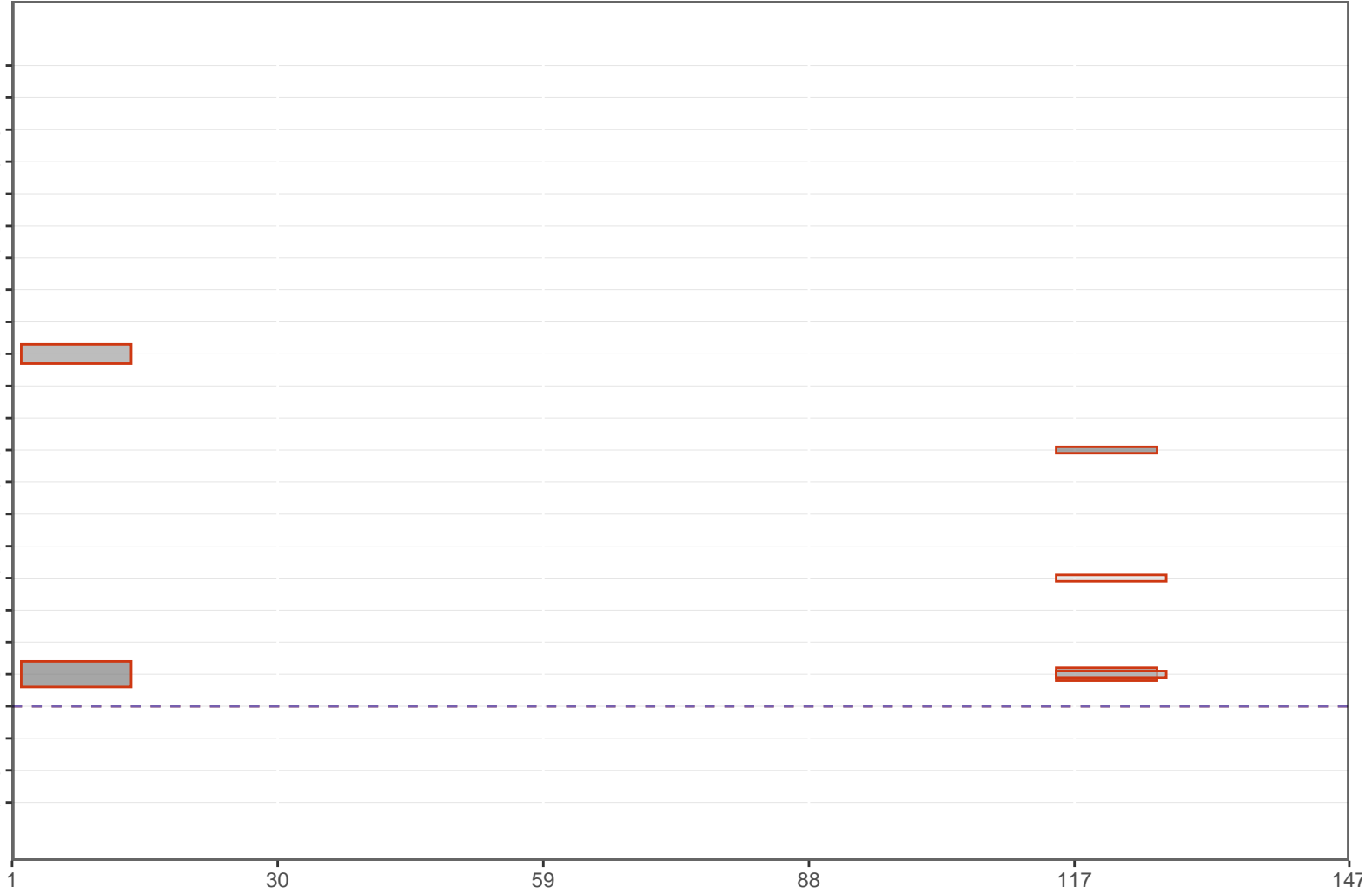
MW indication



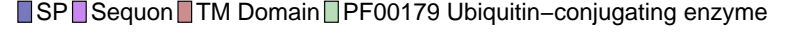
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

1HGRIYQLKLFCDKDKYPEKPPSVRFHSRINMAGVNHETGVVEPKKFDLLANWQREYTMEDLTLQKKEMASPHNRKLVDPPEGTYP

NbL05g00410.1 toplless-related_protein_4-like [MW = 124.36 kDa]

No. of times detected



log(intensity)



Values from



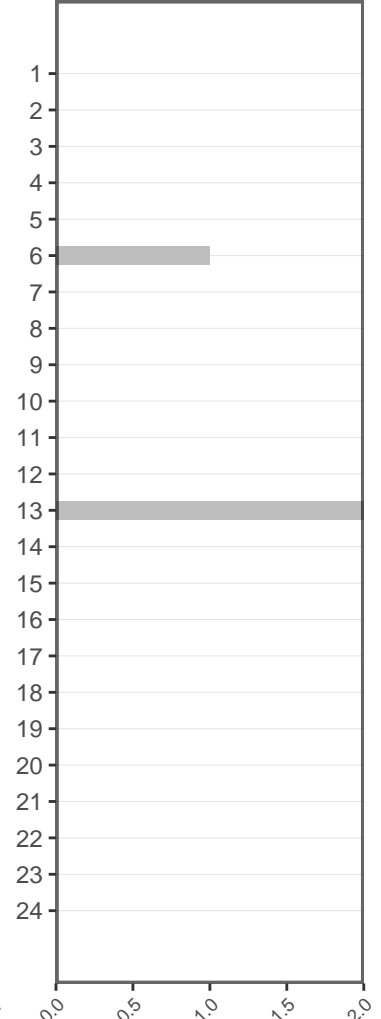
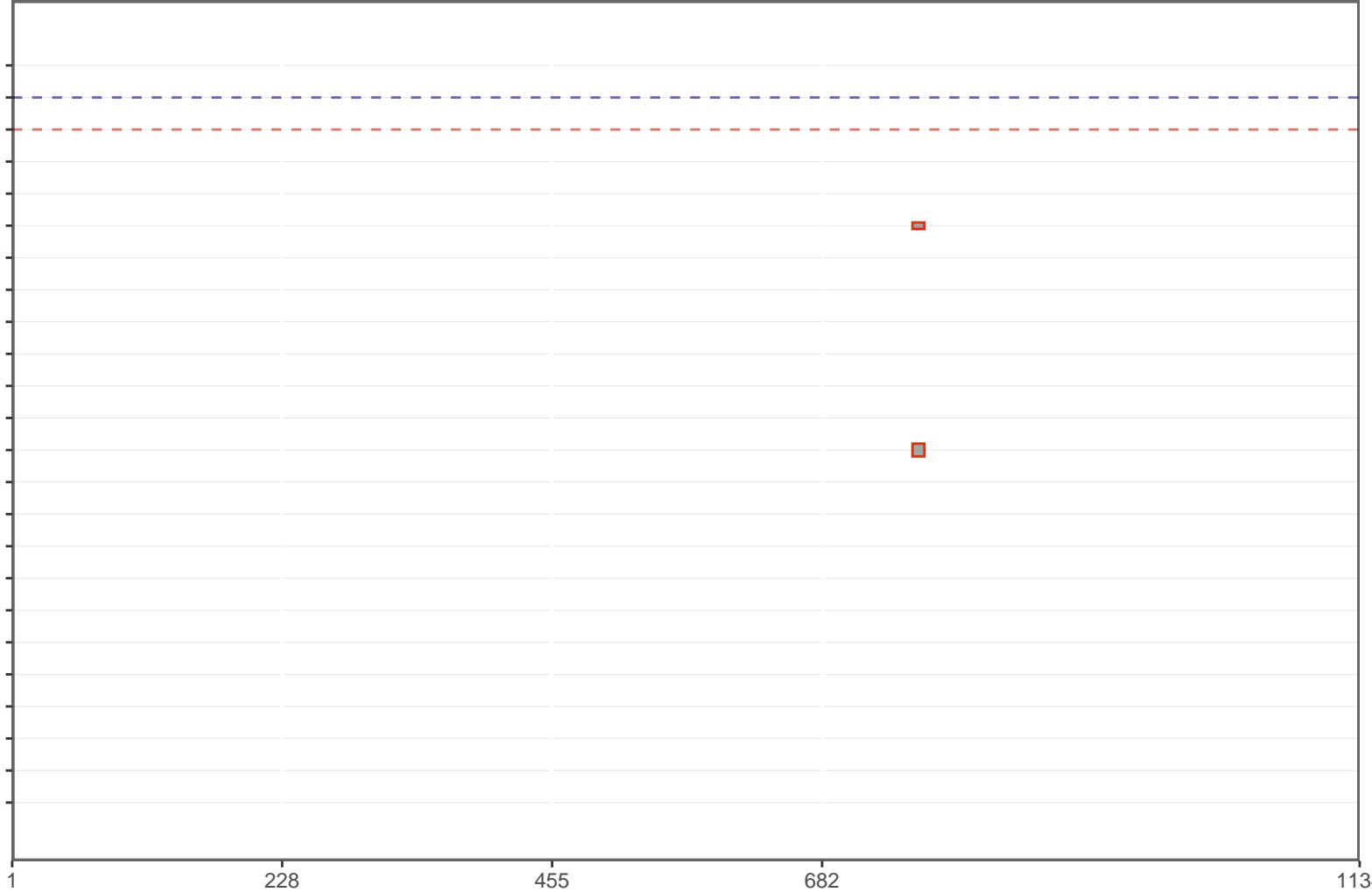
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ISCTTMYADGCAFLFSGGTEKDGESYLVWEVNESEGAVKRTYVIGLQKRSVGVVGFDDTKNRFLLAAGDFVWVDMNTLTLTSDAEGGLPAKPIRFSEKGTLLAVSTSENGVKKLANADGVRLLRAIESRALDPRVPPGAVAKPMISTYGASSSTAGTSMIAIDRTAPVNAVVLQNGDNRELQDAKPRVDELEKIKWKLTEISEPAQVRSRRLPDLLEVRIRLMTNNGAAILALAVNAVHKLWVPRNERNATGKASTAVPPQLWGPSSGLMTNDSSETNLEEAV

NbL05g00330.1 malate_dehydrogenase_[NADP]_chloroplastic [MW - SP = 50.52 kDa]

No. of times detected



log(intensity)



Values from



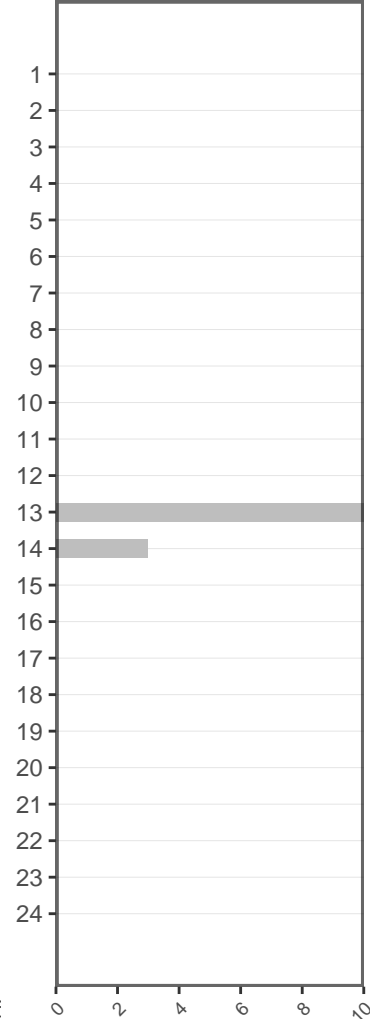
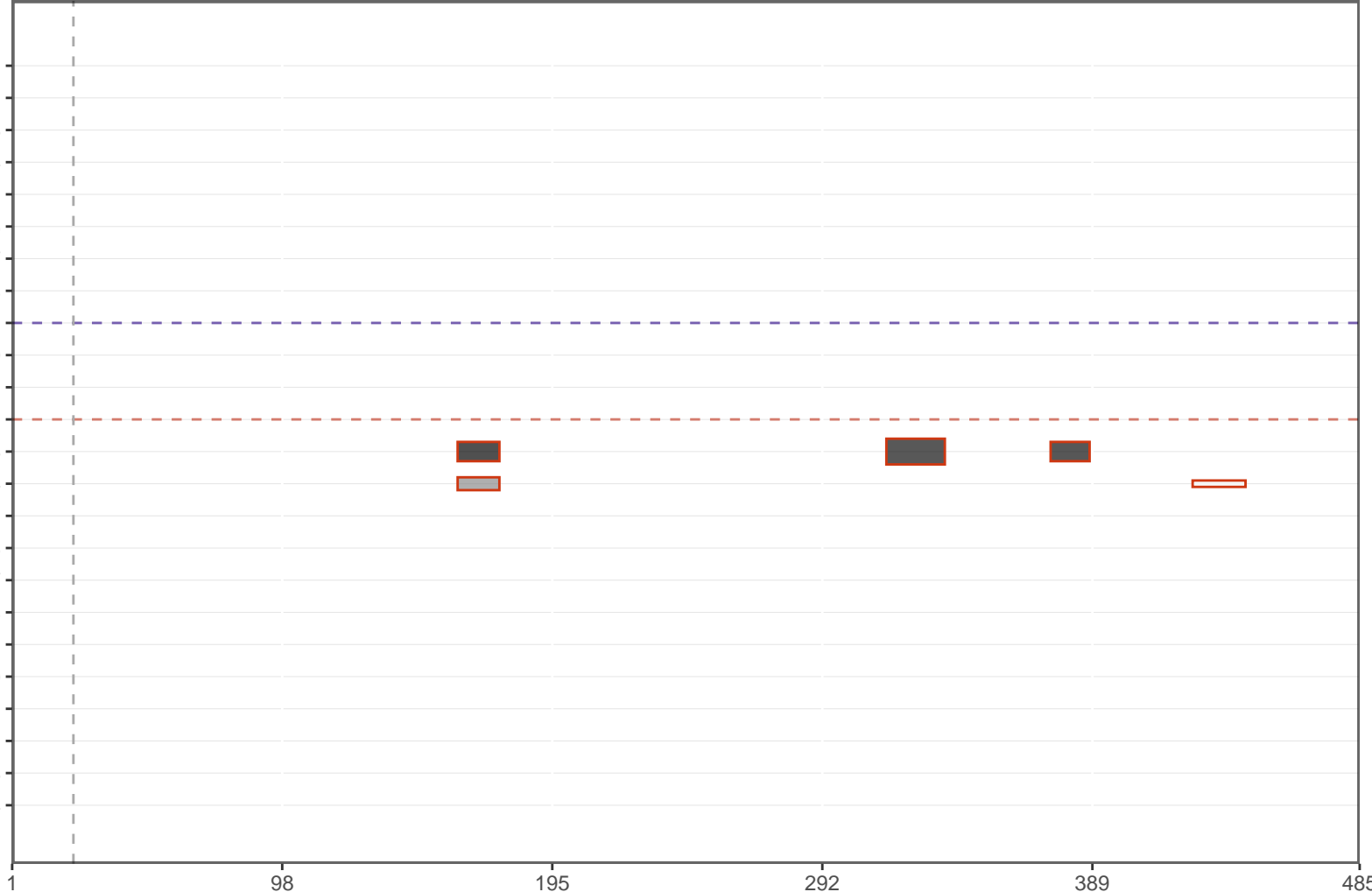
MW indication



Molecular weight



Gel Slice

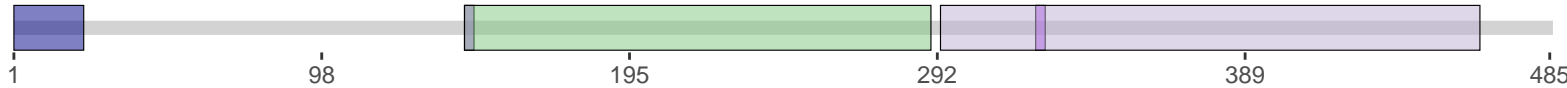


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF00056 lactate/malate dehydrogenase, NAD binding domain
- PF02866 lactate/malate dehydrogenase, alpha/beta C-terminal domain

Protein sequence:

PGMERADLLDNGGIFAEQGLKALNAVSRNKKVIVGNPONTNALIGLKNAPGPAKMFHALTRLDENRAKGLALKAGVFEYKVKVSNVIWGNHSTAGVPPVLAKEKNGFPVKEVIRDTRWLEEFETKVKRGGVLIQKWRGSSAATAVSVDAIRLVTPTPEGDWFTGTGVYTDGNPKYGAEGVIFEMPCRSGGDGVKELKVDYIDVLRIRIKKSEDELLAEKRGVAHILTGEGIAVCDLPGDTMLPGEM

NbL05g00280.1 non-symbiotic_hemoglobin_2 [MW = 17.63 kDa]

No. of times detected



log(intensity)



Values from



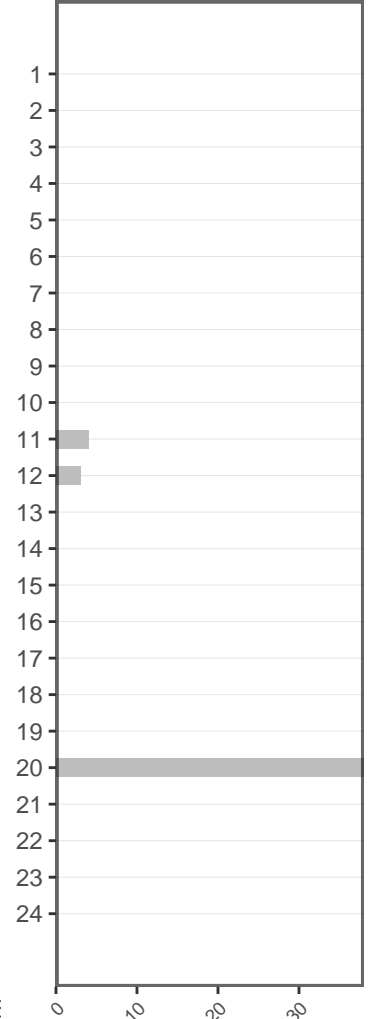
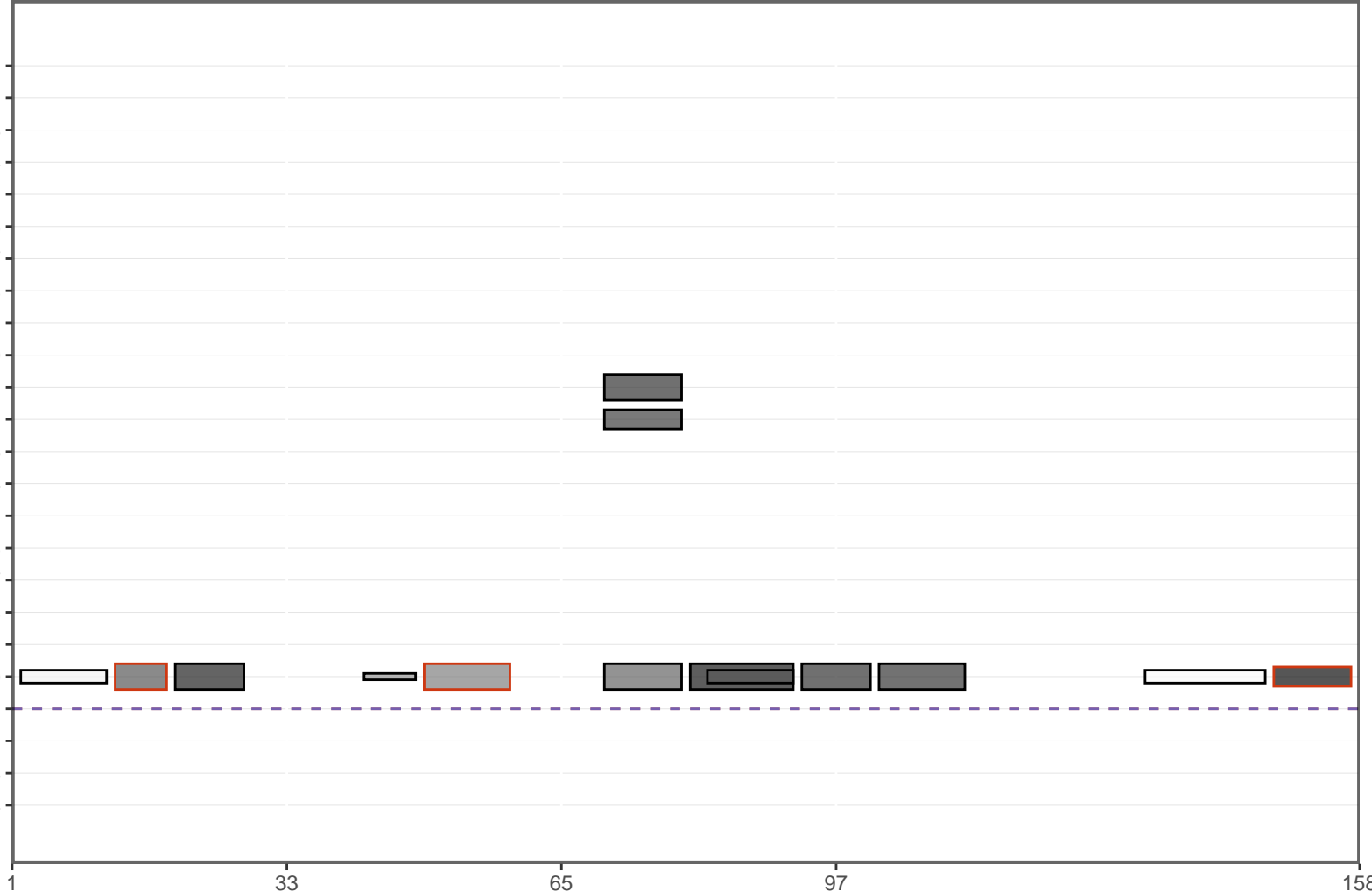
MW indication



Molecular weight

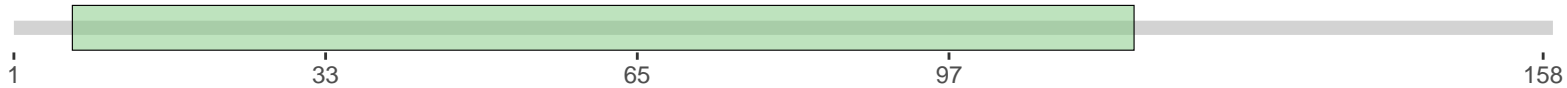


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

/FMTCESAVQLREKGEVWGETFLKYLGSVHKGKGVDRHFEVWKEALKTKVKEAMGKERWSEEMKEAWGEAVDGLAAAKAEMHAEAAAP

NbL05g00230.1 wall-associated_receptor_kinase-like_20 [MW - SP = 65.73 kDa]

No. of times detected



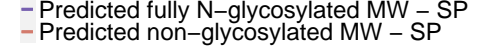
log(intensity)



Values from

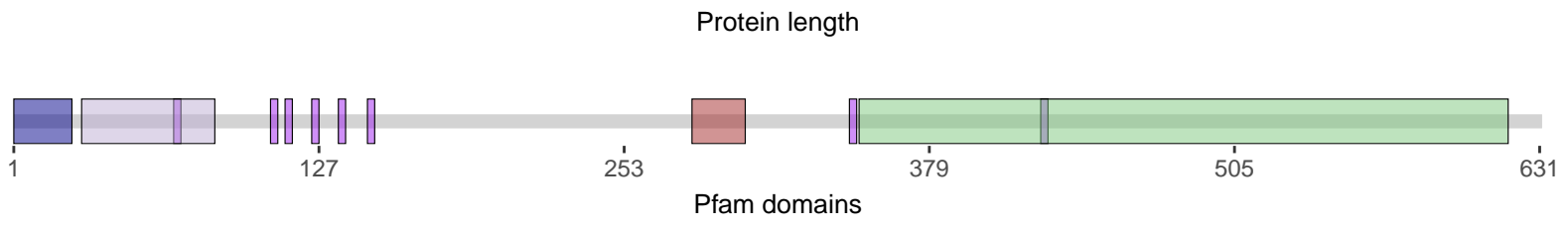
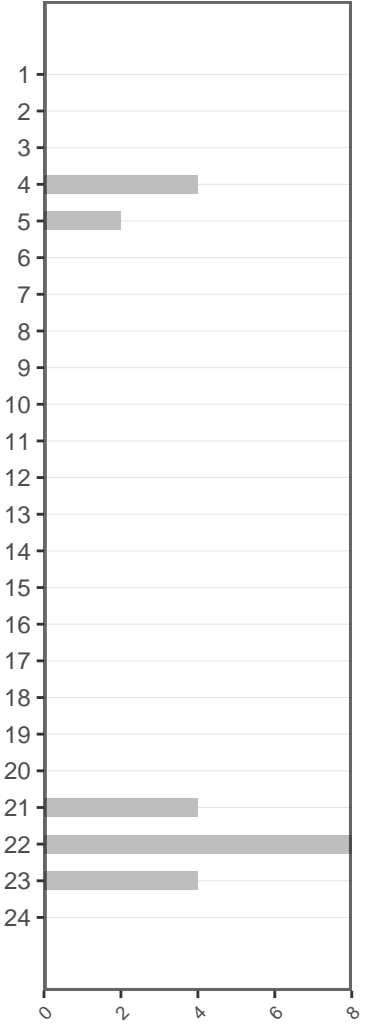
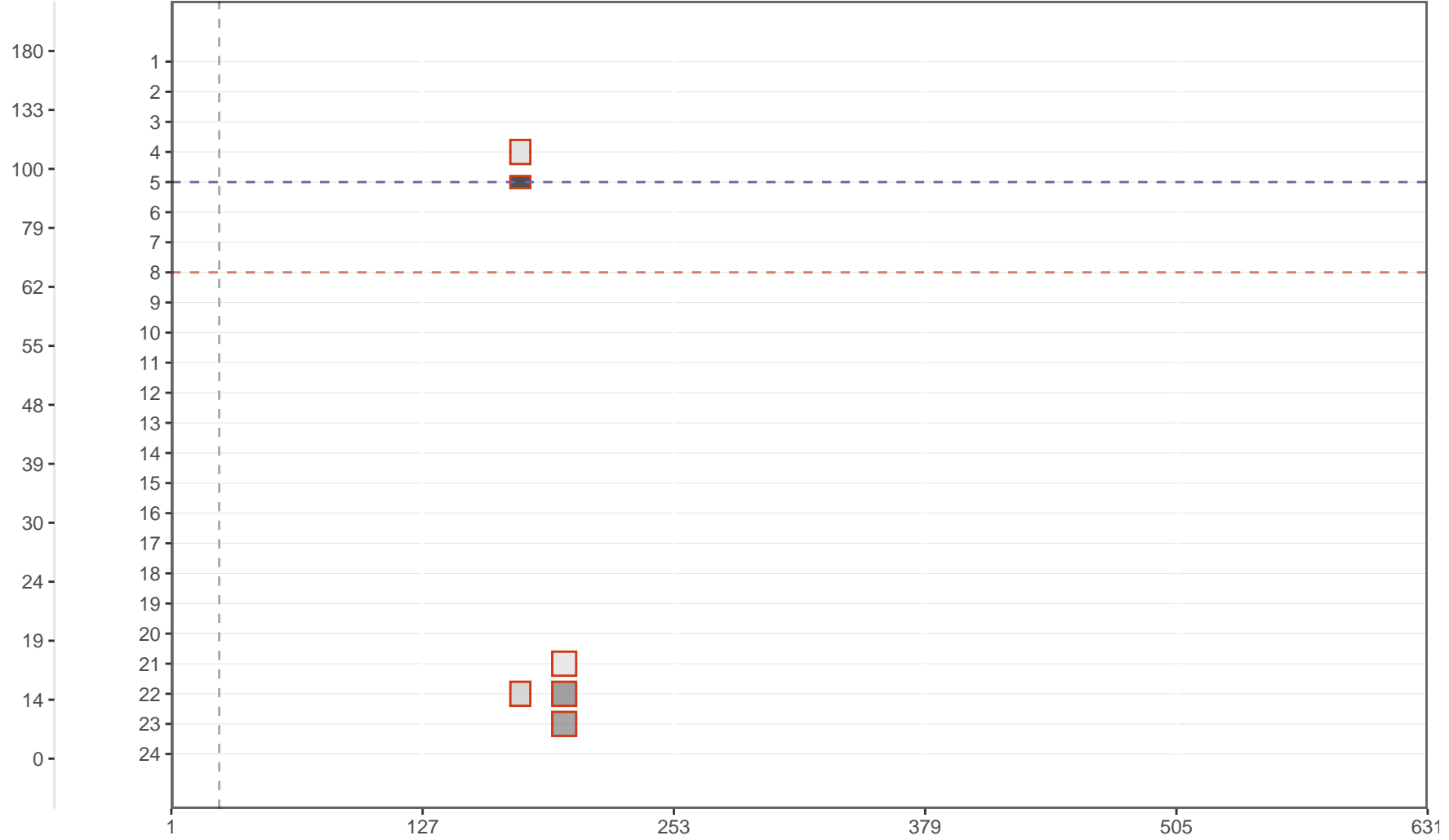


MW indication

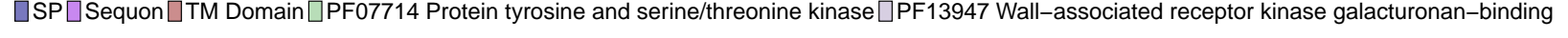


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

YRRHKRIKDAQDRLAREREDILSSGGVKNAKLFTGKEIRKATNFRDRLLGAGGYGEVYKGLDDGTDAAWKAKLGNKGTGDVINEVRLGGVNHKSLRLGCCGVELEGPLLVVEYVNGTLDHGGPPRKLITWDRLLVAHATAEGLAYLHFSAVPPYHRDKSKENLLDESLNKKVSDPGLSLRAHADLSHVSTCGAGTGLYLDPEYFRNYQLTQKSDVYSGFVLLLELTSQKAIDFRAGDDVNLAVYGRVLEERIMDAVDPALKERASSLQLETMKALGF

NbL05g00150.1 vacuolar_protein_sorting-associated_protein_27 [MW = 30.85 kDa]

No. of times detected



log(intensity)



Values from



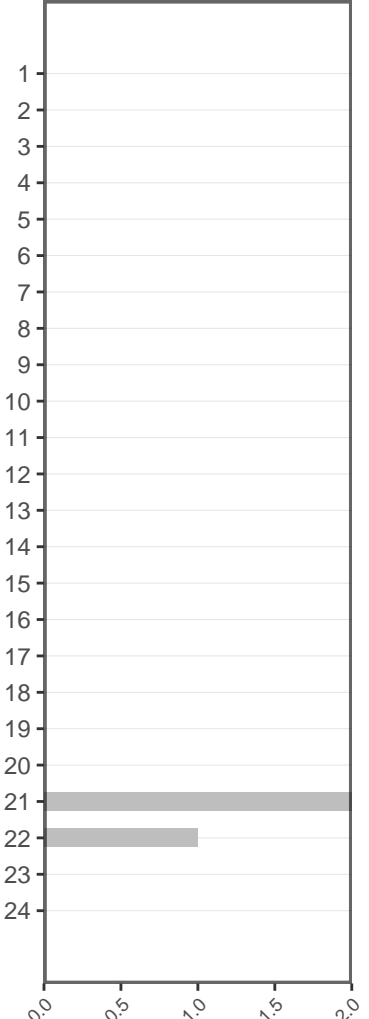
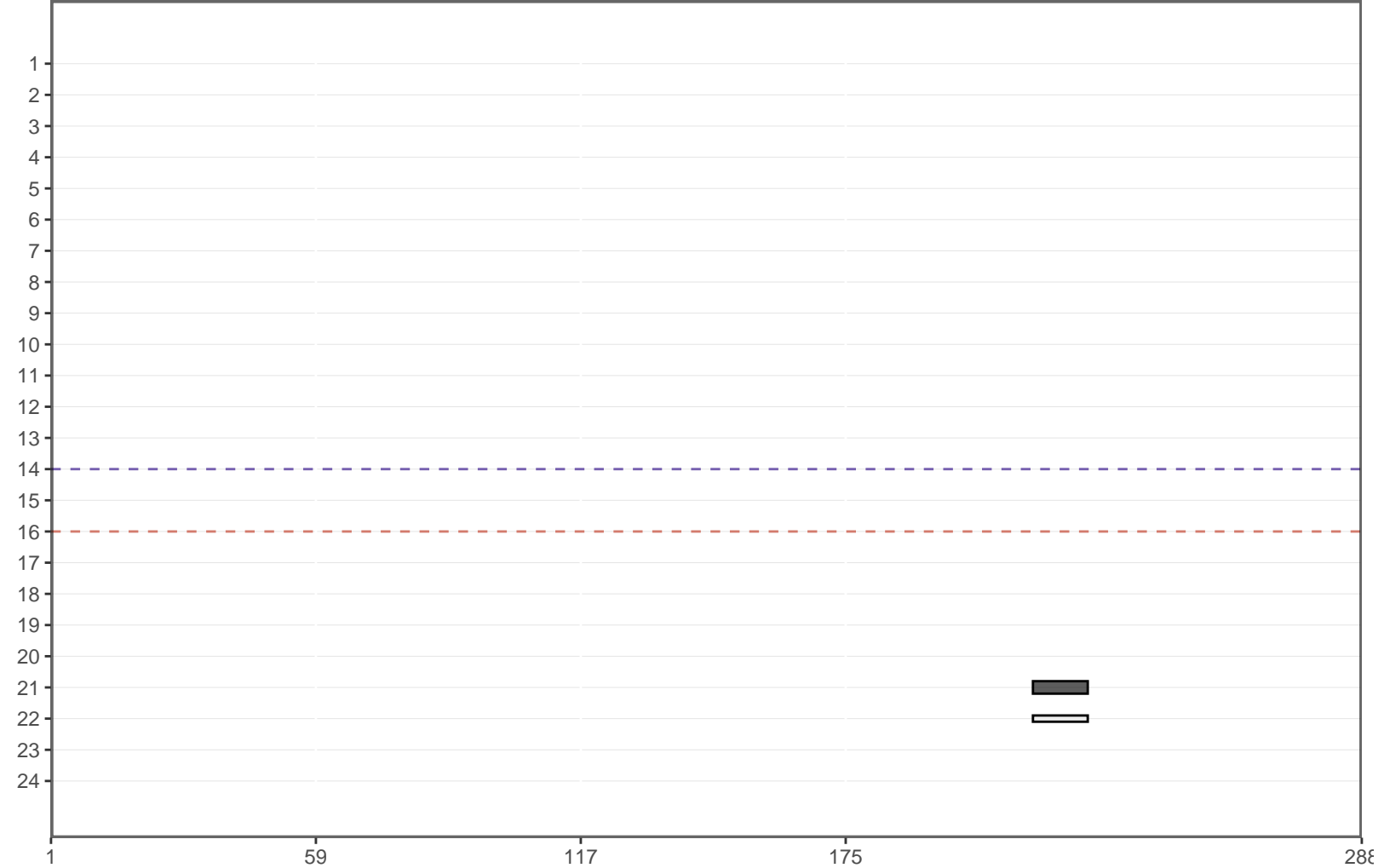
MW indication



Molecular weight



Gel Slice



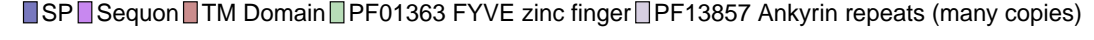
Protein length



Pfam domains



Pfam Description



Protein sequence:

ATPTTSVTPQSKTMPNPIVNTNPKPKKENRIPTRSGSTSNKKGFTFRNTPGPTNDSMETMSADVEVSGEGLREAIKNGDVAANKLLNGGVDANYLDKGGSELLHLAAVFNRIETAFALMESSGASLYCKNSGGETPLDCAFPLQFKMKKKMEEGD*

No. of times detected



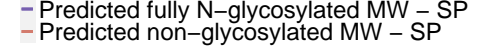
log(intensity)



Values from



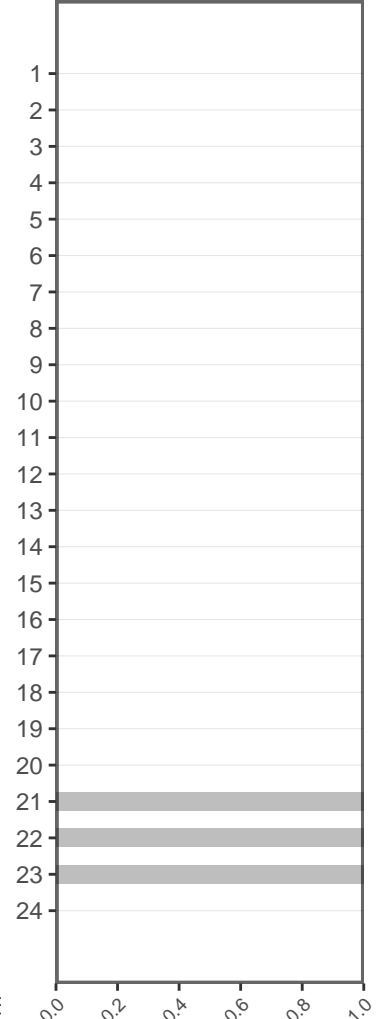
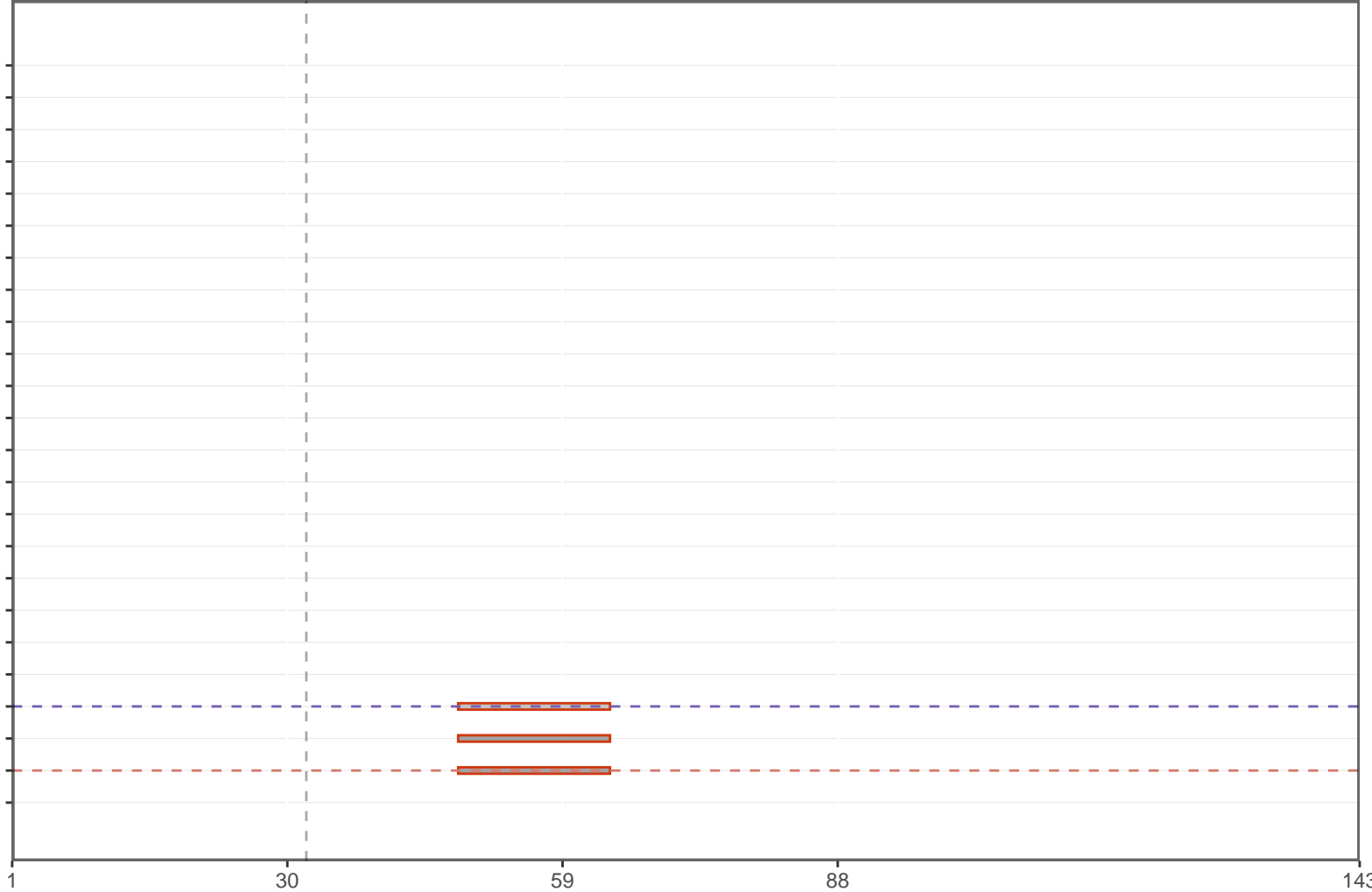
MW indication



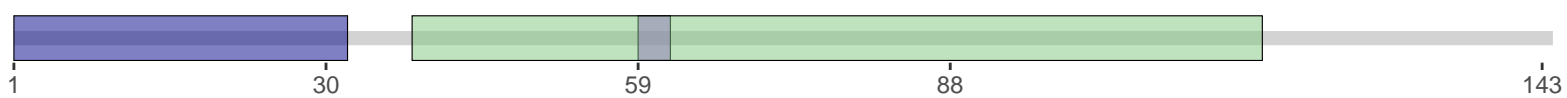
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

NASVSRSCCOIQIKLGGNPKGLGAVMLNNTANDSGAKPEVWTFPKRGLANRPVGYKGGRLNHWALKAAEDLDFMDVMLLW*

NbL04g20090.1 uncharacterized_LOC109229657 [MW = 37.31 kDa]

No. of times detected



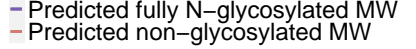
log(intensity)



Values from



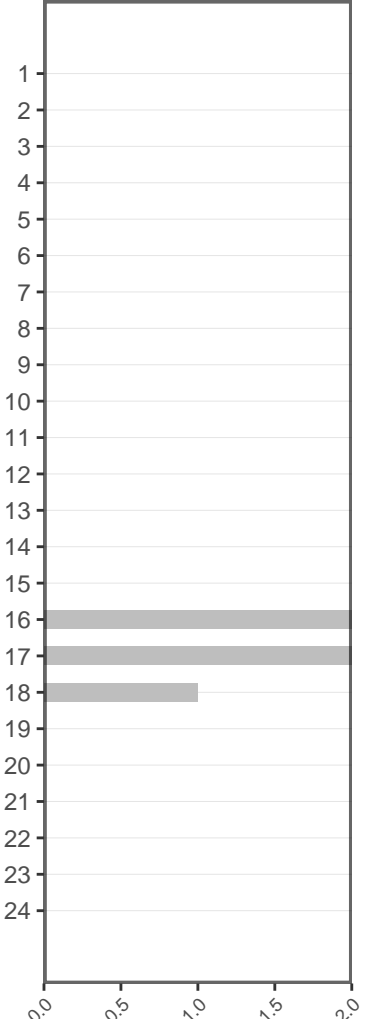
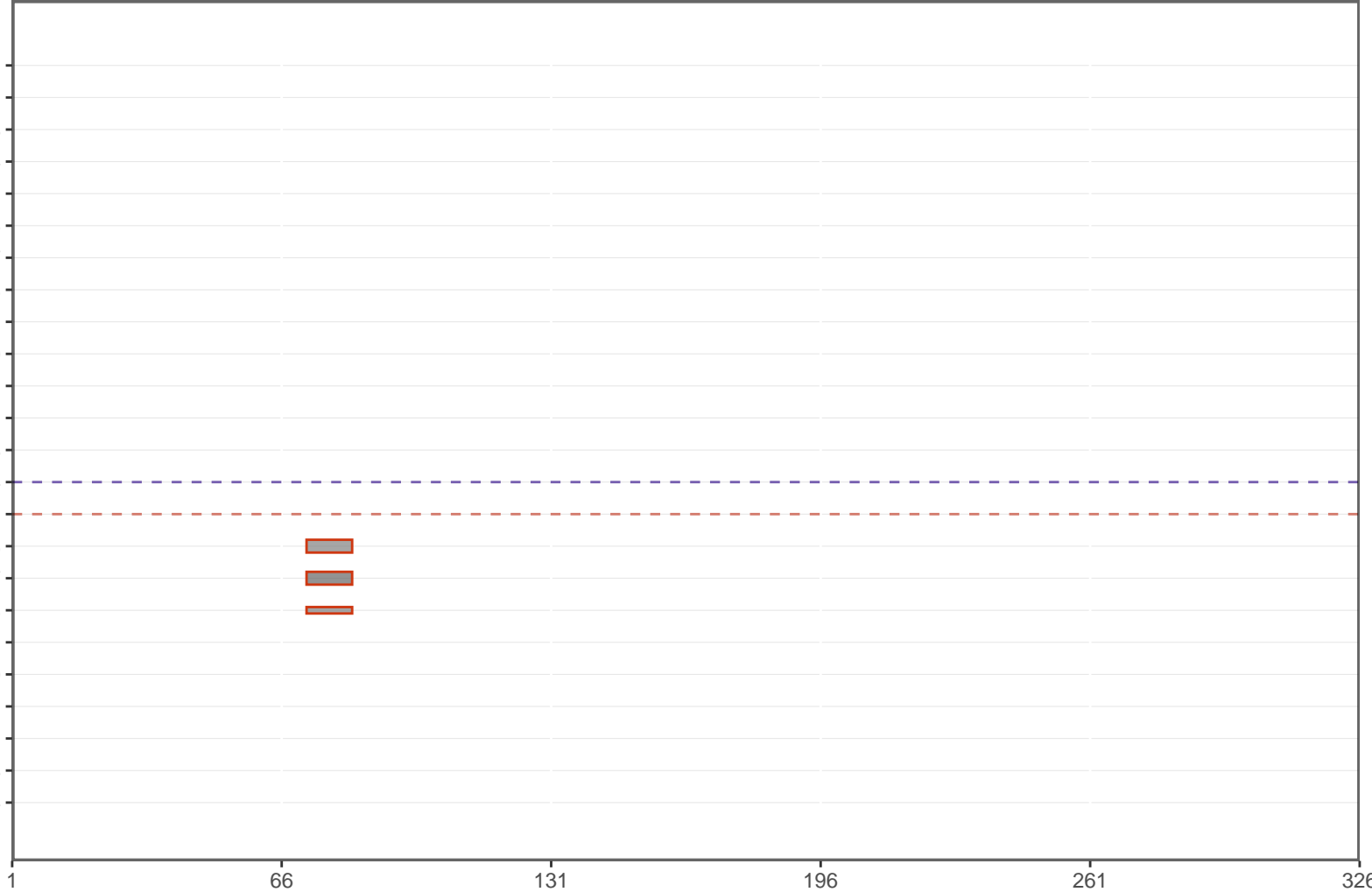
MW indication



Molecular weight



Gel Slice



Protein length

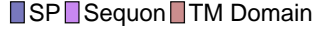


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

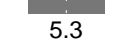
ITDVAEYLYOINPDLGLKFLGKDLTKAGKASFPVPKNIRAPGEFPVSKGSKAEAEKLMRSMQMGMPGAPGMQMYSRDLNNGNFGDEADGDDDDDEGGFPKGLKVLKCKEKRNKNDVWGWAKGIGDTSEVLKTHAVRVSHRMRNWWGARKVQWKKNKSTKSGEL

NbL04g19980.1 uncharacterized_LOC107790078 [MW = 34.77 kDa]

No. of times detected



log(intensity)



Values from



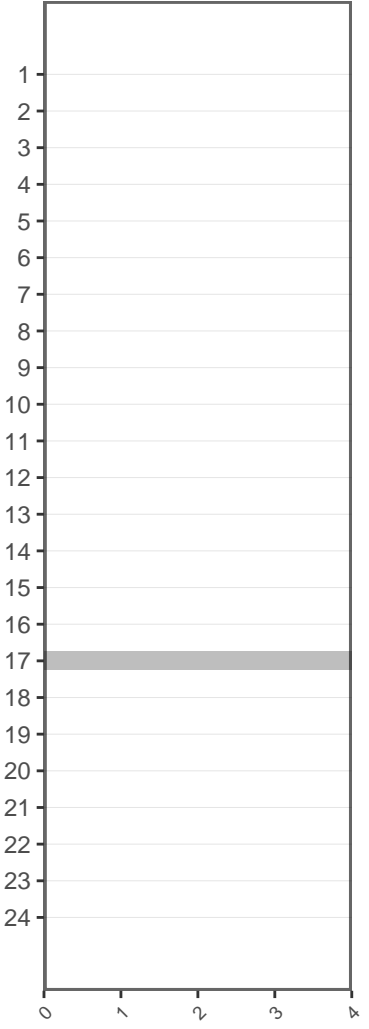
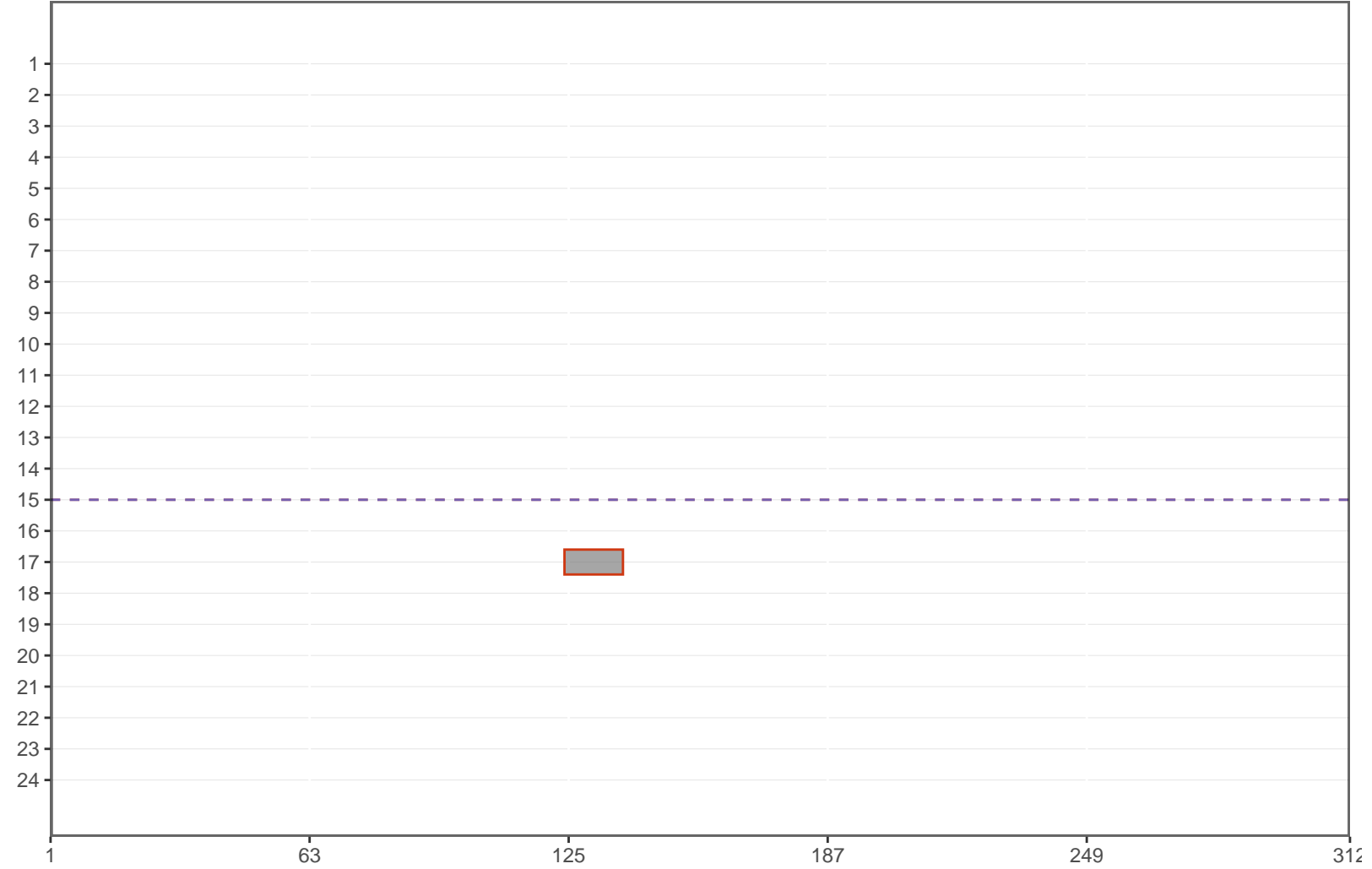
MW indication



Molecular weight

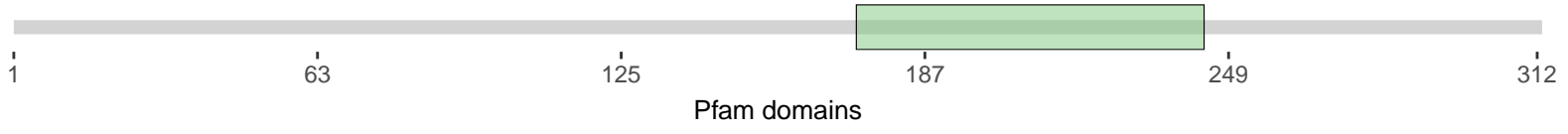


Gel Slice



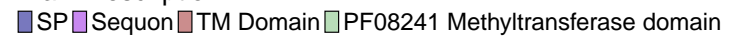
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EVLPPSNAPGVALLDMCSWVSHYPMGYKGERHVGMLNEELKRNPLVEYVVDLNSNPKLPGDNTFDVITNVVSDVLTPLDVFKEMSRIKPGGLAIMSFNRCFFTKAHSWTSTGDADHVMVGGYFHYAGGFEPQAVDSEPNPGGSDPMYVYSRIKATA*

NbL04g19960.1 thioredoxin-like_2_chloroplastic [MW = 25.46 kDa]

No. of times detected



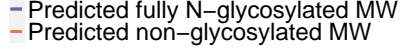
log(intensity)



Values from



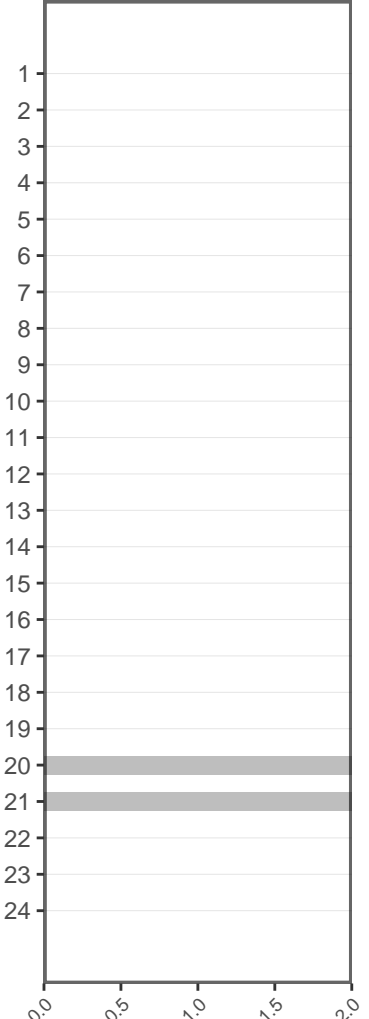
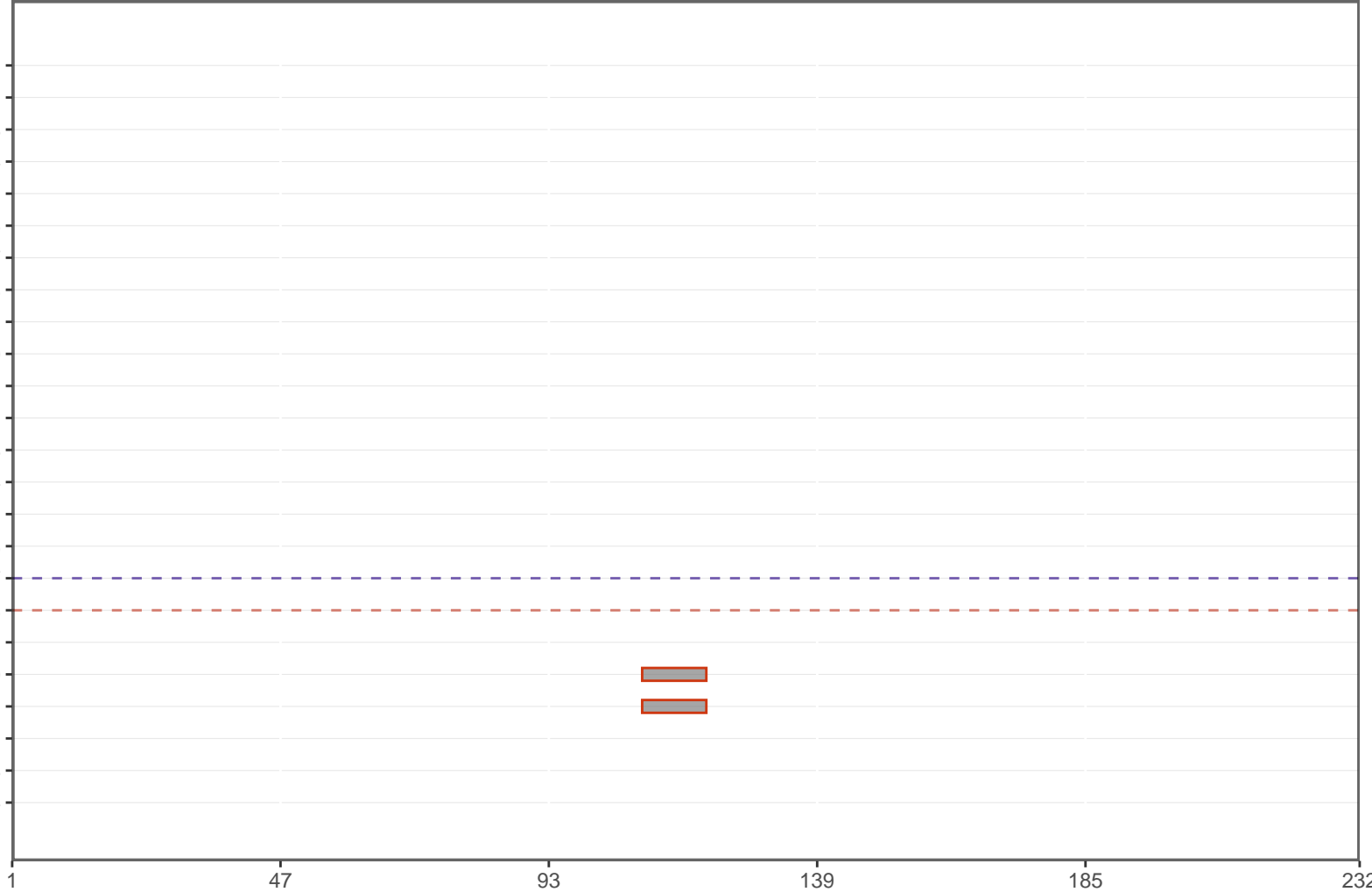
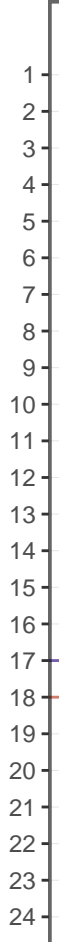
MW indication



Molecular weight



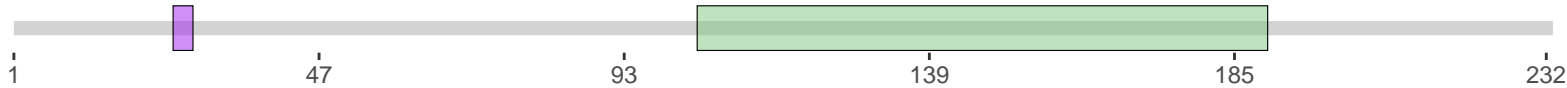
Gel Slice



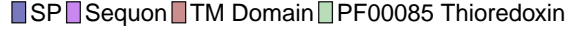
Protein length



Pfam domains



Pfam Description



Protein sequence:

/D/HSTKEFLDLSGAGERLWVEFYGTWASGSKALEFKLGRTAGENPEIMFLKWNFDANKPMCKALNWWLPLFYHFHYRGADGQLESFSGSLAKFKQIKDAQLHNTARGSGPPGVDGDLLELGGTK*

NbL04g19940.1 ectonucleotide_pyrophosphatase/phosphodiesterase_family_member_3-like [MW = 54.93 kDa]

No. of times detected



log(intensity)



Values from



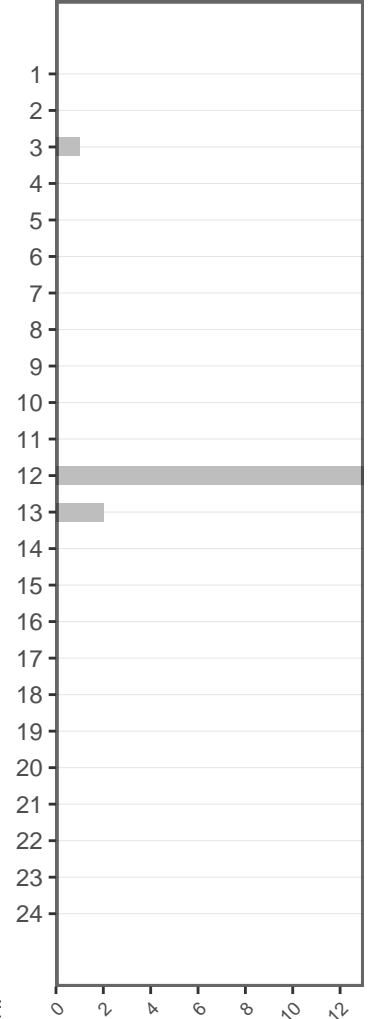
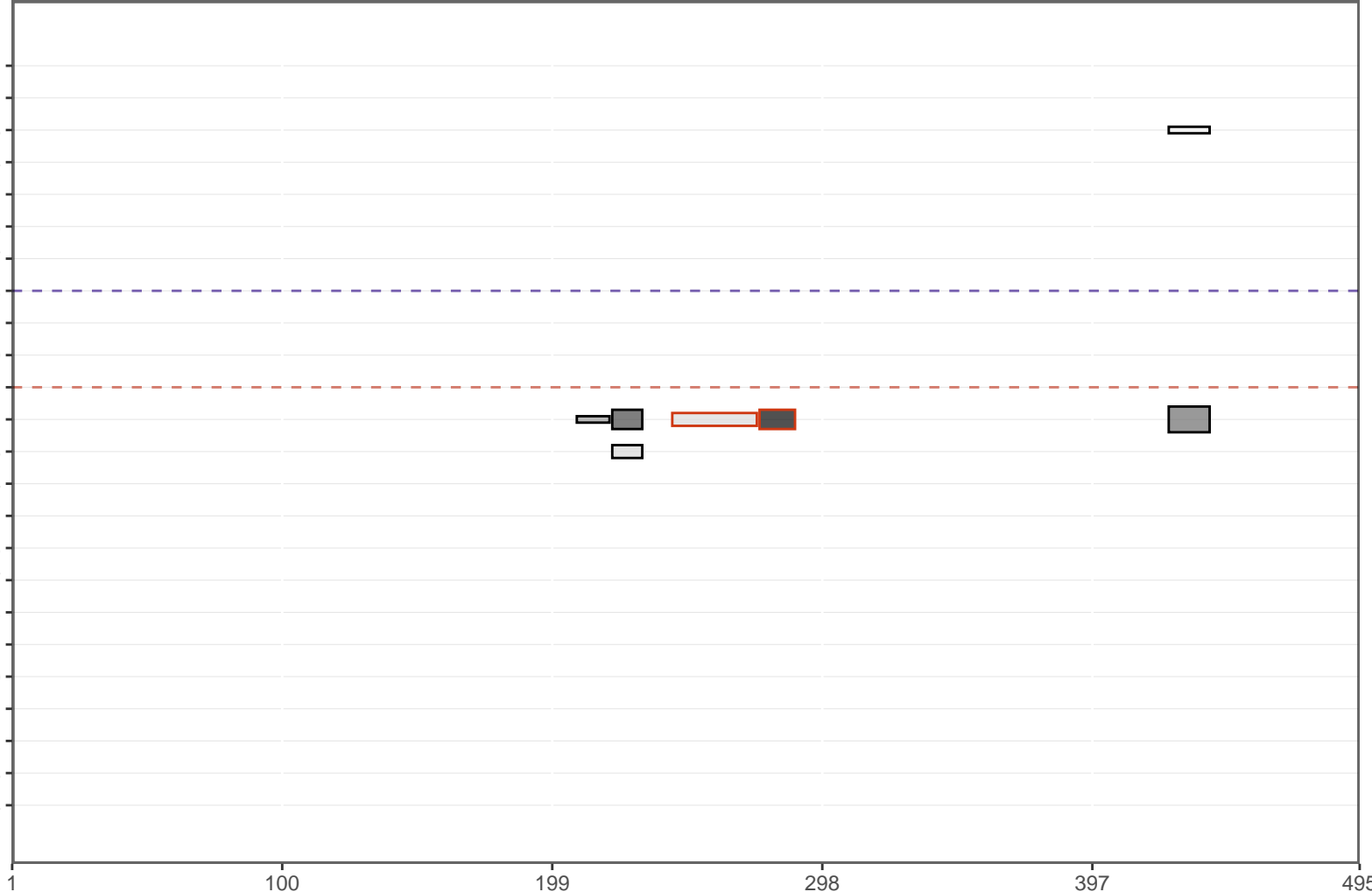
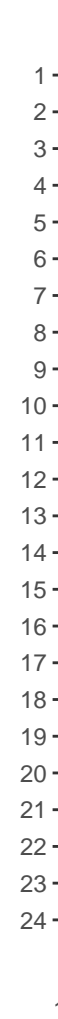
MW indication



Molecular weight



Gel Slice

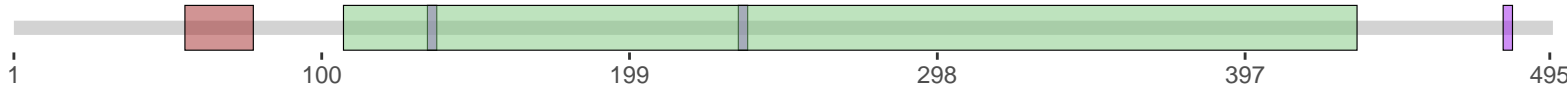


Protein length

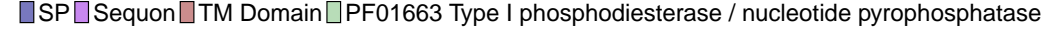


Peptide counts over 4 repeats

Pfam domains



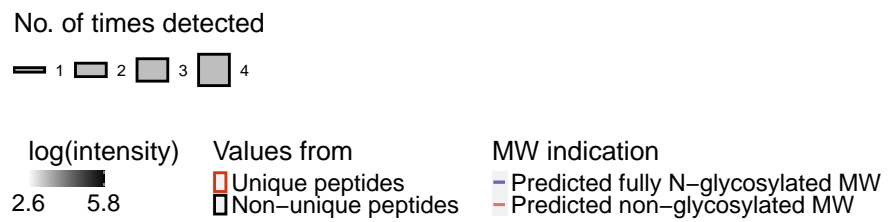
Pfam Description



Protein sequence:

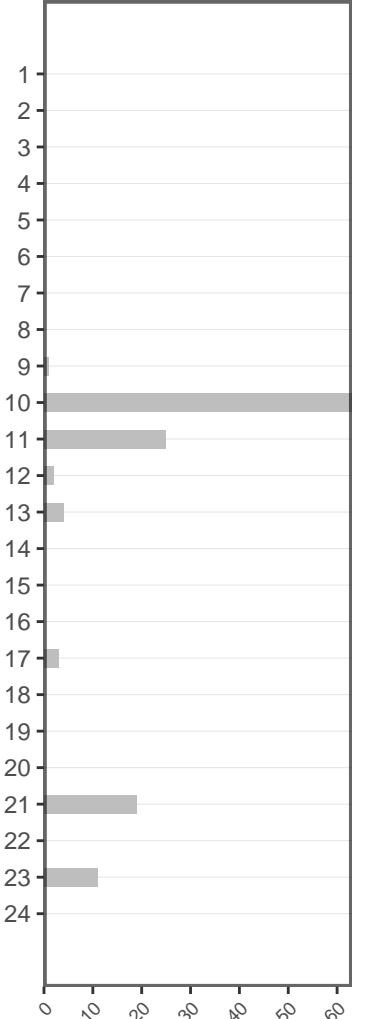
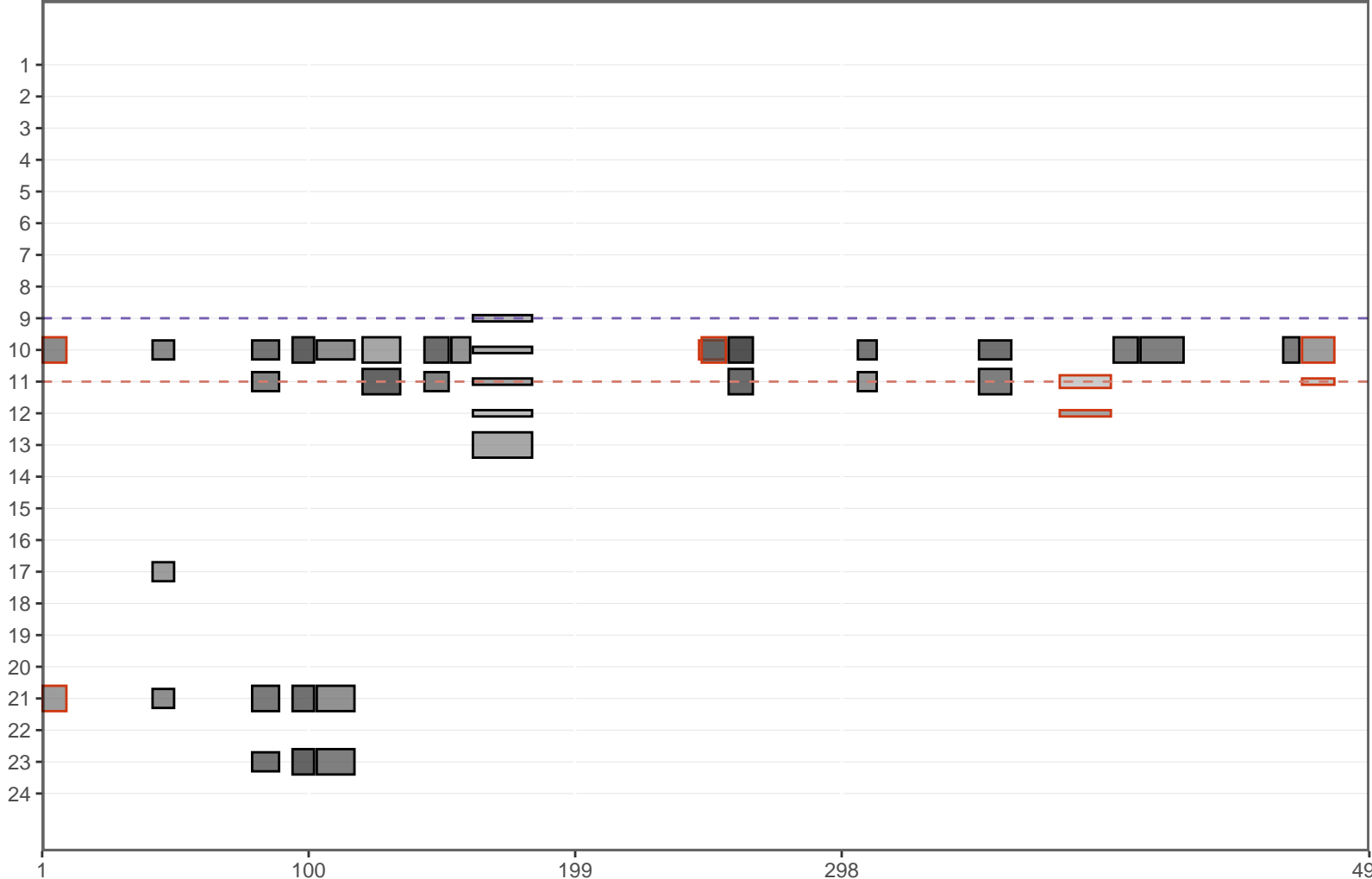
SSVFEERVDYLVNYFDLPTDEIPFMTLYFEDPDHGHKVGDPDPQNEAVARVDMGRLRGLLEKGVFEDLNIMVGDHGMVGTGDKLFLFLEDAFVWIEIPKDWISYSPLLSIRPPTTSVSAKDVATMNEGLKGGKQNGQYLVKYLKEELPARLHYSAEDRIPRIGLIDESFKVQKSSKRKEGGSHGVYDIAFFSMRTFIAHGPKPFARGSKVPSFENVGVNVLVTTLNIGQSAENGTTSFPTKILLPSH

NbL04g19850.1 WD-40_repeat-containing_protein_MSI4-like [MW = 54.72 kDa]



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00400 WD domain, G-beta repeat
- PF12265 Histone-binding protein RBBP4 or subunit C of CAF1 complex

Protein sequence:

ISTLAADANKLAGSAGSRIKADNPISGRIFQGHEDTVDVGFQPSGGDFCFSGVDDSGSLHWDAKRVGNPFVVKVEKAHQADLHGVDPWNPVHDLITGSDANISVRLFRNRNITSDGVSPVHKFEHHTAAVLGVQVQPPORTSEVFGSSAEDGLLHWDAKRVGETTDTTEAKSGDDPPPLGFFQHGASHRDKIVDFHWNASDPWTVVSDDLTETSGGGGTLQHWRMSDLVYRQEEVLAELQGFQKHVSNQAPKPGA

NbL04g19790.1 uncharacterized_LOC104097489 [MW = 29.08 kDa]

No. of times detected



log(intensity)



Values from



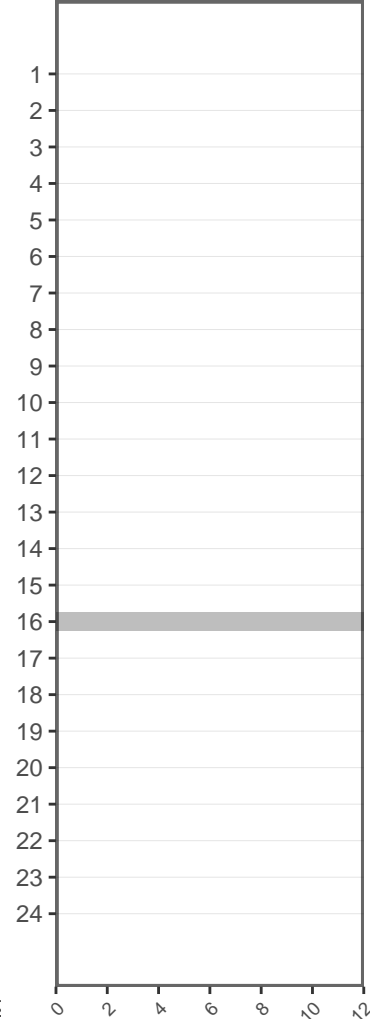
MW indication



Molecular weight

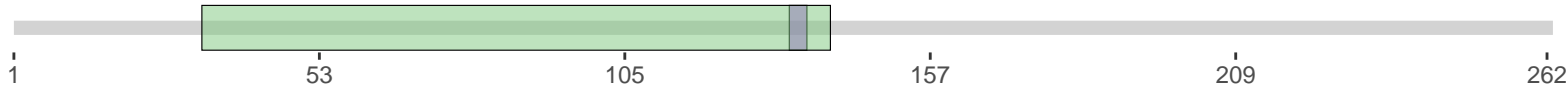


Gel Slice



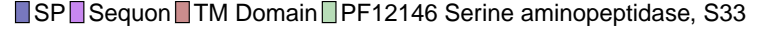
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

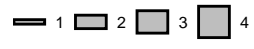


Protein sequence:

IGDVLVLLYASKYIDVHTFVNLGGRYLNLEKGIARLGEDPFLRIRKDKDFIDVKNKAGEVDYRVSEESLMDRLRHTNMHDACLQIDKGRVLTVHGSADHRVEDALEFDKIPNKKLHIEGANHCYTSHLAELTFALPFIKEGLQKNV

NbL04g19770.1 proteasome_subunit_alpha_type-2-A [MW = 25.54 kDa]

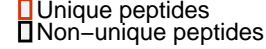
No. of times detected



log(intensity)



Values from



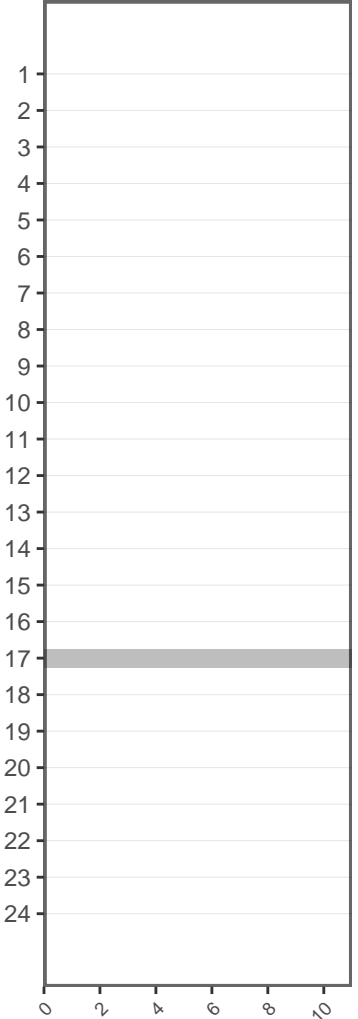
MW indication



Molecular weight



Gel Slice



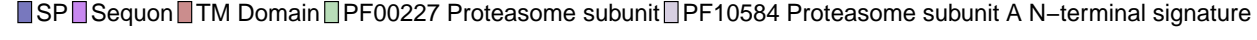
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IPVITQLVREIAVIMGEFTQSGGVRFFGVSLLWGFDDKGPQLQVDPGSGYFSGWKASAMGNVSNAKTFLEKRYTEDELDVAVHTALTLEKGFEGGSGKHEIGVGTOKVFKVLPKEDDYLGEVEI

NbL04g19730.1 probable_protein_phosphatase_2C_58 [MW = 32.19 kDa]

No. of times detected



log(intensity)



Values from



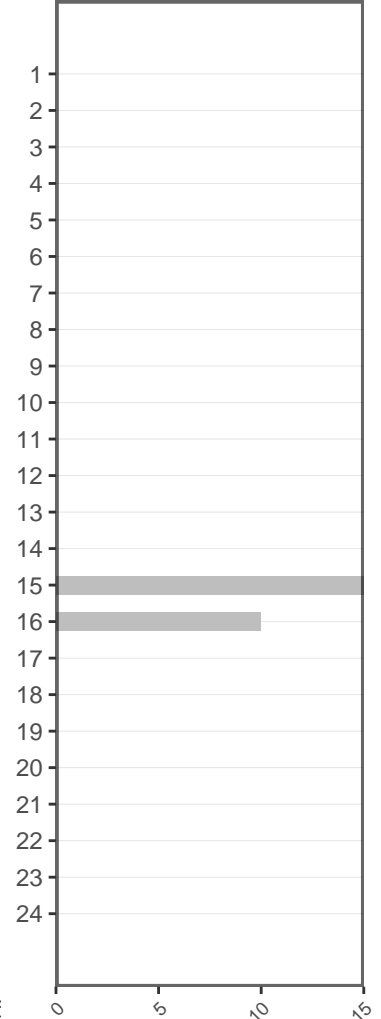
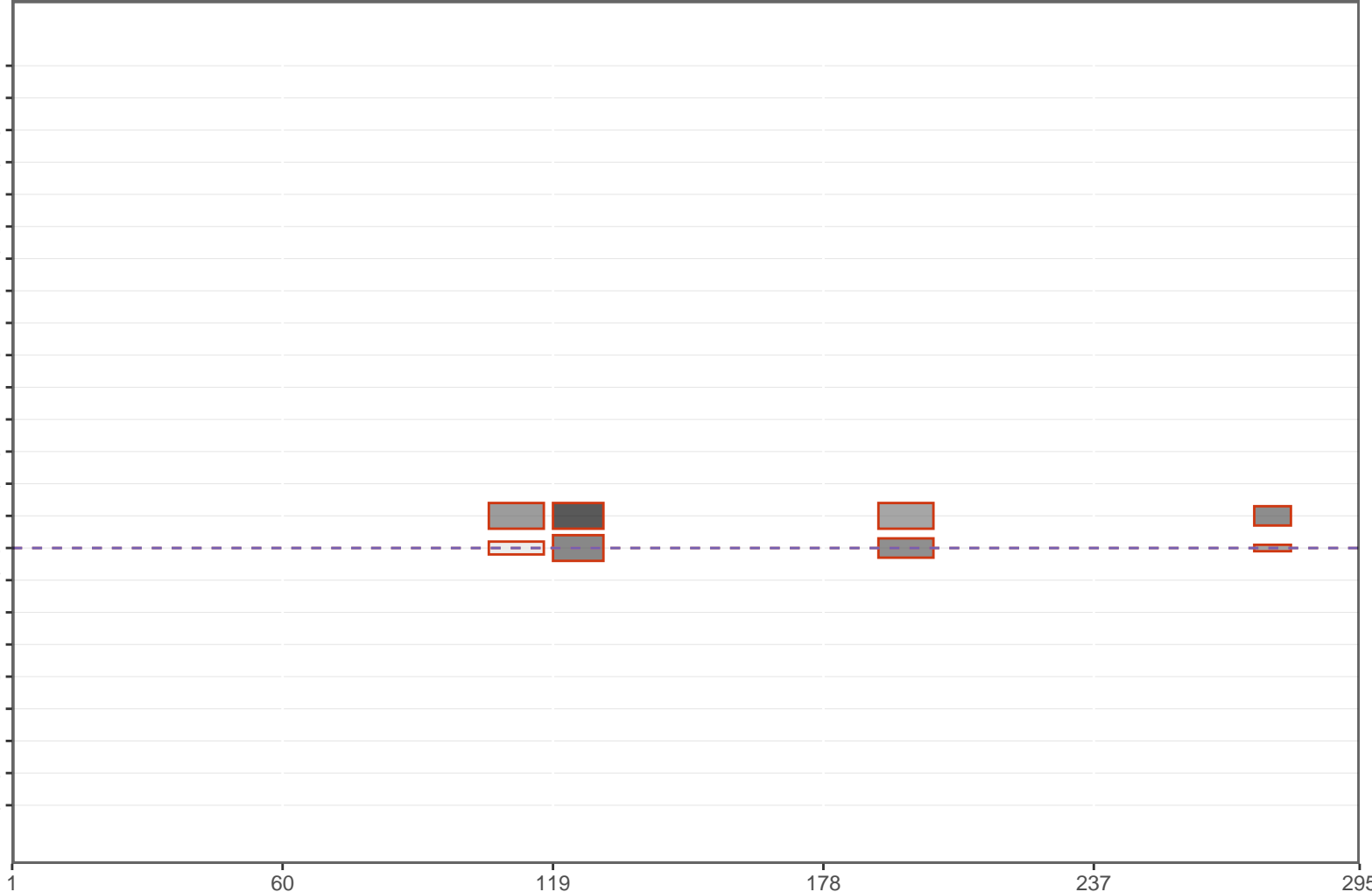
MW indication



Molecular weight

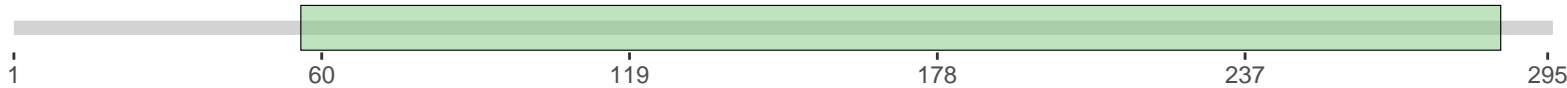


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

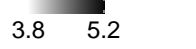
SLGKGGSTAVTAMLSNGQLVAVVNGDRRAVSKKSVKGLGVDHEPNREKEIEESKGGFVSNLPGDPRVVDGGLAVARAFGDKLKKHLSSDPDVIEIUNDDVLLILASDGLWVVMNSNGEAVDCRNMKDAKAAKHLAELASRKKKDDISGIVVVFQ

NbL04g19690.1 uncharacterized_protein_At4g28440-like [MW = 16.18 kDa]

No. of times detected



log(intensity)



Values from



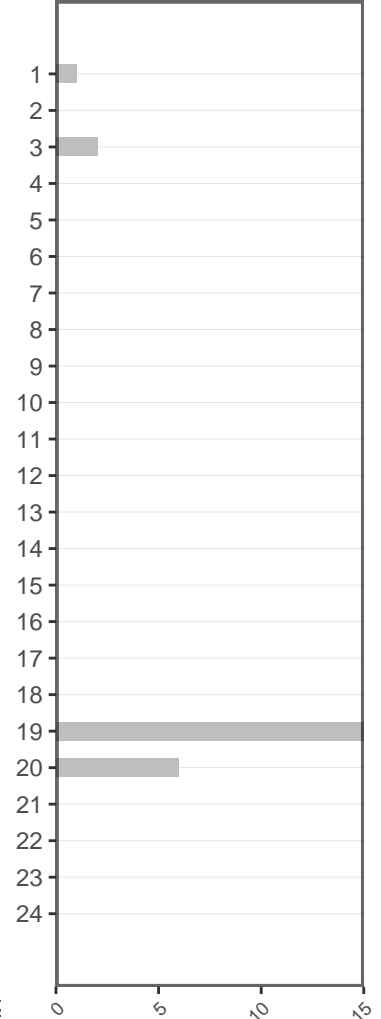
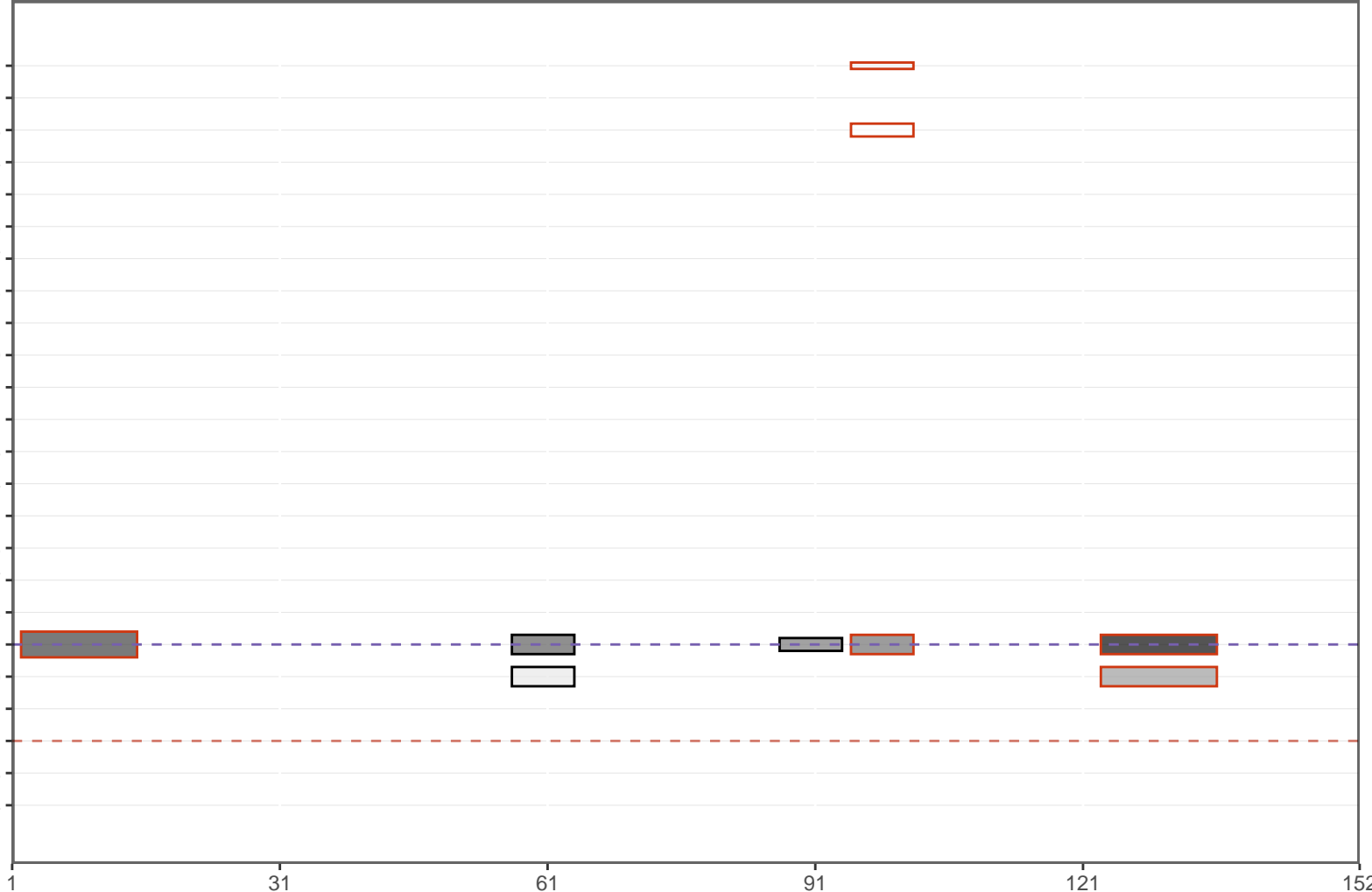
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PRGPRRLAECLVGGDTGSILFTARNEGVDMMKADAVILRLNAKIDMFKGMRLAVDKWGRVEVTEFRDFGVNEKNLILVEYELNVEE*

NbL04g19670.1 26S_proteasome_non-ATPase_regulatory_subunit_2_homolog_A-like [MW = 98.45 kDa]

No. of times detected



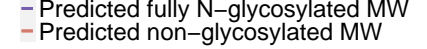
log(intensity)



Values from



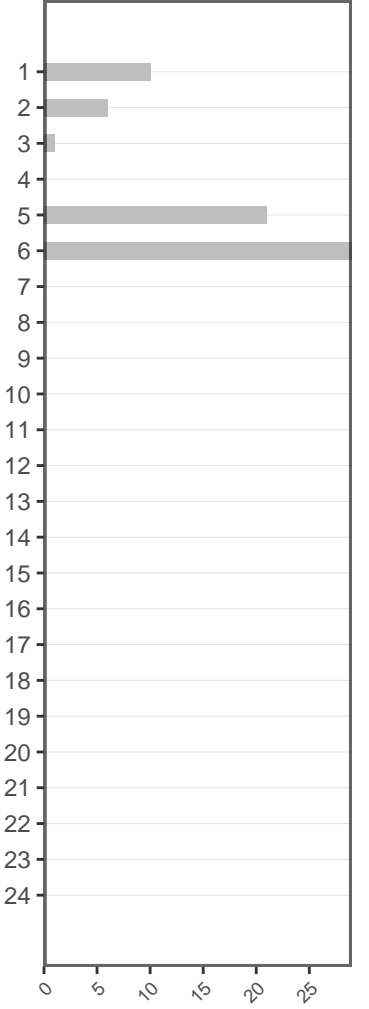
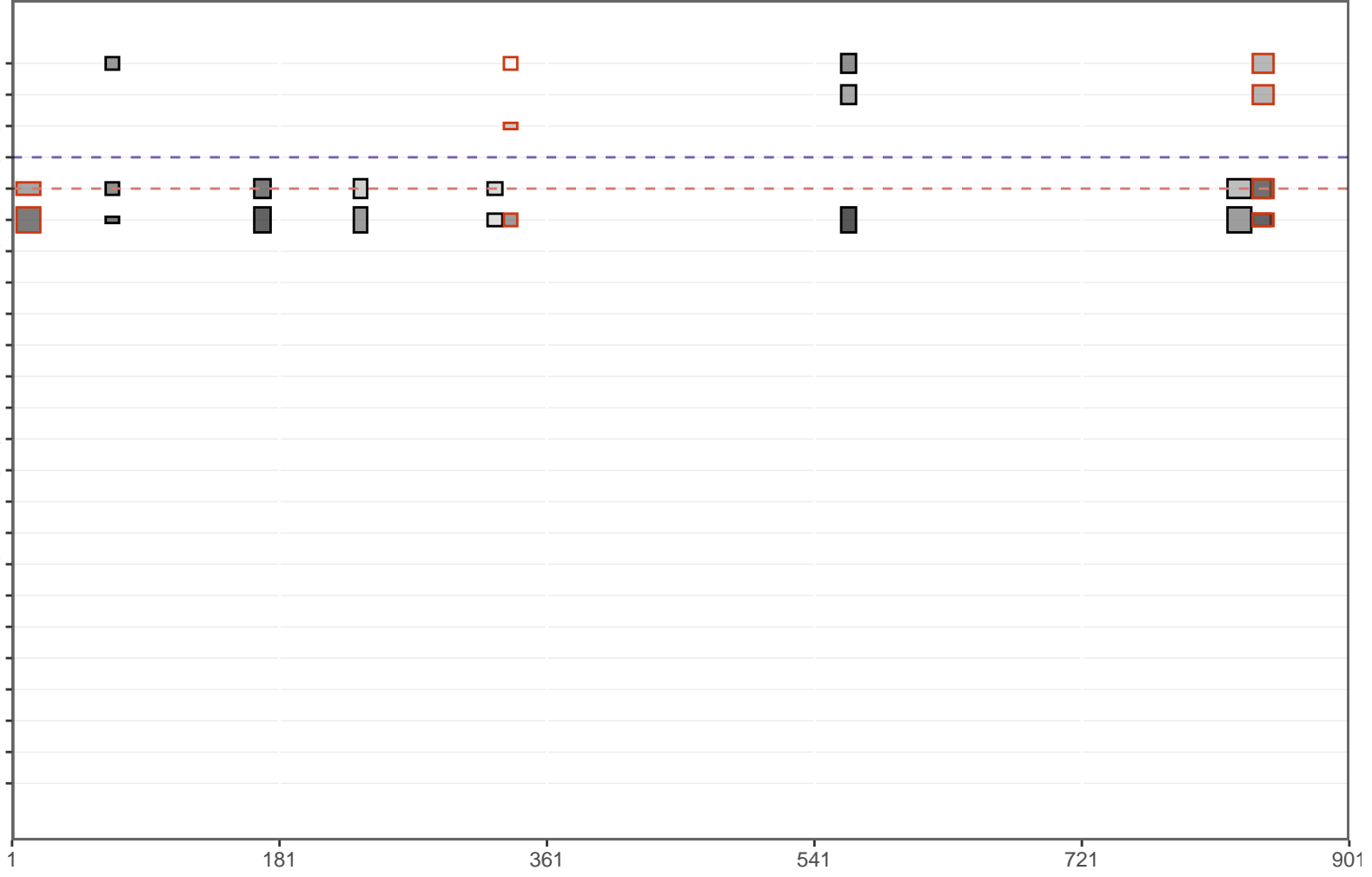
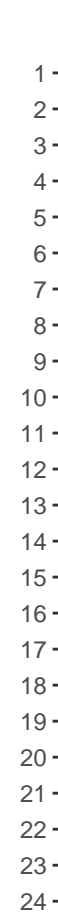
MW indication



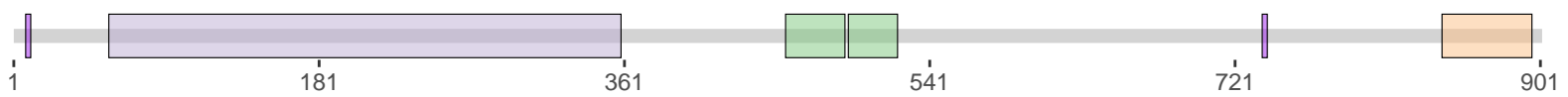
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01851 Proteasome/cyclosome repeat
- PF17781 RPN1/RPN2 N-terminal domain
- PF18051 26S proteasome non-ATPase regulatory subunit RPN1 C-terminal

Protein sequence:

ILLVDYDSGLAQIDKYFHSTDAHVAGALLGVGVNDGINKNEGDPALALLAEYDKEDPSRIGAMSLGLAVAGSDNEGRKLTPLIGDQKAELELAFATVSLGVVYVSGDNEEIQGAIFALMERSESELEGEFARLLFLGLGLLVLGKQDSVEATAEVSKTFTNEKIRKHCDMTLSCAVAGTGNALKVQVHFLGDCAGHFKEKGETFGQPWVLGIAMVMAAEELGEMAIRLEHLLQVGEQNRIRAVPLALALLGHNPKVNMVDTLSRLSHDSDSEVMAAISLQLGAGTNNARI

NbL04g19520.1 fasciclin-like_arabinogalactan_protein_9 [MW = 32.43 kDa]

No. of times detected



log(intensity)



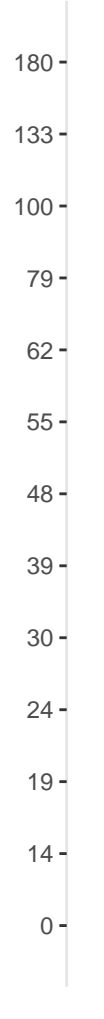
Values from



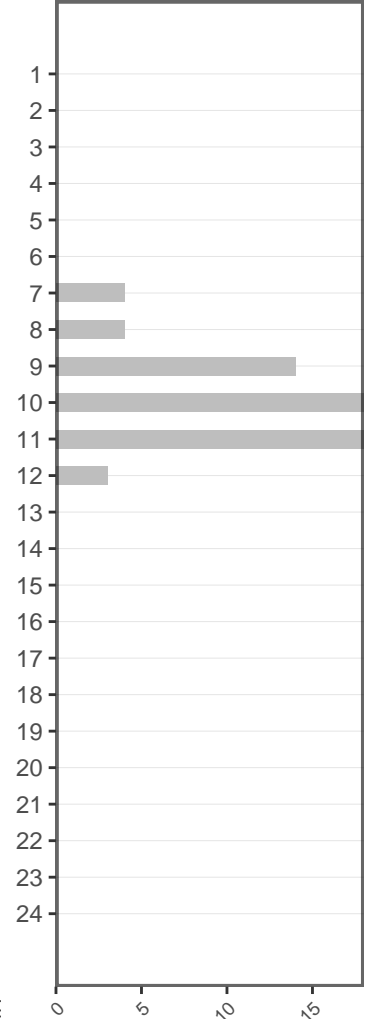
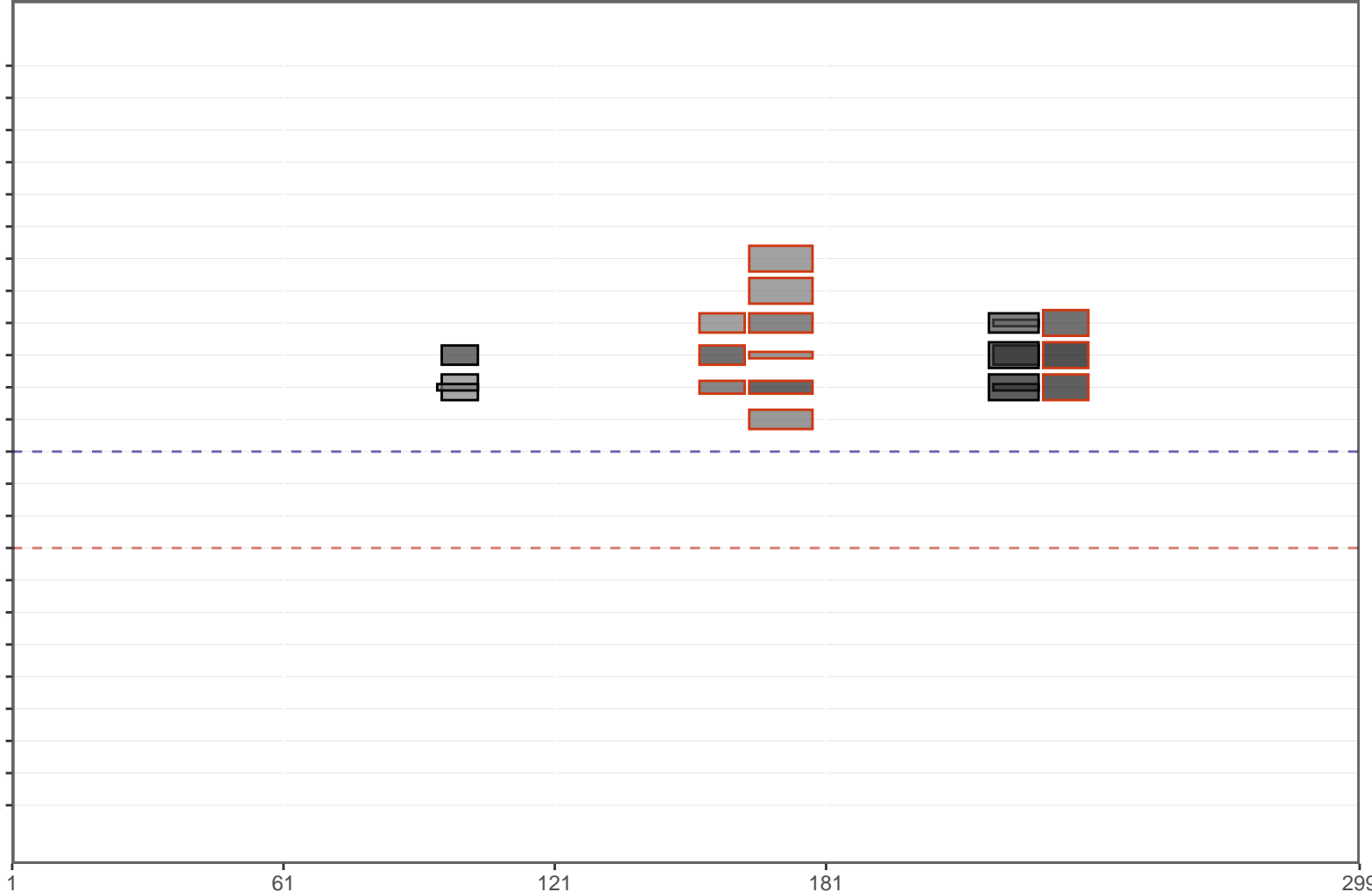
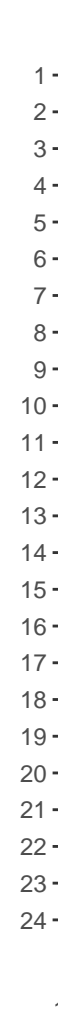
MW indication



Molecular weight



Gel Slice

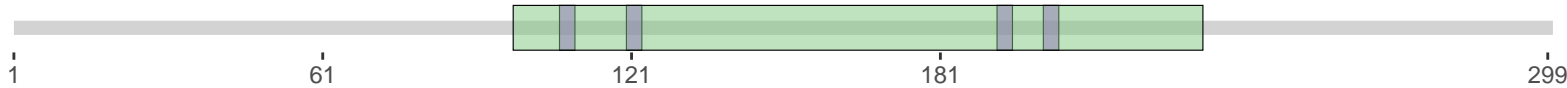


Protein length

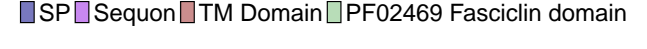


Peptide counts over 4 repeats

Pfam domains



Pfam Description

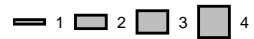


Protein sequence:

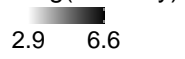
.PGSTLNKLSDOCKVQLGHHVYKPKYFSEDLQTVENPVRTQATGGKGEAFGLNFTFGNNQVNVSSGAVETNINAIKDKPPLAVYGLDKVLIPLAFTDTKTPSSDAPAFPTDDEAKGGSTADTKAKKEPSPAPNGAKRINWVFLGSLGVFLFCMGALS

NbL04g19280.1 ketol-acid_reductoisomerase_chloroplastic [MW = 63.26 kDa]

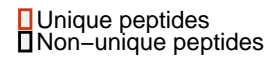
No. of times detected



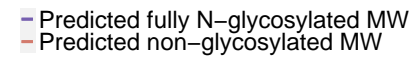
log(intensity)



Values from

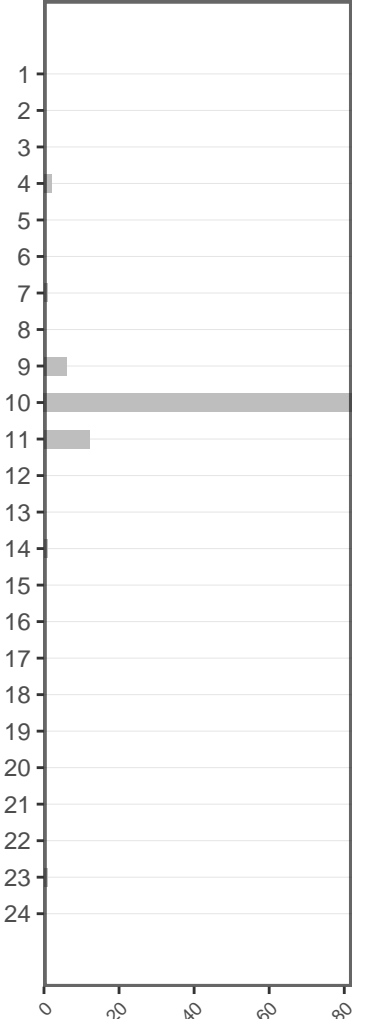
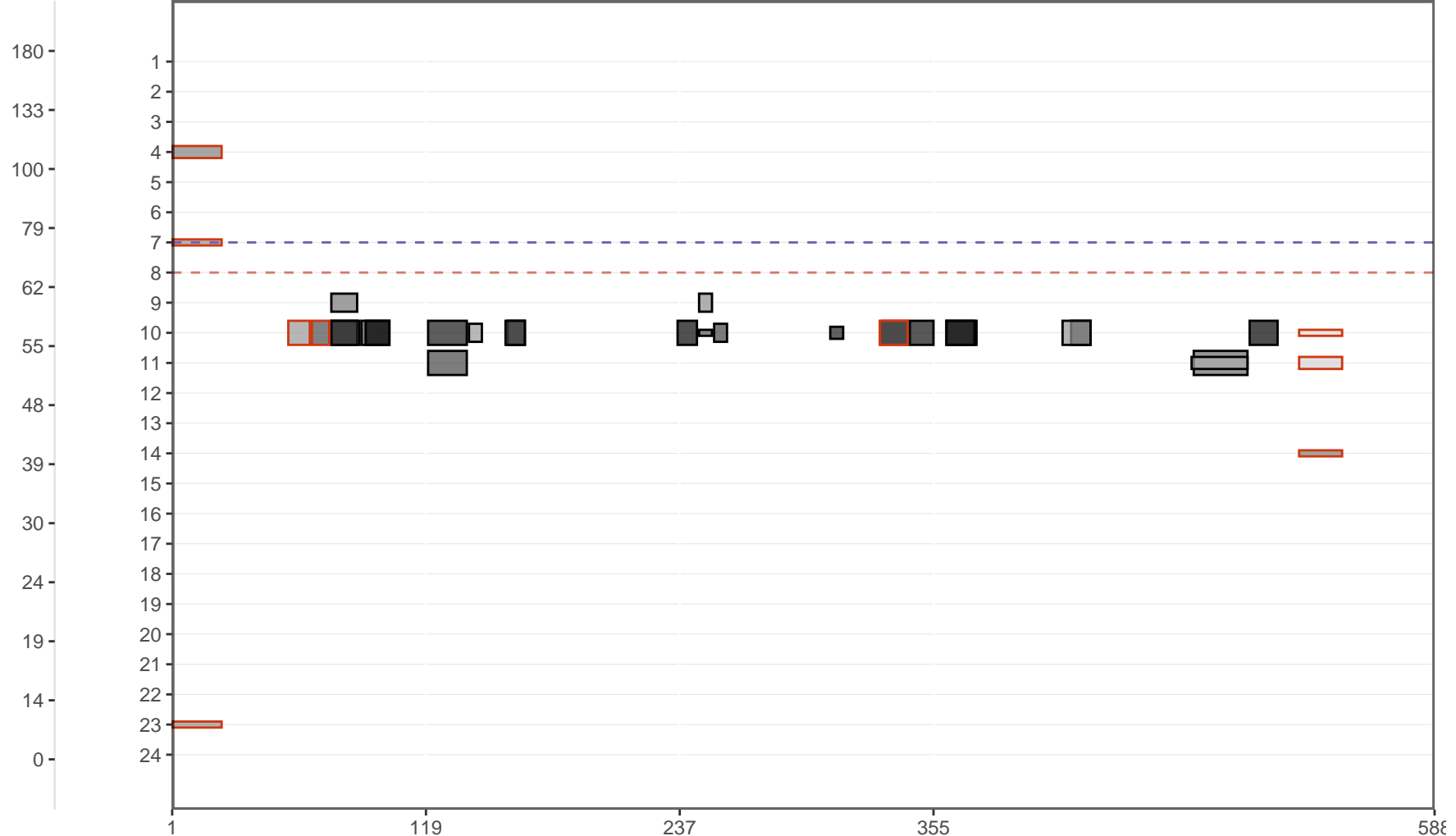


MW indication



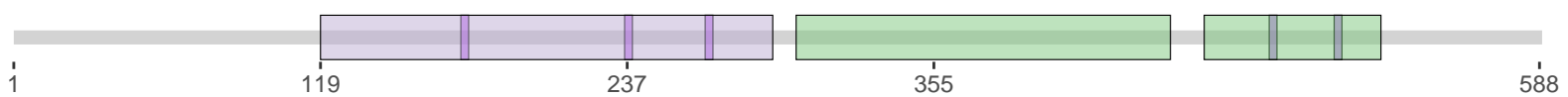
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01450 Acetohydroxy acid isomeroeductase, catalytic domain
- PF07991 Acetohydroxy acid isomeroeductase, NADPH-binding domain

Protein sequence:

ITDAVLGWSVALGSPFTFATLLEQEKVSDIFGFRGRLGLAVHGVVVELFRFRFTENGMDLAKYKNTVECFGHSKTIETKGLAVVNSLSTEEGKKEFEAAVSAASYVPMELVECYEDATGSEIRSVVLAGRRFYEKEGLFAFMGHIDQTRMVKVGERVRAKRPAGDLGPMYPTAGVYVALLMADQELRKKGHVSEHINESVIEVDLSLNFPMHARGVSVFMVDSNSTARLGSFRKWAAPRFDFVLTQQALVAVDNNAINRDUISNLFSDPHGAEVGAQLRPTVDSVTDAA

NbL04g19260.1 14-3-3_protein_9 [MW = 29.54 kDa]

No. of times detected



log(intensity)



Values from



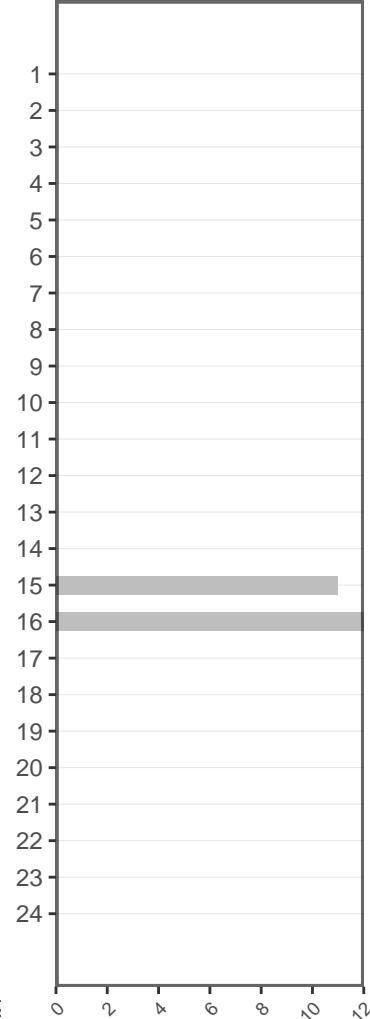
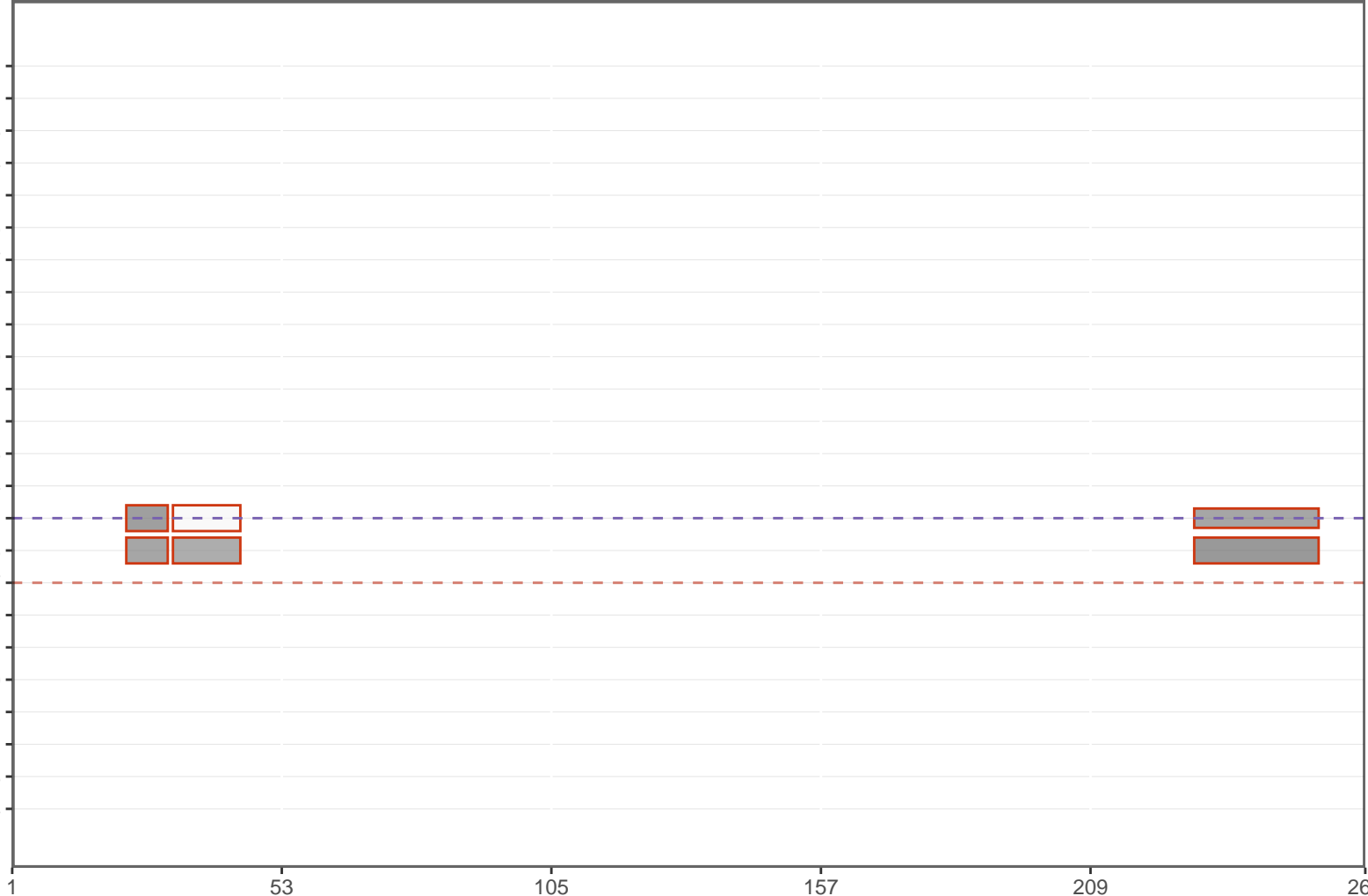
MW indication



Molecular weight



Gel Slice

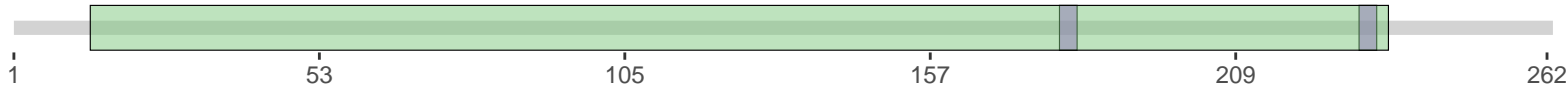


Protein length

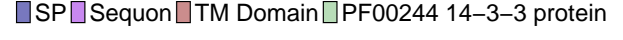


Peptide counts over 4 repeats

Pfam domains



Pfam Description

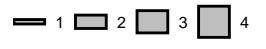


Protein sequence:

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NbL04g19240.1 phosphoenolpyruvate_carboxylase-like [MW = 110.03 kDa]

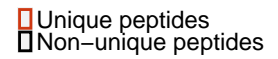
No. of times detected



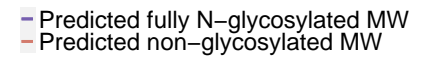
log(intensity)



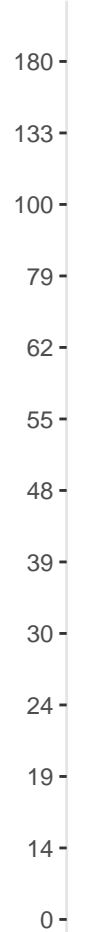
Values from



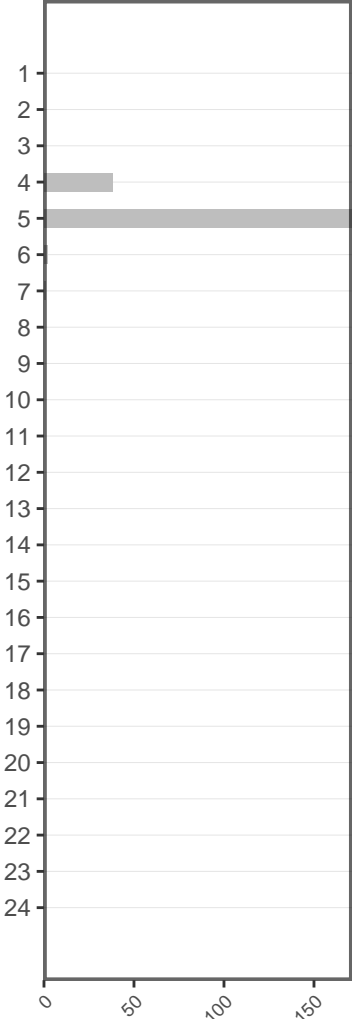
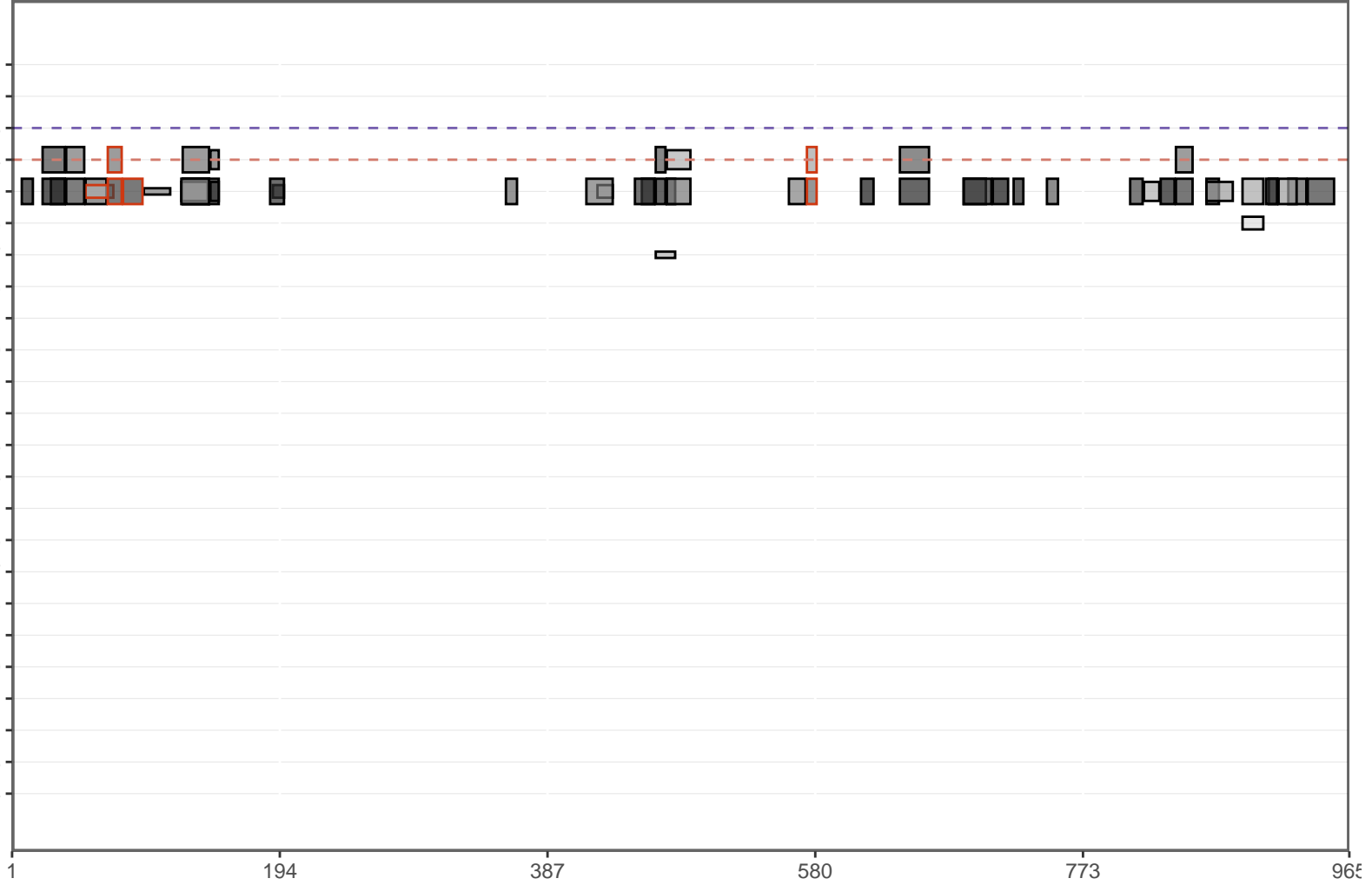
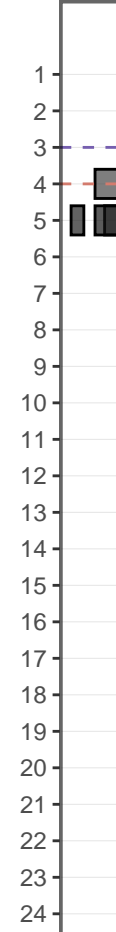
MW indication



Molecular weight

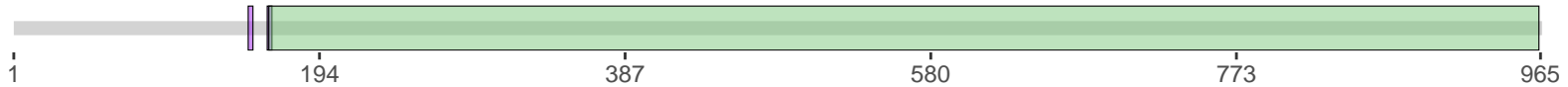


Gel Slice



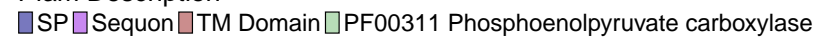
Protein length

Peptide counts over 4 repeats



Pfam domains

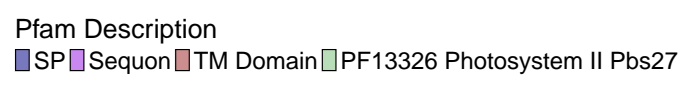
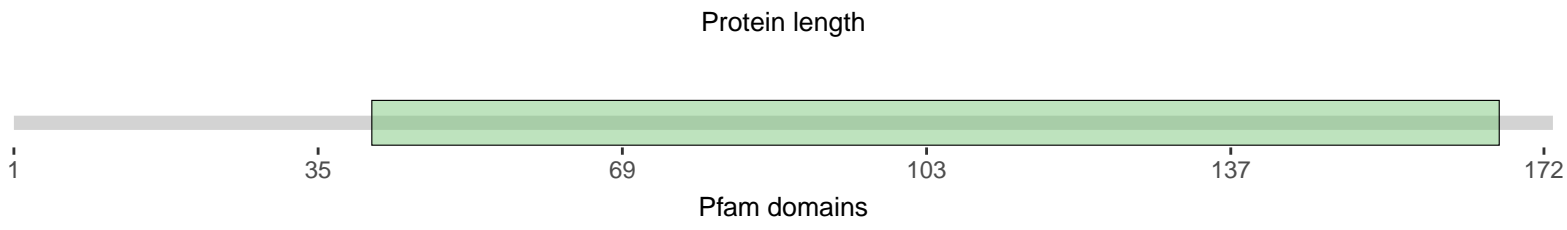
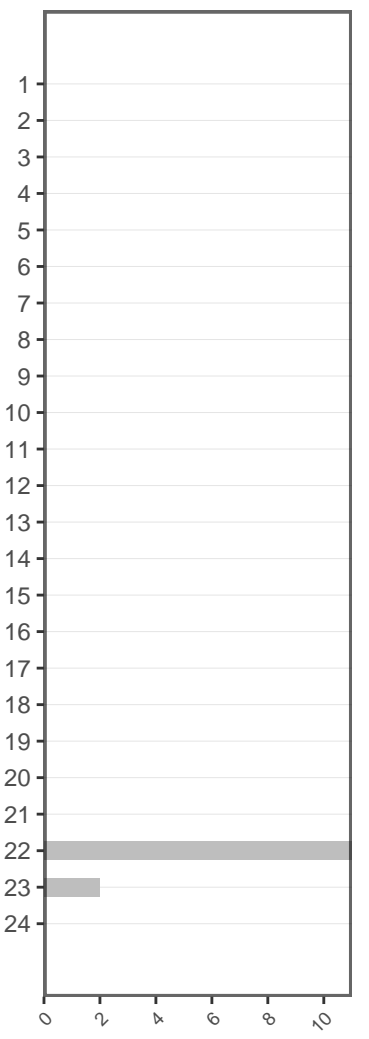
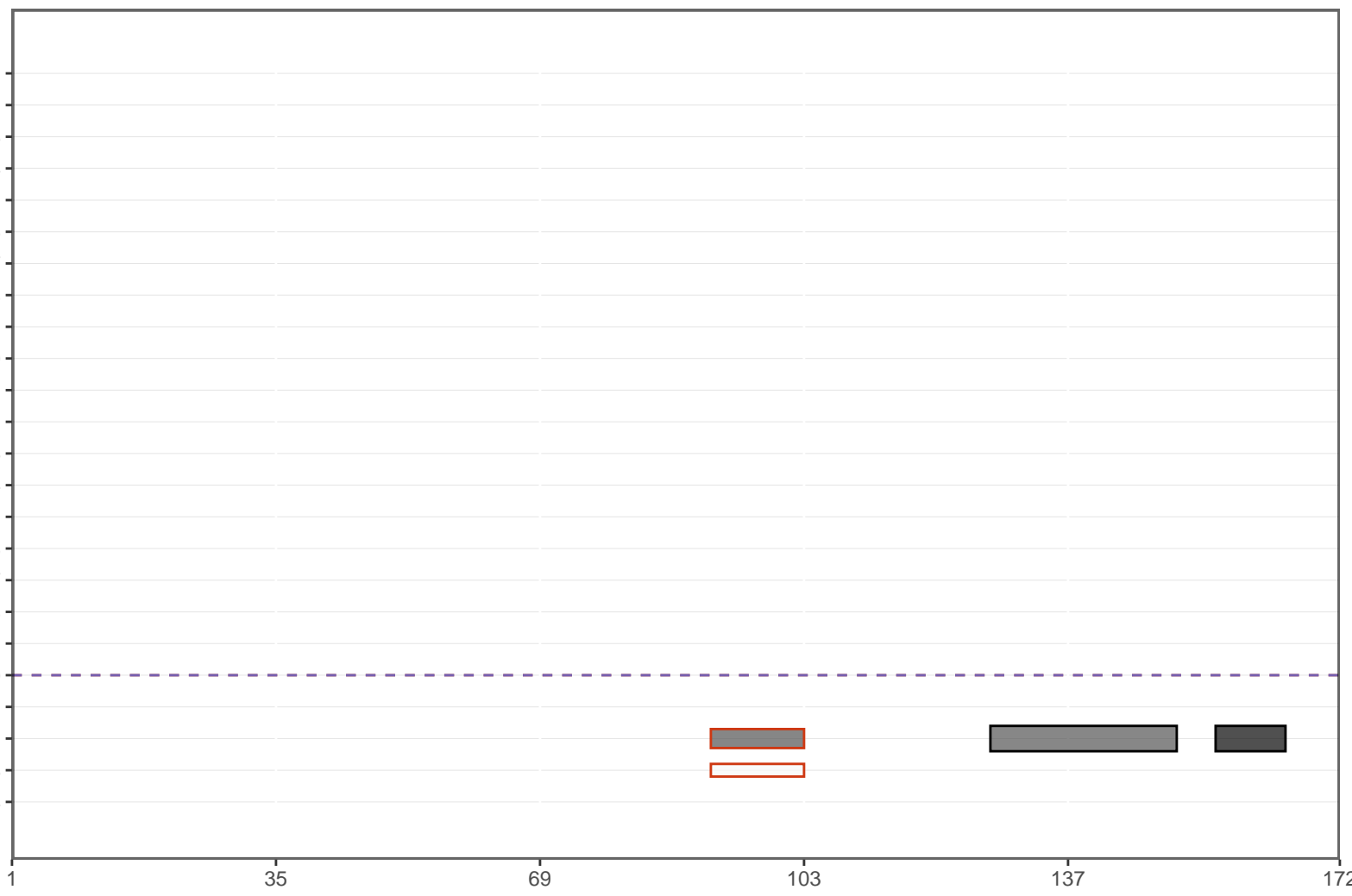
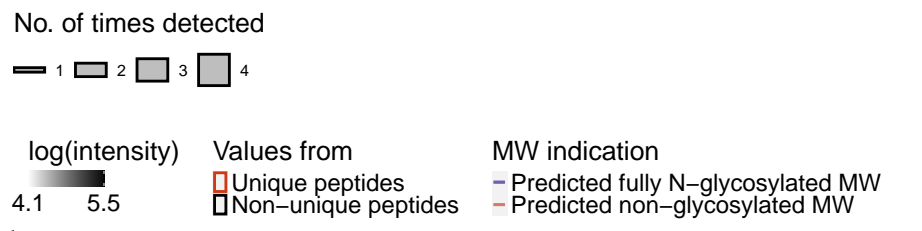
Pfam Description



Protein sequence:

SYKEVSEERQCEWLLGELSGKRPFLFGDLPKTDIADVLDLTFNVAELPADNFGAYHISMTAPSDVLAVELLQRECHVNSPLRVPLFEKLADESAPASVRLFSISWYRNNNGKGEVMGYSDSGKDAGRLSAAWGLYKAGDELVVAKEFGVKLMTFHGRGGTVGRGGPTHLALSGPPDTHGSLRVTVGGEVEGEGFGEELCFRLLGRFTAATLEHGMNPPVAKPEWRALLDEMSVATKEVRSLSVFGDPRPFVEYFRLATPELEYGRMNGSRPWKXPSGGII

NbL04g18830.1 photosystem_II_repair_protein_PSB27-H1_chloroplastic-like [MW = 18.79 kDa]



Protein sequence:
 ASEVKKVRSSTLSMEKSDPNADSVTELREASNYWAKYRREKDLLGRASFRRDYSALNAVSGHYVYFGPTTPIPAKRKGRILEEMDTAEKALGRGR

NbL04g18670.1 lipoyl_synthase_2_mitochondrial-like [MW = 26.4 kDa]

No. of times detected



log(intensity)



Values from



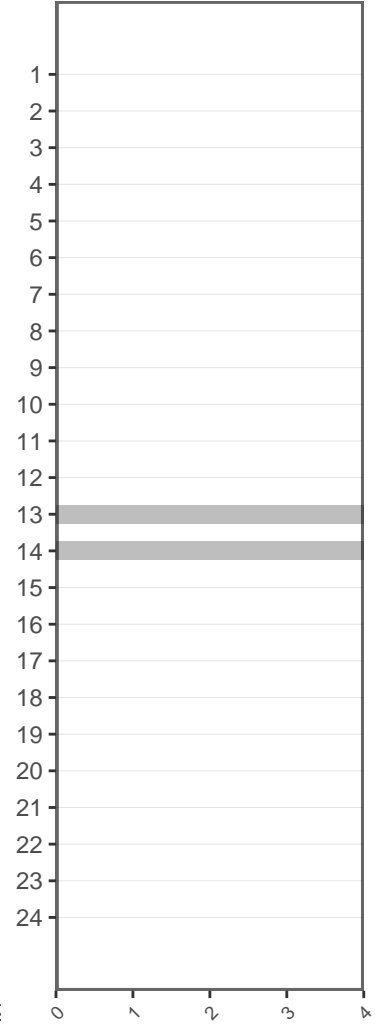
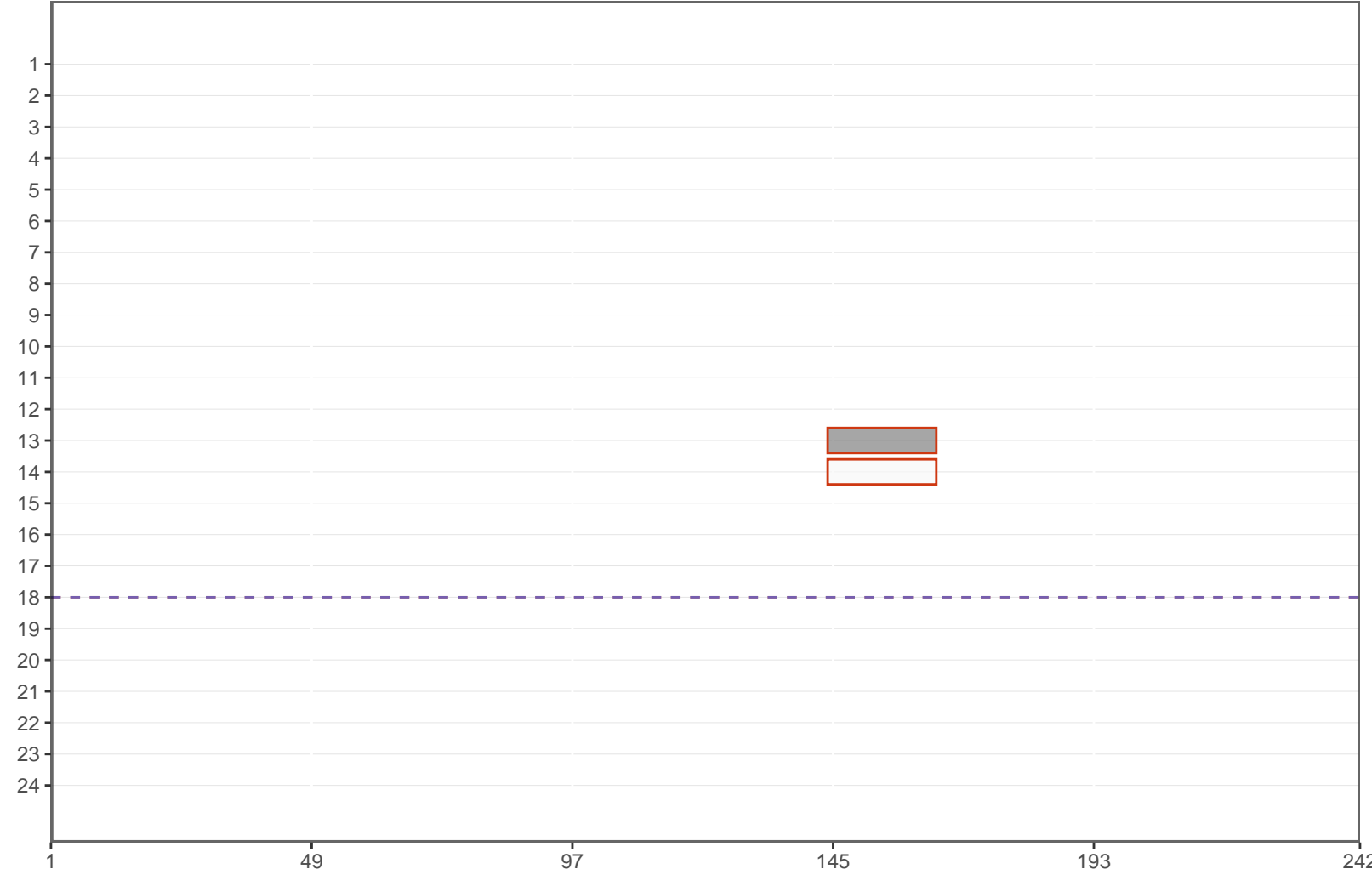
MW indication



Molecular weight



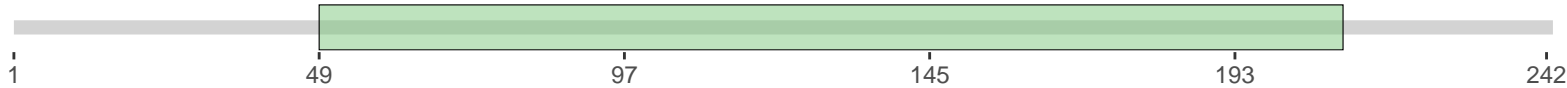
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

TETVQKLGKALKPNMLKALTPDFRGGPGGVEKVAKSGLEVFVFAHNIETVEELGQVVRDHRANFKQSMVLLKMKGVAPANTLTKTSMILGGCETPEQGVCKTMEKVRAGVDVMTFGQYMRPSKGHMPVSEVYTP

NbL04g18290.1 GDSL_esterase/lipase_At4g26790-like [MW - SP = 36.27 kDa]

No. of times detected



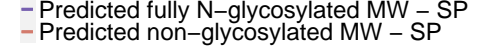
log(intensity)



Values from



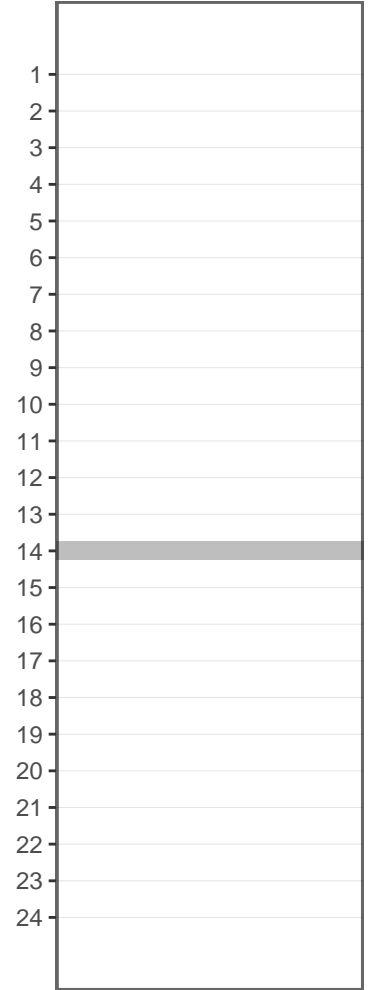
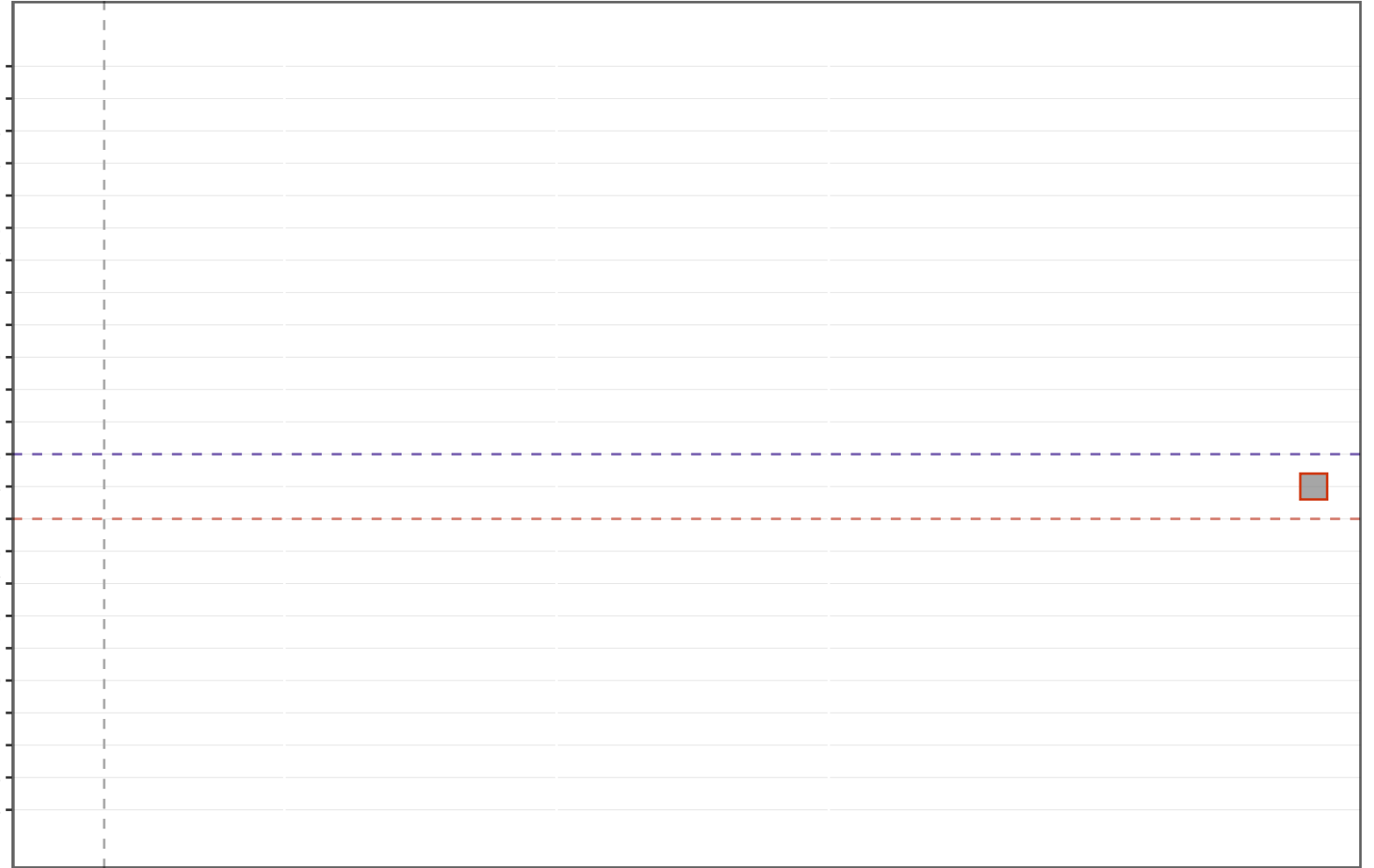
MW indication



Molecular weight



Gel Slice

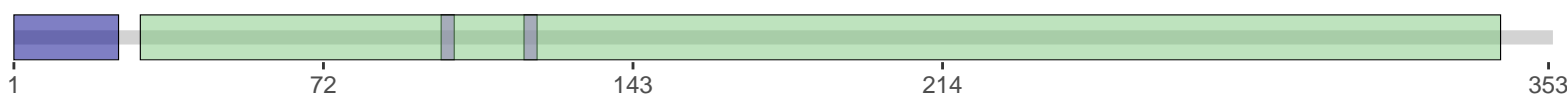


Protein length

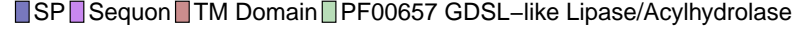


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

STNDFLENYITMPGRRSQYTVDDGQTFLLGIANNFTNLYLGGARKIKLGGLLPPMGCMPLERTSNMANGNEGLESYVAMNFNDKLSGLVIELNKLGGQVYVLENPPYVNLGMKIKPSLYGFEVAVSLACCATGLFEMGVAGDPPNLFYFGKDKANKYHFWDAFHPTKTEKDRIDAHVVKTALSKFLV

NbL04g18230.1 L-ascorbate_oxidase_homolog [MW - SP = 57.45 kDa]

No. of times detected



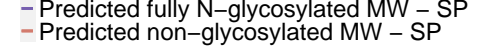
log(intensity)



Values from



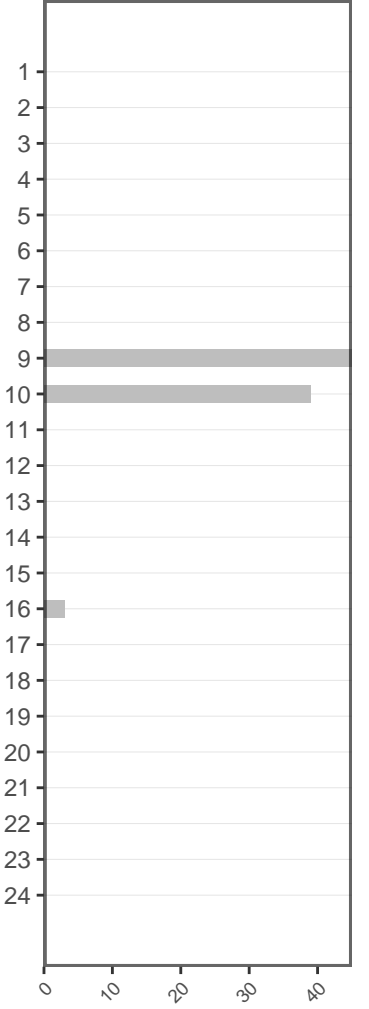
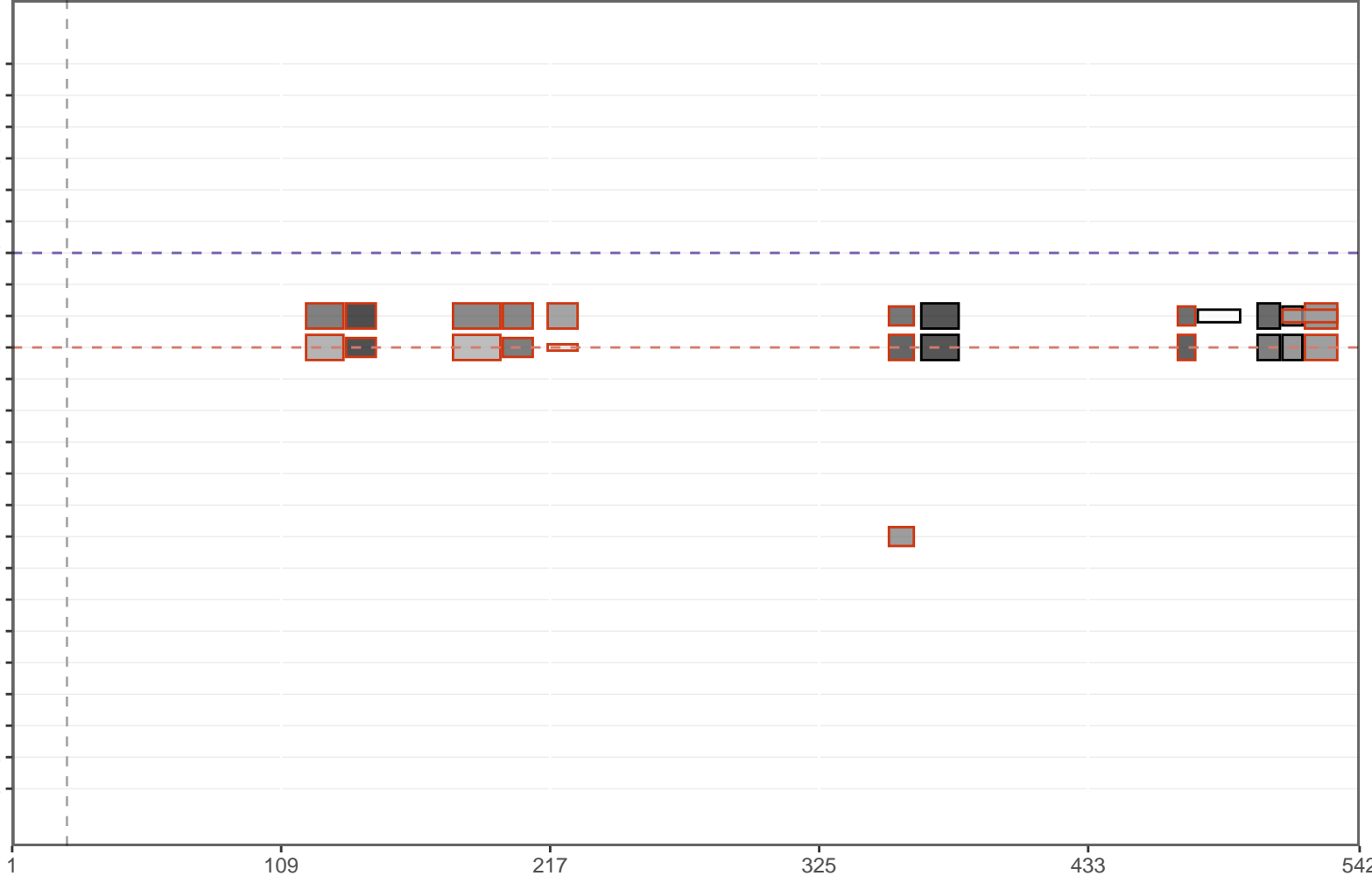
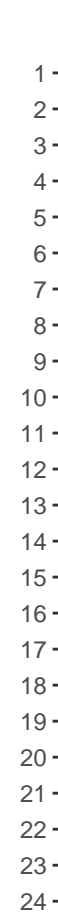
MW indication



Molecular weight

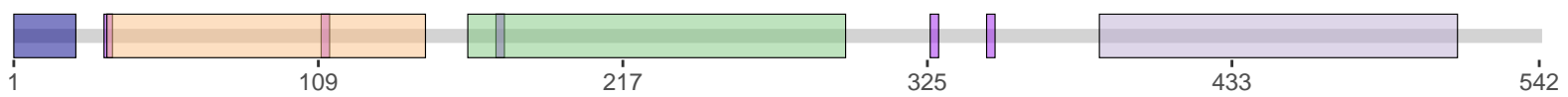


Gel Slice



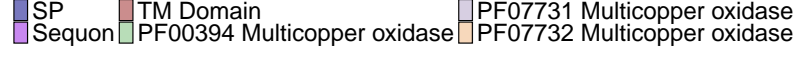
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

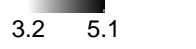
SYSVLLADQPKDKVIVVSTRFSQVLTATSTLHYNSAGSVSGPPPGPTTEIDWLSLNGARSLRRNLGASGRFRNPGSGHYHGLNTRTRIRLNSAPVINGKGRVAINVSEFVADTFLKLAHFNIPGVFSLGSPDPTGGGAVLQTSVMAADFRAYTEVFENLEVSQGHGHHFFVYVMGGGEWTPASRLTYNLRDTRSTVQVYPKSWTALVMPLENVGMWNRSGNWARGVLDGDFYLRVYSPANBWRDEYIPRNALLGGRASTRLN

NbL04g18220.1 L-ascorbate_oxidase_homolog [MW - SP = 57.85 kDa]

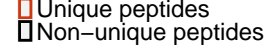
No. of times detected



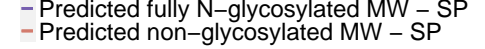
log(intensity)



Values from



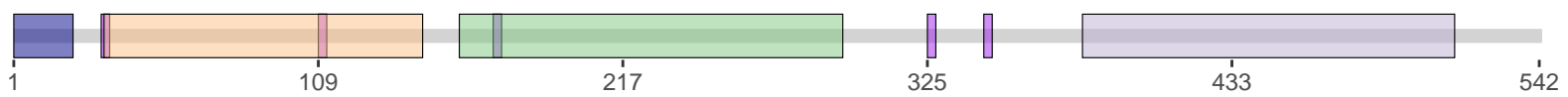
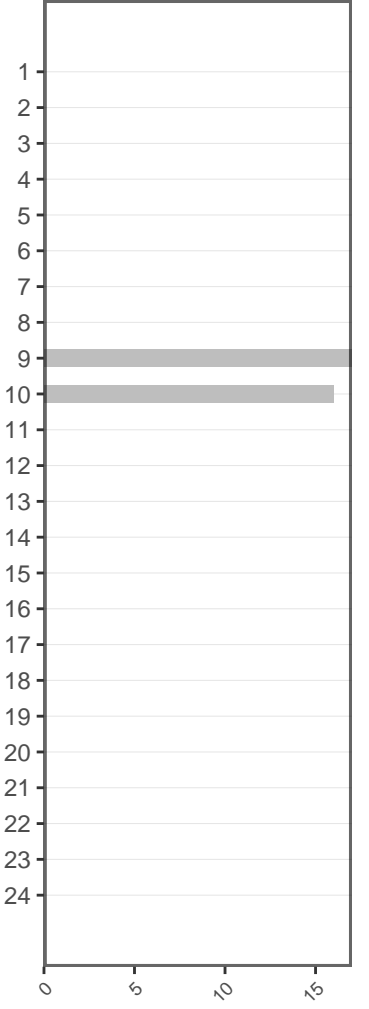
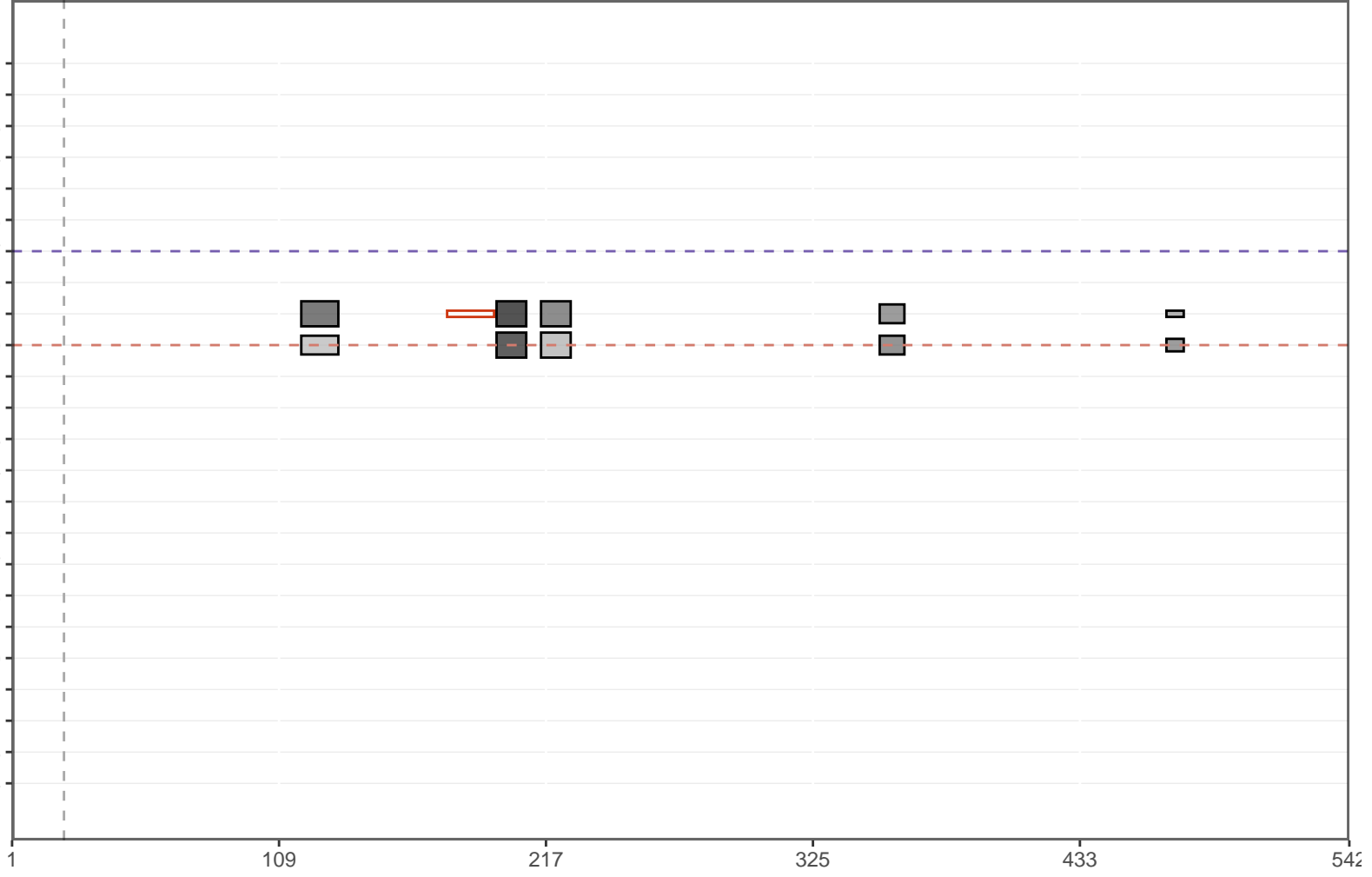
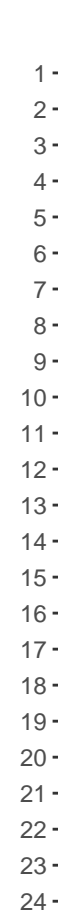
MW indication



Molecular weight

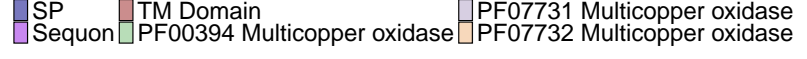


Gel Slice



Pfam domains

Pfam Description

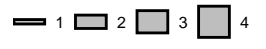


Protein sequence:

'SVLVITMDQPODYYWASTRTFTSGVLTATGILHYNSAGSEVSGPPGGPTIEDWLNAGARSFRONLTASGPRPNQDGSYHGLVNTTRTRILANSAPMINKQRWVNSVSRIPADTRFLKLDVFKIPGVFNLSGSDNPTGGGGYLGTSVMAADRFAFVEVVFENFEDVGSWHDDGHFFVVGMDGGQWSPASRLNVLNRDGBRGTQVYVPEKWTALVMPLENVGMNIRSENWARQYLGQGFYLRVYFRANSWRDEYPIPKNALVCGRASGRTRPL'

NbL04g18140.1 aconitate_hydratase_cytoplasmic [MW = 108.63 kDa]

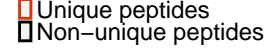
No. of times detected



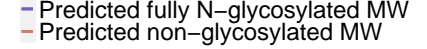
log(intensity)



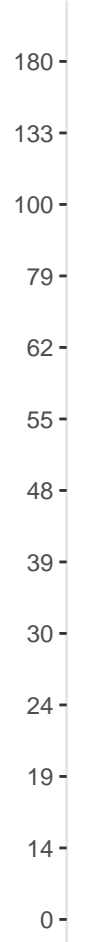
Values from



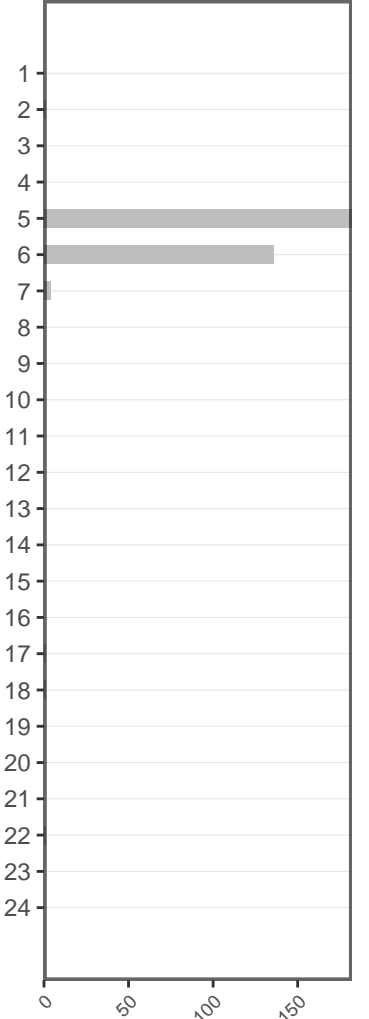
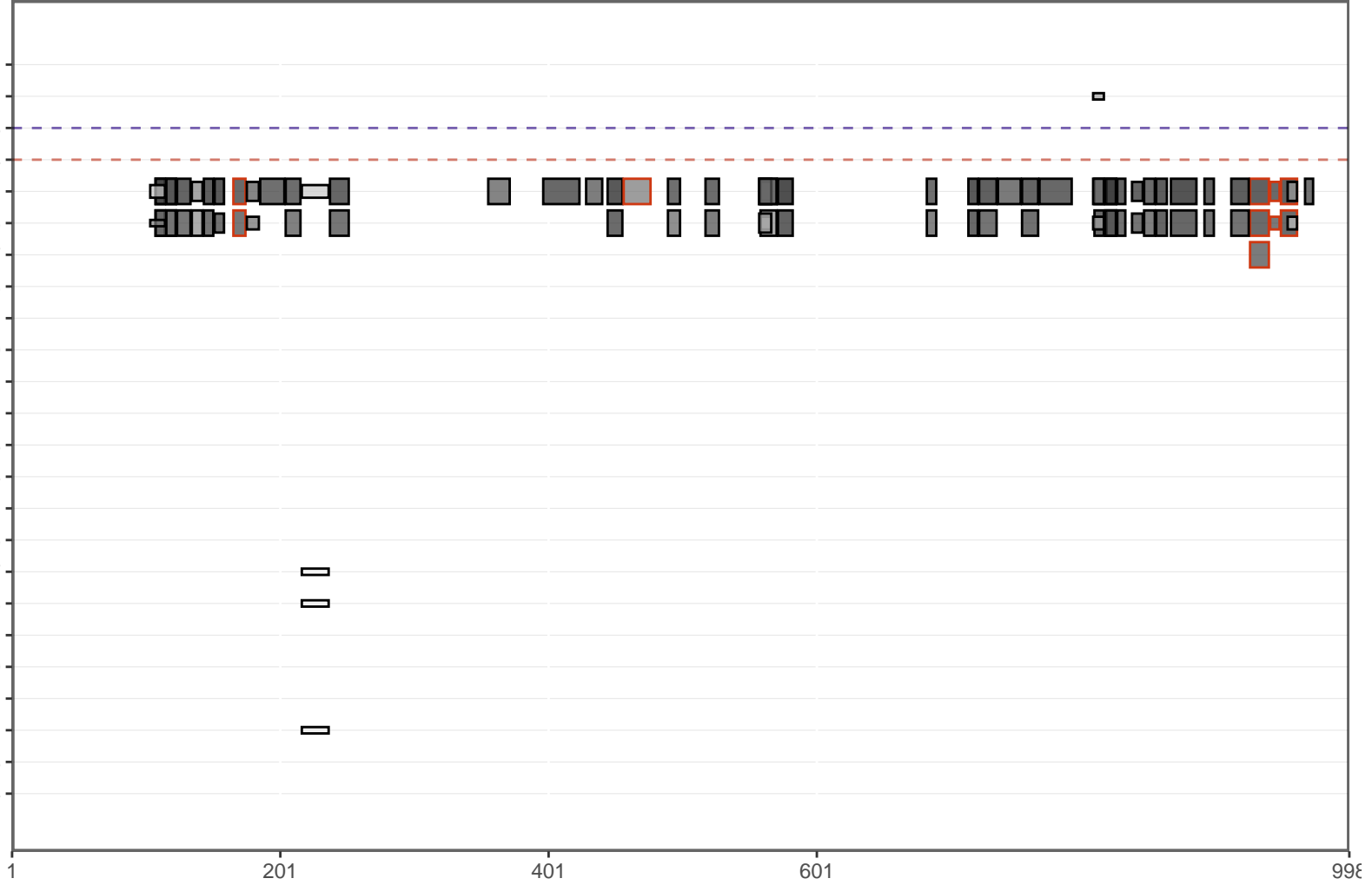
MW indication



Molecular weight

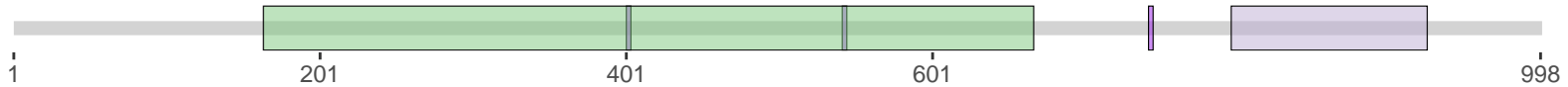


Gel Slice



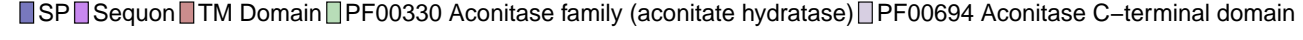
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LKEMKSDWIACLDNKVGKGFVAKVEGDKKAKFDHFGDPAELKHGSEVIAAITSNTSNFPMVLMGALWAKKASELGLHVKPWWKTSIAPGSGGVVTKYLLKGLGKYLNGGQFNIVSYGGTTCIGNSGDLDESVASISENDIVAAVLSGNRNFEGRVHALTRANYLASPLLVAVLAGTVDIDFKDPIGVSKDKGKDYVFRDIWPGTEIEAEVQSGEVLPMDFKSTYEATKGNMTMWNELVPTAKLYSWDRNSTYIHEPPYFKGMTMDRPPGHSYKDAYCLLFGD

NbL04g17910.1 beta-amylase-like [MW = 65.45 kDa]

No. of times detected



log(intensity)



Values from



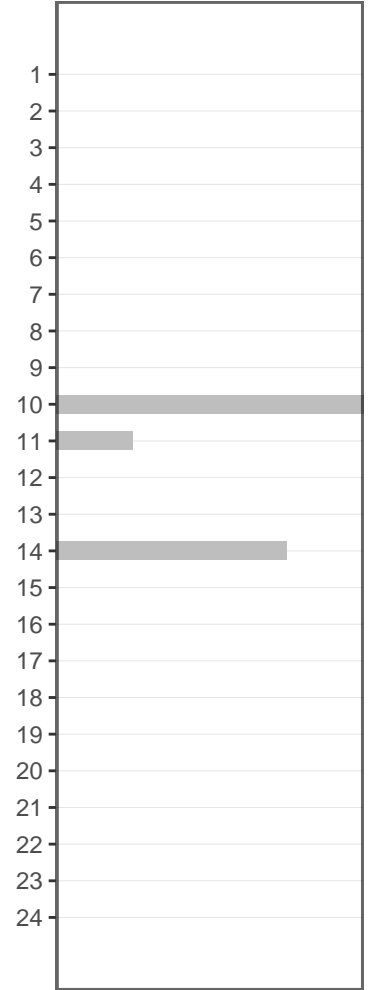
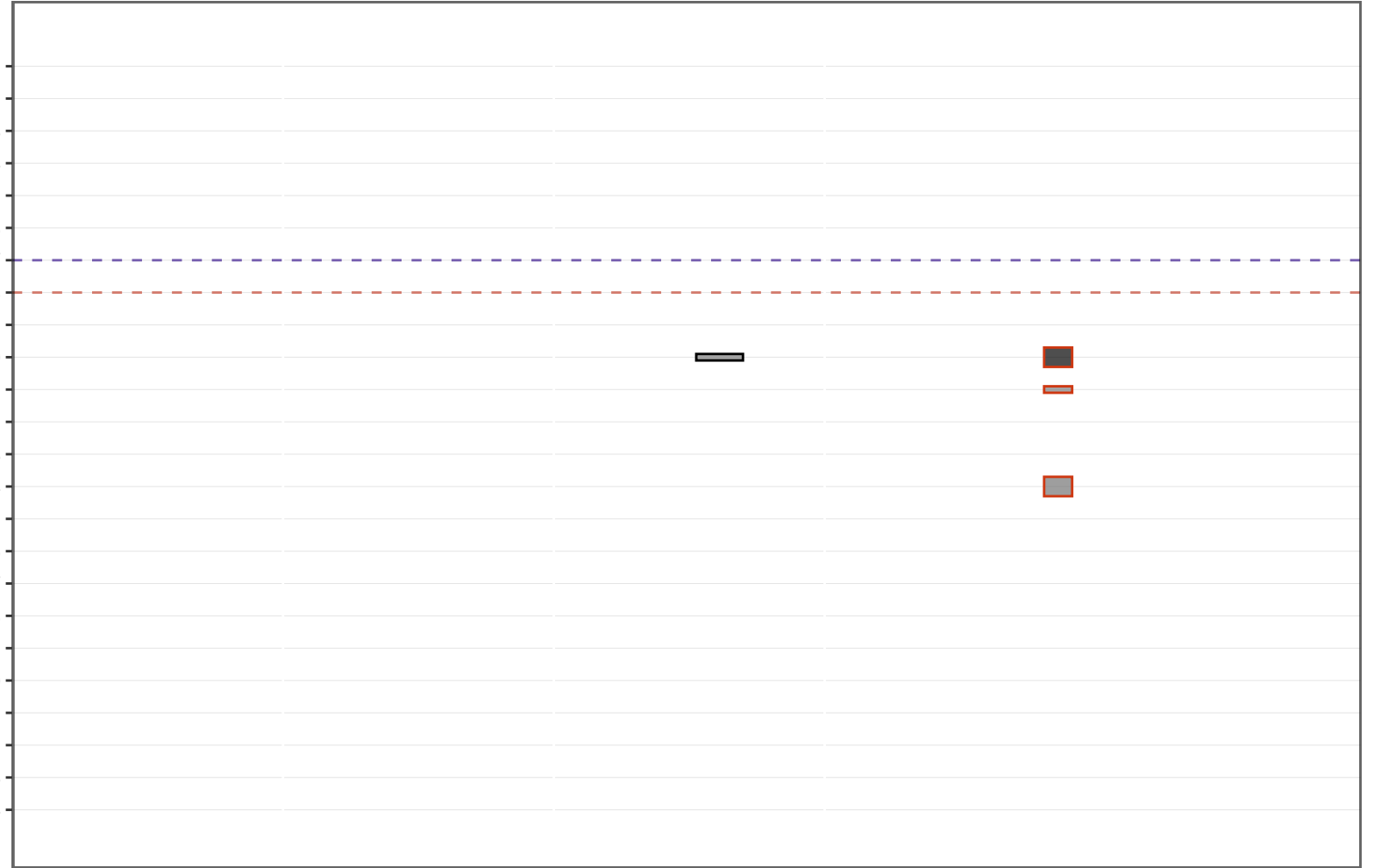
MW indication



Molecular weight

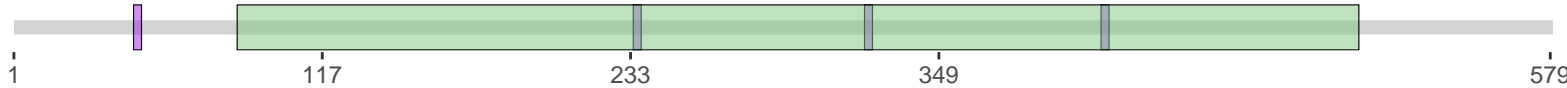


Gel Slice



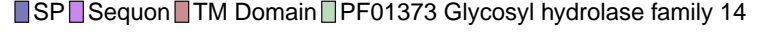
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ICYDKYMRDFTKEAVTKAGYQWDLDPDADGTYNDHPVKTFGGFGNGTYLTKKGFLLTWYSKLLHSGDGLDEANKAFLGKVKLSAKVAGHHWWKQASHAAELTGGYFNLDNRDGYRIPARMLSRHHGTLNFTGLEMRNSEQPVAKGGPQELVQGVLEGVWKENIEVAGENALSRVDSYVWNGILLNARNPQINNGPPKGMAGETYLRLSEKLLGGRFNFTKFTFVKKMHADLVYCFPEYKLAFLSRGKMEISIDELVTATQRTKPFPPWDEQTDARIGGLAEYWI

NbL04g17790.1 xyloglucan_endotransglucosylase/hydrolase_protein_9 [MW – SP = 31.48 kDa]

No. of times detected



log(intensity)



Values from



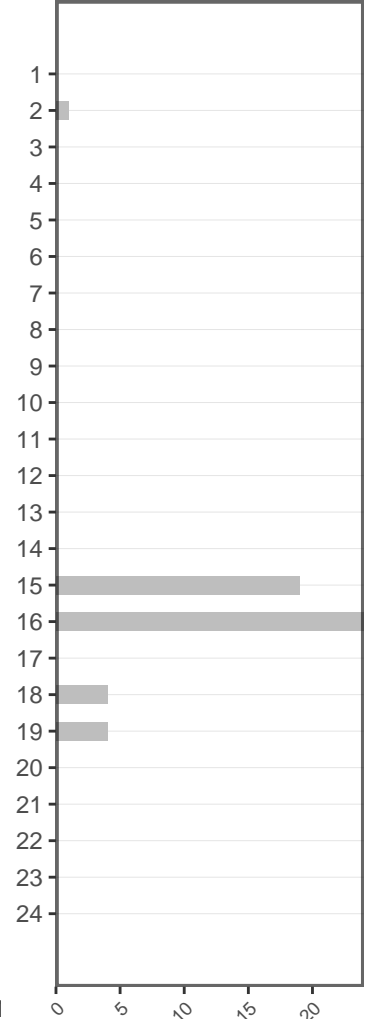
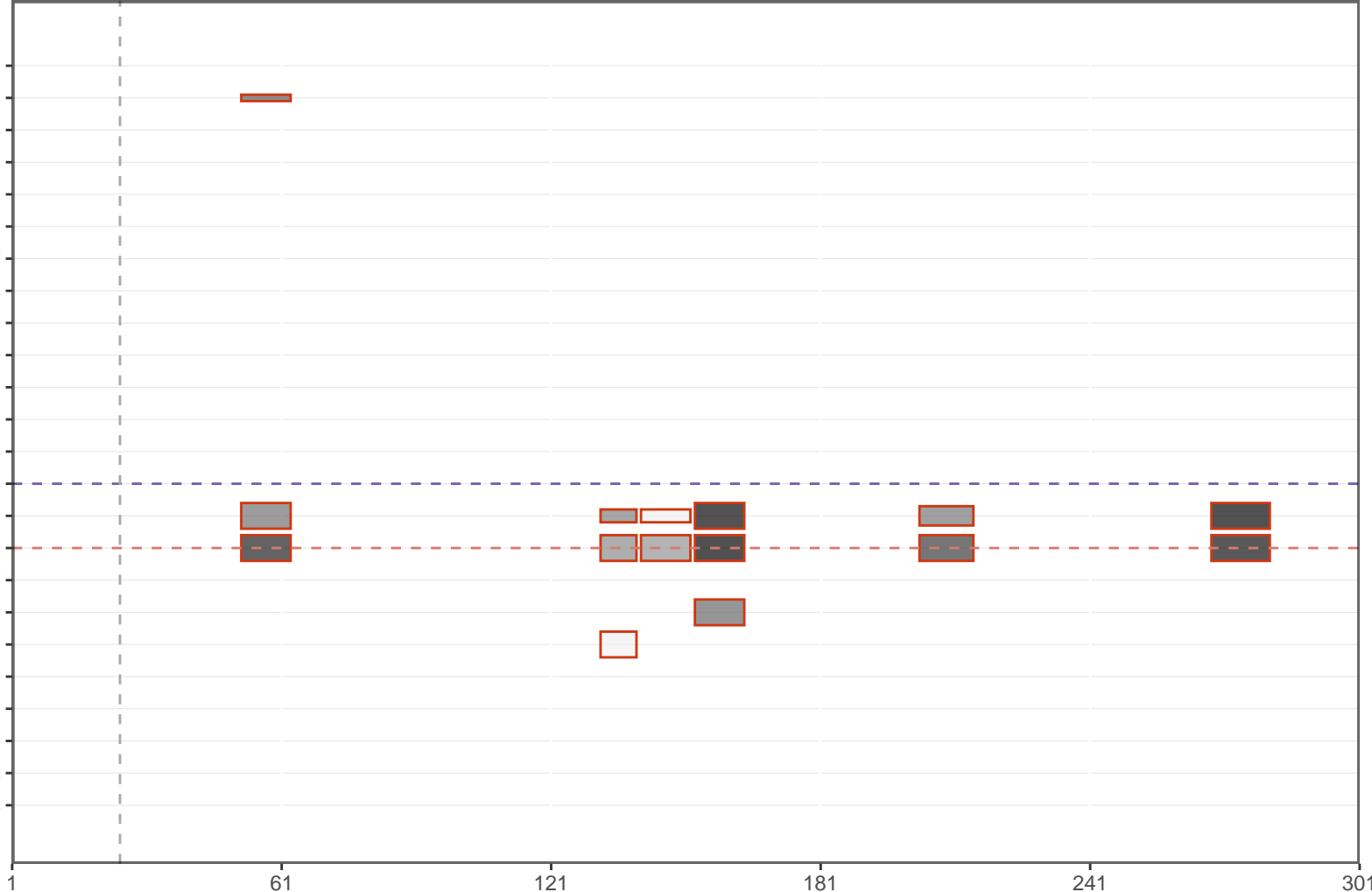
MW indication



Molecular weight



Gel Slice



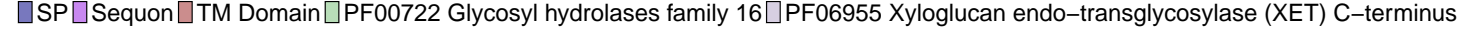
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SKEFHSYLSLWNCRQVFLVDTPVRRHSNLEHKGIFFPKDQAMGVYSSINADDWATGGGRVKTQWHSAPFFVASYRGFEDGCECPATVAAENSKRSGSTAEKRYWWDDEPTMSELSLHGSHQLWVRANHMVYVGTDTARFPVAPVEGQHGHKHKTRN

NbL04g17670.1 frataxin_mitochondrial [MW = 22.86 kDa]

No. of times detected



log(intensity)



Values from



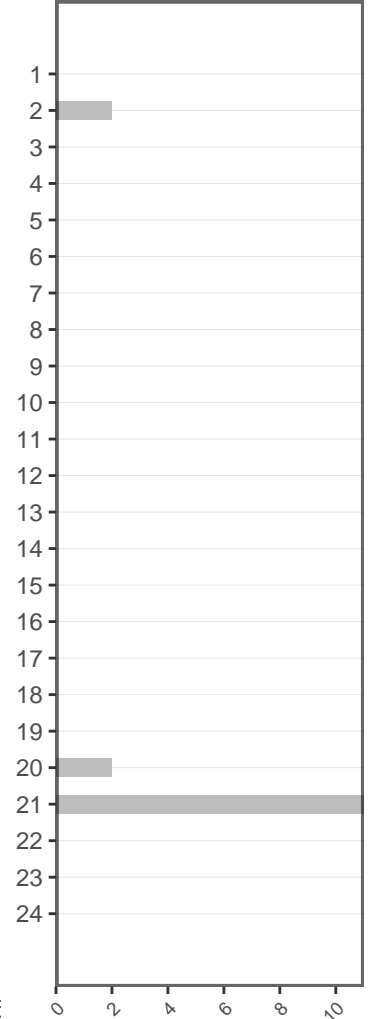
MW indication



Molecular weight



Gel Slice

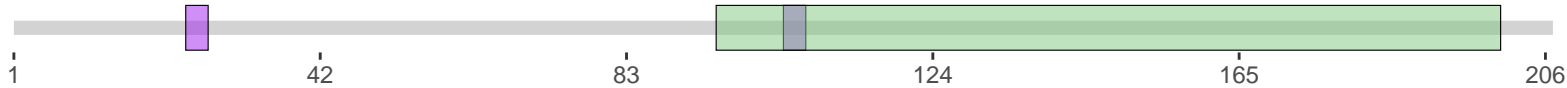


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

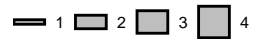


Protein sequence:

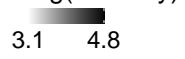
ISLLQEDYHRLANATHHLLDLKLEKDGSDVDIDGFDVYDYGNEVLFKLKLDLGTYYWIKQTFNRQIWMSSPVSQPSRFDFWDQNSQGWYRRRTKANLRTVLEDELEKLGSAITLS*

NbL04g17520.1 uncharacterized_GPI-anchored_protein_At4g28100 [MW – SP = 31.99 kDa]

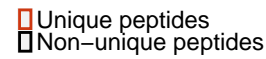
No. of times detected



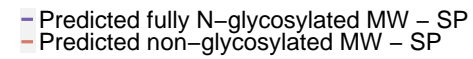
log(intensity)



Values from



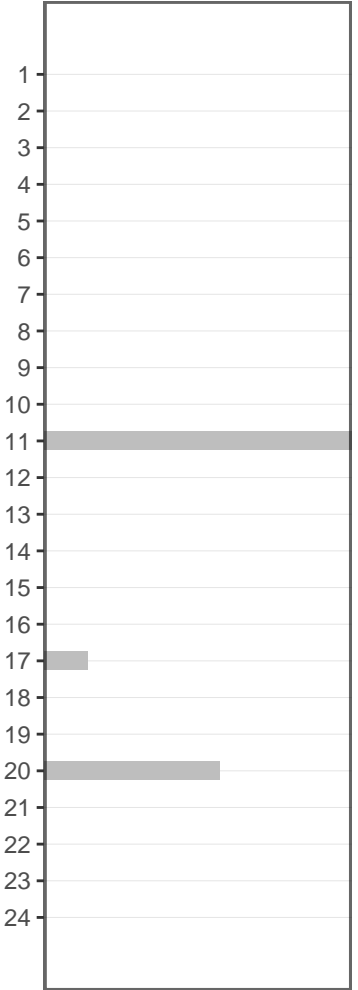
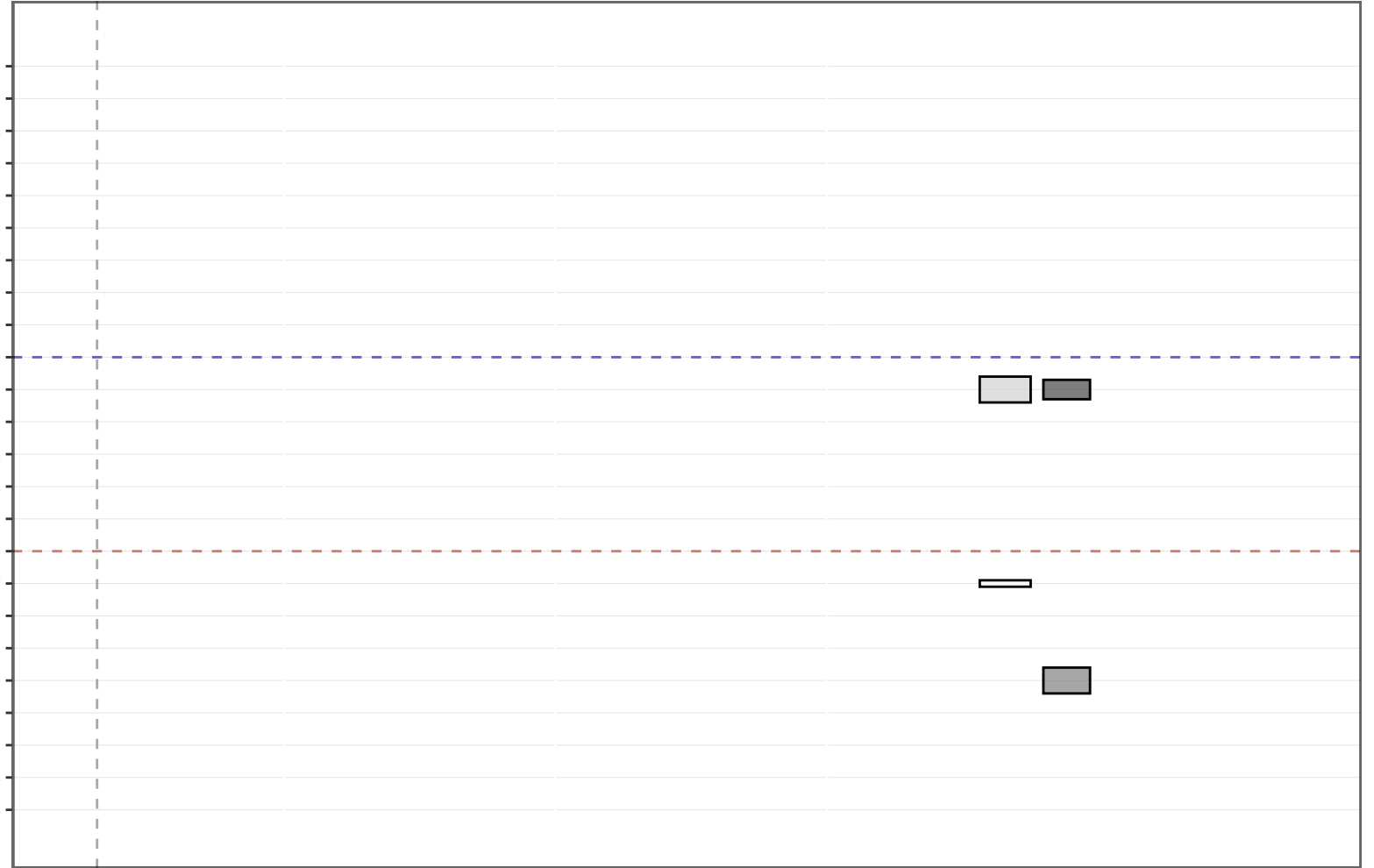
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

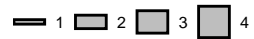


Protein sequence:

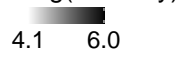
LCFCGRLHQITSLSGPAMFNLGSKNATPTAAVNRNLERNGRNSVGGCTRLGALGKLNDDGKRRTHKMDVIGGDRVSKMLTRDCQLMGLTWLARNKTAHPITVSAVLRRAIMVYSHPHHEKCSFDGEMPLAVDSLQFEKTDGSPSPGVSERFAIFFPMLILLNLYLFG

NbL04g17500.1 protein_THYLAKOID_FORMATION1_chloroplastic [MW = 33.94 kDa]

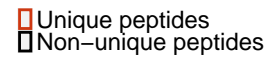
No. of times detected



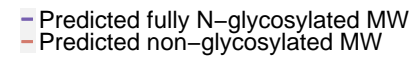
log(intensity)



Values from



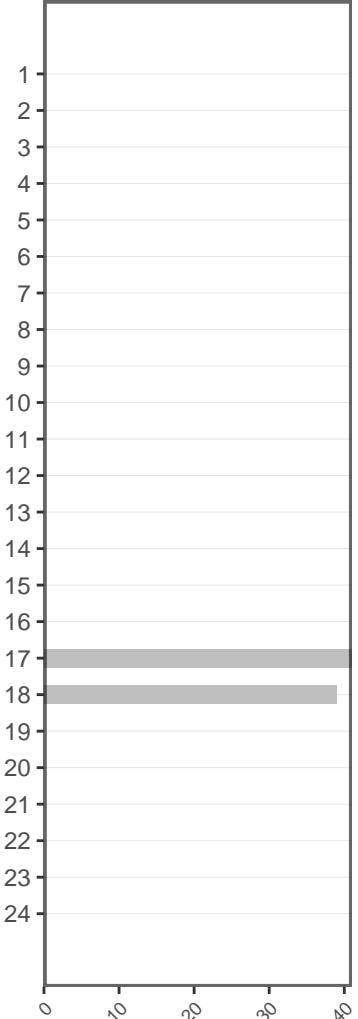
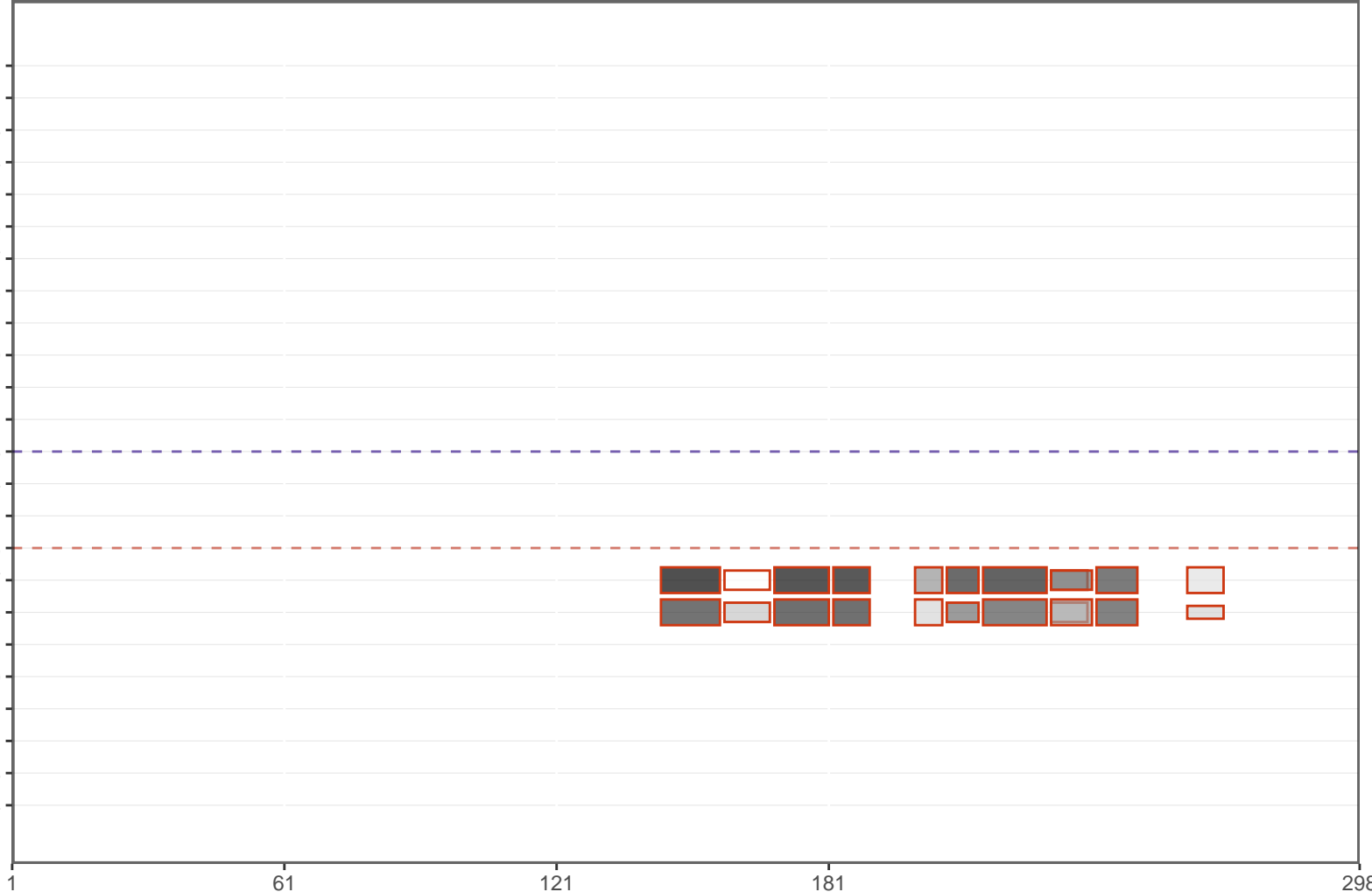
MW indication



Molecular weight



Gel Slice

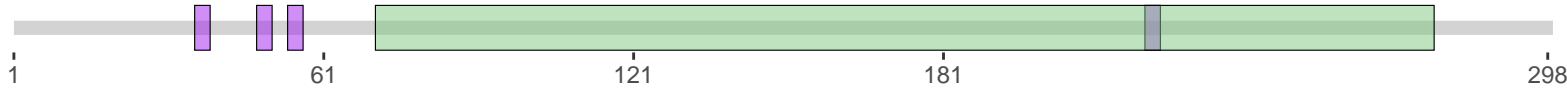


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IEDRDAIFKAYIEALNEDPVGVRADAGKFEFEWARTGNANTLDFDSRDGVEVENLKDADRAGTKDSFQYRLLFAVGLFRLLLELANVTDPFLKLGASLNKKGVDRDLQVYRNLKSLVDAKELLKKEYVEREKKKRGERESQKANEVTKLGLGDQVYAGR

NbL04g17440.1 fasciclin-like_arabinogalactan_protein_7 [MW - SP = 25.77 kDa]

No. of times detected



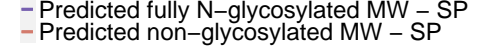
log(intensity)



Values from



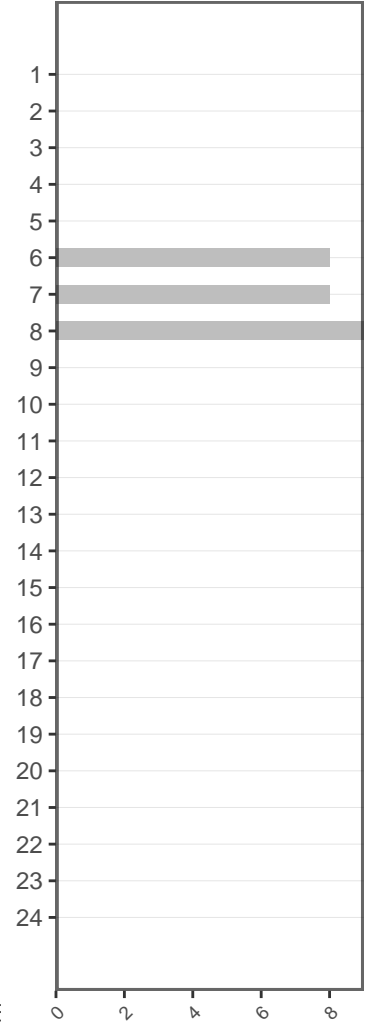
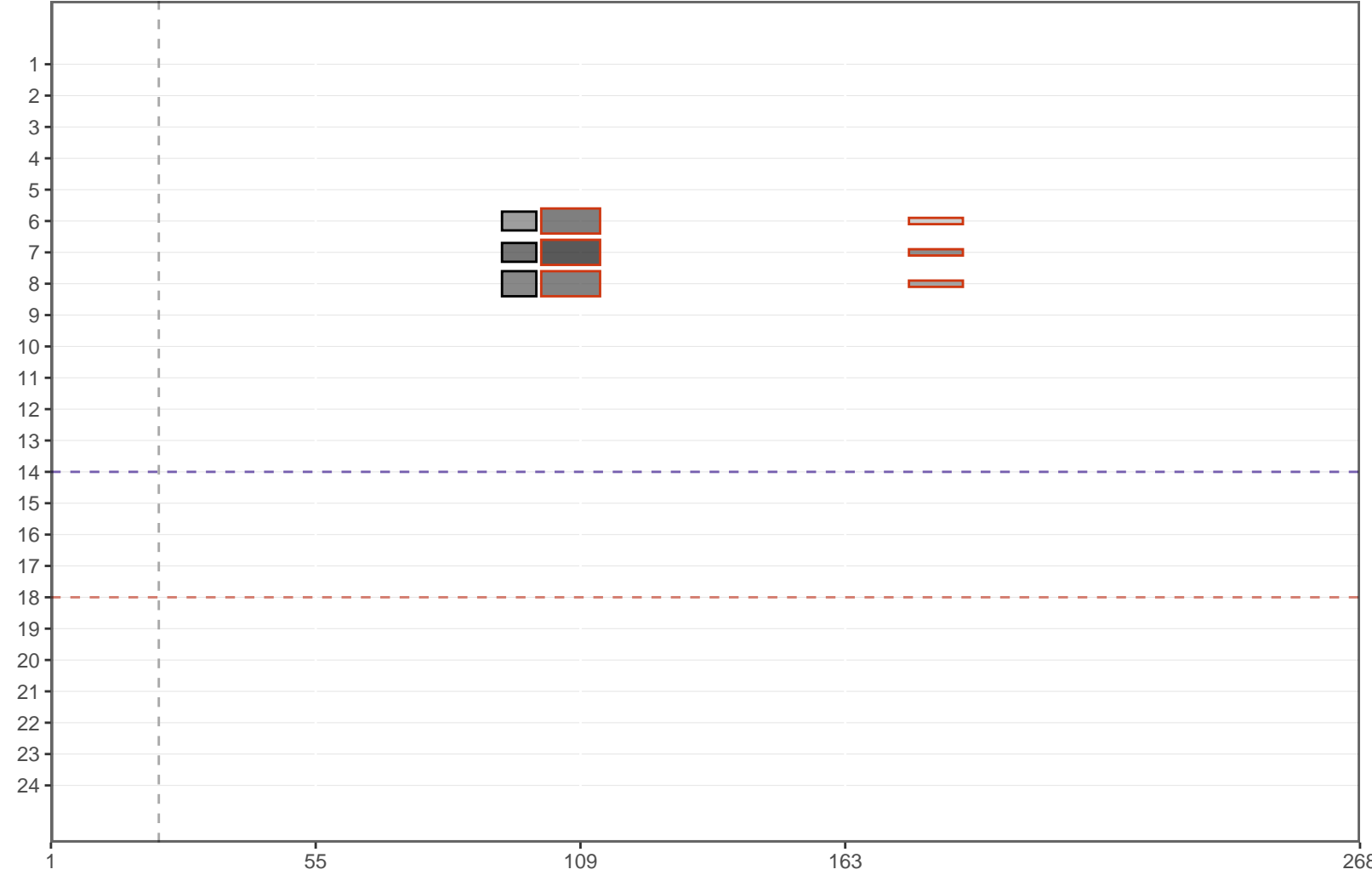
MW indication



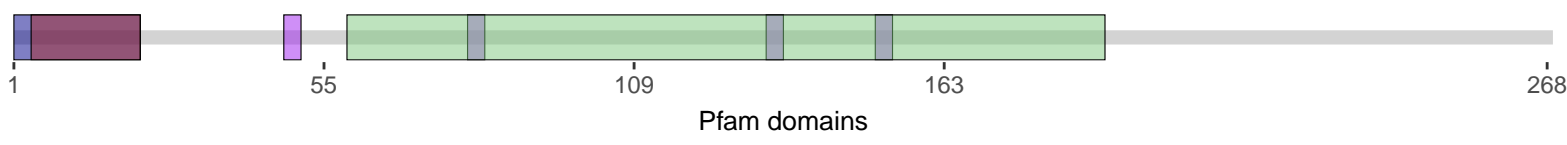
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

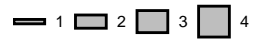


Protein sequence:

HYSLADFKNLSDMSPNTFAGGNLYSLNFTYDGGTVHLNSGWSRRTKYSVAVRATFPVAVYQVQKVLFEAFGTDLPPMPAPAPAPETDAPTADSPAADDTGKARAASSPDSPPSASHRMMMSWGLNHLVLIAGGFLMLL*

NbL04g17290.1 plant_UBX_domain-containing_protein_4-like [MW = 42.64 kDa]

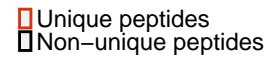
No. of times detected



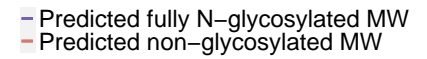
log(intensity)



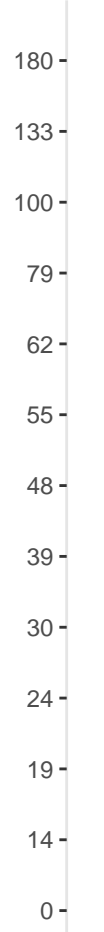
Values from



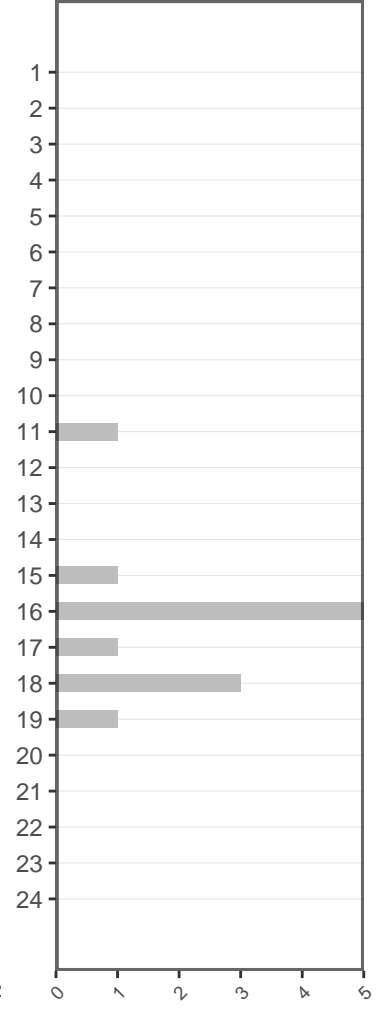
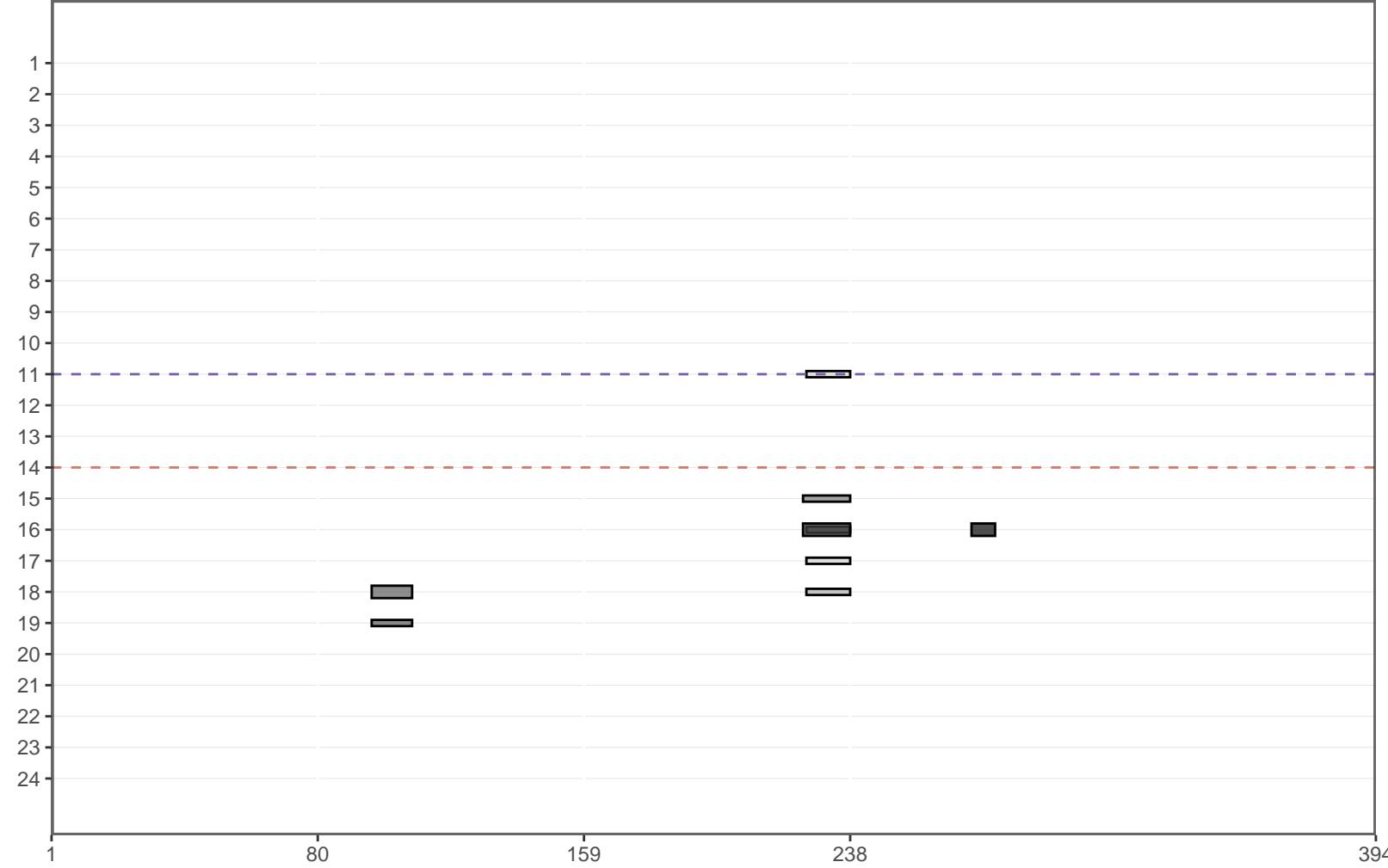
MW indication



Molecular weight

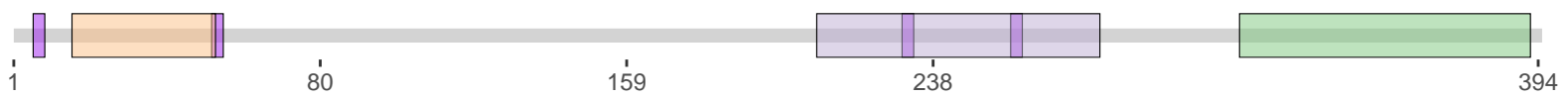


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SGTARRLTGETVSAAPQPPESRTHVTFWTFNGFTDDGFLRRFDDEPENASFLGIRKKECPKELEPEDRRRTSVRVLNTRREEDGCPVPEKRRATFGVGRRLGSTNSAEGVDGIGAVSSEFTAAPTPSEVLVDDGSGTSTGILRLADGTRMVRFRNFQHTIRDRGFDASRPGGPRGKLTGTVGFPFKQLGDLDTGEGAGLANSVVIQKL

NbL04g17270.1 pyrophosphate--fructose_6-phosphate_1-phosphotransferase_subunit_beta-like [MW = 60.48 kDa]

No. of times detected



log(intensity)



Values from



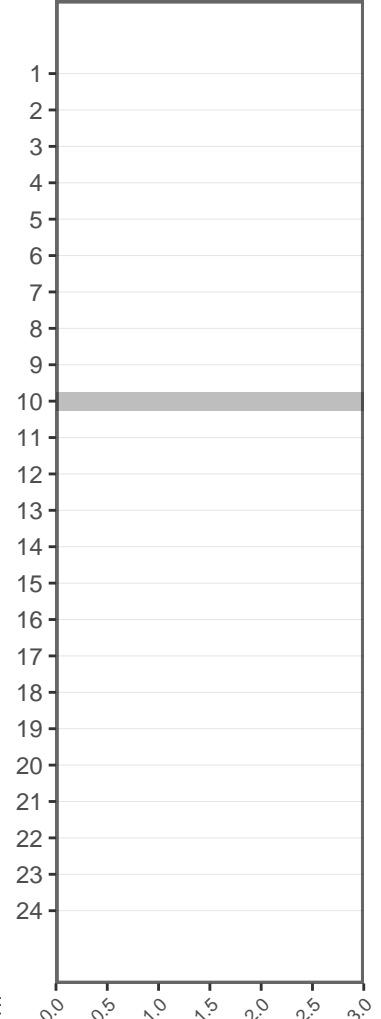
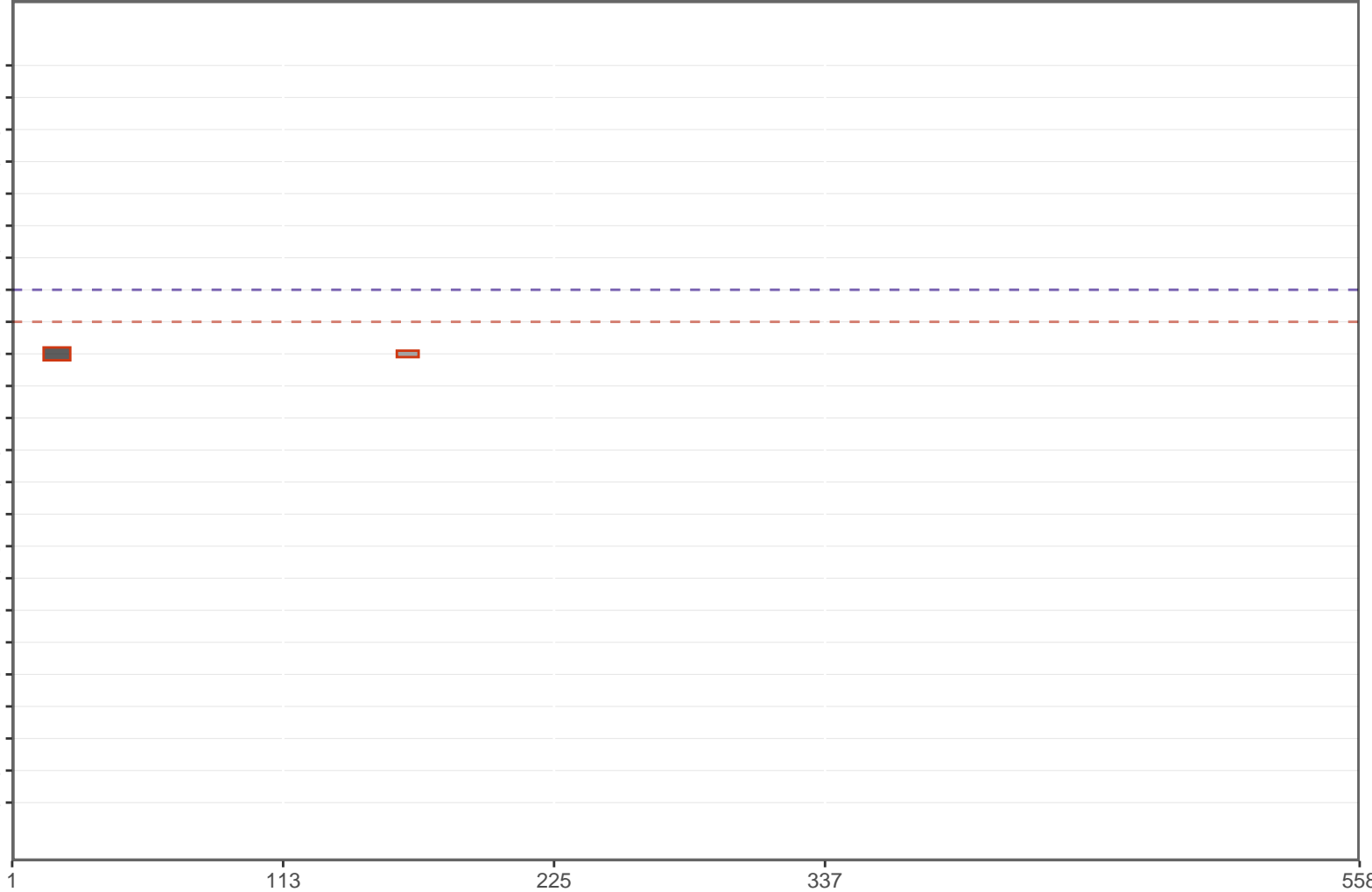
MW indication



Molecular weight

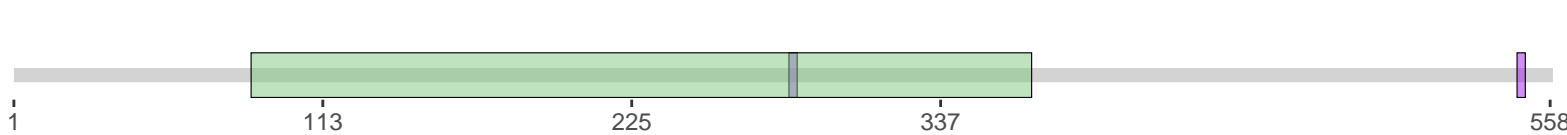


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

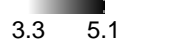
IGRAASHITLICALGTHPNITGEEVAAKQGLKSVTDYVWGHCKRAKLGYNVYVILPEGLHDFPEVQGLIAELNELANDVDEAGNWKLRBSQHELFEFLPAQDEGLLLERDPHGNNVQVANKETKMLIQMVEALENKKEGYSYTHKFKGQSHFFSYEGRCGLPSNFDNRYVALGYGAGALLHSGKHELISEVGNLRAPVLEDVTVGGTALTSLSMDVERRRHGKFKPVRKAMVELDGAPRFKFSALREEWALKNRYFSPGLQFVGPITANEINHTLMLELGAKA*

NbL04g17180.1 heterogeneous_nuclear_ribonucleoprotein_1-like [MW = 49.76 kDa]

No. of times detected



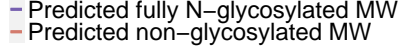
log(intensity)



Values from



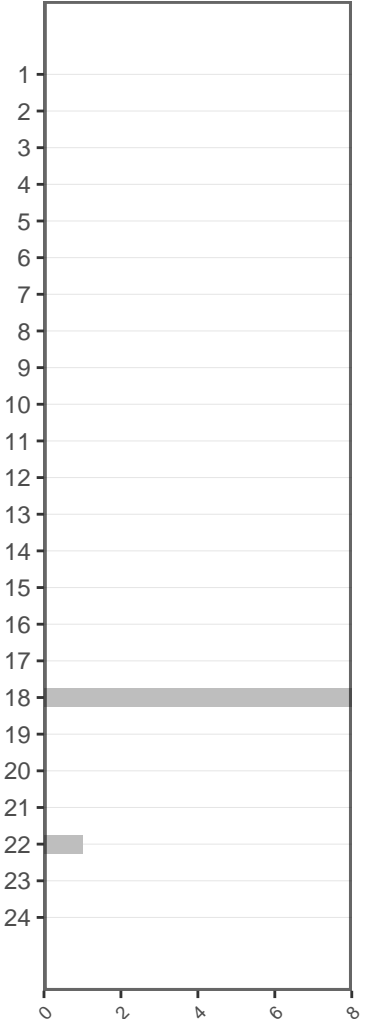
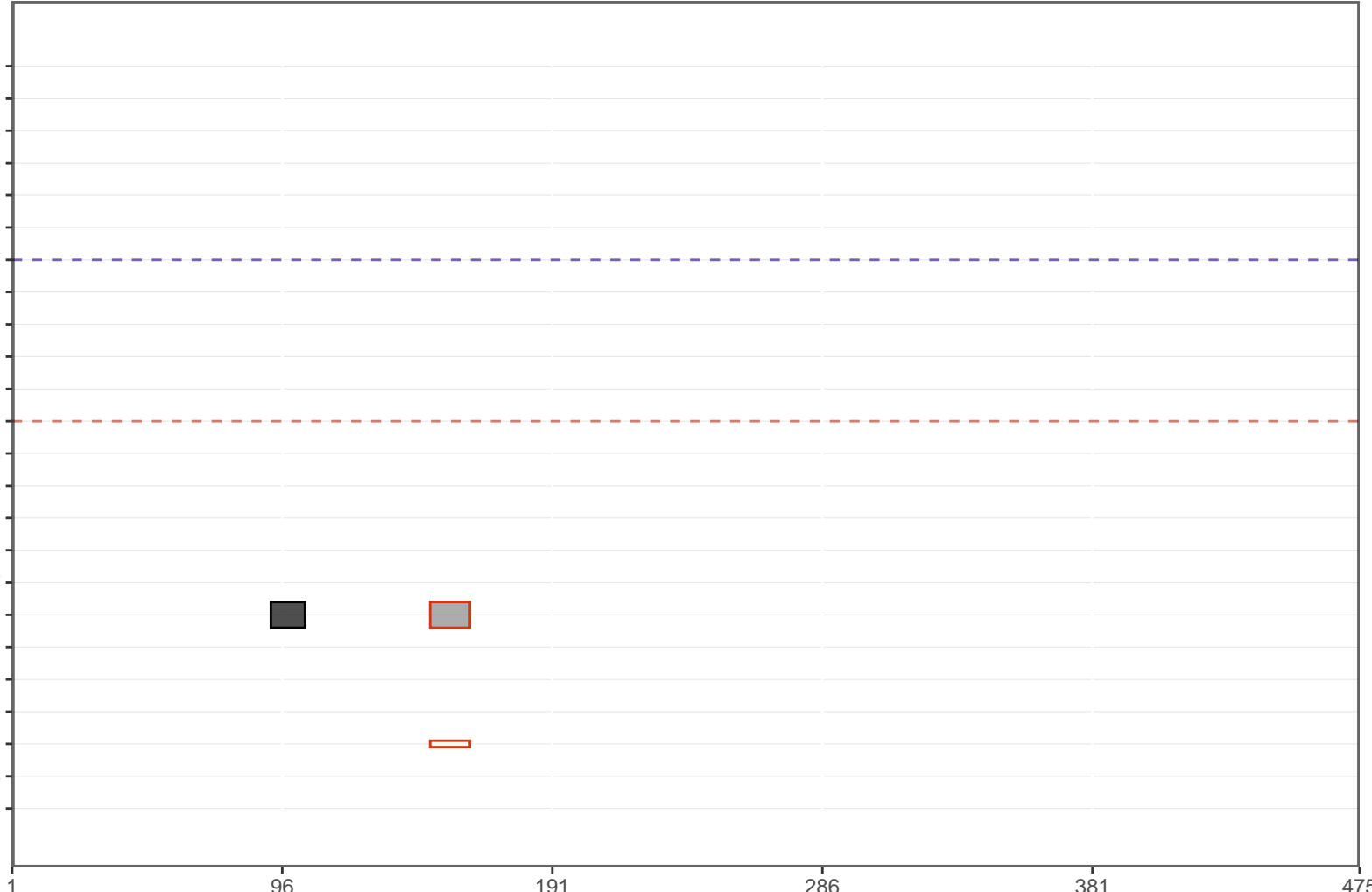
MW indication



Molecular weight



Gel Slice



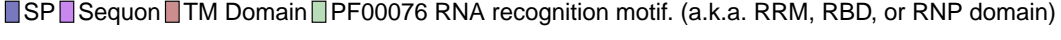
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FSPIAQRSGFAGFGSGYGMGLNFEPLGPGYGGNANFN6SLVYGRGMPPYYVNSNRFGGPGFDGGNGGSS6FFSATRNWGNGLGYGTN6T65NFVAVGSGNMGAGNFENTGVVGS66IS6GGGGANVSN6GNLGYGGDDTLVGL6GGYGRNVTTSGAPAS6YPA6NS6YD6GALADLY6GGLGY6SD6WR6AN6SER6D6G6S6IGYGL6T6P6MPP6AS6Y6G6Y6G6K6R6T6R6IG6D

NbL04g17030.1 heat_shock_protein_83 [MW = 90.16 kDa]

No. of times detected



log(intensity)



Values from

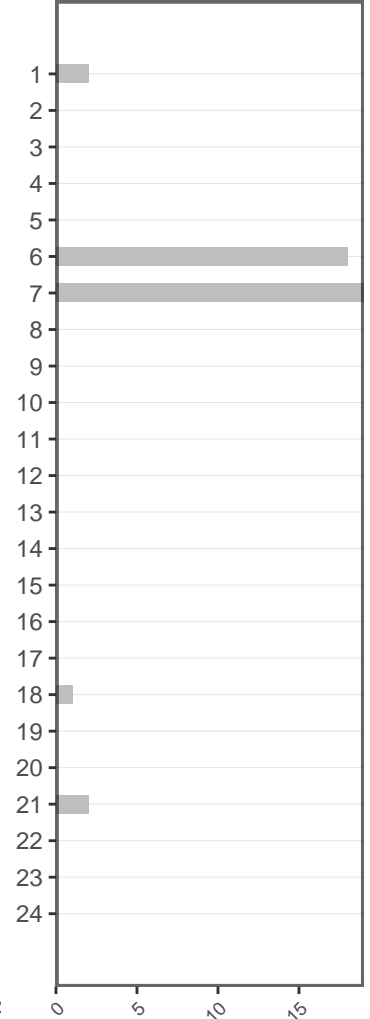
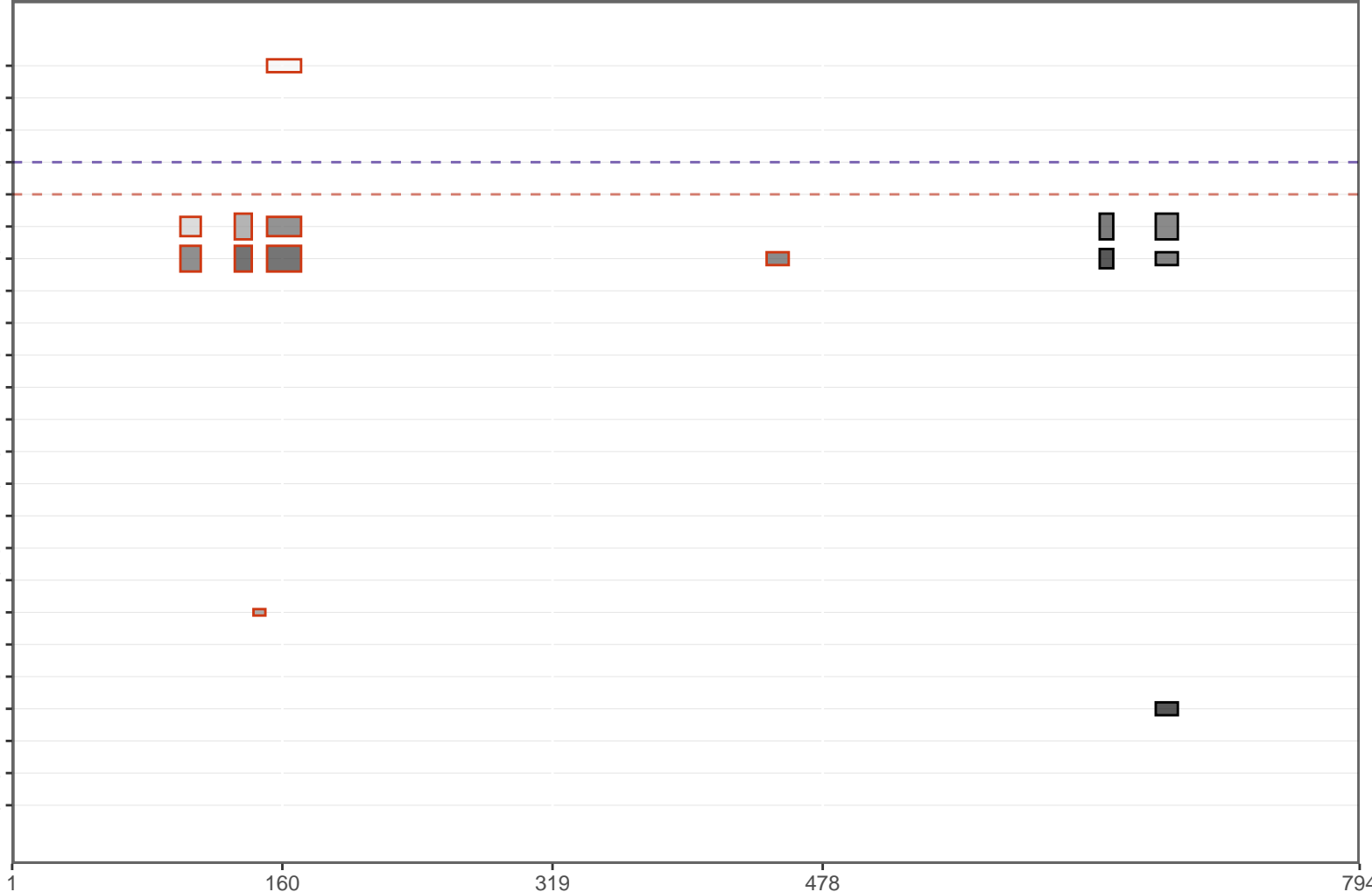
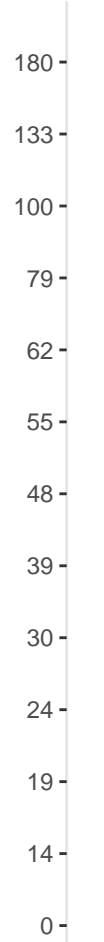


MW indication



Molecular weight

Gel Slice



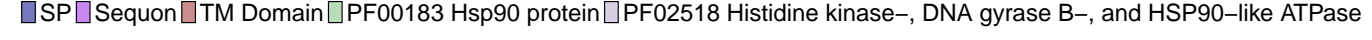
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SHFTTEGEVEFRSIVYPEVSSMGKGDVNPKNTRNIRLVWRVIFSDDFGELFPRVLFKIGVYVDSNDLPLNVSRILGSRVVRIMKKRLVYKAFEMGGISLSENKDDYKFWENYGRHLKLGIEDRENKKRLAPLRFSSGGSEDFETISLDEVYENMKPDGKDYVYASDSITSAKNTFFLEKLEKDLVFLVDPIDEVAIGNLKYKFNKFNVSKEKDLGDKNEDKEKEKDFEGQGTGDWIKKRLGDKYVAGVQINRLS66PQVLVSGKFGVSWANMERLMAKQVGD!

NbL04g16800.1 low-temperature-induced_cysteine_proteinase-like [MW - SP = 48.94 kDa]

No. of times detected



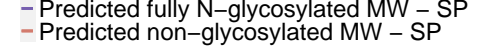
log(intensity)



Values from



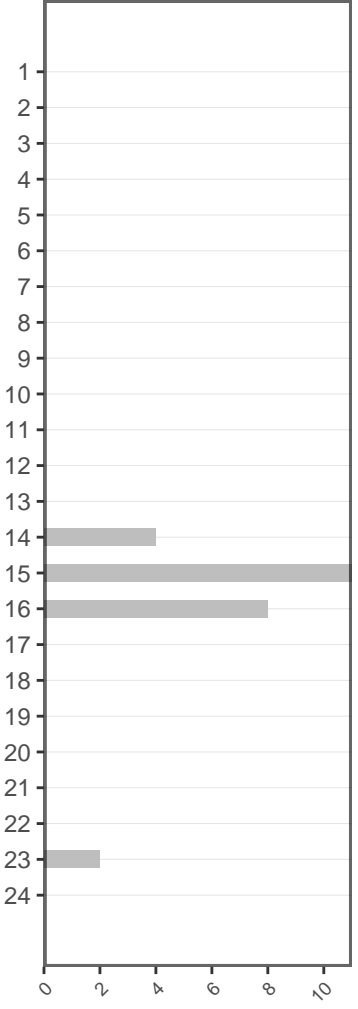
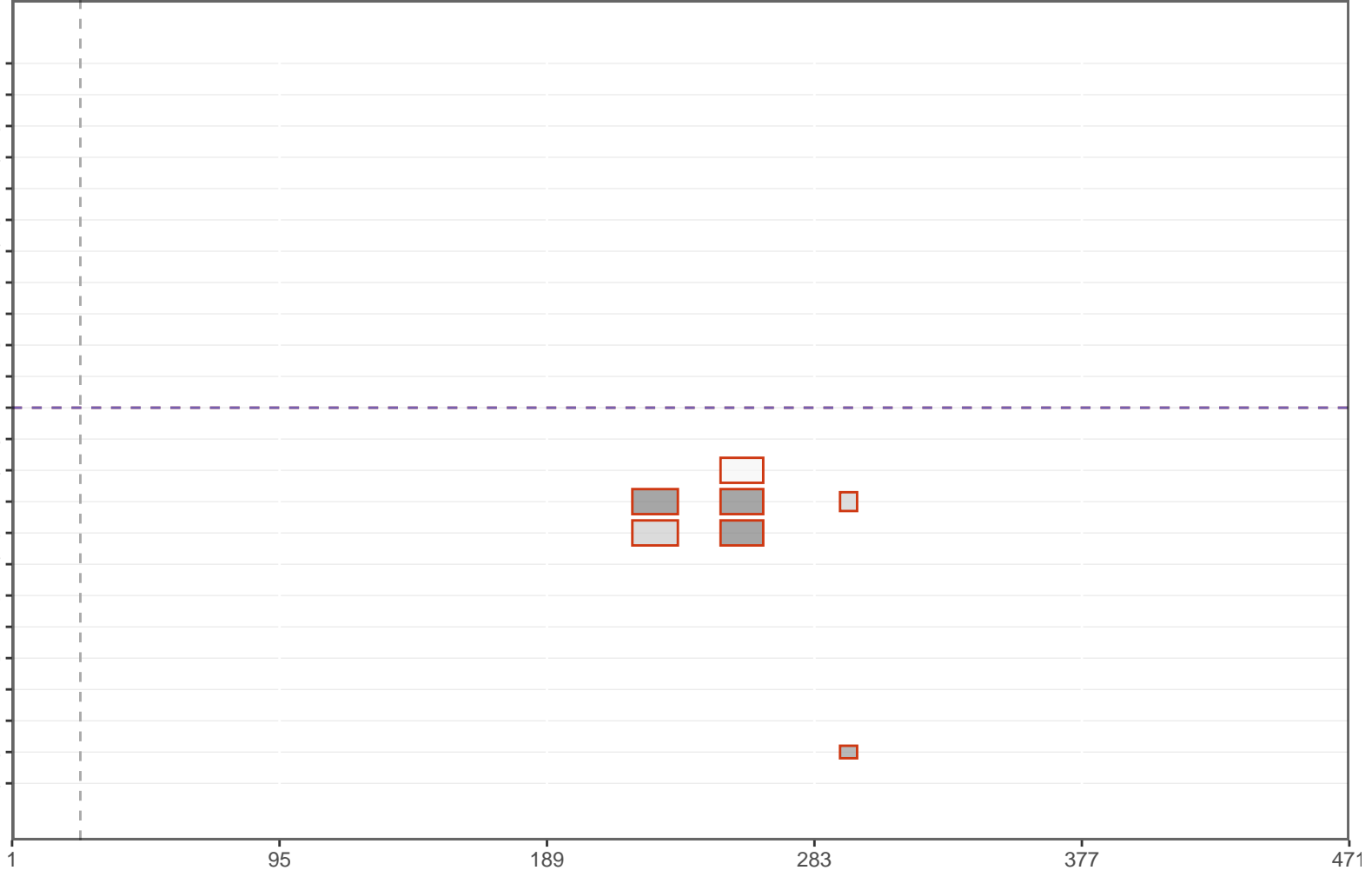
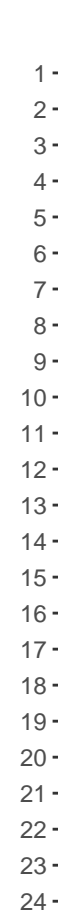
MW indication



Molecular weight

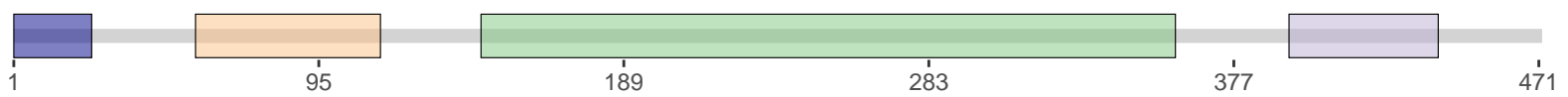


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

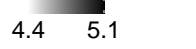
IDTEEDYFYKAKDGGKDDQARKNARVITDMYEDVPADEKALKKAVAGQFVVAIEAGKDFQHYKSGIFTCGKGAEVHGVVAWVYGVSENGMDYVIRINSGWGAISVSENGVYLRMQRNIGNPKGLGGATIASYPVKTGQNGNPKPKPSPFPSPKPKPTGQDNNNECPAGTTCGCVYKYYKGFVWGGCPMEGATGNDHNSGCPHDYFVQCNKAGTGSISKNPLGVKAMQHLAKPIGTFQNEGNM

NbL04g16640.1 phosphoglycerate_mutase-like_protein_1 [MW = 31.4 kDa]

No. of times detected



log(intensity)



Values from



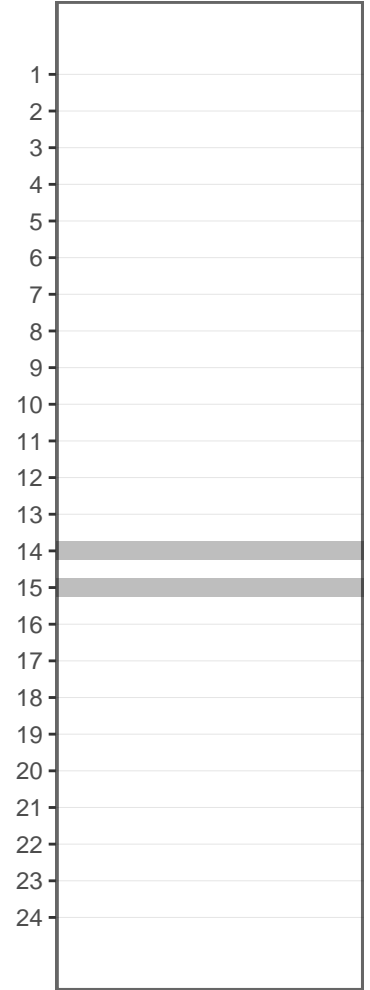
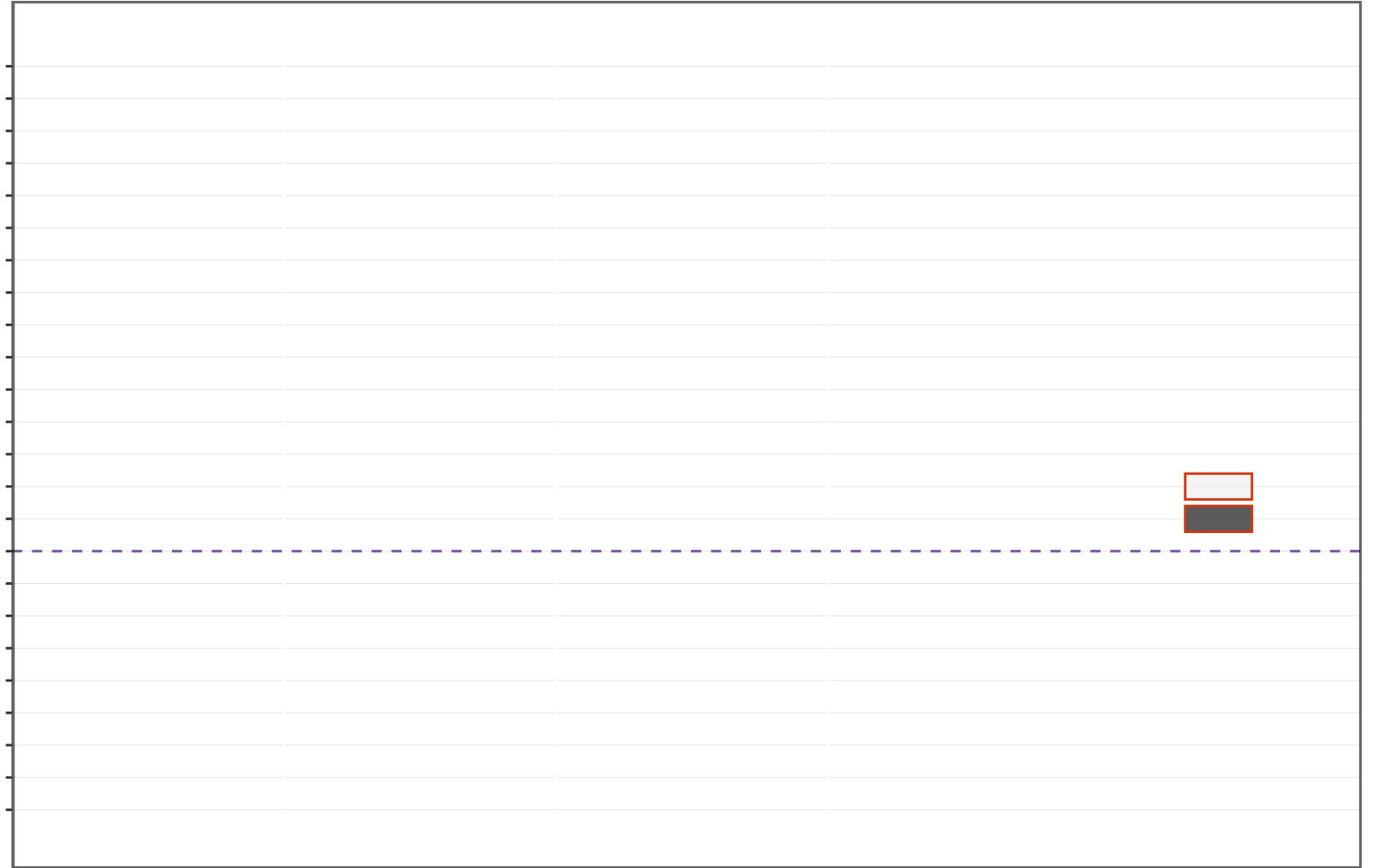
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SVECCREHLGVYWGDKRRBSEYKPLFMDLSLIEGDDDLWEFDIREPNEHLASRGMEFLKWLWTRKEKEAWVTHSGFLIHLTSAFGNDCHPDVNDKICRFFNDELRSMMVDRGMIGSD66STDDYPKPKPSGVDEVPDSDDTGNIHPDGLLN

NbL04g16410.1 protein_DCL_chloroplastic [MW = 26.26 kDa]

No. of times detected



log(intensity)



Values from



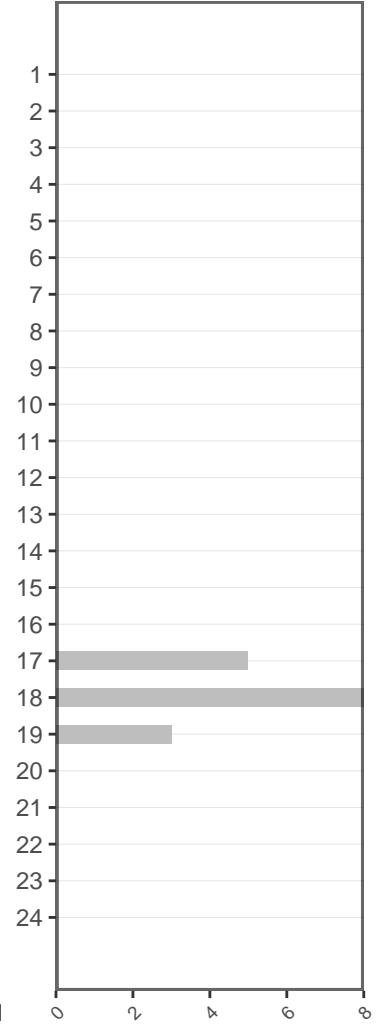
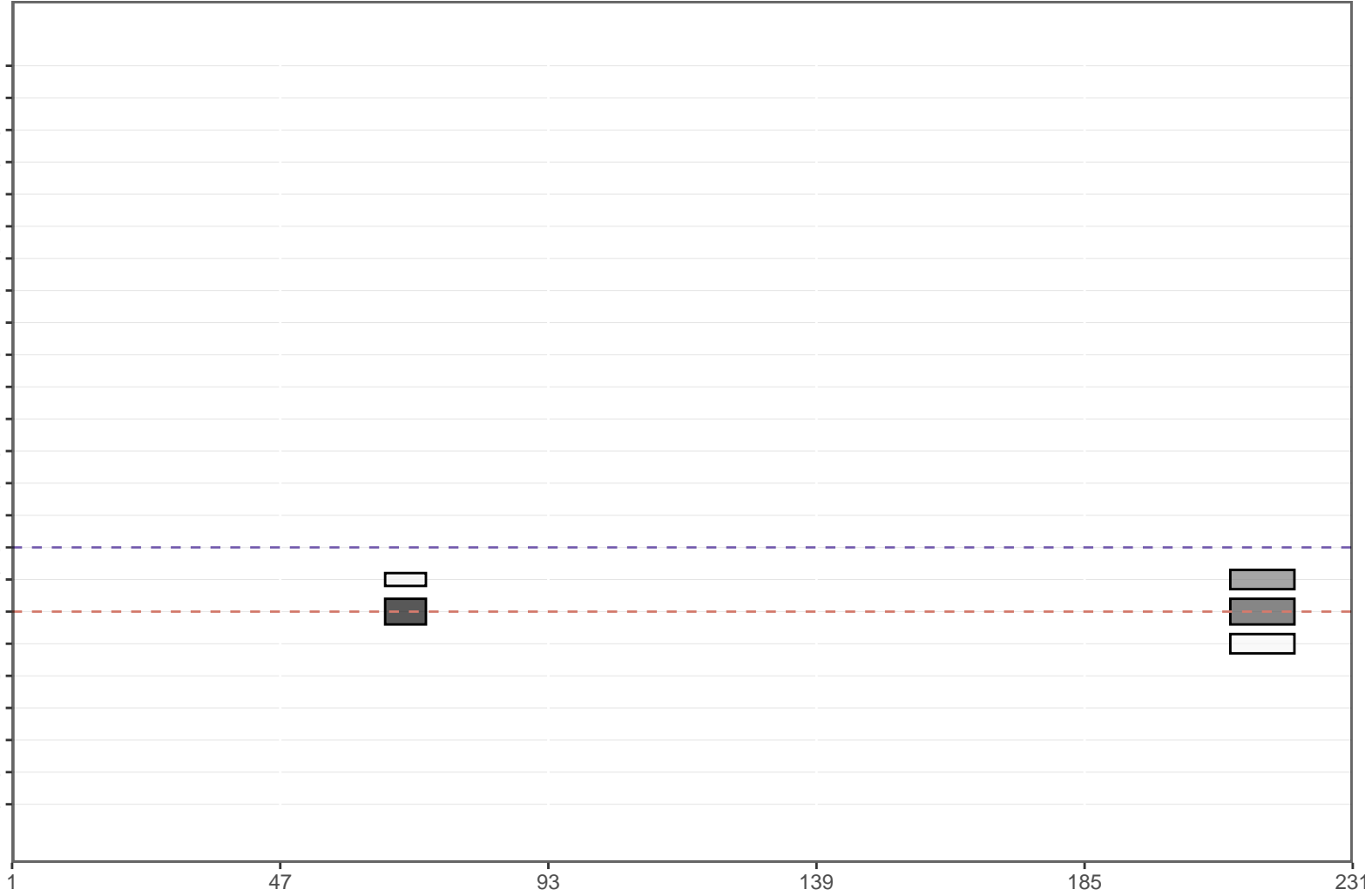
MW indication



Molecular weight



Gel Slice



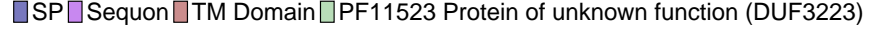
Protein length



Pfam domains



Pfam Description



Protein sequence:

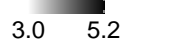
NGDEQNWDVDEGLEDVPLVGFVIMLHSGKAVGDRLSPDHQRTILGRLLPYPHPECEKIGSGVDVITVGVHPDFESSKGLFIVRKDGELVDFSGVWKGKGLRKNYPLVADGFLRHFRRRRNDP

NbL04g16340.1 thioredoxin-like_4_chloroplastic [MW = 24.44 kDa]

No. of times detected



log(intensity)



Values from



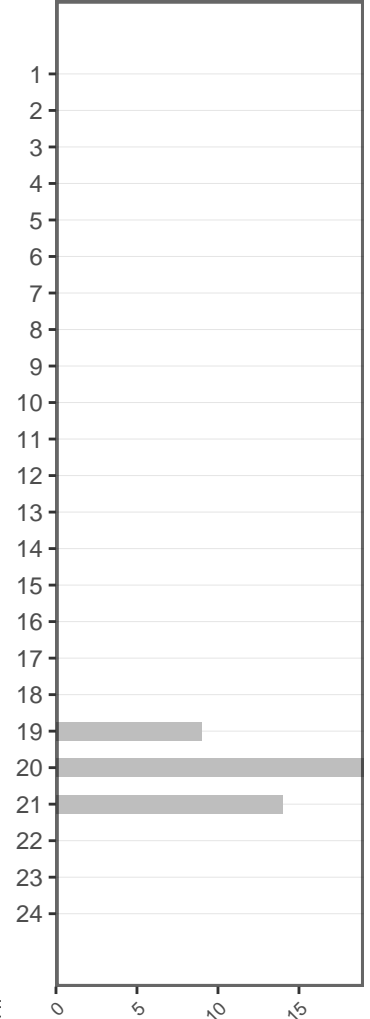
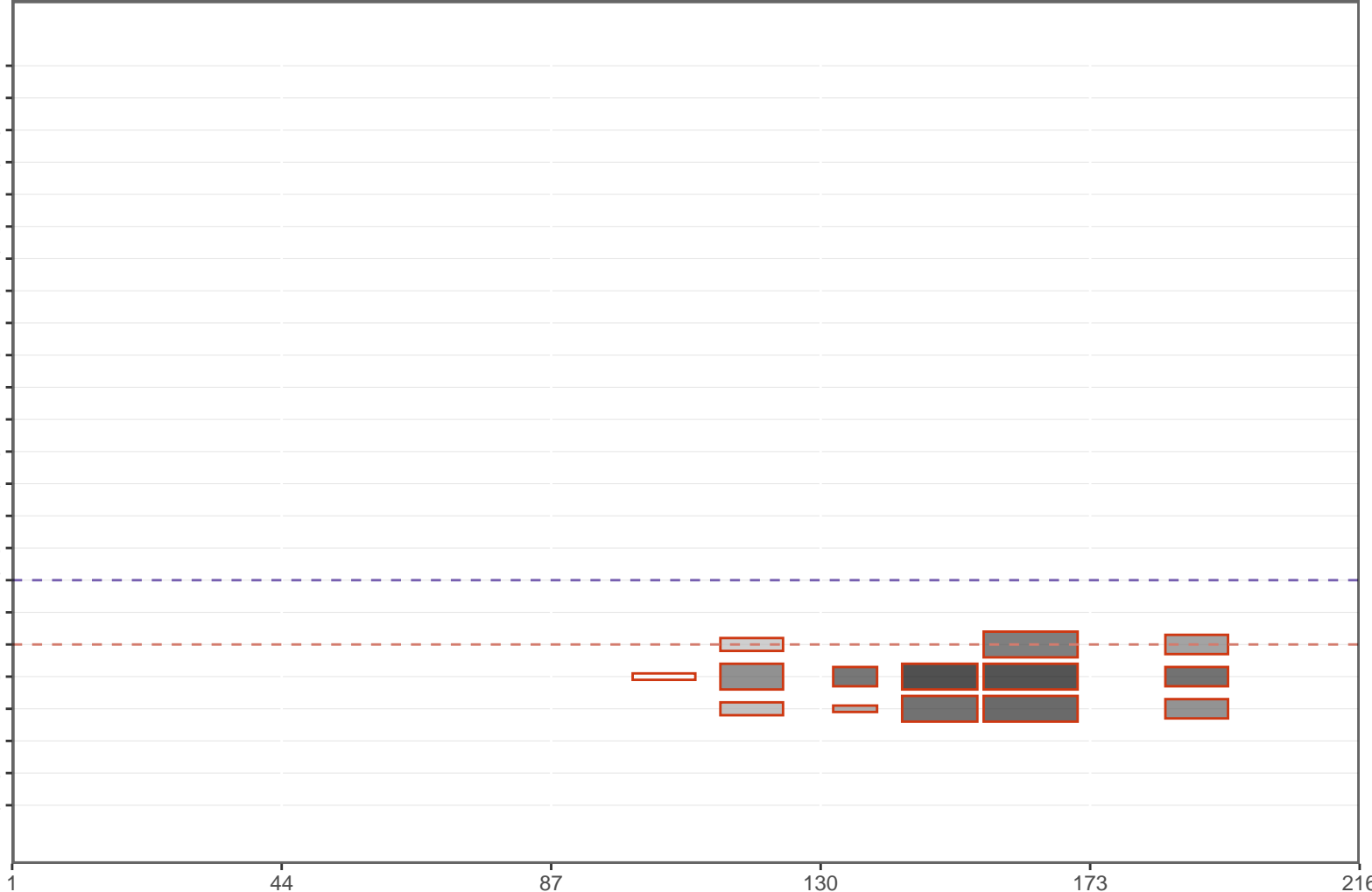
MW indication



Molecular weight



Gel Slice

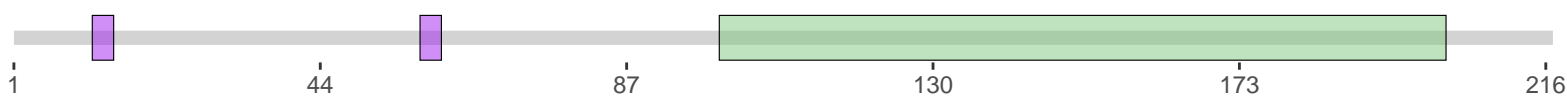


Protein length

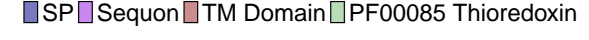


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ICVREFKTDDEFFILEKAKKAGSLVVDFYRTAGSGSKYEGGFAMLRGAGDDEQAPVFLKHNVIDEYDGGSEVAERLRKTVPLRHFYKNGVLLFAFTRDKERLAAALKYAPASADA

NbL04g16320.1 non-specific_lipid-transfer_protein-like [MW = 13.76 kDa]

No. of times detected



log(intensity)



Values from



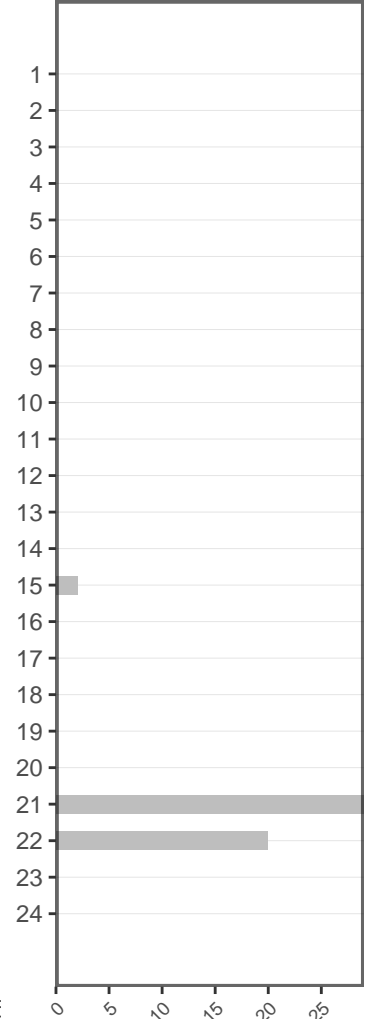
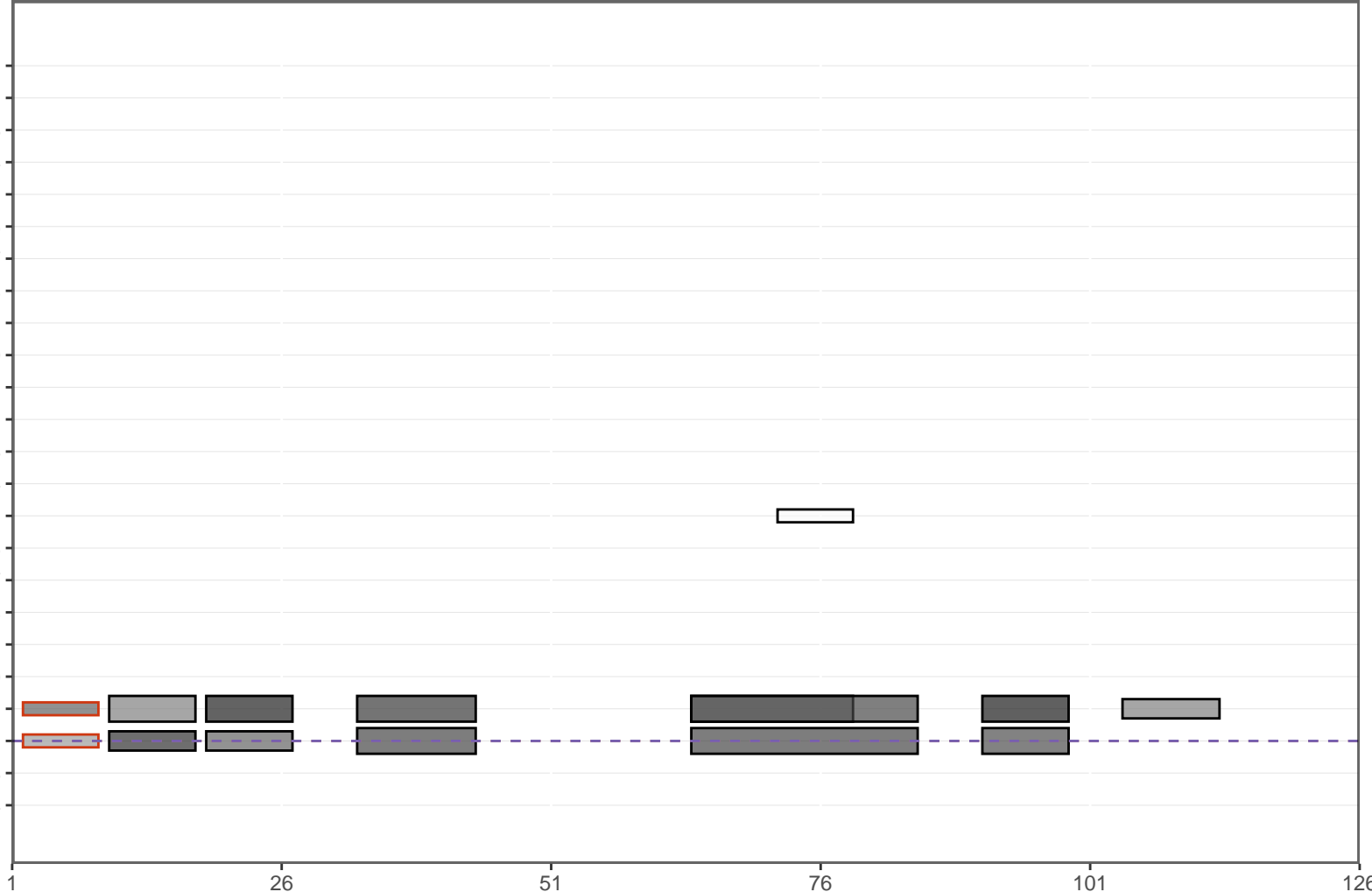
MW indication



Molecular weight

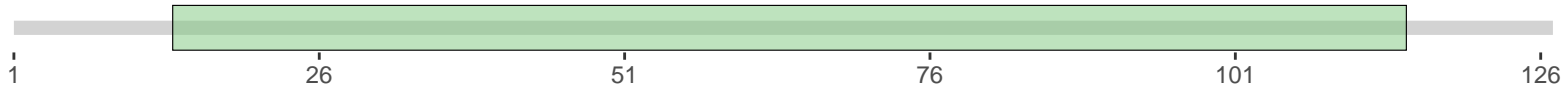


Gel Slice



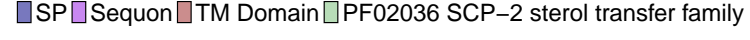
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

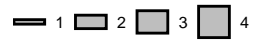


Protein sequence:

VVYVLDLKKGETKEGPEYEGGKPDATFSFKDDDFVKATGKMPQWFMFGAMKIKGISISAQKFTDFDFKPKSM

NbL04g16240.1 protein_TIC_22_chloroplastic [MW = 31.49 kDa]

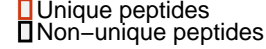
No. of times detected



log(intensity)



Values from



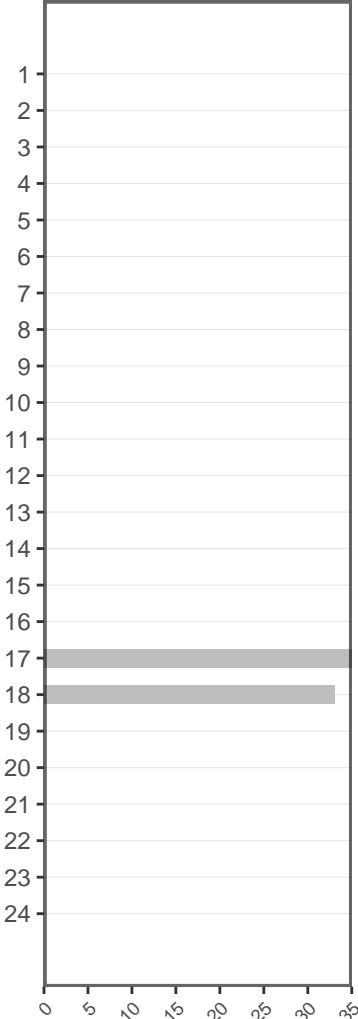
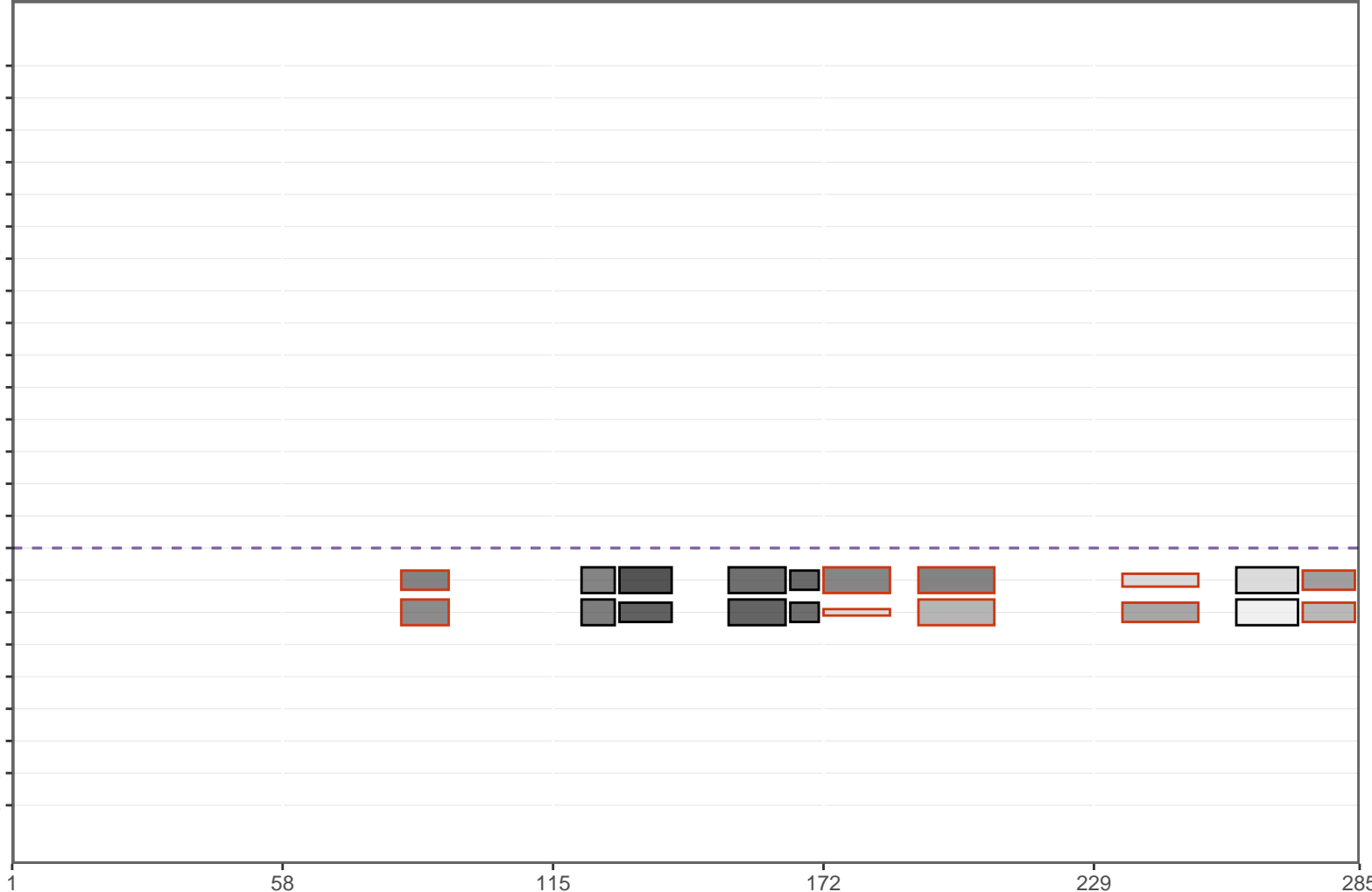
MW indication



Molecular weight



Gel Slice

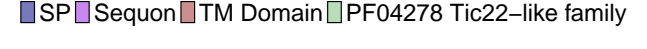


Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

DAEAFLAGVIRMRKGEVRRGGAKVPLFDGQVYMLKVEGIAFRFLPDPVQGNALKASDVKTFDGVFVFGSDLLWKRNRRCYPIYFRKEDIKELSSRASRGASQHMVGSLEDVLRKMEISQRHSGWEDLIFPPCKSHSGHQDVTKYV

NbL04g16180.1 uncharacterized_LOC107761413 [MW = 46.16 kDa]

No. of times detected



log(intensity)



Values from



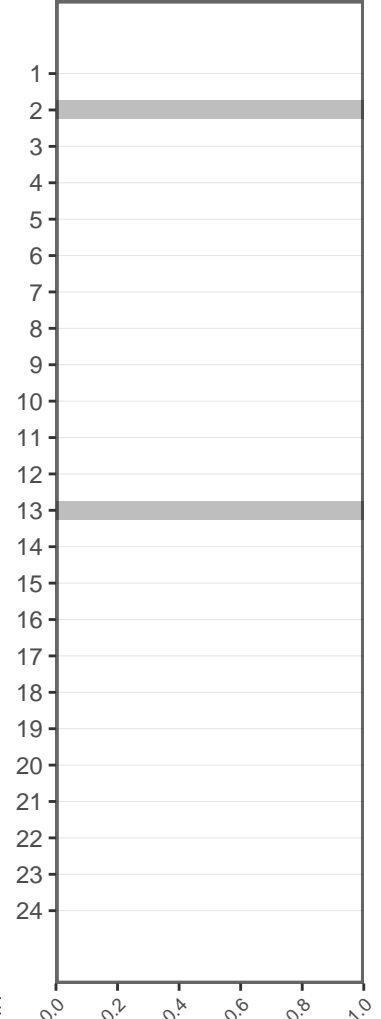
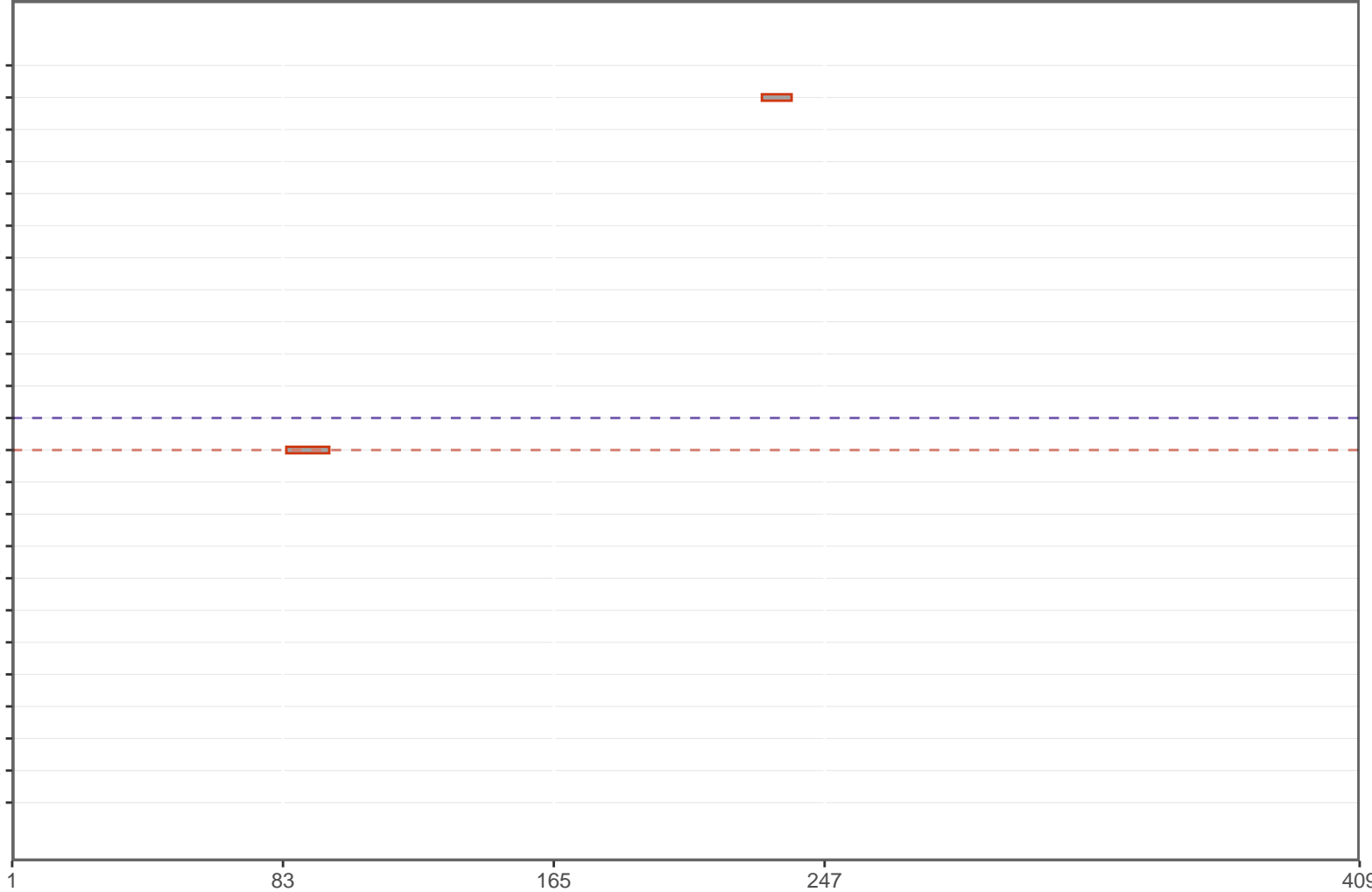
MW indication



Molecular weight



Gel Slice

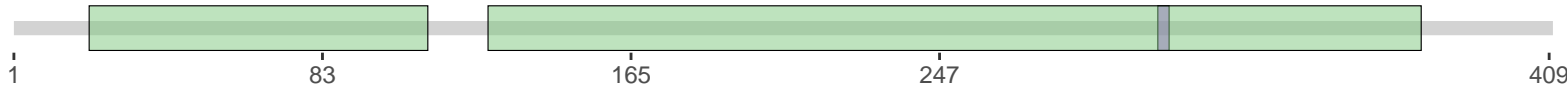


Peptide counts over 4 repeats

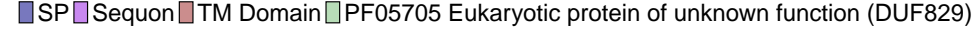
Protein length



Pfam domains



Pfam Description



Protein sequence:

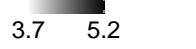
VQTLVAVSSTGAPVHILGSEDDDLAPVGTICNFAGRLLKDKLGGSDVKKLWGISPHVGHYRHYHOLEYKAAVTEVLGKAAVYSGRIQLEGEKMGLEGGHDEIDPLGNLRKAAATANGSFRALAELENDRFVYVPSVEVYHEGKSNVGGHGEQKERYHPLSEFPRINAHGVLGQLFDVQVPKVVEEDWDIRDSSSEFKAASFSTRRHSPFNPMKQIRREL

NbL04g16150.1 uncharacterized_protein_At1g47420_mitochondrial-like [MW = 33.79 kDa]

No. of times detected



log(intensity)



Values from



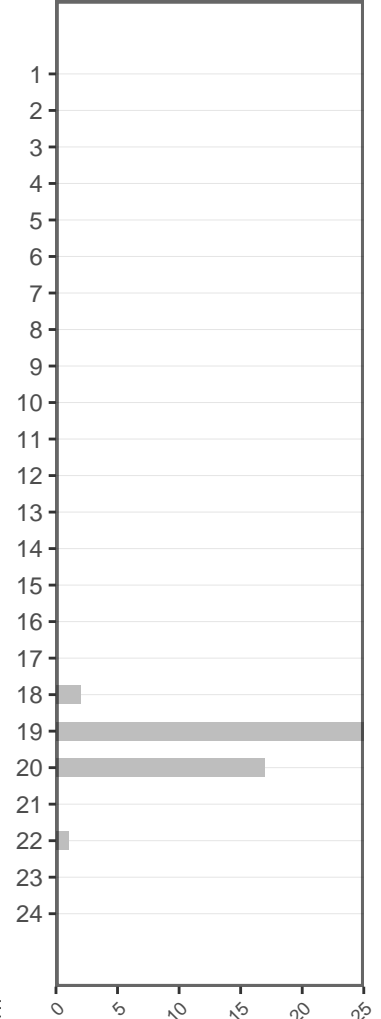
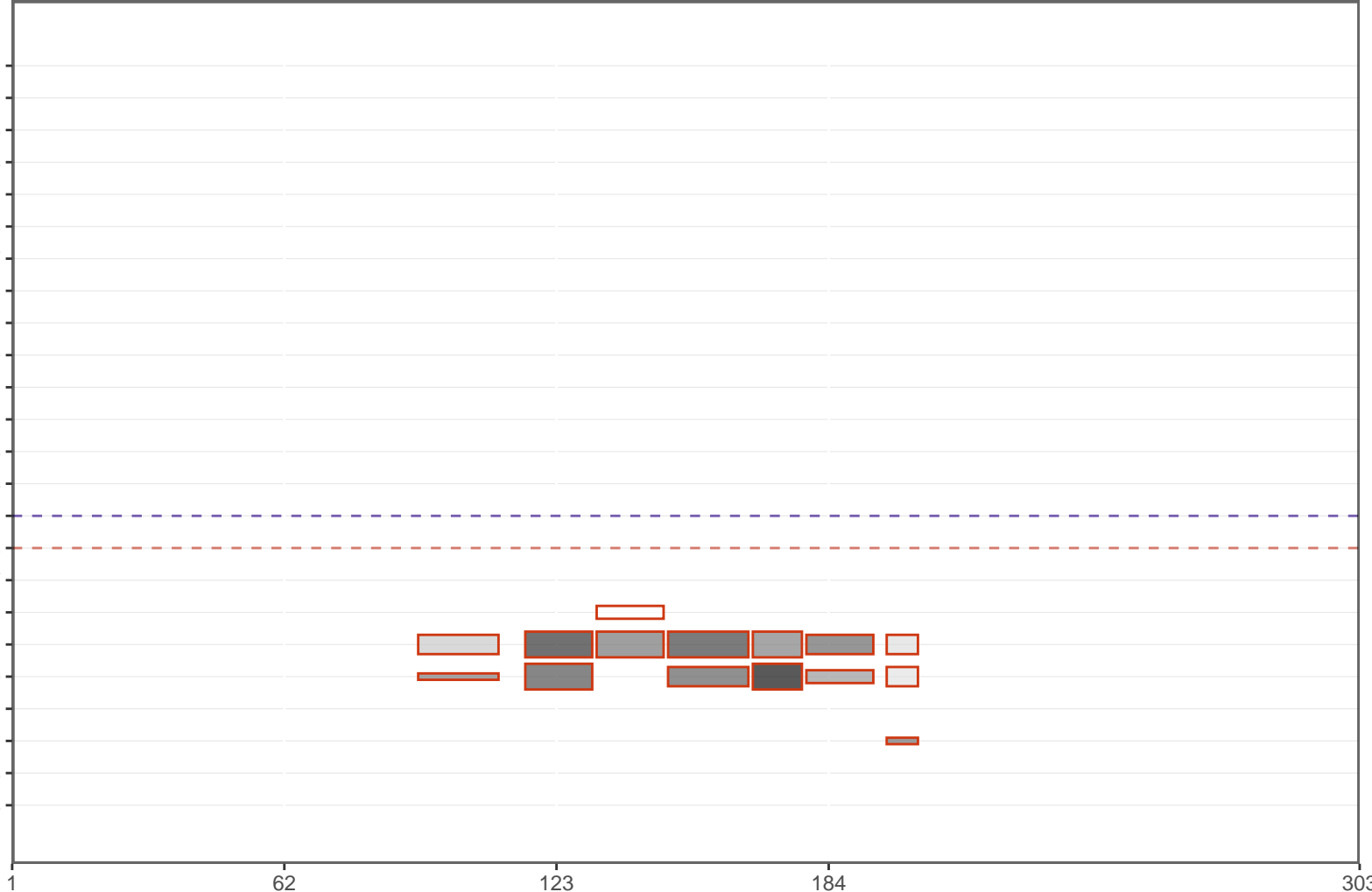
MW indication



Molecular weight

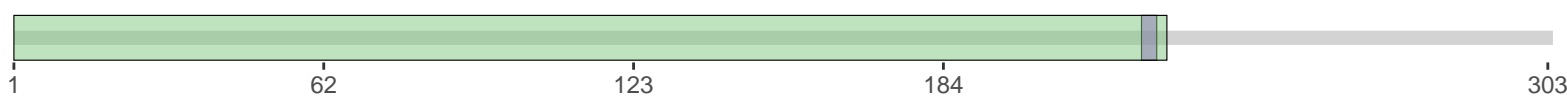


Gel Slice



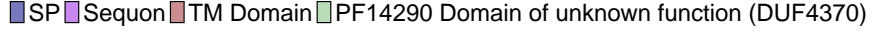
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEEFTGLTSLKMEIDDAAGLSGDDVPLKKEVSDALQTVFQRYNAYMSAFGPEEGYLRKKVEMELGTRMHLKMRSGSIDSEWGKVNTEASWLHVQFFQRLQLGLPTQASISAFSVVYFLNENQITSEYVLLGDKKAVDTSCNLNLSLWKLHNSDFFFSMVPKFI

NbL04g16110.1 26S_proteasome_non-ATPase_regulatory_subunit_14_homolog [MW = 36.52 kDa]

No. of times detected



log(intensity)



Values from



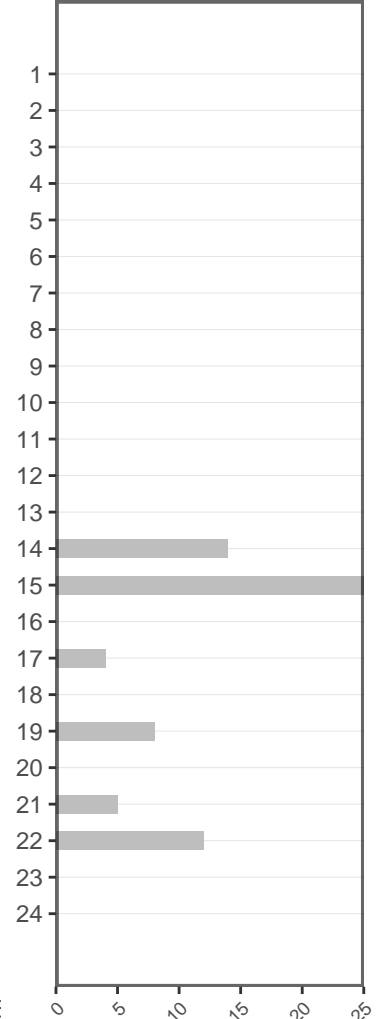
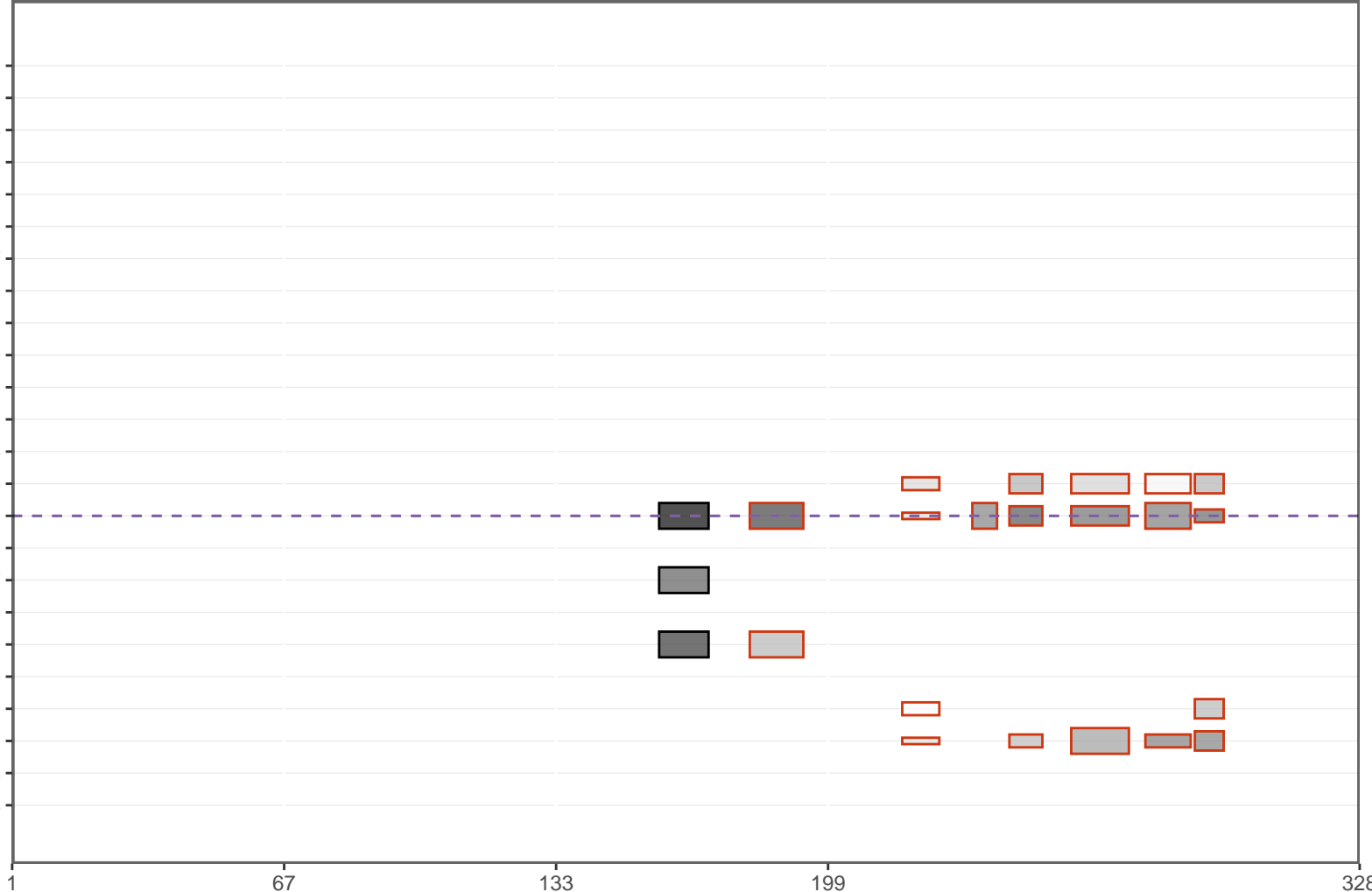
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

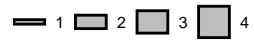
- SP
- Sequon
- TM Domain
- PF01398 JAB1/Mov34/MPN/PAD-1 ubiquitin protease
- PF13012 Maintenance of mitochondrial structure and function

Protein sequence:

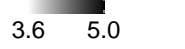
IQSFEALNQRVAIVVDPDPSGKGGKVVDFRLINPQTMLDGPGRGTTSNLGHUNKPSIGALHGLNRHYYSIANYRKNLEEKMLNLHKKKWTDLGLTGRFDAHSKTKNEGTQDEMNLAVYNNKAVQEEDELPPKLAIAANVGRGDANKHEEHVSNLMSNIVDTLGTMLDTVVF

NbL04g15990.1 uroporphyrinogen-III_synthase_chloroplastic [MW = 32 kDa]

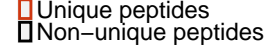
No. of times detected



log(intensity)



Values from



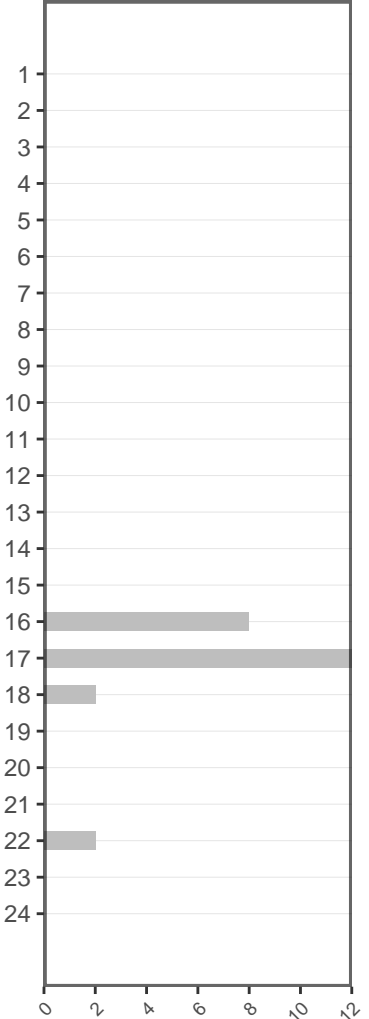
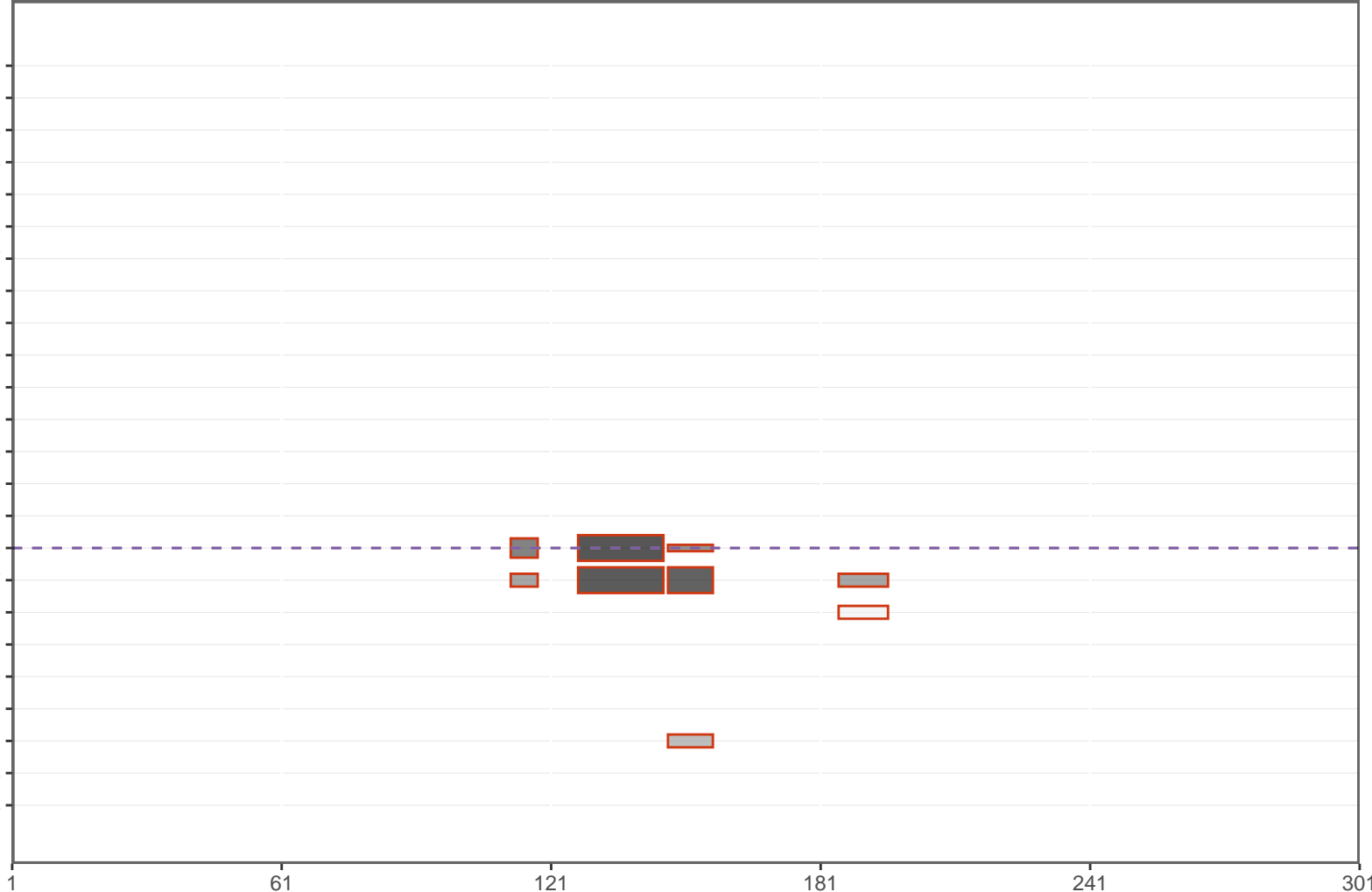
MW indication



Molecular weight



Gel Slice

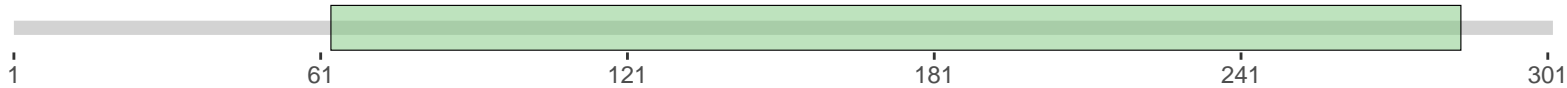


Protein length

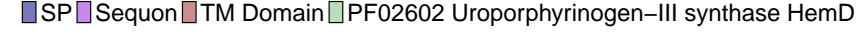


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IFDEAVQSSKQYLQVAFTRPSKATGKVLASELPKNGDKCTVLYPAEKAGTDIEEGLSERGFVTRLNITYTTPVNVQVDGYLELALGAPVVAWASPAIRVWTLNLPASGQWQNVAVAGIGETTASAAKRLGLRNYYFTSPGLEGWWSBIEALSVNEQVQKV

NbL04g15770.1 serpin-ZX [MW = 42.69 kDa]

No. of times detected



log(intensity)



Values from



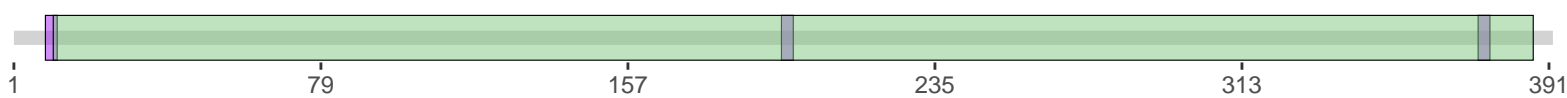
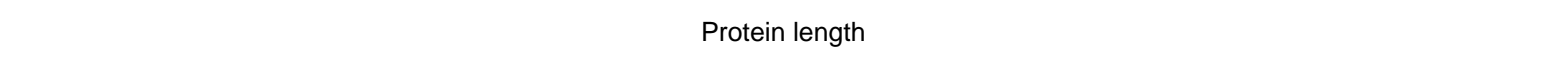
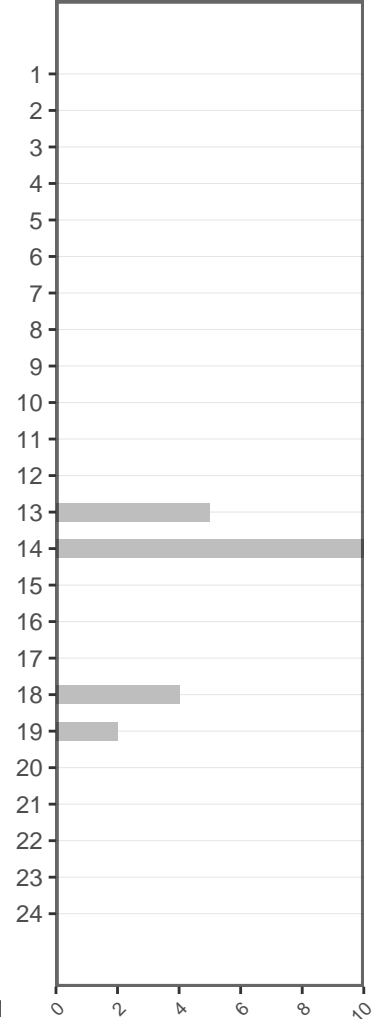
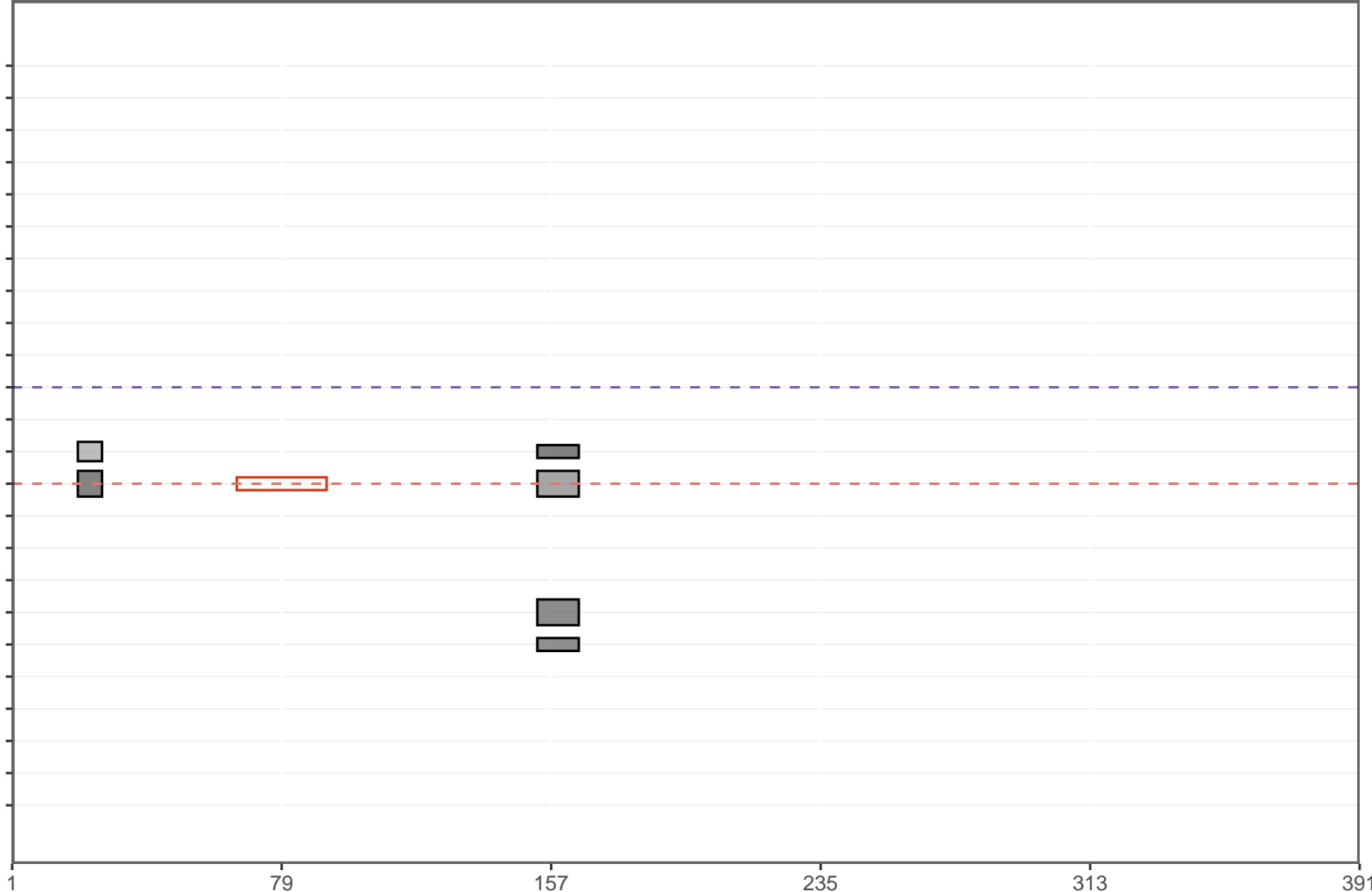
MW indication



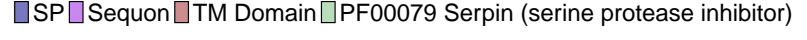
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

FDASVTKDNEFHLLNGTSEWVPMFSKKGQVWAFDGRVVLGLPYKHGSDRRRFTMFFLPDANDGLFALVQVSSGGFLGSLPYQKVEVGEFRIPKIKISGFSEASNLKGLGLVLPFGDGLTEMVDGDFVGNLYVSGIFHKRFIEVNEEGTEAAATAGVILKRALMVEEKVDFADHPVLFJIRENATGVLVFGVGNPLVDI

NbL04g15650.1 plastidial_lipoyltransferase_2-like [MW = 33.52 kDa]

No. of times detected



log(intensity)



Values from



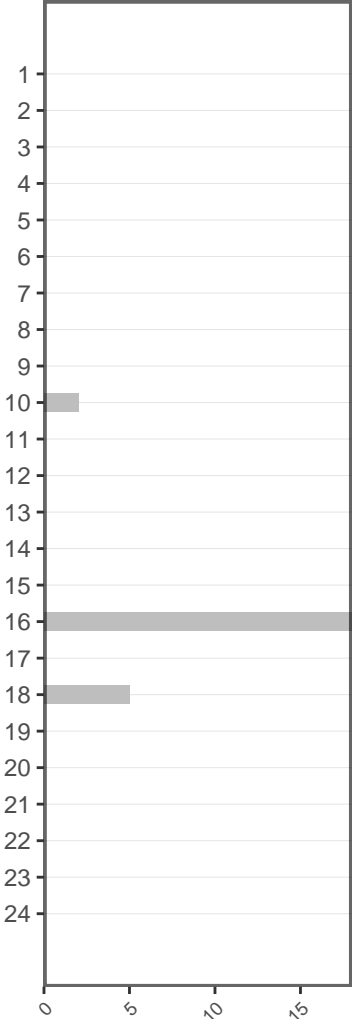
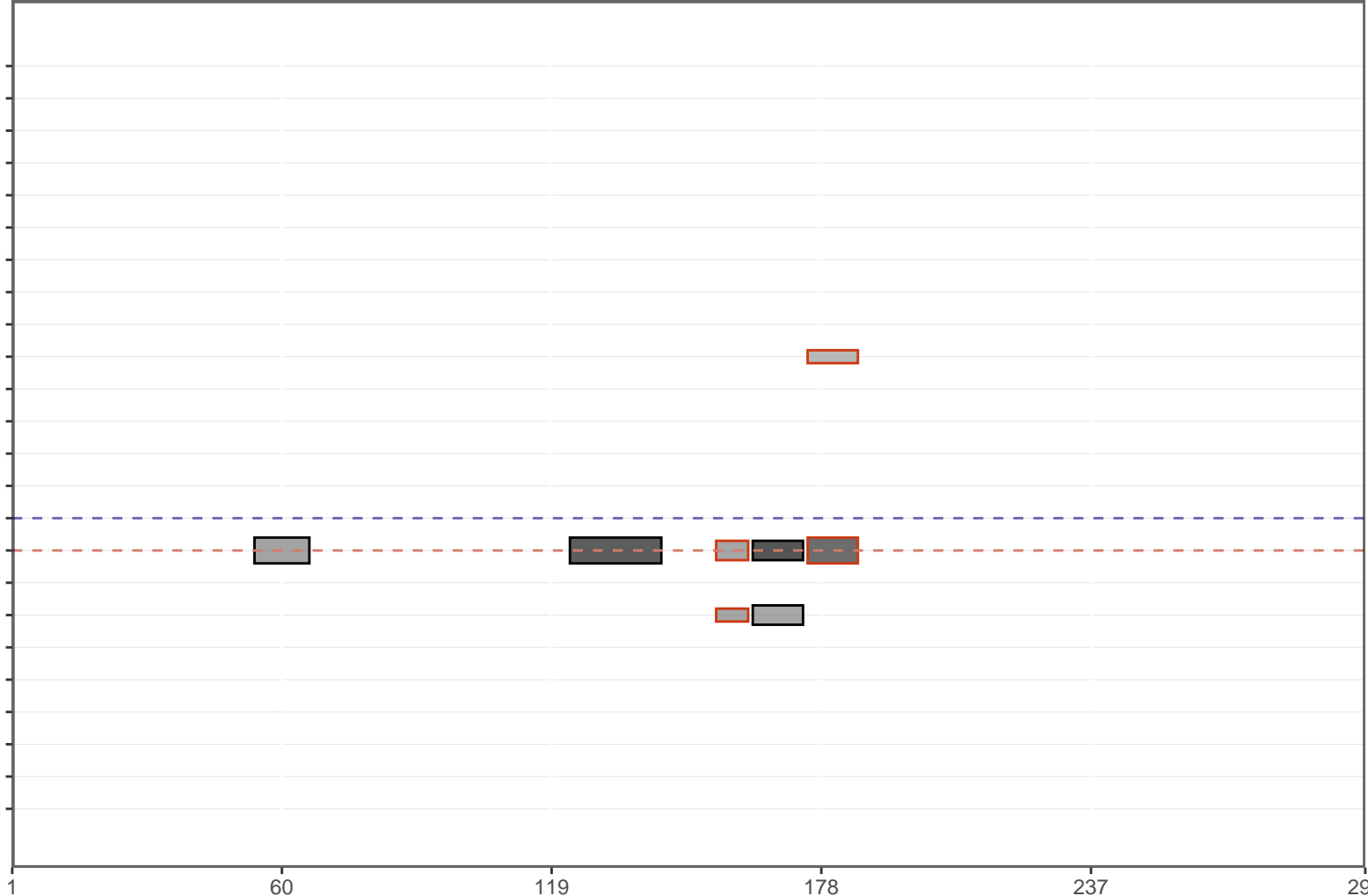
MW indication



Molecular weight



Gel Slice

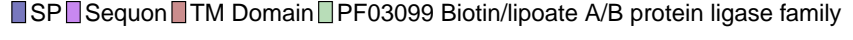


Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

.VMYPINLRYSKMDLHWLRBLEEVRVLS66SFMEASRIDGLTGVWVEGRKLAIGIRV60WVYHGLALNVTTDLTPFQGVPCGIRDRGVGKIKGLKLPVSN6GGTENHQDADDVQLDIAHKSLVKEFEVDFQVDHFKPTPLVLSAEKPF6WLD

NbL04g15610.1 30S_ribosomal_protein_S9_chloroplastic [MW = 22.85 kDa]

No. of times detected



log(intensity)



Values from



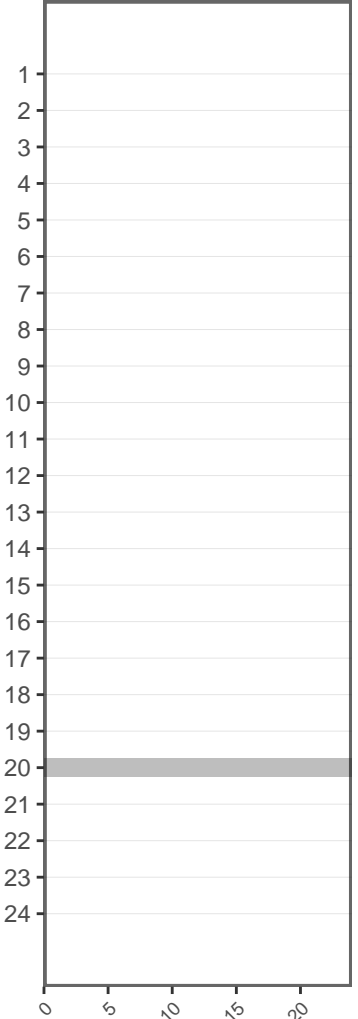
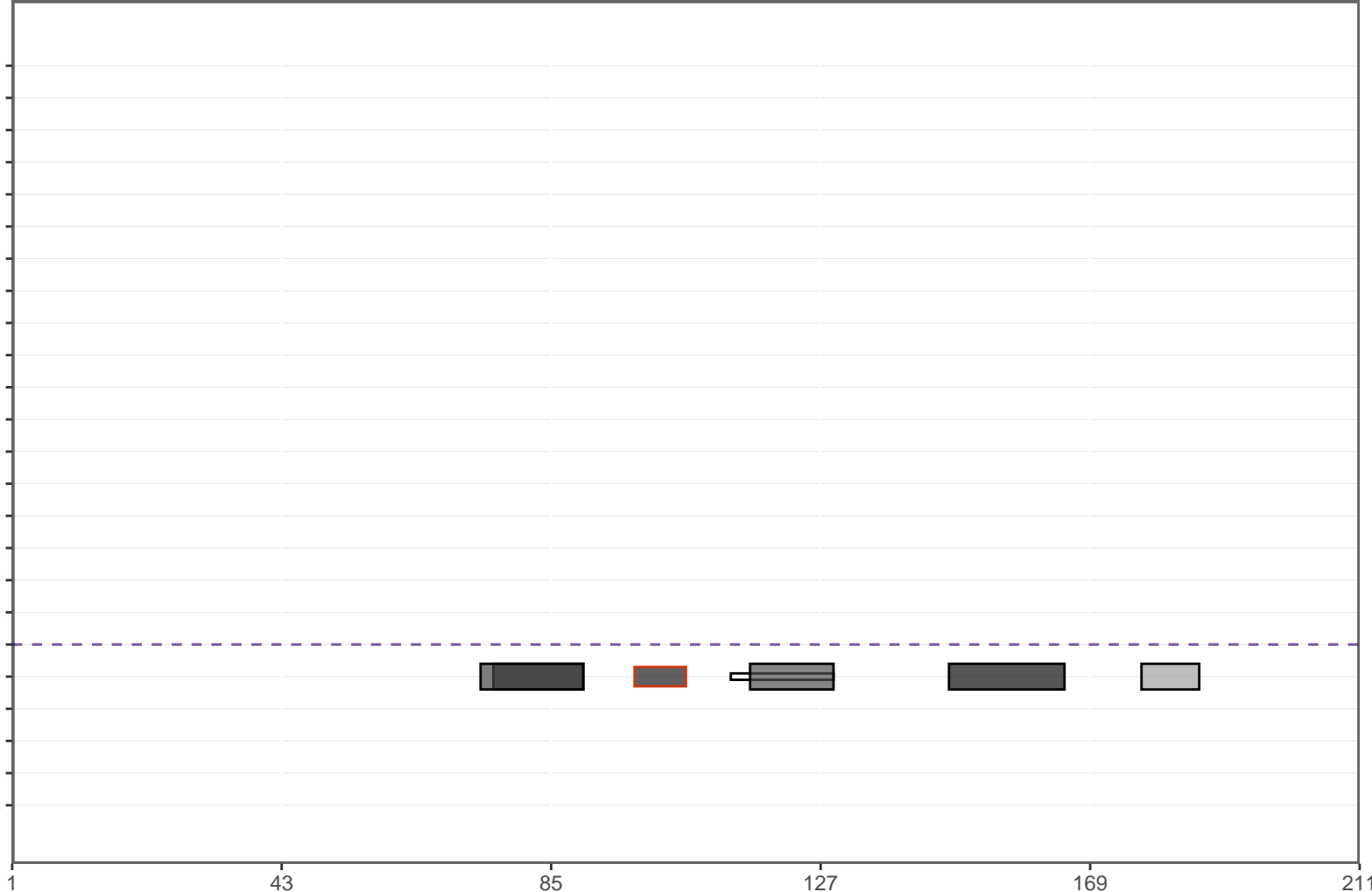
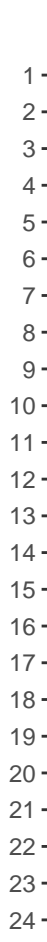
MW indication



Molecular weight



Gel Slice

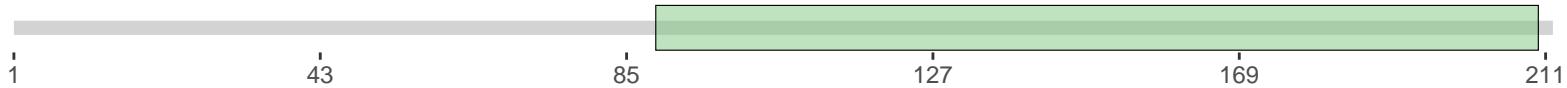


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

ASARVYLQEGSGKHINFRDAKEYLGGNPLWQYVKTPLATLGVYEAHYDIFVYVGGGLGGAGASLGAARALLKVSSESHRKLPRREGGLTRDARVVERKVKGLKAKRKPQFQKR

NbL04g15140.1 uncharacterized_LOC109224904 [MW = 200.4 kDa]

No. of times detected



log(intensity)



Values from



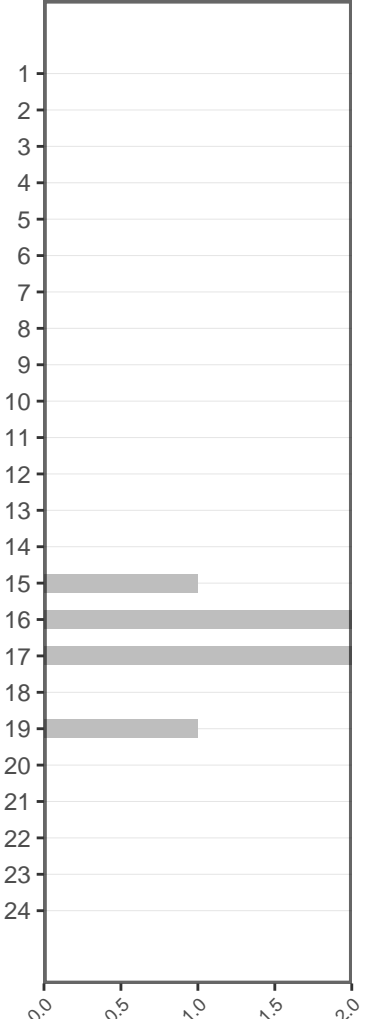
MW indication



Molecular weight



Gel Slice



Protein length

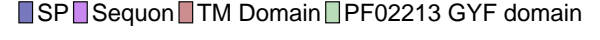


Peptide counts over 4 repeats

Pfam domains



Pfam Description

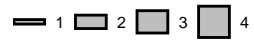


Protein sequence:

ILLQQOYLMLQLSGAAALGGPQGLSLLKLLMLKGGGGGGGGKQEEQGLLRGGGGLLGGVLSLHPHQPFGEQPYGKLPPTPGISGGNATVDTRFRQPSNLFMSNITQVQHPVMEEAHAFNVLPPSISGGDVTQGGFETSLLHPGGGMFKDASSQRSGWGFEEGIDDDQKVPKPRMATAMDPSHTEIAEKDPLEDAENNEPLAVTTFTVIEASHPLPGEQVEKSMPPPPPVAVDNLSLHQQNKLESPPAIPSEPGQVERDPHNGLSVTKELKGVPEPREVKKSSSEKSKXQKST

NbL04g14860.1 maf-like_protein_DDB_G0281937 [MW = 25.31 kDa]

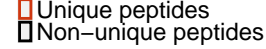
No. of times detected



log(intensity)



Values from



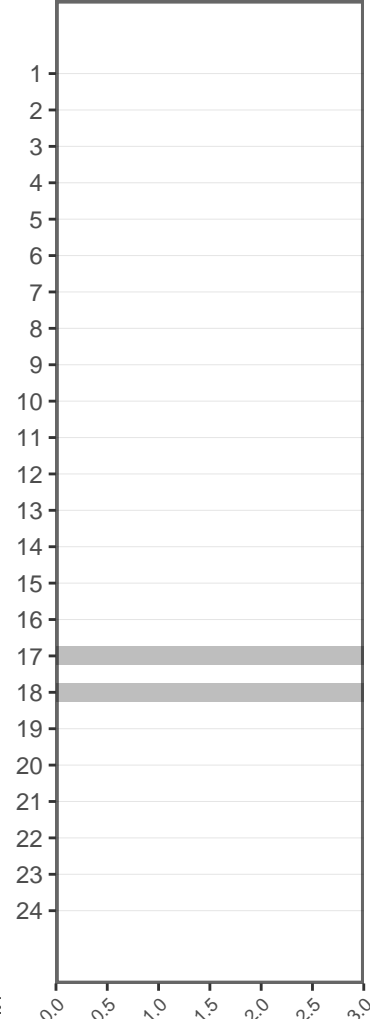
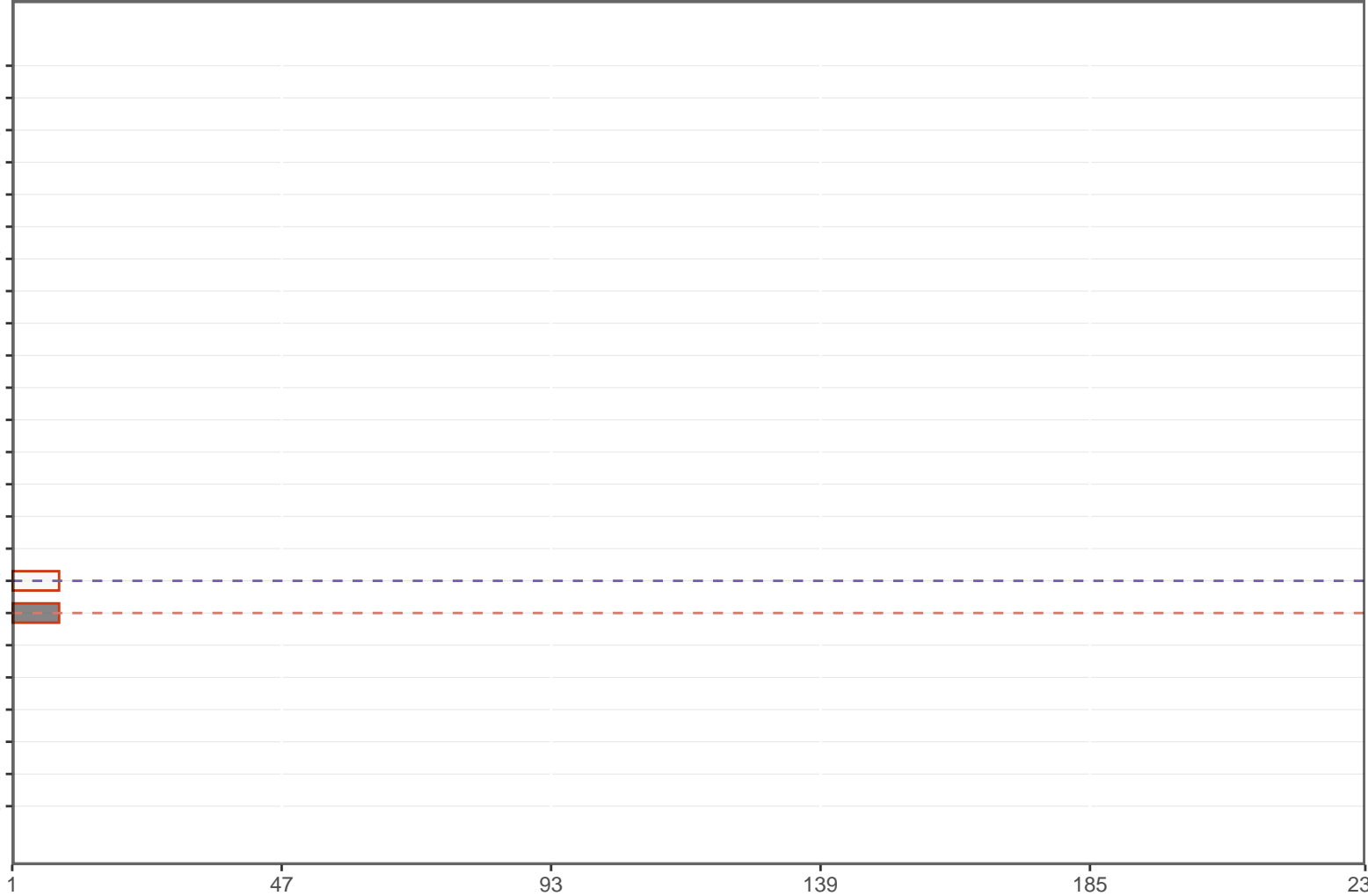
MW indication



Molecular weight



Gel Slice

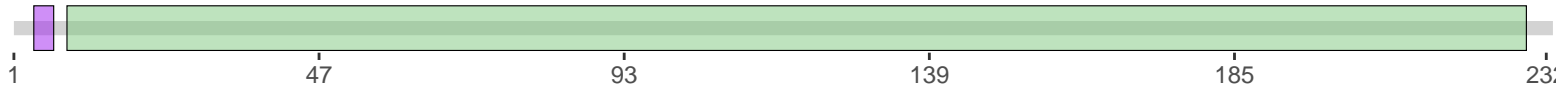


Protein length

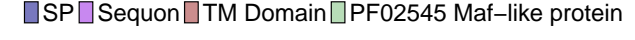


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

AEPTLLTCDVVVVEGMVREKPSSEAEARGFMKDVAHGHAATVSSVLTNLVFGRRGEWDKVEYFHDIPDQVIDRLEEGLVVAAGLIEHPLLPQIKVEVGGTDSVMGLPKALTERLUKEV*

NbL04g14800.1 isoflavone_reductase-like_protein [MW = 34 kDa]

No. of times detected



log(intensity)



Values from



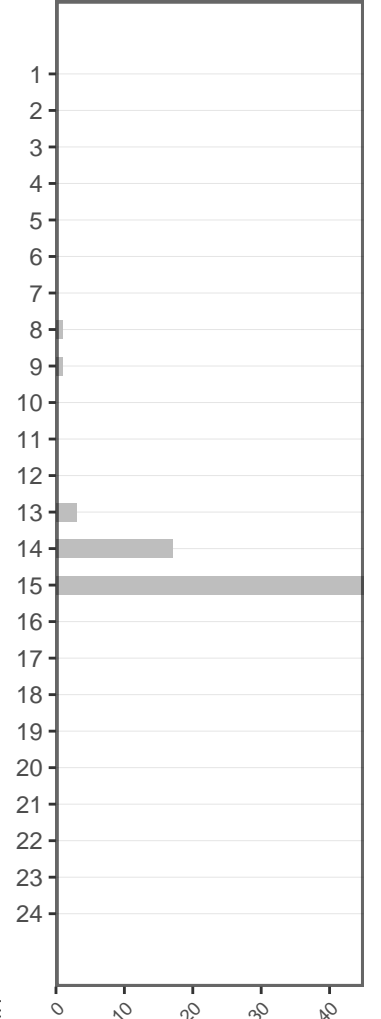
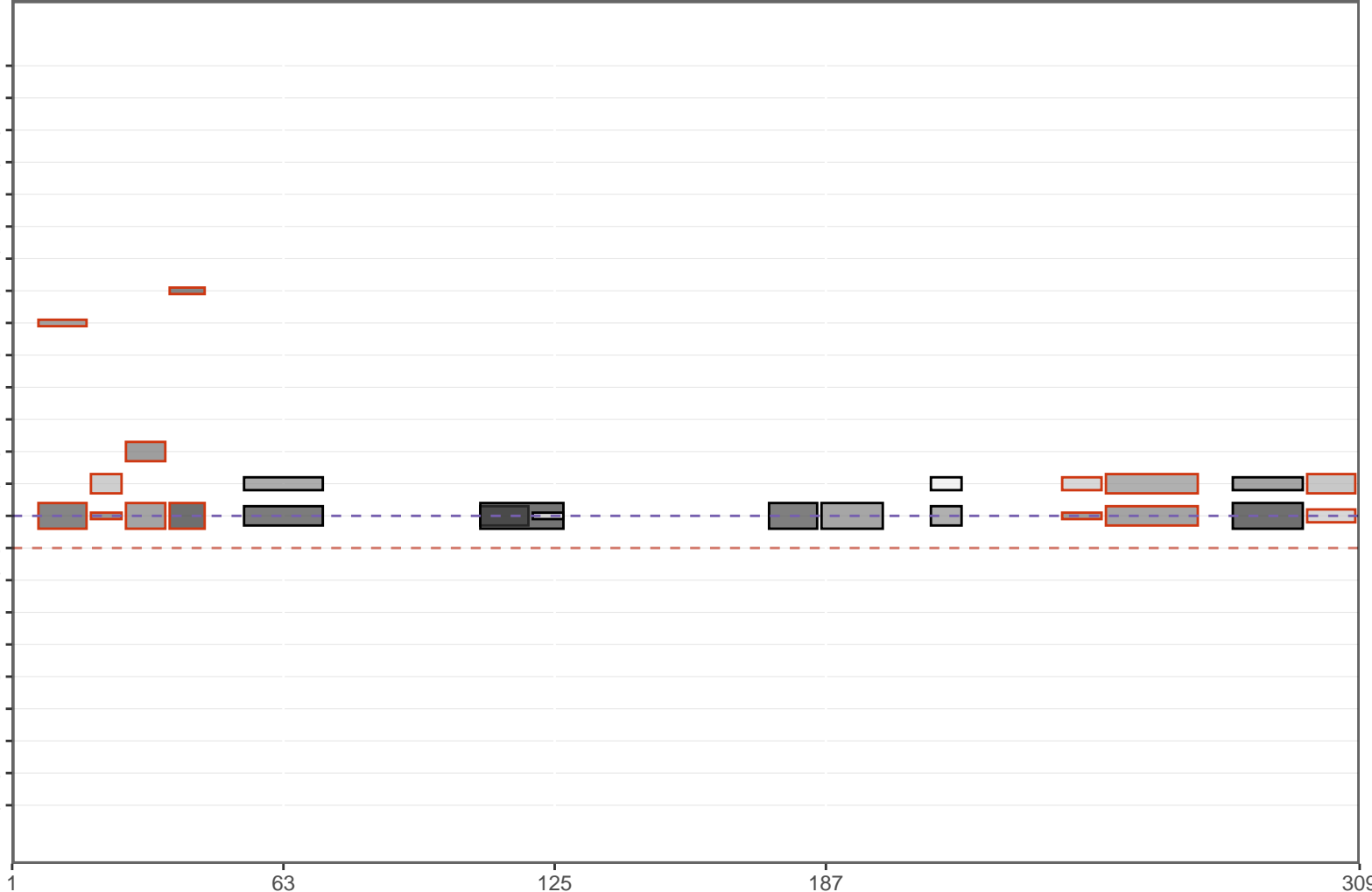
MW indication



Molecular weight

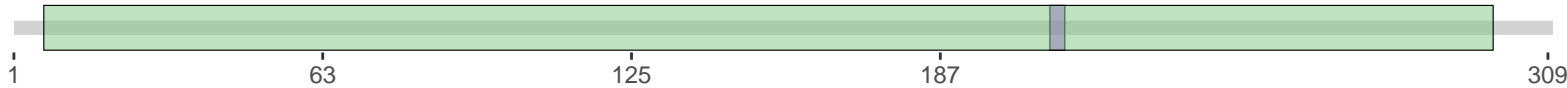


Gel Slice



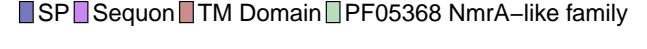
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEAEGPYYTYSCNFGAGYFLPIMVPGATAPRRDKVIRPGDGNVAVFNEEHDGTYTKAVDDPRTLNKTLYKPKWNTLSFNEIWAWEKMGKTKLEKYLPEEGIKDKIETSPMLPLVLANHATFVKGDDGTFKIEPSFGVEASELVPDKVYTTVEEYLGHFI

NbL04g14790.1 gamma_carbonic_anhydrase_2_mitochondrial-like [MW = 29.6 kDa]

No. of times detected



log(intensity)



Values from



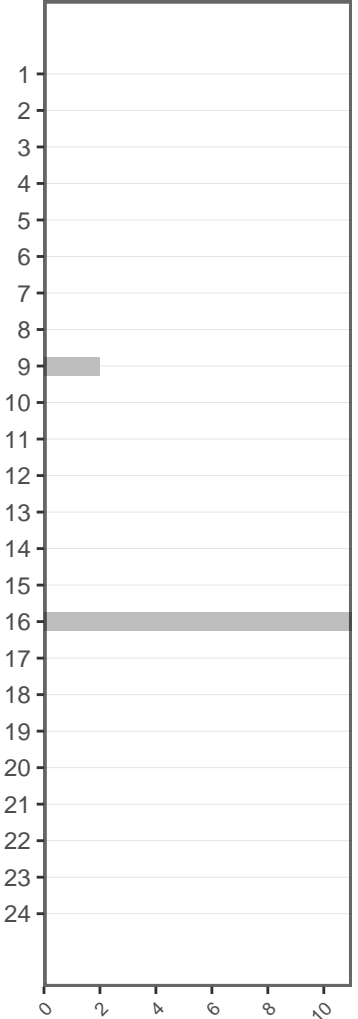
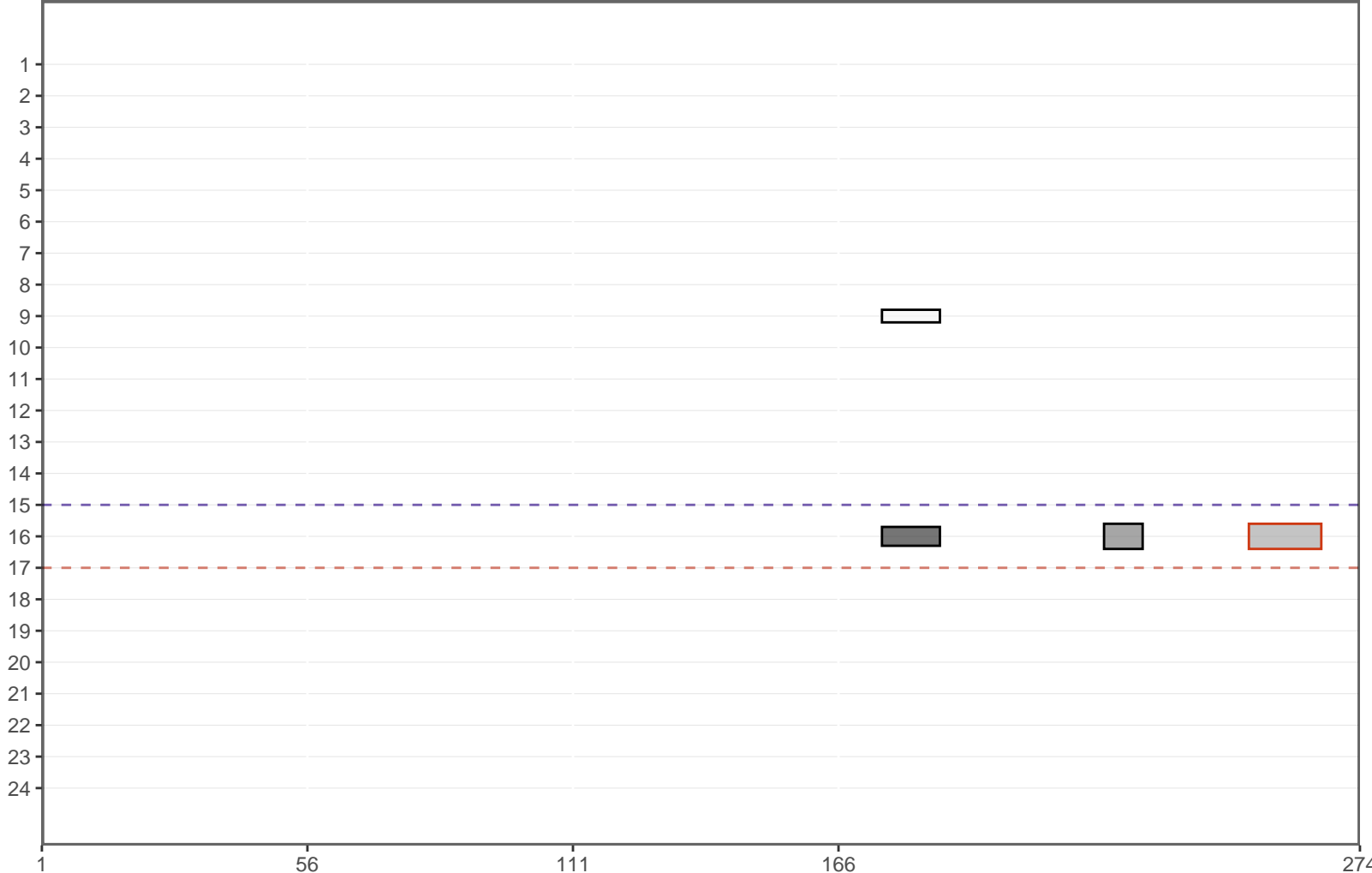
MW indication



Molecular weight

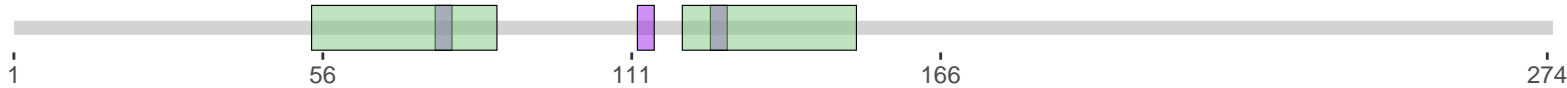


Gel Slice



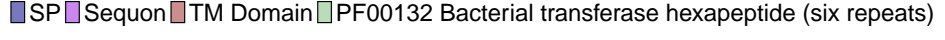
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

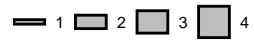


Protein sequence:

INVTYGHSAVIVHGGTIEDEAFKMGATLLDGVHVEKHAMVAAGALVRQNTRIPIGSEVWAGNPAKFLKLSDEEIAFAGSATNYGNLARVHAAENSKSDFEIEFEKMLRKYKRDVEYDSMGVIVRETPPELVLPNLPPEKAKKIQ

NbL04g14770.1 proteasome_subunit_alpha_type-1-B-like [MW = 29.54 kDa]

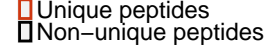
No. of times detected



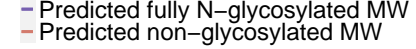
log(intensity)



Values from



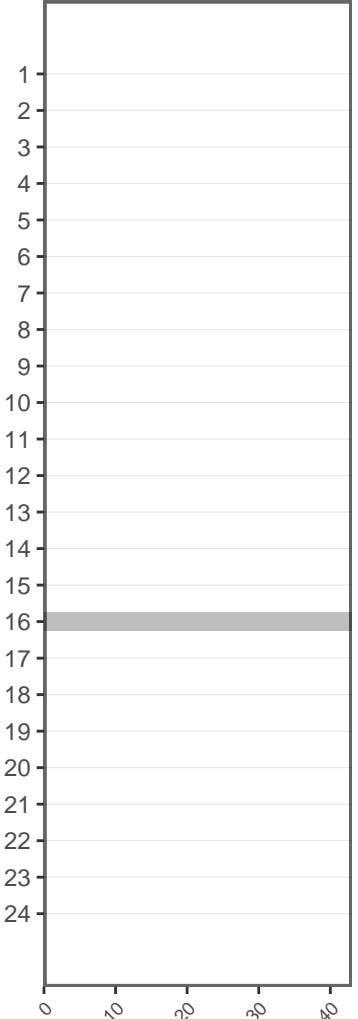
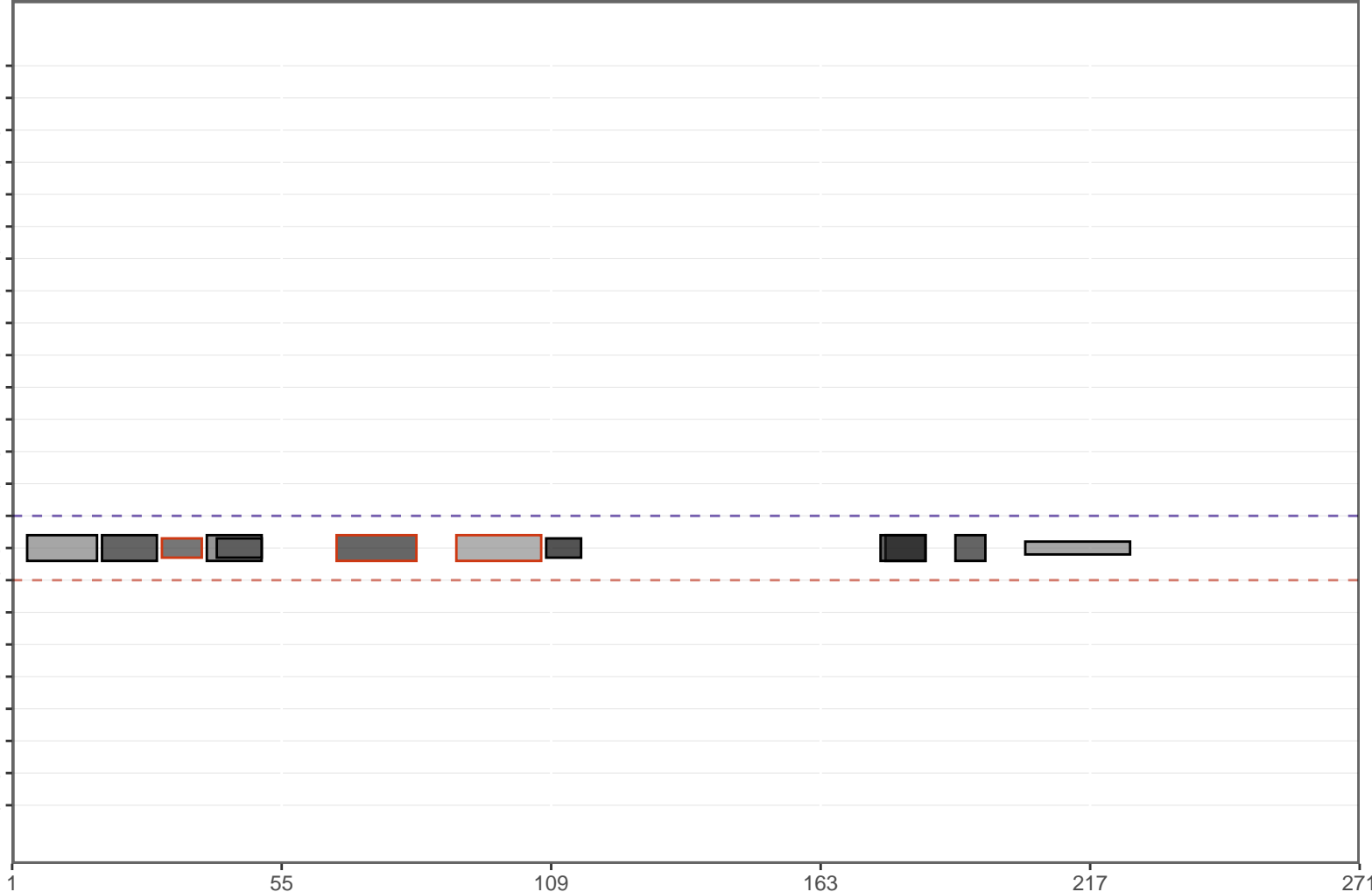
MW indication



Molecular weight

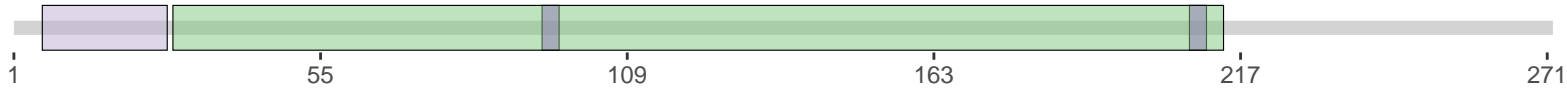
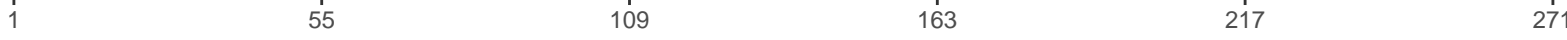


Gel Slice



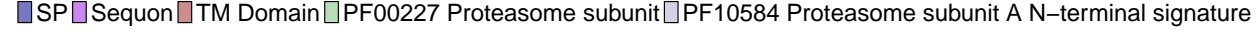
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

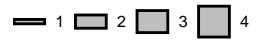


Protein sequence:

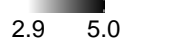
SVKRPYGVGLLVGGLEDSGAHLYNDRPSGNYFEYQFAIGRSQAAKTYLERRFETFMDSRESLLKDALFALRETLOGEKLSTNGTVAVGVGEAFHMLDKETIQALINEFEIAGEAPAAAPDEAGSDEFAAPAPADGGAAPMDV

NbL04g14600.1 GTPase_HfIX-like [MW = 62.93 kDa]

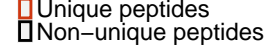
No. of times detected



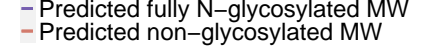
log(intensity)



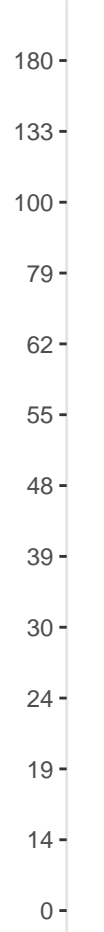
Values from



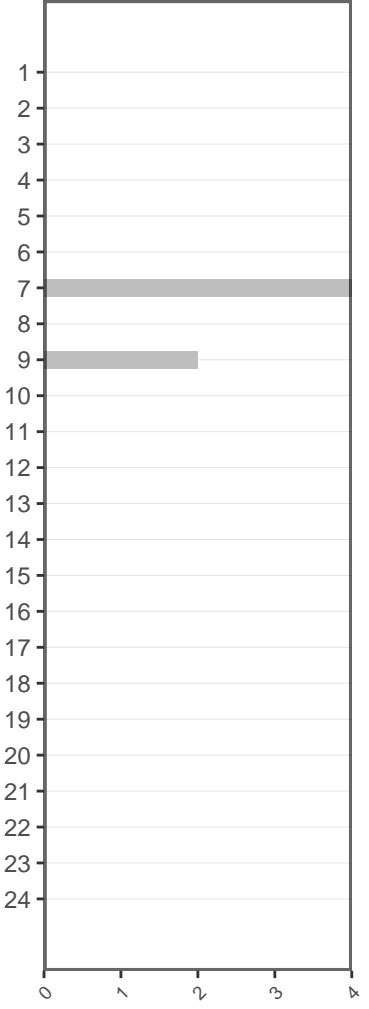
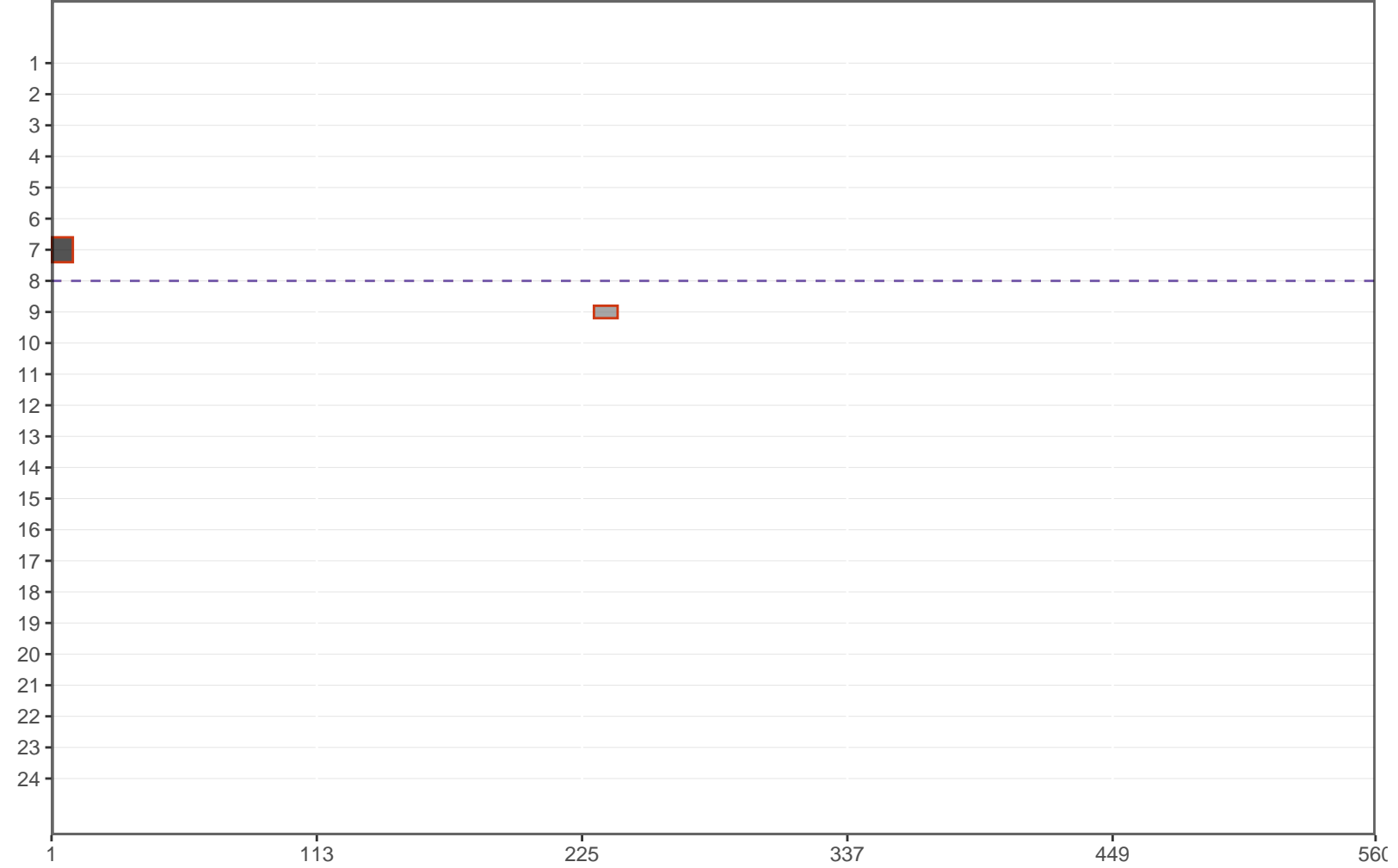
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

THLEROAGGVYKGMGEKQIEVDKRLRTQKIVLKKLEESVYKHKYRNRVSPVFPVSLVGYTNAGKSTLNLRLTGADVLAEDRLFATLDPITTRRVGMKNGKEFLTDYVFGIKLPTLVAFRATLEEAIESSELVHVVDISHPLAEIQEAVKVLSELDVNSIPKLMVWVYVQKARDPEKIKLEAKTKNDVYCVSALTEGGLDFGNEIQNRLKDTMVAWVLEALPFDKGEILLSTHHVGMVVERTMHTAGFFTSLNFKYETKGTLVRAHVPLRFRALLTPMRQMCYS*

NbL04g14570.1 ribosomal_RNA_small_subunit_methyltransferase_I [MW = 41.51 kDa]

No. of times detected



log(intensity)



Values from



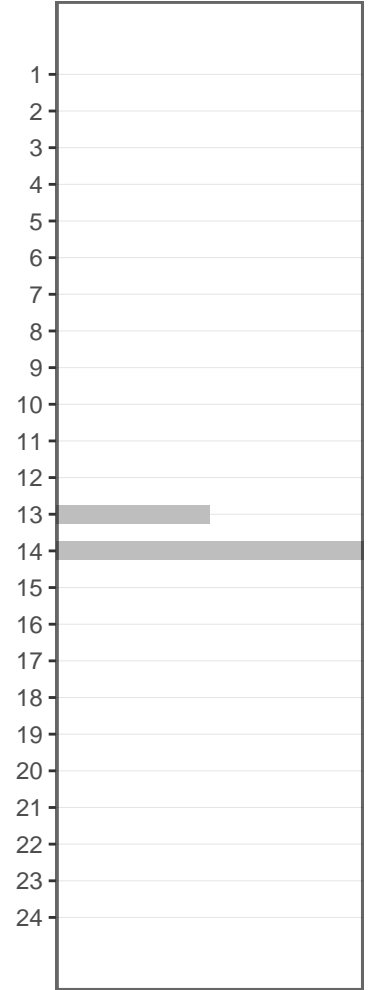
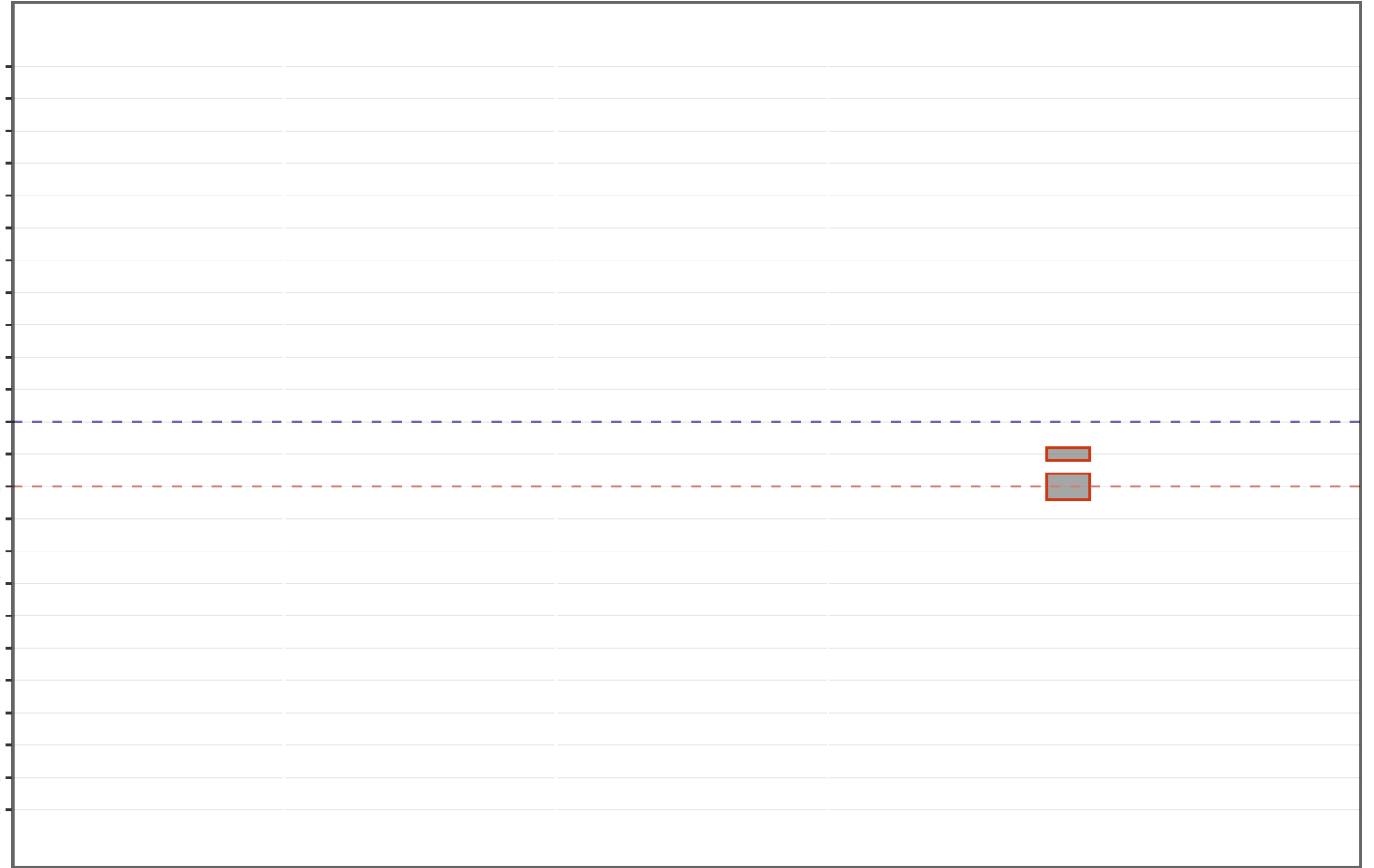
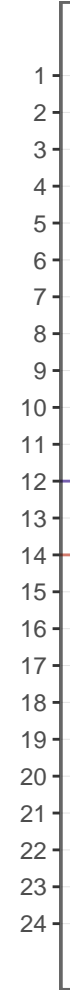
MW indication



Molecular weight



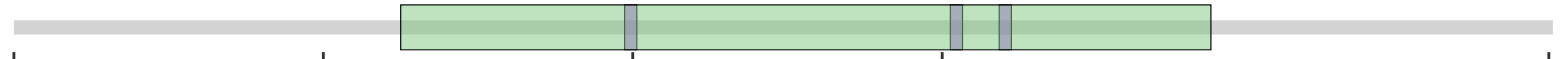
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

TPGISDPMELAKLGVKNNLVVPIPGSAVVTALASAGLPTNEFTFVGLFKHNSRKEKILSEANESATQIFPPHRLSGFLEEAANFGESRQCVMAEMTKVHEEFWRGTGSEANEFLARQLKGEITFLIECKGISIDESPDSGQLENELRELISEGHLSMAVKLWASGKSVRRKAYSLARLKFDDGLESEDEI

NbL04g14540.1 thioredoxin_H-type_1-like [MW = 13.55 kDa]

No. of times detected



log(intensity)



Values from



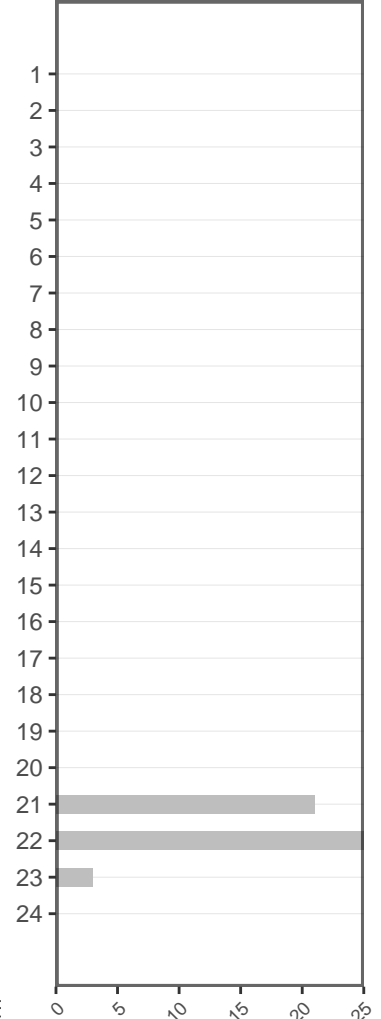
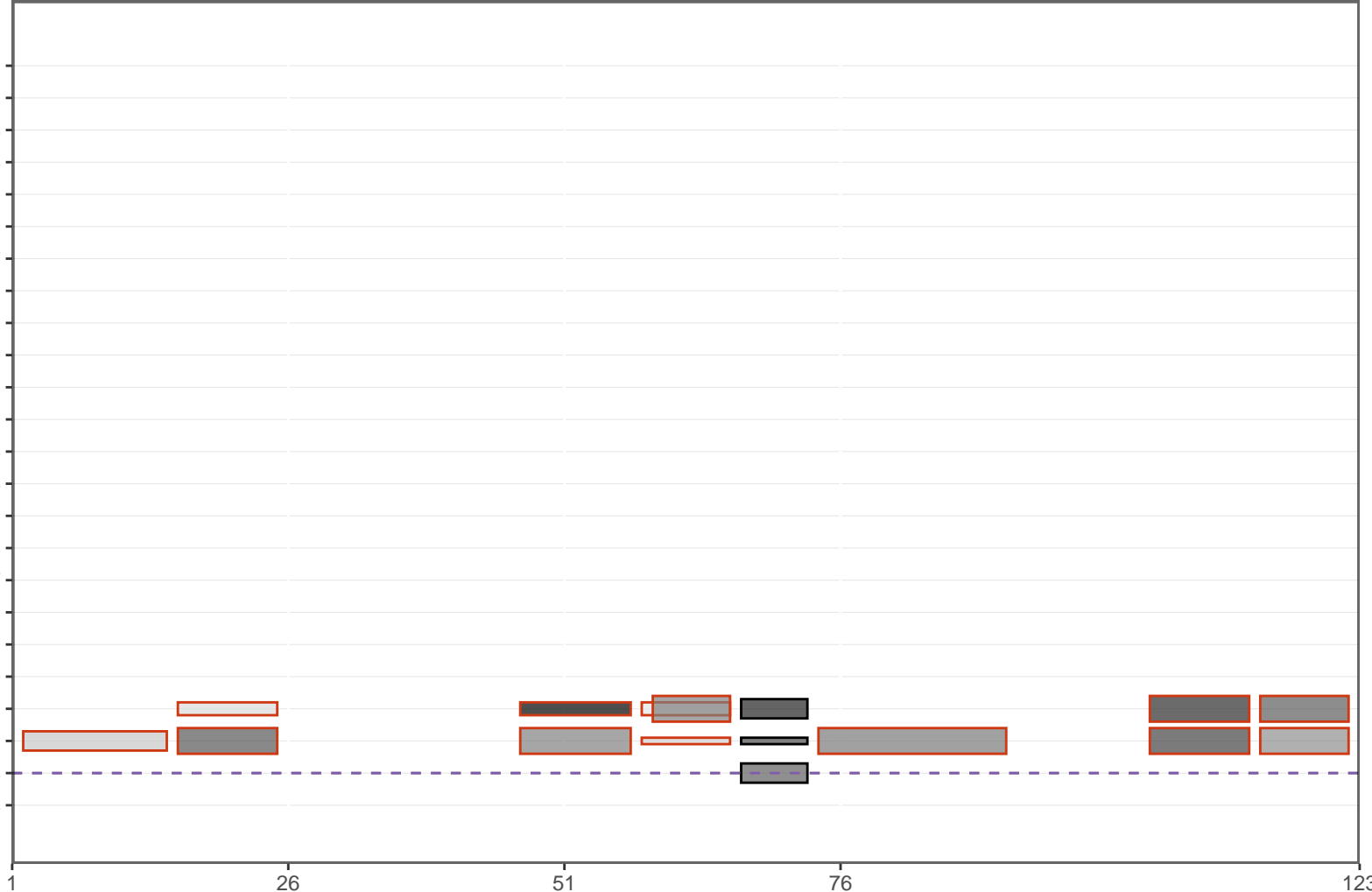
MW indication



Molecular weight

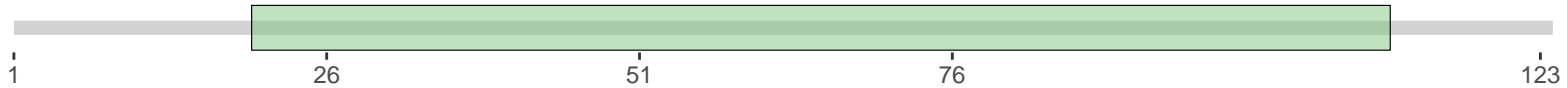


Gel Slice



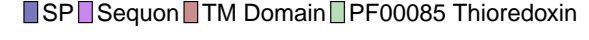
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

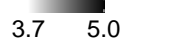
FIAPVLDIAKXKMPHWFLKRVVDEKRTVAEEWVEAMPTTFVFLKDGKEVDRVVGAKKEELGGTWNHAAKPTVTA

NbL04g14510.1 zingipain-2-like [MW - SP = 45.66 kDa]

No. of times detected



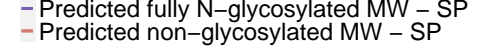
log(intensity)



Values from



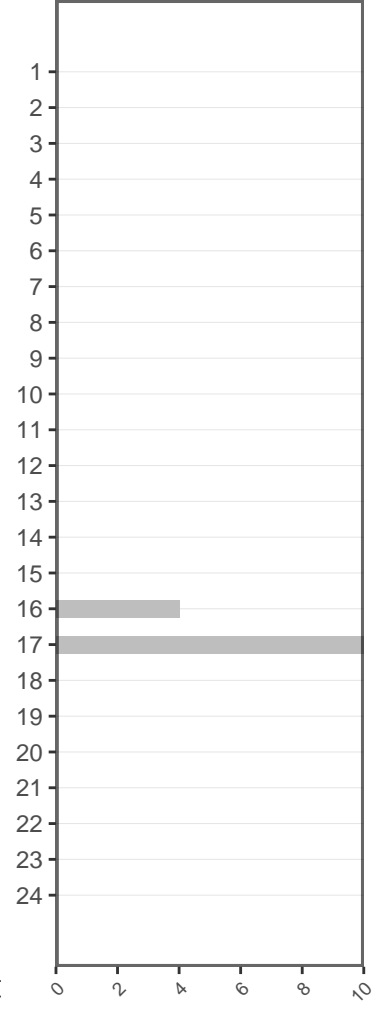
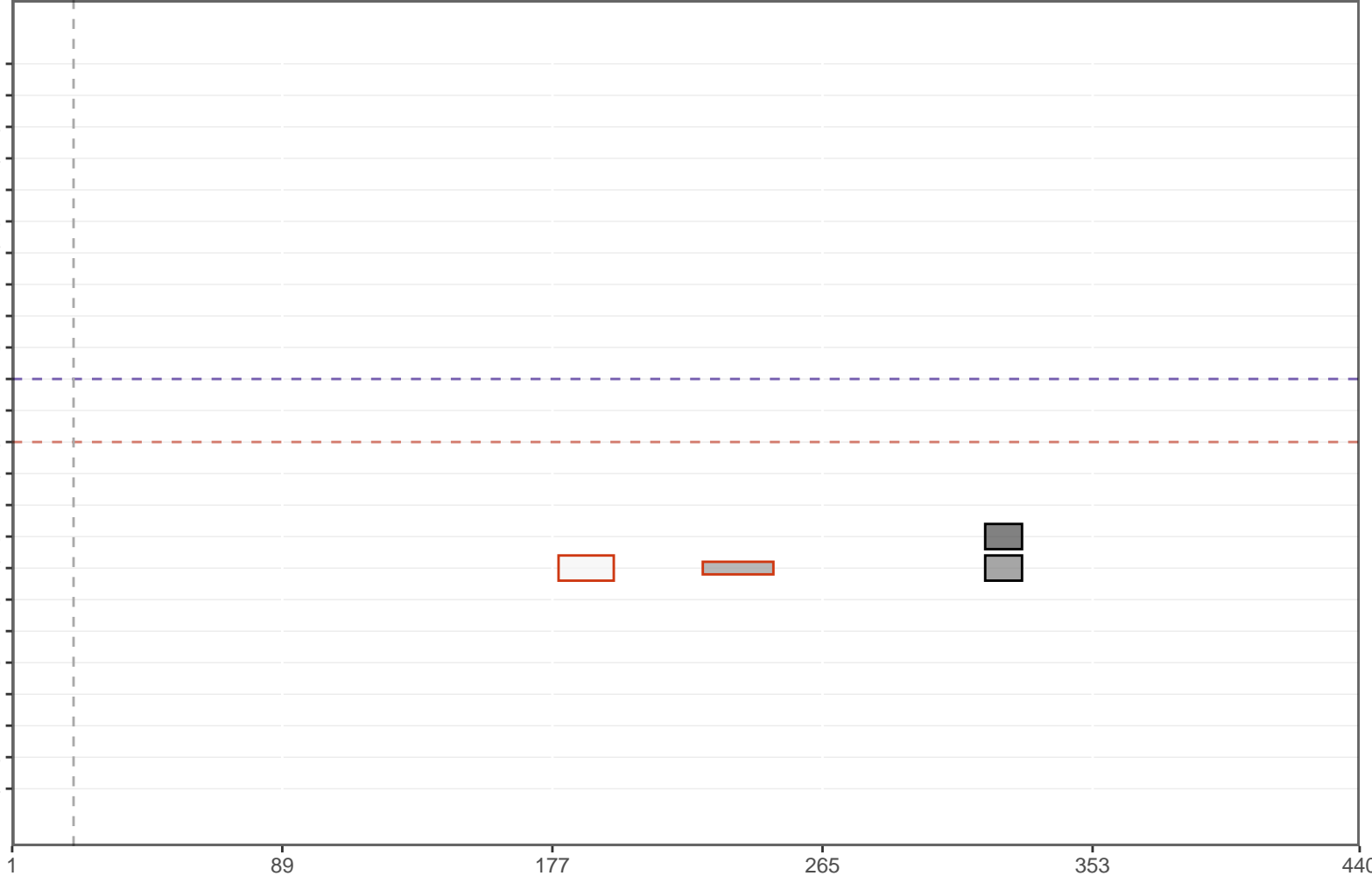
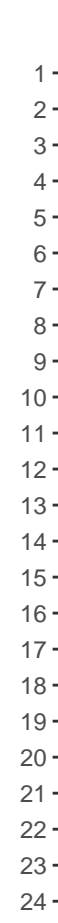
MW indication



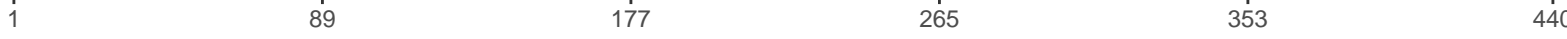
Molecular weight



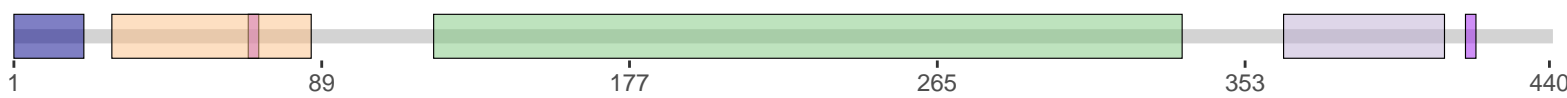
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

NEREGTCNKNLGRRVVTDGVTDFPNDKLLNAWAKGPIVGVGKGERAFDQVSKGIFTPGISTALLHVALVIVGSGENGVDVWIKNSWGTISWINGVYHMQGRNSGNGEGIGINLALAYPTKSSPNPPSPGPKGSMFTSGGGGETCCGGWLLGVCLLWVWCGGLDVAWCKKDRHDCGHPYPCDTRNRLGLKGMENATVWQGPKEAFSGKFGGLLYPF

NbL04g14460.1 cysteine_proteinase_15A-like [MW - SP = 38.09 kDa]

No. of times detected



log(intensity)



Values from



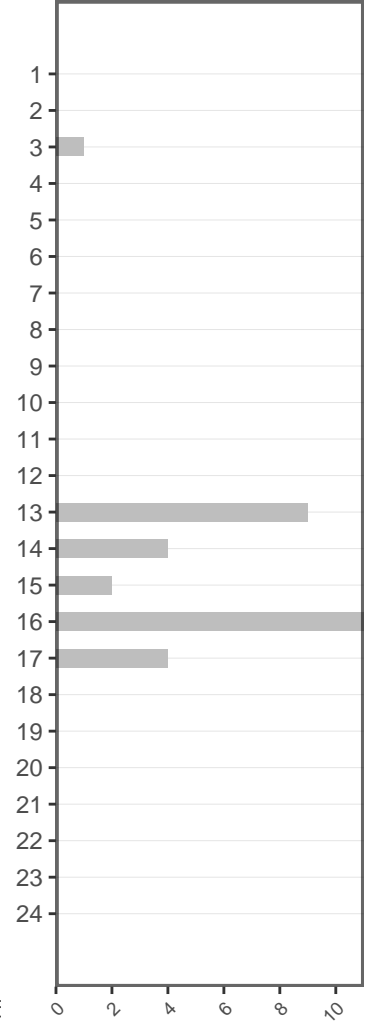
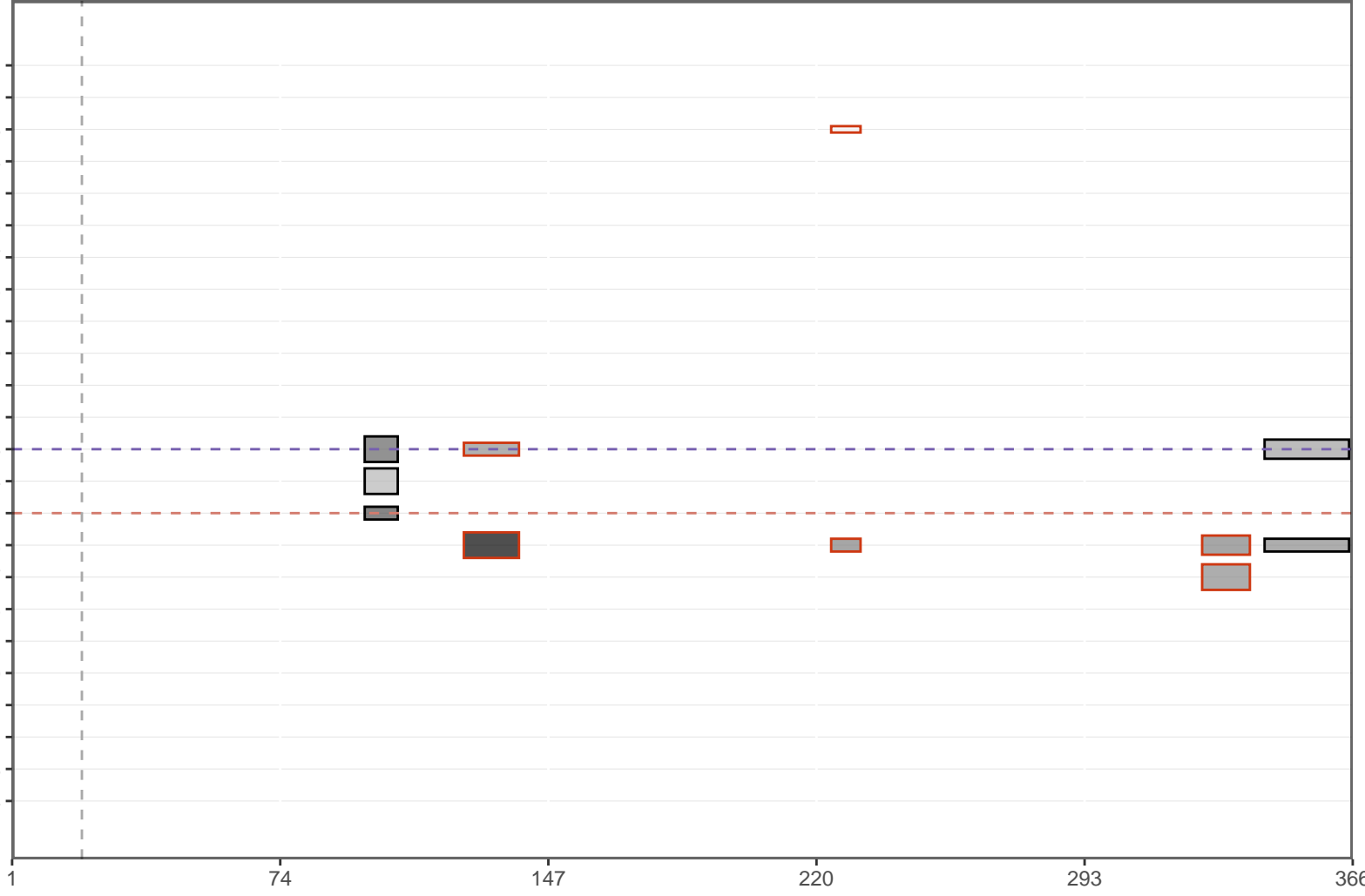
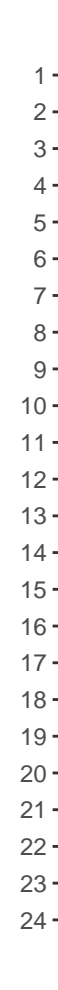
MW indication



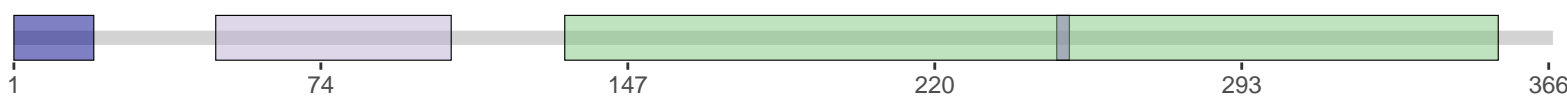
Molecular weight



Gel Slice

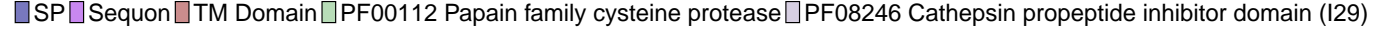


Protein length



Pfam domains

Pfam Description

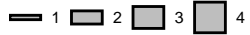


Protein sequence:

LATGELVLSLSEQLVDCDHEGPEGGD6GDAAG66GLMTAFEYFLKAGLGRKEDVPTGKDGKGFHFKSKIAAVTFNFSVGLDEDDQIAANLVKHGFLAVGINAAWMGTVYGGV6EPLICFKRRGDHGVLIVDYGSHGFAPIRLKEKAYWIKNSWGENWGEHGYKICRGNHGGVDAMVETVTAHTTNPNI

NbL04g14430.1 coatomer_subunit_alpha-1-like [MW = 137.14 kDa]

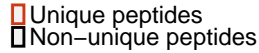
No. of times detected



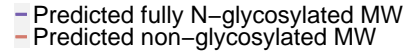
log(intensity)



Values from

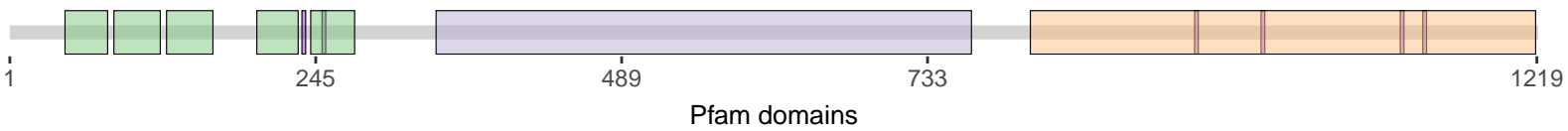
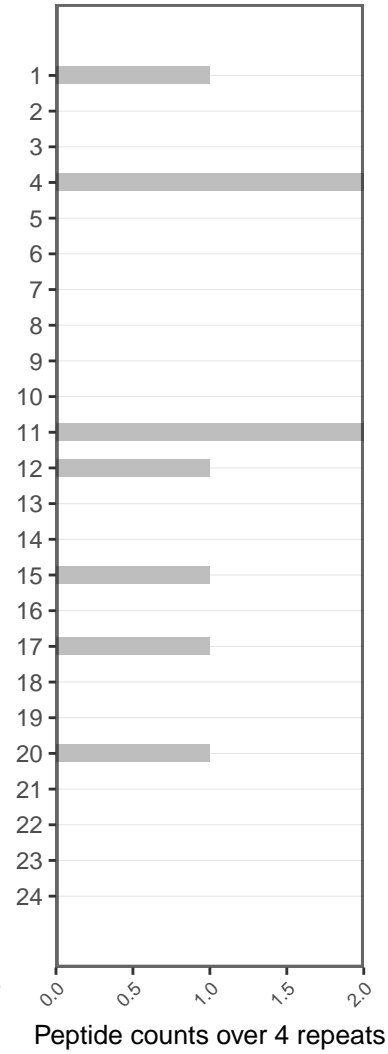
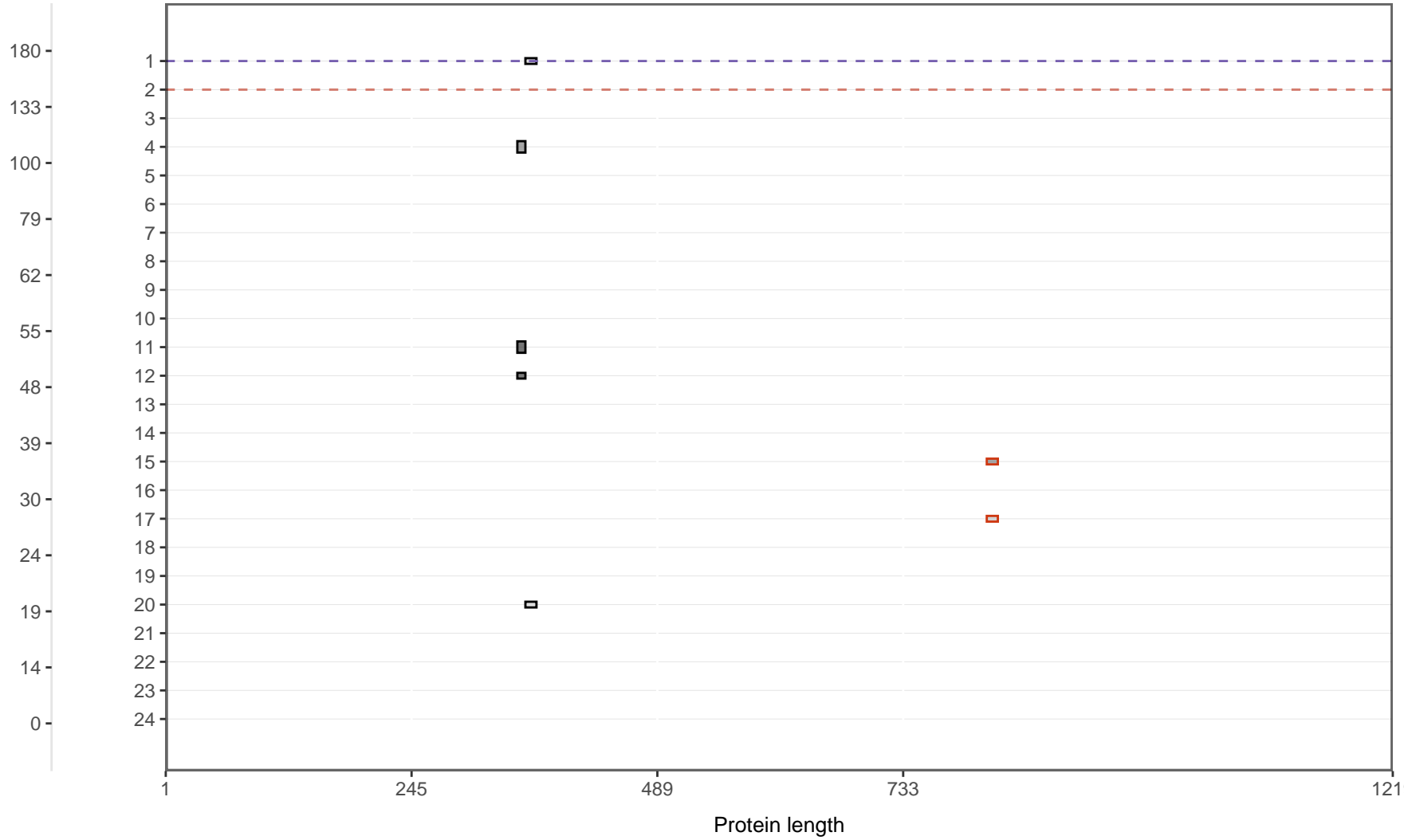


MW indication



Molecular weight

Gel Slice



Pfam Description



Protein sequence:

YFKLALKRKYDQVMSMRINSELOGGAMIAVLOGKGFPEVALHFVKDELTRFNLALESQNEIALESAAKLDGQDHWYRLGVEALRQGNAGVVEYQKTKNFRFLSFLYFTGNLQKSKMMKIAADVKNVMDGFHDALYLGQVRRVKKILENAGHPLAVYATATHLGLKDAERLGEELGENVPLPKKKAASLLPPTPLGGGDWPLMVTYKGFEGGLDQVYRGGHEEYEAADANWGESLDIGEVENLQNGDISMVLDEDEDDGOEENDEEVGVWLELDLPPDPTDTPK

NbL04g14070.1 endoglucanase_2-like [MW = 57.2 kDa]

No. of times detected



log(intensity)



Values from



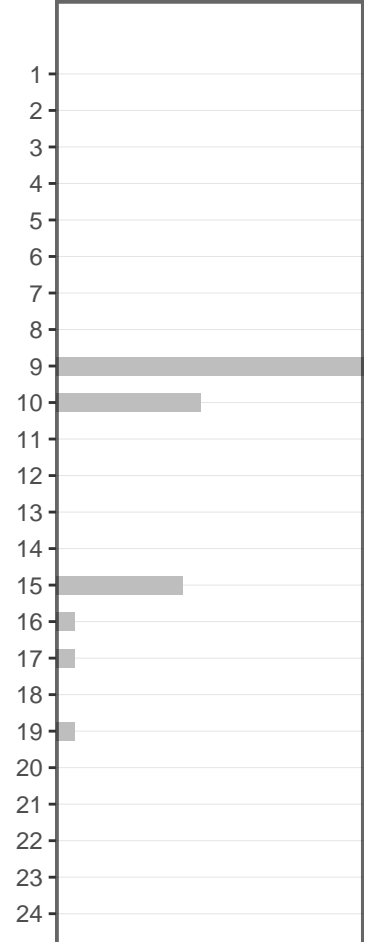
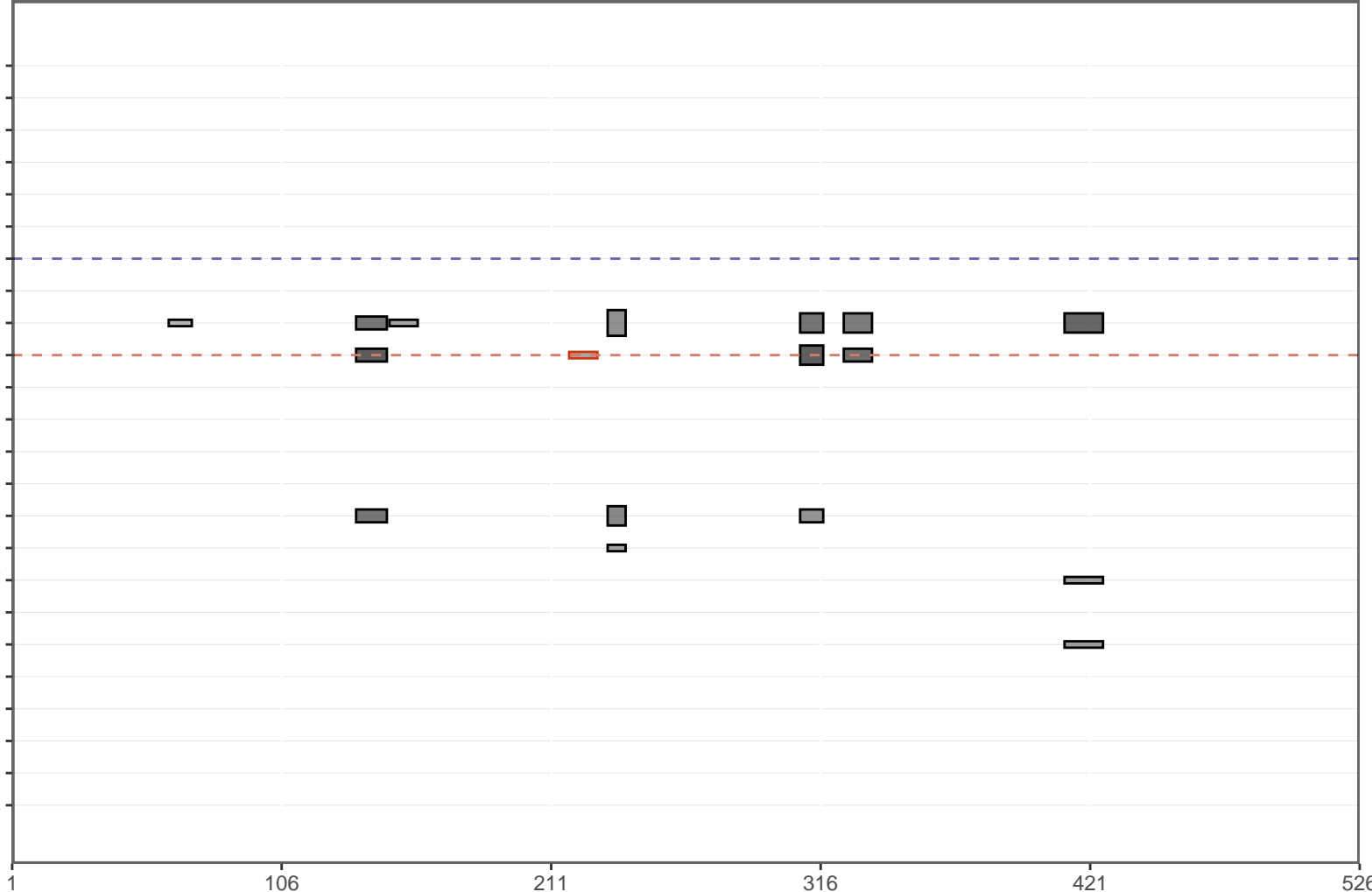
MW indication



Molecular weight

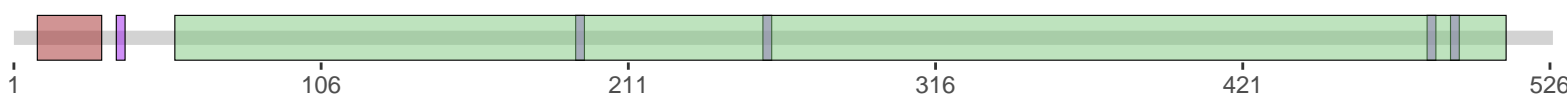


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EVATYYNSTGYDELLWAASWLYHATGGDSYVDWATGKNNADSGFNGFNPTWFSWQNKLAGTQVLLSRVGFDFDKGTNSBETLQEVKRTAEAVMGLLKPSPATSSRTDGLIWEVWNLQHPVASFALVLYSDVMLTERTAKTNGSDAYTPSGLRKFASGADYVLDGNPKMEHLVSGYGNYPQYVHHRGASPKDADTGGKDGWVWLDSTEPNPNVATGALVGGPFLNETYIDGRNNSMQAEPFTYNSAVIVGLLGLVTTSSVQSEFT---

NbL04g14030.1 tRNA_(adenine(58)-N(1))-methyltransferase_non-catalytic_subunit_trm6-like [MW = 48.75 kDa]

No. of times detected



log(intensity)



Values from



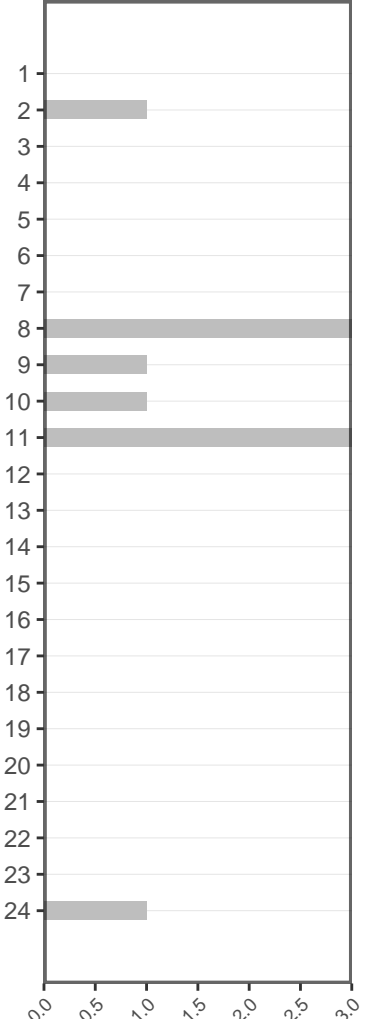
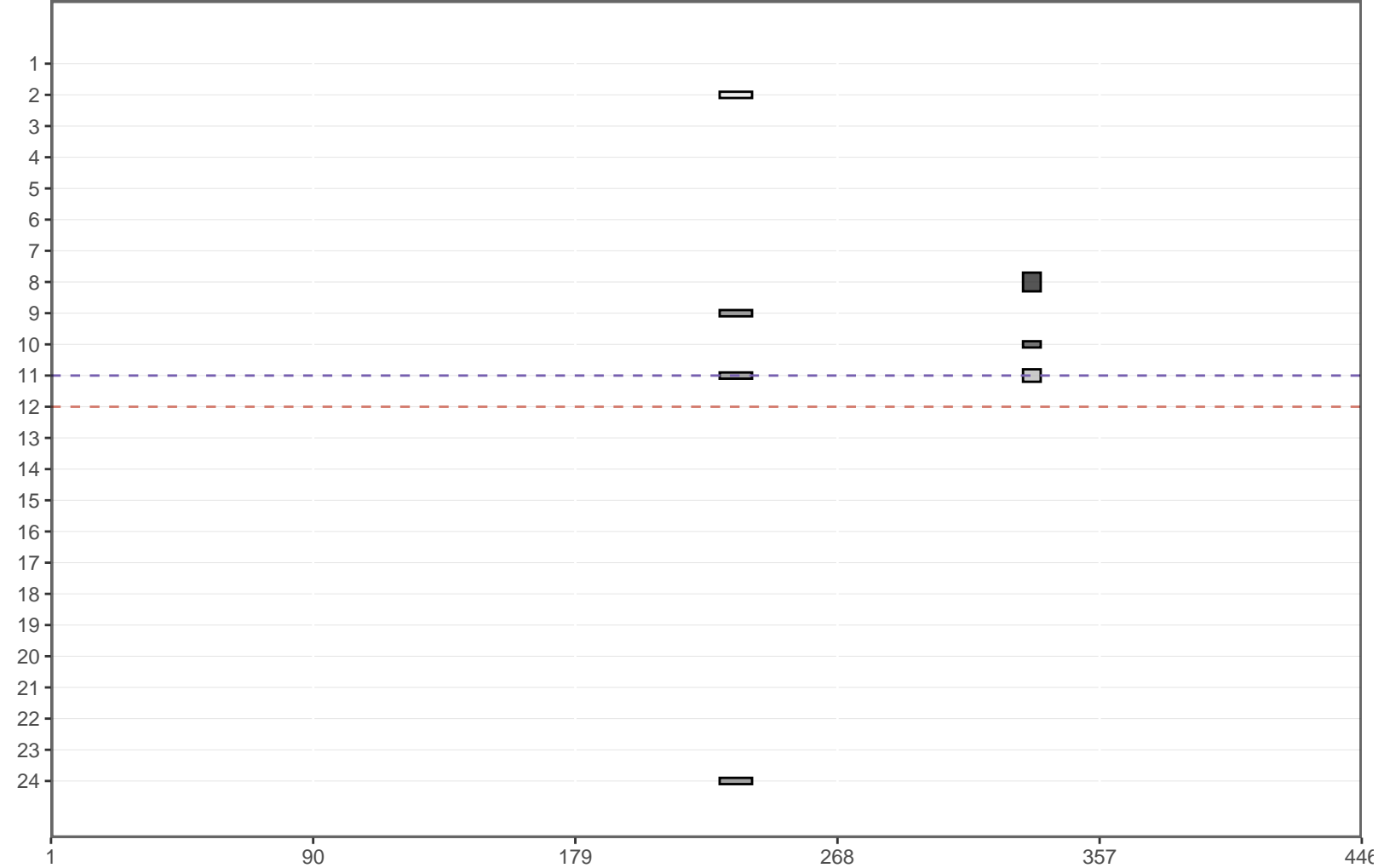
MW indication



Molecular weight

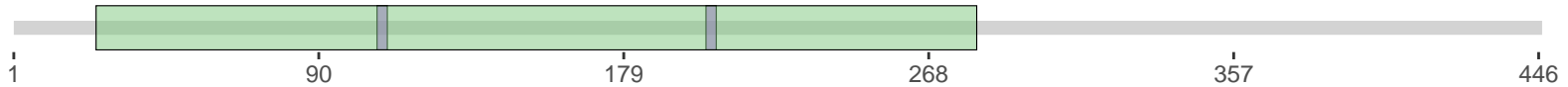


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YLVVDVYGGILTGAAERLGGTGVYGVNTYRGSPPVVDITRMFNINDEICKRIVHSLSDNLKLTGAIVSSEGGEEVLPATHSGGLEEVGSSEHSBMDITPEVSPPIKPKCKIKPGQKAPLEAKLWKENGFSSLIIAAPELDPWGIKEVLLPLAFSAPFAYVHQYVYQPLATCMHNLGIEKMAIGLQISEPWLREYGVLPSPRTHPHMQMSAFGGVILEGTRISSSEPTVTSN

NbL04g13960.1 hexokinase-2_chloroplastic-like [MW = 54.04 kDa]

No. of times detected



log(intensity)



Values from



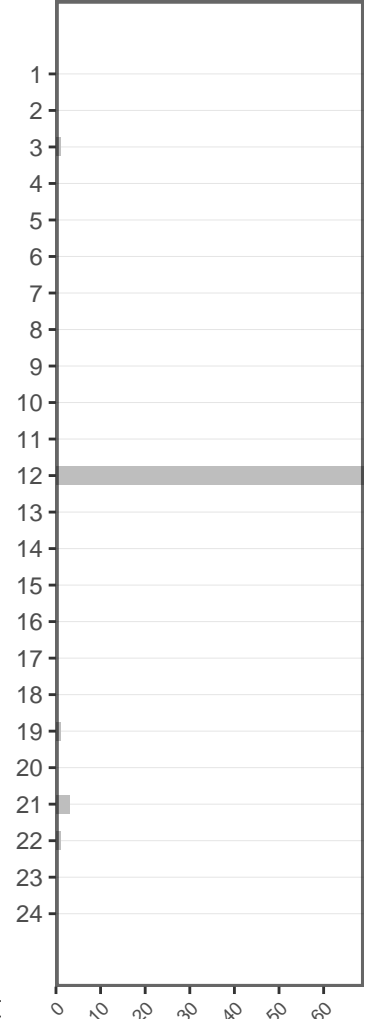
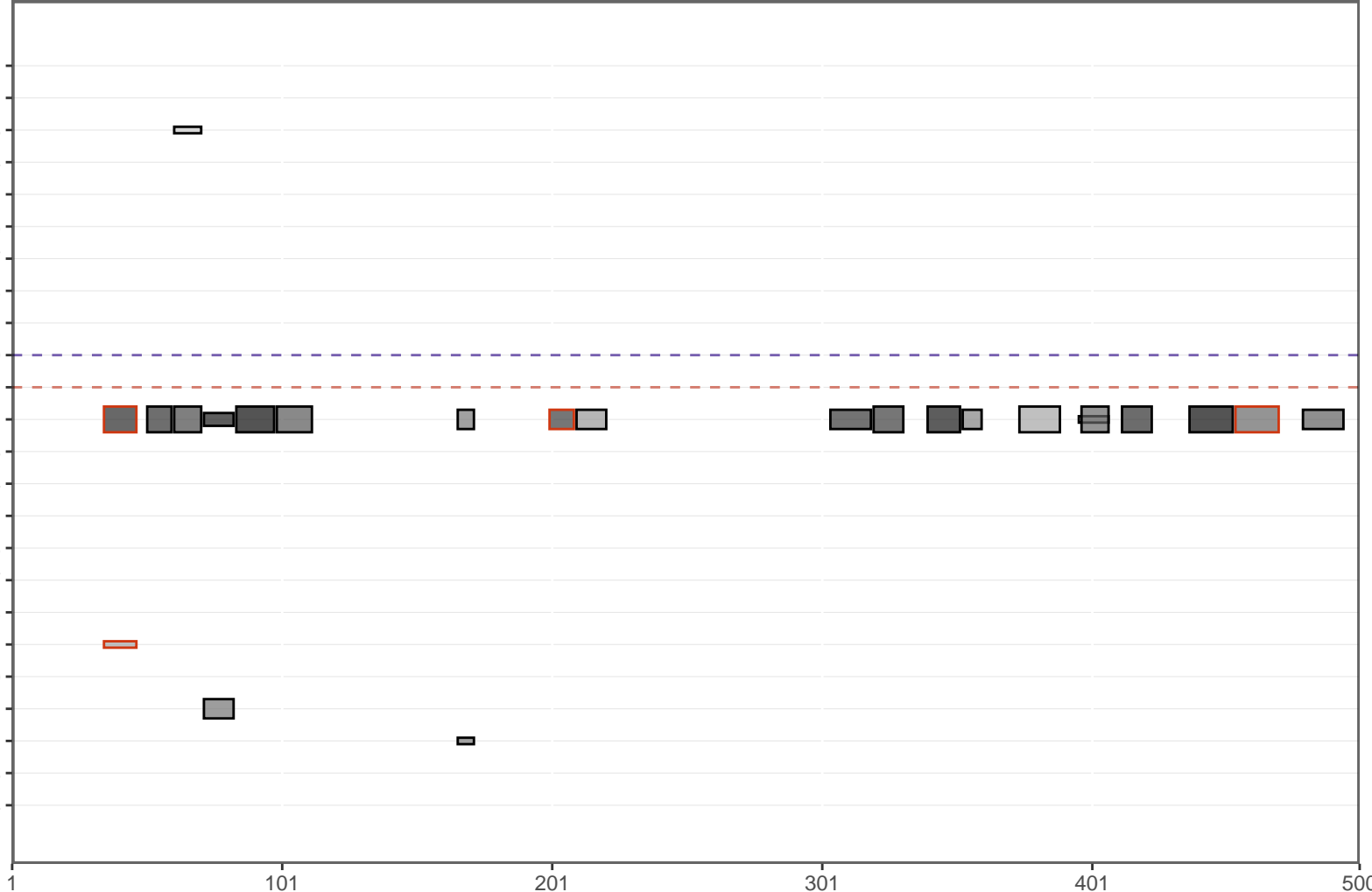
MW indication



Molecular weight

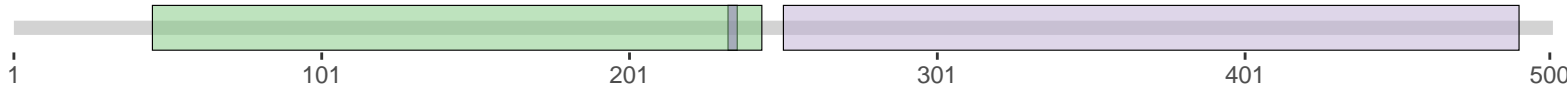


Gel Slice



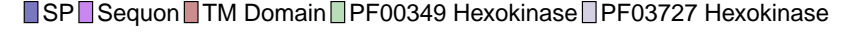
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ATLAGARYWDNDMMAVLGTGTNAGYVERVDMPKLPKRMBNSPVTIVFEWGFNSGLPLTFEDREMDASNPGEQFEKTHSGMYLGEIVRRVLRVMKVKVGLFGGGYVPEKLYTPFLRTPDCAHMGDTSRDLEAVESVLDIAGVKSGLNARKTVVDIGDTIAKRRGLAGAGIVGLKMEEDLKVGFGRKRTVAMDGGLYEHYKVPQYREVLGEAVTELLGSEISKNVIEHSNDGGGAAALAAANKYEHDY

NbL04g13880.1 tubulin_beta-1_chain [MW = 50.5 kDa]

No. of times detected



log(intensity)



Values from



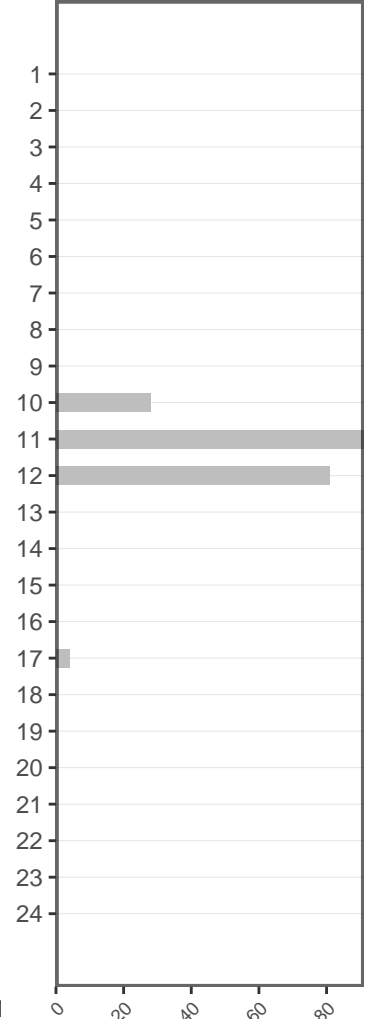
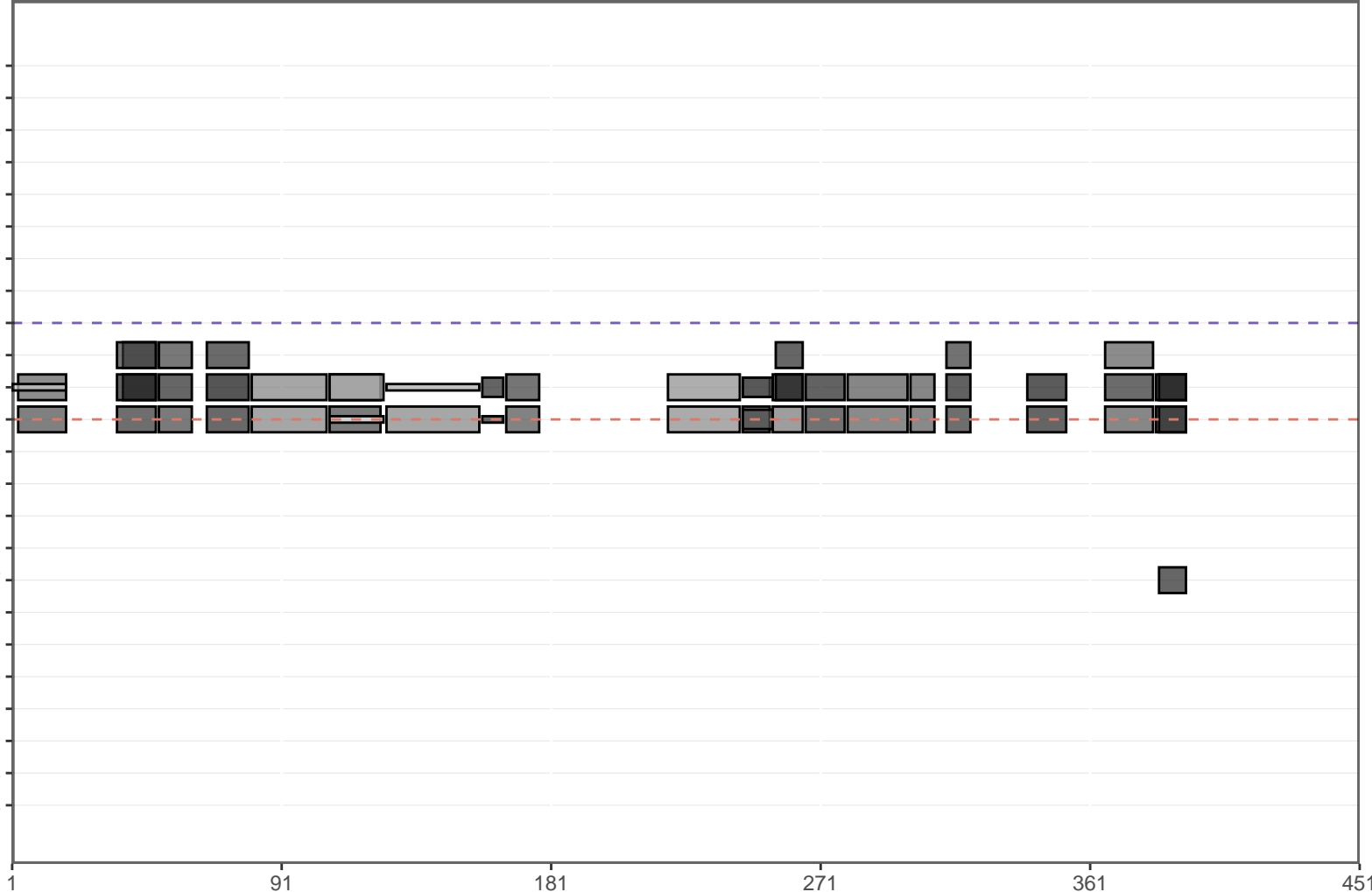
MW indication



Molecular weight



Gel Slice



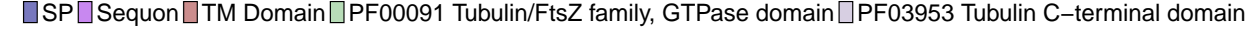
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ICFRTLKLTPSFGLNHLISATMSGVYTGGLRFPGLNSDLRKLAVLIPFRLHFFMVFAPLIRGSGGYSILTVPELTQGMVDAKNMCAADPRHGRVLTASAMFRGKMSTKEVDEGMINVGNKNSVYFVEWPNVNVKSSVGDIPPTGLKMASTFVGNSTSGEMFRFRVSEQFTAMFRKAKFLHWYTGEGMDEMEFTAEAGNMDLVAEYGGYGDATADDEEYEEEGAEHYES*

NbL04g13830.1 thaumatin-like_protein_1b [MW = 39.48 kDa]

No. of times detected



log(intensity)



Values from



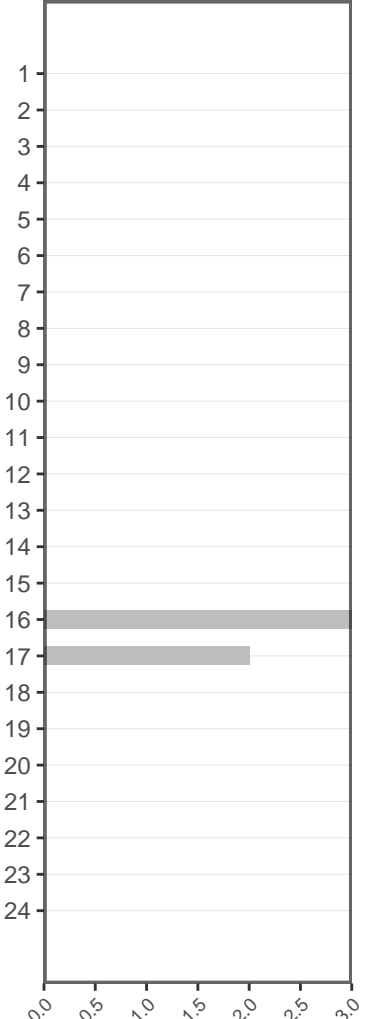
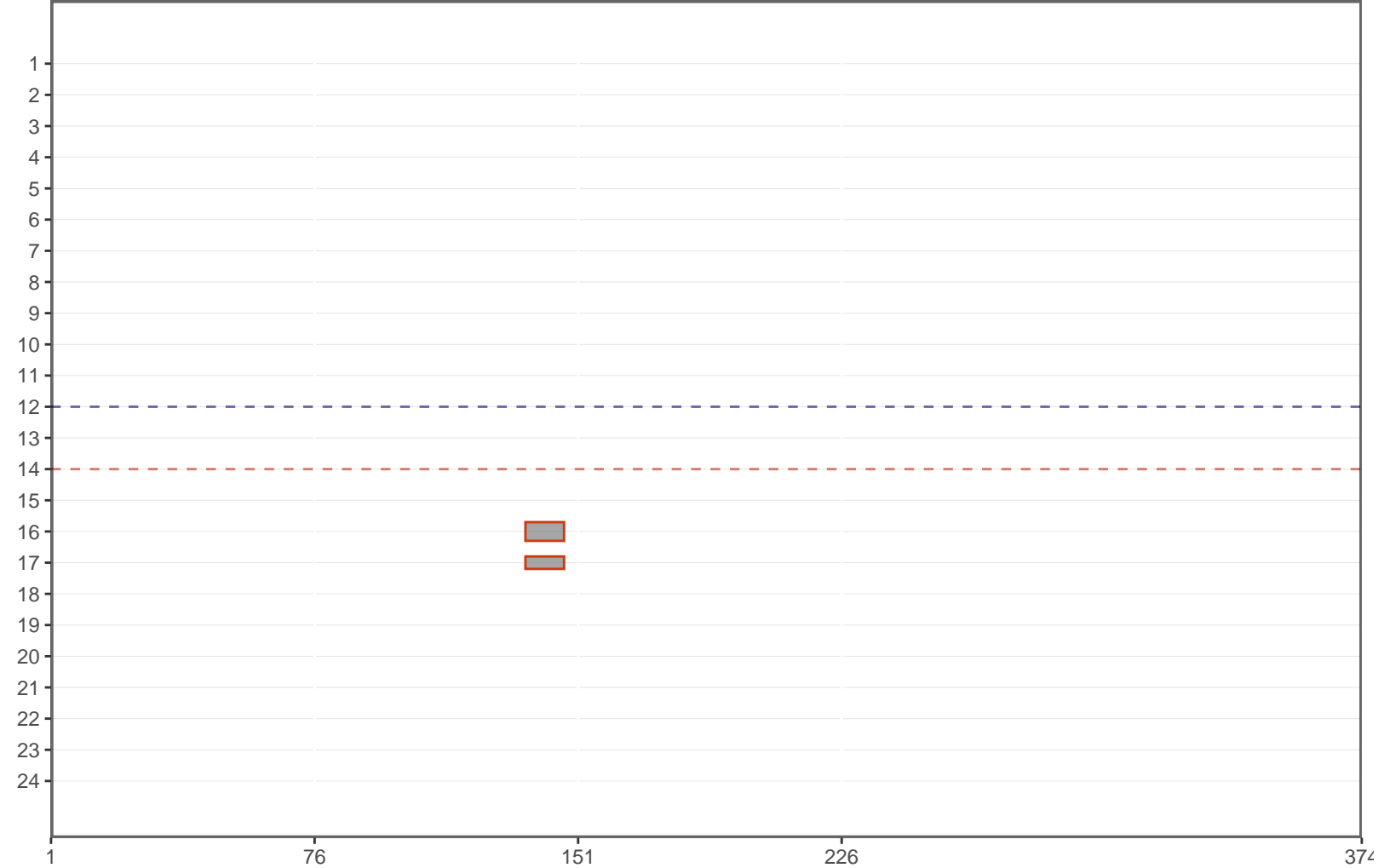
MW indication



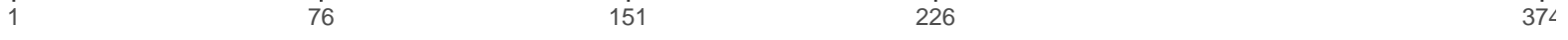
Molecular weight



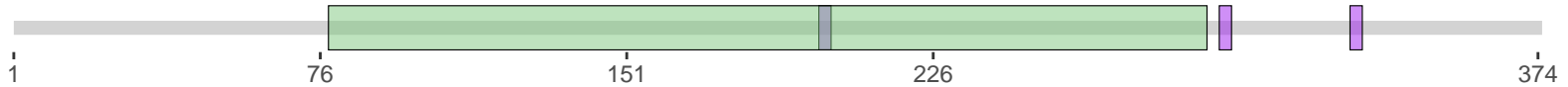
Gel Slice



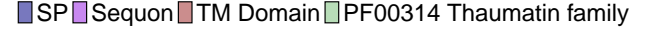
Protein length



Pfam domains



Pfam Description



Protein sequence:

YSLVDQYNLPLMLVFDGSSGNNCTSTGGVVDLNGACPBEKLVTSVGGVWVACKSAGEAFRRDEYCGAGAVNSPICKPSSVEMLFKKKAPRAYFAVDDKSTFTTGTGANLYITFCPSFNTGQKSSSTGGGNFRNGEPEDNSGNNVNPSTINGEMVYDGAWDVBSASSTTCAHVLSSPMMAGSIAFLTAWQLRHLP

NbL04g13750.1 prostaglandin_E_synthase_2-like [MW = 35.55 kDa]

No. of times detected



log(intensity)



Values from



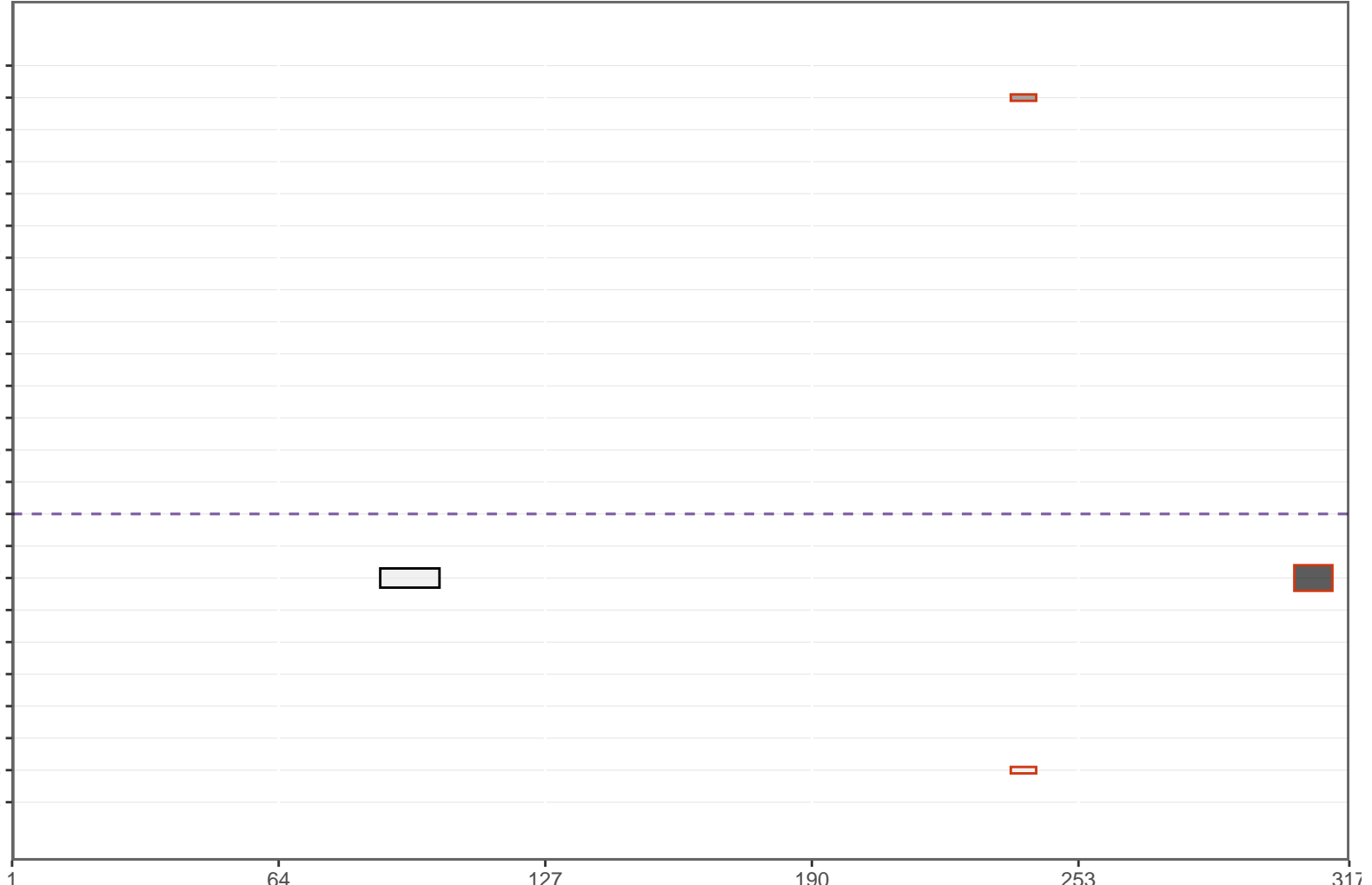
MW indication



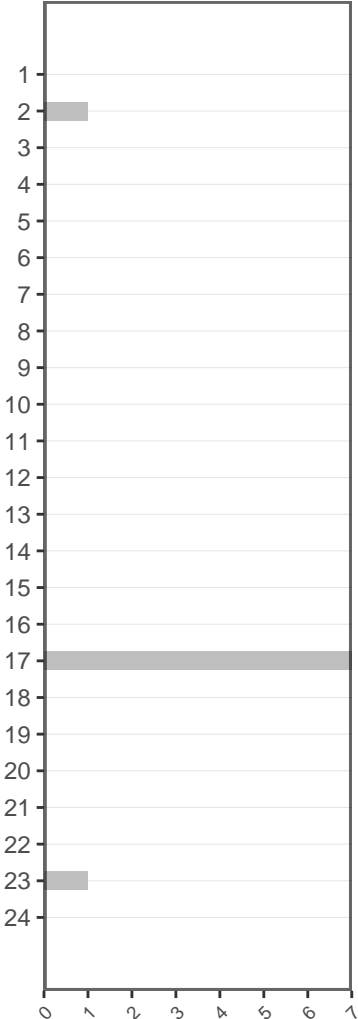
Molecular weight



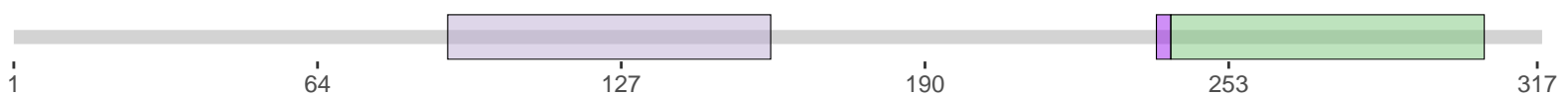
Gel Slice



Protein length

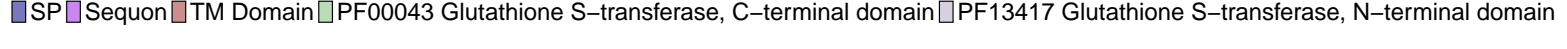


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

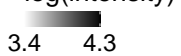
SSDIDKLFKYSVSDSTENADEESKWRKWDNHLVHLAPNIYRTTSEALESEFYTSHGNGFGRFTVKKYGGASMYFVSKRLKKKYNITDERAALYEAETWVDLKGKGRDFGGSKPLADLAVYGVLRPIRRLKSGRDMVENTHIGDWYGRMESAVGLSARIQA

NbL04g13700.1 CO(2)-response_secreted_protease-like [MW - SP = 84.43 kDa]

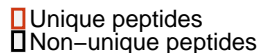
No. of times detected



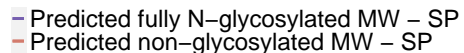
log(intensity)



Values from



MW indication

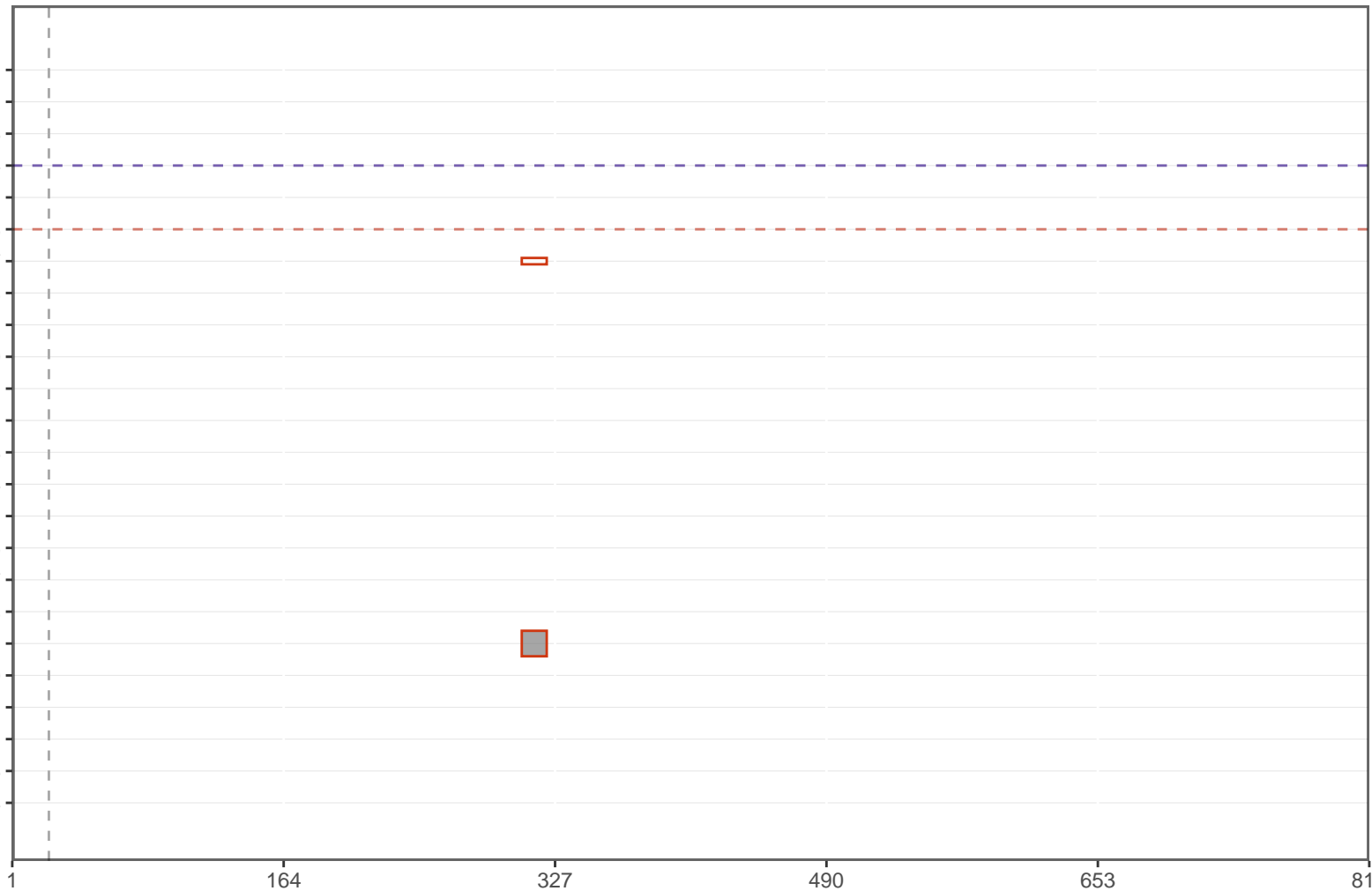


Molecular weight

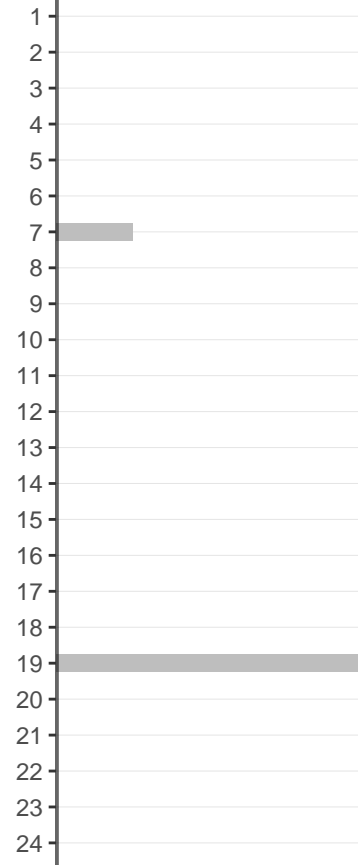
Gel Slice

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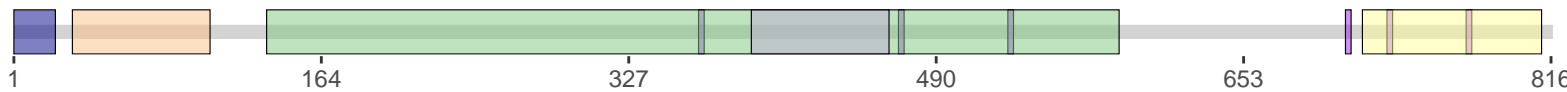
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Protein length

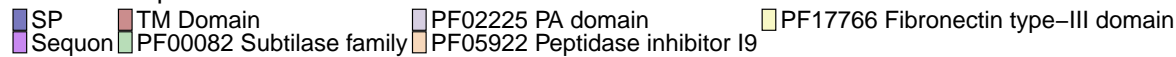


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

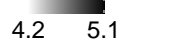
IARSCVPSLNEKKKYGKVLGHNHDEGYSPDKLEEKGGKGGIFLVDDNARTVAPKFSFAAAVTEKDGNEILSYINSTRNIPVABILPTVSKTKNKPVPVAVYFSRRGPNVTYLLKPKDTAPGVALAAWPGNDKTEAVFGGEPPLFNLGGTSMGCPHVGGIAAAKHAHNPWSFSAKSAKAMTTGKKSNLGYTDFQVWVMVRPPFGRPTLQELNAPSYLVYLVSEVFVTAQTNNLKASIFITNGSIAITPYDIGAGEASPGANPGLVYETVYADYLFQFLCSIGYDT

NbL04g13640.1 expansin-A11-like [MW - SP = 25.23 kDa]

No. of times detected



log(intensity)



Values from



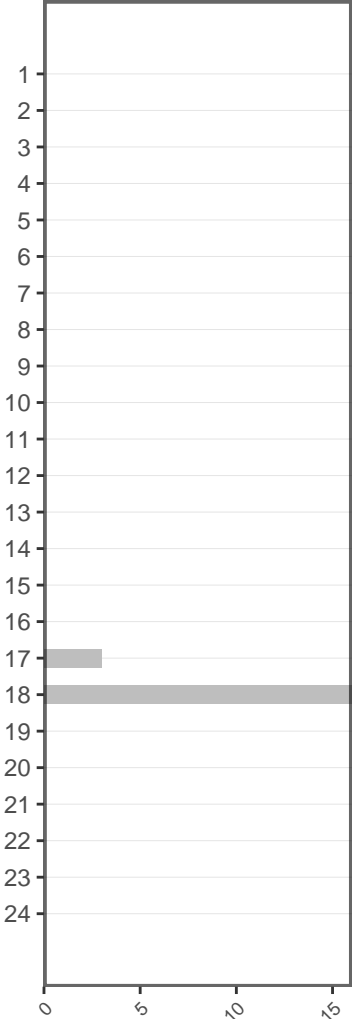
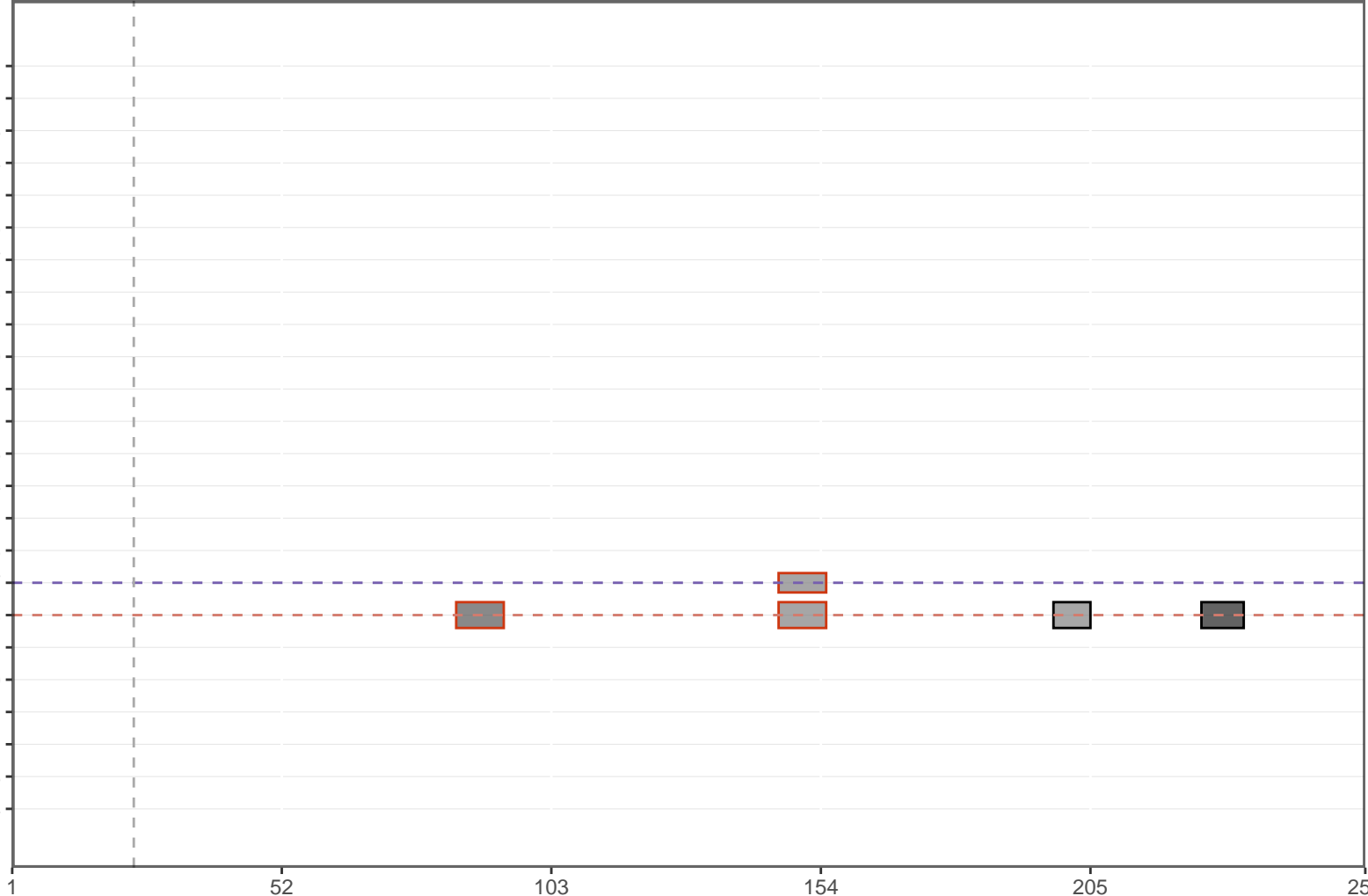
MW indication



Molecular weight

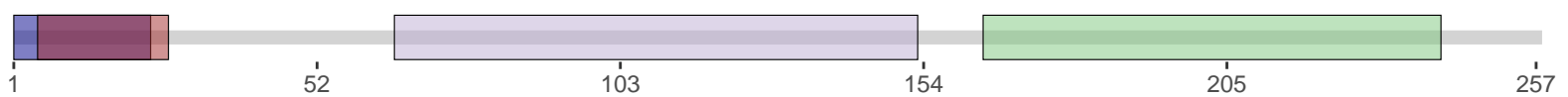


Gel Slice



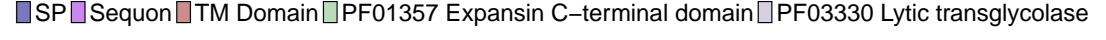
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

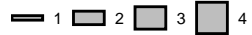


Protein sequence:

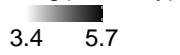
*SNNGGWCNPPRRHFDMAQWENHIGRGGVPGVQYGRIPCEKHKGGVRFETNGRNYFELLMISNHYGGAGSVDGSDVQKSKTNWMTMSRNSWGANVGSNLFNGDPLSRKVTITDQVTKTFLNAVPSNWHFGQTYETSINF

NbL04g13630.1 ribonuclease_P_protein_subunit_p25-like_protein [MW = 28.06 kDa]

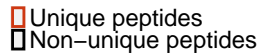
No. of times detected



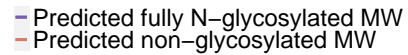
log(intensity)



Values from



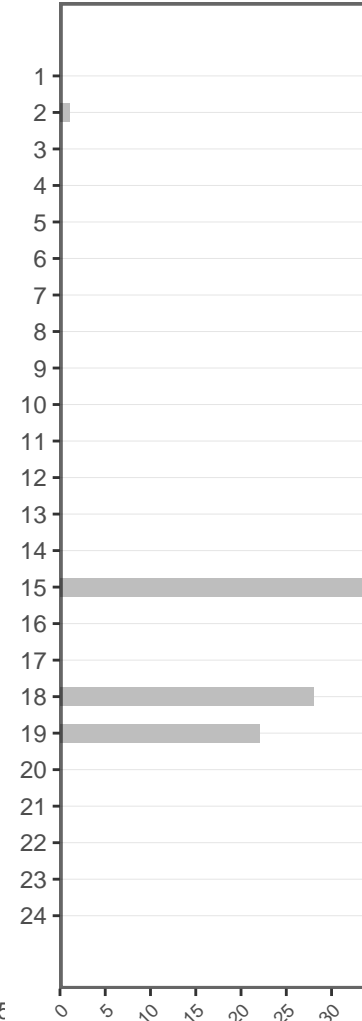
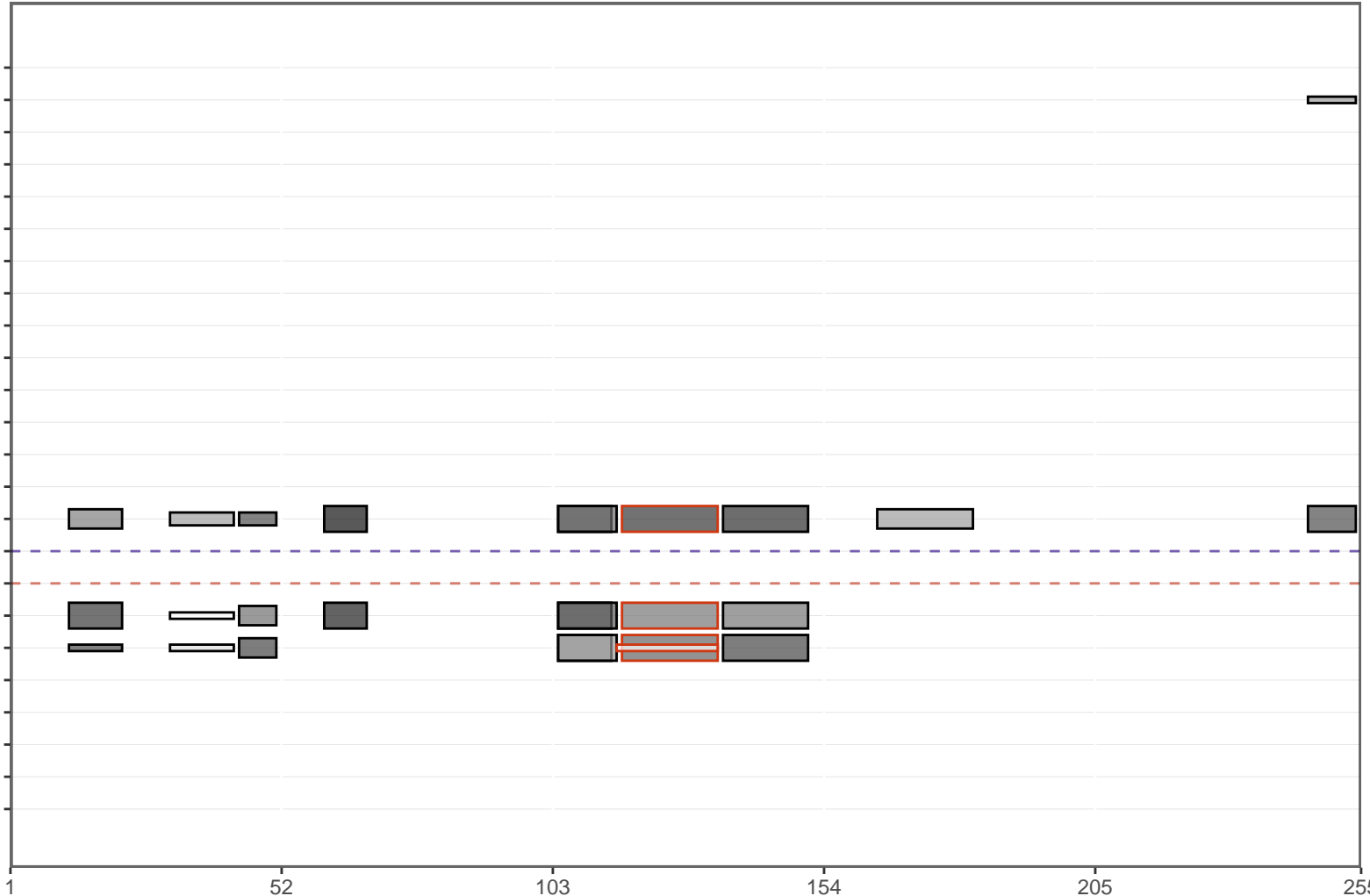
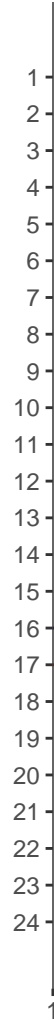
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL04g13360.1 enoyl-CoA_hydratase_2_peroxisomal-like [MW = 34.07 kDa]

No. of times detected



log(intensity)



Values from



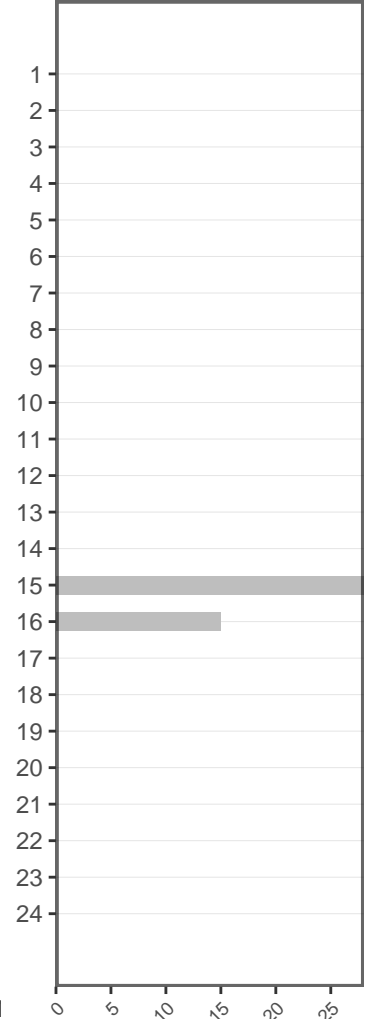
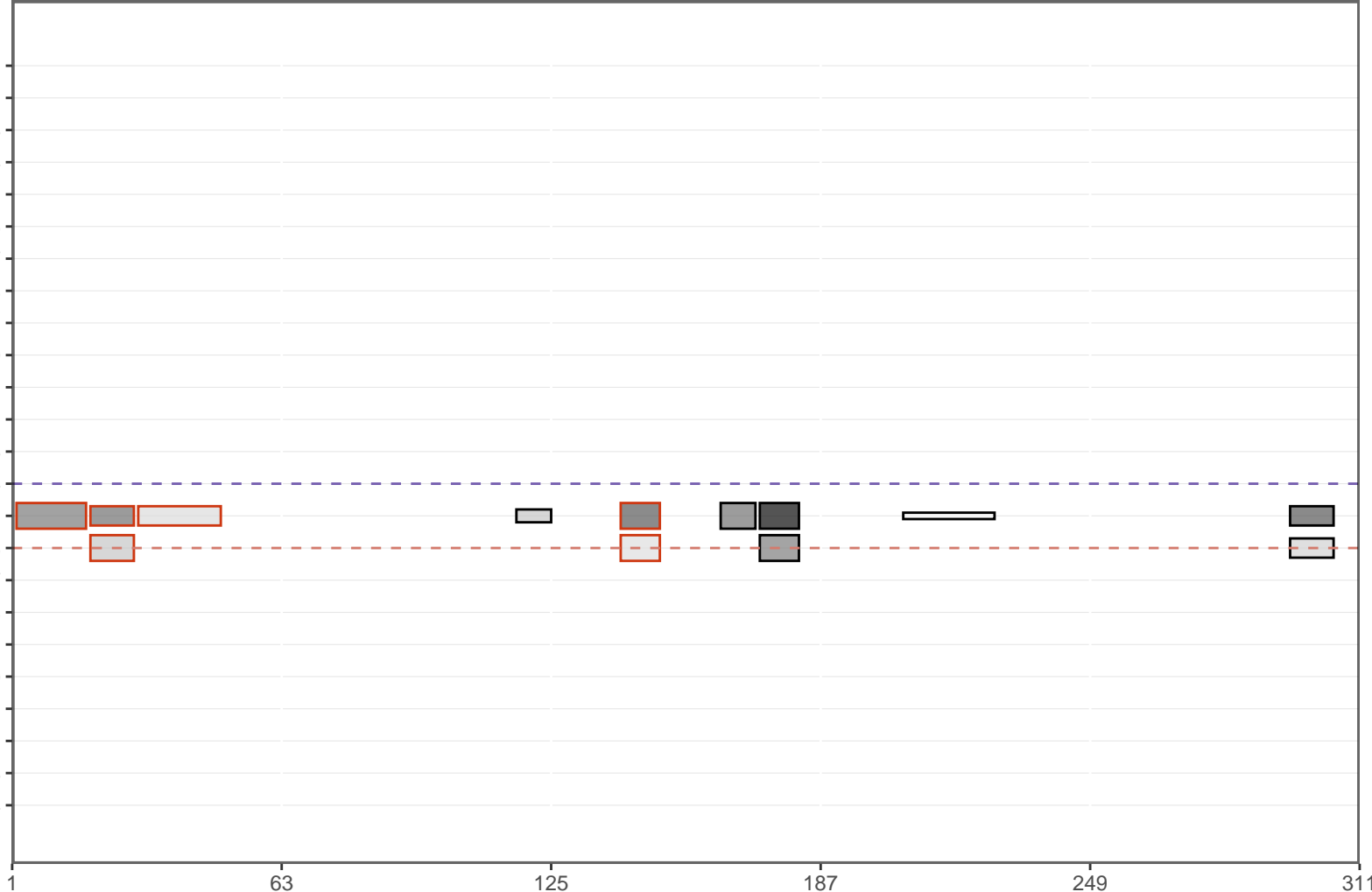
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

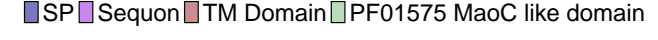
Protein length



Pfam domains



Pfam Description

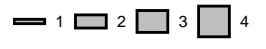


Protein sequence:

GEPLCMNRMSIYLRSGGGFKSRPYSYGRNPNENQTAFFPKPKGQPFVFEFGCTHAGDALLYRLSGDYNPLHSDPLWASAGFSRPLHGLGTLGFAIRAIGRIGRQDHTLKSIGSGLFLHLYVPGETLITEMWFEASRVIYQVWVKERNRAVLLGPFVLDLRINSEL

NbL04g13340.1 L-ascorbate oxidase homolog [MW - SP = 57.82 kDa]

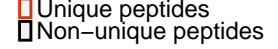
No. of times detected



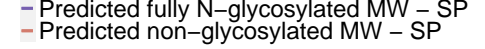
log(intensity)



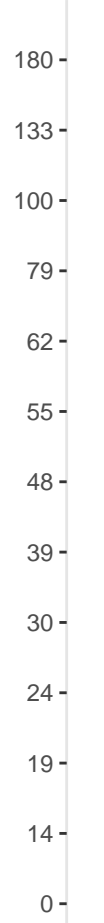
Values from



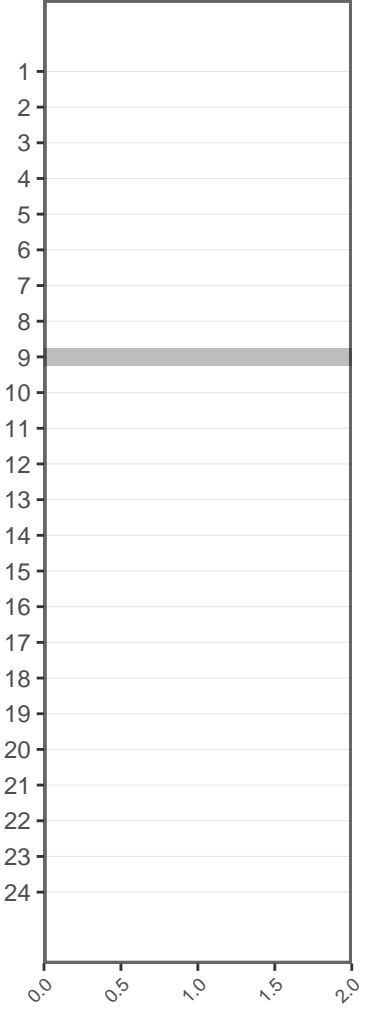
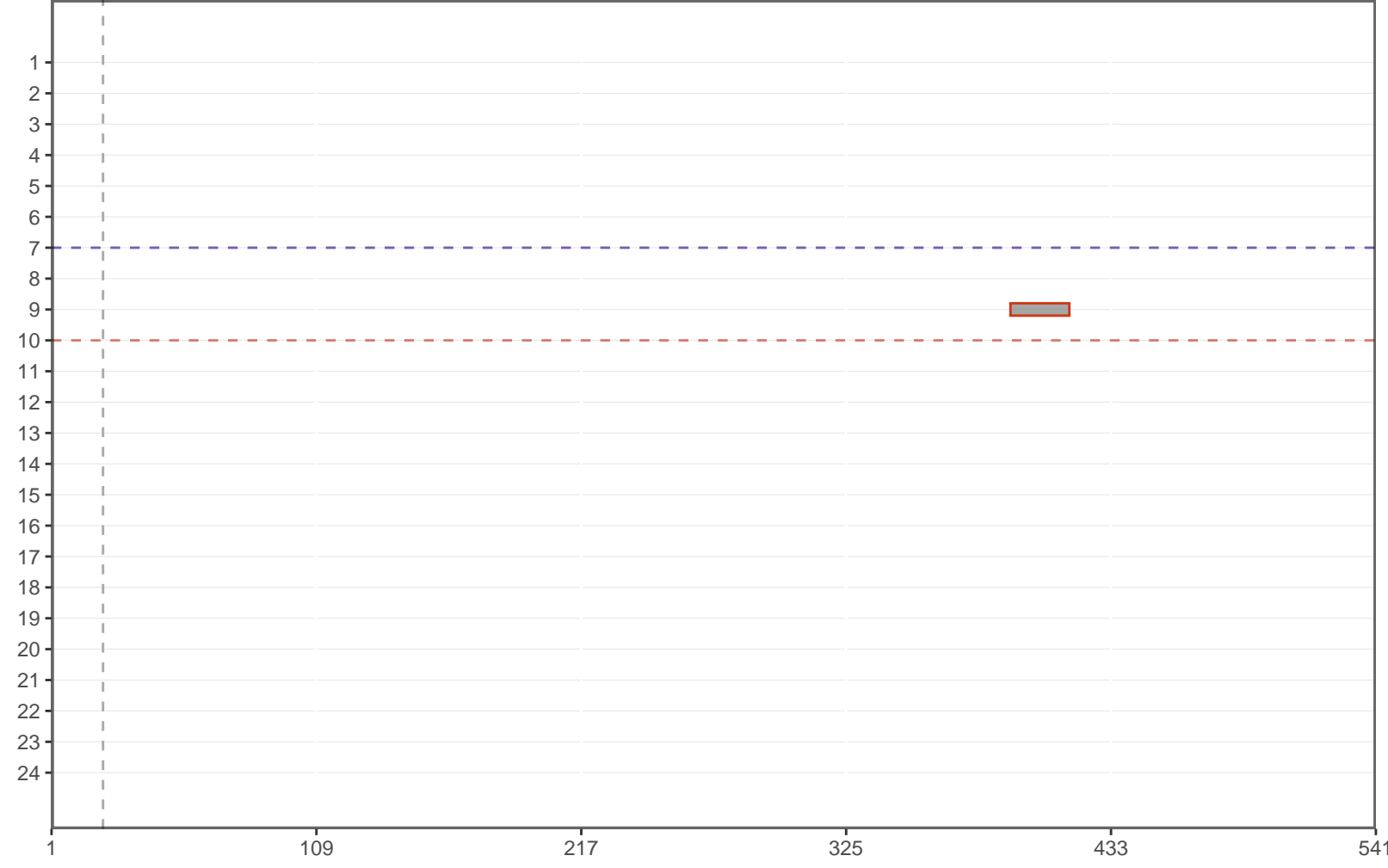
MW indication



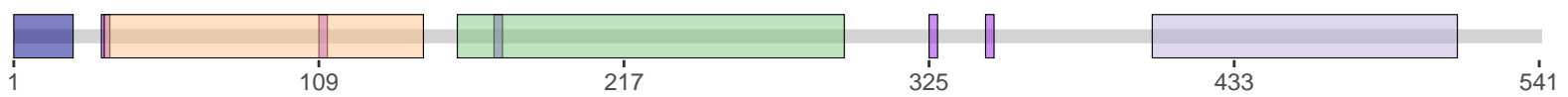
Molecular weight



Gel Slice

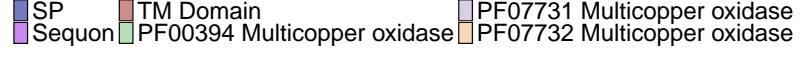


Protein length



Pfam domains

Pfam Description



Protein sequence:

LVLTADGEAKDHYVYVSSRFTSQVLTFTGVLYHYNSNTFVSGPPPGGPTQIDWELNDGRSRITLNSASGPRFNPQGGSYHYGMNTRTRIRLASSAGGVNKGQRYWVNVSVFPLDTPLKLLDFKVGGRVSGISDAPSGGGIFLDSVLGVDYRQFIEVFNENEDIVQGWLNGYVFWVYMGDGGVWTQASRNGYNLRDVAWRCFTQVYVYKSWYHIALDNLVGMANLRTEFWARQHLGGQLMRYVYFTSTLSLRDEVPVPRNARLGGKVRGRTRPL*

NbL04g13310.1 alcohol_dehydrogenase-like_7 [MW = 42.51 kDa]

No. of times detected



log(intensity)



Values from



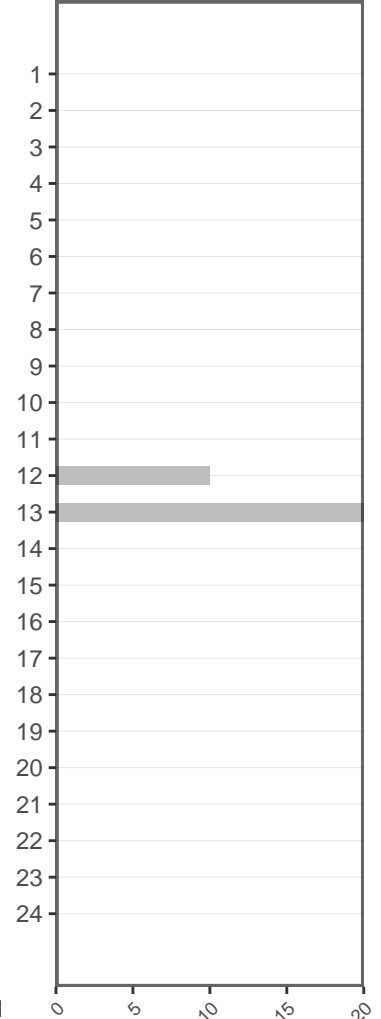
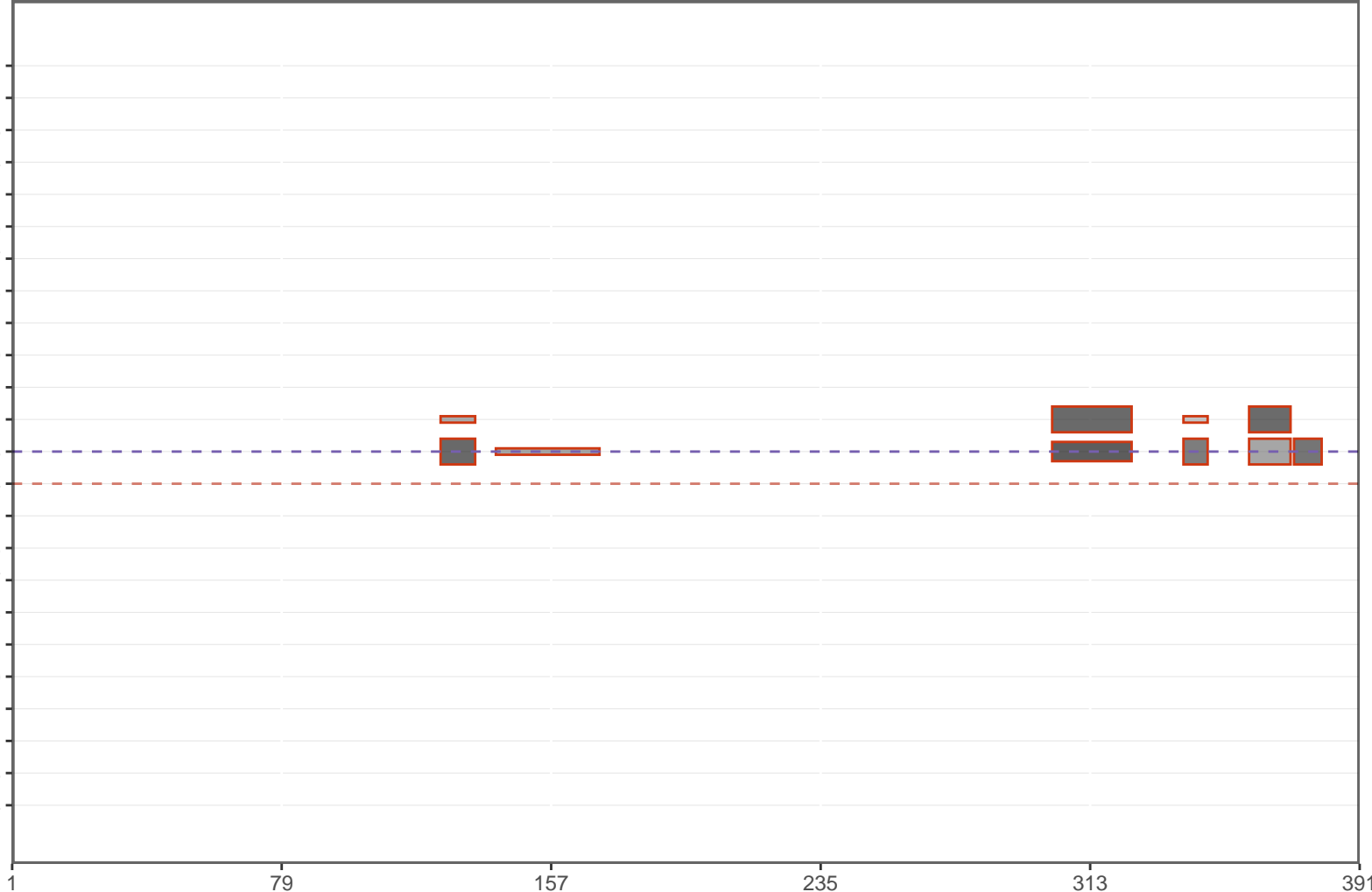
MW indication



Molecular weight



Gel Slice

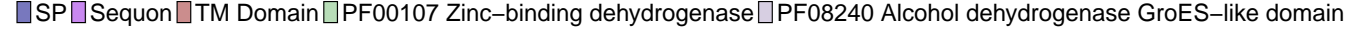


Protein length



Pfam domains

Pfam Description



Protein sequence:

IFSCCVSTGVGAAWKTANVEPGETVVFVFLGAGLAWAEGARLGDTRIGVDVNSDKFEKGFVDFNSNCGGDKFNSQVIEMTNGGADYCFEGVGLGTLVGEAFACRRKGGVKTIVLVGVKPKGAGLNLSFEVLSKTKLTGALFGGLKPKGSDVPLVVKRYLQKELQDKFVTHEVNFEDNKAFFDLIGGKSLRCVIMMDK*

NbL04g13290.1 phosphoprotein_ECPP44-like [MW = 23.61 kDa]

No. of times detected



log(intensity)



Values from



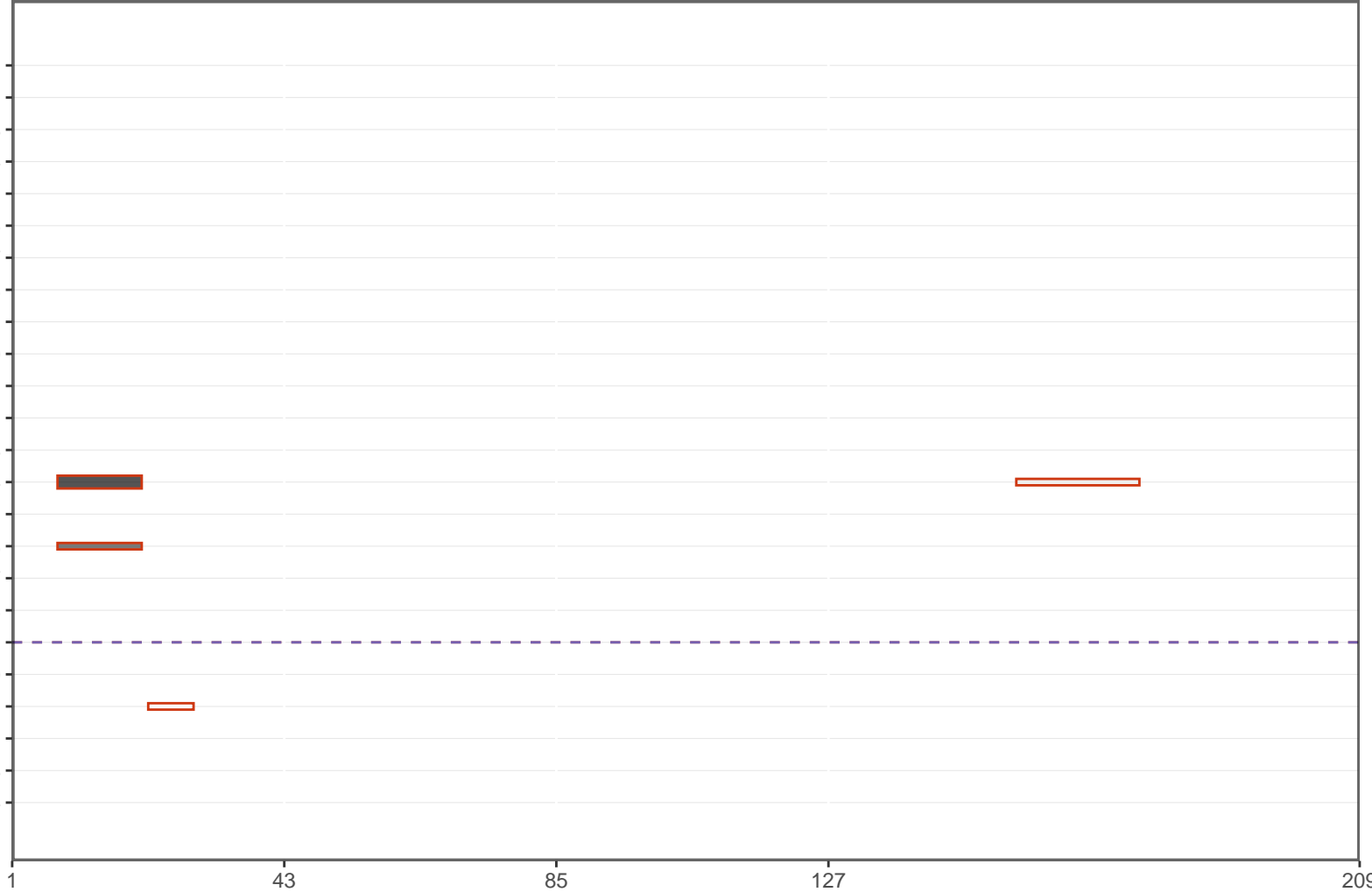
MW indication



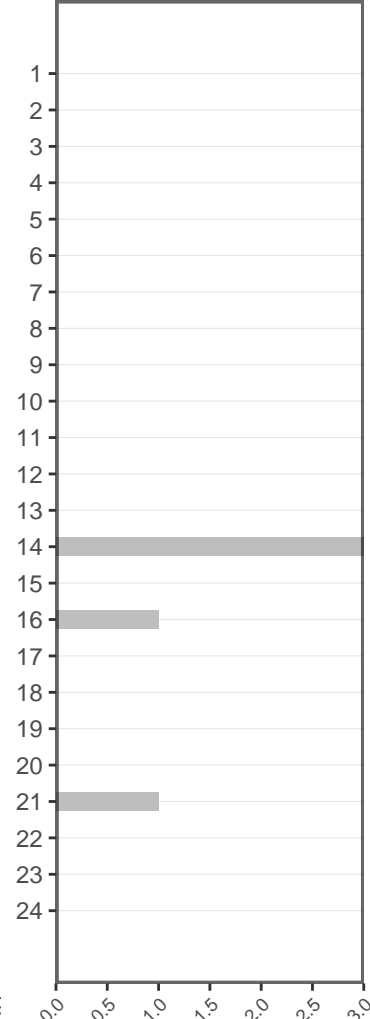
Molecular weight



Gel Slice



Protein length

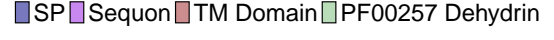


Peptide counts over 4 repeats



Pfam domains

Pfam Description

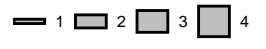


Protein sequence:

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NbL04g13150.1 14-alpha-glucan-branching_enzyme-like [MW = 97.47 kDa]

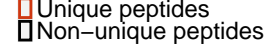
No. of times detected



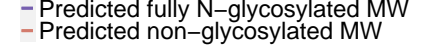
log(intensity)



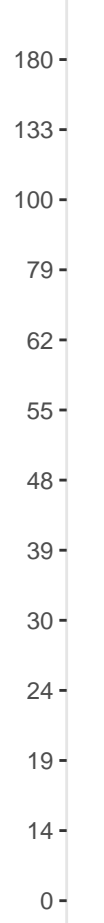
Values from



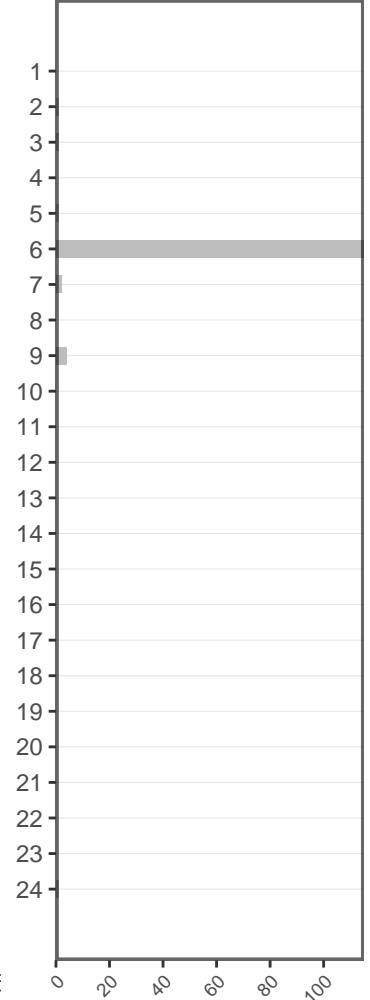
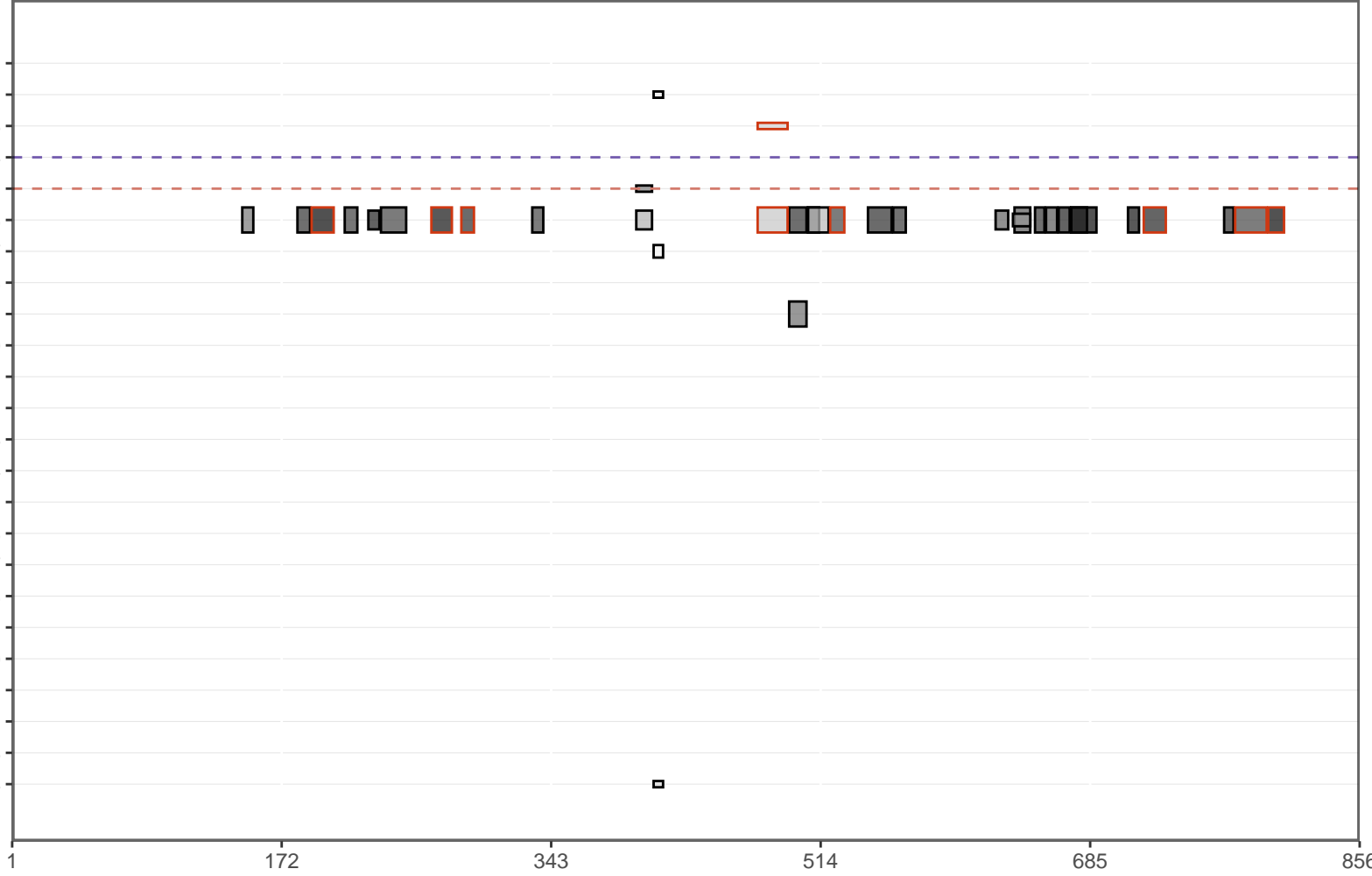
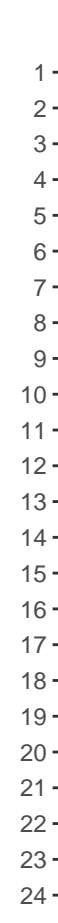
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00128 Alpha amylase, catalytic domain
- PF02806 Alpha amylase, C-terminal all-beta domain
- PF02922 Carbohydrate-binding module 48 (Isoamylase N-terminal domain)

Protein sequence:

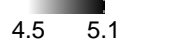
IWVLDENYFDGFRFDGIFSMVYVHHGINMGFTGNYHEVFSFATDVAIVVYLLANLNIHKVFDATVAEDVSGMPLGRPVSEGGIGFDVRLAAMPDKWIDPLKNNKDEWDSKMEVTRSLTNRRYTKNGIWAESHDDGIVGDKTIALFLMKEMVSGMSGLIDASPVVDGIALHKMHFFTMALGGEGYLNFMGNFEGHPKPEWDFPREGNHWSYDKCRRWQNLADSEHLRYKFMNAFRDAMNSLDEKFSFLAGKGVSTDEEDKVVVFERGDLVYVYFNPENA

NbL04g13100.1 isozyme_3_(LOC107771182)_mRNA_HF564633.1_Nicotiana_tabacum_mRNA_for_catalase_3 [MW = 57.02 kDa]

No. of times detected



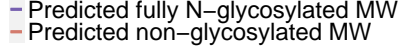
log(intensity)



Values from



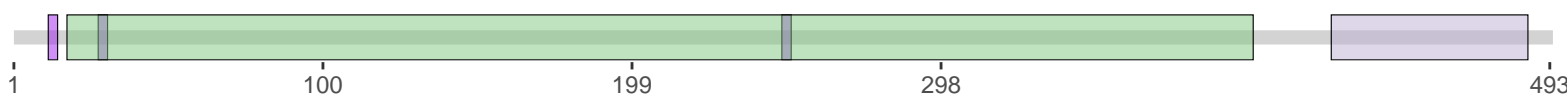
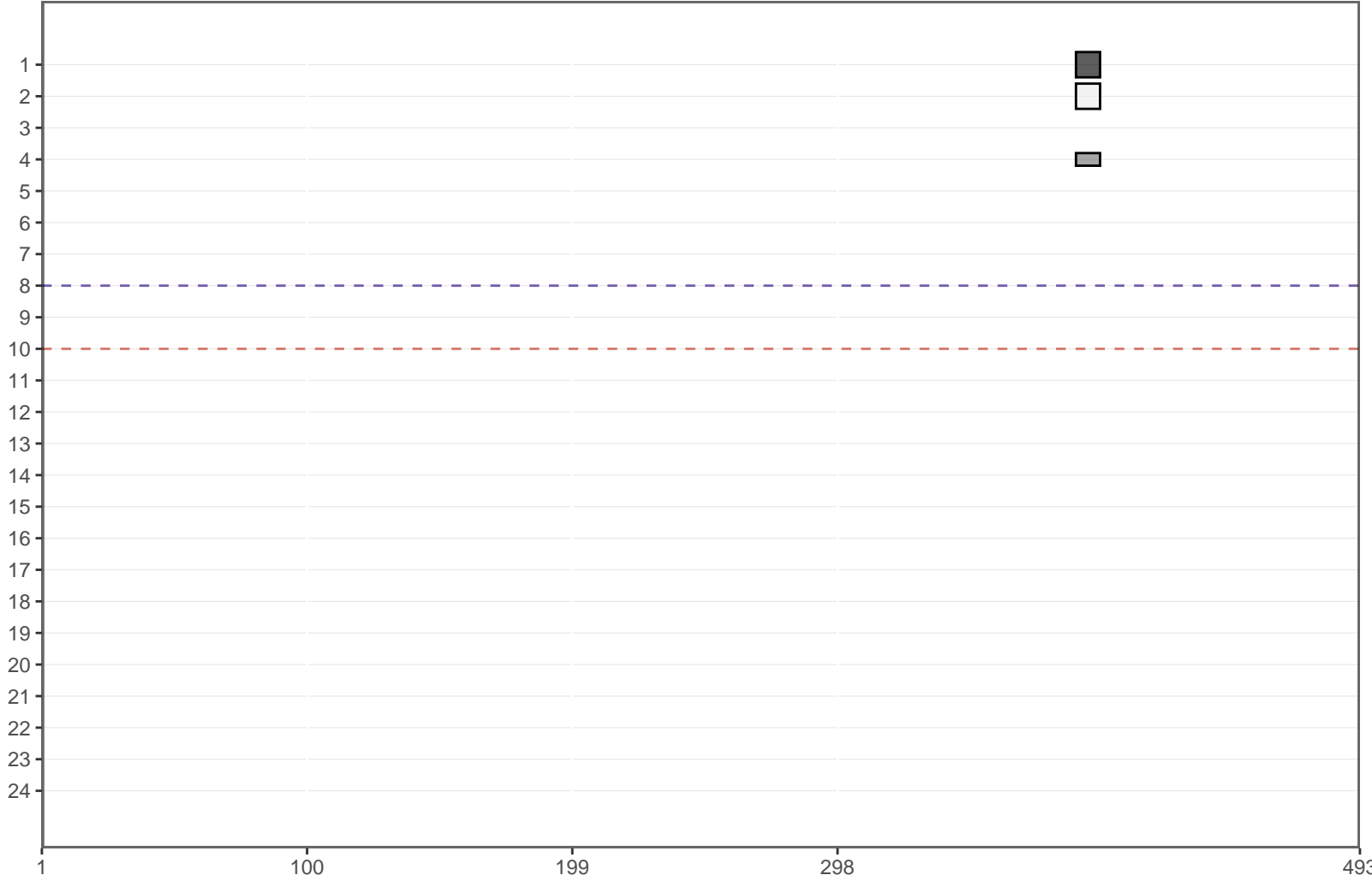
MW indication



Molecular weight



Gel Slice



Pfam Description



Protein sequence:

VKCLLEEEAKVGGANHEHATKDKLVDIAAGNYPWKLFGHQIDPDHEDRFDFDLVTKTWPEDLFLGFGVGLVLANKNDFFAENEGLAFQDPVAVPGVYSDGDKLLGTRFYSYEDTQRHRLGPNVYGLPNAKPKGAHNNHHEGFNFMIRDEEVNYFSPRFDCRIHAEGYPIPPRVLTGKRDKCKIEKNFKYQPGERYRSWTLDRGERFGRWWDALSDPRVTHEIRSIWISYWSGADKTLGGKASRLNVRPTM

NbL04g13010.1 epidermal_growth_factor_receptor_substrate_15-like [MW = 107.69 kDa]

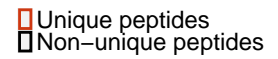
No. of times detected



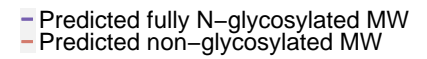
log(intensity)



Values from



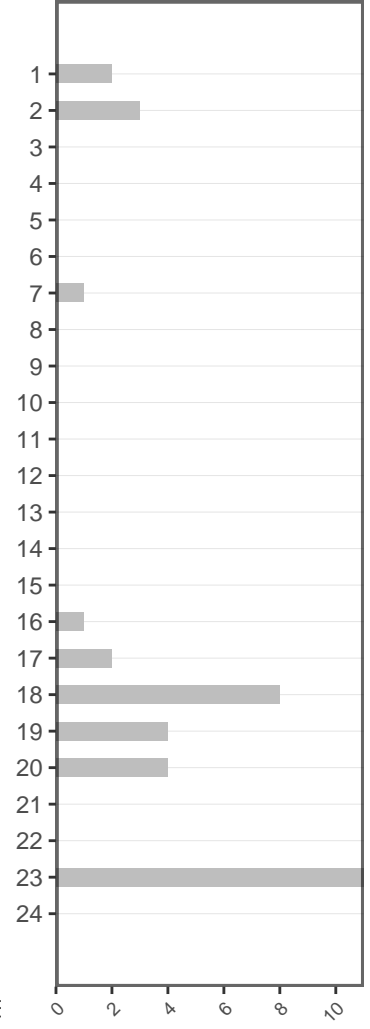
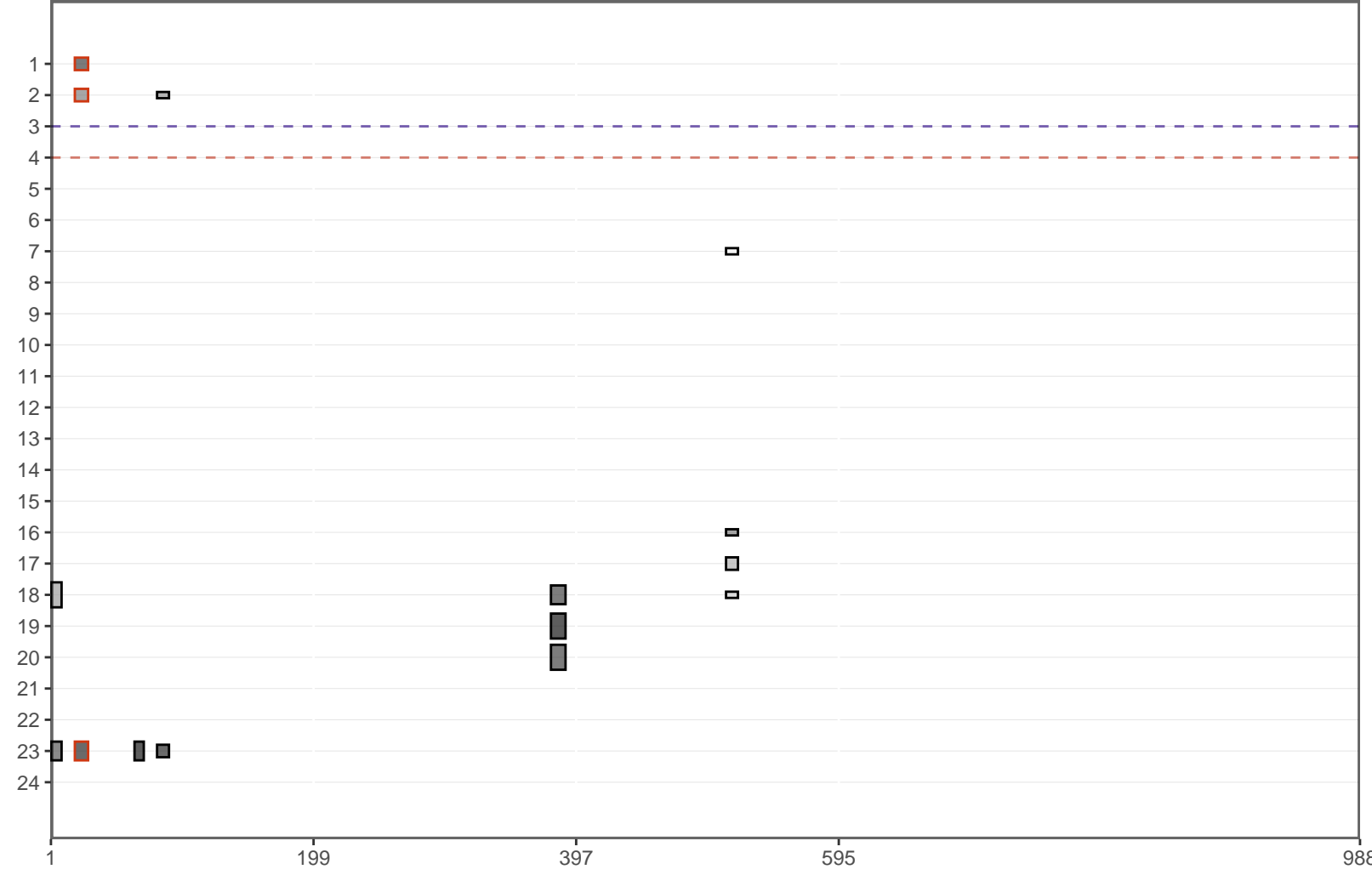
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CGLPGVQPCGAPGSLRPPPTGGVFPQDRBMGFNGQGNARATSMNSHMDQLSNGEONKLEPKREDVAWGEKDESKDNLVLDREKLEFYRTRMDQVLLYKRSKGNLNEITERALADKREAEMLAKKYEEKYKLVAEIAEKLTIEASFRDQERKLELGGAIKMGEGGSDGLGVADRVDQHDELELLKALADRKKHLELNKSTALIELPPQWGPPIVSAVWDEDDWIKFEDEGFSDVAAPANSKSTENGKKEIPKHGSDPDMMSNADTKSENYSAXONNNFET

NbL04g12970.1 protein_canopy_homolog_1-like [MW - SP = 18.82 kDa]

No. of times detected



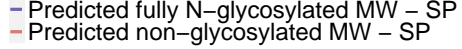
log(intensity)



Values from



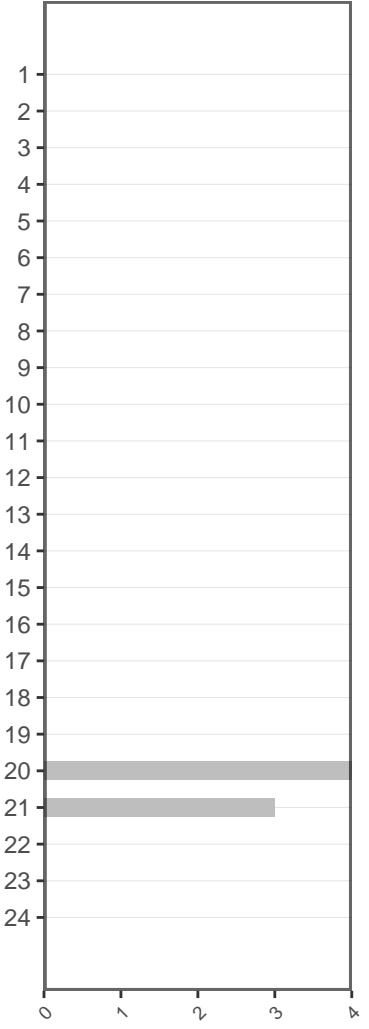
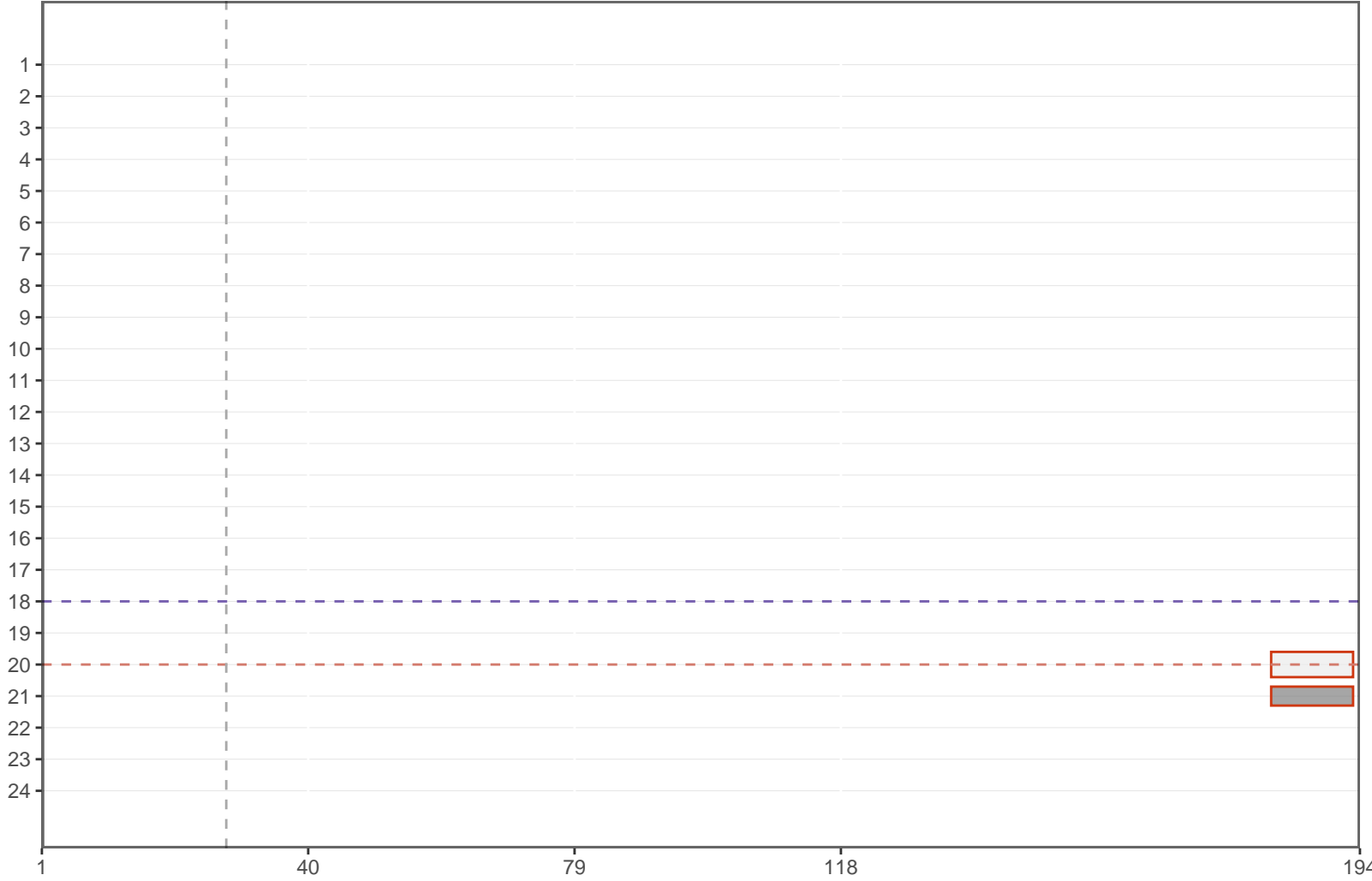
MW indication



Molecular weight



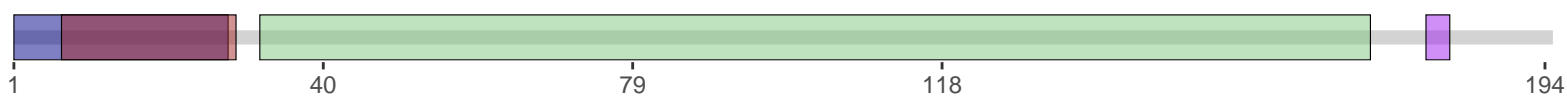
Gel Slice



Protein length

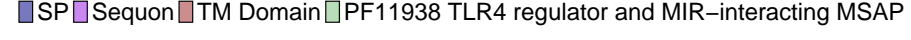


Peptide counts over 4 repeats



Pfam domains

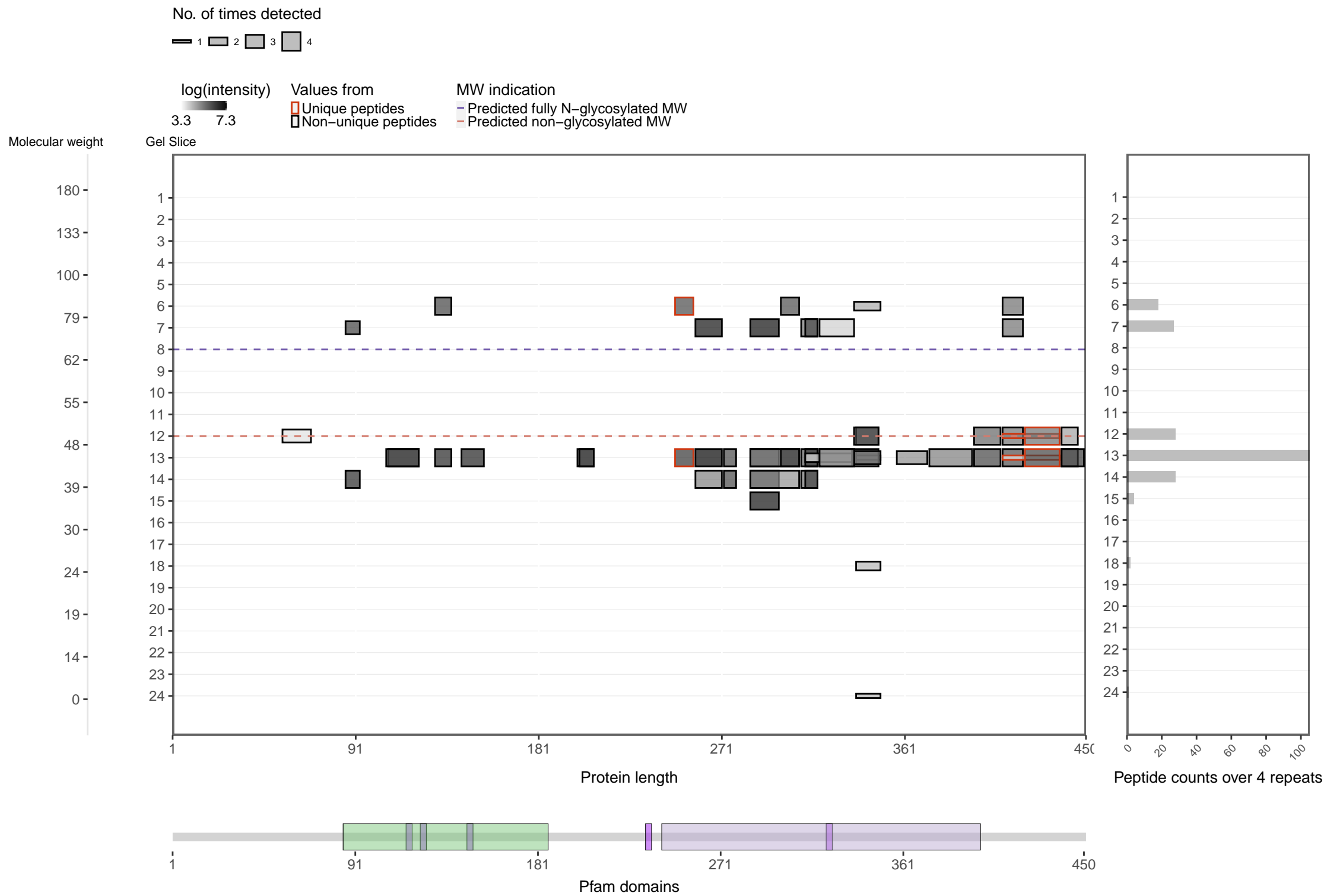
Pfam Description



Protein sequence:

EDLCEKMODYTLKIVDSSTKTKWVNNVLLKTKNDEARAHKKAISFGRLLEGTEDDFTLMKKGSGVGVGDVSKLLCEDLSNYGNGKSSNKTVGDENEDTDREL*

NbL04g12940.1 glyceraldehyde-3-phosphate_dehydrogenase_B_chloroplastic-like [MW = 48 kDa]



Pfam Description

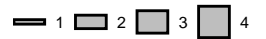
SP Sequon TM Domain PF00044 Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain PF02800 Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain

Protein sequence:

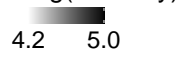
TYVGVNEQDY SHEVADHSNASCTFNGLAPFVWVWDEELSVKGTMTTHSYTGDRLLDASHRDLRRARAAALNVPTSTGAAKAVSLVLPQLKGLNGLAIRVPTFNVSVDIVVNAVKIGTAEQVNAFRKAAADGPKGLVAVGDEPLVSVDFRGSVDSSTIDSSLTMMVSGDDMKVWVWVNEWGYGSRVVDLAHLVANKVPGVWVAGSGDPLDFQCKTNPADDEEGKYVE

NbL04g12870.1 thiamine_pyrophosphokinase_2-like [MW = 29.53 kDa]

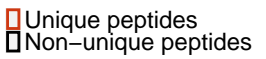
No. of times detected



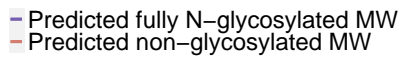
log(intensity)



Values from



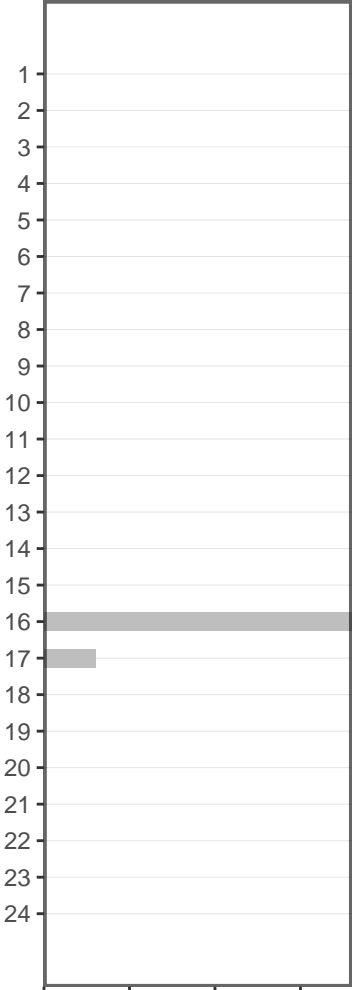
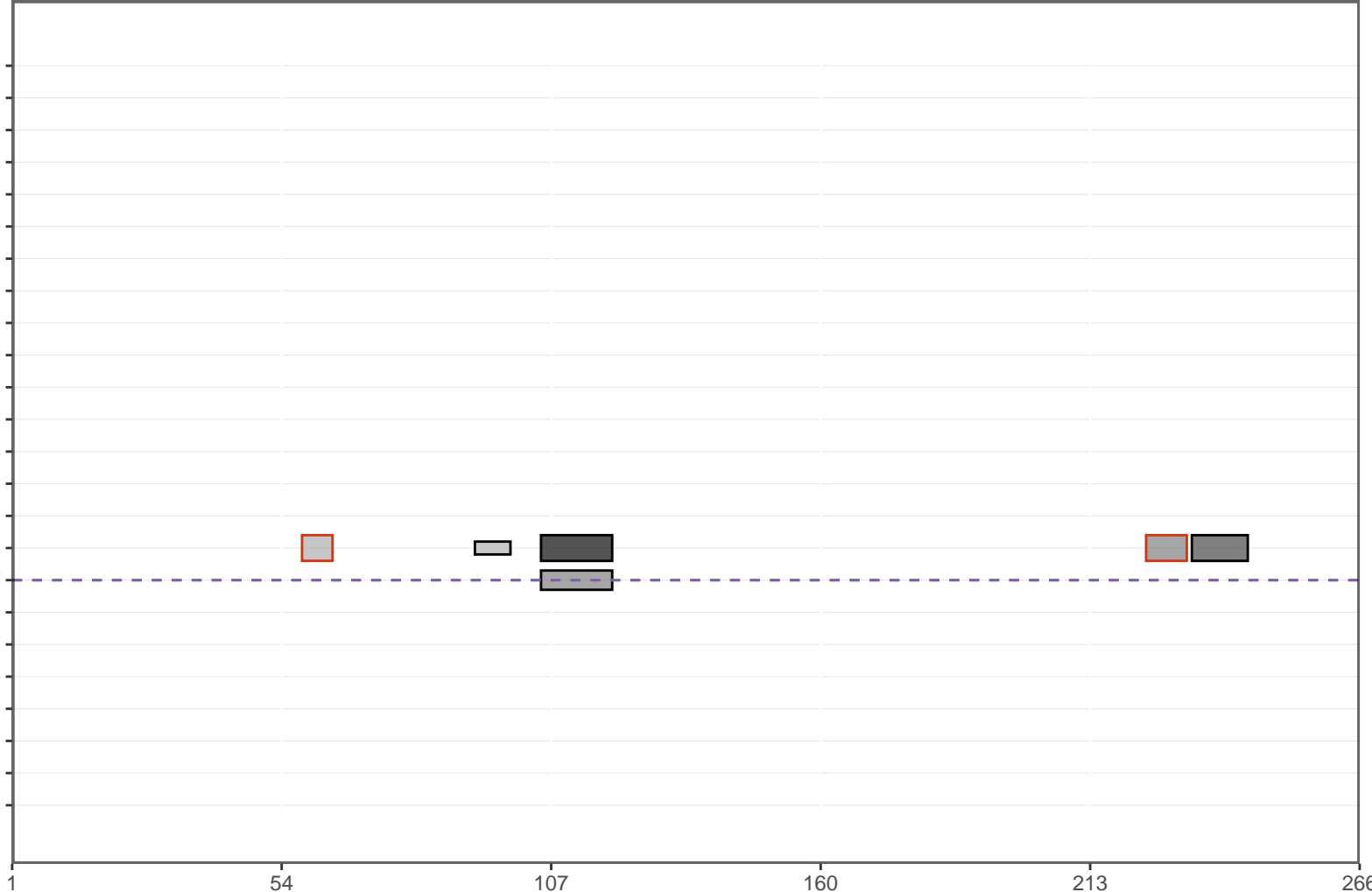
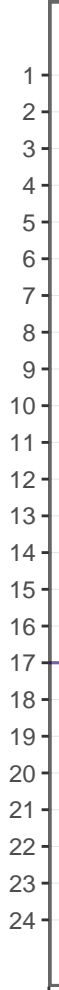
MW indication



Molecular weight



Gel Slice

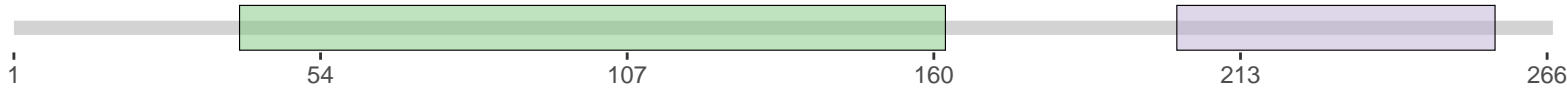


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF04263 Thiamin pyrophosphokinase, catalytic domain
- PF04265 Thiamin pyrophosphokinase, vitamin B1 binding domain

Protein sequence:

HKCVYRELLNLEHPNGLVTGALGGRFDEMGNNVGHFFSPMPILLSDDCUQLLPSTHKKHGHSSVEGPHGGLPIGTAGLKPIGTAAGRFTTTGLKWNLDDETEMRFGGLVSTSNVKNVITVQGESDQLWTRISKEE

NbL04g12720.1 cinnamoyl-CoA_reductase_2-like [MW = 43.43 kDa]

No. of times detected



log(intensity)



Values from



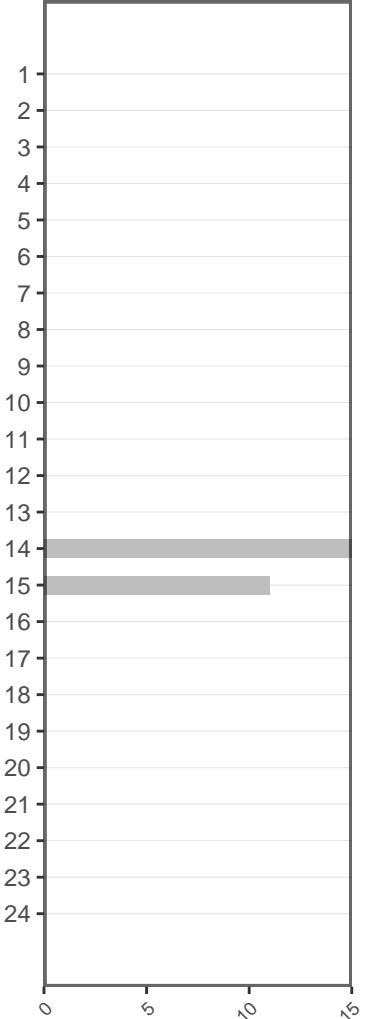
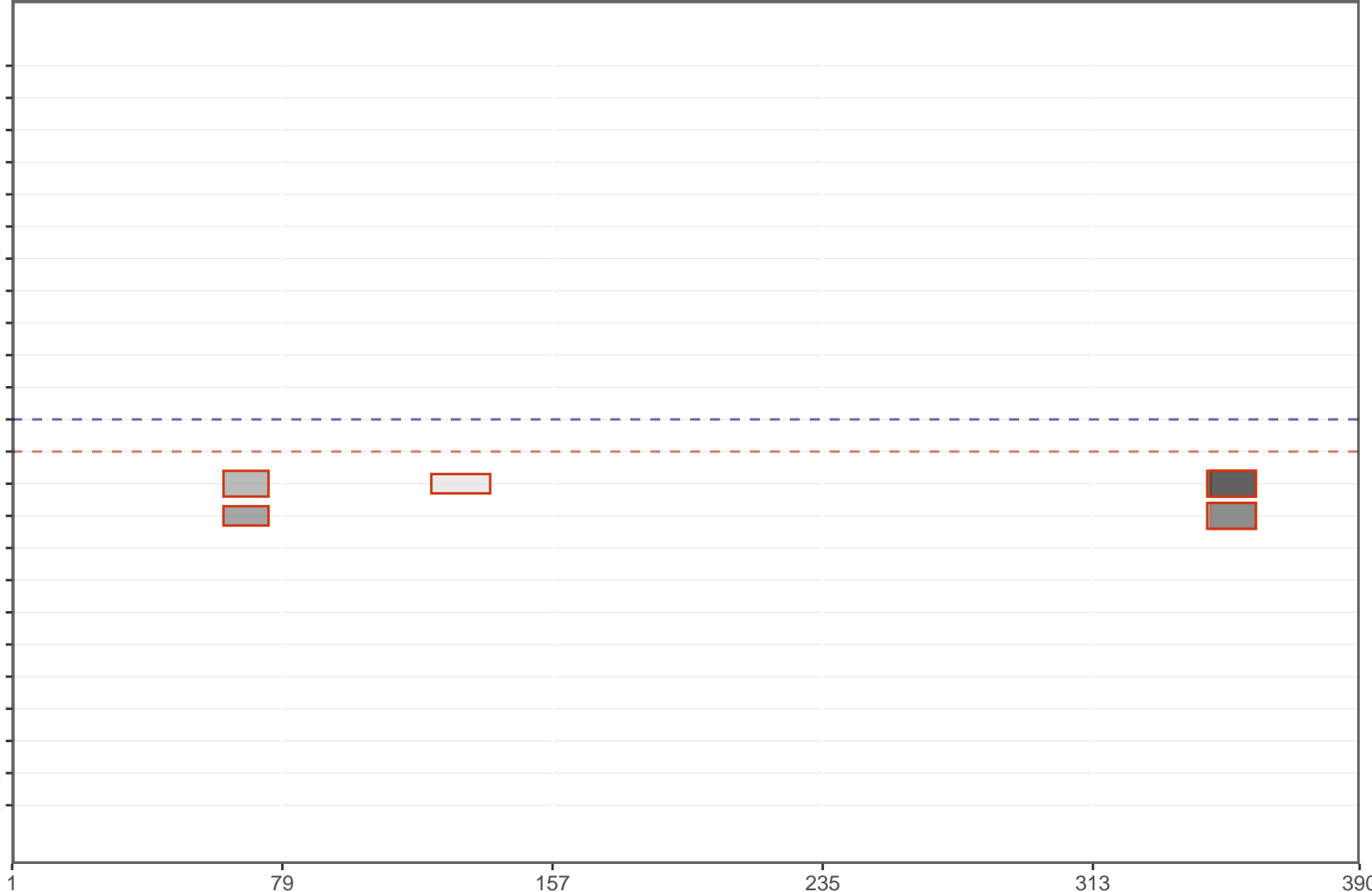
MW indication



Molecular weight

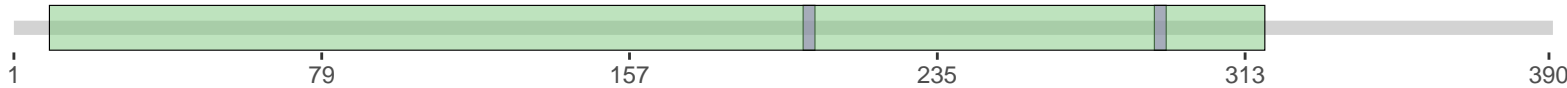


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

GLDLVLTPTVWGPMLQKFTNASSLKLKSGPTFGSPKVFLLNVEWLAELLCVAWLPQHGIVETLSRPPVGHVLTFSAWVSMFSFGNLSIALAKRVEELENKTRFDIVRDLEALVLYEKPEAGRHDMAHKAAGSDLVMLKRHPVNYNYKRFTEVMEEGSYSTEKLGKGLKRPLEETLVDAWEGYKAGILD*

NbL04g12620.1 pyrophosphate--fructose_6-phosphate_1-phosphotransferase_subunit_alpha [MW = 67.33 kDa]

No. of times detected



log(intensity)



Values from

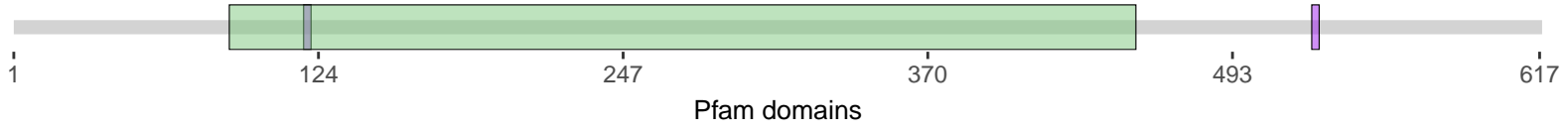
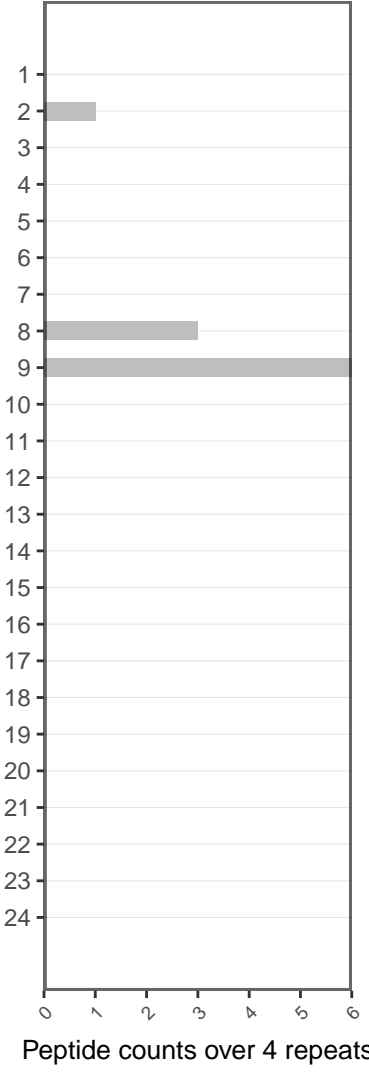
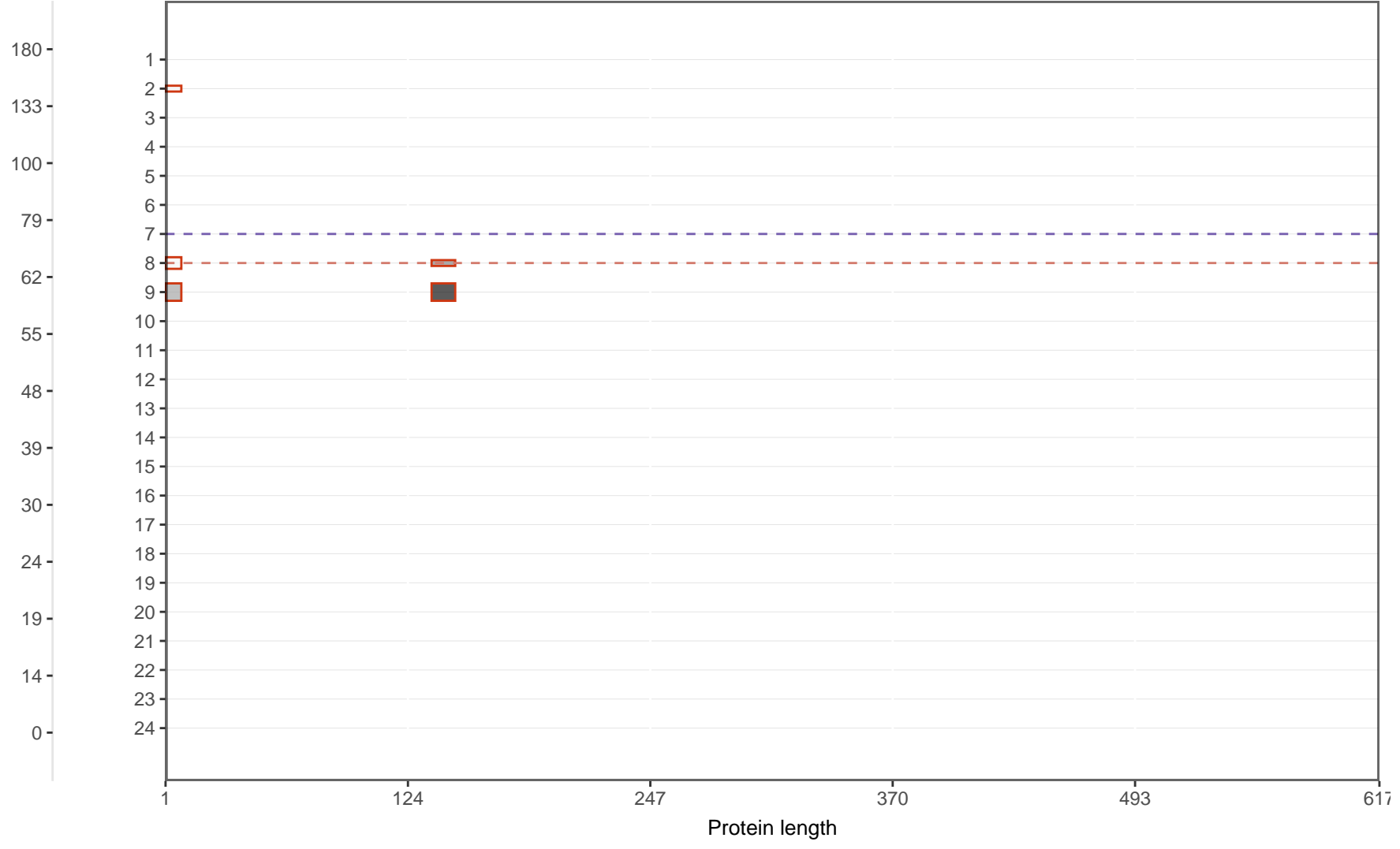


MW indication



Molecular weight

Gel Slice



Pfam Description
 ■ SP ■ Sequon ■ TM Domain ■ PF00365 Phosphofructokinase

Protein sequence:

KXLTLDITKIQICDAVQARAENKDHGIVLLPEGLIEIPEVYALLGEHGLLRQGVSAADKISSQLSPWASALFEFLPFRKQLLLHPESDSSAQLSGDIETEKLIAMHVEAEMNKRLKEGNYGKFKNAICHFQYQARGSLSPKFDGDDAVVVLGHVGYHIAAAGLNGYMATVTLNKNFVKNWHQSGAARISAMMTVKRYGRGPKASIGVPAIHPRTVDLKGKVEYELLSGNATKFLDDVYRNPGLQFDGPGADANAVTLGVEDDGYMGRKKLQGEVLDKVRTIVKPGCSDDVU

NbL04g12580.1 calvin_cycle_protein_CP12-3_chloroplastic-like [MW = 13.91 kDa]

No. of times detected



log(intensity)



Values from



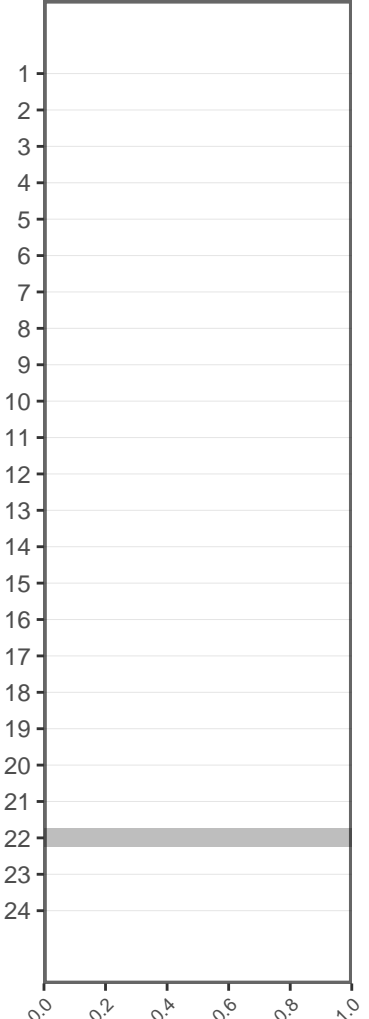
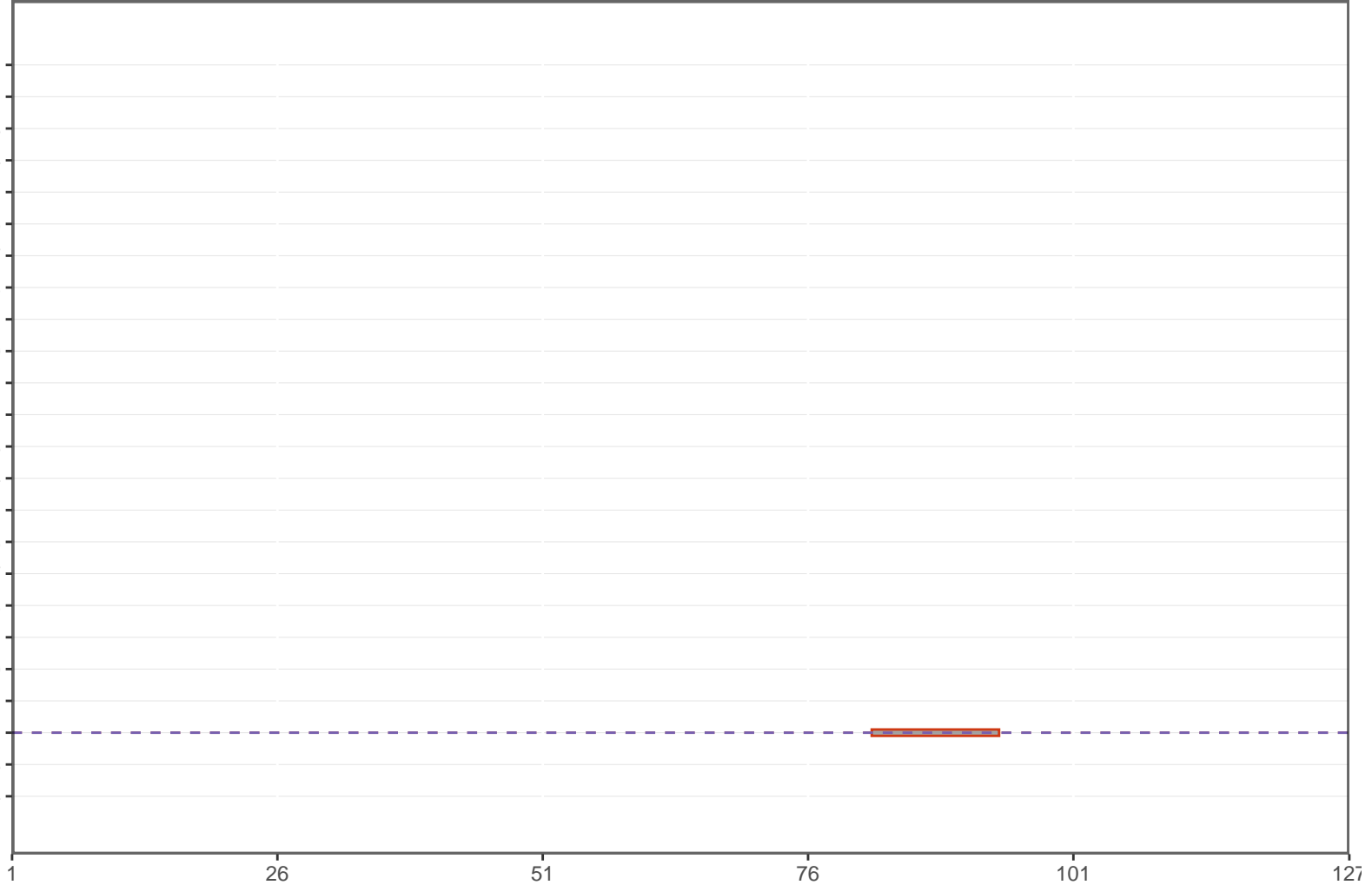
MW indication



Molecular weight

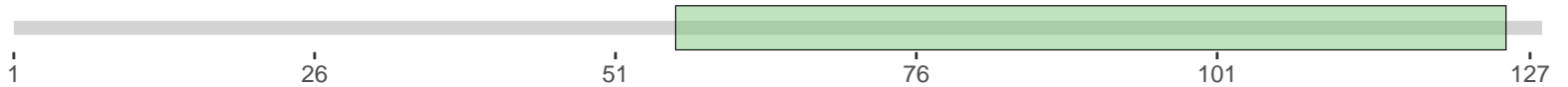


Gel Slice



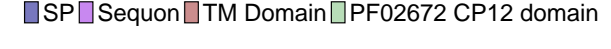
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MIREKQLTEMEKKWKEAKAVGEGDARSDEGKAWDVEEVEVSGAKAHLRIKILGLNGDPLSEFGDGNPETDECRIVED

NbL04g12210.1 50S_ribosomal_protein_6_chloroplastic [MW = 11.44 kDa]

No. of times detected



log(intensity)



Values from

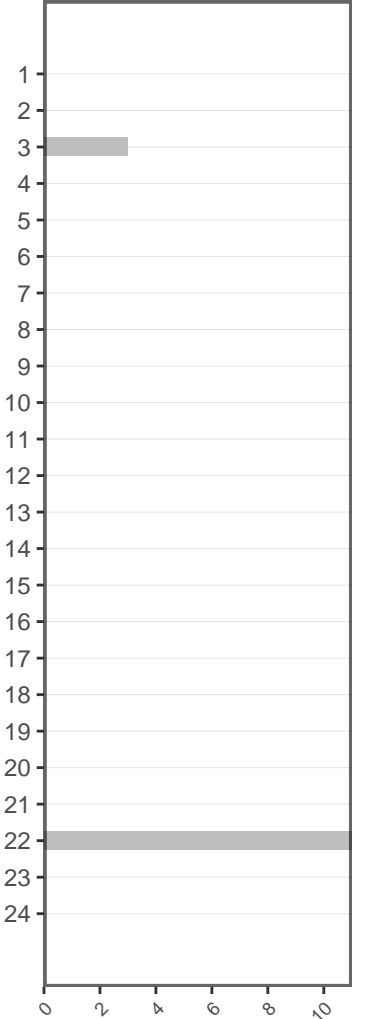
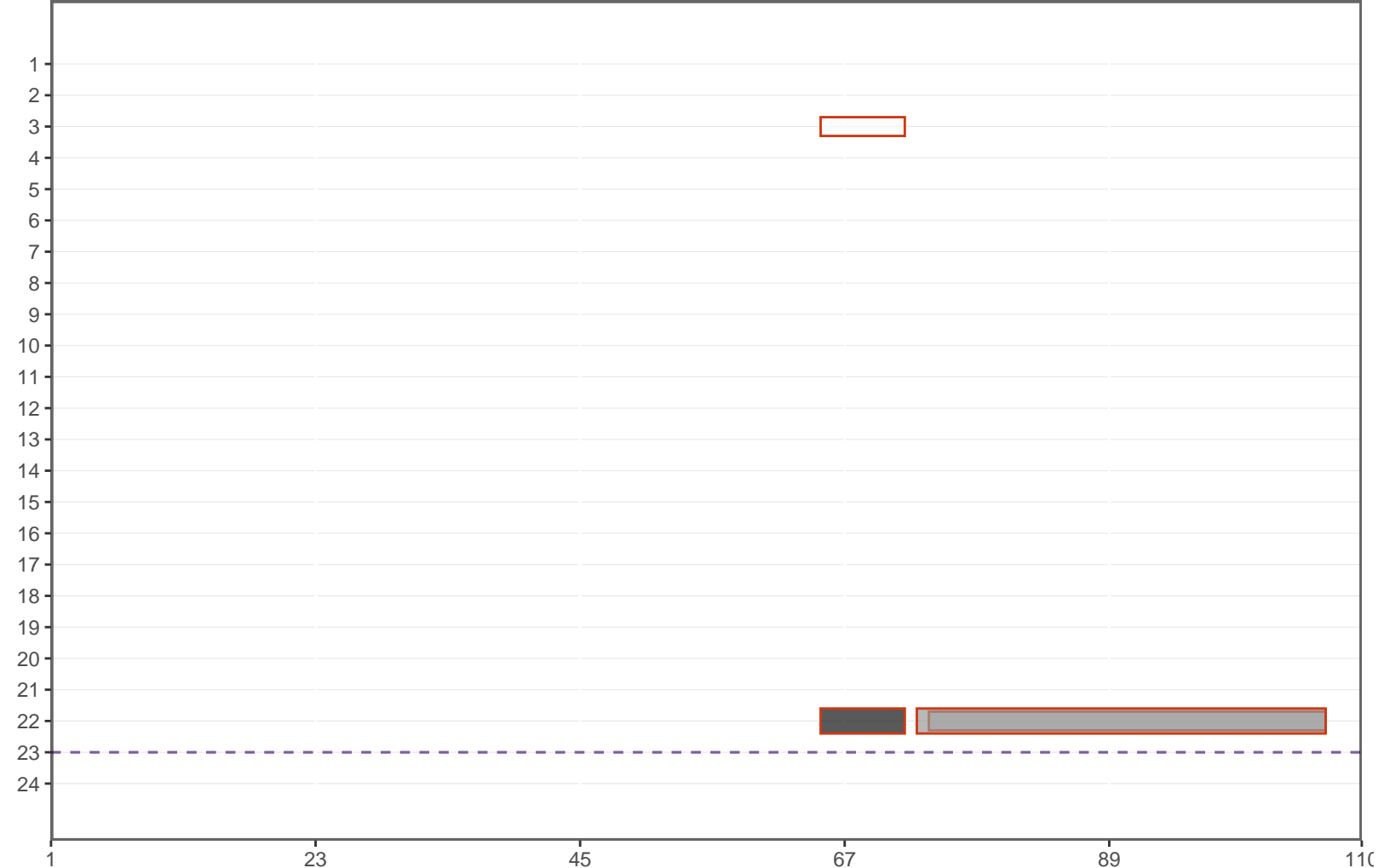
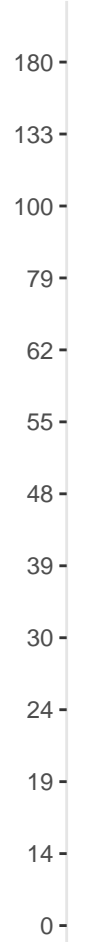


MW indication



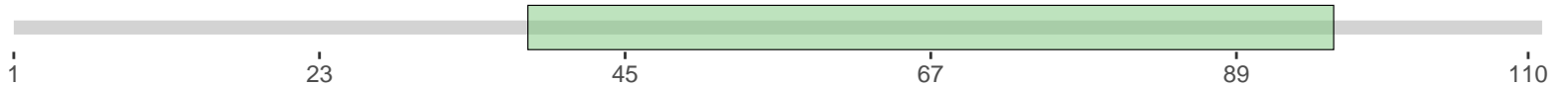
Molecular weight

Gel Slice



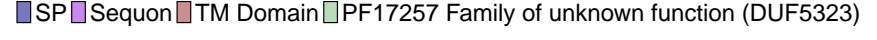
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AIECSSRPQKKATANHHKTRPRKTAQWDIRRGPVYPLPALPPEWFSFATDESQPMSSGASEPKTE

NbL04g12160.1 uncharacterized_LOC104213280 [MW = 108.29 kDa]

No. of times detected



log(intensity)



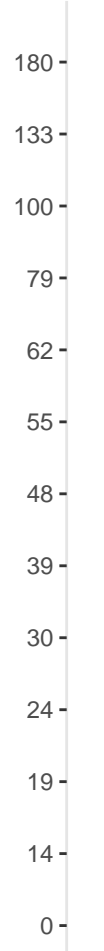
Values from



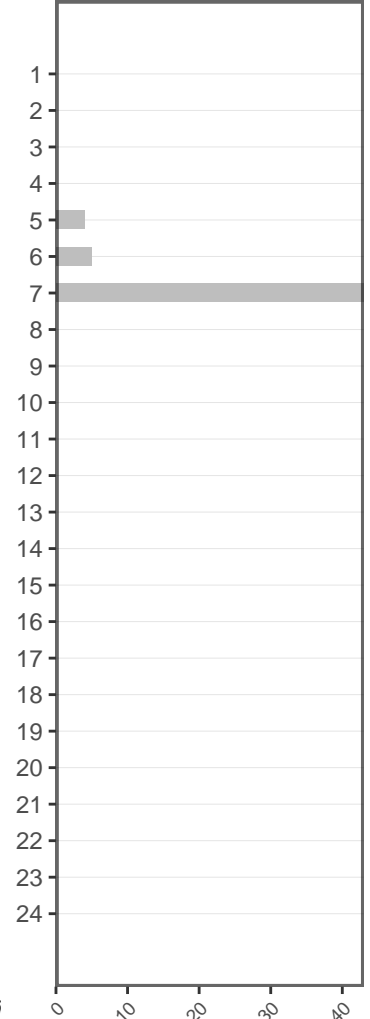
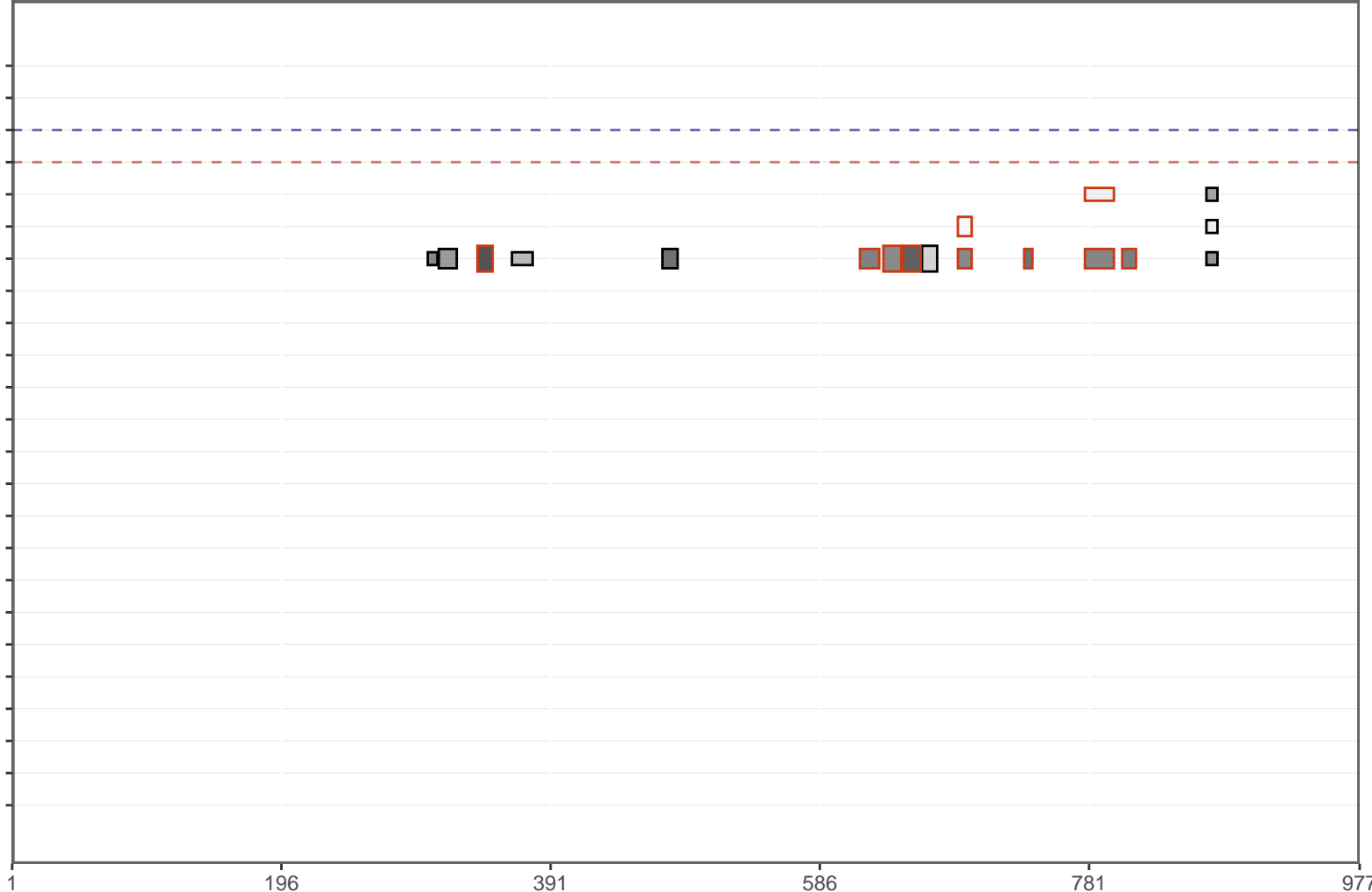
MW indication



Molecular weight

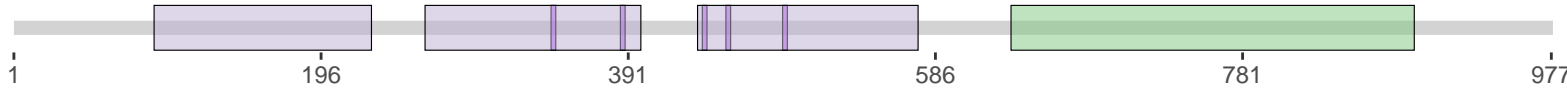


Gel Slice



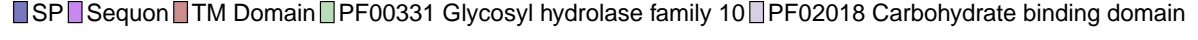
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

EPLSGRYLVLTNRITGNMMPGAMIFDKVRLTYGVSAWVKIGQASGPGSNVVALGVDSQWVNGGQVEISDRWHEIGGSFRIEKQAANKVMVYIGGPMAGVLDLMAAGLQIFVDRRARFRHLKRGTAIRKREVMKFSGSDGSLHGTFRIRVRQLQNSFFPGSAISRTNMDNEDFAFFVKNFNWVAVGQELKWWVTEAQQGNFNPKYKDADELDFGCTNKNIGVRGHGIFWEVVGAVGAWVQSLNKNLDLMTAWGNRLTGLLFRYKGFHEHYVWNEMMHIGSFYQDRL

NbL04g11990.1 uncharacterized_LOC109240426 [MW = 23.78 kDa]

No. of times detected



log(intensity)



Values from



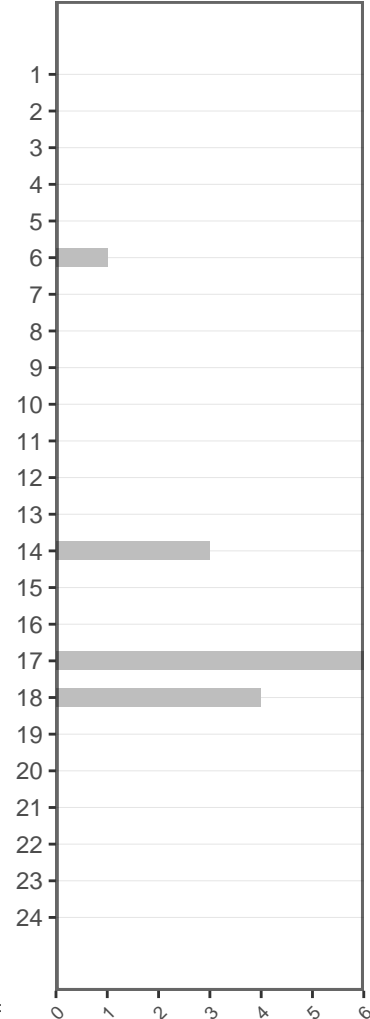
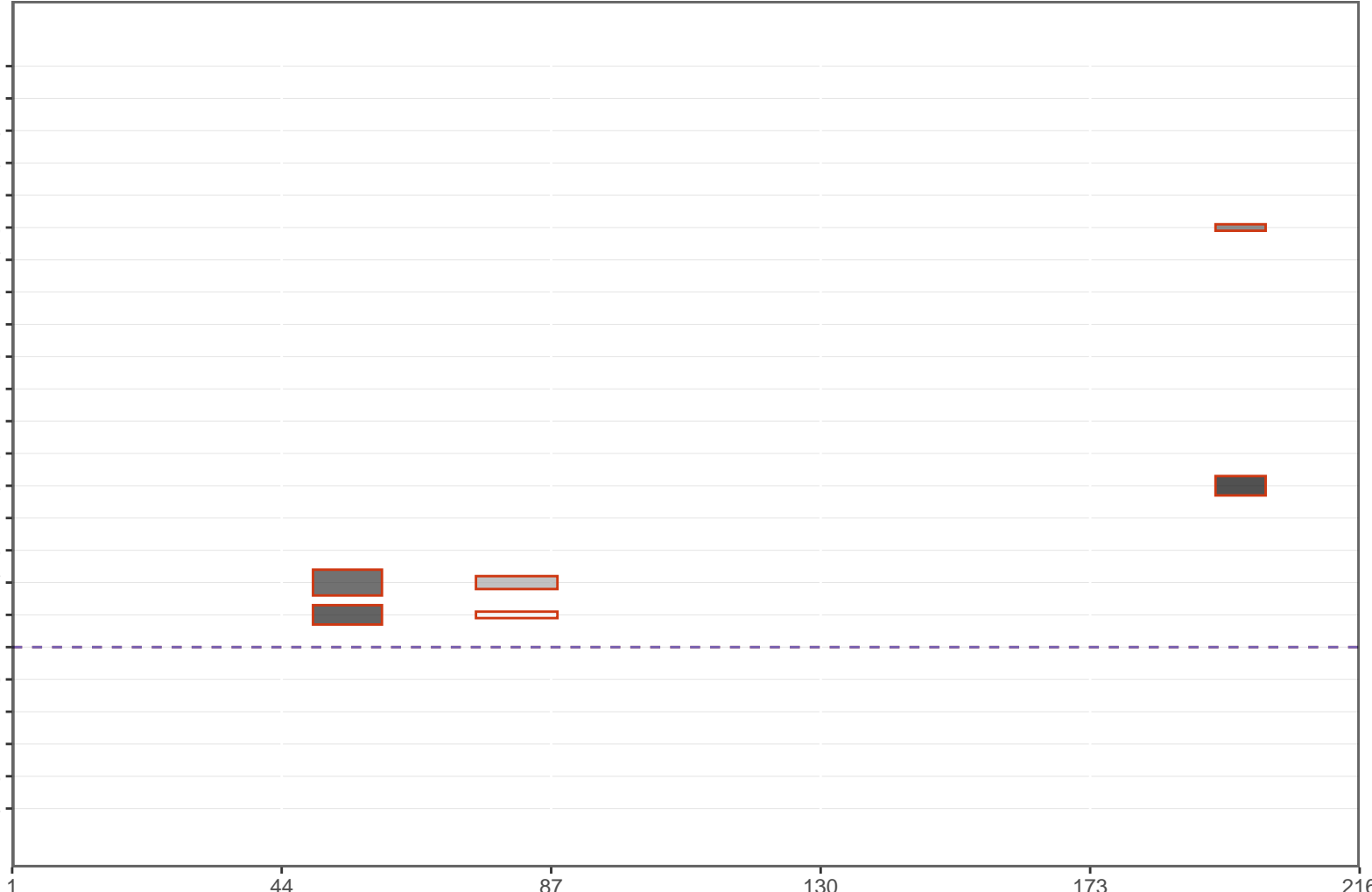
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains

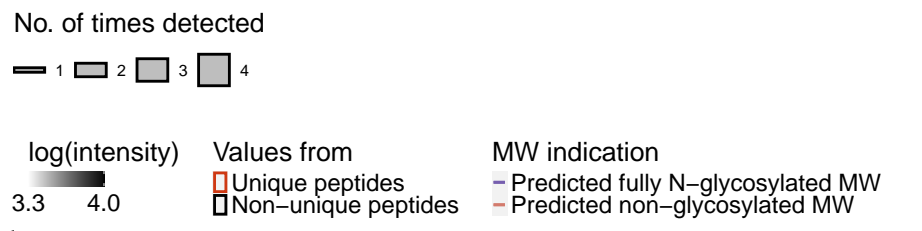


Pfam Description
 SP Sequon TM Domain

Protein sequence:

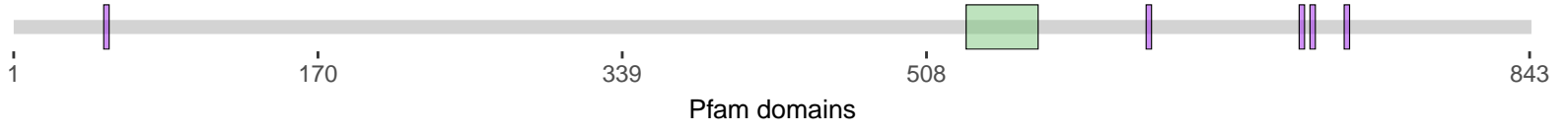
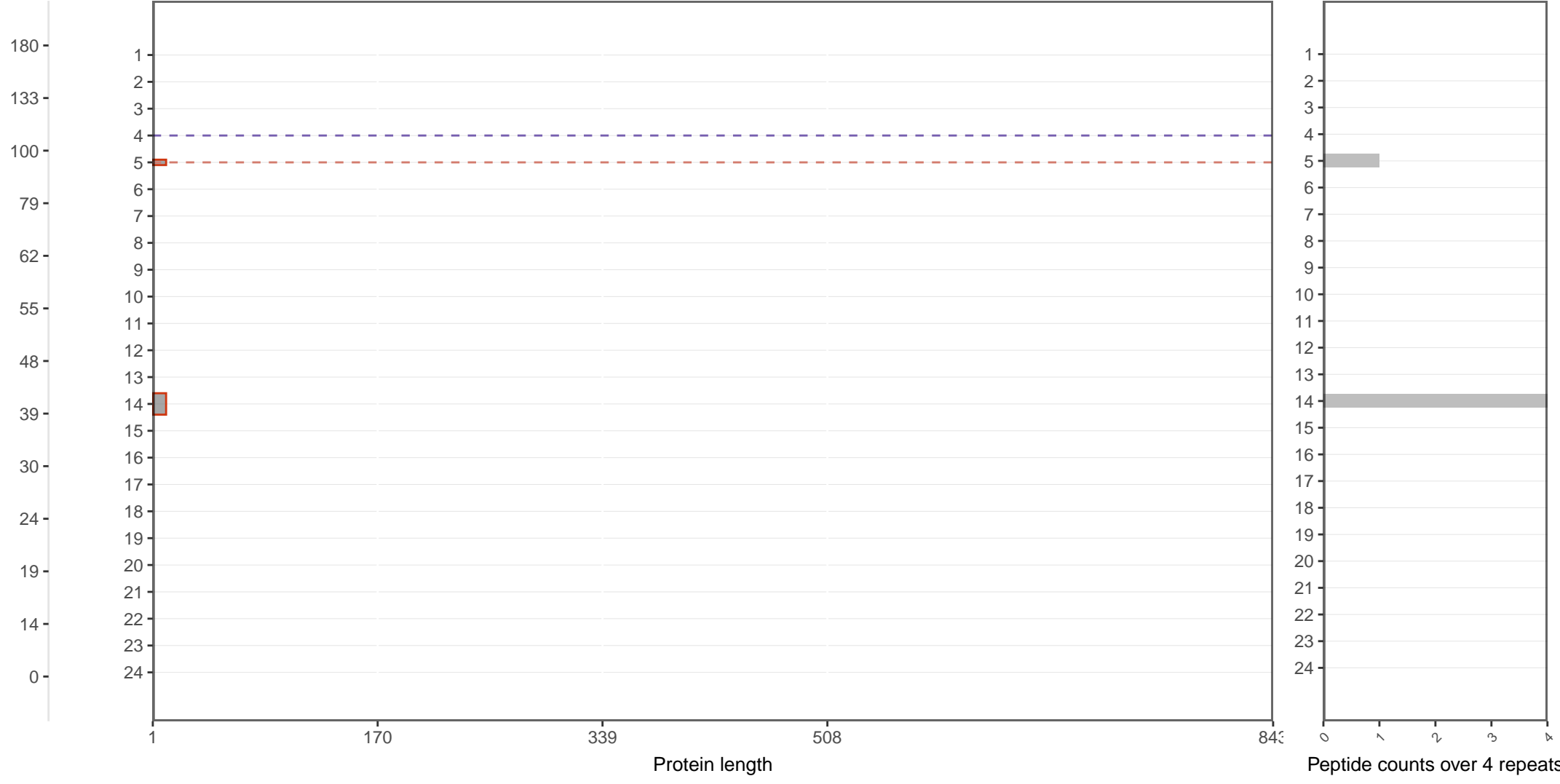
VFQSLPDISKASELFTLVKGVGPTASAVLAFAFADIAPIFMSDEAMVAANGNSKIDYTLKGVYLVLEKLGAKSEKELSAKGGDCTFPSDVERALWSSAVGAKLDGLGSEPEKVELKRGSKRRVRI

NbL04g11670.1 activating_signal_cointegrator_1_complex_subunit_2-like [MW = 93.59 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF02845 CUE domain

Protein sequence:
 FVSSPLPATMAMFPTNVEDPRIRADILVQGVRRDINGDYSQALEGHSKGTFLQIDKNNIMSRRELLRNTGTGWSMDQDQFKFLSGIMVHPVEDNFGGAHHPVSGKQKNGPPVDEDNAIMESKISQKDLFFDYGKGLAAGLEVYLNLRPEEVDRILEGTHLEDLQSLDLSLEKSDGPKSGVPSMTRNDKNGKGLVEPVVPPRNRIMPAATPYQAEGSSNSGTTTSVGRFIRKTTTTEEPAGLTLDSREANDLAKTIALS6QLEVEDEYDSDGFDLGLSGD6SAFETESLQKSNFGI

NbL04g11430.1 subtilisin-like_protease_SBT1.7 [MW - SP = 78.45 kDa]

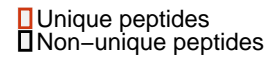
No. of times detected



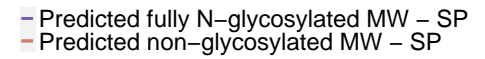
log(intensity)



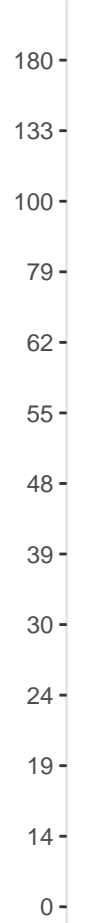
Values from



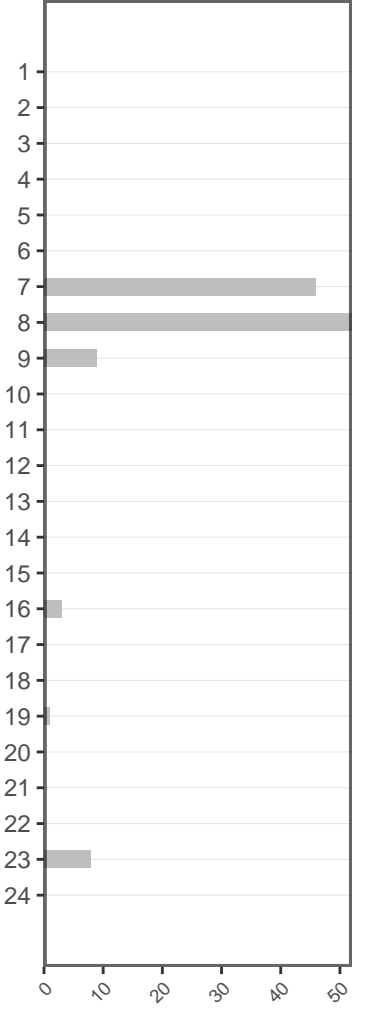
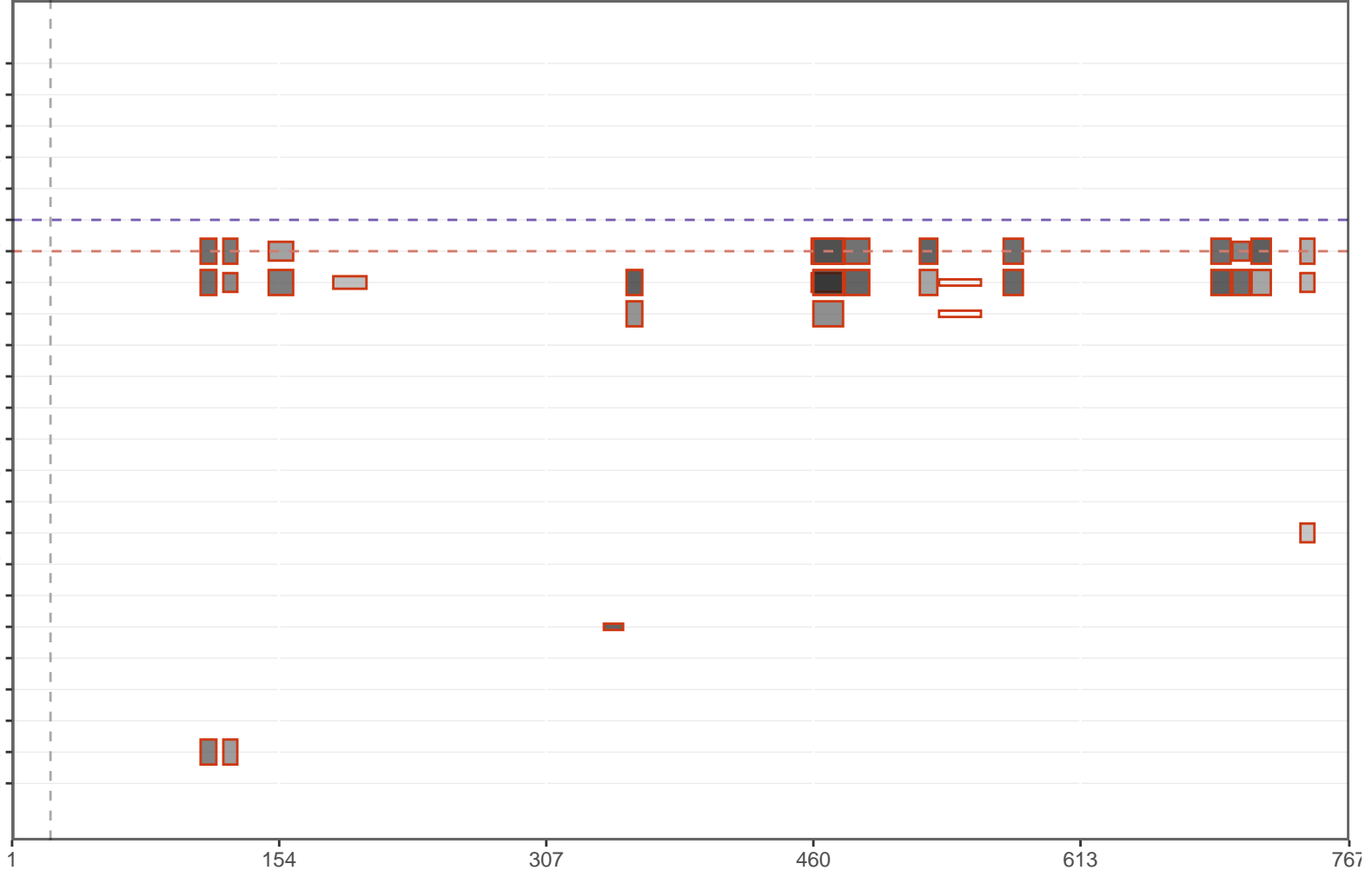
MW indication



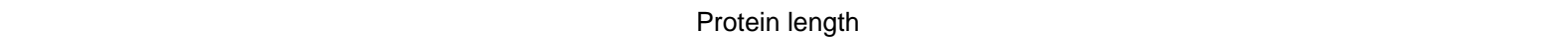
Molecular weight



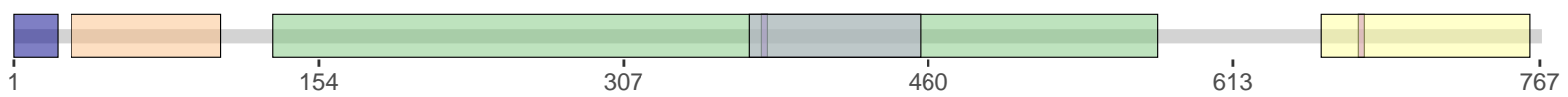
Gel Slice



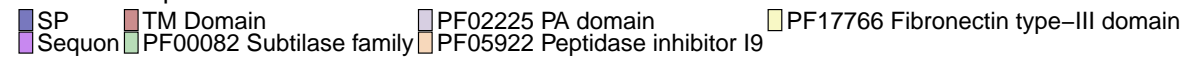
Protein length



Pfam domains



Pfam Description



Protein sequence:

...MPLVYAGN...SQA...NGNL...GTSGSL...PEKVDGKH...V...DRGMN...RAK...GLV...K...V...K...D...AGG...G...M...L...A...N...T...D...S...Y...G...D...E...L...V...A...D...A...L...I...P...T...A...V...G...G...T...A...G...D...L...K...R...Y...A...S...D...E...N...P...T...T...T...I...A...F...G...G...T...K...L...G...V...G...P...P...V...A...A...F...S...R...G...P...N...I...P...E...L...K...P...L...A...P...G...V...N...L...A...G...W...T...K...V...G...P...T...G...L...P...E...D...T...R...N...V...G...F...N...I...S...G...T...S...M...S...G...P...H...V...G...L...A...A...L...K...A...H...R...E...W...E...P...A...I...R...S...A...L...M...T...G...Y...S...T...Y...K...N...K...M...E...D...V...A...T...G...M...S...T...P...E...H...G...A...G...H...N...P...A...A...L...N...P...G...L...V...D...L...T...V...D...Y...I...N...F...L...G...L...E...Y...G...P...M...K...V...A...K...R...D...I...S...G...E...N...K...E...Y...R...V...A...D...L...N...Y...S...F...A

NbL04g11170.1 geranylgeranyl_transferase_type-2_subunit_alpha_1 [MW = 81.01 kDa]

No. of times detected



log(intensity)



Values from



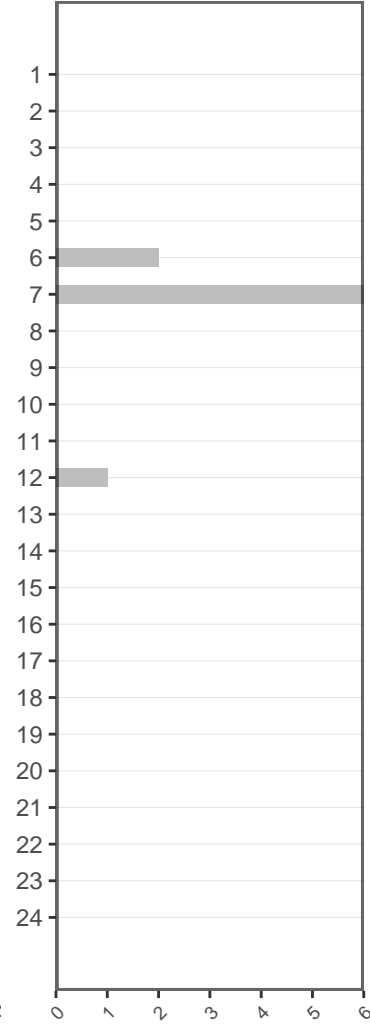
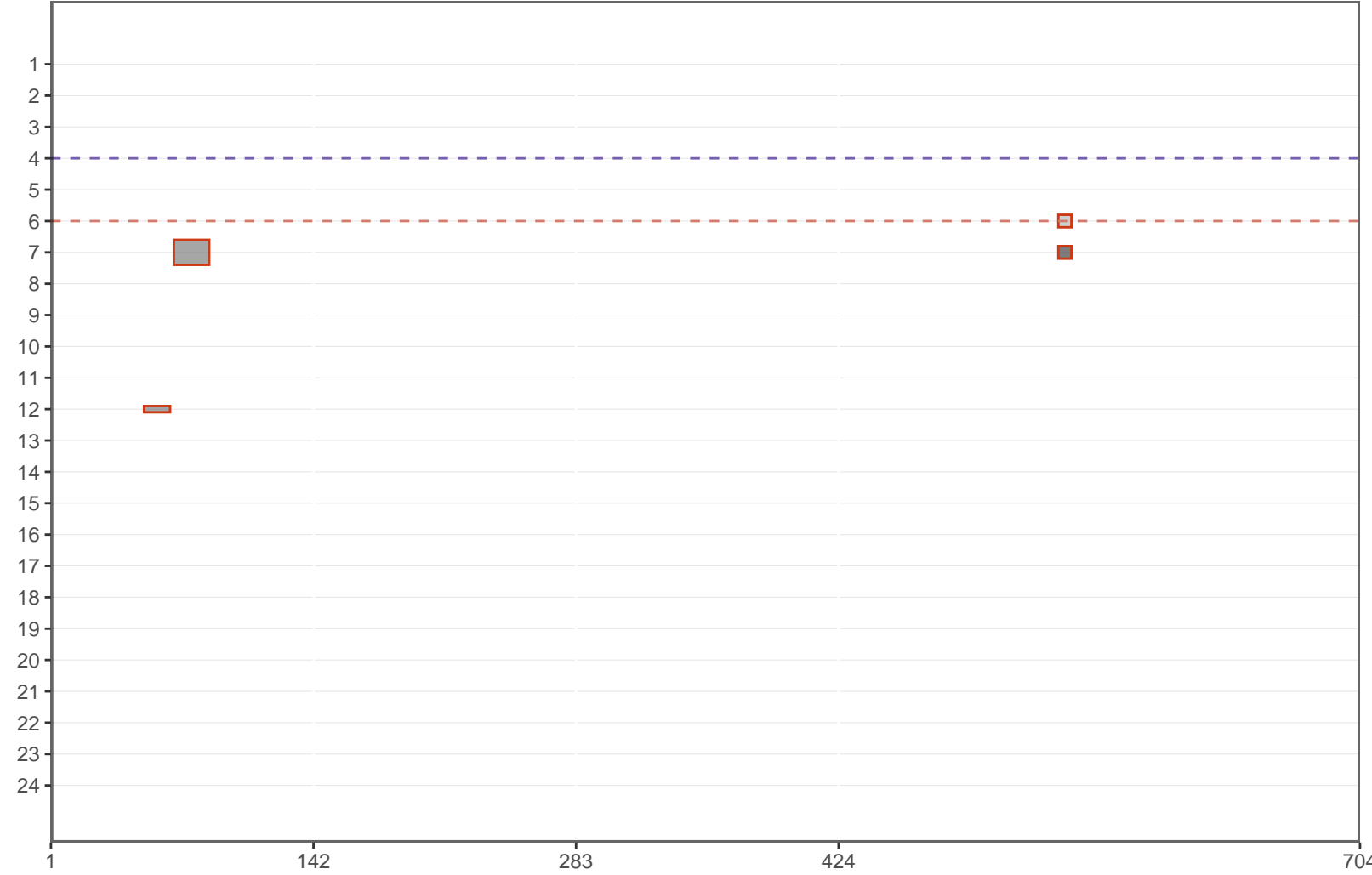
MW indication



Molecular weight

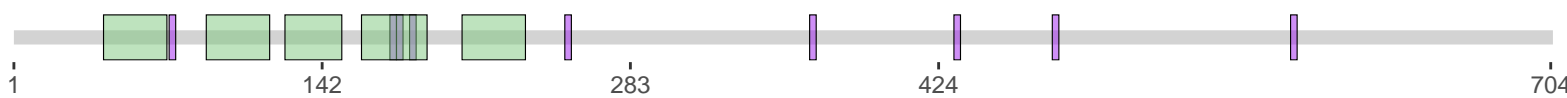


Gel Slice



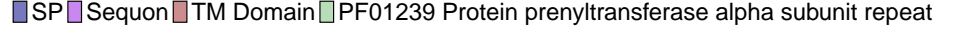
Protein length

Peptide counts over 4 repeats



Pfam domains

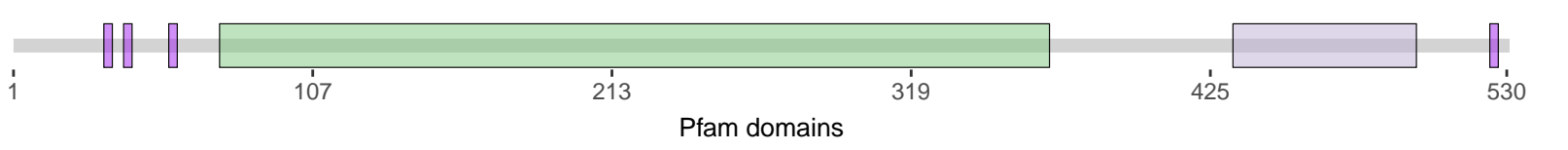
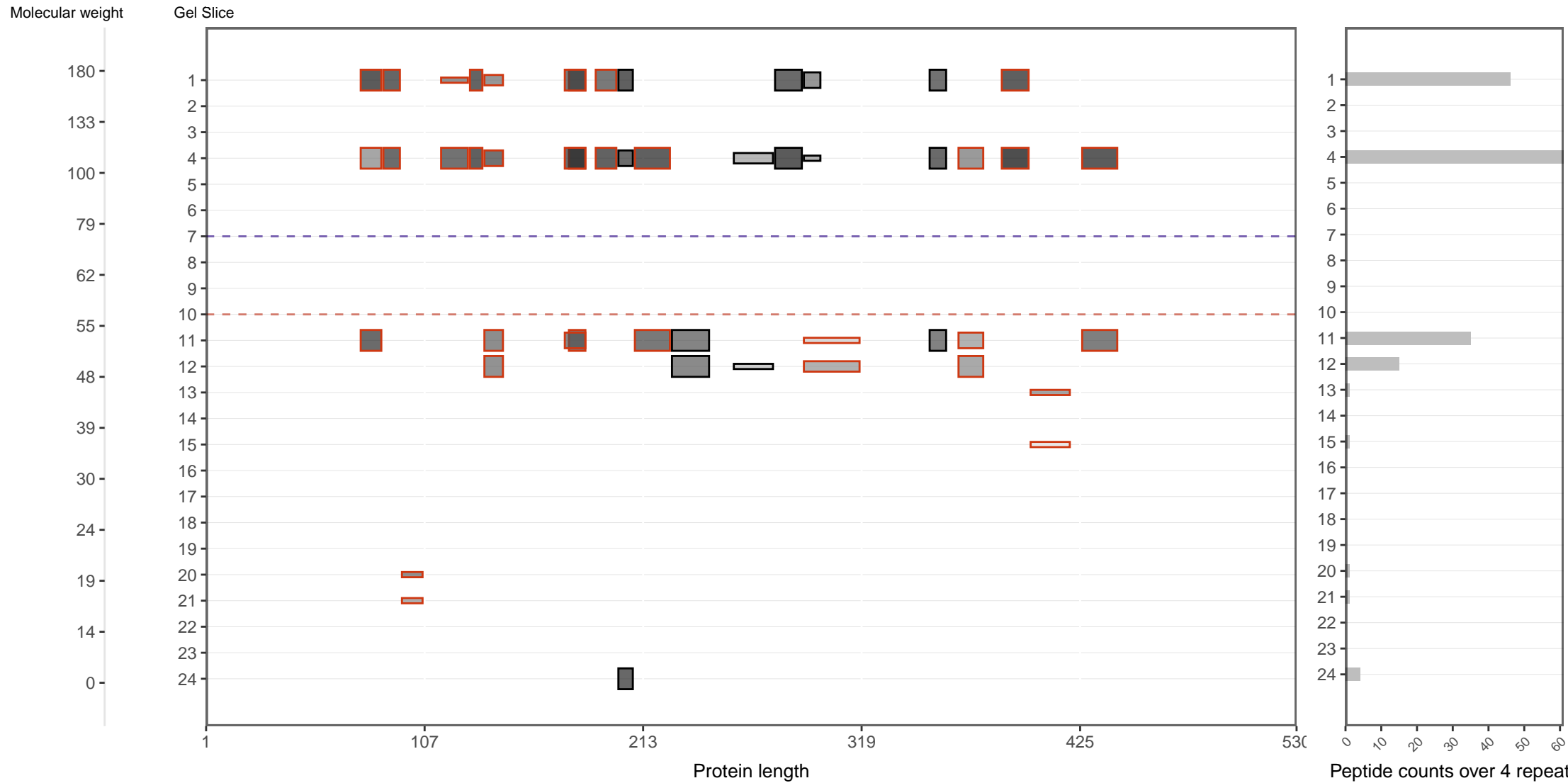
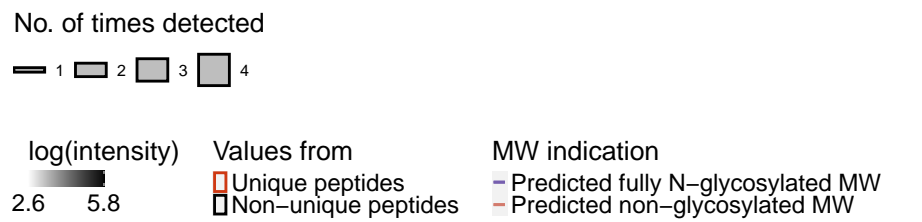
Pfam Description



Protein sequence:

IANLSKSYQVYVNLARSGDFSSGTGANHGNNSHAFTVSGIPYRSEHVDLKNKEEKISWSEESFGPHEAGFLSEVLNLFHIERTKVDEKVVYGVNITTVNEIAHYRELLATMNGKIGKLTLLARLLMHDITVGTGSHRNVSHHTEVLQYDOLKMDPMHFHYGDEYSLVLLKHISQELLKHKCGKYRDPSPKINFLRLNDLSLRIGSMERKLWAVQVLDLSNNGLQSELEGLVMQLTGLNVSNNKLGFTALEPLRLLRKVLDSVNEIGAHISDTRRYLCCSPL

NbL04g11060.1 argininosuccinate_lyase_chloroplastic [MW = 58.32 kDa]



Pfam Description
 SP Sequon TM Domain PF00206 Lyase PF14698 Argininosuccinate lyase C-terminal

Protein sequence:
 CRTLNFCPLGACALAGTGLPDRFMTSDALGFAAFMRNSIDAVSDRDFVLELLSANSITAVHLSRLGEEWVWVASEEFGFLTPSDVSTGSSMPQKNPDMELVRGKSAVGVGDVLSLLVGGKGLPHAYNRDLGDEKPEVDFVKTIVGMLVSAEFAQWAFNRRERIKTLPAGHLDTADLVVKKGIPFRTRSHDVLVGRVAGLGVSRNGLGDLDELNLSLWFDKDYEFGLGVENSKKFRVGVGSGTSGSEVAGQLDYWDKLNIGRES

NbL04g11000.1 chaperone_protein_DnaJ-like [MW = 46.42 kDa]

No. of times detected



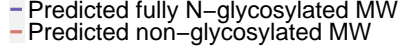
log(intensity)



Values from



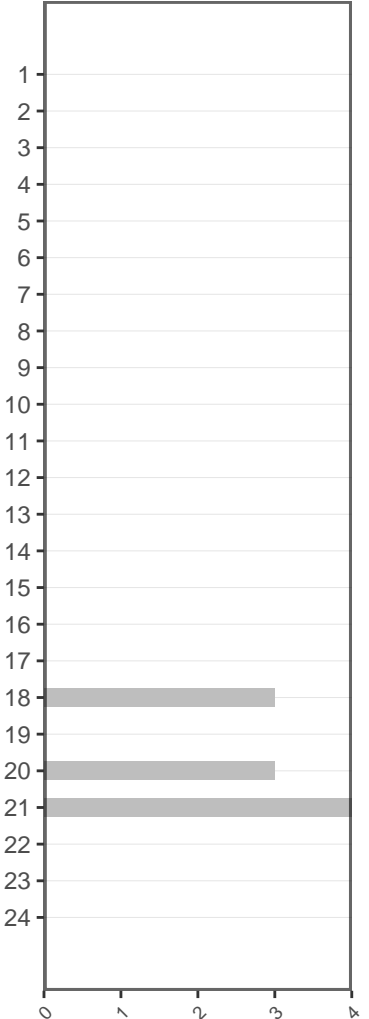
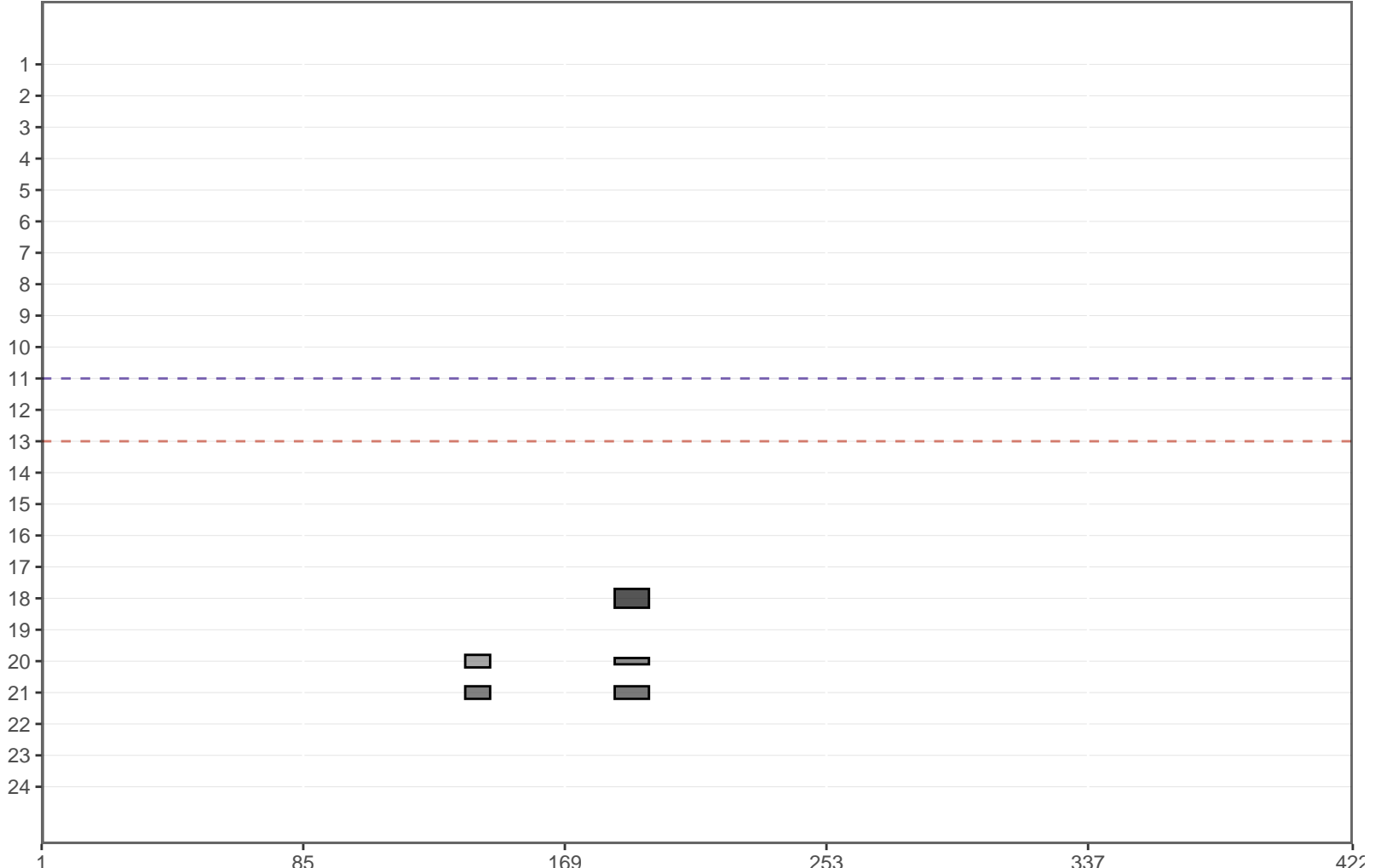
MW indication



Molecular weight



Gel Slice



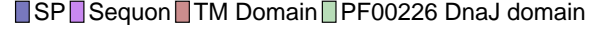
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

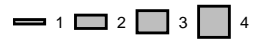


Protein sequence:

IRPKSYNKQOKRGGDEKLPVRRRSRABGGSSGGQNGNPSFVNFQNRVPGPQPKTATPVSQGMRRGGVNLWTAQPYGVNLFYPRVVEGGDLRGEKONRAFTATELELSPPLVPGREAYVGIWFFPFMGDFVNGDLENGKSHAAGDGFPSWMPMPFSSSEGVNVAQNTATPTTPAPAPAPAPVQAGAQGTQAPASAPRPMGAPFTGAKRRGRPRKYN

NbL04g10850.1 glucose-6-phosphate_isomerase_1_chloroplastic [MW = 67.52 kDa]

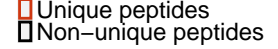
No. of times detected



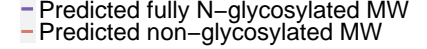
log(intensity)



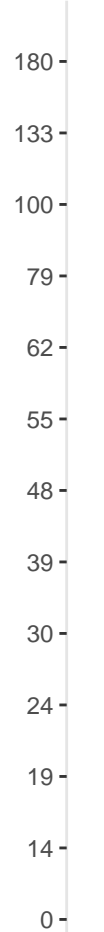
Values from



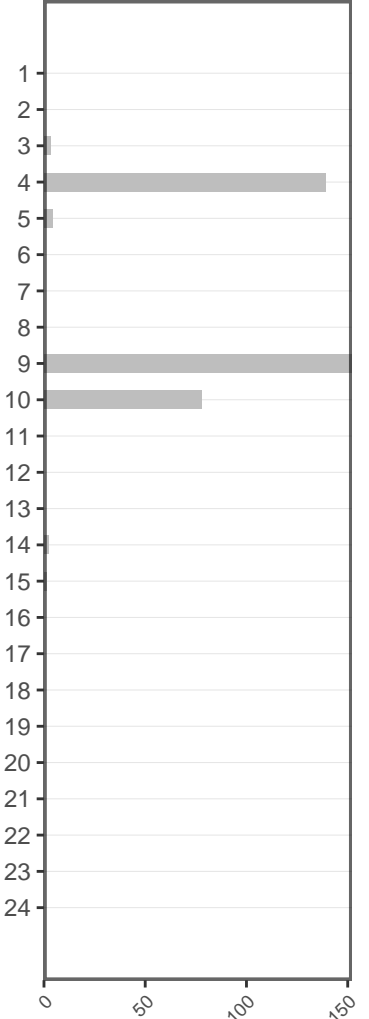
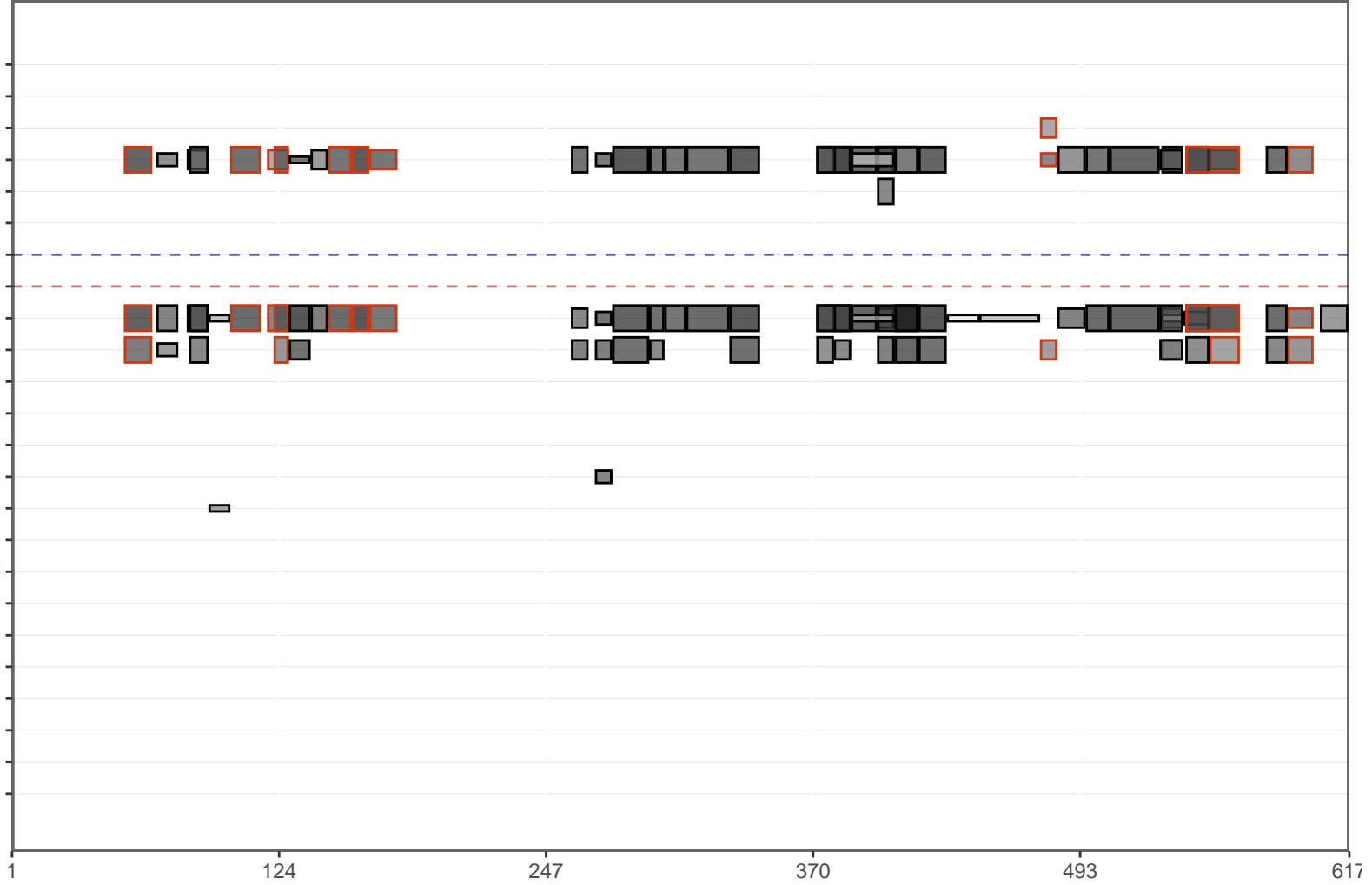
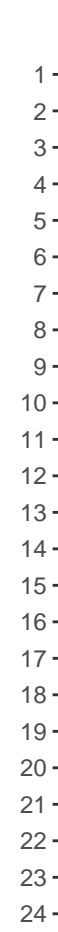
MW indication



Molecular weight

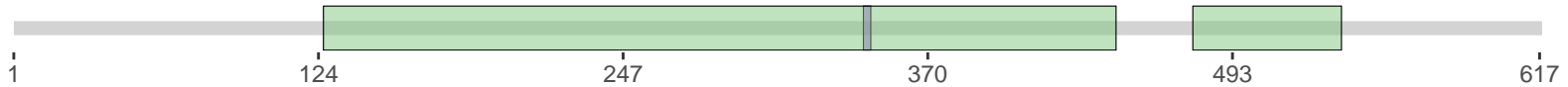


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VLAARFPMFDVYGGRTSELGAVGLPALGINIREMLTGAALMDEANRTTVVRDNPAAALLGWWATDGVGSKDMVLPVKDLSLLFSRYLGGVMESELGKEFDLGNRNVNGGIVGKNGKSTDDHAYVGGQLREGVHNFATFIEVLRDRPPGHQWLEPQVTOGDVLFGLMGGTRISALVANDRESTVTVQGVETPRSRVGLALYERAVGIVASLVNINAYHQPGVVEAGKAAAGEVLAQKRVLAVALNEASCKEPVEPFLDEAERGHGEEDEMIYKIIAIIAANDRALI

NbL04g10760.1 14-3-3_protein_10 [MW = 30.01 kDa]

No. of times detected



log(intensity)



Values from



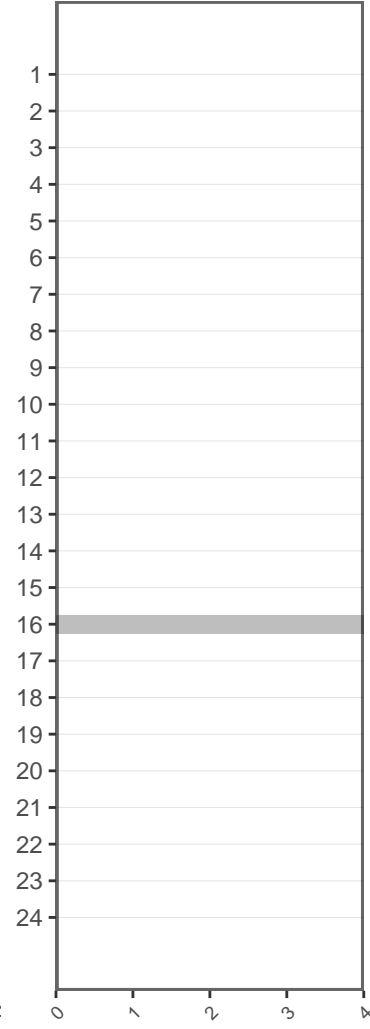
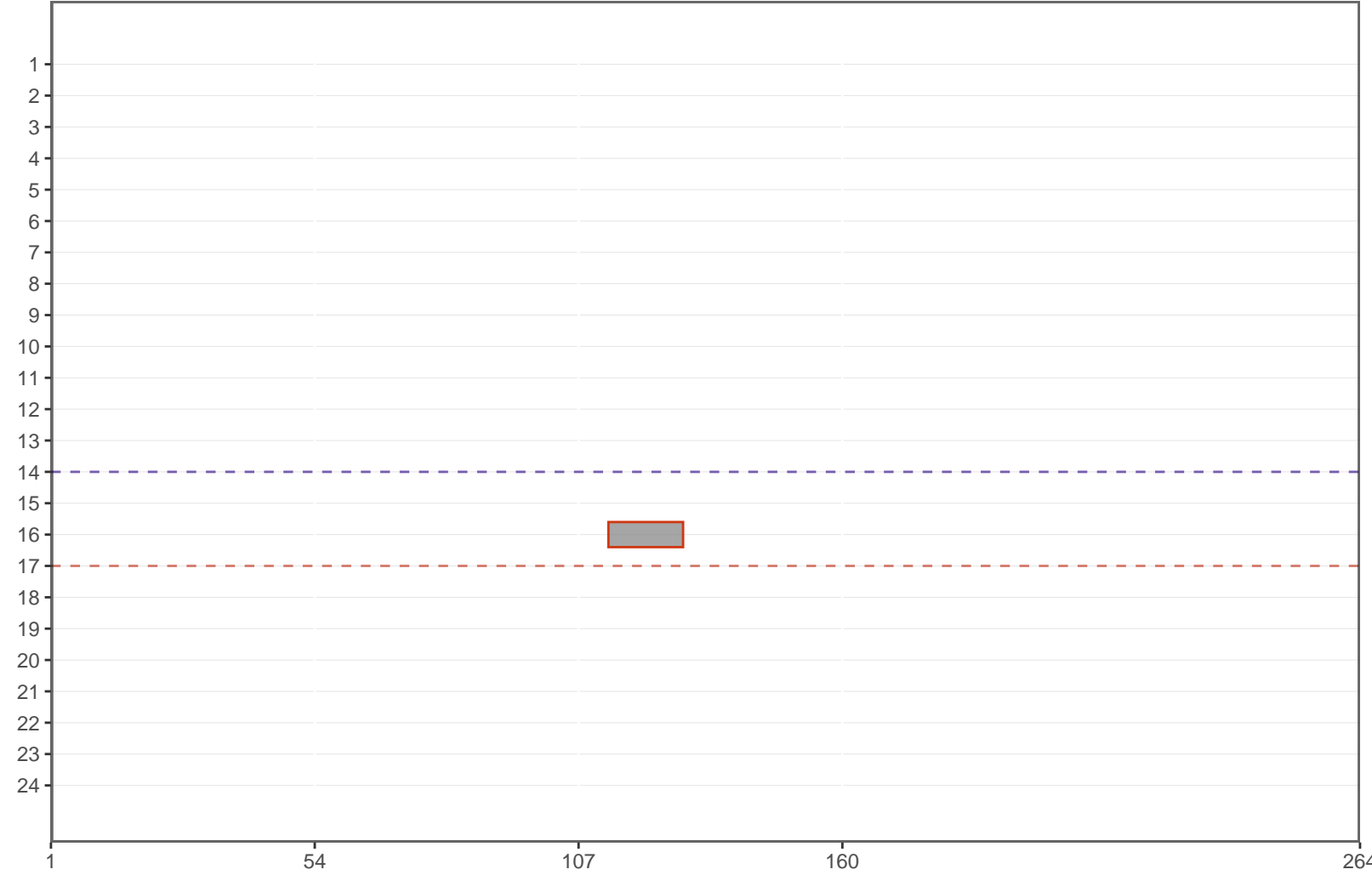
MW indication



Molecular weight

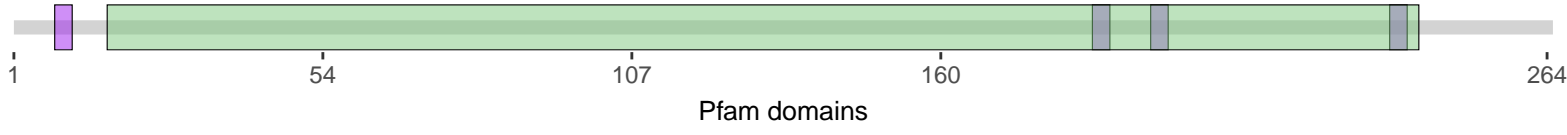


Gel Slice



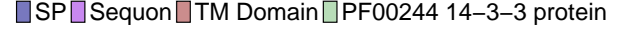
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PSASTGESRIVYLYLMMGGDHYRRLAEFRVSDERKQAAEDTMMNBYKAAQDEIADLPPTHRIHLGLAINFSVYFELINSEDKADSMKAGAFEEAAIELDTLGEESYKDGSTLMLLRDNLTLWTSQMGVCTLLRAVTRHRHMQTR

NbL04g10720.1 esterase_AGAP003155-like [MW = 24.99 kDa]

No. of times detected



log(intensity)



Values from



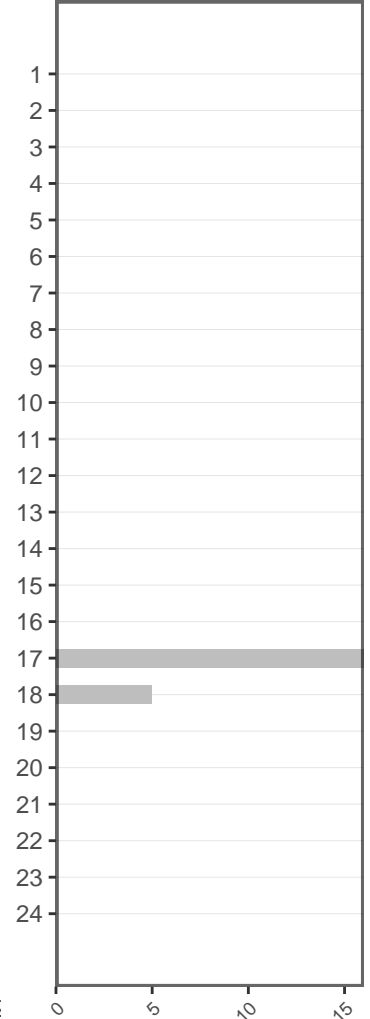
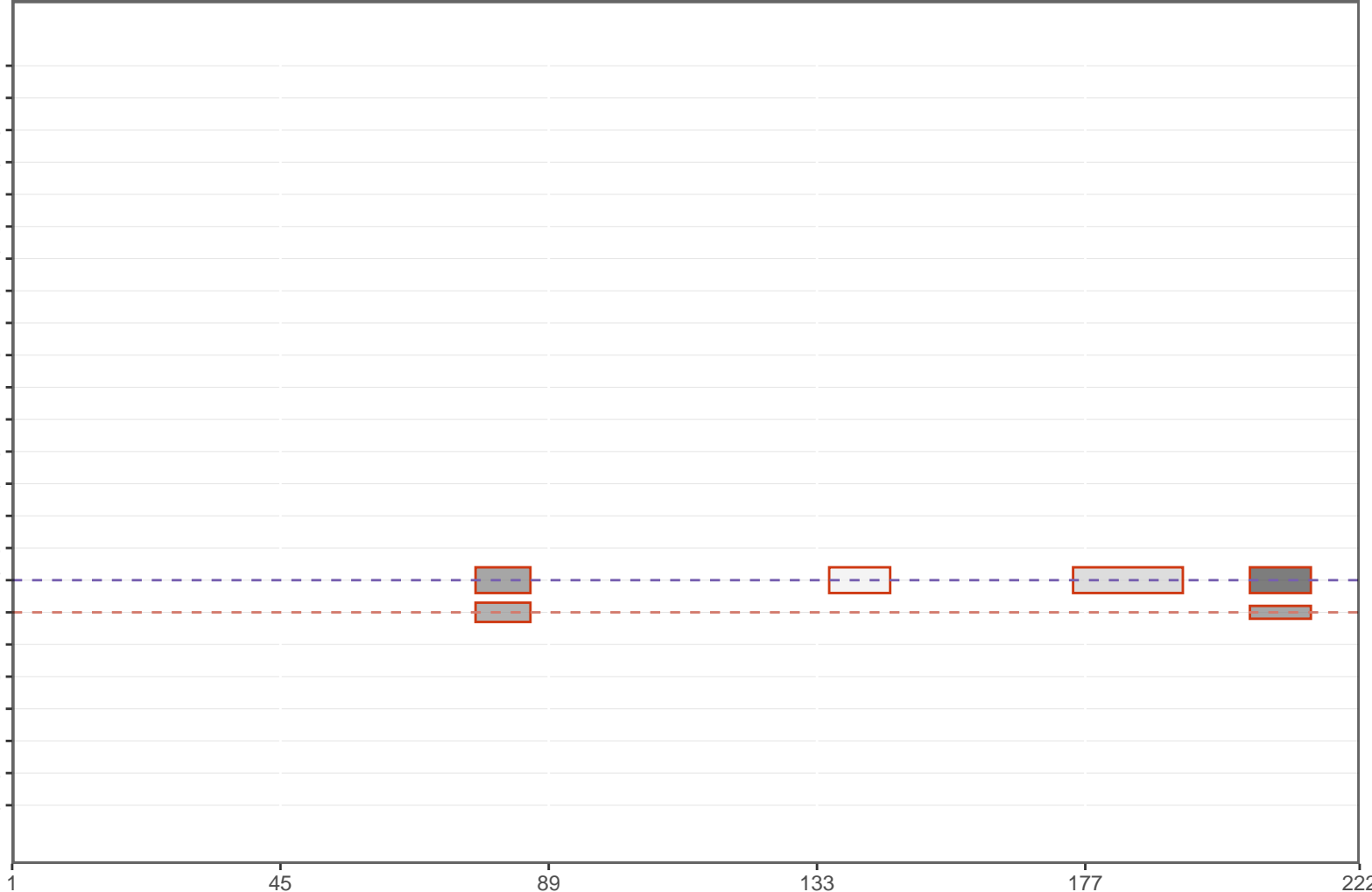
MW indication



Molecular weight

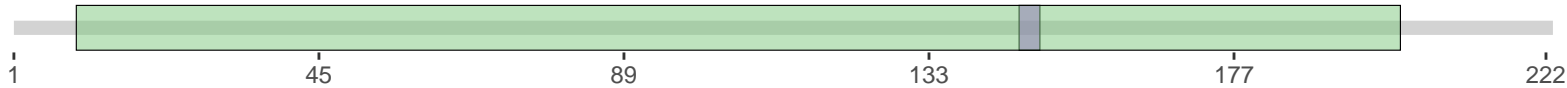


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MRKIGPFDQLLQFSQGANLGGALSGLQEKGVALTVPKIKYLIHGGAGFRNKNVAKAYSSSITGPEVHFLGEGDYLKRYGIELLESVVDPAVHHKPKGHITPIRFDKGLSEMLSFIEKVAIEIK*

NbL04g10700.1 purine_permease_3-like [MW = 14.4 kDa]

No. of times detected



log(intensity)



Values from



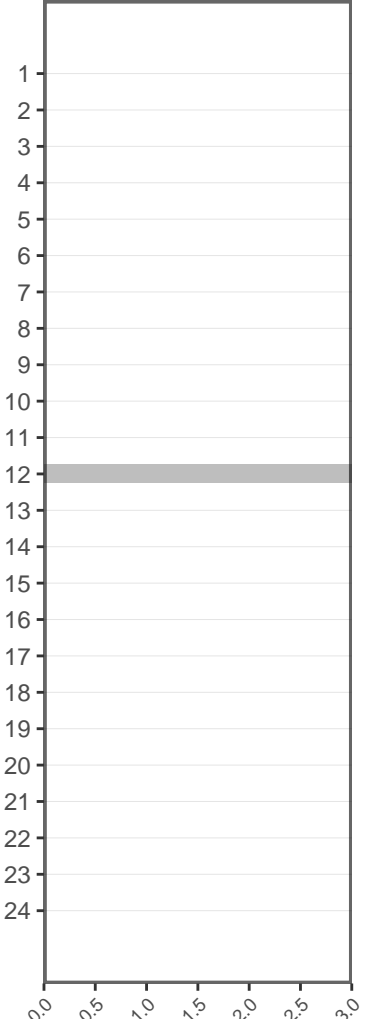
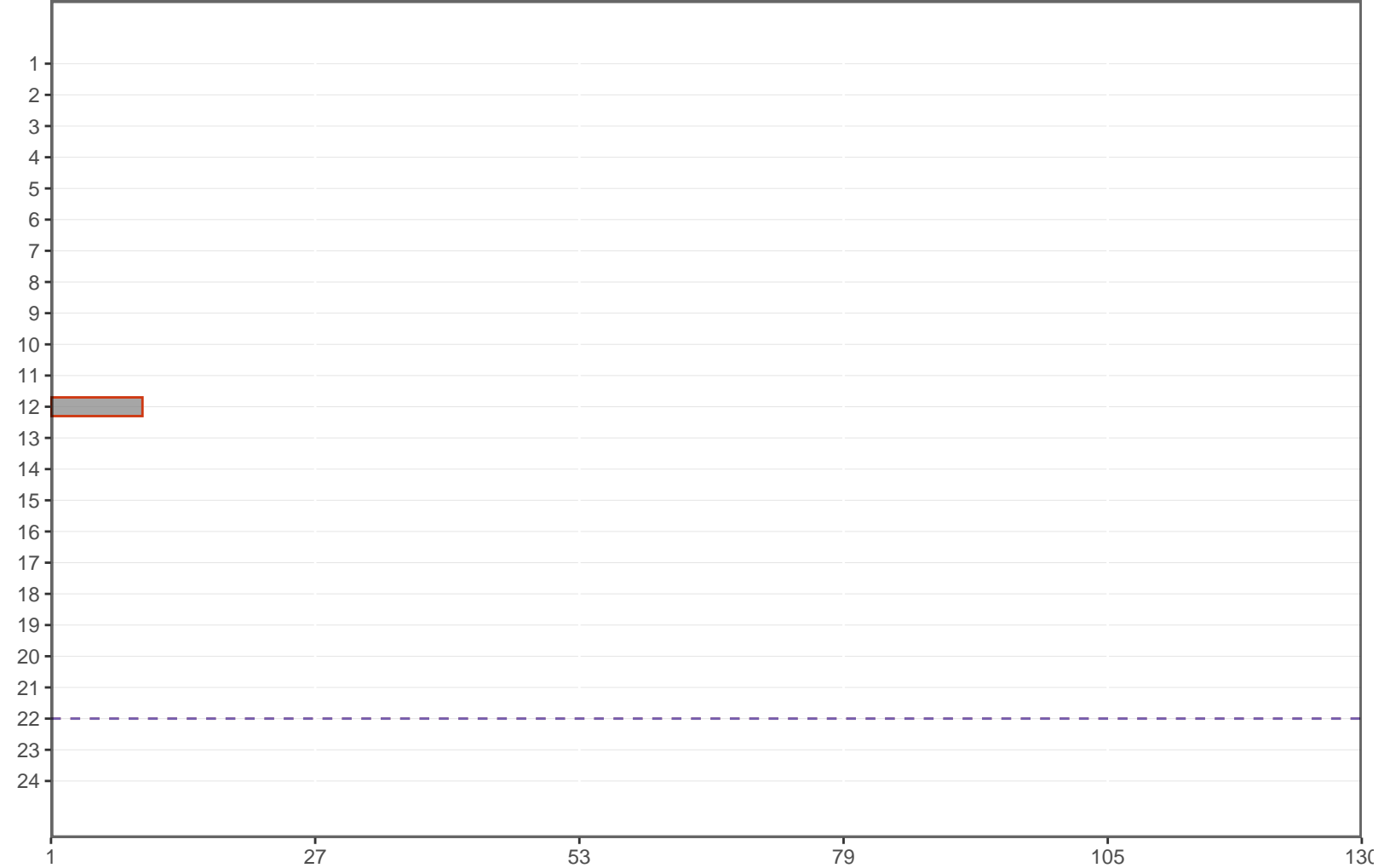
MW indication



Molecular weight



Gel Slice



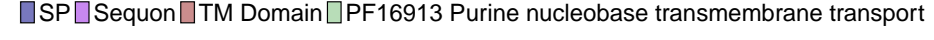
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISSLLSGVIAVLLPVTEVLAVIFHEKFGTEKGVALFLBVGFRISFYFYGEMKQHNKEKQTELEEMATTGSSNPPLESAA

NbL04g10610.1 28_kDa_ribonucleoprotein_chloroplastic [MW = 32.84 kDa]

No. of times detected



log(intensity)



Values from



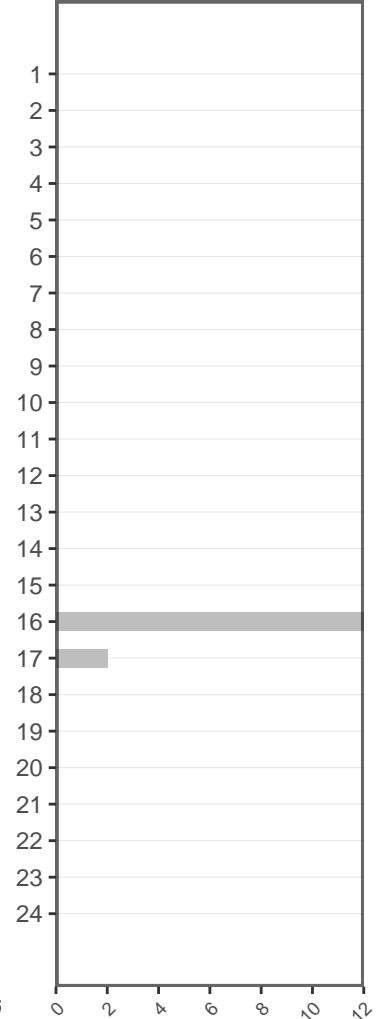
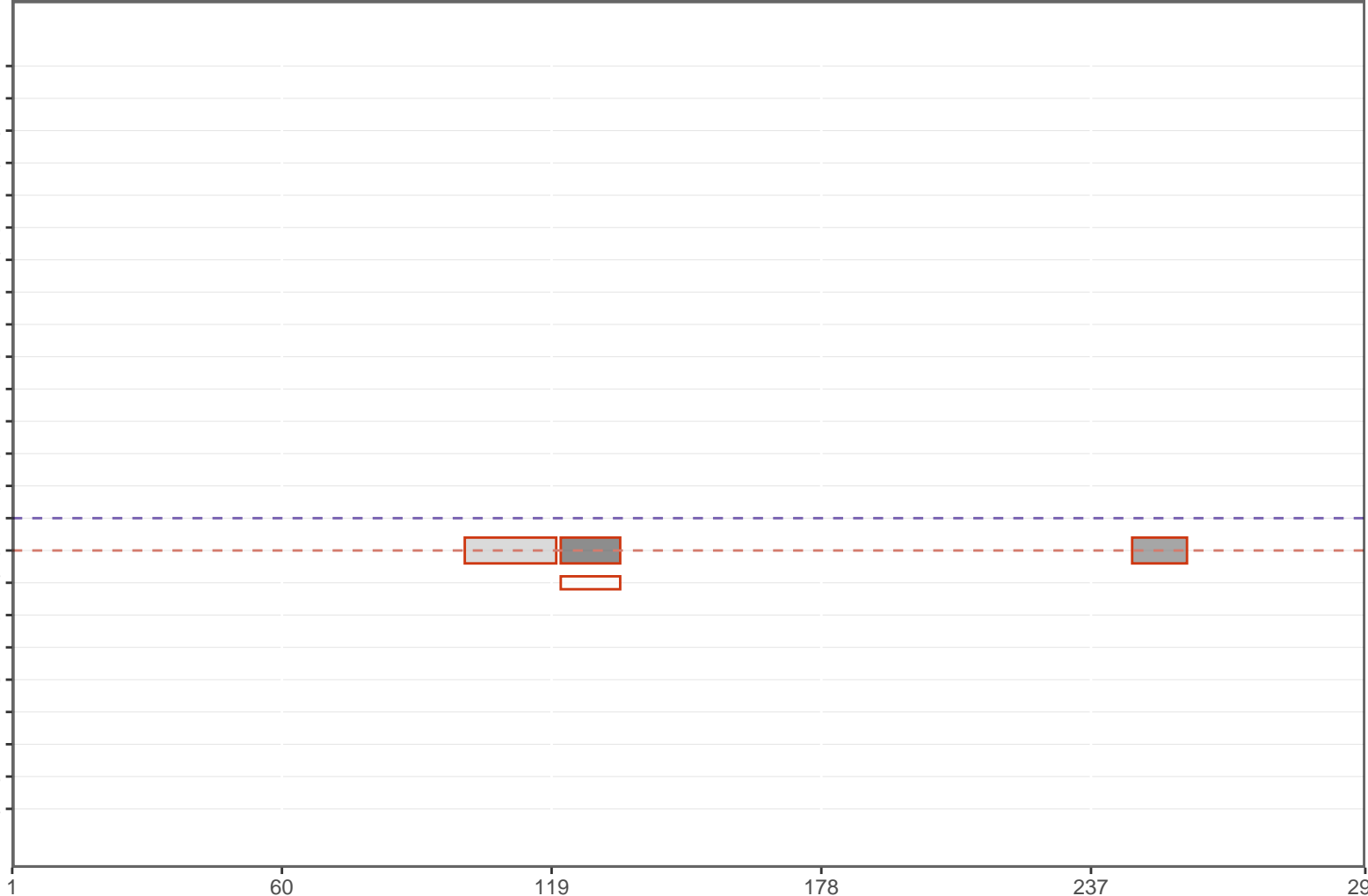
MW indication



Molecular weight

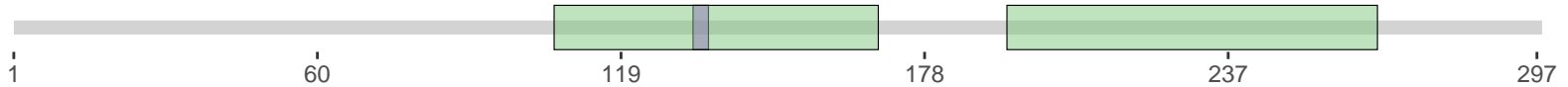


Gel Slice



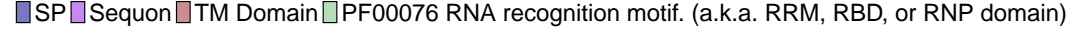
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IRGLVFTVMSGHEAKAVLEALEVELEGRLRLAWKPKTKVPSPPPKRLPVHNVFVNDLHFEARSKDLMFEFFKANGADVSAEIVFNSDNRPRRSAGYGFVFNFKVEADALSSFDCKEFMGRPRIRVAHSHKRFMRGETKKILGSGEVSELSISVAE*

NbL04g10500.1 14-3-3_protein_7 [MW = 29.34 kDa]

No. of times detected



log(intensity)



Values from



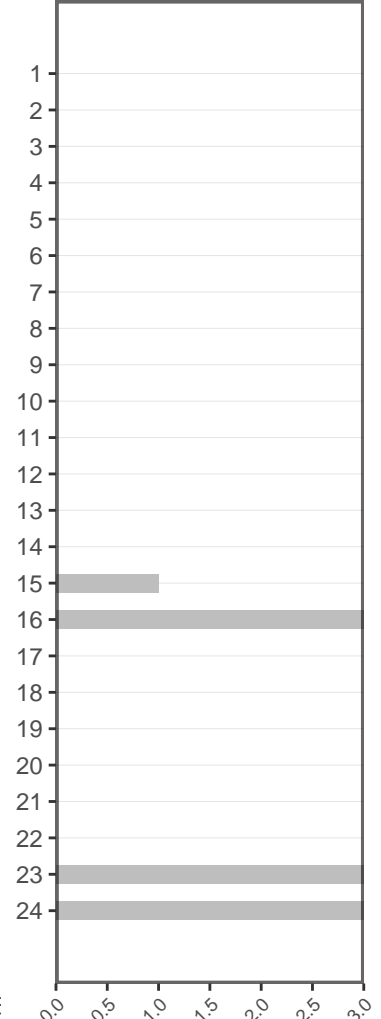
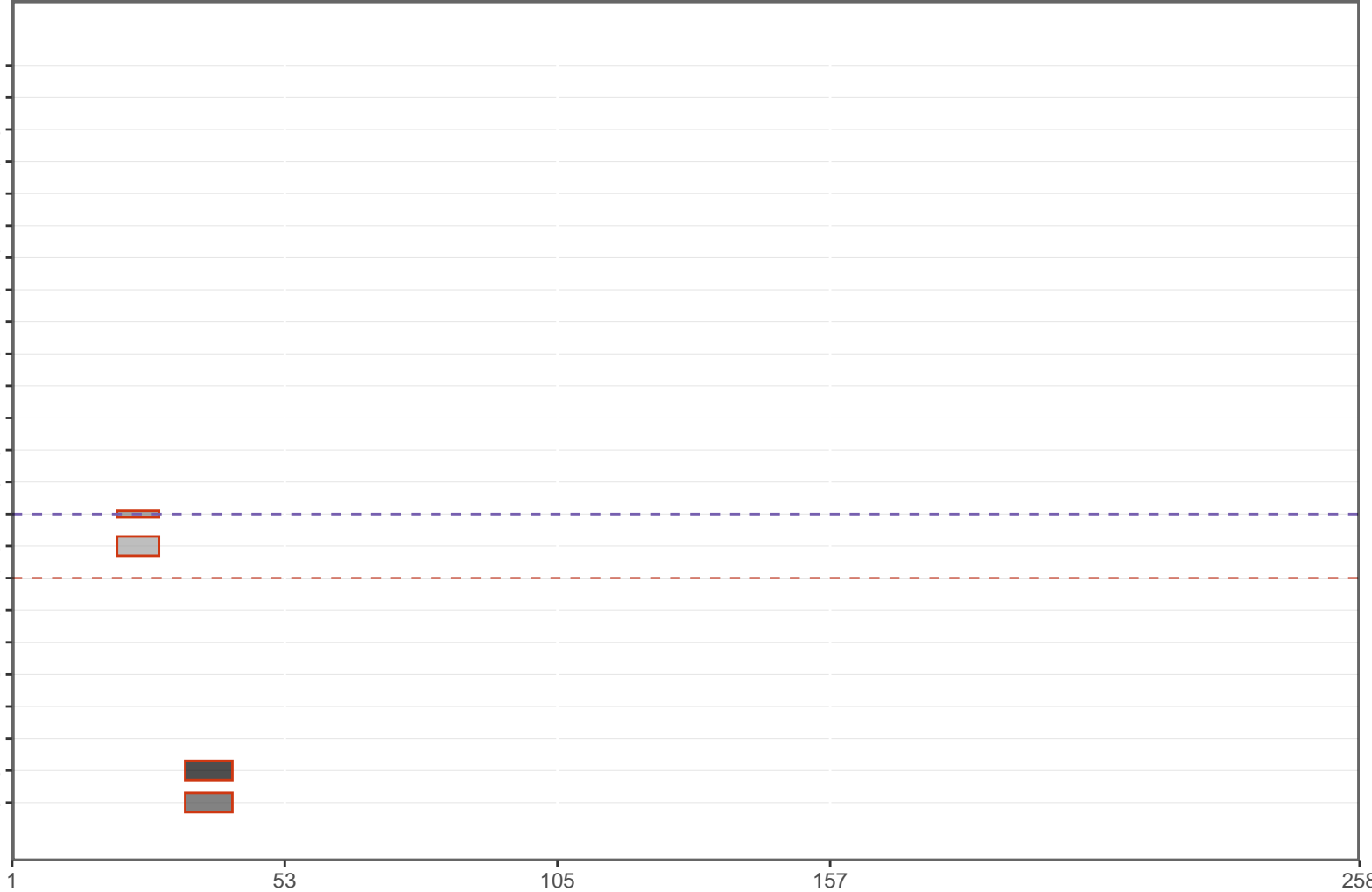
MW indication



Molecular weight

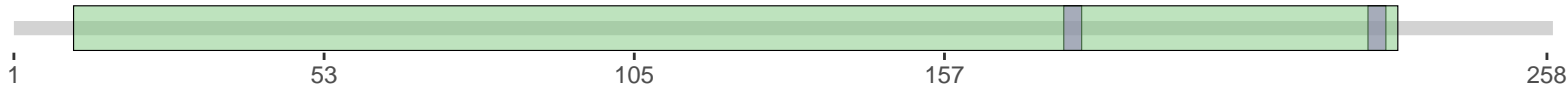


Gel Slice



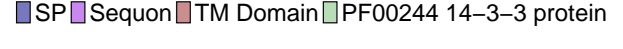
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AGESTVFFYYMKGGVYRFLAEFKSGDGRKEAADQSLNVAEATATASADLAPTHIRLGLALNFSVFFYEILNSPERAGHLAKGAFDEAAELDLSSEESYKDTLIMQLLRNLTUWTSDEEGGDISASISWLIIPFMVR

NbL04g10330.1 aldolase_1_chloroplastic [MW = 59.94 kDa]

No. of times detected



log(intensity)



Values from



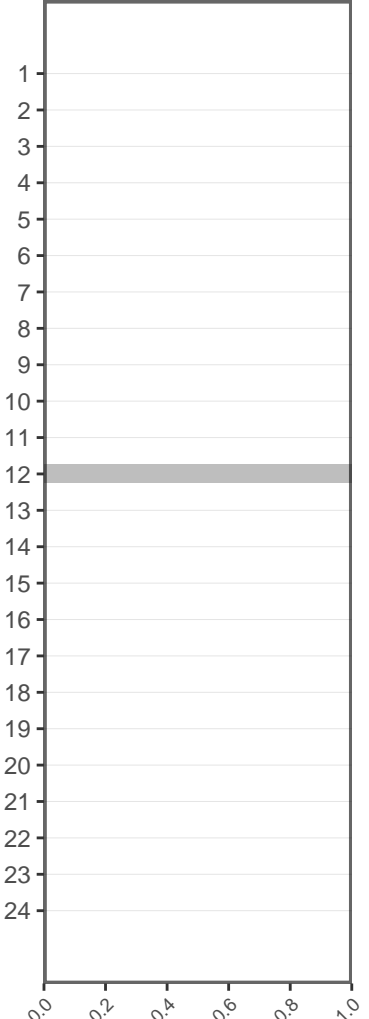
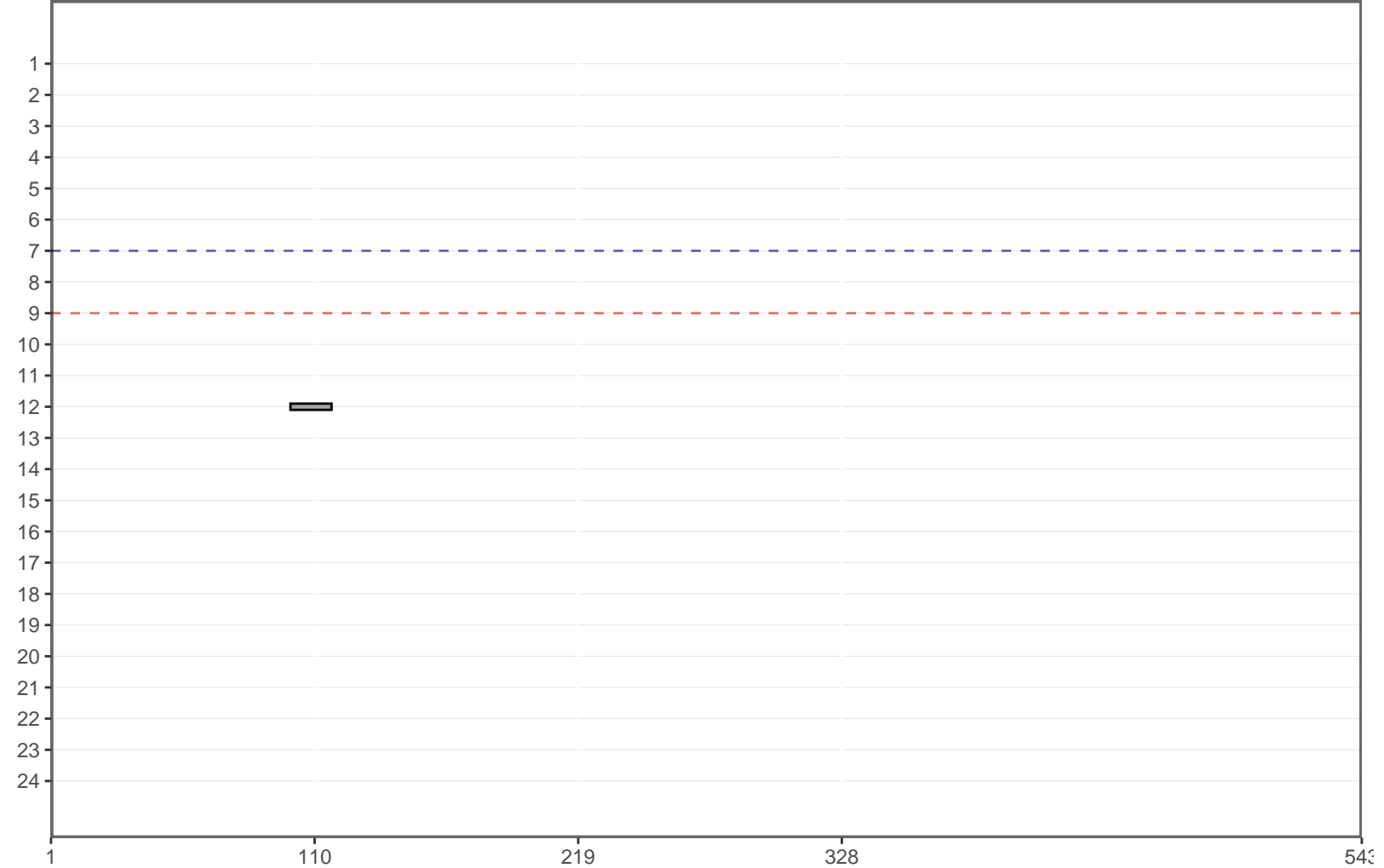
MW indication



Molecular weight

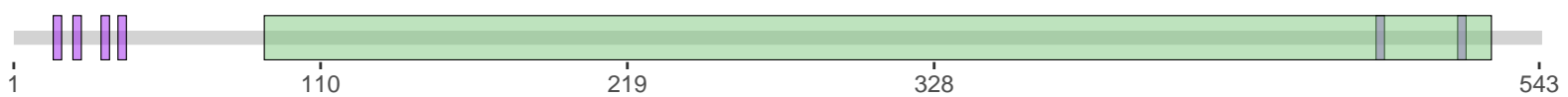


Gel Slice



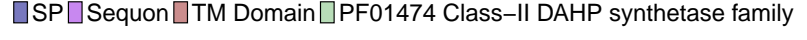
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGYAMQRINQWNLDFTEHSEGGDRYRELNRVDEALGFMAAAGLTVDPIMKTFEFVTSHEGILLPEYQGLTRLDSTGSLYDGSAPFLWVGERTRLDGAAHYEFLRQWVNFPLGIKYSQKMDPSALVLELNFENKAGRTFTRMGAENMRVKLPHLRRAVRAGGIVTWSDPMHGNTKAPGGLKTRPFDGSAEVRRAFFDVFHEQEGSHPGGVHLEMTGGNVTEGIGGSRVTFDDLSGRYHTHGDPRLNAGQBLELAFIAERLKRRLGSGGVLGQ*

NbL04g10260.1 thylakoid_luminal_29_kDa_protein_chloroplastic-like [MW = 37.7 kDa]

No. of times detected



log(intensity)



Values from



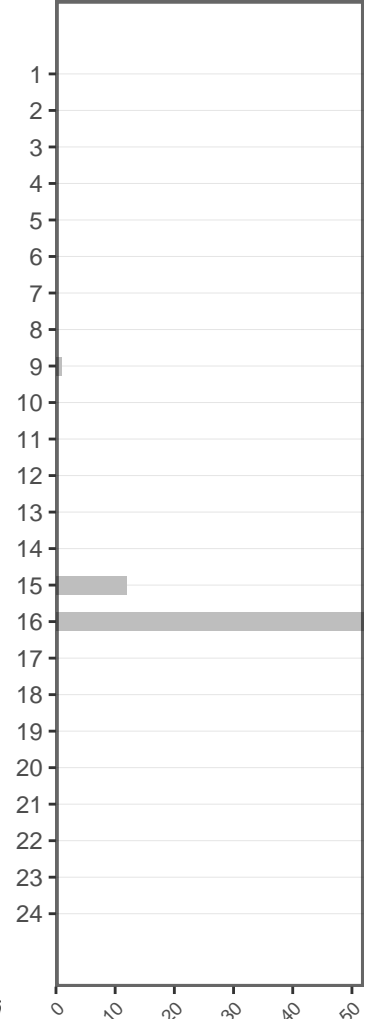
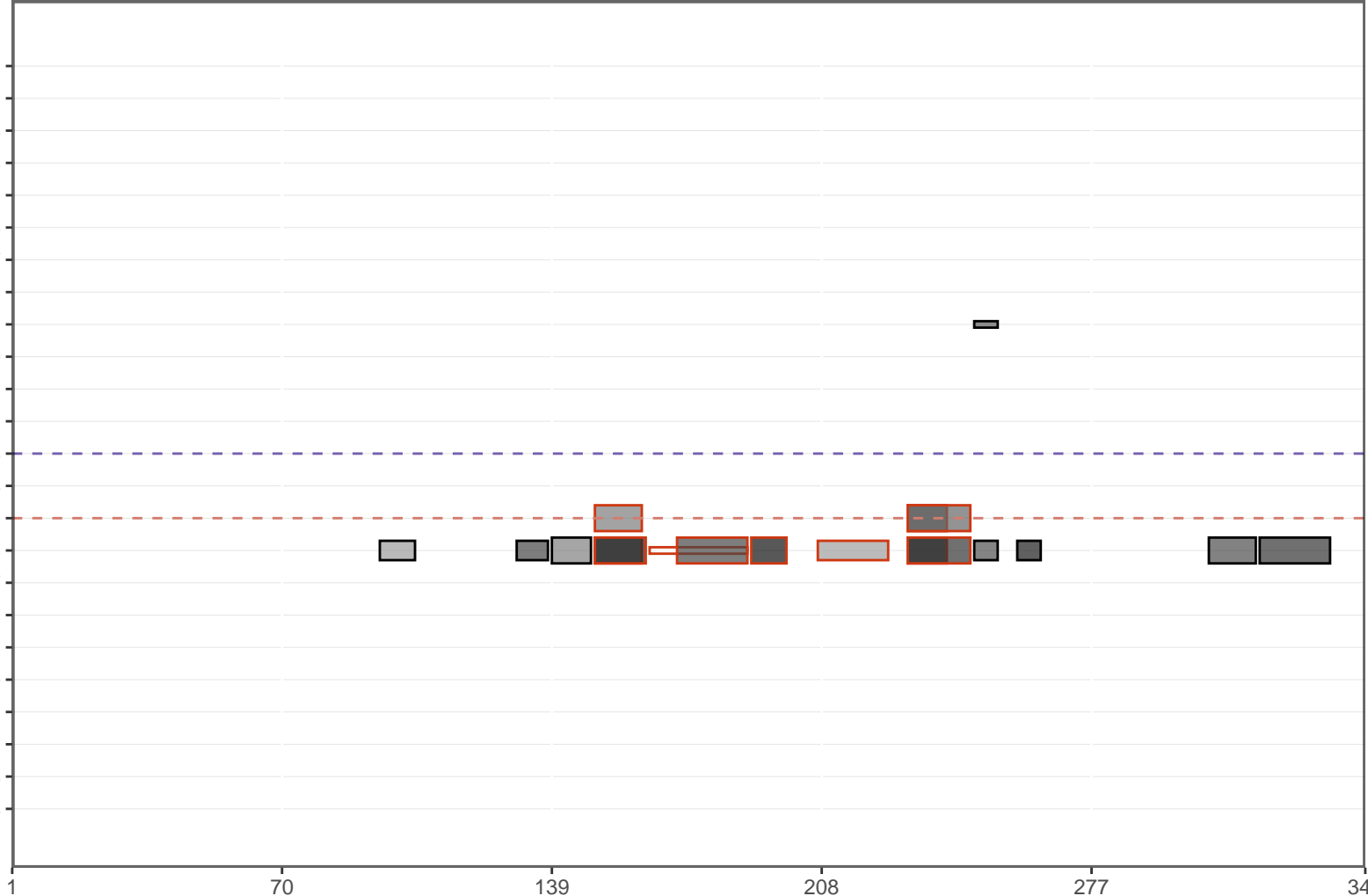
MW indication



Molecular weight



Gel Slice



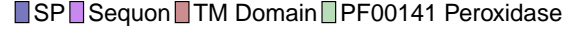
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EIDADSKGGPSSYADLQILAAGSAVKSTFLASAEKGGNGVKEKGSLLYSAYGNGQWGLFDKQFGRSDAGEFPQGEGRVQWDKASVQEMKDKFKAVGFGPRGLAVMVFVFGPDGQATELLASDFEVLPLVWQKYGSRRETVSRDTVEVDLFTLTKLSGLGGQNYEAYSYPVQKIDVTKLKL*

NbL04g10250.1 serine--tRNA_ligase_chloroplastic/mitochondrial [MW = 59.73 kDa]

No. of times detected



log(intensity)



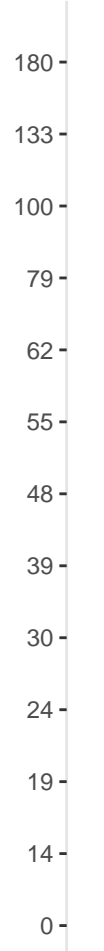
Values from



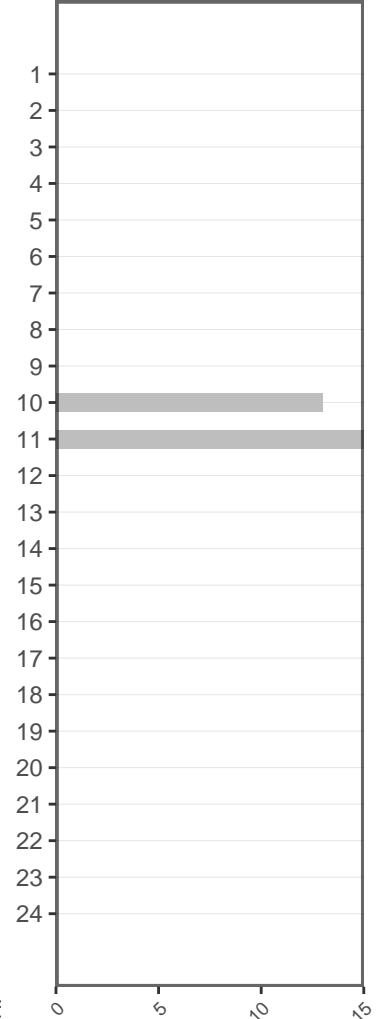
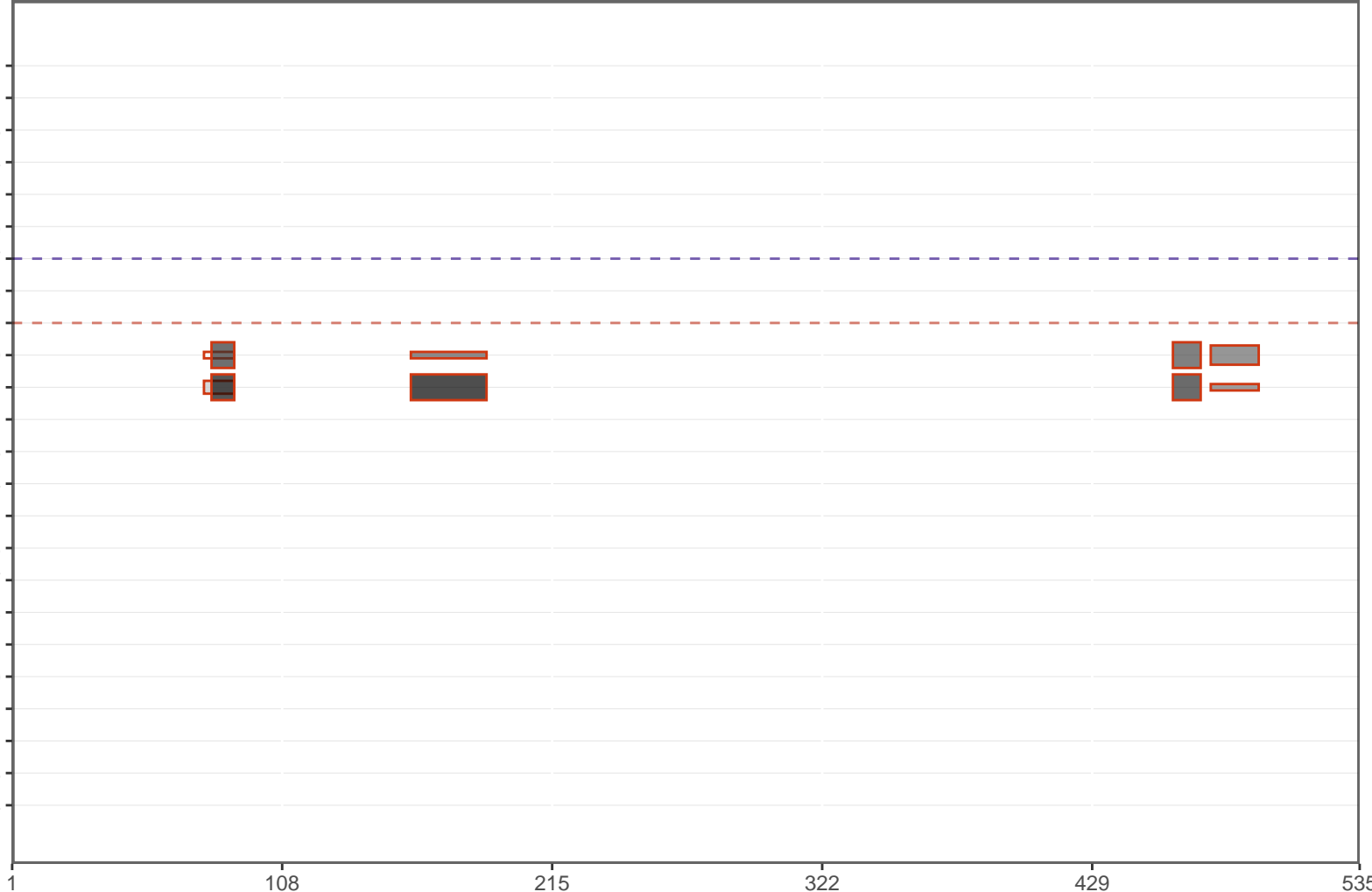
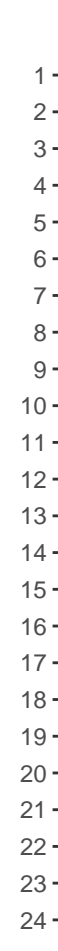
MW indication



Molecular weight

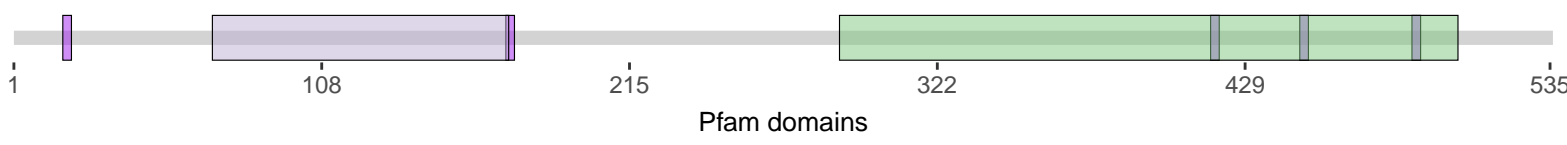


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

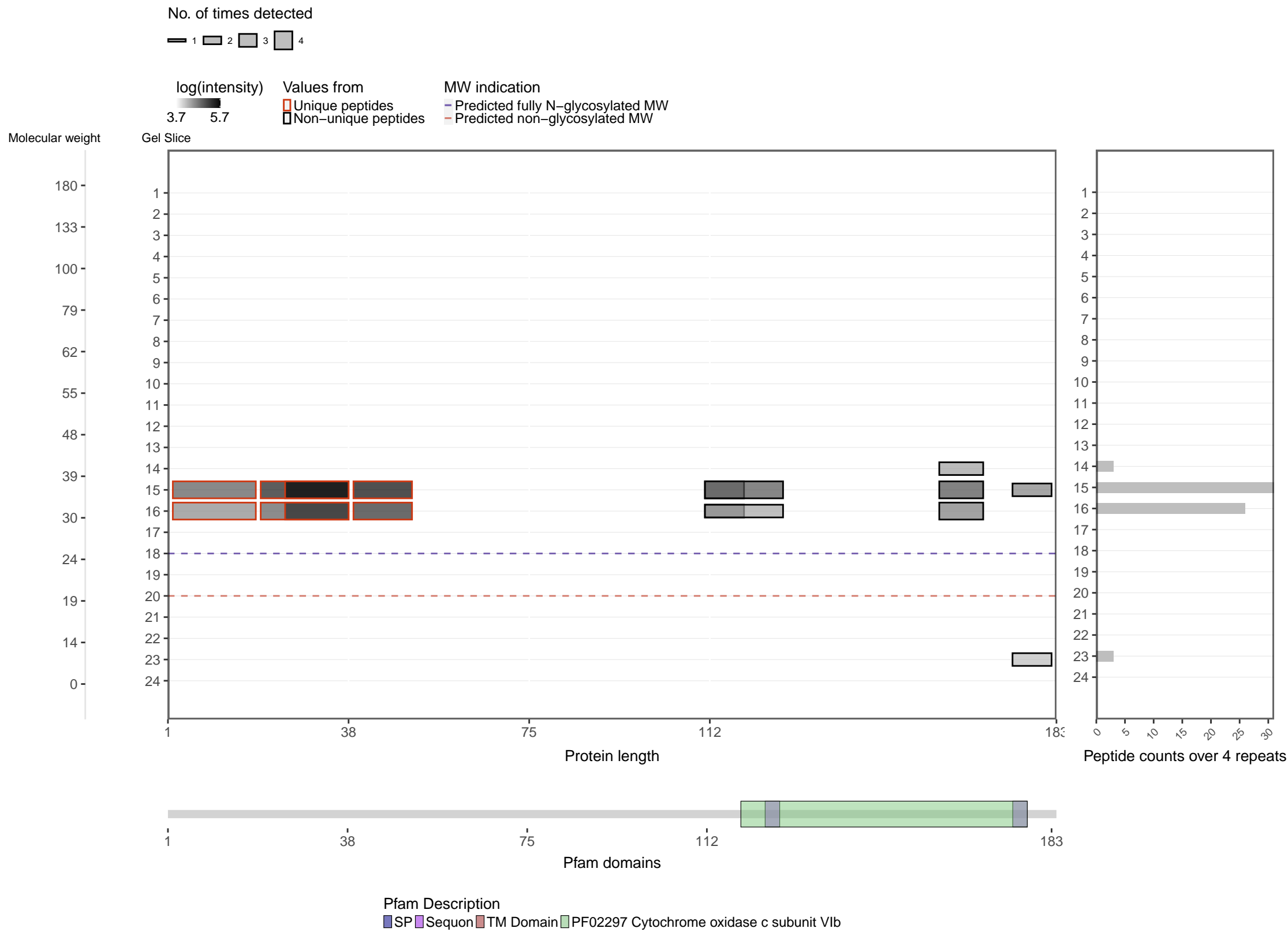
Pfam Description

- SP
- Sequon
- TM Domain
- PF00587 tRNA synthetase class II core domain (G, H, P, S and T)
- PF02403 Seryl-tRNA synthetase N-terminal domain

Protein sequence:

3FTPLTTEIVRSSVWEKGGFQPRGNTQVYBIENSDDGLIGTAEPVGGIHMDSILSESLPLKYAFSHGFRTEAAGAAATRGLRVHGFQSKVEMFILCRPDESDDYHEELIEEEDLFSSLGFHFKTLDMAAGDGLGAPAVKFDVEAVMPLGLRVEGEVNDTKSVTFFTTANWKPDTLHGFKYKPVWISSASNTAVGSRRLGHRVRFEPGASGGPKKGSSEAPTQGFVHTLNATACAVPRMVGLENFQDGDGVDVPELRFPRFMGGLHKKPKHGNP

NbL04g10240.1 cytochrome_c_oxidase_subunit_6b-1-like [MW = 20.02 kDa]



Protein sequence:

PVEASDESSESTNDETSGNEESAVETPEIKLETAFADFRFPFTTNGTRHGFTRVVEYHRGVAAKGEGAPEGDKFAKYRSLGPGIEWDRWNEGRENGTFPGPL

NbL04g10230.1 14-3-3-like_protein_C [MW = 29.36 kDa]

No. of times detected



log(intensity)



Values from



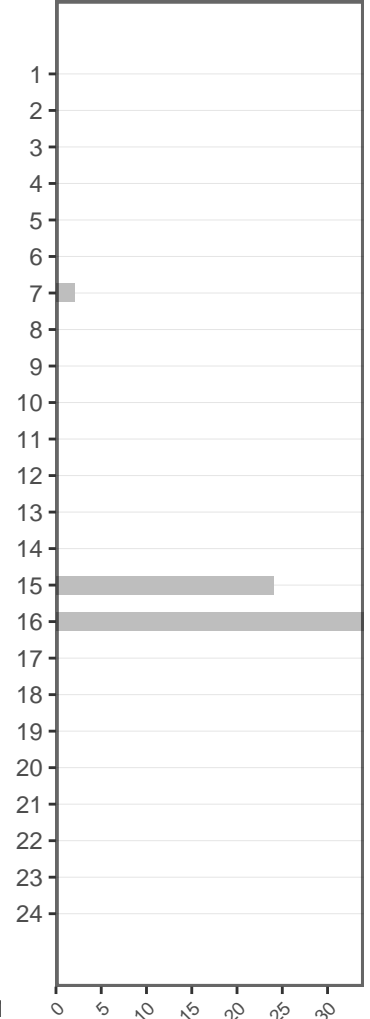
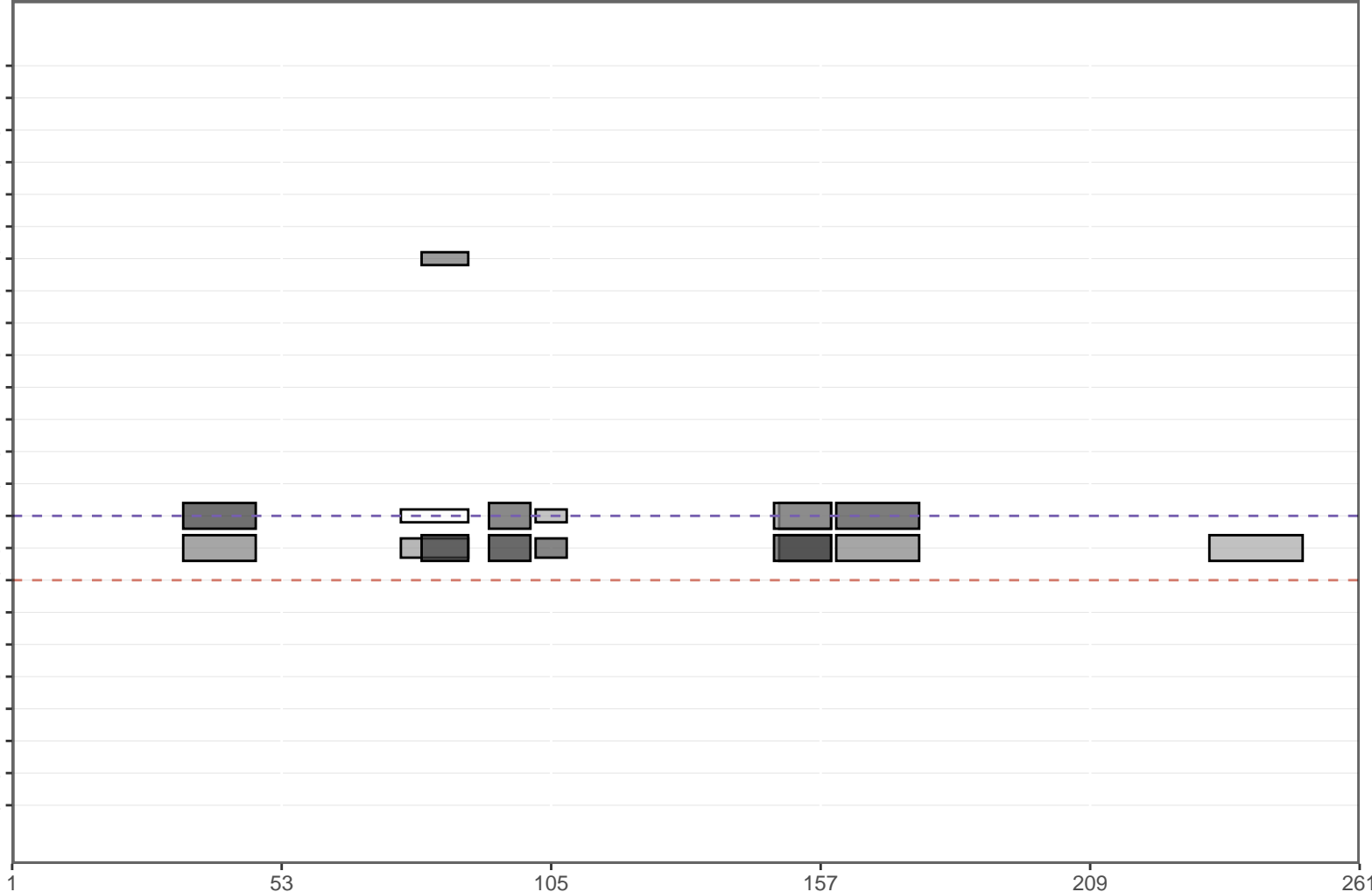
MW indication



Molecular weight

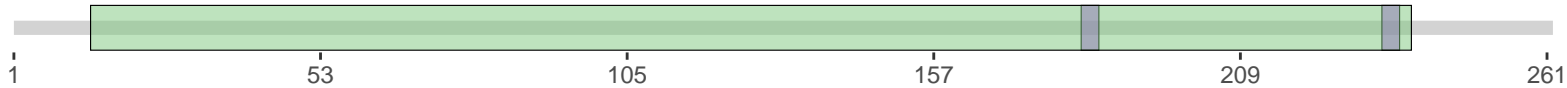


Gel Slice



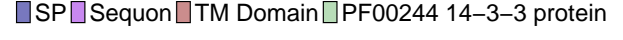
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IASGDSKVPYLYKIMGSDHRYVLAEFKFGAERKEAESTLITAYKAAQDIATTELAPTHPIRLGLALNFSVFYIEKLSNPDRAQNLAKGAFDEAIELDTLGEESKDDTLIMQLRDNLWTSDMDDGDAEIKEDPKPDEAKN

NbL04g10020.1 probable_beta-D-xylosidase_7 [MW - SP = 82.37 kDa]

No. of times detected



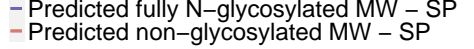
log(intensity)



Values from

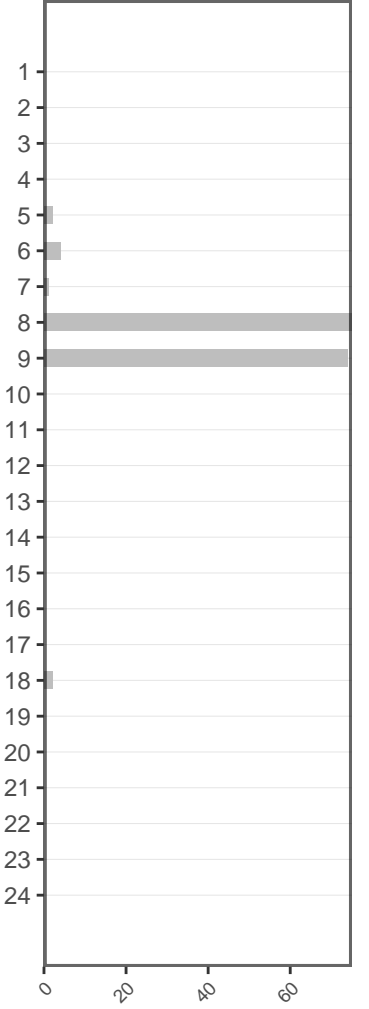
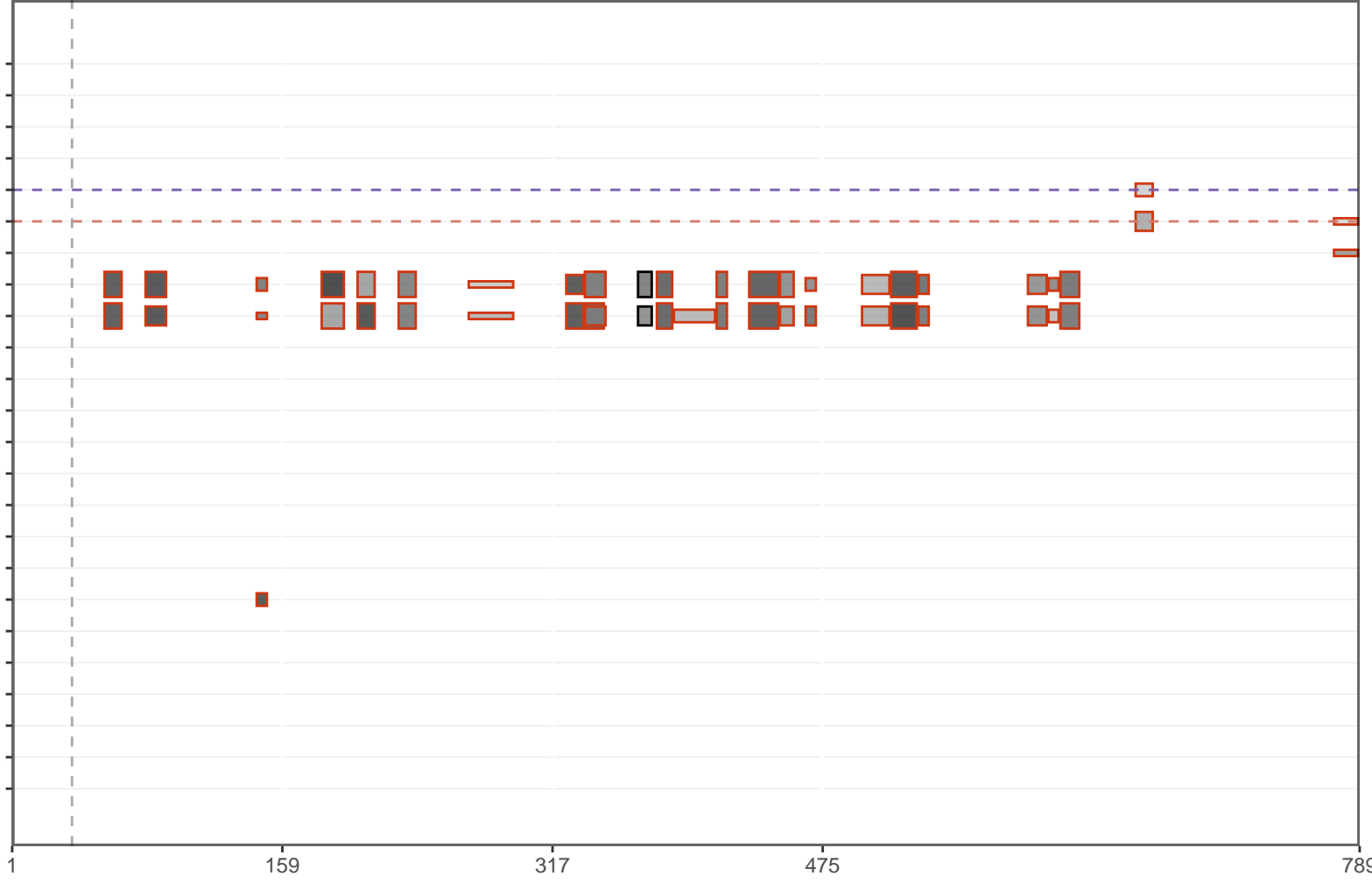
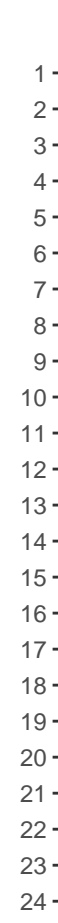
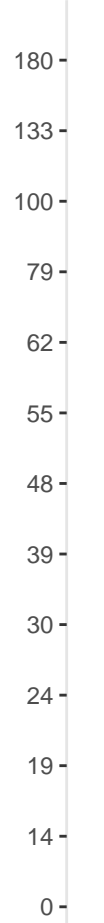


MW indication



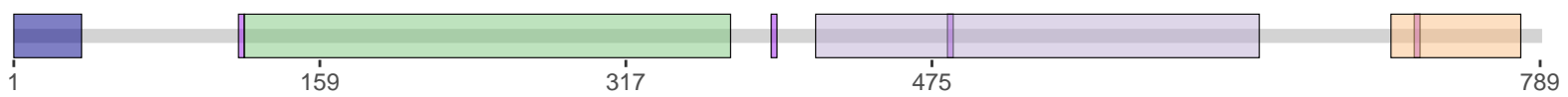
Molecular weight

Gel Slice



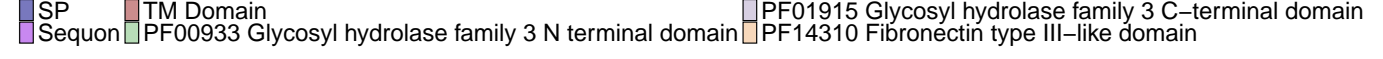
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FNGNPTKQLFGNSPILVCGAGHGELEAARSGGLKNTGKLLPLSKAKTNSLAVGPNANNAFVLRGNVGGPPKGEIKALSGYVKVGVYHPGNAVNGTSVAIDQAVNAKNDVYVLMGLDGGDEREQDFRDDLVLPGGQEKLTSTVAKAAKPVVILVLSGGPVDISFAKTNPKIGSILWAGVYDGEAGGLALAEIFGEHNPGGKLPITWYDQEFKIPMTDMRMRPNPTTGYPGRTRFVYKGPVVEFGVGLGYFTFYVYEFSSVTRKTVQLNQLSTAKTVQSSDSI

NbL04g09850.1 uncharacterized_LOC107766695 [MW = 30.56 kDa]

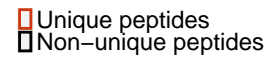
No. of times detected



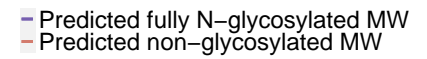
log(intensity)



Values from



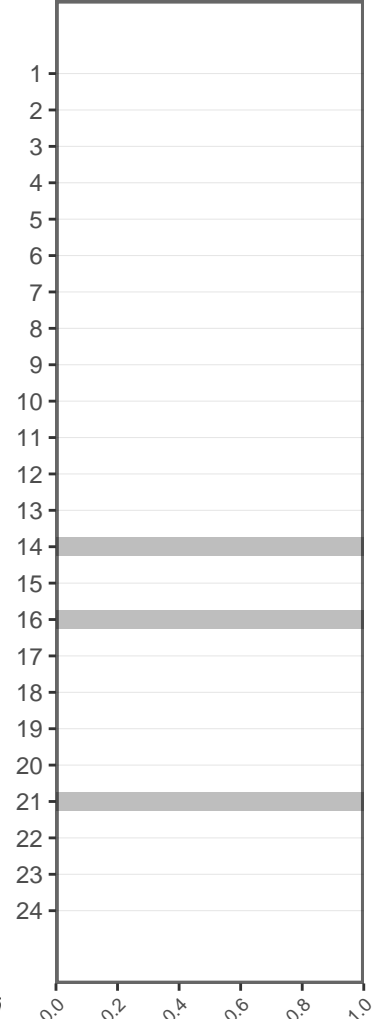
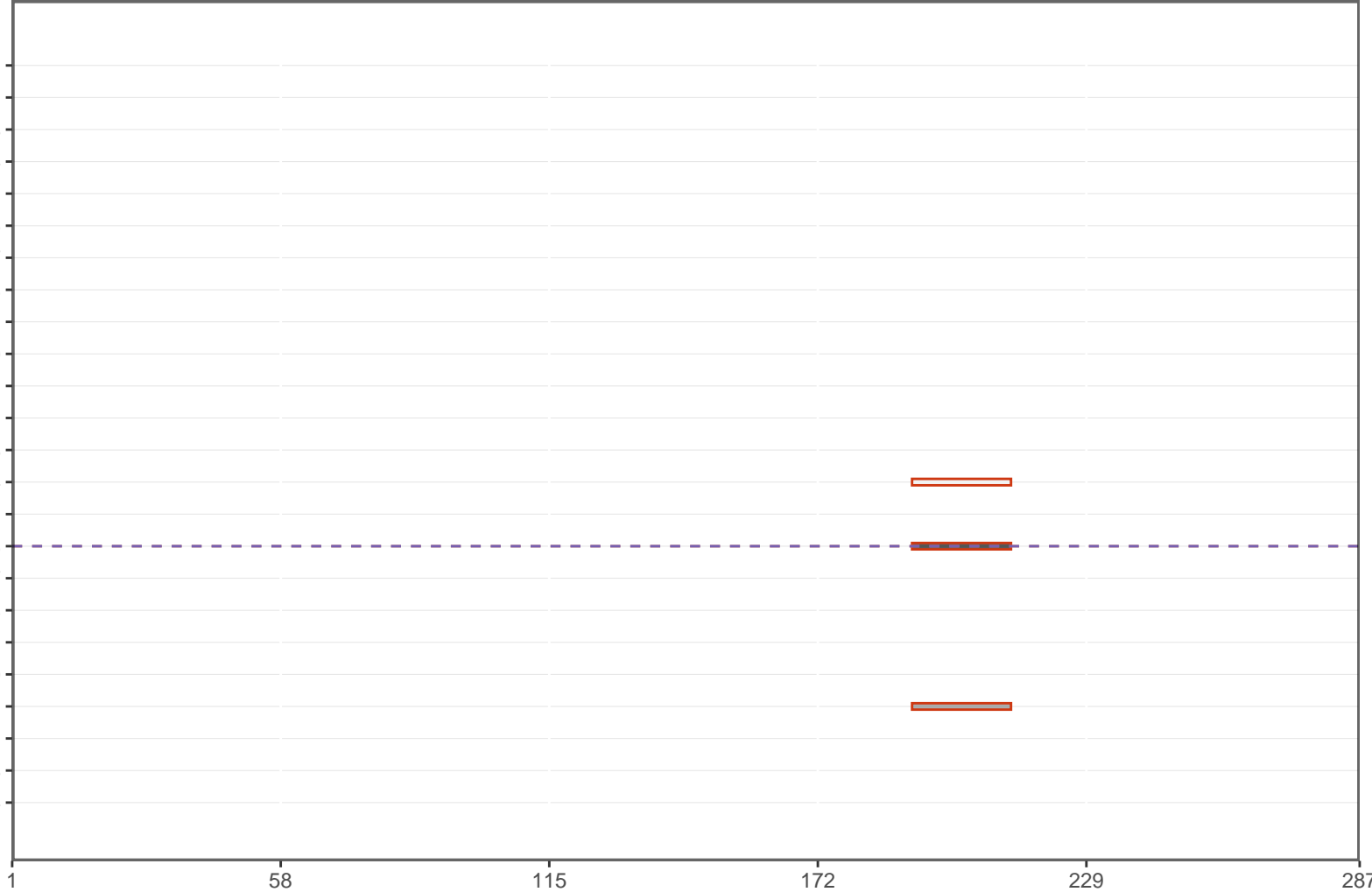
MW indication



Molecular weight

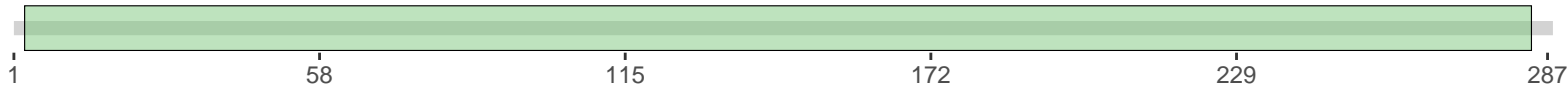


Gel Slice



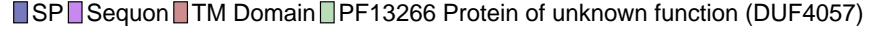
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

XPVTIPEVAKQRELGGTLESEAEMKLNKGLSDAKTKELVGHDFAPPEIGRPLAARALALRESITGFTNNGDVGGDEQAVKTKAHPENKLAELTGNDFIKGDTTPPAEKHLSSAKLREMSGNFADKQVESRDFYGGVRKPPGGESIAIV

NbL04g09750.1 aspartic_proteinase-like_protein_1 [MW - SP = 54.41 kDa]

No. of times detected



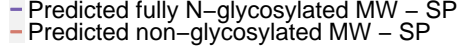
log(intensity)



Values from



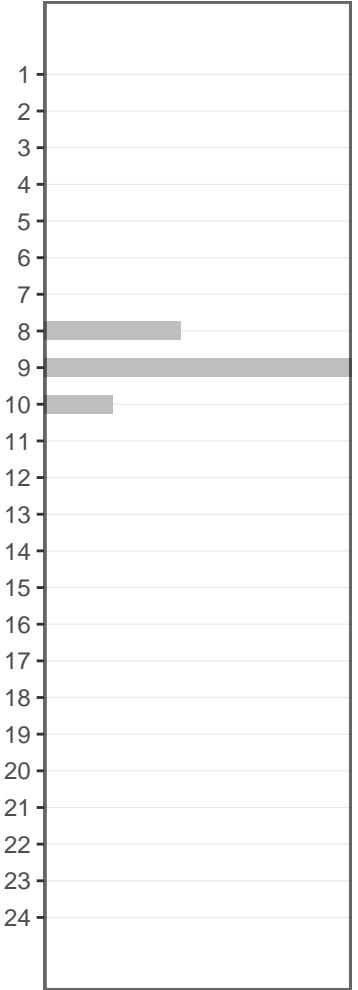
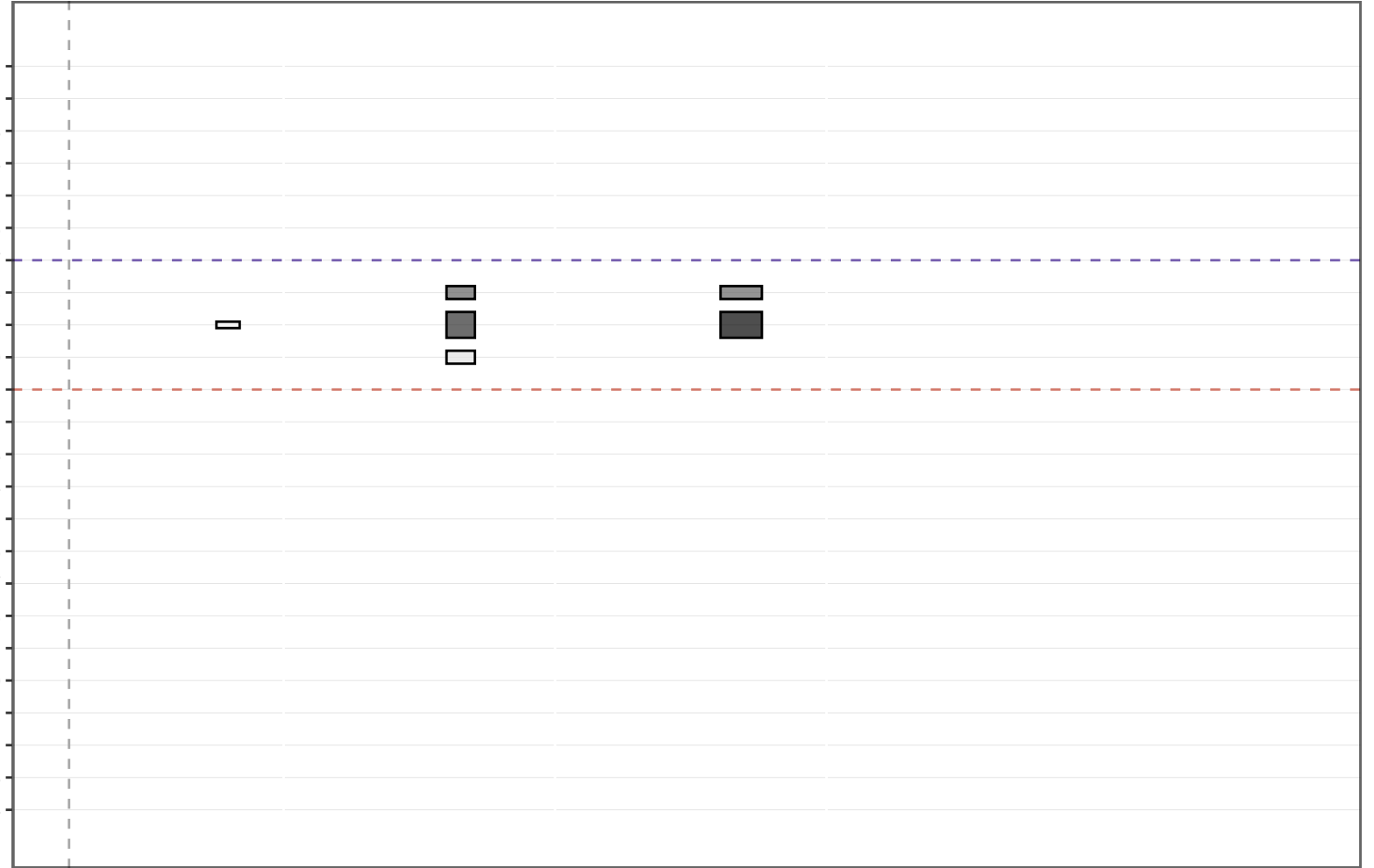
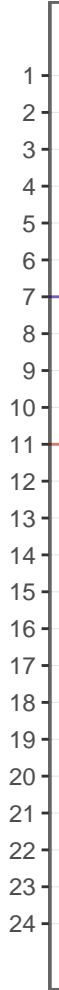
MW indication



Molecular weight



Gel Slice



Protein length

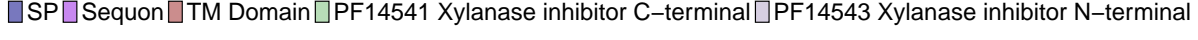


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LGPGEISVPSFLAKGGFVPHFSLGFDKTNIGSTIFFGDDGPENGRLSSEFVSLDGNNTYVYEVQRVYFGDTLQKGGGFDALVDGSGSFTYLPSEIFTEVTEFDDQINATRLPTEDFFVYKASGRGLFNPISMKVLAANGSFFVQINPVFTISDGDNFYGVGLPEGMIGIGQNLMEGVRMVFQWQNMKLGWVSHSKGDDIEGSAKVTAPPFGSLASNPFTNEQGRSPQGHAWAPAMAGKPSAASHAVSCLHCAMSGLLLSLVWLPVLP

NbL04g09740.1 60S_ribosomal_protein_L30-like [MW = 12.4 kDa]

No. of times detected



log(intensity)



Values from



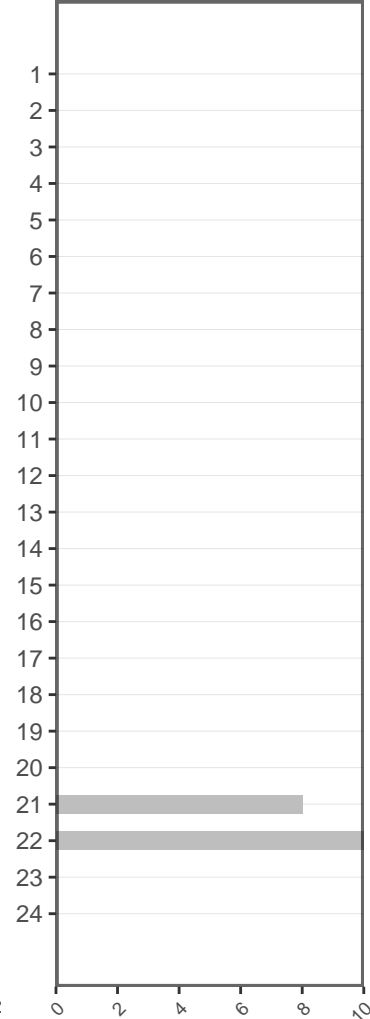
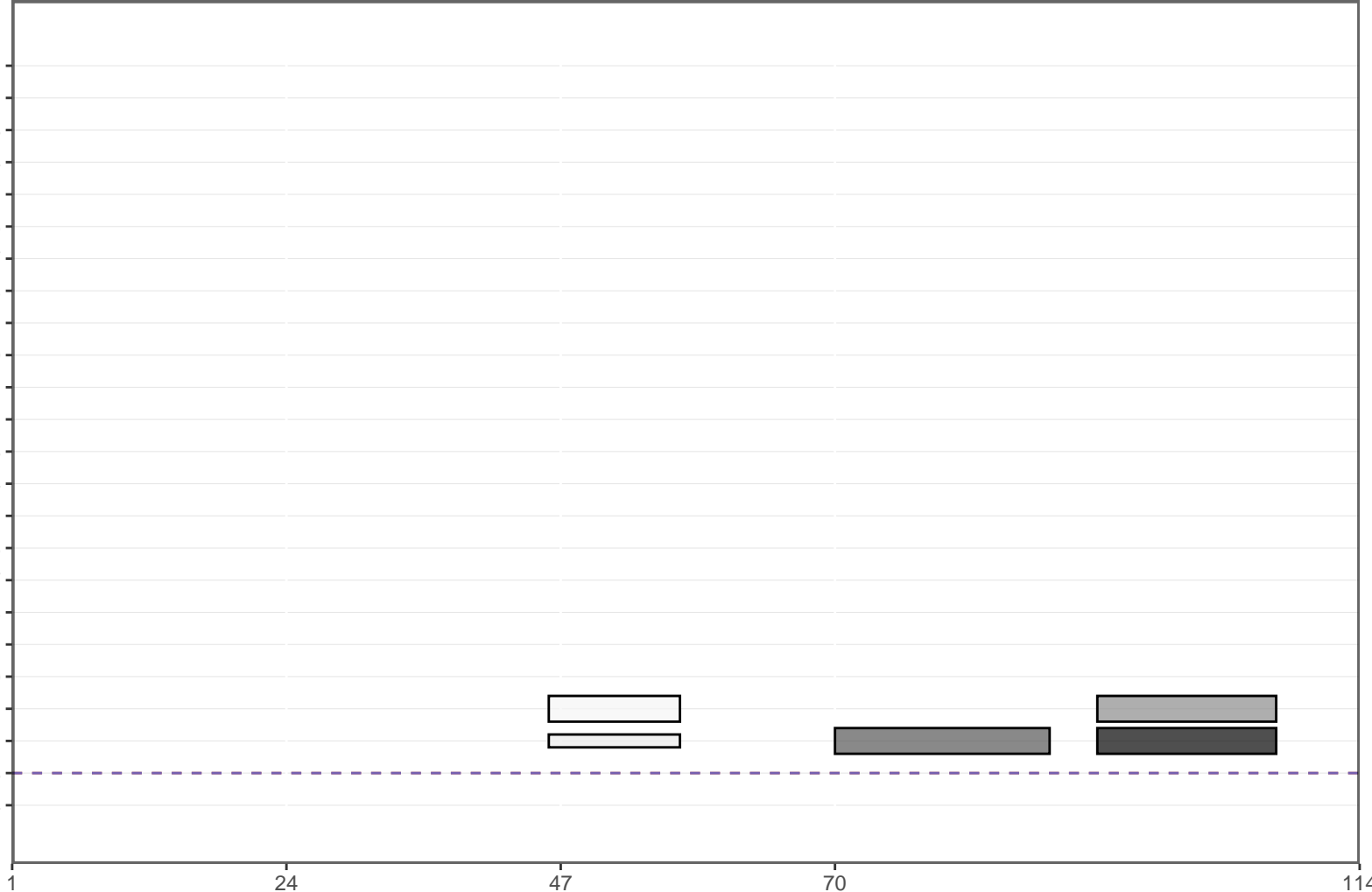
MW indication



Molecular weight



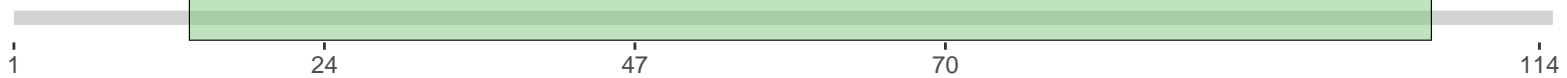
Gel Slice



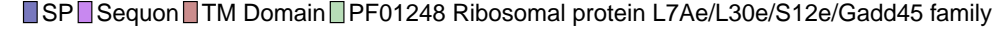
Protein length



Pfam domains



Pfam Description



Protein sequence:

GGKLLISNNCPPLRKSEIEYVAMLAQVGHFNNGNNVDLGTADGKYFRVSGLSHPGDSQIKLPGDH

NbL04g09530.1 uncharacterized_LOC107779703 [MW = 58.14 kDa]

No. of times detected



log(intensity)



Values from



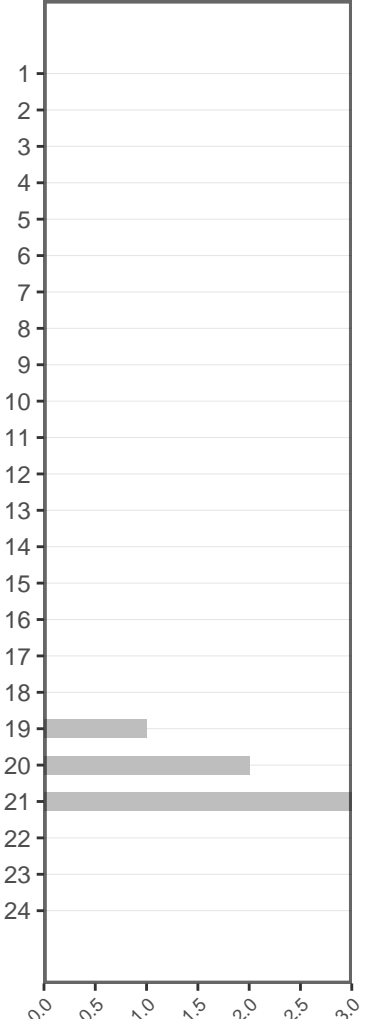
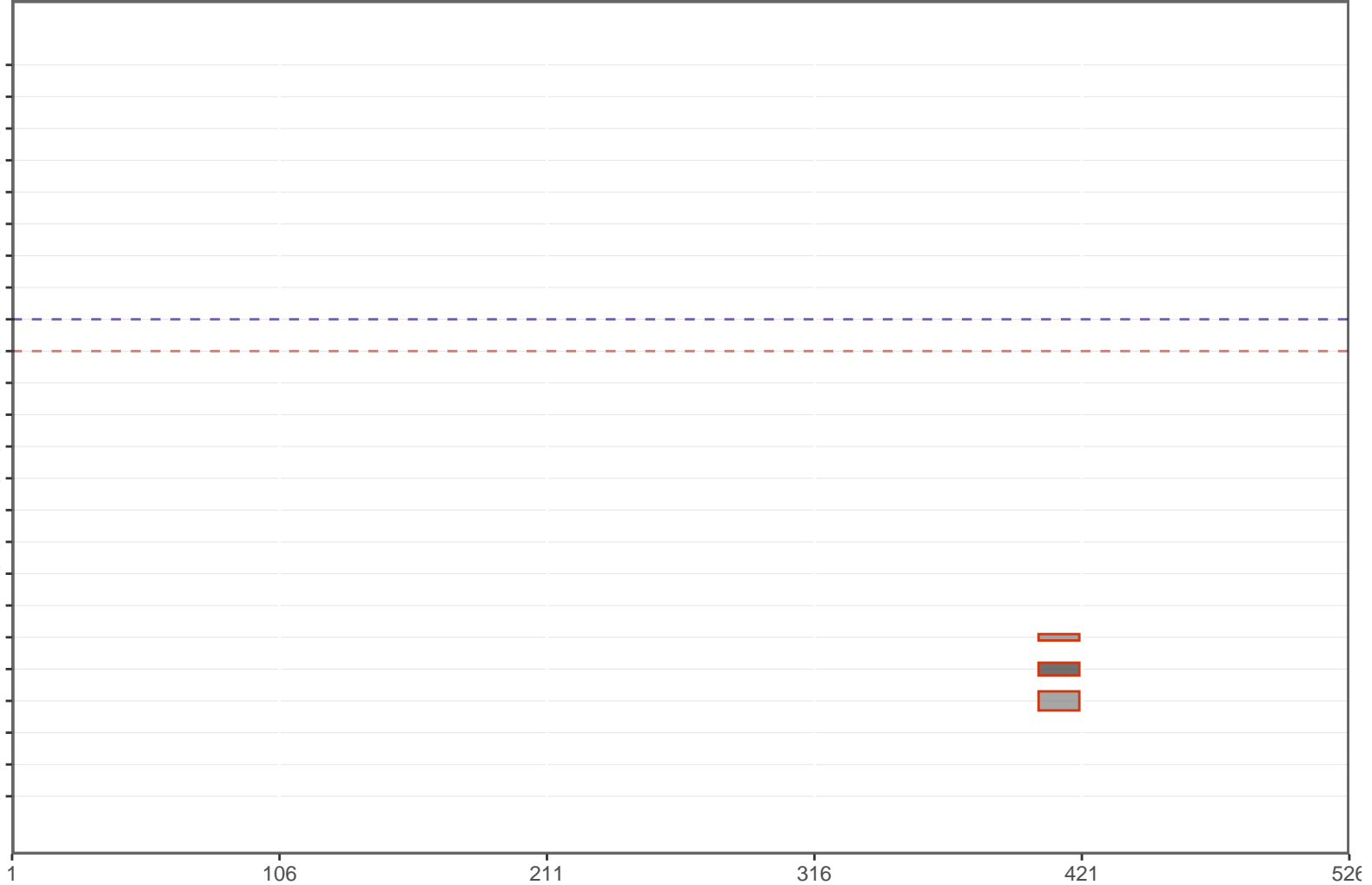
MW indication



Molecular weight



Gel Slice



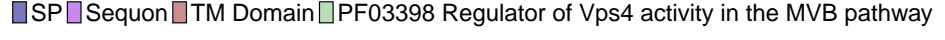
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

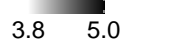
IPSIGVSAPEMLFFPASALGSDSEEMAKPEDEMLKSHKGNVERDEVLQEKVYKDKLGGPETLSAPEEEKGFLEFVPPQRLGPFSSGQTFTTQSGIPRFTKTAESDDIDLDVLAANAANAESAERAAAAARSANLADFRISLFRKRSEEVPGSTSENSEGEGRILEKAPFDLGHQLSNDGIPSPHSGPPEHGVSNVPSGDATVGFEGFMSTNHHPAPGTALHGQRLPELDDETYYGYPNLFITNGSNPSSRGGQSFKNIKSTHWK

NbL04g09390.1 uncharacterized_protein_Osl_027940-like [MW = 26.12 kDa]

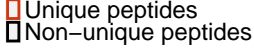
No. of times detected



log(intensity)



Values from



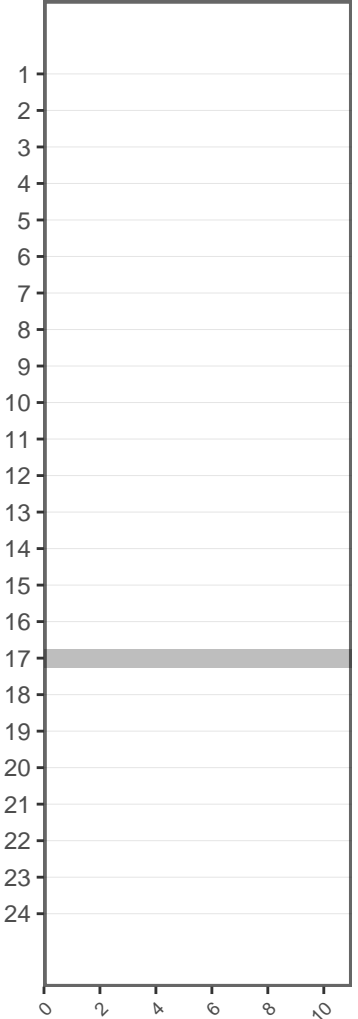
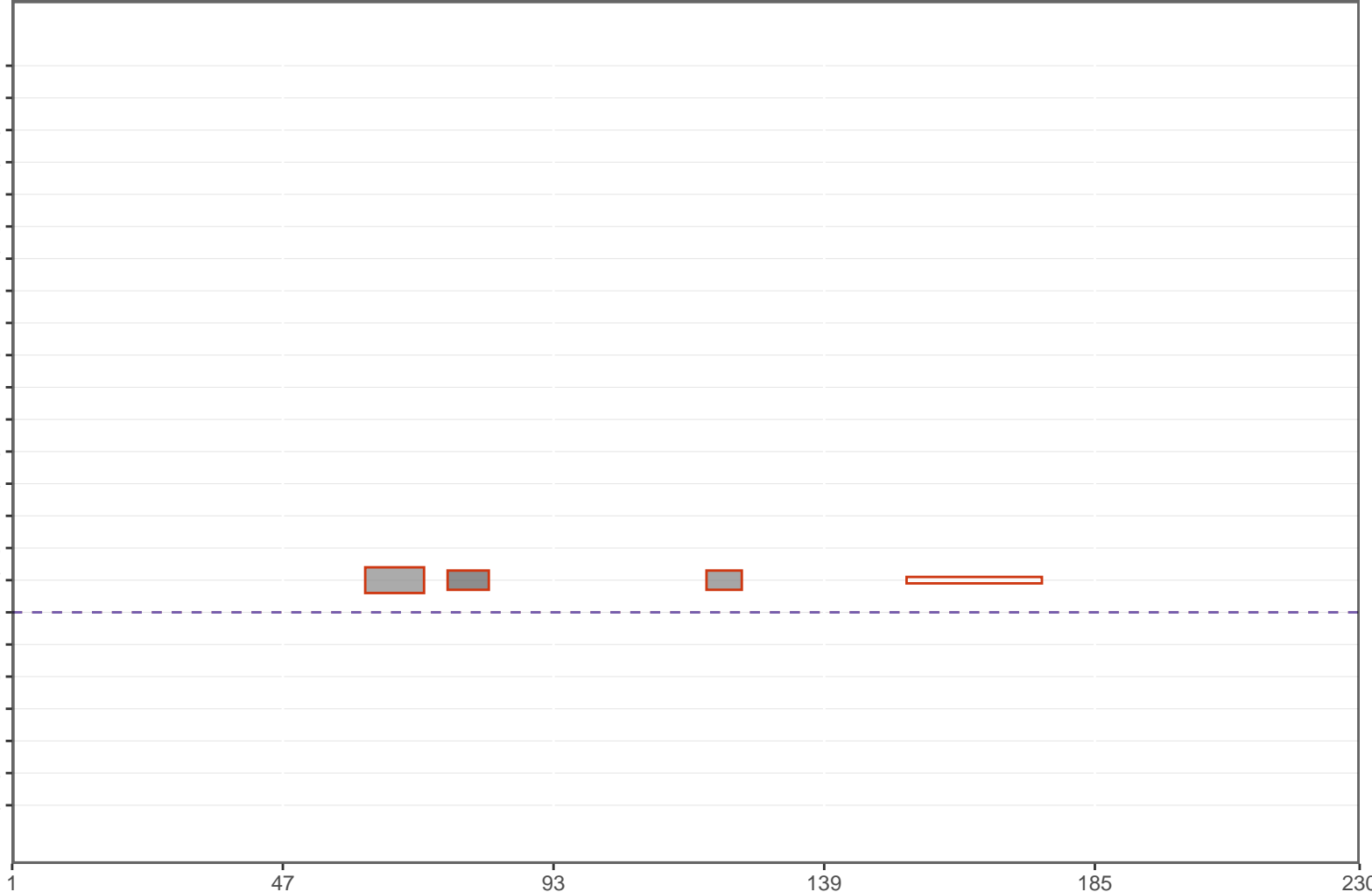
MW indication



Molecular weight

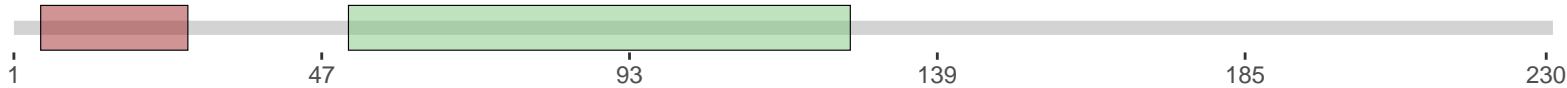


Gel Slice



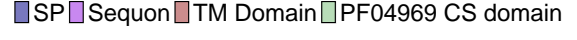
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

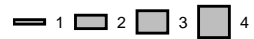


Protein sequence:

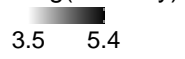
NYDESKTSTTSRSHVLYKKAEKHWWRLLKGEGRVRFVFKVDVWKWVDEDEEDTKPGTMDFGDIDFSKLNMOGGPSDFDADVPEGDGDDSDTEEEVREEENSADNEPKAAVFPSTEPKAKA

NbL04g09320.1 probable_ATP_synthase_24_kDa_subunit_mitochondrial [MW = 27.47 kDa]

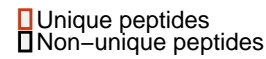
No. of times detected



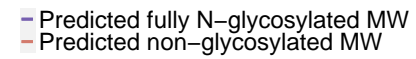
log(intensity)



Values from



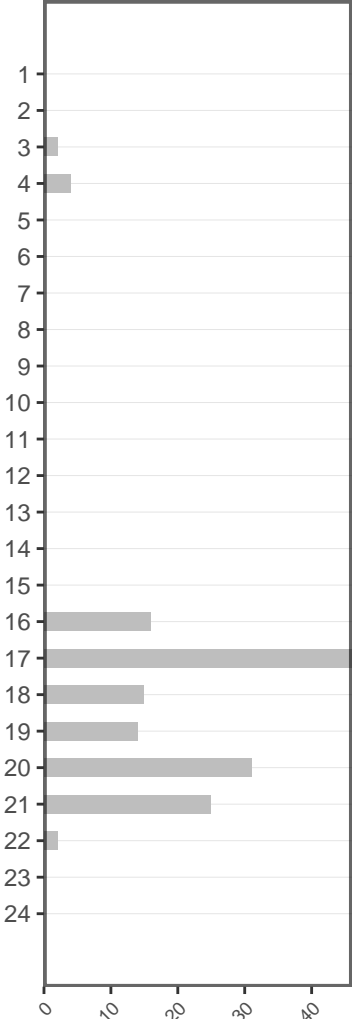
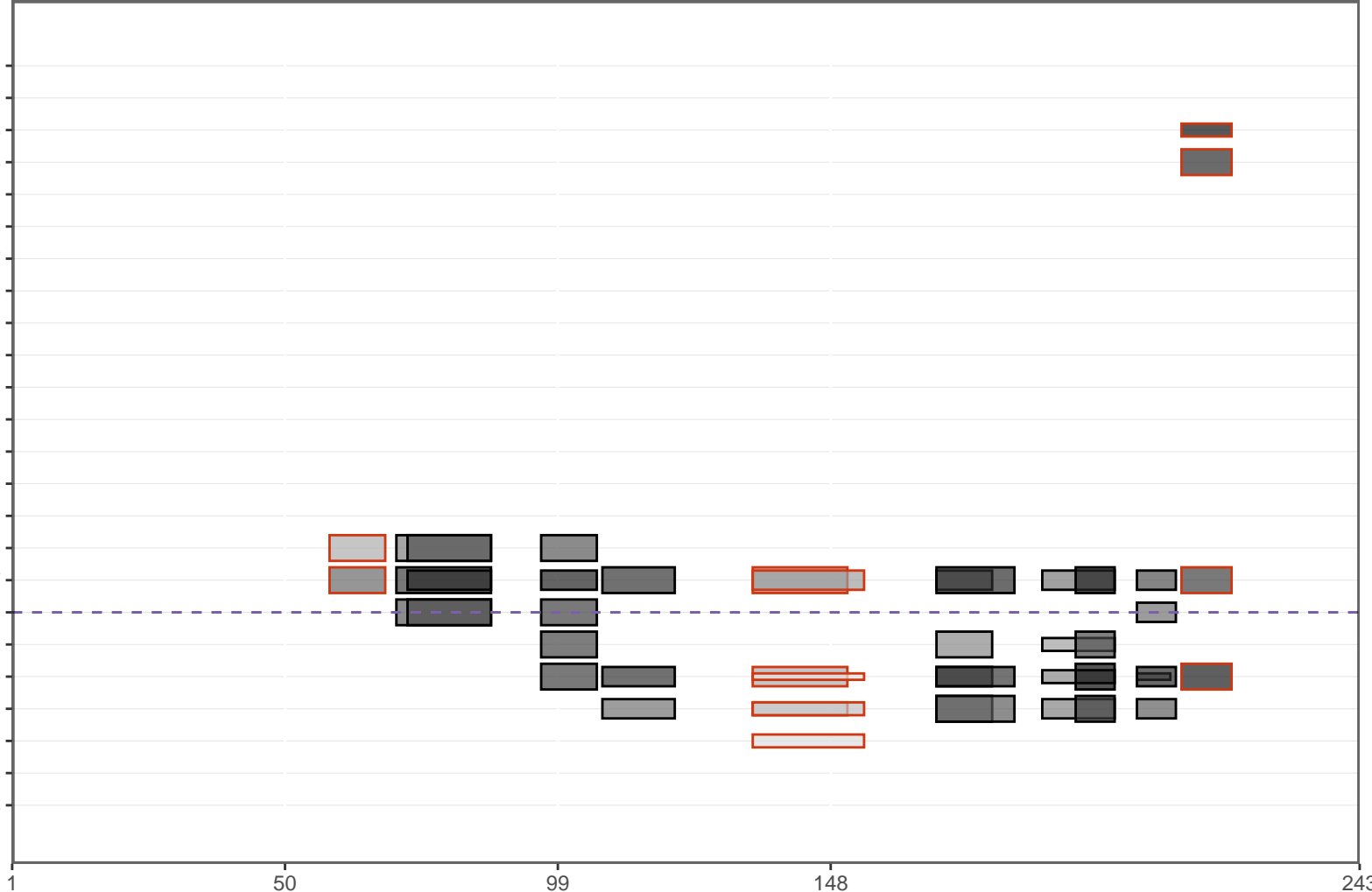
MW indication



Molecular weight

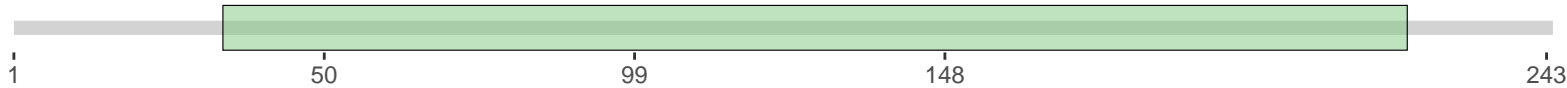


Gel Slice



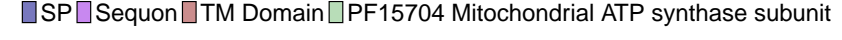
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NIETVETHEIPDARTYLLKLEKEMRVRKGLIDGGEDLQMAALDKVEKEHKPLMRNDKKGIALTAEFDKINQKLGIRKEDLPKYEEGLEKIAKAGLEELKDKDALEAMEAGKRRFEFKDEEMPSVWLSLRNFI

NbL04g09270.1 hypoxanthine-guanine_phosphoribosyltransferase [MW = 24.52 kDa]

No. of times detected



log(intensity)



Values from



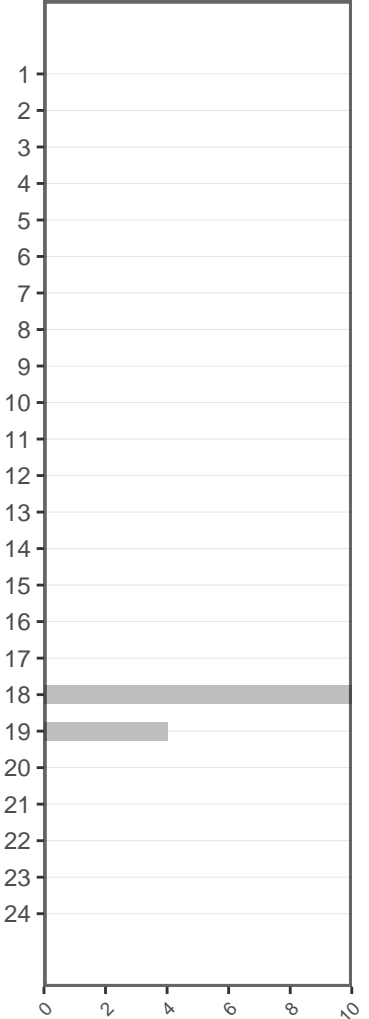
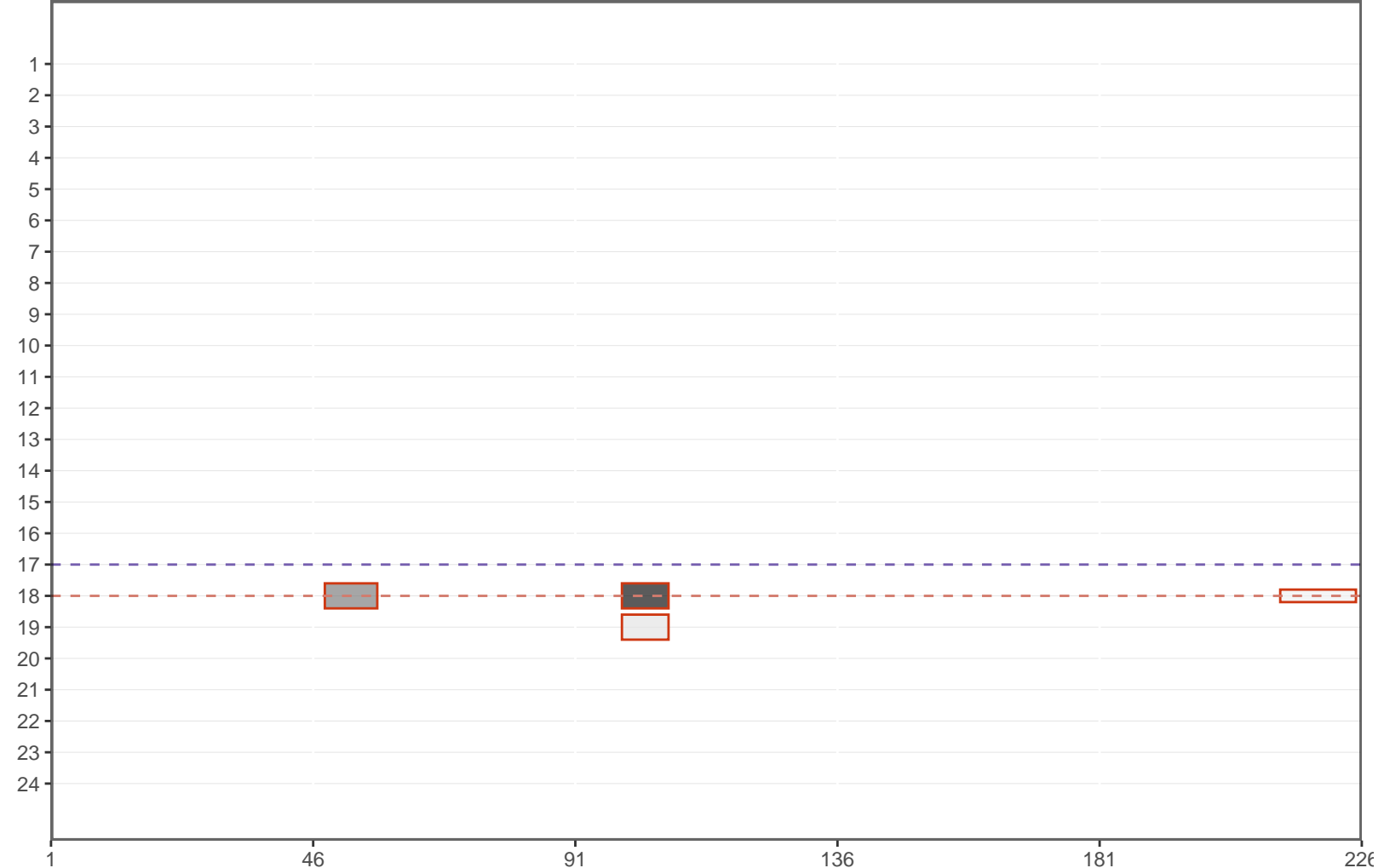
MW indication



Molecular weight

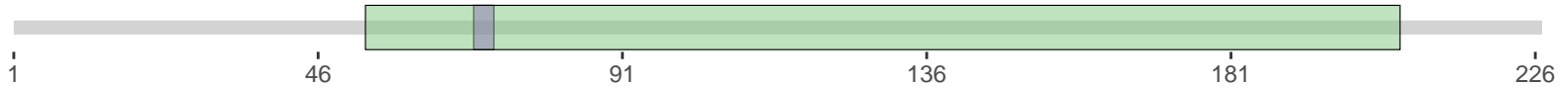


Gel Slice



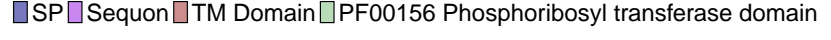
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IYDFVRYVESYGGSTVSNKPKWISGDLNIDVTGKHVILVEDIVDTGNTLSGLIEHLKSGASSISVCTLLDKPKRKYVLELVGEGMFEVRFEGCPDYFVAGYGLDFAELVRLNLPYVGVLPKPMYS*

NbL04g09260.1 uncharacterized_LOC104248969 [MW = 20.43 kDa]

No. of times detected



log(intensity)



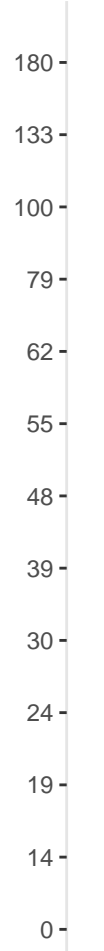
Values from



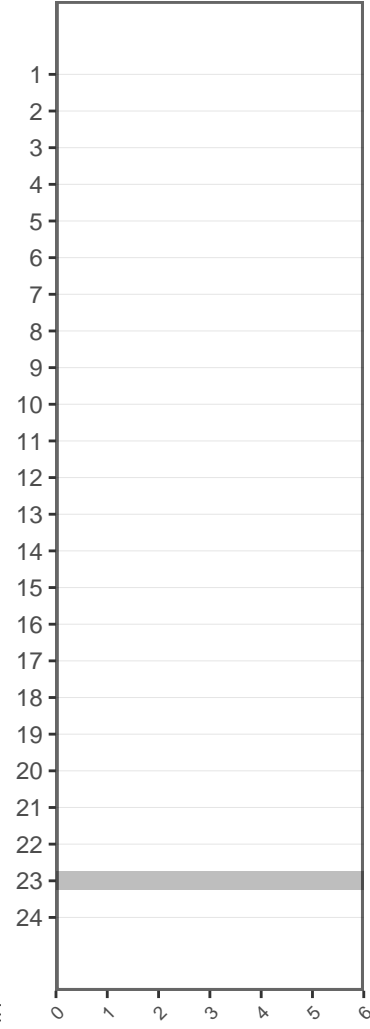
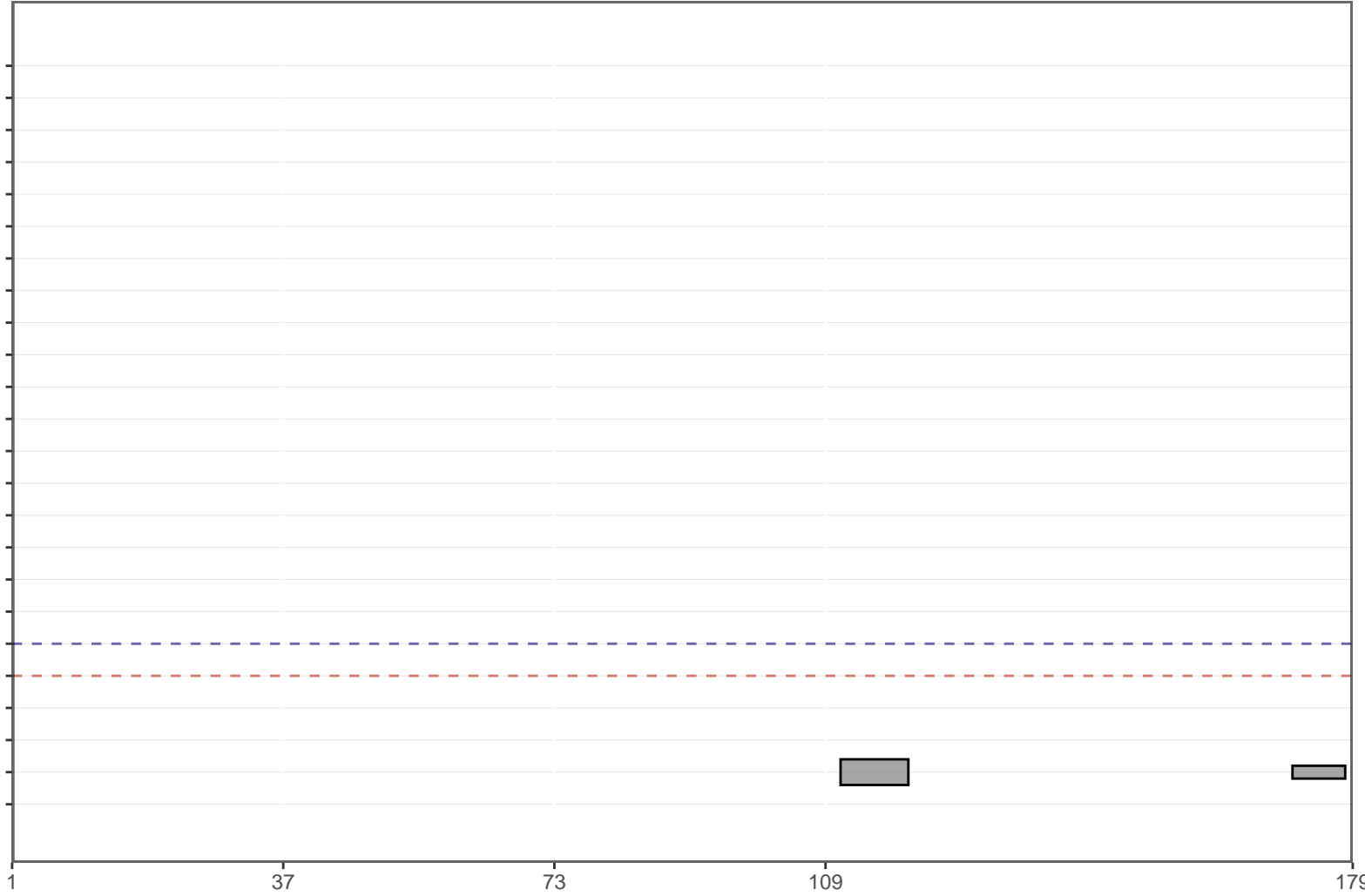
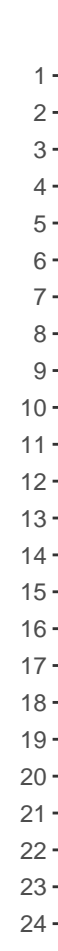
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

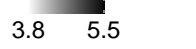
ISSSTQFISQNVRYKYGVDYDKEVDKINLKFAEAREEIESAMEGKETVYFNEEAEGARAANKVEFDLYVGLLEKLESESEKGVIGRSMQLNEQLKAELEQLNE

NbL04g09150.1 xanthoxin_dehydrogenase-like [MW = 29.68 kDa]

No. of times detected



log(intensity)



Values from



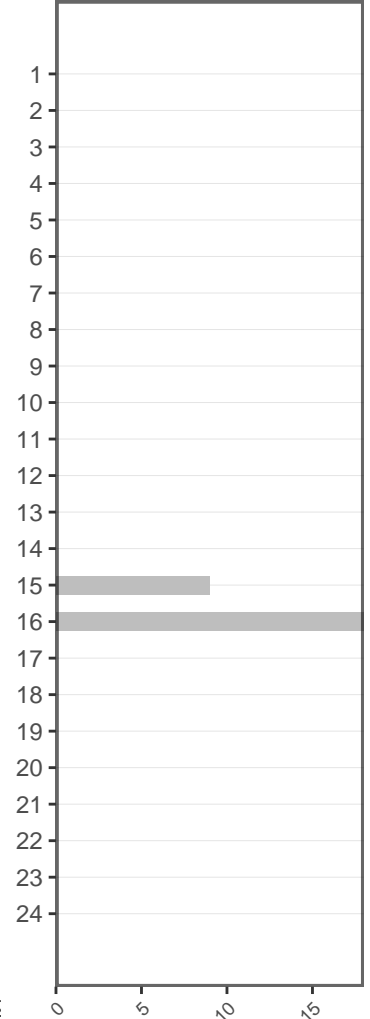
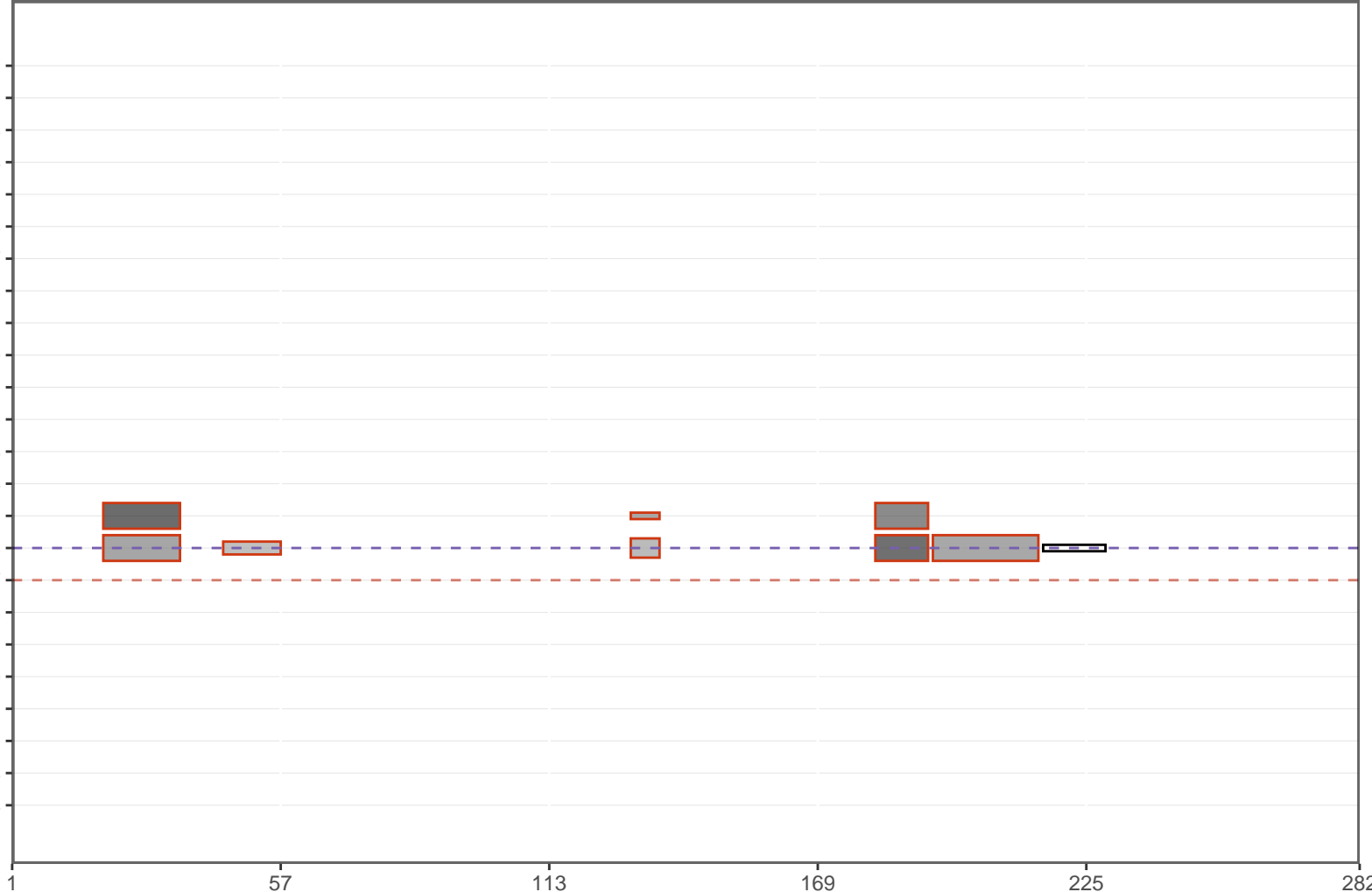
MW indication



Molecular weight

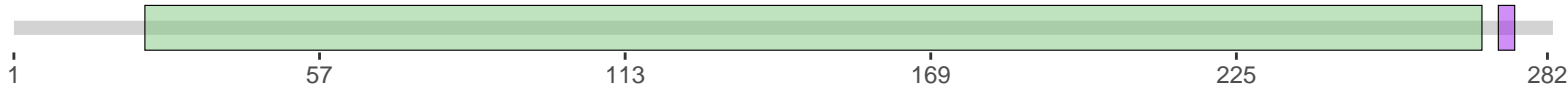


Gel Slice



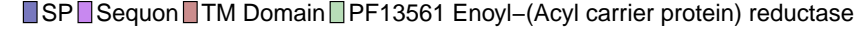
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VKGVFLGMKHIAIRIMPLKKGIVSLSSAAASIAIAGLAPHAYTTSKHAISGLTKNVAEELGGHGIRVNCVSPYAWTGLSLPHLPEDGRINDDAADPHAVFGKLANGGVDLLVGDVAVAVFLASAEARVYHSGHNLMDGGFSGVNHSLKVFRE

NbL04g09130.1 peroxidase_12-like [MW - SP = 36.38 kDa]

No. of times detected



log(intensity)



Values from



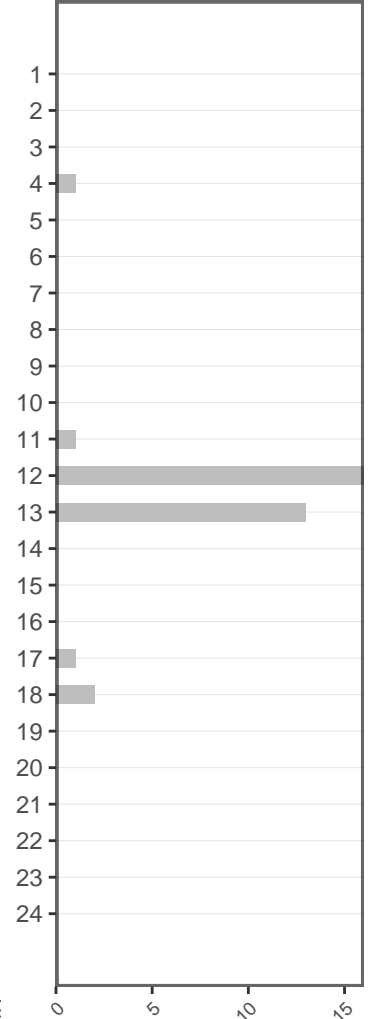
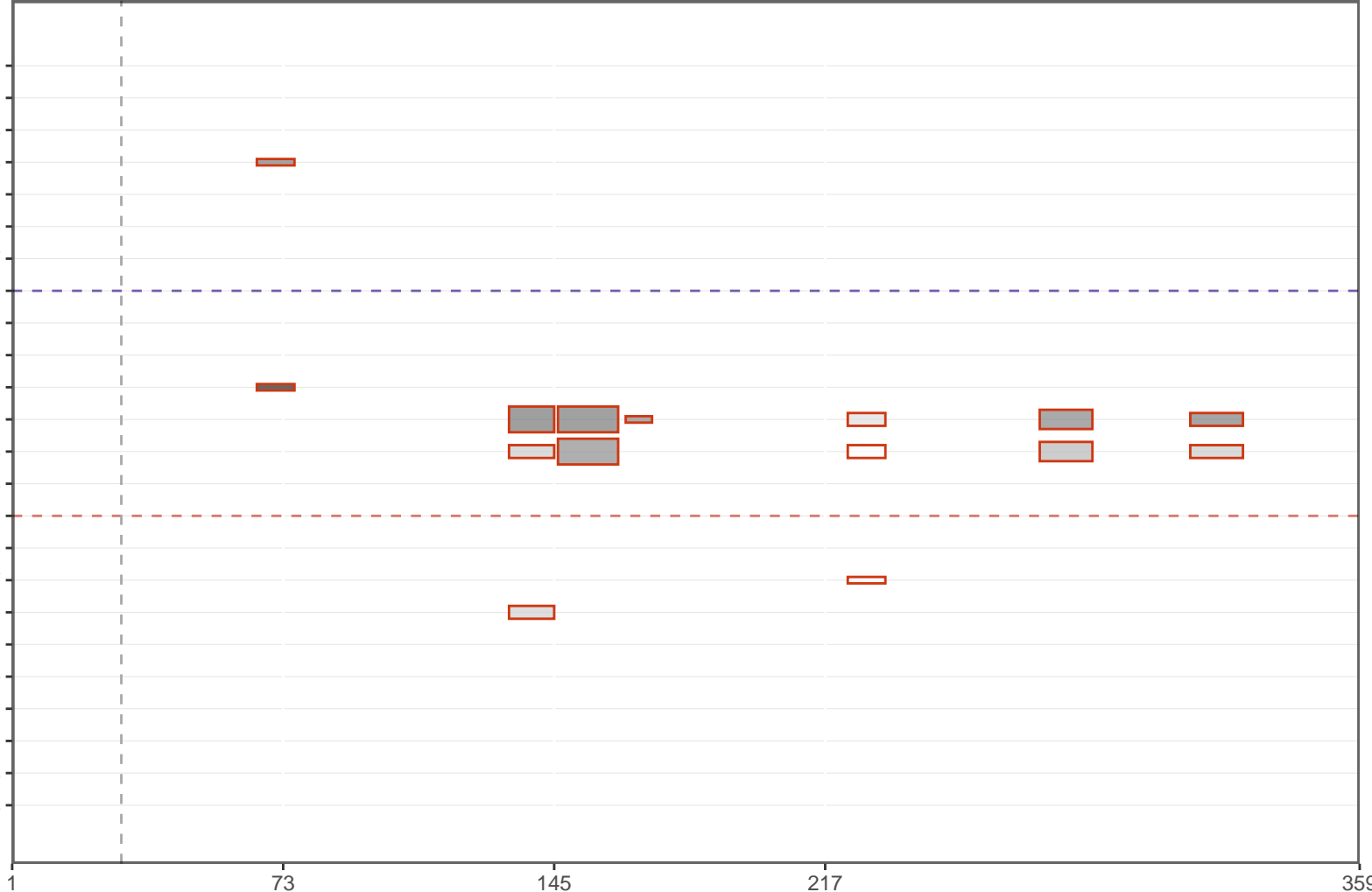
MW indication



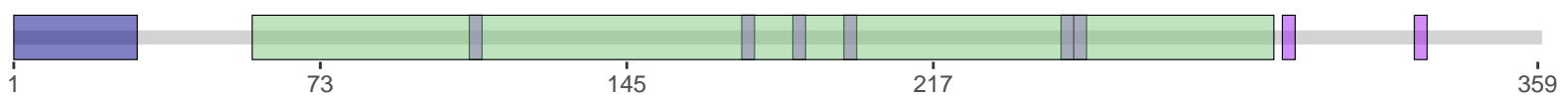
Molecular weight



Gel Slice

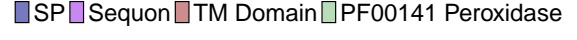


Protein length



Pfam domains

Pfam Description



Protein sequence:

.NFATRNELIANLPPSPFNTSALTSALTKNFPTTDDVALGGGHTIGIGHGTSTFERLYPNQDPSMDKTFANKLNKNTGPTSNSTNTVLDIRSPNKFQNYVYDLMMNRQGLTSDQDLYTDRRTRGVITSPFANESGLFEEFVKSMKMGQLNLTGTQGEIRANGGVIRNSANYNLLSSVLEEEQKTSWEI

NbL04g09110.1 peroxidase_12-like [MW - SP = 35.87 kDa]

No. of times detected



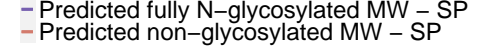
log(intensity)



Values from



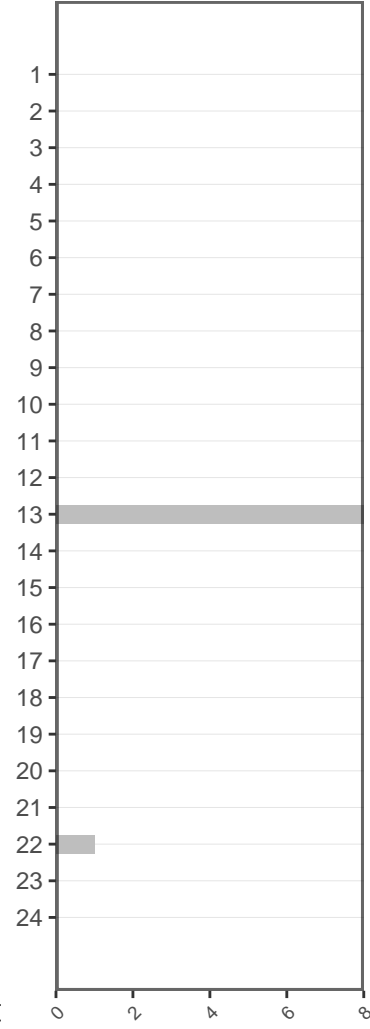
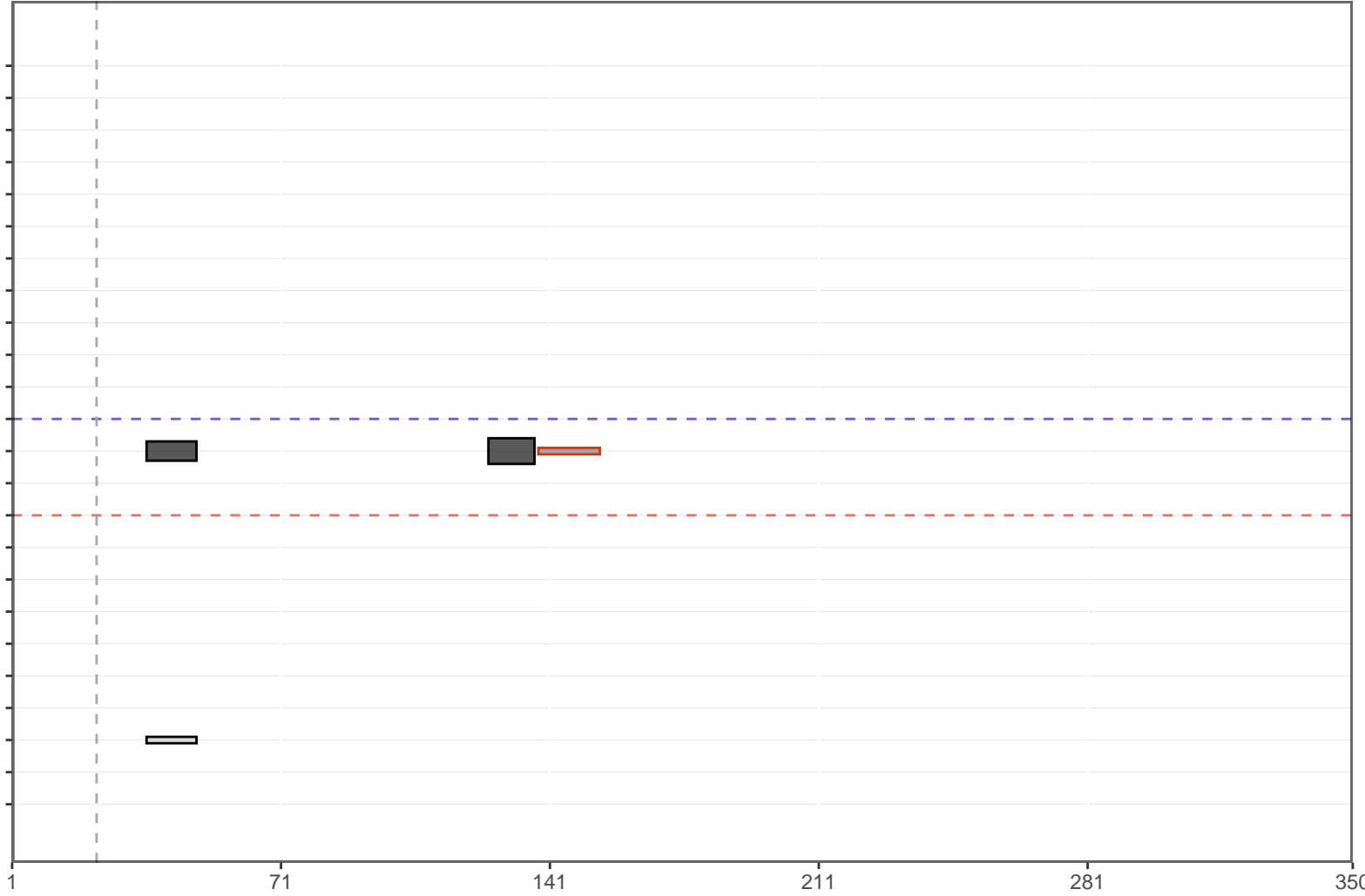
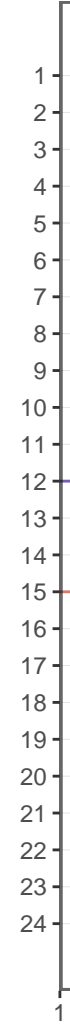
MW indication



Molecular weight

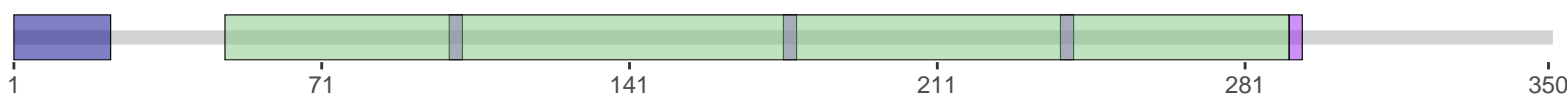


Gel Slice



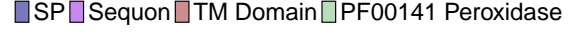
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EQATLDNLVAFANFTFVLSRLATKGLDADVAWLSGAHFGISGICSTFDRLPFNQDPTMDKTFANLKTSCPTANSTNTVDMDIRTPALFDNKYYVDLMNRGLFTSDQDLFTDRRTGRGVEGFAKNGSLFFDKFVIGMIKMGQLNVAVTGGNGEIRTRCDRRNKDKKVDIATVVEEDVEETFSALP

NbL04g09010.1 5-formyltetrahydrofolate_cyclo-ligase-like_protein_COG0212 [MW = 39.89 kDa]

No. of times detected



log(intensity)



Values from



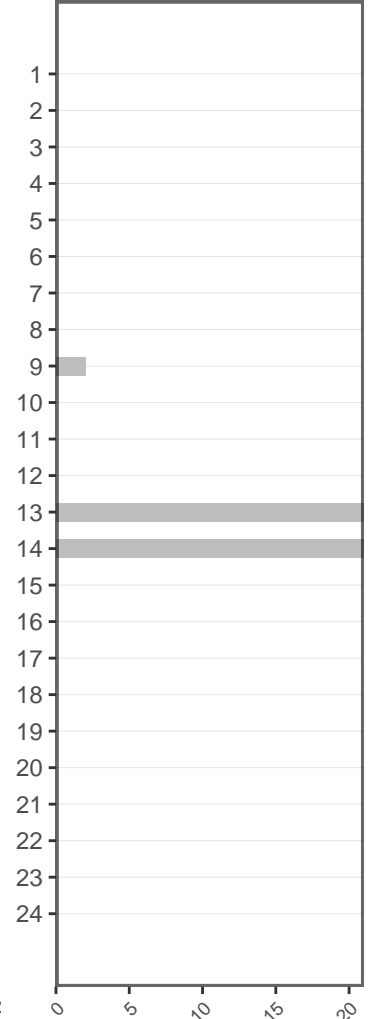
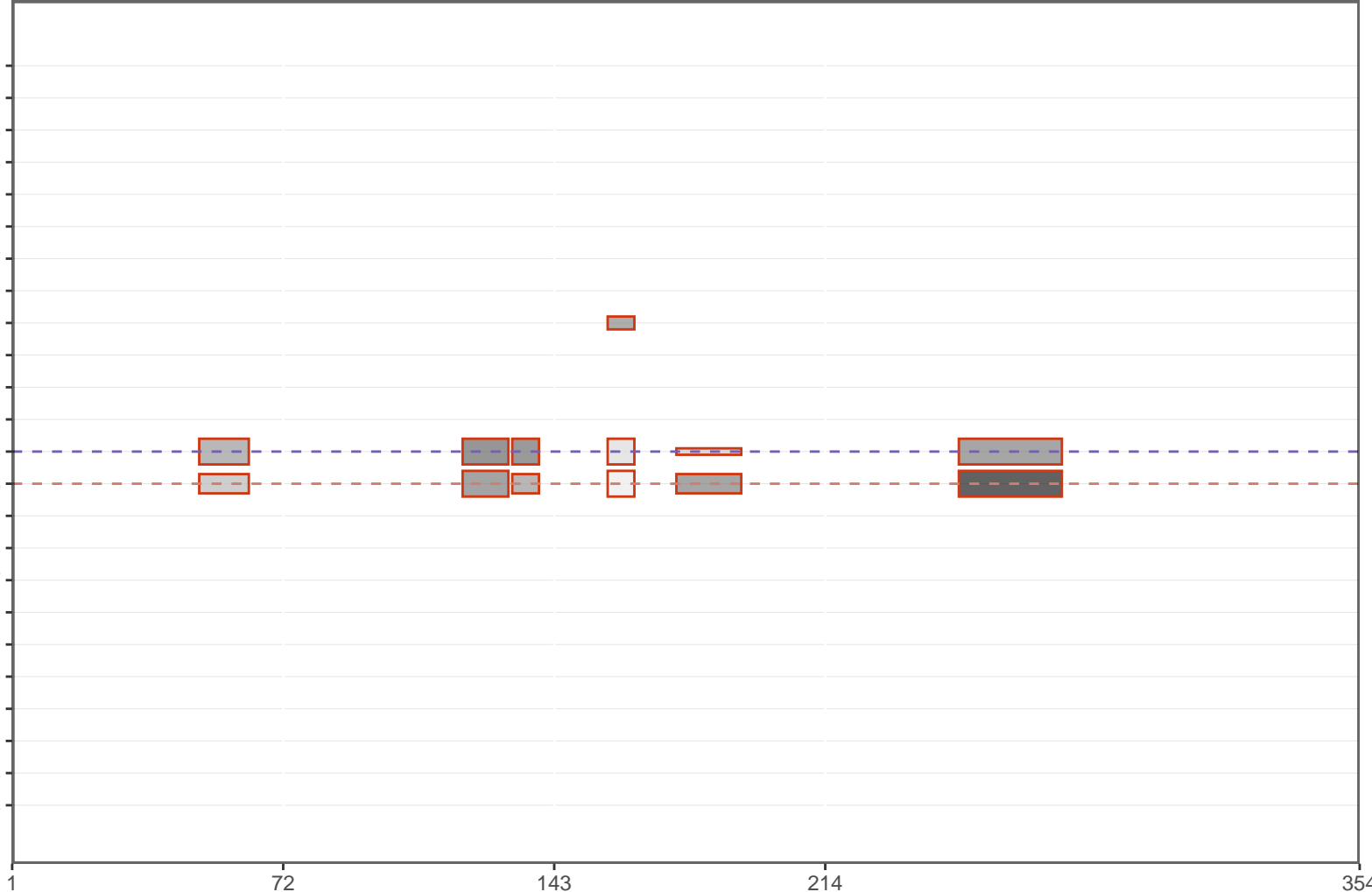
MW indication



Molecular weight

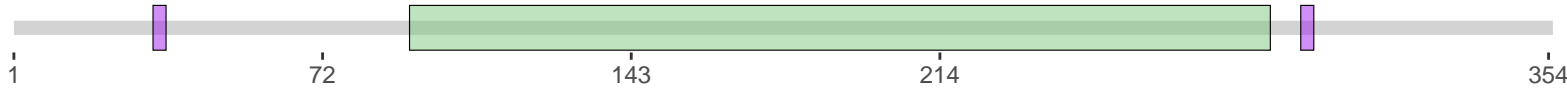


Gel Slice



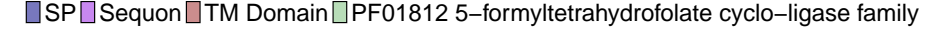
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SGGKLLTPQRLRTGFFVLESEMLSPGTKEACTSAGVAKYGRPIGLEEKIKVLNIGSVAWPKTGAALGKGEFALEFYGLRVMGADDDSTFVVTVDHEQLVDPIKLLIHDPVDDICTPTQVETNTSIPKPGGYWENLYPEKLSQIRLRQLKKEIQETGRRLPTGPEKLPPTAQRRI

NbL04g08930.1 aminoacylase-1 [MW - SP = 47.74 kDa]

No. of times detected



log(intensity)



Values from



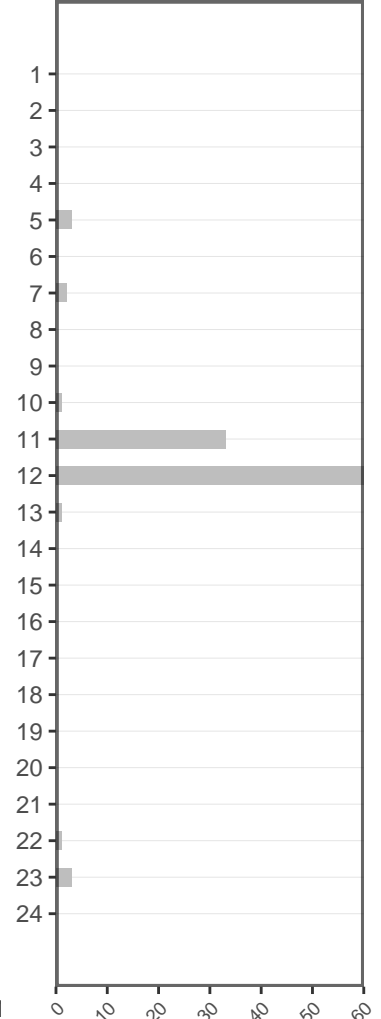
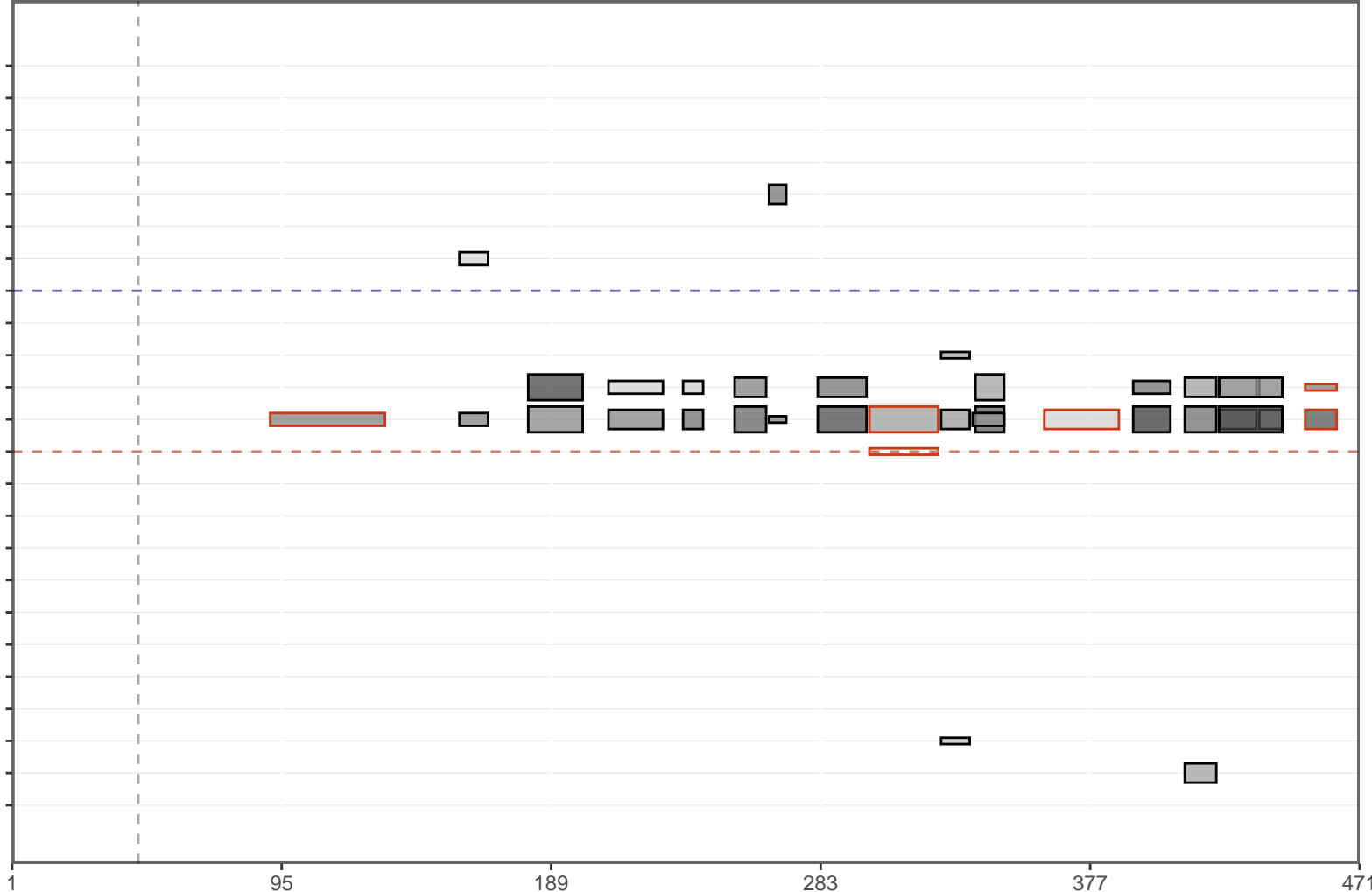
MW indication



Molecular weight

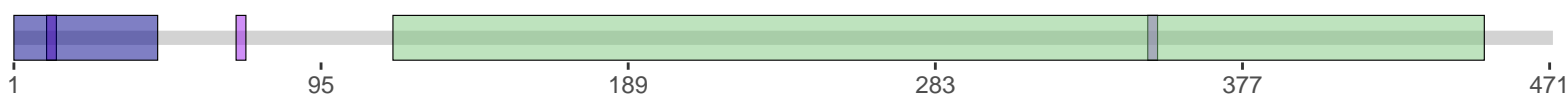


Gel Slice



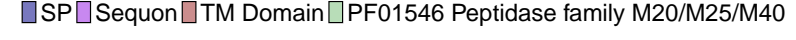
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DEFRFYADRTPTVWMMKAVGSPGHGRLVNTAMENLMKSEIVTKFRGSKFDVKKAGLAANESEVSNPFLKAGIPSTGFMNMGPSAEAGFDIRMPPTADPQLMRKIEEQWAPWRNMTFYETEKGLRDNMGCLMLTSDSNPWSVFNQAVTKSGGKLEKPELASTDARFMRRLGPTFGFSPMKNTPILLHDHNEFLKDTVYLEGKVVYESIKLSGFDGSEYHRCNAVSGQ

NbL04g08840.1 synthase/flavanone_3-hydroxylase-like [MW = 39.87 kDa]

No. of times detected



log(intensity)



Values from



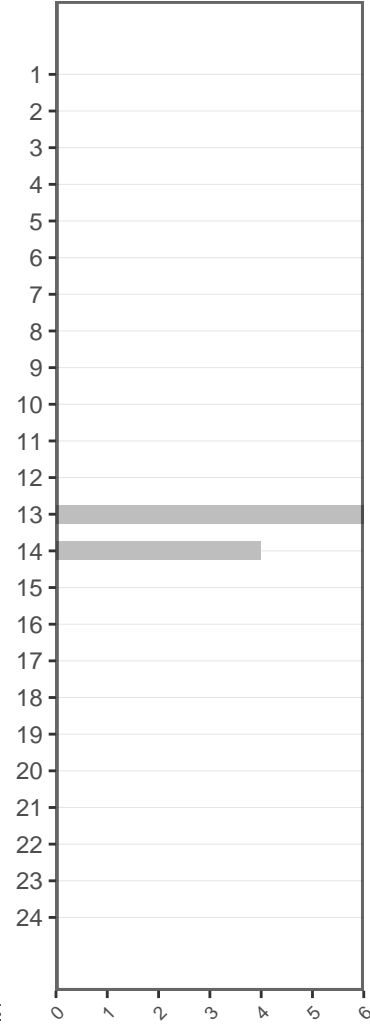
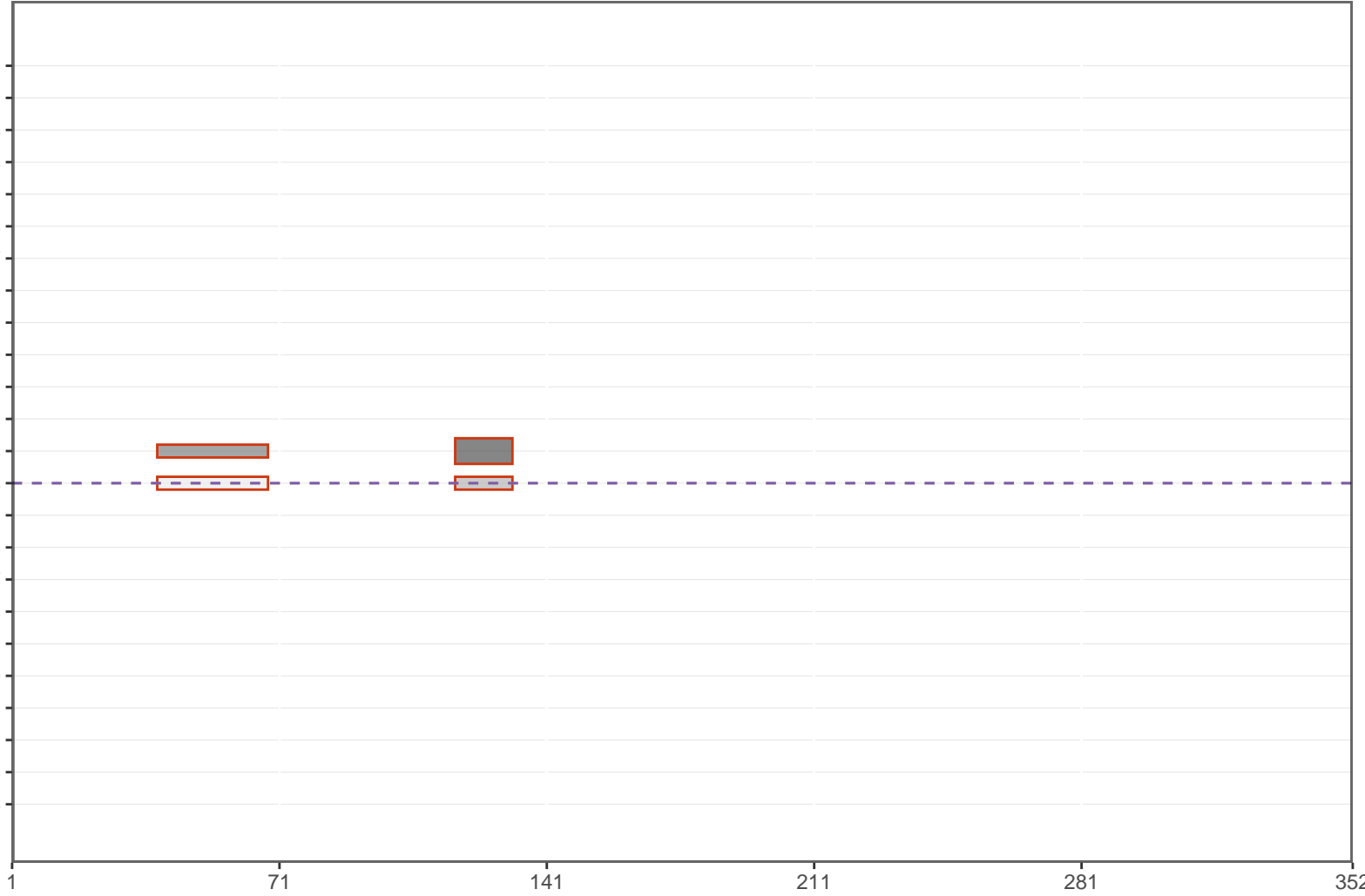
MW indication



Molecular weight

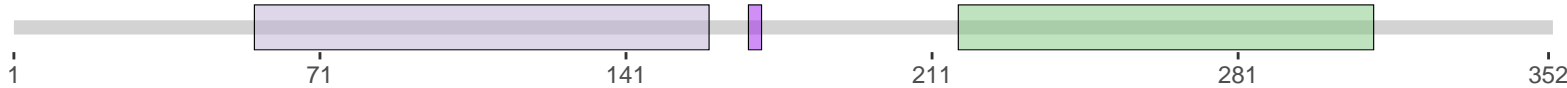


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

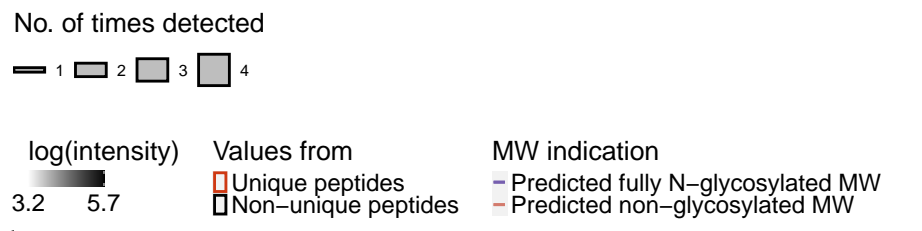
Pfam Description

- SP
- Sequon
- TM Domain
- PF03171 2OG-Fe(II) oxygenase superfamily
- PF14226 non-haem dioxygenase in morphine synthesis N-terminal

Protein sequence:

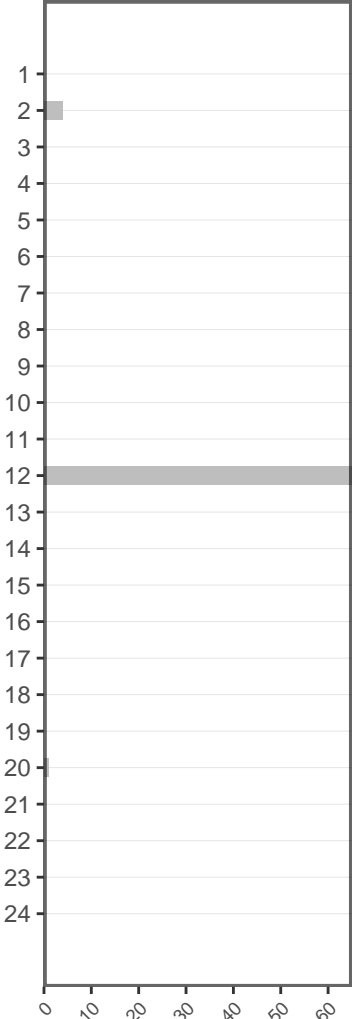
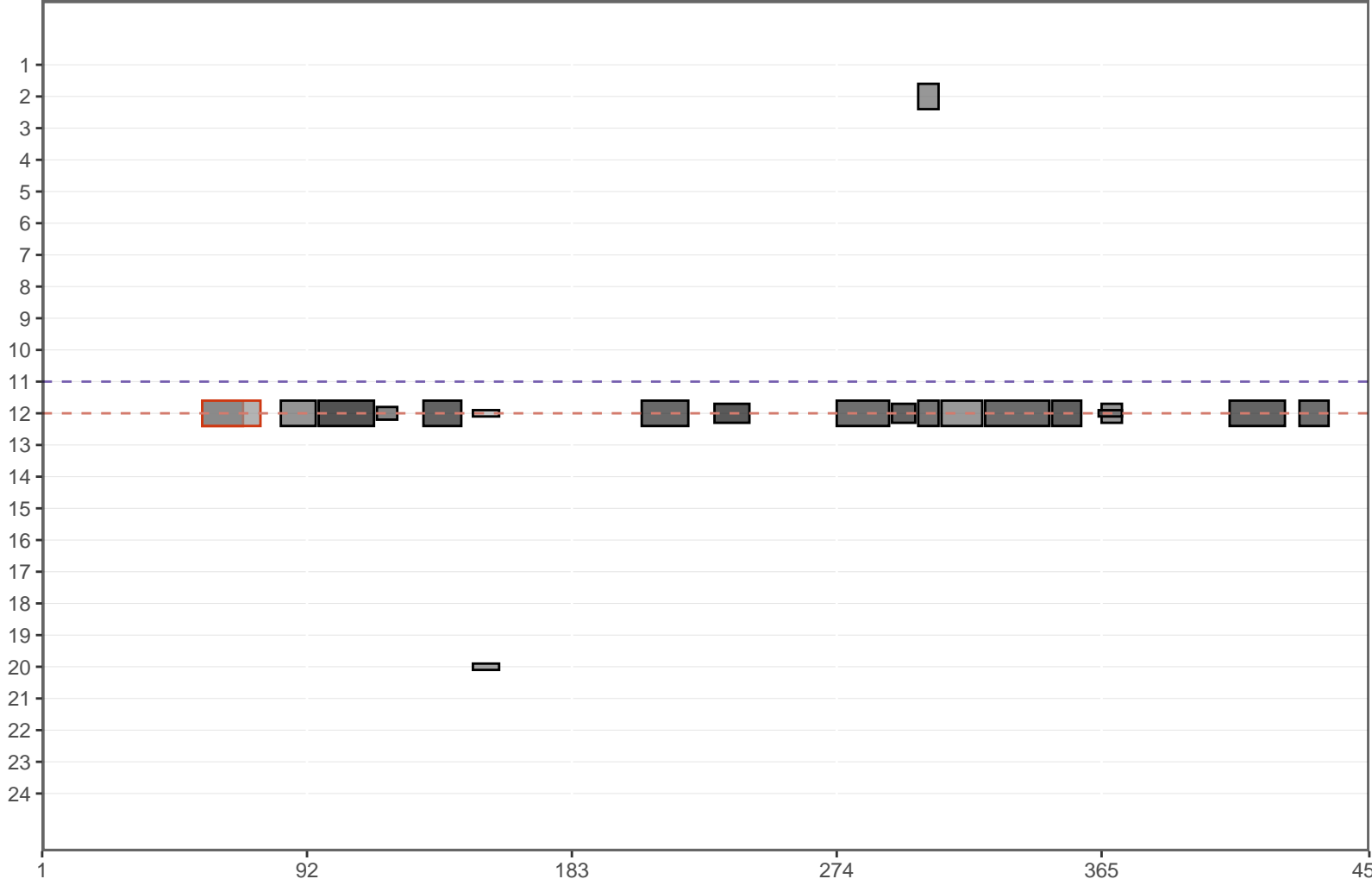
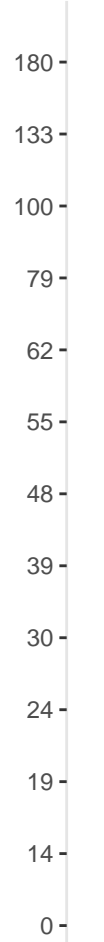
SYRKNLSREANEYAEERMEVVEKFKLSLGLGLEAHEMMEAGGEDVLLKINYPGPRDLALGVVHTDMSYITLVPNEVGLGVFKDGVVVDVYIPNALIVHGDGVEILSNGKYKSVYHRTVTKDKTRMSWPFLEPPSEREVGPIKLVNEANPKFKTKYKVDVYCKLNKLPQ

NbL04g08780.1 probable_N-succinyldiaminopimelate_aminotransferase_DapC [MW = 50.65 kDa]



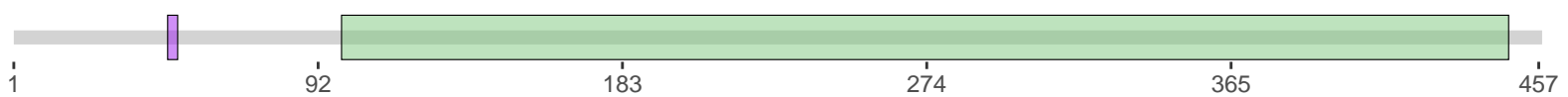
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00155 Aminotransferase class I and II

Protein sequence:

FSLPDELKSAVSKNTRAILNTPHPTGKMFREELNVIASLGIENDILVFADEVYDKLAFEMEHISIALPQMYERTVTMNSLGIKTFSLTGWIKGWAIPPHLTVGWRGAHSLYLFATSTPMDYAAATALRAPDSYVEELKRDYSANKALVEGLKAAGFTVYPSGGTYFVAVDHTFPFGLNDIAFGELYIKEVGVWAIPTSVYLYLNPPEGKLVRFRTFKDDDTLKEAVQRMKELSKK

NbL04g08680.1 pathogenesis-related_protein_5-like [MW - SP = 27.88 kDa]

No. of times detected



log(intensity)



Values from



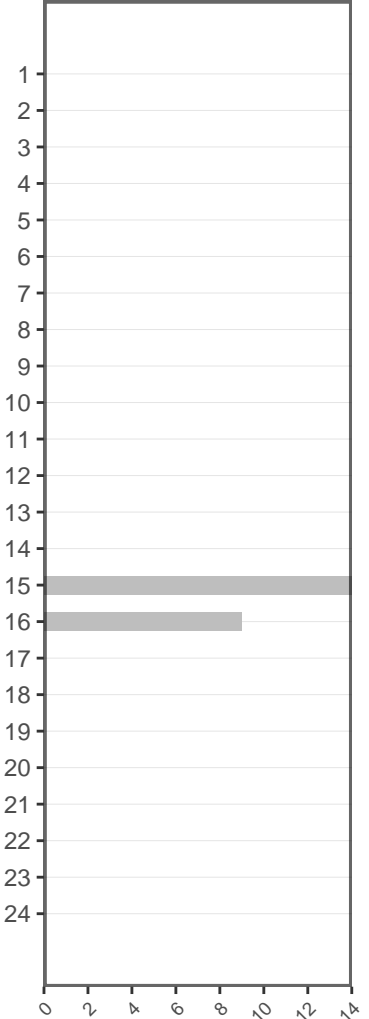
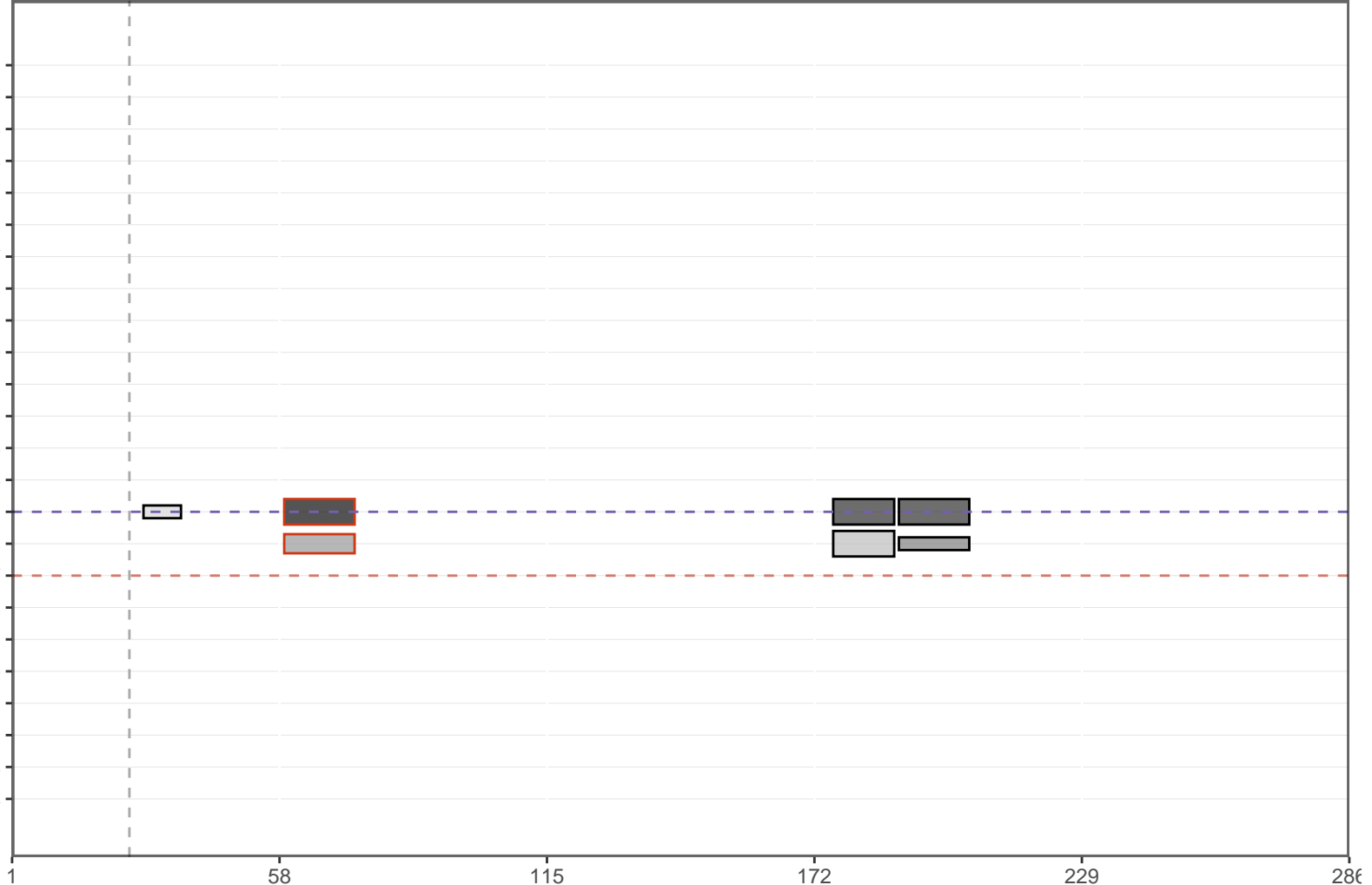
MW indication



Molecular weight



Gel Slice



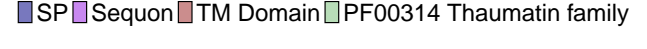
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

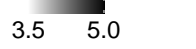
GFNVPMSVTPINGKGNKNSIAGDGDRLRQDQPKELAVKANKGVVAGREAGDFDTEYCGRGNVGNPTTCOPTYYKSKFKNGVPTAYSVAYDDPTSIFFTCGGTDYVAFQSSKRPVCTYHDHKLVDGGSGNLRBLISLNLWMLGLFLIANLNF

NbL04g08580.1 protein_GrpE-like [MW = 36.73 kDa]

No. of times detected



log(intensity)



Values from



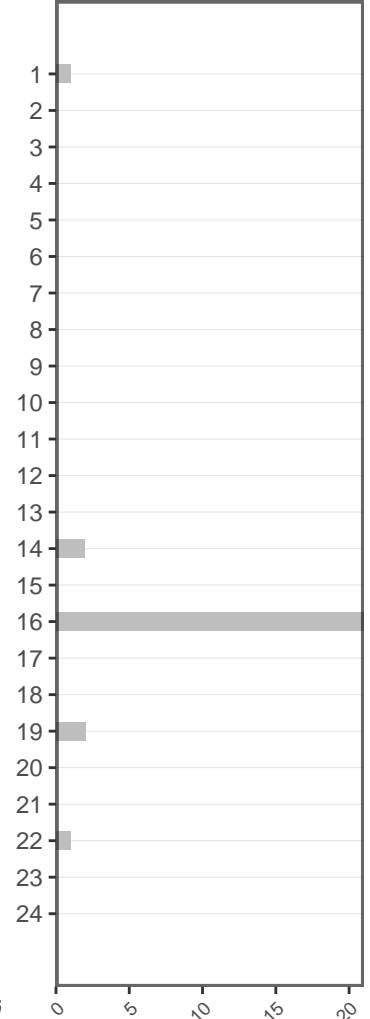
MW indication



Molecular weight



Gel Slice

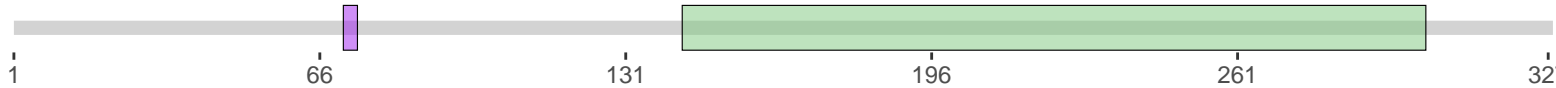


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

DLLAQKYSLSLSAEIDSGKEKYRILQADFDFNFRKRSEKERLFRITFGGEIEGLLPMVDNFERAMRQKLETETEKKIDASYGGYKGFVEIMKSLRVAAPVTGKPDFPALHEAVAREESGQFTDGIIEFRFRGFLLDGRLLRPMVKVSGPKRIPSSVAGKSAATARVDDN

NbL04g08430.1 nitrate_reductase_[NADH]_2 [MW = 102.02 kDa]

No. of times detected



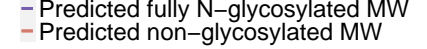
log(intensity)



Values from

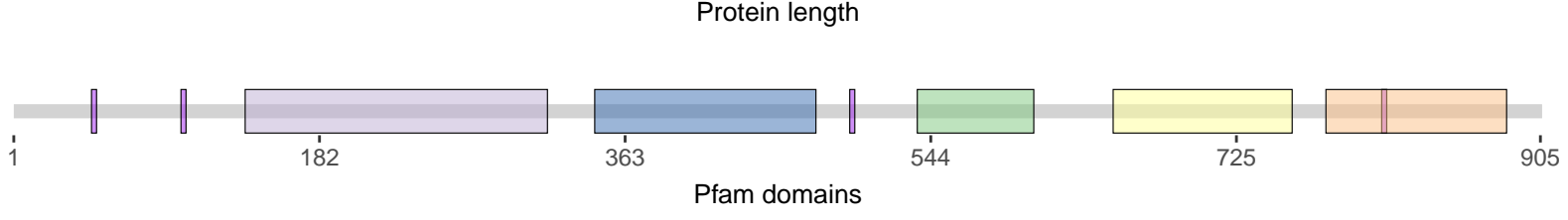
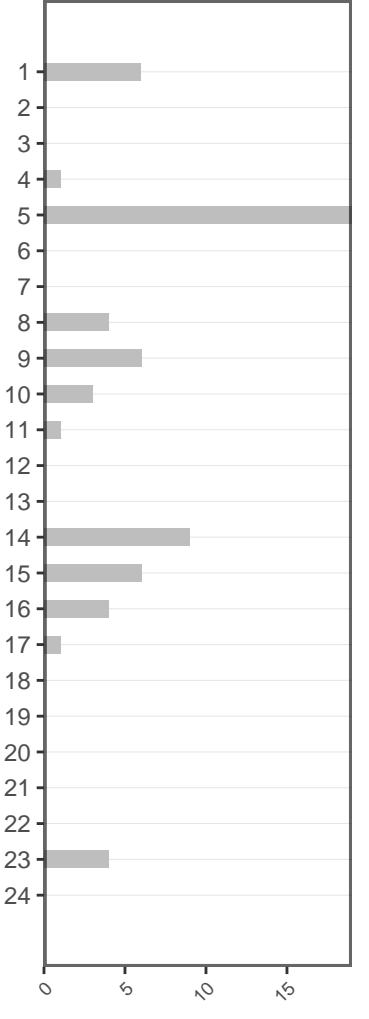
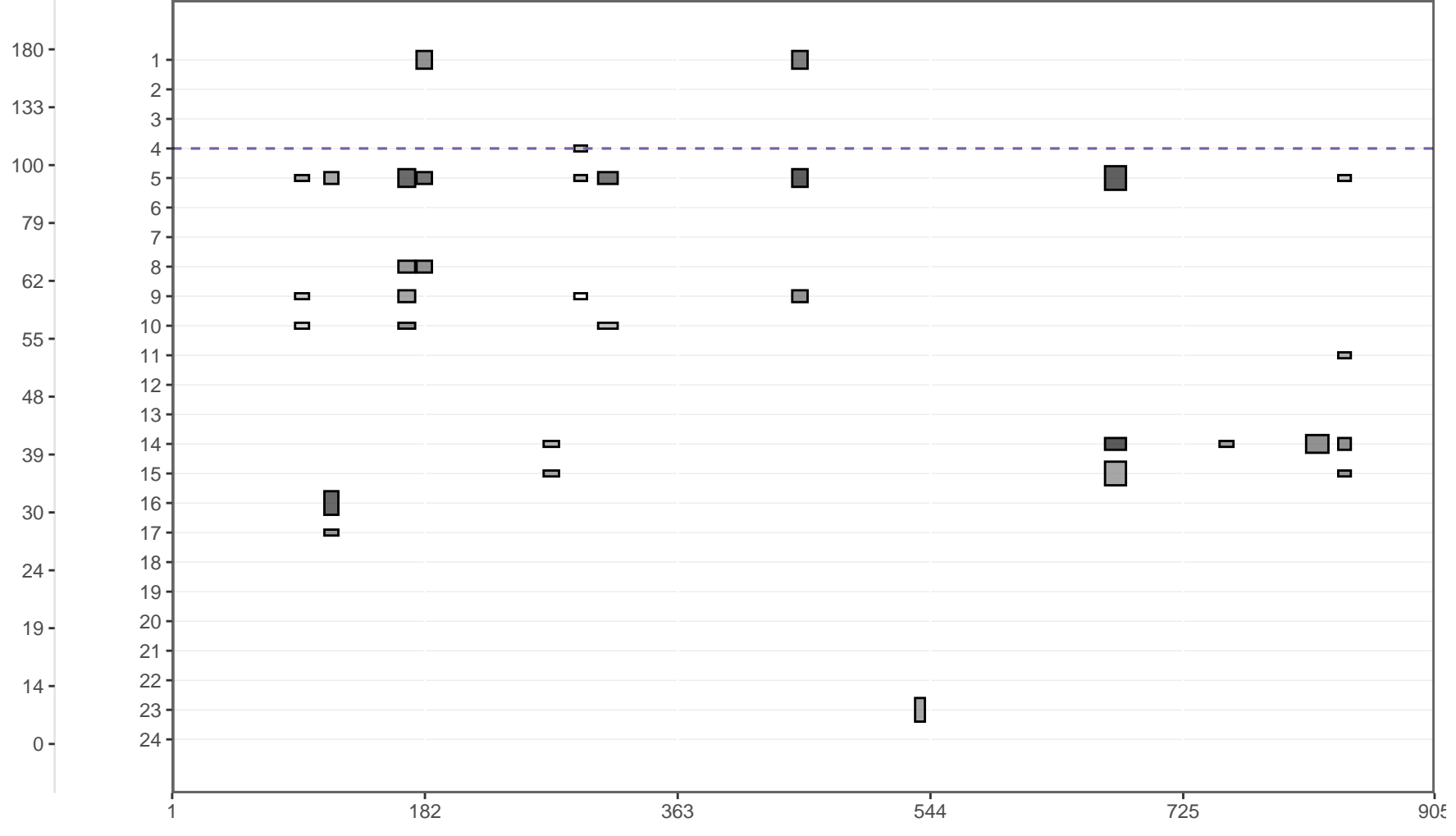


MW indication



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00173 Cytochrome b5-like Heme/Steroid binding domain
- PF00174 Oxidoreductase molybdopterin binding domain
- PF00175 Oxidoreductase NAD-binding domain
- PF00970 Oxidoreductase FAD-binding domain
- PF03404 Mo-co oxidoreductase dimerisation domain

Protein sequence:

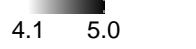
DLLSAKEAVRAWDEFLNTGPEKLMVNVGMNNGWFRVKNMVDKPKHKEIGVFEHPTQPGNGSGGVMMAKERHLEISAEAPPTLKKSGISTPMTASKMYSMEVRRKHSASDAWVHGHVYDTRFLKDKHPGGTDSLINAGTDCITEEFDAHSDAKKLLDFRIGELITTGYSDFQGNVHSGSSFSFLAPIKELVPPQRRVVALPREKIPCKLIDKQSGISHDVKRFRFALPSEDDVGLGFPVGHKFLCAVIDDKLGMRAYTPTSTDEVGYFELVVKIYFKGHPKFPIK

NbL04g08230.1 eukaryotic_translation_initiation_factor_3_subunit_I-like [MW = 19.54 kDa]

No. of times detected



log(intensity)



Values from



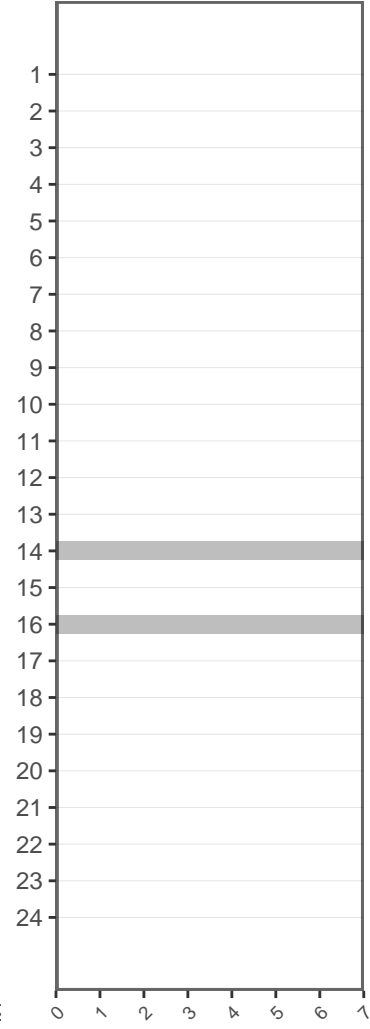
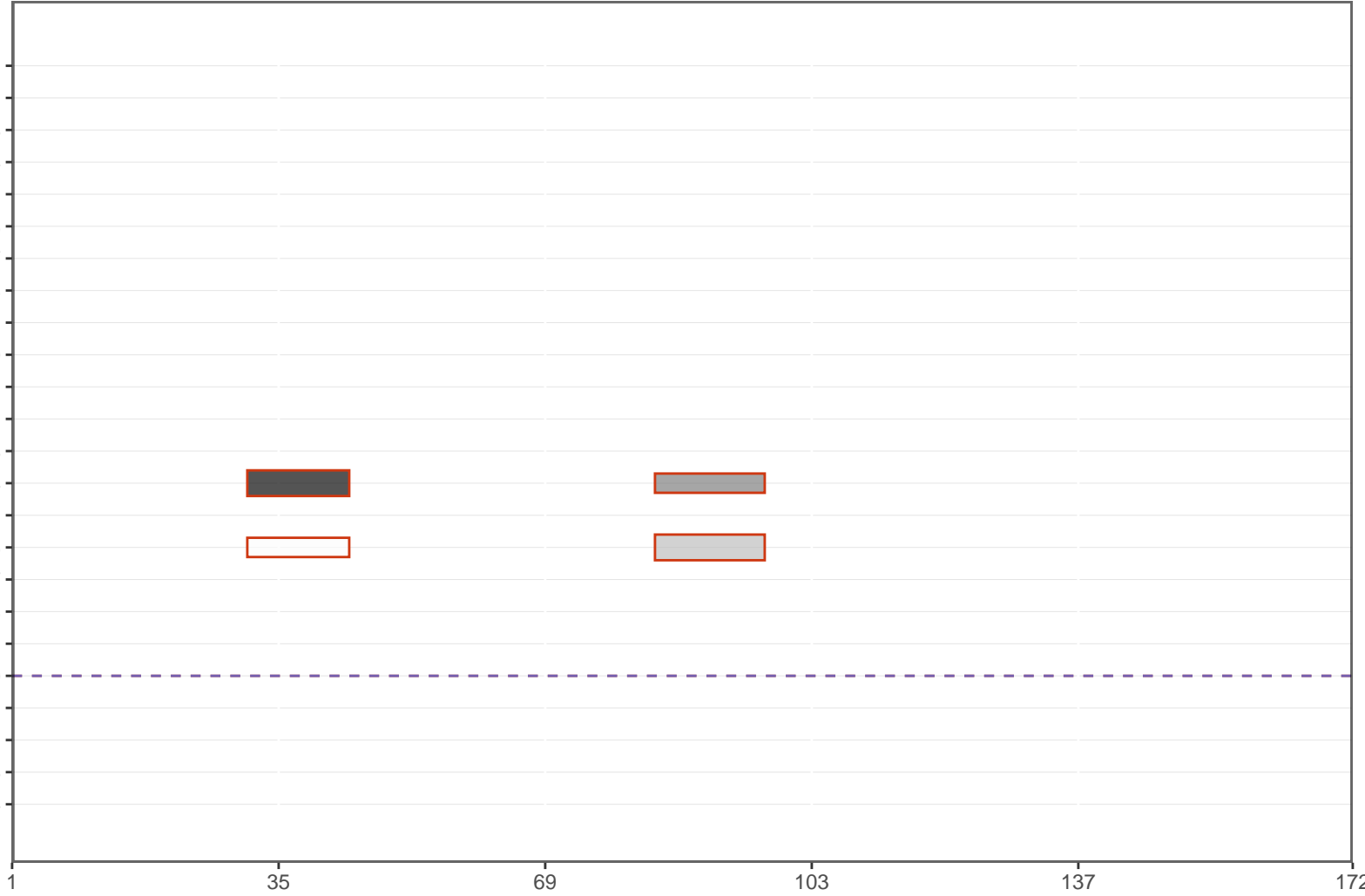
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ADQSALWLDVIRGTGLFTFRNFDSPARVDFSVGDKLAWITDFPFMGLPSAIIKVRISGRDPSDRHPVHLSVSRLEYLHWPLSPRLRYLLVLEHDTFGYVK

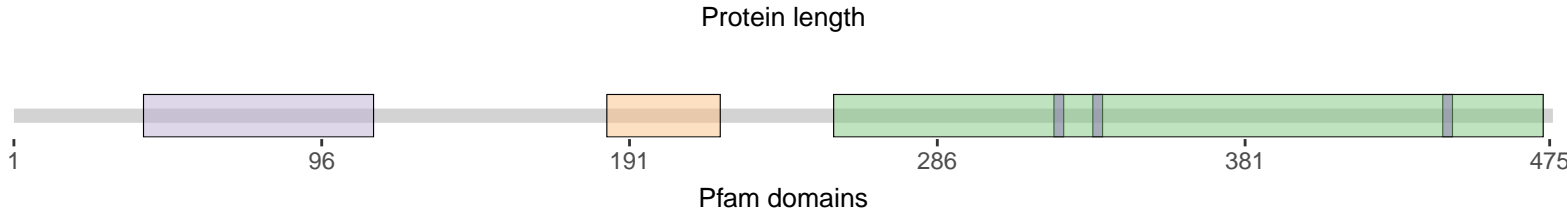
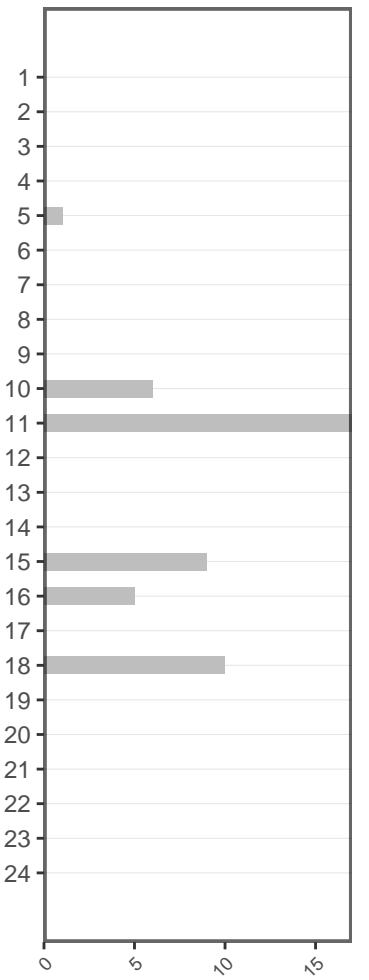
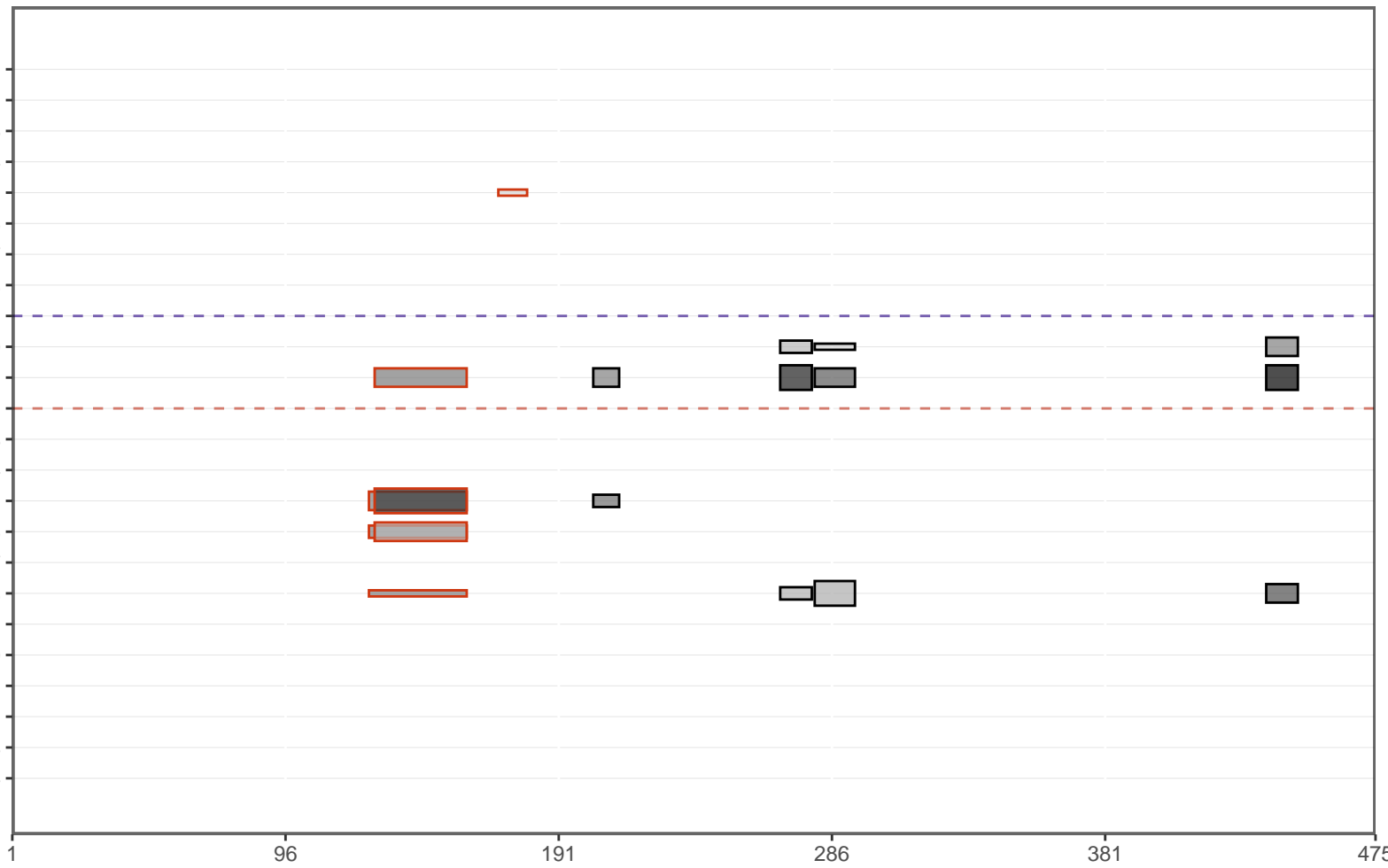
NbL04g08140.1 dihydrolipoyllysine-residue_acetyltransferase_component_5_of_pyruvate_dehydrogenase_complex_chloroplastic [MW = 49.49 kDa]

No. of times detected
 1 2 3 4

log(intensity) Values from MW indication
 3.5 4.9 Unique peptides Non-unique peptides Predicted fully N-glycosylated MW Predicted non-glycosylated MW

Molecular weight
 180
 133
 100
 79
 62
 55
 48
 39
 30
 24
 19
 14
 0

Gel Slice
 1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24



Pfam Description
 SP TM Domain PF00364 Biotin-requiring enzyme
 Sequon PF00198 2-oxoacid dehydrogenases acyltransferase (catalytic domain) PF02817 e3 binding domain

Protein sequence:
 IAASTAPAVGTTVMPSGGAPVAPVVELGTFVPTFTMGNVSRNMVESLAVPTFRVGYTFTFNALDALYKIKSKGVMTALLAKATALAKHPVYNSSCRDDGKSFYNSRINAVAWDDGLFTPLVLDADKVDIYSLSRKWKELVDKARAKLOPHEYTTGFTLSLNLGMFGVDLFDALPPGTGAIMVAGASHPALYKDKDRIGLKNQMVNVYADHRVYVYQADLAFLOTLAGIEQPKDLT

NbL04g07980.1 uncharacterized_LOC109225373 [MW = 82.78 kDa]

No. of times detected



log(intensity)



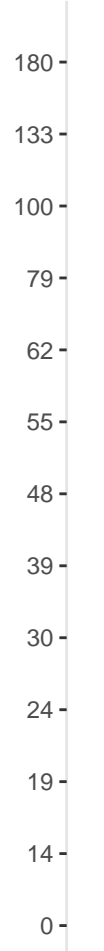
Values from



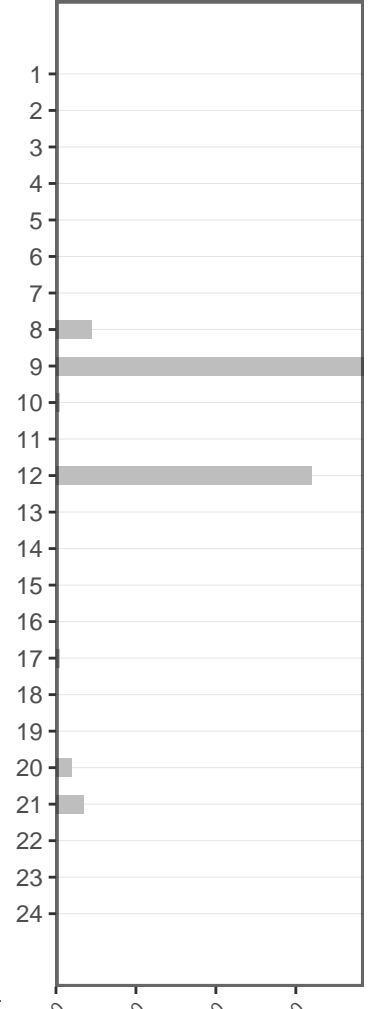
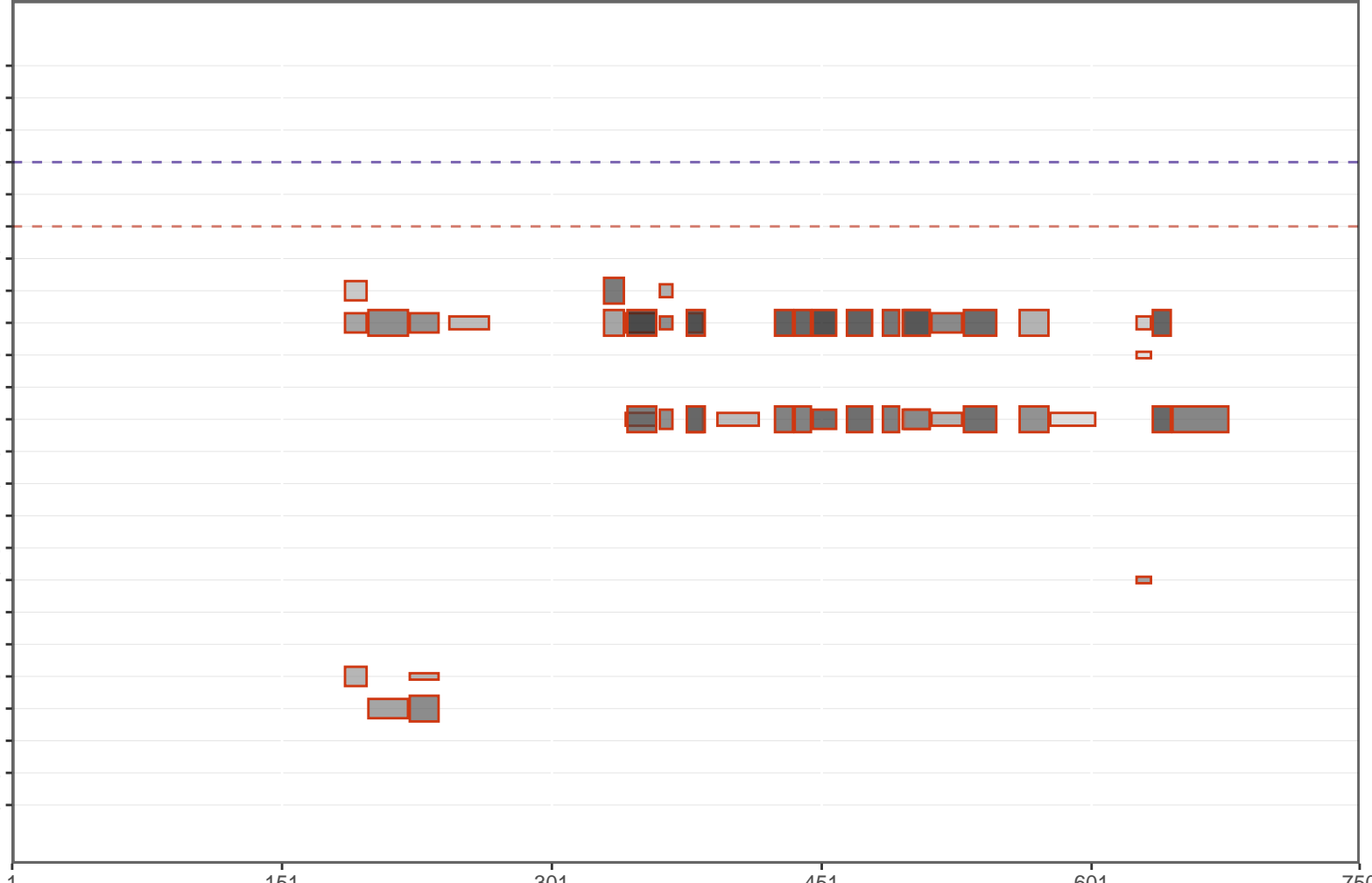
MW indication



Molecular weight



Gel Slice



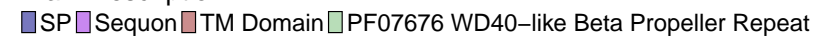
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RASSEYRHELFDAVKKFEITRASPAAHHLNPFSPD66WVGYHKRGSTGNKGG6DILLLENLKNPQISLFRVDG6FSP6SP6DRIVAKMPLVYVWYD66GLRGLVSTRMAFSTAWDPKRRKGVVYTSVGTFFASERTEVDN6IN6DKDL6LYK6LTTGG6NNAF6P6P6DKWVFR6GR6GH6K6LV6Y6DALE6T6GL6Y6L6TE6GS6W6TD6M6N6SP6DD6W6AF6AS6DR6N6P6G6G6F6M6M6H6N6GT6L6R6K6V6Q6S6EG6GR6N6H6Y6F6P6DK6Y6Y6T6S6Y6A6V6S6

NbL04g07770.1 NAD(P)H-quinone_oxidoreductase_subunit_M_chloroplastic [MW = 17.18 kDa]

No. of times detected



log(intensity)



Values from



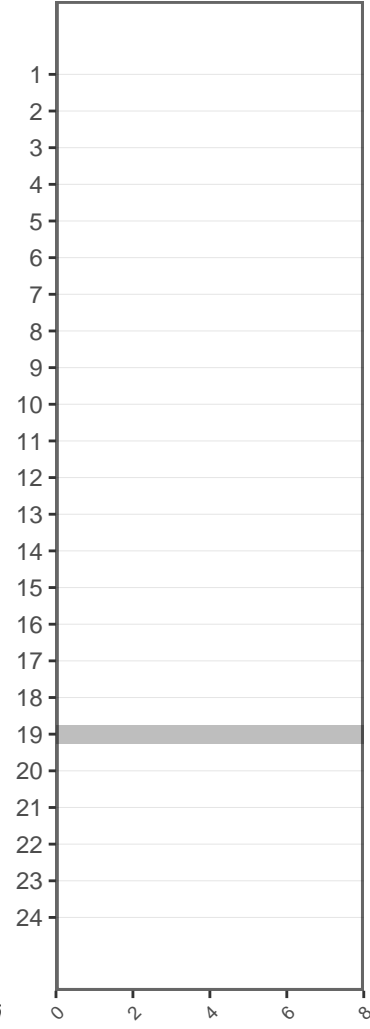
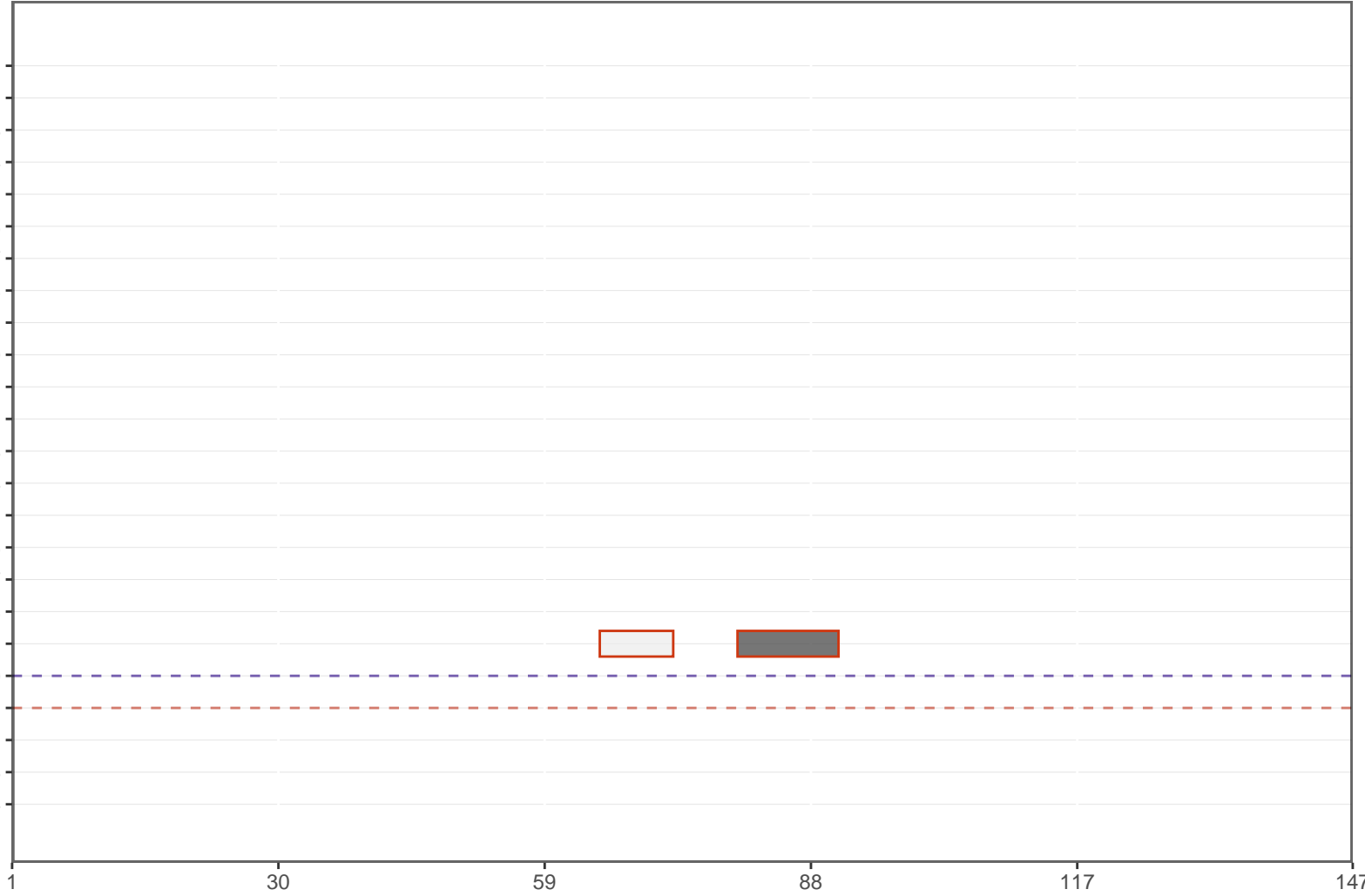
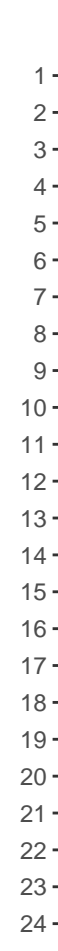
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

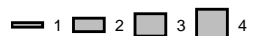


Protein sequence:

MGQPRPVEAQINVSKNMSREYGGQWLSBATHRVRIYVYIDRETFAFDQGMKLTULDPTDFEYVTDGDTKRVYGFQELVYHYE

NbL04g07740.1 UDP-sugar_pyrophosphorylase [MW = 78.37 kDa]

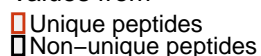
No. of times detected



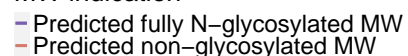
log(intensity)



Values from



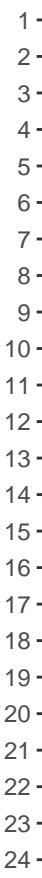
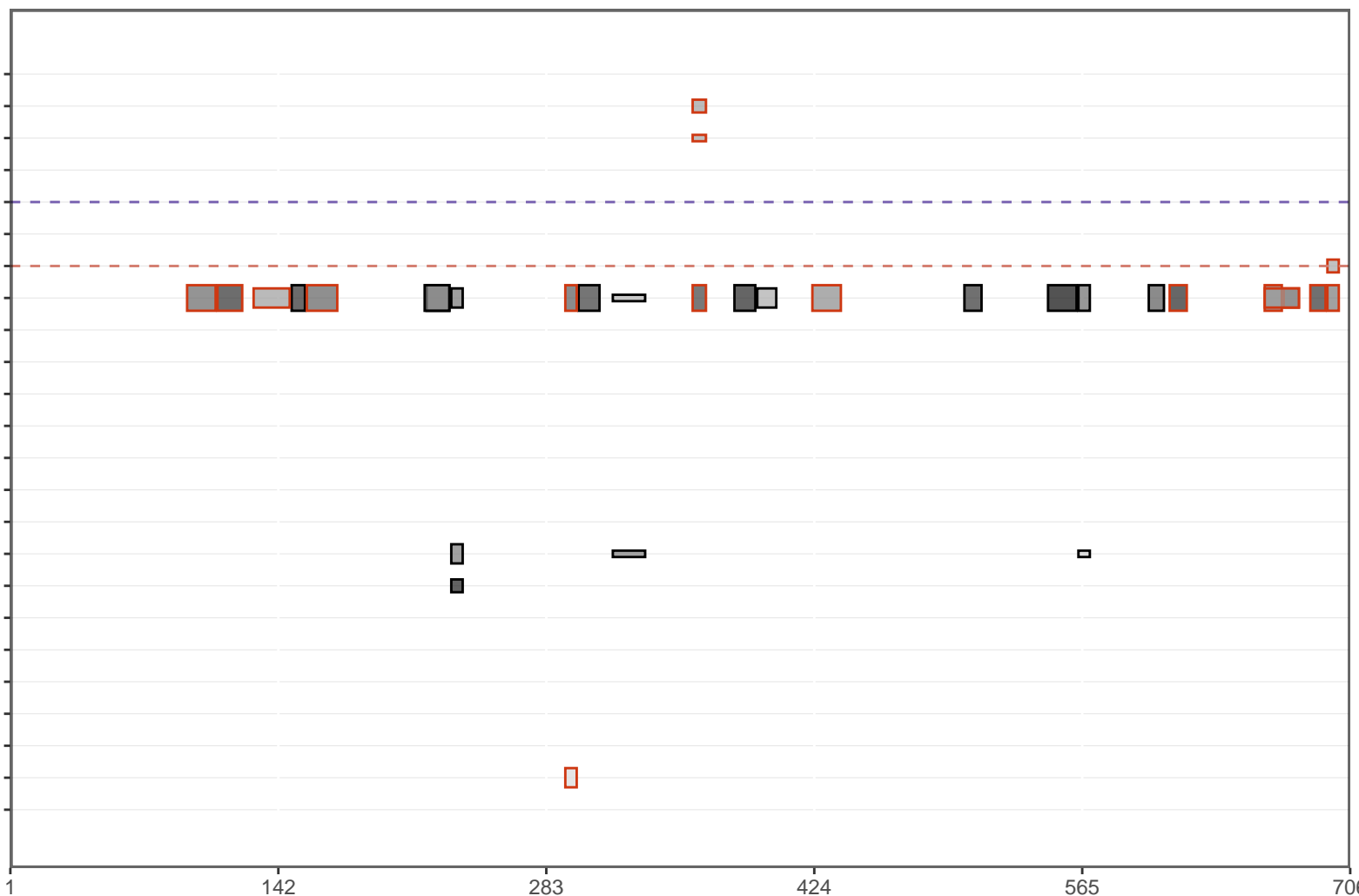
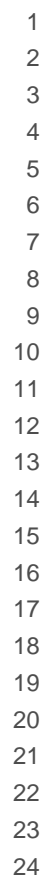
MW indication



Molecular weight

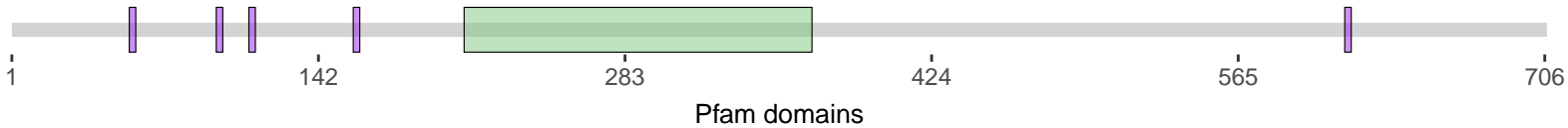


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

MRQTKPHIGGDVHSLLYSSGLLKVDDAGLRWVLFQDFTNGLFKAPALGVSAIKGHHNSLAVPRKAKEGGDTLTKHKDGRITMIVNVEYVNGLDPLLRASGYPDDGNSETGYSFPFGNGLFEIGFYHEELTKTGGAKEFVNPYKDKATKAFK6STRLEGMDDYKTLSPPEARVGFYVDAWLVAPVKNNPEDAANKVPKGNPYHSATSGEMAHFRSHSLRKKAGVMDPKIQVFNNGGEVWWRVWVKPKWALTFSEVYKSKVSGNSGSGERSTIAKGRDAL

NbL04g07720.1 phosphoribosylformylglycinamide_cyclo-ligase_chloroplastic-like [MW = 49.34 kDa]

No. of times detected



log(intensity)



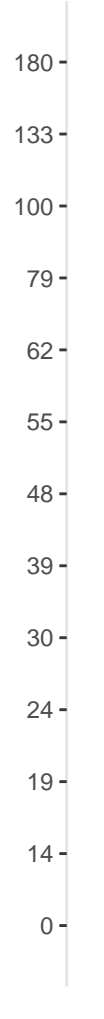
Values from



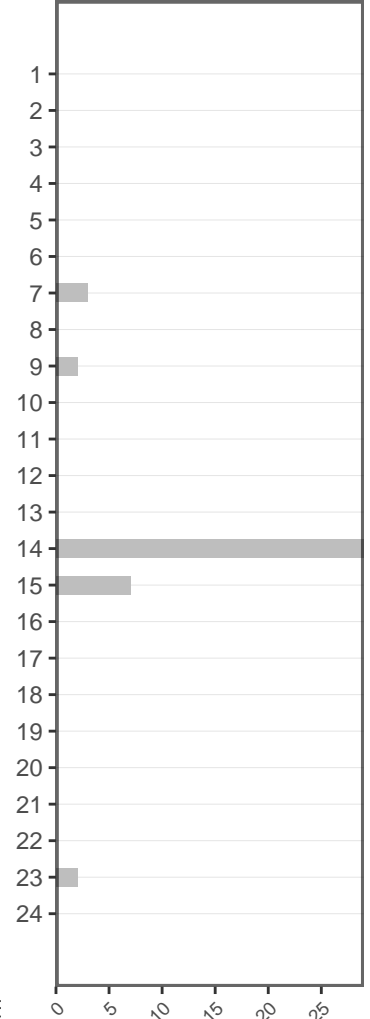
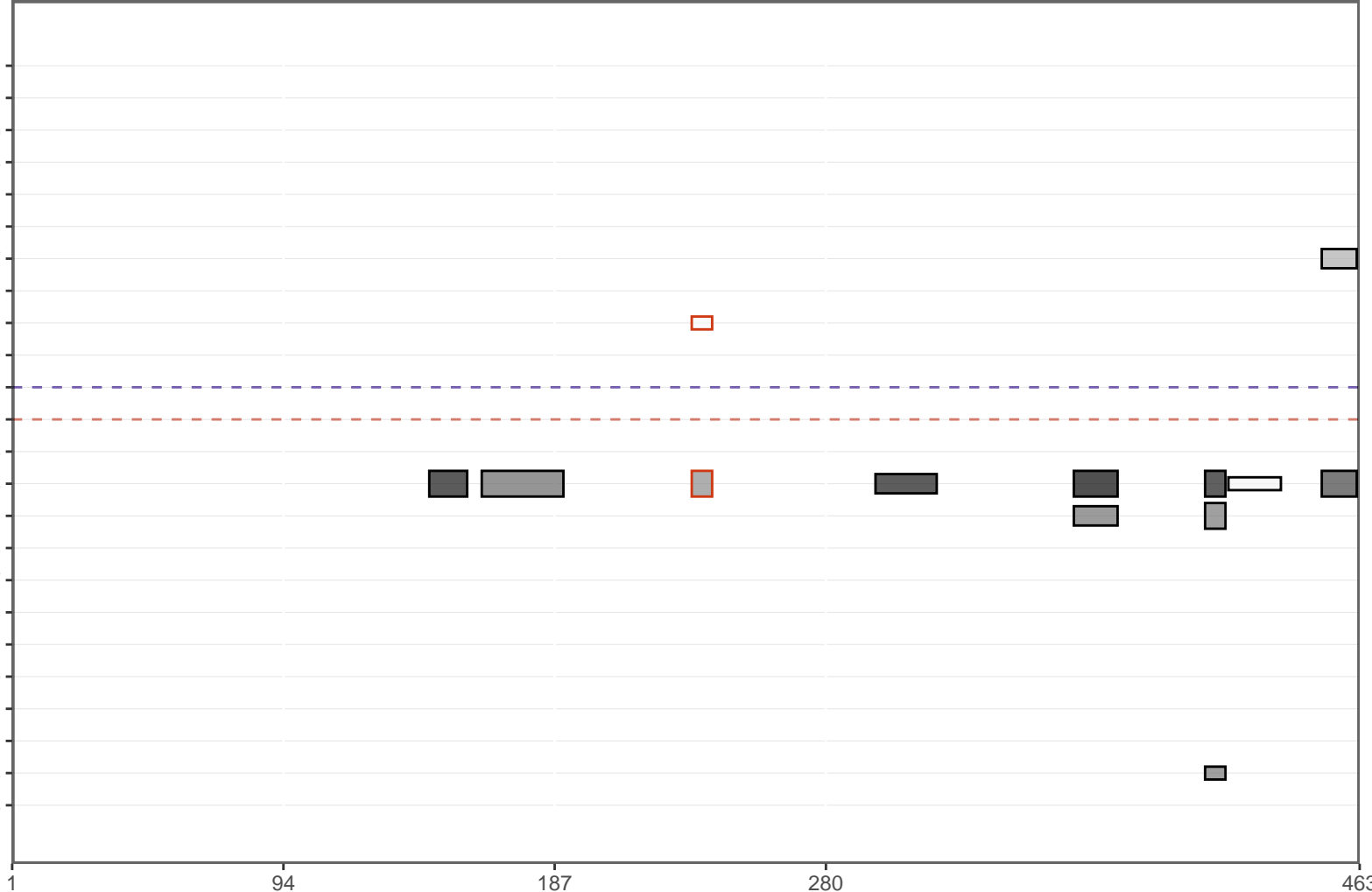
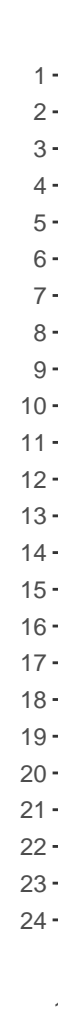
MW indication



Molecular weight



Gel Slice



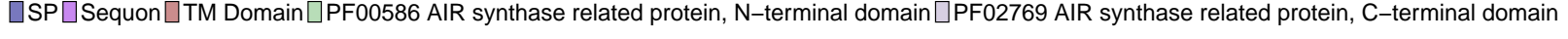
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

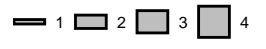


Protein sequence:

IAKPLFLDYFATSRLEVDLAEKVKGNDGGGQSDGALLGGETAEMPDPFAEGEYDLGDFAVGIVKKGDEVIDGKSKVGDVXLHGLPSSGVHNSGFLVRRVLRKGGSLKLDLPGETTFLGEALAPTVVYKQVLDISKGGVKGIAHTGGGFTDNPRVFPKGLGAIYEDGSAWVPPVFKVWQKAGRIEDGEMMRTFNMGIGMVLVSPPEAADRLGEVQKTAIYRIGEVAKGGDGVSYE

NbL04g07640.1 probable_methyltransferase_PMT24 [MW = 85.49 kDa]

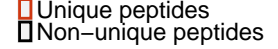
No. of times detected



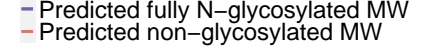
log(intensity)



Values from

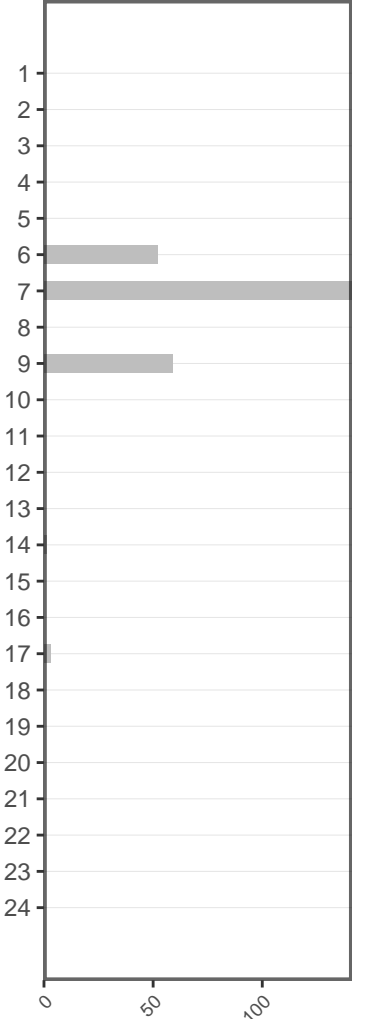
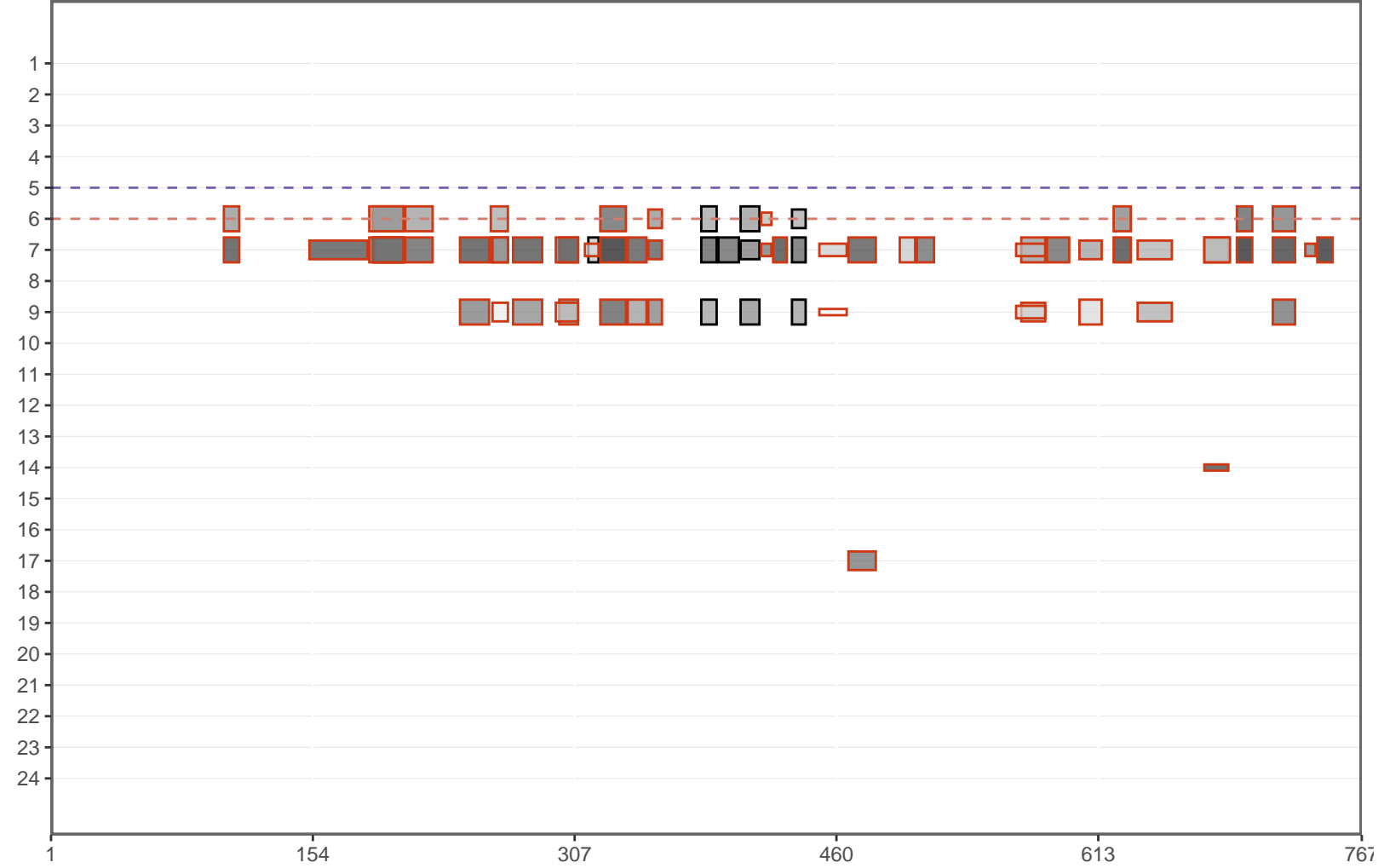


MW indication



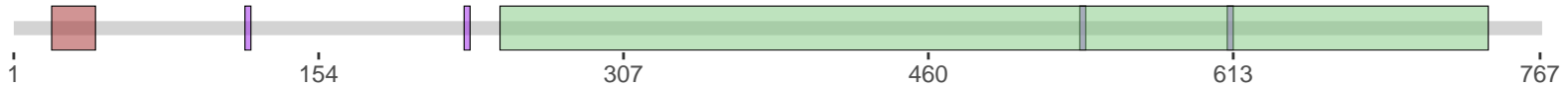
Molecular weight

Gel Slice



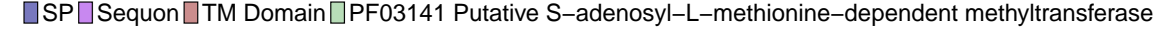
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IVASFGYLFRDVAAMSLAPKDEHEADVGFALERGPASAVMGTRKLPFRSKVFDVAHCAARGRVPVHHEGGKLLLENRVLRFQGHFLWATPVYRKDEESVGVWEAMSELTSMGOWELLENEKLNKLVGAFKRPKTSNDCKVSRQNDPPMGEAEADPDAAWNTLEAMKHKAPEDASARGSRVPSKWLRSKLPVWLTSGVGVYQKAAADFAADVHWKHYVSKVYLNGLGINSVSRVMDMKAVYGGFAALKDKLWVMMVVPVDSPTLPIYER

NbL04g07620.1 TOM1-like_protein_2 [MW = 56.25 kDa]

No. of times detected



log(intensity)



Values from



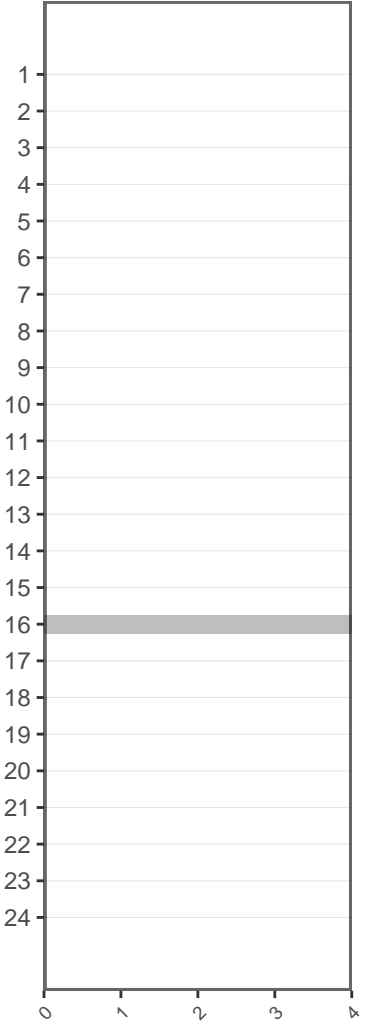
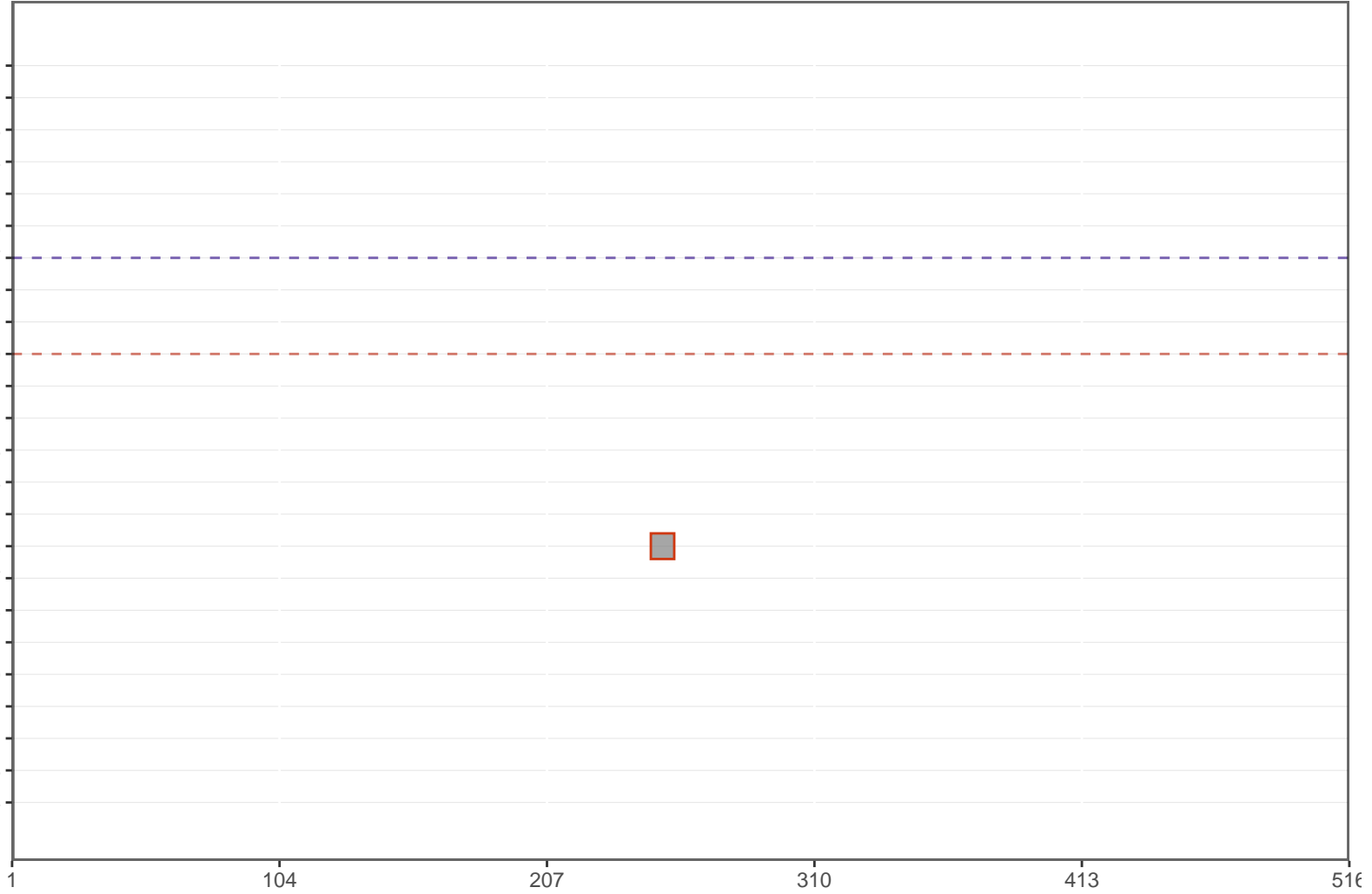
MW indication



Molecular weight

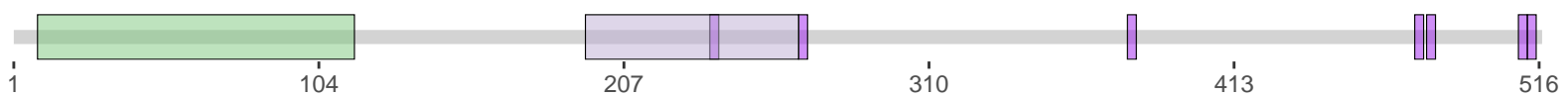


Gel Slice



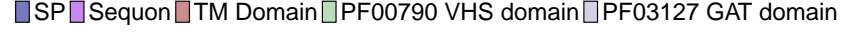
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ALNDGLQVLRRIHDDMANGTSTITVQPRETHAPLMNWNHEDDESEDDFSLIARRSSEKDPGAGGRKTVDKSEPMRITPTLPPPPGRRPVGTDMGMVDVLSGERFESERSFGTAGSSPIAVSTNENNVSGIPRSPSPDDLLNPTADDQFVNPISLFTGKNNNGESDTKAKKADHLPPAFWDAPPTTLPPDPARYNQRQGVFEKNVFGGGSSVDSVVGQTNLENSSSSPKQKPEDALFKDLVDFAKAKSSSSNNGSNRSP

NbL04g07590.1 aspartic_proteinase_Asp1-like [MW - SP = 45.2 kDa]

No. of times detected



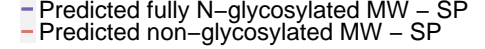
log(intensity)



Values from



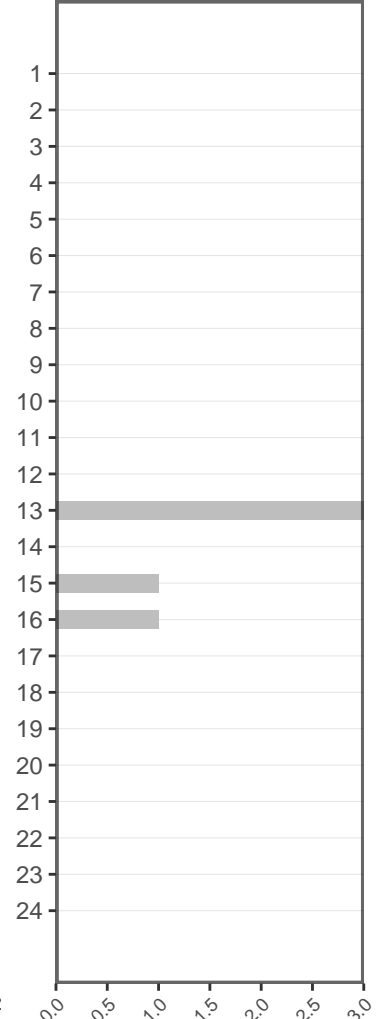
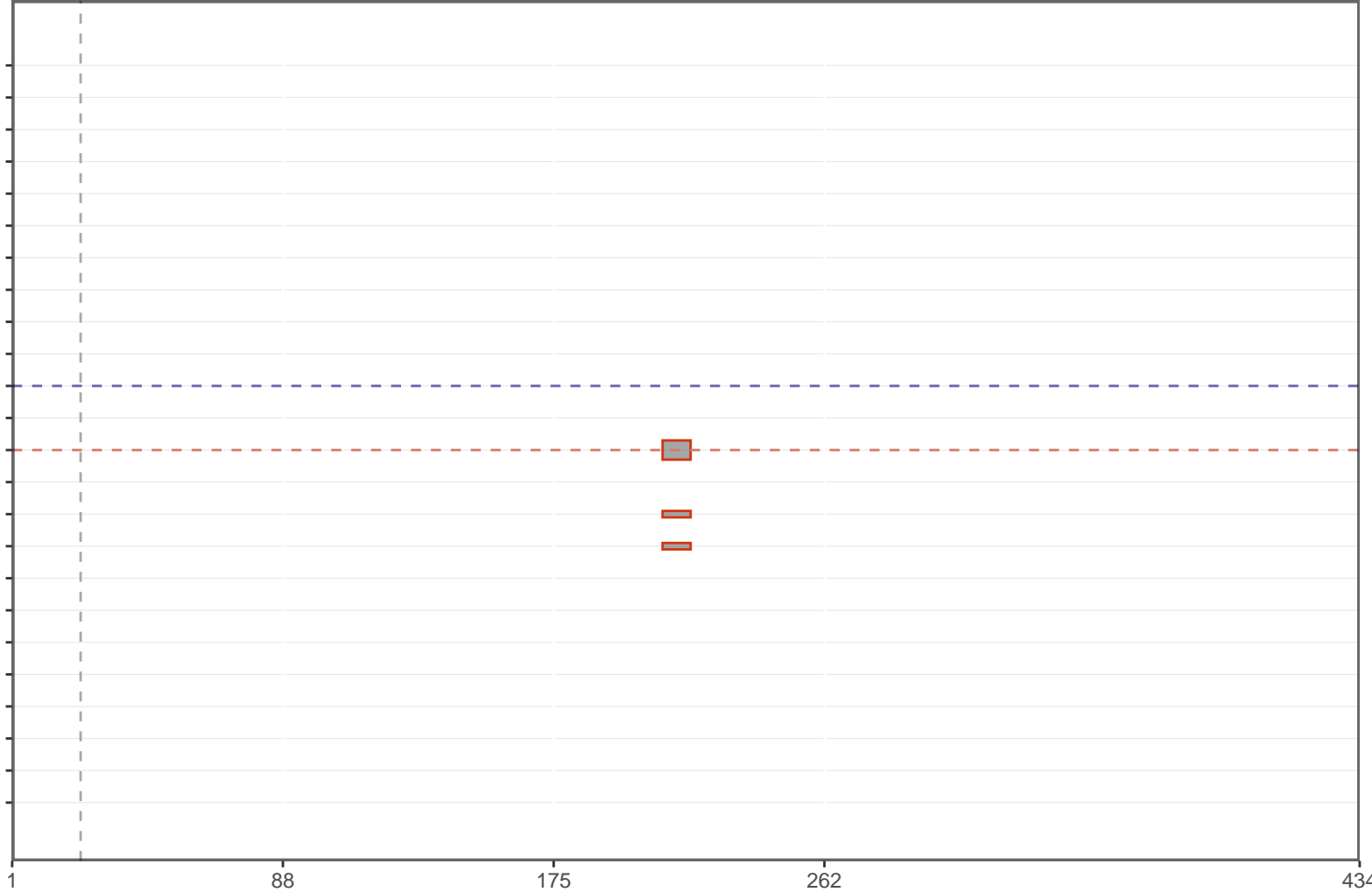
MW indication



Molecular weight



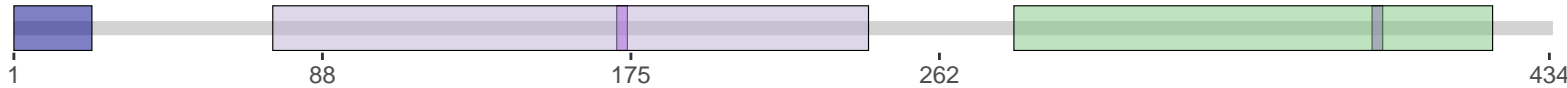
Gel Slice



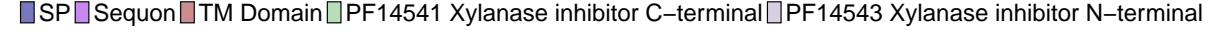
Protein length



Pfam domains



Pfam Description



Protein sequence:

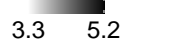
LDLGLKGGKASIVSOLHSKGLVIRNVGHLSLGGKGGGLFFGDEVDVDSRIVWTFMAHDRMKHYSAGSGELFFGKATGFKNLVYVDFDGGSSFLVNAQTYGGISLLKELNGKPLKEAKDDVTLPLQWGRPRPFKSNVKKYFKNFALNPHGHWKSKAHEIPPEYLIISGKGVCLGVNLGTEAGLGNVNLIGDISMGDKMVIYDNEKQAIQWSPNCDRPPKSNMMI

NbL04g07580.1 2-oxoisovalerate_dehydrogenase_subunit_alpha_1_mitochondrial-like [MW = 51.33 kDa]

No. of times detected



log(intensity)



Values from



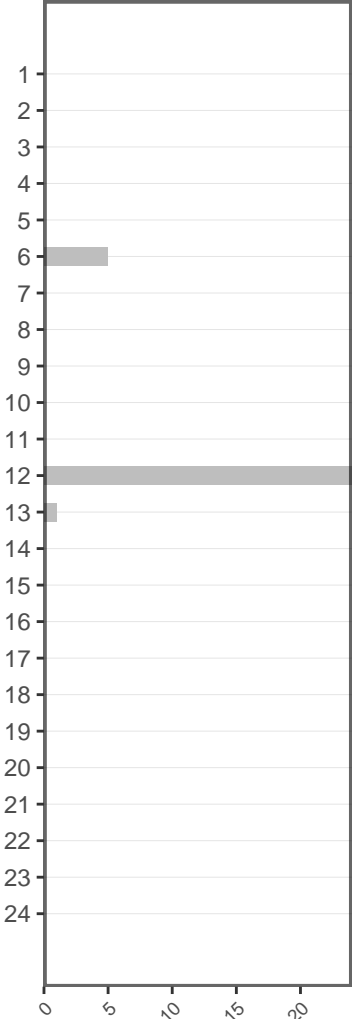
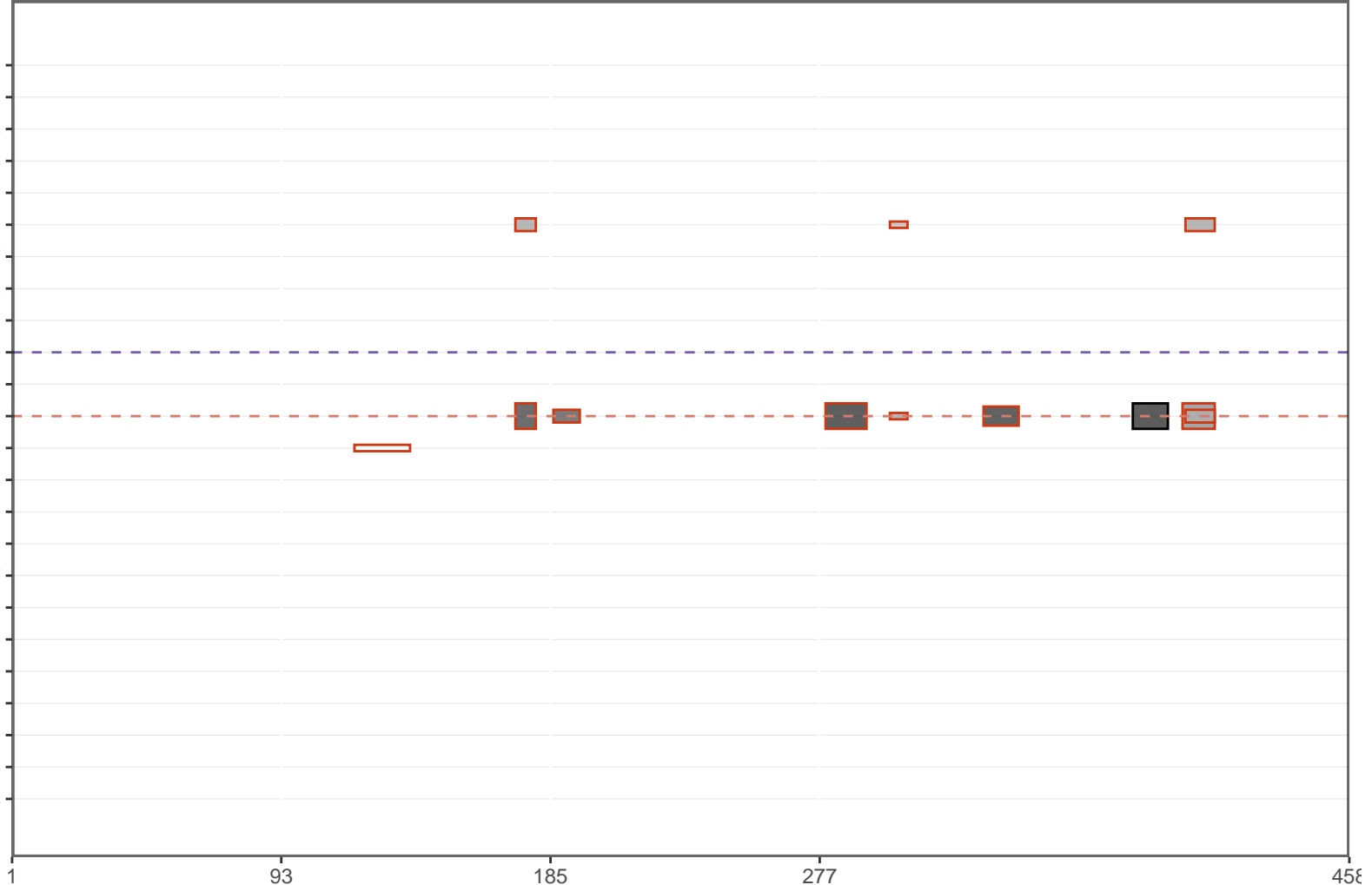
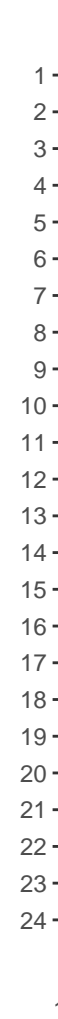
MW indication



Molecular weight

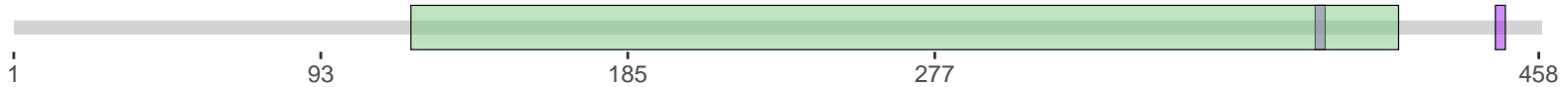


Gel Slice



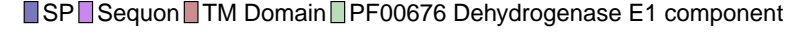
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LTISPIATQIPQAGVWVSLKMDKKEADAVTYLGGDGTSEGDGFHAALNFAAVLDAPVVFQIRNNGWIASTPINEQFRSDGVASKGGVAGIRSRVDDGNDLATYSAHAAREMAIKKQKPLVEAMTYRVAHSTSDSTKYRPFVEEIEHWKTKAIPISRFKWIQRNGWVWVNDENESELRGDRTRKQVIGAMQAAEKVKEKPLDLETEVVDKVPNLNLEGQHKFRIDAVNISPKYKPSDVPV

NbL04g07300.1 serine_carboxypeptidase-like_42 [MW - SP = 37.74 kDa]

No. of times detected



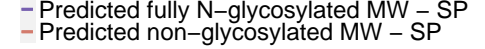
log(intensity)



Values from



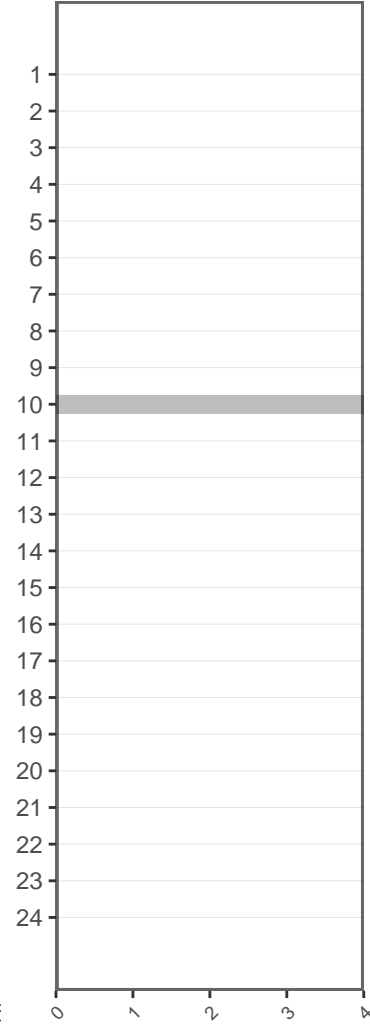
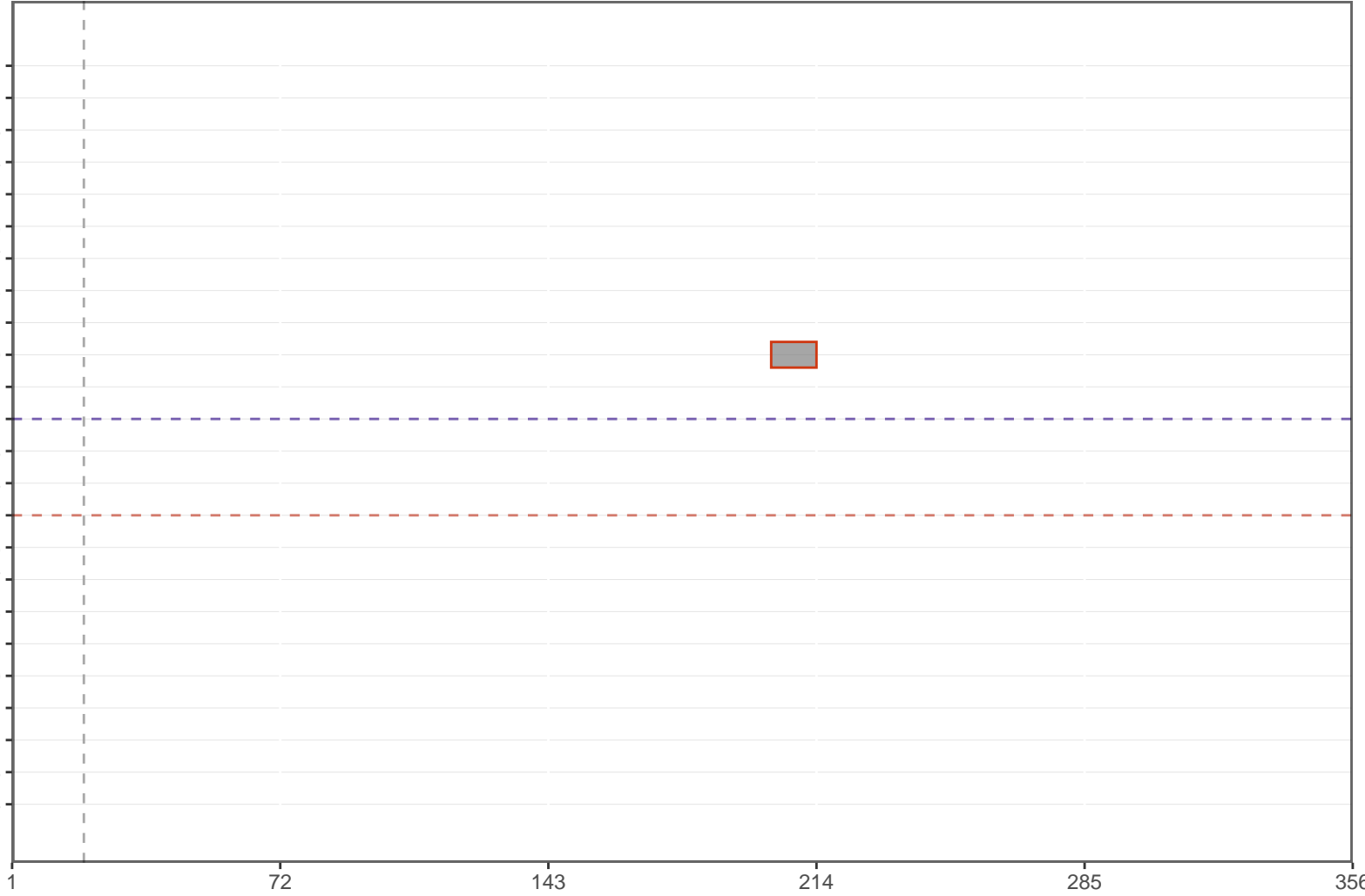
MW indication



Molecular weight

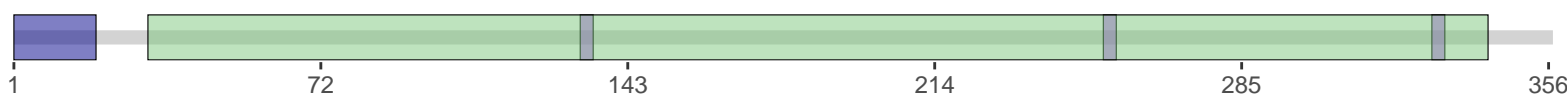


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

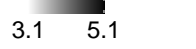
RSRELYLTGESYAGHYIPQLAWALLDHNENHKEYKFNKGVAGNPLNLDRDVPATYEFVFWSHQMSDEVLAMNGCDFEFTFGSPKINVSHEGNAISEANDHSKYYNNYDVLVDVCPVPEVEGELRLRKMATKMEVGVDMVQMSYERRFYFNLELVQKALHANRTNLAYSWMSMGSGTGLLLLLLOYSEIQ

NbL04g07230.1 pathogen-related_protein-like [MW = 26.7 kDa]

No. of times detected



log(intensity)



Values from



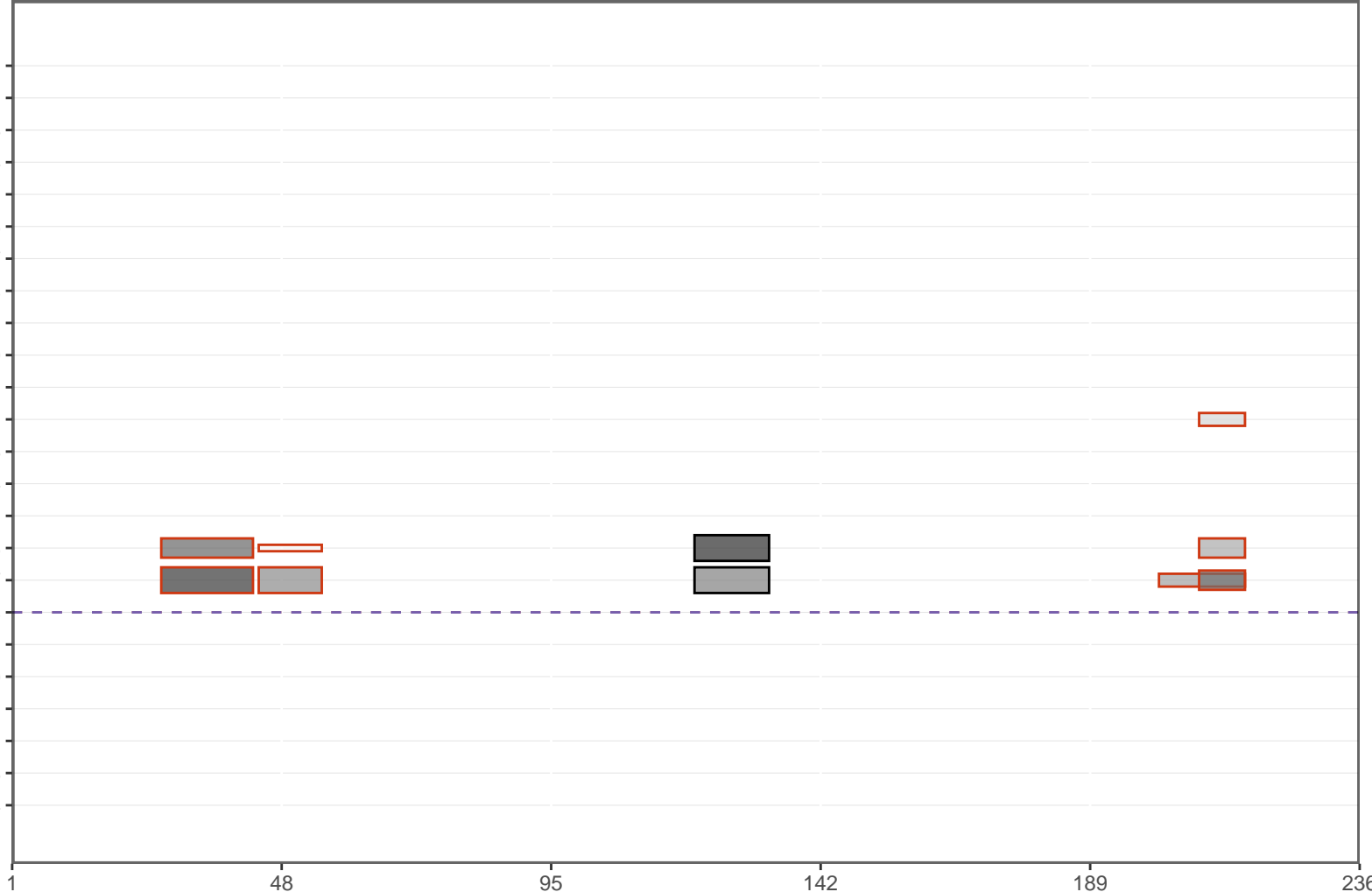
MW indication



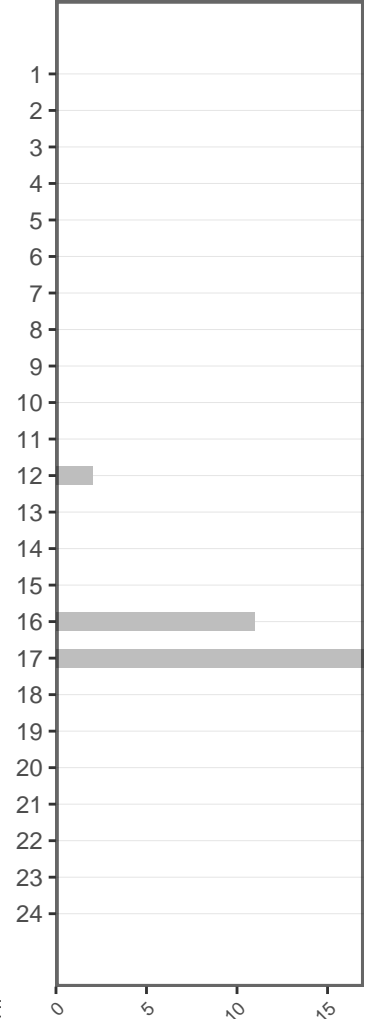
Molecular weight



Gel Slice



Protein length



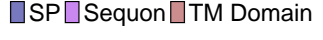
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

GGYNTFLQTSLEPEISVRYVNPDEETFE66GKVRISFLRGAIEILHV56PPEIVYKFRHWGHMEGPFKGHATGELVOLFQIGFEVYKESNKKVKAFFFDRLGELLGPLVKGKNGD6THAMALACP6MK

NbL04g07120.1 long_chain_acyl-CoA_synthetase_9_chloroplastic [MW = 76.01 kDa]

No. of times detected



log(intensity)



Values from



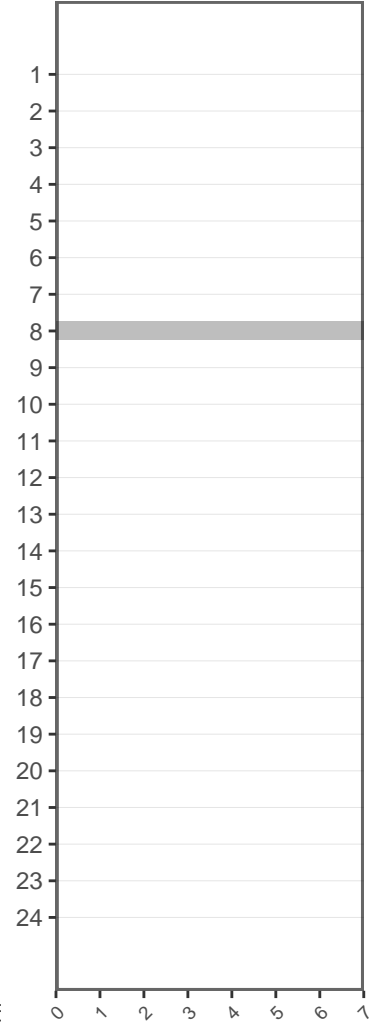
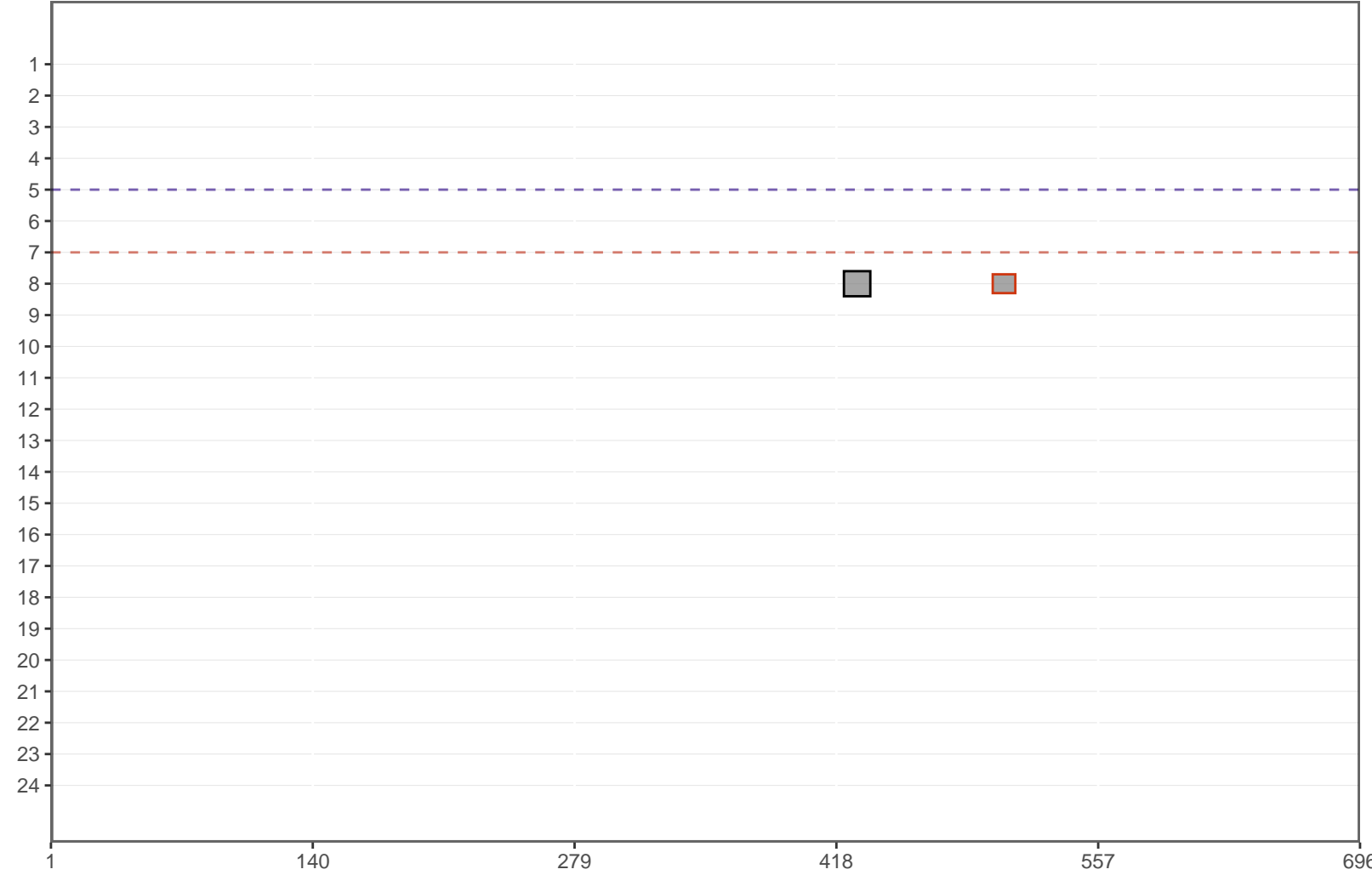
MW indication



Molecular weight

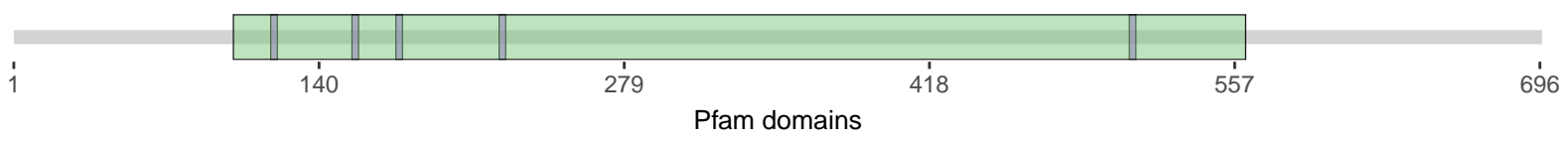


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TKGDLSVLRPTVMAMFNLDRVRDGVKXVDAAGLGGKFLDLAYSRRQEAINGNWFQAWGLEKQFVNLVFKKXVQALGGRRIFLGGGAPLGGDTGRFINCLGAPIGGGYGLTETCAGCTFSQVDDTSEVGRVGLPPLGSRGKLDVAEEGGYLTGDSFMPRGEIVGGPNVTVRYVFNNEEKSEKVVYKVDERGMWVFTGDIQGFHADGGLERDKKDIVKLGHEVYVSLGKVEAALSISPVVDNIMLHANPHSYGVAVVAAGAEEGWAKNHGIDFGDFPELCCNEE

NbL04g07090.1 50S_ribosomal_protein_L25-like [MW = 31.45 kDa]

No. of times detected



log(intensity)



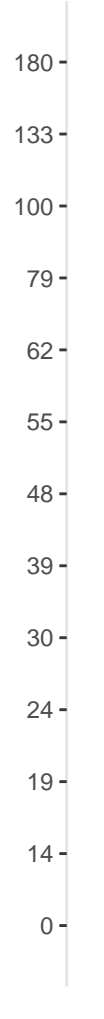
Values from



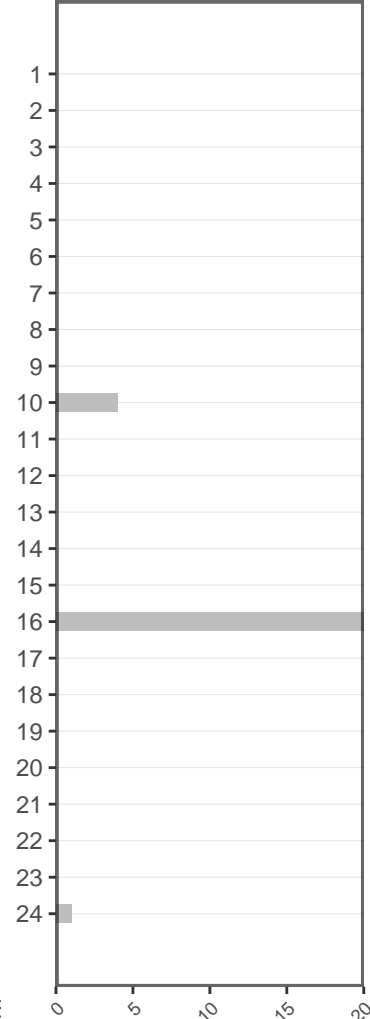
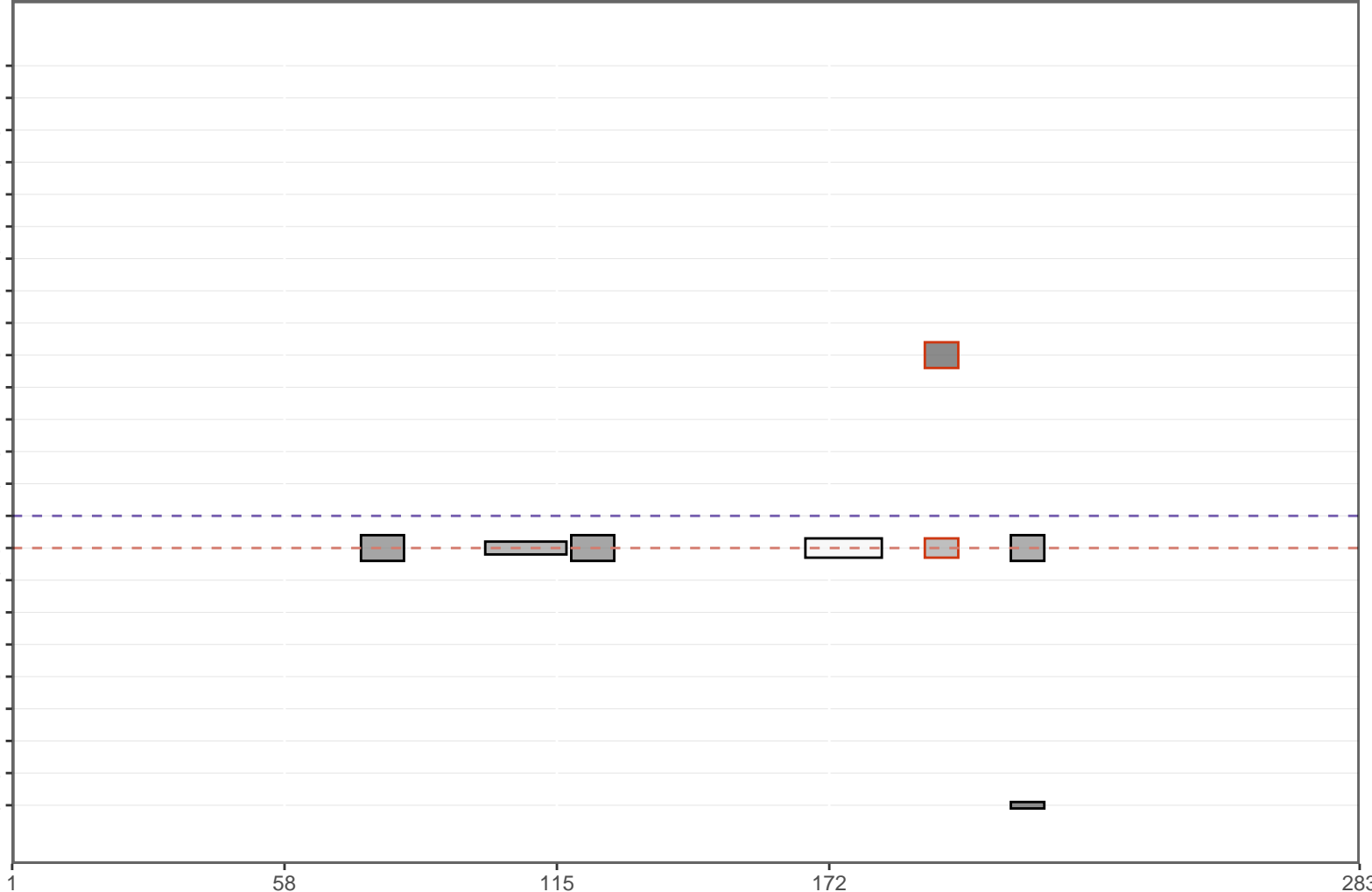
MW indication



Molecular weight

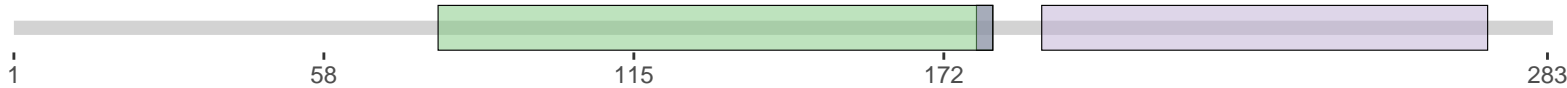


Gel Slice



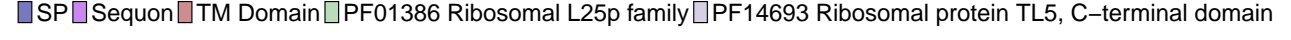
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LVNHLGRSHFLSLRFLDLEVRPDPFDVEVEKVKVLPKRVHLEAGSDAPLNVTFIRAPSSALKKVDPLFRGEDVSPGLKKGVEYLNKIKRTWYKLPADVIPPVIVDLSLELVGQKLVMGDLKVVHFKLKLQPKDHPVYKIMGARVSDGKKA

NbL04g07080.1 probable_L-ascorbate_peroxidase_6_chloroplastic [MW = 47.21 kDa]

No. of times detected



log(intensity)



Values from



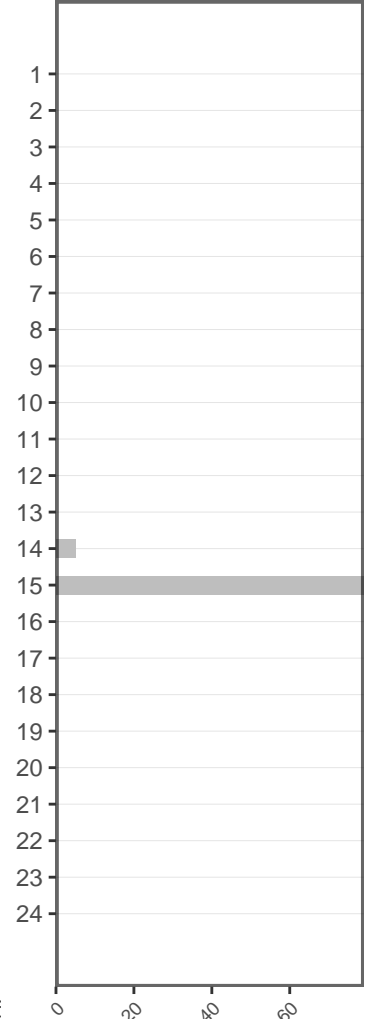
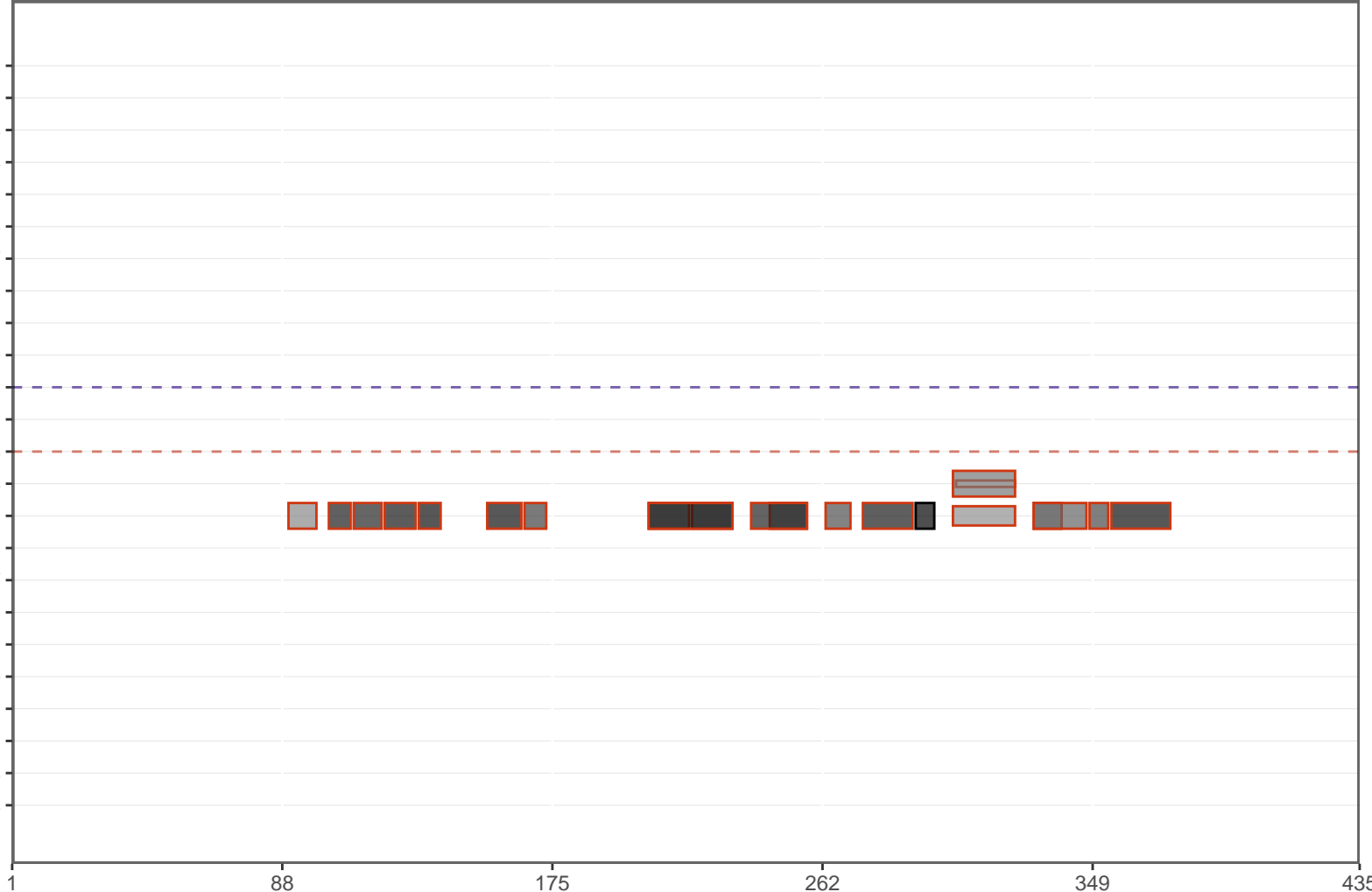
MW indication



Molecular weight



Gel Slice

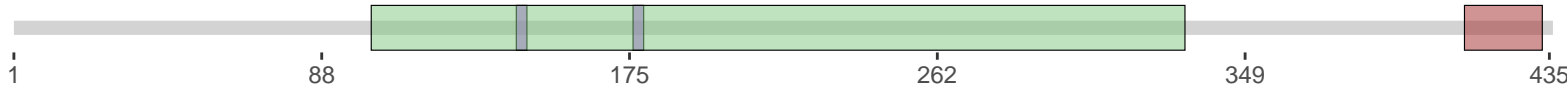


Peptide counts over 4 repeats

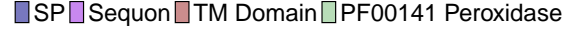
Protein length



Pfam domains



Pfam Description



Protein sequence:

DVSYPEECPEEGRLPDGPPRSHLRDVFYRMGLNDKKEVALSGAHTLGRSRPERSGWGKPEYKTYNDGPNPCCGGSSWTQWLKFDNSYFKDKERRDEDLVLPDIALFEDDSFKEYAEKYNWINDVFFKDAEAAHAKLENLGAKFDPPEGFSIDNTPFGGQPEKFAAKYSTGKRELSDAKGGKRAEYEGFGSSGADKPLPTNYFLNIMVGLAVTSLGN

NbL04g06910.1 thioredoxin_Y1_chloroplastic-like [MW = 18.96 kDa]

No. of times detected



log(intensity)



Values from



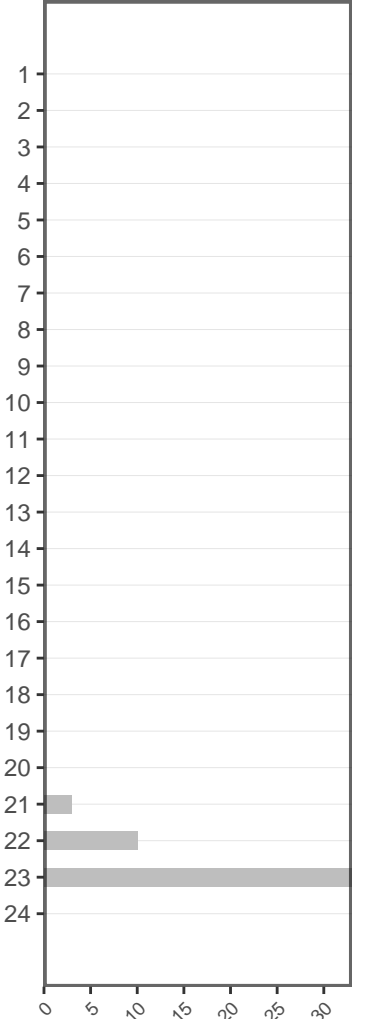
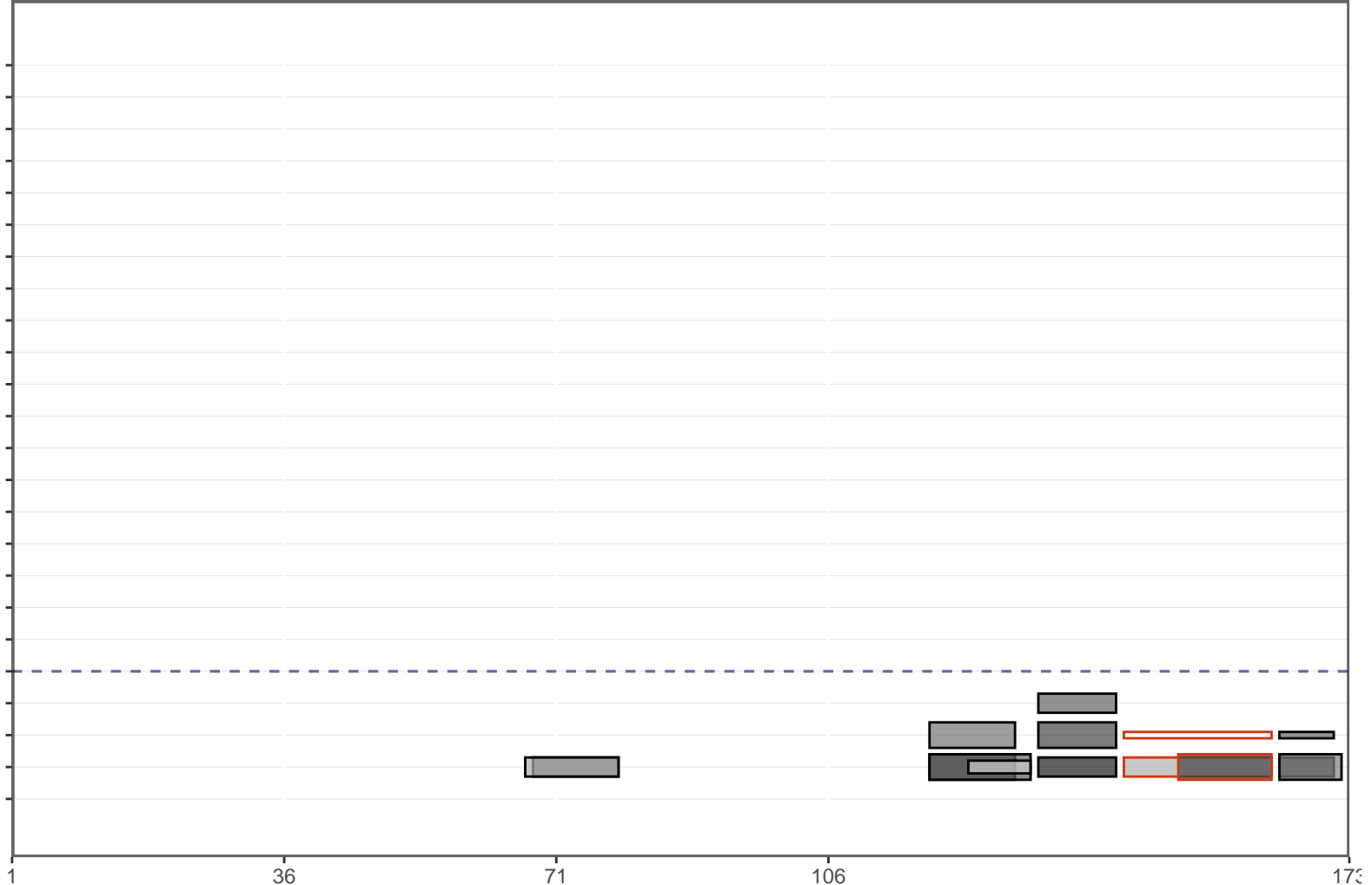
MW indication



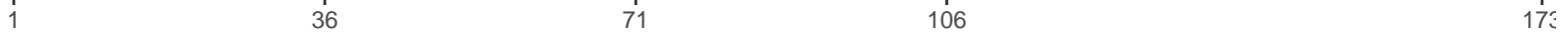
Molecular weight



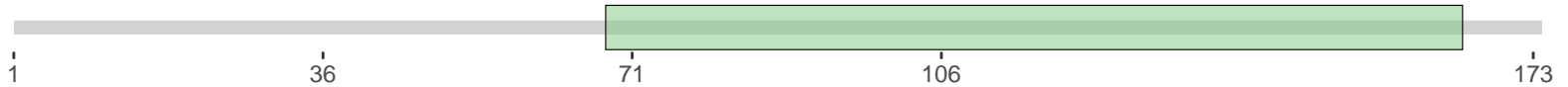
Gel Slice



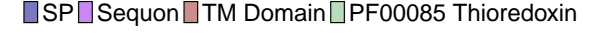
Protein length



Pfam domains



Pfam Description



Protein sequence:

FEELLEKSEKPLLVDFYATWCGPGQFMVPLNEVGE6MKDKHVKWIDSEKYPALADKYKIGALPTFLFKDGEVCDRFEGALNAPTLQRIESALEVKQ

NbL04g06790.1 trihelix_transcription_factor_GT-2-like [MW = 76.1 kDa]

No. of times detected



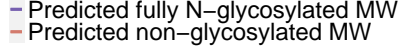
log(intensity)



Values from



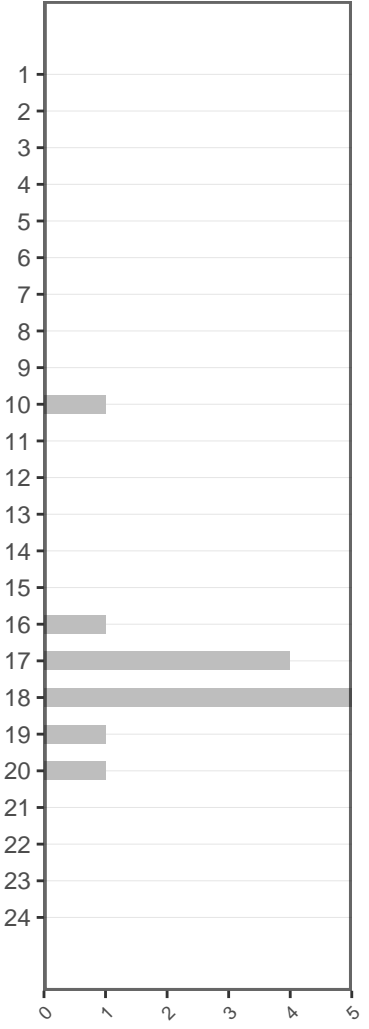
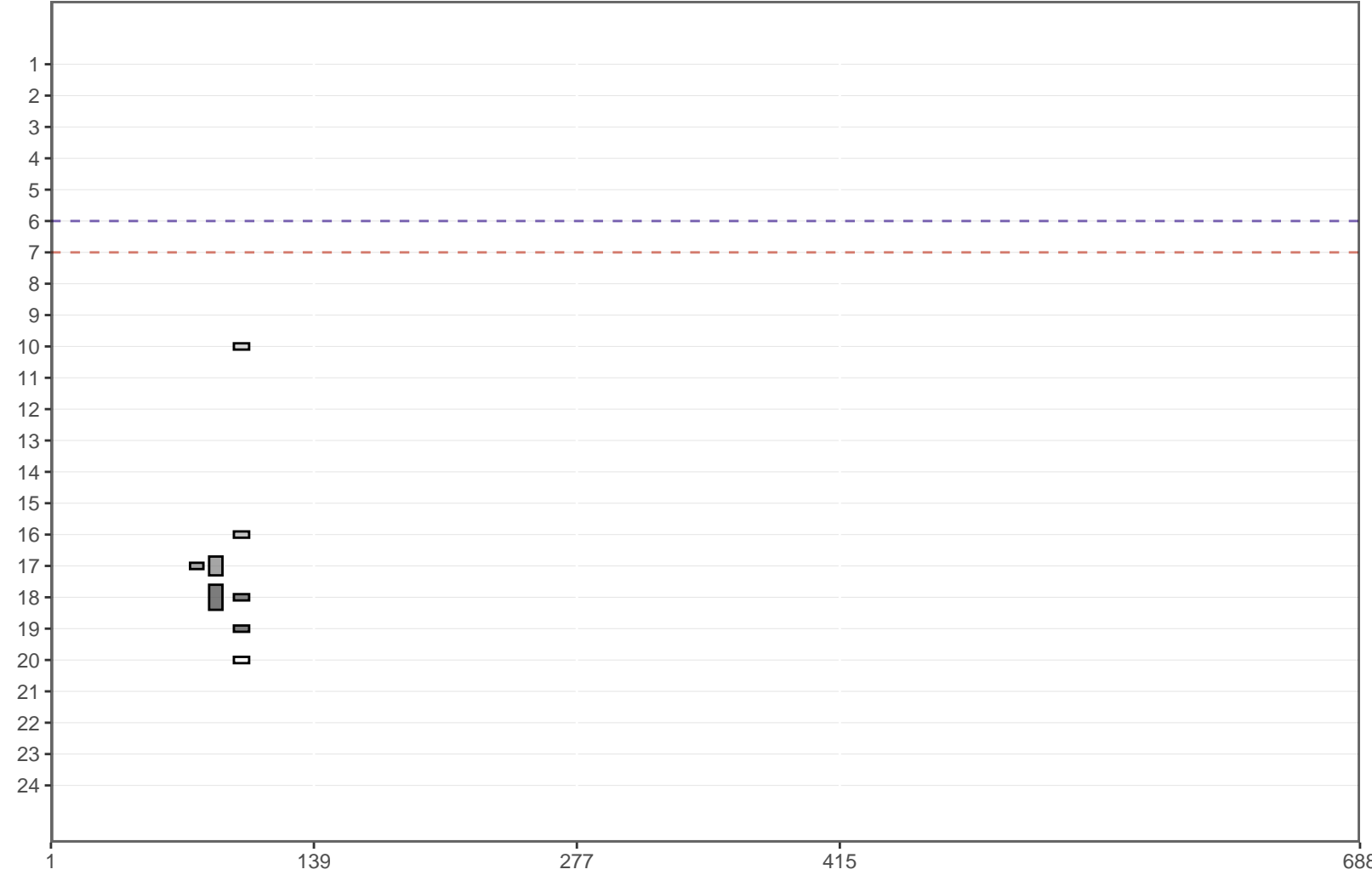
MW indication



Molecular weight



Gel Slice

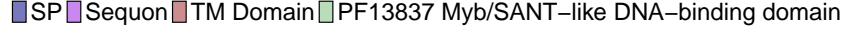


Protein length



Pfam domains

Pfam Description

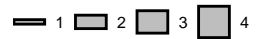


Protein sequence:

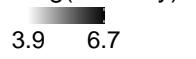
.EKRRDRMVRSEAWRVGQVARMNRHDLVQERSTAAAKDAVIFLQKTFEGNQIPENIVAFPSAQVQGLPENPPPPSETRSGVVHQGTQPTAVLVSPAPFTQSPATAPVSLPFRKQGLPLTFPPVPAKSVELTFPKSDNGEGYSPASSRRVWPKAEVEALMLRTQLQVYKYGNSPKGFLVWEEISAGMKKLVGNRNRNAKRCKEHWENIKYFKYKVESNKKRPEDSKTQYFHQLDALYKEKAKNETSSGFENPSAAGFALNPNFMPMPMARPECOQVPRPHH

NbL04g06760.1 fructose-16-bisphosphatase_cytosolic [MW = 37.19 kDa]

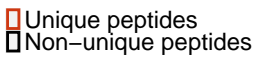
No. of times detected



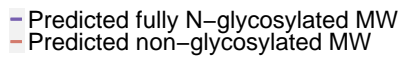
log(intensity)



Values from

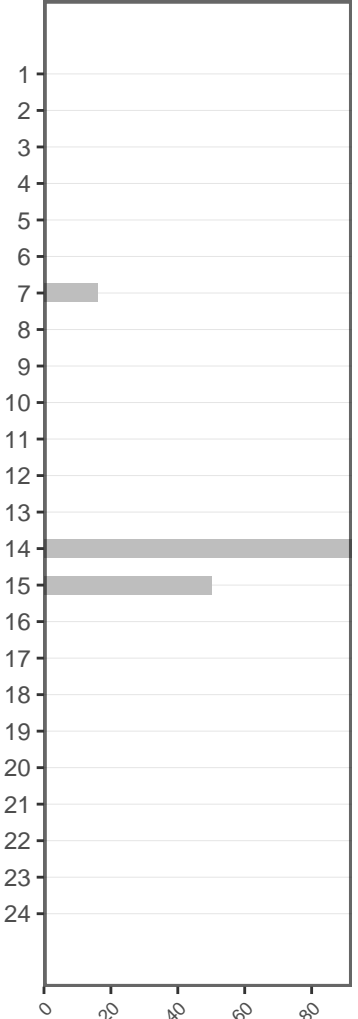
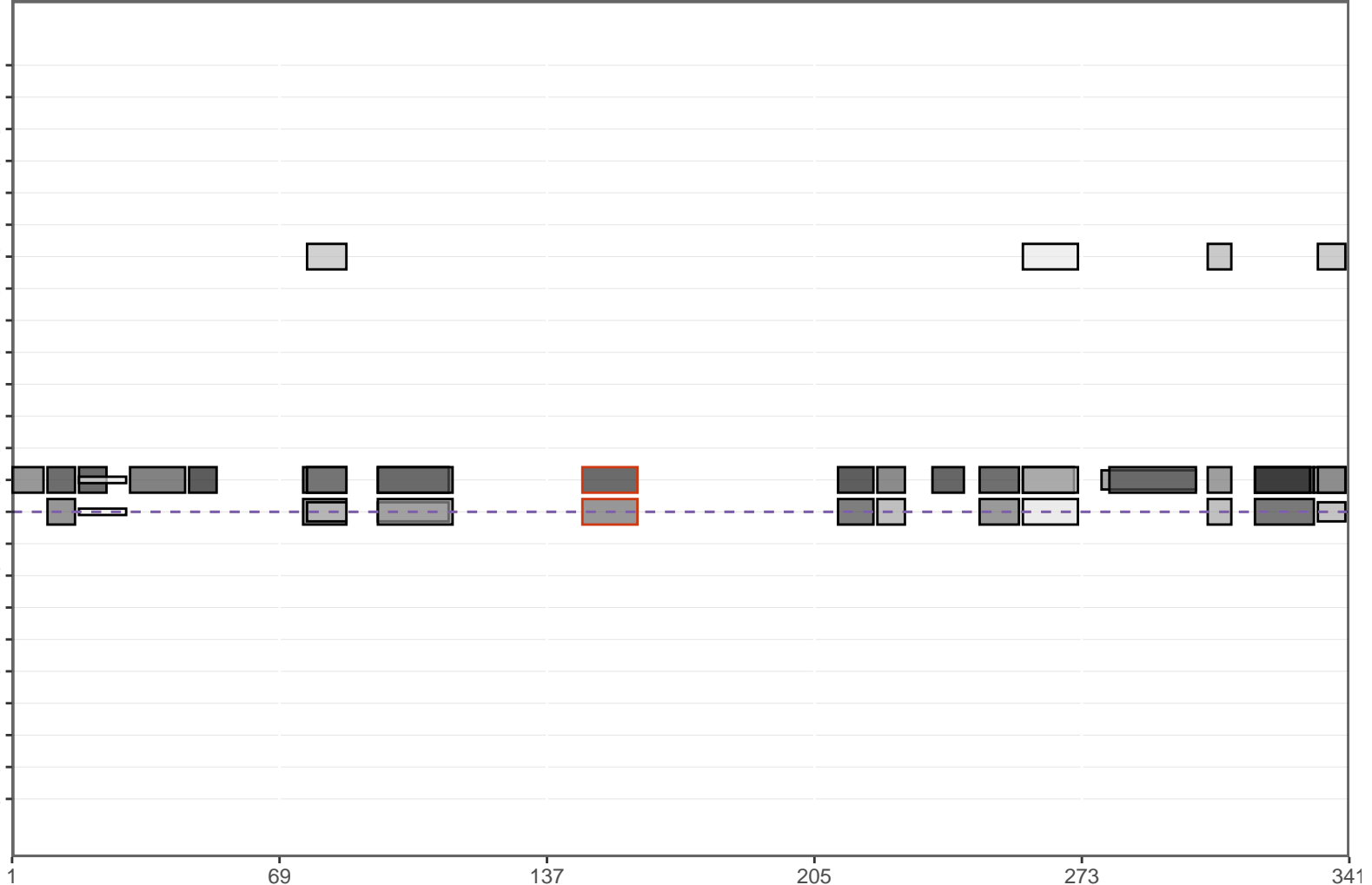
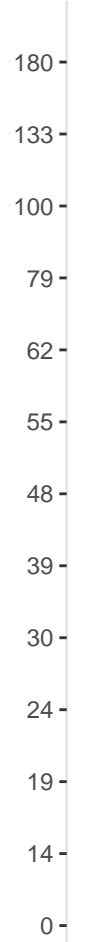


MW indication



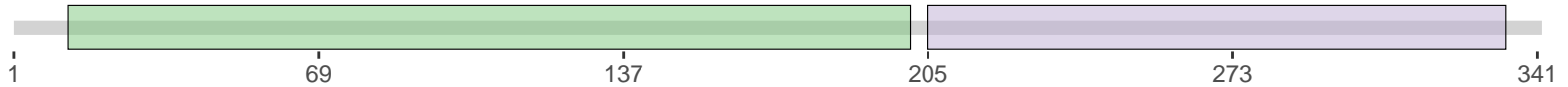
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

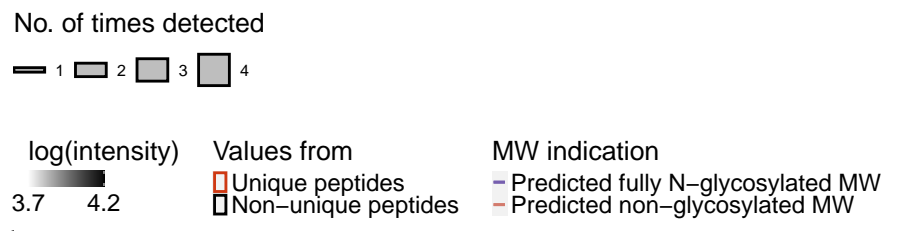
Pfam Description

- SP
- Sequon
- TM Domain
- PF00316 Fructose-1-6-bisphosphatase, N-terminal domain
- PF18913 Fructose-1-6-bisphosphatase, C-terminal domain

Protein sequence:

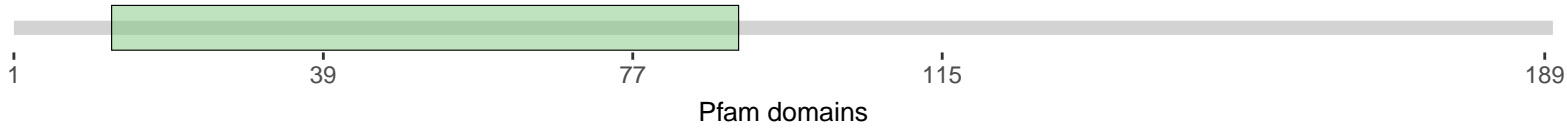
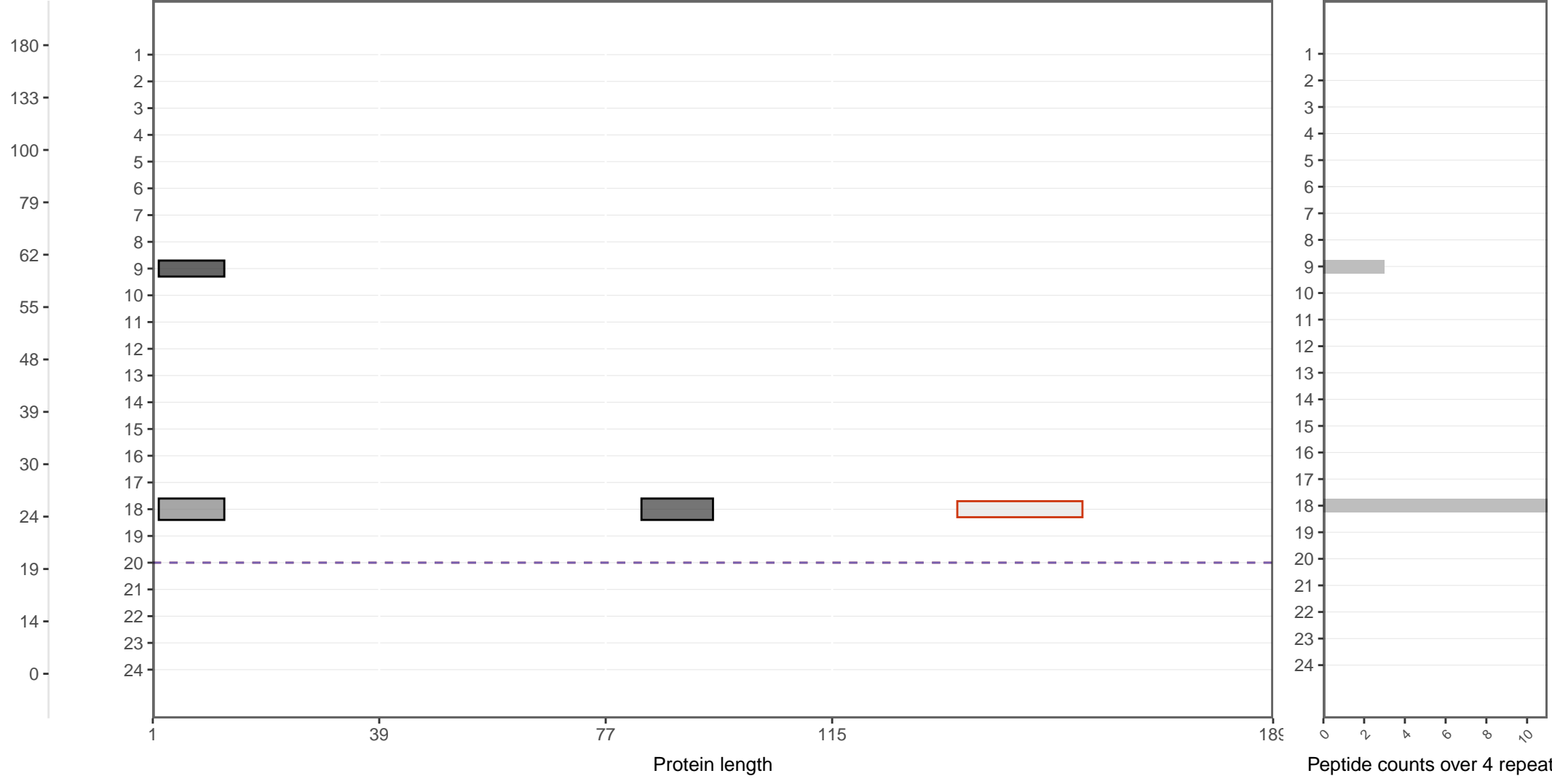
GKNMLAAGYCMYGGSSCTLVLTGGVNGFTLDPDLGELFTHPDKIPKIKKIKYVNEGNAKRWDPSTKIVQNKYPTDGGSPKRLRYGSMADVHRTLLYGGIFLPADKPKSPNGKLRVLYVTFPMFLMEQAGGGGFTGKGRALDNLVPKKHERRAPILGSDYDVEERKLLAAEEGN

NbL04g06740.1 uncharacterized_LOC107817613 [MW = 20.35 kDa]



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain PF06391 CDK-activating kinase assembly factor MAT1

Protein sequence:

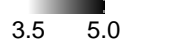
AEEYAAALAAASKGPTQPDGDAALGLGPDAGSSTGPDGHYAPWAGGIQPRPTQPLPVGSSPGLVEYDEETMKLKAEEKARAGGWLSLEISKRKALEEAFGLWV

NbL04g06600.1 RNA-binding_protein_2-like [MW = 27.37 kDa]

No. of times detected



log(intensity)



Values from



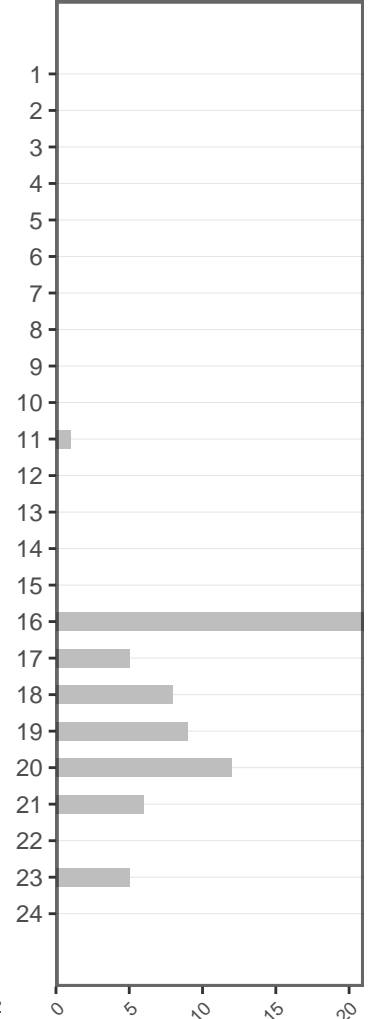
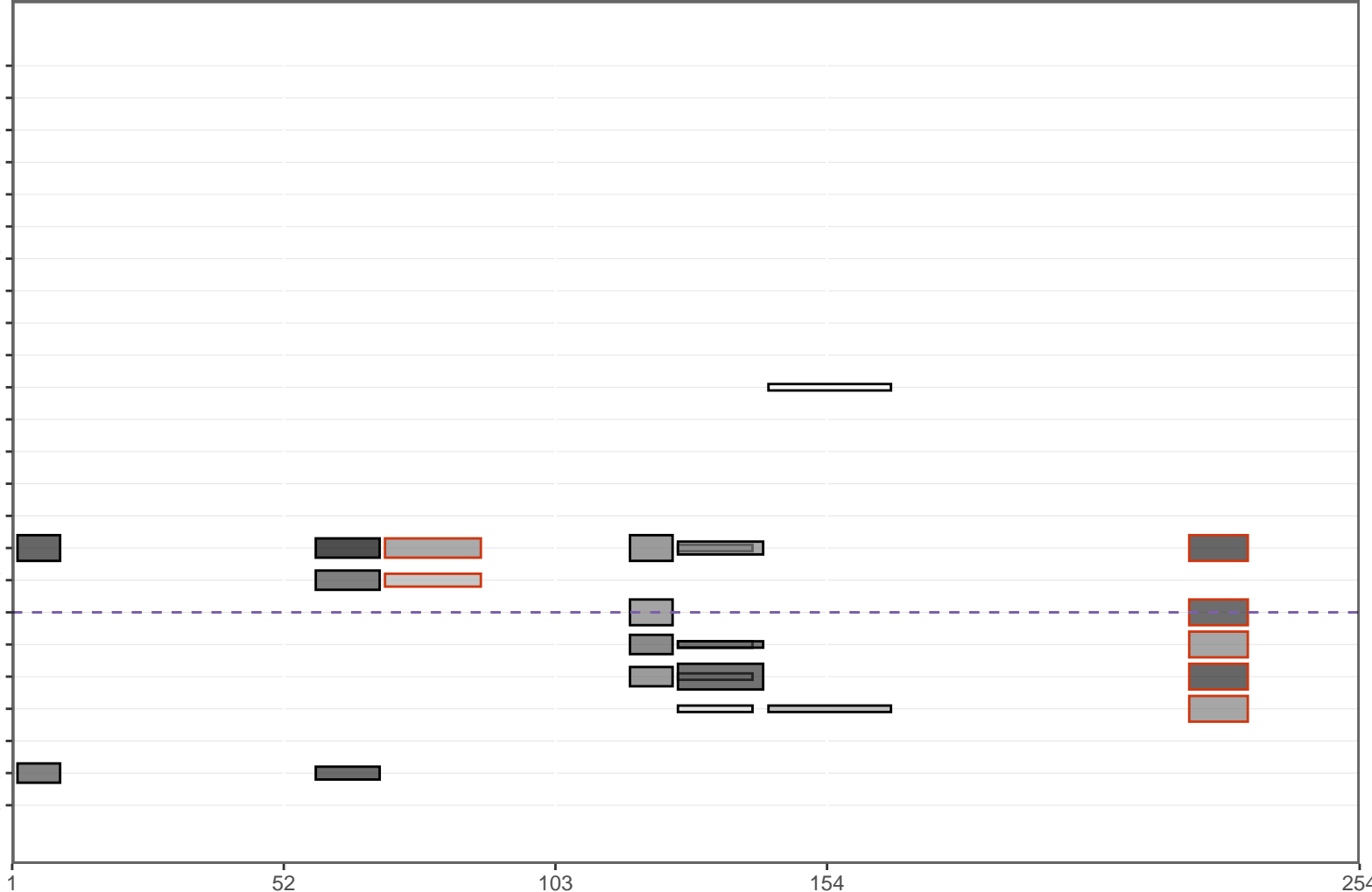
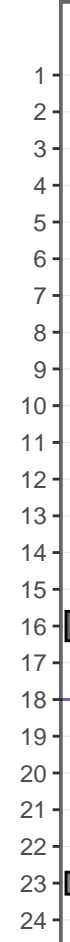
MW indication



Molecular weight



Gel Slice



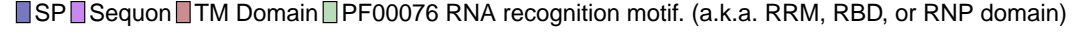
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MSARGPELAPNGRAMVLSGGMPVEIQLRRPRETLPLPPDAINTLYEGLPADSSRREVAHFRRPFVGYKEVRLVRIKESKIRGGDPLILGFVDFMDPAAGATAALSALGGYKMDHDFDSAVLRILGFQFKFQPRGGGSSGRKR

NbL04g06540.1 cycloartenol_Synthase-like [MW = 86.02 kDa]

No. of times detected



log(intensity)



Values from



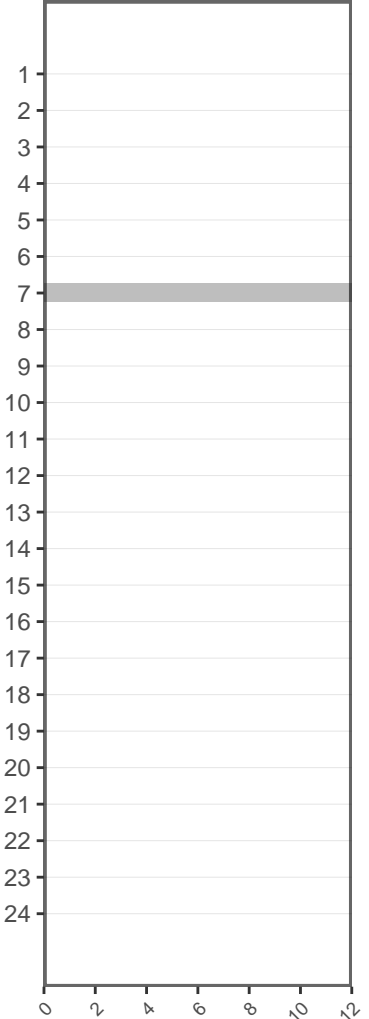
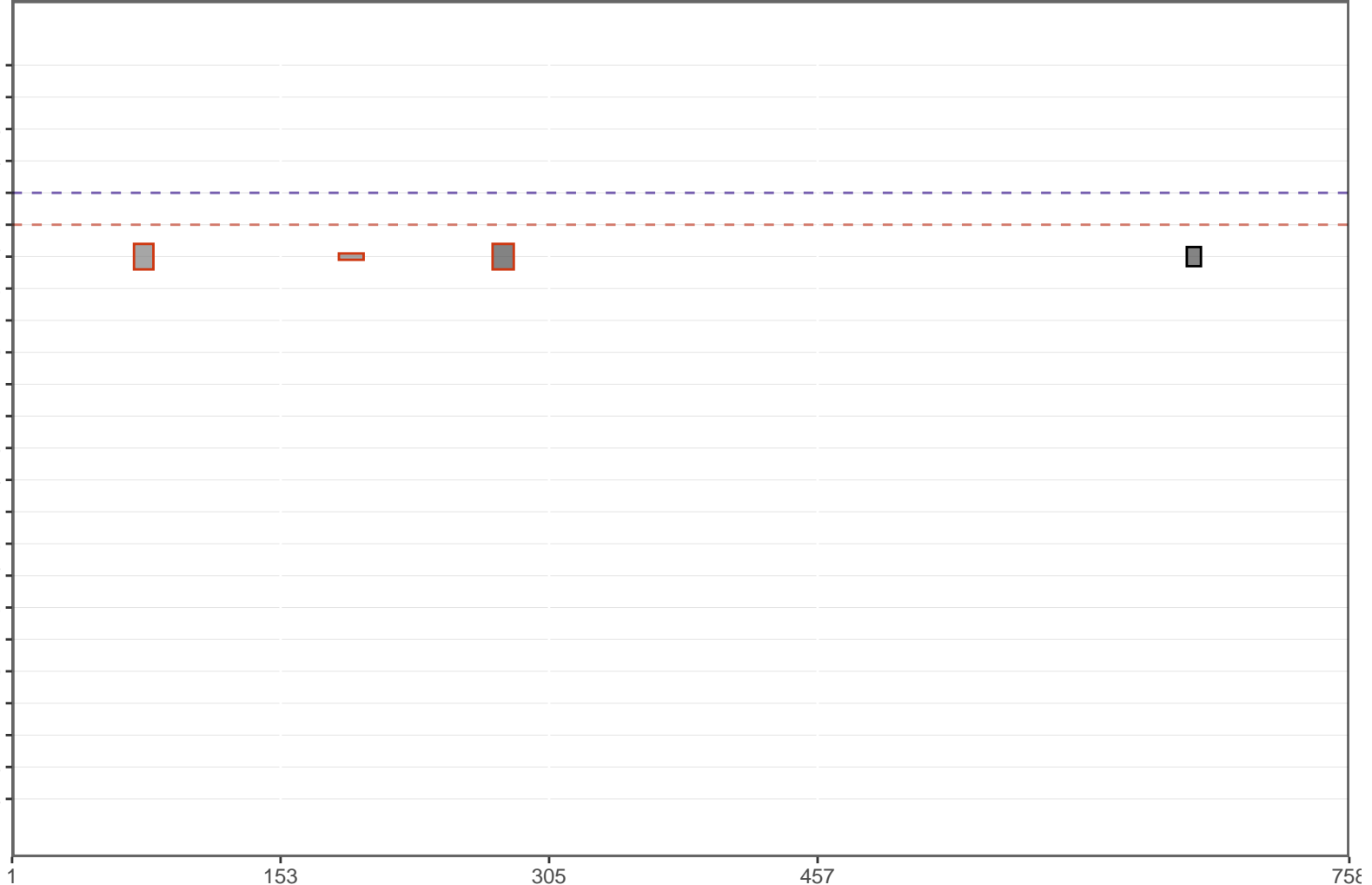
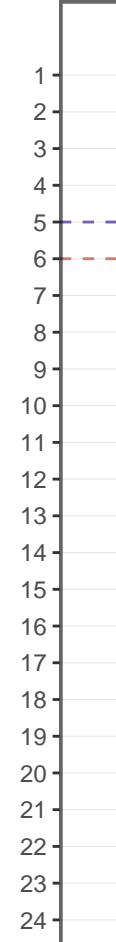
MW indication



Molecular weight

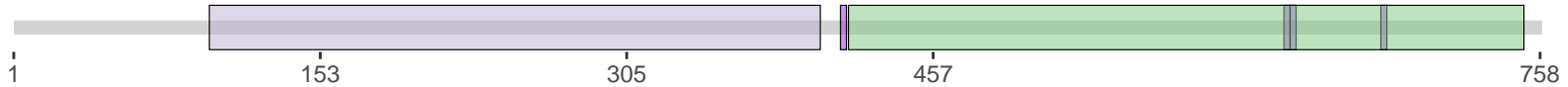


Gel Slice



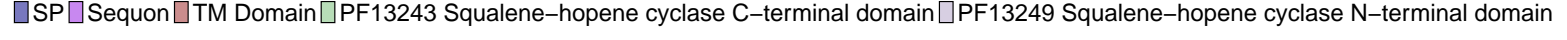
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

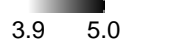
ICIGPVNKLNMLCWVEDPHSEAFRLHLPRHIDYMWVAEDGMKMGYNGSGSDTSAQAIATELGEYGSALRKAHSFKNTQVLDGPGNLDYWRHSHKGAWPFSTADHGWPIPSDCTAEGLKASLLSKLPSEIVGDPLEAKRFYDAVWVLLSLGNSSGGGFATYLSRSEYVWLEINPAETFGDNDYDFWVEGSSAAGALTAFRKLYPQHRKEEVERCIAKAAAFIEKIGSEADSGSWVGGWVGFYGTWFGVLGLLAAGRNVTN66SIRKAGDFLLSKQISSGGWGE

NbL04g06400.1 uncharacterized_LOC109240968 [MW = 113.46 kDa]

No. of times detected



log(intensity)



Values from



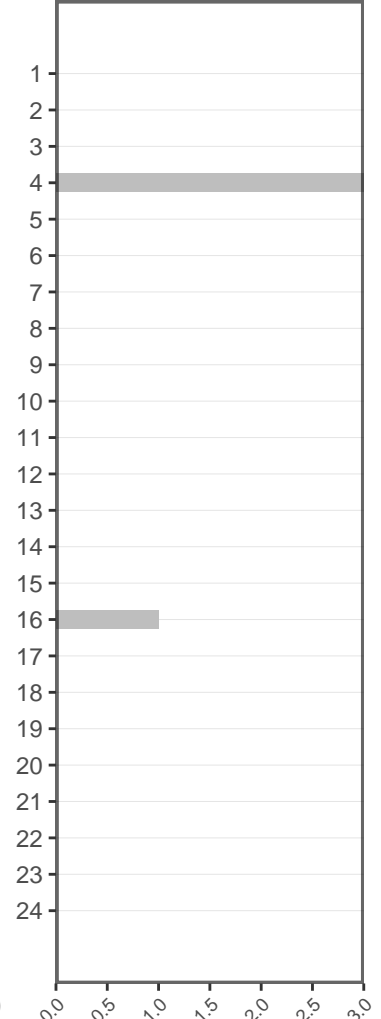
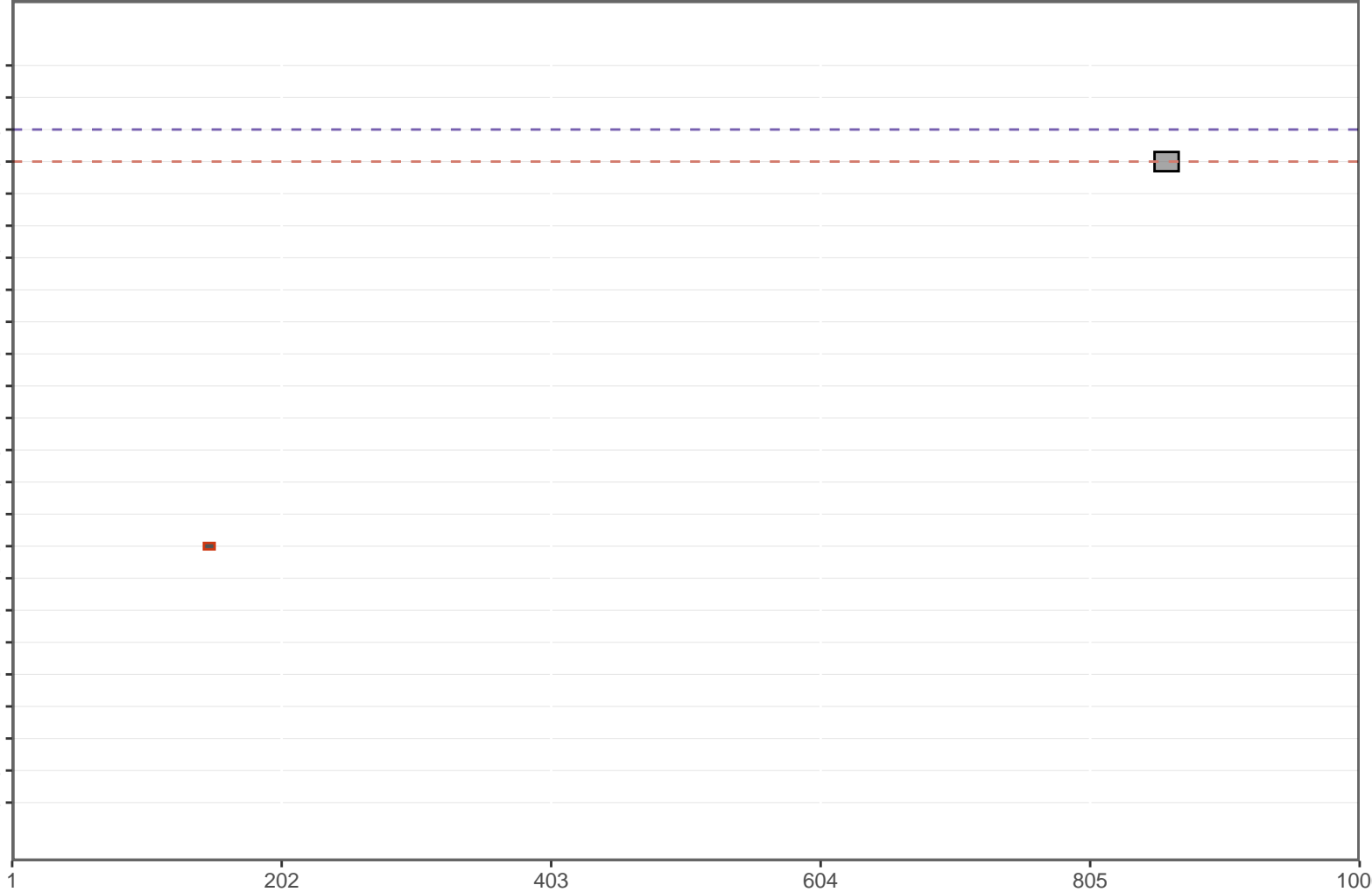
MW indication



Molecular weight



Gel Slice



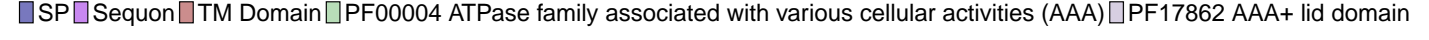
Protein length



Pfam domains



Pfam Description



Protein sequence:

SKANRKEFVHKVQEMFDQLSEVFPVLCGRNKNVETGSKKEKFTMLPNLGRLLAKLPLSLKRLTEGLRATKRSVDDDHKLFENVMHSHPKKEEDLLSTFNKQIEEDRKVIARENLMELVYVLEHLSGIDLLHNTDGVLTQKKAKEKVGWANNHYLFTGLQPSKGRDRLVLPRESLETAILRLKEQETMSKQSGNKNLAKDEYENNFVSAVPPGEGVWFDDGALSEEKVALNELVLPMRPELFSRGNLLRPPQKGLFGPPPTGKTLWAKALATEAGANFISITGSLT

NbL04g06390.1 nucleolin_1 [MW = 69.01 kDa]

No. of times detected



log(intensity)



Values from



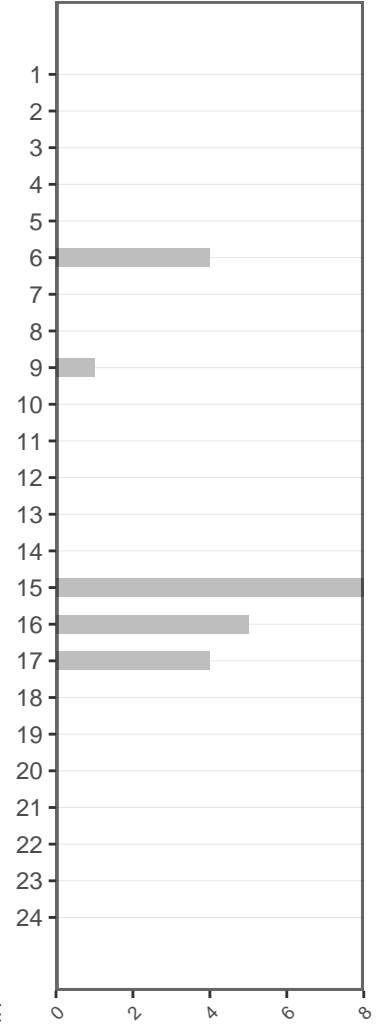
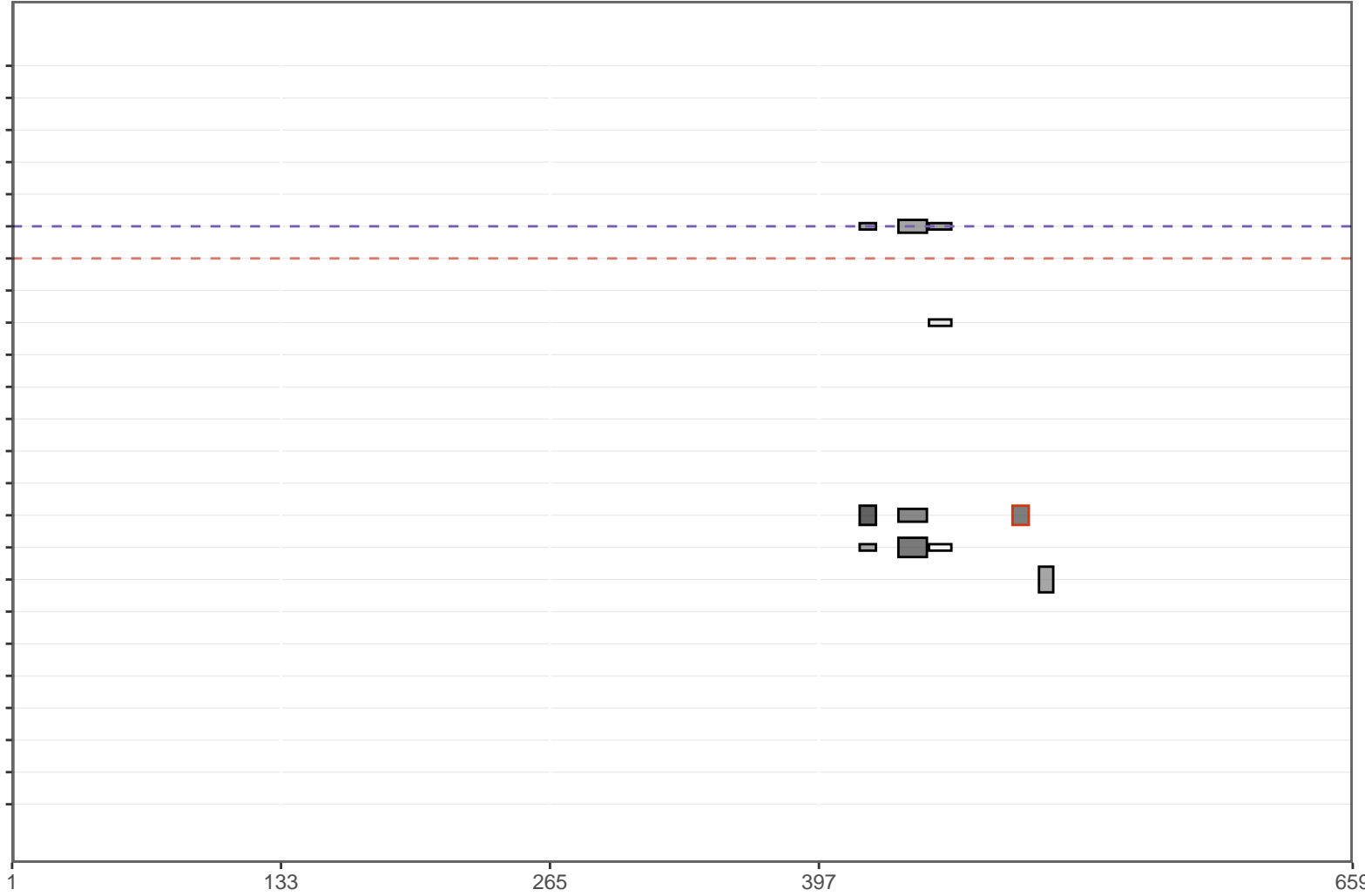
MW indication



Molecular weight



Gel Slice



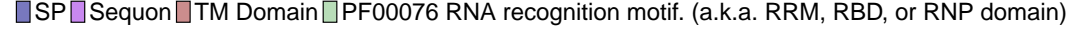
Protein length

Peptide counts over 4 repeats



Pfam domains

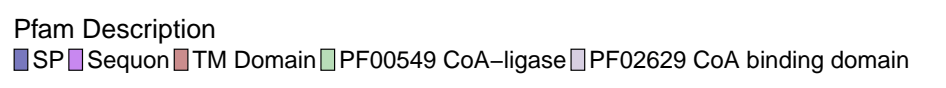
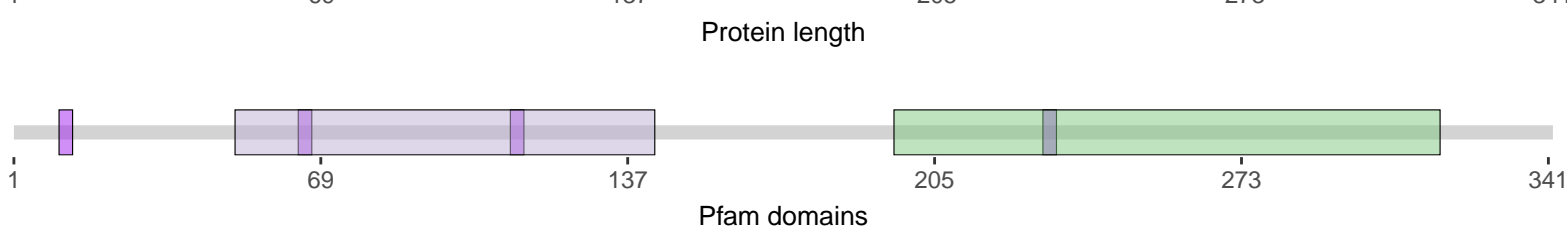
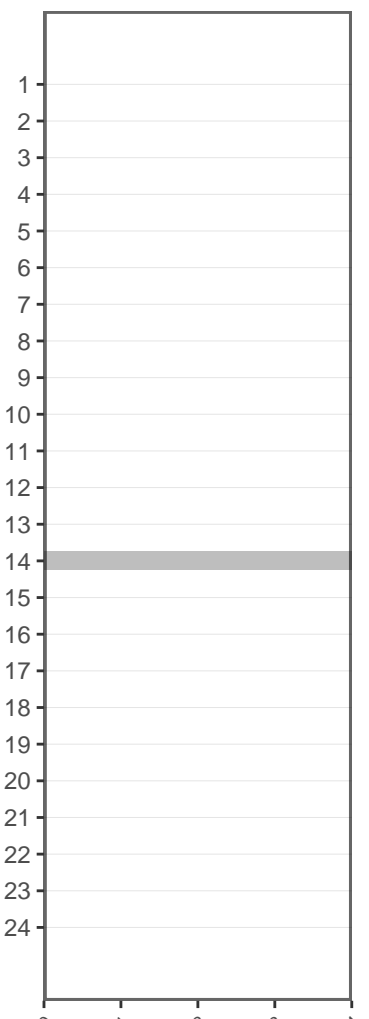
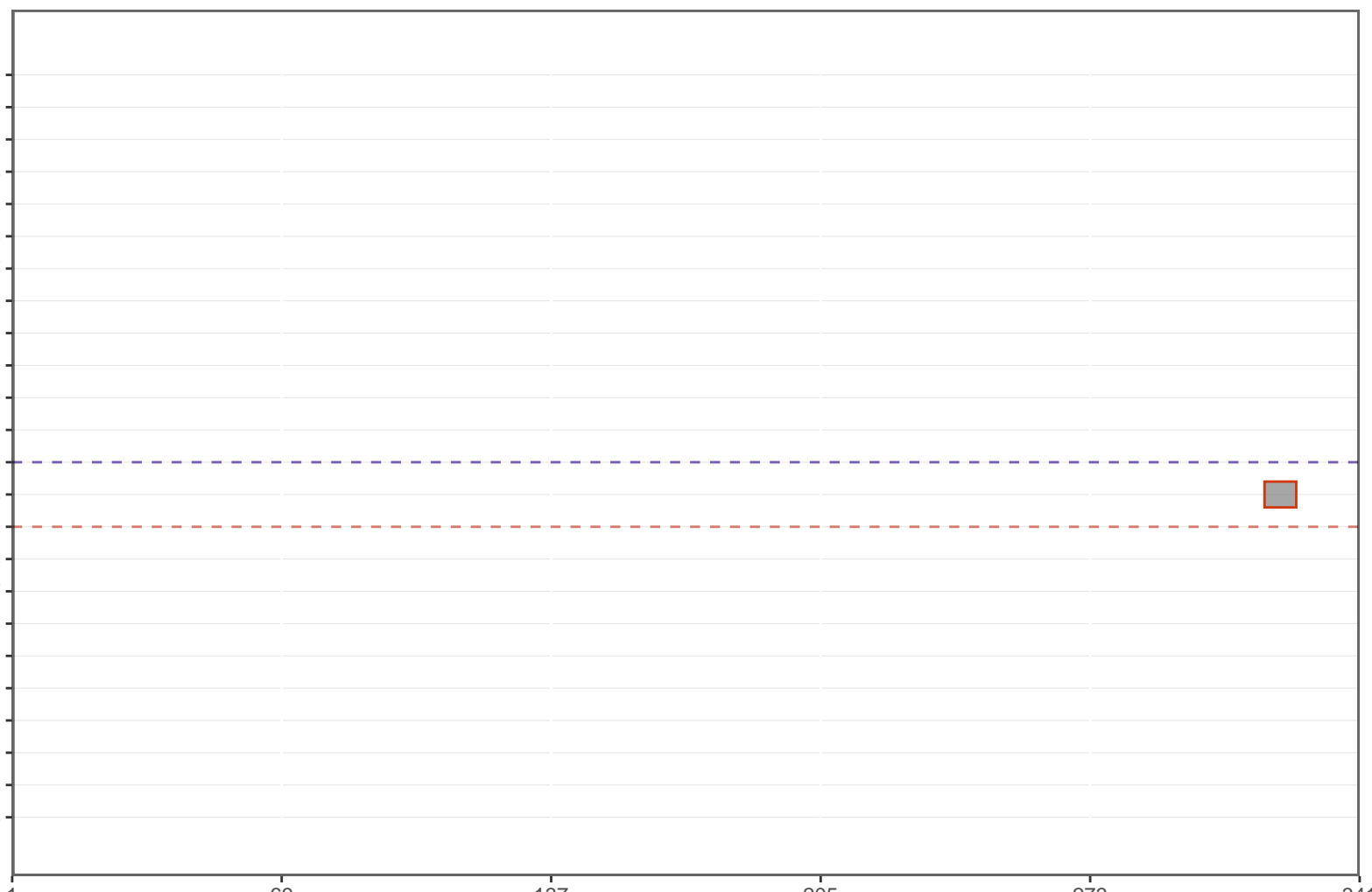
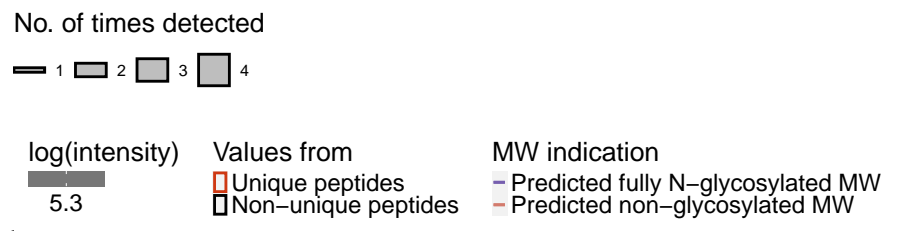
Pfam Description



Protein sequence:

EEESQKKKPSSTPWGKKESSSEEEDEEEDENKPKTKKQDQVEMVDADDFKAGKTRPTPKAGTPTCTKLVGNLGVYVEQADVENFFKMDGSEVGEVRFSTHEDGSKYGVHVEFVTEAAGKALELNGDILLGRAVRLDLARERGEYTPRTGREENSFQRGRGREGTTFVRFGRFDKNEAEDQIRBSLEEHPASGGKIKTRIPDPEGVKGMVVEFANADSDANKALELDGSEVGGYNLTVQEAAPROGDSGGGRGFGRRGGRRGGRRDGGRRFGC

NbL04g06300.1 succinate--CoA_ligase_[ADP-forming]_subunit_alpha-2_mitochondrial [MW = 35.61 kDa]



Protein sequence:
 LLKKQSKTRLLGPNPGRGKPKGEEKIKGMPGYYHKPRGRIGVSRSGTLTYEAVFQTTAVGLGGSTGVGGGDFNQTNTFVQLEKFIADPQTEGIVLSEGGTAEEDAALIKESGTFQKPVVFIAGLTAPPGRMRMGHAGAVSGGKGTAGDKIKALKEAKVTVGGSPKIGVTMLDVFQKRGLA*

NbL04g06220.1 photosystem_II_stability/assembly_factor_HCF136_chloroplastic [MW = 49.14 kDa]

No. of times detected



log(intensity)



Values from



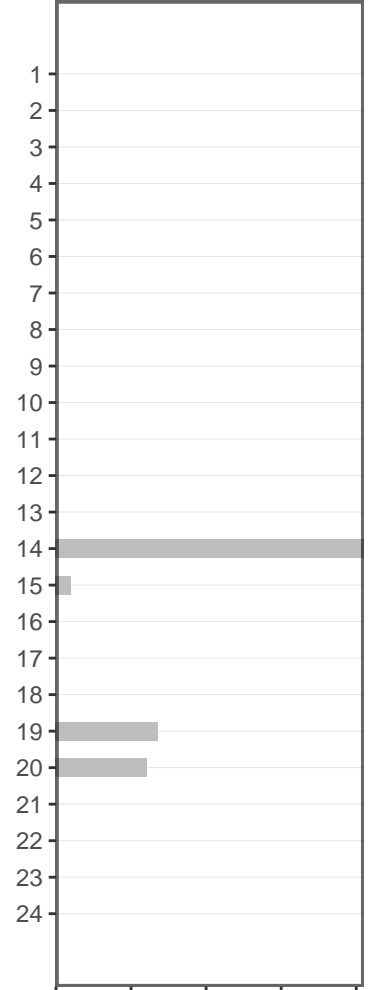
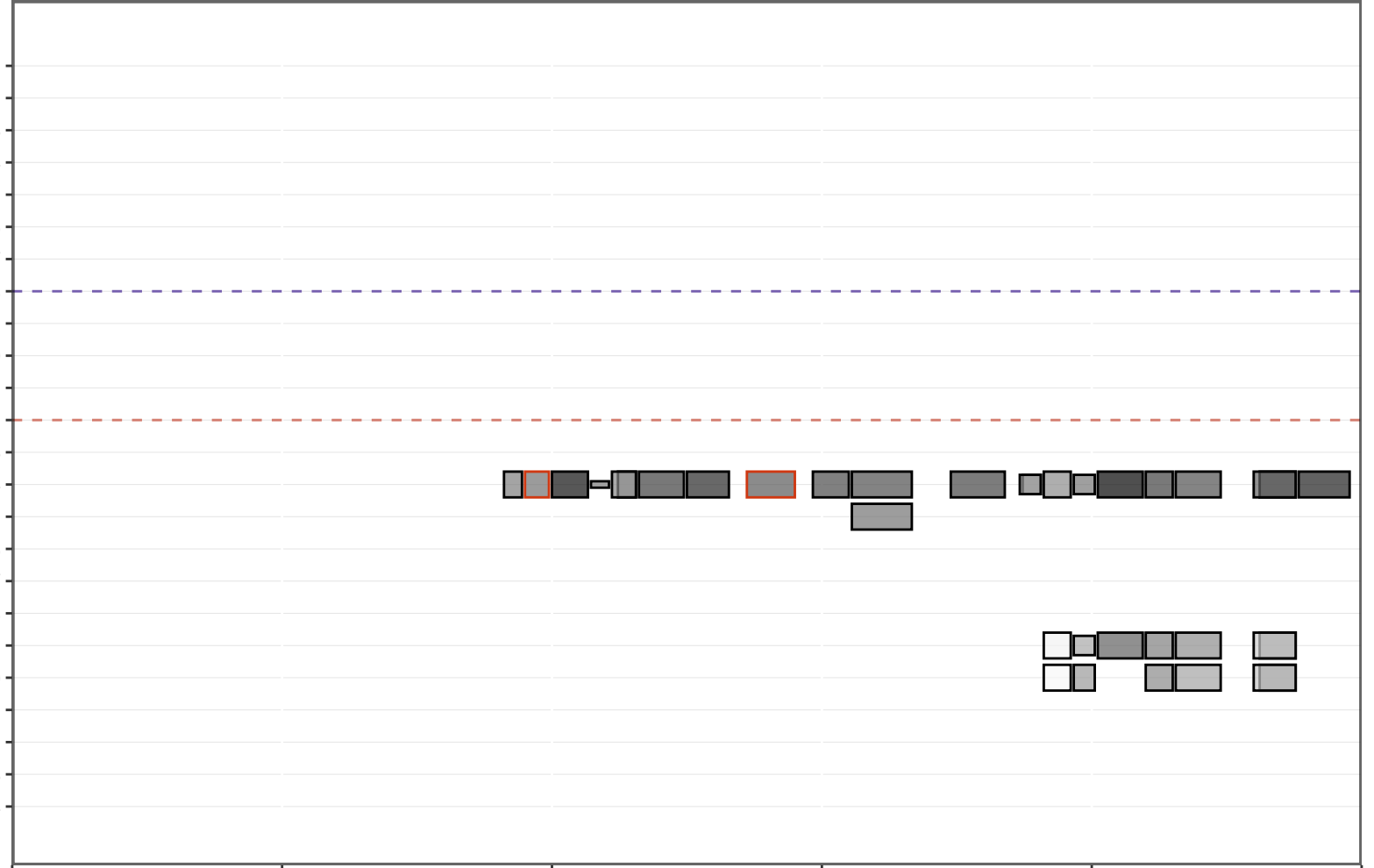
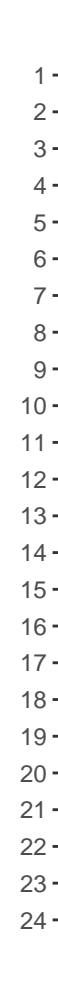
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

'SDAGETVQR'PLSSGLPQDMYYKATGKSAEMVTDDEGAYVTSNKGYNWKAAGETVSATLNRTVSSGGISGASYVTGTFSTVNRSPDGRVYVWSRSGNFYLTWEPGGAYWQPHNRSVARRKQNMGWADGGLLWLLRGGGLYLSKGTGLSEDFEESVDSRSGFLELVGYSQDEAWAAGSGSILLKTRNGGKTWIRDKAADNAANLYSVKRFINDNGGFLVNDGVLKLYLG'

NbL04g06030.1 pyruvate_kinase_cytosolic_isozyme [MW = 54.99 kDa]

No. of times detected



log(intensity)



Values from



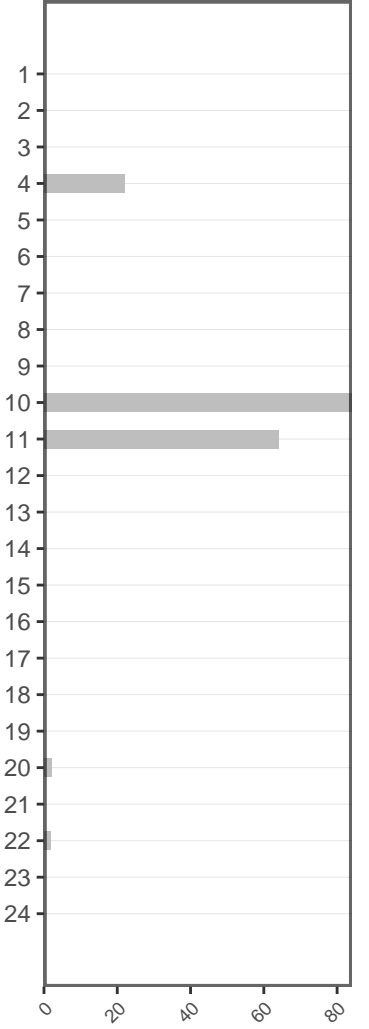
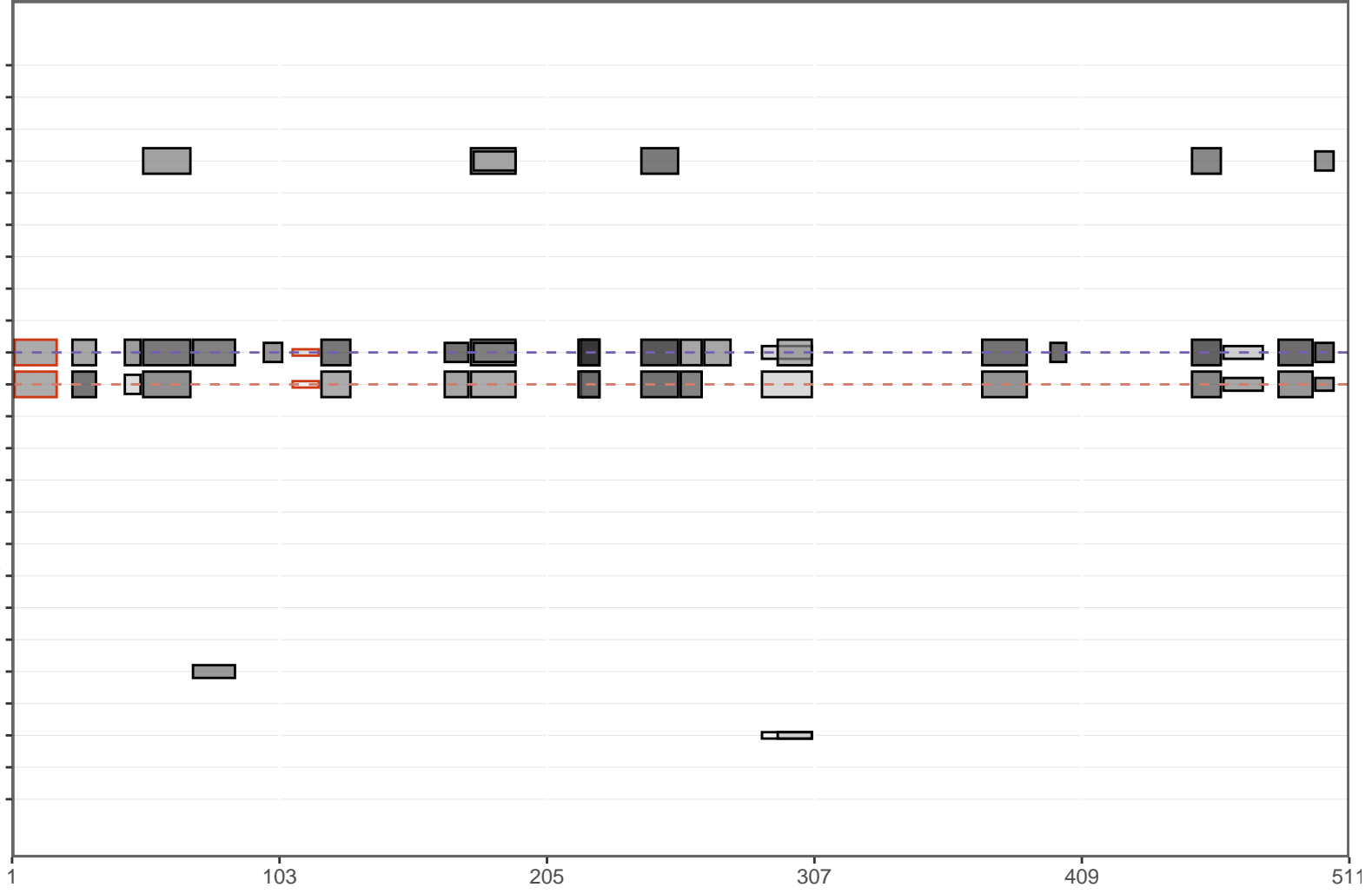
MW indication



Molecular weight

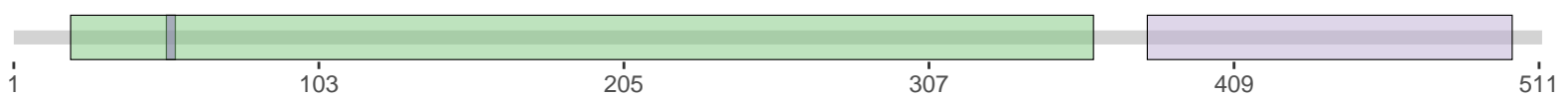


Gel Slice



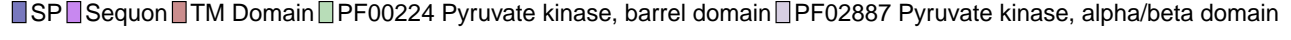
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VENQEGVYVNFDEILRETDSEFMVARGDLGMEIPVEKFLAGKMMIYKGNLVGKPVVYATQMLESMIKRPRPTRAEATDVAANVLDGTDGVMLSGESAGAYPELAWKIMARIGEAESLQGAIFKEMRSTPLPMSPLESLASSAVRAANKANAKLVVLRTRGGTTAKLVAKYRVAIVVGVVPLVLTDSGDFWRFDETRARHSLIYRGLIPLLAEGGSAKATDAEESTEVILGASLKSATEKGLGTPGDVWALHRIGAAEVKIKLVK

NbL04g05680.1 uncharacterized_LOC109225794 [MW = 39.85 kDa]

No. of times detected



log(intensity)



Values from



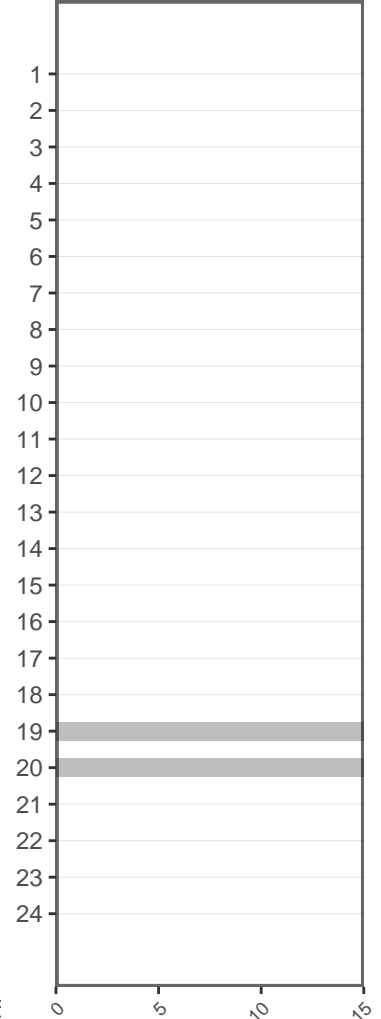
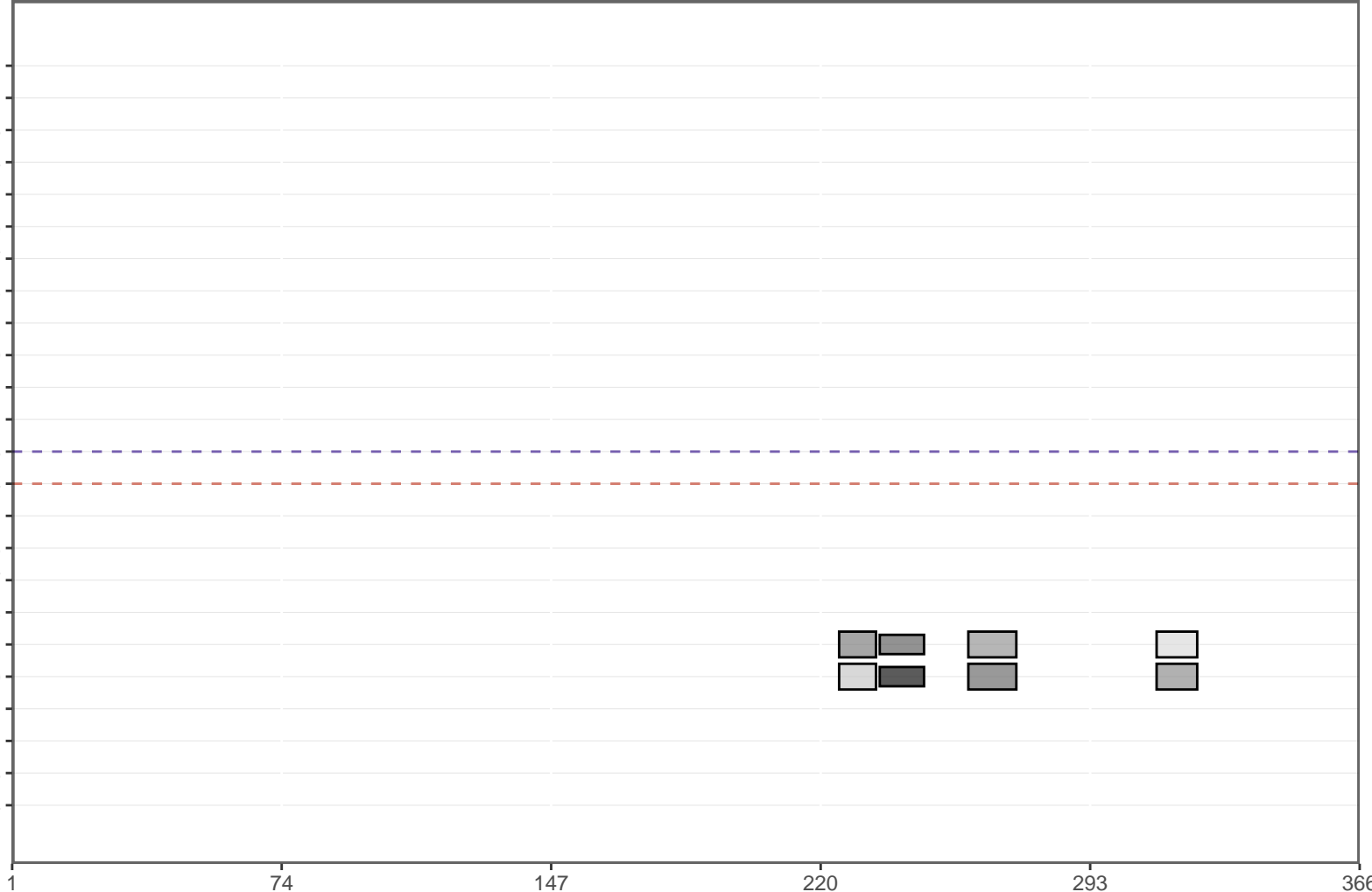
MW indication



Molecular weight



Gel Slice



Protein length

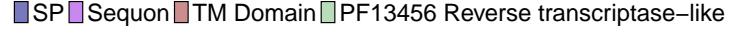


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SRGGMPERMPKRRGDEVMLESECTDMVGSVAIENDFLRKHVLLDDHKVQGAIPGRGCTLEFDGAEKGNPGLAGAGAVLRADGGSPRRLREGLVGATNAAEYRGIHLGLKVALSKGFTNIRVGGDSKLVCMQIGLWVKNQNIETLYEQAKLQKDFLFRHIIHLRENSDADVQANLGVLEAGGIGEEIK*

NbL04g05200.1 probable_inactive_purple_acid_phosphatase_2 [MW - SP = 70.79 kDa]

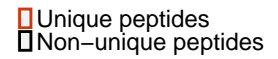
No. of times detected



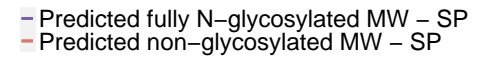
log(intensity)



Values from



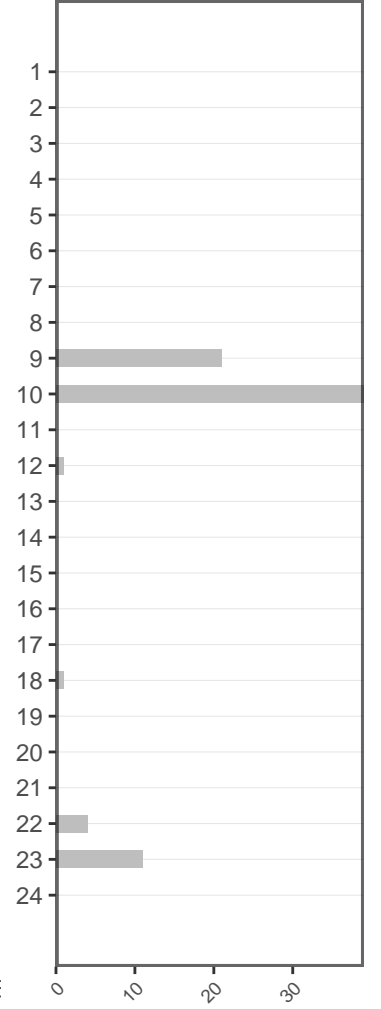
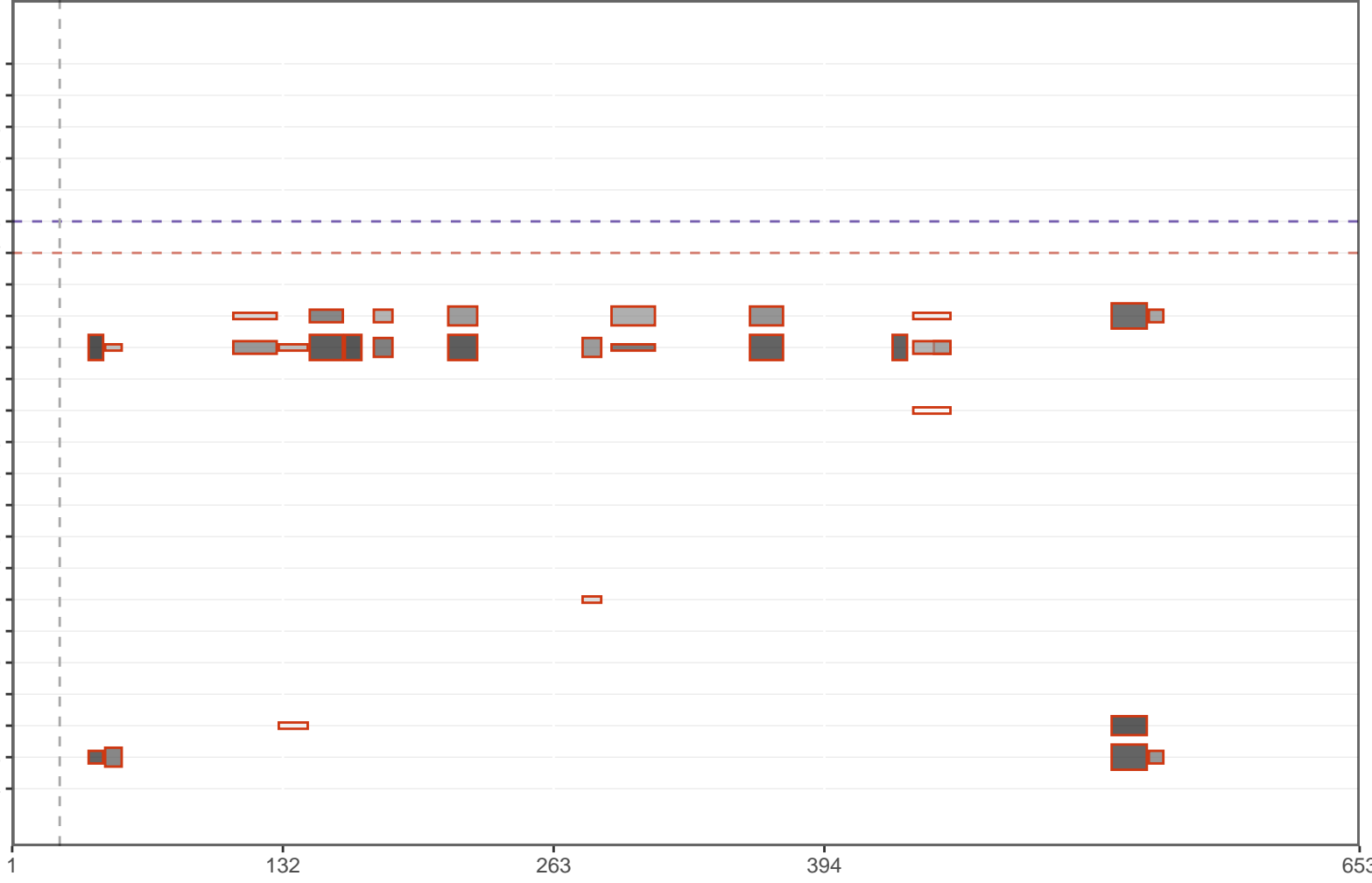
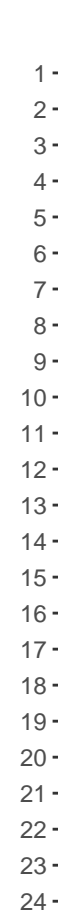
MW indication



Molecular weight

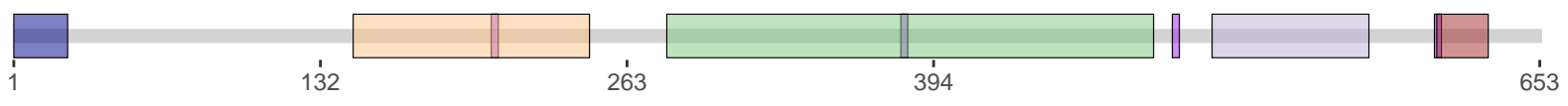


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

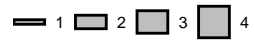


Protein sequence:

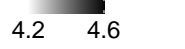
LDNFFSQVEPLASRNPPYHVDIGNHEYDQPLQPKWQWBSRLVGTGGGEGGVYSLKFKHMPGNSSEPTGMRAPATRNLYFSFDGSGPVHIVVMSTETNLFQSGS69YDFLKHDLSEVDRIKTFPIVFDGHRPMYTTSEKKDAPIREKMLAHLLEFLVNNHVNVLVWGHVHRVERFDPLNFTGSSGLDGKEWKAFFMHNVIGMAAGDGDWQRPVNHFTDPRVPGPVGSLYRGDFEGYMLRHATKEKLTFSYGNHDSGEVHDIVTEILASGGVNLGGSHDGHATMEI

NbL04g05180.1 PLASMODESMATA_CALLOSE-BINDING_PROTEIN_3-like [MW - SP = 27.13 kDa]

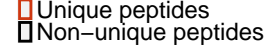
No. of times detected



log(intensity)



Values from



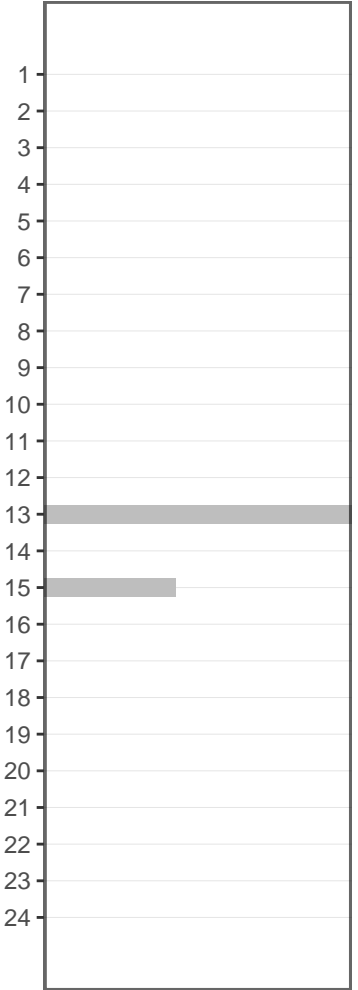
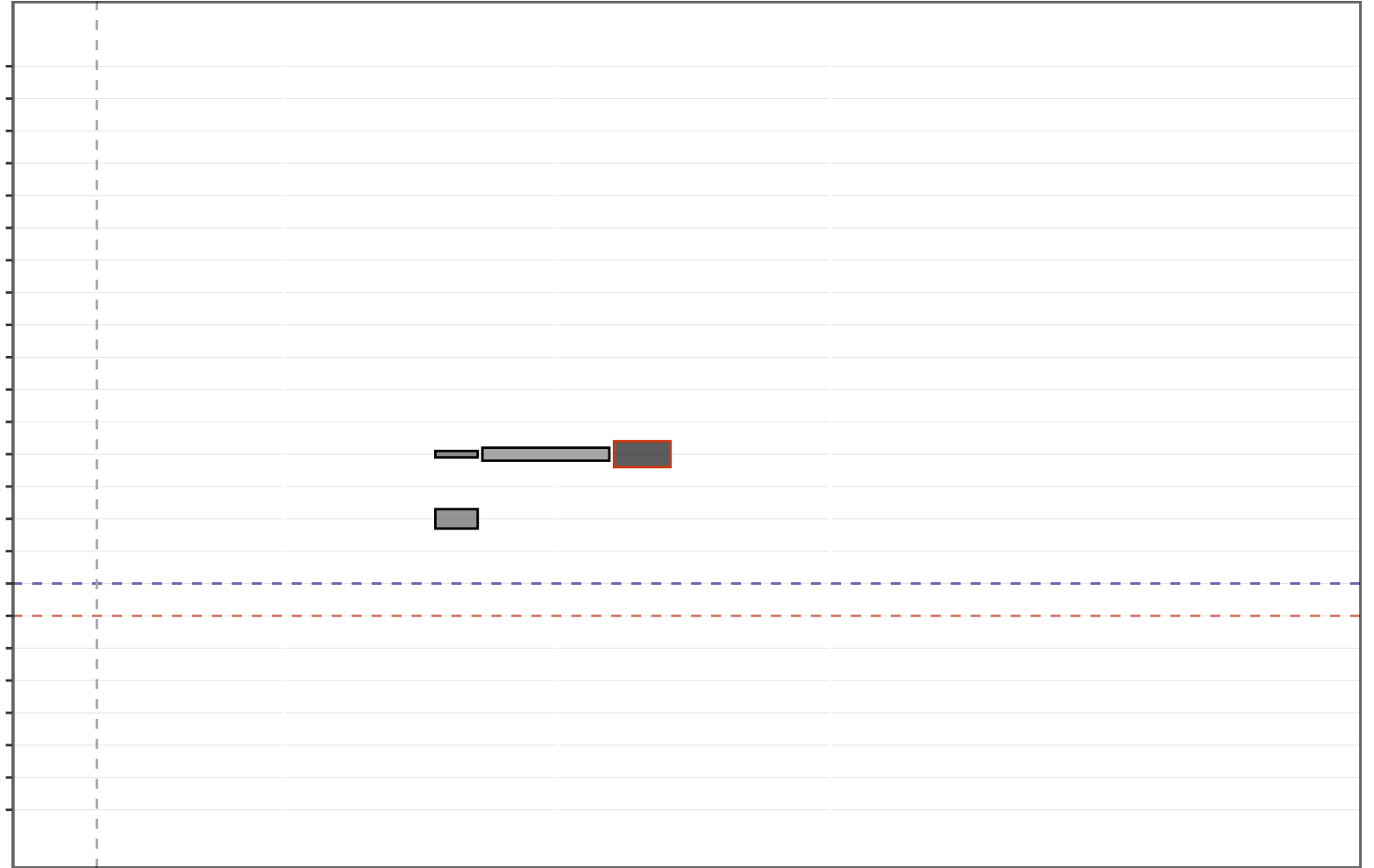
MW indication



Molecular weight



Gel Slice



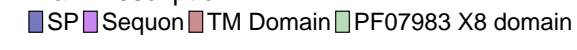
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IYVNSYQRKGAAGASGDFSGTATTEPNPPTTGGGGVGGSTGNTGGGGSTTTPAPGGSTTTPVPPGSTTTPVAPPQTTPPTAPPQTTPGIGTGGTGTGIATTPGNTNPFVFGPGSGGGIENTDGNAAGHFRNSIFLALLAISLGLRA*

NbL04g05120.1 alpha-14-glucan-protein_synthase_[UDP-forming]_2-like [MW = 41.35 kDa]

No. of times detected



log(intensity)



Values from



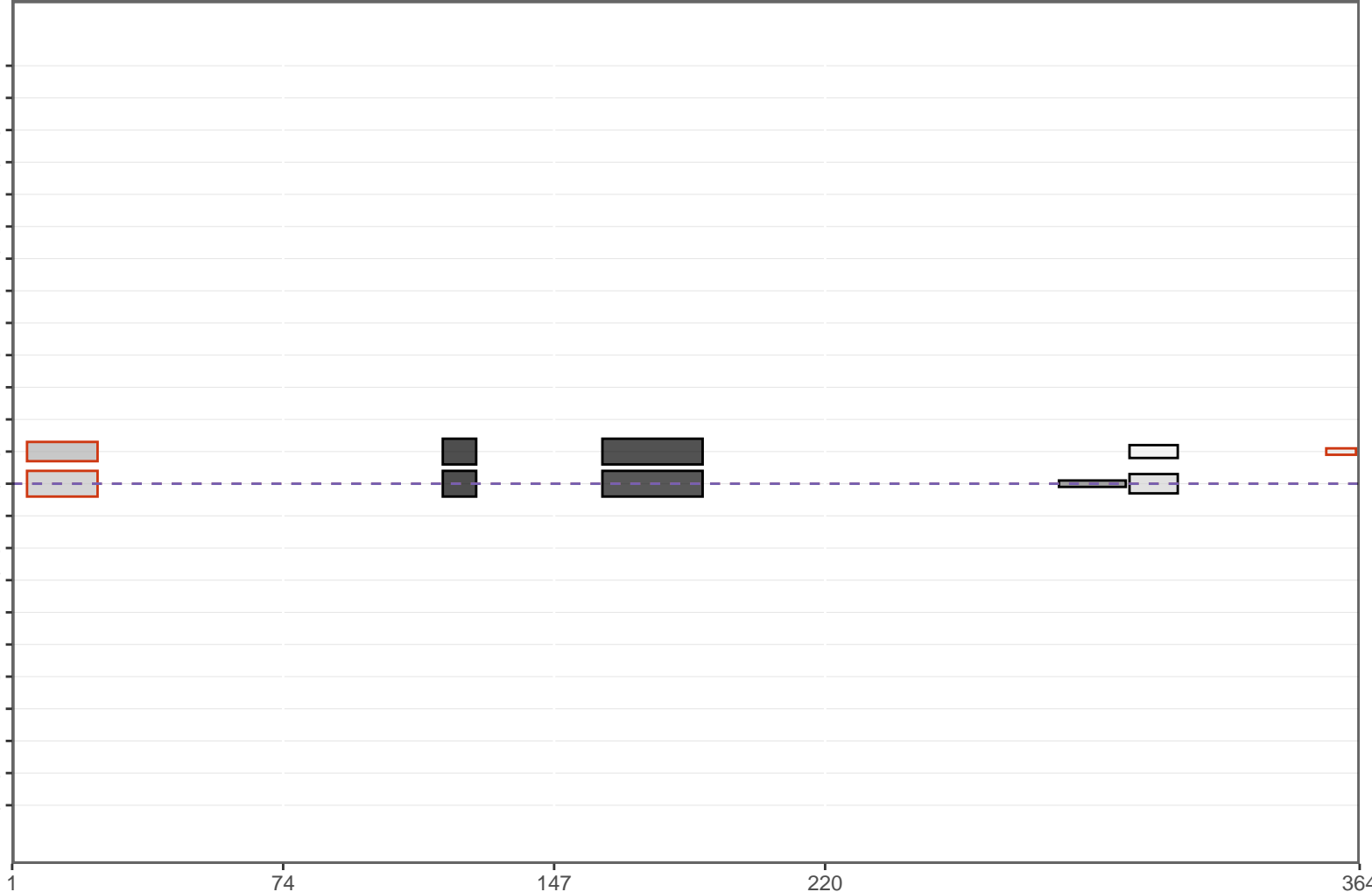
MW indication



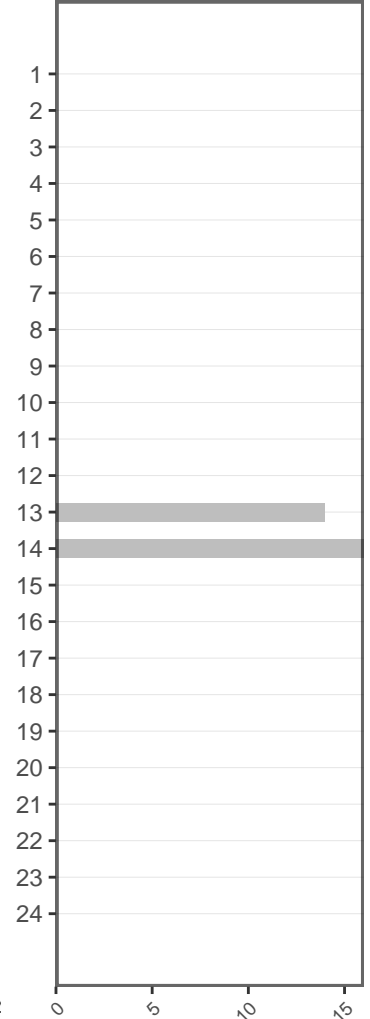
Molecular weight



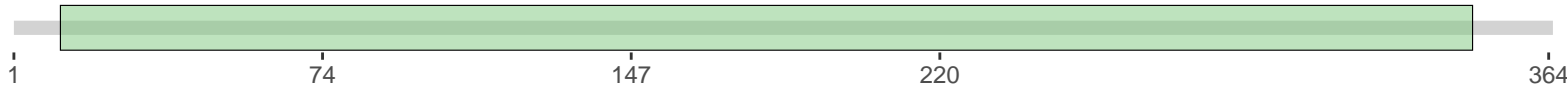
Gel Slice



Protein length

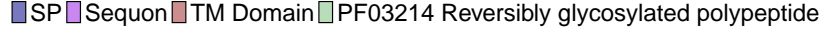


Peptide counts over 4 repeats



Pfam domains

Pfam Description

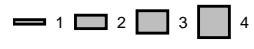


Protein sequence:

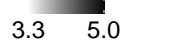
VLNIPDYDAPTCLWPRENTRVDAVMTIPKGLFPKMGMLAFDRELIGPMVYGLMDDGQPIGRVYDMMWAGWTKVGDHLGLGKTKLPIYHWSKASNPVNLKKEYKGIYWGEEIPFFQSATLFPKDCTEVGGQYIELSGVNDKLSKVDPIYFKLADAMVTWEAWDELNPTSEGLAKLSISNGPKA

NbL04g05090.1 translin-associated_protein_X [MW = 33.65 kDa]

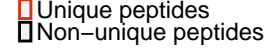
No. of times detected



log(intensity)



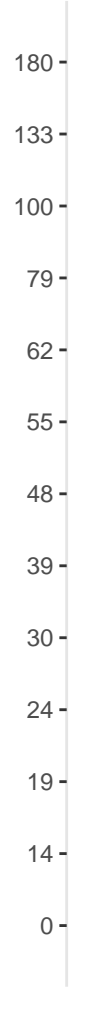
Values from



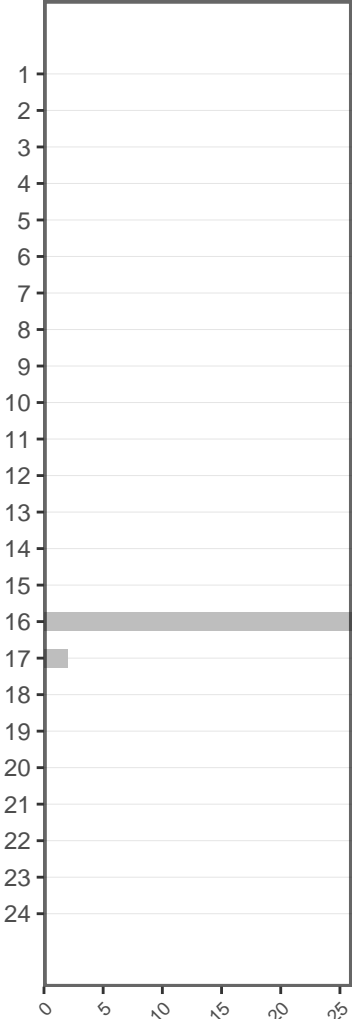
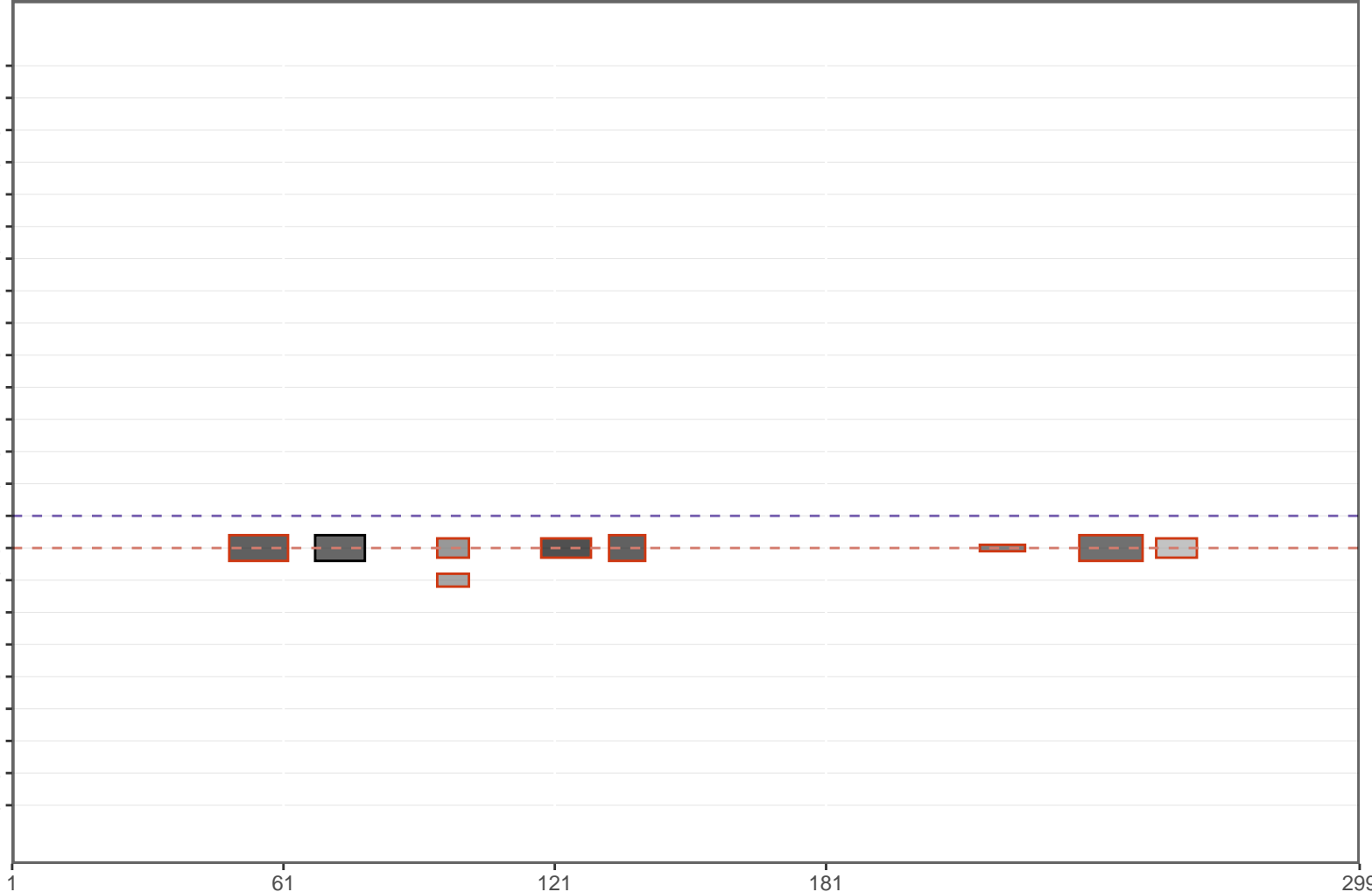
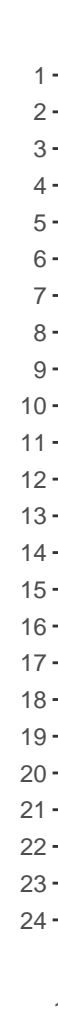
MW indication



Molecular weight

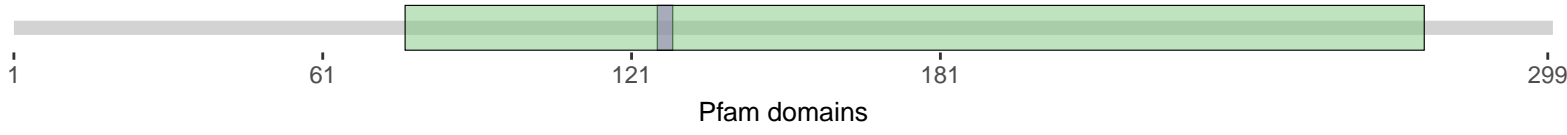


Gel Slice



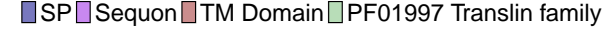
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

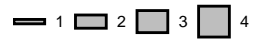


Protein sequence:

CGTDFWKLRRAYSPGVGVEVAATLGNFGTGTGLTLDEINAAFLPLSDPSVEFLQNLQVLDVGLGADLTGELMRLAIGRISEGELOFAEKICGFVREIYRKLFLIAPEMDDPSDMKQKMETMLQGVMMKIENACFSVHYRGEYIPLGSAEFSYLLGMPDVE

NbL04g04980.1 protein_PHYLLO_chloroplastic [MW = 157.84 kDa]

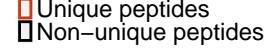
No. of times detected



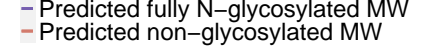
log(intensity)



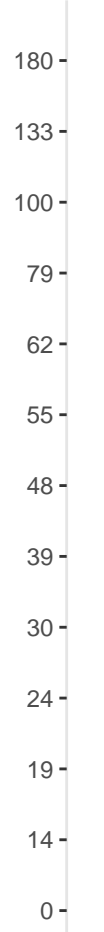
Values from



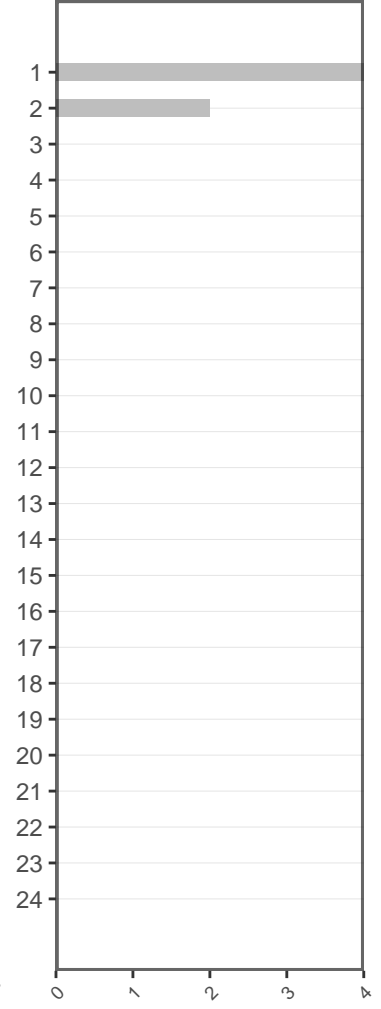
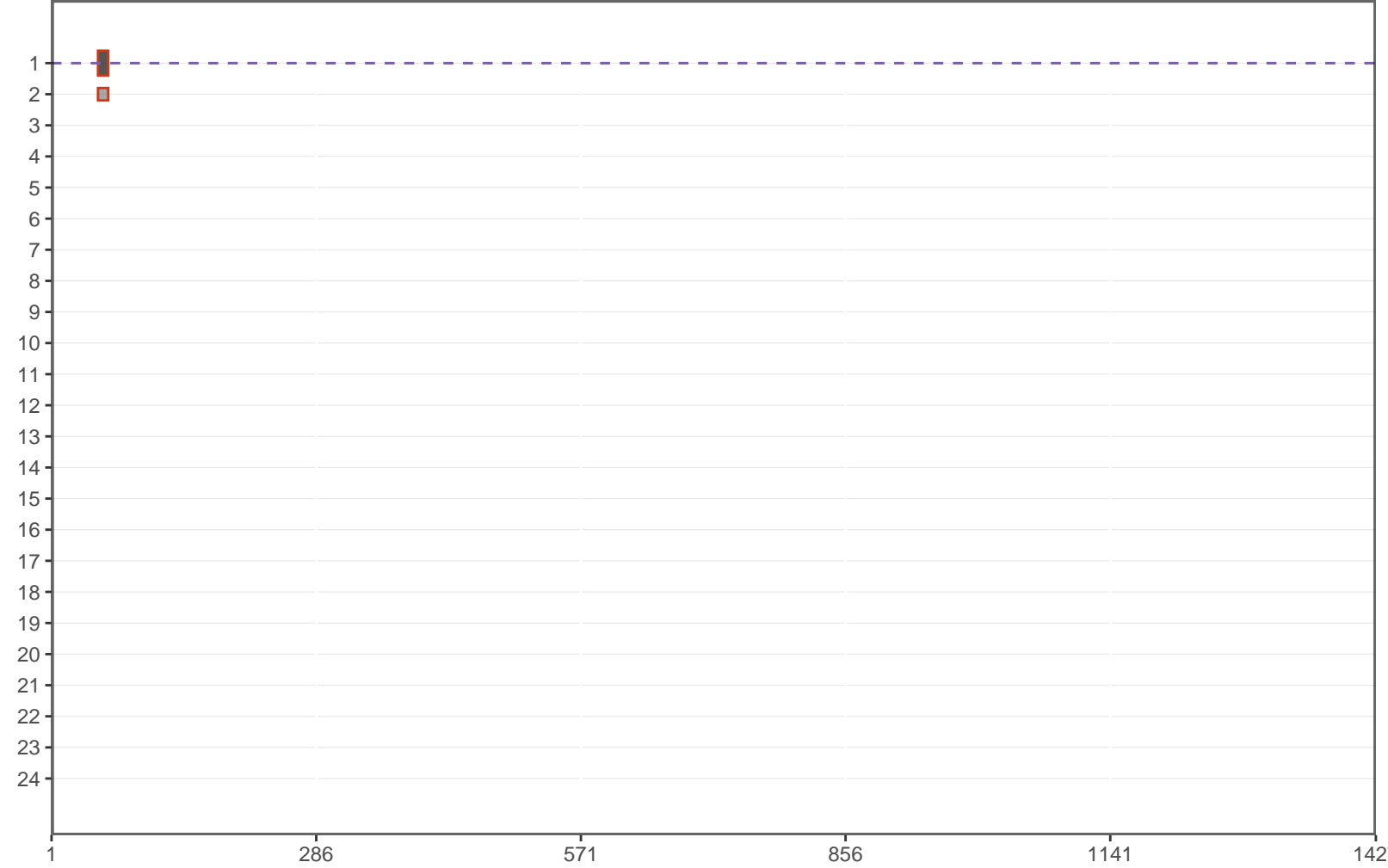
MW indication



Molecular weight



Gel Slice

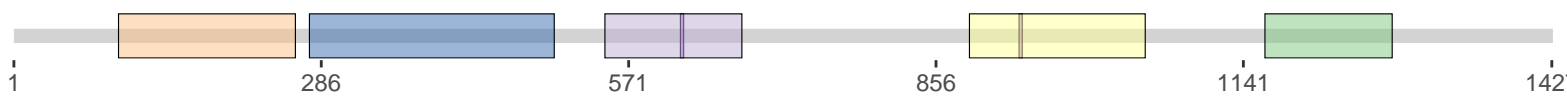


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

- SP
- TM Domain
- PF02775 Thiamine pyrophosphate enzyme, C-terminal TPP binding domain
- PF13378 Enolase C-terminal domain-like
- Sequon
- PF00561 alpha/beta hydrolase fold
- PF02776 Thiamine pyrophosphate enzyme, N-terminal TPP binding domain
- PF16582 Middle domain of thiamine pyrophosphate

Protein sequence:

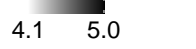
AFNRFSKLVNLSMINDGLSSKVGKMGYSKYRIQLGSPPTSSSAIHSTYHREGFISLFLEDGNTGYGEVAFLEHKNLLDVEEQLGLMHVVEGVADHFLPLLRGQSFRRWVHSLGIGQNPSPVRFGLMEVNLNAAAREGSSLLNVLVQGTVEGTGRSFDVYVGALEENGGPNEMALWATTLVKEGFTAKLKVARGADPTVDIAIKERIKGVSWIEELRADANRISWNYDEAAKFGLSKDSGLQVIEEPVNDADDHDKFGEETGLPVALDETNSRKNHLLKVLAKYTHP

NbL04g04780.1 acyl-acyl_carrier_protein_thioesterase_ATL3_chloroplastic-like [MW = 24.1 kDa]

No. of times detected



log(intensity)



Values from



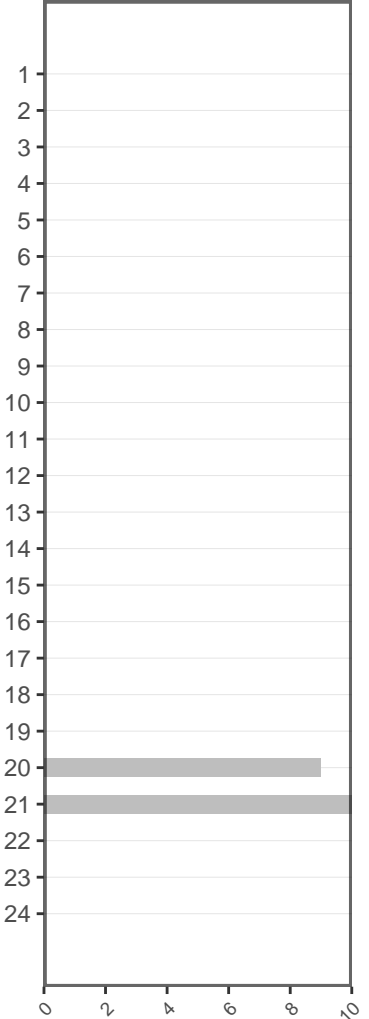
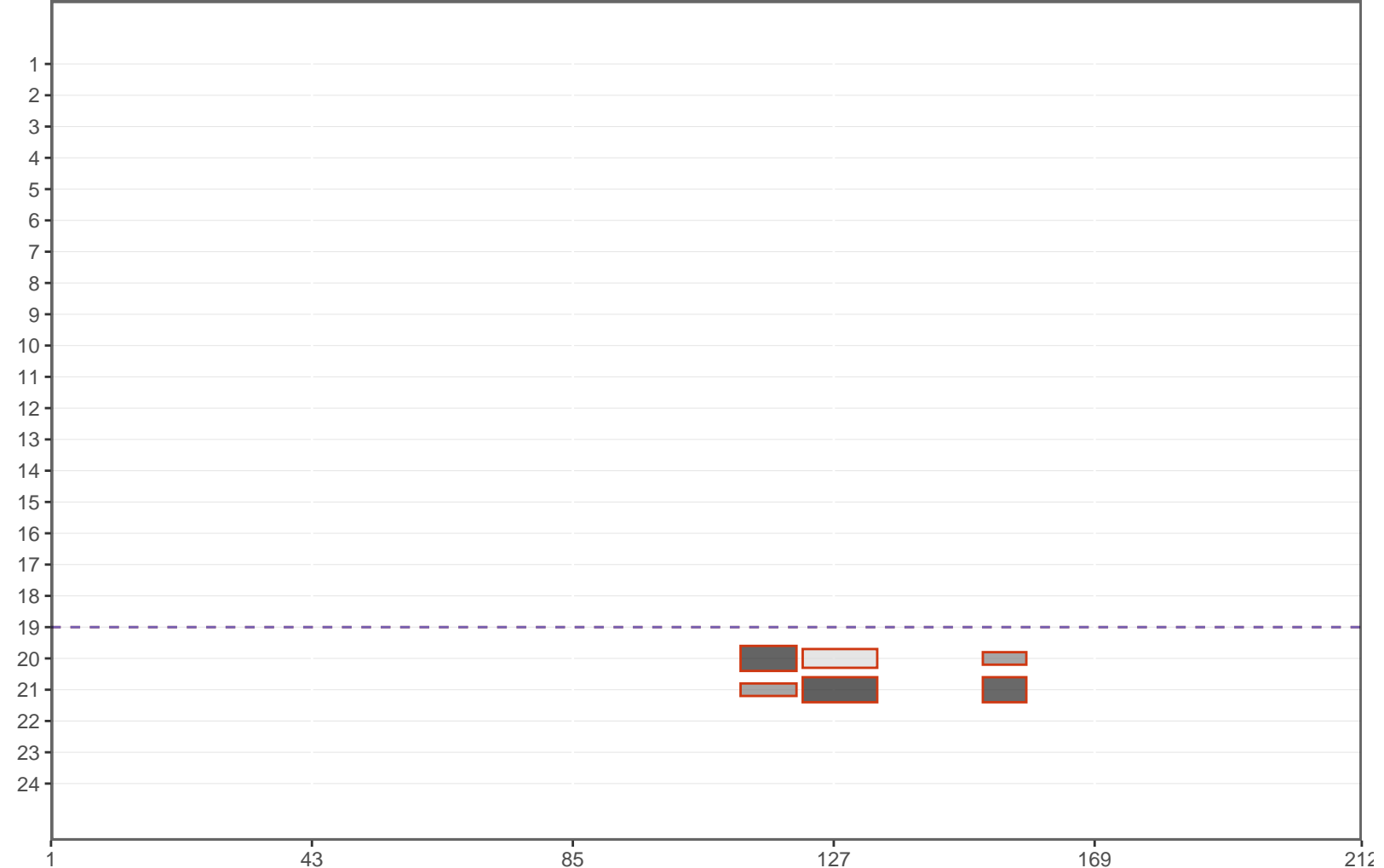
MW indication



Molecular weight

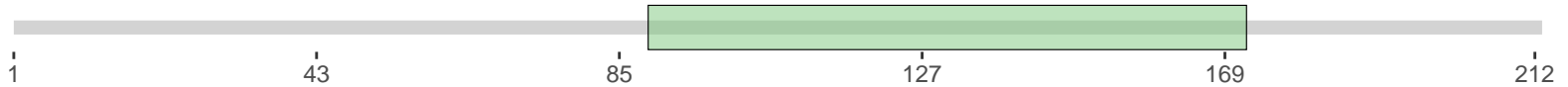


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VNNAIAYSYCHCRHELLERLGVSDAVARNGDAMLTDLGSKYLAPLRSGDRFVWVRIDDSAVRLLFFEHFIFKLPDGGPLEATGTAWLWLNKYNRPVRIAEFRKPKVQFLRQESK

NbL04g04700.1 acetylajmalan_esterase-like [MW - SP = 37.62 kDa]

No. of times detected



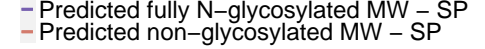
log(intensity)



Values from



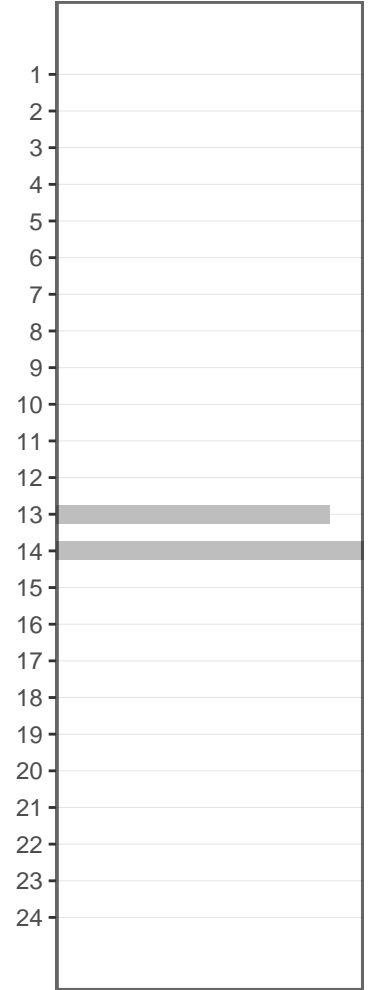
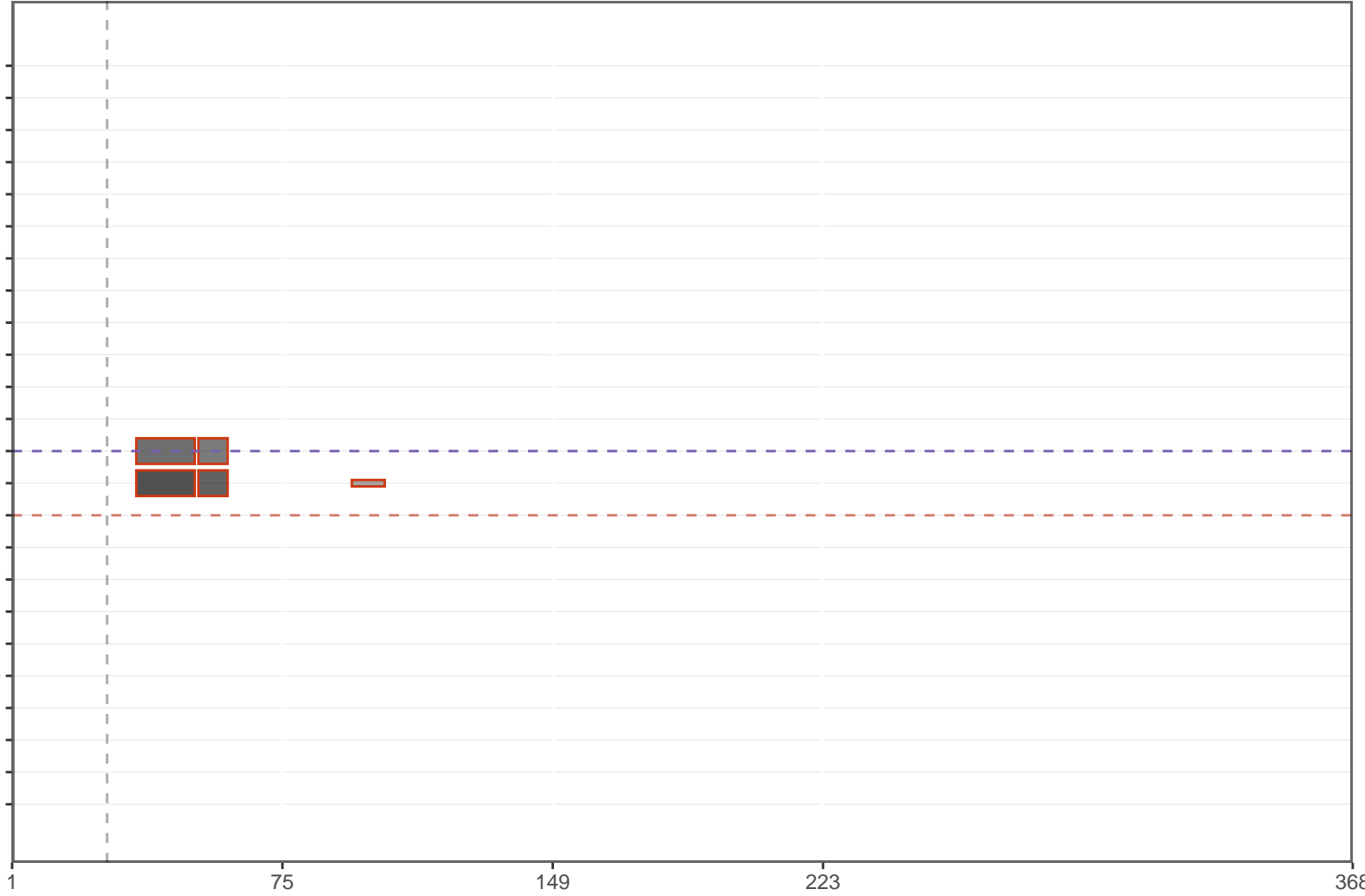
MW indication



Molecular weight

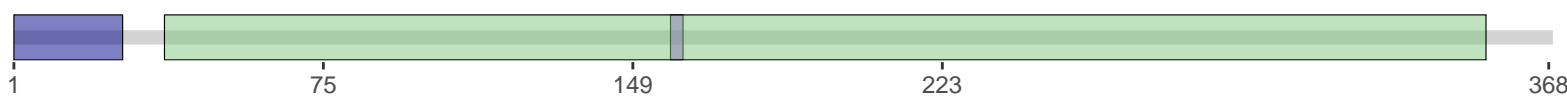


Gel Slice



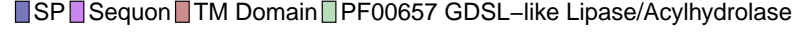
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

EWGGNDYINGFFGRKQLPEVRTYVFFVAGIMRSIKDHLGATRIIVPGIYVGLGLFLVLTFFDSENANGYDQLGCLRNVNDFABYLNRLGLASLGRQGFVRIIVYGDHYGALLTLRSPSSFGFNGLTLTADCGTGGRYNFRFRVCGSASVRCADENWQYVHWGHLTDEAHRHMTDIAVVDLLRFSCTV

NbL04g04560.1 ATP_synthase_subunit_beta_mitochondrial [MW = 59.81kDa]

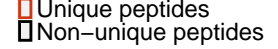
No. of times detected



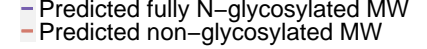
log(intensity)



Values from



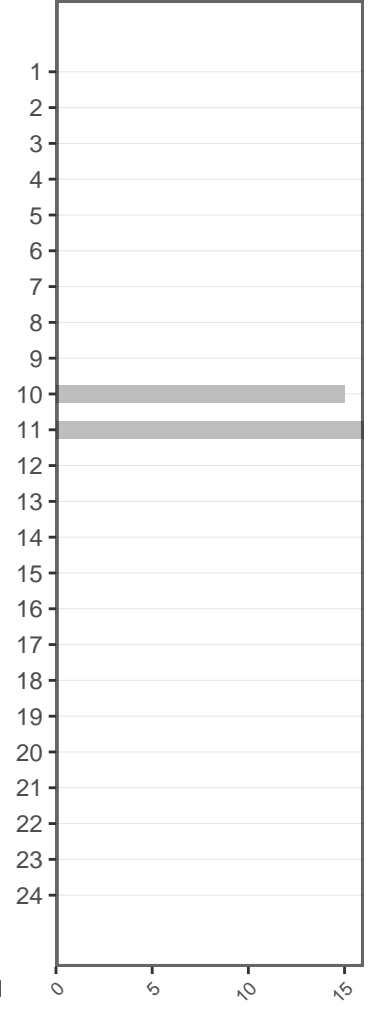
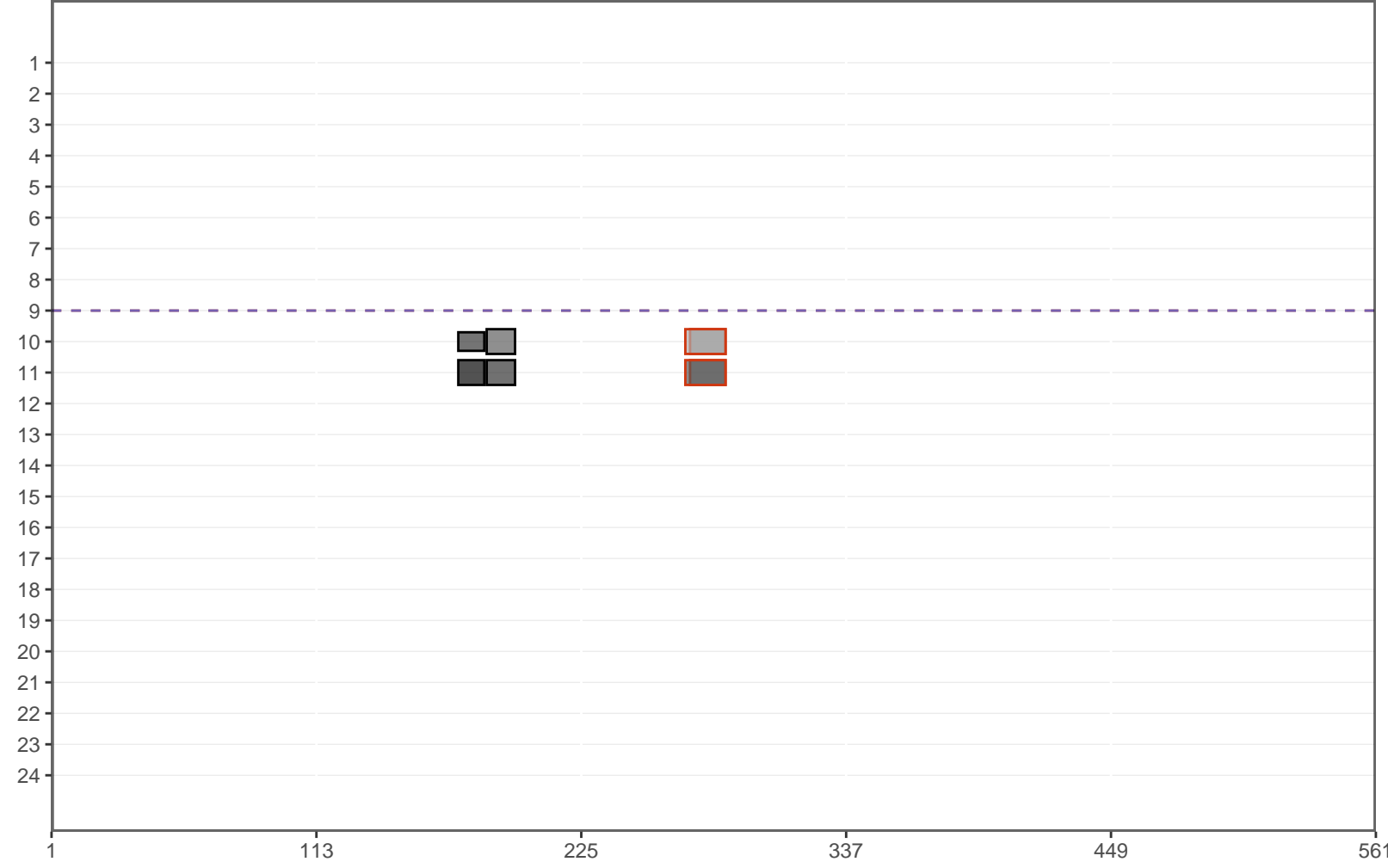
MW indication



Molecular weight



Gel Slice

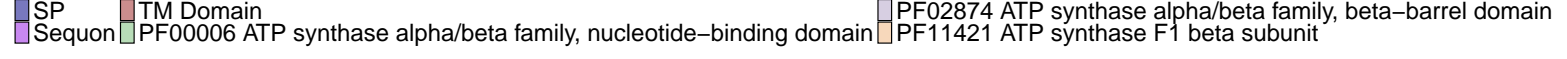


Protein length



Pfam domains

Pfam Description



Protein sequence:

RTREGNDLYOEMIESGDKLGEKQSEKGAALVYGMNEPPGARARVGLTVAEHRDAEGDDLLFDFNFRFTQANSEVSALLGRIPAVGVQPTLATDLGGLGRIFFTKKGSITSVDAIYVADLTDPAWTFFAHLDTTVALRQISELGGYVWDLPLDSTRMLSPHLGEGHYNTARGVQKVLQNYKLDGHALGMDLSEDDKMTVARARKIQLSGQPHVAEVFTGAPKVVDLKESINFGQVLDGKYDDLSEQSFYMWGGIDEVIAKAEIKAESAA

NbL04g04320.1 kirola-like [MW = 18.71 kDa]

No. of times detected



log(intensity)



Values from



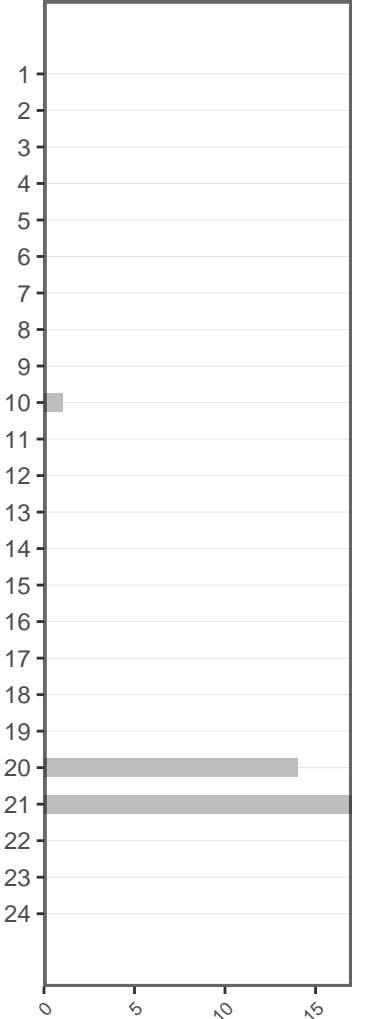
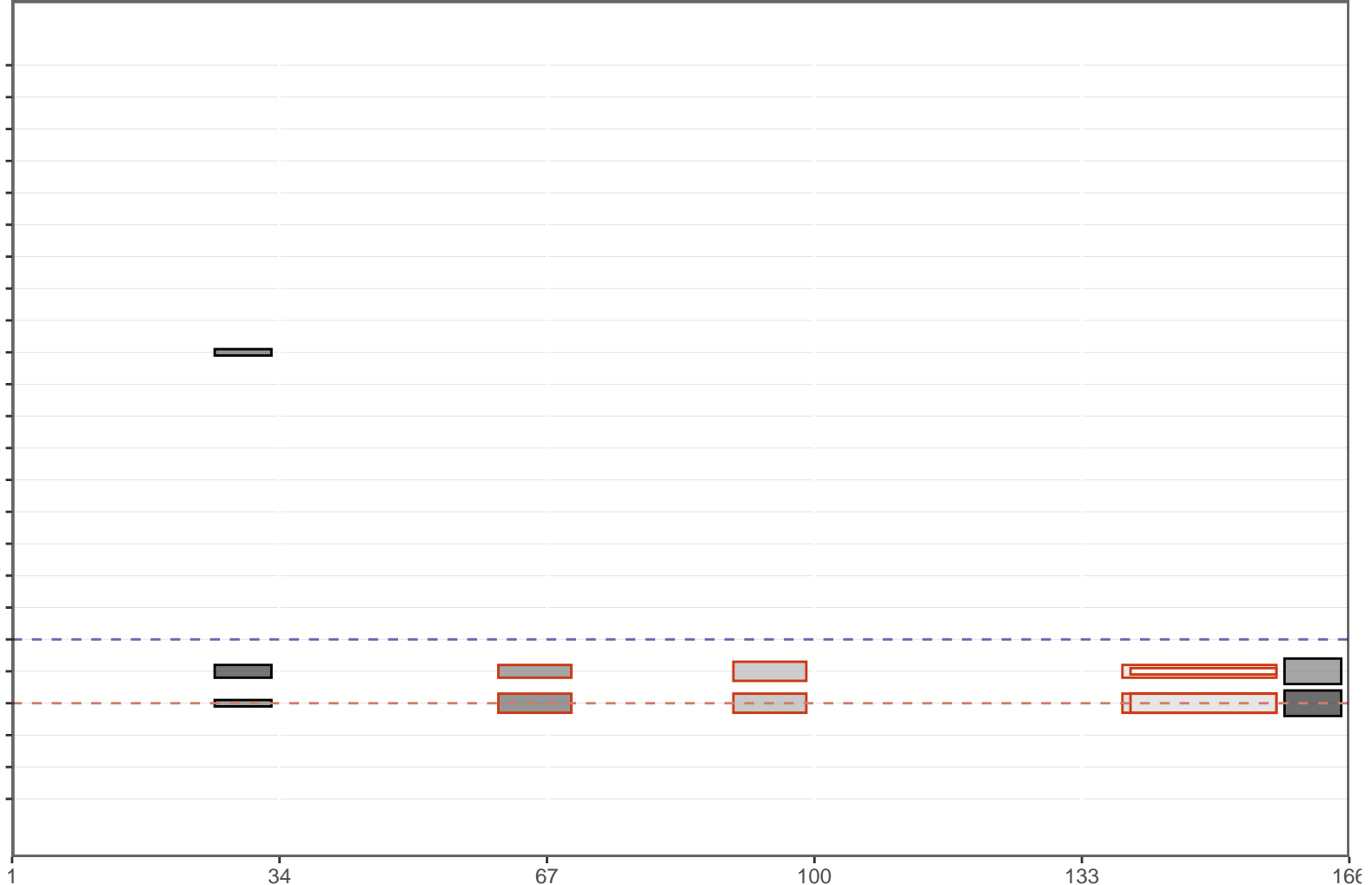
MW indication



Molecular weight

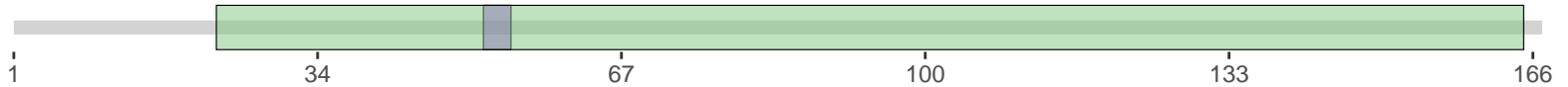


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

/GSVSYWKYNDGKDKKGVIEAVDQKKGKBITWVKVIGDGLLESYNSFTITTSHQHQWTTWTFVYEKKTEDTPEPLVPLGLLHNTKDIQGHLLK

NbL04g04200.1 HMG-Y-related_protein_B-like [MW = 21.16 kDa]

No. of times detected



log(intensity)



Values from



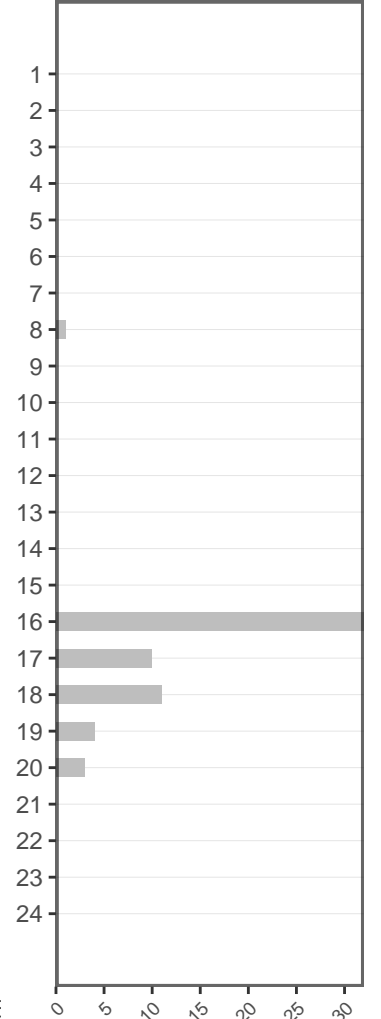
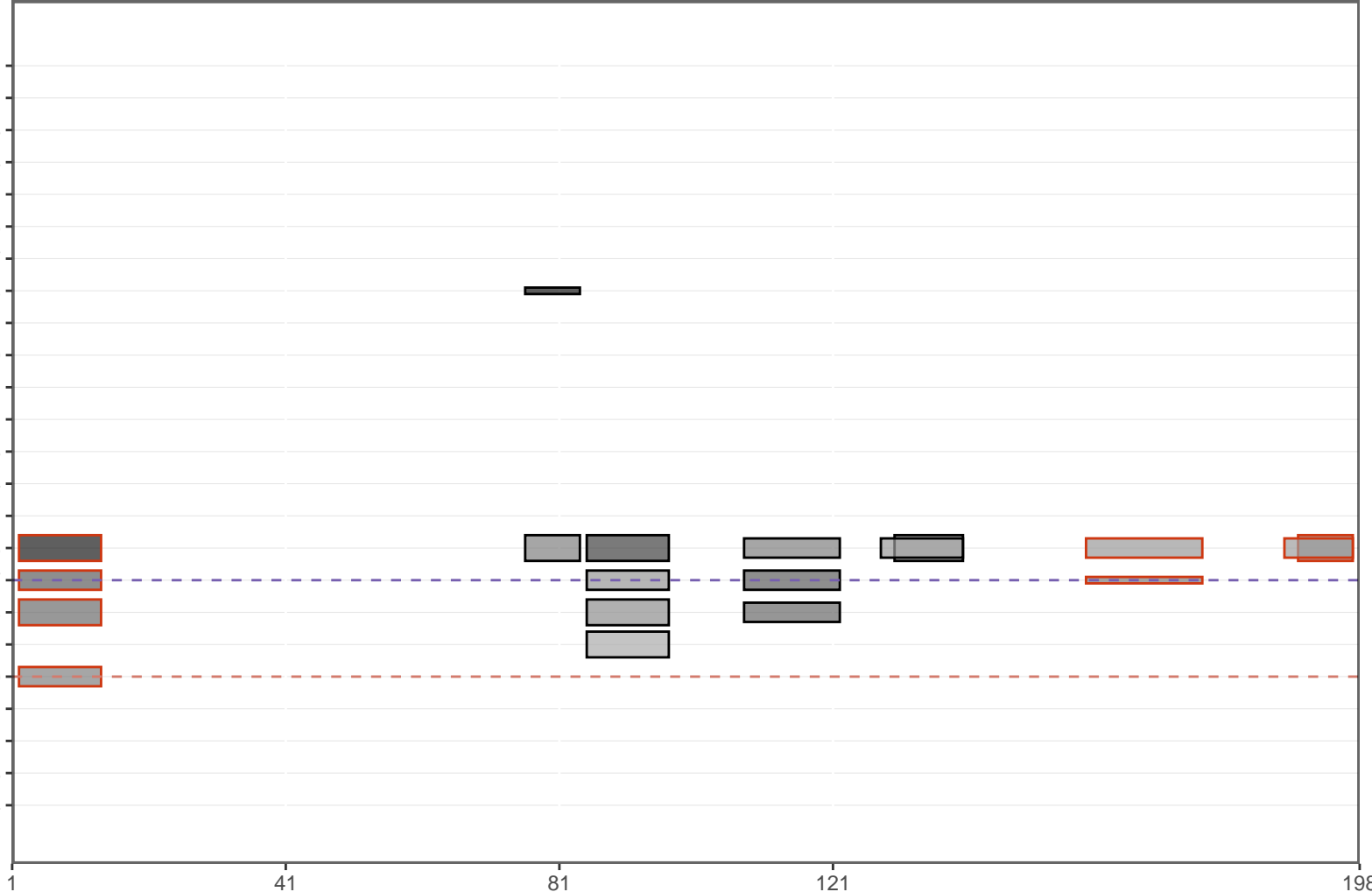
MW indication



Molecular weight



Gel Slice



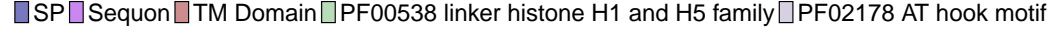
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

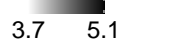
IKPDNAPRRGRGRPPKPKAPLPEGVVPPPPRRGRPPKERRDPHAPISVFMKVTSPSSGGTGKKRGRPRKYPNDTSSPSAVLPPRGTFRGRGRPPKVKTPVAEEVA*

NbL04g04190.1 glucan_endo-13-beta-glucosidase_3-like [MW - SP = 52.07 kDa]

No. of times detected



log(intensity)



Values from



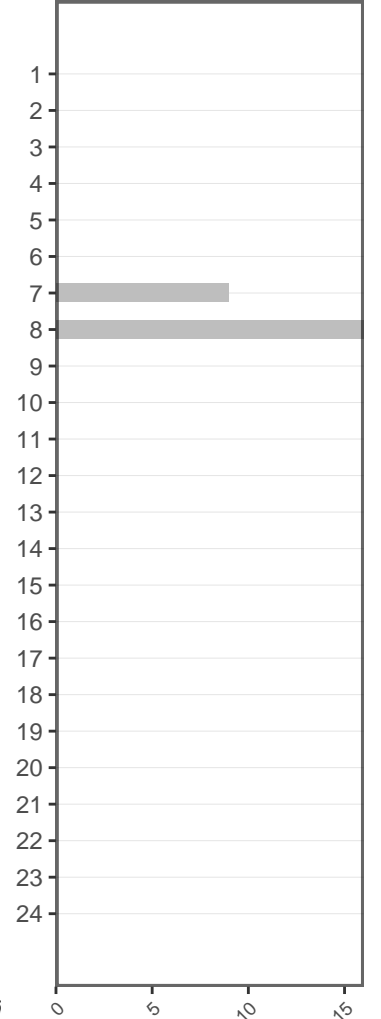
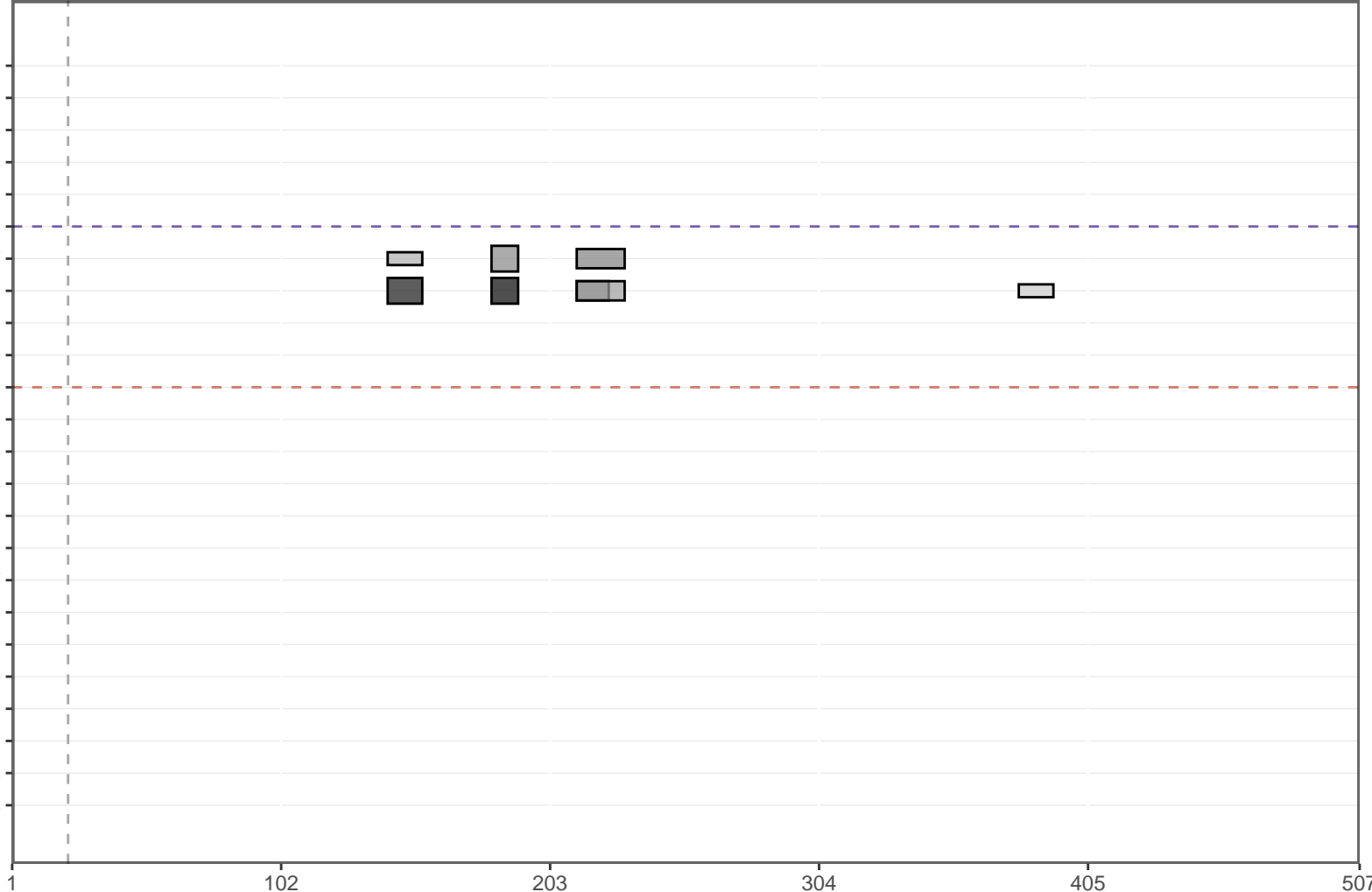
MW indication



Molecular weight



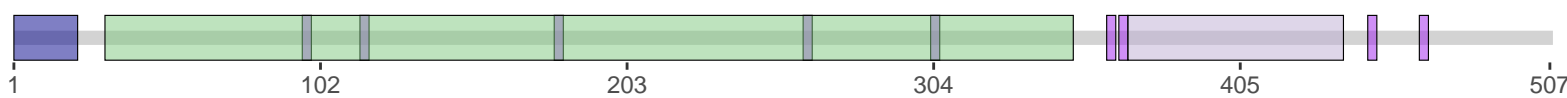
Gel Slice



Protein length

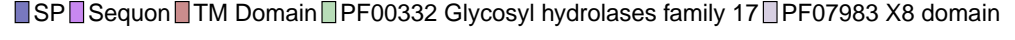


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VVFDVVDAAYTSMKYLNFNPIVTEGGWPSKGDSSPEAEALDANNTYNSNLRIRHVLNNTGTRPKPGIAISTVYVELYNEDLRHDSISEKNWGLFDSGGMPVYTMHLTGGSTVLANDTTNGTFYVAKENAEKMMVQAALDVAAGGPKVDCFTLLGGNPKVPEPNTVIAHASYAFDAYYRKMGMADGTCNFGVATVSTTDFPNSGGGIVPGSGGRTGTLTN6SSHAPSSDSTA6GCH8GQYSHDVRTFL6SLVGLVLTAAGL

NbL04g04180.1 cysteine-rich_repeat_secretory_protein_12-like [MW - SP = 27.31 kDa]

No. of times detected



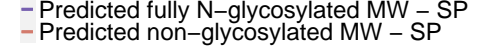
log(intensity)



Values from



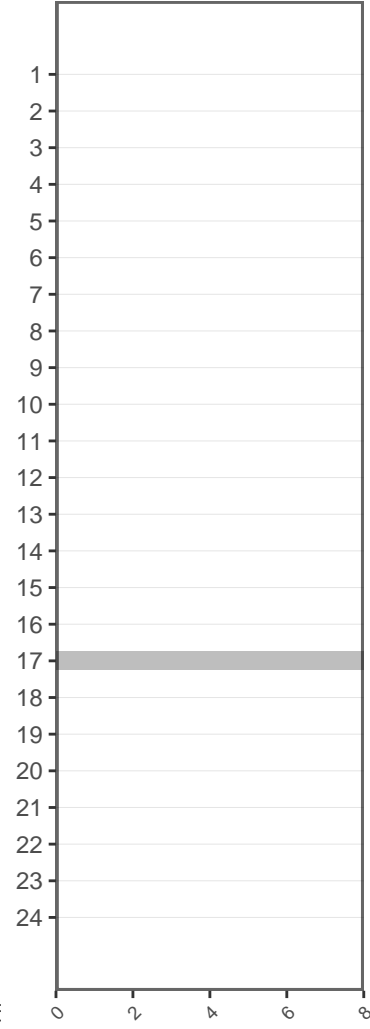
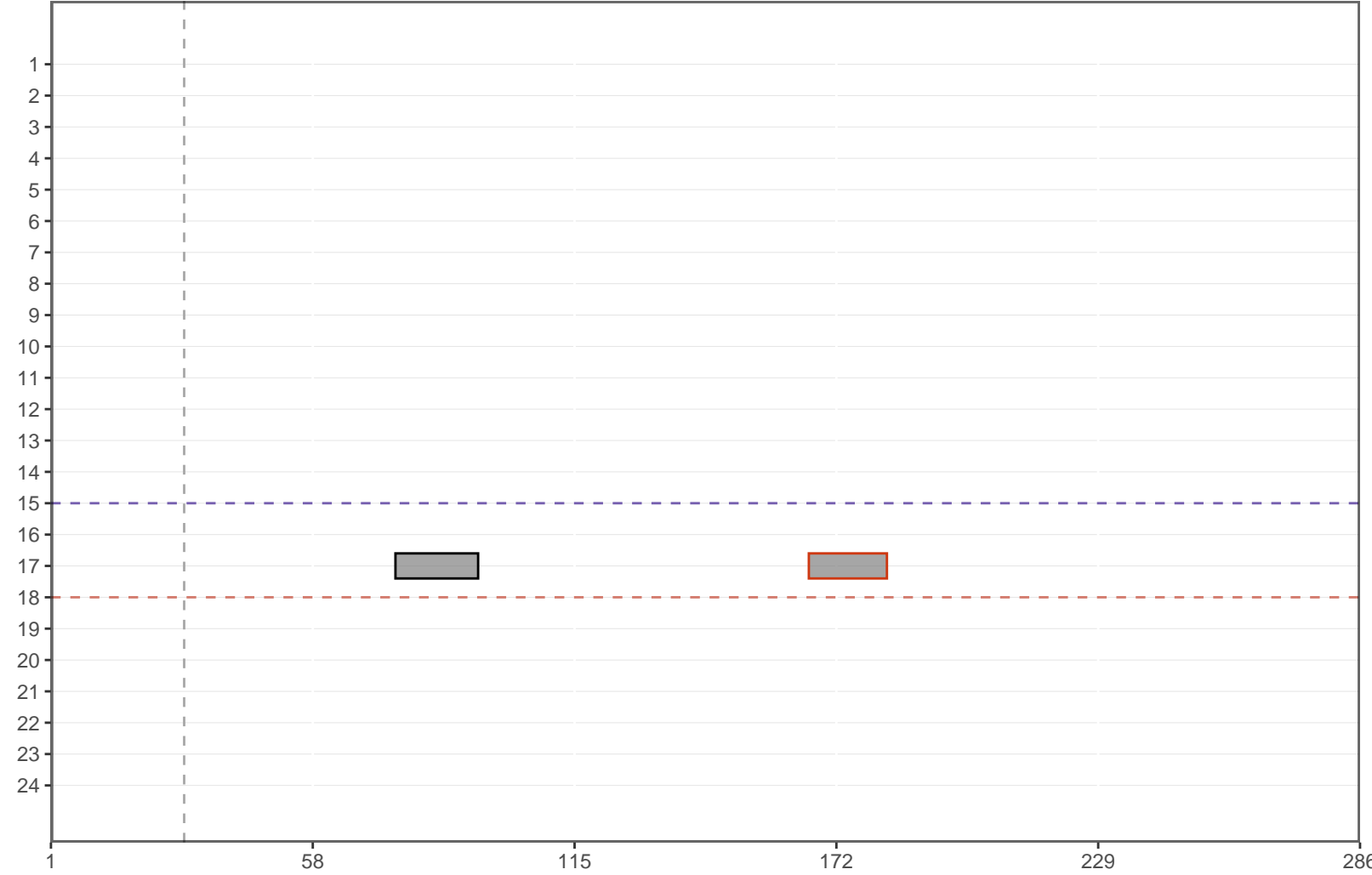
MW indication



Molecular weight



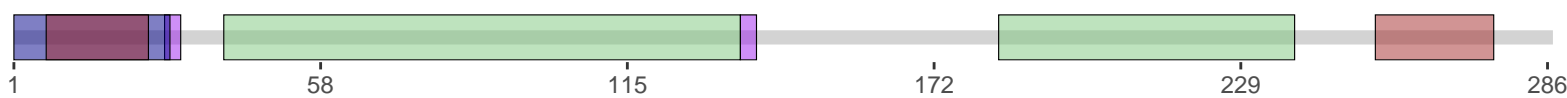
Gel Slice



Protein length

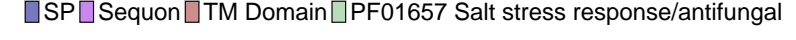


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LVKYNV/SFLGVEKGVVMMHKDGPSSMDNEMLTRNDVAVLTYLGVVPGQGFYFRVGGSSGKQVAAGCTQDLVSGEGDDGLSEAIRQLKSEGGSPWGDPMFTKGVARFSEKGFSSKSGDEVEKTLAITGLIGVAVLIVFLSVLKNLGEKKGCK

NbL04g04140.1 1-aminocyclopropane-1-carboxylate_oxidase_homolog_4-like [MW = 49.16 kDa]

No. of times detected



log(intensity)



Values from

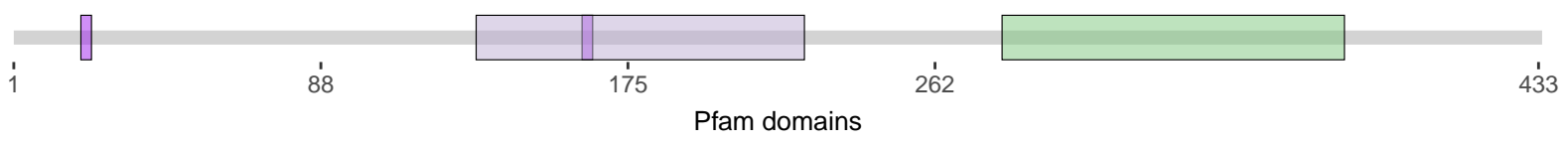
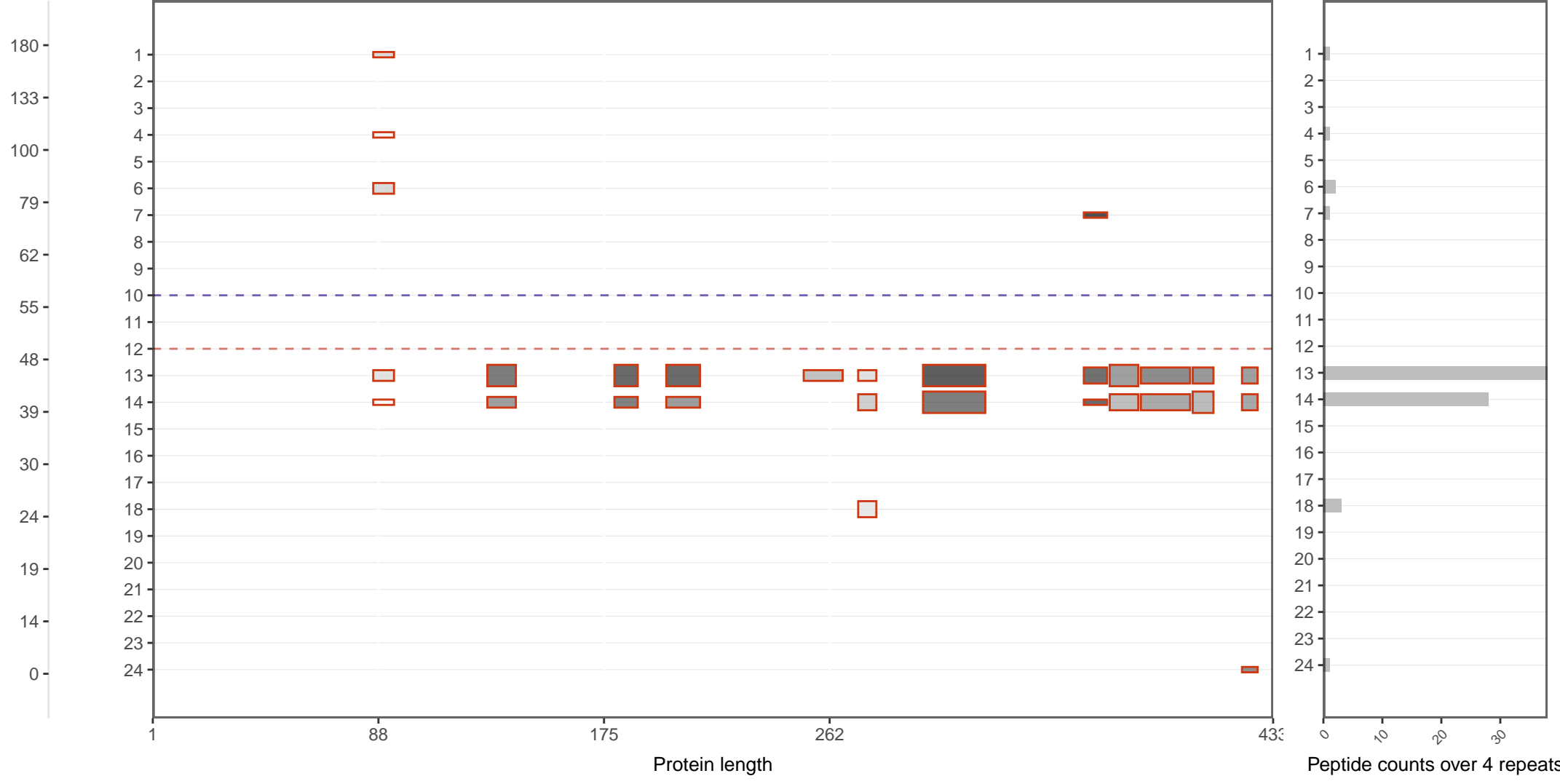


MW indication



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF03171 2OG-Fe(II) oxygenase superfamily
- PF14226 non-haem dioxygenase in morphine synthesis N-terminal

Protein sequence:

IFDLYNSKASIVRDTLGMRLGPTFPDWEHVEVGRDVAVEWDEKVEVKGEEELMGLLCEGLGKVKDRUKELSGLDARIMAAHYYPGPELTKGLTPTDFDQVLTVLVQNEVTGLGVKFGDDVVDLEPPGAIINIGDILGINSDEYKSEVHRVLANPFGQPRVSVAVFVFNPSGRNHLFGPLPELISDEKPAVYRFLFMDVMRRFFSKELDGKTLNYYRVSNDM

NbL04g03820.1 putative_methyltransferase_DDB_G0268948 [MW = 29.98 kDa]

No. of times detected



log(intensity)



Values from



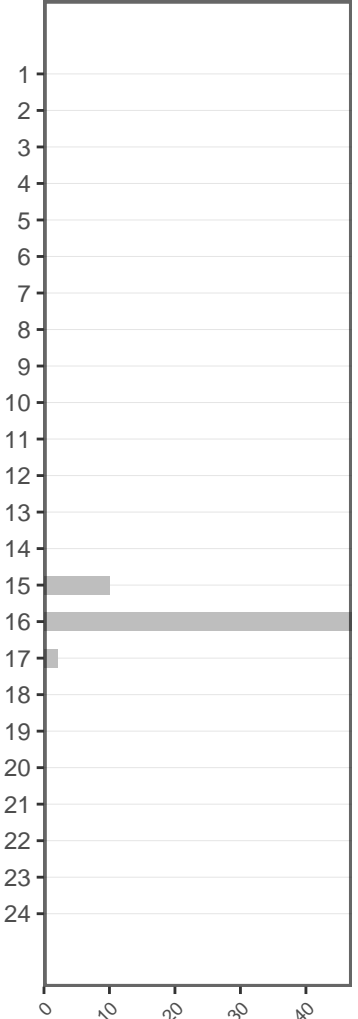
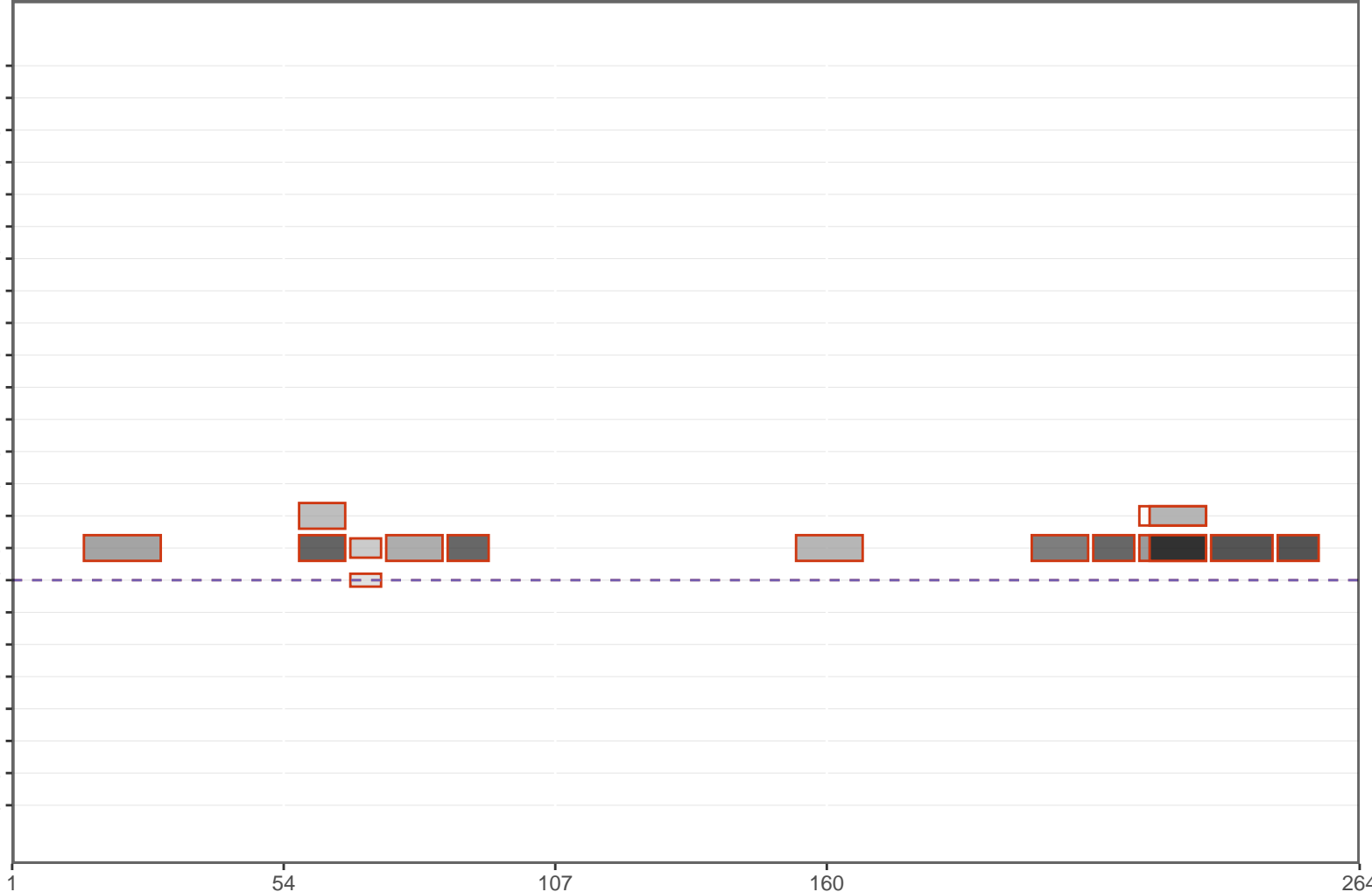
MW indication



Molecular weight

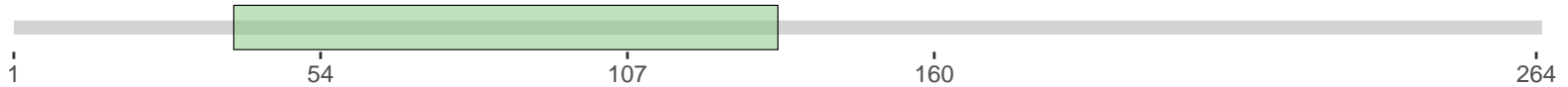


Gel Slice



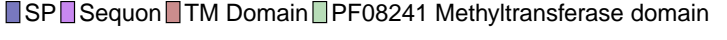
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DSVKKLLKPKNGVAAWQKTVPEVSNVDFEFKFTVDAGPYWECPRKLVDERVYKIDFFPEFVSGYDHNNGPFEFKKVMDLNSVFTYLVKWSAVGTAKKGVLLTDDVVEKFTSVWNEDESQKTVSFFYLRIQKVGNI

NbL04g03540.1 vegetative_cell_wall_protein_gp1-like [MW - SP = 8.7 kDa]

No. of times detected



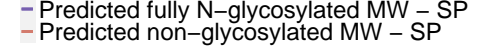
log(intensity)



Values from



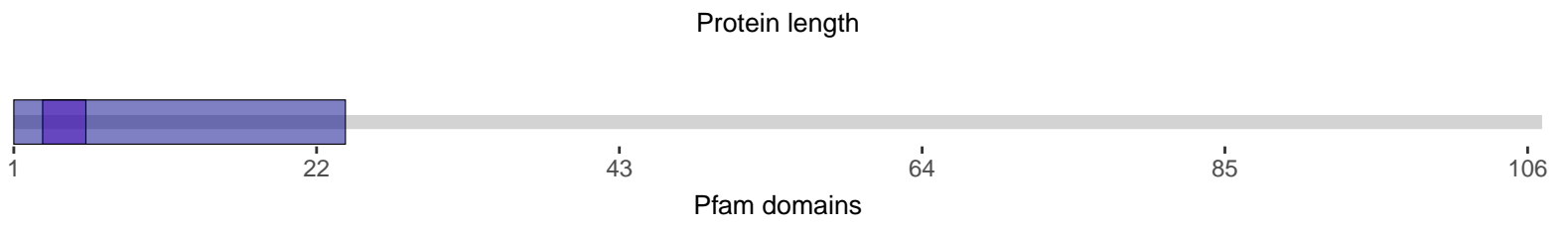
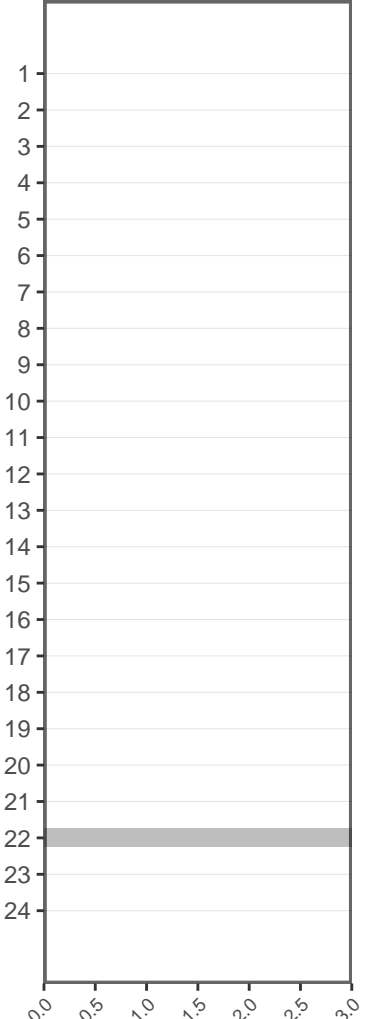
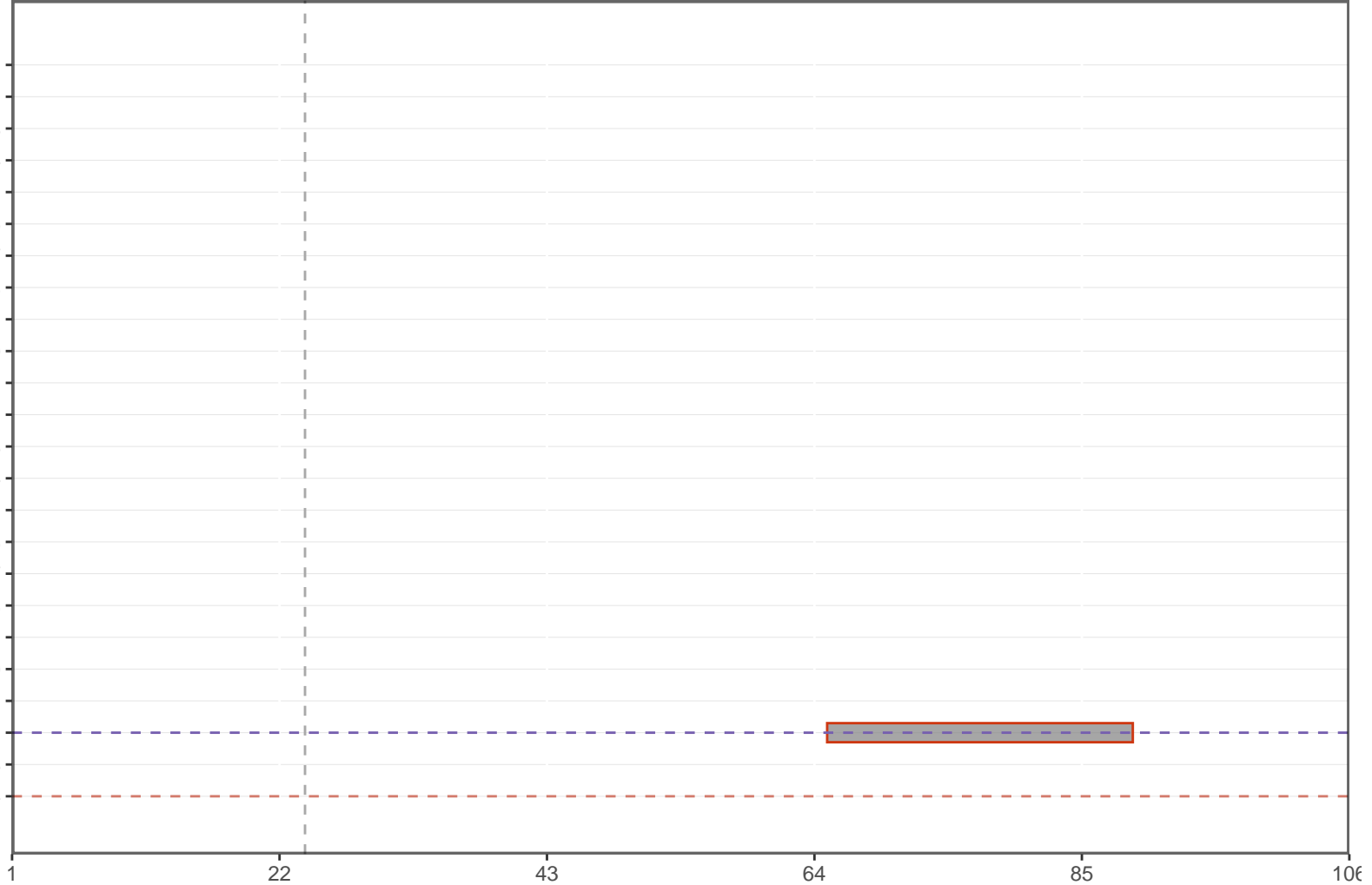
MW indication



Molecular weight



Gel Slice



Pfam Description
 SP Sequon TM Domain

Protein sequence:
 ILPKPEIPLPQGLPFLPFLFMPKPLPLPQLPMPQLPFLFTPQLPVPKPLPLPELPVPLPLPSP

NbL04g03500.1 alpha-galactosidase_1-like [MW = 48.21 kDa]

No. of times detected



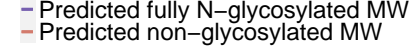
log(intensity)



Values from



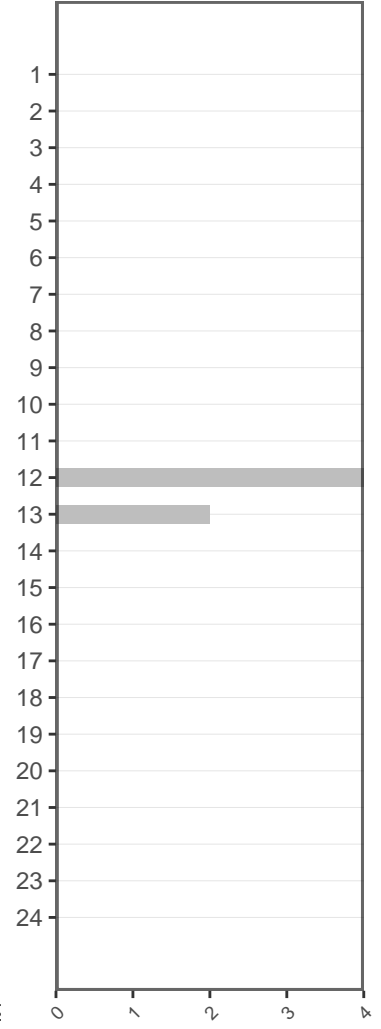
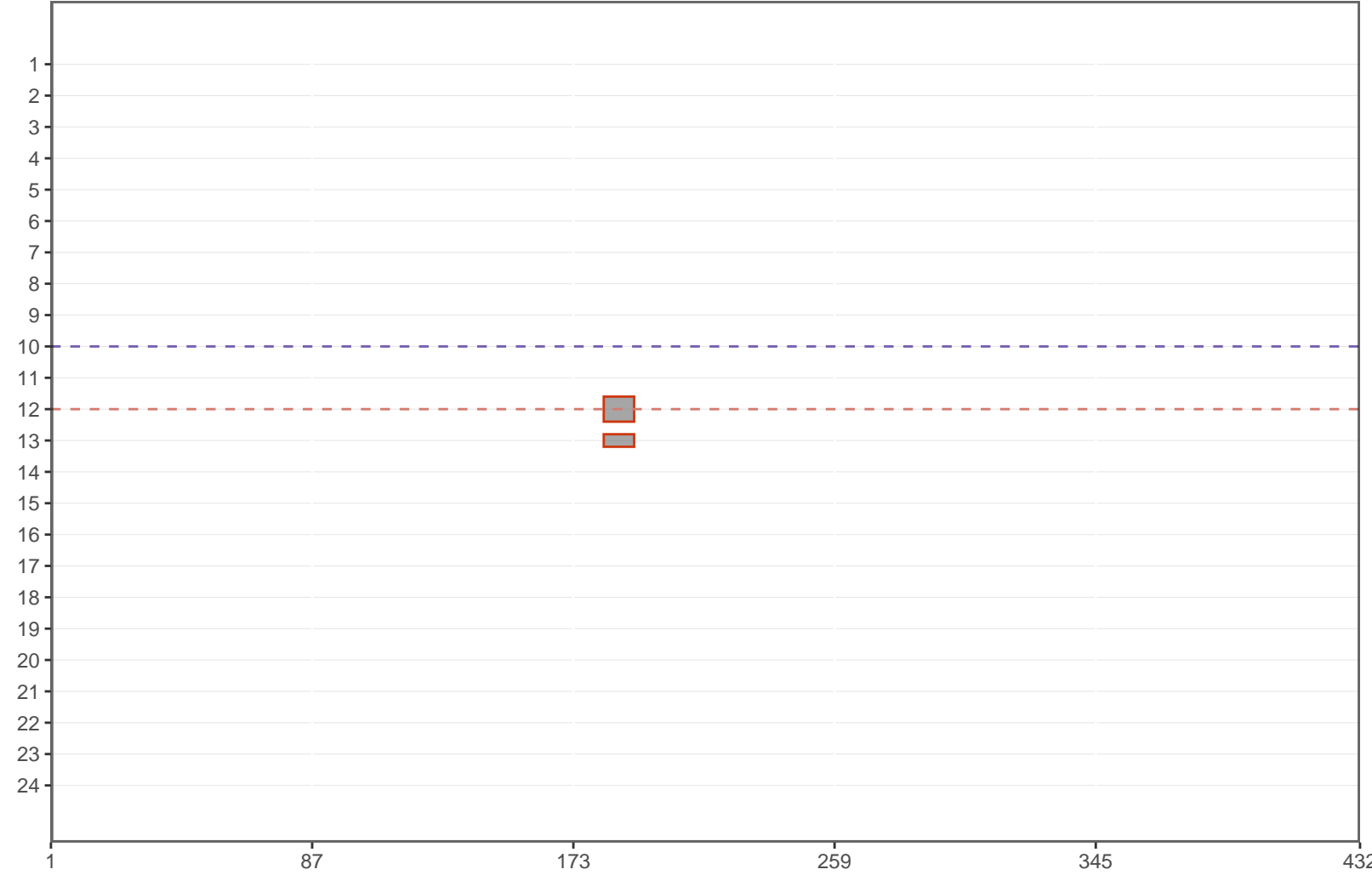
MW indication



Molecular weight



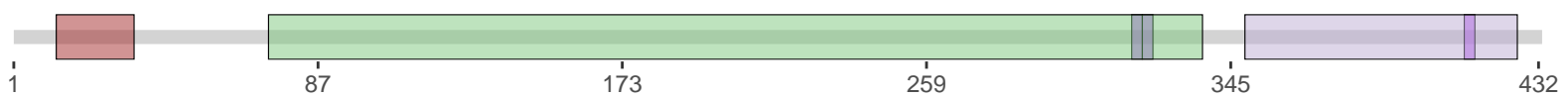
Gel Slice



Protein length



Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF16499 Alpha galactosidase A
- PF17801 Alpha galactosidase C-terminal beta sandwich domain

Protein sequence:

GTKPARYPMTRALMAGRIFFSLGEWGDHLHPLWGGKVGNSWRNTDGDGTSWESMRADQNEVYADLRPPGGVNDPDMLEVNGMGMTKDEVYHFSLWISKAPLIGQVRLNLENDTKEILANKDVAWNGDELGGGKVRMGQDLEVWAGPLSGYRVALLNRRSGTKEITALEWEDIGPPIPVVARDLWEHKTLETRFVGNSTATVMSHACKMFKPIAS

NbL04g03480.1 pyruvate_kinase_cytosolic_isozyme [MW = 55.06 kDa]

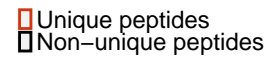
No. of times detected



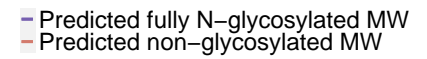
log(intensity)



Values from



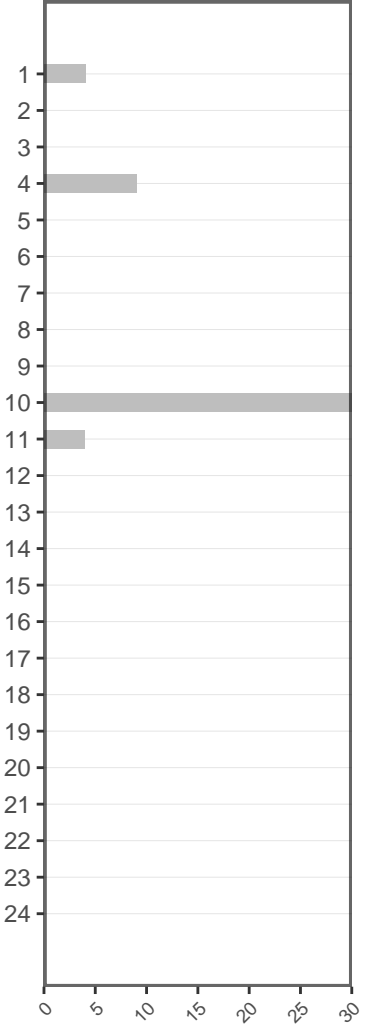
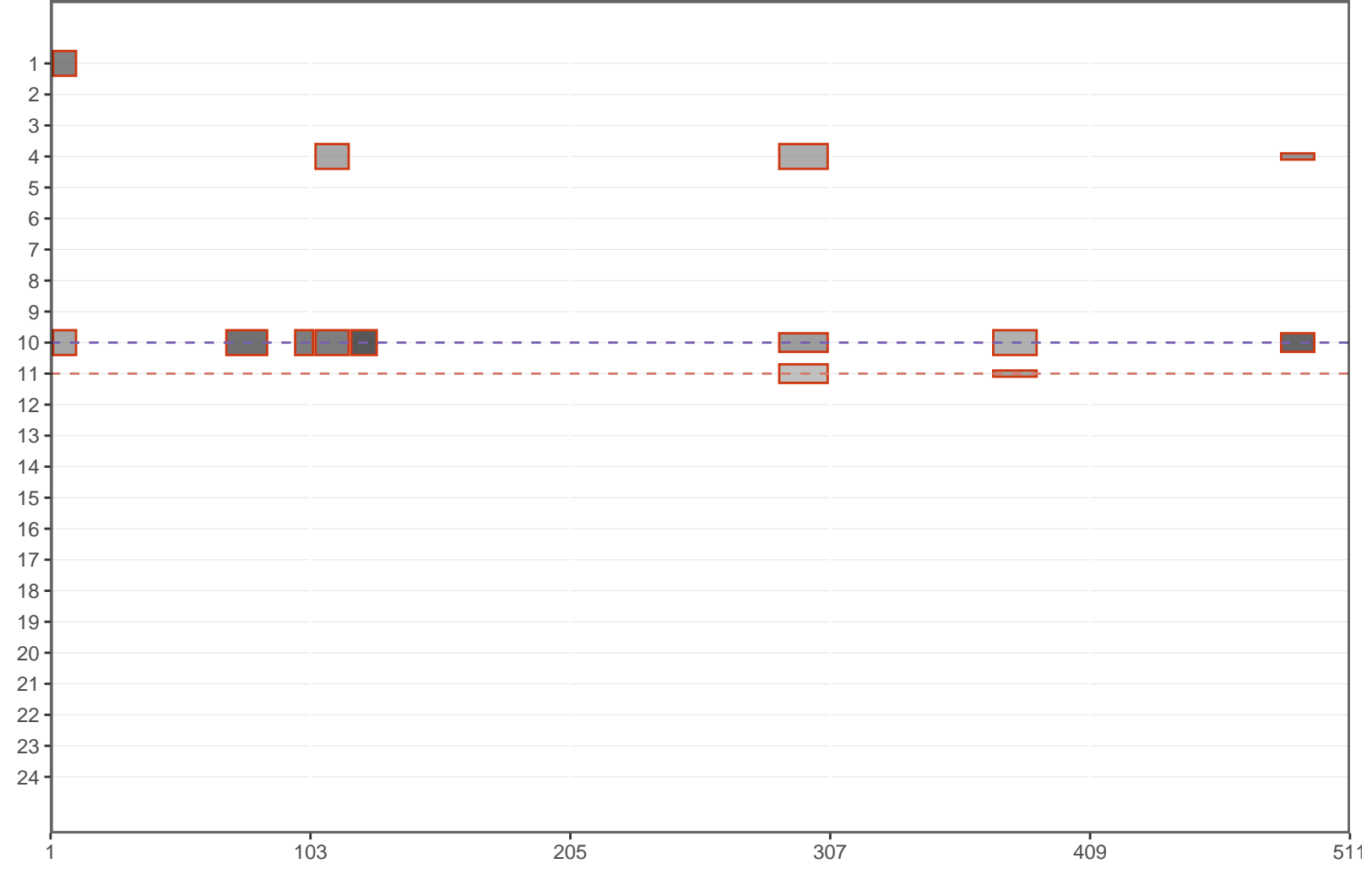
MW indication



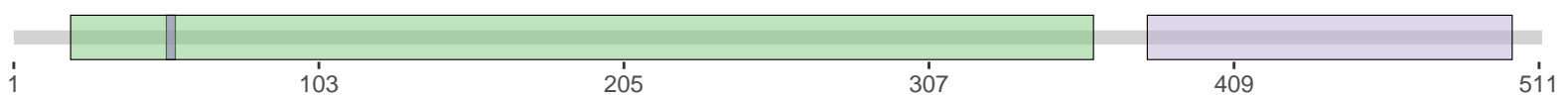
Molecular weight



Gel Slice

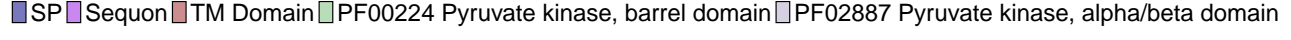


Protein length



Pfam domains

Pfam Description



Protein sequence:

YVENEGVYVNFDELRRETDFSMVARGDLGMEIPVKEIFLAGKMMYKGNLAKPKPVVATQMLLEEMKSPRTRAEATDMANAVLDGTDCVMLSGESAAGAYPELAWKMSKICIEAESLSDYGAIFKEMIRGTPLEMLSPLESLAGSAVRTANKAHANLIVLTRGTTANLVAKYRPPVPLSGVVPVLTDFDFDWSIGDETPARHSLVYRGLIPLLAEGSAKATDSESETEVLEASLKSAAVANGLOKPGDAVVALHRIQAASVRIQLVK

NbL04g03430.1 probable_leucine-rich_repeat_receptor-like_protein_kinase_At1g35710 [MW - SP = 63.27 kDa]

No. of times detected



log(intensity)



Values from



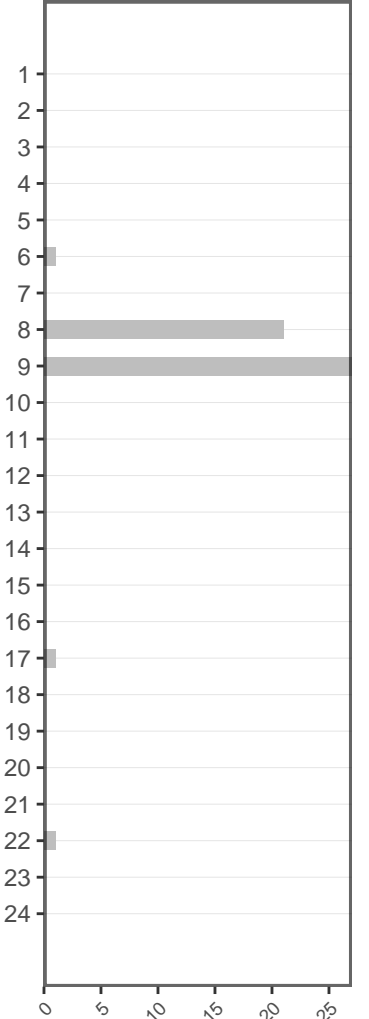
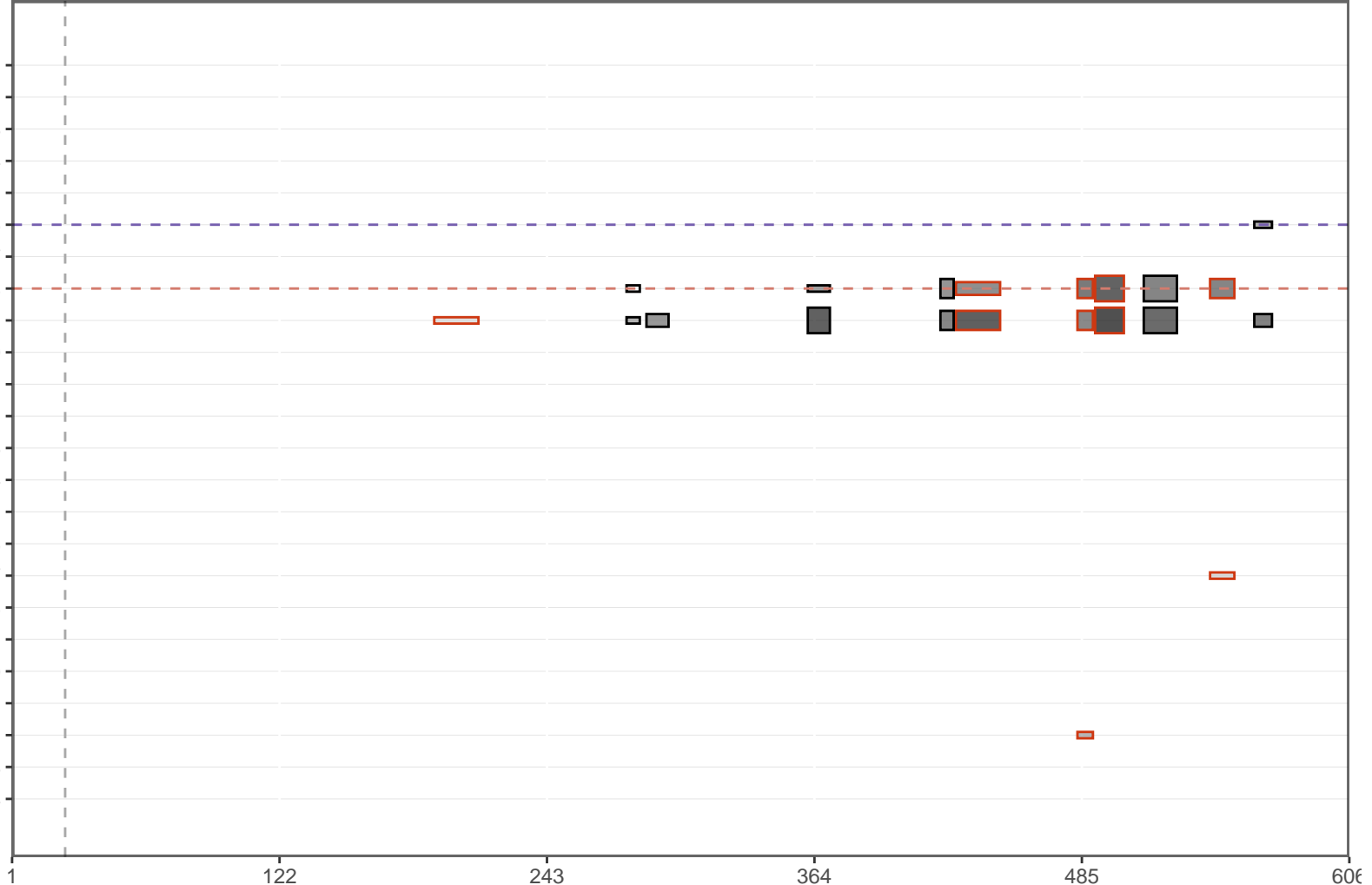
MW indication



Molecular weight

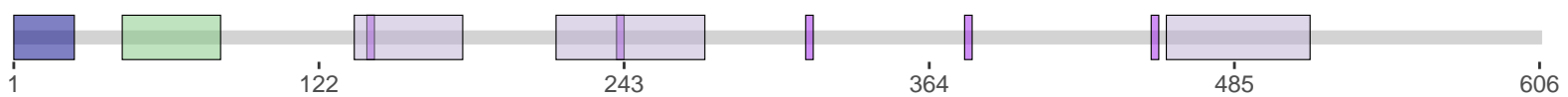


Gel Slice



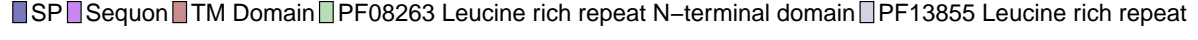
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SLSLSFNKLTGQFASAGLPLNWNLSLRNSLSDPLAFASNGLPSELLSDLEVYNNFNLGTPDPIWRNRELSQVNLGGKLRGMLPNFTRPNSLSDLSGNFFTFNNGSNFFTRMSLGGKANSNNGKSDVALLKLPDGTSSLDLHSGNLGFSLSRMLSENKTSKFLVEDVSNNGLSGNPELNSGLNLYNLGSKNAGGIFTSISNINMLERLDGSRNGIAGTIPGLGELLKLGWLDELGNKAGRPDLSLEIEELRHANFRANRLGGEIPGRPNYFPAAYANLCLCGKPL

NbL04g03320.1 FAD_synthetase_2_chloroplastic-like [MW = 40.55 kDa]

No. of times detected



log(intensity)



Values from



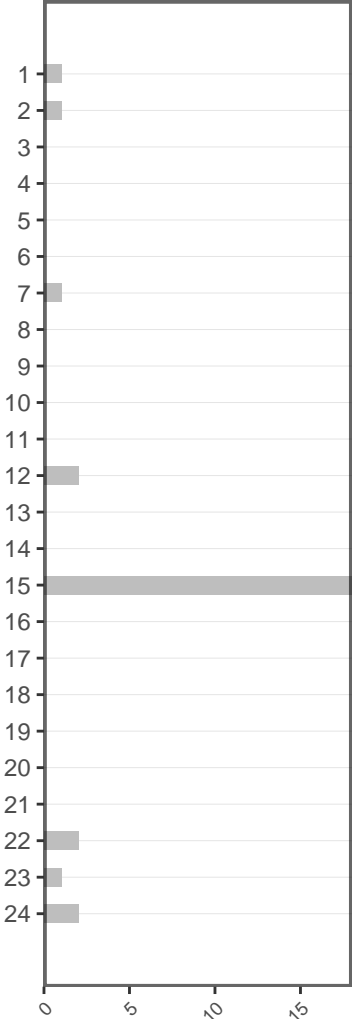
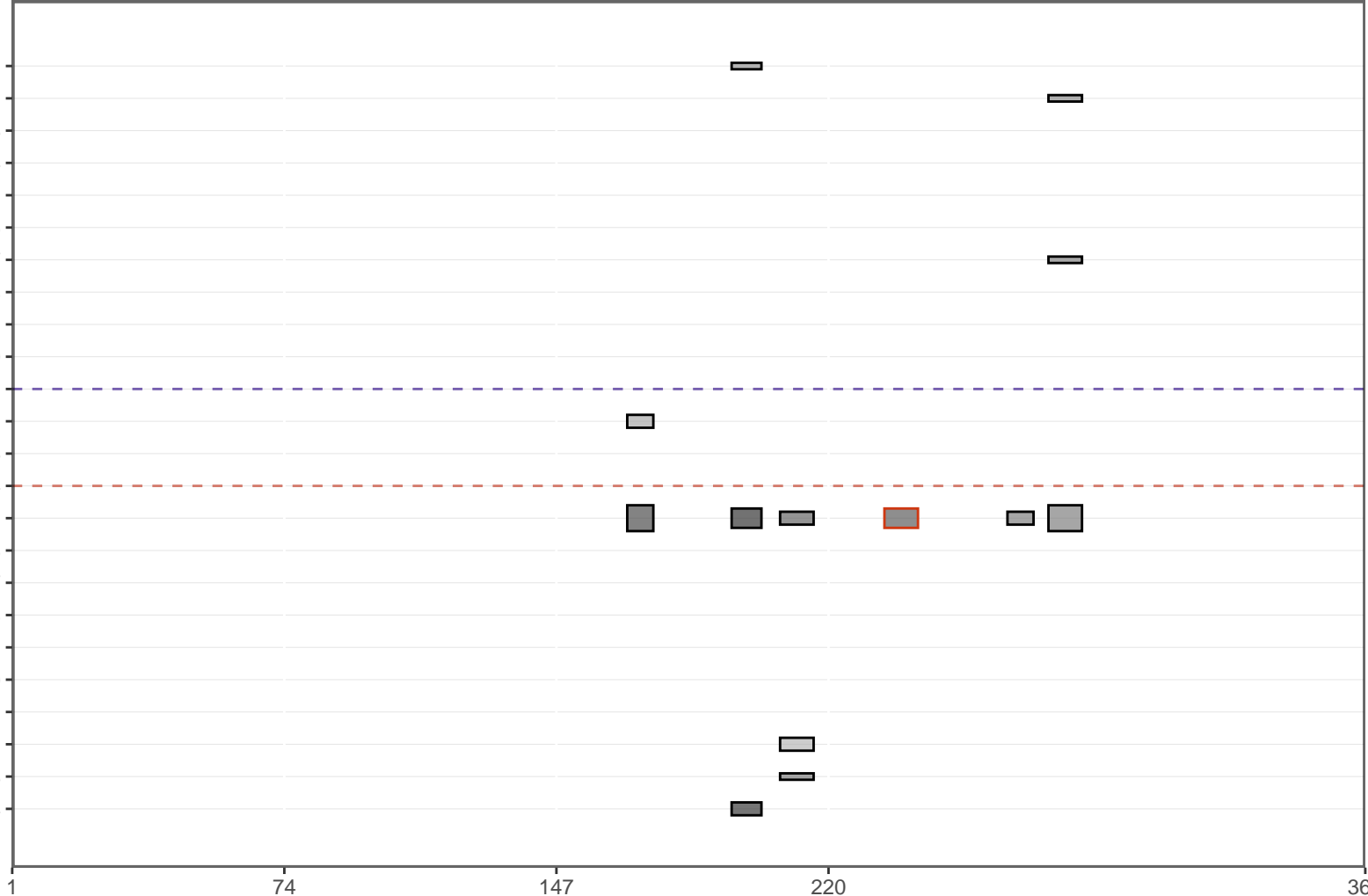
MW indication



Molecular weight

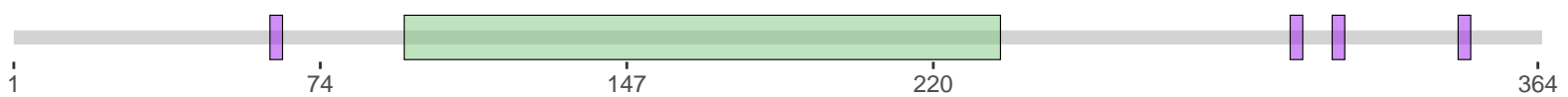


Gel Slice



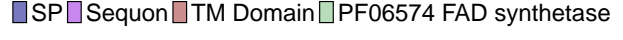
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

QIEFSKYRSLTFRQFVEKLSKELGVRGVVAGENYRFGYRAGGDADIVLKLCEEYGLEAVHNSVMEKNGISIEDLNSREKKEKGGVSTRVRYVALDKGDMKYVSELLGRNHRVLLMEDGERFTSEKSRLSAPKSGLLNLSPEKGLYENSGISIDENVPRVIVDTHLIECYEVAWFTQITSRDKILGIDFGS

NbL04g03270.1 glyceraldehyde-3-phosphate_dehydrogenase_A_chloroplastic [MW - SP = 41.06 kDa]

No. of times detected



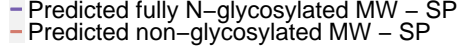
log(intensity)



Values from

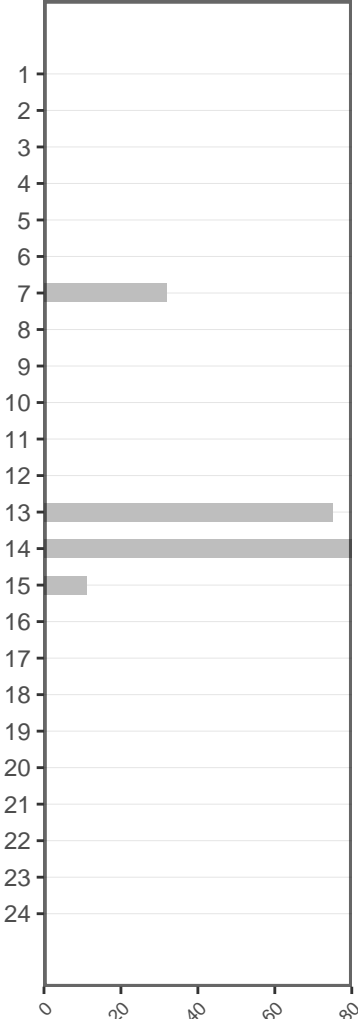
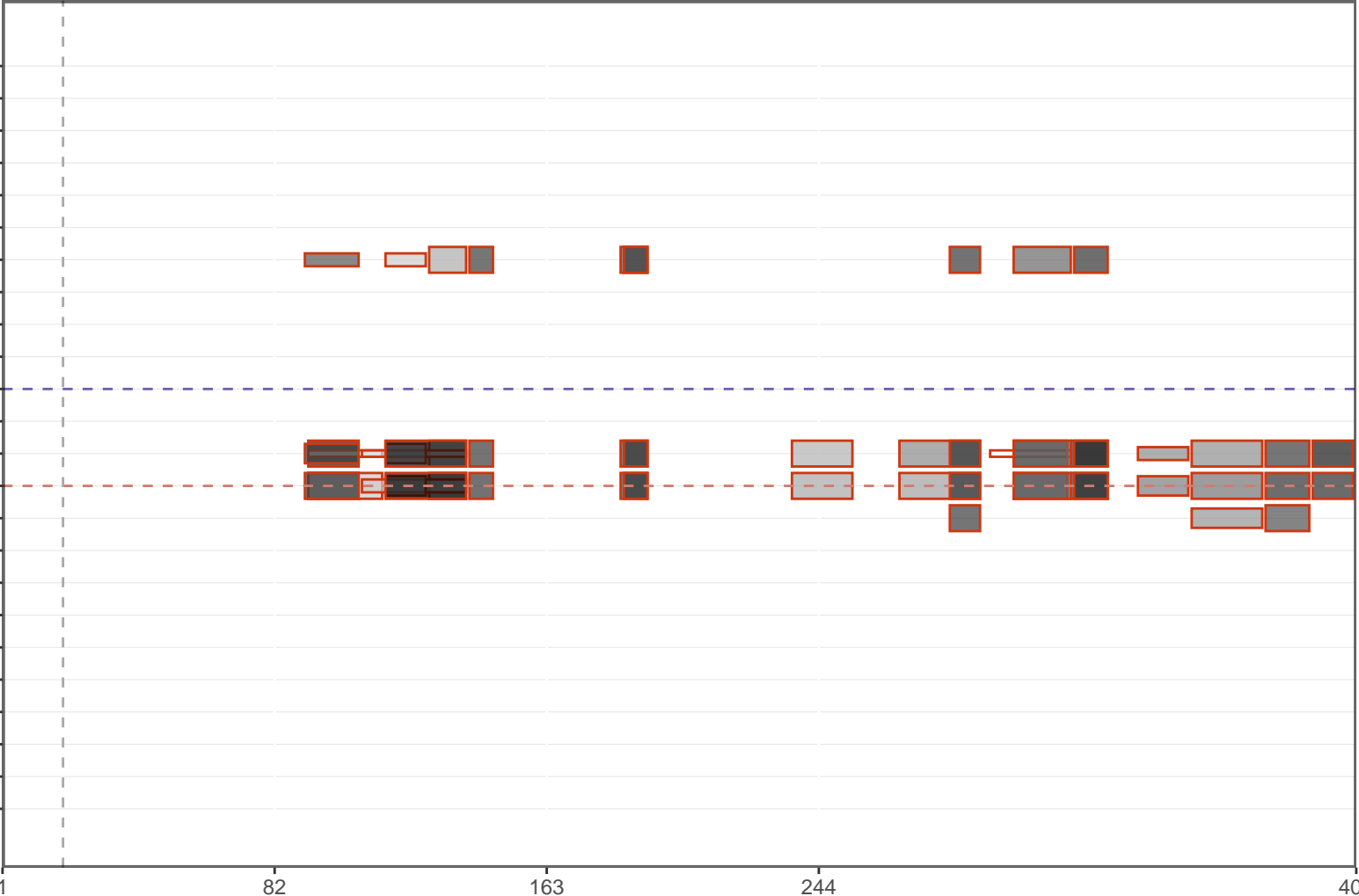
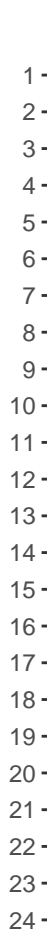
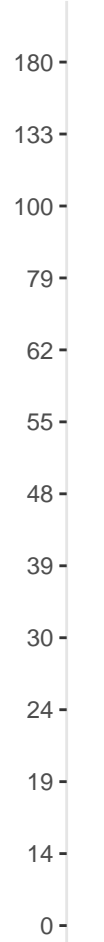


MW indication



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00044 Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain
- PF02800 Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain

Protein sequence:

TAPGKGDPTTYVGVNADLVNFDPEISNAAGCTTNGLAAPFVKVLDQKFGIKGIMTTTHSYTGDORLLDASHRDLRRARAALNVPSTGAAKAWALVPLKIKLNGIALRVPFPNVSVVLLVGVQSKTFAEVNAAFRESADKELKGLDVGDEPLVSVDFRGSVDSVSTVASLTMVMGDDMKVVAWVYDNEWGYSGRVLDLADIVANGWK

NbL04g03230.1 glutamate-1-semialdehyde_21-aminomutase_chloroplastical [MW = 58.46 kDa]

No. of times detected



log(intensity)



Values from



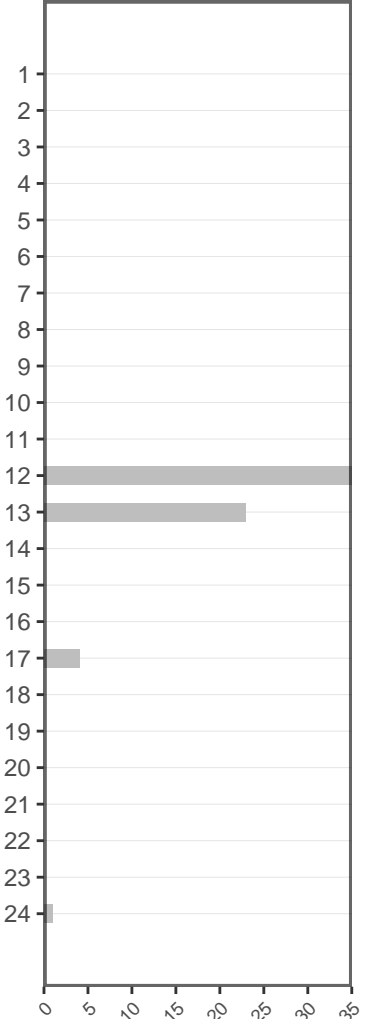
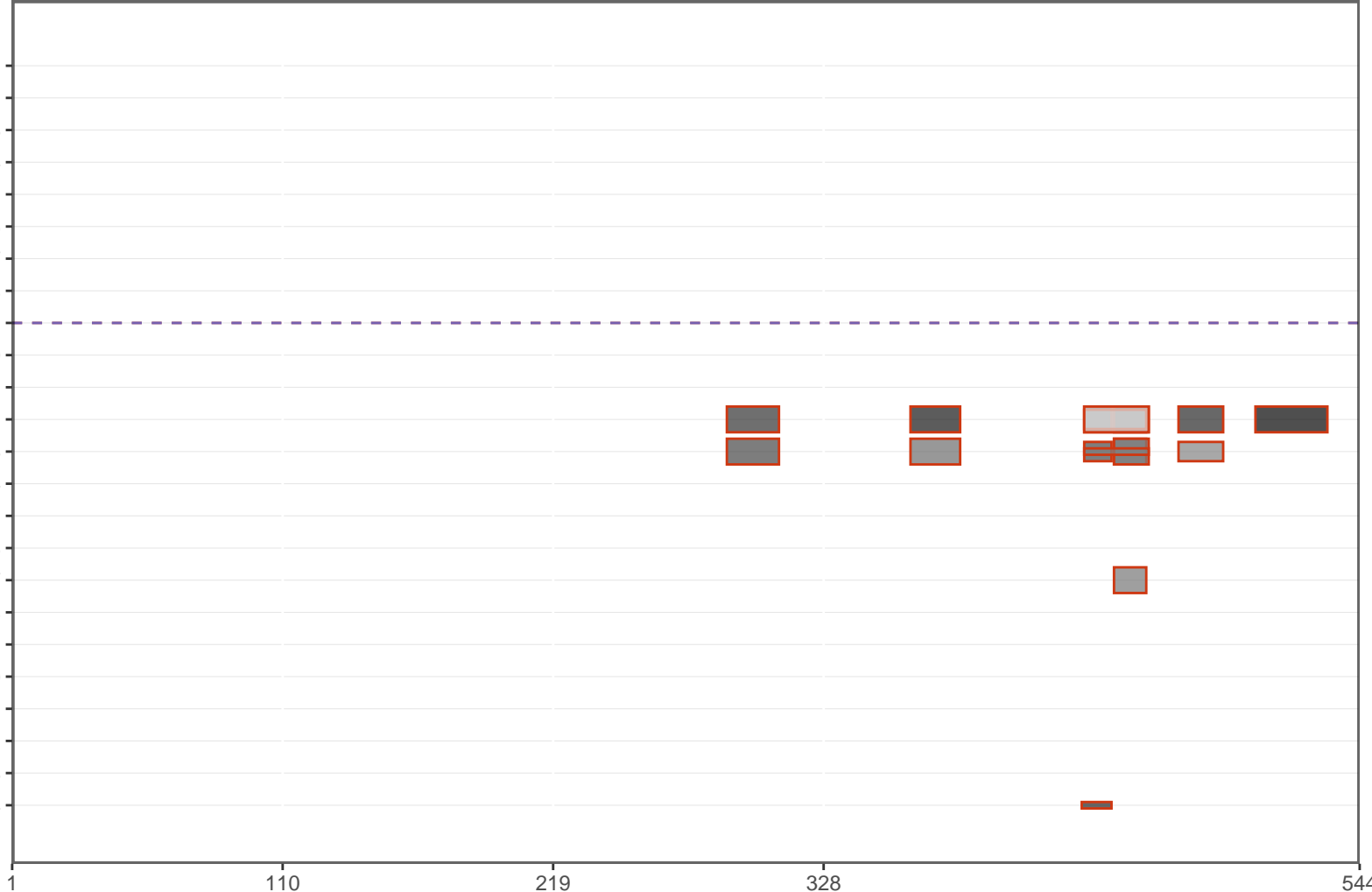
MW indication



Molecular weight



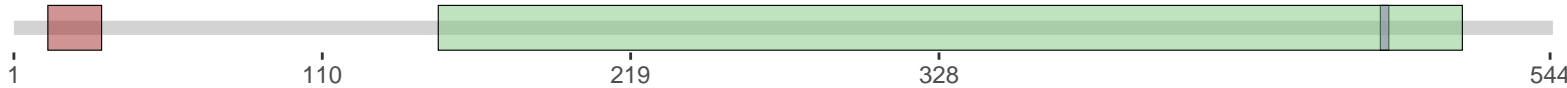
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL04g03110.1 lignin-forming_anionic_peroxidase-like [MW - SP = 31.82 kDa]

No. of times detected



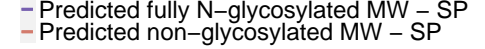
log(intensity)



Values from



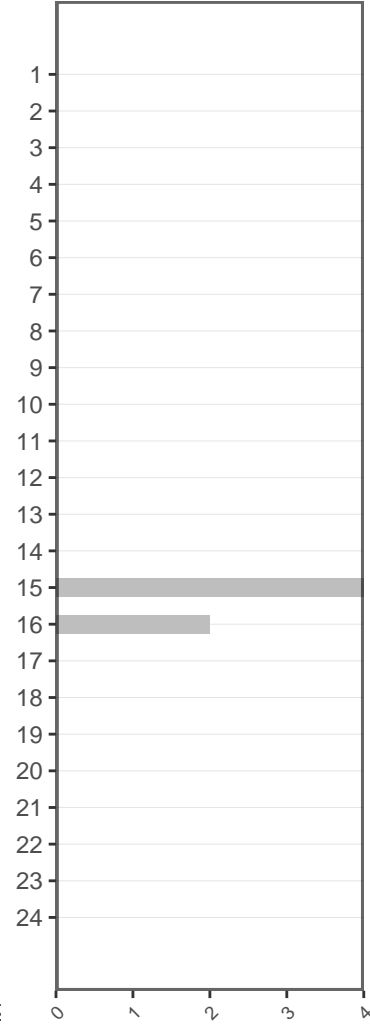
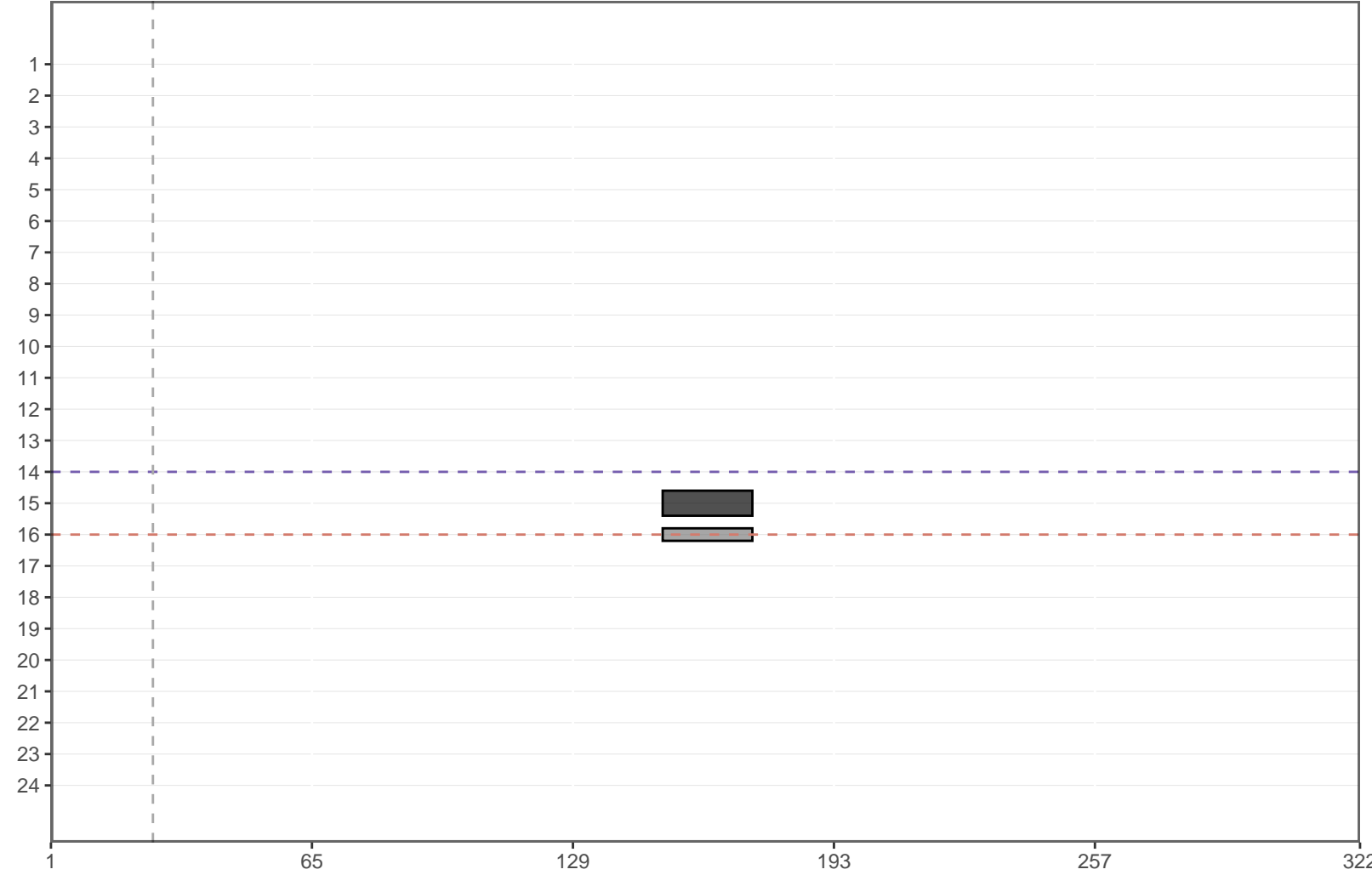
MW indication



Molecular weight

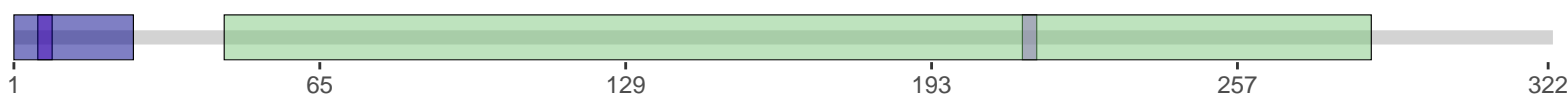


Gel Slice



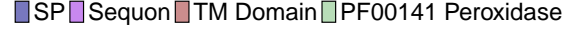
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RRDSTASHTLAETDLPGFPDPLNRLISGFASKGLSTRDMVALSGAHSIGQAGFLFRDRIYNGTEDIAGFASTRRRGCPKEDQNGNLAFLDLTFNGLNDFYFNFLRFRKGLGSDQILLGGSGTDDHSEYNSNPRFAFDFAAAMIRMGDISPLTGNGIRTVGGSN

NbL04g03100.1 lignin-forming_anionic_peroxidase-like [MW - SP = 31.79 kDa]

No. of times detected



log(intensity)



Values from



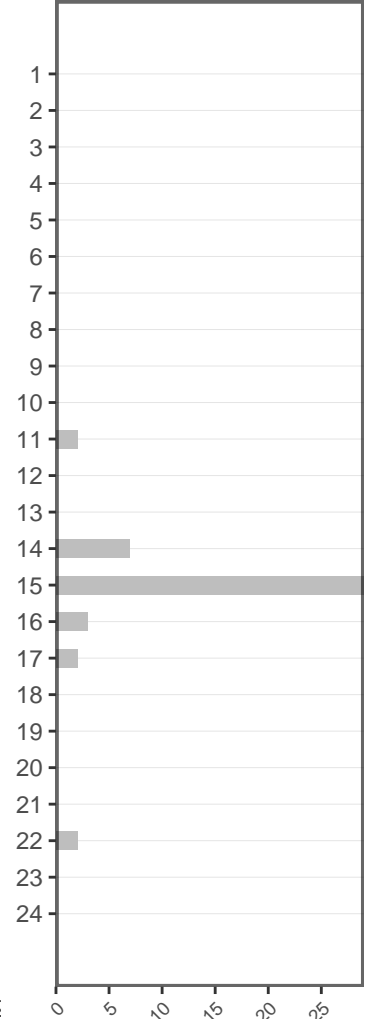
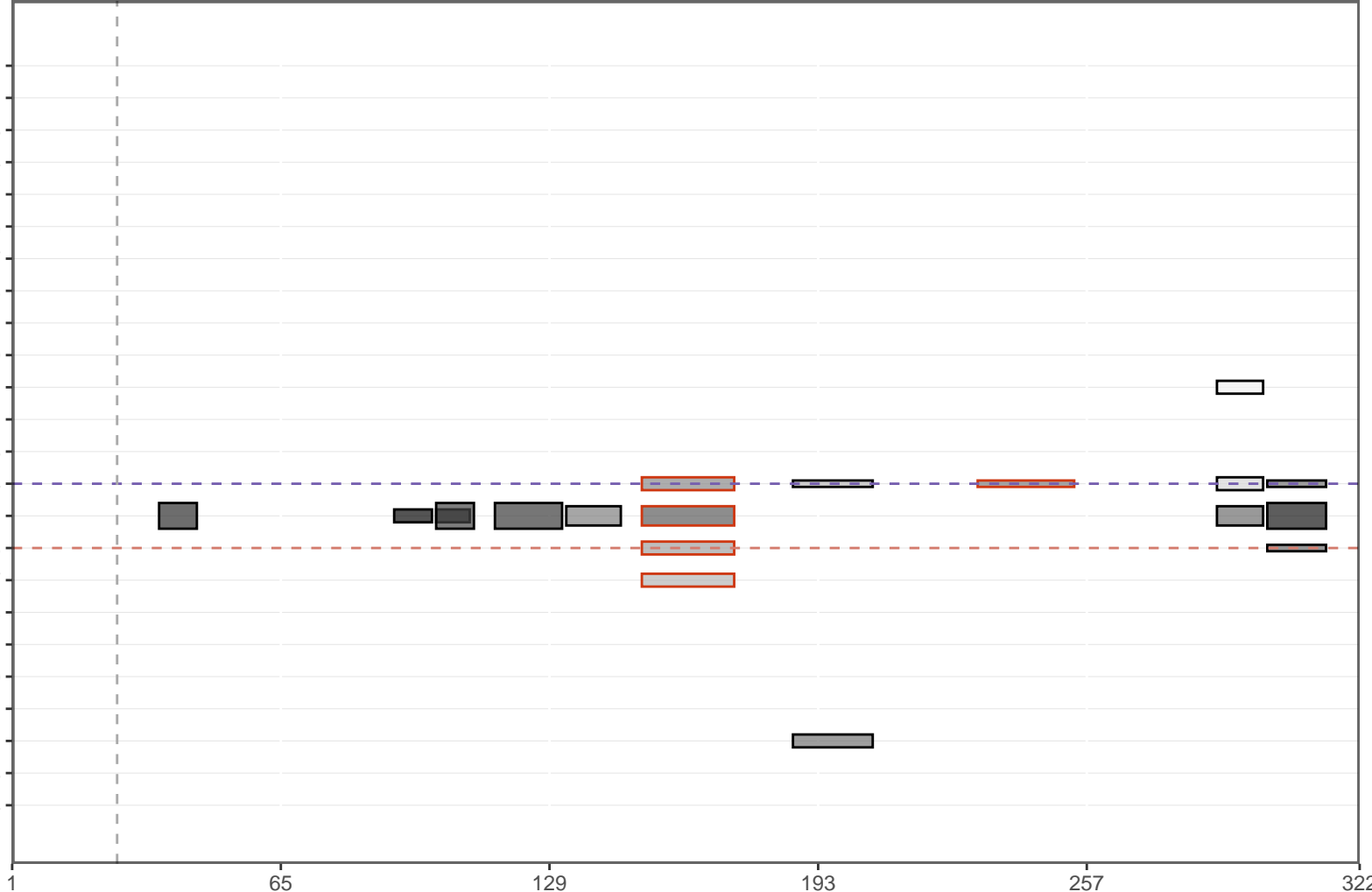
MW indication



Molecular weight



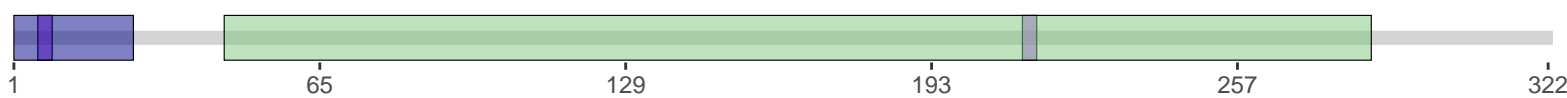
Gel Slice



Protein length

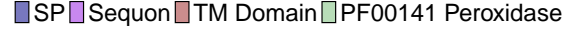


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

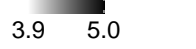
RDSTASHLLETGLGPPDPLNRLISGFABKGLSTRDMVALSQAHSIGQAQGLFRDRIRYNGTIDAGFASTRRRGCPKEDQNGNALAPLDLVTPNGLDNNYFNKLRQRKGLLQSDQVLLGGSTDDIVSEYNSPRAFAFDFAAMIRMGDISPLTGGNGHIRTVGGSN

NbL04g03020.1 histidinol-phosphate_aminotransferase_chloroplastic [MW = 46.23 kDa]

No. of times detected



log(intensity)



Values from



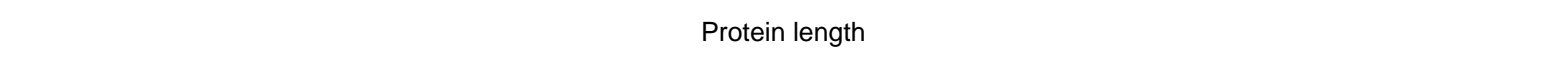
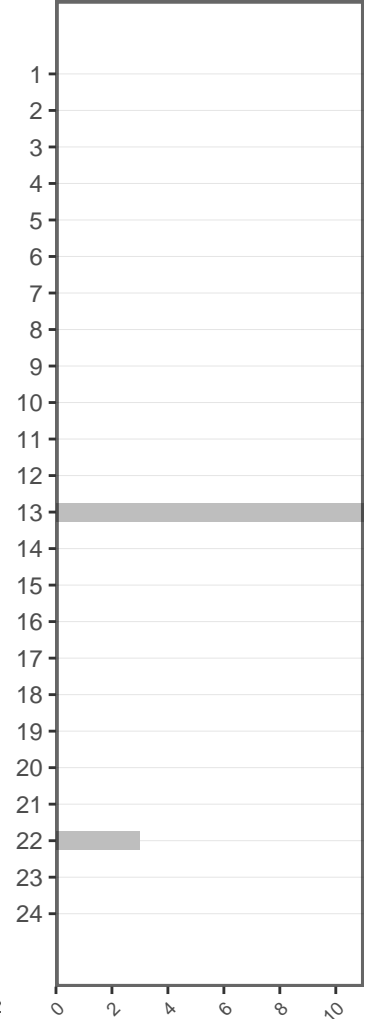
MW indication



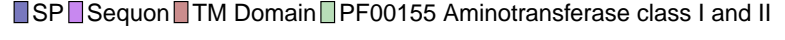
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

'SLDVERIAEYVEHEKPKGIFLTPNPFQGIIDGETLLKLDLPLVILDEAVVEFSQMESKMKWKKHKNLVLRTFKRAGLAGLRVGYGAPFKSIEFLWRKQPNVSVAAEVAAGALNPNVYLENKKVALVGERERLFLNLLKEVFLDPVPSYSNFLGKGVTSMDANKLKEADLTMGVMRHYNKSKELGIVRVVSGKPEHTEALMKLKHFY'

NbL04g02980.1 DNA_repair_RAD52-like_protein_2_chloroplastic [MW = 23.13 kDa]

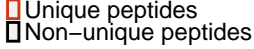
No. of times detected



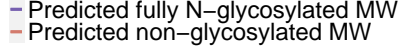
log(intensity)



Values from



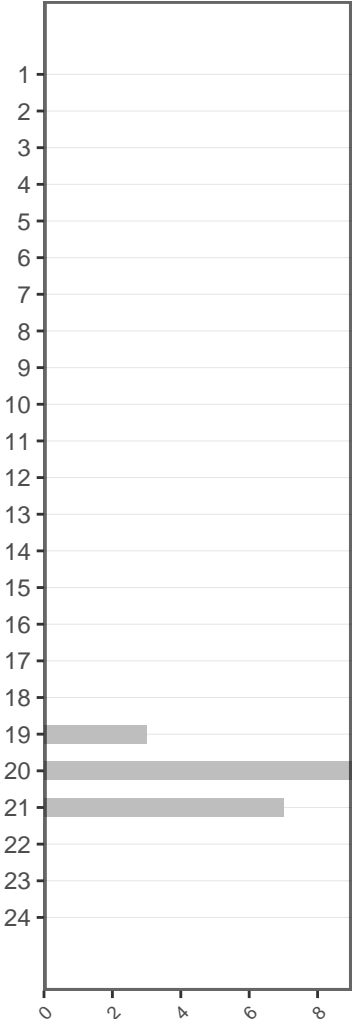
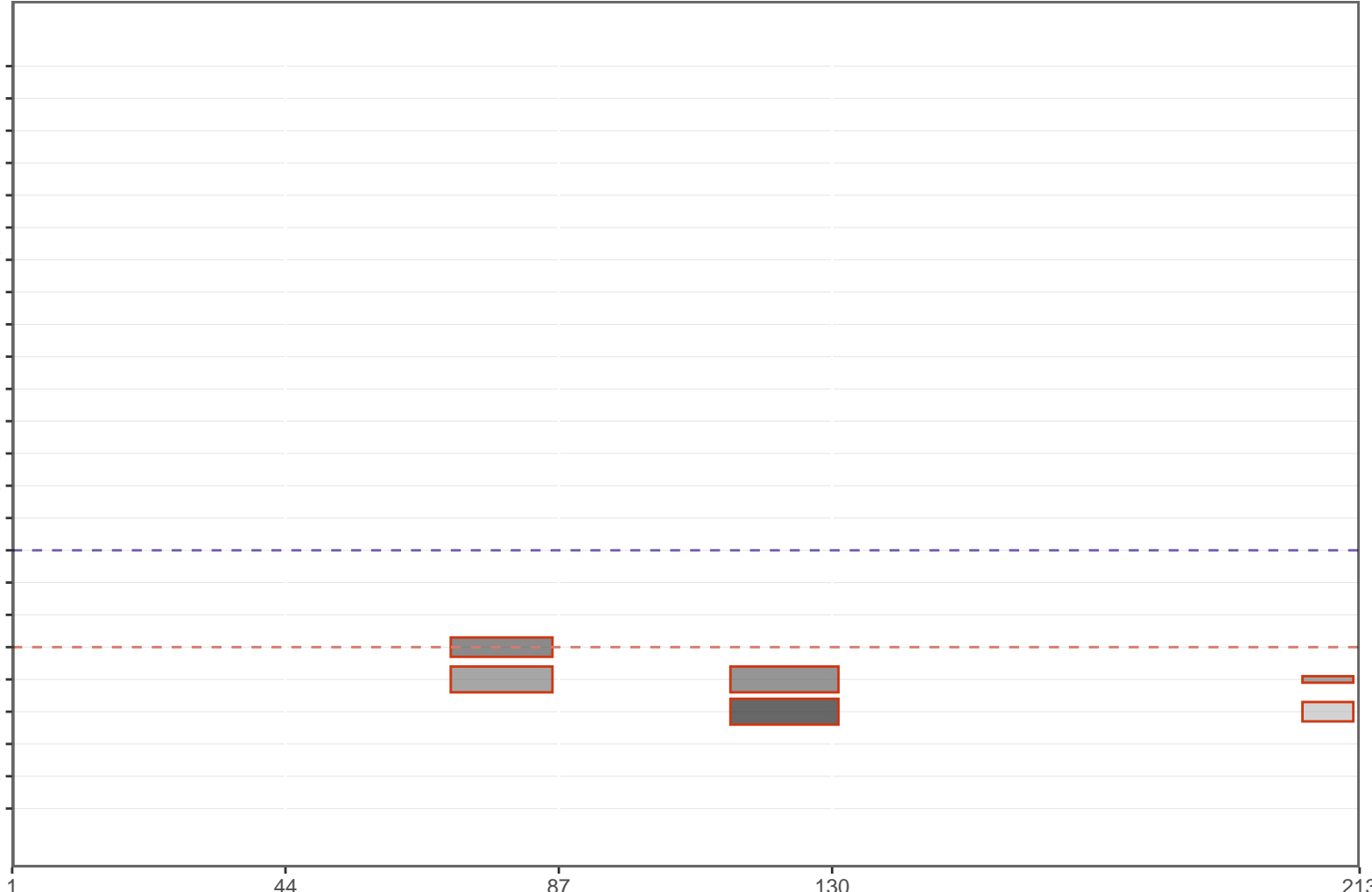
MW indication



Molecular weight



Gel Slice



Protein length

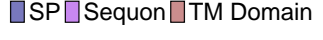


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IRPLAEILROLNKRADNIKANDGDDNSTFRPWWHANRMLSFYAPGWGGEVRDITFSDNGSVTVVYRVTIRGSDGEAHRREBTGTVSPGNGPSTDLWAAEEIIFGRAGARFGLGLVLYH*

NbL04g02880.1 glycine--tRNA_ligase_mitochondrial_1-like [MW = 81.33 kDa]

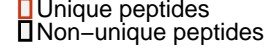
No. of times detected



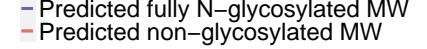
log(intensity)



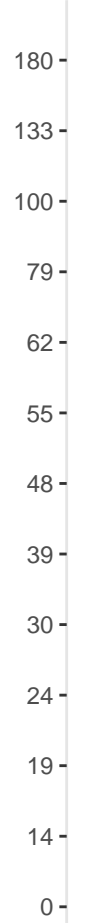
Values from



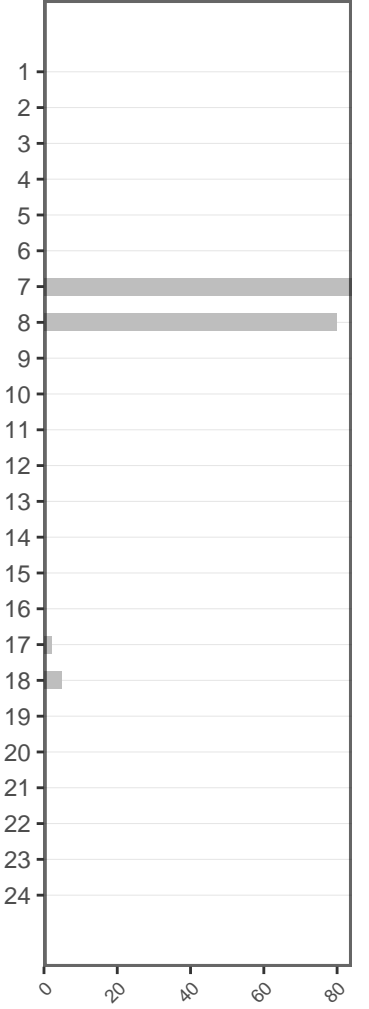
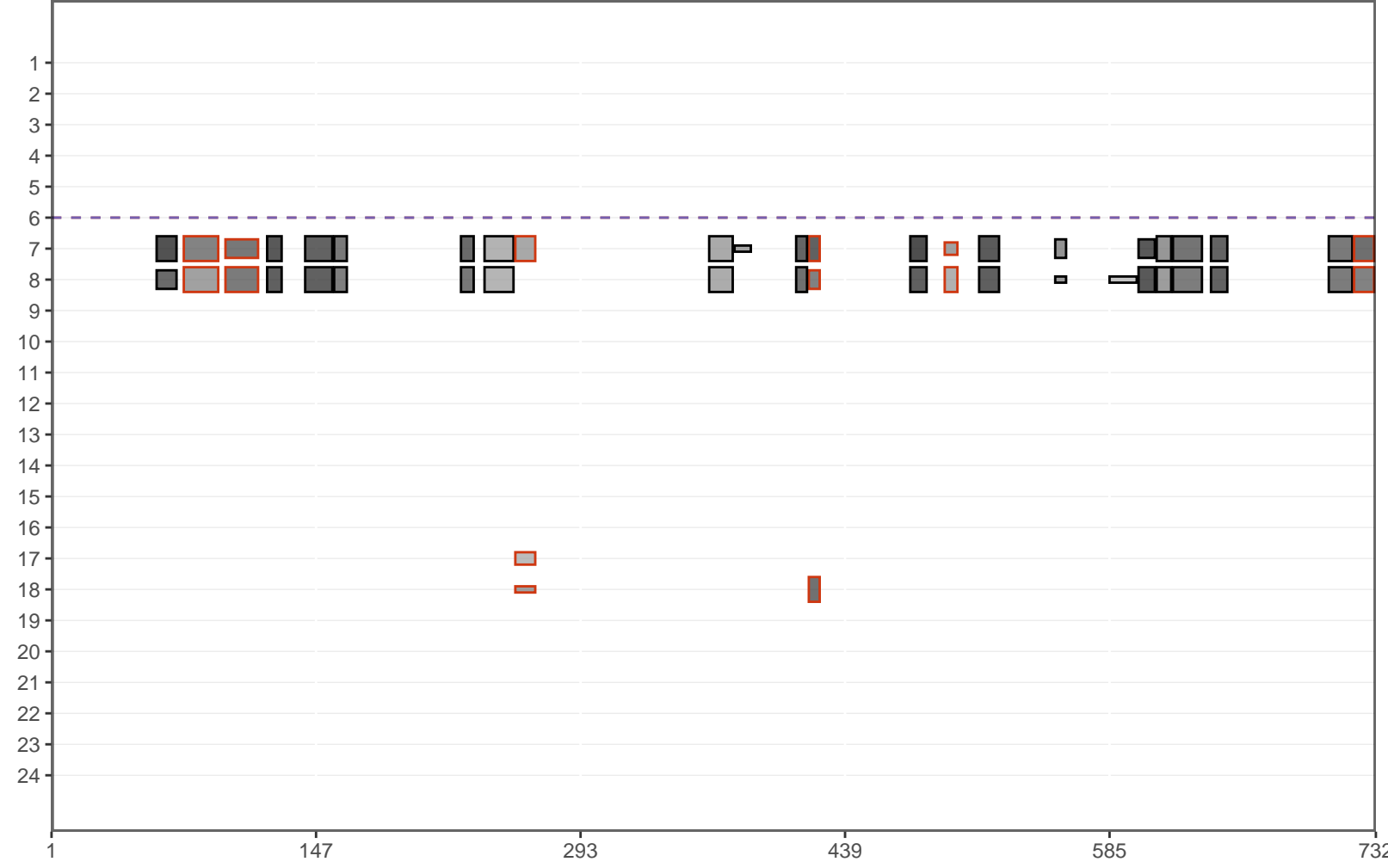
MW indication



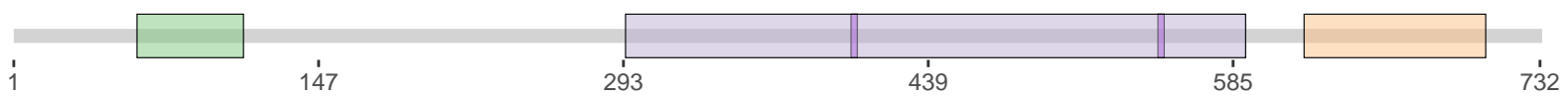
Molecular weight



Gel Slice

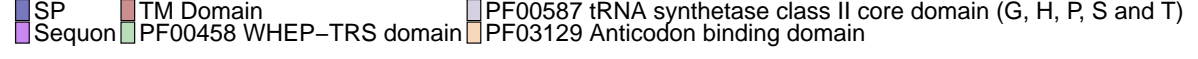


Protein length



Pfam domains

Pfam Description



Protein sequence:

IFVDPQDSIPKFSQWALEFLMFRDEQVSGGCAKRLQGLGEAVSGGVNNETLGYFGRVYFLFRLGIDQERLRFRRGLANEMAHYAADCWDAEIESGSGVIEGVGADRSANDLRAHSEKSSVALVADENKFSRPREVEKLVIPKKEGLGAFKGNQKMWTEALEAMEEKVAMEMKADLESKGEVGFHCTLGKNTIKKGMVSIKSKKKEKHORVFTSPVIEPFGIGRIYLYEHSFYTRPSKGGDEQLNFRFRPLVAPKGTVFFPLVGNQGGYEEVAKLISKSLTAIGS

NbL04g02860.1 proteasome_subunit_beta_type-3-A-like [MW = 22.69 kDa]

No. of times detected



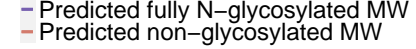
log(intensity)



Values from



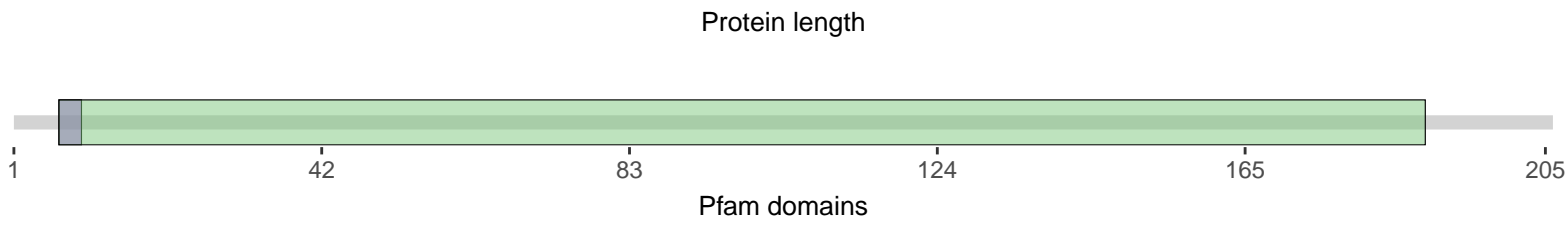
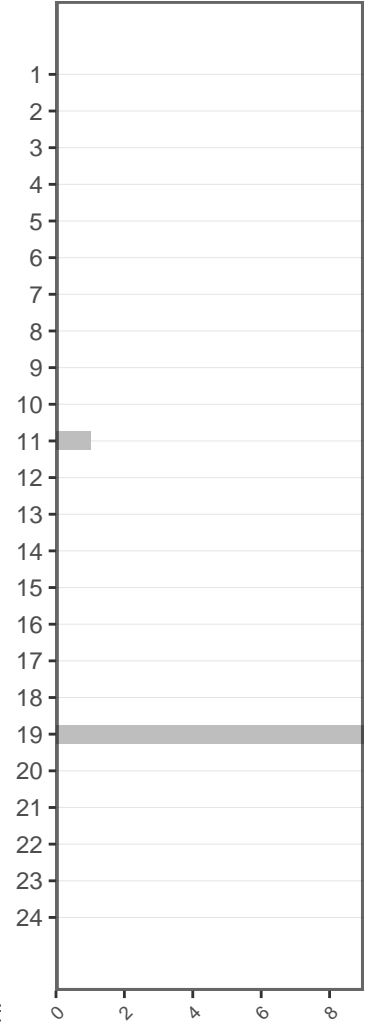
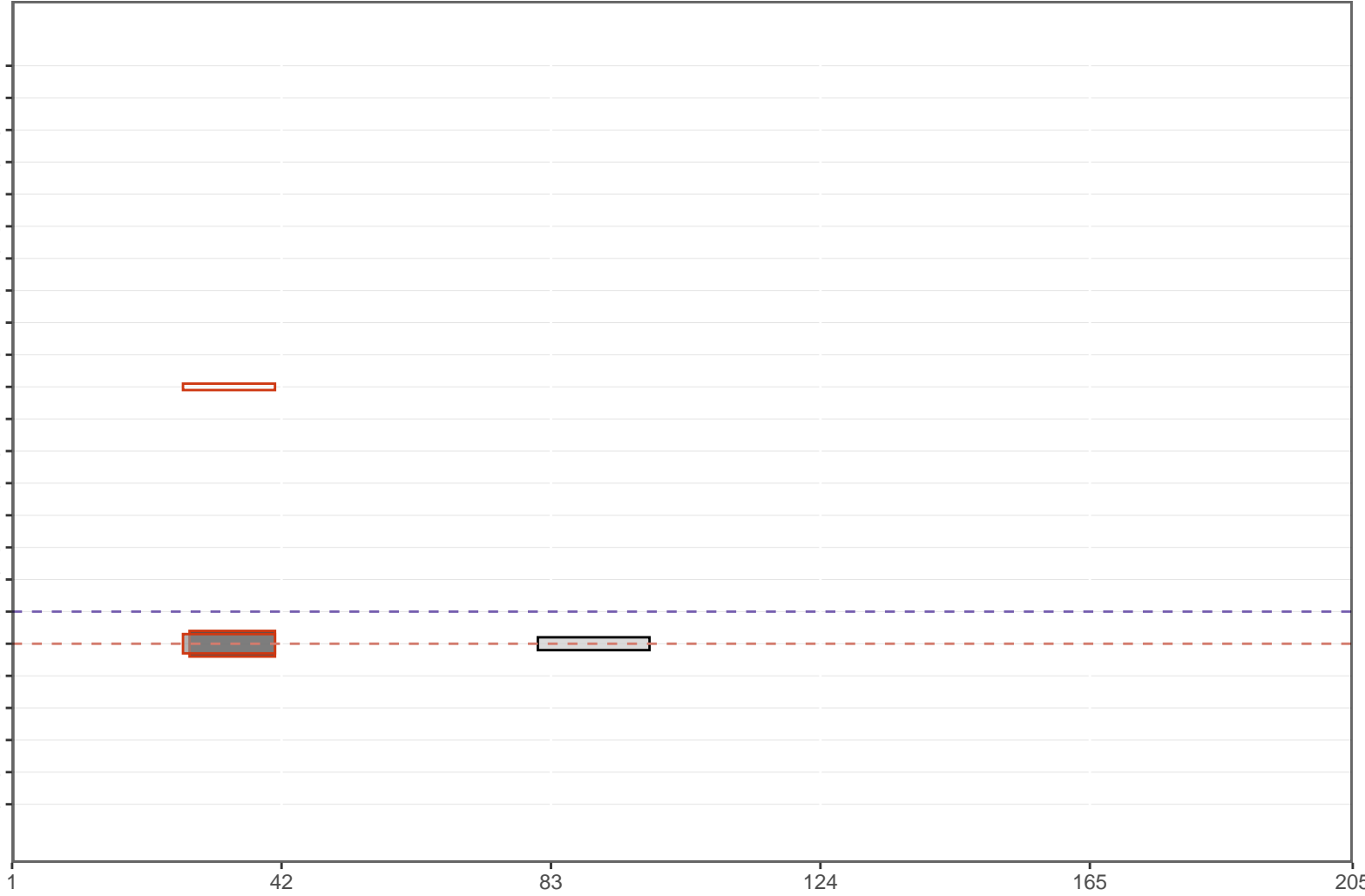
MW indication



Molecular weight



Gel Slice



Pfam Description



Protein sequence:

VSAIYKRFQPFYQRPVAGLGGDDKPFICTMDAIGAKELAKDFVAGTASESLYGACEAMFKPDMGPEELFETISQALLSSVDRDGLSGWGCHVYVYTFTEVTEKILKGRMD*

NbL04g02850.1 psbP_domain-containing_protein_2_chloroplastic-like [MW = 28.07 kDa]

No. of times detected



log(intensity)



Values from



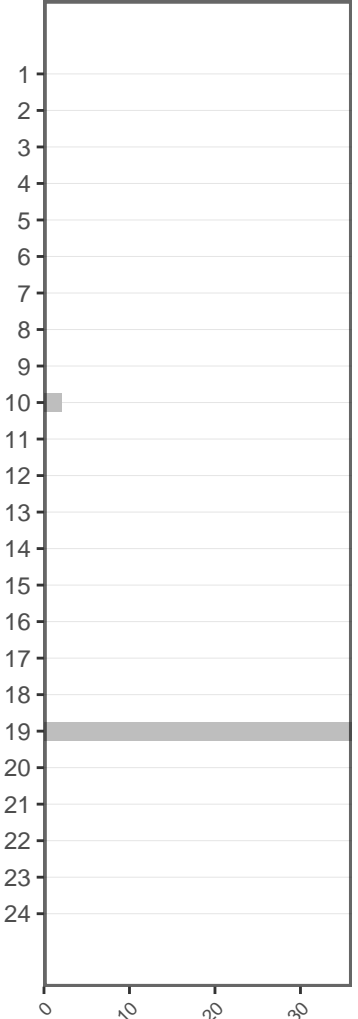
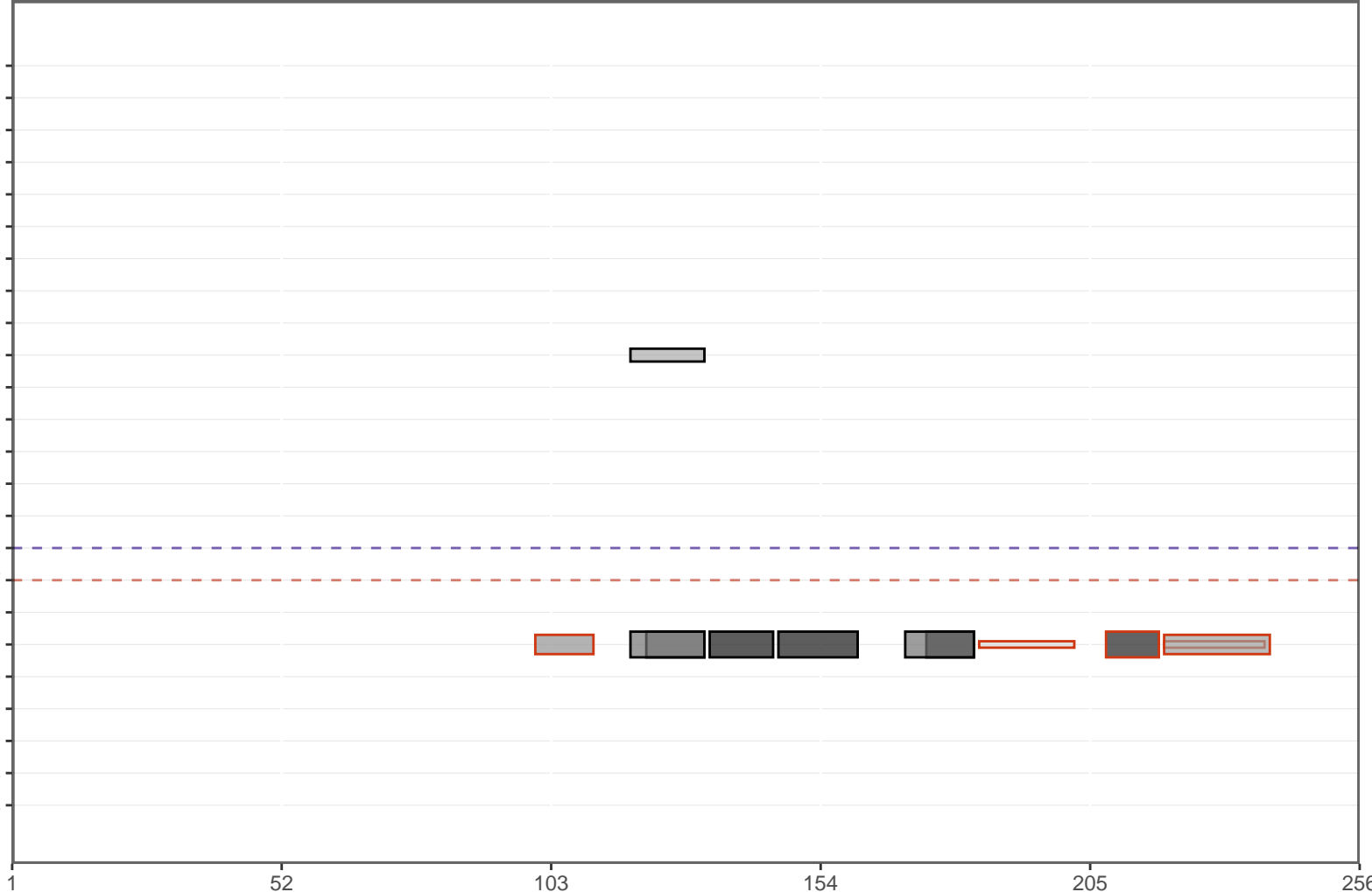
MW indication



Molecular weight

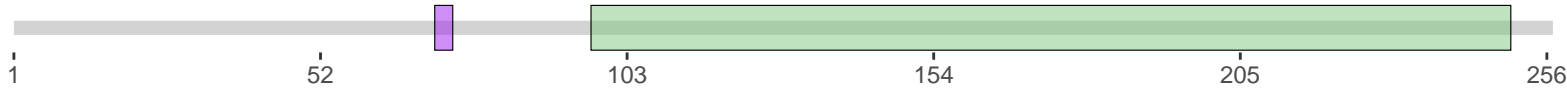


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MKYDKAGATLVLFQDANKGNSNVDVVIPKIFLISGFTQDFADKLLAEKRKESTNEAEVVAWSEKTEGEGGLVYEFETYIDSTRGKKRIFSAFVAGKLYLLNIANSGLSEPIQDPRINTLEQLHSDFTAPST

NbL04g02500.1 cell_division_cycle_5-like_protein [MW = 118.18 kDa]

No. of times detected



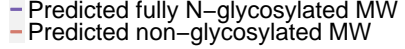
log(intensity)



Values from

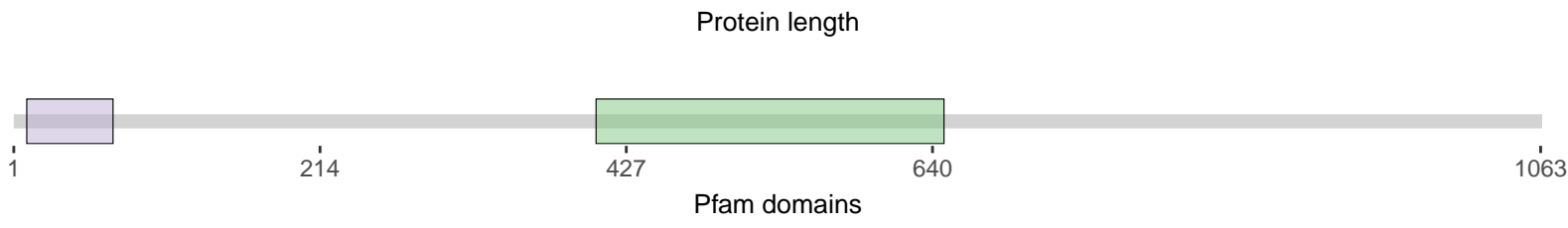
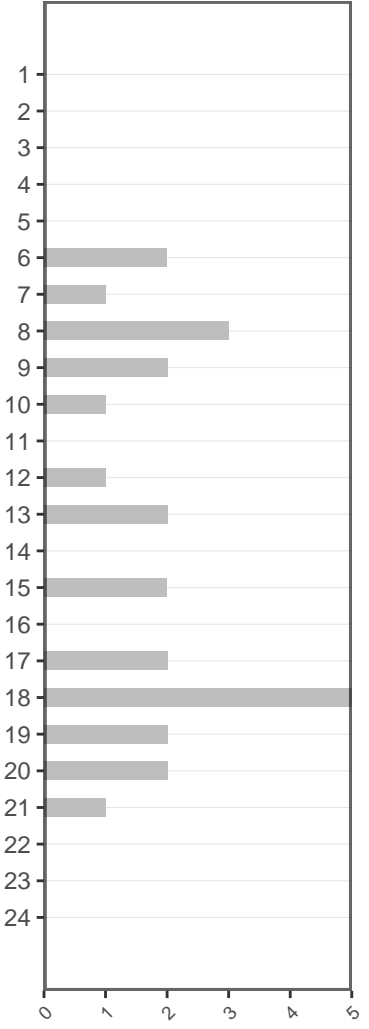
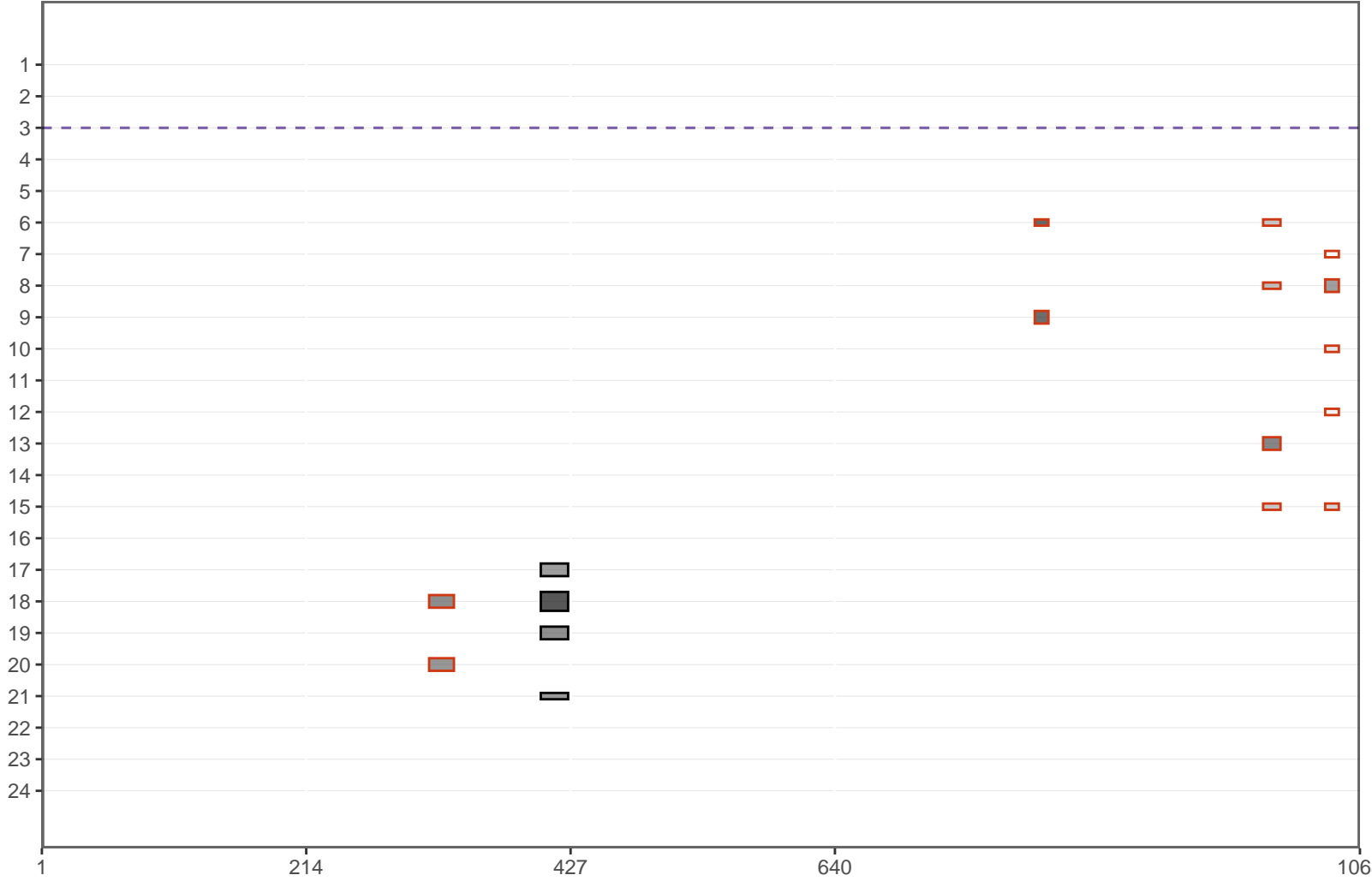


MW indication

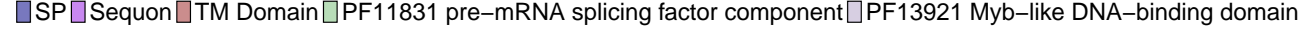


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

EEARQALLRRKSKVLGRELPRPPIASLELRISLLRADEDEKSFVPTTJEGADEMRKELLSLEHDSNKYPLDVKAEKKNKGVKRRKVAEPRIEDFDEDELKADGLKDEAGFVRVAMGHEGSELDEFVEAHKFTLNDIMYFPTTRNAVGLSVAQNMELKLAALQNEFENLKKKMDDTKATKLEQKIKVLTNGYQMRAGKLIWBGIEATFKGMDTAGTELEFRALQKGEQLAASHRRINLWEEVQKQKELERTLQKRYGDLIADKEMQHLMDFRIDQAGMGEIYA

NbL04g02300.1 splicing_factor_3B_subunit_3-like [MW = 134.62 kDa]

No. of times detected



log(intensity)



Values from



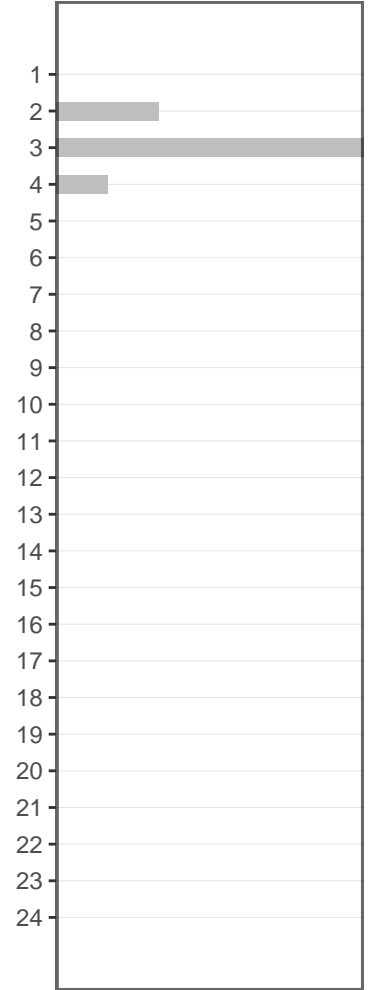
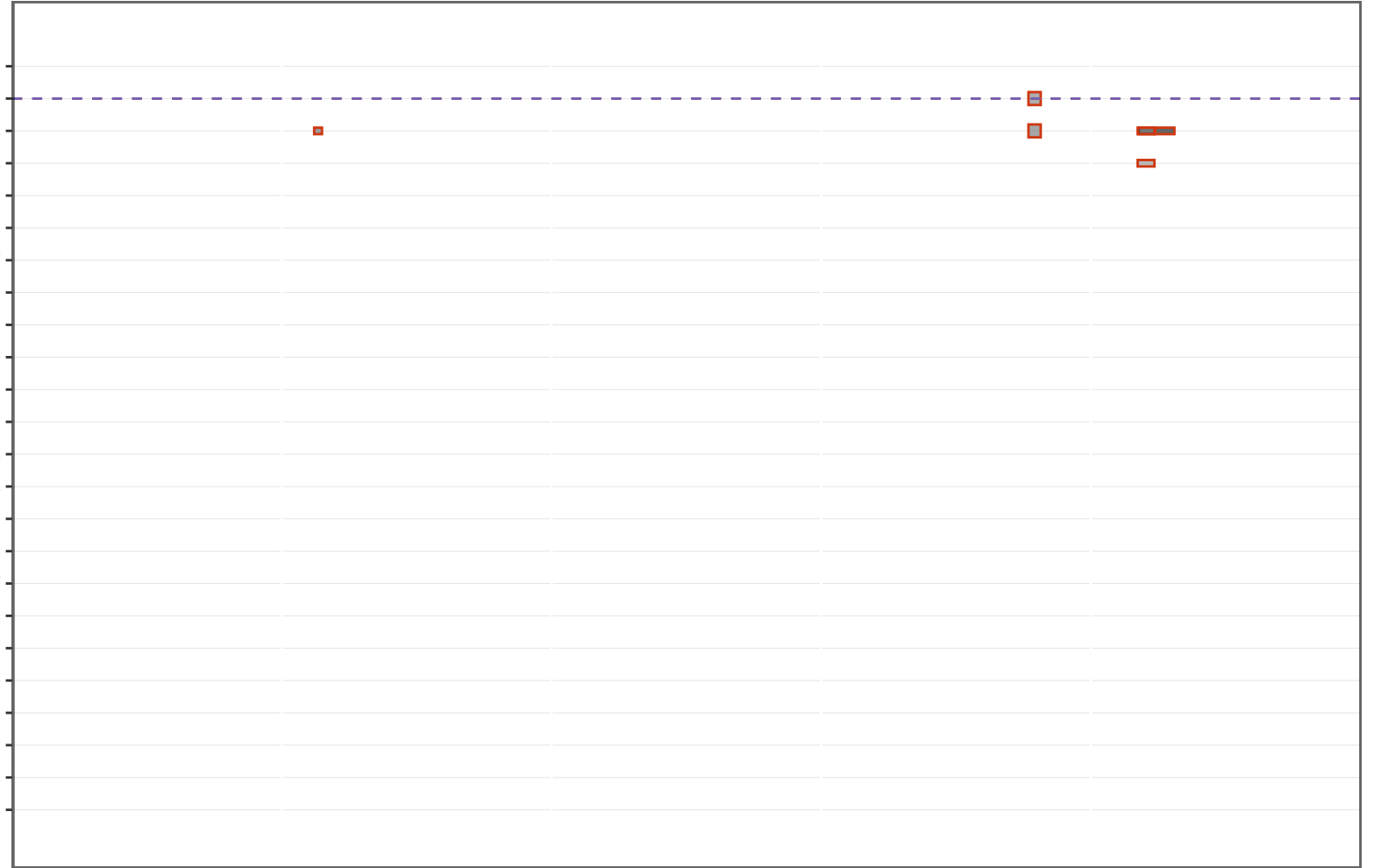
MW indication



Molecular weight



Gel Slice

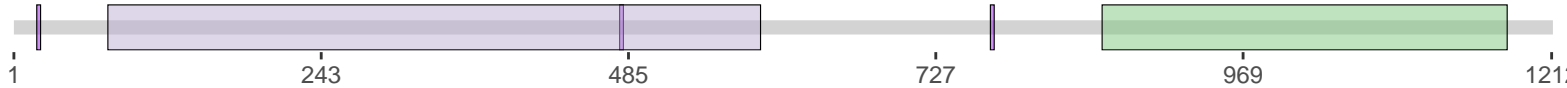


Protein length

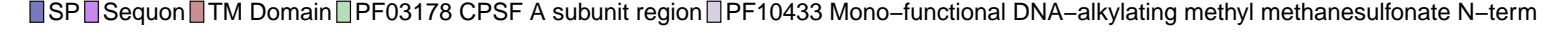


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

QRSRFLAVGYSYDNTIRRLSLDPDDGMVLSLGGVSSPPEILLFLFVQASIGGDEGADHPASLFLNAGLGNGLFRFTVDMITGQLSDARSRFLGLRAPKLFSLVVRGRRAMCLGSSRPVLGYHQGHFLTLPVSEYLETFAAFSSDDQCAEGVWVAGDALRVFTIERLGETFNETAIPRLVTPRRFVLPKPKRMVIMESDQGAYTAEREAAKKECFETAGNGENGAEGVENSDEEDGNDPLSDQEGYKPKSESGRWVSGIRVLDPRSTFTTLLLEODNEAAAFSCTVA

NbL04g02270.1 histidine_biosynthesis_bifunctional_protein_hisIE_chloroplastic [MW = 31.45 kDa]

No. of times detected



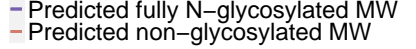
log(intensity)



Values from



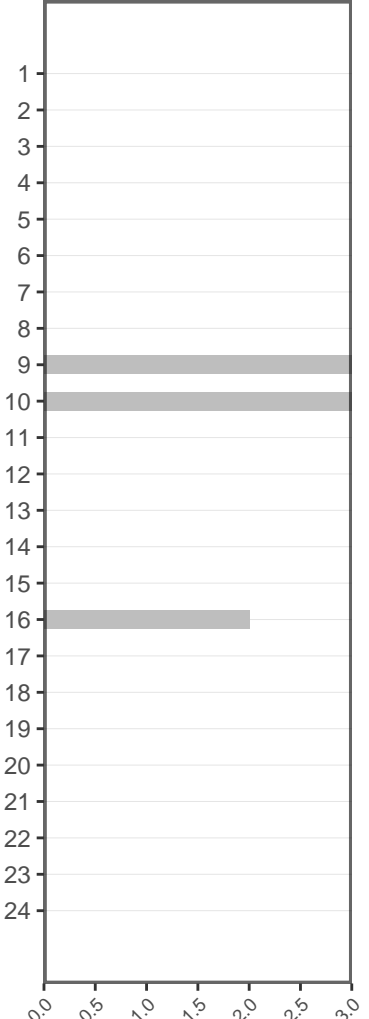
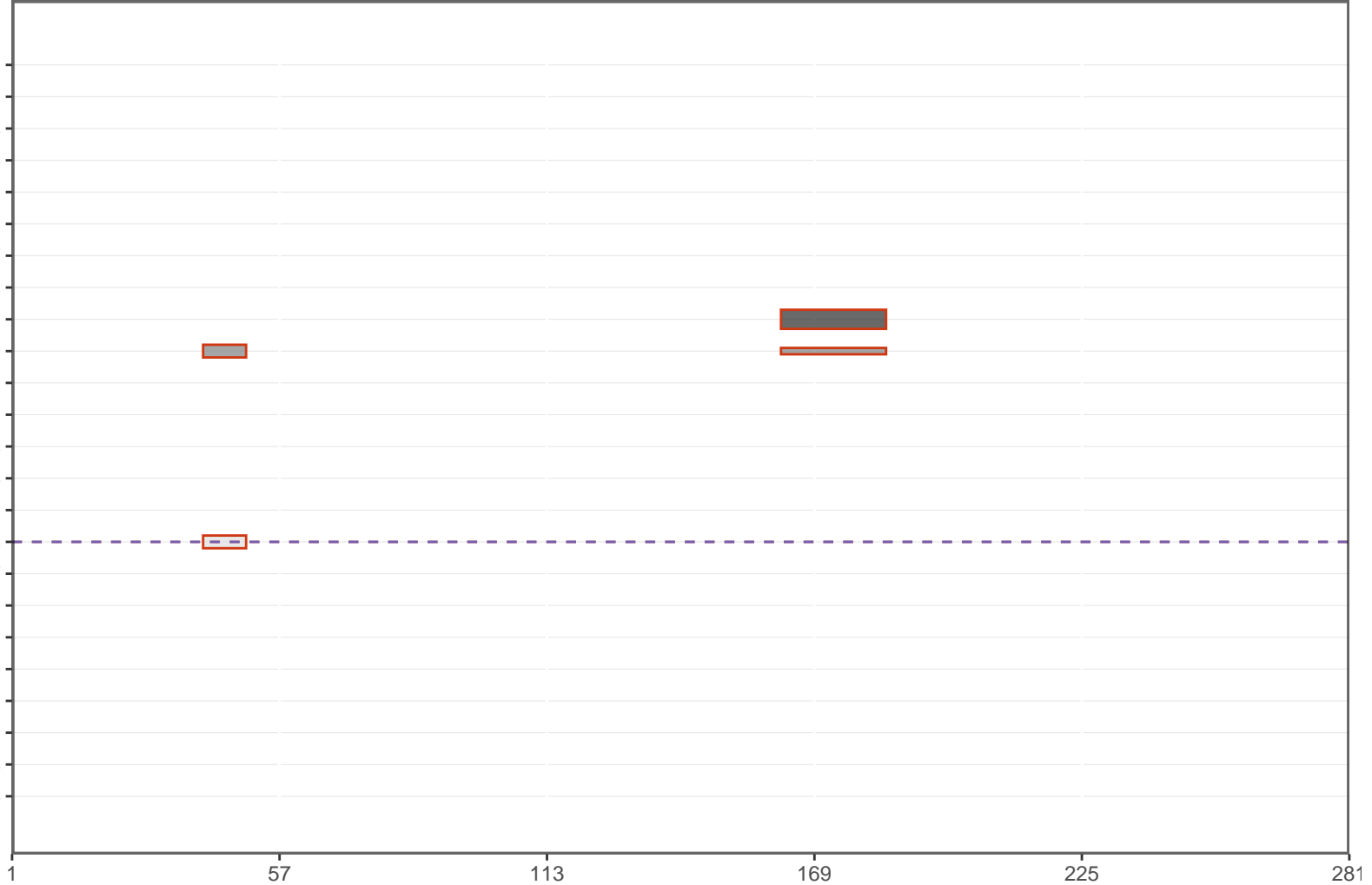
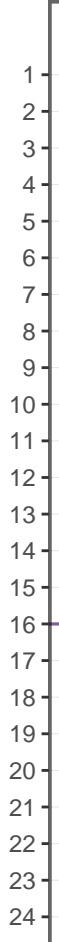
MW indication



Molecular weight



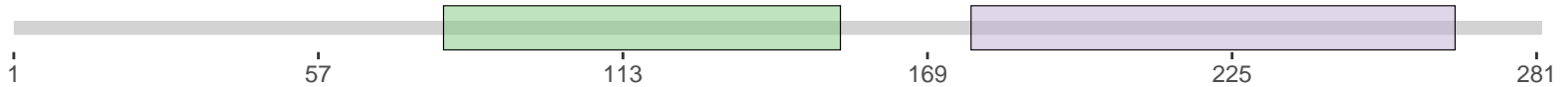
Gel Slice



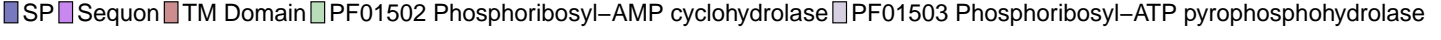
Protein length



Pfam domains



Pfam Description

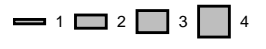


Protein sequence:

ICDRDSIYLKQPDGPTGHTGSETGYVYTVGDLKNTVEKENELAMFTFLVALESTNKKAETSSSSSSGKPPWTKRLLLDKLLCGKIREAEDELGRLEENEDKGRITASEMADAVYHAMVLLSLRQVWIEEVLQVLRQRFKSGGIEENRKE

NbL04g02220.1 2-oxoglutarate_dehydrogenase_mitochondrial-like [MW = 115.56 kDa]

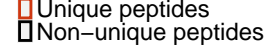
No. of times detected



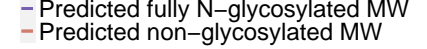
log(intensity)



Values from



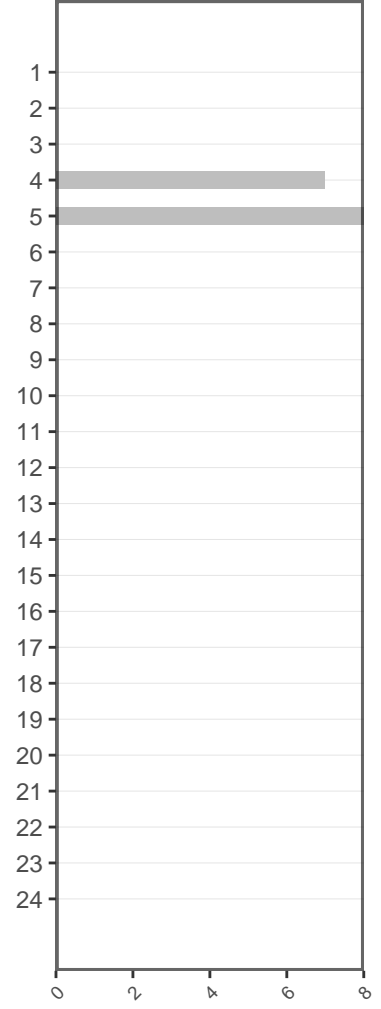
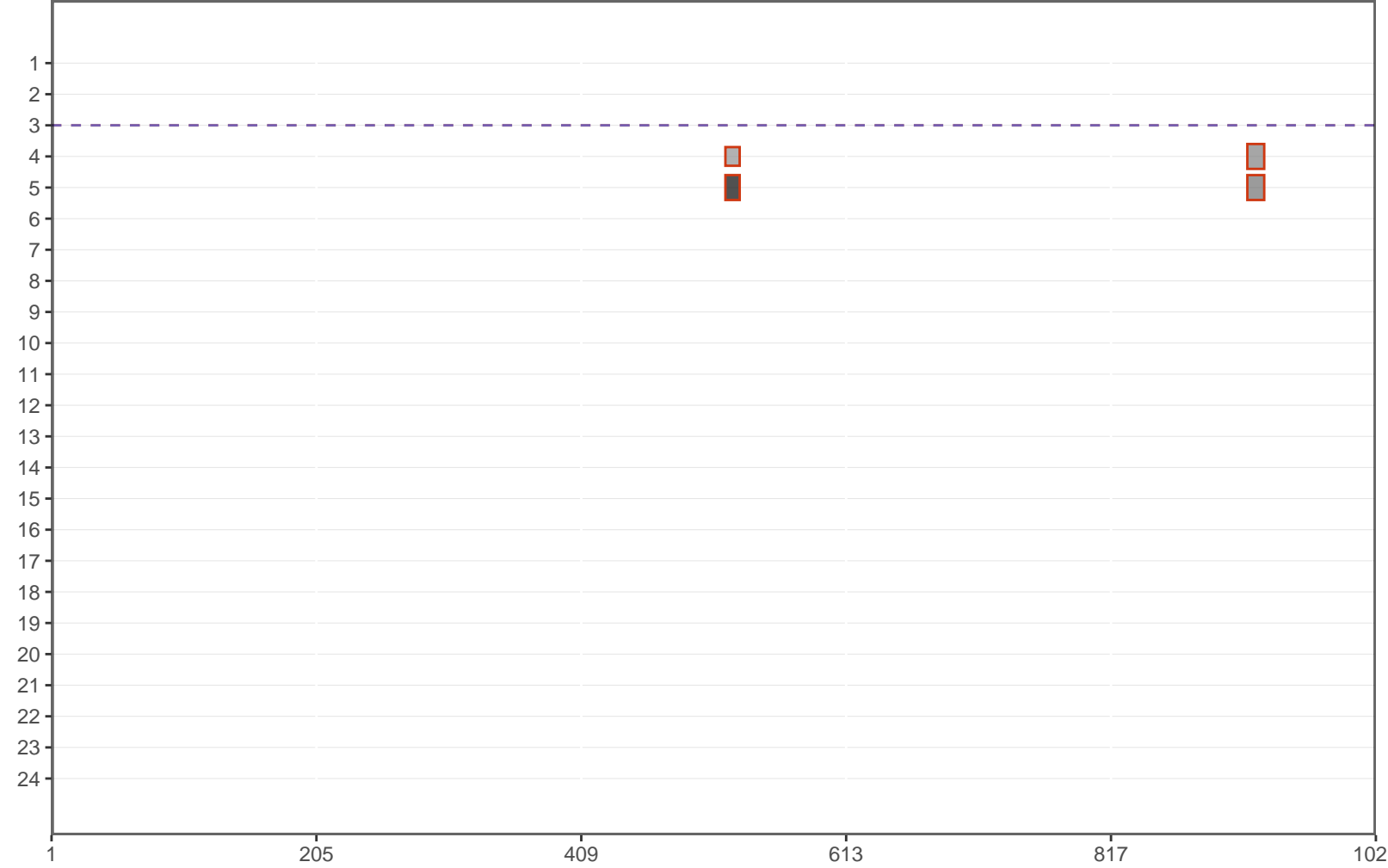
MW indication



Molecular weight



Gel Slice

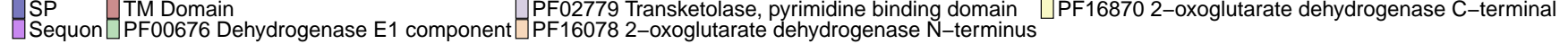


Protein length



Pfam domains

Pfam Description



Protein sequence:

IRFGHNEDEPSFTGPKMKYKVRSHPSALEIVGDKLLOGSGVTKDDVEKIHKNKINLNEEFVASKDHPQKRDLWLSAFVSGFKSPAGLSRVNRTGVNPEIKDKGKATFLPEDFKPRAIKVYDERKKMETGERVDWALGEALAFATLLVEGNHVRLLSGQDVERGTFSRHSHVLIHQETGAKYCPLDHVMNMGNEEMFTVSNLSLSEFGVLGFELGYEMENPNLSLWLAQDFGDFENGAGVIFDQFLSSGSEAKWLROTGLVLLPHGYDGGGPEHSARLERFLQMS

NbL04g02200.1 actin-depolymerizing_factor_2 [MW = 23.93 kDa]

No. of times detected



log(intensity)



Values from



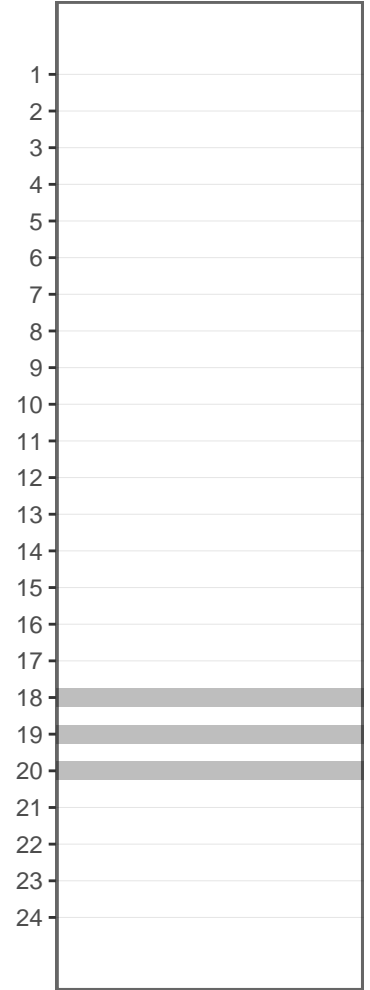
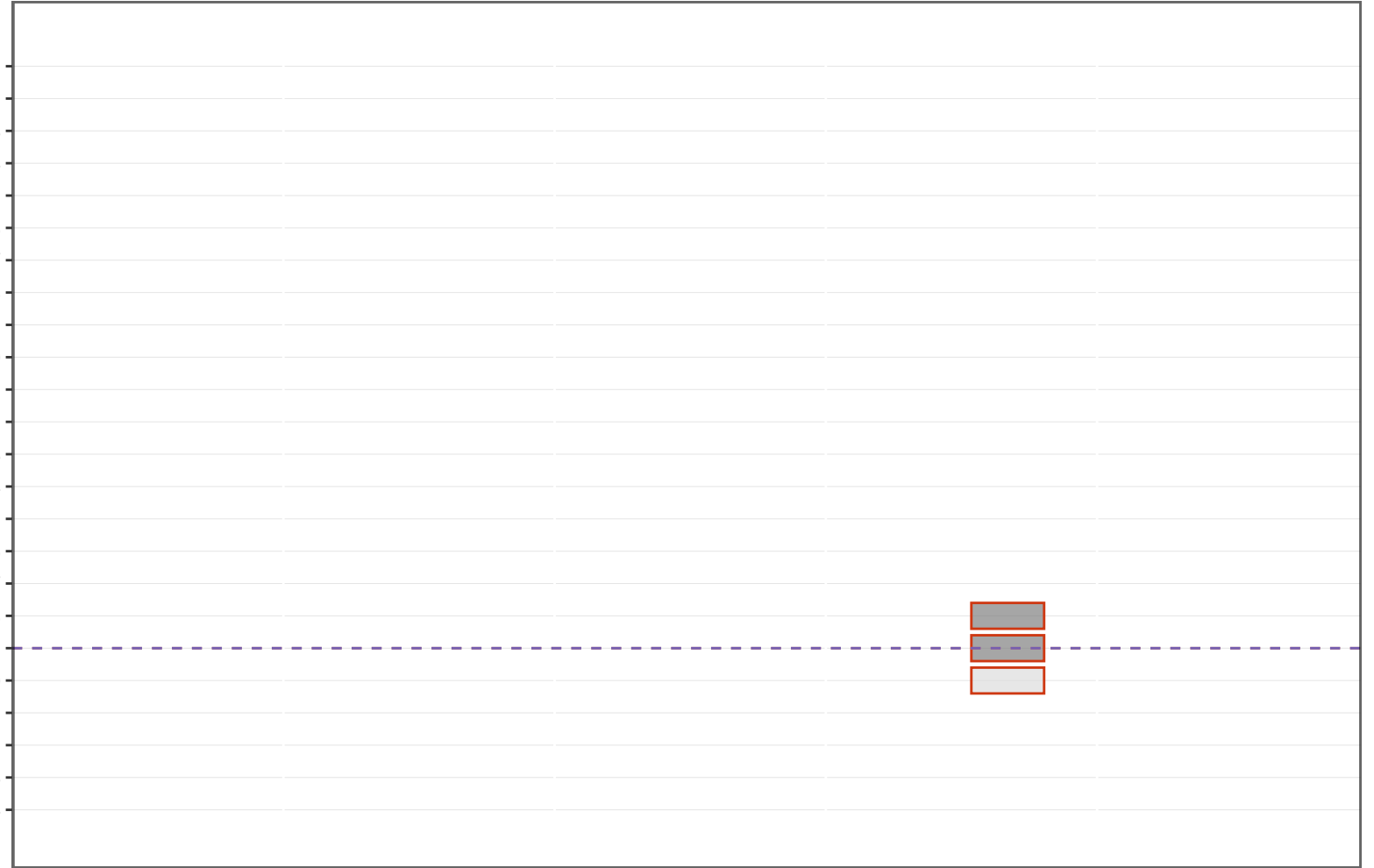
MW indication



Molecular weight



Gel Slice

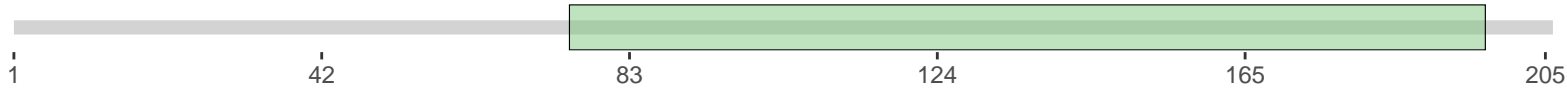


Protein length

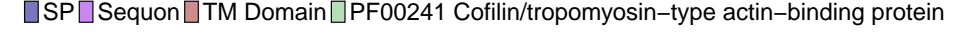


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

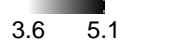
IFIIYKIEEKQKQVYVEKLGEPTEFSYEDFTAGLPADEGRWAVYDFDTEENVQKGRFFFAWSPDARVRKMMYASGKDRFKRELDGFVQLGATDPTMGLDVFRRRVGGED*

NbL04g02180.1 heat_shock_cognate_70_kDa_protein_2-like [MW = 71.31 kDa]

No. of times detected



log(intensity)



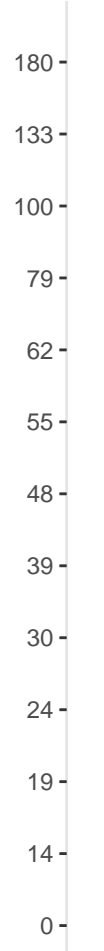
Values from



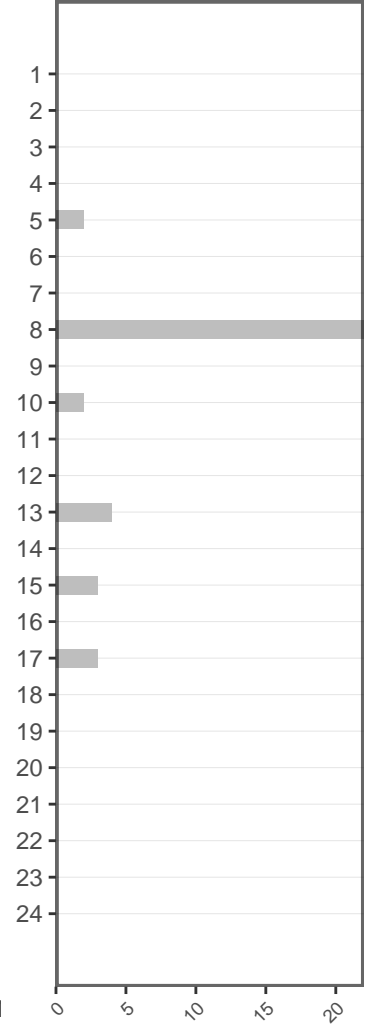
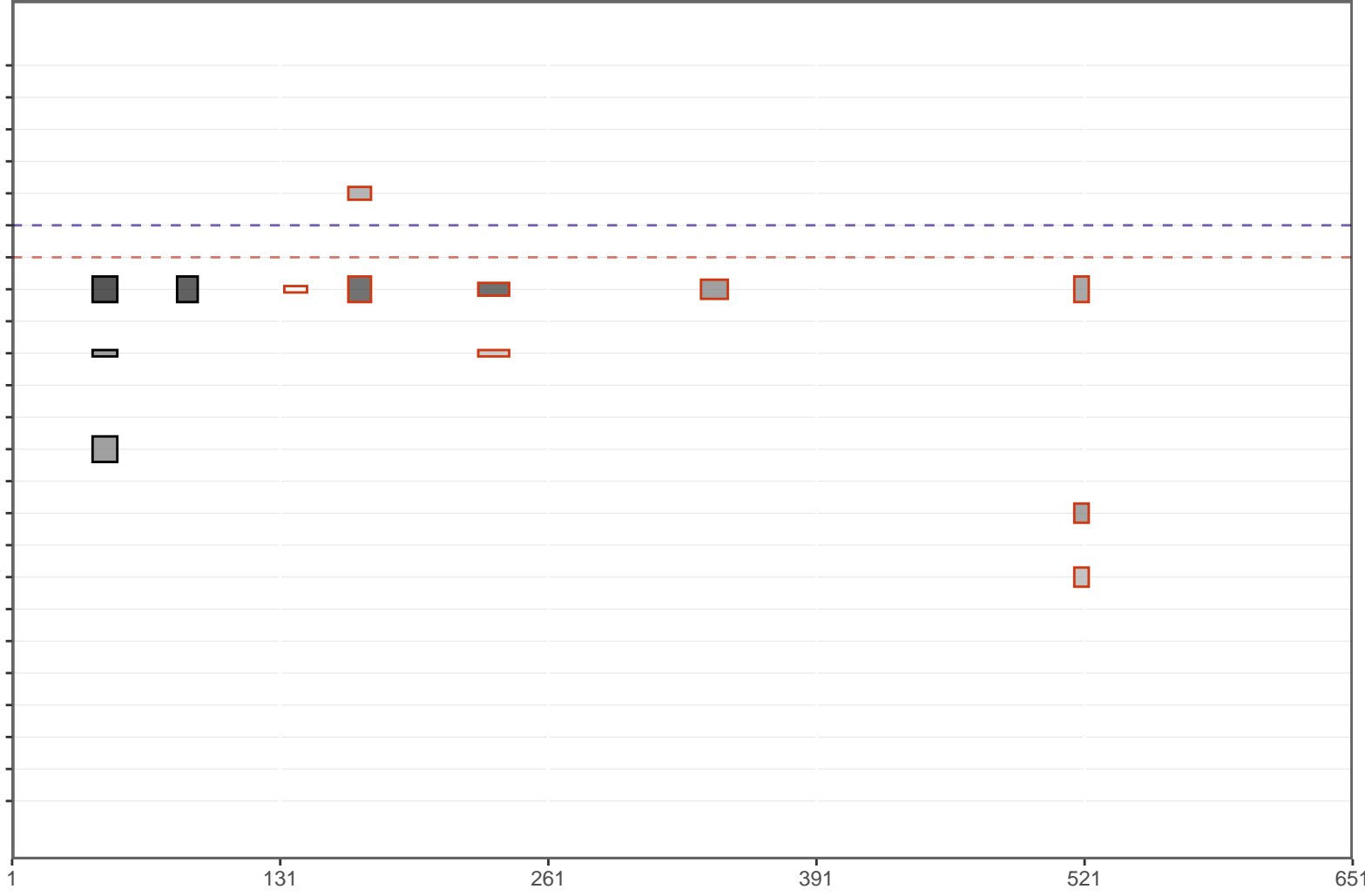
MW indication



Molecular weight

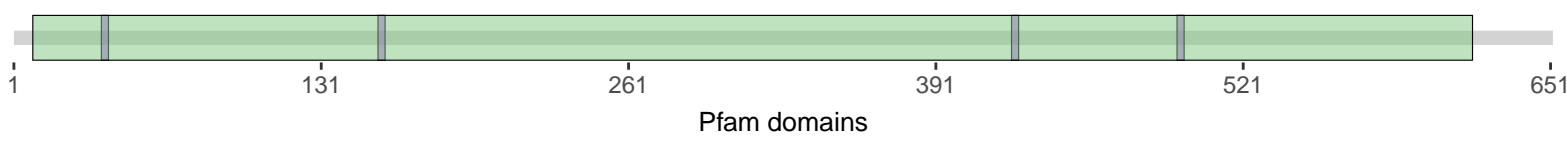


Gel Slice

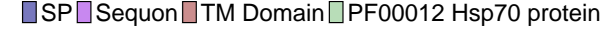


Protein length

Peptide counts over 4 repeats



Pfam Description



Protein sequence:

LFRRKCEPVEKCLRDAKMDKSGVHDVLLVGGSTRIPKVGQLGDFRNKELGKSNPDEAWYGAAGQAALSGEGNEKVDLILLVDFPLSLGLETAGVMTVLRNRTTPTTKQEGVFTYSNGPGVLIQVVEGERARTRNLLKGFELSGIPAPRGPVQITVCFDIDANGILNVAEDKTTGQKNITITNDKGRLEKDEIKMVGQEAERYKAEDEEHKKKVEAKNALENYWMNRNTKDEKIGAKLSPDQKKKIEDAIDGSHWLEGNLGAEEDEFDDKMKLESICP

NbL04g02150.1 triosephosphate_isomerase_cytosolic [MW = 27.56 kDa]

No. of times detected



log(intensity)



Values from



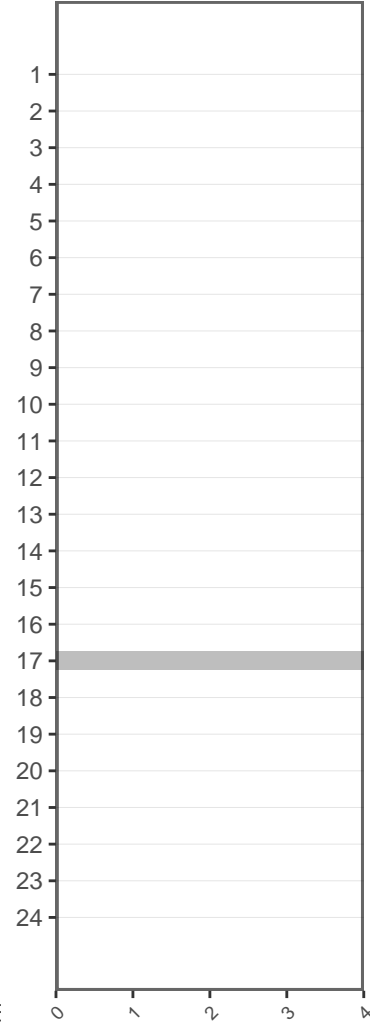
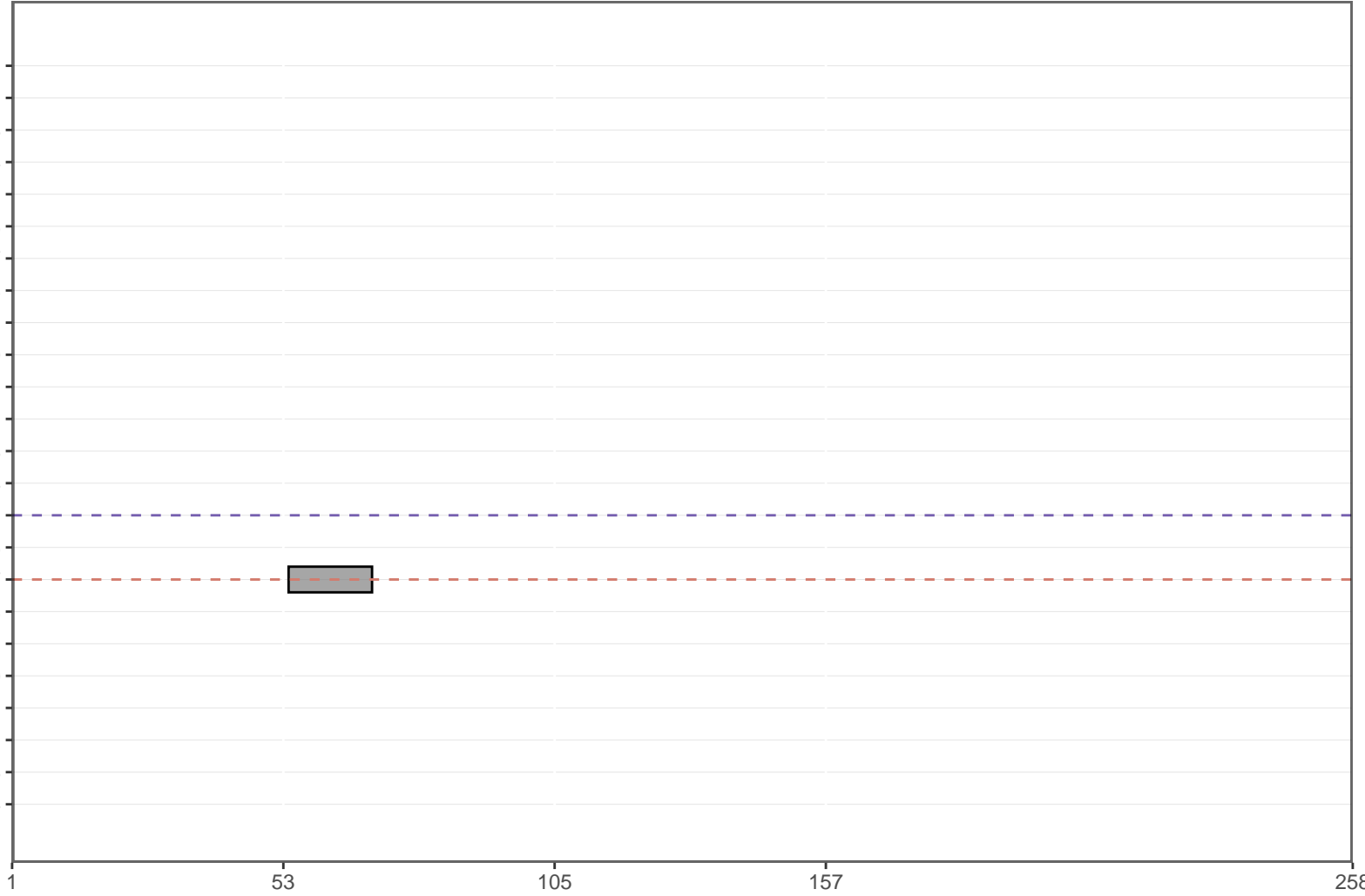
MW indication



Molecular weight

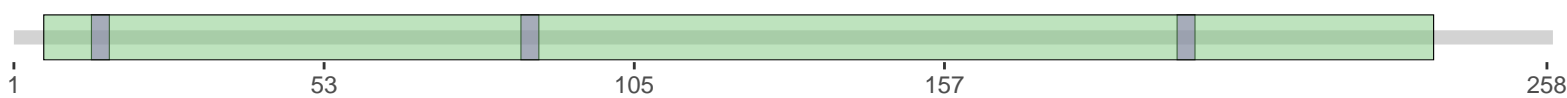


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AYAISQGLKVIACVGETLEGRREGSGTIDVAAQTKAADRKYKDWTKVAVVEPFWAAGTGRKVASFRQAGDEVHAELRRWLGQVNSAEVASTRHHYGGSGVNGANGKELAGPDDIGFLVGGASLKVQENTLELLSSVYVWLNKG

NbL04g02080.1 peptidyl-prolyl_cis-trans_isomerase_FKBP20-1 [MW = 20 kDa]

No. of times detected



log(intensity)



Values from



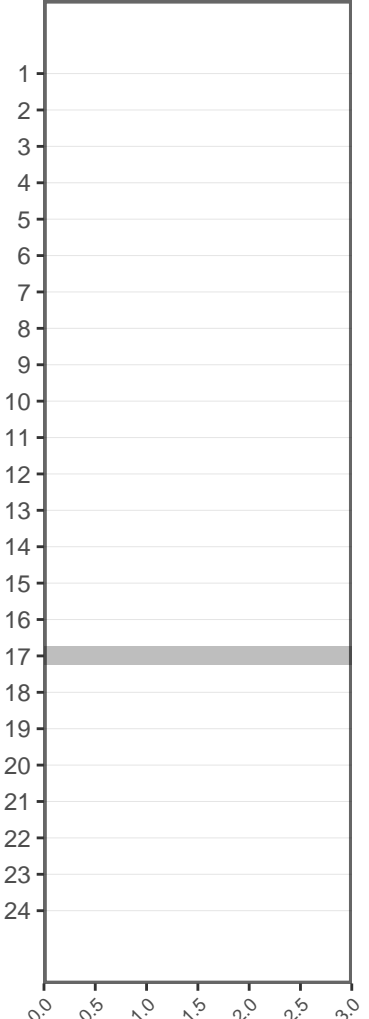
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

KVGEIAVITCKPEYANGSAGSPDPDPDTLVFEVELVACRRKRGGSISVSDERARLEELKKGREMAAAKKEEKKREAAKAAARIGAKLEAKKGGKGGKAKI

NbL04g01920.1 uncharacterized_LOC107771755 [MW = 35.97 kDa]

No. of times detected



log(intensity)



Values from



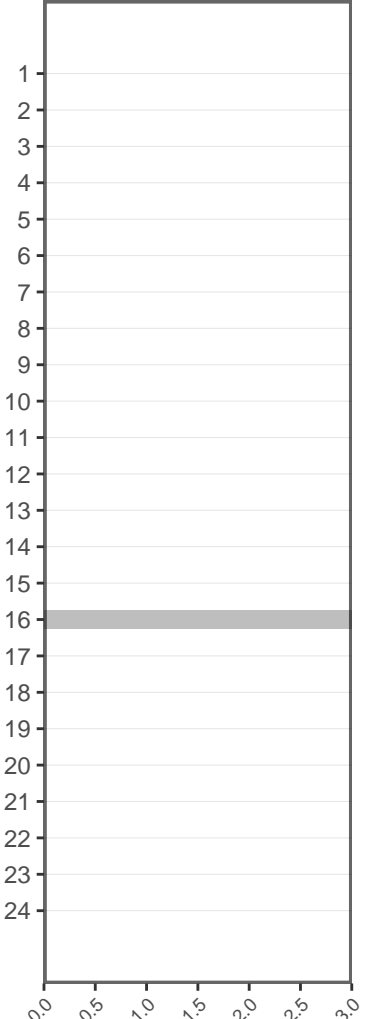
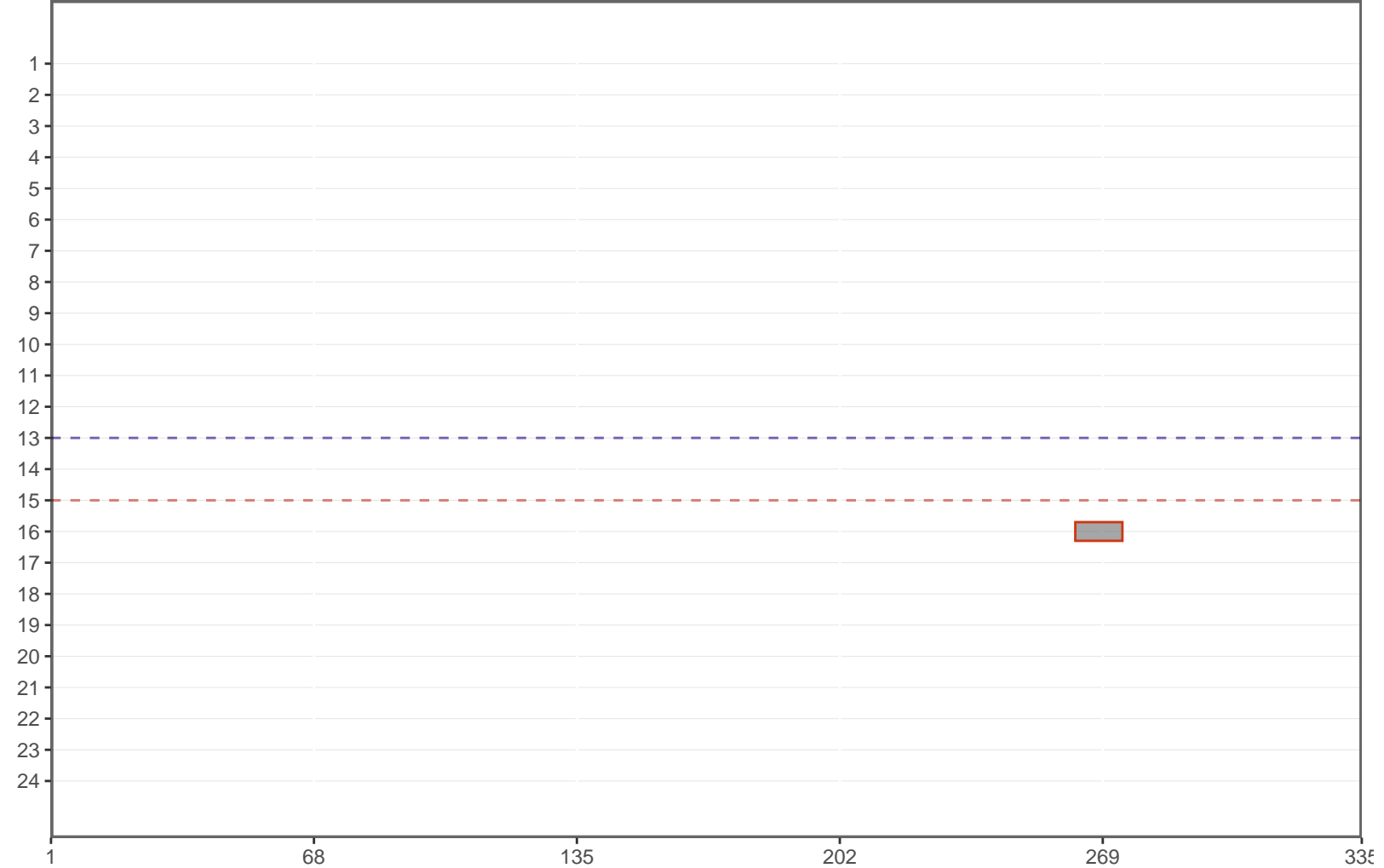
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

YLGISLVLVIGISTPGLLGAADGFSFPPDYGERIARHEAAHFLVWVIGLPLIGYSLDKGKEHVNVDRELEKLYSGGLDKELDRLLAWAMAGLAAEGLYDVKVIGGSAIDLFTLGRFLNRKSPSLKDDGGGNLTRWVLFAGSLKNNKLEHALITAMTNKASVTEGIEAEKAA*

NbL04g01860.1 acylsugar_acyltransferase_3-like [MW = 51.42 kDa]

No. of times detected



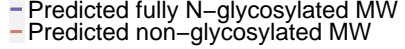
log(intensity)



Values from



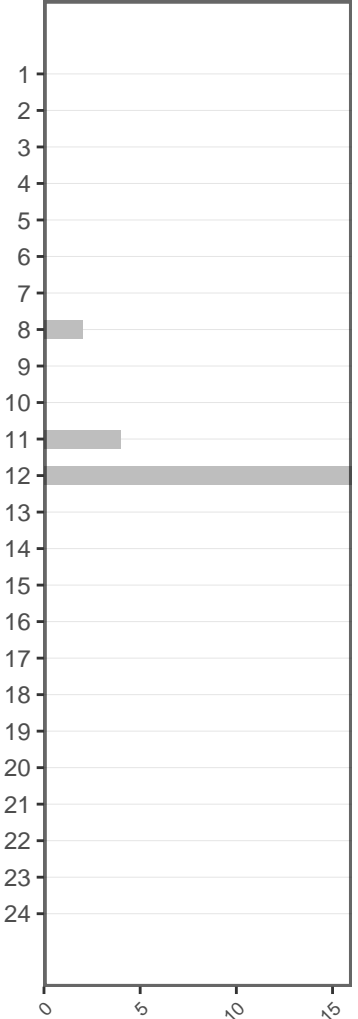
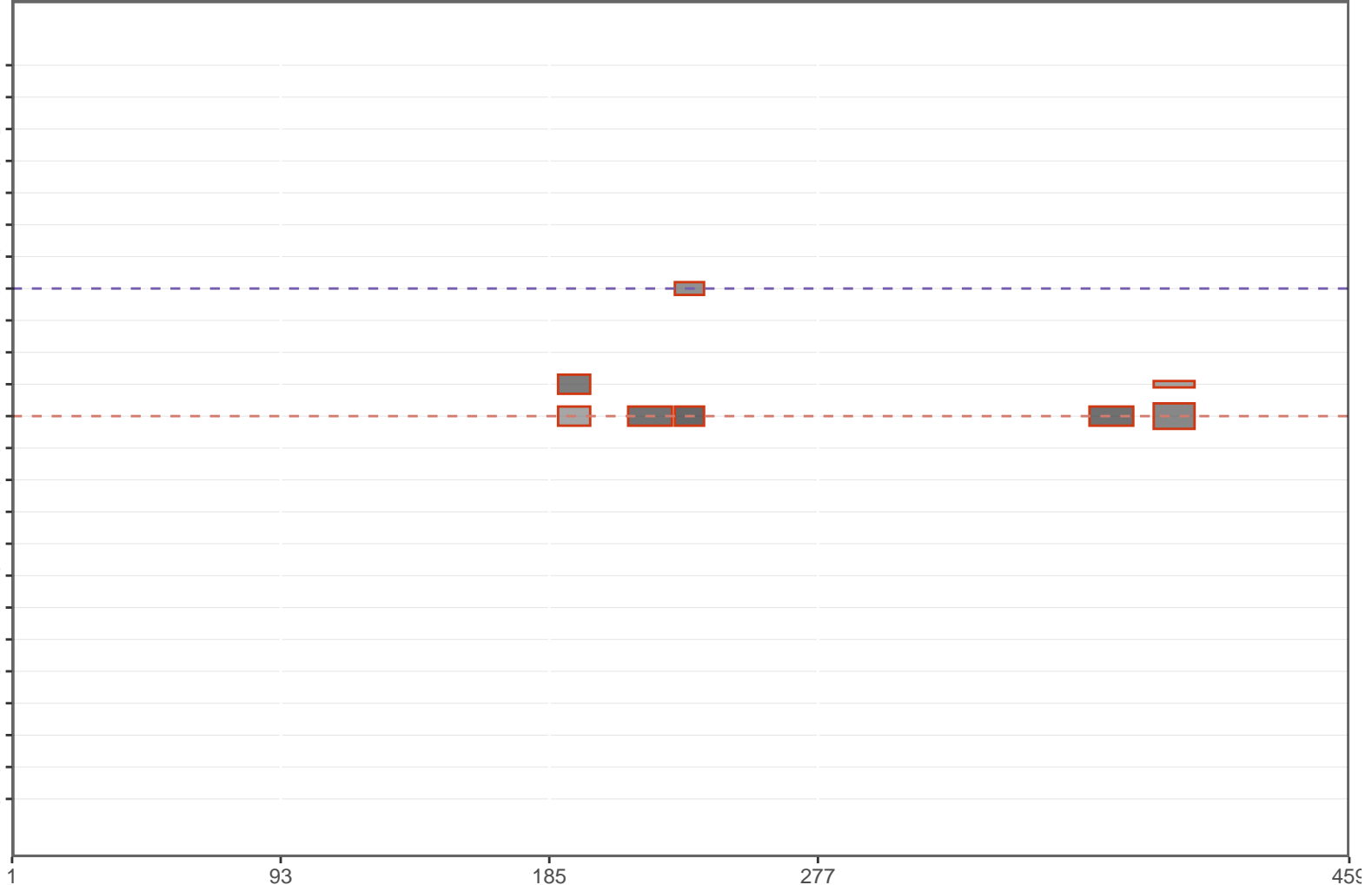
MW indication



Molecular weight

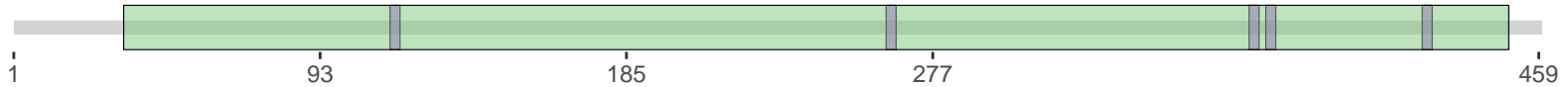


Gel Slice



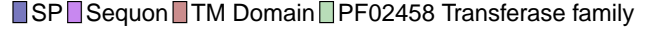
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

AASLYPPTKDMANLPEVYKPGKEGSGKFTFSBKLALRARVINNSNGINPTTEVSAFYIGRAMATKKKSLGSGPVALQAMNLRPLPKTLMGNGSFFVITDEKEMDLRLLVGLKLEAKEEVRKRYKHDKTDFLPTTIELYKEANDSFFNNGCYDHYRFSBKNKFFPNVDFGWGKPEKVSSSGNGPVKNMLVMDNKGDDGVVYVYKMEQDMSALEKDEELLEFAFSPNM

NbL04g01850.1 acylsugar_acyltransferase_3-like [MW = 51.4 kDa]

No. of times detected



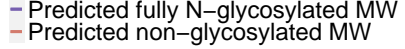
log(intensity)



Values from



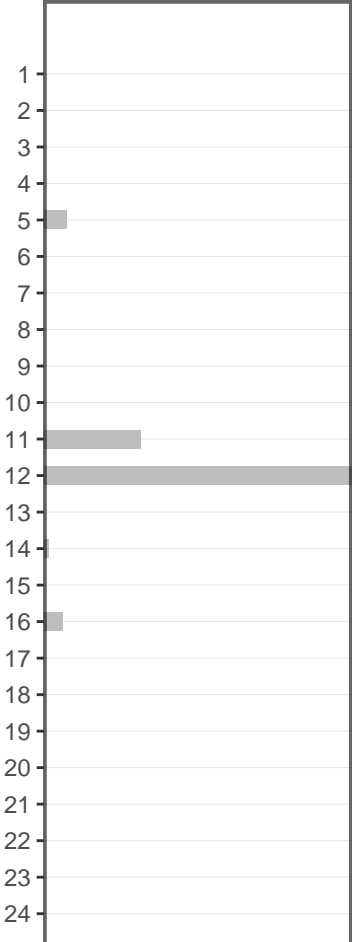
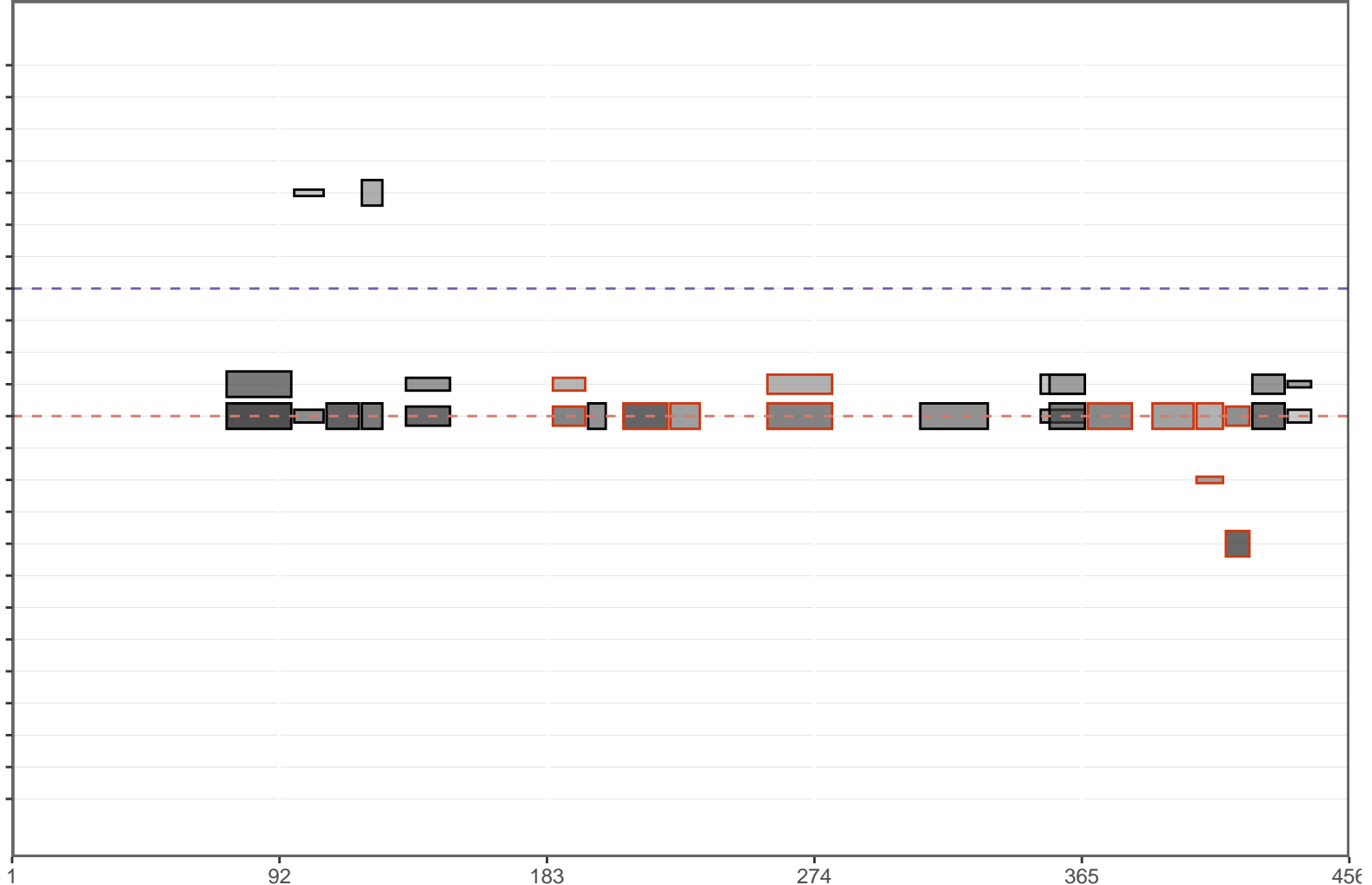
MW indication



Molecular weight

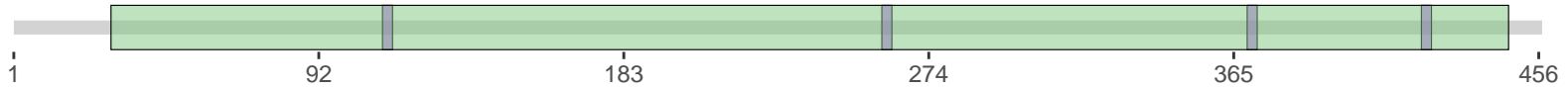


Gel Slice



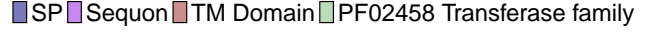
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

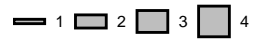


Protein sequence:

SIFPPTXDMNLLVWPKGEEGSSKGF7FSSKLAALRARINNSNIGNPPTTEIVSAFYGRAMATKTKTSGGSGPSVLVQAMNLRPLPKTKLMGNGSFFVITDEKEMDLPRLLVGLKREAKEEVRKRYKHDKTDFLPTTHLKYEGNDGFYNSGVDYHFRFSSVHKPFYVNDMDFGWQKPEKVMSSNGPKNVNTLMLMDNKGSDGVEVYVYMKEGDMSALEKDELELFASPM

NbL04g01810.1 reductase_large_subunit-like [MW = 91.34 kDa]

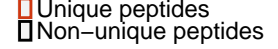
No. of times detected



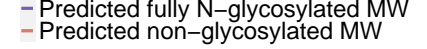
log(intensity)



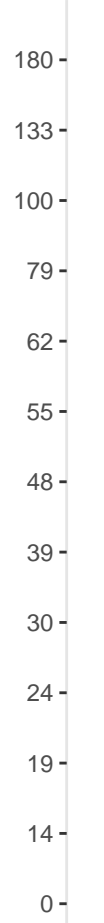
Values from



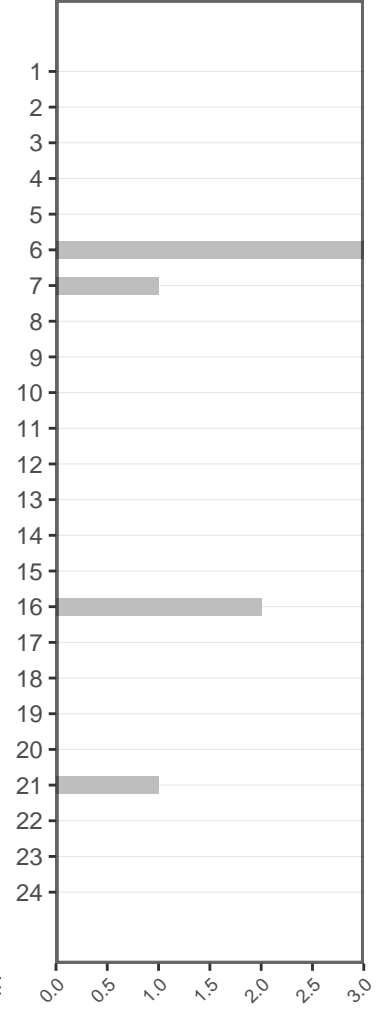
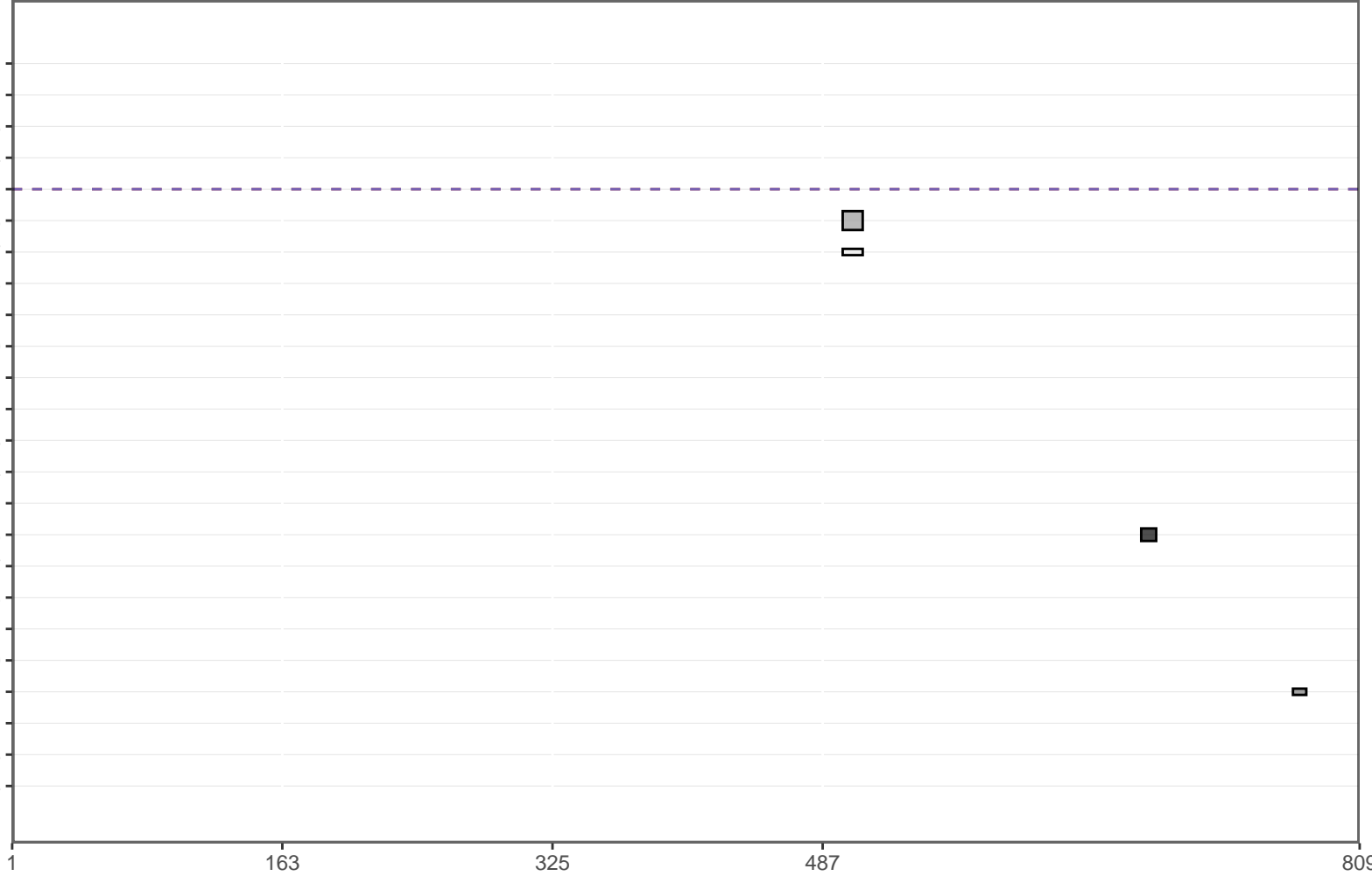
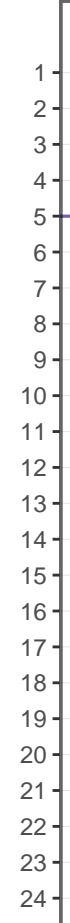
MW indication



Molecular weight



Gel Slice

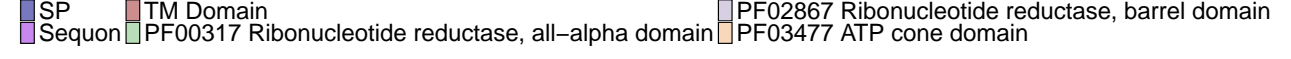


Protein length



Pfam domains

Pfam Description



Protein sequence:

VFELKSOIETGTPYMLYKIDSCARKSNQGNLGTIKSNLCTEHEYSPSTETAVGNLALPRVYREKEVPTESGPKLVGSRGSKNRYDFDKLAEVYALVSTLNKIDNYYVETAKRMSLNRHPISGLGVGDLADTFILLGMSFDPEAGDLKDFETIYHAKASSELAAKEGPEYTAGSPVSKGILQPDMMVGVTSPNRIWDWGVLEMIKNGVNRNSLLVAFMPTASTSQILGNNEGFEPYTSNYSRRVLSGEFVWVNNKHLHLDTMGLWSPTLKNRIYDDGSVQ

NbL04g01790.1 ras-related_protein_Rab11D [MW = 24.59 kDa]

No. of times detected



log(intensity)



Values from



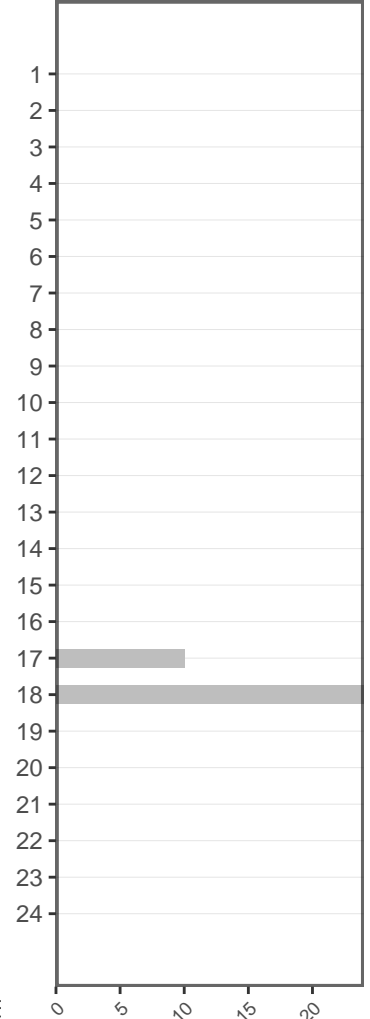
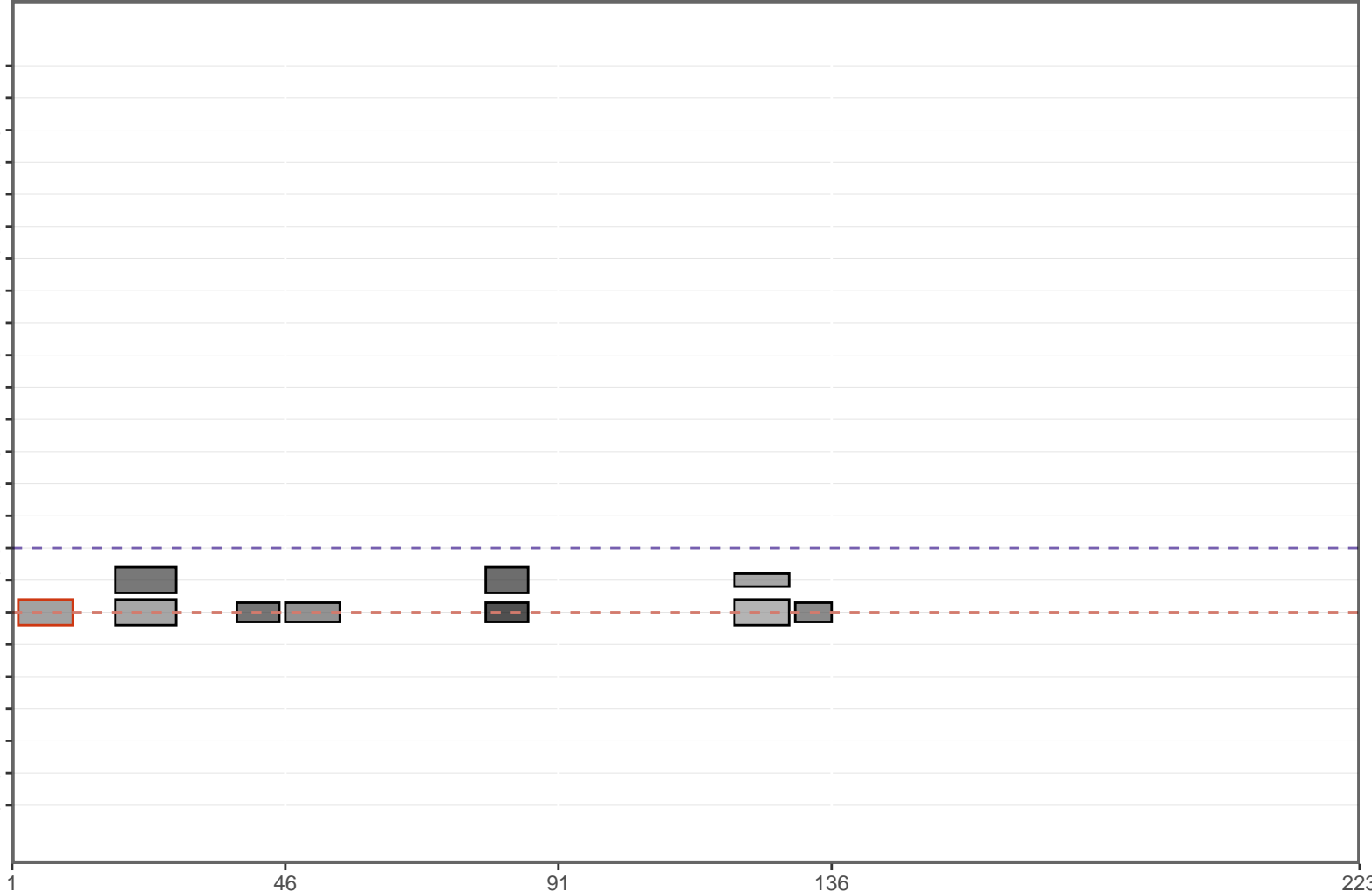
MW indication



Molecular weight

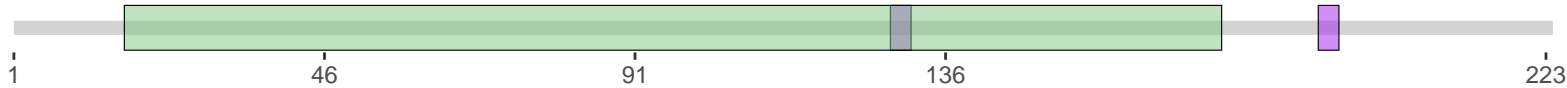


Gel Slice



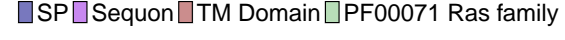
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TKRQTDFHIPRWLEELRAHADRNIVMLIGNKTDLEDRVPTEDAKFEFAQKGLFLETSGAMEATNVEDAFITVLTETFRNIVNKKNLVADENSGNPNASLTGKKLVPQGVPIPKKACGS*

NbL04g01770.1 14-3-3-like_protein_A [MW = 30.25 kDa]

No. of times detected



log(intensity)



Values from



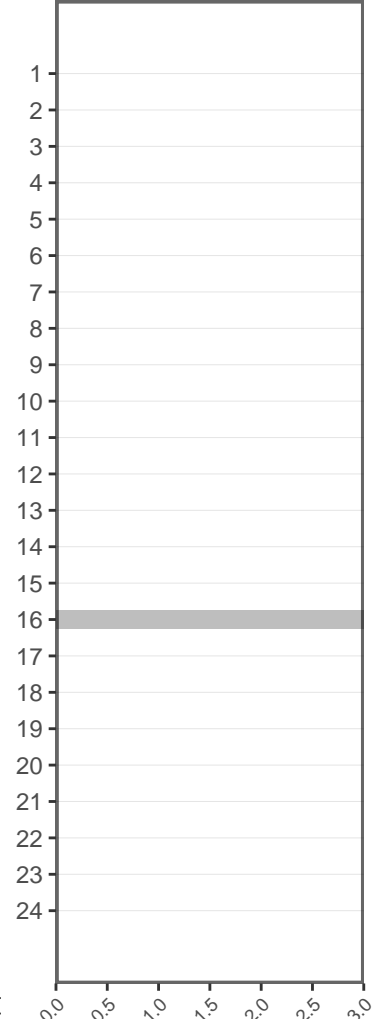
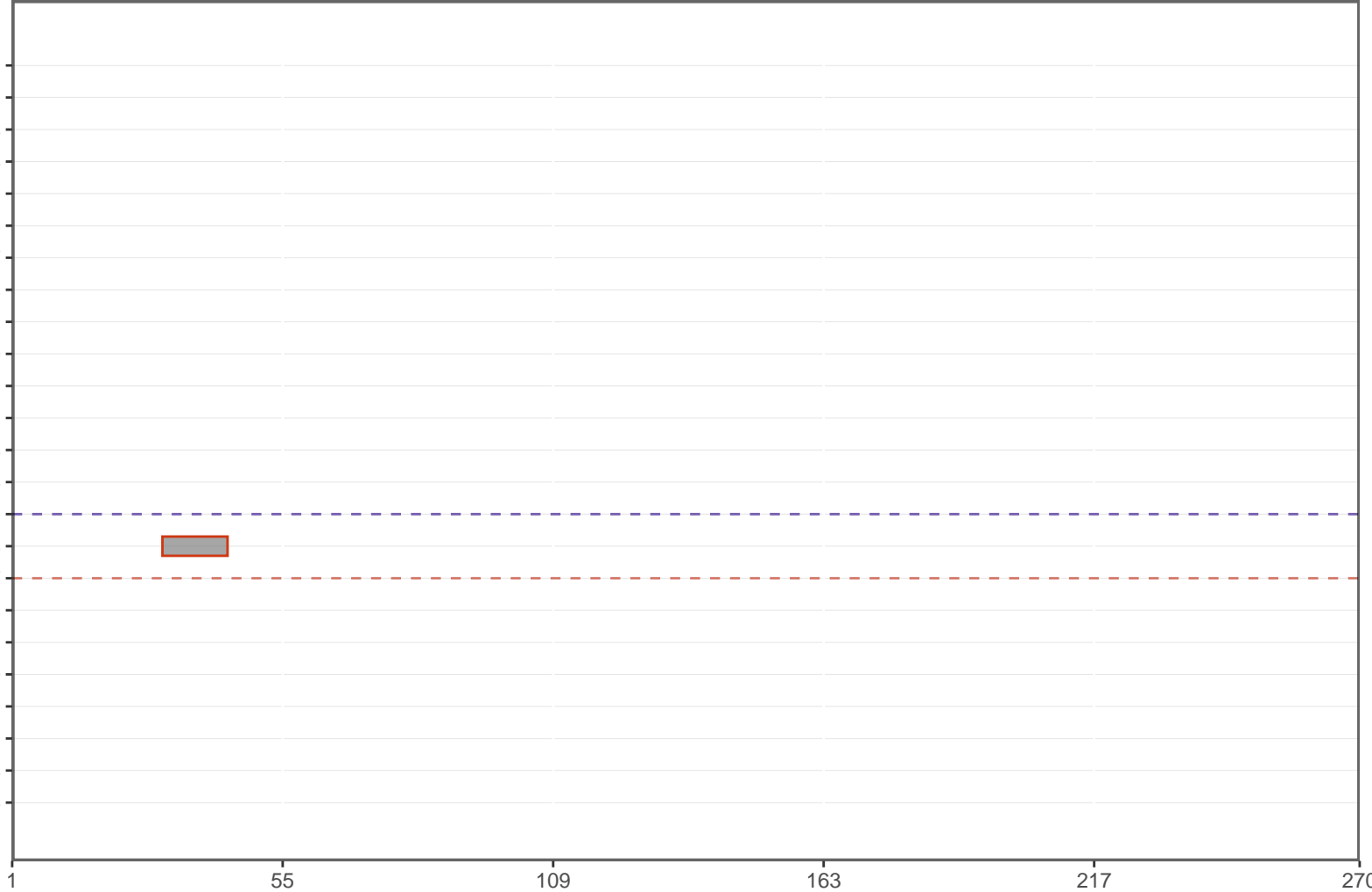
MW indication



Molecular weight

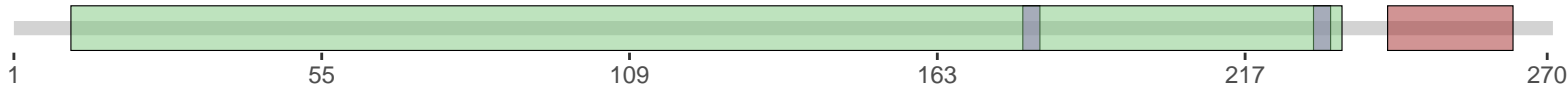


Gel Slice



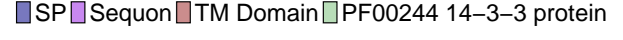
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

YLLKMKGDYRYLLAEFKTGAERKEAENTLSAYKSAGDIANNELAPTHPIRLGLANFVFFYVELNSPDRACNLAKGAFDEAAELDTLGEESYKDDTLIMQLLRDNLTLWTSMDMQVSSFYLLFGLVYLLFFDLSLANPVLVGFSSGGV

NbL04g01670.1 ATP-dependent_6-phosphofructokinase_5_chloroplastic [MW = 60.76 kDa]

No. of times detected



log(intensity)



Values from

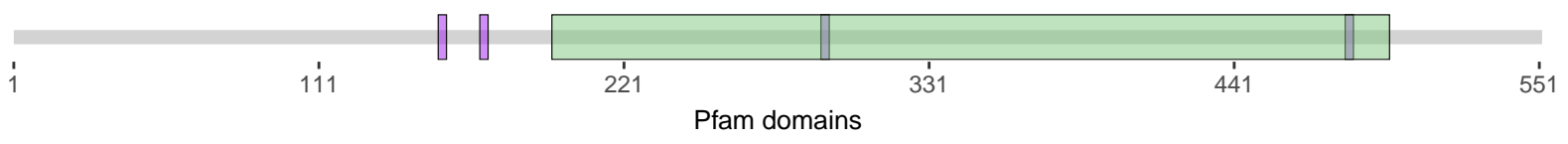
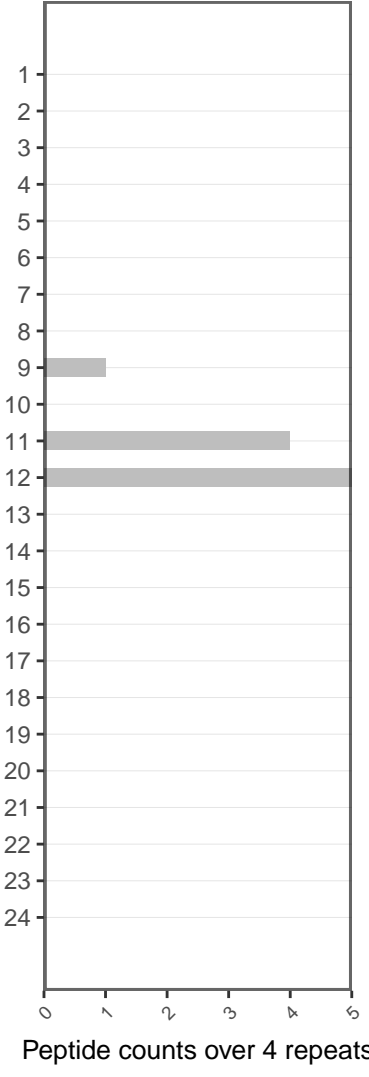
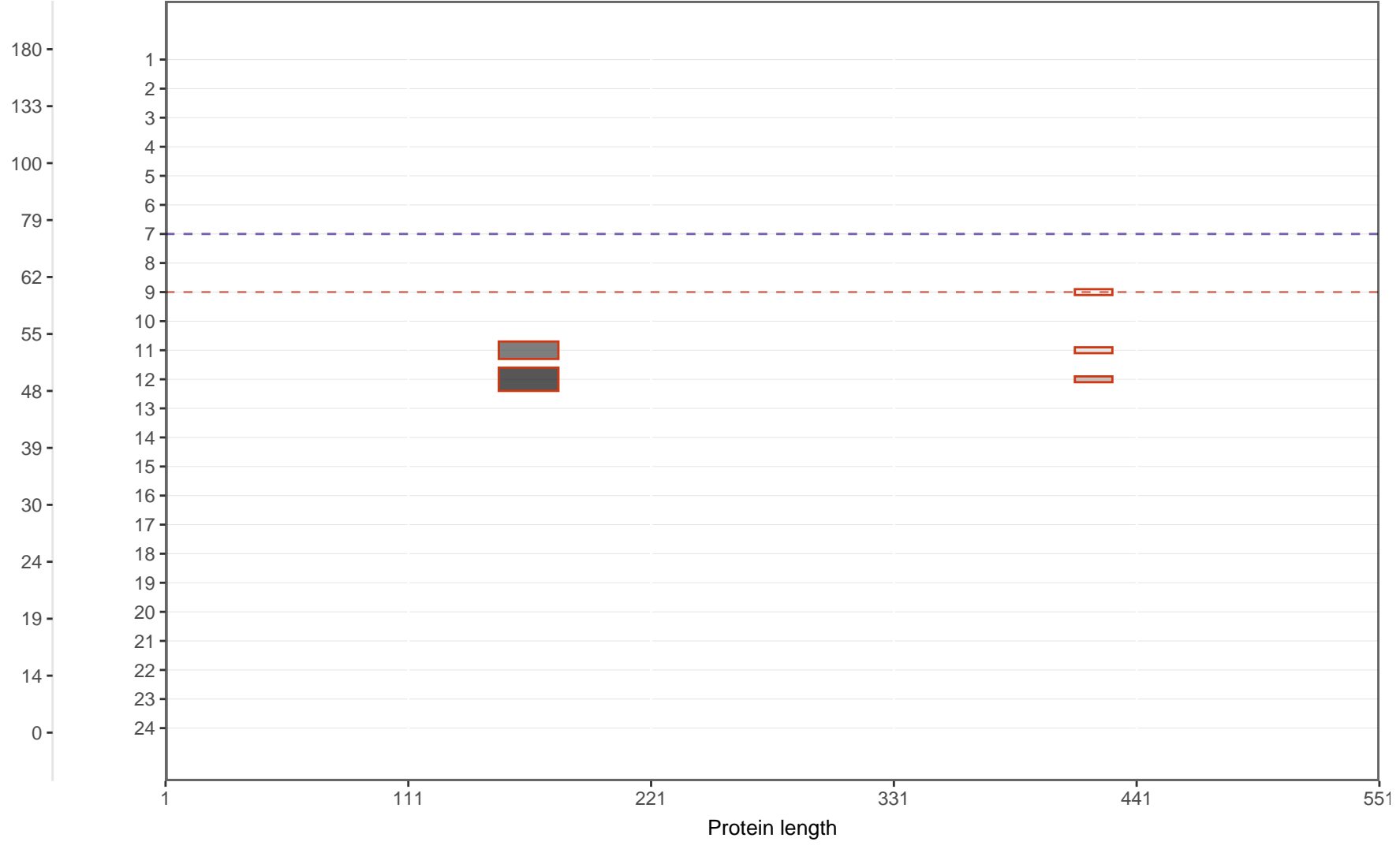


MW indication



Molecular weight

Gel Slice



Pfam Description



Protein sequence:

GVSRGGPKYSDIVDSIGERGINMLFVGGNGTHAGANAHDECRKRHKMKVAAGVVPKTDNDMLMKTGFGFDVAEEAGRAINSAYEASHAVRGVIGVLMGRSSGFAMQASLASGGIDKCLIPFVFNLHGHVGLRHLKYLETNGSAVYVAEGAGDDFLEKTNKADASGNVLDGNGVYLGQEKYFKEMGETSDVWYDPTYMRACRANASDGLCTVLGQNAVHGAFAGYSGFTVSGINTHYVVFPIPEVSKPRVVDNRSMAHRLGFTSGPDFL

NbL04g01590.1 54S_ribosomal_protein_L51_mitochondrial-like [MW = 14.53 kDa]

No. of times detected



log(intensity)



Values from



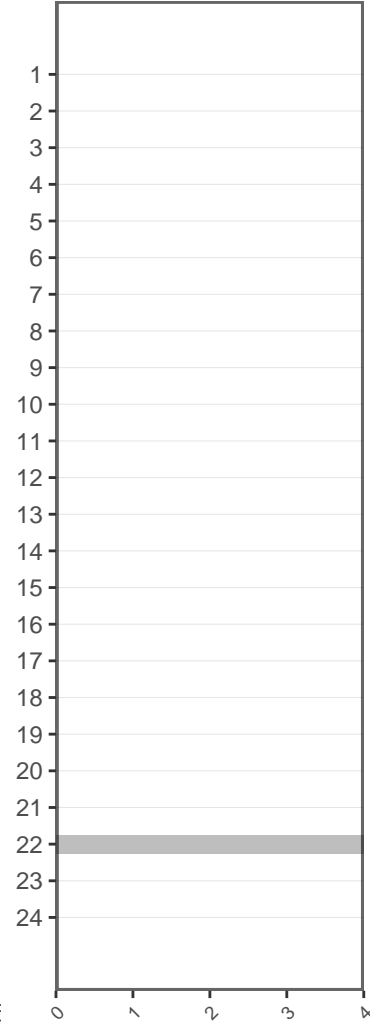
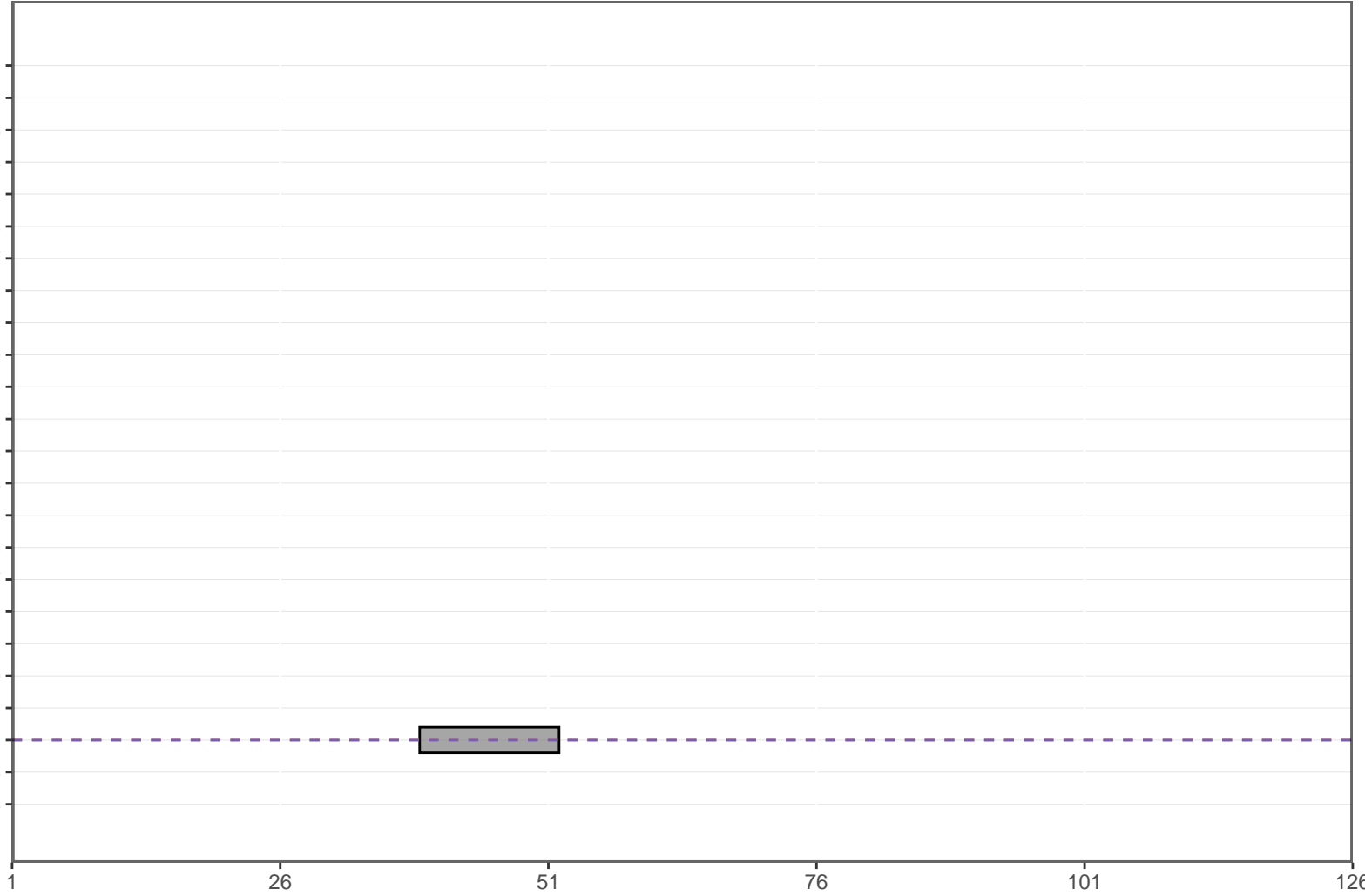
MW indication



Molecular weight

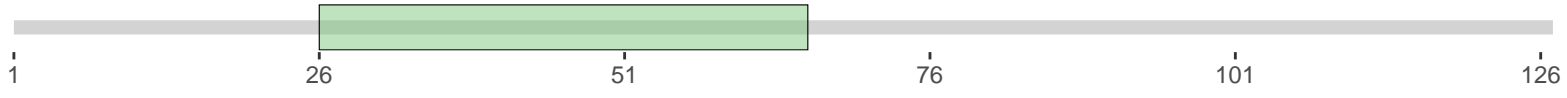


Gel Slice



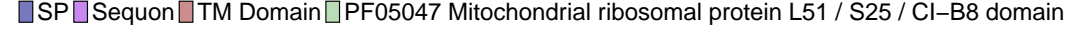
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

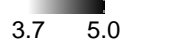
.NRGQHPLKGLYKDERAGCMCEKFEERRRTRBSNQAKEFAWQKGGEDSDSADYKTKRISRYMMNSIEVSLQKFF

NbL04g01440.1 glutamine_synthetase_cytosolic_isozyme_1-1-like [MW = 39.18 kDa]

No. of times detected



log(intensity)



Values from



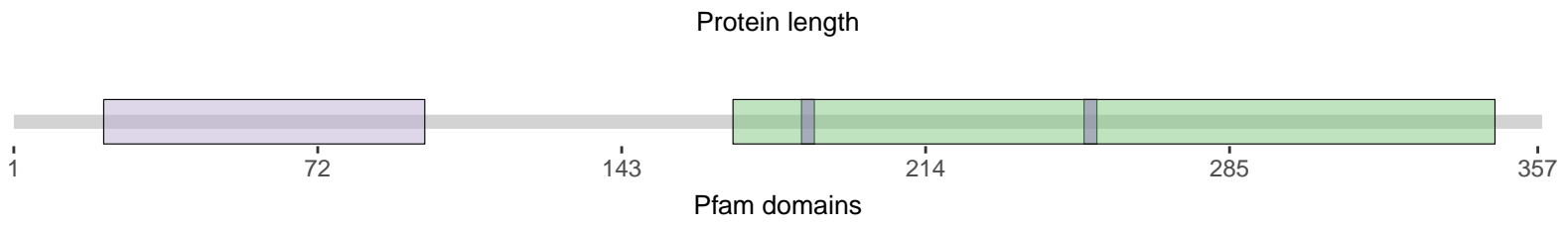
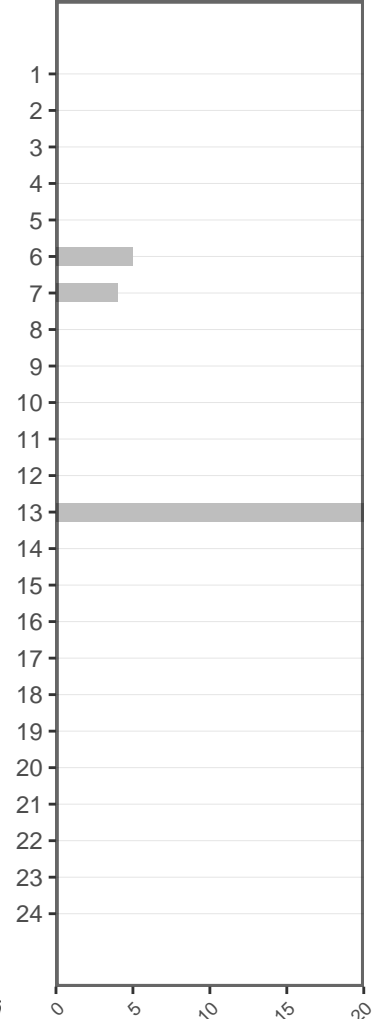
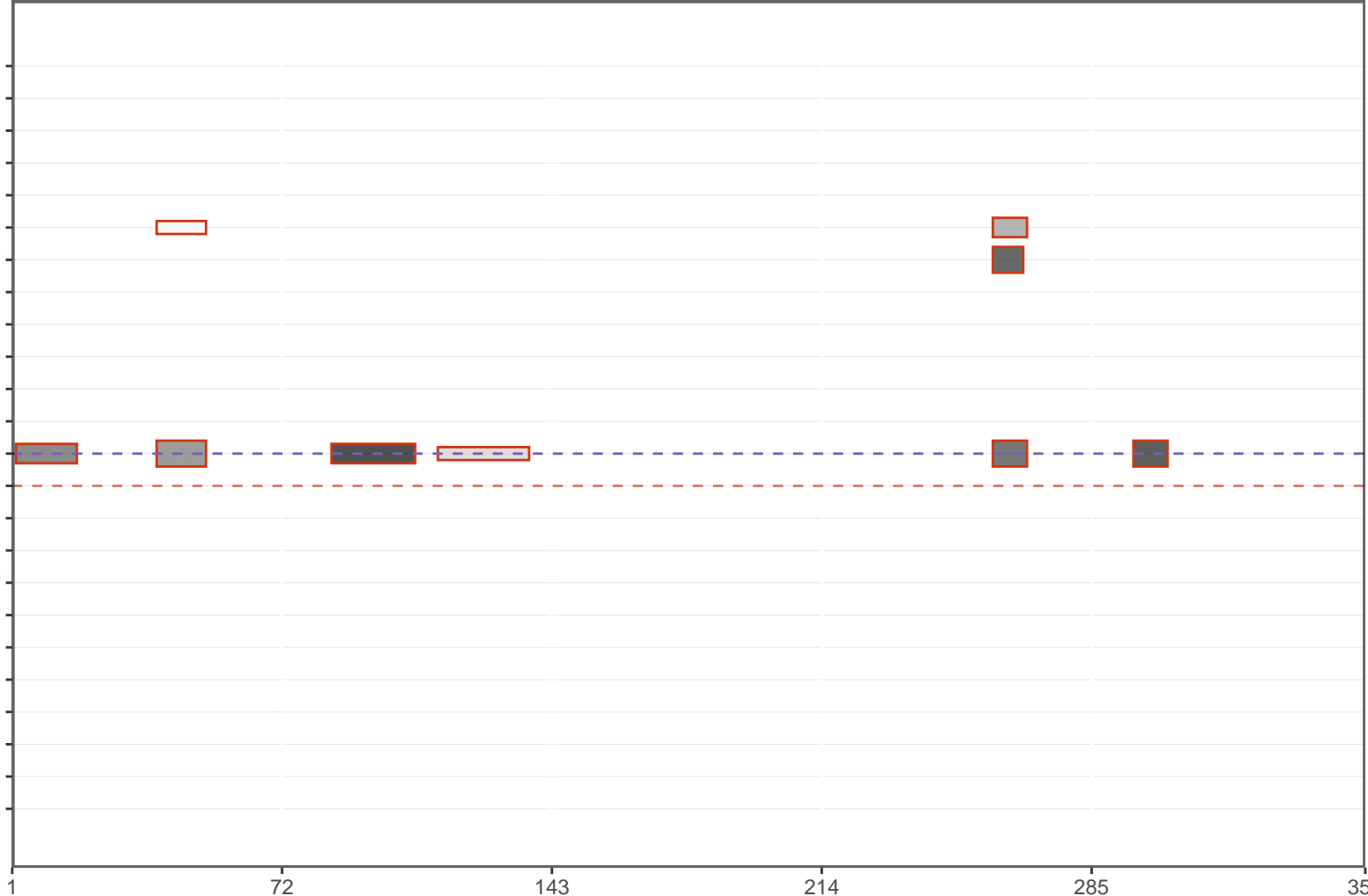
MW indication



Molecular weight



Gel Slice



Pfam Description



Protein sequence:

NAFGRDIDVSHYKAGLYAGINSGINGEMPPGQWFEQVSPVSGISADELWAARVILERITEAGVAVVFDKPKPIPGDWNGAGHTNYSTKMRNEGGEYEVKKAQKGLRLHKEHIAAYGEGNERRLTGRHETADNTFKWGVANRGSIRVGRDTEKEGKGVYFEDRRPASMMDPKVYVTSMAETTLVELV

NbL04g01370.1 universal_stress_protein_PHOS32 [MW = 17.82 kDa]

No. of times detected



log(intensity)



Values from



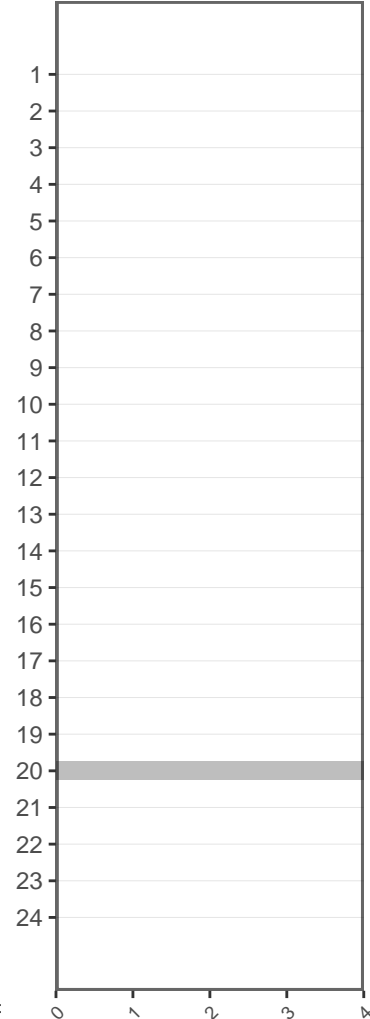
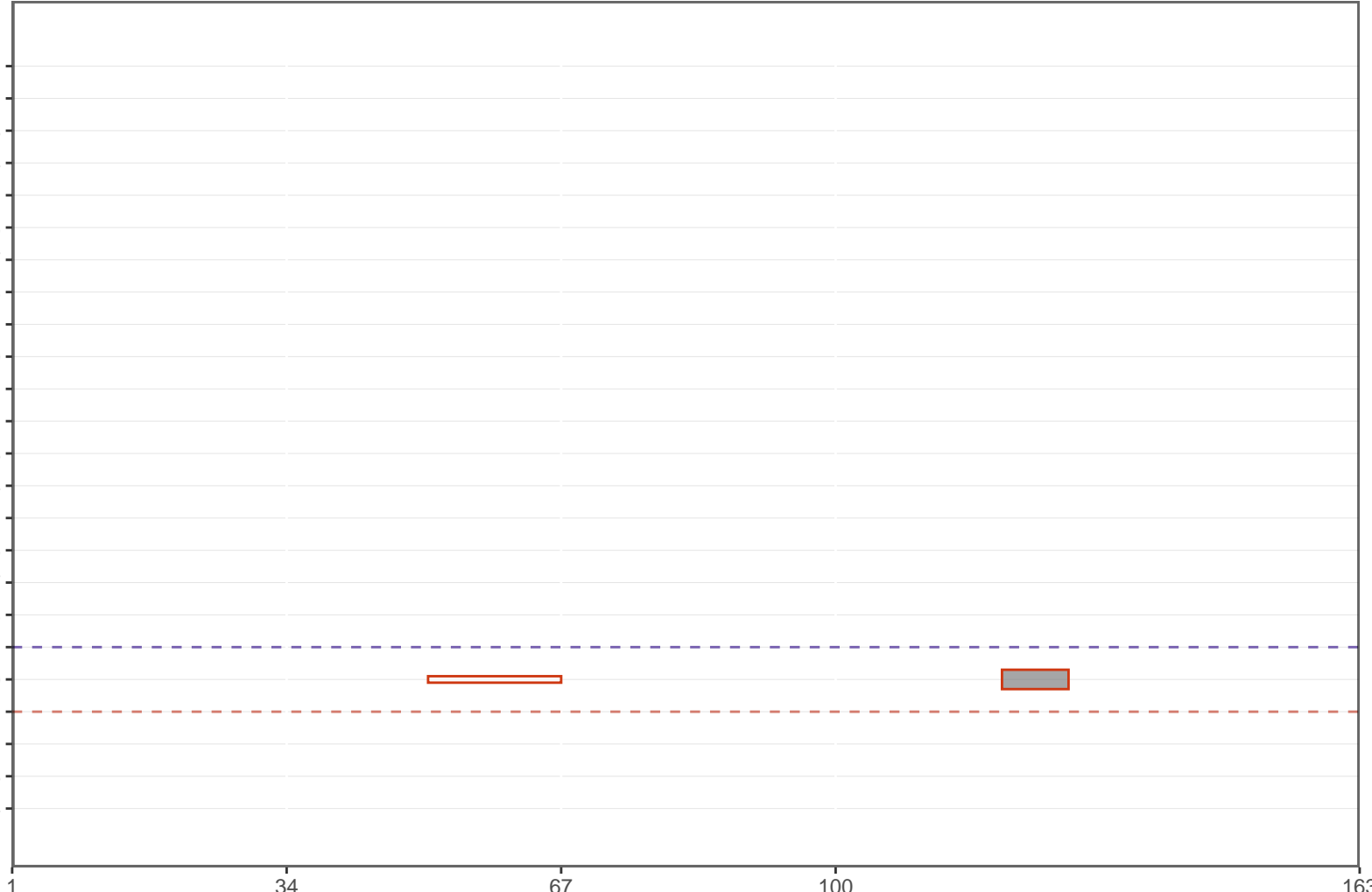
MW indication



Molecular weight

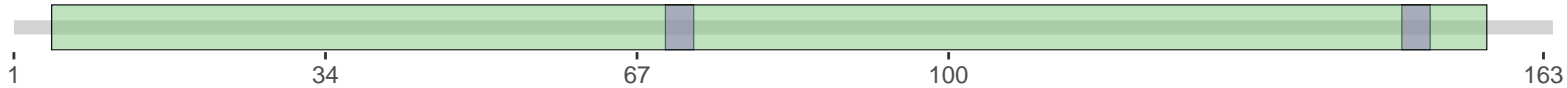


Gel Slice



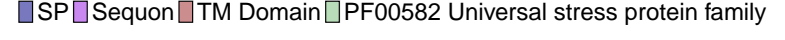
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

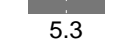
ISKYYGLDPREVLQMLDTVEKIKKVVWAKVYVWGDAREKLGDAEHLKLDLQMLGSRGLGVLRMLGSEVNHVGNATGPTVWKSFPK*

NbL04g01330.1 tropinone_reductase-like_3 [MW = 26.95 kDa]

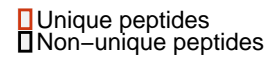
No. of times detected



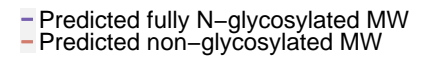
log(intensity)



Values from



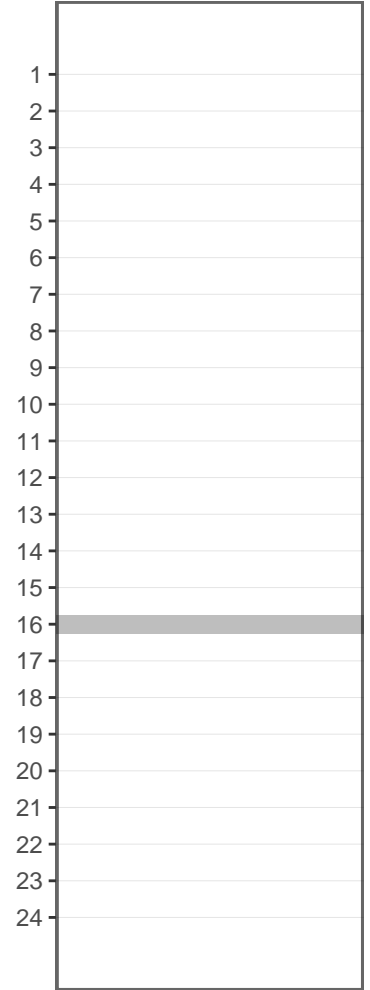
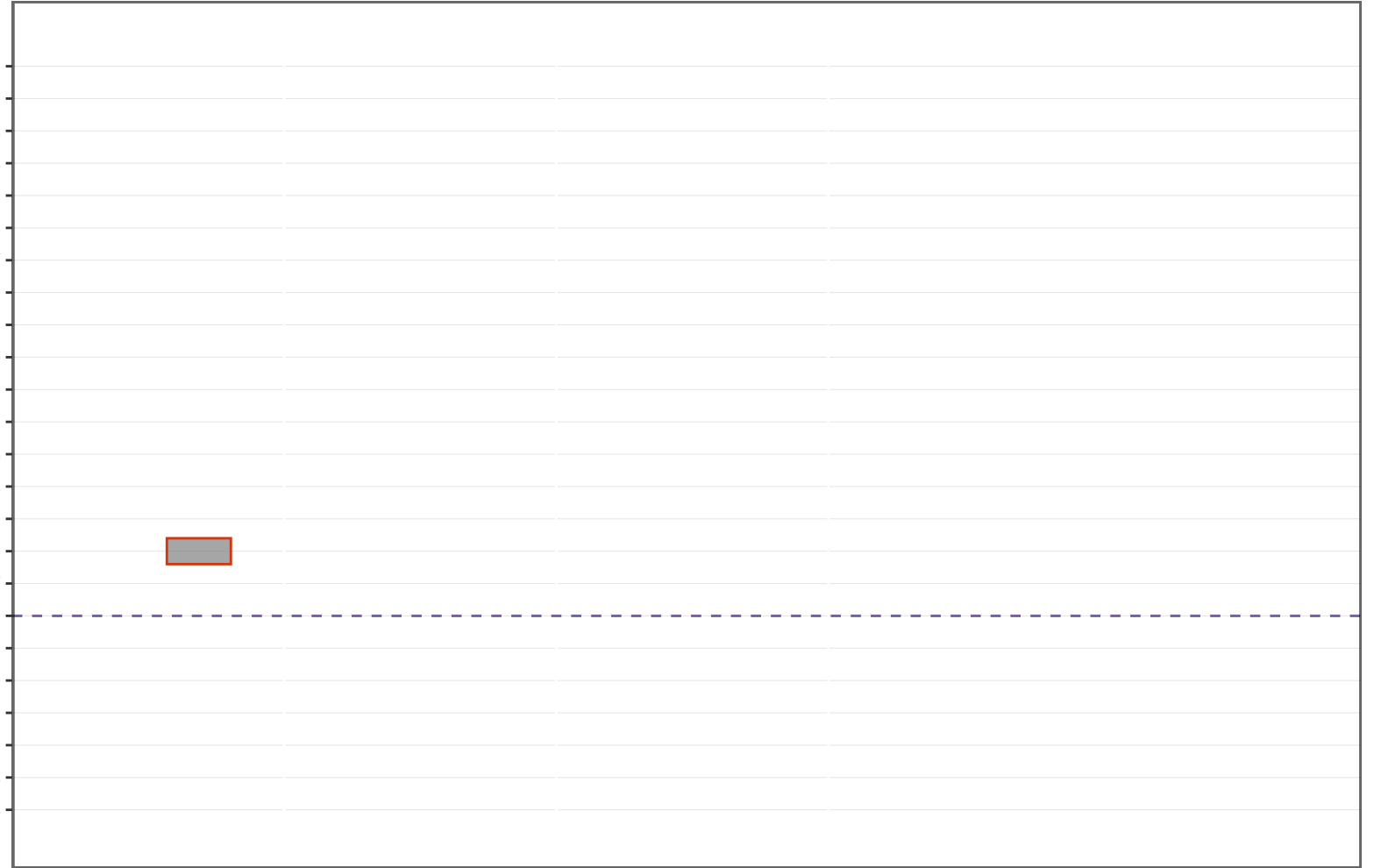
MW indication



Molecular weight



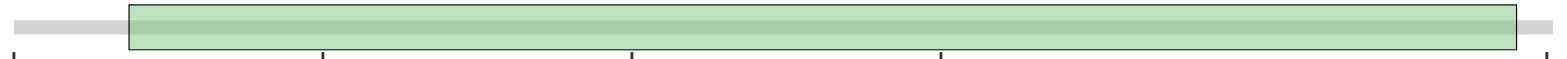
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

CLWDINVKASILLQDAAPYLKKGSSVLISSISAYFPASMGAMGVTKTALLGLTKALASEMSPDTRVNGVAFGFVPTHADLTQNEHVRREIEGKTLNLRGFTQDMAAAVGYLASDDAAVVTGETLVVAGGMP SRL

NbL04g01160.1 peptidyl-prolyl_cis-trans_isomerase_FKBP16-3_chloroplastic [MW = 27.14 kDa]

No. of times detected



log(intensity)



Values from



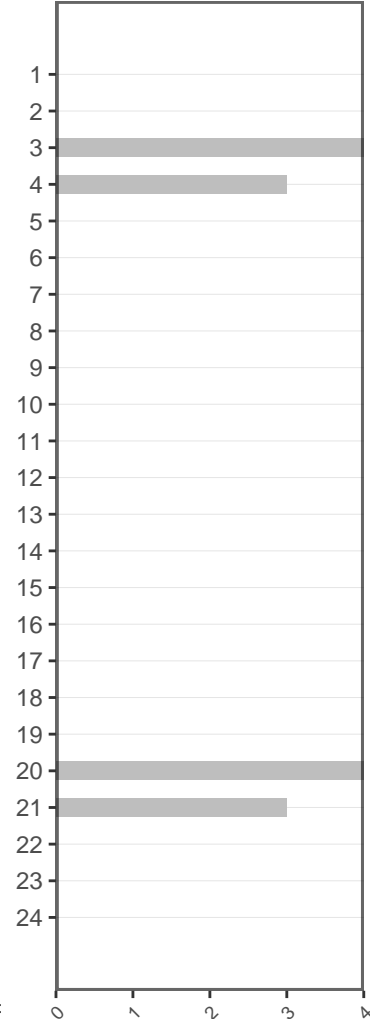
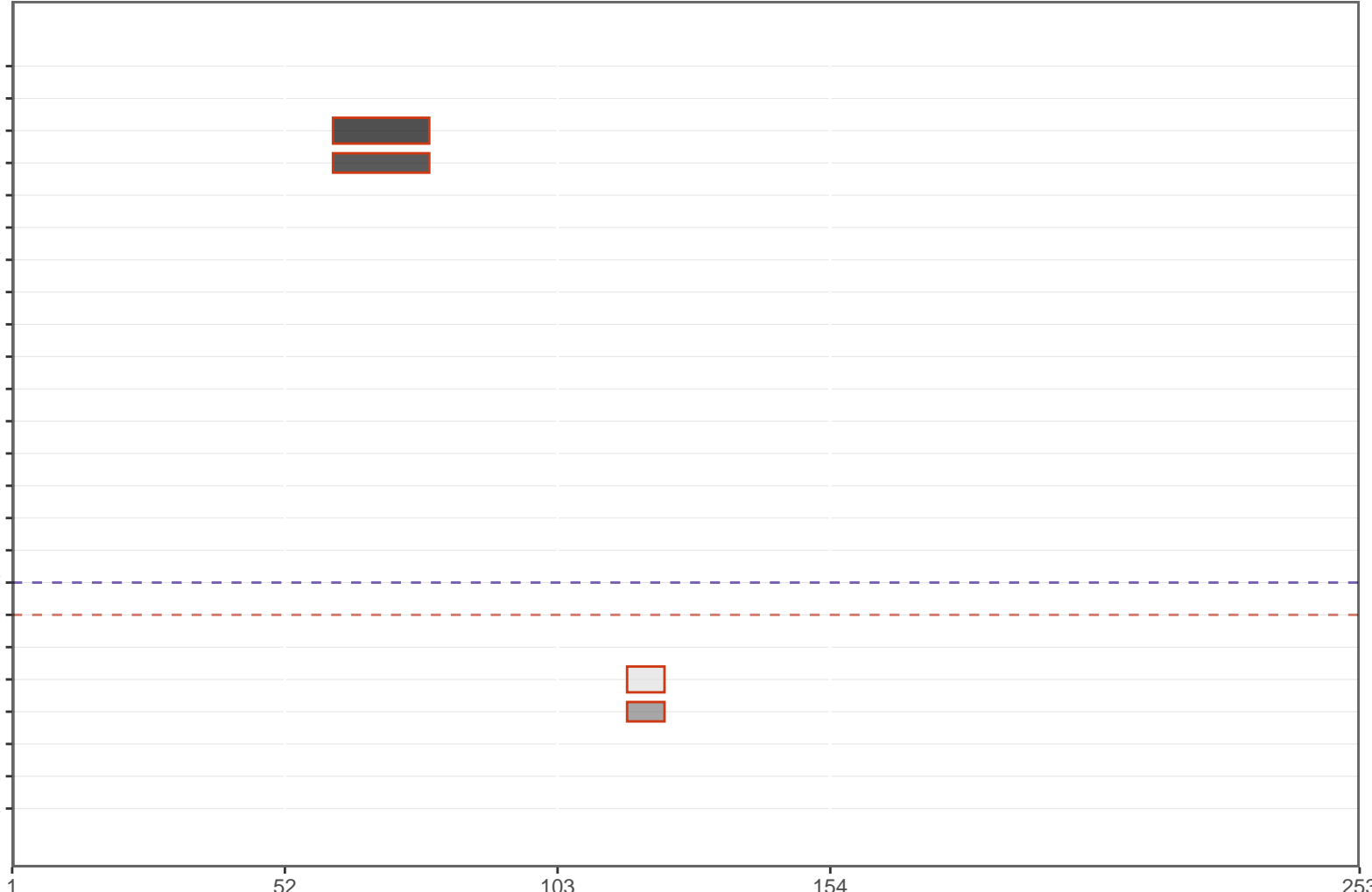
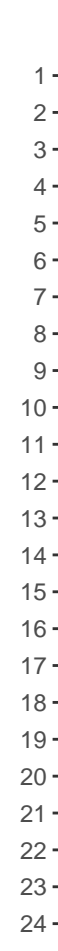
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

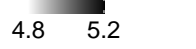
PKLCDATCAKELNFMVFTTEGGIGYKDKVGGGSPRPVGFQVAANGVAMVPSGGIFDSLEKGGLYFRVGGAGGVKGLDEGLSMKVGKRRLLVPGELAFPKGLTSAPGRPRVAFNSPFIQVLEIYIPGLESDDEE

NbL04g01150.1 trafficking_protein_particle_complex_subunit_5 [MW = 24.39 kDa]

No. of times detected



log(intensity)



Values from



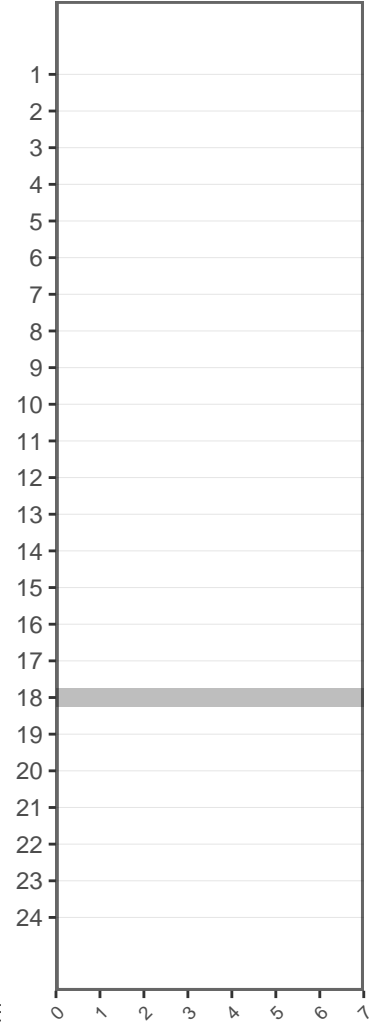
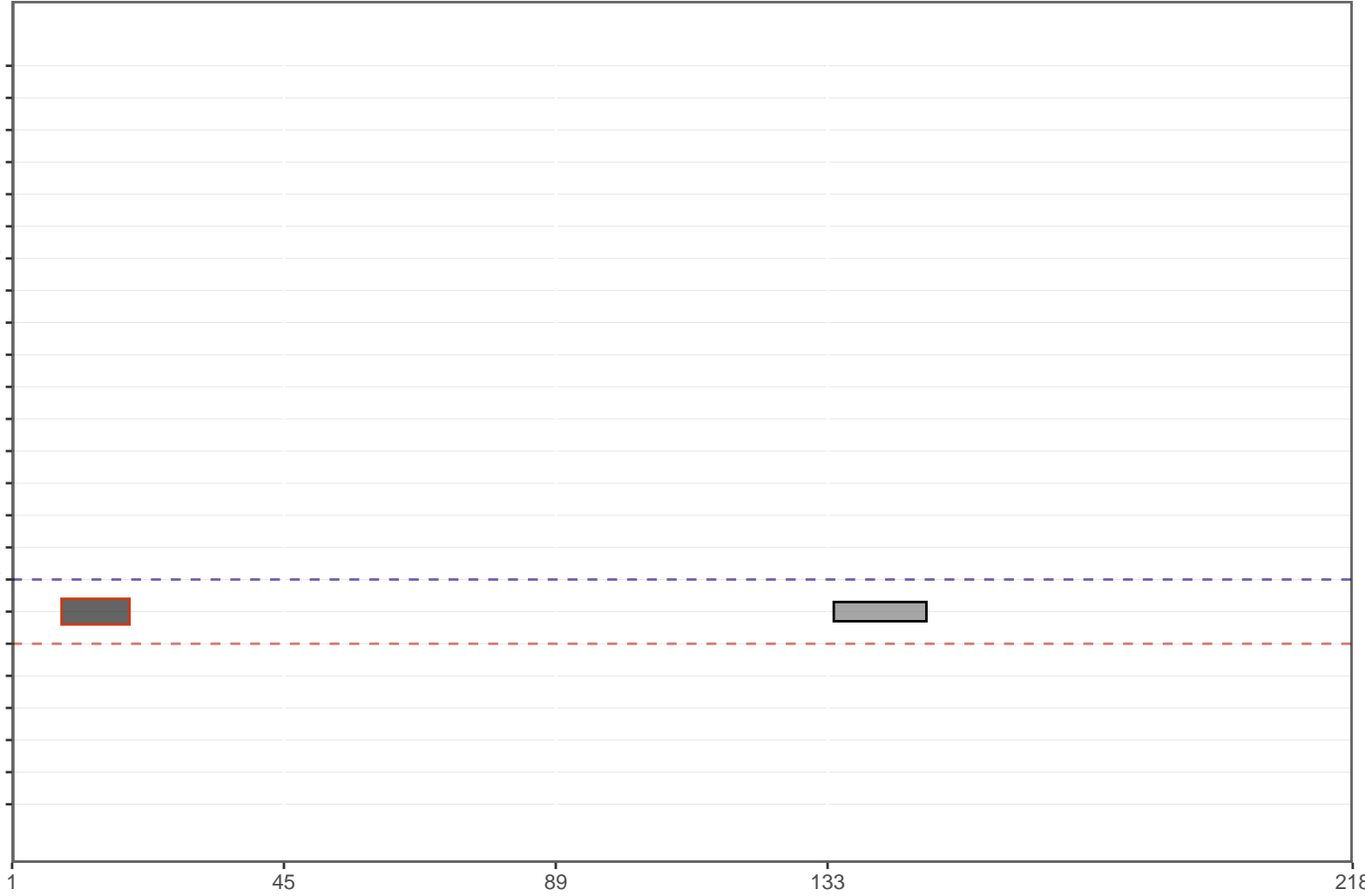
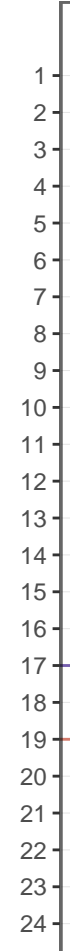
MW indication



Molecular weight



Gel Slice

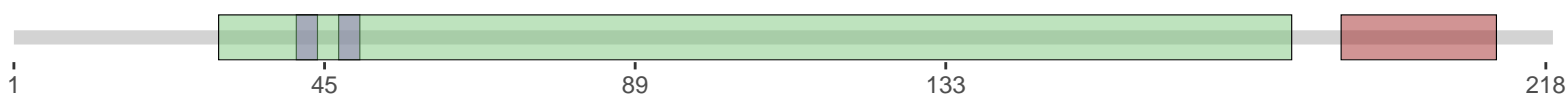


Protein length

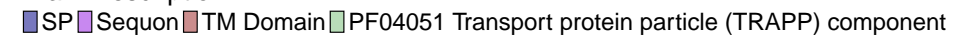


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

WKVLFQKVASDLEKNGTEHEDEYMISEKELLNRFISIPKDMGFNGGAFVAGIVRGLVLENGFRWVYAHFVVEGGQRPRTRILUKFAEEVNGFFLFGSGTLVVGSGTDFLPIAFVTVYFFT

NbL04g01110.1 acetyl-CoA_acetyltransferase_cytosolic_1-like [MW = 43.11 kDa]

No. of times detected



log(intensity)



Values from



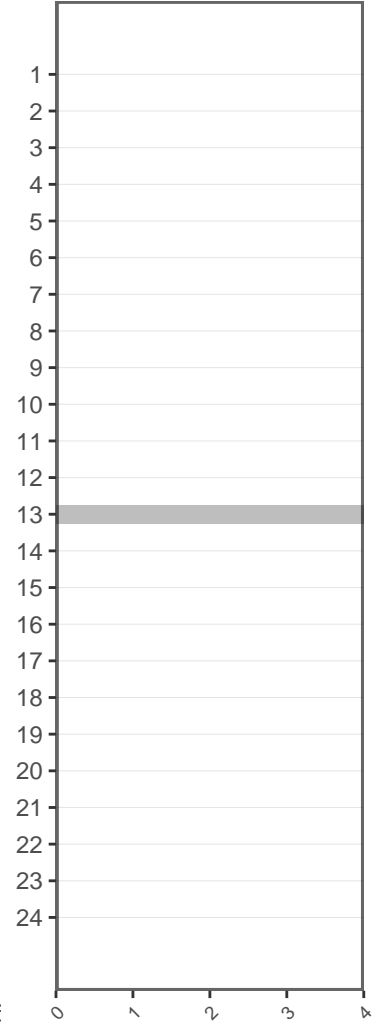
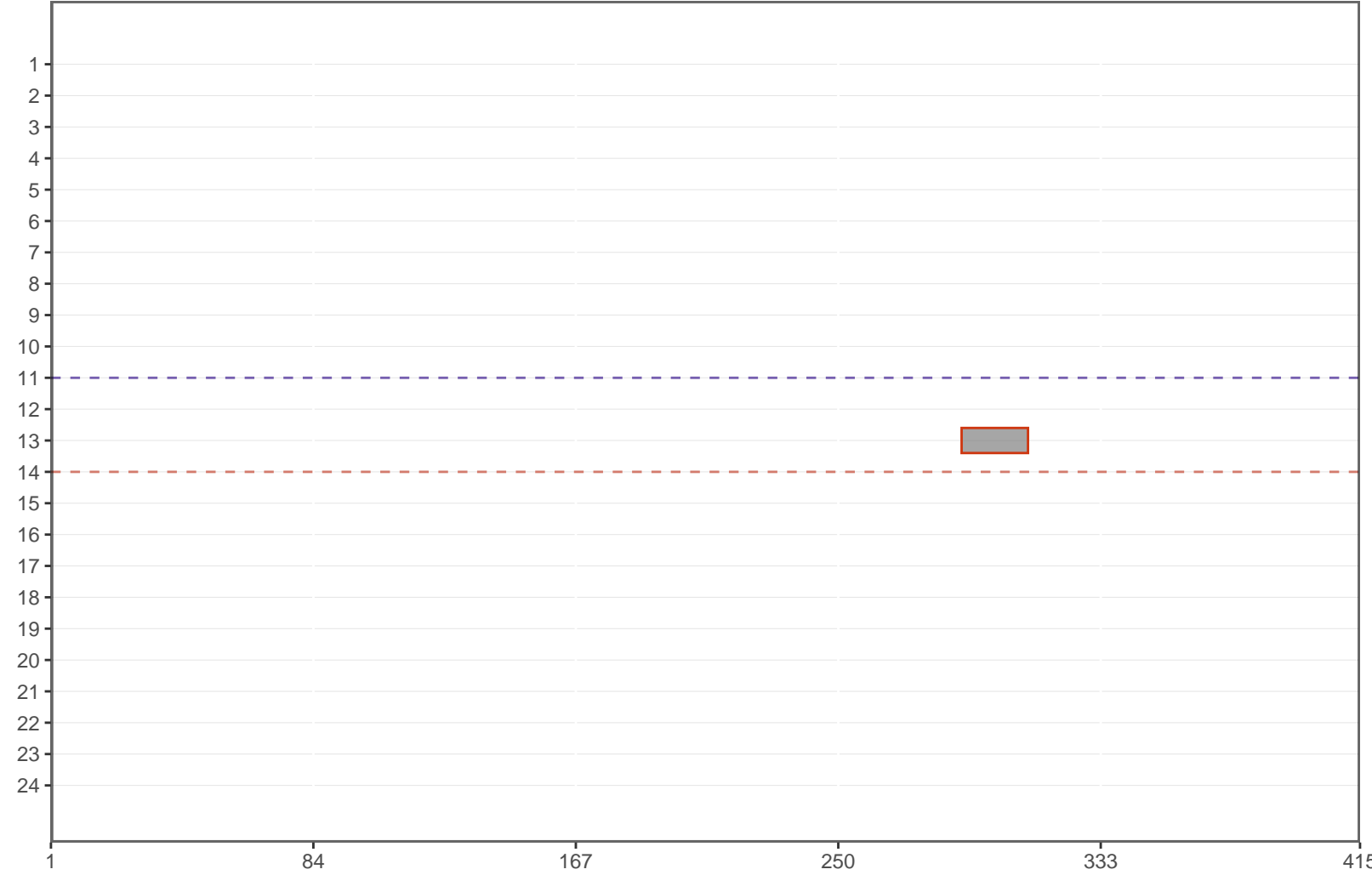
MW indication



Molecular weight



Gel Slice

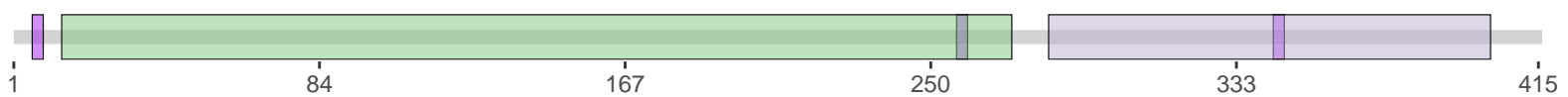


Protein length

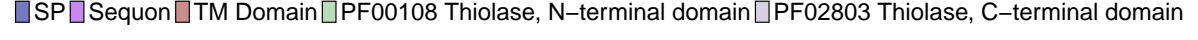


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SFERGIAQRSGCAFVWVPEISGGRRPPTFDVNDKDEGLKFDKLLKLPSTFKENGSGVTDGNASHISDGAALVLSGGKALELGLVIGRIRGFADAGAPELFTTAPALAFKAKNSGLESSDIDYKINEAFSVVALANRLLNITSGKLNHGGAVSLGHPGCGSARLVTLGLVLRKHKNGKFGVAGICNGGGASALVVELMIRIMVARSLS*

NbL04g01060.1 phosphoglycolate_phosphatase_2-like [MW = 34.55 kDa]

No. of times detected



log(intensity)



Values from



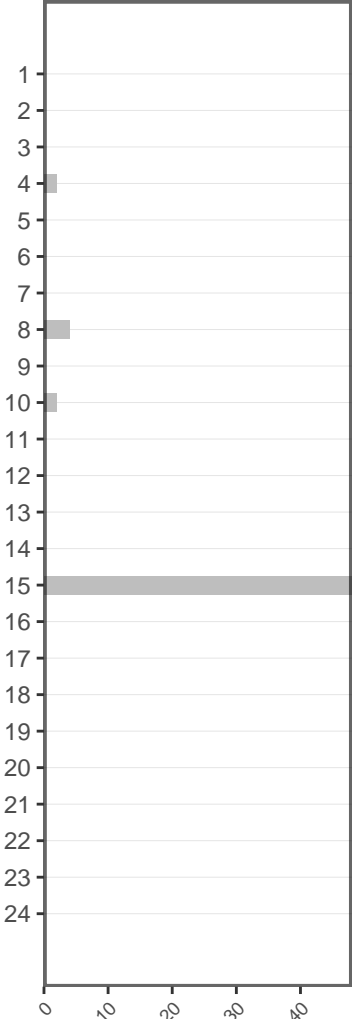
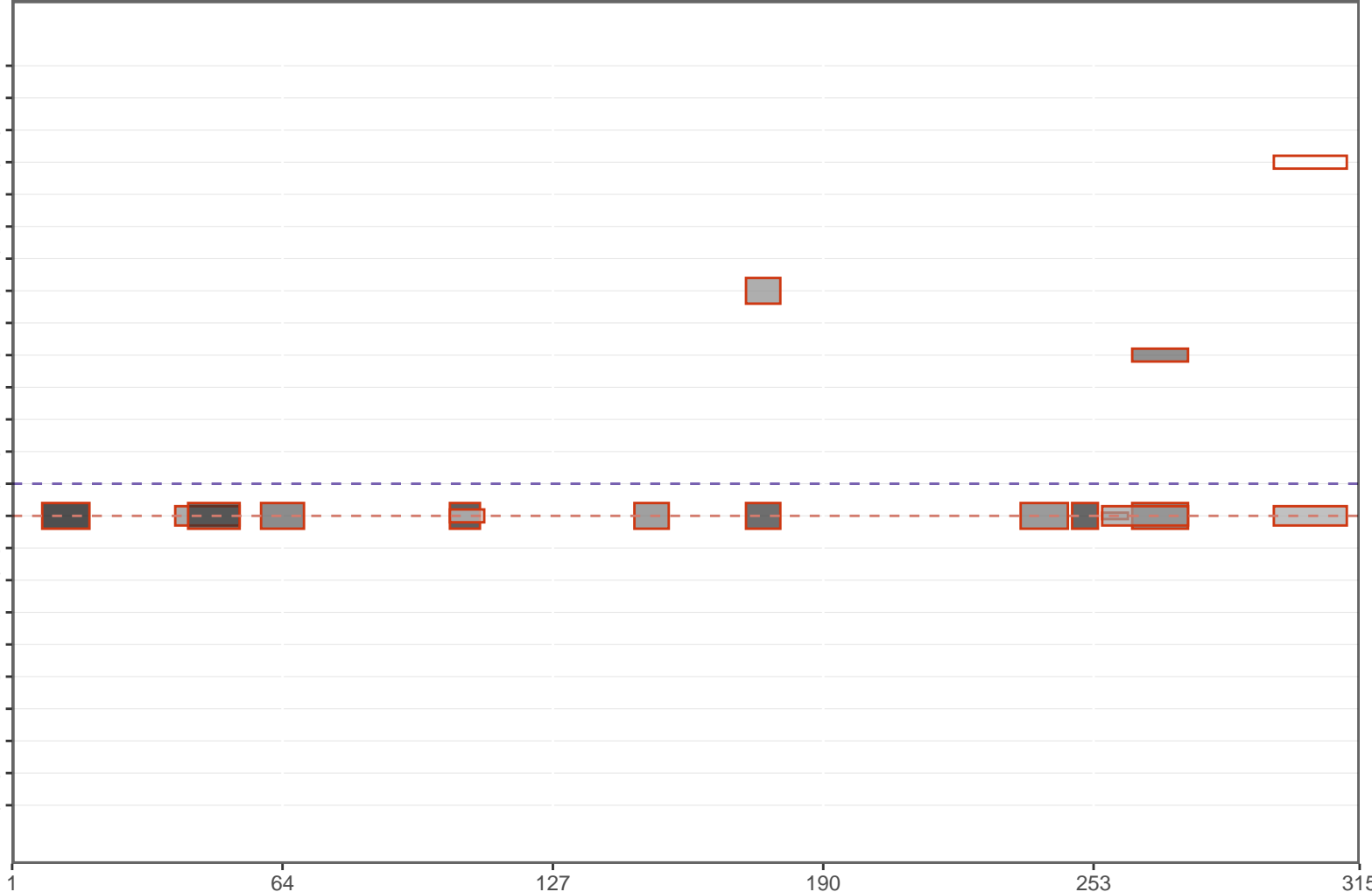
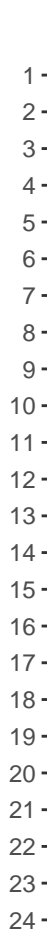
MW indication



Molecular weight



Gel Slice



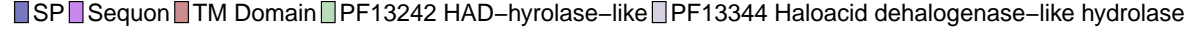
Peptide counts over 4 repeats

Protein length

Pfam domains



Pfam Description



Protein sequence:

CSNCLFEHDKSIVGAVVGLDGGYNYFLKGLYALGIRENPGCLFIATNRDASGHILTDLGEWPDTSFLVTVGAGGMVAVGGATQKEPIVVGKPKSTFLMDFLLGKYNFTSRMGVMDRLDITDLFGGNAGRRLLVFSGVVTESAFQGLSKELQVQPEYFTNVSVDLKYV

NbL04g00830.1 uncharacterized_LOC109239397 [MW = 35.51 kDa]

No. of times detected



log(intensity)



Values from



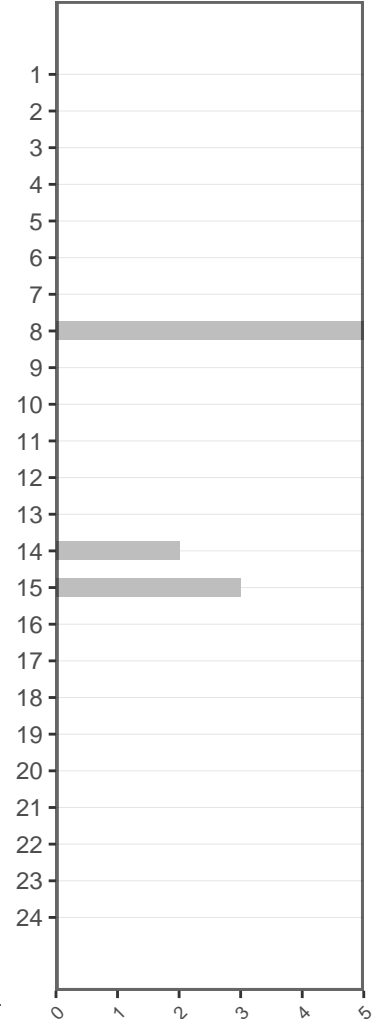
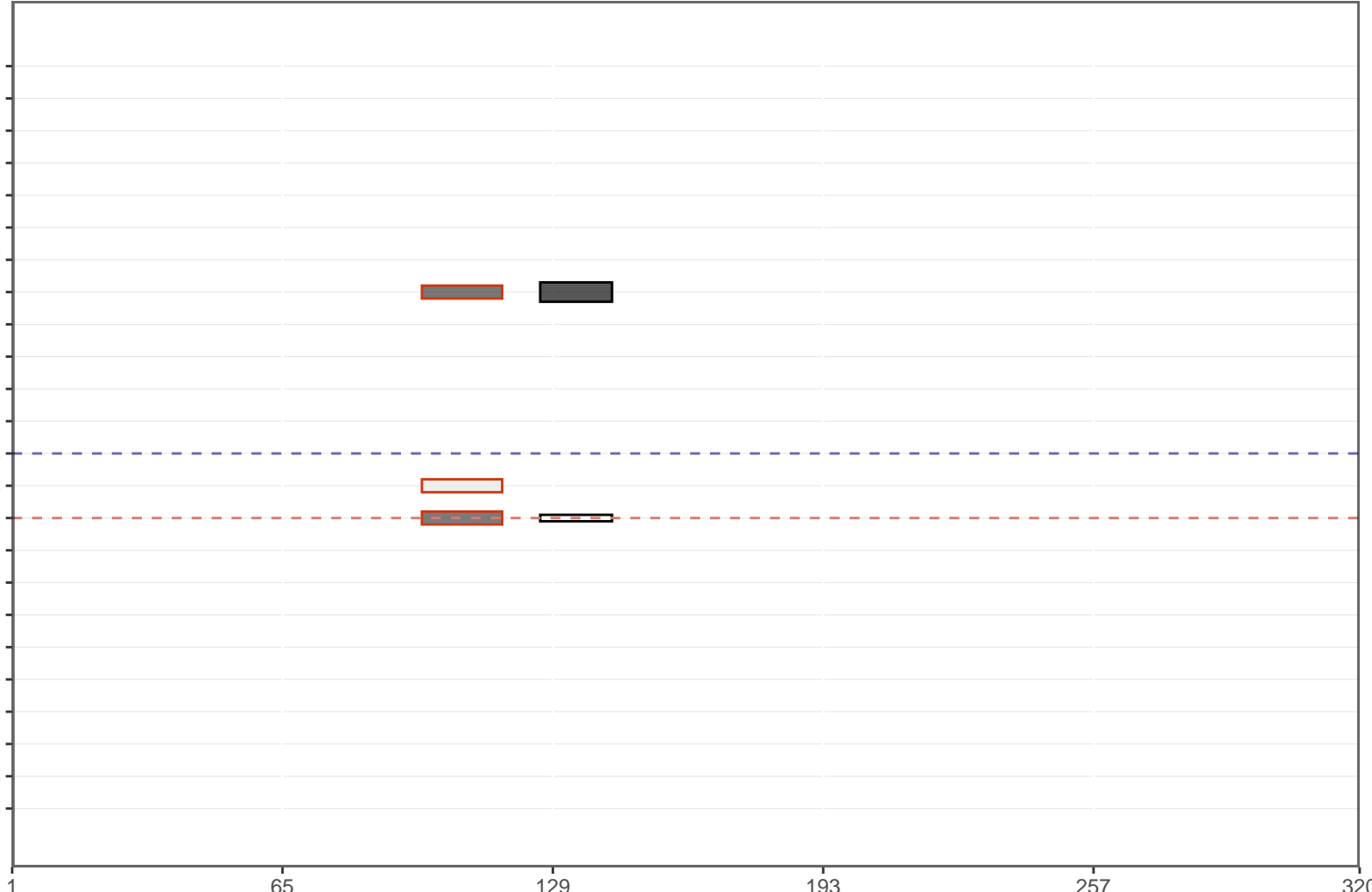
MW indication



Molecular weight



Gel Slice

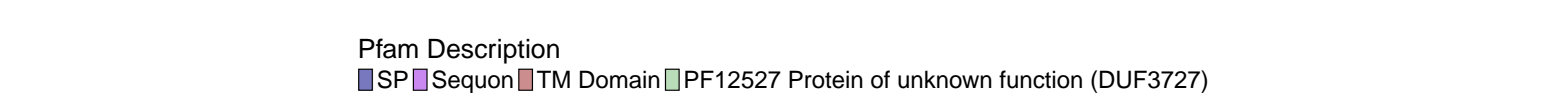


Peptide counts over 4 repeats

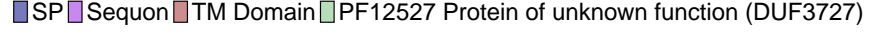
Protein length



Pfam domains



Pfam Description

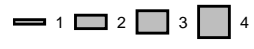


Protein sequence:

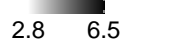
RSLSREDECLLCFVDMPIVQLKSTNVEGWSAVSDEVEAHLPTAAALAKHMMALVYSGFDYARGGFCYTEDDFEFRFRDGGDDGLPSEGIETGFHMDGSHYMIYTPSDPLFVWKGKDGLLQADDELLEDPNISAIDEETEFNALVEEAAALLESLLGERFKFYI

NbL04g00760.1 beta-glucosidase_BoGH3B-like [MW - SP = 66.09 kDa]

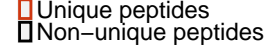
No. of times detected



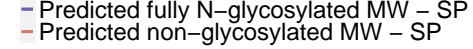
log(intensity)



Values from

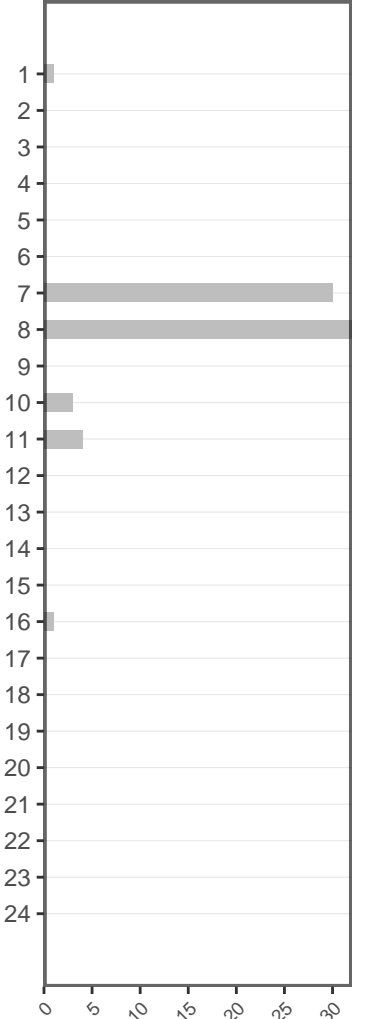
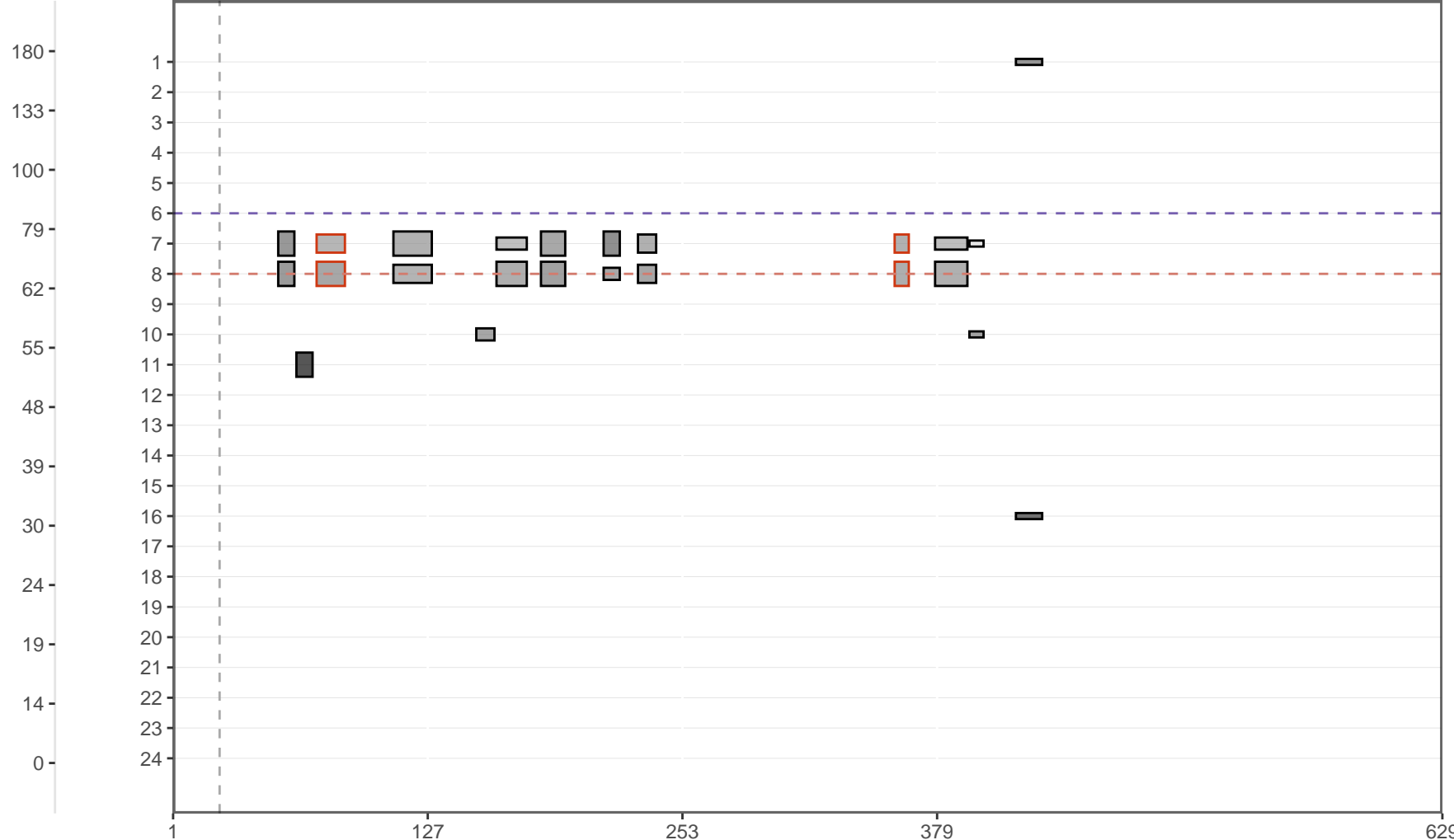


MW indication



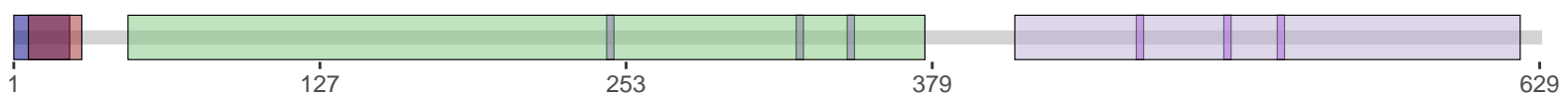
Molecular weight

Gel Slice



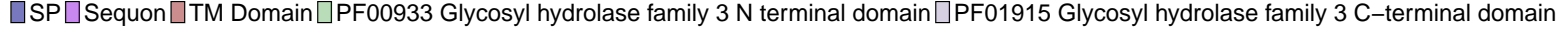
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RFRRFGVYSDWAGIDALTYPPWHANYFYSLLEGVNAQIDMMMLFPVNTTFERFDGLTYLVKNNFVQMSRIDDAVKRLRWFQMLGFESPLADYSMKVYLSAEHRELAREAVRSLVLLKNGANADEPVLPLPKKTSLSLVAGHANMMGVGGGQWTTWQGLSGNTTIGTTLTSLAENTVDPEKRVVFKENPDAEFIKSNFNFYAVAVGETPVAEGGSDSLNLRTPAGPDTMTTVCASVKNVYVLLTGRPMVMDPPLAQIDALVAWLPSTEGGGIADLVFGDYGTGKLRITWFKT

NbL04g00720.1 anthocyanidin_reductase_((2S)-flavan-3-ol-forming)-like [MW = 25.24 kDa]

No. of times detected



log(intensity)



Values from



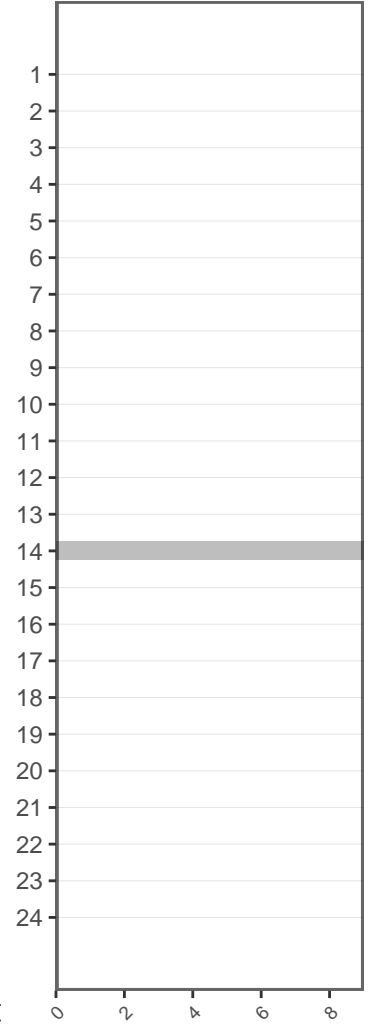
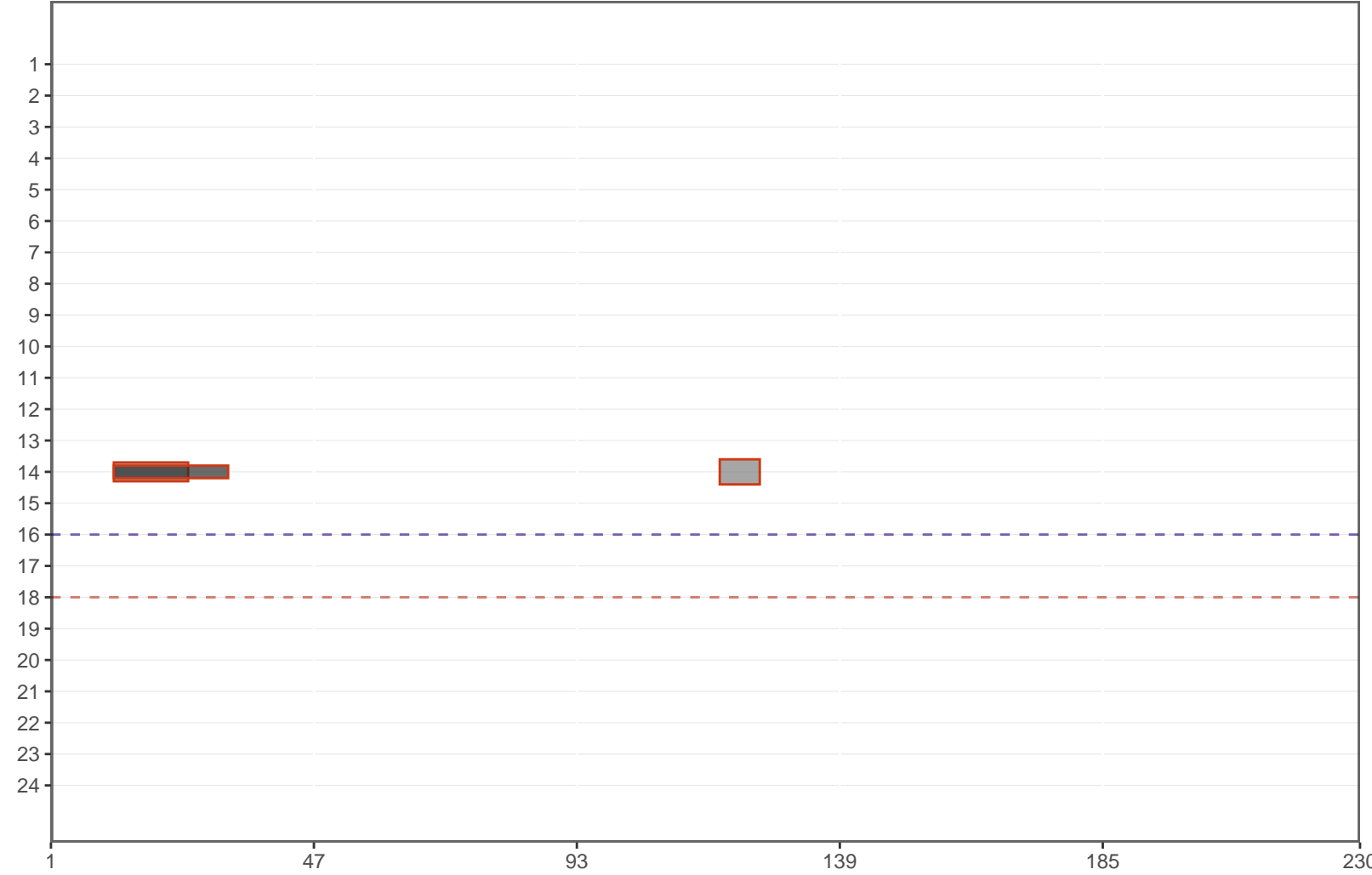
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

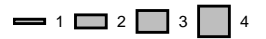
Pfam Description
 SP Sequon TM Domain

Protein sequence:

ALSLVYTGDEISYQGLKFRIEVDGKAPVHEDVGEAHIFGMETASINRFLGASAFVSSAEIAEYKKEKYPEFHANGRYLDDPKREVKVGSKKIKGKGFVYKDKMKILDNISCAKEIGVALNLPPEA*

NbL04g00660.1 insulin-degrading_enzyme-like_1_peroxisomal [MW = 112.06 kDa]

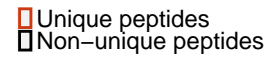
No. of times detected



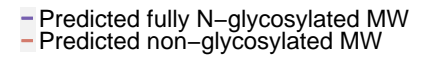
log(intensity)



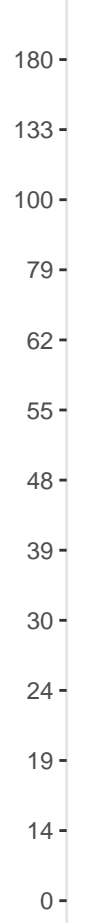
Values from



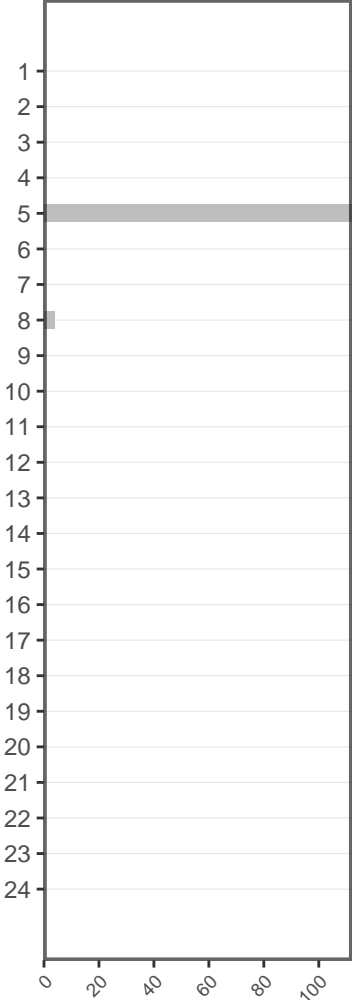
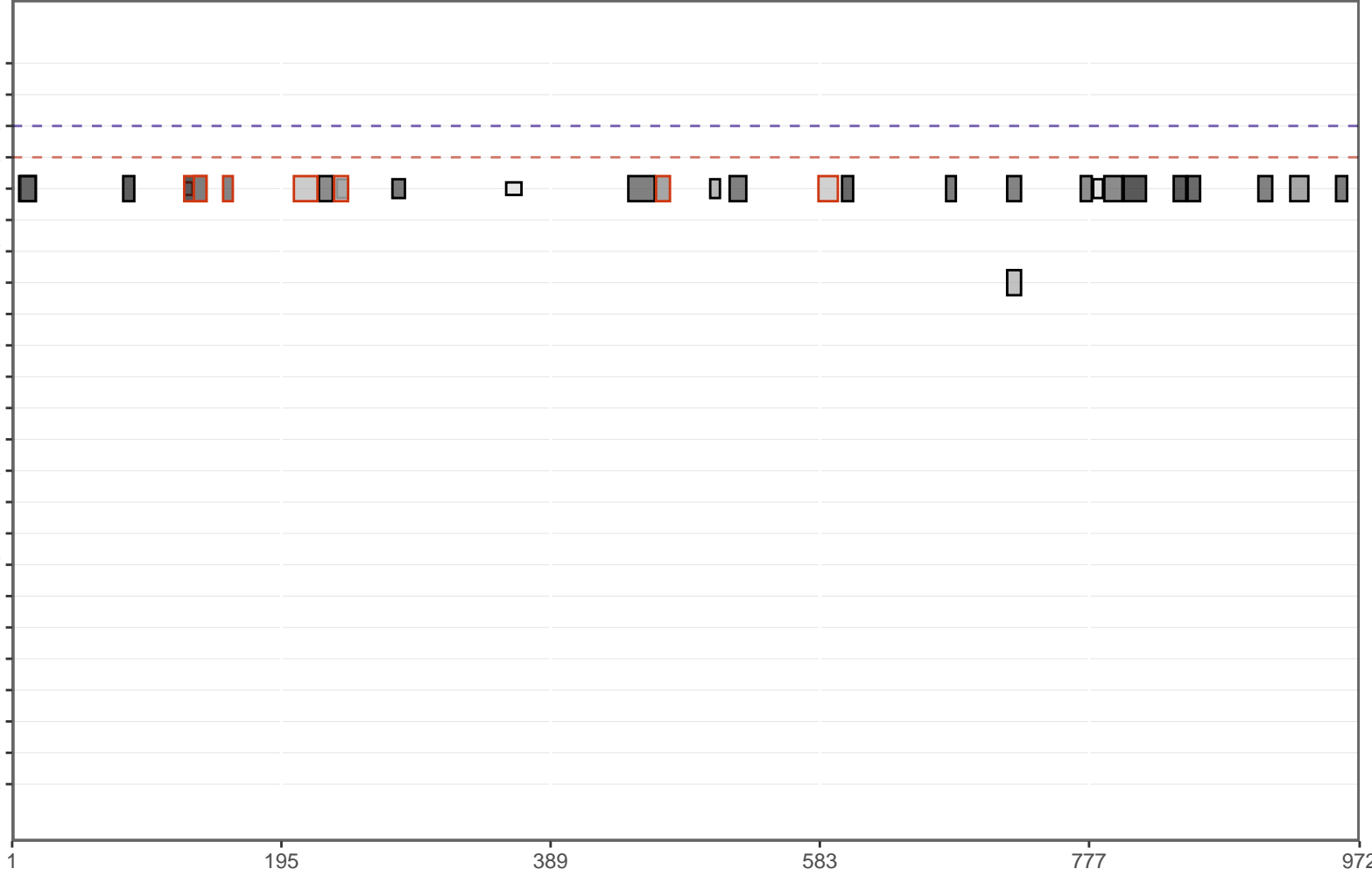
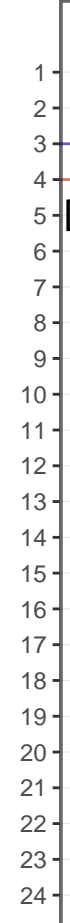
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

WMKQAPSEDLHLPANVRIPTDLSLKPVFEKTKVPLLRKSPYSRLWYKPDATFSSPKAYVMDFGCPFGGHSPEAEVLTEIFRLLMDVLENAVYHAGVLYGINKTNVNGFLTVFGYNDKLRVLEAVVEKIKFEVYKDFRPFVKEVLTGKGFNYKFGQPGQGMYYGSLLEQENTWVPTDELEVYHPLKEDDLWYFVPLLLARGLFQVYVGNIEQAEAESMTQLIEDVFFNPGPQPSIKPLFASGHITNRVNLERGVNYFYAAEGLNPNDENSLLIHYIQVHQDDFTI

NbL04g00620.1 magnesium-chelatase_subunit_ChIH_chloroplastic [MW = 153.89 kDa]

No. of times detected



log(intensity)



Values from



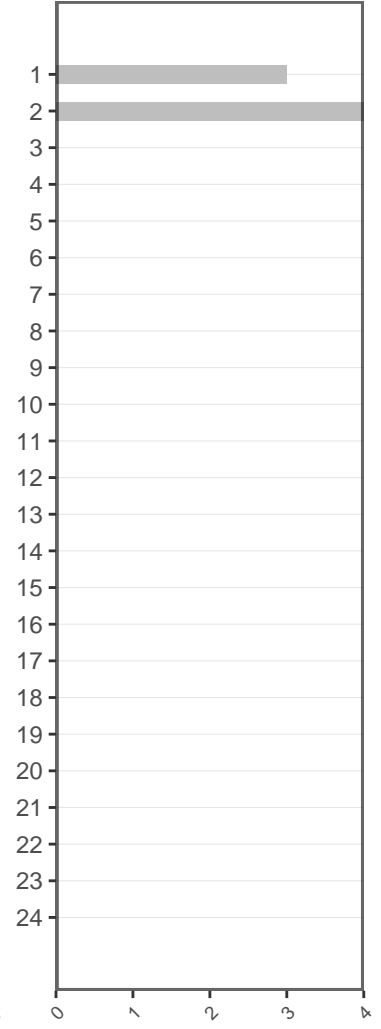
MW indication



Molecular weight



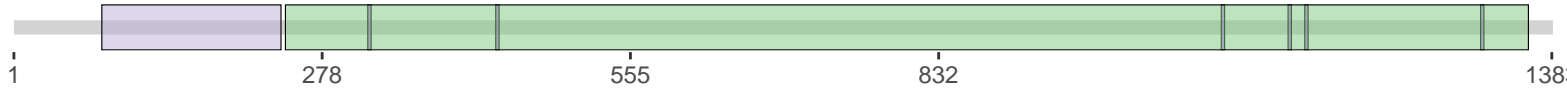
Gel Slice



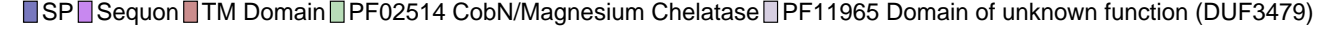
Protein length



Pfam domains



Pfam Description



Protein sequence:

I/VGMSDACPDSLIGNIPNYYFYAANNPSEATIAKRRSYANTISVLTTPPENAGLYKGLKQLSELSESYVGLKDSGRGGQIVNSIHTARGCNLKDIVDLPSEEGEISAKERDLVGRKYVSKIMEIESRLPQGLHIGEPPTAMEAVATLVNIALDRPEDGISALPBLAATVGRSIEEYRGNDDQGLRDLVELLRQITEASRGAISAFVVERTTNKKGQVANNNDKLTSLGFGINEPWWVGLVNTQFYRADREKLRVLFQFLGEOGLKLIWANNEVGLKQALEGRVYEPGPGDPIRNP

NbL04g00610.1 villin-3-like [MW = 104.24 kDa]

No. of times detected



log(intensity)



Values from

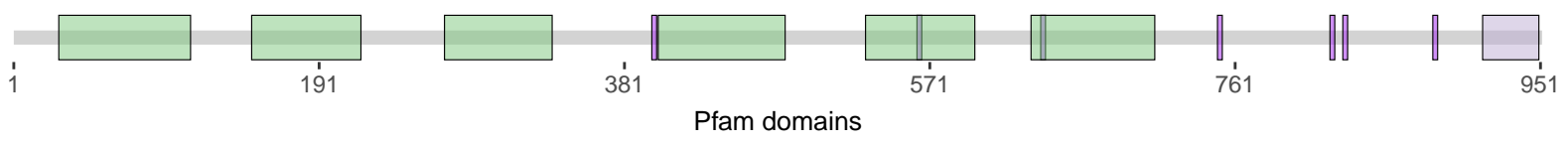
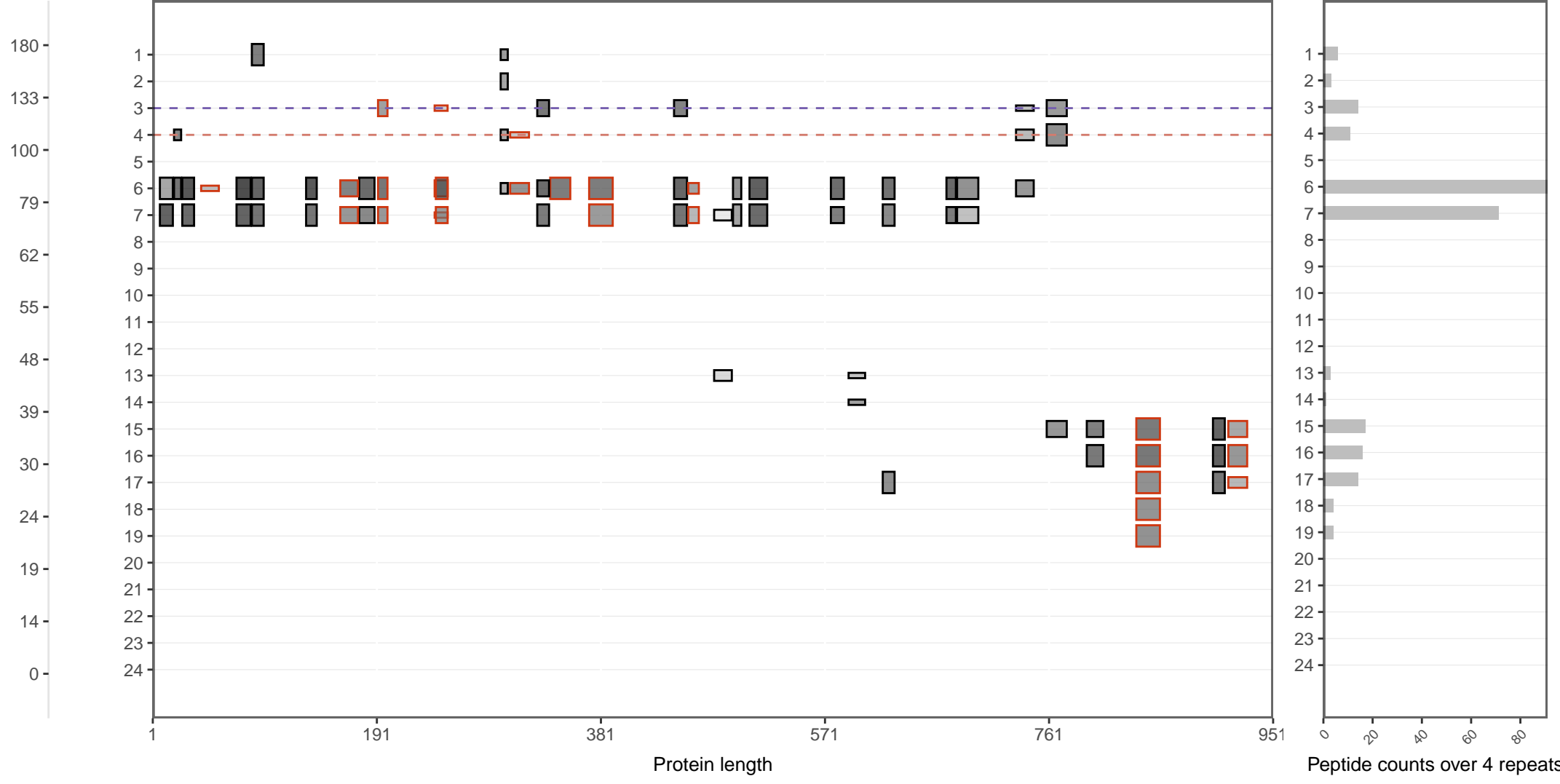


MW indication

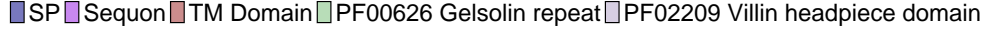


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

RPVLGRVFOGKEPPQFVAFQPMVLMVGLGSGYKVIADKGLNDETYAADSVAIRLISGTSVHNKAVGVDAVFAFLNSNEGLRGGSSSLFSWHGNGSTYEQOGLAAKVAEFLKPGATVVKHTKEGTSSAFVWALGDKGQSYTSKVAPEVSRDPHLFAVGFNKGVEEVEEYVNFSDDLTEVLLLDTHAEVFTVWIGGSDAKKQKSAFDGKGVYEMAALEGLSPNPLVYKVTGEGKPFVFTTFFSVDPAKASAHGKGFQKVMLLFGVHASENDOORSNGSGG

NbL04g00570.1 L-ascorbate_oxidase_homolog [MW = 19.51 kDa]

No. of times detected



log(intensity)



Values from



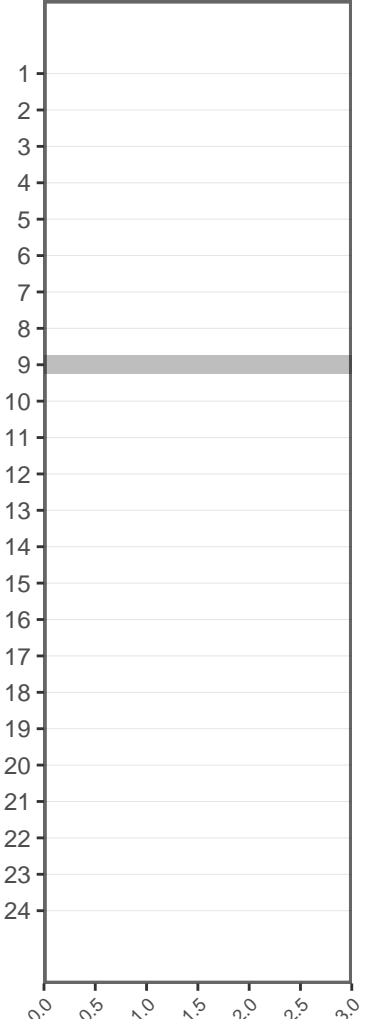
MW indication



Molecular weight

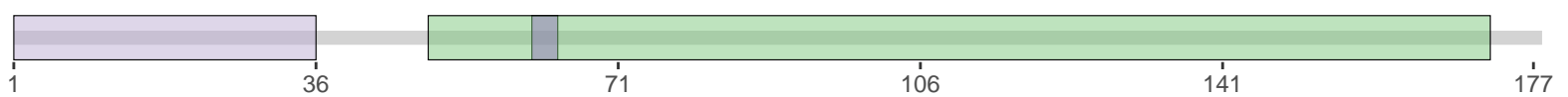


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

.PPFDQLLNGRGSNLSLTFVDDGRTRYFRISNVLGFTAINFRDGHKMLVVEEGHFLQNTYESIDHLGGSYSLVVTMDQPGDYYIAGTRFTSGVLT...

NbL04g00540.1 dihydroneopterin_aldolase_1-like [MW = 14.25 kDa]

No. of times detected



log(intensity)



Values from



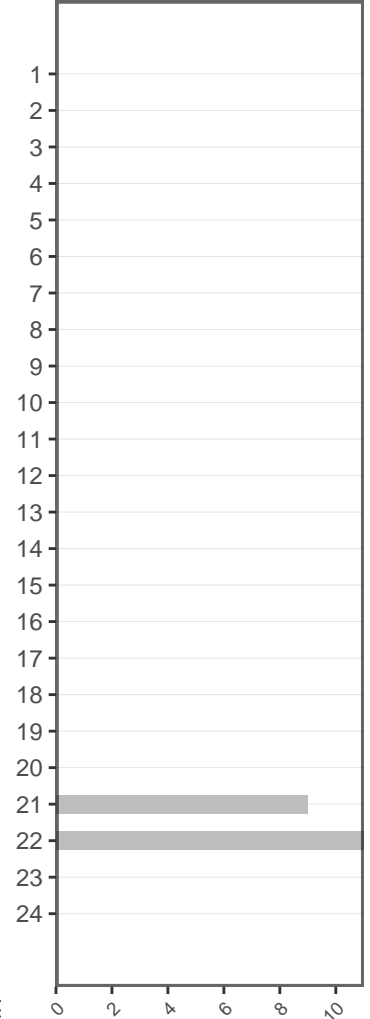
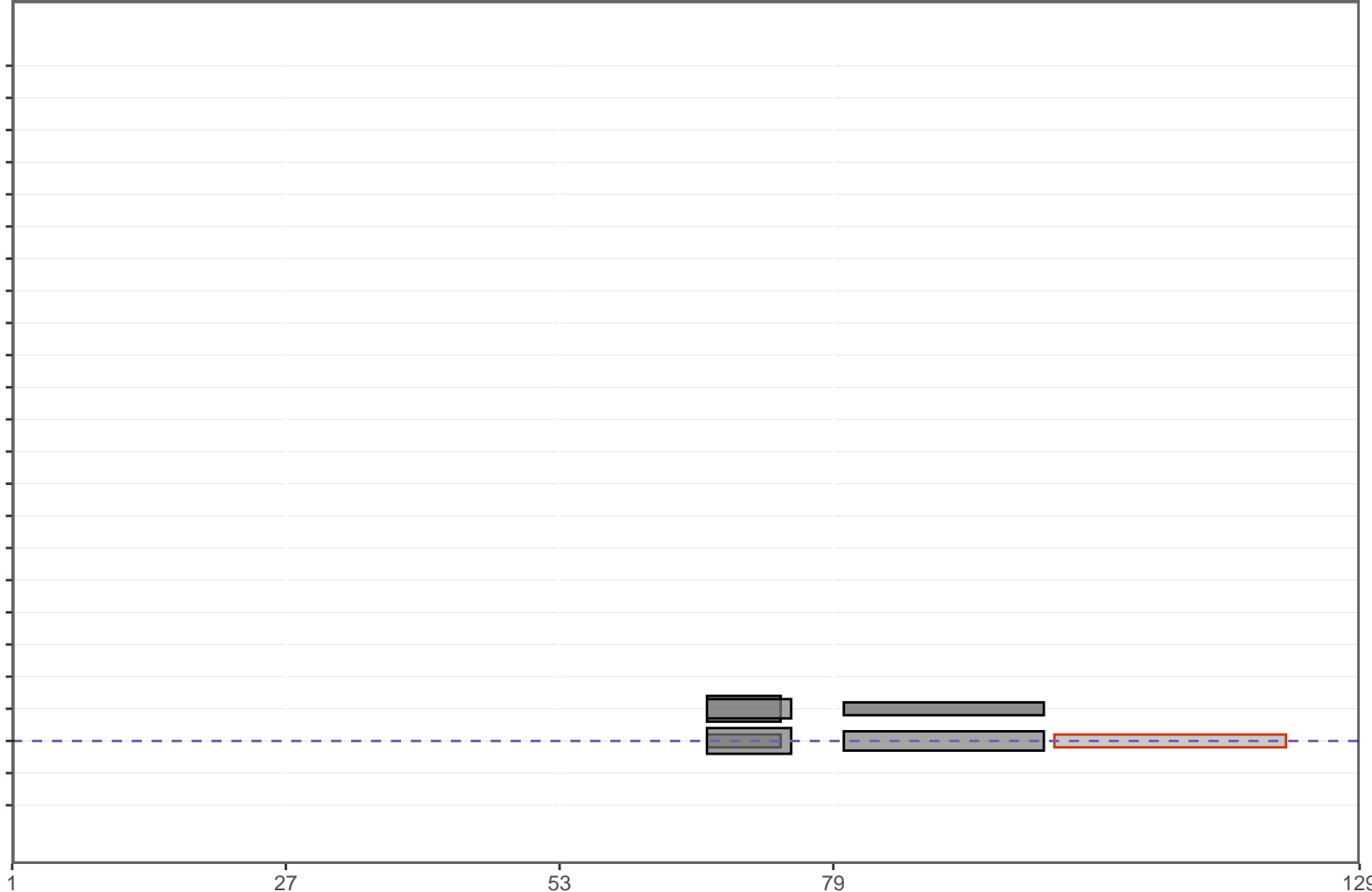
MW indication



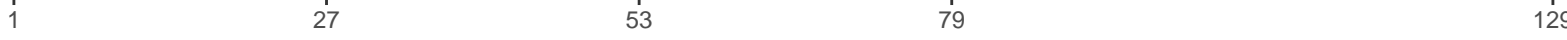
Molecular weight



Gel Slice

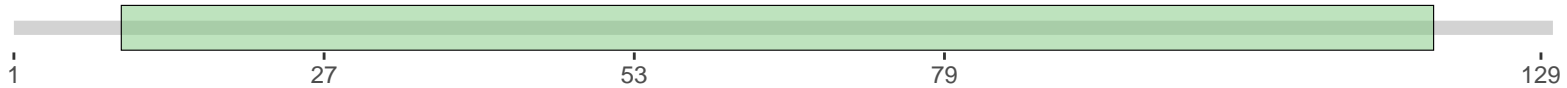


Protein length

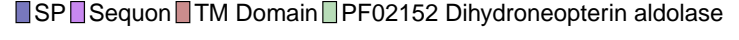


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

DCLSDTLSTYDIYKWKKEVEGPPRKLEKVAELASTLIDKYPQVSAVRVQVQKPHVAVGGSDVFLGVEIRHRDLDP

NbL04g00380.1 DNA-(apurinic_or_apyrimidinic_site)_lyase_chloroplastic [MW = 59.58 kDa]

No. of times detected



log(intensity)



Values from



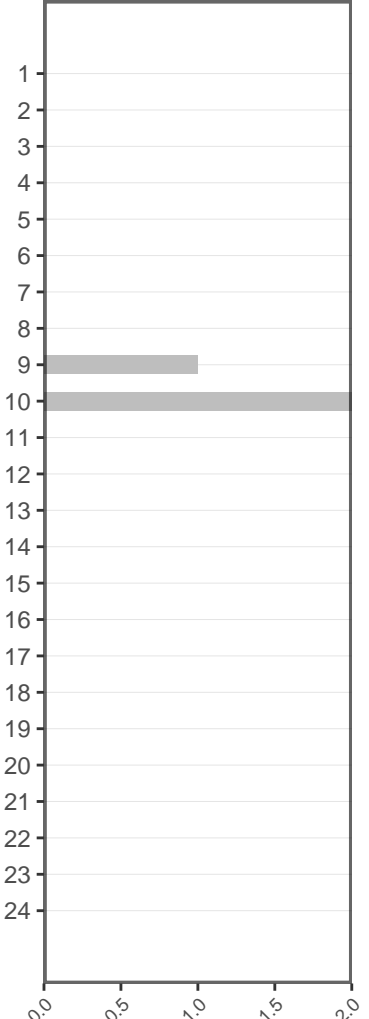
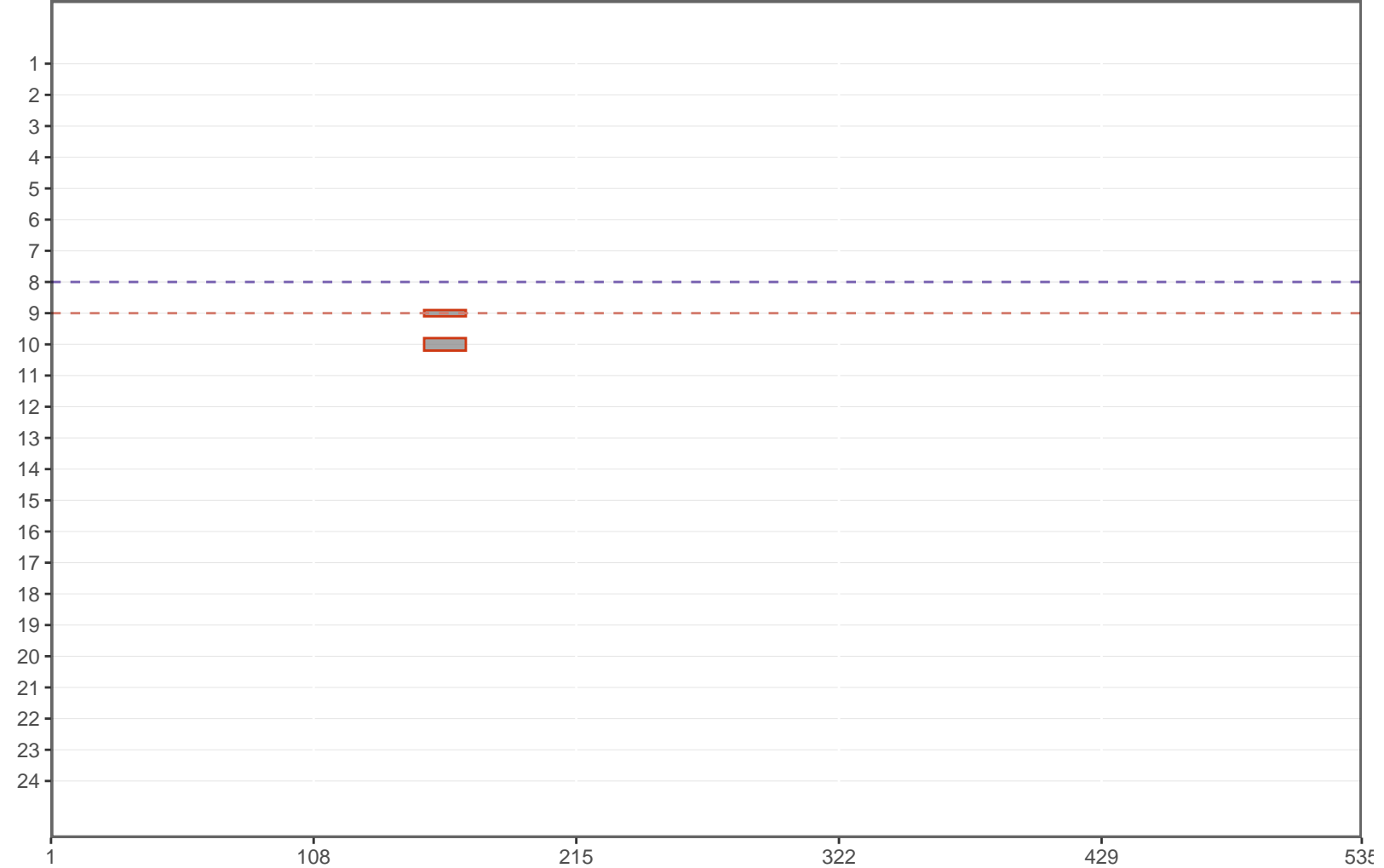
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VVYVPTTMRPPLSEKDKTKYKLLSWVNGLRALLKLNKLIQGLADREDFDLGLGETKLGDKDVEAIKESLGGYENSFWTQSEVAKLGYSGTARISRKPLSVRYGLGIPDHDTEGRVLTVEFDNPFLLGGYVFNSSGDLRLRLTYRTEWDPGLGNVYKKELEKPKVLTGDLNGAHEEIDVYVPMGNKRASGFTDEERGSGFETNFKNGFVDFTRFKGHPGVVGYTYWGYRHHGRKTKNGWRLEDFLVLSERIAIDNVHDSVLPDVGSDHSPGLKLLK

NbL04g00160.1 protochlorophyllide-dependent_translocon_component_52_chloroplastic-like [MW - SP = 64.46 kDa]

No. of times detected



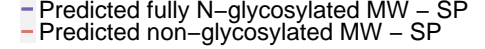
log(intensity)



Values from



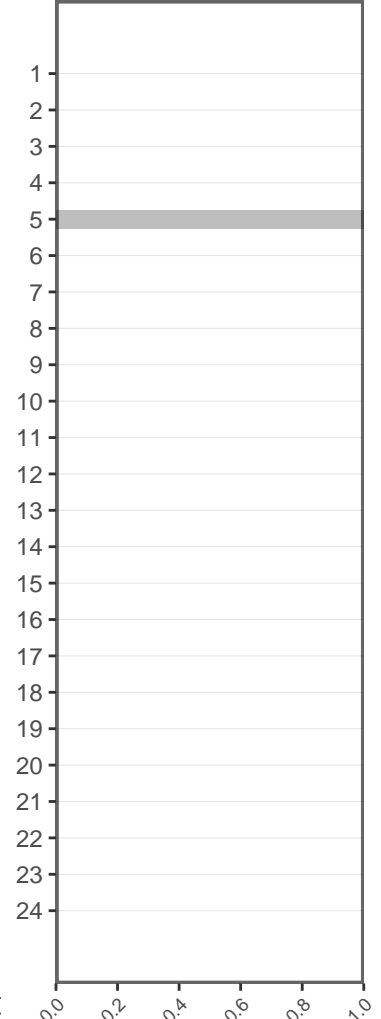
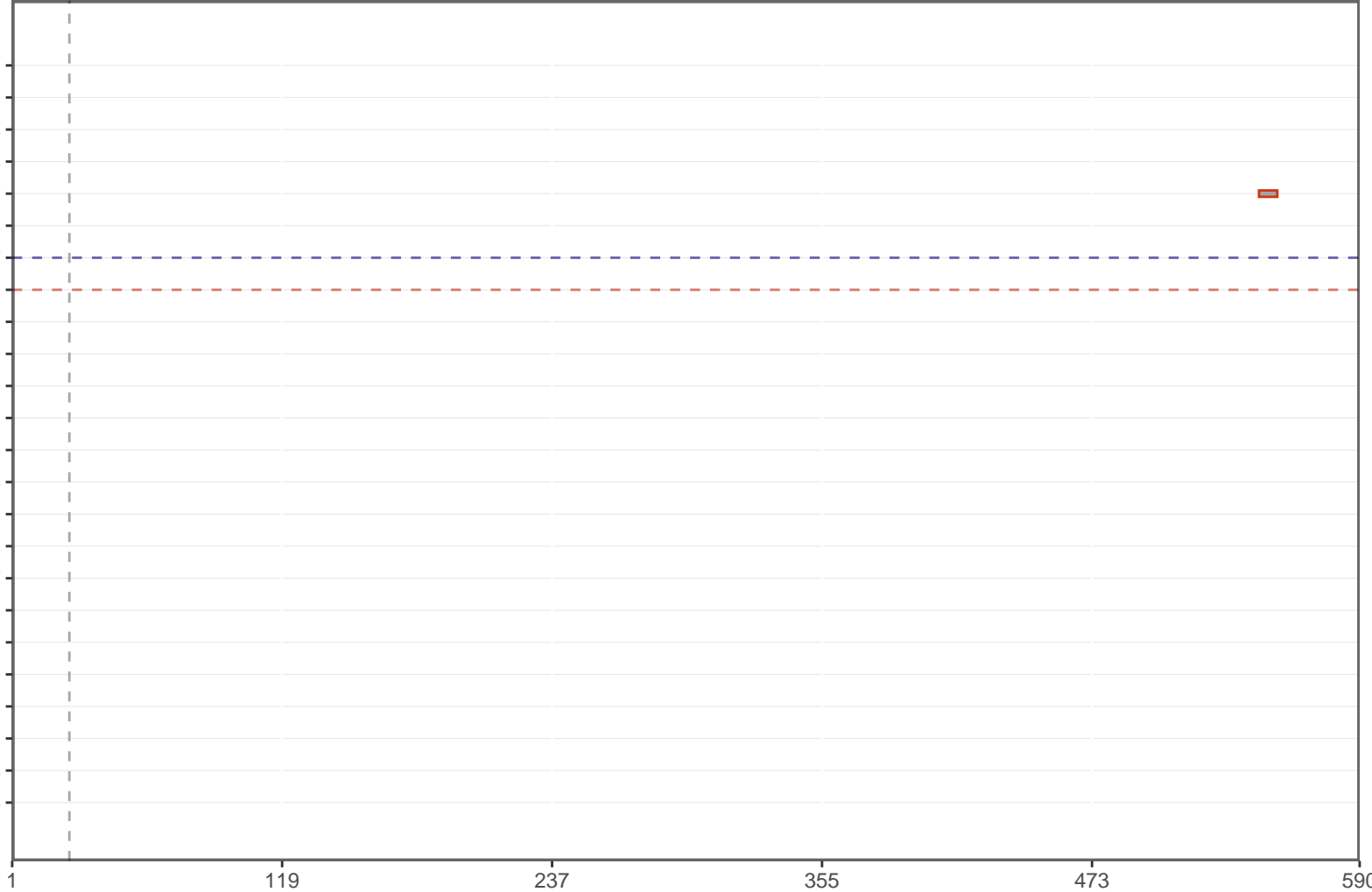
MW indication



Molecular weight



Gel Slice



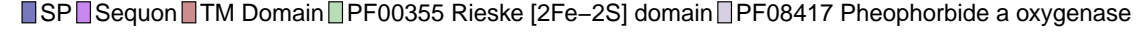
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

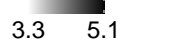
RDISYQYELLENLMDPMHVGYSHYGIMVDPQPKKVKADREGGRPLDITVTKLDVNSITANGGPRNTEAFQVYVYSLFAFGNGGKTSAVSSGTVQEKPSAEKQKQKALLIFIGIPVSPGHRIFASPRNFATWADRIPIRFIFHLGQNLIDSDVLLHVEEHKLEIGPYVYVWVNAQIMPTKADAVVAFRRWLNKYAGGGVDRWRAKYNGDLPTPPREQLLDRVWTHVTVNGTSCNFAYKGLNGLEILQIASIGMIGVAAAKGGMLSMVMRYSLVSIALLCFVASRWLSHFY

NbL03g24920.1 glutamyl-tRNA_reductase-binding_protein_chloroplastic [MW = 35.8 kDa]

No. of times detected



log(intensity)



Values from



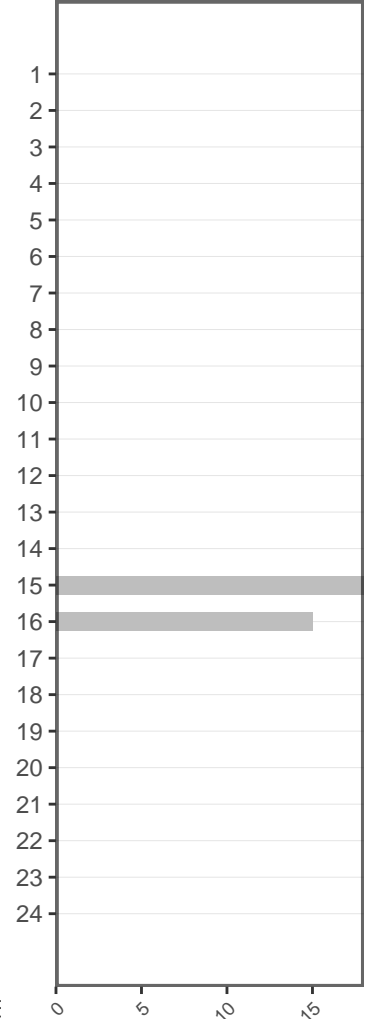
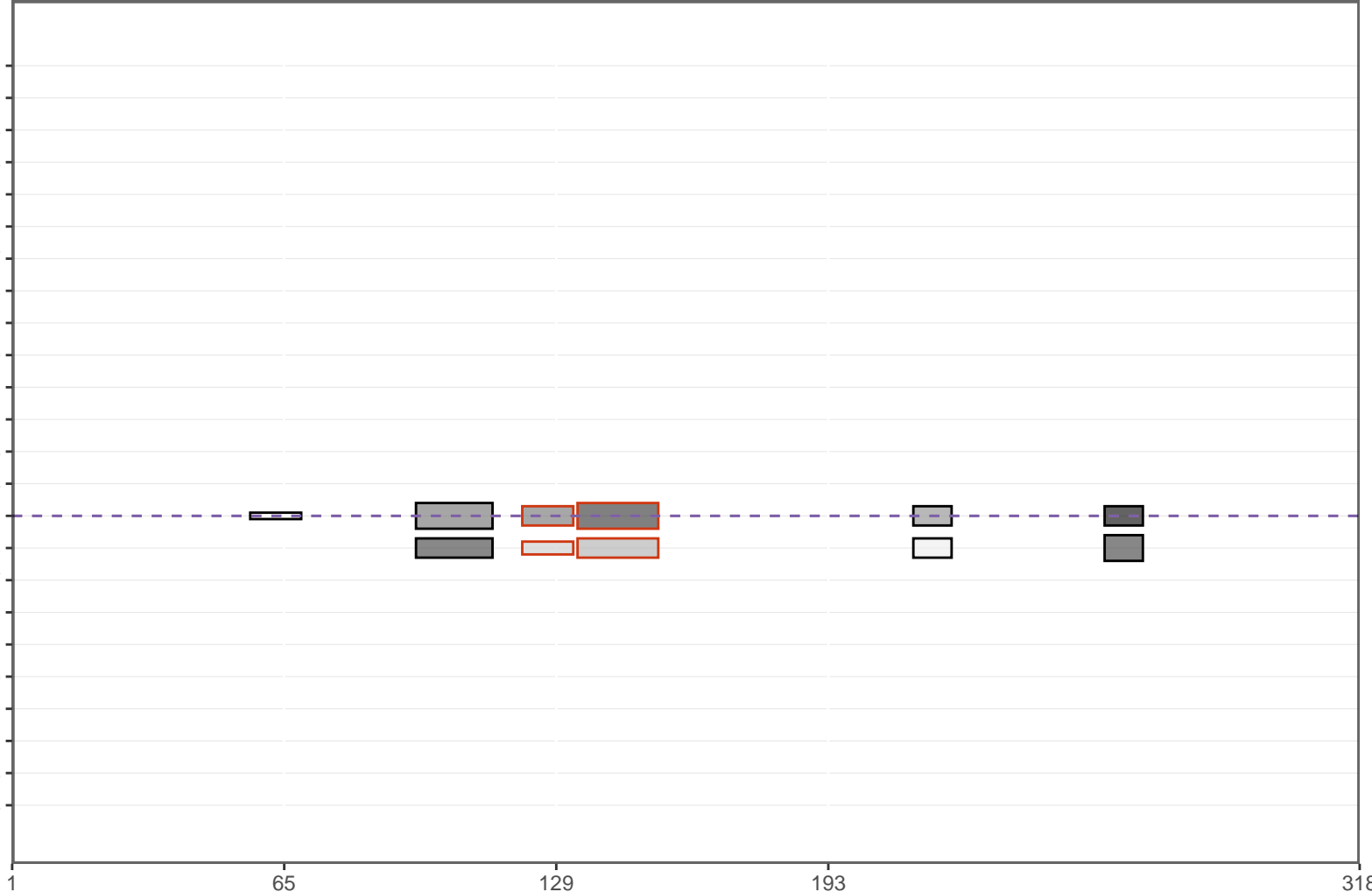
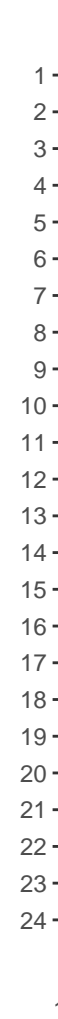
MW indication



Molecular weight



Gel Slice

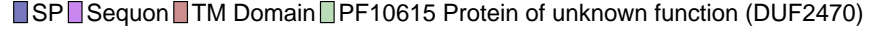


Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

EDTTLAKXLIHSYWKRFQHEDEKHLFLLSVERVLGLEDFAEEDGAWVTSSDVKLANPDLRDFAEARMIEENTHNRDELRFQNYHLDLQFQVSDAKMLWDRDLGFDVRFRRSPQNDVFEARIPFFREVTEDEKGAKSSFNQMSGLAWVEVKNPHAAEFKAKGLKKIEVTGL*

NbL03g24910.1 uncharacterized_LOC104100193 [MW = 28.76 kDa]

No. of times detected



log(intensity)



Values from



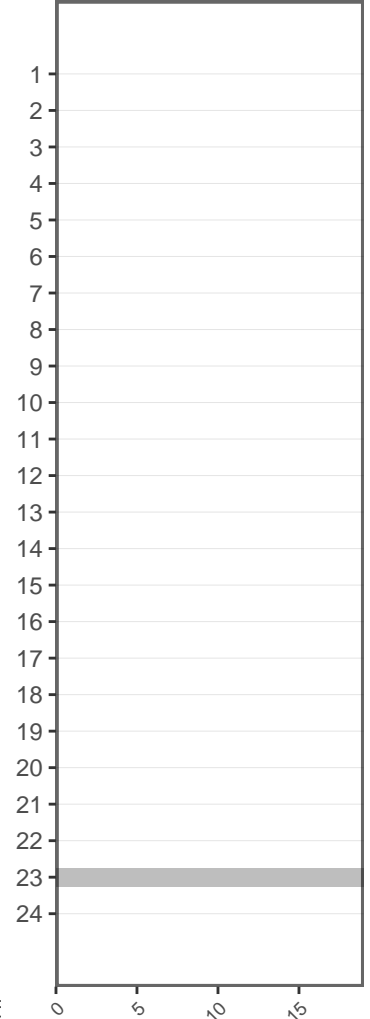
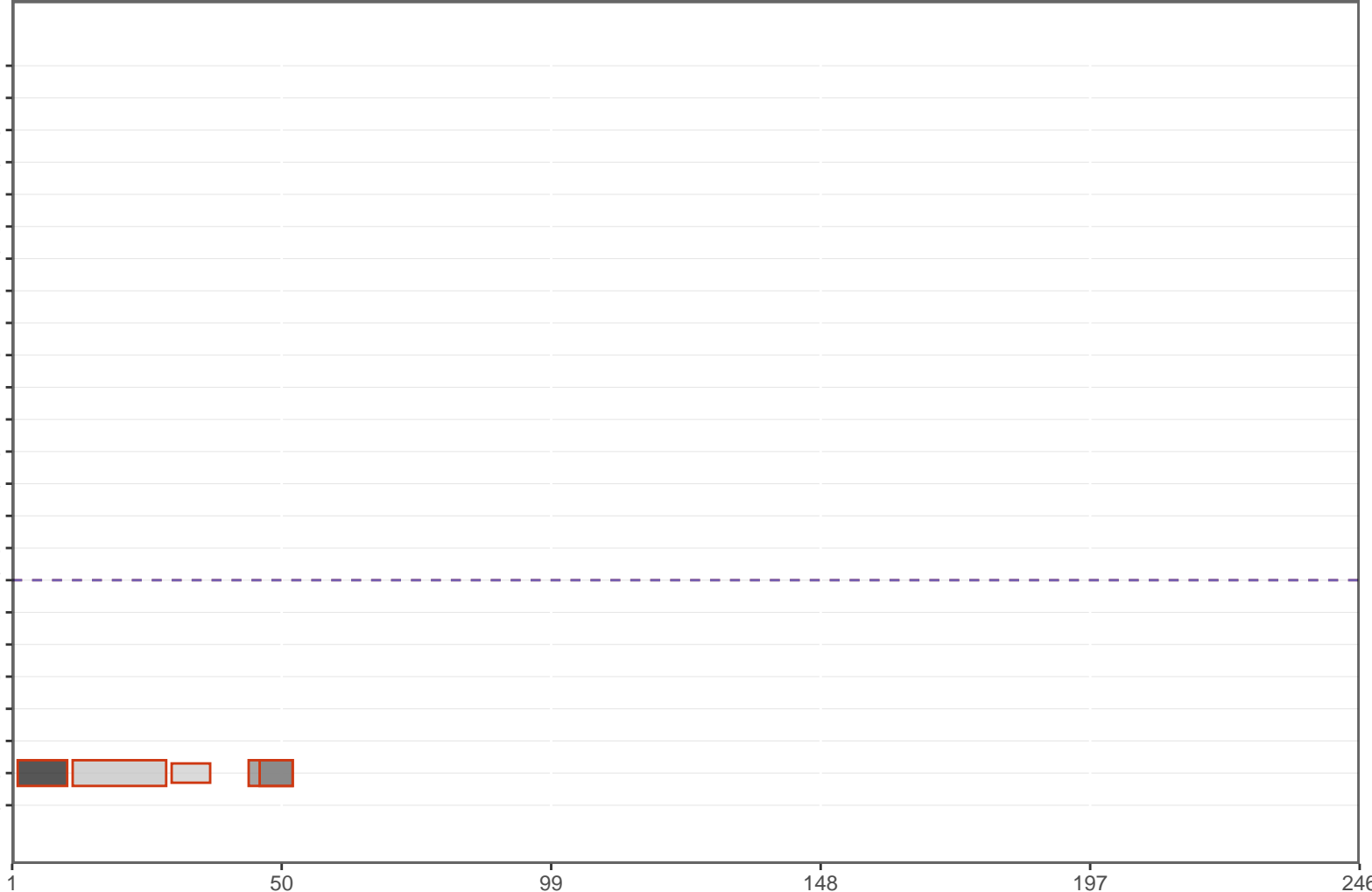
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KFGAEPTEALVEYRRYSHFVPRGSGSKYLRALVRPMLVGTGKWPVKNSHQKMKVAEMRMLRWMCGHTRMDLKNEDREKVGVPAMEDKMRERARLRWFGHGHRNTDAPVRRCEERLAVVGTGRGRGPKKY

NbL03g24880.1 cell_wall_integrity_protein_scw1 [MW = 35.03 kDa]

No. of times detected



log(intensity)



Values from



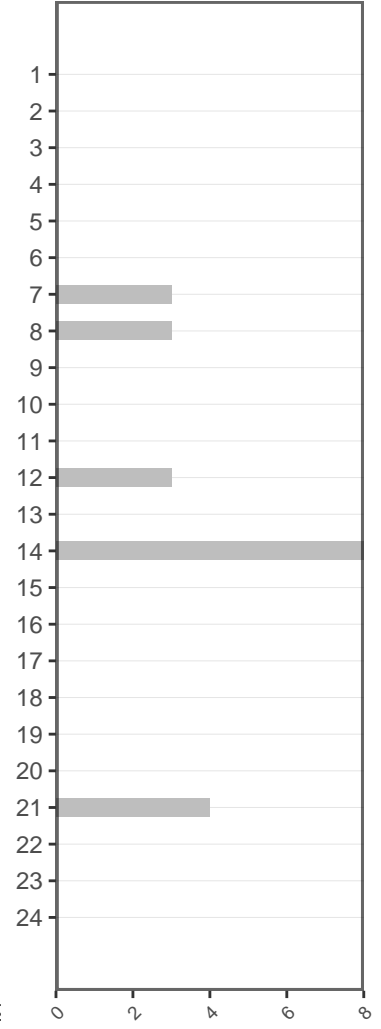
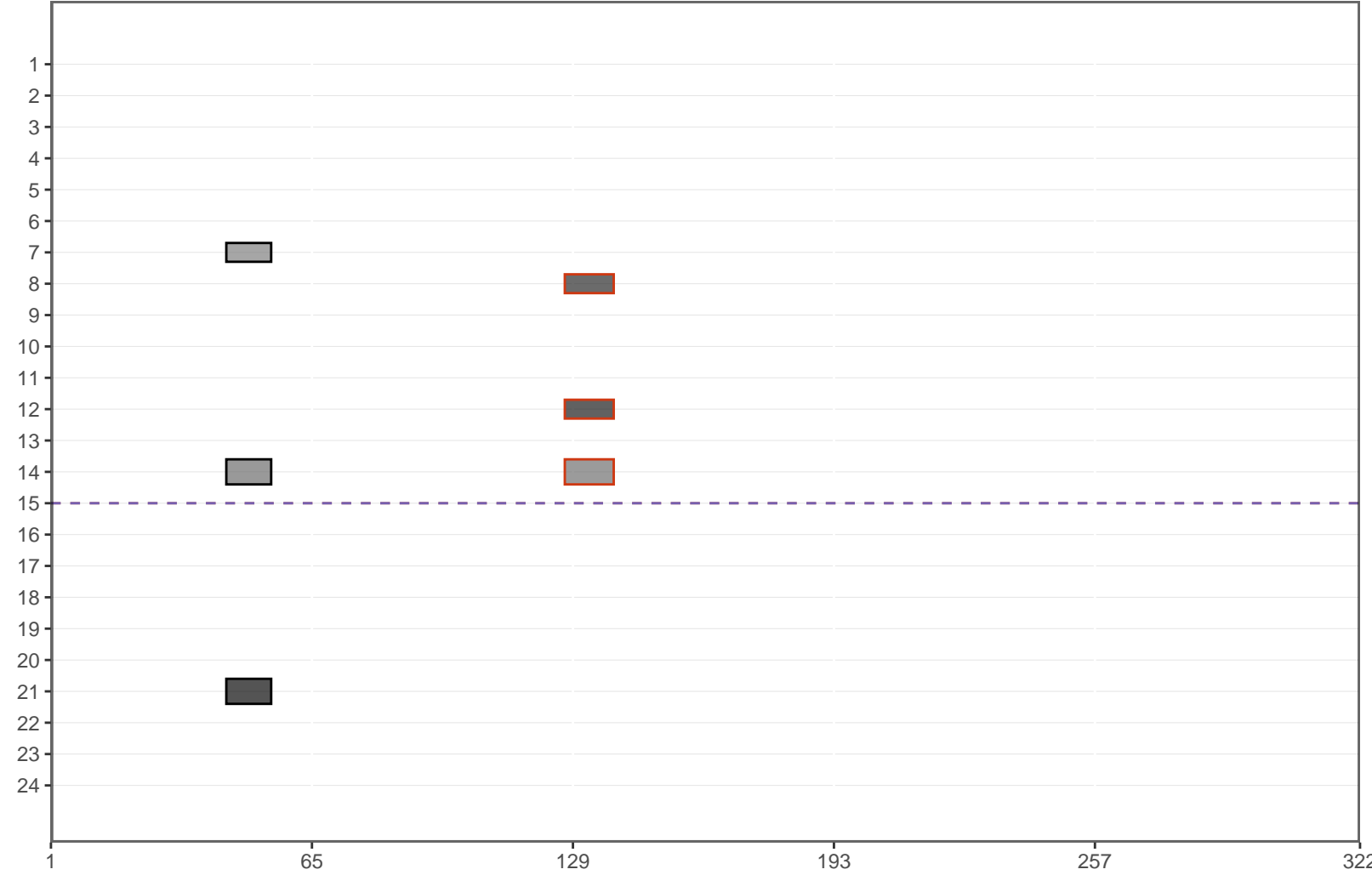
MW indication



Molecular weight



Gel Slice



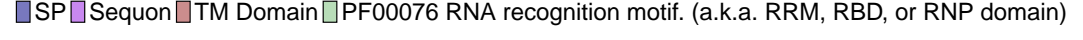
Protein length

Peptide counts over 4 repeats



Pfam domains

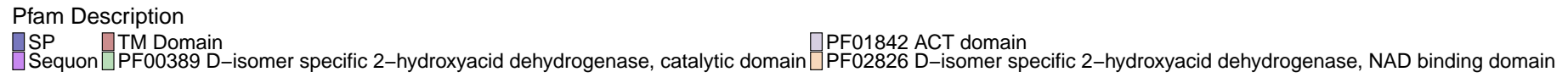
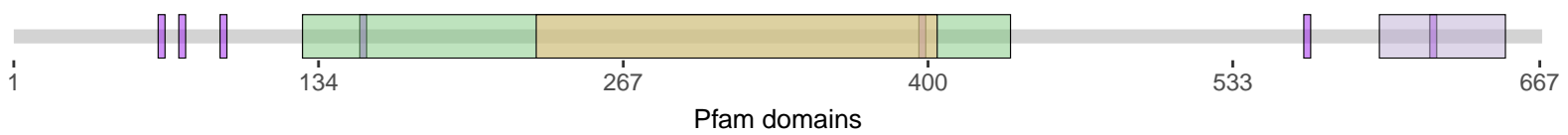
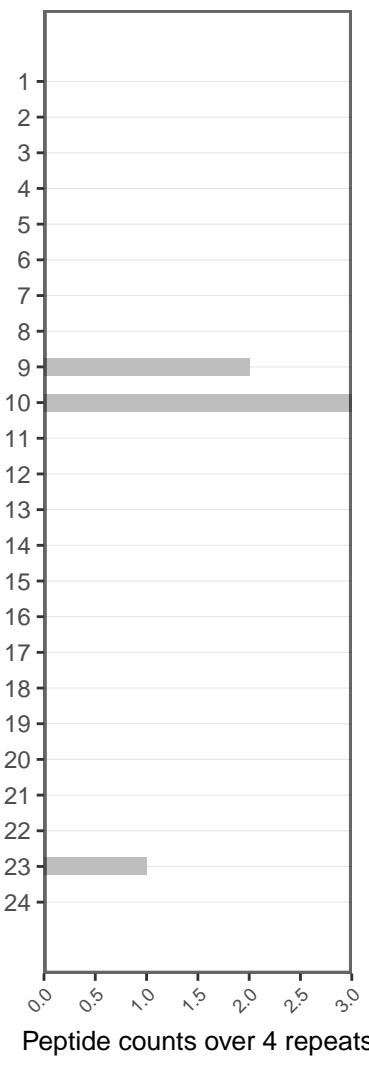
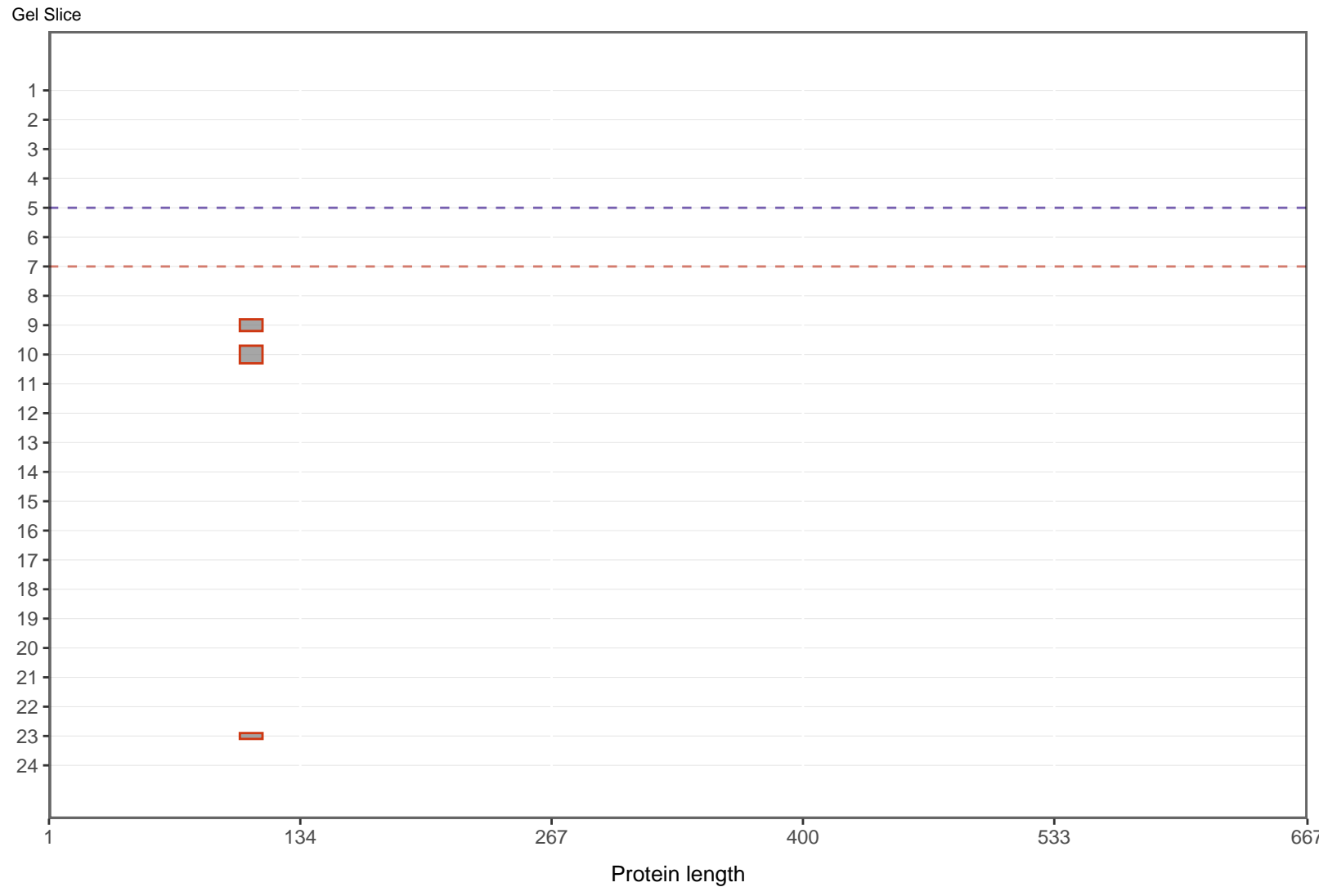
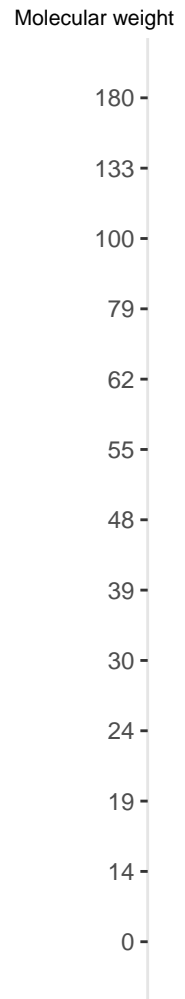
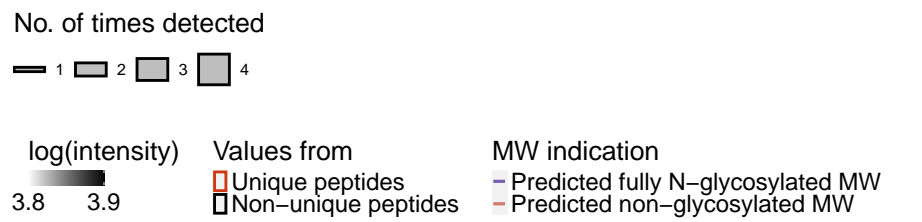
Pfam Description



Protein sequence:

DSGYSSPSPFHPPPAPVWGHVGLAGAPRPYDYGVPVPHMFMAPAPVPAFSSVYPIQNTKDNPPCNTLFGNIGENNEEELRGLFSTPGFGKMKVLRGERHTVCFIEFEDMNEATNVHHSLOGAVIPSSSSVGMRIQYKINPFGRRKDGHPVGAIPVNGAPPPLTKV

NbL03g24870.1 D-3-phosphoglycerate_dehydrogenase_2_chloroplastic-like [MW = 70.64 kDa]



Protein sequence:

VSLIIMPLTPTATKKVFNDDTFAMKKGVRLINVARGGVDEDAIYRALDGGVAGAAALDVFTEPPKDKSLVQHENVTVTPHLAGSTKEAQEGWIEIAEAVVAGALNGELSATVNAIPVPEVLSLAPVYVLAEKLRGLAVQLVTGGSGGQINVYVYKSAARDPSLDRLLLRAMVTKGIETPISDTINLWNAFSAKGGKGRISEERWVDS6PEYVVEHQVQINLVGSRFASALBENGNISIEGKVKYGVPHLTRVGSFSDVSLSEGNILKGVDPGPMQGVGNLGSENVN

NbL03g24800.1 protein_STRUBBELIG-RECEPTOR_FAMILY_6 [MW - SP = 74.66 kDa]

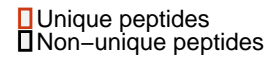
No. of times detected



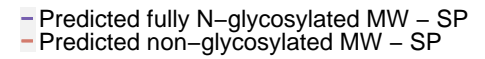
log(intensity)



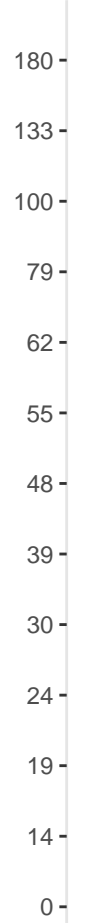
Values from



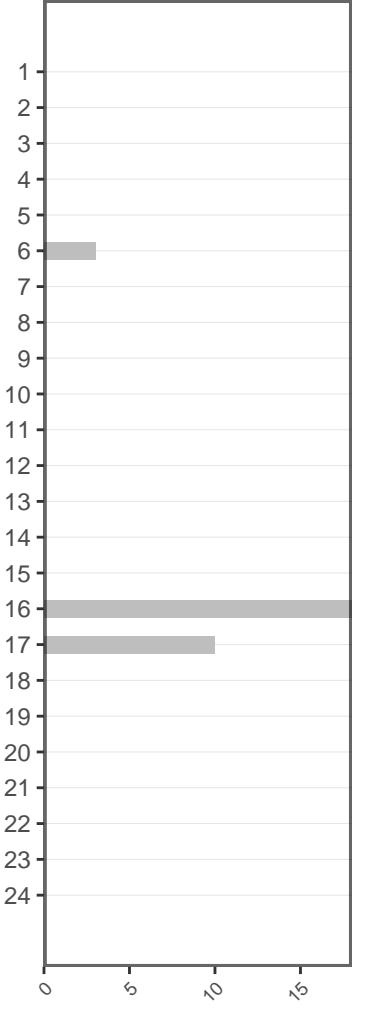
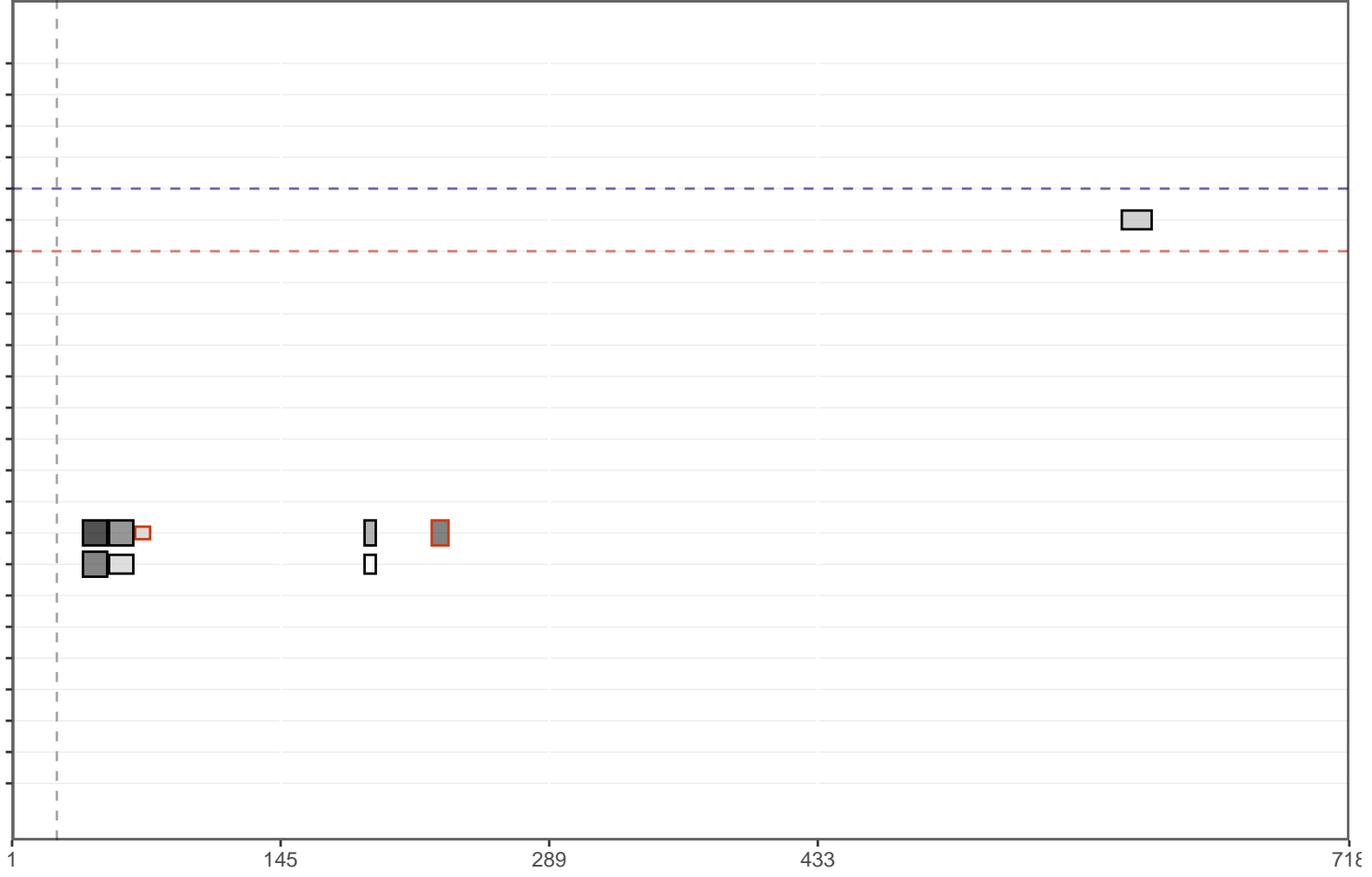
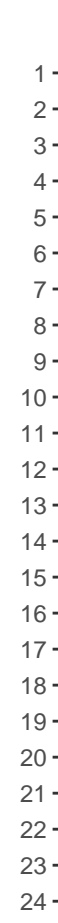
MW indication



Molecular weight



Gel Slice



Protein length

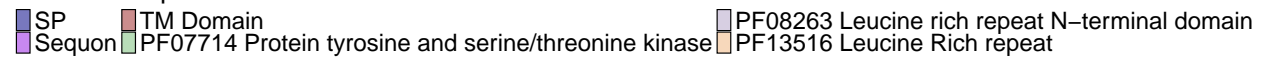


Peptide counts over 4 repeats



Pfam domains

Pfam Description

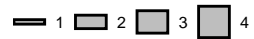


Protein sequence:

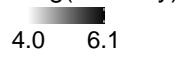
IKTNQASSAPSYKTFEAPWVWLRPPPIRHKSFDEDEAAKPIVPPKKVNTAKINARGYSIADLQMATDSFVSNLHGEQGFGRVYRAGFDGKVLAVKKNKSNALNPEDFLDIVSEISGLHHPNVTETLVGYGSEHGQHLVYEFHKNKALHDFLHLDENSKPLTWNRSVKALGTARALEVYHEVCGSPVWVKKKNSANILLDAELNPHLSDGGLASLADVDGALNHNNTGSGYGAPEVAMSGGFTIKSDVYFSGVWMLLELFGKPFDDGGRTRSEQSLVRWATPCLHIDDAI

NbL03g24710.1 pectinesterase/pectinesterase_inhibitor_U1 [MW = 64.44 kDa]

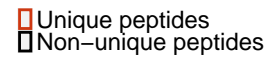
No. of times detected



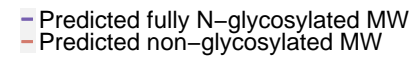
log(intensity)



Values from

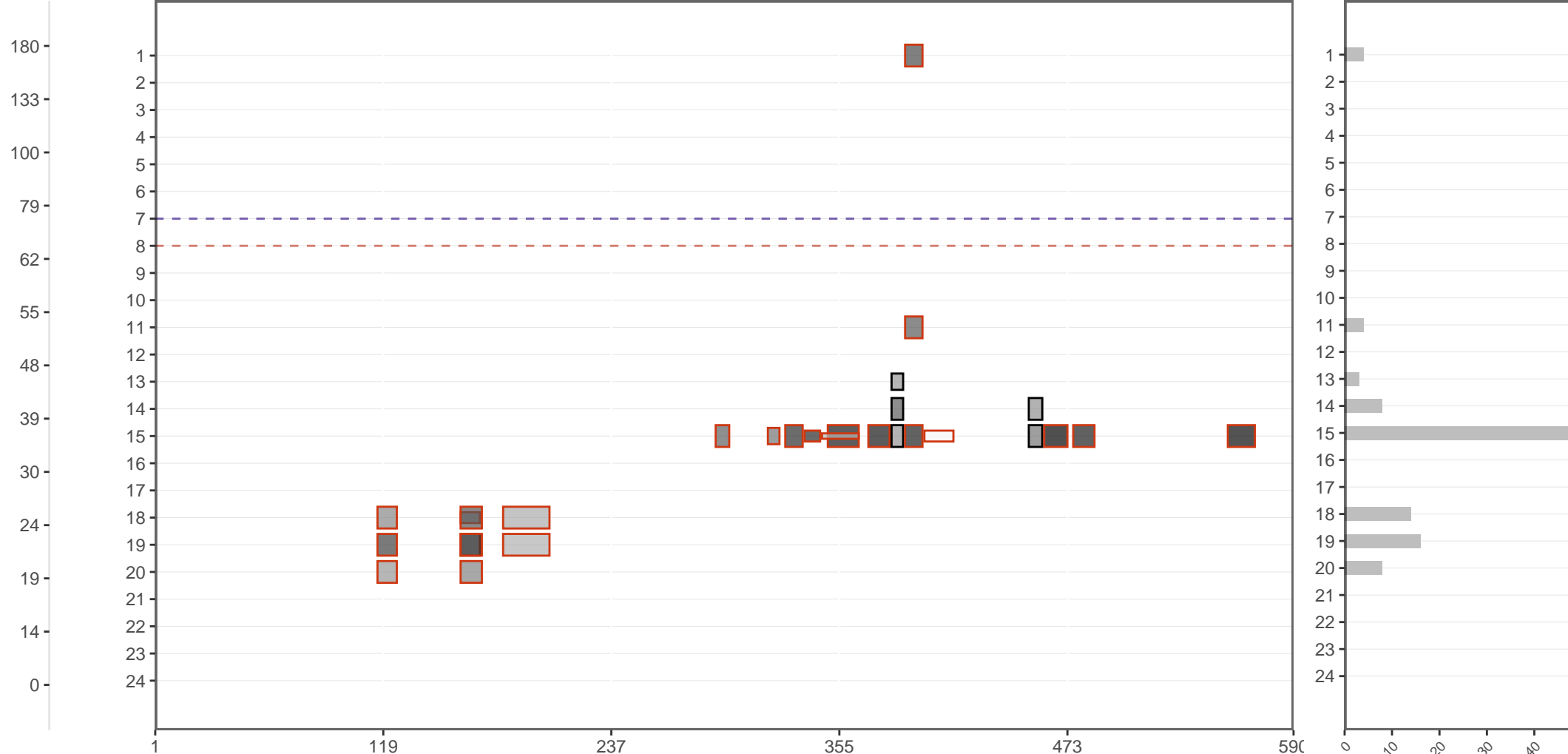


MW indication



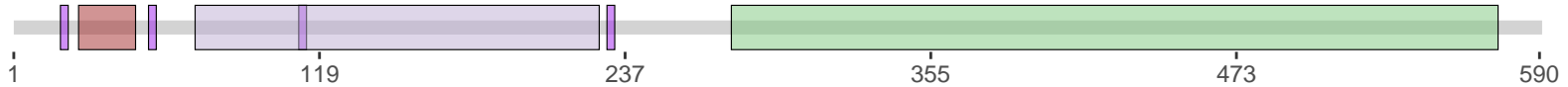
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

XGSGNFKTYSEAVARAFPEKSKRYVIRKAGVYRENVDPVKKKTNMFMMDGRGRNTITGSRNRYKDGSTTFNSATVAVGEKFLARDITFQNTAGAAKHQAVLRVGSGLSAFYRGDLAVQDLSLVYHNRQGVFVQGLAGTVDFIFGNAAVAVGGDGHARRPQGGKNNVTAQGRSDPNQNTGIVGKGRIGATSDLRPVQKSFPTLGRPWKEYSRTVMQSSIFDVINSAGWHEWNGFNALTLFYGEYQNTGAGAGTSGRVWRGFKVTSATEAQAYTPGRFTAGGS

NbL03g24700.1 pectinesterase_3 [MW = 64.33 kDa]

No. of times detected



log(intensity)



Values from



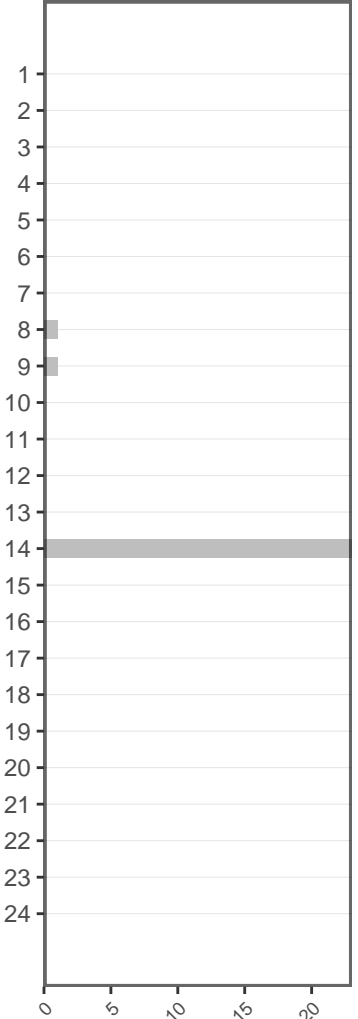
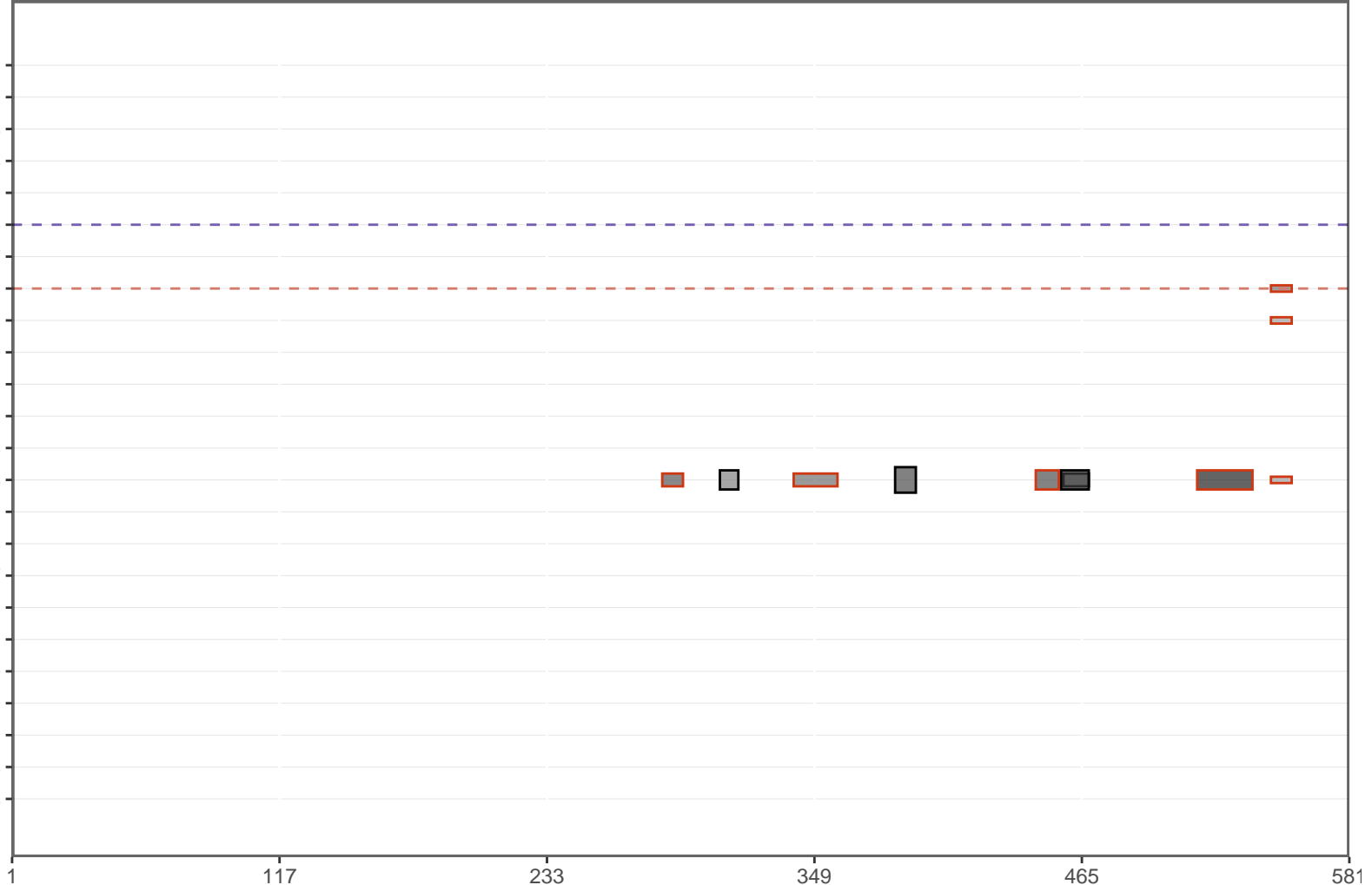
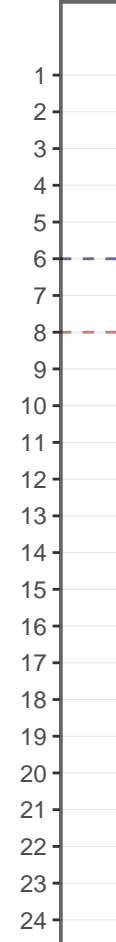
MW indication



Molecular weight

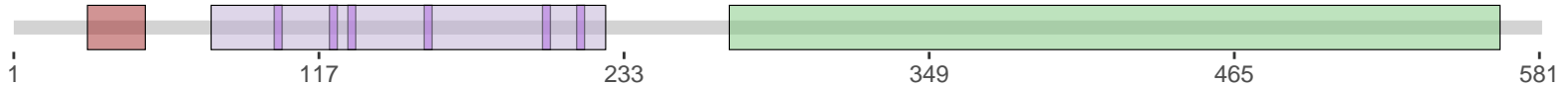


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ITRDVLTIQEAVKRVFKKSKVRFVWYKAGEVYETVRIMDKSHVWMMYGGDKTKTVVSGRLNFVGGTPTFDATFAVAGRGIARDMAFNKNTAGAAHGAAMRSGSDHSEVYRGLFDGFDGLYAHNSNRGFYRECDTGTIDRFQSAVAVFGSGKIPRQPLRNGFVTTAGKQKIPNGMNGMSKGGDLSPDLDTARTYLGKRPVKGYSTVVMGNSIAFLHPVGVIEWVWVGVVERADTFYAEVQNTGPGAAVQRVWVAGYKSTTPEAAKYTVQSLGGDTVLPTD7

NbL03g24680.1 alanine_aminotransferase_2-like [MW = 59.88 kDa]

No. of times detected



log(intensity)



Values from



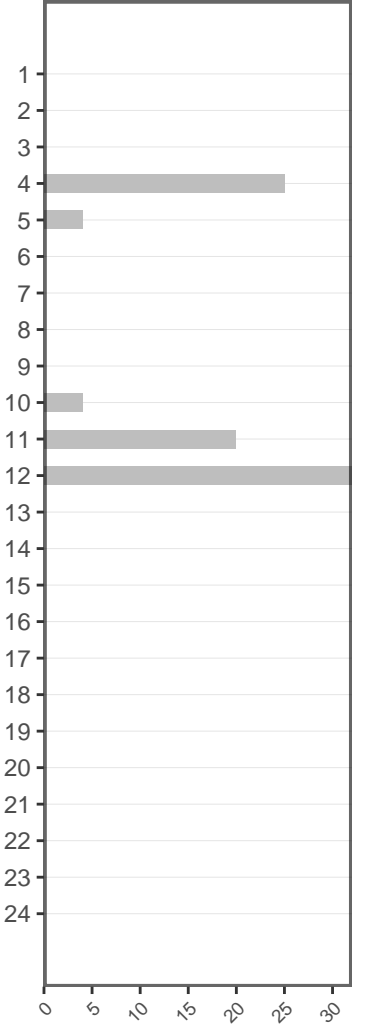
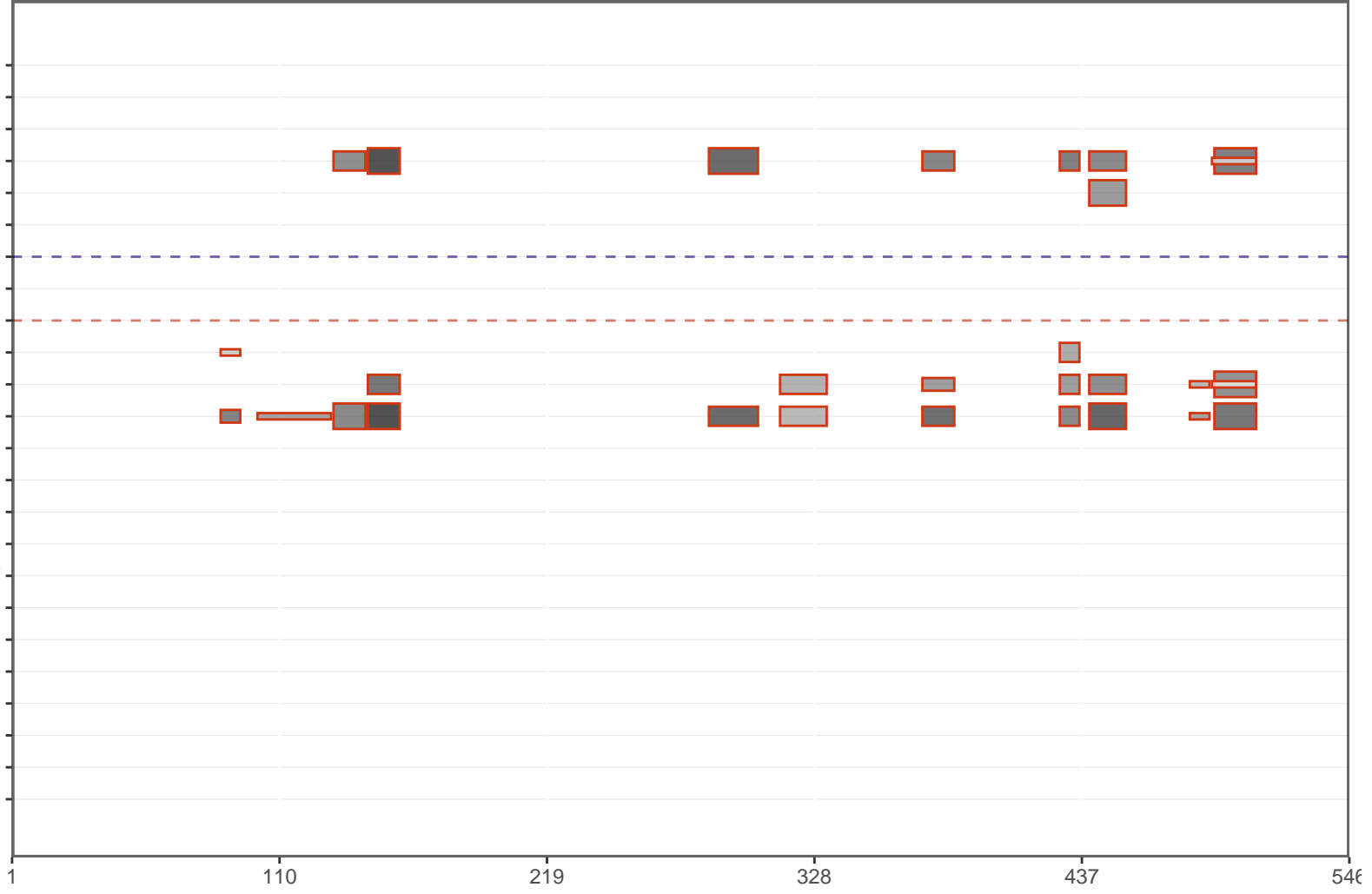
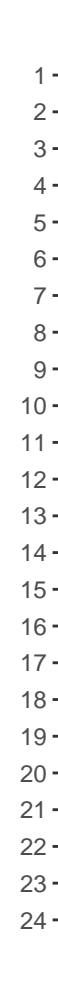
MW indication



Molecular weight



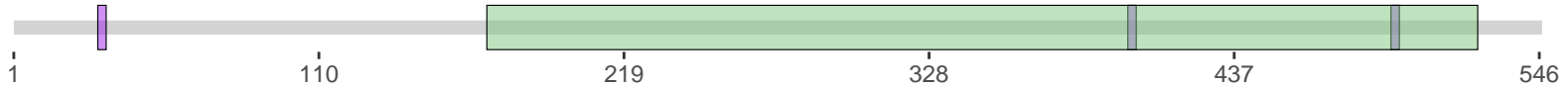
Gel Slice



Protein length

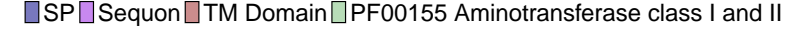


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SWGLSELENLQKTKAKGKIVKRVLWVNPQNTGGVLAEANQRDIVEFCKKKEGLVLLADEVYQENVYVPEKQHFHSFKKIKARMSDFGKDKSLVDFQGVKSGFYGGCKRGGYMEVTFGSPFIREQHYKVASVNLGNSGQGLASLVMSPPKVGDSEVYSFSAEKEALSSLRRAKTLQDAFNLSLQVTFQKVAEGAMVLFRRINLPWAKAIAEAEAKTAPDGFYARRLLNATGAAVYVPGSGFGQRPQTWHFRCTILPQEEKIPAVSRRLTDFHKGFMDFRS*

NbL03g24600.1 serine/threonine-protein_kinase_Aurora-3-like [MW = 12.24 kDa]

No. of times detected



log(intensity)



Values from



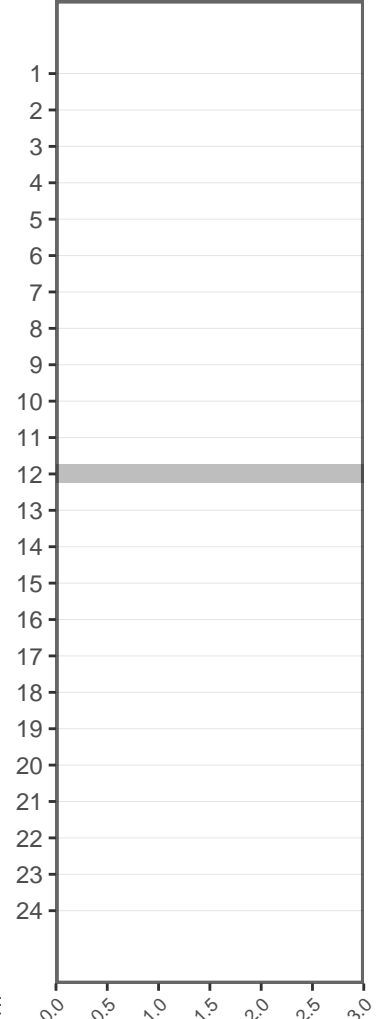
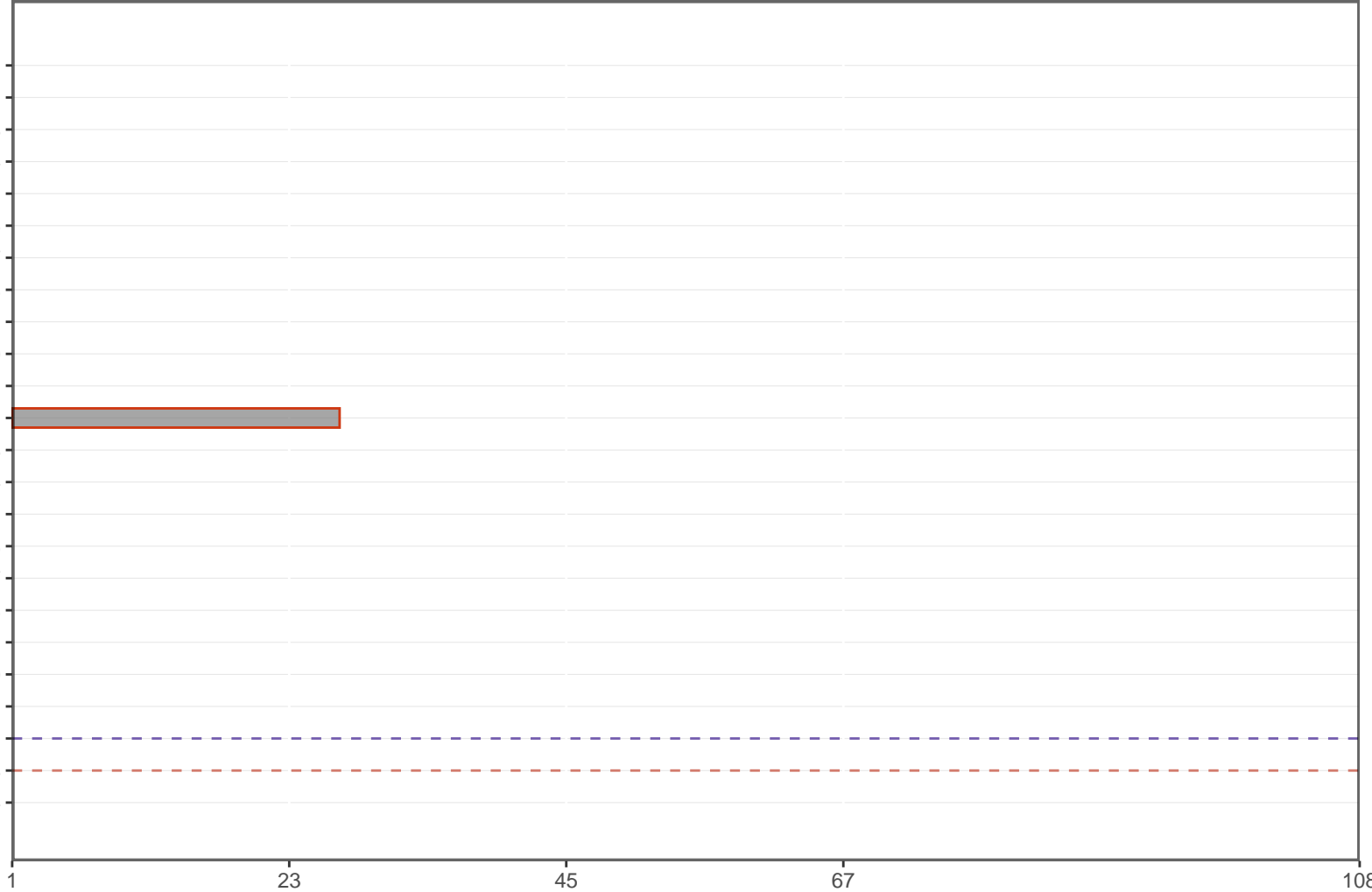
MW indication



Molecular weight



Gel Slice



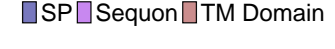
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DLEILEGPLLTGSFWLFDGFRGVNLFQGHFDKGLGKTASVDFNMWREIGVAALLRGGYDFVF

NbL03g24550.1 subtilisin-like_protease_SBT1.5 [MW - SP = 80.57 kDa]

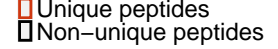
No. of times detected



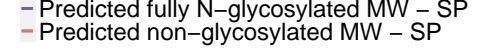
log(intensity)



Values from

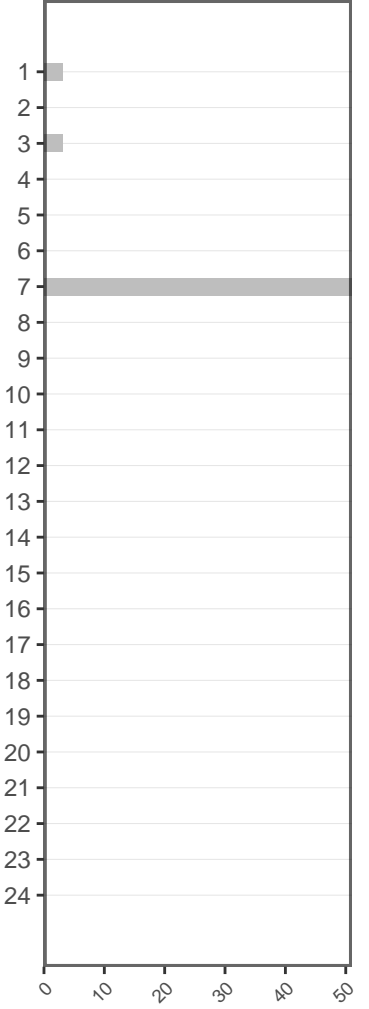
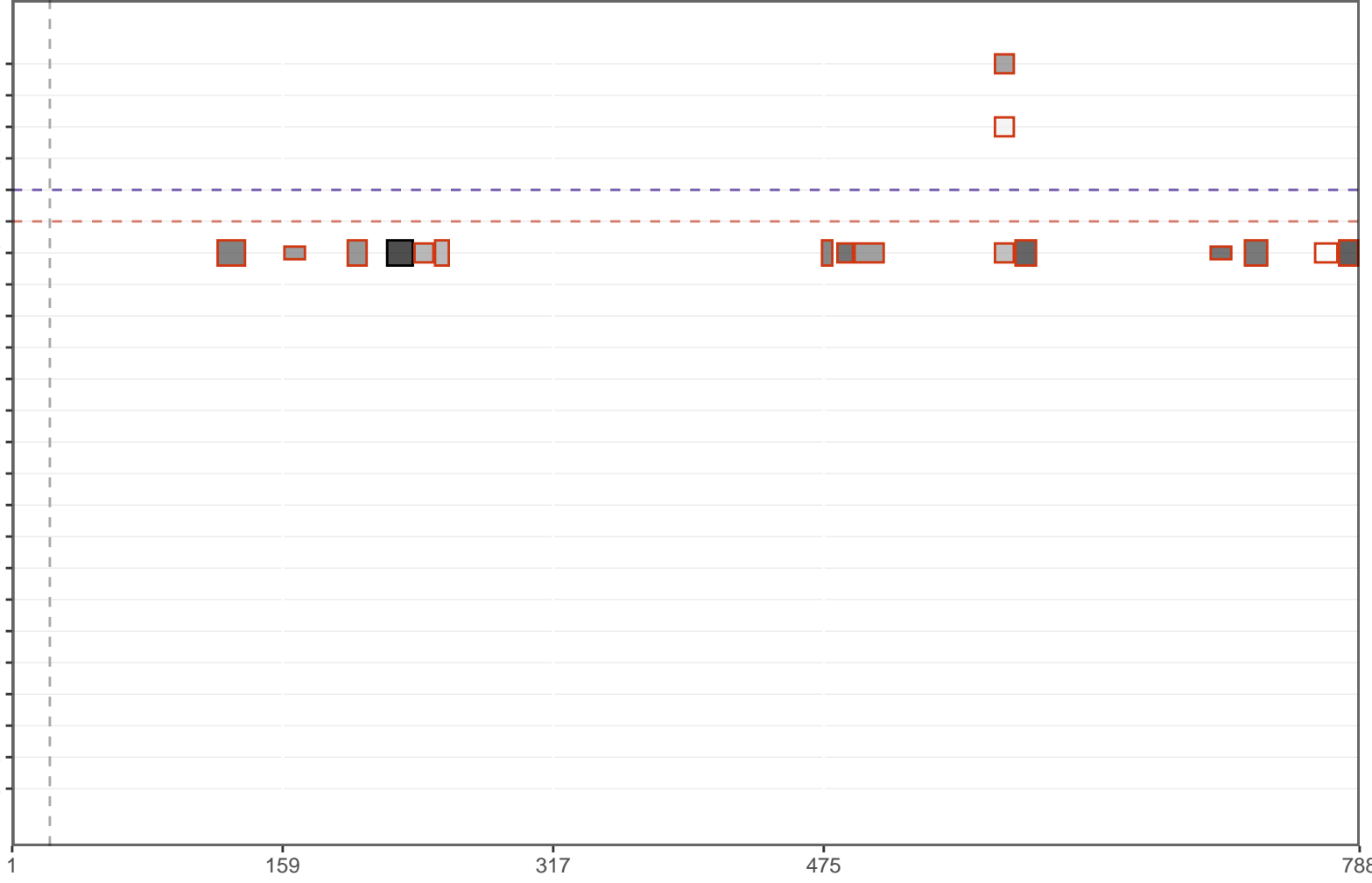
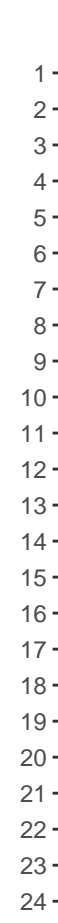
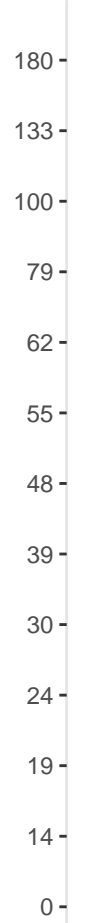


MW indication



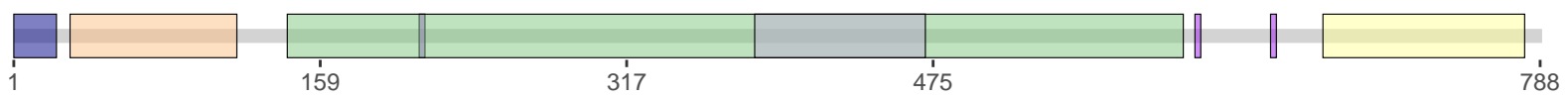
Molecular weight

Gel Slice



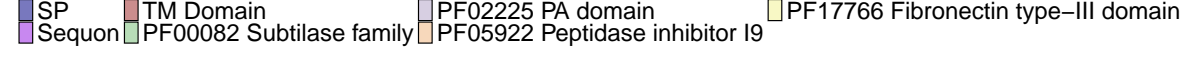
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MLIYAGSEGDSDYSSBLGLEGLNPNDEVDGKVLGDRGVNSRAVKGVEVKKAGGGMLANGVDFDGEGLVADCHLPLRTPSVGASAGDEIRKVIETALKSKSRPTATLFRGTIVNWKRPVVAFSFARGPNFETPEILKPDVAHPGLNLAAWPDGVGPSGIPDKRRTFENLISGTSAGCFHVSGLAALLKAAHPGWSRPAIRSAIMFTYATVDNRIGQMDESGNSSTVMDFGAGHVHPGNAMPGLYDILTSYDVAVDLGNENNYFTKNRVVTRKYSDCSGAKRAGHYGA

NbL03g24390.1 linoleate_13S-lipoxygenase_3-1_chloroplastic [MW = 103.33 kDa]

No. of times detected



log(intensity)



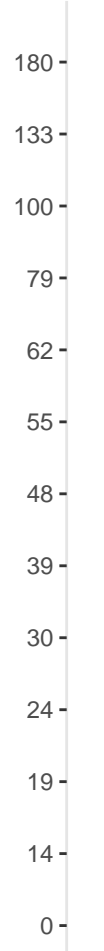
Values from



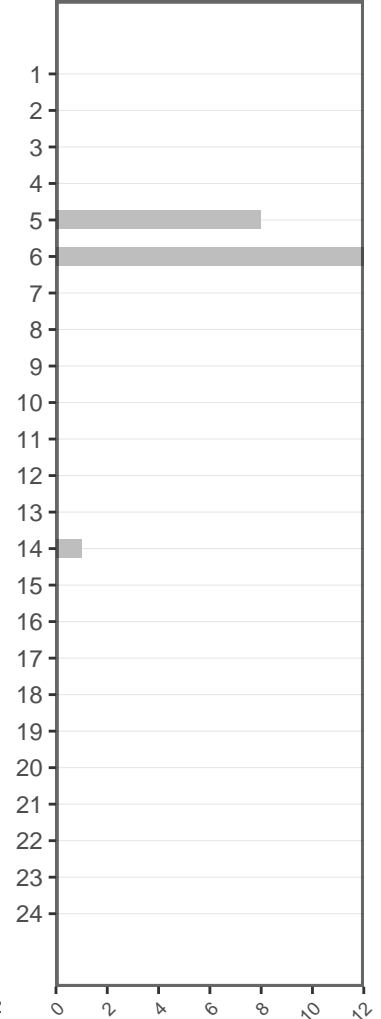
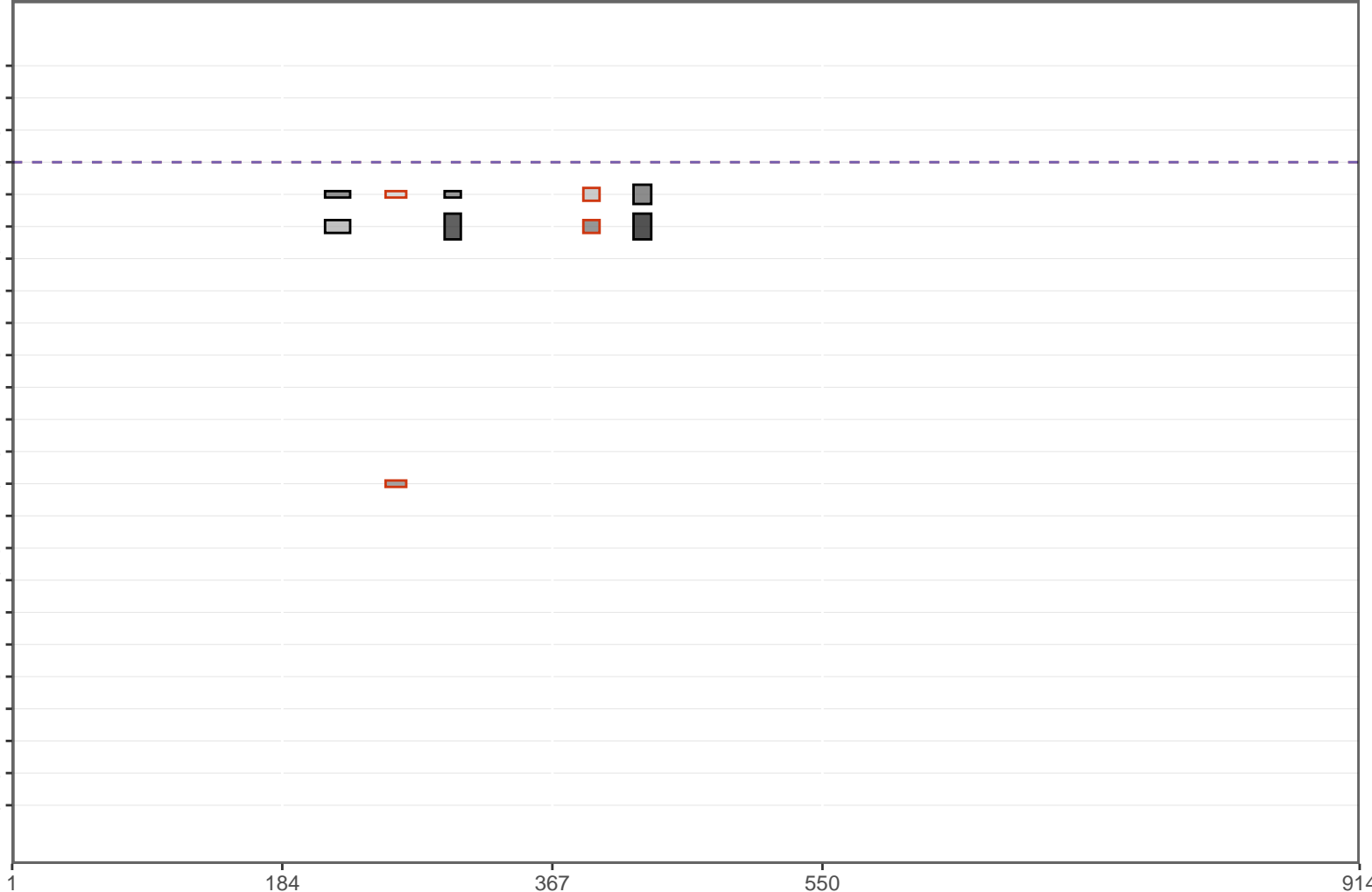
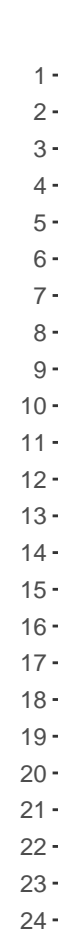
MW indication



Molecular weight

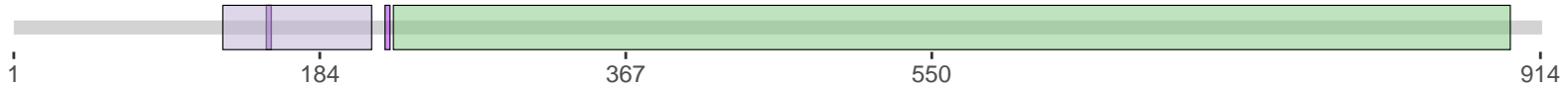


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DPEIYGTQESAIKEEHLGHLNGMTVQGEALDSNRLIYVDYHDVLFPLDRINALDGRKAYATRTIFLSDLGTLKLPVAIELSLPQTGPPSRKHHVYTPPDATGNMWMGLAKAHVGSNDAGVHQLVNHWRTHAGLEFFLAHRGLSAMHPYKLLDPHMYTLEINALARGSLISADGVIEAGFTGPRYGMEMSAANKNFWRFLEGLPADLIRRGMAVDPDTPQHGKLLLEDHPYAADGLMWAIEGWRBKVNHYYPDSAGVNDRELQAWAESINVGADLRNEE

NbL03g24370.1 aldehyde_dehydrogenase_family_7_member_B4 [MW = 54.63 kDa]

No. of times detected



log(intensity)



Values from



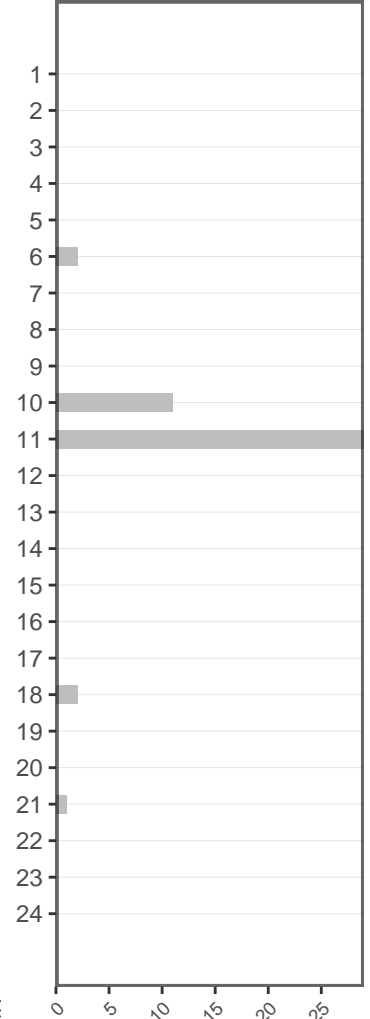
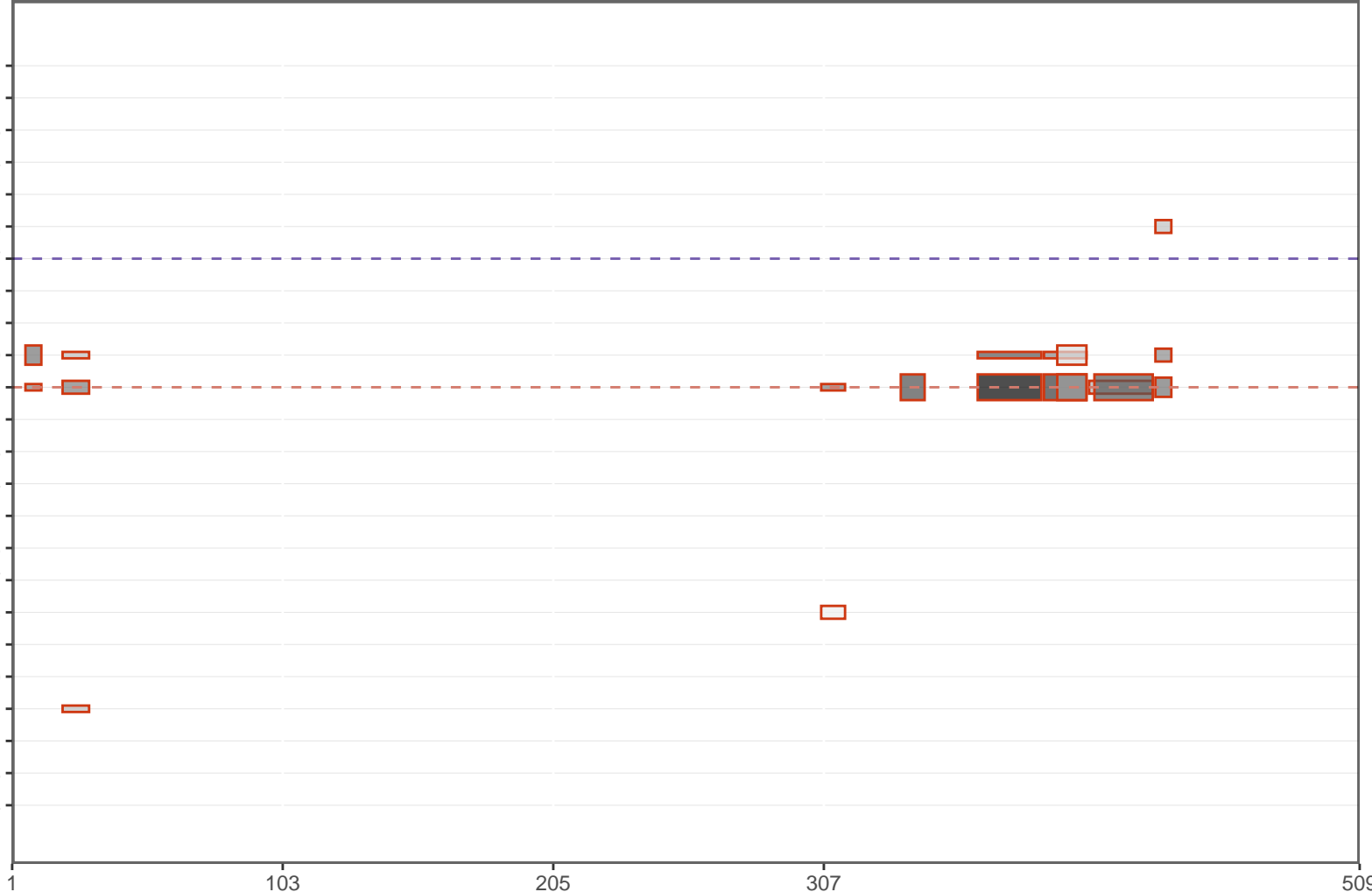
MW indication



Molecular weight



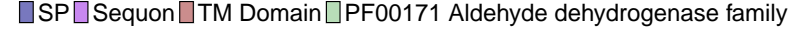
Gel Slice



1 103 205 307 509



Pfam Description



Protein sequence:

SFTGSSKVLAVDGTVNRFRKGLLELGGNMIIMDDADIELAVRSLFAAVGTAGGRCTTCRRLLVHETVYAKVLEPLVDYKGVKIGDPLEKGLFLGPLHRTSRSENFQKGGKGNKSGGGKILTGGVIESEGDFVHPTVIEISKAEVVKEELFAPLVYVKFKTFEEAVENNVDPGLGSSIFTRNPQIMFKWGAAGSDGGIVNNIPTNGAIEGGAFGGKGTGGGREGAGSDSWKGYMRRSTCTNYGNEPLAAGNFG

NbL03g24260.1 peroxisomal_(S)-2-hydroxy-acid_oxidase_GLO4 [MW = 39.73 kDa]

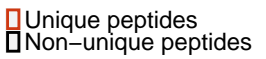
No. of times detected



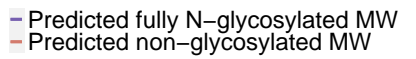
log(intensity)



Values from



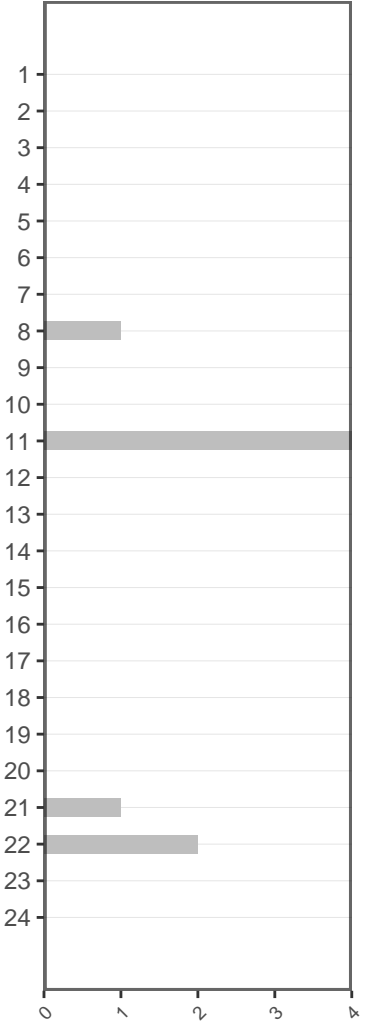
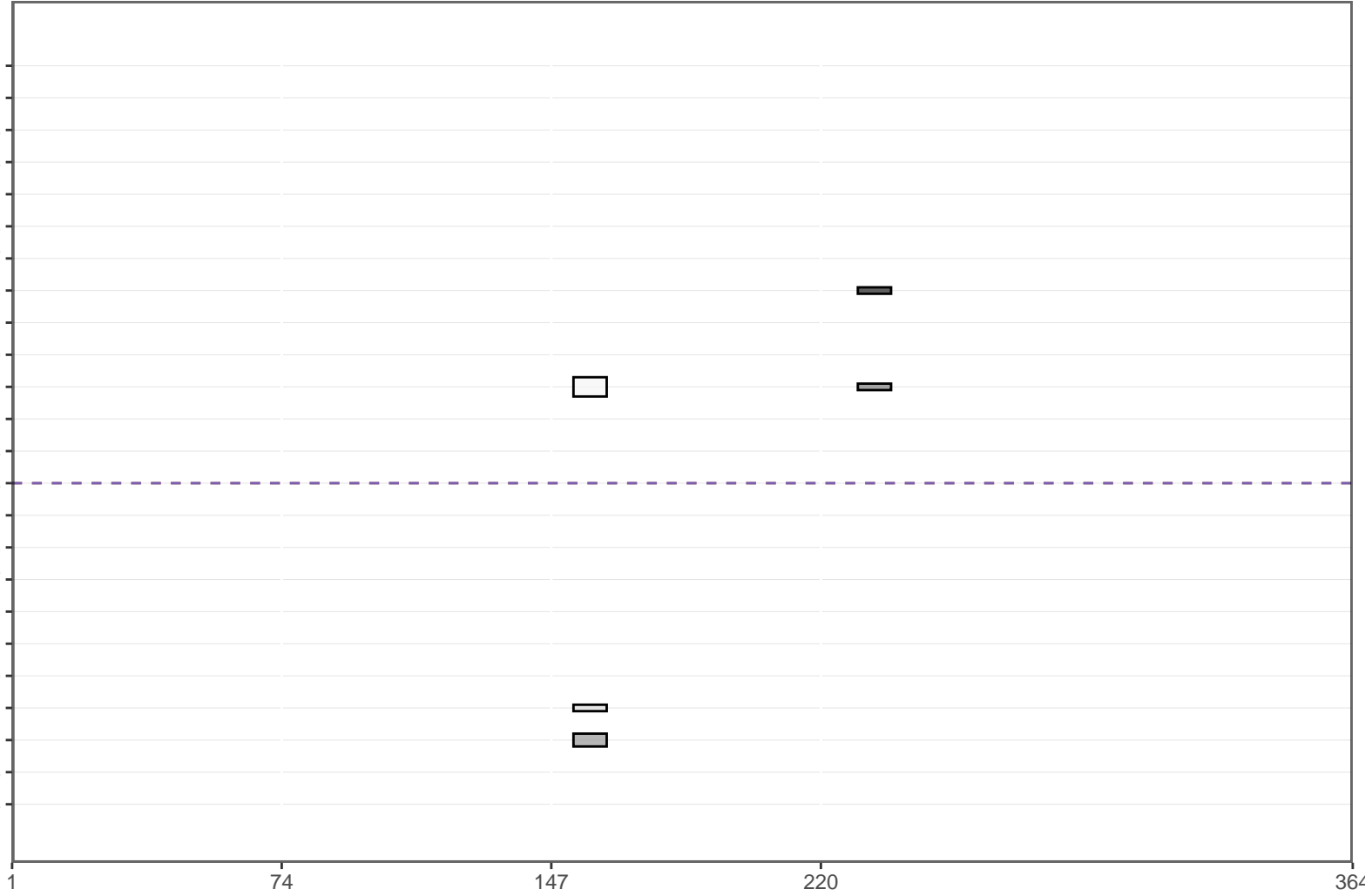
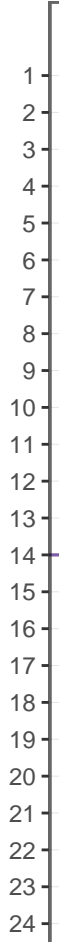
MW indication



Molecular weight

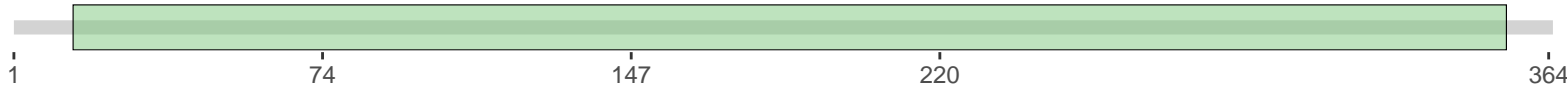


Gel Slice



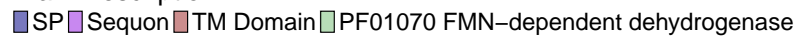
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ADIKNKAVAPRLKINFEGLISTEYVNDKGSNIEAIAAGTFDASLGWWDIPWLKSTKLPKIKGVLTSBDAKAVKAVGVEGIVSNHGARQLNVAATISVLEEYVHVAVGDKVVPVFFDGGISRGTDIFKALALGAKAVLGRVVYGLAAKGEHGVKQVIEMLNKLELTMALSGGCTINDTRSHVKTQKEYGRM

NbL03g23940.1 glyoxylate/succinic_semialdehyde_reductase_2_chloroplastic-like [MW = 39.69 kDa]

No. of times detected



log(intensity)



Values from



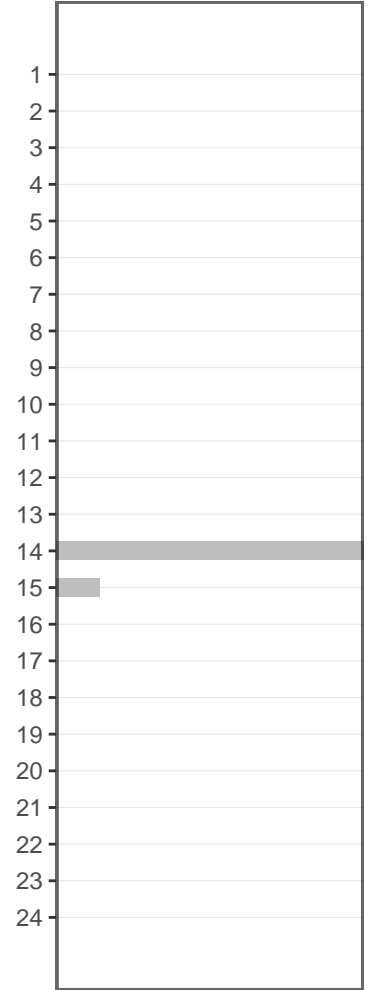
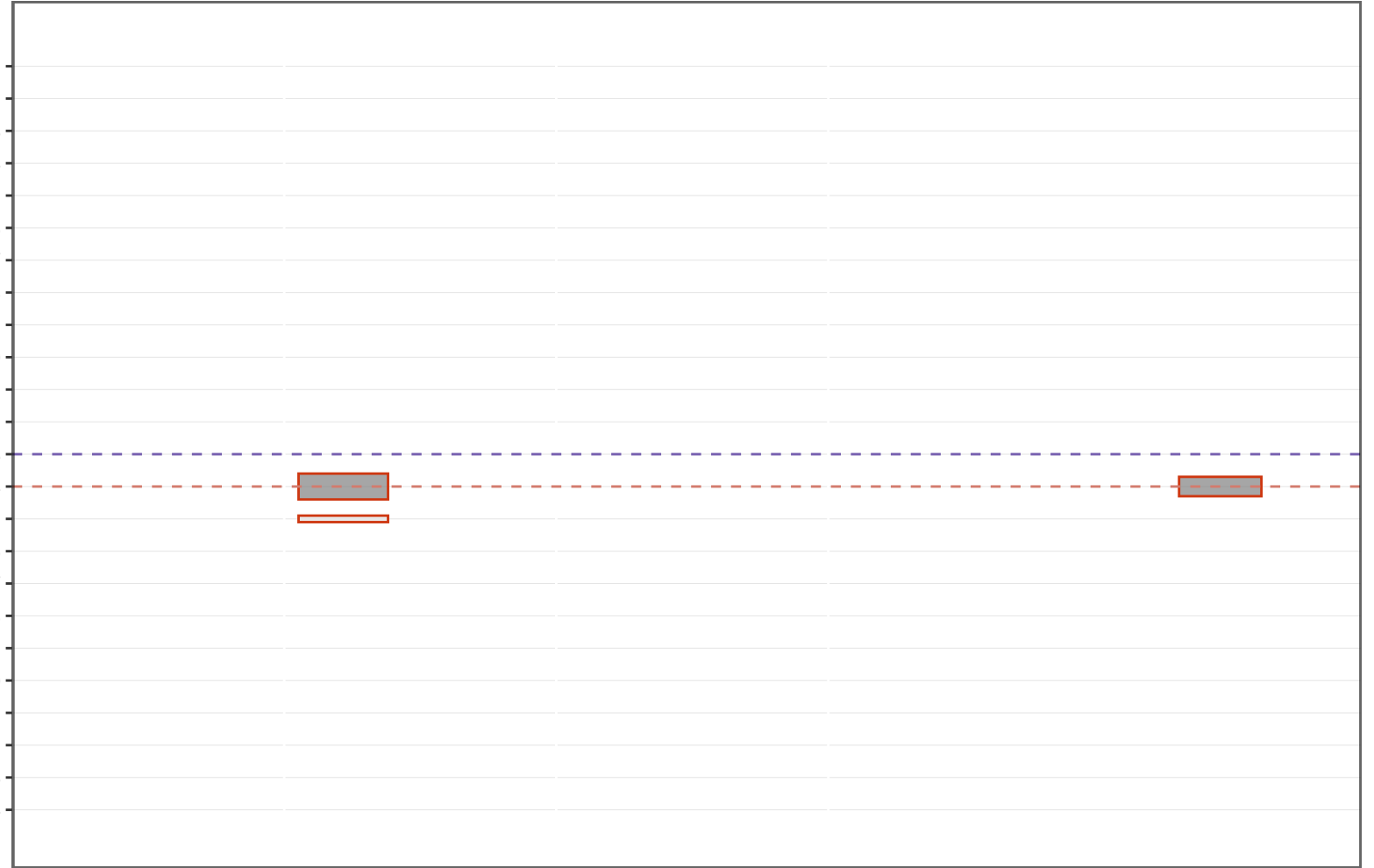
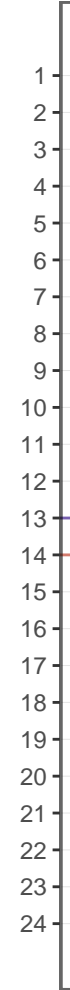
MW indication



Molecular weight



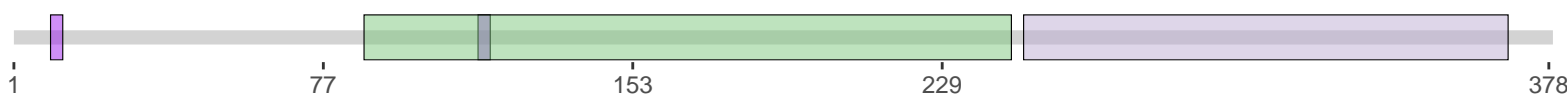
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF03446 NAD binding domain of 6-phosphogluconate dehydrogenase
- PF14833 NAD-binding of NADP-dependent 3-hydroxyisobutyrate dehydrogenase

Protein sequence:

YYVDVSTVDTGGTSHKJGHEHRATGAHFLKFAFVSGGKKPAEDGGQLFRITAGDDVLYETVAPLDDMGKSRFYLGVEVNGAAMKLVNMMVMSGMMASFEGGLVSEKVGLDPSVLEIVSDDGAEAFMAMKGPSMAVKSLYPTAFPLKHQKDLRLALVLAESVSGPTPIAATNELYKWKSHGLSDGDFSAVIEALKVGLGRET

NbL03g23920.1 putative_hydrolase_C777.06c [MW = 39.39 kDa]

No. of times detected



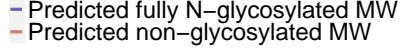
log(intensity)



Values from



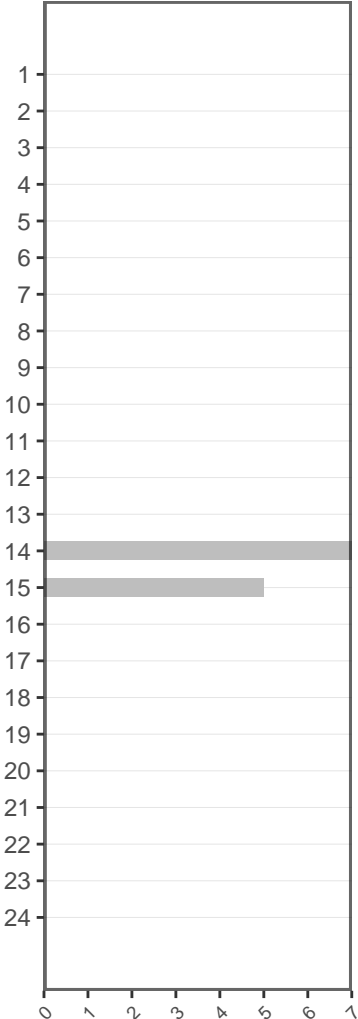
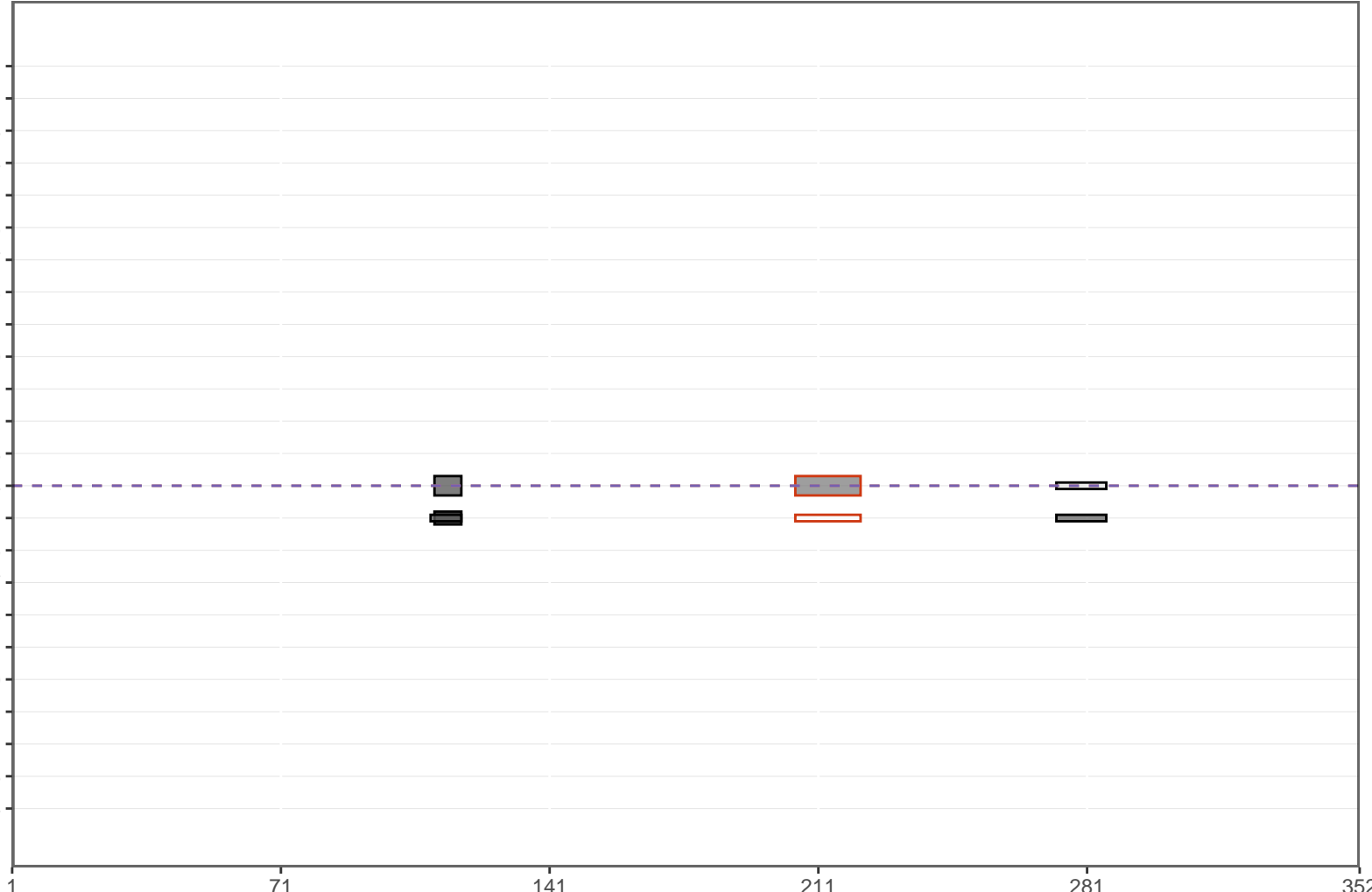
MW indication



Molecular weight

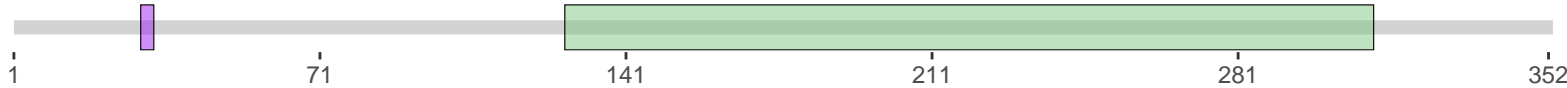


Gel Slice



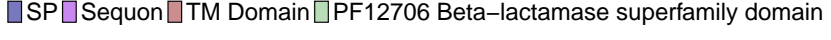
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AIGSLDDLRDVTNVDGPRIVASRDFEVMKTKHYLVDRSGIPGAAVSELGFNKEDFFVNDLEIPLVWVHSGSDYRSLGFRFGDGYHSDVDPEETYPLLKDCHELLMDALRPPRSGSTHFGLPRALEEVRKIKPRITLFTGMMHLMDEHEVNERLLKRETEGGVGLSDGLRVPVSL*

NbL03g23830.1 WD-40_repeat-containing_protein_MSI4-like [MW = 50.78 kDa]

No. of times detected



log(intensity)



Values from



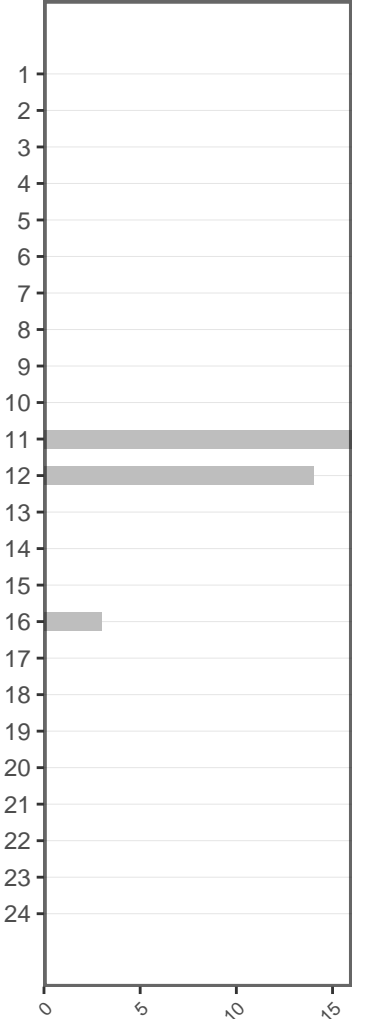
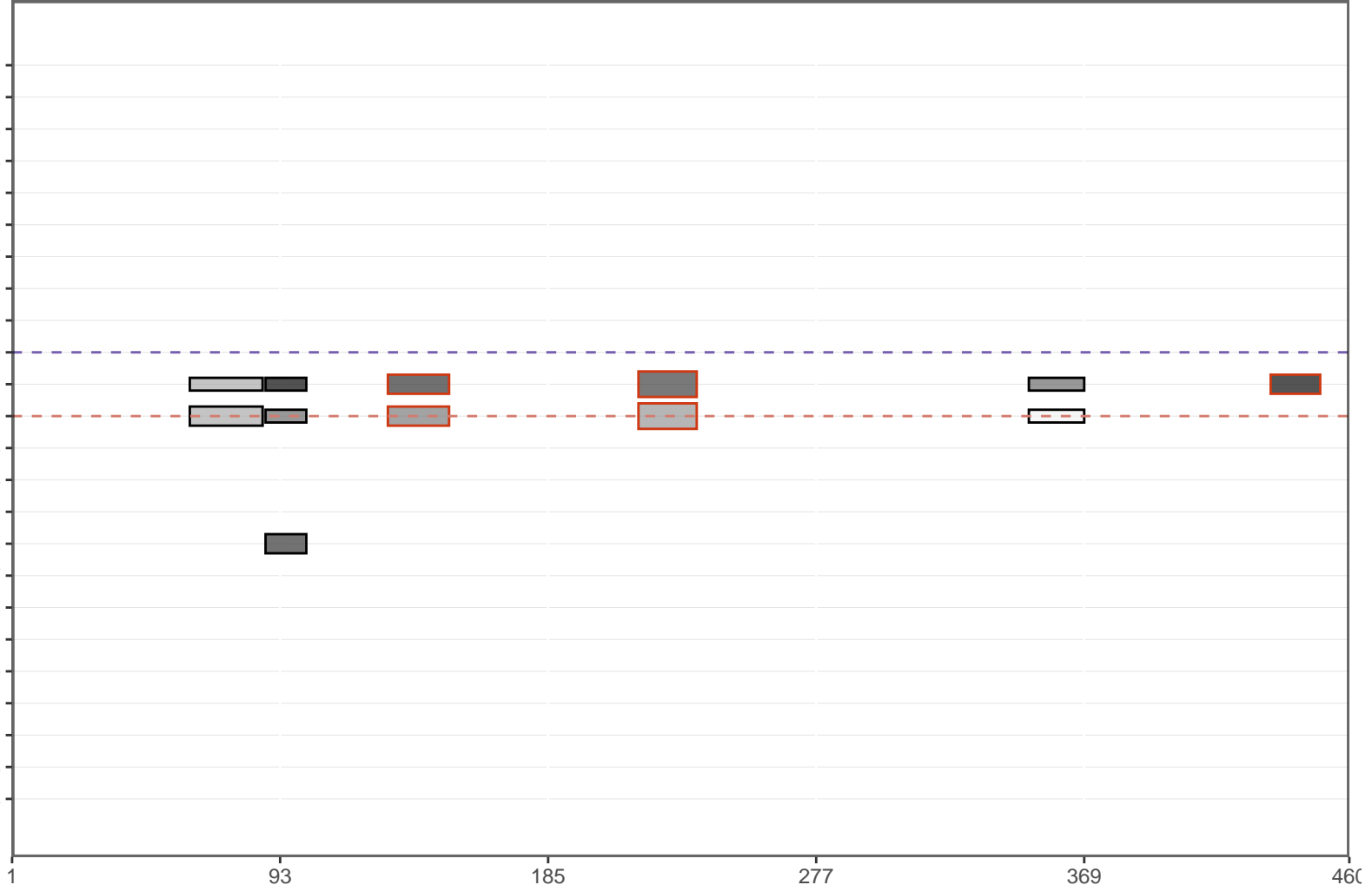
MW indication



Molecular weight

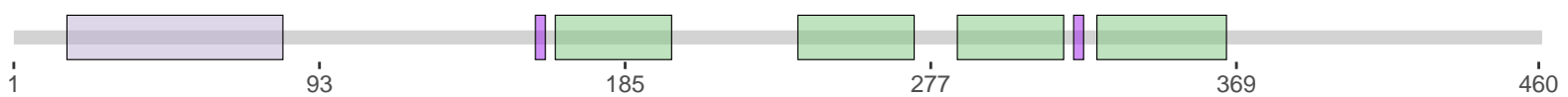


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SSGASNSRPSAEISPTVGARGFGQDDTVEVDFGCPSSADEFQSGVDDSGLLHWDEKRTGSSPAWVVEKAHNAADLHGVQWVNHQVNVILTGSADNTRMFRNLTSGGVGSPHFEGHTAVLVGVQWSPDKSSVFGSSAEDGLNVDHKEKGMEDSAGRKAHSTPPGLFFRHAGHRDKVVDHVAADPWTIVGVSDGSGSTGGGGTGLQWRMDLVRPEDEVLELEKFKSHLTTGS

NbL03g23770.1 eukaryotic_initiation_factor_4A-10-like [MW = 60.8 kDa]

No. of times detected



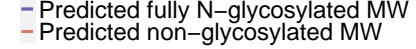
log(intensity)



Values from



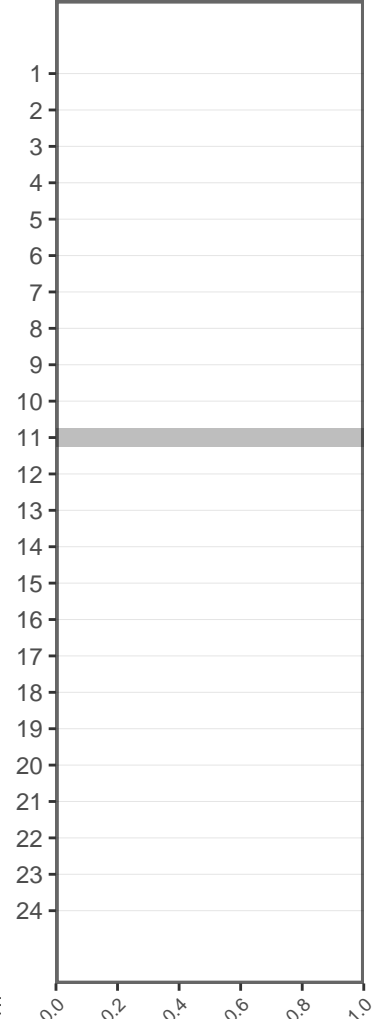
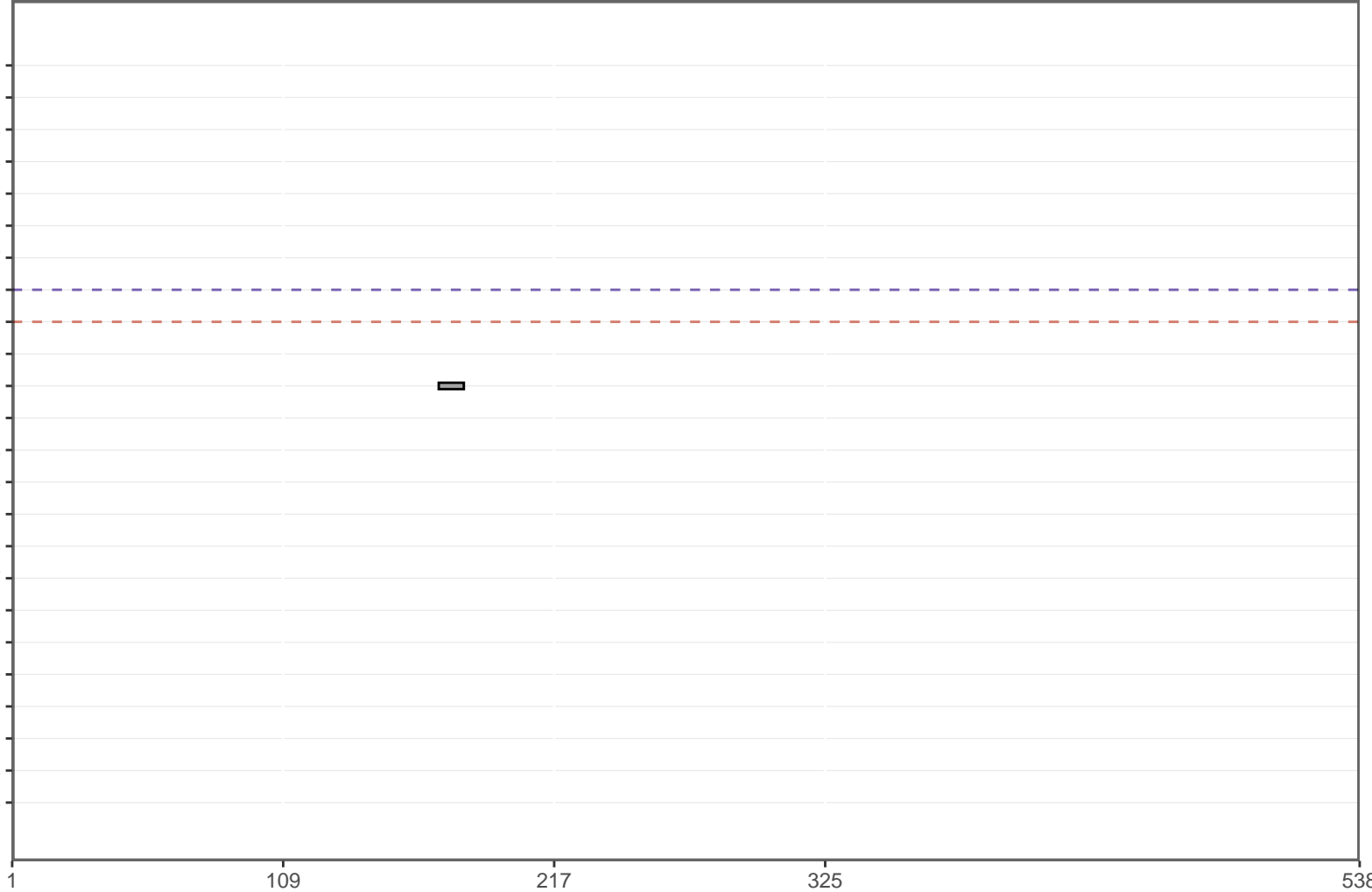
MW indication



Molecular weight



Gel Slice

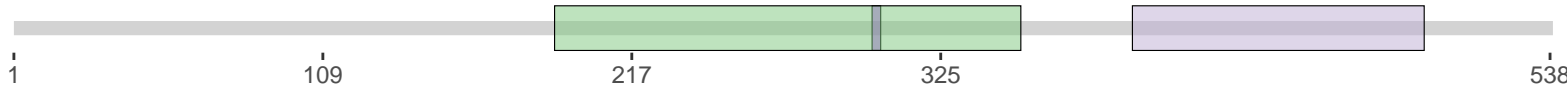


Peptide counts over 4 repeats

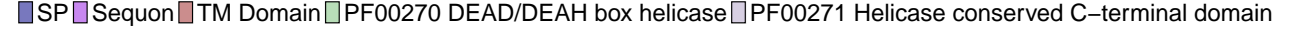
Protein length



Pfam domains



Pfam Description



Protein sequence:

LGDP...LVKFCVGNIGEDKHLGAGVHLYVGTGPGVFDMLGRKNGSLLLDHIRMFLDEADEMLSRGFKDQYDILQLLPAKVVHVVYFATMPADALETFRKFMKPVKVLKFDLLELGKGFVNVVREERKLGAVDLYDRLLIAKSVIFVNSRLKVVNLTKMRBRGHTVSATHGKMDQKARDKIMHEFGSGSSSILITDLGARVIDVQGVGVINVDLPTOLENHLRRIGSGEFESKGVAINFVTADEEKMLEDGRFVNVVIDELPENVADEP-

NbL03g23740.1 PRA1_family_protein_F2-like [MW = 20.27 kDa]

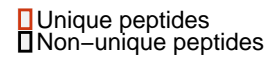
No. of times detected



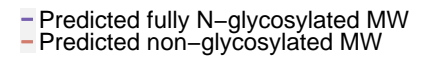
log(intensity)



Values from



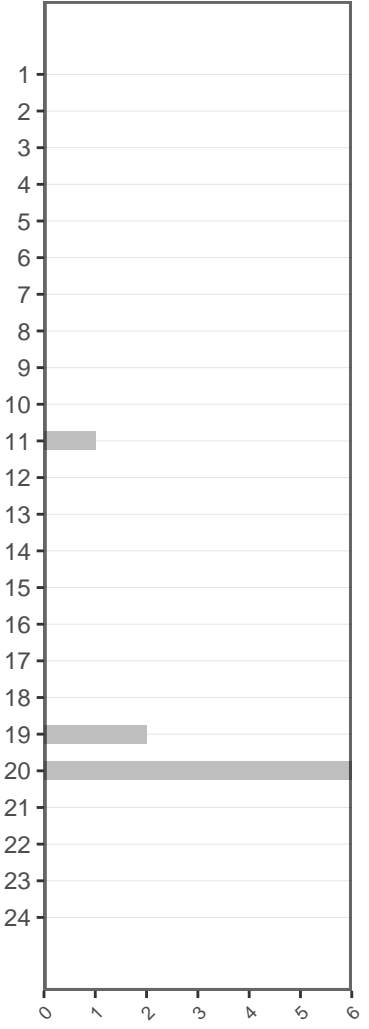
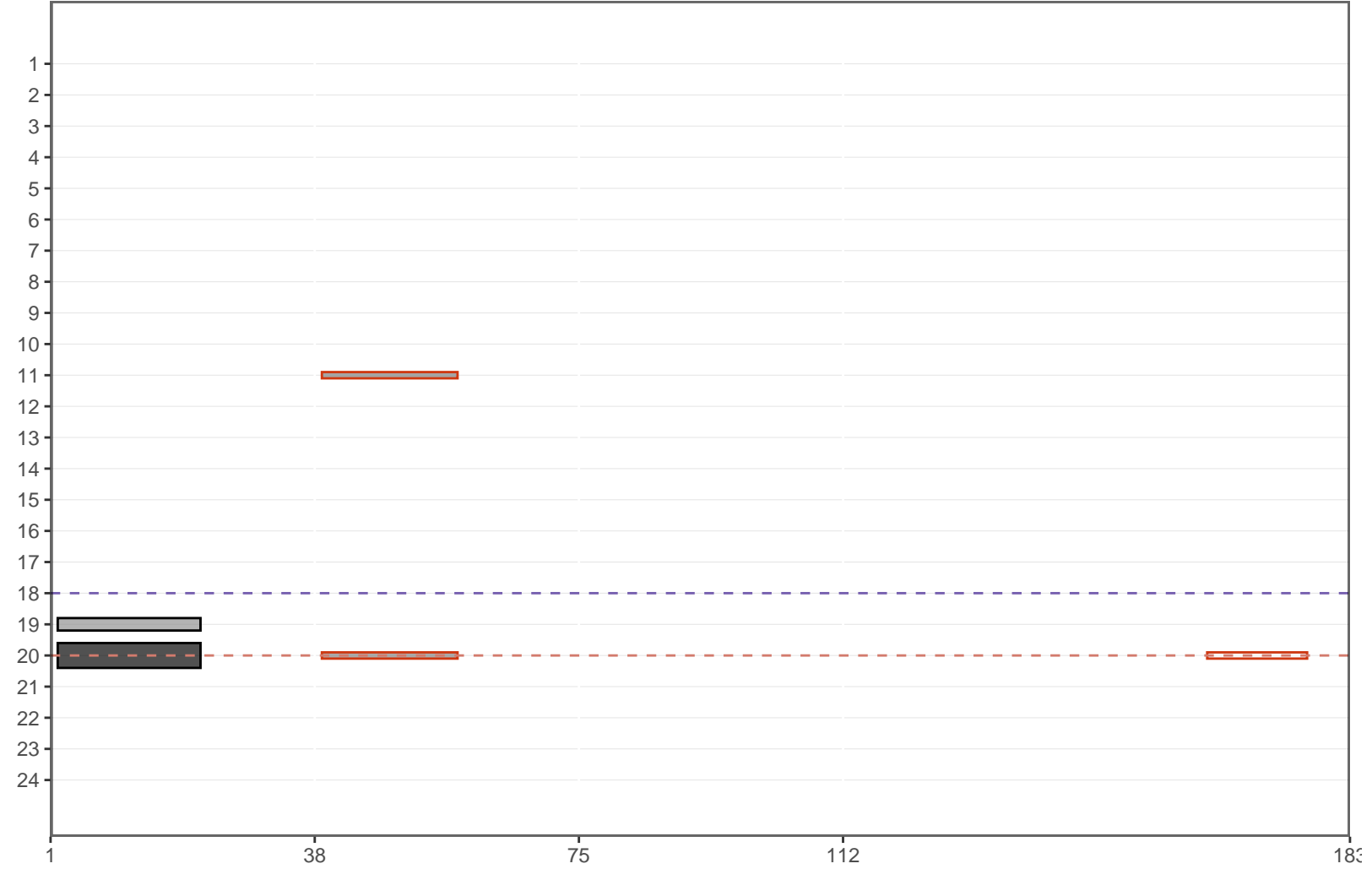
MW indication



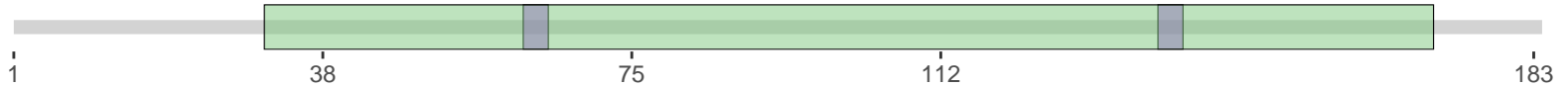
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

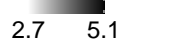
LGIIVFLSLWHPISLIVFLVLMAMWFLVFLRDEPLVFGRLRISDHVVLVLSVFTGILLTNTATSNILSLAWWFVVLHARIRKTDOLFMDDEAAAGFLRAPPSSV

NbL03g23530.1 IAA-amino_acid_hydrolase_ILR1-like_4 [MW - SP = 45.63 kDa]

No. of times detected



log(intensity)



Values from



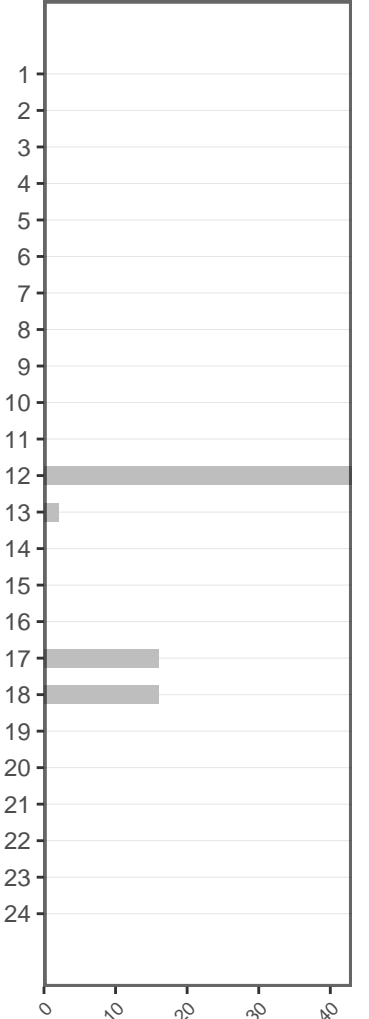
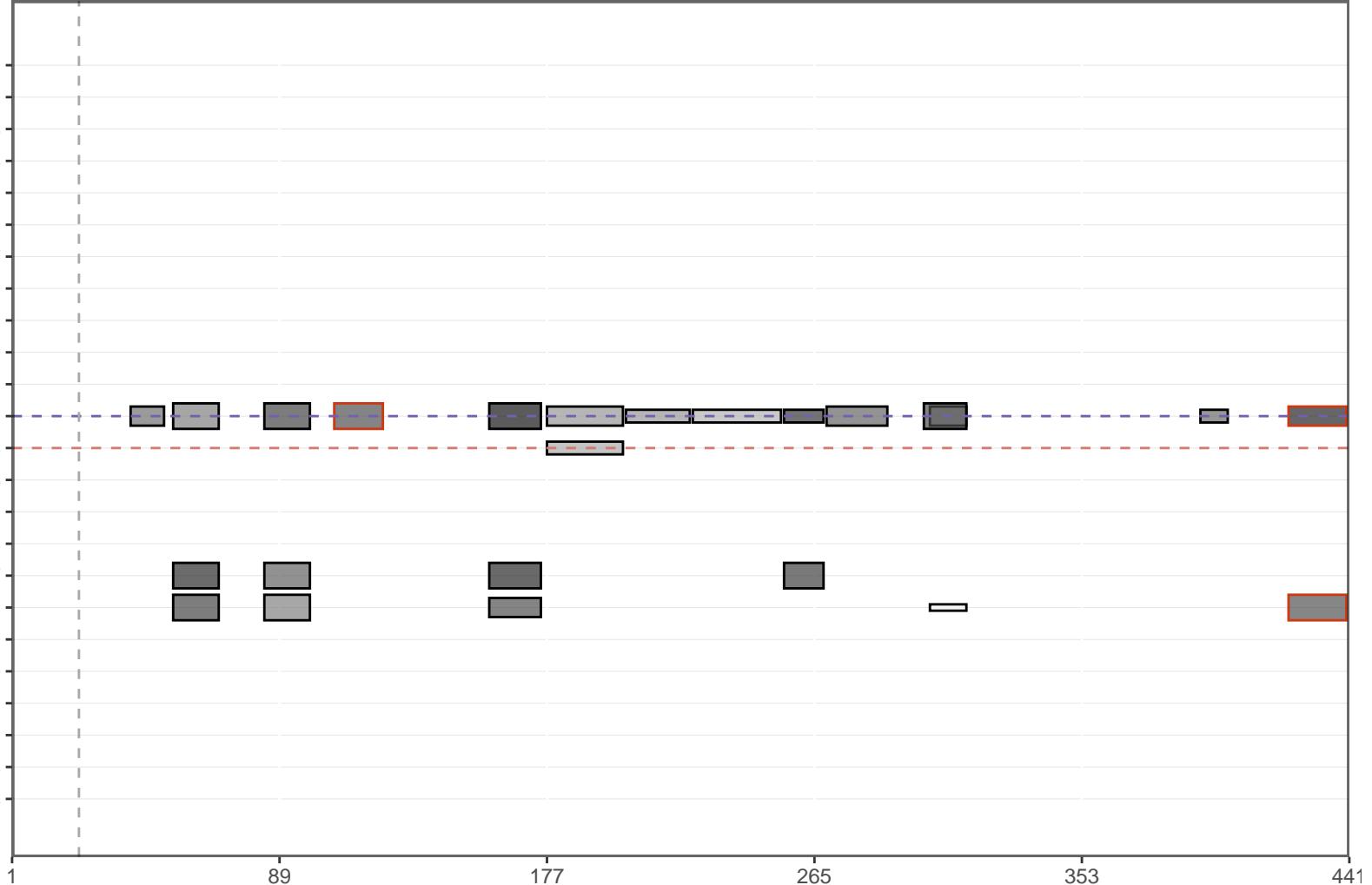
MW indication



Molecular weight

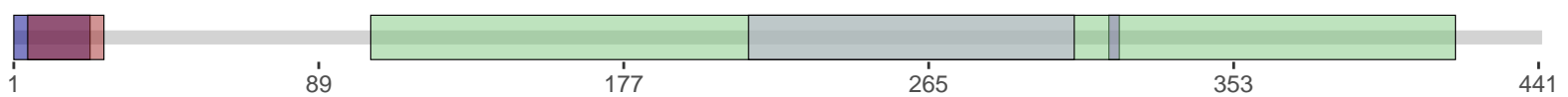


Gel Slice



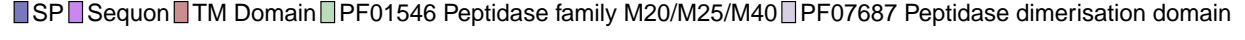
Protein length

Peptide counts over 4 repeats



Pfam domains

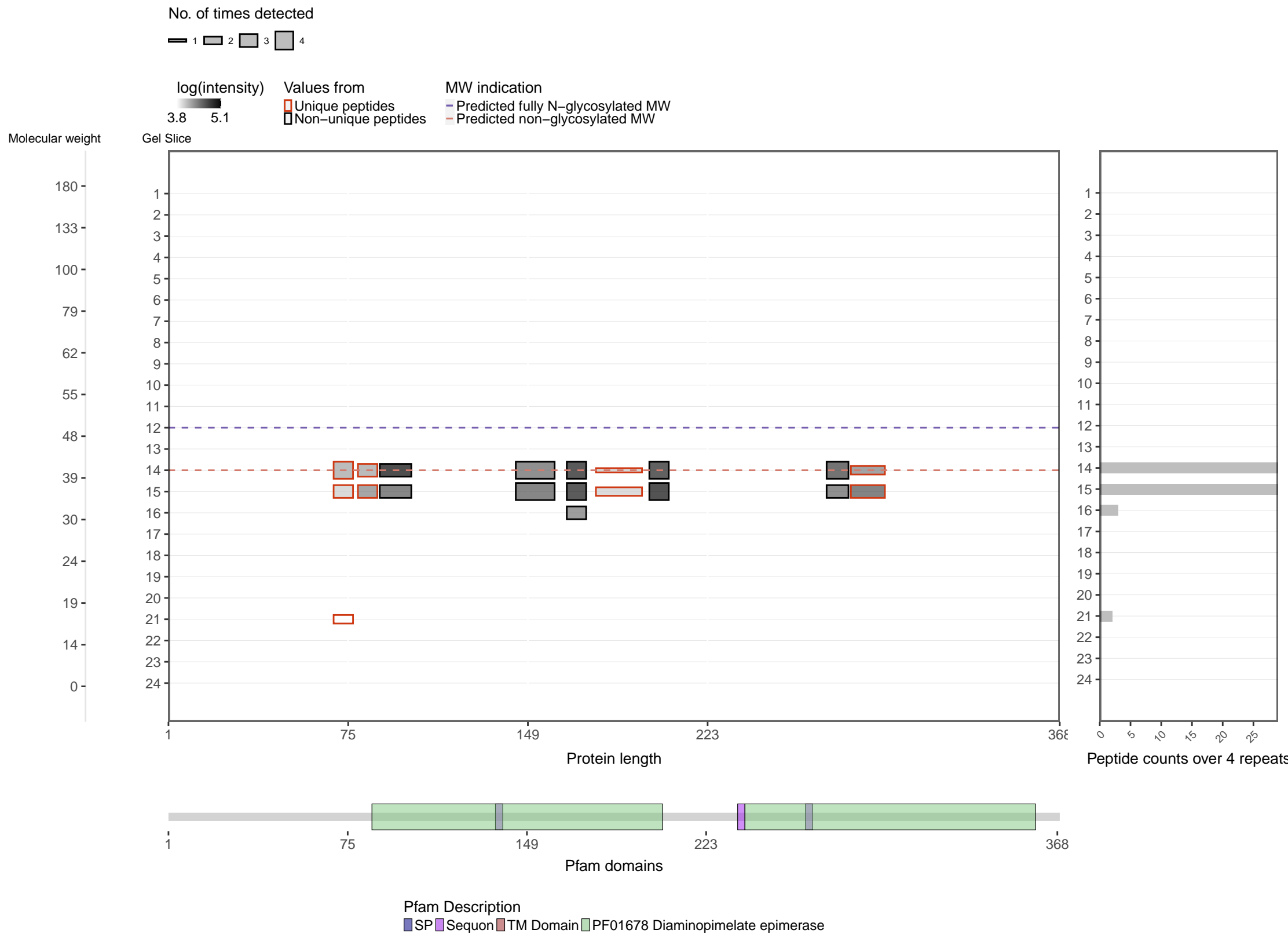
Pfam Description



Protein sequence:

PFLGSGFFEAVISGKGGHAIPQHSIDPLAAASNVVSLQHLVREADPLD6GVVTVAKFGGGAFNVIPDSVTGGTFRAFSEKSFQGLRORIEVIVGQAAVGRGNATVDFLTKKFFPPFTVNDKLNKHFQRFVAGDMLGNDHVKDMEPLMGSEDFAFYQEVIPGVYFLLGMQDETNEKLVVHSPYFKINEALPGALGASLARLYLEAGSGVPSISDHHDEL

NbL03g23450.1 diaminopimelate_epimerase_chloroplastic [MW = 39.69 kDa]



Protein sequence:

SKRSFTHTGAGLVPEIGEDGKVRVDMGEPLKASDVPTKLPFNKDGSAVWAKRLVDGSAWNVTCVSMGNPHCVTFCTSGGGDLGVDELNLSDGPKFHHVMPFARTNTEFVQVFSPTLKMRRWERRGAGATLGGTGACAVVAWALEGRAARWCTVPLPGGPLDEWSEKDNHYMTGPAEIVFYGVPLV

NbL03g23220.1 protein_transport_protein_SEC13_homolog_B-like [MW = 19.23 kDa]

No. of times detected



log(intensity)



Values from



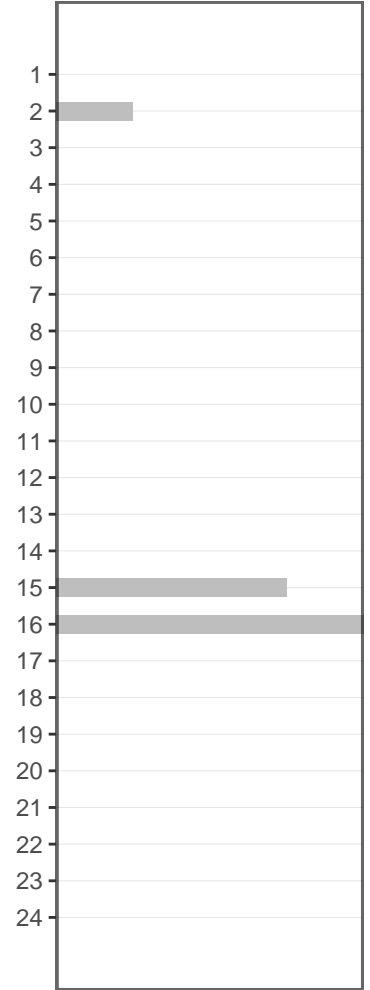
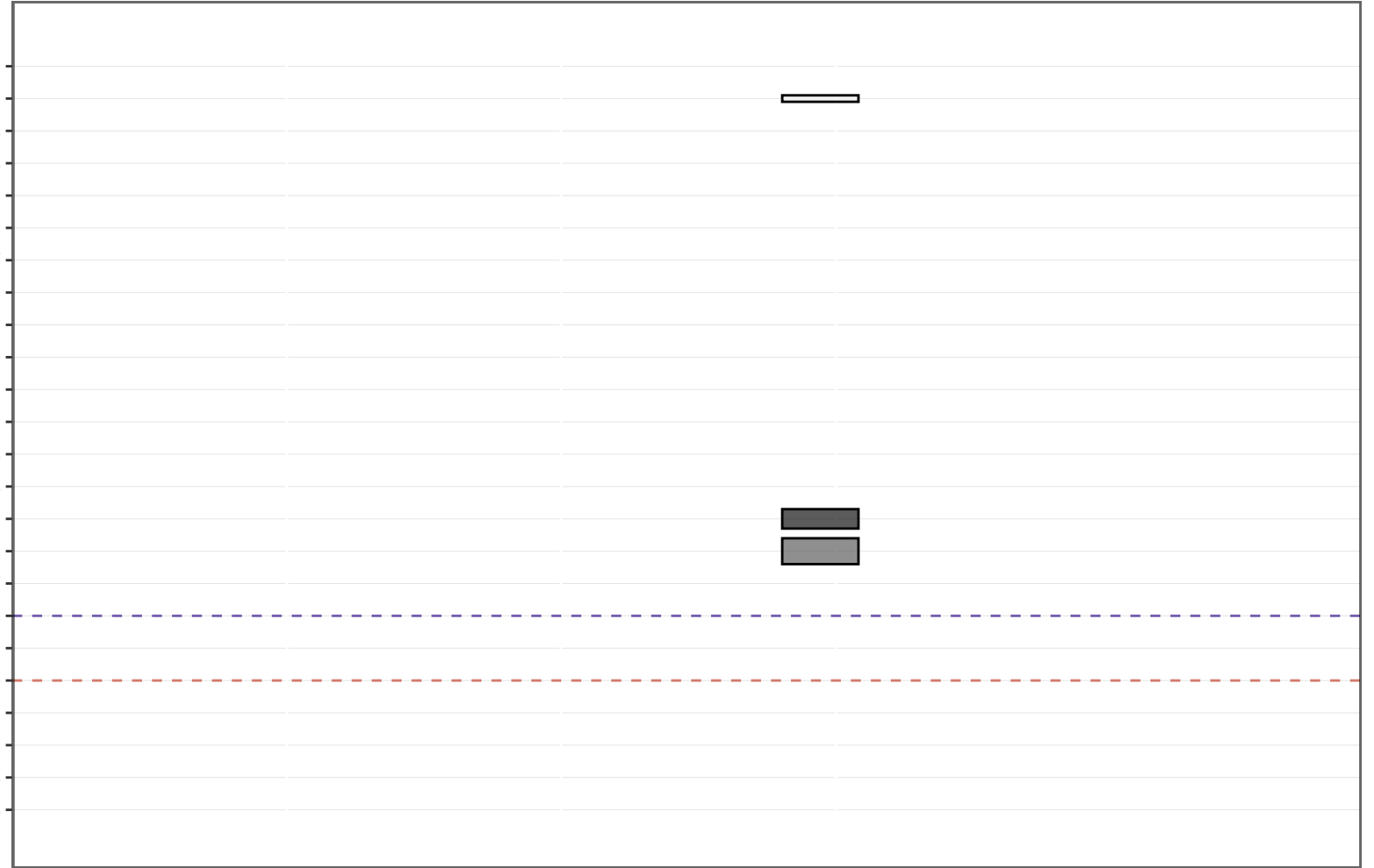
MW indication



Molecular weight



Gel Slice

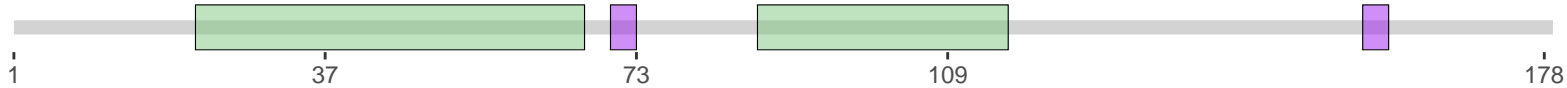


Protein length



Peptide counts over 4 repeats

Pfam domains



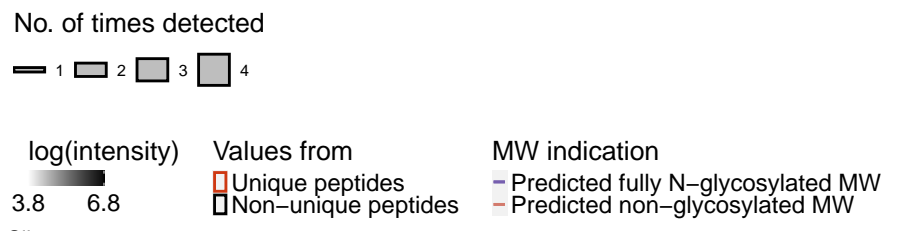
Pfam Description



Protein sequence:

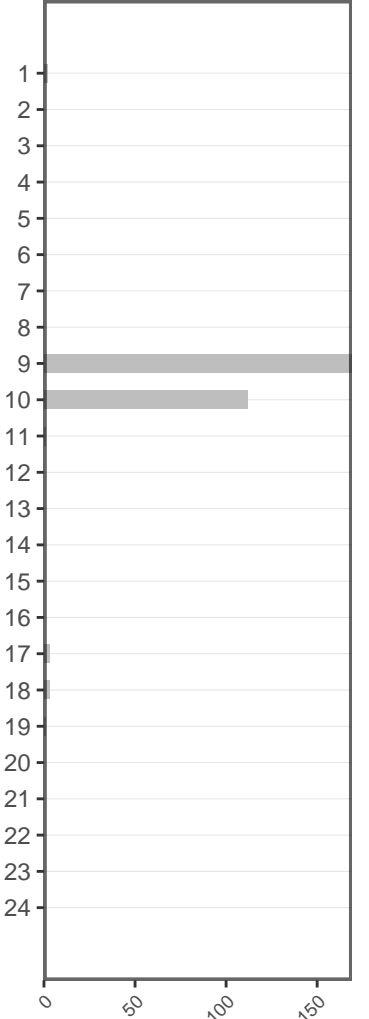
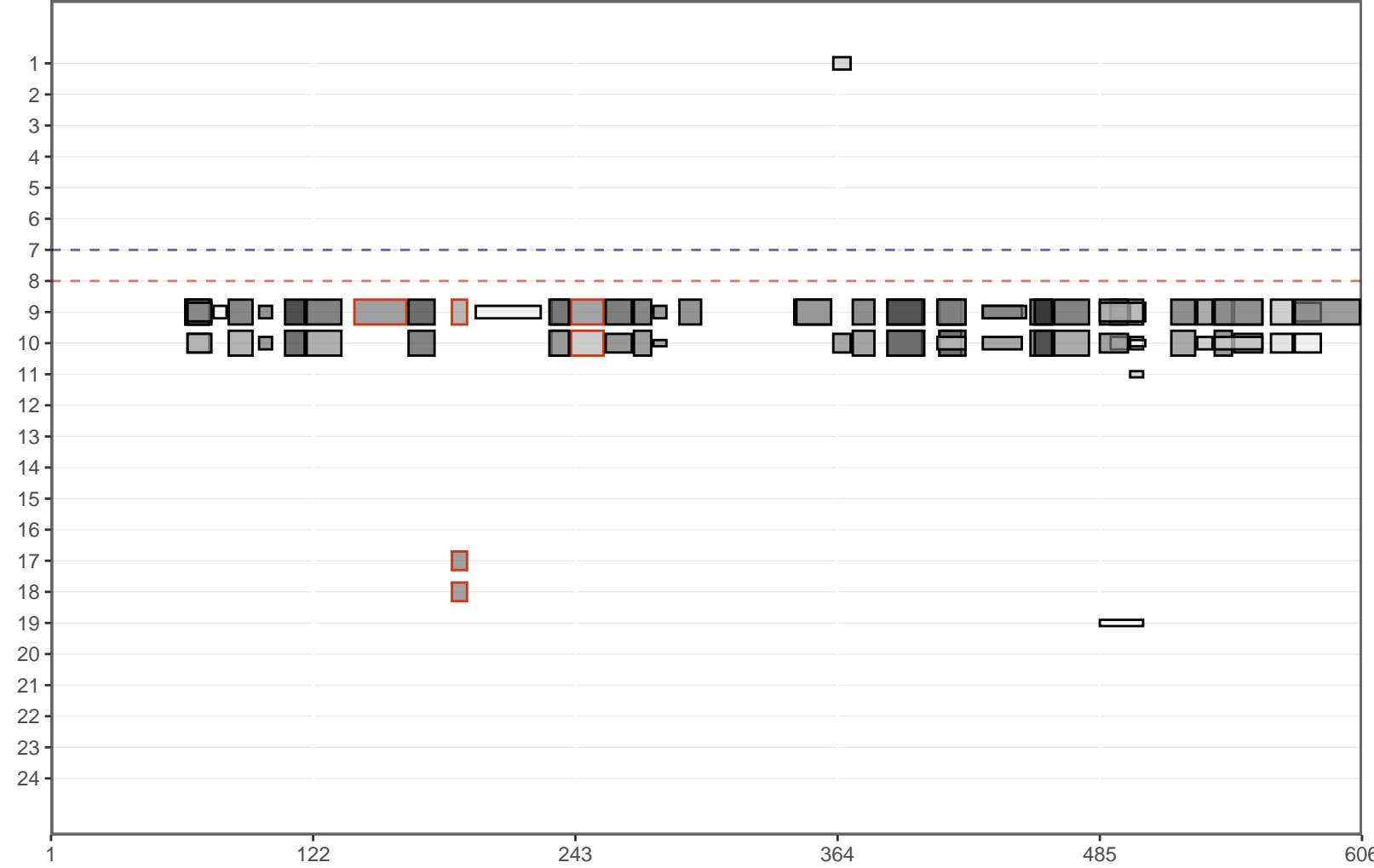
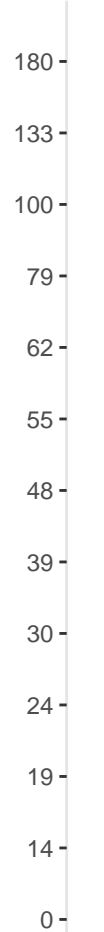
ICFPAIQMYYTDWVREDAWAPNLGLPKTTIABASEDGRVHWFTVAKEGDQWEGKVKDFGSPVWRVRSWBLTGNLAWADGNHNYTLWNEAVDGEWQPIVTVDA

NbL03g23160.1 ruBisCO_large_subunit-binding_protein_subunit_beta_chloroplastic-like [MW = 64.44 kDa]



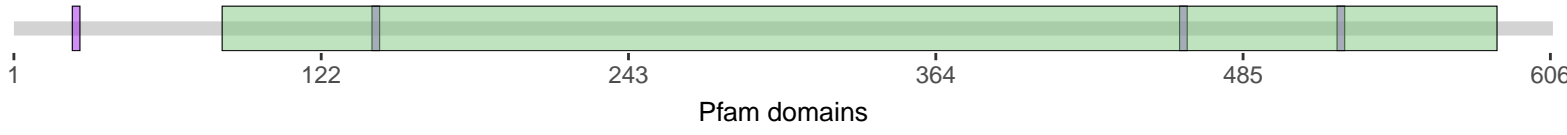
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam Description
 SP Sequon TM Domain PF00118 TCP-1/cpn60 chaperonin family

Protein sequence:

NARDLVNYLEAARGDYPILIAEDIEQELATLVWNLKRGALKIAALKAFQFGRKKSQYLDQALTGQTVVREEVSLKLDKDRAGSEVLGHAGKVLKSDFTTIVGDSGSGEAVNKRIQKRIVEAFEGDYEKELNERIAKLGSGVAVVGVGAGTETELKELKRVEDALNATKAAVEEGAVVGGGTLRLAAKVEDIKGTLDDDEQKIGADIVKRALRYPMKLIANNAGVNSGVVIEKVLSDNPKYGYNAATGKYEDLMAAGIDPTKAVRQGLEHAASVARTLTSDAVVTENKE

NbL03g23070.1 uncharacterized_LOC109224015 [MW = 17.81 kDa]

No. of times detected



log(intensity)



Values from



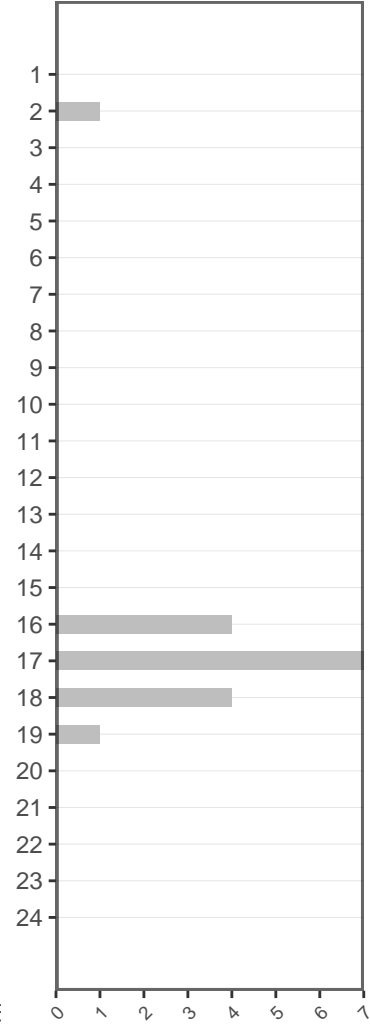
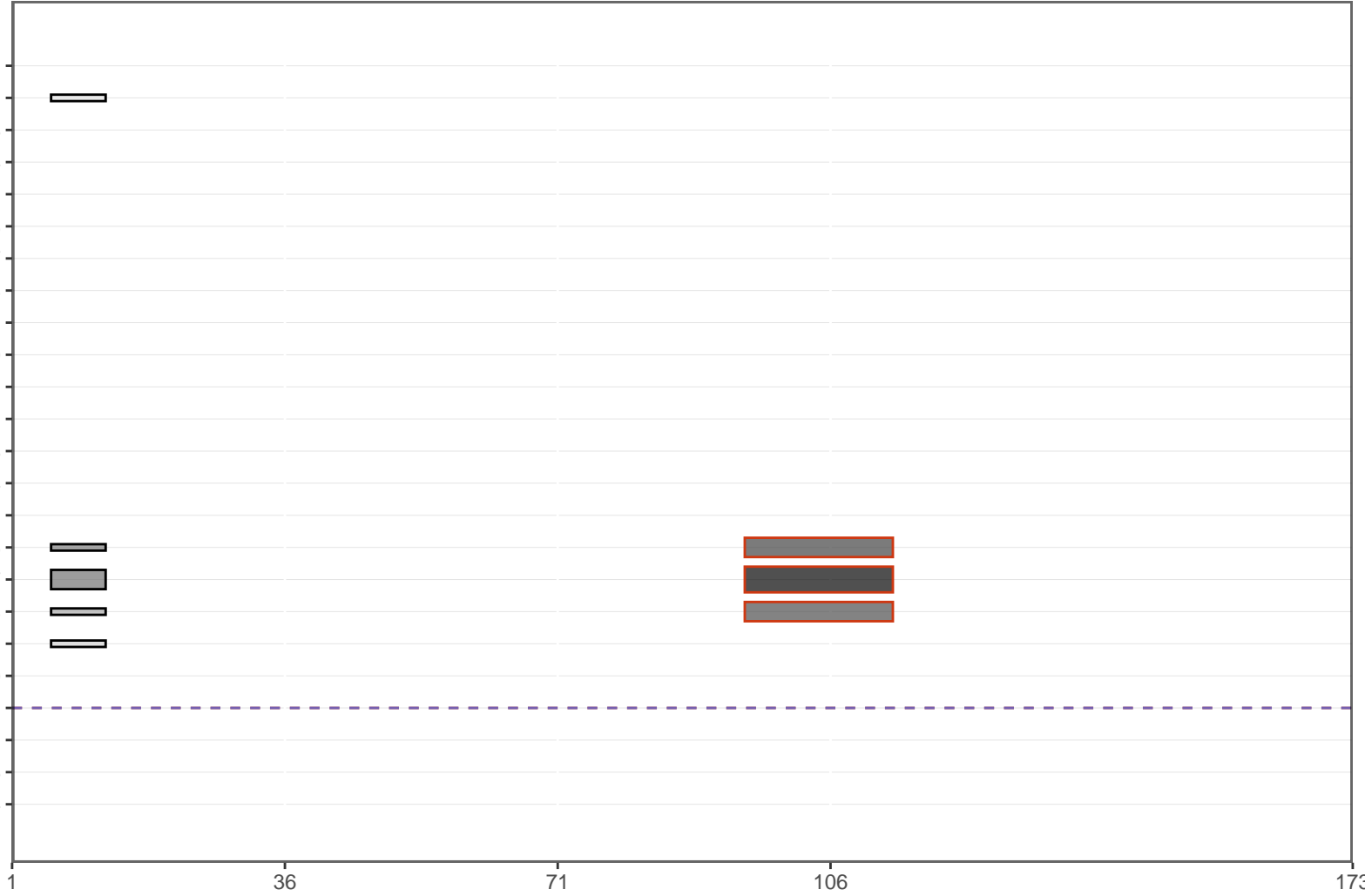
MW indication



Molecular weight



Gel Slice



Protein length

Pfam domains

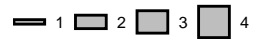
Pfam Description
 SP Sequon TM Domain

Protein sequence:

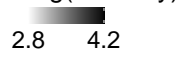
LLVGIAVAEENLGGKTEKSGSGVEVPEGTTTWWWVDGAEHNSGDIVGERSLPEGGESGVDSLGLGLEGGKGGKKEVKEEGEGSGKPTLVGEGVW

NbL03g23030.1 hydroxyphenylpyruvate_reductase-like [MW = 33.78 kDa]

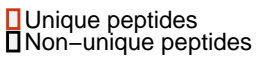
No. of times detected



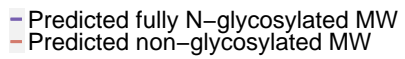
log(intensity)



Values from

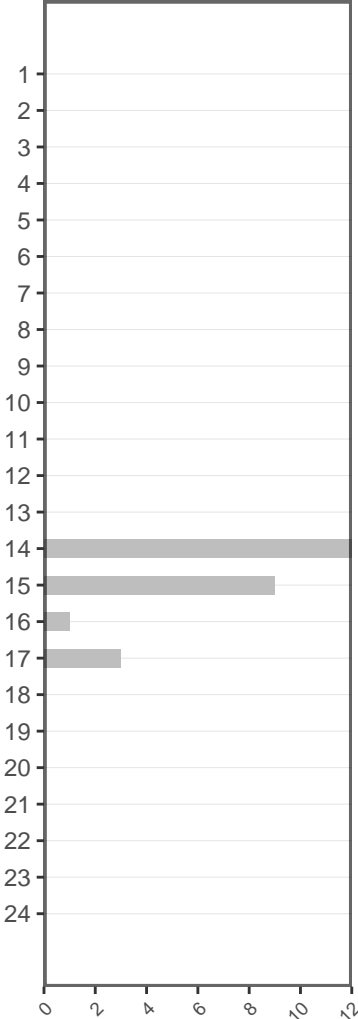
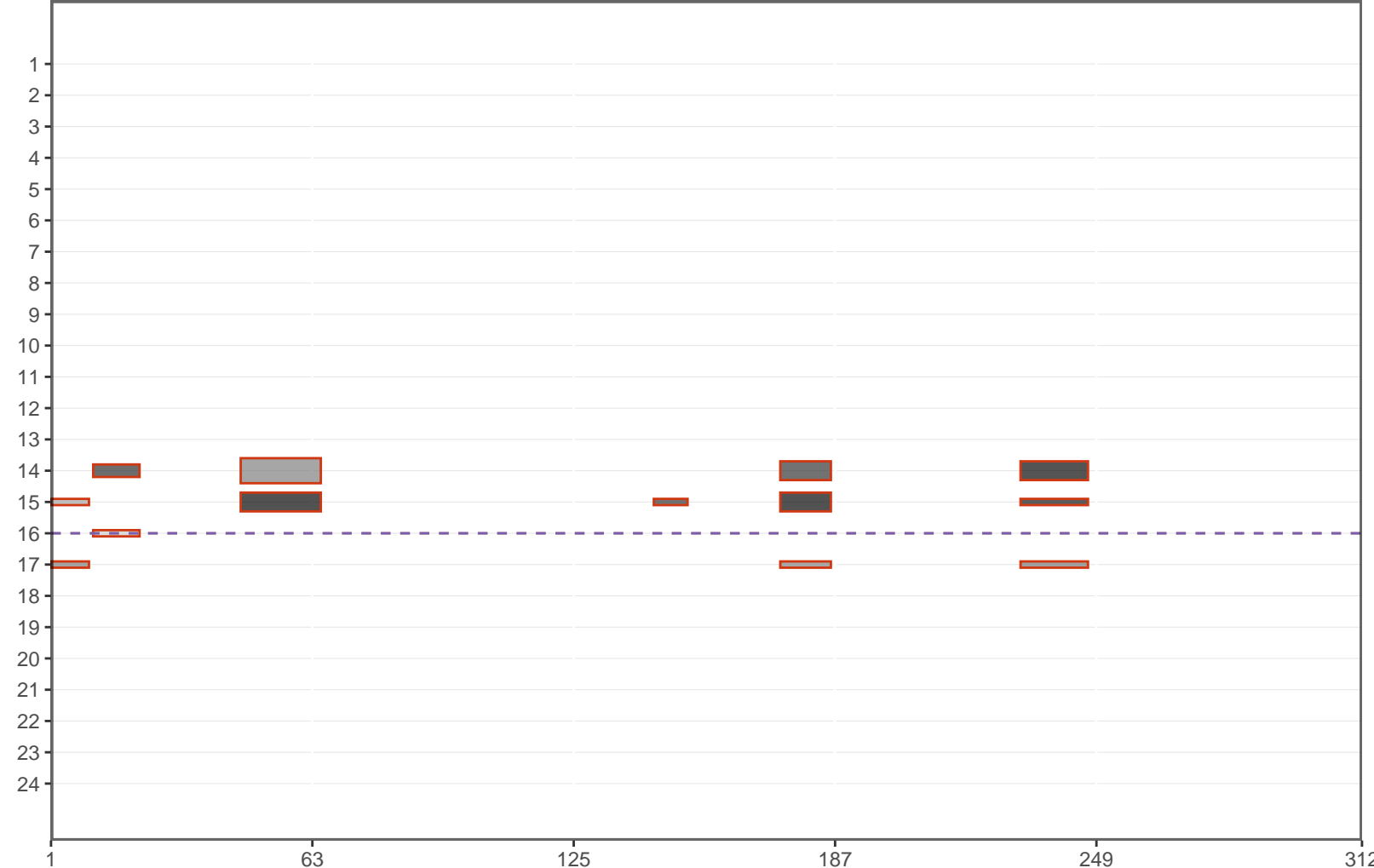
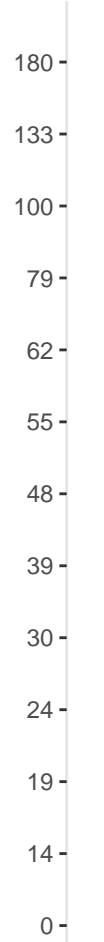


MW indication



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF00389 D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain
- PF02826 D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain

Protein sequence:

SKSGIVGLGRIGSAAKRAEAFGGSSVHRSQKPESTYTYPRVIDIASNGQLVAGALDETHHINREVIALLGPNQVWVNRGSHIDSELSVAALAEGRLLGAGLDVLEYEAPVLLAGLQNVVLSFPHVAASTLETRKDMADLVANLEAHFHKPLTPV

NbL03g23020.1 hydroxyphenylpyruvate_reductase-like [MW = 34.16 kDa]

No. of times detected



log(intensity)



Values from



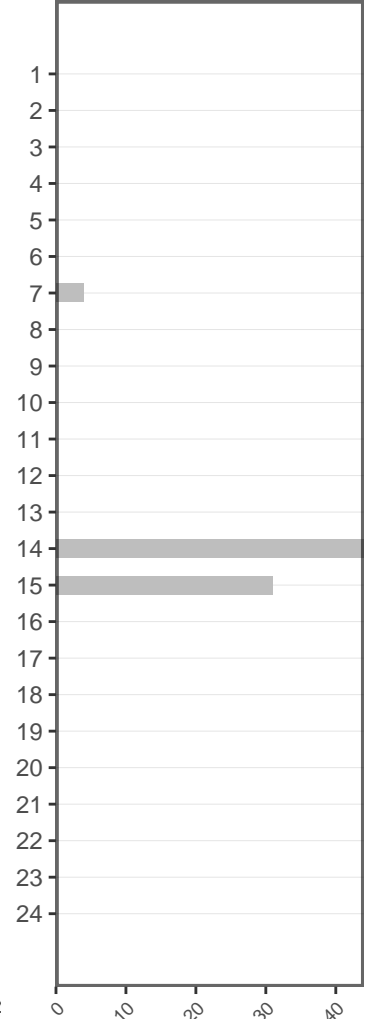
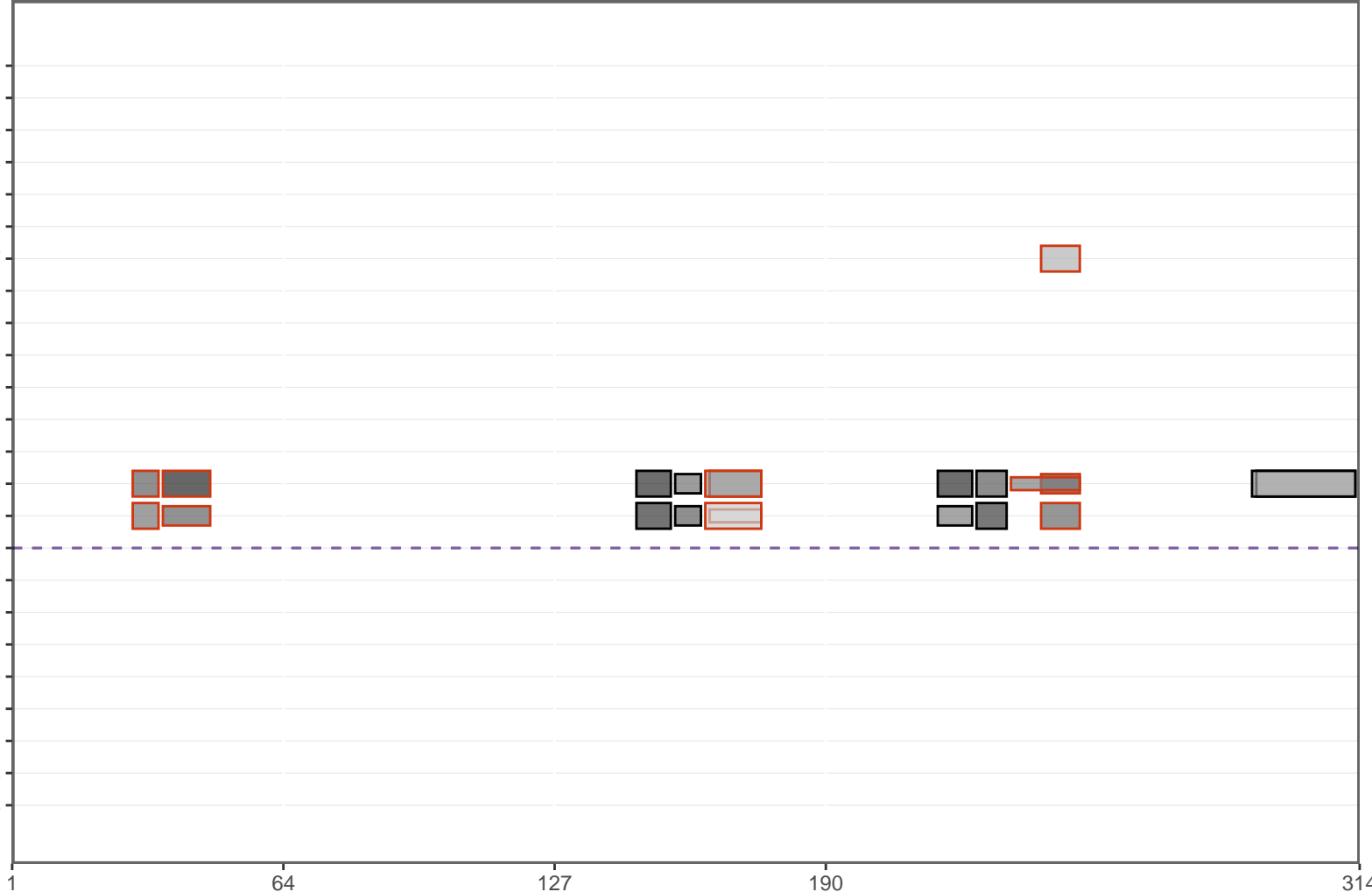
MW indication



Molecular weight

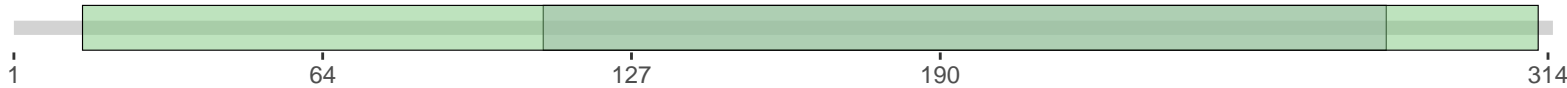


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF00389 D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain
- PF02826 D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain

Protein sequence:

GKSVGIQLGRLIAAKRAEAFGGPSVYHTRSEKPNTHYKYPPEVVELASNDGILVACALTPETRNINRVEIEALGSGVLIINGRPHVDEKELVSAVESRLGGAGLDVFNENEPEVPEGLFLENVLLPHVSGGTVETRKAMADLVLGNLEAHLNKLPTPVV

NbL03g23000.1 30S_ribosomal_protein_S17_chloroplastic [MW = 17.59 kDa]

No. of times detected



log(intensity)



Values from



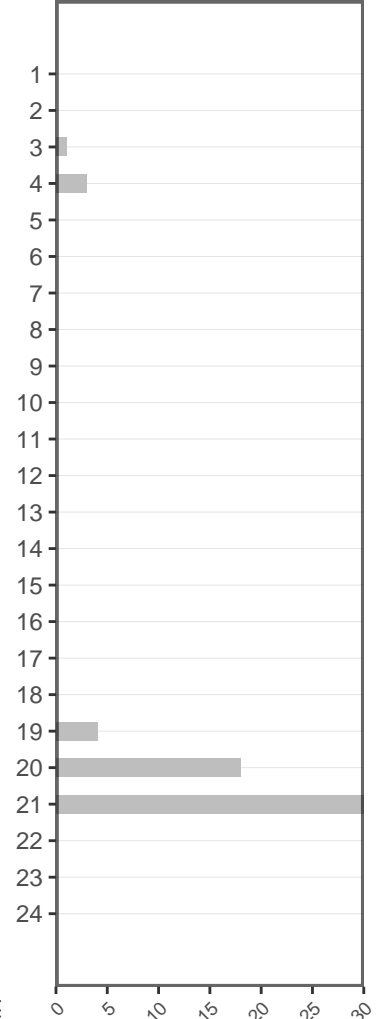
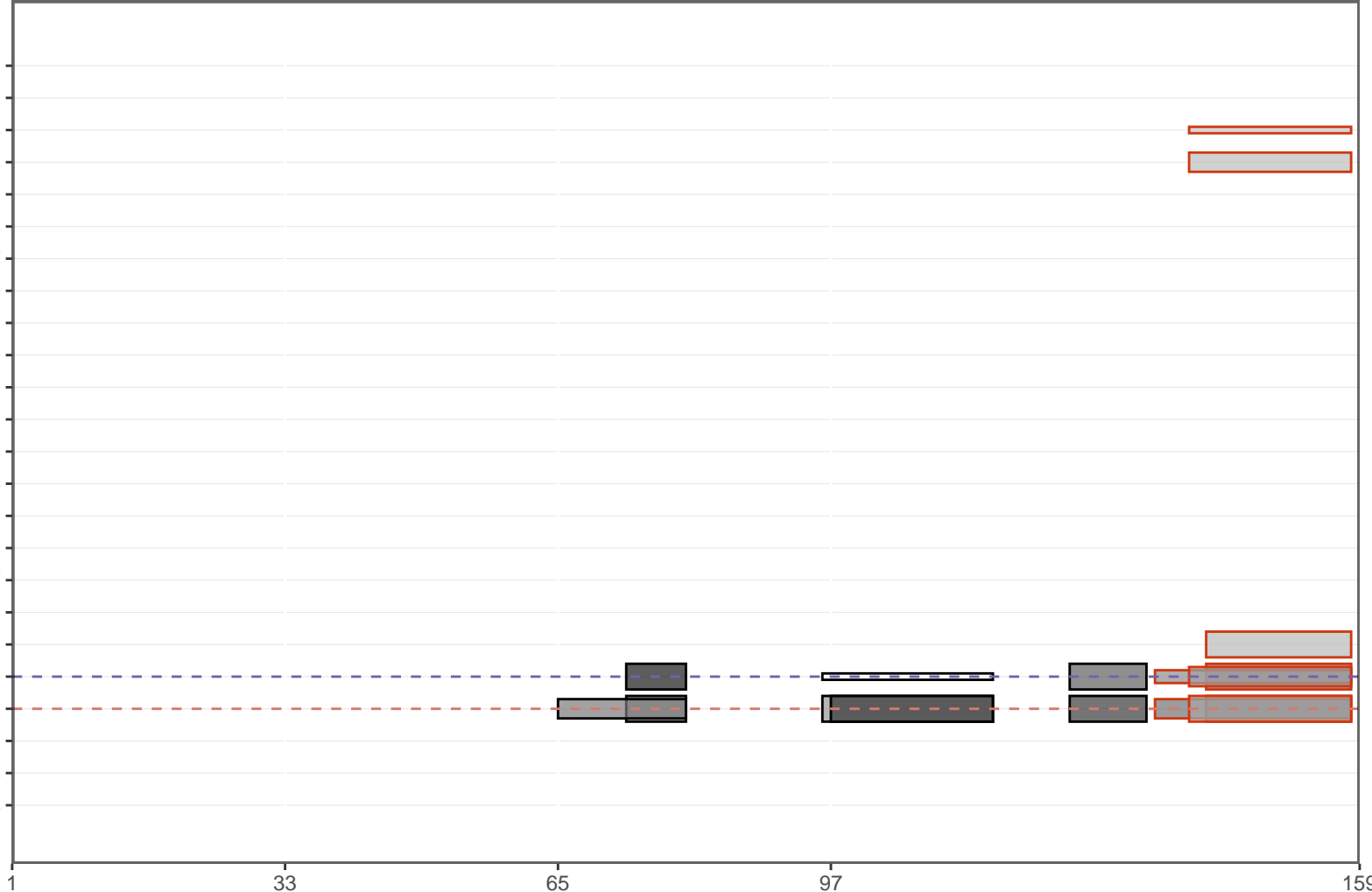
MW indication



Molecular weight

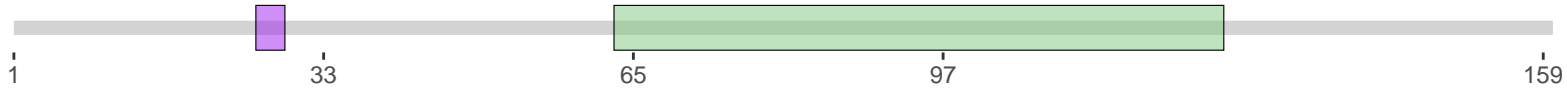


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

STNDKTVSEVETRLAHPKVKRRVRRKKKKYGAHDPLNGFQVGFVLEKTAPIKTKTKFLAVFVPRNGPKPKKEENGELVPLESSLGGP

NbL03g22950.1 malonate--CoA_ligase [MW = 67.3 kDa]

No. of times detected



log(intensity)



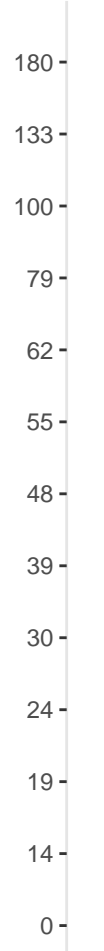
Values from



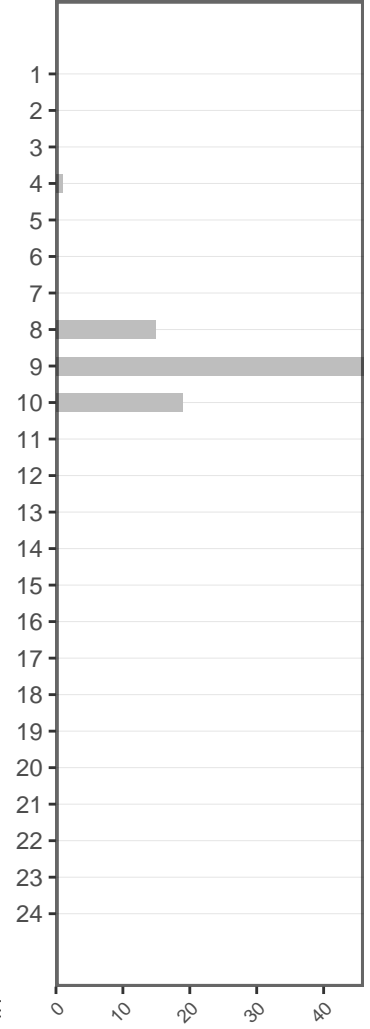
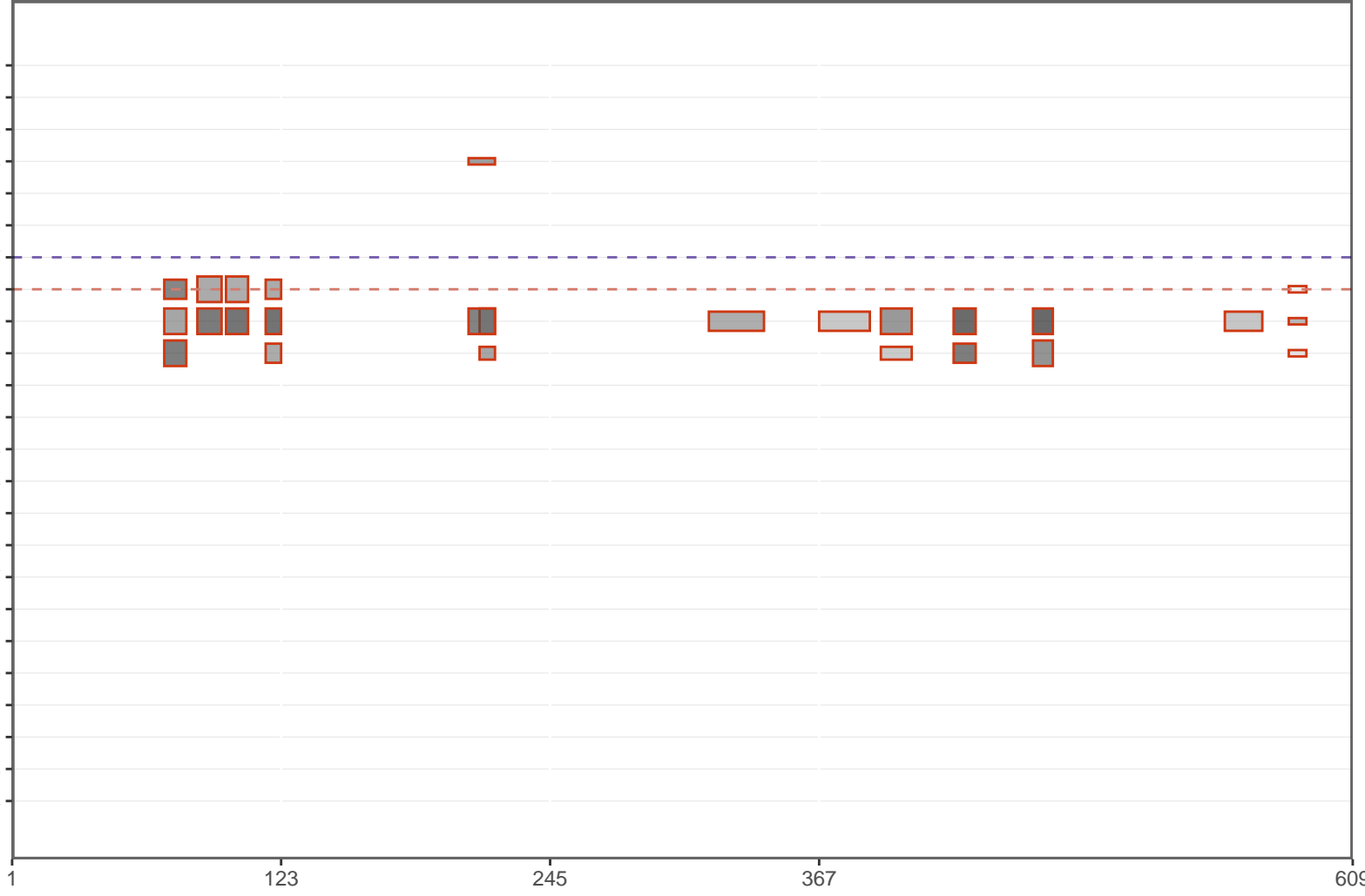
MW indication



Molecular weight

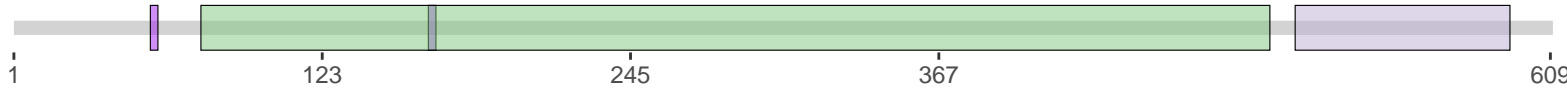


Gel Slice



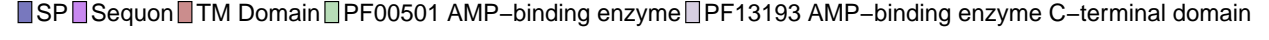
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AGSTYDFMPKFSVIRGWGKWRRESYPTDGTETDNATVFTGVPTMYTRLIGGYEAMDPELKAASASAAARHLRLMMCGSSALPLPVMQGWETITGHRILLERYMTEFVMAENPKGRKRGGTVGKPFSGVQAKILLDDEGGSDKTGVRELCKPPLFKNEYWRLESEVTKQGSFTDGGFFKTDGAVTVDEEDGYHILGRNADIMKVGNGYKLSALEIAVLEHPWSEGGVILGLPKDYGVEVCGAVIPDTELKRRRDEELKPLSLGELSDWAKERLAPKIPSRFLVWDSLPI

NbL03g22850.1 aspartate_aminotransferase [MW = 43.39 kDa]

No. of times detected



log(intensity)



Values from



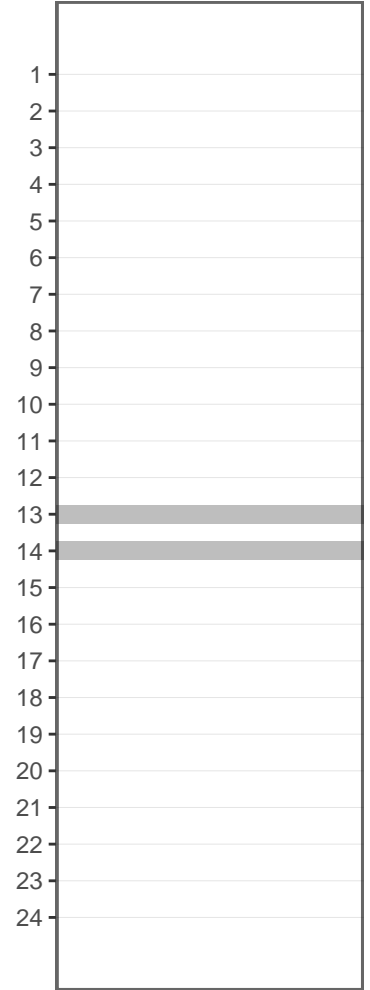
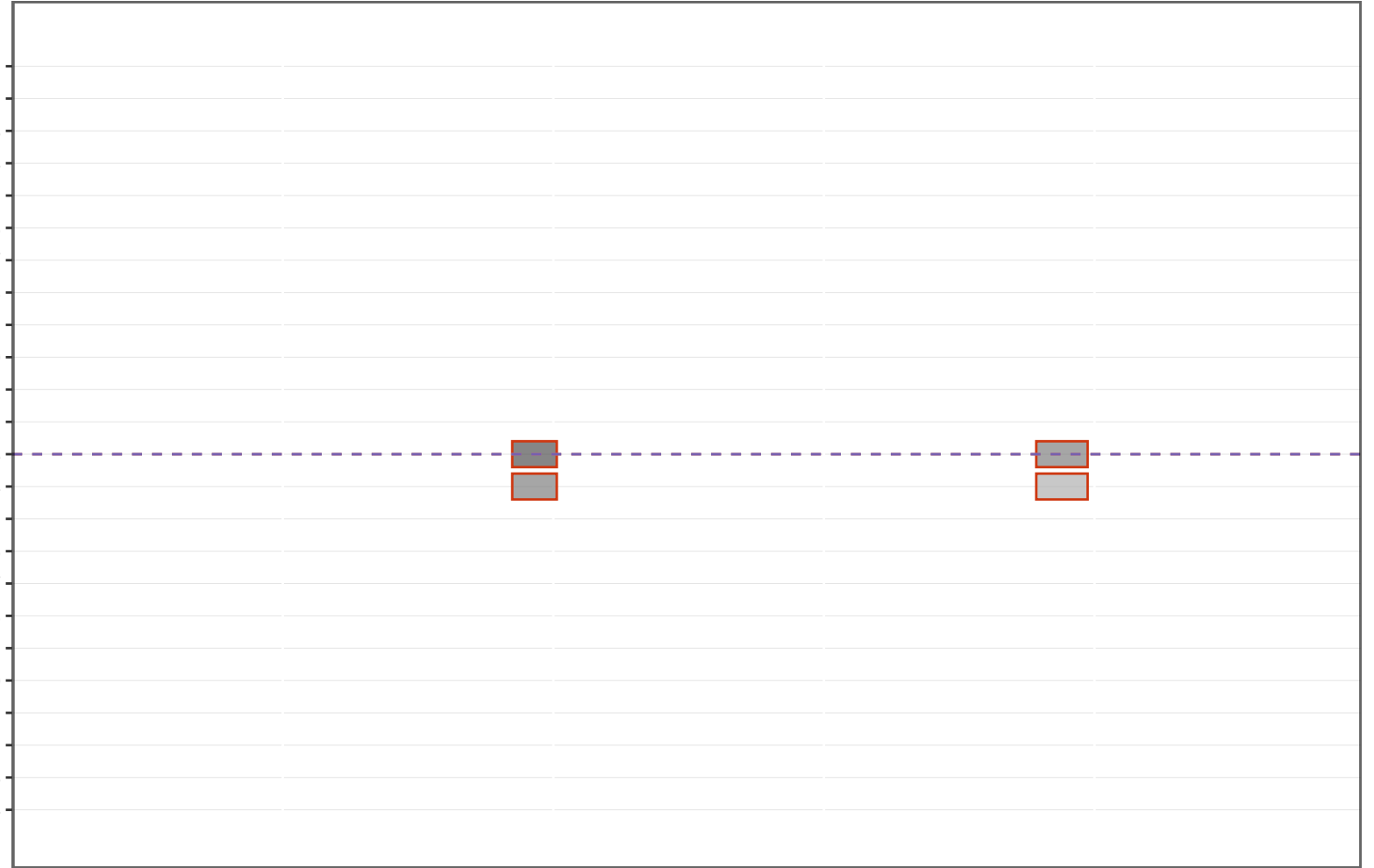
MW indication



Molecular weight



Gel Slice

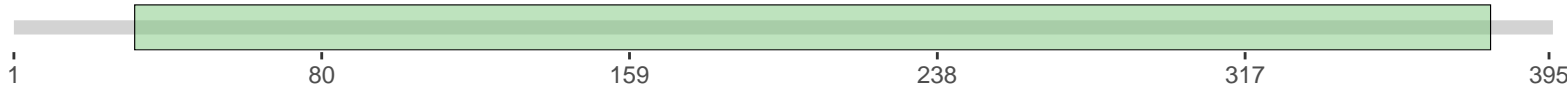


Protein length

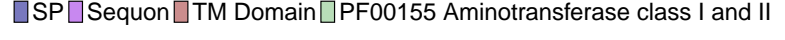
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

ESLLKRSIDICKEAGDWLVNDTYEYFMVDKRNKIVDIEGHNHVFISFKAYGMMGWVRVGVIAVPSVEVEGLAQLKVDNPNPGASISQRLALYSMEMPEVWTDQVNDLVNRELLLEALSPLGEEAVKGGEGGAIYVWAKLPKQYENDFEVVHVLAKRHGIVLPQSSGCGPQHVRIISFGLEKDCRVAERLRKGLLELVNSGMIS

NbL03g22830.1 D-glycerate_3-kinase_chloroplastic [MW = 51.1 kDa]

No. of times detected



log(intensity)



Values from



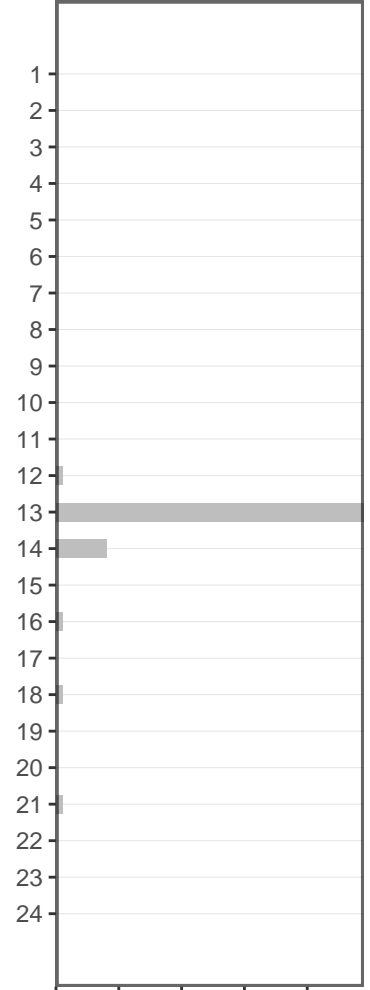
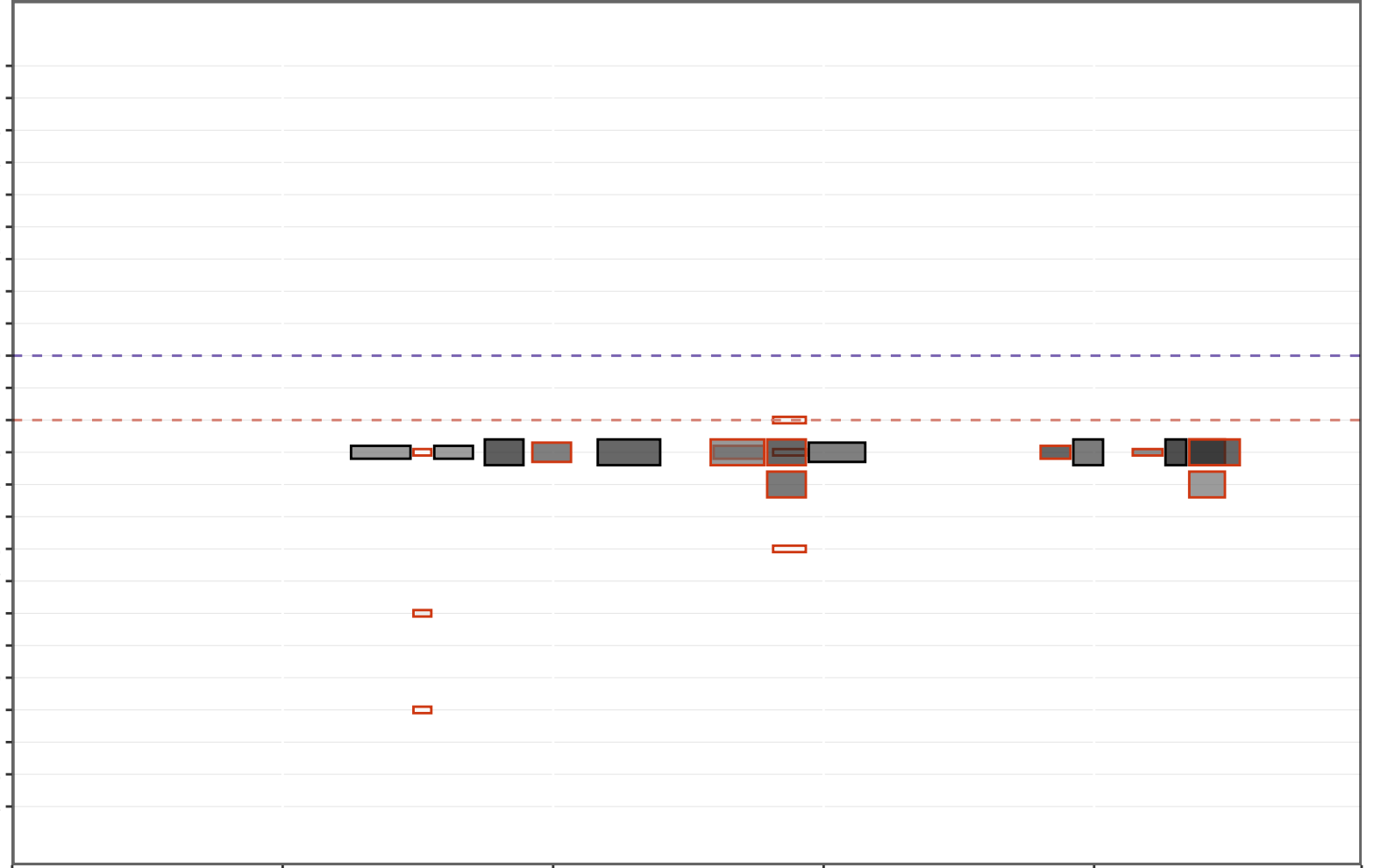
MW indication



Molecular weight



Gel Slice



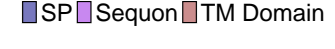
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

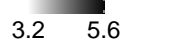
DGCGKTLVFALELYFKITGRKAATLSIDDFYLAEEGAKLRREDNPNDLLEFRGNAGSHLSVETLFTLSKVTKEGVKMLPRYDKSAVNGRGRDAPSTVPEVEGPLTVLFEQWMLGFKPLPPEVKKVVDPOLETNNKLEAYDAWYKVKSWIHKIGDPSVYQWRLGAEAMRADGNPQMGSDDEVRDVSRYLFWYKALPTLYSEGPTGADPEHLLIEIDGRNPLGS

NbL03g22820.1 protein_CDI-like [MW = 31.98 kDa]

No. of times detected



log(intensity)



Values from



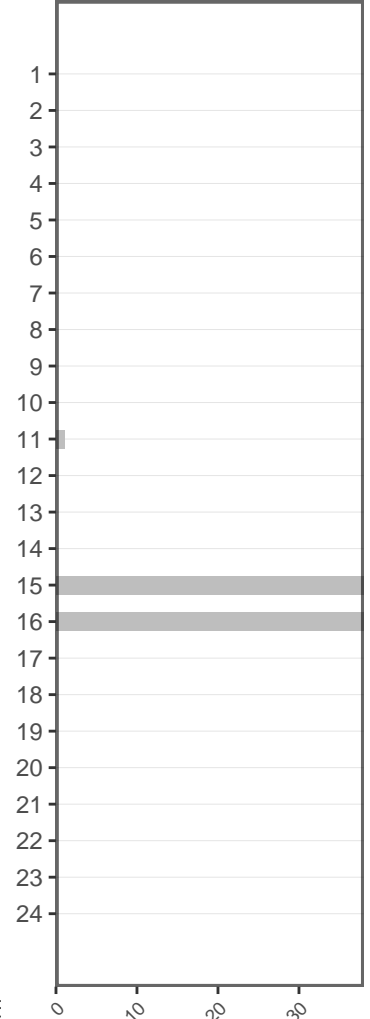
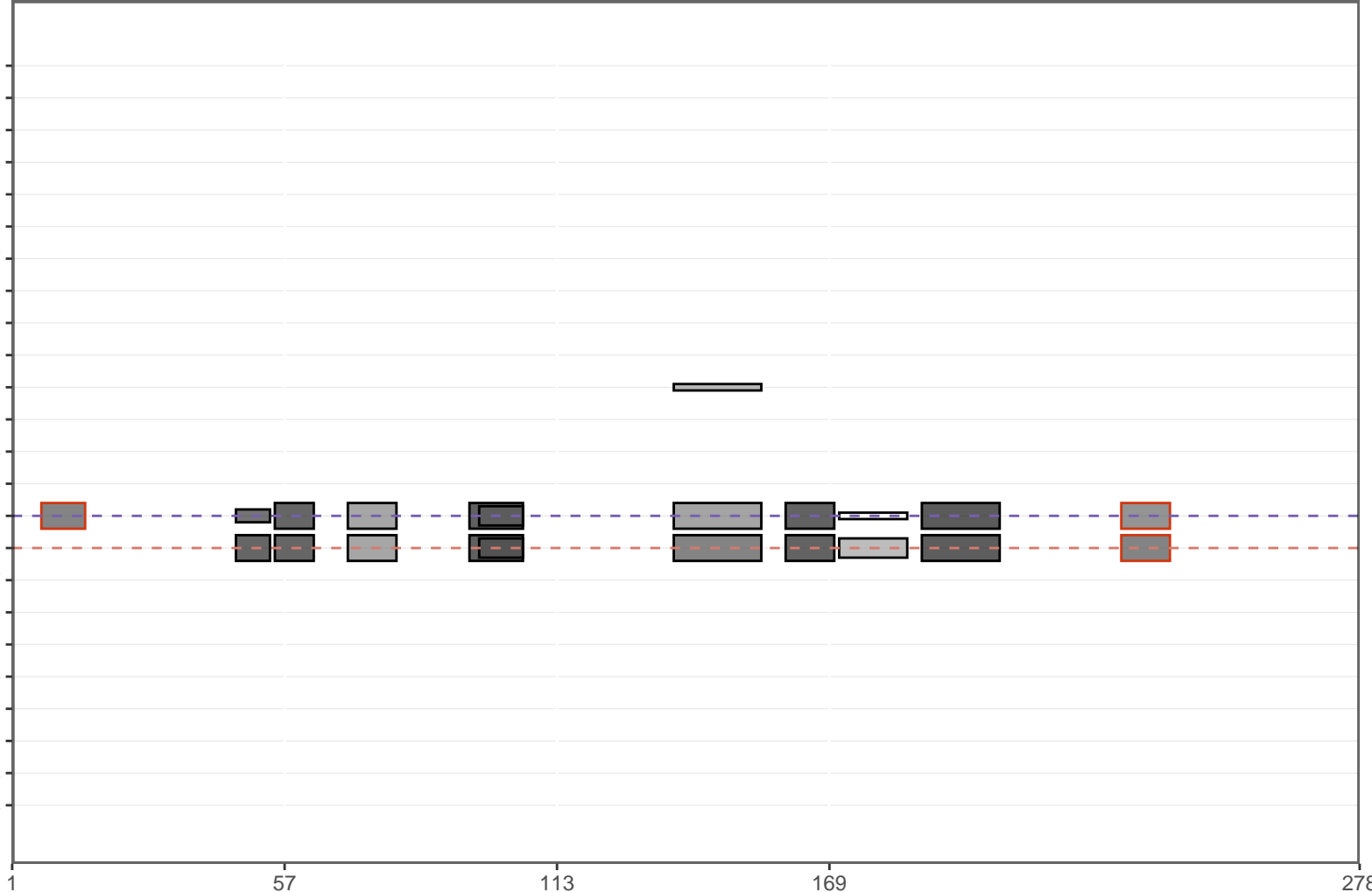
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

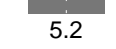
YLDDIKELRDLYDDKVALMCDVQHDYTRKETFKMDGAVQTVYPRKKNVSSMLVNDGHPKNRKALTPEVVNSSEGAFIHRFMALDEDEEGEVFVNFVLVGHNKVYKDDPTEPKAIHYTLGGPWFEAIWKDGEFGDLWLKELEGEKAKEKLG

NbL03g22790.1 uncharacterized_LOC109210747 [MW = 83.38 kDa]

No. of times detected



log(intensity)



Values from



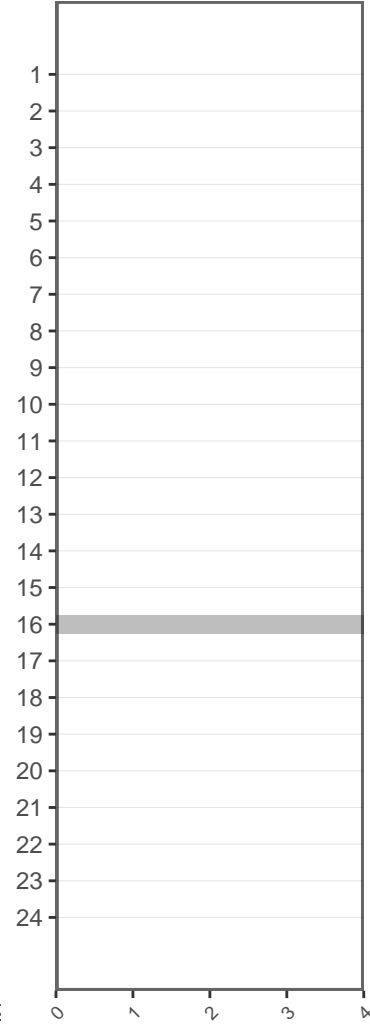
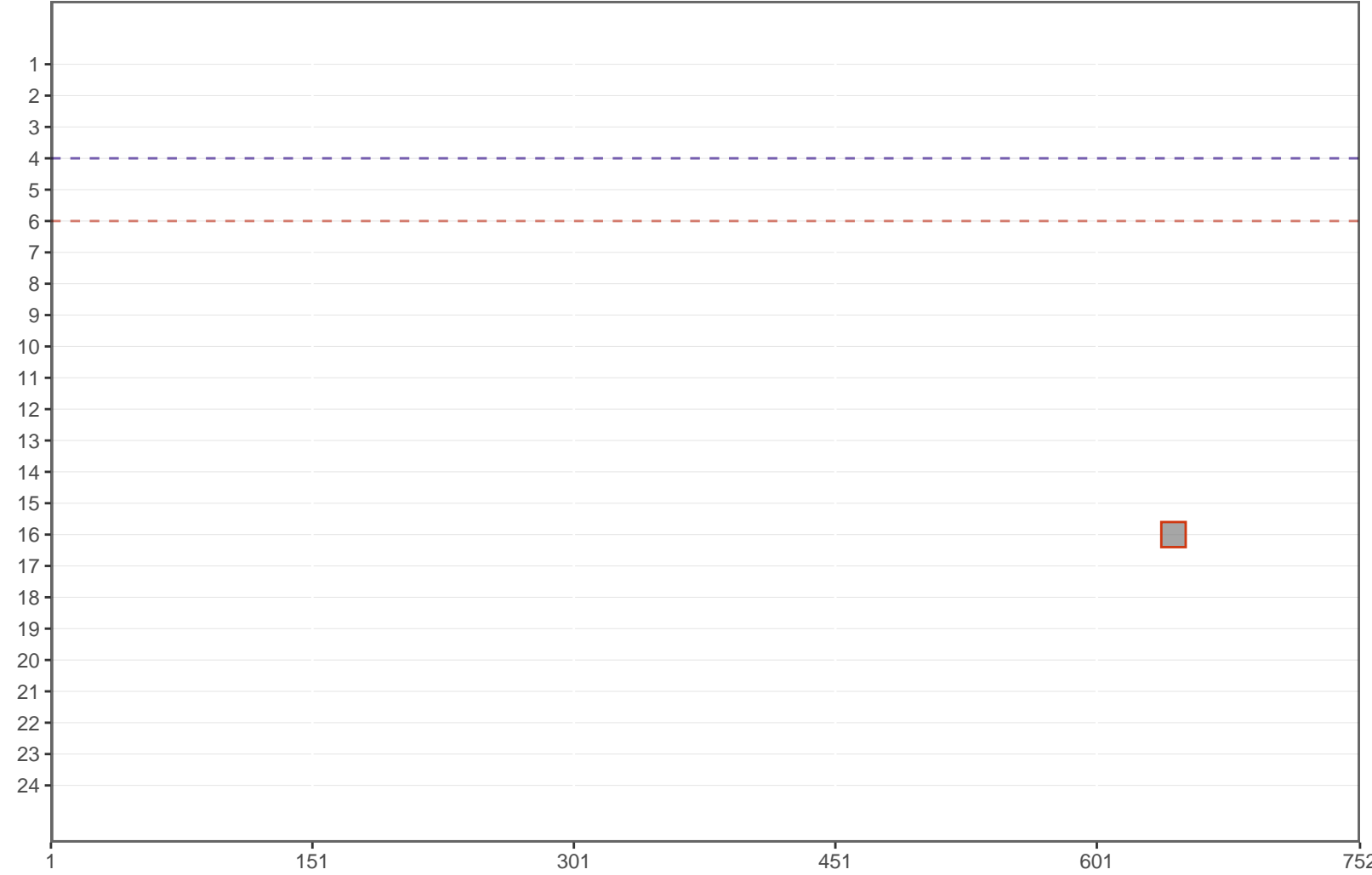
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

LRDPFSPLNLDLYNNDGSGSDHPDWSMKMNPQGISNAGPTESHGETETAGSDNTNMMKMPQGISNAGPTESHGETETAGSDNTNIVPLSGSDFSHEGLMKNDSGKDKIKTGPNGSGSEKLENGYDDDDINNDINLNRINMDSYEEGVLKVDVAVVNDVKIKDQGLGTESSISGONMGDGEVLAETLSGPAQRKADDTTHNYGIETVAADSGSESDRQVDHMLPLGREHSAEGDHYFEDSVKDVDTSDQLRVAWEVHSTEVRLVLSGMSPOHYAQAXCK

NbL03g22780.1 N-alpha-acetyltransferase_15_NatA_auxiliary_subunit-like [MW = 52 kDa]

No. of times detected



log(intensity)



Values from



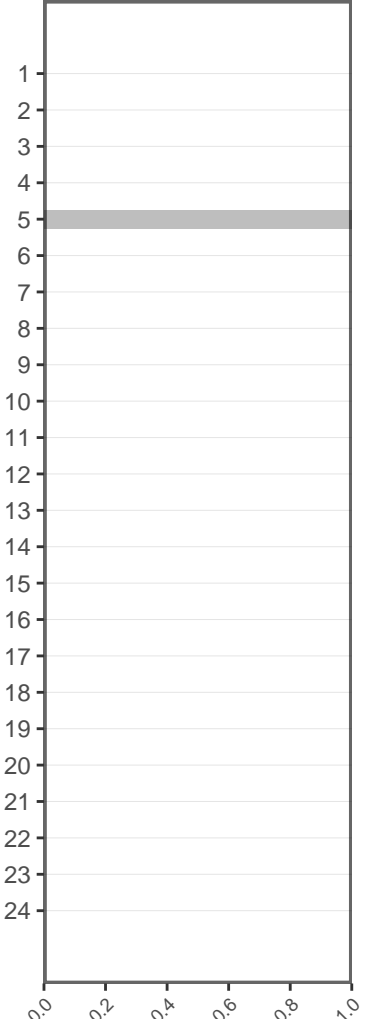
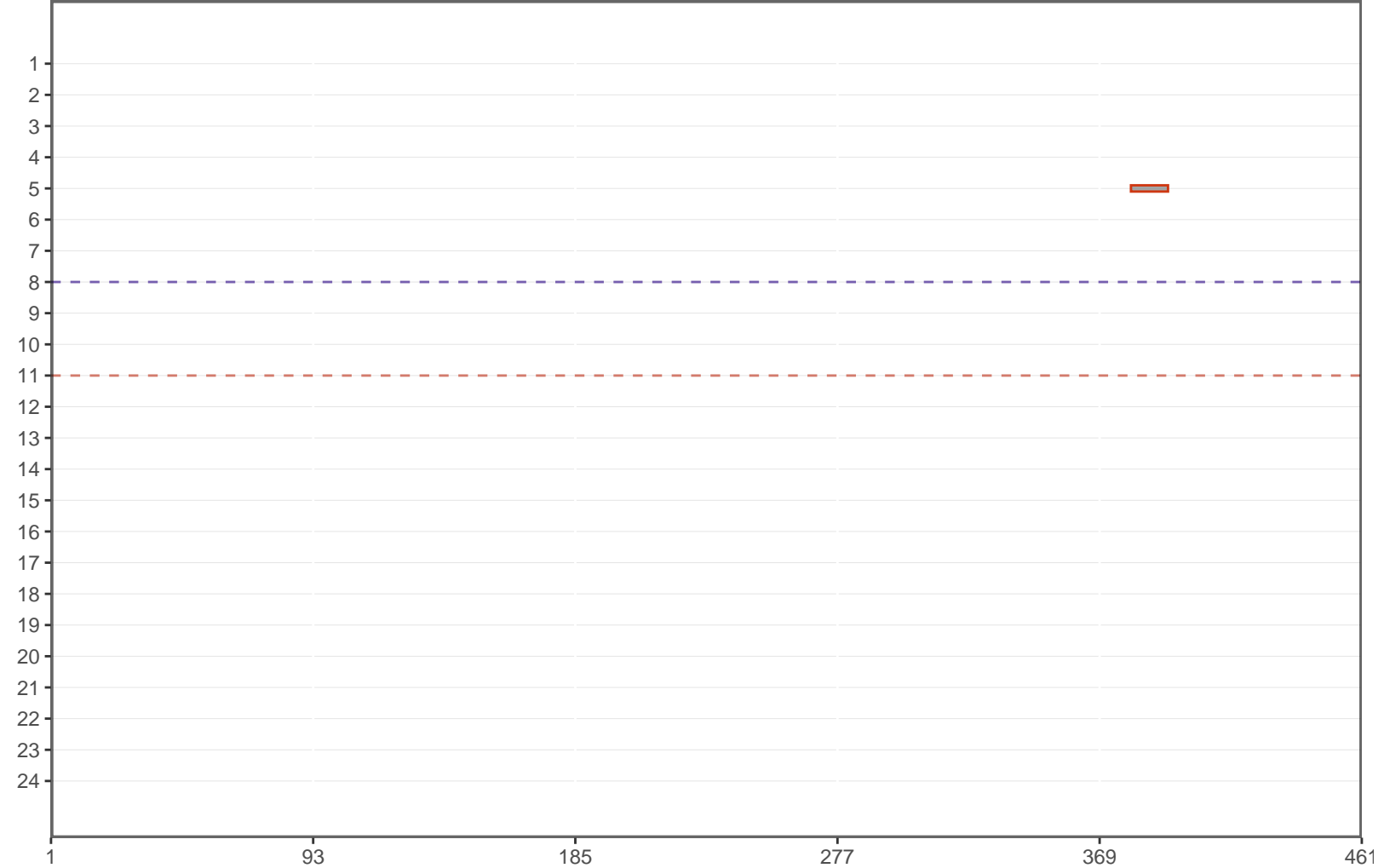
MW indication



Molecular weight



Gel Slice

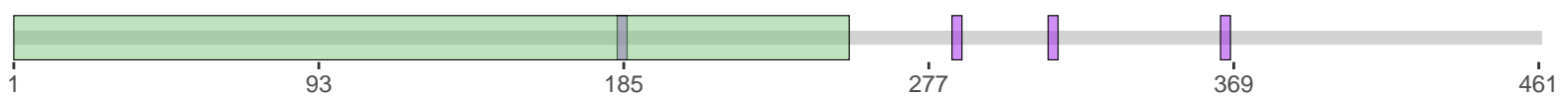


Protein length

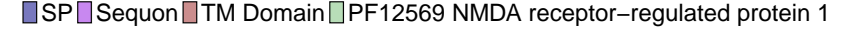


Peptide counts over 4 repeats

Pfam domains



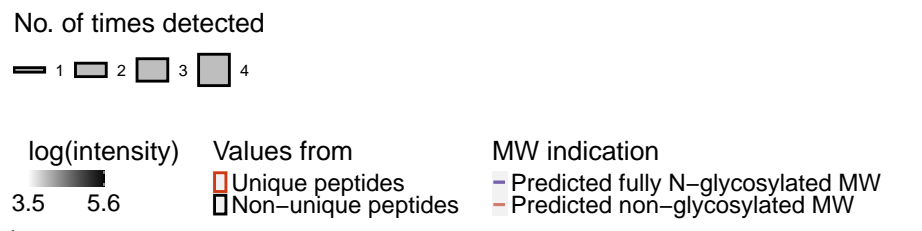
Pfam Description



Protein sequence:

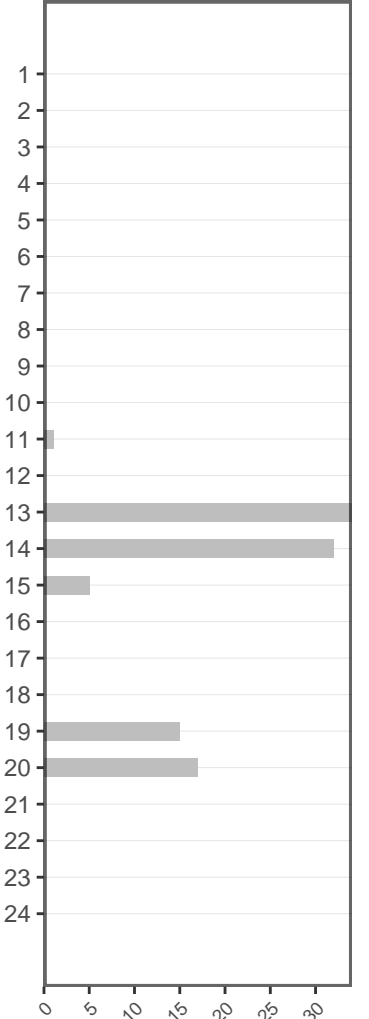
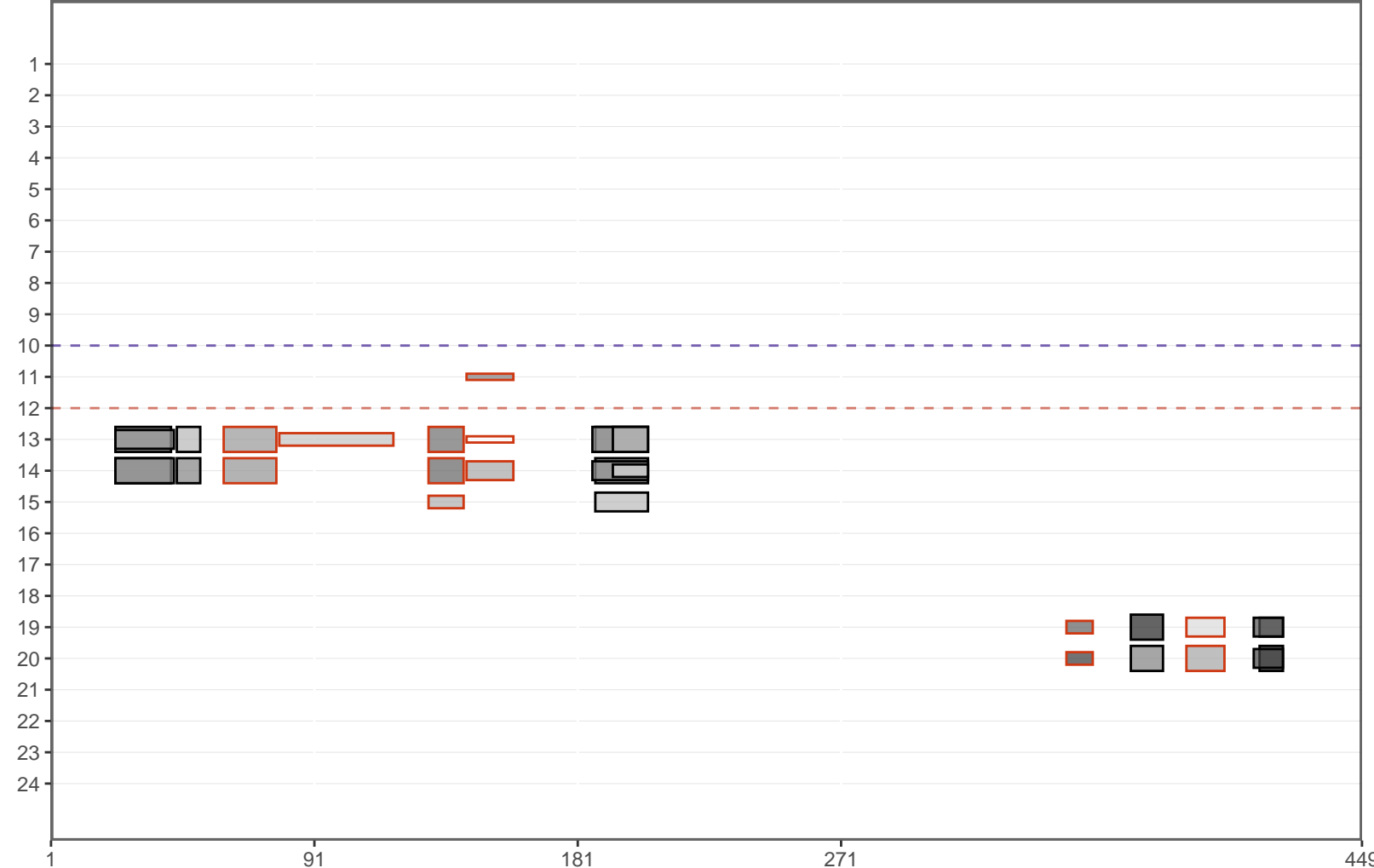
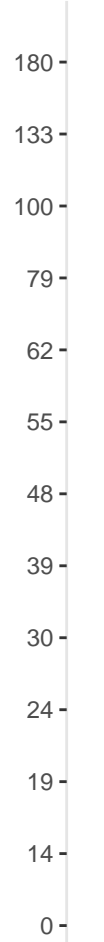
ASKYKLLLIKHSDDLETHLSEFVEMRKKKILLGAIKYLMLRLDADDPKSHLGLKFFHNDLSLTFPNDTEKLIWGVLEAERTISQLHGKSLIDANNITFEKIHRESLMHRAVAVLLELVLEPNKKAEAVKLLDSTNDLVSIDGAGGNVSSWKLNDGIVYHKLLETLLADSDASRWKVRCAEYFYSYHFGFGFQSSAATSSANNQIKGSSANGALGLNADGDSLSNGRLKLNALKDLH*

NbL03g22690.1 nuclear_pore_complex_protein_NUP50A-like [MW = 47.84 kDa]



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain PF00638 RanBP1 domain PF08911 NUP50 (Nucleoporin 50 kDa)

Protein sequence:

ETASFSFQQLSSSQNAFTGLAGTGFSTFFVFGAISKKEGKPLFGG6DAGAG6GSLFGAKSDQPSFGLPLFTNGANNLSLFGNSGSIIMNKGEGETAFPSKEEVSIVETGEENEKPVFTADSVLFEFLDGGWKEKGGKELKVVNVTAGEGKARLVMRTKGNVRLINASLVPENKLTNMDKRGILTFAGLNSAGDQKGLSTALKFKDASIVEEFAAAWAKHKGTTTGLKTPENSPKASDD

NbL03g22650.1 MAR-binding_filament-like_protein_1-1 [MW = 82.35 kDa]

No. of times detected



log(intensity)



Values from



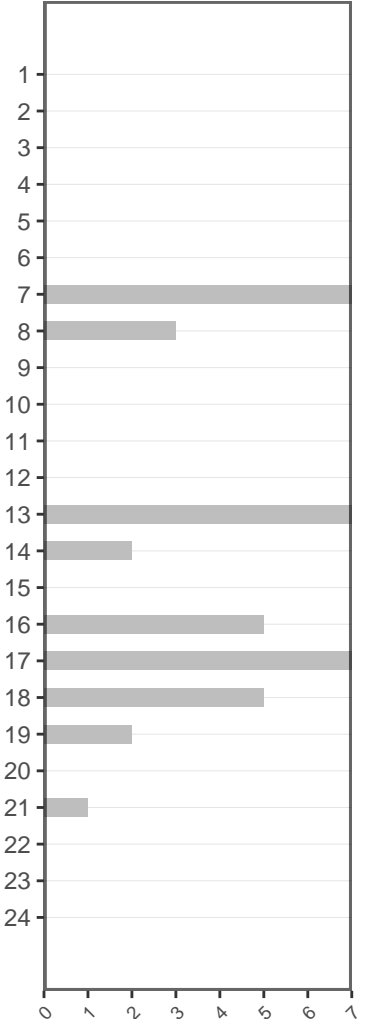
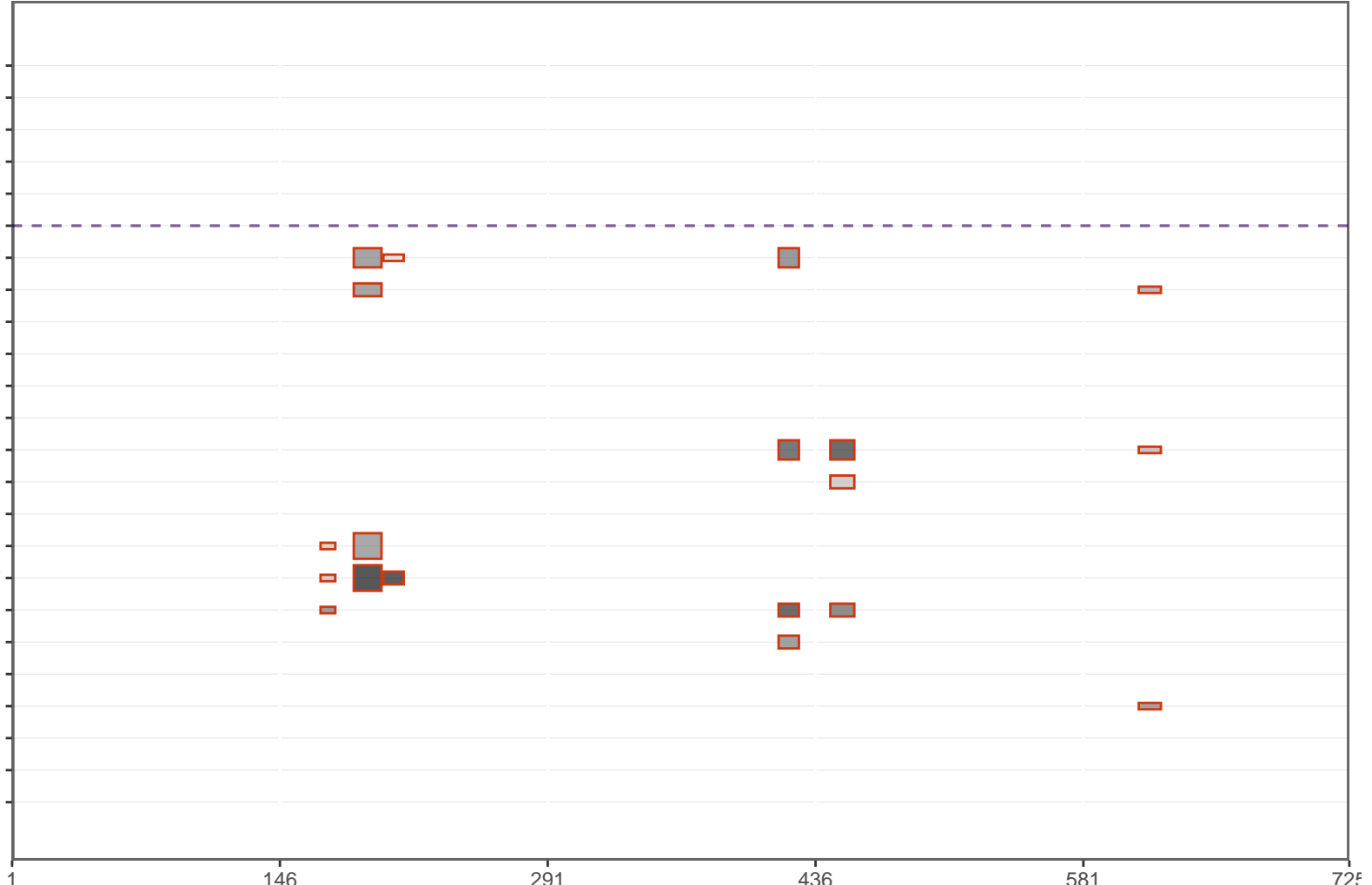
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

CELDAQKEYNEFKSISEKKNVADAKLLGEGEKRLHOLEEQLGAAADDEVKRNKVLVDTGQEKENRTVLDALLENKSKLALKEVQVTRFTELEKRRSDADAEQIQGSRHLSKLEAEVSKLQMLEETRTLLGRKIDETKRGAEALLAELTTRELLKKTNEEMHTMSENELAAVTENRDMLGTELVDVYKKAERTADELQGEKRVVLEKELFLEAQITREKESRKNLEEELEERATERGSLDEMNRNALALAKELKELANSRISGLEDEREVLQKLSLQKGLQAEARENLEDAHSL

NbL03g22570.1 pyridoxal_5'-phosphate_synthase-like_subunit_PDX1.2 [MW = 32.88 kDa]

No. of times detected



log(intensity)



Values from



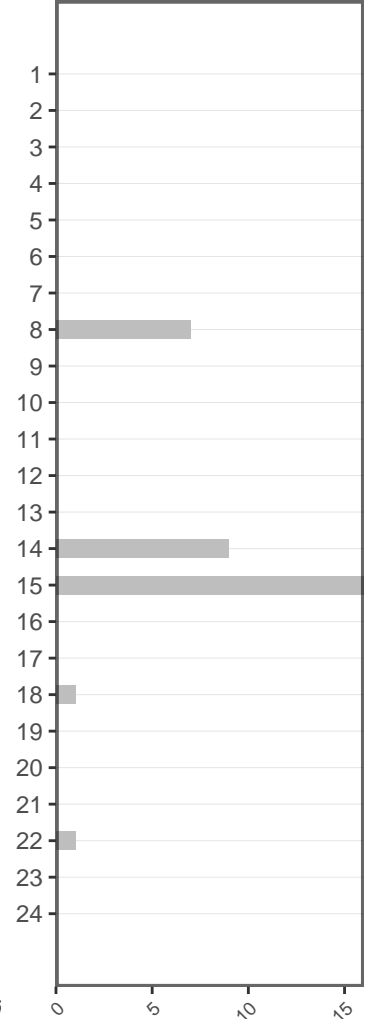
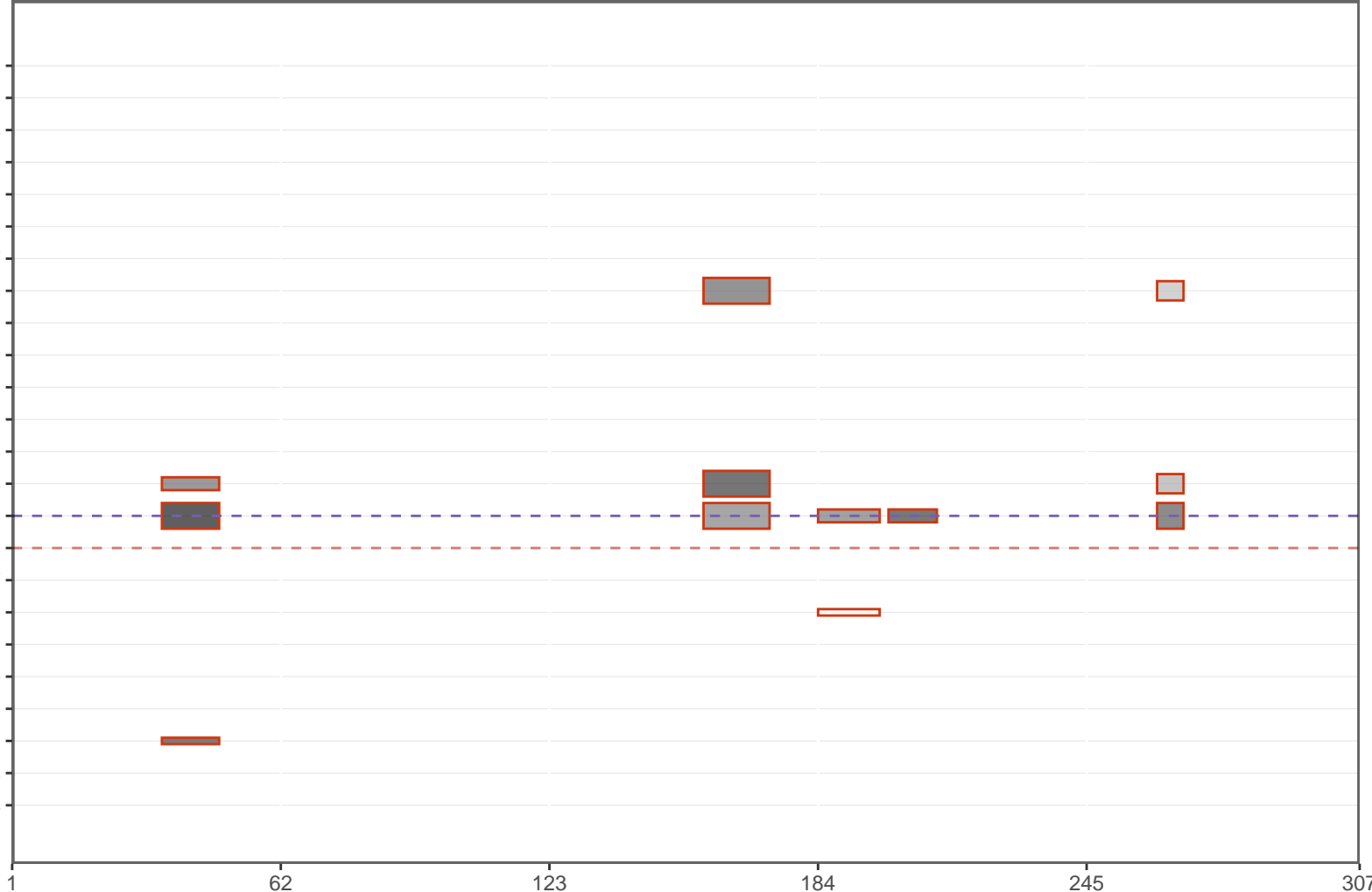
MW indication



Molecular weight

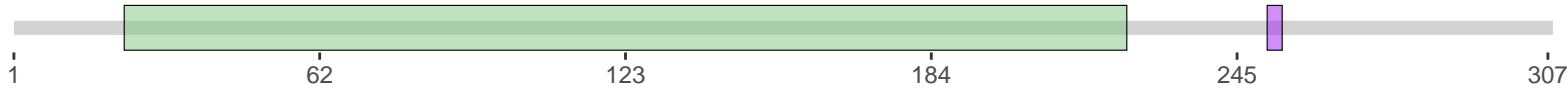


Gel Slice



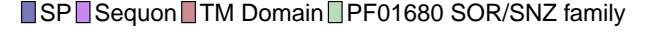
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LGEALRRVREGAAMIRITGGDLGTGNIVDTVRNVRKVMGDRLLSNMDEDEVFTFSKIGAPYDVAQTQMGRLPVVHFAAGGIVTPDAALMMGLGGDGVFLGPDIFNGSNPYKVRVAVRNVNDRPHLAAASGLLEAMGGLNLENRVERFVSAEETV

NbL03g22550.1 uncharacterized_LOC107817663 [MW - SP = 38.57 kDa]

No. of times detected



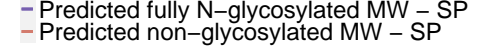
log(intensity)



Values from



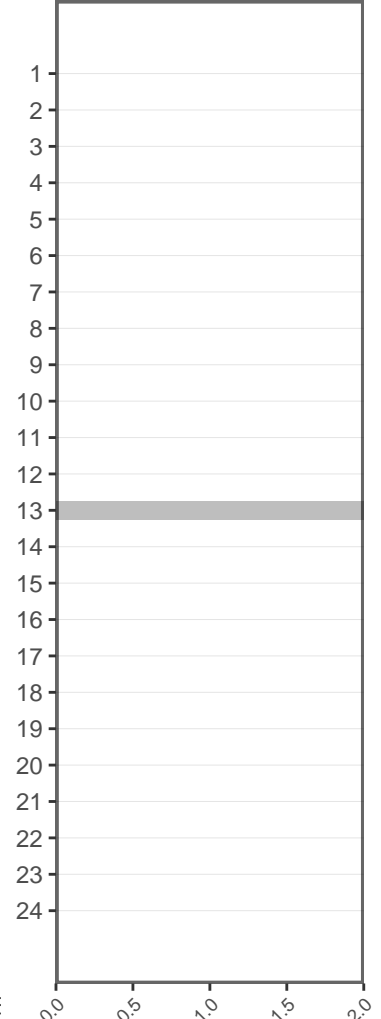
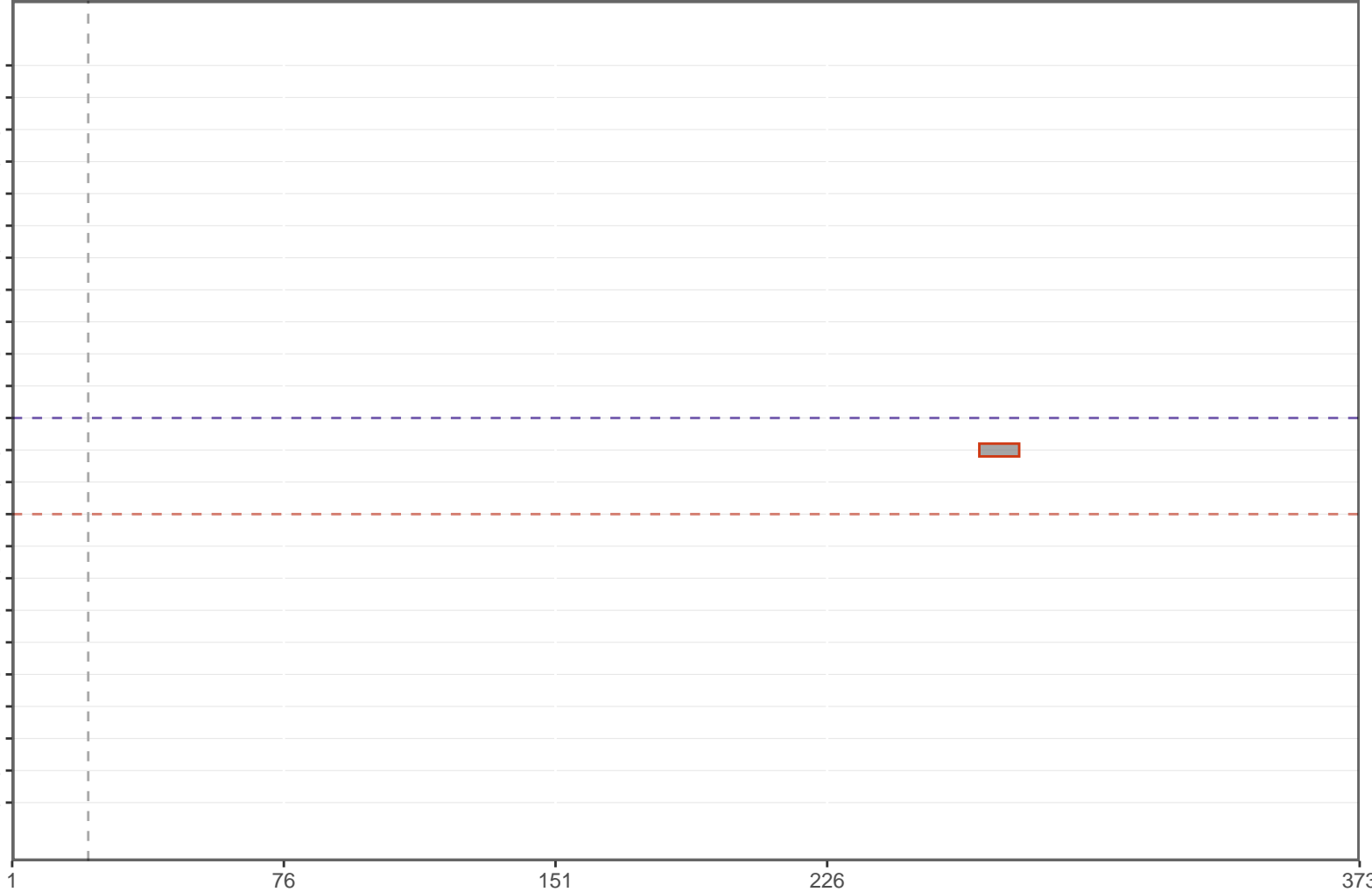
MW indication



Molecular weight

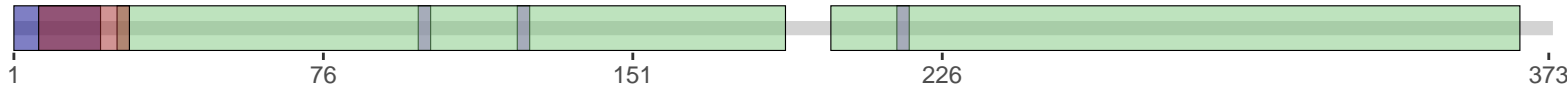


Gel Slice



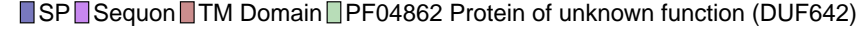
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

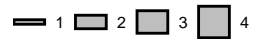


Protein sequence:

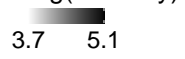
IKDPAAGPLDIFALKLNKPHRPGKGNLKNFEEGPIYFPNTFSWGLIPNIEDDHSPLPGWMIESLKAQKYYDAAHFTVPEGKRAIELVAGREITAGGVITTKGKYVDMFVSVDASNSDGGSLIEAFAGQNLQVFPVESTGNGGPKRAKLRKFAVSETRVRFLLSTYYHMKSDHSGSLGCPVDDDLVGVRRHP

NbL03g22480.1 serine-threonine_kinase_receptor-associated_protein-like [MW = 38.43 kDa]

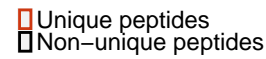
No. of times detected



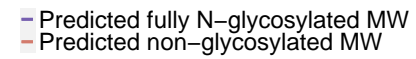
log(intensity)



Values from



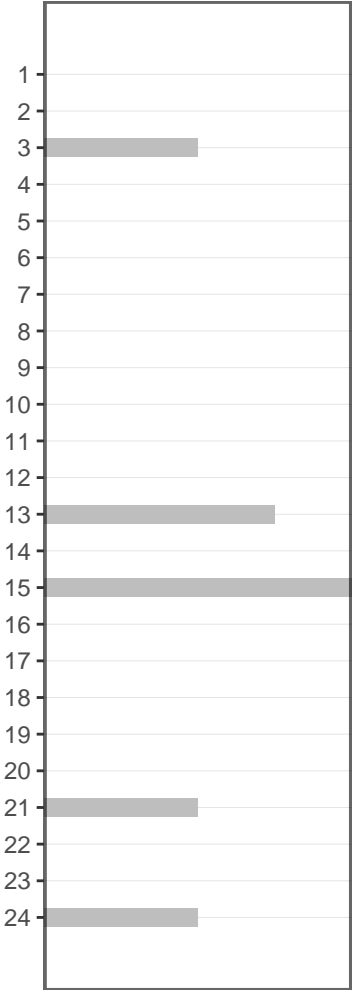
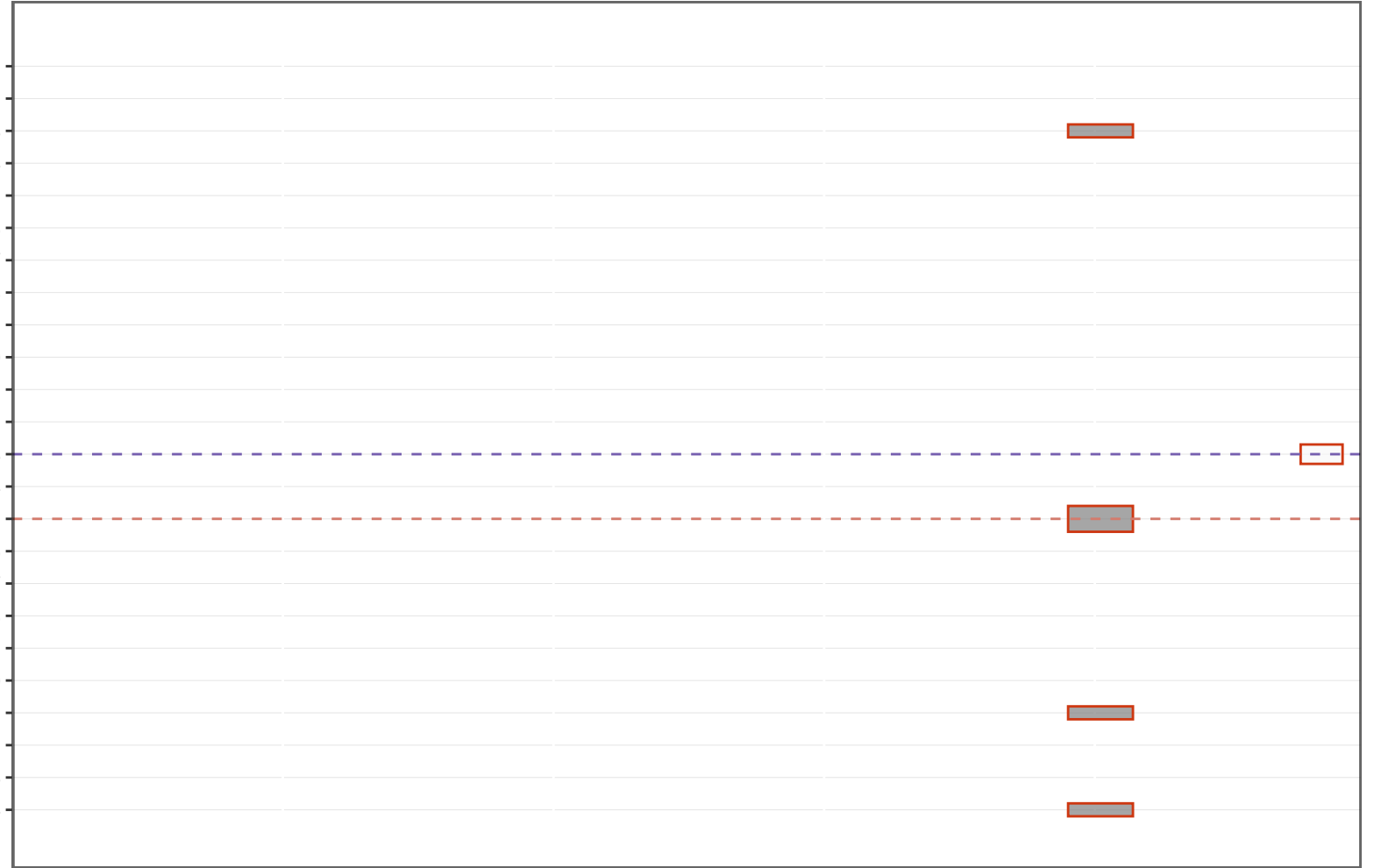
MW indication



Molecular weight



Gel Slice

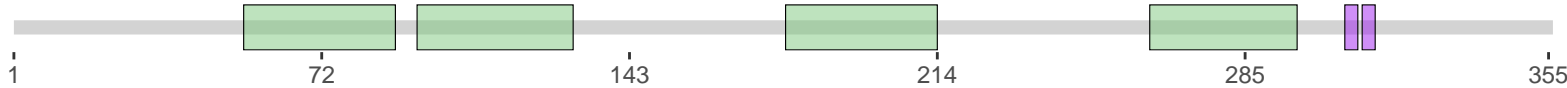


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

MAAGSLRLWDVRSQKVVQTLFETKFPVTSAEVSDGCRVYFTADGSSVKFWDANHFGLVKSKYDLPCKVKSASLEPKFGRNFIAGGEDMWWVHFDFDTGEEIKGNKGGHGPVHQLRFSPGGESVYASGSEDGTRIRWQLGPLGGNEGNSIANGSIANKDDMGVEVYQKIEELVSEANKTEETQIDGAAKVVADV

NbL03g22400.1 beta-galactosidase_9 [MW = 104.99 kDa]

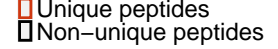
No. of times detected



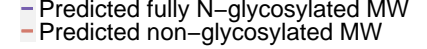
log(intensity)



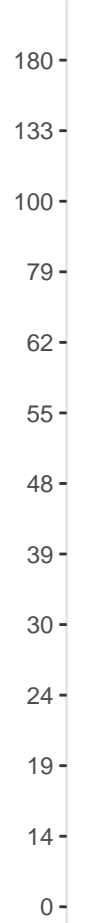
Values from



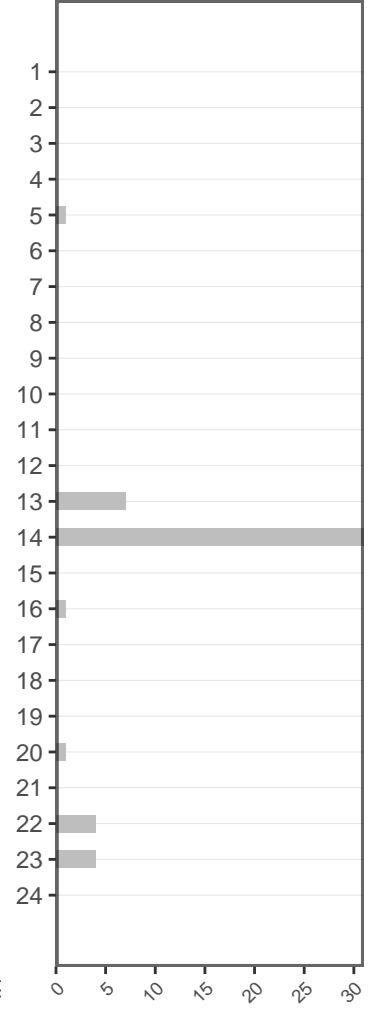
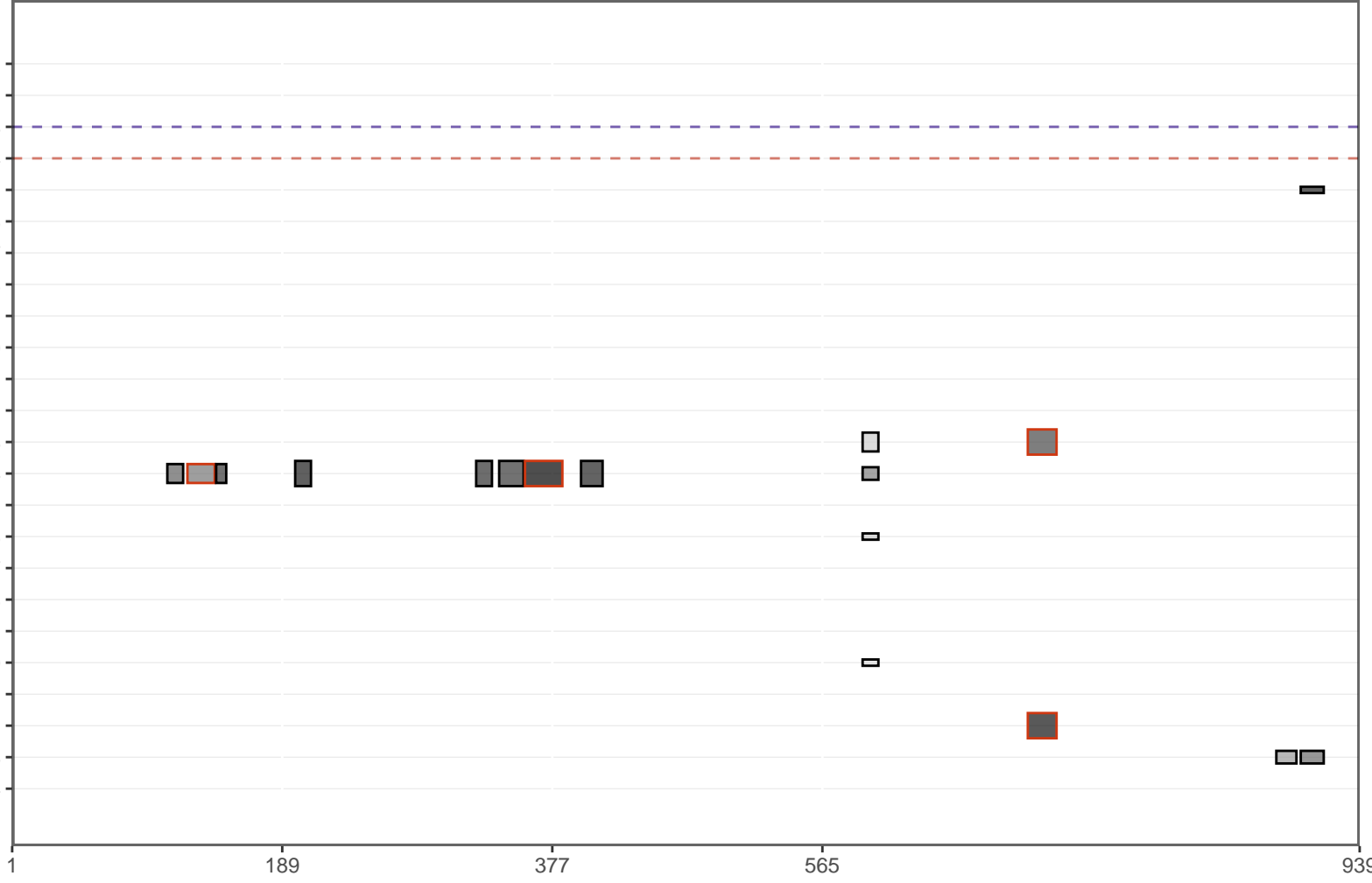
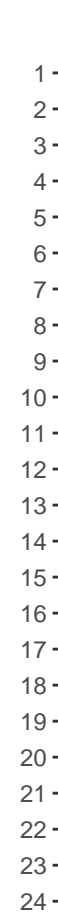
MW indication



Molecular weight

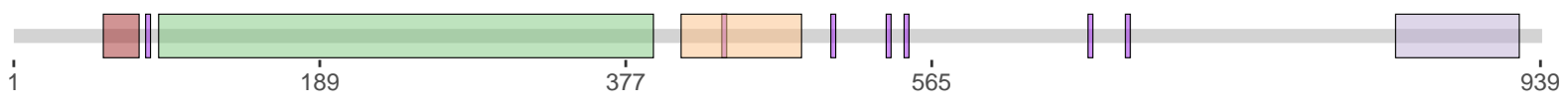


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SEYTLPPVYSILFDGRNTAFNTAKVGGTSRIKIVGLDEIVGNGNBLFFOLRIKSKLRISIGSWMALKERLGVWGDKNFTSTGLEHLNVTKDQSDHLYVLTIRYISDDDSFWEENDVSPFTGIDSMRDFVRFVINGLAGSMKGVKIKVGPVKLVGGYNDILLSETVGLGNYGAFLEKDGAGFKDGLKLTGGRNGDNLFTSLWTVYGVGLKGEFLKVVYDYNSTESAAWTELPNDMPVFSWYWRKFDAPGGTDPVALDFSGMKGQAWVNGNHGRYWTUAAKNGCC

NbL03g22220.1 protein_ASPARTIC_PROTEASE_IN_GUARD_CELL_1-like [MW – SP = 49.16 kDa]

No. of times detected



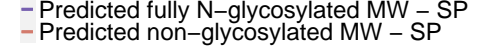
log(intensity)



Values from



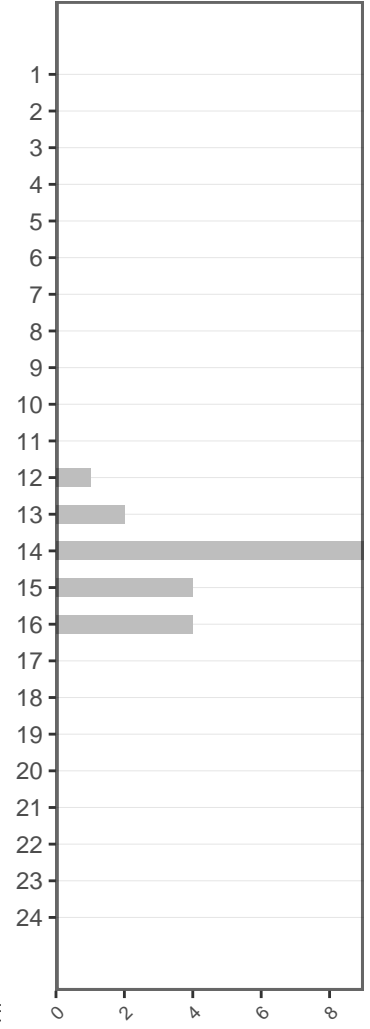
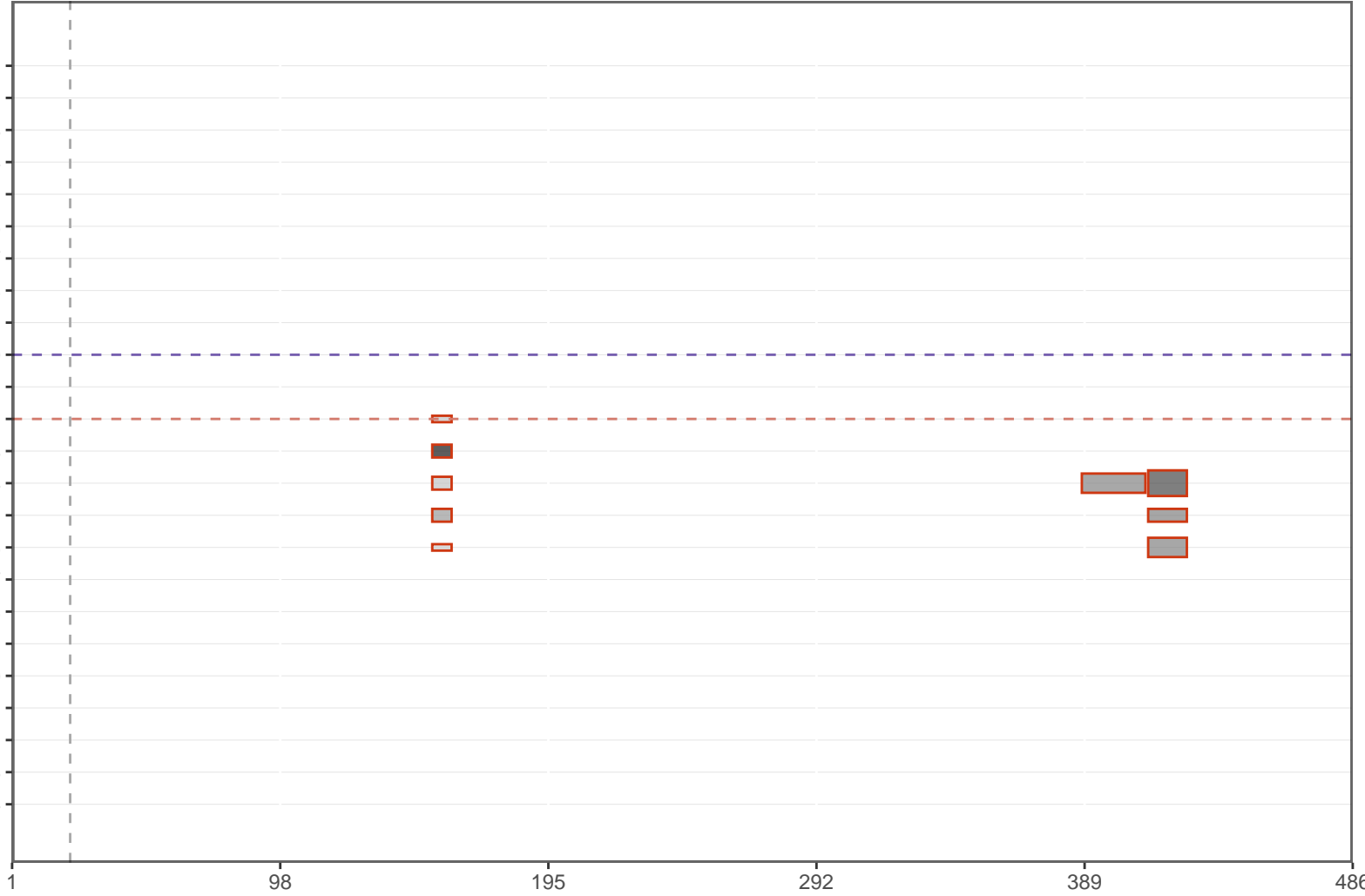
MW indication



Molecular weight

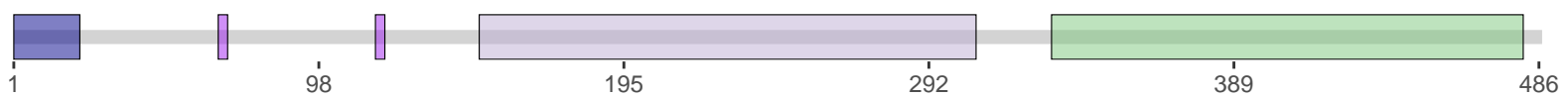


Gel Slice



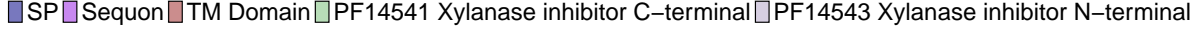
Protein length

Peptide counts over 4 repeats



Pfam domains

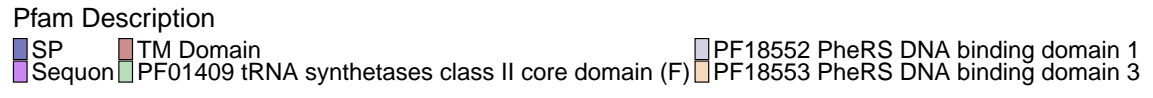
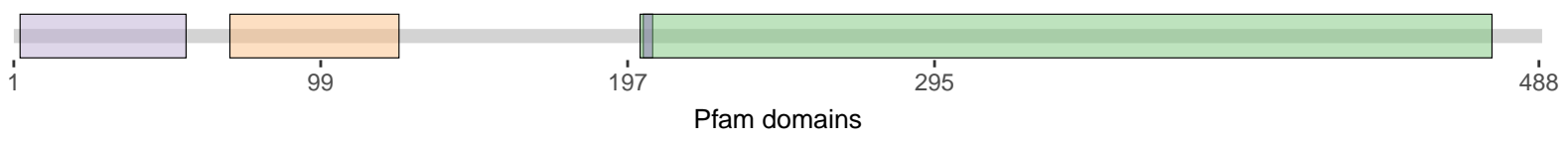
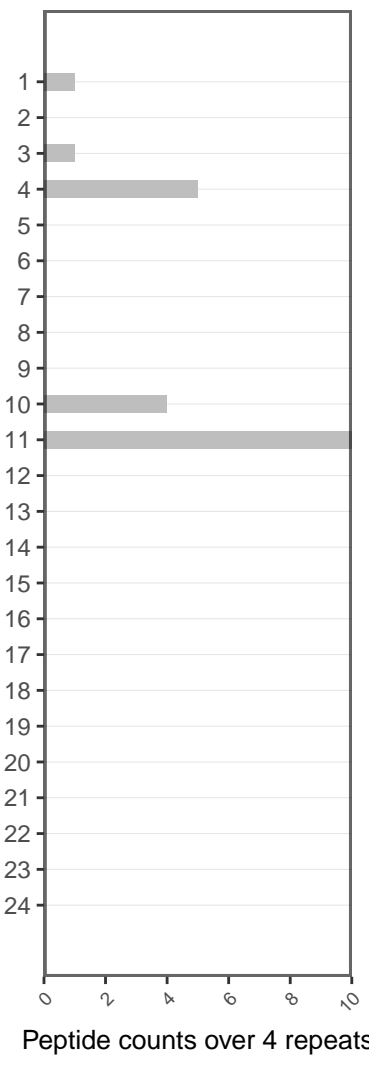
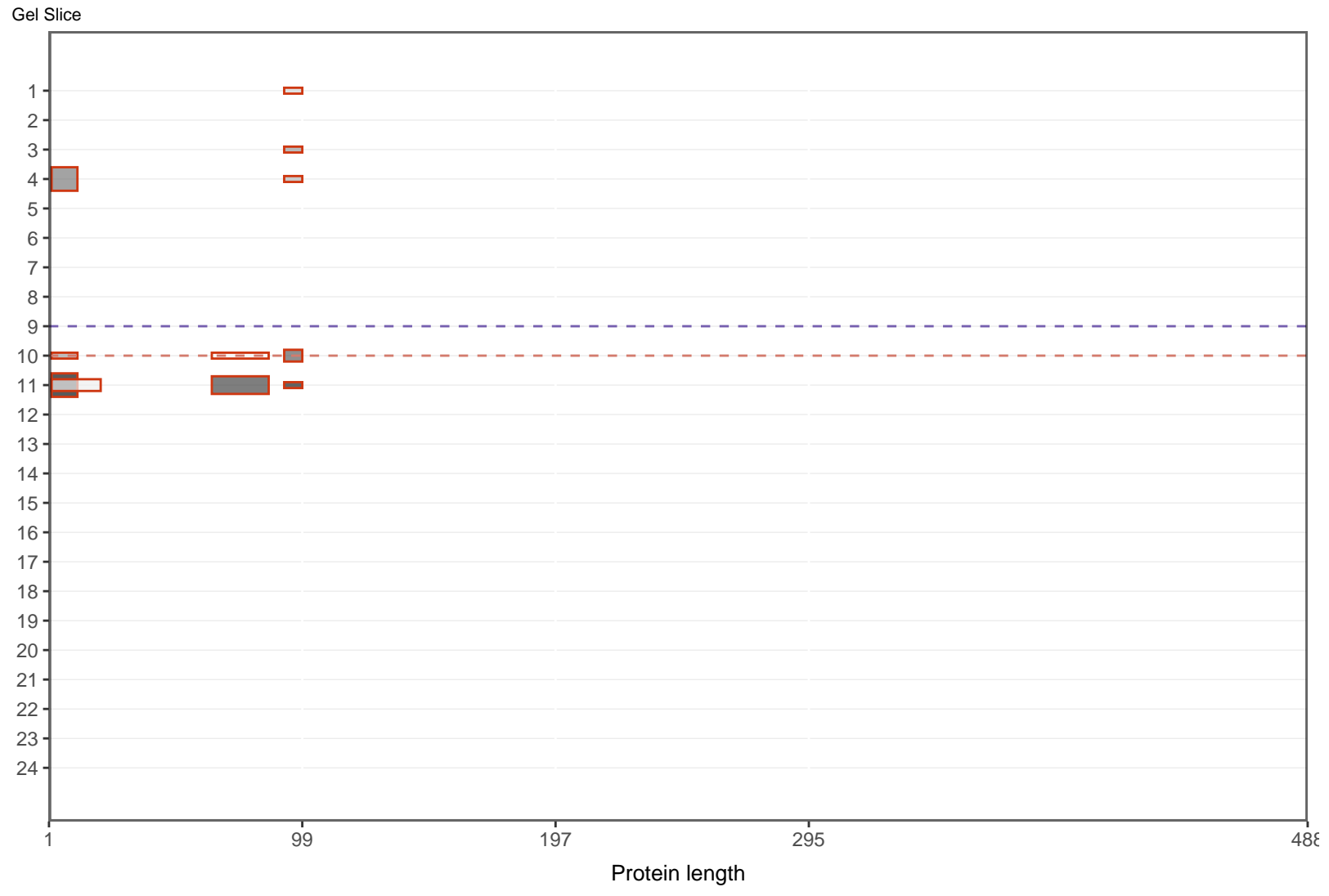
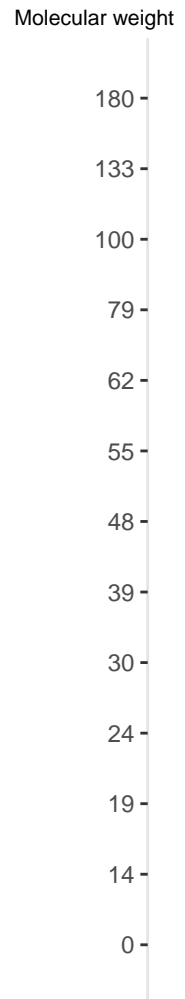
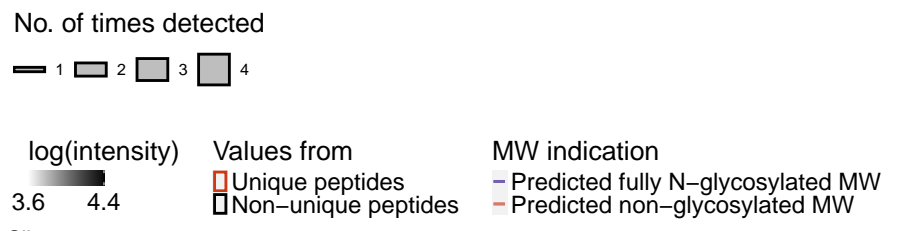
Pfam Description



Protein sequence:

IGSFTVGEFATEYVDFGNIGSDFSKVAVGGCHDNEGLFVGAAGLIAAGGGTSLPLPQKASDFYCFVDRDSASBSTLDFNSARPGDSDVAPLLRNSRRGTFYVGLGIVGGVGMSPASVDFQVDSGNGGIVDSGTAVTRLQTTAVNALRDFKFTQNLPSGGGFALFDTCYDLSSMKTVEVPTVALHFTGDKTLSLHPKXVLPVDSGKFLAFAPTEGSLSGHIOGGGTRVSYDLANNLVGFSPPDKC

NbL03g22110.1 phenylalanine--tRNA_ligase_alpha_subunit_cytoplasmic-like [MW = 56.26 kDa]



Protein sequence:
 MGFEEPTNPFVSSFWFDALFQPGQHARDSDHDFFLKVPSTTKMLPEEYVERVKQVHESGGYQSRGYDWRKEANKNLLRTHHTAVSRMLRALAQKPFAPKPKYVSDRIVRNEAVDRTHLAEFHQIEGLGCDRLGLTLDGLGVLHDFFARLGMKSLRFPKPNVPTPEPMEIFSHYEGLNKVVVEVGNNGMFRPEMLLPMGLPEDVFRVIAWGLSLEPRTMLYGGIDNRDLFGPKVDGLKRNPKRLGI

NbL03g21930.1 histidine--tRNA_ligase_chloroplastic/mitochondrial [MW = 56.75 kDa]

No. of times detected



log(intensity)



Values from



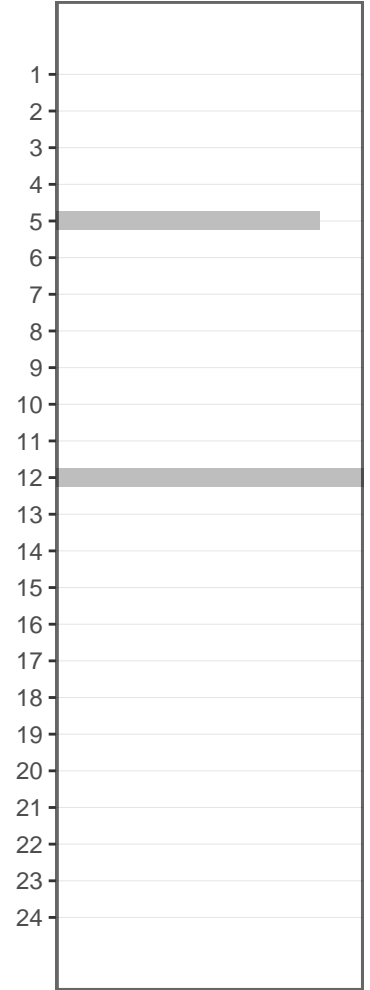
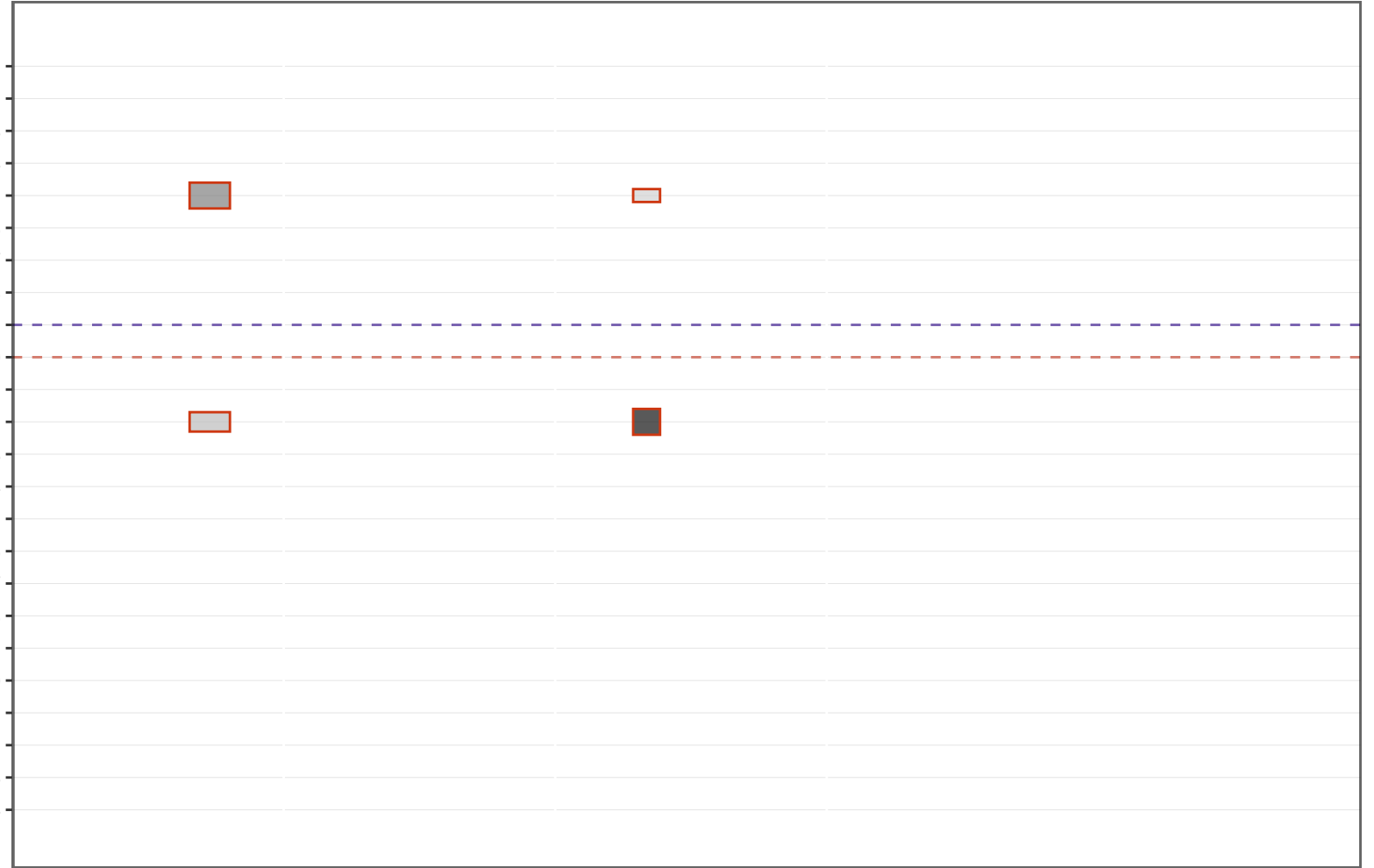
MW indication



Molecular weight

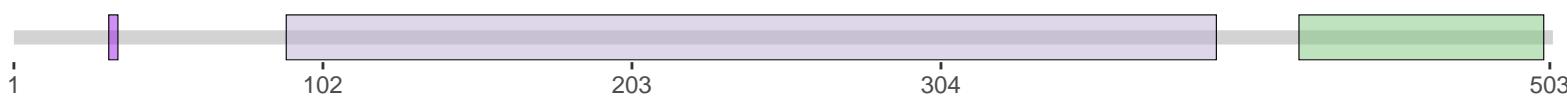


Gel Slice



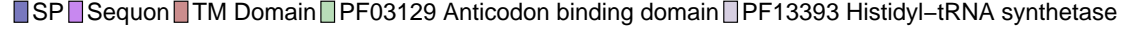
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

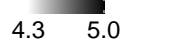
YVGFKSSRKYLQEVLRGYSVPEPMFGRVGHIDKIHPIIMDDIRKDIQSDMSEVAIEELGVLGLKSLAKLEEKLGASGEALSDLKQLFSLAEKYGYSSEWQFDASIVRGLAYVTGIVFEGFRKGLRAIQGGGRYDRLLSTFGDDLPACGFGGDVAIVVELLKERGLLPELNLQVENIVDELDELQGAASAWATLREKGGSDLVLENKPLKVVFRRAARINARRLLVGNAEVQKGMVWKTLSFGQGVKIVDELEI

NbL03g21830.1 SH3_domain-containing_protein_C23A1.17-like [MW = 57.53 kDa]

No. of times detected



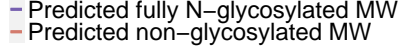
log(intensity)



Values from



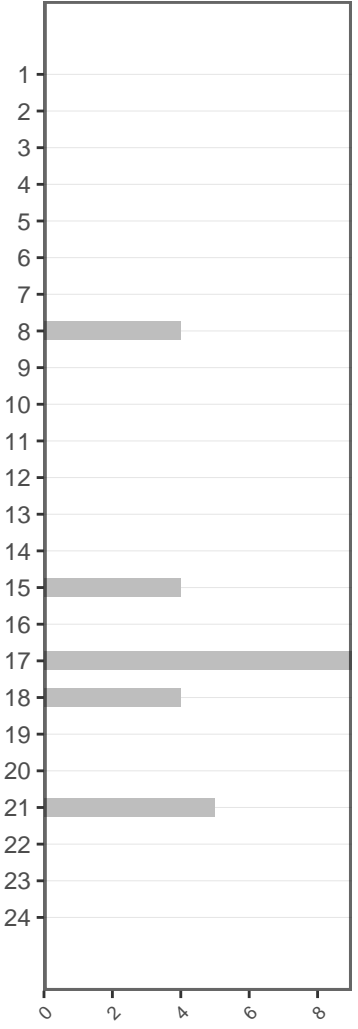
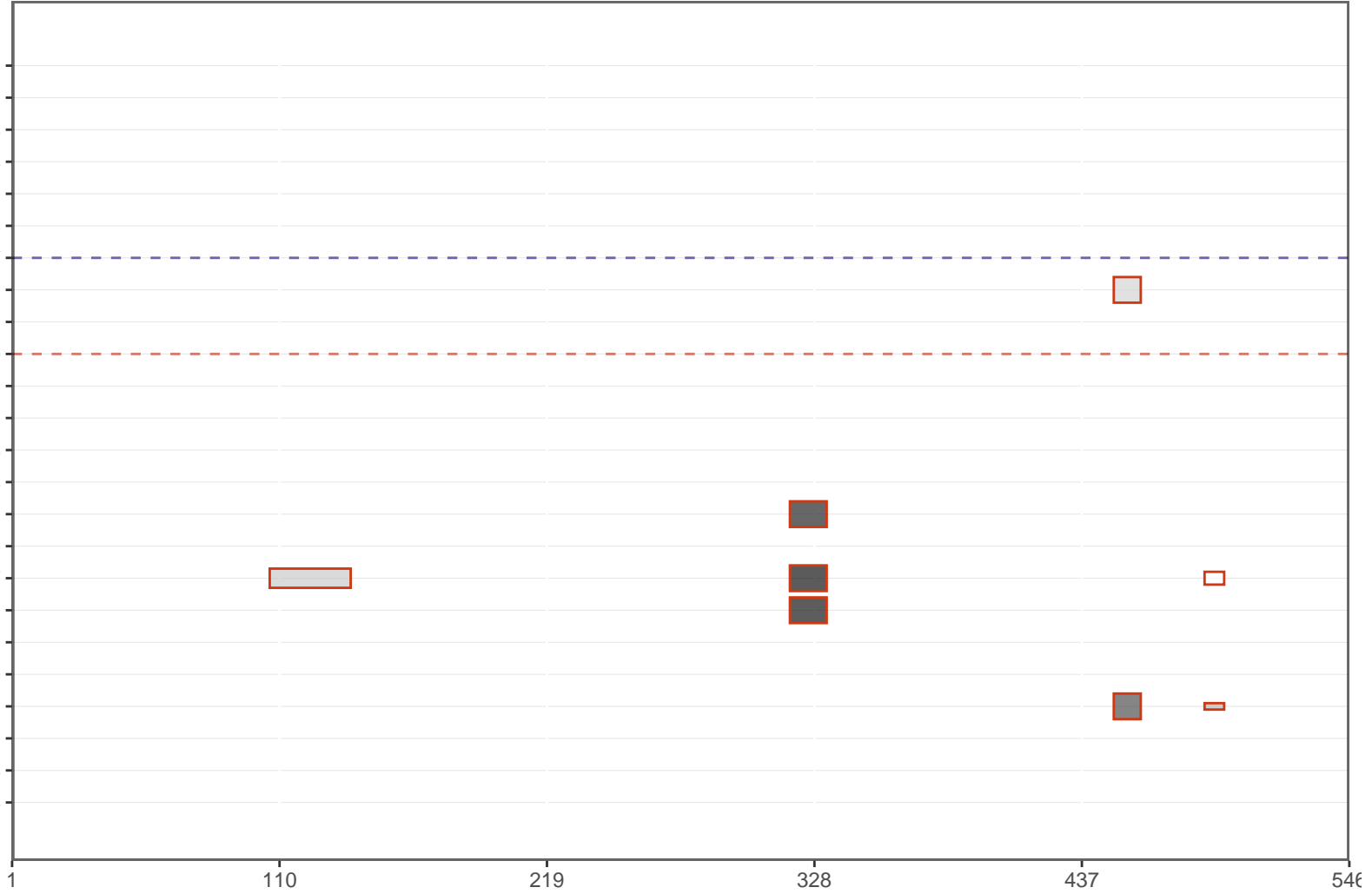
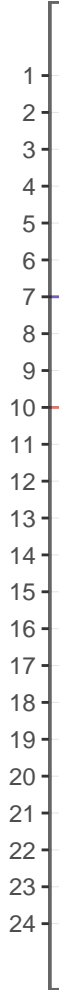
MW indication



Molecular weight



Gel Slice



Protein length

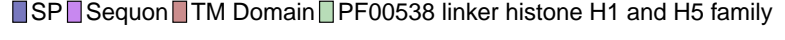


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SVHNFVGLPALGAEESTTKRRPRGRKDGSTVVKPEKPLDQSGGTRRRPGRPKSTTVDAAGSSMGTTARRGRPRKNSPTGRGRPRKNAWAATNGGGVWNPISVGNVTVNPKGGVPSGAISTKRRGRPRRSGGPTATGVVTDVPAAAFETENLPTNGGGVTVNNGSIPPLGKRRGRPPKSYSAIAAPTIVKRRPKLSGKPLGRPRKIVTSAASDPKLVVAWEELNGKLECMGSRKEAAEALKPCVNAESPWALALQLEELASAGVNPVQON

NbL03g21790.1 66_kDa_stress_protein-like [MW = 66.03 kDa]

No. of times detected



log(intensity)



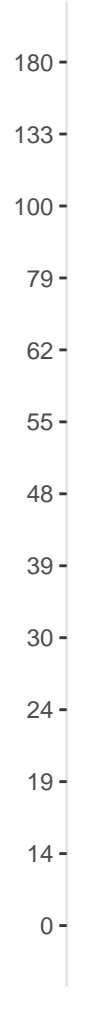
Values from



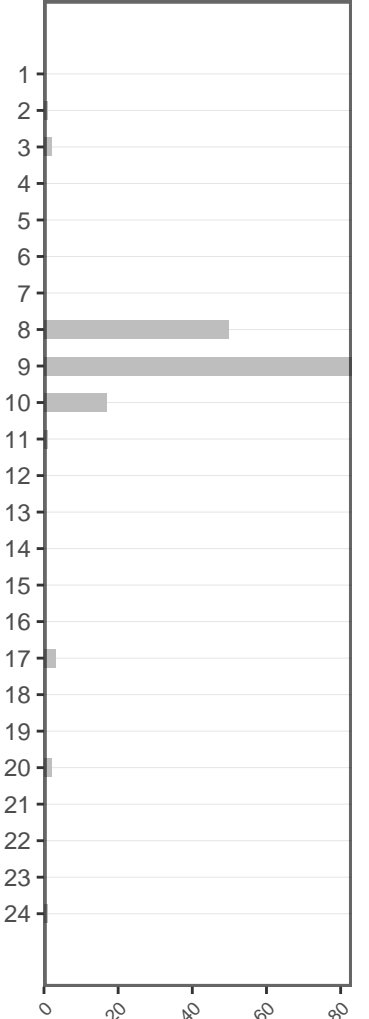
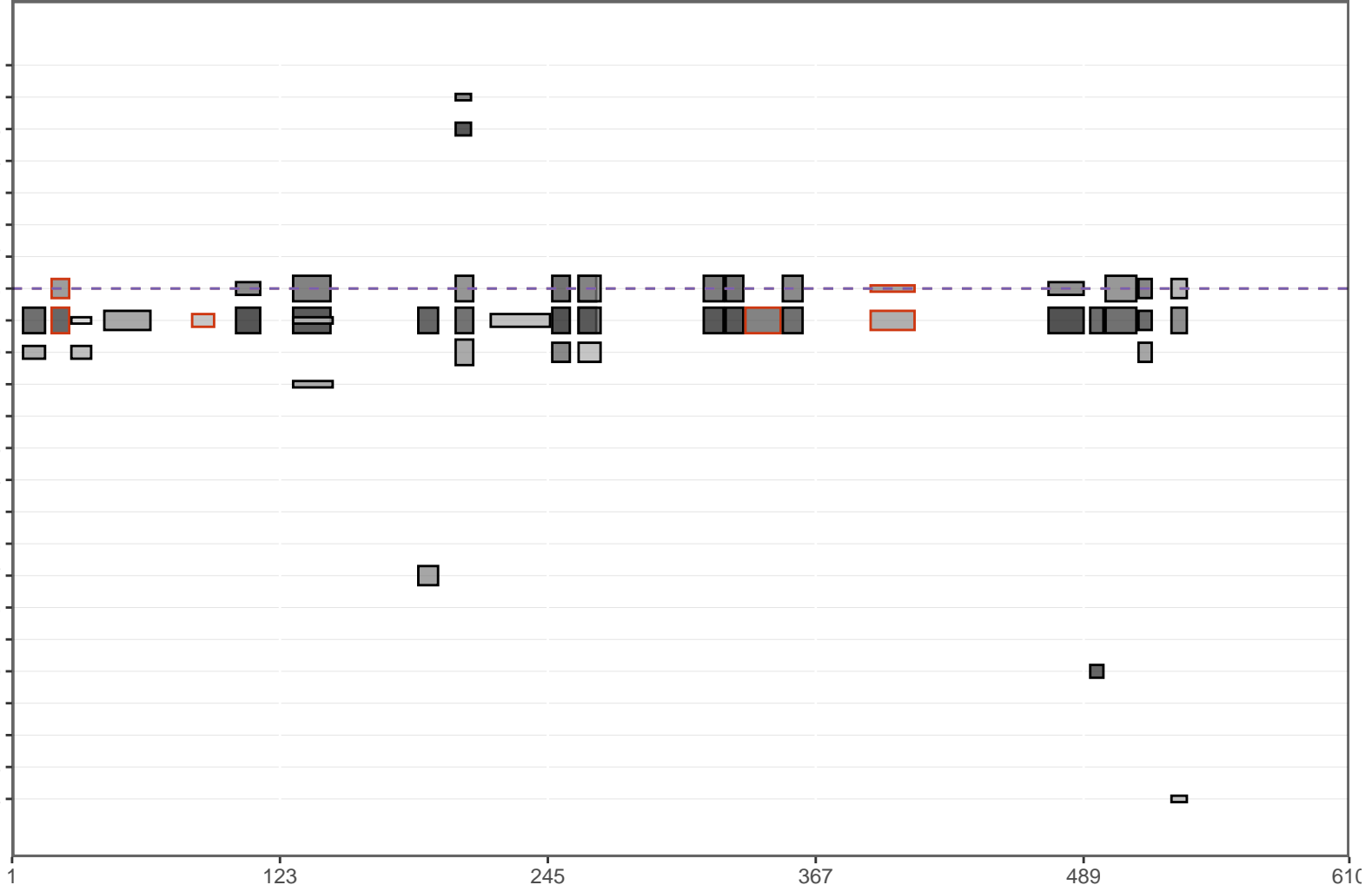
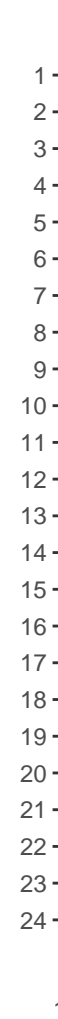
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

.WQNDHLVTVLSLGGTISFASAELEKSPVSEFGHMKNVNLSLAVLKSDDPQIMLSSSEYDGLVWVWQDGYSGKLERKVNSSQKGFVVEGEVSCGFQDNKVRVRLSGDQGGDANSDVGVNGKDLGLALSSPEATLVSFDTGVLLFRGTVKLVLETIDLGFVTVASAPDGGSEAVVGGQDGLRVLVSTGDTLNEEAVLEKRGATVIRVSPDVMFASGADVREAAVWDRASREVLKKNMLYHTARINGLAWSPDNTMTATGSLDTEVIVYDQKPKASRTIKGAHLGGVYGLAFTT

NbL03g21780.1 beta-glucosidase_44-like [MW = 60.33 kDa]

No. of times detected



log(intensity)



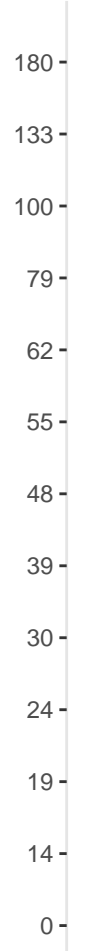
Values from



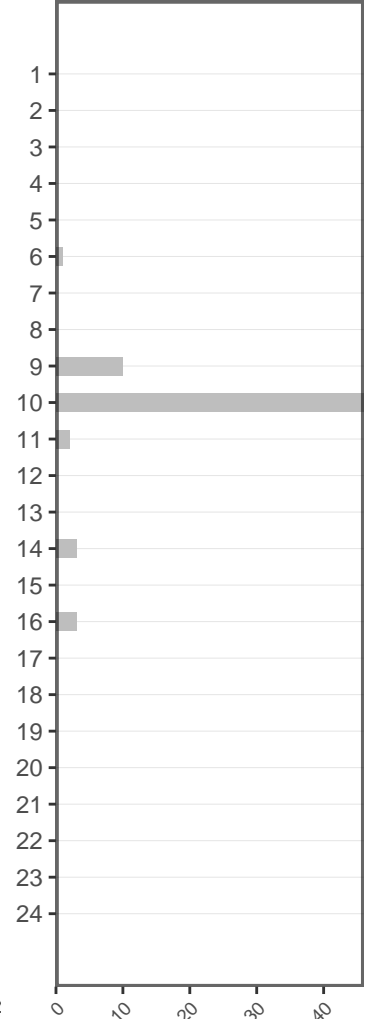
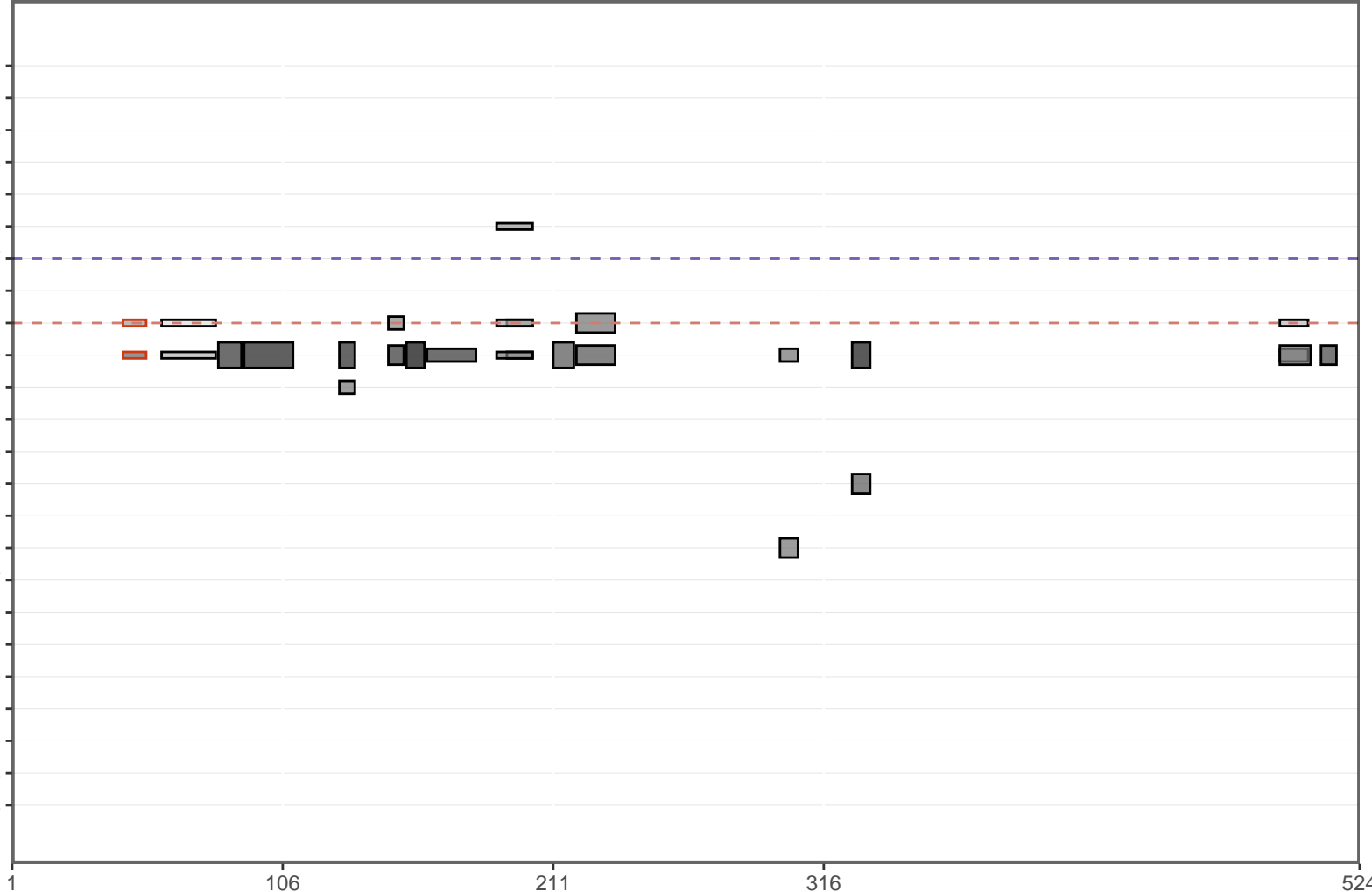
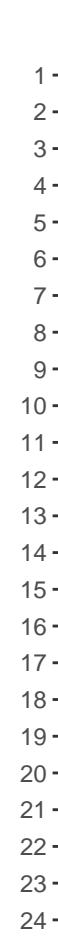
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

[P]Y[VA]N[L]L[C]H[A]N[A]G[R]Y[R]E[K]Y[G]K[G]K[G]L[L]D[F]V[W]Y[E]P[L]R[G]K[A]D[N]Y[A]G[R]A[R]D[F]L[G]W[F]L[P]L[V]Y[G]E[Y]P[K]T[M]N[V]G[K]R[L]P[K]F[K]E[E]V[M]K[M]G[S]D[L]L[G]I[G]Y[T]A[Y]M[Y]D[H]Y[T]P[G]L[Y]Q[G]D[W]N[V]G[F]A[Y]D[R]K[G]V[P]G[P]R[A]H[S]D[W]L[V]P[W]G[L]H[K]A[V]N[Y]K[E]R[Y]G[N]P[T]M[L]E[N]G[M]D[V]A[G]N[T]L[P]K[A]L[Y]D[T]K[R]I[S]Y[K]Y[K]L[E]L[K]K[T]D[E]G[A]N[H]G[Y]F[A]W[L]V[D]N[F]E[W]R[L]G[Y]T[S]R[F]G[V]Y[V]D[F]N[T]L[K]R[Y]P[L]S[A]L[W]K[M]L[R]R[H]G[...]

NbL03g21740.1 guanine_nucleotide-binding_protein_subunit_beta-like_protein [MW = 35.99 kDa]

No. of times detected



log(intensity)



Values from



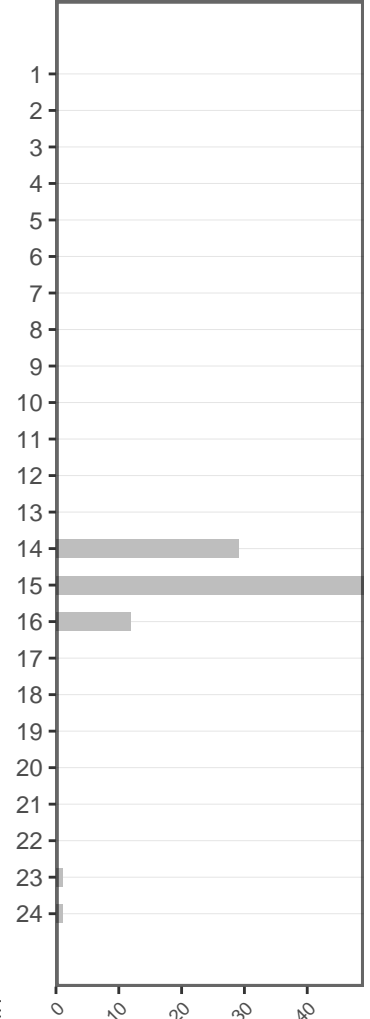
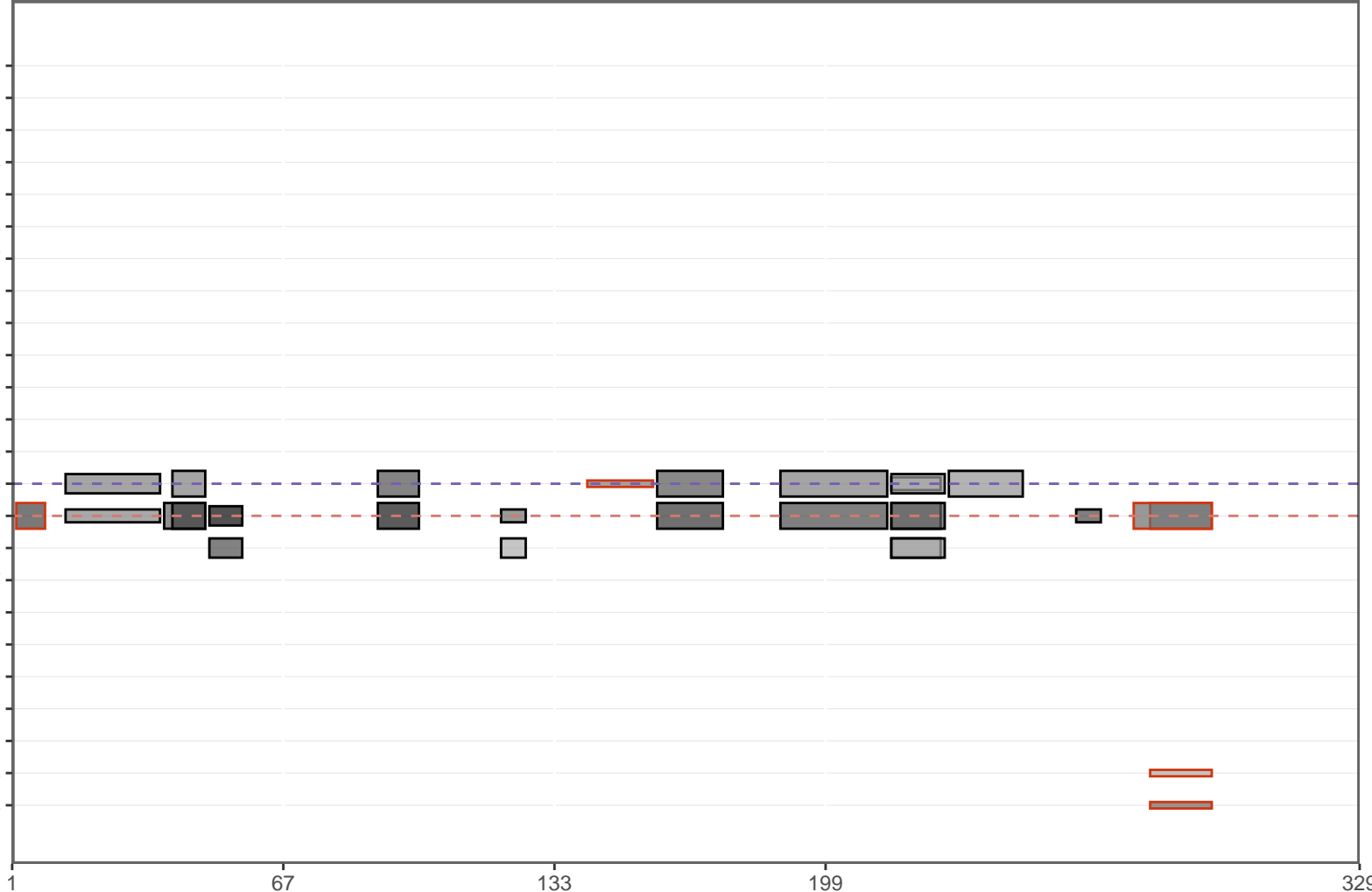
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DWVSCYRFSPNTLQPTFVGGSDWRTVKWNLNGLRSLRFLAGHAGYNTVAVSPDGLGASGGKDGTLWDLAEGLKLYSLDAGSHALGFSPNRYWLGATETSRIKWDLESKIVVDLKVLDKGESEMATGTTGSAACKNKIMVGTCLSWADGSLFSGYTDGLHVVWIGIRY*

NbL03g21700.1 eukaryotic_peptide_chain_release_factor_GTP-binding_subunit_ERF3A-like [MW = 57.42 kDa]

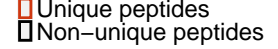
No. of times detected



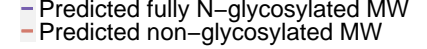
log(intensity)



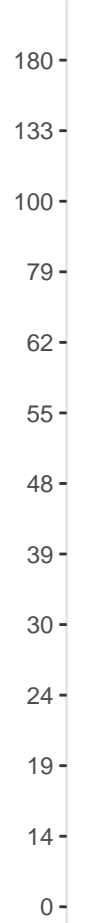
Values from



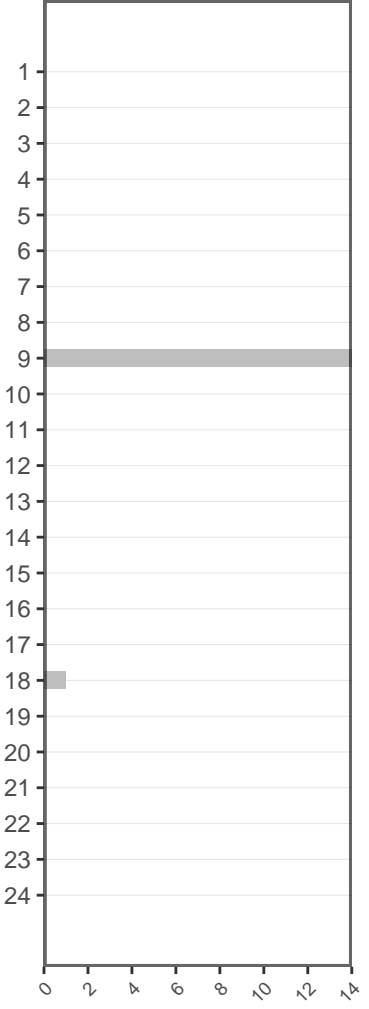
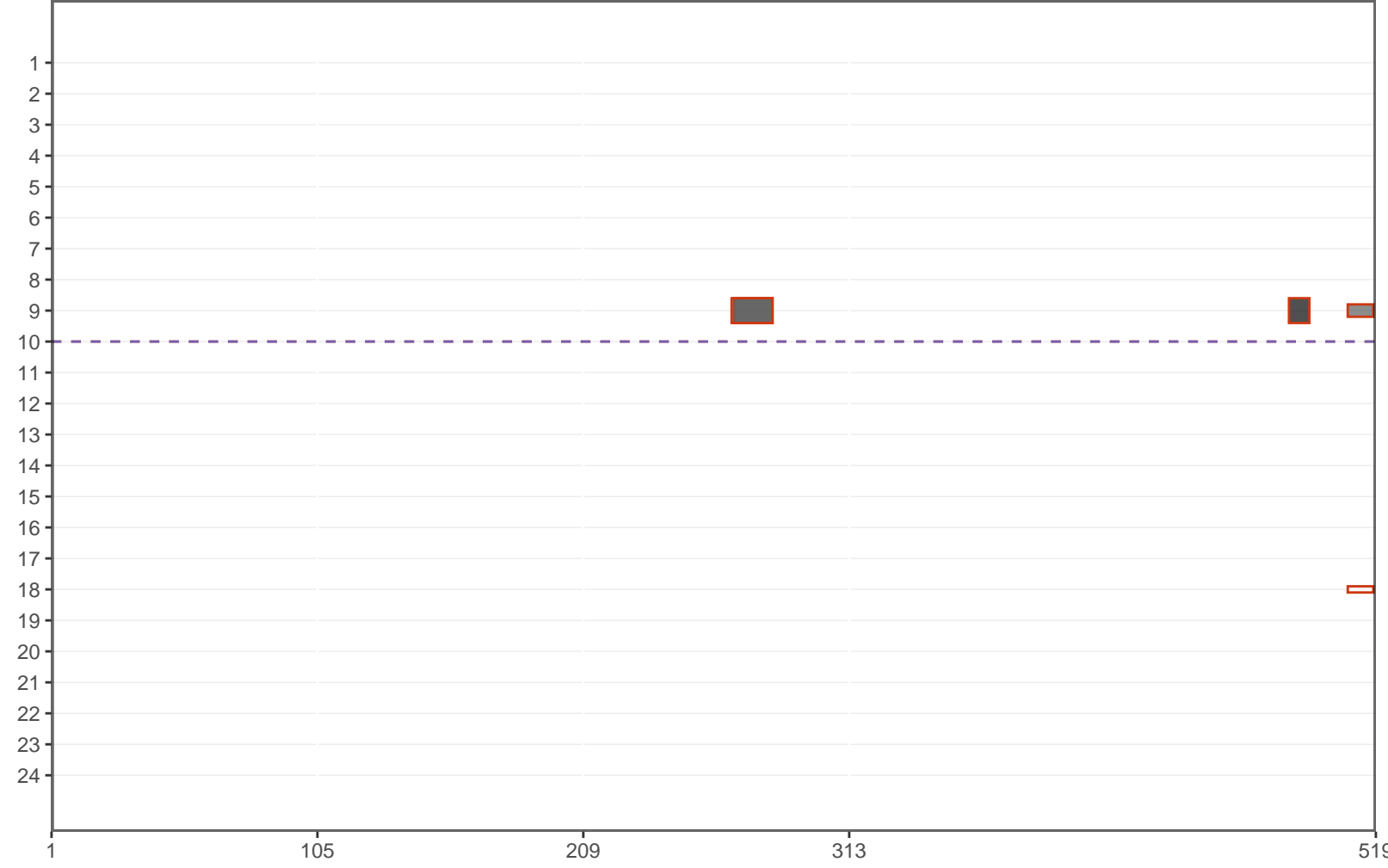
MW indication



Molecular weight



Gel Slice

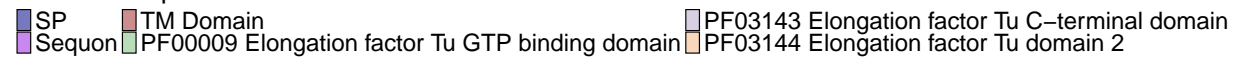


Protein length



Pfam domains

Pfam Description



Protein sequence:

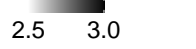
YAKERYDEIESKIMFLKSSGYNWKKDVFPLPIBGLLGSNMKNRVEKSVGSWVWNGPLFEALDAVEVPRDPKGPLRIPIDKFKDMGTVMKGIKESGSRGDNLLVMPNKAIVKGLAIFQDEDRVIRGAGPCGENRVRRLSGIEEEDIMSGFVLSGVAQPIAVTEFVAQLQILELLEDAFTAGYKVALHHAVVEEGEIVELHQGLDKTKKPKMKKPLFVWNGAILGRVQVNNLQIEKFSDFPQLGRFRLRTEGKTVAVGKVALPQVADNAI

NbL03g21620.1 probable_protein_phosphatase_2C_8 [MW = 24.86 kDa]

No. of times detected



log(intensity)



Values from



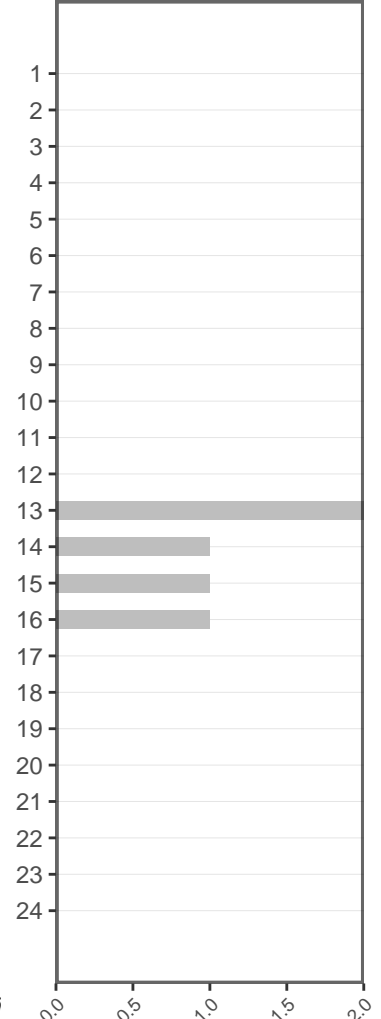
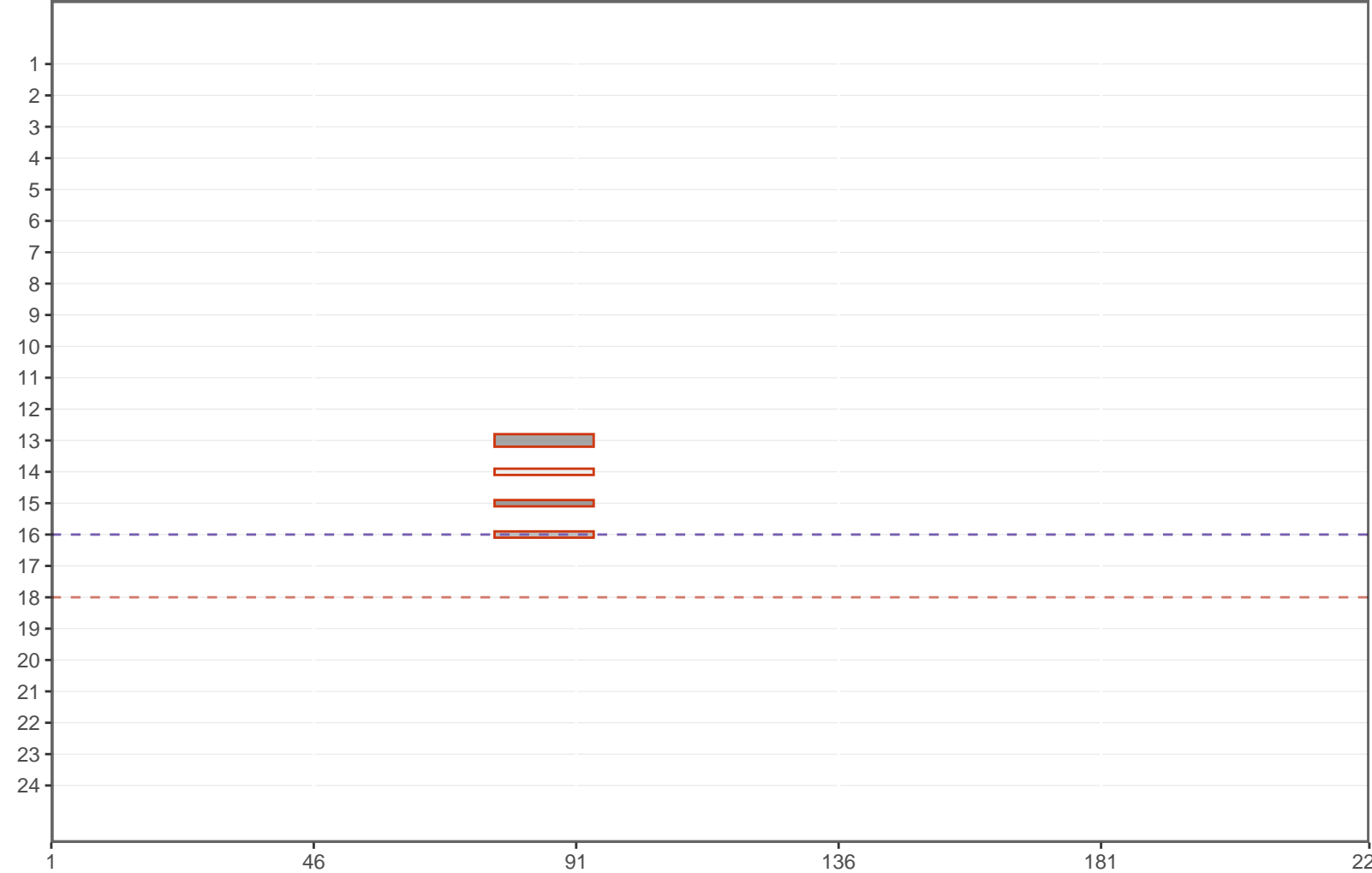
MW indication



Molecular weight



Gel Slice

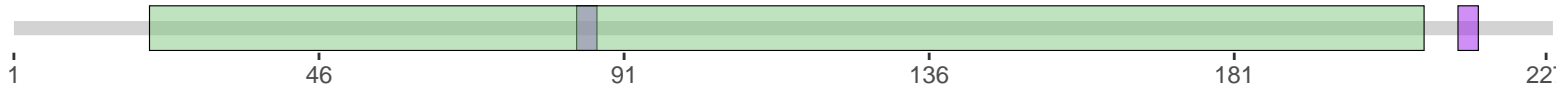


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IHKATYPQERARICKAGGSVBSNGLRQARLEVERAFSDRGRFKKGVVATPQVHGFDLTERDHFILGCDGLWGVFGPSDAVDFVQKLEKGLPVSVVRRLVREAVRERGGKNGSAAVAFRRKQ*

NbL03g21550.1 calcium-binding_allergen_Ole_e_8-like [MW = 18.74 kDa]

No. of times detected



log(intensity)



Values from



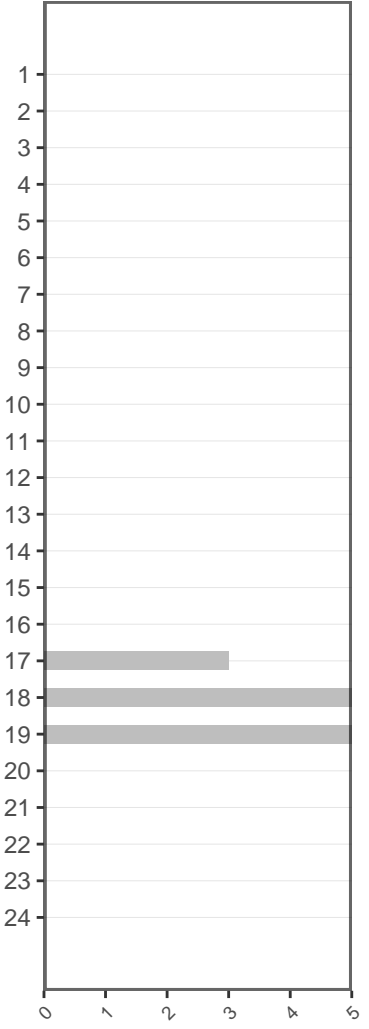
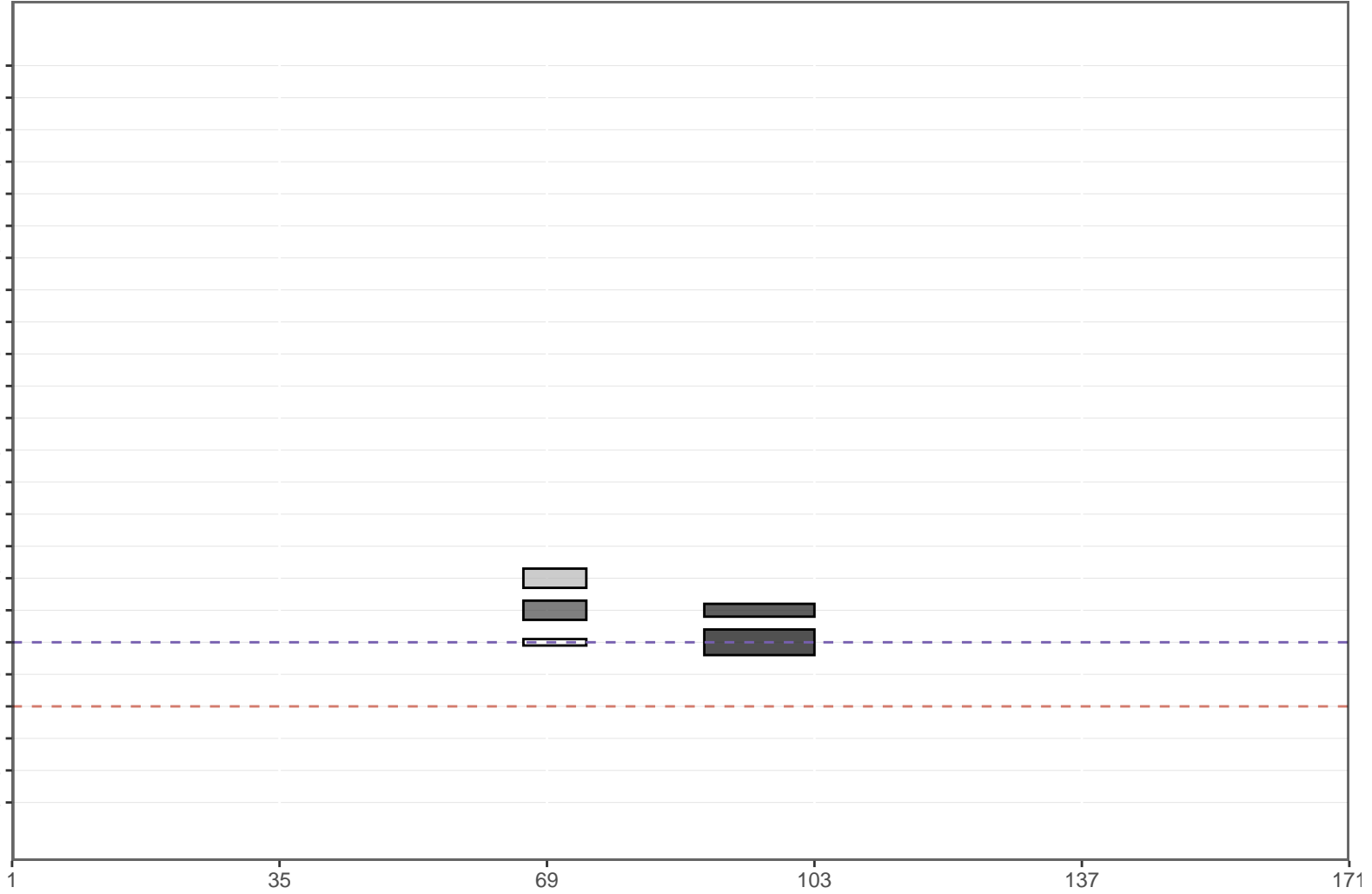
MW indication



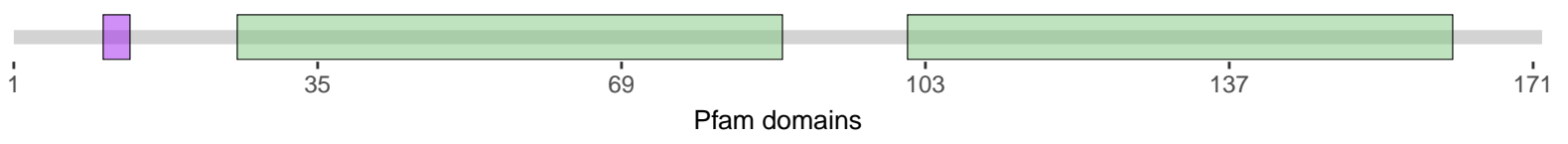
Molecular weight



Gel Slice



Protein length



Pfam domains

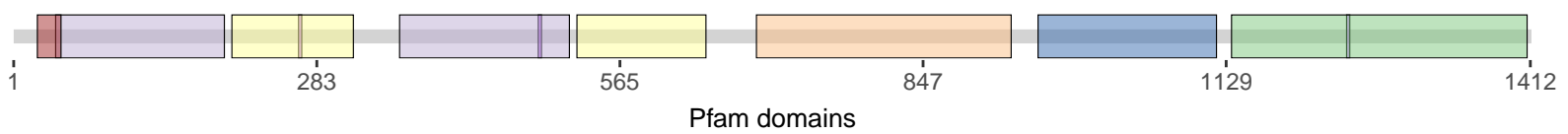
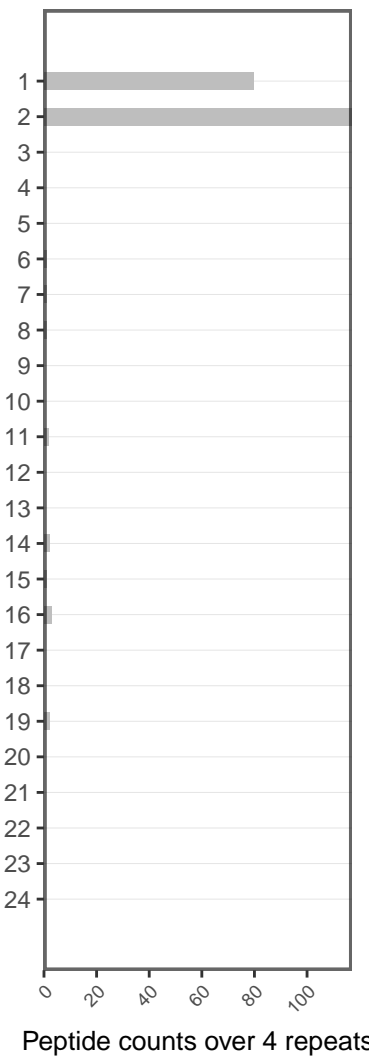
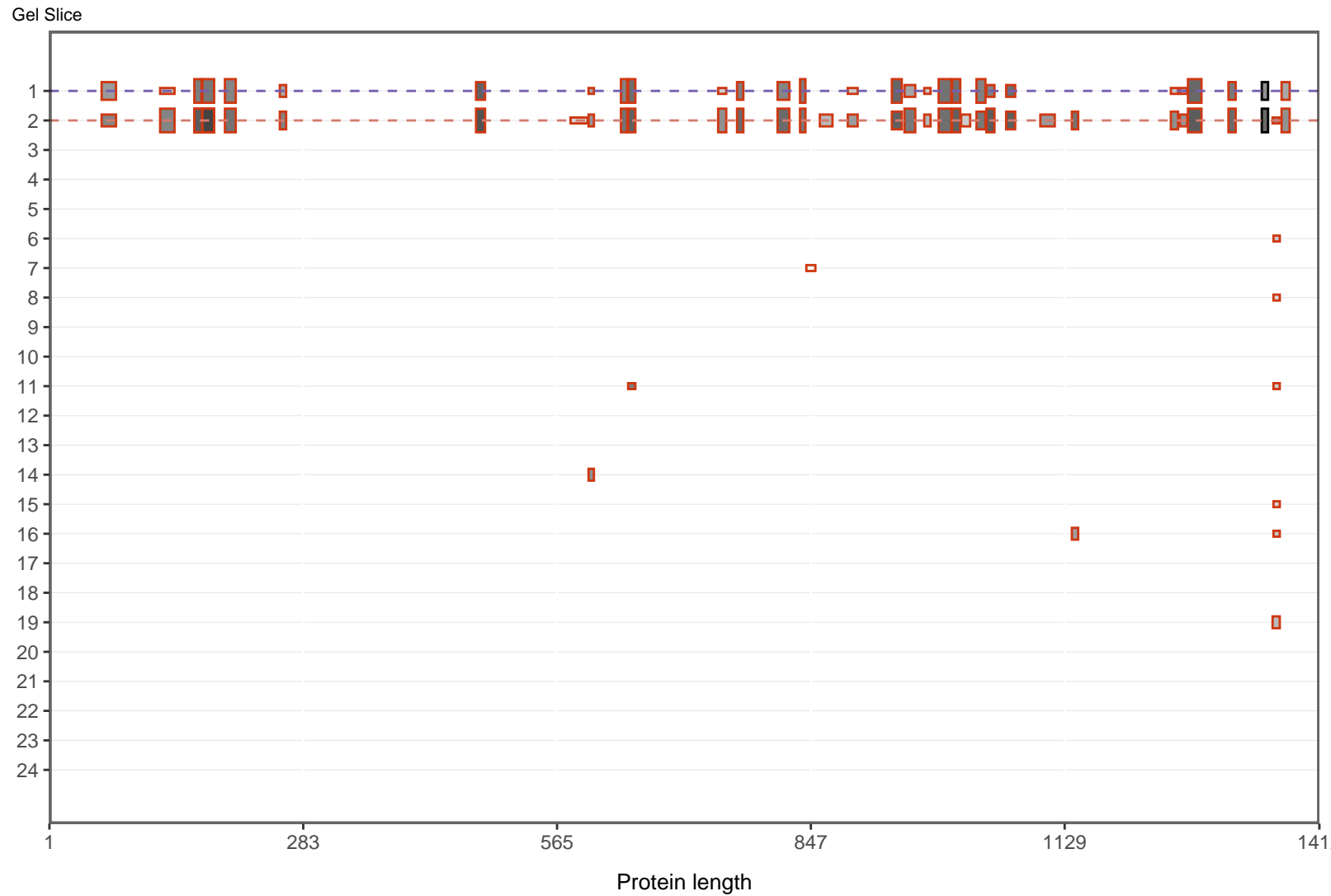
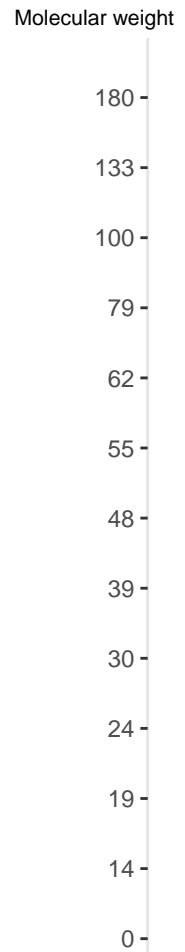
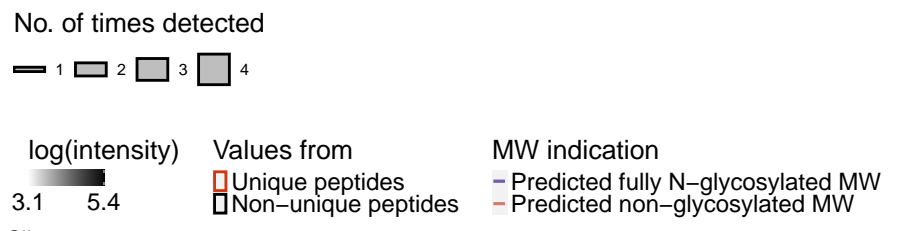
Pfam Description



Protein sequence:

DRDGYNLDFAEFGKGVNGVGGVNEIRAFDLYDGDNNGLISDAELHQILTRLGEGGVGGCTKMISSVDADGGYVVFDEFKMMTNNFQKQ

NbL03g21410.1 uncharacterized_LOC109223953 [MW = 151.74 kDa]



Protein Description

- PF01116 Fructose-bisphosphate aldolase class-II
- PF07005 Sugar-binding N-terminal domain
- PF03446 NAD binding domain of 6-phosphogluconate dehydrogenase
- PF17042 Nucleotide-binding C-terminal domain
- PF14833 NAD-binding of NADP-dependent 3-hydroxyisobutyrate dehydrogenase

Protein sequence:

ILVLDQDPTGTTQTVHNDIEVLTSEWSEVLSVSEPKRKRKPGFFILNRSALTSKASALADIGRINDTAAKSVKADYTVVLRGDSLRGHFPEEADAAVSLGEMDAWILLPFLLGGGRYTGIDHYYADSDRLVPGGETEFKDAAFQYKSNLCEWVEEKTGRIPATGVSSISQLLRGGSPDAVCEHLNENLQKGGSTGIVNAASERDMAVFAAGMGAELKGGHFLGRTAASFVSRARVGVQKSPLENDIGNRERNGSLVVGSVVPKTKTGVEELKLGVGH/LKTIETSYNKVAMI

NbL03g21350.1 geranylgeranyl_transferase_type-2_subunit_beta_1-like [MW = 34.61 kDa]

No. of times detected



log(intensity)



Values from



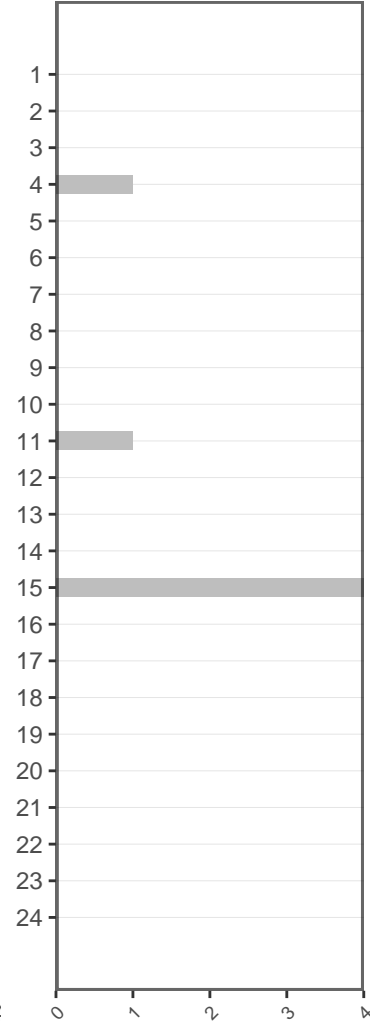
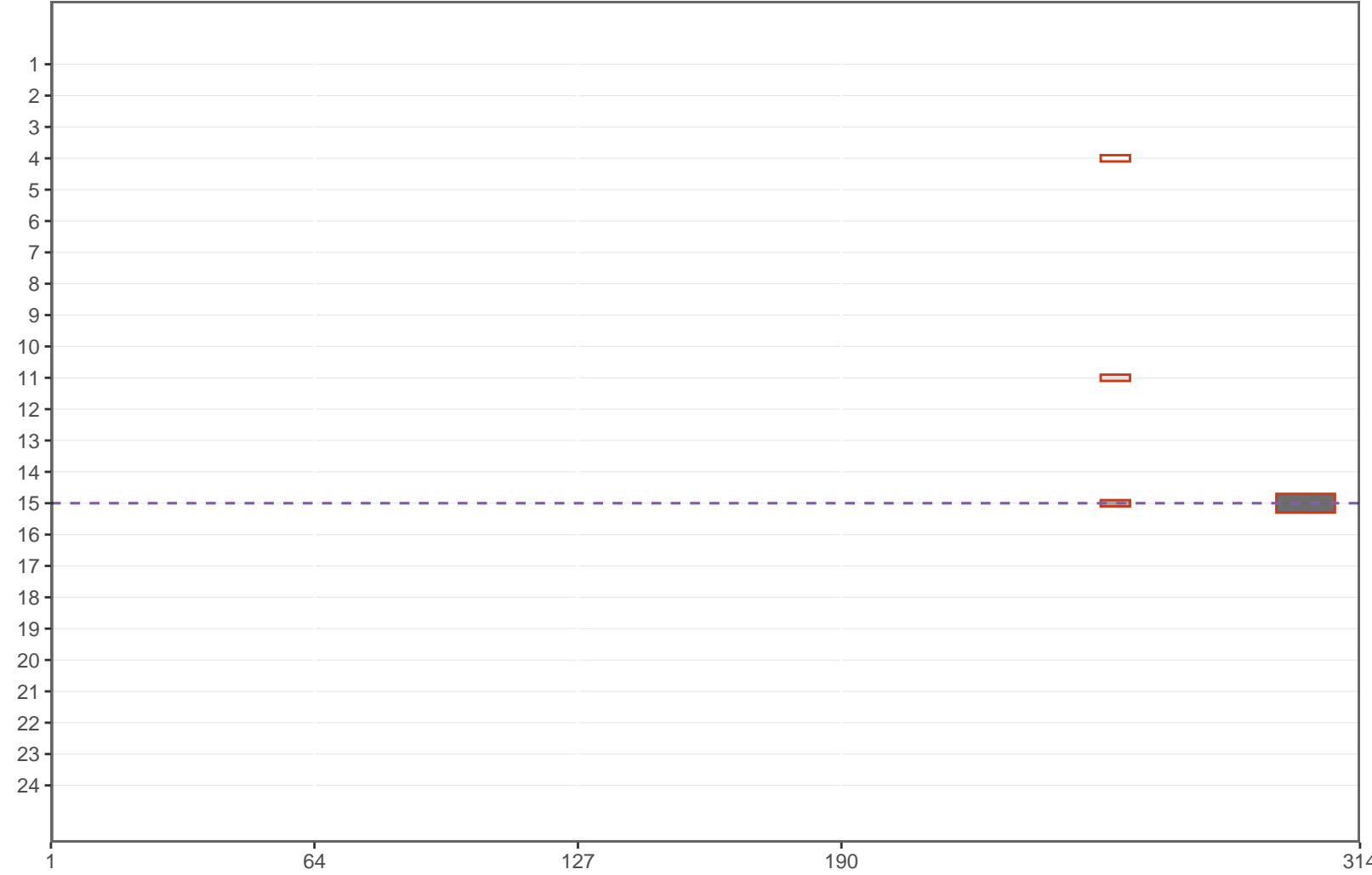
MW indication



Molecular weight

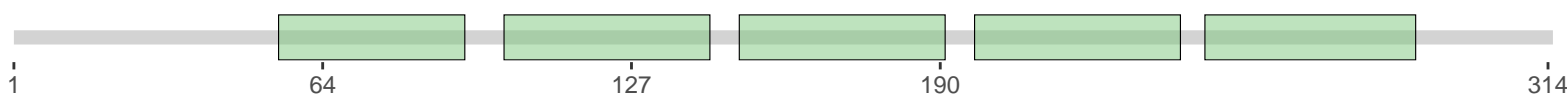


Gel Slice



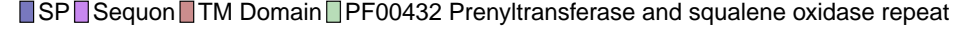
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

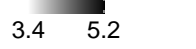
SLDKVYGGKAVYILSDKNVDDGGFGTPGAESHAGGDFGCVAAIATGSLHHVDKDLGWALLCERQVKSGLNGRPEKLPVQCYGVWVLSLIMDRVHWIKGKLVKFLDCGKENGSGISDRPDADVDVFTYFGVAGLSLLEYPGKIPDAVALPVQVNRVILGR

NbL03g21200.1 stromal_processing_peptidase_chloroplastic [MW = 116.49 kDa]

No. of times detected



log(intensity)



Values from

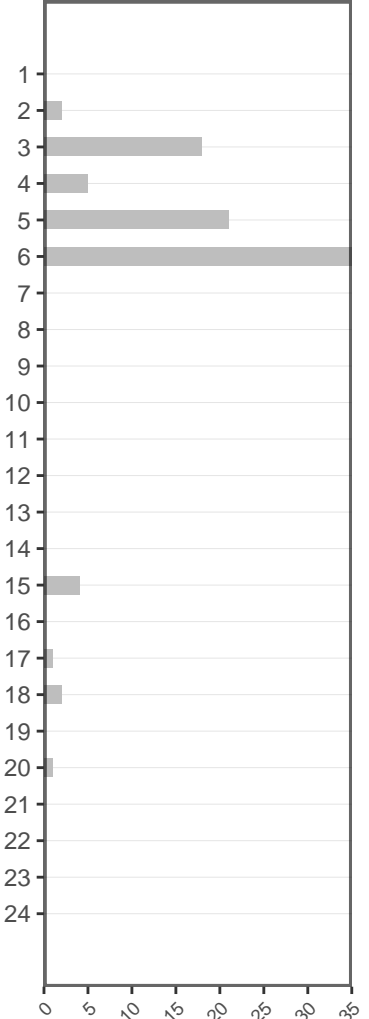
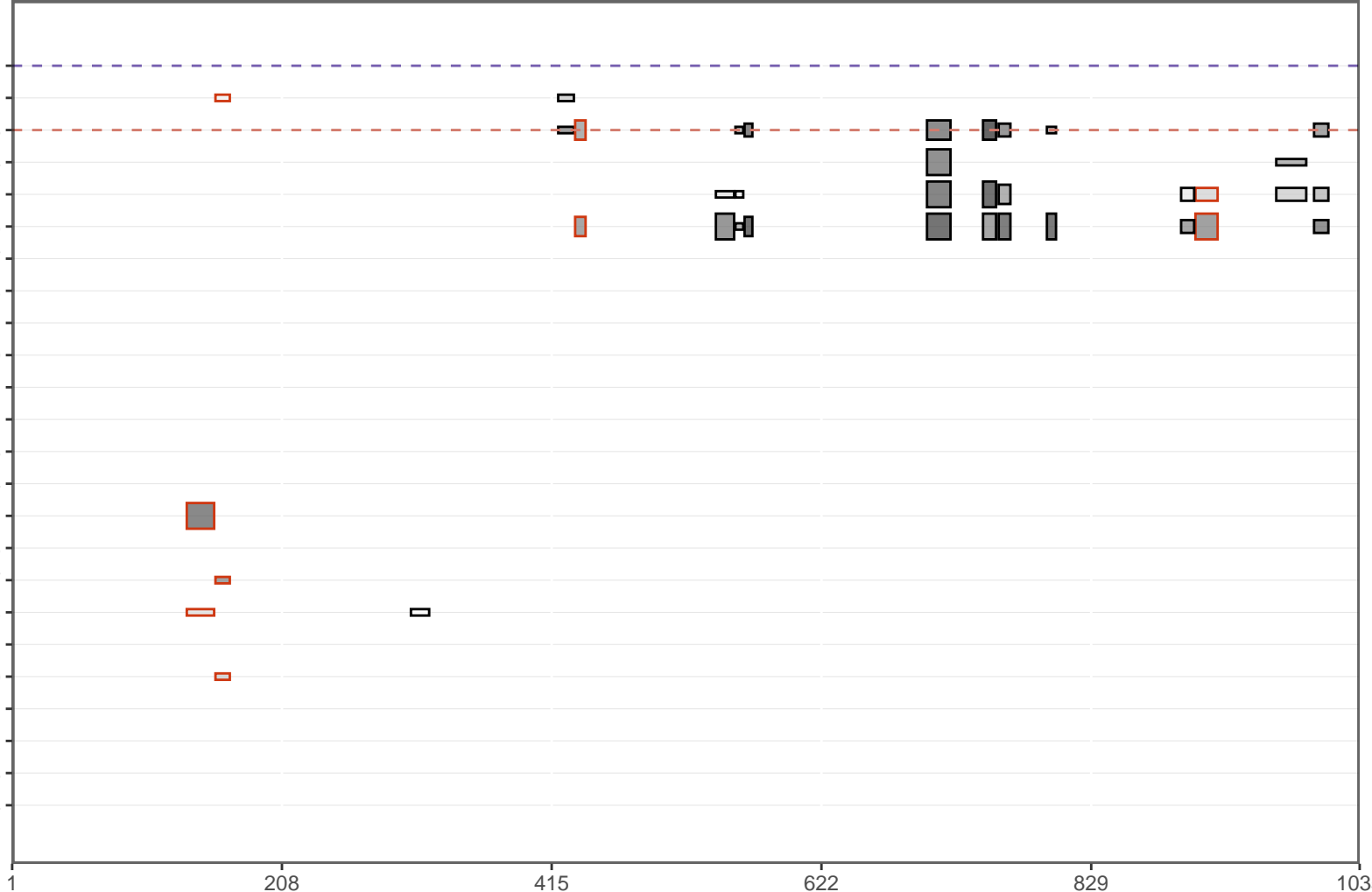


MW indication



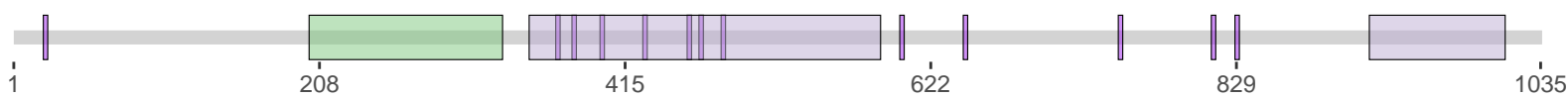
Molecular weight

Gel Slice



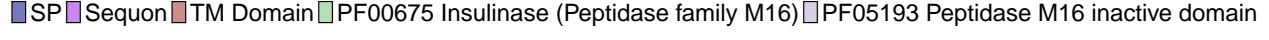
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILVMKRFLSALHFRINTRYKSNFPFTVELHSDSGREGGTVTLFVTAEPKNWGNVAWVQVEYRRLKKEFGVTKGELARYTDALKDSEQLAAMDNVSGVNDLDFVMESDALGHTVMDQRRGHEGFLAVAGTITLVEVWATGAEVLEVISDFGKPSALPLAAVAQVPSKVVHYEGGGSEAEFRISPEEFTTAMISGLKESIEPEPELEVPTELUTSKGLEELRLKRCPSFVPAVNSDITKEVDNETGVQRRLNGIPNKKTKNEANGVMRLVSGGAAEESHEKGSVYC

NbL03g21010.1 uncharacterized_protein_At4g14100-like [MW - SP = 22.88 kDa]

No. of times detected



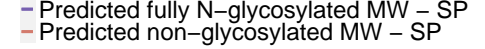
log(intensity)



Values from



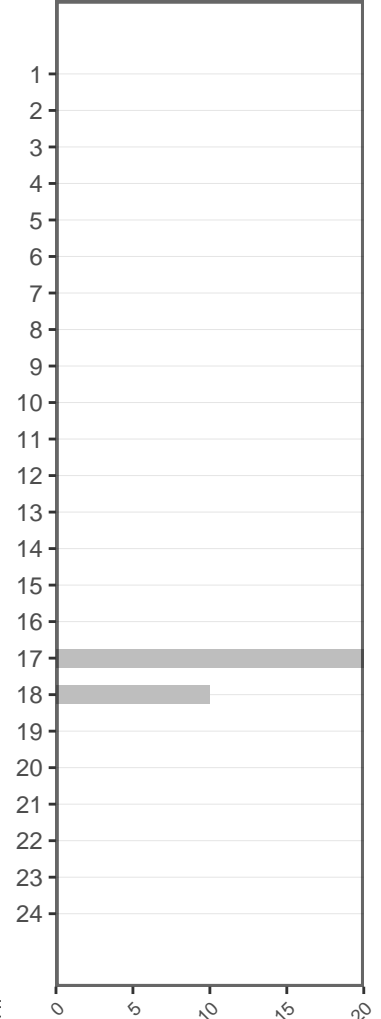
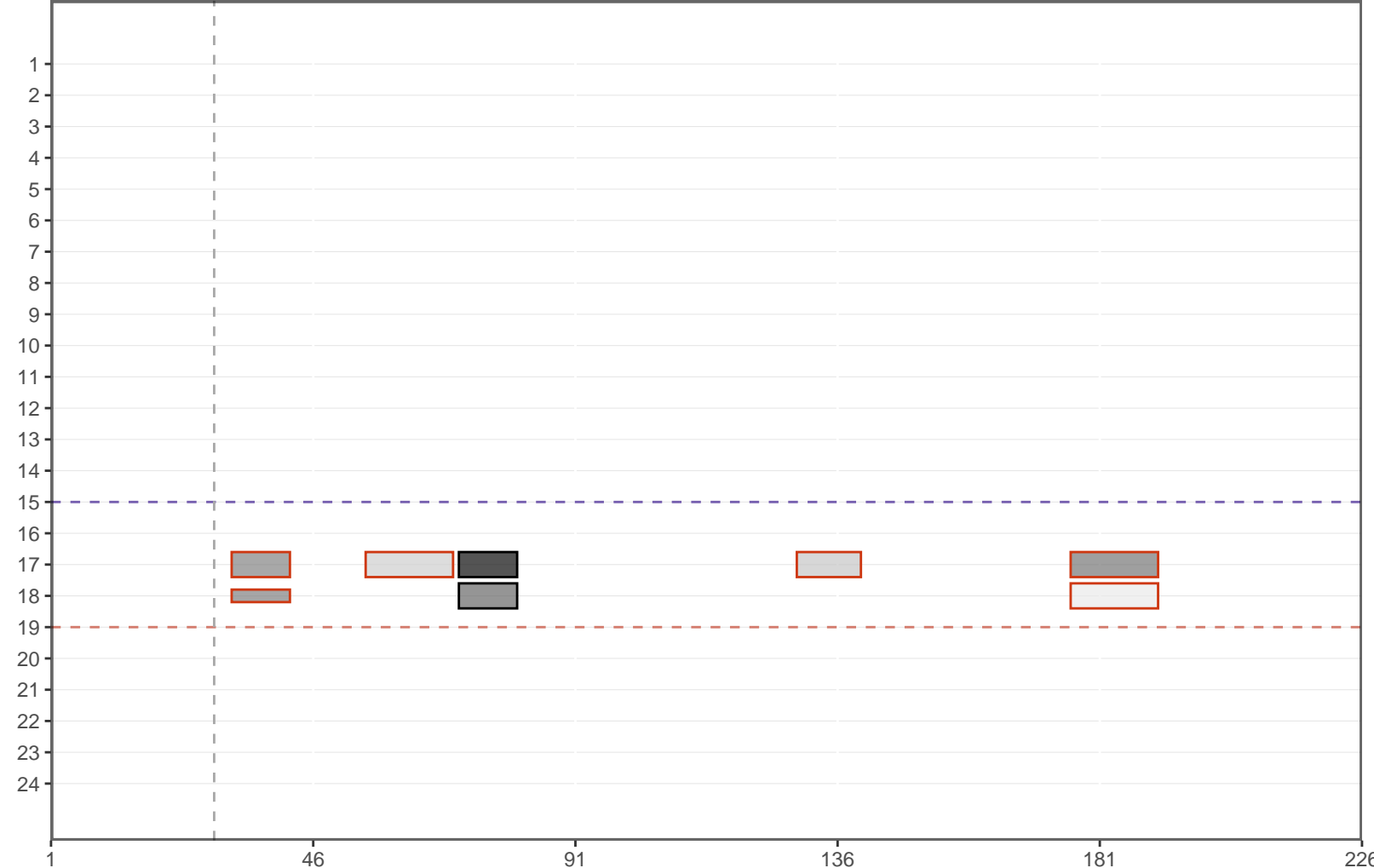
MW indication



Molecular weight



Gel Slice

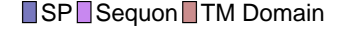


Protein length



Pfam domains

Pfam Description



Protein sequence:

ECRVMHFPVGLRPNALGGKYLGGRYMDGLGNWEKDFRWFYVEDIVTKRPLVYAFFTGMIANHMTFEVGVKLEDPNWGAPVYGFNKALEGEKSPVIEIENLGLDAEVSRLMGSVVDVSELLL*

NbL03g21000.1 succinate_dehydrogenase_assembly_factor_2_mitochondrial-like [MW = 21.03 kDa]

No. of times detected



log(intensity)



Values from



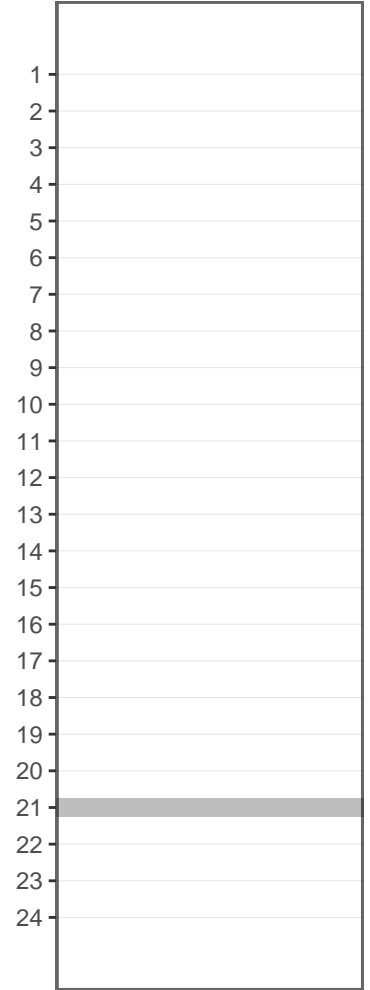
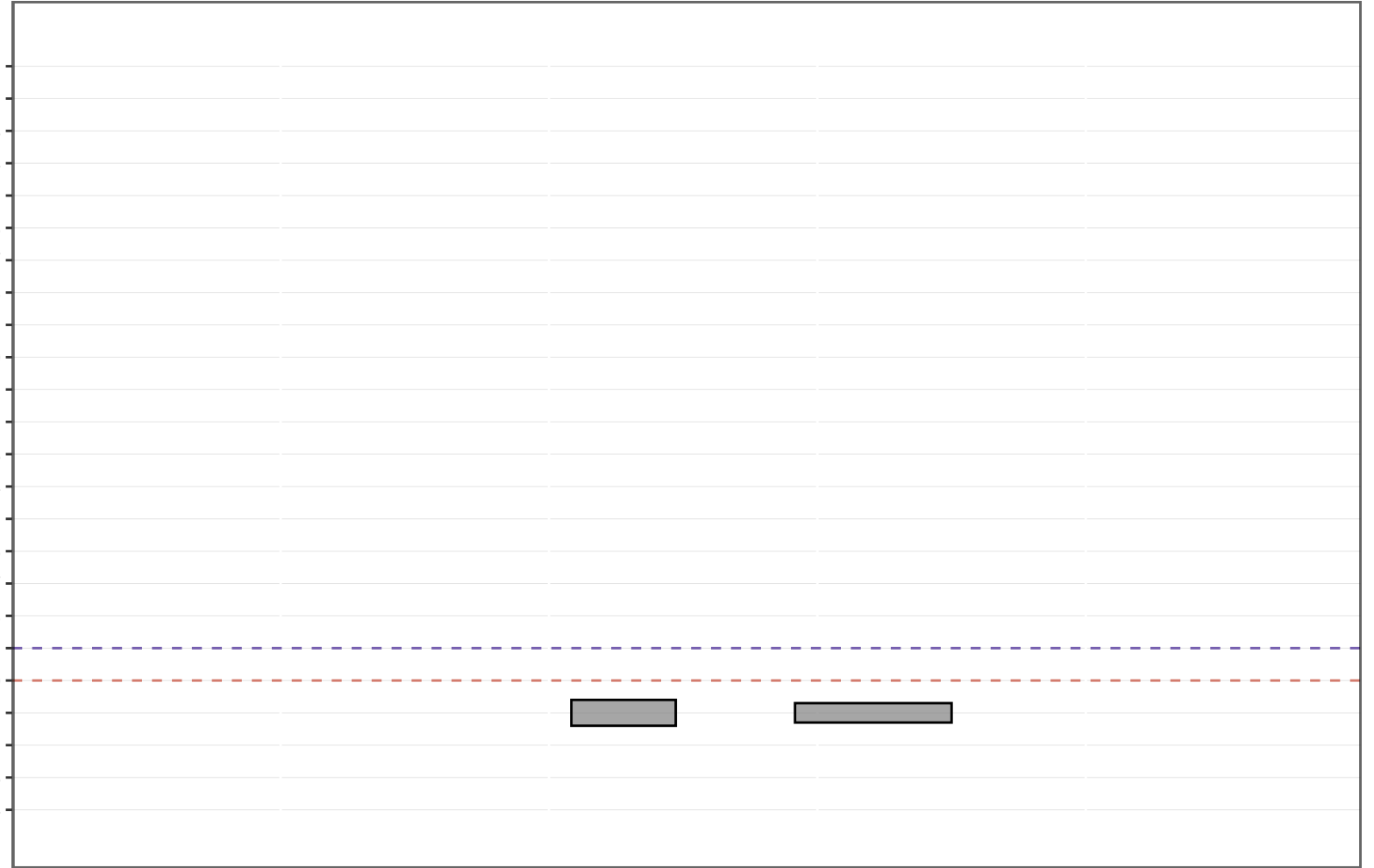
MW indication



Molecular weight



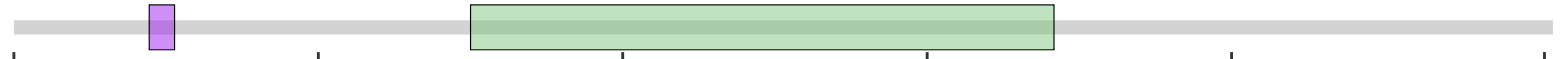
Gel Slice



Peptide counts over 4 repeats

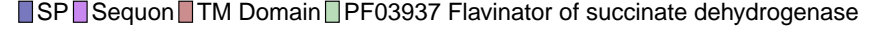


Protein length



Pfam domains

Pfam Description



Protein sequence:

EHQSMDENGKFLVHYLDGEPDIIWALTGGEOPPDIAISTNPVFSVAVREKVINNLQKHSFETRLFLFNGLGLEDGMSREVMRVLLEIGRSFYCWAEAKNI

NbL03g20930.1 ribonuclease_TUDOR_1-like [MW = 107.67 kDa]

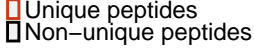
No. of times detected



log(intensity)



Values from



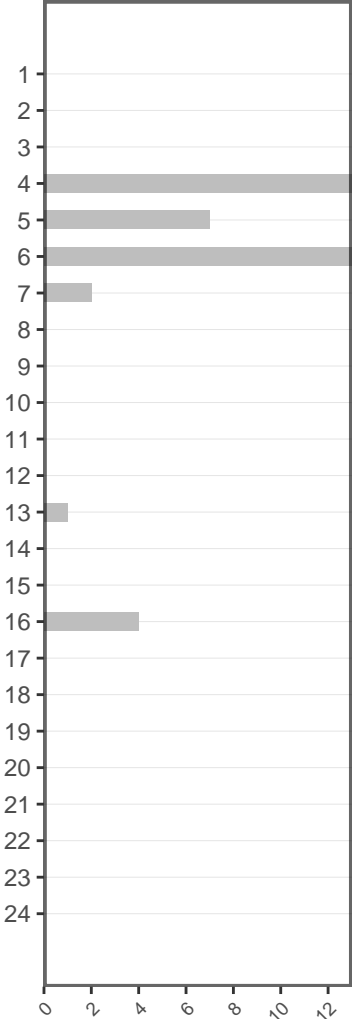
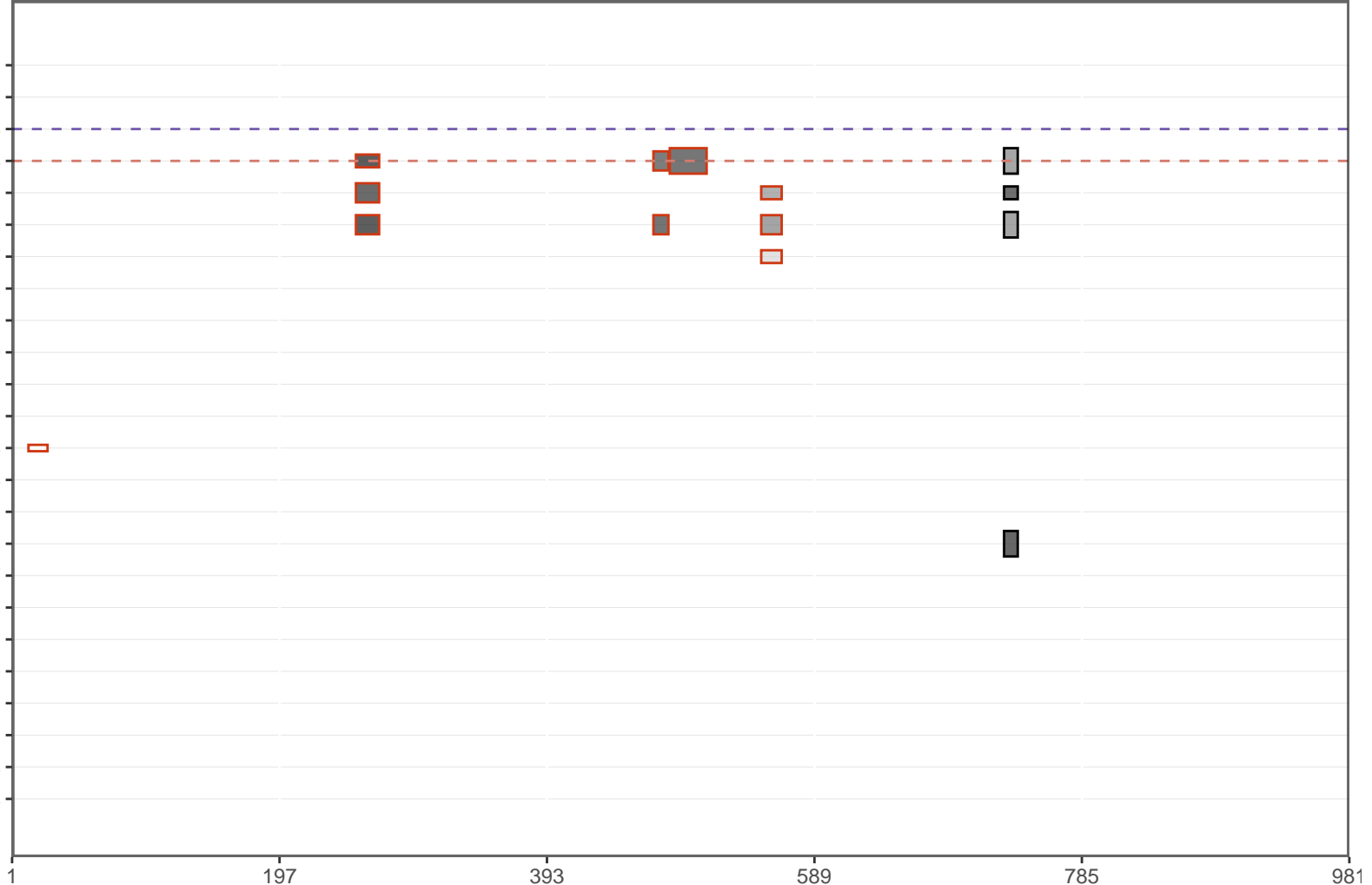
MW indication



Molecular weight



Gel Slice



Protein length

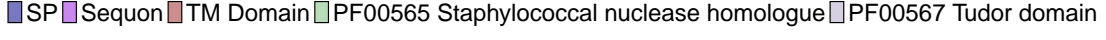


Peptide counts over 4 repeats

Pfam domains



Pfam Description

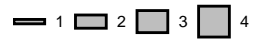


Protein sequence:

FLASKGGDDASPLPAAAGNGLAGVWAEELVGRGFATVVRHRDFEERENYVDALLSAESRAISGKKMGHPKPEPLVHTDLLAGSAKKARDFLPLQNRNRMVAIVYVLSGHRFLFKPKETGSAFBSISGVRGPGRDEPFVSEEAALMRKRIMGRDVEIEVETVDRTOFTLGTLWESRENWATLLEAGLARLQISFGTDRIGDAHLLMQAEGAAAKRQKLKVVWENYVEGDEVANGGAAEKRQKEEVKVTVEVLGGGKFFVQLVSDGKVAANKQLASLHLEQAPVGA

NbL03g20890.1 respiratory_burst_oxidase_homolog_protein_C [MW = 105.92 kDa]

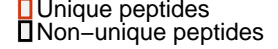
No. of times detected



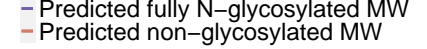
log(intensity)



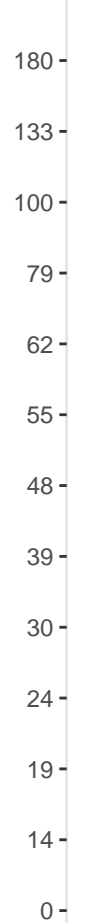
Values from



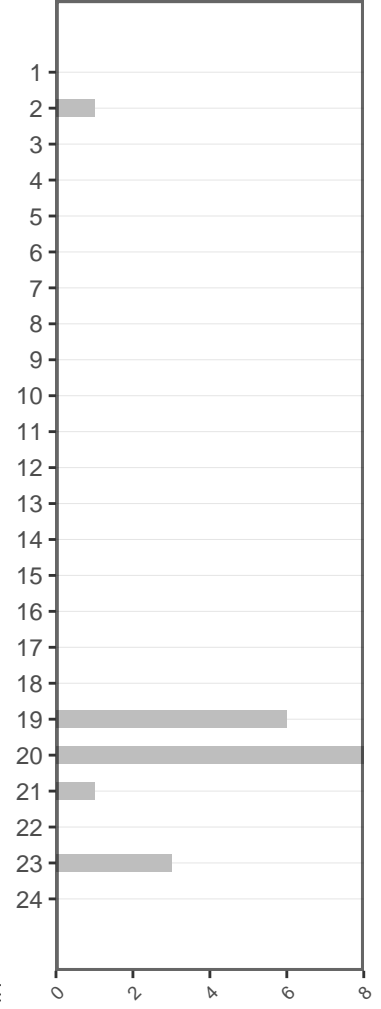
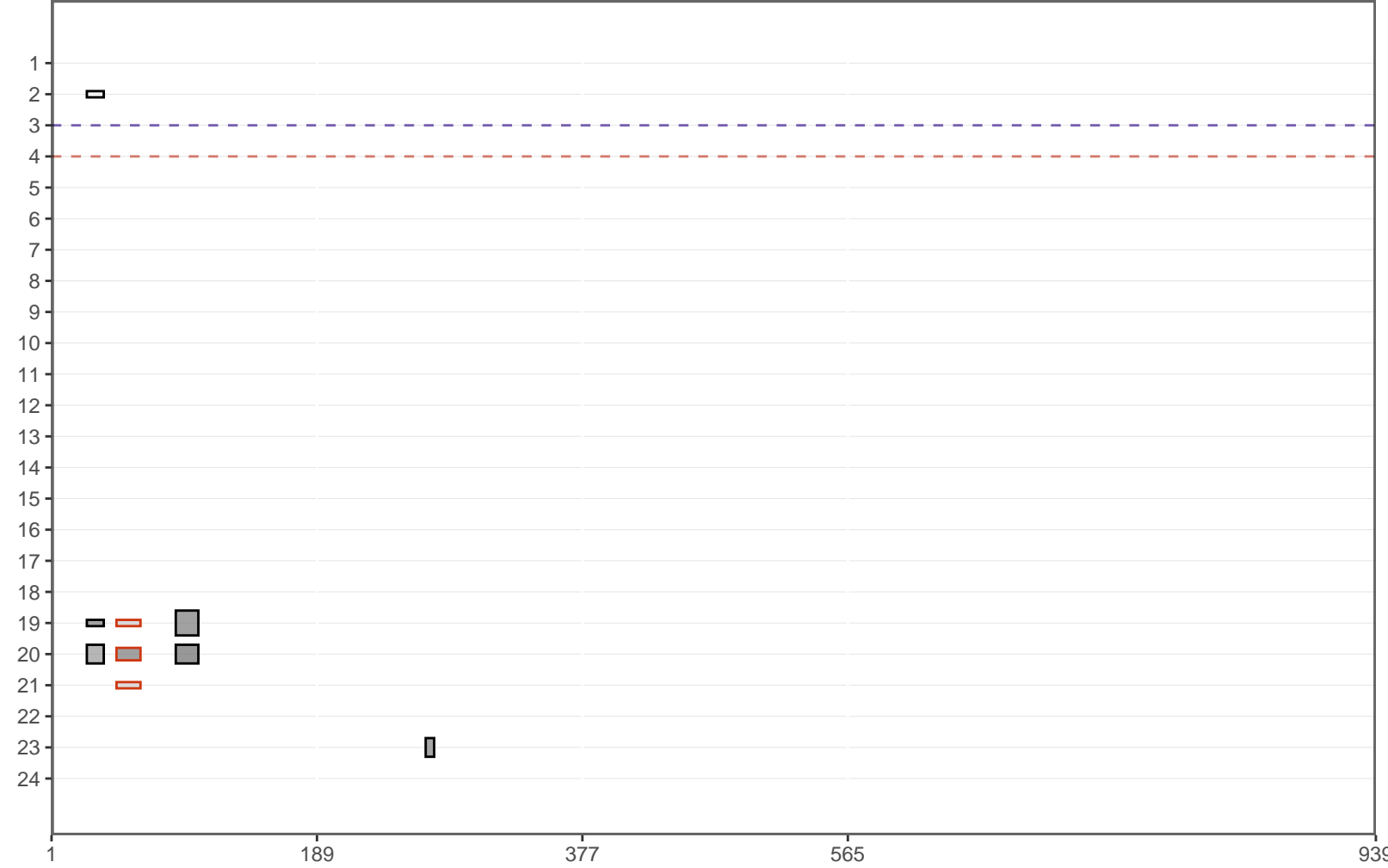
MW indication



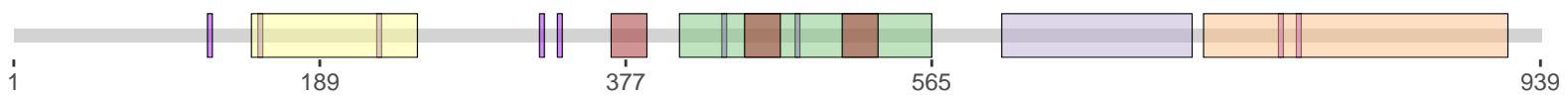
Molecular weight



Gel Slice

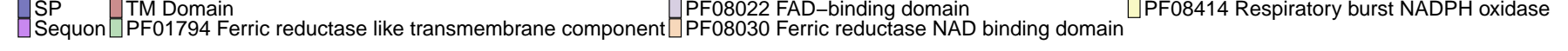


Protein length



Pfam domains

Pfam Description



Protein sequence:

MAAALGVGVHQLSRLTGDFFRLLNASEEEVEFMKYYFGDQPEGWVFRKGVGVGTQIMVYLMAAFLATPWFRRNRVSLPKPHKLTGFNAFWYSHLFFVIVYTLFVHVGKELVTKDWWYKRTTVMYLTPIIYASERLIRAFRSKIKAKILKVVYVPGNVALAHMKGPDGYYKSGQVMEVNDAAVSPFEVWHPFSITGAPGDGVLSEVHIRTLDGWRTRGLKTVFSEVCGPPFPNGKSGLLRADHLOGENNPFRVLDGPGYAPAGDYYKVEVLLWELGIGATPMSIVKDI

NbL03g20860.1 U2_small_nuclear_ribonucleoprotein_A'-like [MW = 32.63 kDa]

No. of times detected



log(intensity)



Values from



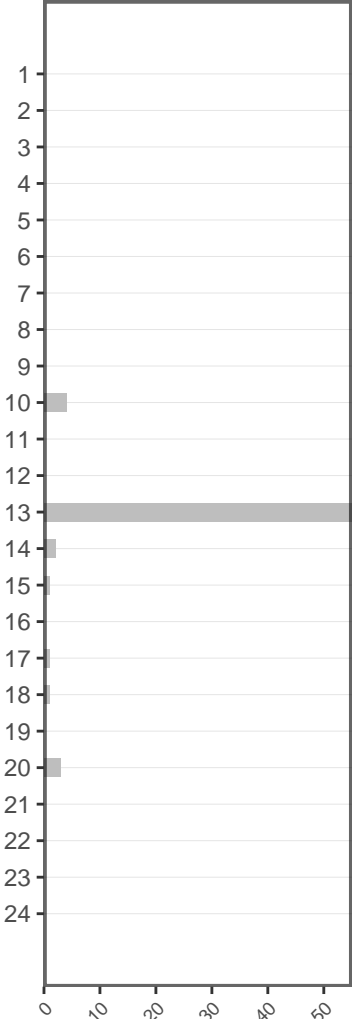
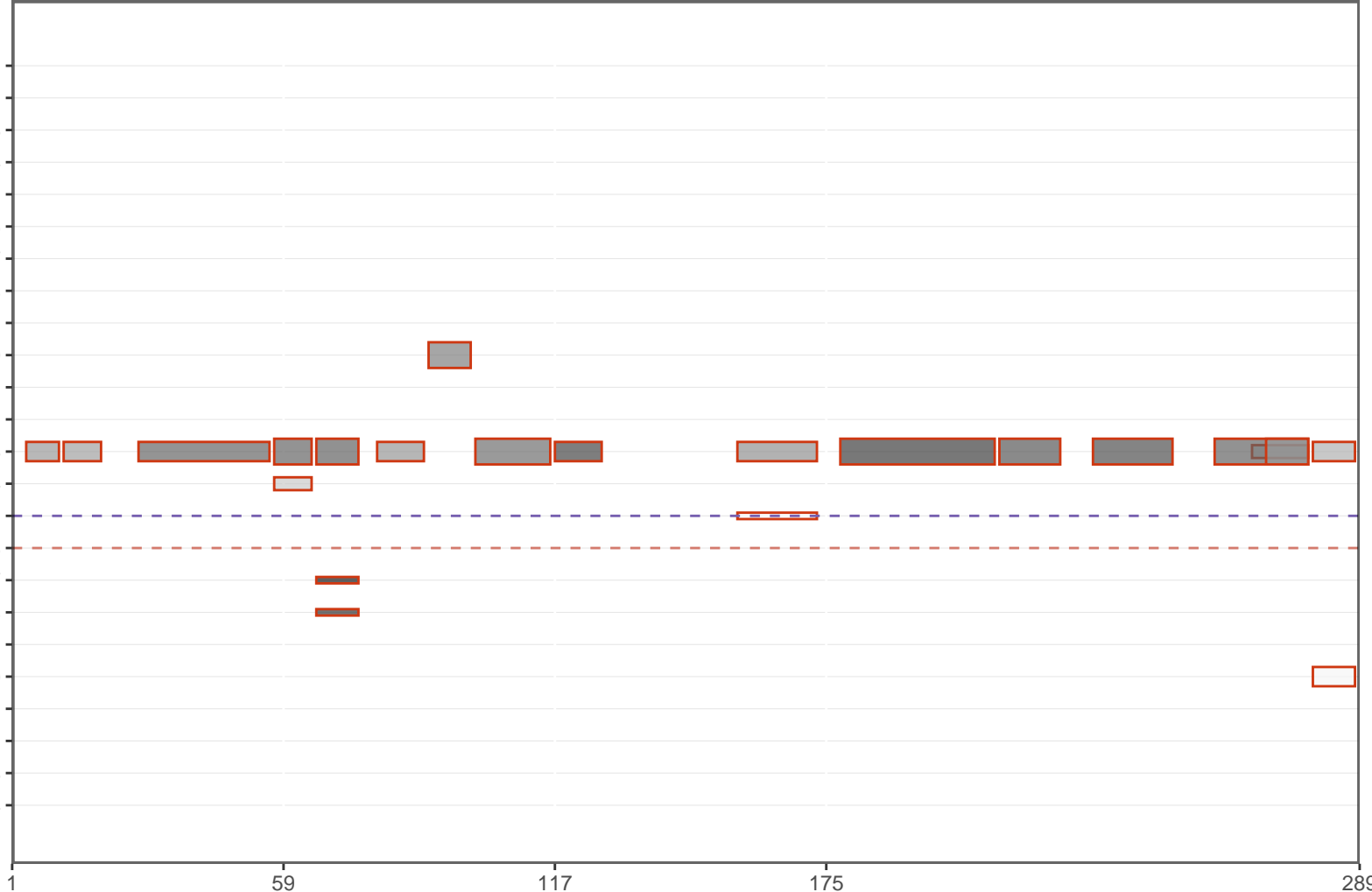
MW indication



Molecular weight

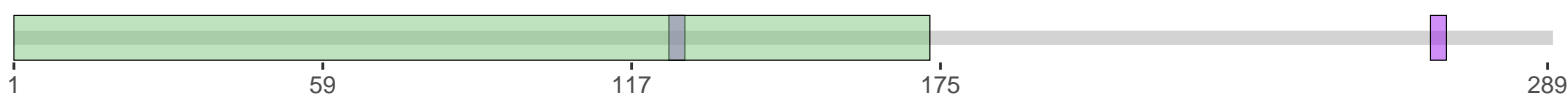


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YVHKLSRLLDYFRKVGKERLEASNFASEEAEAEKKEGVKTEVPGEVPAAPPEERKEDAEAPKPAAPTPPEQIAKAAVINGDTLEEVARLEQALRGGQLPADLNIGDYDAKKEKEDAKEDNMVTDGDDKANKTEENPEQKTDGPTDMEQE

NbL03g20830.1 ACT_domain-containing_protein_DS12_chloroplastic-like [MW = 31.04 kDa]

No. of times detected



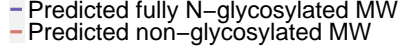
log(intensity)



Values from



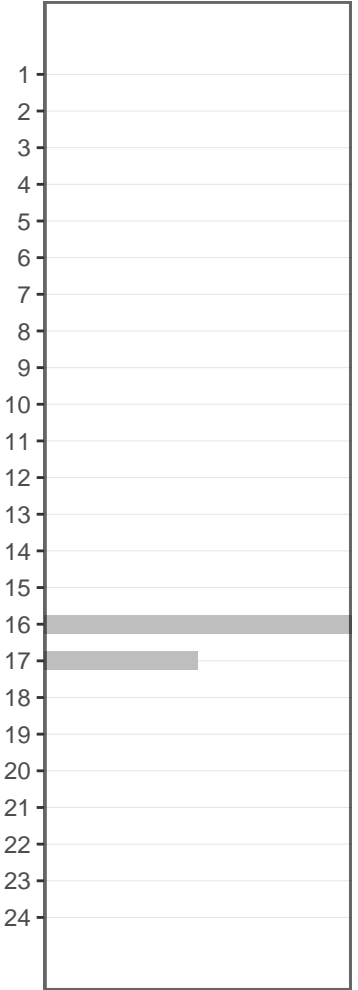
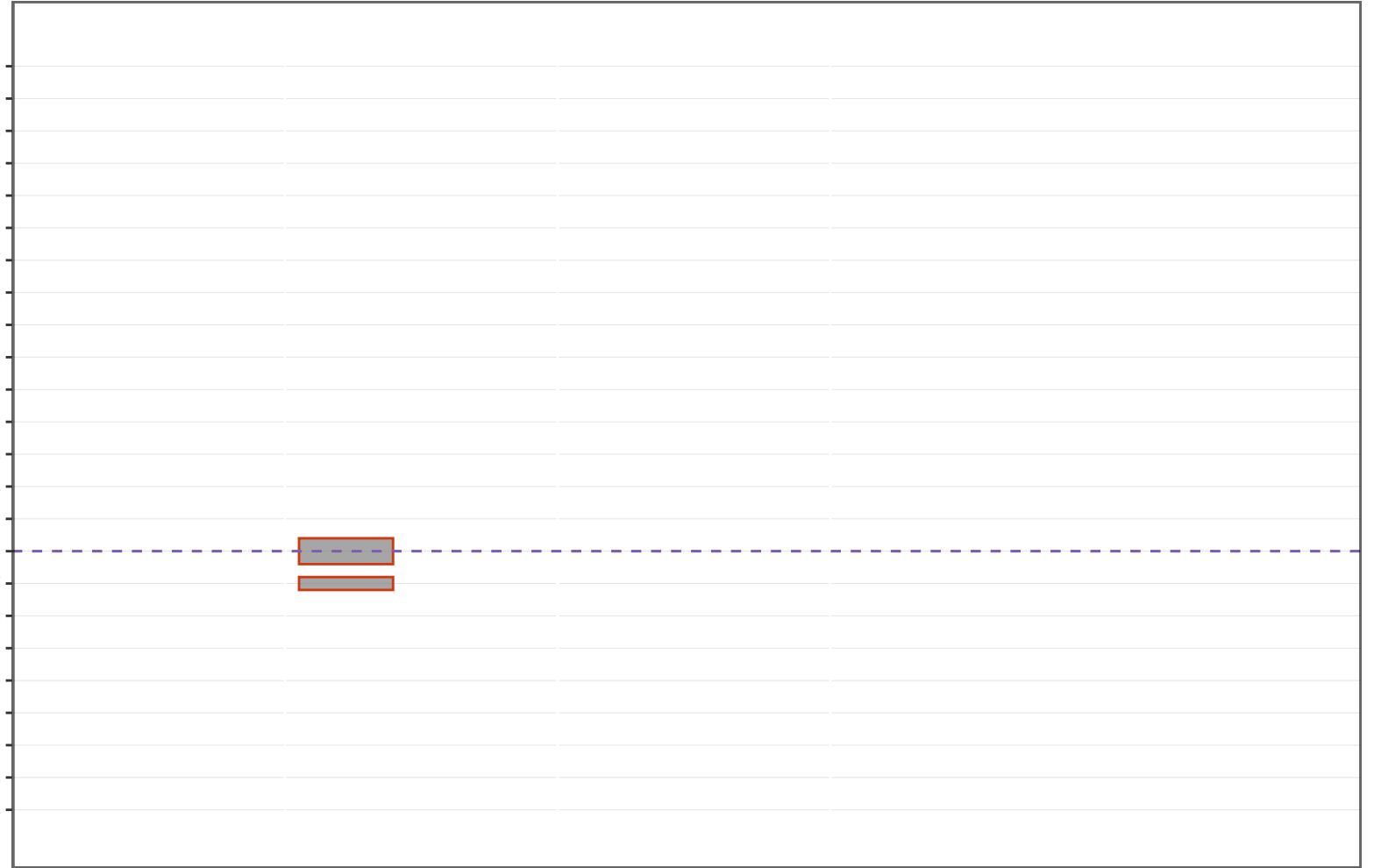
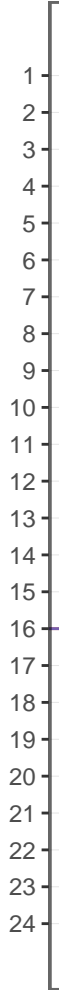
MW indication



Molecular weight



Gel Slice

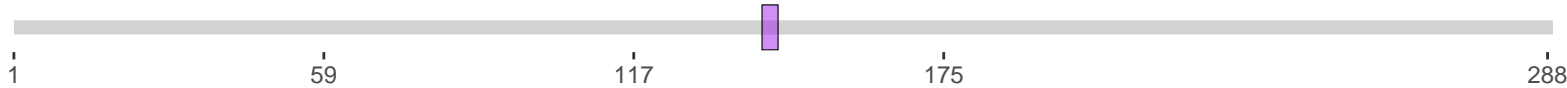


Protein length

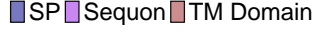


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

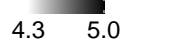
ISGKHTLCTINASTGRKVDPEGLEAIRLTHINMIEFHPSSAGLAMGEVFGAYQFNKLDVDATHHVVYDDGPDRLVVEAADRPGLVDLWKHTEINDVESGEFTEGLLAKAKFHVSYNNKALIKPQQVLANSLRYLRRPTTEESF

NbL03g20820.1 4-coumarate--CoA_ligase_1 [MW = 59.56 kDa]

No. of times detected



log(intensity)



Values from



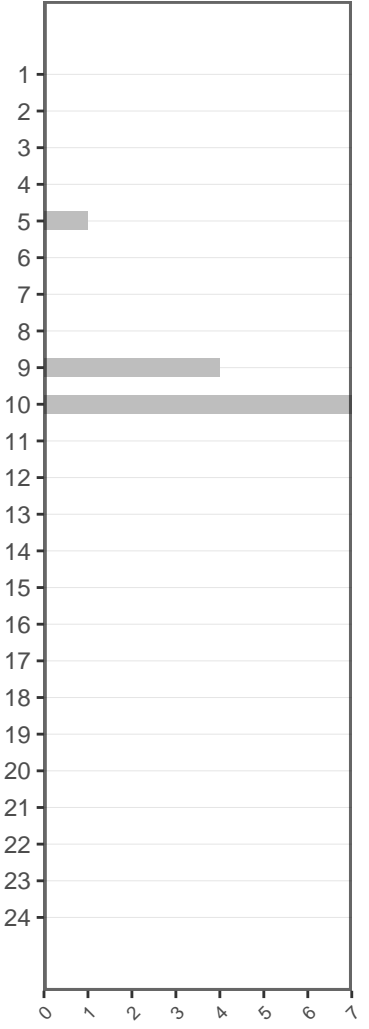
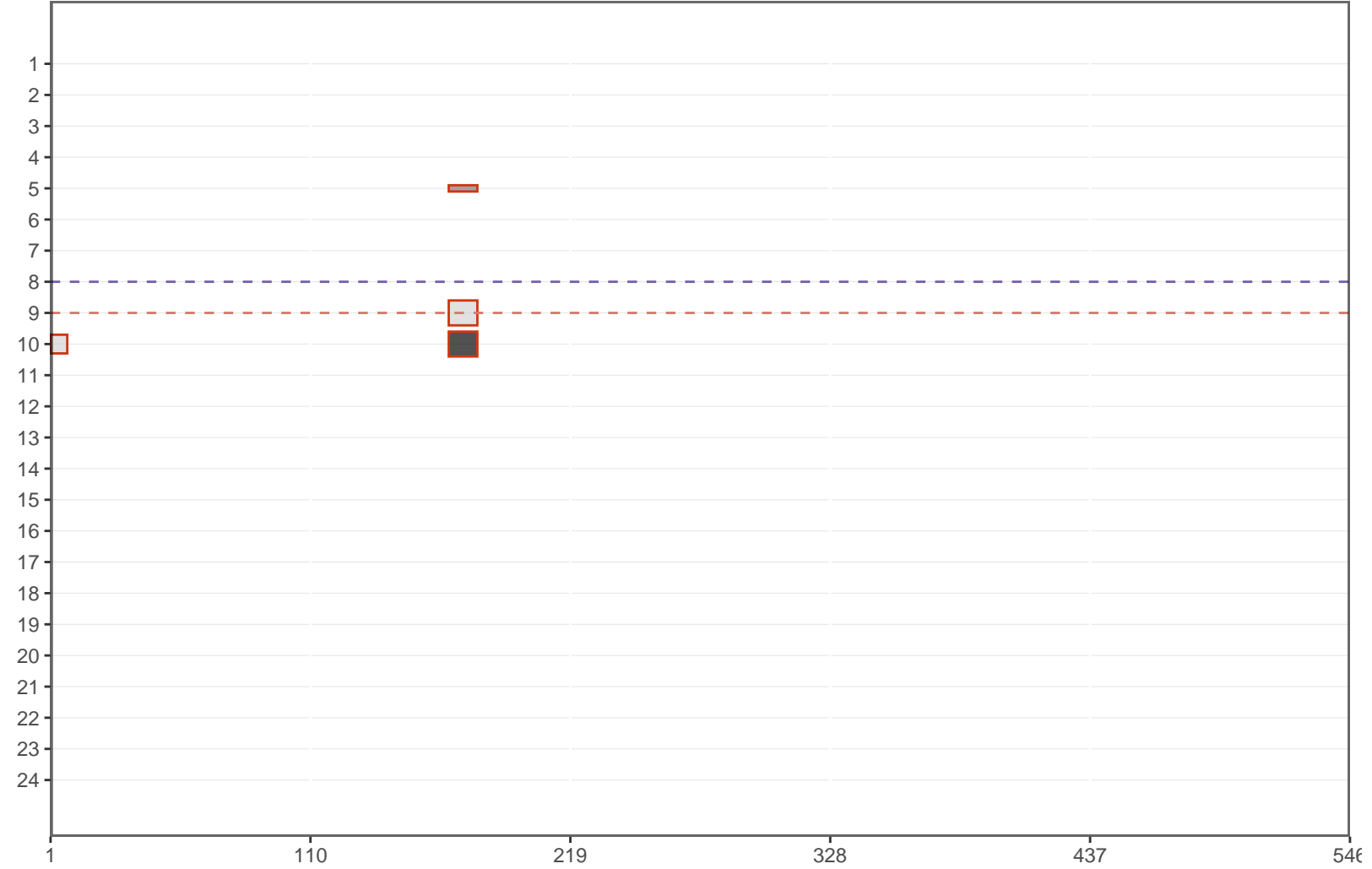
MW indication



Molecular weight

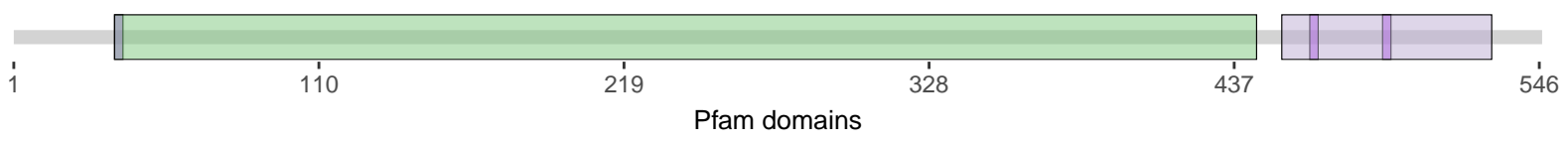


Gel Slice



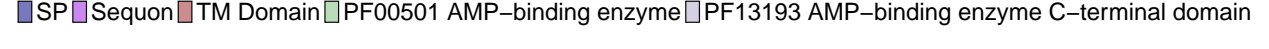
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

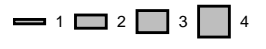


Protein sequence:

QKFDAPFLLELQKWKVSGPEVPPVLAAKSPVDSYDLSSVRTVMSSGAAPLQKLEDAVRRKFKKAKLGGGYSMTAGPVLAMCLAFANEKFDKAGAGSTVVRNAEMKIVDPDTGGSLRNPQFGEIGRGGDMKGYLNDPEATTRIDKEGWLHTGDGFDDEDELFDRLKELKIKYGFQVAFRAEIEALLLNHPNBSAAVVFMKDELAGEVPPVAFVRSNGSATEDEVKDFVSKGVVFEYKRVKRVFVETVPKPSGKHLKDLRAKLAAGVPI

NbL03g20730.1 ubiquitin_receptor_RAD23b-like [MW = 39.28 kDa]

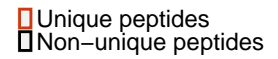
No. of times detected



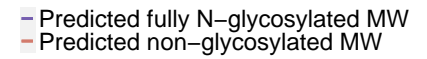
log(intensity)



Values from



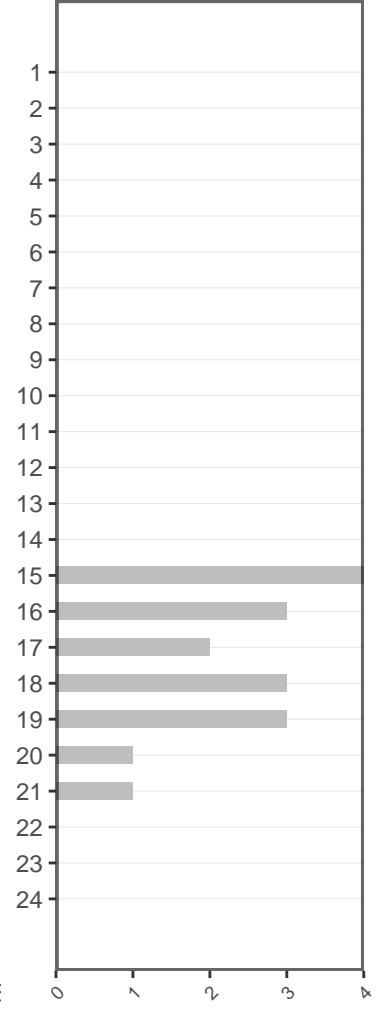
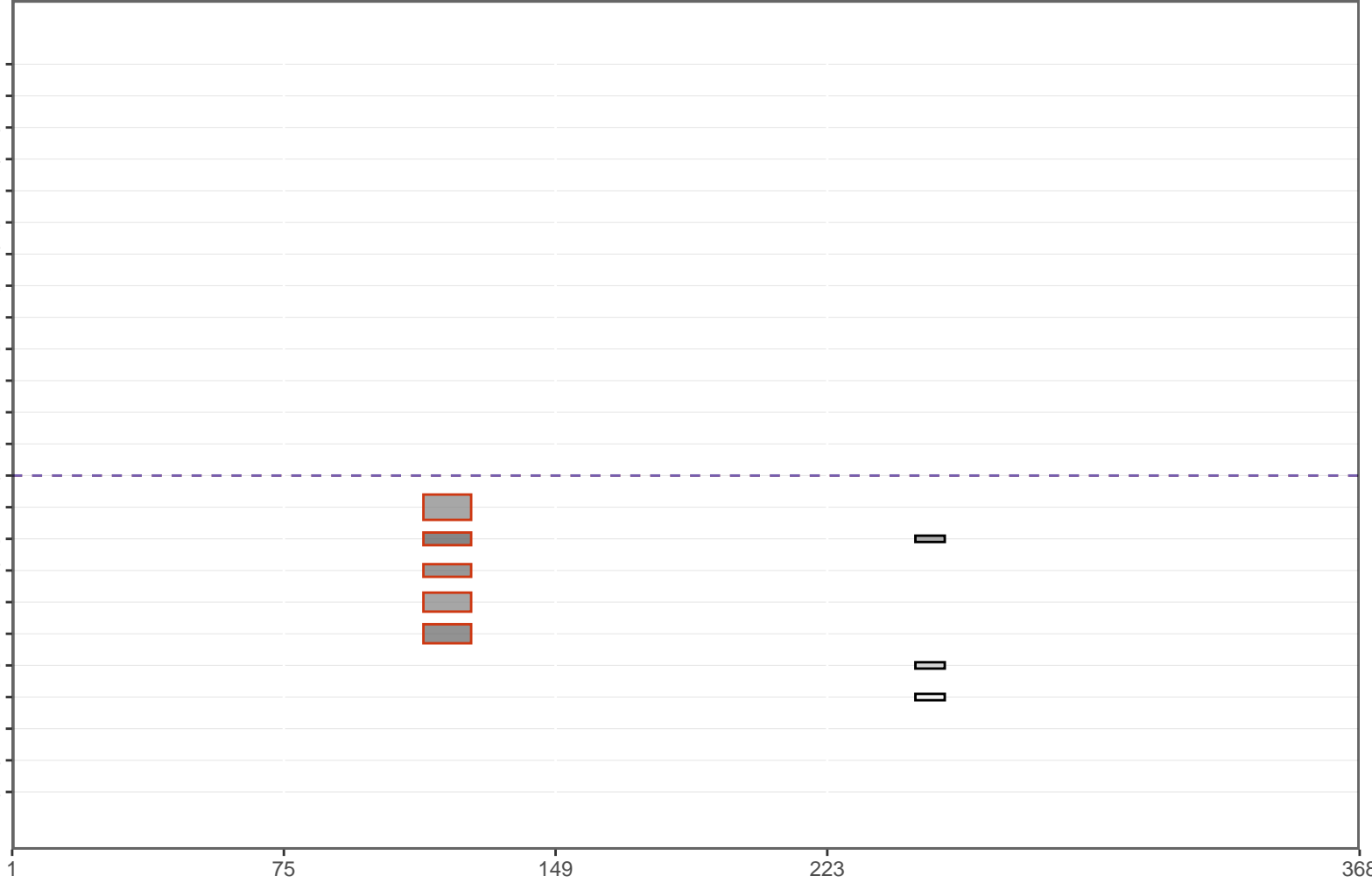
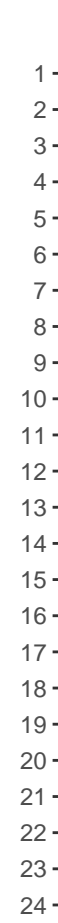
MW indication



Molecular weight



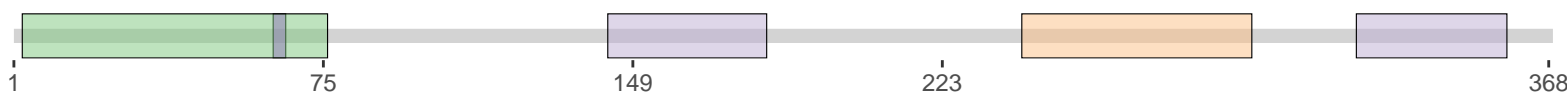
Gel Slice



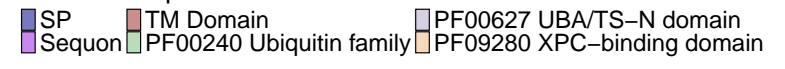
Protein length



Pfam domains



Pfam Description



Protein sequence:

YNNPERAVDLYLSGIPETAEVWVPAWHGGVNSAAGTAAPTAPSSGGPNSAPLNLFQENVAGAGGAGLGLSDFLRNNGQFQALRSMVQANPQLQPMGLGELGKGNPOLLRSIGEHGDFLQLNEPVMHSGEDFDHAEQGEIPHTVSVTPPEQAVIERLEAMGFDRALVIEAFLAGDRNEELAVNYLLEHAGDVED

NbL03g20680.1 uncharacterized_LOC107804369 [MW = 33.66 kDa]

No. of times detected



log(intensity)



Values from



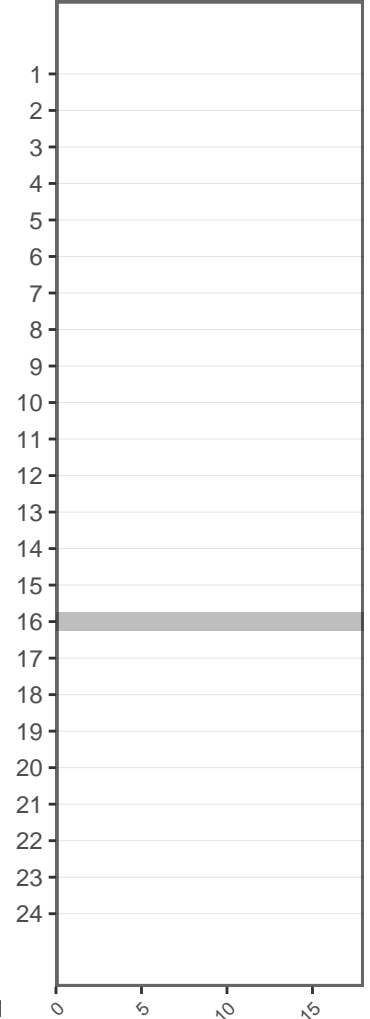
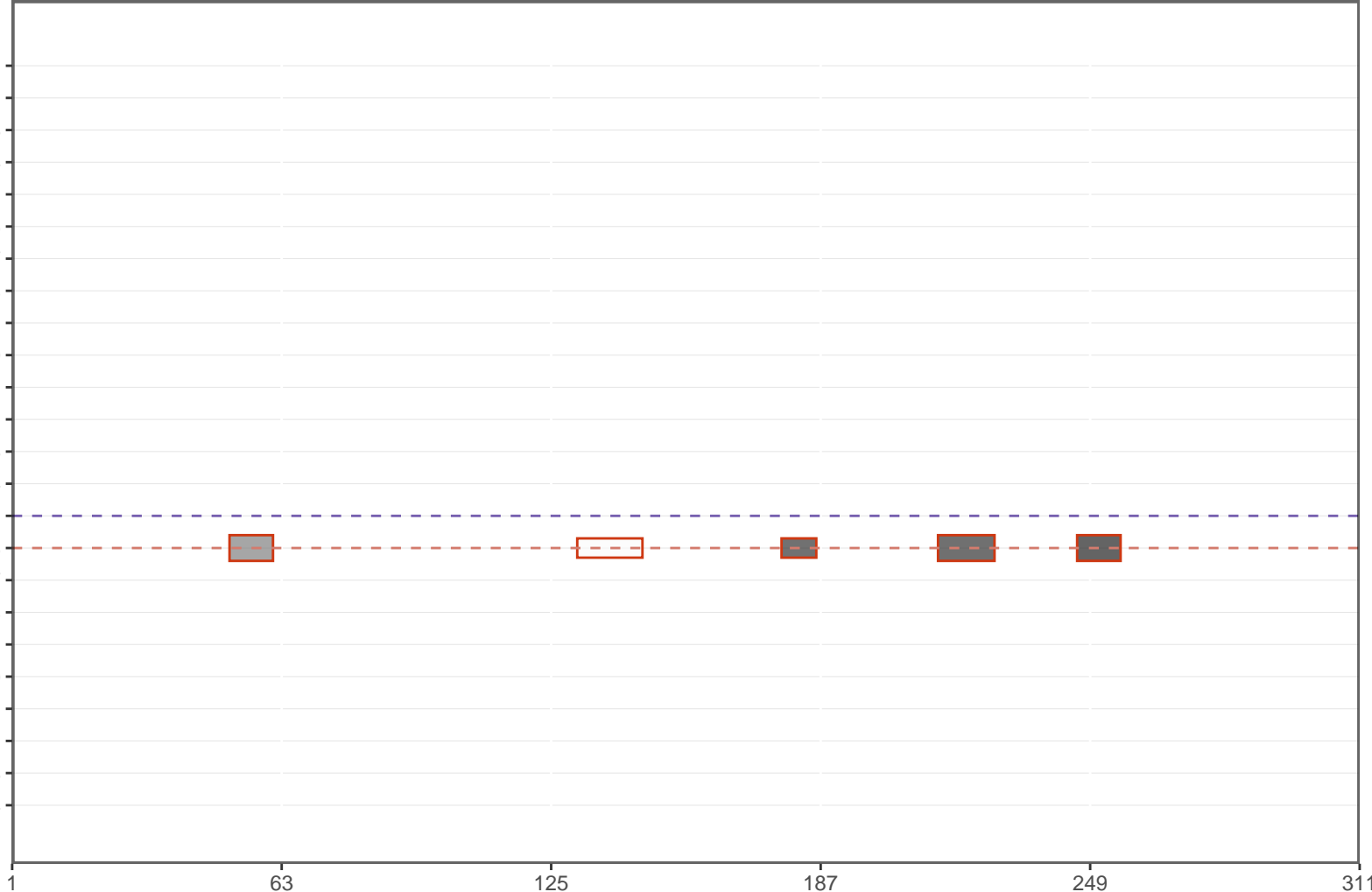
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

VSKLGEPPDQKTDNPEGLTAAYGKWBAAWRLQAGLSGKVKLEKFPQKMLEKIWIGAFMLVGARHPGATVGAWEVEEYRSEVSGLIAELAAAAAEKGLVFEEAMEDRLGAYSRVAHFPTAVKEFKWRNGWYFSLSEKIAEKGKPDPLHTAWLKEKLV

NbL03g20580.1 heat_shock_70_kDa_protein [MW = 71.92 kDa]

No. of times detected



log(intensity)



Values from



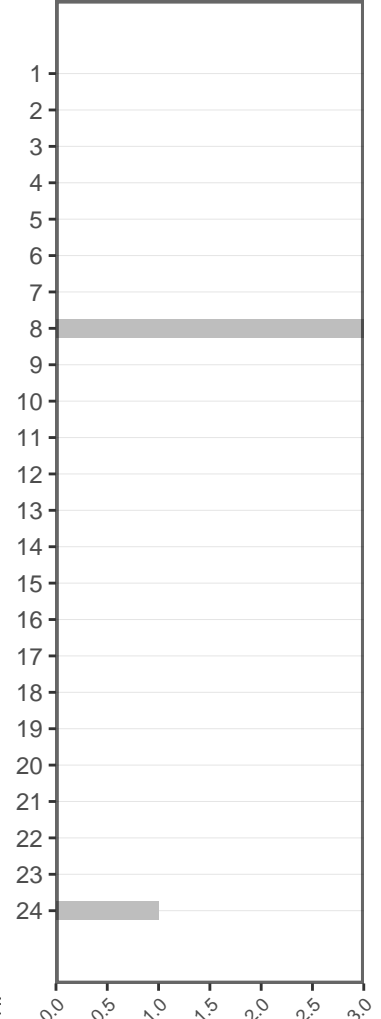
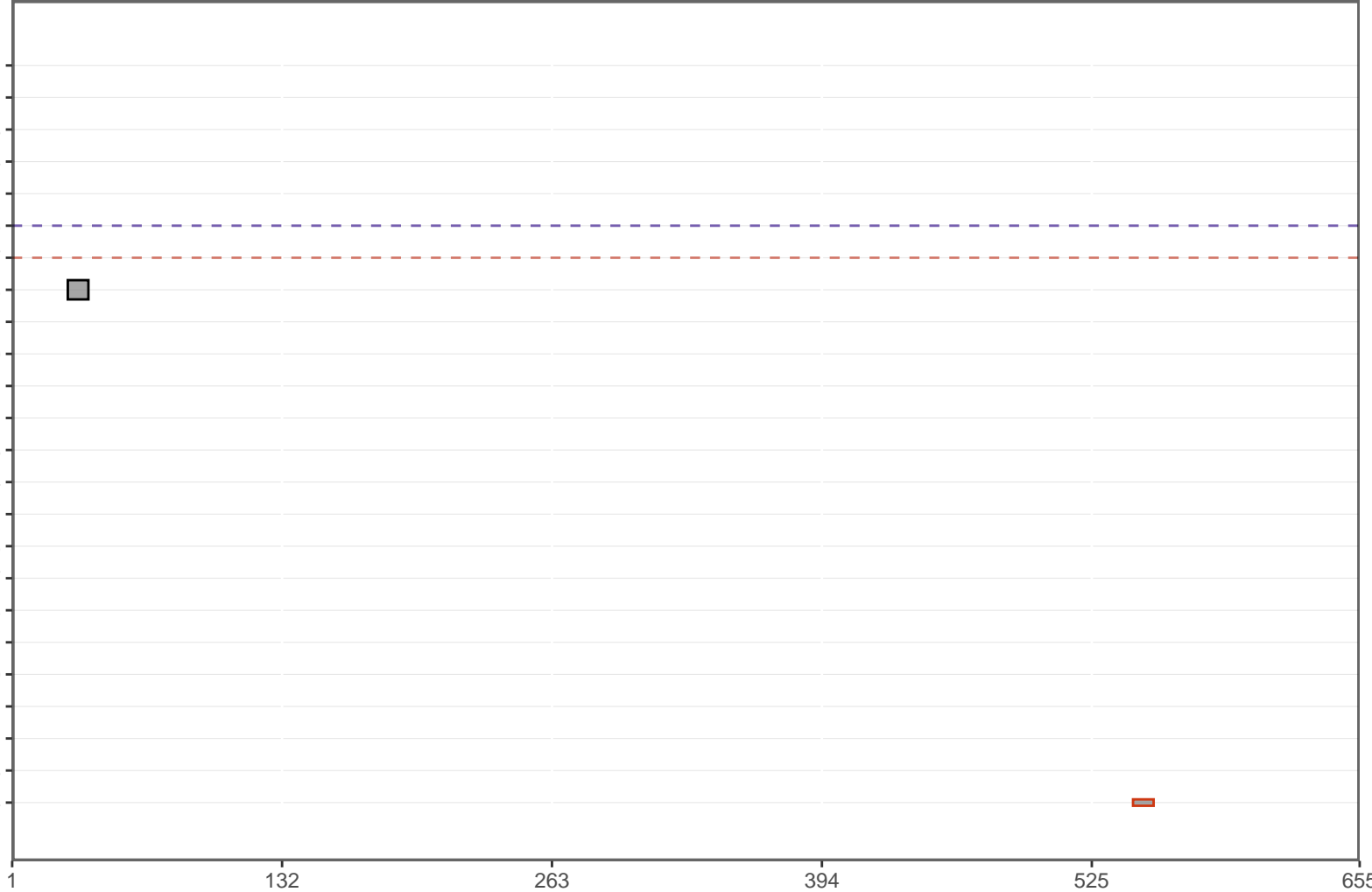
MW indication



Molecular weight

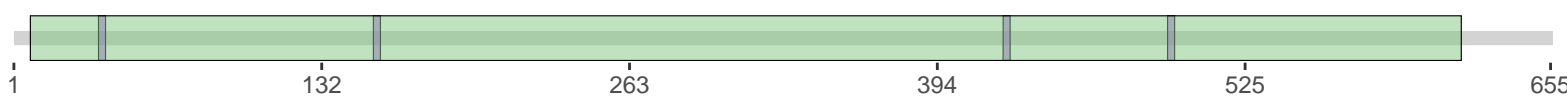


Gel Slice



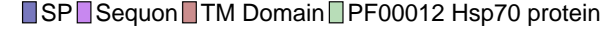
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KKCEPVEKLRDAKIDKSHYHDVYLVGGSTRIPKVGQLLGGFFNKKELGKSNPDEAVWGAAGVQAALLEGEGDQKVDLLLDVTFLSLGLTAGGVMTVLPNRTTPTTKGQIFSTYDQNGPGLVDYVEGERPMTKNNLLGKFLKGIIPAPRGVPGINVCFDIDANGILNVAEDKTAGVKNKTTITNDKGRLSKEEIERLVGEAERYKAEDESMKKKVEAKNLENYAYNMRNTVYRDEKFGKLDPSGKQKIEKAVDEMIDWLDRLNGLAEVDFEDKLDLENLCP

NbL03g20570.1 shikimate_O-hydroxycinnamoyltransferase [MW = 48.4 kDa]

No. of times detected



log(intensity)



Values from



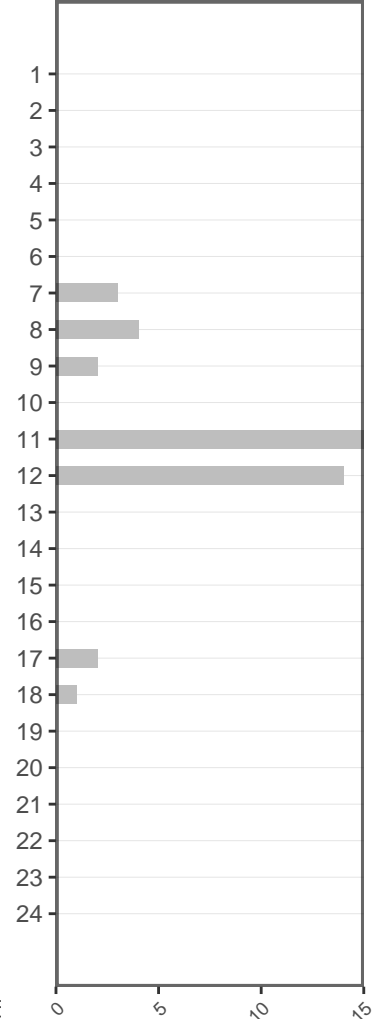
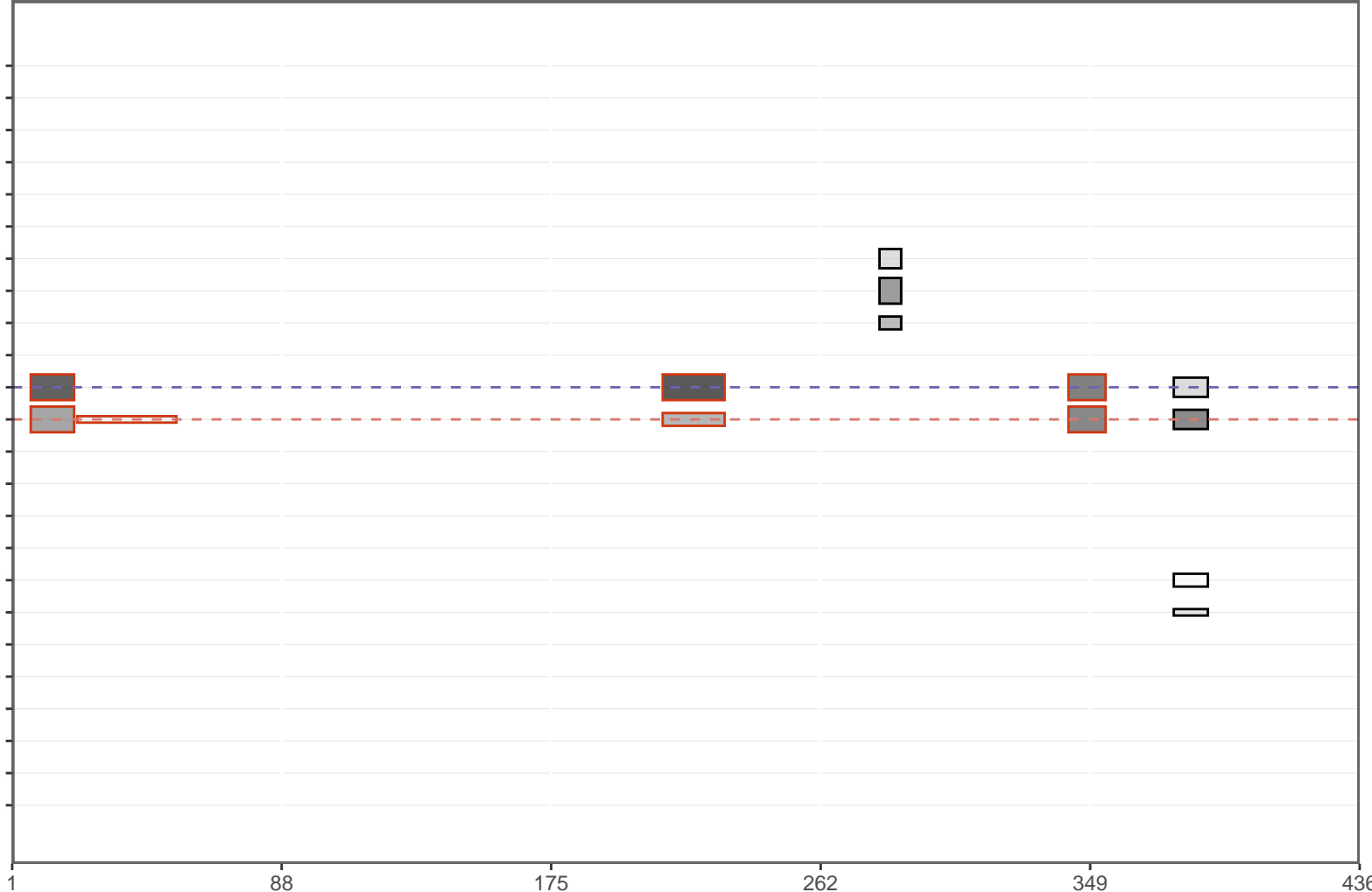
MW indication



Molecular weight

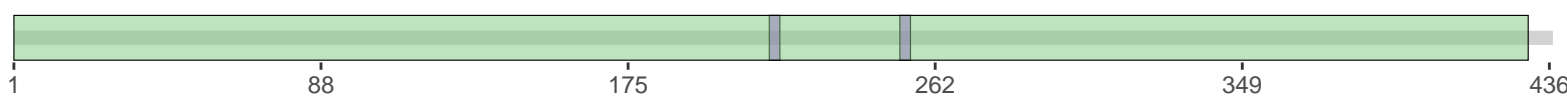


Gel Slice



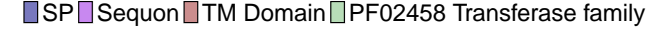
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

QPPPTLKYTPENTINPEIVPETSIVSFKLTRDQINTLKAASKEDGNTVNVYSVEMLAGHWRRSTGMARGLAHQDETKLYATDGRSLRRLPPLPGYFGNVIFFTTFAVAGDGGKPIWVAASKLHDALARMNDVYLSALDHLLELQFDLKAIVRGVHFTFKGPNLIGITWSRLPHDAIDFGWGRPFMGGPGGAYEGLSFLPSPPTNDGSGSVAISLQAEHMKLFEKFLYDF

NbL03g20470.1 glycerol_kinase [MW = 56.56 kDa]

No. of times detected



log(intensity)



Values from



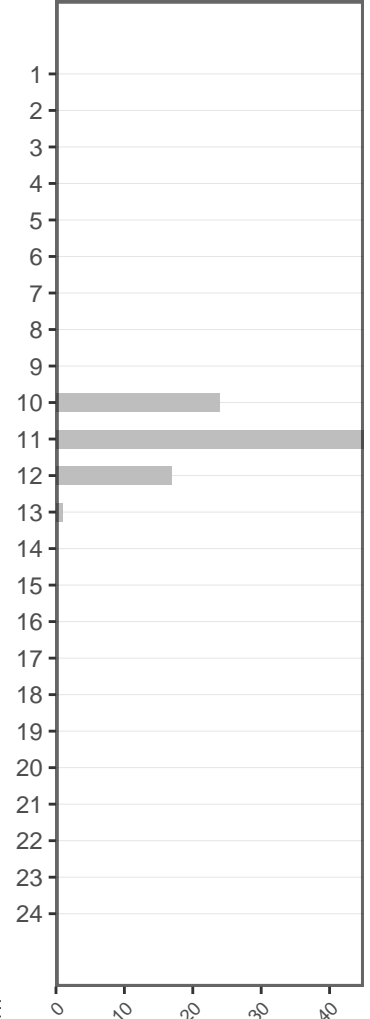
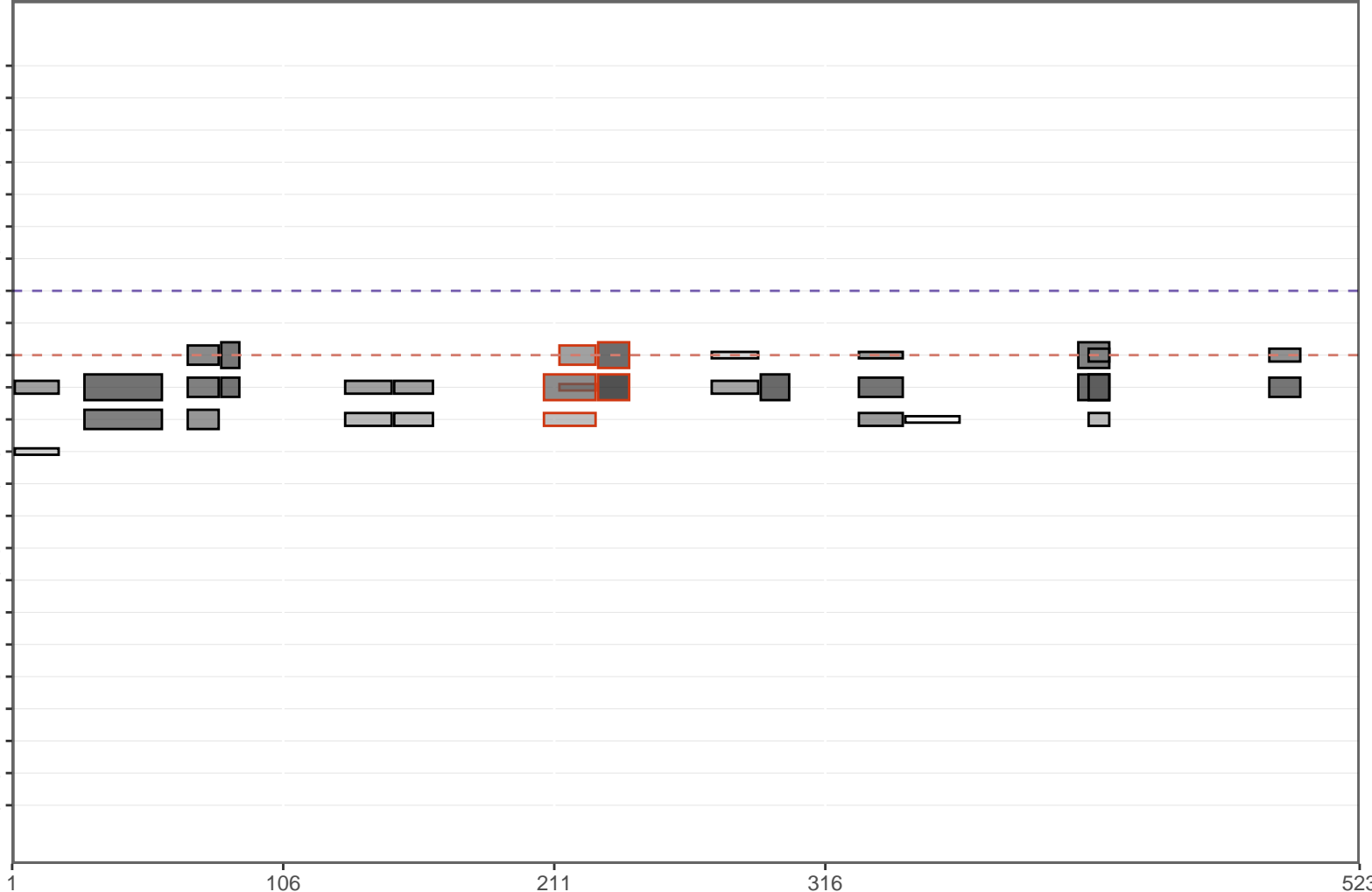
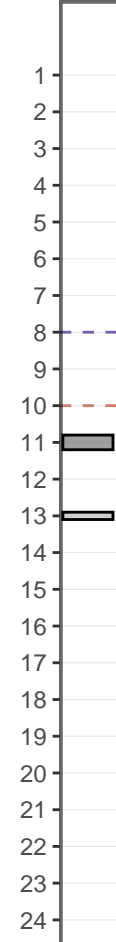
MW indication



Molecular weight

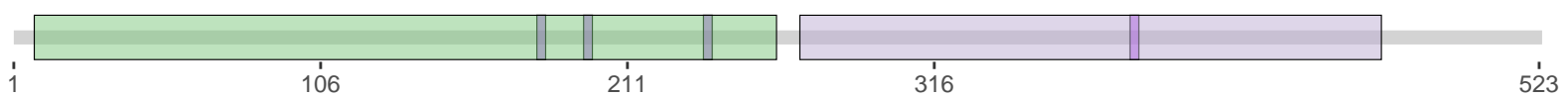


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00370 FGGY family of carbohydrate kinases, N-terminal domain
- PF02782 FGGY family of carbohydrate kinases, C-terminal domain

Protein sequence:

IGCLGDQHHAMVGGSCRKGEAKSFYGTGAFLLNTGEEIMKSNHLLSTFWVKLGPKAPNVALEGGSIADGAAVQWLRDGLGHSSANEIEELASKVTSTGGVYFPAFNGLFAFWRRDARGICVGTFRFNKSHIRAVLESMGFGVKDVLDSMHKDAAGKSDGKTEETEFLLRVDGGATVNNLMDQADLLGSPVYFRADIETTLGAWAAGLAVGVYTDDEFSSGEMKKATTFKPALEELRKKKVDWGLAVRSRFDLADLSL

NbL03g20410.1 protein_TOPLESS-like [MW - SP = 126.47 kDa]

No. of times detected



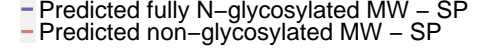
log(intensity)



Values from



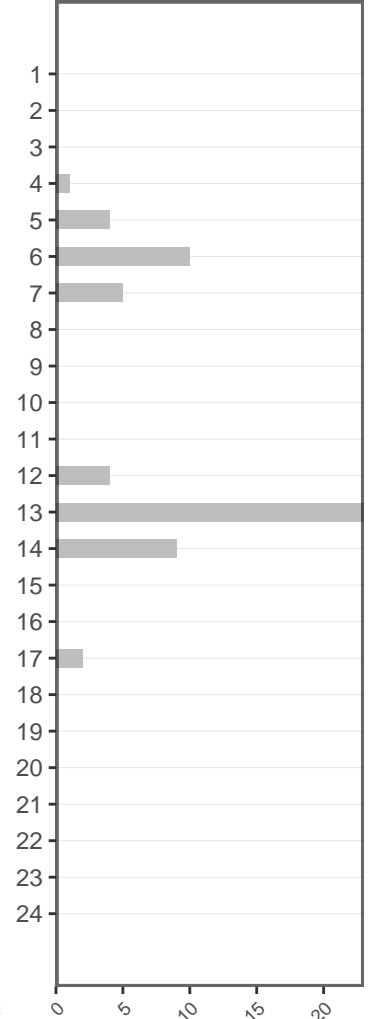
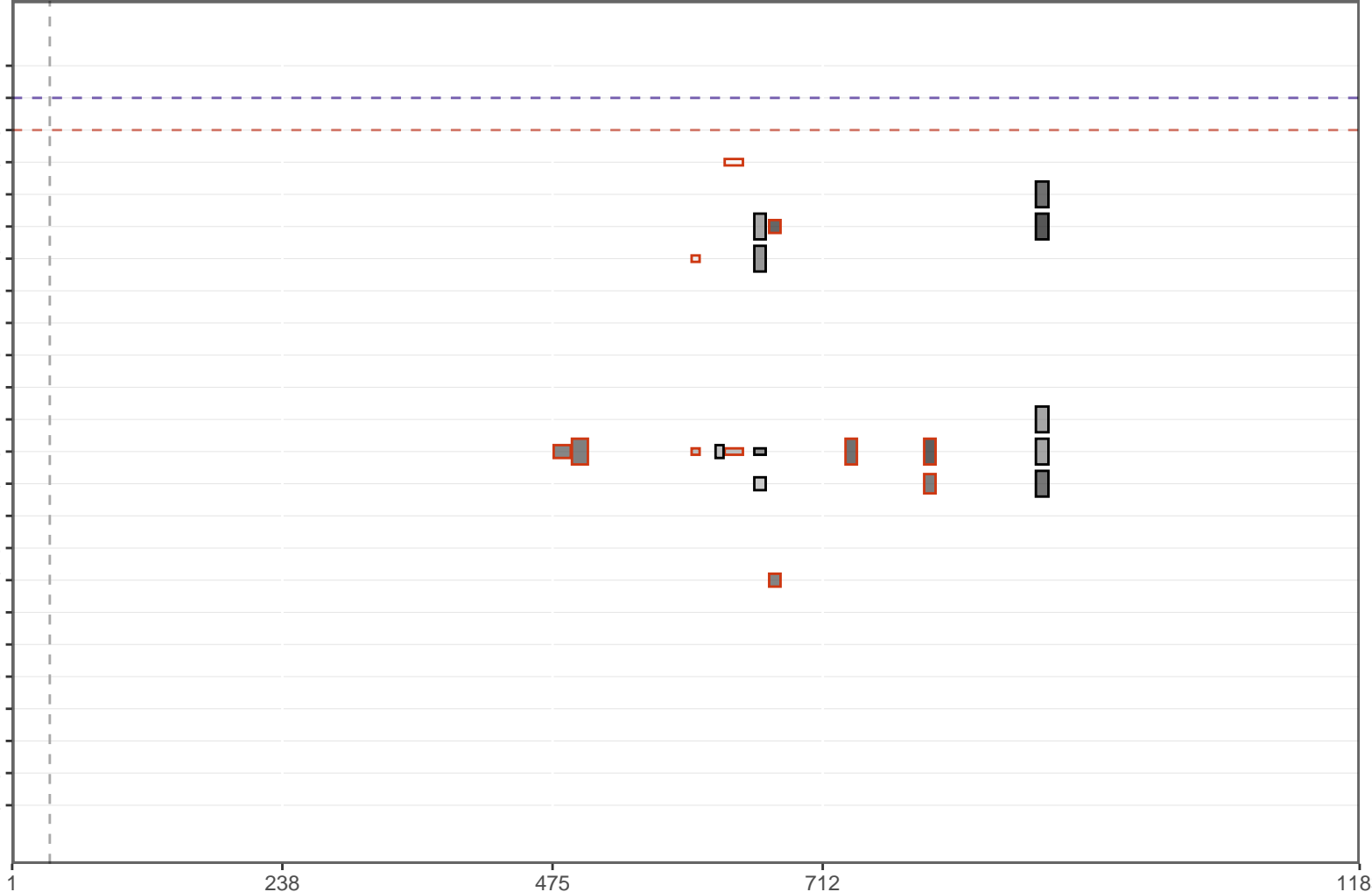
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

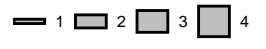


Protein sequence:

ITALDQKIKAWLYDNLGSRVDYDAPGRVCTMAYSDGTRLFGCGTSGKDGESHVEVNESEGAVKRTYLGFRKRSLGVVGFDTTKNRFLLAAGDGFRIKFWMDMDKIVQLLTSIDADGGLPAEPRIRFNKDGSLLAWSANENGIKLANSDGIRLVRTFENLAYDASRASESAKPTVNGISASSSSGFADRVAAGDVGISGMNDARNVTVDKPRIVEEPNDKSKWKLTEITEPSSGCRSLKLPENLRVTKISRLVYTNESGNAIALALASNAIHLKWKVWRNERNSSGKATASVSPQLVDF

NbL03g20380.1 proline--tRNA_ligase_cytoplasmic-like [MW = 58.76 kDa]

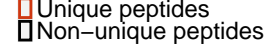
No. of times detected



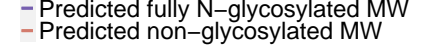
log(intensity)



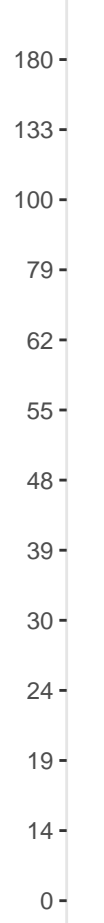
Values from



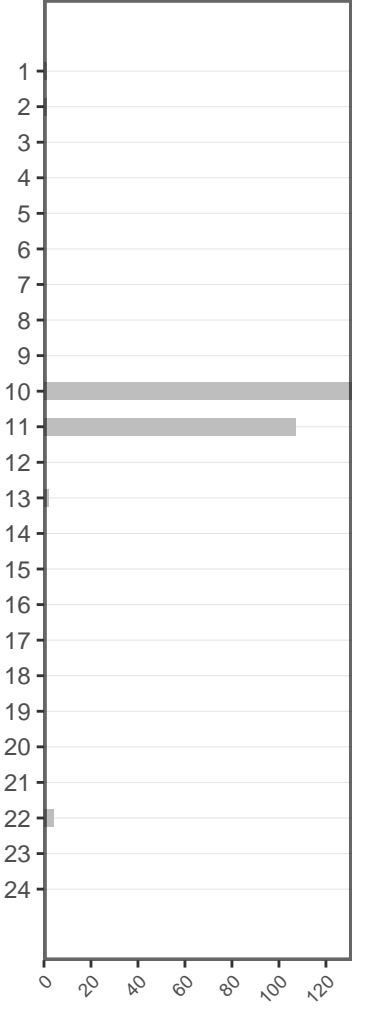
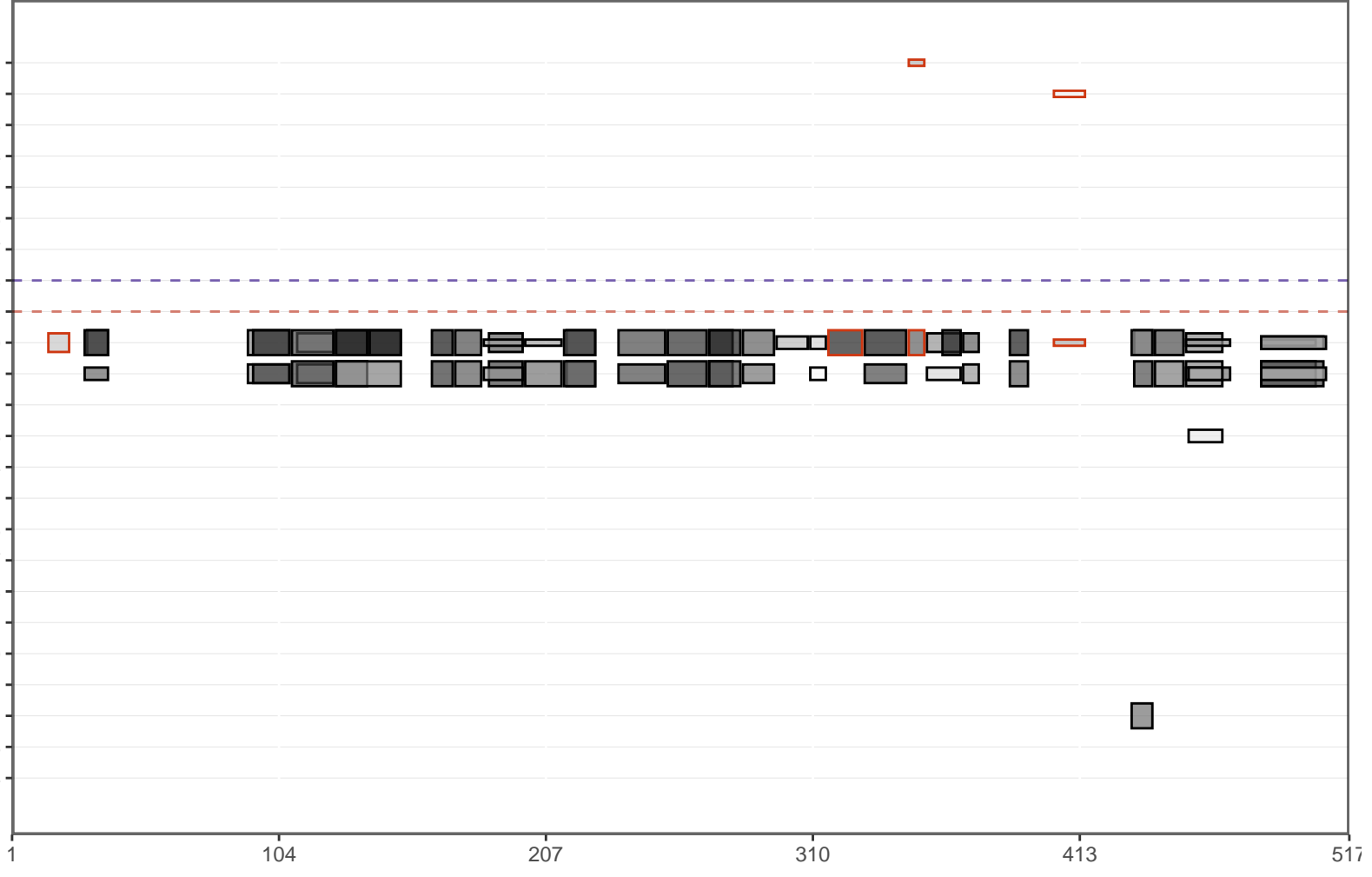
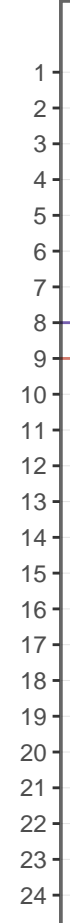
MW indication



Molecular weight

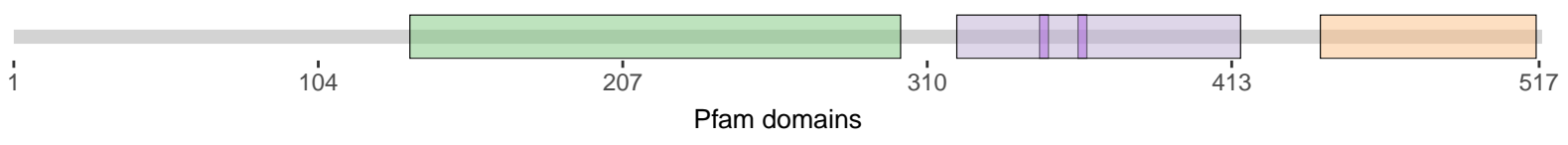


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam Description

- SP
- Sequon
- TM Domain
- PF00587 tRNA synthetase class II core domain (G, H, P, S and T)
- PF03129 Anticodon binding domain
- PF09180 Prolyl-tRNA synthetase, C-terminal

Protein sequence:

IPNTGRGIGGATSHKLGQNFAMKFEFENEKGEKAMVWQNBWAYTTRTIGVMIMVHSDDKGLVLPKVASTGVVPIVPIKDNATGGIFDGAATVEKLNESGGVRAEADFBNVSPGWKYSHWEMKGVPLRIEIGPKDLANNQVRAVRRDNGAKTDIPMDNLVEQLKDLATIGENLFDNAKGRDAGVQIVRTWDEFTVALGGKLVLPWGDCEDEEVKDKARTKGEMGAANKLSPFDQPELPEGLTGFASGPKAKKWTYWGKSY

NbL03g20320.1 uncharacterized_LOC109223891 [MW - SP = 55.22 kDa]

No. of times detected



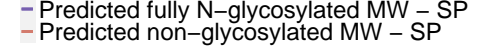
log(intensity)



Values from



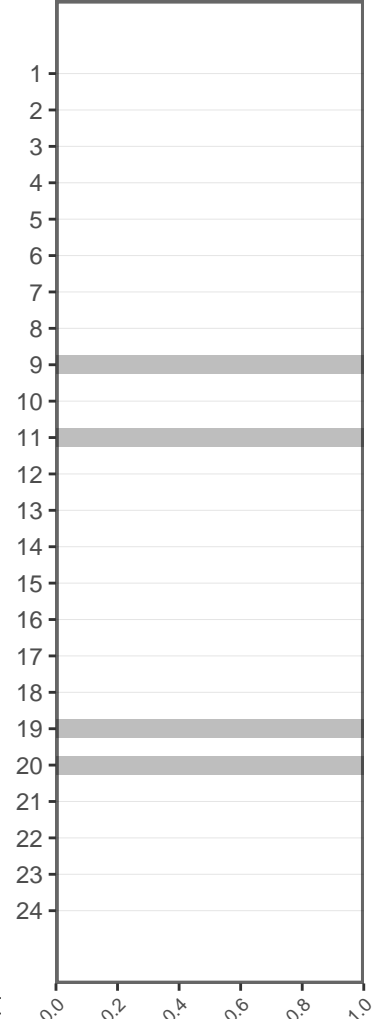
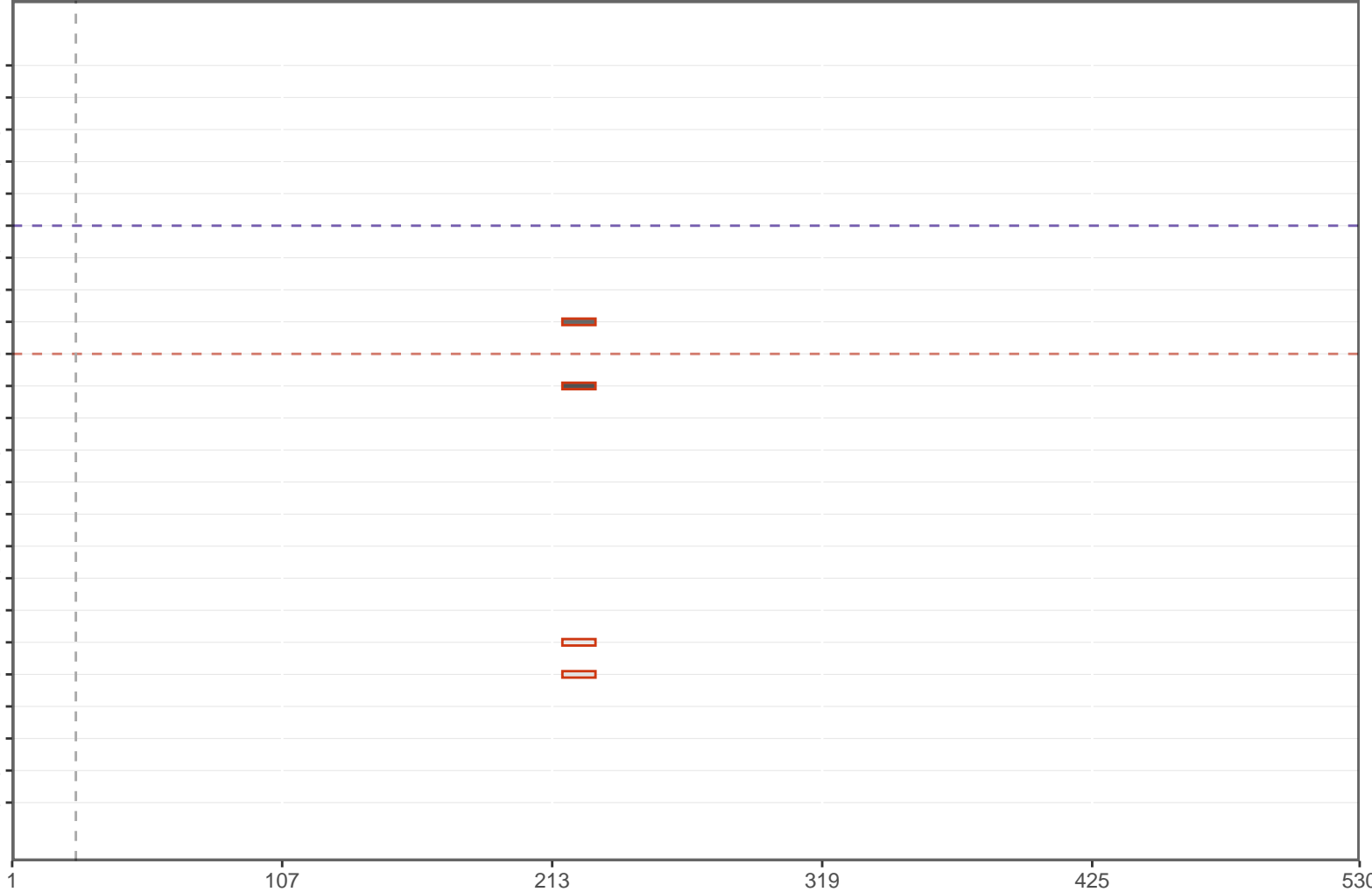
MW indication



Molecular weight



Gel Slice

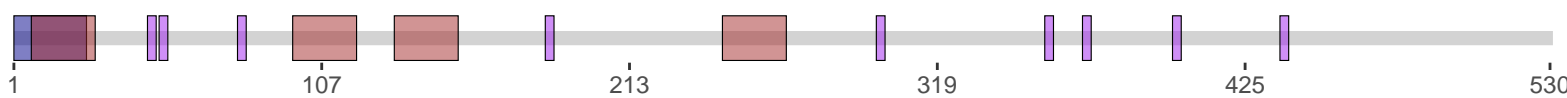


Protein length

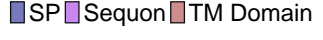


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LGLAALGFLSILGQVLYVWGLWAVTFILGDFALVLIHNTGDTQVAMNDWKNPTAHTALDDHPCVDATAGETLGGSEKVTYQLVGVANRIFTNVSNIDPPSGVYNGSGFLVPLGNPFNSDKDRKGANGEVELSNATGVWRNRYGVGSASNVGCTVGMTPDMYNGMTGVVWVSEGLYHWGPFSELLDCTFLRDTVGVHDEHGPDLTRYKWWYKGLALVSAWMLSLGHWLVARERRHRYKTKLVDTSGOESLAGKSGE

NbL03g19970.1 protein_LURP-one-related_12-like [MW = 23.63 kDa]

No. of times detected



log(intensity)



Values from



MW indication



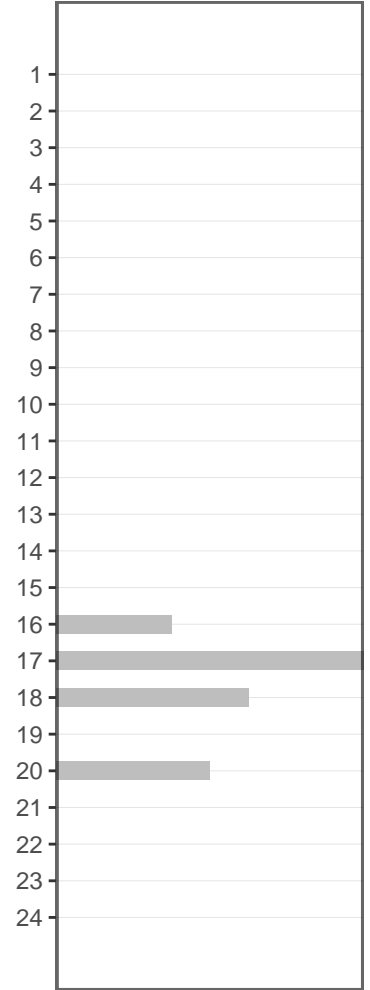
Molecular weight



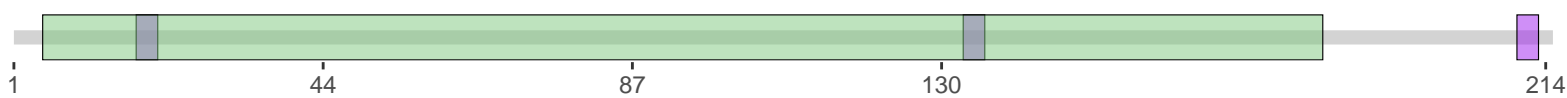
Gel Slice



Protein length

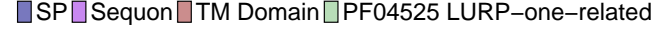


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IQKPFVSRSSIIIGRISVTAEVYGNPMEYVQIEGFAQRNCTFFNADKVSVAERIRKVDACANVVLGKDFSLSEVVKPGFDGAFAMGLVLLDGGDGGVWPNPNRNRVDGQPIEDDPLNLS*

NbL03g19960.1 cucumber_peeling_cupredoxin-like [MW - SP = 16.34 kDa]

No. of times detected



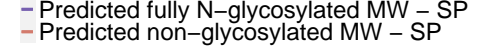
log(intensity)



Values from



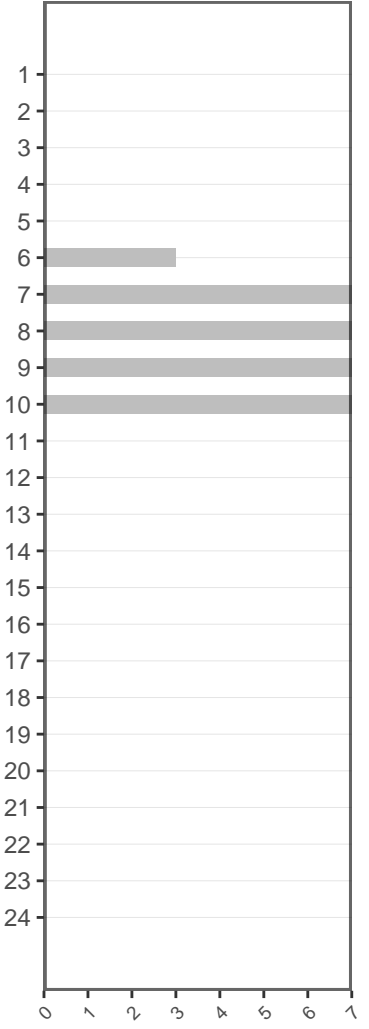
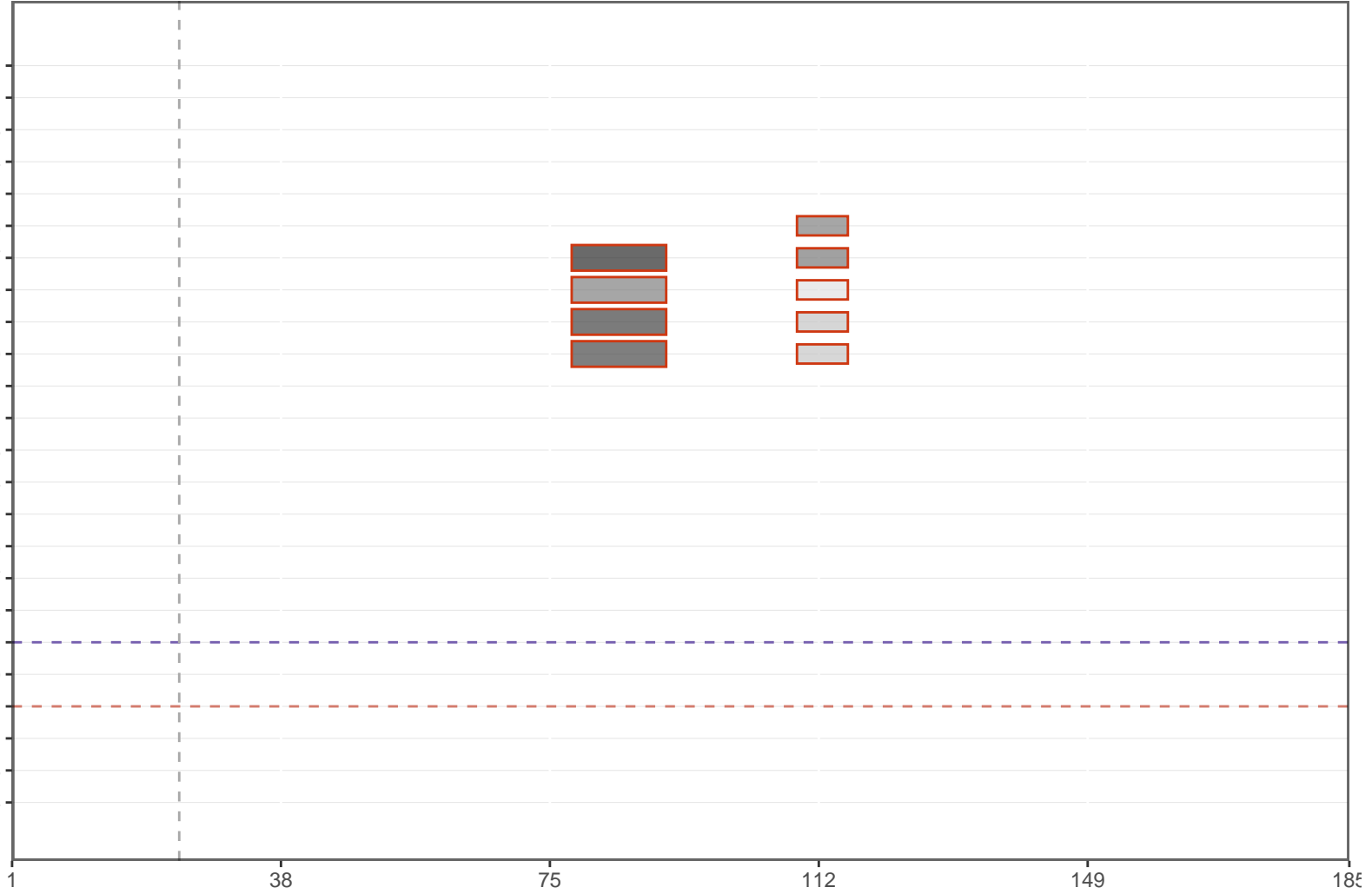
MW indication



Molecular weight



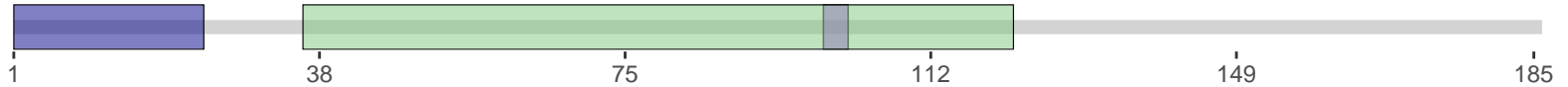
Gel Slice



Protein length



Pfam domains



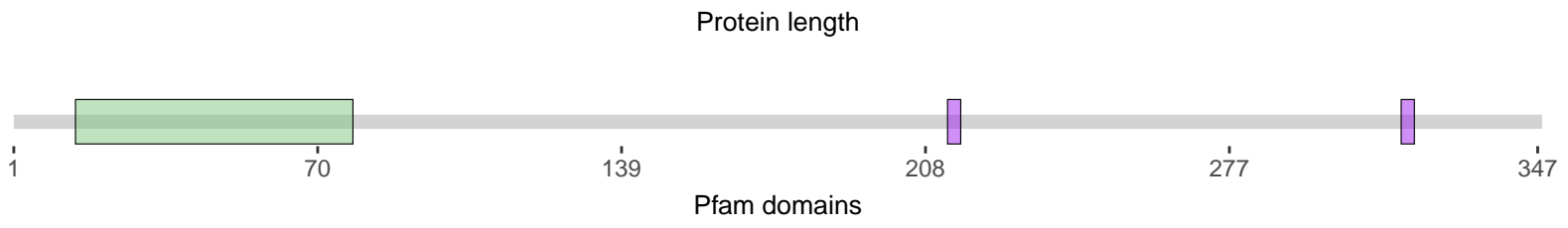
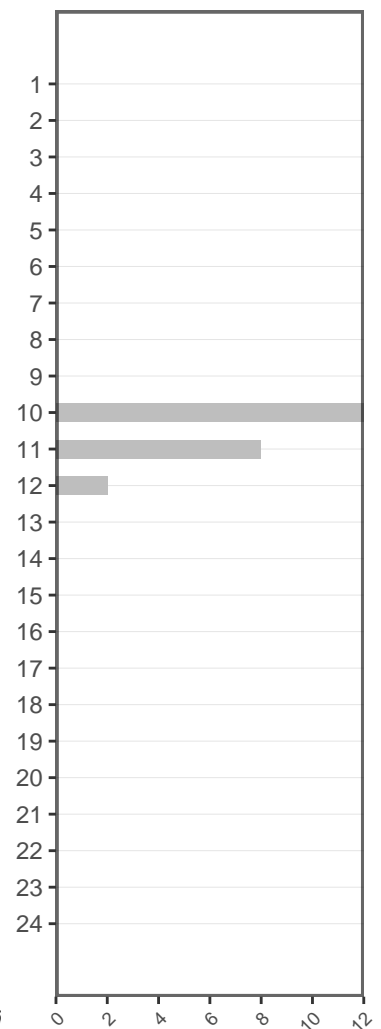
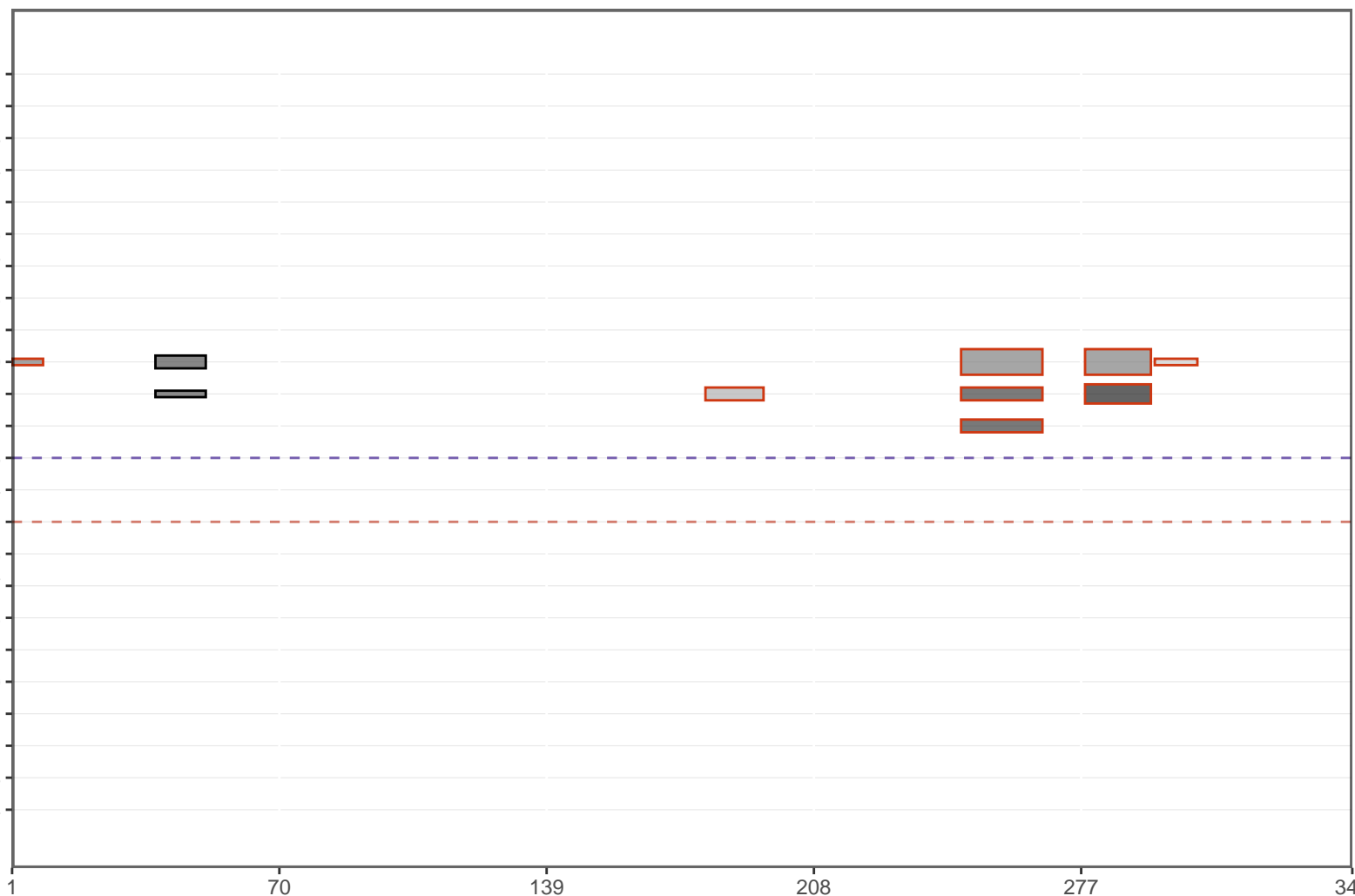
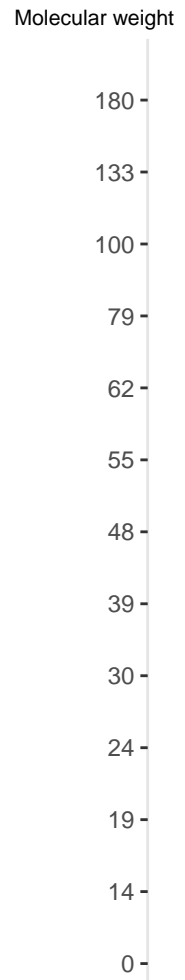
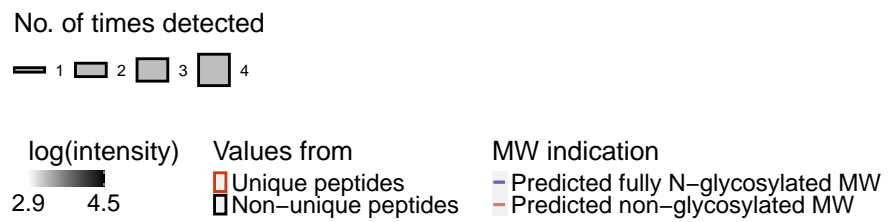
Pfam Description



Protein sequence:

ASFDCSSQNAIGRAINGRANVLEDEGERYVICTFGRHCQNGOKLATVSSSTGTPGANPPTFSAAGPSSGVPOGIAPPPPSSTIVFAFLLSLSSIAALFL

NbL03g19950.1 methyl-CpG-binding_domain-containing_protein_11-like [MW = 38.26 kDa]



Pfam Description

- SP
- Sequon
- TM Domain
- PF01429 Methyl-CpG binding domain

Protein sequence:

VTEHKKKEEMPDKDASEKKKMEASDETEVDNGRDKMAGHGSSEETIADNVEVHNNSTKDKNFEGVSDAIGSEANAAAGLEVEEKHGSGEKFKETQIDSDGAGVNRDVPKVKYTPERSVAGDGTGNIGEPGLVQKATNSVNFGEYRSLSEGEKKNRTSLMMDNGEINGPGRNHTPQHGPASISGQ

NbL03g19560.1 protein_RKD1 [MW = 16.14 kDa]

No. of times detected



log(intensity)



Values from



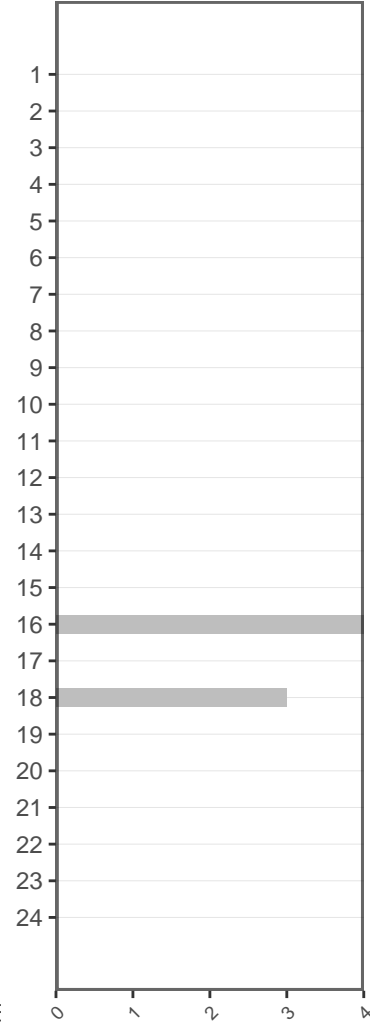
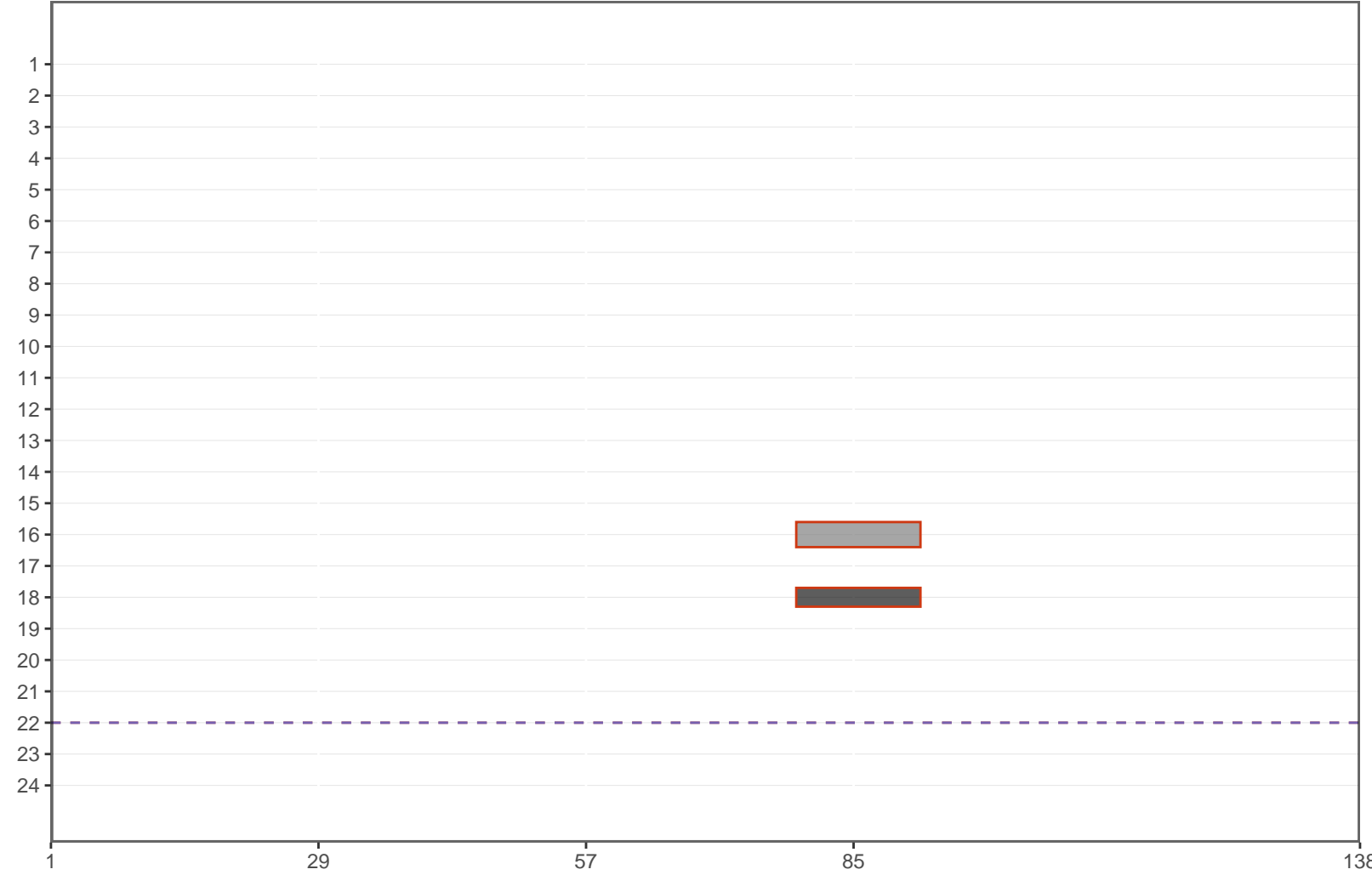
MW indication



Molecular weight



Gel Slice



Pfam domains

Pfam Description



Protein sequence:

SGGSGMEQKLDKDWLLEEEKMLEEVPDMELEEKTKRLRGRFKNYKRKRLMSMTELOASFGDYCNPNPWGIGYGHRE

NbL03g19540.1 malate_dehydrogenase_chloroplastic [MW = 43.39 kDa]

No. of times detected



log(intensity)



Values from



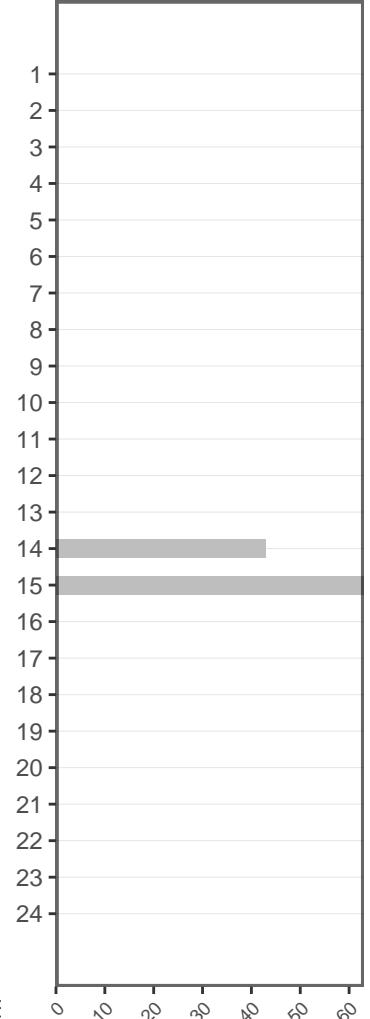
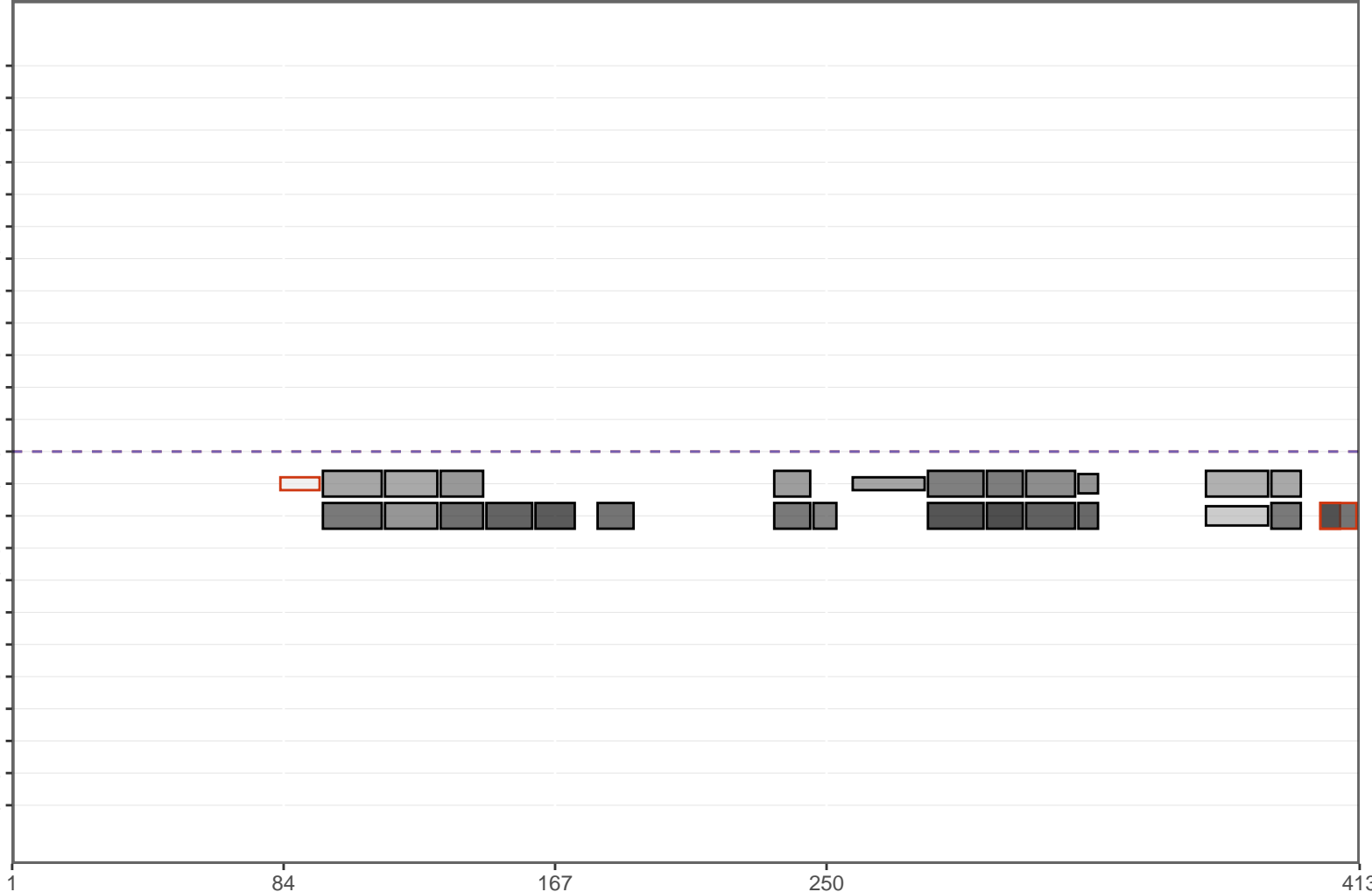
MW indication



Molecular weight



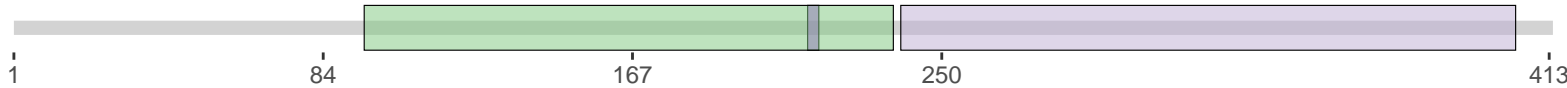
Gel Slice



Protein length



Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF00056 lactate/malate dehydrogenase, NAD binding domain
- PF02866 lactate/malate dehydrogenase, alpha/beta C-terminal domain

Protein sequence:

KTLLVEAVDNCPCDFRHSINPVNSTVPIAAEVLKRRKGVYDPKILFGVTTLDVVRANTFVAGKNNLRLLIDVDVPIVGGHAGITLPLLSKTKPSTFTTDEEVEGELTVRIGNAGTEVVEAKAGAGAGATLGMVAARFVVEGSLRALDGDSDVVECAFVHSDITEVFFAFRRVRLGKNGVETALPDLQGLTEYEGKALDALKPELKAIEKIGFVQKEPWA*

NbL03g19530.1 geranylgeranyl_diphosphate_reductase_chloroplastic [MW = 51.25 kDa]

No. of times detected



log(intensity)



Values from



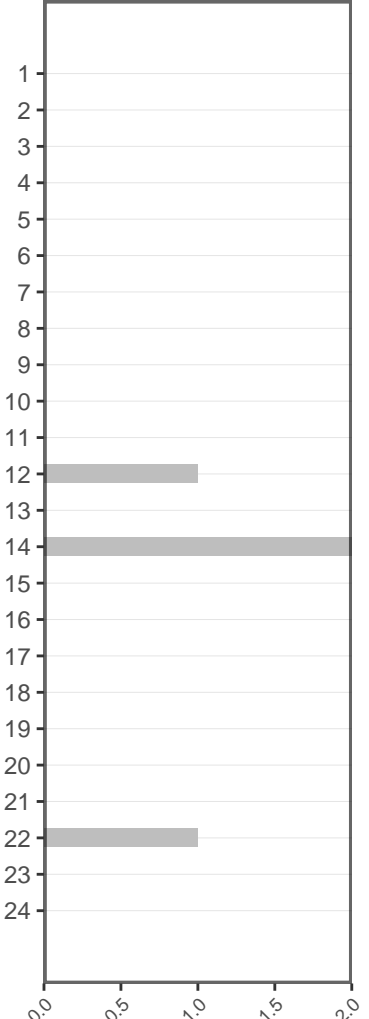
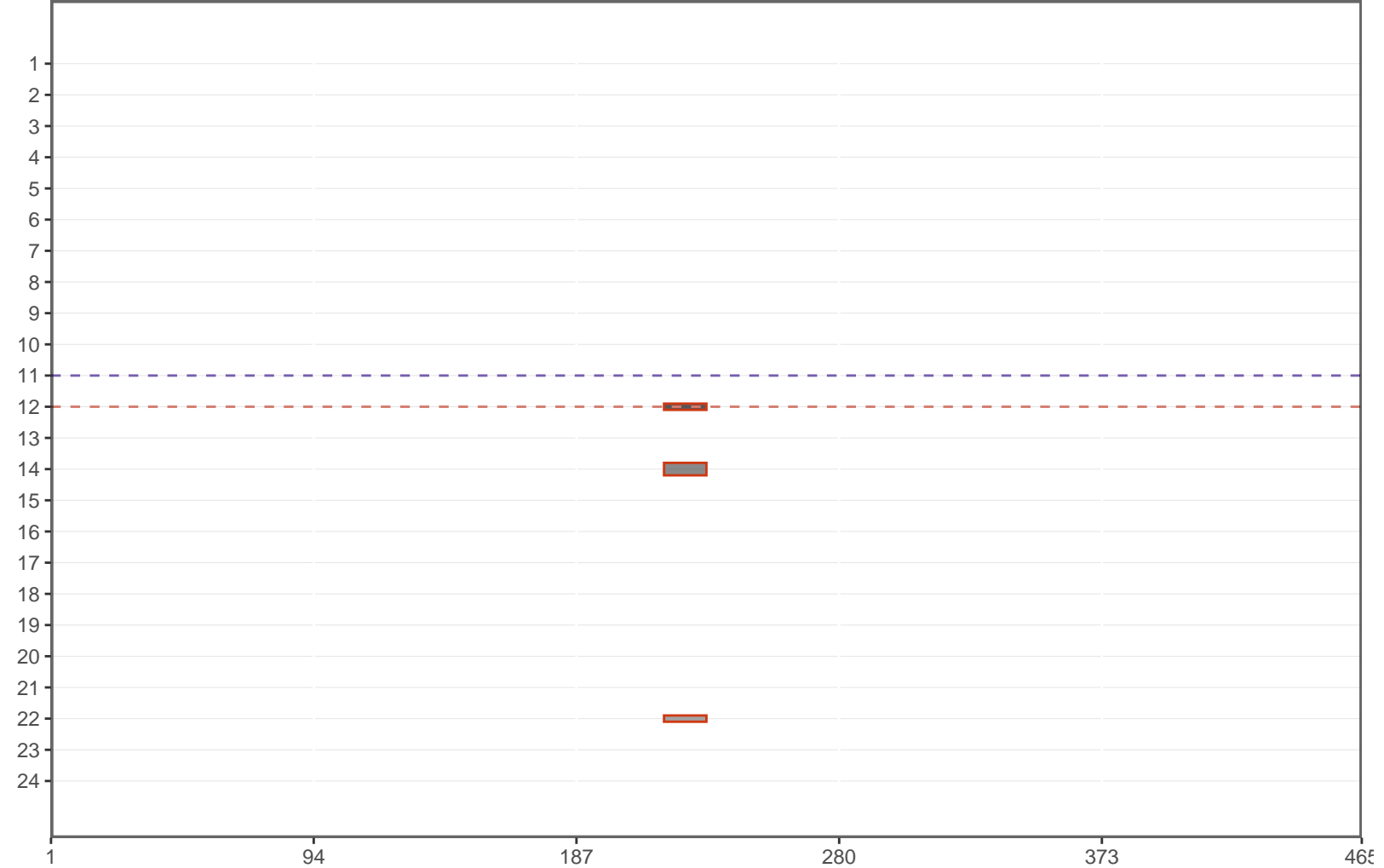
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AGDYEAIAFQERIRISDDKMKYYENLAEMVGGDVPDFYGVWVFPKGDHWVGTGTVTKADKKFQLATRLRADSKITGGKIRVFAHPPEHPRRRLRDRVALVGDAAAGVYTKGSGEGHYFAAKSGRMCAEAIVEGSEMGRMVDGSLRKYLEKWKDKTVPPTKYVLDLGGVYFRSNAPREAFVEMCADEYVQKMTFDSYLYKKVAPGNPIEDLKLAVNTIGSLVRANALRKMEDKLEV

NbL03g19430.1 ribulose-phosphate_3-epimerase_chloroplastic [MW = 30.6 kDa]

No. of times detected



log(intensity)



Values from



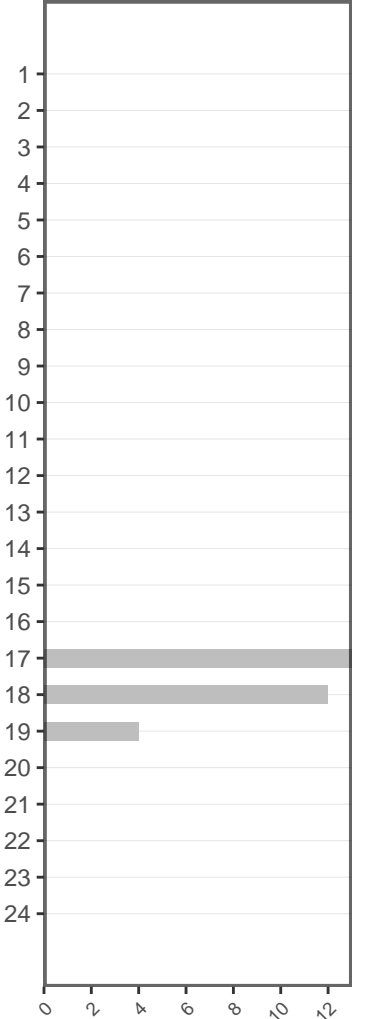
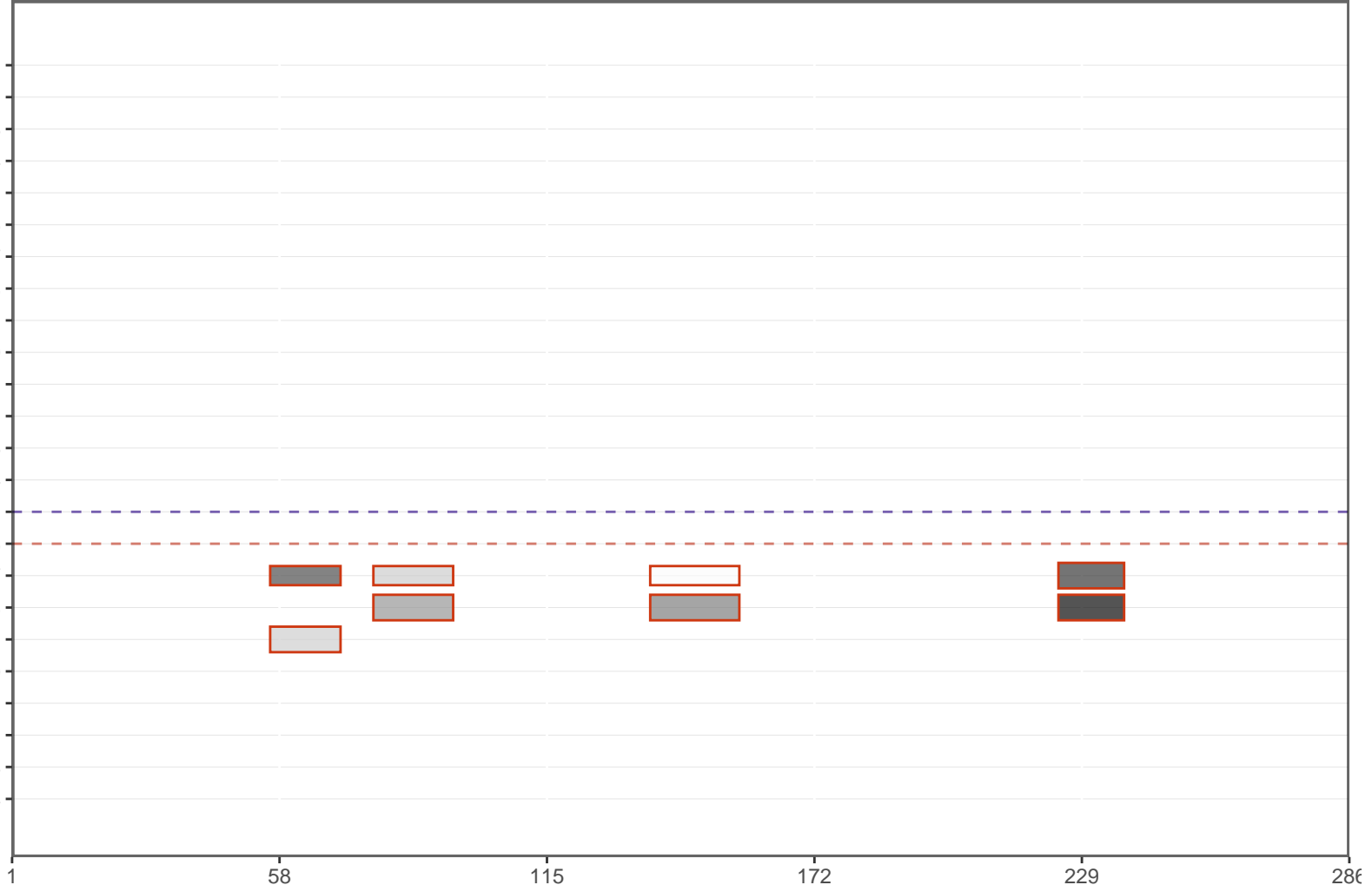
MW indication



Molecular weight

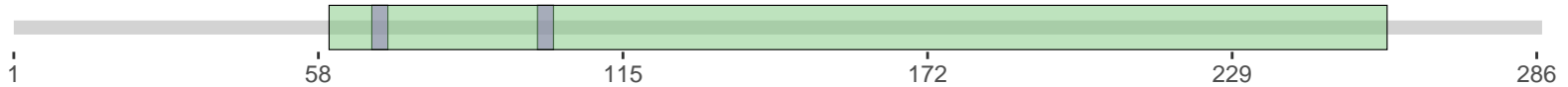


Gel Slice



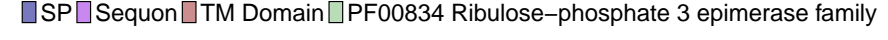
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

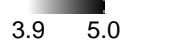
DRVPDFIKAGADISVHGE66STHLHRTINGIKELGAKAGVLANPQTPLEAVLDAVDLVLMSVNPFGGG6FIE9GKKISDLRKKICAEERGLNPIWEVDGGVSPKNAYKVEAGANALVAGSAVFGAPDAEGKYLNTLYASLRDAELDLY

NbL03g19370.1 vesicle_transport_v-SNARE_13-like [MW = 25.11 kDa]

No. of times detected



log(intensity)



Values from

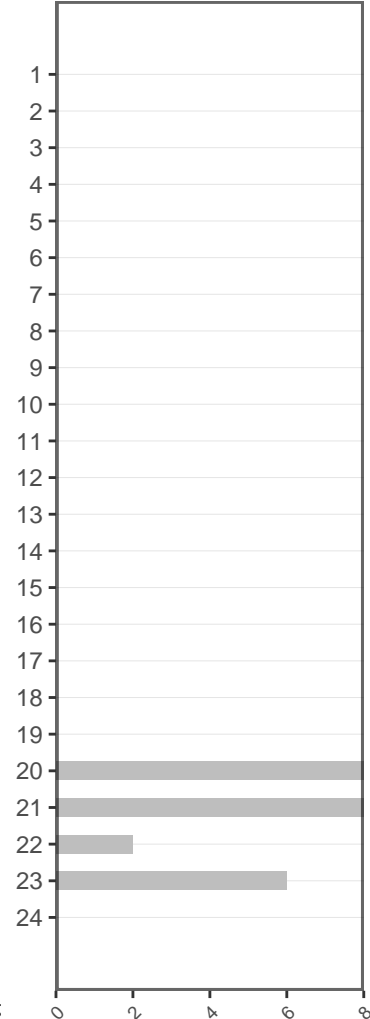
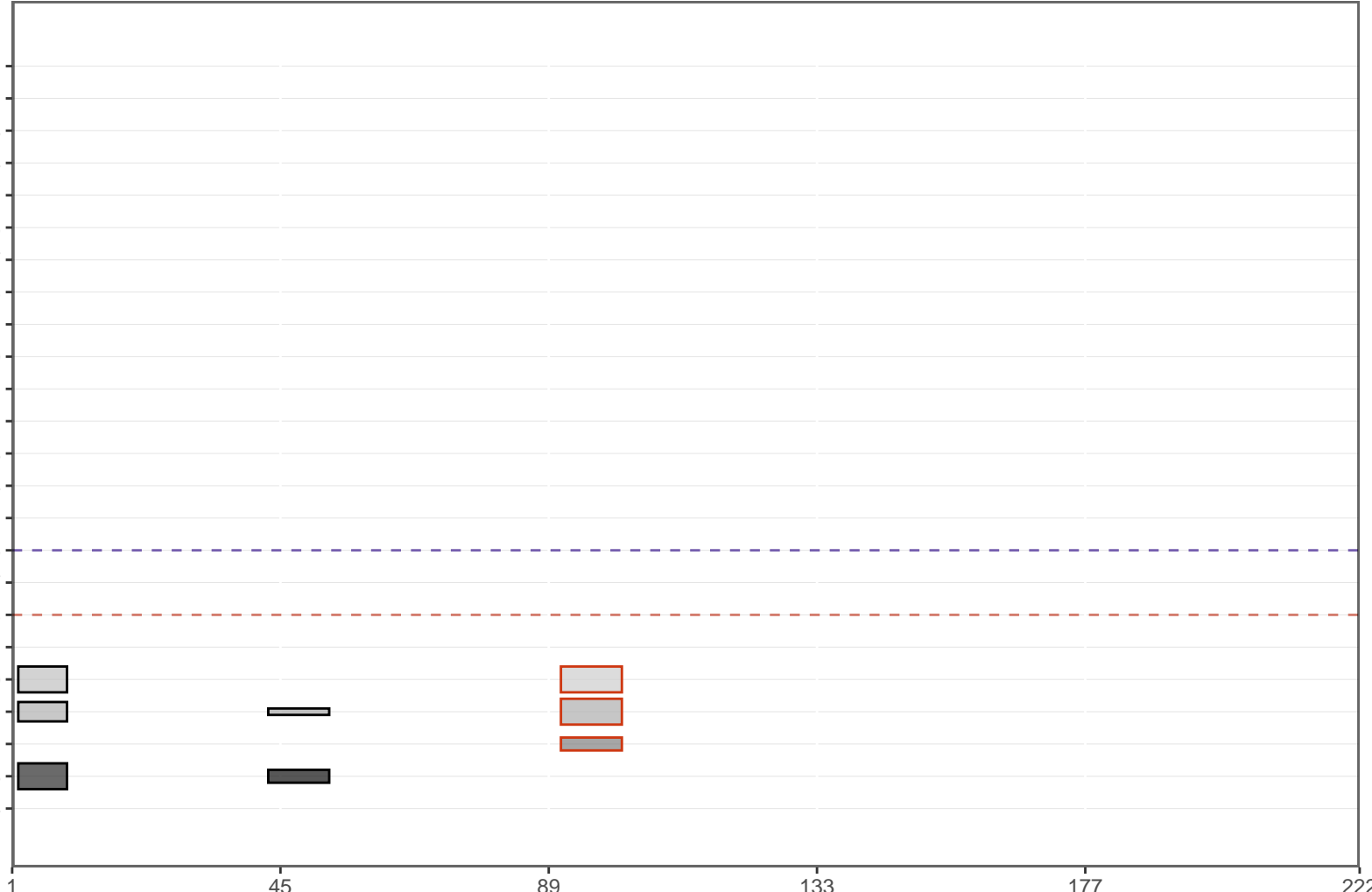
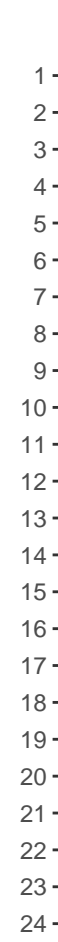
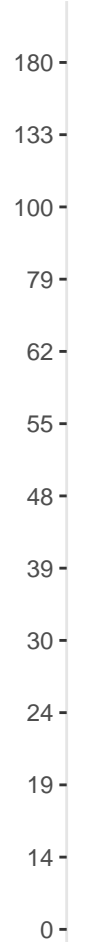


MW indication



Molecular weight

Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

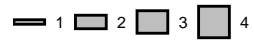
- SP
- Sequon
- TM Domain
- PF05008 Vesicle transport v-SNARE protein N-terminus
- PF12352 Snare region anchored in the vesicle membrane C-terminus

Protein sequence:

DAARDLLESGMVDMMVSDAGRGRLLMMSTERLNHSDRIRESRKTMLETEELGVSILODLHGGRGSLHAAHDTLHGVDNISRKIKLTMRRMSRNKHWIGSHAVLVLLLVYFKLAF

NbL03g19290.1 eukaryotic_translation_initiation_factor_5A-1 [MW = 17.37 kDa]

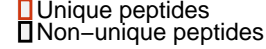
No. of times detected



log(intensity)



Values from



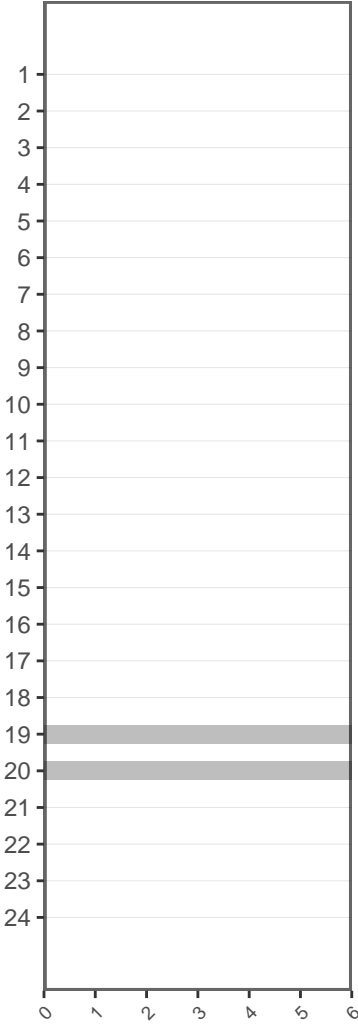
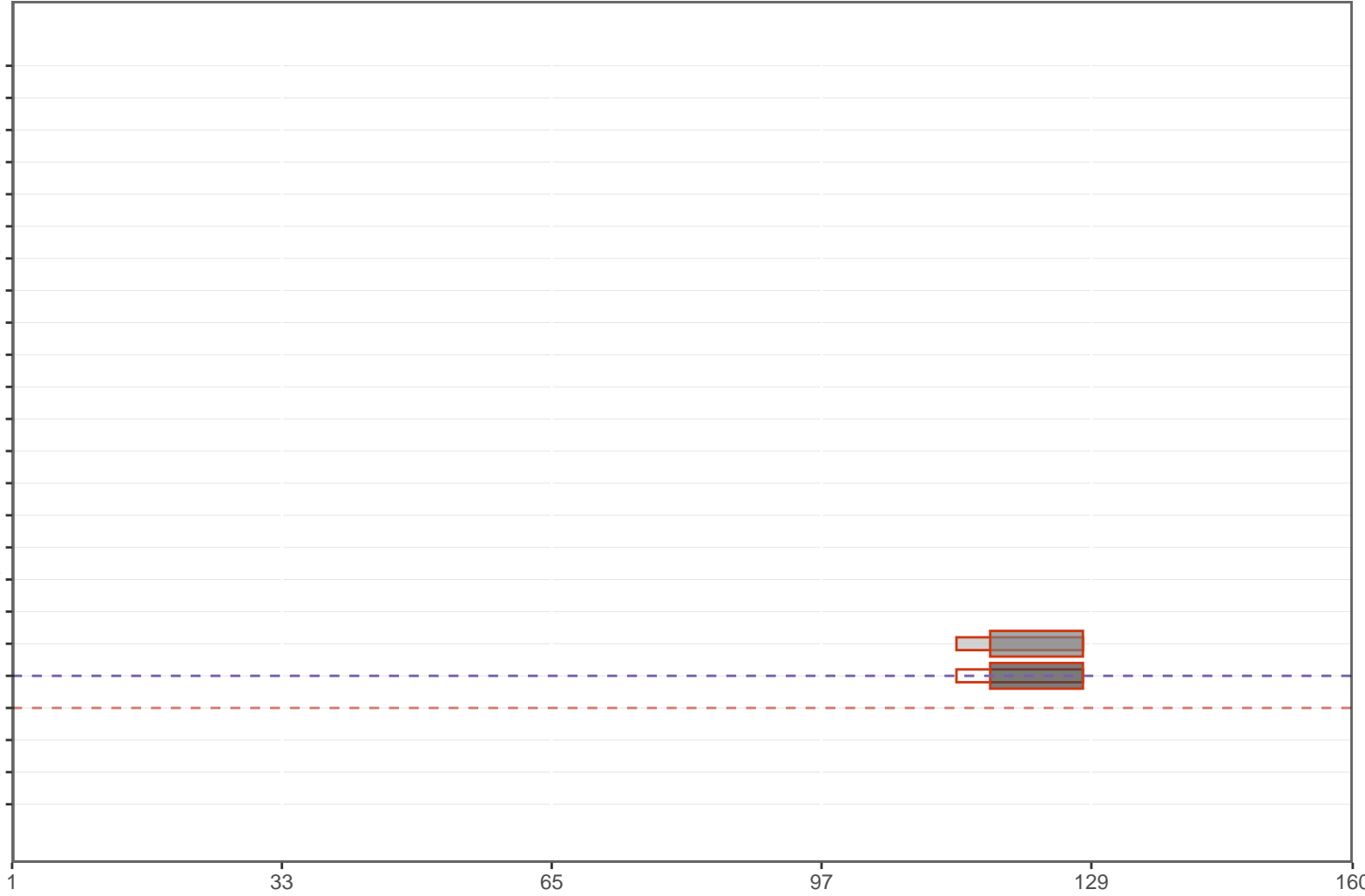
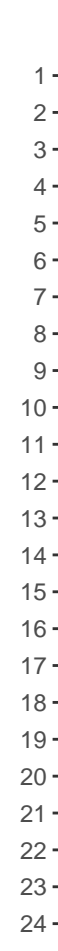
MW indication



Molecular weight



Gel Slice



Protein length

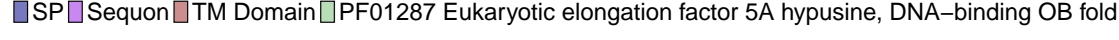


Peptide counts over 4 repeats

Pfam domains



Pfam Description

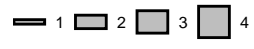


Protein sequence:

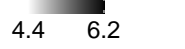
TGKKLEIDVPSSTINGDVPVHNRFDVGLIDISGDFVSLTFENGNTKDDLRLLPTDQNLALLKNDGFAEGKDLVLEVMAMGEEGIGKIDVGPK

NbL03g19180.1 LYR_motif-containing_protein_4 [MW = 9.88 kDa]

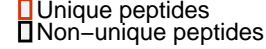
No. of times detected



log(intensity)



Values from



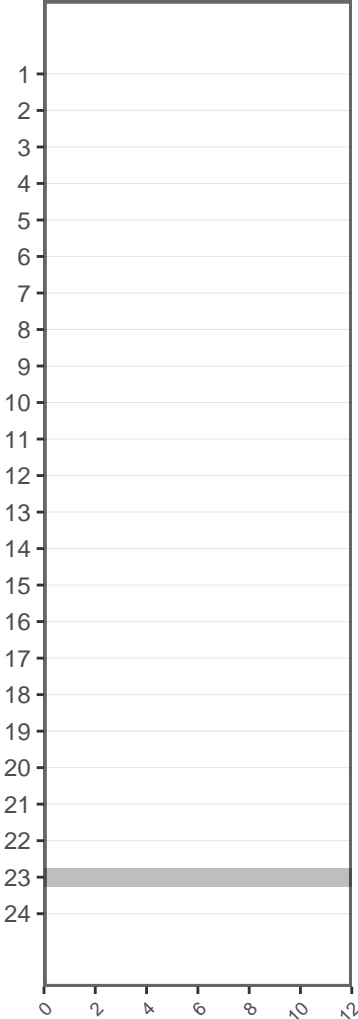
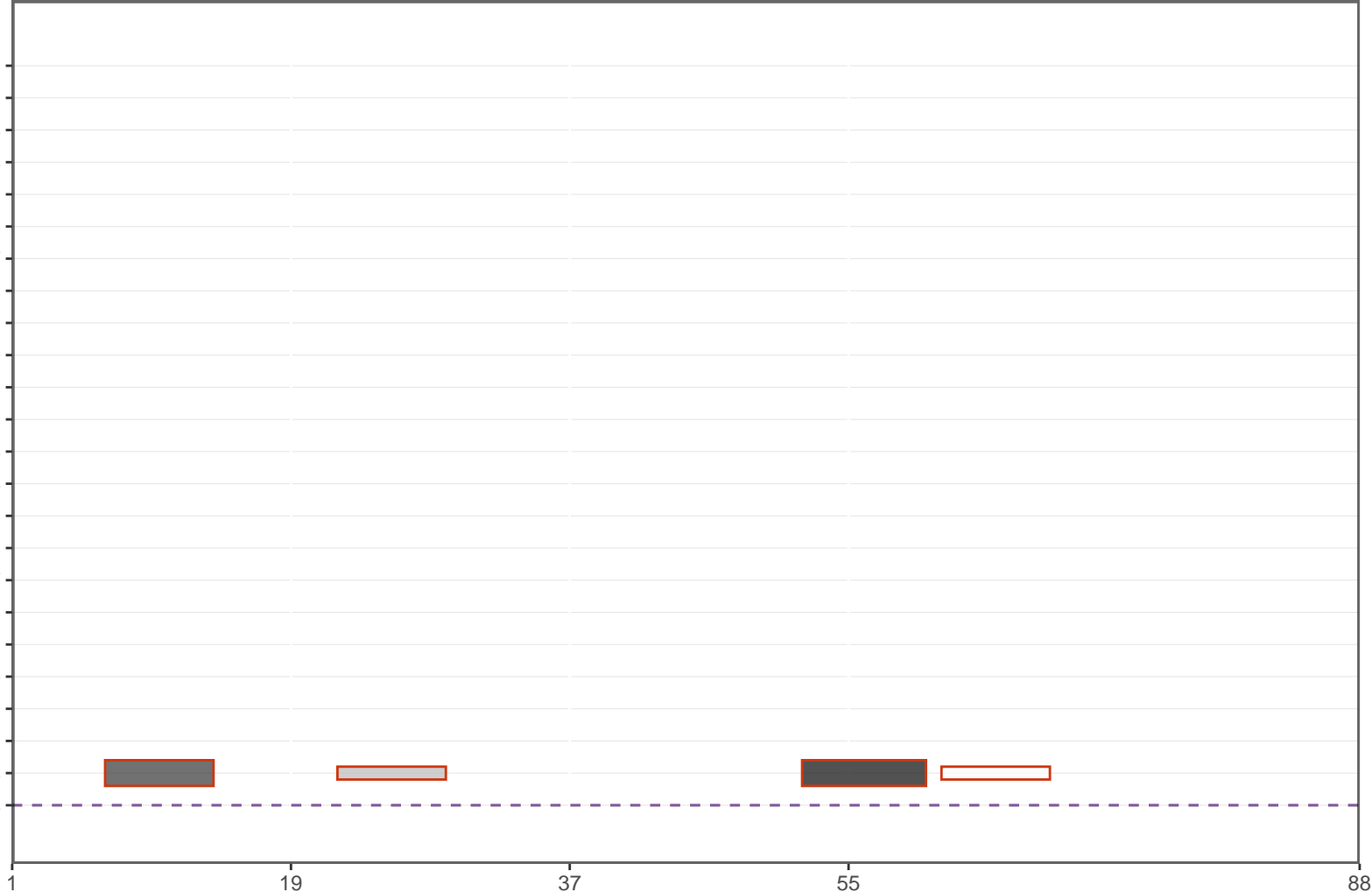
MW indication



Molecular weight



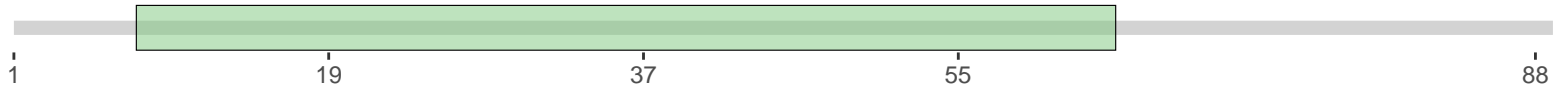
Gel Slice



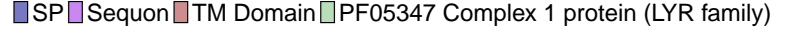
Protein length



Pfam domains



Pfam Description

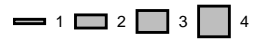


Protein sequence:

TKRRIDGFRNKGLESDPSKVAAFSEGRGILEVAKRGAVVSLVAPKVKVMELN

NbL03g19120.1 pre-mRNA-splicing_factor_ATP-dependent_RNA_helicase_DEAH1-like [MW = 119.68 kDa]

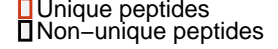
No. of times detected



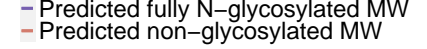
log(intensity)



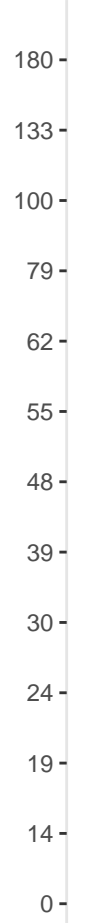
Values from



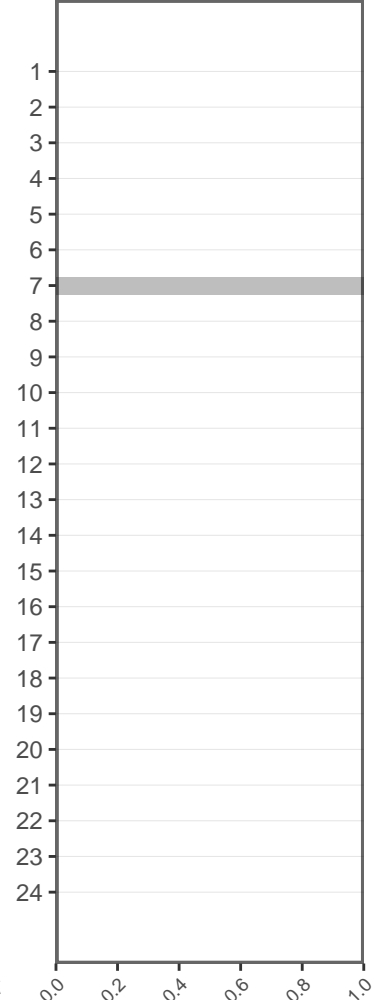
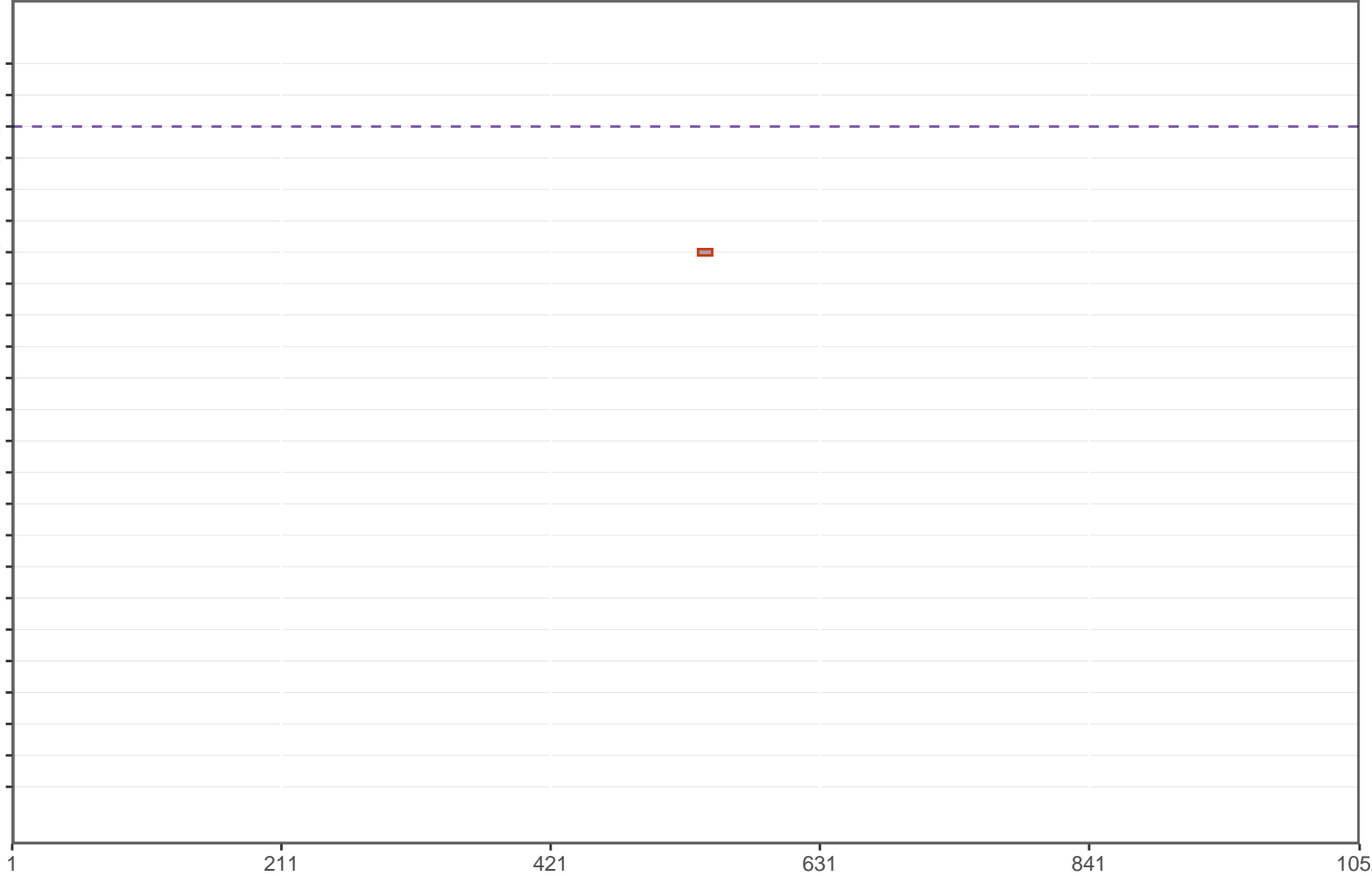
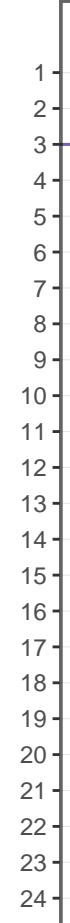
MW indication



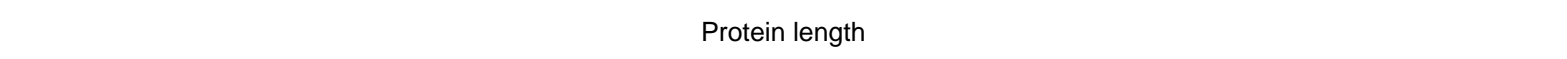
Molecular weight



Gel Slice

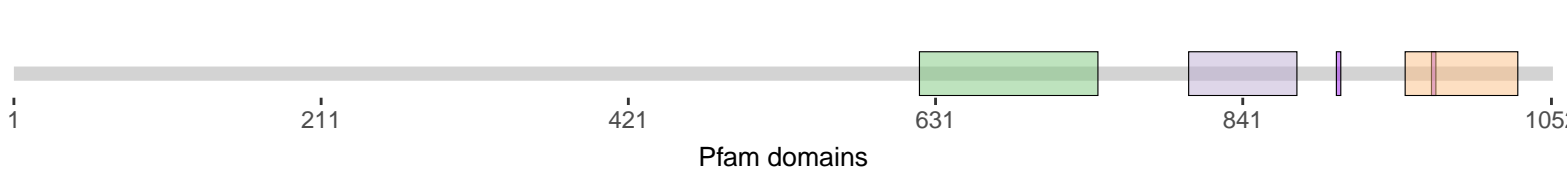


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

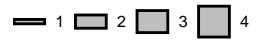


Protein sequence:

YMTDGMLLREFLGEPLASYSVIMVDEAHERFLSTDLFGLVKDIARFRPDLKLISSATLDAEKFSDFVDCAPFKPGRFFVEHHTYKPEADYLDAAVATLQIHTQPPGDDLFLTGOEETAEIHKRIKGLGTRIAELICPIVANIPTLQAKFEPTPEGARKVVLATNAETSLTDGKYVVDGPFKMKSYNPRTGMEISLITPISKASANDRAGRSGRTGPGKGFALTYAVNYMNDLEONTVPEIQRNLANVVLGKSLGHLNLFDFMDPPPEALLKALEMLF

NbL03g19100.1 UDP-glucose_6-dehydrogenase_5-like [MW = 52.91 kDa]

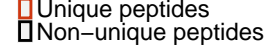
No. of times detected



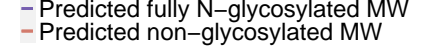
log(intensity)



Values from



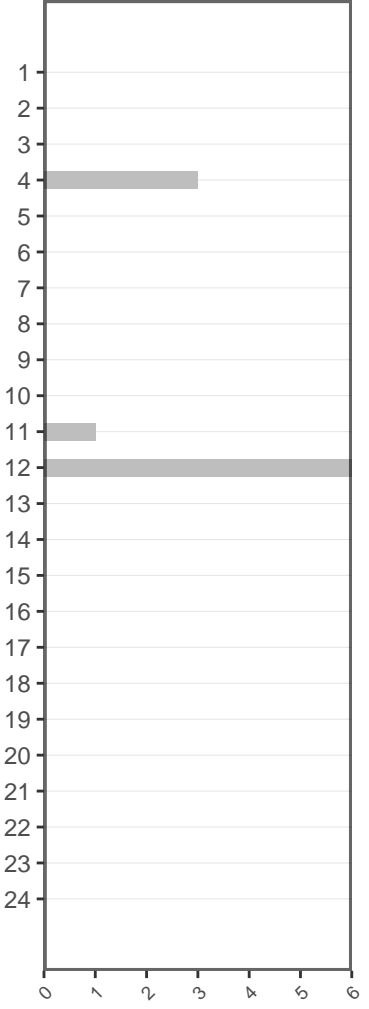
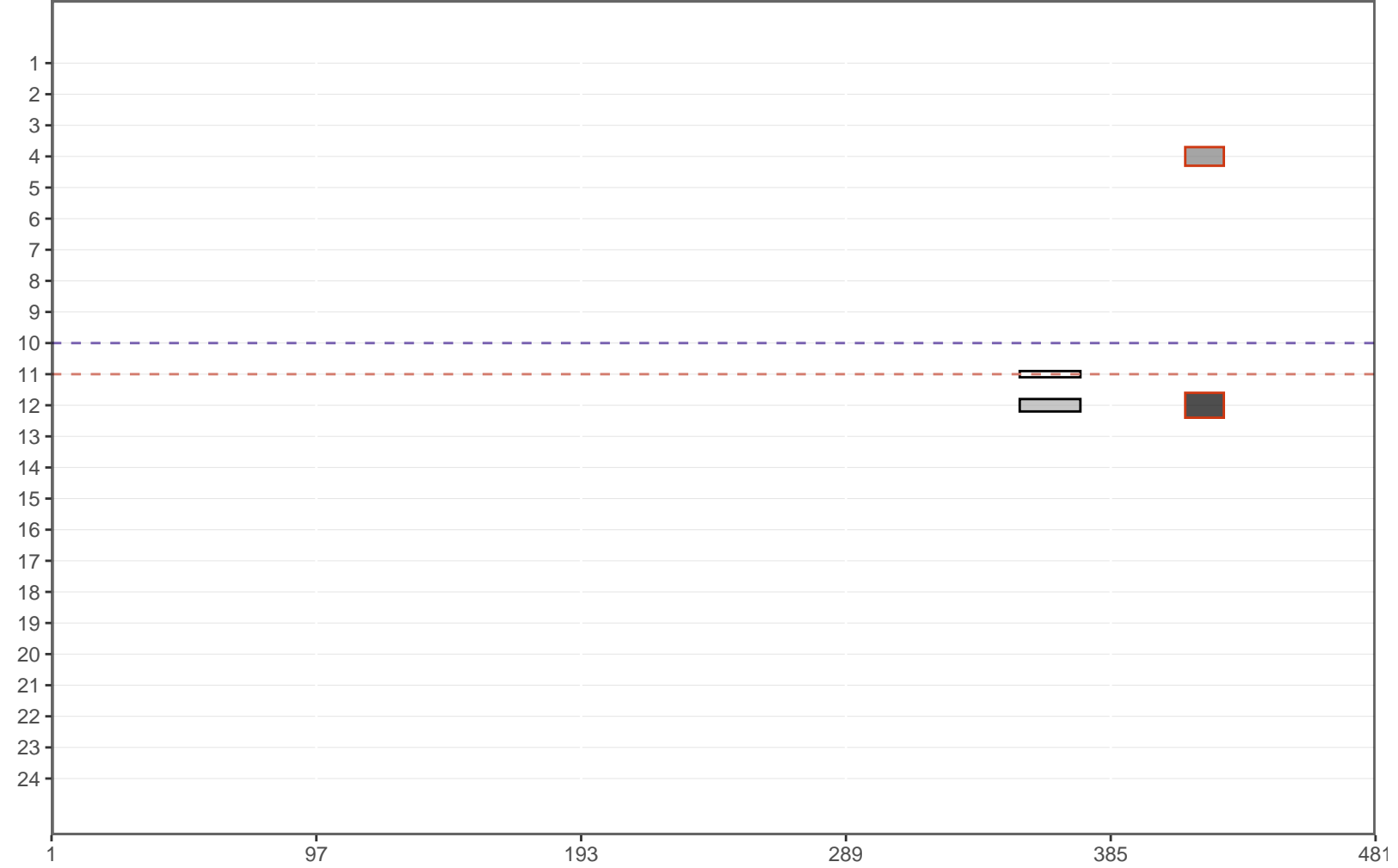
MW indication



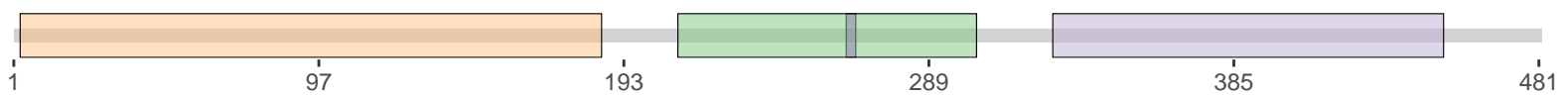
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00984 UDP-glucose/GDP-mannose dehydrogenase family, central domain
- PF03720 UDP-glucose/GDP-mannose dehydrogenase family, UDP binding domain
- PF03721 UDP-glucose/GDP-mannose dehydrogenase family, NAD binding domain

Protein sequence:

NAMISALCEATGADVTVQVSNAGKIDTRIGPKFLNHSVFGGSGFGKIDLNLYVIGEGNGLKEVANYWYGVKVNQVYGNFRFVNRVSSMFTVSGKKVALGFAFKKDTGDTRETPAIVDVGKLLGDNAHLSHYDQGVTEDDGDKLMSMKFDWDHPTLHGFMSPCAIVKQANVVDVAYEATKDAHSLGLTEWDFKTLGPKVYDSMGKPAFVFDGRNVVDAEKLREIGFVYVSGKPLDMLKMPAAV

NbL03g19080.1 40S_ribosomal_protein_S19-3-like [MW = 16.03 kDa]

No. of times detected



log(intensity)



Values from



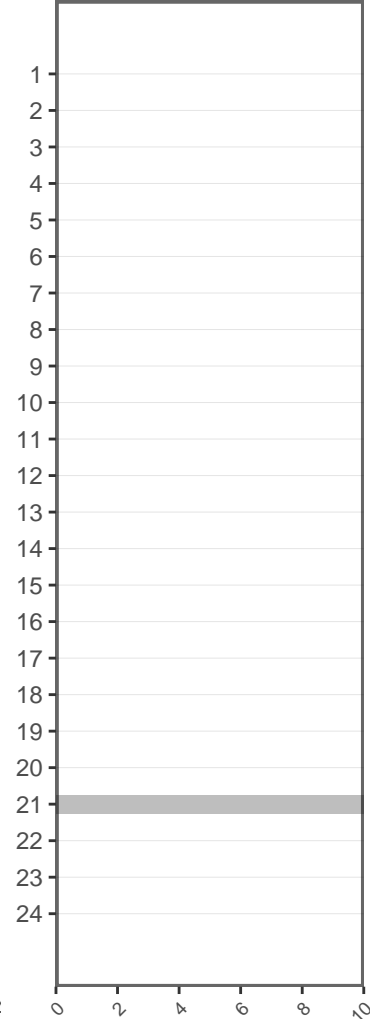
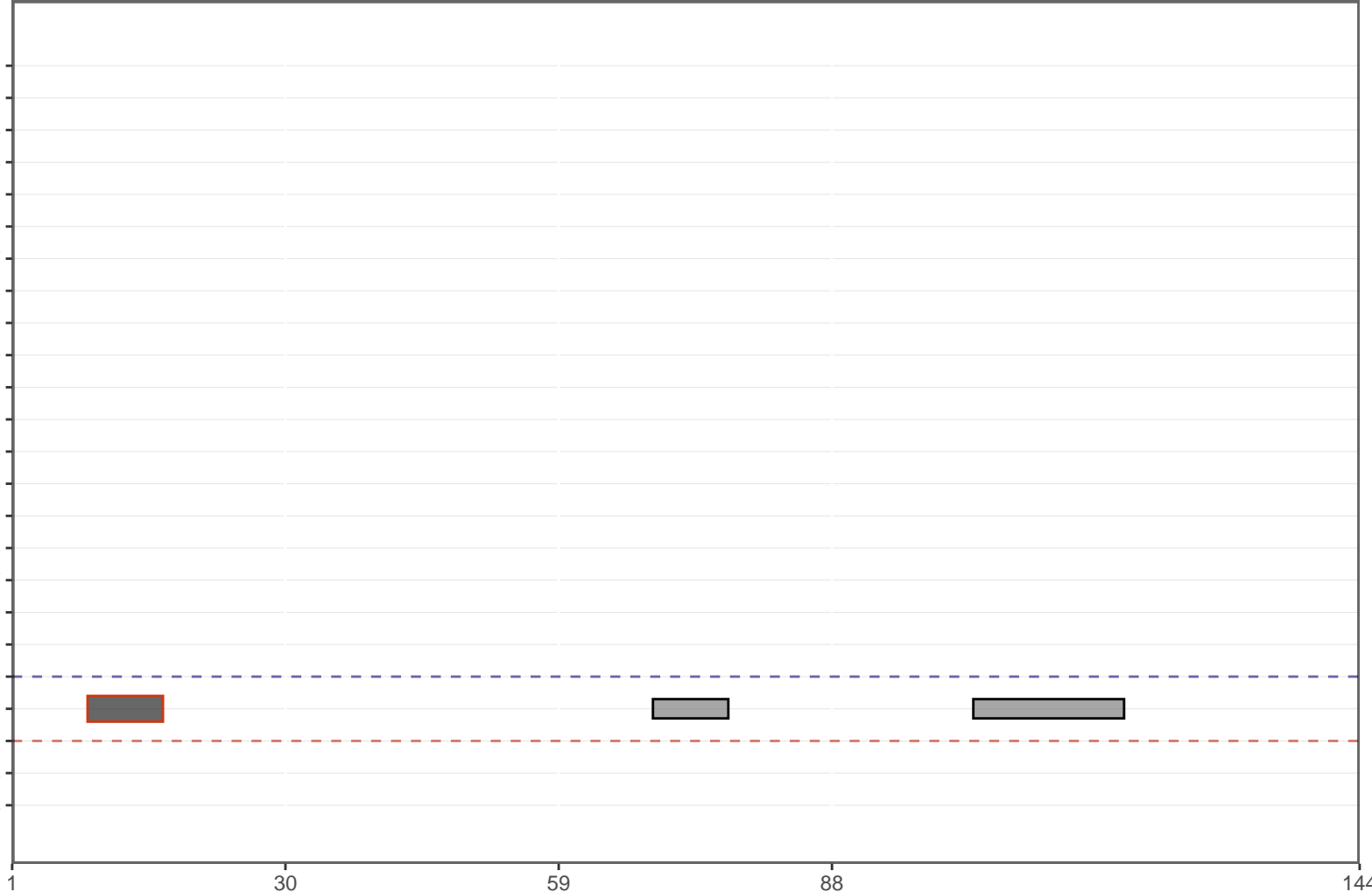
MW indication



Molecular weight



Gel Slice

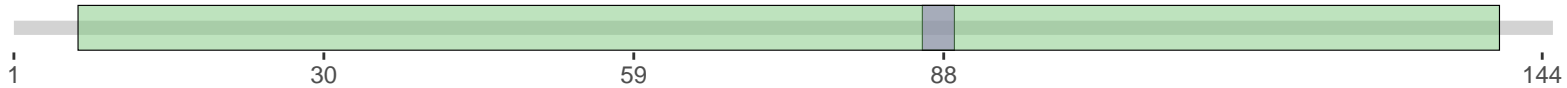


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ISMARKYLRIGQLGVGGFRRIHGGNGRNGRPRRHFCIKSGSGVARNLQQLQNMNIDFPKGGRRITFNSGGRDLDDVAGRIAW*

NbL03g18870.1 uncharacterized_LOC109223785 [MW = 18.77 kDa]

No. of times detected



log(intensity)



Values from



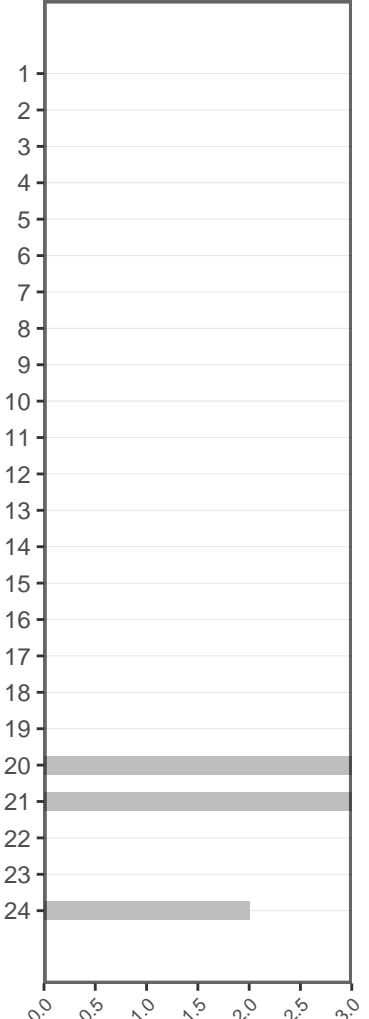
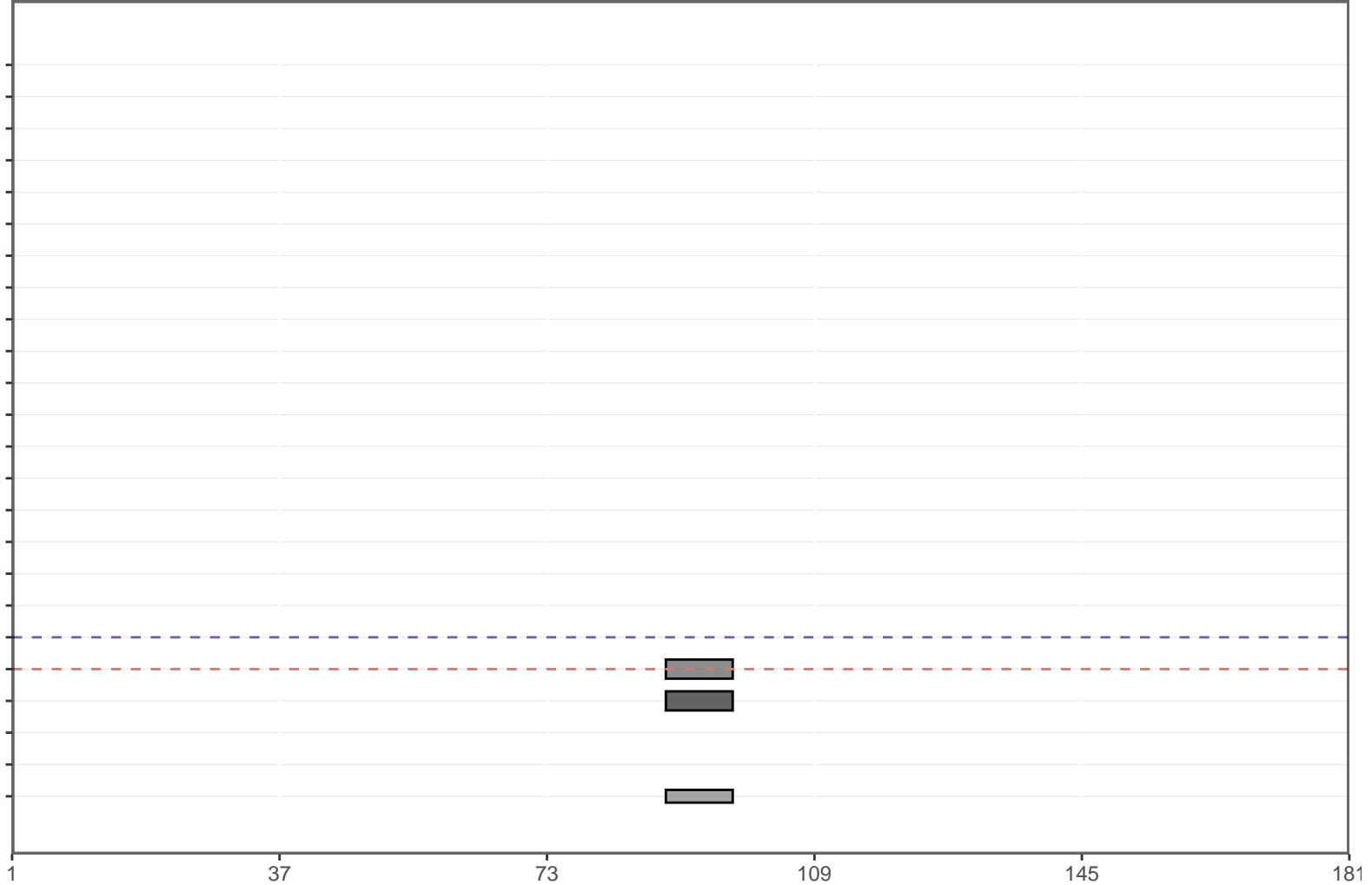
MW indication



Molecular weight



Gel Slice

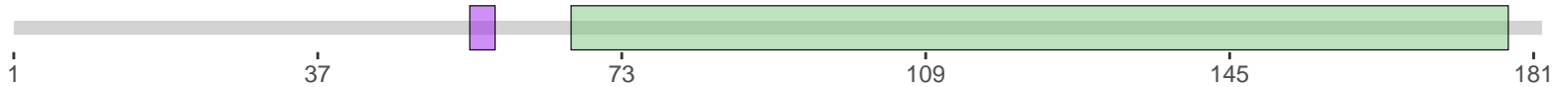


Peptide counts over 4 repeats

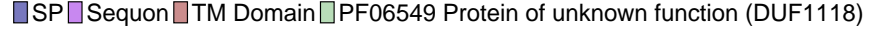
Protein length



Pfam domains



Pfam Description



Protein sequence:

LEKAGLLSAEKSGLSLSTIERLGLLKAEEFGILSAATDPTPRAALFSLRLGLLVLGPMGVVLPEDYPPWGVVGVVLLVLLVVGGSAAFGAENLVNLSQKIK*

NbL03g18790.1 probable_UDP-arabinopyranose_mutase_2 [MW = 41.18 kDa]

No. of times detected



log(intensity)



Values from



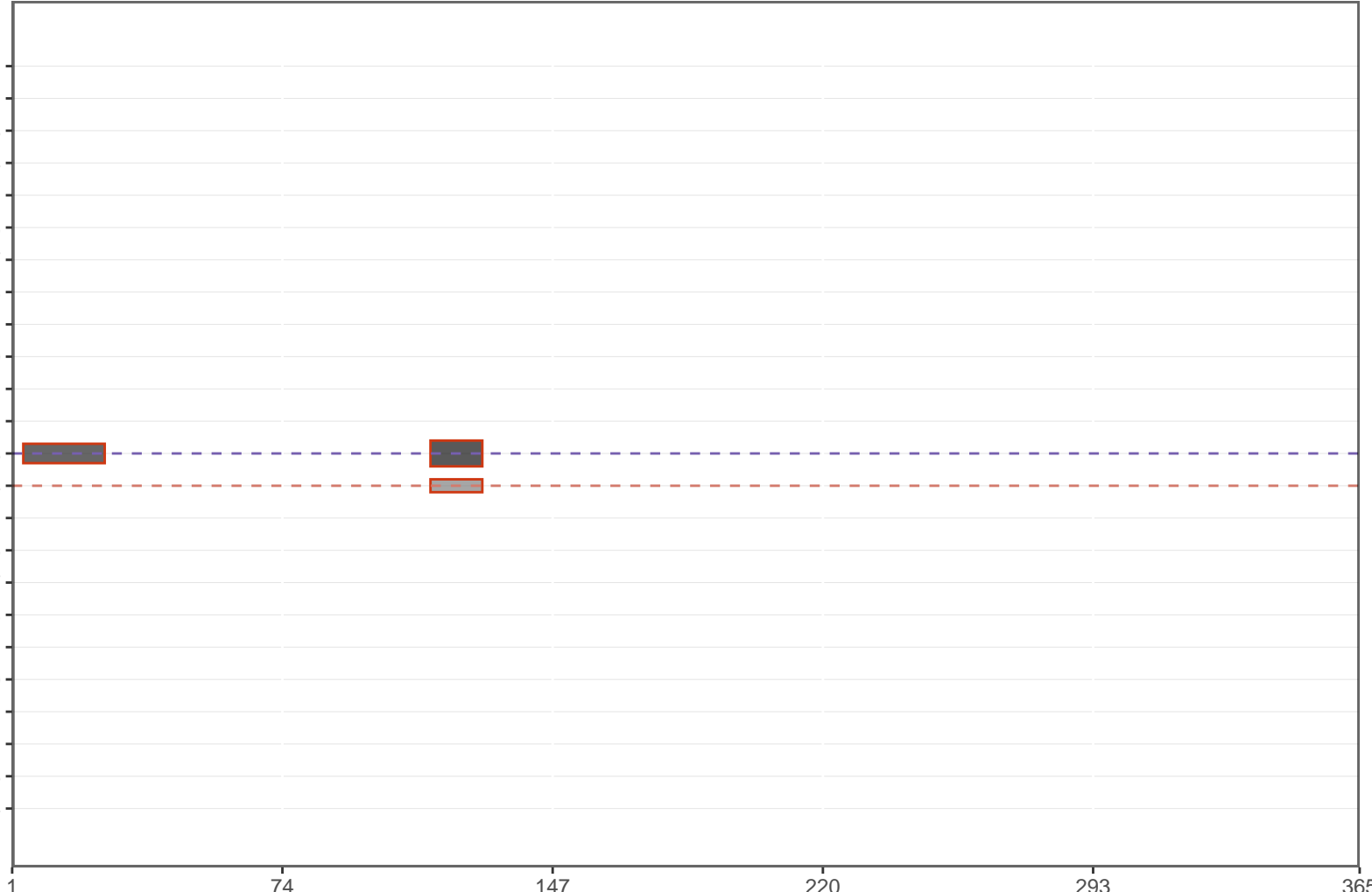
MW indication



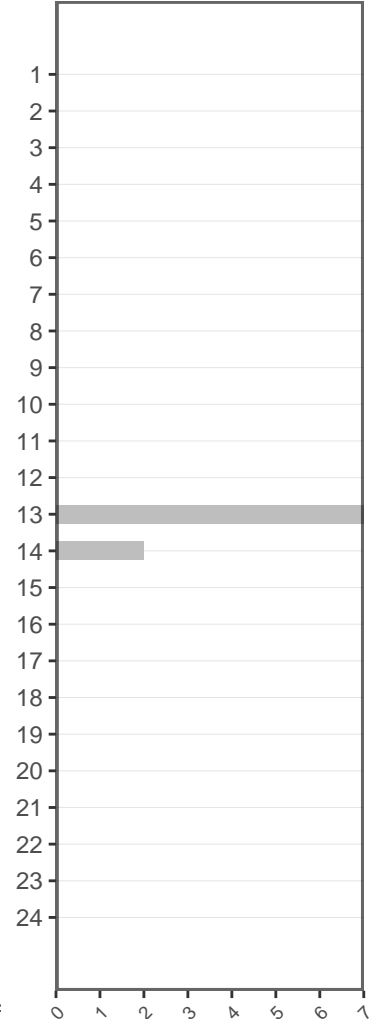
Molecular weight



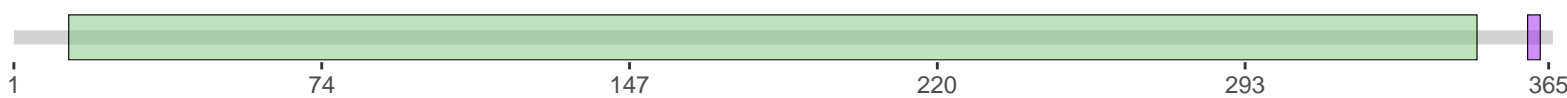
Gel Slice



Protein length

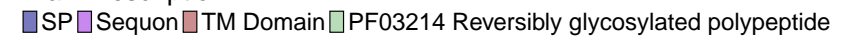


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LWLNPDYDAPTLQVPLERNTRYVDAMTPIKGTLFPMDCGMNLAFDRELSGPMYFGLMGDDGPGIRYDMMVAAGWCTKVCDELGLGVKTLGPIYWHKSNPFVNLKKEYKGRVWDEELPFQGVTLFVKDCTSVQKCYLELQKQVKAALGKVDVDFNKLADAMITWIEAWDELNPSATATAKIPNGSSK

NbL03g18730.1 flavonol_3-sulfotransferase-like [MW = 14.89 kDa]

No. of times detected



log(intensity)



Values from



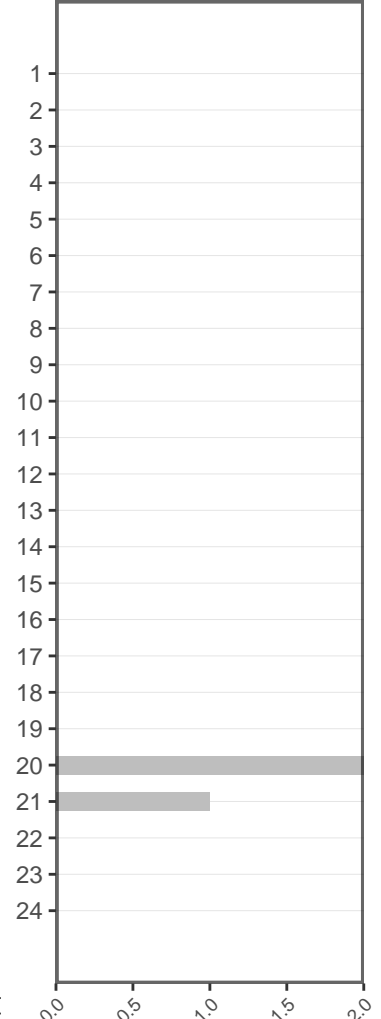
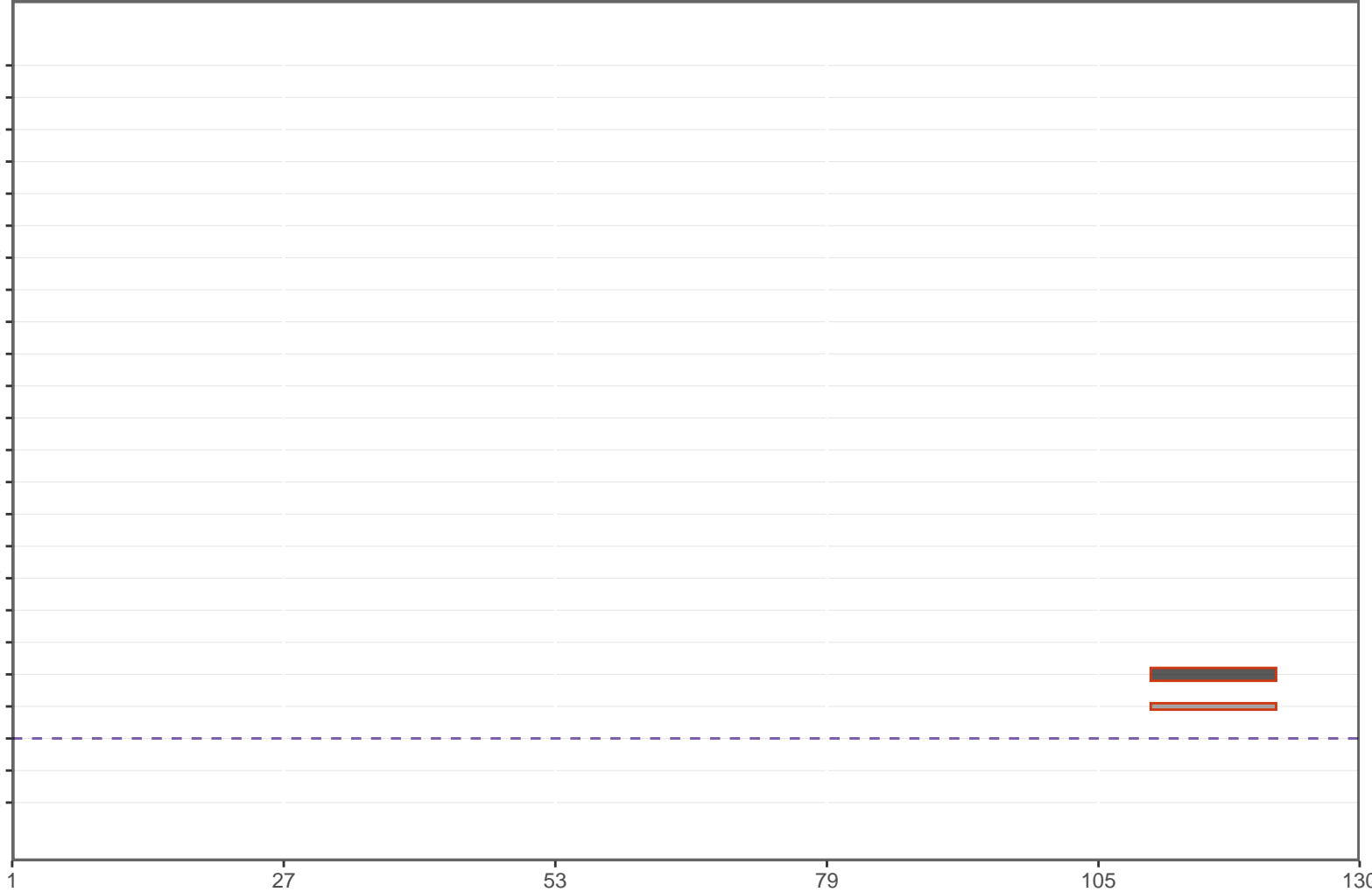
MW indication



Molecular weight



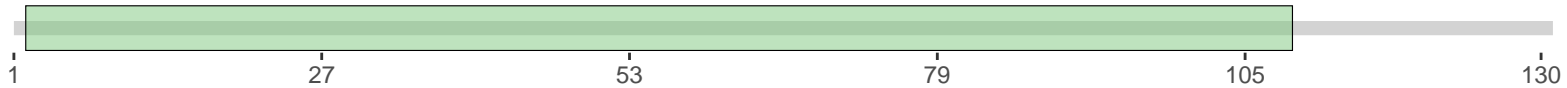
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

MLPPISLQEAFDQDFTEGGSPFGPFWDHVRGYYKASLEFPKSVFLRYEDLKKDPMFHAKNKLEEESEGIVKTEISDF

NbL03g18610.1 UDP-glycosyltransferase_89B2-like [MW = 53.43 kDa]

No. of times detected



log(intensity)



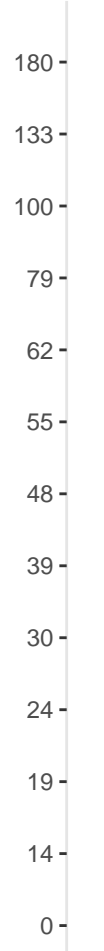
Values from



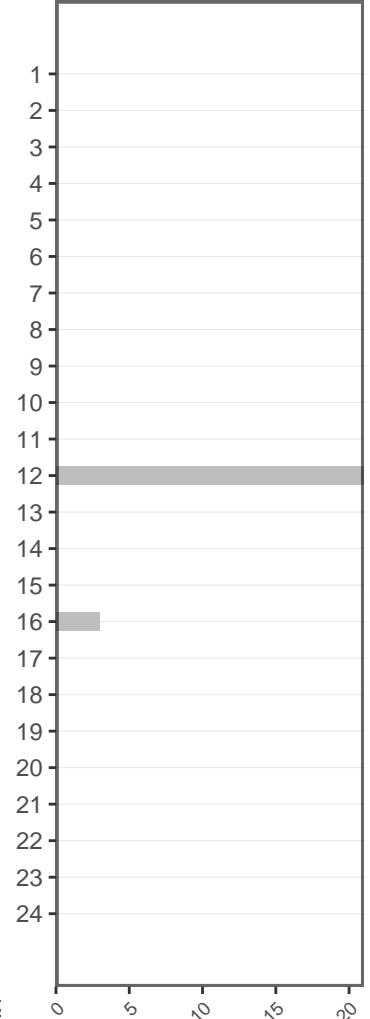
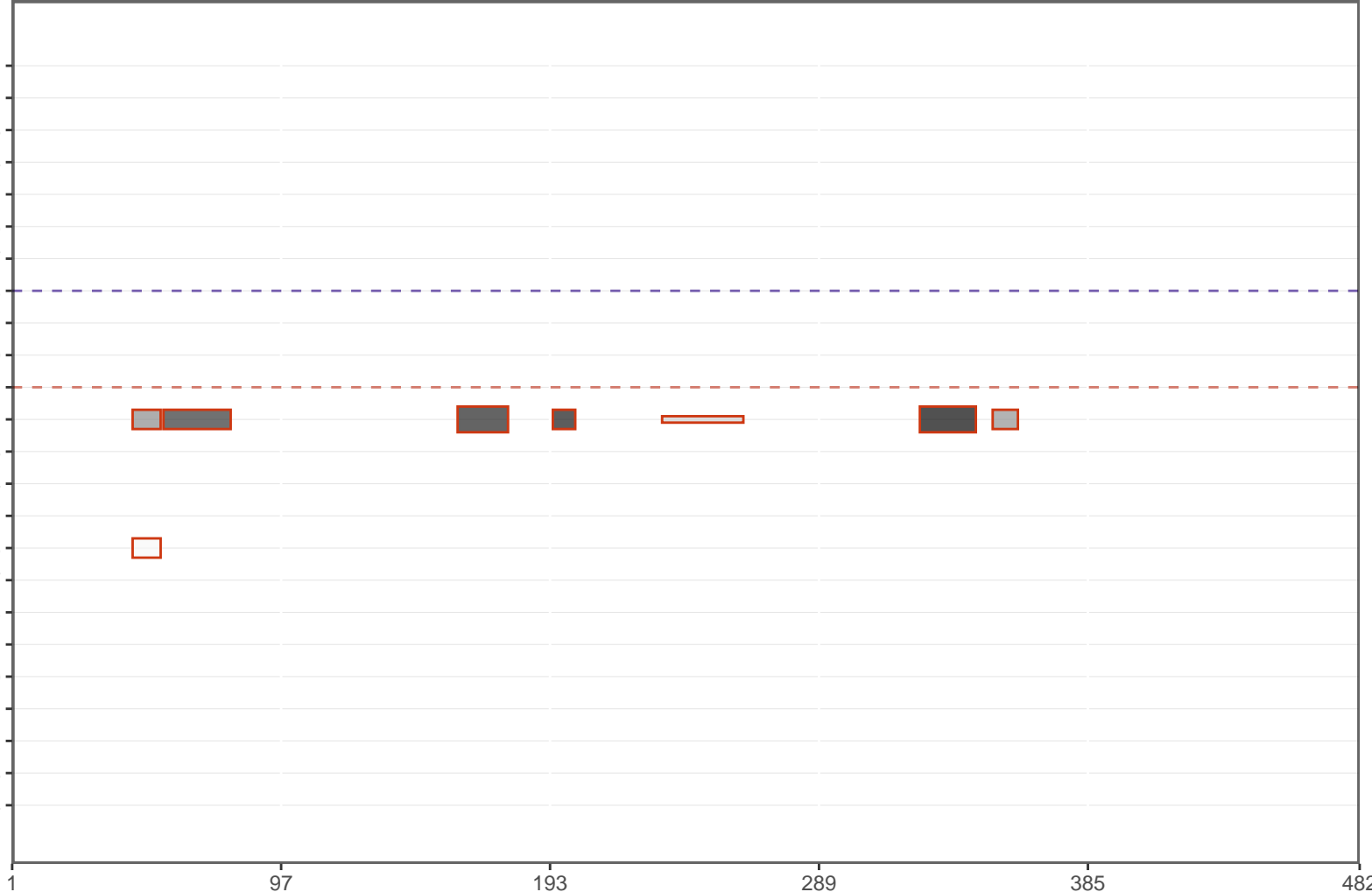
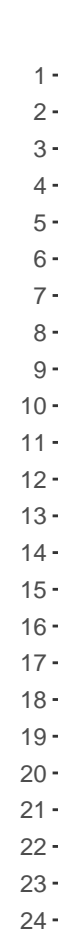
MW indication



Molecular weight

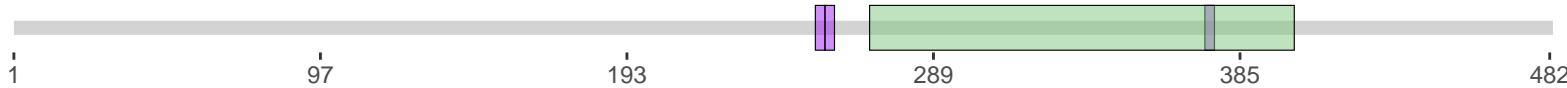


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

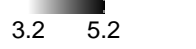
IKDLGHSVWVWVGPVLPDDENDTNGSSNRGGSSVLAELAWLDTGCDNSVYVFGSGAVLTNGMEELAALEKSGVFIWSAKRATKGVHSTNYGVVPSWFEFEIAGRGLVIRDWAPQVLUKHRVAFGLTHDGVNBTLEGLVAVPMLTWPMGADQFANALLDEHKVAFRASEGAKTPTNDELAKLAEAVGGKGVERRERASELRKAAALNGIKEGGNSFKDLKLEIFVWHLSEEAAKIKR

NbL03g18430.1 calcium_sensing_receptor_chloroplastic-like [MW = 41.87 kDa]

No. of times detected



log(intensity)



Values from



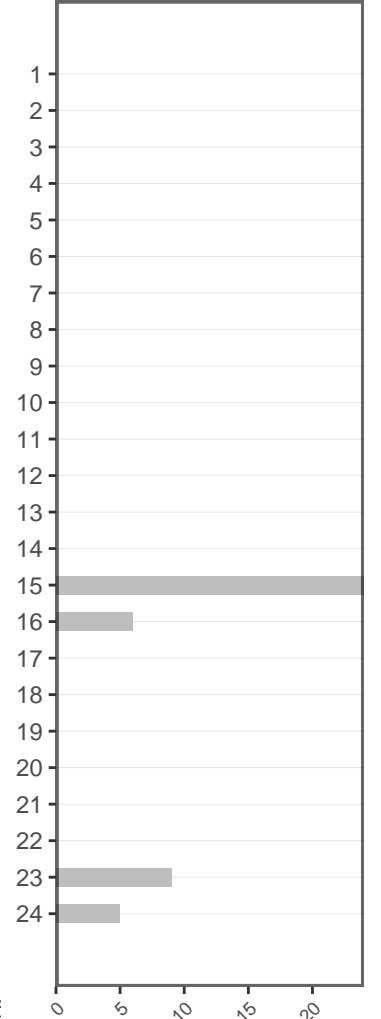
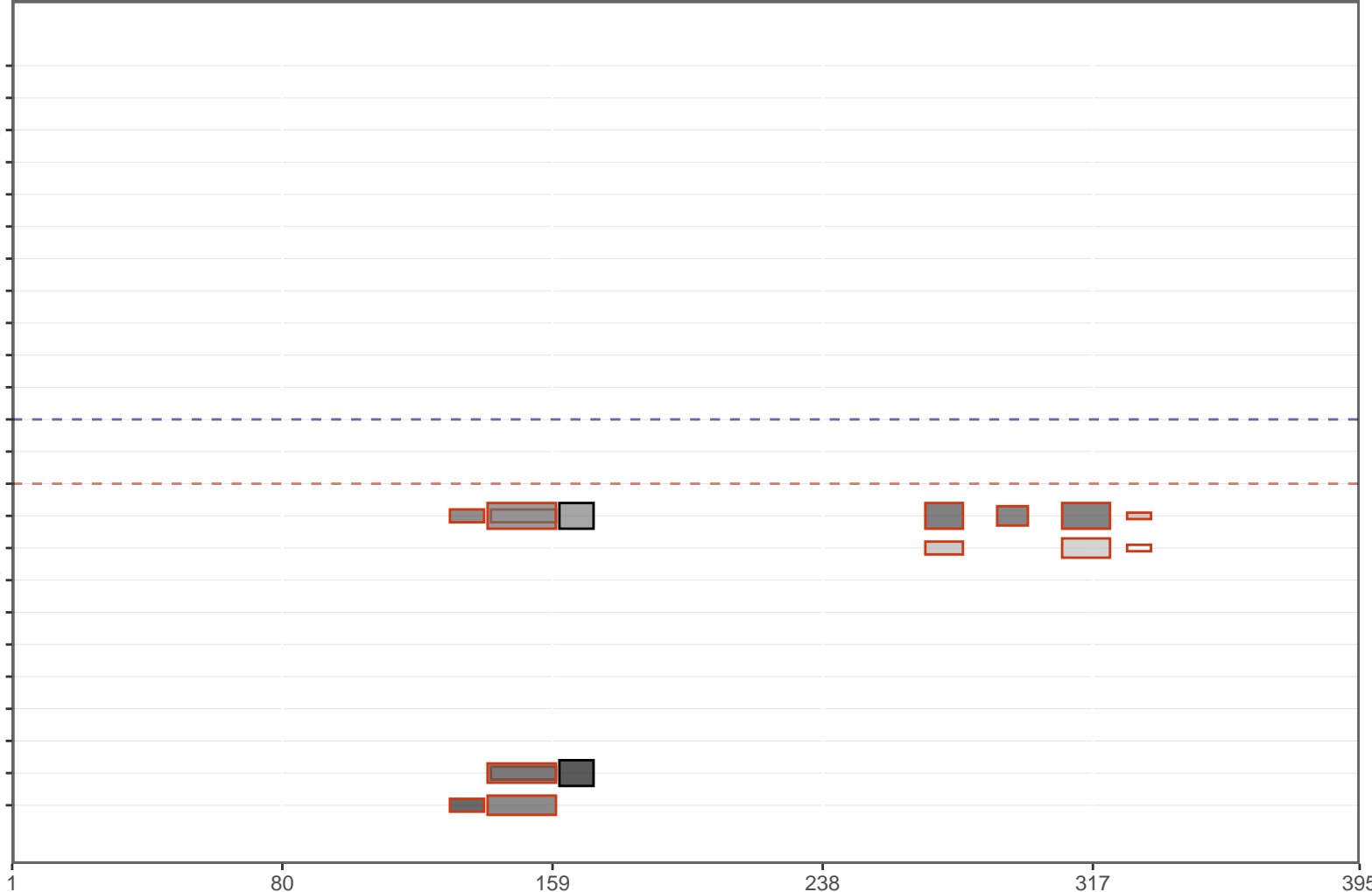
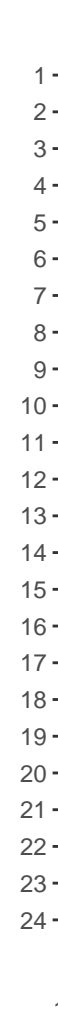
MW indication



Molecular weight



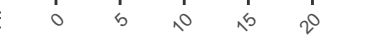
Gel Slice



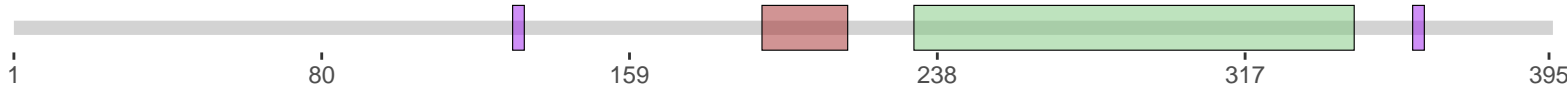
Protein length



Peptide counts over 4 repeats



Pfam domains



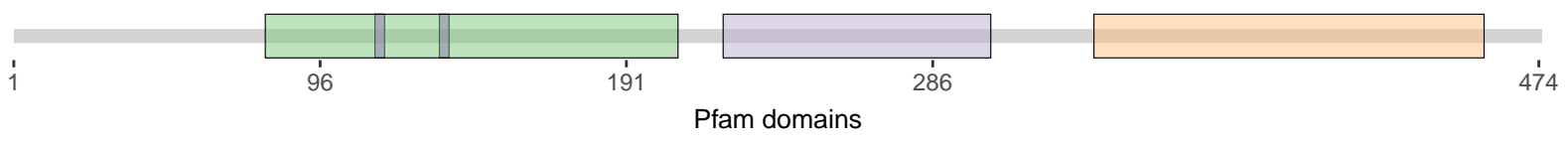
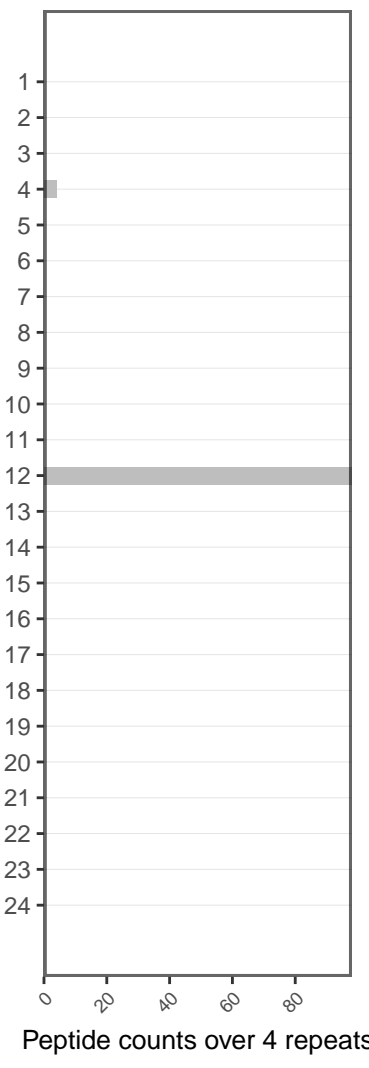
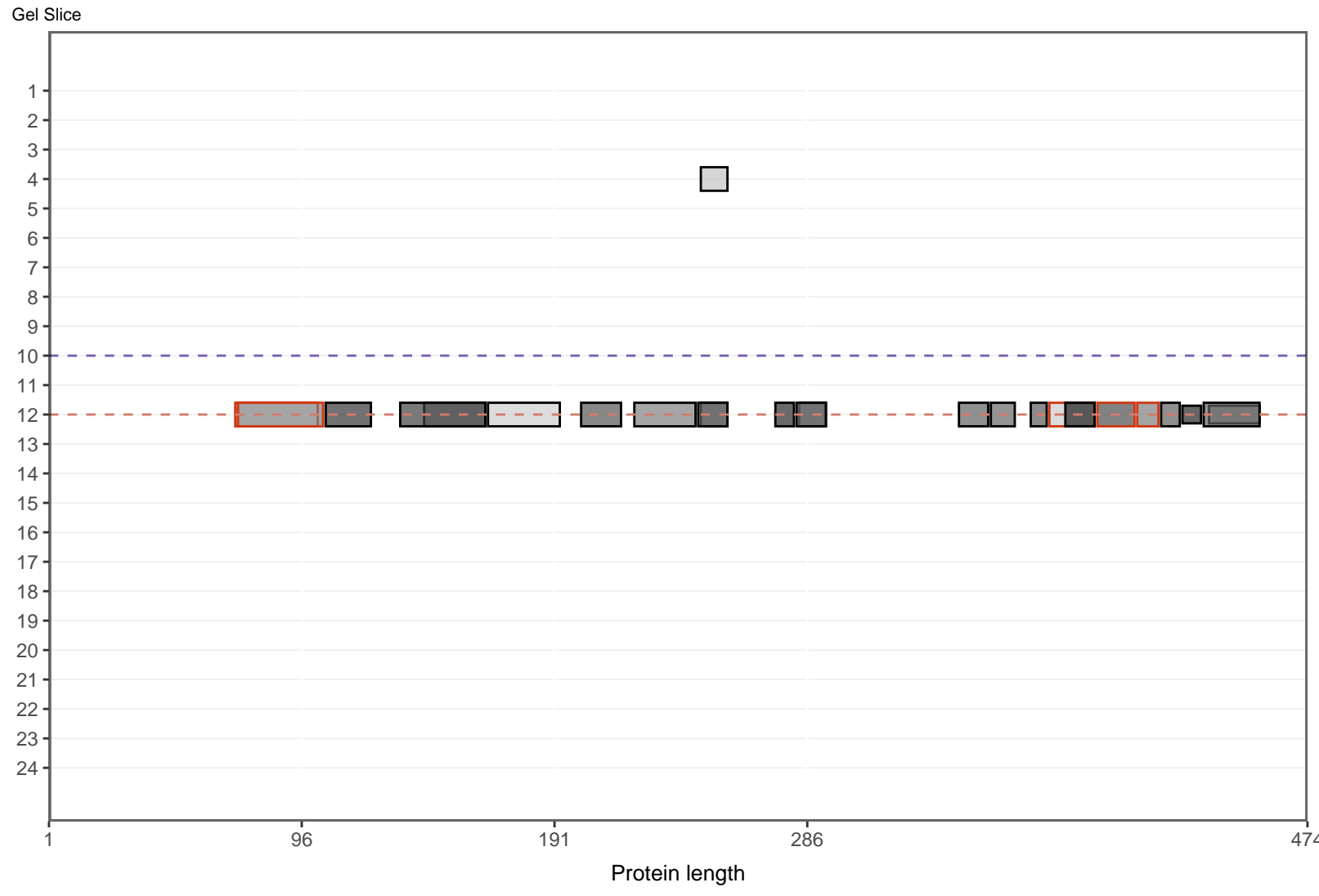
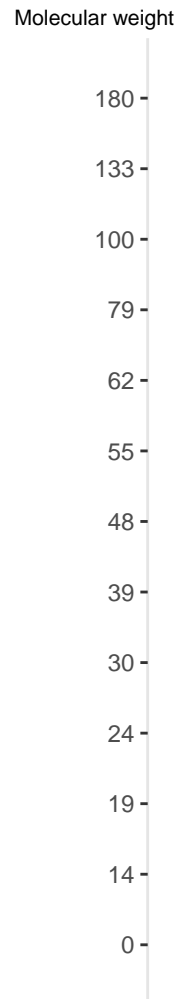
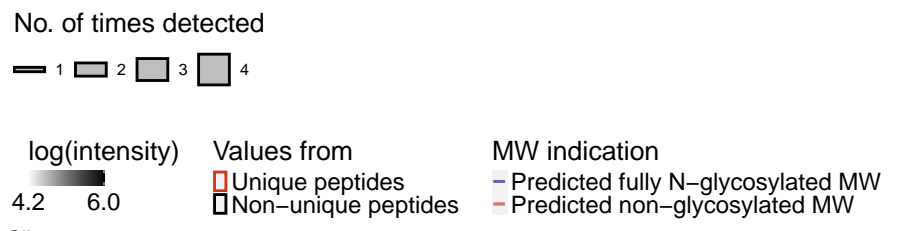
Pfam Description



Protein sequence:

VETISSADPAIIAVGGTFLAVLFPPLVLSALSFBLRGVYKGLTPAGTLDQMSKHYVLDIRTEKDKKAGIPRLPSANKNKIQPLEDLPSKRLSLVRAKVAEALVALKISYLVKKNKGSNIVMDSYDSEAKTVAKTLTSLGPKNKWMTDGFSGGRGWLQSKLGTDSYNFSAQVLSRVRVRAARRFDTGTVKLLSGGSD

NbL03g18370.1 1-deoxy-D-xylulose_5-phosphate_reductoisomerase_chloroplastic [MW = 51.29 kDa]



Protein sequence:

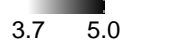
ADSEHSAIFQCIQGLPEGARLRRLTASGGAFRLDLPVEKLEKVKVADALKHPNWNMGKNTVDGATLFNKGLVEIAHYLFGAEYDEIEIVHPQSHSMVETQDSVLAGLWPDMLRPLVLTLSWPDRIYCEVITWPRLDLGLKLSLTFKAFDNNKYVPMDLAWAAGRAGTMTGVLGAANEKAVELFISERISVLDPKIVELTCAKHREELVSSPSEEEIHYDLWARDVAASLETSAQFSPALV

NbL03g18270.1 uncharacterized_LOC109214664 [MW = 33.39 kDa]

No. of times detected



log(intensity)



Values from



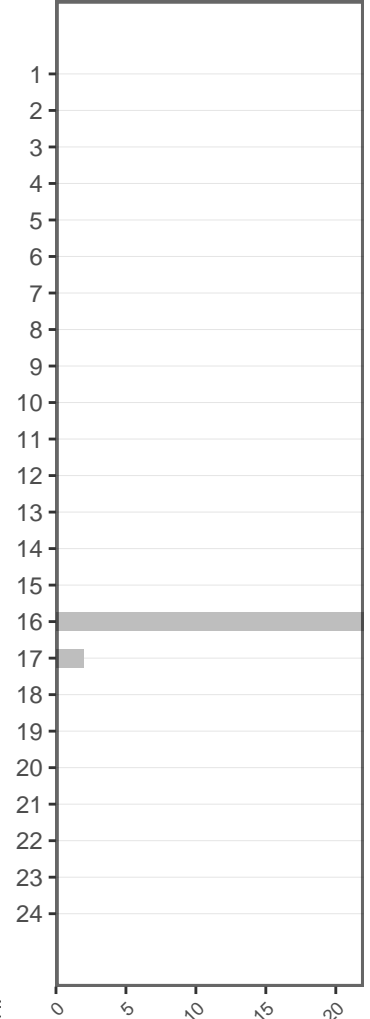
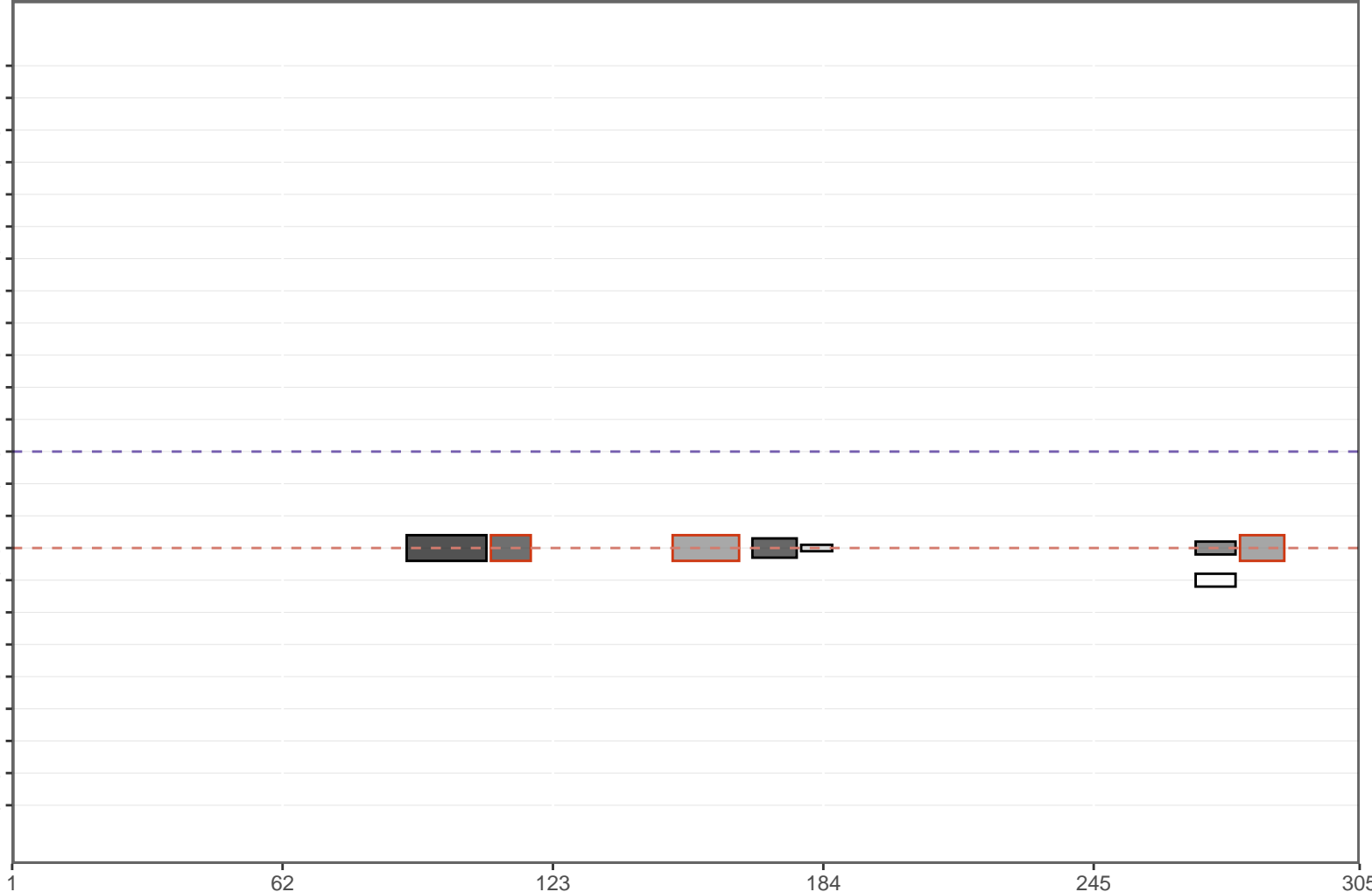
MW indication



Molecular weight

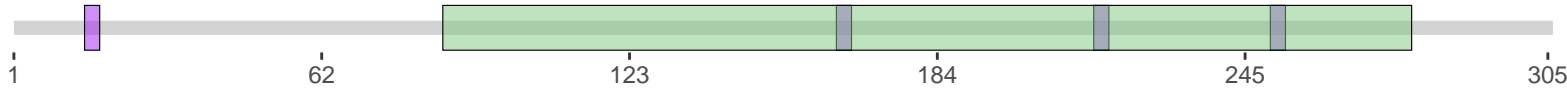


Gel Slice



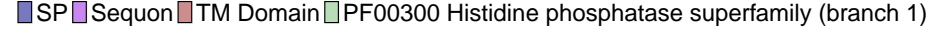
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ICWVWPSITQRAYCTAEIAAVNGVNRIRVPEYSLDARGLGAVEGEKSLDLAEVYEESSLSFNKPPPTDGGTPESEVSDVFRVVTQVMSEVLETQVSEDTVIHVSFDSNLFLQAGLTLGLRLRRHRLSFGPGEVRYVDSGSIPTYKGPASKVYKGLNPPGCT

NbL03g18210.1 UDP-glycosyltransferase_90A1-like [MW = 54.62 kDa]

No. of times detected



log(intensity)



Values from



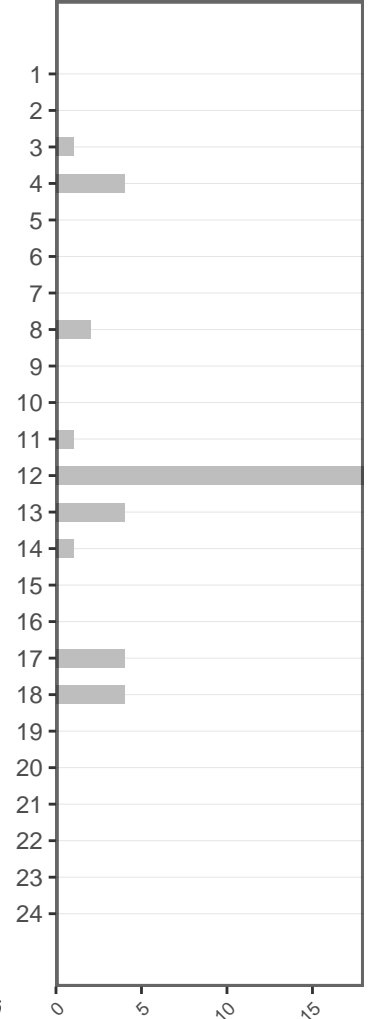
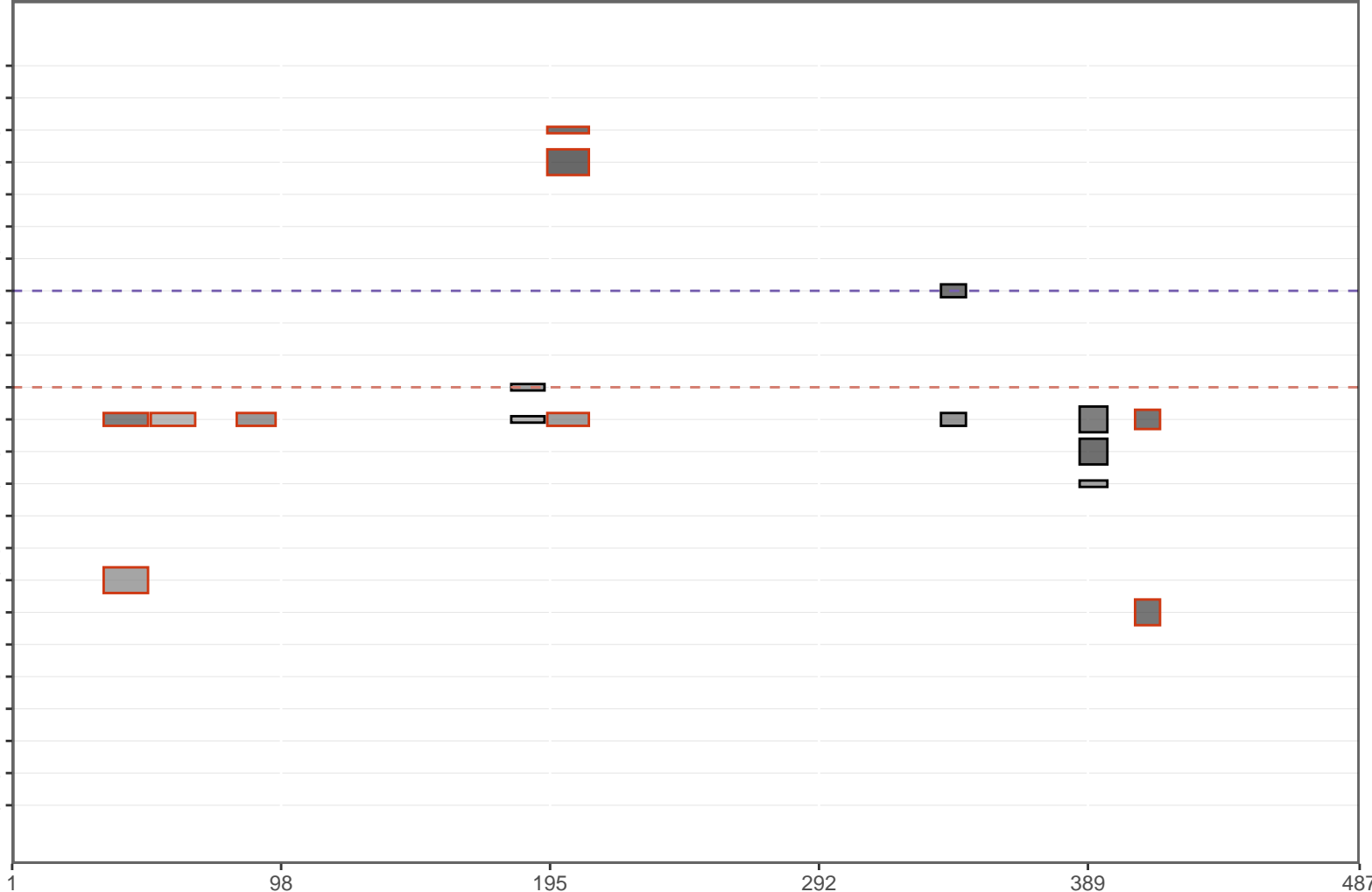
MW indication



Molecular weight



Gel Slice



Protein length

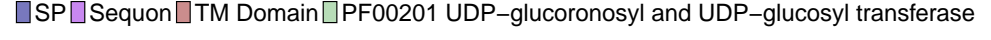


Peptide counts over 4 repeats

Pfam domains



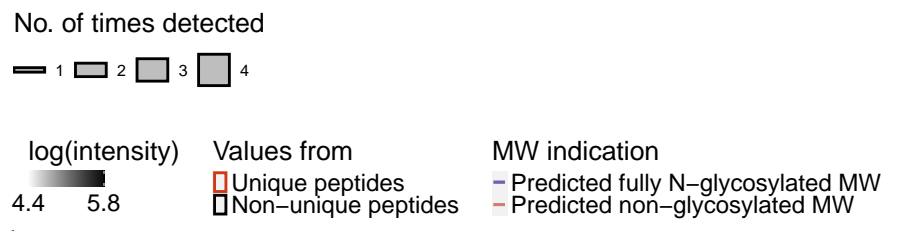
Pfam Description



Protein sequence:

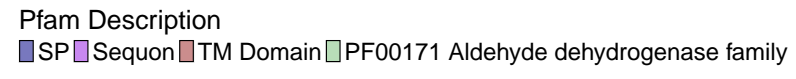
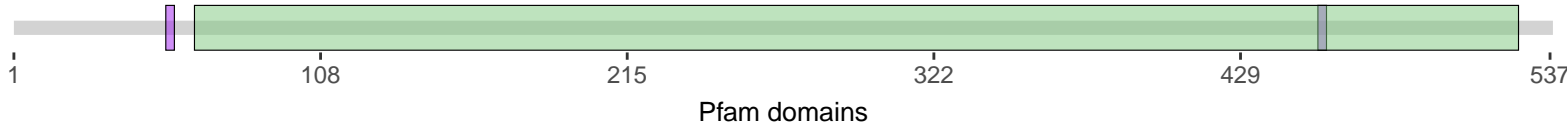
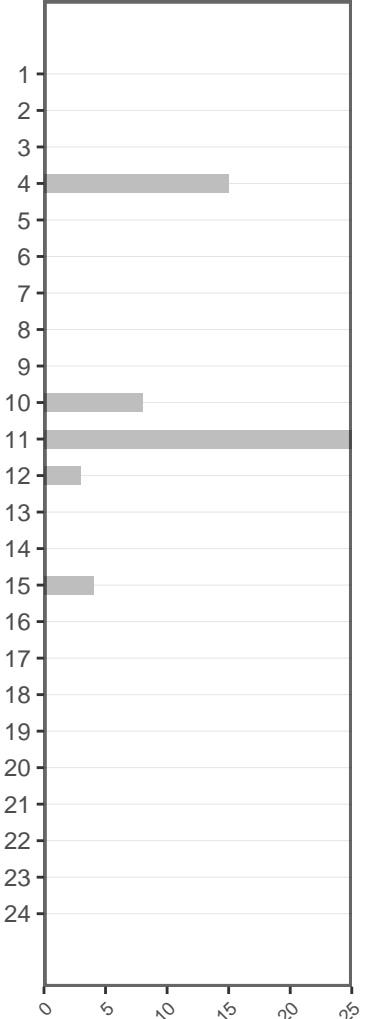
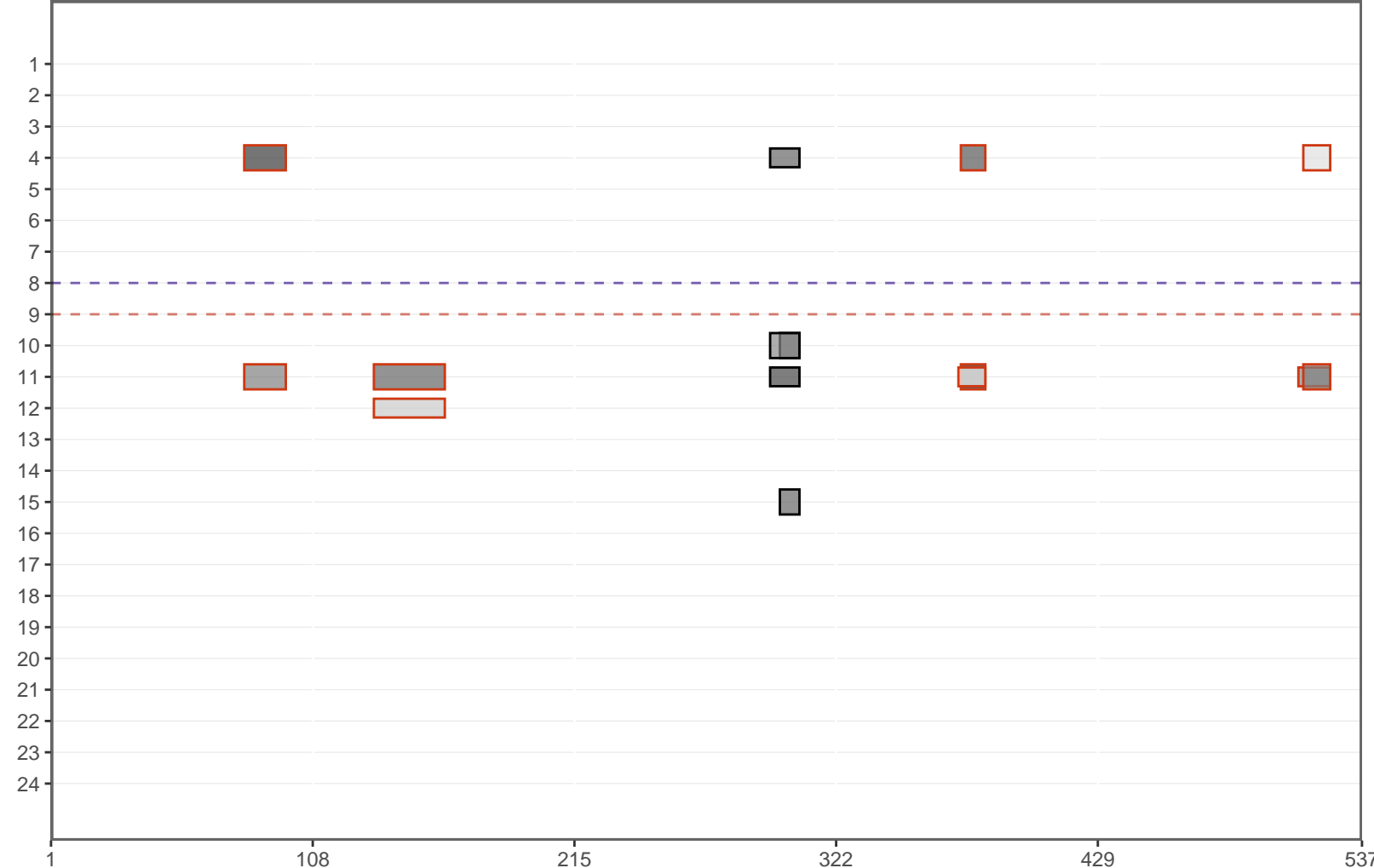
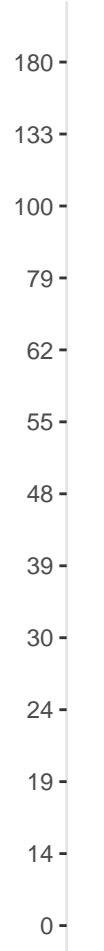
KSWCVGFLCLAKGPMNTNTDPRDKHETWIMQWLNKSLADRQPLVYVAFGTQAEISAEQIGEARGLLELNTSFLIYVTRPKVLYHLKGFEEVRYKDRALVKEVVDQSEVLRHRSKGFGLCHGQWVNSMESICAKVPLSLPLMAEQHIANRFVVEEIGVGLRIMPVNGSVIRGFVEAEVEKMMVRELMEGEKGLRKKVKEMGENAWDSMKEGLRKKVKEMGENAWDSMKEGGSSWTLGLLDDAGDGKIK

NbL03g18170.1 aldehyde_dehydrogenase_family_2_member_B4_mitochondrial-like [MW = 58.53 kDa]



Molecular weight

Gel Slice



Protein sequence:

SGFGPTAGALASHMVDKLAFTGSETGKTVLELAAKSNLKPVTLELGGKSPFICEADADHVAELAHFALFFNNOGCCCCAGSRITYHERVYDERIEKAKRANRRVYGDPRFKGVGEGPQDSKQFKVLRHR6GRD6SATLEGGDRFSGKGYFQPTVFSNWKEDMLAGDEIFGPVQCVFKFKDGEVKRANRNYGLAAGVFTKNIDTANTLTRGLRAGTVVWNCYDFDAGIPFGGKMSGMSGREKGYLSNLYLKKAVVTLKKNPWW

NbL03g18140.1 protein_NUCLEAR_FUSION_DEFECTIVE_2 [MW – SP = 17.02 kDa]

No. of times detected



log(intensity)



Values from



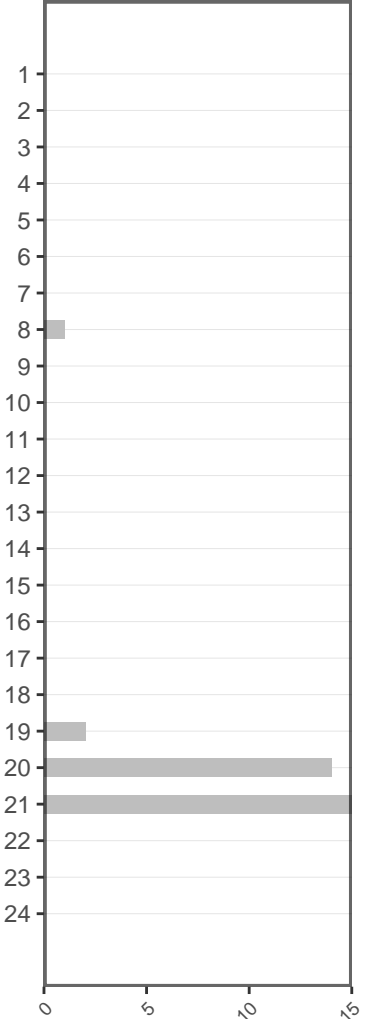
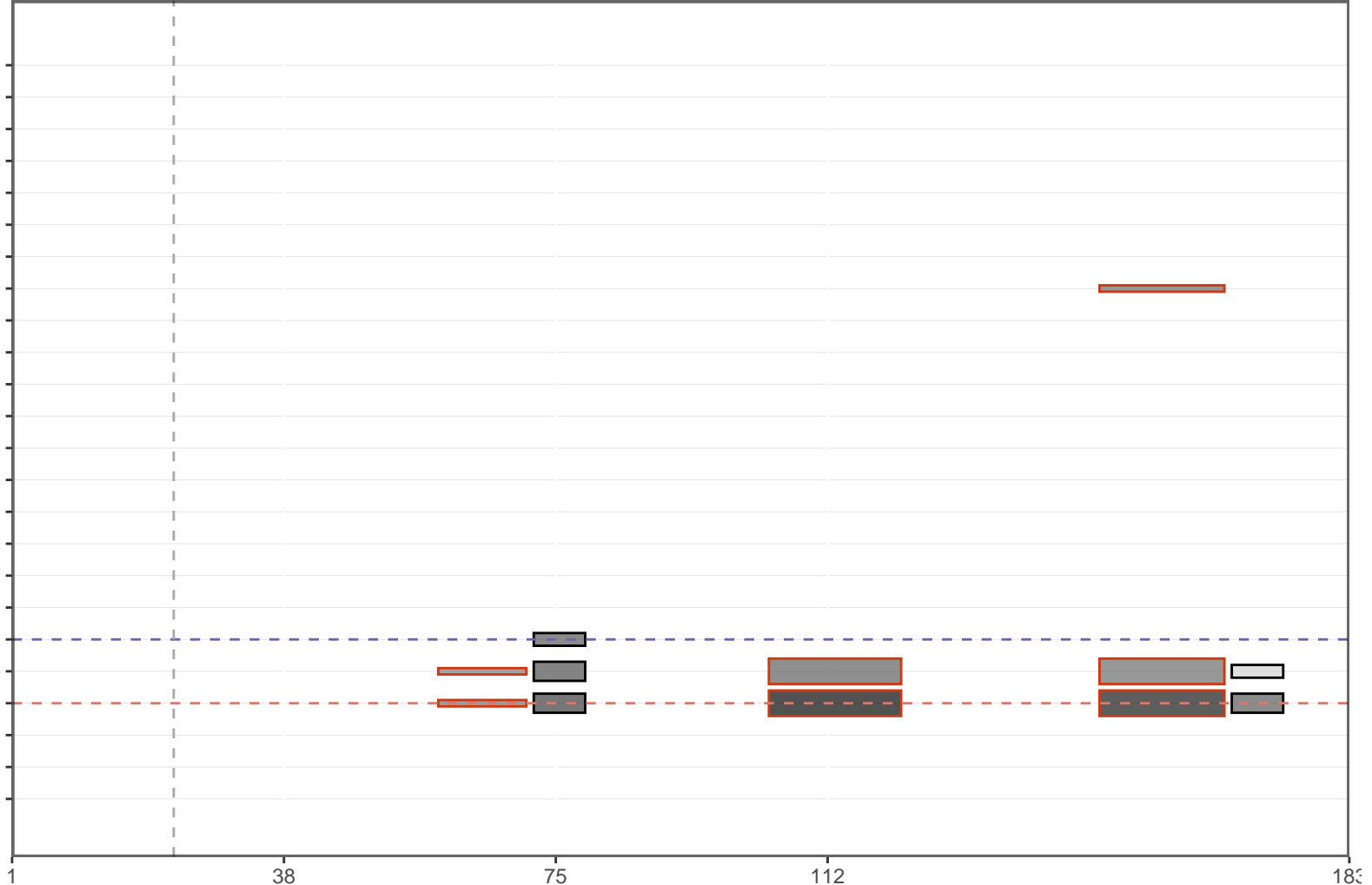
MW indication



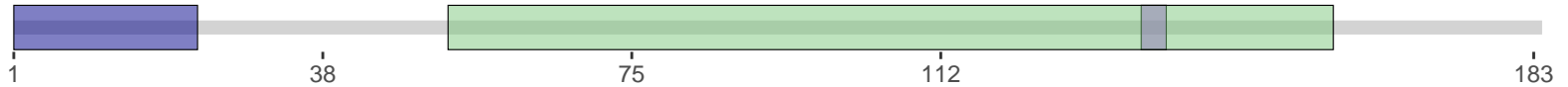
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

KAIEGSVSLQLLRKNDMPKDLNRAIAELSNVFTSGAADGERLGLQKIVRVSHKTNSSAPVWCGAFRAMFGAIDTSSLNAGKVFVFGHGKGMEGAMAM*

NbL03g18090.1 39S_ribosomal_protein_L47_mitochondrial-like [MW = 18.97 kDa]

No. of times detected



log(intensity)



Values from



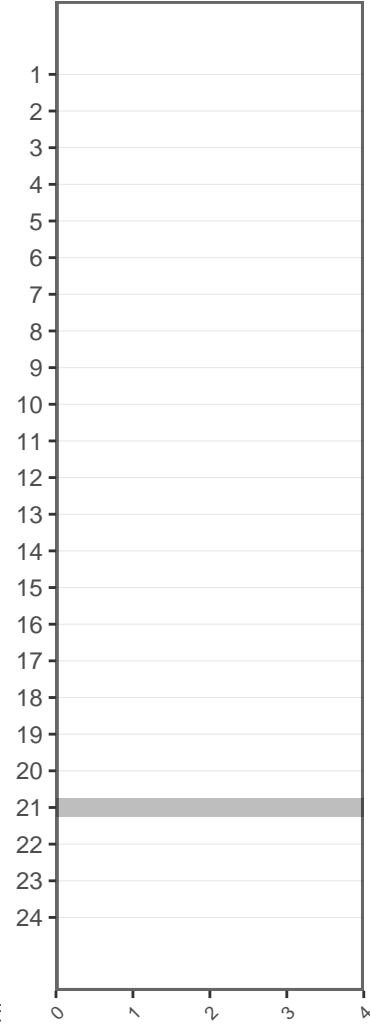
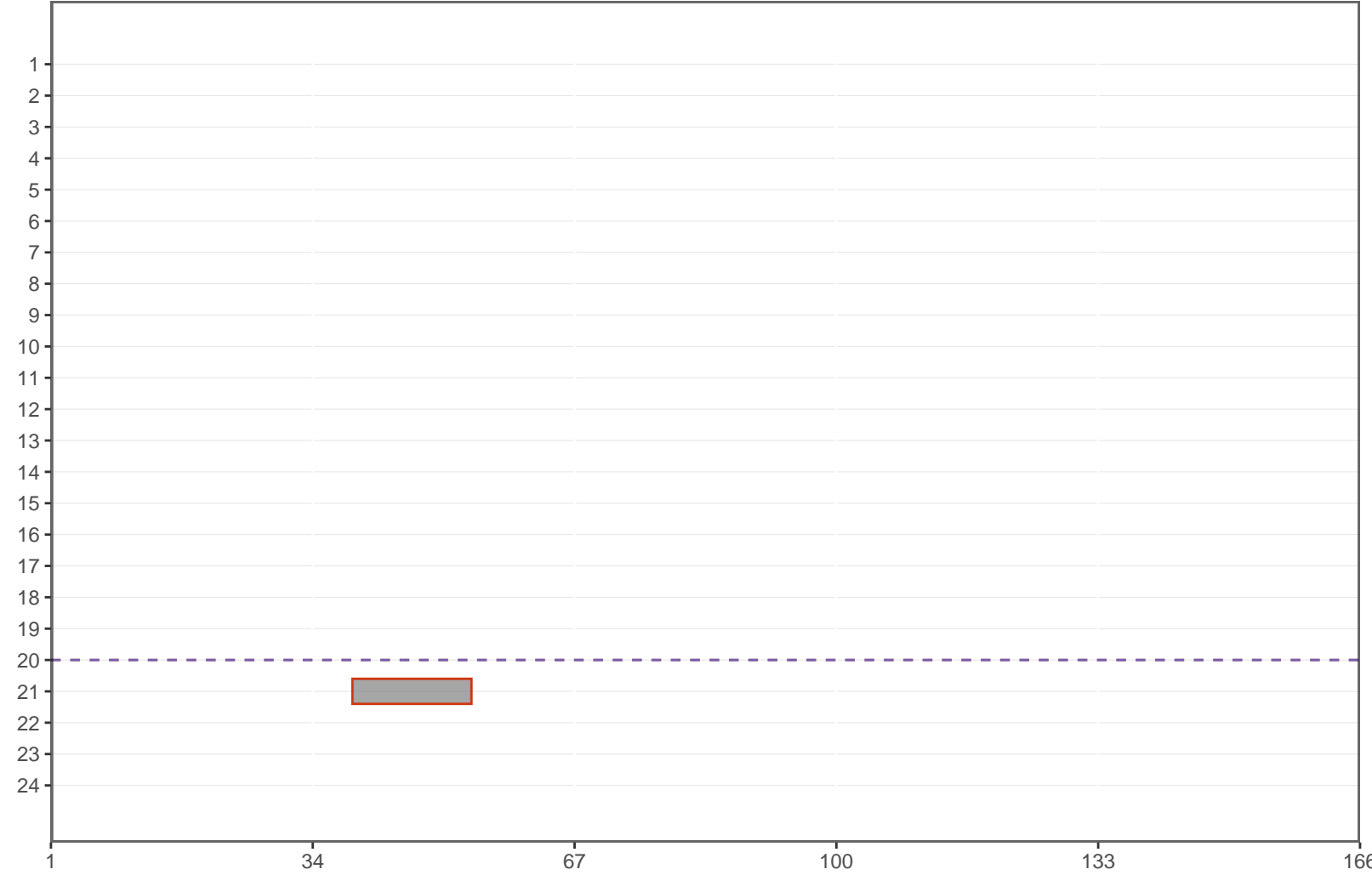
MW indication



Molecular weight

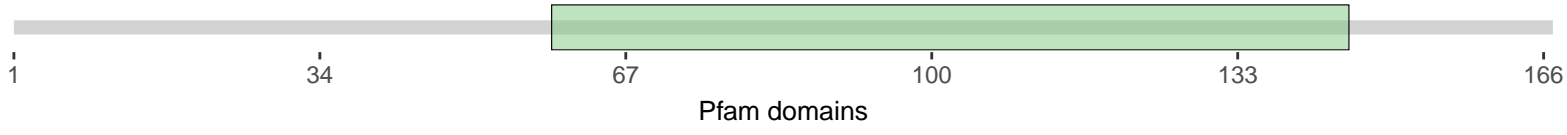


Gel Slice



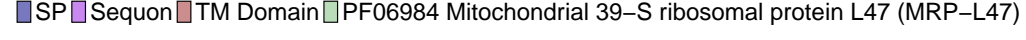
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKKPLVYGRGWKASELRKSWDDLHKLWVLMKEKNMLMFORQMLNAGNLRFPNPERISKVRKEMCRKHVLTERRAIDEADPRRSTEMKRMNAL

NbL03g17910.1 betaine_aldehyde_dehydrogenase_chloroplastic-like [MW = 55.67 kDa]

No. of times detected



log(intensity)



Values from



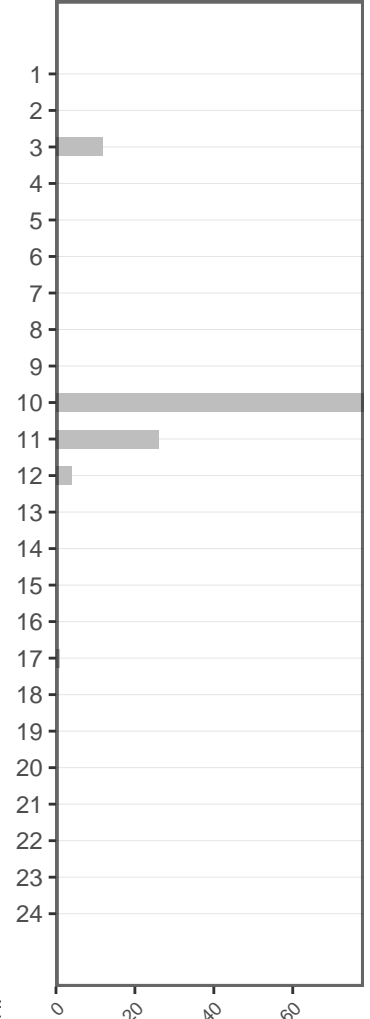
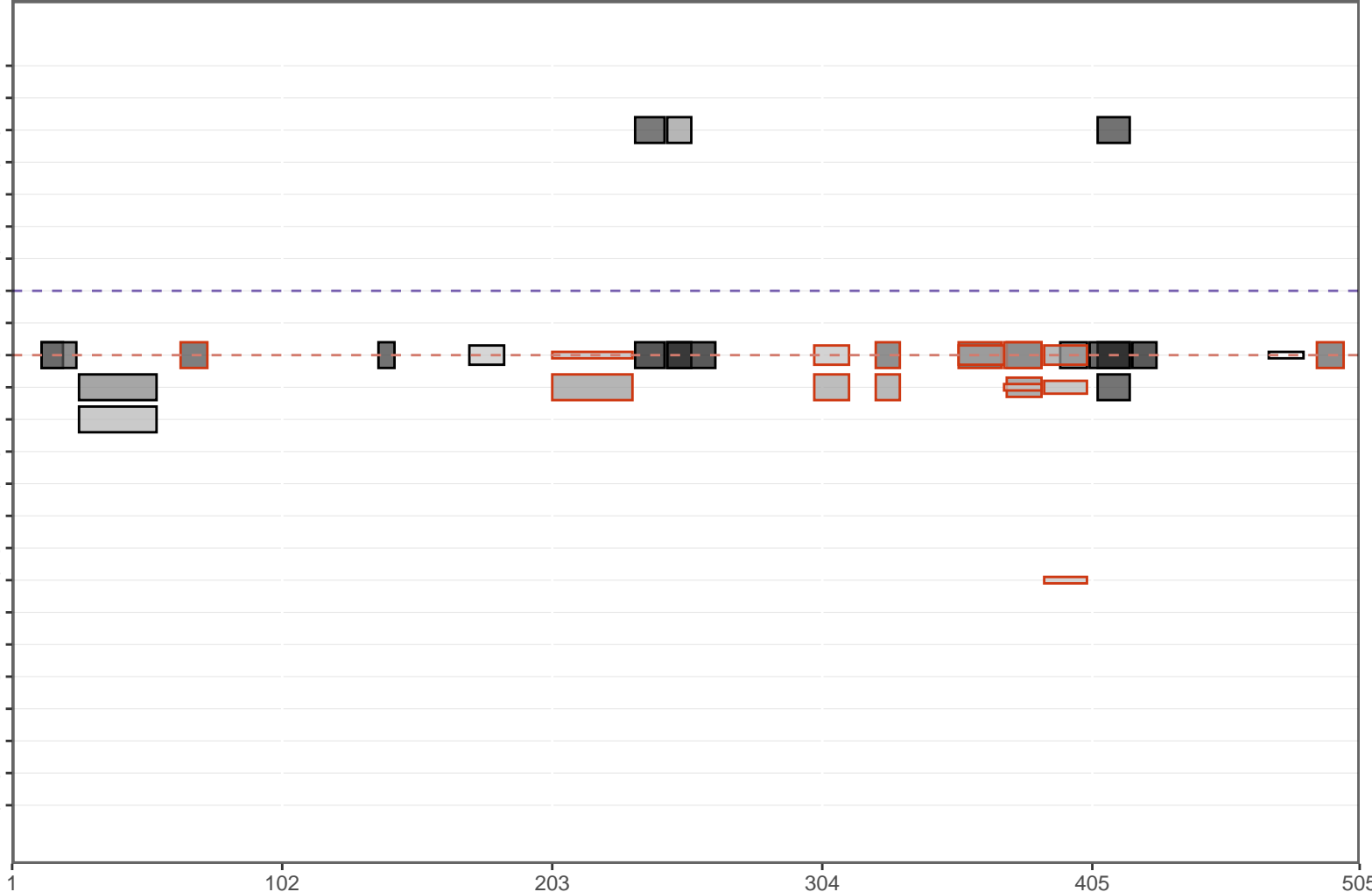
MW indication



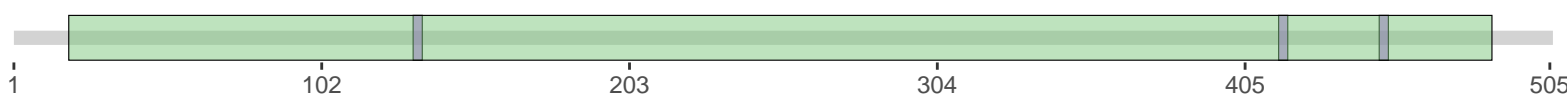
Molecular weight



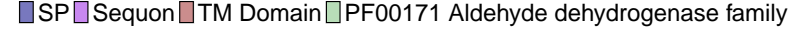
Gel Slice



1 102 203 304 405 505



Pfam Description



Protein sequence:

GPTGIKIMTAAALQVLPVTLLELGGKSPVFFDDPNIDITVEVTLFGGFVWNGQIGSATSLRHQDTASQFLDRLLEWTRKIKSDPLGDECKLGPVIRSGQYKVKLSTAKNEGATLVGGDRPQHLKKGYYQPTITVDVRSMEIKKEEVFGPVLGVKTFKTEEEAEIELANDTRYKGLGAAILSKDLRGERFTRKAFGGGIVWNGSQPFGPFPVWGGKRRSGFGRELGEWLENLKNQVTRYVSDERWAFYKSPKLI

NbL03g17900.1 mannose-1-phosphate_guanyltransferase_alpha-B-like [MW = 45.58 kDa]

No. of times detected



log(intensity)



Values from



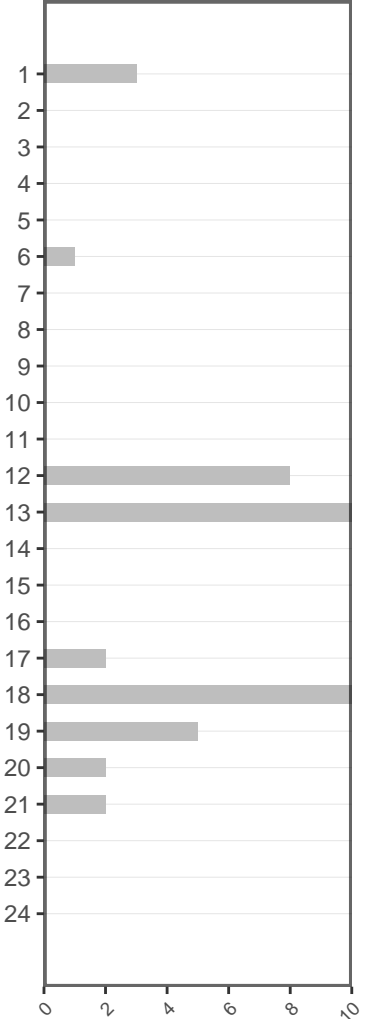
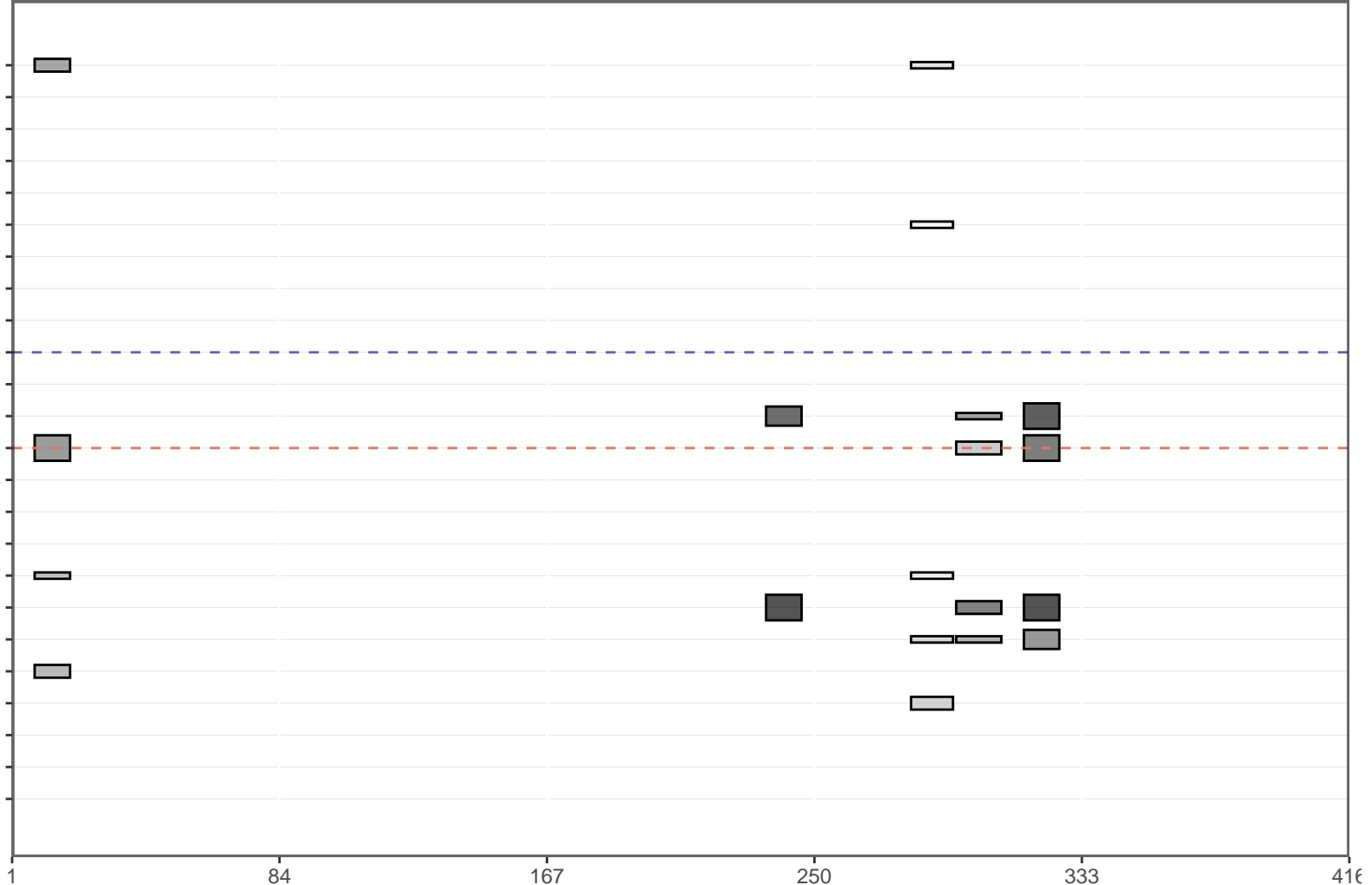
MW indication



Molecular weight

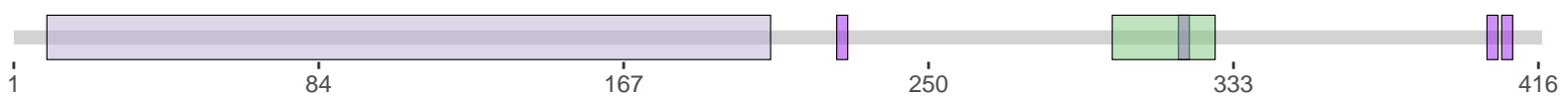


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

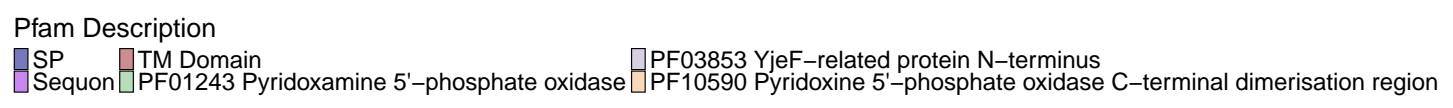
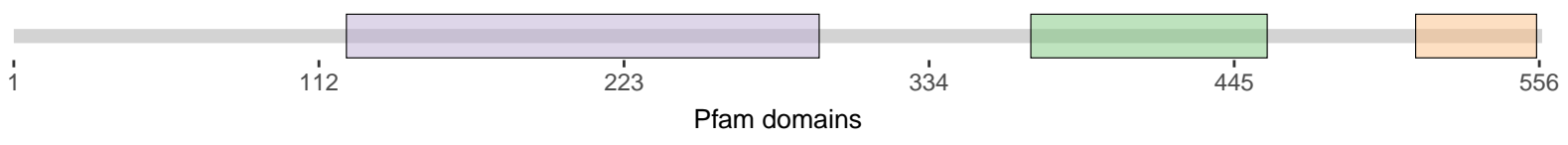
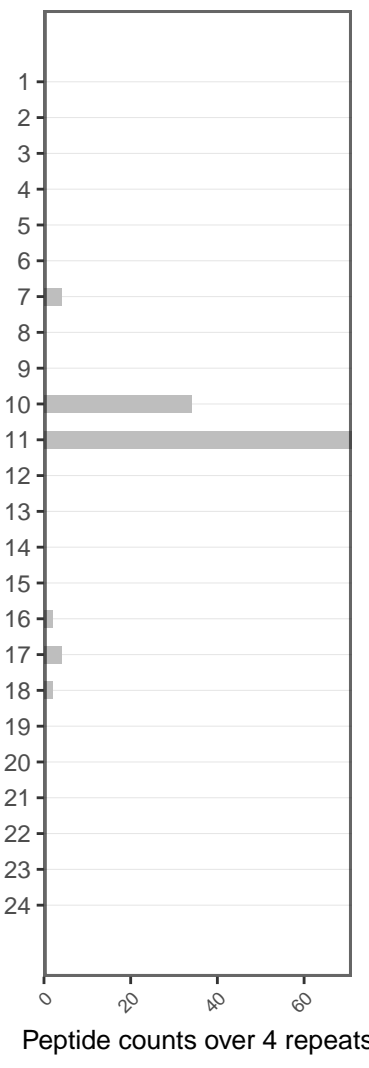
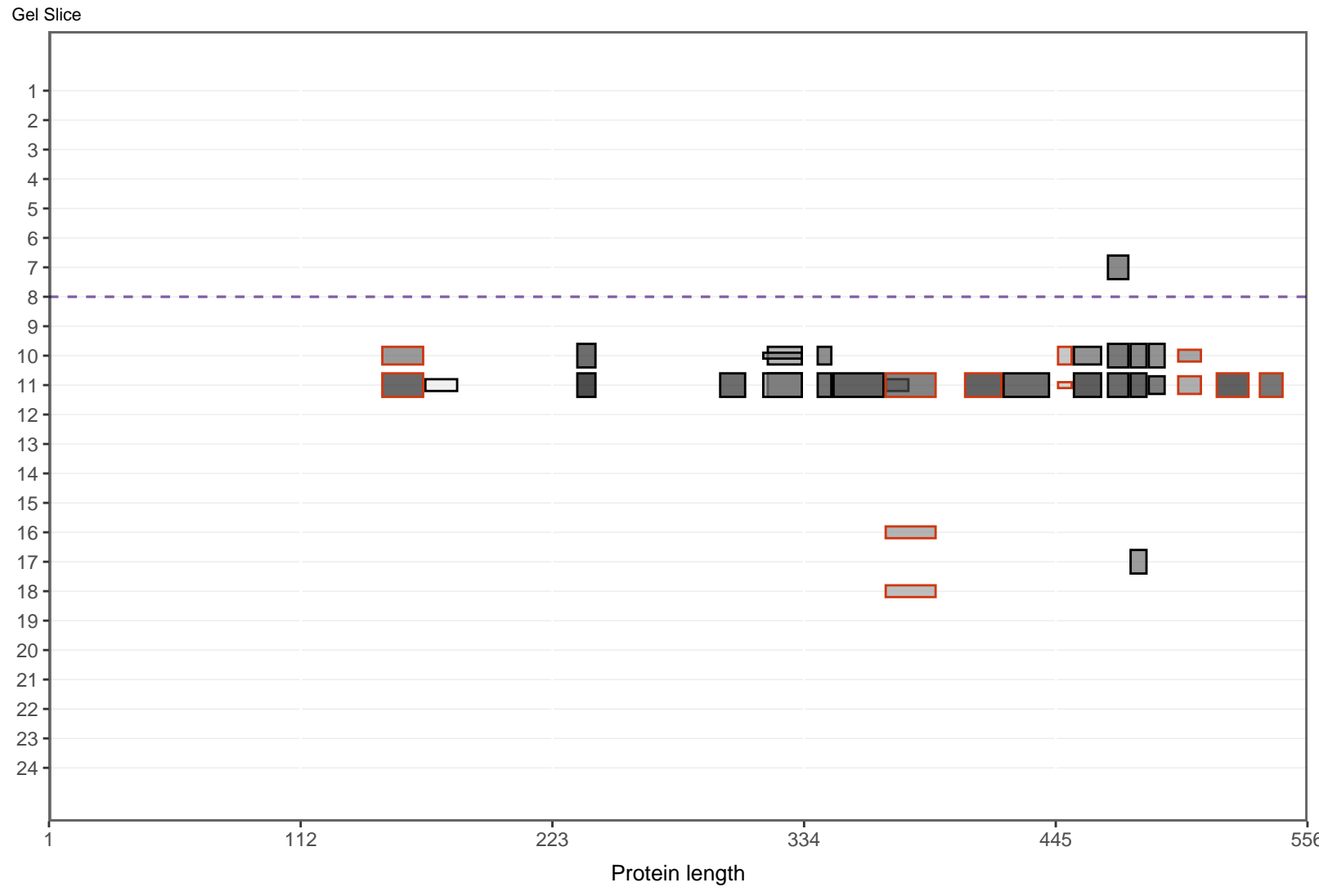
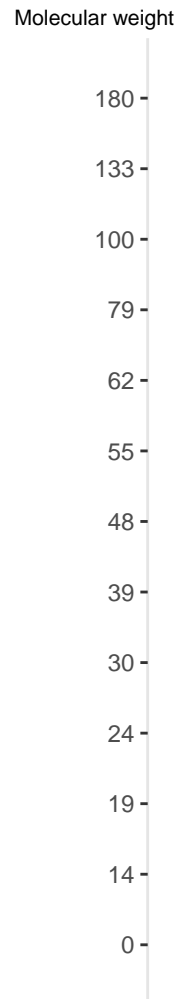
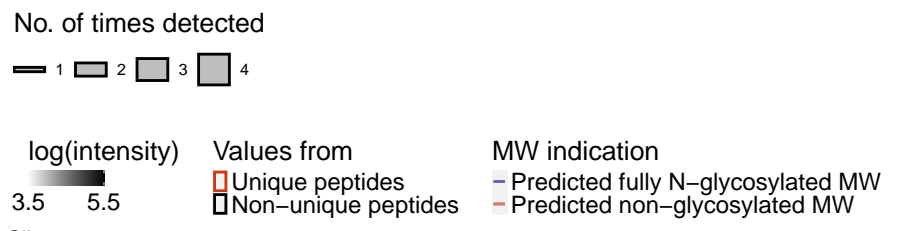
Pfam Description

- SP
- Sequon
- TM Domain
- PF00132 Bacterial transferase hexapeptide (six repeats)
- PF00483 Nucleotidyl transferase

Protein sequence:

MDIFNAIQGYSSQRKDRANLRFRVBSFEALGPNRSLPTDFVRLDGDILPLAGKKLYTYETMDVFEKIQTPGMSLKGSGLYALVIRSTPHLLASGDGSKTAANGDVIYHPSAKVHPTAKGPNVVISANARIGAGARLISCHLDLQVEKENGIVYHANGVWKSIGRWSRVGAGDYNNAKLGITLGEVSGVDEDEVVINSIVLPNKTLNVSVQEEEL

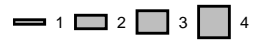
NbL03g17890.1 pyridoxine/pyridoxamine_5'-phosphate_oxidase_1_chloroplastic-like [MW = 62.16 kDa]



Protein sequence:
 JEECDLSGEGYKFDMLVSLTAPKLGAKSFGDTHIFLGRFVPPSIRKFNQLQFAVPGTSMCVRIKPKPKIDISMRNENYISPALLEEVAADPFDFQKWFDDMTAGLKEPNAMALSTTEKDGKPSRRVLLKGFQKDGFRVWYTNVEGSGQGIENFHAALLFYWDLNRQVRIEGPVQKVSDEESEQYFHSRPRGSGLGAISKSGSTVPGRQFLIDEYNGLEAKYSDGGGLIKPKHWGGVRLKPEMFEFVWGGDGRHLHRLGYNPETVDGRREWRIRKLAP

NbL03g17770.1 5-formyltetrahydrofolate_cyclo-ligase_mitochondrial-like [MW = 31.68 kDa]

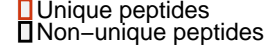
No. of times detected



log(intensity)



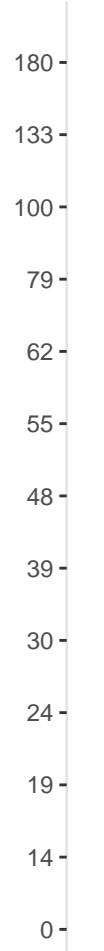
Values from



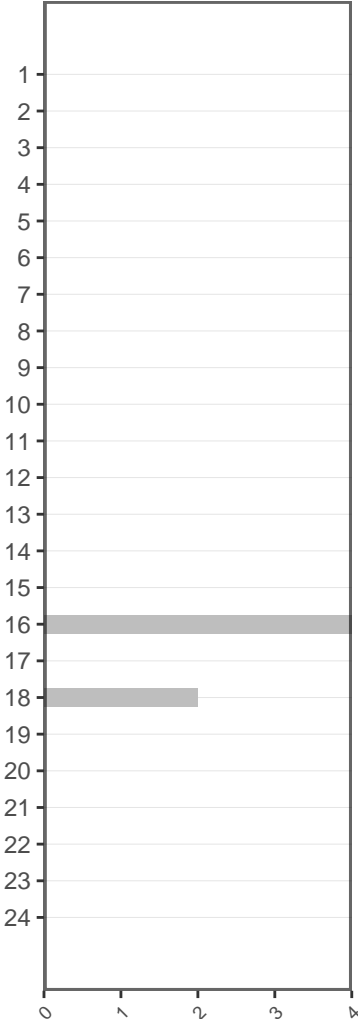
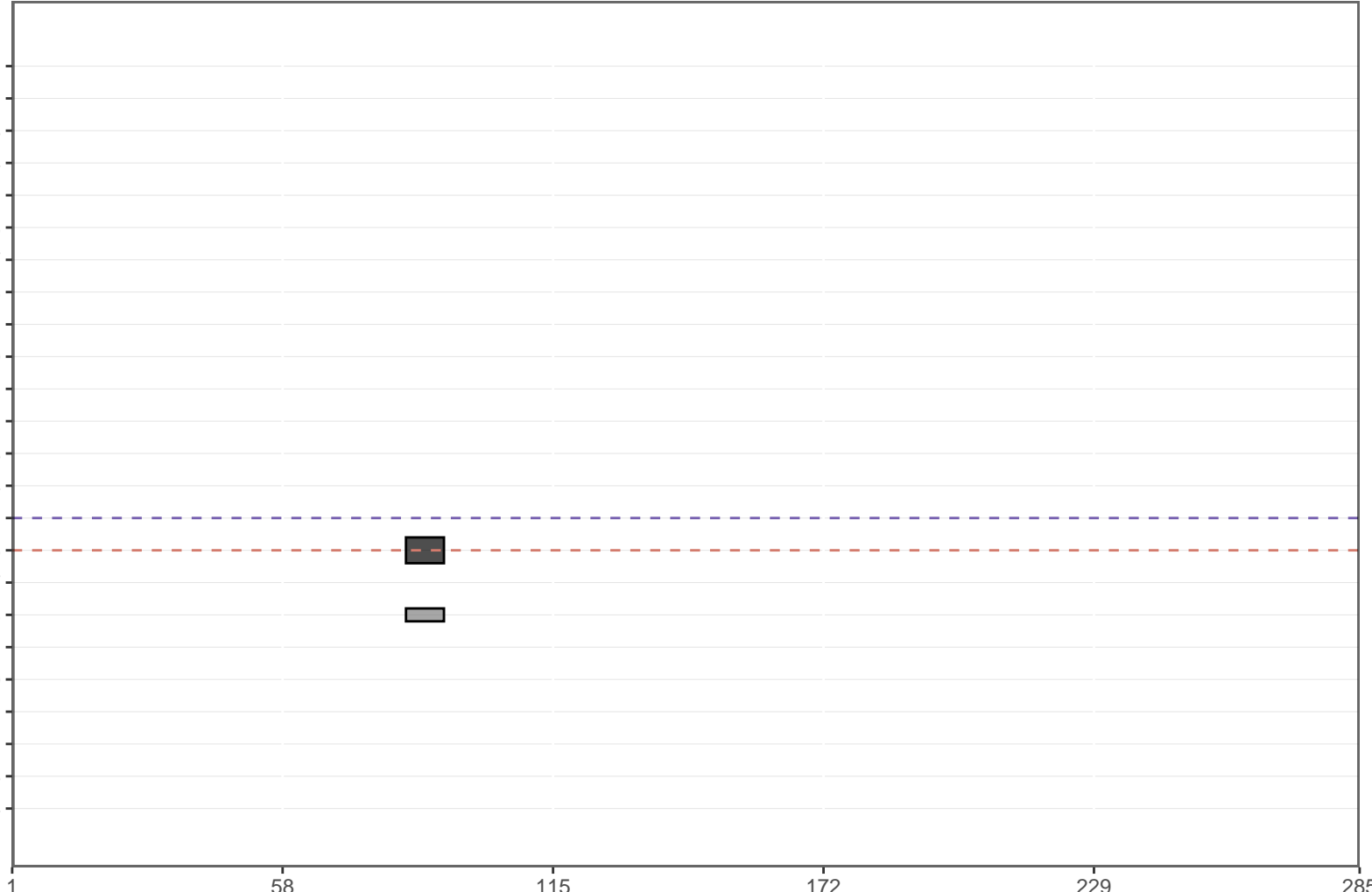
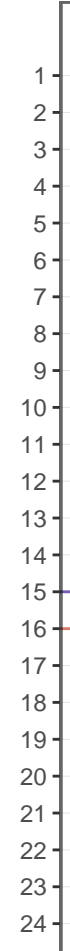
MW indication



Molecular weight



Gel Slice

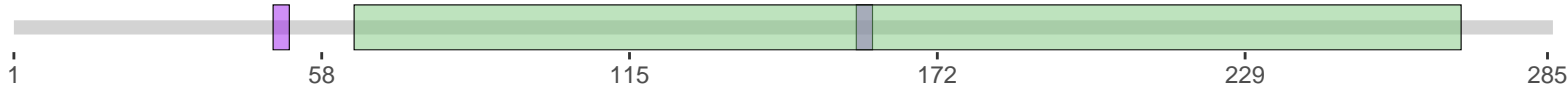


Protein length

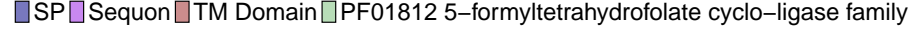


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

GSHPELDIQKLLFVPRVEDRNRNMRMLNISSTEDLIANSMDLEPAPVDAGNEREDVLFANEPVDFLLPLGLAFDKAGRRLLGRGGGYDFTLSRYGELAVDRNWKQLKIALGYSMQIVDDGTPLTPNDLIDVALVSPGGVIRIPVALEIGH

NbL03g17740.1 HIPL1_protein-like [MW - SP = 72.57 kDa]

No. of times detected



log(intensity)



Values from



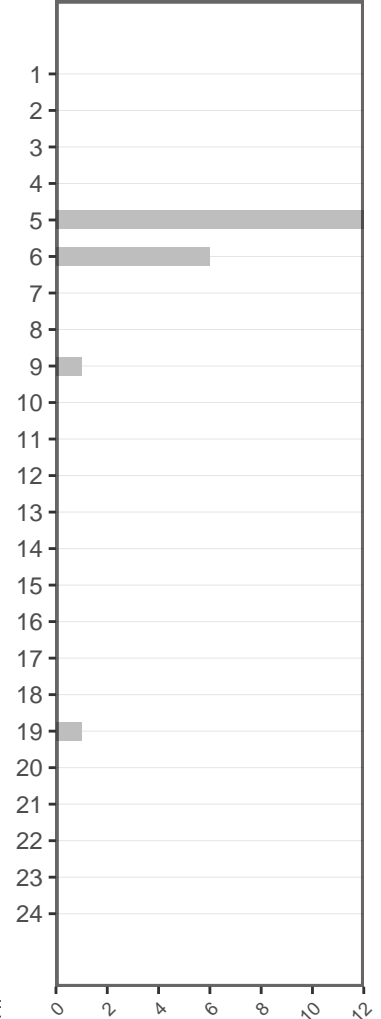
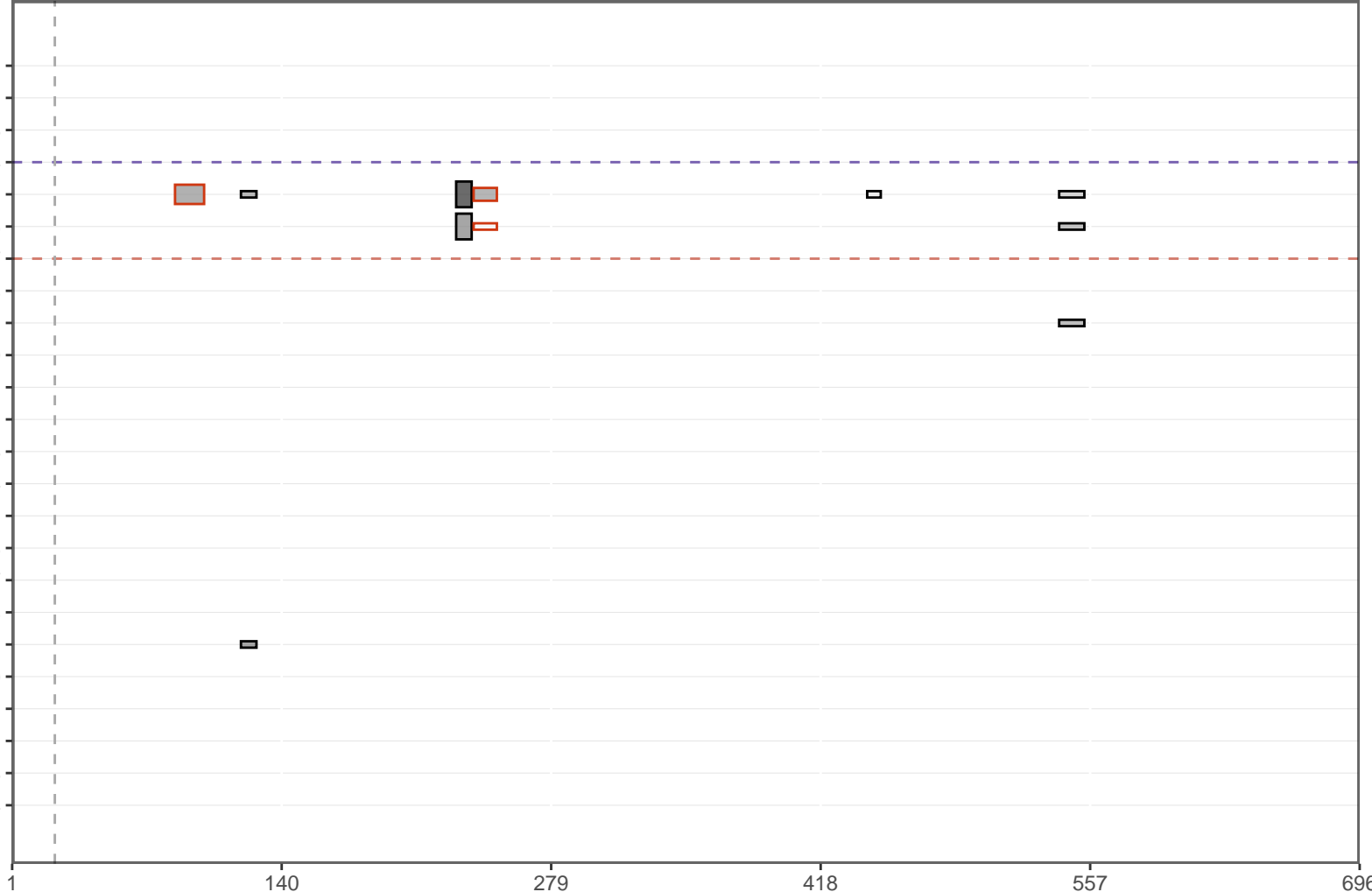
MW indication



Molecular weight



Gel Slice



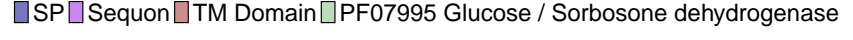
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

QSVIAEFTANGTASQPSLAKTBAKEVRRIFMGLPFTSHHGGQILFGPKDGYLYFMMDGGGGTGDVYNFQNKKSLGKIMRFDDVDSRPAEEISGLGLWQNTIPKDNFYIEDKLGPEWALGMRNPNWRQSFDSARPFVMAQADGDDHYEEVDITKGGNYGWNLYEGAPFPAPPKSPGKNTSMSSINRPFPMVNYHSEVKNKEGASBITGGYFYVRSADPCMSGRVLFADLVAGAMWAGTESPENSGFNTEISFTGAGNSPINCALVPGESVPLQGYFSFGEI

NbL03g17690.1 heterogeneous_nuclear_ribonucleoprotein_1-like [MW = 34.84 kDa]

No. of times detected
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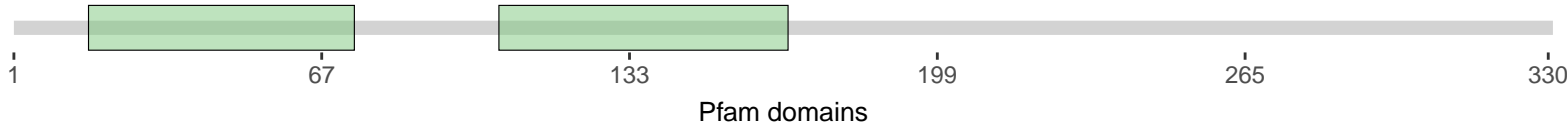
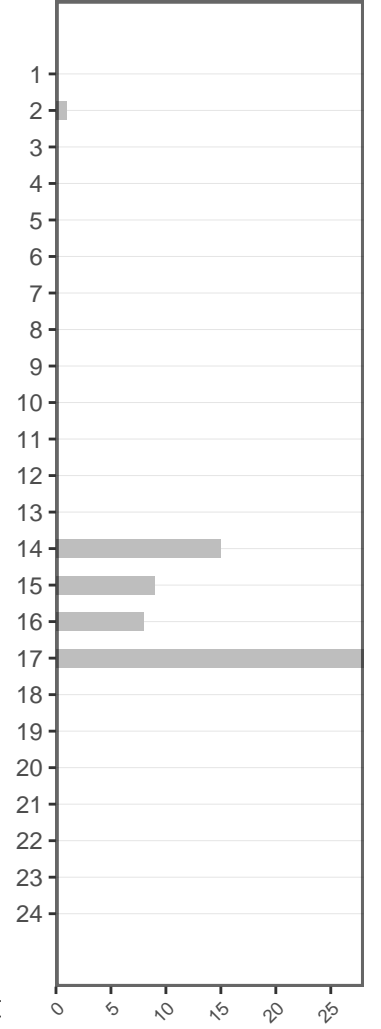
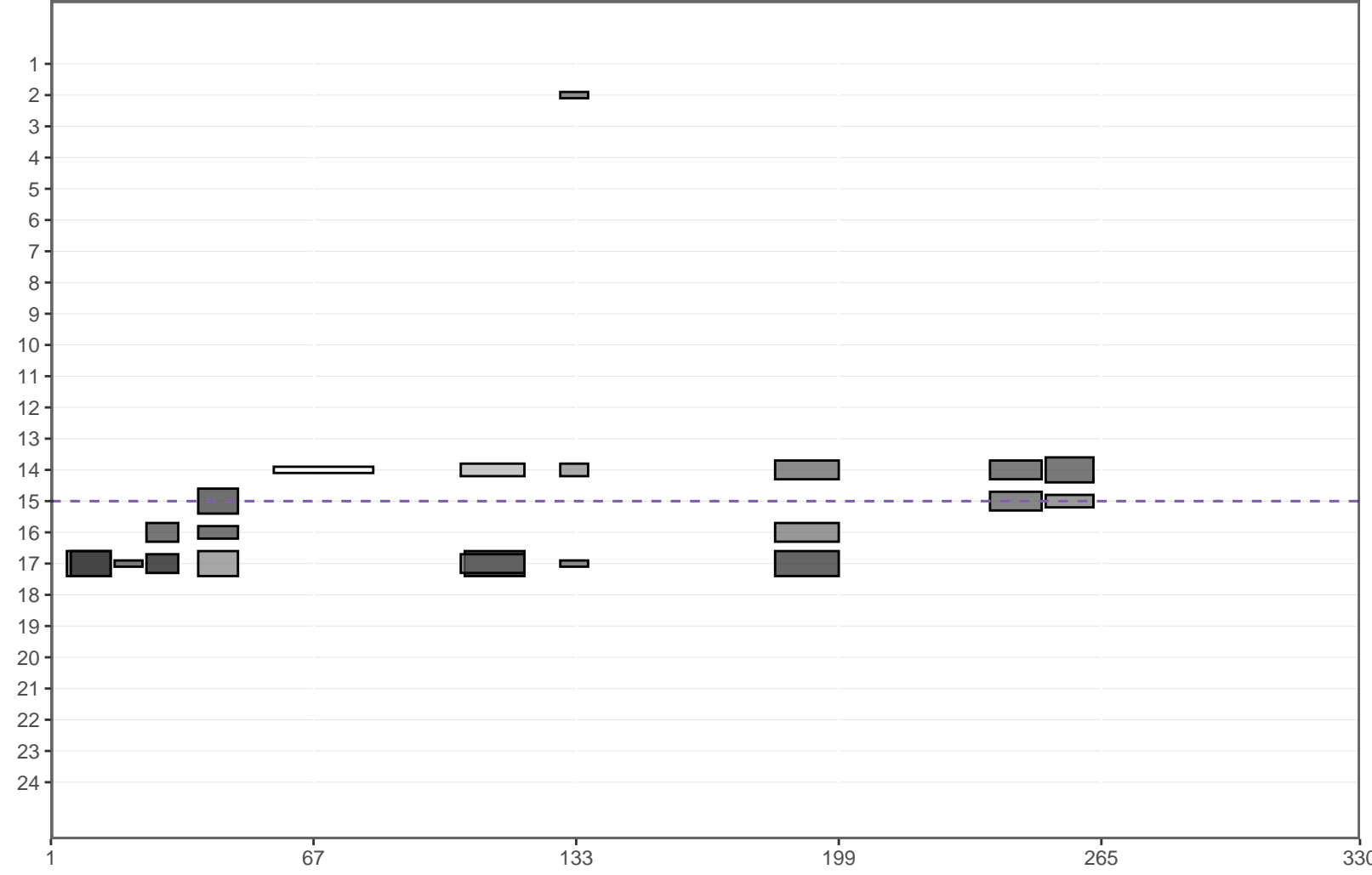
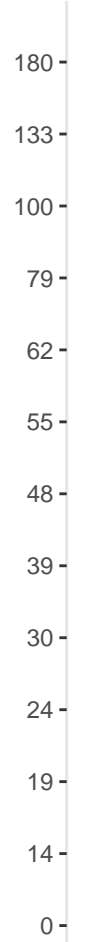
log(intensity)
 2.7 5.3

Values from
 Unique peptides
 Non-unique peptides

MW indication
 Predicted fully N-glycosylated MW
 Predicted non-glycosylated MW

Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

Protein sequence:
 VVLSQNMIDMLGTQVEKKKPKPKPNPMSGGHGYGSGSRGRGVSDSYGGFQNSYSGFGGFGPMSYRSGGGMGRFQDVGYGSGGEGGRYDFQGGEGFGVGRDPELGYSSRYGAVGGFGGGAGGGGGLMAYGRGADYGGYGGAGGAGYDVLALMMVDQEVFM

NbL03g17480.1 protein_QUIRKY [MW = 118.43 kDa]

No. of times detected



log(intensity)



Values from



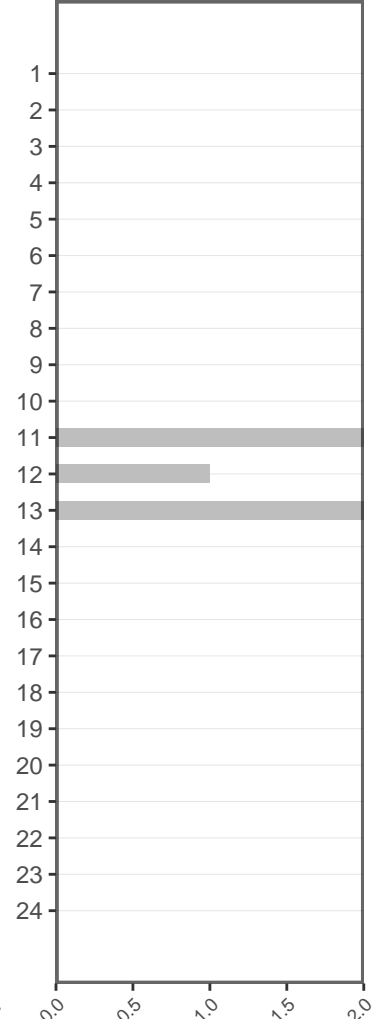
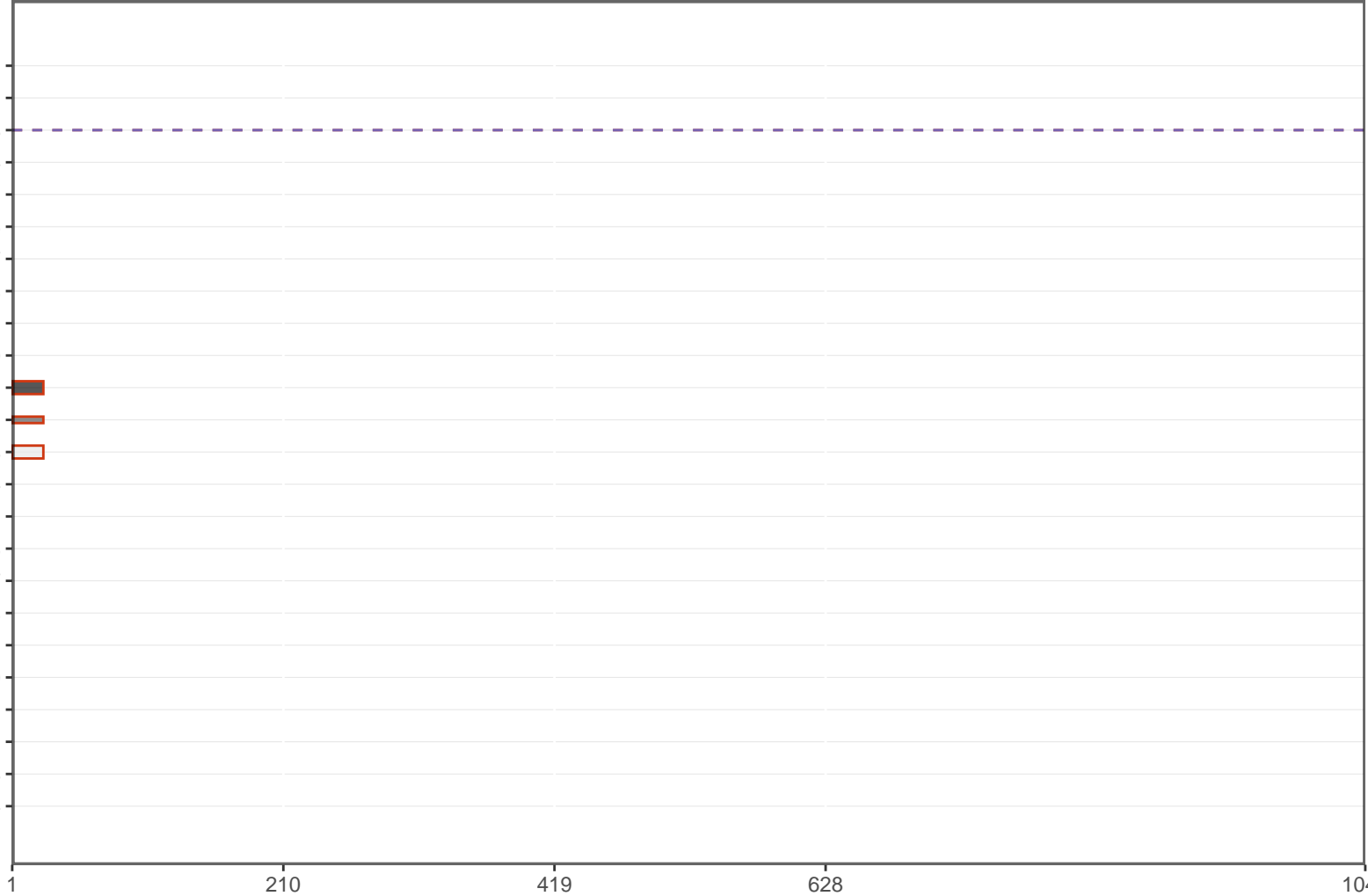
MW indication



Molecular weight



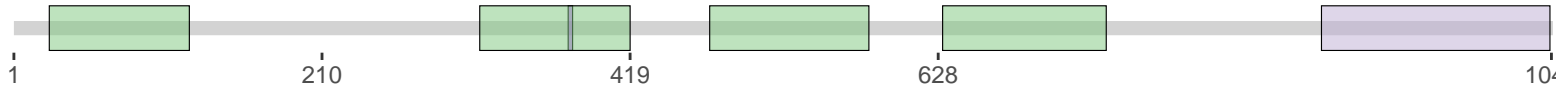
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

QLGFGSVTRRRGSMNHHSFAHWEDLIFVAGEPLEDGLLLVEDRTKDPVLLGHIPVSEEGQLDERLVSAKWFGLEGGPGGSGVGRVNLRMGLGGYHVLDEAAHVCSDFRPTANQLKPPVIGLELGLGARGLLFLKSGKPGKSTDAVCAVAKYGRKWWRTTRITFTDFDPRIWNEGYTWGVYDFCTVLTIGVFDNWHMFADAGDKKPDVPIGKVRIRVSTLENKKVYTNISYPLMLLRBGLKMGEEIVARFVPSLIPETGAVYGGPVALPKMHYLRPLGVAQGE

NbL03g17140.1 probable_3-hydroxyisobutyrate_dehydrogenase-like_1_mitochondrial [MW = 37.81 kDa]

No. of times detected



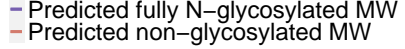
log(intensity)



Values from



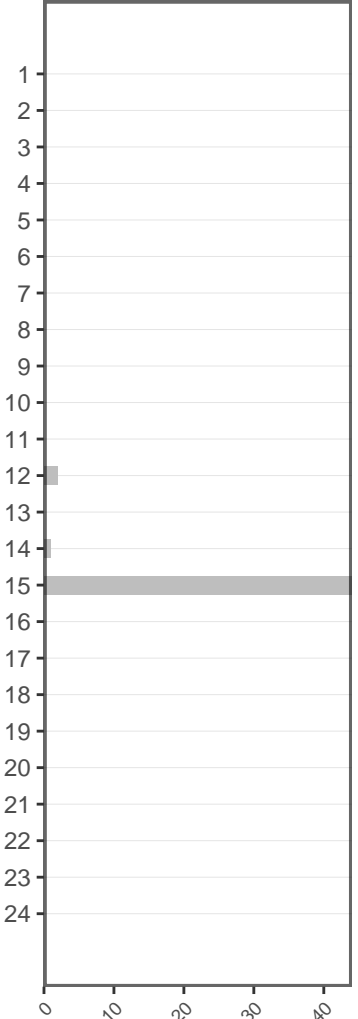
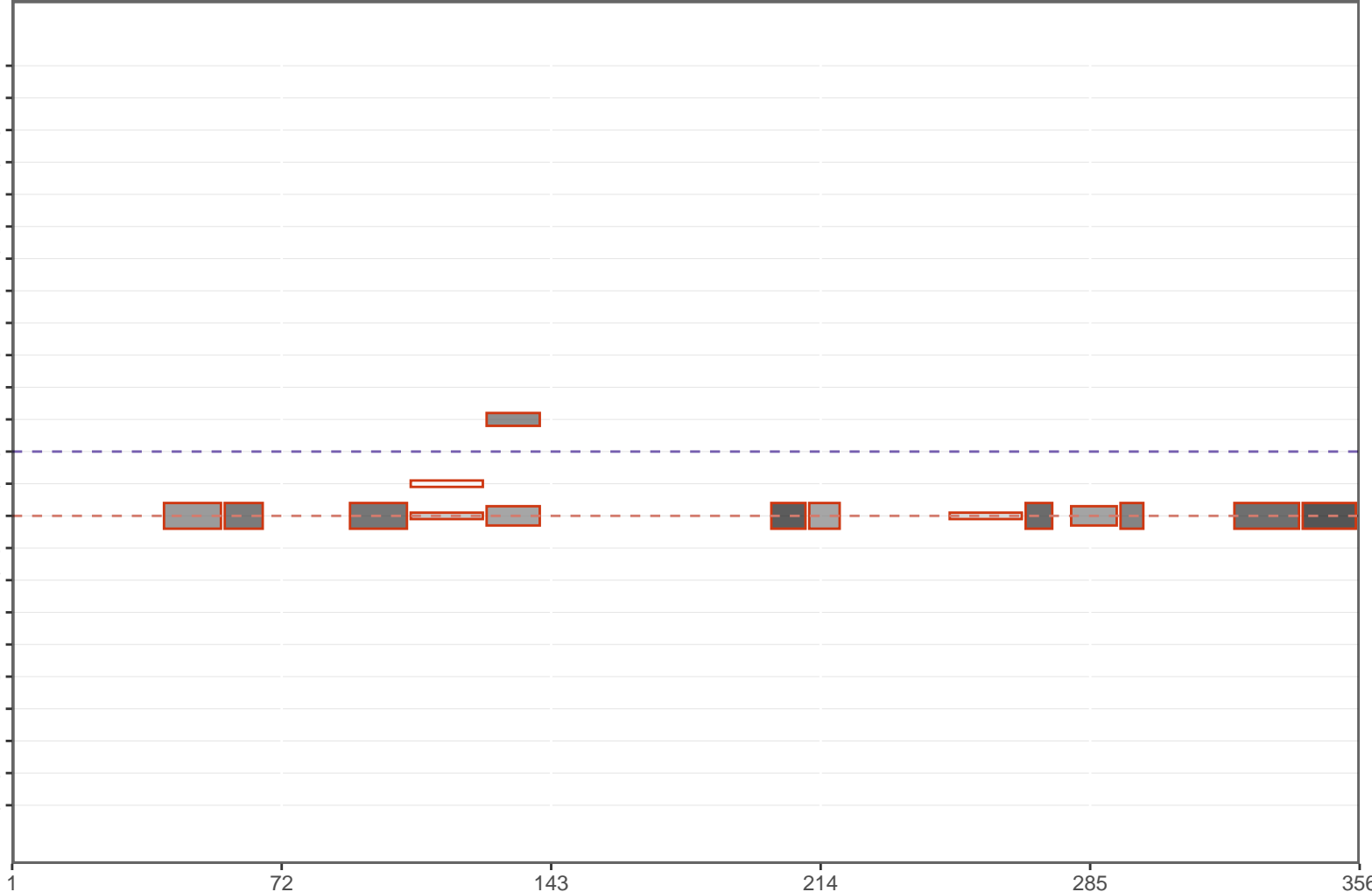
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF03446 NAD binding domain of 6-phosphogluconate dehydrogenase
- PF14833 NAD-binding of NADP-dependent 3-hydroxyisobutyrate dehydrogenase

Protein sequence:

AAGCSAVDAPVYSGGDLGARNAAISFAGGEEISIRLNPLNLLGRVYYMGAPGKGFTRLGNQVWASTMVLGEGLYAHKAGLDLNLNMAISTGAAGSKBLDLYGSRHRDRFEPGFYVNHFWKDLGICLREGQNMGLALPGLAAGQLYLSKXAHGEGNLGTQALILALERINNLASSSSEVQKPI

NbL03g16810.1 60S_ribosomal_protein_L27a-3 [MW = 16.46 kDa]

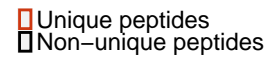
No. of times detected



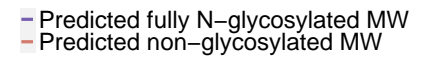
log(intensity)



Values from



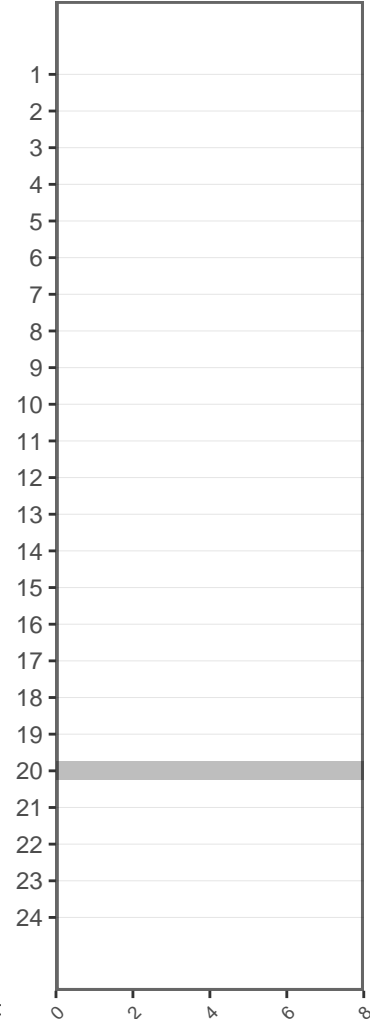
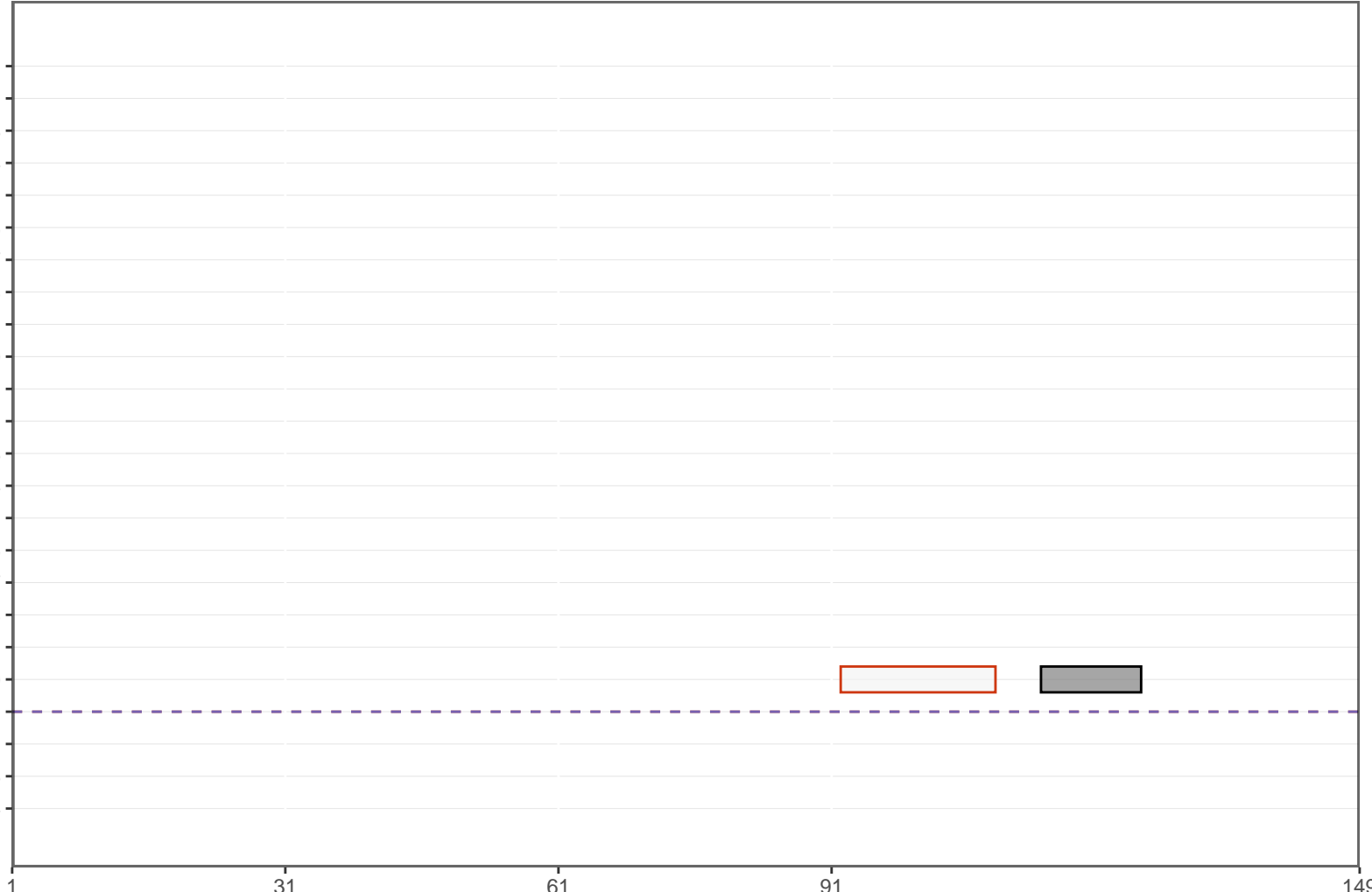
MW indication



Molecular weight

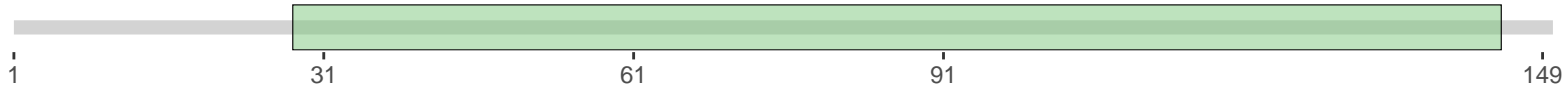


Gel Slice



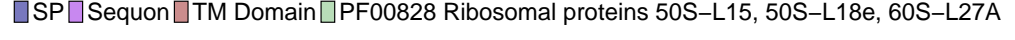
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

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NbL03g16740.1 histidinol_dehydrogenase_chloroplastic-like [MW = 53.14 kDa]

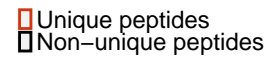
No. of times detected



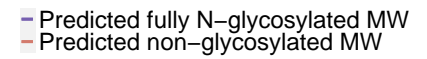
log(intensity)



Values from



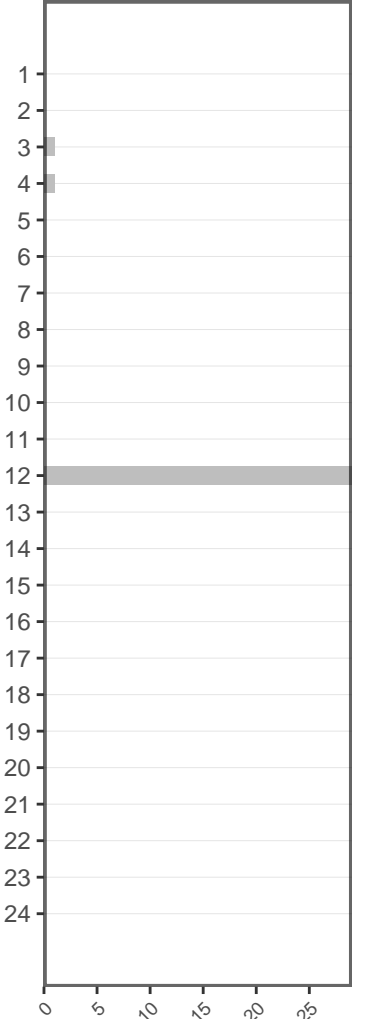
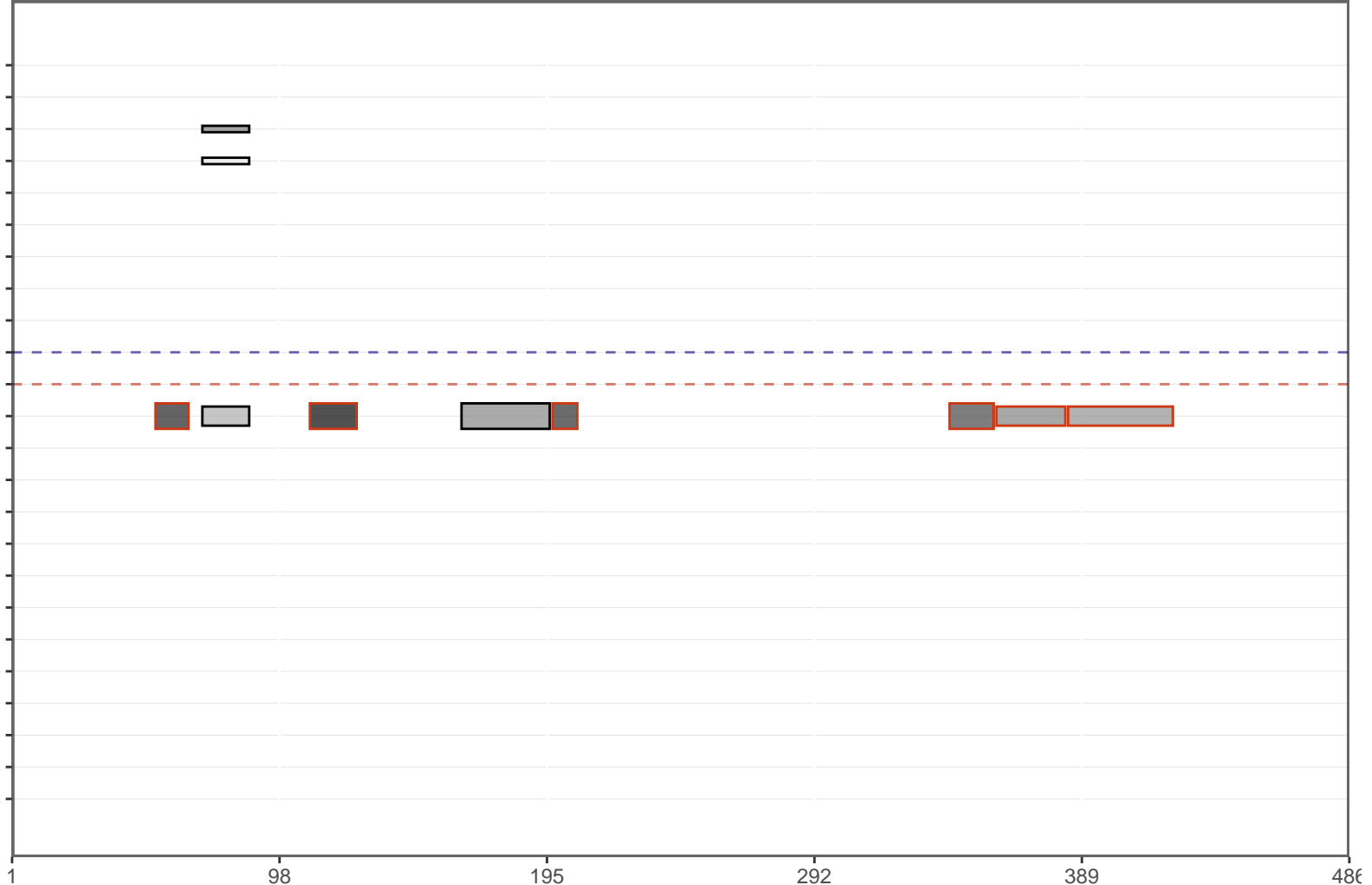
MW indication



Molecular weight

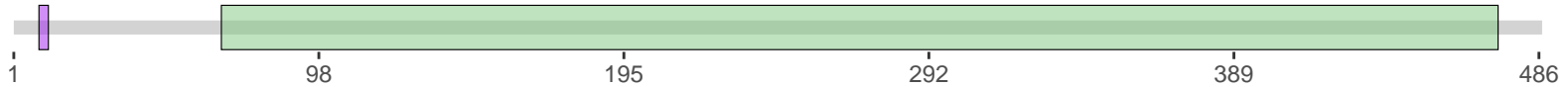


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

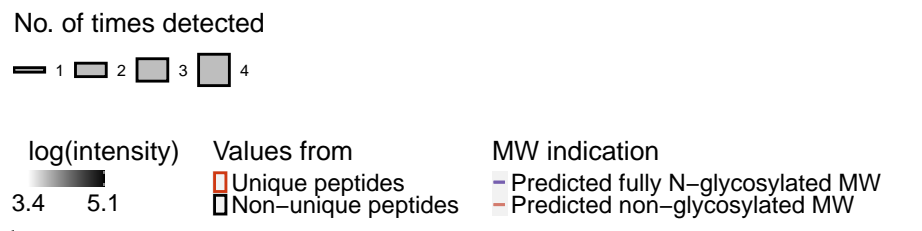
Pfam Description



Protein sequence:

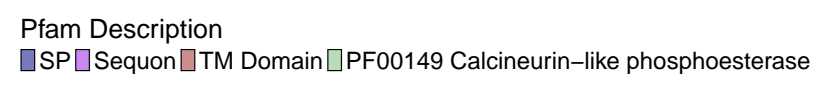
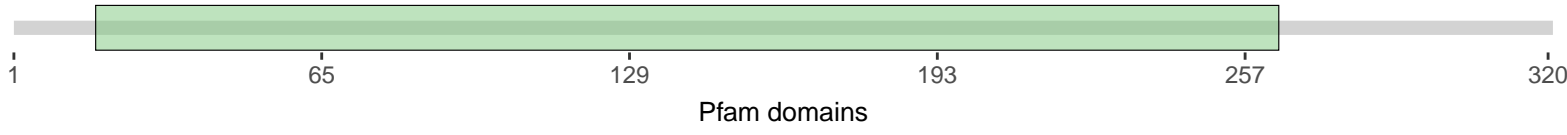
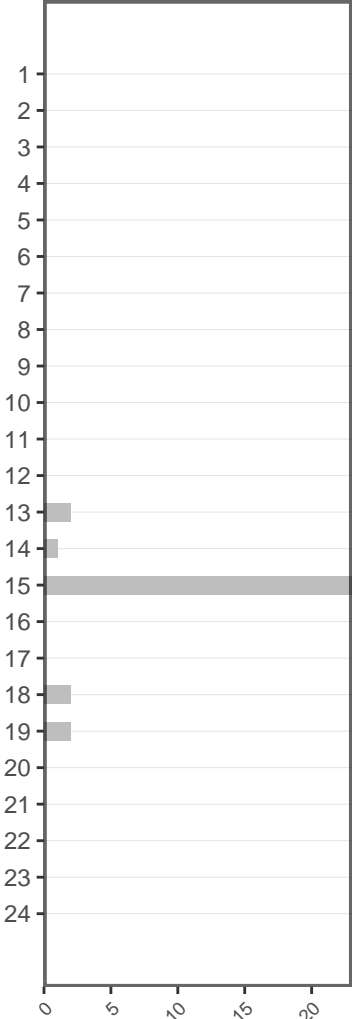
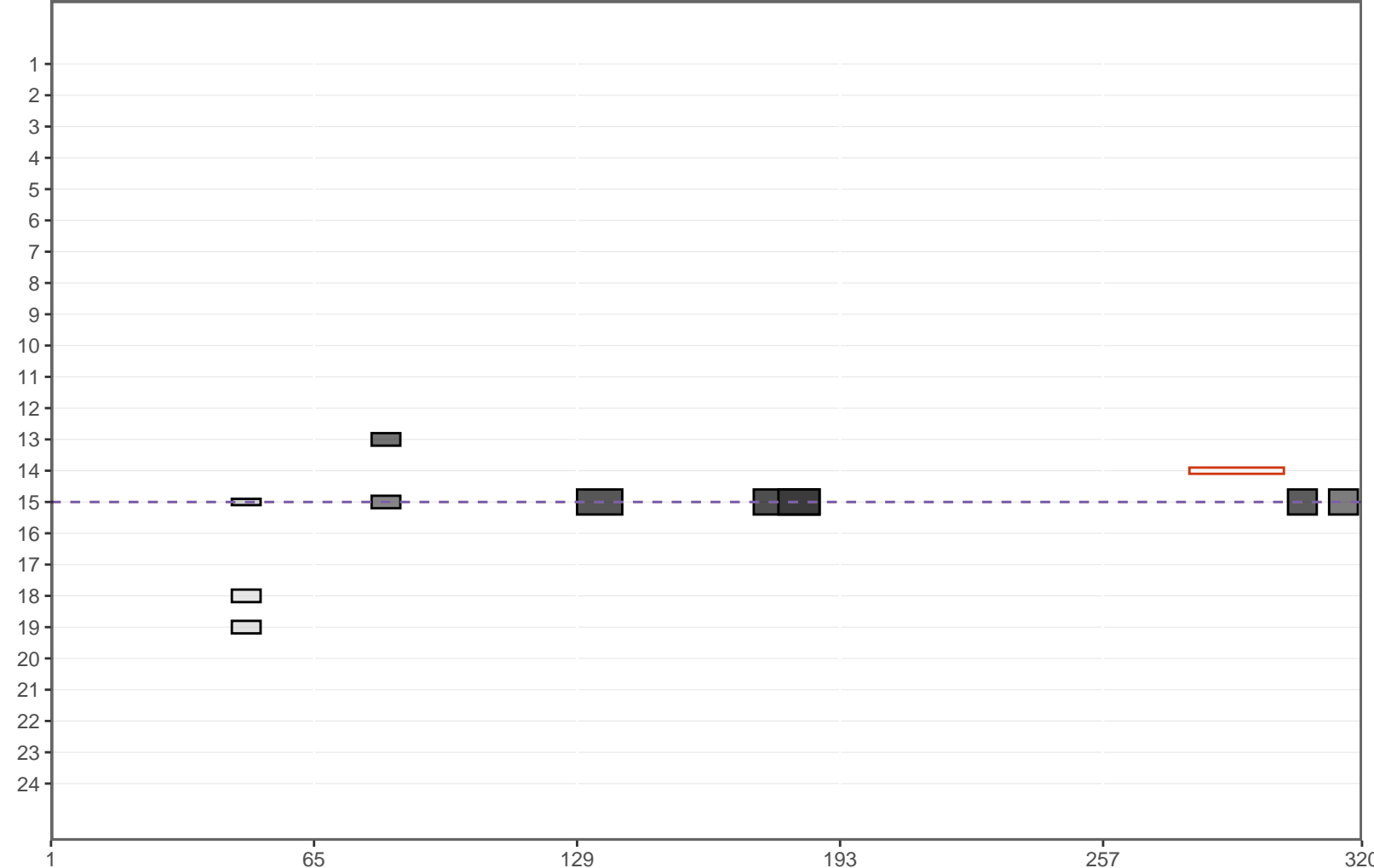
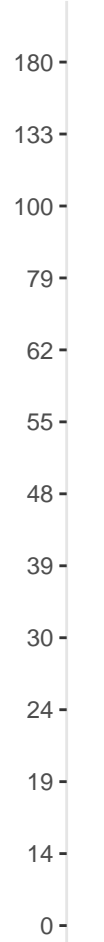
IQAISAMAVGTESGPKVEKYGPGNGYVTAAXKMLGNSEAMVSDMPGPREVLVADKHSPHVAADLLSQAEGPDGQVLLVAGDQVNLDAIQEIRKGGGALPREEFALGALSHSFTVLARDVLEAISFNMVAPHLINVNEAEKWESSIENAGVFMGGWTPESVGDVAGSTNIVLPTFYGVARMYGGVSLDFLKYTVQSLTEGLRNLGPIVVEKMAEVEGLDAHKRAVTLRLGDQEARQVSHER

NbL03g16620.1 manganese-dependent_ADP-ribose/CDP-alcohol_diphosphatase-like [MW = 35.73 kDa]



Molecular weight

Gel Slice



Protein sequence:

IAIGWPEDEHPNLTAKALKVIGERNFNDSKNSPNGLVGLERRFLKFNQGVGKQLEWLDHVLGEATELNGNVAVVCCHLFLDPGASFAALLWNYDEVMDVHCVGKVLQGLGHAHKGSGVDSHGVRHRLVLEALEGPPGTDAGFHIDAFSDRLSLFGNDRMKSTEMVFGH

NbL03g16530.1 indole-3-glycerol_phosphate_synthase_chloroplastic-like [MW = 45.03 kDa]

No. of times detected



log(intensity)



Values from



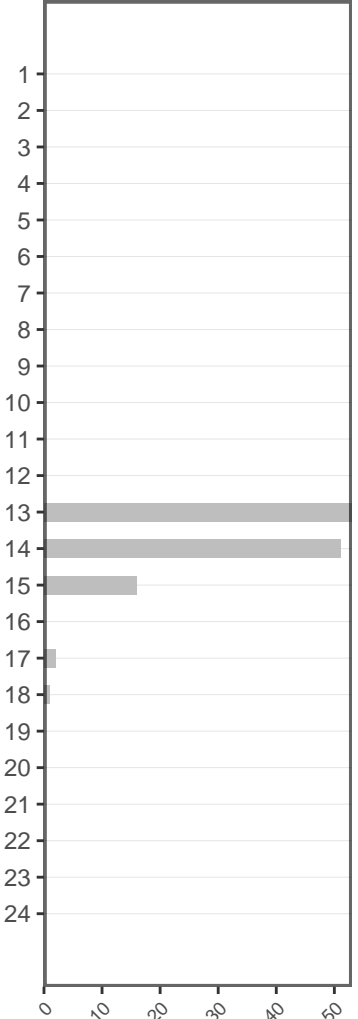
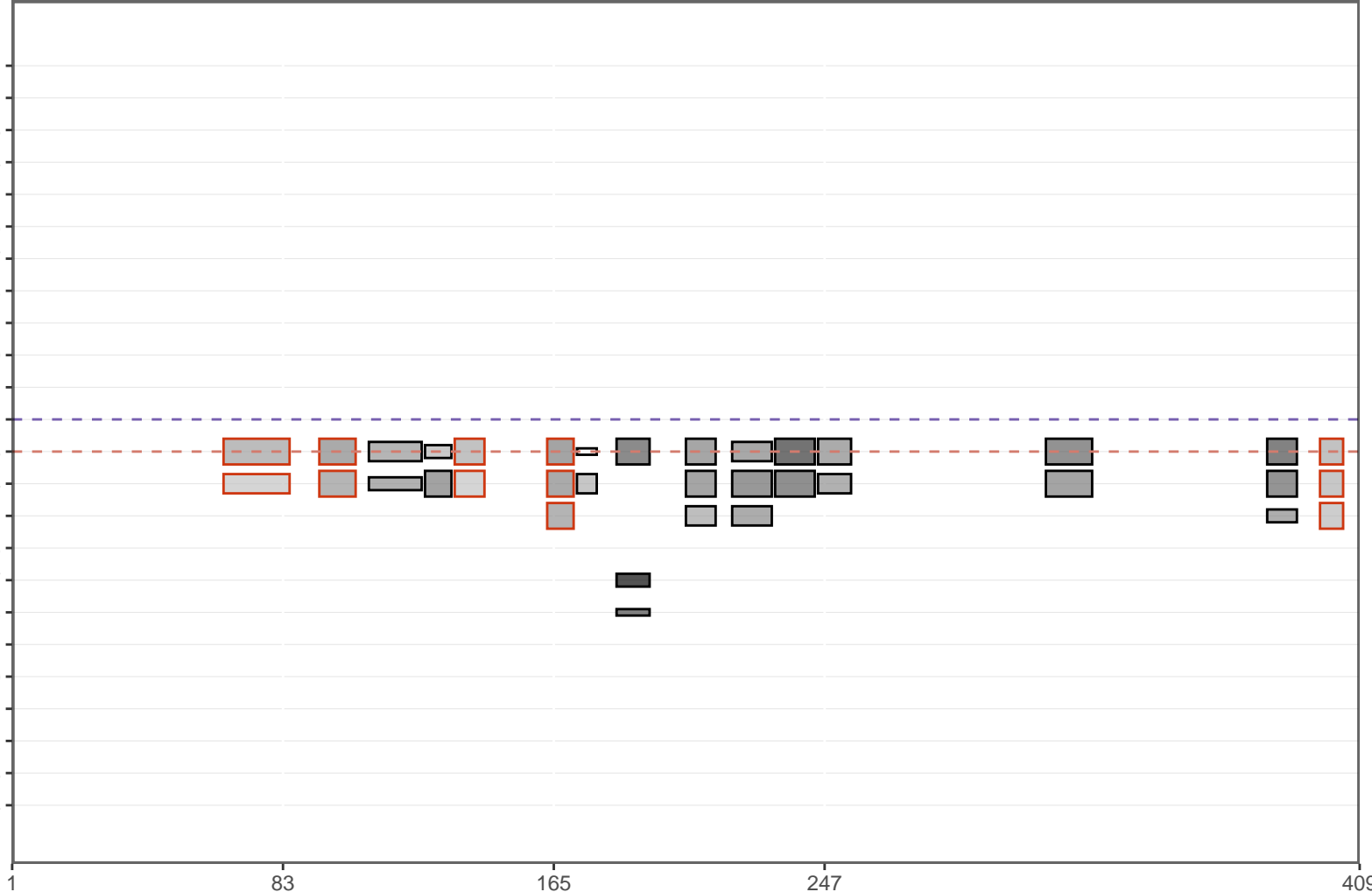
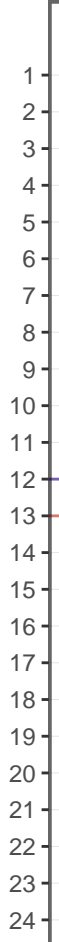
MW indication



Molecular weight

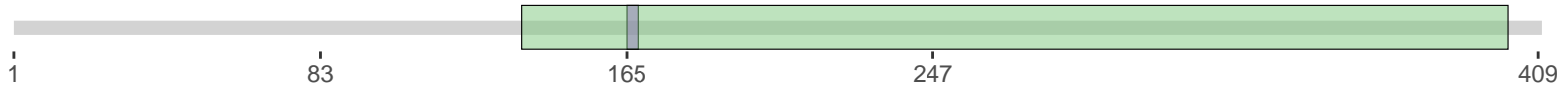


Gel Slice



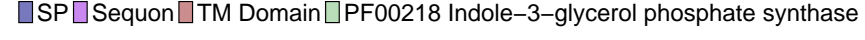
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

JAEVYKASPSRGVLRGDFNVEIAKAVKGGAGLGLVLDQKYFGGSEFNLAIRNAGVEPLLCKEFVIEAWGLYARVKGADAVLLAAVPLDLDKMYKIKGLLGLTALIEVHDEREMDRVLGIDGVELGHNINRDLGTFKVDISNTKLLLEGERGERIRERGHVVEGSLFTRPADIAVQDEAGVKAVALVGLSELVKGDPPTKIGSELFGKDISG

NbL03g16510.1 28_kDa_ribonucleoprotein_chloroplastic [MW = 32.19 kDa]

No. of times detected



log(intensity)



Values from



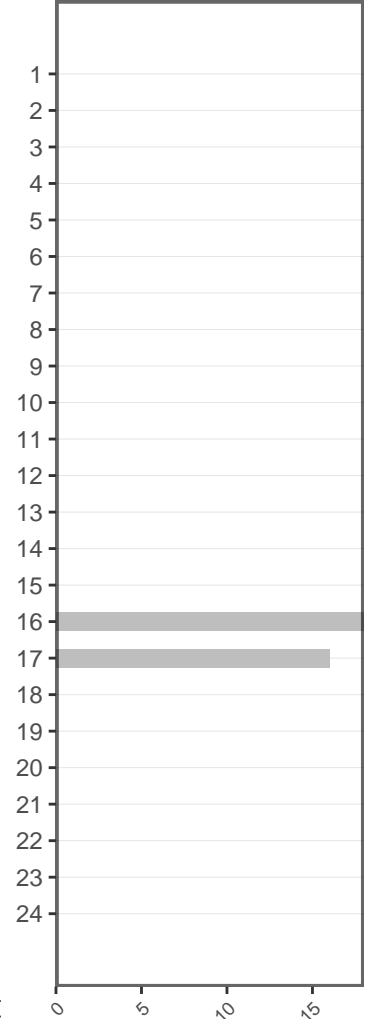
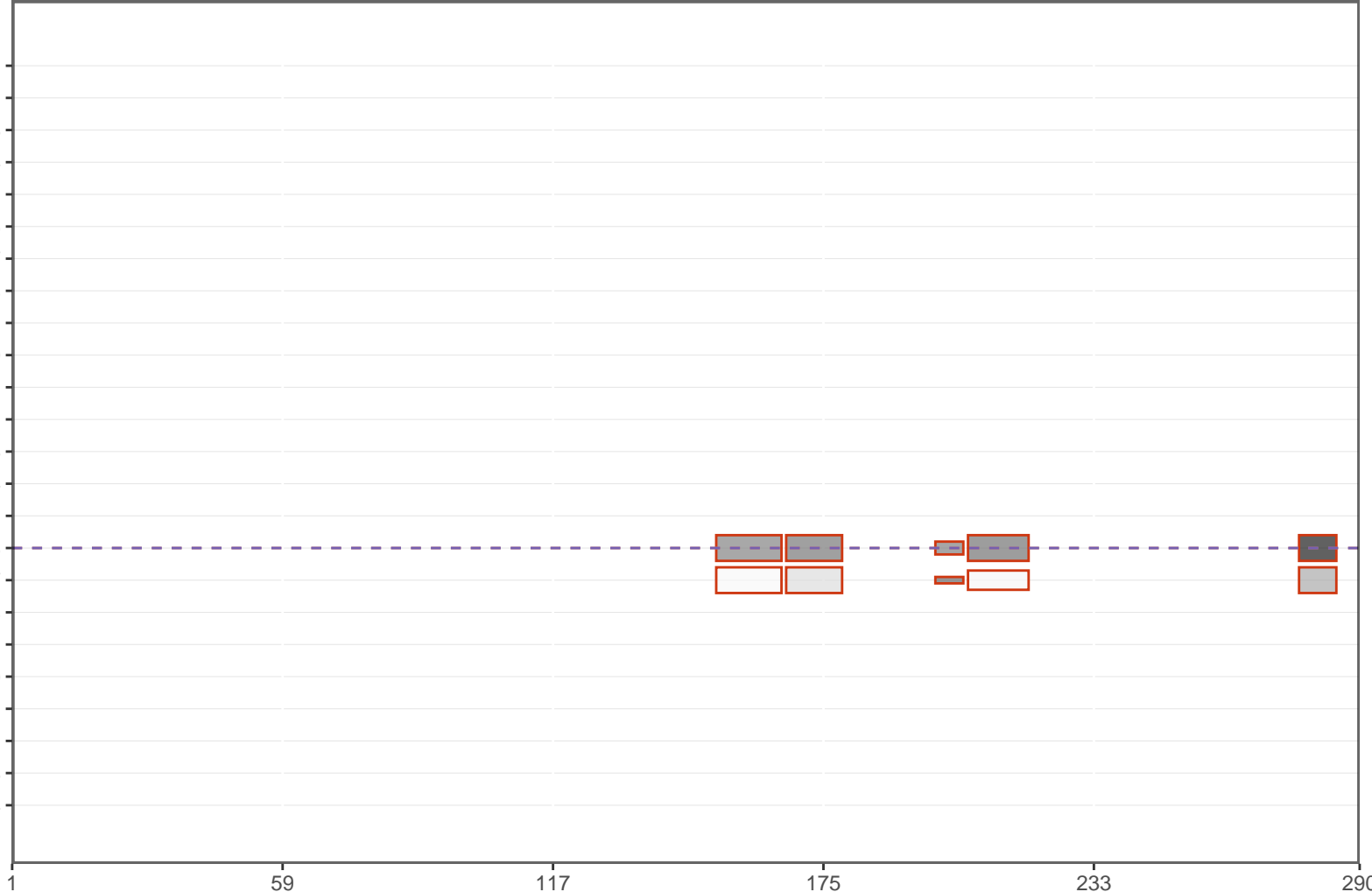
MW indication



Molecular weight

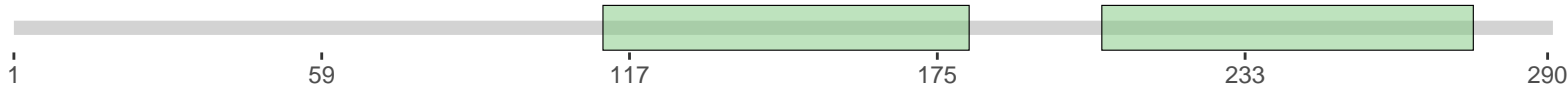


Gel Slice



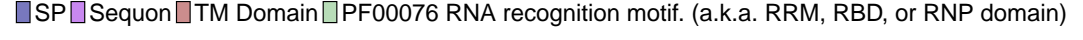
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SVVEAEVYNYRETRDRSRGFGFVMTSTVEEADKAEVLSGVDLNGRLITVVKAAAPRGRFPERPRPTFQPTVYRIVYGNFVDDIDARLEQIFSEHGKVVSAVYVDFREGSRGRGFGFVMMSSSEAEAMALDGGTLDGRTRIVAAEERPRNTVY

NbL03g16360.1 uncharacterized_LOC107819570 [MW = 116.33 kDa]

No. of times detected



log(intensity)



Values from



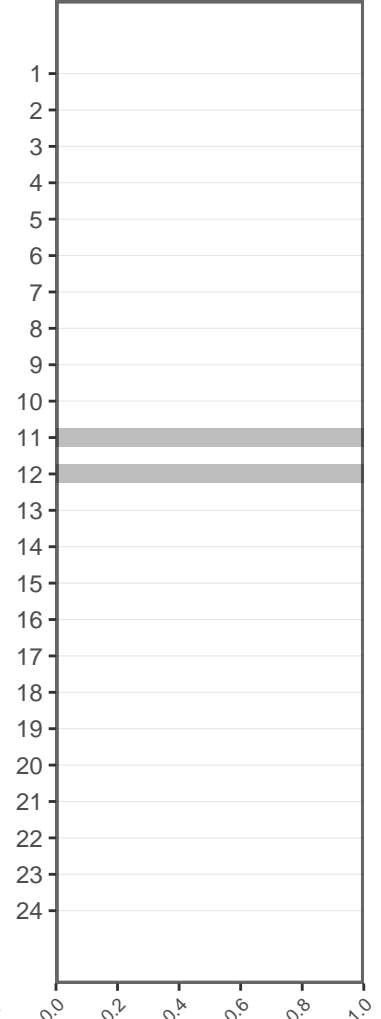
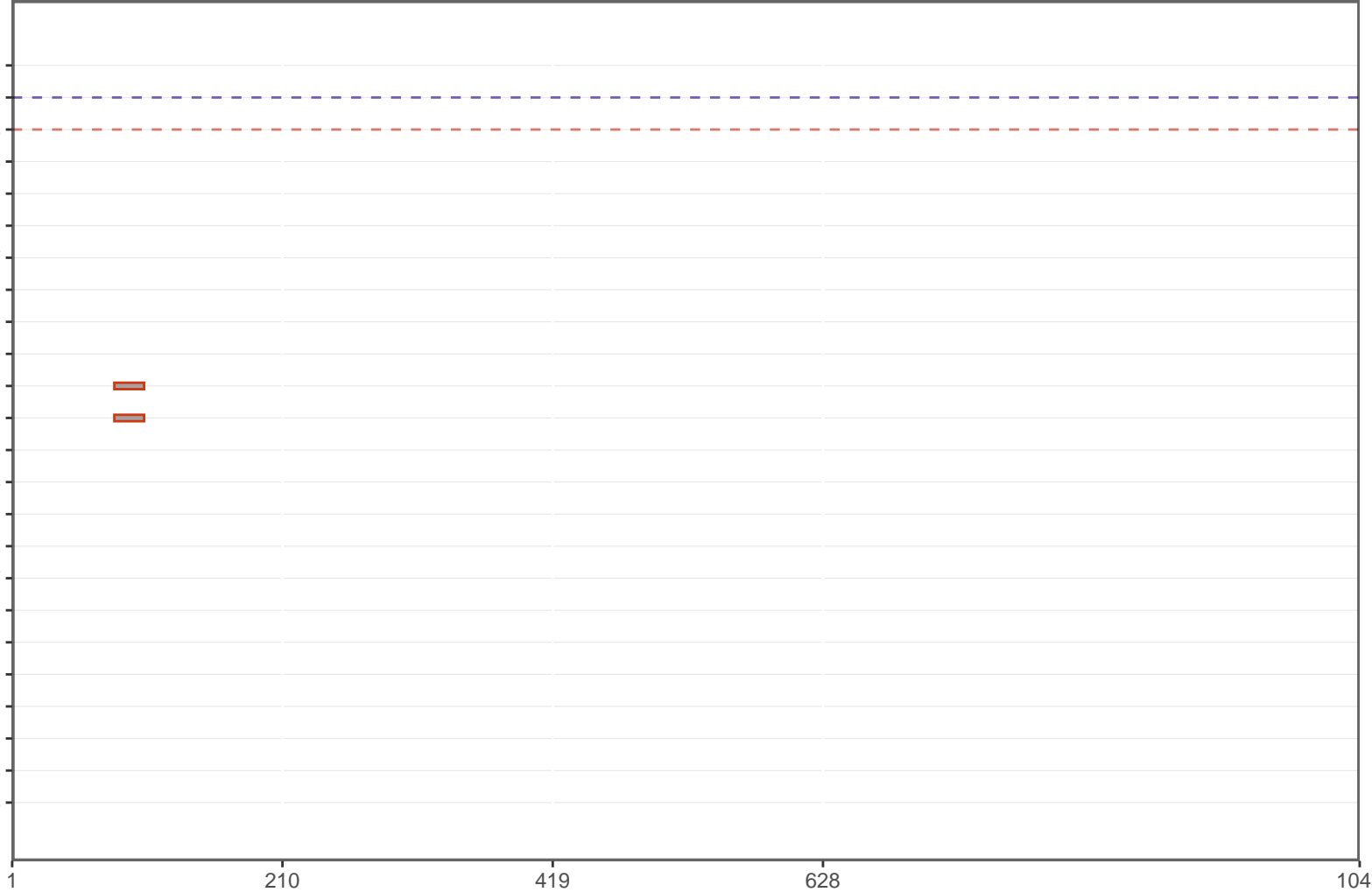
MW indication



Molecular weight

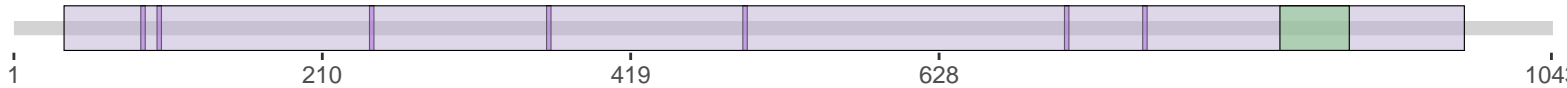


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

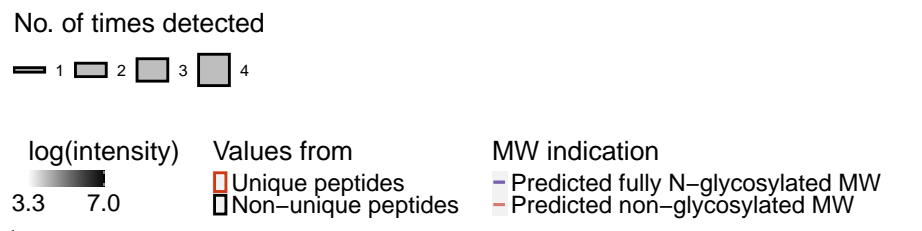
Pfam Description

- SP
- Sequon
- TM Domain
- PF00670 S-adenosyl-L-homocysteine hydrolase, NAD binding domain
- PF05221 S-adenosyl-L-homocysteine hydrolase

Protein sequence:

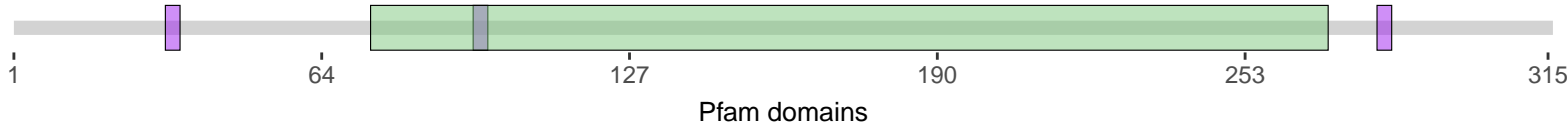
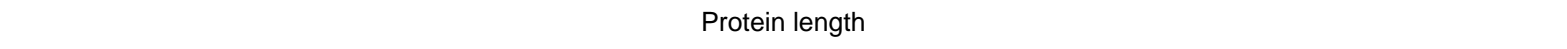
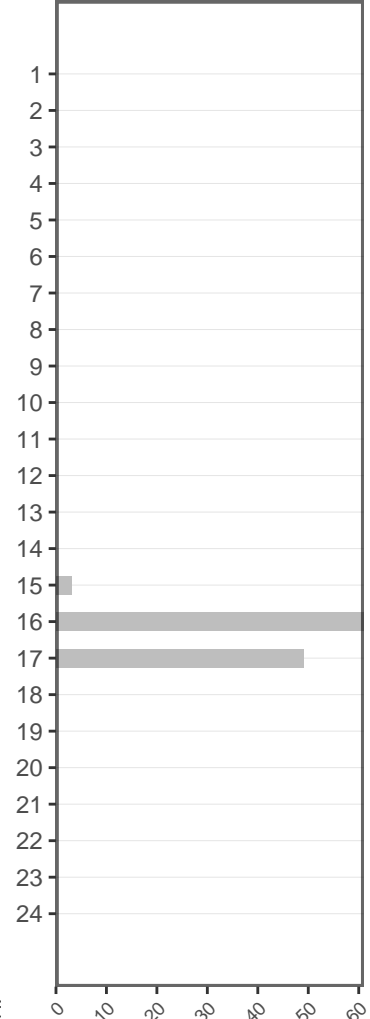
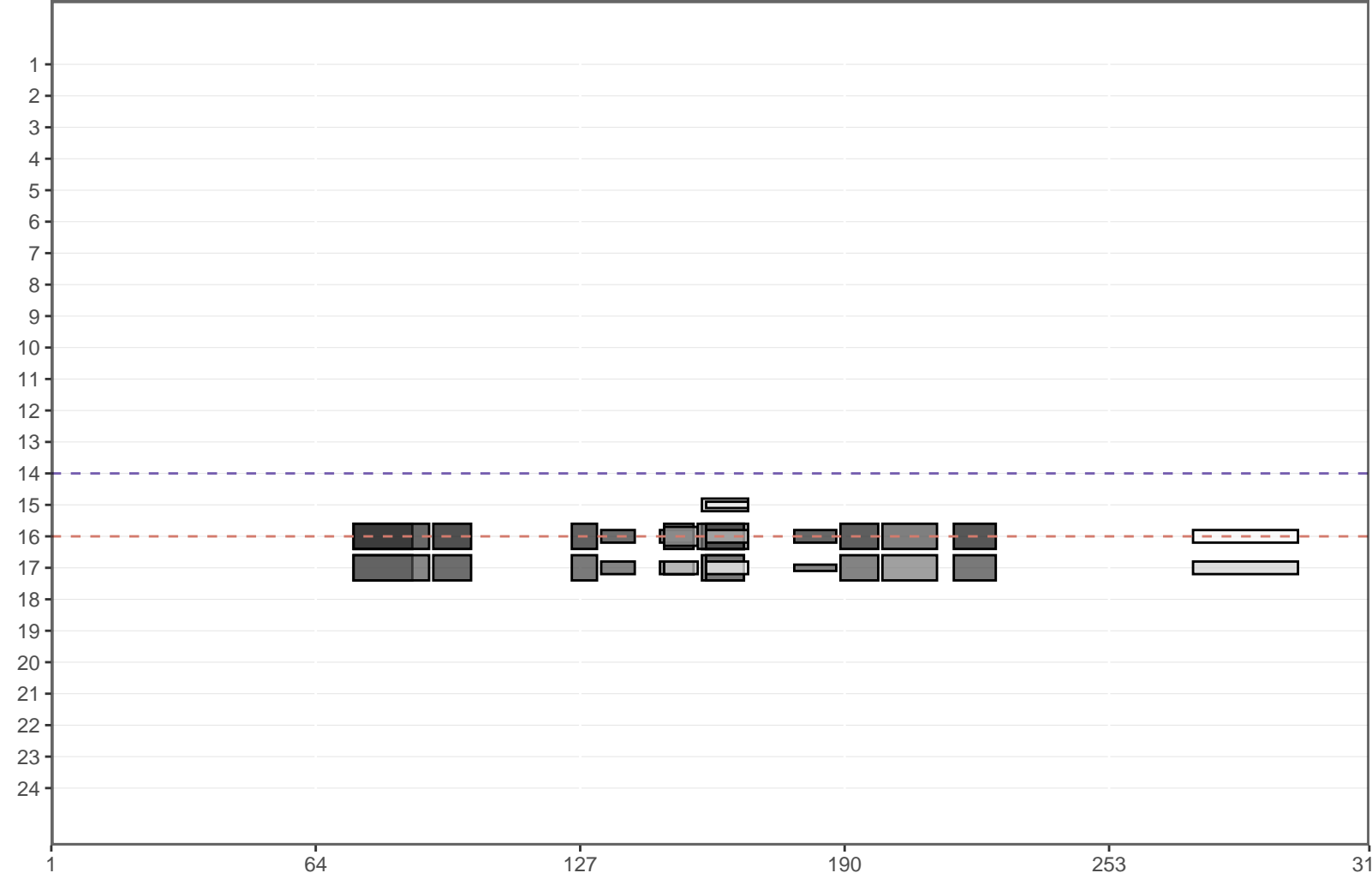
LLLEVEELTELTEVWEGSQWEKWEKMEQAAEHVAPILPENSNNKELVSNAGRGRARLCKDDEEGSNVAKFDFGLSTMTLGTGSGAVIRPVMQKINIMSLAVYTKLIGRAPPVYMLLQLYDTYKRPEDFDVLLVGVGKLVLAHHVILDGVVDEEIPILGRFFLATGRALIDGDTGKLMRLIDEEVFNVQGSRRRPFSEVANGSLVDAVDLKGKDDTTLTVNPNLEAGLNLEKMDGEGIAEWEVERLLHLRENKTIHWMTANIEDISPAFYMKILLLEEGYKPLREH

NbL03g16310.1 haloacid_dehalogenase-like_hydrolase_domain-containing_protein_At3g48420 [MW = 33.64 kDa]



Molecular weight

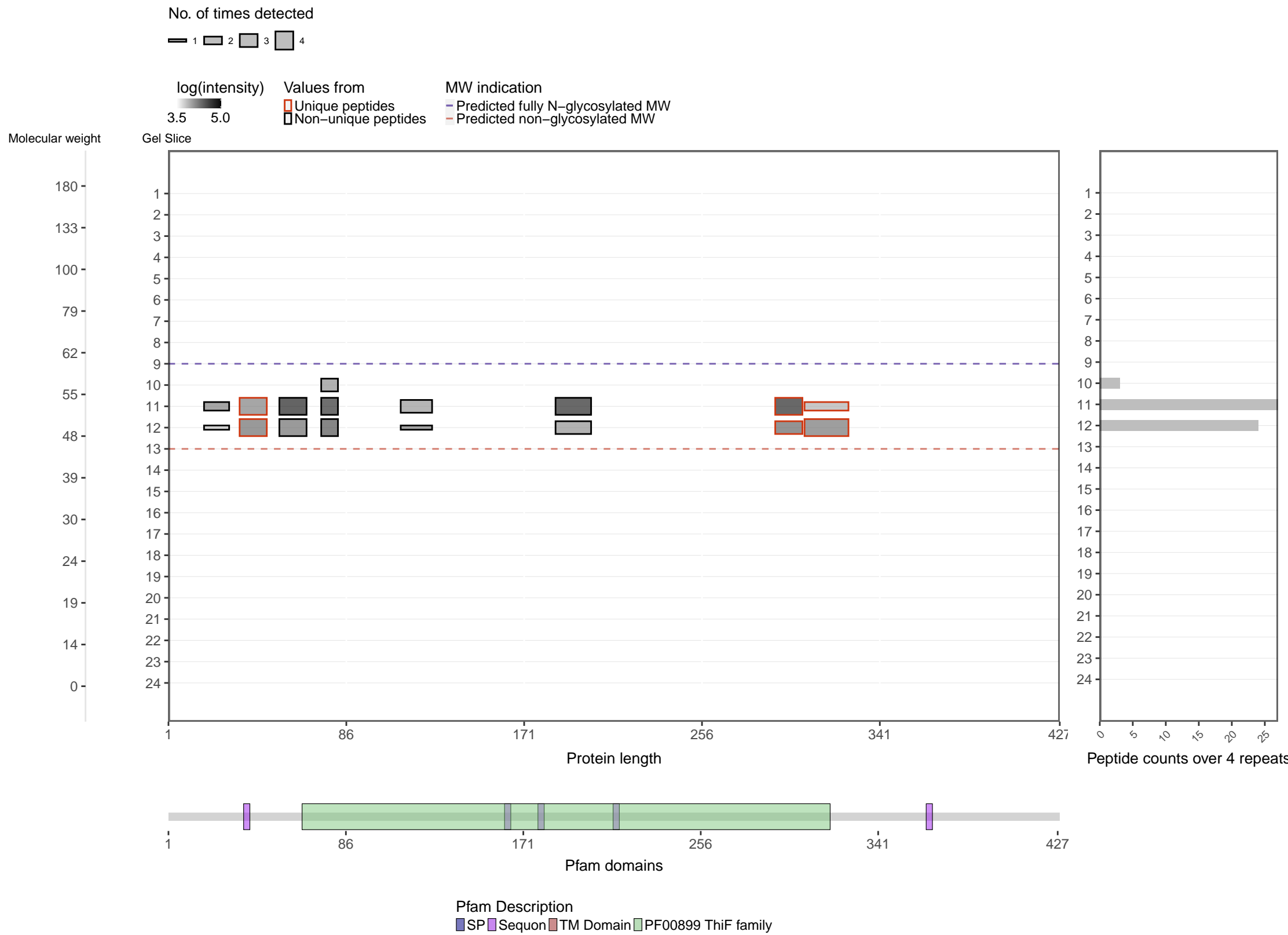
Gel Slice



Pfam Description
 SP Sequon TM Domain PF13419 Haloacid dehalogenase-like hydrolase

Protein sequence:
 ERKQFIAGLHKRKTFLFMALIEKLLPLRPGVAVLVDDALGNQVAVVGGSTNEKAVSAIVSGLLSPERAEKIQVAGVVRPKKDPNVLAAADTLGVDPSSGVVVEDSGIGLAAKAAKMGIVTKSGYTDENFENADAVFDGKDPPEERFDLAFDGGLEKGVVSE

NbL03g16220.1 ubiquitin-like_modifier-activating_enzyme_5 [MW = 46.66 kDa]



Protein sequence:
 .RMVYVQACNELNGTWMEGGVSEDAVSGHQILIPGESAGFACVPLRVVASGIDERTLKREGVGAALFTTMGVVAGLLVQNTLKYLLKFGQVSPVLYGNALKDVFPTMEMKPNITGGSNAAGLERQKEVILAKPTRDAAKAKADKKEALSAPENIVHADNEWNISVDDNEVDGTVTGHSGVLPQGVHPELVADEYKPKPATFETVGPADDELELRQLEALNAE

NbL03g16130.1 uncharacterized_LOC104224837 [MW = 93.85 kDa]

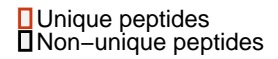
No. of times detected



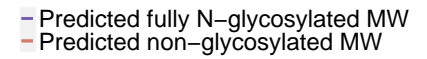
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Values from



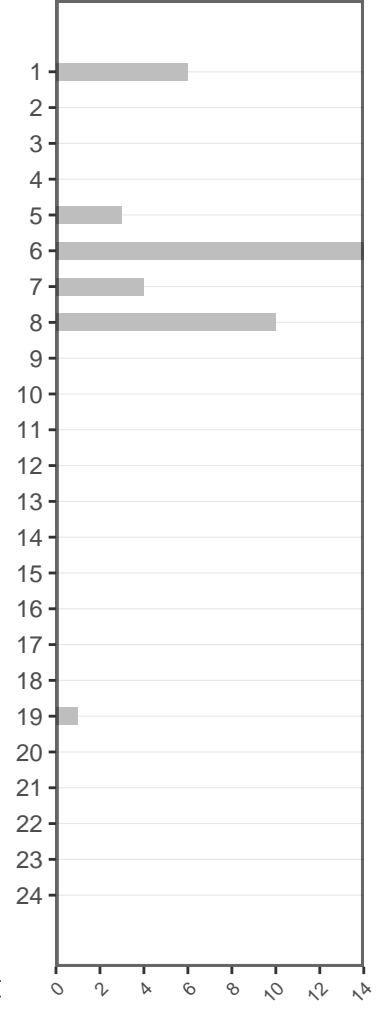
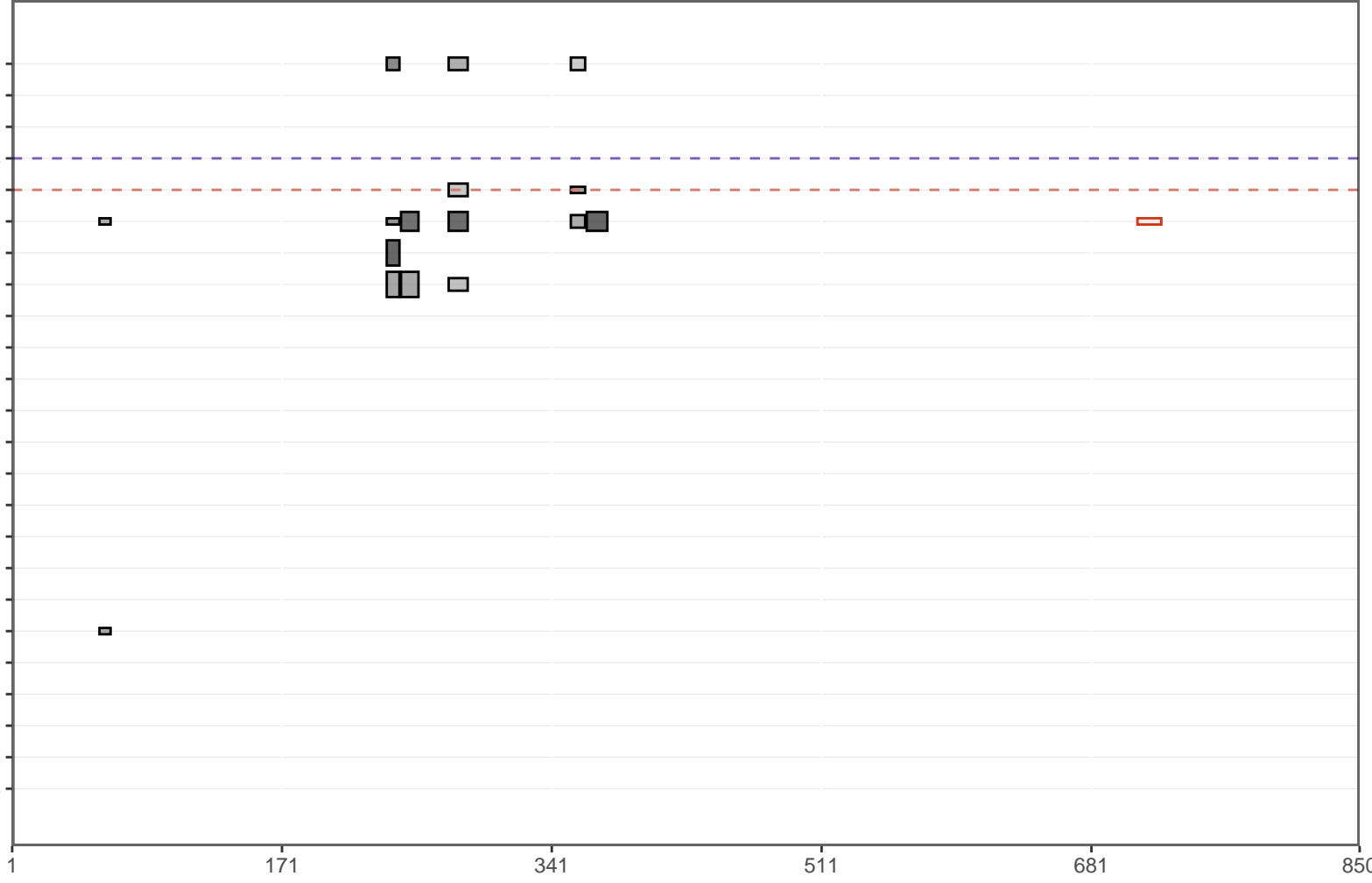
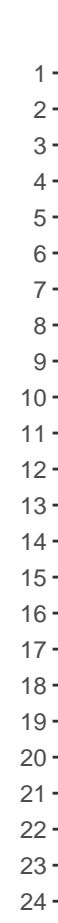
MW indication



Molecular weight

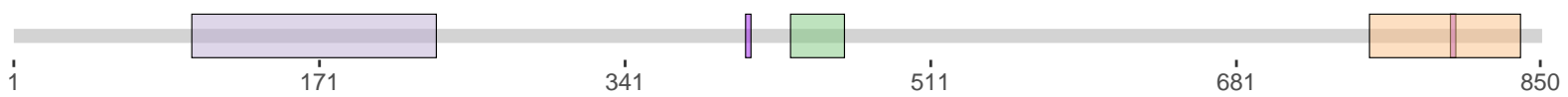


Gel Slice



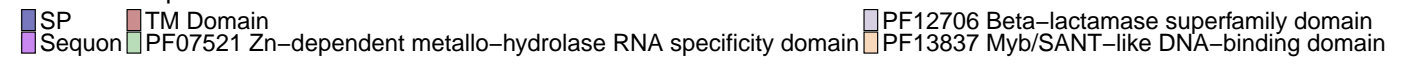
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ILNRISDGSITVYMGKNEILLHTSGHARREELLEVLYKWKPKQFLPHNGELLFLKHELLGKSTGRHTAVKNGEMLVGSHLRNRKVLNNGFBLGKENVQLMYSDGQAFGTAAELGIDERGRASDGVVSMELLRPQGMGDKATEKALKGKIRITRGLWLDKGLLDLHKAHAALSSCLSGPLHMERITVSEVLRKMWRYKYSKRPVIAAFENPAGVLADEINGKLSGKSHGFGIEALRNVMDEDQKGGQASEARAEEGPGYPIDAAEQVEGVMDIERLTHDRGT

NbL03g16090.1 probable_aspartyl_aminopeptidase [MW = 52.65 kDa]

No. of times detected



log(intensity)



Values from



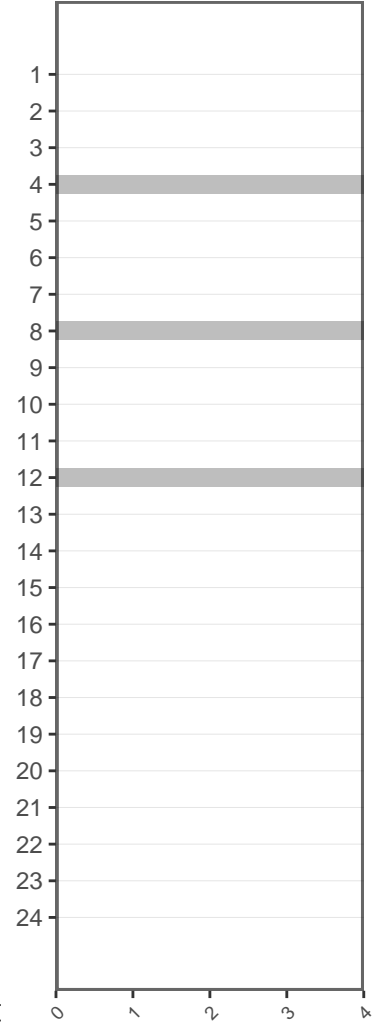
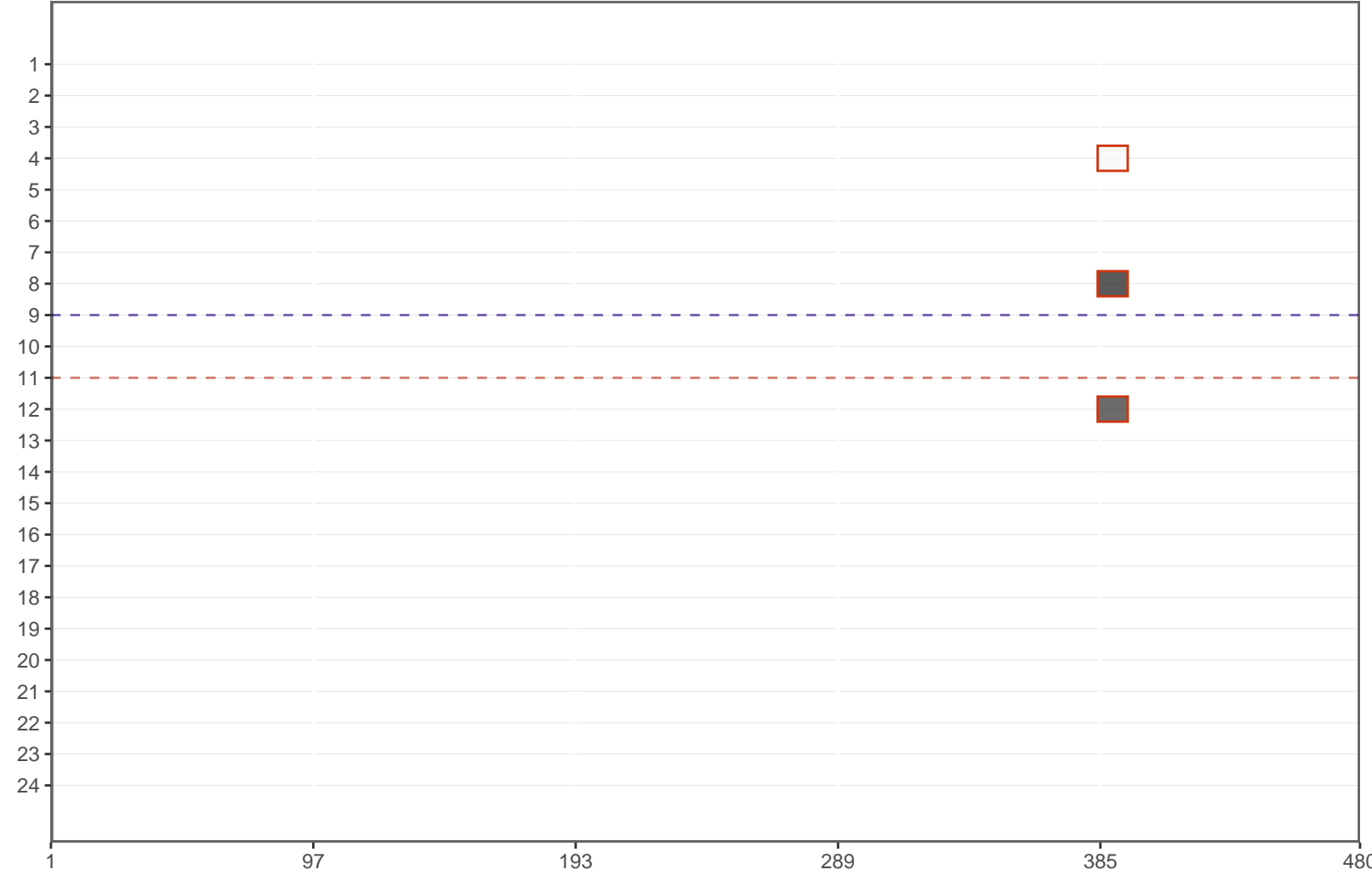
MW indication



Molecular weight



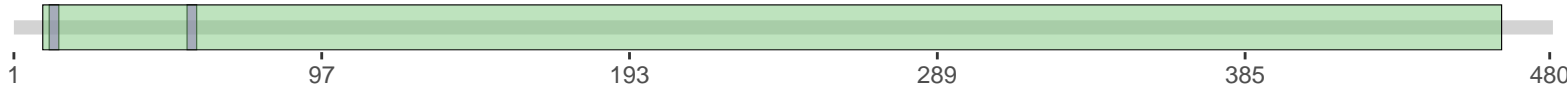
Gel Slice



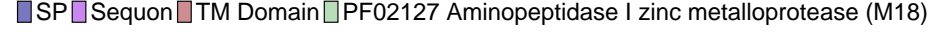
Protein length



Pfam domains



Pfam Description



Protein sequence:

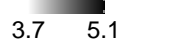
AAQAGCCPSDIDCFELGQDDTQPSVWAGAKKEFVFSGRLENIQSFQSLKALQATSGNSLEDEVGVRMVALFDHEEVGSDSAQAGSPVMDALSRITSTFSPDLKLPKAGRSFLVSDMMAHALHPVYDKHEENHQPKFHGLVKKHNAQRVATNAVTSFLFRFAAANKHPIDQFVIRNDMPGSGSTIGPLASGIGRTVDVQAPQWEMHRSREMGAVDDVKKHAYHFFKAFQDFSHLDAMAVDVI

NbL03g16080.1 4-coumarate--CoA_ligase-like_9 [MW = 59.66 kDa]

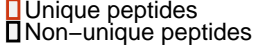
No. of times detected



log(intensity)



Values from



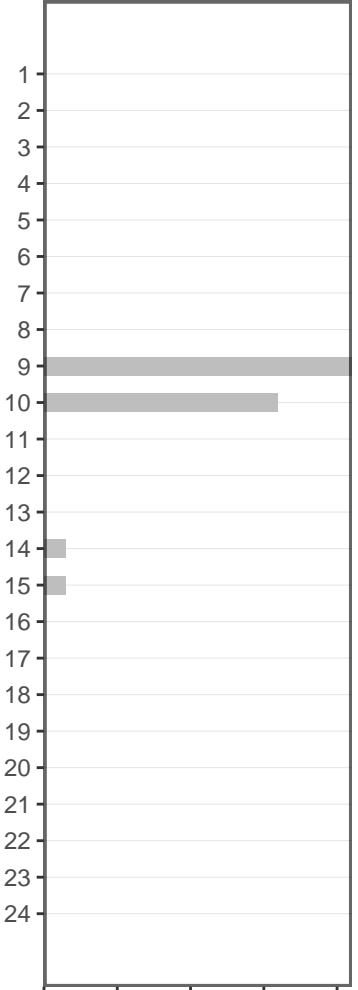
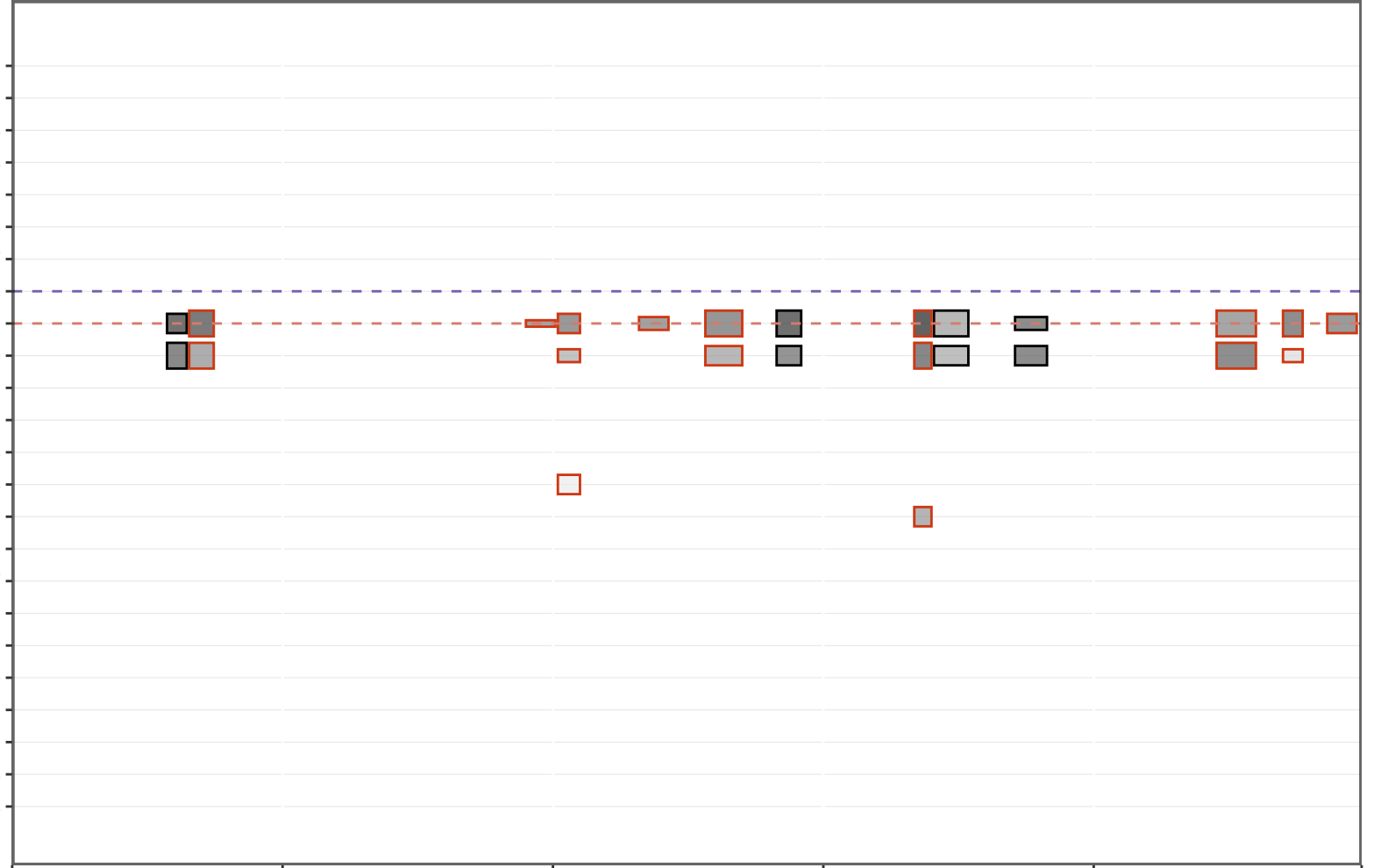
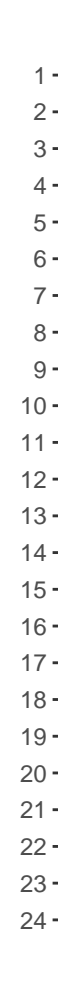
MW indication



Molecular weight

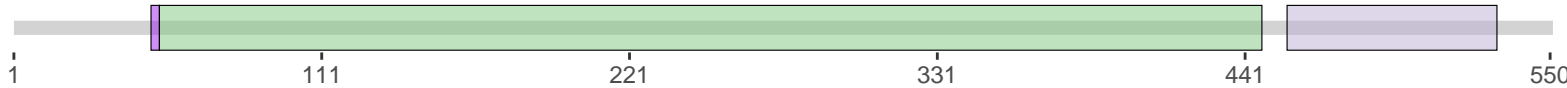


Gel Slice



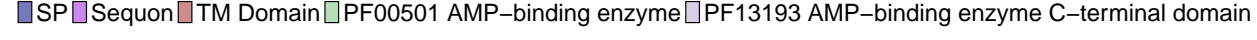
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MIERFDPEKMLAAVEKYYRVTYMPVSPPLVAMAKSDLAHKHLSLKLKLAGGAPLGEVAERFKRRFFNVEHGGYGLTFTTGGATGMSGPEESDRYGSAGRLAVNVAEKVDPDNGETLPPQGRGELWIRGPTMKGVYDQKQATSATLNSGWLKTDGLCYFDADGFLVYVDRLKEIKYKAVQVPPALEHLLQSPDVAWAVPYDPEEAGEIPMAVYVRRPQGTISEAQIDAAKQVAPYKIRRVAFIDAPKSPAGKILRRELINHASGGASRL*

NbL03g15940.1 nucleoside_diphosphate_kinase_2_chloroplastic [MW = 25.38 kDa]

No. of times detected



log(intensity)



Values from



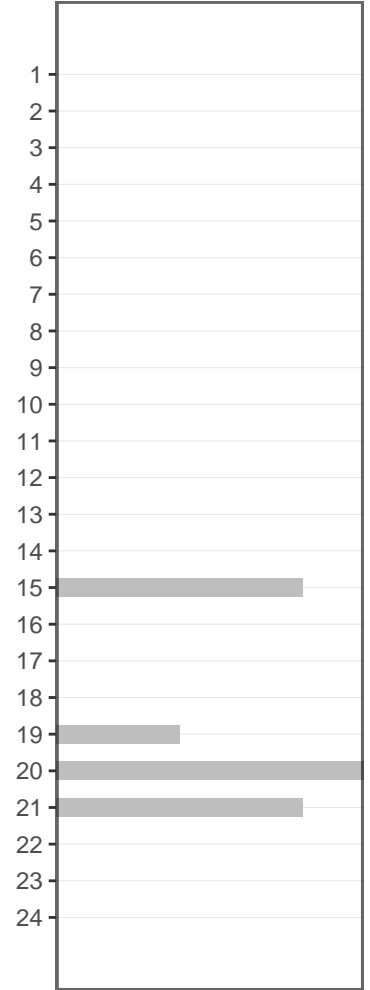
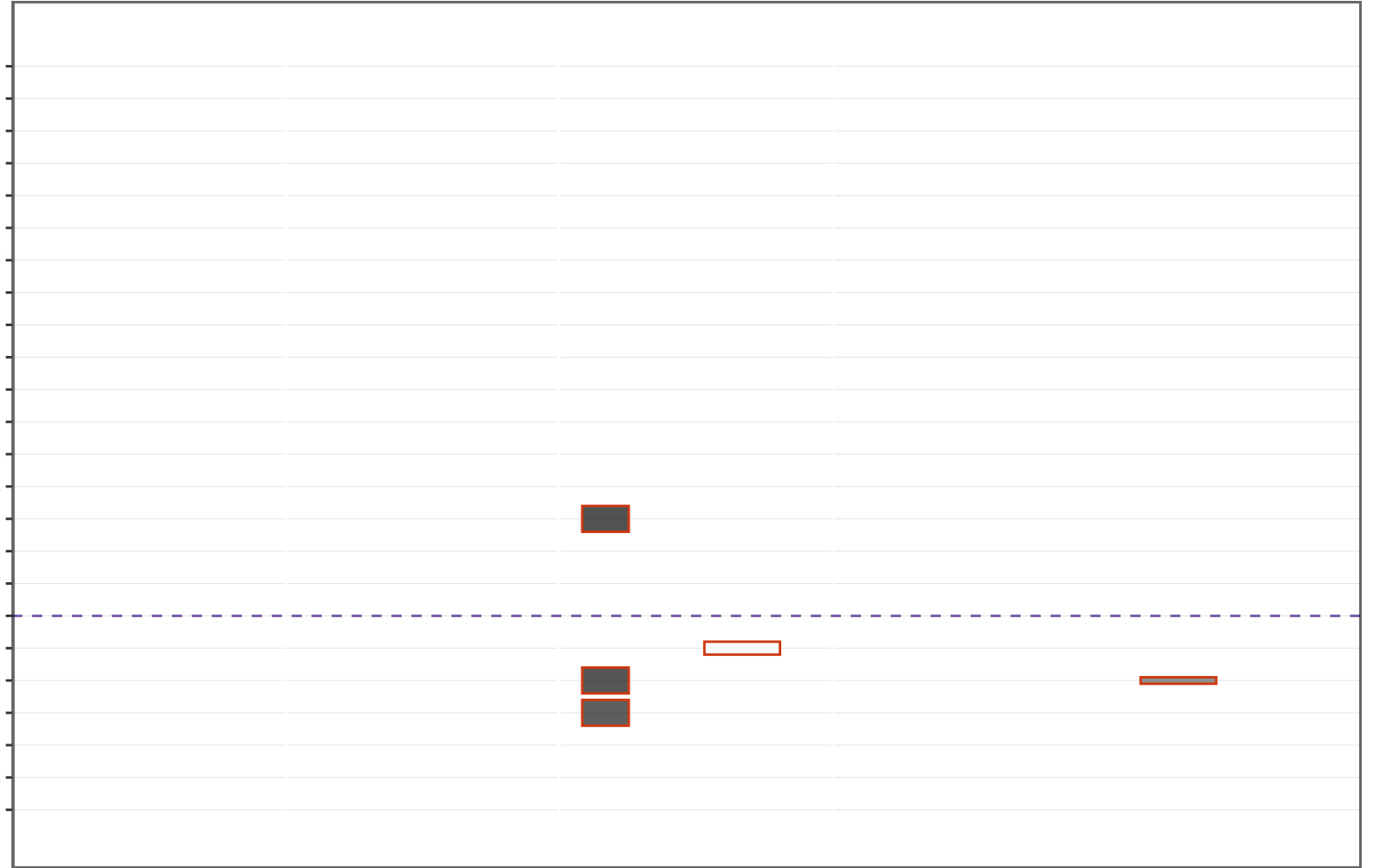
MW indication



Molecular weight



Gel Slice

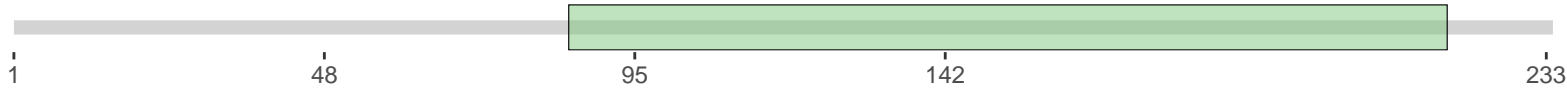


Protein length

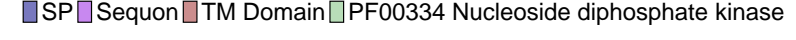


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

TSRFEKGFKLTGKLFEGPKELAEHHKDLGKSGFFPKLDIWTSGPVMMAWEGVGVVASARKLIGATNPLNAEPTGIRGLAVDTGRNVVHGSDSPDKKREIALWREGELGSWTAVGEPWLE-

NbL03g15780.1 gamma_carbonic_anhydrase-like_2_mitochondrial [MW = 33.12 kDa]

No. of times detected



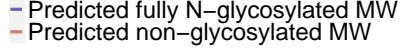
log(intensity)



Values from



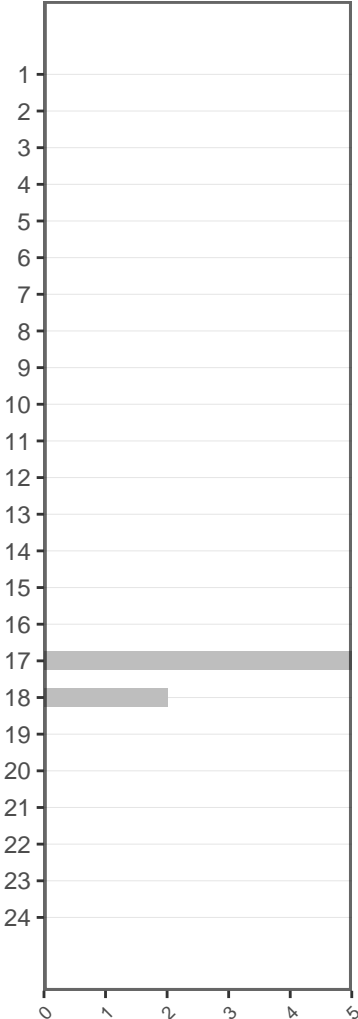
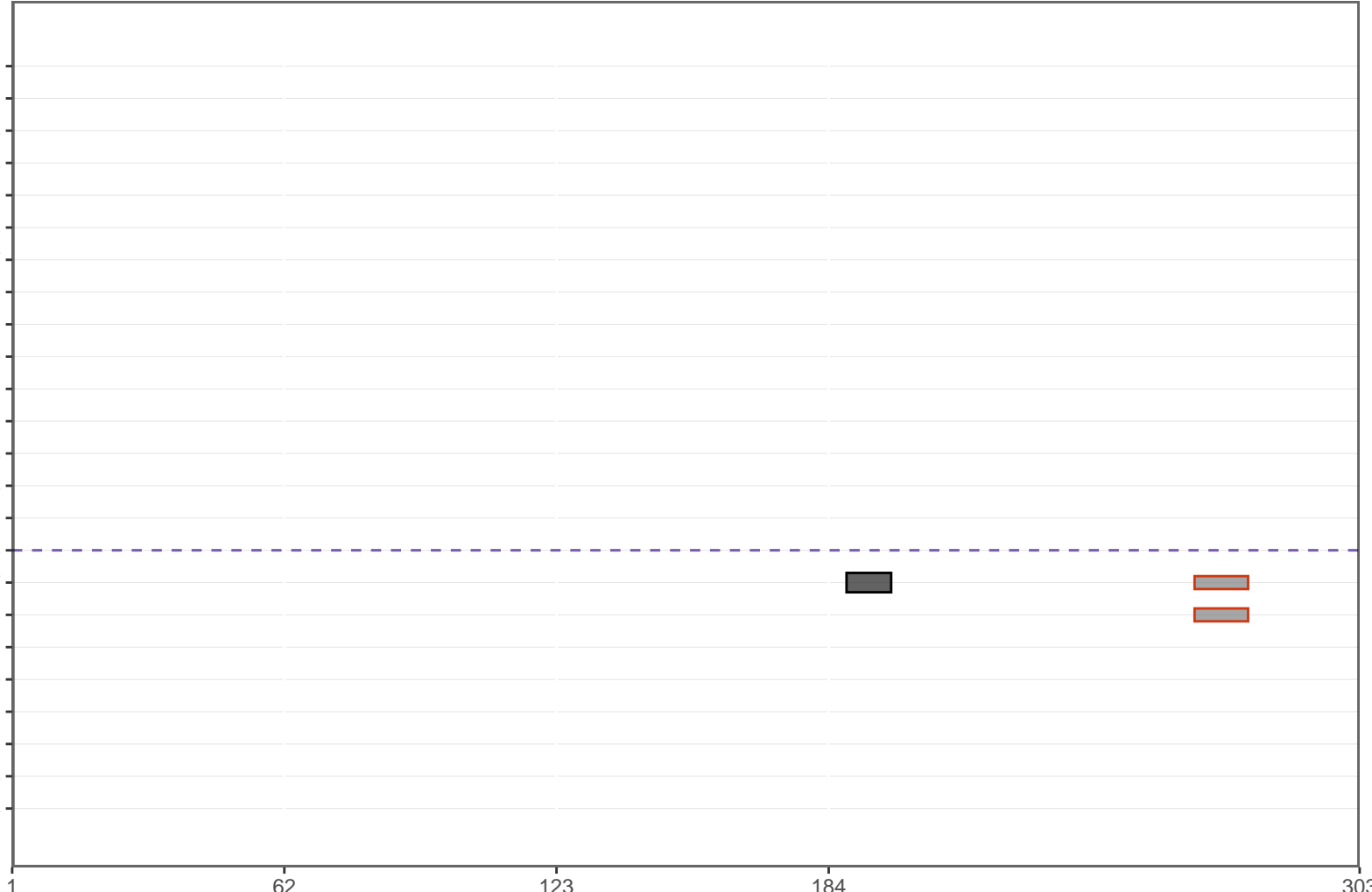
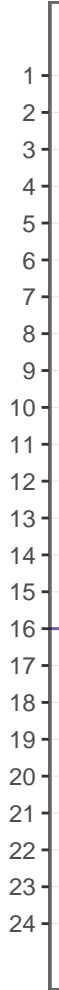
MW indication



Molecular weight



Gel Slice



Protein length

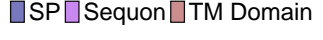


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

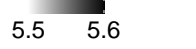
YDGSVYVNGAVLRGDLNKTIGFSSHQEKGVVHAAWBSPTGLPMTLVDRVYVVGAYSLRSCETIEPEGIGQHSILMEGGLVETNSILEAGSVLPPGRIRPISGELWAGNPARFRVTLTHEEKEIPRLSAAINDLANAHRSEFLPSTVYVLEVEKLLKKSFGISL

NbL03g15750.1 alpha-14-glucan-protein_synthase_[UDP-forming]-like [MW = 35.11 kDa]

No. of times detected



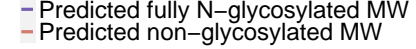
log(intensity)



Values from



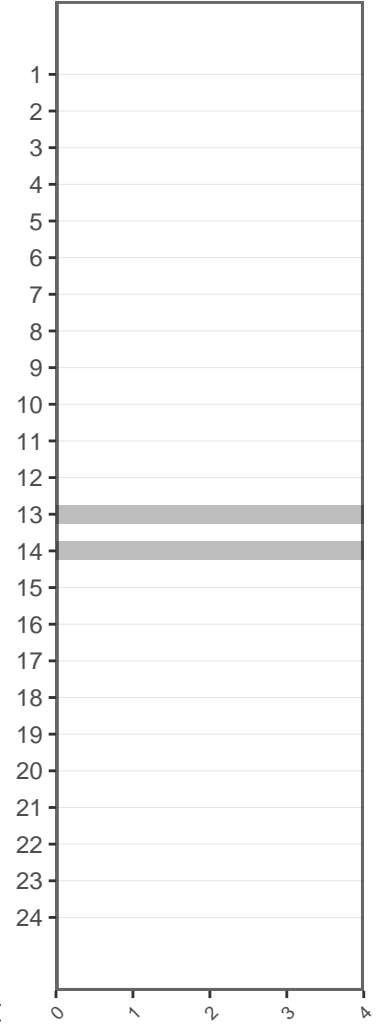
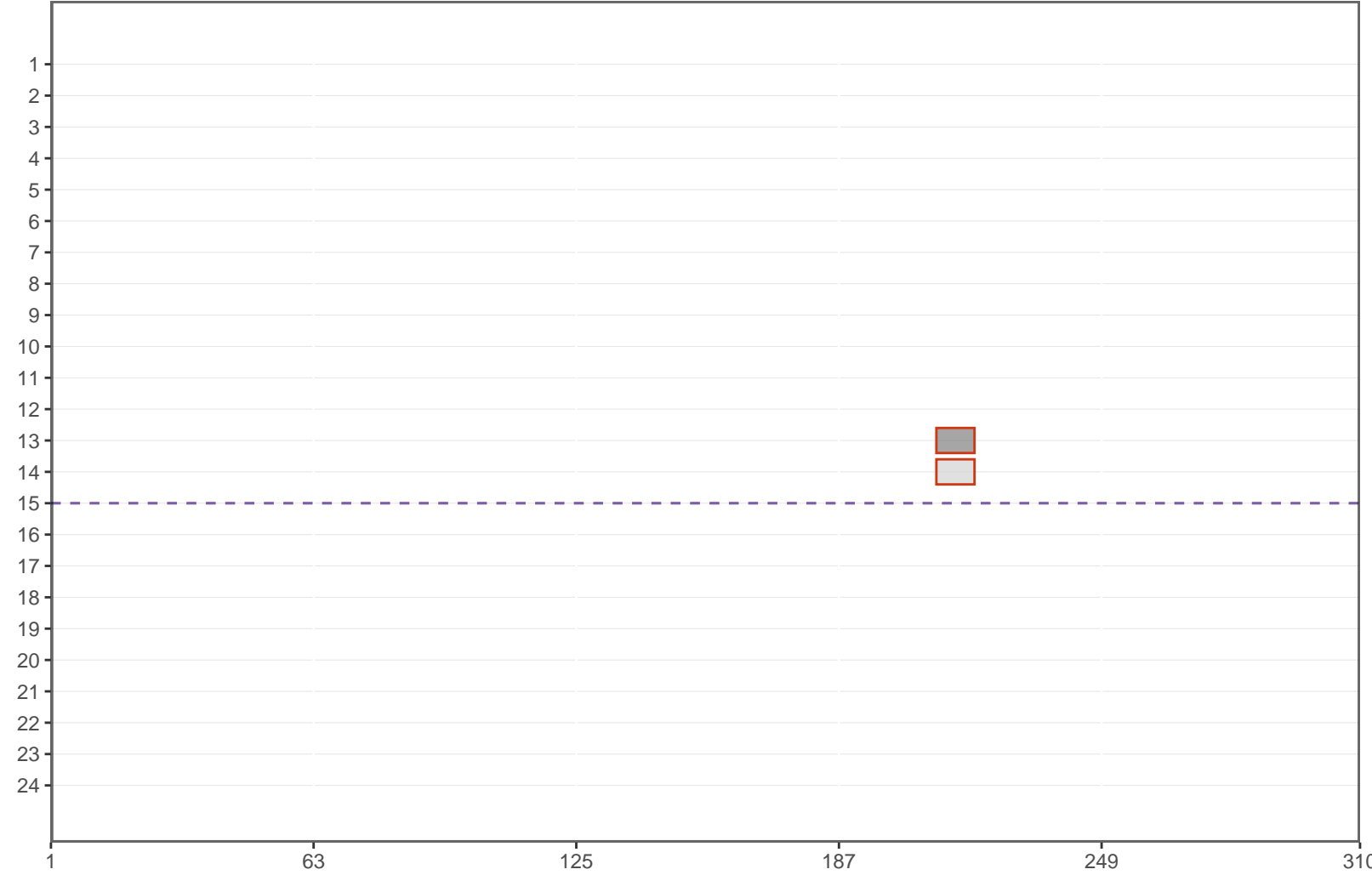
MW indication



Molecular weight



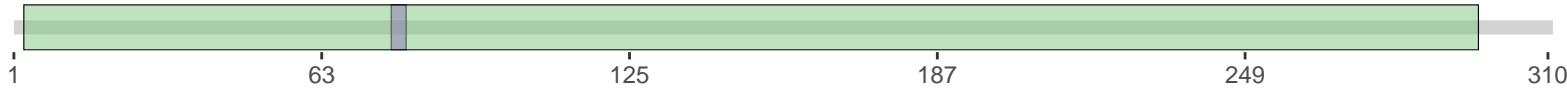
Gel Slice



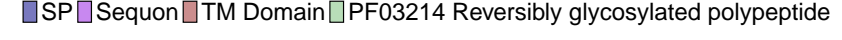
Protein length



Pfam domains



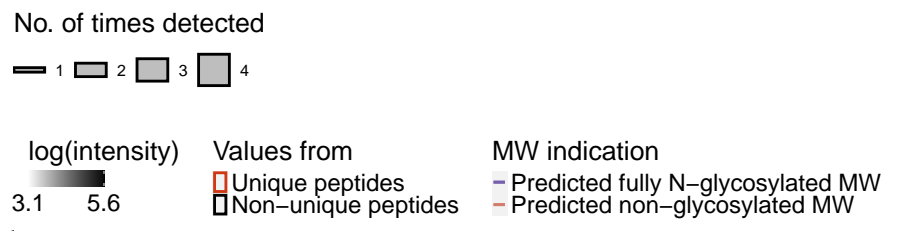
Pfam Description



Protein sequence:

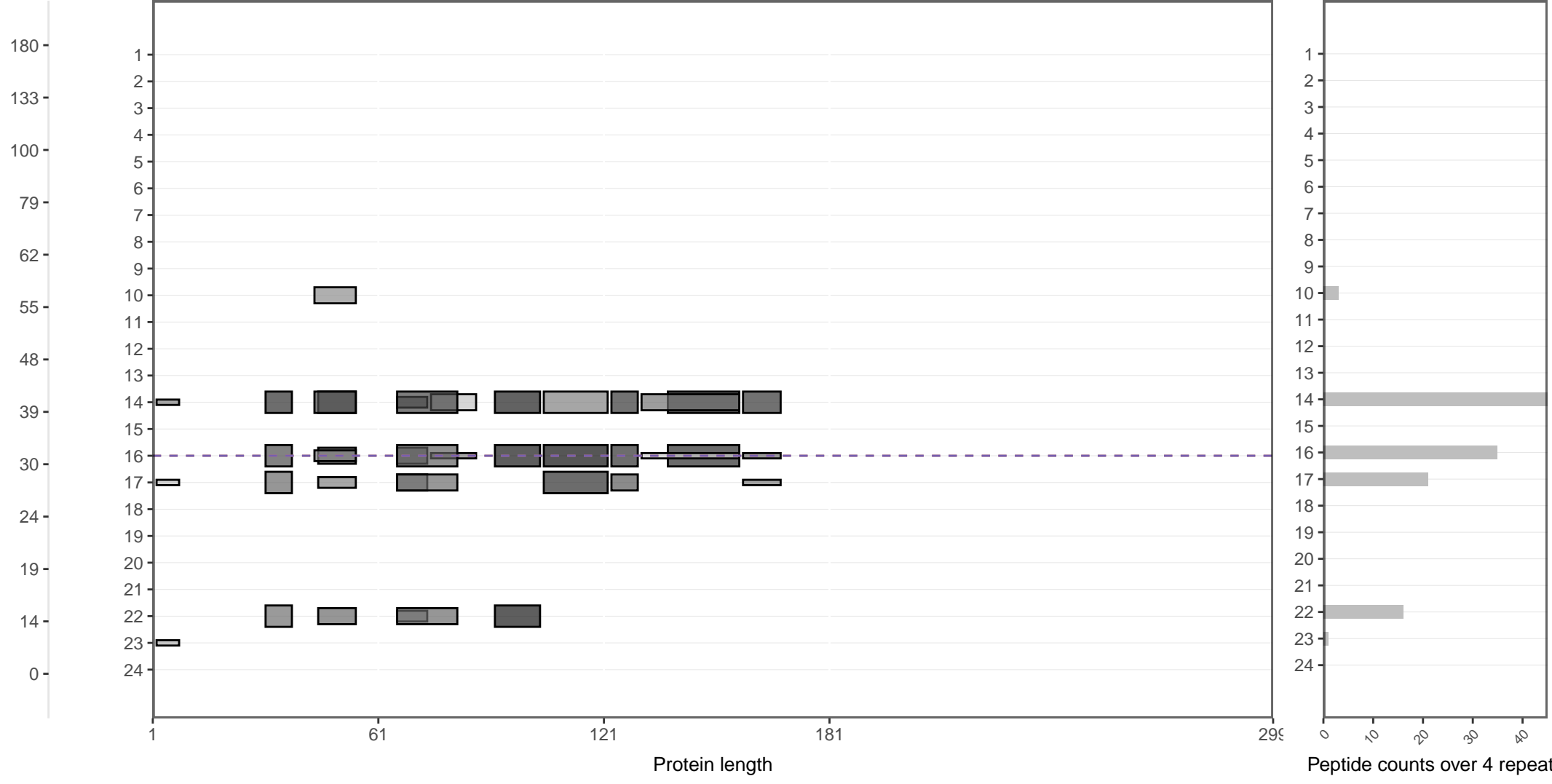
DAVMTIPKGTLYPAGAAANLAFNRELVGPMVFGIMGGDGLRGRYDDMWAGWCKVCCDHLGFGVKTGLPLVWHSKASNPFWLKKFKGLFWGEEIMPPFGSVVFKECTNAQQCYLELAKMVEKLGRIIDYFPHNFAAAMVTWIEAWEEFNAPKAKIDSVKSA*

NbL03g15710.1 40S_ribosomal_protein_SA-like [MW = 32.49 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF00318 Ribosomal protein S2

Protein sequence:

VALGNPTAFCDTDSMRVYVDIGPANNKGGKHIGVLFWLLGRMVLGMKRGSPQGHKWDVMDLFFVREPEEAKEGGEEEPADYAEVGGALGGDWSGNDPDAQWADGAPVVRVAASGWTGGDAVEGGWDAAPRAQVAGAEVFRATPTGWDI

NbL03g15700.1 alpha-galactosidase [MW - SP = 42.75 kDa]

No. of times detected



log(intensity)



Values from

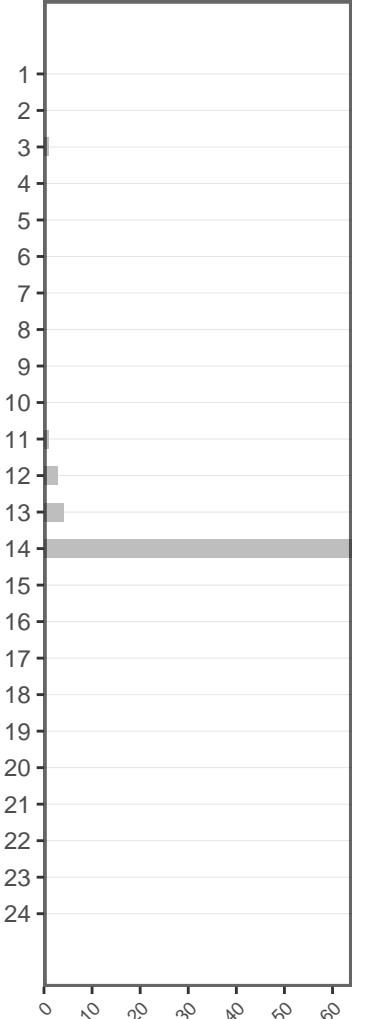
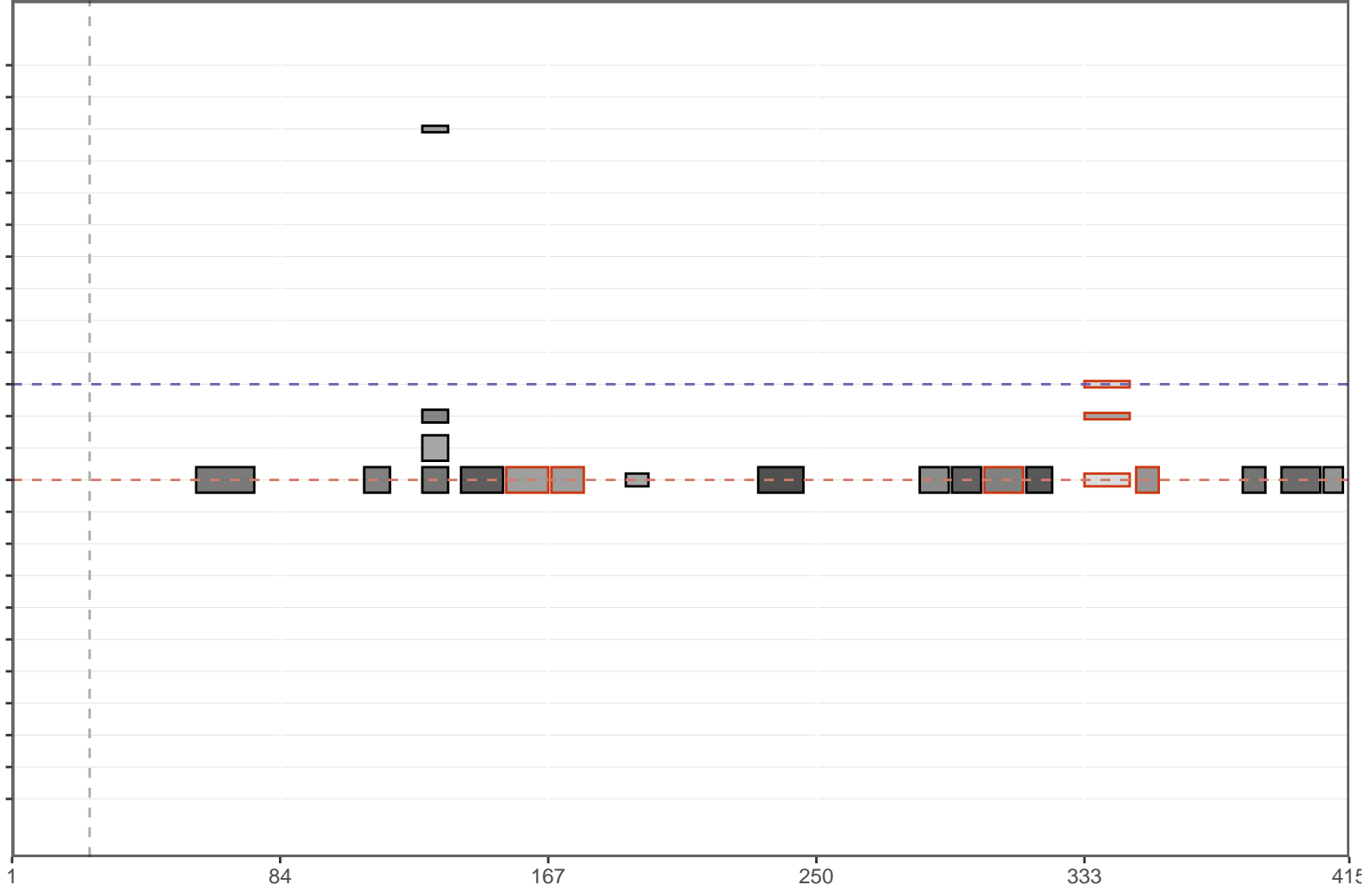
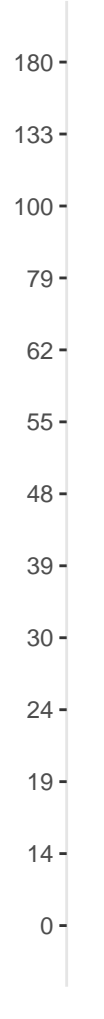


MW indication



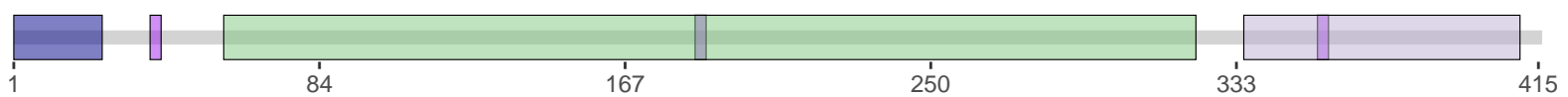
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISKALQNSGRAIFYSLGEWGGDDDPATWASVGVNSWRRTTGDGDDNWDGMSRADMDKHWASVAGPGGVDNDPDMLEVNGDMTAEYRSHFISHWLAKPLIGGDLRSMDGTAHELSNKEVIAVWQDKLVGQCKKVKNGSDLEWVAGPLSGKRVALVWNRSSKADITAVWSDGLDGGSTVVDARDLWAKSTKGEVKGQHSABDSHDCRMVLTFRK

NbL03g15610.1 beta-galactosidase_10 [MW - SP = 97.02 kDa]

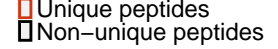
No. of times detected



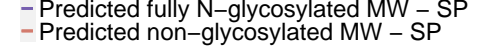
log(intensity)



Values from



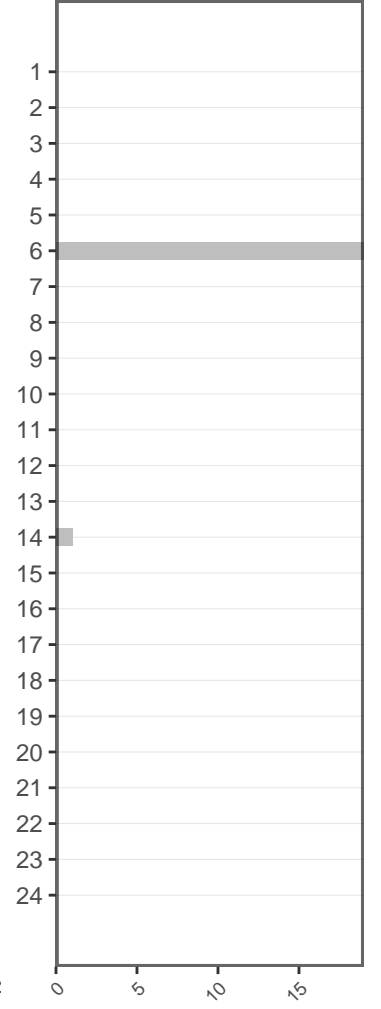
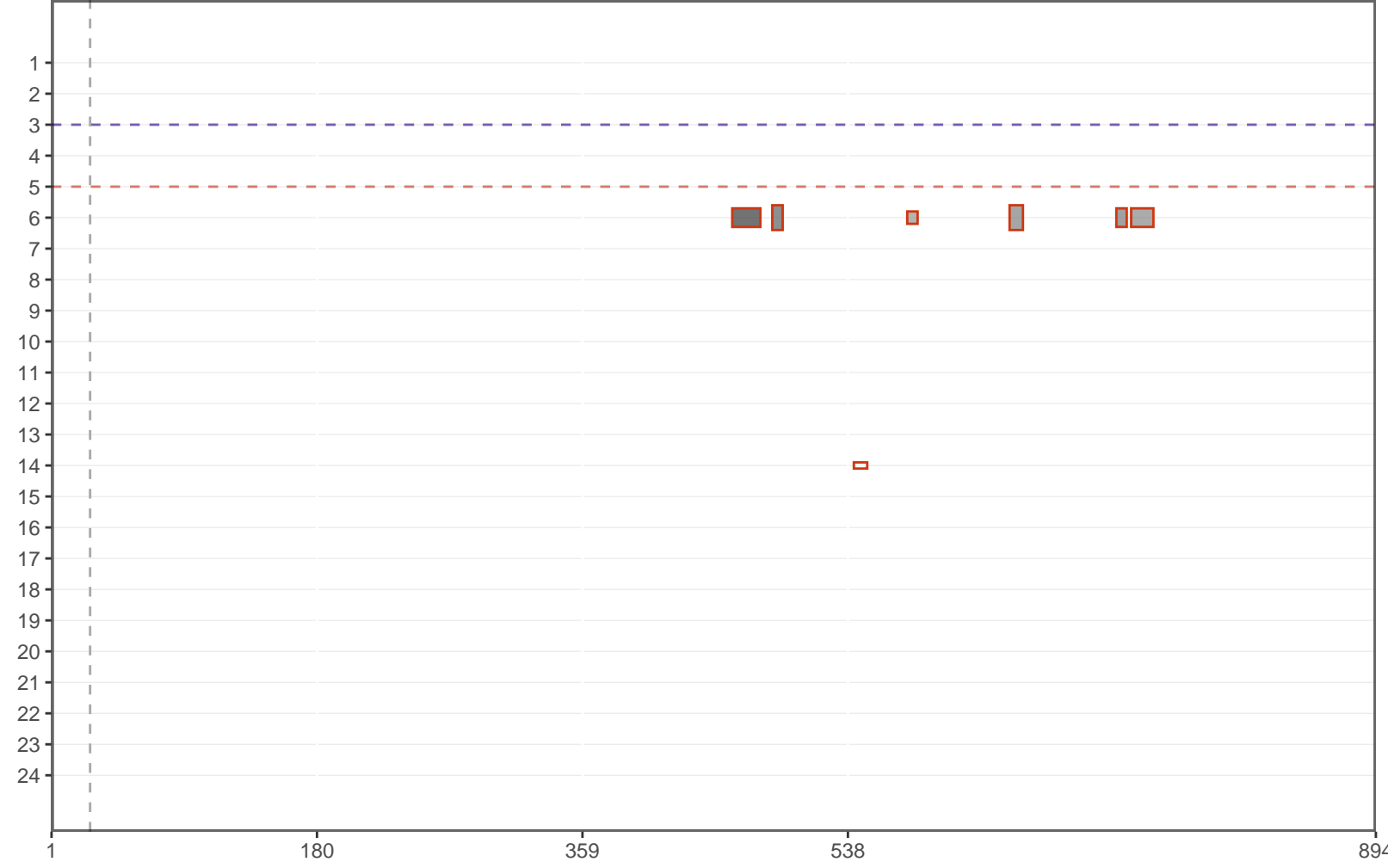
MW indication



Molecular weight

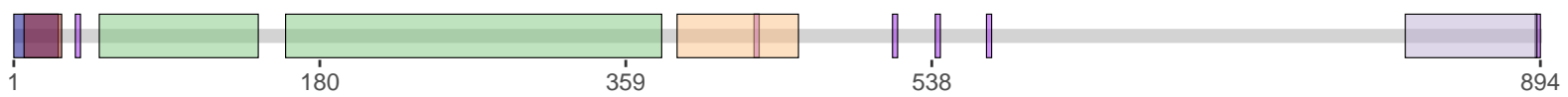


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SYQLFAWSVLSLPQDKNAVFNTAKVGGGTSIVNMEPVDLHPTVRSPKRDKALGWEVFKETAGWGWVDFTRNGFVDHINTTKDFTVLLWYTFISFVNEEFLQNKSSAMLPVESKHAMHVFHNLVGLASASNGTVPHFKGTPLVKAGKNDIALLSMTVGLGTAGSFYEWIGAGPTSVKVEGFNSGTVLBSASTWYKVGHLGHEVLRVYESGGLNNKHWALTSSEPPKQDPLTWYKAVDVPKGPDEPVALDMHMGKGLAWLNGEIGRVPKRSKLEKCYTCDDY

NbL03g15600.1 phytochrome-associated_serine/threonine-protein_phosphatase_3 [MW = 34.84 kDa]

No. of times detected



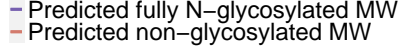
log(intensity)



Values from



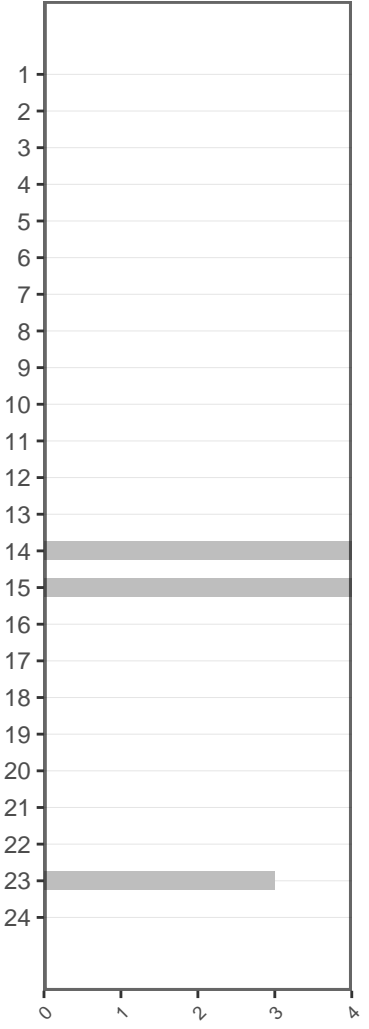
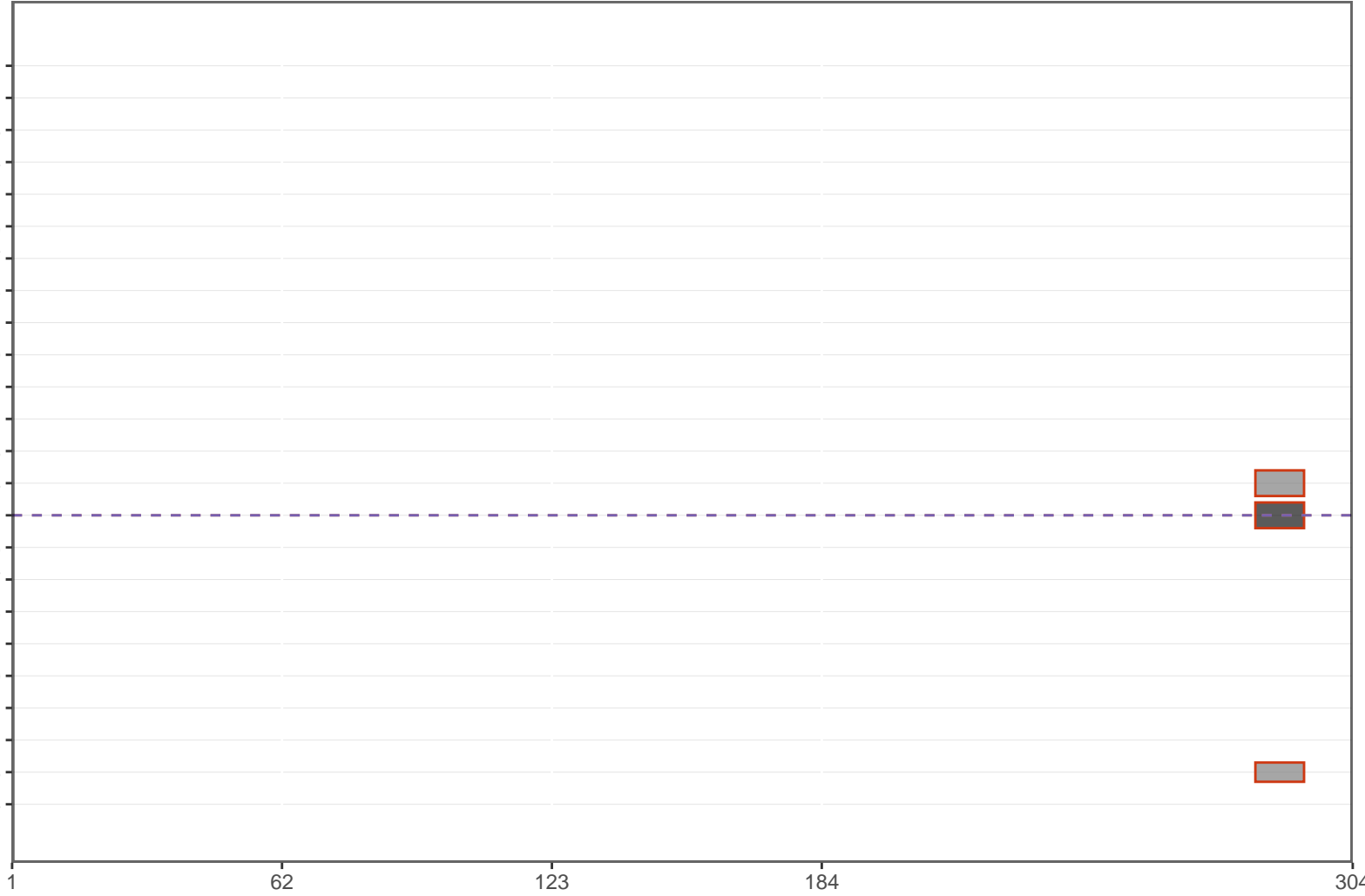
MW indication



Molecular weight



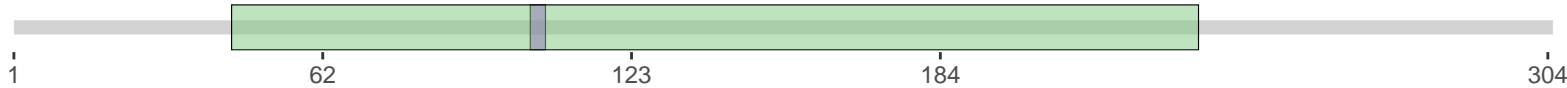
Gel Slice



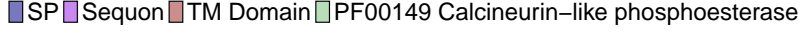
Protein length



Pfam domains



Pfam Description



Protein sequence:

CTDVFDYLTLSAIDGTVLGVHGGLSFDVRIIDGIRVIERNCEIPEHGFDDLMWSDPEIDETWVSPRGAGWLFGRVTFTEENHNKLDLVRAGHGVDEGLKMFQDKGLVTVWSPAPNYCYRQGNVASILSFENMEREWFFSETEENNQRGPRTGVPVFL*

NbL03g15570.1 asparagine--tRNA_ligase_chloroplastic/mitochondrial-like [MW = 66.02 kDa]

No. of times detected



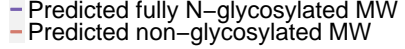
log(intensity)



Values from

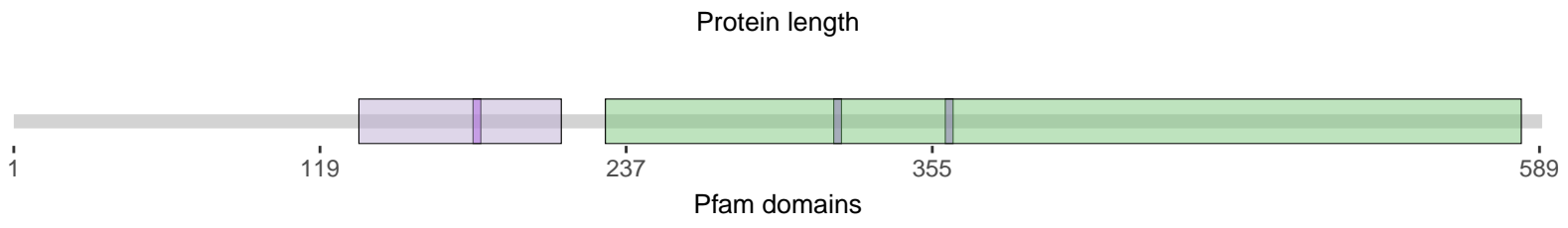
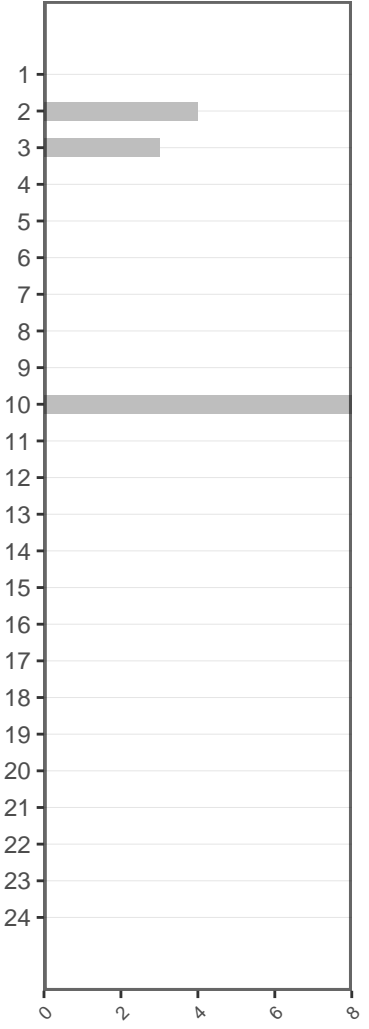
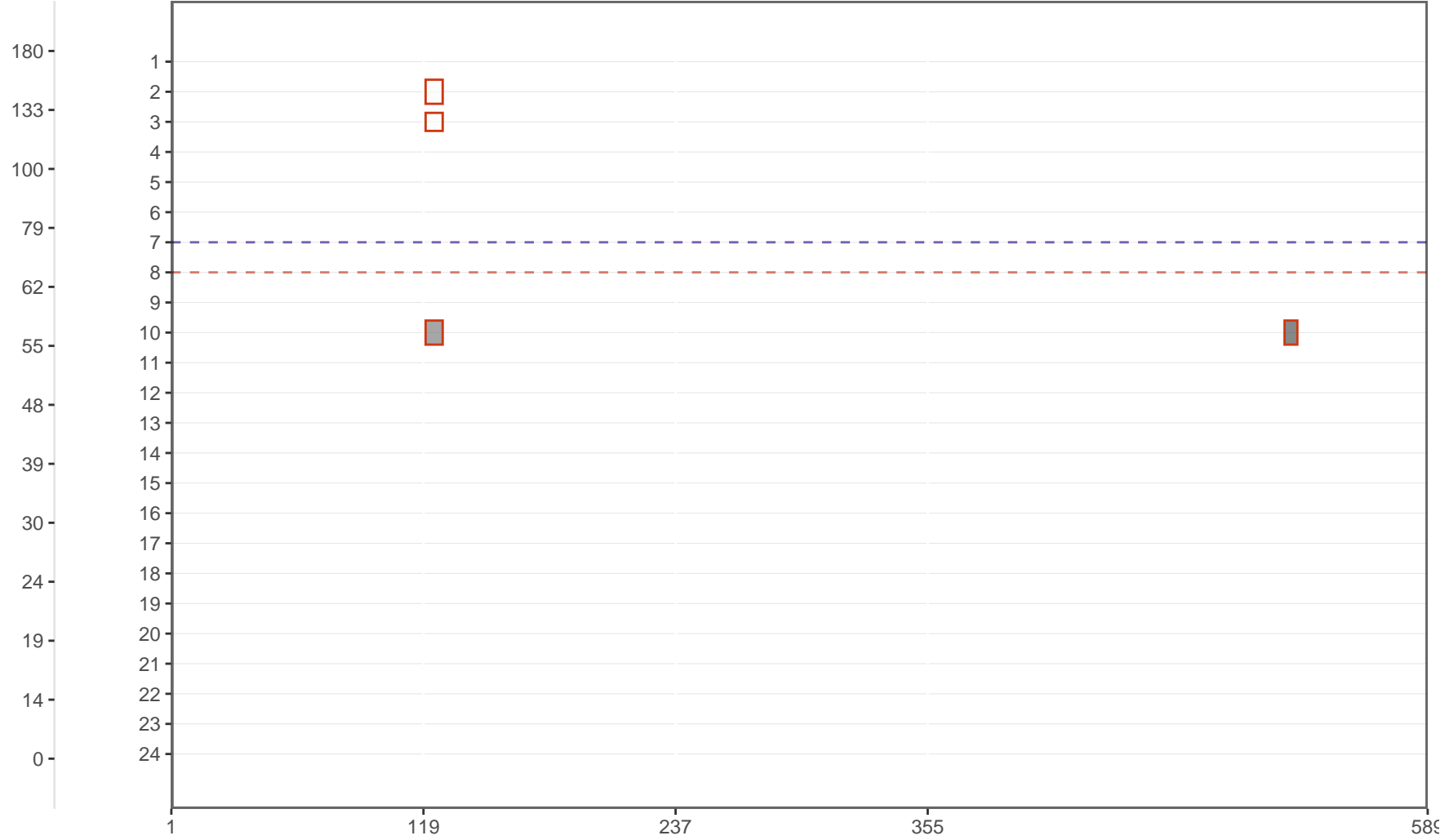


MW indication

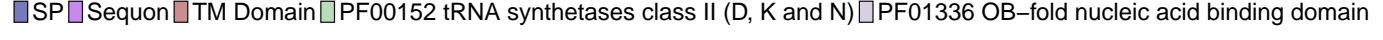


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

EGAGEQFRVYTLIPITIKREGGDSFVNAIPTEEGGQVNWWSQDFFGKQAFVLSGGLNGETVATLSDNYTFGPTFRANSENTRHLAEFRVMEPELAFADLDDMGATAVLQVYVQVLENCCKEDMDFNTWIEKGIITRLSDVVEKRFVQLTYTDVALELLKARKKDFDFVWVGGDLGSEHERVITEEAFGGCPVIRDPKDKAFYMRQNDGDKTVAAMDMLVPRVGEIIGSGQREERLGVLEERLDNLKLNKESFVWYLDLRRYGVPHAGFGLGFERLLVQFATGIDNR

NbL03g15530.1 serine_protease_inhibitor_1-like [MW - SP = 23.95 kDa]

No. of times detected



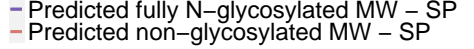
log(intensity)



Values from



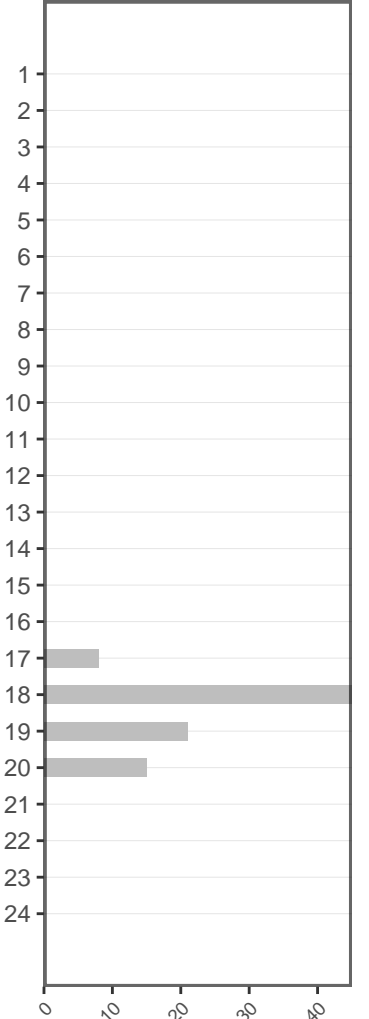
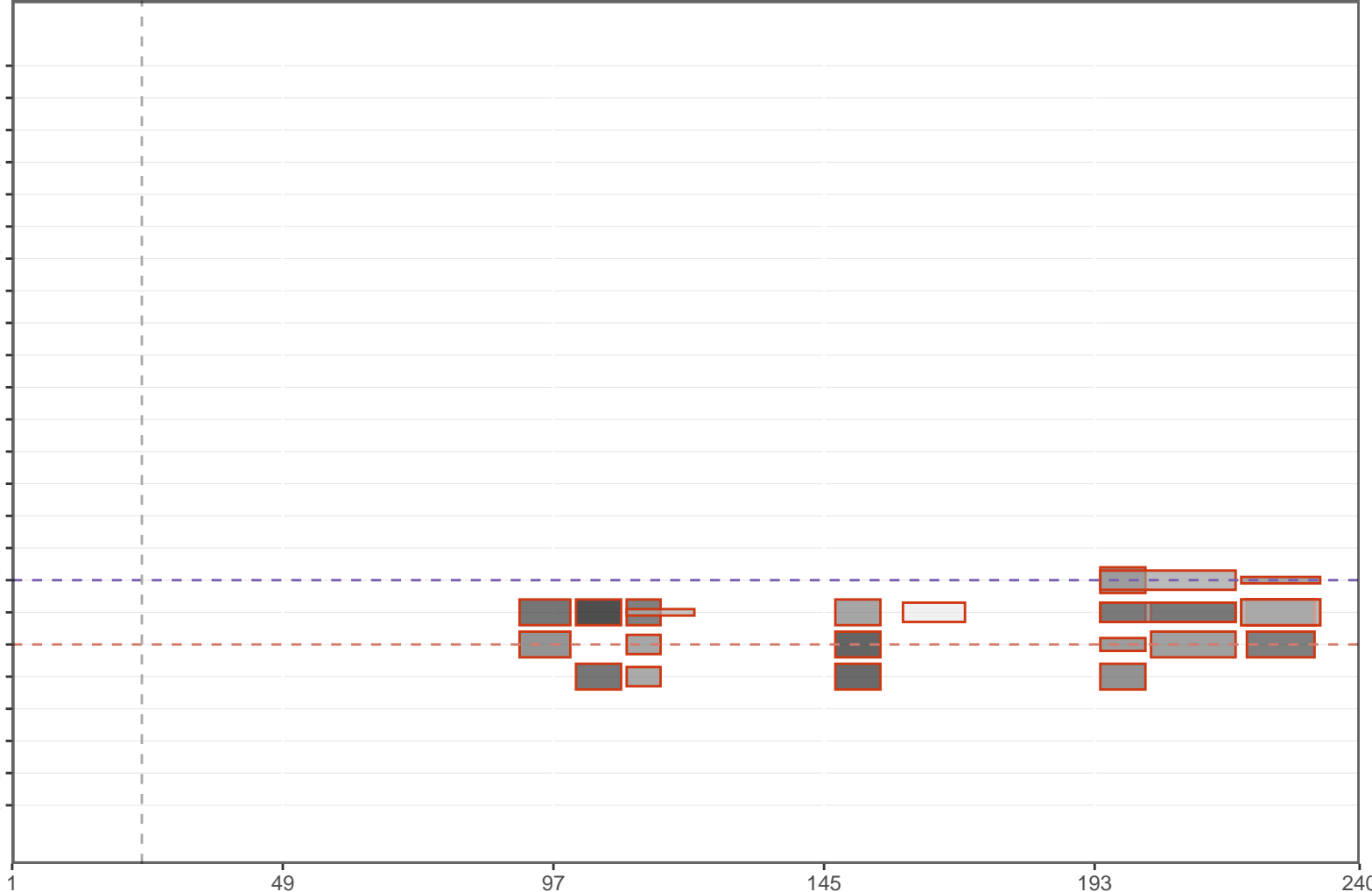
MW indication



Molecular weight

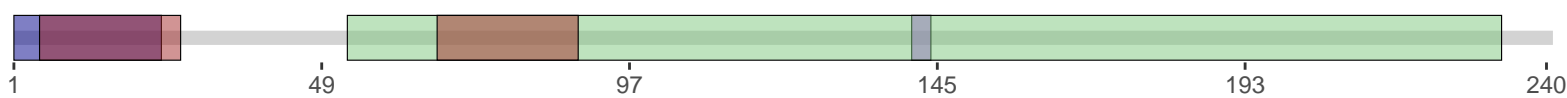


Gel Slice



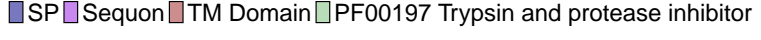
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

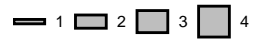


Protein sequence:

VKFTTHPRPLNVRRENTDNMFSAITRLGVNETVWVGGDPEIARLTREVLGGTLGNLRPENSDFWFKIERVTKGGPFYKLRVGPATDSRPVVGSDGVTHVFGVRRLLALNQPFAVVFRRKFGKTDG

NbL03g15280.1 protein_argonaute_1-like [MW = 76.89 kDa]

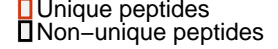
No. of times detected



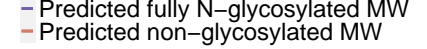
log(intensity)



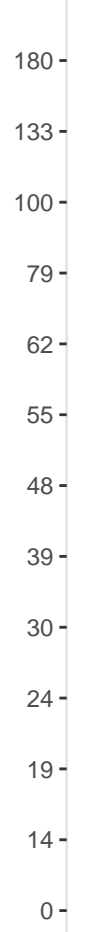
Values from



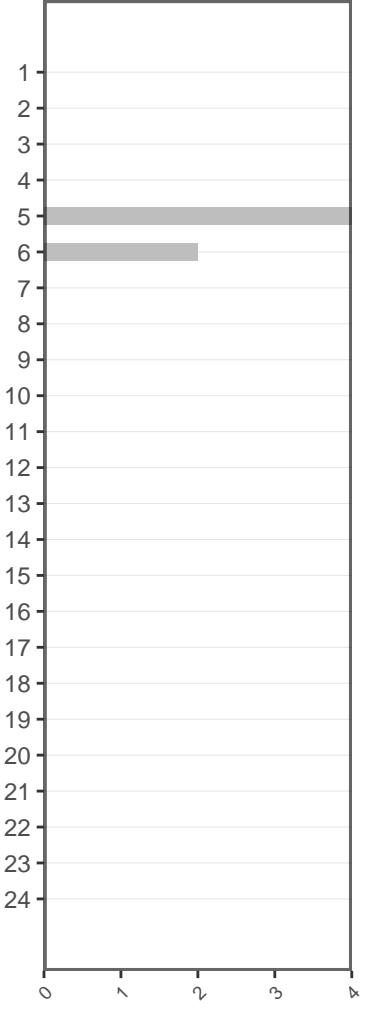
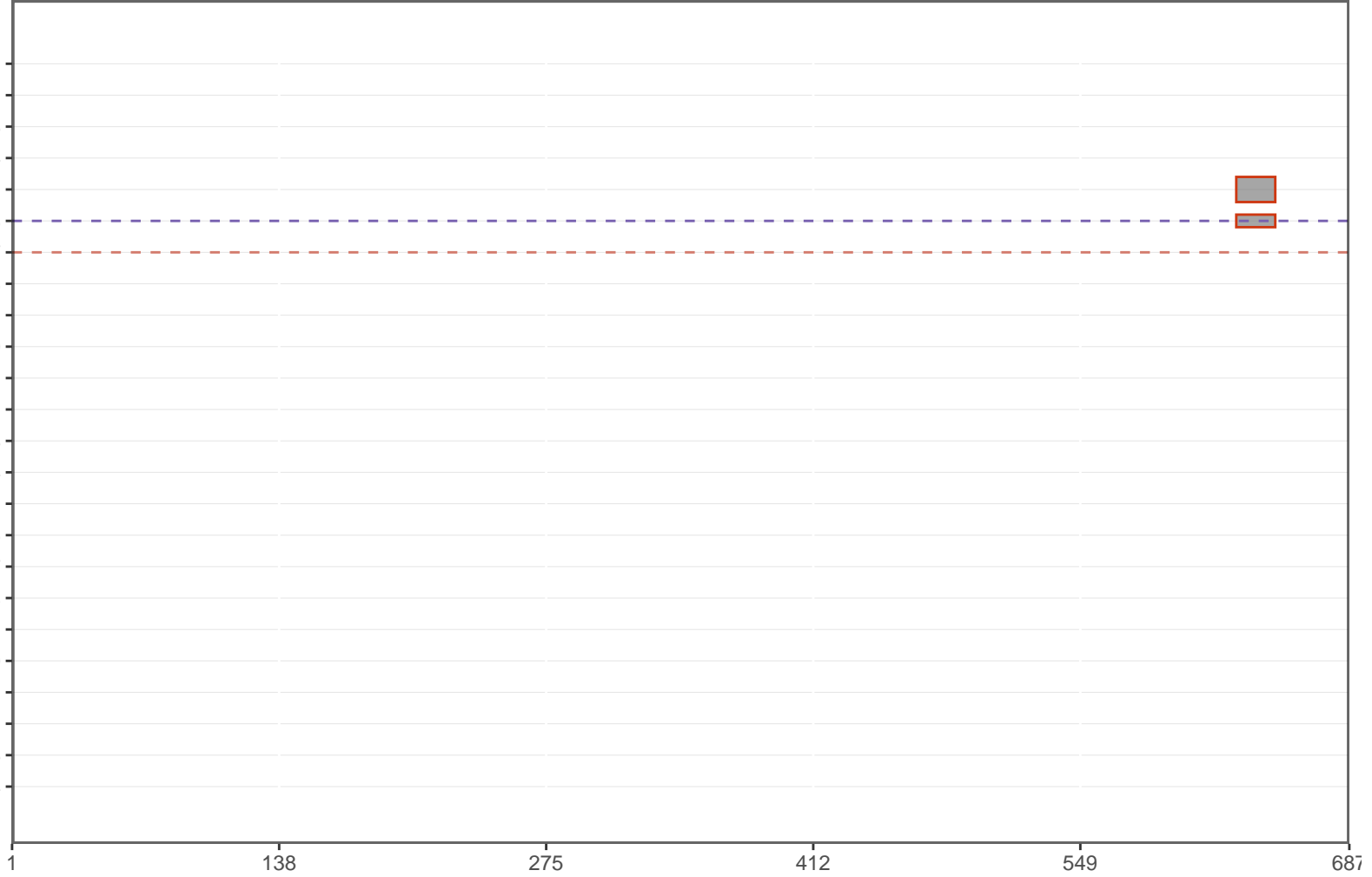
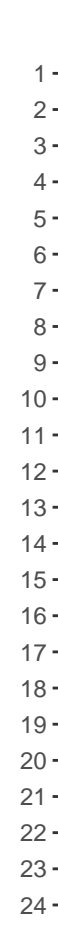
MW indication



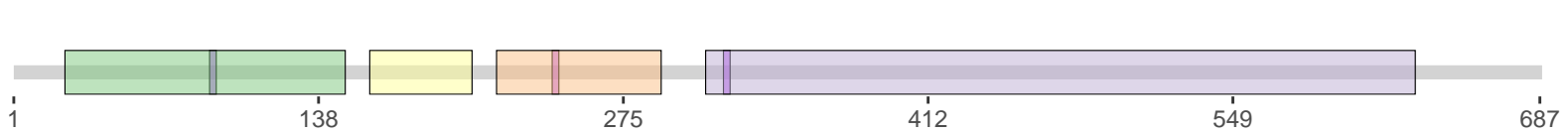
Molecular weight



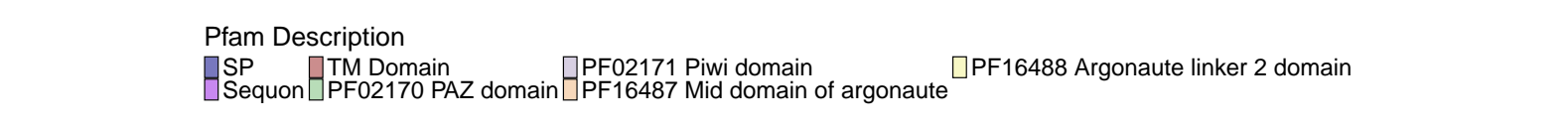
Gel Slice



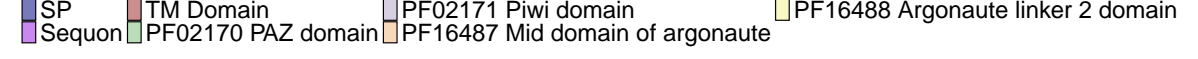
Protein length



Pfam domains



Pfam Description



Protein sequence:

IRICETELGVVSOCELTKHVFVKMSKGYLANWALKNKVYGRNLTVLVDASRRIPLVSDRPTIFGADVTHFHPGDESDSPBAVAVAGDQWPEIKYAGLVSAQAHKQELIGDLYTTRQDPVKGTVVDSKMKDLISFRFRATGKPKPQRIHFYRDGVSEGGFYQVLLFELDKARKACASLEPNYQPPVTFVAVVQKRIHITRLFANNHRDRNAVDRSGNIPGTVVDSKMKCHPTEFDVFLGSHAGIGGTSRPAHYHVLVDENKFTADALQGLTNLGYTVARCTRGSVYPPAYAHLAAFI

NbL03g15240.1 glutamate_decarboxylase-like [MW = 58.69 kDa]

No. of times detected



log(intensity)



Values from

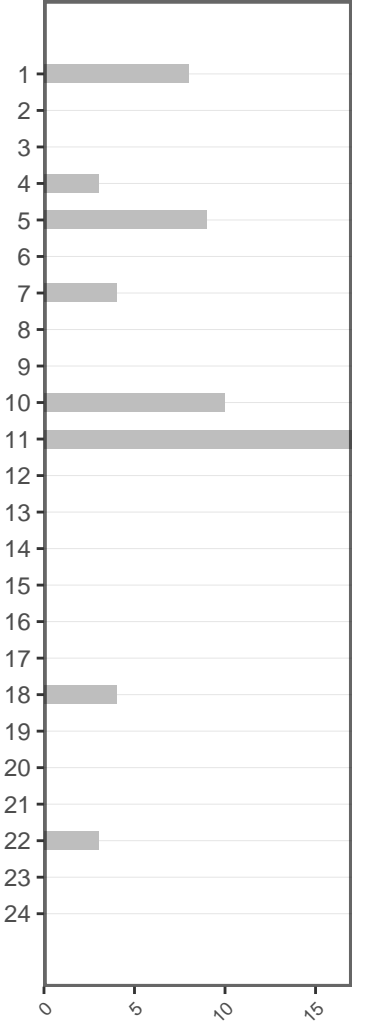
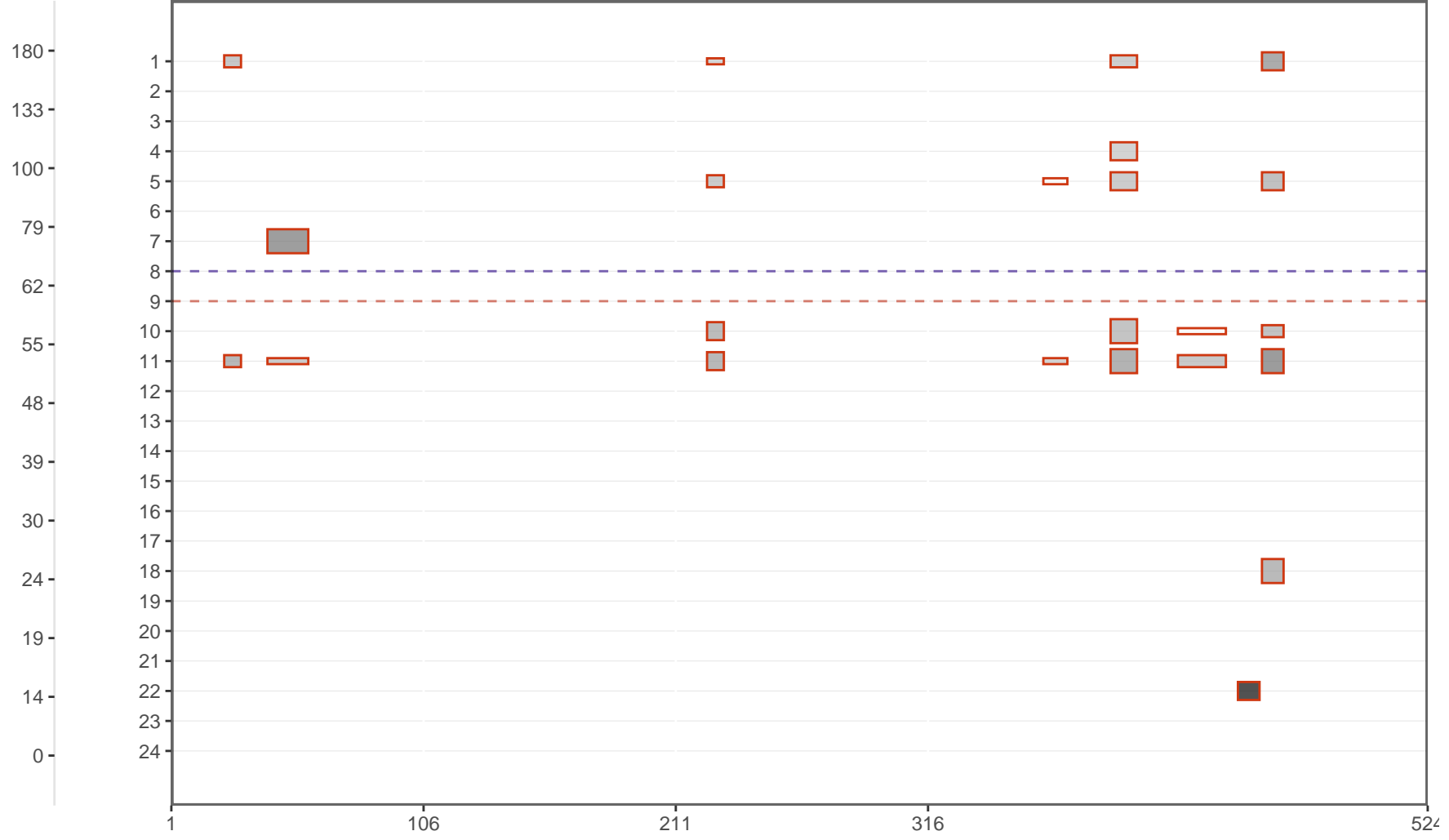


MW indication



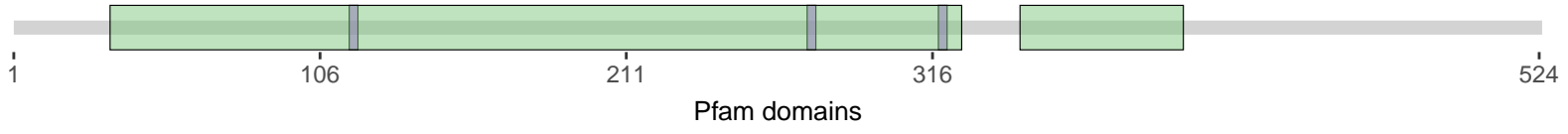
Molecular weight

Gel Slice

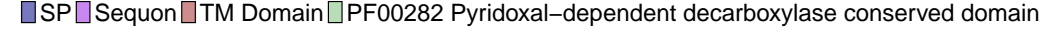


Protein length

Peptide counts over 4 repeats



Pfam Description



Protein sequence:

SGGFIAFLVLPDLEWDFRLPAKSNVSGHKYGLVYGVGWLWRKSKEDLPDELVFHINYLGSDDPTFTLNFSGKGSAAAMSGVRVYKAGAGSIRBYGIAQYVQLRFGFGYKSIEMENCMANAAVLTAGTMMGRFDVSKDKVGVVAFBLRDSKSKYTFEVSFLRRFGVWVWVATMPPDAEHWVLRVVIREDFSHLSAERLVSDEIENVLKELDTHPPRLPTKAARVTAEEVHNDKGDGLHDFHTDVFETQDKLKHWRKIAGKKTSGVCI

NbL03g15140.1 uncharacterized_LOC109207500 [MW = 41.82 kDa]

No. of times detected



log(intensity)



Values from



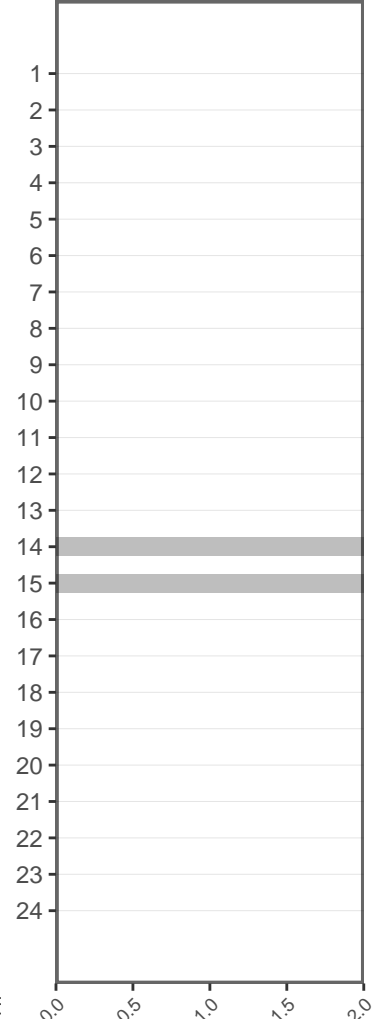
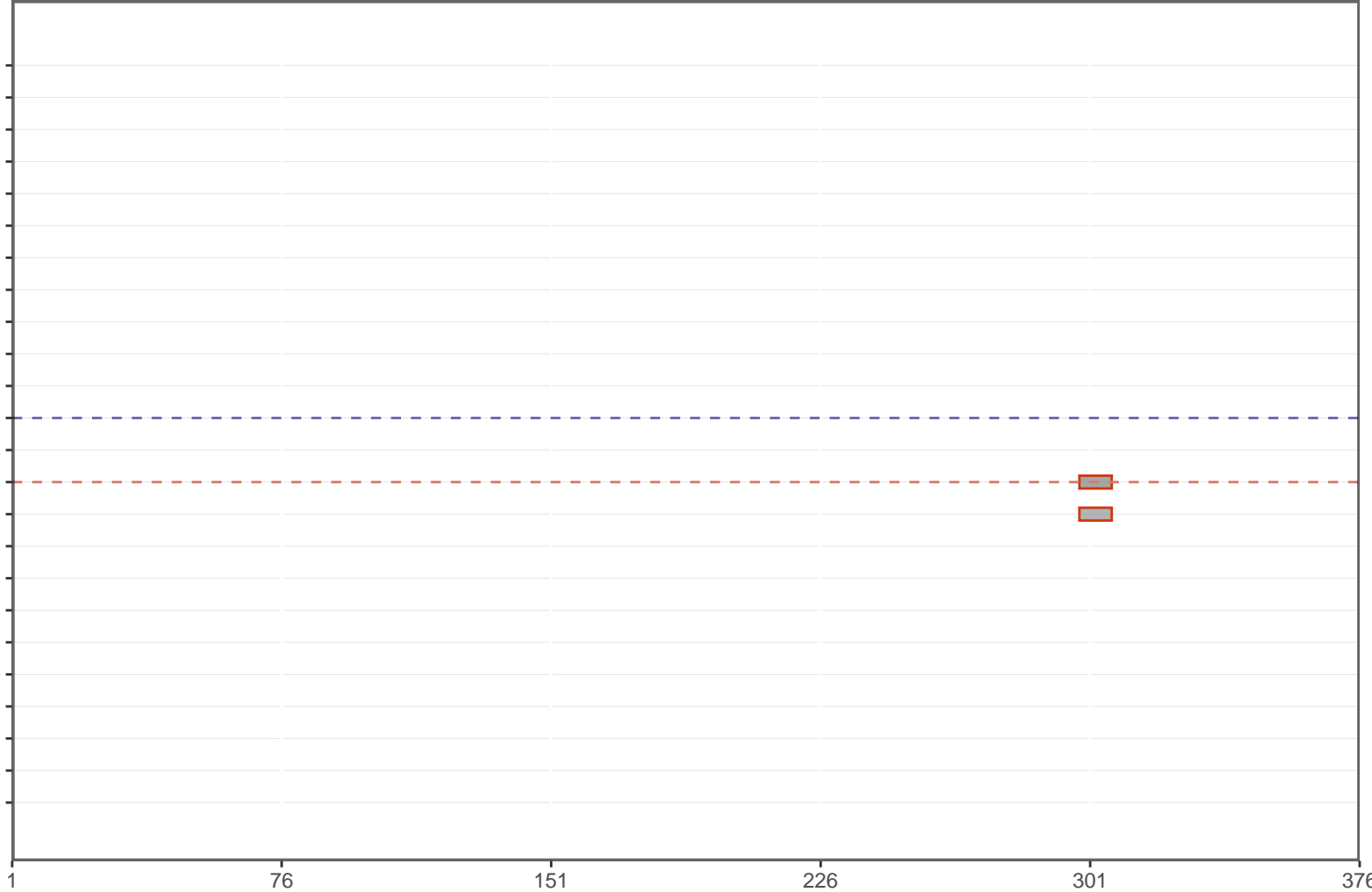
MW indication



Molecular weight



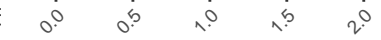
Gel Slice



Protein length



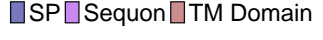
Peptide counts over 4 repeats



Pfam domains



Pfam Description



Protein sequence:

IDNNRAADVDALQIGEFDRVRRRFEYEDRDLRWRWKLPSKAFSGLDCCNIEYDINLPGLFQGLLALDLKSLIEGGKLSLGHKGRIDEVLEKSFELGAGTFCGGLAVNADLSLSLSELGNQLAARSRNKKFRGIVAVVYKYPELENDQMLKVLRLRIGDDEDTTSIGQAFGGGHRNASSFMLNTEFENWKVK

NbL03g14930.1 dihydropyrimidine_dehydrogenase_(NADP(+))_chloroplastic-like [MW = 47.15 kDa]

No. of times detected



log(intensity)



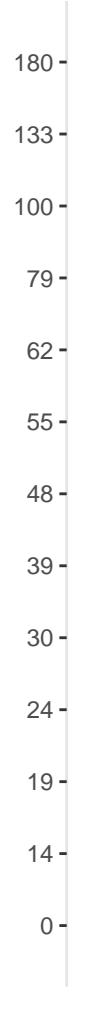
Values from



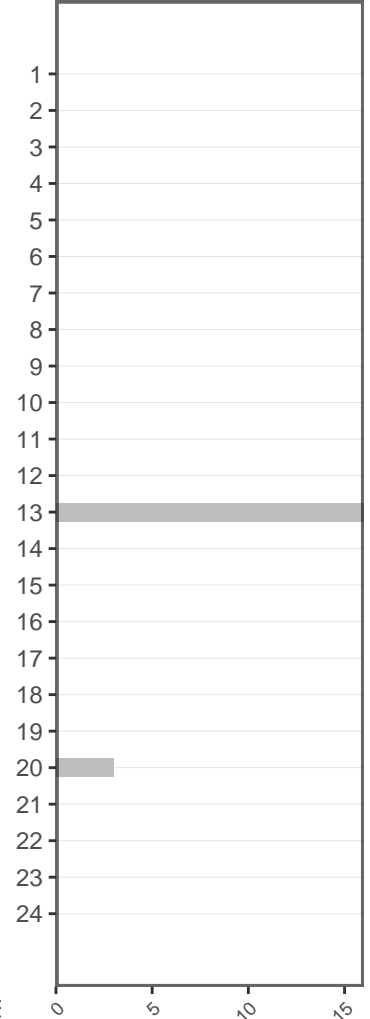
MW indication



Molecular weight

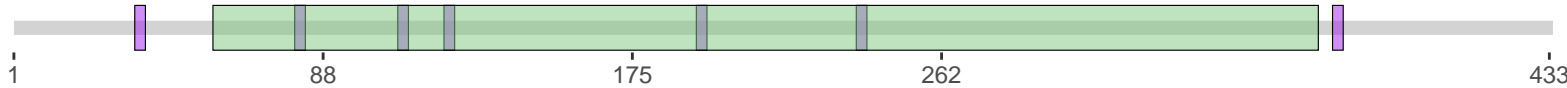


Gel Slice



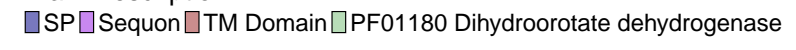
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MGAALVGGDCCLLEEVGGWNAWVFWVWAKMTPNITDTPKRVSLNNGGEGVSAINTMVMGINLFLRPEPCVEGYSTPGYSKAVHPALAKVIAKMMKSEFGDKDYSLSAIGGVETGGDAEAFILLGANTVGVCTGVMMHGYGLVKTLSSELKDFMRKHFSSIEDFRGASLEYFTTHTDLVLRGQEAIRGRKAIAKGLGSDKDWTDGDFVQETESMVEN

NbL03g14920.1 40S_ribosomal_protein_S3a-like [MW = 29.7 kDa]

No. of times detected



log(intensity)



Values from



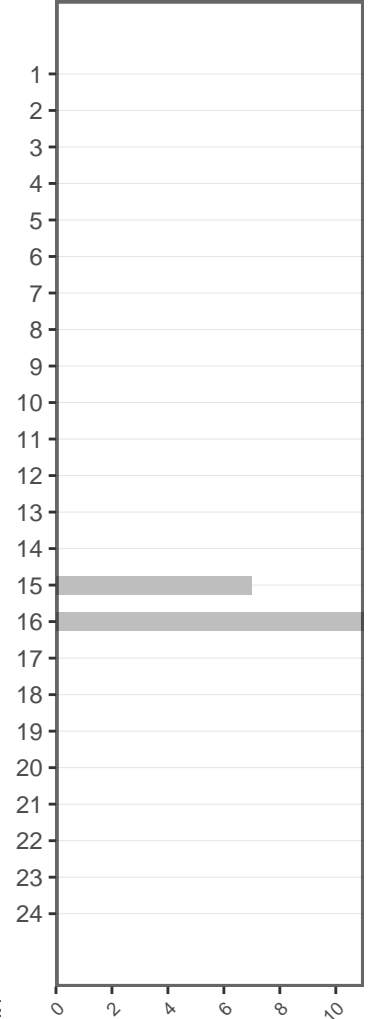
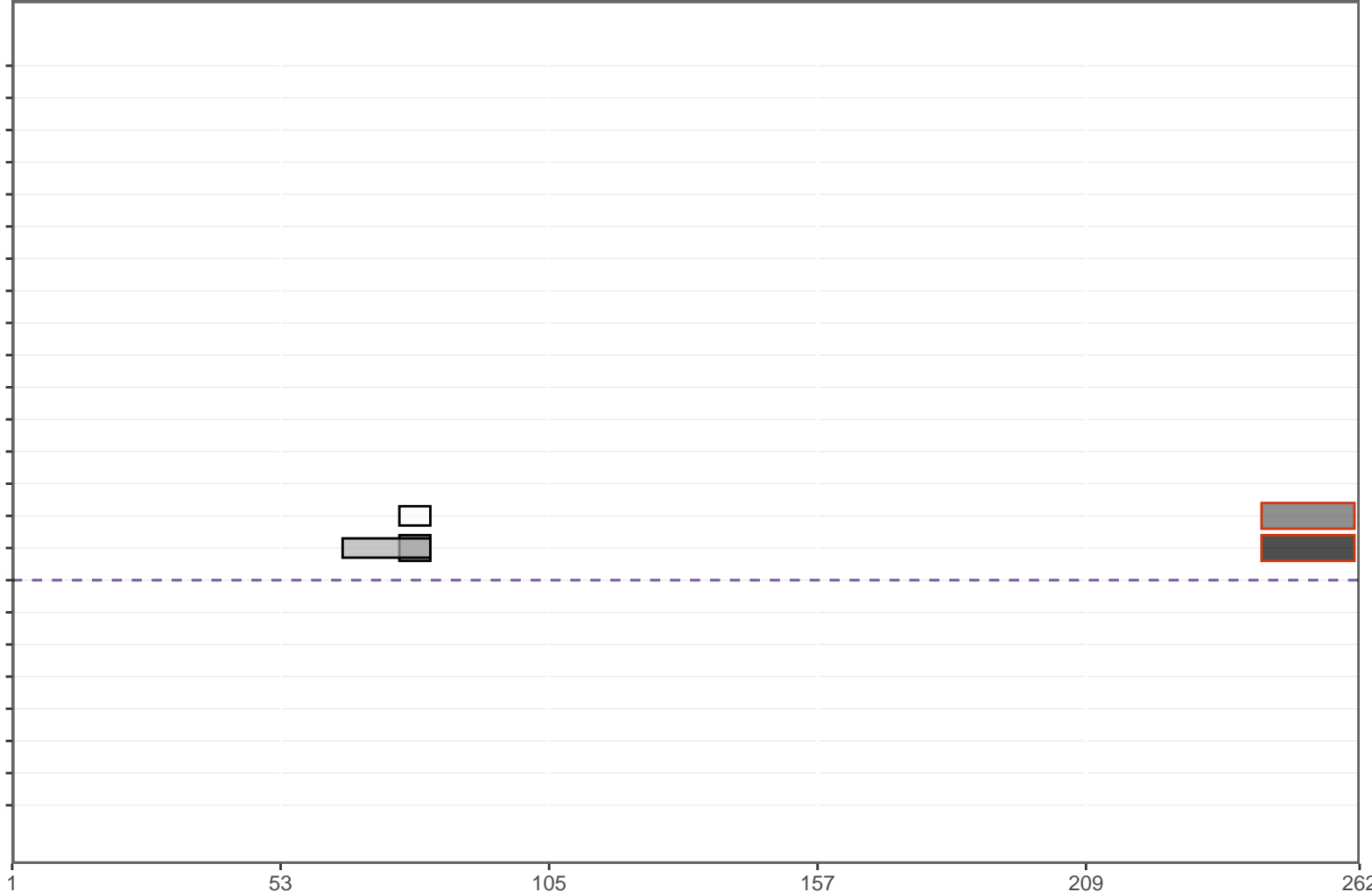
MW indication



Molecular weight



Gel Slice

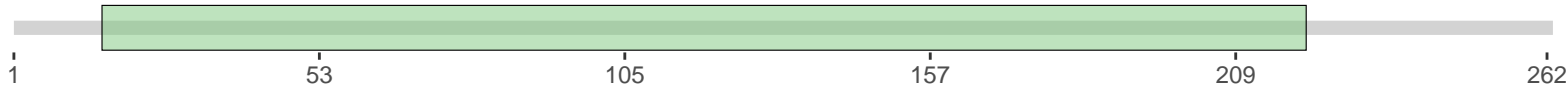


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

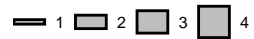


Protein sequence:

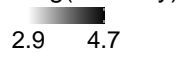
WQTLIEAHVDYKTFDEYTLRMFGAFTKRRPNQGRKRTGYAGSSGIRGIRRMVEMIRNNGASSCDLKELVKFFPEISGREIEKATSSIFPLQNVYIRKWKILKAPKFDGKLMVEVHGDQSEEDVGVKLRPQDETAEEAEPEVPGA

NbL03g14870.1 V-type_proton_ATPase_subunit_C-like [MW = 42.92 kDa]

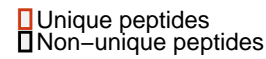
No. of times detected



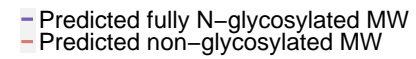
log(intensity)



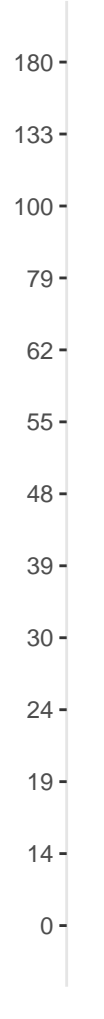
Values from



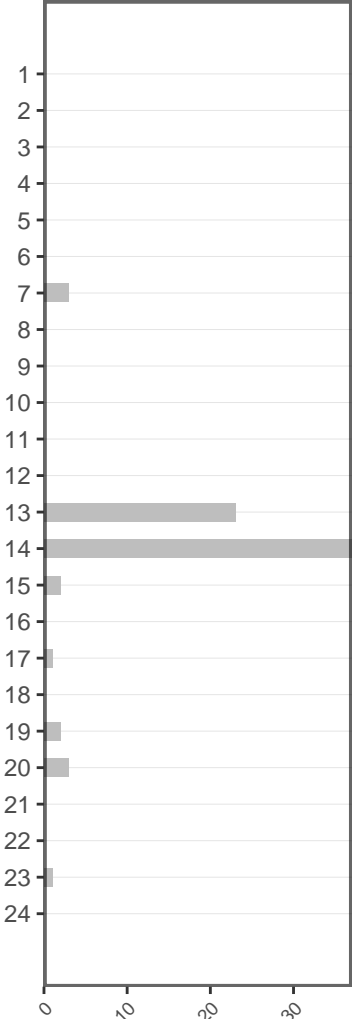
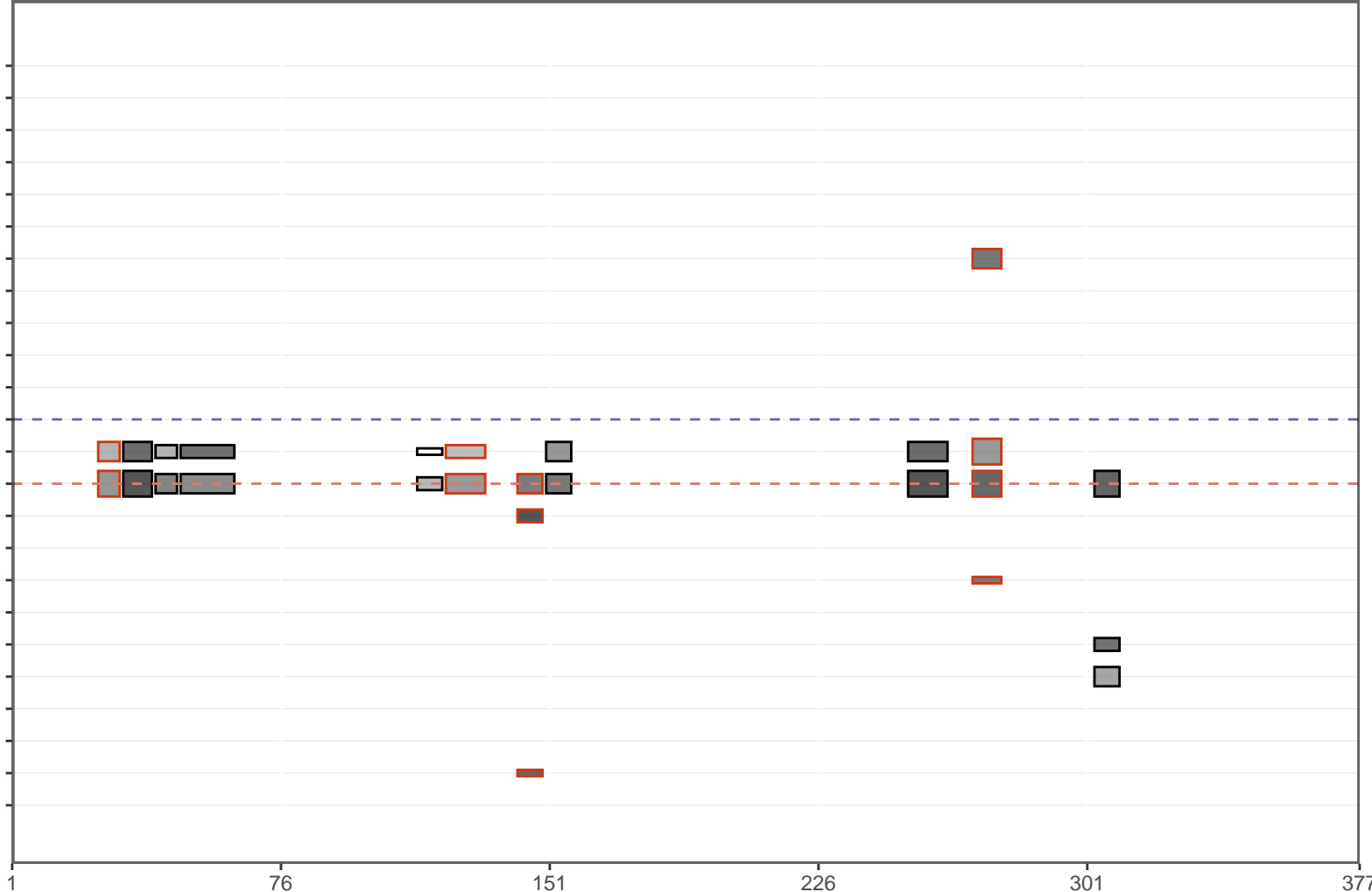
MW indication



Molecular weight

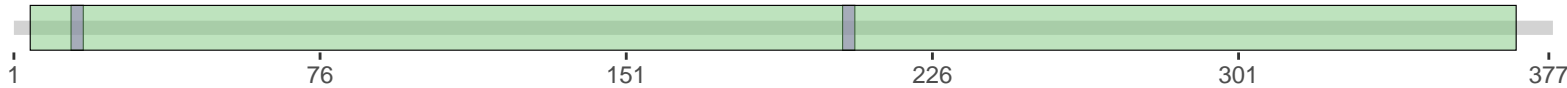


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YVTSSEHLTLAVVSKYSGKDWLSSVENLTYVYVPRSSKMLYEDNEVALYTVLFRNRDADNFKIKARERGFQIRDFEHNPEQESGRKQELKMDQDQETFRSGLLQWCYTSYGEVFSQWMLFCQAVRIFAESLRYGLPPSFLVVLAPSTKSEKIVRSILELGDSSNSNFWKSEDEGGMGFGDGTAAHPYVVFNTNLV

NbL03g14600.1 3-oxoacyl-[acyl-carrier-protein]_synthase_3_A_chloroplastic-like [MW = 46.66 kDa]

No. of times detected



log(intensity)



Values from

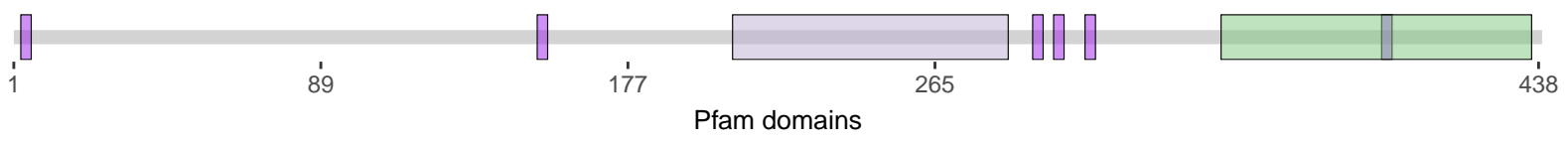
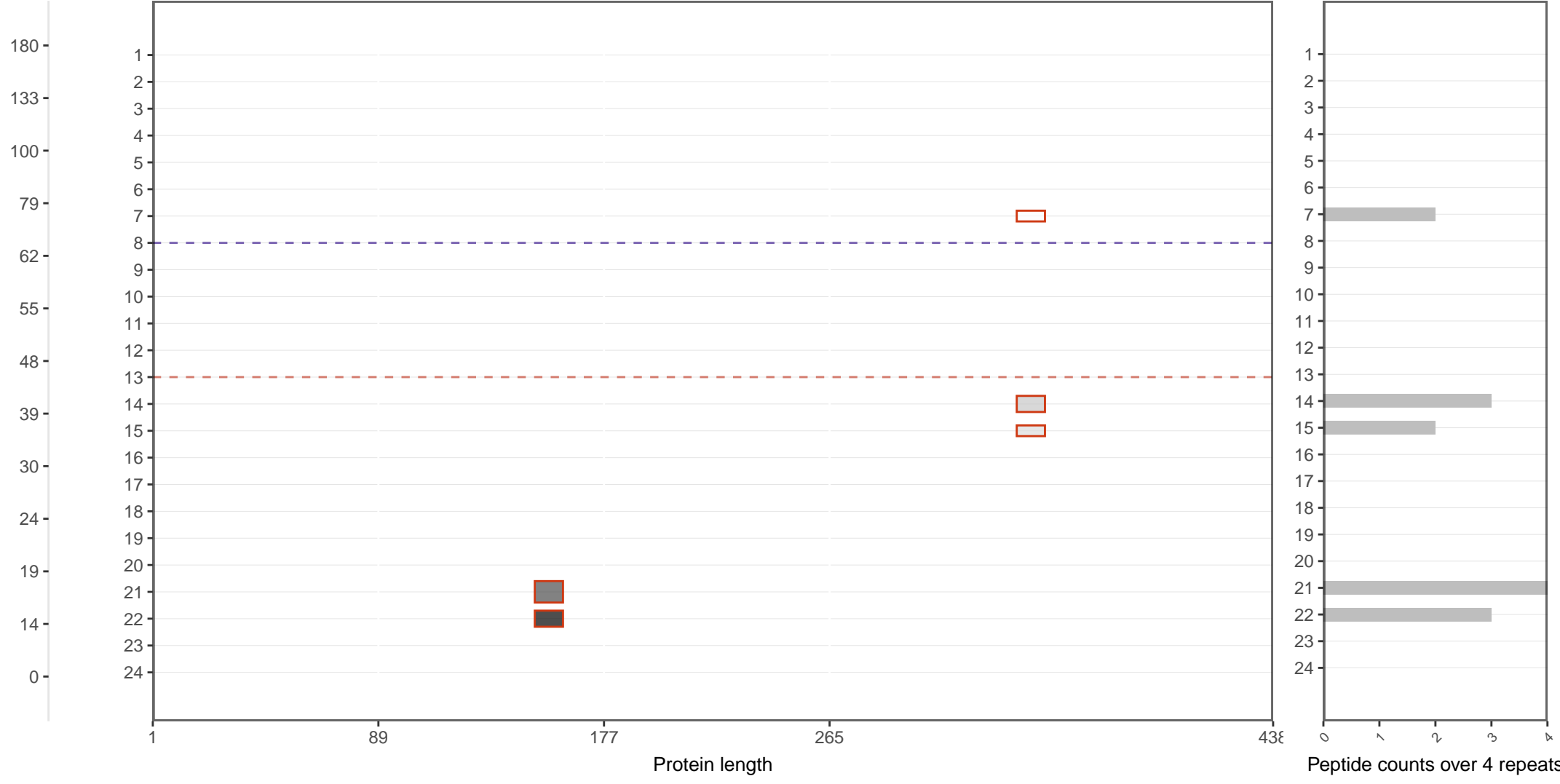


MW indication



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF08541 3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III C terminal
- PF08545 3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III

Protein sequence:

FDITACSGFMLGLVSAADYHRGGVFNKLVIGADALSRVVDWSDRGTOLFGDAAGAVVMDACDDEGDLFGDLHSDGEGORHLNASKENETDHFAGTNGSVGFGAPKGGSSYGIMNGKVFRRFAVRVPLSEIAALEKAGLPGSKIDWLLHQAQNRIDGWATRLVPSERVISRLNLYNGTSSAASIPALDEAVRSGKVGAGHVAAGFGAGLTWGSAILRWG

NbL03g14500.1 DNA-binding_protein_SMUBP-2 [MW = 108.1 kDa]

No. of times detected



log(intensity)



Values from



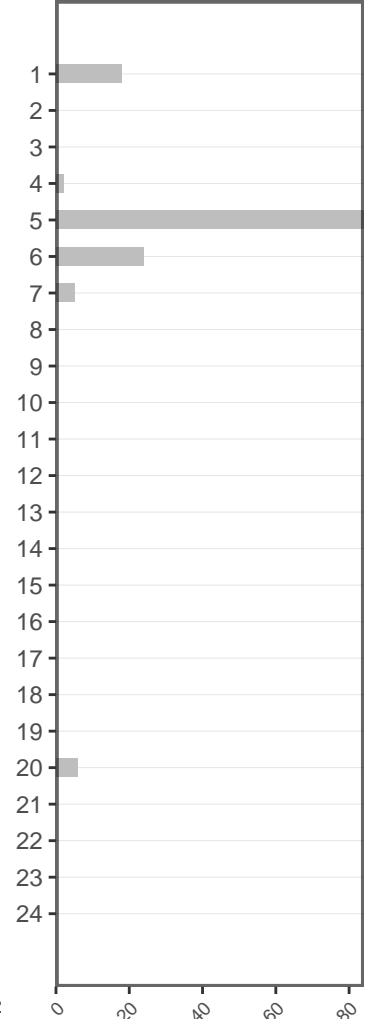
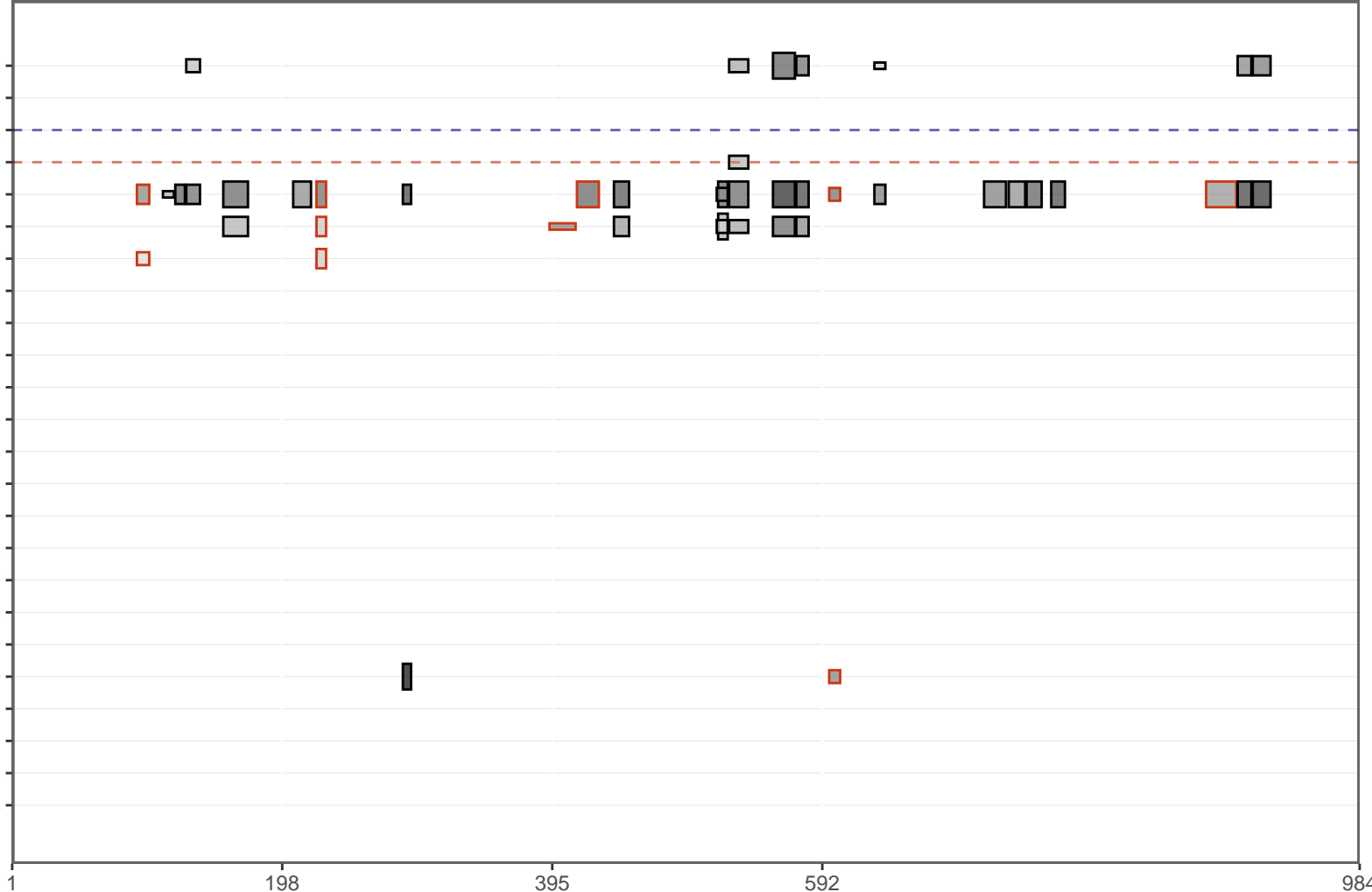
MW indication



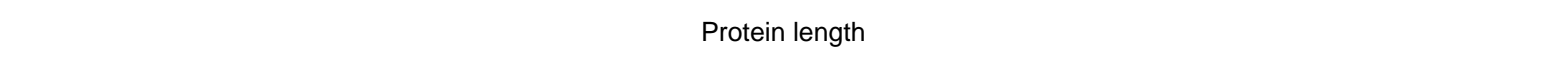
Molecular weight



Gel Slice

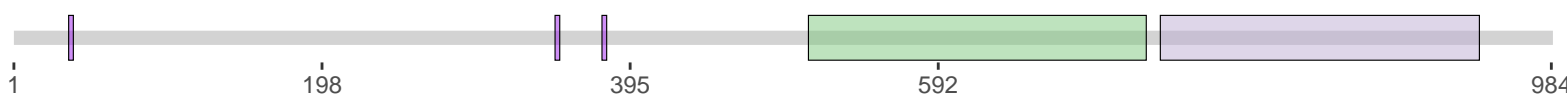


Protein length

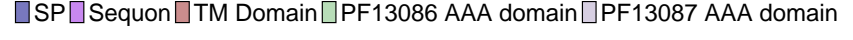


Peptide counts over 4 repeats

Pfam domains



Pfam Description

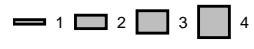


Protein sequence:

/VATLFGDKEDLVVALEENGMAADVSEVELPDGSTRDRKSFDFTSQRKAALGLNLRNRPIMGPPGTGKTGMKELISLAWKQGERVIVTAPTNAAVDNMEKLSIDGLNVRVGNPARIQSPWASKSLTEVNTKLAADFRAEIERKKKGLRDLRYLGLKDDSLAAGIRQLLKLGLKSKREEKETVELSSAGVVLATNNGAADPURLDITFDLVIDEAGGAIEPSCWIPILLAKRGLAGDQFQLAPVILSRKALEGGGLVSLLEERAASLHDGMLSTKLTQYRMNNAUASVWASKEMYC

NbL03g14490.1 protein_BOLA4_chloroplastic/mitochondrial [MW = 17.23 kDa]

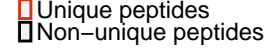
No. of times detected



log(intensity)



Values from



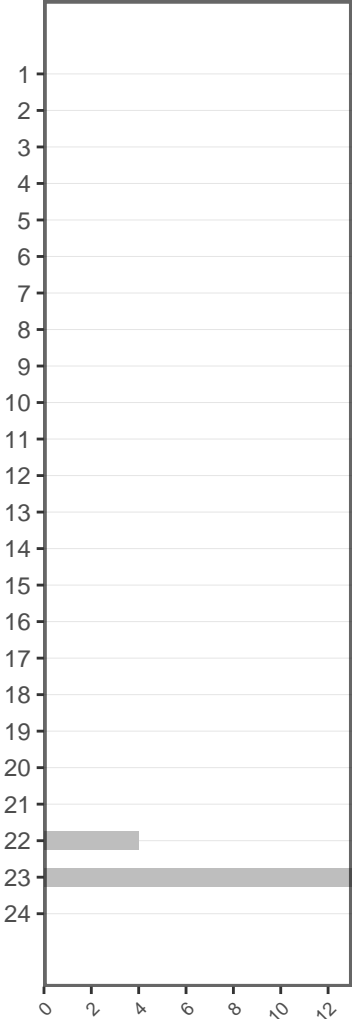
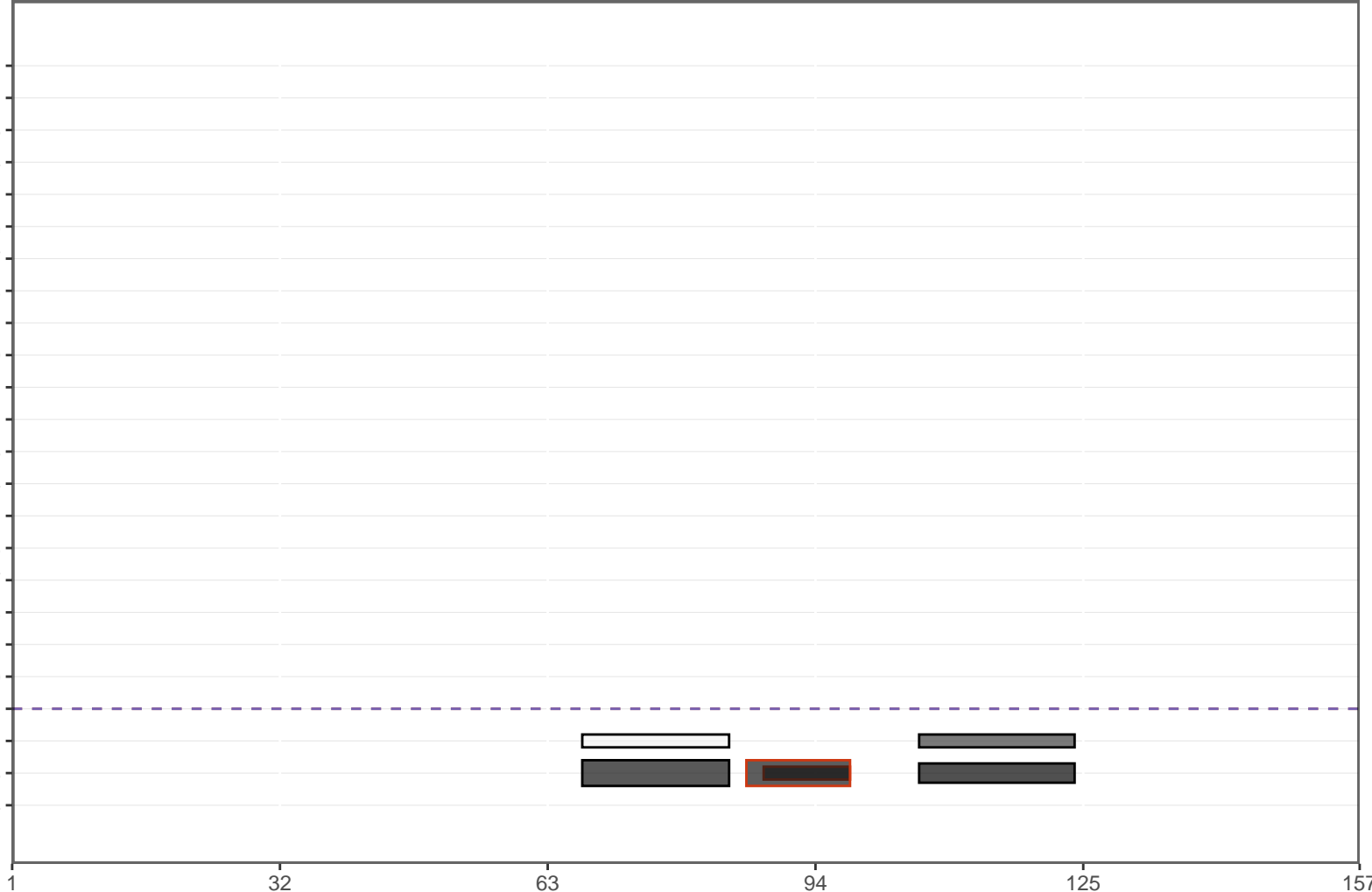
MW indication



Molecular weight



Gel Slice



Protein length

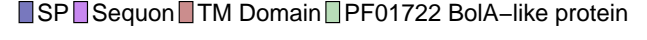


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VTSDTGSIDSLMEEMQKKEQLNADSVVVKDAVGDGRHVSDVVSFAFEGGSANRGRMVKKAIWEELGNTVHVDQMTTRTRAEAGK

NbL03g14430.1 cysteine_proteinase_inhibitor_6 [MW – SP = 29.48 kDa]

No. of times detected



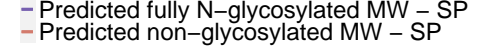
log(intensity)



Values from



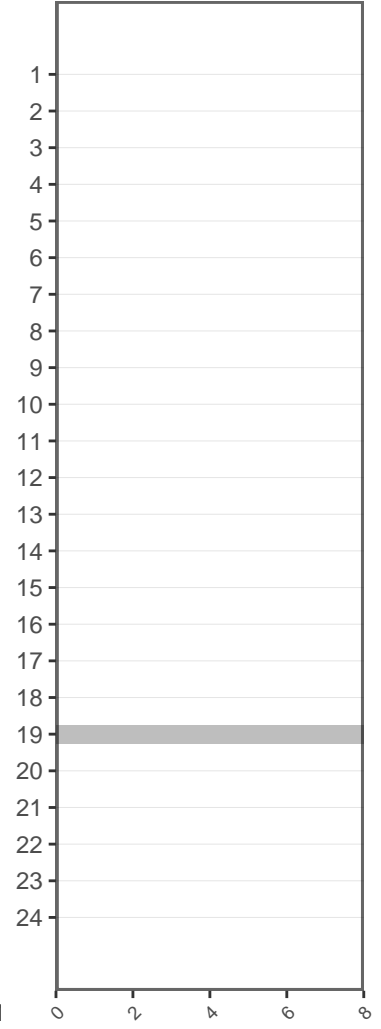
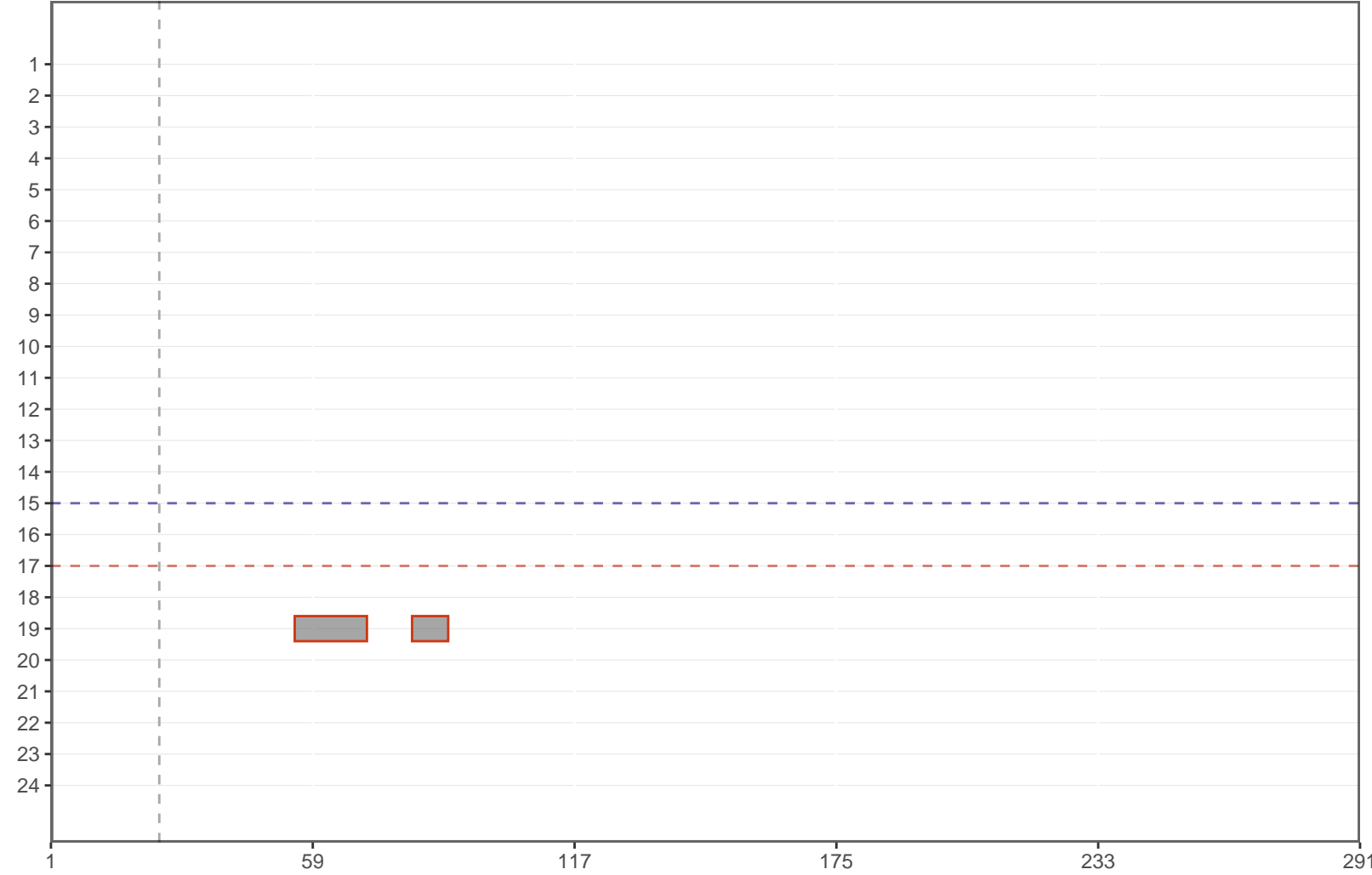
MW indication



Molecular weight



Gel Slice



Protein length

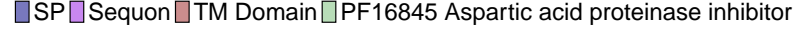


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

QDEFTYIVEDVPTLTSSDLGKGGDMSLGGVGVYQKILDSISGVNRKKGSSVLIQHSARFYEEEGSGLKGVVPHDPIVQEAADHAIKTKGQRSNLSLPIYELGEVHANAEEVIGEDNMLKLMILKTSRGGKQKFKVQVHHNNEGAFQLNHMERDHS

NbL03g14420.1 alanine--tRNA_ligase-like [MW = 112.75 kDa]

No. of times detected



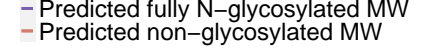
log(intensity)



Values from



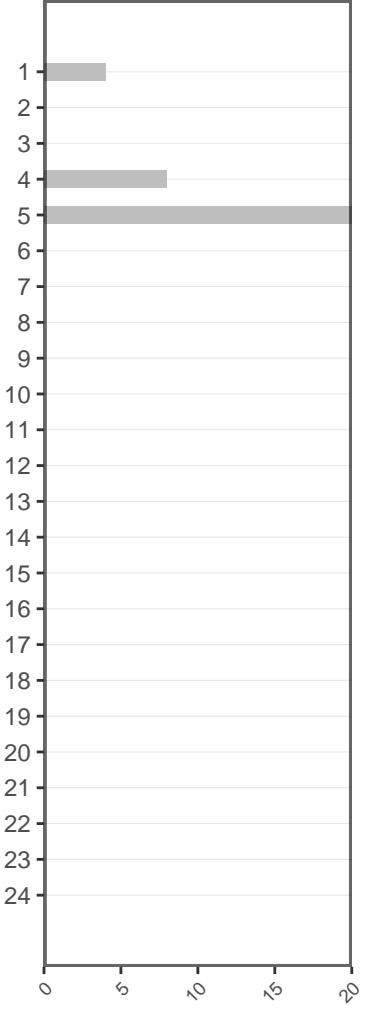
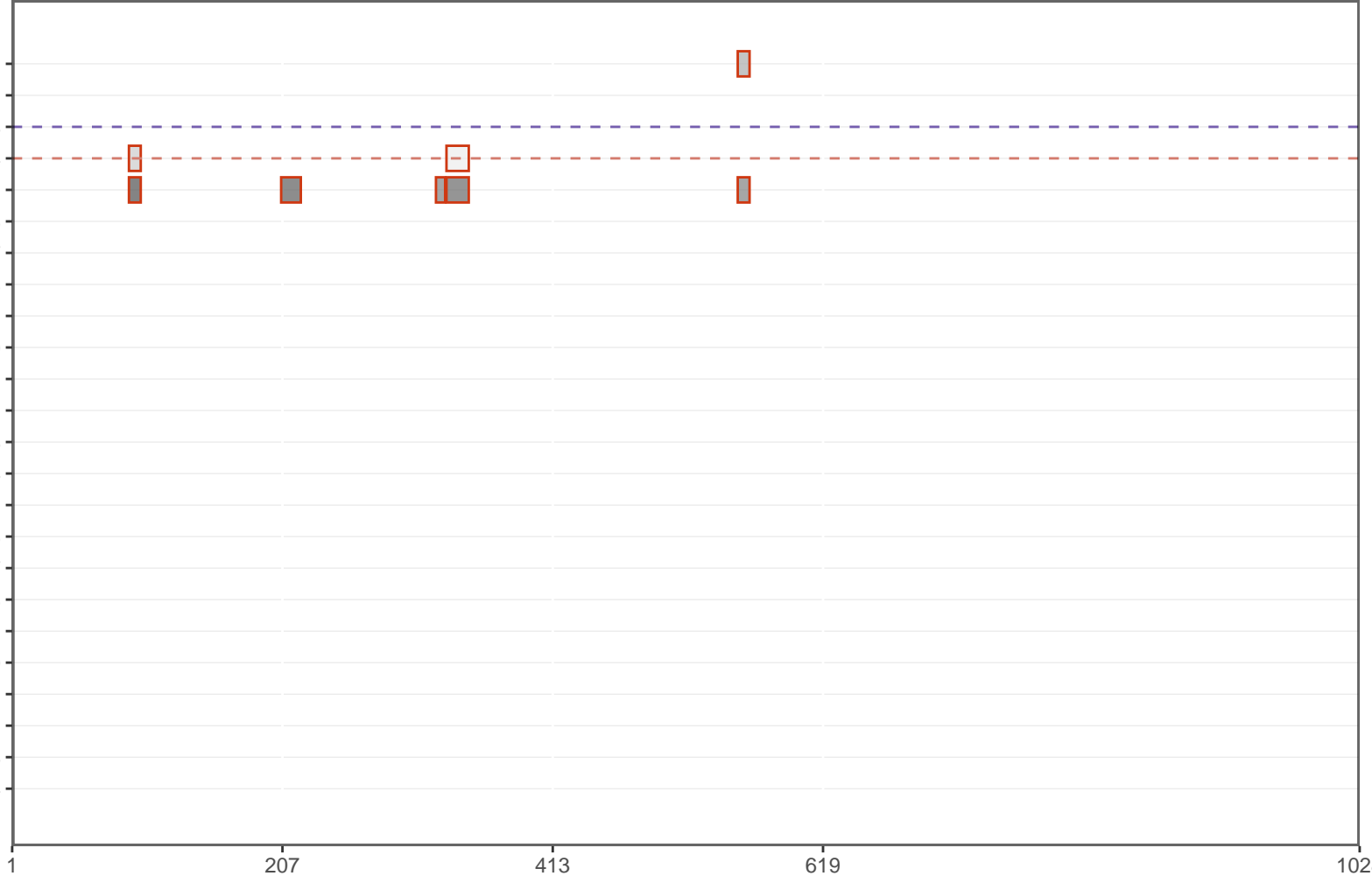
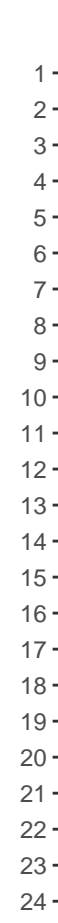
MW indication



Molecular weight



Gel Slice



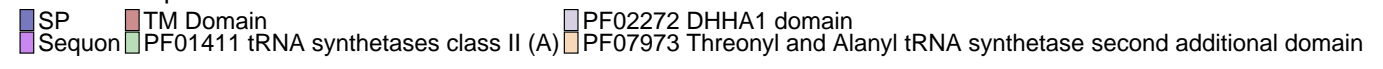
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

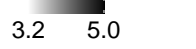
TQLMAEERGLVVDVDFGNVAMDARERSRNAGSKNAGGAAMDATLAKKGVATNDSEKFTWFDHSESEKAYHGNFLESAAAGDEVGHELESTFVWEGGGGQVDTGSELESSESGFQVGNVQVYGGFVLIHGSFSGDAHKFSVGVKGVCKVQVYNNRRTLVAPNHTGTHMLNFKLKEVLDGHDVDDKGSVLPKELRFDPSHGKPKVPEELRKESVNEQKSELDVFSKEALSDAKSKGLRAVFGVEVYDPVRIIVSVGRKVEDLLANPENEEVLSYSALCGQTHI

NbL03g14350.1 WEB_family_protein_At3g02930_chloroplastic-like [MW = 109.69 kDa]

No. of times detected



log(intensity)



Values from



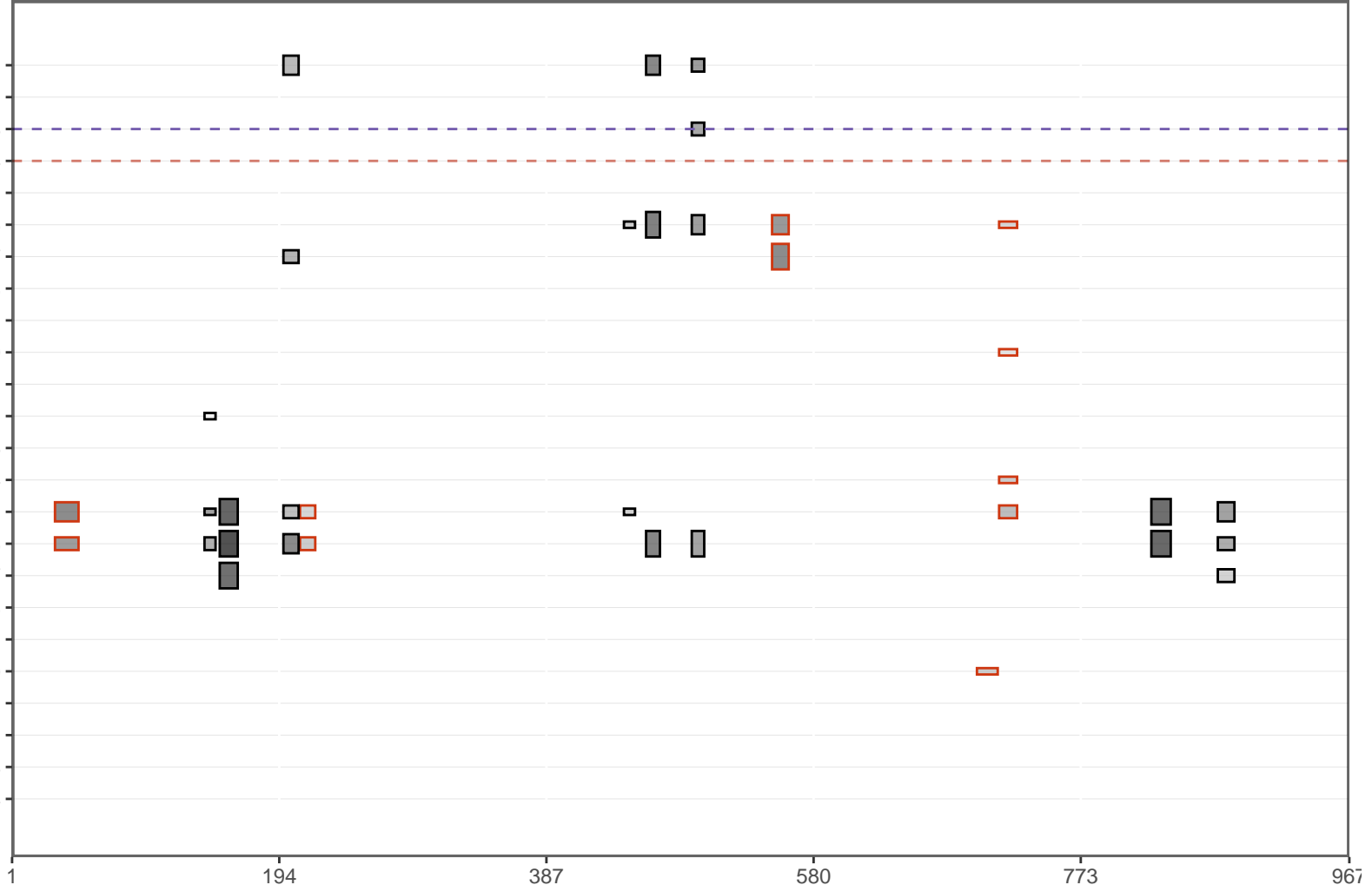
MW indication



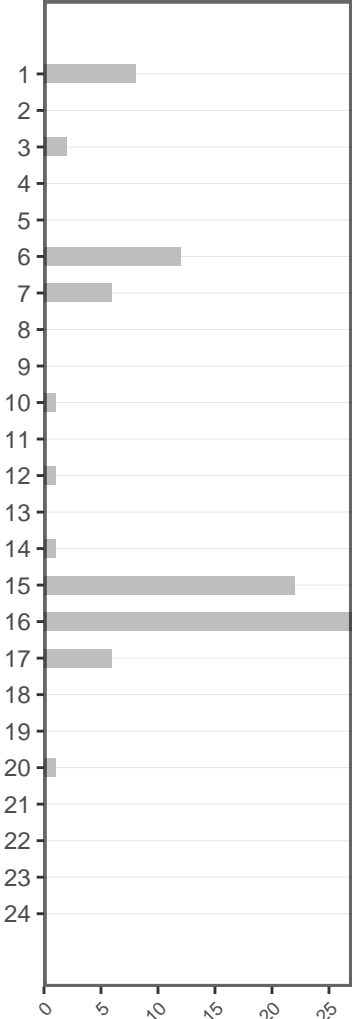
Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

GSNDLLHDAESEIARLKEKVGLEEMSTTRQKGDLEESERRAGIAKKEEASAMKAVESLAELETVKKEKTAQAEHEKLAENVQGLLEEKNLINLELNSRREEEEKKPKKAMEGLASALHSEVSEAREAKERWLVSSQAQAEHYETQIEDKLVKATNKAEKVESLLEDAEAKKIDDLTNSVEGSKNEHDSKAEVDEKELVLMNVKTKTEENSSMEKEINRLVLLKKEAQEASDFEEEAIVQLKNSLNEAESEVTVLKEVLGEAKGEGMKLKEGLLDKENEVQNLQENEELRSRA

NbL03g14250.1 binding_partner_of_ACD11_1-like [MW = 29.58 kDa]

No. of times detected



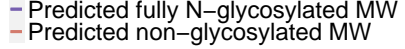
log(intensity)



Values from



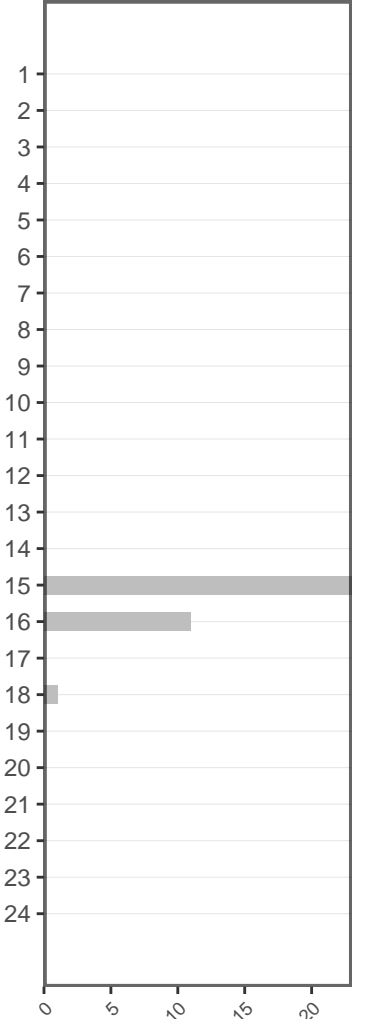
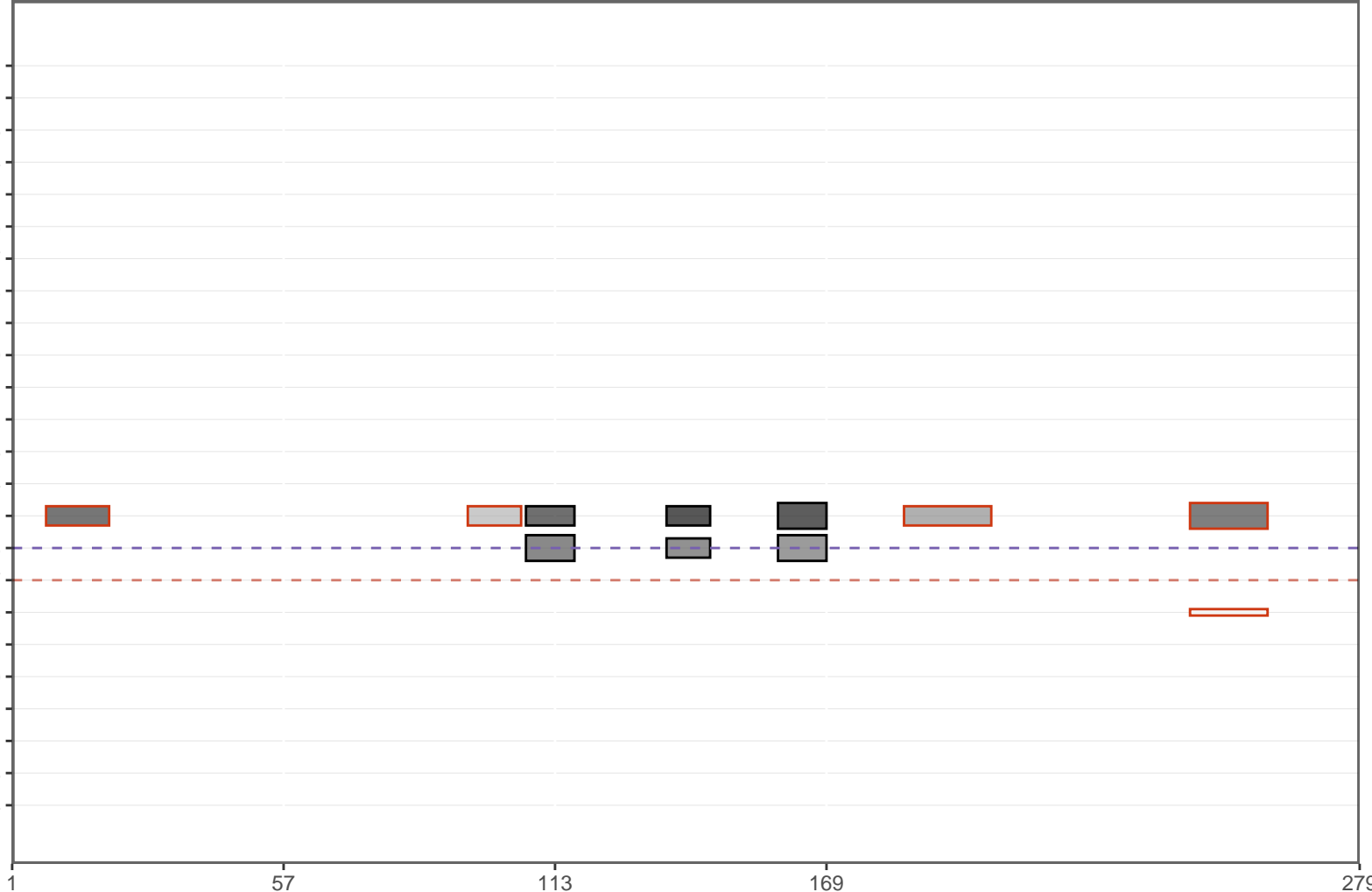
MW indication



Molecular weight



Gel Slice



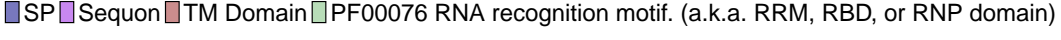
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

KAIKTFDEKHQFISTASAKVAELDQKGLSEKINMGTRIVNDKVKEMDQKQFQVTEKTKALAAAEQTVSTAGSAMKKNRYVLTGASWVTDGAFNKVTKAAGEVGQKTEKMAEEEGGRSATSQVYPIHAFSESPKASKTEEPWPKSPKGLL

NbL03g14230.1 TOM1-like_protein_1 [MW = 43.75 kDa]

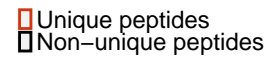
No. of times detected



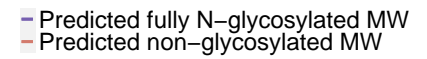
log(intensity)



Values from



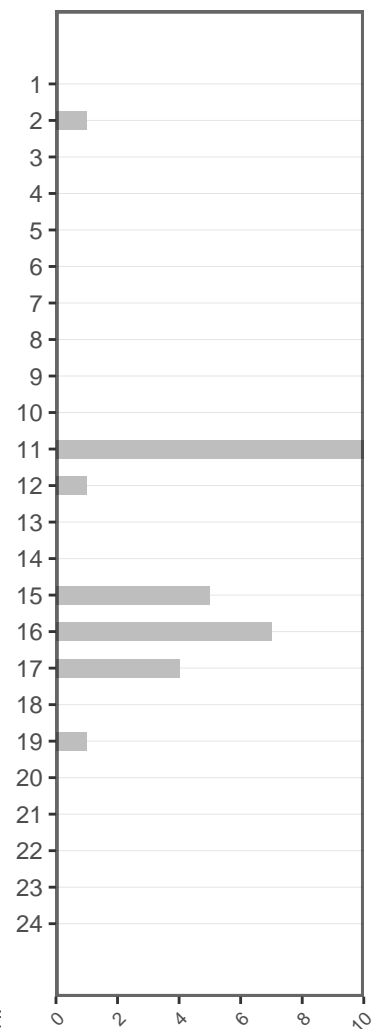
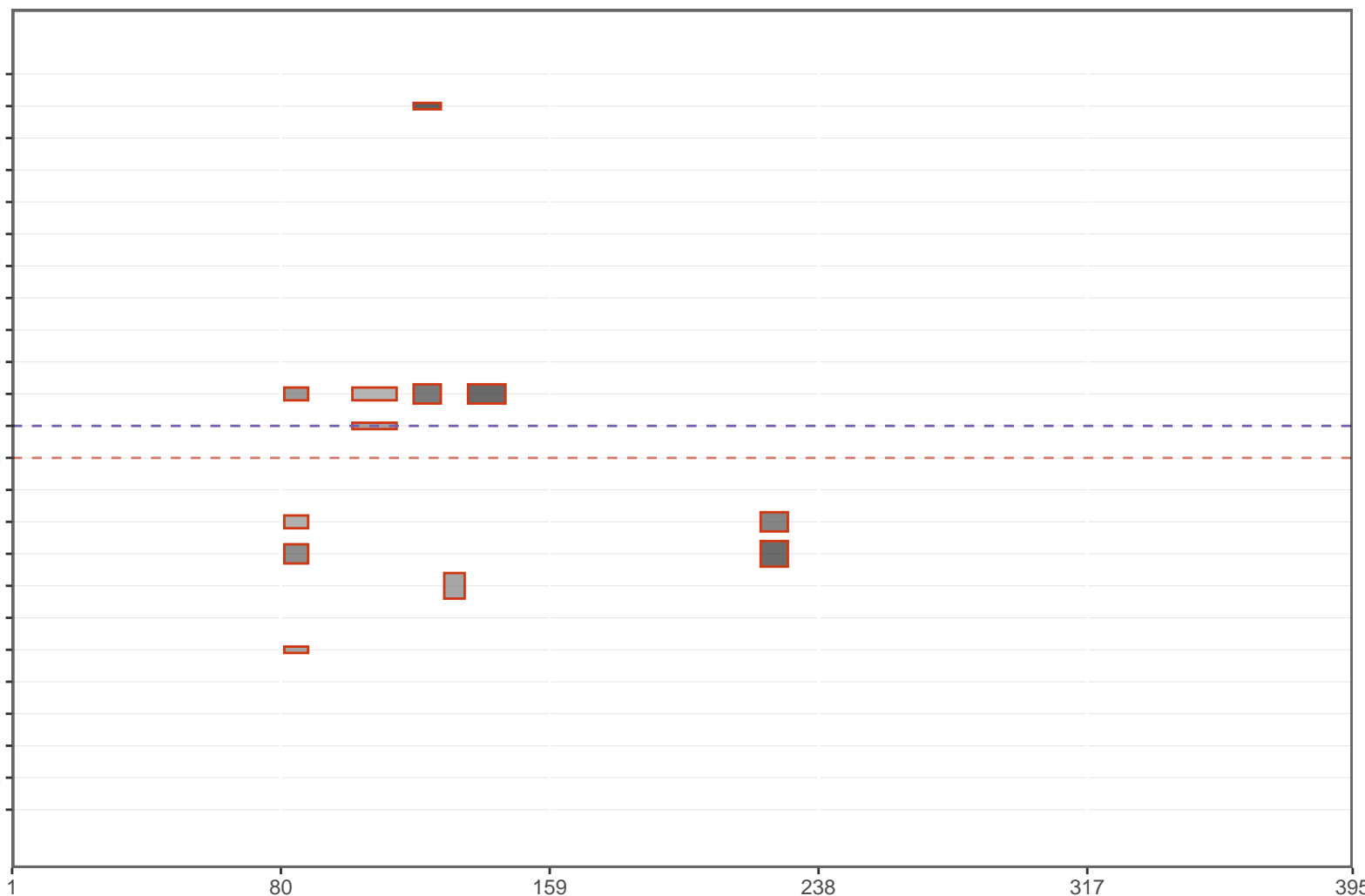
MW indication



Molecular weight



Gel Slice



Protein length

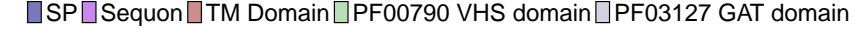


Peptide counts over 4 repeats

Pfam domains



Pfam Description

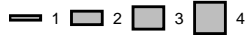


Protein sequence:

GRDHELSLAPITPPRRVTSASEPDTLADQIQGHEIPRENFSAEQTKAEAFDVARNSVELLTVLSSSPQGDALGGDLTTLLVQDQRGSLNIVQRIHETGALLFEALNINDEVGKALKSKYDELKPKPLVVSSEPERMMPVAVEPDESPRAGKEDALIRKPKGGQSAVHGGDDMMDDLDLDEMFGKKAGGTSEAGHDTKKGGSPKDDLSF

NbL03g14200.1 4-coumarate--CoA_ligase_2 [MW = 67.08 kDa]

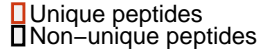
No. of times detected



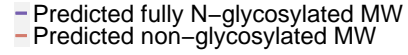
log(intensity)



Values from



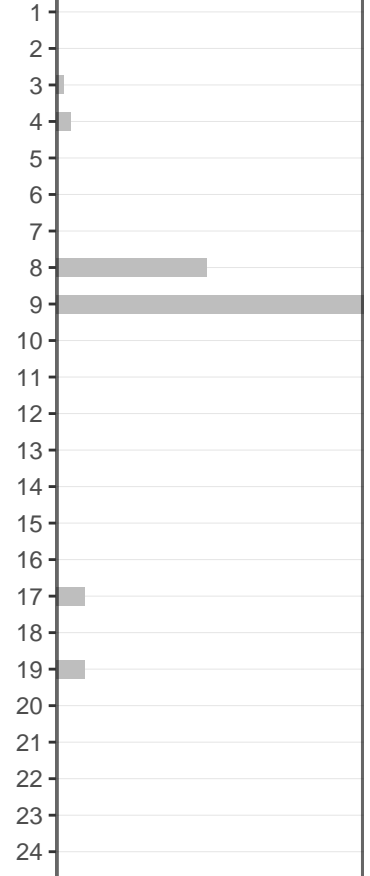
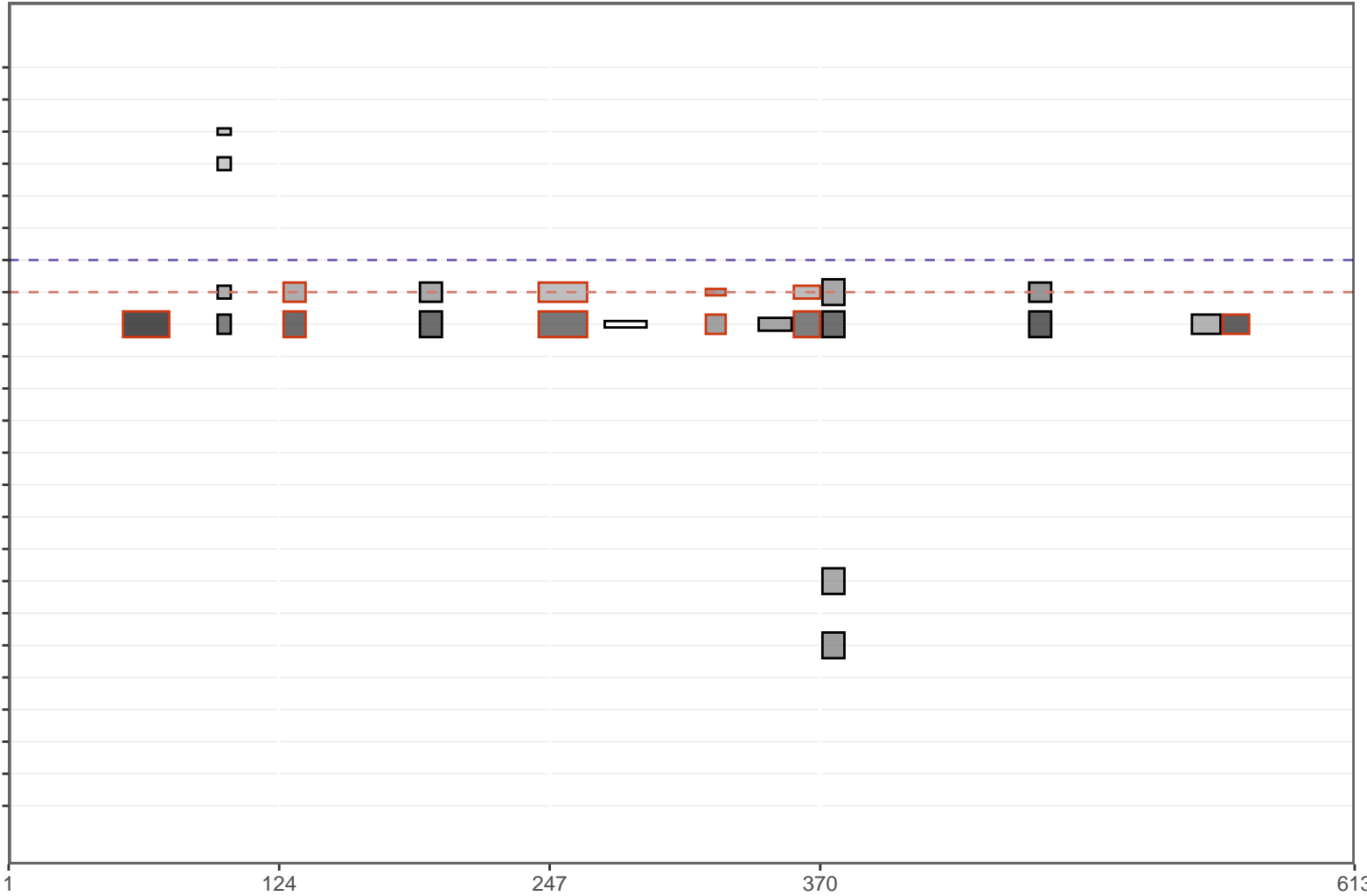
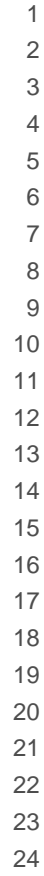
MW indication



Molecular weight

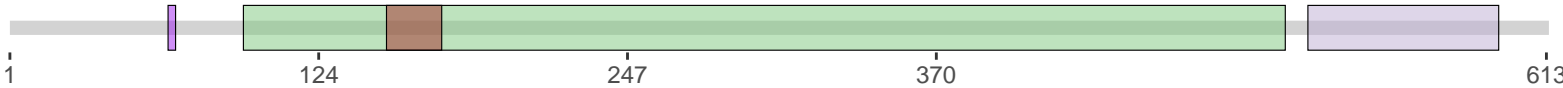


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description
 ■ SP ■ Sequon ■ TM Domain ■ PF00501 AMP-binding enzyme ■ PF13193 AMP-binding enzyme C-terminal domain

Protein sequence:
 *YVLCVLPPIHFDALNBYLIVSLRAGATVLMQKFEIGALLELGHYRVVAVVPLVLAANKPMVDSFDLSSIRLVLSGAAPLQKLEELHRRVQAFVGGYGGYVTEAGPVVTPMCPFAKQPFSTKSGSGGGVVRNADKVVDPETGGSLGRNPGEGIRGSGMKGVLNDDAETARTGVDDGLHTGDIGYVDDDDIYVDRVVKELKFKGQVPPAELEGLVHPDQADAVVPKDDAAAGEVPAFVVRSPDGFETEAEKFEIAKQVIFVKRLKYYFHAIPKSPSC

NbL03g14050.1 oleoyl-acyl_carrier_protein_thioesterase_chloroplastic-like [MW = 41.42 kDa]

No. of times detected



log(intensity)



Values from



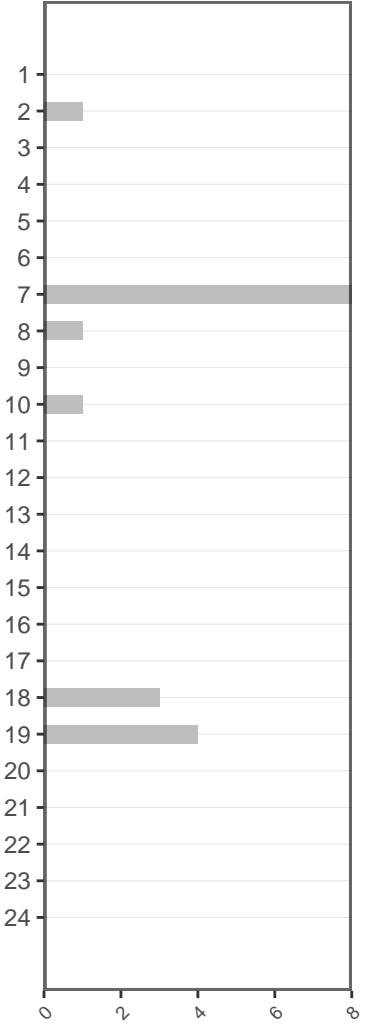
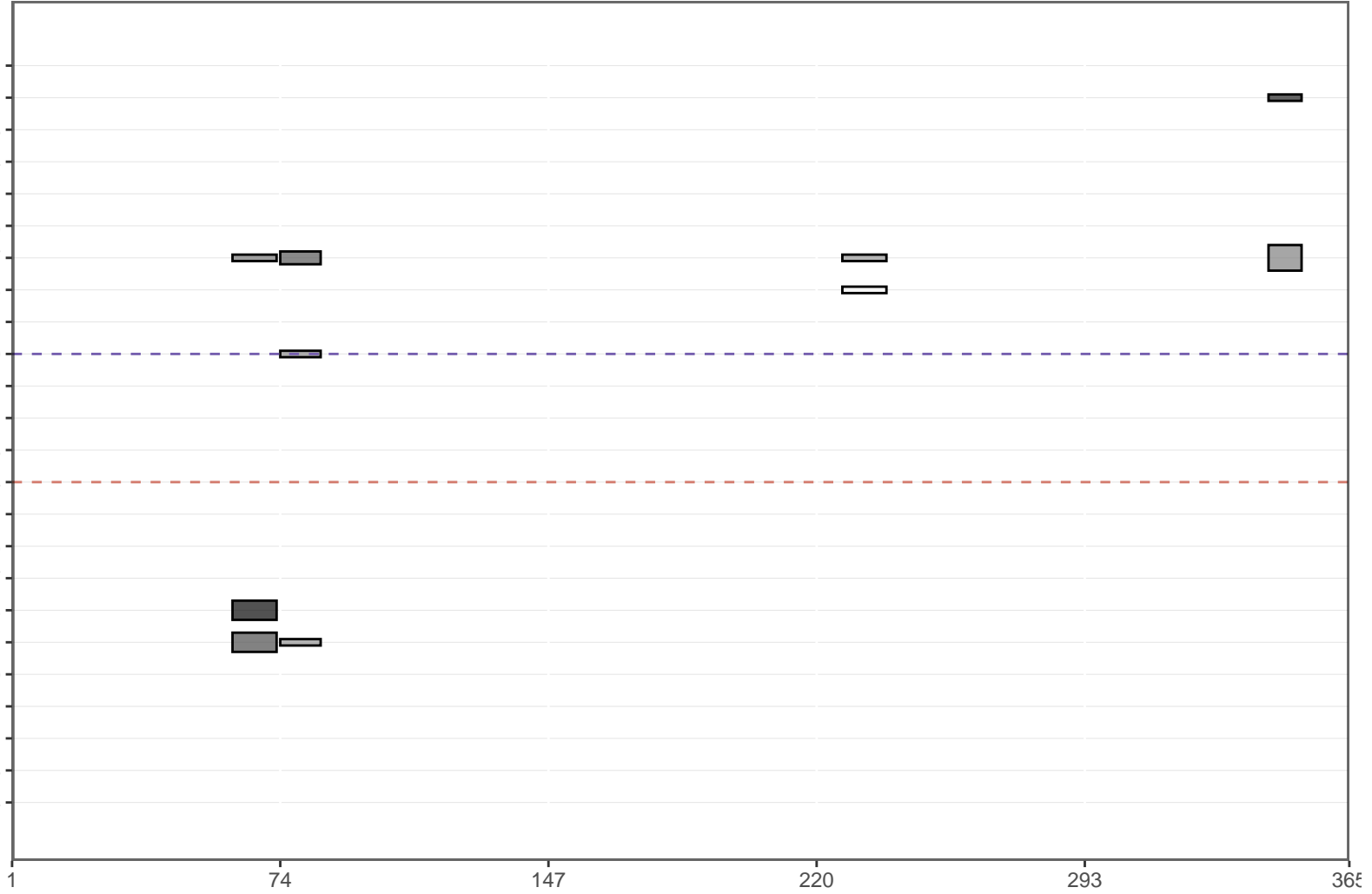
MW indication



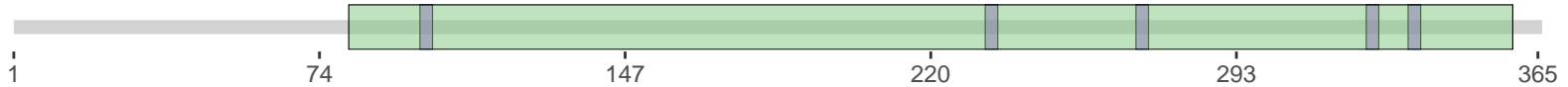
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

IRIGTRDVLKDYATGEGFRATSKWVMMNGDTRRLGKIVTDVHHEVYVFGPKELRLAFPEENNSLKKIKLEDPH6SRLLGLAPRRADLDMNKHVNNVYTGWVLESPDQILDTHELQITLDVYRREGQHDVVDLSLTGLESFEDSALGTNGSASGRENKSFHLVRLSGDGLNRRGTEWRKKSVKV

NbL03g14020.1 uncharacterized_LOC109209395 [MW = 29.13 kDa]

No. of times detected



log(intensity)



Values from



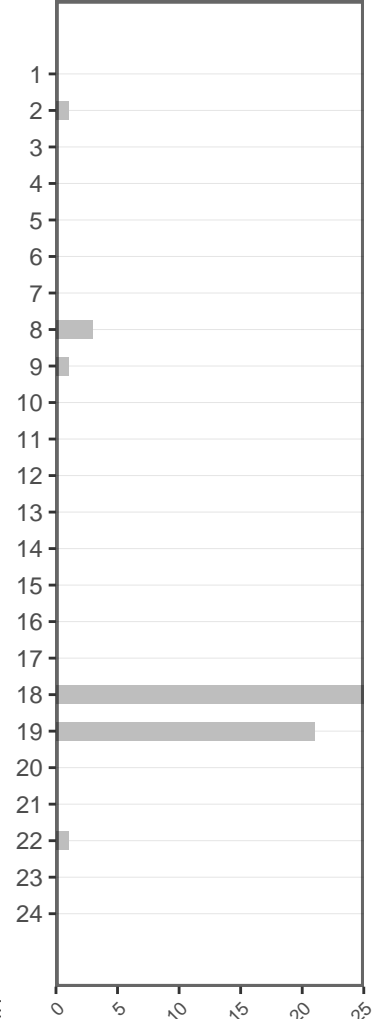
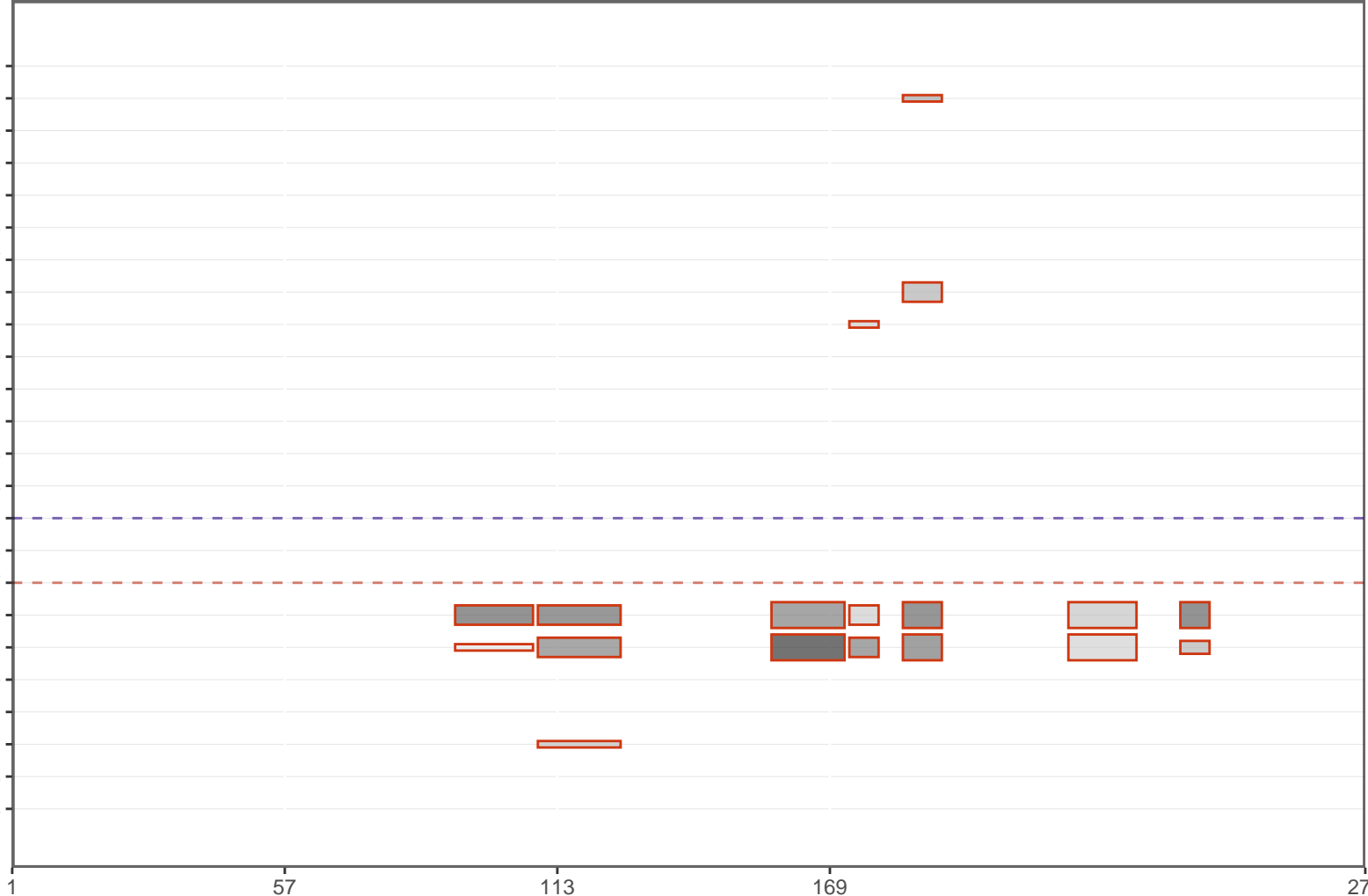
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

AGLKVGDGVVYTSFFGDELWPAKLGFTKTAIGAKPDSVYFVSRGVDDVKRLPKRRAPDQFGRKLTDMQKARATHICLDCGVYFLPKSFDDQPEVACPGQGRAPKRFKAYDVTNGRAIGGGLPNGVHGLIAGIGGVGALLVGLGQ

NbL03g13970.1 membrane_protein_of_ER_body-like_protein [MW = 132.66 kDa]

No. of times detected



log(intensity)



Values from



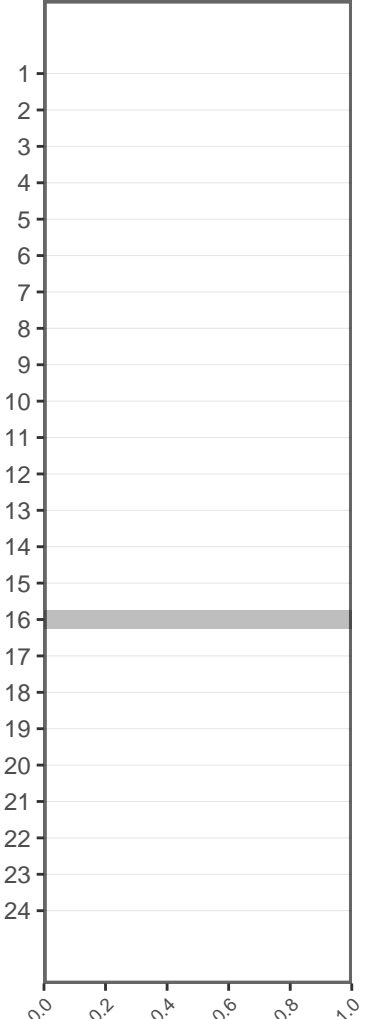
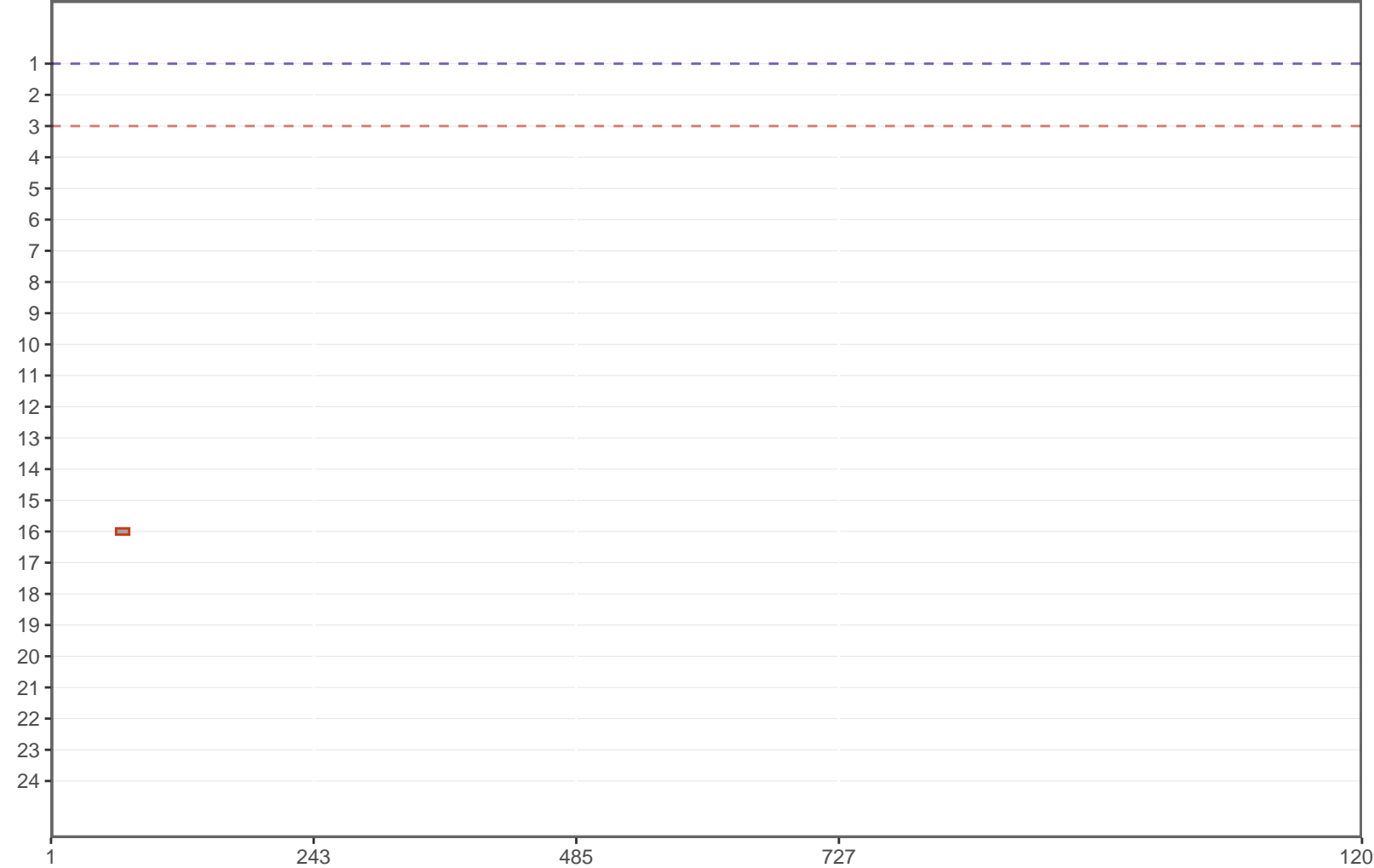
MW indication



Molecular weight



Gel Slice



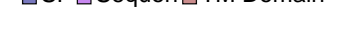
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

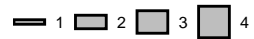


Protein sequence:

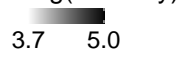
LSCSFSPFTGNGFRLFRFFGEGKDKGNVKGEGIPITTKNWFSSIFASGDKGASVEGGSGTGANAVKNDAGVLRPSDNFKDGSAPLVIREAPVYSSGGTGEAGHILGSENGDANKMGKMAINTVQKSVNATKSGAGGSVDFDFEEGILNLPVVAASSEEVKGNDRNDELRLTAGRIQVSNGLAGEPLPASGGTGGKVLITSTKEESLTIKSRTELKSDVMITSTKEESLTIKSESDLTKSDMTLLKNGPDNEGLLSAATTSFALNGLDENGKPKFTELPOEHCQVKA

NbL03g13790.1 nascent_polypeptide-associated_complex_subunit_alpha-like_protein_2 [MW = 23.2 kDa]

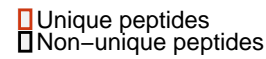
No. of times detected



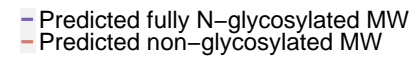
log(intensity)



Values from



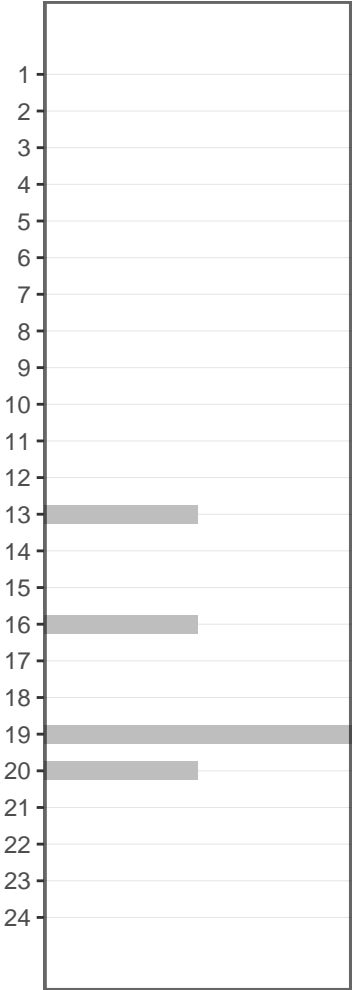
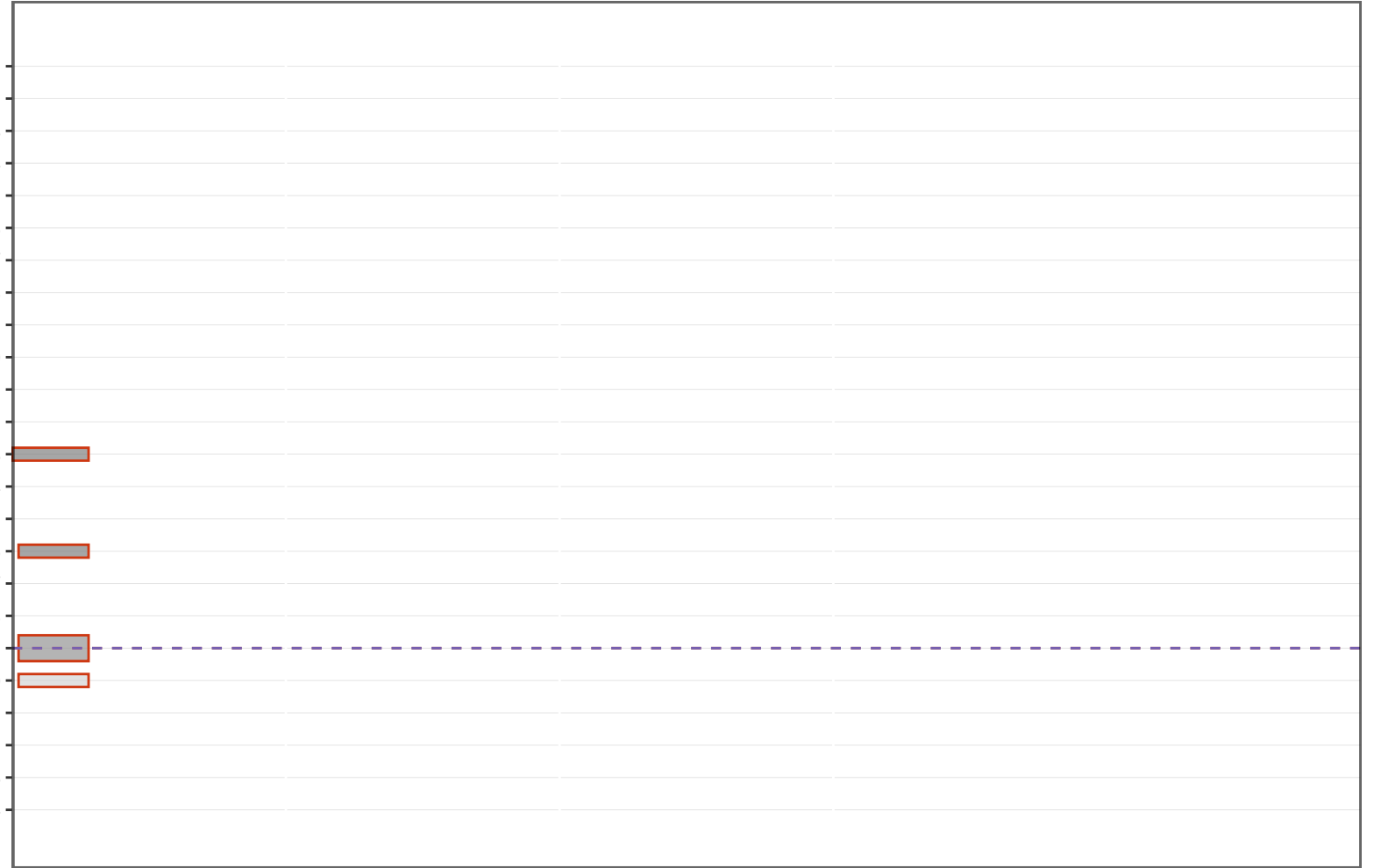
MW indication



Molecular weight

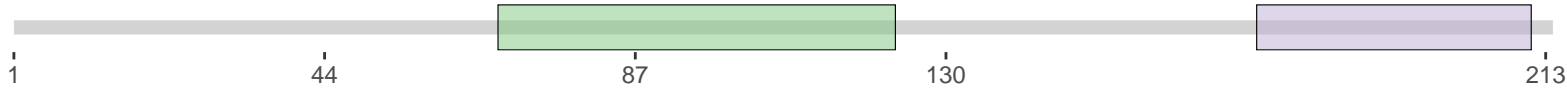


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

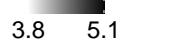
RTKNVLFISKPDVFKKFNSETYVIFGEAKIEDLSSGLGTAAAGQFRMPDMGSMVMAKSDVSPSTAVAEADDEEEVEDETGVPRDIDLMTGAGVGRSKAVKALKCHNGDIVSAIMELT*

NbL03g13770.1 caffeic_acid_3-O-methyltransferase-like [MW = 39.6 kDa]

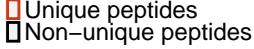
No. of times detected



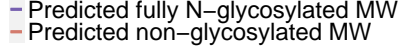
log(intensity)



Values from



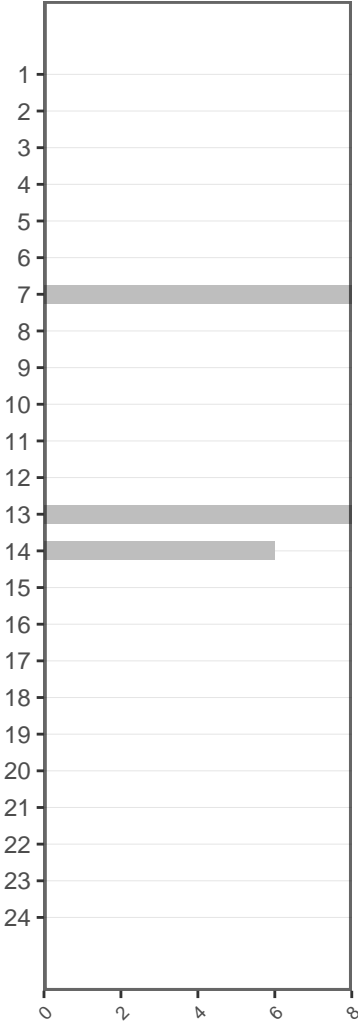
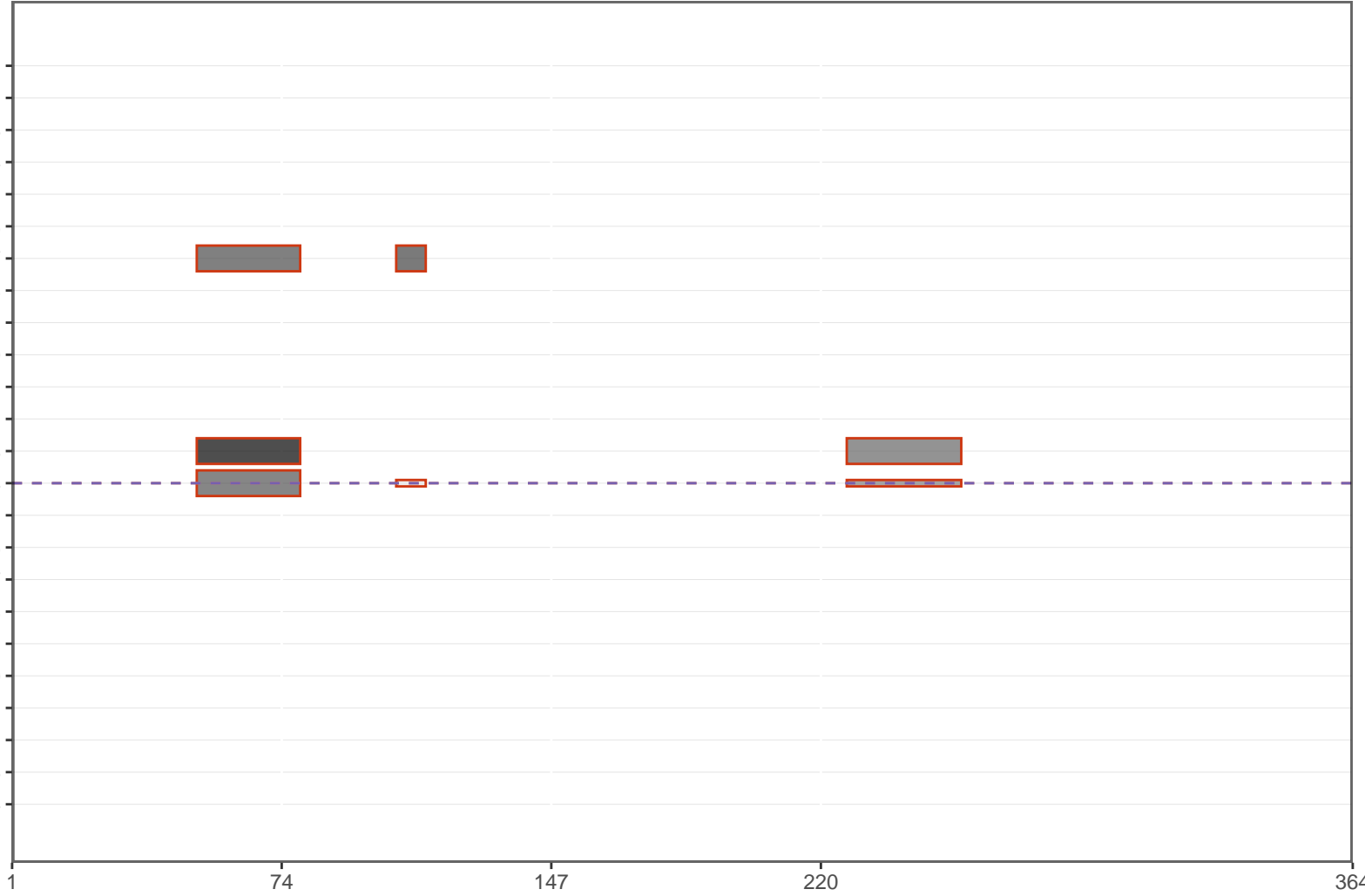
MW indication



Molecular weight



Gel Slice

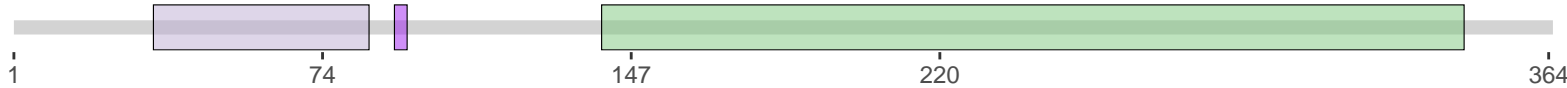


Protein length

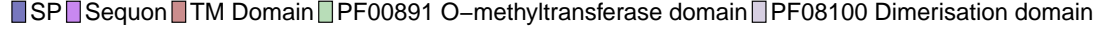


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

DFRFNKVFNRRGMSDHSSTMSMKLEEDKGFEGELNSIVDVGGGTGTATNMMVSKYPSIKGINFDLPHVIGDAPVPGVEHVGDDMFASVPKADAFIMKWIWDHSDHEHLKFLKNGYEALPANGKVIWAEGLPEAPDTSLATNTVHIDIVMLAHPDCKERTETEKEFQALAKAGAGFTGFHKACGANTWVMEFNK

NbL03g13630.1 probable_6-phosphogluconolactonase_4_chloroplastic [MW = 37.26 kDa]

No. of times detected



log(intensity)



Values from



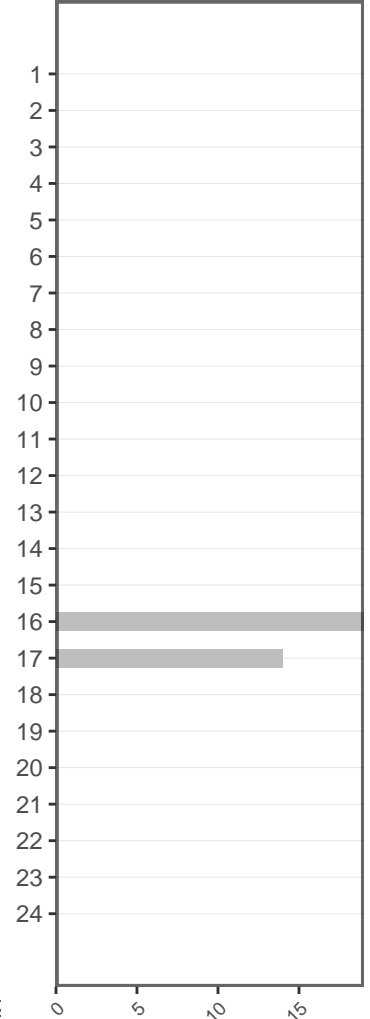
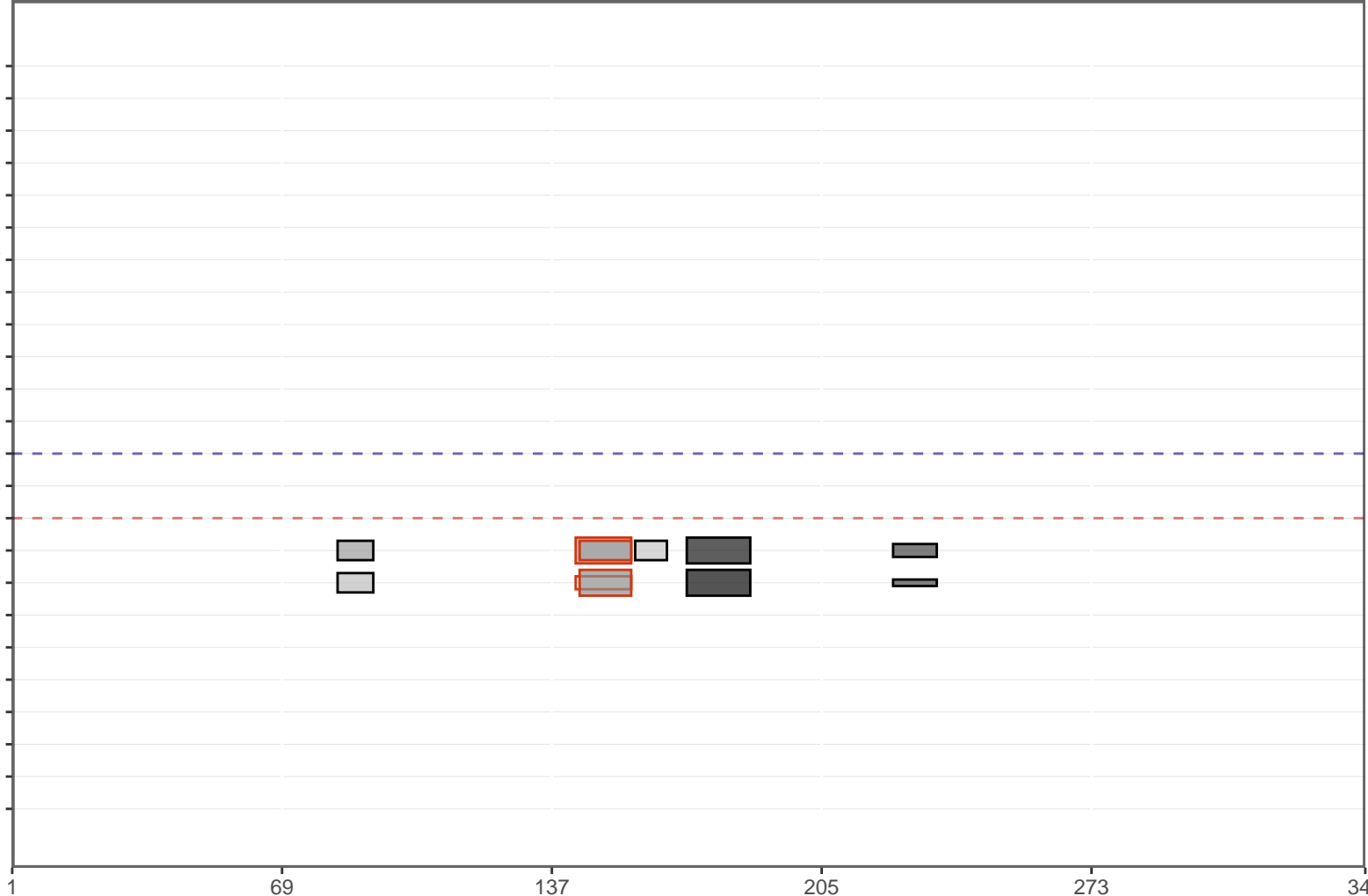
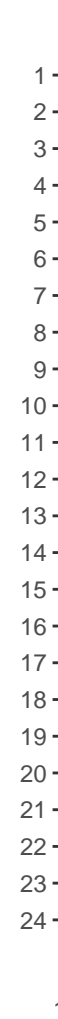
MW indication



Molecular weight



Gel Slice

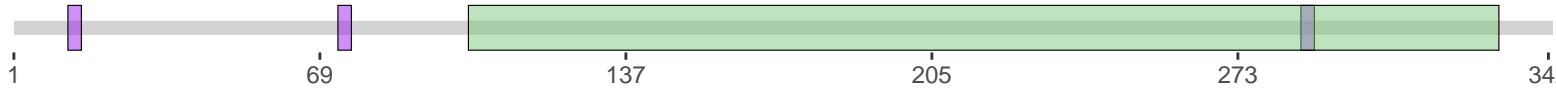


Peptide counts over 4 repeats

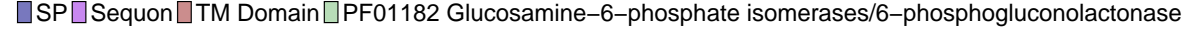
Protein length



Pfam domains



Pfam Description



Protein sequence:

HHVYVYDERVYPKDHPDGNLYLADAFLSKIPSPGNVYVNDALSAEGAADDYETCLRHLVSKIVDISDATGFPKFDMLLGMGPDGHVSLFPGHPLVHEKEKVVTFIKESPKPPPERITFTFPVINSANIALVAGAGKADVYHKSIGDSESDLLPVQMVPEGELIWFLDKAAAEKLI

NbL03g13390.1 protein_yippee-like_At4g27740 [MW = 12.01 kDa]

No. of times detected



log(intensity)



Values from



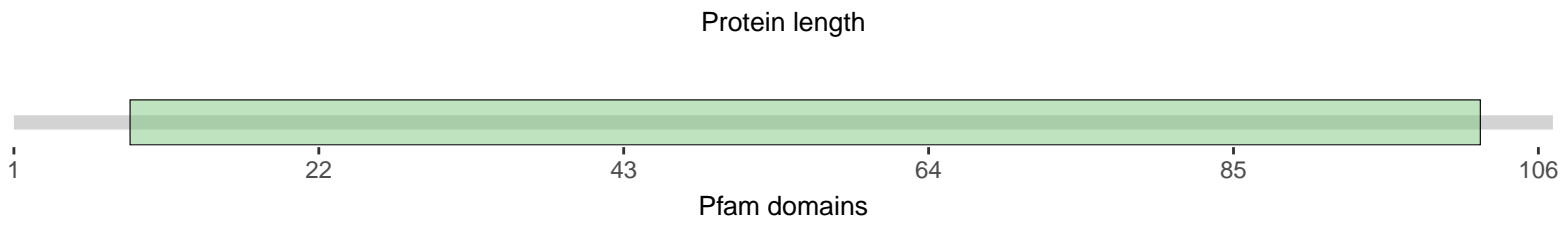
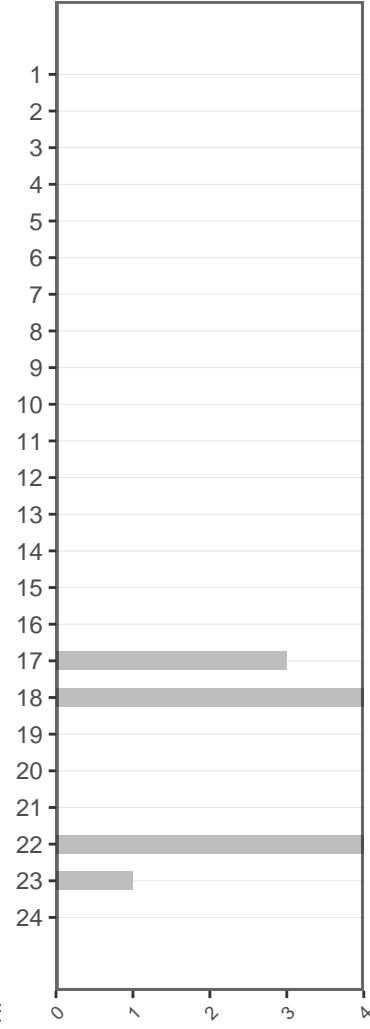
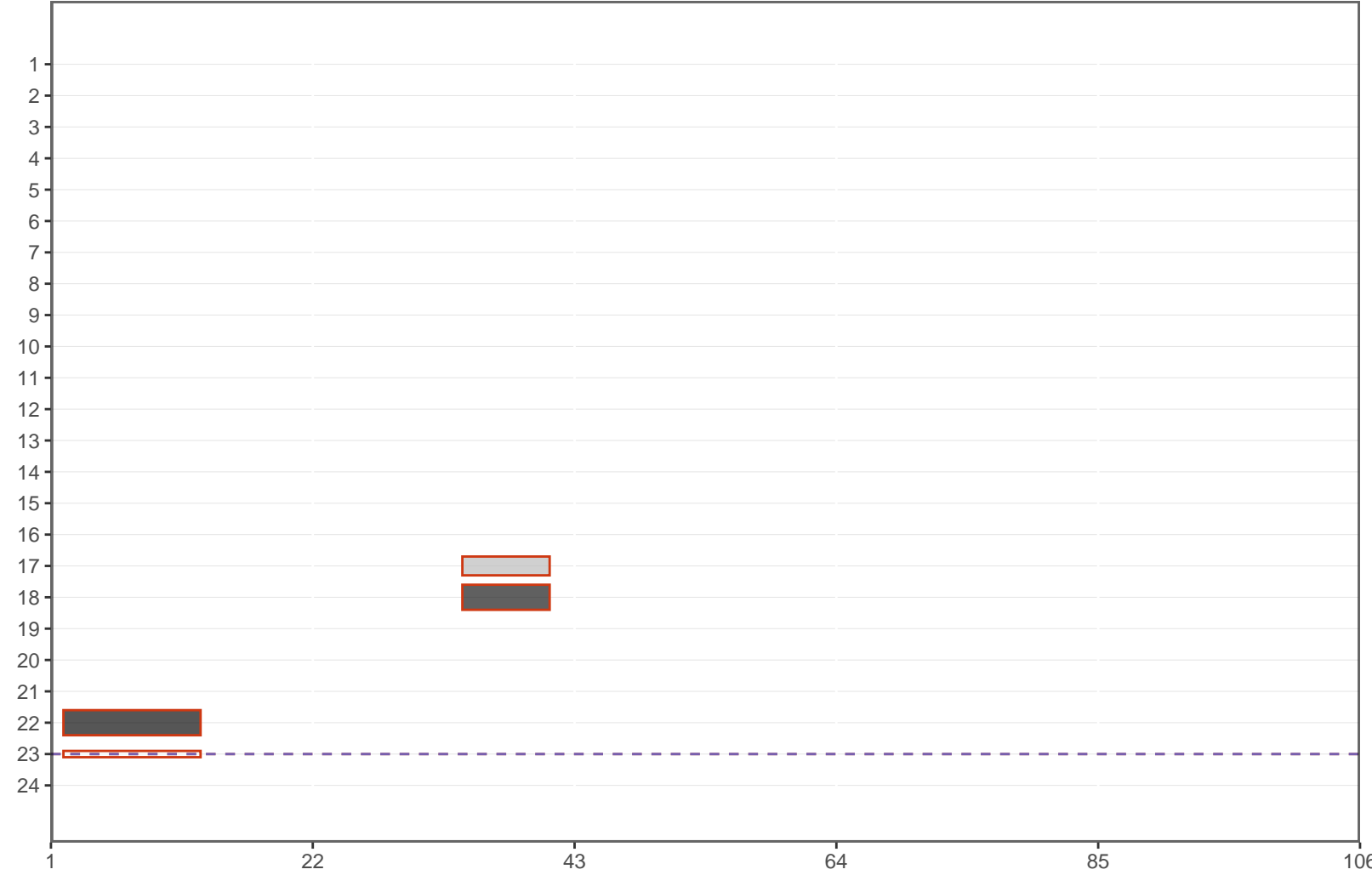
MW indication



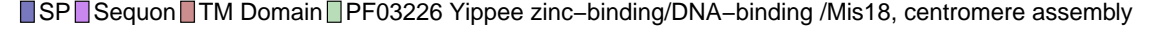
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

FDHAMNLYGKKEEDRQLTGFVSDIFGKGGEEELGWYKAVDPGKQYKEGRFIETAKLKEY*

NbL03g13270.1 thylakoid_luminal_17.4_kDa_protein_chloroplastic [MW = 27.68 kDa]

No. of times detected



log(intensity)



Values from



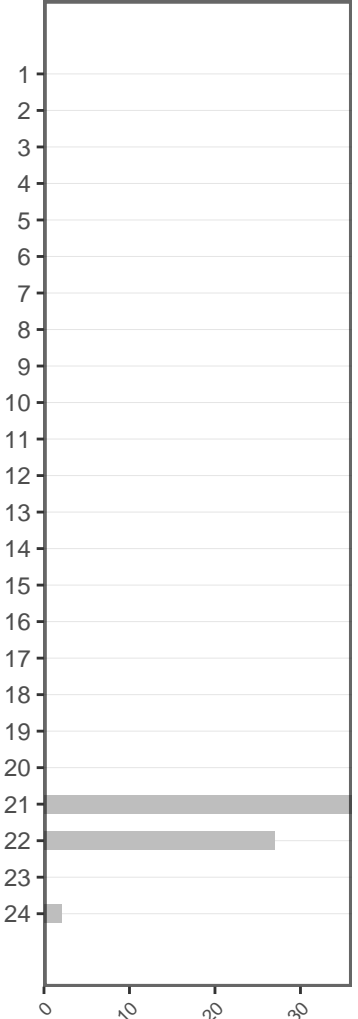
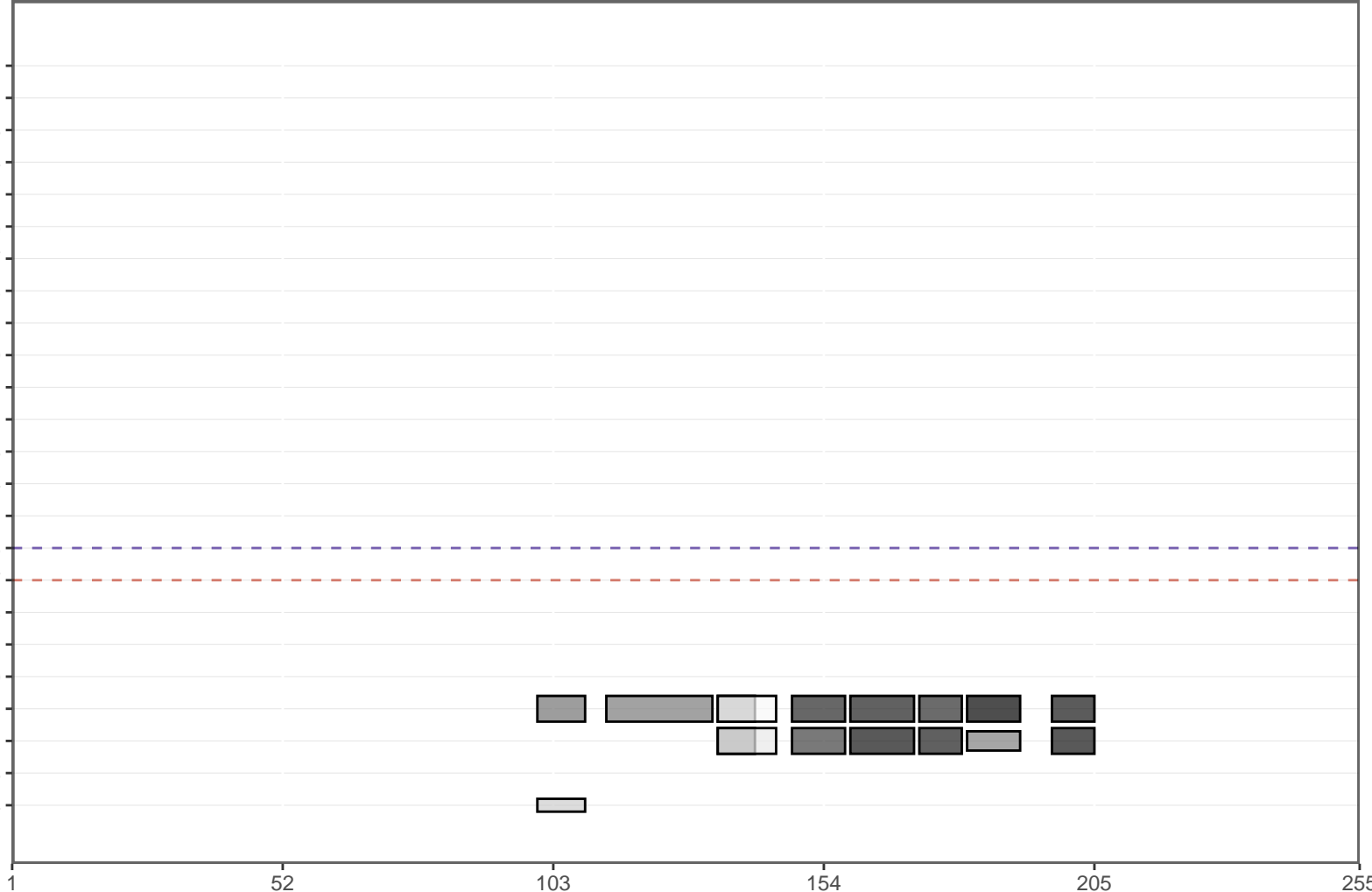
MW indication



Molecular weight



Gel Slice



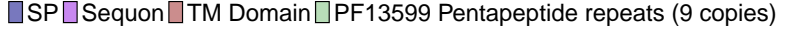
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VGNITGQANGVYDKPLDLRFQDYTKENKIKGKSLAALMSGANFQDADMTEVMSKAWVGAFKGTDFSNALDRVFEKANLGGASFNTVLSGETFNDAGLEADAFEDTTHGVDLQKGLKTKTNEEGRVNLGGR

NbL03g13240.1 luminal-binding_protein_5 [MW - SP = 70.7 kDa]

No. of times detected



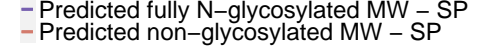
log(intensity)



Values from



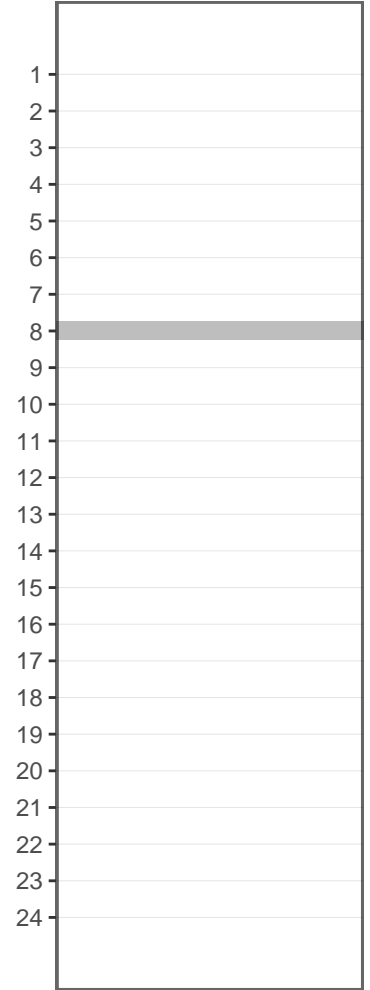
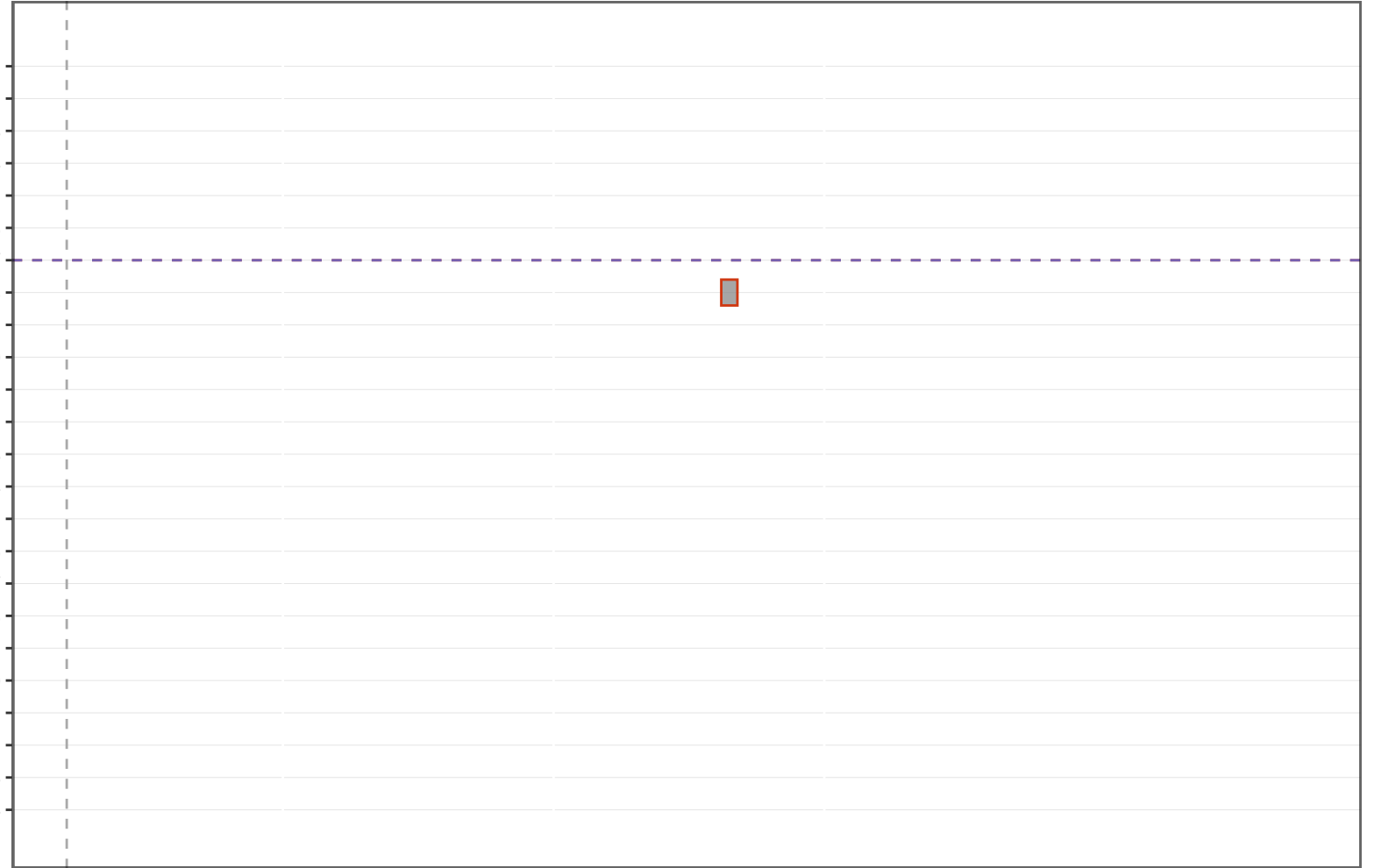
MW indication



Molecular weight



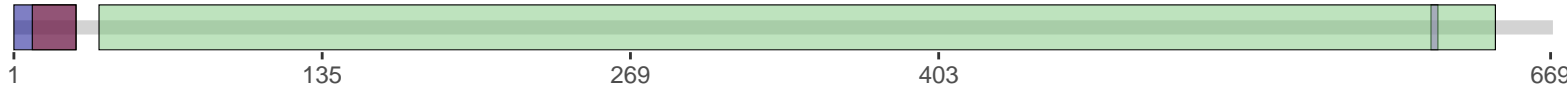
Gel Slice



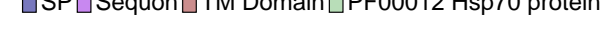
Protein length



Pfam domains



Pfam Description



Protein sequence:

FSEPLTRARFEELNDLFRKTMGPKKAMEDAGLQKNGIDEVLVGGSTRPKVQGLKDFDQKEPKNGVNPDEAWYGAAVQGGLSGEGGDETKLLDLPFLFLGIEYVGGVMTKLRIPNTVPTKKSQVFTTYDQDQQTIVISVFEGERLTKDGRLLGKFDLGTIAPAPRGTPQIEVTFEVDANGLNVAEKEDKASGKSEKRTITNDKGRLSQEEIERMVAEAEFAEEDKKVKERIDARNSLETYYNMRNGINDKOKLADKLESDEKEKIEATKALEVLLDNGSAE

NbL03g13200.1 KH_domain-containing_protein_At4g18375 [MW = 74.11 kDa]

No. of times detected



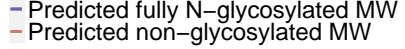
log(intensity)



Values from



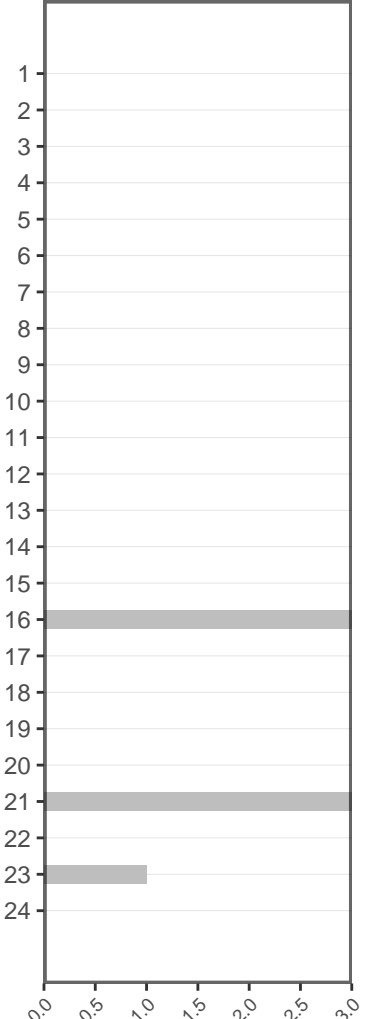
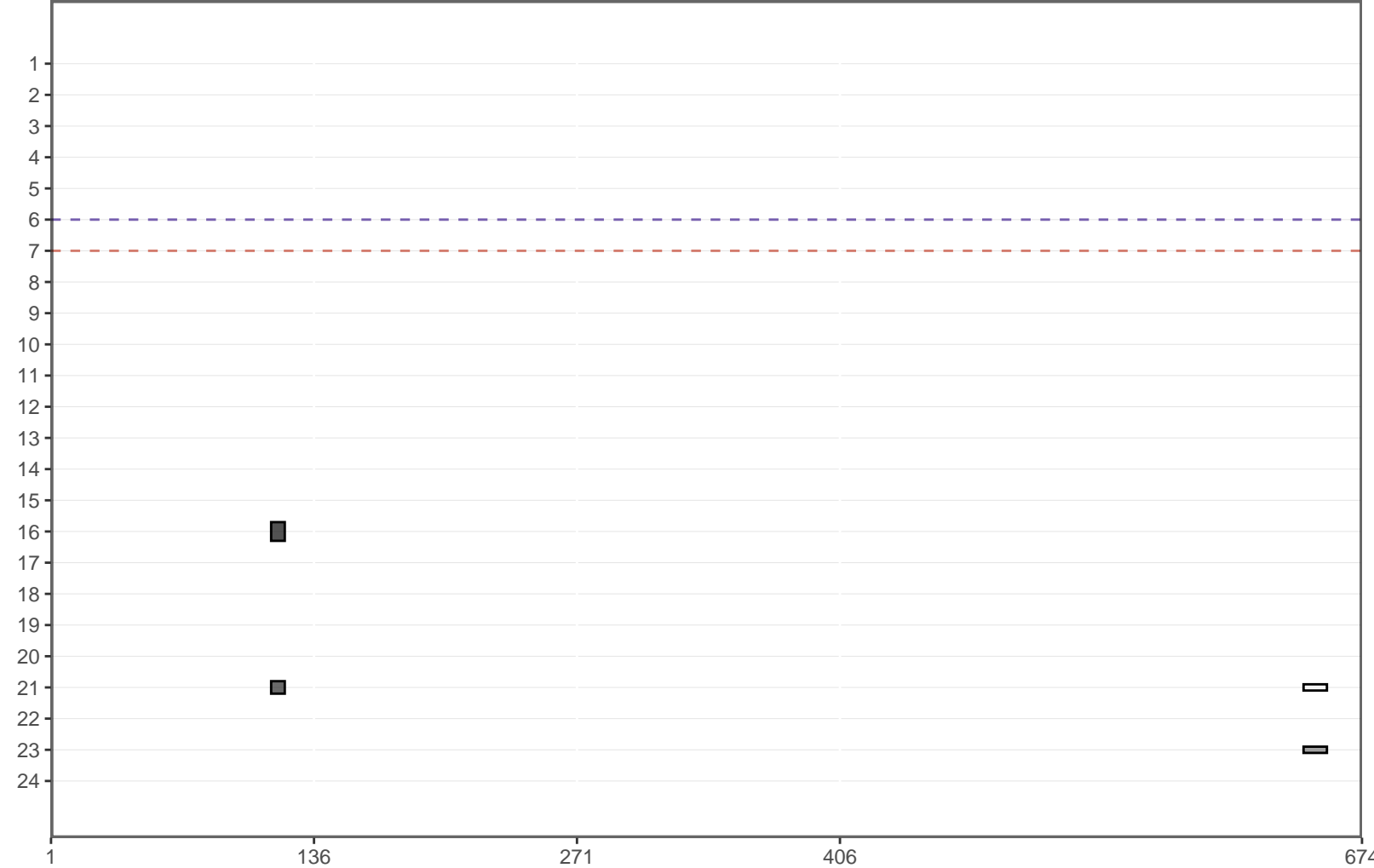
MW indication



Molecular weight



Gel Slice



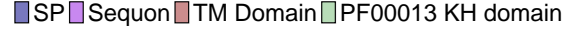
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

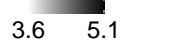
YAVESGKAPGNENGPVIMYVEDLVFRILGPKVDKVDYVAGESSDGHIELLQNEIGVDKILNIPVASSNEQVIMMSDEGPDDELFPAGEALLHIGTRIVDLVPEKENVYTRVLVGTDEVEGLGGDRDGLSDMKTKTGATVQILPKLELPPVGVSTDEIHNQVGEKAAREALVEVTSMLRCELYREFFQKDFPSPRVFASPARGNGADKSVNNTSPSGQNVNNDVQTSIVGNAPAKLMTGPKVNETGASASEIAKGNENERGEDIPSGLNRMHVPVLRSTLELVIPPIAVPKLTKSF

NbL03g12940.1 dipeptidyl_aminopeptidase_4 [MW = 87.25 kDa]

No. of times detected



log(intensity)



Values from



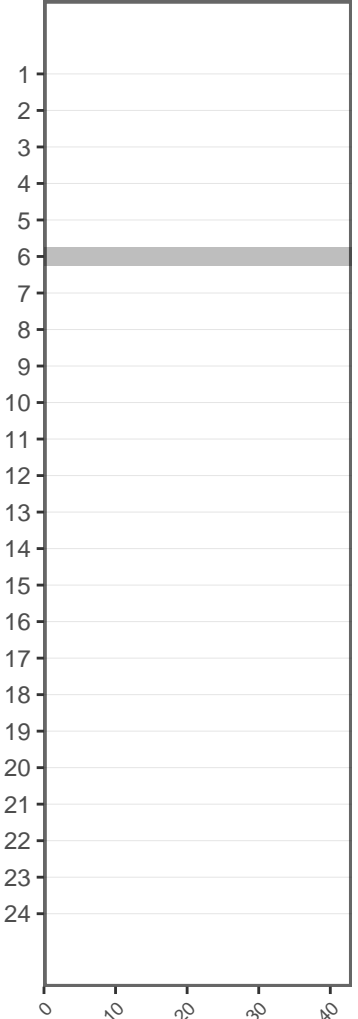
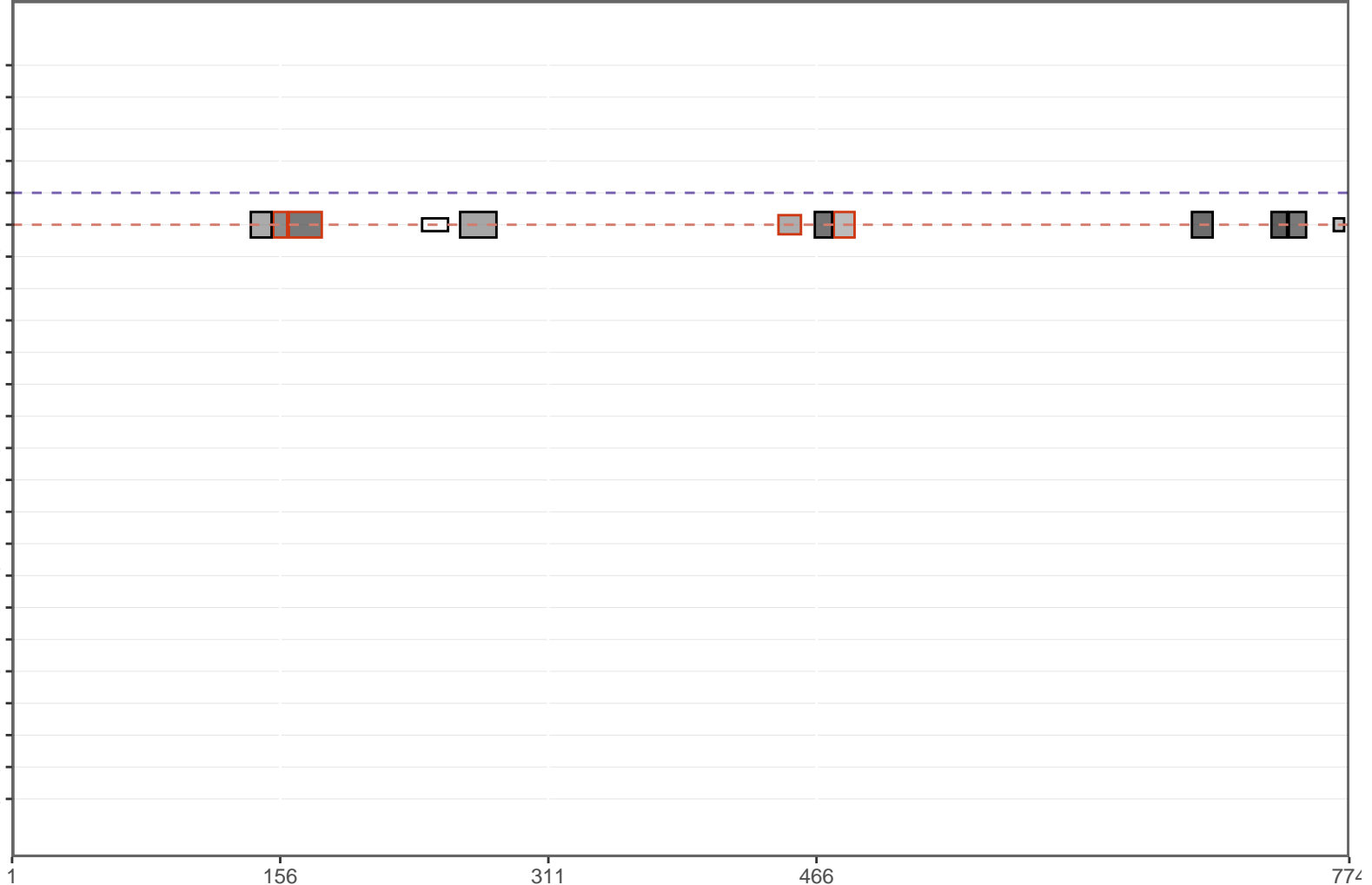
MW indication



Molecular weight

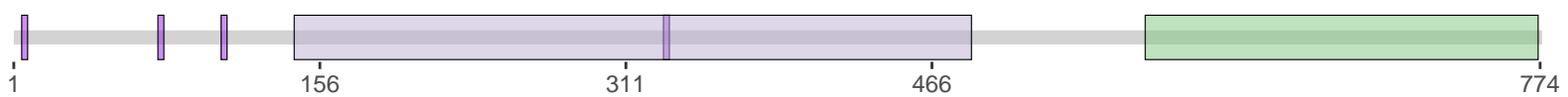


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00326 Prolyl oligopeptidase family
- PF00930 Dipeptidyl peptidase IV (DPP IV) N-terminal region

Protein sequence:

INGAFIWASEKTFGRHLYLHDTNGVGLGRITGGDWLVEQVAGVNEVTEGLYFTGTLDDGPLESHYGAKLFFDANSPLEGPMRLTNGRKHAVLHDHGMORFDIHDHSLVSPKISLSSLDGSLMHLFDQPVSEVPGFRKHLLESPEIKGAGDDGTALYGLYKPPDMKFGAPPYRTMEVYGGFPEVQLVDGSDWNTNTVDMRAGYLRKSGILYWKMDNNGRTARRGLMFEQALKYNOGLVDAEDQLTGAEWLLKQGLAKGHHGLYGVWYGGVLSAMTLARFPEVFKCAVSG

NbL03g12880.1 protein_BOBBER_1-like [MW = 33.98 kDa]

No. of times detected



log(intensity)



Values from



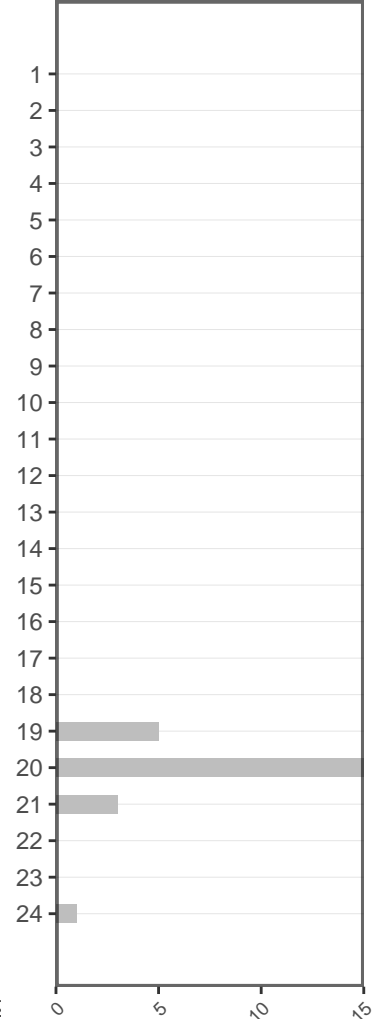
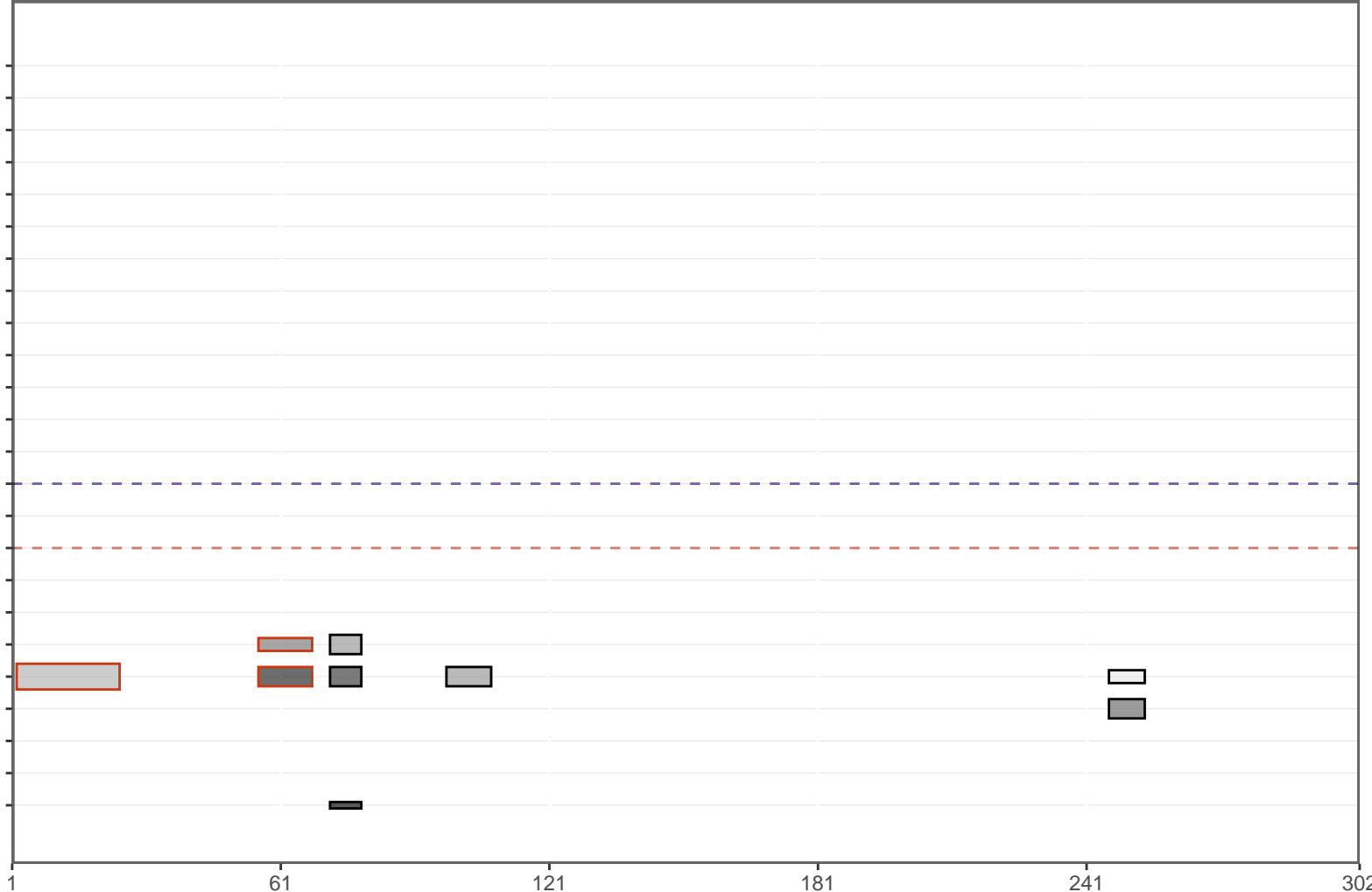
MW indication



Molecular weight



Gel Slice



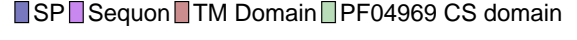
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DLENYSWNSLSLEAVNIPVPHGTGRFRVCDIKNHLKVLGKGGPPIDGELYRPPVWVDDCFWVLEDDQKISVLLTKKDGMEWVKCCVKGPEIDTQKAEPESKLIADLPETRSTVEKMMFDRGQKSMGLPTSDETQKQKGLKFMMEHPEDMDFSKAKIE

NbL03g12860.1 probable_plastid-lipid-associated_protein_14_chloroplastic [MW = 75.92 kDa]

No. of times detected



log(intensity)



Values from



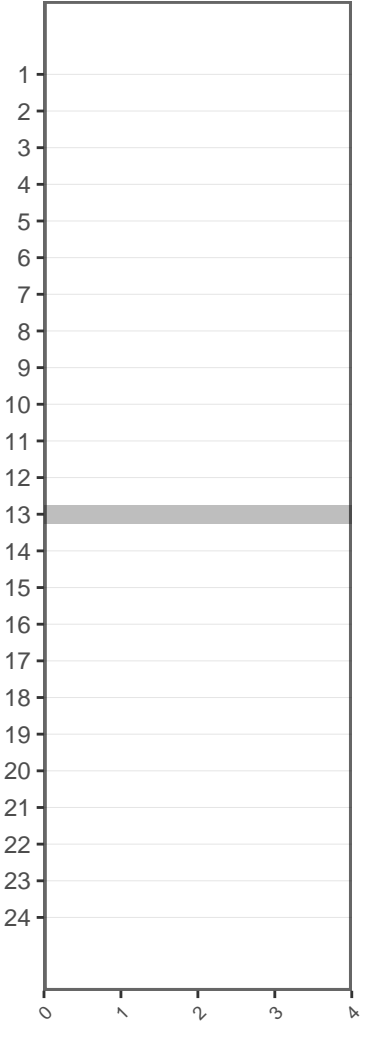
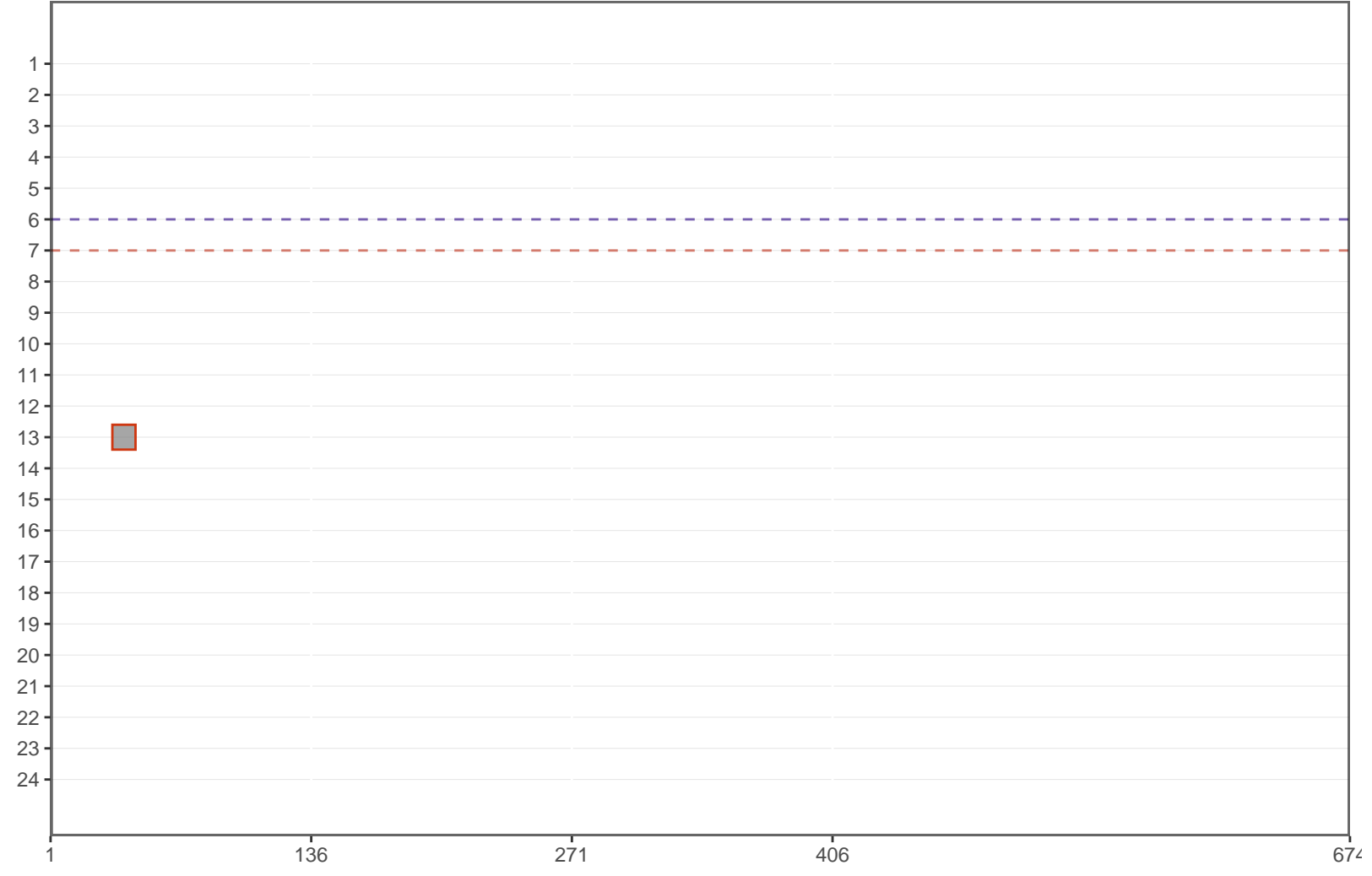
MW indication



Molecular weight



Gel Slice



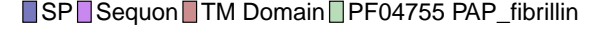
Protein length



Pfam domains



Pfam Description

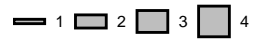


Protein sequence:

LRLEMDPTIFAKFKALFTKGNDFSLREFLLHAKRNSAGNFGQILDNRNWSAGWHLLELLLPKPLDRISGLNLRHPFLOGPKWRVSPSIVRWLSGTTVRAIEEYVGGQGRRLAHFELMEMLNPPYKPKHWRARAFPGKWRLLVYGTGRHGLTLPQPSVRLVGEVYLTGKASTPKTTFSAASHSFTMPGGDWRHDKSGVGGKLVNTYFRLLRGRRLVKEETDTGKFPATPAGGSVAKRLSCKTWRKAIPVNEFFSBLPAKLVSAETEVTMSLQKPLS

NbL03g12840.1 splicing_factor_3A_subunit_3-like [MW = 59.76 kDa]

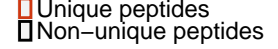
No. of times detected



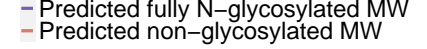
log(intensity)



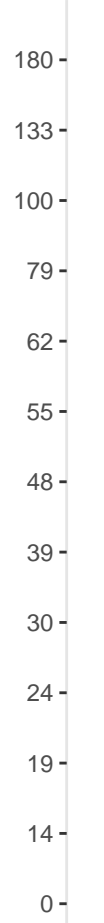
Values from



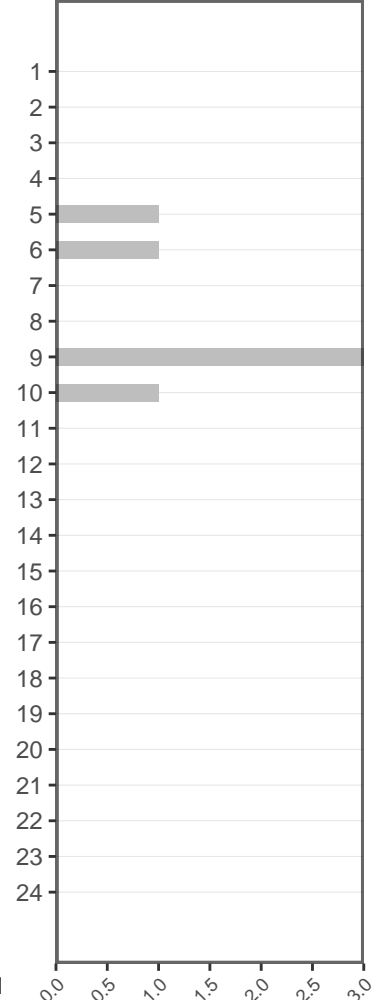
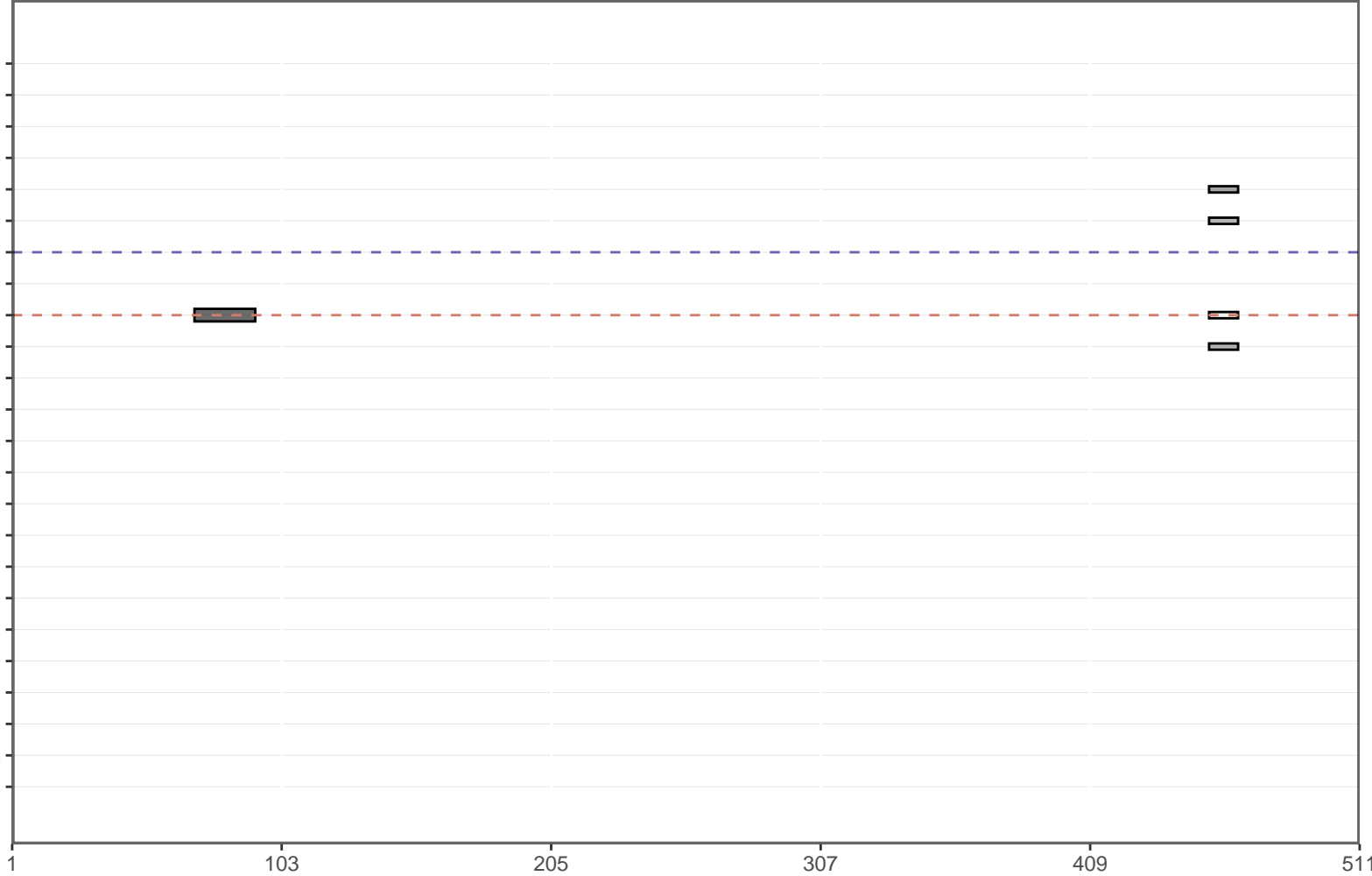
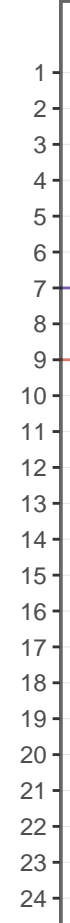
MW indication



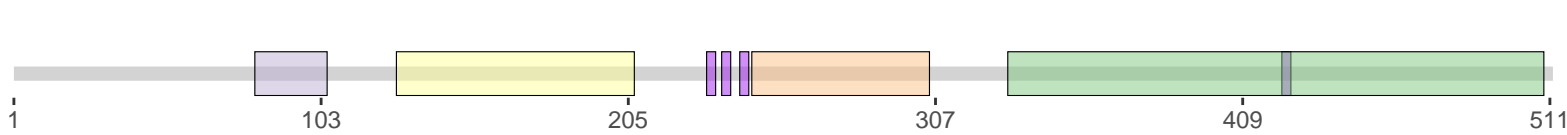
Molecular weight



Gel Slice

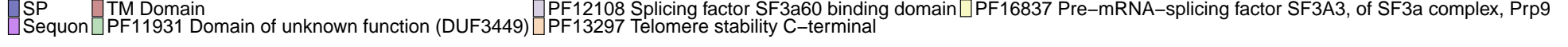


Protein length



Pfam domains

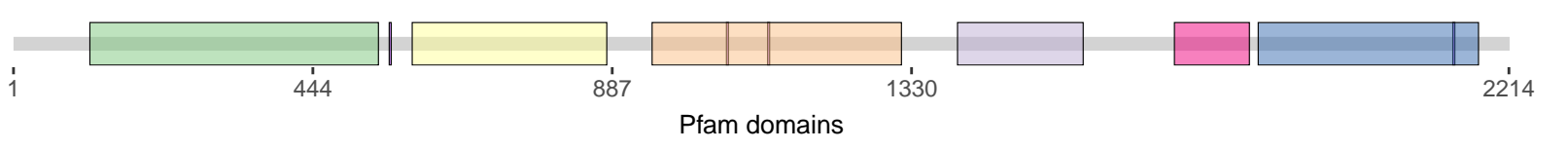
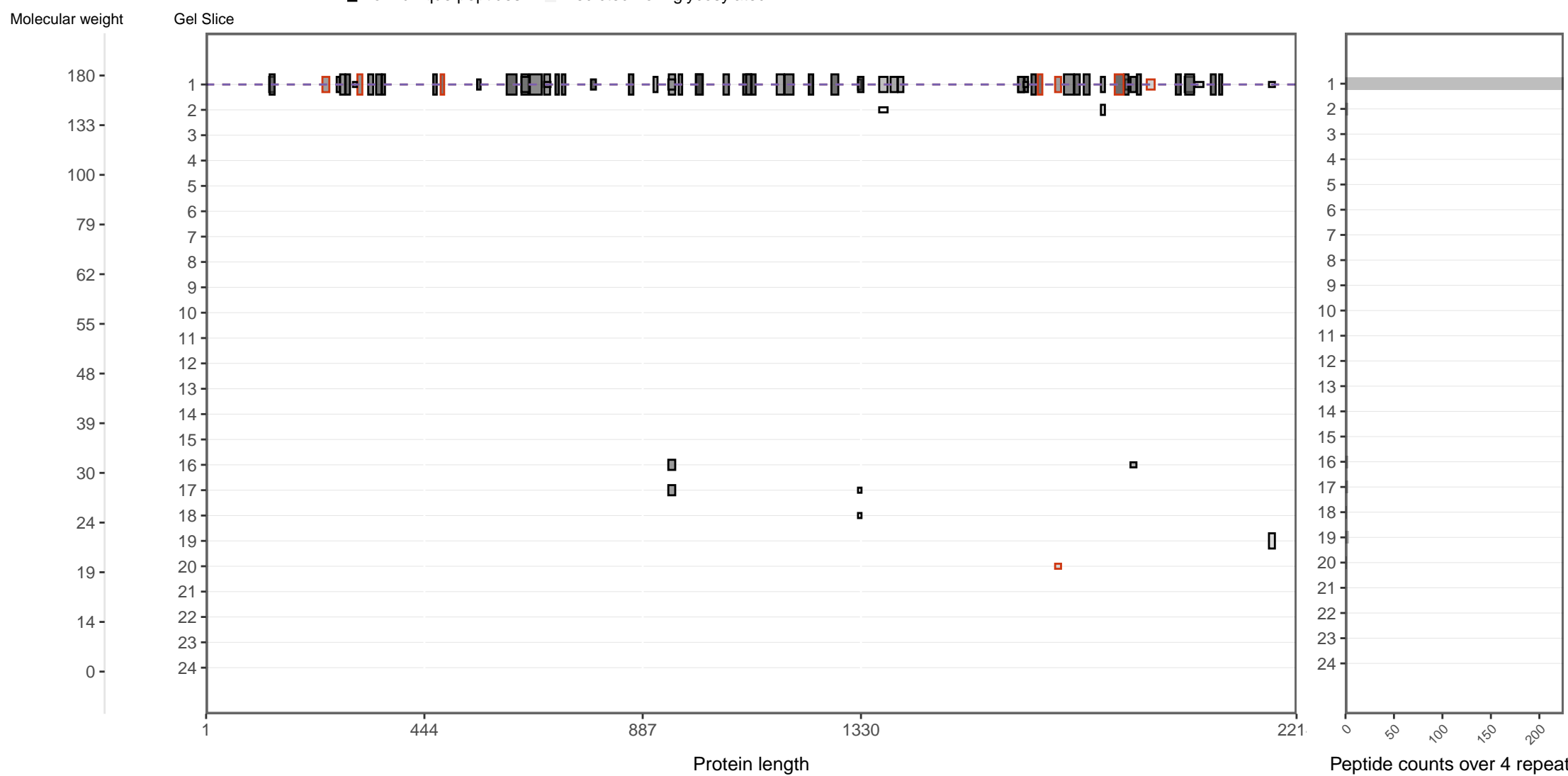
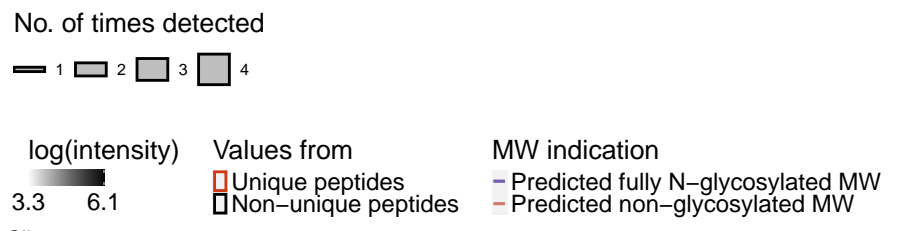
Pfam Description



Protein sequence:

VIDLNSYSTVEELMEGPDKLEKALGALGKTKGGTGGTQGRARLFLTRHTPLKLRDRKHFAGSRKPEQNGVMPAPQVSDDKKEALMEAKIRKLDLDETIVRTKENVEKGGALTYEEMEAREEDDVAEAESEDEEDDQIYNPLKPMGWDGKPIPVWLYKLHGLGDFKCEGCGNHSHYWRGRAYERHFKEWRHQHGMRLGIPNTNFMNEITSIEEAKQLWERIGDEKGLNKRWRPDLLEEVEEDQEGNIVNKKTYTDLGRGGI

NbL03g12820.1 glutamate_synthase_1_[NADH]_chloroplastic [MW = 243.02 kDa]



- PF01493 GXGXG motif
- PF04898 Glutamate synthase central domain
- PF14691 Dihydropyrimidine dehydrogenase domain II, 4Fe-S
- PF0310 Glutamine amidotransferases class-II
- PF01645 Conserved region in glutamate synthase
- PF07992 Pyridine nucleotide-disulphide oxidoreductase

Protein sequence:
 QGAKPGEGLPGHKVGDVAFRNRTAGVGLSPPHHDIVSDIEAQLIHLKLNANPEARVSVKLVSEAGVGVVAGVWKGHADHVLISGHGGGTGASRWVTKIKSAGLPLWELGLAETHGTLWANDLRGRFTLGTGGKTKGRDVAWALLGAEEFGFSTAPULFGIMMRKHGNTGPGVGIATDQDLRLREKFAGEPEHVFHFFFMIAEEVREIMSHLGFRTLFEMVGRSDMLELKDNDLTKNNDKLNDLGLLLRPAADRPEAAGVGVGQKGDHGLDMALDNNLJLSKAALE

NbL03g12720.1 probable_protein_phosphatase_2C_76 [MW = 38.77 kDa]

No. of times detected



log(intensity)



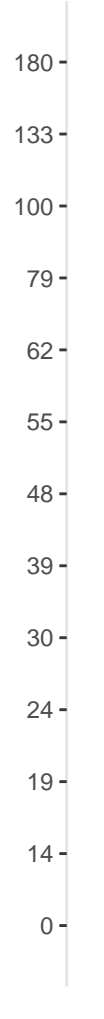
Values from



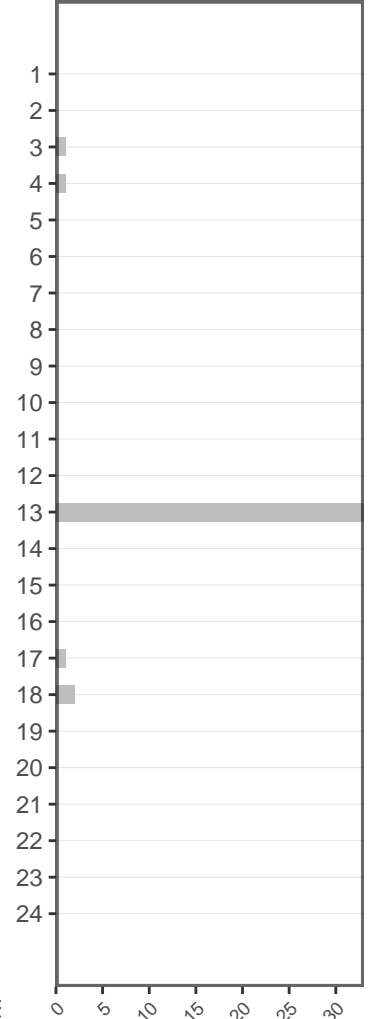
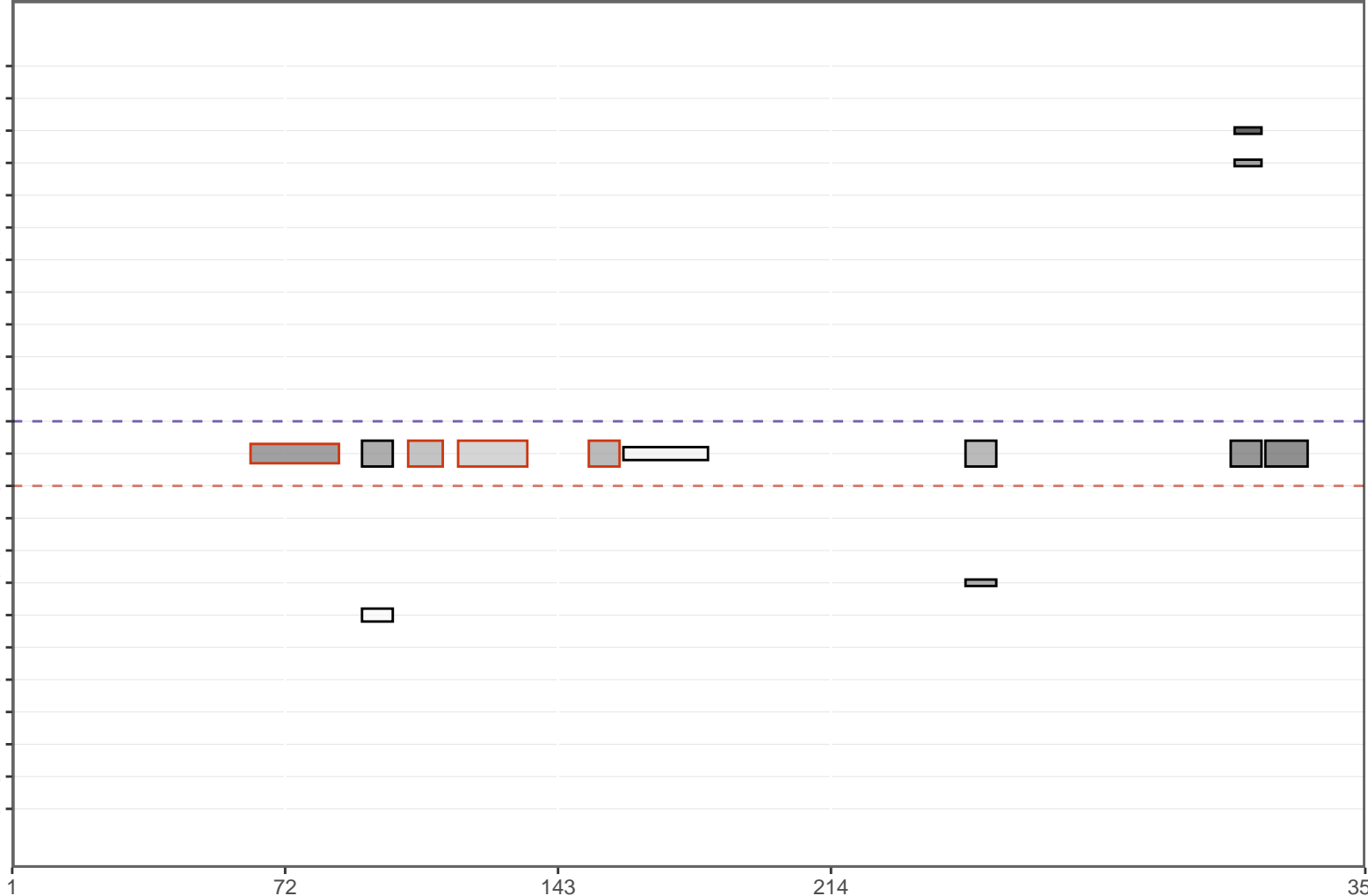
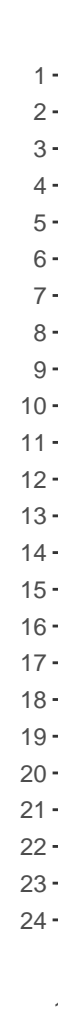
MW indication



Molecular weight

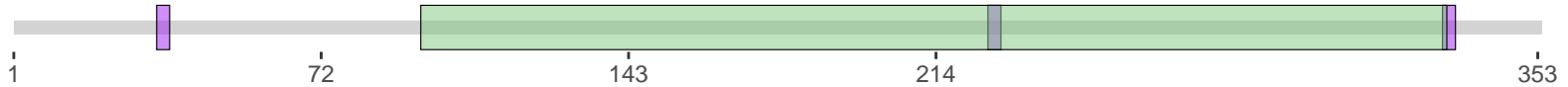


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SETYQDTMDIFLDEKDFRDDGGSTASTAVLVGNHLYVAVVGDSTRHSGKKAIALSEEDHKPKRTDERKRRESAGGVVMMAGTWRVGGVLA MSRAGFRNMLKGFVAEPEIQDGEIDEEILLVLSADGLWVVPNEDAI SLAEAEPEEAARAKITETAFTFRGSA DNTGIVVVFHKKVPEPSSGGG

NbL03g12490.1 uncharacterized_LOC109206341 [MW = 19.05 kDa]

No. of times detected



log(intensity)



Values from



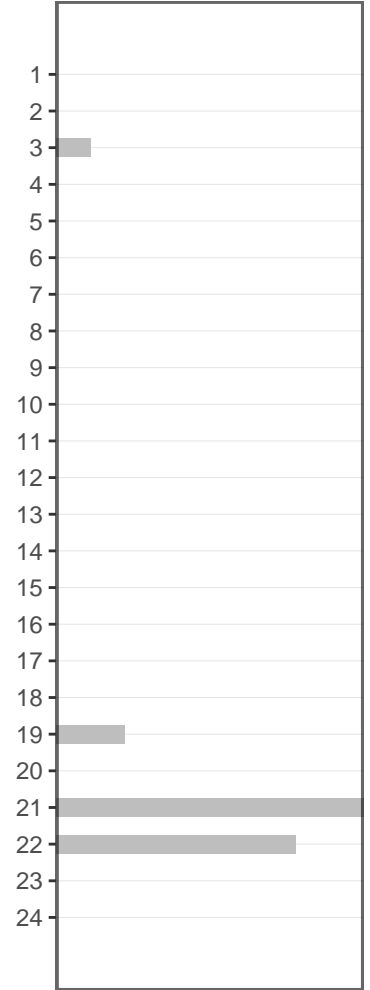
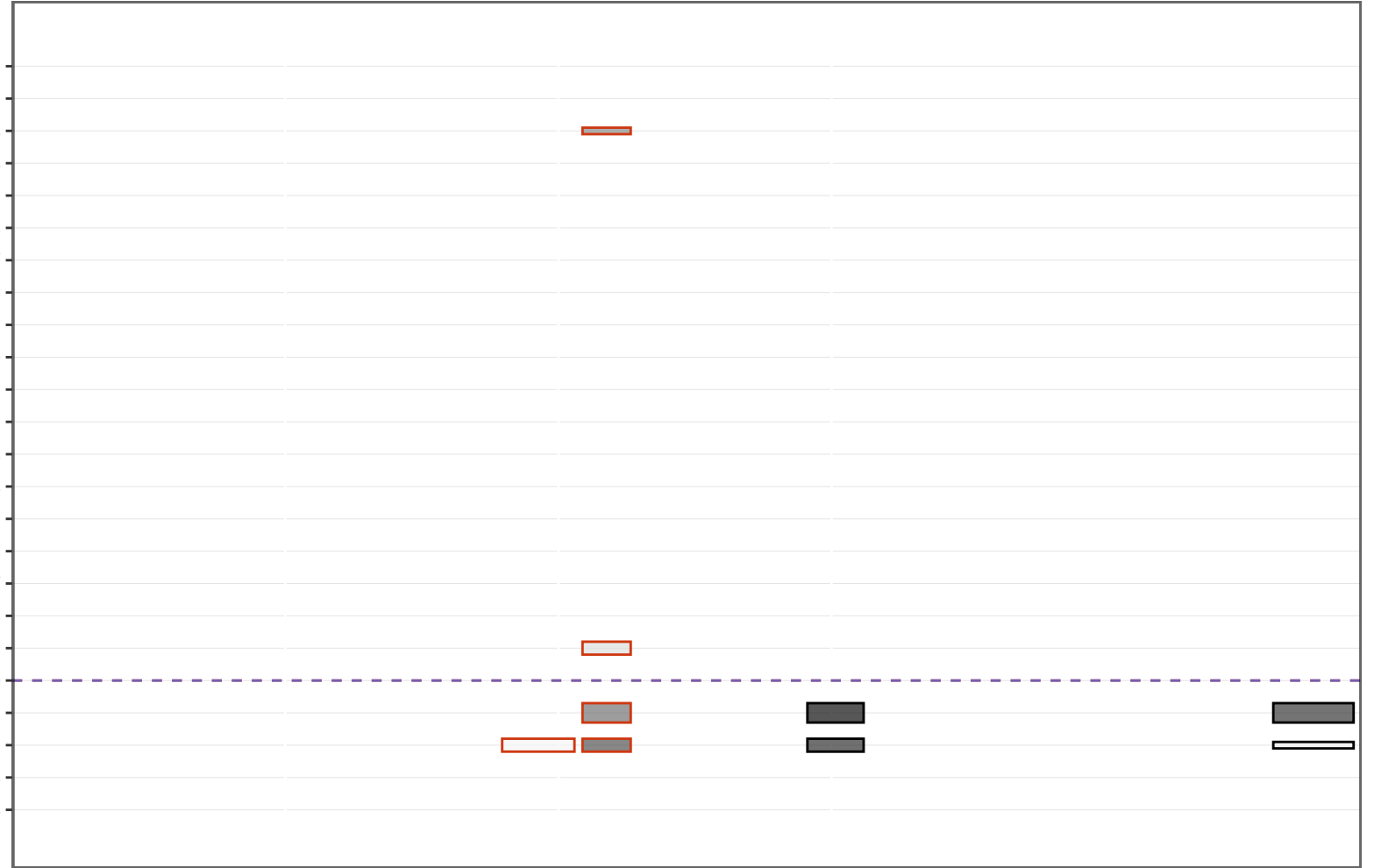
MW indication



Molecular weight



Gel Slice



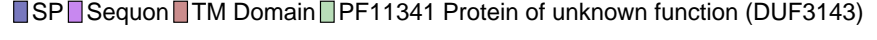
Protein length



Pfam domains



Pfam Description



Protein sequence:

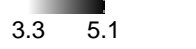
DEVLQKLPDKKKALYSHSLFDIEAWLRSLGFGYGRDRRALWFVEKPKDWAHLSLDTDHYRVLKNGPGNLEKDIERRFYSVALSRDENALGGP

NbL03g12390.1 probable_NADH_dehydrogenase_[ubiquinone]_1_alpha_subcomplex_subunit_5_mitochondrial [MW = 25.77 kDa]

No. of times detected



log(intensity)



Values from



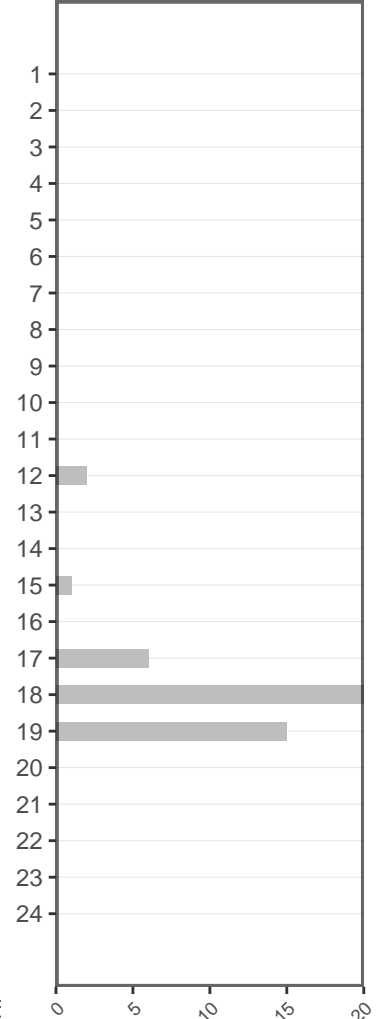
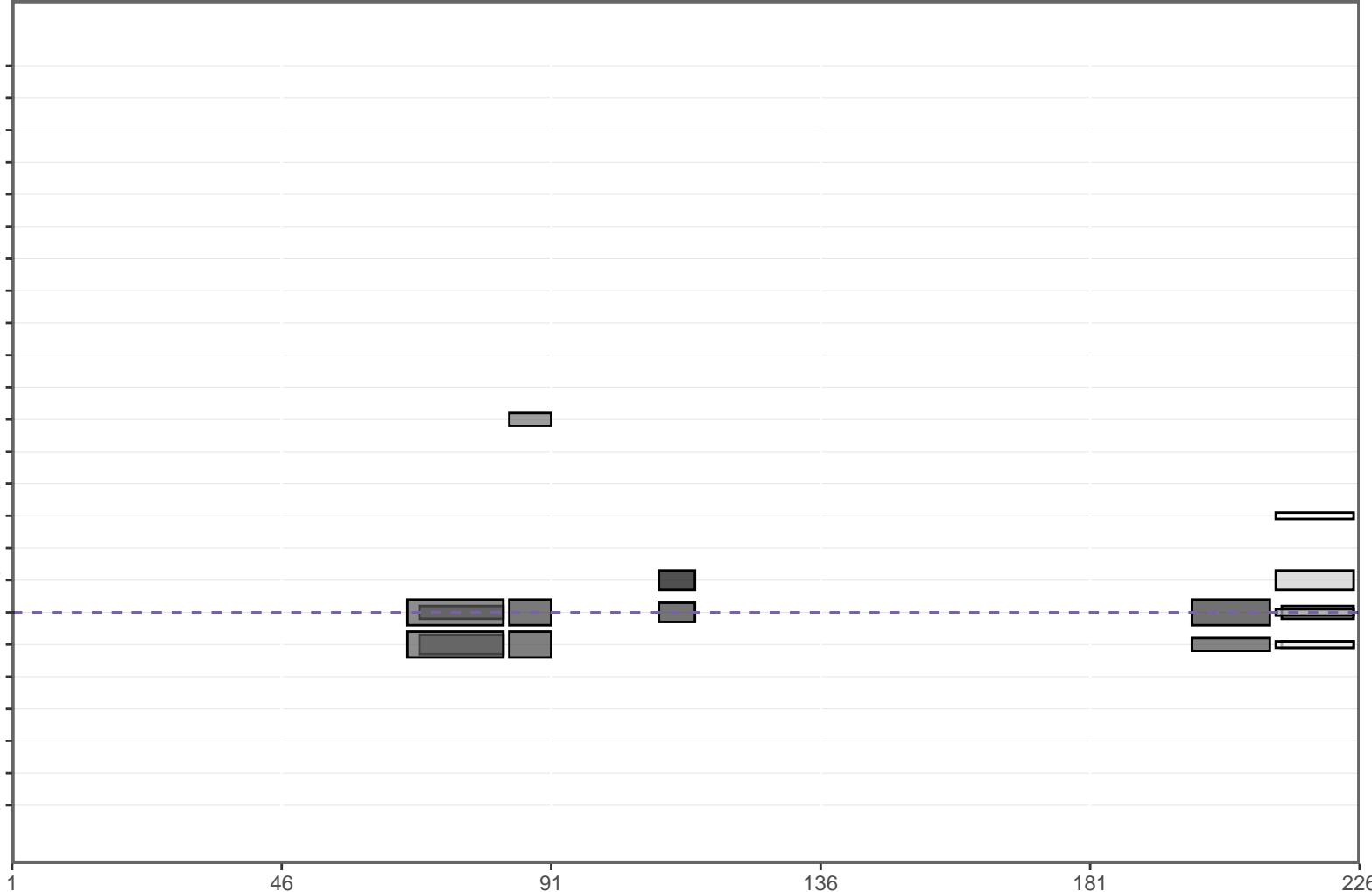
MW indication



Molecular weight

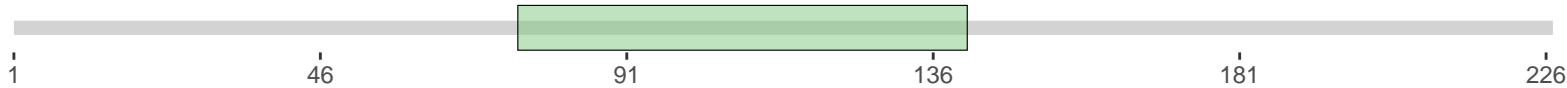


Gel Slice



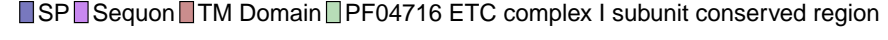
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

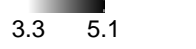
EDEGTRKAVESFTRHRLVVDGEEDEMEKRLGGGQVEUEEAGDELKLGHMNEWKPWGVDPDYEGEVIENDAPVPKHPLHRRPGLPEEFYKLEAVTSGTLETSSKDFEPAASGEGQPK

NbL03g12380.1 protein_SGT1_homolog [MW = 47.56 kDa]

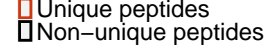
No. of times detected



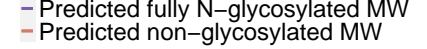
log(intensity)



Values from



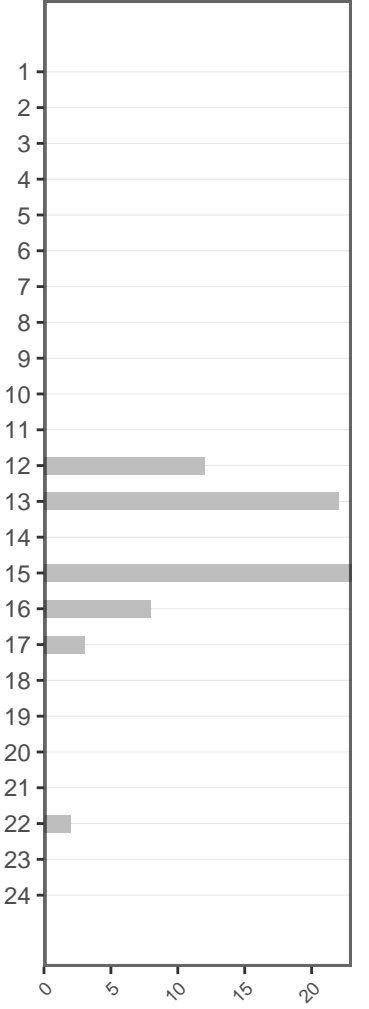
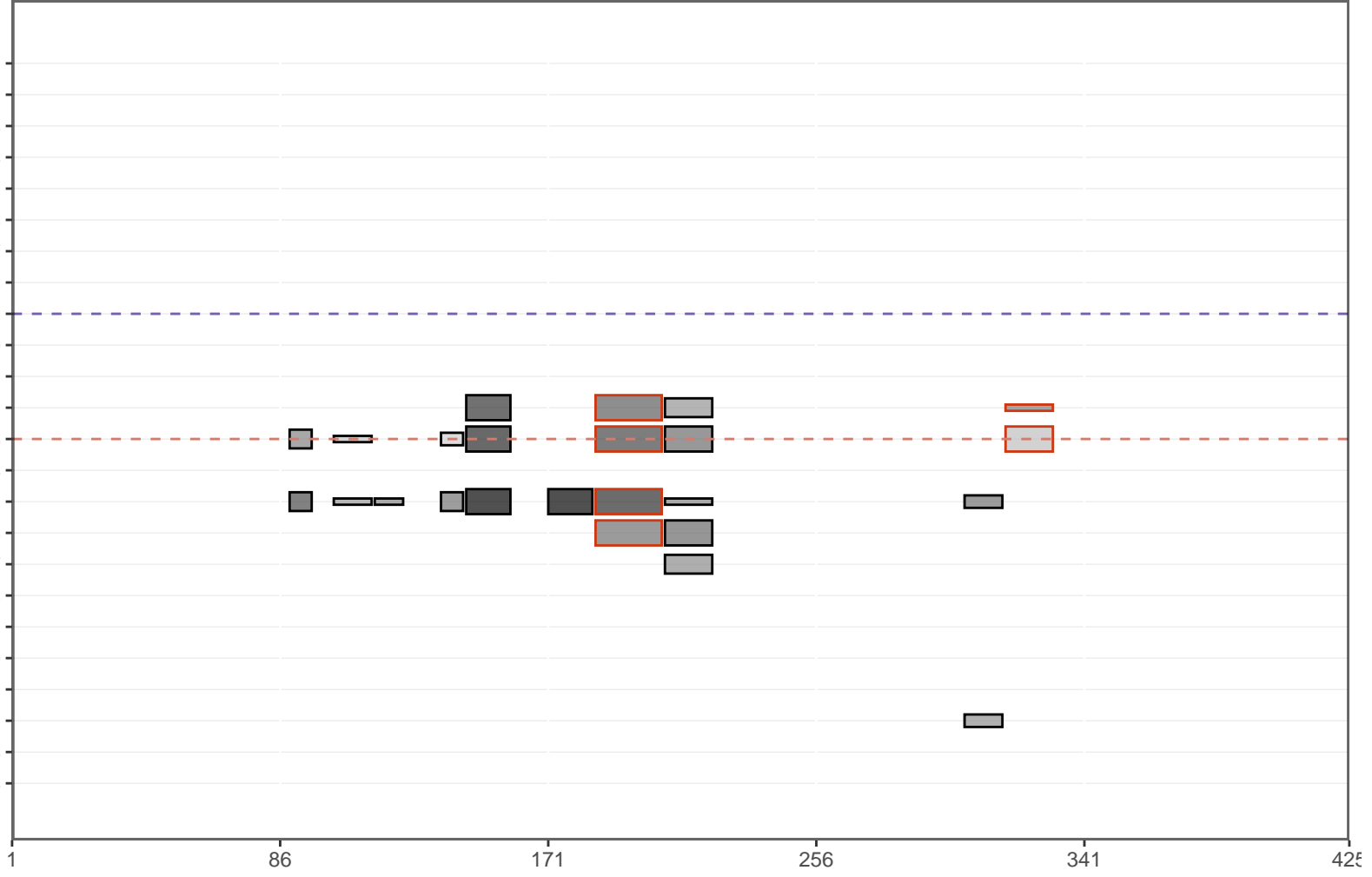
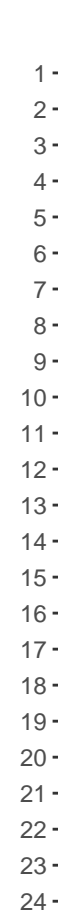
MW indication



Molecular weight

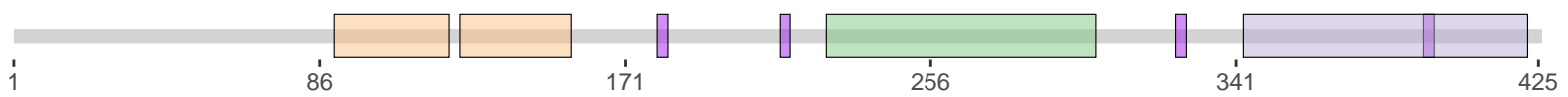


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VAPKDAQPTVNLISVGGGAARPKYRHEFYQKPEEVWVTFKAGIPAKNIVVDFGEQLVSVIOPGDETVSFGPRLFGKTPAKGRVEVMSTWIERLAKAEPLHWTSLEYTRGSAVQRFNVSDDAPRPVYVPSKLRHTDWDKLEAEVYKKEEKDEKLDGDAALNKFRDHYKDAEDTRRAMKSPFVESNGTVLSTNWKVEGAKKVEGSPDGMELKKWEI

NbL03g12220.1 heat_shock_protein_82 [MW = 80.76 kDa]

No. of times detected



log(intensity)



Values from



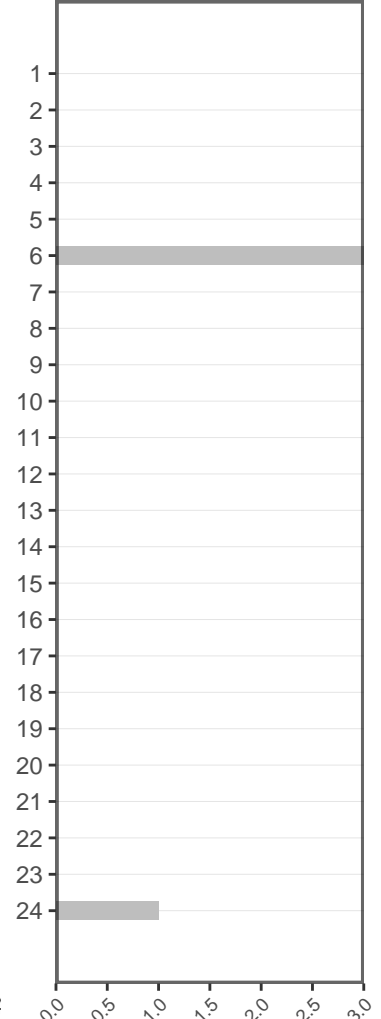
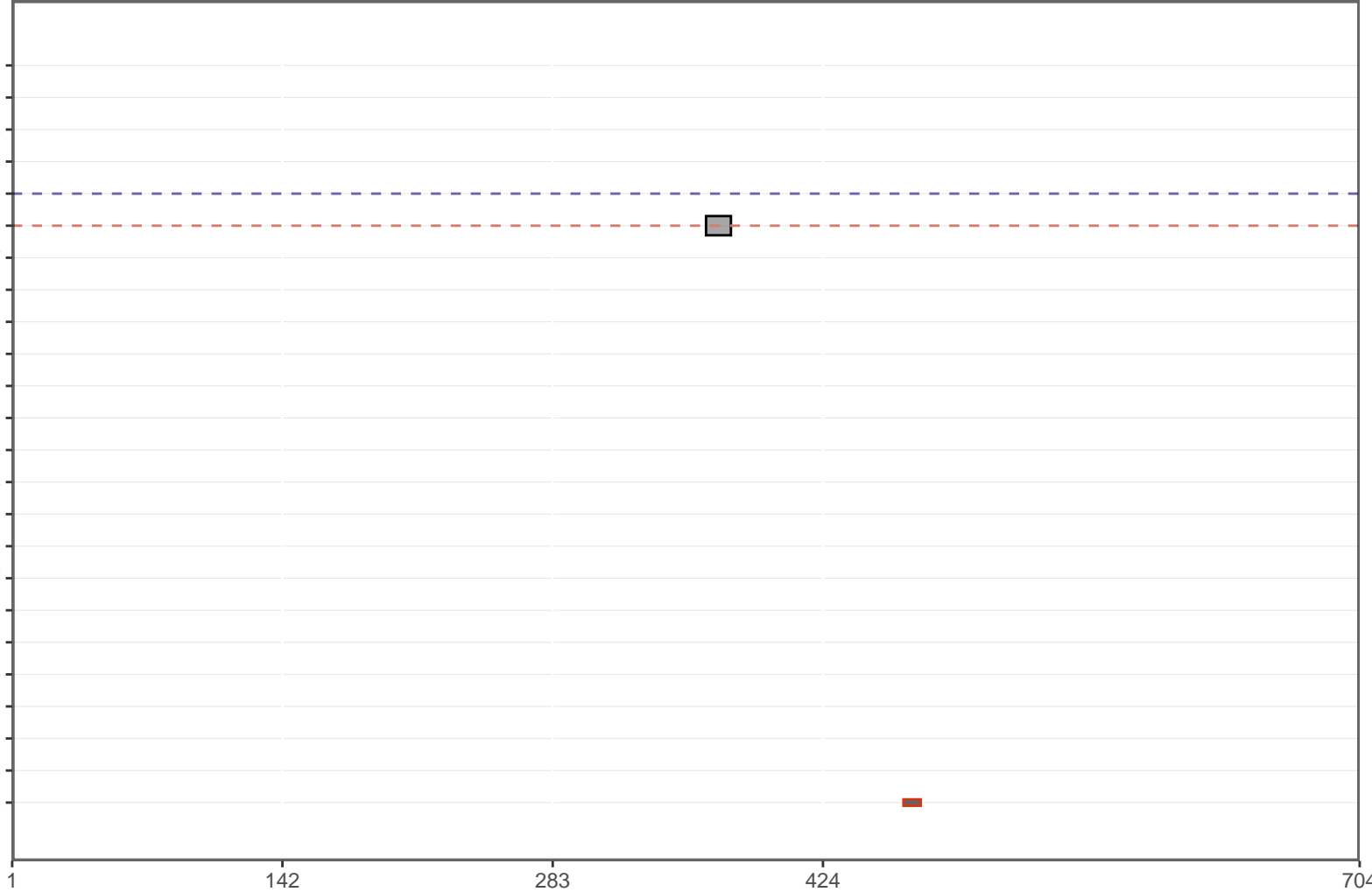
MW indication



Molecular weight



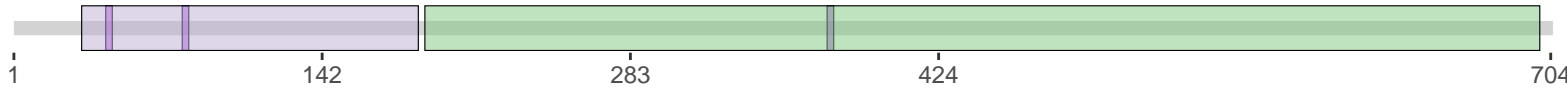
Gel Slice



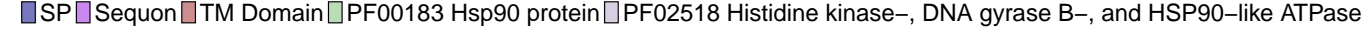
Protein length



Pfam domains



Pfam Description



Protein sequence:

/RRVFIMDNCEELIPEYLGFVKGVDSDDLPLNIGREMLQGNKILKIRKLVKKKGIEMFNIEAKEDYKFKYEFAGKNIKLGHEDEGSRRAKADLRLRYHSTKSGDEMTSLKDYVTRMKEGGKDYVYTGESKQAVENSPLERLKKKGGVEVLVMDAIDEYAVGDLKEYDGSKILVSATKEGLKDDSEEEKKKKKEKSFENLQKIKKLDGKVEKVVSDRIVDSPGGLVTGEYGWITANMERIMKAGALRDSMSVMSKKTMEINPQNGIMEELRKRRAEADKNDK

NbL03g12140.1 plastidial_pyruvate_kinase_2-like [MW = 66.32 kDa]

No. of times detected



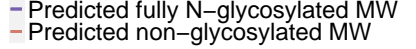
log(intensity)



Values from



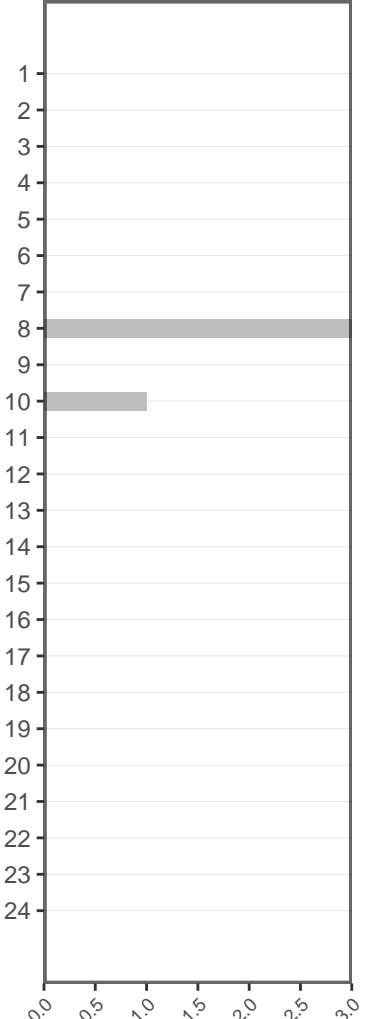
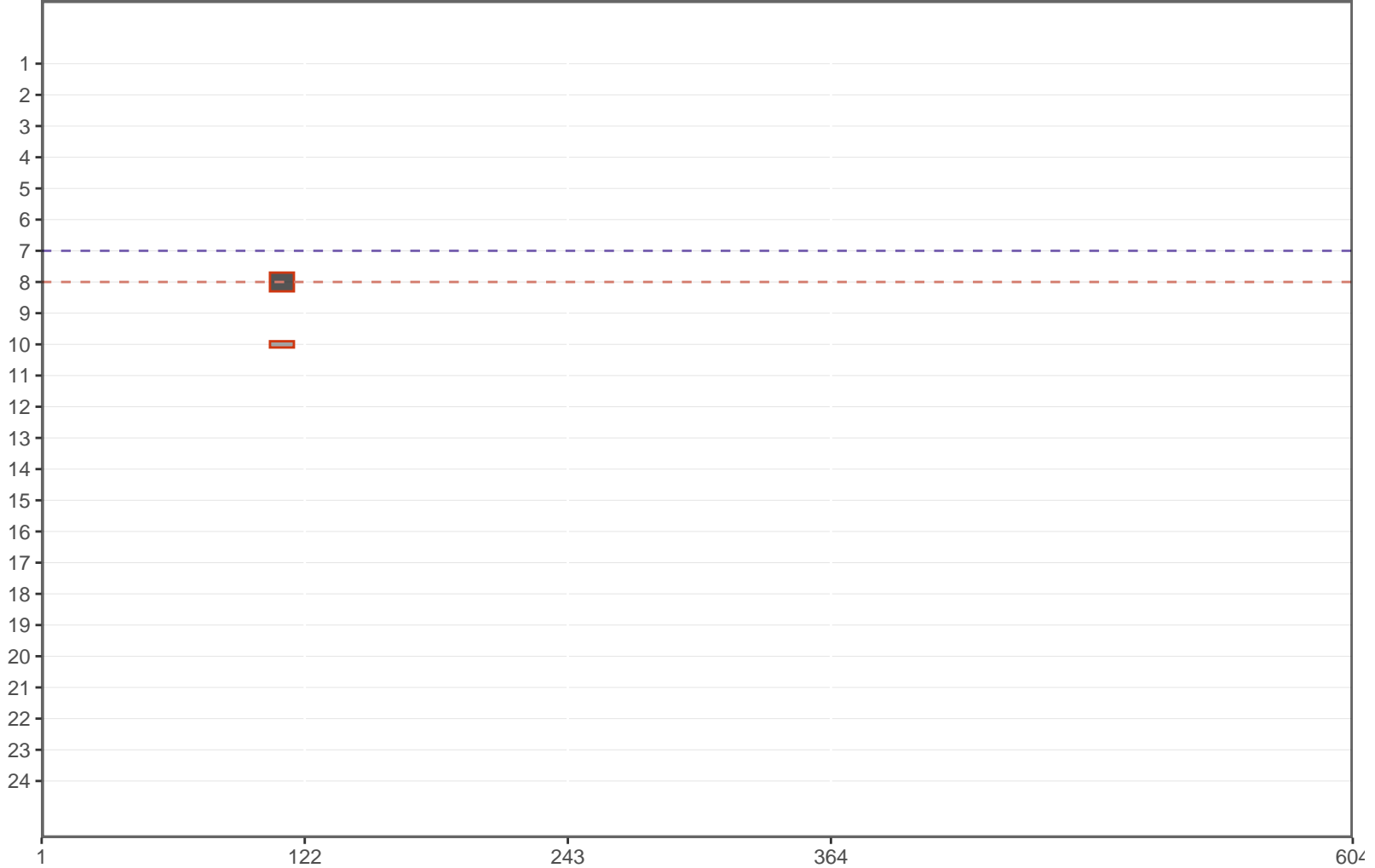
MW indication



Molecular weight



Gel Slice



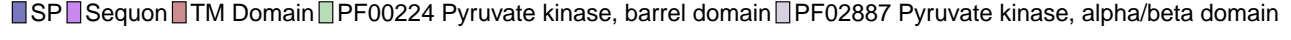
Protein length



Pfam domains



Pfam Description



Protein sequence:

HLNVRGKSTALPSTFKDWDKIFGVNGIDFYAVSFKDAVAVHELKLNKSGGADIKVVKESADSPNLIHSITASDGMVARGDLAGELPIEEVPLLQEEHINIGRSMGKAVVATNMLESMVHPTPTTRAEVSDAAVREGADAVMLSGETAHKGFKPLKAVKVMHTVBLRTEATVGGETPPNLGGAFKNHMESEMFAFHATMMGNTLGTISIVVETRTGFMAILLSHYRPGDTFAFTNDKKVQGRALALYGGVCPVMEFSEGAEETFTNALSLGKGGMVKVEGEQVALVQSI

NbL03g11990.1 sec-independent_protein_translocase_protein_TATB_chloroplastic [MW = 35.09 kDa]

No. of times detected



log(intensity)



Values from



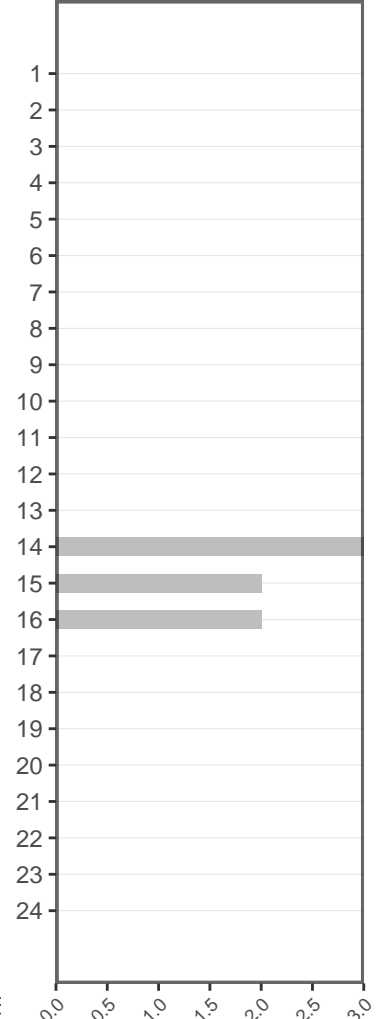
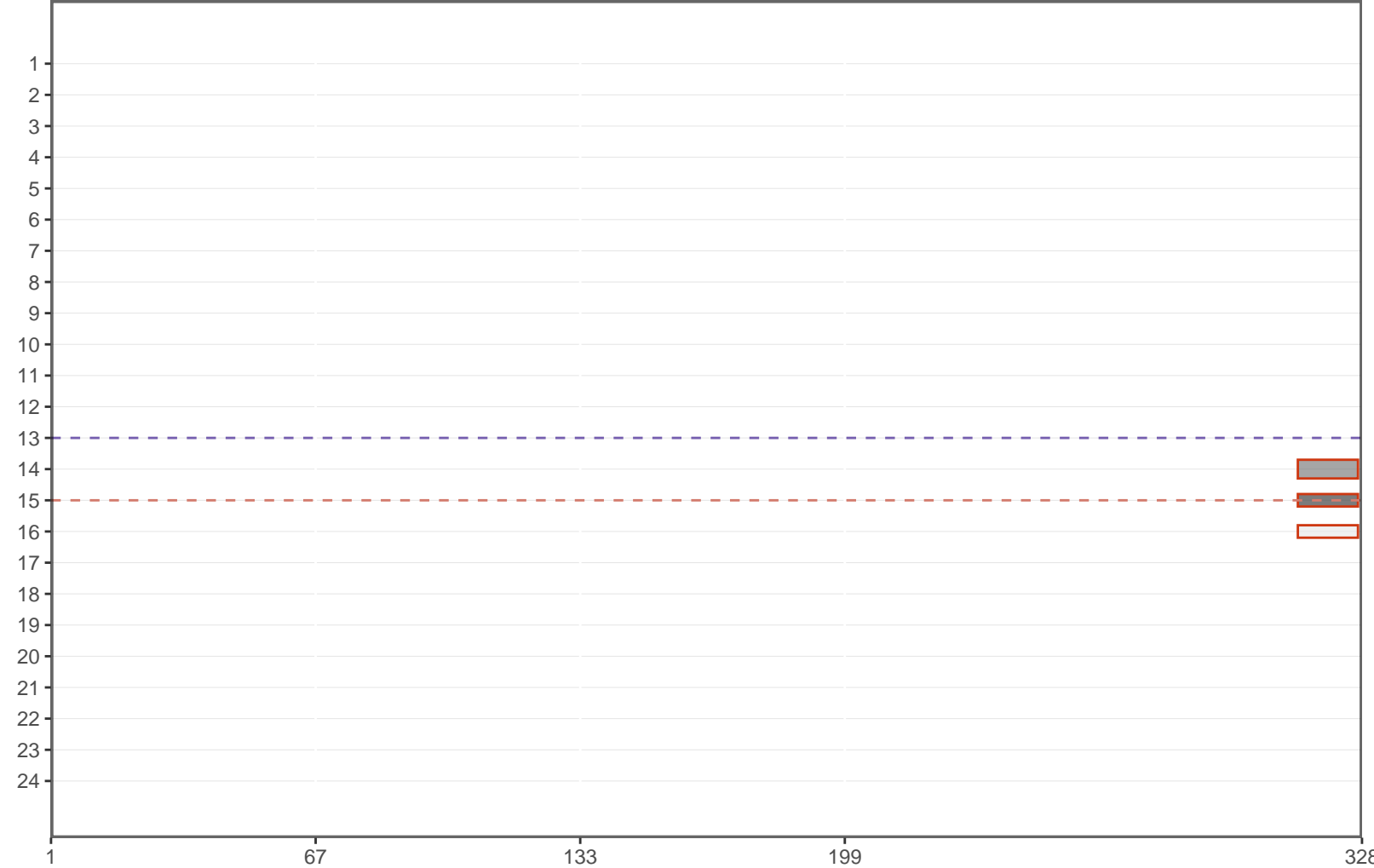
MW indication



Molecular weight



Gel Slice



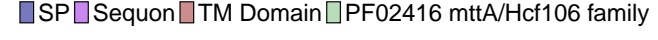
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKIGSGQDTIKSSTTRGGEVDPNGSPFIASSSEEDMERLLRIAEAEKQAEKDLASLLESGSEERTVGVQVADNSGSAVSTEDYIKITEEQLKAAAGQGNESGPEIGQISSNAGLSGADNSGSSDQAVSTDEVKITEGGPSPQGLSNAQGLLEETLKEAASAPPSGQKPESET

NbL03g11960.1 protein_SRC2_homolog [MW = 34.9 kDa]

No. of times detected



log(intensity)



Values from



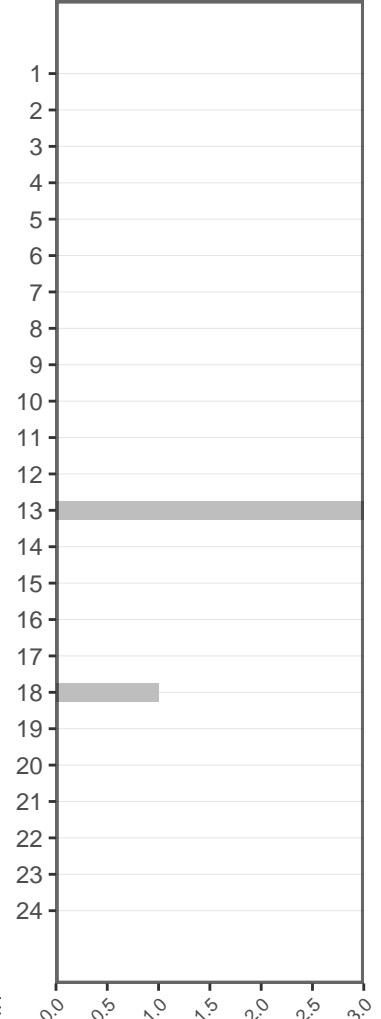
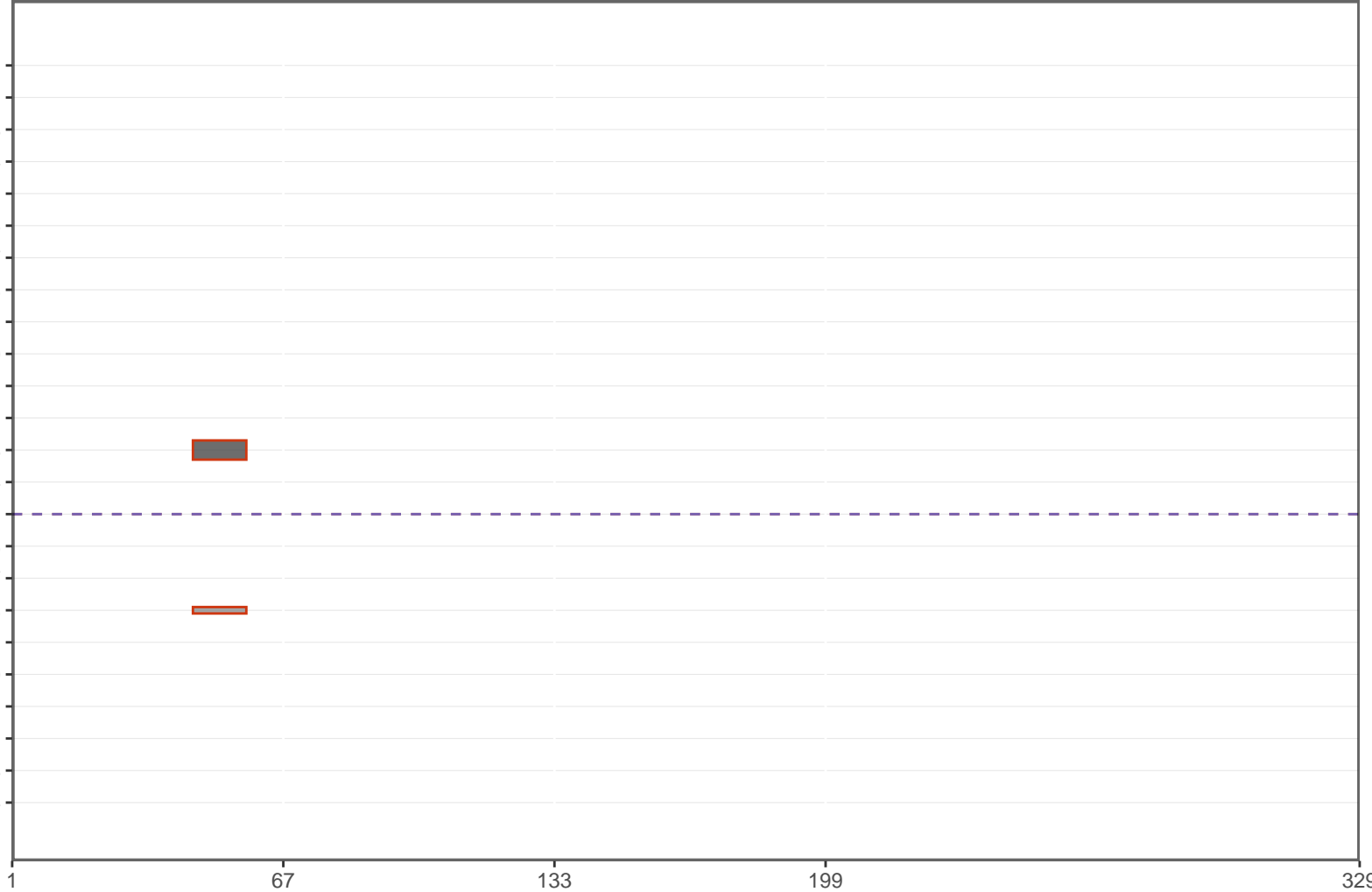
MW indication



Molecular weight



Gel Slice



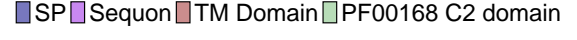
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISRDYPAAPFPQFYGGSYGAPSPAPSAAPQPVGGSEYGAAPFYAAPPSGYPYSAAPAPAPFYGGGGPNYGAAPPAPYSGGGSYGGPQYSMTGYGGGGNYYGASVYGGQSGYKCEEEKKKGKFGGMGLGAGLAMSAWAGALGGLAISEGIDHEDNIADKAAEKVEDDLADDYDGGDF

NbL03g11930.1 short-chain_dehydrogenase_TIC_32_chloroplastic-like [MW = 39.32 kDa]

No. of times detected



log(intensity)



Values from



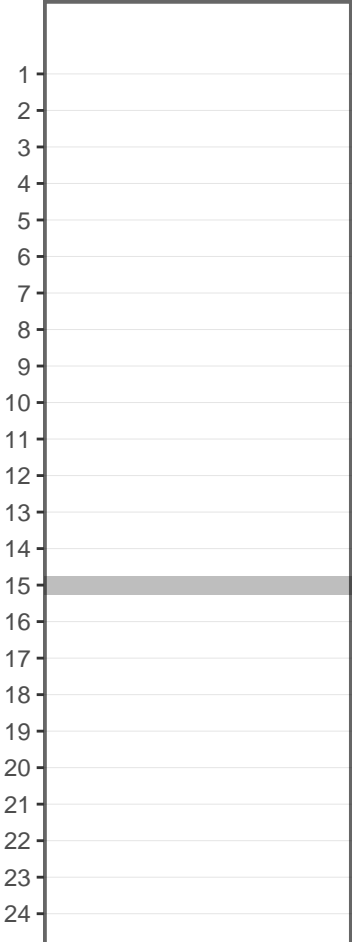
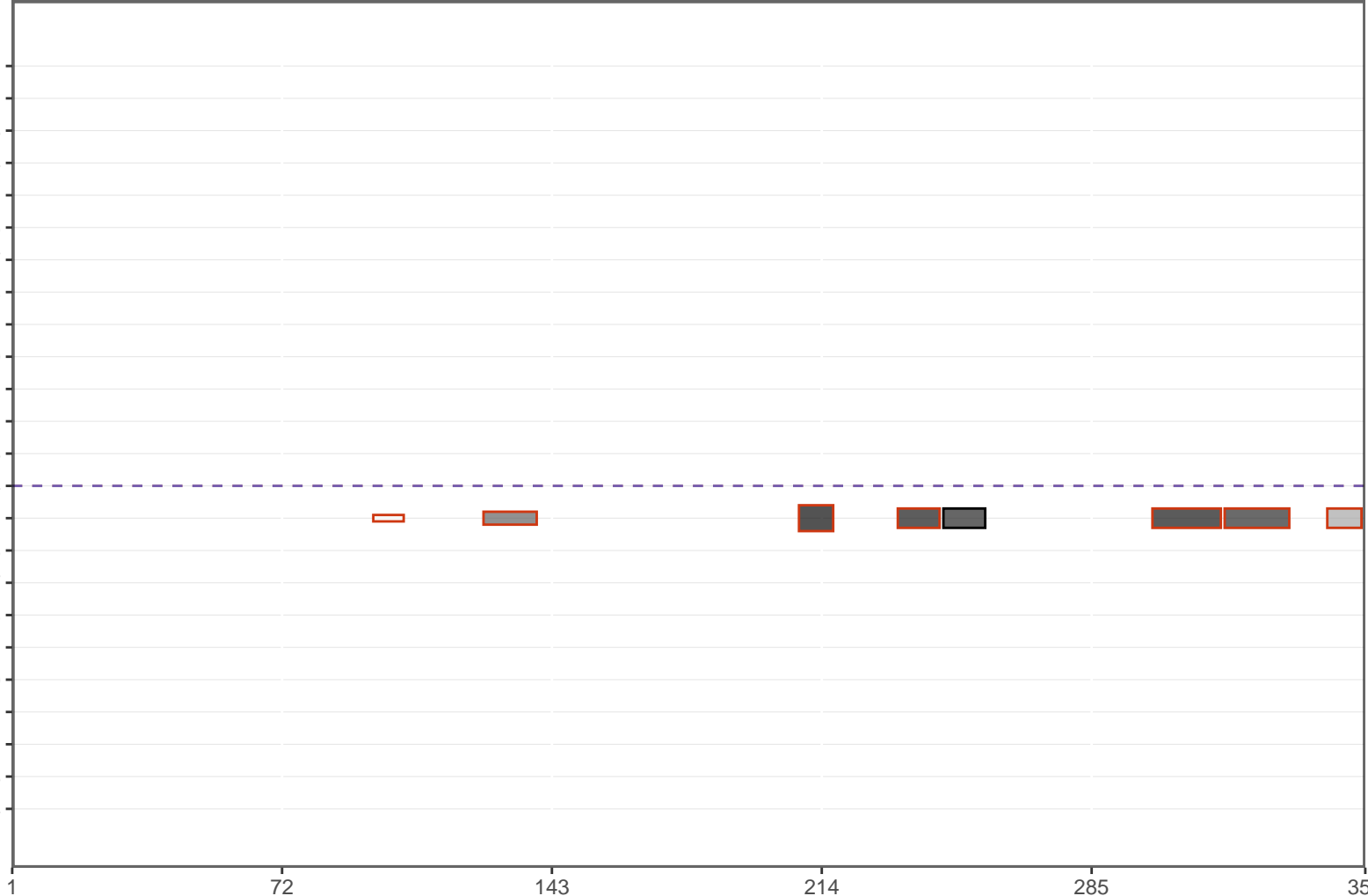
MW indication



Molecular weight



Gel Slice

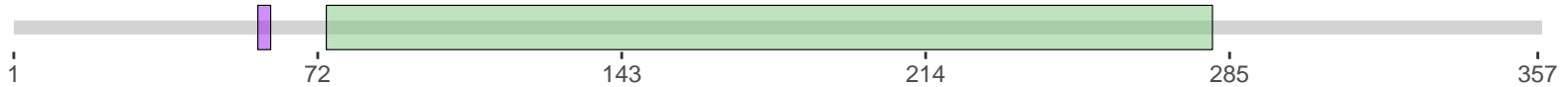


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

MLSKDNIELQFATNHLGHLELTLNLLKRNKTRKTRKREGRRVNWASEAHRFAVREGVRFKINDRKSYNFSGAVQGSKLANKLHANELTRRLKEDGAEIANSLHPGMITNLFPHMGSVFDGLVNLKLVKKNVQGSASTTQYLALHPQVKGVSQGEVFLDNIATTTAKKDMDLAKRLWDFSMDLVK

NbL03g11800.1 pectin_acetyltransferase_9-like [MW - SP = 17.07 kDa]

No. of times detected



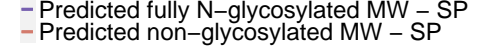
log(intensity)



Values from



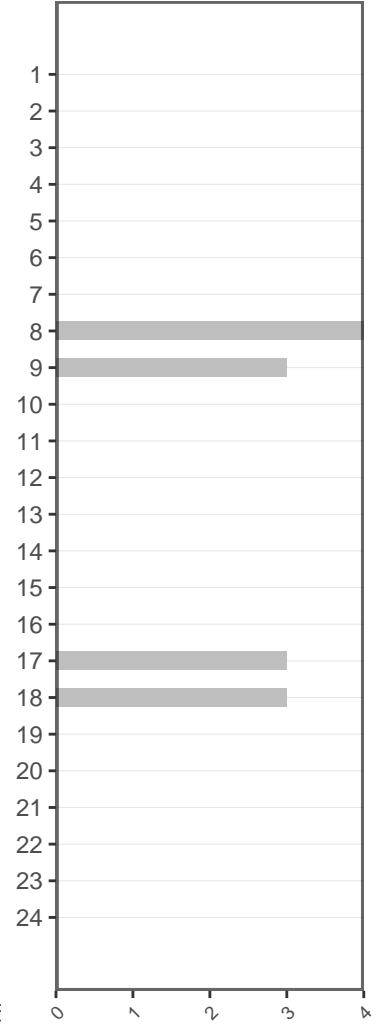
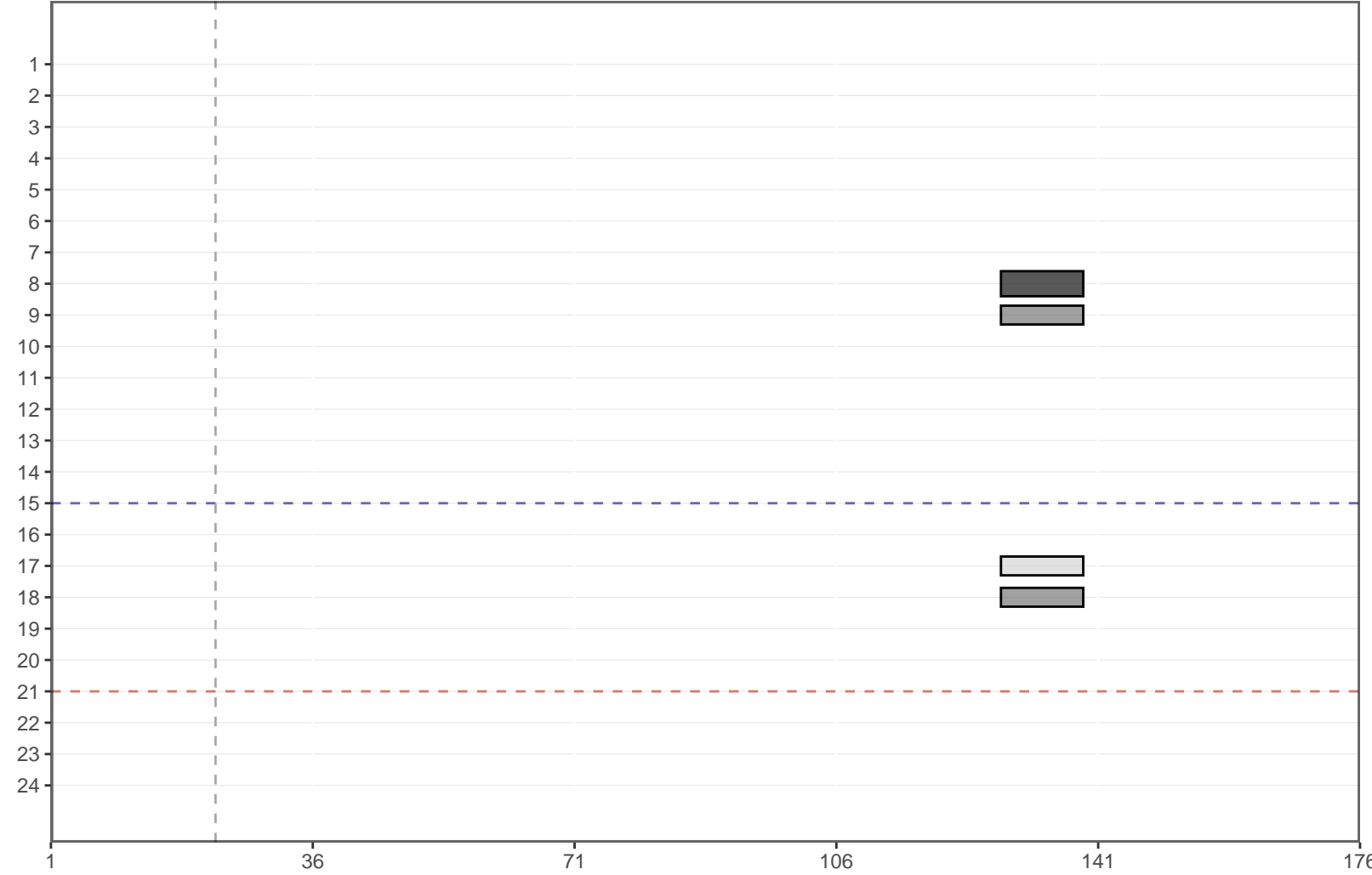
MW indication



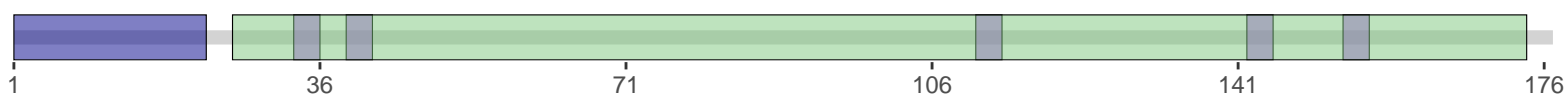
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

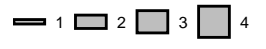


Protein sequence:

GWVNDKSCLDLRSTTRHGSTRYMNKWEVFGILSNNAFLNPDFYVWNRVRLRYCDGASAFAGDSKFNQTYR6SSSERNGSTLLYFRGQRWKAHLDLPL

NbL03g11790.1 tripeptidyl-peptidase_2 [MW = 149.42 kDa]

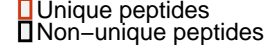
No. of times detected



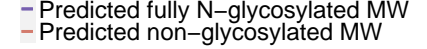
log(intensity)



Values from

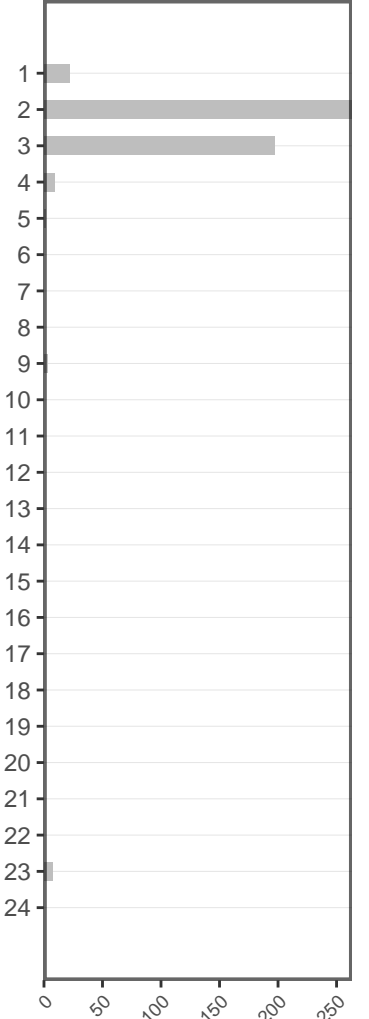
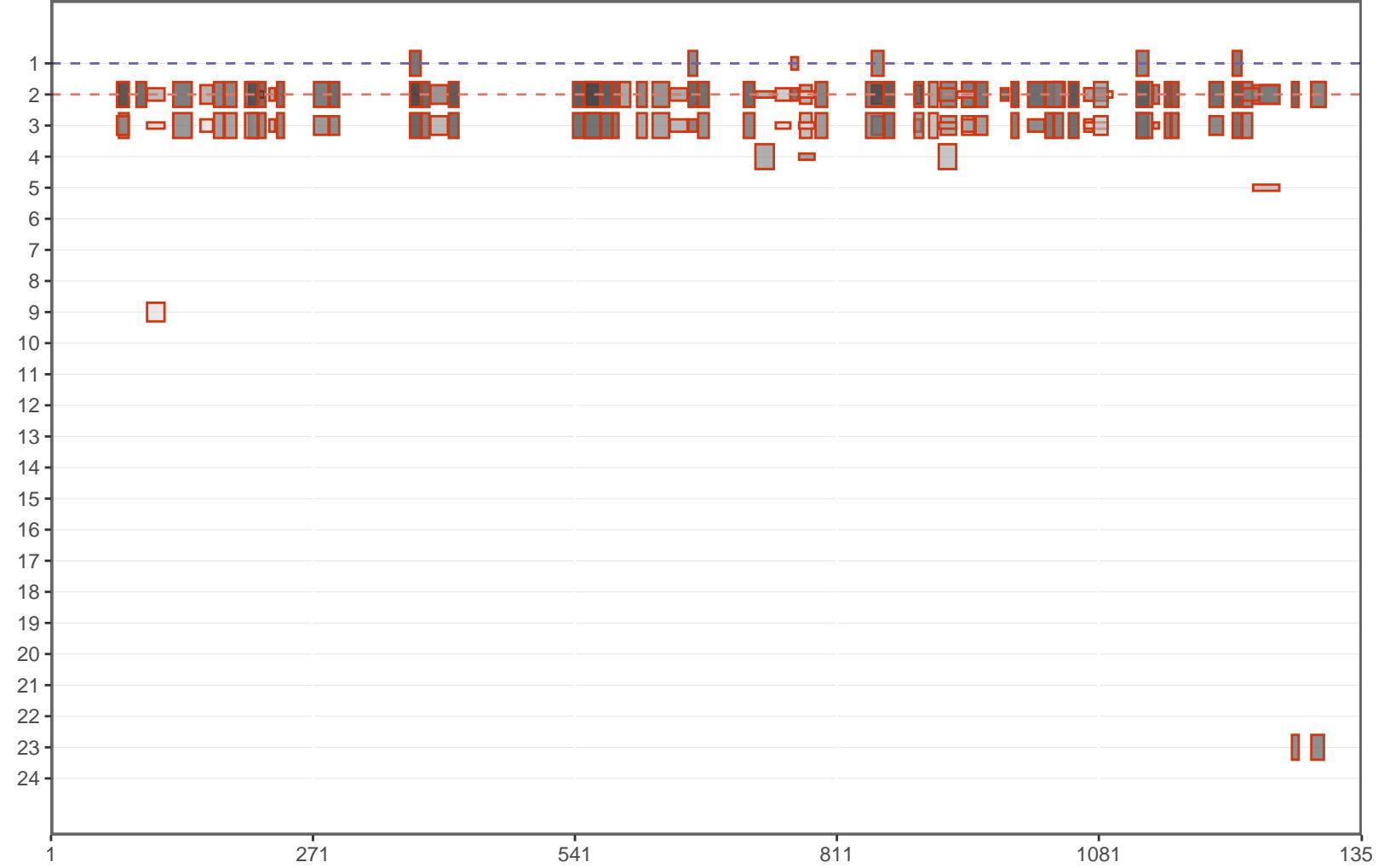
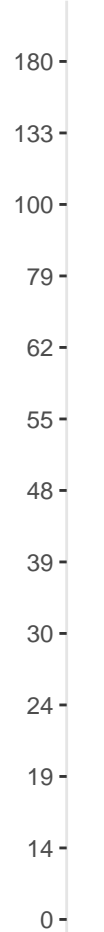


MW indication



Molecular weight

Gel Slice



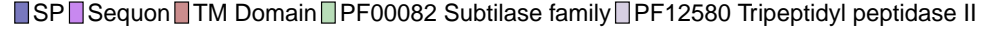
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KLFSTGDAVYKAPFYLHLLHNGRFSFVADPTNLSGHLHYVEVGGDSKSPWRGFLFRIPVITTKPTAVKRRPPLSFQSGFVPGIERRRFEVPGATVVEATMRTYGFDTARRFDITVQLGFLQRPKWESWATFSPPSKSFAFRVEGGRTMELAWQFVSGGGSHETTVDFAFRGINSKEEVLDGSEAPVRIDEALLAERLVPVSAVLKIRVYRPRIDAKLHALSADRDKLPSGKQRLALTUYKLEDEGAELKPPQPLLNRYDYNKFEFGFYMISDYNKRVYHMG

NbL03g11750.1 oxalate--CoA_ligase-like [MW = 56.21 kDa]

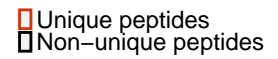
No. of times detected



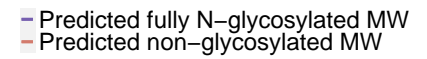
log(intensity)



Values from



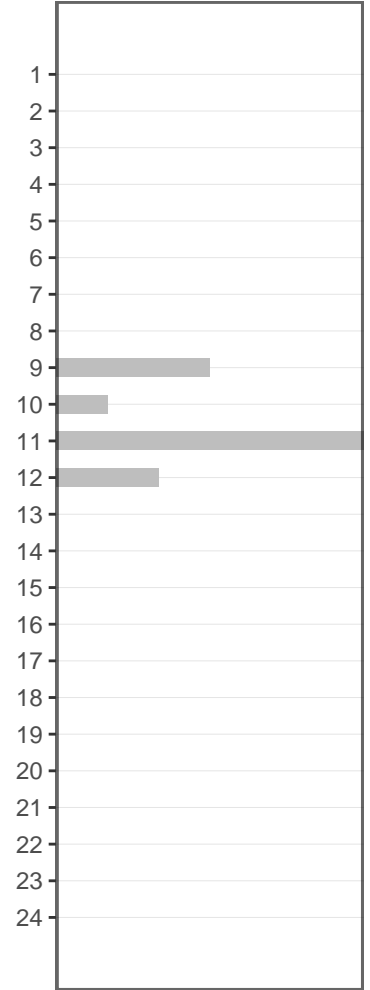
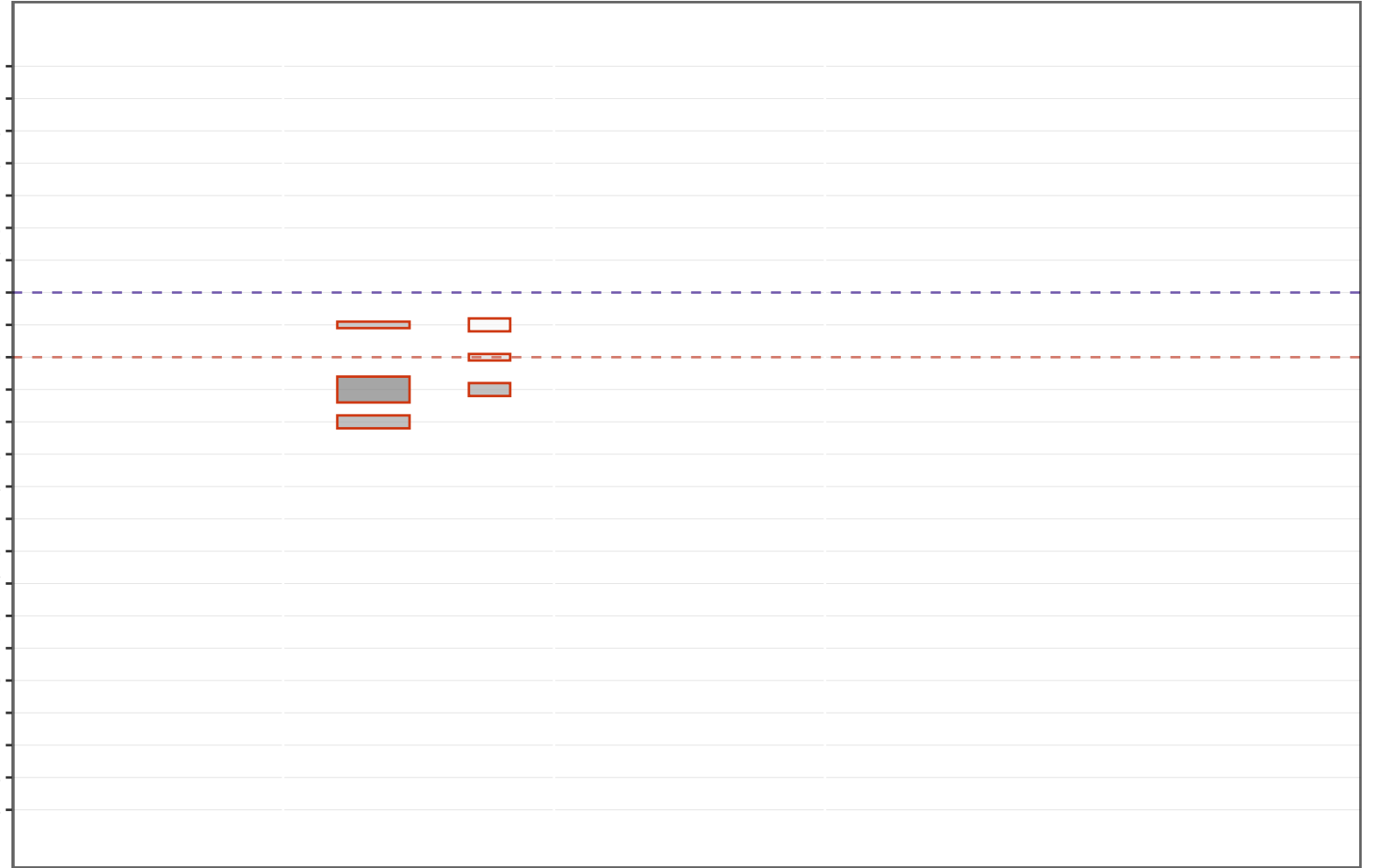
MW indication



Molecular weight



Gel Slice



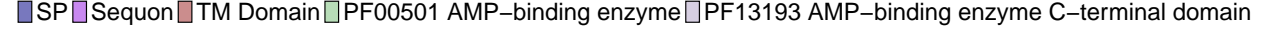
Protein length



Pfam domains



Pfam Description



Protein sequence:

NATVYTAVPTHQILLDGHLSKPESEYKLRFRIRGSAALAPVMMARLEEAFGAPVLEAVAMTEATHLMASNPLFENGPHIPGSGVKPVGQEMAILDENGVIGGANAKGEVGRISPVTKGKYNPEANKSAFQGFVHTGDGVYLDSDGVLHLVGRIKELNRRGGKSPFIEVDALVLSHAEIAQAWAFGVDPDKYGGEEINAVIPREGSNDIETELRFQKKNLAARVKKVFMFDLPLKATATGKIGRRLVAEHLAQISTKVKPKFGA

NbL03g11650.1 remorin-like [MW = 23.17 kDa]

No. of times detected



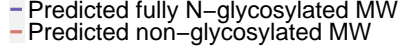
log(intensity)



Values from



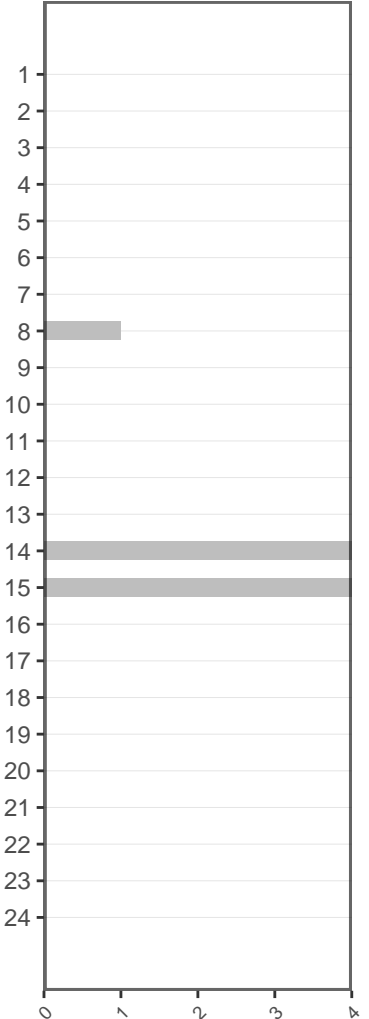
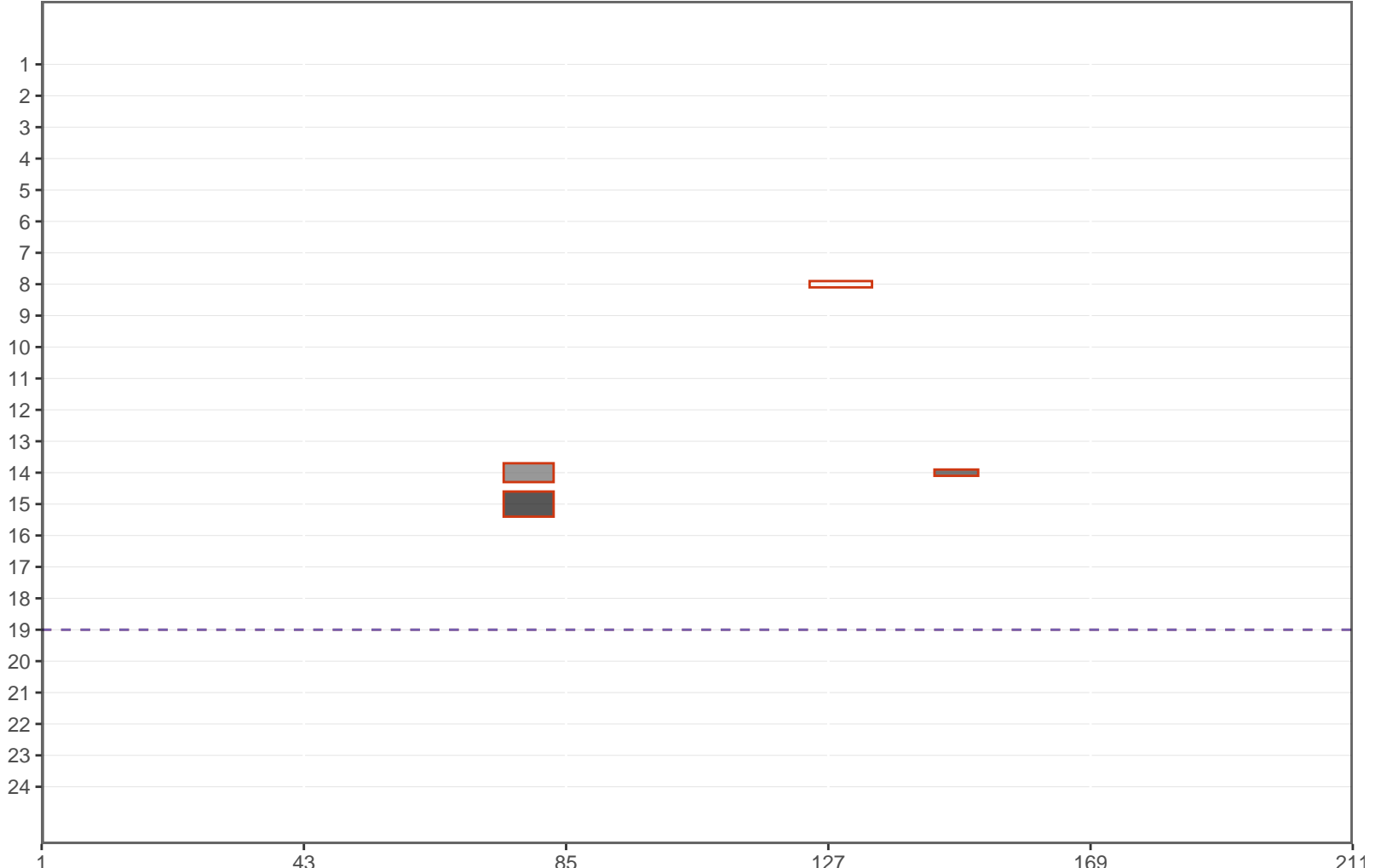
MW indication



Molecular weight

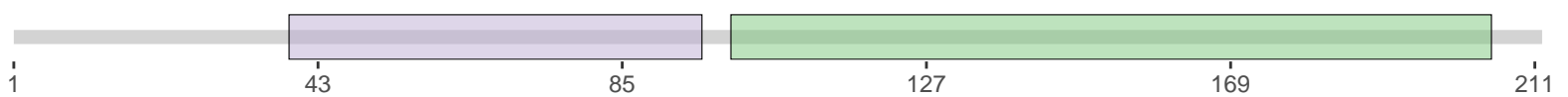


Gel Slice



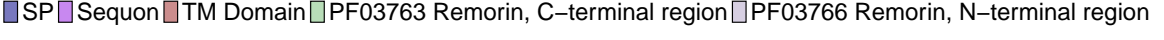
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LSARVATEKRLSLIKAWEESEKKAENKAGKVKVSAIAAWENSKKANLEAELEKMKMEEQLEKKAIEYIEKMRNKALLHKEAEKRAMIAKRGEDLLKAEELAAKYRATGTAIPKLLGGP

NbL03g11550.1 3-hexulose-6-phosphate_isomerase [MW = 21.42 kDa]

No. of times detected



log(intensity)



Values from



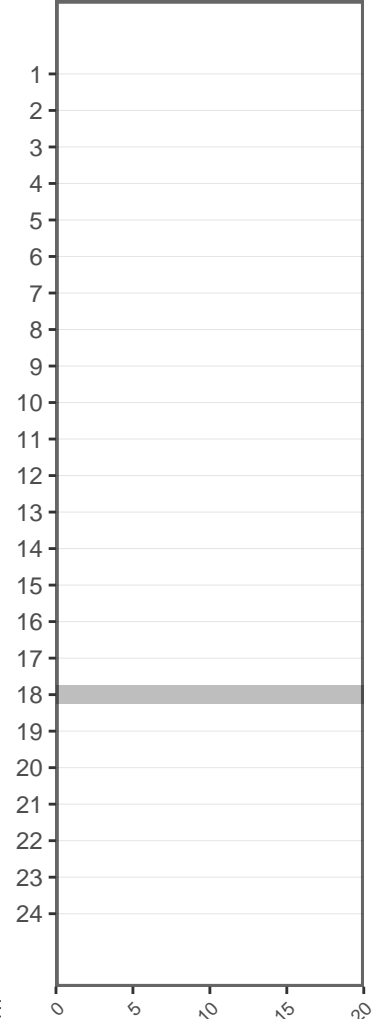
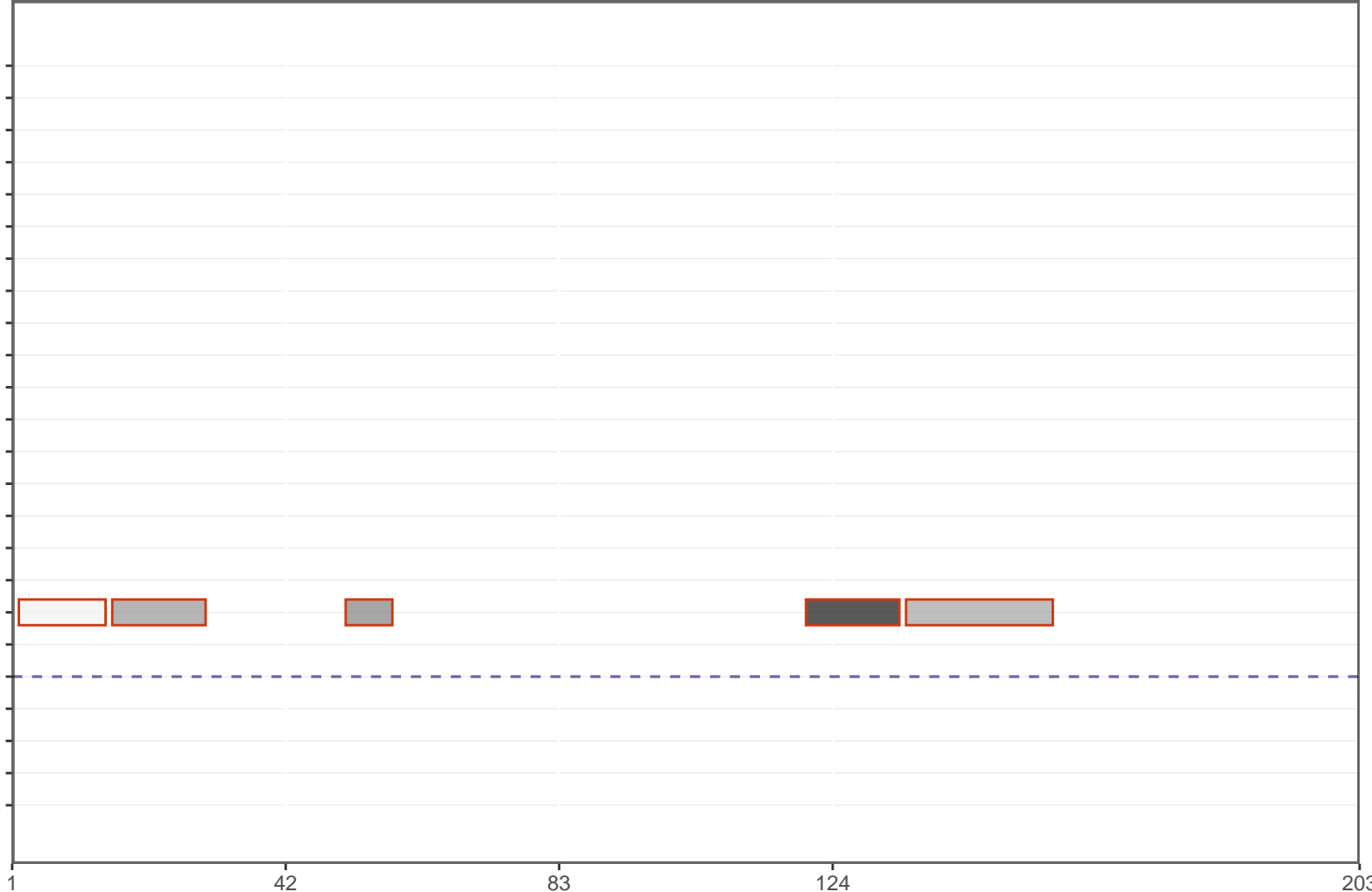
MW indication



Molecular weight



Gel Slice



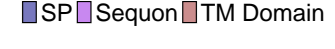
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RPPDLLIASAGFGFSTVDAAGVAKSNGARVLLTADPEGGSSVWYASVWVIRPQTMADDSAGDAERERPLLMGSLVEGAMFVLFEMVVKFLADLKQSPVARRRHTLE

NbL03g11380.1 putative_4-hydroxy-tetrahydrodipicolinate_reductase_3_chloroplastic [MW = 26.96 kDa]

No. of times detected



log(intensity)



Values from



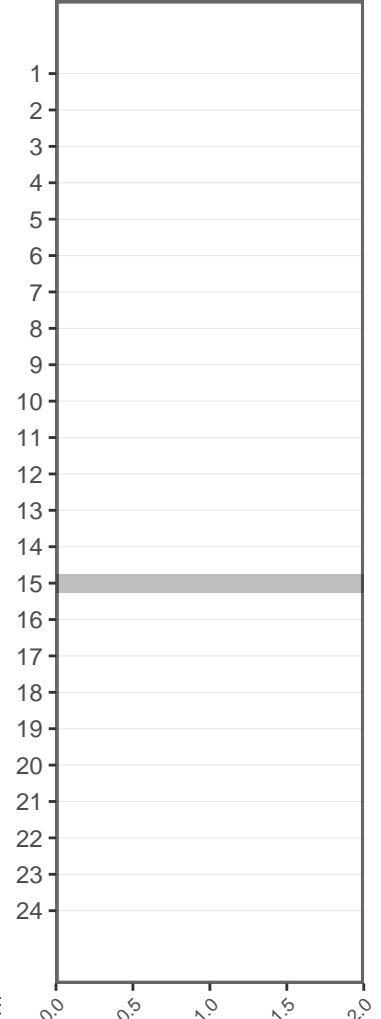
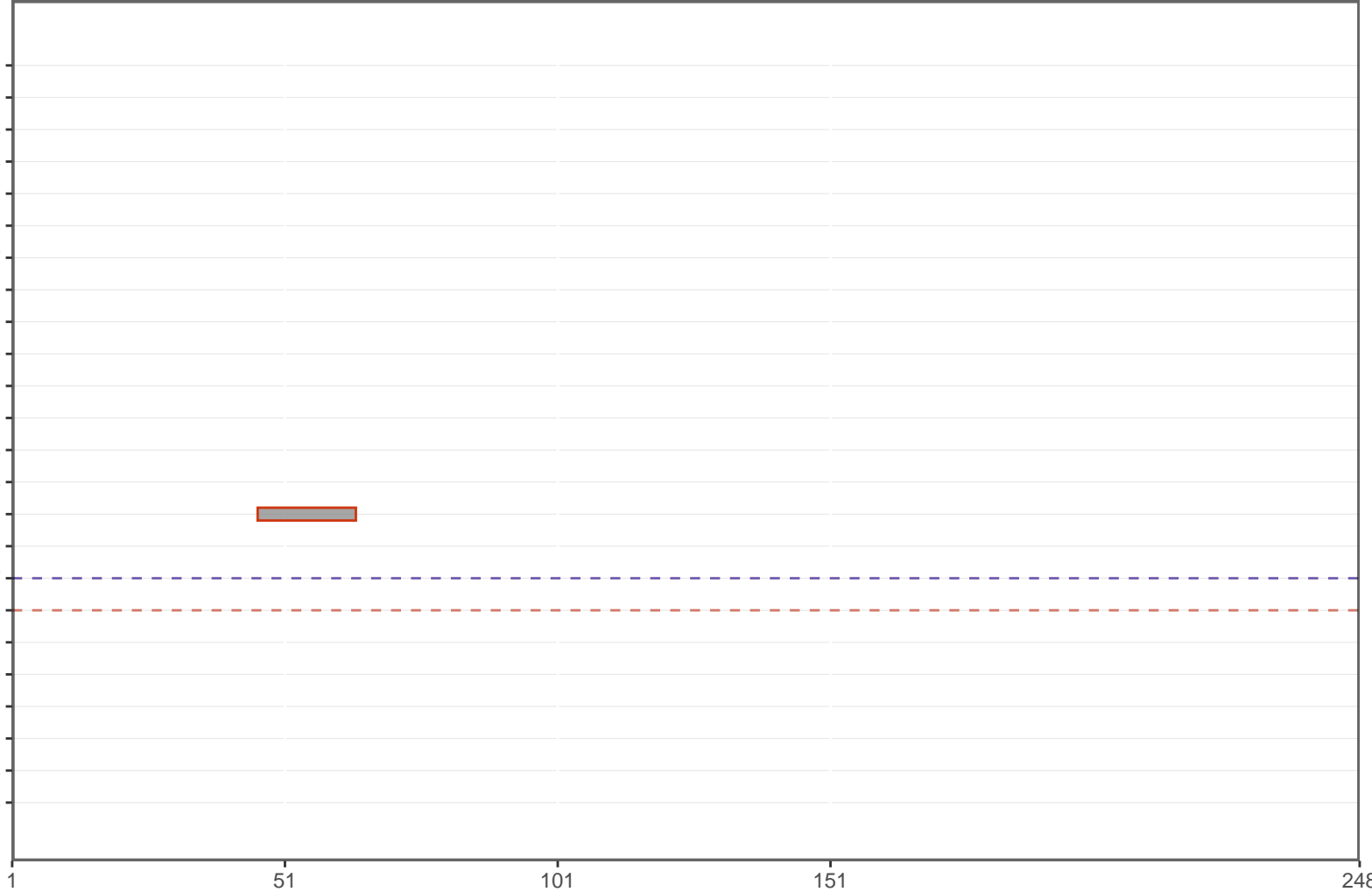
MW indication



Molecular weight



Gel Slice



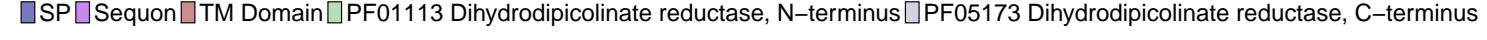
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

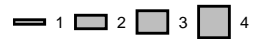


Protein sequence:

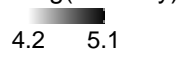
LDQAISASFIYINVEVESRANAVDFPTQDAVGIANNLNLSGGLYNREDISTDIPARGGILGEDGVYVHSLVPLGLPSSTSYVFEKPGEVYTLQHDITDVGCLMPGLIARLFAERTWSMAWRSFYKQGTVRG

NbL03g11080.1 ATP-dependent_Clp_protease_ATP-binding_subunit_CLPT1_chloroplastic-like [MW = 25.99 kDa]

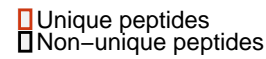
No. of times detected



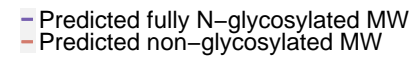
log(intensity)



Values from



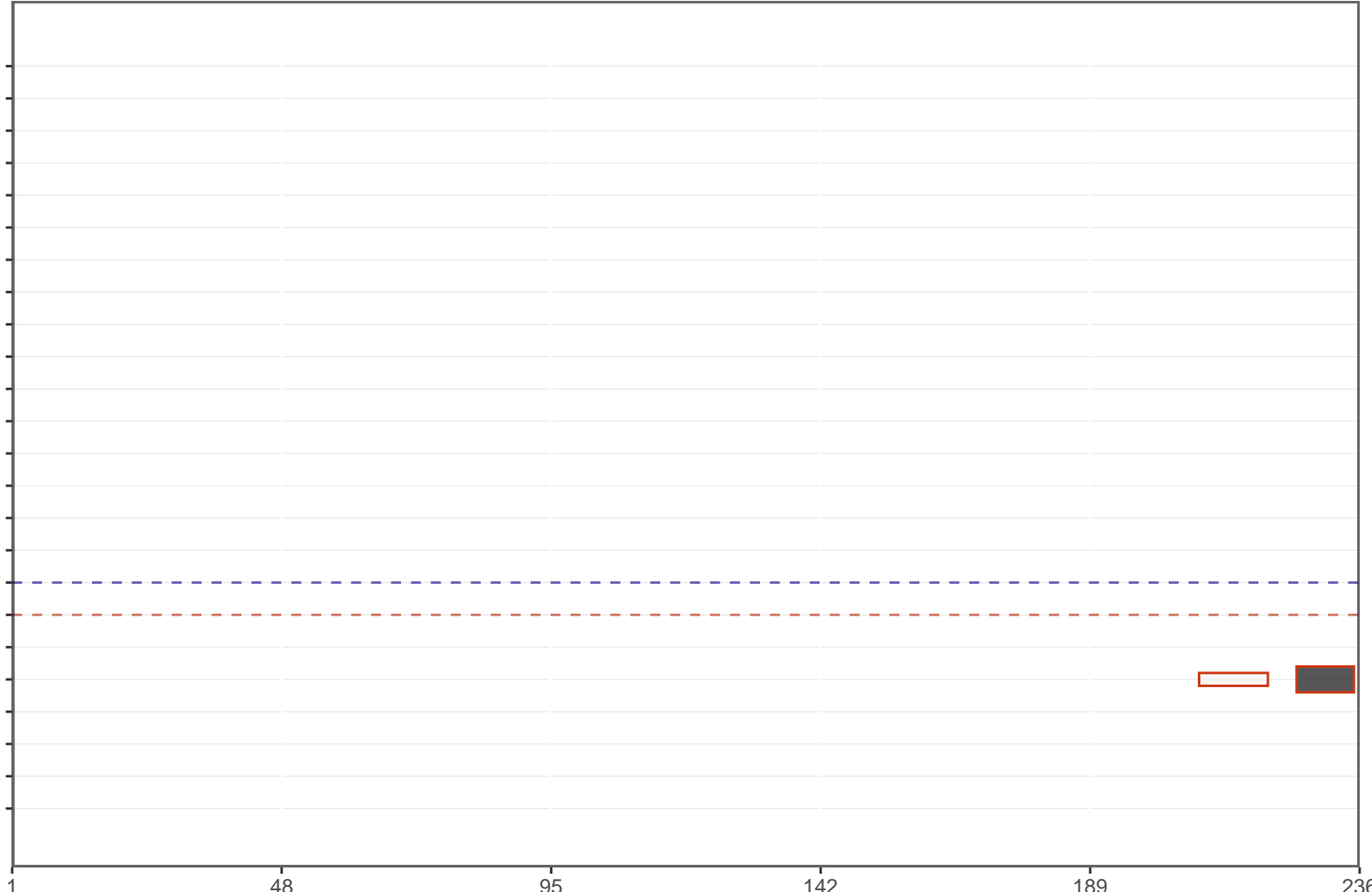
MW indication



Molecular weight



Gel Slice

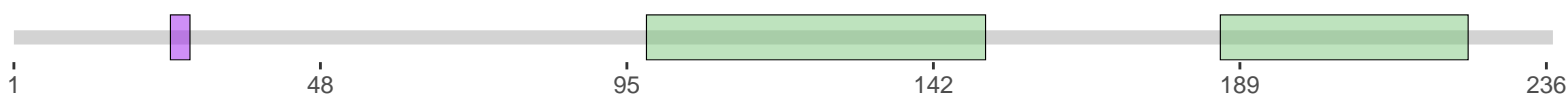


Protein length

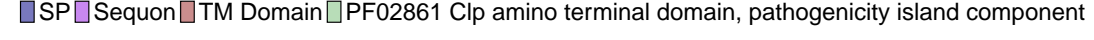


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KYPNTGTEALLMGALVEGTSAAKFLRANGVTLKVKREETVLLGKSDMYFFSFEPHPLTEPMQRALDWVDEKIKSGEGEITIAHLALGIWSEKESAGHKIMATLGFDDKARELANSMKDIEMSYT

NbL03g10900.1 UMP-CMP_kinase [MW = 26.78 kDa]

No. of times detected



log(intensity)



Values from



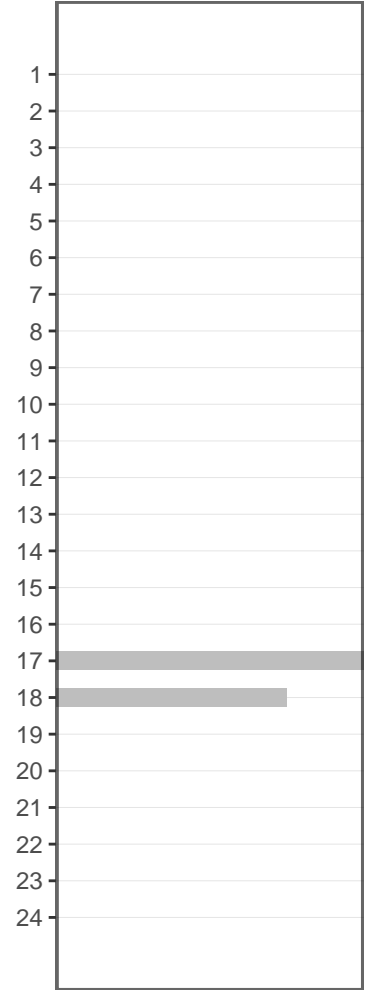
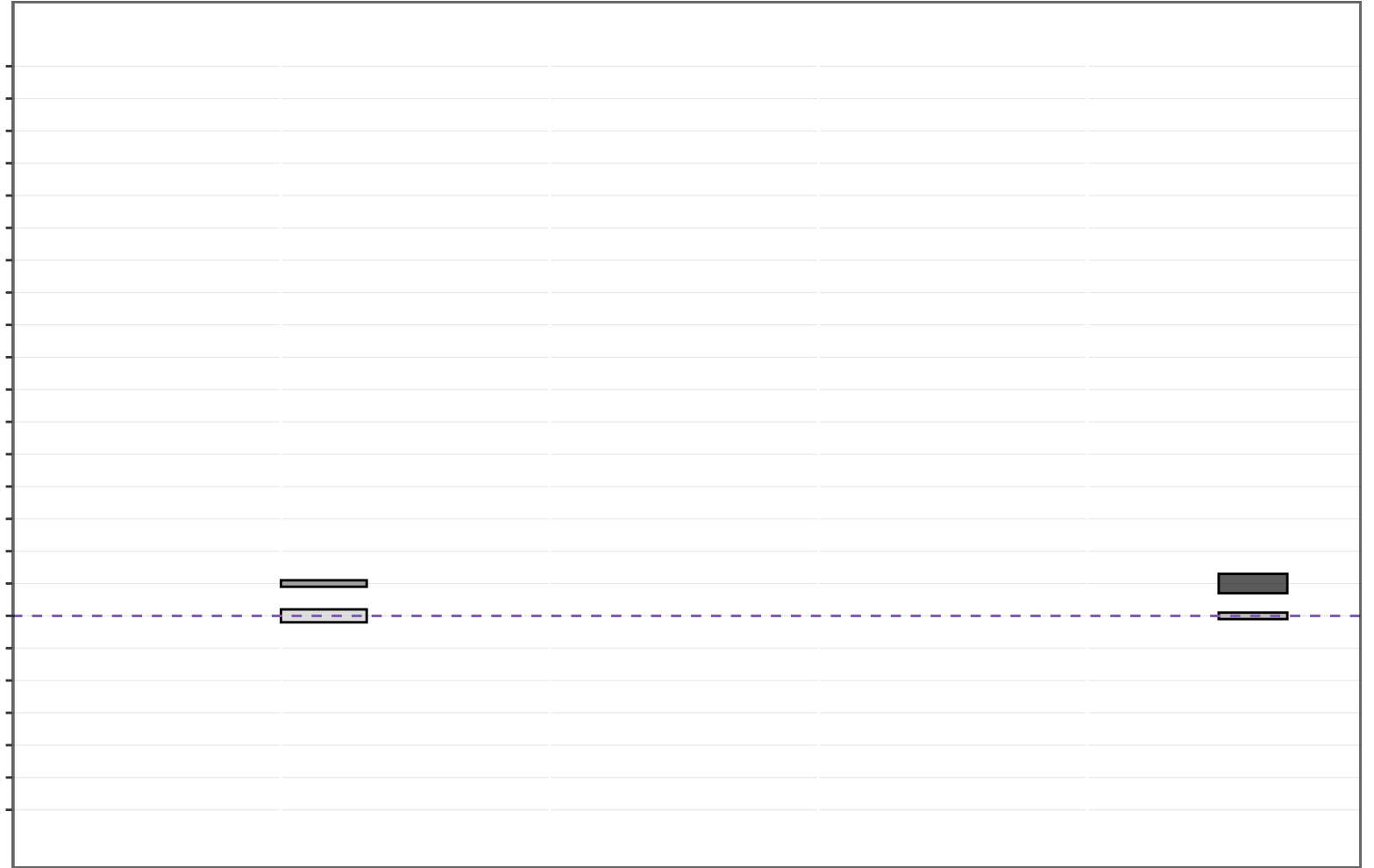
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

IEGSIAPSEVTVYKLRKAESAEHKKFLIDGFRBEENRMAVERIGAEPNVLFFDQPEEVMKRVLNREGRVDDNEHTVKEKLVKAVKTLFVAVNHAYKGGKLVKIDGTGTGEEIFERVPIFSLSSLV

NbL03g10880.1 21_kDa_protein-like [MW - SP = 18.69 kDa]

No. of times detected



log(intensity)



Values from



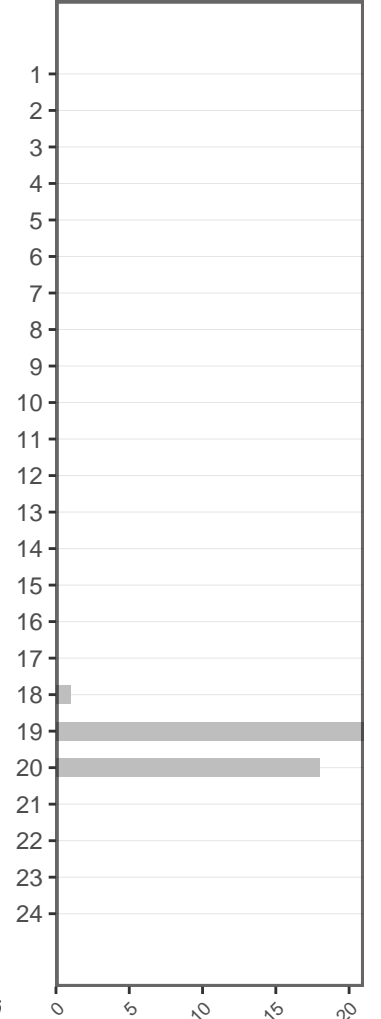
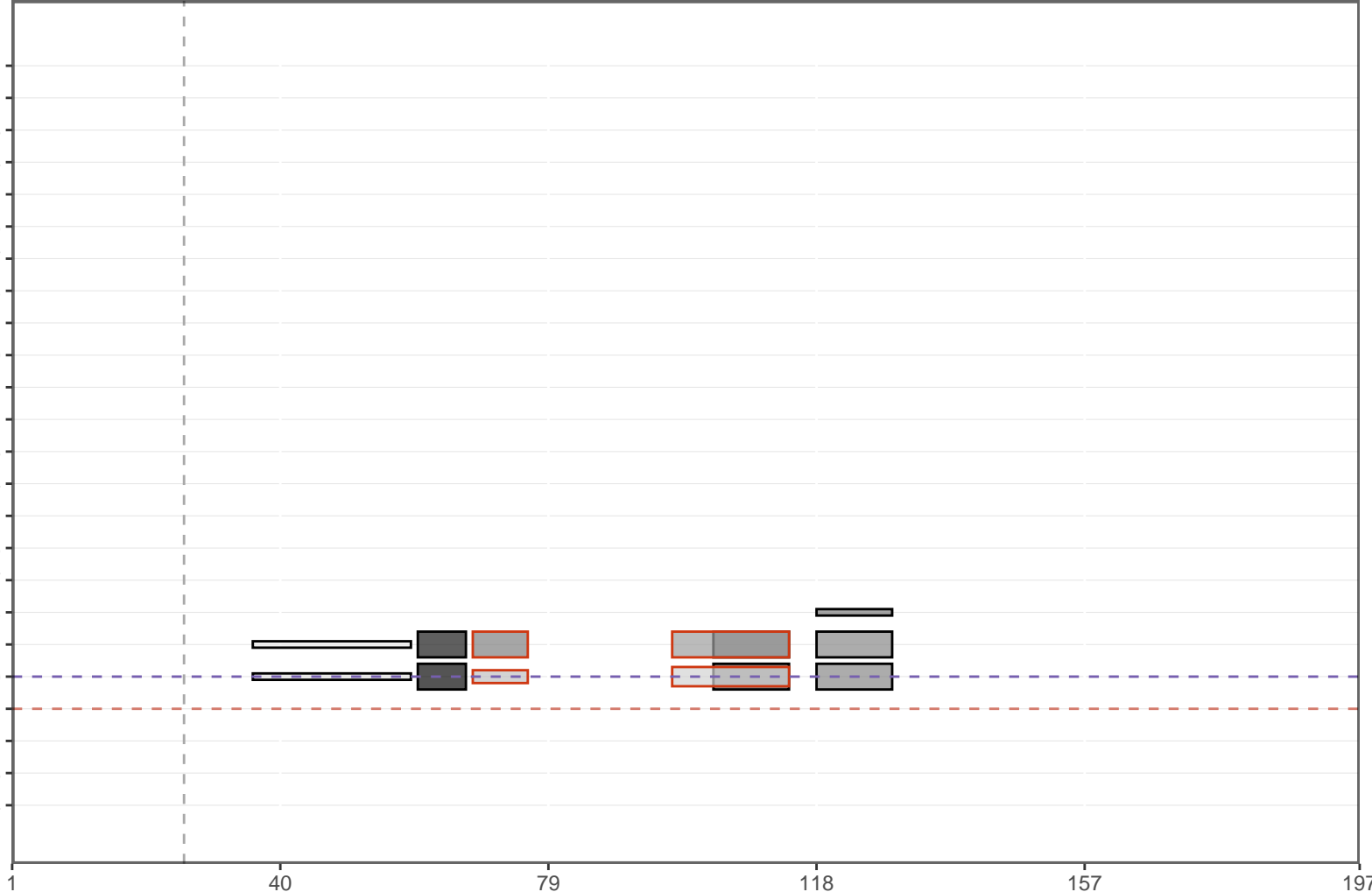
MW indication



Molecular weight



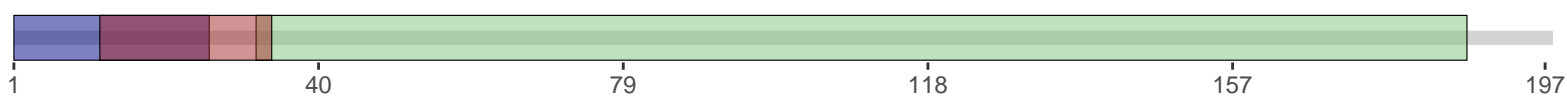
Gel Slice



Protein length

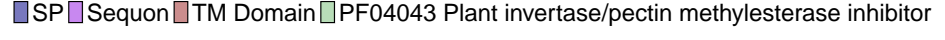


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CLLKFGLKPREYEAIKDCIEETSDDVDRLKSKVSELKEVDHGRGKDLHWHNVEYWSAATDENTCTDGFAGRALNGRIKASIRNRIRLAEVTSNALGLINQYAAKH

NbL03g10800.1 monocopper_oxidase-like_protein_SKS1 [MW - SP = 63.52 kDa]

No. of times detected



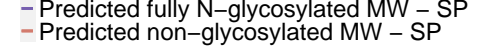
log(intensity)



Values from



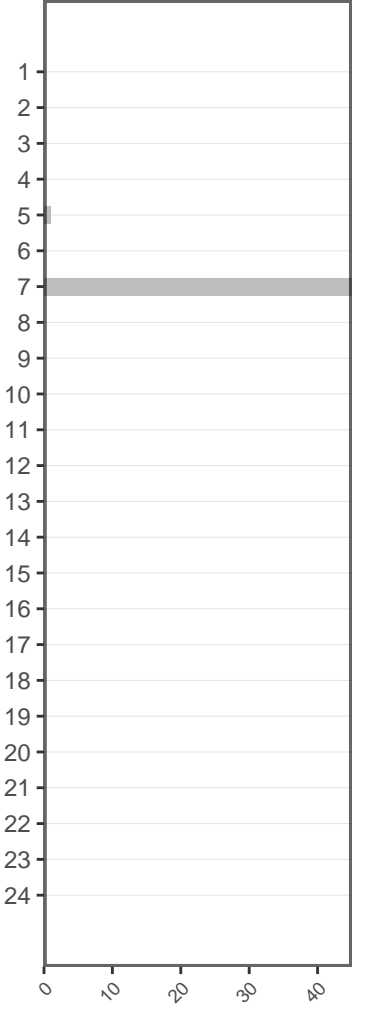
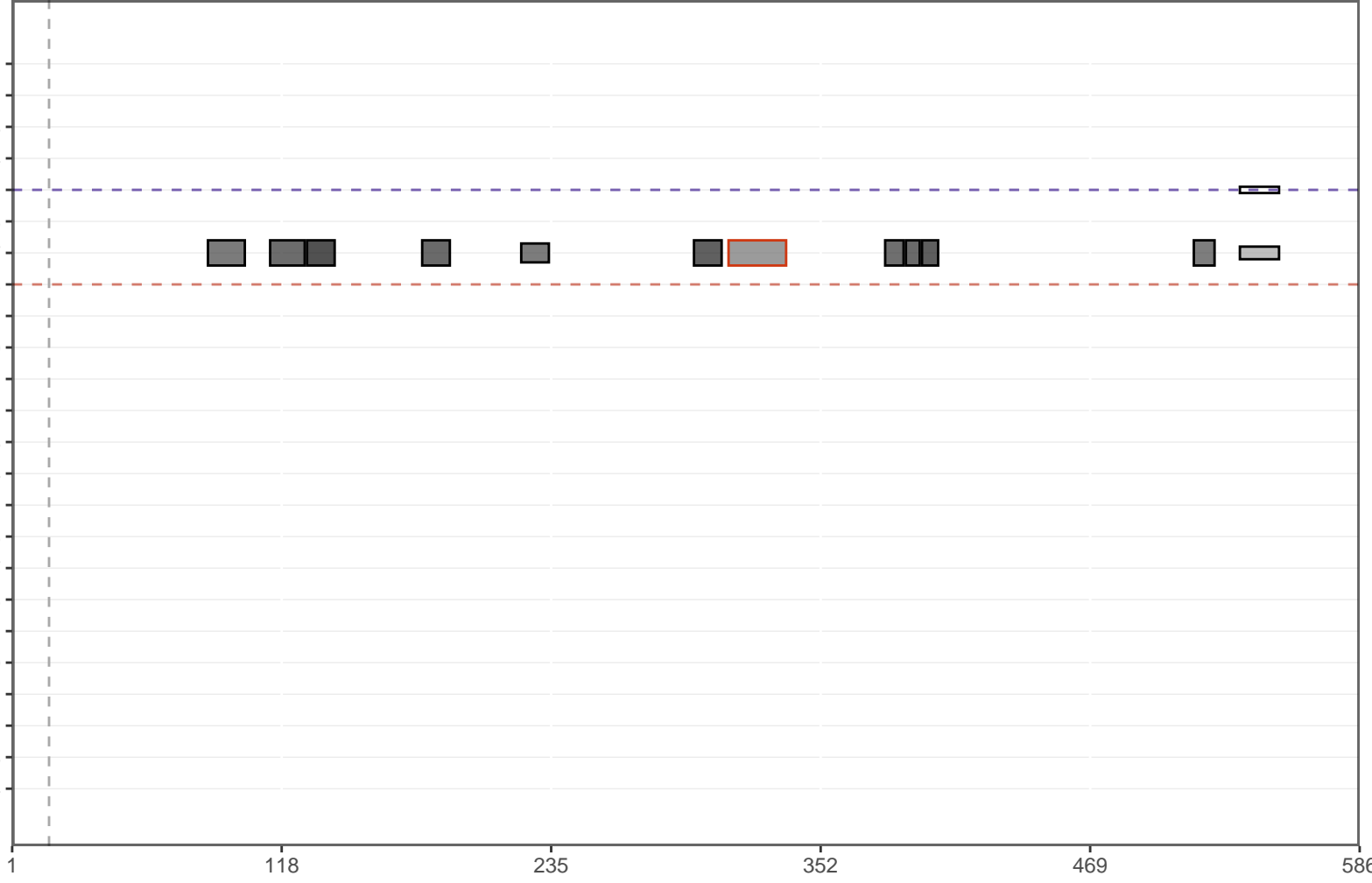
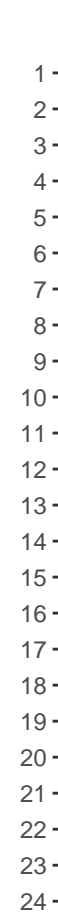
MW indication



Molecular weight

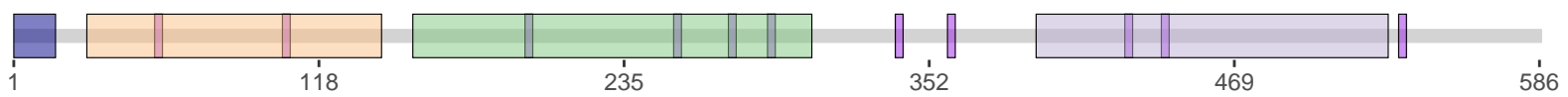


Gel Slice



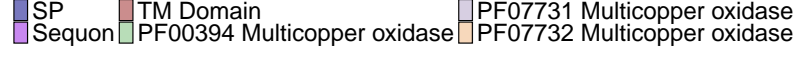
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

TVASPRFVNSQLWGVKTVGVAWLVHYSNKGKAGGPLPDPNDVDTSYALNDAMSRGNVSASGARINPQGSFHYGGNVTQVYLLKSVPPVAIDGKLRATYNGISFKNPETPIRLADVYHYKGDYKDFPTKPMNRPPKVDTSLNATYKGFIEVLGNNDTVAQGFHMDGYEFFVYGMGFGEVTEENRGGVYNRWDAIFRSTQVFPGGWTAHMASLQNVGVWNLRAENLDRWYLGQETVMRINFEIHSNKTQLPVSFNALYGGALASKGKPKQTSATIFRSESMYL

NbL03g10790.1 acid_beta-fructofuranosidase_AIV-18-like [MW = 74.77 kDa]

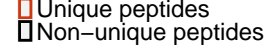
No. of times detected



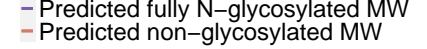
log(intensity)



Values from



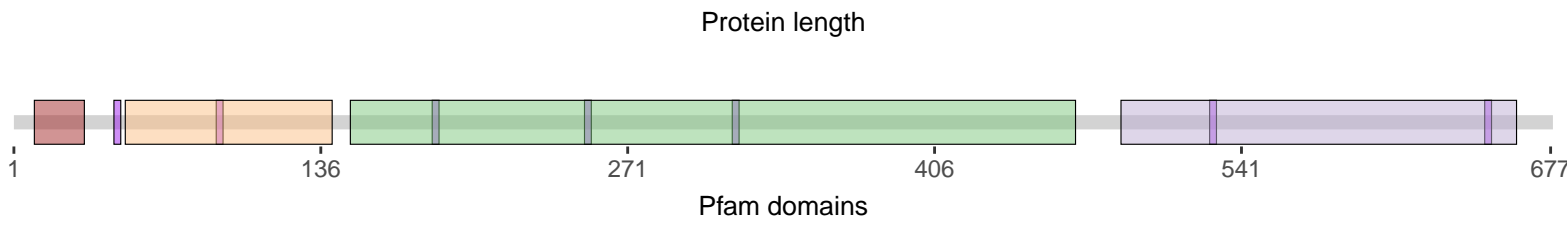
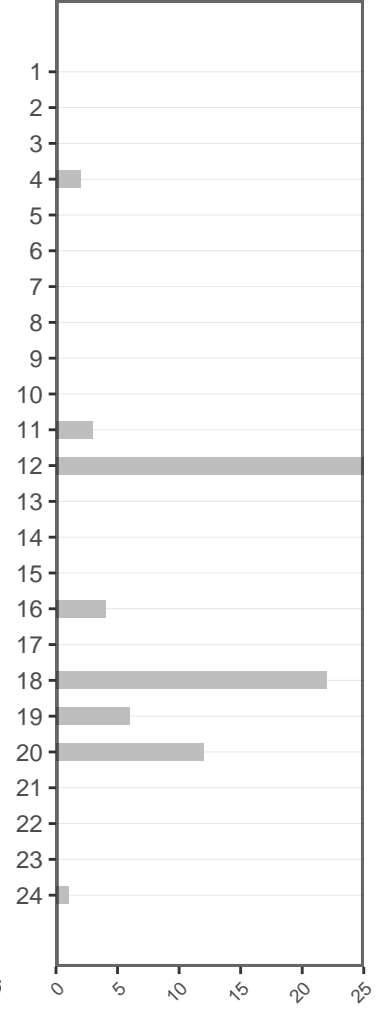
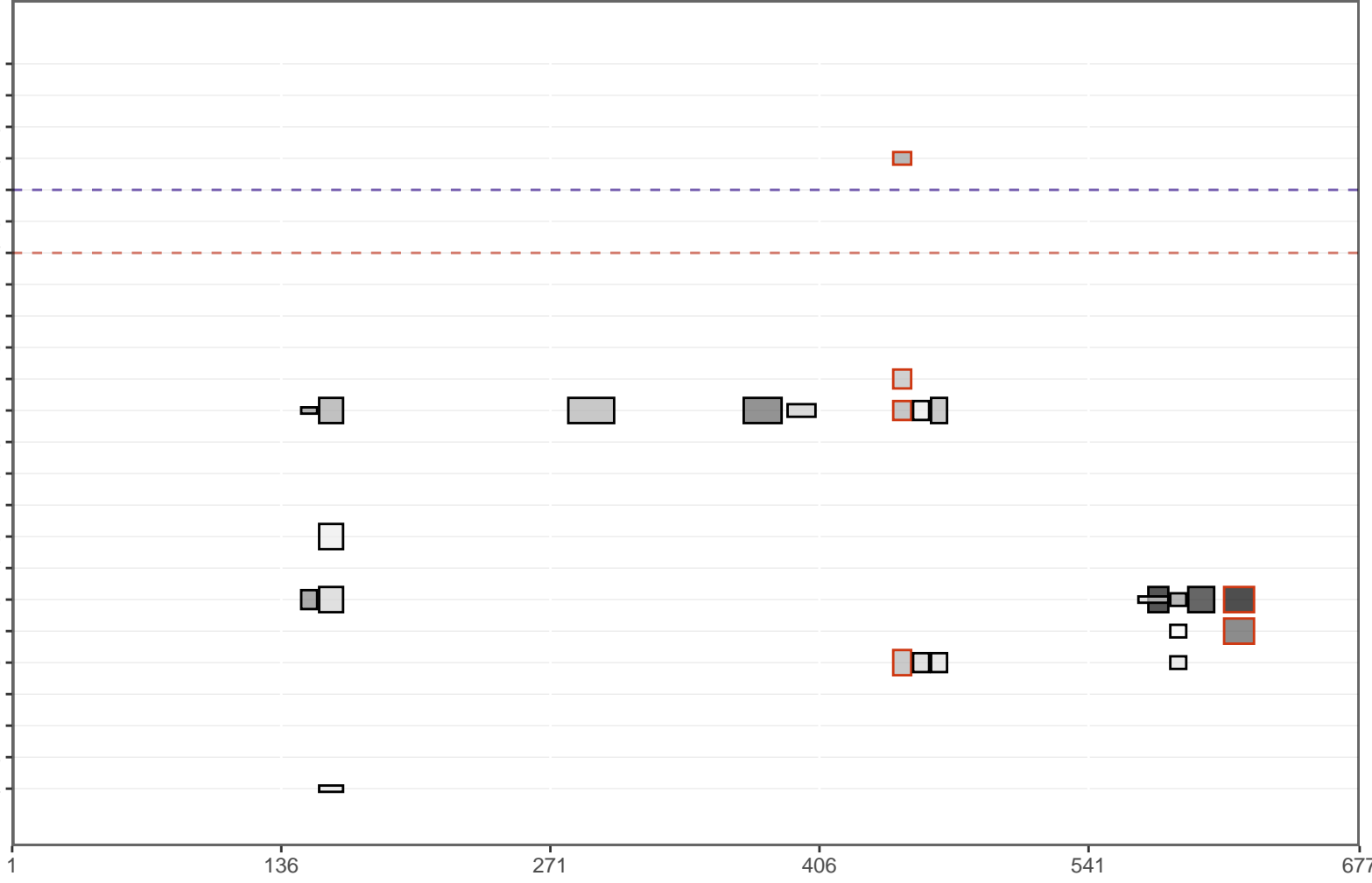
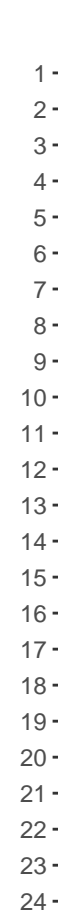
MW indication



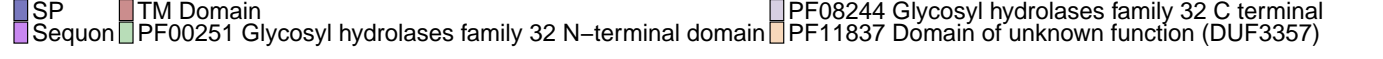
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

DDVLIHAVPGTGMMEGVDFYFVSTVETNGLDTSVNGPGIKHVKASLDDDKHDYIAIGTYDPVKNKWTDPNPELVDGGLRDLDFYKFAKTFYDPKQRRIILWGWIGETDSEADLKGWASVQTRPTVLYDKETRTHVLDGWPKIEISLRIGDPLAKGLNLQPGSELVHYDGAQLDVEAFSEVDKAALEATREADVGFNGSTGGSAKRGLGPFQGVVVAADGTLSELTPVYFYAKGTDRGAETVFCADETRSEAFQVAKGVYVGSVPLDGENISMRLLDHDSIVEE

NbL03g10460.1 acid_phosphatase_1-like [MW - SP = 28.53 kDa]

No. of times detected



log(intensity)



Values from



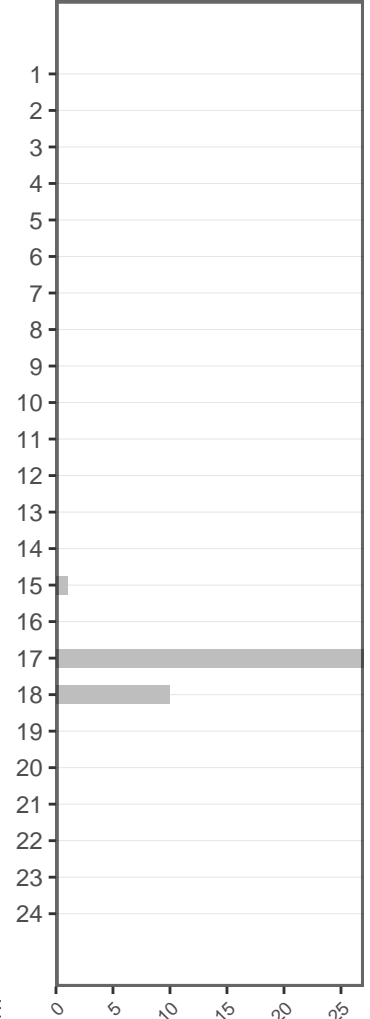
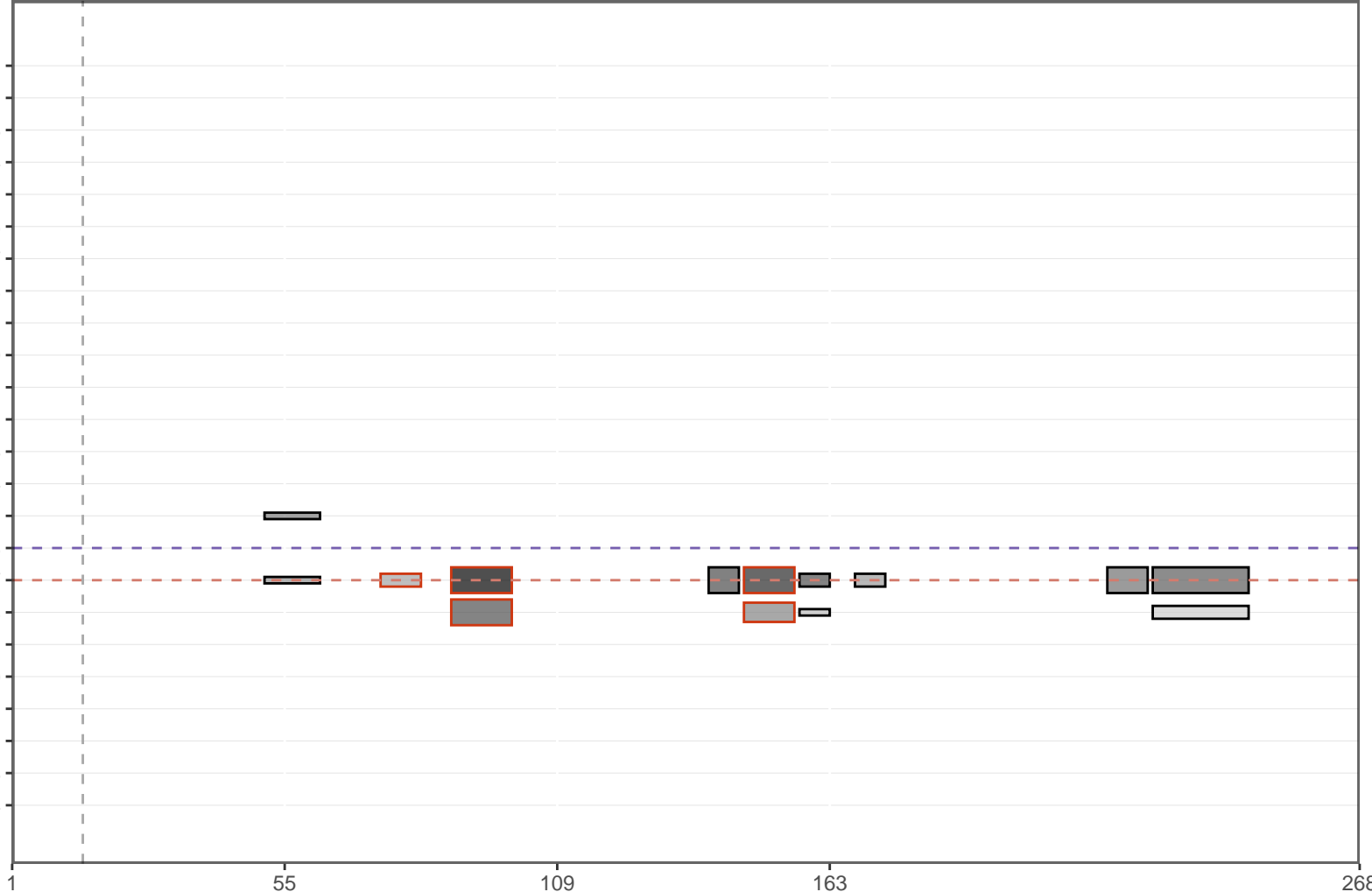
MW indication



Molecular weight

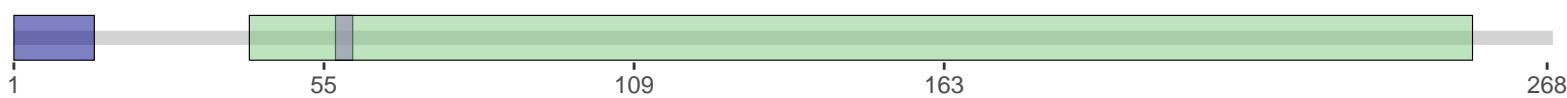


Gel Slice



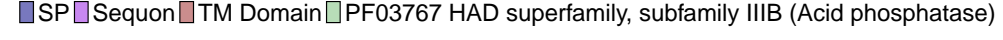
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YYSQHGYGLEVYDSKWFDEWKEKGVPIVIGSSKLYGVDMRLGKVFLLTGRERHRIVTVENLMNAGFDQWDKLLRGGKDHGKATHYKSEKRDEMVEEGFRIVGNSGDQWSDLLGSSAERSPKLPNPFISRTSGSGGFFP

NbL03g10410.1 ATP-dependent_6-phosphofructokinase_4_chloroplastic [MW = 61.97 kDa]

No. of times detected



log(intensity)



Values from



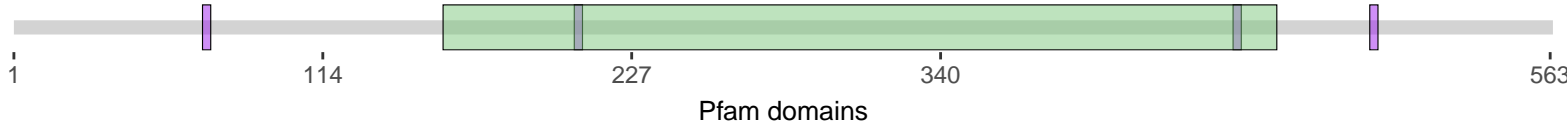
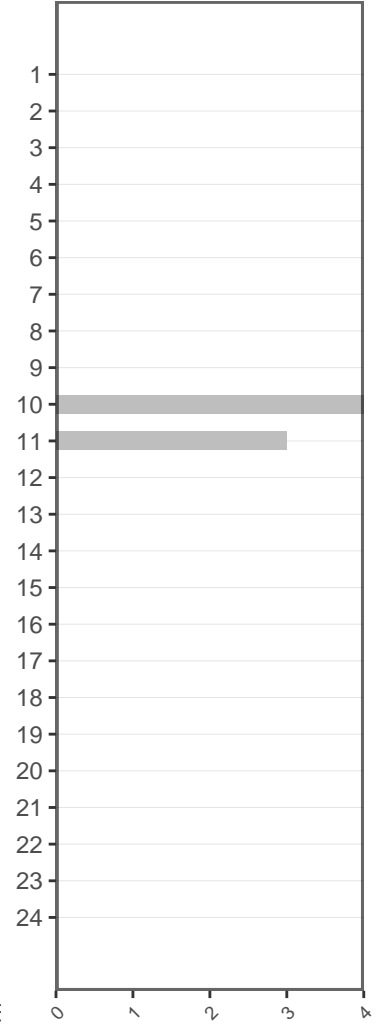
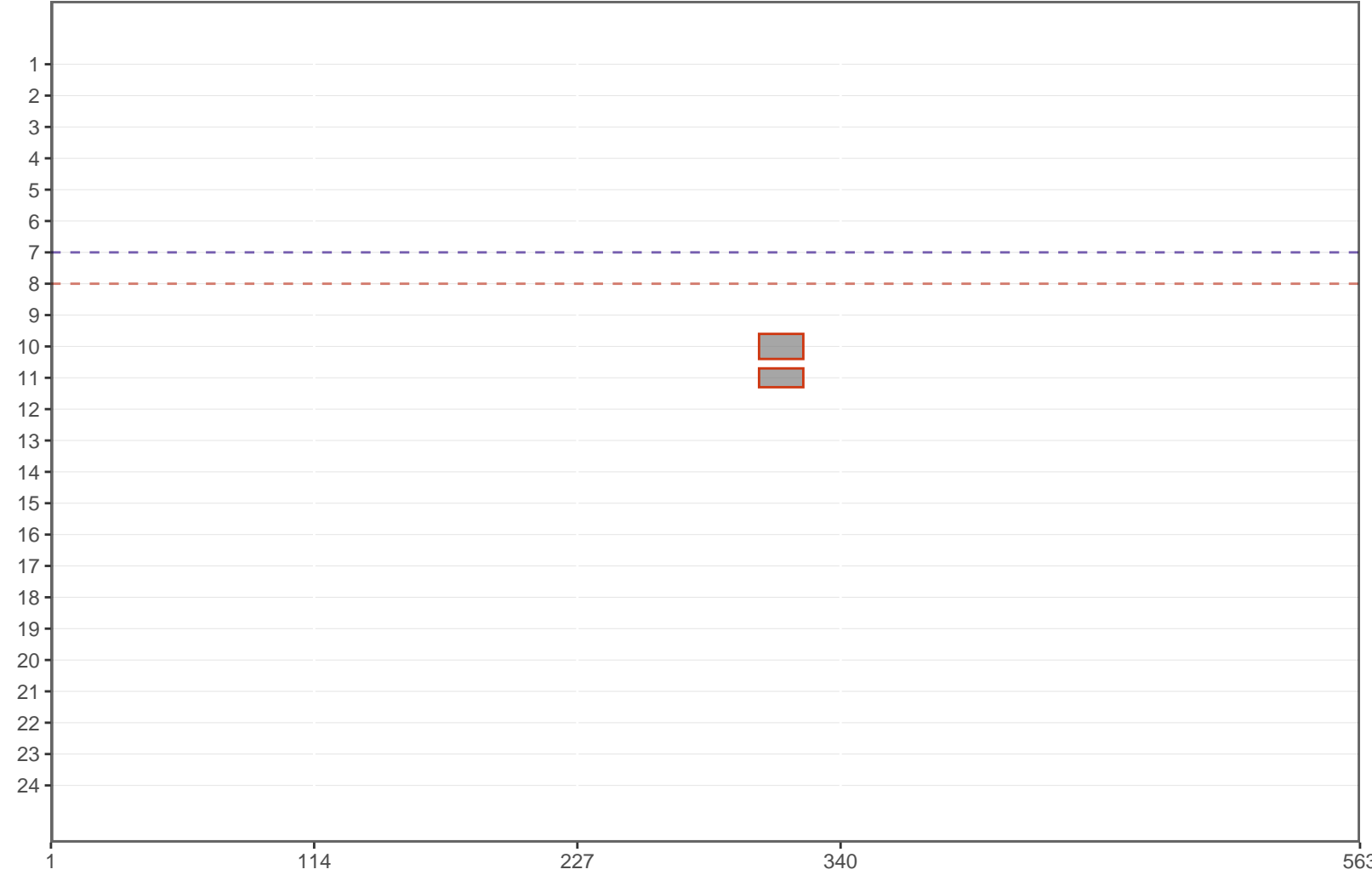
MW indication



Molecular weight



Gel Slice



Pfam Description
 ■ SP ■ Sequon ■ TM Domain ■ PF00365 Phosphofructokinase

Protein sequence:

IKRGKVAAGIPKTDNDIAVDKSGFDTAEEAGRAINAHVEAESEVGVGKMLGRVSGFRAMLATLGNRDVDCGLPEPFFLEGGPGLVEYVEQRKENGKHLVLAEGAGGEYVAGSMQAFQENBAGSNRLLLDVGLWLTQHKDHFTRIRKTKNMKYIDPTFMIRAPSNASDNFYCTLLAGSAVHGAMAGFTGFTVGPVNSRHAYIPDRVTETFTNTVLTGRMVARLLASTNGPSFQDSGAVRRKVDKQFDIAHKFMVIDGGTADALAHVRDVEETALHLV

NbL03g10290.1 protein_mago_nashi_homolog [MW = 17.83 kDa]

No. of times detected



log(intensity)



Values from



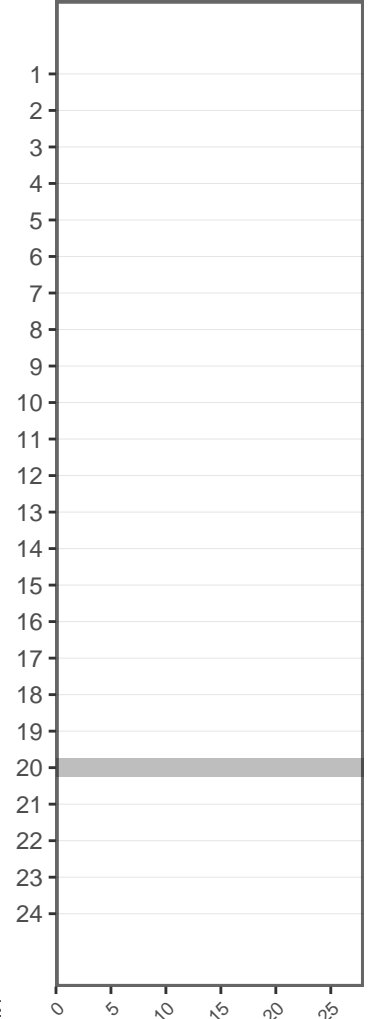
MW indication



Molecular weight

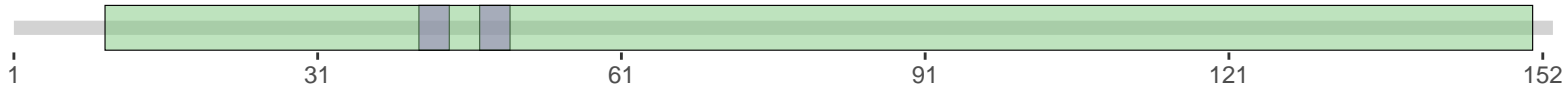


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

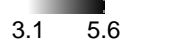
LRRCRRIVADSEIMKEDDNNWPEPRDVRGRGLEVMGNHHSFTTSKIGSLMDVGTGKDPGLRIFYYLVGDLKGFVFSLSLHFNIKPI

NbL03g10150.1 superoxide_dismutase_[Fe]_chloroplastic-like [MW = 34.8 kDa]

No. of times detected



log(intensity)



Values from



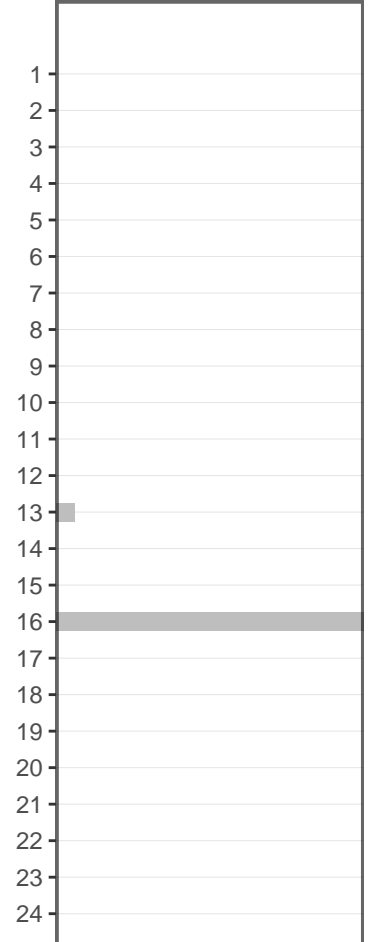
MW indication



Molecular weight

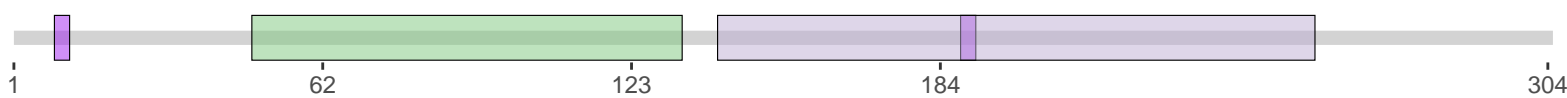


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00081 Iron/manganese superoxide dismutases, alpha-hairpin domain
- PF02777 Iron/manganese superoxide dismutases, C-terminal domain

Protein sequence:

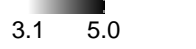
KPSGELLEINRDFGSEAFVKEFKAAATDFGGGWAWLAVKANRLNMGNSNPHPTDEKLLVVKTPNFWFLWVDSPLLTIDWEHAYLDFRNRDPVGSIFMEKLVGEAVSRLEVAKARVAEREEREEERKRREREEERKAGGEVREMYVEGTHSDTE

NbL03g10050.1 quinone_oxidoreductase-like_protein_2_homolog [MW = 37.32 kDa]

No. of times detected



log(intensity)



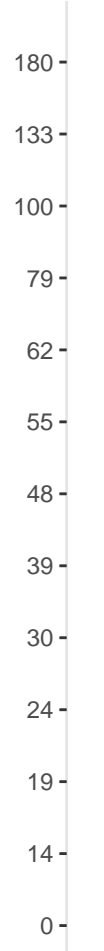
Values from



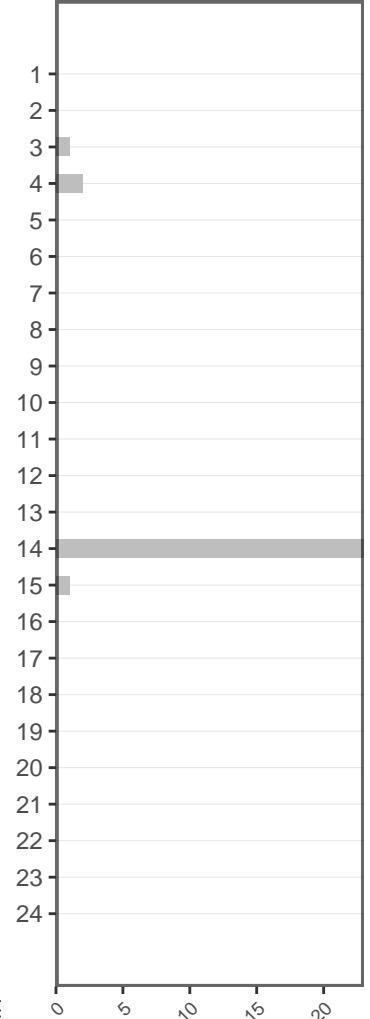
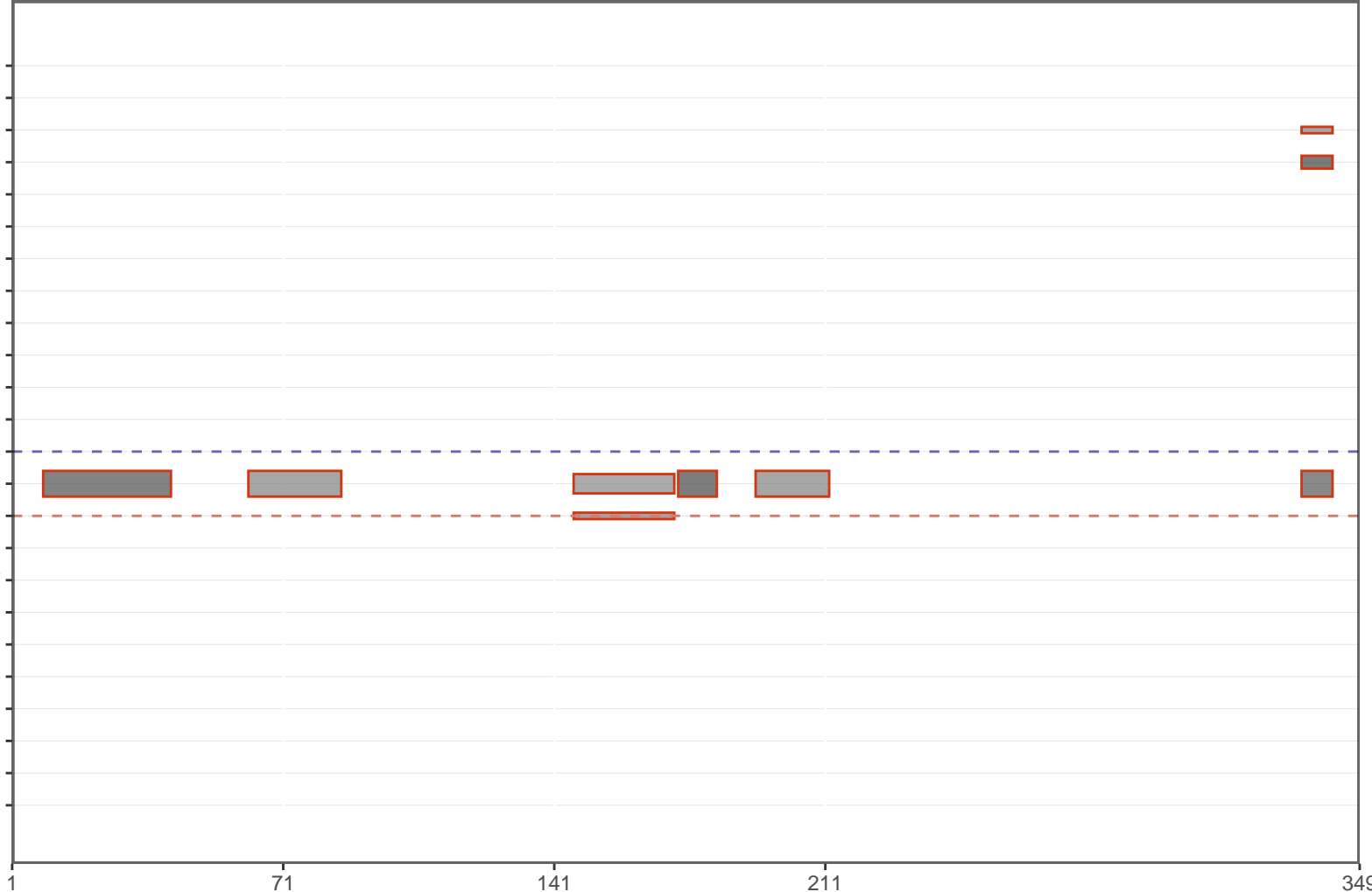
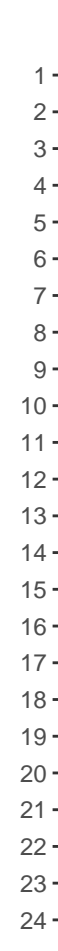
MW indication



Molecular weight



Gel Slice



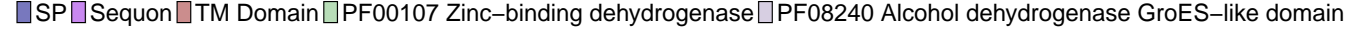
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AAGVQLSAVQIQKGGATVAARNGNEKVFLLKLGVDHVDLSNANVIESVKGFLKSRKLGVDVLDVDPVGGKLTKHSMKLLNWGADILVGFASGEVPIIPANALVKNVTHGLVWGRHKVGPVNLGDGLNELLSWLSKGLTINISHTFLAEAHLAFTALKDRRAIGKVMITFDEDRTLKEL*

NbL03g09750.1 expansin-A4-like [MW - SP = 24.07 kDa]

No. of times detected



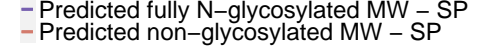
log(intensity)



Values from



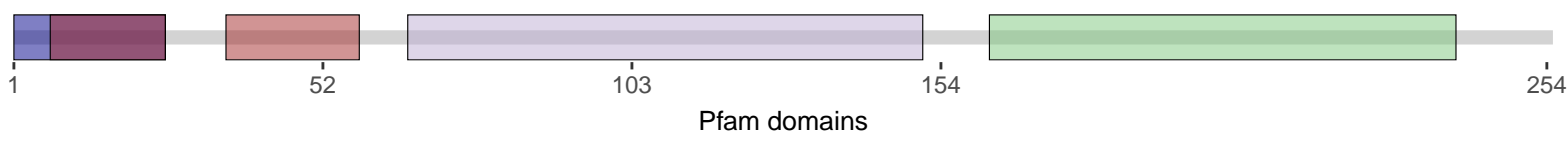
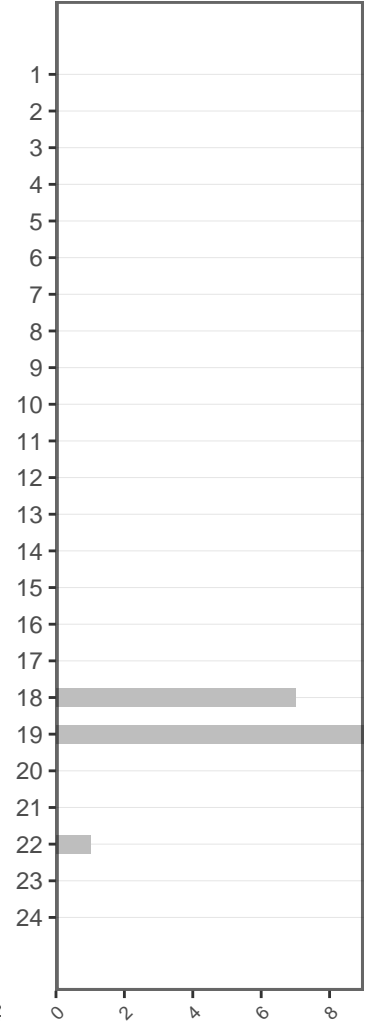
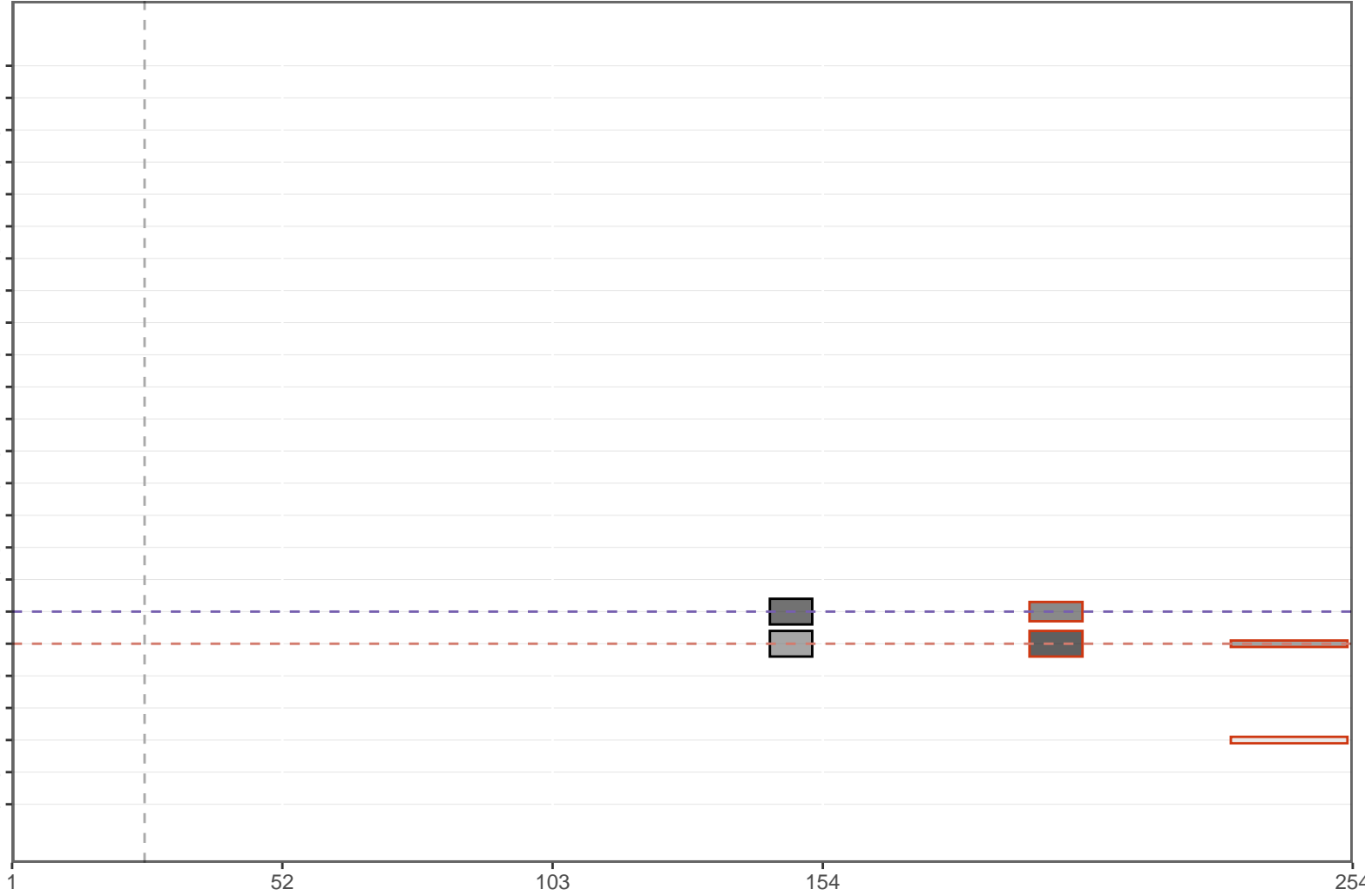
MW indication



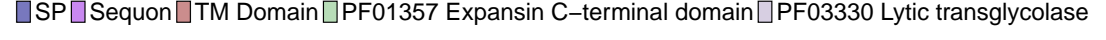
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

INNGGWCHPPLQHFDLADPFLGIAKVRAGIVVDFRRVPCRRKGGIRFTNGHSFFNLVLTNVTNCGGAGDQGEVSIKGENSGWGTMSRINWGGNWNANLNGQLSFGVITTSDDRLESNNAAPNINWFGGTFEGAGP

NbL03g09710.1 alpha-galactosidase-like [MW = 47.85 kDa]

No. of times detected



log(intensity)



Values from



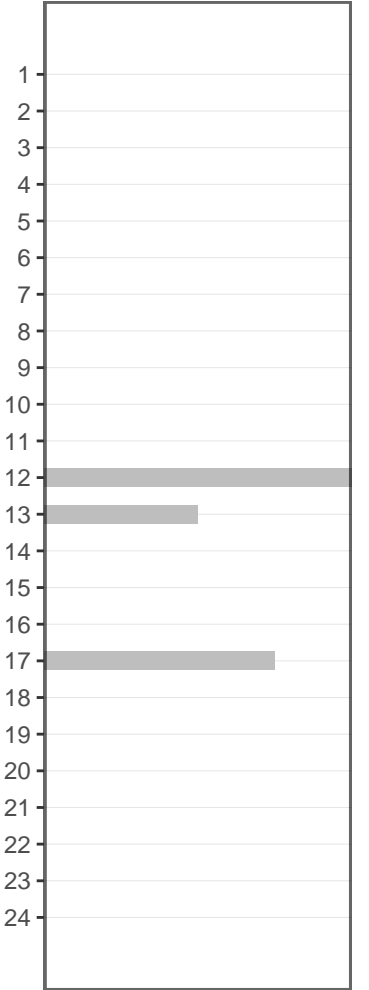
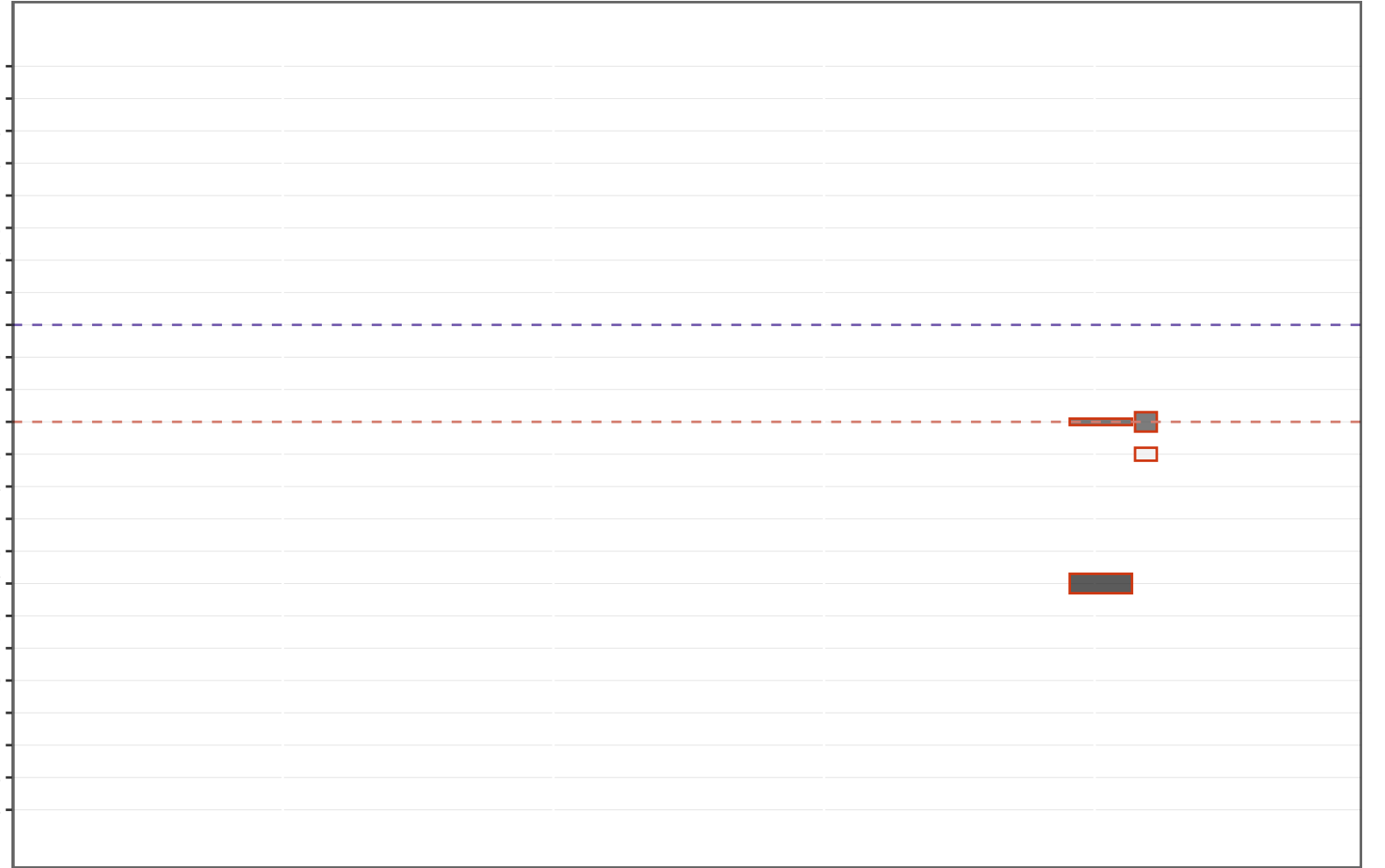
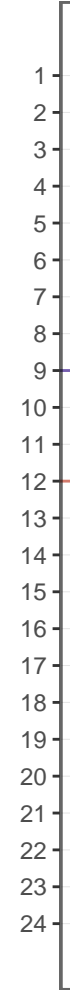
MW indication



Molecular weight



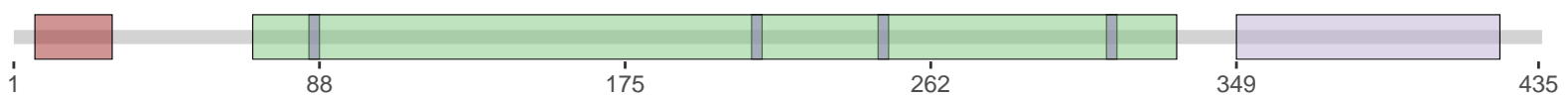
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IRDALNATGRITFYALGEWGVDDPKKAWGKIGNSWRFTDDNDTWASMTFIADINDKIASVAGPGGWNDFDMLLEVAGGGMNHYEYKGFHSWALMKAPLHGCGVRNITAELEFISNKEVAVDGGDFLVGQRRVYAAGPDGEGVWAGPLSGNRLAIVLWNRGKAAISITAKWCAGLGGSSIVSRDLWKHEVSENTVGSFSARVDHAGGEMVILTPKRATRAISL

NbL03g09700.1 uncharacterized_LOC107819606 [MW = 19.28 kDa]

No. of times detected



log(intensity)



Values from



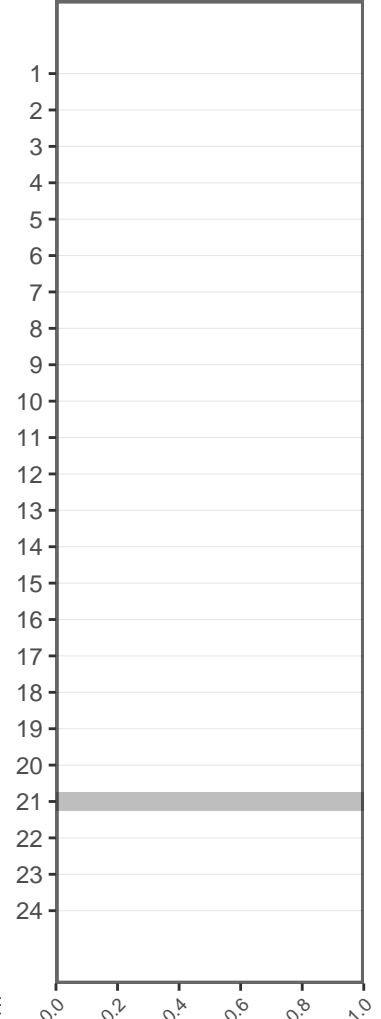
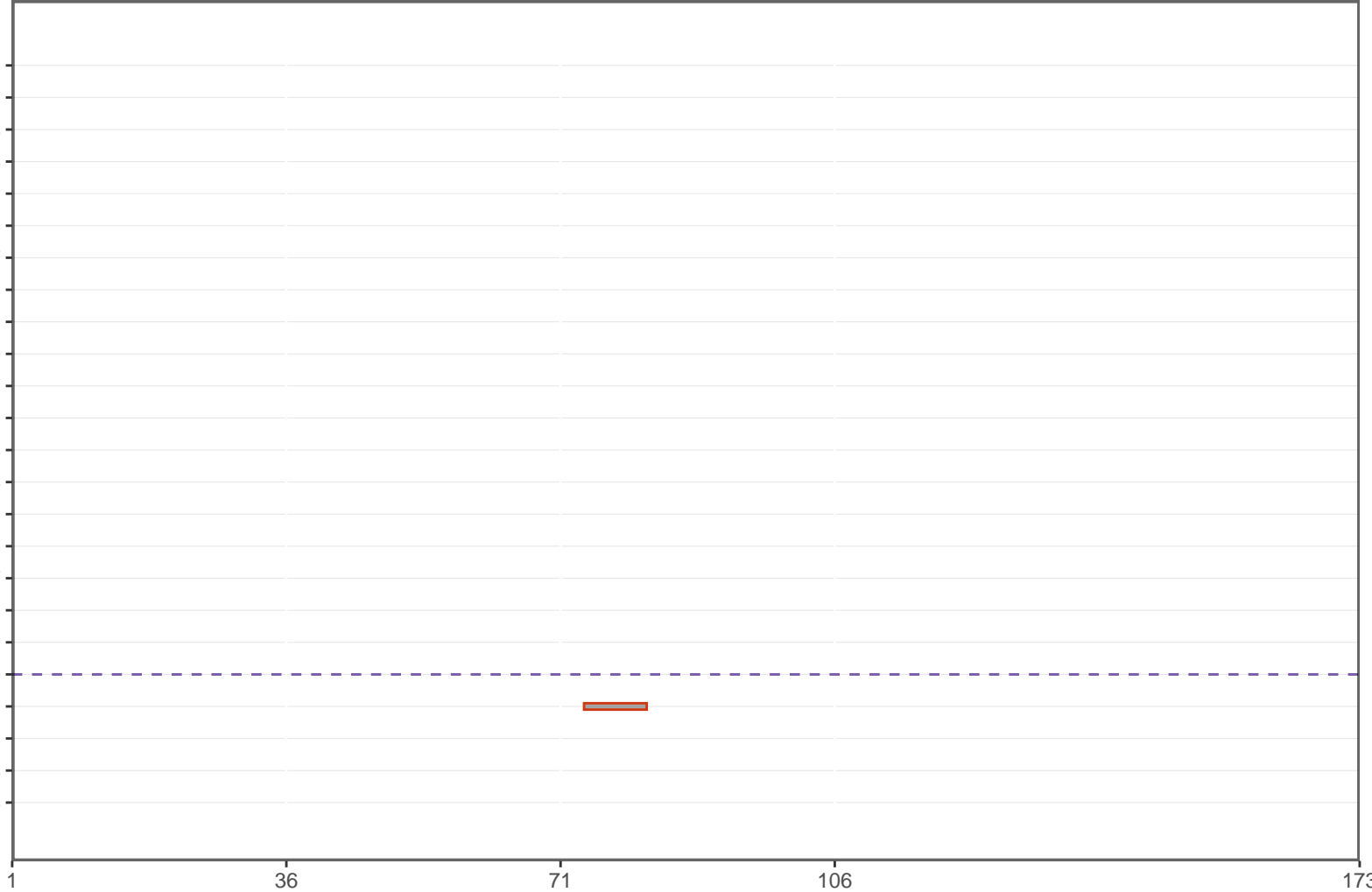
MW indication



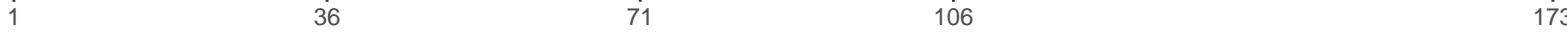
Molecular weight



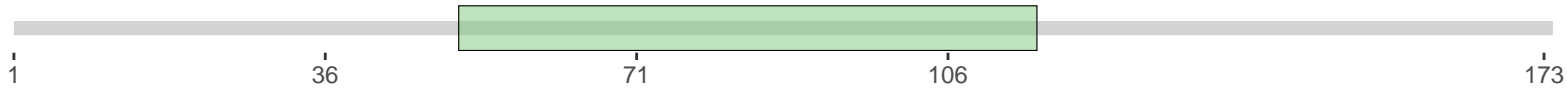
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

MELEIDAEAREATQSGVIRMSREGYALRRKIGSTYKDFKSKYEVKGEYVEEGVWVKTKKVKCKDTRGEARGVDNFGRIYHVAGLDKSKSGFFNTLFSR

NbL03g09650.1 uroporphyrinogen_decarboxylase_chloroplastic [MW = 43.33 kDa]

No. of times detected



log(intensity)



Values from



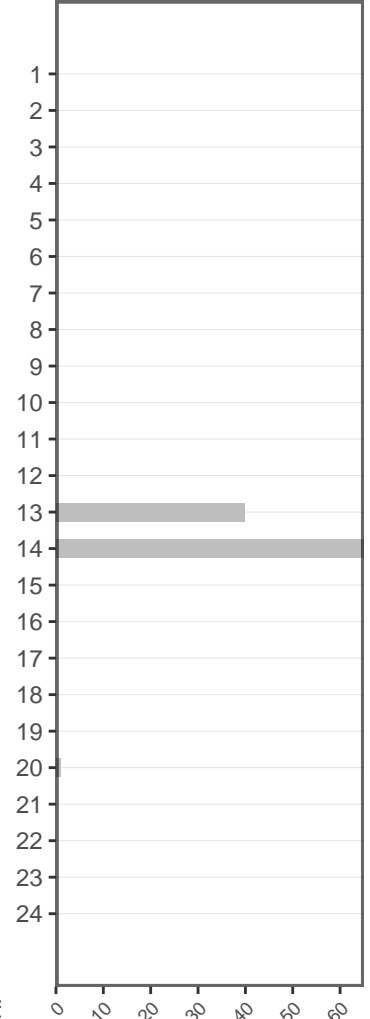
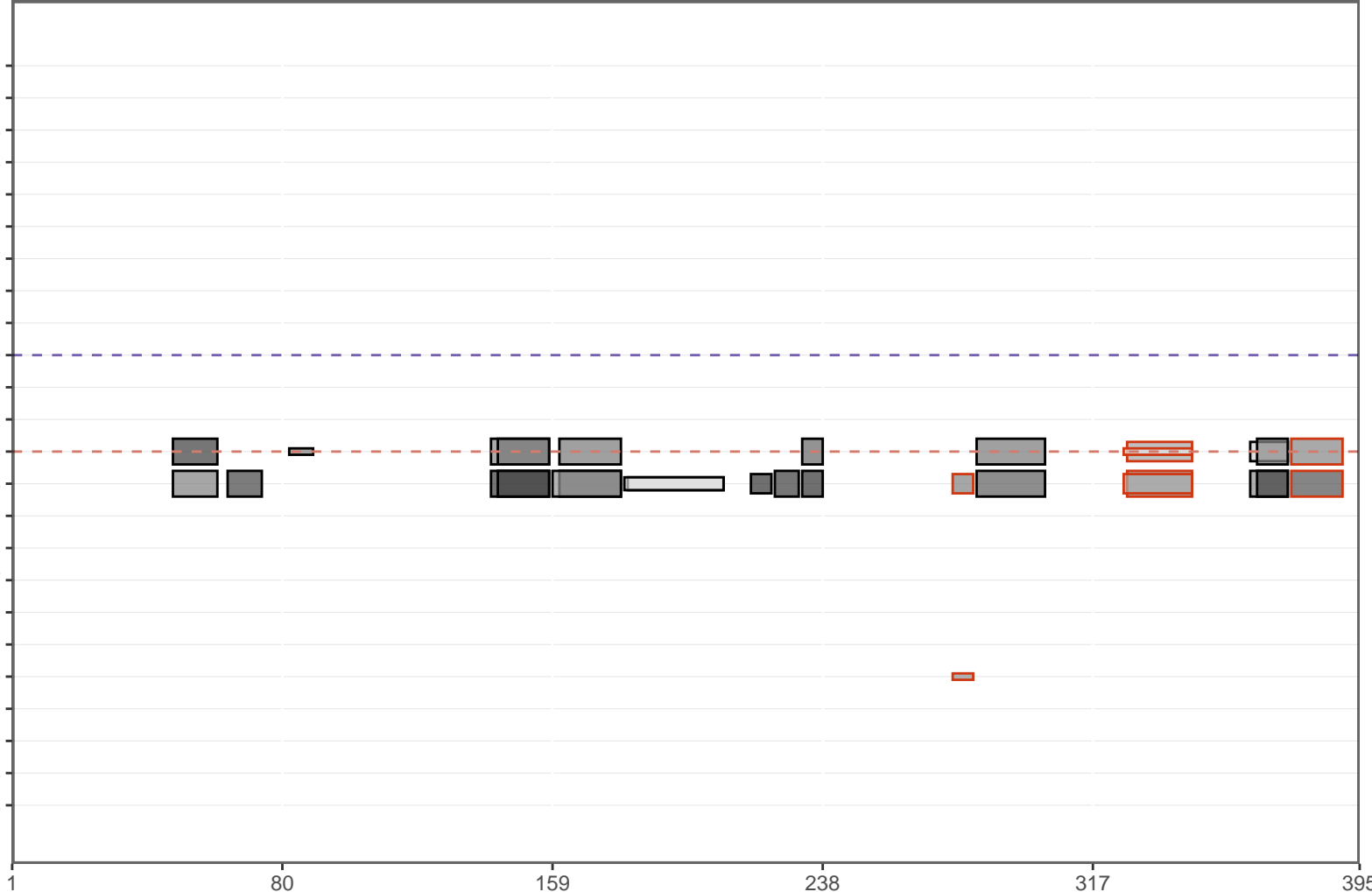
MW indication



Molecular weight

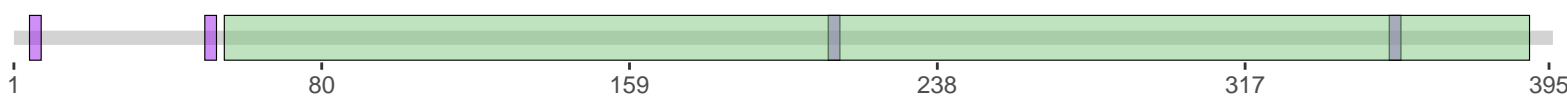


Gel Slice



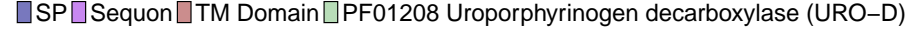
Protein length

Peptide counts over 4 repeats



Pfam domains

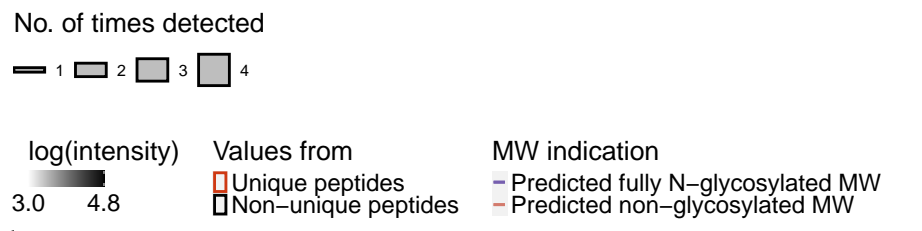
Pfam Description



Protein sequence:

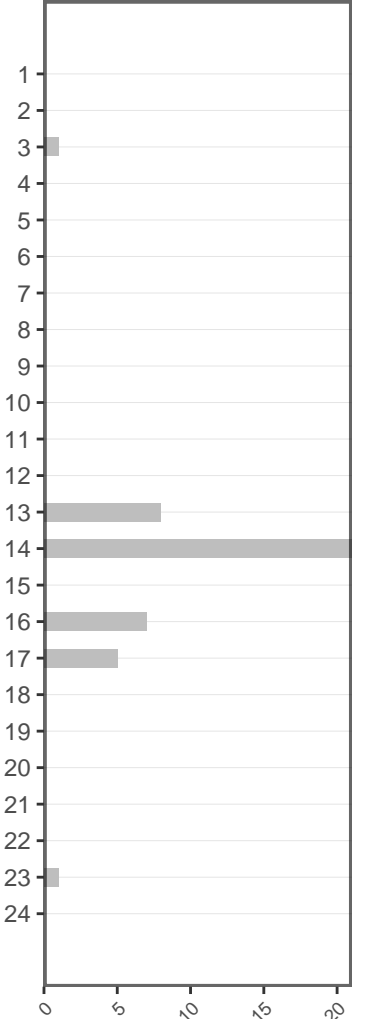
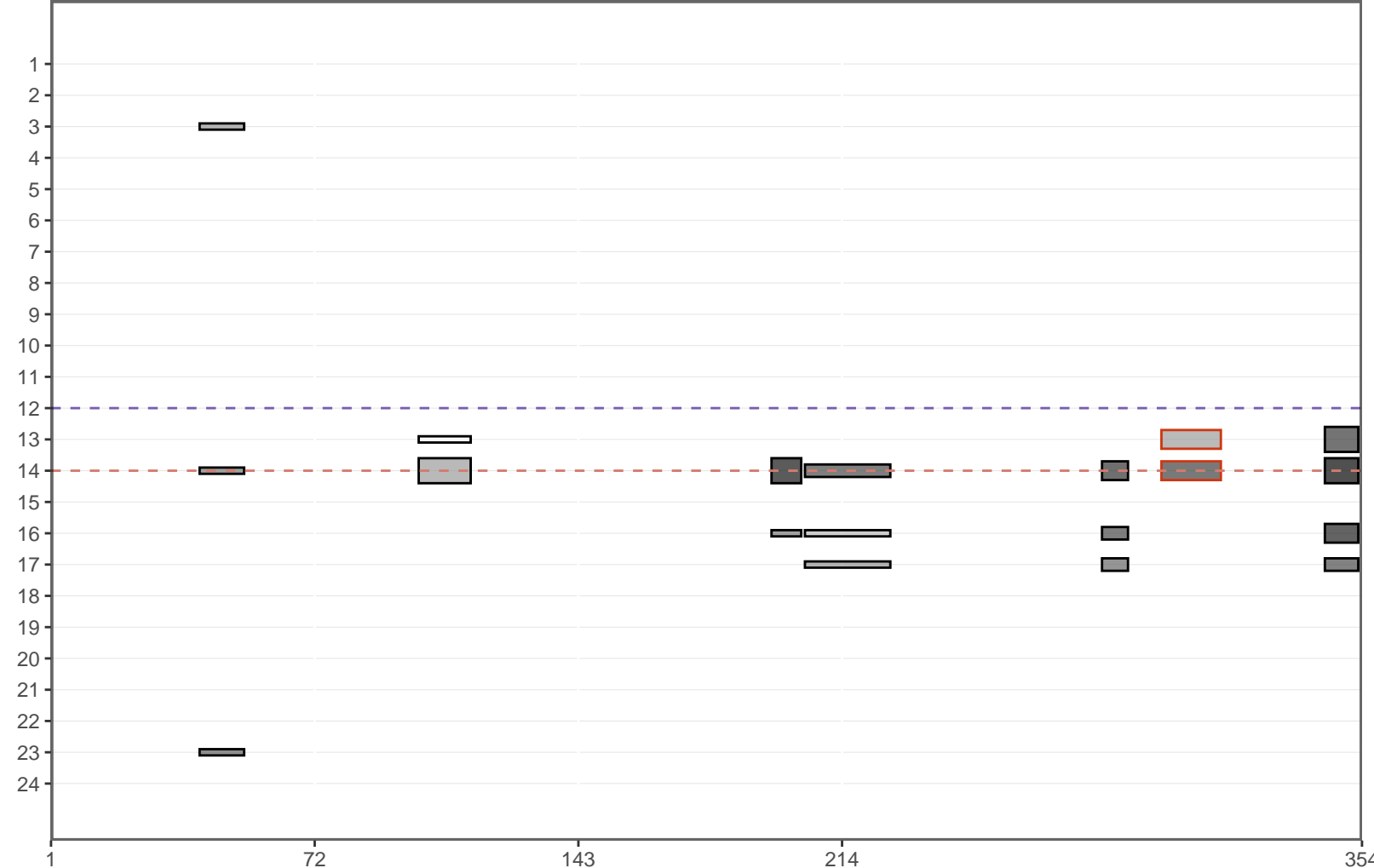
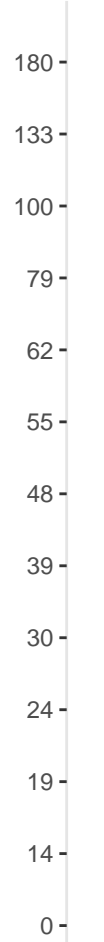
IQAAVLGFGAPFTLAEYVVEGGSSKNFTKRLKLAFAEKVHLHALQKFAFMSAKYRIVYQADSGAGAVQIFDSWATELSPVDFEESFLPKGIVDSVLTHTPMLPLIIVAGSGGGLLELRPLTGVDSVLSLWTVDMADGRRRLGPDVAIGNIVDPGLVFGSKEFTIRINDTVKKAGKQKHLNLGHGKIVGTPPEENVAHFFEIAKGLKY

NbL03g09540.1 photosynthetic_NDH_subunit_of_subcomplex_B_2_chloroplastic-like [MW = 38.79 kDa]



Molecular weight

Gel Slice



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

IMATAVYKNNGRKPKVLTSAIASHLKSRTKTRGDTGIQGLRSGTYGAHPRPLSSPEELSPGEAMKTEEPQLFSGWPELKPQHSAGQWPTVLKHKLSRLVSVPPPEERAKEFYNSPSKYETDQGRLEFRIRMGFEDYLSPPGFSKYGKDYFICTGASMLIPLVNPNGEEWRGAQVIEHNL

NbL03g09520.1 ADP-glucose_phosphorylase [MW = 37.84 kDa]

No. of times detected



log(intensity)



Values from



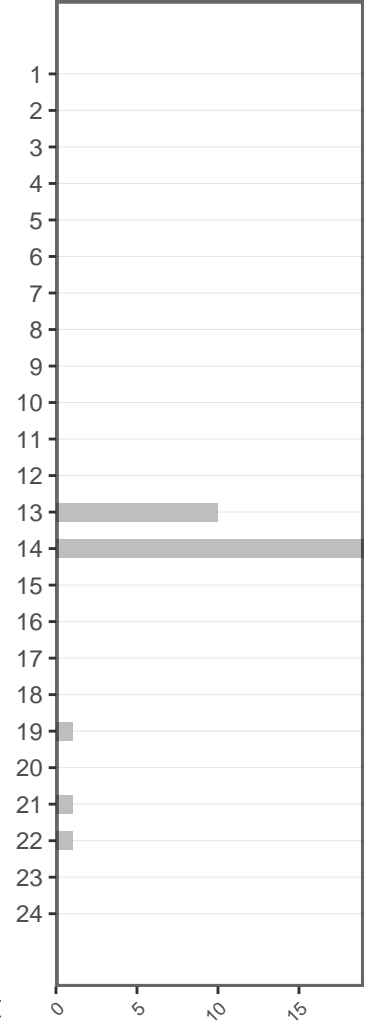
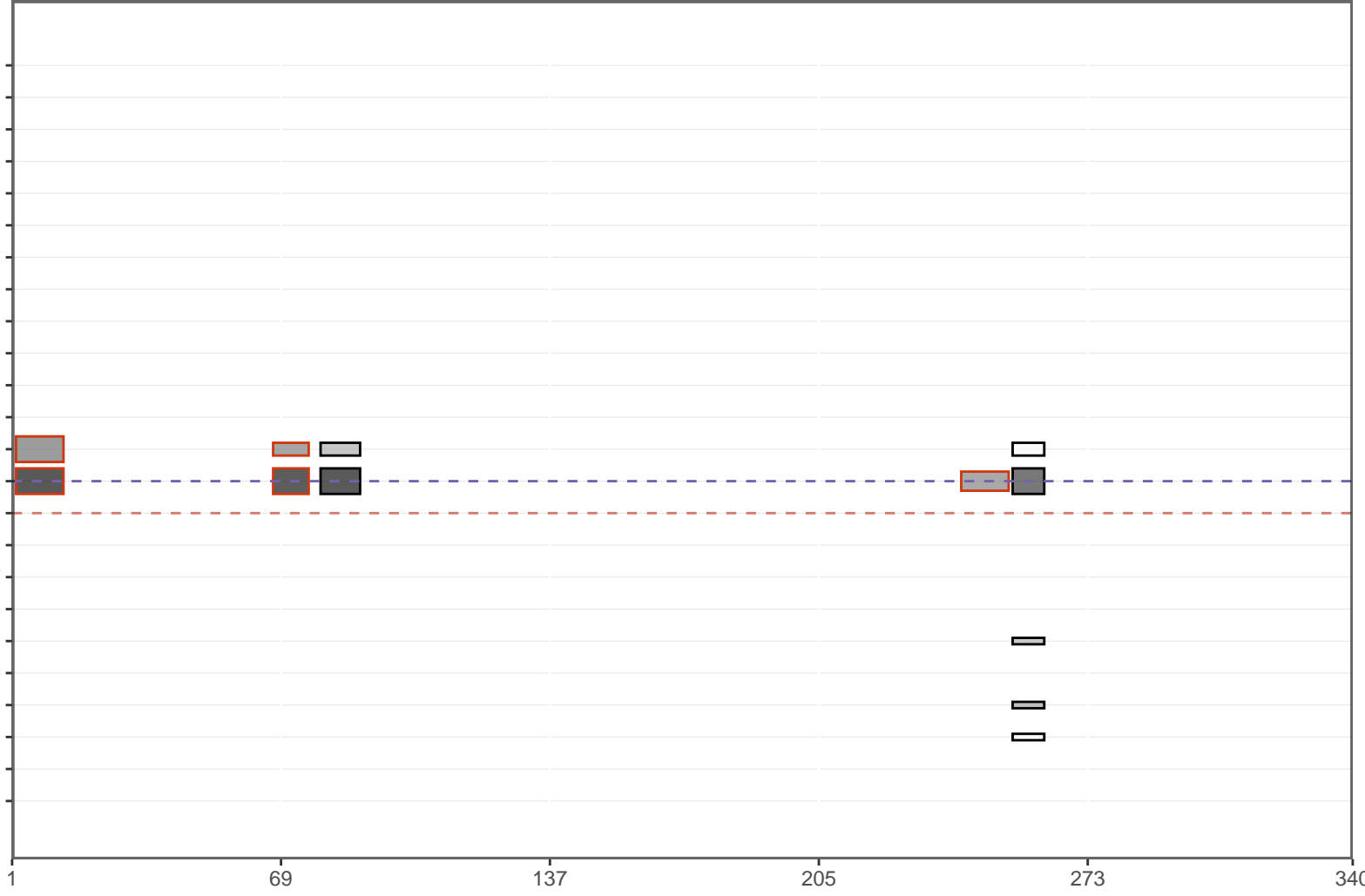
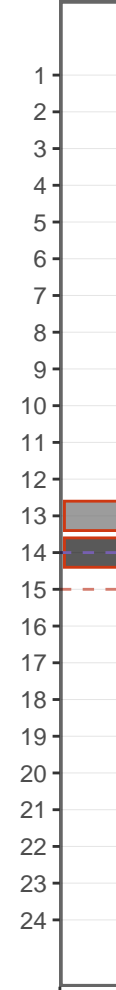
MW indication



Molecular weight

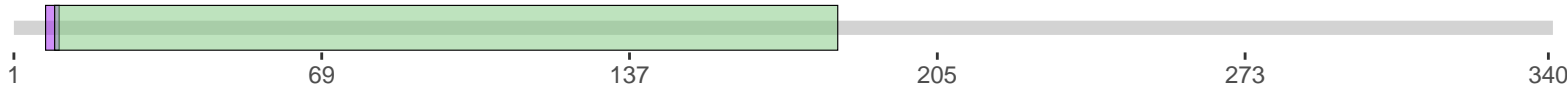


Gel Slice



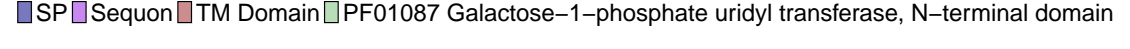
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VQVFNHGASAGAMSHSHGSMALPVPPTVSARLDDMREYYKGTGKGLGDIQPNELLIDGSAHFISLVFFAATFAFEWIIPRDHSHFHQLDNEKANDLGLLKLMLKMSLQLNPPFNLLHSTSPFQVDPFSYASSTHWFLQIAPHLSVVGGEIATGCHNPVPEDAKILRDVRLN

NbL03g09500.1 probable_phosphatase_SPAC5H10.03 [MW = 32.26 kDa]

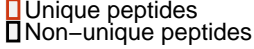
No. of times detected



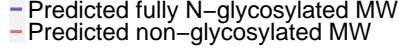
log(intensity)



Values from



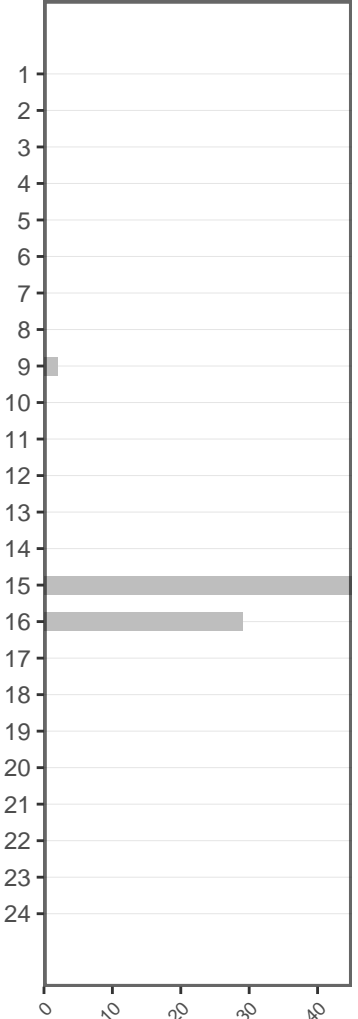
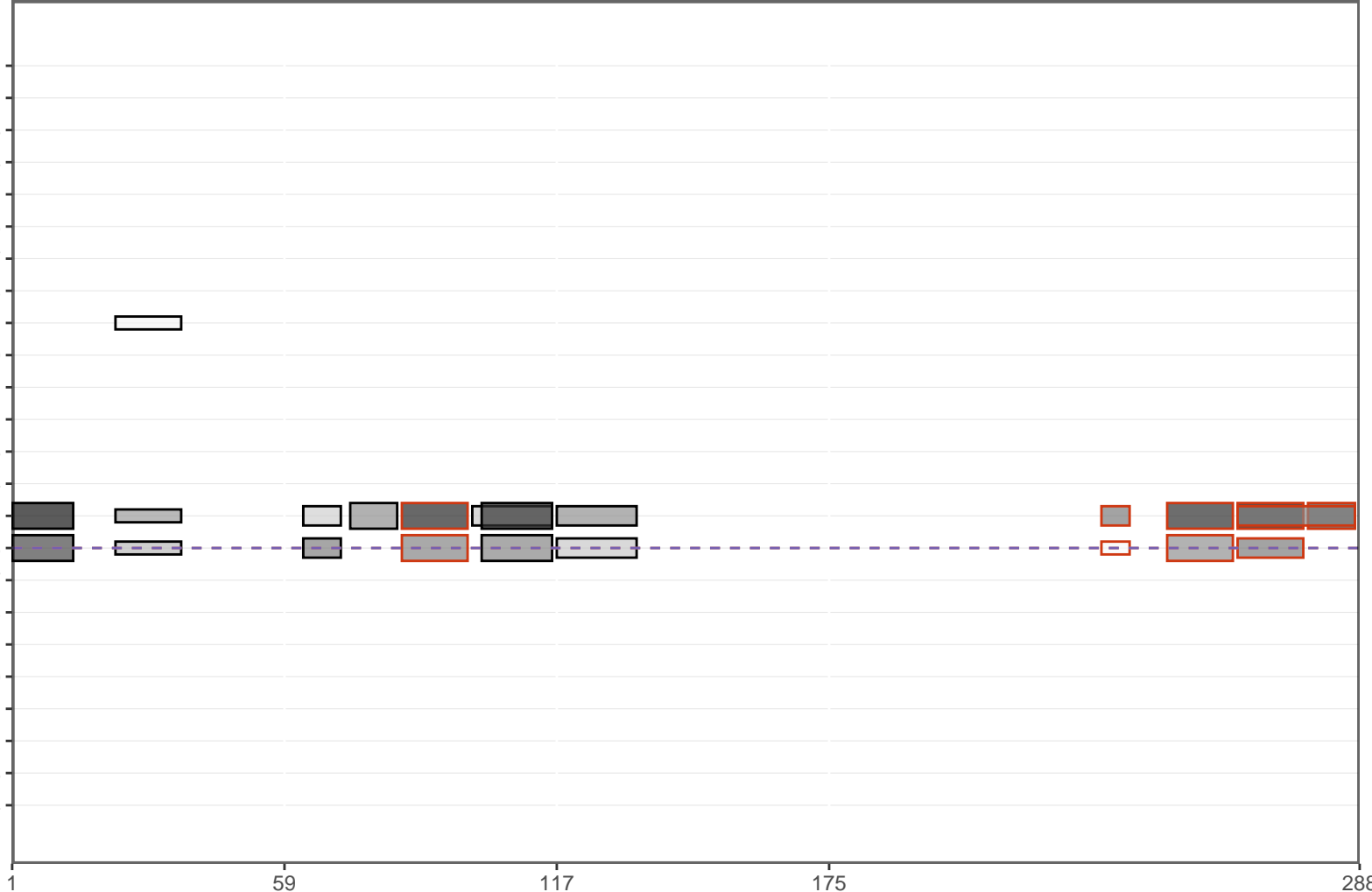
MW indication



Molecular weight



Gel Slice



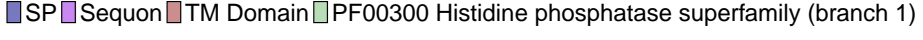
Peptide counts over 4 repeats

Protein length

Pfam domains



Pfam Description



Protein sequence:

IELCREHLGVIPCDERRRVEYEQGLFFADLSLIESDEDTLWKANVRETKEEVMARGKFLNWLTRKEKEIIVSHVGLLFLHAFGTDCIHPFKVKEIKRFRANGLERLMMVDFRSMIGSDSSITNYPGKIPGAANLPSEPADEKLENDNNLNK

NbL03g09230.1 beta_carbonic_anhydrase_5_chloroplastic-like [MW = 33.78 kDa]

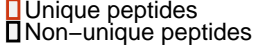
No. of times detected



log(intensity)



Values from



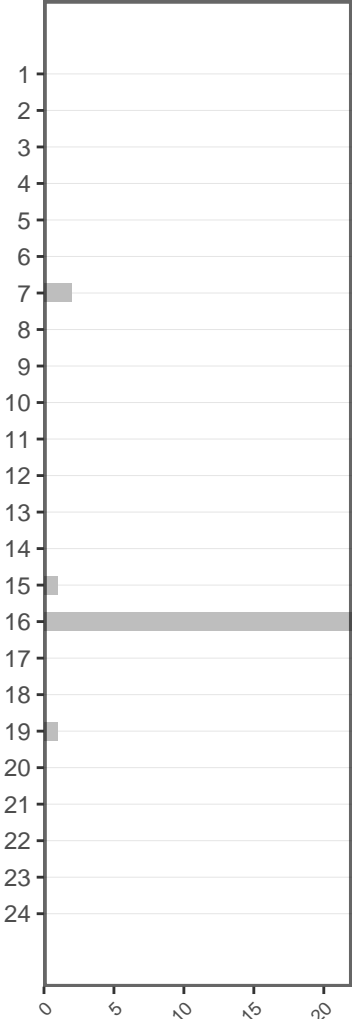
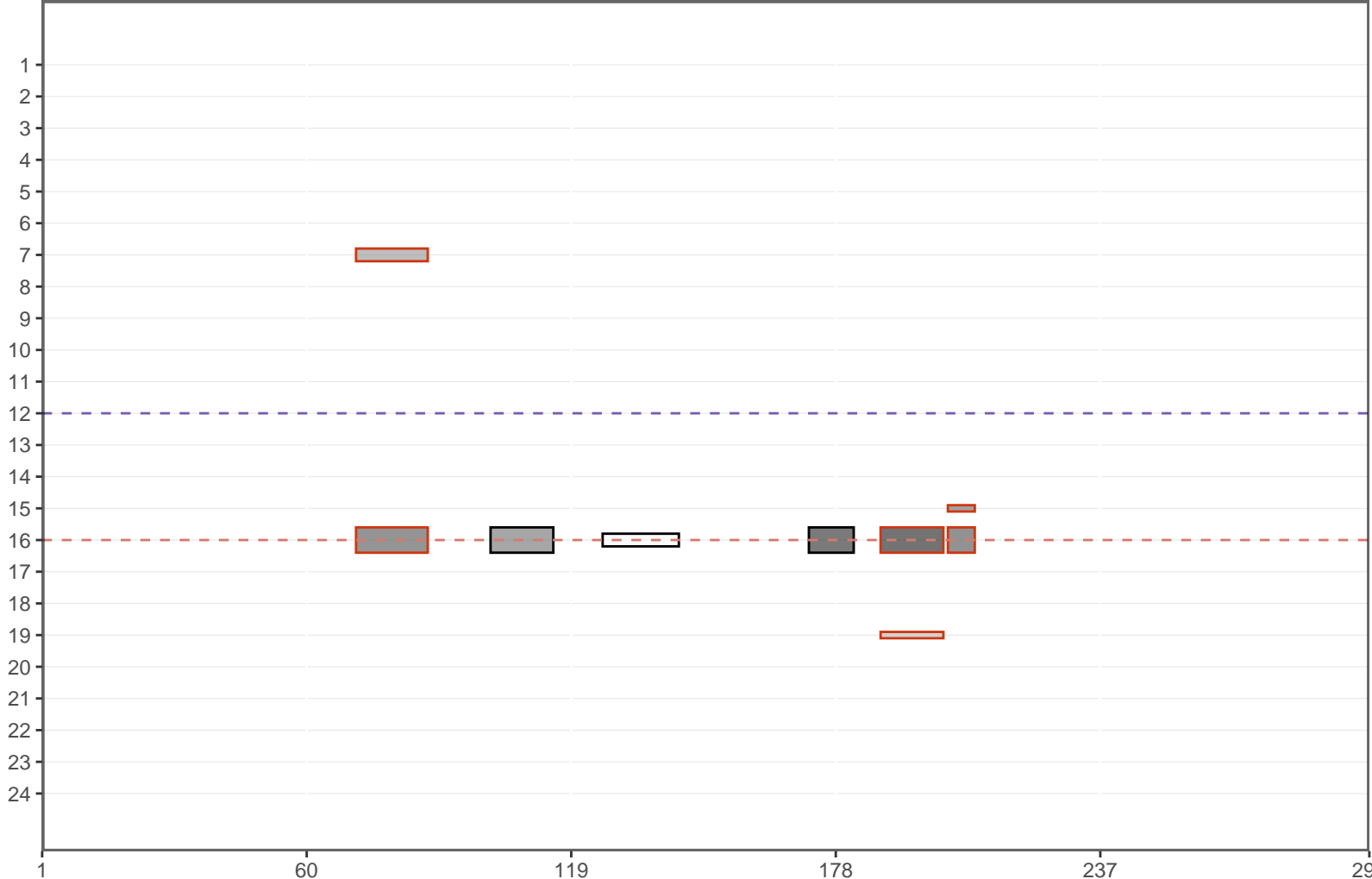
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

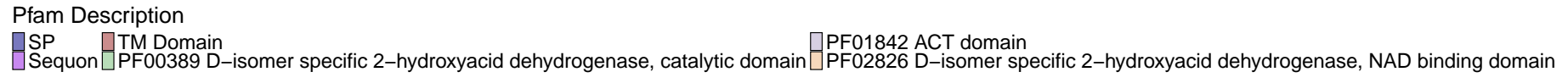
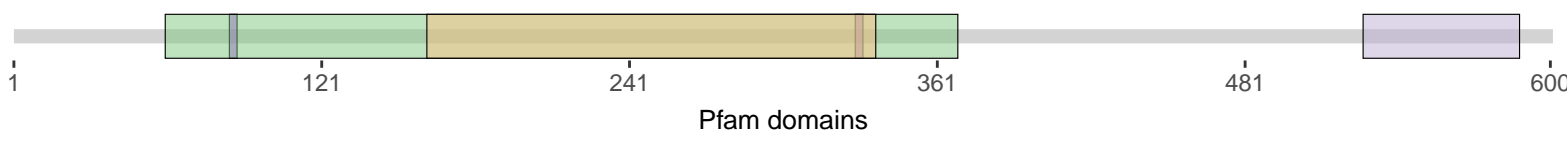
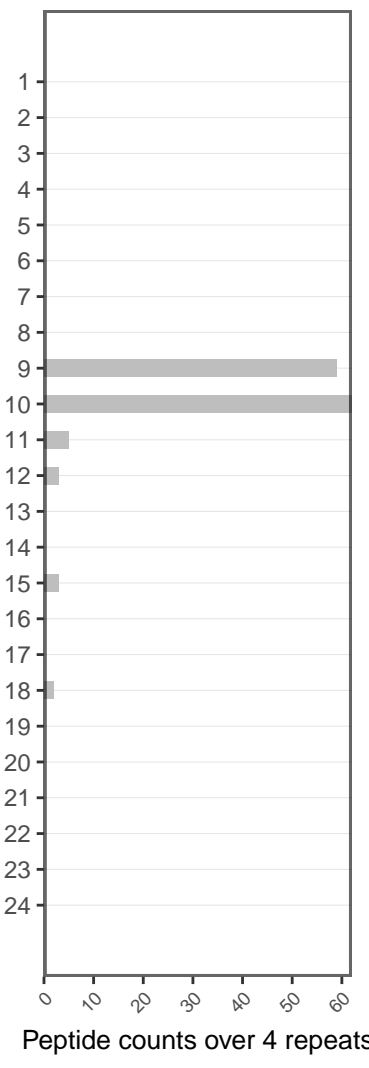
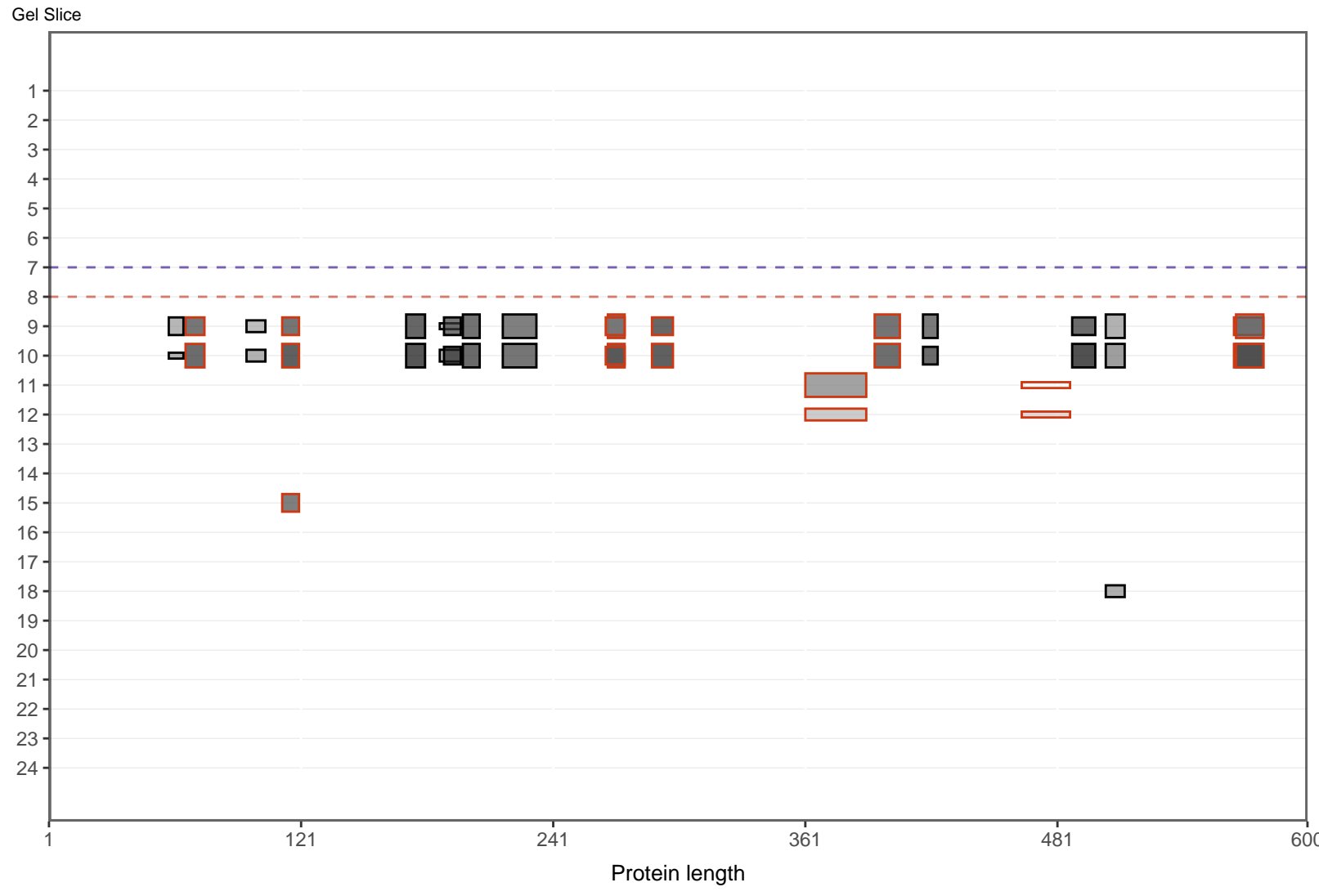
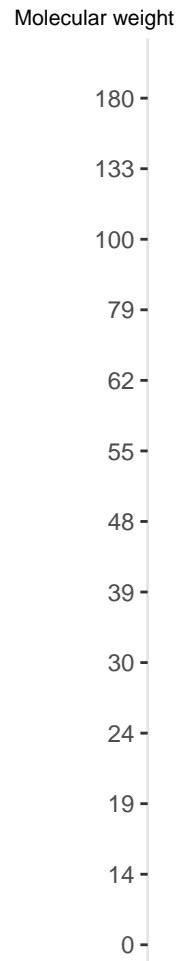
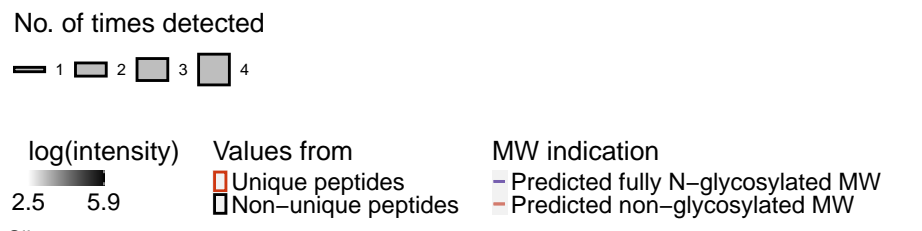
Pfam Description



Protein sequence:

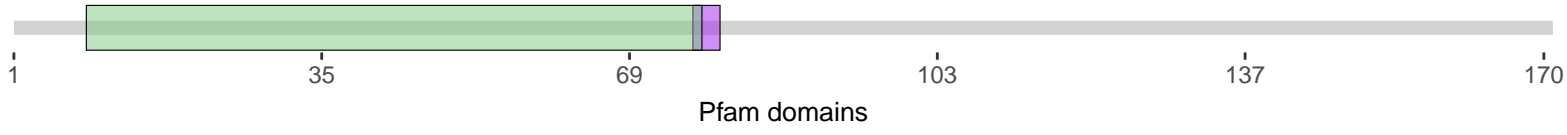
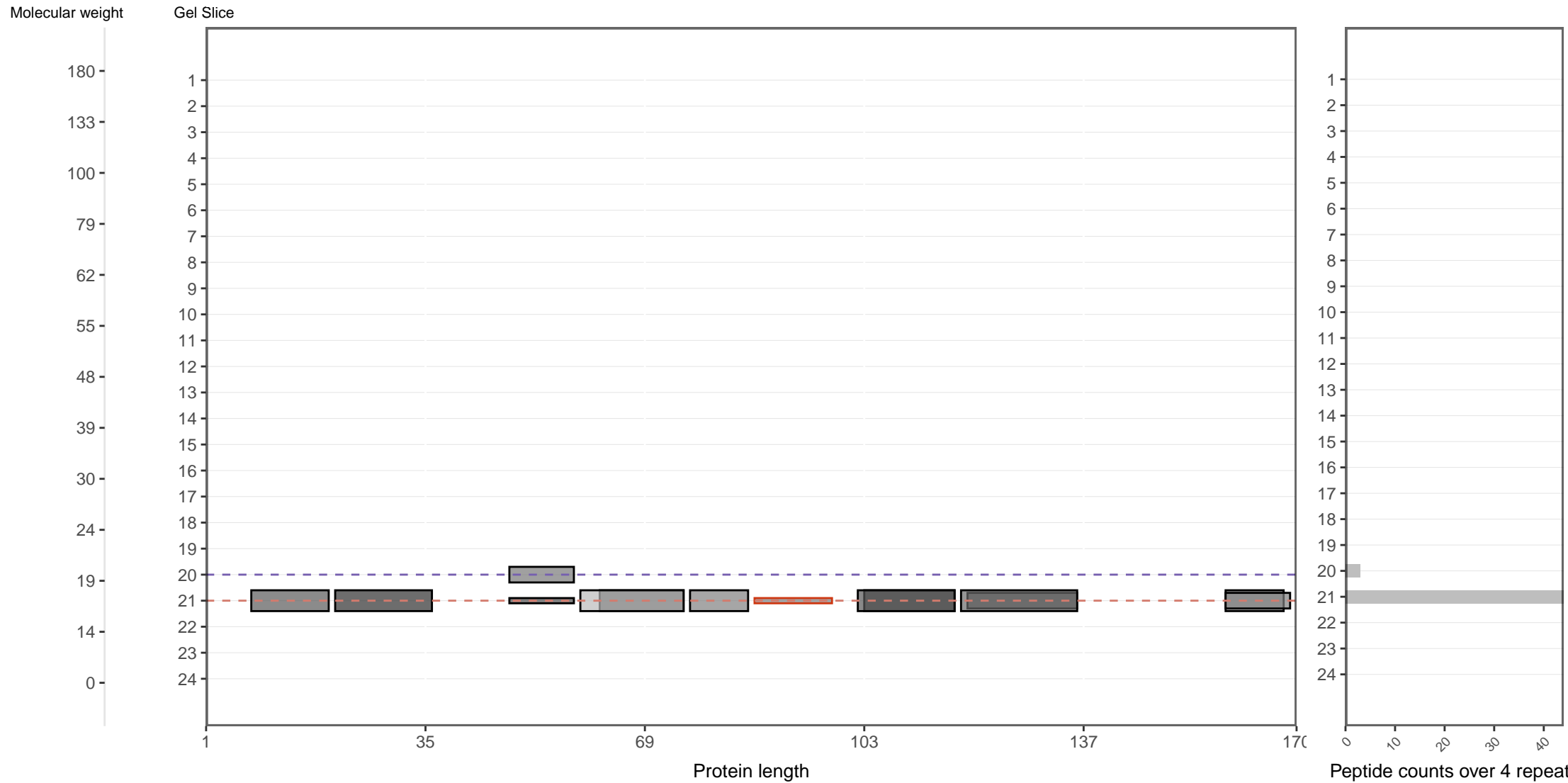
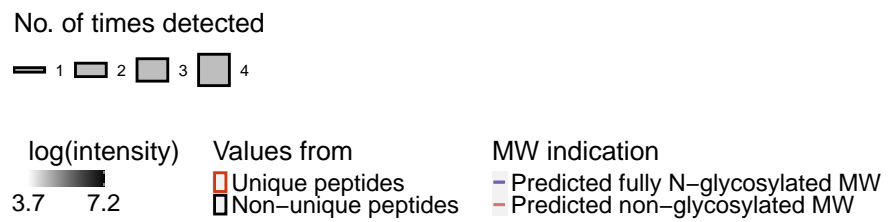
GEAFVVRNIVANLVPPVYENGPSSETNALEFVNTLKVQNLVGHHSRGGIRALMSMDNETPSSGFRBWWVLGKSARASTKAAASNLGFDGQGHCKEKEVNSGLMNLLETYPWIKDKVKNKGELLHGGYYDFVDCFTFEKWTLENNRVRVNDQVSRINREFWVY

NbL03g09110.1 D-3-phosphoglycerate_dehydrogenase_1_chloroplastic-like [MW = 63.29 kDa]



Protein sequence:
 VARGGVDEEALVRALEDAGVAGAALEDVFTVEPPPKDKSLQIHNVTATPHLGASTMEAGVQVMEVAVVAGALKGELSATVNAFVPAEVLSELKPYVLAELGRLAVGLVAGGGGKVKVYTYGSRAPDQLDTRLLRAMITKGLIEPISVFNINVAIDFTAKGRGLRAIEERILLDGGSPSPVEFHQVQIANVESKFAISDSGIEIRVGRVKGDKVPHLTKVGFSEVDSLEGGHLCGQVDDQPMGKVGSEVLEGENVNVNFMTVGRIPRQKQVAMVGVDEQPSKSLI

NbL03g08920.1 glycine-rich_RNA-binding_protein-like [MW = 16.97 kDa]



Pfam Description

SP Sequon TM Domain PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

Protein sequence:
 ITVNEAQRSGSGGGGGGGGFRGRRREGGGYGGGGYGGGRREGGGGGYGGGGYGGGRDRYGGGGDRYGGGGGSRYRGGGGDDGNWRN

NbL03g08910.1 probable_pinoresinol-lariciresinol_reductase_3 [MW = 34.6 kDa]

No. of times detected



log(intensity)



Values from



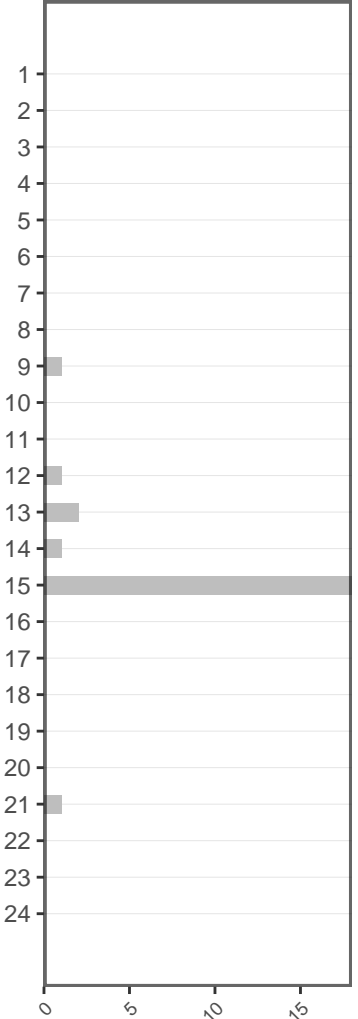
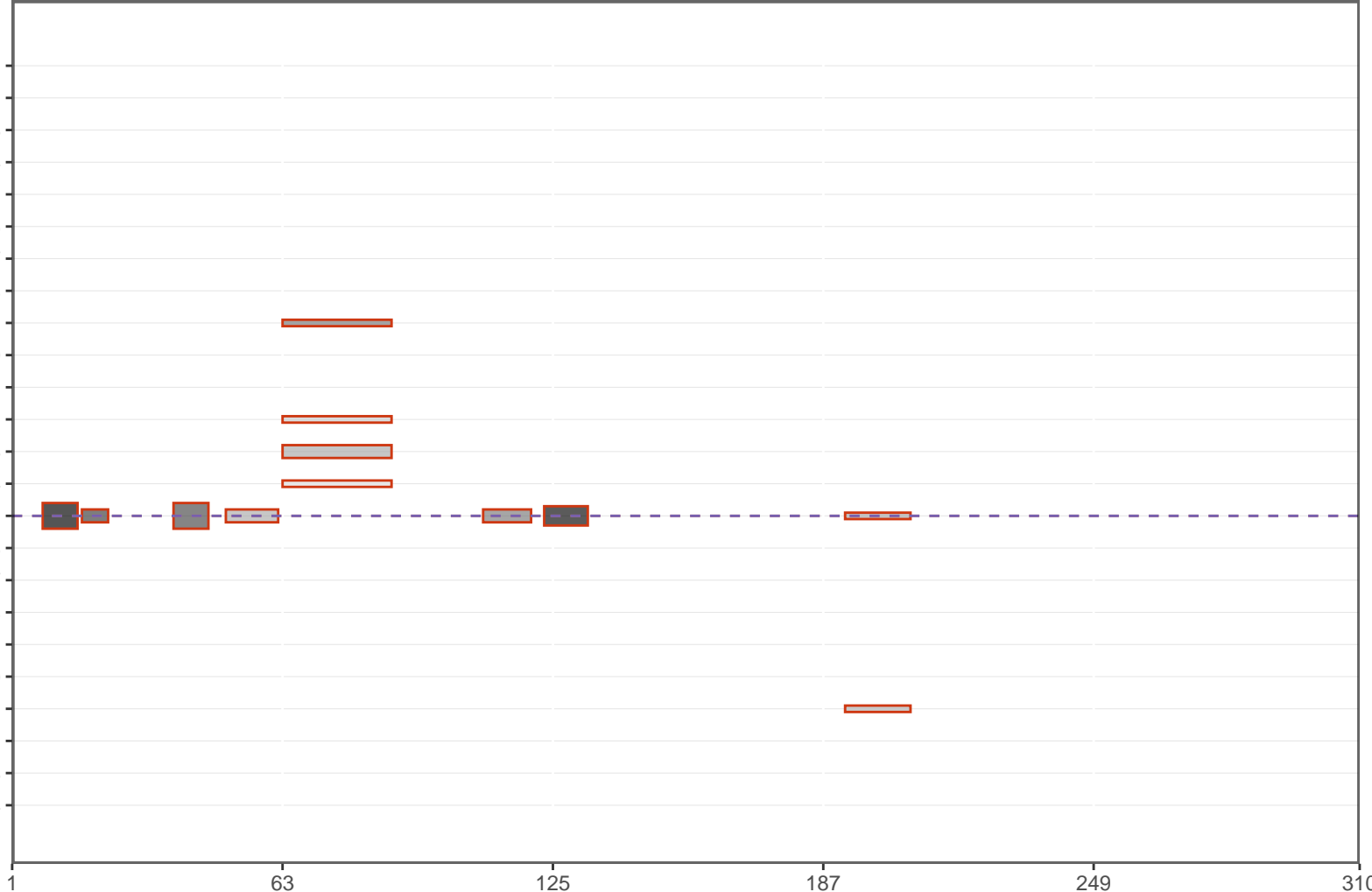
MW indication



Molecular weight

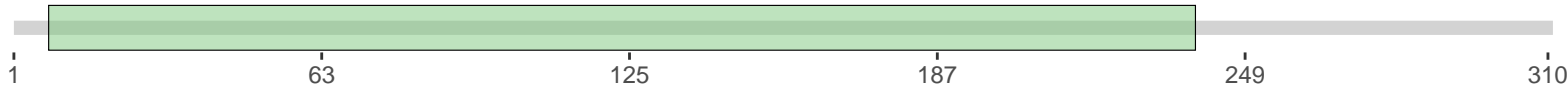


Gel Slice



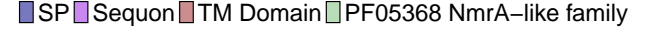
Peptide counts over 4 repeats

Protein length



Pfam domains

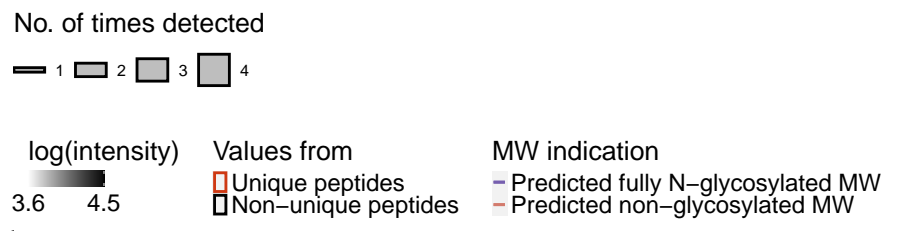
Pfam Description



Protein sequence:

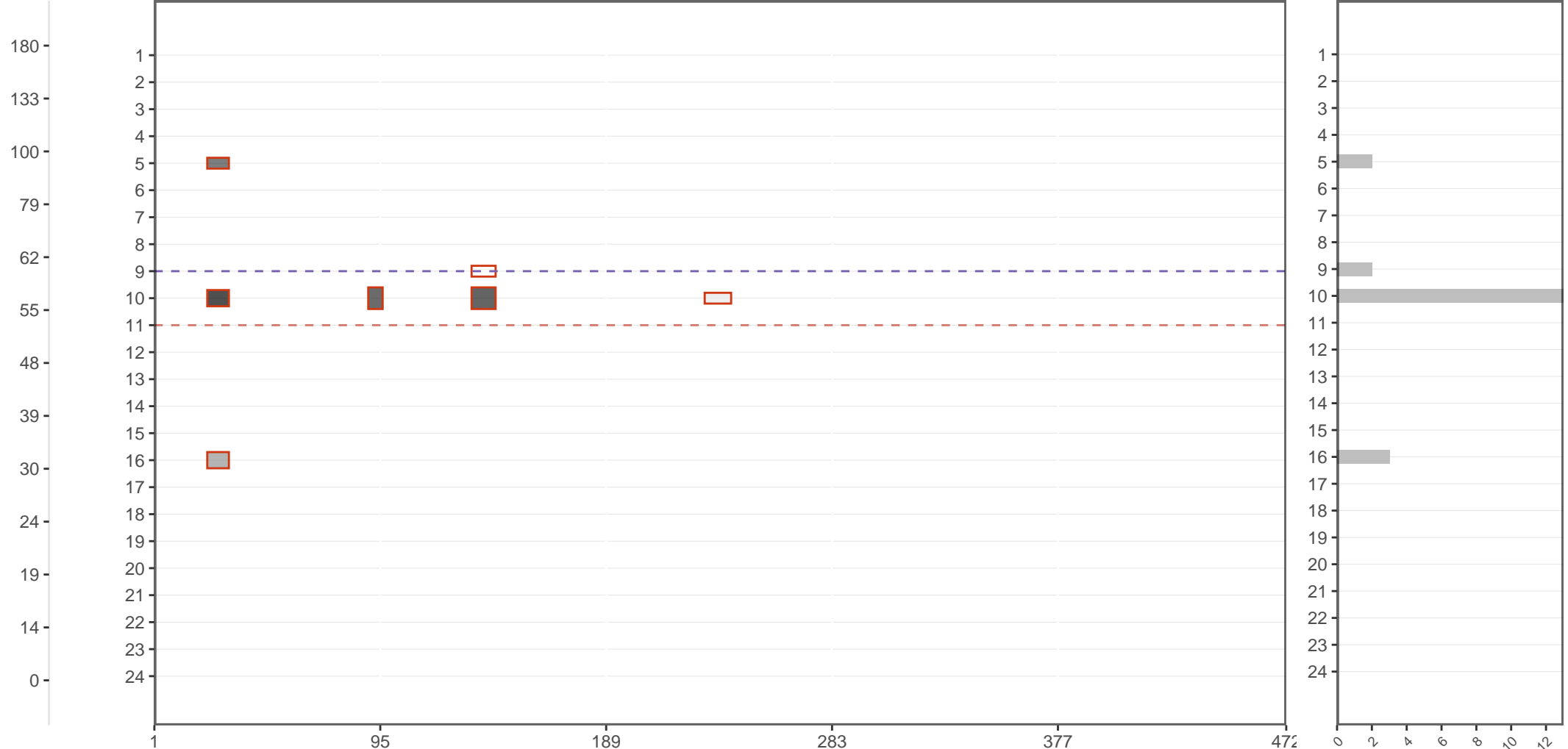
AEGIPYTYCCNFFTSFLPELGPGRKTRPRDEVSIFGDGTAKAVFKENDAAAFANTVDDLRTLNKKVHLRPPGNVYSMNELVDIWEKIGKALKRNYFTEDELLKRIKREMPYFENMELVIFYSAFVKGDDTYFSIDSSGGLEGQIQYPIQTYTRISEFLDTLL*

NbL03g08870.1 bifunctional_dihydrofolate_reductase-thymidylate_synthase-like [MW = 52.67 kDa]



Molecular weight

Gel Slice



Protein length

Pfam domains

Pfam Description

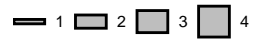
- SP Sequon
- TM Domain
- PF00186 Dihydrofolate reductase
- PF00303 Thymidylate synthase

Protein sequence:

DEVKTFSFLPNMFEKHEEYKFLRLVEEISNGMPKDDRTGTGLSKFGGQMRFLNKSPFLTKKVFWRGVVEELLWFISGSTSSKVLQKQGHKHWGDNAGRDLVDIGLNDREEGDLPVYGFQWRHFGARYDMHTDYSGGFDGLADVNIKIKNPPDDRRLILSAWNPSSDKLMLPFCHEMFAQFYVANGELSGQMYGRSADMLGLGVPEFIASVALLTCMAHVTDLVPGDFVHWGDAHW

NbL03g08820.1 purple_acid_phosphatase_2-like [MW - SP = 51.45 kDa]

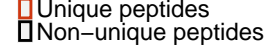
No. of times detected



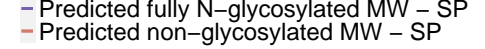
log(intensity)



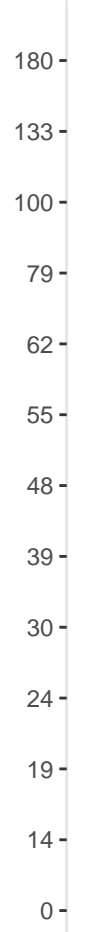
Values from



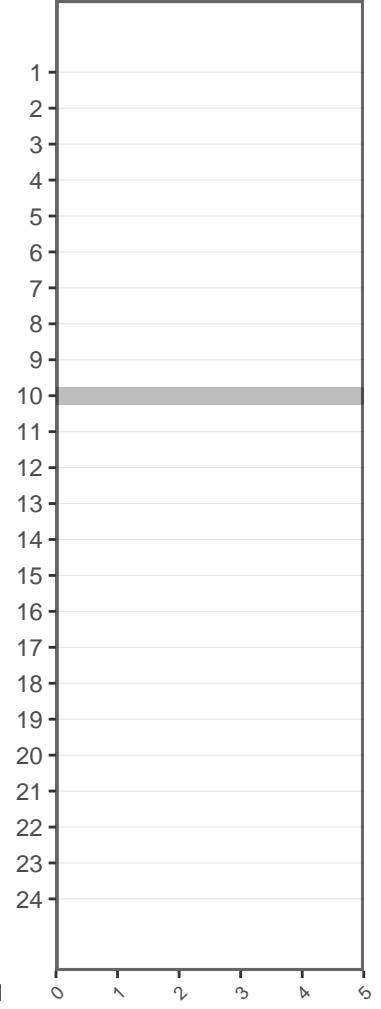
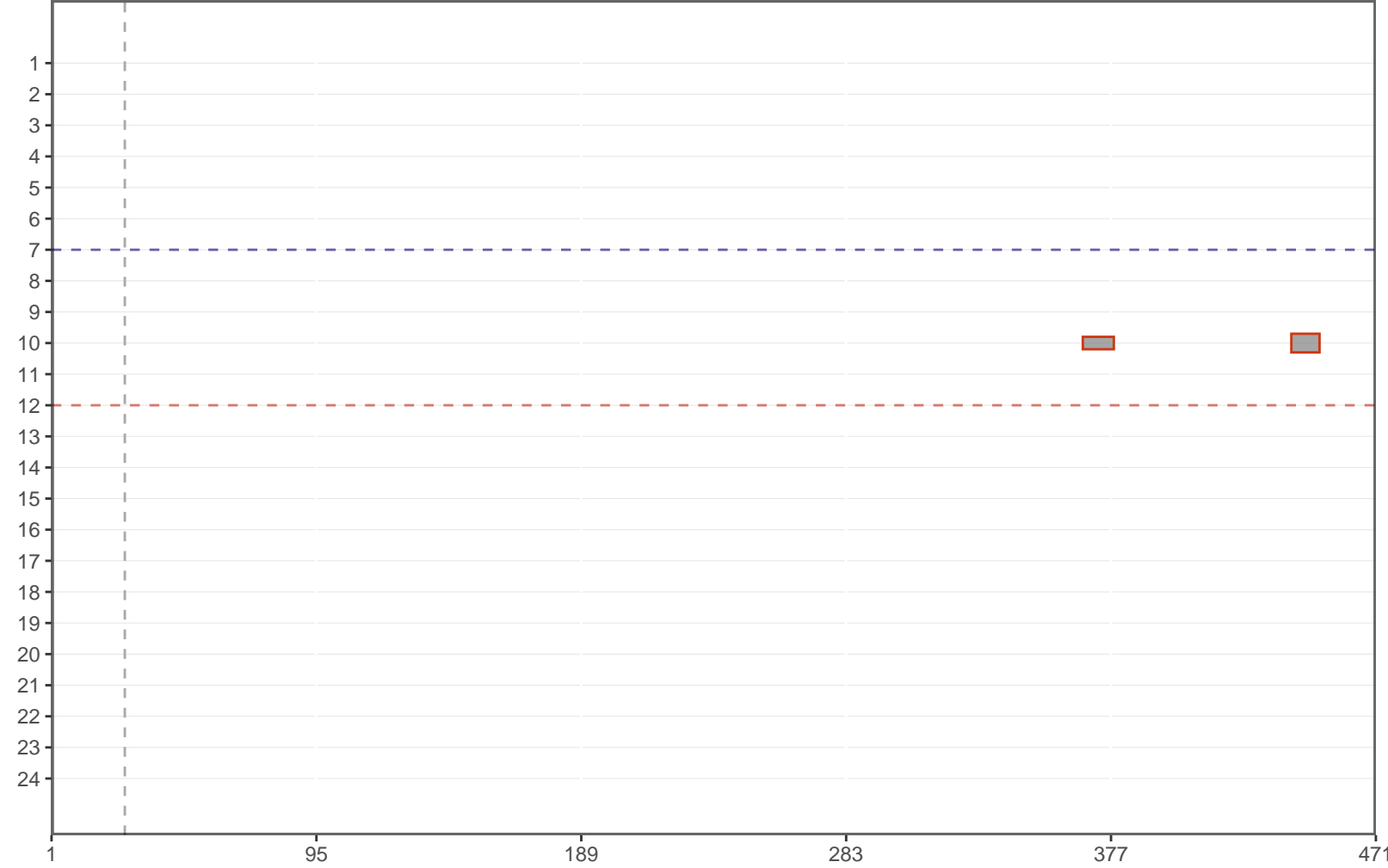
MW indication



Molecular weight



Gel Slice

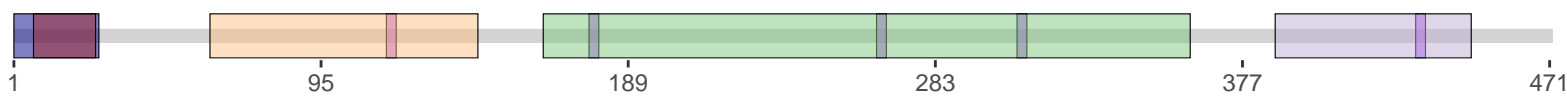


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SVAYQPWVWTTGNHEIDFAPEIGETPKPKPYTHRYRVVPYKSSNSTAPFVYSIKRASAVHVLSSYSAVGMYPQVQWLYEELPKVNRSETPALVLLHSPWVNYHMEGETMRVAVYEPVQVYKVDVVFAGHVAHYERSERVSNWAVYVNGKCTPRDGSAPVYTRDGGNIEGLANEMTEPQPEVSAFREASFGHATLDKNRTHAYVSWHRNKGQYTVKADKLLVYVRFVHPVDDSTAPKQ

NbL03g08800.1 xylulose_kinase-like [MW = 52.42 kDa]

No. of times detected



log(intensity)



Values from



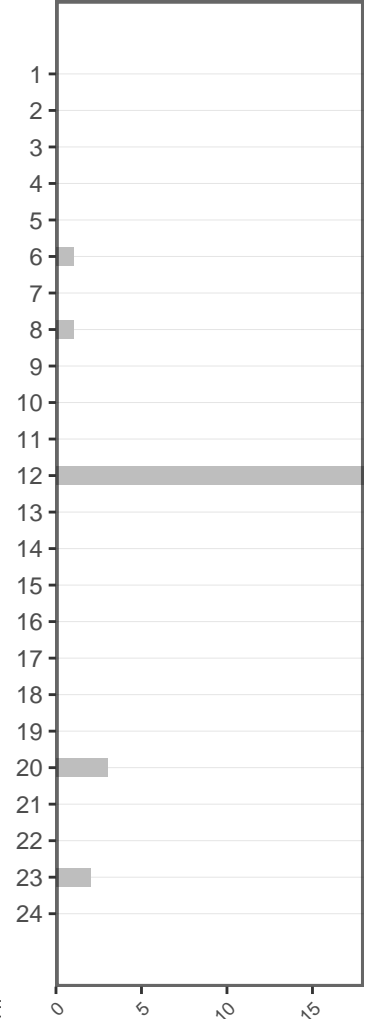
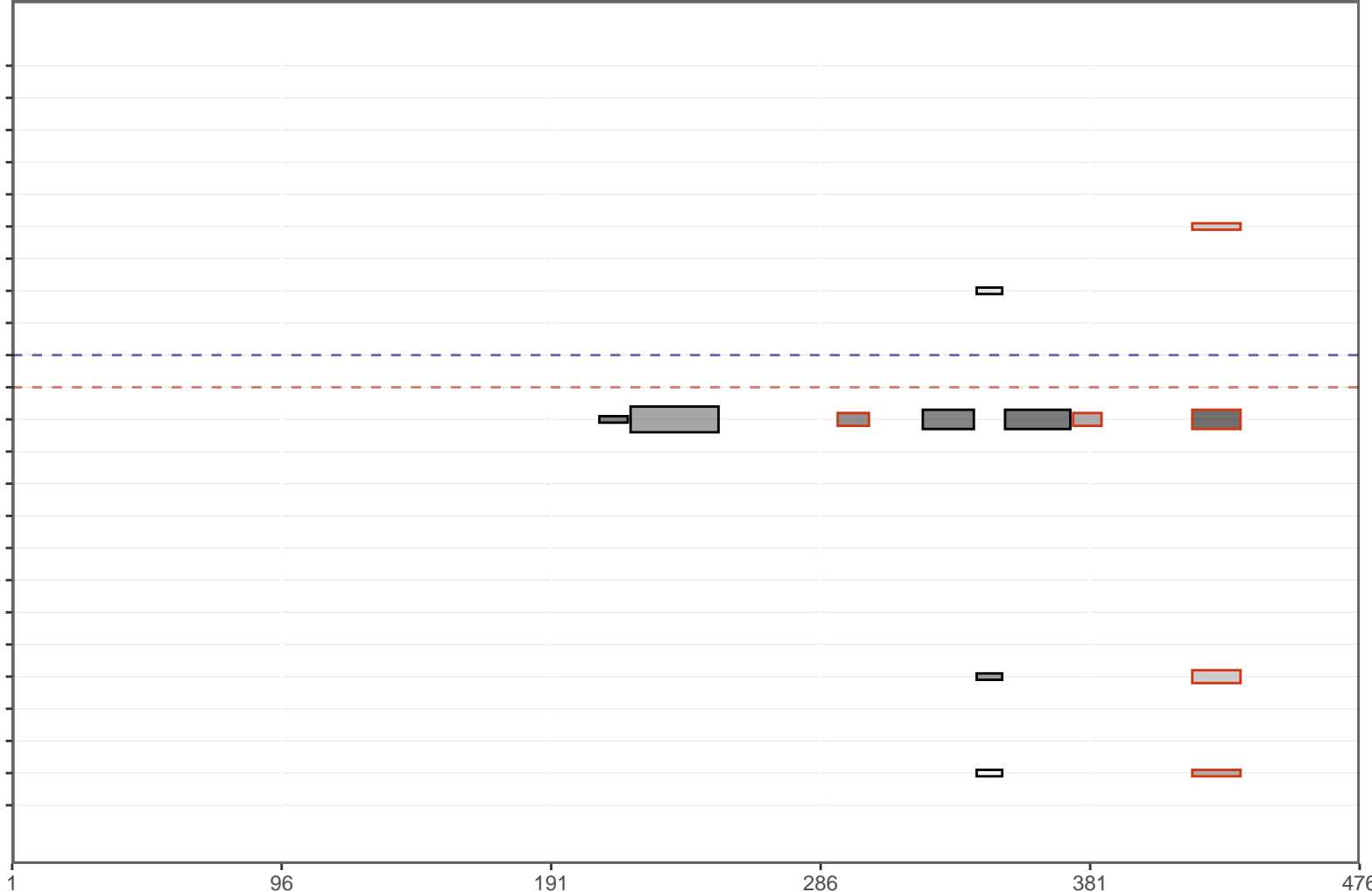
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00370 FGGY family of carbohydrate kinases, N-terminal domain
- PF02782 FGGY family of carbohydrate kinases, C-terminal domain

Protein sequence:

ITDSYPSVLLSOPYSKLLPEVGAQPGTKGCKEDIRTFQFGYPKDGAICTGTTDSIAFLAARATQPKAVTSLGSLAKLLSTRVEDARFGVYSHRLDDKWLVGSAINTGGAVLRQLFTDEQLAKLSEGINPLEASPLDVIPLGAVGERFFPADPNMEPRLHPPENDVEYKHLGILEGRIEAKGVNLLKDLGATPVEEVITSGGGKNEKWTQKRRERVLGLPVRADQTEAVGAALLAKGGSENIP

NbL03g08720.1 epimerase_family_protein_SDR39U1 [MW = 38.71 kDa]

No. of times detected



log(intensity)



Values from



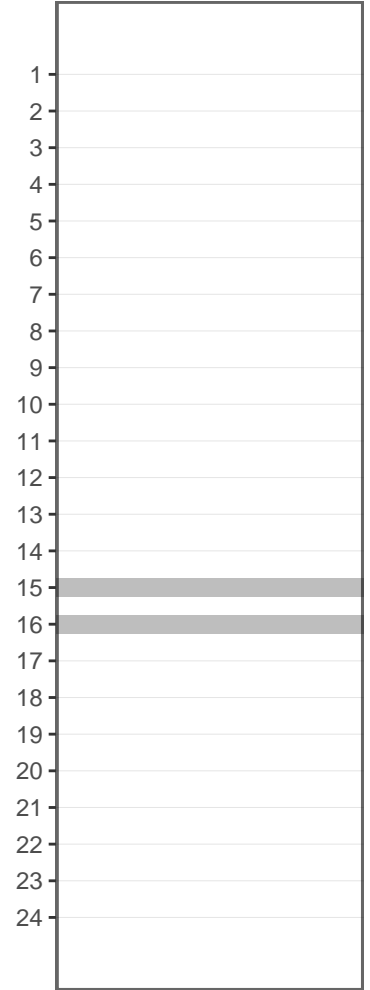
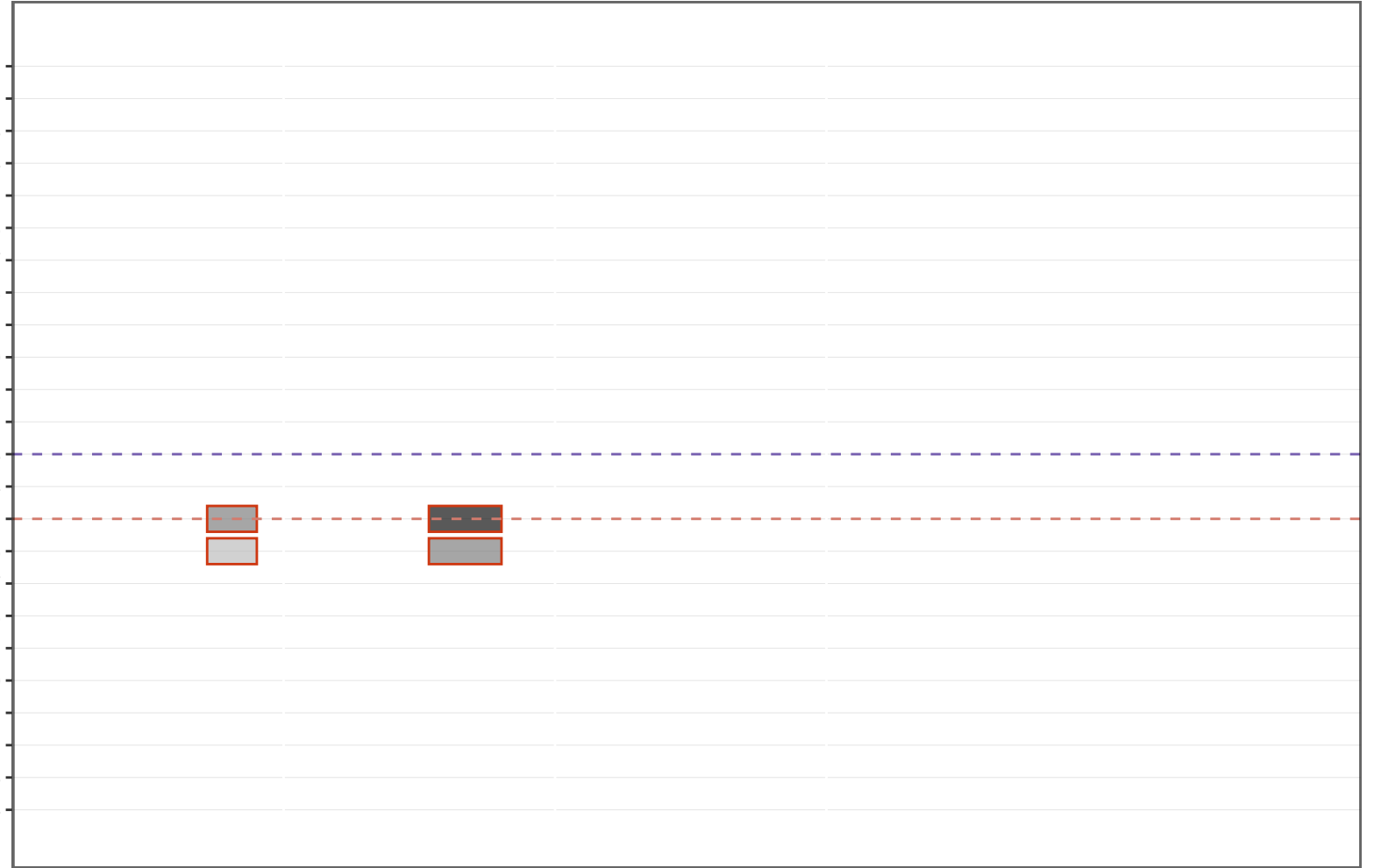
MW indication



Molecular weight



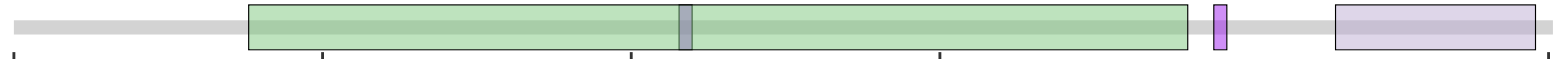
Gel Slice



Peptide counts over 4 repeats

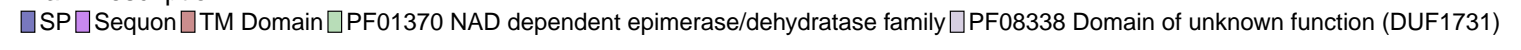


Protein length



Pfam domains

Pfam Description



Protein sequence:

FISASAVYYGISETRVFDGSPGNDYLAEGREWEGAALKVNDVRLALIRGVVLDKDGALAKMPFMMFAGPLGGNGWFWHLDDLVLEALSNFYKGVINGTAPNPNVLAEMCEQLGSLGRPWLVPPEIALKAVLGGASVLLDGGKVPTRAKELGFFKRYKDKALKAIMS

NbL03g08710.1 ubiquitin_fusion_degradation_protein_1_homolog [MW = 35.69 kDa]

No. of times detected



log(intensity)



Values from



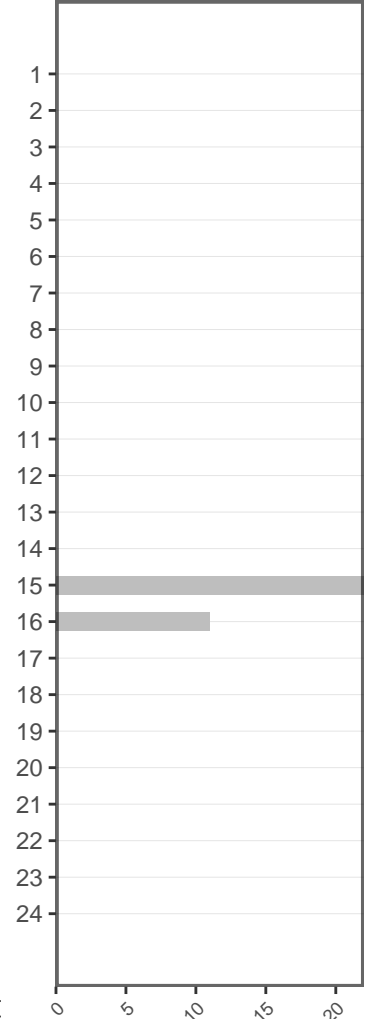
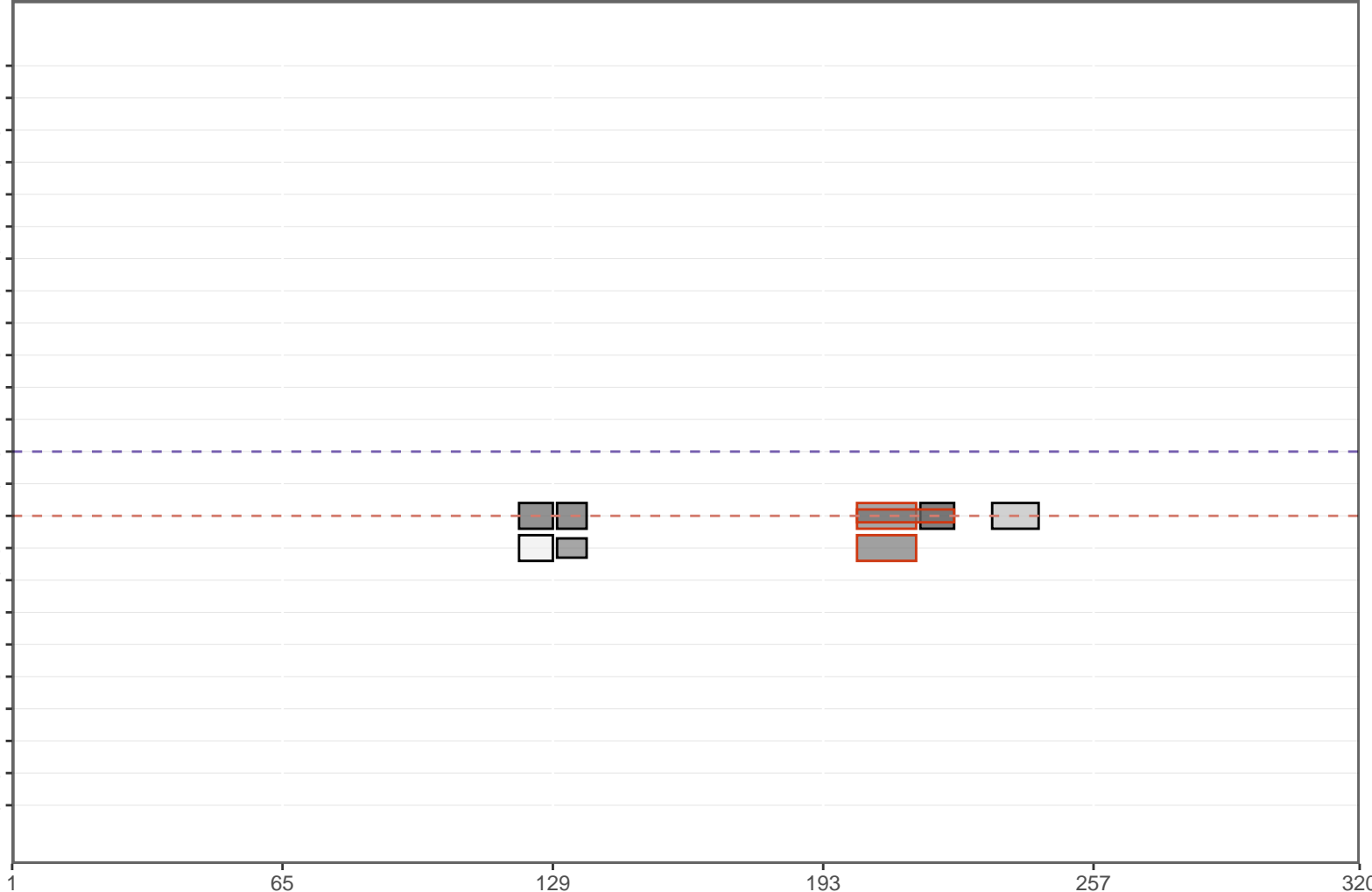
MW indication



Molecular weight



Gel Slice

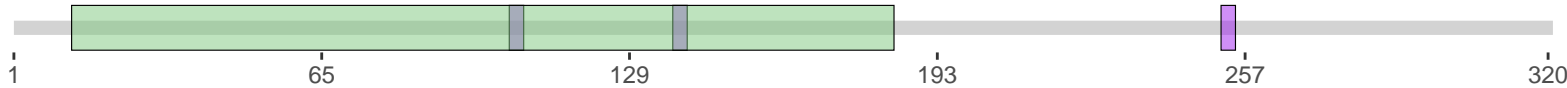


Protein length

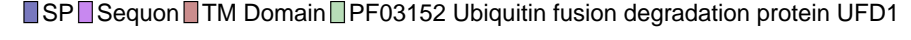


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

AAWYNNKYYIDIVIEKPEKPAISHSIETDGEVDFAPPLDYKPERPVPPLPKTRPEEGEAAAEEEPKFNFTGSARRLDGKPLKGGPPVSTSGSKDKRPFDMANATGSGAAGSSGSGSNRGTQGLVFGDANANRLDKQKEPKVKEEPEKQKRAFTGKHYLRG

NbL03g08590.1 SKP1-like_protein_1A [MW = 17.51 kDa]

No. of times detected



log(intensity)



Values from



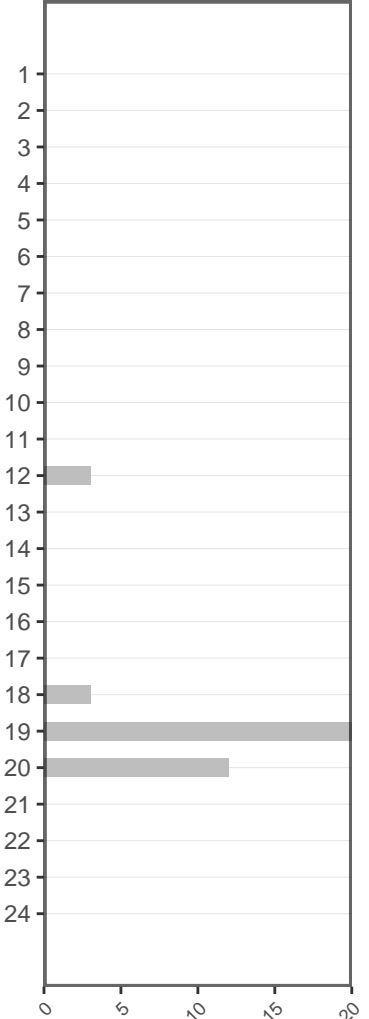
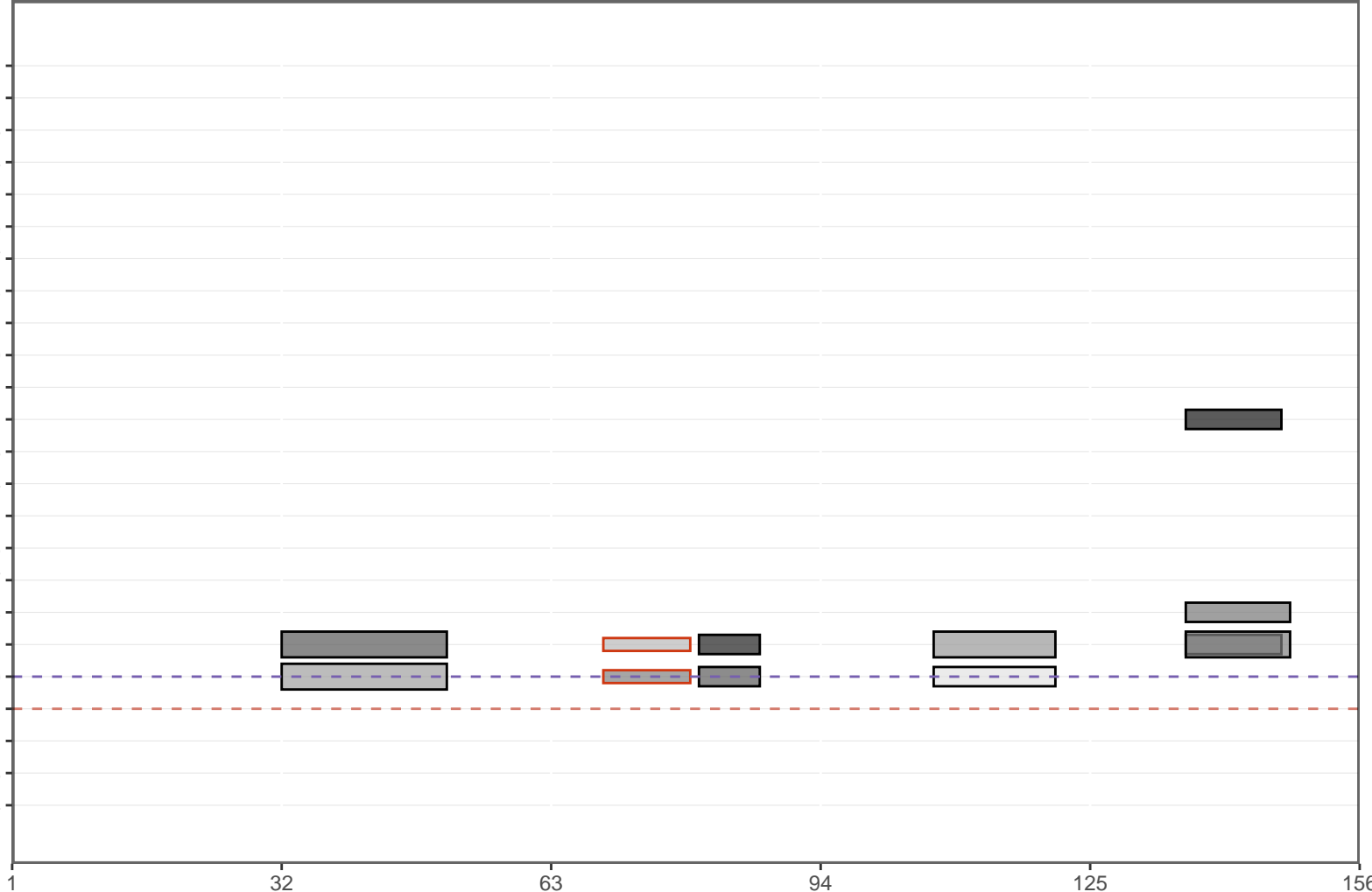
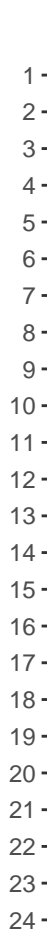
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

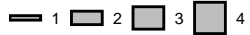


Protein sequence:

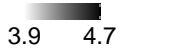
DAAKTEDKASEDELMKAFDSDFVKGVDGATLFDLHLAANYLNKIKLLDLTGQTVADMIGKTPFEEIRKTFKNDFTPEEEEEVRRENWAFEE

NbL03g08470.1 expansin-like_A2 [MW - SP = 26.52 kDa]

No. of times detected



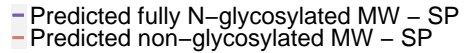
log(intensity)



Values from

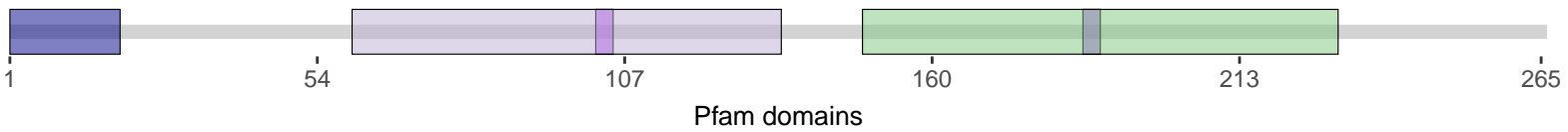
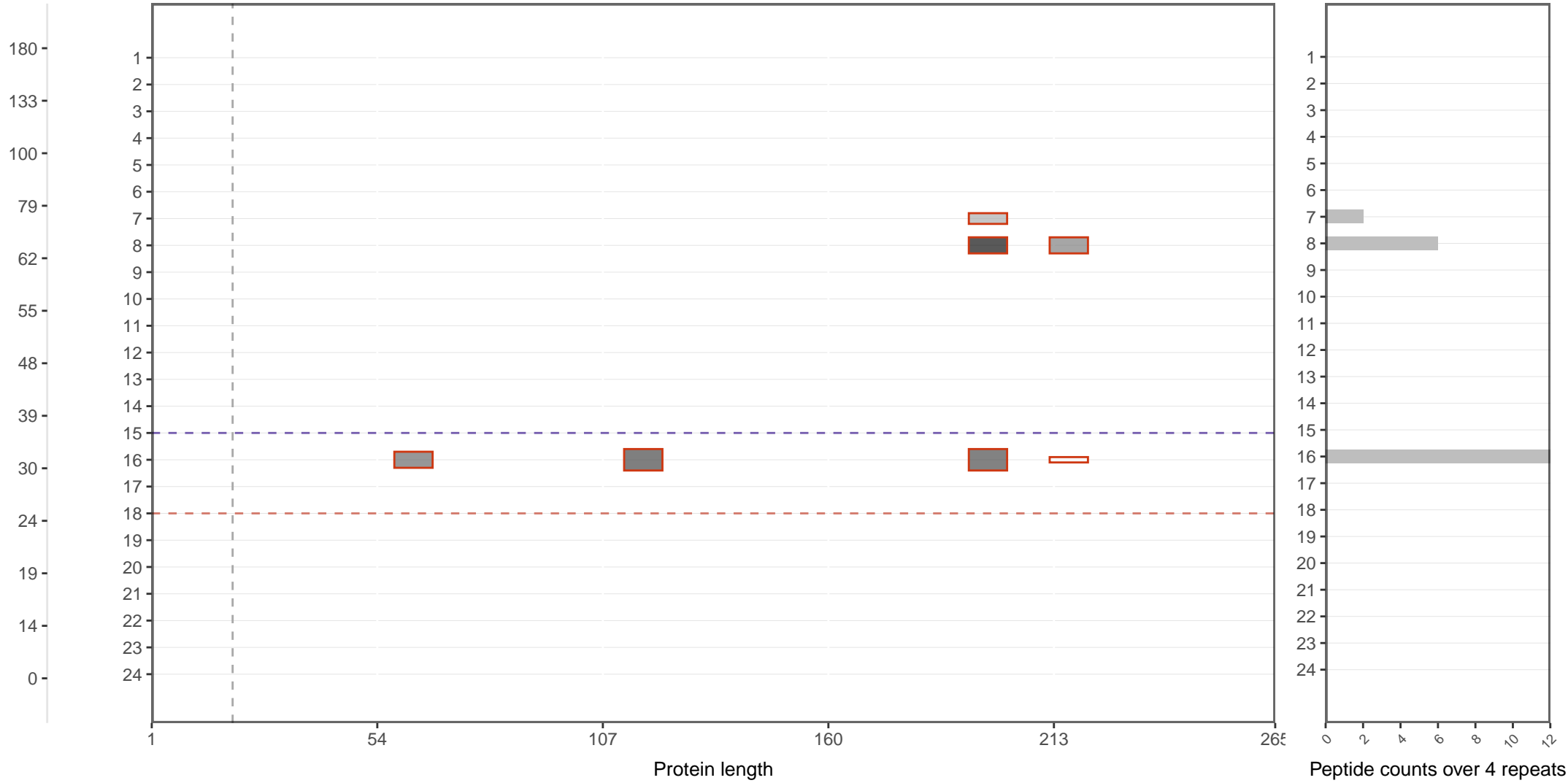


MW indication

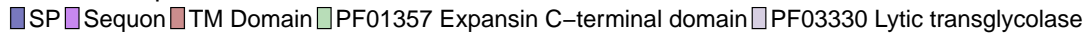


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

SKADLLKLAIVYDVEKRVPCDFKKNLARVEGSSKFNFLAIFLVGGGQTEIVGVDAVGVGSSNWFMSRNDGAWWDTSRVPKGALGRLLVTAFGFDGKWFWAKVLPANWRNGVHYDRLGIFDAEGGCEPCDDGTWKLPI

NbL03g08400.1 DNA_repair_RAD52-like_protein_1_mitochondrial [MW = 21.27 kDa]

No. of times detected



log(intensity)



Values from



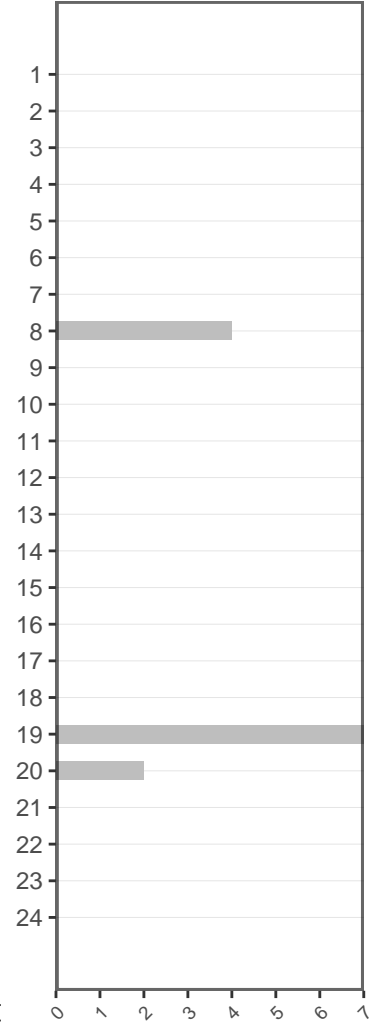
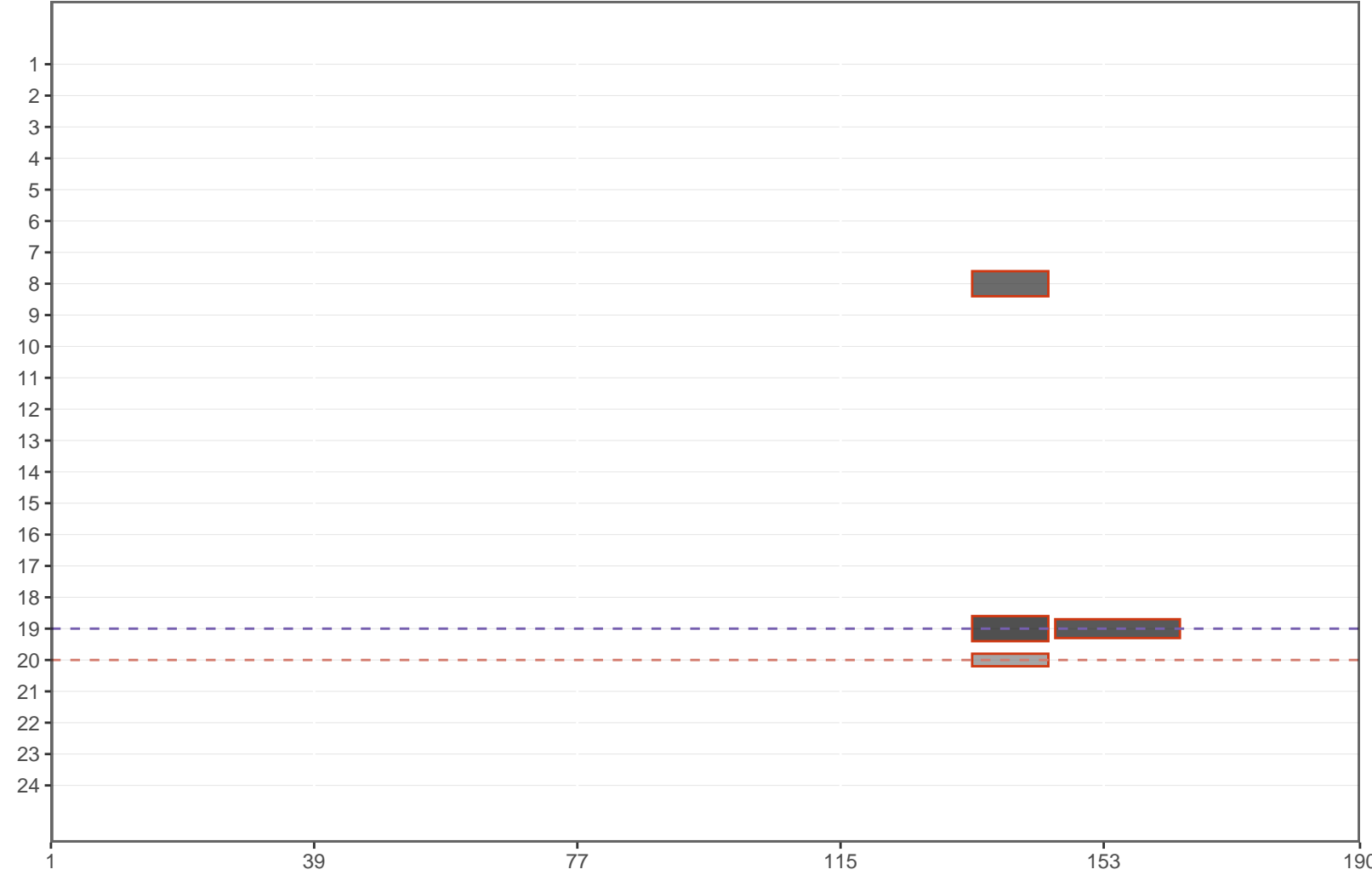
MW indication



Molecular weight



Gel Slice

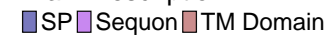


Protein length



Pfam domains

Pfam Description



Protein sequence:

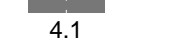
IKFRHIEPNIGSLKYIPWHVNRNLNHAPEWVSGEVRBINY6SDGK6V6VVRVFLYGTDAEIVRESTGTASVDDPGYGDPPVQKAEGMFRACARFGLGHLHYEDMS*

NbL03g08350.1 single-stranded_DNA-binding_protein_WHY2_mitochondrial [MW = 26.82 kDa]

No. of times detected



log(intensity)



Values from



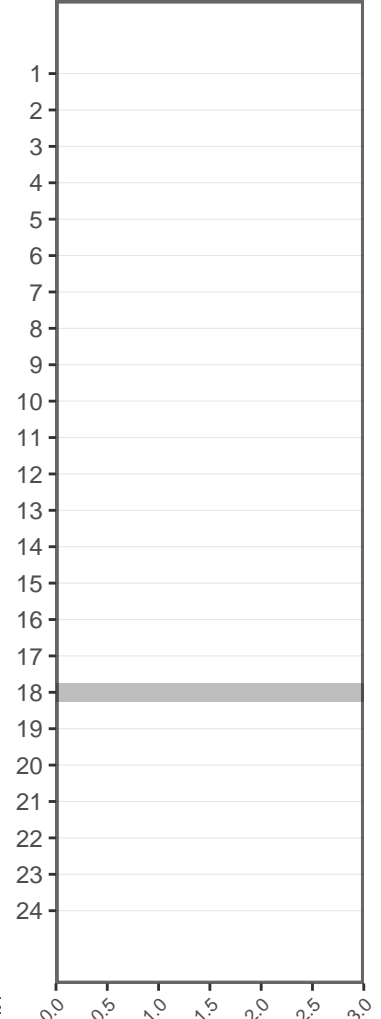
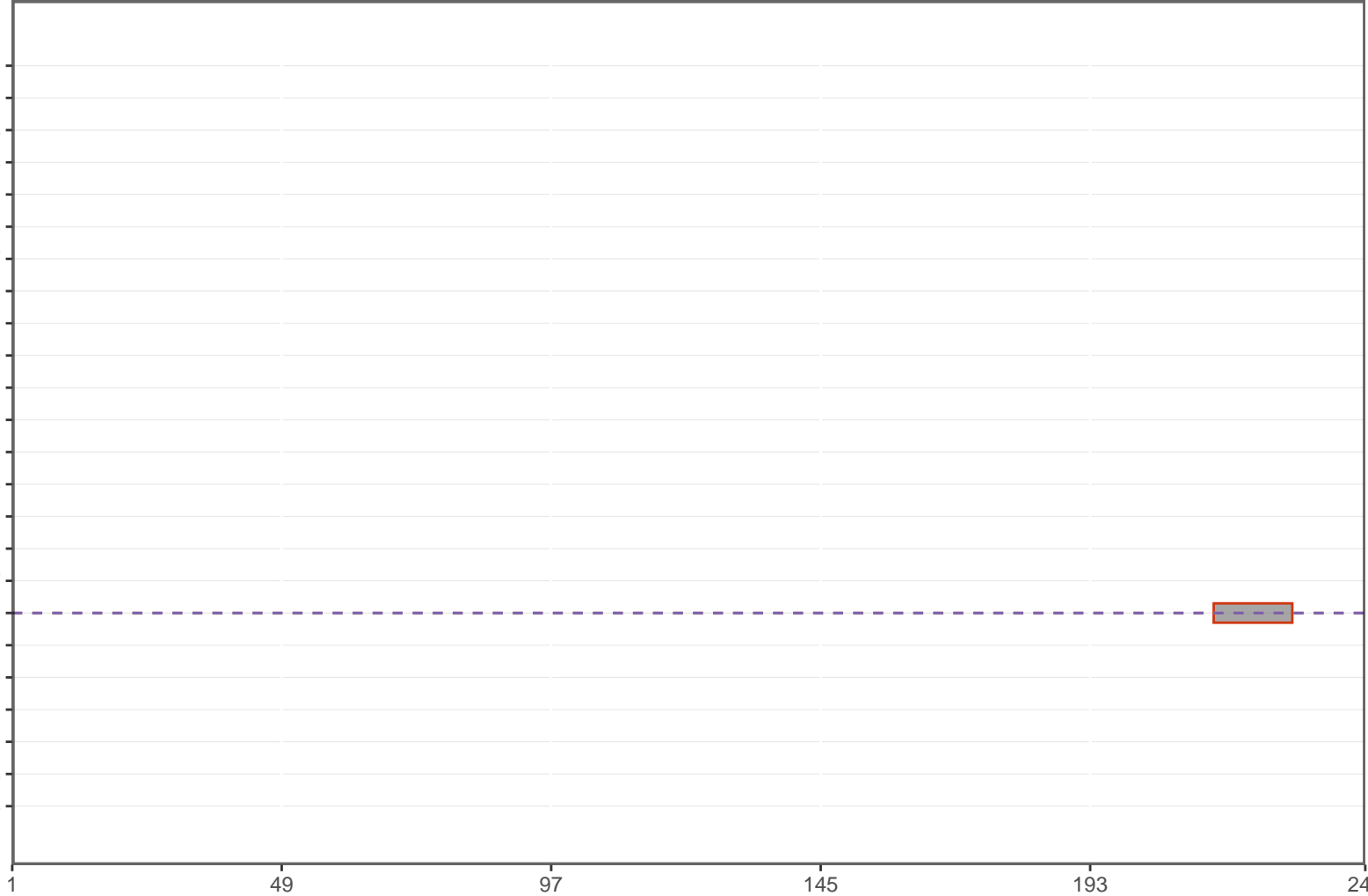
MW indication



Molecular weight

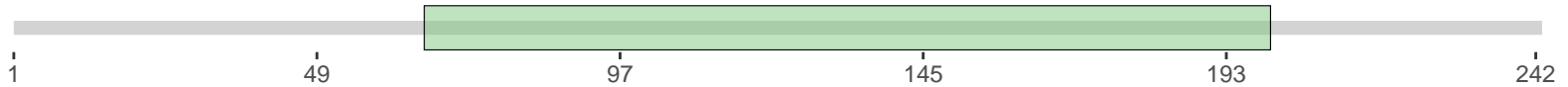


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

RKYDYVEKRLQFLGATEVGLISIGTRDGGCEFFHDFPSMLSSNAGQVRKLSLKPKNADGTCYFSLGIVNNLNKNNRFTVPVTTAEFAVMRTAFSFLPHIMGWDRFTNQPSEGGTPSKVVPQLMETEWDRI

NbL03g08280.1 60S_ribosomal_protein_L7a-2-like [MW = 29.35 kDa]

No. of times detected



log(intensity)



Values from



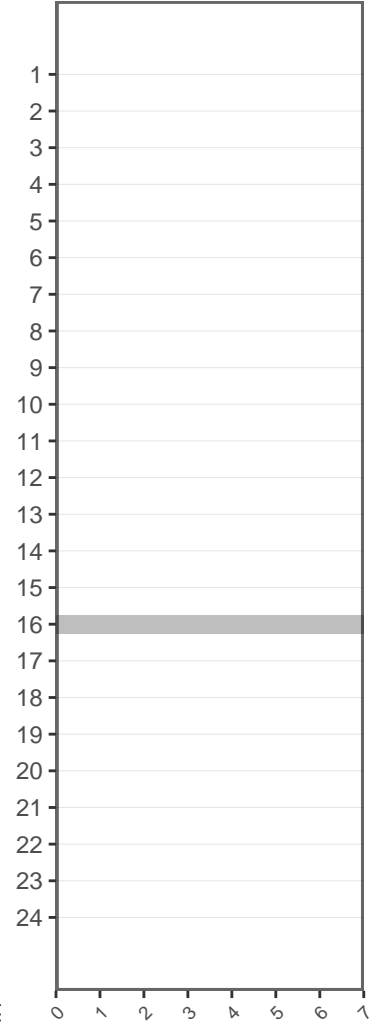
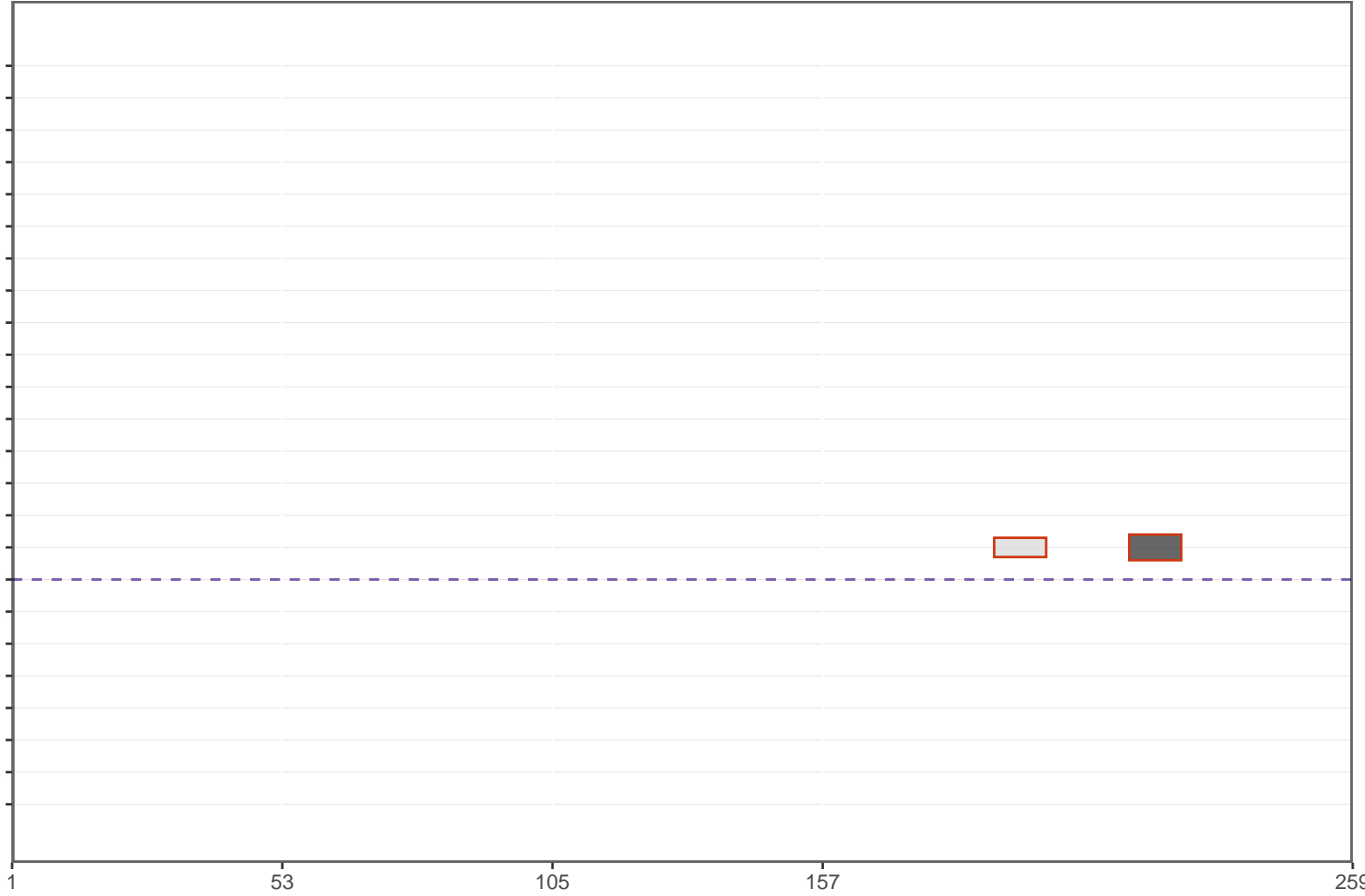
MW indication



Molecular weight



Gel Slice

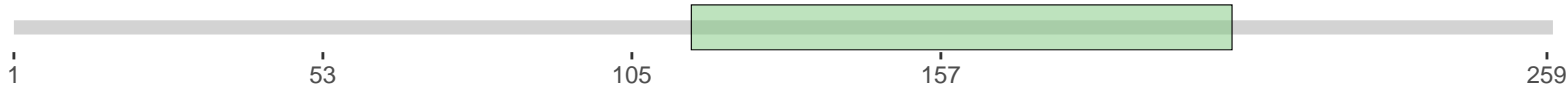


Peptide counts over 4 repeats

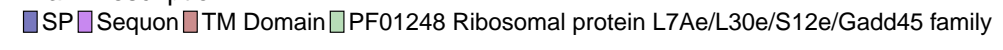
Protein length



Pfam domains



Pfam Description



Protein sequence:

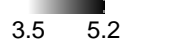
LEGKTPETKXPPIIVKGLKHTYLEGNKAGLVVAHHDVDPHELWVWLPALGRKMEIPYGVKGGKARLGVVHKKTASALGLTTLKNEGKMEFRILEAKANFNDFEENRKKVGGGVMDGKSGQARTKAKERVLAKAEADRMI

NbL03g08120.1 2-alkenal_reductase_(NADP(+)-dependent)-like [MW = 44.46 kDa]

No. of times detected



log(intensity)



Values from



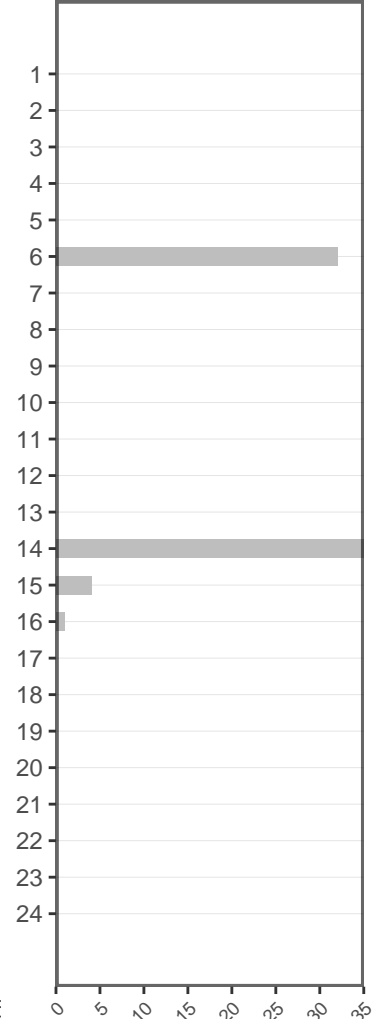
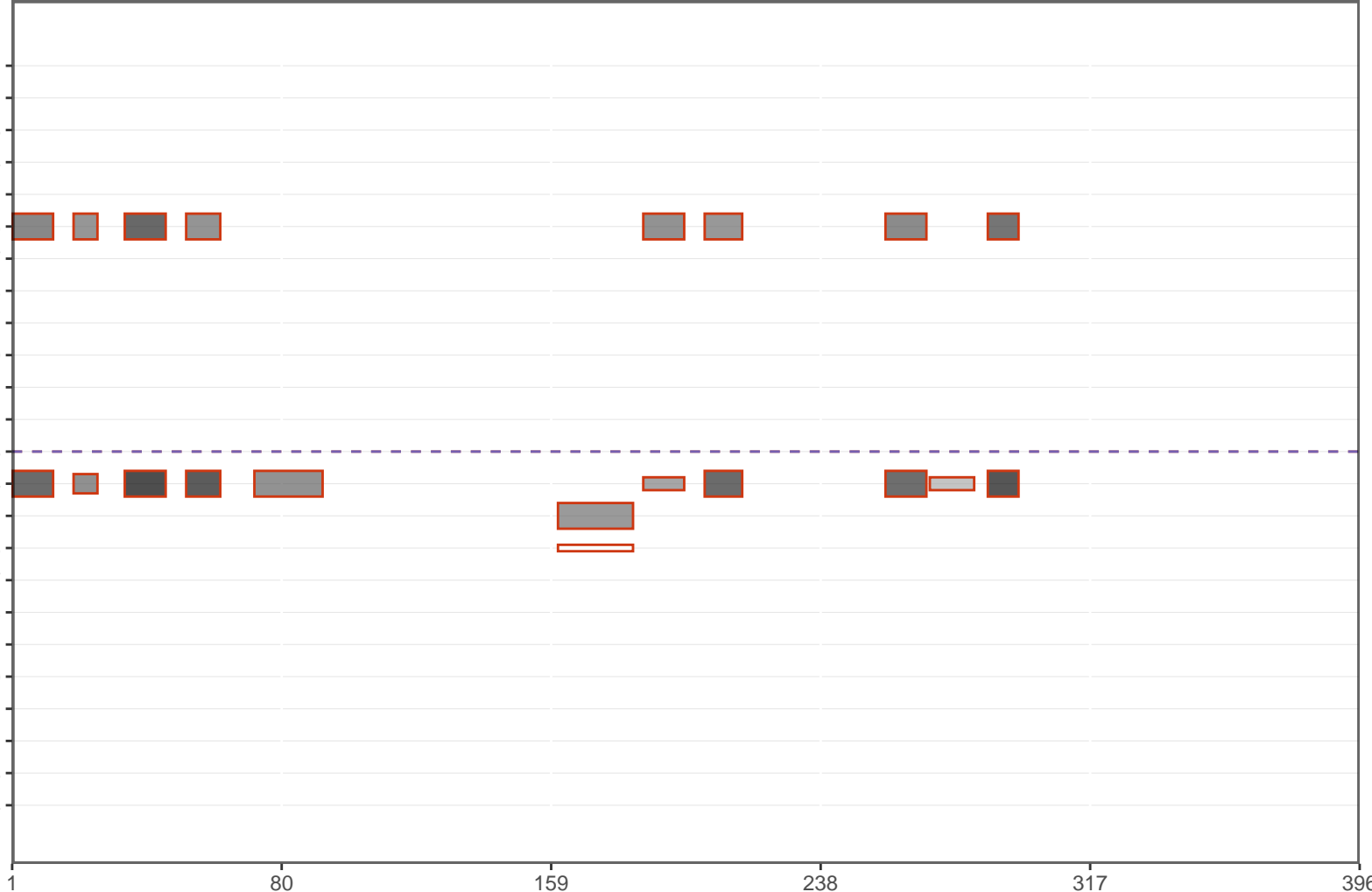
MW indication



Molecular weight



Gel Slice

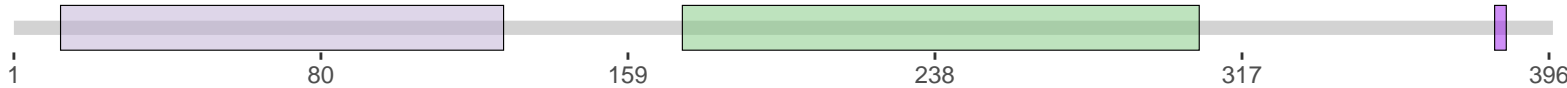


Protein length

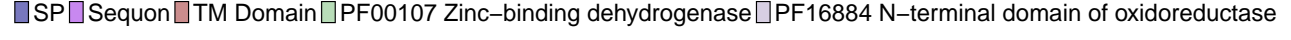


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IKGCYVYGSASTDEKVNLIKSELGFDFAFNKKEGDDFAGAKRHFPKGIDVYFENYGGNMLDEVLLHMLYGRITVGGMISQYNKPKPDGHNLFGLTKRLRMEGSELDFRHKVPELEFVQLREKKLVFEDIAEGLNENASAFVGVYHGRNKGKIQHRLNRDKWELRKNGFARFREFVKEKVCLSSTRMYSNESSLFGVNIWLSR

NbL03g08110.1 UPF0301_protein_TC_0483 [MW = 53.28 kDa]

No. of times detected



log(intensity)



Values from



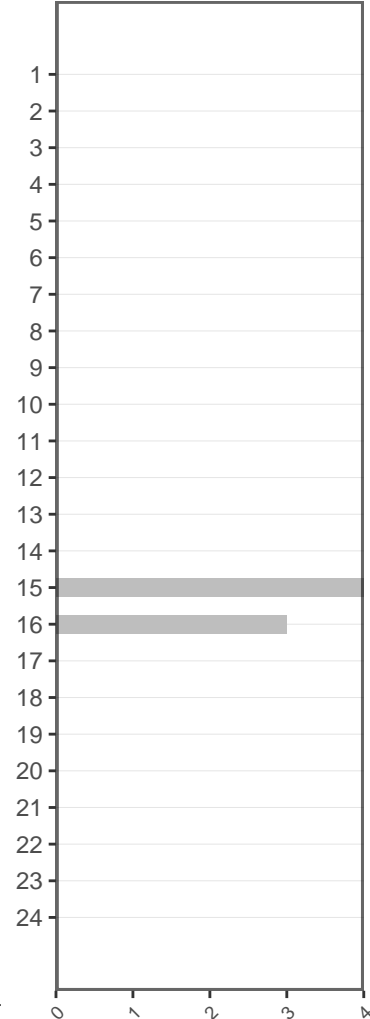
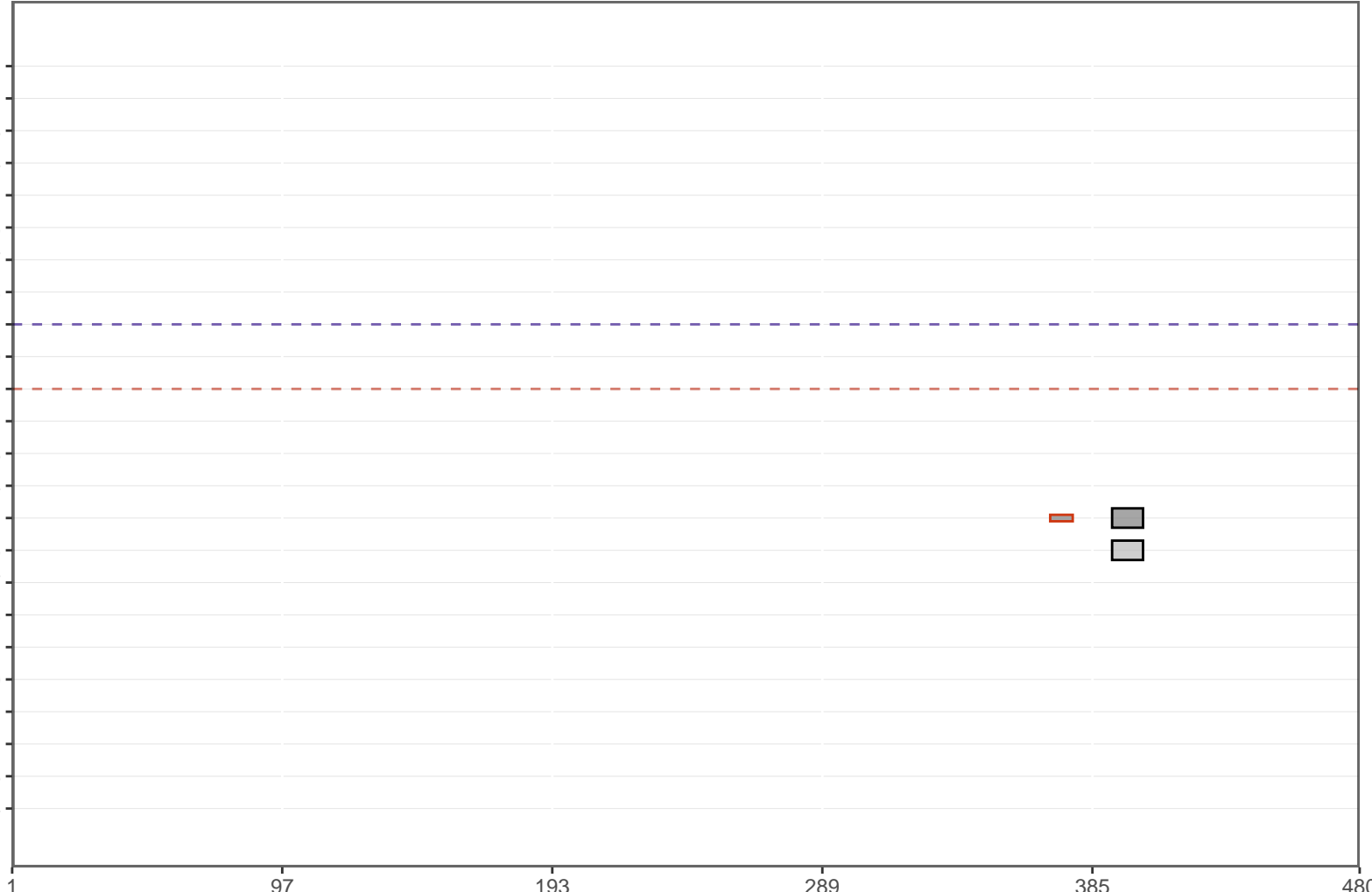
MW indication



Molecular weight



Gel Slice



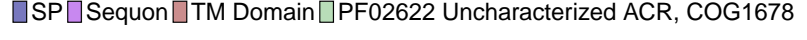
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IPKSHQKFLDVRFRFRASLYHQEQGAAATVSDTHKQEGTSFGPKALPLKVAHRIAPENQGVAVATEKLDGVRFTFERTVALLRSQTRHPQEGPFGVWVNRPLKQKIKHKMPTNLDLDTTADGSLHFGGPLEAMFLLRGSASSELPFRFEVPIGVCFGARNSLEEAIVLNKGVLLKPGQFRFFVGVAGWQLDQLRLEIEEGYVWVAGCSNLFAGSOTSSSESLWGEILQLMGGQYSEVSRKPKGDI

NbL03g08020.1 uncharacterized_LOC104218509 [MW = 31.34 kDa]

No. of times detected



log(intensity)



Values from



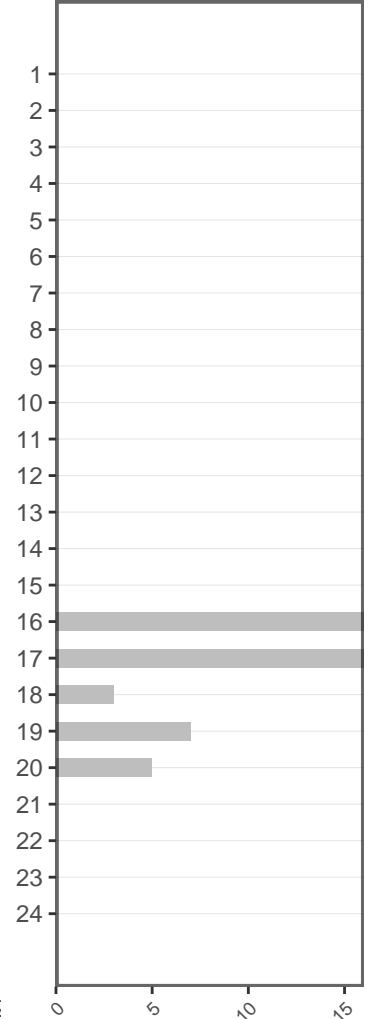
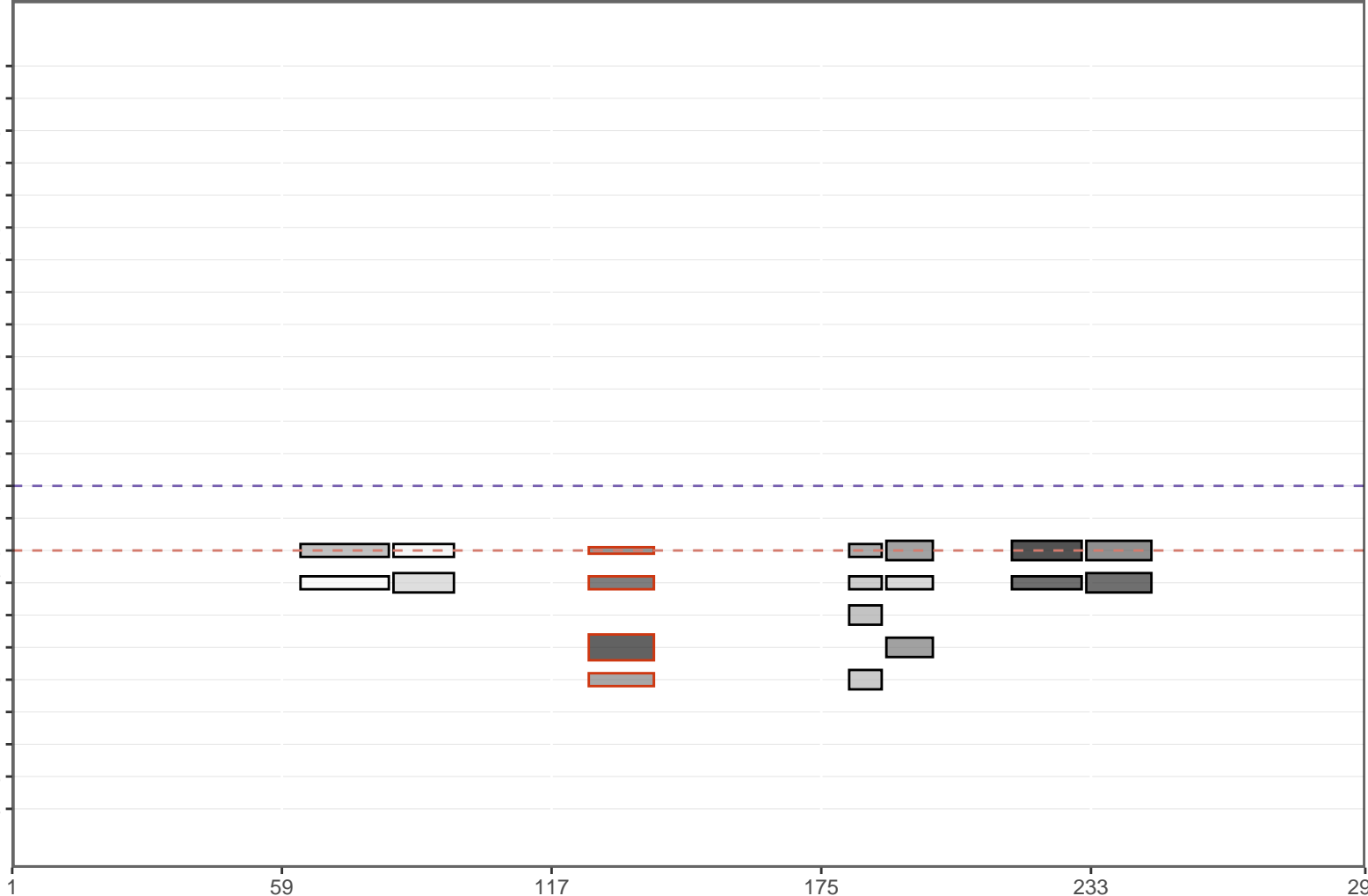
MW indication



Molecular weight

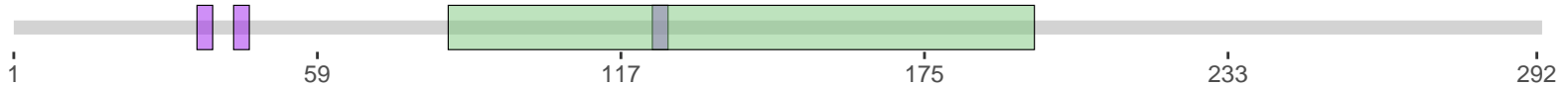


Gel Slice



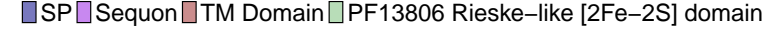
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

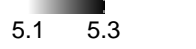
IGLLNAKLTDDCCVQPTDSTFFLNGAKWEYVNNPILRVLTPALRNLFVYKTTDDENIYSMRGGGKVDASEIVFSGKAGPVTASDNNVDEVRMVIDEGGEAFGFTGRNELNGKAVVIGFLLDFELLTGKGLLKGTFGLDFYVSVSDAFK

NbL03g07950.1 cytochrome_c-like [MW = 12.07 kDa]

No. of times detected



log(intensity)



Values from



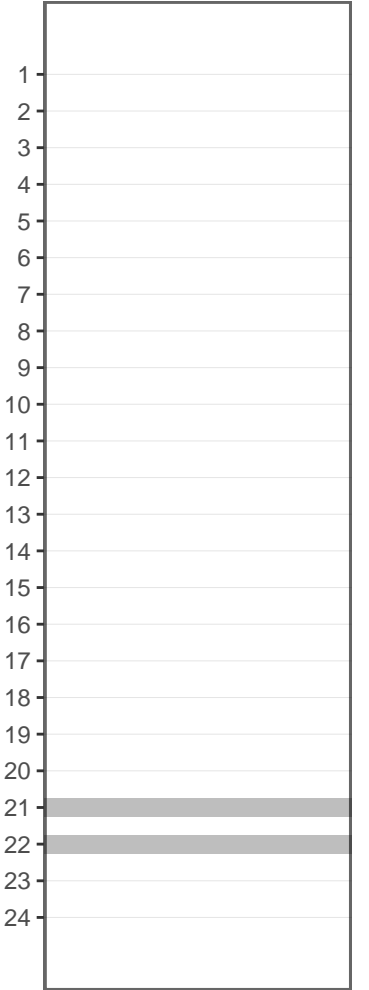
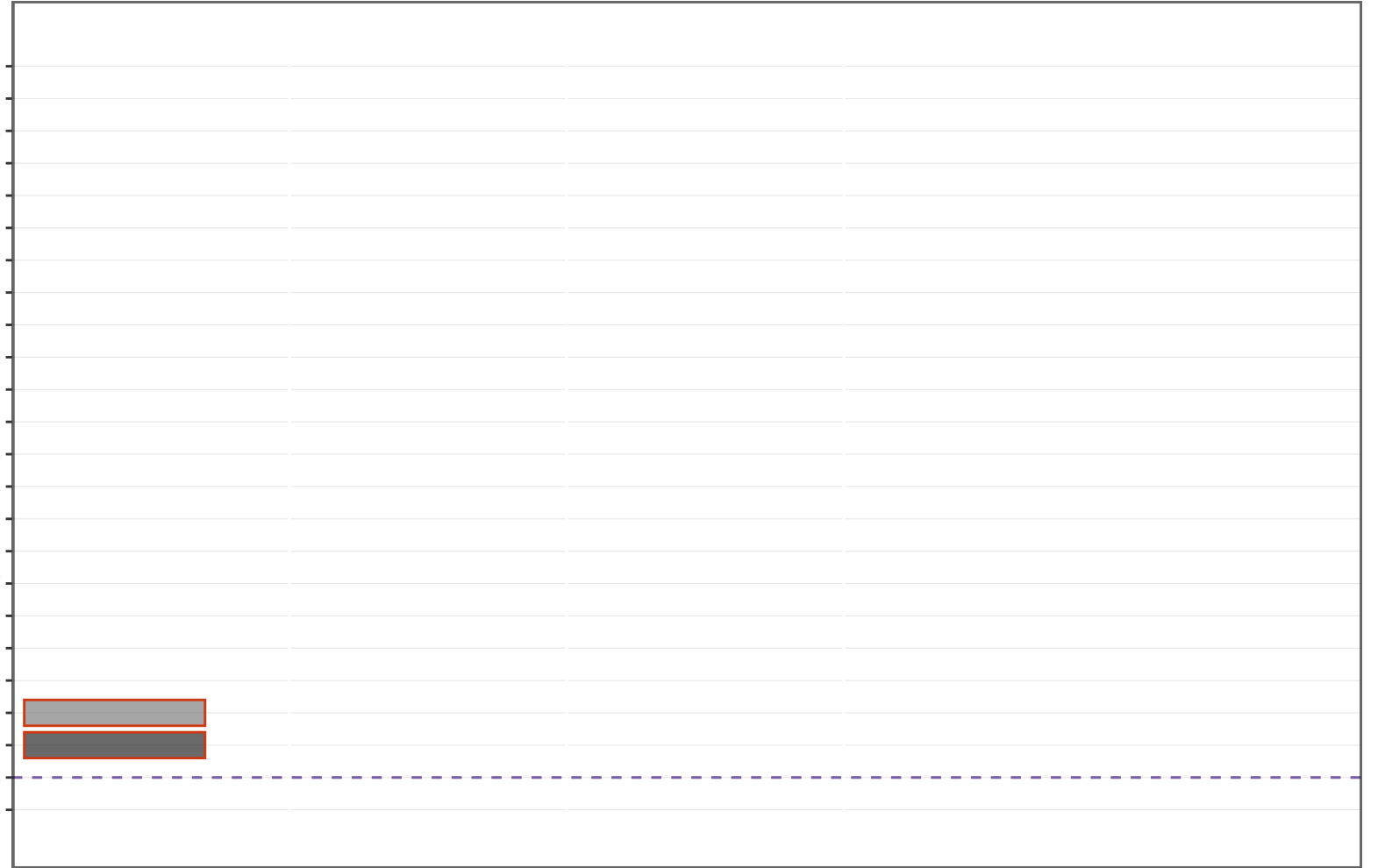
MW indication



Molecular weight



Gel Slice

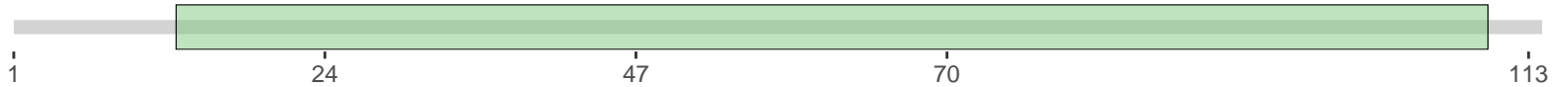


Protein length

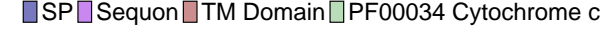


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

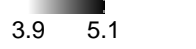
SLEGRSGSTAGYSEYSAANKNNMAMWVEEKTLDVLLNPKKYPGTRMVFPLGLKPKQDRADLAVLKATA*

NbL03g07860.1 far_upstream_element-binding_protein_1-like [MW = 84.09 kDa]

No. of times detected



log(intensity)



Values from

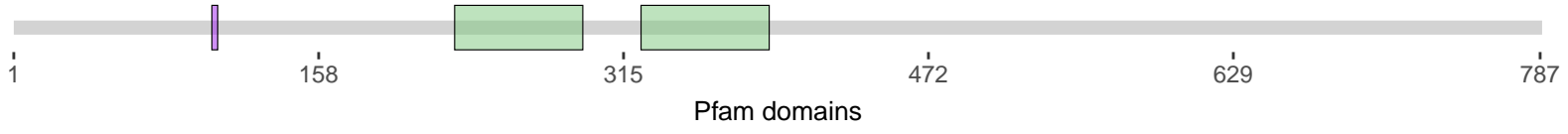
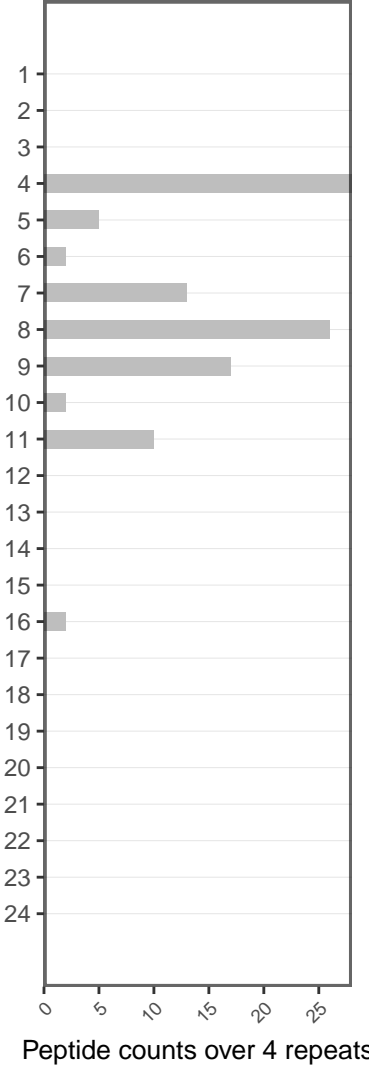
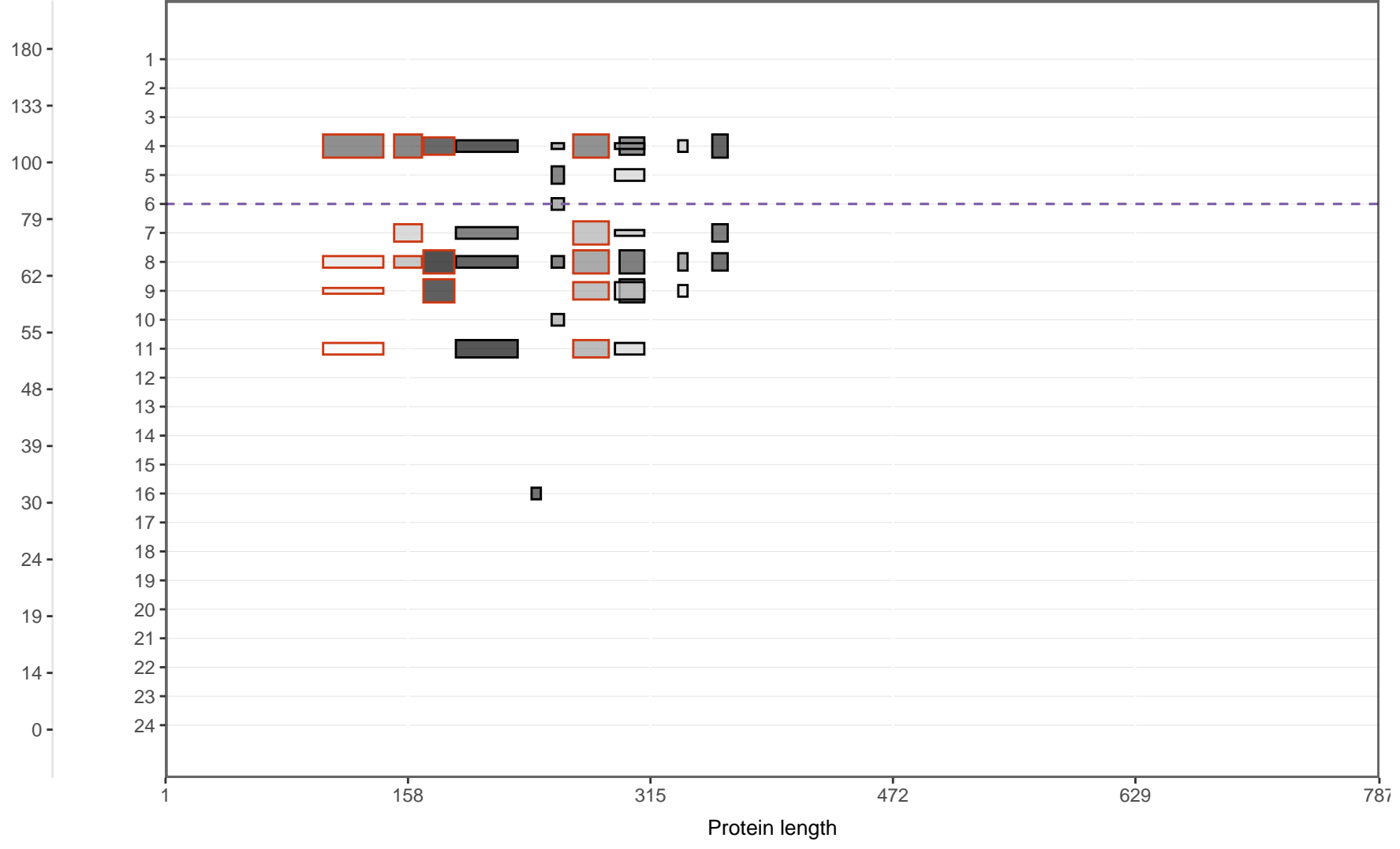


MW indication

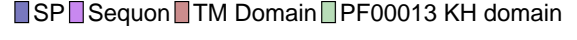


Molecular weight

Gel Slice



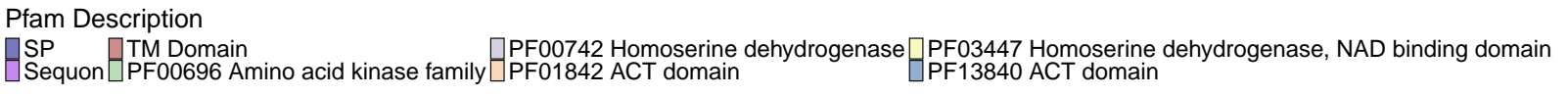
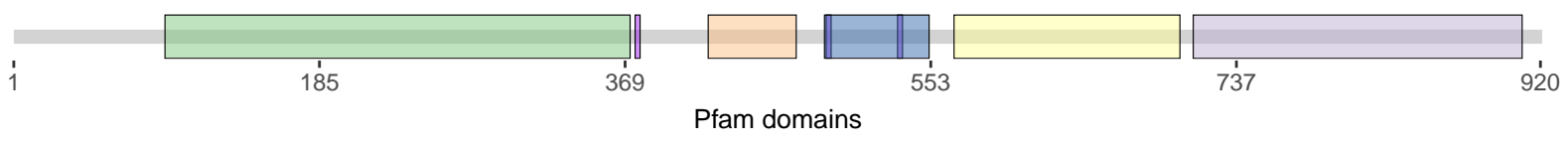
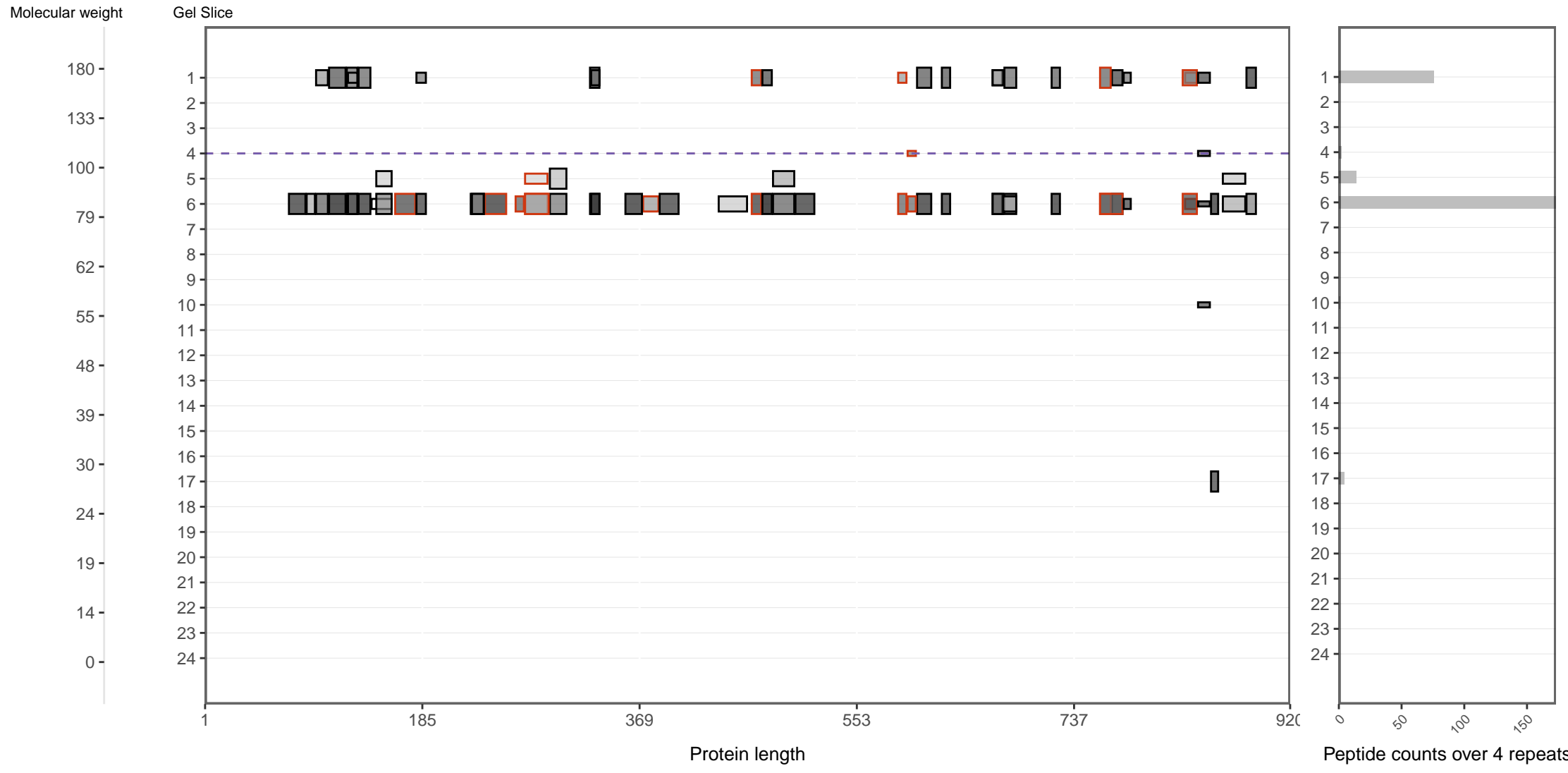
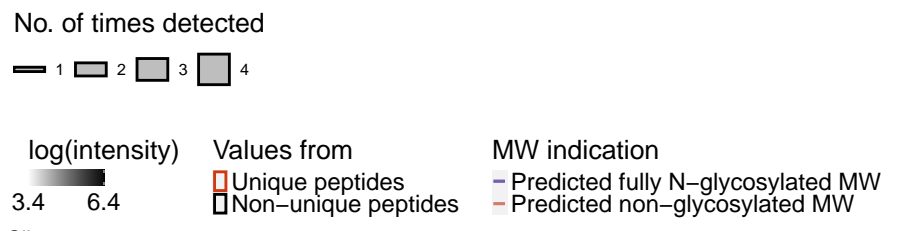
Pfam Description



Protein sequence:

ISQPIRPFSTQSSGVGGQAFRRRGGAAFPQWGRPGHGGDFGVDYHGRGGYSERSQYPPAVYGNYPFGAPRGGFGGGVEGRPPASMSGGPPSSGANNVYNGAHPDYGQVYVPHDAPHGGGGYGHGYTDVYKVDHMAPNGVYGGHSGPQFTSYTGAAHPHYGTHEDYGGKPPSYGVHPQASHGGQYVSHRANRAGPEVYGGGAPRSTGGYGGASMPGGGGGGGYPVASEGFMGGTYVWVGGSTATDGVNHPQAAFGSGPYRQGSAGPVPYGYGQPI

NbL03g07800.1 bifunctional_aspartokinase/homoserine_dehydrogenase_chloroplastic-like [MW = 100.37 kDa]



Protein sequence:

SOASSEHSVCFVAPEKEVKAVADLDSRFGGALSAGRLSGIWIIPNGSILAAVGGIRMASSTPGVSAITLFTALAKANIRRAIAGDGETEYNTFVVKREDQVRLRAVHSHKFKYLSRTIIVYGVGPGIGATLSDQLKDTAVLKDKFNIDLRVMGITGTRTMLLSEGGIDLSKWRELLSLRGEMADLSEKFWHVRGNHFIPNTVLVDCDADSHASHYDWLHKGHHVTFPNKKNKNSGPLDQYLKLRALGRGSYTHYFEATVGGAGLPISTLRLGLETGDKLRIEGIFSGTLLSYFNFA

NbL03g07790.1 histone_H2B-like [MW = 18.82 kDa]

No. of times detected



log(intensity)



Values from



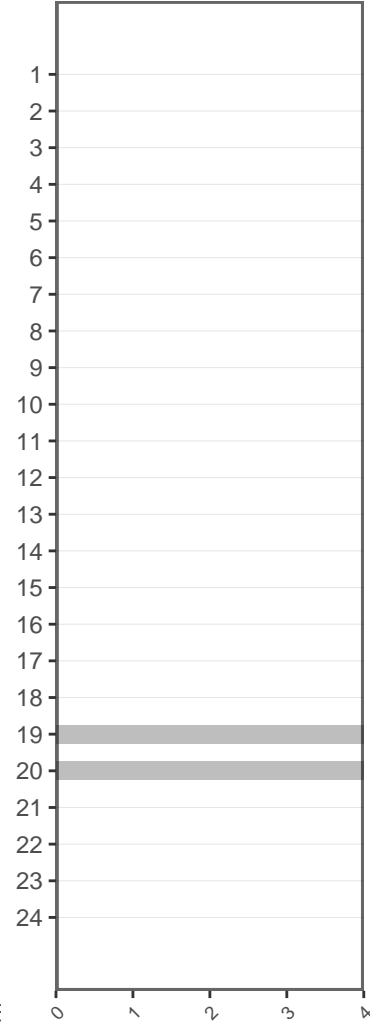
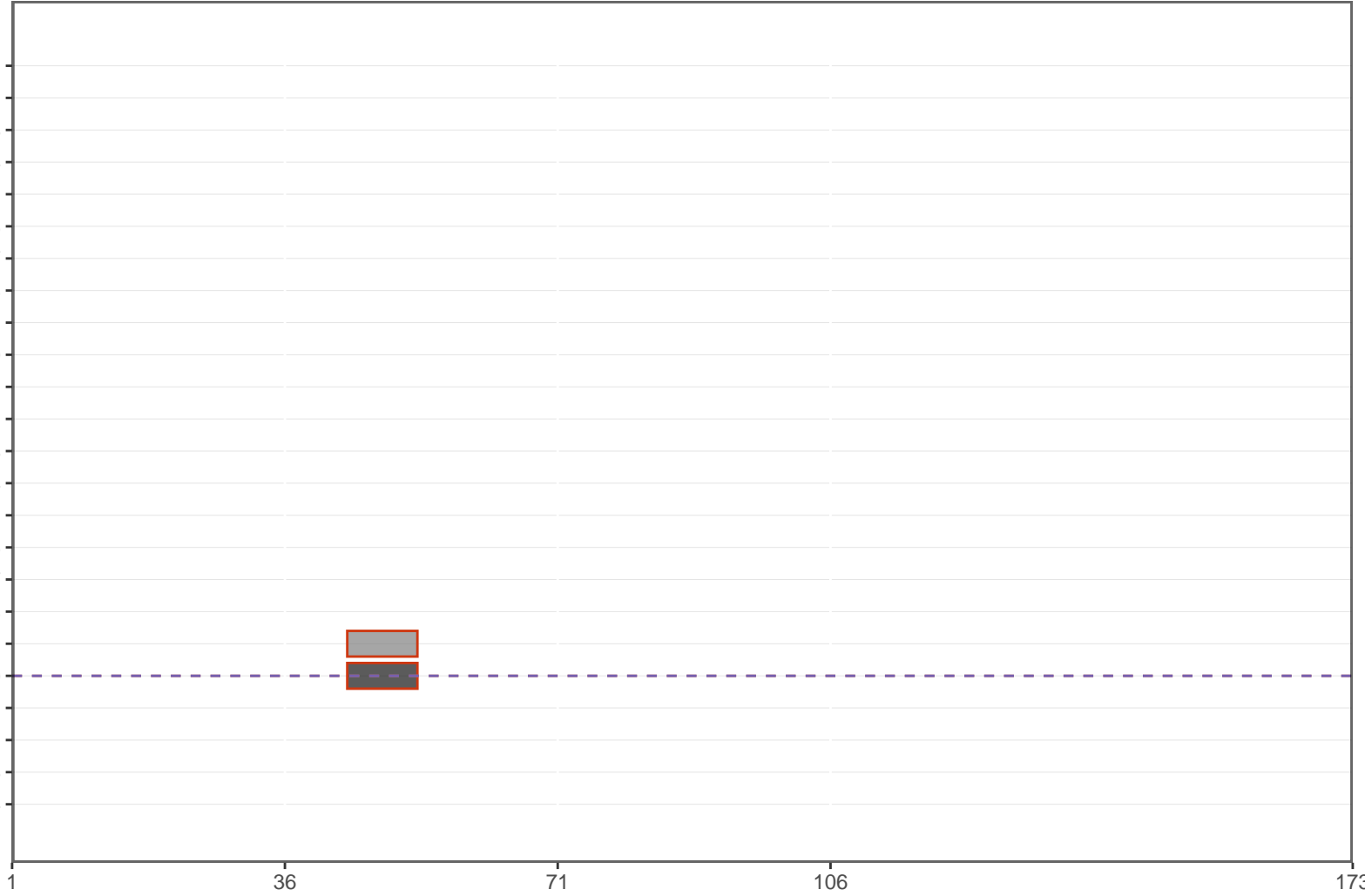
MW indication



Molecular weight

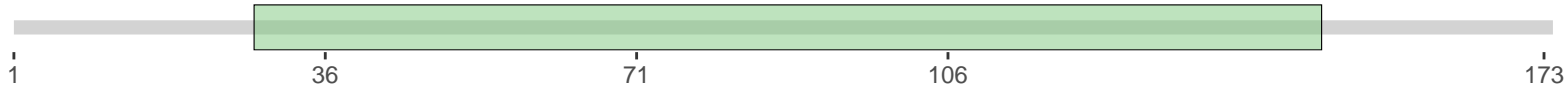


Gel Slice



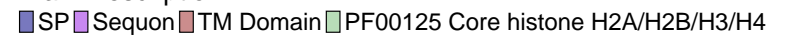
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

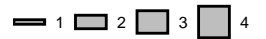


Protein sequence:

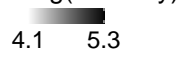
DKKKRLLKLSVETWYKIFKVLKGVHFDIGISKAMGIMNMFINDIFEKLADESSLARYNKKPTTSREIQTAIVRLVLPDELAKHAVSEGKAVKTFKTSQ

NbL03g07780.1 histone_H2B-like [MW = 19.72 kDa]

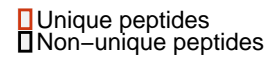
No. of times detected



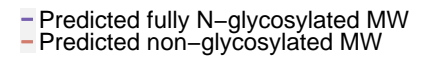
log(intensity)



Values from



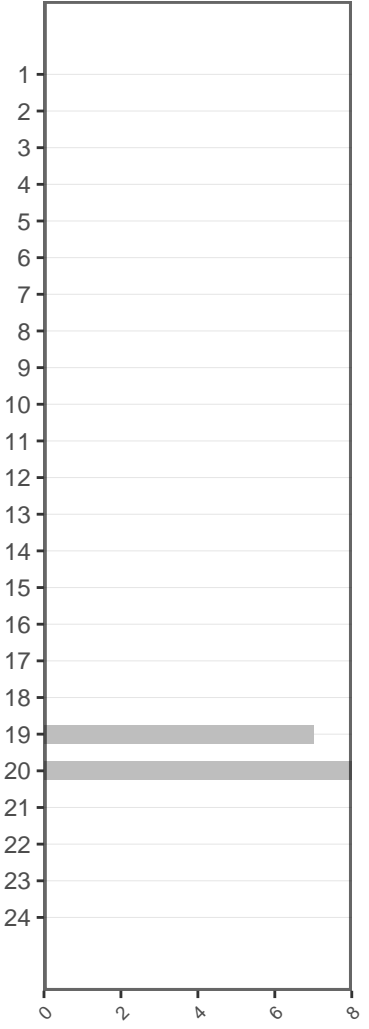
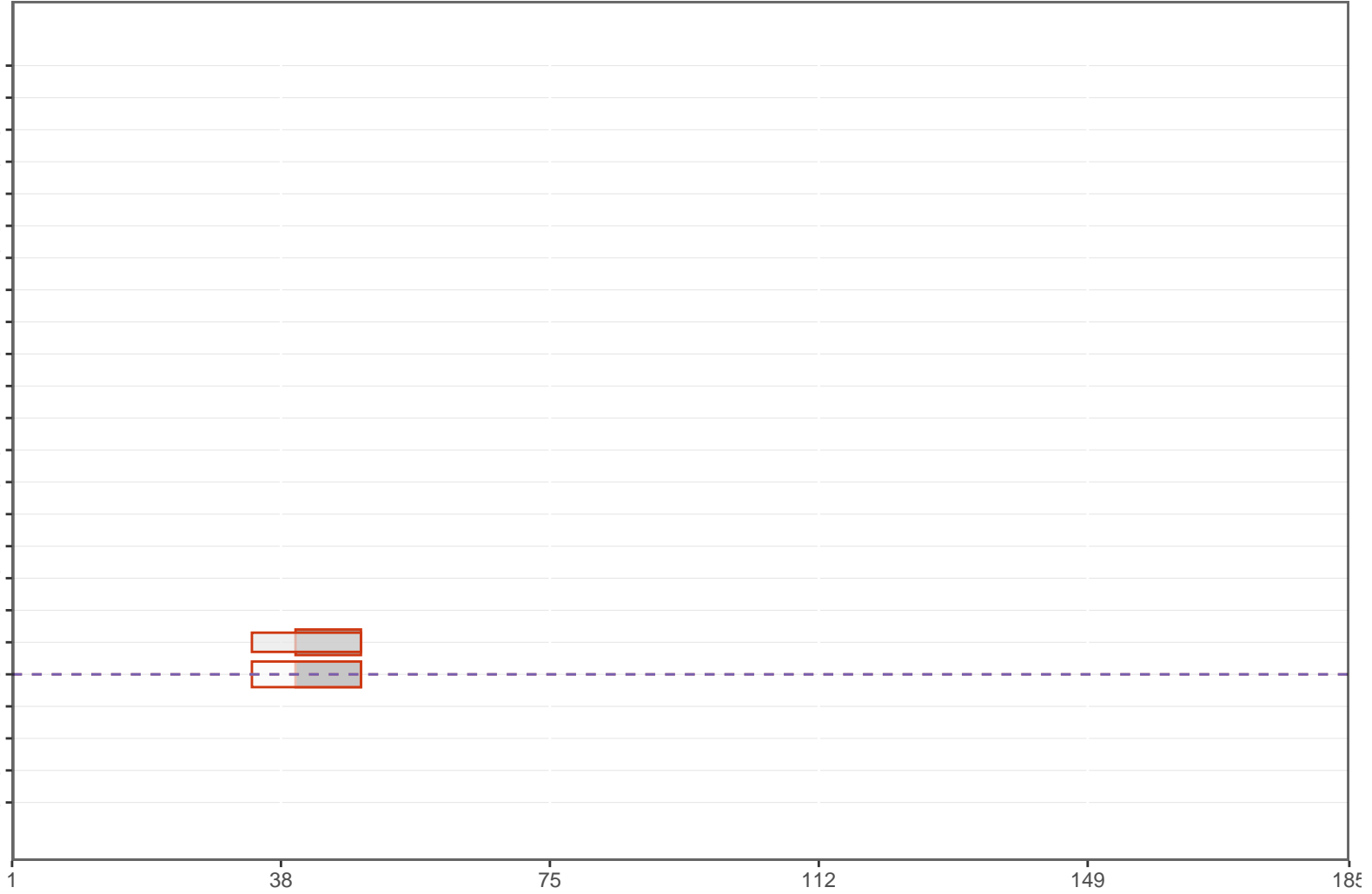
MW indication



Molecular weight



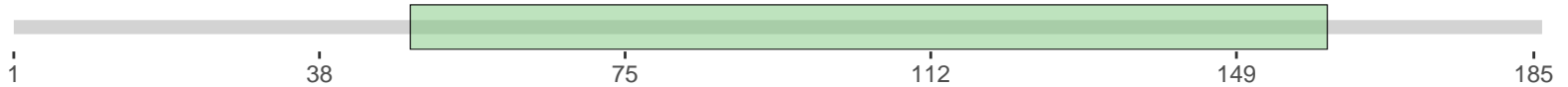
Gel Slice



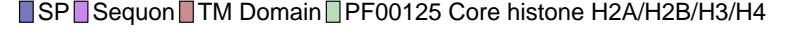
Protein length



Pfam domains



Pfam Description



Protein sequence:

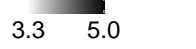
AGAAAGDXXXXRLKKEVETNKKYFVILKGVHPDQIGISKAMGIMNSFINDFEKLAGESSRLARYNKKPTTTSREIGTAVRLVLPQELAKHAWSEGTRKAVTKFTSSP

NbL03g07700.1 serine/threonine-protein_phosphatase_PP1_isozyme_3 [MW = 34.52 kDa]

No. of times detected



log(intensity)



Values from



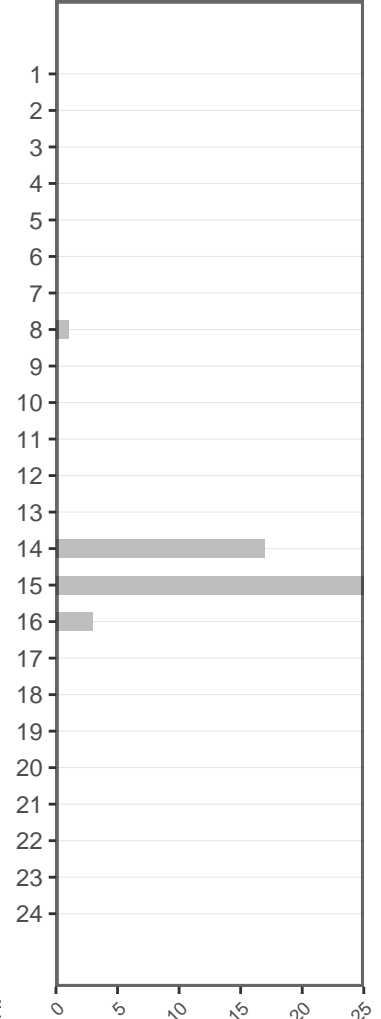
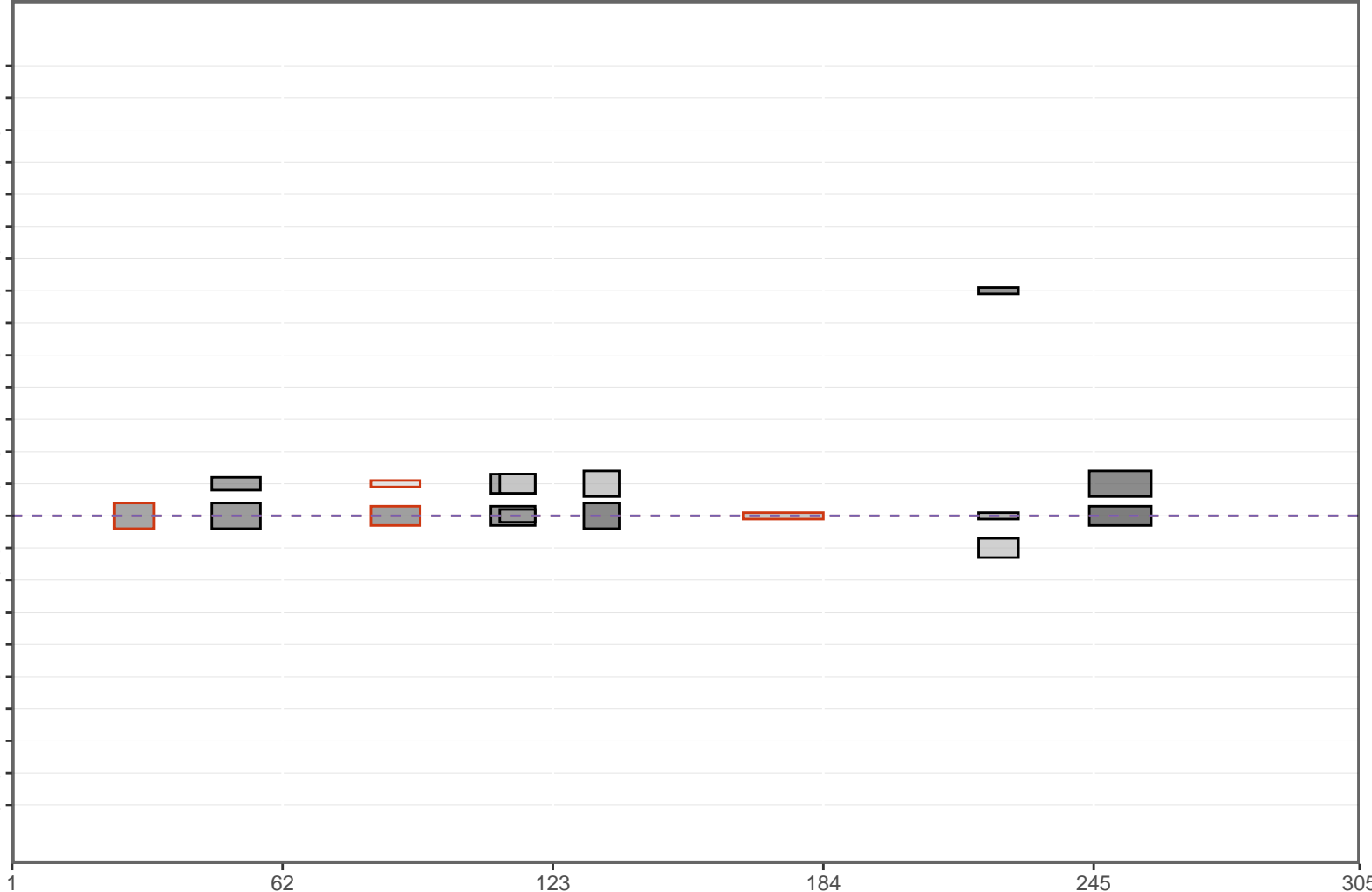
MW indication



Molecular weight

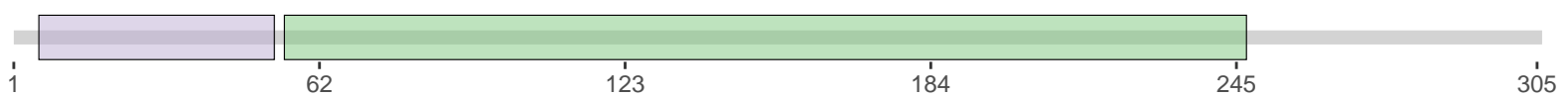


Gel Slice



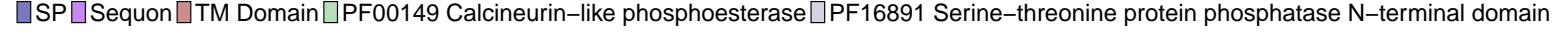
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

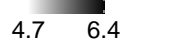
VKLVKSFDTDFNCLPVAALDEKILGMHGGLSFDLSLDQIRNLPRTAIPDTGLLGDLLWSDPKDKVKGWGMNDRGVYTFGPKVSEFLSKHDLDLVCRHQVVEDGYEFAERQLVTIFSAFNYYGGEFDNAGAMMSVDENLGSFQLKPAEKKNKFMV

NbL03g07670.1 small_nuclear_ribonucleoprotein_E-like [MW = 10.31 kDa]

No. of times detected



log(intensity)



Values from



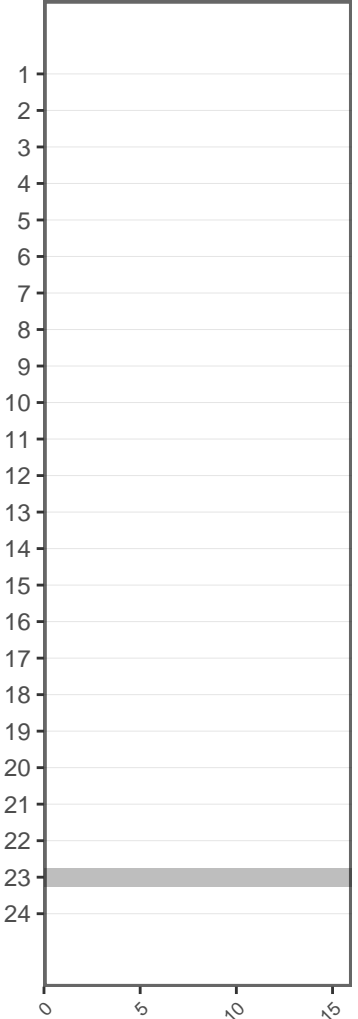
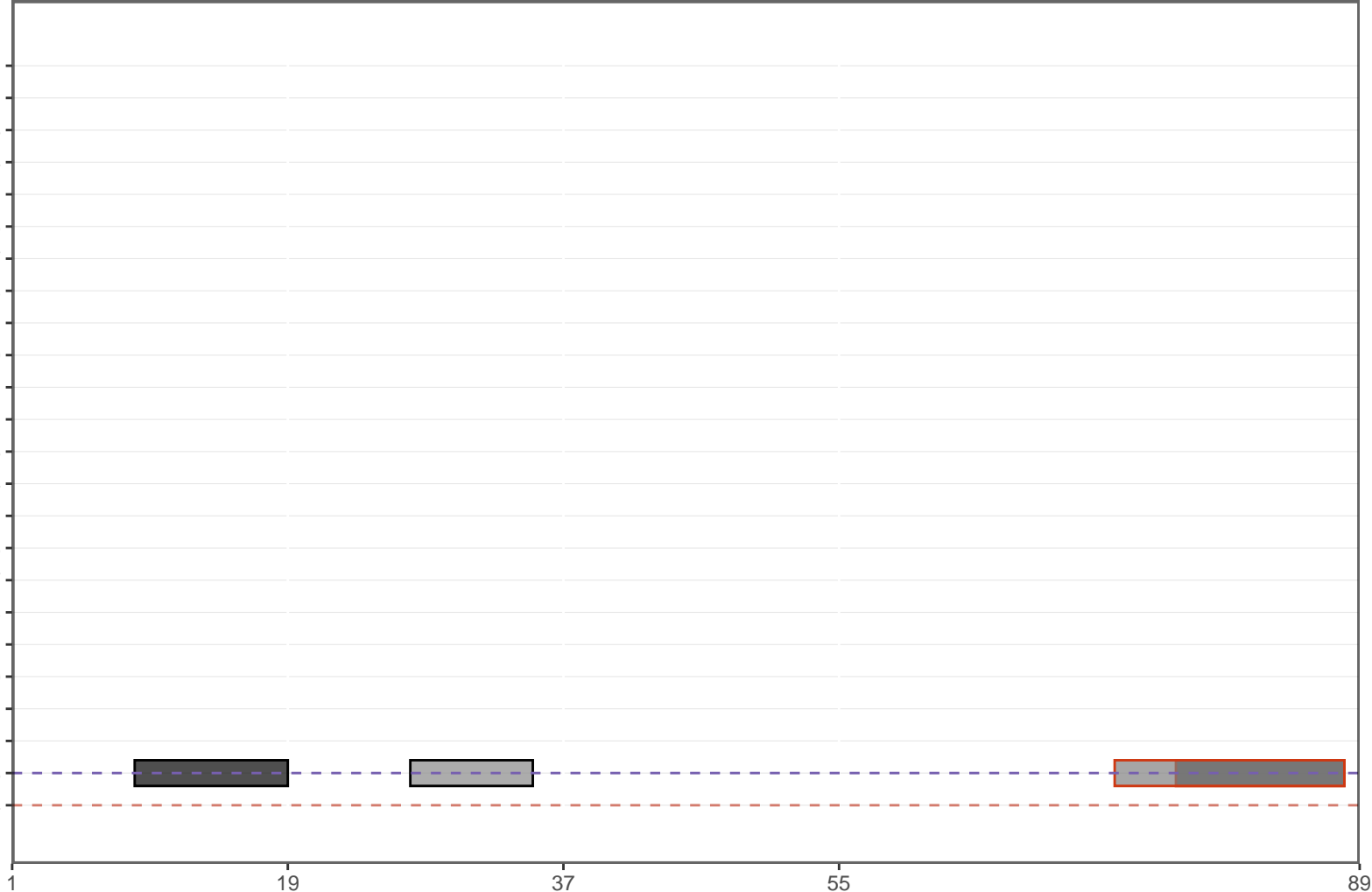
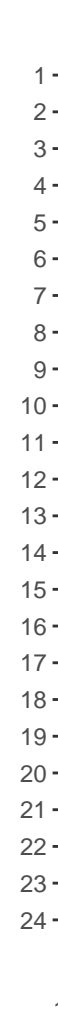
MW indication



Molecular weight



Gel Slice

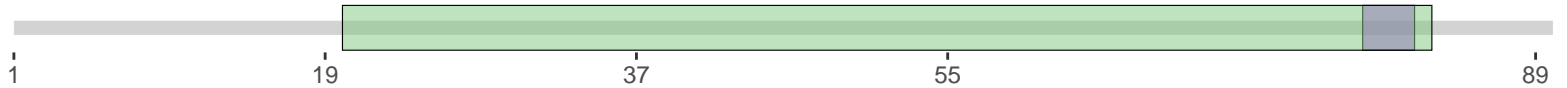


Protein length

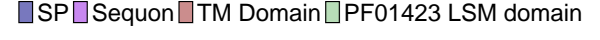


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

FEQKDLREGRIIGFDEVMNLVDDAEVSVKKKSRKQLGRLLKGDNTFLMMNTGK*

NbL03g07640.1 delta-1-pyrroline-5-carboxylate_synthase-like [MW = 77.87 kDa]

No. of times detected



log(intensity)



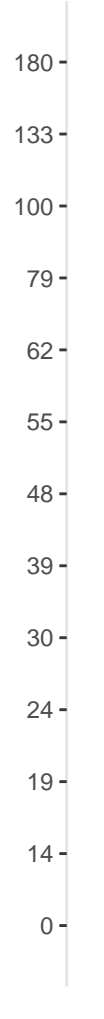
Values from



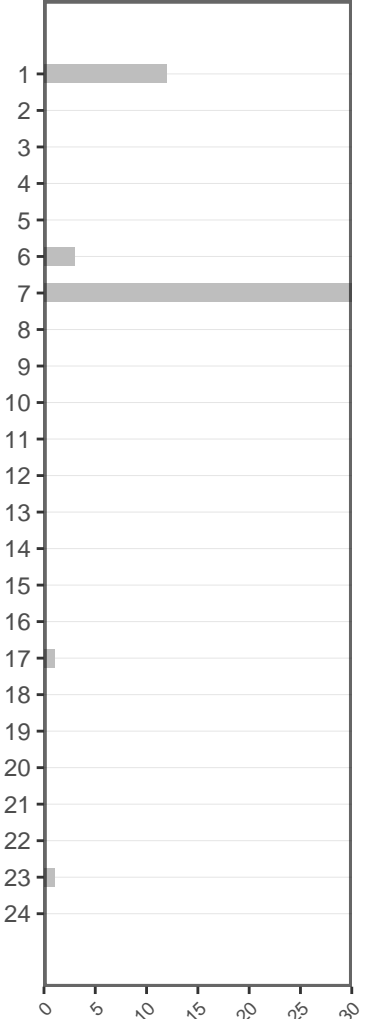
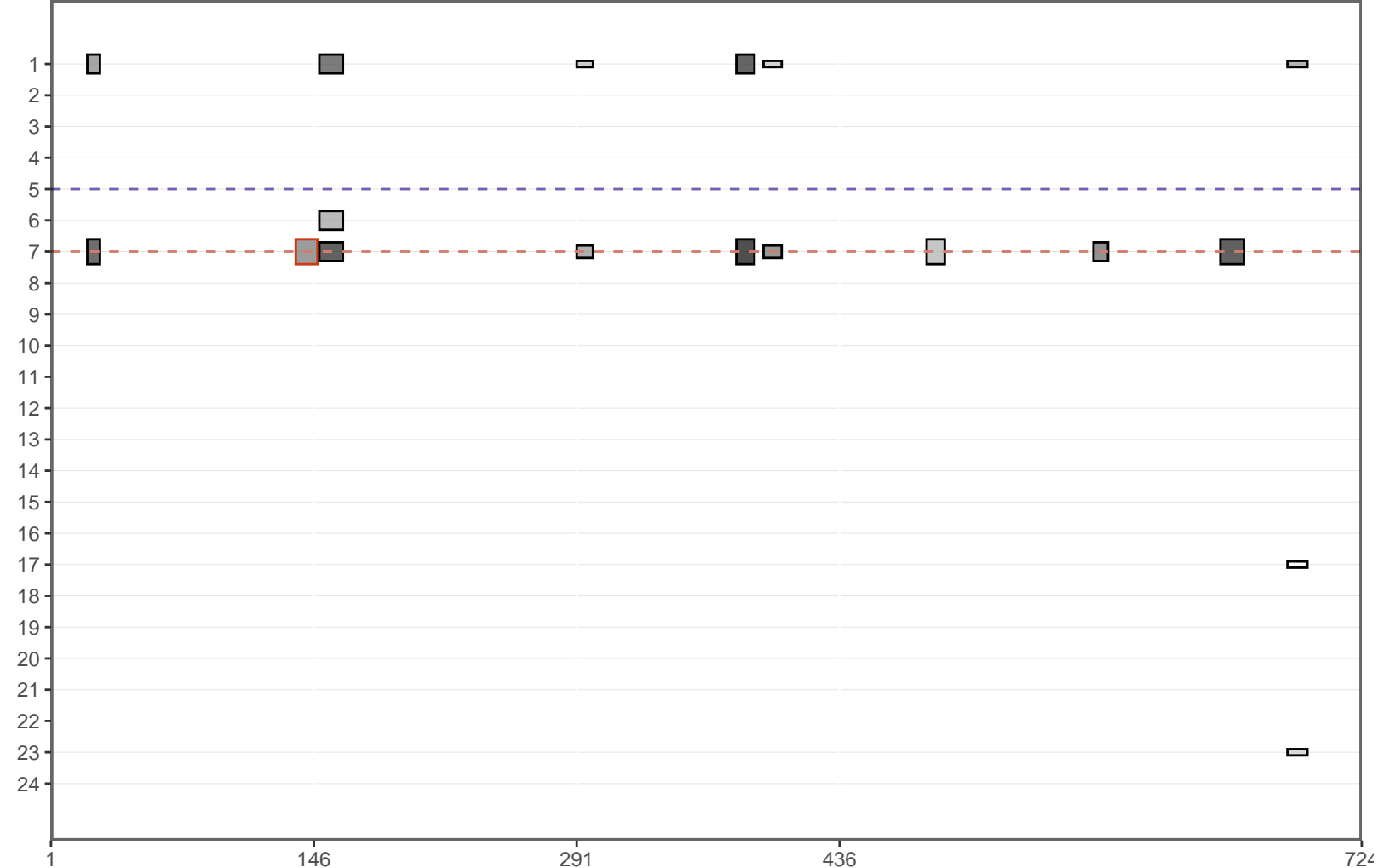
MW indication



Molecular weight

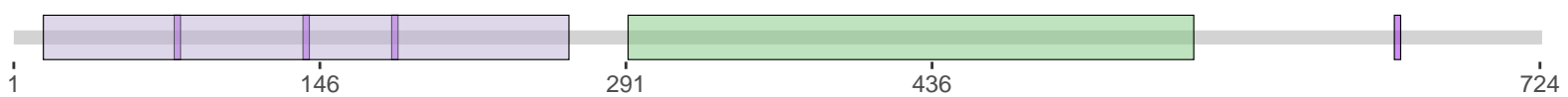


Gel Slice



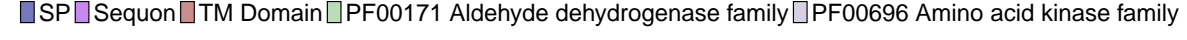
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DVAIAAQAGYEKAIJIRLAKPKGIISLANVSRVLANMDEPIGRILKRTELADGILEKTSPLGLLIFESRFDALVQIADLAVRSGNGLLKGKKAERNAIHLKVTSAVPPVSGEKIGLIVTSREIEPELLLDVNDLIPRGNKLVSGIKAKTIPVLAHGADGICHFIDKSAIDLMAKRVLDKATDYPAAGNAMETLLVHKDLVGTGGINDLILEGKGVSLFGGPKASLLSIPENSFHNEYGALACTIVEVVEDVNAIDHHRHSGAHTDSITEKQVLELFLROVDSA

NbL03g07630.1 uncharacterized_protein_At2g39795_mitochondrial-like [MW = 28.9 kDa]

No. of times detected



log(intensity)



Values from



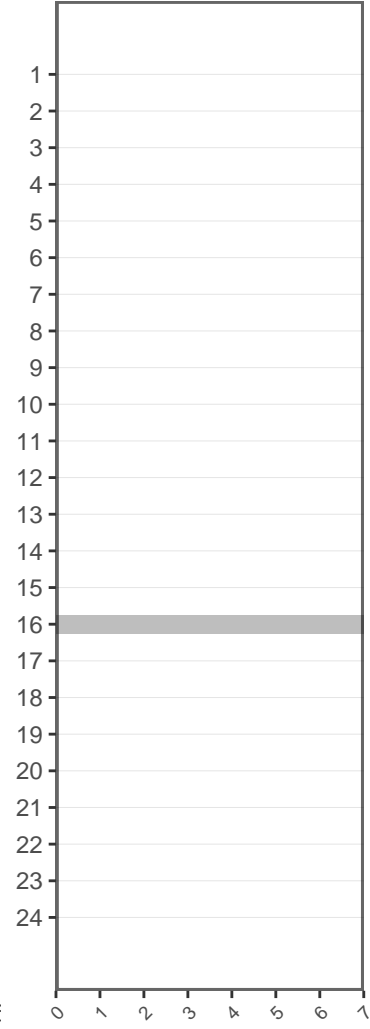
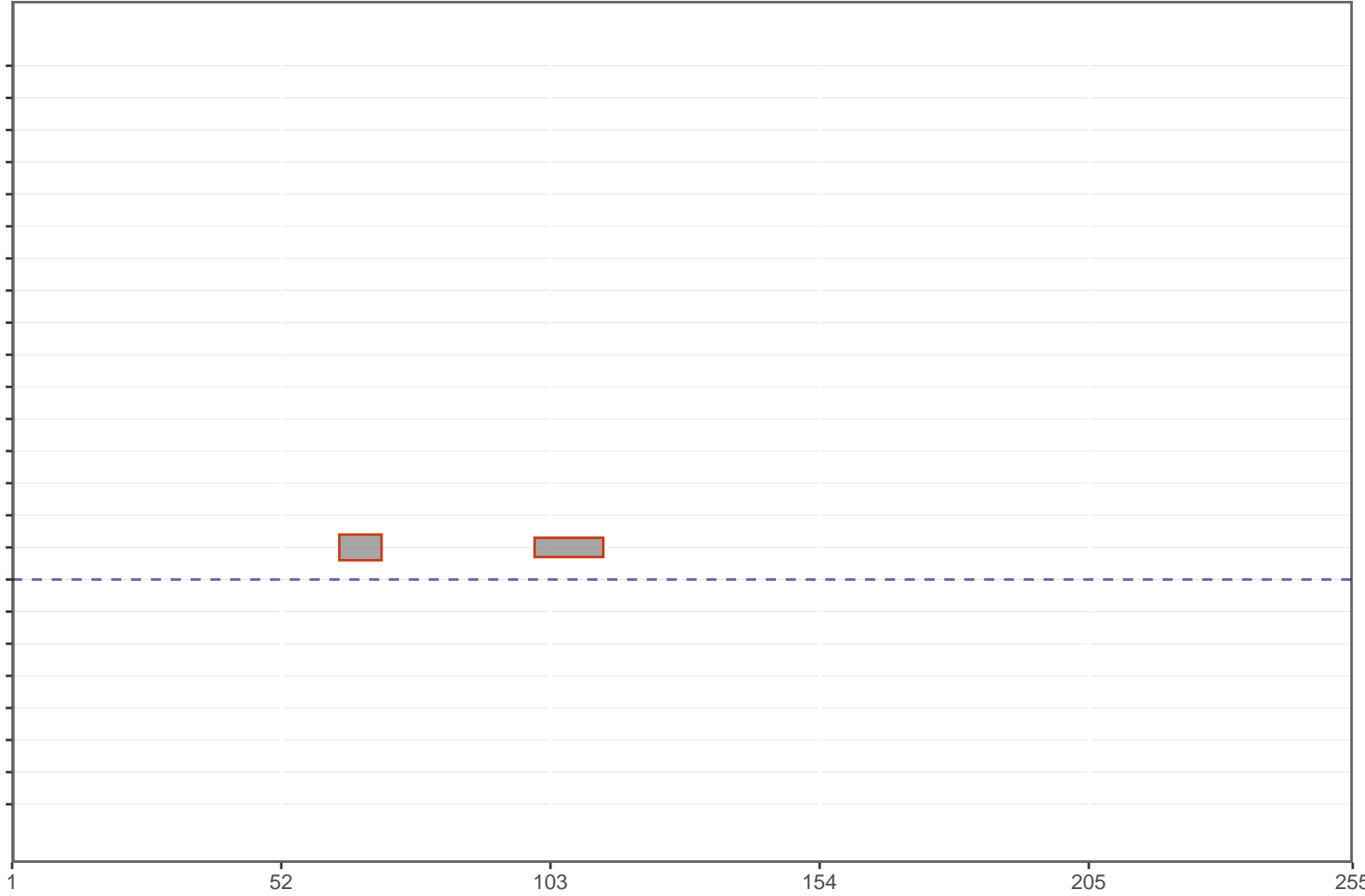
MW indication



Molecular weight

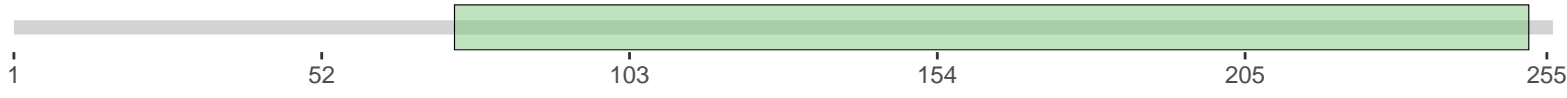


Gel Slice



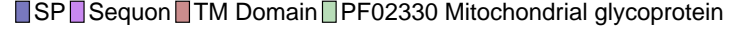
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YQGETVVEVHMPDLVFGDEDEGNDNDTERPWGSLPLVVRVSKRNGPCLFEGGTAYPDEVVHHLAKDPAADEGVAEGPEFSDLDENLQKAFHKYLEIRGKIPSTNLFHEVYMINKDSREYLMWIKVKKFIEA

NbL03g07510.1 anthranilate_synthase_alpha_subunit_1_chloroplastic-like [MW = 60.3 kDa]

No. of times detected



log(intensity)



Values from



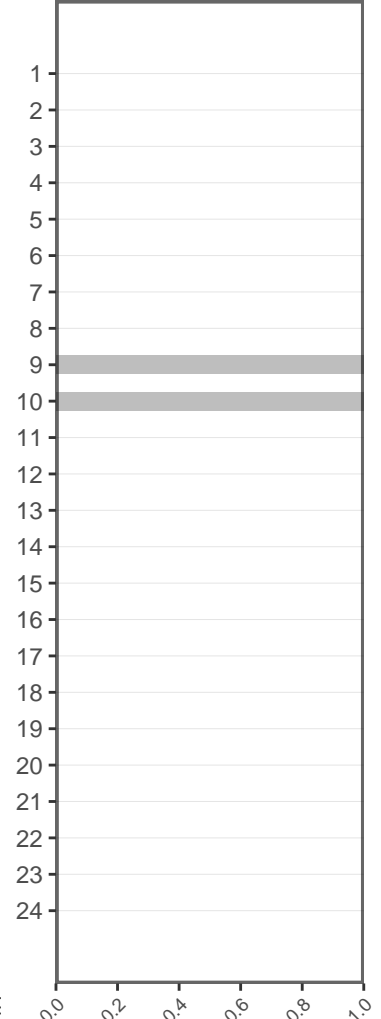
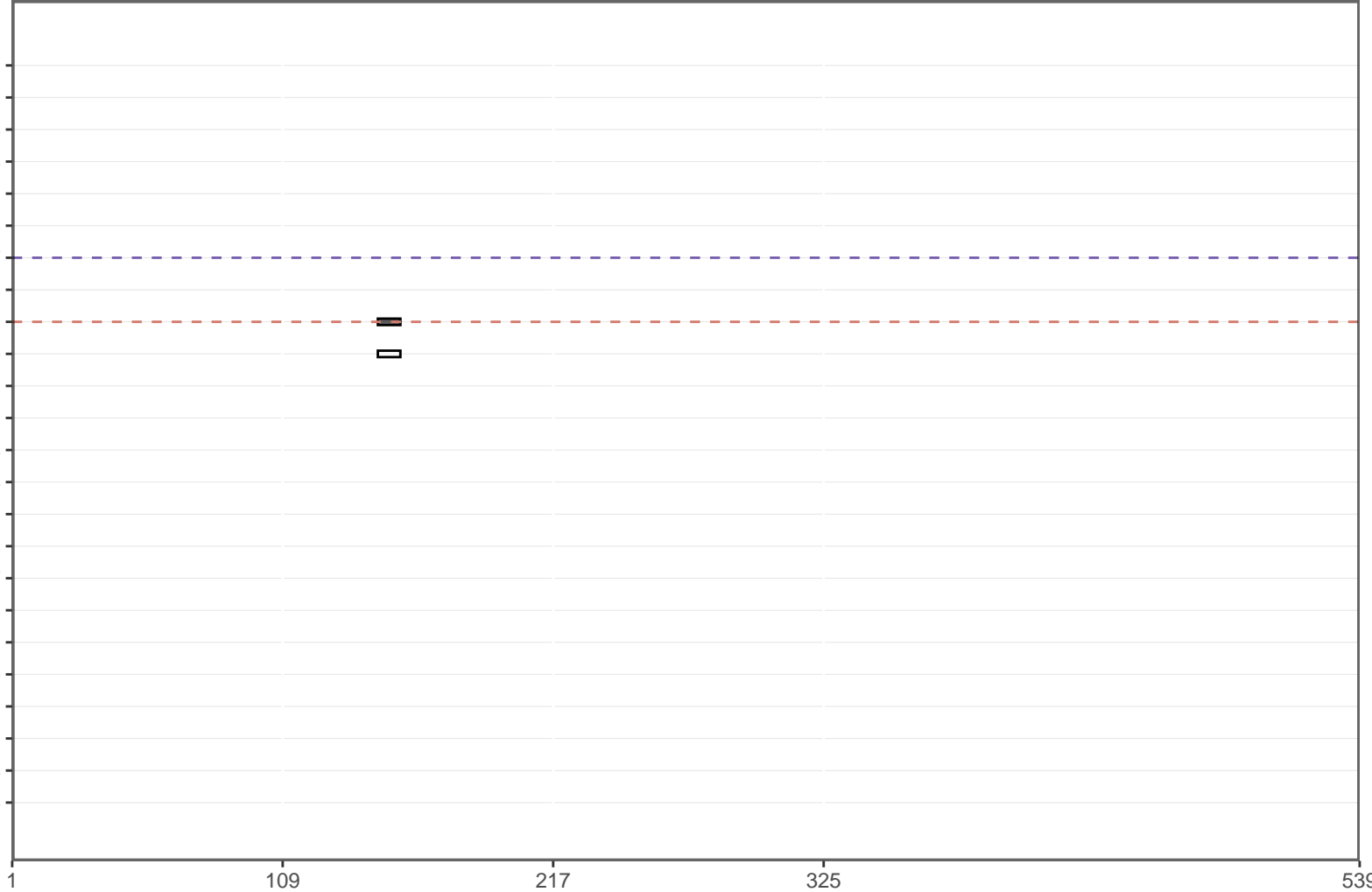
MW indication



Molecular weight



Gel Slice



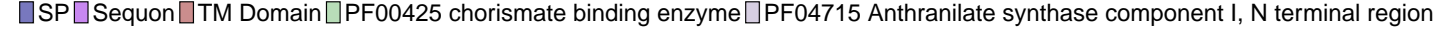
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

'SRVGGIESPRLSPGGVDFCTHTFGPELANGMTSEEYKAWLGAKEHAAAGDFQVLGGRFERRTFADPFEVYRALRIVNGSPYMTYQARGGLVASSPELIRVKKVSGELLDHLTGWDLRALALPVGTVSGAPKVKAMELIDQLEVRGPIVSGGFGGIFSGGMDLALALRTMFLNGARYDTMYSYTDASRRDEWVAHLGGAGVADSNPDEEQECENKVAGLGRADMAESAFVWGRHRLSEVINGSVPLFSRVGHGTSGMSKDRHEKRN'

NbL03g07310.1 sedoheptulose-17-bisphosphatase_chloroplastic-like [MW = 42.43 kDa]

No. of times detected



log(intensity)



Values from



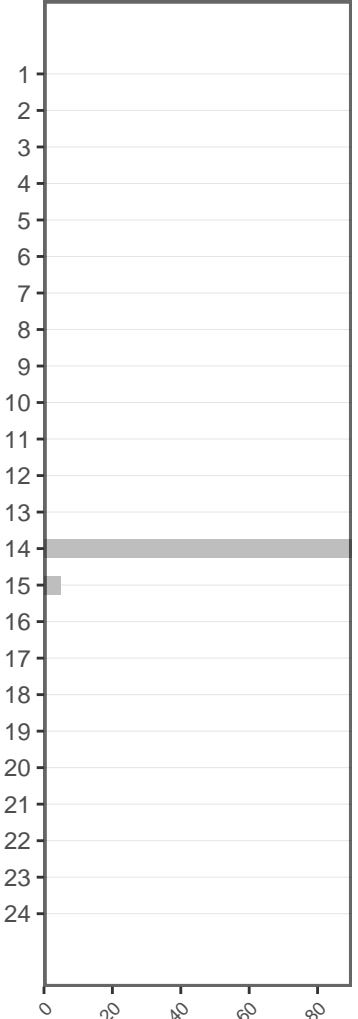
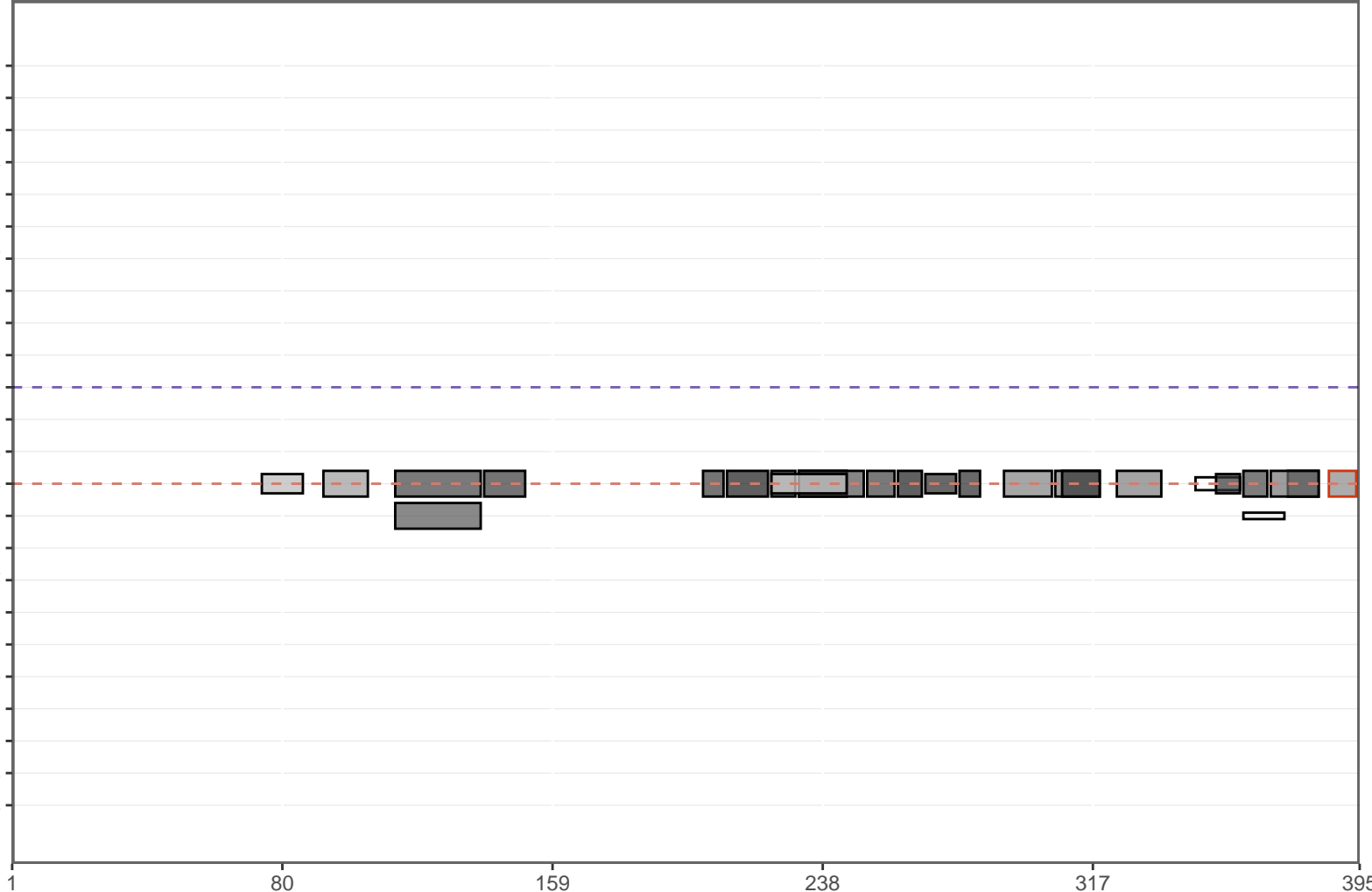
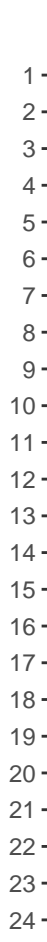
MW indication



Molecular weight

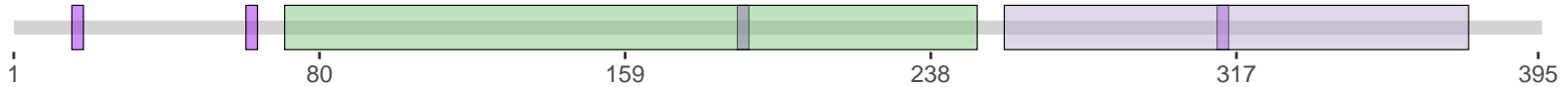


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00316 Fructose-1-6-bisphosphatase, N-terminal domain
- PF18913 Fructose-1-6-bisphosphatase, C-terminal domain

Protein sequence:

IVDTNFTVGTIFGVVWPGDKLTGIFGRDQVAAAMGIFGRPTTYVLAALKDVPSTHEFLLLDEGKWKWHVYKDTTEIGEGKMFSPGNLRATFDNADVAKILDYVYKELYLRVYTGSMVPPVNIQIVKEKGFITNVTSPATAKALLLFEVAPLGLIEKAGGVSDGKGGVLDKVIKGLDERTQVAYGSKNEIRFEETLVGSSRLKAAEPVGAAY

NbL03g07090.1 GDSL_esterase/lipase_CPRD49-like [MW = 28.91 kDa]

No. of times detected



log(intensity)



Values from



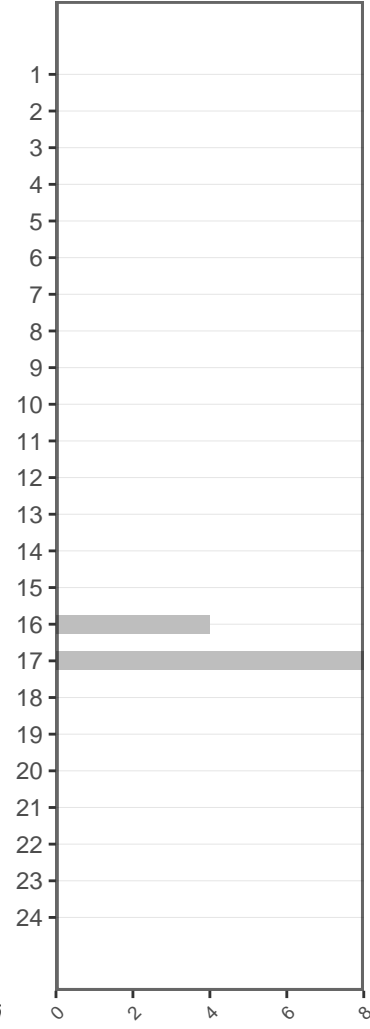
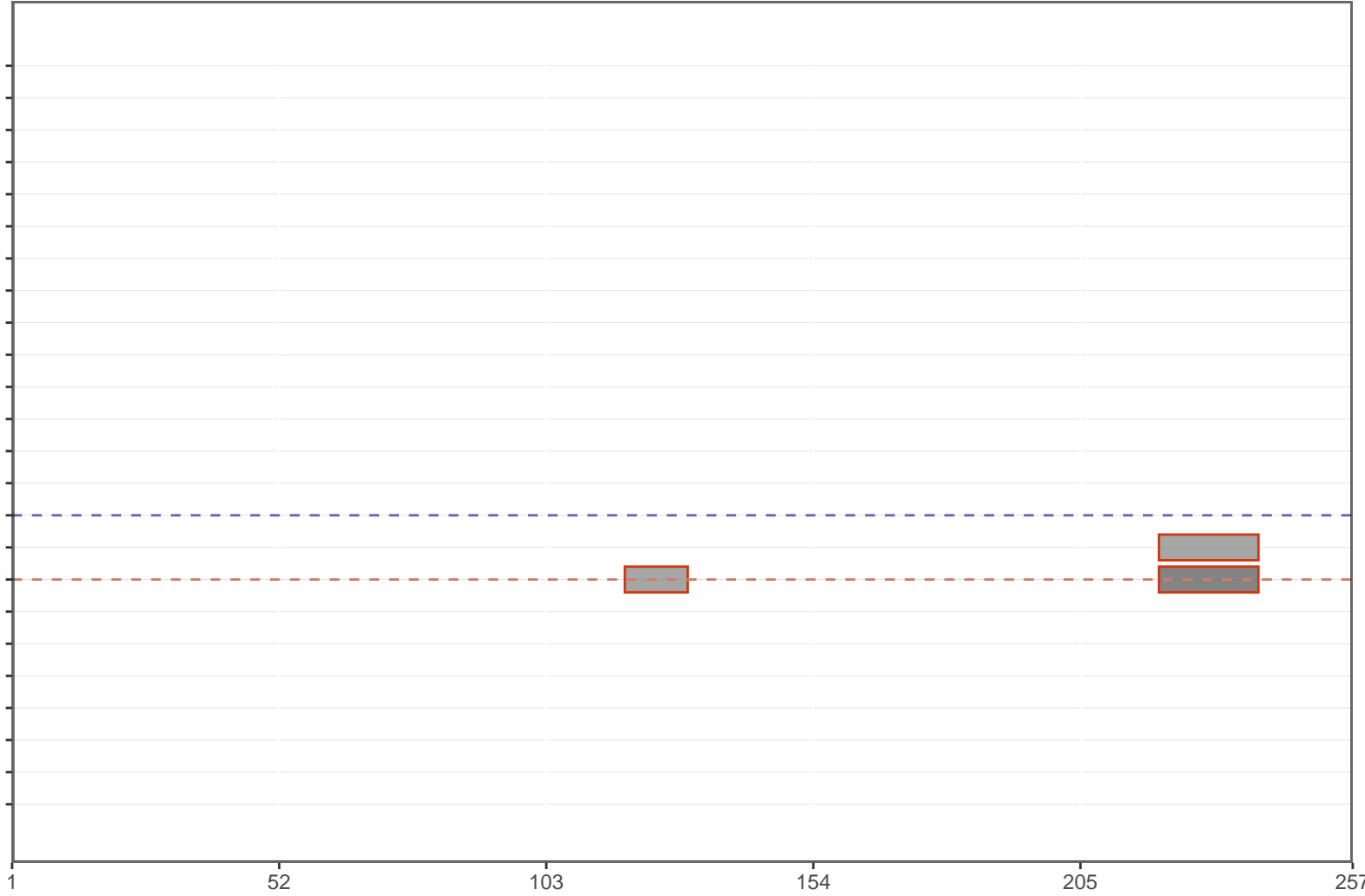
MW indication



Molecular weight

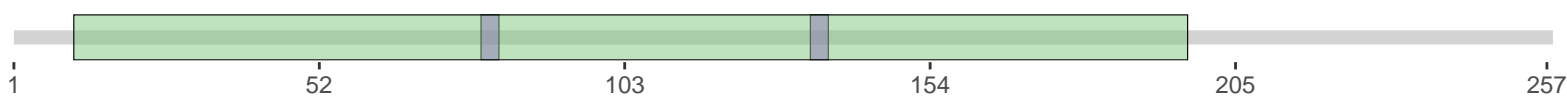


Gel Slice



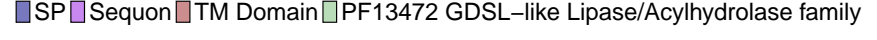
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

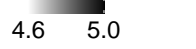
INRIIVLSCPVPYDEARVRENTSDFYFSELVRTNELGRQYSDAGIELGNEMNLKVVQVWITALQKREWLTAGFTDGHLEAGSKVVEEIKVLKEAGWTRPSLWVWKMPTFEAEEDSPYDLVLDGKTTINPSDWYHYRREIRWD

NbL03g06650.1 ferritin-1_chloroplastic [MW = 27.87 kDa]

No. of times detected



log(intensity)



Values from



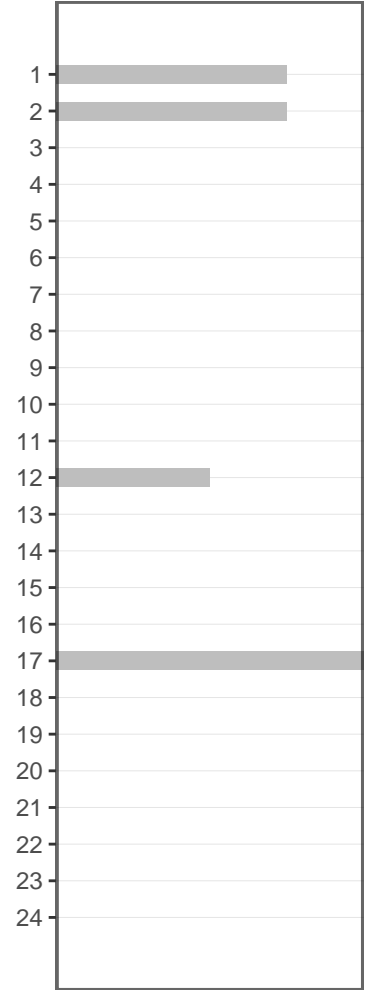
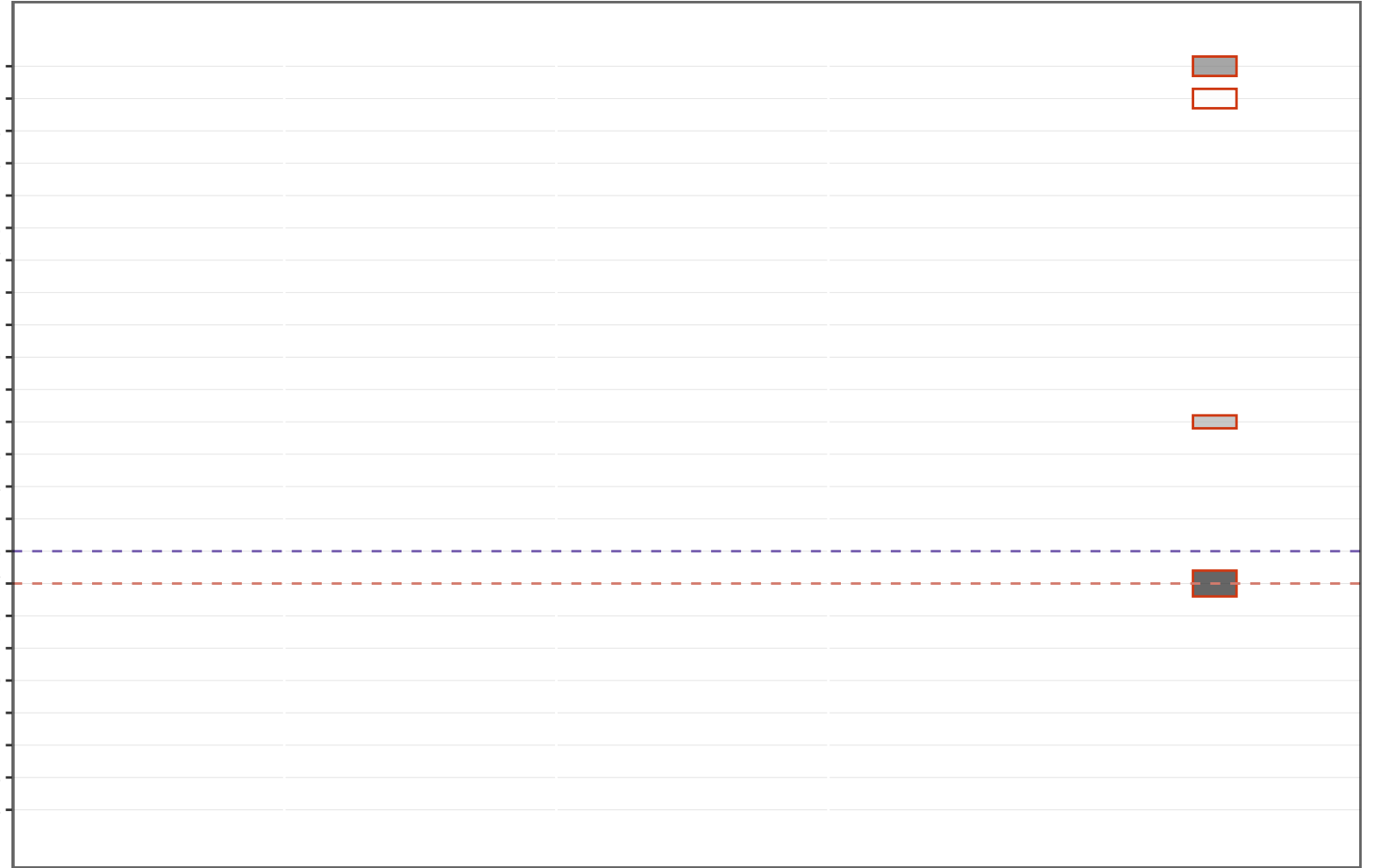
MW indication



Molecular weight

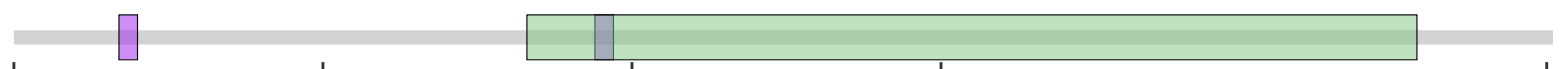


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

VALKGLAIFXKSSLEERDHAELKMFQNGRGRWKLKSGAPTFDFHCEKGDALYAMELALGLEKLTNRLLNLHVAASRNDVHLADFLSESEFLVEQVDAIKKISEYVAGLRVRVGGHGVWFDFDMLNEGAAI

NbL03g06630.1 cytosolic_endo-beta-N-acetylglucosaminidase_1-like [MW = 81.99 kDa]

No. of times detected



log(intensity)



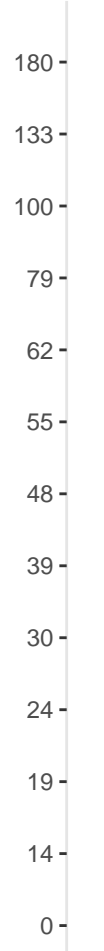
Values from



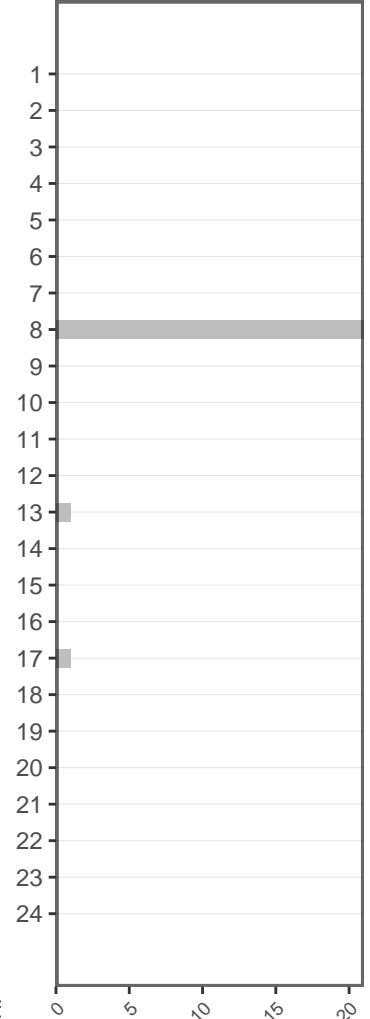
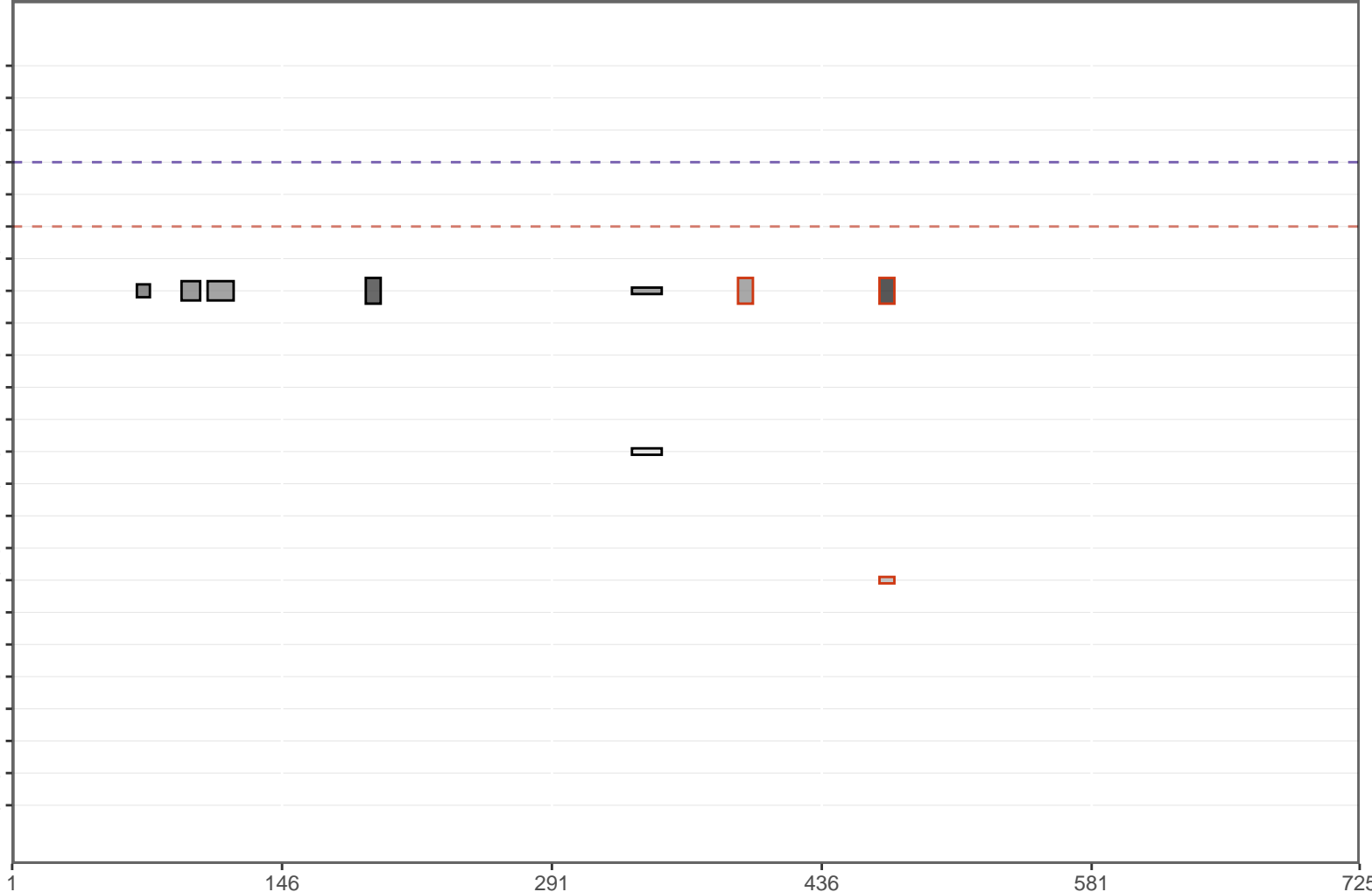
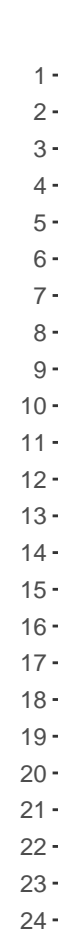
MW indication



Molecular weight



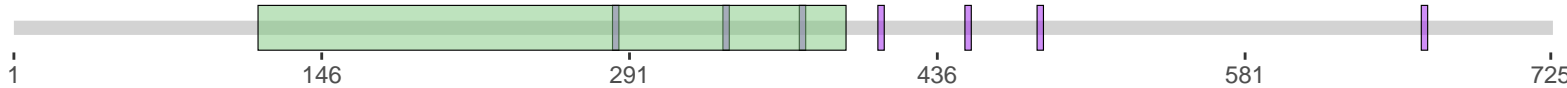
Gel Slice



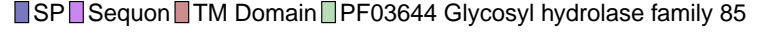
Peptide counts over 4 repeats

Protein length

Pfam domains



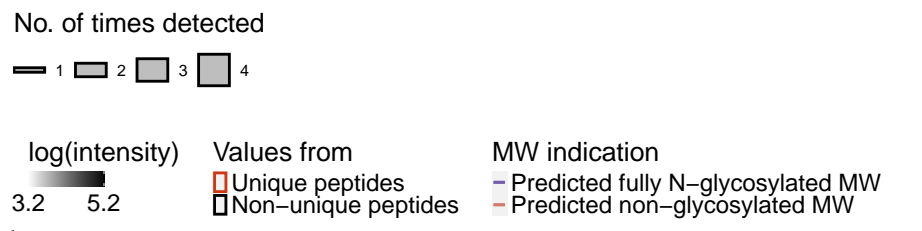
Pfam Description



Protein sequence:

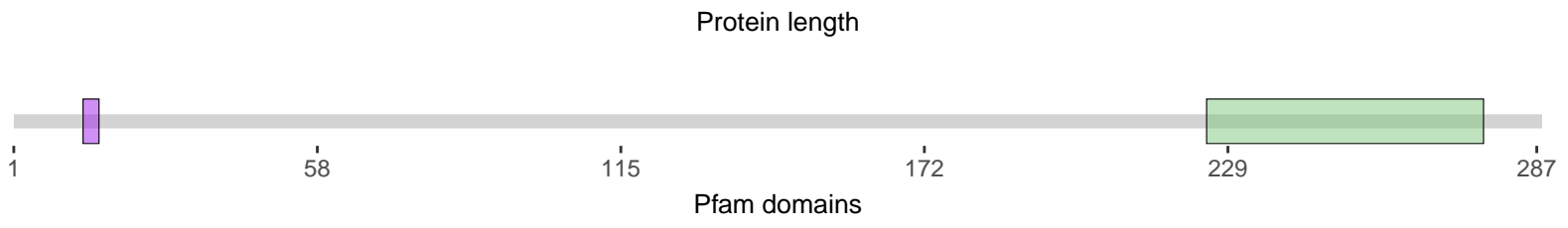
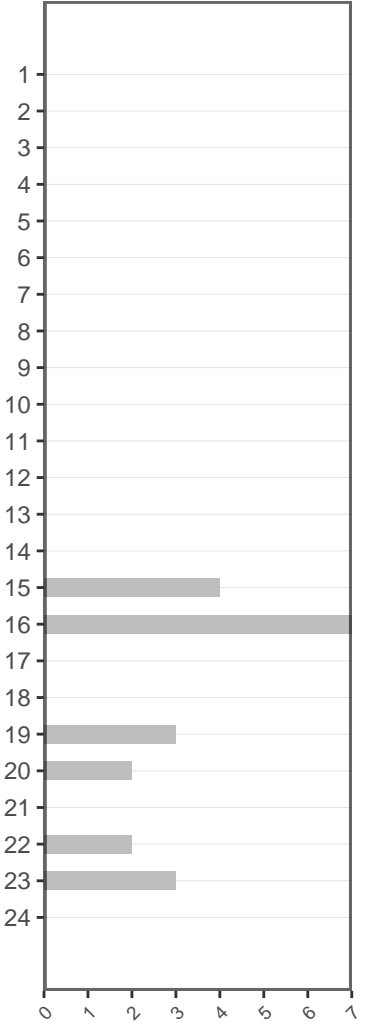
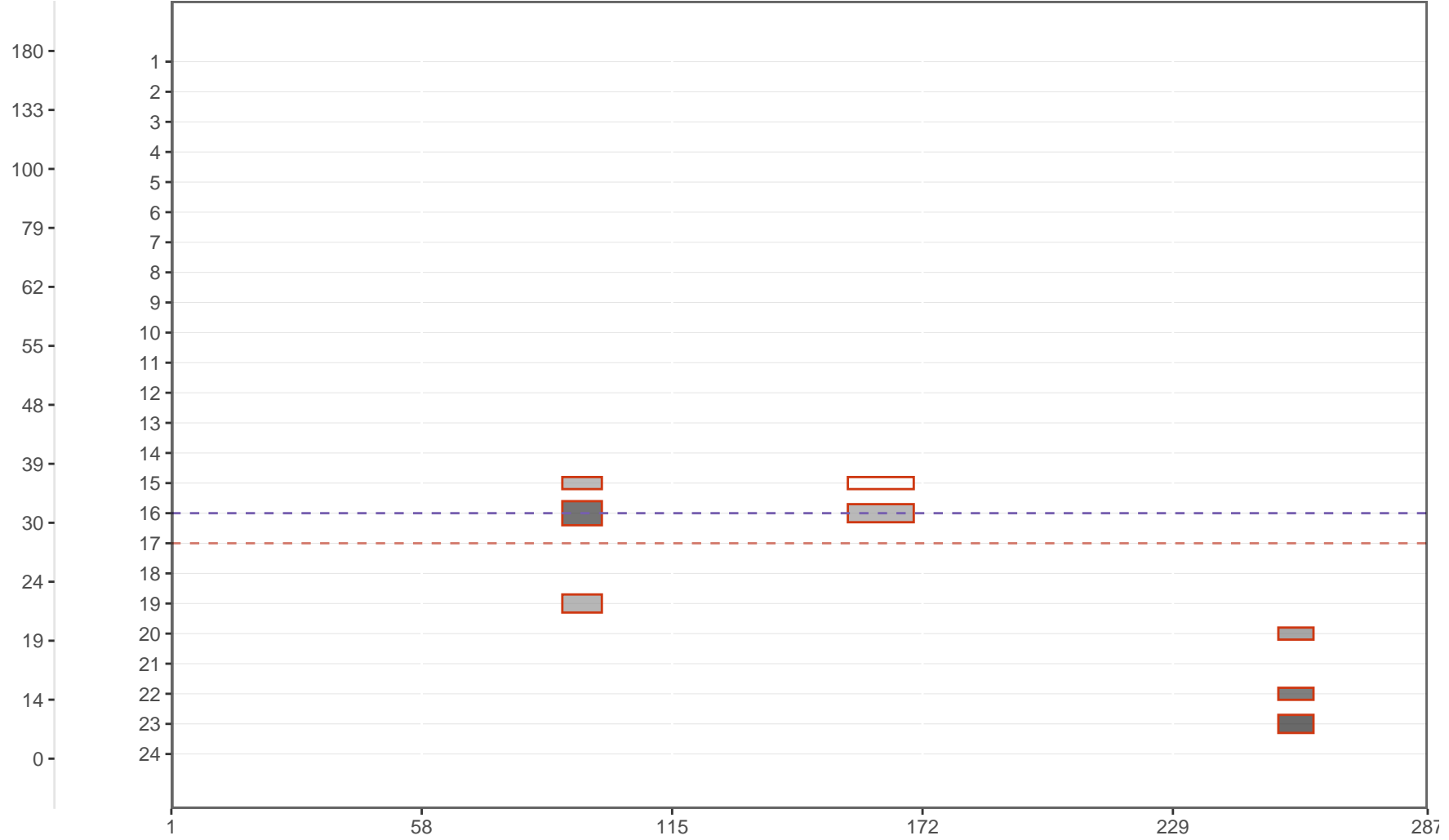
KQLPDTQTQNRWVGLVERBWNISGNYPFLTPFYVNFNDGGRGHHGVDDGKGGPTWANNISGGSGFQLLFFSGESTAGLEVVVQLKEPBYVNGGGLAFNGTLDHIFEARLFEQKGLADSPVRFYVGVKNGSLLGLSLEFN SAVRKGKSVLLASGDSLLMTRFVRGFDNVIMPRRVTKLETPEPSWVQGESVTEMGVMTKIHAVGVKLRPEVHKSESQAKIMAFSPTEYHVAHGLAIDRRLNEDFFPPTSLWLDGNYHEWFGHGRKLNKLVKLDK

NbL03g06530.1 biotin_carboxyl_carrier_protein_of_acetyl-CoA_carboxylase [MW = 30.03 kDa]



Molecular weight

Gel Slice



Pfam Description

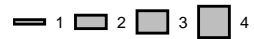
- SP
- Sequon
- TM Domain
- PF00364 Biotin-requiring enzyme

Protein sequence:

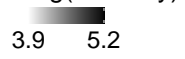
RDIEAPLVPAFVSSPPPPPSASKPTASTAASPMSPGKSSSEKISPTNVAEKBAKLAALSTGASGYVAVSCPTVSGFRFRARTLKGKQPPMKEGDVKKEGGHGLDFGTLPVRSDAAGELLKLFNDGEAVGYGQPLIWLPSFRGI

NbL03g06460.1 alpha-soluble_NSF_attachment_protein [MW = 32.68 kDa]

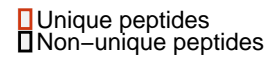
No. of times detected



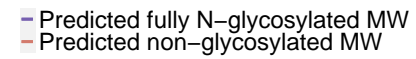
log(intensity)



Values from



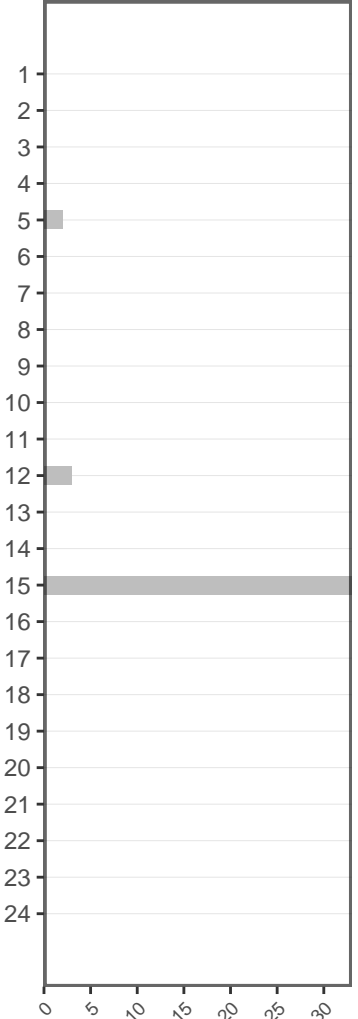
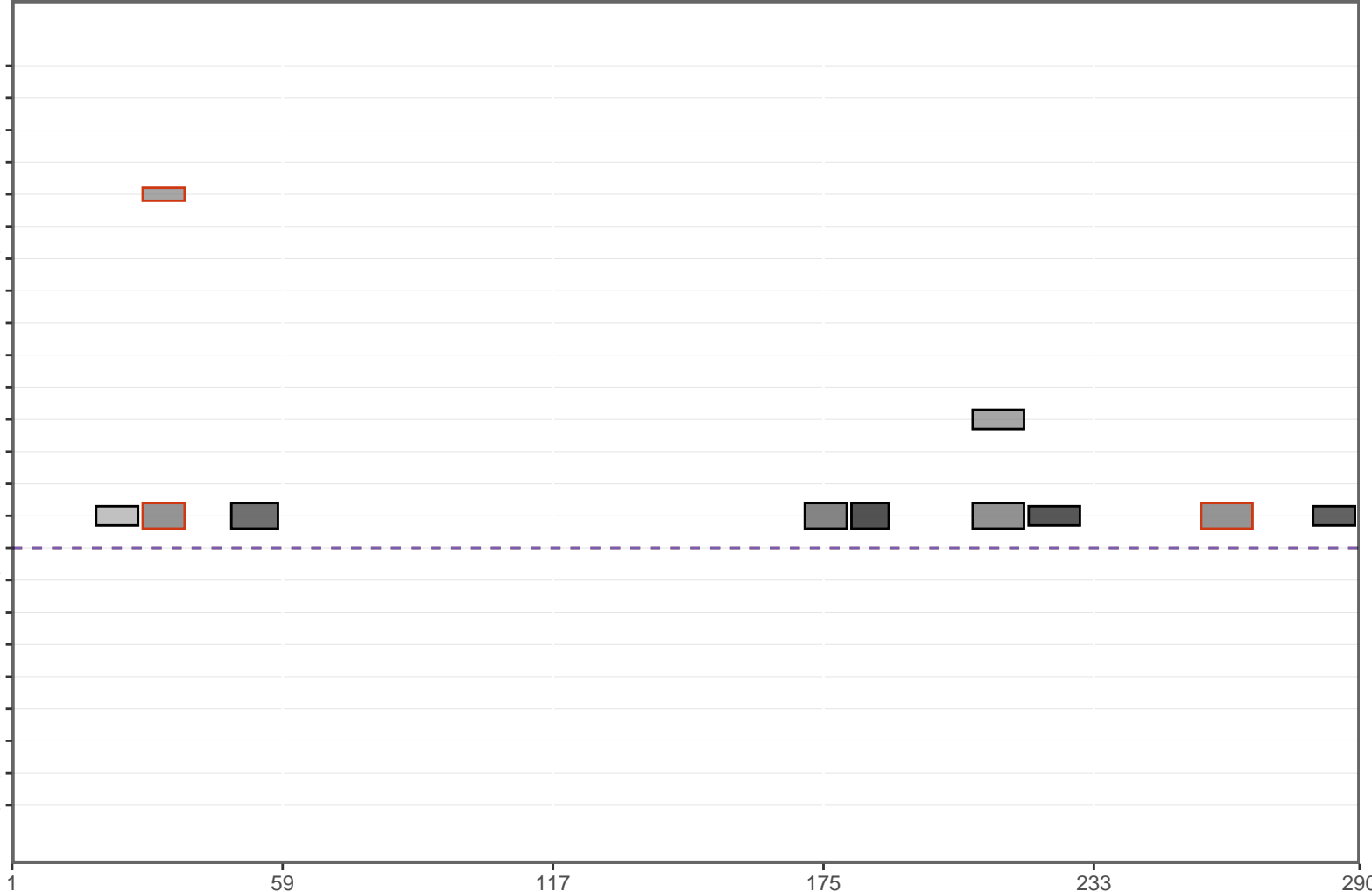
MW indication



Molecular weight

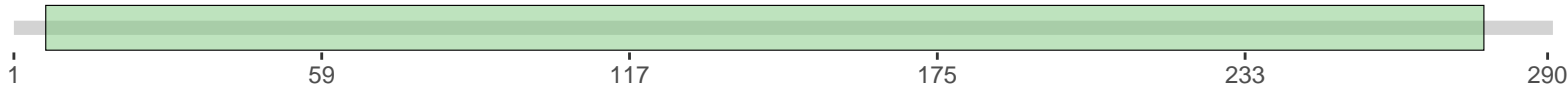


Gel Slice



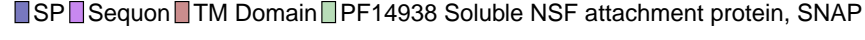
Peptide counts over 4 repeats

Protein length



Pfam domains

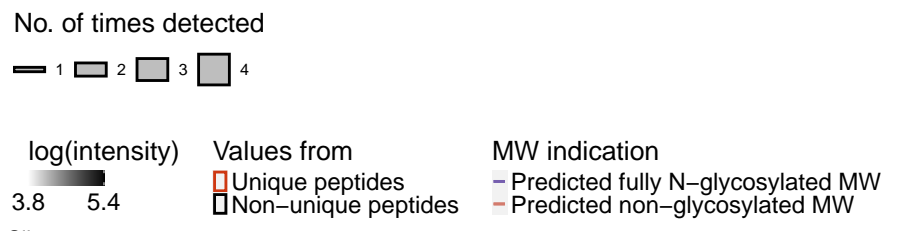
Pfam Description



Protein sequence:

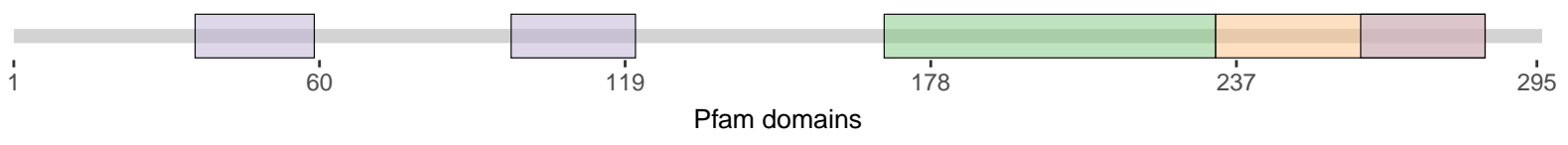
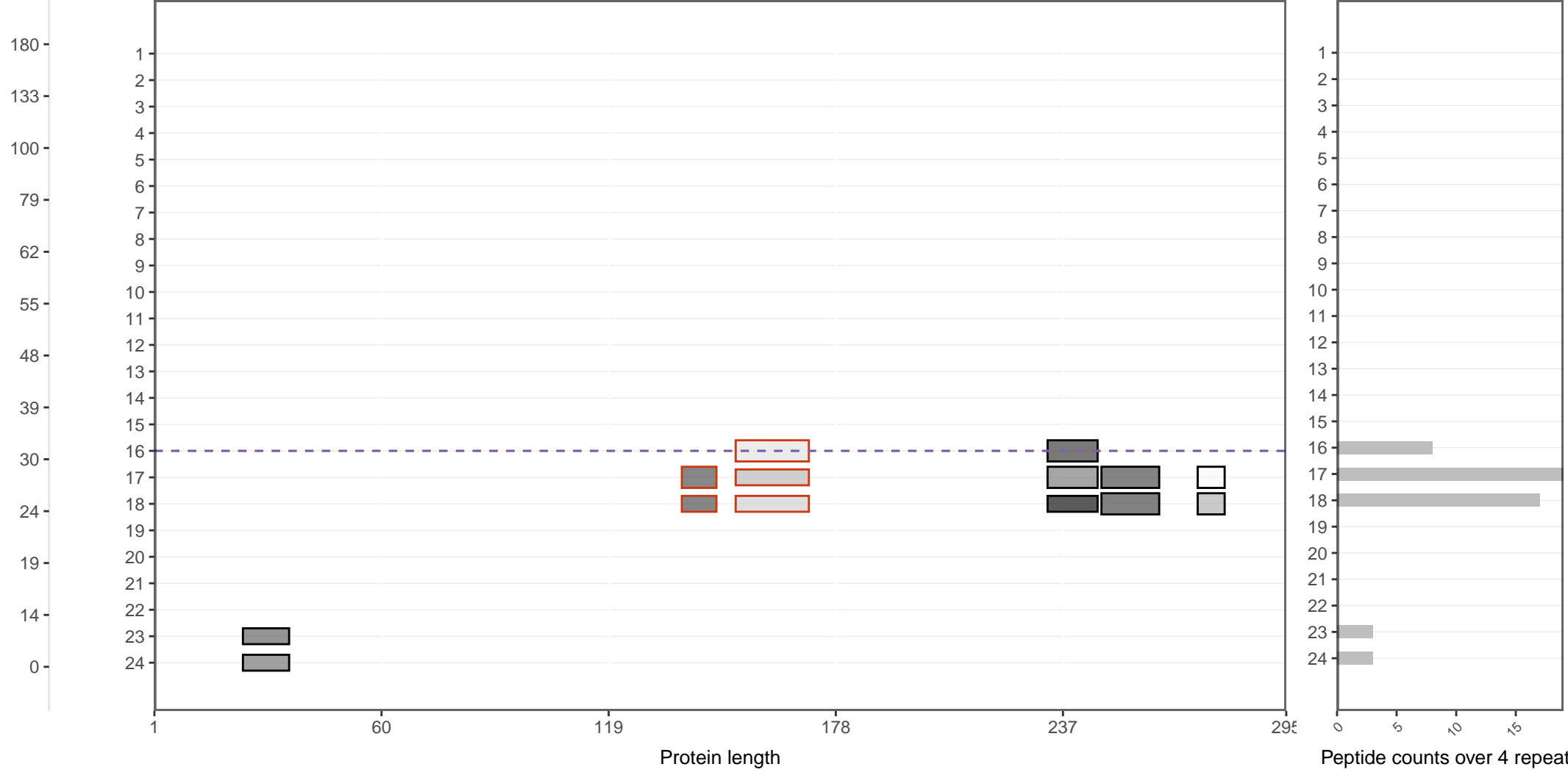
IQAISYYEKADLYGSEEDVFTTANGCKKQKVGFSAGIEYPRAFIEFEIARHSVNNLNLLKYGVRGHLNAGIGOLGKGDVVAANNALERYGELDPTFSGTRECKLLVDLAAIIDEEDVAKFTDAVKEYVDEMTQLDWARVTFLLLRVKETLKAKELEEDDLT

NbL03g06040.1 zinc_finger_CCCH_domain-containing_protein_14-like [MW = 30.88 kDa]



Molecular weight

Gel Slice



Protein sequence:

QEDPRAMGAGPIPIGRFGGRMEPPPIISGPAASFGTSTATAKISVDASLAGAIGKGVNSKIGCRGTGAKLAIREHETDKNLRNIELEGTFFEQISQASAMVRELISSLGVLGPGRAFWQGGPPPMENYKTKLGFENFANGSGTFRGERCHFAGHAELRKTGV

NbL03g06030.1 enoyl-[acyl-carrier-protein]_reductase_[NADH]_2_chloroplastic-like [MW = 41.35 kDa]

No. of times detected



log(intensity)



Values from



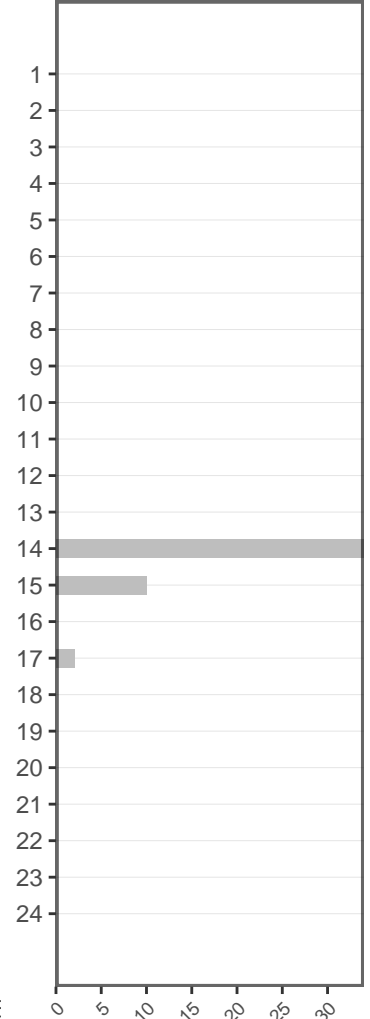
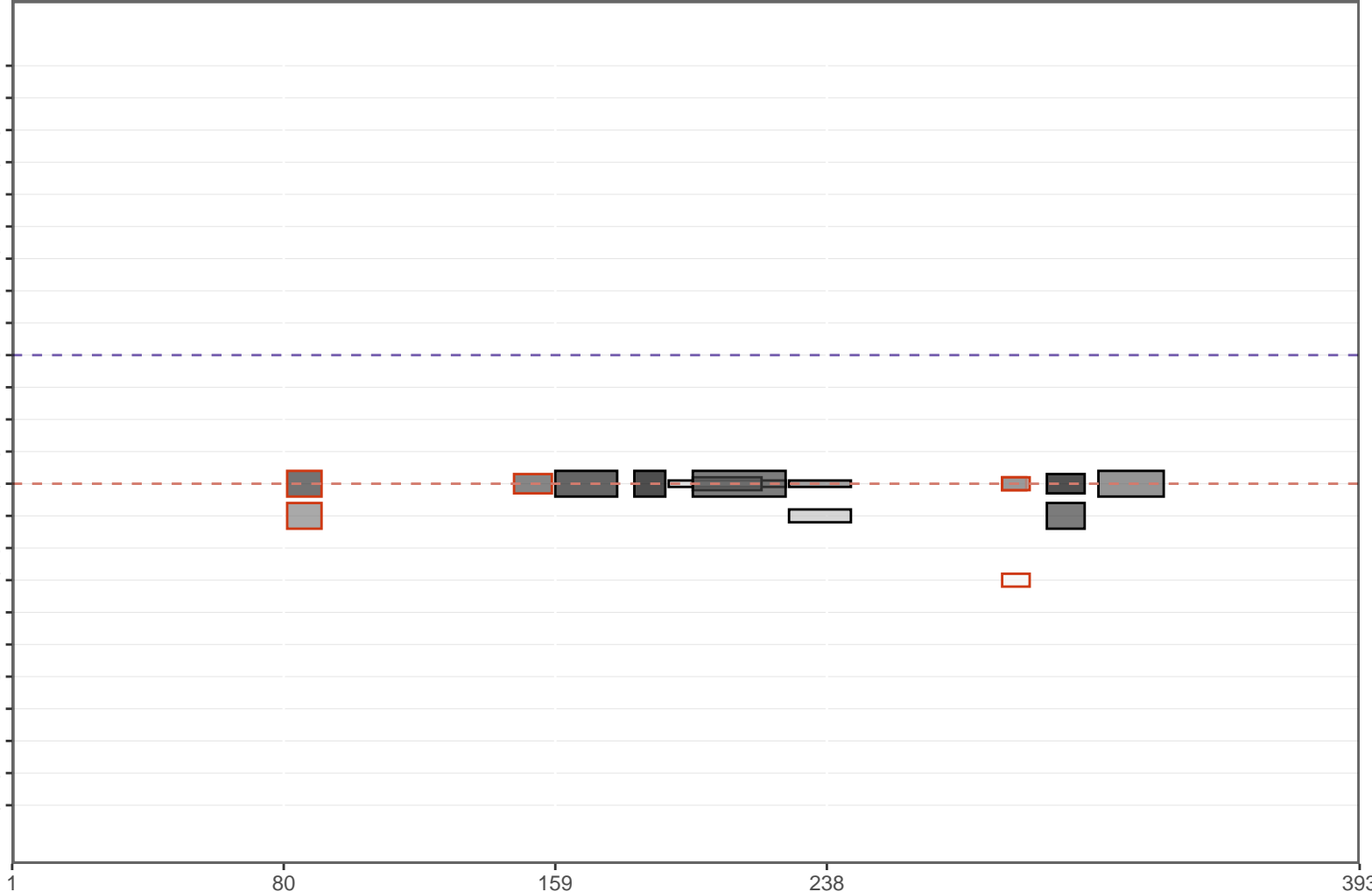
MW indication



Molecular weight



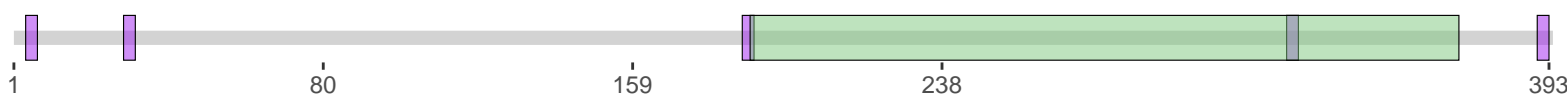
Gel Slice



Protein length

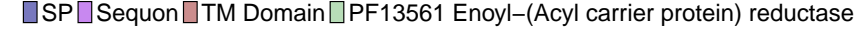


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

/AGSSNWYKELAEVSEVKQDFGTDLVHSLANGPEVKPILLETGRKGYLAASASGYSFVSLRLHFLPILNPGGASISLTYASERIPGVGGGMSAKAALESDDTKVLVFEAGRKNKRVVNTSEAGPLGERRAAKAGFDIMMNVSLLENPLQKELYAEVEVGNAAAFVSPPLASATGATVVDNGLNAMGVGVDSPRFEGLDIPKDKNS

NbL03g06000.1 nudix_hydrolase_23_chloroplastic-like [MW = 31.85 kDa]

No. of times detected



log(intensity)



Values from



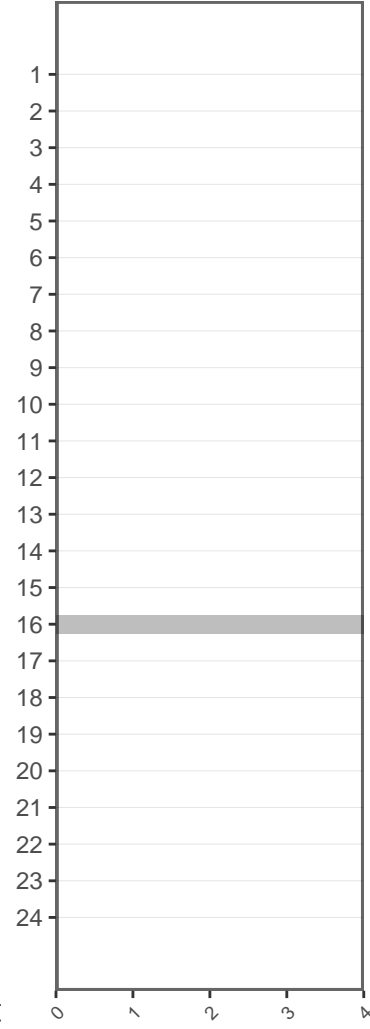
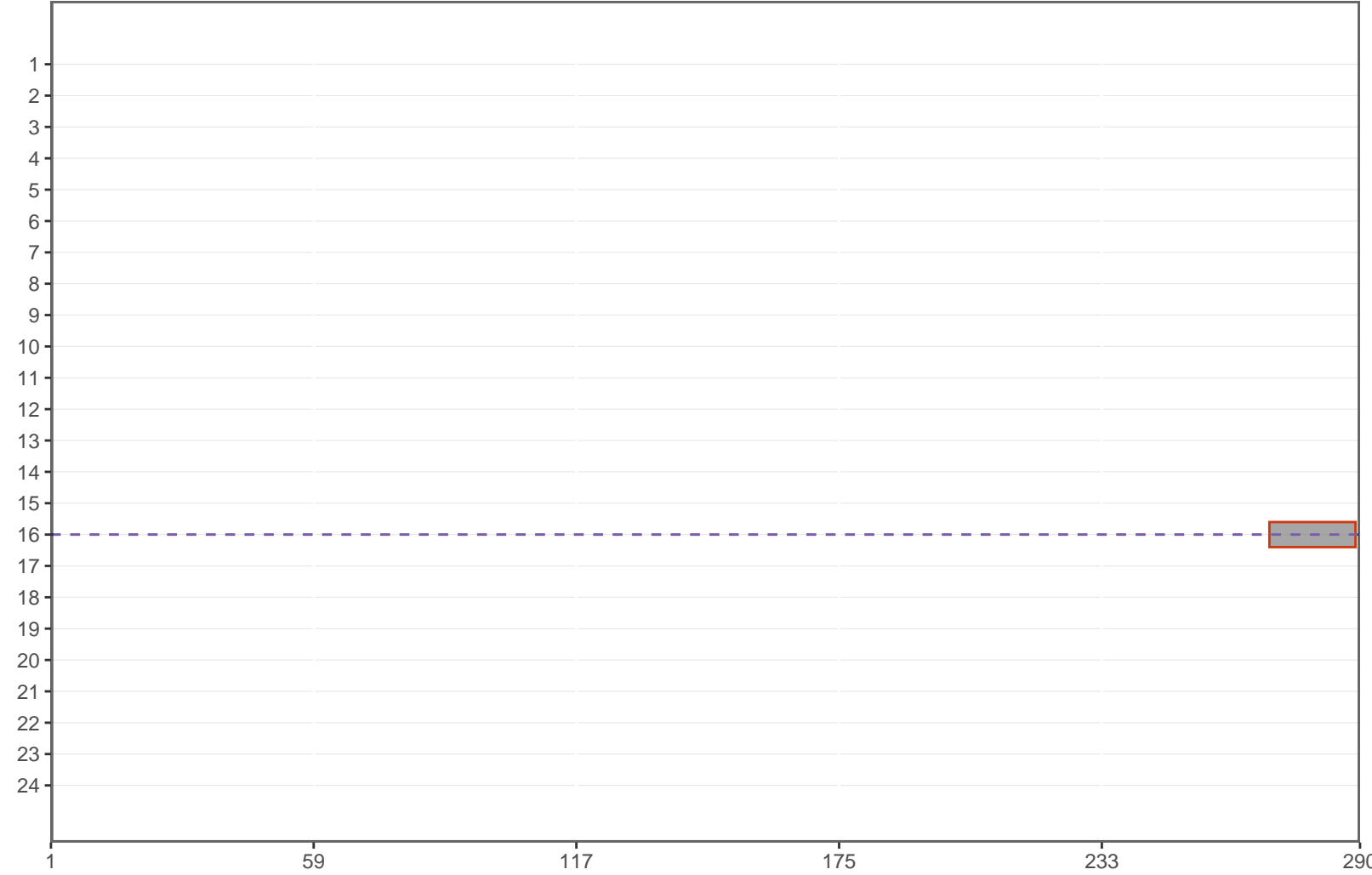
MW indication



Molecular weight

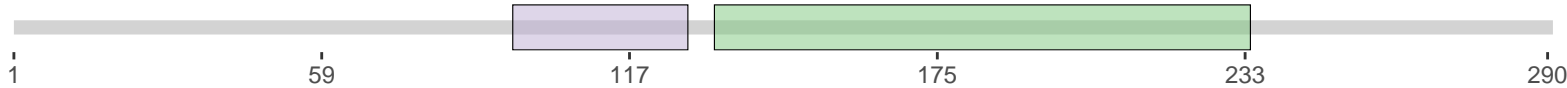


Gel Slice



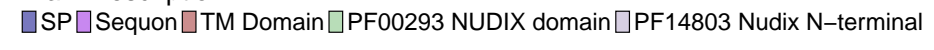
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KMIVGCLLEHDKKGLMCRKRKQKQPSGLWTLPGYMEIGESAAGARETLEENAEVEVESFFAQLDPLHGQTYMFLAALKTRHFRSPGPESSSECRVLEDDPFDLSLAFSSMLVTLKLYVEDKVGKPKFKHYGINKRPTGEPSEKAVYLEVHMGS'

NbL03g05910.1 probable_ribosomal_protein_S11_mitochondrial [MW = 26.13 kDa]

No. of times detected



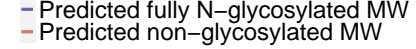
log(intensity)



Values from



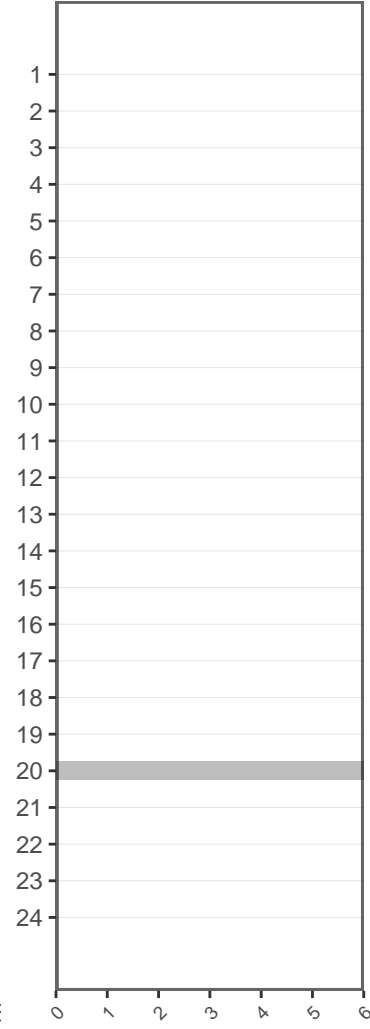
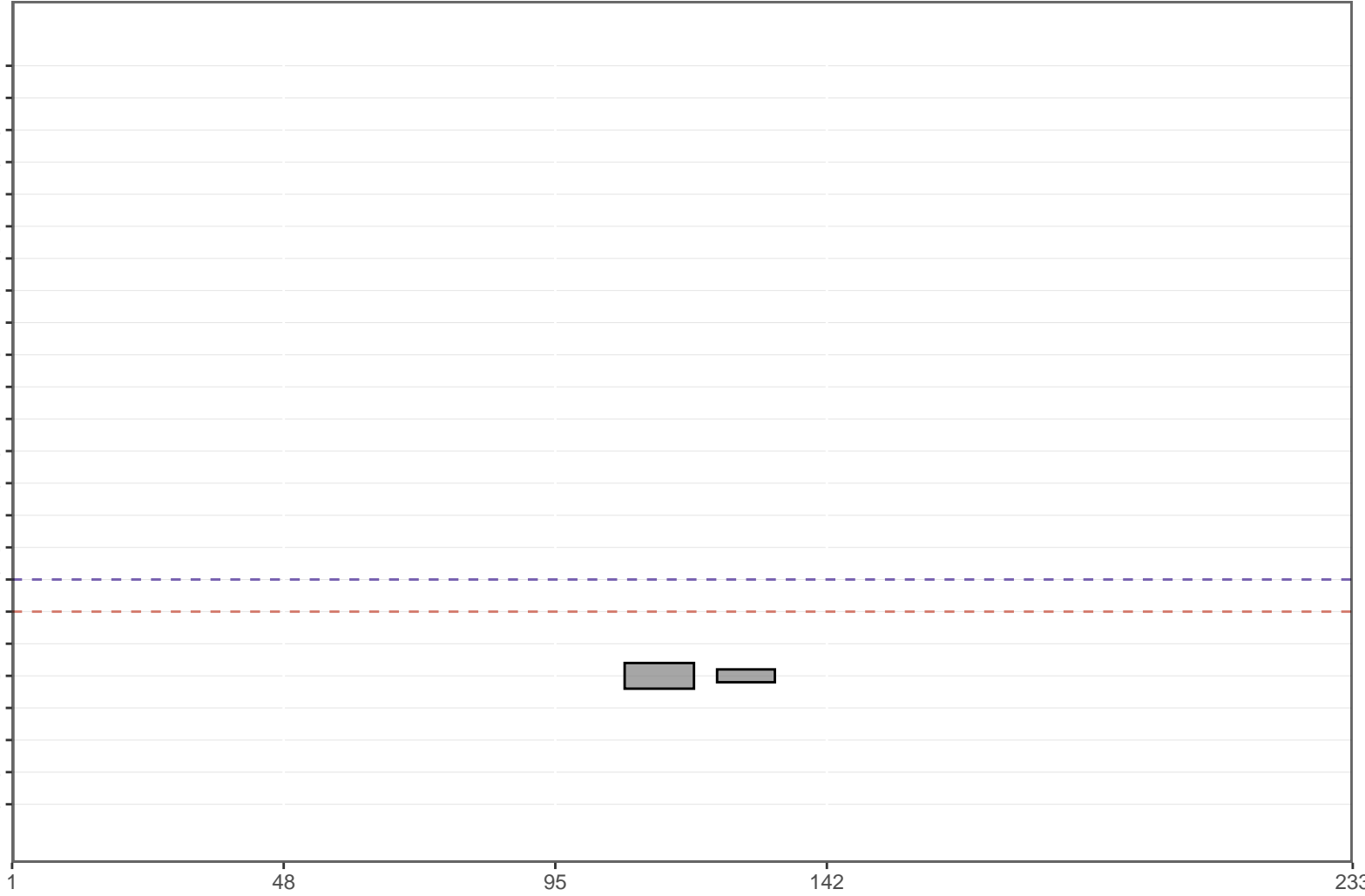
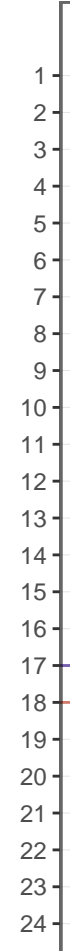
MW indication



Molecular weight

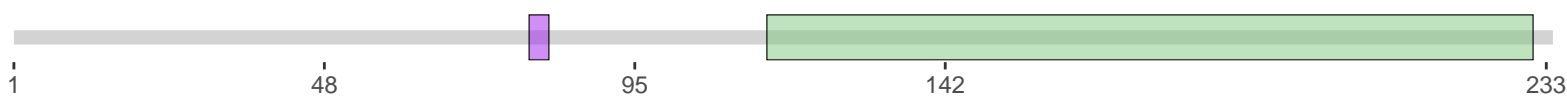


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PLSRYYVEQQADVHKVLRNNAFVTVDSKGNKKFGATAGKITGKGTAKIARYAAEATAEHVGREARDRGLREVVMMKVGFTFFKKGKGAISFREQYTHRGDKNPVVFIEDTRRPHNGRLPKKRRP

NbL03g05820.1 uncharacterized_LOC107781405 [MW = 31.43 kDa]

No. of times detected



log(intensity)



Values from



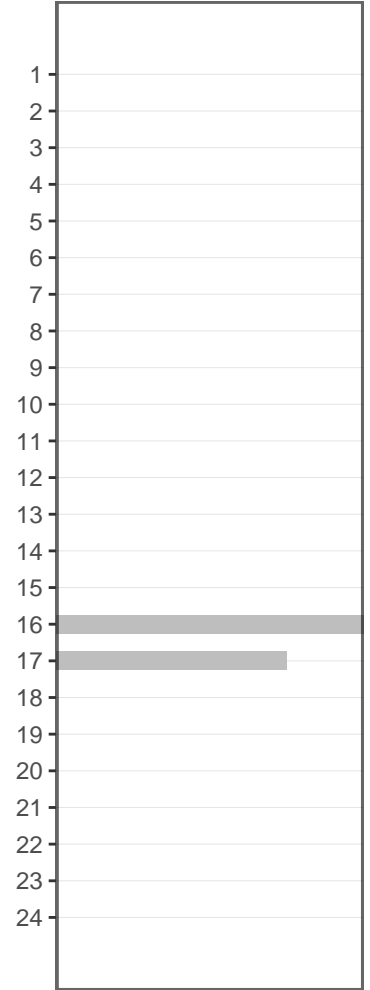
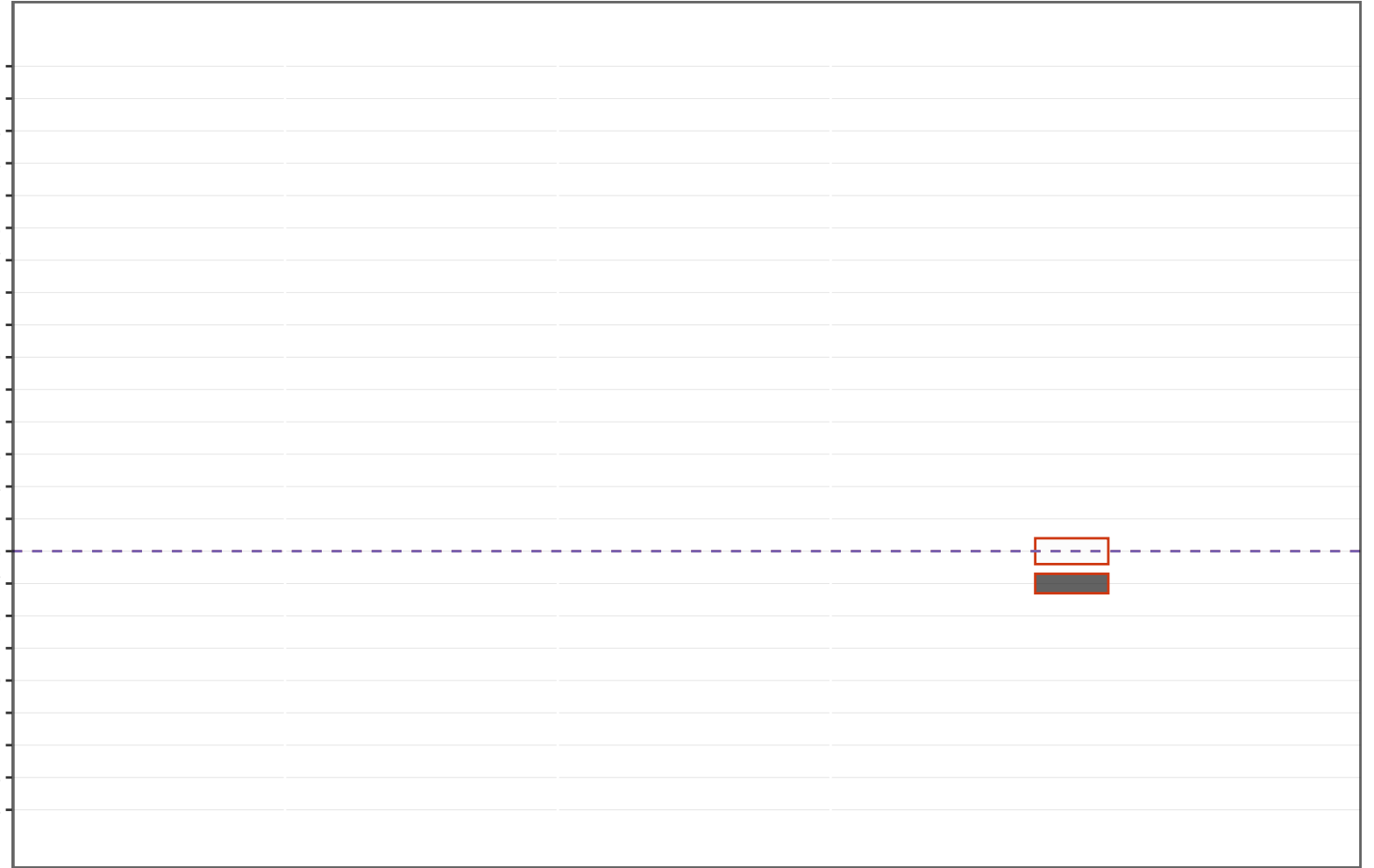
MW indication



Molecular weight



Gel Slice



Protein length

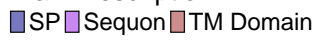


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IEFYDRVYDSSNCRQLLVVHDSLFMLADIKERKDKVKGWGGELVYVPEKWTSTFDVIFLFLPALAFELGGIMEVLRKRKGLGARVWISHPGGSDVVEEGRKLYPDVYVSNLPEKMLGNAAEHSEFVYKFTDEPGFYLAIKFEPENKNDI

NbL03g05600.1 uncharacterized_LOC107780098 [MW = 38.03 kDa]

No. of times detected



log(intensity)



Values from



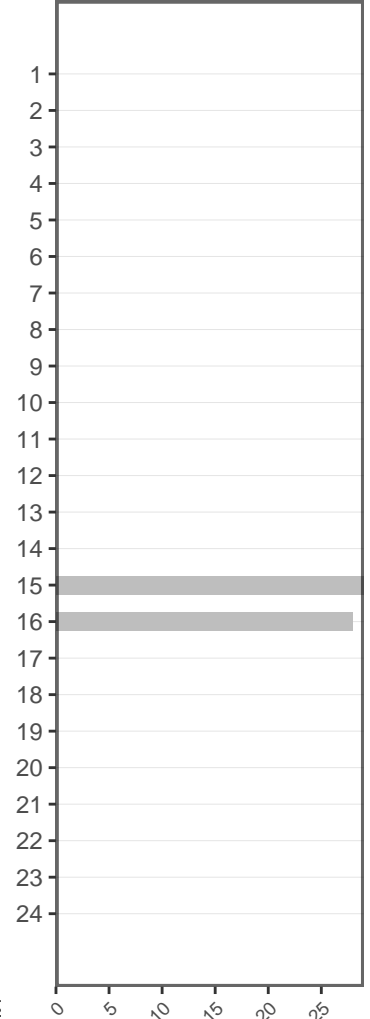
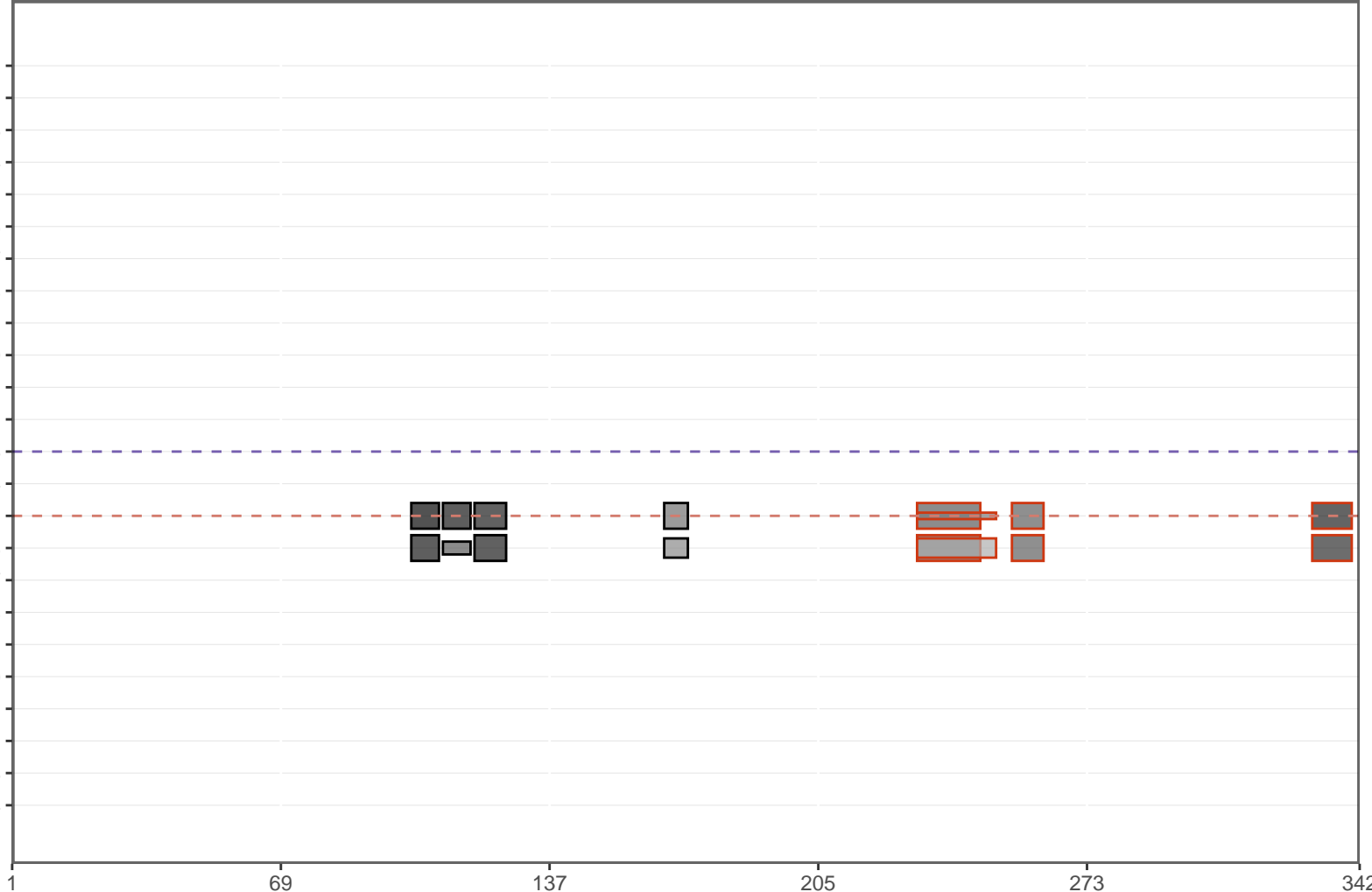
MW indication



Molecular weight

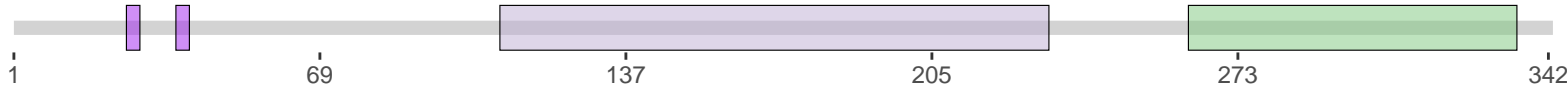


Gel Slice



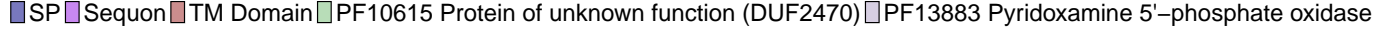
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TKOLLANSKCSLLVARDPEDRTDLVTVHGDVAVPVPETEKEGHRAAVLAHPEAFVWDFGDFQFMRIEPRVRYVSGVATLGGSEFSKEEFRTAKIDPIYQFSKPTSHMKNKDAEDTKLVVHSTVSPVDFAYMLDNDLGINAKAGYKNTFKLRFVPPFRRAVDRKDKTKLIVEMLGAARS

NbL03g05540.1 50S_ribosomal_protein_L18-like [MW = 26.06 kDa]

No. of times detected



log(intensity)



Values from



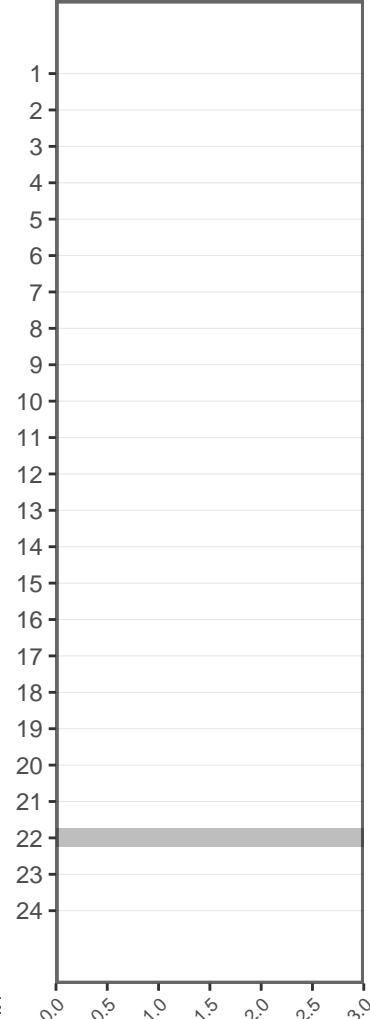
MW indication



Molecular weight



Gel Slice



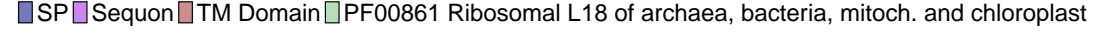
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKIASFNVEISRMVPPPIRDRVTRKYLKPYLRLMHFTNKYVNAQVWHPTPTVAASASTQEKGLRLAMVEGKENTRDVAAAKIGKLLGERLGAKGPIASVFFKREQRVHGKKAVIDSVKEVGIELV

NbL03g05470.1 uncharacterized_LOC107828093 [MW = 72.43 kDa]

No. of times detected



log(intensity)



Values from



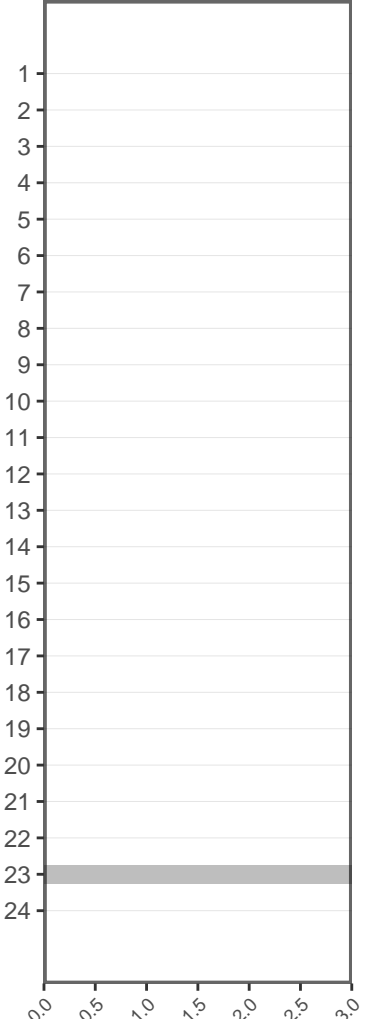
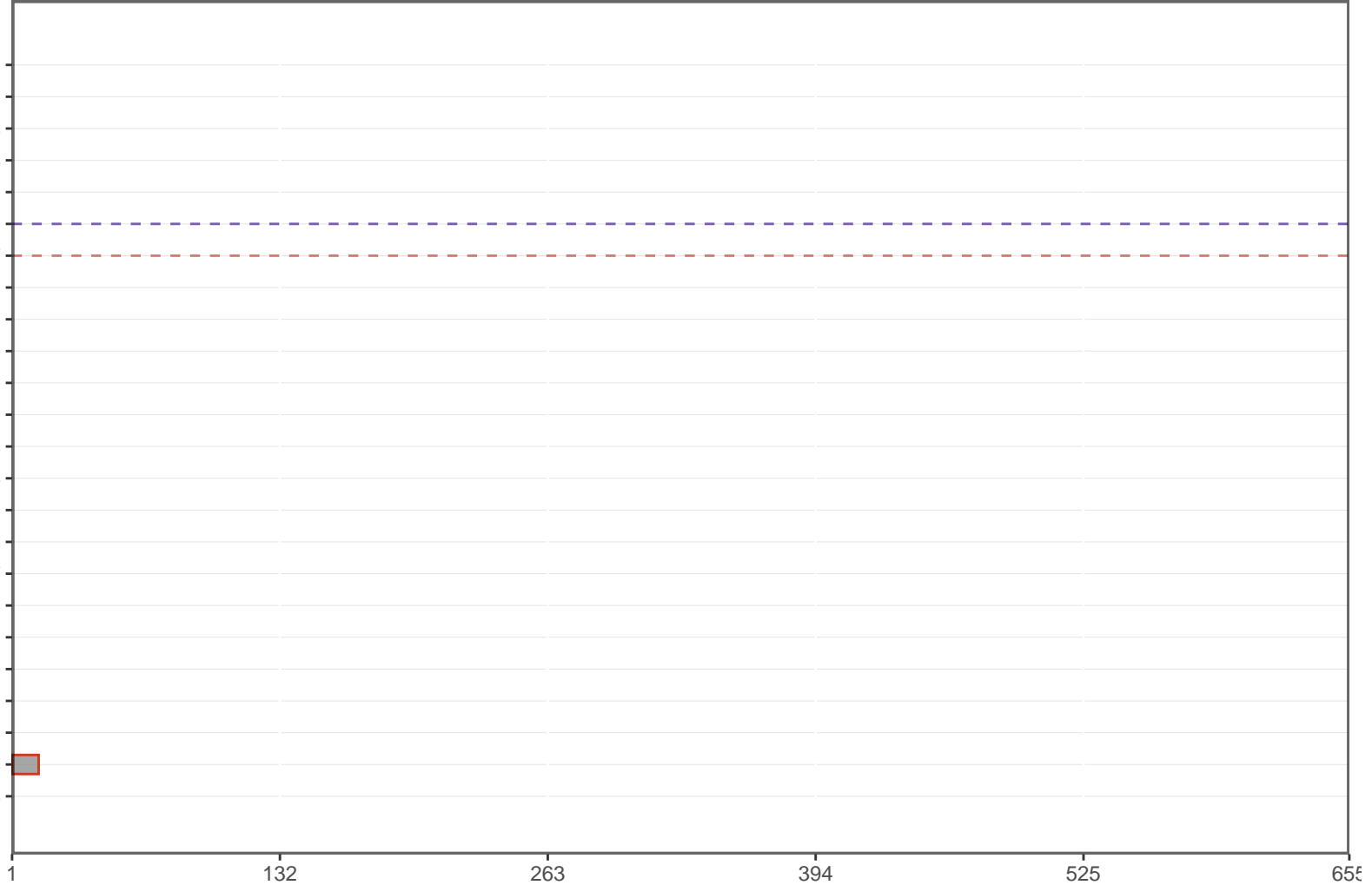
MW indication



Molecular weight

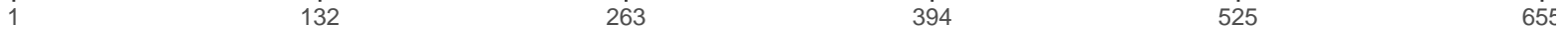


Gel Slice



Peptide counts over 4 repeats

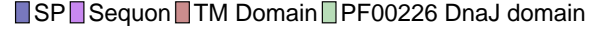
Protein length



Pfam domains



Pfam Description



Protein sequence:

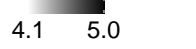
IGNENRSASTSDNIVSNANKEGNVDAEDNRIRSFVITAGPGYIMVEFPLEYADCTLRGNGKRAFQAVIASPPPIIDGKDVFQGWGFMPPLGLLENFERNRDGGSGWSPFSPMFTGPHVGGDGGENHNRVYGGHSHVDNLGALHNADATISGGDREHFSRPIYVDDDDVFEVSEAGEEEDSDWRDKERNKAKSGKWSARTGAPSKNANKQGVAKKRVEGANDNLRDGLATDQGVEMSHVAVESNKKGIASKTRRLPGRVAKHFGSLDLNVEFSND

NbL03g05330.1 adenylosuccinate_synthetase_chloroplastic-like [MW = 54.86 kDa]

No. of times detected



log(intensity)



Values from



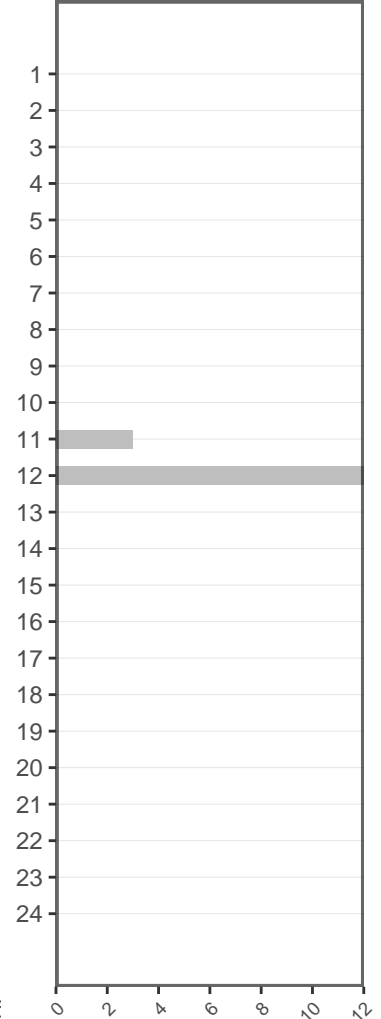
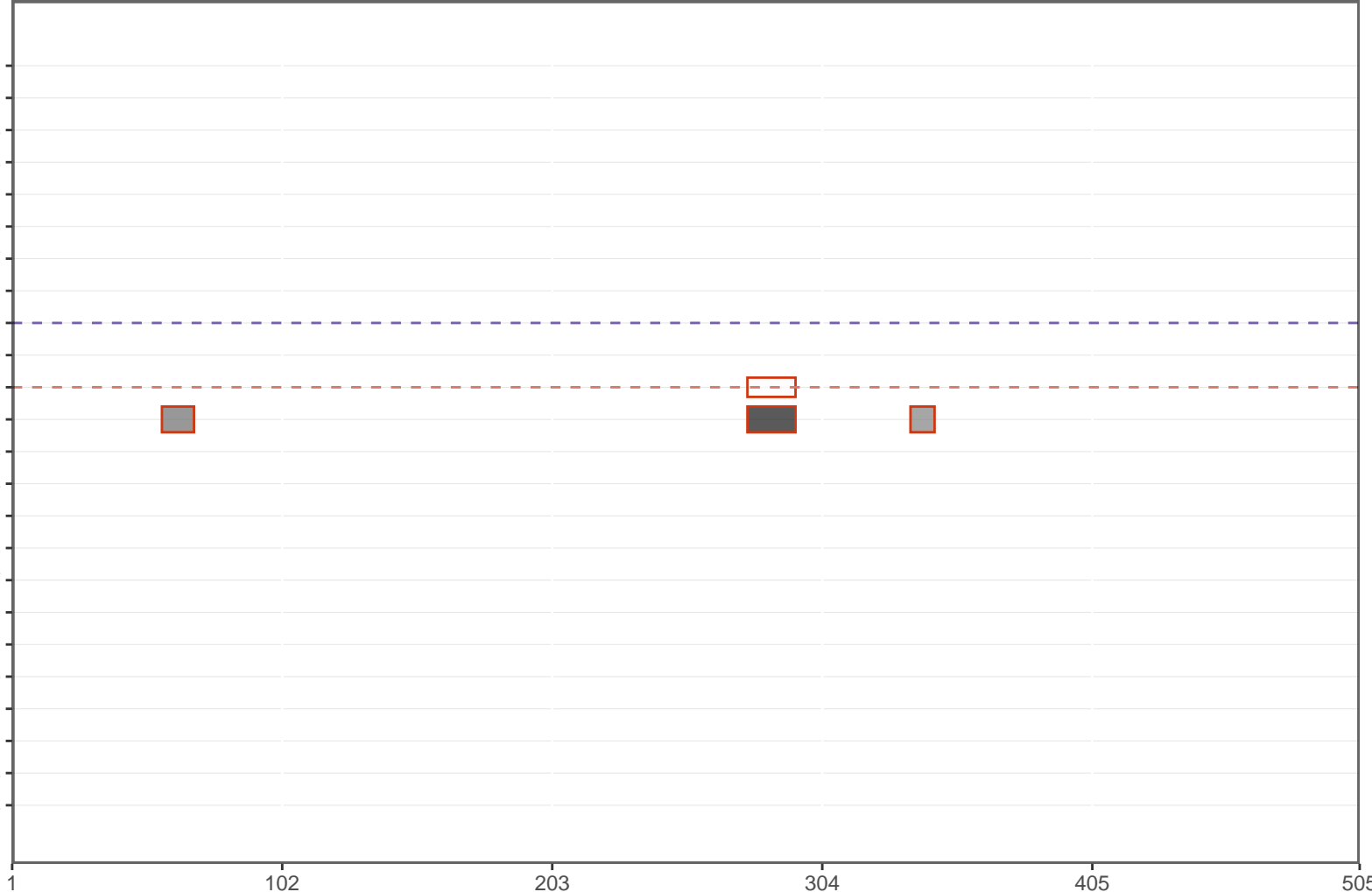
MW indication



Molecular weight

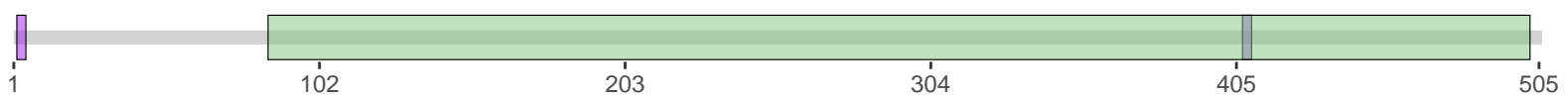


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PKKDLLLSDASRFKGFNYGPDMLREEVERYKFAERLEFFITNTYHFMNDAISGKIKLVEGGGATMLDIDFGTYFVTS66PSAGGKIGTLGIAPRMVGDGKLVKAYTTRVGS6FFPTEILGKGGDLRFAGQEFGTTTGRPRRGGWLDIHALRFCCGQINGFASLNTKLDVLSLSEIELGVYRPPDGTPIVEGFPDRLLLDQIKVEYEVLPQWQTDSSIRKYSELPKAARDHIERIEELGVPHYIGVSGDRDALYK

NbL03g05170.1 aspartate_carbamoyltransferase_1_chloroplastic [MW = 45.34 kDa]

No. of times detected



log(intensity)



Values from



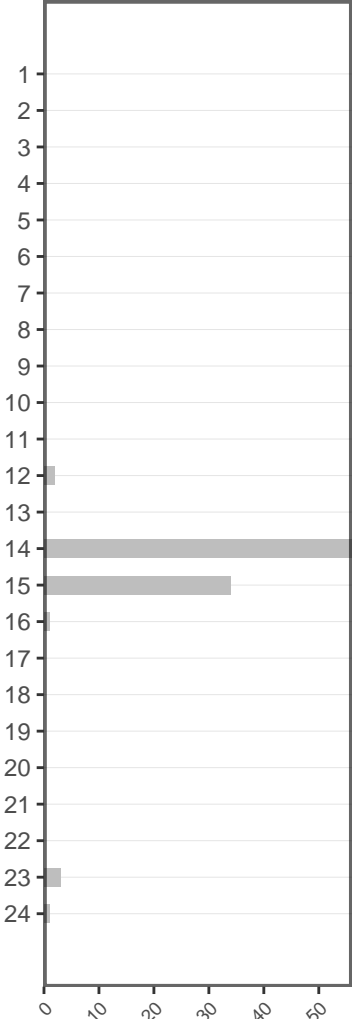
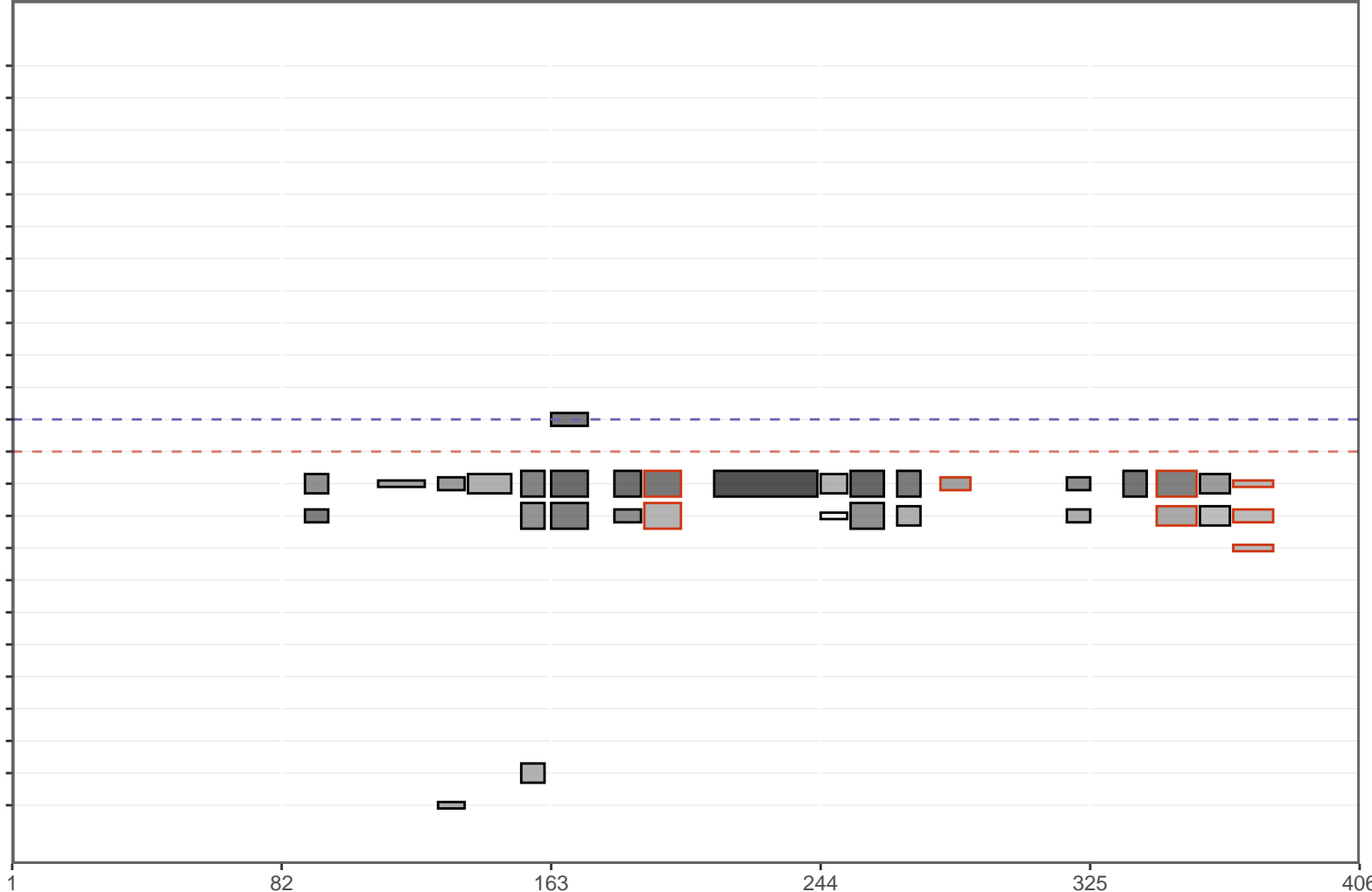
MW indication



Molecular weight

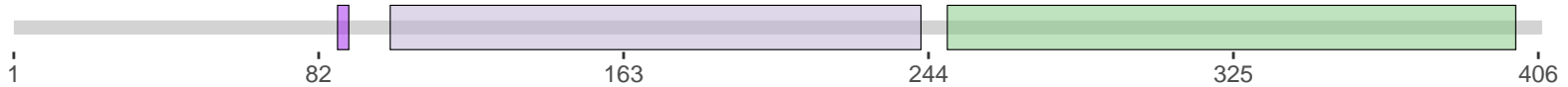


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00185 Aspartate/ornithine carbamoyltransferase, Asp/Orn binding domain
- PF02729 Aspartate/ornithine carbamoyltransferase, carbamoyl-P binding domain

Protein sequence:

MSIRTVETGYSDIVMRHFESGAAKRAAATASIPINAGDGGPHPTQALLDVTIEREIGKLDGRIKVALVDGLAYGRTRVRSLLAYLLAKYGDVKKYVSPDVAVKMKDDKDKLFTMGSGVQWEEESADLVDAASKGDVYVYQTRIGRERFGERVDLYEARGKIVYDLGVLNAMGKHVAVMHPPLRLEDFITDVEDDPRAYFRGAKNGLYRIMALKLLLLGW

NbL03g05150.1 eukaryotic_translation_initiation_factor_5B-like [MW = 152.47 kDa]

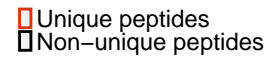
No. of times detected



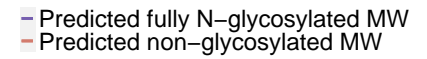
log(intensity)



Values from

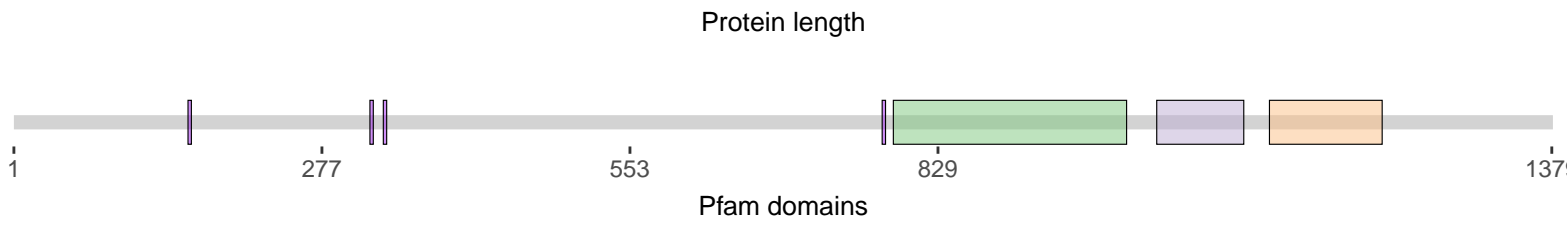
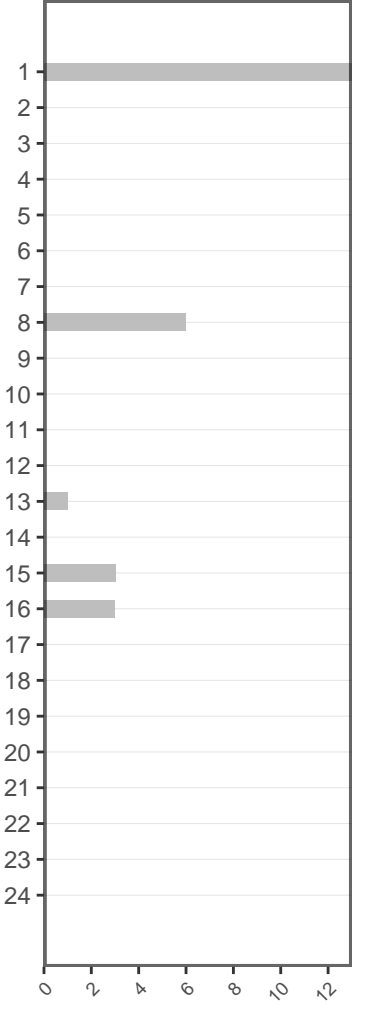
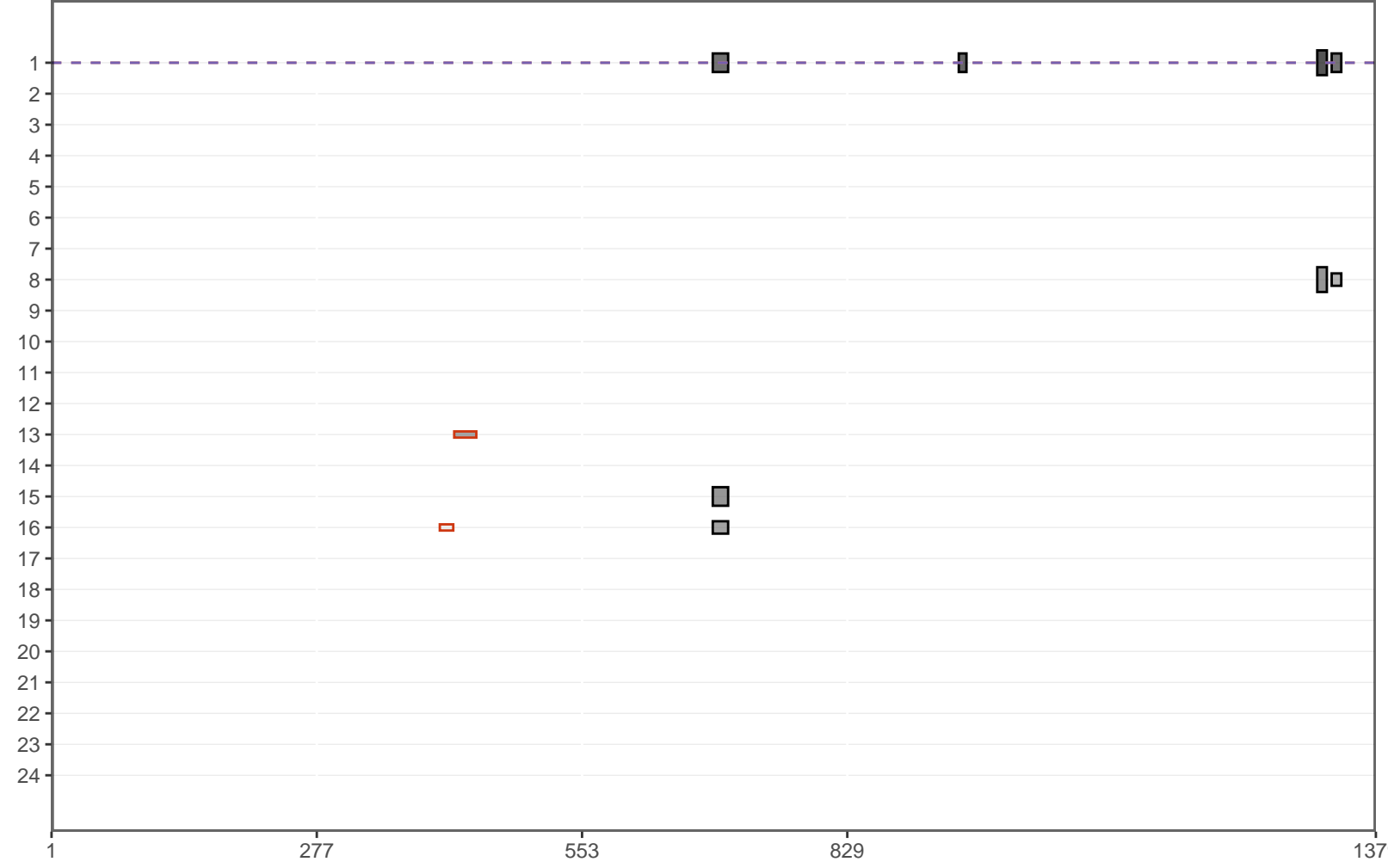
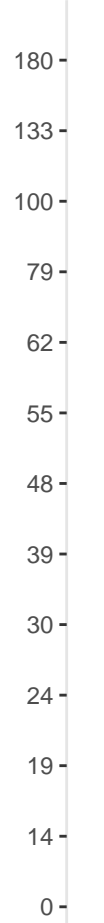


MW indication

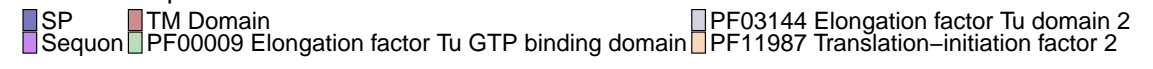


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

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NbL03g05060.1 stearoyl-[acyl-carrier-protein]₉-desaturase_chloroplastic [MW = 44.88 kDa]

No. of times detected



log(intensity)



Values from



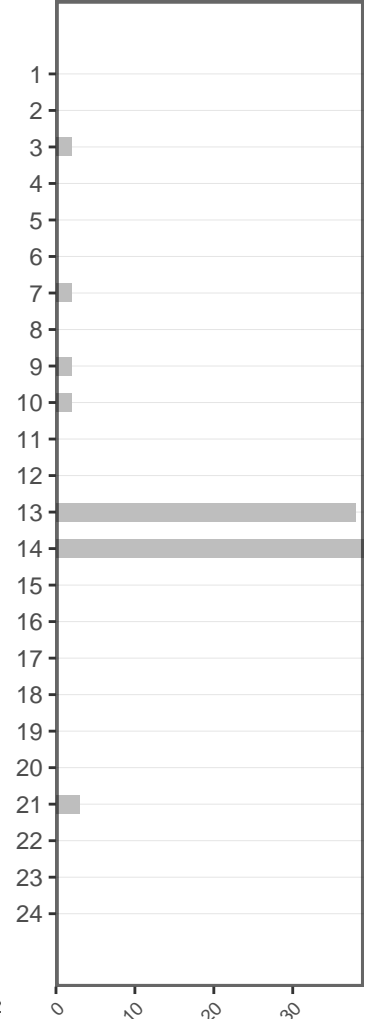
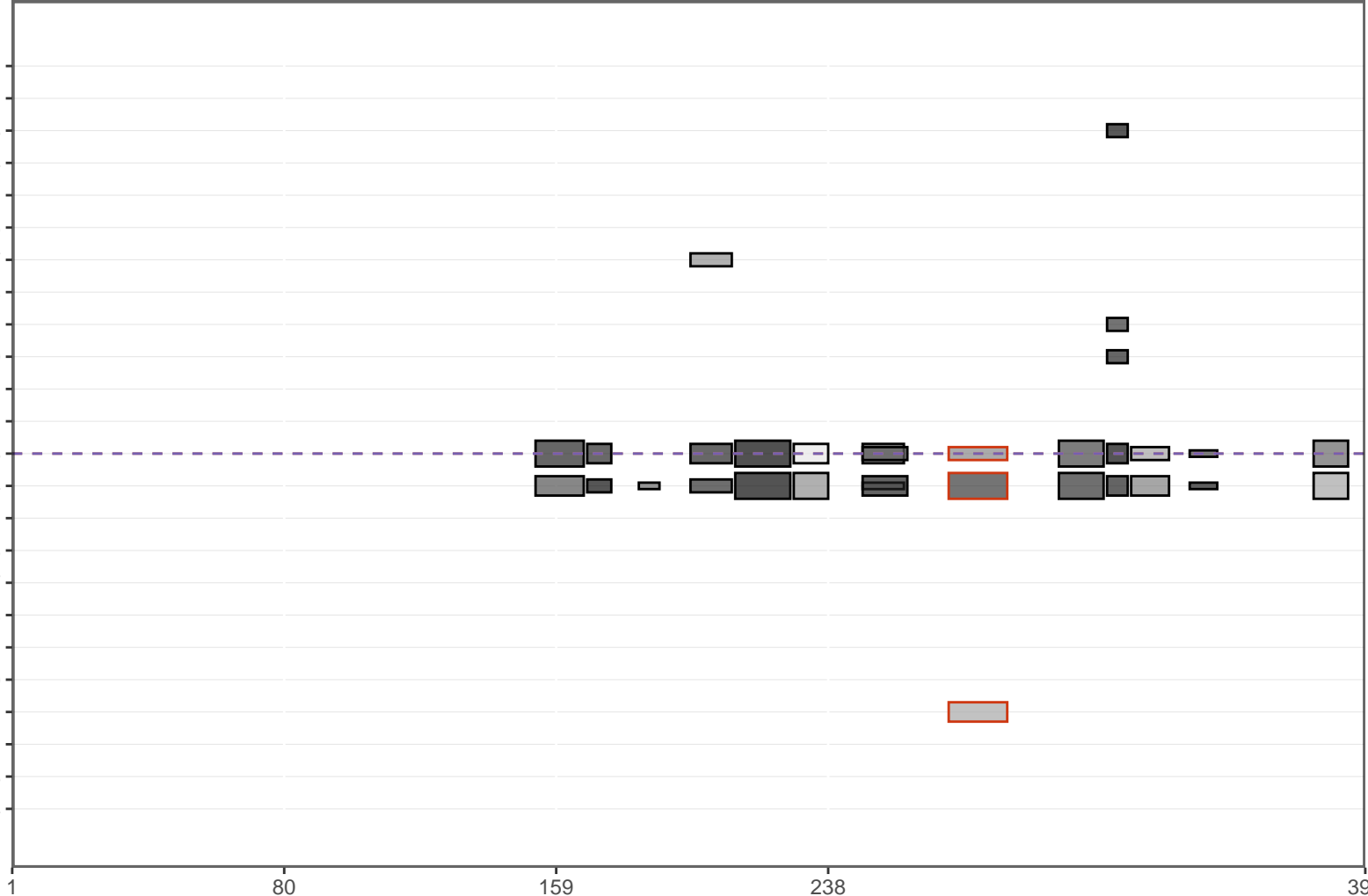
MW indication



Molecular weight

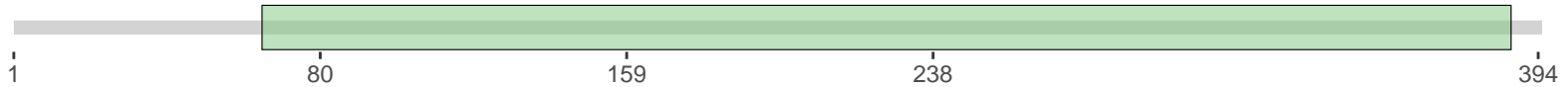


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YLLYSGRVDMDRCIEKTKYLGSGMDPRFENPNYLGFRYTSFQERATFISHGNTARLAKEHGDLLAGVGGHMADEKRHETATYTKIVEKLFVDPDGTLLAWADMRRKKSMPHLMVYDGRDNLFEHFSVAQRLGVYTKADYADILEFLVGRWEMEKLTGLSGEGRKADYVCGGLAFRRIKLEERADARAKEKAPVPSWVFGREIKL

NbL03g04950.1 probable_LRR_receptor-like_serine/threonine-protein_kinase_At1g53430 [MW - SP = 109 kDa]

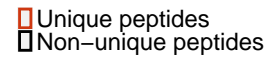
No. of times detected



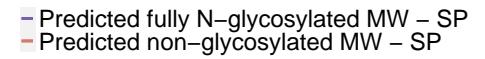
log(intensity)



Values from



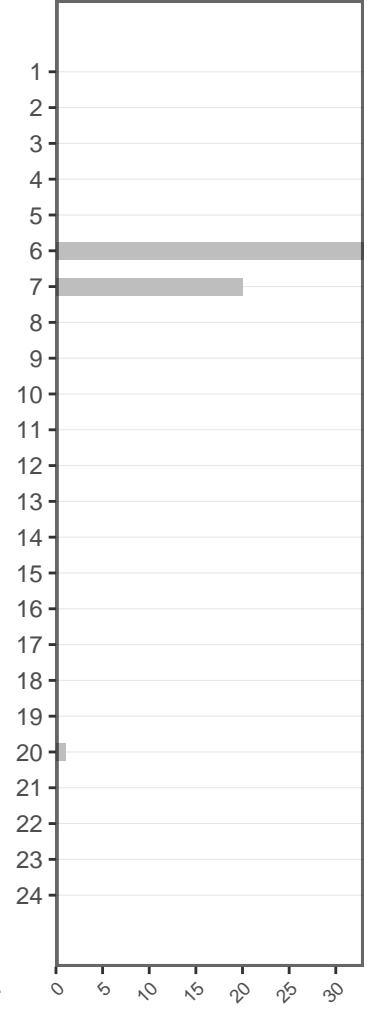
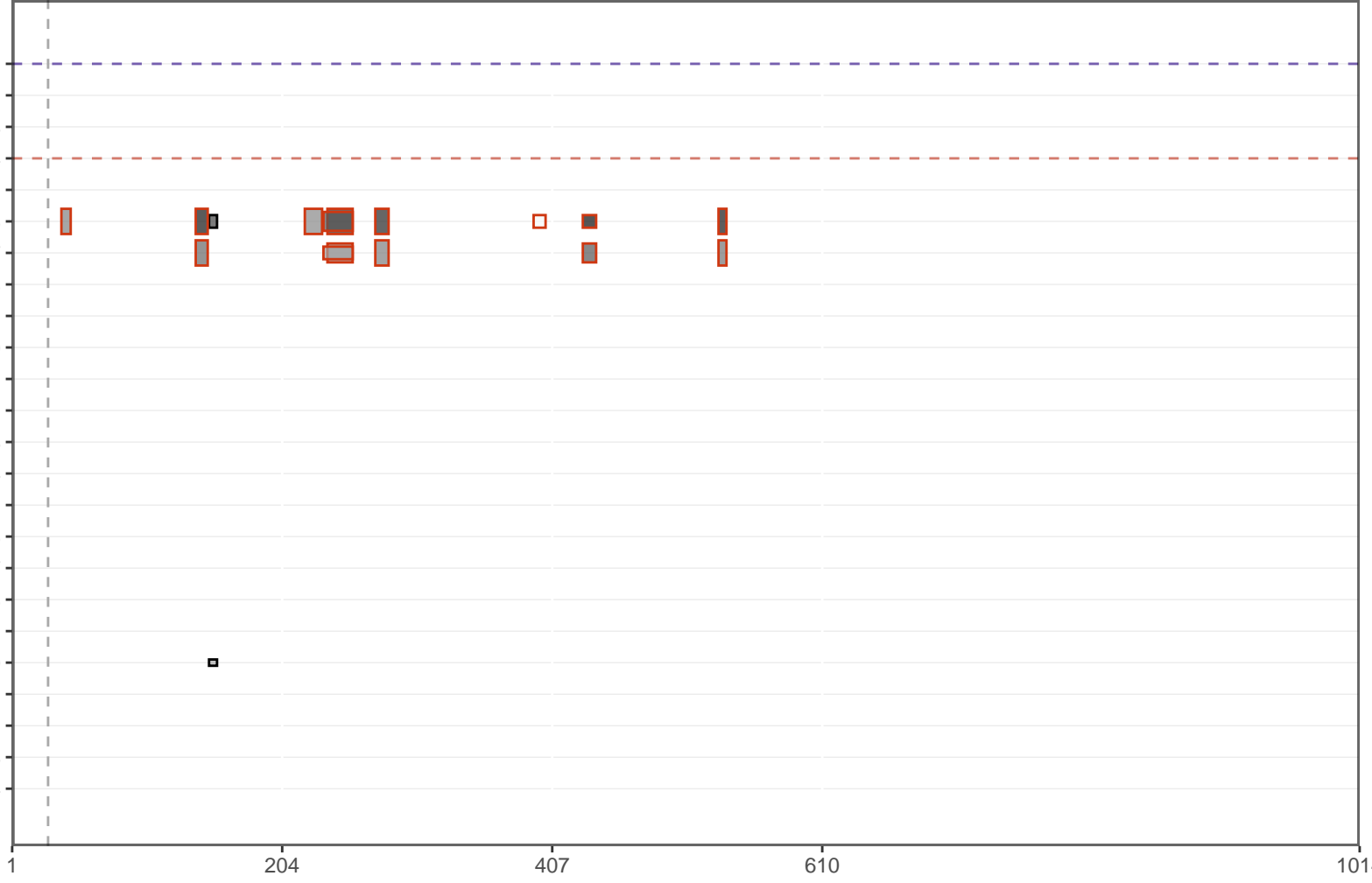
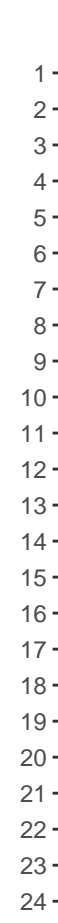
MW indication



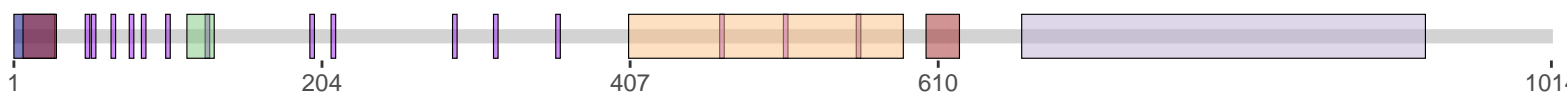
Molecular weight



Gel Slice

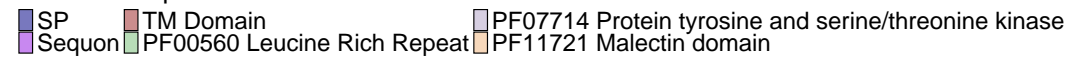


Protein length



Pfam domains

Pfam Description



Protein sequence:

RVRLHFAMFSDNDSYSSLGRIFDFVSGKGNVSKDFNIMERAKGVSKFEMDFKVFVNGSTLEHLYWTGKGTAFDRGVYGLHSAITVFNVNDTGRHLVGVAVIGVLSGAVLLIIVVLLVKKGLGKKNKELELRALDLQTHFRLRKQKAAATNFDPAKIKGEGGFGPYYKGVLDGAMAVKQLSSKSKGGRNFVNEIGMISALHHPNLRVLYGGCIEGNQLWVEYEMENGLARALFGRDDQRLNLDWPTTRKRIGLGARGLAVLHEESALKIVHRDIKATNLLD

NbL03g04820.1 peptidyl-prolyl_cis-trans_isomerase_CYP37_chloroplastic [MW = 50.71 kDa]

No. of times detected



log(intensity)



Values from



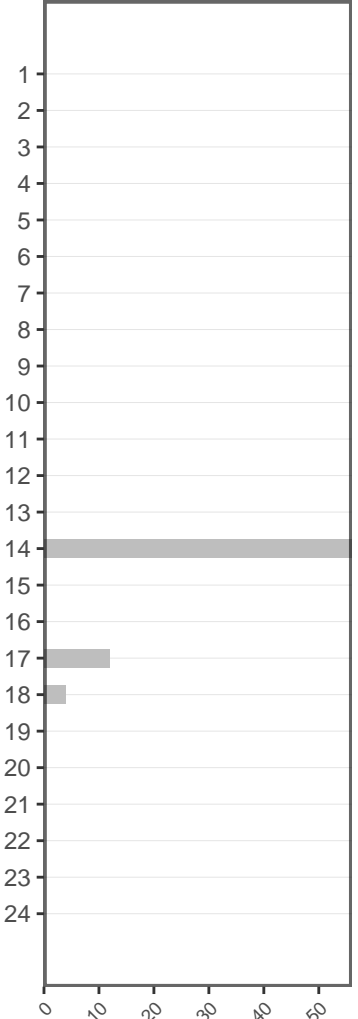
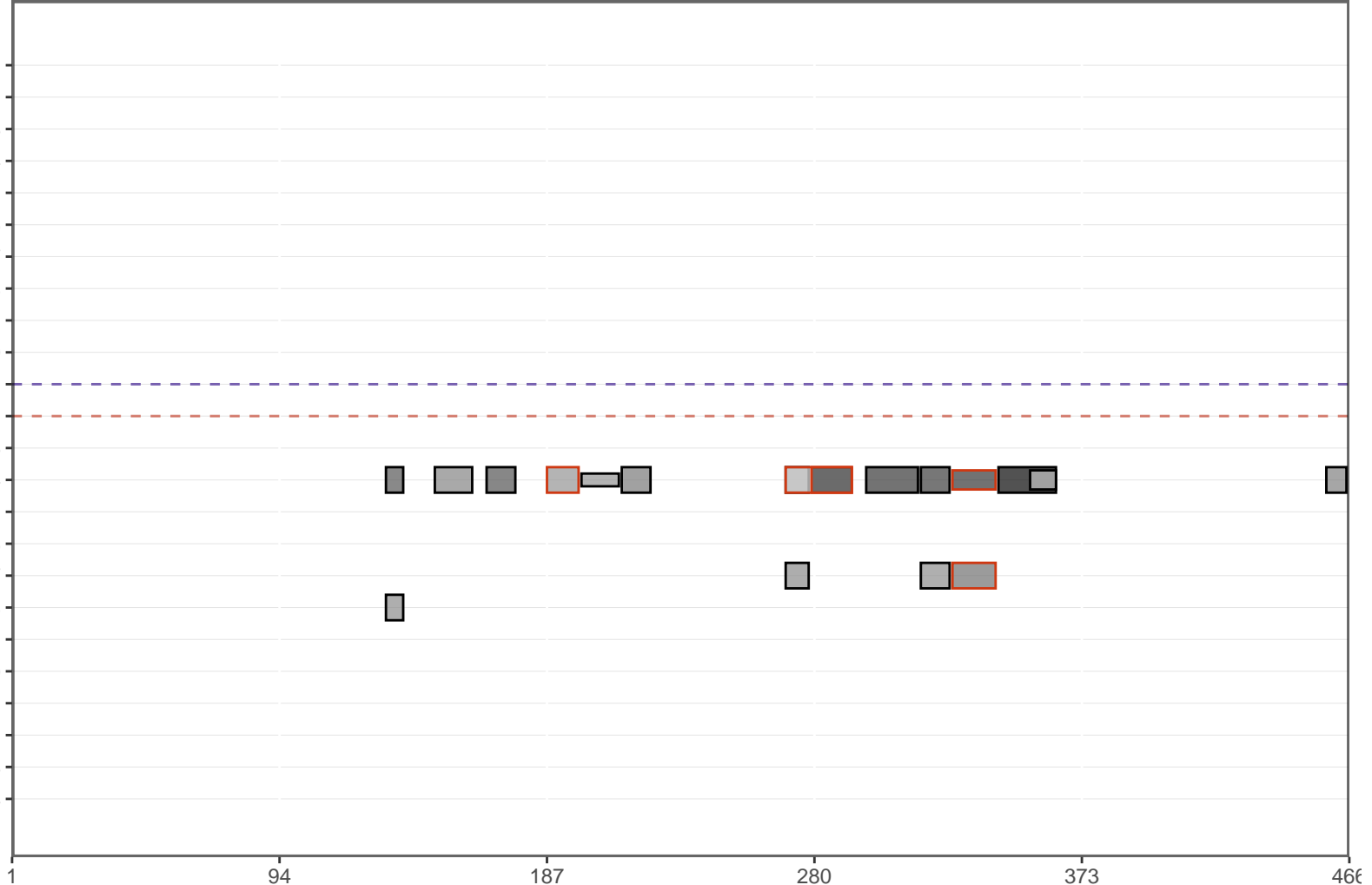
MW indication



Molecular weight



Gel Slice



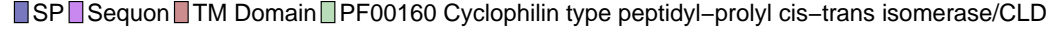
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KDKDPKYSVGLASTLDTVAQLELLGAPGLSFLLPQGHLYKPRLRGRGVVEFTVEKVDGSTFSPEAAGVAKSTAKIVVLDGYSAPLTAGNFAKLVDGAYDMKLTNANGALSDELEKATGYGVPLKIKPSGGFELPYRTFLSVODGELPVLPVLYGVAVAMAHSDVSEELSSPQOFFFYVDKRNLSGLGGLSFEEGGQFVFGYTTIGRDLHPKQTGDNRIRSAKLVGGDRLLVLPQEN

NbL03g04700.1 thioredoxin-1-like [MW = 19.73 kDa]

No. of times detected



log(intensity)



Values from



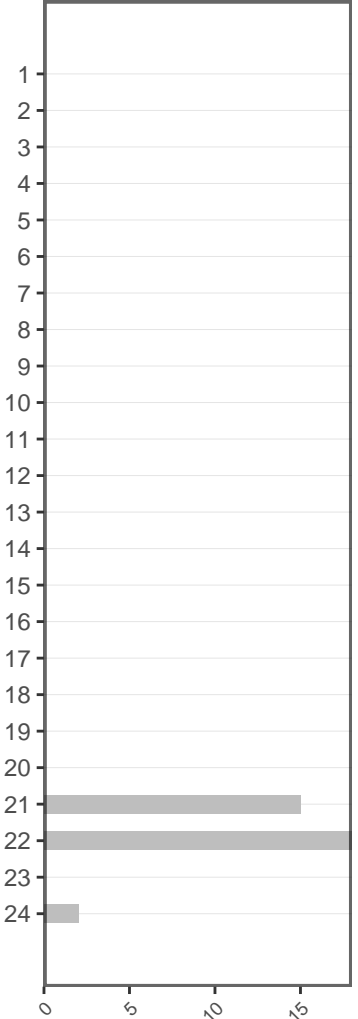
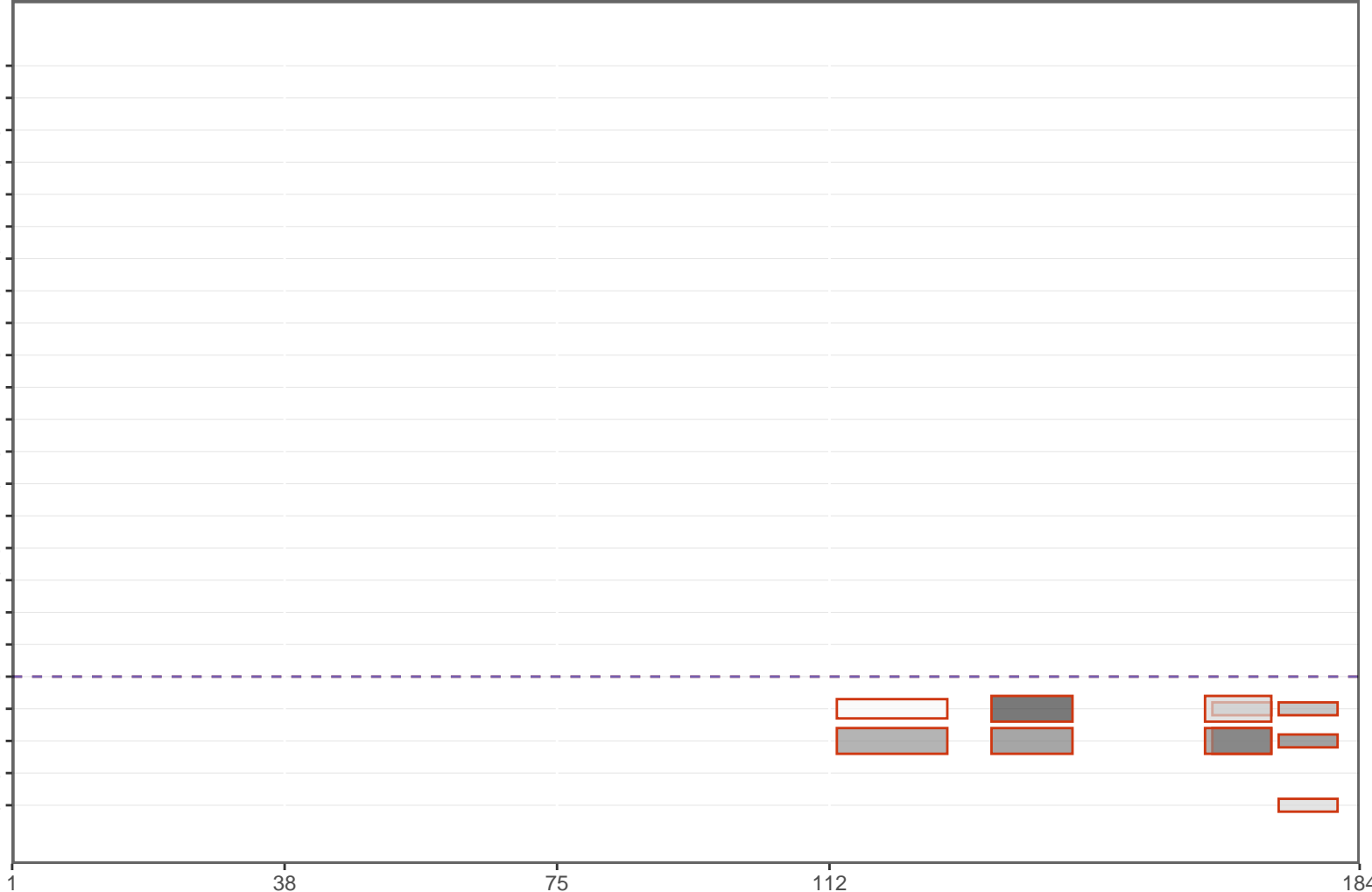
MW indication



Molecular weight



Gel Slice

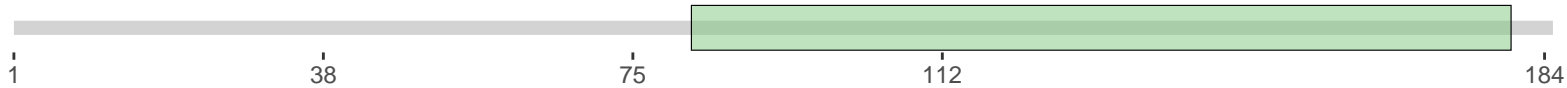


Protein length

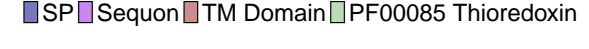


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VLPVPYNDQTVESLVIGSDVPLVLEFVAPWGGPCRMIHPTVDLAGEFAGKFKFKYKNTDESRIATRYGIRBIFTVMFKDGEKKDTVIGAPKTLTASIEKFL*

NbL03g04620.1 early_nodulin-like_protein_2 [MW - SP = 40.58 kDa]

No. of times detected



log(intensity)



Values from

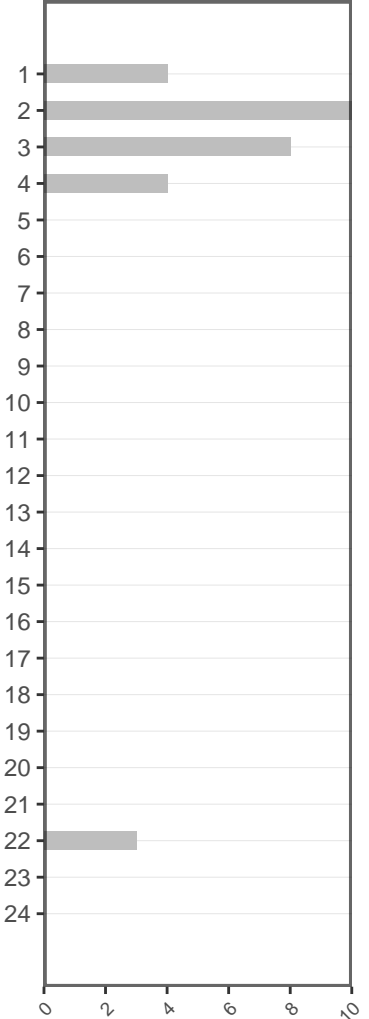
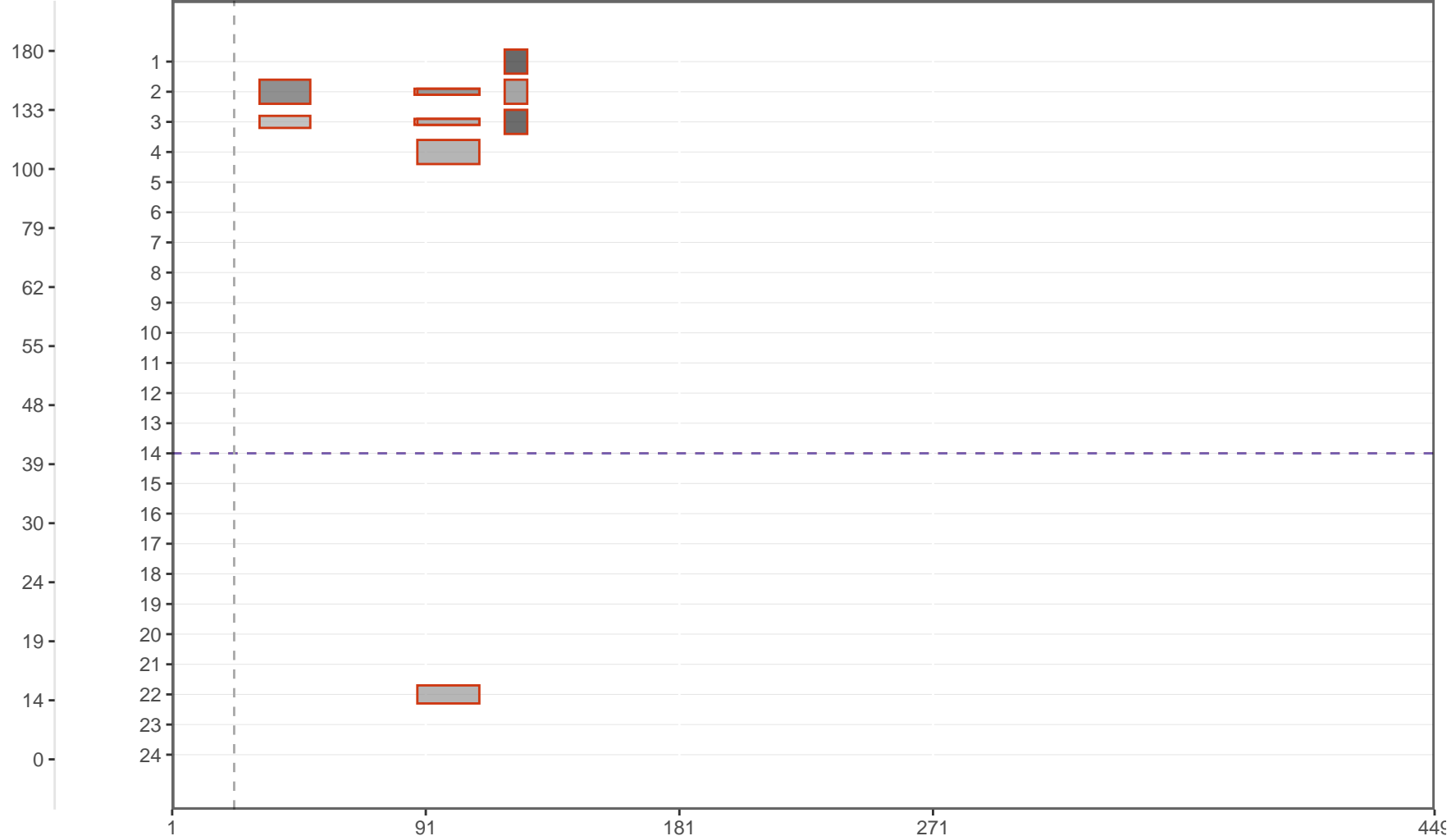


MW indication



Molecular weight

Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

TPSGGSATPPTPSGGSATPPSPGGGATPPNPGGGGTRPWAGKPKGGSTPTSPSMGVPSGSAAGSTTPPTPTTSAPSATTMAGAPKGGSTTPTDTSPPNGAPVAVSPAGKPKTSSTPTAGSIVFNTSGMPTTGGPAPKGGASDLSPSPSSSLAPGSSALSPGGIAPKGGTSSMAPGGMAPGAGAGSTPADNSPAGAPSNPNSFVAKFTPSVLLSTVSLTMAFGFISPT

NbL03g04490.1 homogentisate_12-dioxygenase [MW = 51.69 kDa]

No. of times detected



log(intensity)



Values from



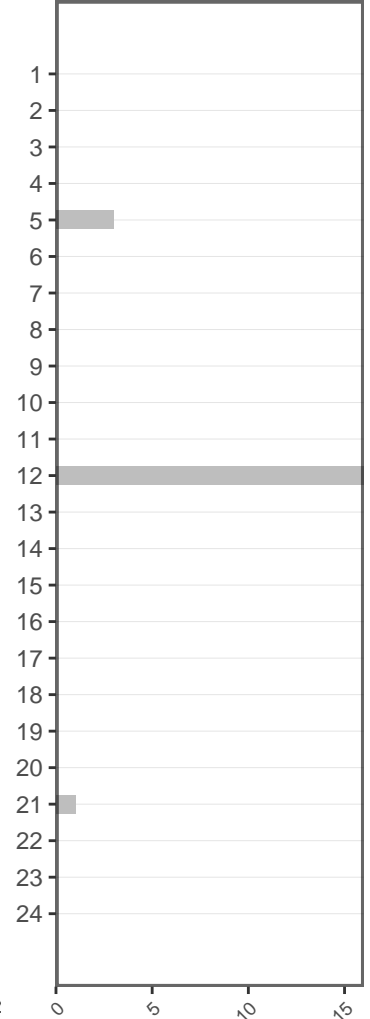
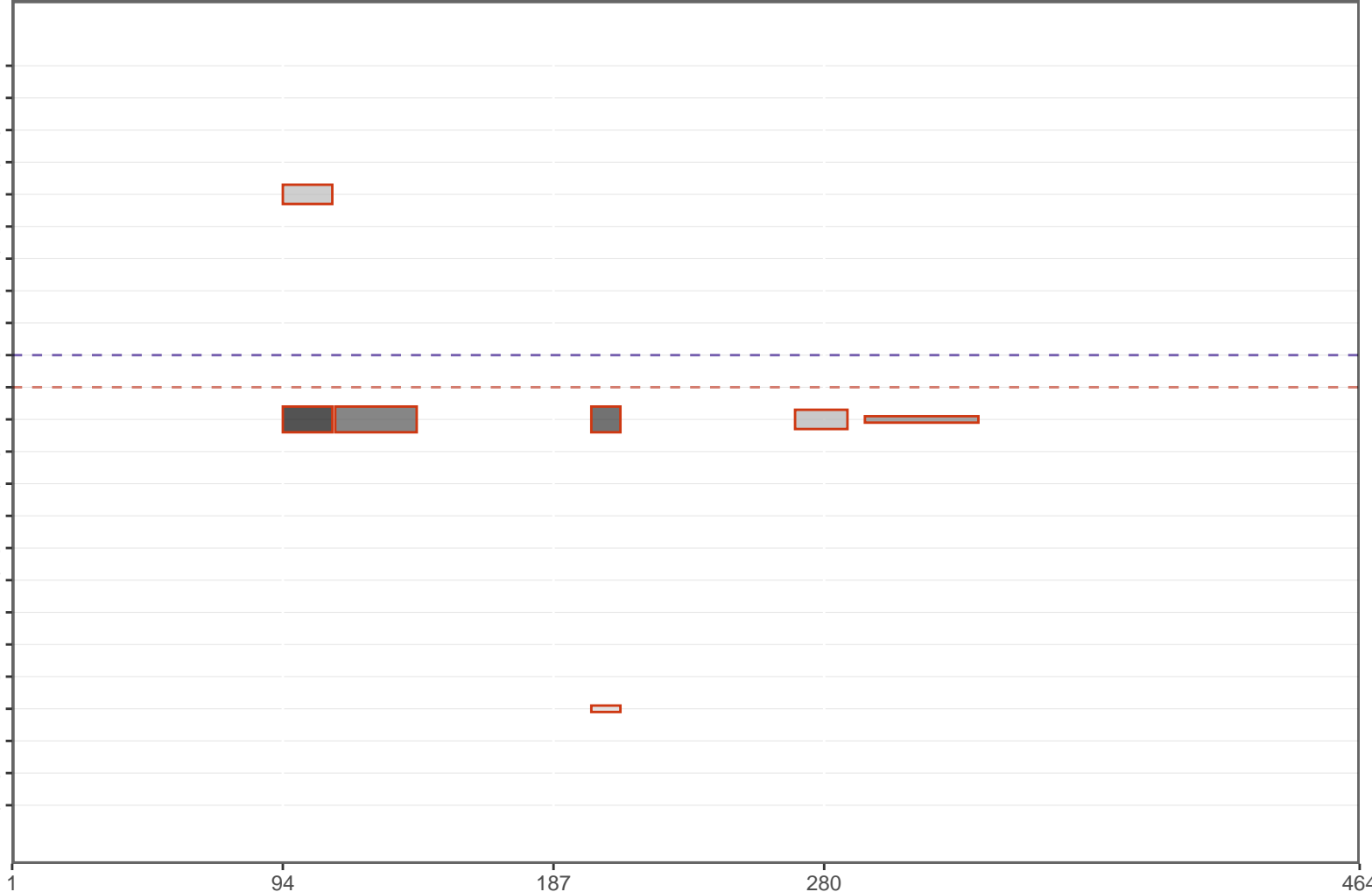
MW indication



Molecular weight

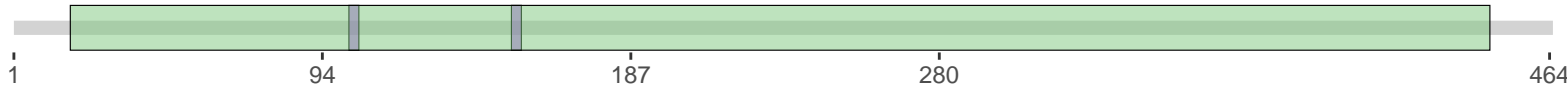


Gel Slice

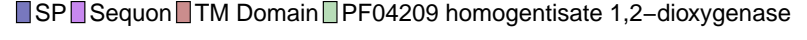


Protein length

Peptide counts over 4 repeats



Pfam Description



Protein sequence:

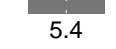
HFQLPDLGPICANGLAAPRDFLPIAWYEDGSRPGYIVIKYGGELFIAKQDFSPFNVAWQGNVYPIKYDLKFGPNTVLIDHSDPSINTVITAPTQKPGVALLDFVFPFRWVAEHTFRPPYHYHRNMGSEFMGLYGGYEAAKADGFHPGGASLHSGMTPHGPDTTKTYEATALGNEAGHPKIADTMAFMFESGLIPRVGSALESPEFMDHVDYQGVGLKSHFSGLSAMQGTATFRMENG

NbL03g04400.1 malate_dehydrogenase_2_mitochondrial [MW = 35.59 kDa]

No. of times detected



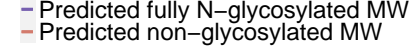
log(intensity)



Values from



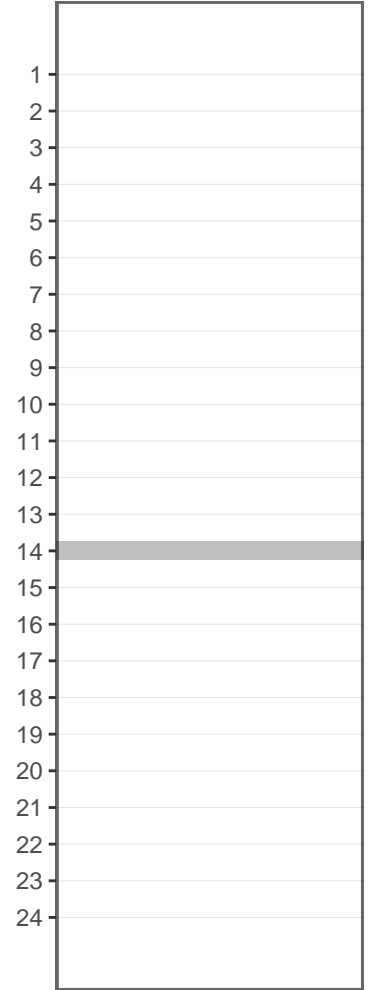
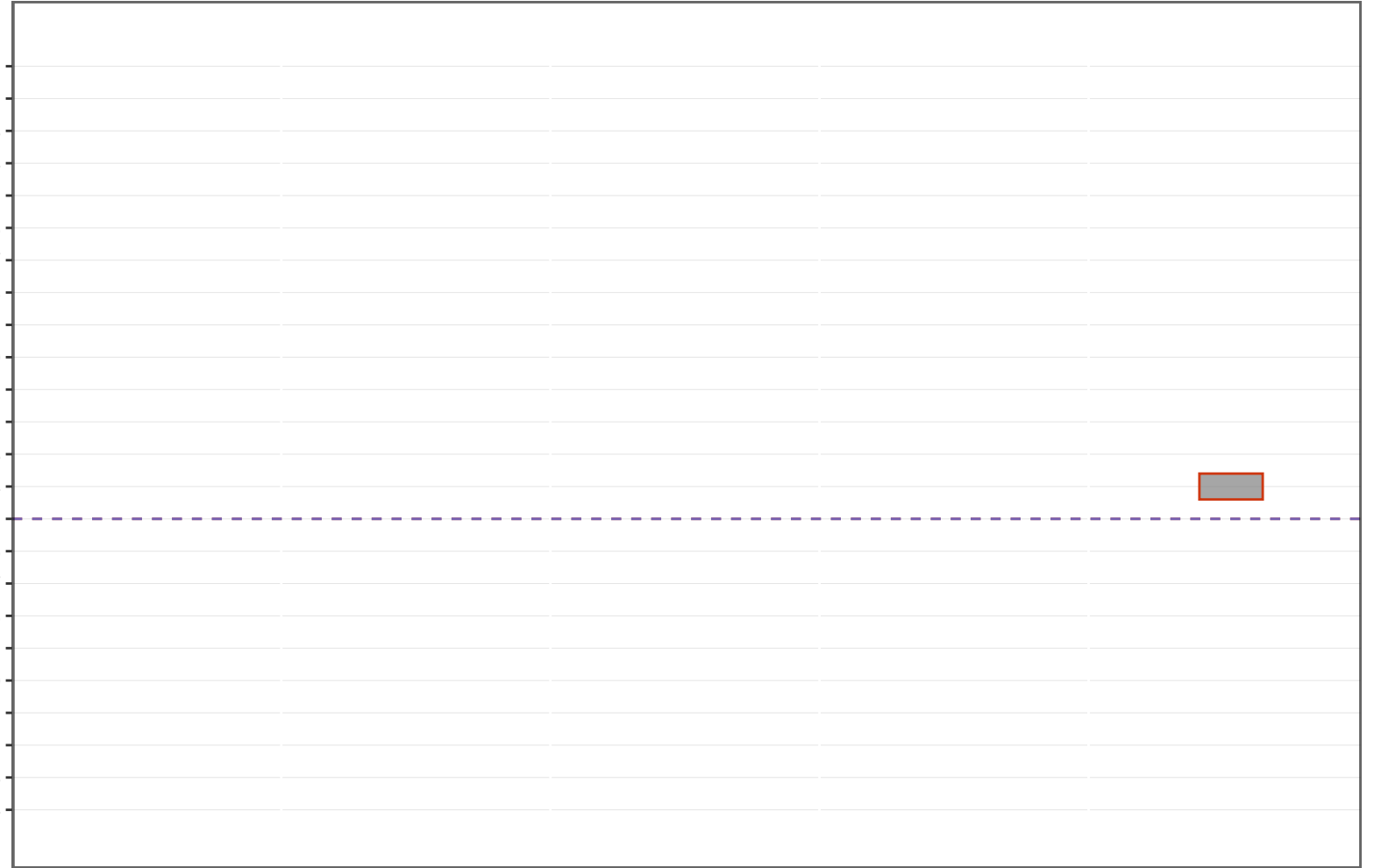
MW indication



Molecular weight



Gel Slice

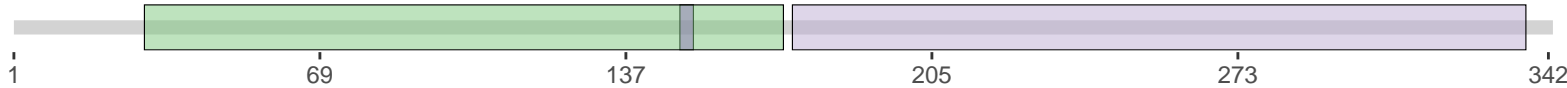


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF00056 lactate/malate dehydrogenase, NAD binding domain
- PF02866 lactate/malate dehydrogenase, alpha/beta C-terminal domain

Protein sequence:

FKXAGTYDEKRLFGVTTLEIVRAKTFYAGKAKVNWADIVIPVVGHAIGITLPLFGDAPKANLGDDEIEALTKRTDGGTEVVEAKAGKGSATLSEMWAGAIFADAQKLGKNGVDPVVEGSEFVQSTVTDLPLFFAFKRVLGGKNGVEEVLGLGFLSVFERKQGLEALKPELKSSEIKGKIFAND*

NbL03g04250.1 interactor_of_constitutive_active_ROPs_1-like [MW = 35.85 kDa]

No. of times detected



log(intensity)



Values from



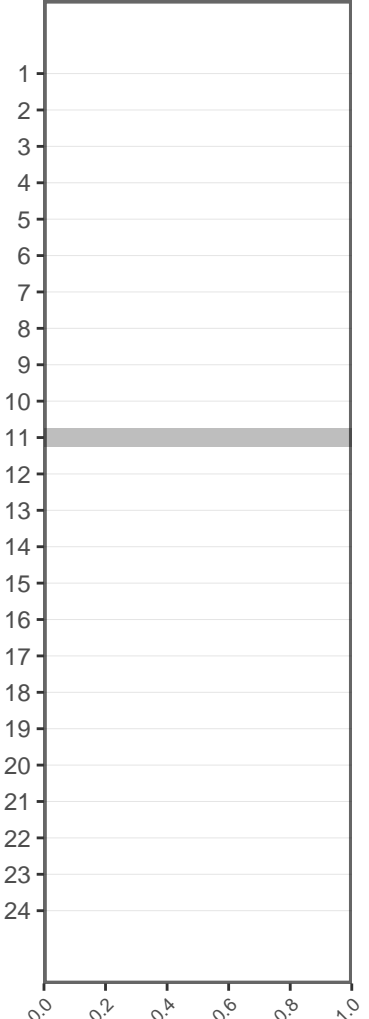
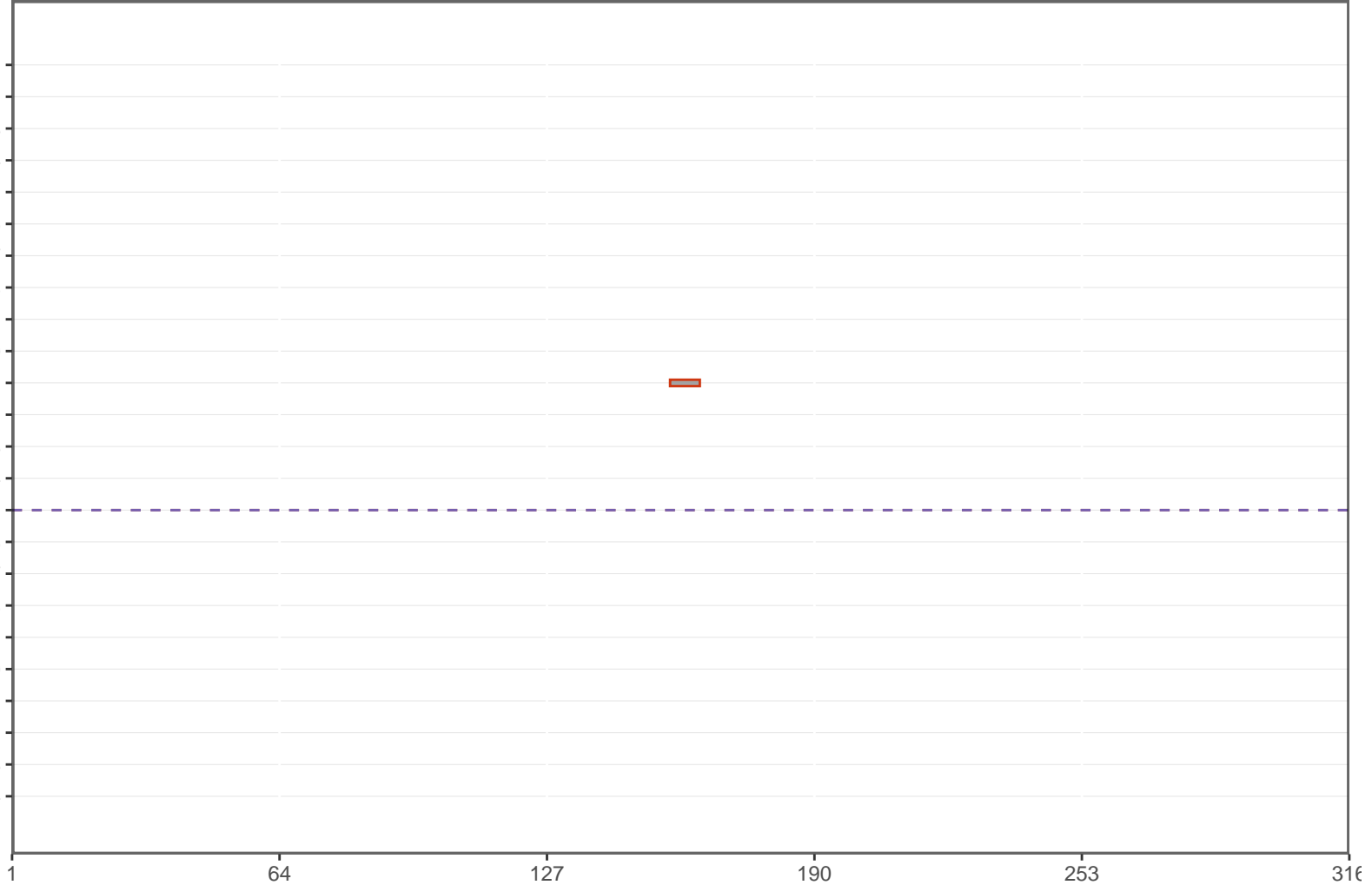
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

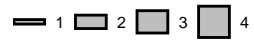


Protein sequence:

ALSQYKELDLNKEEIMLKAKLEEKEKQVFGGENENLJKELNDKTLKLEISSTKANTEEMNLFKFNQVQLETTKRNFAFEINEKLEAESEKAKDELESEMMLKLRVQTEGWRKAADAAAALLAGEVEVNGRRLLSERQSGMDYKRYGNVFEPEVGGYGVYGVPLNDDSDDAFG

NbL03g04160.1 elongation_factor_Ts_mitochondrial-like [MW = 43.07 kDa]

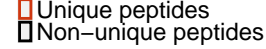
No. of times detected



log(intensity)



Values from



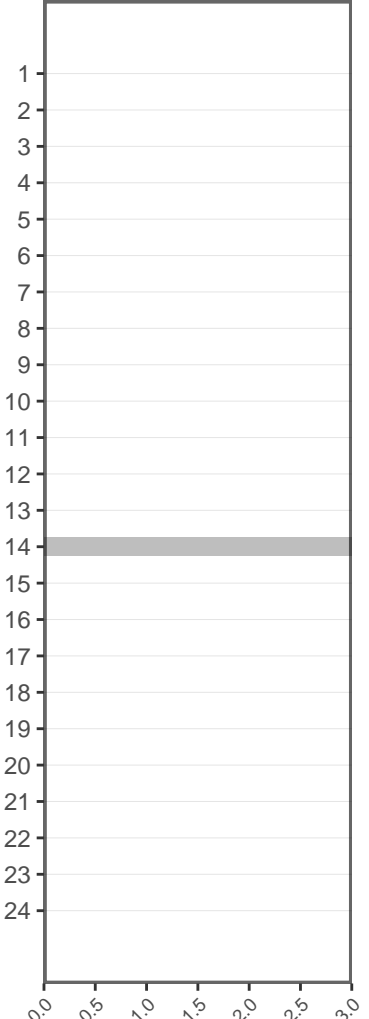
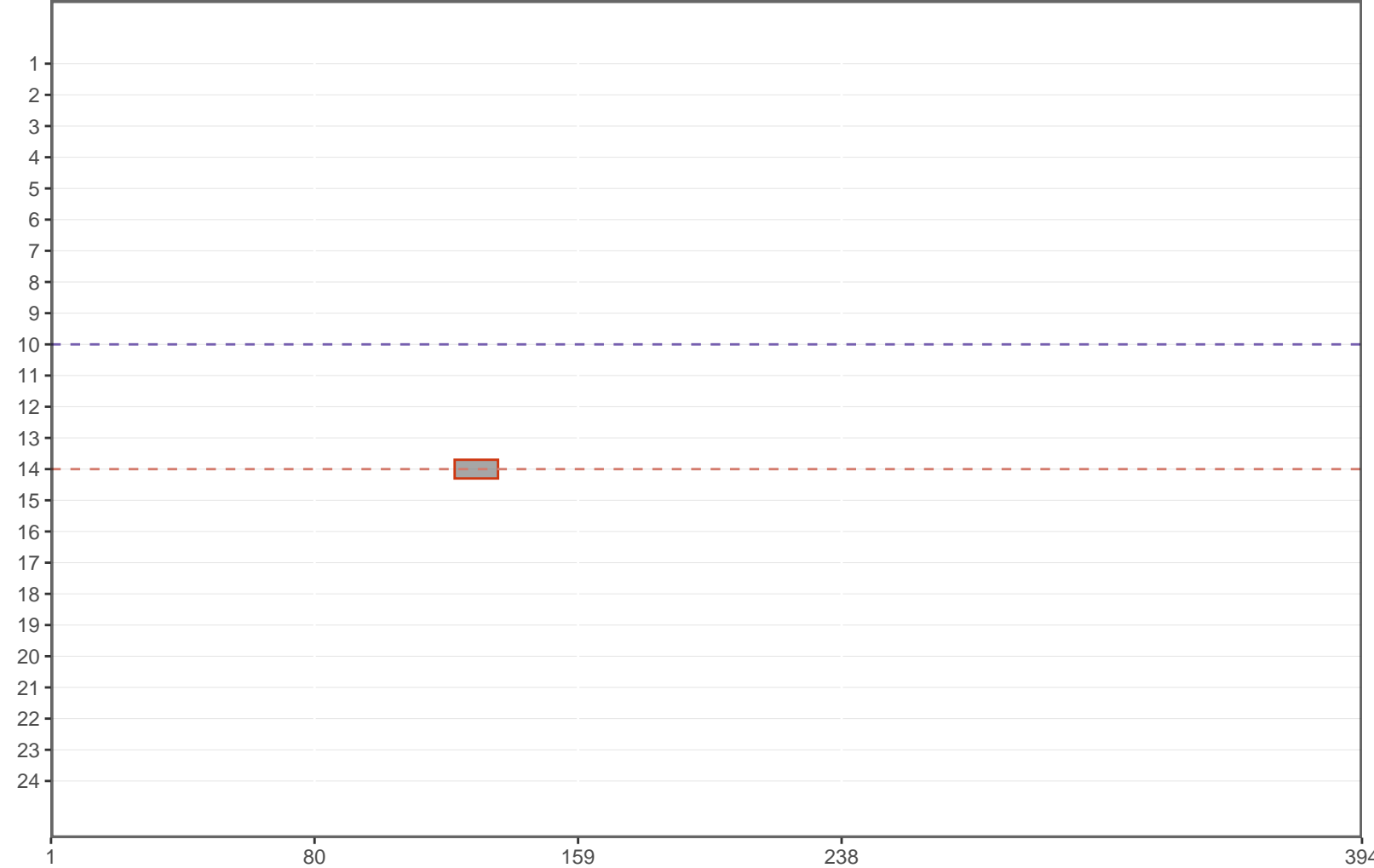
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

I L E D L K M N L D I H P K L E G E K S V Q N A T E V A A M M G E N V K L R R G F A M S T P S I G V S T Y L H T F P Q P G V R I A G L S L E V E D Q N V P G D A L G R V G S E I A M H V A A K P L F L T K E D V S D A L S N E R D I L K S Q A E S S G R P Q I A E K M V E G R M R K Y F E E V A L M E G K F V V N D T I N V K T L S E I K E V S P V K G G F L R M E V G E G L Q R L E A S N E S E P L A N A A

NbL03g04080.1 3-hydroxyisobutyryl-CoA_hydrolase-like_protein_5 [MW = 42.78 kDa]

No. of times detected



log(intensity)



Values from



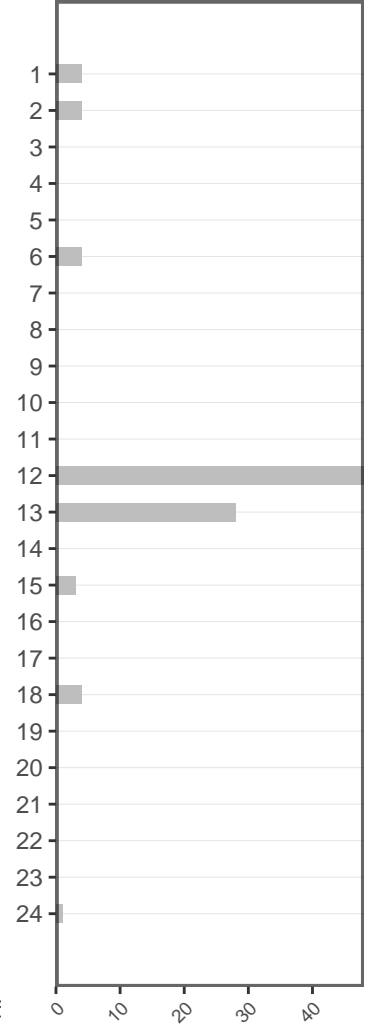
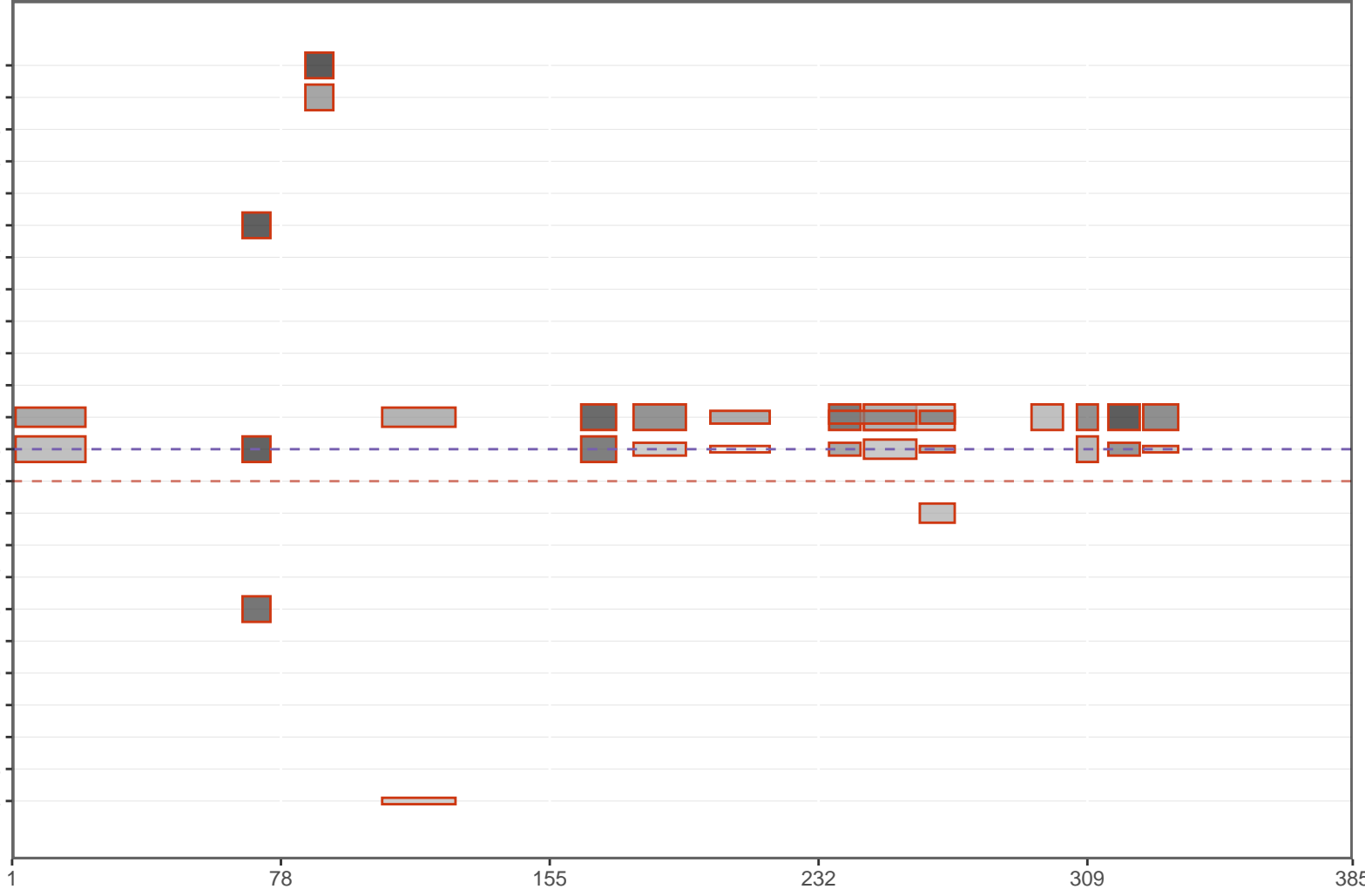
MW indication



Molecular weight

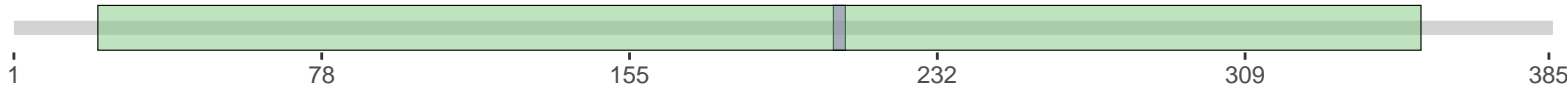


Gel Slice



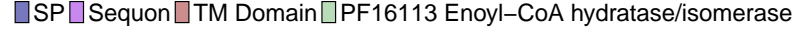
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGKELVAAGLATHFVPLPEKLEKLEKHLNLTSDSEAVVSSAIKEFSTDVQIDEEVLYKKQAIQDEGFSKIDVWAEIHSFEAEAGKEGNSWVPLVGLKRSSPTGLNITLRSRREGKQGLSECLNKEFRITNINLRTKISGDVVEGIRALTDKDKNSPKWDPFTLEKDDERVNLVFGPFEEDELEKIVSENEGQRWDGKVEDSAYGRO

NbL03g03970.1 citrate_synthase_glyoxysomal-like [MW = 56.07 kDa]

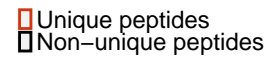
No. of times detected



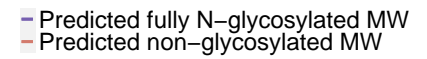
log(intensity)



Values from



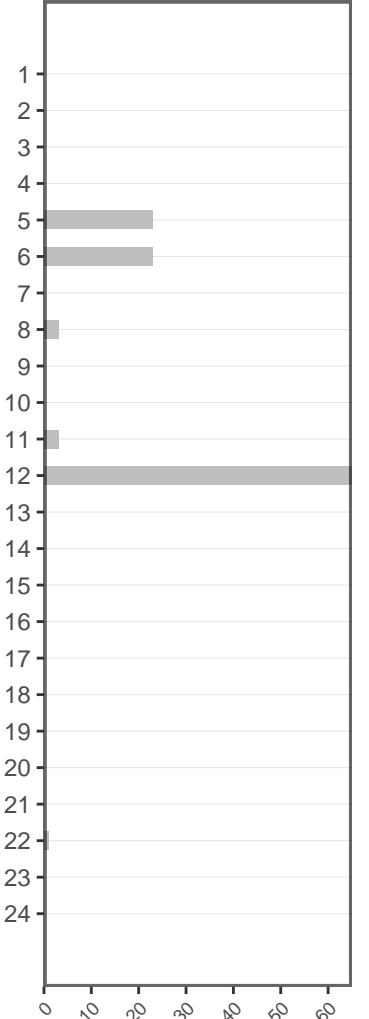
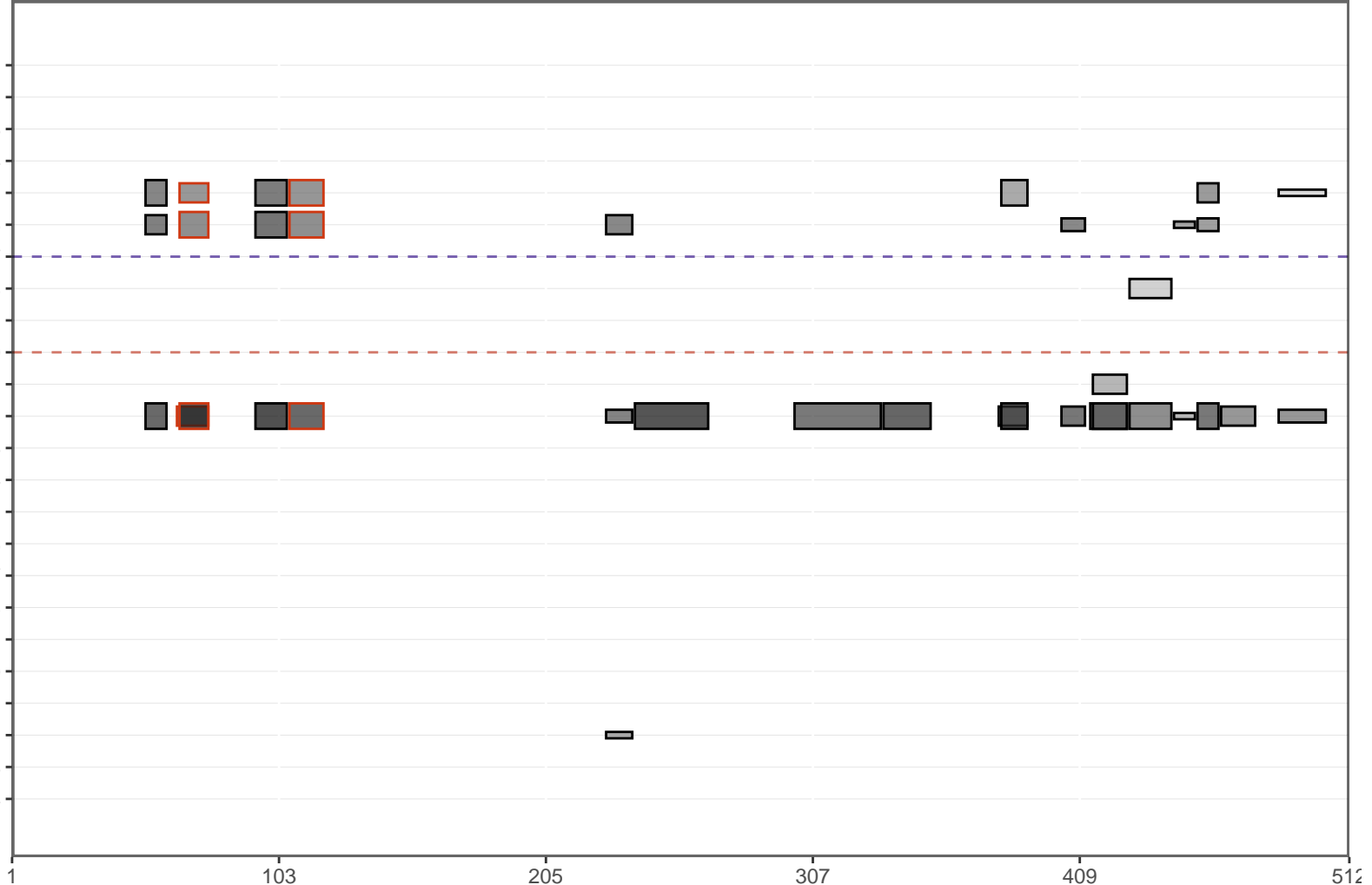
MW indication



Molecular weight

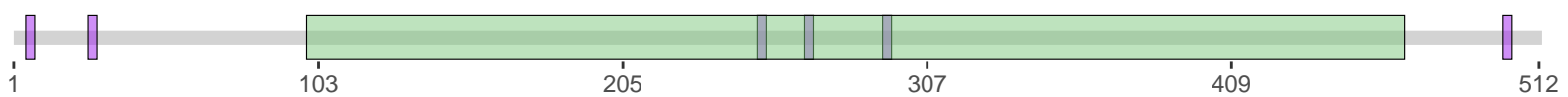


Gel Slice



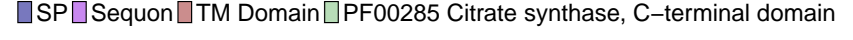
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL03g03880.1 14-3-3_protein_9-like [MW = 28.55 kDa]

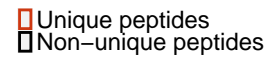
No. of times detected



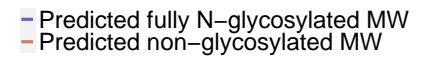
log(intensity)



Values from



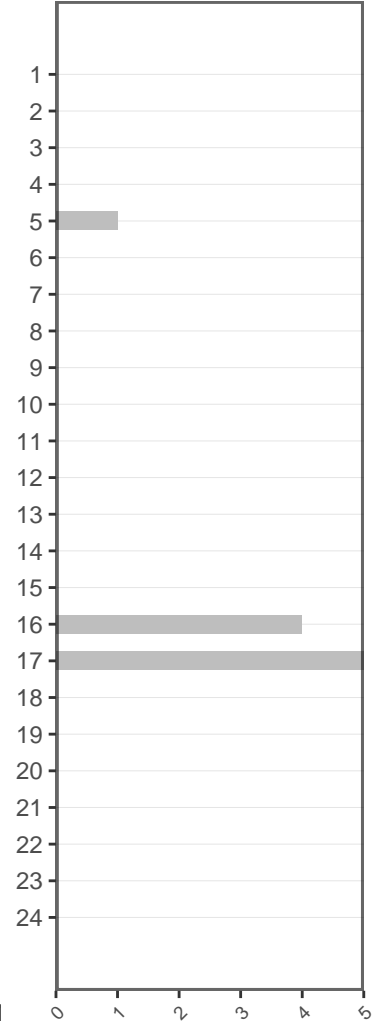
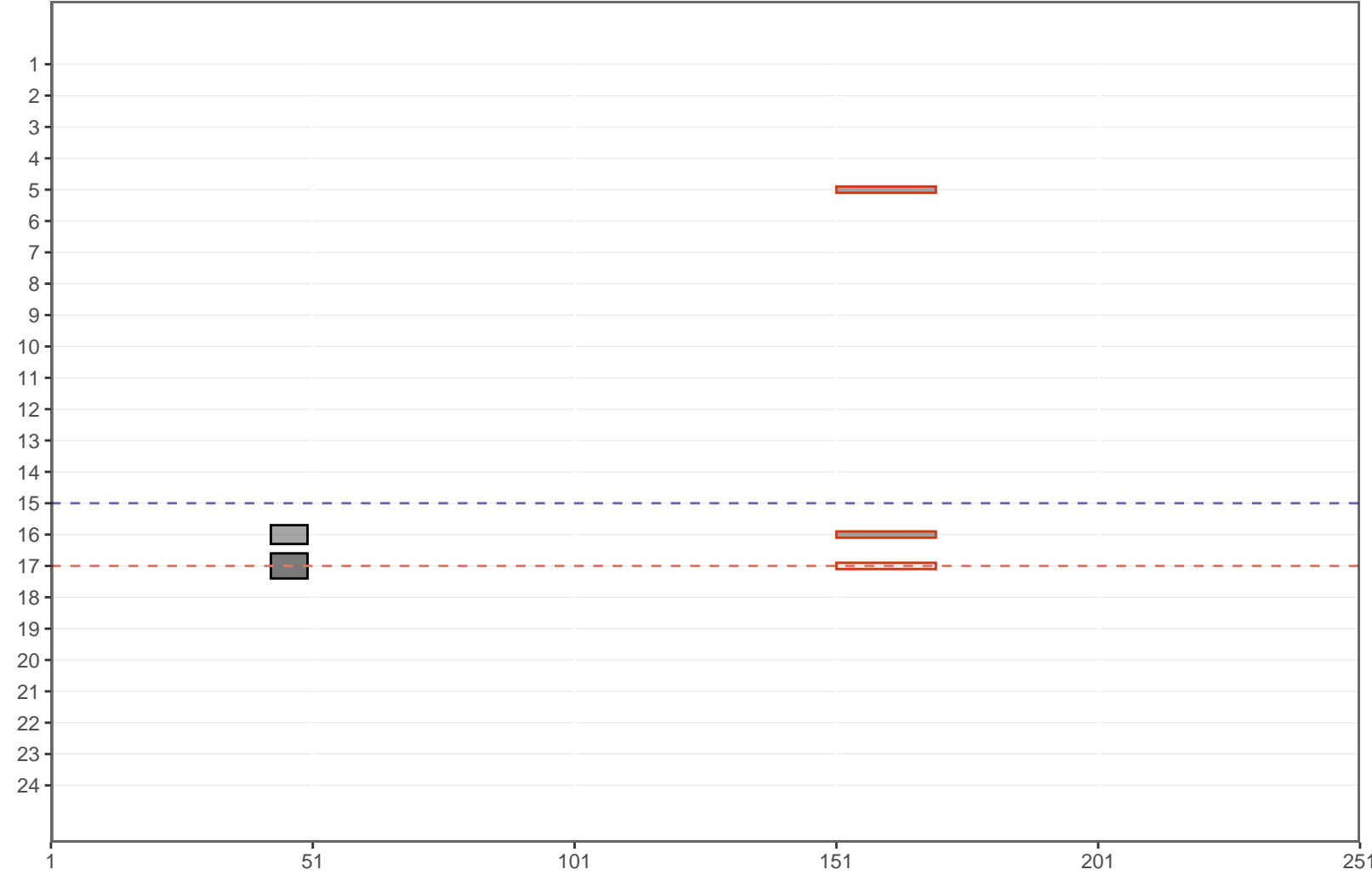
MW indication



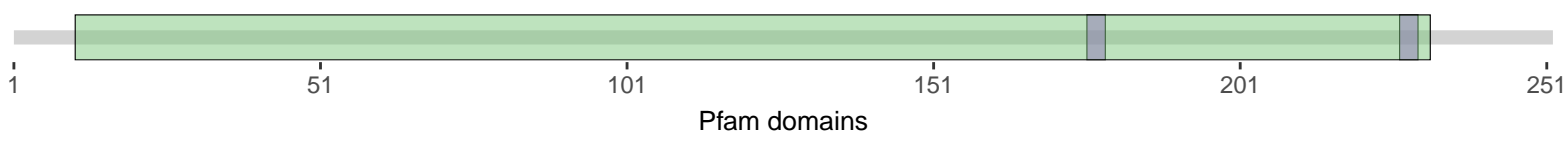
Molecular weight



Gel Slice

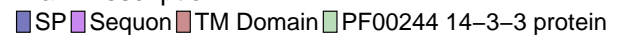


Protein length



Pfam domains

Pfam Description



Protein sequence:

CTSGSESVFYKMGDYYRRLAELKTKGNDKKEVDSLSKAVQTATATAEAELESTHPIRLGLALNFSVFFYYEIMNSPERAGHLAKGAFDEAISELDALNEDSVKDGSTLMQLLRDNLFWTSDIPDAGMCKAFSDQDA*

NbL03g03800.1 ethylene-responsive_transcription_factor_4-like [MW = 31.04 kDa]

No. of times detected



log(intensity)



Values from



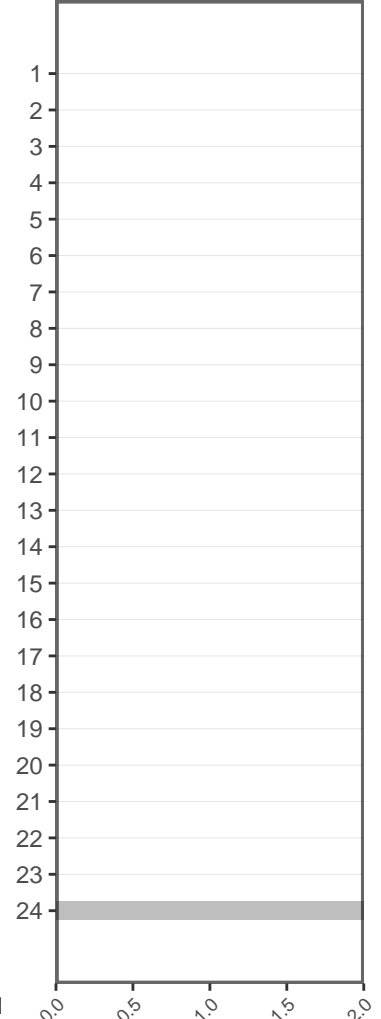
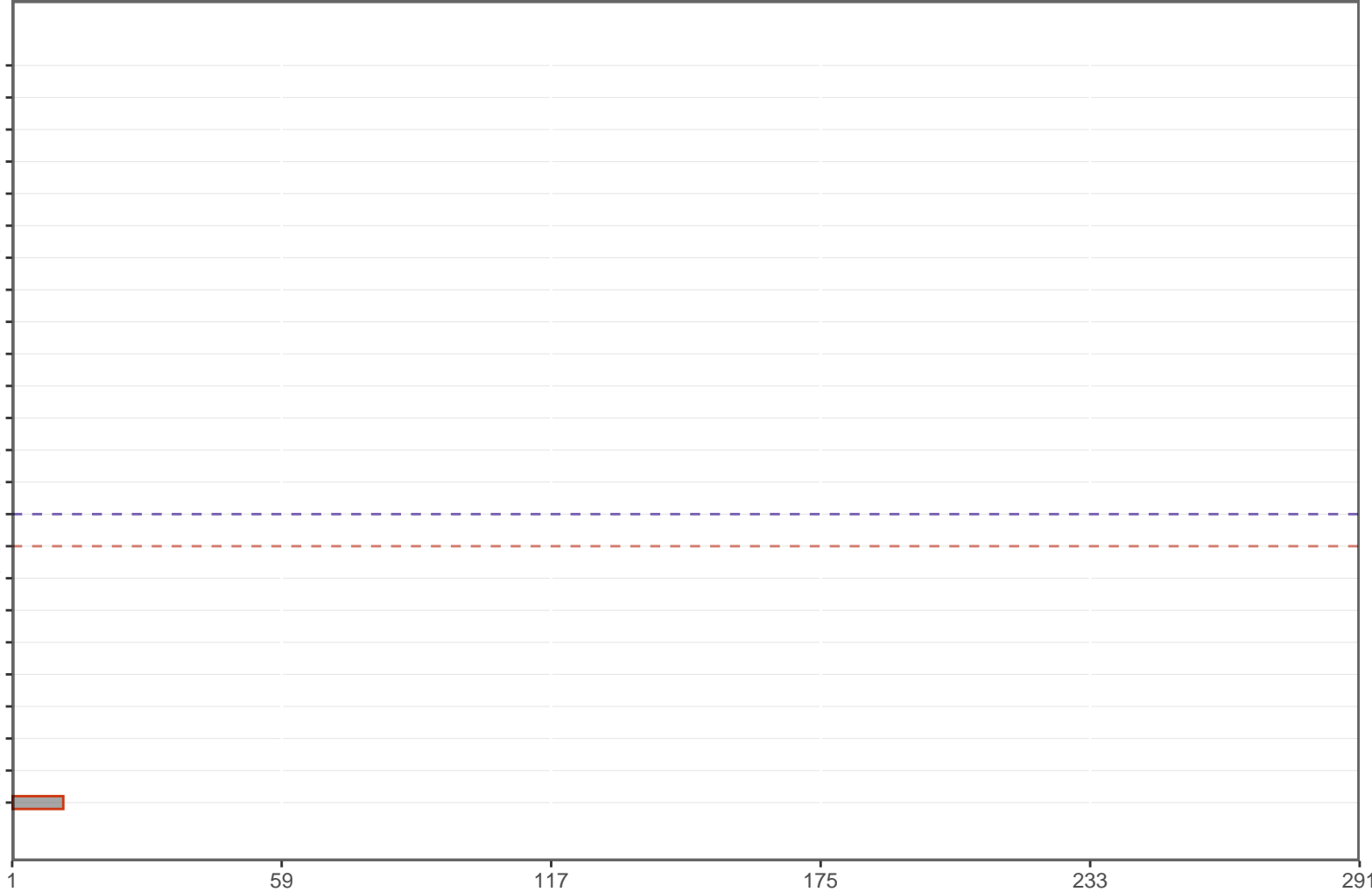
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

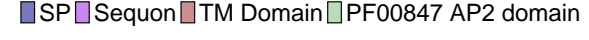
Protein length



Pfam domains



Pfam Description



Protein sequence:

ICKSEVGLVIRNGFPIHQPVMGALTSQSSPVESSGGETGVHAPLELDLSTRRLGAVGEGGNHVRINGFPFIHQDPTWVLPNGQPIILFDENFVPTGVLNRPMPYRFQGVTVFENGVSGRVYHSDSSSFTTVENYFGGGVSRRELNDLNLSPIMEA

NbL03g03630.1 probable_cinnamyl_alcohol_dehydrogenase_6 [MW = 42.55 kDa]

No. of times detected



log(intensity)



Values from



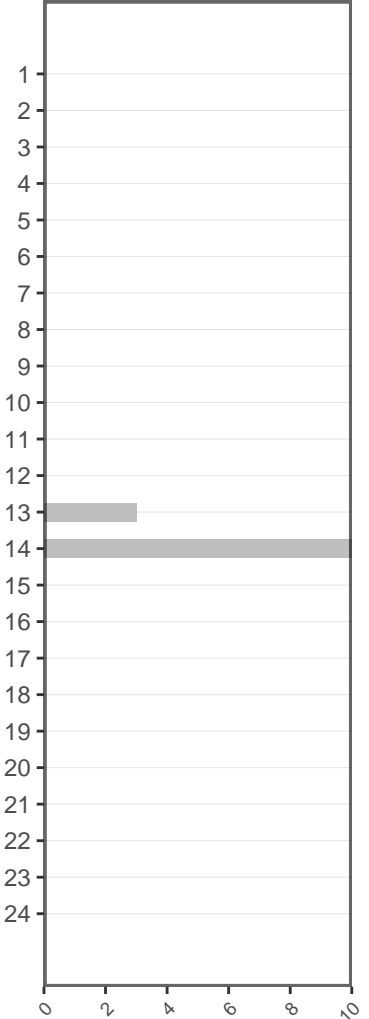
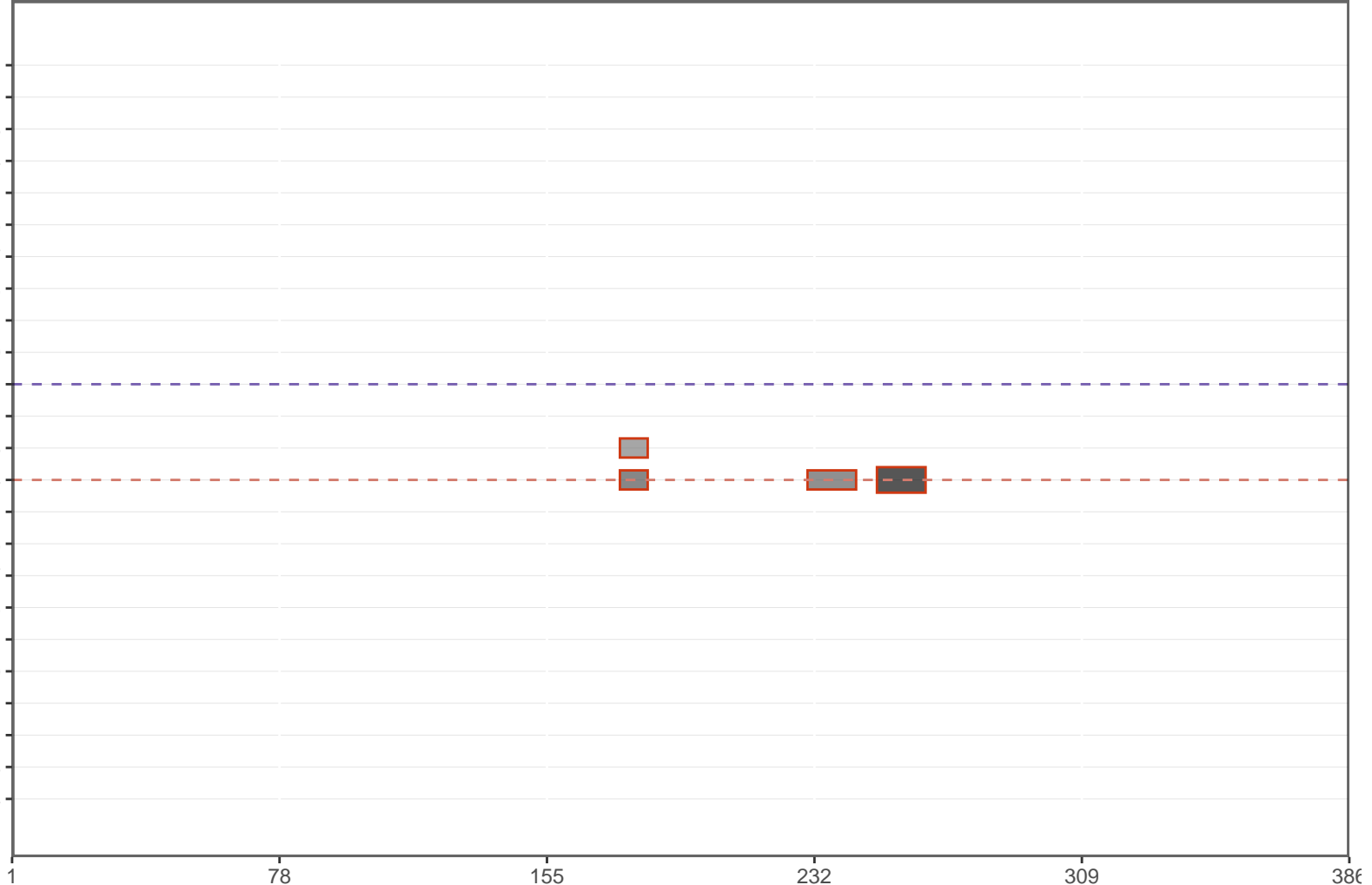
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

PDNLAMDRAATPLLGAGTIVYSPKDNVIVETKGRIGVIGLGGLGHHAVKFGKAFGHVTVISTSPKQGEAKHNLGADDFILSTNPKQIGAKRRTFLDFTVAANHSLGLYLELLKVNGLTVIVGAPFKPDLPAFPMFGKRNKVKGGMGSEETQEMMDLGEKHNLSDIEHTDQINEGLDRLANNDKVRFLVDAAGQSENLY

NbL03g03540.1 cytochrome_b6-f_complex_iron-sulfur_subunit_2_chloroplastic [MW = 26.13 kDa]

No. of times detected



log(intensity)



Values from



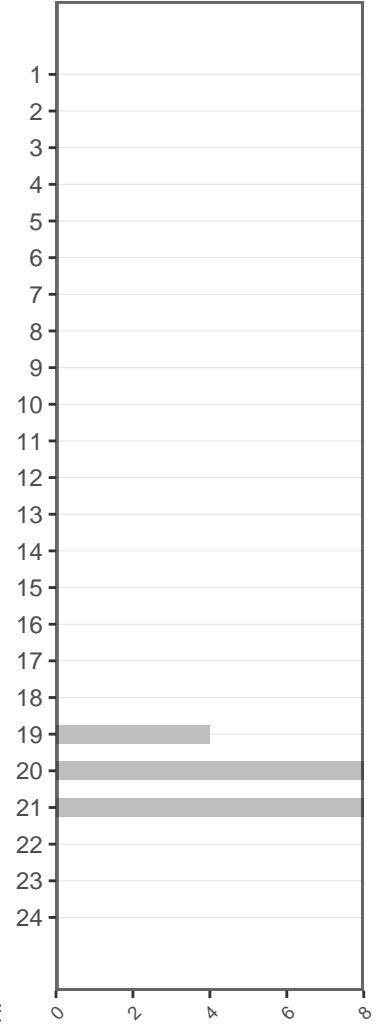
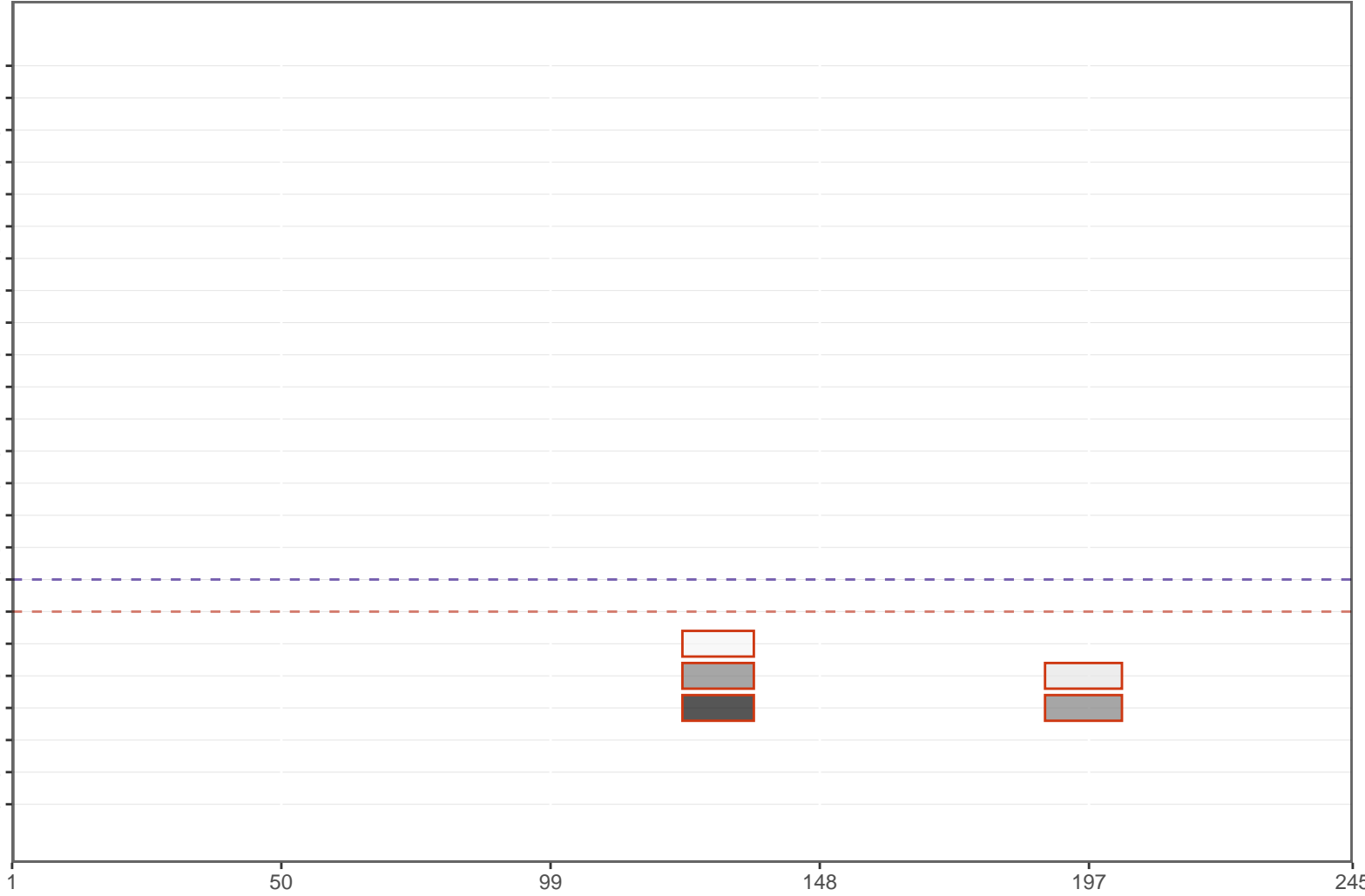
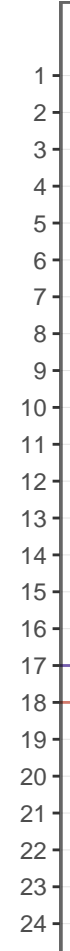
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

ISGGGGGIPKXDAIGNDVAISEWIKTHPPGNRTLFGGLKGDPTYLVAVENDGLTATYGINWCTHLLGGVYFPAENKFKPCHGSGYNNQGRVVRGPPALGLALAHADIDGKVVYFVFWETDFRTGEPVWV

NbL03g03390.1 uncharacterized_LOC107778869 [MW = 10.46 kDa]

No. of times detected



log(intensity)



Values from



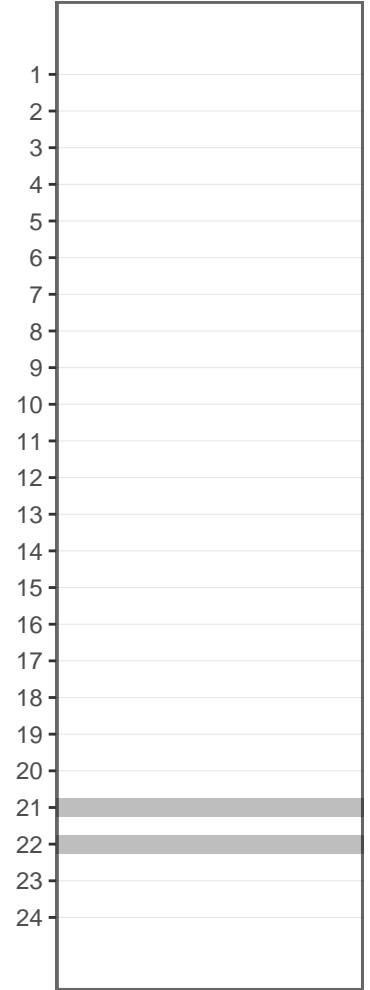
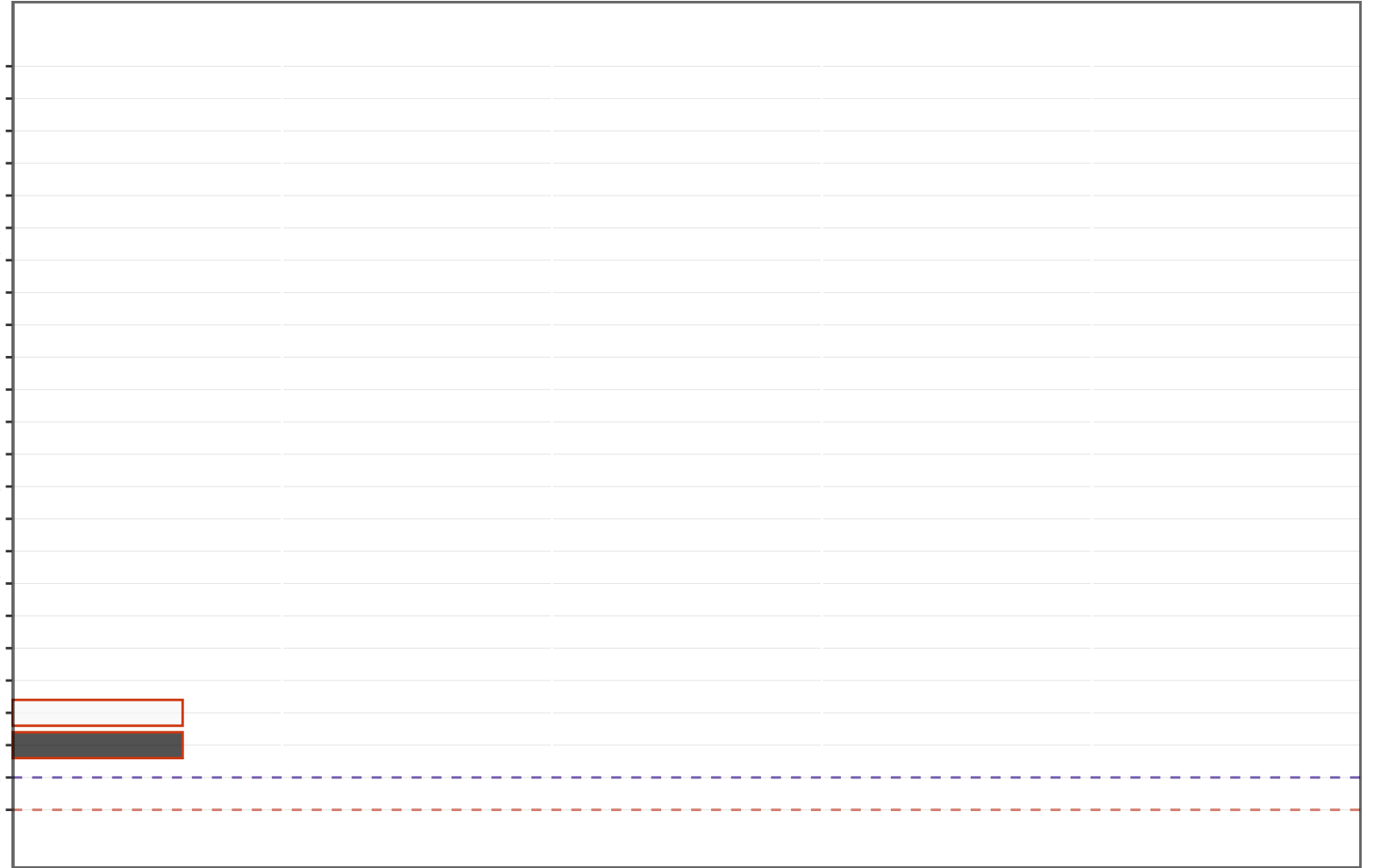
MW indication



Molecular weight



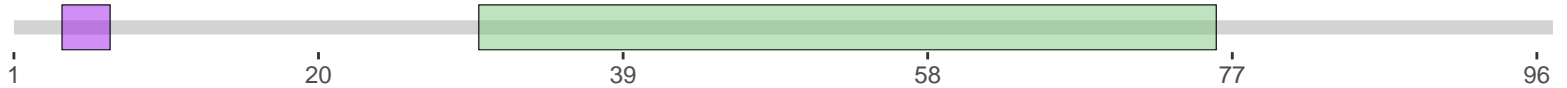
Gel Slice



Peptide counts over 4 repeats

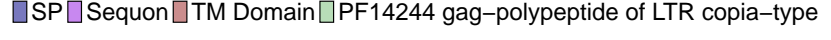


Protein length



Pfam domains

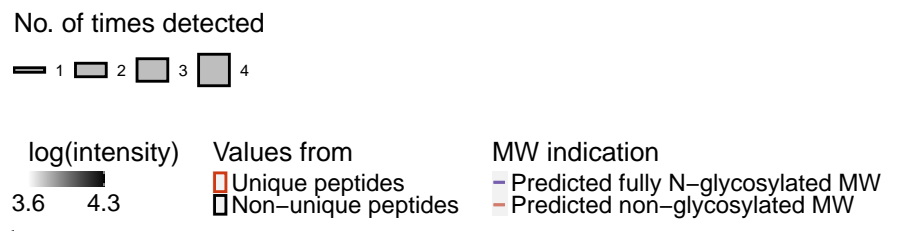
Pfam Description



Protein sequence:

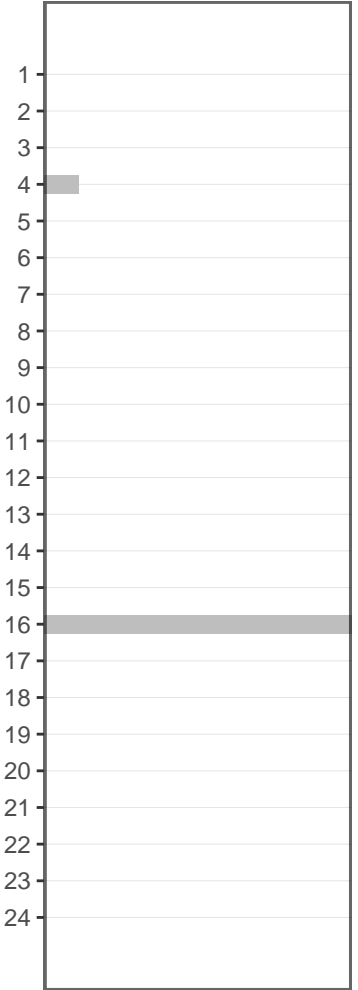
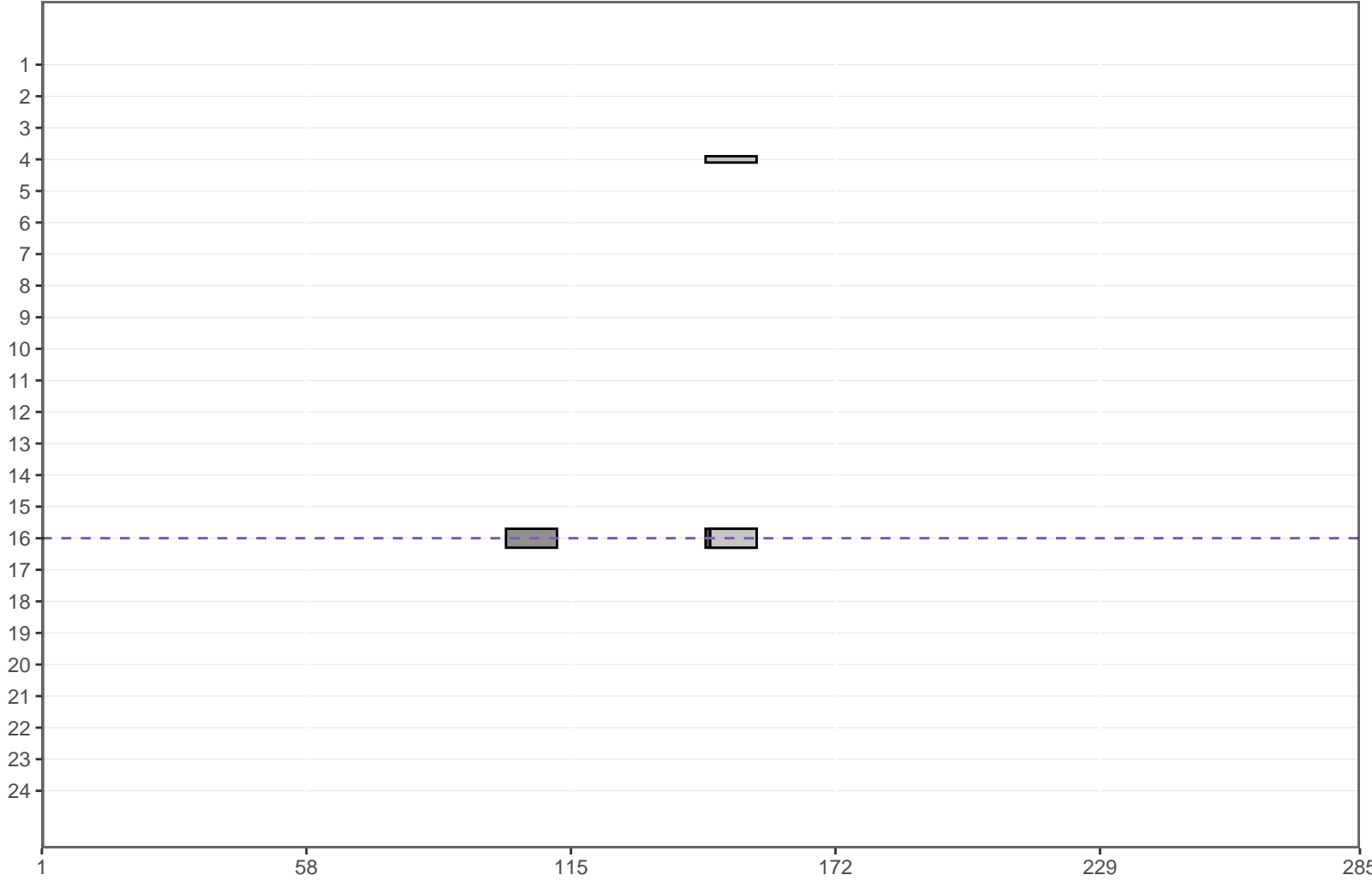
SMVLLNSVFDGKEVGGWNRRAVAALSSKNLGFIDGTFFEPDASSTDFKQWNGNDMMVSE

NbL03g03170.1 ACT_domain-containing_protein_DS12_chloroplastic-like [MW = 30.88 kDa]



Molecular weight

Gel Slice



Peptide counts over 4 repeats



Pfam domains

Pfam Description

SP Sequon TM Domain

Protein sequence:

IGKIINKFAITKASTGRKVDPELLEAIFRLTINNMMEVHPESSEMLAMGEAFGVFQPYQKQVDIATHHHYDDGPERBLLQVETADRPGLVLDVNIITDINVDVESGEGFTEGLLAKAKAFHVSYYGKALKPKQGVLANSLRYFLRRPTTEDASEF

NbL03g03130.1 calnexin_homolog_1-like [MW = 65.27 kDa]

No. of times detected



log(intensity)



Values from



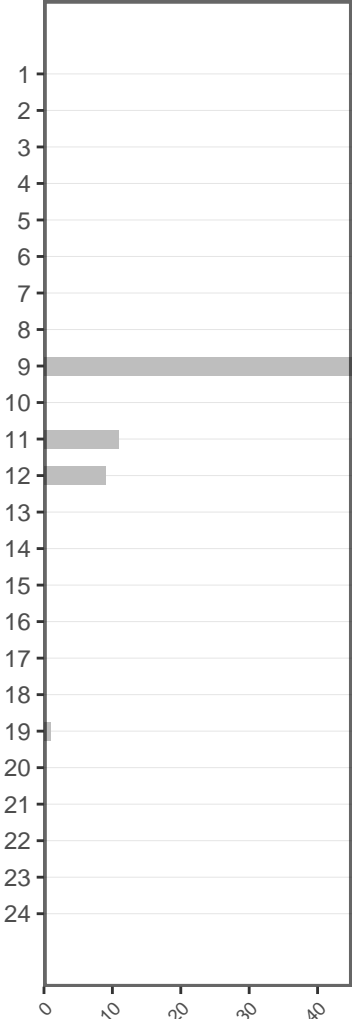
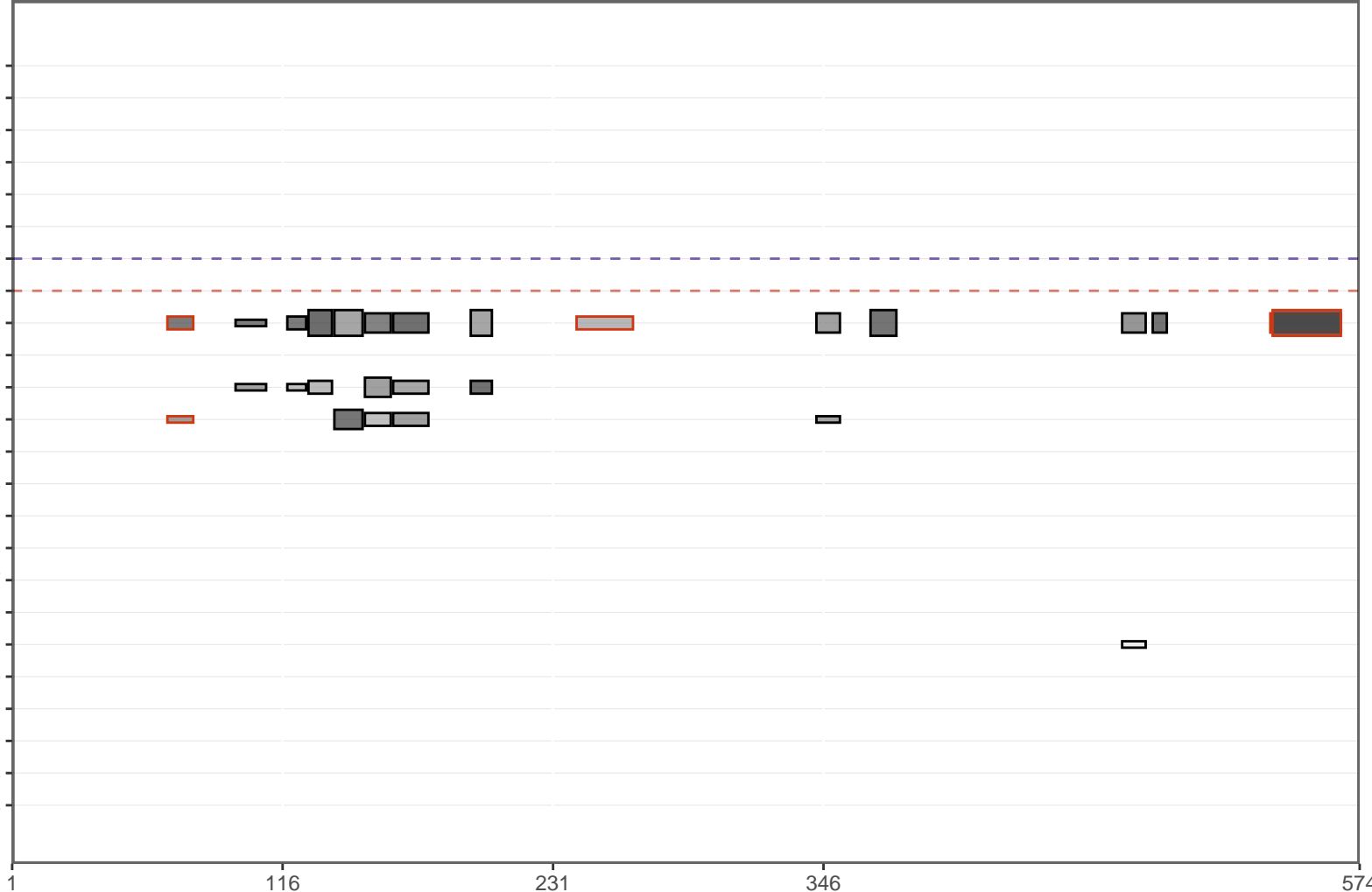
MW indication



Molecular weight

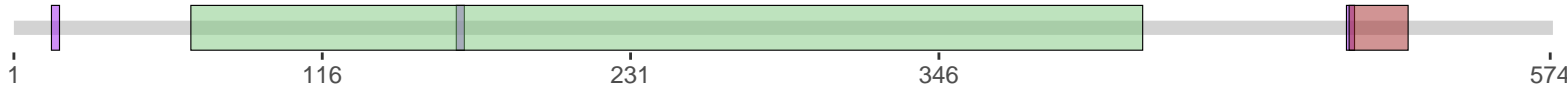


Gel Slice



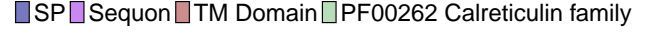
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DKPDPDAKXPCDWDDEDAFMEIIEDEGAEPKQWLDDEPEIEIDDPKATKPEDWVDEEDGEWEAPGIDNPKGAEGPQGGGEWRPMSKSNPKYKQHWAPLIDNPNKYGWPRDIPNPNYFELDRPNFEPVAAIGIEIWTMGDGLFDNIIAASDEKVAEYRNTAWKSKFAEAEKQKAEVAYSGGLKGFQKVVFDLLKYNADIPLLGEHKIKVLDLLEKAEIQTGNLTGVVIVSIVIFVFLKLTFGGKQKQPARATEEERKR6SDGAEASTENISGGATEEKECONEDATAAPRR

NbL03g02970.1 lysosomal_alpha-mannosidase-like [MW - SP = 113.57 kDa]

No. of times detected



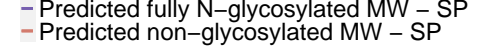
log(intensity)



Values from



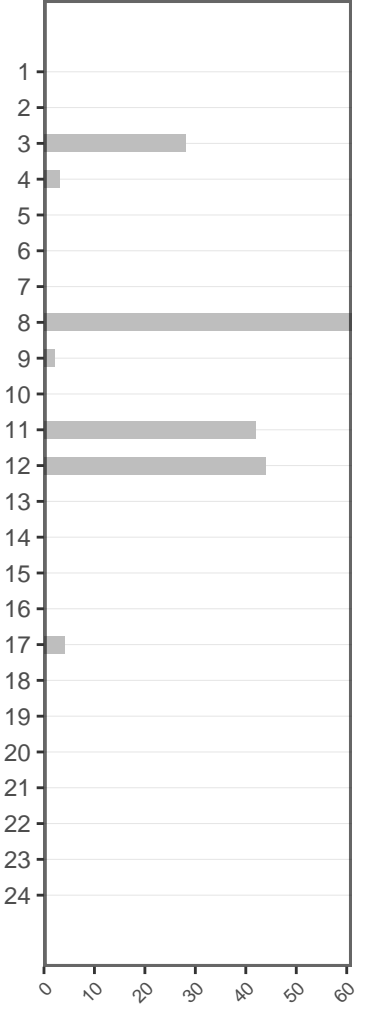
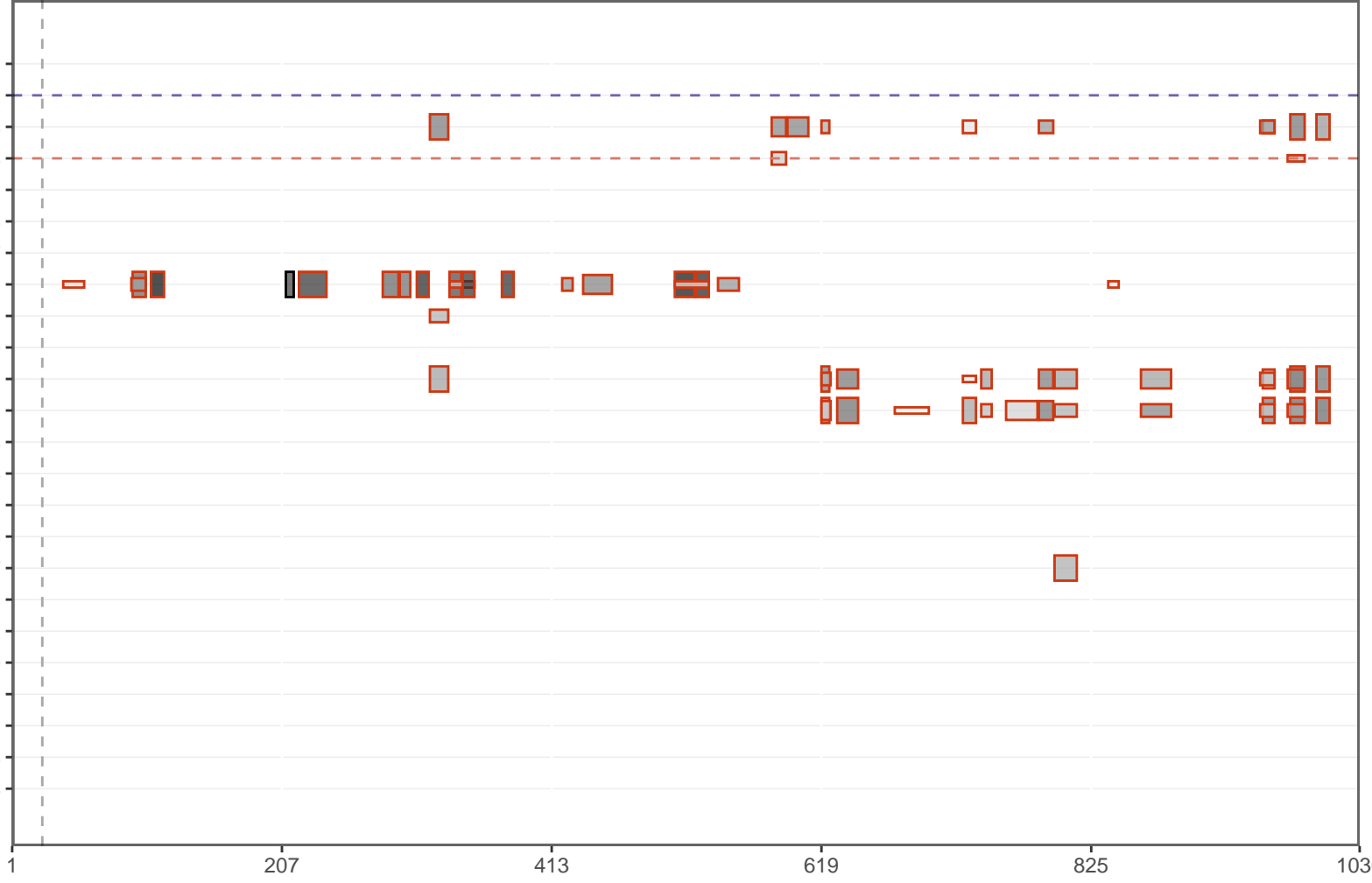
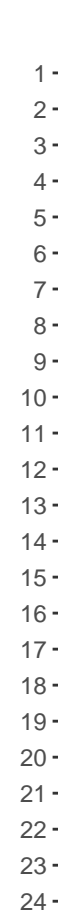
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01074 Glycosyl hydrolases family 38 N-terminal domain
- PF09261 Alpha mannosidase middle domain
- PF07748 Glycosyl hydrolases family 38 C-terminal domain
- PF17677 Glycosyl hydrolases family 38 C-terminal beta sandwich domain

Protein sequence:

AKRDTVLRIPVYVNEVYVQDSTGKEIEGQLLPVKAIAIRDFYVYVAYGESPSTSSPKYWLAFATVYPLPLGNSVYVTSQKRAVAASIPQTFYKTEGSSGSDAVEVGPNGNLVLYSADGGKFTGQYVNRKRVGRSSLEQSFYSYASADDSKDAWKDLGASGAVYFRPNSGFPVHSEKVPVYTLHGPLLDEVHQINNSWYQTRVYKEKEHVEVEFTVGPVPIQNGIGKELVHQTDKSNKTFYTDNSNGRDLKRRIRDRADWDLGVNGPAAQNYVPLNGMFLKDNSNEFSVLY

NbL03g02850.1 ubiquitin-conjugating_enzyme_E2_variant_1C-like [MW = 16.77 kDa]

No. of times detected



log(intensity)



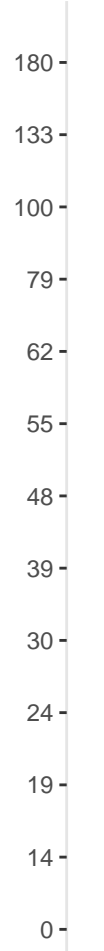
Values from



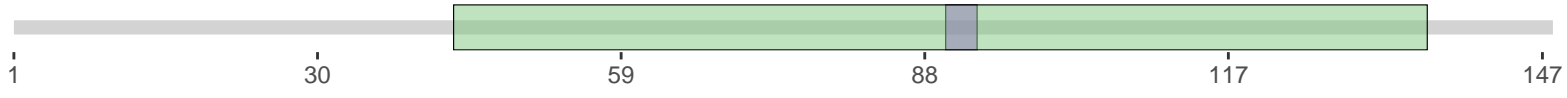
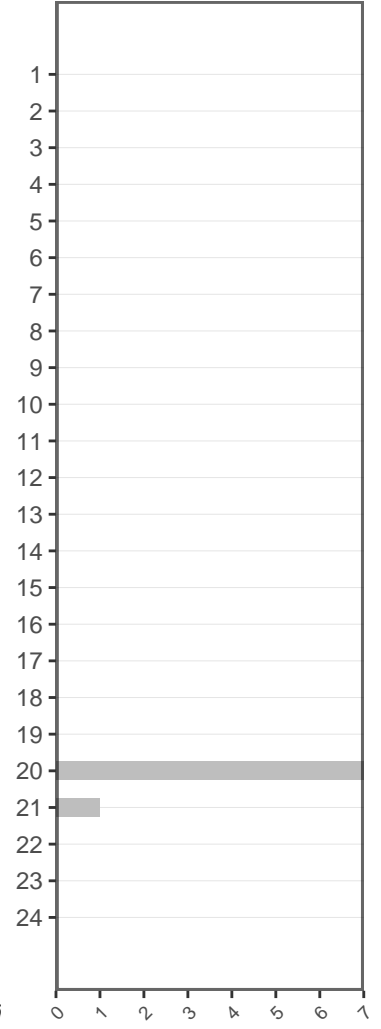
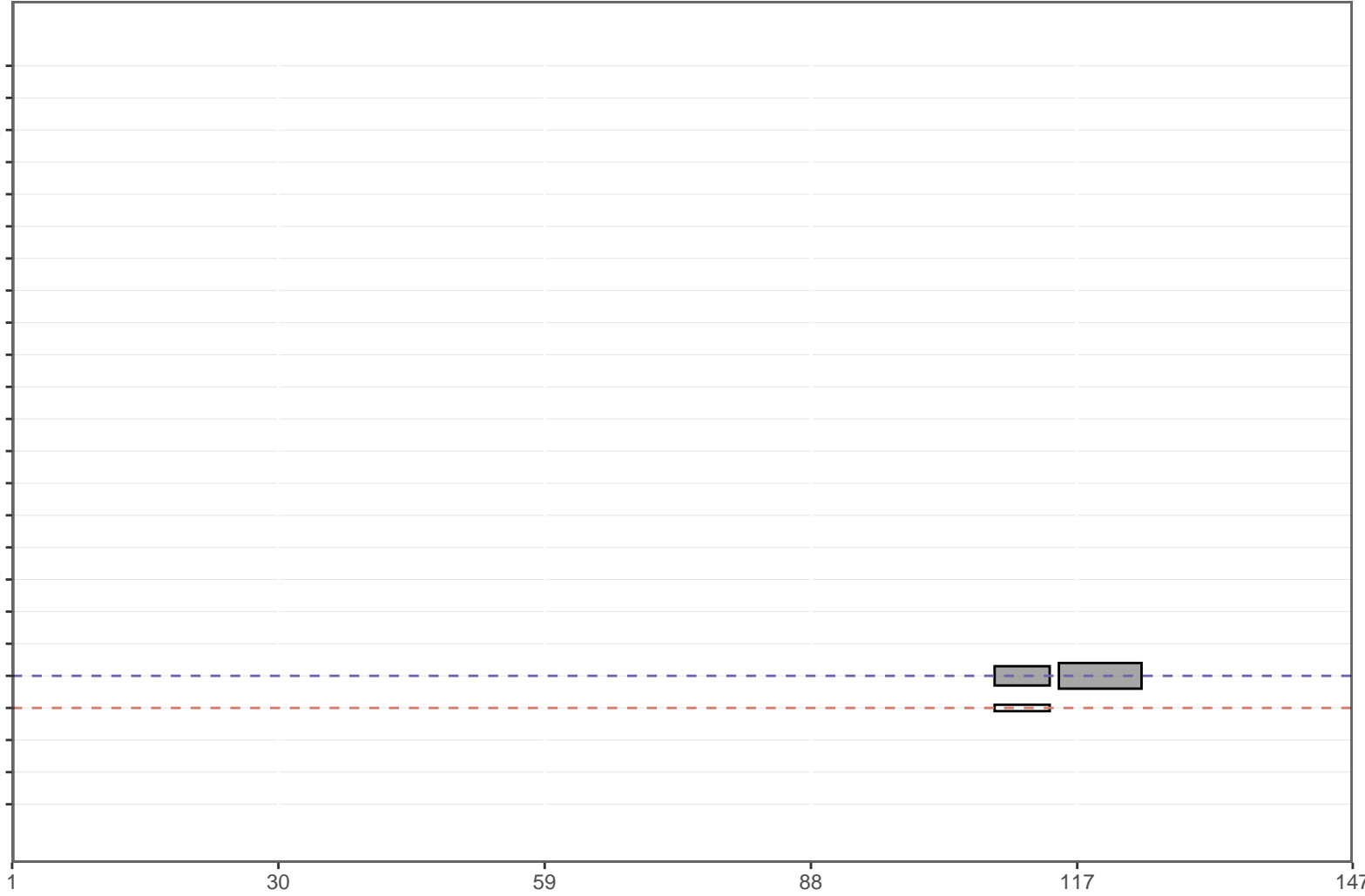
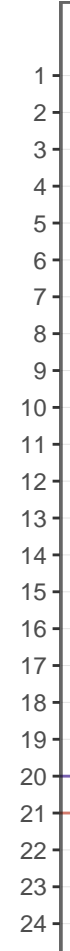
MW indication



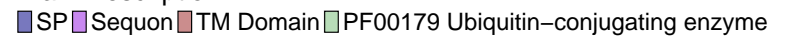
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

HGGRIYQLKLFCDKDKYPEKPPSVRFHGRINMTGVNPEGGVDAKKFRMLENWRQREYTMEDLTKLRKEMVAPQNRKLVDPREGTFP

NbL03g02720.1 serine/threonine-protein_phosphatase_BSL3 [MW = 108.97 kDa]

No. of times detected



log(intensity)



Values from



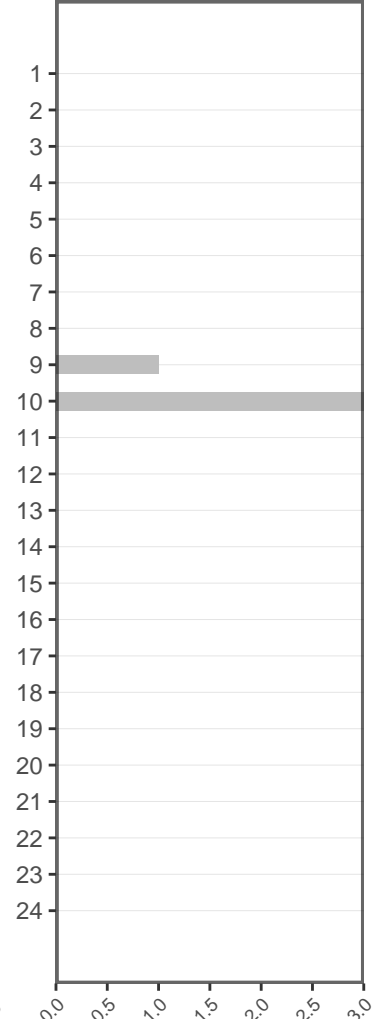
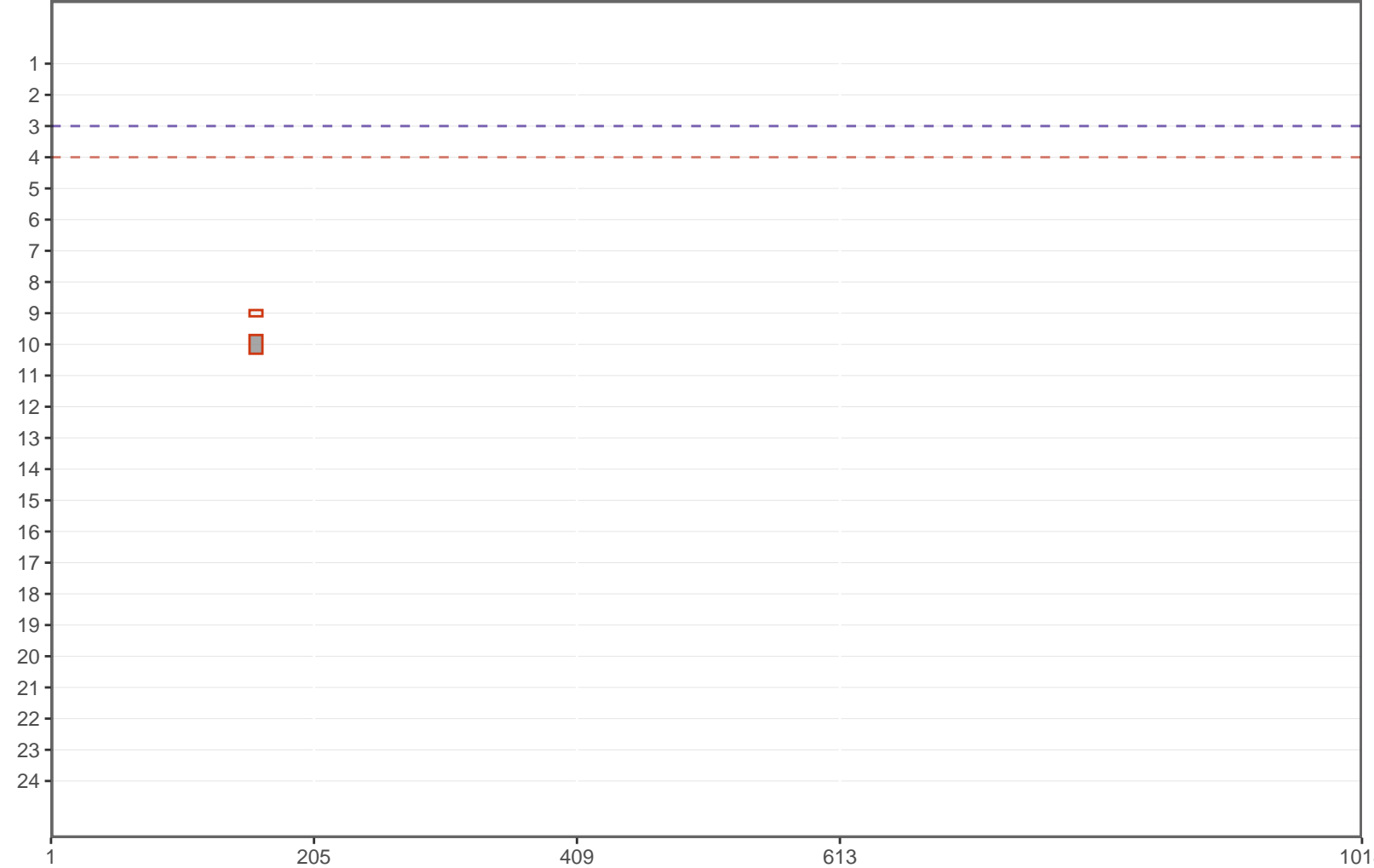
MW indication



Molecular weight



Gel Slice



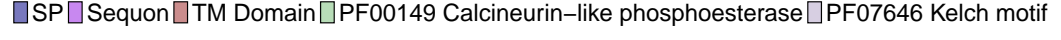
Protein length

Peptide counts over 4 repeats



Pfam domains

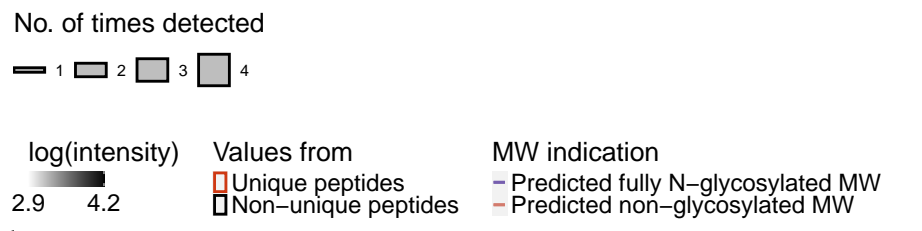
Pfam Description



Protein sequence:

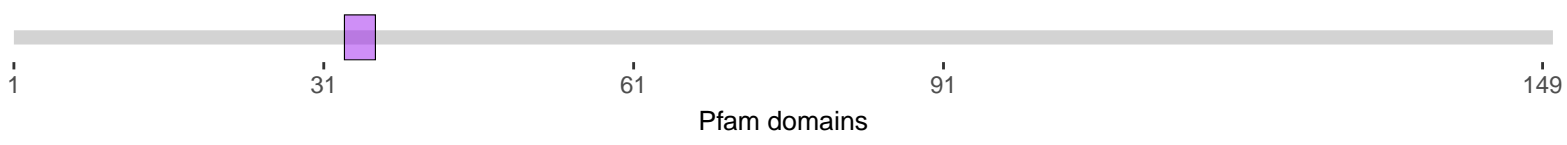
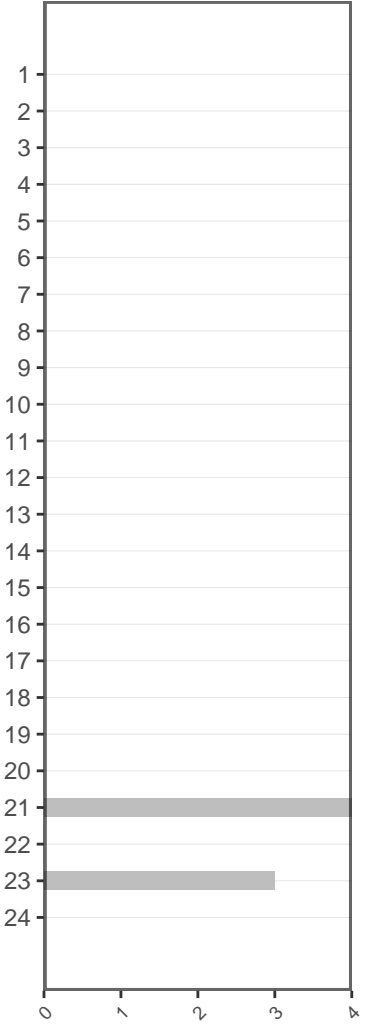
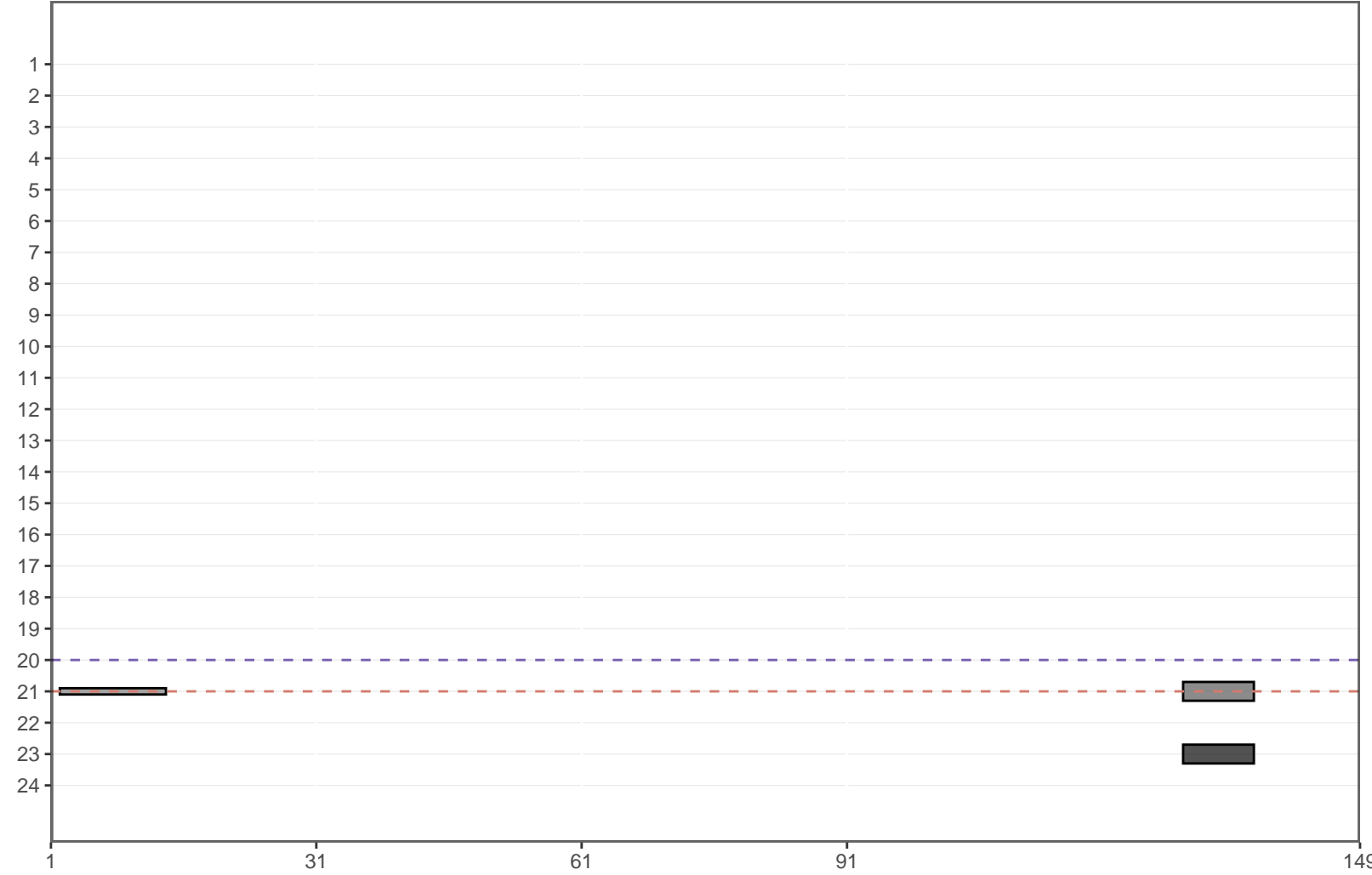
'SDISTENATLQGSRRRLKGVYELVEASAAEAETATLAAAKARGGGNGEVELPDRDRGAEATPSSGKQAPSLIKPDGVPVGVRLHHRVAVAAETGGALGGMVRLGSDGFENEGRRVSYGTFENATAARKLLDRGMSINSVPKVIAHLKPRGWPVPRRQFFLDCEYEMVLDGSAERIFASEPSVLQLRAPKIFGDLHGDFGDLMLRFLDEYVSPSTAGDSYDYLFLGDDVDRGGHSELTFTLLALKVEYPLNVLHVRGNHEAADINALGFRIEGRMGERGGIWA

NbL03g02670.1 succinate_dehydrogenase_subunit_6_mitochondrial-like [MW = 16.75 kDa]



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain

Protein sequence:
HGPTLRTAREAAKQSAVGGIGAVSTAGVWVKYGRSLHGTALFGAGAVFGWTFGGGEVANNWLGKYLQDTMAAGVKFMWVWQNKVEG*

NbL03g02440.1 enoyl-CoA_delta_isomerase_2_peroxisomal-like [MW = 25.68 kDa]

No. of times detected



log(intensity)



Values from



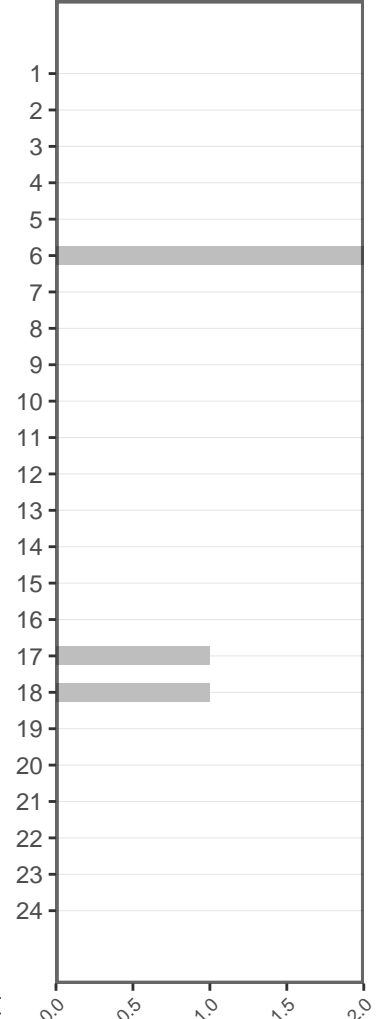
MW indication



Molecular weight

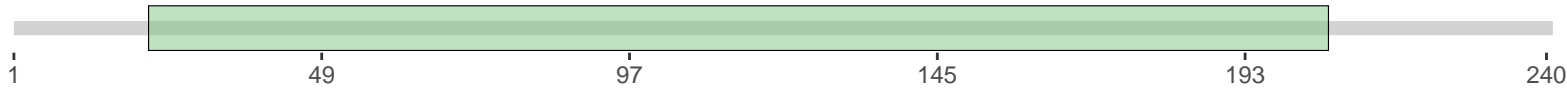


Gel Slice



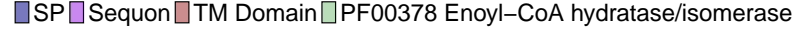
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VAAGLLLAICHQYVTMRSDKGVVYMSLELDKGMTLPDVFVTAMIRSKVGSAAARRNLVJKATKMKAEQVAMGILDSAHPTAEAAVAVRLAEELGKRRWDGKTFAELRKLKSLVPEVCGVLGKHTVLPRL*

NbL03g02400.1 signal_recognition_particle_14_kDa_protein-like [MW = 14.22 kDa]

No. of times detected



log(intensity)



Values from



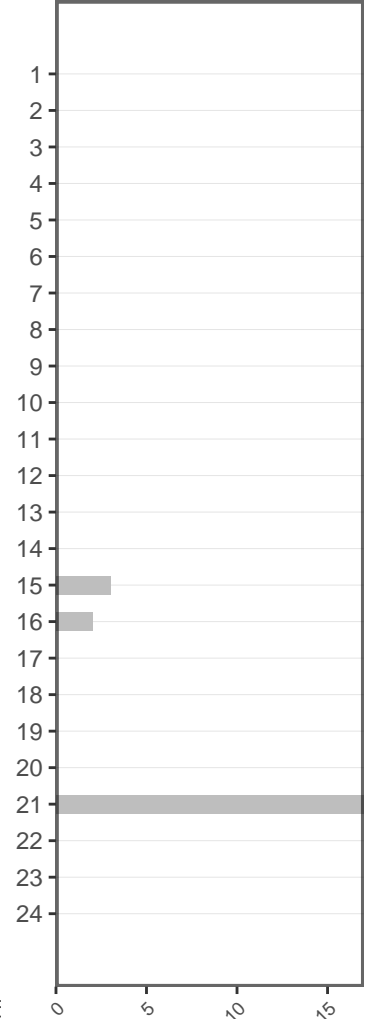
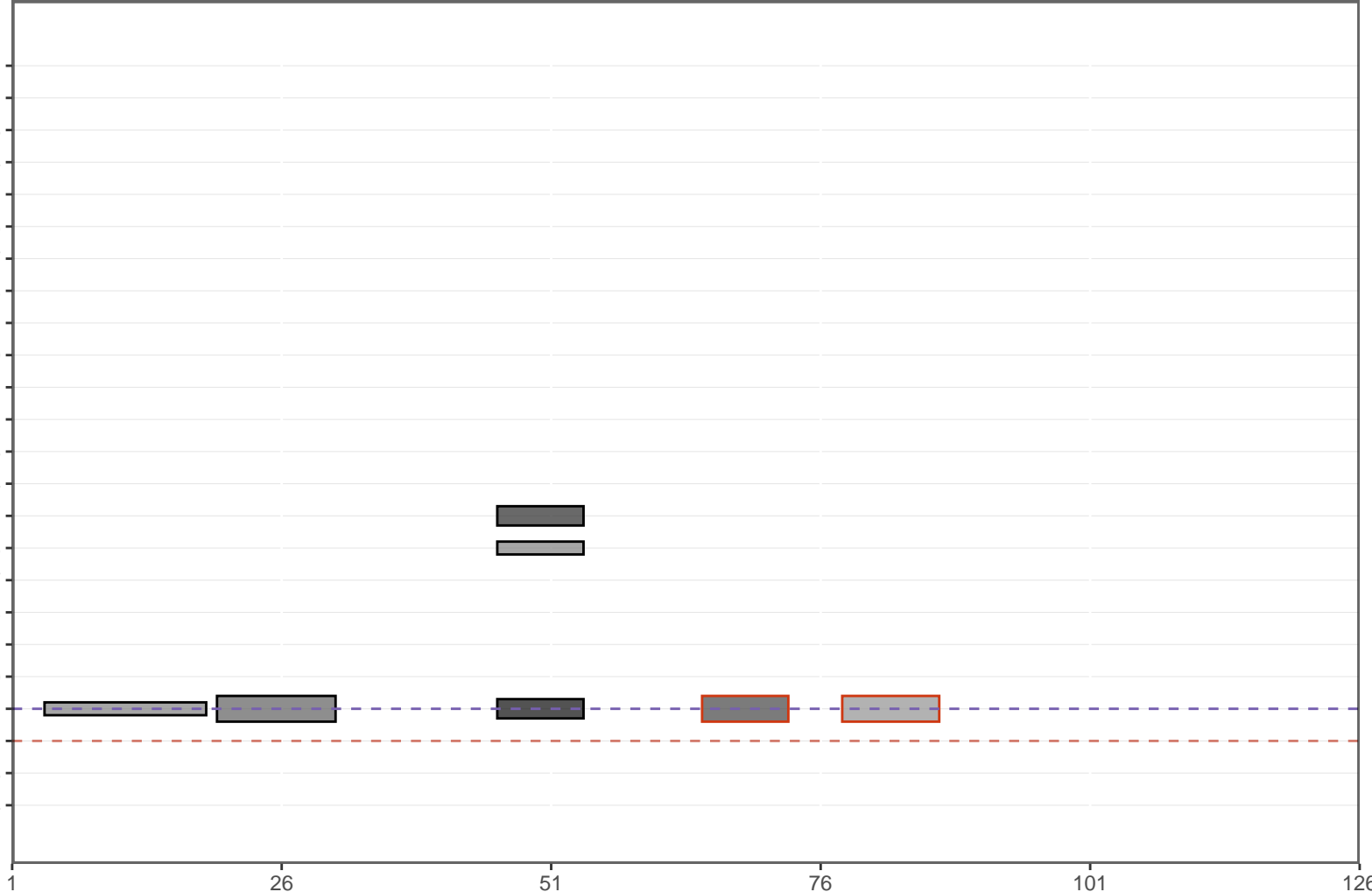
MW indication



Molecular weight

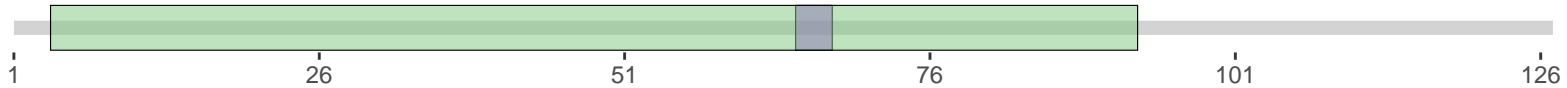


Gel Slice



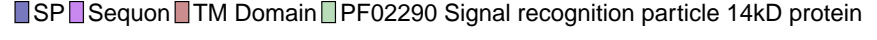
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ENIEFXCLRATDGGKNIETMVGANDHGRFGAIEVALLKARLTALKKRERKDKRKAADSDKLEKSKKSAAGKAST

NbL03g02340.1 2-isopropylmalate_synthase_B [MW = 65.79 kDa]

No. of times detected



log(intensity)



Values from



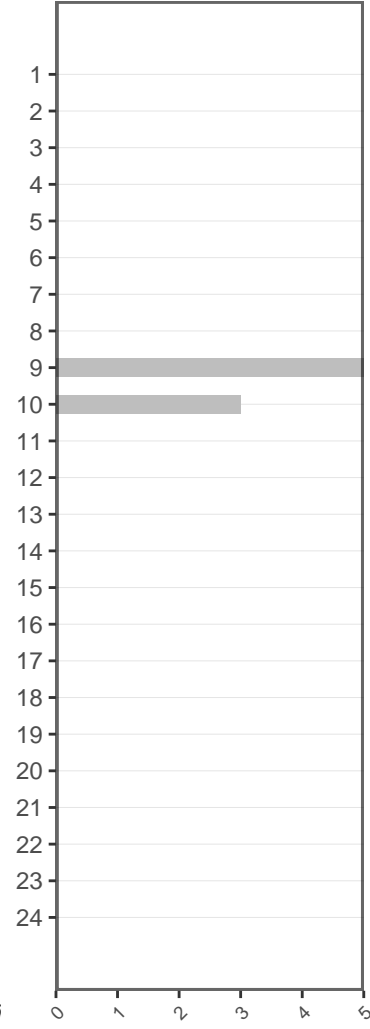
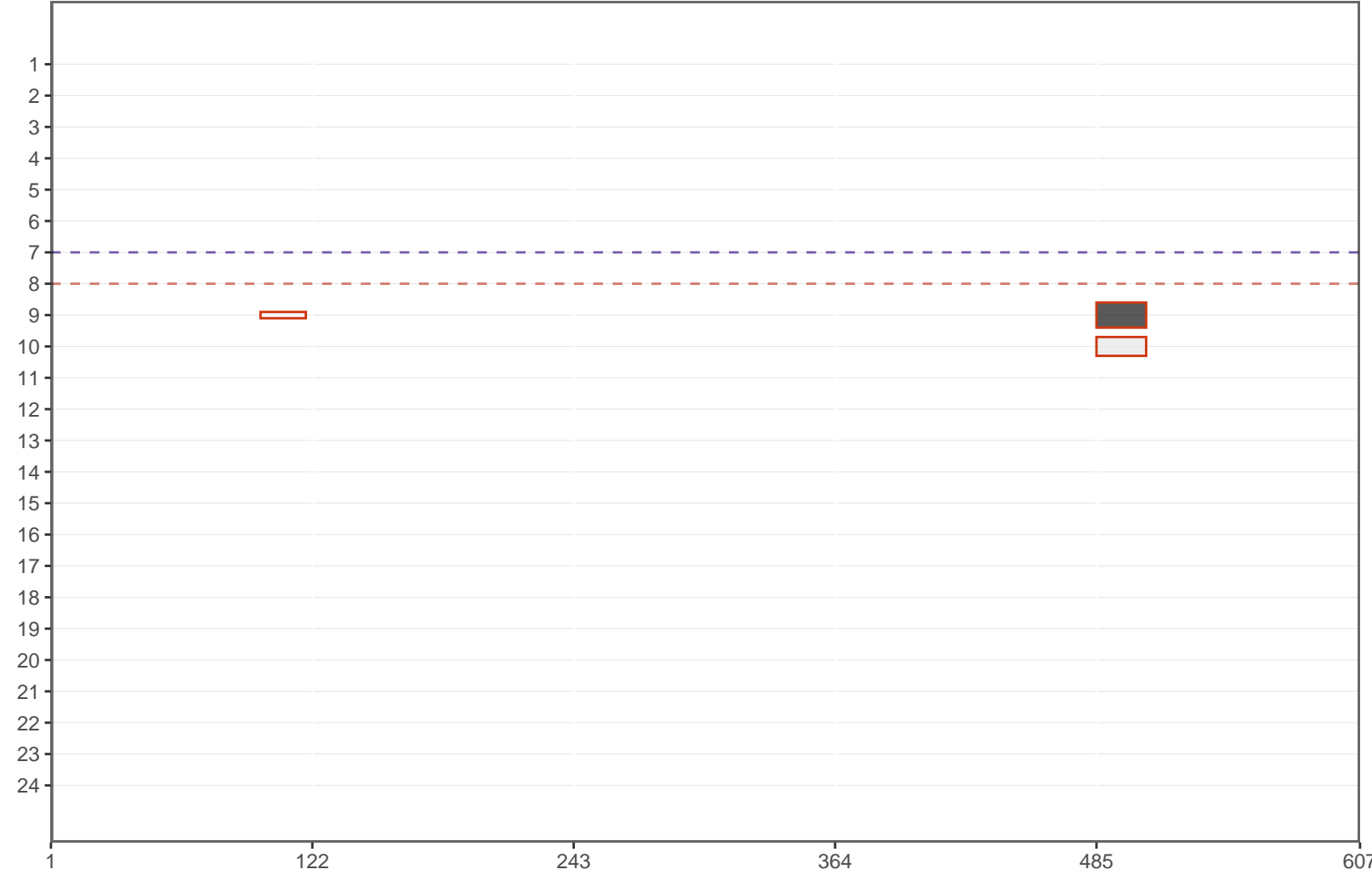
MW indication



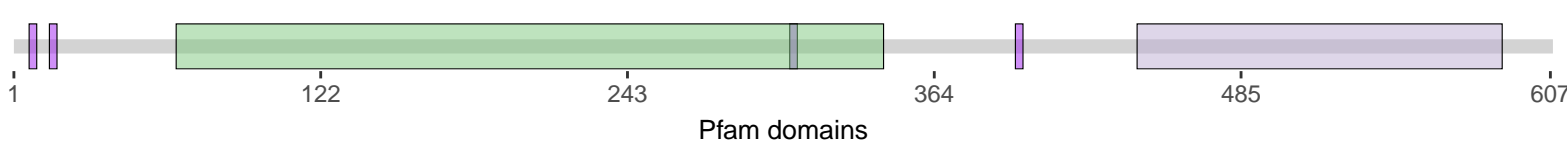
Molecular weight



Gel Slice



Protein length



Pfam Description



Protein sequence:

VEVTNGIGGERAGNASLEEVVMAALKRGEQVGGVLTGINTGHILMSGKMEVEYTGHHVQPHKAVGANAFHESGHGDDGMLKHKDTYEIHPEDIDGLNRANESGIVLGLKSGRHALQAKMLELGYDIEGKELEDLFWRFKSAEKKKIFDQDLALMSDEVFQDFVWQLENVQVTOGELGISTATVKLIDADGGHVSQVGTGPRVDAKKAVDLKVYVVALEVEVSNVTEGIDMASTRVLRGENGHTSTHALTGETVHRFSFGTGADMDMIVSEVRYAYIGALNKMLSI

NbL03g02330.1 15_kDa_selenoprotein [MW – SP = 16.28 kDa]

No. of times detected



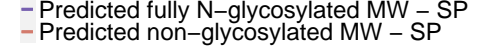
log(intensity)



Values from



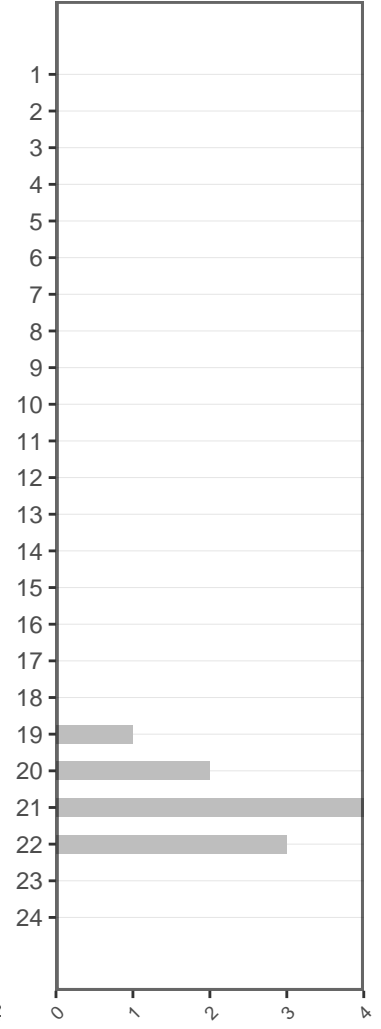
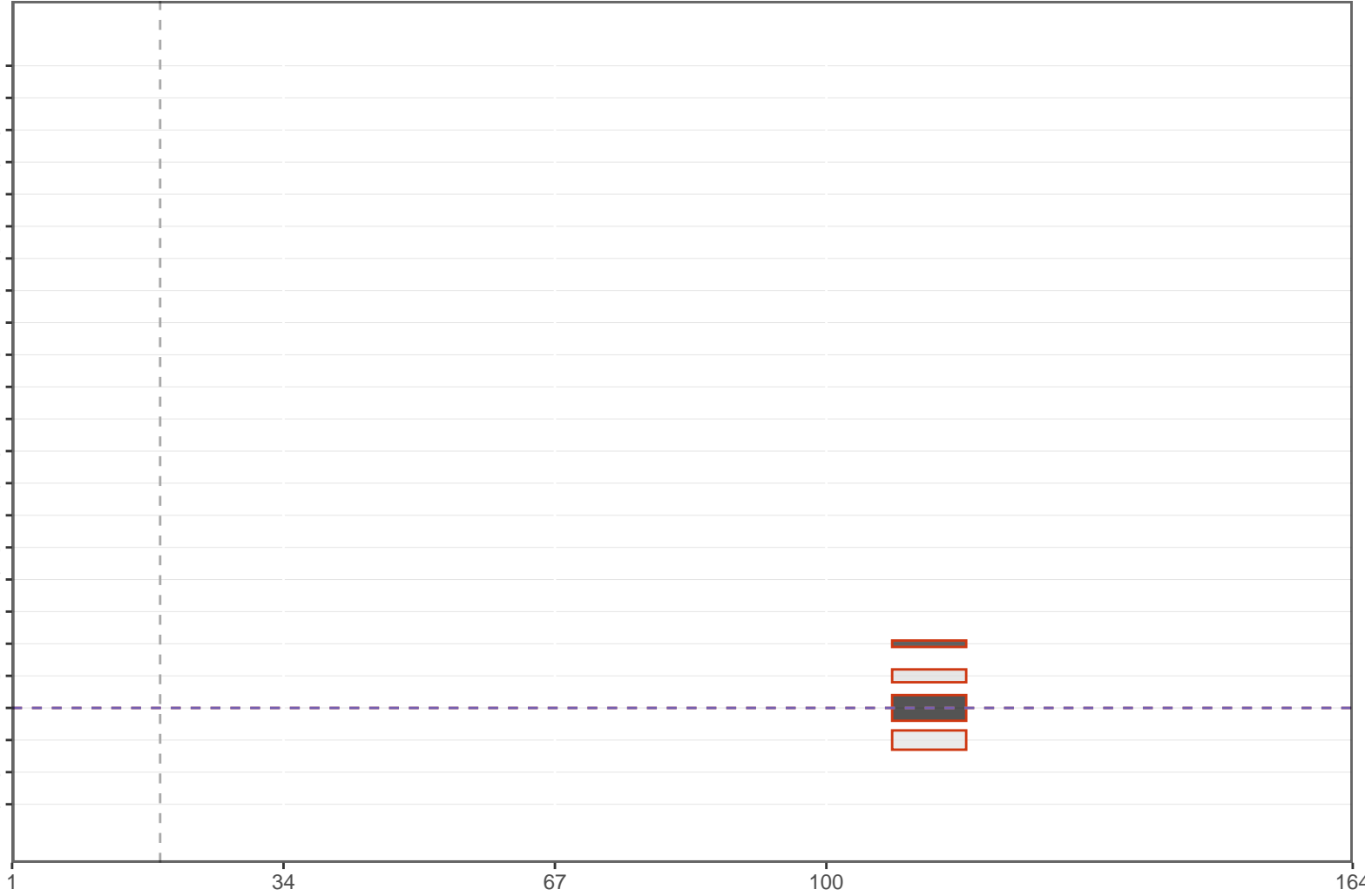
MW indication



Molecular weight



Gel Slice

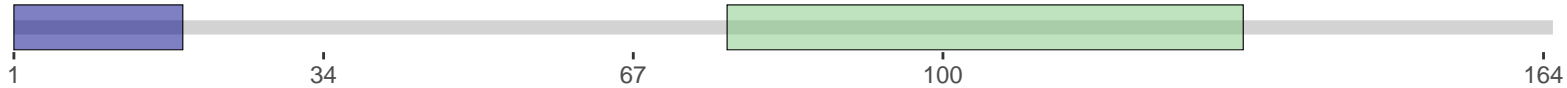


Protein length

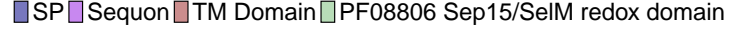


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

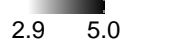
MSKVVYSGALEVGMKRLVFEVVGRIEEKKFPVYVGVQWYNSPKLIMLDHGHGHEKARISSECLLFRFLQVMGIDGPISYFYWFKVH

NbL03g02270.1 probable_prefoldin_subunit_2 [MW = 16.19 kDa]

No. of times detected



log(intensity)



Values from



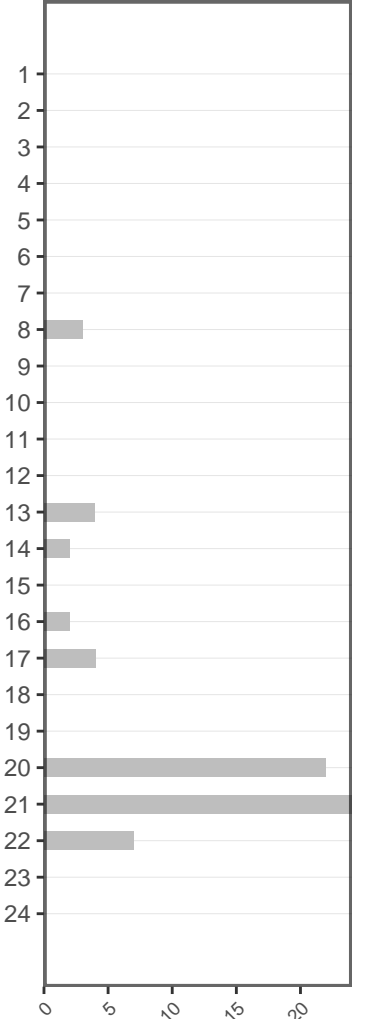
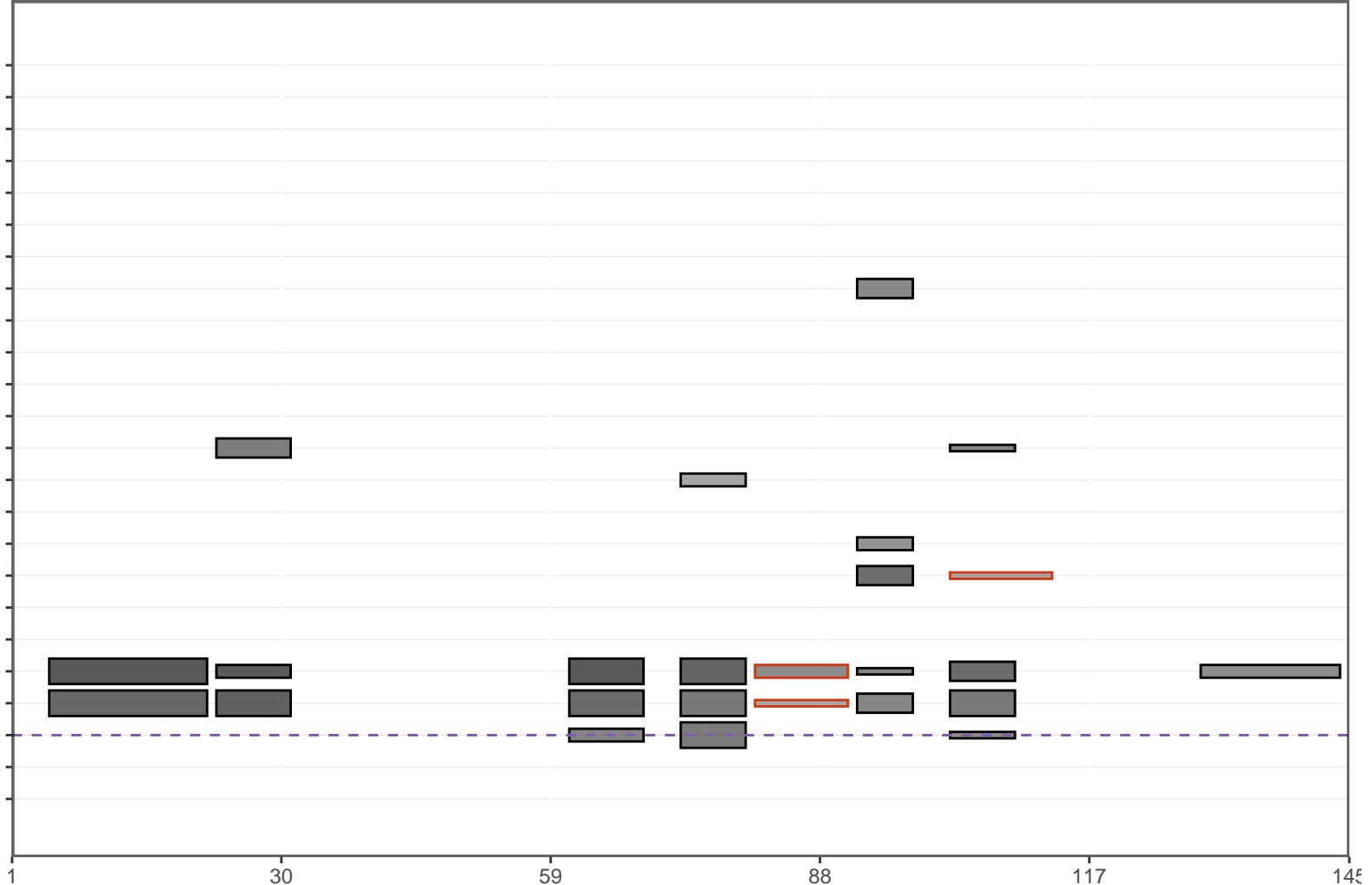
MW indication



Molecular weight

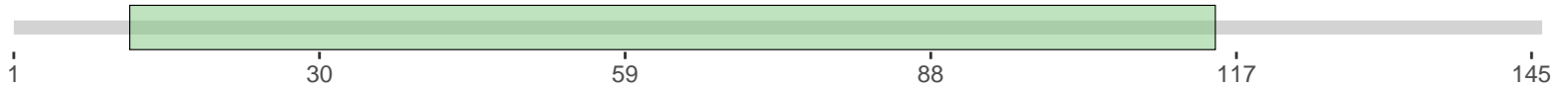


Gel Slice



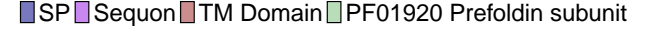
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RMIGGLVVERTKEVLPVQRNKKEGIEVTRLNLEALEKKKKKIDFETKYQIRMRKPAEVEKKEESGRKEGSAQGVLVGPRGNE*

NbL03g02250.1 stearoyl-[acyl-carrier-protein]_9-desaturase_chloroplastic [MW = 45.14 kDa]

No. of times detected



log(intensity)



Values from



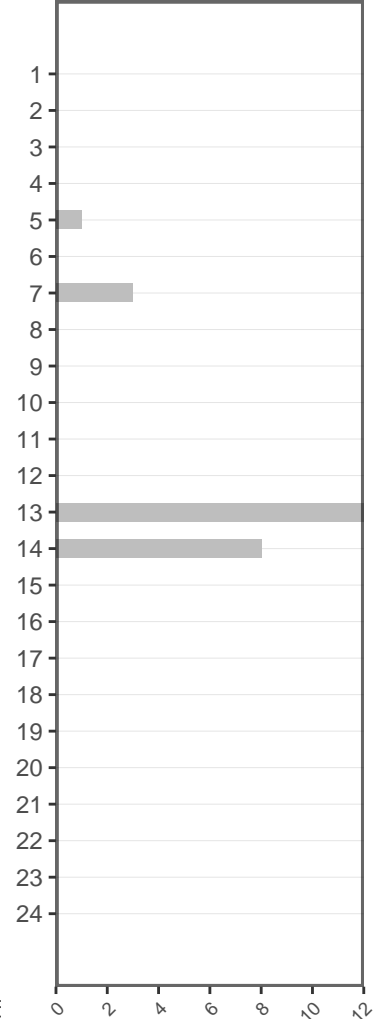
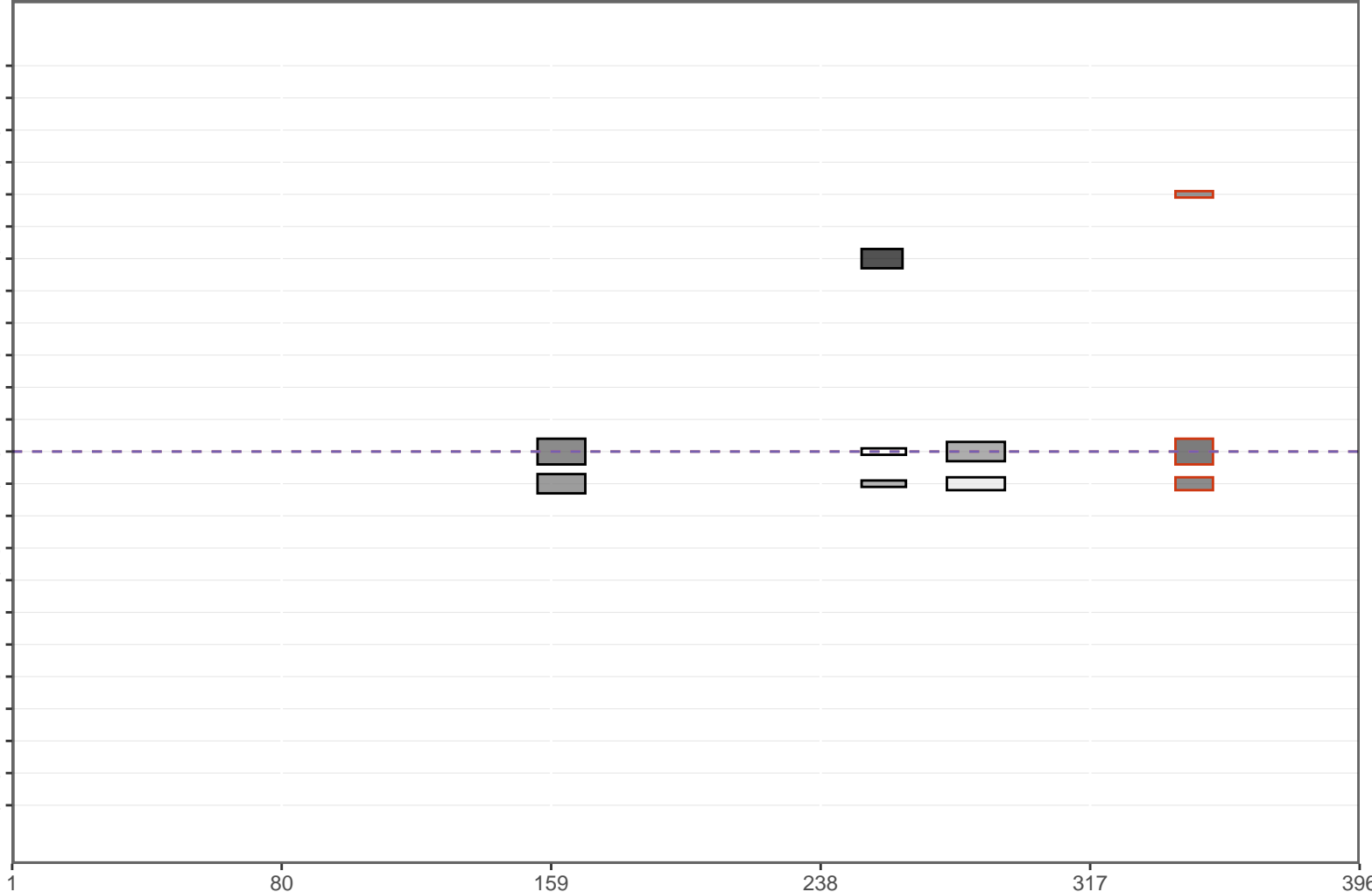
MW indication



Molecular weight

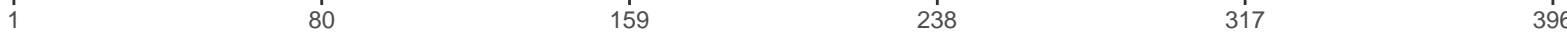


Gel Slice

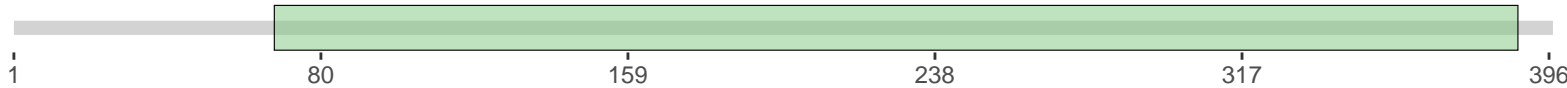


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

LNKLYLISGRVDMRAIEKTIQYLGGSDPRTEENPYLGFVYTSFGERATFVSHGNTARLAKHEHGDKLAKICGIIAADEKRHEIATKIVKLEFDPDGTLYLAFADMMRKIKISMPHLMYDGRDESLFDHFEAVADRGLGVYTAHDVADILEFLVGRWIKWADLTGLSGEGRKADEYVCGLPPIRIRLEERADGRAGKSGPMPFESWIVDREVKL

NbL03g02240.1 protein_FAM136A-like [MW = 17.09 kDa]

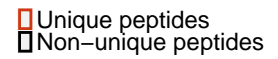
No. of times detected



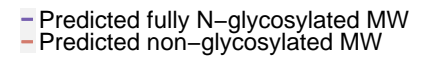
log(intensity)



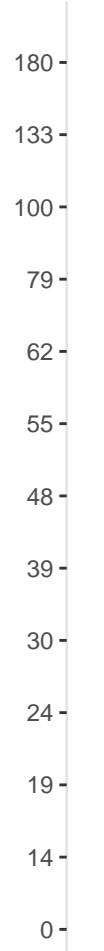
Values from



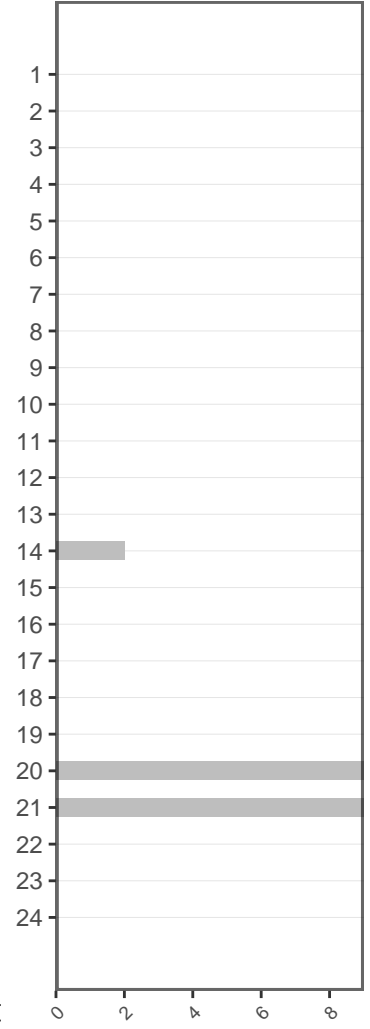
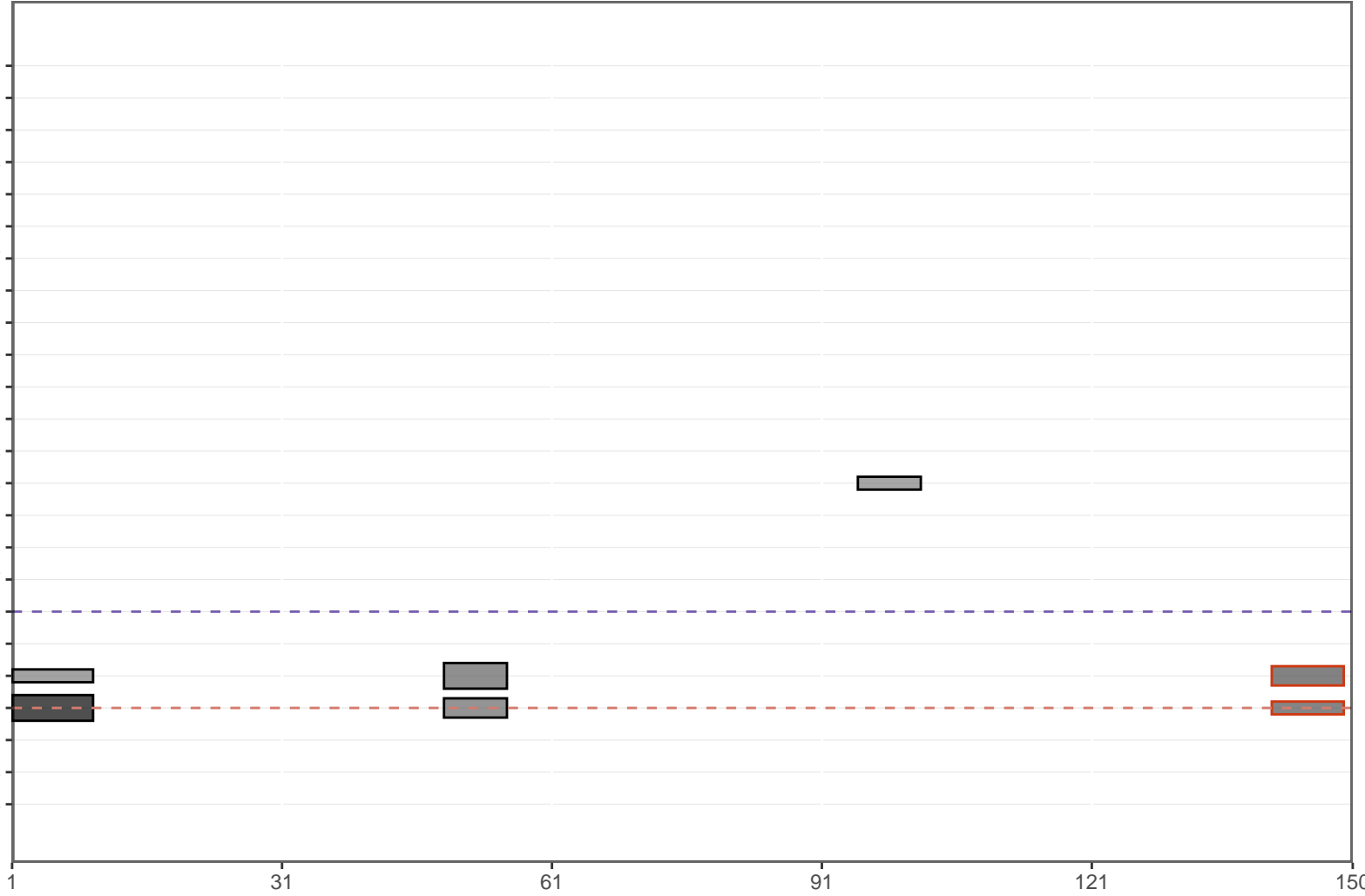
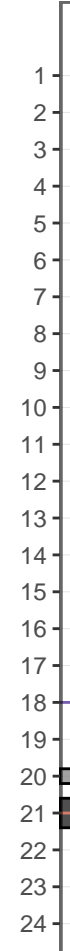
MW indication



Molecular weight

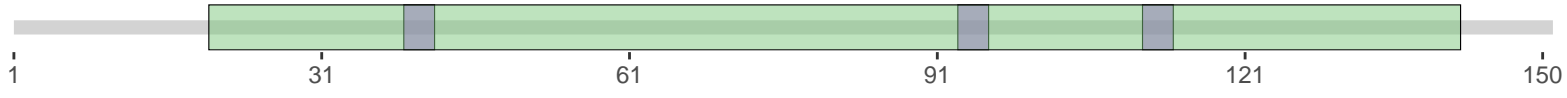


Gel Slice



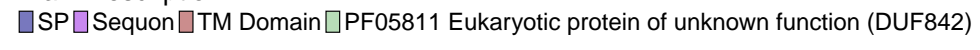
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGHCVEHCSYHYVWNAQNLVQNEAKPGERMNRSLMVGGDHYETAKLQKRRSDATKDLGGVDQGVHDSINTLPHLVARLKSGLGFN

NbL03g02160.1 nuclear-pore_anchor [MW = 229.78 kDa]

No. of times detected



log(intensity)



Values from

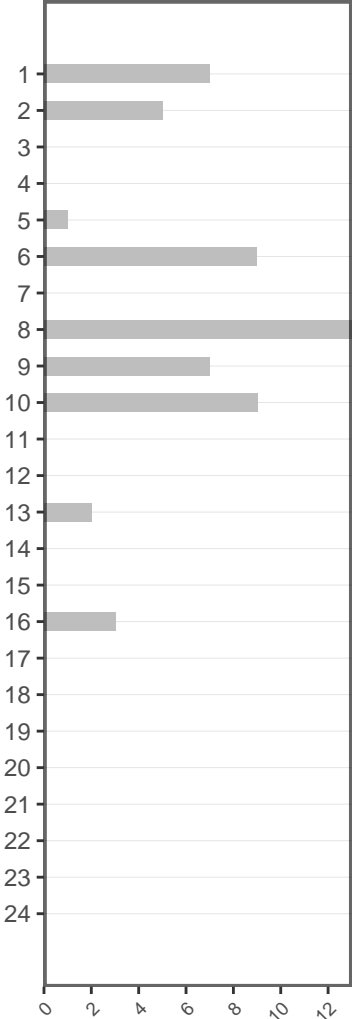


MW indication



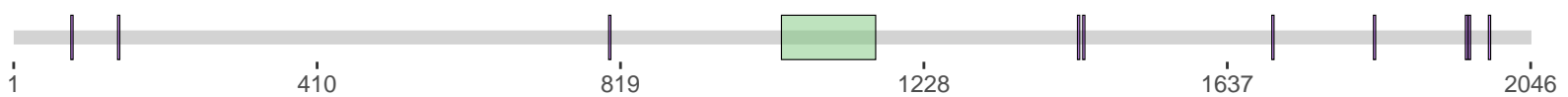
Molecular weight

Gel Slice



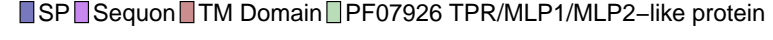
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

INCTYKSEAAASATAGKEEAAVATLAIEISLKEEDNSAKMMSQGNLEALITLKDLDLKEHQRWHAAGVNYNERYVLSGETIQDELTRTSGALAAEGEESSELKRSIKLKTENNELKAKWGAEMSALEVSKTEAKNYTEANEQNKILLDRLEGLHKLAEKDRBSLGTSSGSETTASDDGLMNVNLYLRRKDKAETELGLRDKELRLGGOLENAGRRADIAEASLNSERENSRAGVLYNEEFKALGLQVRELNLRLREGNLGLREKHFEEGGKLRAAQKMKIEVDGLQK

NbL03g02150.1 aldo-keto_reductase [MW = 47 kDa]

No. of times detected



log(intensity)



Values from



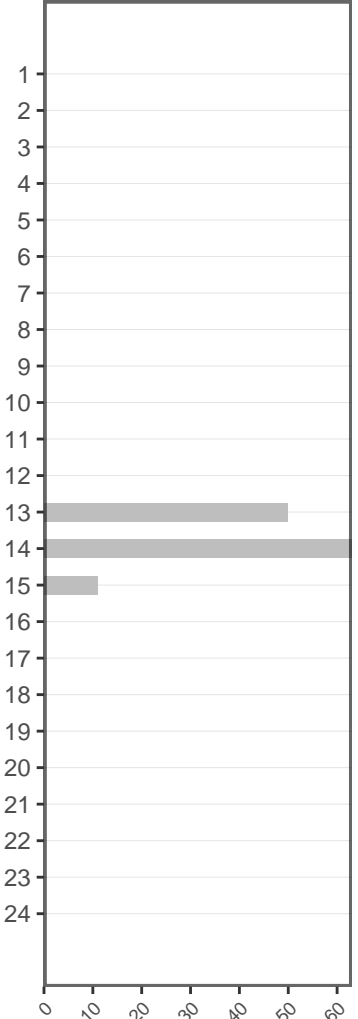
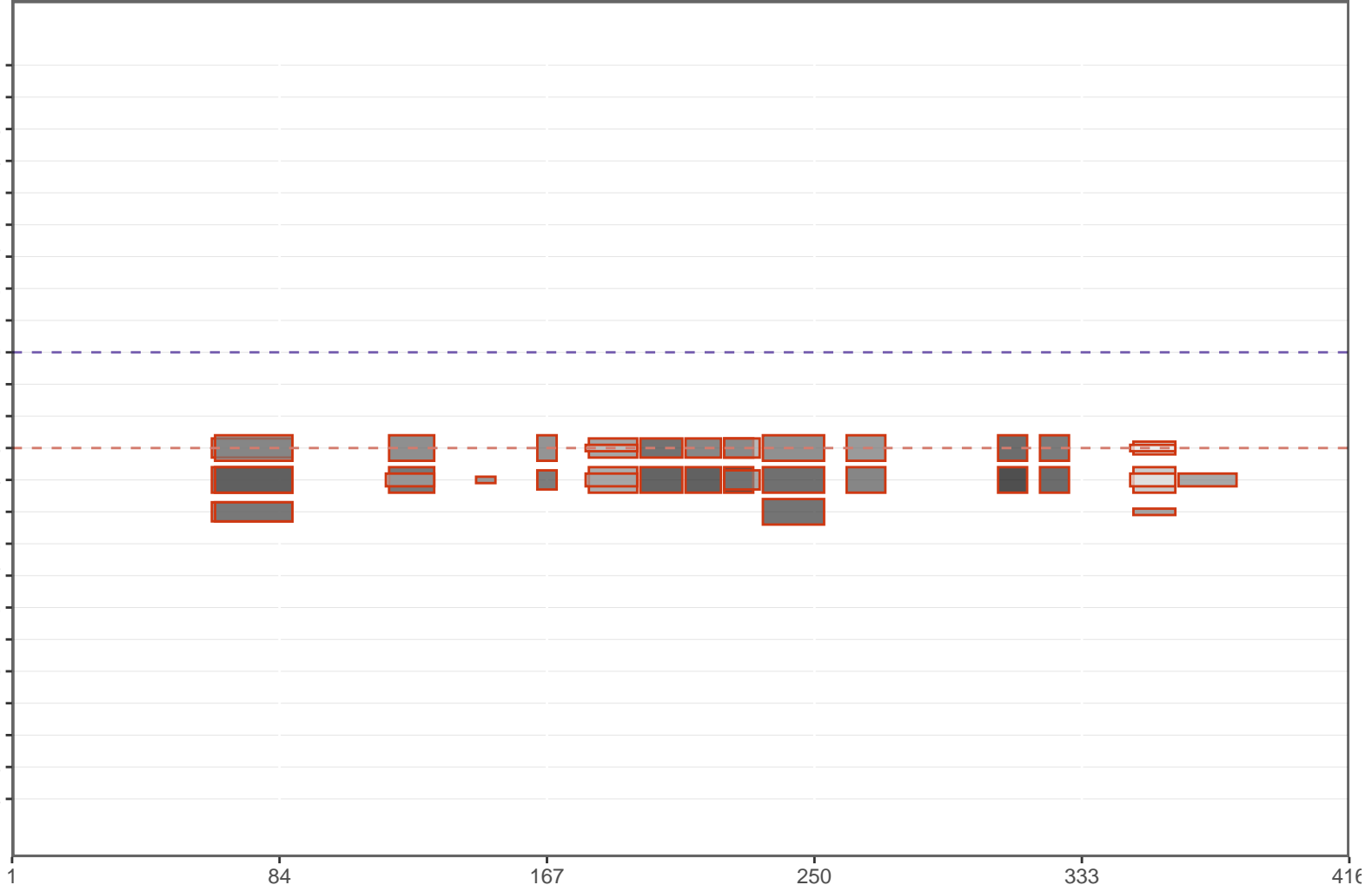
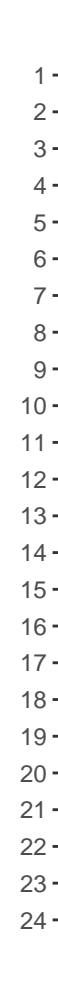
MW indication



Molecular weight

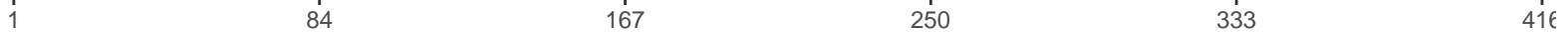


Gel Slice

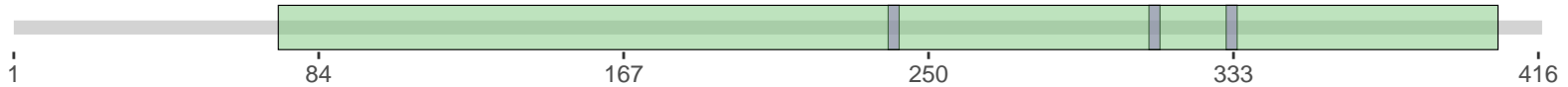


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

VVPLFGFFYESSKWRPVPFVEQLRAFGLDEGKVRVYGVNSETSYGVMEFVHAAKVEGMPKRVGIGNVSLLVKRGHFVLDVEVGHVNNNGILLVSLVPLAGGTLGSKYLDNNSEAAARKGLNLFPGVYMERVYKSLAKEATKRYEEVAKKHGLTVELALGFARDPFPMTSSIGATSEVGLKEDDAFLTERPLPPQVMDDEDIFKRVKDPASR

NbL03g02120.1 serine/threonine-protein_phosphatase_PP1_isozyme_2-like [MW = 36.7 kDa]

No. of times detected



log(intensity)



Values from



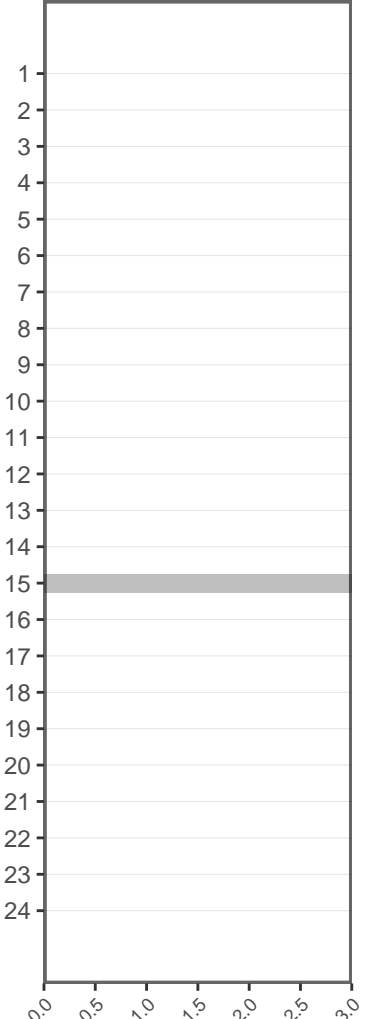
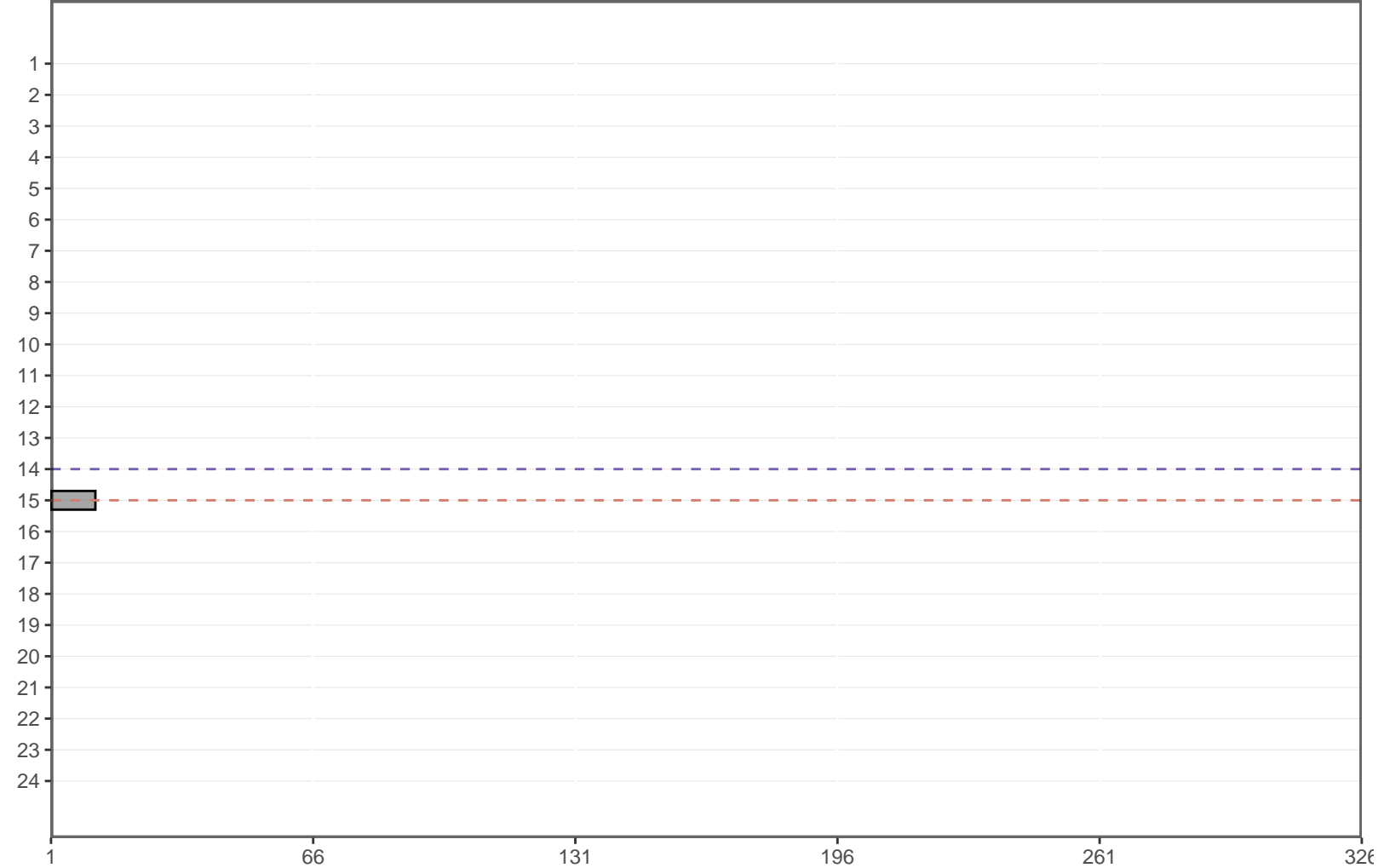
MW indication



Molecular weight

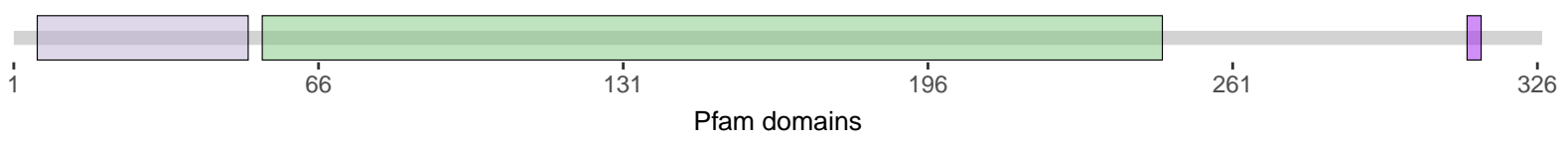


Gel Slice



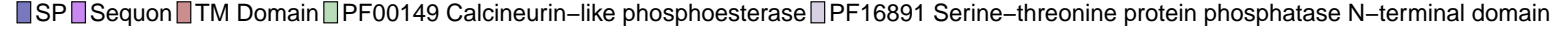
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

"NCLPVAALIDEKILGMHGLSPDLNHLQIRNLQRPTDVPETGLGLDLWSDPKDYKGVGSMNDRGVSTFGPKVTEFLQKLDLVLGRAHGVVDDGYEFFADRGLVTFISAPNYVGEFDNAGAMMSVDETLMSGFQILPKAEKPKFGFGGATSANNATPTKESFLGKIG"

NbL03g01910.1 probable_hydroxyacylglutathione_hydrolase_2_chloroplastic [MW = 36.22 kDa]

No. of times detected



log(intensity)



Values from



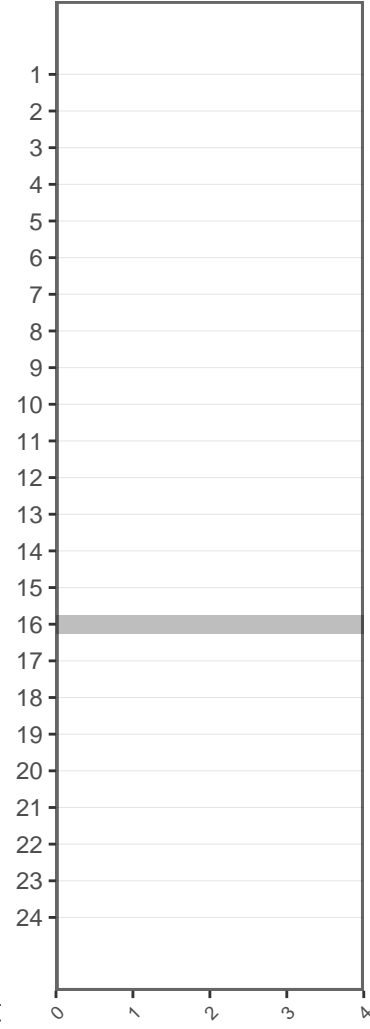
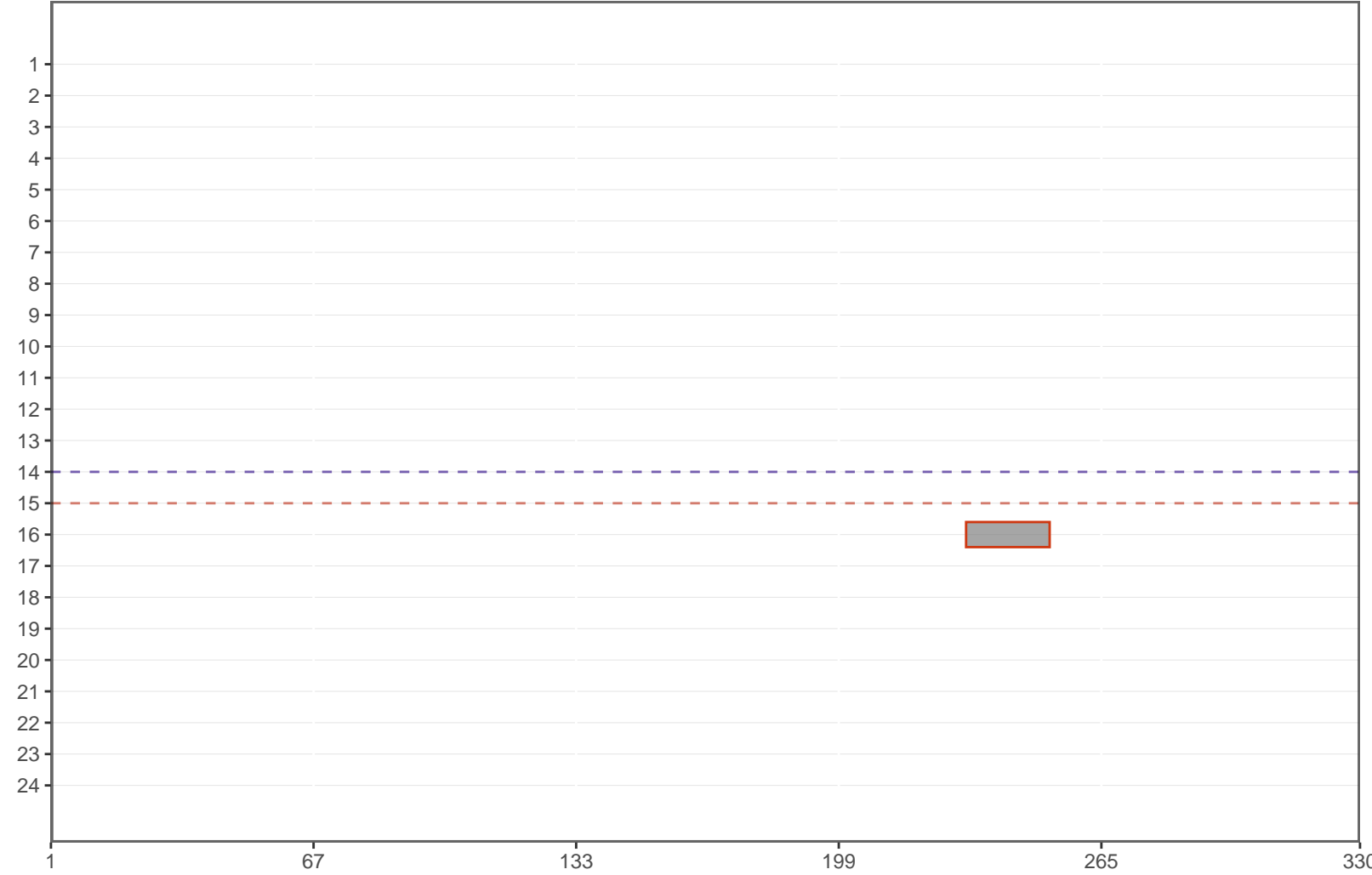
MW indication



Molecular weight

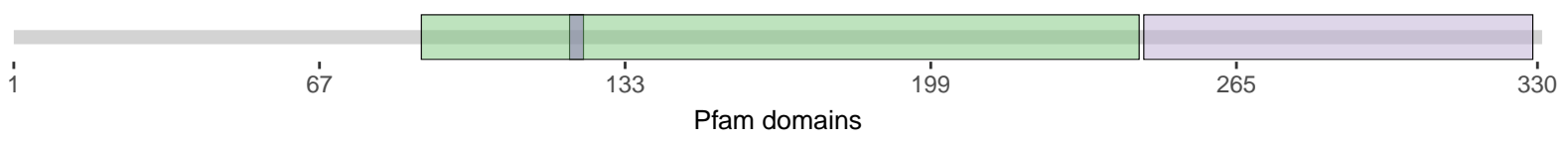


Gel Slice



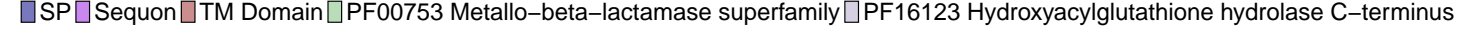
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISGADSDRIPGIDAIANDGDQWFMFAGHEVLMETPGHTRGHSHFYFRSKAIFTGDTLFLSLGCKLFEQTPQGMLSLRLKIMLPPDNTNYYGHEYTLNFKFALSVEPQNEELQGVAAQVYVNLKQKGLPTPTTLTKAEKLGMPFLRSTSEIRKLLNFPPTADDAEALGARRANDTE

NbL03g01870.1 30S_ribosomal_protein_S16-like [MW = 14.65 kDa]

No. of times detected



log(intensity)



Values from



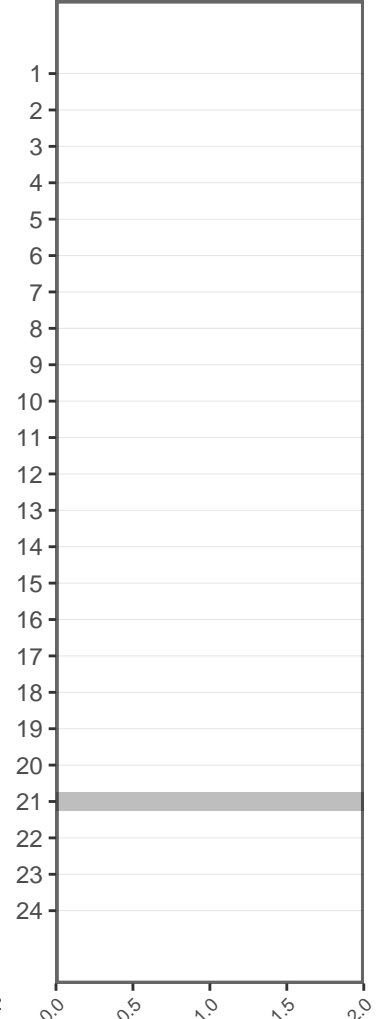
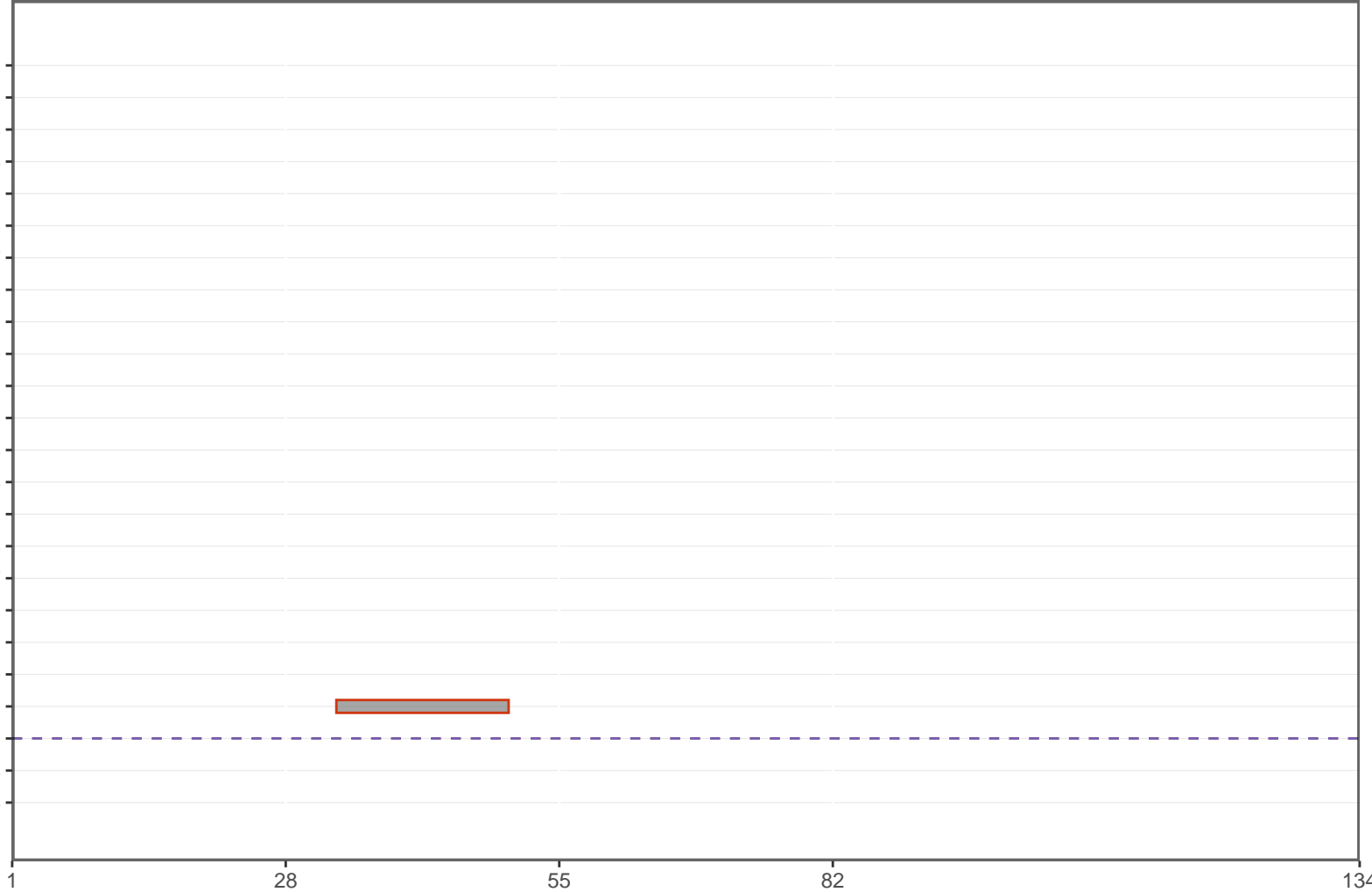
MW indication



Molecular weight

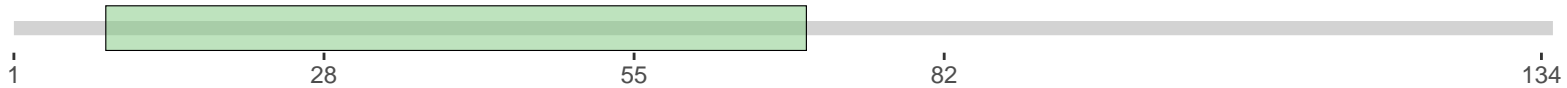


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LNFDKRYKYLTVGAGPSEPEVERLLFRAGVLPPLPMLAMGKGGPRDTRPVHFMTRGRVAPESEVWADPKVSAKVGDDKA*

NbL03g01820.1 methyl-CpG-binding_domain-containing_protein_11-like [MW = 37.48 kDa]

No. of times detected



log(intensity)



Values from



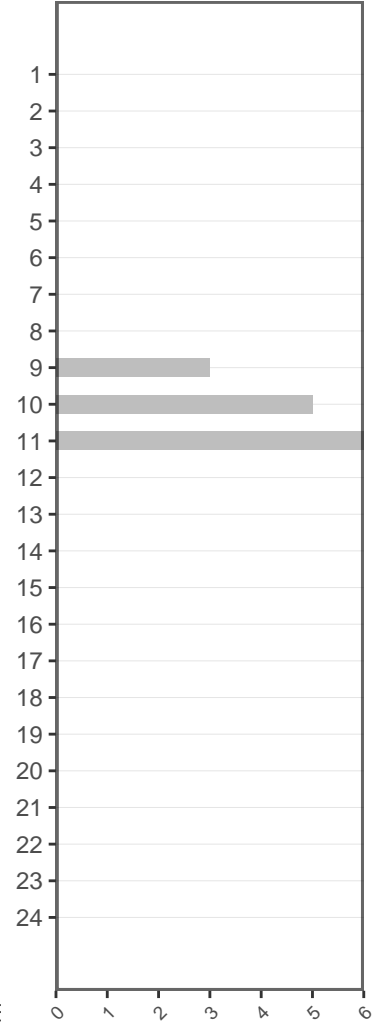
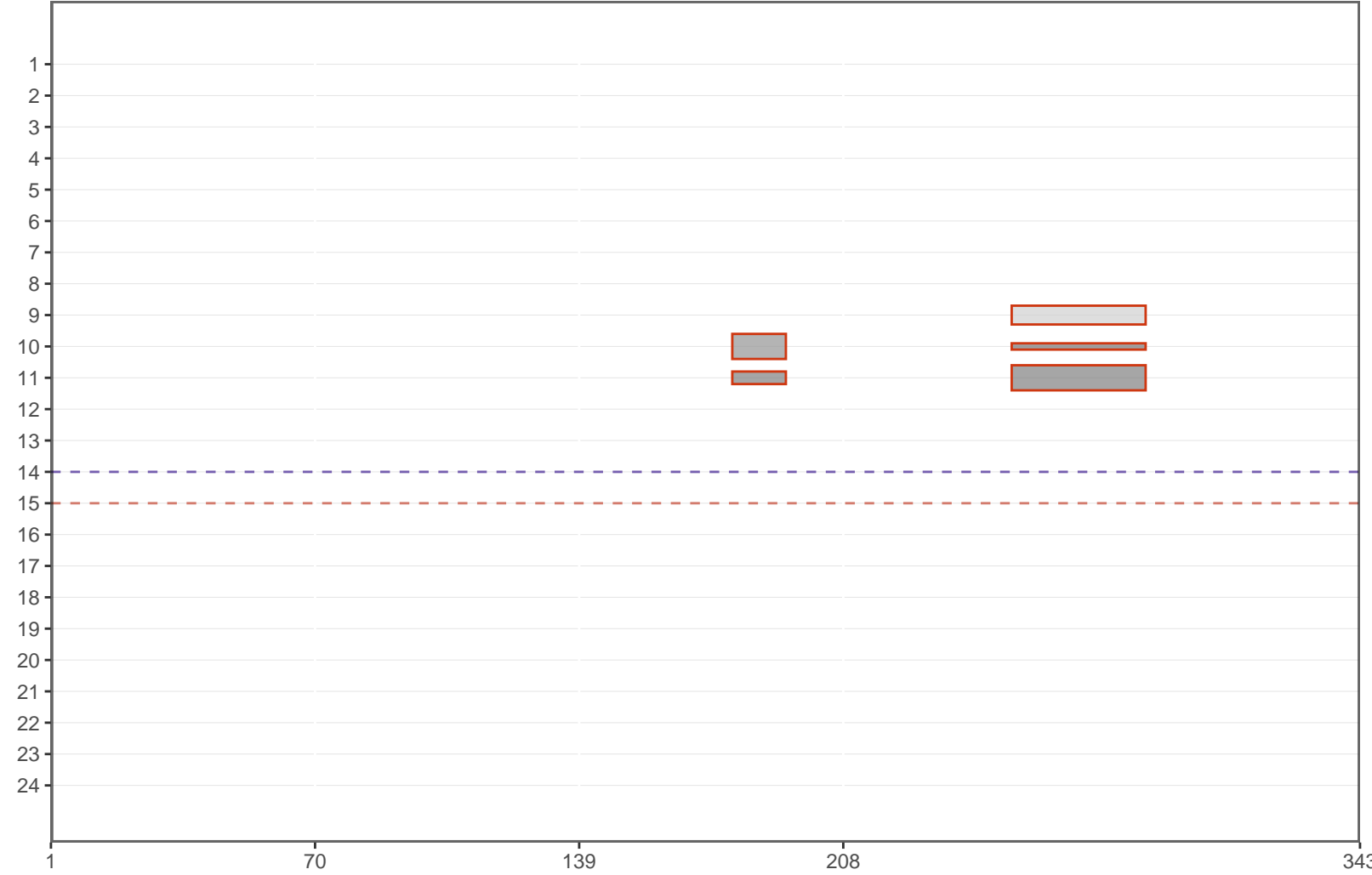
MW indication



Molecular weight



Gel Slice

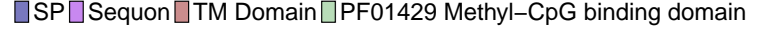


Protein length



Pfam domains

Pfam Description



Protein sequence:

INKGKQKEVAADDEAEAGMKGALHPPEEKPEMDDKQKKEVEAAANEAEAGMKGALHPPEEKPESEPKVDSADDGKQKSDNAKIEKLVSGEKLESLSKSDKSPAADVNEKNPEVVTAEQNEAVGGSSKDKVEHAGNGESNNGENRSGEEKEEMKGTDLVMSGNKNKNGPQPMHSDQHSGRPISG

NbL03g01790.1 phospholipase_D_alpha_1-like [MW = 92.19 kDa]

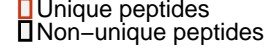
No. of times detected



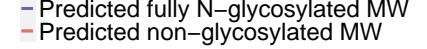
log(intensity)



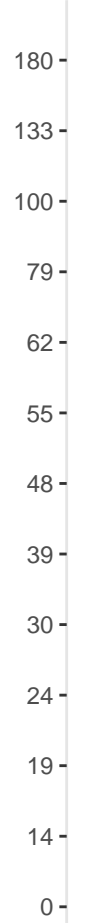
Values from



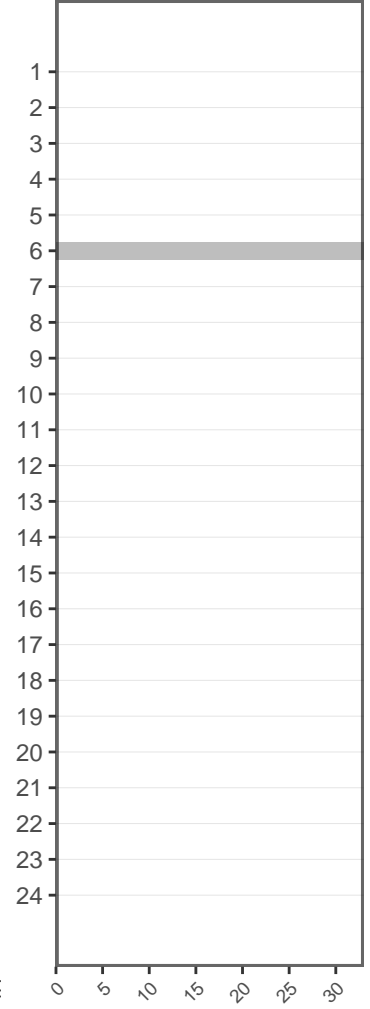
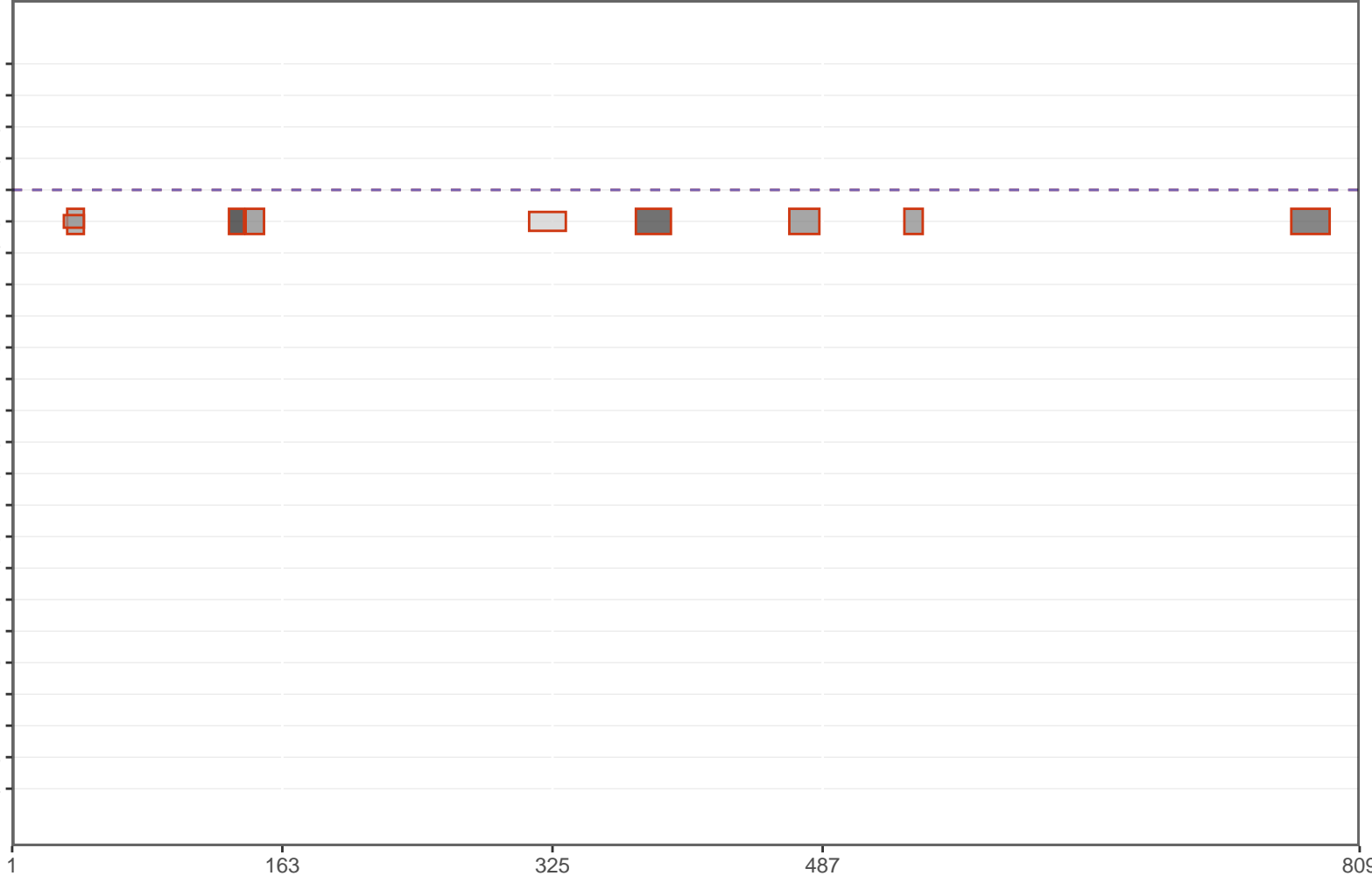
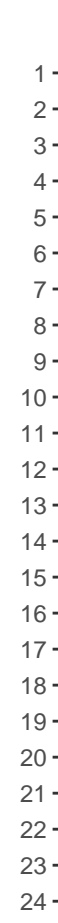
MW indication



Molecular weight



Gel Slice



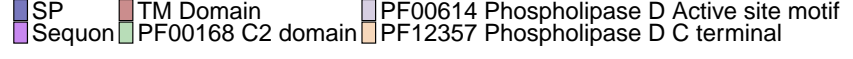
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SAITKGGPREPWIDHSRLGPIAWDLNFEGRWRKGGGKDKLVNFRLELDHHPPEPVMVLDQSETWVQLFRSIDEGAAGFPDTPEDAANKAGLVGKDKNIDRSIQDAYHARRAKNFYIENGVFLGSSVYWGSDDKIVEIGLHHPKELALKIVSKIEAGERFTVYVPMWPEGFESASVQALDVGRRTMEMMYKHVQALNAKGIEDPRNVLFFCGNREVKSGEVEPESETPEPQSDVMRAGEARRFMVYHSGMMVDEYHVGANINQRSMQARD

NbL03g01770.1 probable_polygalacturonase_At1g80170 [MW = 49.3 kDa]

No. of times detected



log(intensity)



Values from



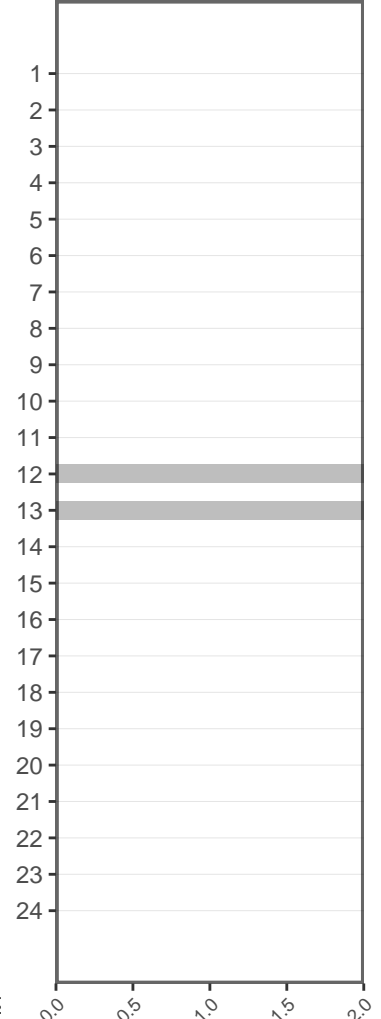
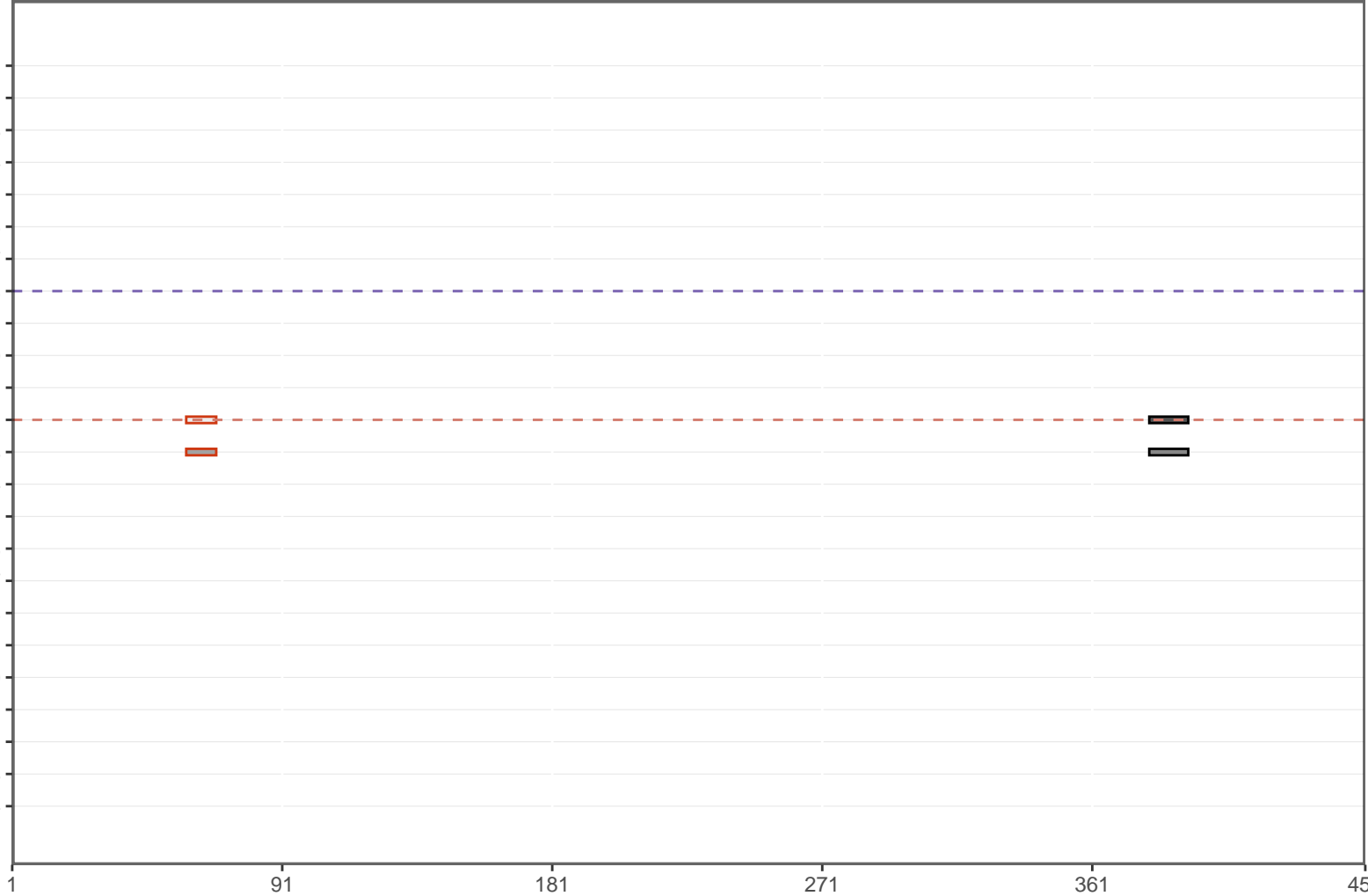
MW indication



Molecular weight



Gel Slice

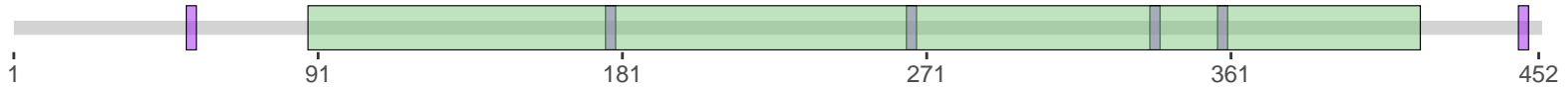


Protein length

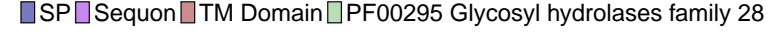


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ISISKCHVEYVSHLQAFAPKSPNTDGHISSEBHVGRDSSIGTGGDDCSIVGNSSRLVKNACGPGHSGISGLGKSNRRGVDVVDGAYLNTENGVRKTKWGGSGGFVRKIAFANVAMENVSNPIWQYVQDGRQACPNGLAISINVSFVGRGSSATKNATFFAGSDSSPCRNLYLEDQGLVFLFEPFTTSFGWNAVGGSTSGFNPNPSLGFPSGETIQHPTLESLNLSKSF

NbL03g01760.1 trafficking_protein_particle_complex_subunit_2-like [MW = 15.35 kDa]

No. of times detected



log(intensity)



Values from



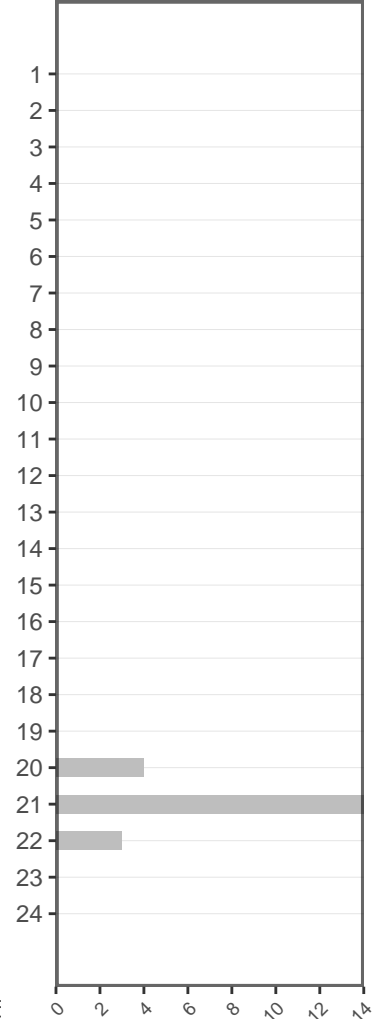
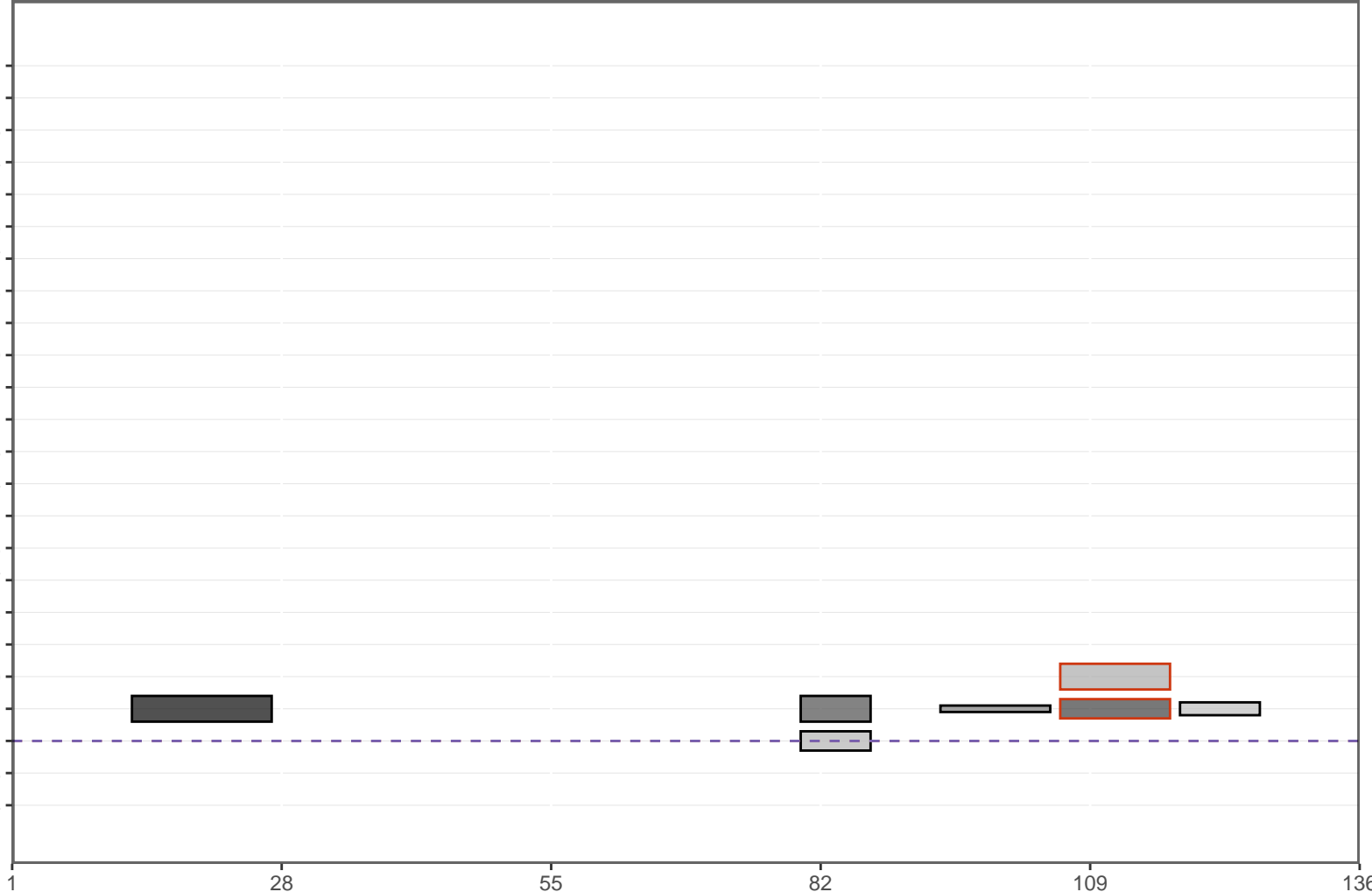
MW indication



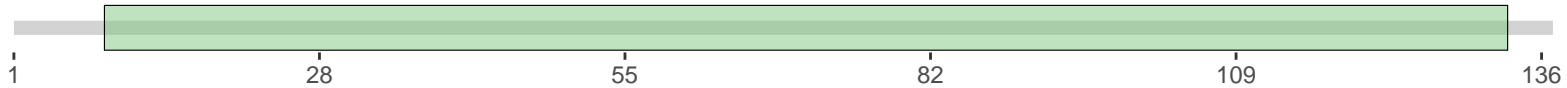
Molecular weight



Gel Slice

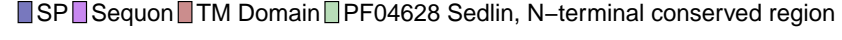


Protein length



Pfam domains

Pfam Description



Protein sequence:

AMFLKSIDRFNDLVASVYVYAGHTRILMLLHDSRNDGDKSFFQEVHELYKILLNPLVLPGRITSSHFDTKVRALARKYL

NbL03g01750.1 biotin_carboxyl_carrier_protein_of_acetyl-CoA_carboxylase_1_chloroplastic-like [MW = 29.49 kDa]

No. of times detected



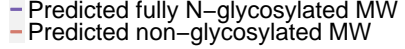
log(intensity)



Values from



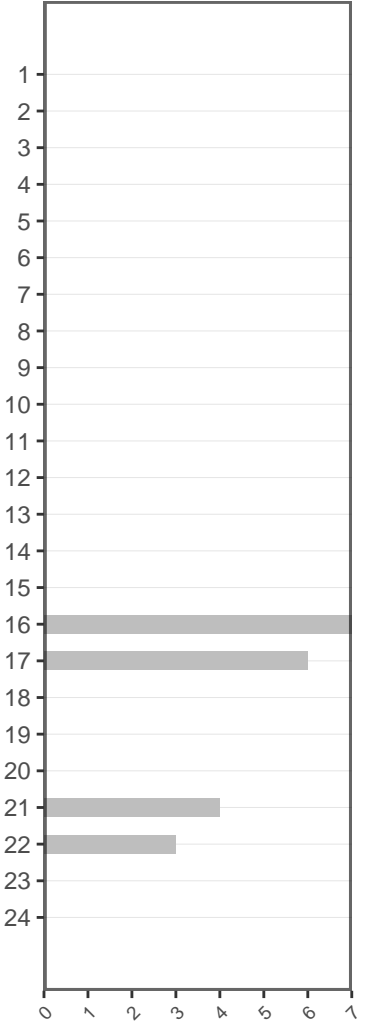
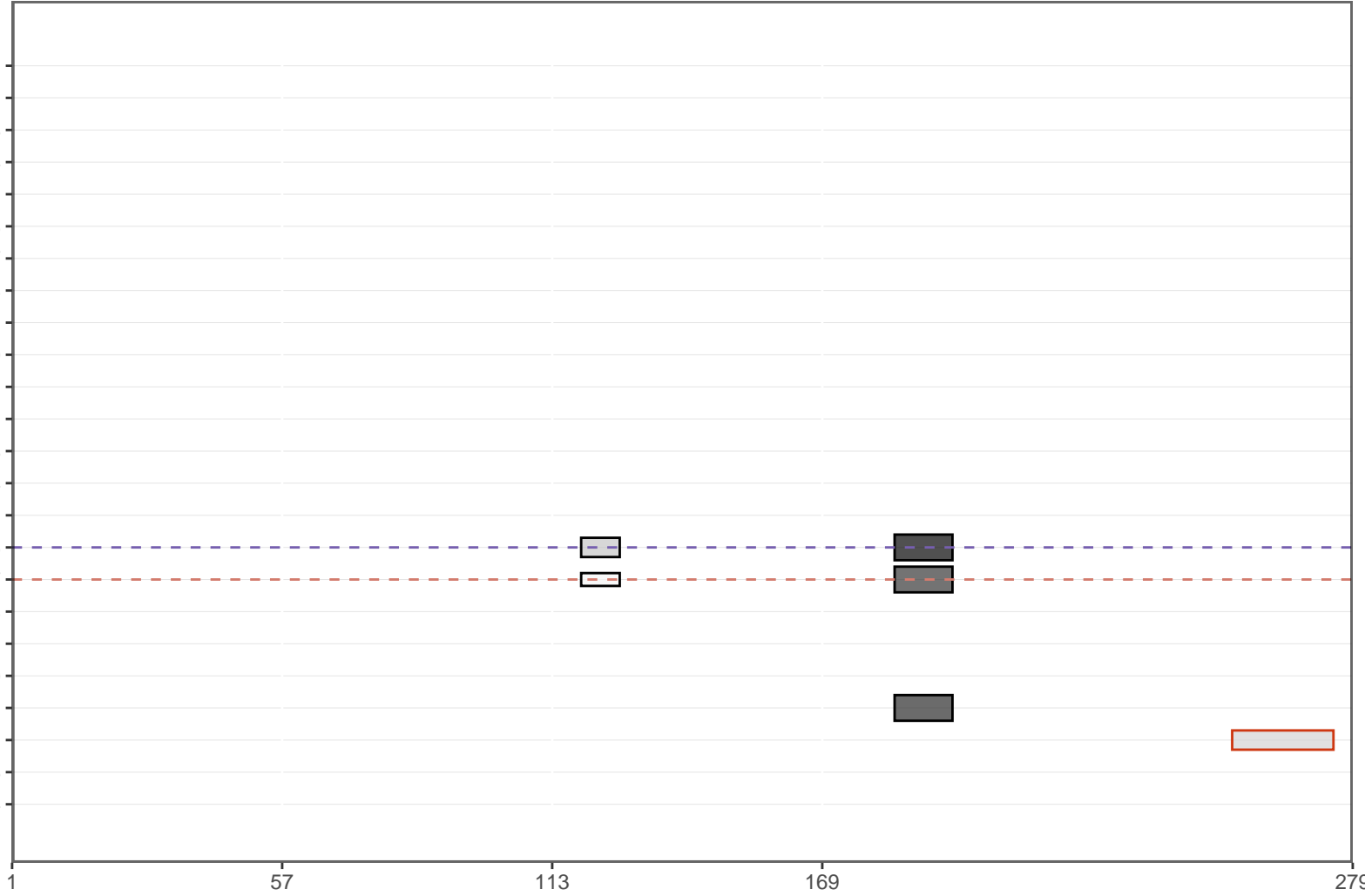
MW indication



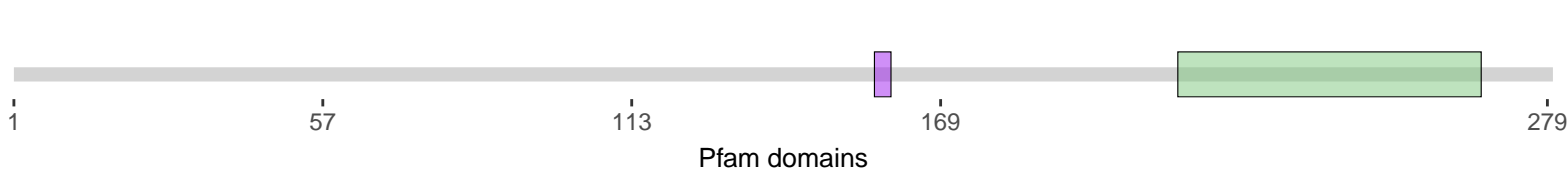
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

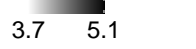
/KRDLYGPTSTLSLPMNPNVNHSSVEAANDNGSABSPSLATKSSPPSDGIRTMIDKAADEGLVIGSPRVGYFRRSRTWKGRAPPSCKEKQGVKEGVGFIEQLGGLPEVSDVSGEVKLGKDKDGPVGYGDLISLRFPPGIKKLQ

NbL03g01710.1 monothiol_glutaredoxin-S15_mitochondrial-like [MW = 18.96 kDa]

No. of times detected



log(intensity)



Values from



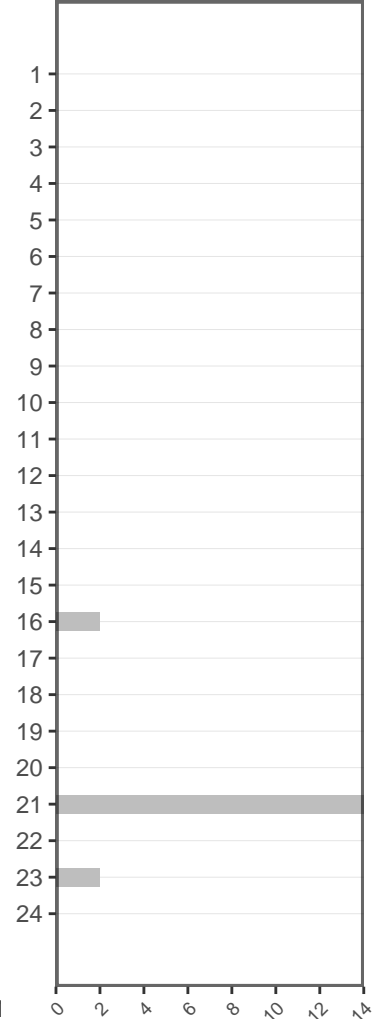
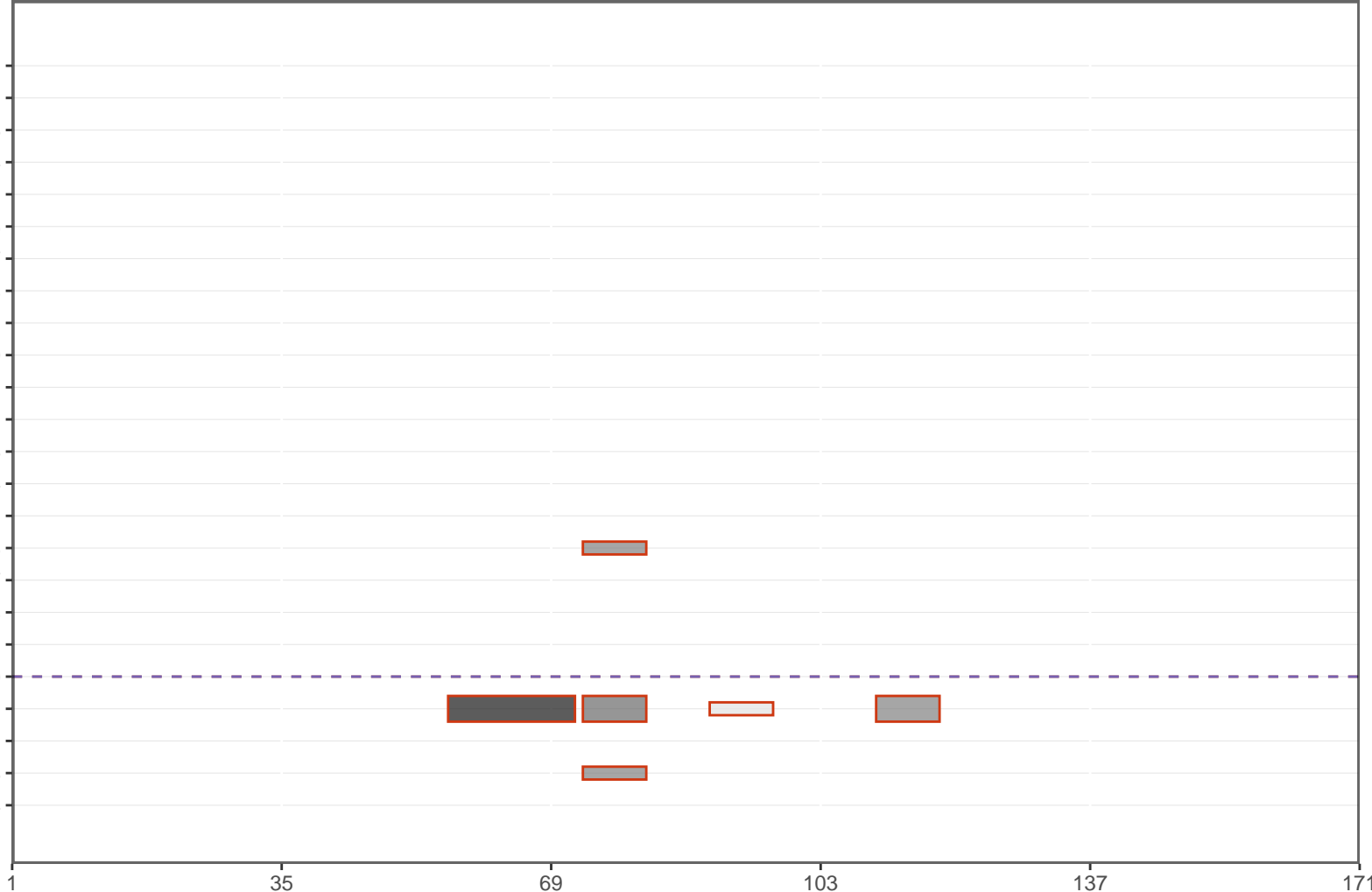
MW indication



Molecular weight

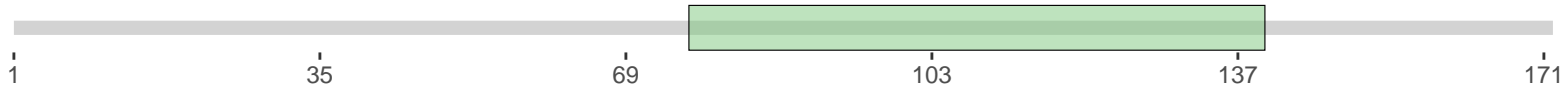


Gel Slice



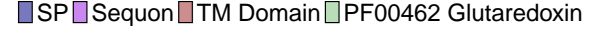
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

KENPVMYMKGVPELPRGFSLLAVRLKEVSPVIBARNILEDPELKNVAKFASHWPTFFQIFNGEFIGGSDILNMHGSGELKEKLTIAANGQKAE

NbL03g01650.1 uncharacterized_LOC107814272 [MW - SP = 38.87 kDa]

No. of times detected



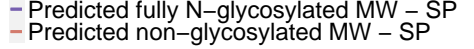
log(intensity)



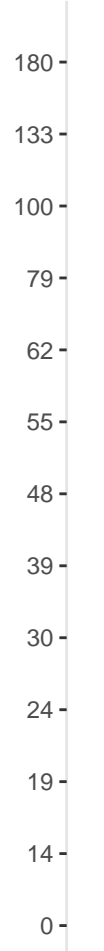
Values from



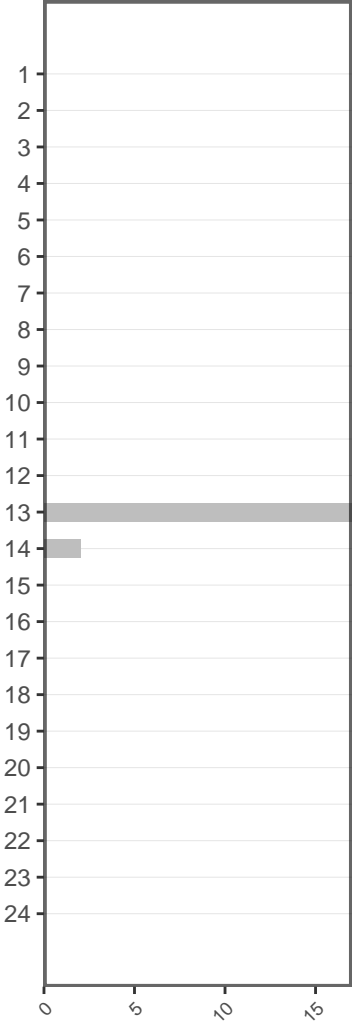
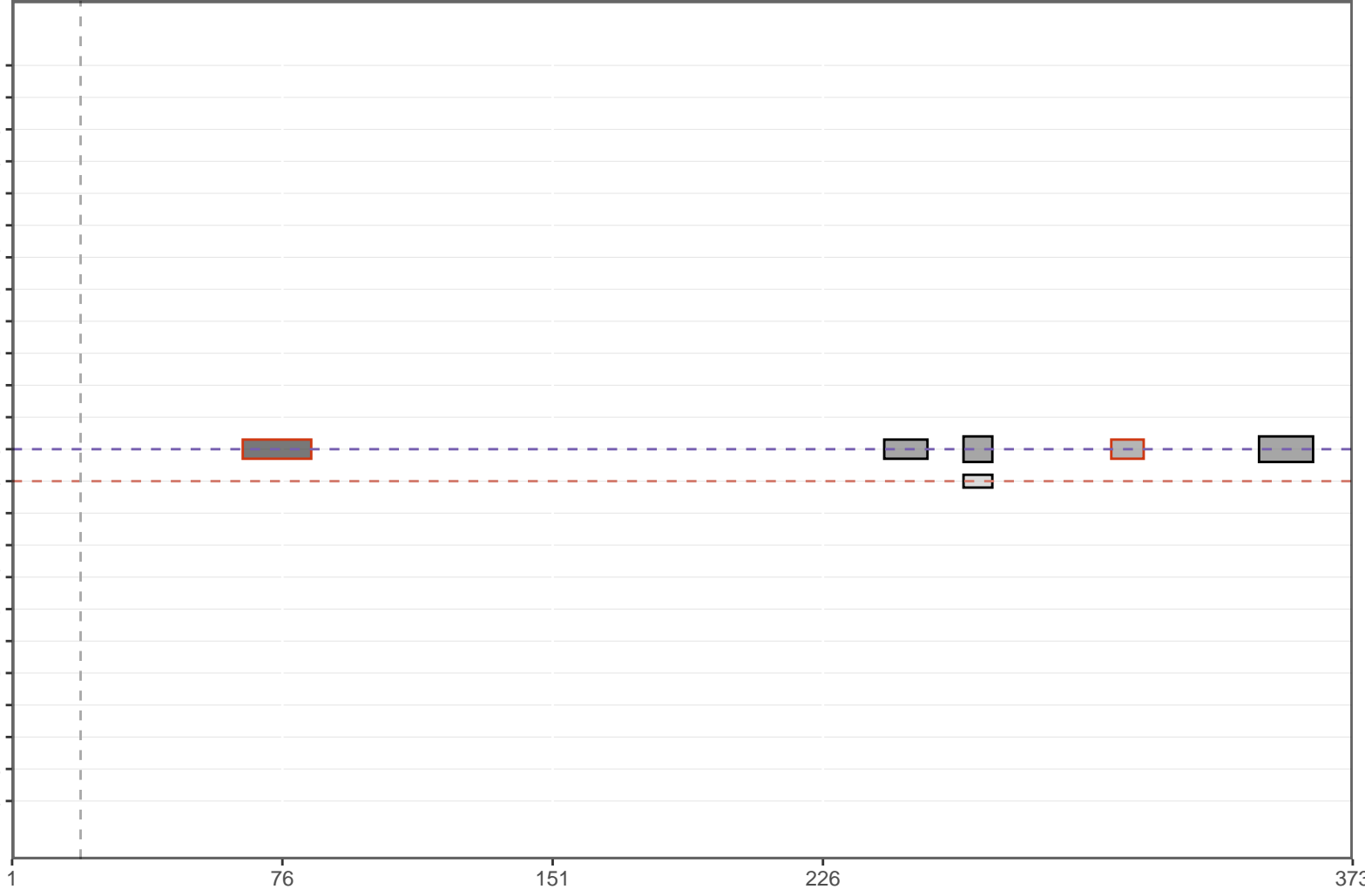
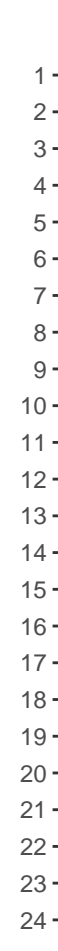
MW indication



Molecular weight

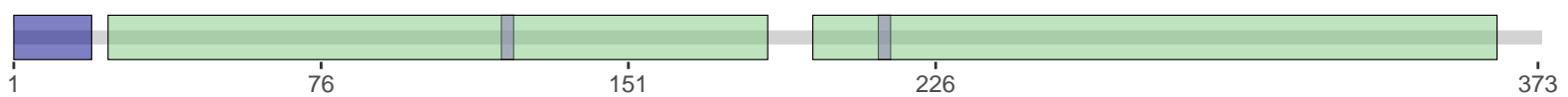


Gel Slice



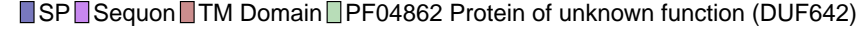
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

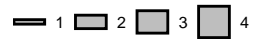


Protein sequence:

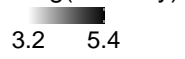
PACGFLIDFVALKAKTKRPRKGNMLKNGFEEGPIYFNTTWGVLIPNIEDHSPLLGWMEISKAVKVDKAEHETVPEGKRAVELVAGRESAAGVVRTRPGKIKYDLFISIGDAENSCEGEMLVEAFAGKNTMGFPYESKGGGFKRARLRLFTAISPRTRVRFLLSTYYHMKSDNSGSLGGPVDVDRVLGVGRNRPPI

NbL03g01570.1 heat_shock_70_kDa_protein_15-like [MW = 93.68 kDa]

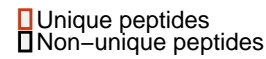
No. of times detected



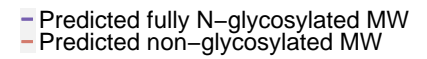
log(intensity)



Values from



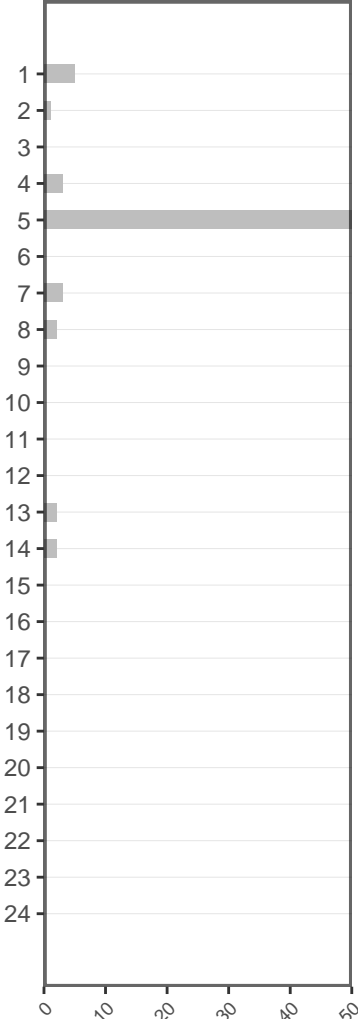
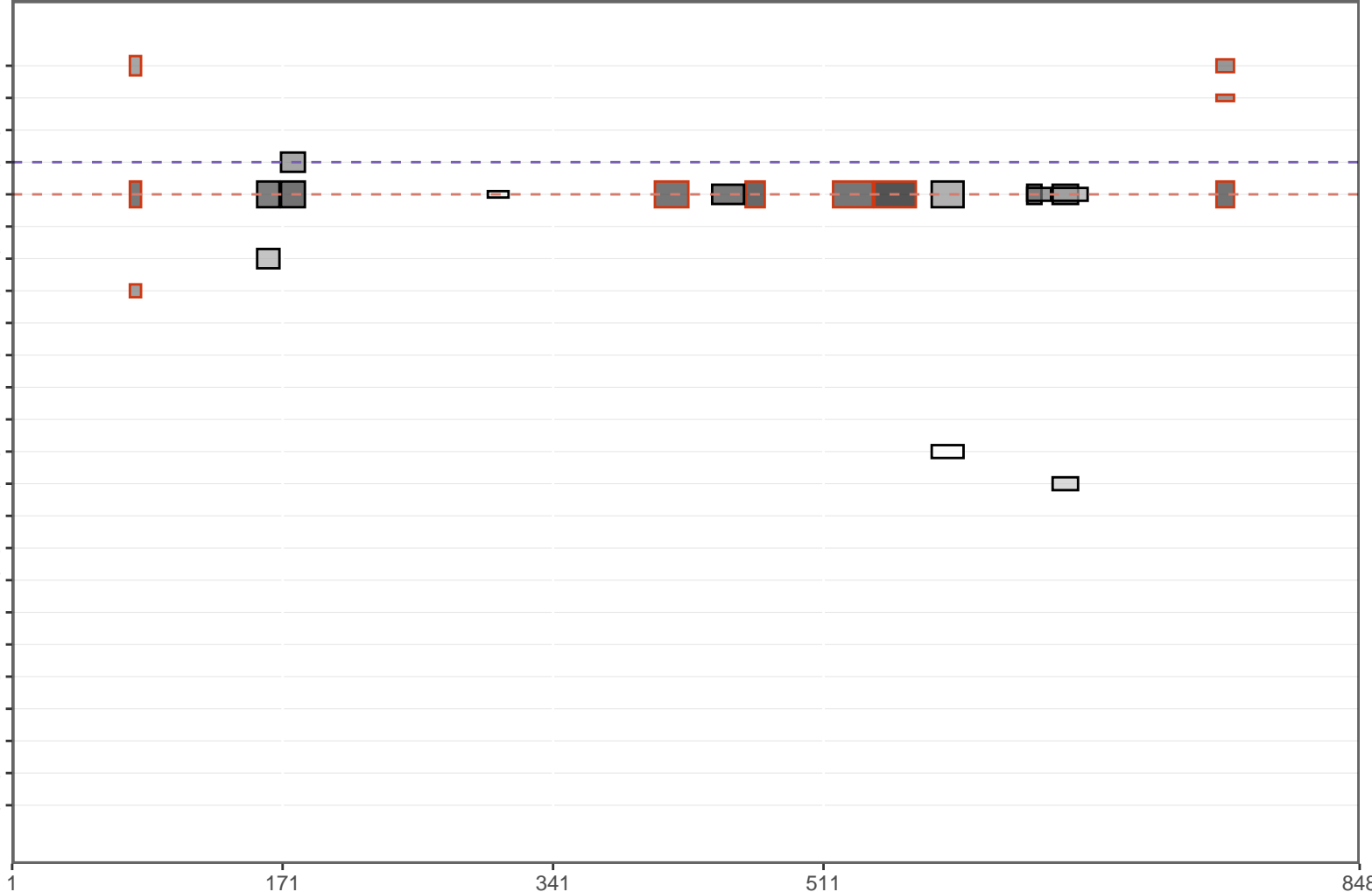
MW indication



Molecular weight

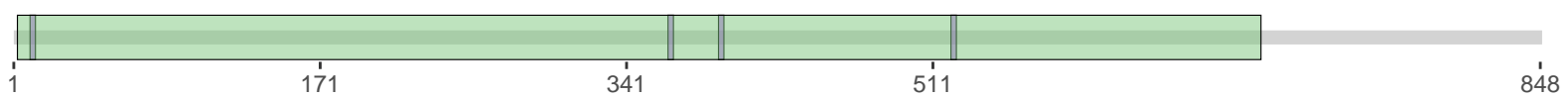


Gel Slice



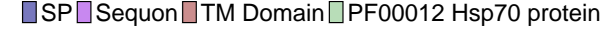
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

INQOSTIVFPKGNPPEVKALTFYRSGTFTDVAQADVSELGAPANISTYRIGPFQSTKGERAKLKWVRLNLHGIVVESATLLEEVEEVPVKEESKMDTNASADAPSTAEITDENMQDANKGADASGVENGVPESGDKPVEMATDKAEAPKIKKVKTNVPTVELVYGALAAADVQKAMEKEFEMALQDRVMEETKDKKNVAEAVYDMRNKLHKYQDFVVDSEREQFIKLGQVEDWLYEDGDEETKGVYAKLEELKGGDPHQRYKEYTERGSDVLAIC

NbL03g01550.1 nuclear_pore_complex_protein_NUP50B-like [MW = 47.73 kDa]

No. of times detected



log(intensity)



Values from



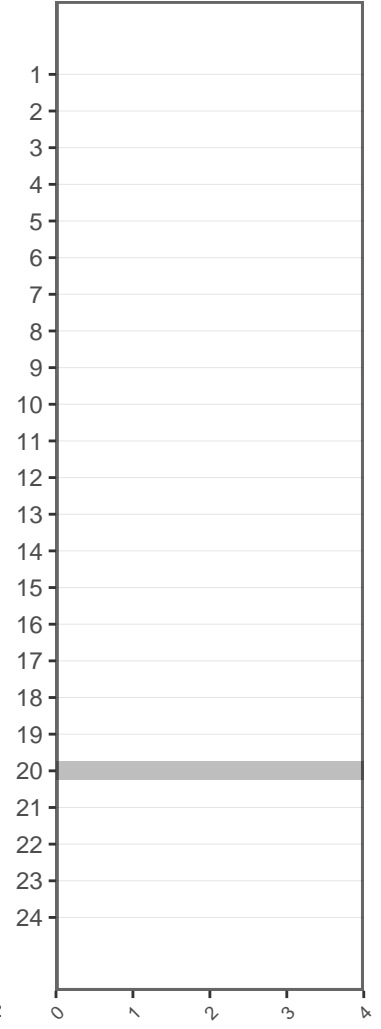
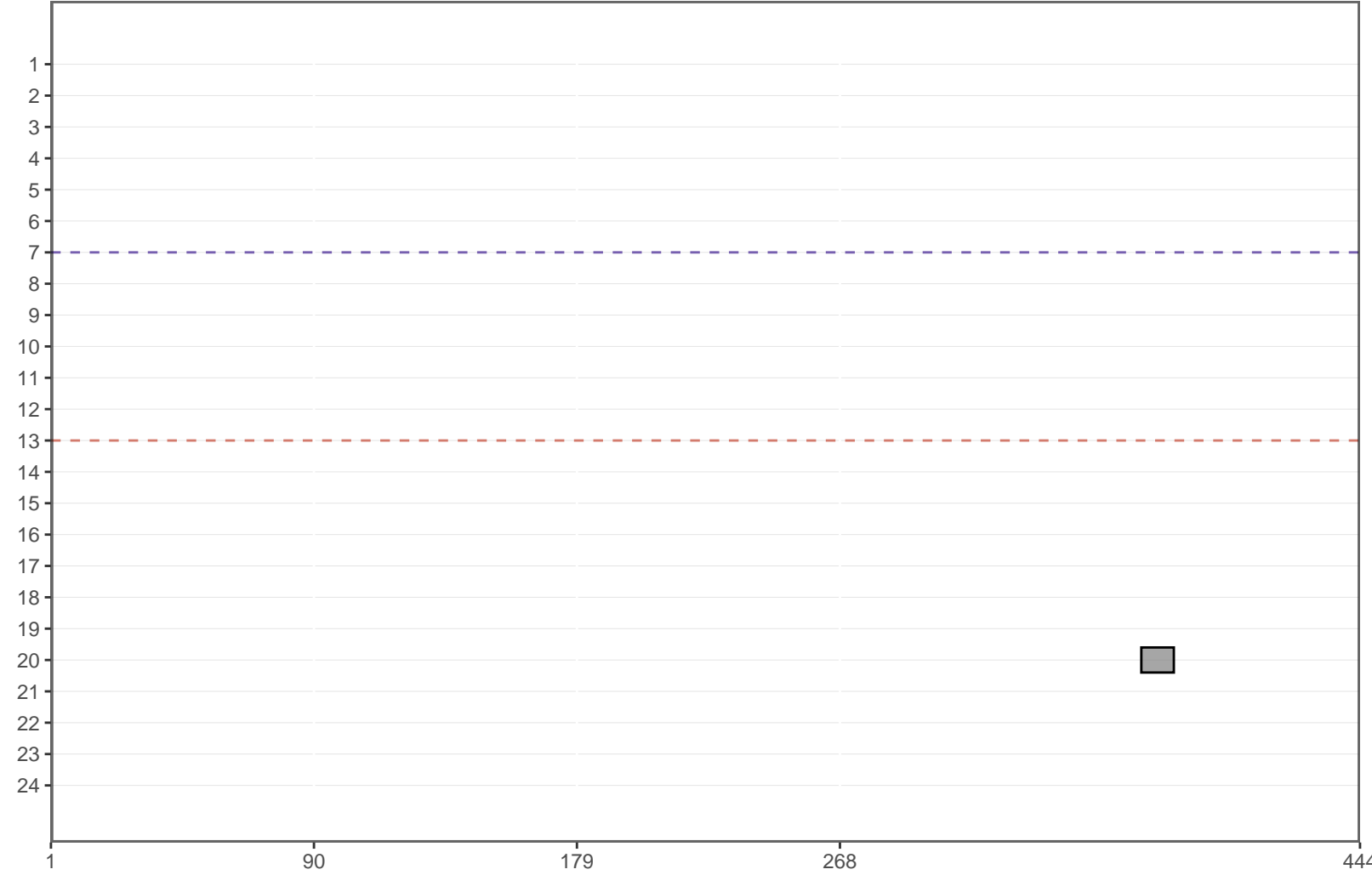
MW indication



Molecular weight



Gel Slice



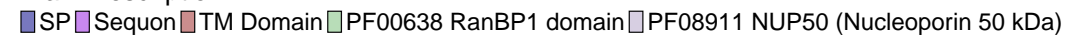
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SDGENEKGAETASFSFQGLS66QNAFTGLAGTGFNFTTFSGFVSSKESGSLPGQGLFGVKSDGSPFGLNLSSTNGNALSFGNSGSS6SVKSGEGHIGPKMGVFPVETGSENEKAIFTADALFEFLNGIWKERKKGELKLNISSETETGKARLVMRTRGNVRLILNANLYPEMKLTNMDKXGVTFACMNSAGDGKDGSLTALFKFDASIVVEFRVAVMEHKDKMPGSLKTPQNSP

NbL03g01480.1 N-alpha-acetyltransferase_16_NatA_auxiliary_subunit [MW = 102.98 kDa]

No. of times detected



log(intensity)



Values from



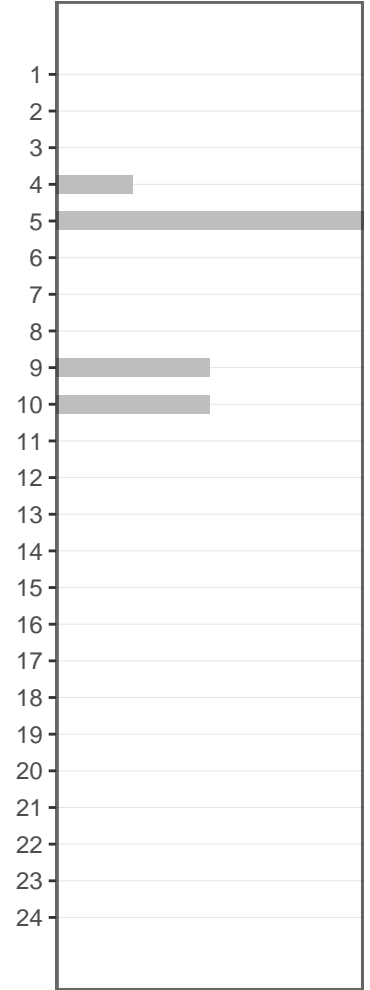
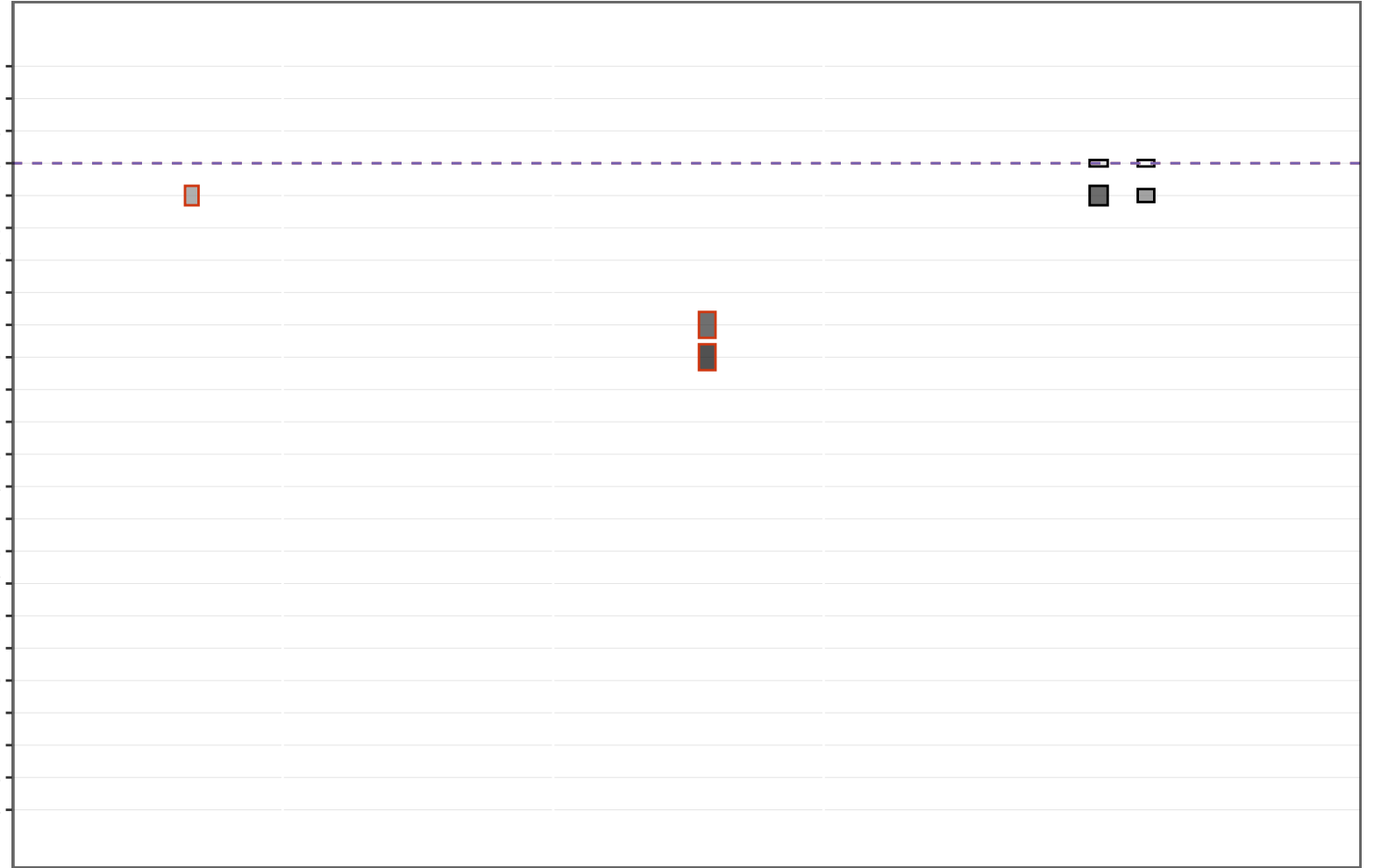
MW indication



Molecular weight



Gel Slice



Protein length

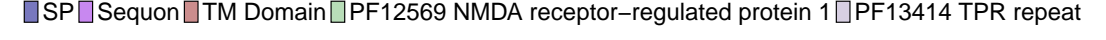


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

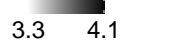
ARCMDLADRYINSEGVKRMIGADLVAAKNTALLFTKDDGDHNNLYDMQGMWVELASGEVYLRQGDLRALKFLAVEKHADITEDGDFDFHGVGLRKMTRMIVEMLKFQDRLHSHAFRKAASGAIRCYLRVYDPPKPSAAEEDDEMFKLPASQKKLFRKLRKAEARAKKEAEVKNESSESSVWKSQRKLRKPVDPDPHSGEKLAQIEDPLAEATKYLRLLLTHSSDFLETHLLSFEVNMRRKQKLLAQVKKHLVRLDADNPKSHLGLKFFKFFRVGALPVPVTDKEL

NbL03g01360.1 golgin_candidate_5 [MW = 114.88 kDa]

No. of times detected



log(intensity)



Values from

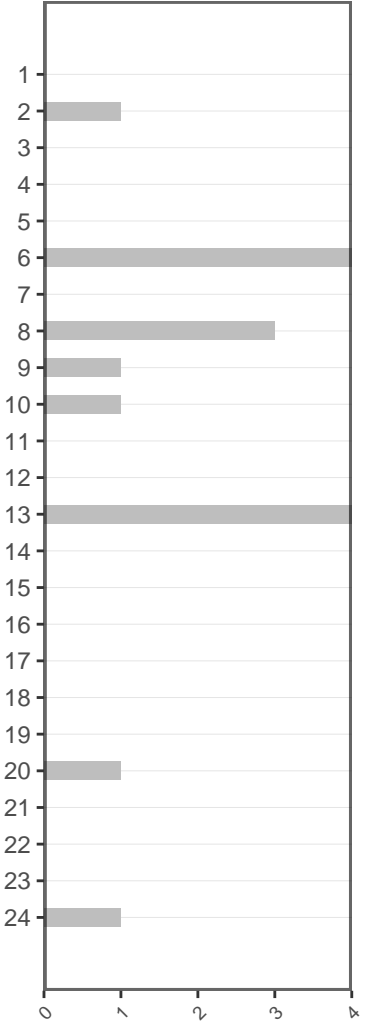
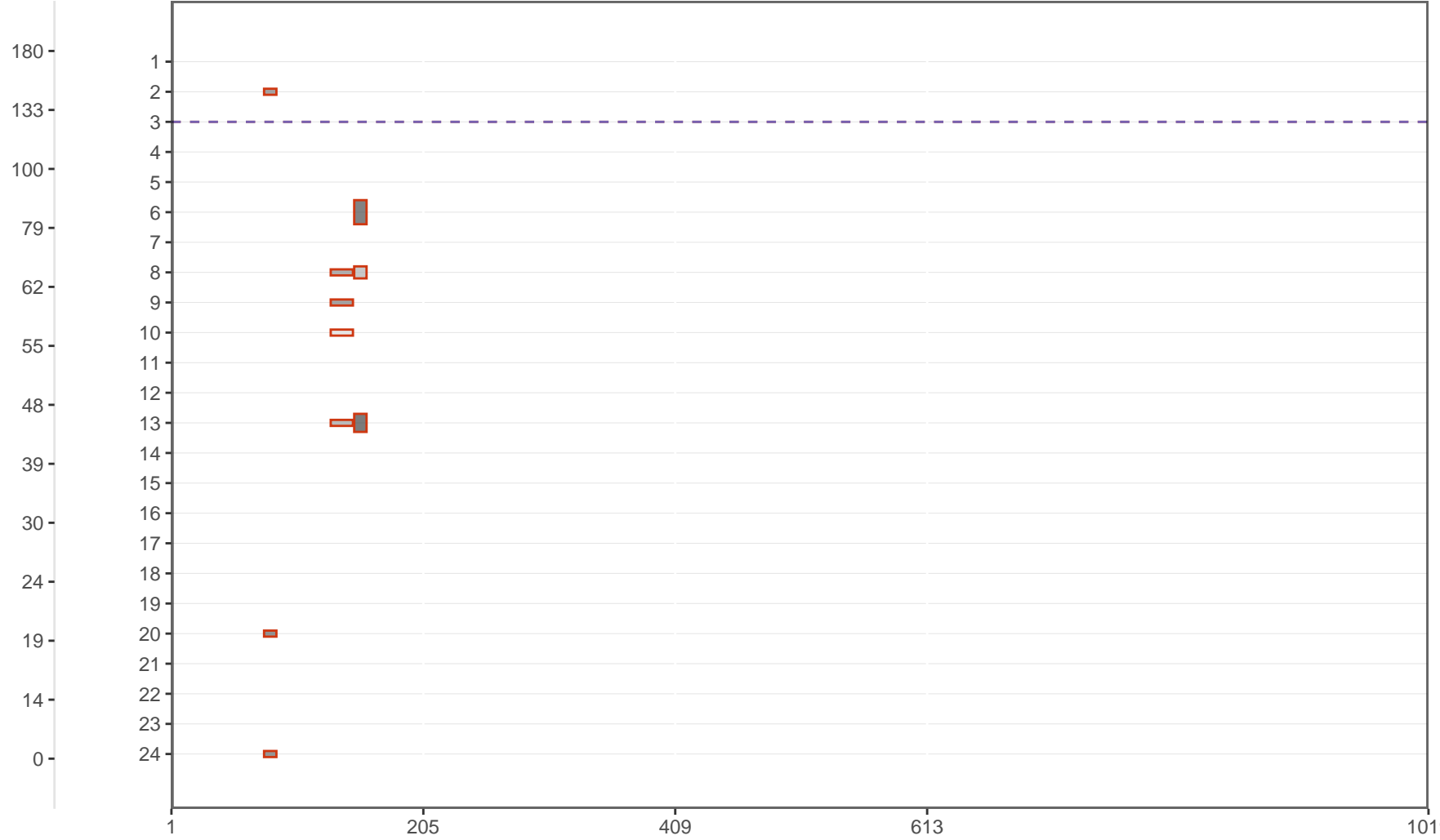


MW indication



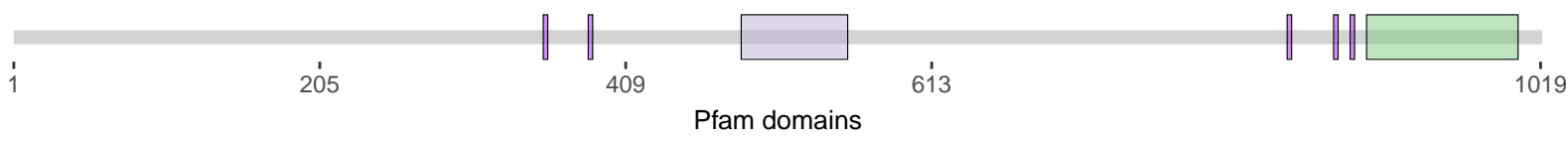
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

SP Sequon TM Domain PF12325 TATA element modulatory factor 1 TATA binding PF12329 TATA element modulatory factor 1 DNA binding

Protein sequence:

CDIETQVMAEGEQLSKQDAAGDAQMRKLRAGIRELEEEKGLLTKLVEEENKVESIKRDKATEKLLHETVKKHGAELATQKDYTNALNAAREAEALAEARANNNEARTQLEGRLEAEQREAMLVQALEELRGLTSRTQGGAVFREDMLRRDIEDLQKRYGASERRRQEEELITQVPESTRPLLRQIEAMQETNARKTTEAWAAVVERTLNRRLQGEAEKAAATAEKERISERLGGTLERINLVLEAGISCLRAEQTQLTRBLDKERORAGENRGEYLAALKEAEASNEGRVYOLE

NbL03g01030.1 beta-galactosidase-like [MW = 93.86 kDa]

No. of times detected



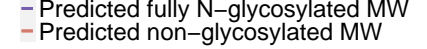
log(intensity)



Values from



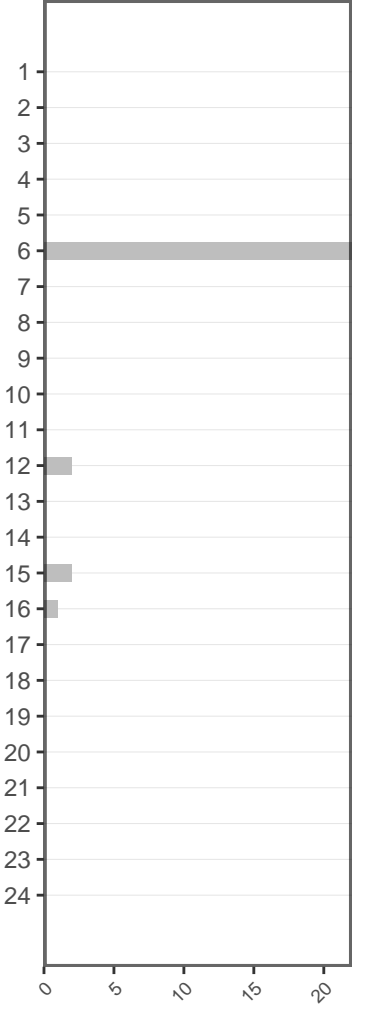
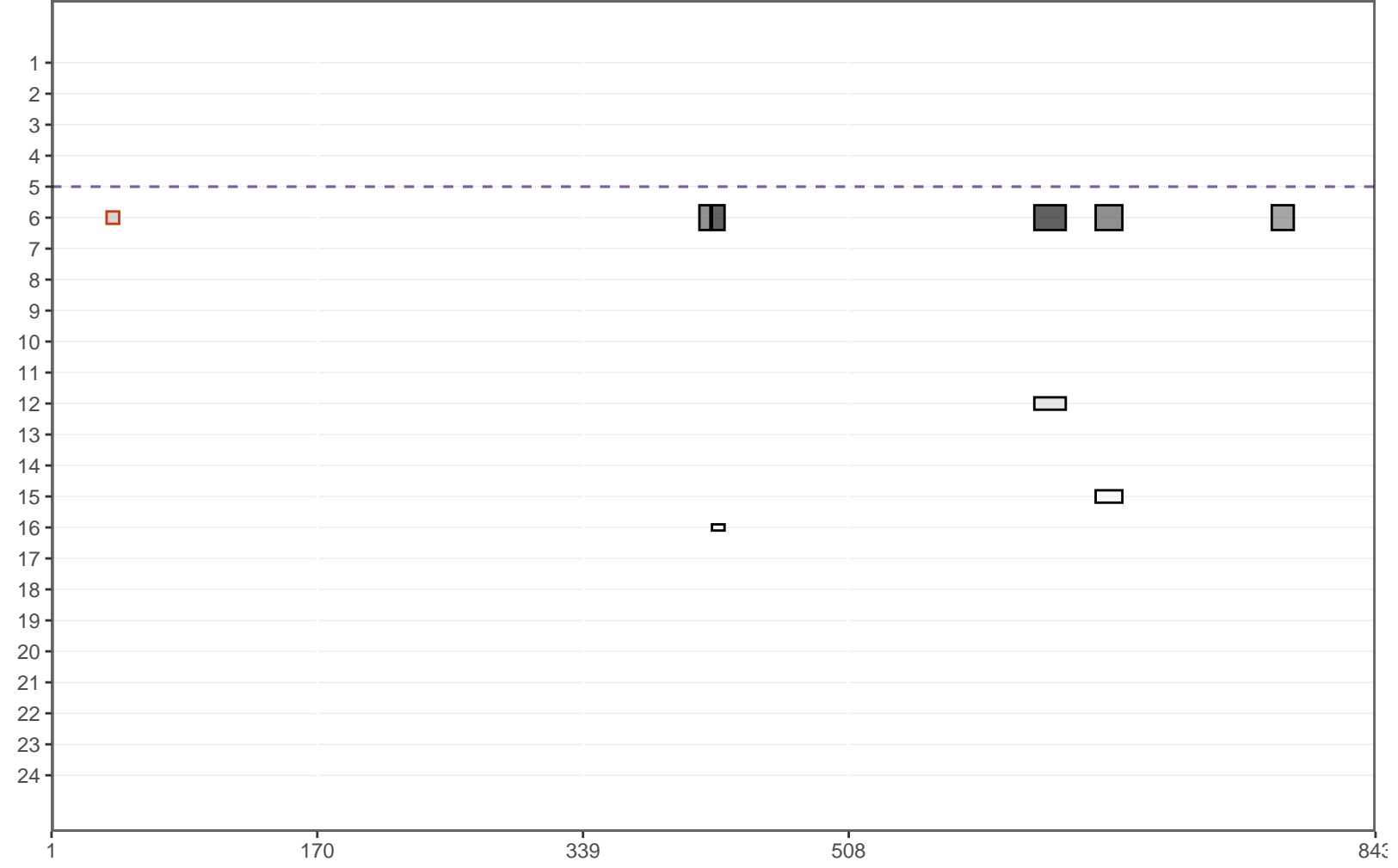
MW indication



Molecular weight

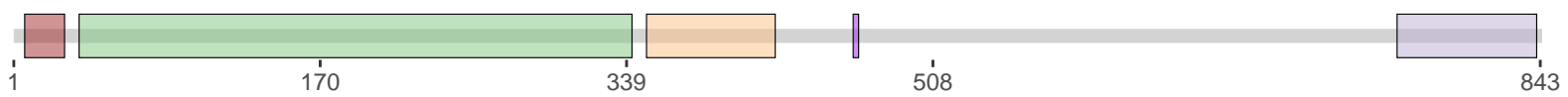


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

INTVYNTARVGLQASALMMKTPNIRGFSWQBYNDPFAVEYEDNTFTVGLLEQINTRDVSQVWYMTDVKIDPREGLFSGGKWPWLRVSSAGPALHVFVNDQLAGVYVGLSKGKLTFNKAVNLRADYVNIKSLLSAVGLNIGHFETVNTGVLGPVLSGLDDEKRDLTWQKWKYVGLKEALNHLGLSGSSVEVVEGSLVAGRQPLTWFKTTFNAPKGNPLALDMNMMGKGGVWVWNGSGRYPWPGYKASGTCGAGNAGYVFNEDKQDNCGEATORWYVVI

NbL03g01000.1 protein_HOTHEAD-like [MW - SP = 63.77 kDa]

No. of times detected



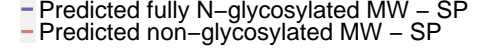
log(intensity)



Values from



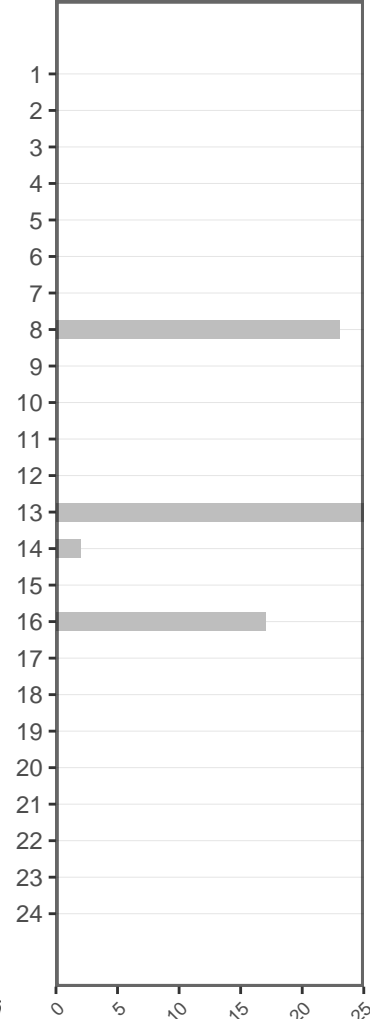
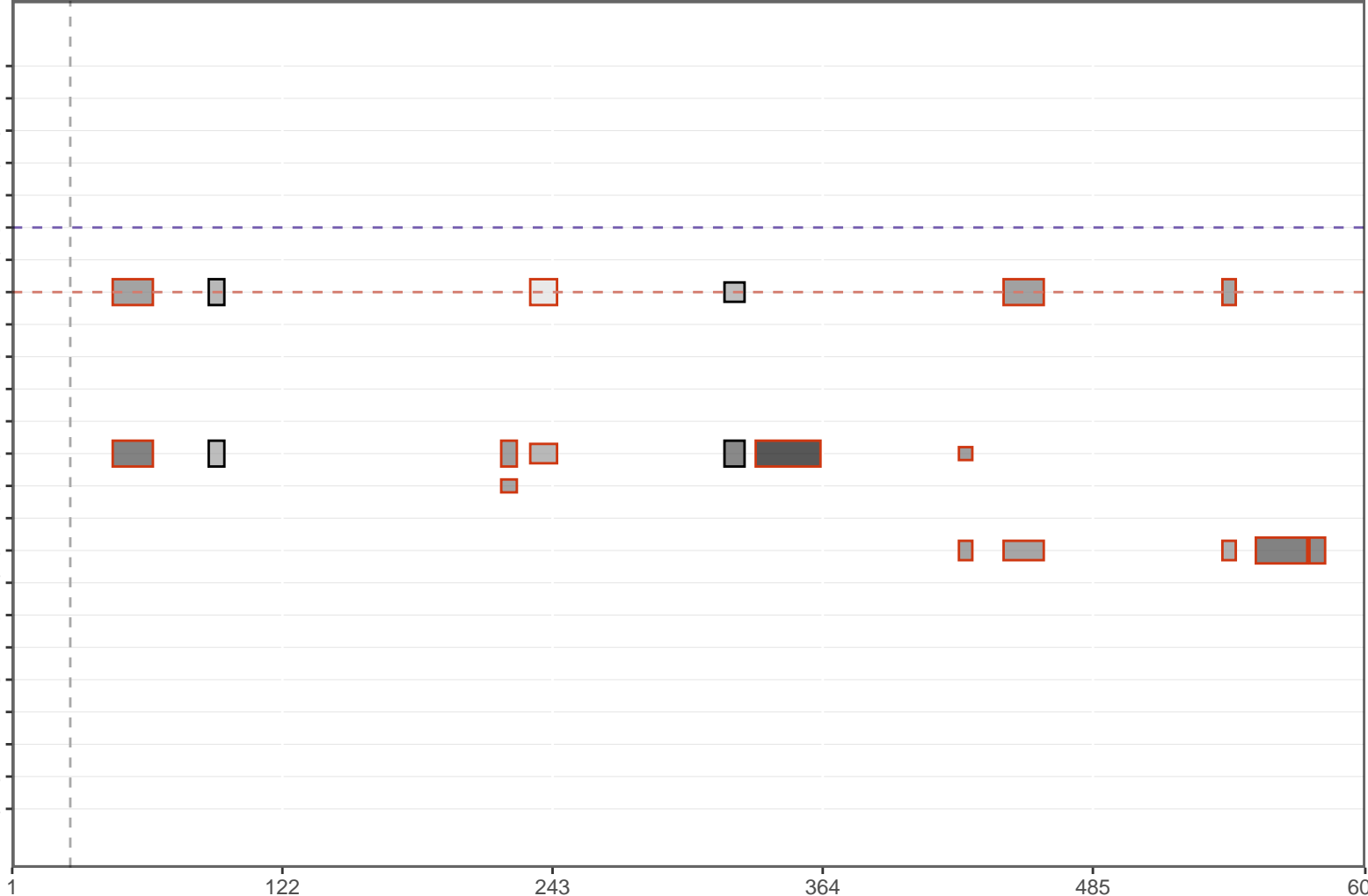
MW indication



Molecular weight



Gel Slice



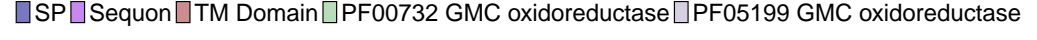
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

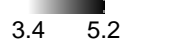
IASLEILSSGAGSPQMLMGGKPKLEKELKINPLVLDNKKFVGGKMSDNLNTIFVPTNRPVEGELKIQTVGDKMGVYIEASGGYGGTDEDIRKNGVSAEIGQLSTIPPEQRAGEAEMKRNKNVPGVEFRGFLAKIATPLSTGKSLKSTNDDNPSEVTFNYSFHPDLKRDVNGIRLMEKLVKSHFNNTYGGKELFLKLLNLSVQANILPKQNTDTESELEGFCKDKLTLTWYHGGGHGKVAFTSDVRYVNIHRLRIVDGGTFTTESPGTNPQATLMMAGRYMGVQI

NbL03g00970.1 beta-galactosidase_17 [MW = 80.87 kDa]

No. of times detected



log(intensity)



Values from



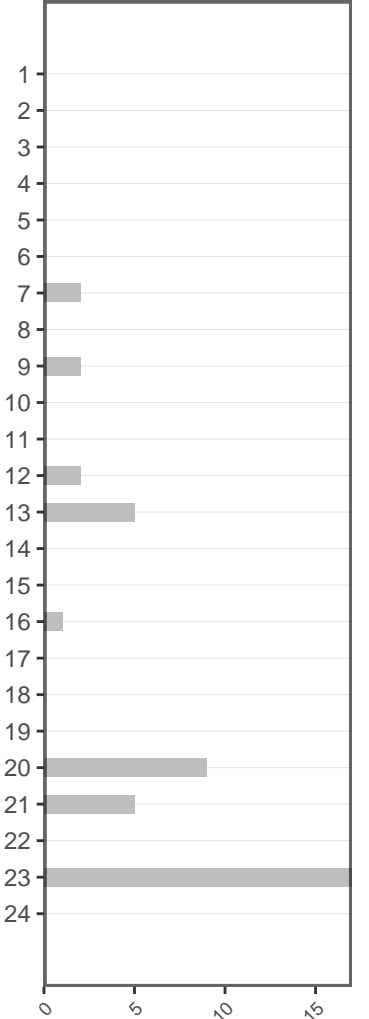
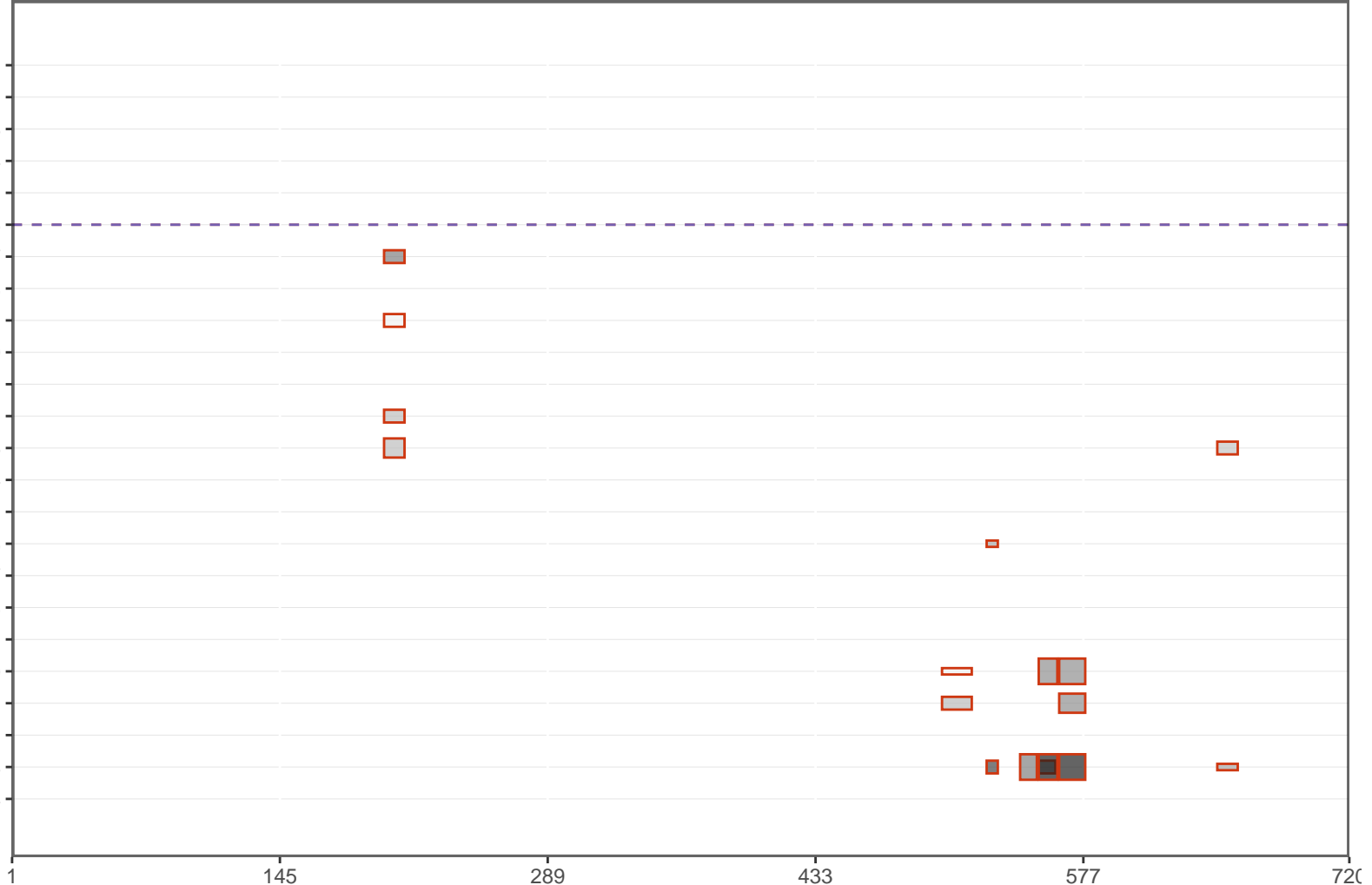
MW indication



Molecular weight



Gel Slice



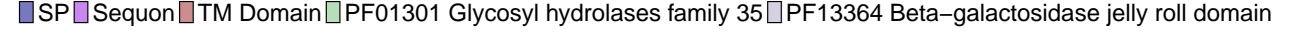
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YLERILSRNGSAVLYMAHGDTNFGFYSGANTGADESDDPKPLTSYDYPDPIKESGDDNPKYQALRRVIAKYTAAPLASVPPNNEKKAYGLIKGQTKSFLNIDTKYFDGVTSEEDPLAMELGGMFGMFYVSDYKAKANGSLLFIPKVRDRGQVFCISPENNEEIPKYVGTIVRWSNTPRLLPHTGCGSSGSKIVLNVEMGRINYGQYFDKNGILSPVYLDGELPHKWKMLPIPFHNLNEDQQGDSVSDAYTNLGNBVRKLNKRNINYPPEAFYAGHLTVDYKDTLSFF

NbL03g00820.1 threonine_synthase_chloroplastic-like [MW = 61.9 kDa]

No. of times detected



log(intensity)



Values from



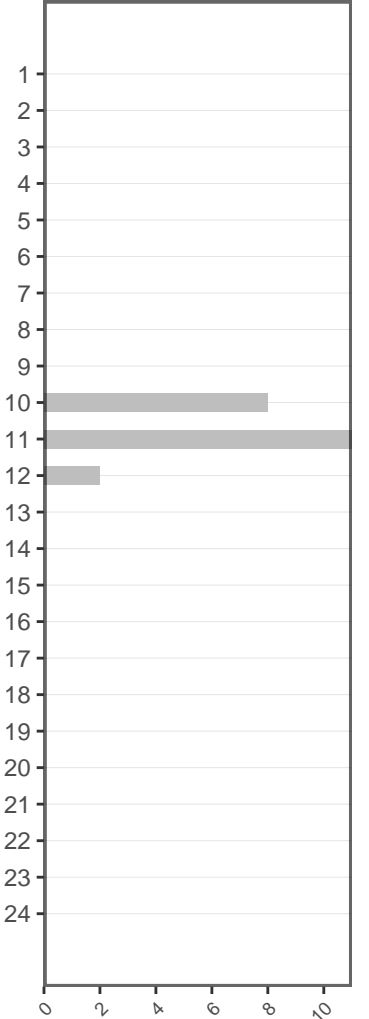
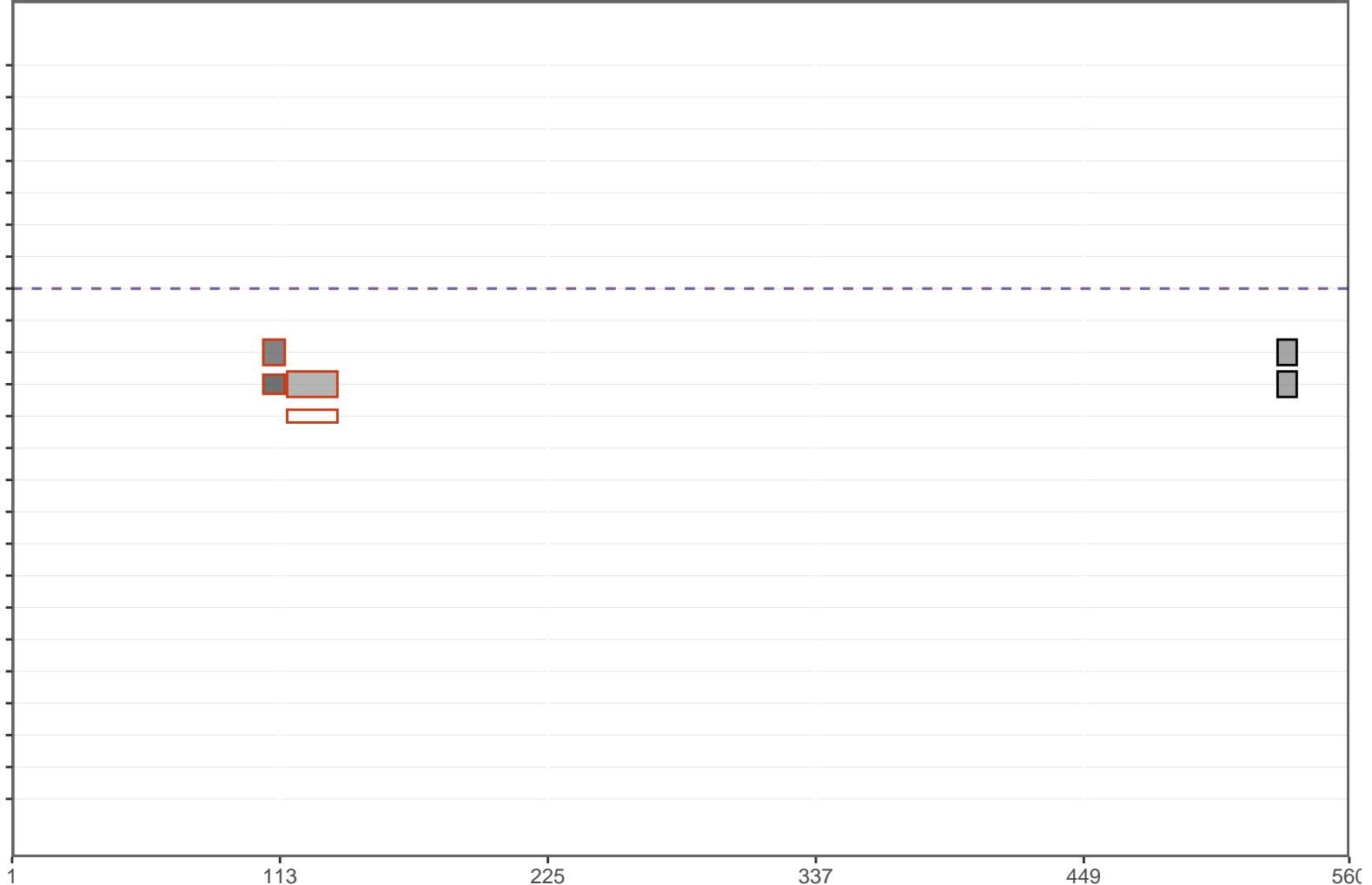
MW indication



Molecular weight



Gel Slice

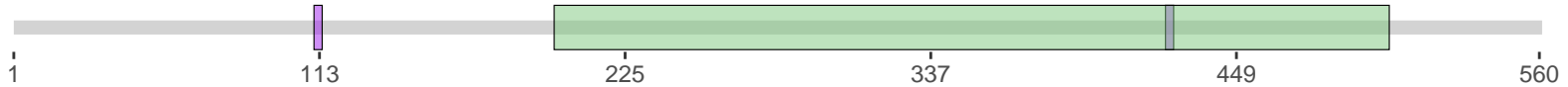


Protein length

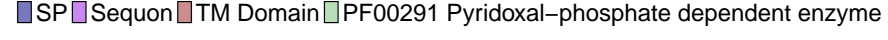


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ISTGDTSAALSAYCASAGIPISVFLPANKISMAGLVPIANGAFVLGLDTDFDGGMQLIREVTALPEYLLANLSLRLEGGKTAIEILGGFDWEVDPDWIIPGGNLGNHAFYKGFQGMCKELGLVDRIPRLVCGAANANPLVLYHYKSGWKEFKSVKANTTFASAIGIGDPVSDRAVALGNSNGIVEEATEEELMDAMAGADSTGMFGICHTGVALTALSKLRKTKGVIRPDRVAVVSTAHGLKFTQSKVQVHSHKEKNMEGRFANPPVQVKAADFGSVMVLLKYLKLSKNSKIP

NbL03g00730.1 subtilisin-like_protease_SBT1.4 [MW - SP = 79.85 kDa]

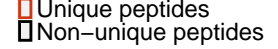
No. of times detected



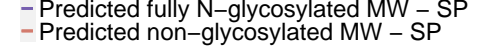
log(intensity)



Values from



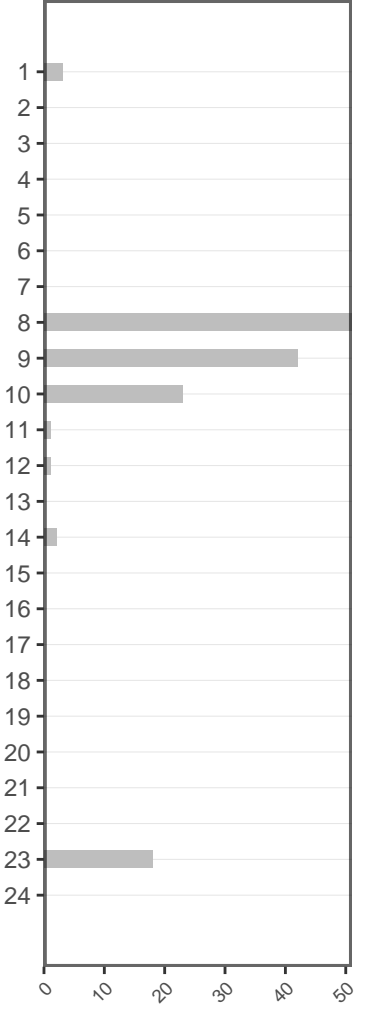
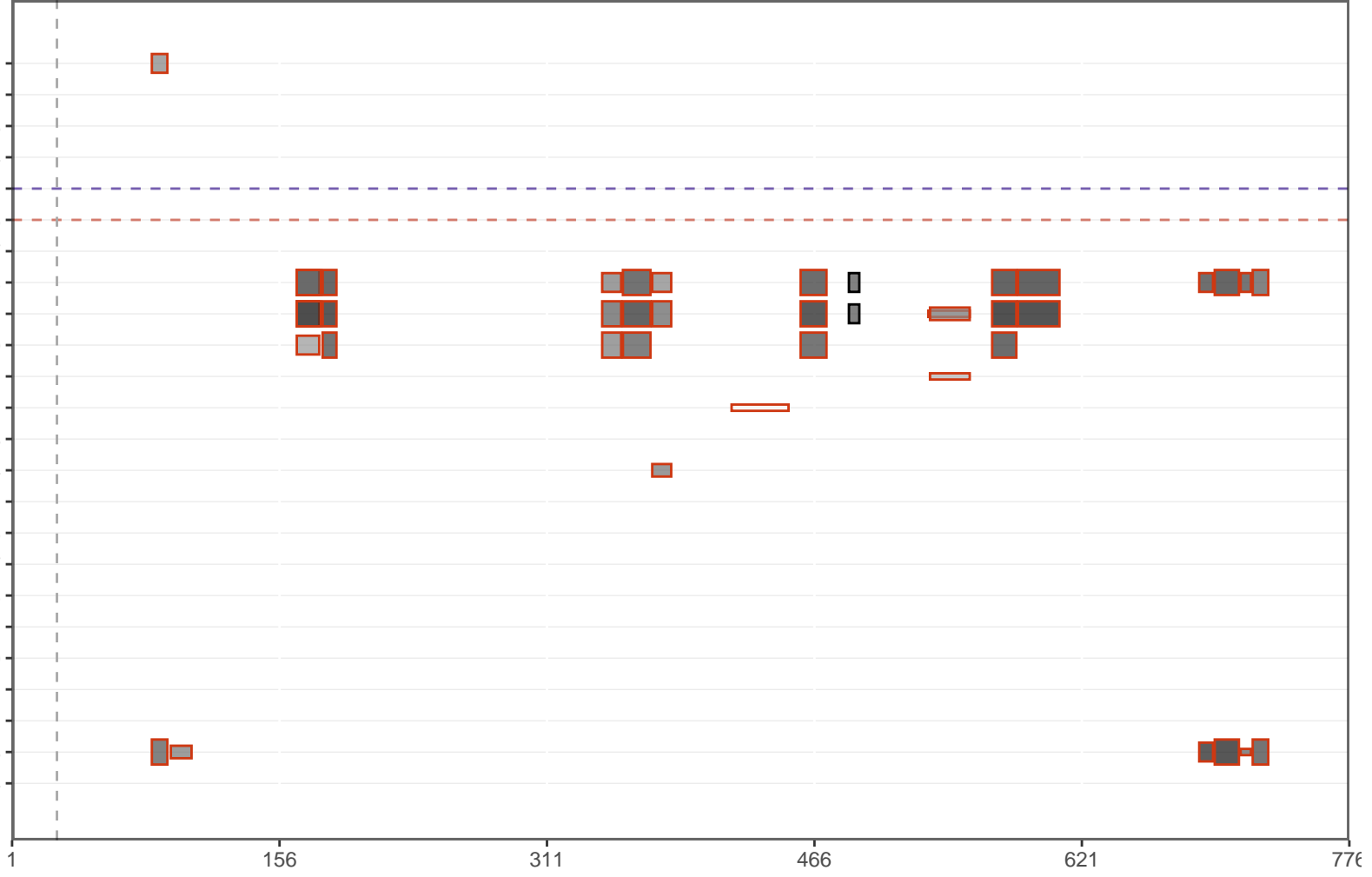
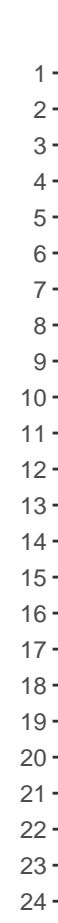
MW indication



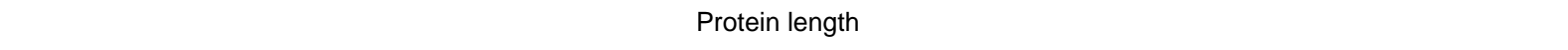
Molecular weight



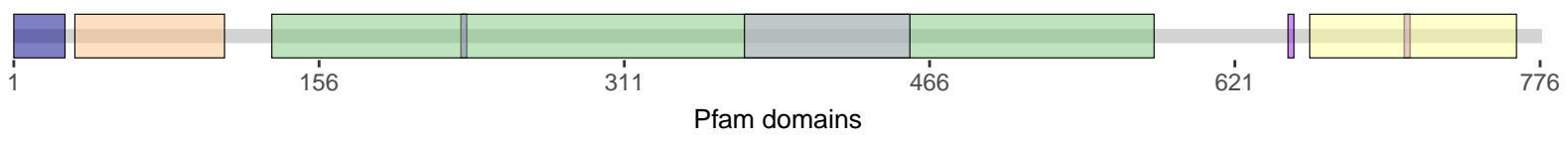
Gel Slice



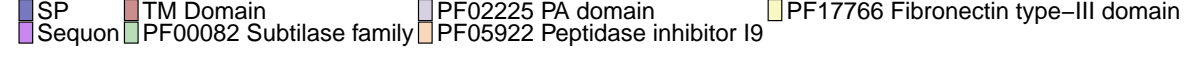
Protein length



Pfam domains



Pfam Description



Protein sequence:

GDCGSKYCYPKLDPKPKVAGKIVLGDGRGGARVKEKSAVKGAGGVMILANLADSGEELVADSHLLPMTMVGKAGDKRHHVTSQPSPTATVFRGTGKGPAPARVAAFSSRGNLTPRELKPKVAPGVNLAGWGTGSGVFTDLDIDTRRVEFNISGTSMSGPHVGGLAALLRRAHFKWTRPAVKSALMTAVNLDNSGKVFDTLDTGGESTPEVHGGSHVDPNRLDPLGVDETSQVNFVLFSGVYDGGDVAVFARDSSRVNDSERSLATPGOLNYPFSVYFTGI

NbL03g00600.1 alanine_aminotransferase_2-like [MW = 58.35 kDa]

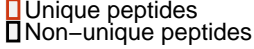
No. of times detected



log(intensity)



Values from



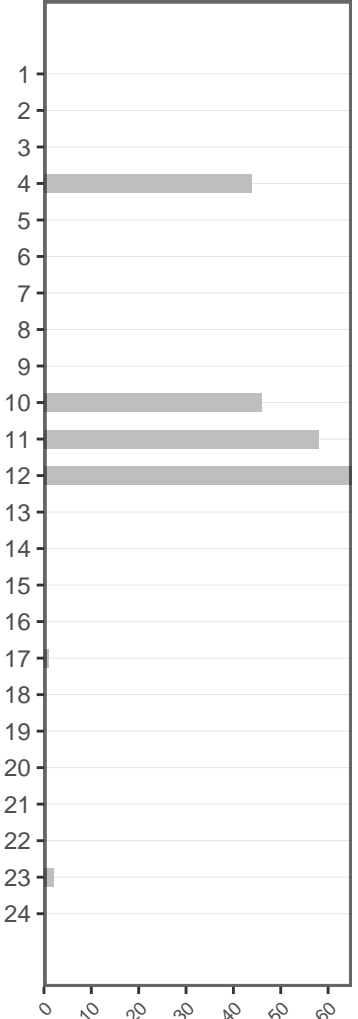
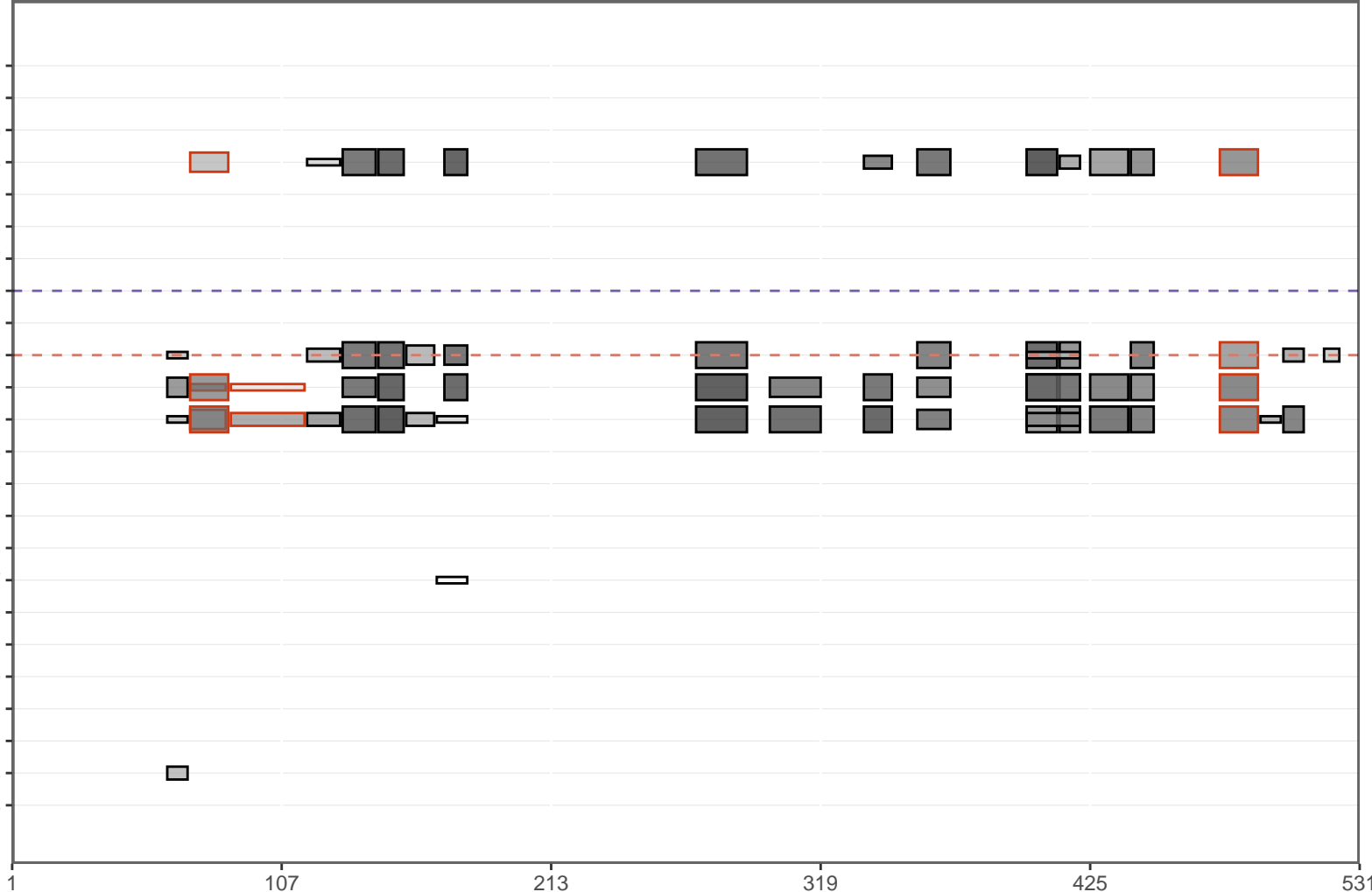
MW indication



Molecular weight

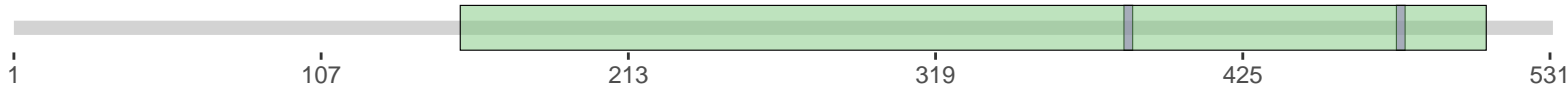


Gel Slice



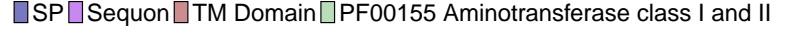
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

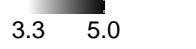
EQQLKTAASKGIDVRAALVNPQNPDTGGVHGEANGREVEFGKREGVLLADEVYGENVYVPDKKFKHSFKVSRBMGYGKNDLVSFGVSGKGFYGEQKRGYMEVTFGFSFEVREGQYKASVNLGNISGGQIAGLMSPPKVGDESYESFSAEKEGLSSLARRAKTLEDALNSLEGVTCNRREGAMYLFRRINLPDKAKAAEAATAPDAFYAKRLNATGVVYVPSGGRQVPGTWHFRCTILPGEENPAVWRILTEFHEKFMNERG

NbL03g00450.1 uncharacterized_LOC107810895 [MW = 44.37 kDa]

No. of times detected



log(intensity)



Values from



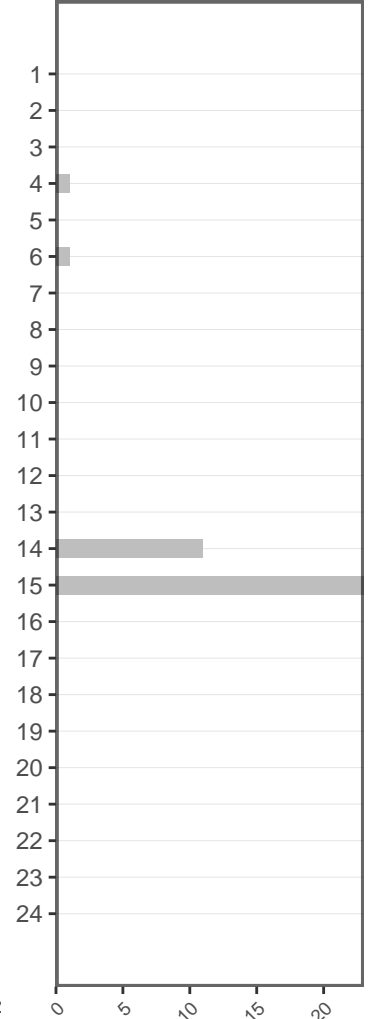
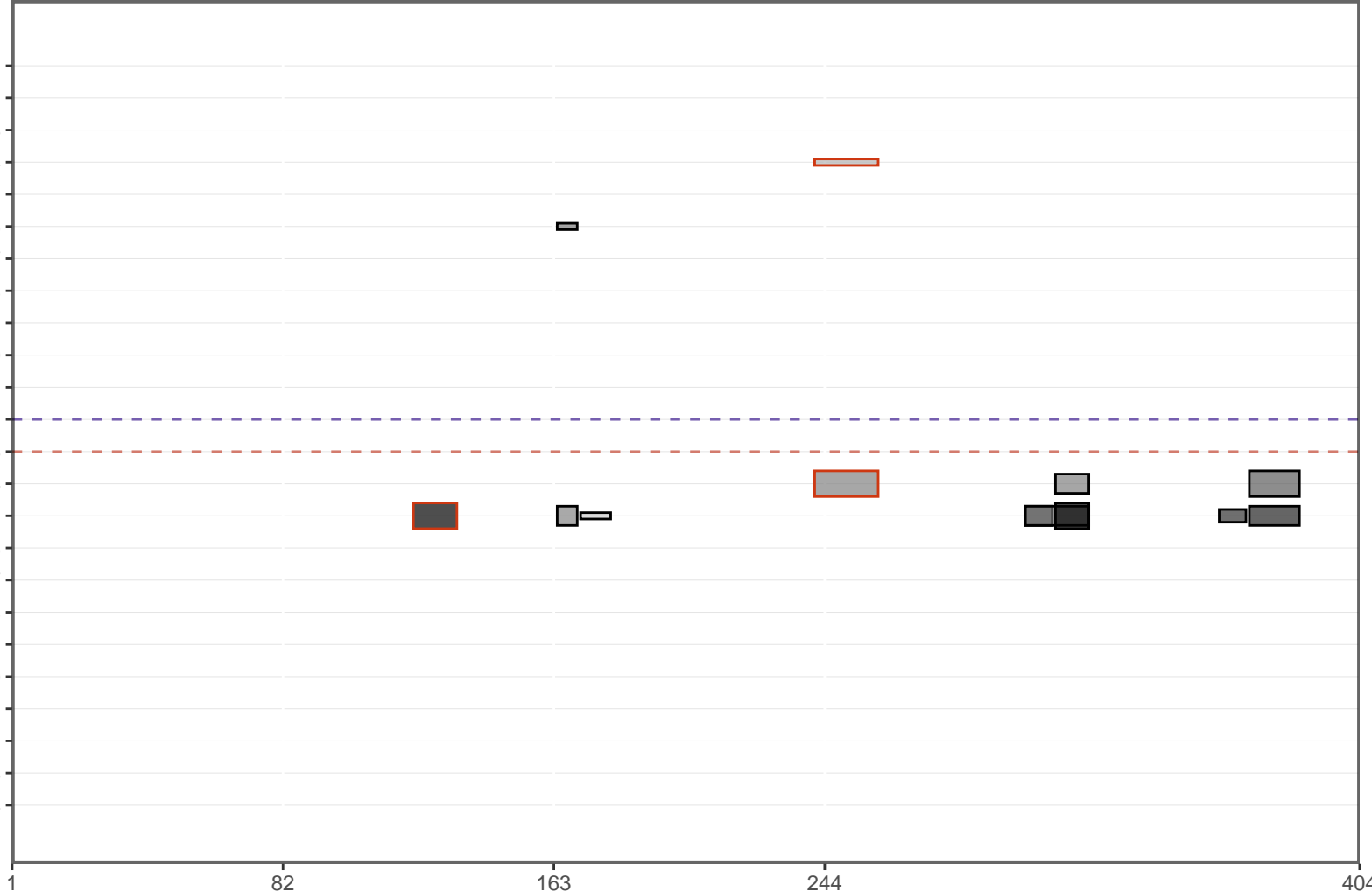
MW indication



Molecular weight



Gel Slice

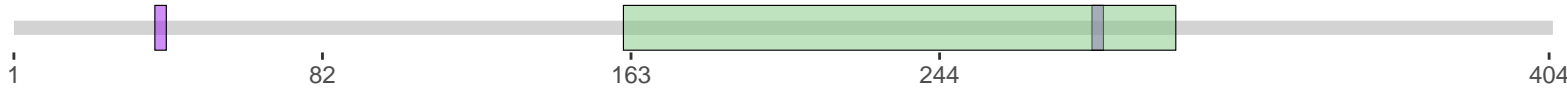


Peptide counts over 4 repeats

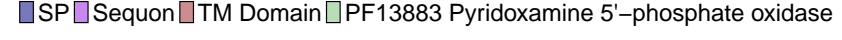
Protein length



Pfam domains



Pfam Description

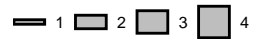


Protein sequence:

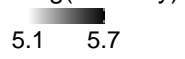
YPFGLVDFAPDSMGHPFSSFLAHTRNLLADPRGTLVQHPQWSSLNARVTFGDVPLPEDDGEWAKKQYIAKHGGPSSQGNFFYFRMGNISDNYFIFGGFTVAWVQVKEYETLQPKIAVDGSEGNLKEINAIFSKPLKDLIGQEAEVDDAALISIDSKGTDVRRVGGAGFNVRISFEVGHVGTLEEAKAALWKLNGGQVYVNGK

NbL03g00400.1 V-type_proton_ATPase_catalytic_subunit_A [MW = 49.81kDa]

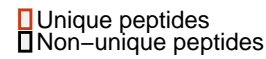
No. of times detected



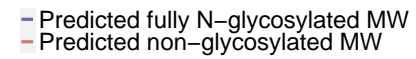
log(intensity)



Values from



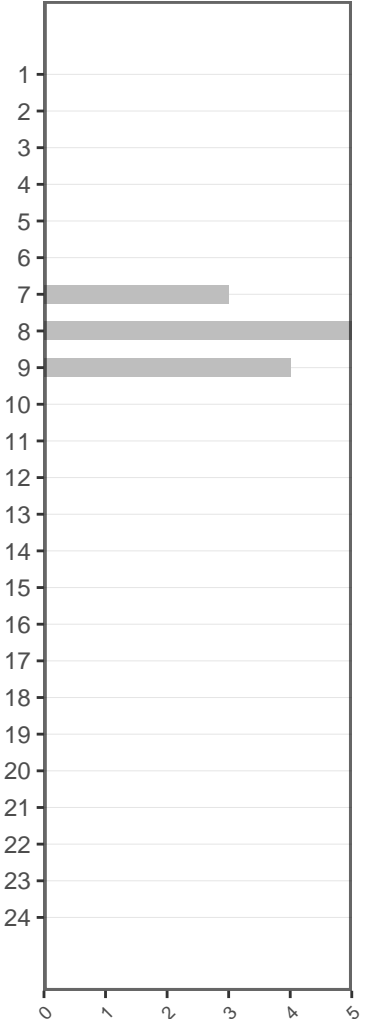
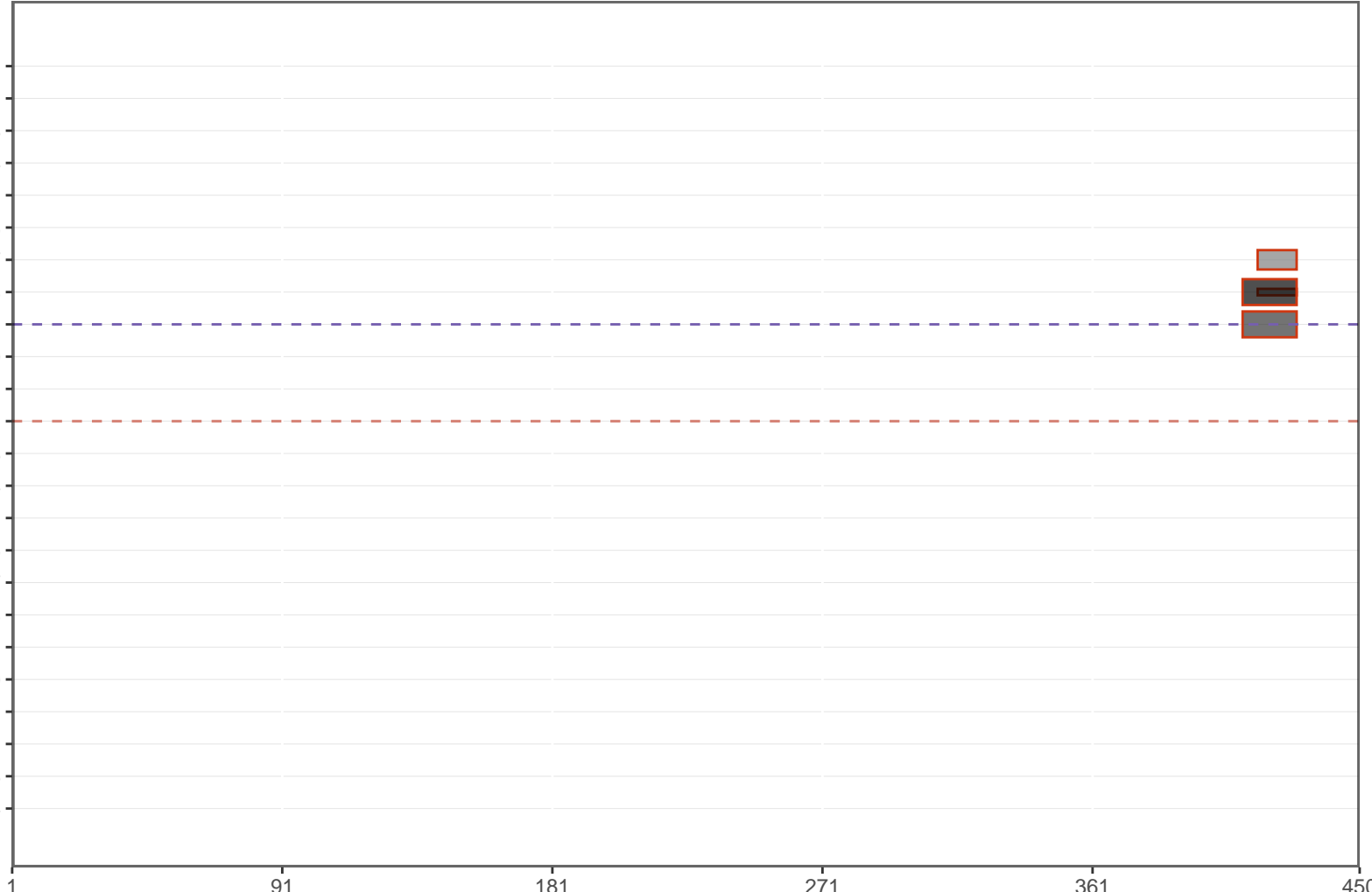
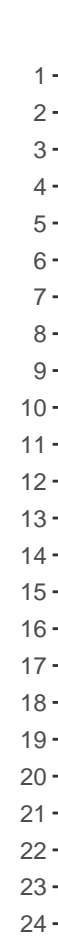
MW indication



Molecular weight



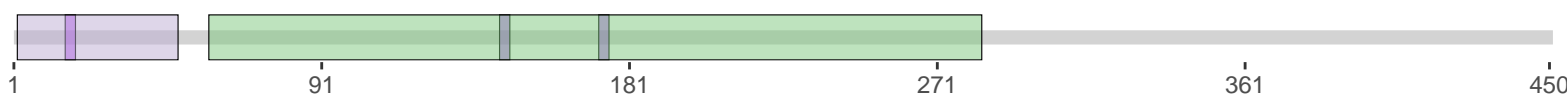
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00006 ATP synthase alpha/beta family, nucleotide-binding domain
- PF16886 ATPsynthase alpha/beta subunit N-term extension

Protein sequence:

RLASPYERAGKYKGLGGPERTGSVITWGAVSPGGDFSDPVTSALGVQVDFVGLDKKLAGRNKIFPQVNWLSYKYGSALESFYKDFSDIFDIRKAREVLGQREDDLNEVQLVGDALAEQDKITLAKLLREDVLAGNAFTPYDKFCPPYKQVWMLRNHIFVSLANGAVERGAGMDGQKTYTLKIRHLGDLFVRLVSGKFDPEGEVGLVGFKKLHDDLTAGFRNLEDETR

NbL03g00220.1 60S_ribosomal_protein_L15-like [MW = 24.19 kDa]

No. of times detected



log(intensity)



Values from



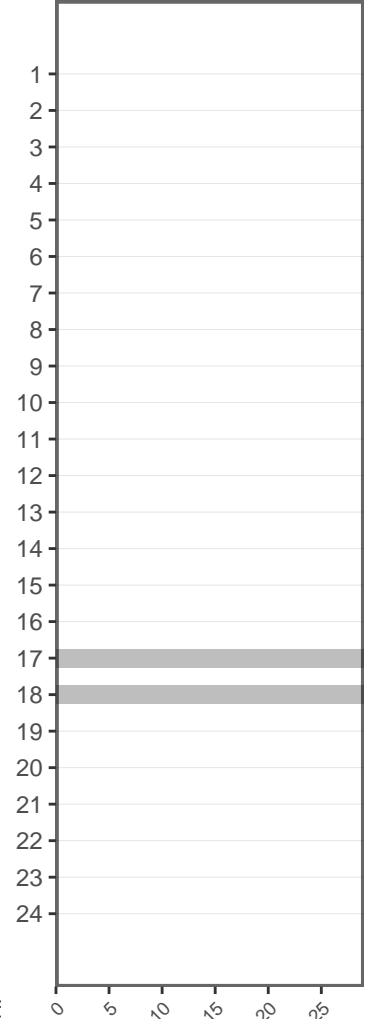
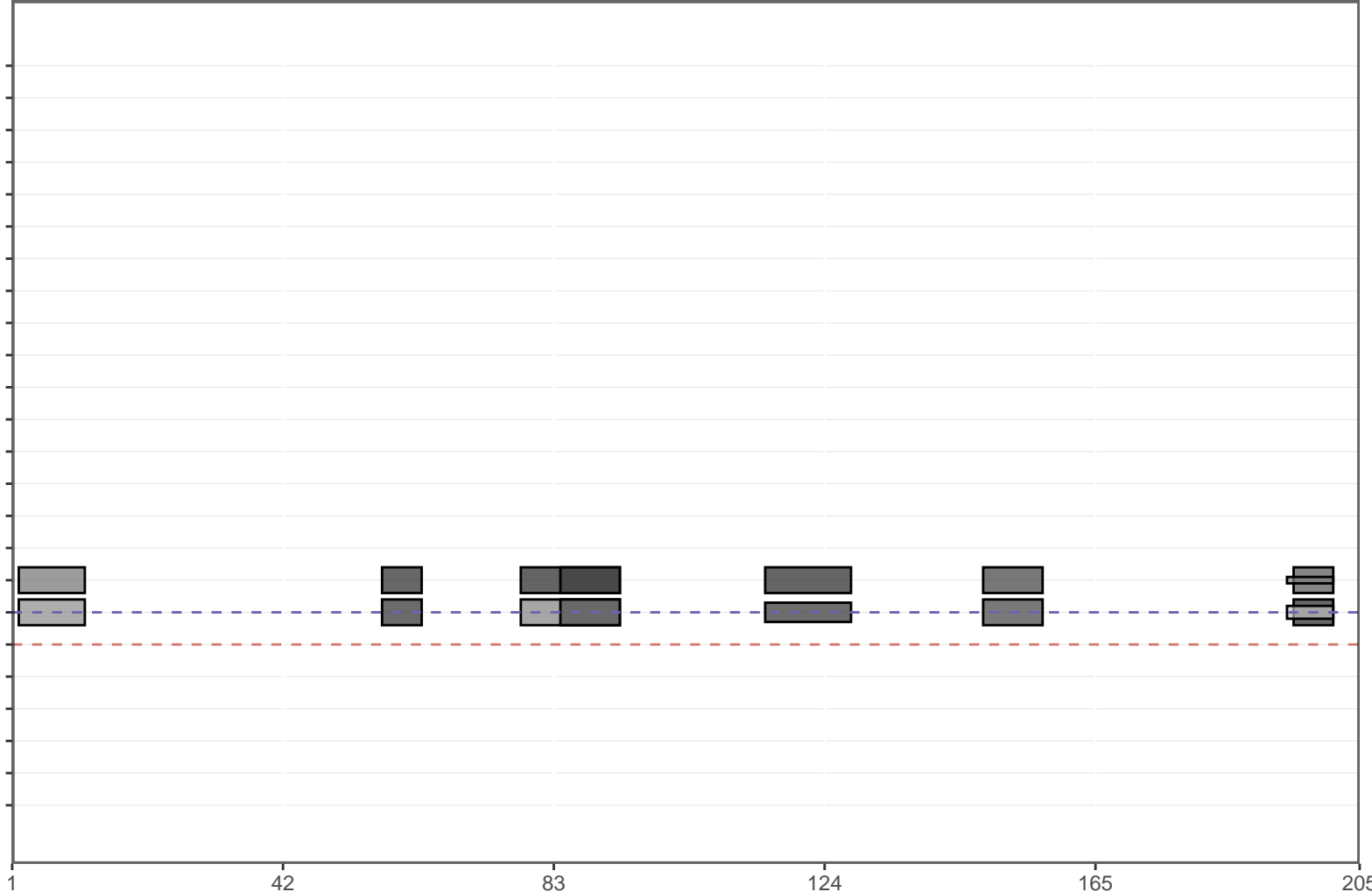
MW indication



Molecular weight

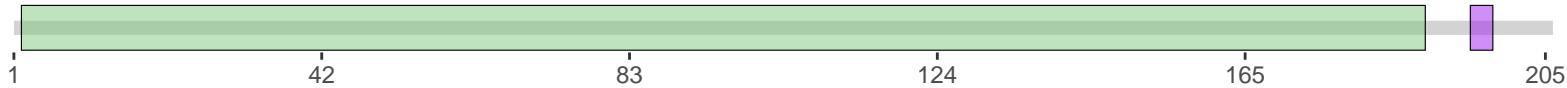


Gel Slice



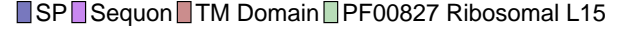
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VTQLKFORSKRSVWEERAGRLKGLKLVLSNYWINEDESTYKYFEVILVDAHAARNDPRINWICNPVKKHRELRLGLTSAGKYYRGLRGLKGLHYLHKNRPSRRGTWKRNGTSLRRVYI

NbL03g00210.1 protein_ABHD11 [MW = 33.15 kDa]

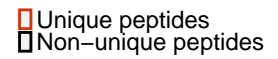
No. of times detected



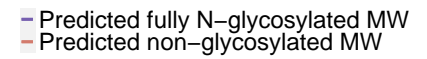
log(intensity)



Values from



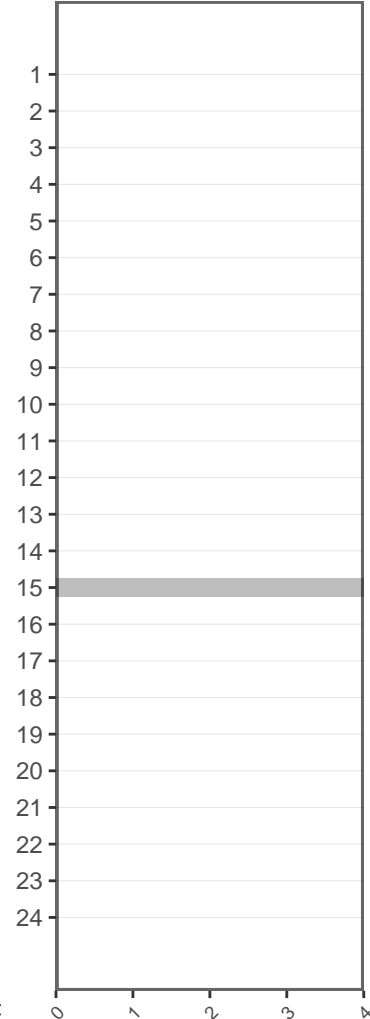
MW indication



Molecular weight



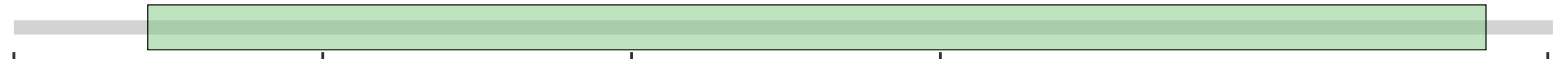
Gel Slice



Peptide counts over 4 repeats

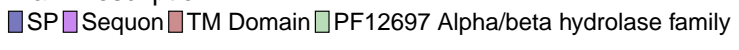
1 61 121 181 299

Protein length



Pfam domains

Pfam Description



Protein sequence:

IAGADGDDHPELELSEFLSKLPEEVSKRDNVALLLEGFSRDVAQWVVTNLRGTNPAGSFSHLSEWFDLKGIAEMVGSVEDTNLWKKIVEDVPRGVHNFKKAERSLHRWALEDRRHVAEEQAVEEGGGVEMHVEDAGHVVHADNPDGLFKILEFSFGQF

NbL03g00170.1 uncharacterized_LOC107816116 [MW = 15.55 kDa]

No. of times detected



log(intensity)



Values from



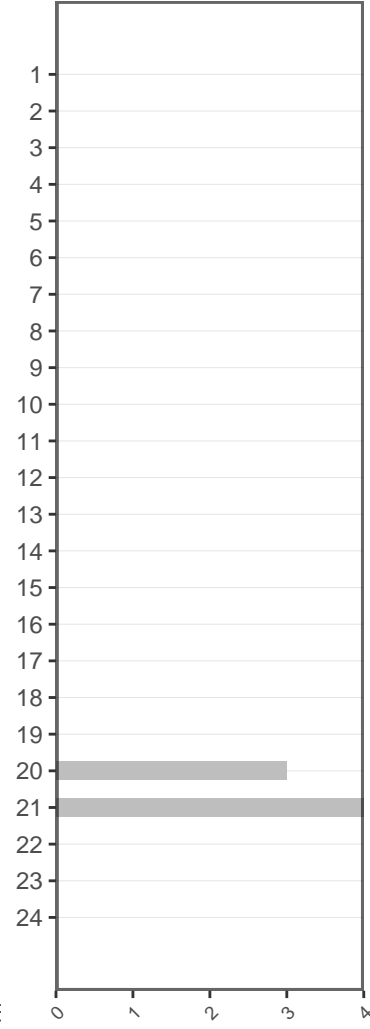
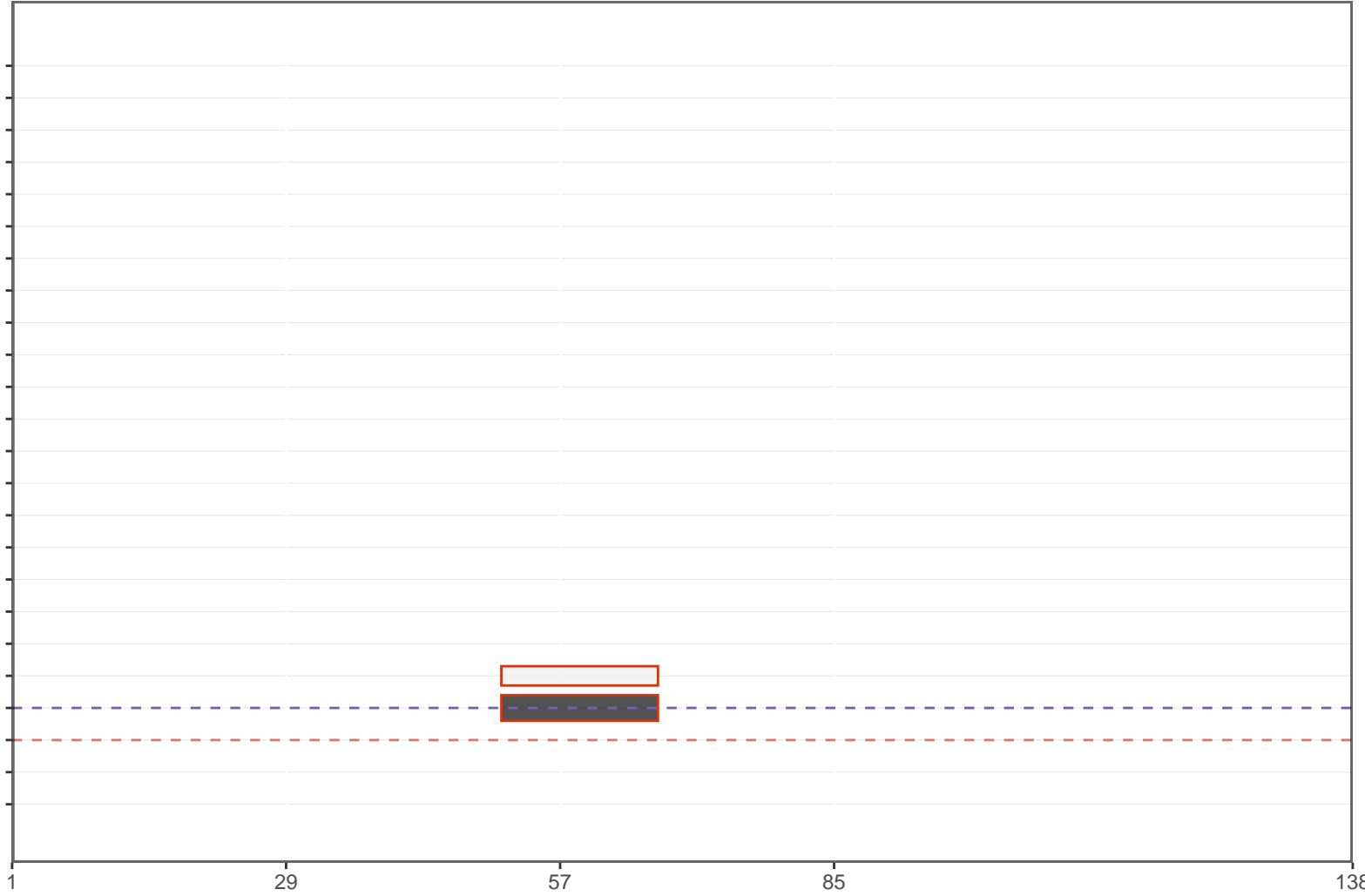
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

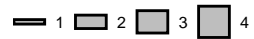


Protein sequence:

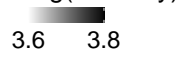
IEADDSLEIDPELRYSGFRNFQFLGRVFSIDTVAKPLPPMAMNVAARNITFTFTGFFDEGANAGKSLGLGGEKVRKVR

NbL03g00060.1 patellin-3-like [MW = 64.31 kDa]

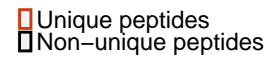
No. of times detected



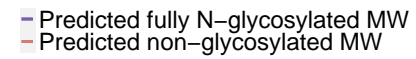
log(intensity)



Values from



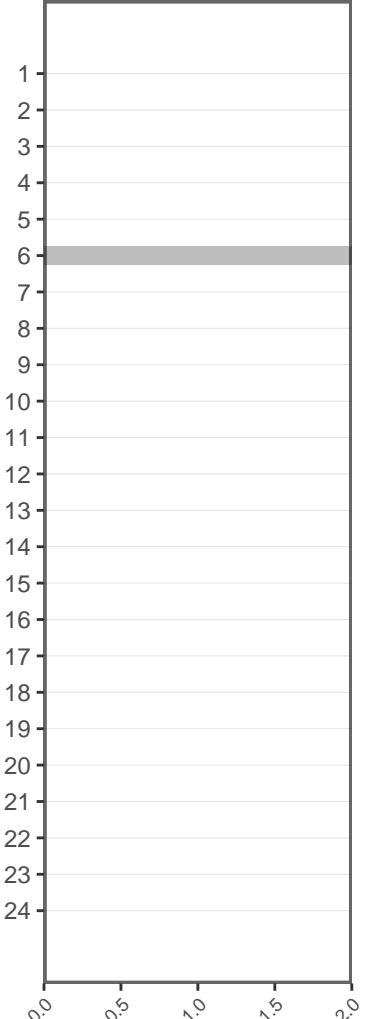
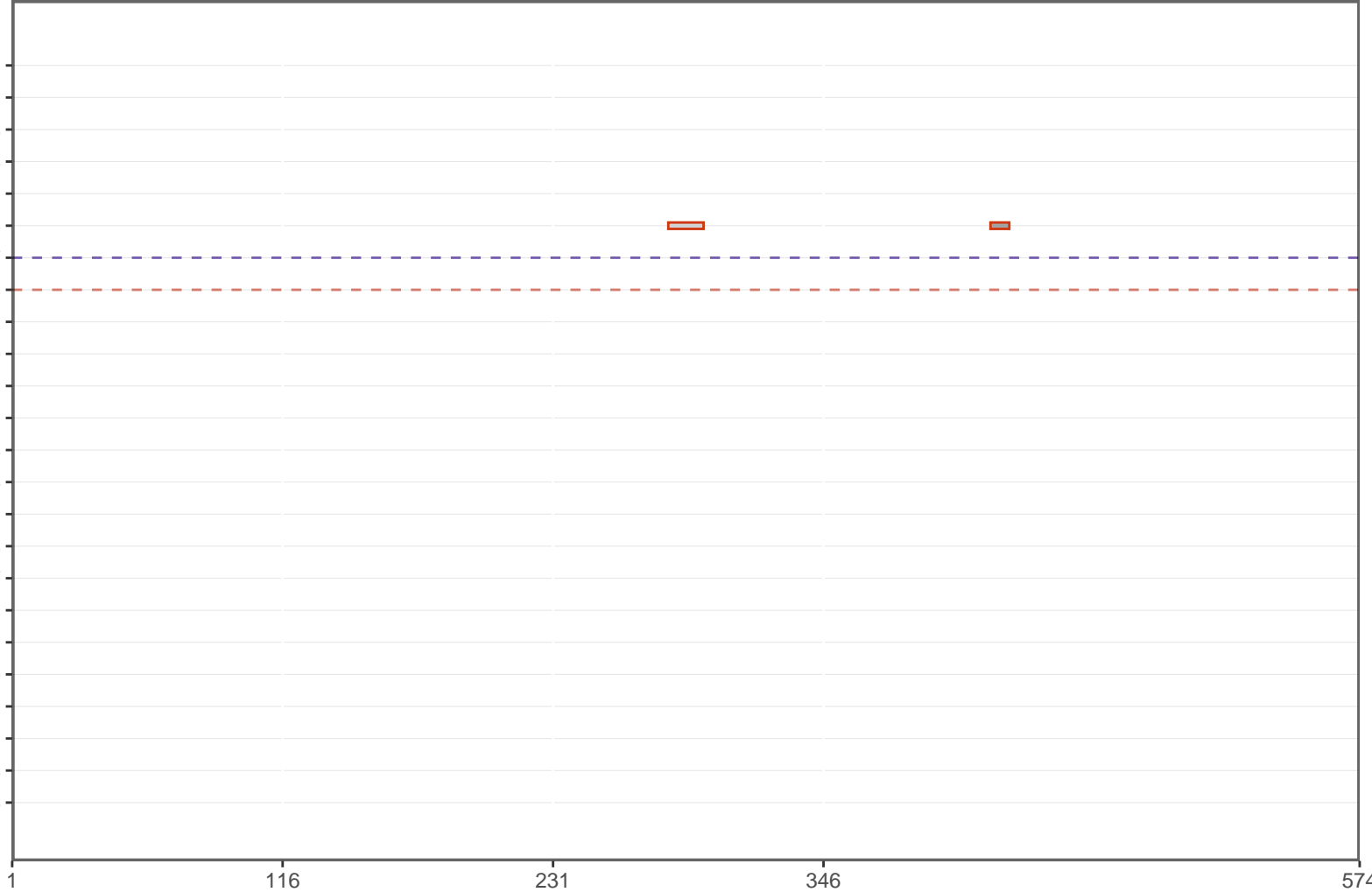
MW indication



Molecular weight



Gel Slice

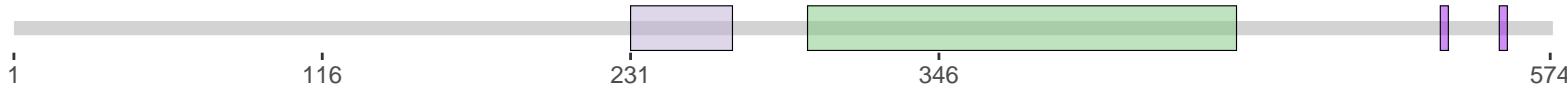


Protein length

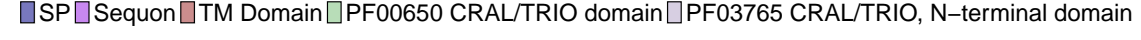


Peptide counts over 4 repeats

Pfam domains



Pfam Description

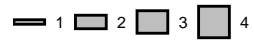


Protein sequence:

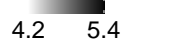
/RKELIDLELDEKELGGGLEKYYVYGLDKEGHPVQYNVAFGEFQNKELYQNTFADKEKLTFLRWIRIQFMKSRINLDFSPDGICTFVQVLDLKNLSPGLFFFKELKRGVYTRALQLLGDNYPEFVAKGVFNVPWYVAYVYRMINGIFTRTRTKSKFVAGPSRBAETLKYITPEQVPAQVGGLSKEGEGEFTVAERTDEIKRASKHTIEFFVTEKGLSWEARVTFQWVDVYVGAEFVPAVEDGYTHIEKSRVVGANETVSNFTWAGEGGKVVITFDNGSSKXXLLVRSKQK

NbL02g26240.1 nuclear_transport_factor_2-like [MW - SP = 17.75 kDa]

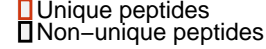
No. of times detected



log(intensity)



Values from



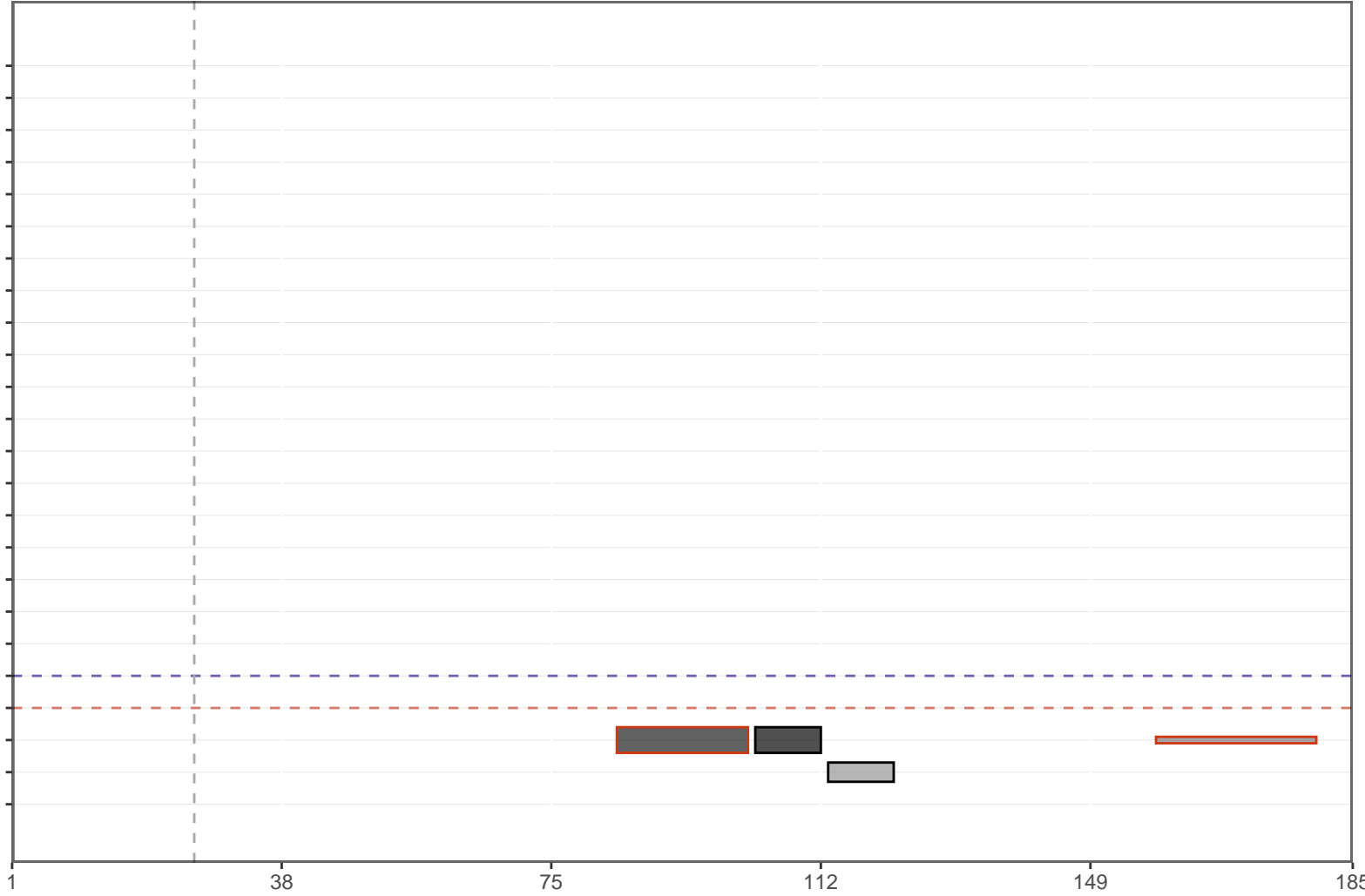
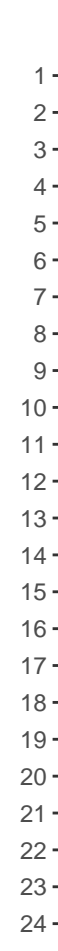
MW indication



Molecular weight

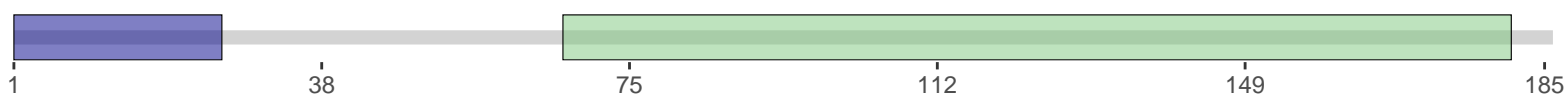


Gel Slice



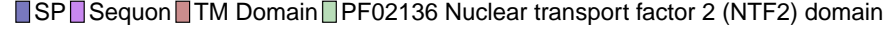
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

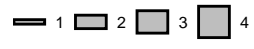


Protein sequence:

NRAGLANLYOENSMLSFEGVRIQGGAGHWKLTSLPFQGGKHQNTVDQDQPGIPGIMLVFSGNLQDFQEEHVKFSQMFHLMPTQGGSFYVMDIFRLNYA

NbL02g26180.1 sulfite_oxidase [MW = 43.51 kDa]

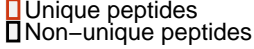
No. of times detected



log(intensity)



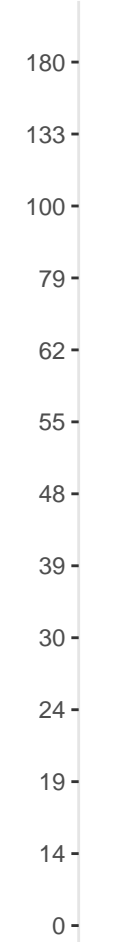
Values from



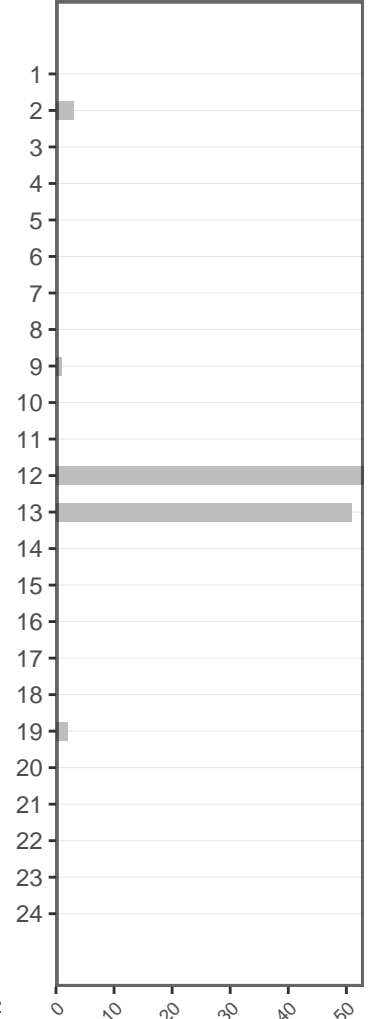
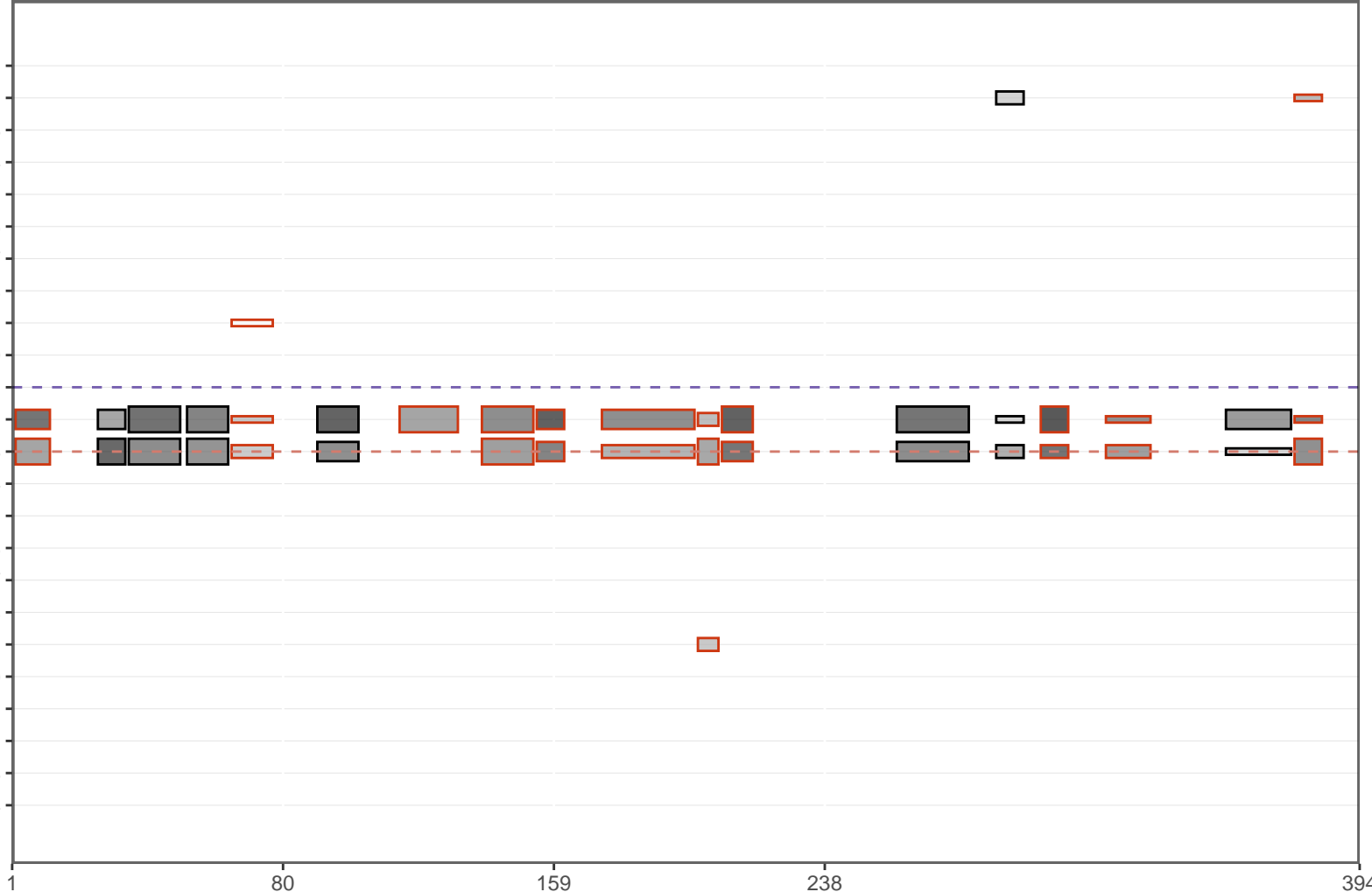
MW indication



Molecular weight

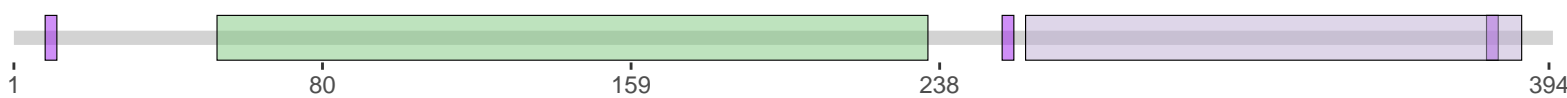


Gel Slice



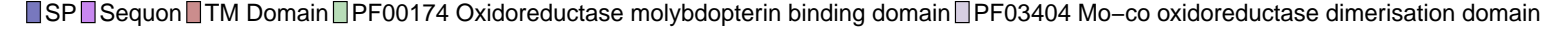
Protein length

Peptide counts over 4 repeats



Pfam domains

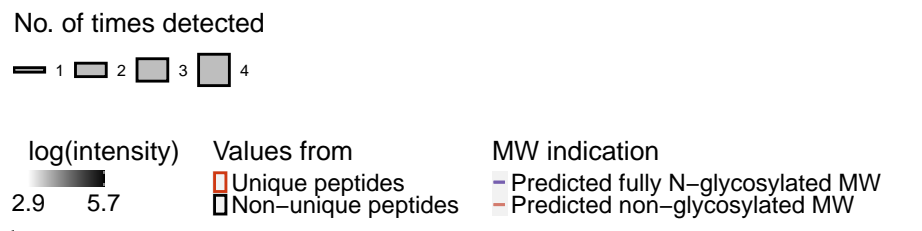
Pfam Description



Protein sequence:

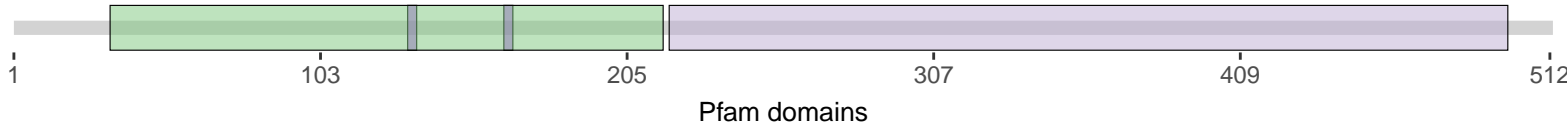
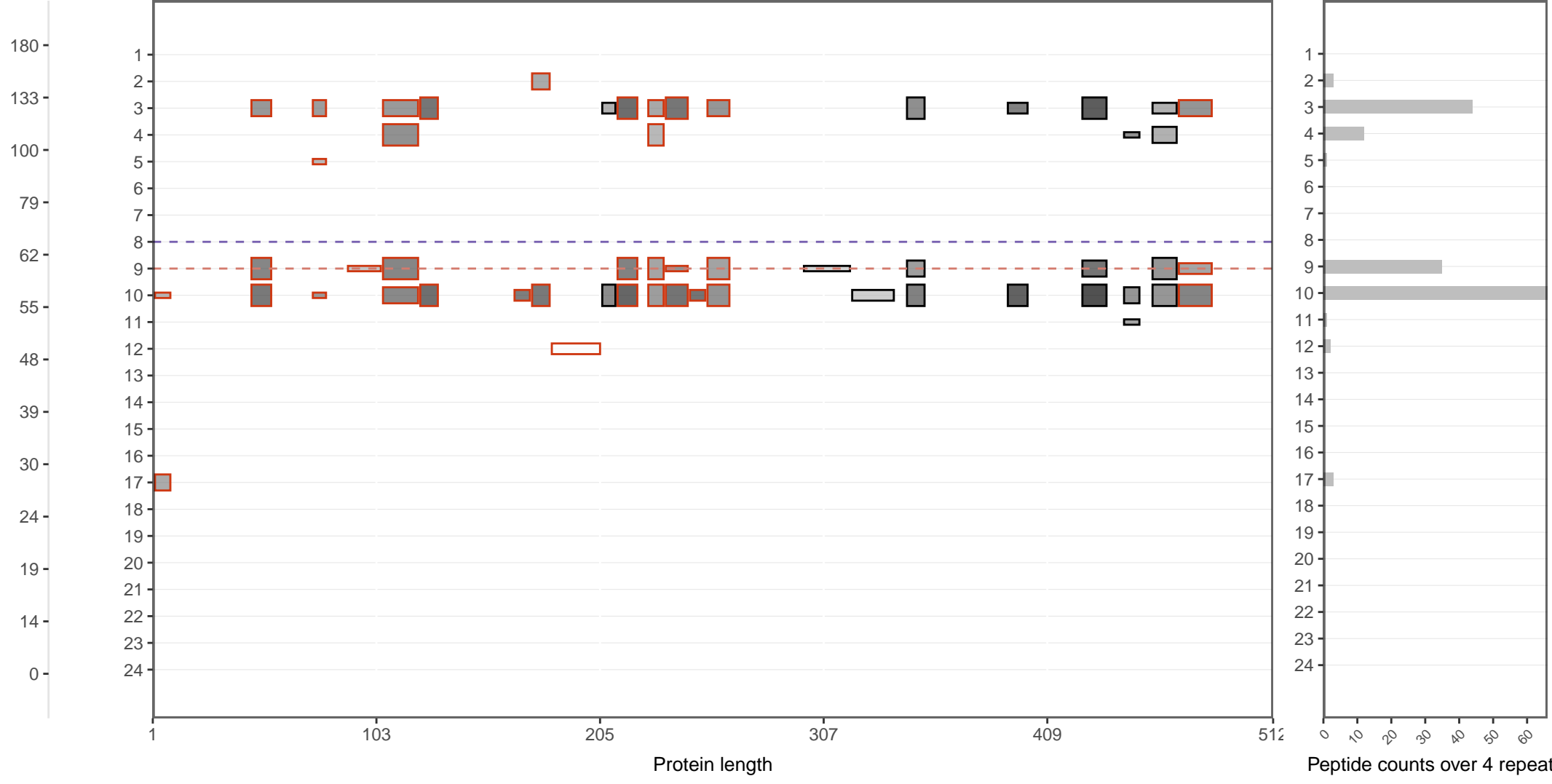
LDVLLAYEMNGQPLNRDHYPLRVVWPGVIGARVWALDGNIAEECGFFVQKDYKMFPTTWNWNNWVSTRPQMDFFVQCAIGSLEDVSVVYHKGITKGYWVSGGGRGIERYDVSDGKTVVEAARYQRTGPIYIADDA6SDKWWVVFEEANIPGSAEIVAKAVDAAVWVQPEISDSWNLRLGILNHSWHRVQVRVGGANL

NbL02g25910.1 glucose-6-phosphate_1-dehydrogenase_cytoplasmic_isoform [MW = 58.7 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00479 Glucose-6-phosphate dehydrogenase, NAD binding domain
- PF02781 Glucose-6-phosphate dehydrogenase, C-terminal domain

Protein sequence:

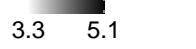
REDFGTEGRGGYFDEYGIIRDIGNHLLGVGLVAMEKPVSGKPEHIREKVKVYQSMPLPKDEEVLGGVEGYKDDPTVPDINSNTPTFATVLRHNRNEWEGVDFMAGKALNSRKAERIVQKVPDFRCKKQGRNEFVIRLQPSSEAMVYKLTIVKQPLGEMSTVQSELDLSEYRIVQGVVPEAYERLILDIRGGQGHFVRRDELKAAWEIFTLRHRIDDEKIPVYKPSGRPAEAEDELLGNVGVYQTHGYWIPPTL

NbL02g25500.1 glucuronokinase_1-like [MW = 39.95 kDa]

No. of times detected



log(intensity)



Values from



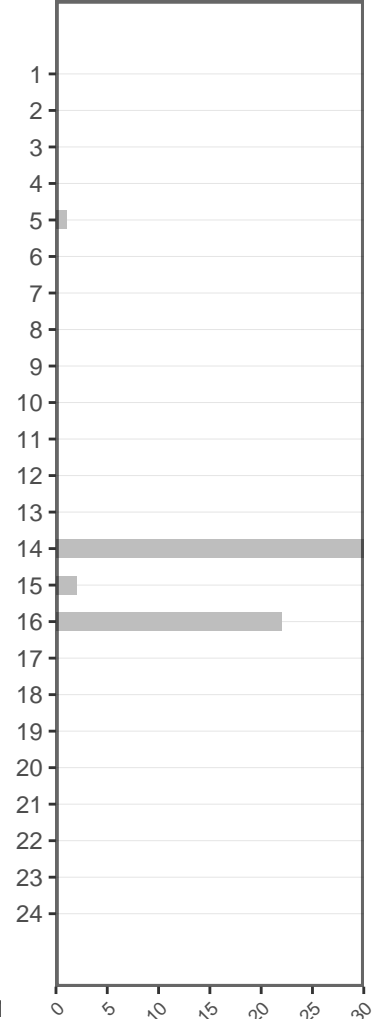
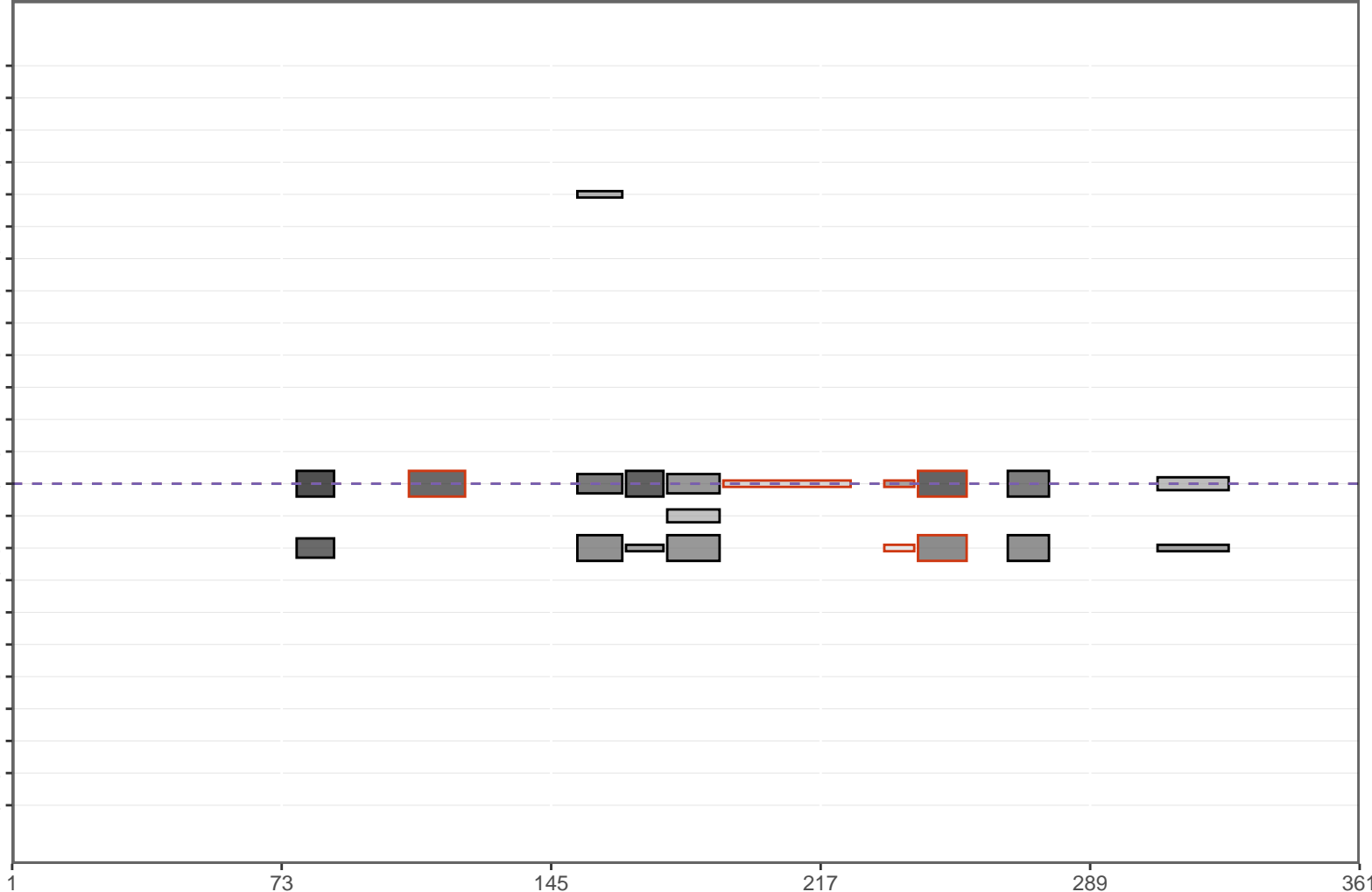
MW indication



Molecular weight

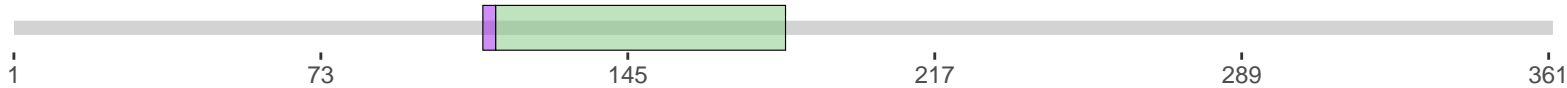


Gel Slice



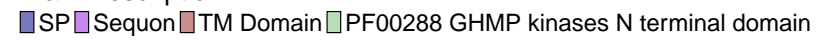
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

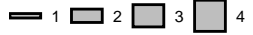


Protein sequence:

IGLQDRVAQVYGGVAVMDFGKNIHMDLGHGIVTPMDVLLPPLVLYAENPDSGKVIHSTVRGRWLEGGDEFIRSTMEEVAVNAVEGRKTLLEKDYKLAALMNHNFDLRRRMFGDDALGAMNEMVEIGRRIGAAKFTGSGGAVVVFQDPSGQWGLLEDAGHTAGFTFGPKVMPFLSEVDLQTLGN

NbL02g25330.1 titin [MW = 427.49 kDa]

No. of times detected



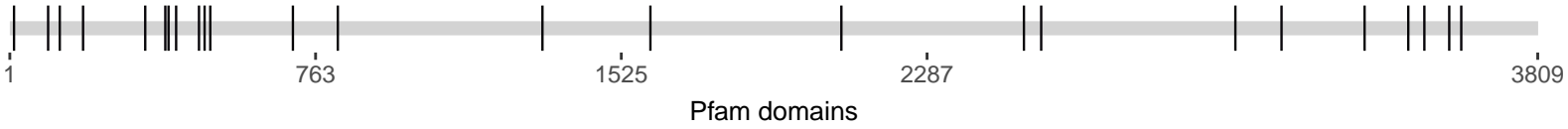
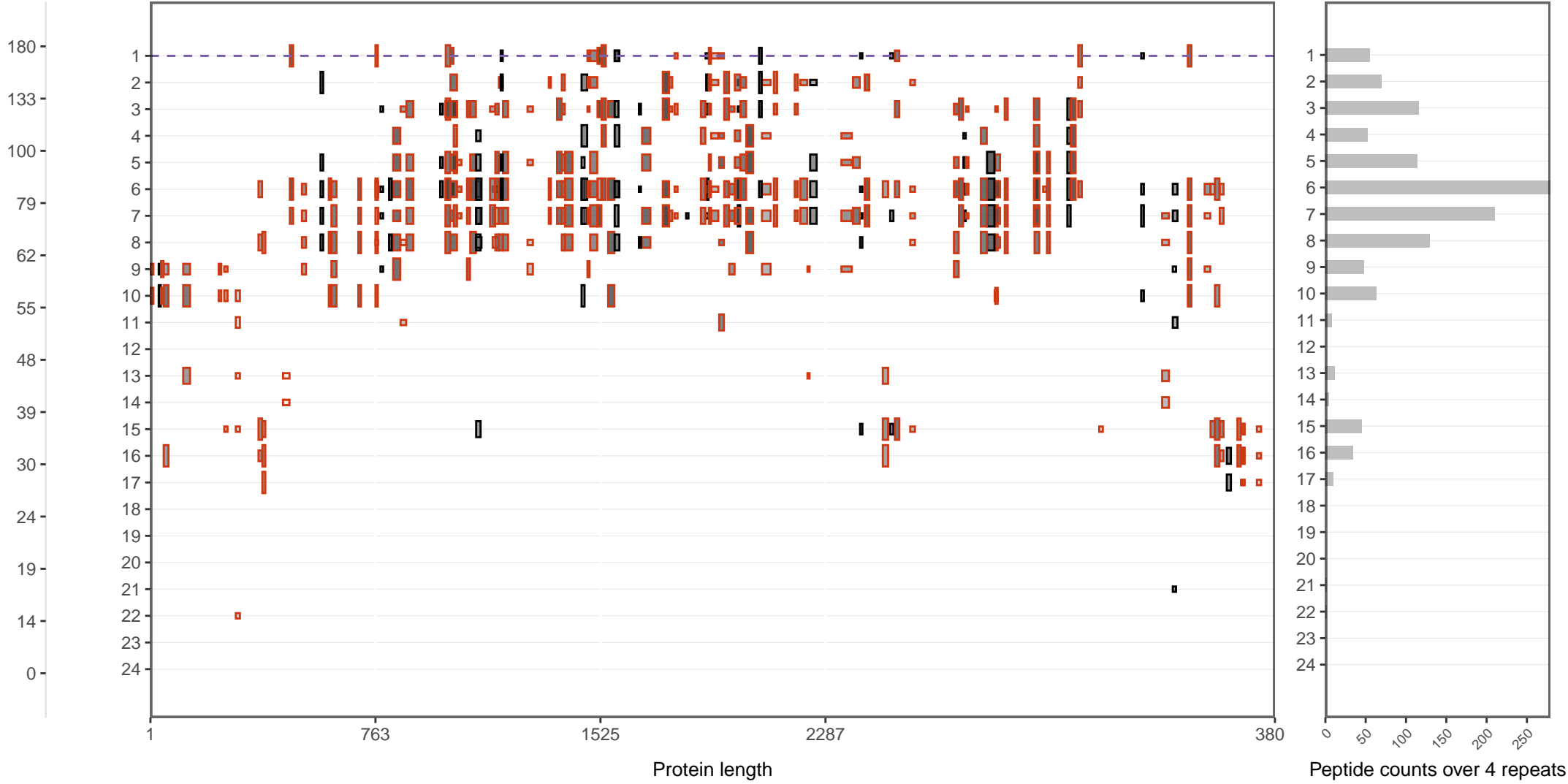
log(intensity)
2.8 5.2

Values from
Unique peptides (orange box)
Non-unique peptides (black box)

MW indication
Predicted fully N-glycosylated MW (blue dashed line)
Predicted non-glycosylated MW (orange dashed line)

Molecular weight

Gel Slice



Pfam Description
SP Sequon TM Domain

Protein sequence:

EPRAEKPEEPVATEKPEEPVATENPEEPKAEKADPEWLEKPEEPVAKKPEEPVATEKPEEPKAEKDDENWGEKPEEPVTEKPKPEEPWVEEKDFEPVAGKSEKPEPVVEQTGPNPWEETPKELAFEKPEEPVEETPEVLAELKPKPKVAGKHEKVTLEKNIPLKNDTATPKNTNNDVADLAVEKPEEPKAEKPEEPMAKELKPEPNVEDKPEKSVVEEKSEKLAEETPEEQAEETPEALVAEENPDOSAVEETVEELAEKPKTATEKPEKPA/TLII

NbL02g25190.1 isocitrate_dehydrogenase_[NADP] [MW = 53.9 kDa]

No. of times detected



log(intensity)



Values from



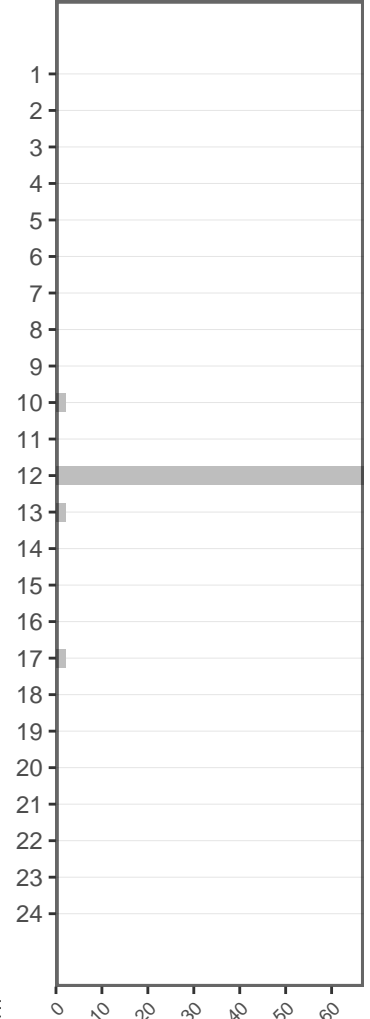
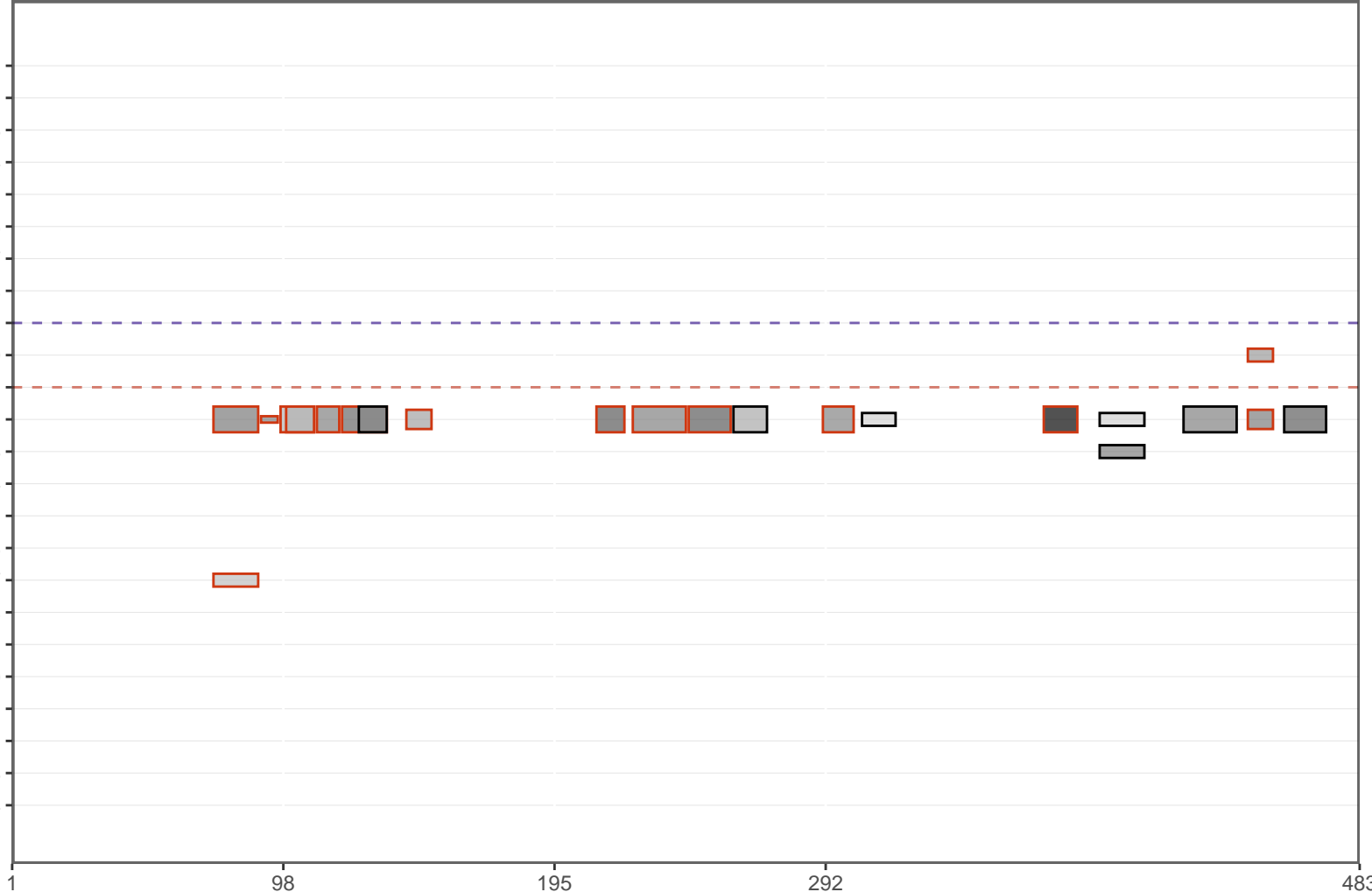
MW indication



Molecular weight

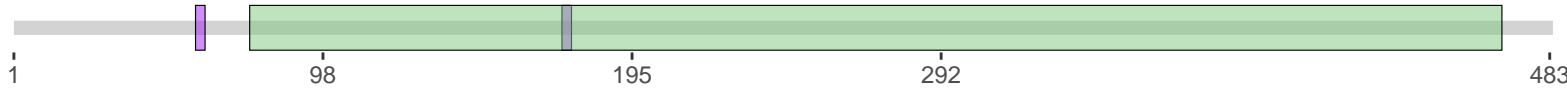


Gel Slice



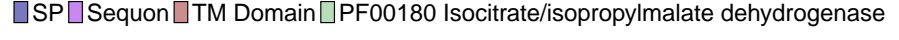
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL02g25170.1 tRNA_(adenine(58)-N(1))-methyltransferase_catalytic_subunit_TRMT61A [MW = 37.99 kDa]

No. of times detected



log(intensity)



Values from



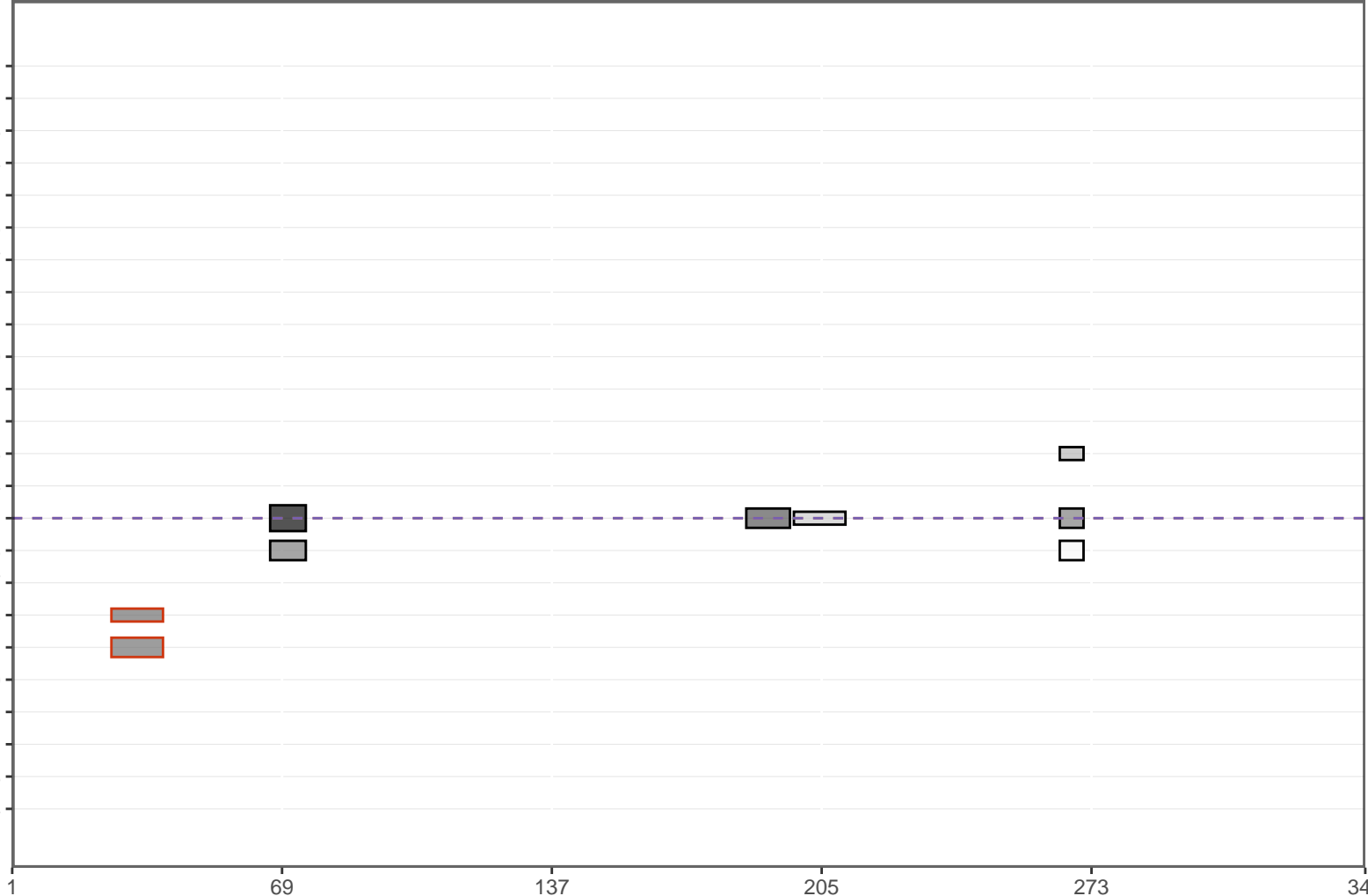
MW indication



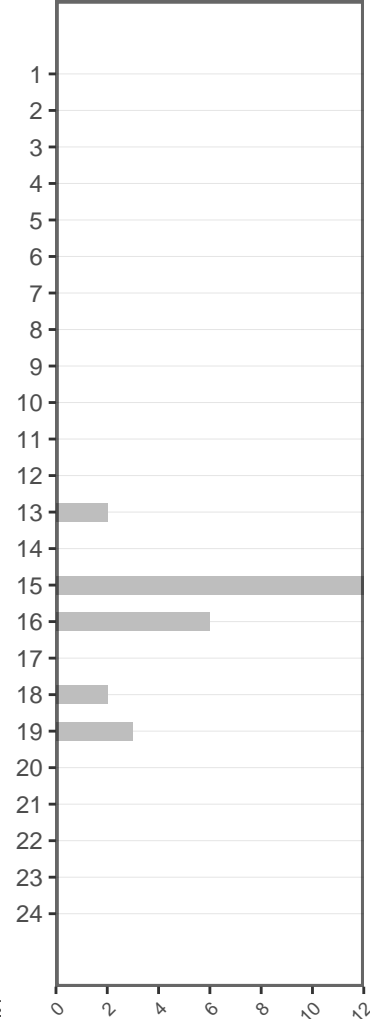
Molecular weight



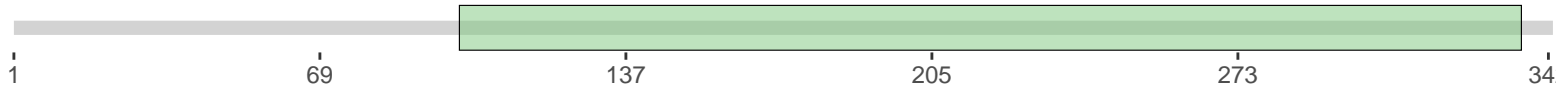
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL02g25140.1 peptide_deformylase_1B_chloroplastic [MW = 30.9 kDa]

No. of times detected



log(intensity)



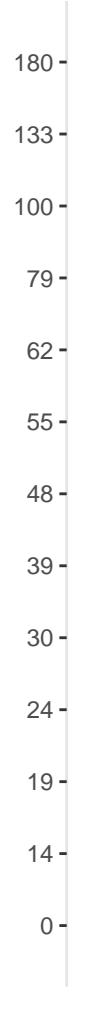
Values from



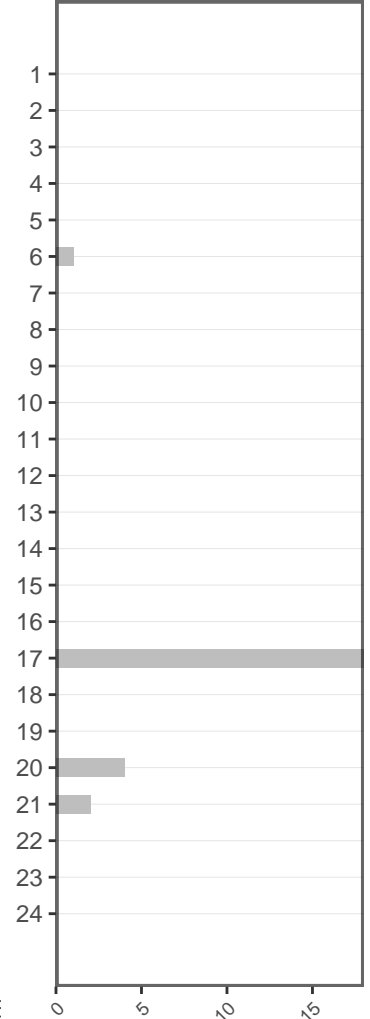
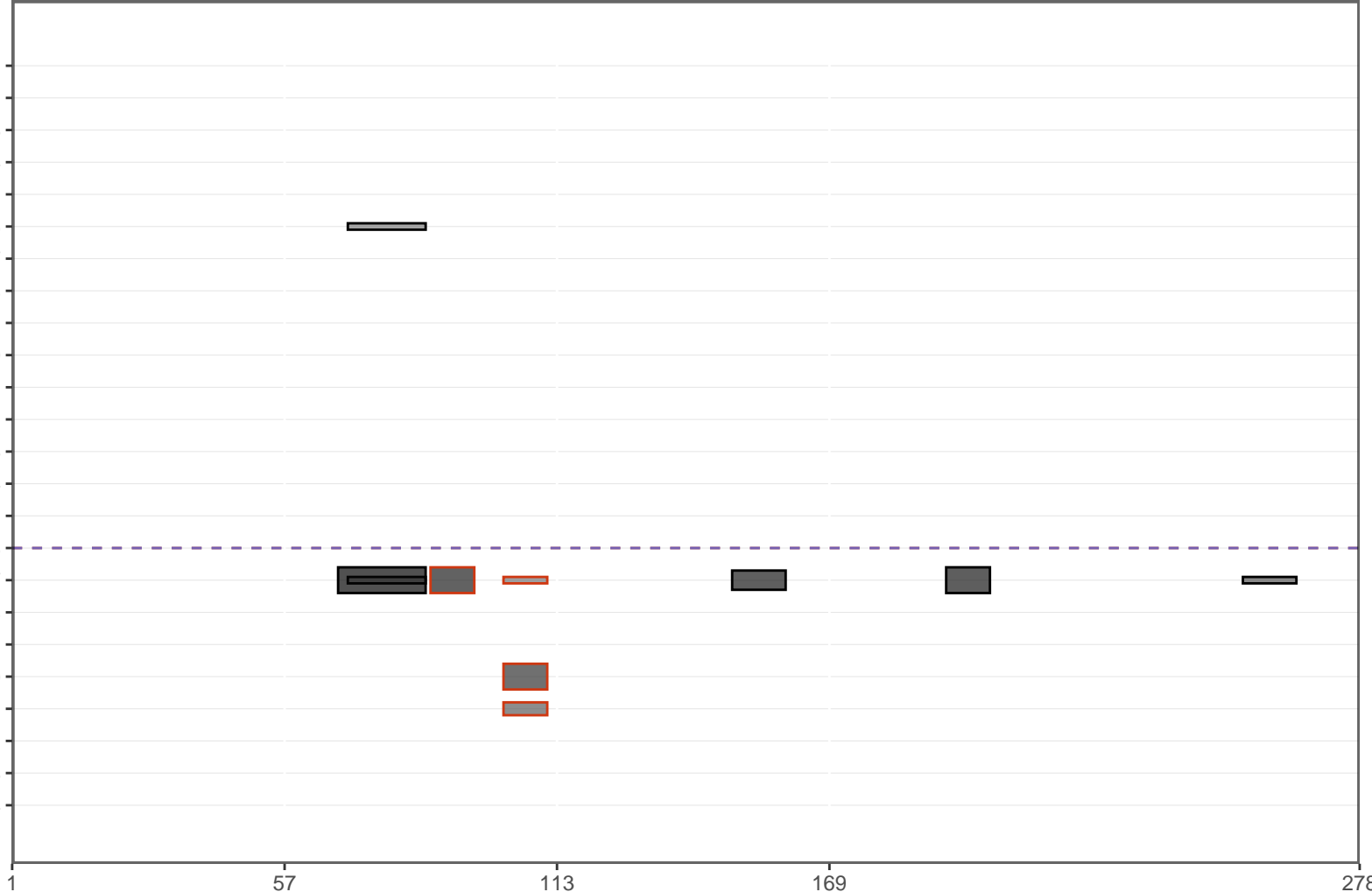
MW indication



Molecular weight

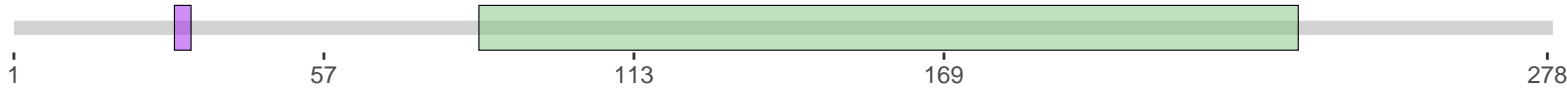


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IGLSAPQVGMNVQLMVFNAAGERGEGEEVLPNPRVSRVSRRIIPYDEGLLFFENGDVERPDSVWVDAGDINGARFELTLTPARVVFQHFHFDHLQGVLFPEKMTDEVLDTRIEDLVALEKKEFEKTLPTPEINTRIKKKAAGVGFGRK

NbL02g25100.1 50S_ribosomal_protein_L12_chloroplastic [MW – SP = 20.26 kDa]

No. of times detected



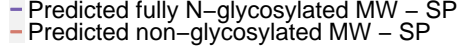
log(intensity)



Values from

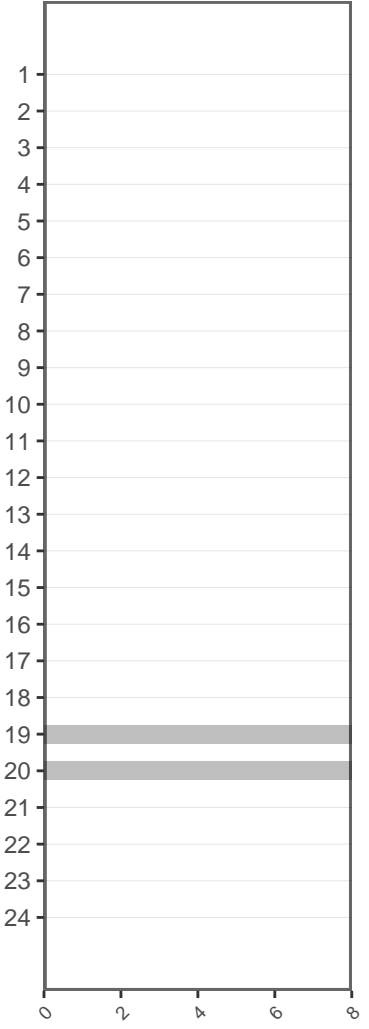
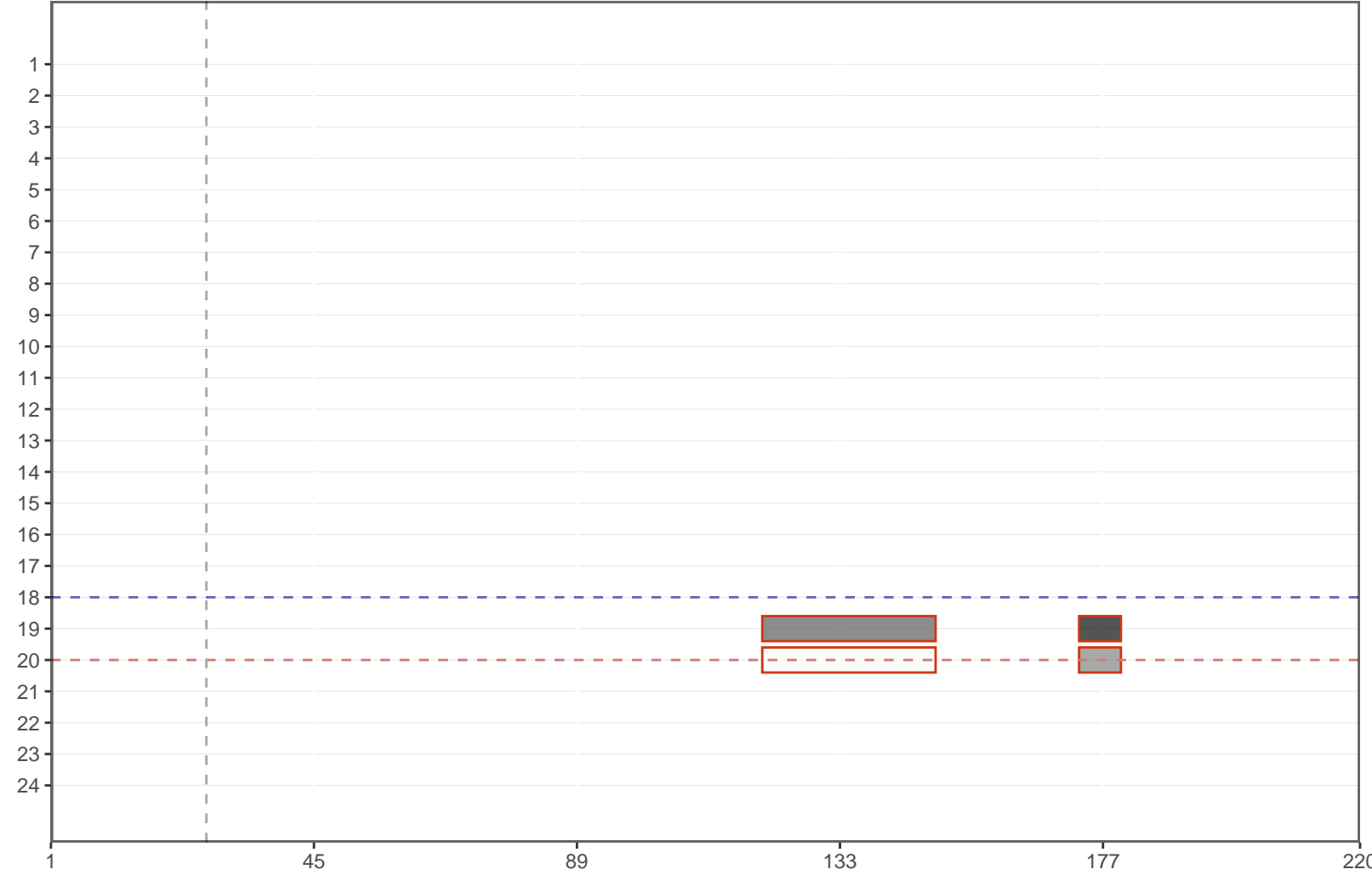


MW indication



Molecular weight

Gel Slice



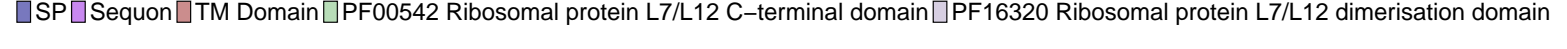
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LDGEISNLTDADQKIVKLVGDKLGVTAASFAPAIAAIPGAAAEAPVVEEKTEFDVVIDEVPGNARIATIKAVRAITSLSLKEAKEIEGLPKKFKREGVSKDEAEDAKKLEEGAGAVSM*

NbL02g25020.1 protease_Do-like_1_chloroplastic [MW = 45.29 kDa]

No. of times detected



log(intensity)



Values from



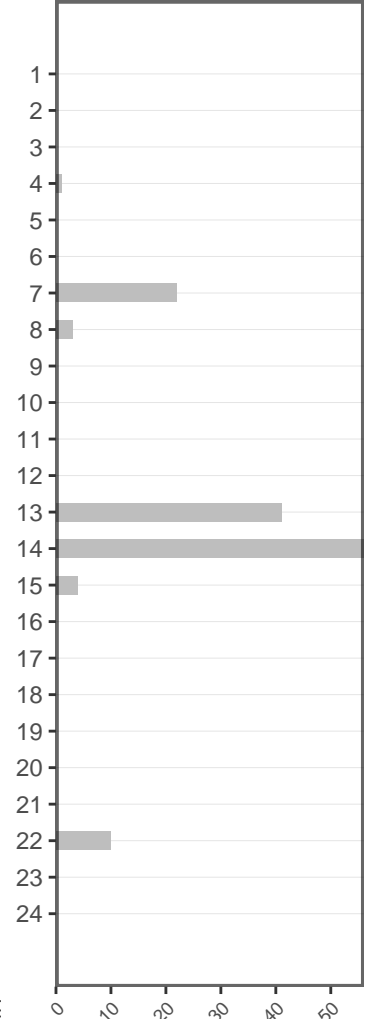
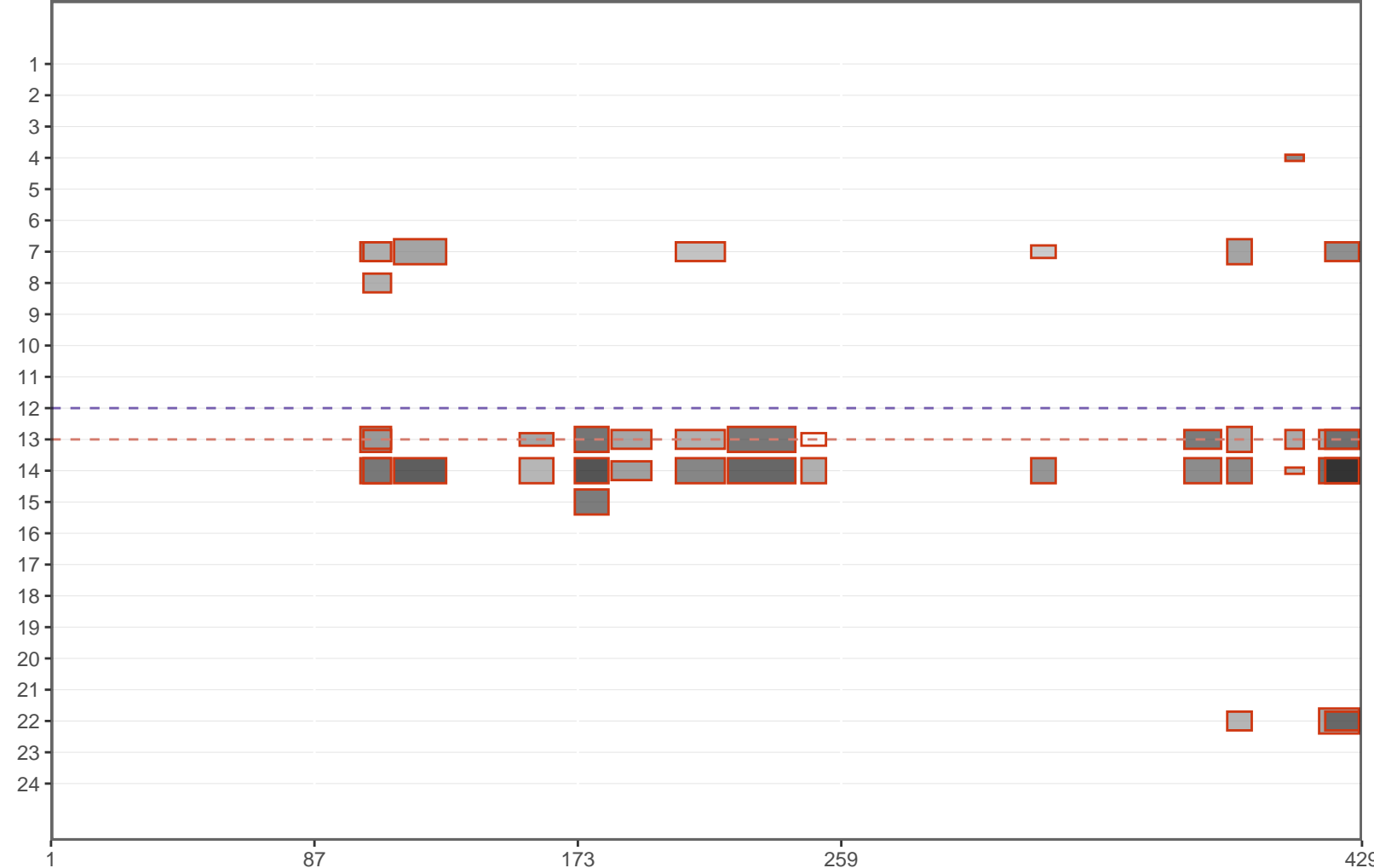
MW indication



Molecular weight

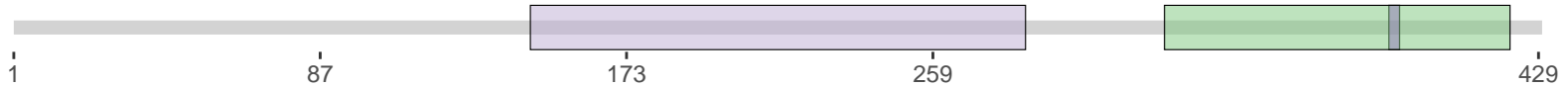


Gel Slice



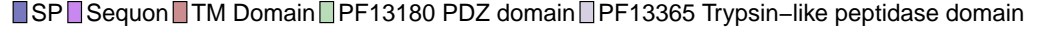
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

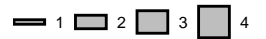


Protein sequence:

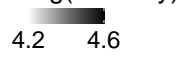
DAPKDKMRPIPIGVSEADLLLVGGKVFAGNPFGLDHLFTTGVISGLRREINSAATGRPIQGVQTDAAINPQNSGGPLLDSGSLNIGINTAYSPGASGGVGFSPIDVTIVSGVDDLVKFKVTRPLKIFKAPDQGVVEQLGVSGLVLDAPPNGFAGKAGLLFTKRDVYGRLLLDGNTSNGKIVSNGTDLVYRILDQCKVGEKIVVEVLRGDQKEKIPVLEPKPEEPI

NbL02g24980.1 formate_dehydrogenase_mitochondrial [MW = 42.47 kDa]

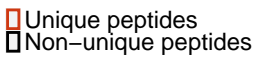
No. of times detected



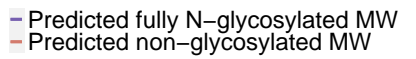
log(intensity)



Values from



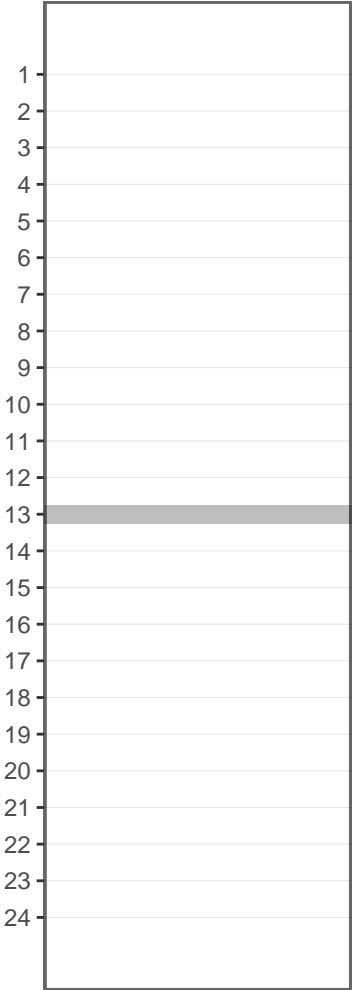
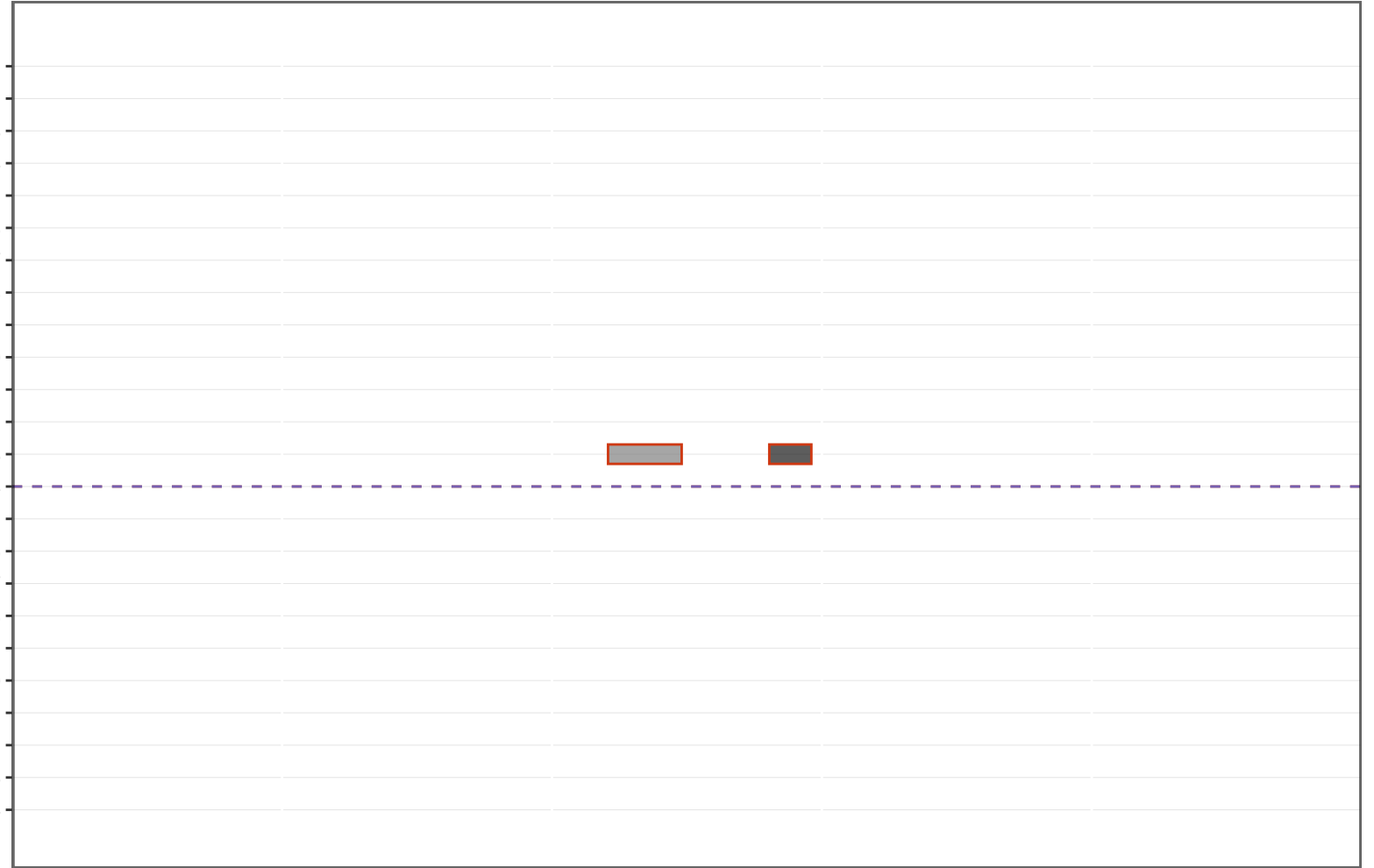
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF00389 D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain
- PF02826 D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain

Protein sequence:

IEWVAGAYRAYDLEGKTVGVGAGRIGRLLLRKLPFNGLLYHDRVMSSELENDGSAKFEEDLKMLESKGDVAVNTPLTEKTKGMFDKERIAKMKKGVLVNNAARGAMDTGAVVDACNNGSHAGYSGDWWYQPPAKDHPWRVMPNGAMTPHISGTTIDQLRVAAGTKQMLDRYFKGEDFPAGNYYKDGELAPQVR

NbL02g24960.1 peptidyl-prolyl_cis-trans_isomerase_CYP38_chloroplastic [MW = 49.39 kDa]

No. of times detected



log(intensity)



Values from



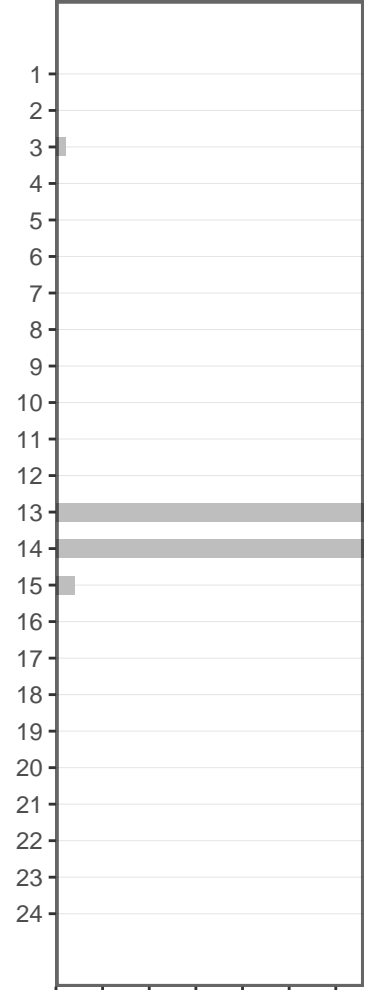
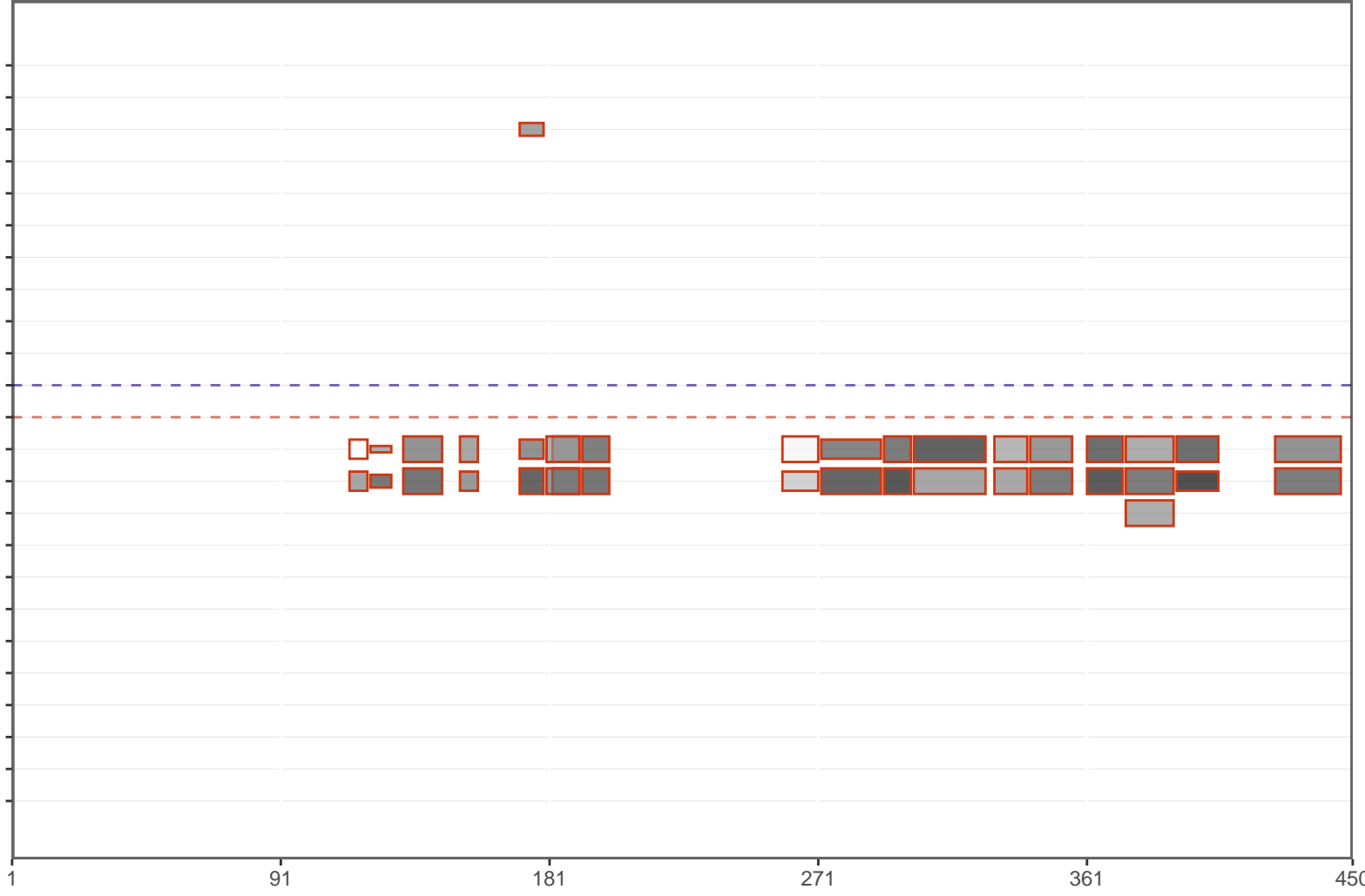
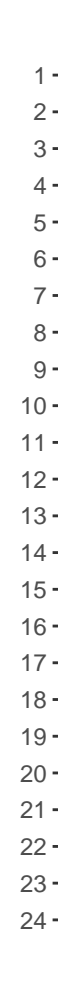
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

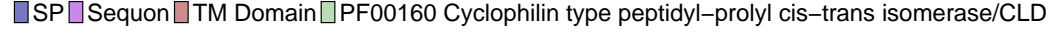
Protein length



Pfam domains



Pfam Description



Protein sequence:

IQKELLYYGGVEEDMVDGFPYVEPEYGNMPLKGRATLDMKVKVNDPNPVEEGVFRVLDGYNAPVTAGNFIDVERHFYDGMELQRADGFVVTGDPGPEGRGFDPTSEKIRTVPLEIMVDGEKVPFYKGETLEDLGLYKAGTRLPFNAGFTMMAMAREEFENNSASSGVFWLKESELTPEANILDGRVWFGVYVTEFEDPLADLKVGDVHDSKVVSGLDNLVNFVYKAGD

NbL02g24790.1 uncharacterized_LOC107798474 [MW = 24.91 kDa]

No. of times detected



log(intensity)



Values from



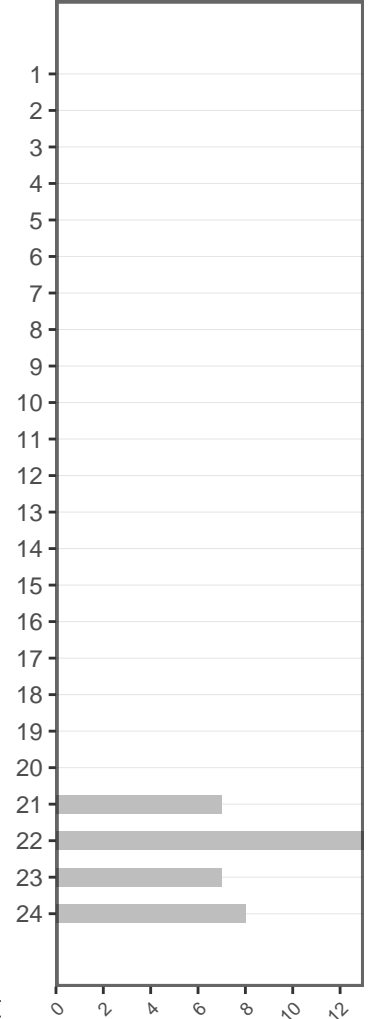
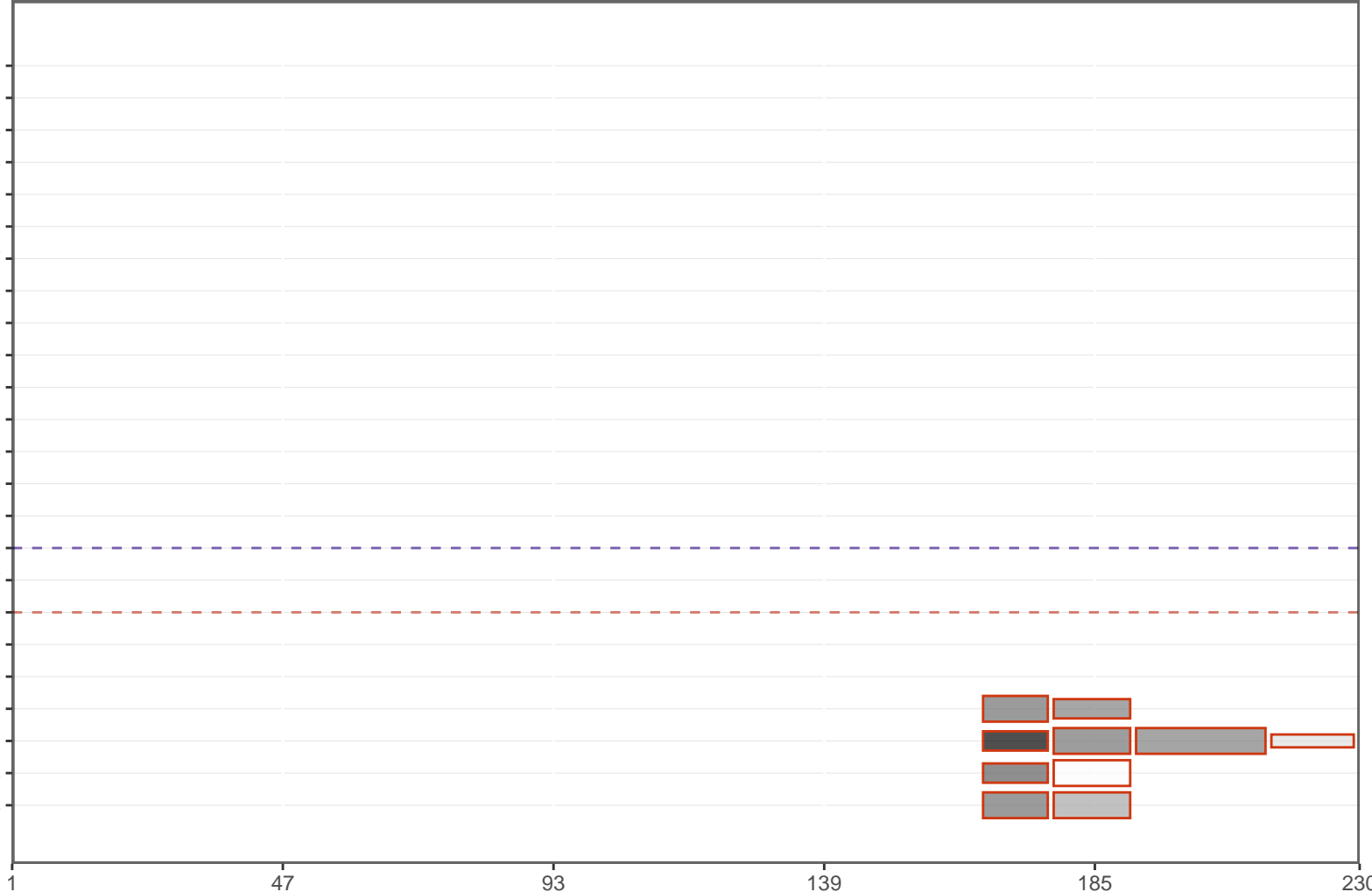
MW indication



Molecular weight



Gel Slice

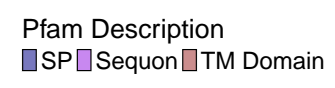


Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:

VTRIVSATEEEEGATAVDEASAAITFTVDGTVSVSVSPSDVLTMFQDQAEGTMNEAAVFNVTKALEEIEGIDLKVGVVEGIAEVELTKGTTIQATGVSSSLVETIQSSGFKLQTLNLSFGDEEDTS*

NbL02g24770.1 translation_initiation_factor_IF-1_chloroplastic [MW = 16.98 kDa]

No. of times detected



log(intensity)



Values from



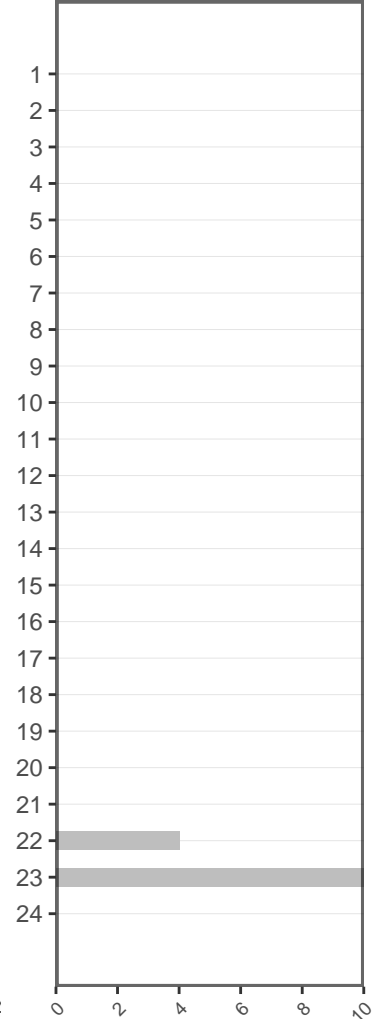
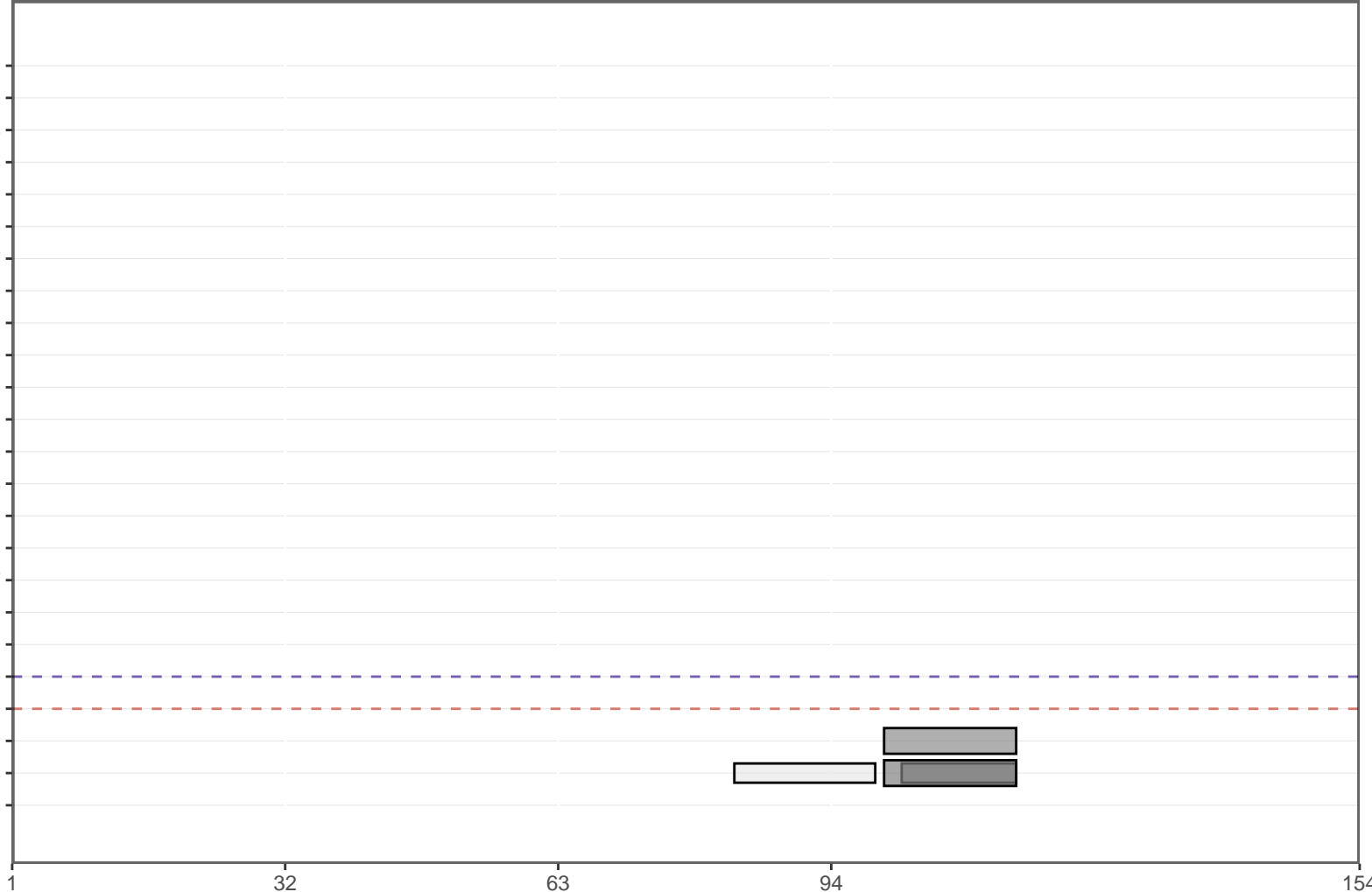
MW indication



Molecular weight



Gel Slice



Protein length

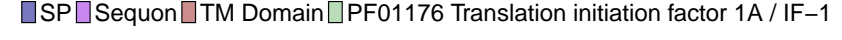


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

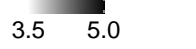
HSFTNSRSQTSIQGLSGEGKWTHEGSDTEELPNGMFRVKLNADVVLGYISGKIRKNFIRLLPGDRVKIEVRYDSTKGRIVYLRGGREGI

NbL02g24750.1 peroxidase_63-like [MW - SP = 34.25 kDa]

No. of times detected



log(intensity)



Values from



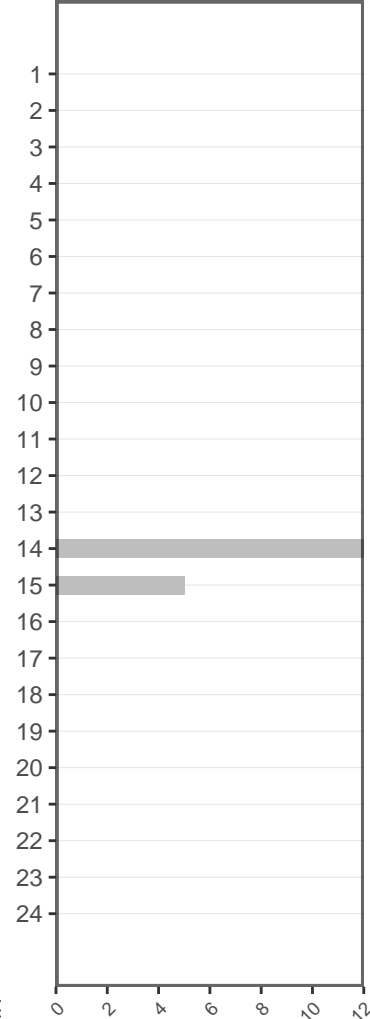
MW indication



Molecular weight



Gel Slice

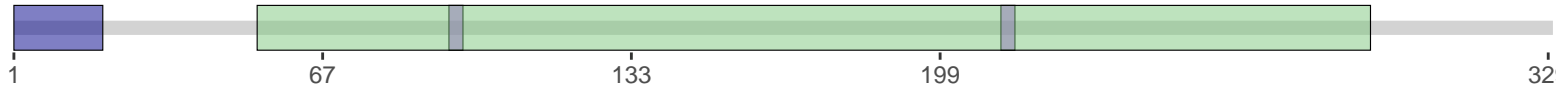


Peptide counts over 4 repeats

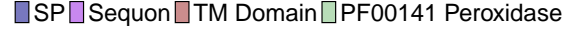
Protein length



Pfam domains



Pfam Description



Protein sequence:

SKASLYEGLNLRPTMPMDGQIKIFERGRFSIQEMVALSGAHTIGFSGHKCFENSDLHHYKNTSGADPQYVPRFAQALKDACSNSGKDPYLEVFNIDMTPNKFDMYYQNLPKGLGLLSSDRGLFSDPRTRIHVEEYVRDQNAFFKAFASAMQKLEHGKVKGKIKGERIHRGDAFNN

NbL02g24730.1 ferredoxin-thioredoxin_reductase_catalytic_chain_chloroplastic [MW = 17.1 kDa]

No. of times detected



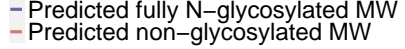
log(intensity)



Values from



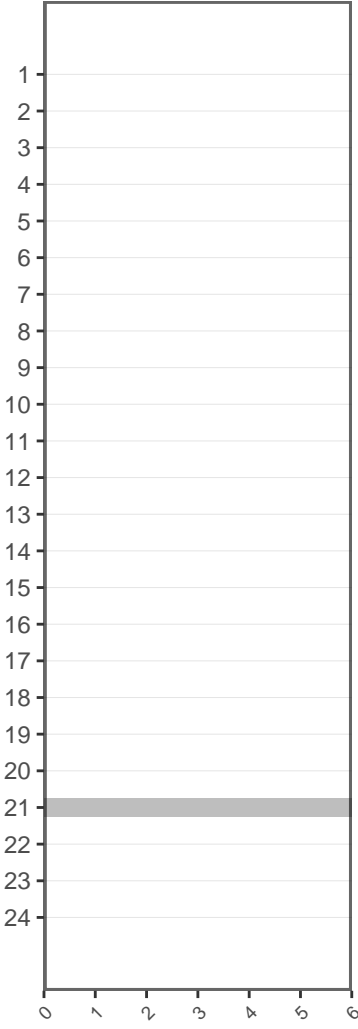
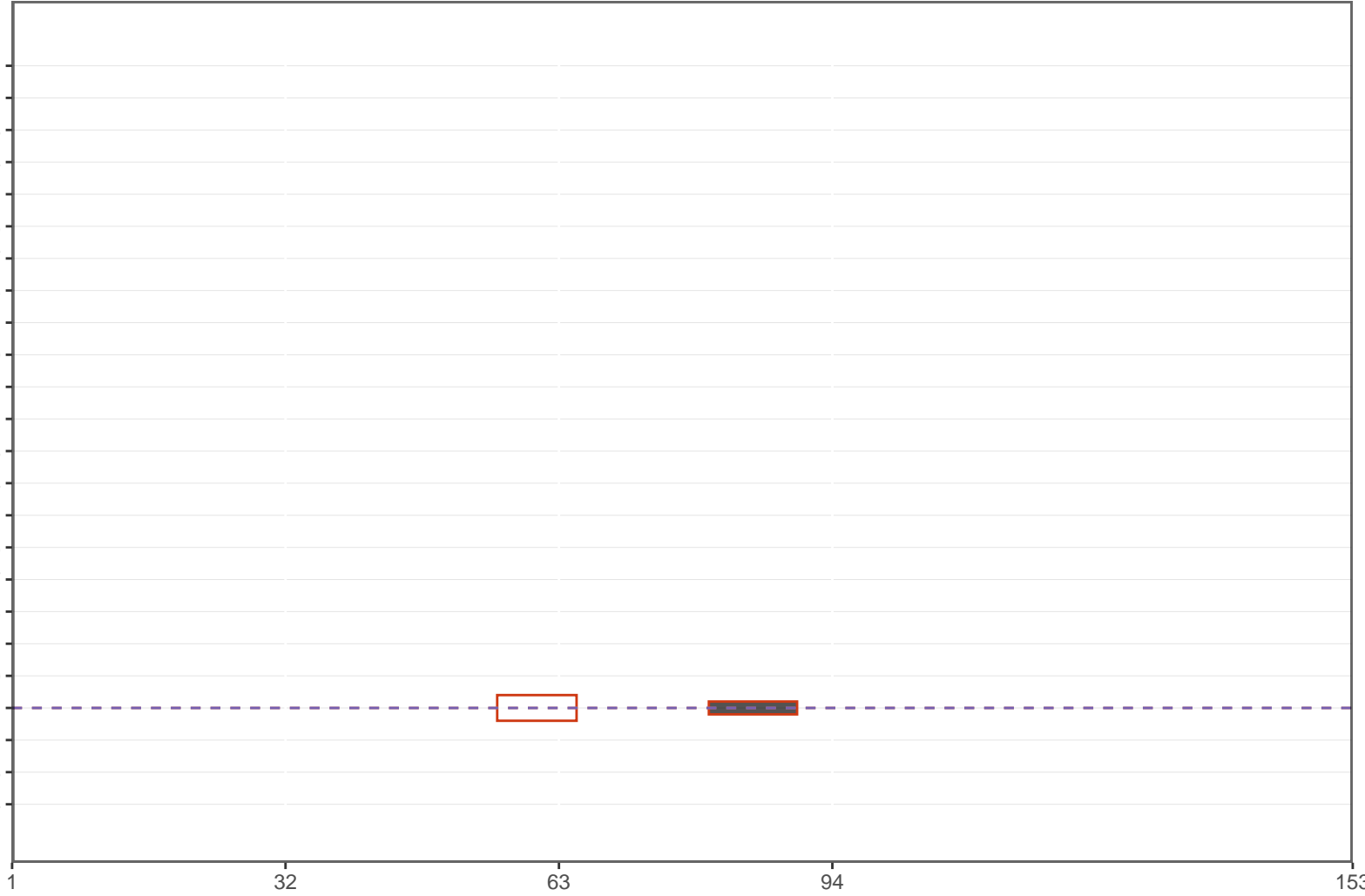
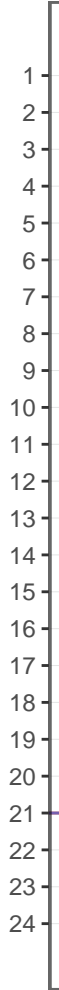
MW indication



Molecular weight

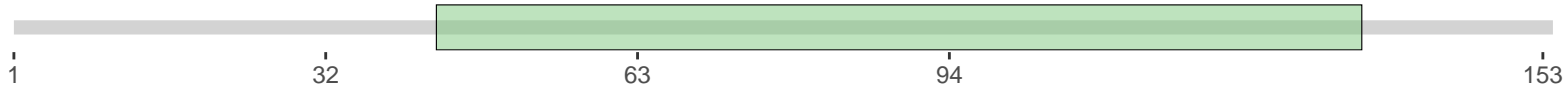


Gel Slice



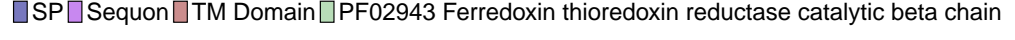
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKGVTSVYKGLAEHKDILGAPLQGRHYDDKAAEAAGGGFWNCPQVPMREKEGHCMLFTFQNDFAEEGVYANMRSLSVSNYLLRLGI

NbL02g24690.1 protein_CREG1 [MW – SP = 20.31 kDa]

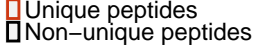
No. of times detected



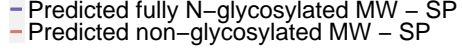
log(intensity)



Values from



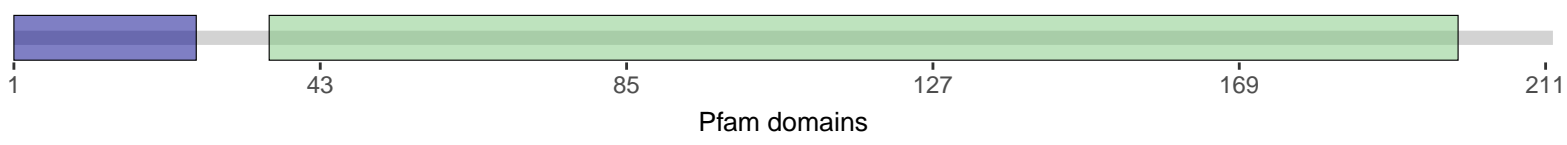
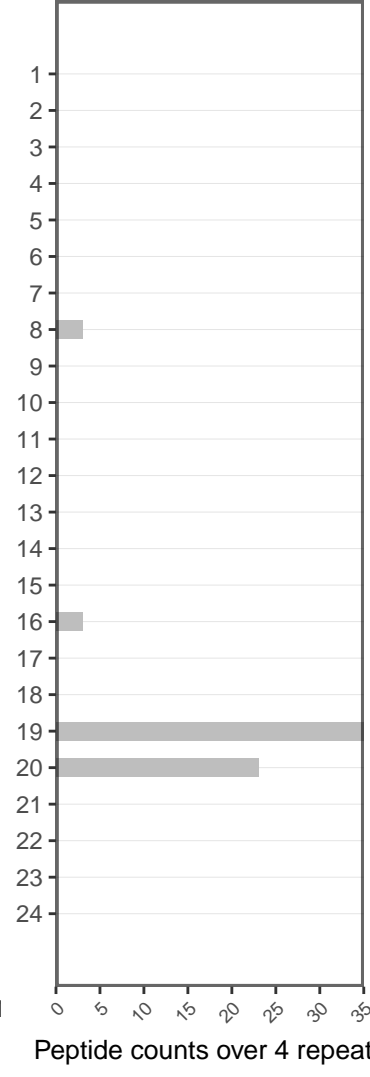
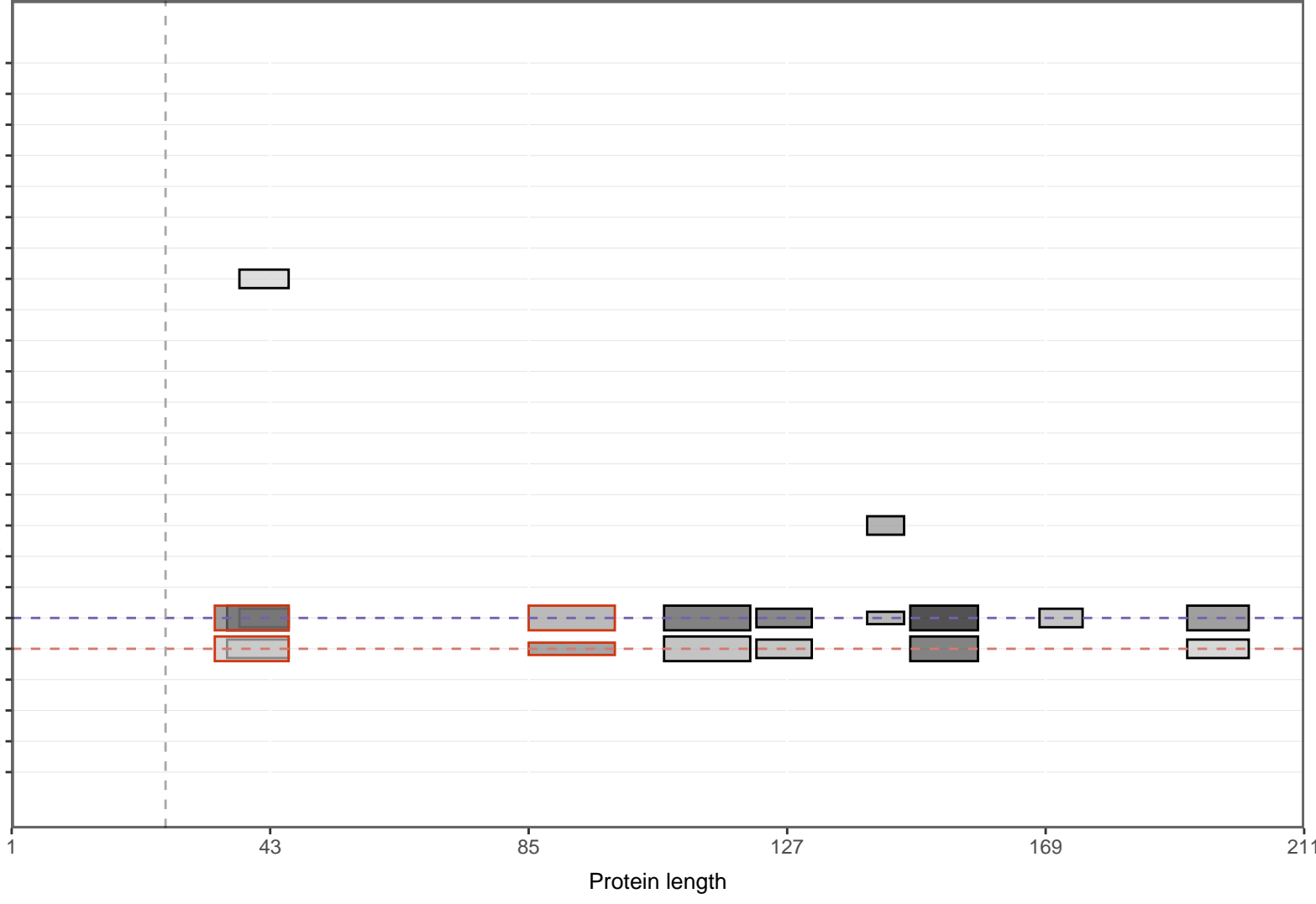
MW indication



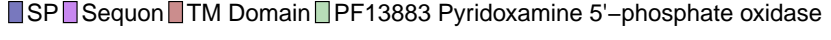
Molecular weight



Gel Slice



Pfam Description

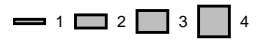


Protein sequence:

JTLDPTRNALKDGRLSLSLSEVANGTGKTPDENPSCAKIFLHGKLLNGDPKETSFAQTALFTRHPEMKGWPKGHNFQFKLEIEEFMINVFGGPKPLVDQYLGAMMDSRVAA

NbL02g24670.1 alpha-mannosidase_2 [MW = 132.39 kDa]

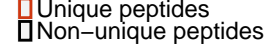
No. of times detected



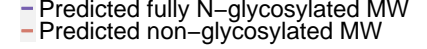
log(intensity)



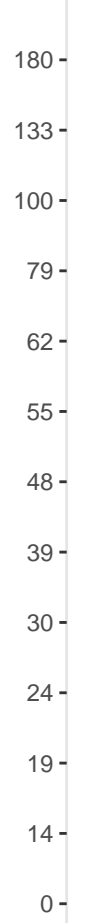
Values from



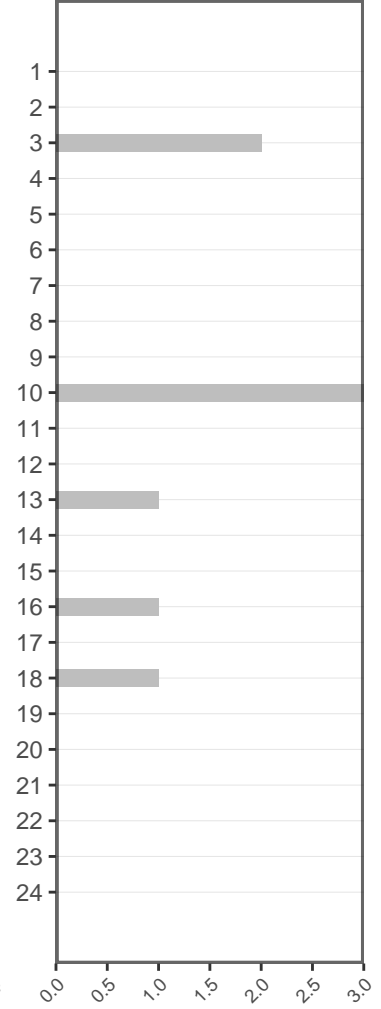
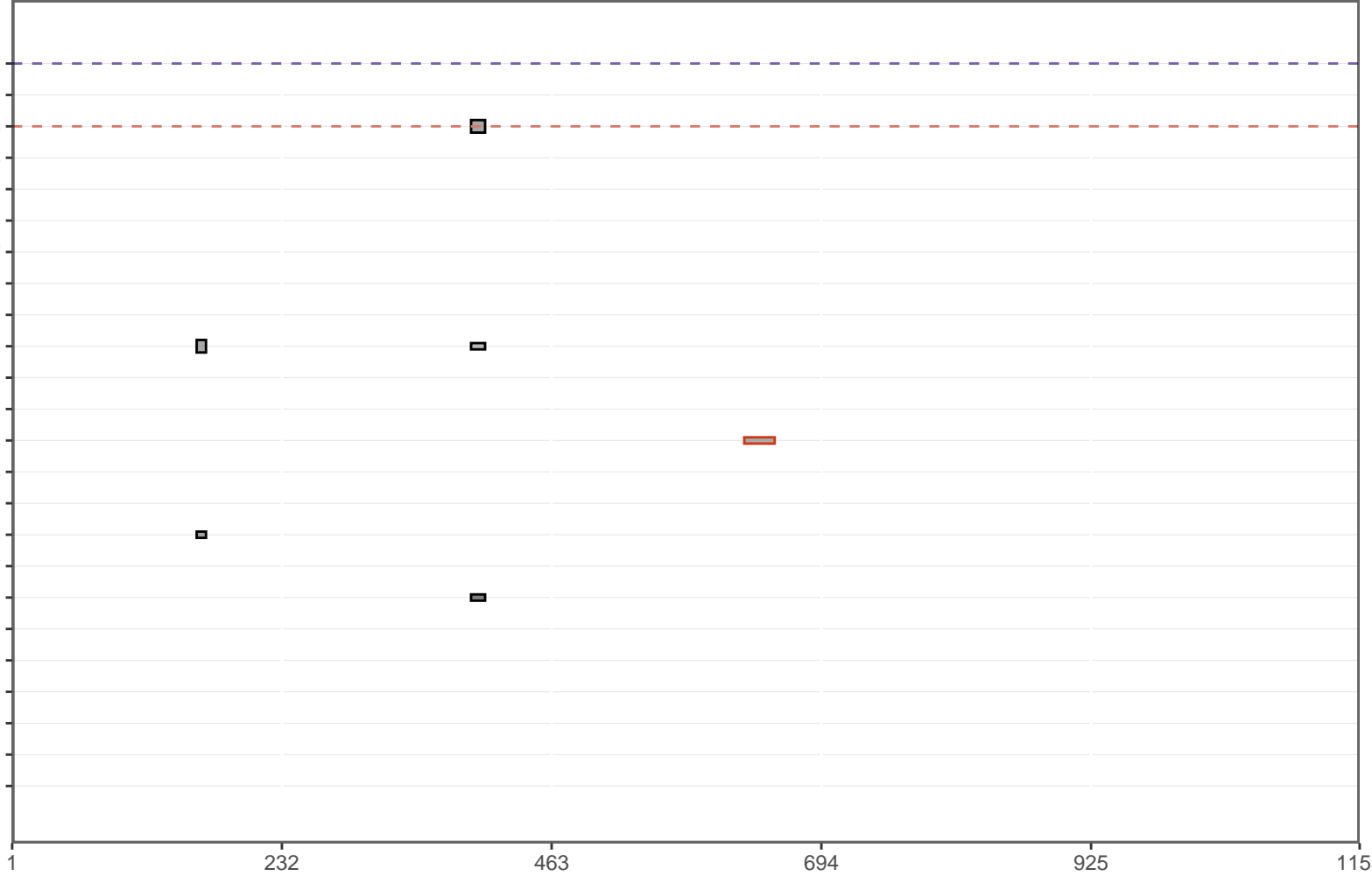
MW indication



Molecular weight

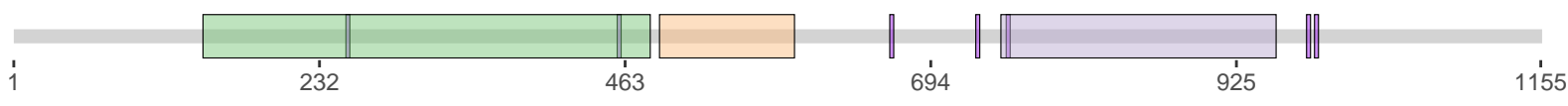


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF01074 Glycosyl hydrolases family 38 N-terminal domain
- PF07748 Glycosyl hydrolases family 38 C-terminal domain
- PF09261 Alpha mannosidase middle domain

Protein sequence:

DHVVQDYGRMIMALGDLGFMKAIEVLLGRHEKNDQHPGDFPQVRSKYDAGPVAWVIAAREGTVGTVALFNPSEGTNEVAVTVERPDP/ILDSNWTCKSGISPELSDKENTFTRRHRYWYKASVPMASLQTYVANGFAGGCKAIPQLRILVPSGNFSCRPYTCDEKLSNEAAIGNENLTVTFSTKFGLLQKVSHPDGRGNVMDIEIDMYS66GAVLFPKPEGEAEPHQAGGMVSEGHVQEVSVYPMATAWDKPSHSTRVNGHNTQDIEHKEYH

NbL02g24660.1 protein_transport_protein_SEC13_homolog_B [MW = 32.63 kDa]

No. of times detected



log(intensity)



Values from



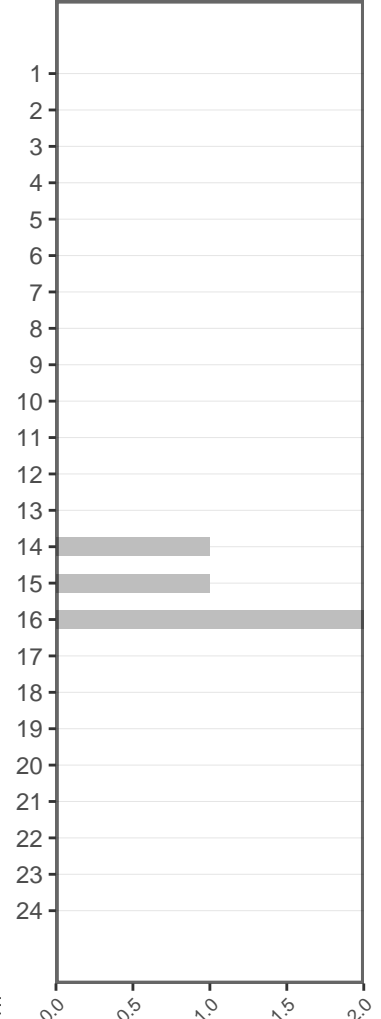
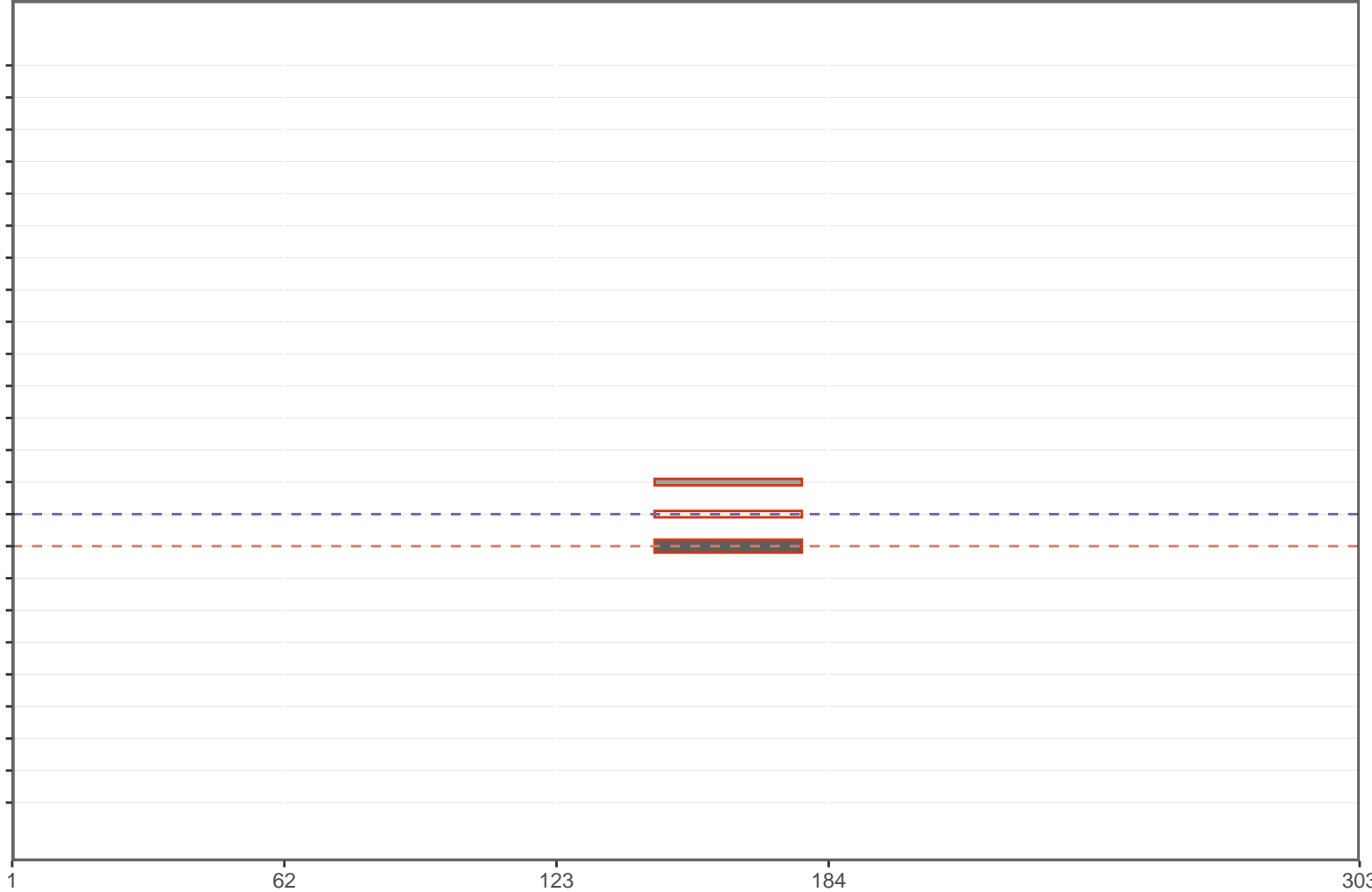
MW indication



Molecular weight



Gel Slice

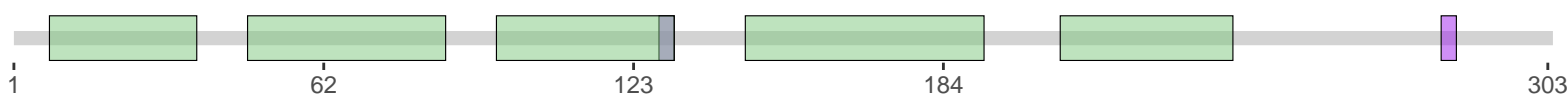


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ITTRIDQJHPVGVTSVSVSWAPSMAPGALVSGVLEPVQKLABGGGDNFVWVWLYNGHWKMDGFRPLQMHFTNWRDVAWAPNLGLPKSTIASASEGDTVVWTFVKEGGQWEGEKVKDFKFTPVWRVSVSLTGNLLVAAGDNNVTLWKEAVDGEWQGAFTVDQ*

NbL02g24600.1 signal_recognition_particle_43_kDa_protein_chloroplastic [MW = 45.36 kDa]

No. of times detected



log(intensity)



Values from



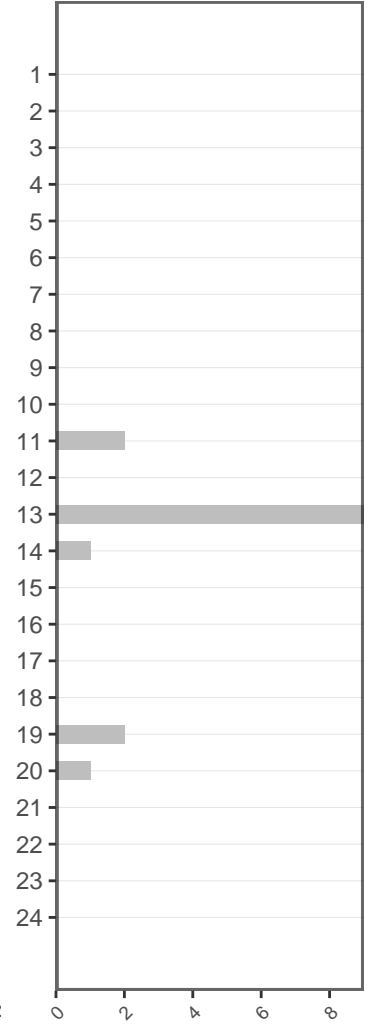
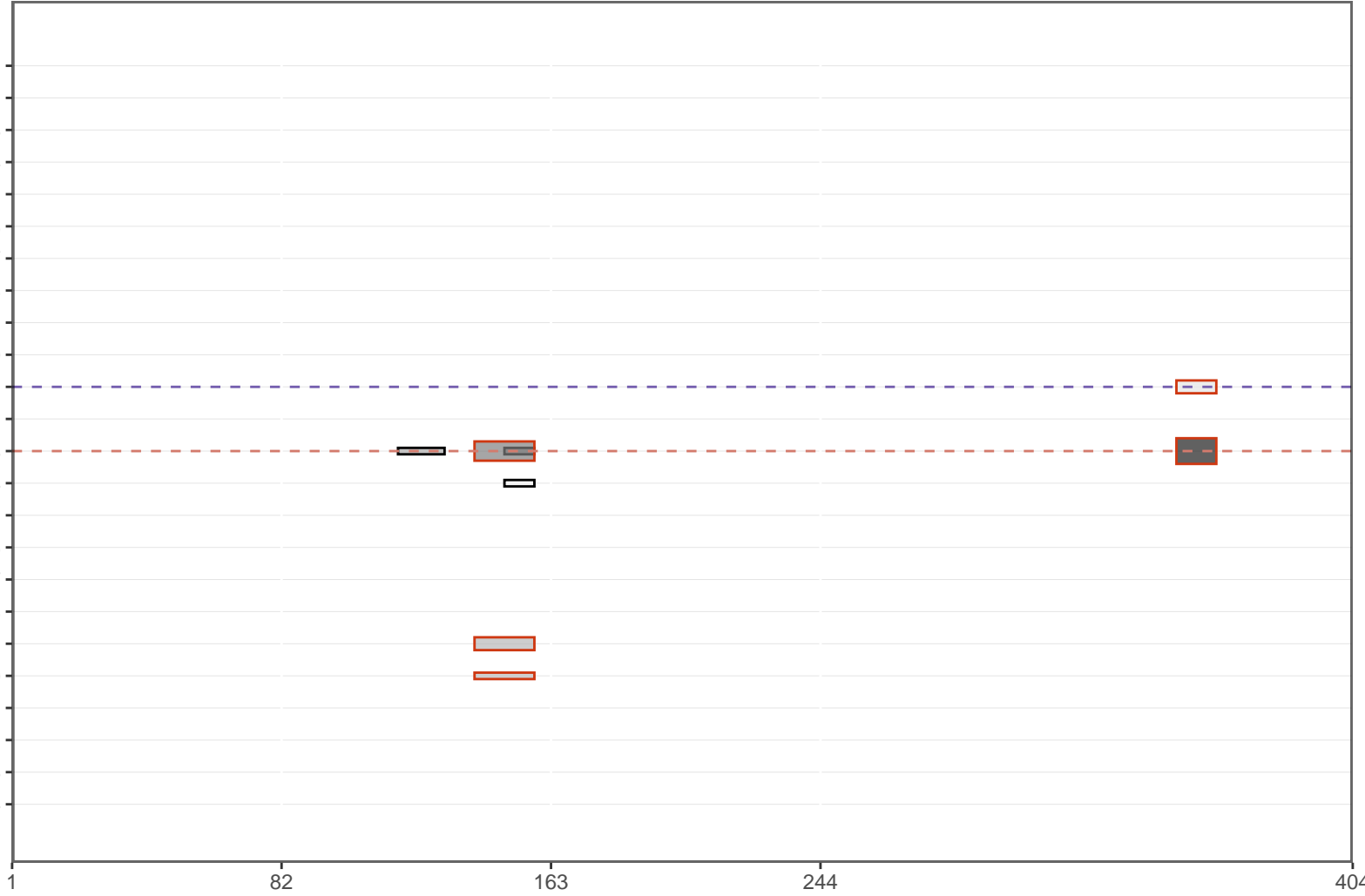
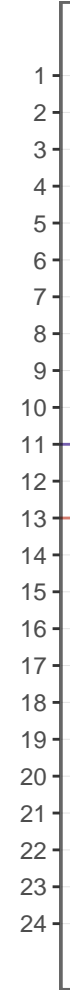
MW indication



Molecular weight

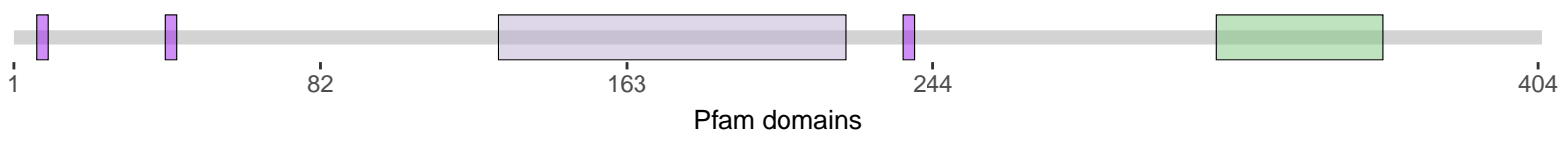


Gel Slice



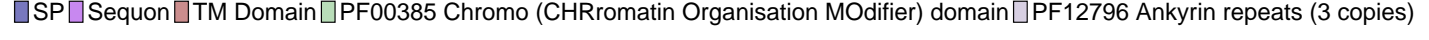
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NGGLTALHMAAGYKPGVAKLLDLGADPEVEDVRRGGTFLSLARMLNQTPKGNPMDGFARRLGLLENVYRILEDAIFEYATVEEILEKRGKGENVEYLKWKDGEDNEWKAWLISEEDVDRDFEAGLEYVAECILEKREAEADKGEVLMKWTDIEEATWEPKENVDFLLIEDFEKGQGNVADLFHGMNEGGVFSKLKSKAEANSGGRVMSFLSY

NbL02g24520.1 inactive_LRR_receptor-like_serine/threonine-protein_kinase_BIR2 [MW - SP = 63.66 kDa]

No. of times detected



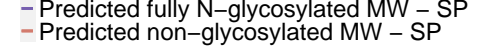
log(intensity)



Values from



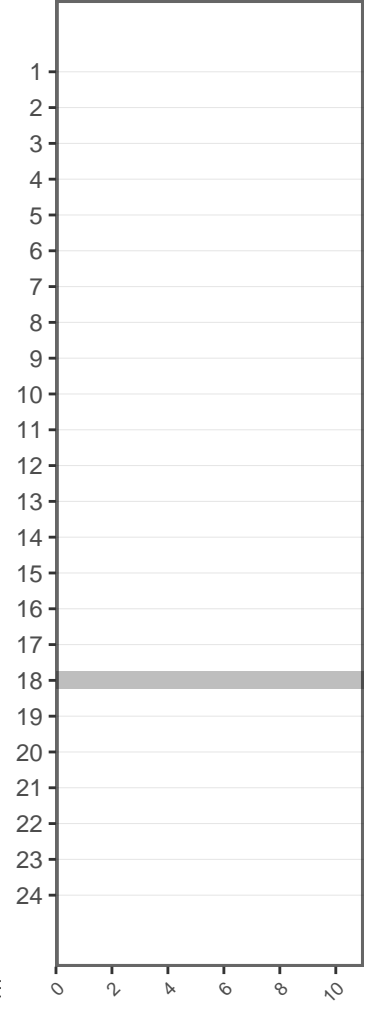
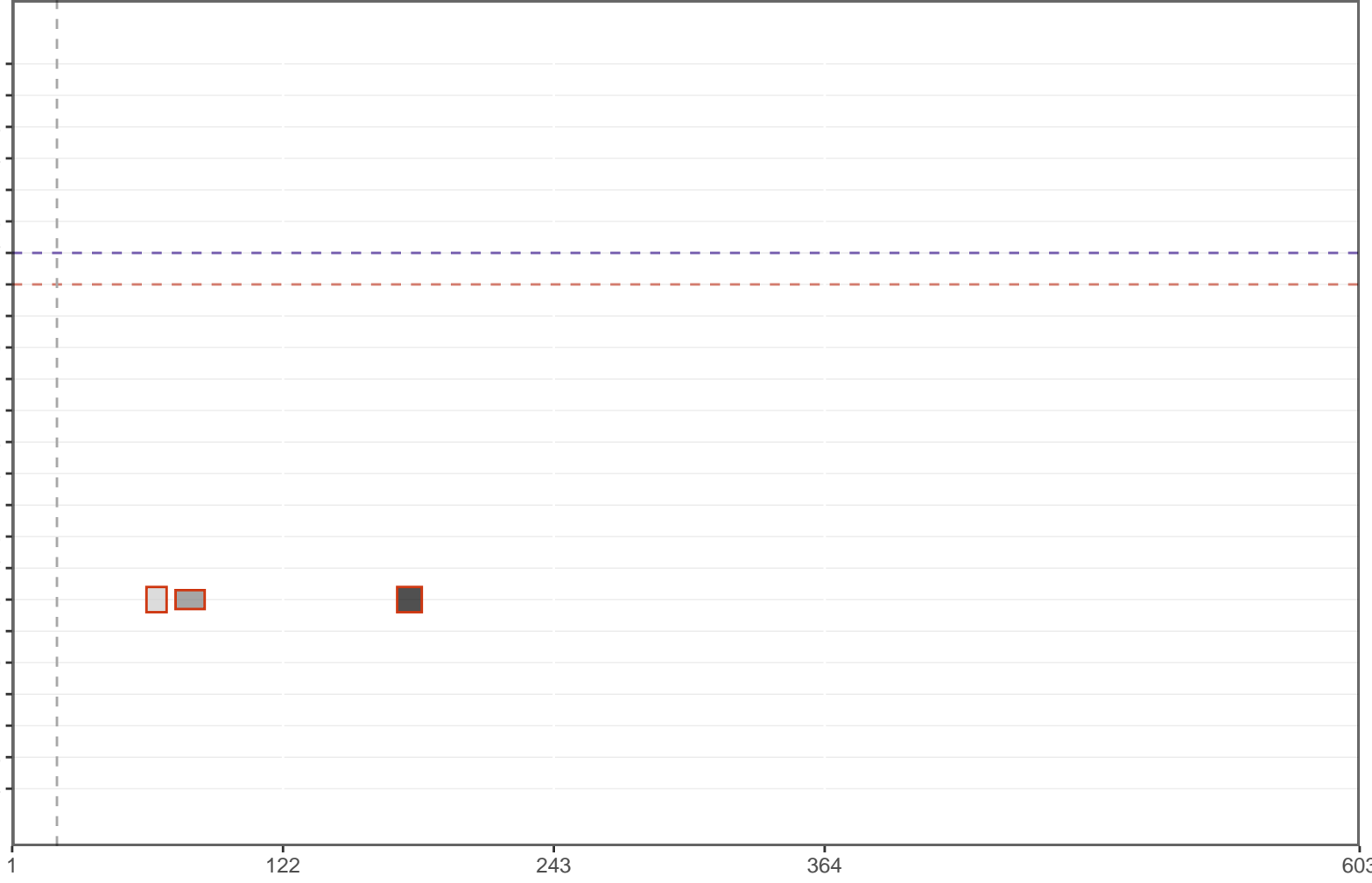
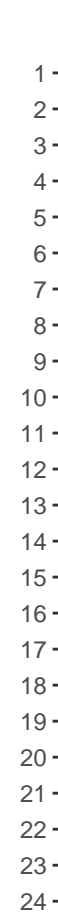
MW indication



Molecular weight

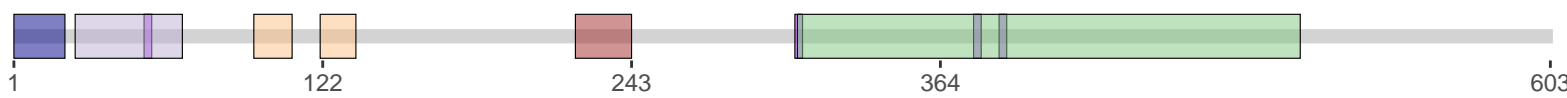


Gel Slice



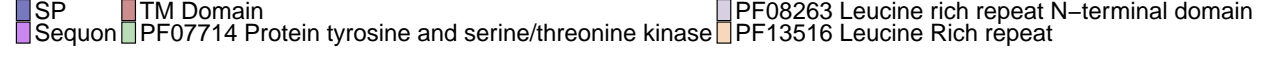
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

LIVDLLVATNSFSDNIVNSTRGTFTYNAVLRDGSALAIKRLNACKLSEKQFRVEMNRLSGLRHPSLVLPLGGYGVVEEKLVYKHLNGLTYSFLNQLSAGLDEWPTFRFRIGLGAARGLAWLHHGGDPLLHQNIGSNVFFLDELDARLMDLGLARLMTPSDAKESFVNGELGEGFYVAPEYSGSTMVPSLKGDAYVSGVAVLELATGQKPLEVTAGEGFRKGNLVDWVAVNGLSASGRKDAIDQNGKGHDEEIVQFLRIACDQVAFRPKERWSMVQVYALKSMAERRGF

NbL02g24440.1 inositol_hexakisphosphate_and_diphosphoinositol-pentakisphosphate_kinase_2-like [MW = 95.13 kDa]

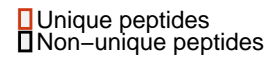
No. of times detected



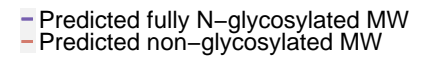
log(intensity)



Values from



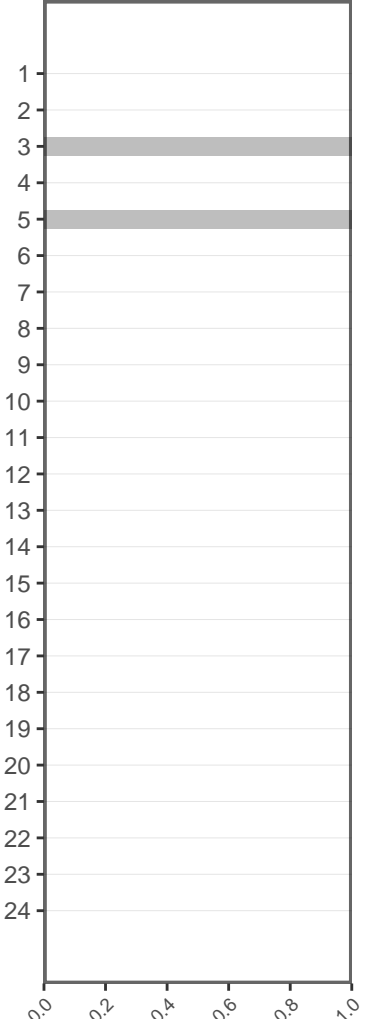
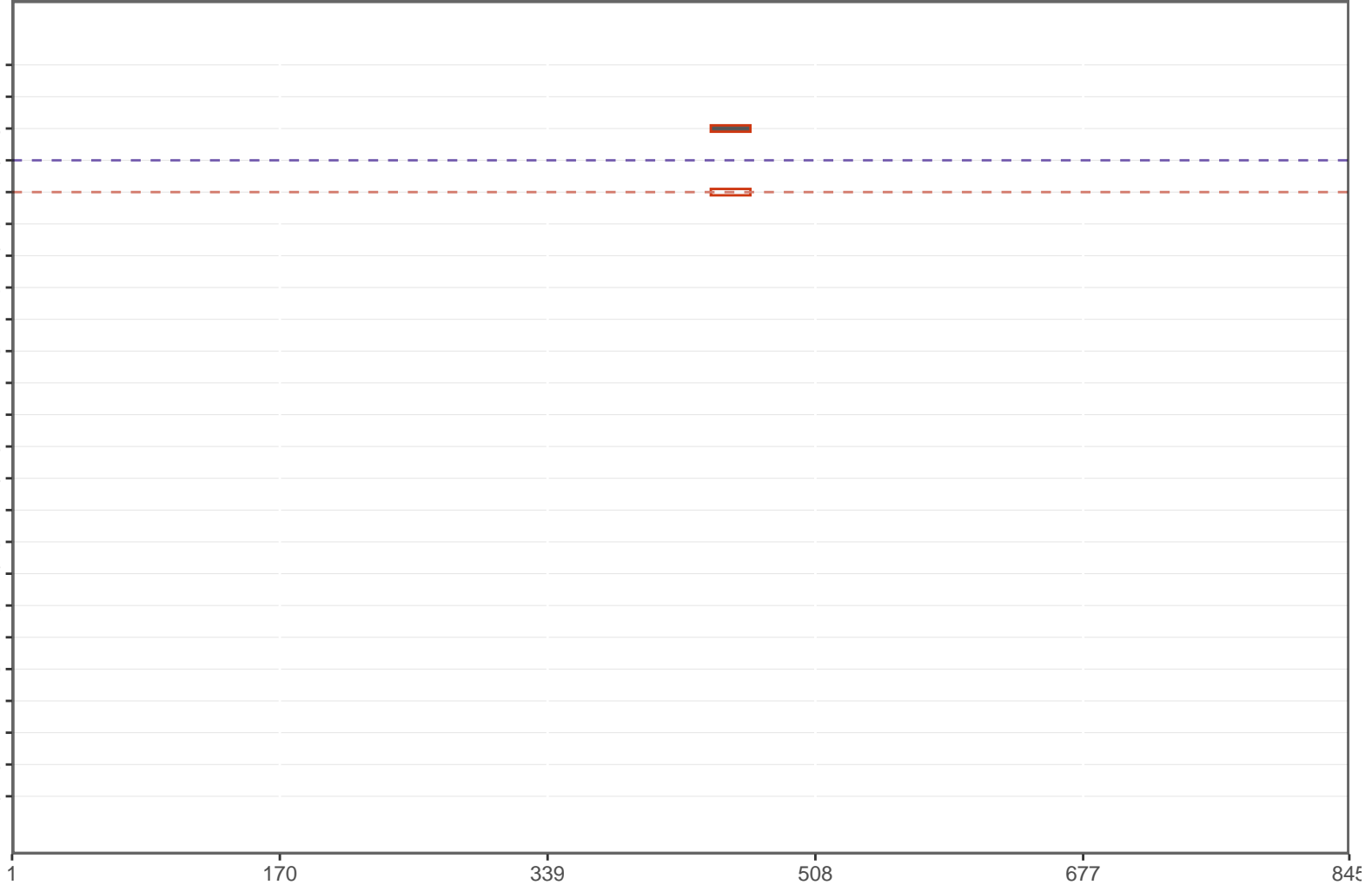
MW indication



Molecular weight



Gel Slice

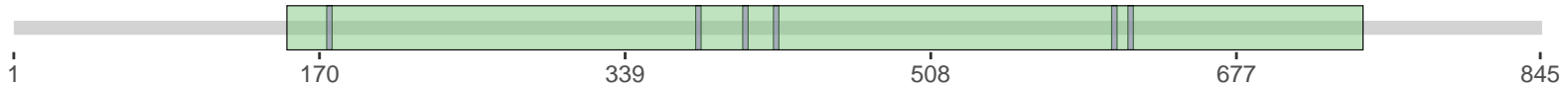


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

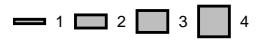


Protein sequence:

SEKPYVMVDSAGLPAKABELLPKLVKTKVTEGVRLLANDEDELEAEASPVDPVPPYDQAKALGKTKNDVDRIAAAGLPGSGEGLLMTAFARWIKLERDLYNERKDRFDIQTIPDYVDSGKYDLHNSHLNLGGLDELFTVAQLLADGVIPNEVGINPKGKLGKSIARRLLGKIMDLRINTREELSAVELKGGDDNHAVNKTFTEDTENHTKPKTRNEESRRTSFNSESRMSDQDDDDDKETRYRLDPKAVANVRTPERHVRTRLYFTSESHLMLNVALRYCNLDESLOEEAS

NbL02g24410.1 FACT_complex_subunit_SSRP1 [MW = 70.83 kDa]

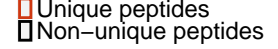
No. of times detected



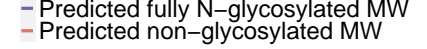
log(intensity)



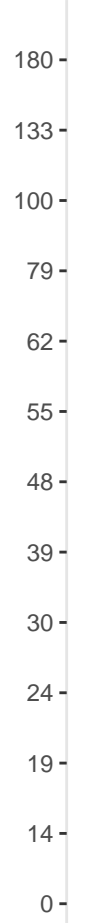
Values from



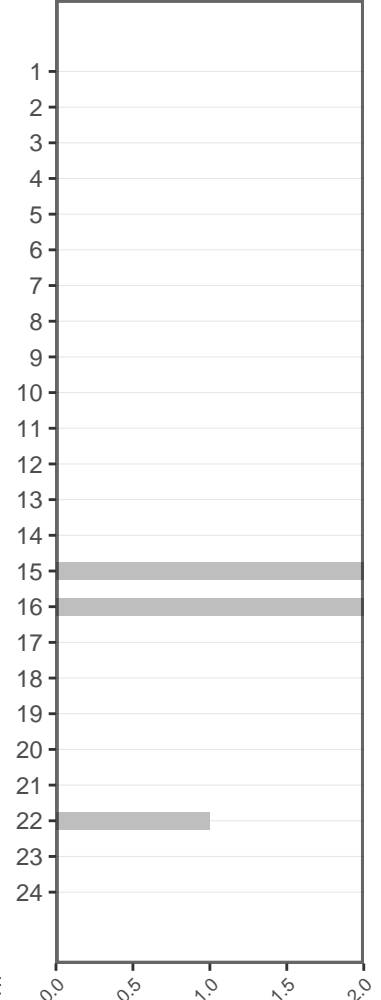
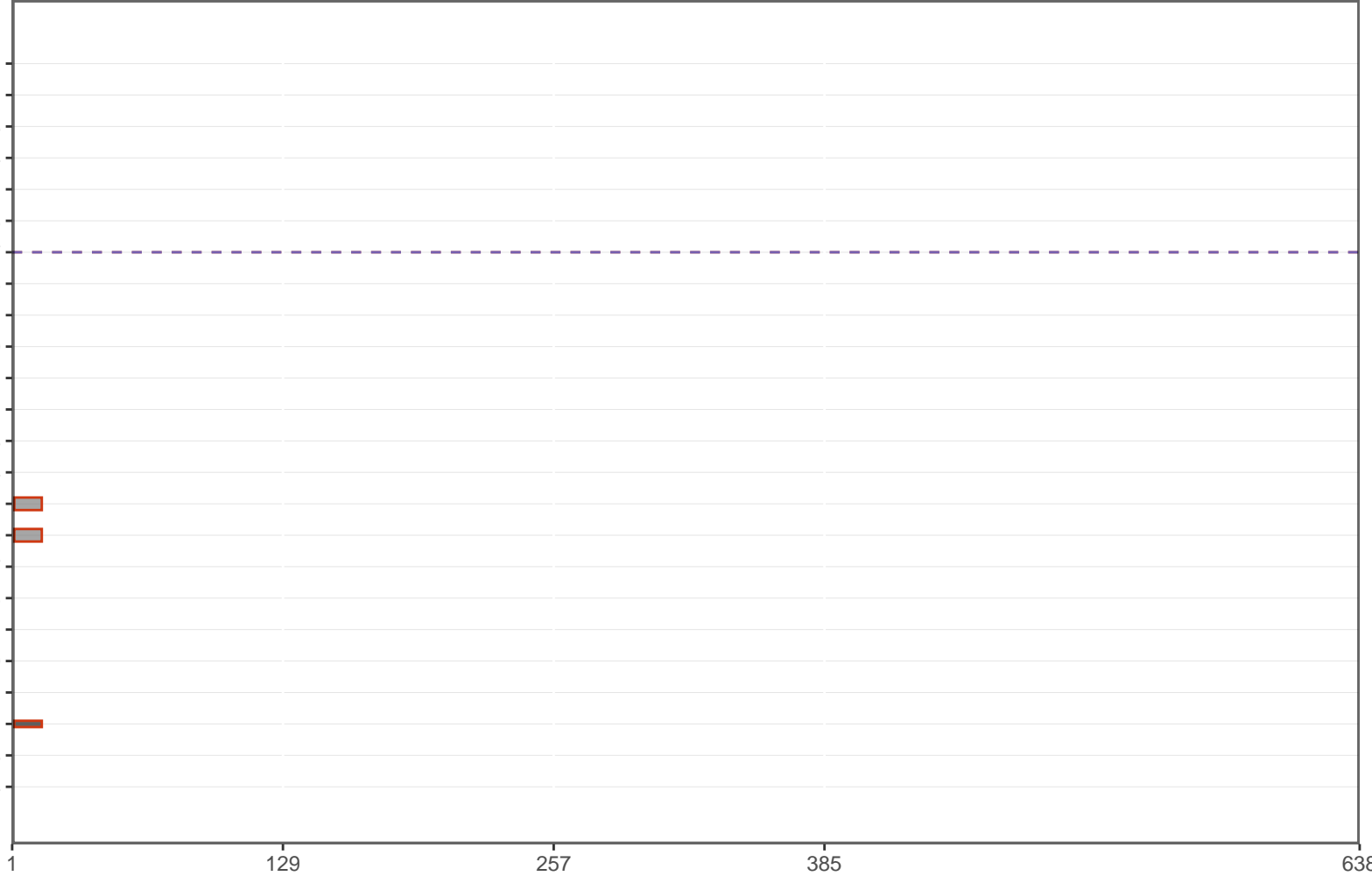
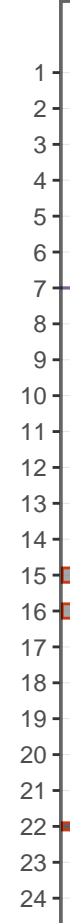
MW indication



Molecular weight



Gel Slice



Protein length

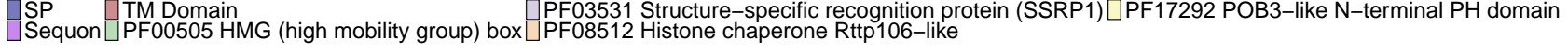


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KYKDRLLPGYKGLHDFITQLRGLSGAKVTKPGKFRSSGDDGYAWKSLKAEDGLLYPLEKSFYFLPKPPTLLHEEIDVVEFERHAAGTANNHYFDLRLRKTQGEHLFRNQRNEVYHNLDFISSKGLKIMLNENARATEGVPLPDEDDAVDPHLERKNEAGDDDEEDEDVFLKDDGGSPDSDGDESDAEDSGGEKEKPKPKKEATVSKPSASRKKADDDGSKKKKKKKDPNAPKRAISAFMFFSGSEREGVKKKFGISFETGRVLRGERVWKLKSAEEK

NbL02g24350.1 ubiquitin-conjugating_enzyme_E2_2 [MW = 17.37 kDa]

No. of times detected



log(intensity)



Values from



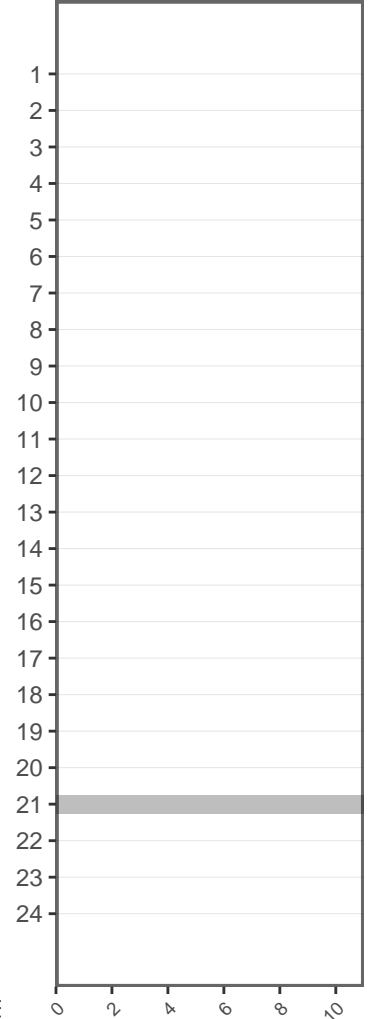
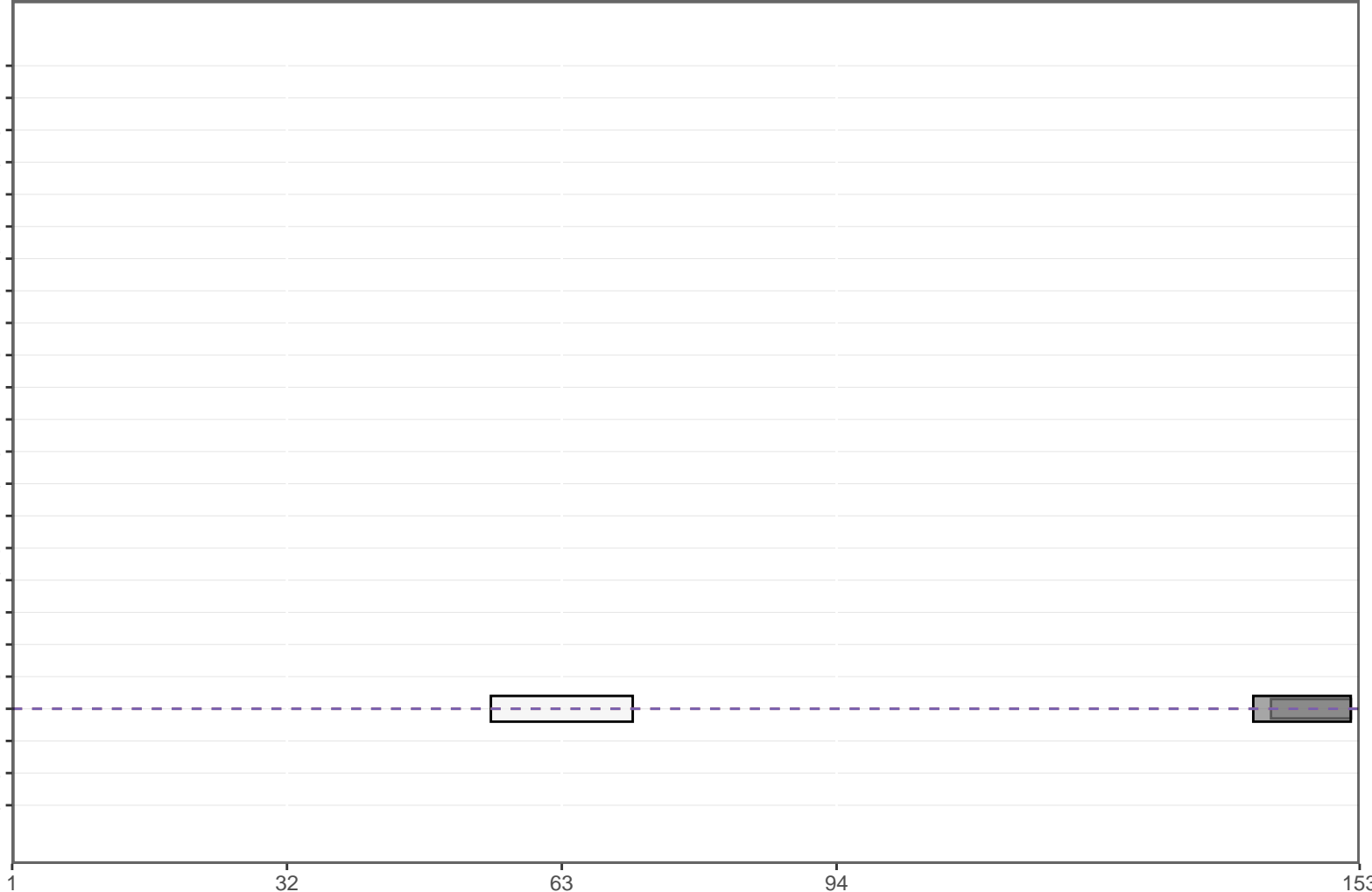
MW indication



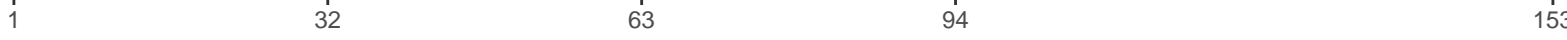
Molecular weight



Gel Slice

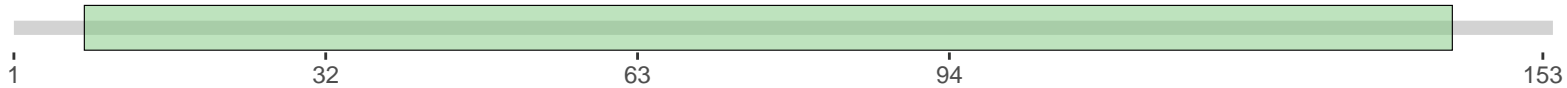


Protein length

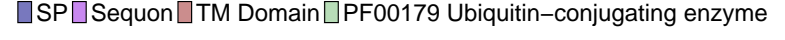


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

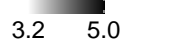
YFNKPPTYRFRSRMFFNIVADGGICLDLQNGWSPYDVAALTSIGSLGDPNPNSEAAARMFSENKREYNRKVREIVEGQWTADP

NbL02g24320.1 aldose_1-epimerase-like [MW - SP = 37.17 kDa]

No. of times detected



log(intensity)



Values from



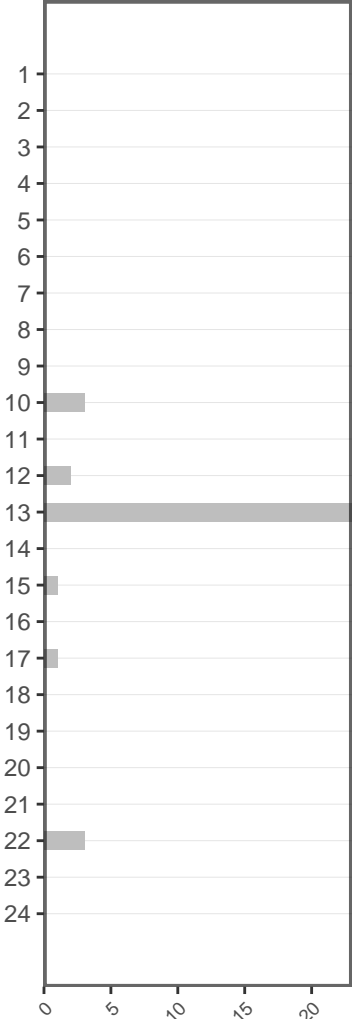
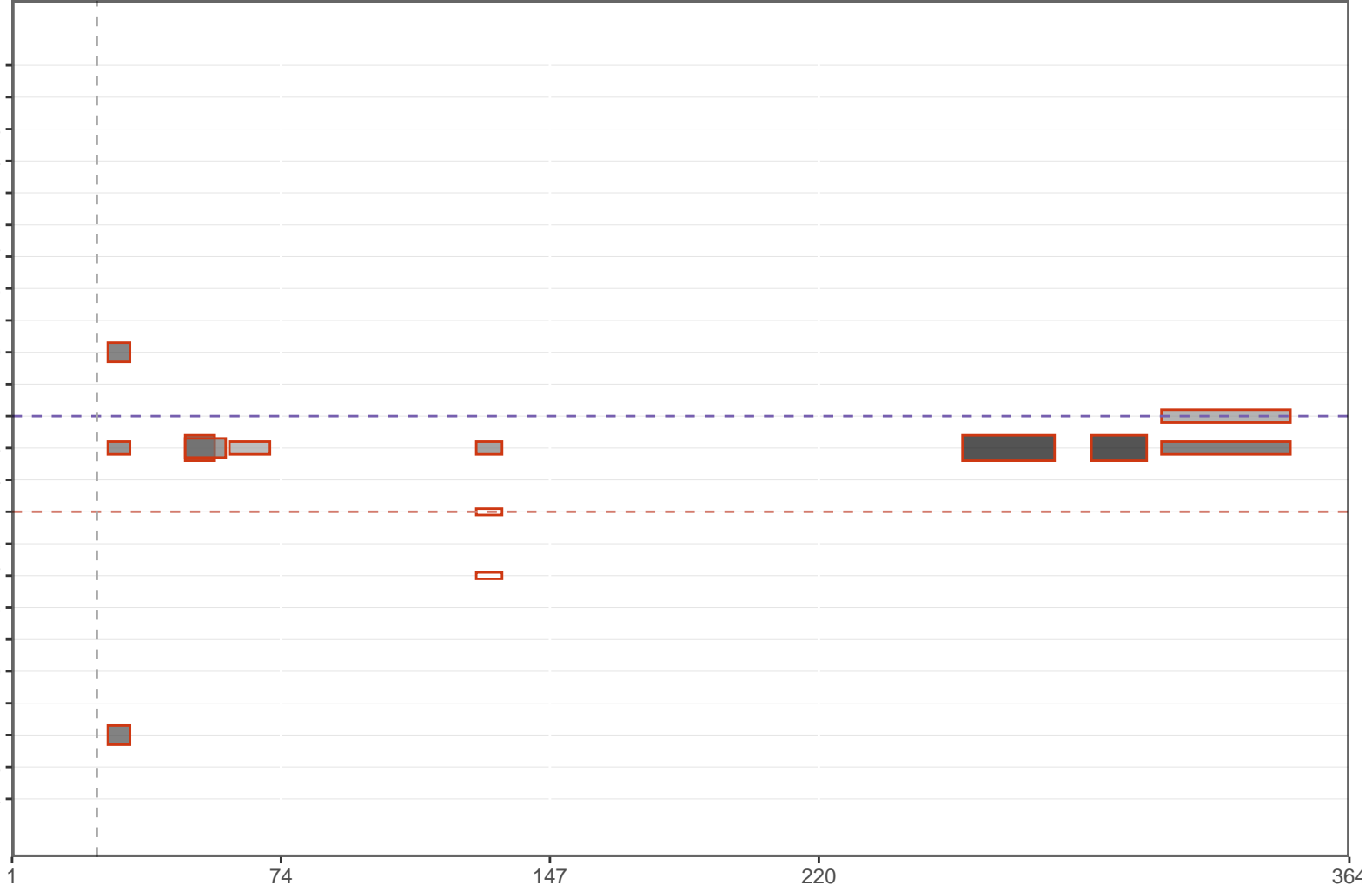
MW indication



Molecular weight

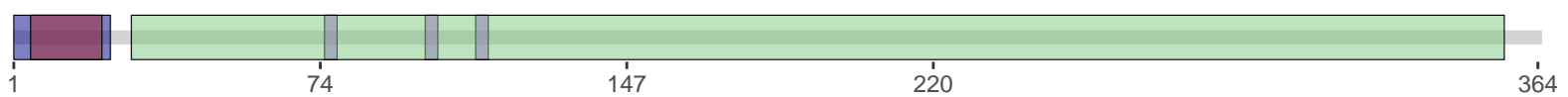


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ALEDPYKLSVVMKAKAKAKATPVLNAGHTFYWNIGGHTSGDLENVIGIFASQIGVDQHLIPTGEFAPVNTAVDFLKPCKVGGQNKLNQGVYDVALDSNENMKPFAVYDRKSGRVMDLKASAPGVGFYTNLSLTKKKGQVYVQPHAAALCLETGGFFDAVNHVNFPTVTPQKSYVHKMLVAFIKKY*

NbL02g24300.1 aldose_1-epimerase-like [MW = 40.23 kDa]

No. of times detected



log(intensity)



Values from



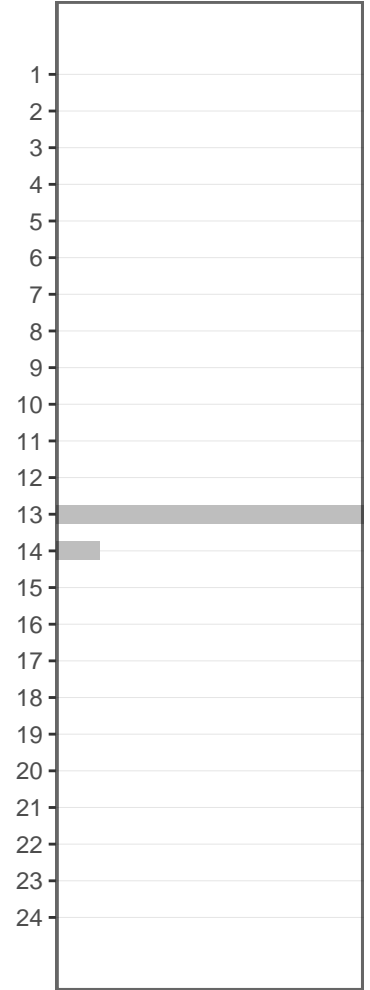
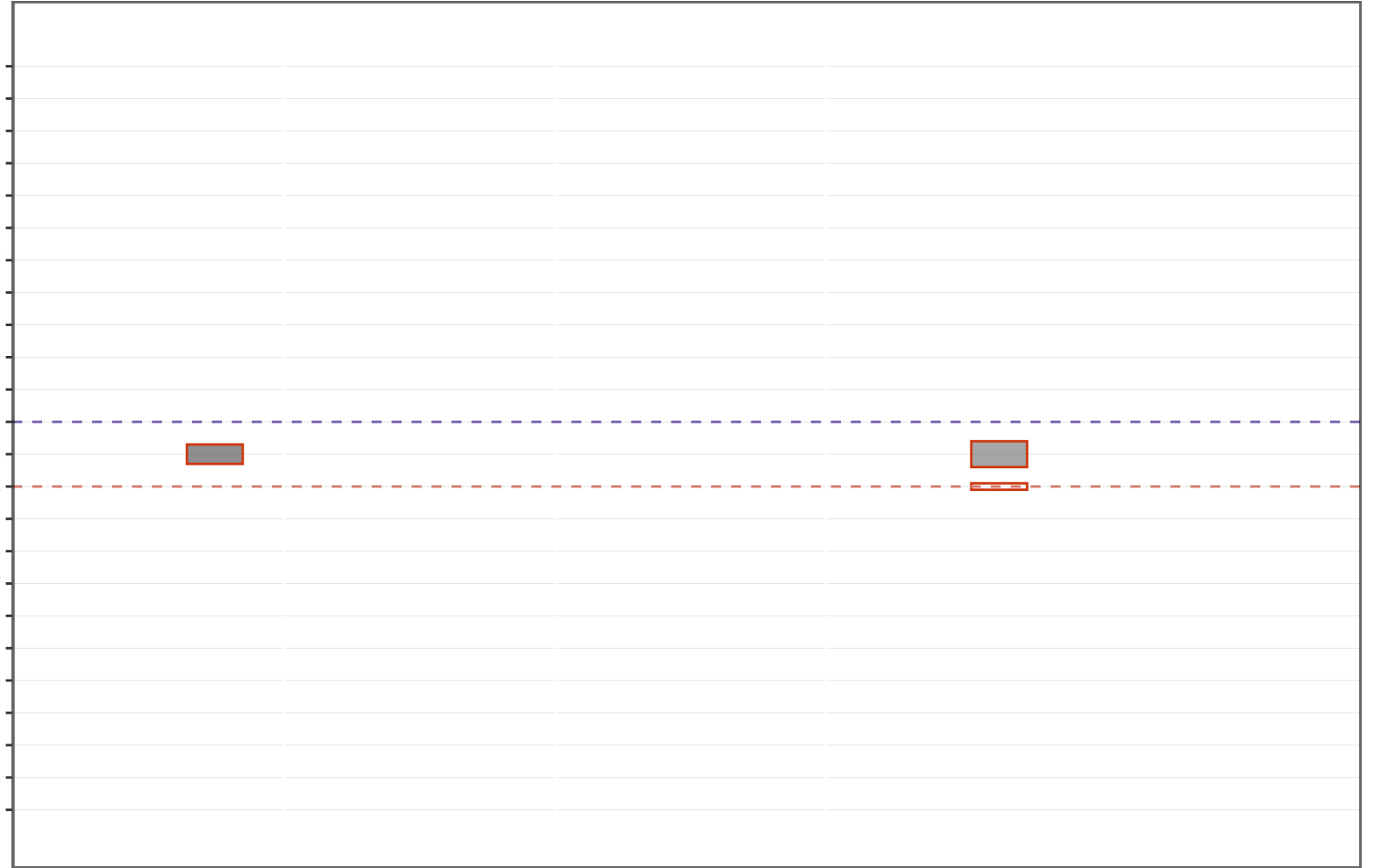
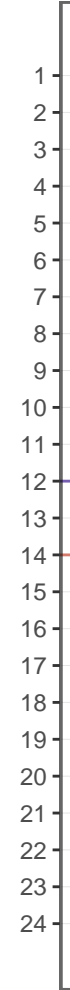
MW indication



Molecular weight



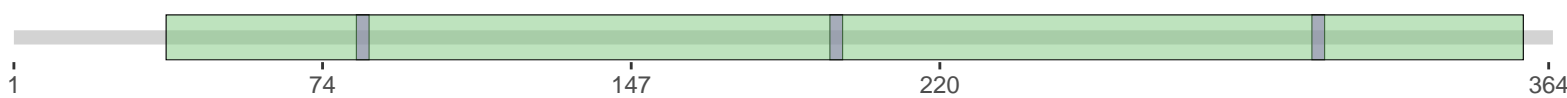
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

ITLKDPIYKLSVYTRAKALNKATPNLSHPYWNNGHNSGDVLSGVLFQSHITLVKELPTGEIAPVKNTPYDLKPRKVGSRINKLNGVDNIVYLDNKKMKFVGLVYDKKSGRVMEDVGAEPGVGYTANFVNTKGGKGFVYQPHALSLETLVFDVAHNPFPSTVNPQDQYVHSVLYTFSSIKI

NbL02g24260.1 tubulin_alpha_chain-like [MW = 49.63 kDa]

No. of times detected



log(intensity)



Values from



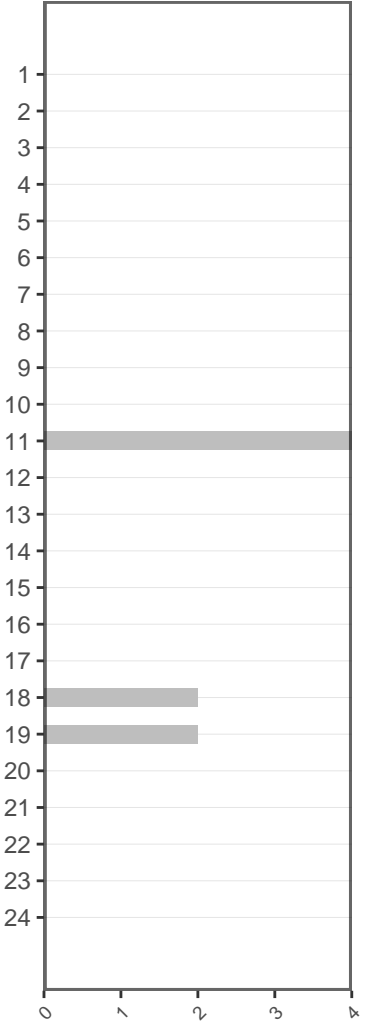
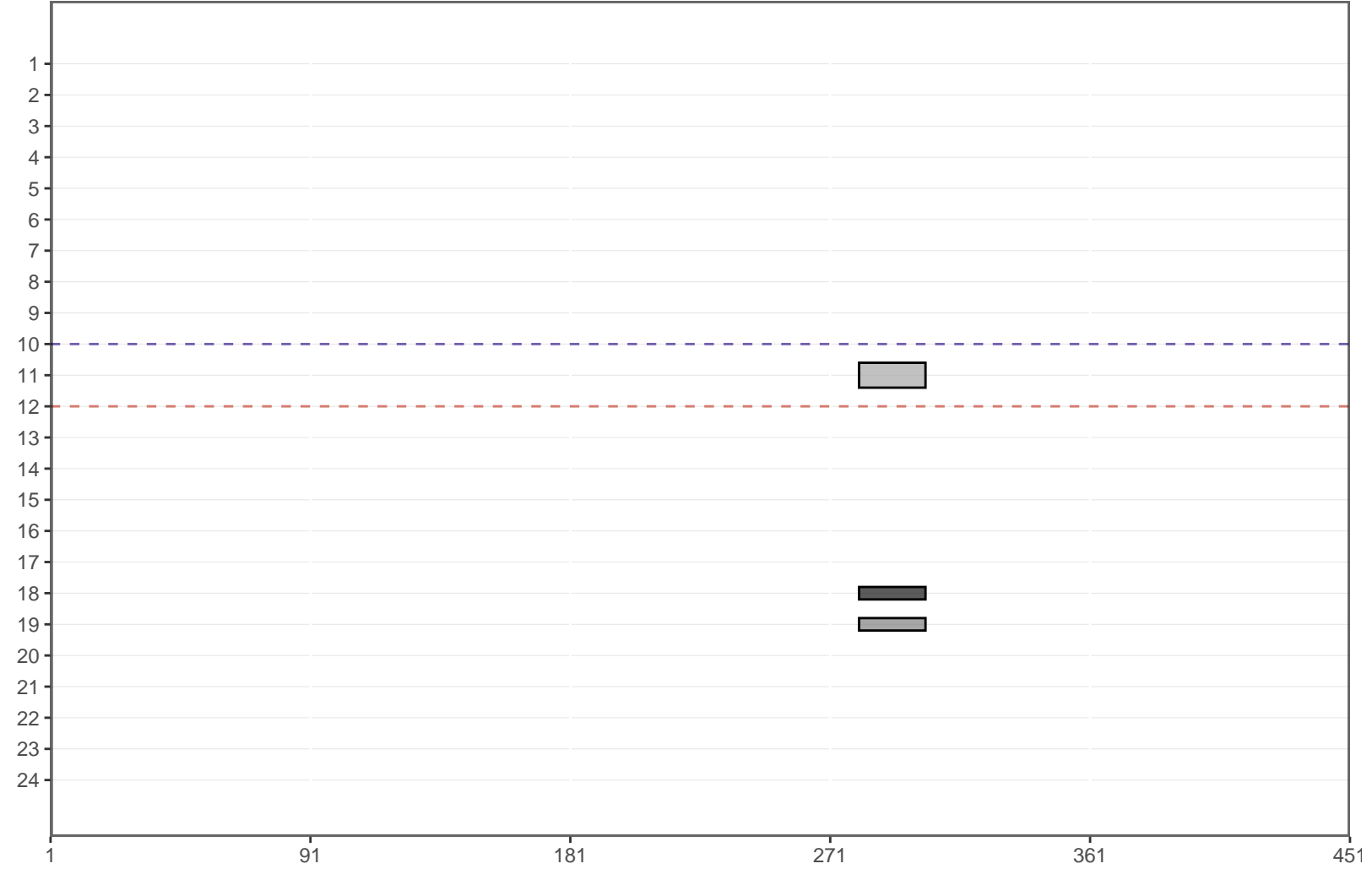
MW indication



Molecular weight



Gel Slice

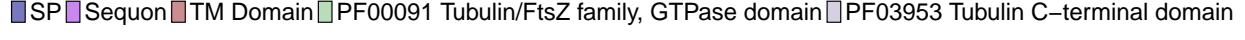


Protein length



Pfam domains

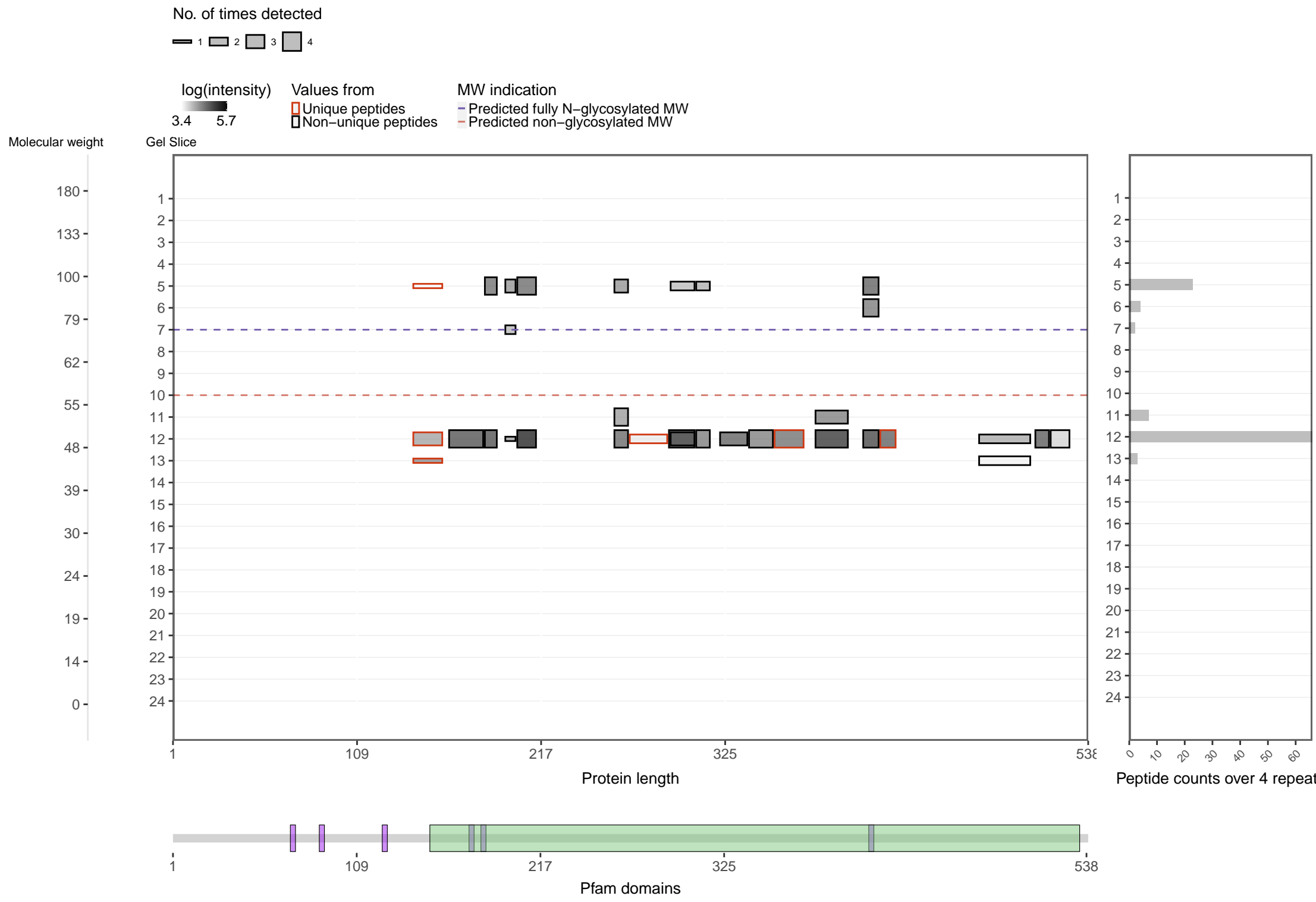
Pfam Description



Protein sequence:

RSKSLDIERPTTYLNLRLSGVHSSLSLRFDGLNVDVNEFQTNLVPYPRHFMLSGYPVSAEKAYHEGLSVAETNTAFEPSSMMVKGDRPHGKYMAAGLGMRYRGDVPKQDVAWAATIKTKRTQGFVDWQPTGFGKGGINYPPTVVPGGDLAKVGRVAVDMENSTSAEIVFGRHKKFDLMYAKRAFVHWYVSGEGMEEGEFSEAREDLAALEKDYEEVGGESGGEDDDVEEY*

NbL02g23980.1 cystathionine_gamma-synthase_1_chloroplastic-like [MW = 57.98 kDa]



Pfam Description
 SP Sequon TM Domain PF01053 Cys/Met metabolism PLP-dependent enzyme

Protein sequence:

CYRKRTRIFETILPKMGTATVIDPADVGTLEALNQKYNLFFTESPTNPLRQVDIEIVSKLCHKEKALVGDIGDTFATPLNQKALALGADLVHLSATKFLGHNDVLAGDGGSEVYKLVSRNLHHLGGALNPNAAVLIIRGMKTLHLRVGGQNGTALRMAEIEAHPKVRHYVYPGLGSHPEHNAKKGMTGFGGVVSEFVDGDLTTAKFVLDALKIFYIAPFSGGSESVDDQRMIMBYWDLGSGDRAKYGMIDNLIYRFSFGVEEDFDLKHADHQLDSF

NbL02g23860.1 uncharacterized_LOC109219811 [MW = 46.51 kDa]

No. of times detected



log(intensity)



Values from



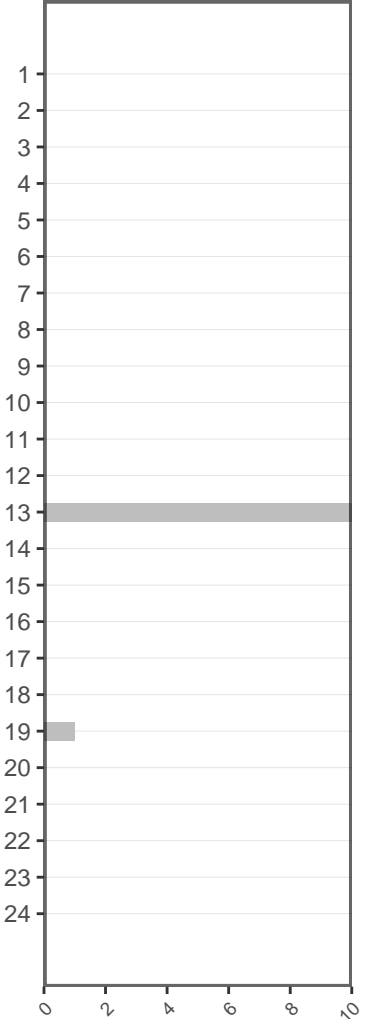
MW indication



Molecular weight

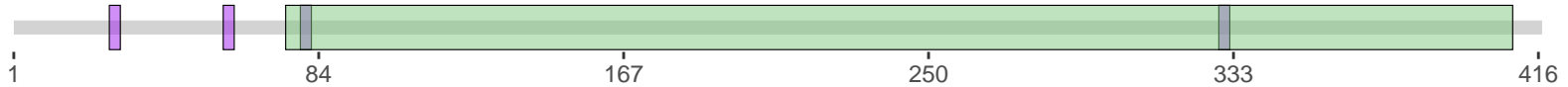


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

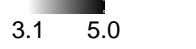
IGYLGEDDGGESPRNLKLPKKPQVIGDNLVBLENDKRVRAFHMDPKGLEMLLVLEERGNQVIPPPLDQFKEDGERIMPHLGTWKGHSLTKRTGVYGATTEAETVALEMMKDKGQLVQDITSTSGASNVITNHHWTGTMQGNLVIQDGGFQLLPGGIYMGVPSDVAHSVQESKSFHLEGLWLEAPGKRQRRLRTYDVEGLAVSSTYFIESK

NbL02g23840.1 chorismate_mutase_1_chloroplastic-like [MW = 36.15 kDa]

No. of times detected



log(intensity)



Values from



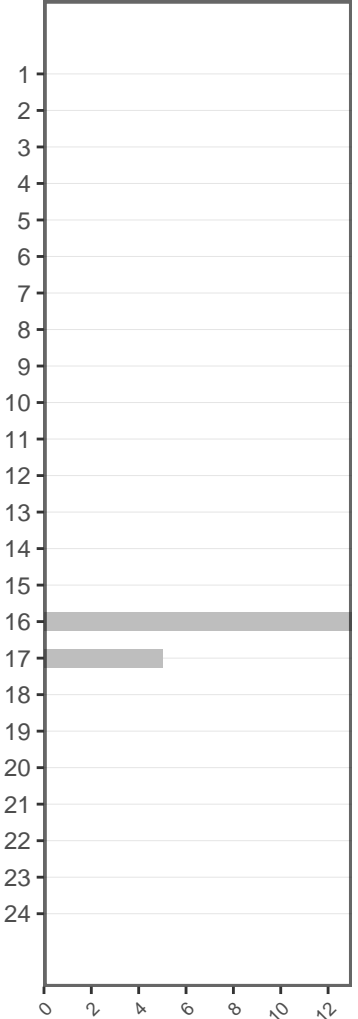
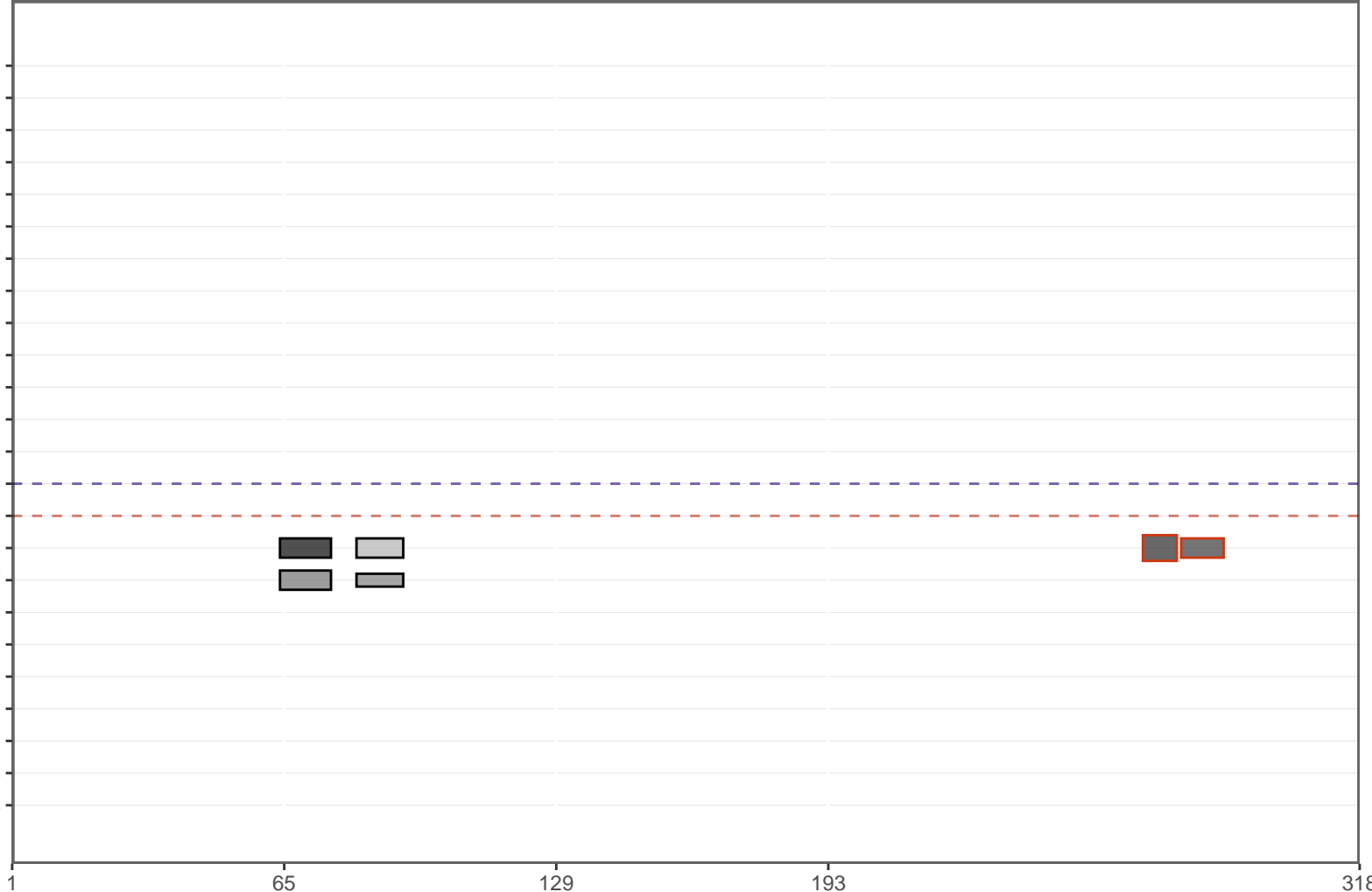
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

ELPEPALPPMCFPKVLHGVADSNVWIKWEMFKNLPRLLKGGDDGNFGSTAVCDTGLQVLSKRHHYGFVAEAKFRASPDVYKAAIRAGDRNGMLDLTYPTVEAATRRVEMKTRTYGDFNKKSPENGDDPVYKIKPSLWELVGDWIMPLTKVQVEVLLRRLD

NbL02g23780.1 probable_ubiquitin_conjugation_factor_E4 [MW = 117.79 kDa]

No. of times detected



log(intensity)



Values from



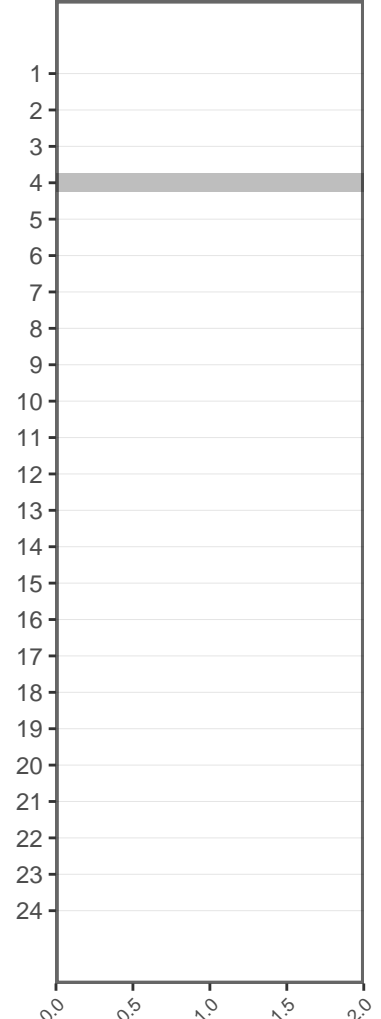
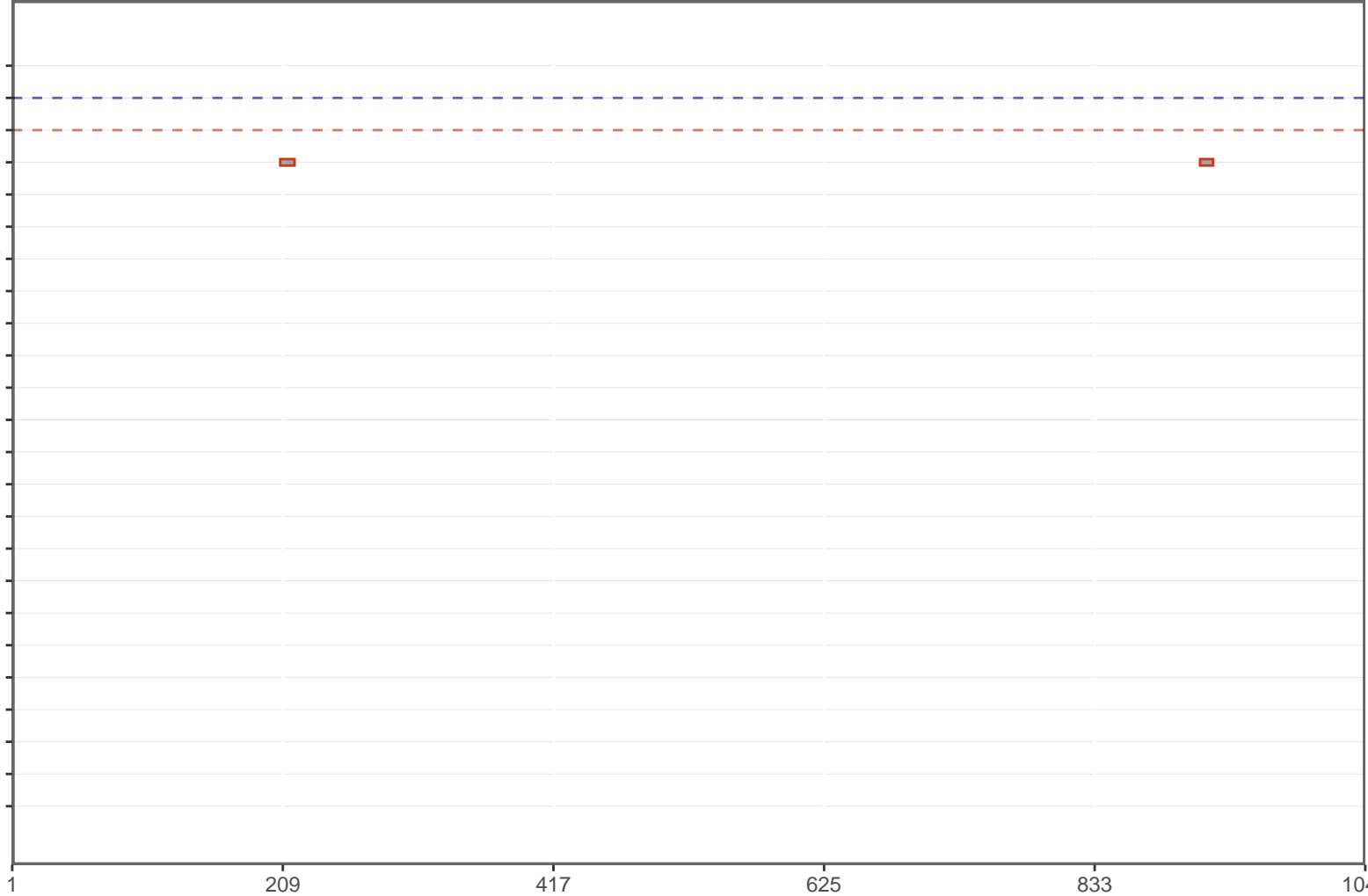
MW indication



Molecular weight



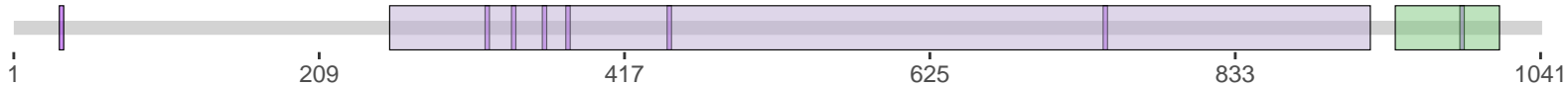
Gel Slice



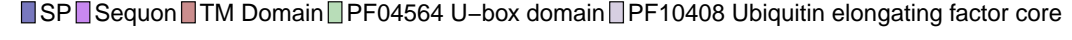
Protein length



Pfam domains



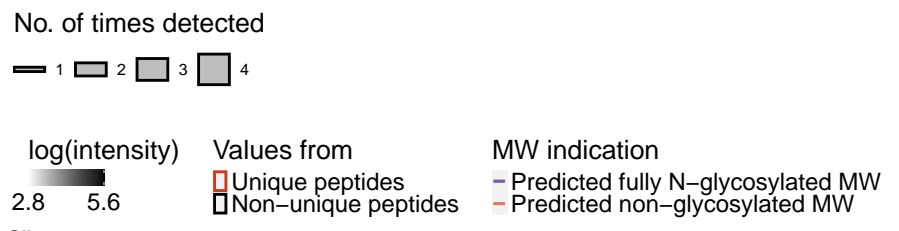
Pfam Description



Protein sequence:

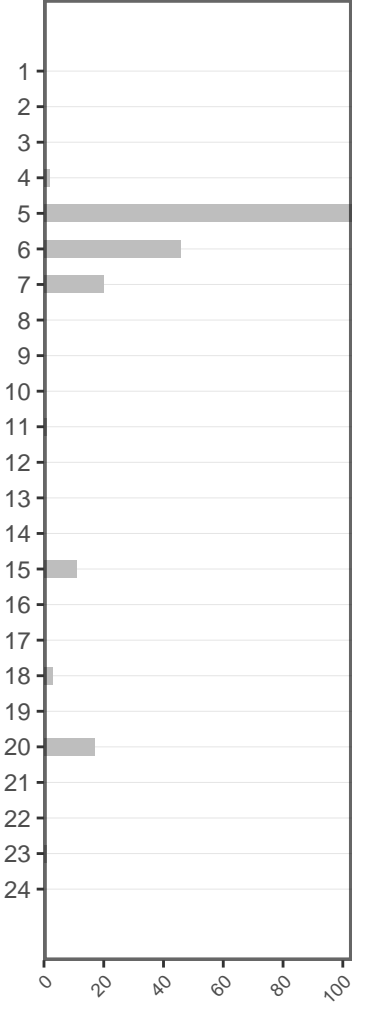
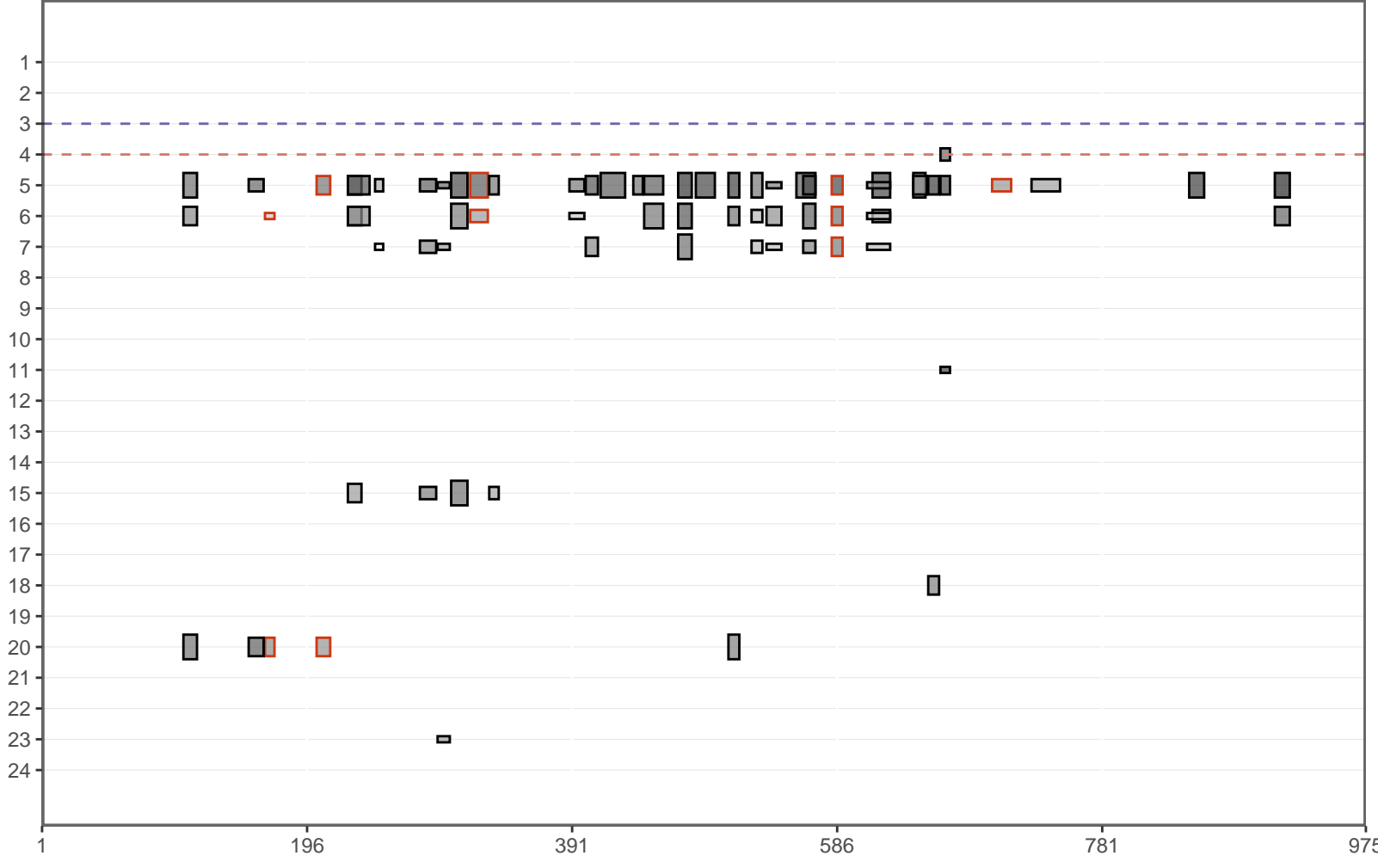
EDILSTMTKMLEQAPSPQLGGESIRLEKELELYSDEKILCYEAQILRDGGLLQRALSFVRLMIVLVGLVGGFKMFLPSPCMQGFASMPHEHLVEDAMELLIFASIRPRALDGLVLLDDFMNIFMFMASPEYIRNPYLRAKMEVVLNGWMPRRSGSTATSTLFEQHQLSELYVRLNLKVVYDFTGSHTFQFYDKFNIRHNAELLELYLVQVPSHRNARFQIAKEEKGVYLNFLNLFINDSIVLLDESLNILELKELEAEMSNTEVWERRRPAQGERGTRLFIHSDENIRIDMKL

NbL02g23710.1 chaperone_protein_ClpB3_chloroplastic [MW = 109.64 kDa]



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

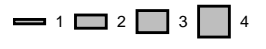
- SP
- Sequon
- TM Domain
- Pf00004 ATPase family associated with various cellular activities (AAA)
- Pf02861 Clp amino terminal domain, pathogenicity island component
- Pf07724 AAA domain (Cdc48 subfamily)
- Pf10431 C-terminal, D2-small domain, of ClpB protein
- Pf17871 AAA lid domain

Protein sequence:

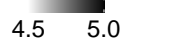
VAALKMETSKPTALDENRAVLKLEMERLSLNDTQKASKDRNLNLEAELELLKKEKQALSTEQWEHEKTVMTIRIGSVKKEEDRVNLEIQQAEREYDNLRAAELEKYSGLNSLQGRGAAAEKELDEVYMGKSGKSMRREVTGNDIAEIVSKVWTGIPVSKLGGSEREKLLHLEELHKKRVVGGDDPRAVAEAGRSRAGLSDPHRIASLAFMFMGPTGVGKTELAKALANLFTTEELVRIDMSEYMEKHAVSRILGAPPVYGVYEEGGQLTEIVRRPWFILFDEIKAHADYF?

NbL02g23660.1 UDP-glucose_6-dehydrogenase_3-like [MW = 53.07 kDa]

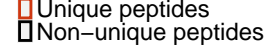
No. of times detected



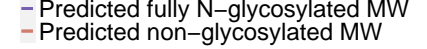
log(intensity)



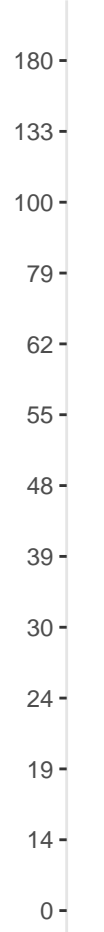
Values from



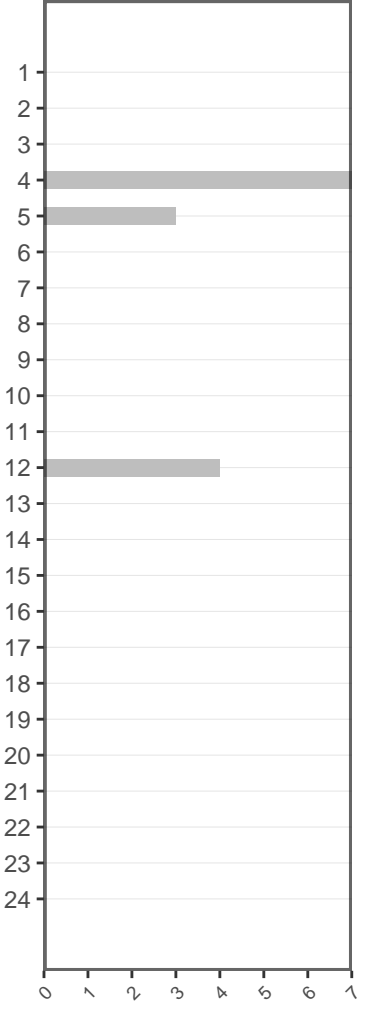
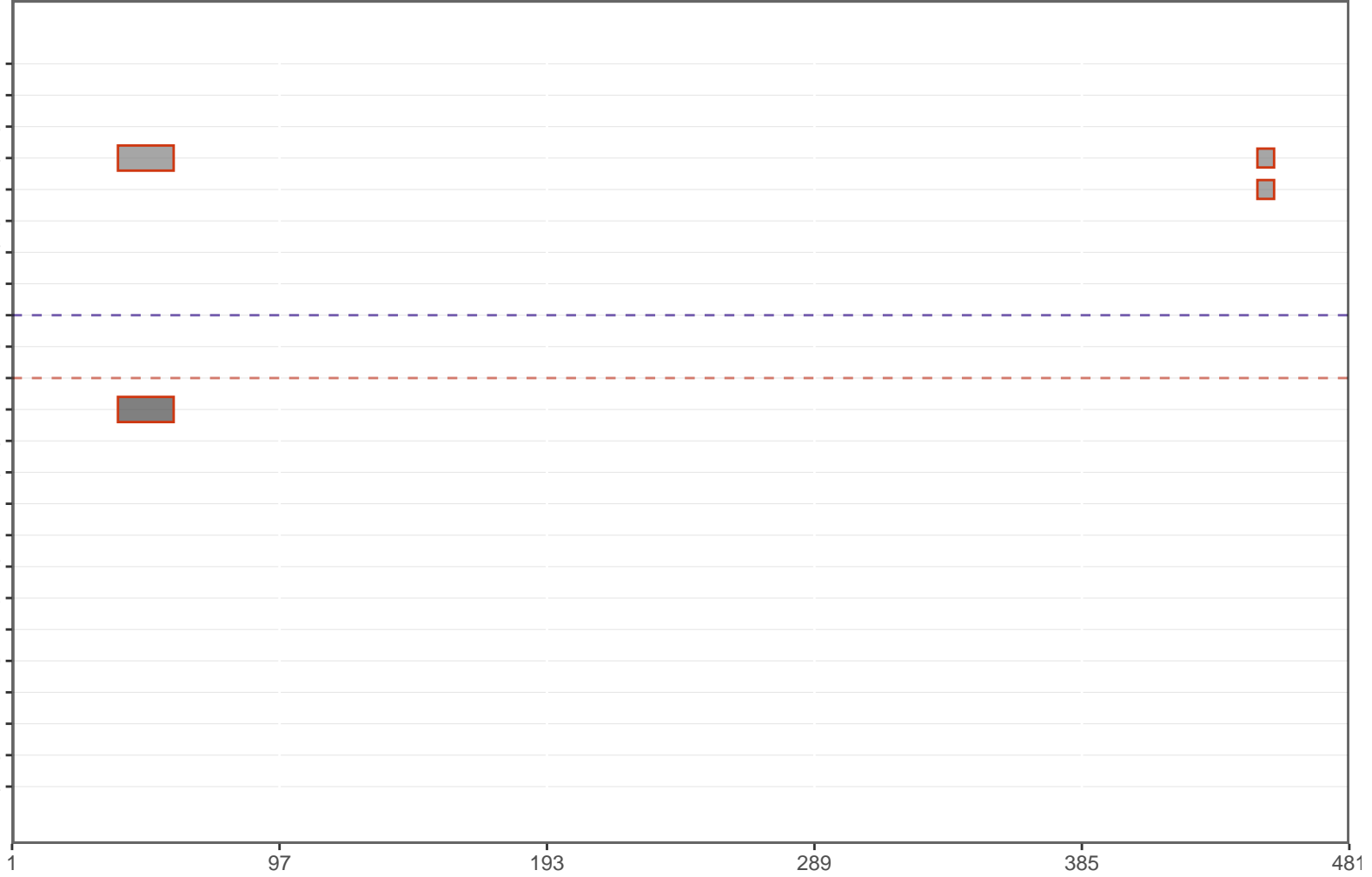
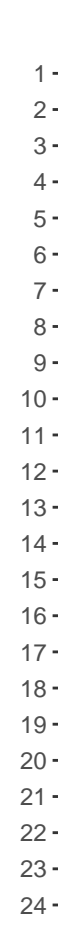
MW indication



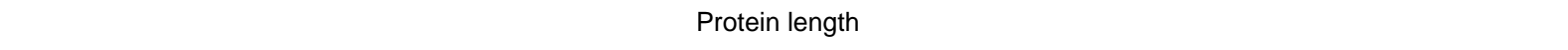
Molecular weight



Gel Slice

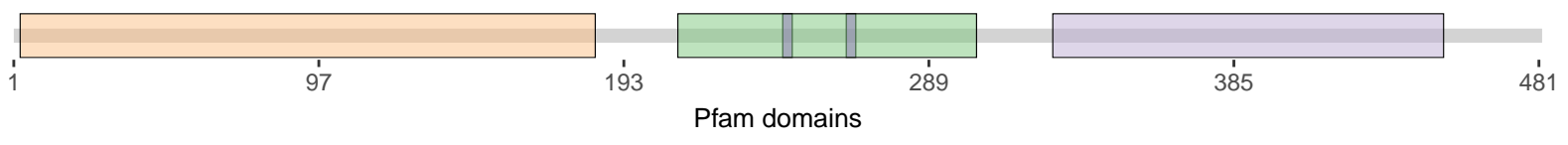


Protein length



Peptide counts over 4 repeats

Pfam domains



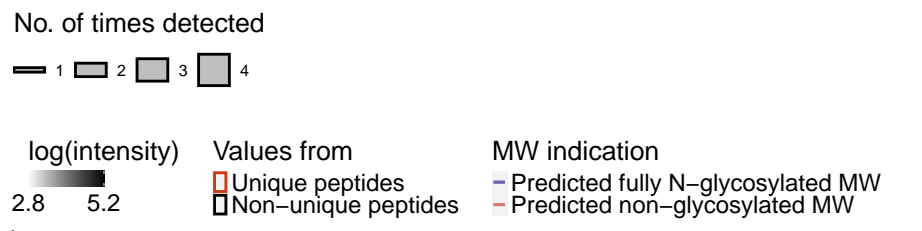
Pfam Description

- SP
- Sequon
- TM Domain
- PF00984 UDP-glucose/GDP-mannose dehydrogenase family, central domain
- PF03720 UDP-glucose/GDP-mannose dehydrogenase family, UDP binding domain
- PF03721 UDP-glucose/GDP-mannose dehydrogenase family, NAD binding domain

Protein sequence:

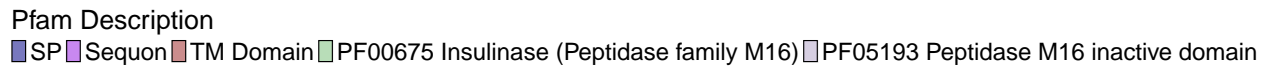
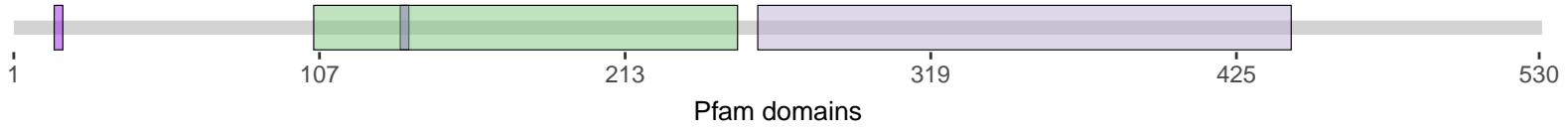
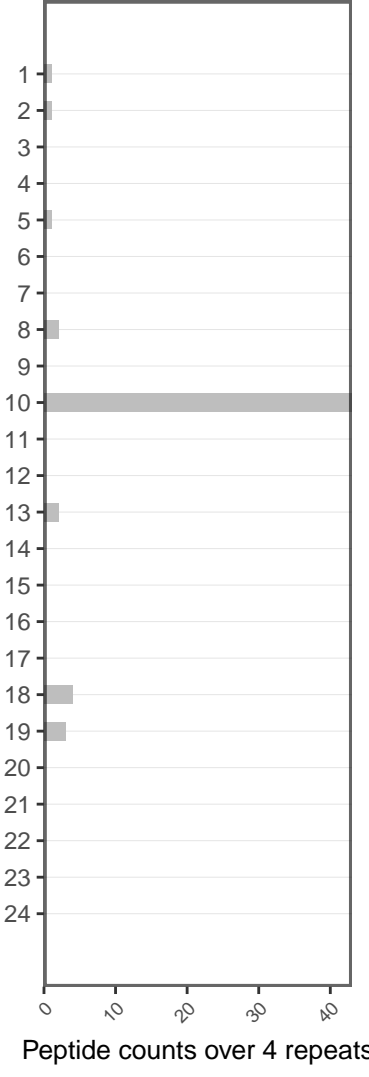
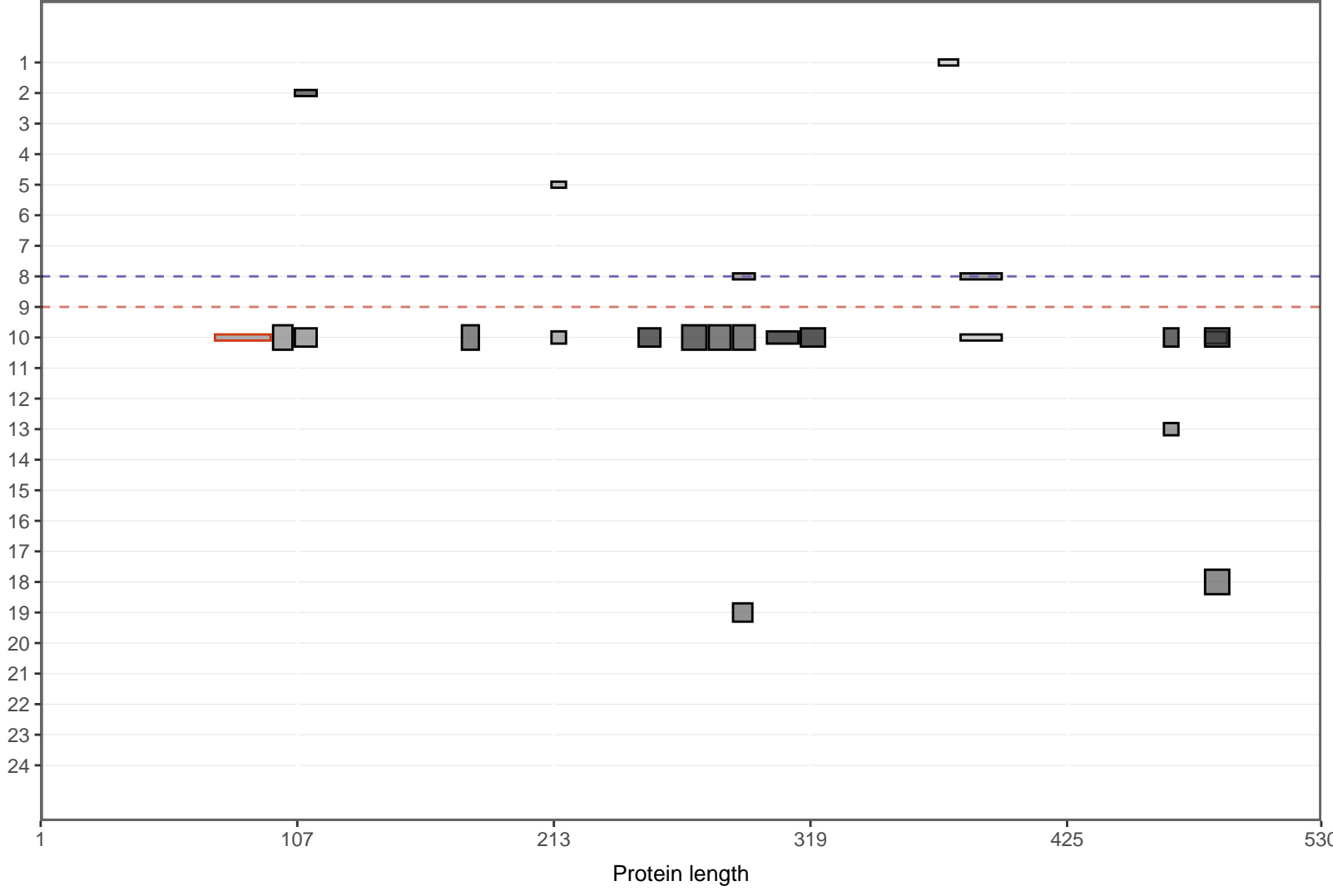
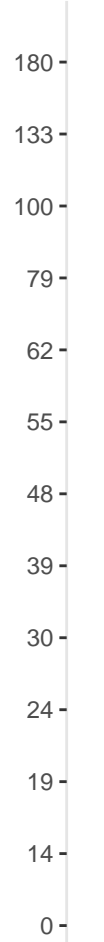
VNMSALCEATGANNVSGVSVAVGKDRIGPKFLNABVGFGGSGFKDILNLYHCEGNGLPEVAEYVWKGVRKINDYQKRFVNRVAAMFNTVSNKKVALGFARFKDTGDTRETPADVCGKGLGDKARLSHYDPQVGGEDQKRDLSMKNKFDWDHPLHLQPMSPFTTKLVSVTWDVYEATNDAAHVCLTEWDFEFTLQYGRHVENMGKPAKRFDGRNIVNVDKLRIGFIVYSGKPLDAWLKMPAAV

NbL02g23640.1 probable_mitochondrial-processing_peptidase_subunit_beta_mitochondrial [MW = 59.07 kDa]



Molecular weight

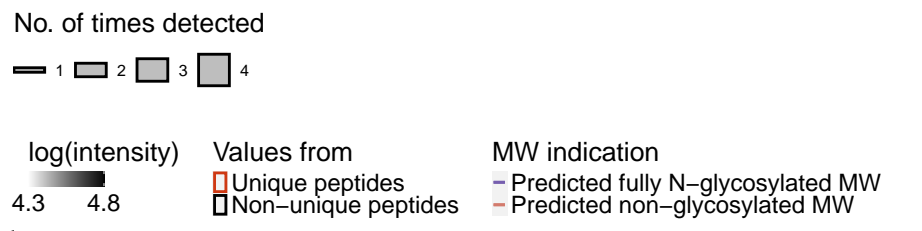
Gel Slice



Protein sequence:

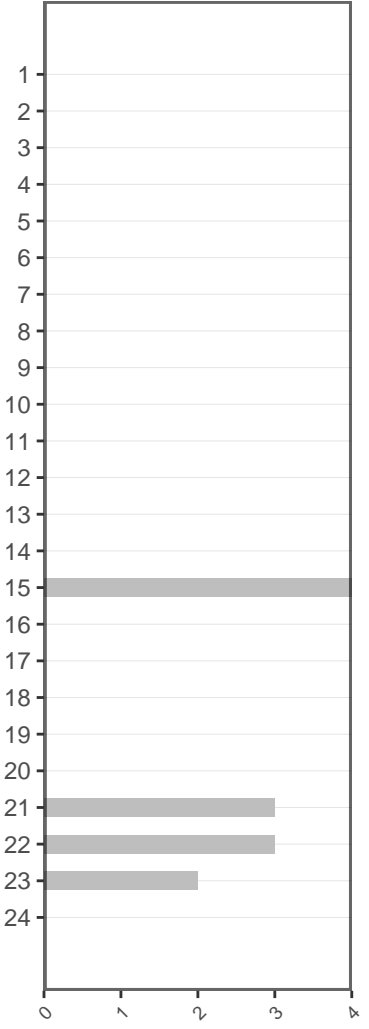
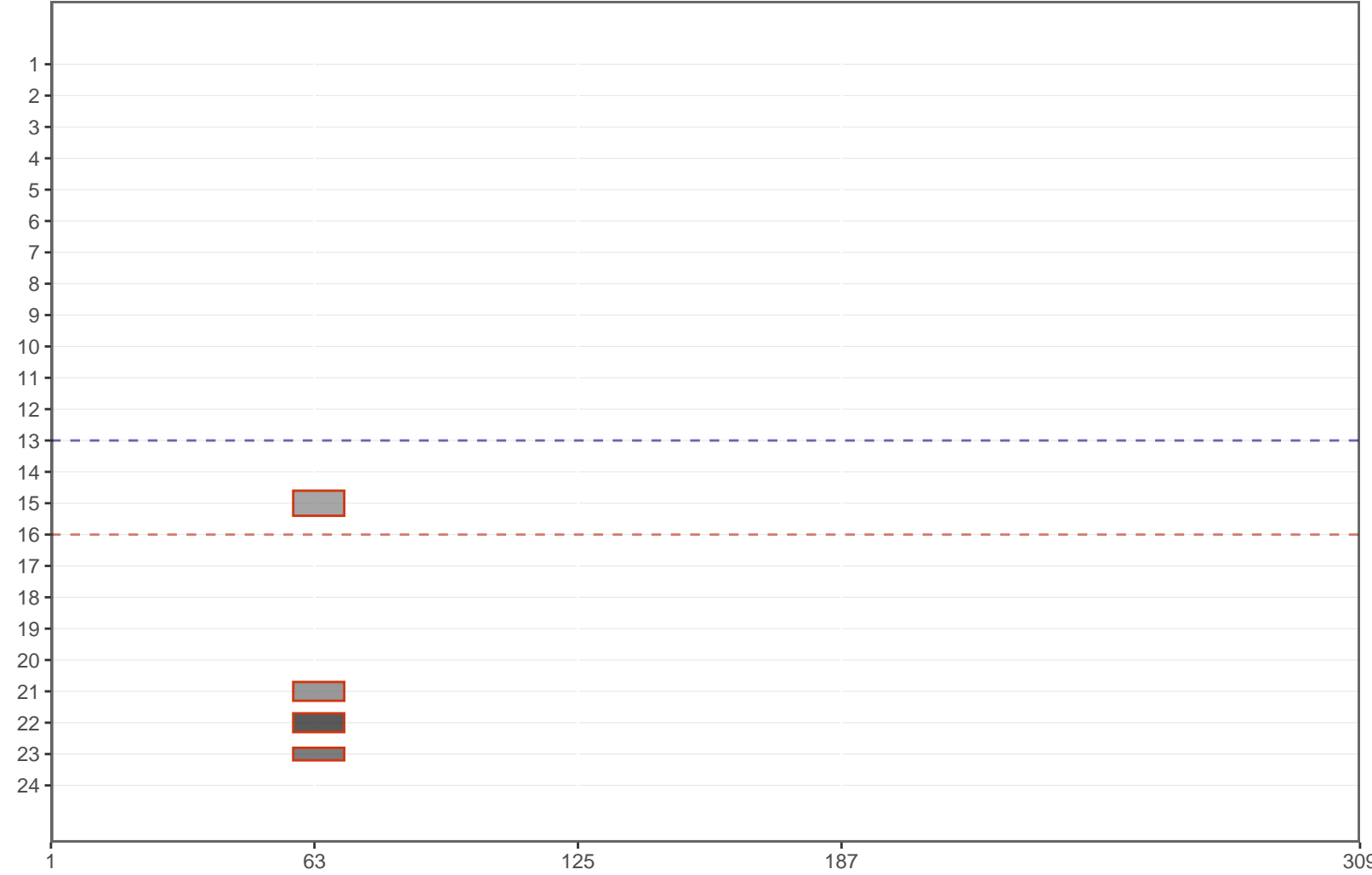
IQNKTTTRGHLKDYISHTYAPRMVAVTGFVKKHEEFDVQVKKQFTKLSDFPTASELVAEREPAFTGSEVRLDDDDPLAGFAVAFQGAPWTDPTIPLMVAQSMGLTWNKNAAGGGKHMGGSLAQRVAINELAESMMAFNTNKKDTGLFGVAVAKPDCGLSDLYGIMGEIVKGYRASDDDVTRACNGLKSSLMHIDGTSFAEDIGRQLLYGRRIPIVTELFARIDAVDASAKRVAARFRIFDGGVAVSAVGPQGLFDPNVFRFRRTYMLRY

NbL02g23580.1 glycine-rich_RNA-binding_protein_3_mitochondrial-like [MW = 31.21 kDa]



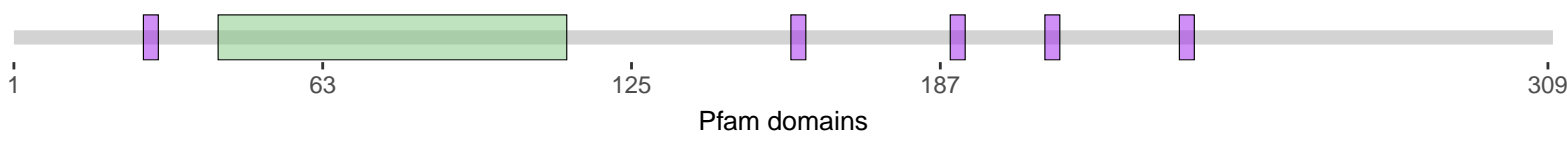
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

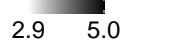
Protein sequence:
 NYGGGGGGYQNSGGFNYYGGGGNSAGAGGYPTENYGGGFSGNSSTGGYGGYGGGGSDYGNMNSPVEGGNFGGGGVYGGGNYQNTPTNSNYGGGGNSFGGGYDGGSSGNFGFGEFPAASFNGGGQGVVDGGGSSLSNEDGGGETSEGNVRDDDDDEPKDFANTRG

NbL02g23560.1 serine_carboxypeptidase-like_25 [MW - SP = 50.53 kDa]

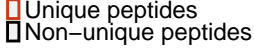
No. of times detected



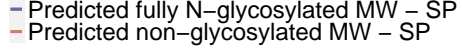
log(intensity)



Values from

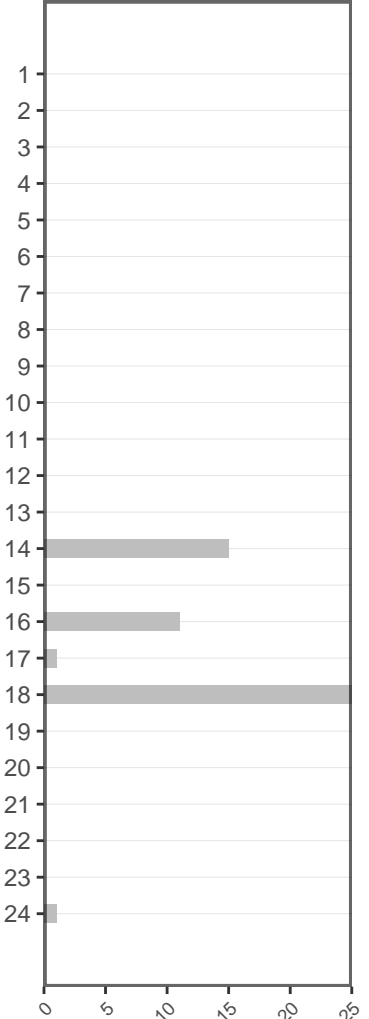
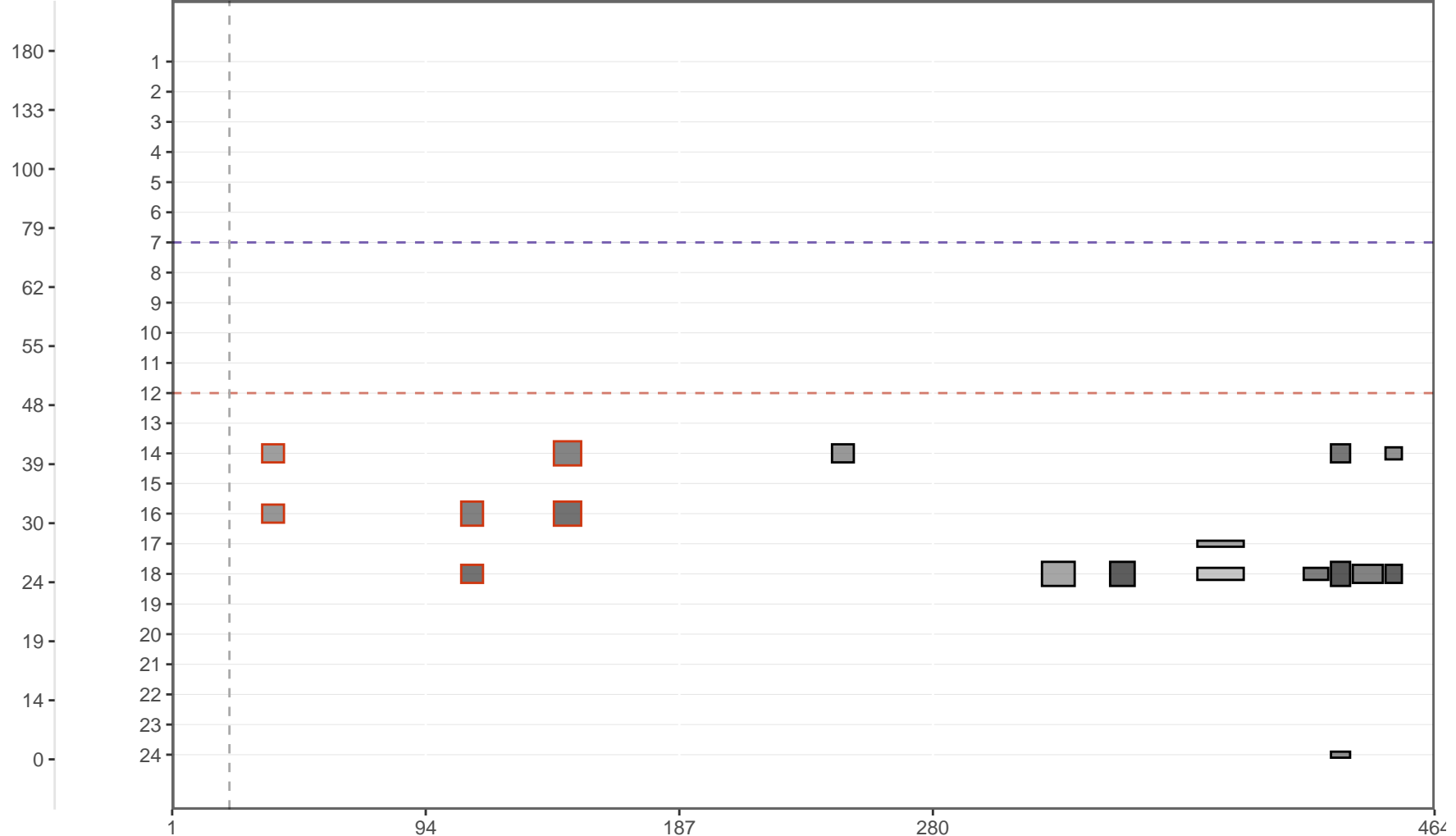


MW indication



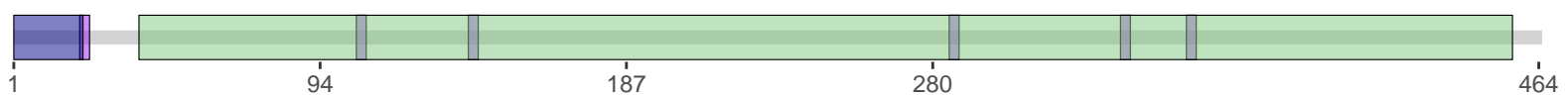
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

/DNLGTVTVYVSHAMISDKTKYKQLVNTGDFRRHKESNEGESLYVYAMDQDFGNIDGYNVYAPQNSDGGSTSTROTMLNPHQPPYKMKQLGGYDPCTEKAEVYVNRFDVQKAMHANTTGPVYKWTACSETLNRNWNDDIDILPIVRELIAGLRVWFSGVDVAVPTATRYLSLAHLKLLSTTRVWYVWYKVKQVGGVTEVYKGLTFATVRGAGHEVLPKRAAYQLFRSLRGEPLPKS

NbL02g23450.1 uncharacterized_LOC109206144 [MW = 20.51 kDa]

No. of times detected



log(intensity)



Values from



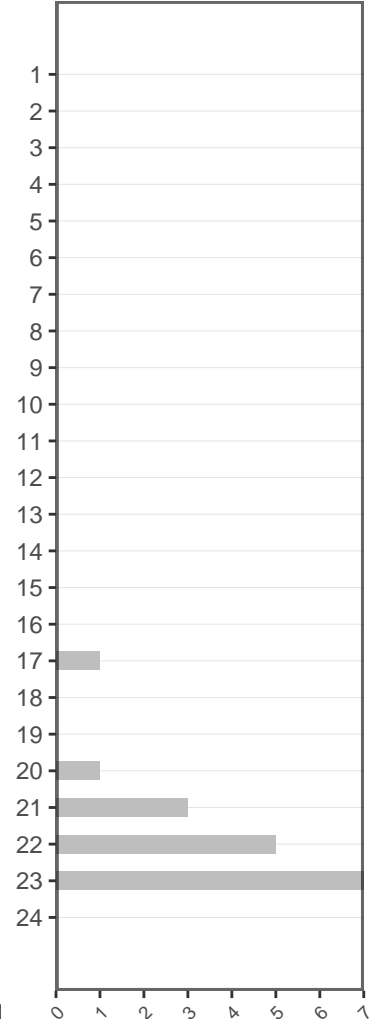
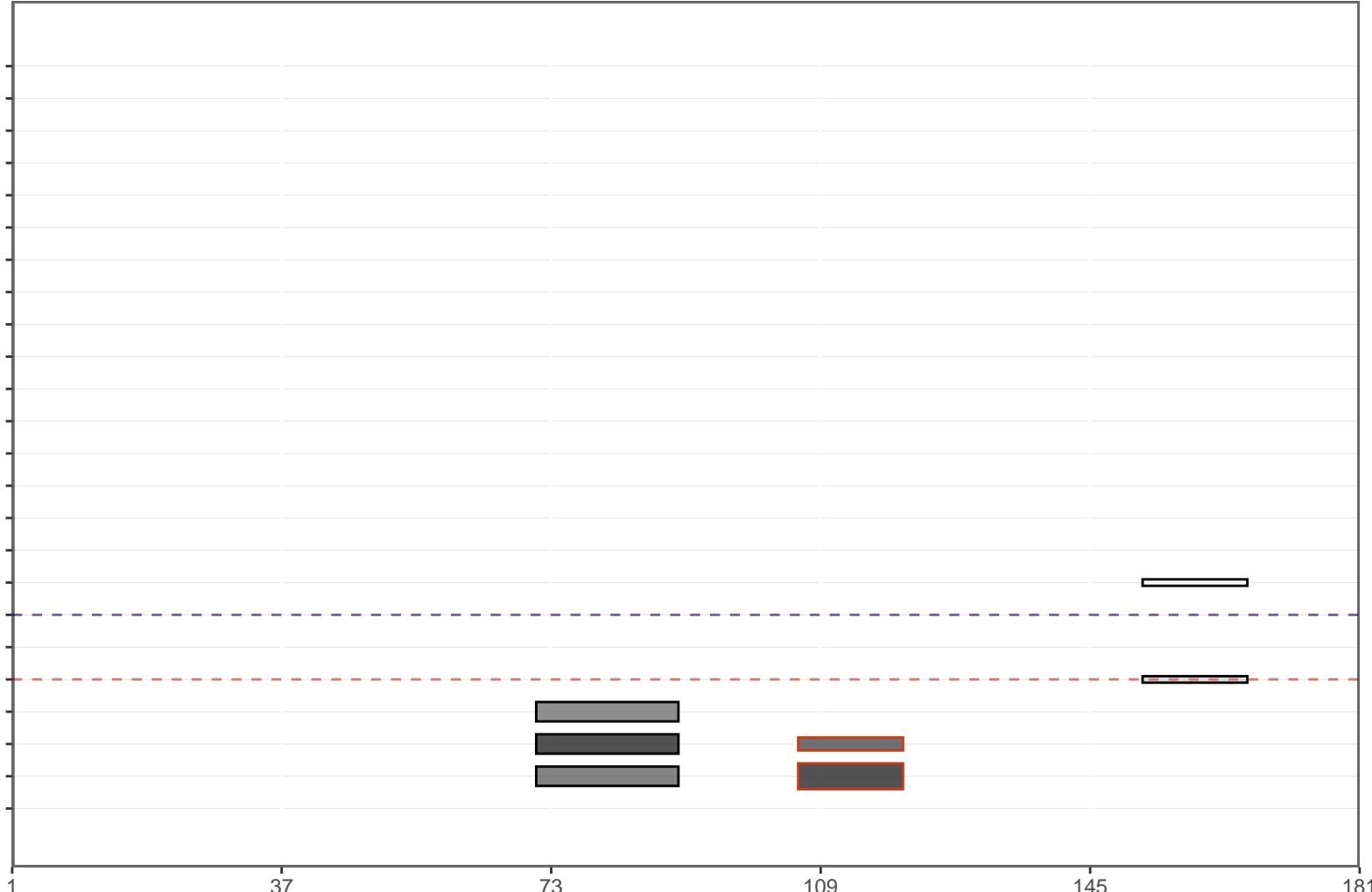
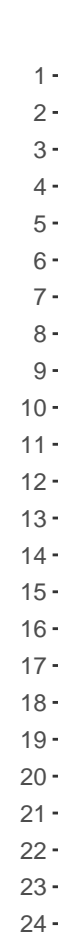
MW indication



Molecular weight



Gel Slice



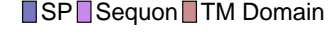
Protein length



Pfam domains



Pfam Description



Protein sequence:

IPQTSPEYLSAVPKATDHRFLGFPATGAKAVPTSDPETVFDIKYFSRDGRRNRPPRRFLNKADEVKMMENKTFDINDFPQRYLTAKIEEDMDAIGGGYQK

NbL02g23340.1 protein_COBRA-like [MW - SP = 46.99 kDa]

No. of times detected



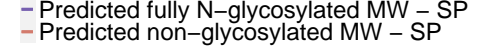
log(intensity)



Values from



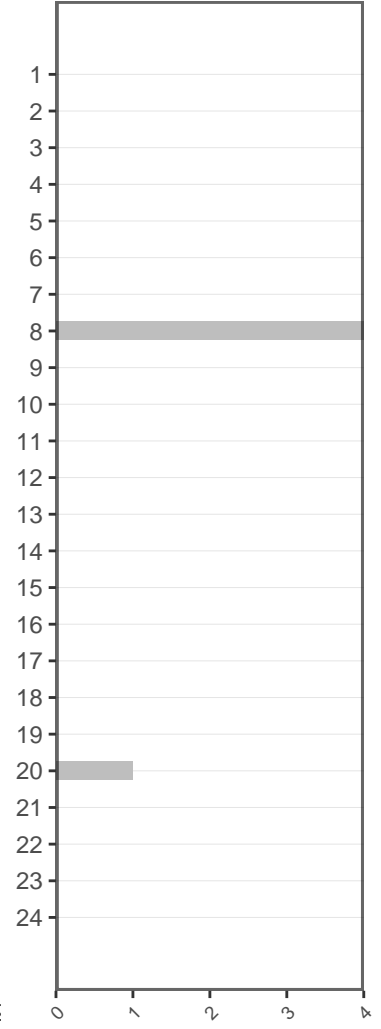
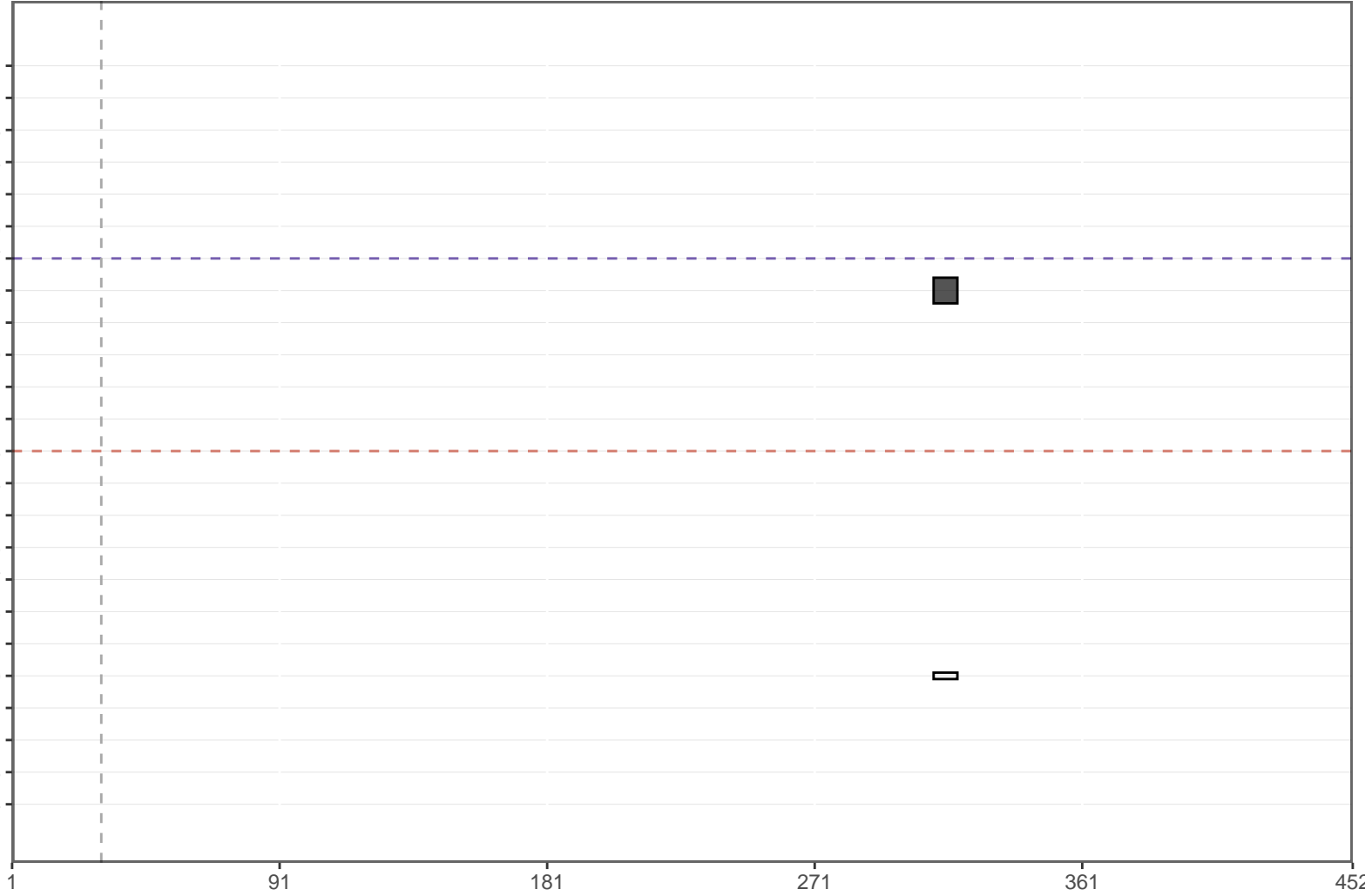
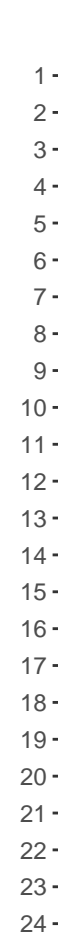
MW indication



Molecular weight

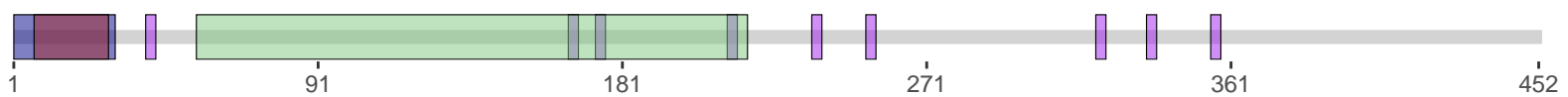


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL02g22940.1 putative_endo-13(4)-beta-glucanase_2 [MW = 75.97 kDa]

No. of times detected



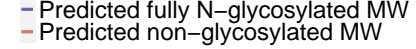
log(intensity)



Values from



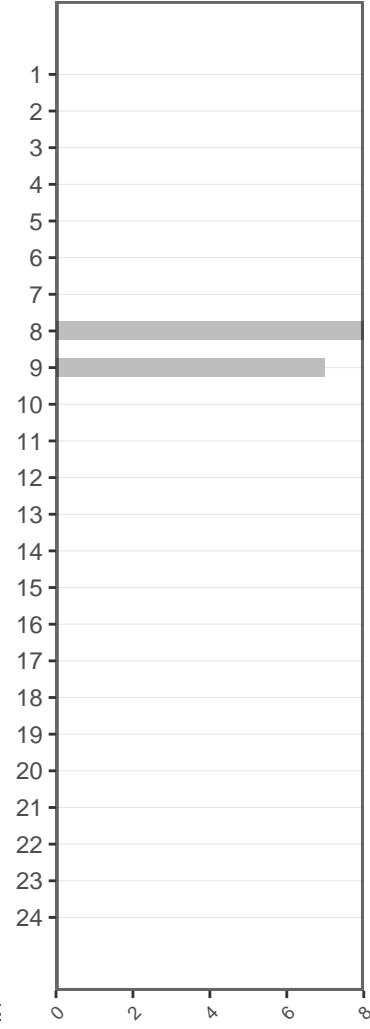
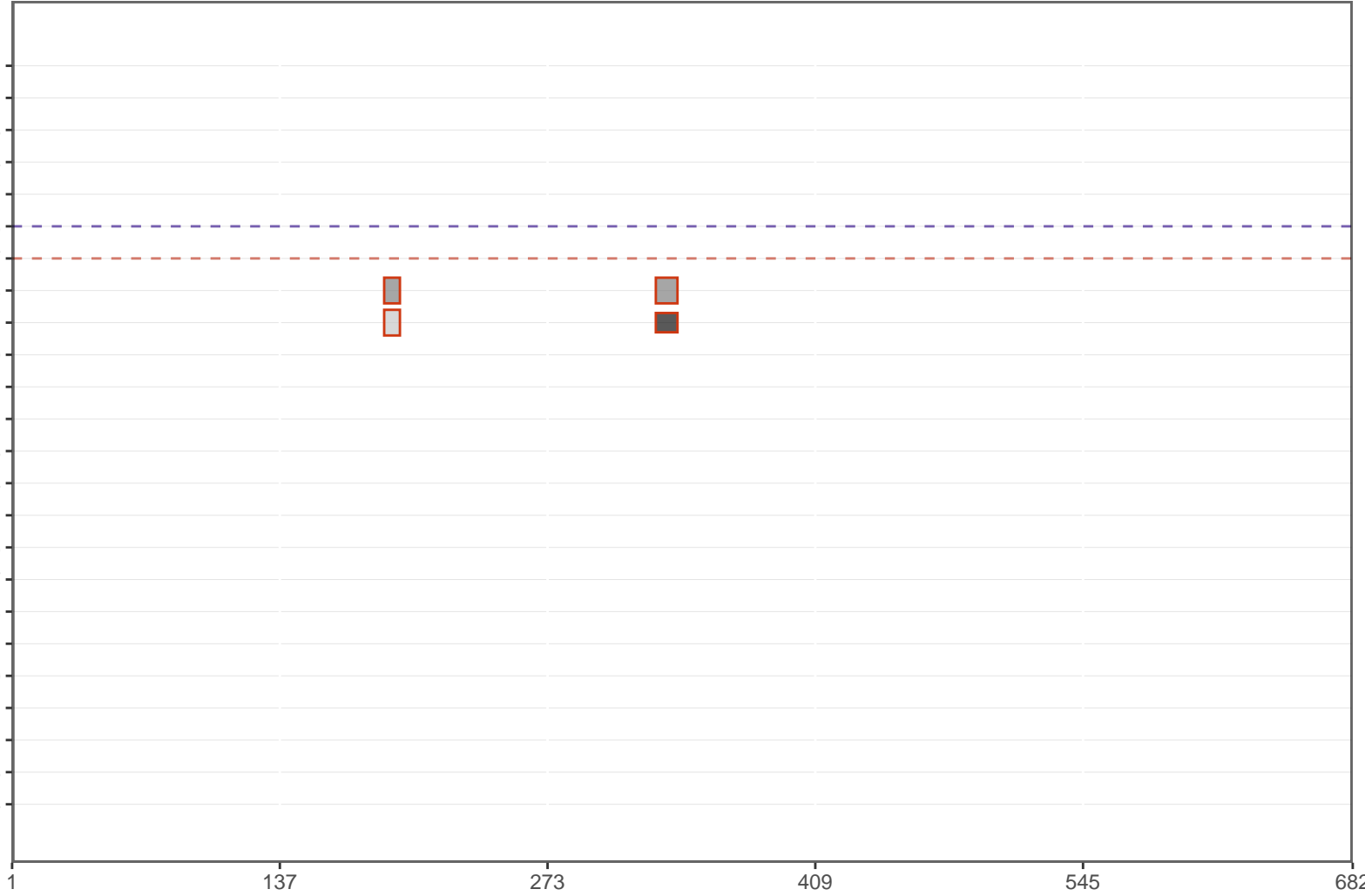
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

SP Sequon TM Domain PF03639 Glycosyl hydrolase family 81 N-terminal domain PF17652 Glycosyl hydrolase family 81 C-terminal domain

Protein sequence:

ISYFYGLIARARALAAIEEVDYLDVPIRIRKFKLDIVPEVWLEGTFEANGFFYEGKGGVYTKQALDSSGADDFGFGVYNDHIFHIGHFLYAVLAKIDPIWGRKYRPAQWALMADFMLSRANRKYARLRCFDLWKLHSHWAGLTFEADGRNGESTSEAVNAYSAALMGLAYGDTNLWIGSTLSAFEIHSAGTWWHHKEGSTLVGEEFTKDNKVVGVLWENKRDSGLWFAEWRREGRLGIGVLPILPITEVLFSDYQFVKGLVEVWTLPALAREGGVCEGWKGFVYTL

NbL02g22710.1 protein_DJ-1_homolog_D [MW = 41.79 kDa]

No. of times detected



log(intensity)



Values from



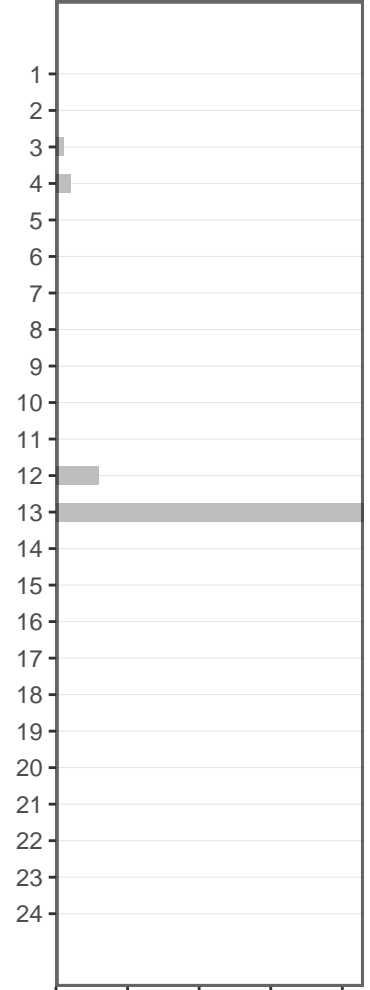
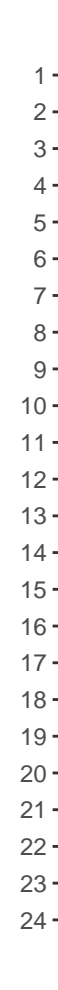
MW indication



Molecular weight

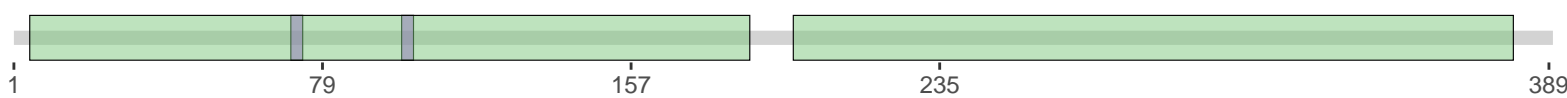


Gel Slice



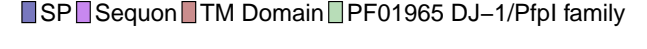
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

RLFVYKALGGSLVIGSKRILFLGGDFMEDVEVMVFFQSLGALSHVDAVPRKKAGDKGPTAVHDFEGDQTYSEKPGHFTLNADFESVDSSVDGLVPPGGRAPFVYLDADAVKLVKFMDSGKFPVAFSICHGQGLSAAGVLKGGKCTAVPWLKLVVGGGTWLEPEPIDRGTGHLVTGAWFGHPFESQFMALGVVHKP

NbL02g22690.1 sucrose_synthase_7-like [MW = 98.82 kDa]

No. of times detected



log(intensity)



Values from



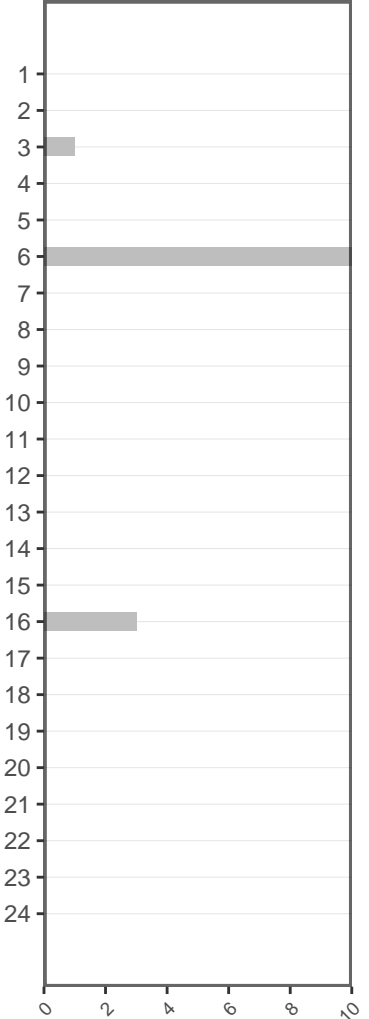
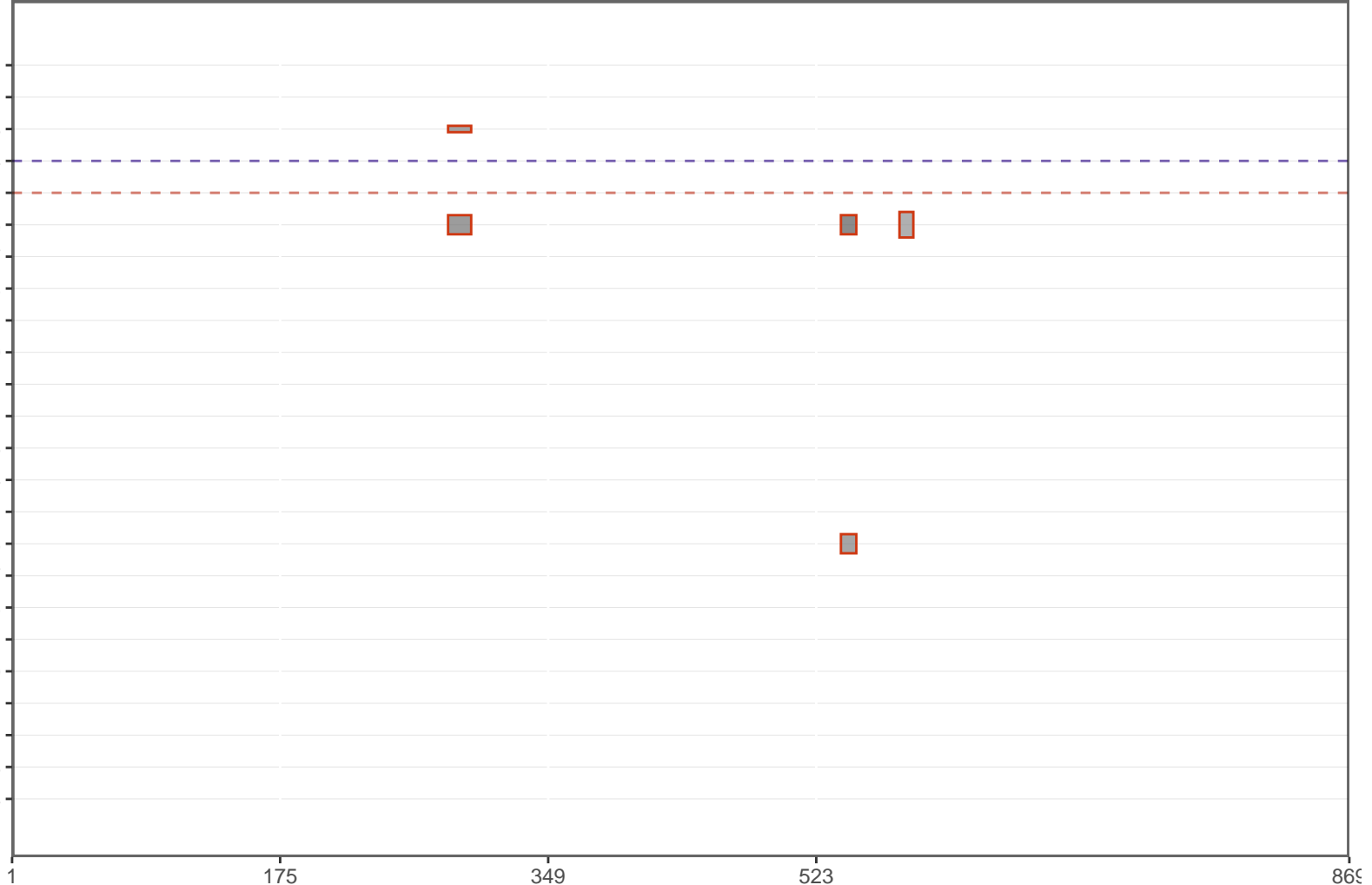
MW indication



Molecular weight

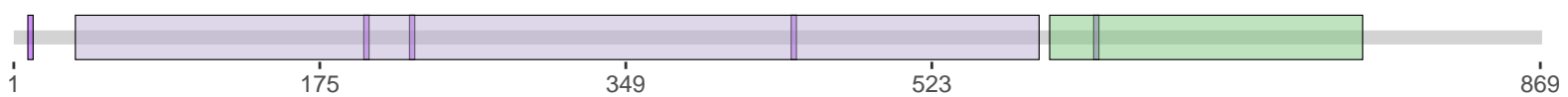


Gel Slice



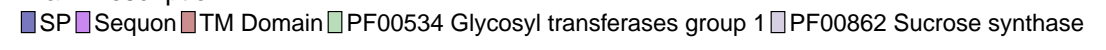
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YTTQDAADKIVELMEGKPDLPKLNFTDGNLVAISLMARKLIGTLGTAHALEKTYVEDSDIKLELQPKYHFSGGFTADLIAMNSADPHSTFYQEIAGSKDRPQVYSHSAFTLPLGIVRVAAGINVDPKFNAAAPGADQSVYFVTEKQKRLTAFRPAIEELLFSKVDNDEHVGLEDRKPKPLFTMARLDIWNKNTSGLTFEYVYGGKKNRRLRLVNLVVGSGFDPTKSKDREEAAEIKKMHLEKYGKGGQIRWAAAGTDRYRINSELYRTIADSKGAFVQRLAYEAFGLTVIEAMNGL

NbL02g22630.1 HSP-interacting_protein-like [MW = 87.91 kDa]

No. of times detected



log(intensity)



Values from



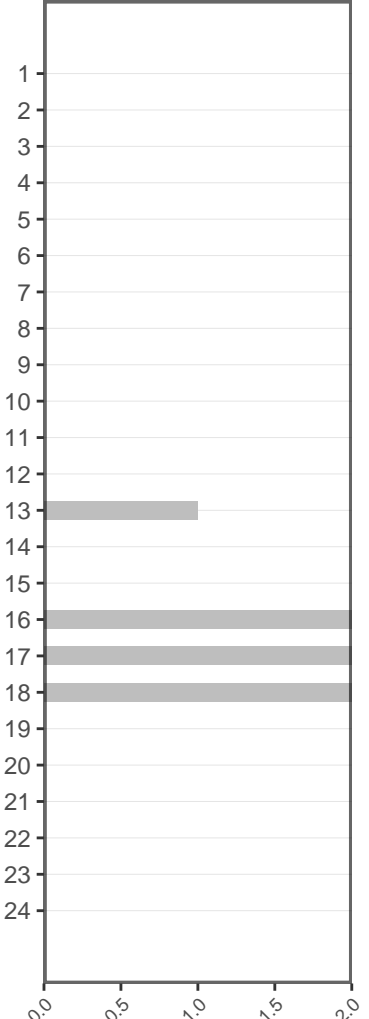
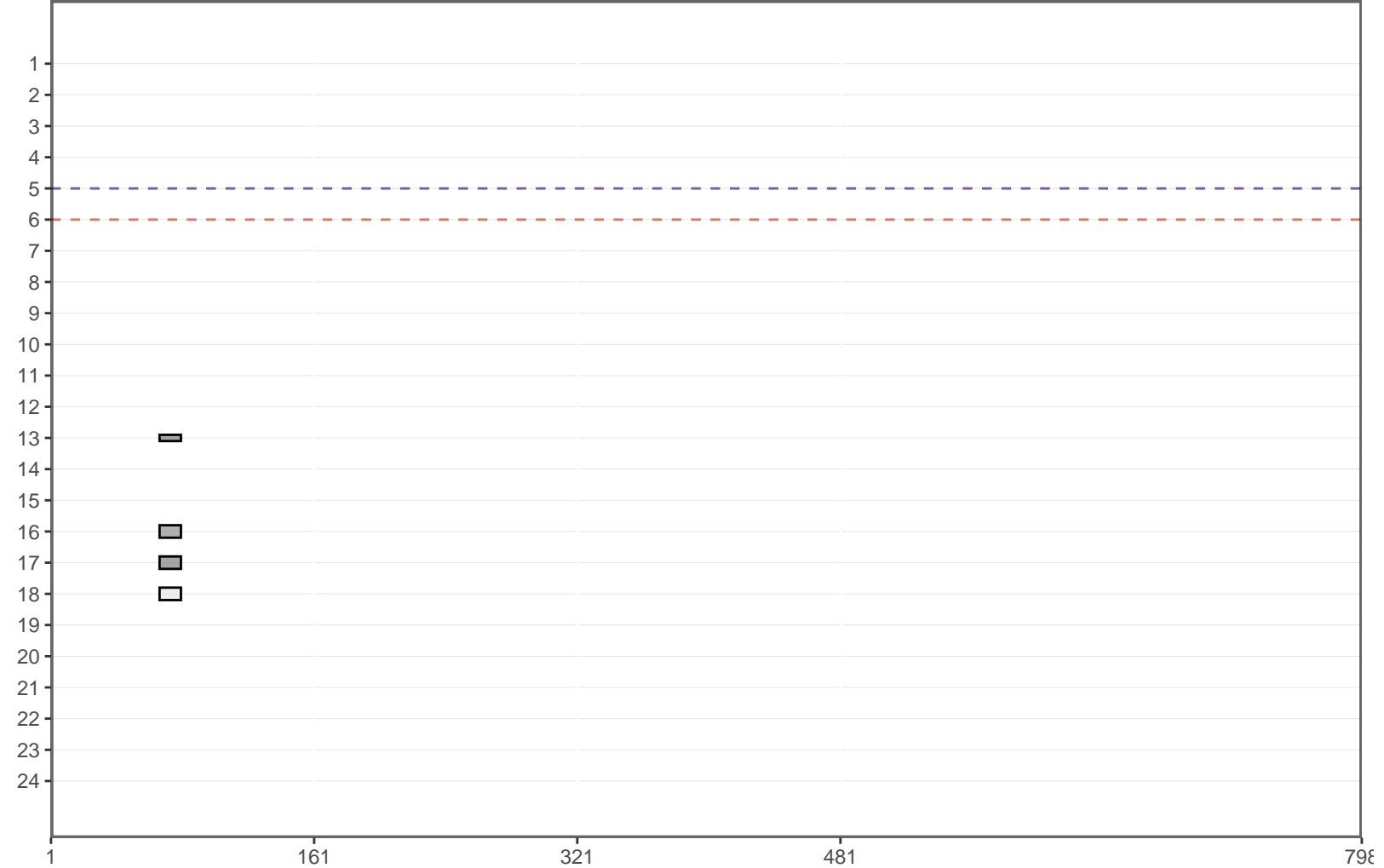
MW indication



Molecular weight



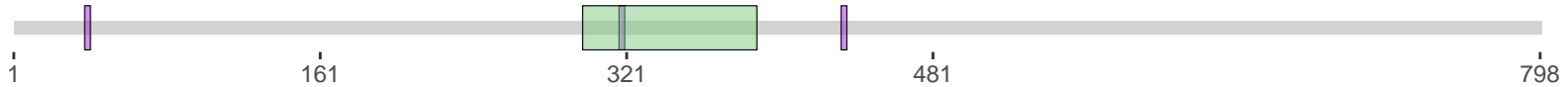
Gel Slice



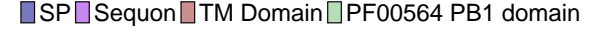
Protein length



Pfam domains



Pfam Description



Protein sequence:

LHVVEVSPCEPALLEEEENLVESEFSGKDDSGSHSISDGVETVQNEENKAEKDTKEKVATTENPDCKEVEIMDDWLFEFAGLFRTHVGDIPDAHDLHELGMELSSALEETVTSSEAGALFDKAAKLFQEVAAALFAFFNVHMGAAARKRIPDDSGASKEMMATOLGAAYDWFYKERYSLAKEKYEEALLIKPDVYEGLLALGQQGFEMAKLYWSEFILAKKEDLLMWDPAETLALFDSAEKMKAAATEMWEKLEEQRAKELKDPASAKDELLRRRXXKGGSGPEGEI

NbL02g22620.1 1-aminocyclopropane-1-carboxylate_oxidase-like [MW = 36.19 kDa]

No. of times detected



log(intensity)



Values from



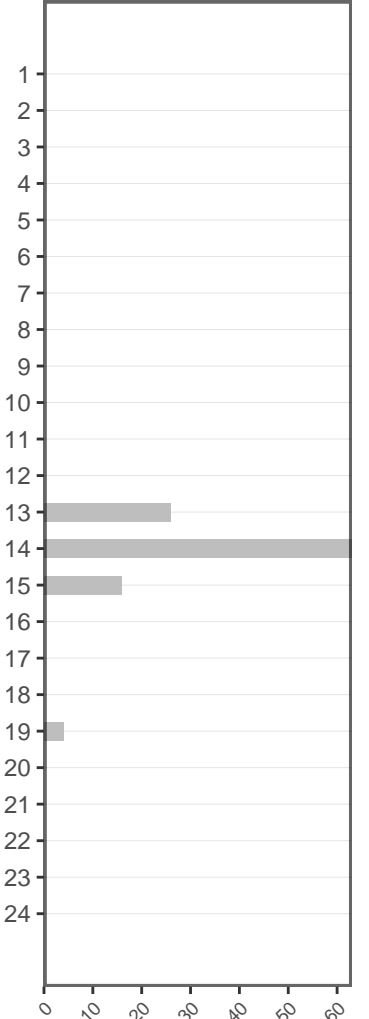
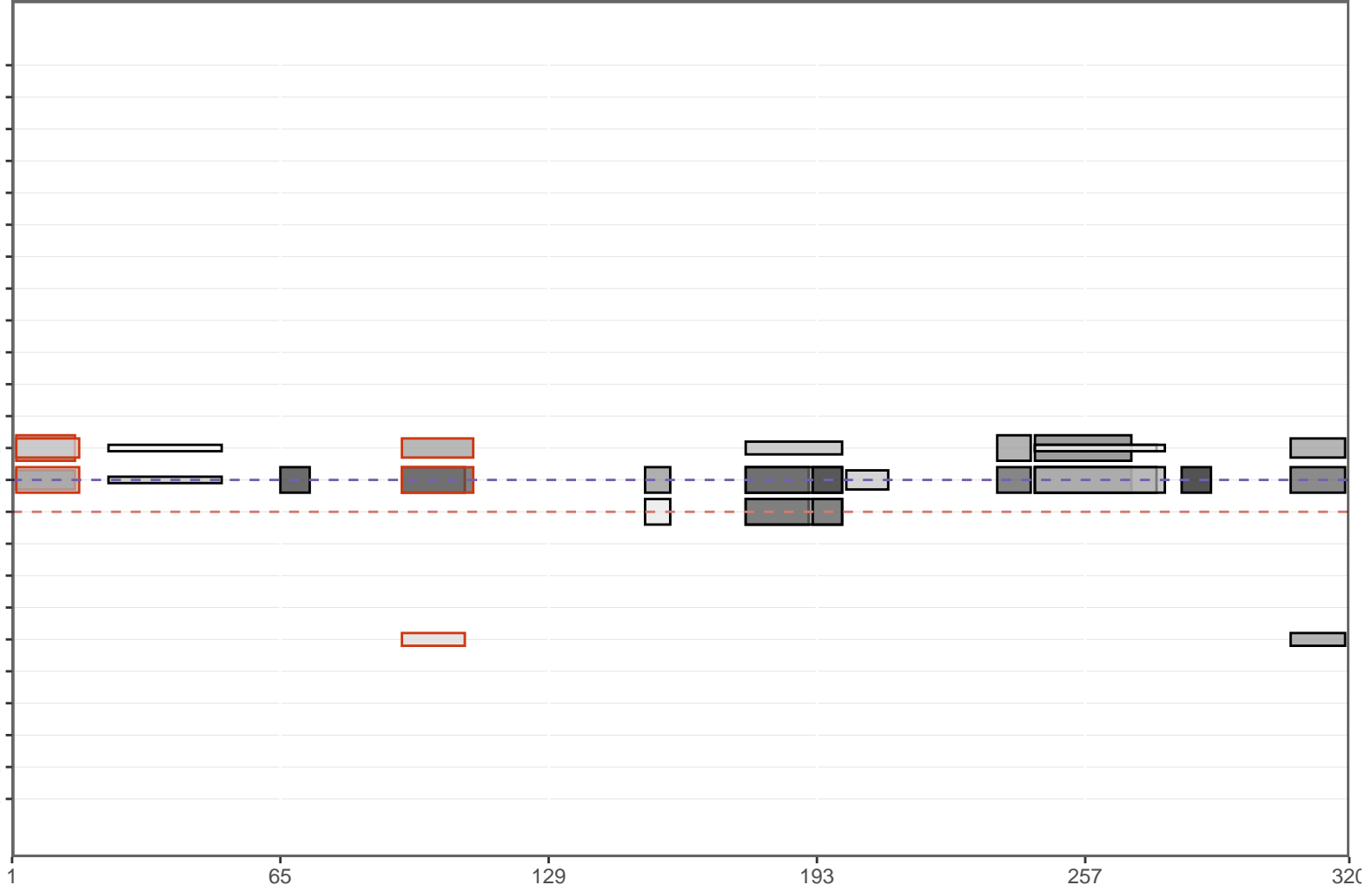
MW indication



Molecular weight

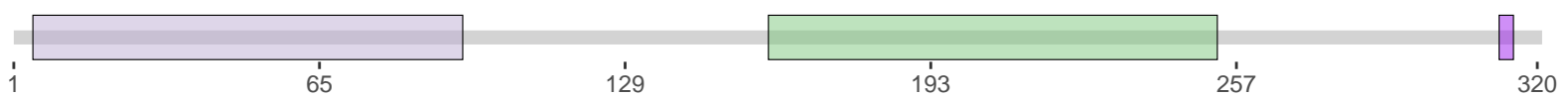


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF03171 2OG-Fe(II) oxygenase superfamily
- PF14226 non-haem dioxygenase in morphine synthesis N-terminal

Protein sequence:

IAFYGSKGPTFTGTVSNVYPPGPKPELKLGRHTDAGGLLIFQDDKVGSLQLKDGWIDVPPMKGHSAVNLGDGLVETNGKYKSHIEHVAQDDGTRMSIASFYAPGSDAVFFAPPELVEKAEENLKYKPFVFEIDMKLVYGLKFGAKEPRFEAMKAVETTIVNSPIETV

NbL02g22600.1 light-induced_protein_chloroplastic [MW = 34.95 kDa]

No. of times detected



log(intensity)



Values from



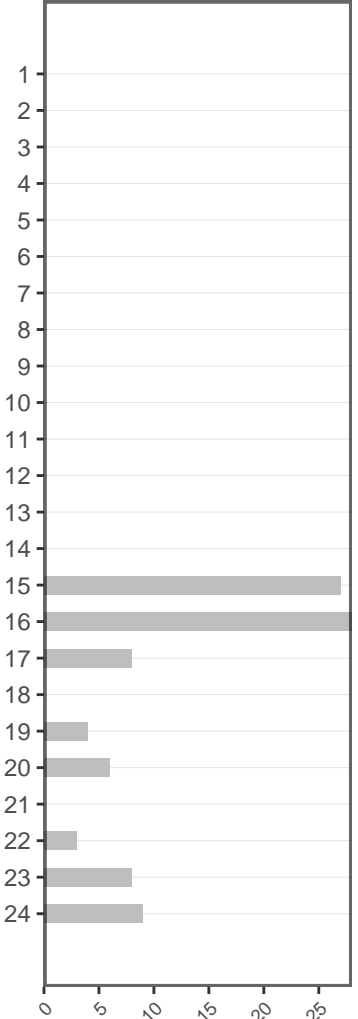
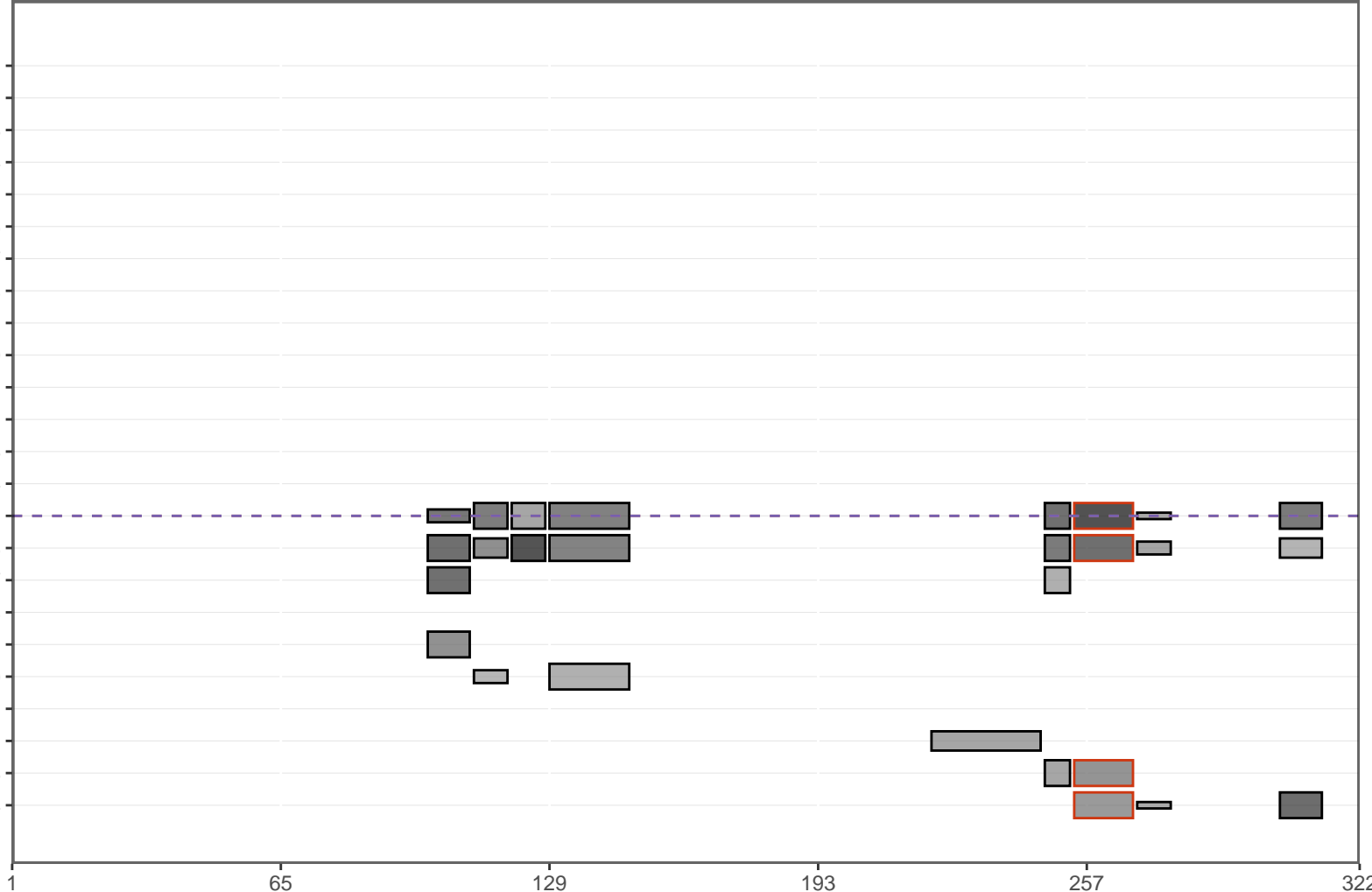
MW indication



Molecular weight



Gel Slice

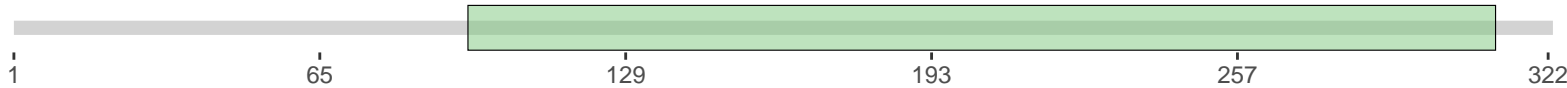


Protein length

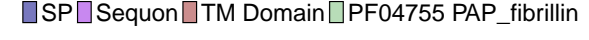


Peptide counts over 4 repeats

Pfam domains



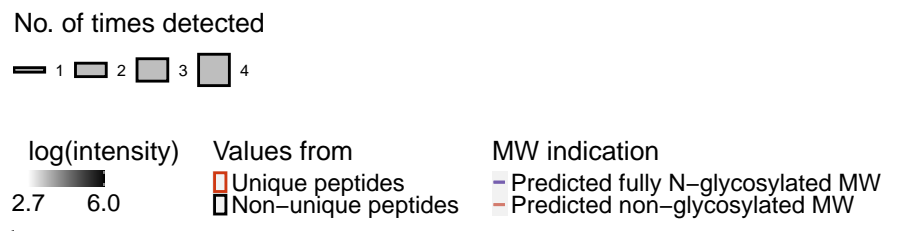
Pfam Description



Protein sequence:

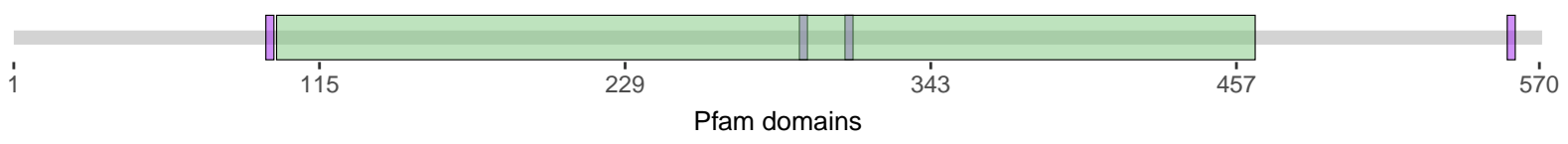
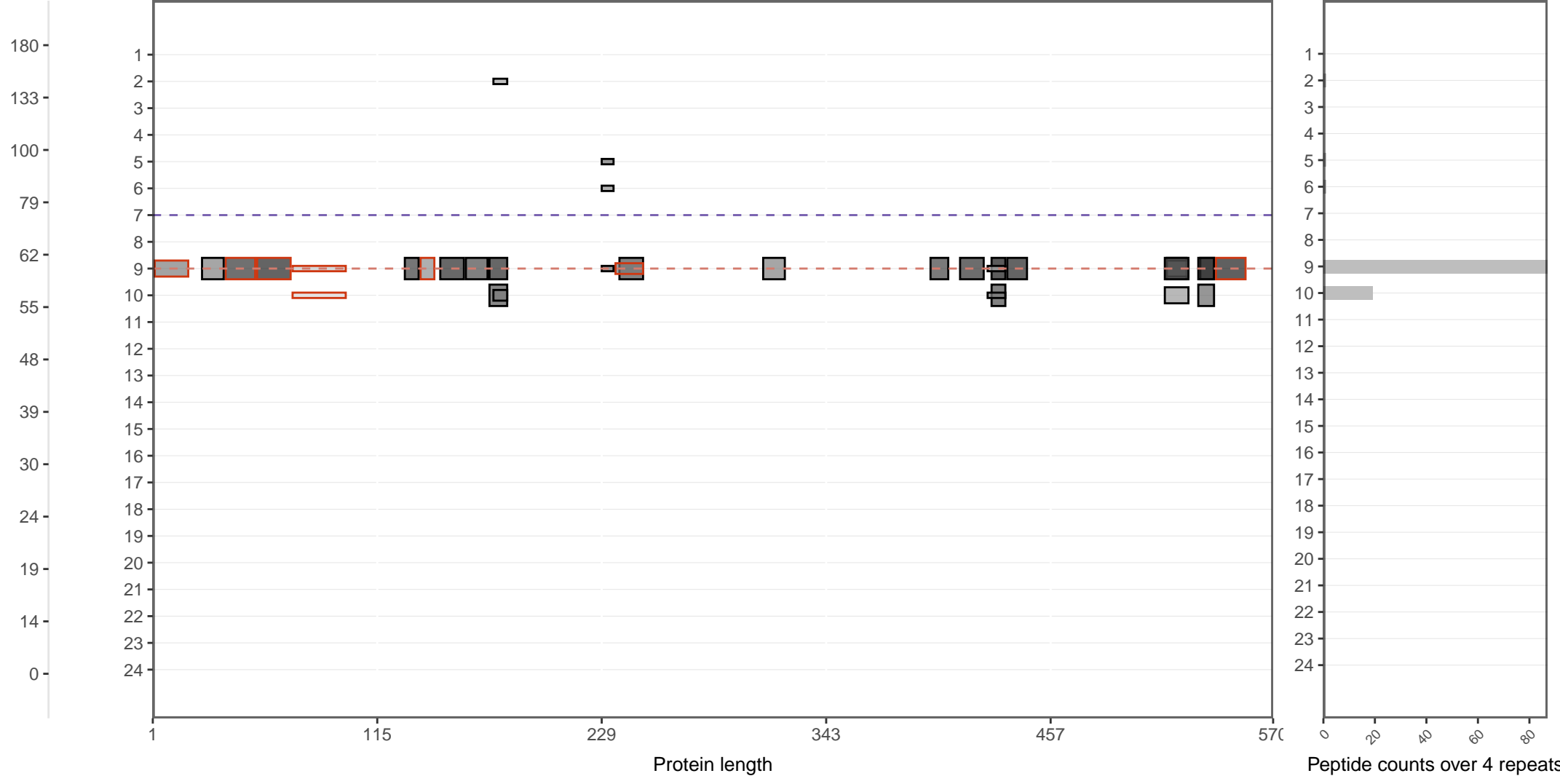
GRKWLAYTSFSQFLPILSRGFLPLVRVEEISGDTSEAFAGVQNVVVFAGPLATTSITNAKFEVRSFKRVQKQKDFDEGHGTPQLTDGHELPEVFEFGKQKIDLSPFKGLVNSVDITASSVAKSISGQPKFKFPIQNSNAGSGLLTTVLDDELRIERGGDGGVFLVKEGSGPLKPI

NbL02g22590.1 pyrophosphate--fructose_6-phosphate_1-phosphotransferase_subunit_beta [MW = 61.78 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00365 Phosphofructokinase

Protein sequence:

/H/FYRLMGRASHSFLEGLGTHFNFILGEEVFVAKKLFKKNVTDYHADVCKRAEGSYNGVLPGLGDFPEKGGIAELNELAHDVVDVAGVWKKLTPGCLLFFLAIGEQLLERDPHGAVGVAKIETKMLKGMVETELGQRKQKGGYNAGFKGDSHFVYEGRGLPSEKDFSTYGVYALGYGAGALLGSKTGLLSSVGLAAPVEEWTVGGTALTALMDVERRHKGKPKVKKKAMVELEGAPFKFKSKREEWALNRRYINPQGFVGPASKLNITLLLELGI

NbL02g22570.1 UBA_and_UBX_domain-containing_protein_At4g15410-like [MW = 32.69 kDa]

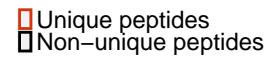
No. of times detected



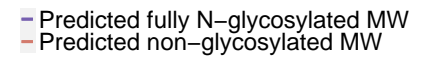
log(intensity)



Values from



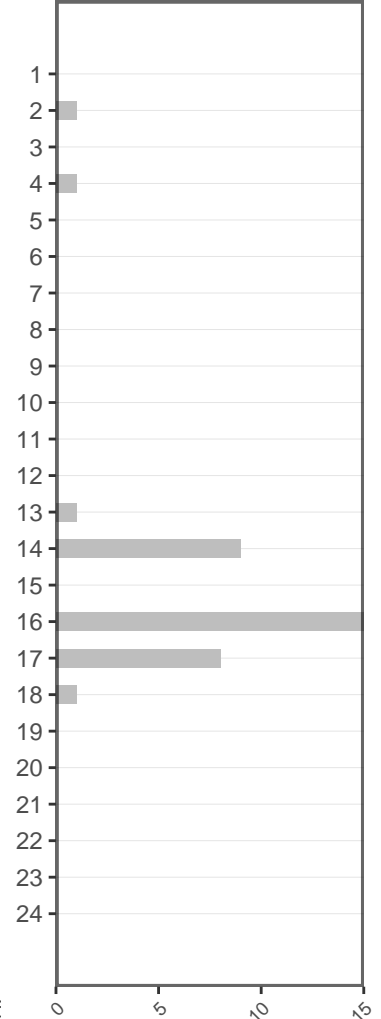
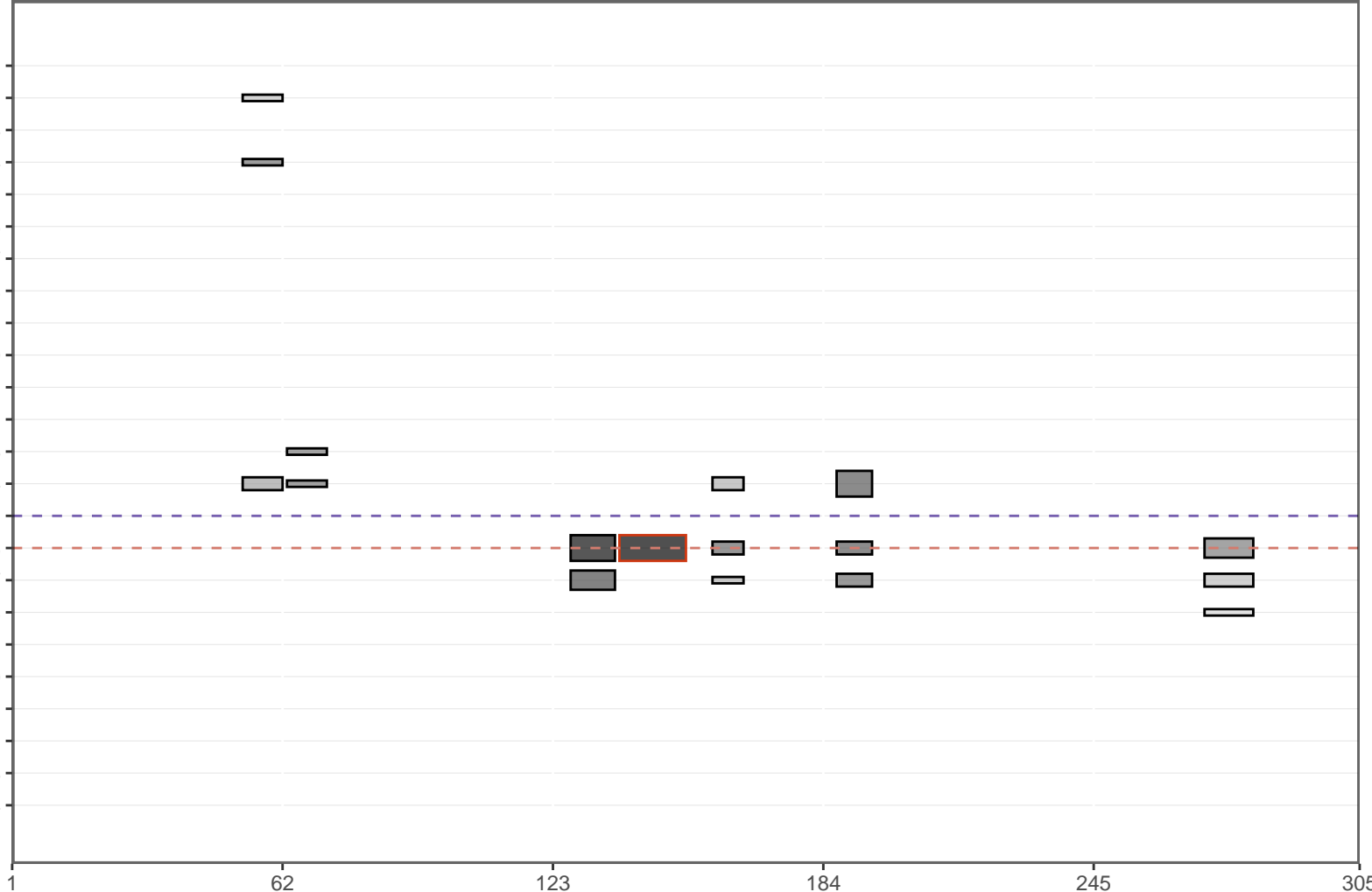
MW indication



Molecular weight

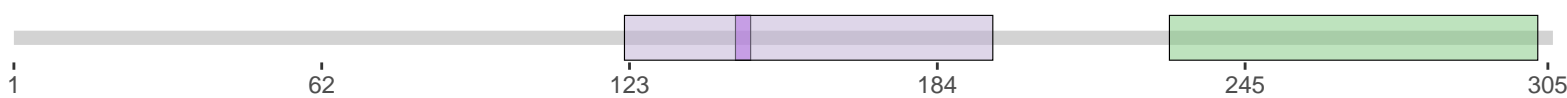


Gel Slice



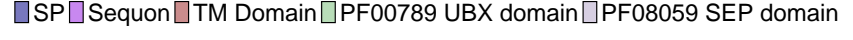
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RSLLDLPENASFLGKITKBECPRELAPADTRSGWVHGNLIRRDENGEPEKRVQVFGVGVGRTLGSSSIPATSEFSAVPISTASAPTSILDOSLPSTLQIRLADGTRVWHFNFQGTVDGIRAFIDARSPDTRAVLLGTGVFPPRLGDTTDTTIEGAGLANSVWIKF

NbL02g22460.1 leucine--tRNA_ligase_chloroplastic/mitochondrial [MW = 110.28 kDa]

No. of times detected



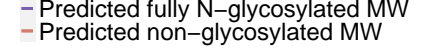
log(intensity)



Values from



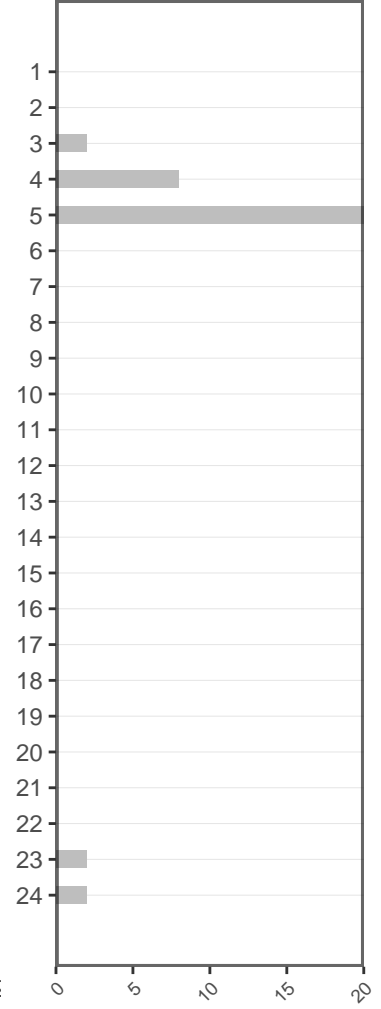
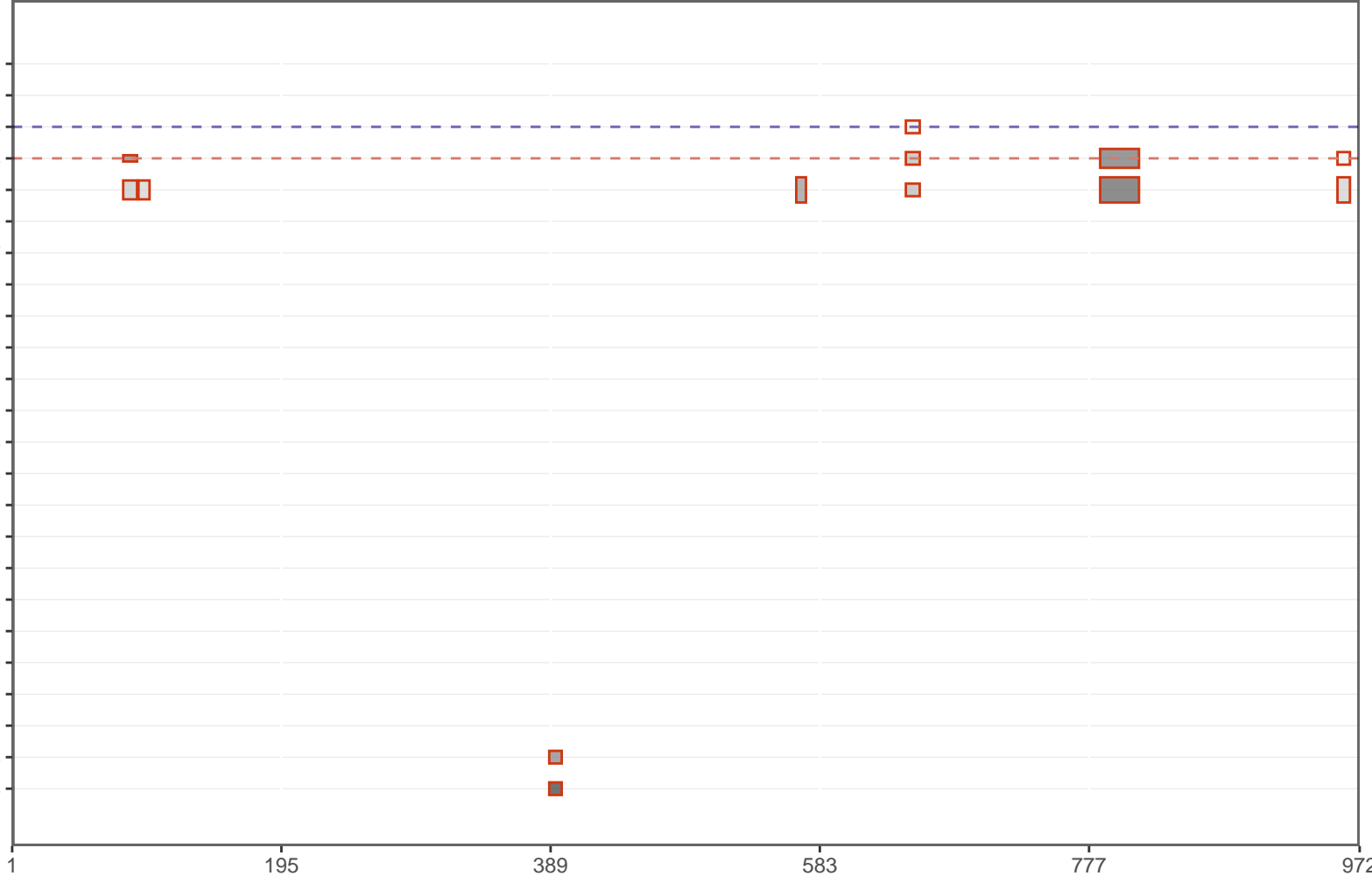
MW indication



Molecular weight

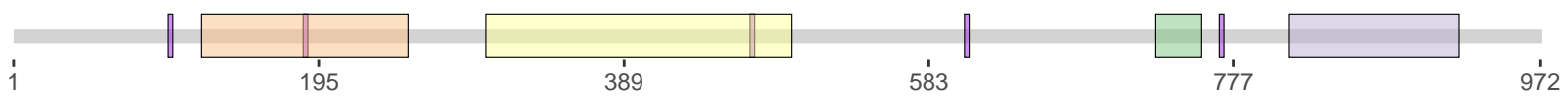


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

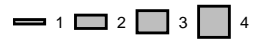
- SP
- Sequon
- TM Domain
- PF00133 tRNA synthetases class I (I, L, M and V)
- PF09334 tRNA synthetases class I (M)
- PF08264 Anticodon-binding domain of tRNA ligase
- PF13603 Leucyl-tRNA synthetase, Domain 2

Protein sequence:

IASSSESGLDINGLPSKEAASRVVQWLEKSGNGKGVNYKLRDLFARGRVYGEPIPVFLDETGGPIVSETELPLTLPEDDFPTPTGTGEPLSKADSVVTKDPLSGKAARRENTMFGWAGSGWYVLRFMQPKNSALVDKAKEGVWSPVDVYVGGAEHVALHLLYARFVHKVLYDGVVYVSTKEPKKGVNQHILGEVQYTKACKDDGNLISADVSELAEYNGEIPFEKVMKSGDGFVLDKDPNPNVRLIARAHKMKRGRGVNPPDDVVALEYGADSLRLYEMFGPI

NbL02g22340.1 aminomethyltransferase_mitochondrial [MW = 44.24 kDa]

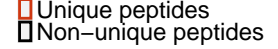
No. of times detected



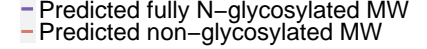
log(intensity)



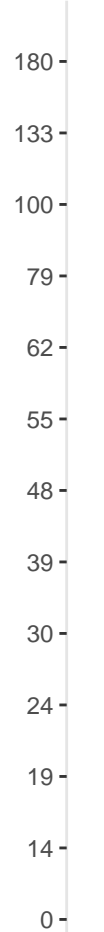
Values from



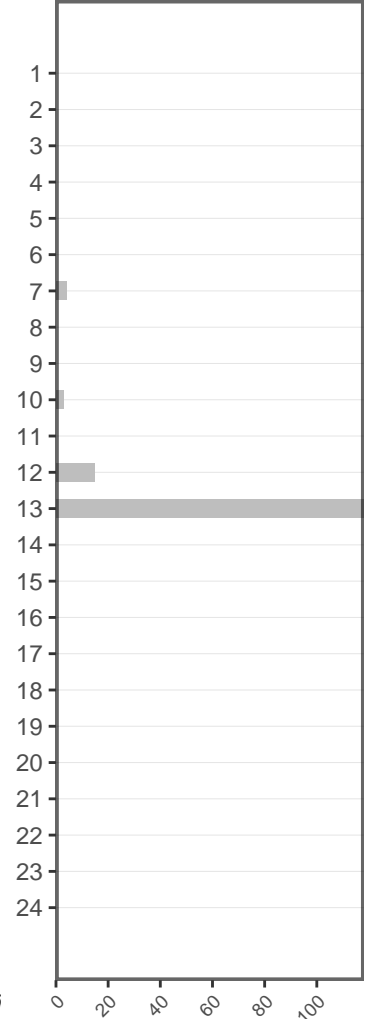
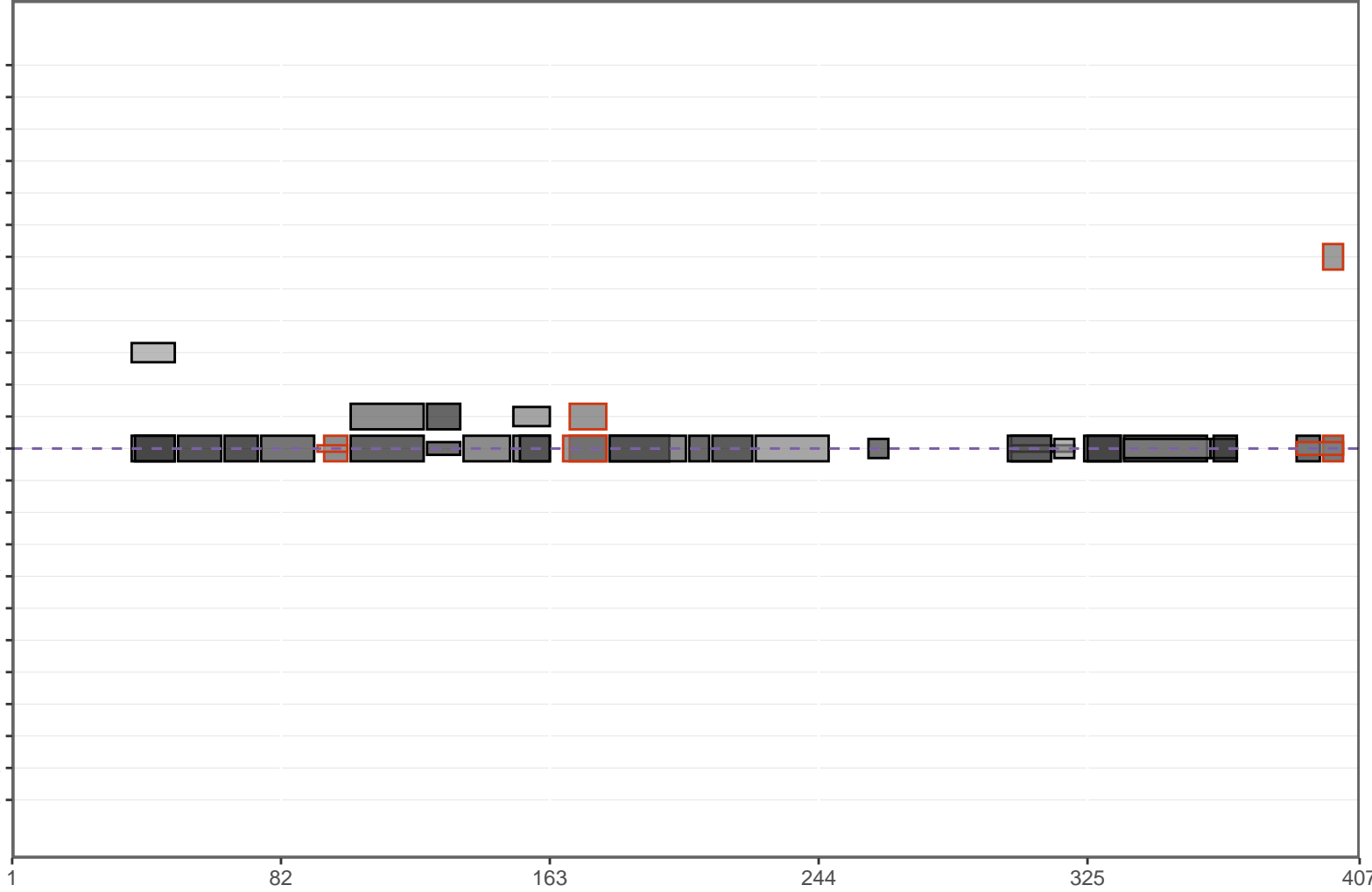
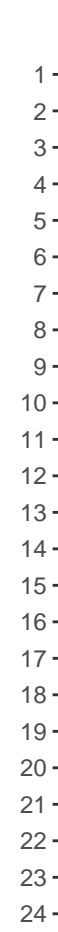
MW indication



Molecular weight

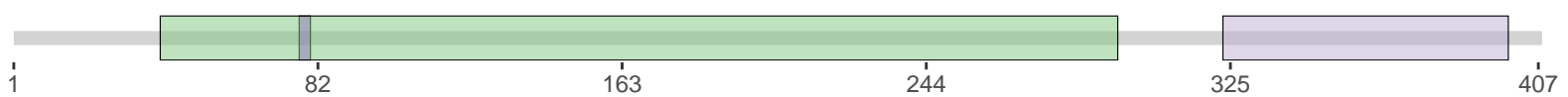


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF01571 Aminomethyltransferase folate-binding domain
- PF08669 Glycine cleavage T-protein C-terminal barrel domain

Protein sequence:

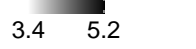
AAPVLOHETKDDLSKMYFGEFRVLDINGASCFLTRTGYTGDEDGFEIVPSENVAIDLAKALEKSEGRILRTGLGARDLSRLLEAGLGLVGNDEMHQHTIVVEAGLTVAWGKRRAEAGGFLGAEVILKQIEEPWIRRVGFFSSGPPRRSHSEIQDSNGNGNGEITSGGFSPLKKNAMGVYKTKGNKKAGTNVKVIRGKGYDGAATKMPFVPTKYKPI

NbL02g22310.1 glucan_endo-13-beta-glucosidase_1 [MW - SP = 54.35 kDa]

No. of times detected



log(intensity)



Values from



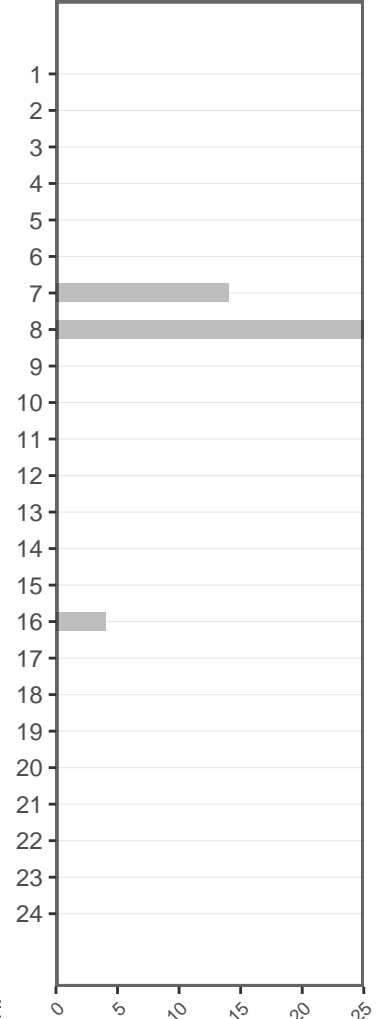
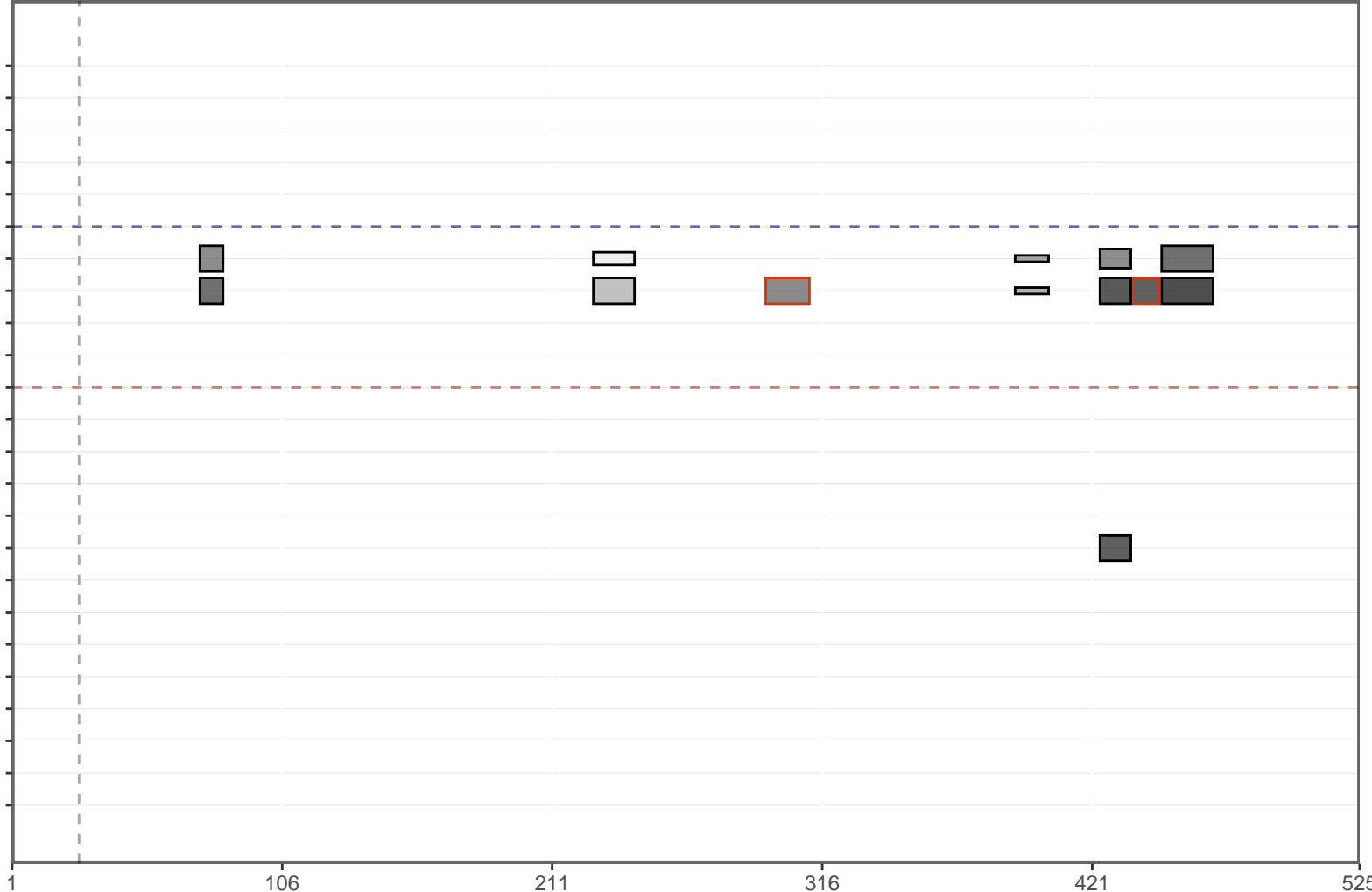
MW indication



Molecular weight



Gel Slice

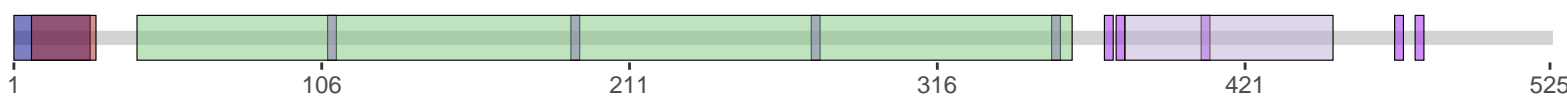


Protein length

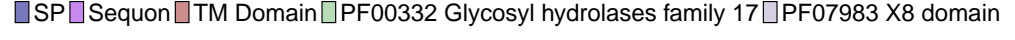


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

YTNVLDAMDSVYFEMKLNLYTDVAVVLTESGWPSPKSGDSKEPVATIDNADTYNENLKHIFDRSGTPLHPEFTSSVYIYELFNEDLRSPVSEANWGLFHGNSTPVLHLVSGSGTFLANDTNTQYGMMDGVDRKTLQAALDWAGGPRGRANKGSEIGPGESEYGFNDVKNHASEVAFDSYKQEGTSPGSDDFKGVAMITTSDFPHGSGCFPPGKTKTENKTQVAVNATQESGANTRIFGAETSLDKNHVHFGVALGLFYSLIQVQLS

NbL02g22290.1 5'-adenylylsulfate_reductase_1_chloroplastic-like [MW = 51.18 kDa]

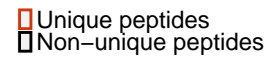
No. of times detected



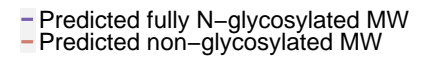
log(intensity)



Values from



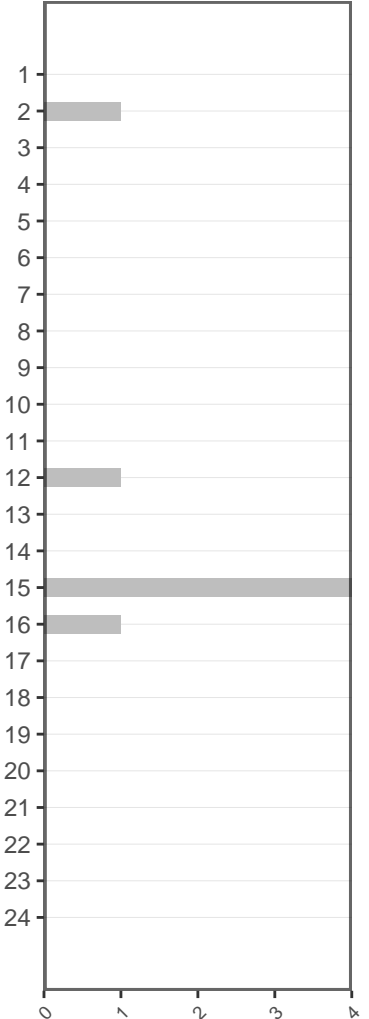
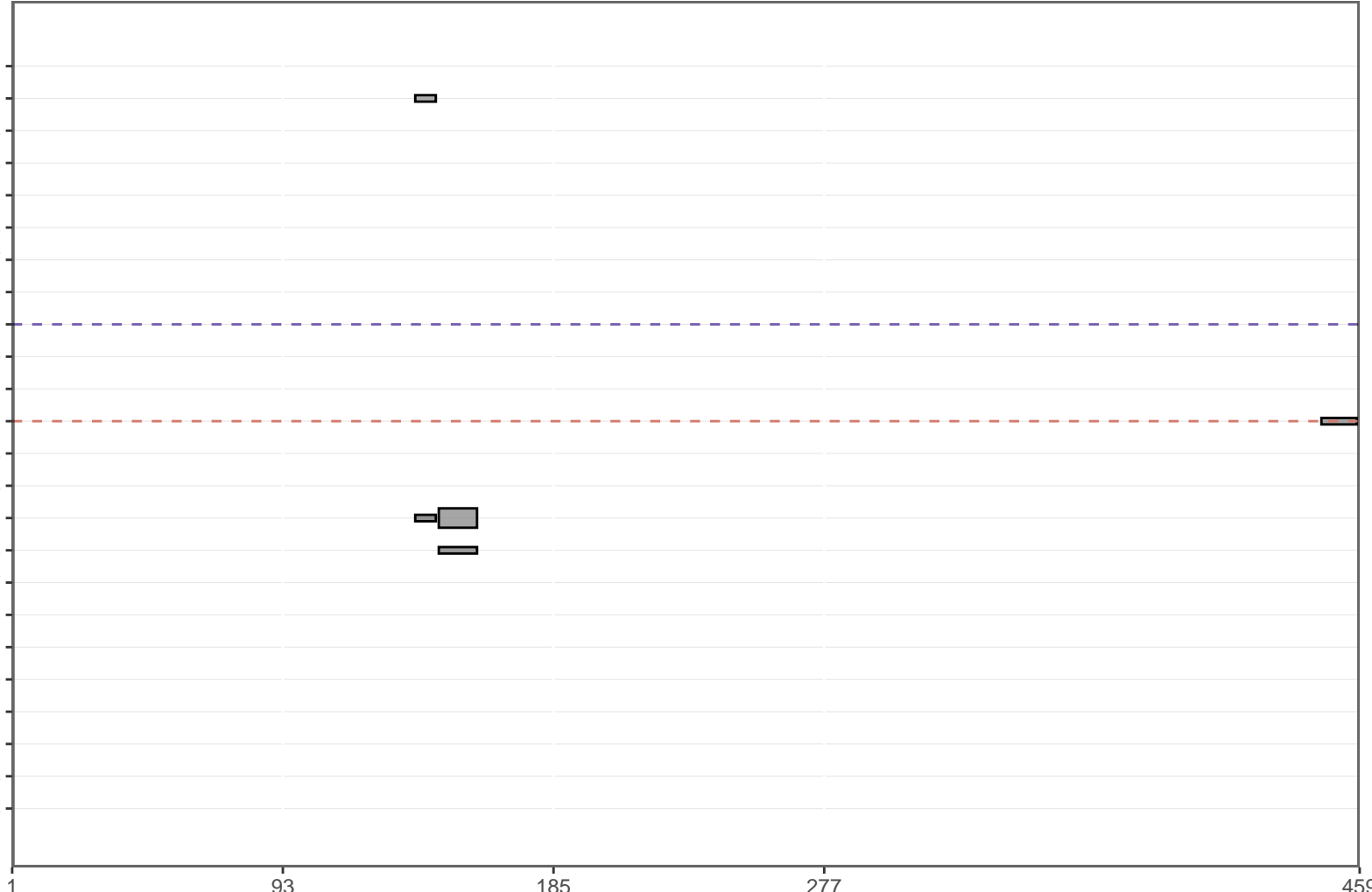
MW indication



Molecular weight

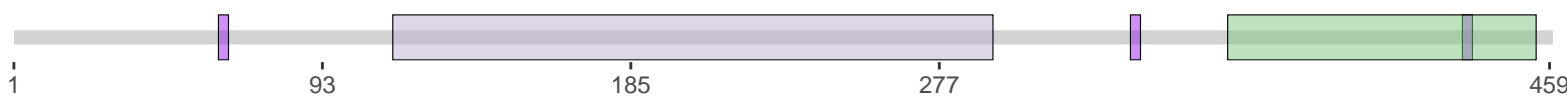


Gel Slice



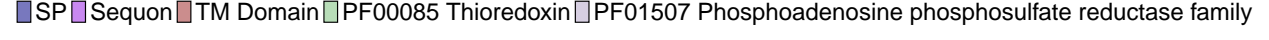
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

KDQSPGTRSEIPVGVQPSFEGLDGGAGLWVNPVAVVQKQKWNFLRAMVFPVNSLHSDGYVSGGSEPCTRPVLPGQHEREGRWWWEDAKAKEGGLHKNKIDETVNGAVQNTGTATADFDTKDVTLSRPGQVENLKLDDRREPVLVLYAPVWQGFQAMEGQVYELAEKLAGWQVYKVKFRADGEGKAFSGQELQLGSPFTLFFPNSEKAIKYPTEKRDVDELLAFVNALR

NbL02g22280.1 lactoylglutathione_lyase_G LX1 [MW = 32.86 kDa]

No. of times detected



log(intensity)



Values from



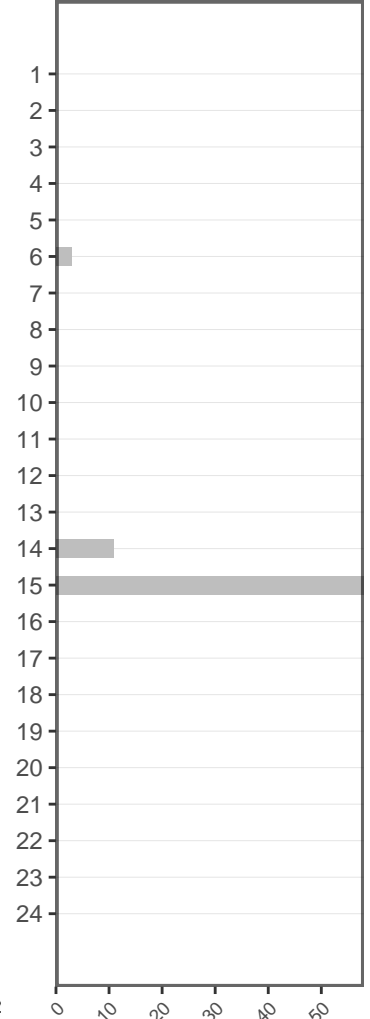
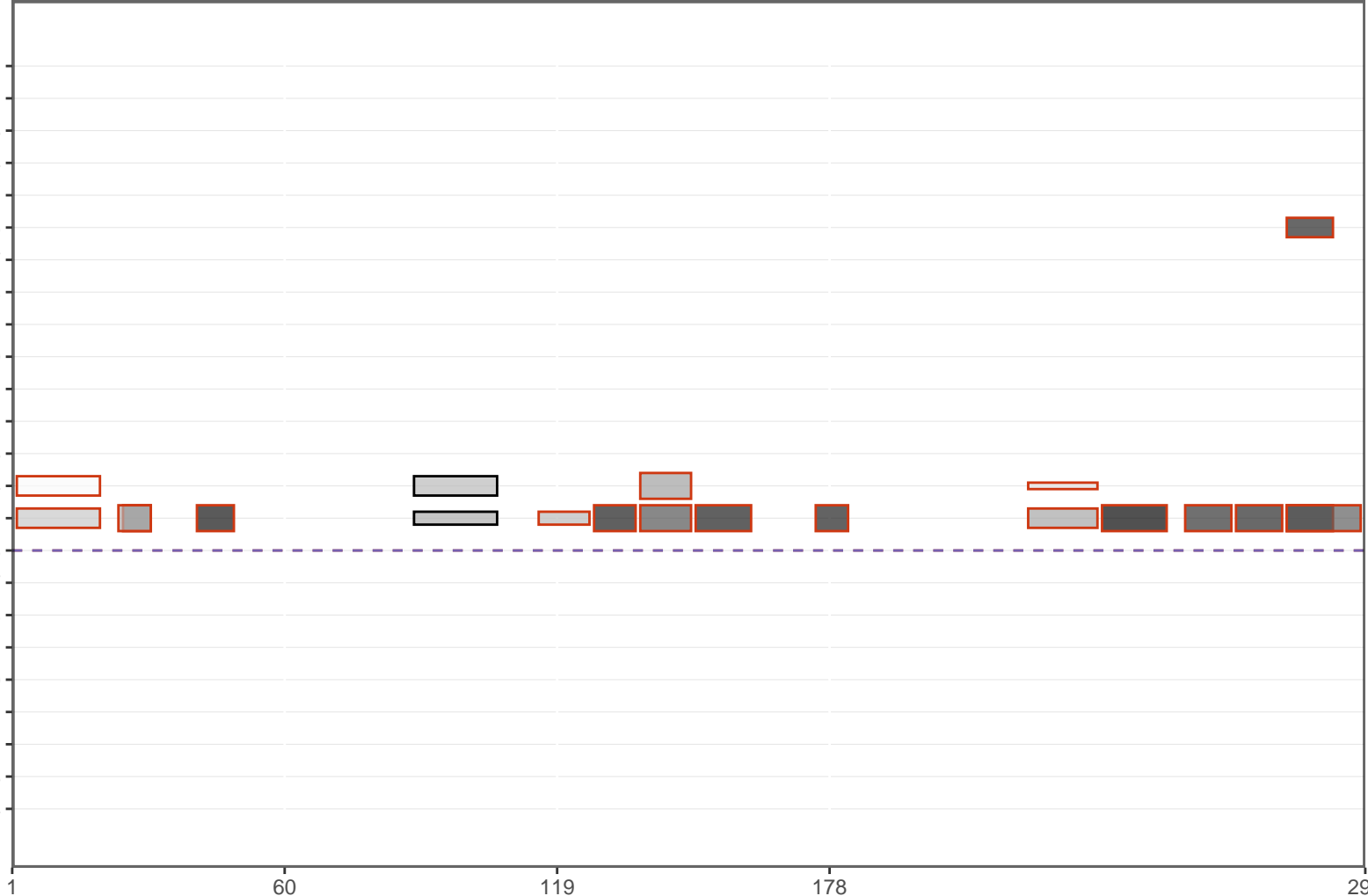
MW indication



Molecular weight



Gel Slice

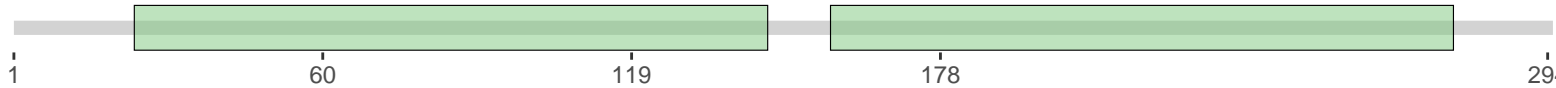


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

VKDPDQYLFELORASTPEPLGGVMLRVGDLERSIKFYKALGMQLKKVDRPEQKYSAMMGVAPEHETVLELTYNYGVTEYTKGNVAGVAGSTDDVYKSAEIVNLVTQELGGKTRGCPPIGLNTRITFLDPDGGWKTFLVNDQDFLKELEESK

NbL02g22190.1 soluble_starch_synthase_3_chloroplastic/amyloplastic [MW = 141.42 kDa]

No. of times detected



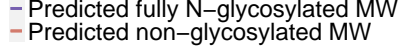
log(intensity)



Values from

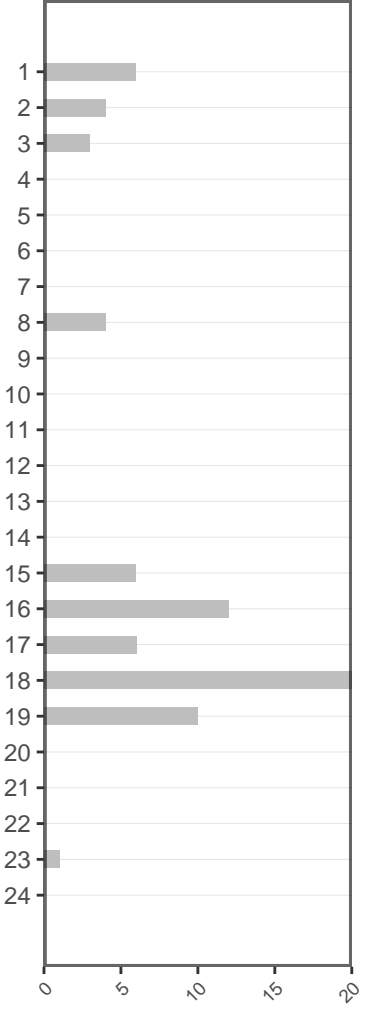
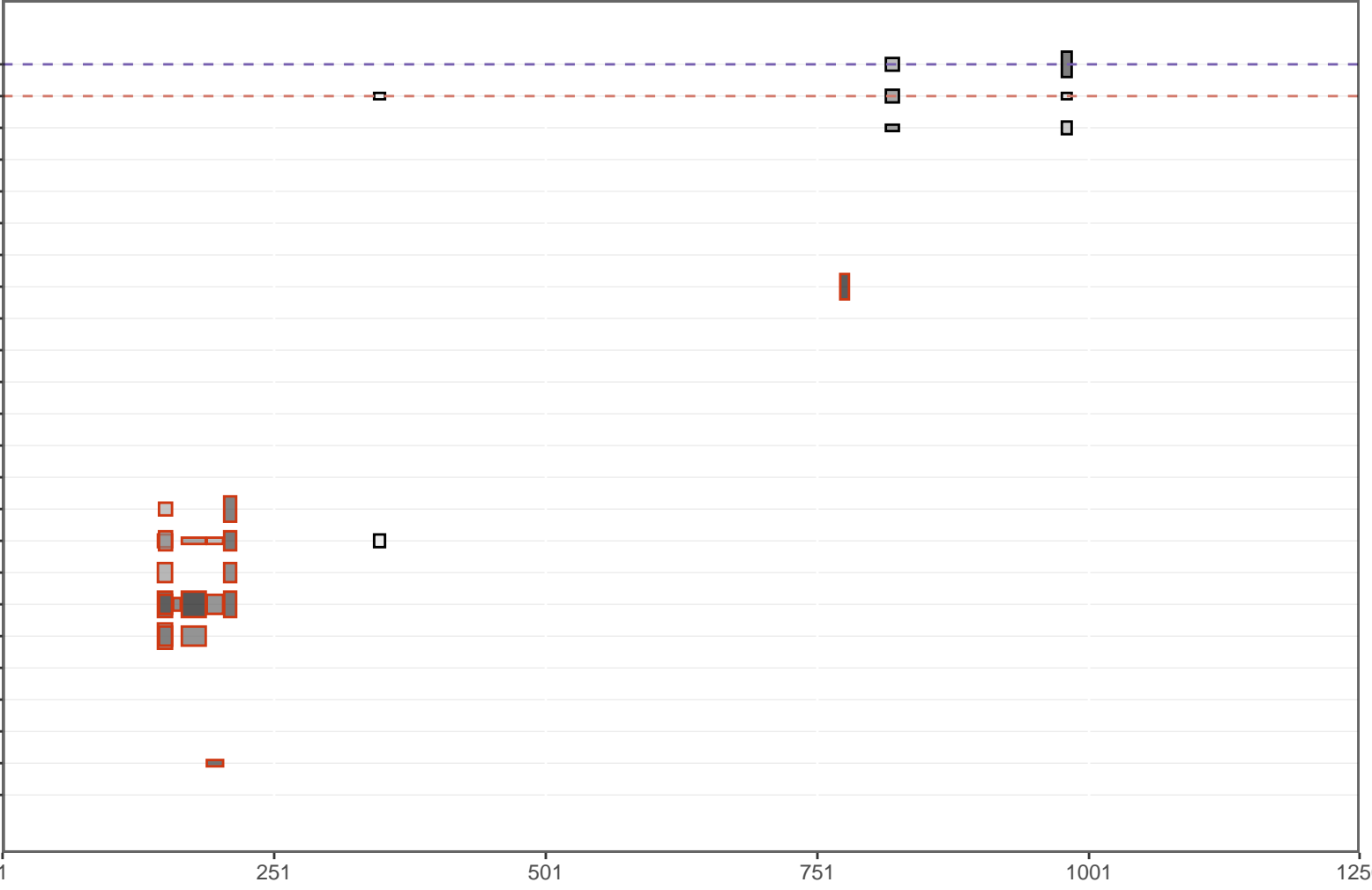
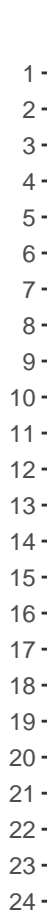
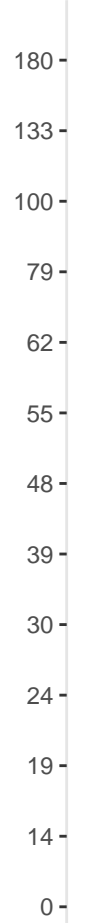


MW indication



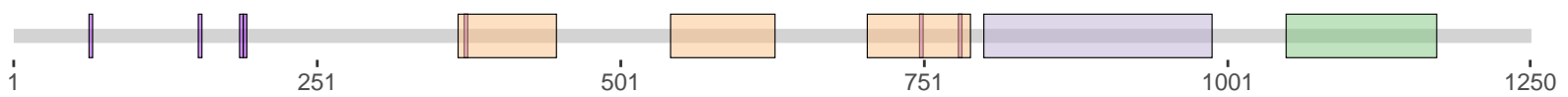
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

*PKIAIAYDNNHRRDGFHVAVFKHPEELWVEEELGIFKTLGERRLRREEMRAKAEKAAARMKAESKERTMKGFLSLGQKHVYVTEPLDVGAGSSTVTVYNPANTVLSNGKPEWFRGFSNRWTRHRLGFLPPKMLPENGTHVKATVKKVPLDAAHMMDFVSEREDGGIFDNRSGMDHHPVFGGVAKEPPMHHVAVEMAPIAKVGGSGDVTSLSRVAGDLNHHVDVILPKYDGLKMGVWDFQFHKKBYFVGGTEKHWVFGKVEGVSIVYFLEPQSLFYKGCYYGCNI

NbL02g22160.1 ATP_synthase_gamma_chain_chloroplastic [MW = 41.43 kDa]

No. of times detected



log(intensity)



Values from

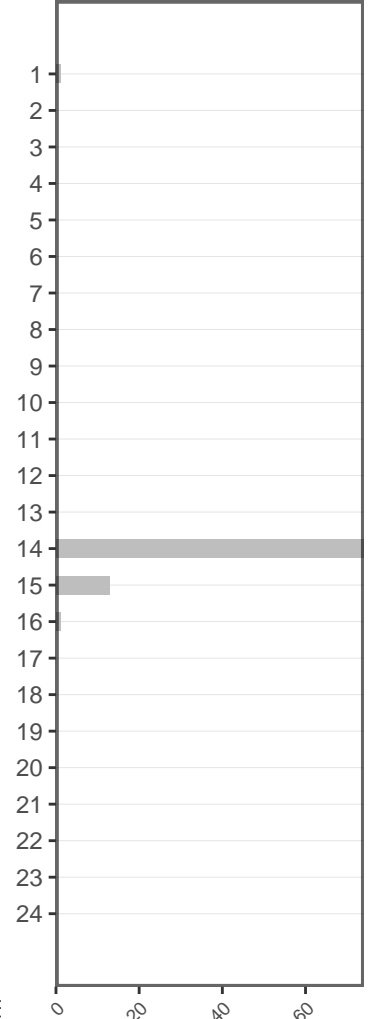
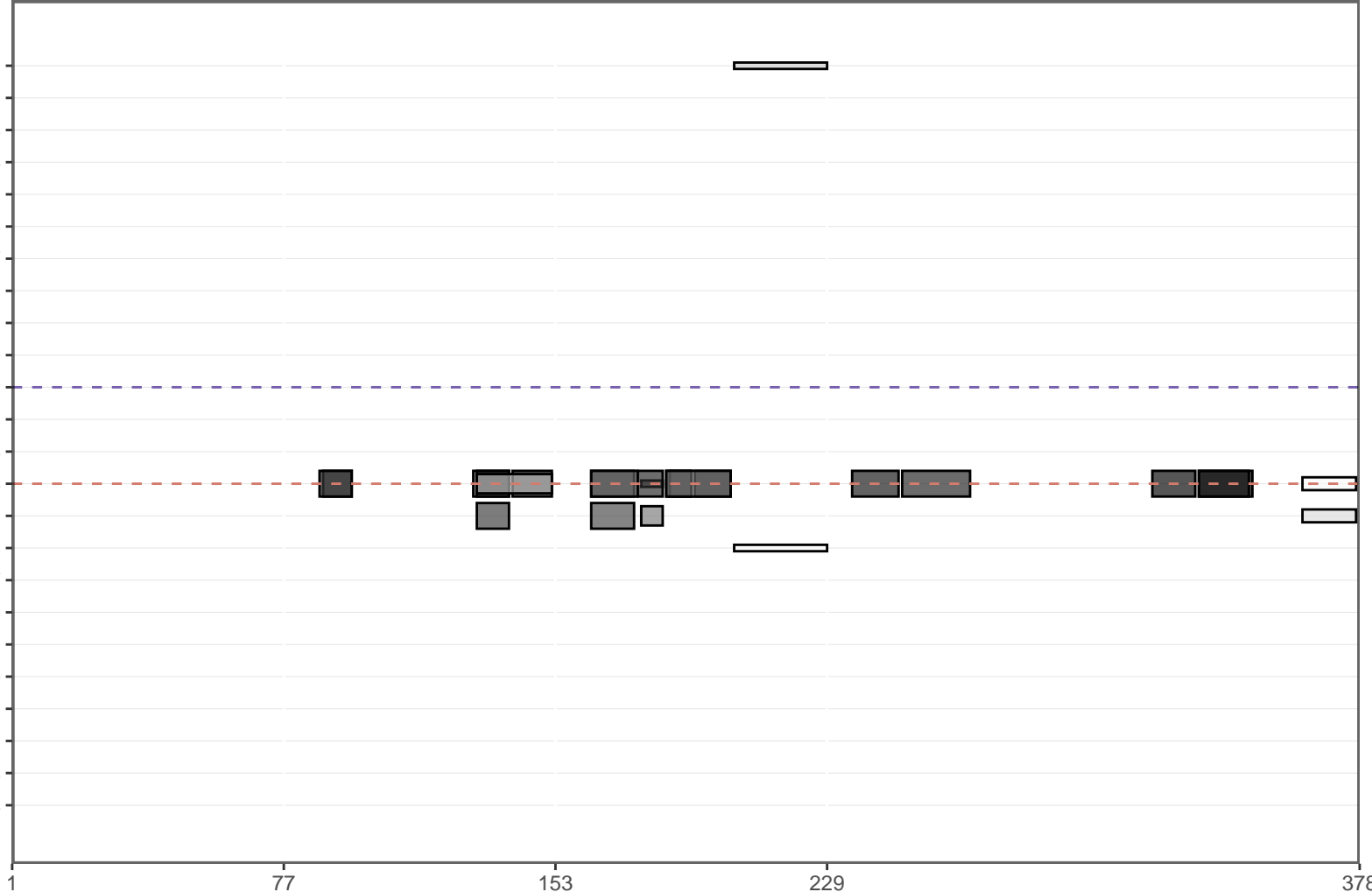
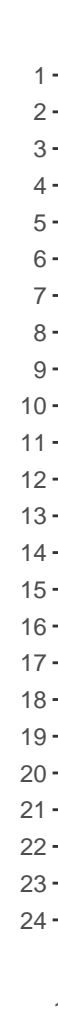


MW indication



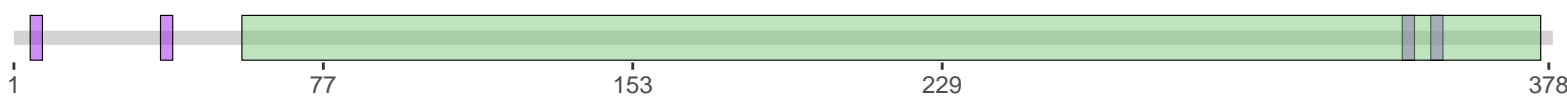
Molecular weight

Gel Slice



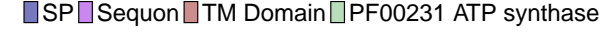
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

KKGNSTYLRFPYIPVQKFLKGNLTKAKDQAIADDDVFLVSEEVQKVELLTKFVSLVSKSEPVHITLLPLSPKGEIDINGNVDAAEDEFRRITKQGLKTVKRDIMRTKTTDFSPILQFEGDPVQGLDALLPLVYNDQILRALQEGELAAARMSSAMSAATNASELKKNLGRVYNNRGRGAKITGELEIIVGADALV

NbL02g22140.1 nucleolar_protein_56-like [MW = 53.86 kDa]

No. of times detected



log(intensity)



Values from



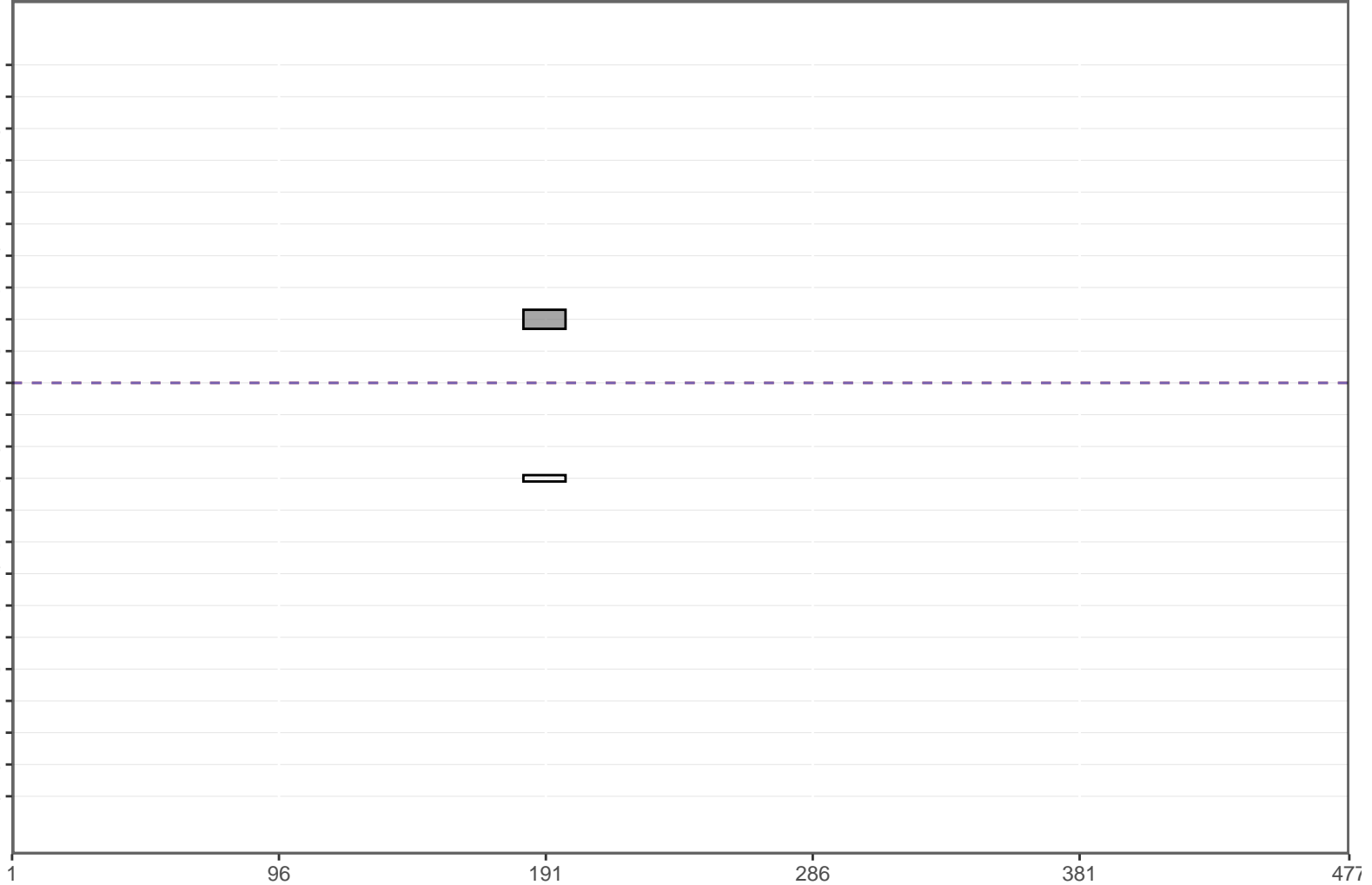
MW indication



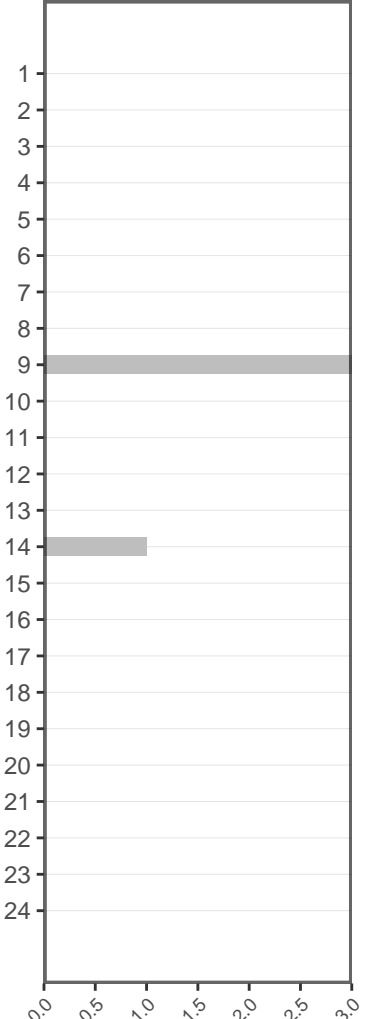
Molecular weight



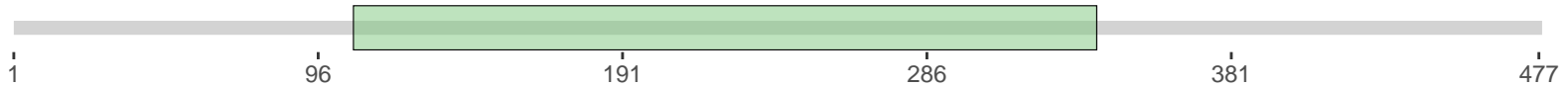
Gel Slice



Protein length

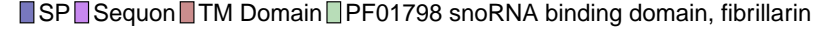


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NLAALIGEVGARLSHAGSLNLAGPSFTLQILGAEKALFRALKTKGNTPKYGLIFHSFGRASARNKGRMARVLANKGBIASRLDCLDFTSTTTFGKELREGVEERLDFYDKGVAPRKIVNVMKSAIETVEGKDAEMDVDEPSAMKSKKKKVEVVEYAGPMEDDPLVNTNVDASEEFPKSEKSKKKKKRKEGEGREHEEDDTNGAPEDGTAKKKKKKEENGEEELQAAAEVKKKKKSKVQDDQ-

NbL02g22060.1 zinc_finger_MYND_domain-containing_protein_15 [MW = 70.51 kDa]

No. of times detected



log(intensity)



Values from



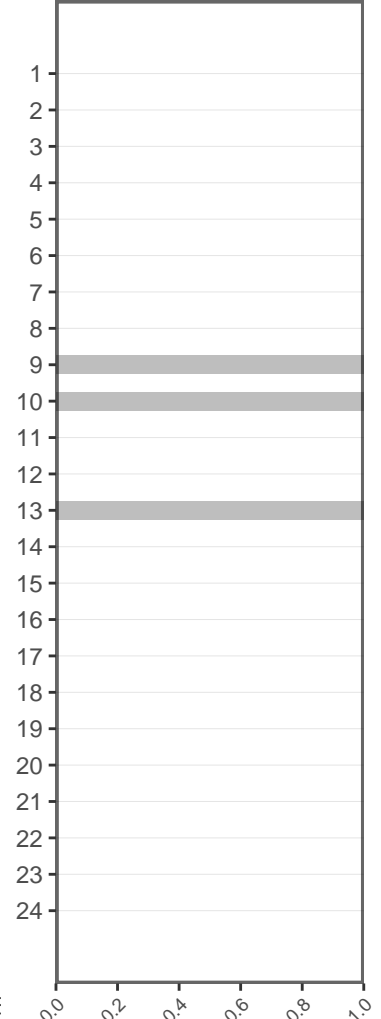
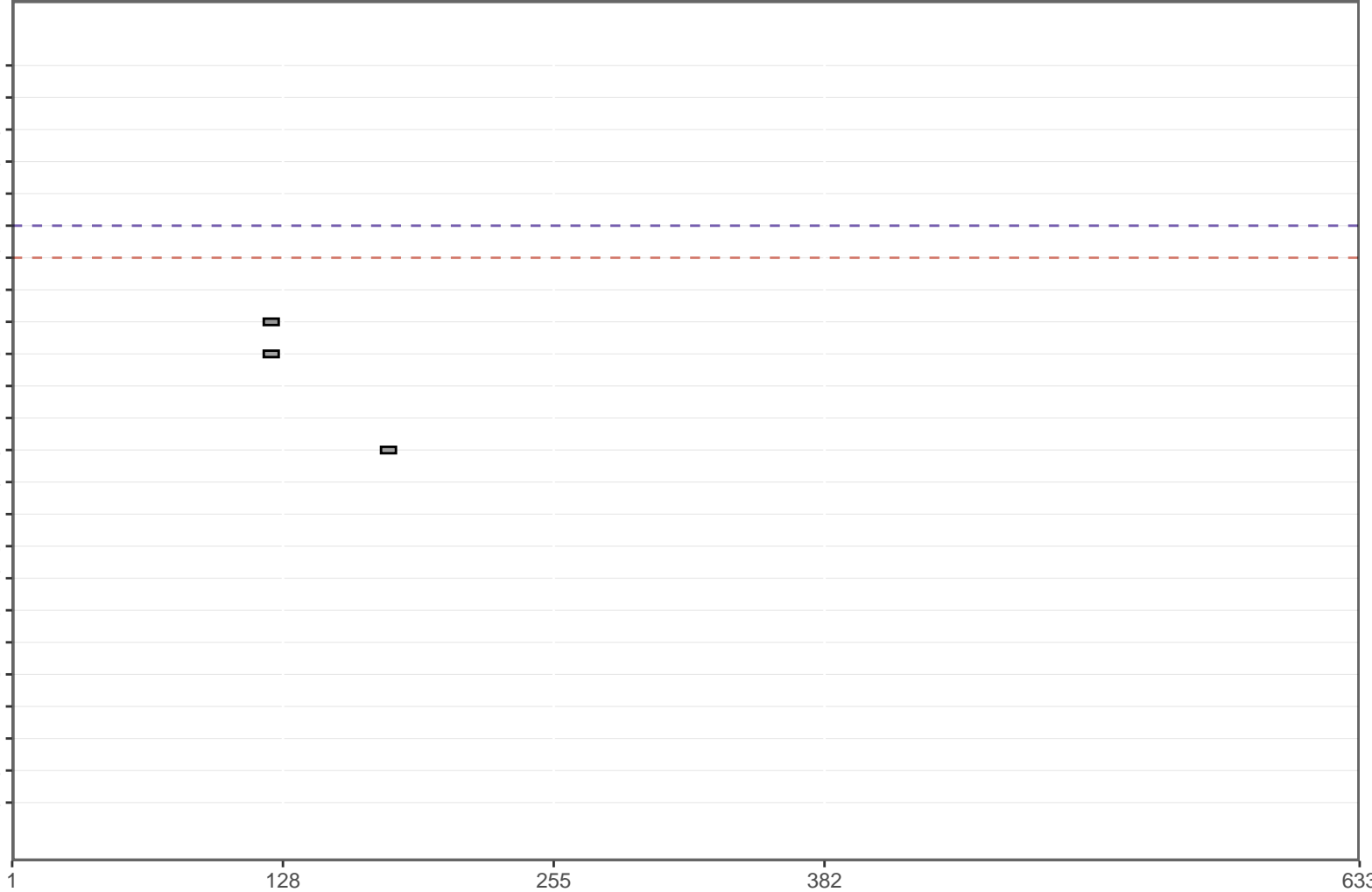
MW indication



Molecular weight



Gel Slice

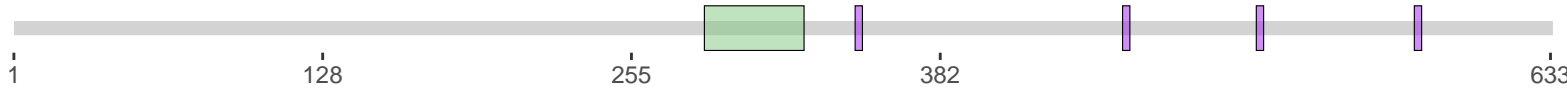


Protein length

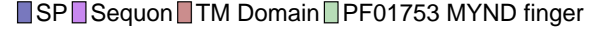


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

CSAVVYCSVCKQGHWKEAHRKIVGQGLYRAMMEREELAMNIFIFNGEAGPKWLESLGHGKGMWRIRKCKGKCYSHCPFGLLPVPGGLWNSWGGLDENEPHDSFHHFRDGISSVFLGDLVYELRSLPLTFPVADLHSLPLTYVMATALNISKILLKIKKLVYHIGPESELDMWFAEIGHLHGMENHIMVGPVPTNLGGTTSGHGSRVRYNIVRGLYGDSEASVLPTRHWIMBLNGLGSGYSGWDGALDKISMVPAVETNESEL6CSSSKOYLRAAG

NbL02g21830.1 pectinesterase-like [MW = 58.73 kDa]

No. of times detected



log(intensity)



Values from



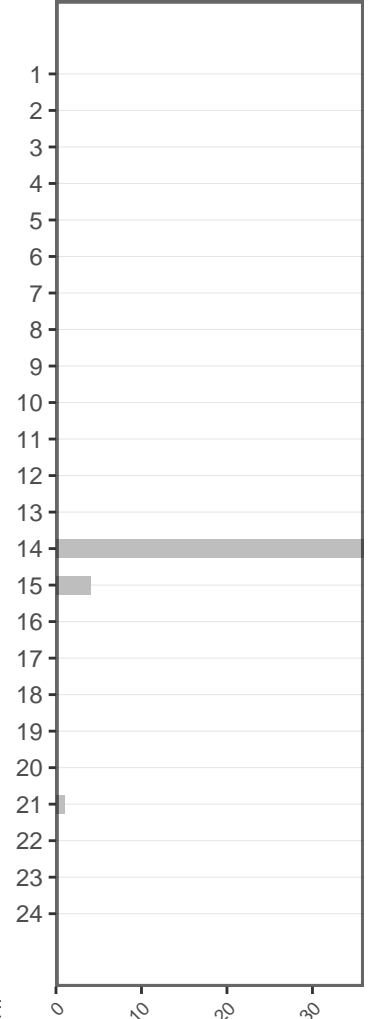
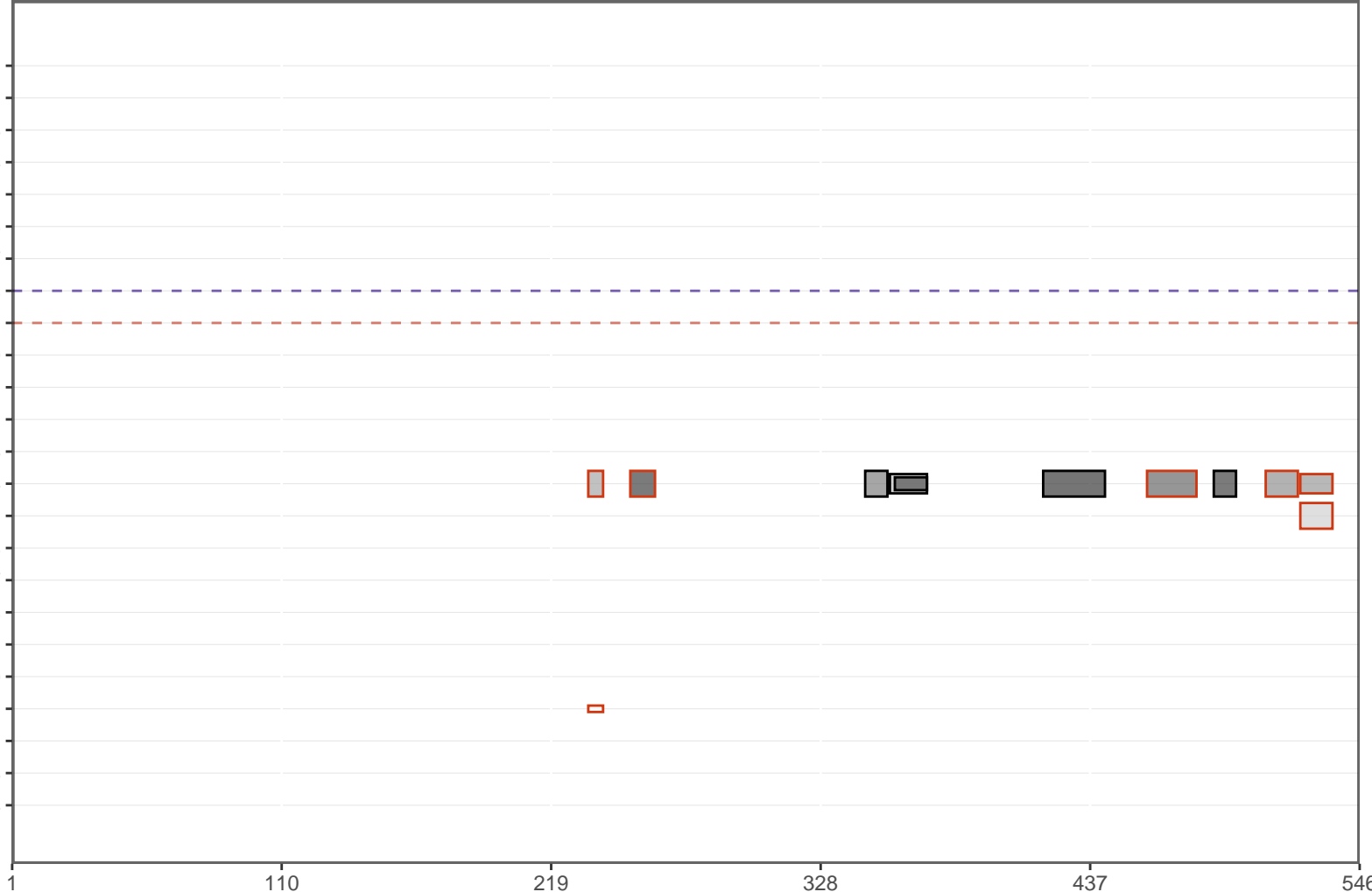
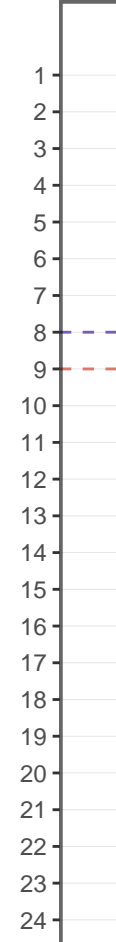
MW indication



Molecular weight

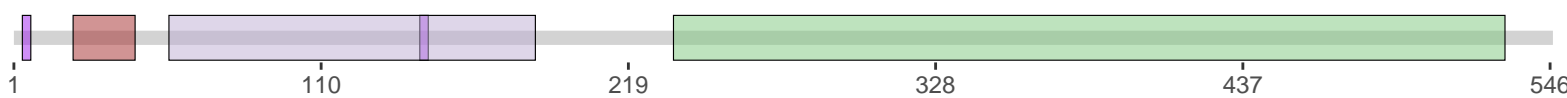


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IKTRYIYYXGIIYKENVEIGKIKKNNVAVLGDGMDATITGSLNVDGATFNATVAAGDGFADGLQFQNTAGAAKHDAWALRVGADGVSINRKHDFQDTLVTLSLRQGFYRDCYAGTDFDFGNMAVVFQNKIAARKPGCGQKNMVTAGGREDPNQNTGTSGNKGDIATSDALPVGSEVKTLLGRPWKAYSRDTLVTMDSNGDHDIDPEGWSVWKGDFAKTLVYGEVMNKGAGAGTSKRWRWPGVHYLSASEATKFTVAGLQGGGAWLKSTGWYTEGL

NbL02g21770.1 putative_receptor-like_protein_kinase_At4g00960 [MW - SP = 72.45 kDa]

No. of times detected



log(intensity)



Values from



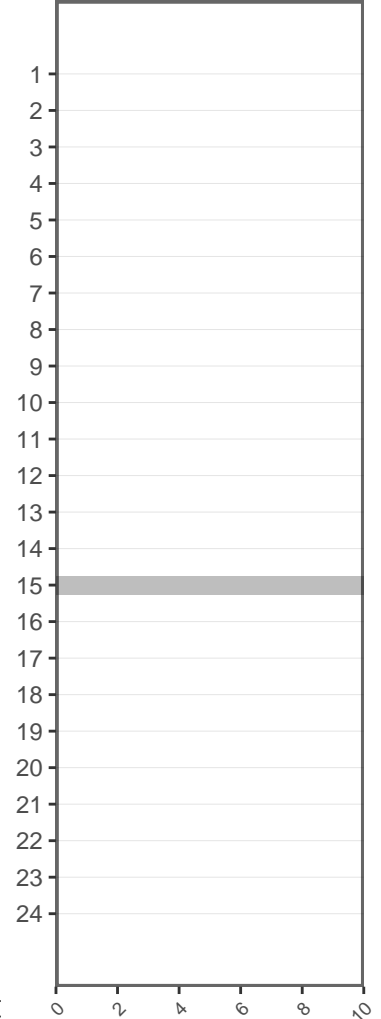
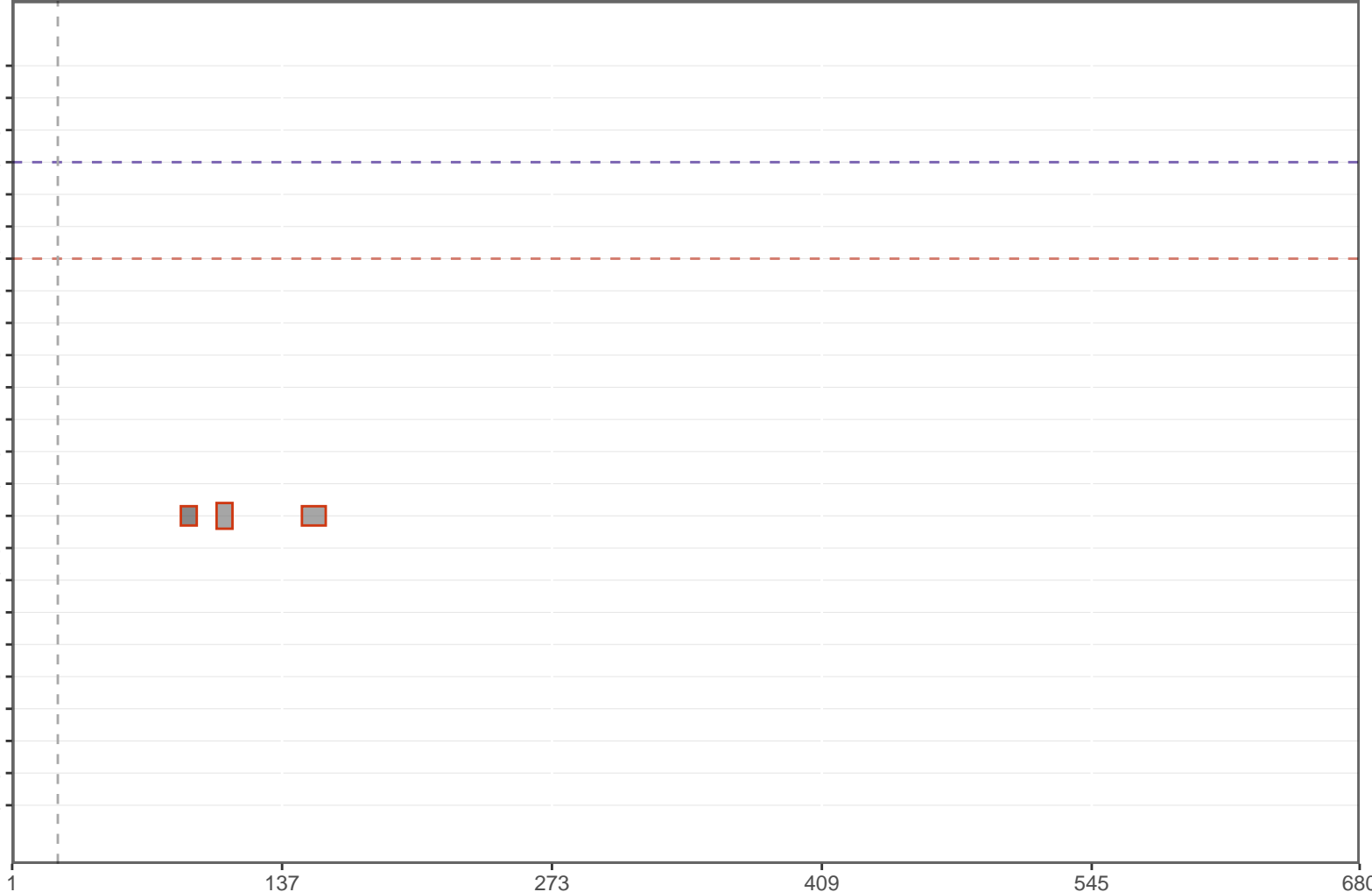
MW indication



Molecular weight

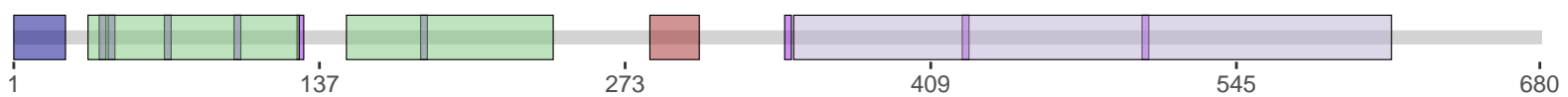


Gel Slice



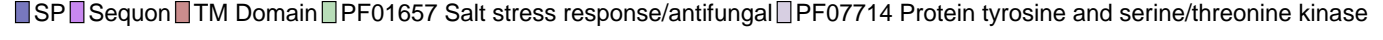
Protein length

Peptide counts over 4 repeats



Pfam domains

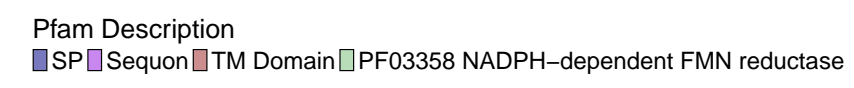
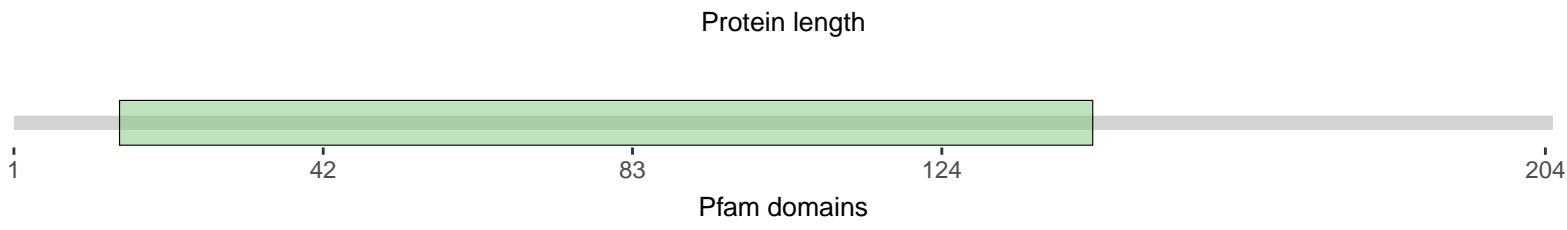
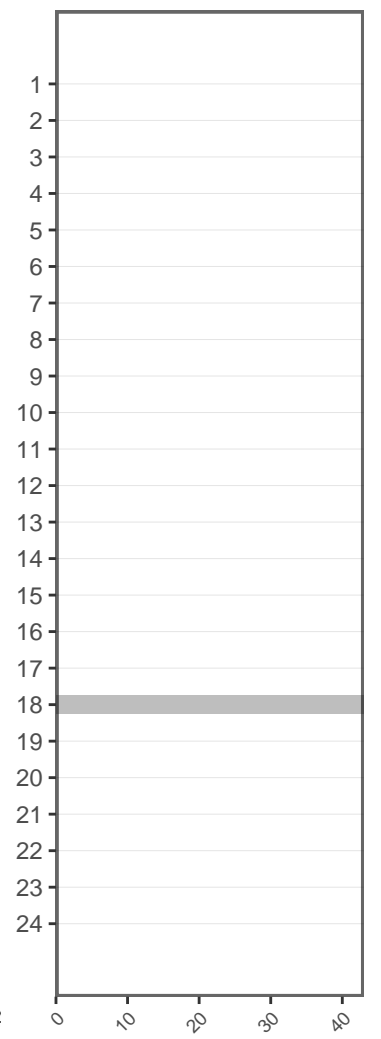
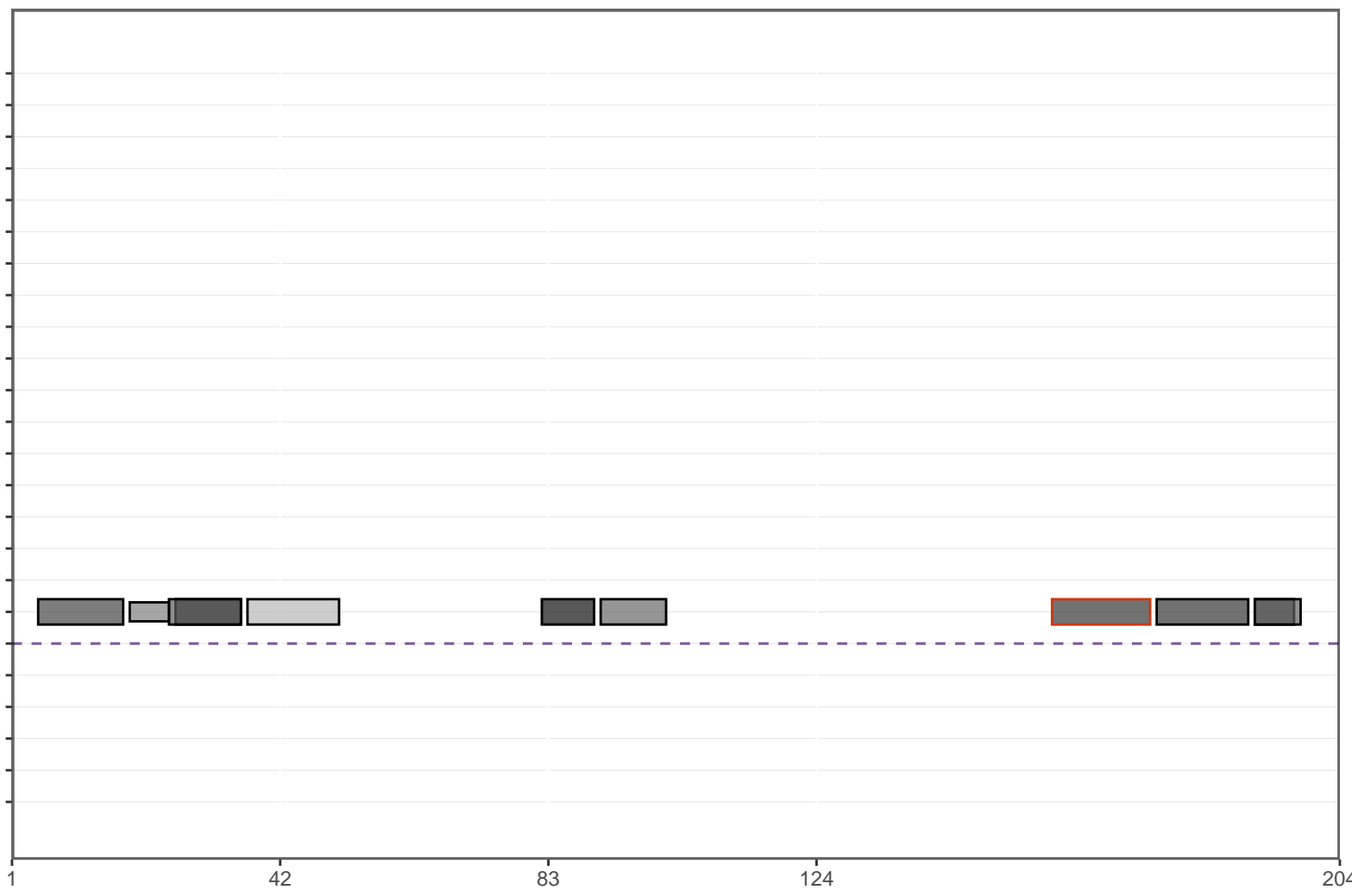
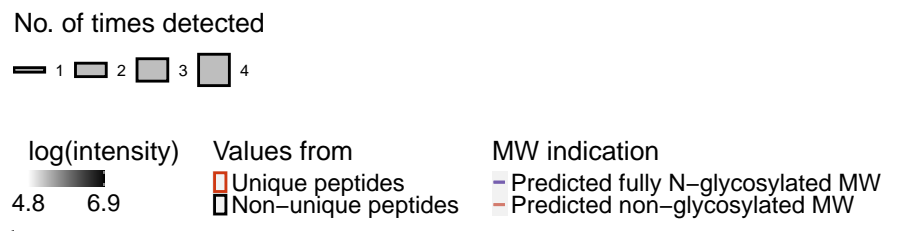
Pfam Description



Protein sequence:

IAESLOYDFSTRVATQNFNSNANKLGGGGFGRVYKGLKNGDGEVWKKLSADSGGGDLEFNEVVLVSRLLGHRNLVRLKGLDGAERLLVYEFVFNASLDDFLFDPVKKRRLDWERRSRRIGGVARGVLLHEDSRLLRIHRLLKASNVLLDAGMNPKISDFGMARLFTLDETGGNTERAGTYGYMAPEVAMHGDGFSVKSDVFSFGVLLVLEILGGQKNTCFRNGSEVEEDLLEVAWSNWRDGTATNIDPMLRGSTVLRDLRSHIALCGVENADRPTMAAVVLMSSL

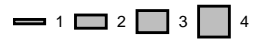
NbL02g21630.1 probable_NAD(P)H_dehydrogenase_(quinone)_FQR1-like_1 [MW = 21.6 kDa]



Protein sequence:
 KAFLDATGGLVIRTDGLAGKPKGLFYBTGGGGGGGQETLTAITGLVHGMIFVPIGYTFGGGMFEMENIKGGSPYAGTYAGDGSRPTELEMEQAFHGGKYATITKILKGS

NbL02g21580.1 G-type_lectin_S-receptor-like_serine/threonine-protein_kinase_At1g11410 [MW - SP = 90.65 kDa]

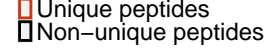
No. of times detected



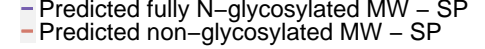
log(intensity)



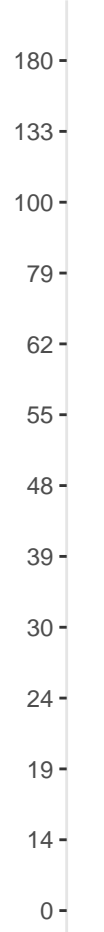
Values from



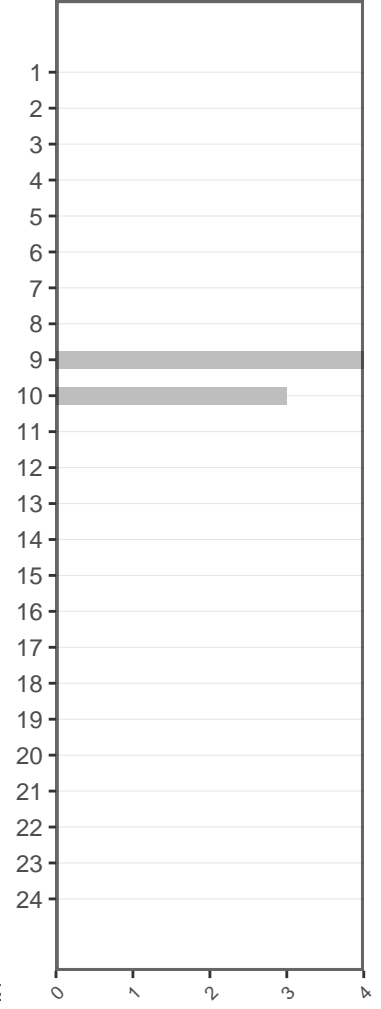
MW indication



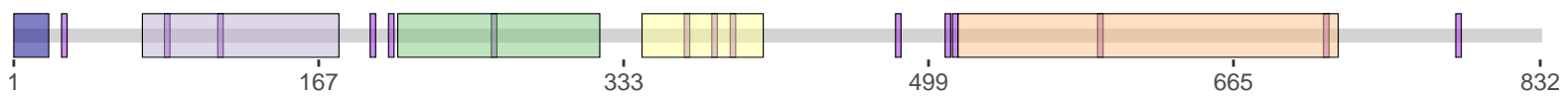
Molecular weight



Gel Slice

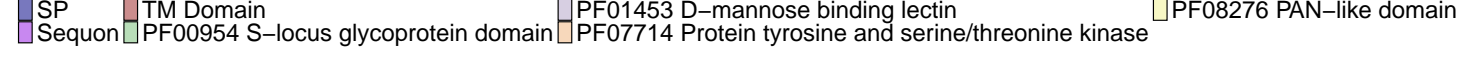


Protein length



Pfam domains

Pfam Description



Protein sequence:

ITWYGLRDKIKFTDGGGDFYSRASASDLAQFSKPNPNHRLKMTAHVGSAAAVIGLLLLAVFLVSKRRKDKKSHENTLNKLSAGEEMDGGSEGTSEIFDLSTISMATDNFVANKLGGEGGFGVYKGHLDKGGVIAVRLKLVTSGGGAKFEFRNEVTLIARLGHRLVRLKGGCSGLGEMLVYVLPKSLDFDFDKTKGILLDFWGRKEIHHGIARGMLVHQDSRLRHHRLKASNVLLDASMQPKISDFGMARIFGVDQVEANTNRVAGTVGYMSPVAMVGFSAK

NbL02g21450.1 universal_stress_protein_PHOS32-like [MW = 26.82 kDa]

No. of times detected



log(intensity)



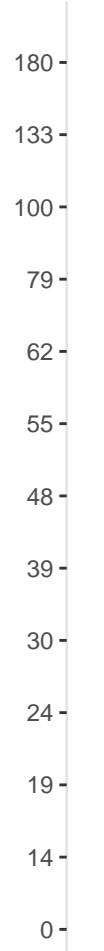
Values from



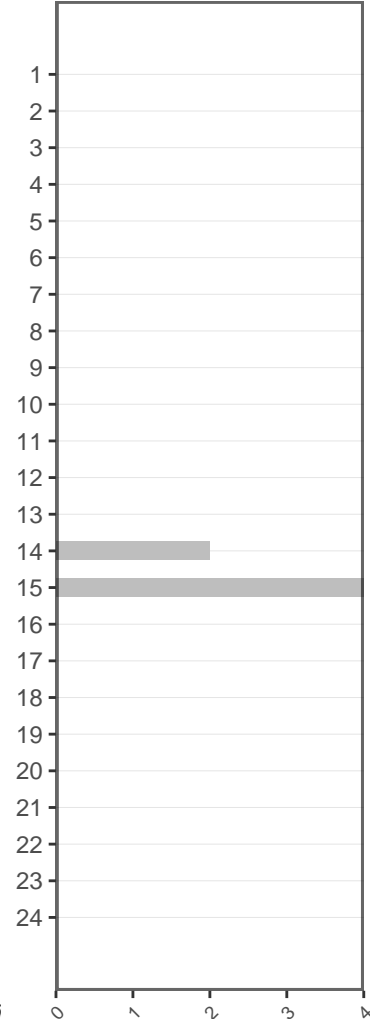
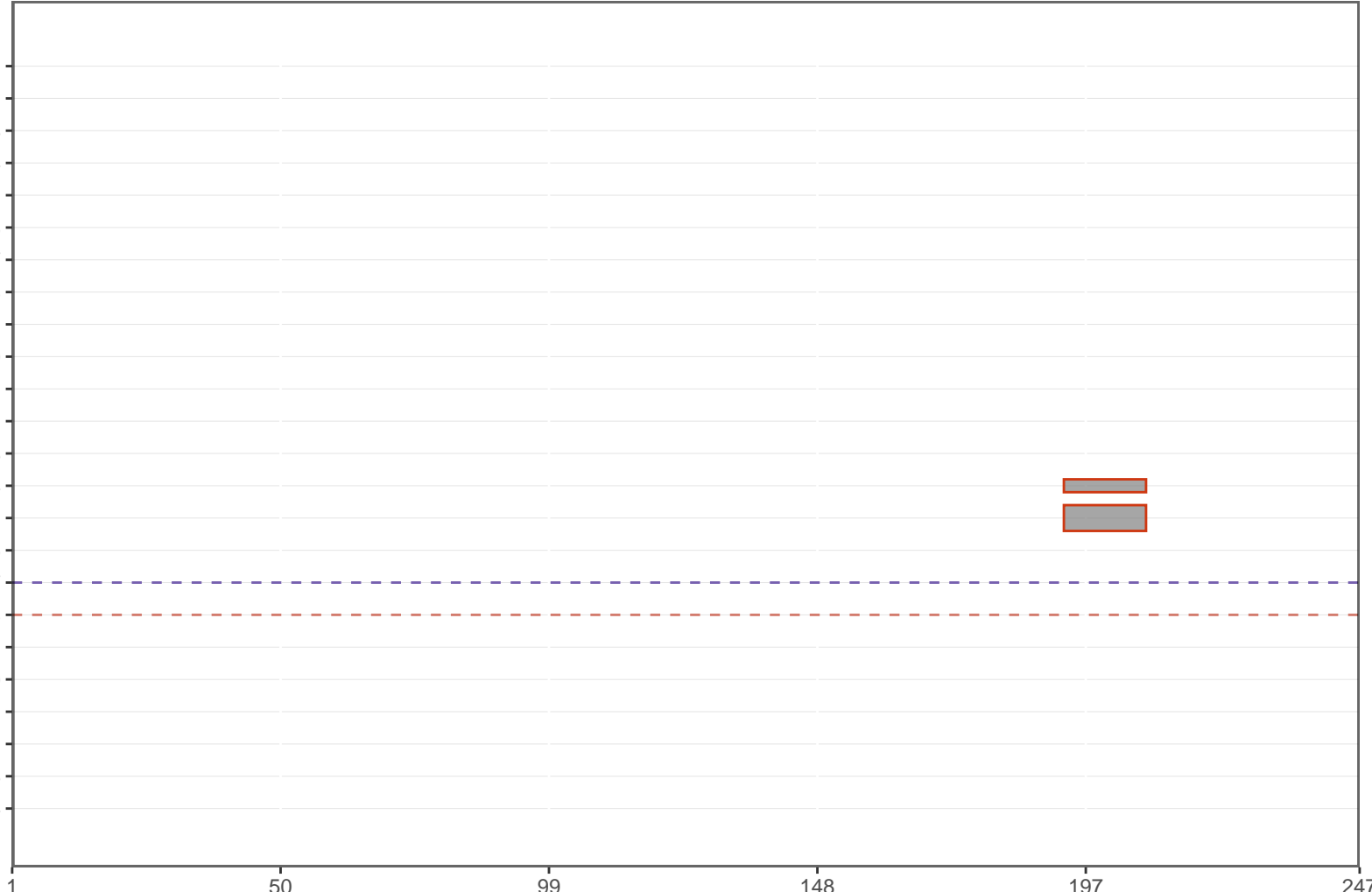
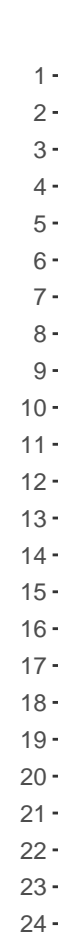
MW indication



Molecular weight

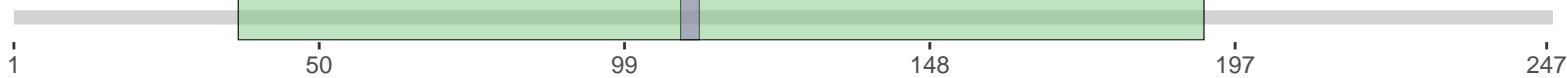


Gel Slice



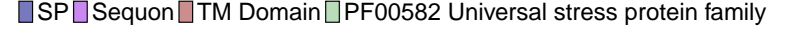
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ITKANDLAQPLVEGNPFKHKYKDHDKMERLGLLEVERLGLSAWIMSGRFGASRRSKGGRLGVSVDYGVHHCVCPVAVRRYPDDKDGWADDANERSVKKETTDCGLVHPVPEDEPIYHDAEDKAAATGQRKGLPI

NbL02g21370.1 putative_PAP-specific_phosphatase_mitochondrial [MW = 21.92 kDa]

No. of times detected



log(intensity)



Values from



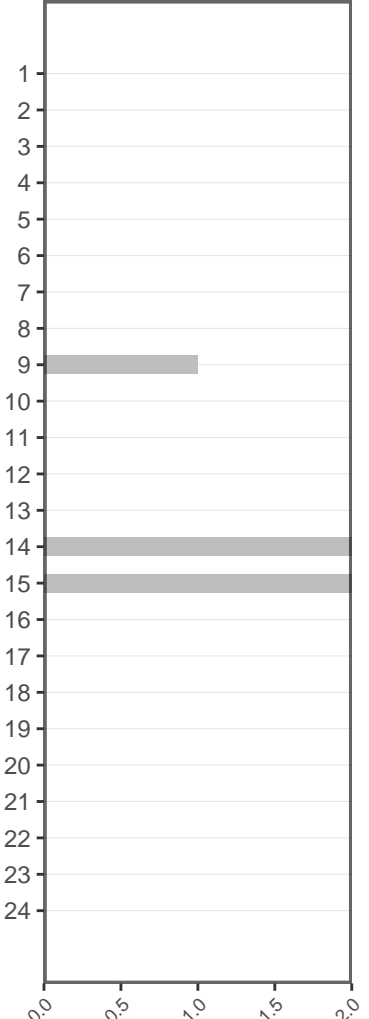
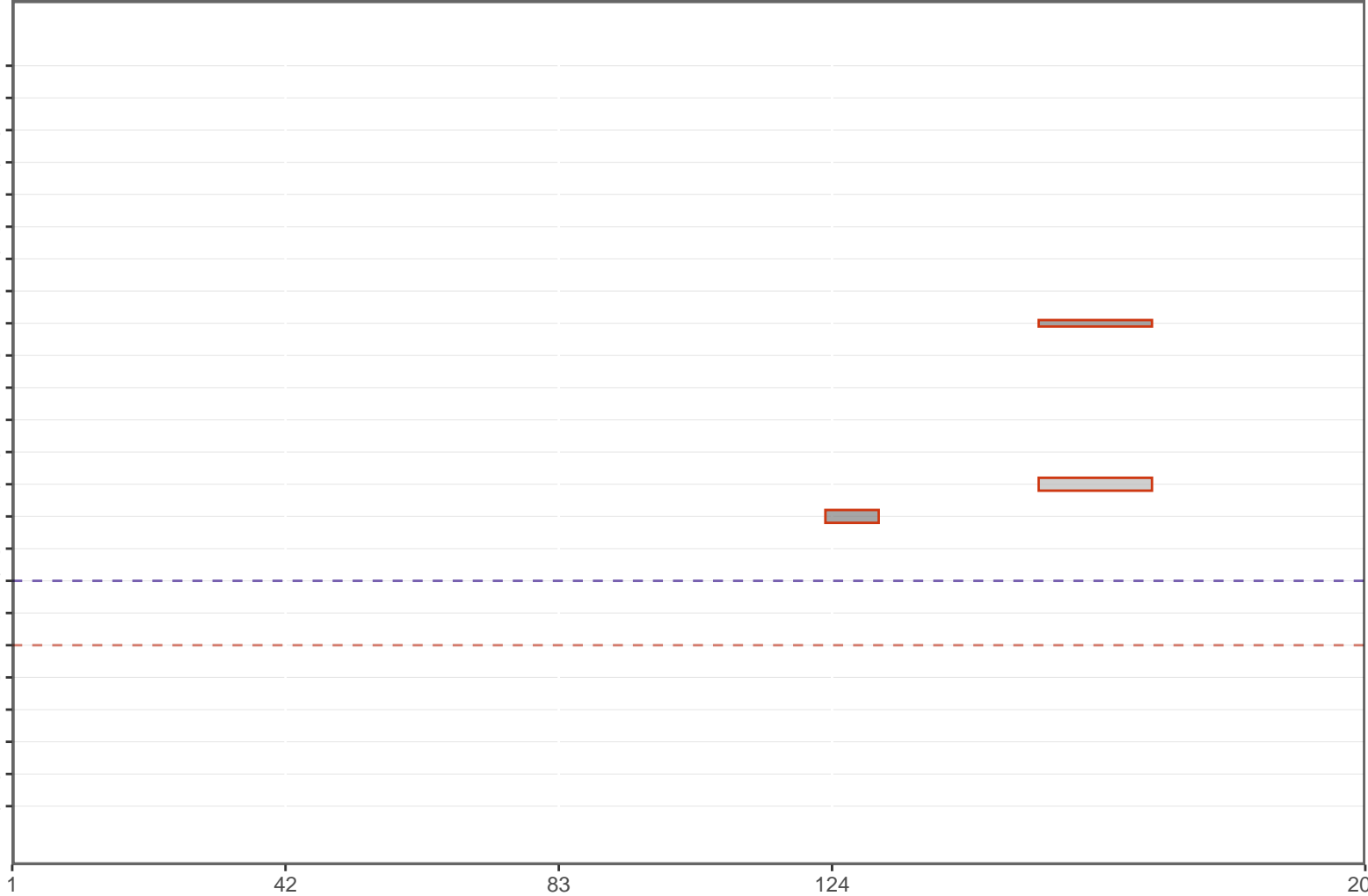
MW indication



Molecular weight

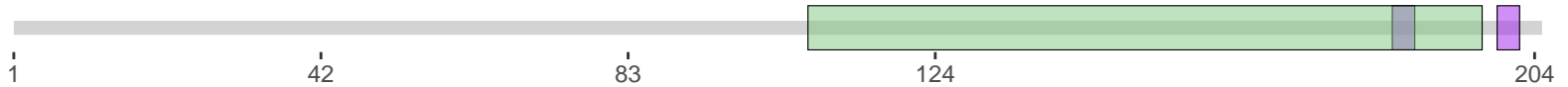


Gel Slice



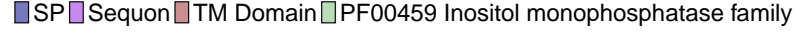
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SFDAERDSENVEGNLLLSADCGSLGKYLVAAGRAVYIQGPKATSTKAWDHWAGICVHEAGKVTQWEGSGLDFAADQGERRLIFP6GGVALVTNGSLHKKIGMISNTFVLT

NbL02g21190.1 eukaryotic_translation_initiation_factor_3_subunit_J-A-like [MW = 25.2 kDa]

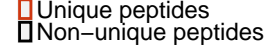
No. of times detected



log(intensity)



Values from



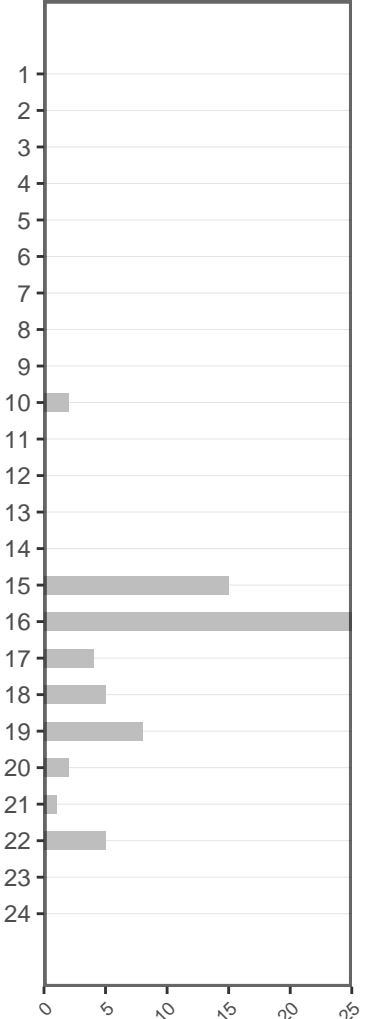
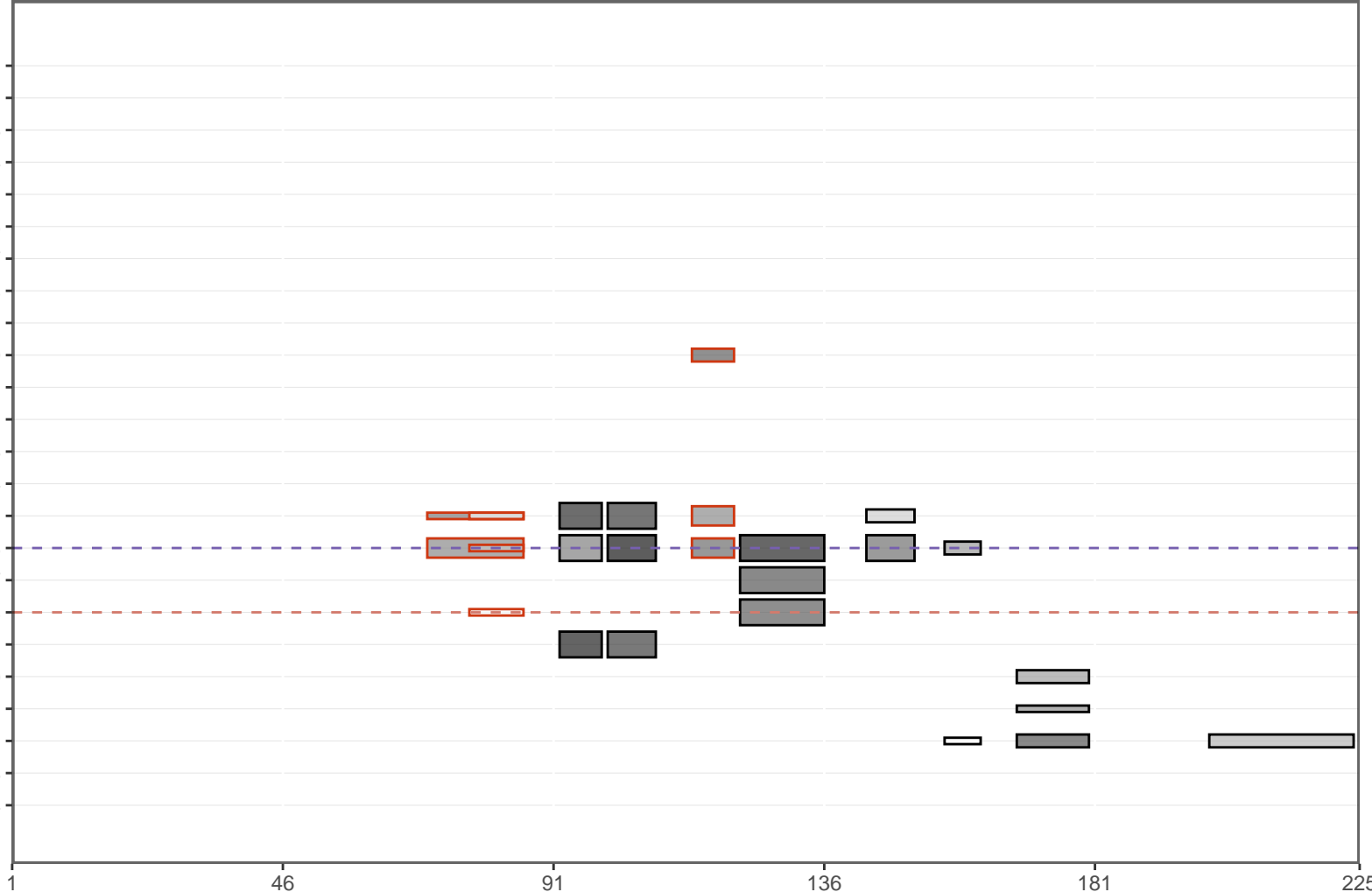
MW indication



Molecular weight



Gel Slice



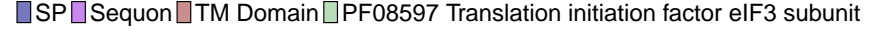
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DYKSTAELEFATKGGGDKNTVDNFRPKSENFLEVAELHSHKLRPYEKSHYIQLLKAWMRLSMTALKGADANEIASSVTAAINEKIKAEKEANAGKKKAGAKKKIHHVDKADDEAVVNAVDDGDDDFDM

NbL02g21100.1 beta-galactosidase_8-like [MW = 19.95 kDa]

No. of times detected



log(intensity)



Values from



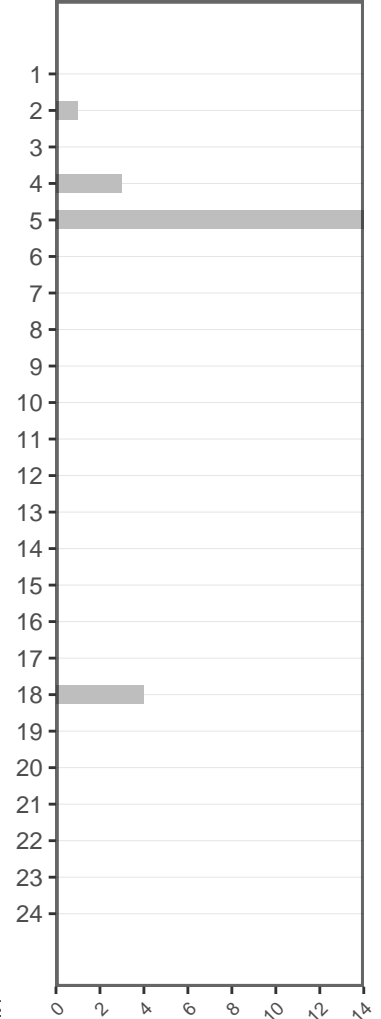
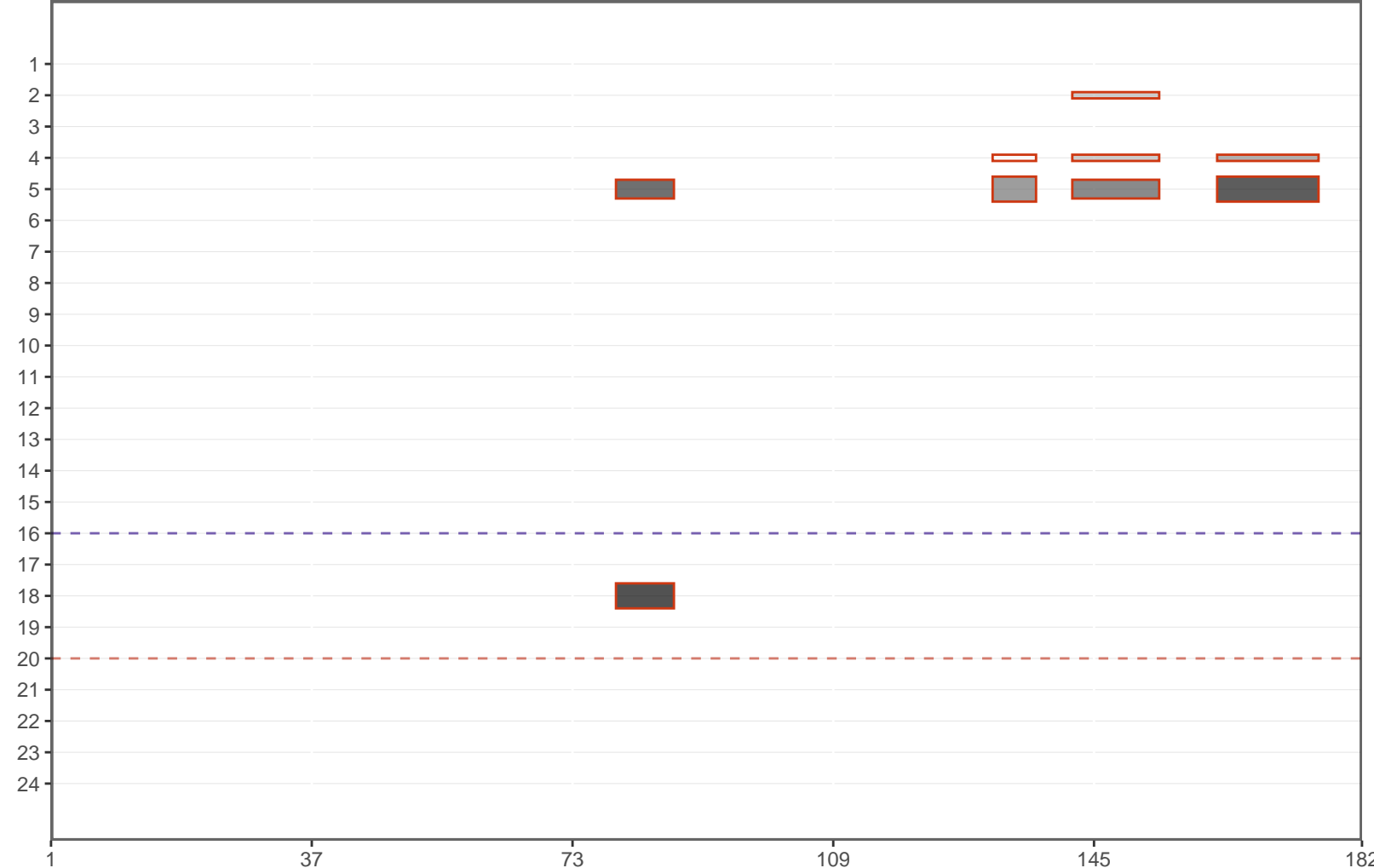
MW indication



Molecular weight

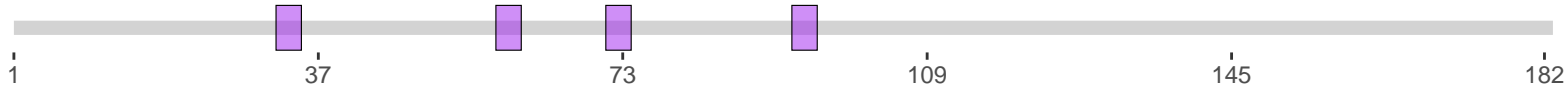


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

ISFSPPEKGGPYSLNLSLSEMGKGGAWNGQVGRYWSYRSPSTGCGNNKDYRGAANSWGLKXKGGPQVLYHYPRRWLTPGKNLVLHEELGGDPKIEFSI

NbL02g21070.1 quinone_oxidoreductase_PIG3 [MW = 34.57 kDa]

No. of times detected



log(intensity)



Values from



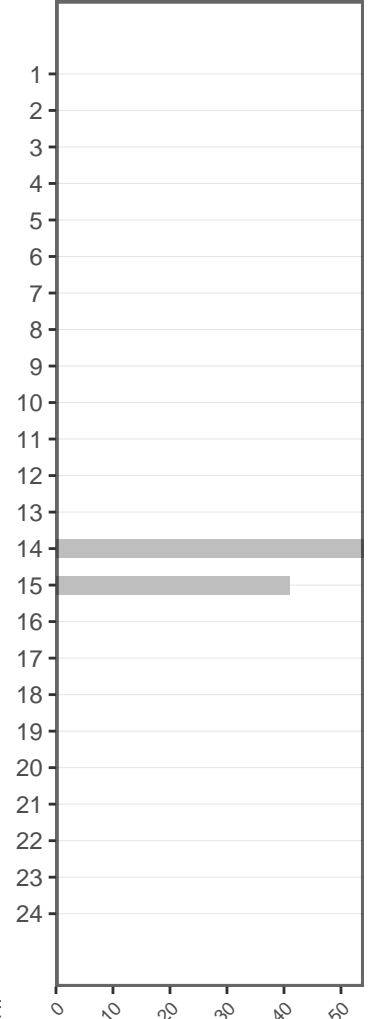
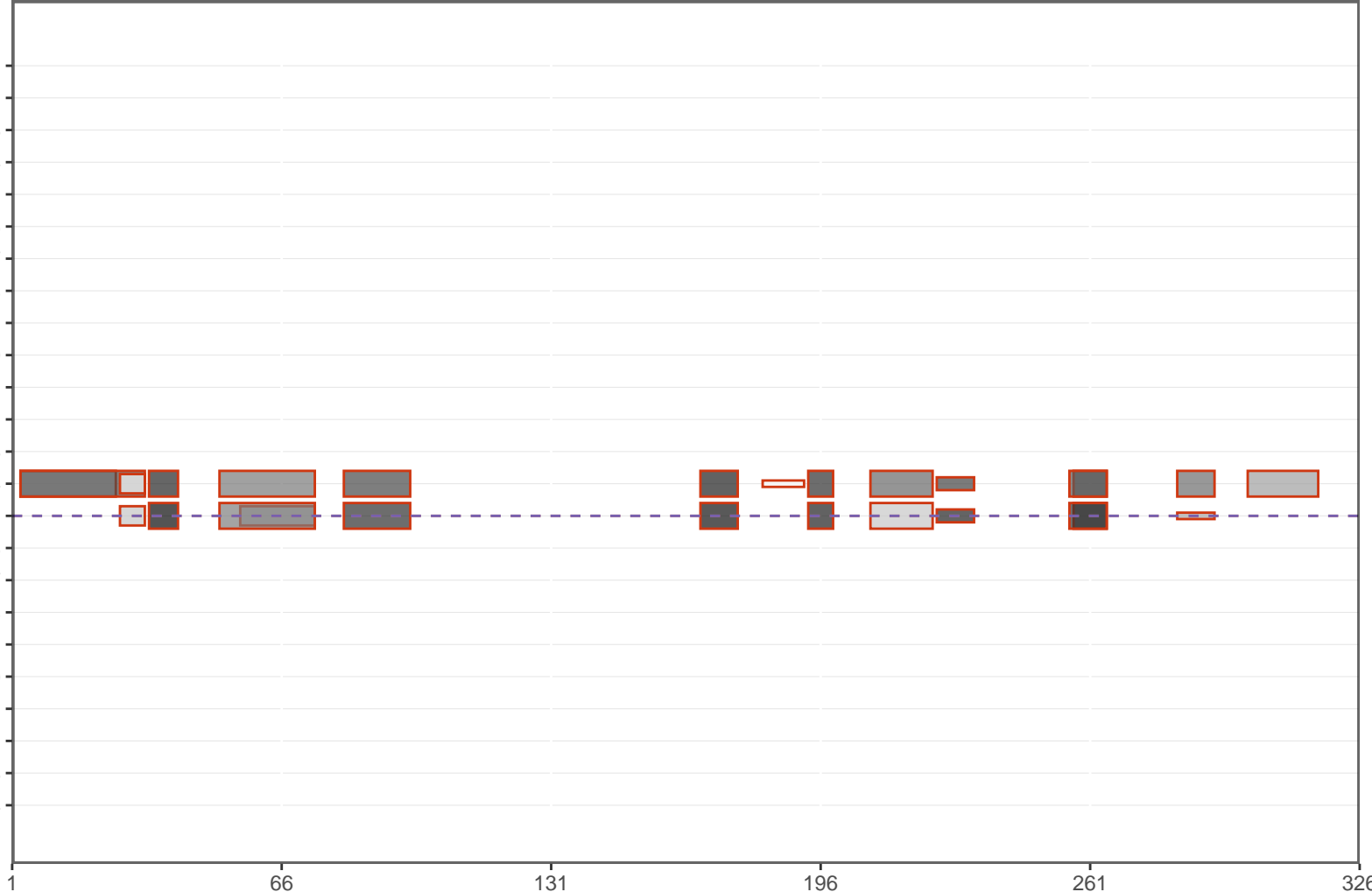
MW indication



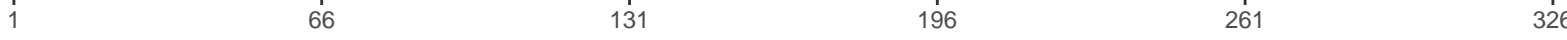
Molecular weight



Gel Slice

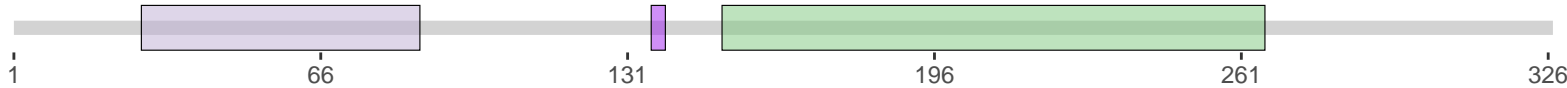


Protein length

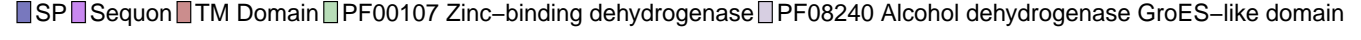


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ISSGIGTFAIQMAKGLGWVFTTAGSEENKVVCKELGADVQINRYKTEDVTRRKEETGGKGVVDVLDSDGDSVFGQRLNDSLNDGRLFIQFMGGTIVGTQVNLAGLLARLLTVGAAGLRSSAOKNKAGIVREKKNVWFAAAGKVKPVVYKYFPLAEAAEAHQLMESSKHGKLLTV*

NbL02g20940.1 glucose-induced_degradation_protein_8_homolog [MW = 27.71 kDa]

No. of times detected



log(intensity)



Values from



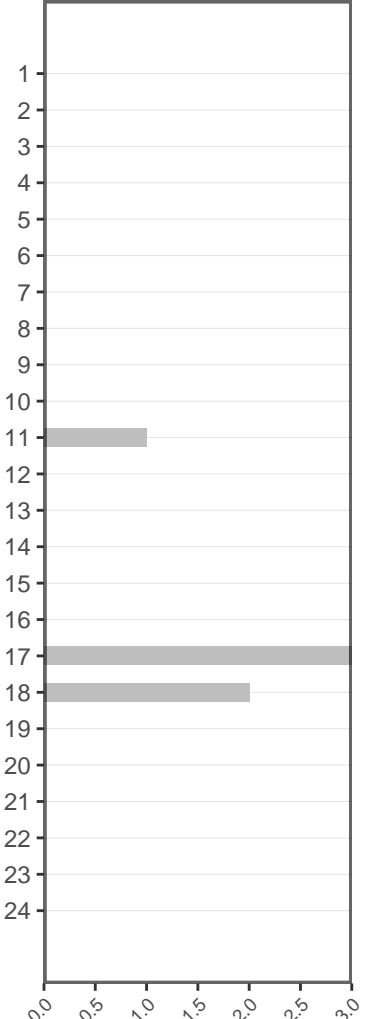
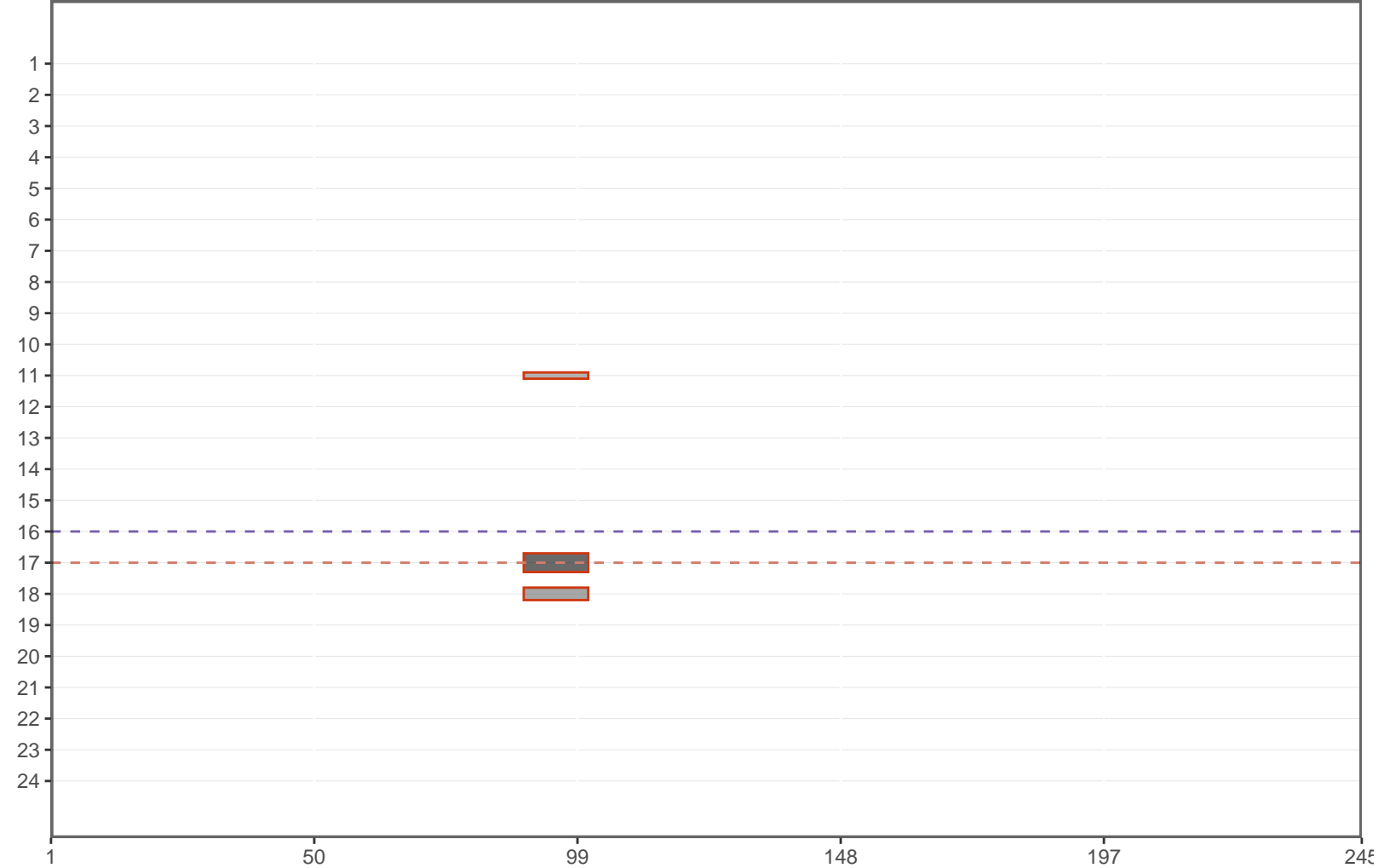
MW indication



Molecular weight

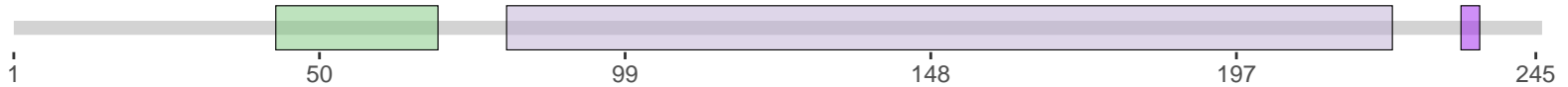


Gel Slice



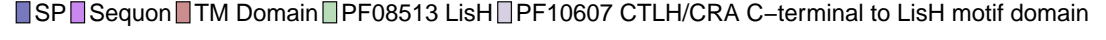
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

I L D T N P Q L F F H L G G R L I E R N G K V E E A L F A G E E L A P R G E N G A F L E E L E K T V A L L A F E D V S N C P V G A L L D V S G R L K T A S E V N A A L T S G S H E K D P K L P S L L K M L I W A G N L D E K A V Y P R I N L S T A S L E D P W I

NbL02g20810.1 bifunctional_epoxide_hydrolase_2-like [MW = 25.24 kDa]

No. of times detected



log(intensity)



Values from



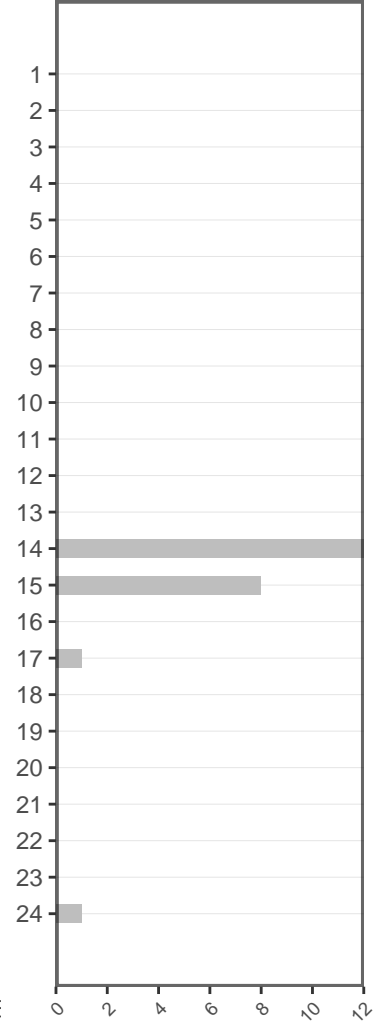
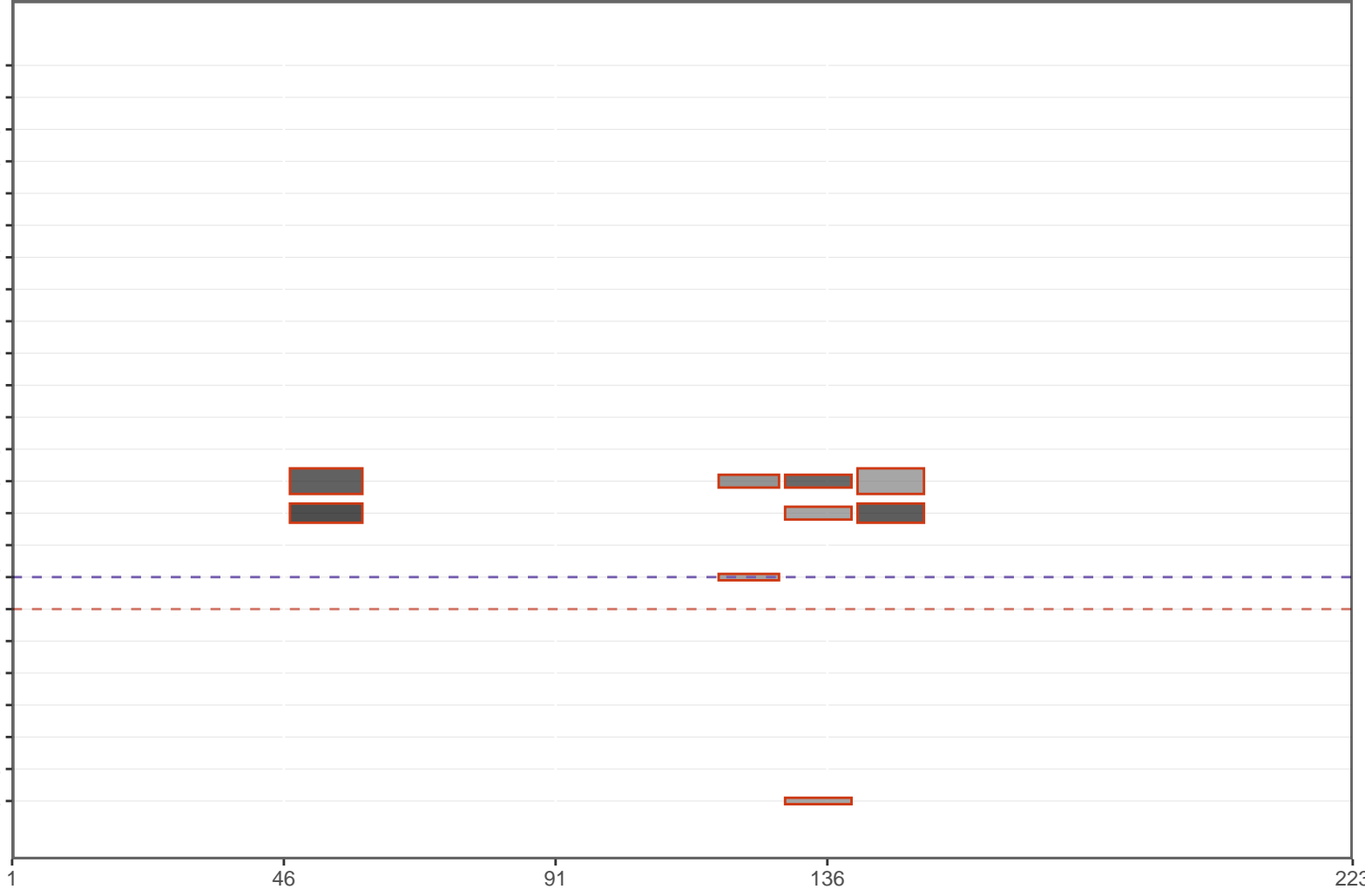
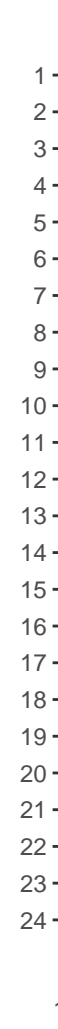
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

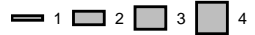
Pfam Description
 SP Sequon TM Domain

Protein sequence:

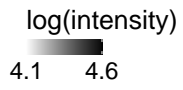
IMDIDVQPTLPVWFSEKDETFYGAIVEKSGFQTALGVPPYRSLLEGANITDPRVHVPAIFVIGEKDFLKFPGVRDVIHSGGLKLSVPLNIGMWNLEGGHFVQEQLPDEVNGVLDFLFRNSGS*

NbL02g20780.1 clathrin_light_chain_1-like [MW = 35.48 kDa]

No. of times detected



log(intensity)
4.1 4.6



Values from

Unique peptides
Non-unique peptides

MW indication

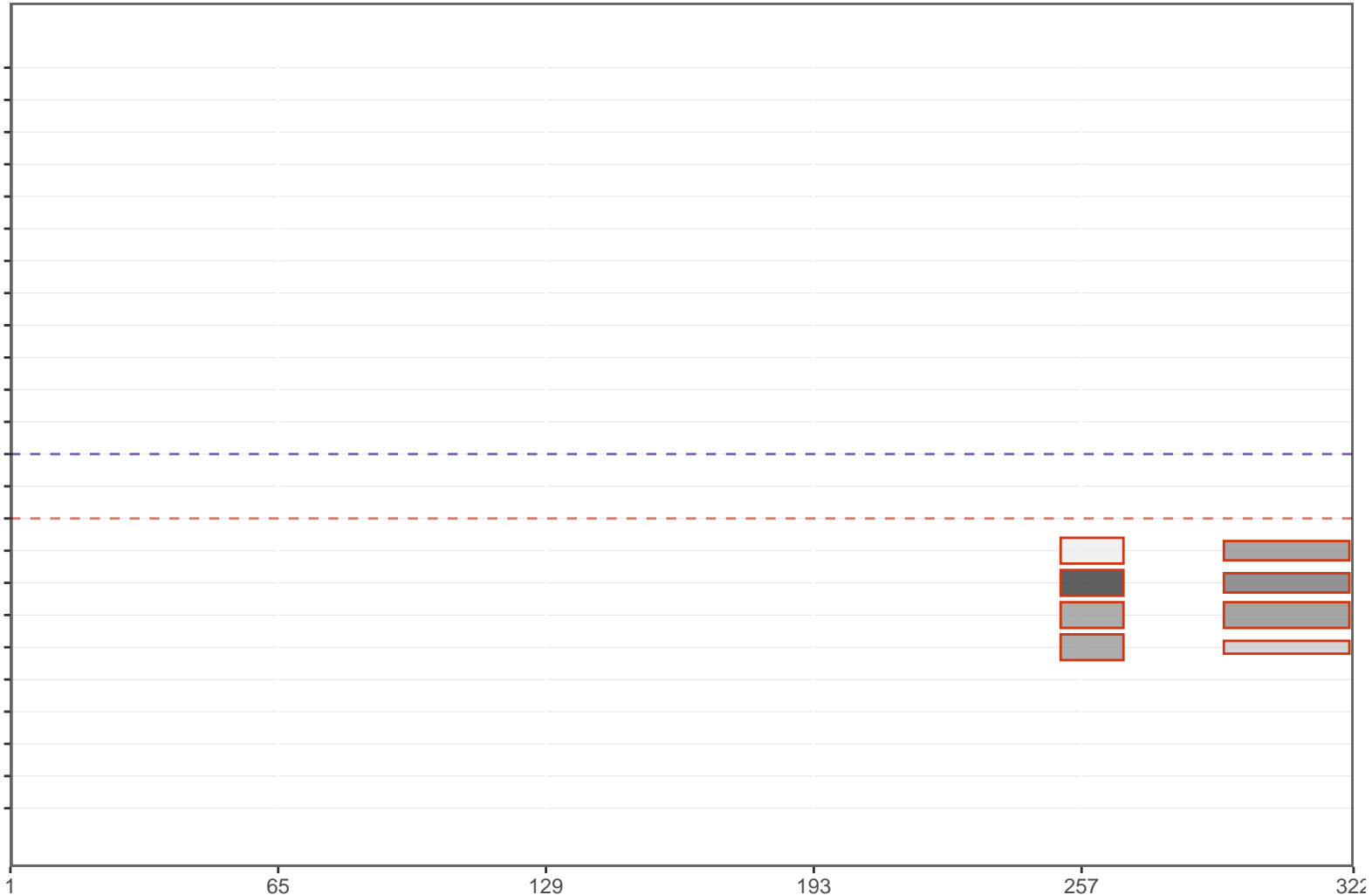
Predicted fully N-glycosylated MW
Predicted non-glycosylated MW

Molecular weight

180
133
100
79
62
55
48
39
30
24
19
14
0

Gel Slice

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22
23
24

Peptide counts over 4 repeats

0 2 4 6 8

1 65 129 193 257 322

Protein length

Pfam domains

Pfam Description

SP Sequon TM Domain PF01086 Clathrin light chain

Protein sequence:

DIEEGEEYKCAFYEKRRLTVEVDGSTRREKEKLVLNDEKFKKADQGWYKAAALPKVEATEKGRKRDGDEKPKSVTVGGPKPKGTLELRMRHLLKLIKHPFPHPMPPPPPKDAKAGKDKGDKDKGDKTKGDKDAKNKAKEAPNGTSDAPPSGANVTGTSEEPAAAEI

NbL02g20660.1 14-dihydroxy-2-naphthoyl-CoA_thioesterase_1-like [MW = 18.96 kDa]

No. of times detected



log(intensity)



Values from



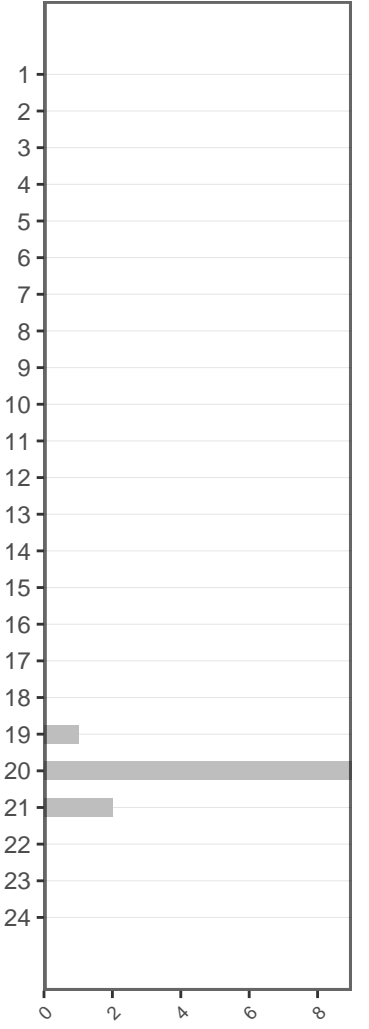
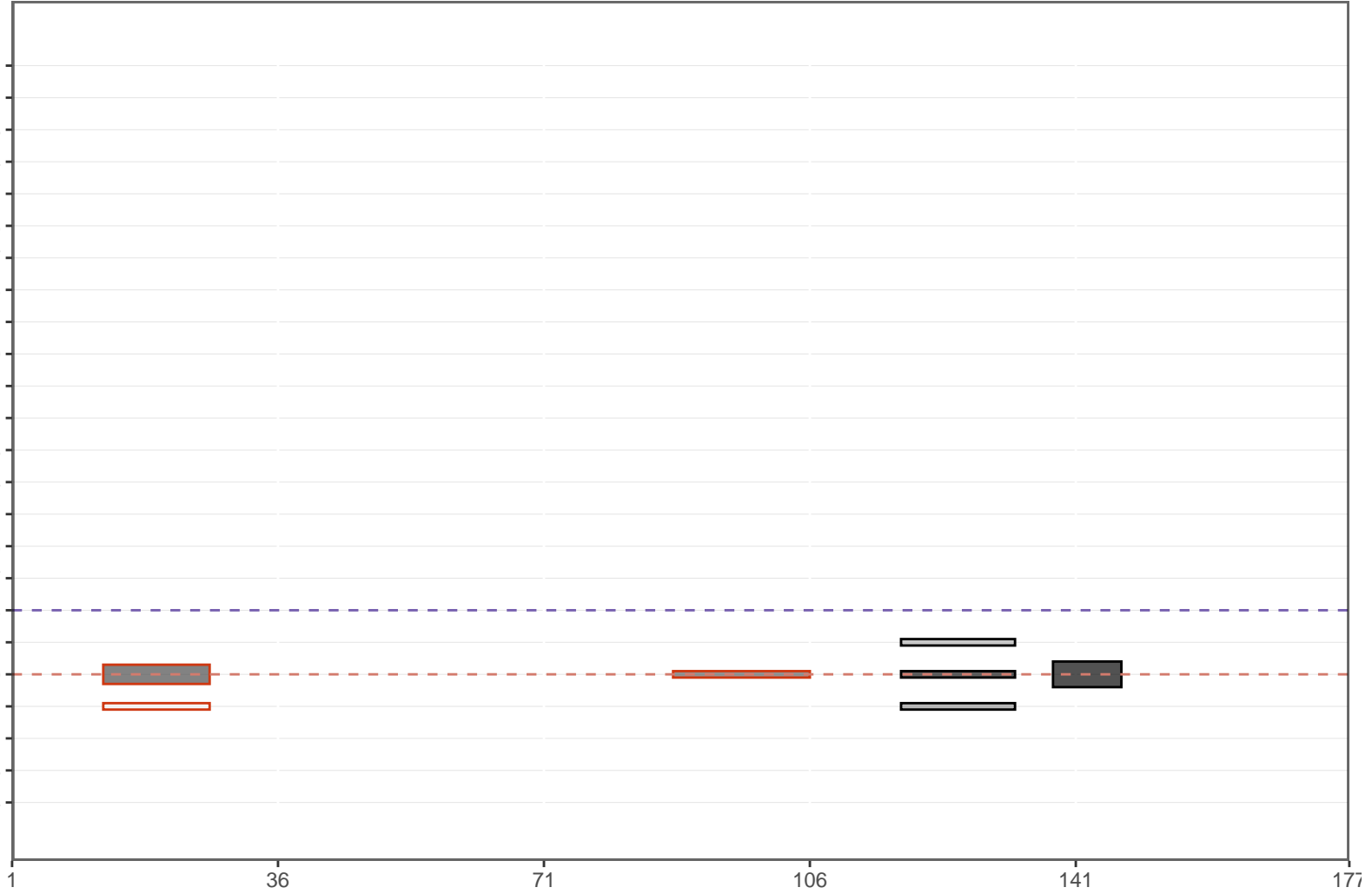
MW indication



Molecular weight

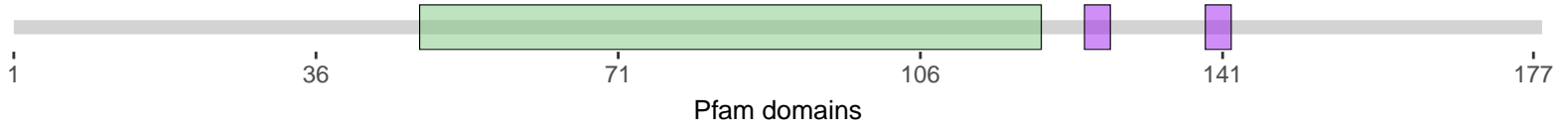


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

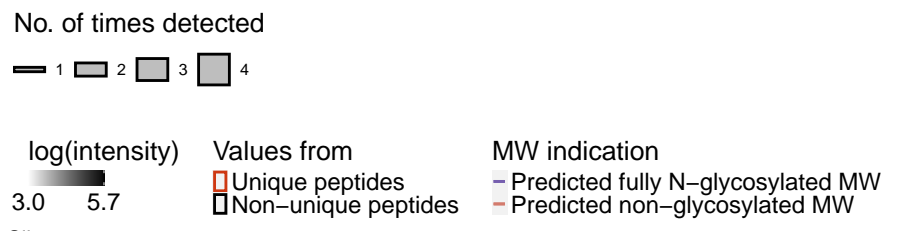
Pfam Description



Protein sequence:

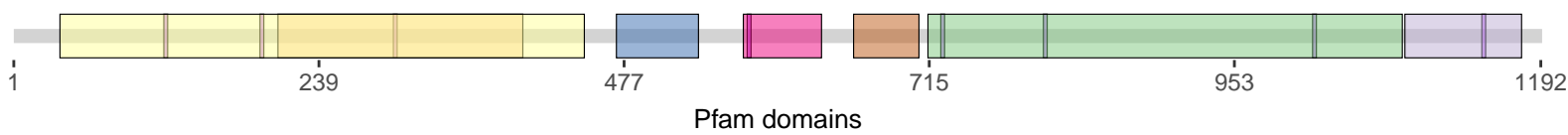
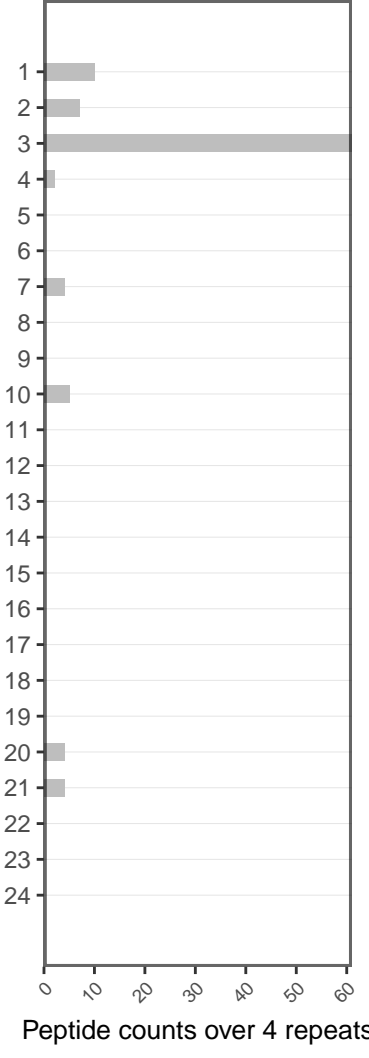
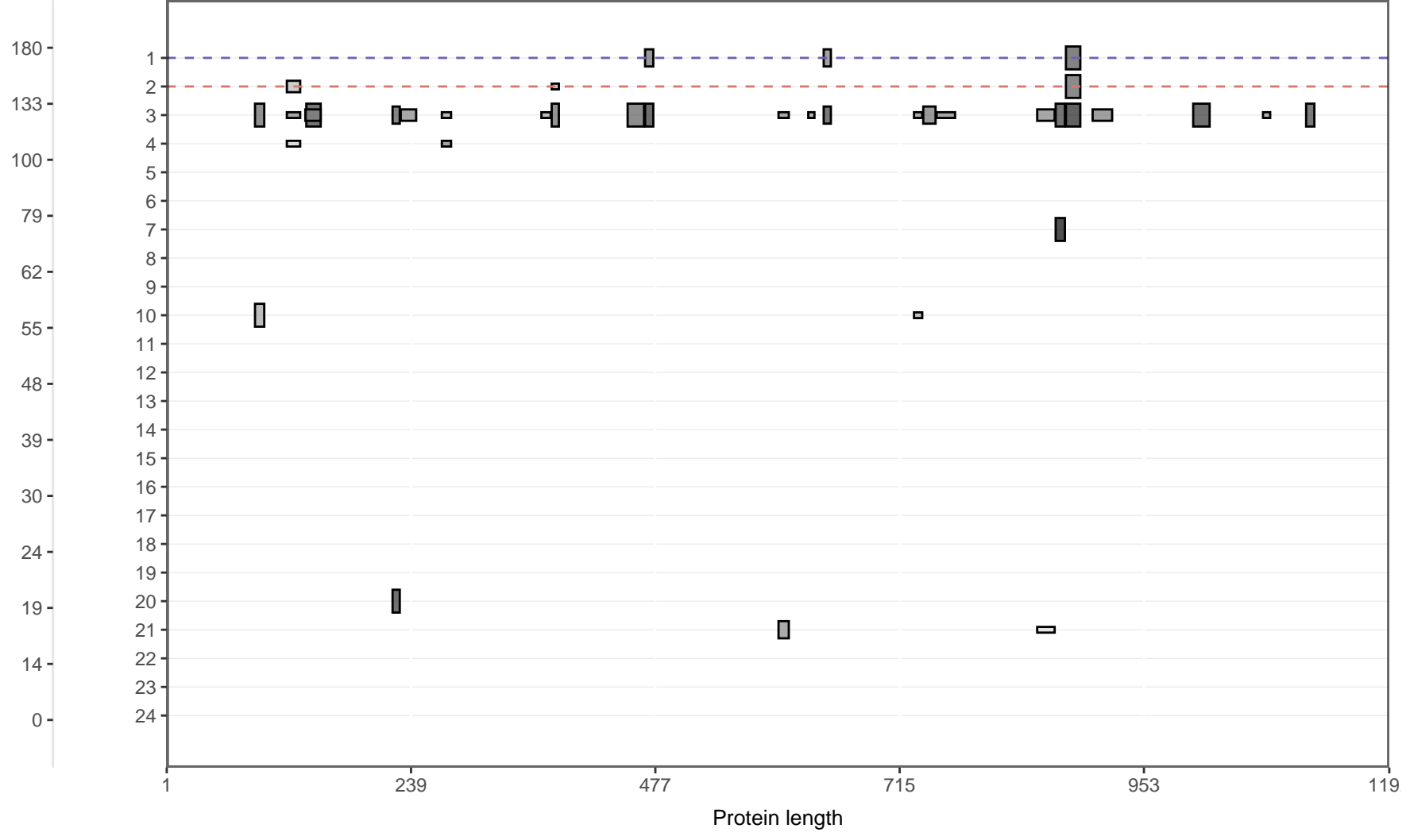
IRVAGYLSRHHLSAHHGDAVFAEAFNIGDKTHVWEVGIWIDPNNEENKTLASRRVTLKANMSPVFNKADAAVNLKKYAKVLPVGGVARRWSEYDI

NbL02g20550.1 DNA-directed_RNA_polymerase_II_subunit_RPB2 [MW = 135.26 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- TM Domain
- PF04560 RNA polymerase Rpb2, domain 7
- PF04563 RNA polymerase beta subunit
- PF04566 RNA polymerase Rpb2, domain 4
- Sequon
- PF00562 RNA polymerase Rpb2, domain 6
- PF04561 RNA polymerase Rpb2, domain 2
- PF04565 RNA polymerase Rpb2, domain 3
- PF04567 RNA polymerase Rpb2, domain 5

Protein sequence:

LVRTLRRLRRVDAITEVGVYRDRRLKELRIKTDYGRGSRPLFVFKGRLLIKKDKDGLQGRSEPEEGGWHDLVAKGYEYDTEEEETMISMFDNLVQARLNPEEAYSDTYTHDEHPSLKGVCSAIFPFDNNGSPRNTYQSGAMGKQAMGVYTNVQFRMDTLAVLYVPOKPLVTTRAMEHLFRQLPAGNAVAISGYSQYNGQSDVMMNGSSDRGFRFLFFRFRVDRDEEKNMGLVKEDFGRPDRASTGMGRHGSYKLDKDDGLAPPGRVYSGEDVYIGKTPISL

NbL02g20540.1 metal-independent_phosphoserine_phosphatase-like [MW = 32.97 kDa]

No. of times detected



log(intensity)



Values from



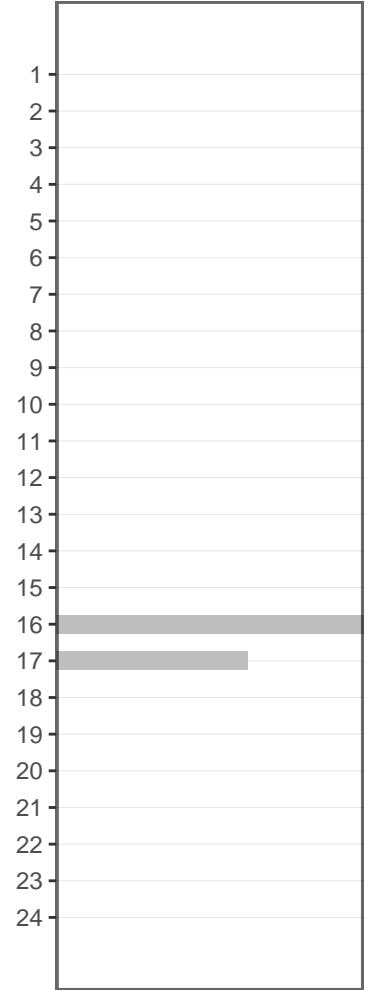
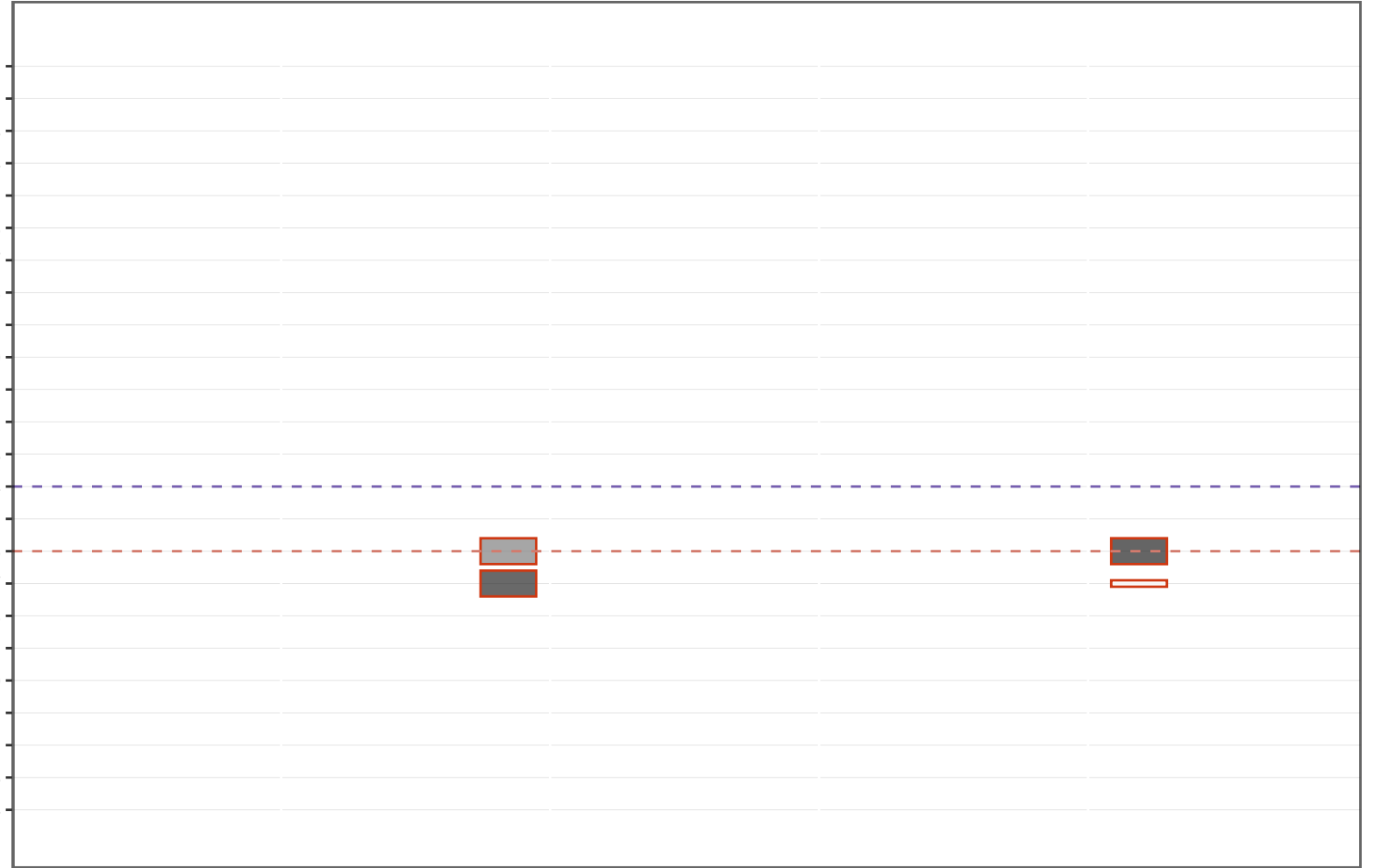
MW indication



Molecular weight

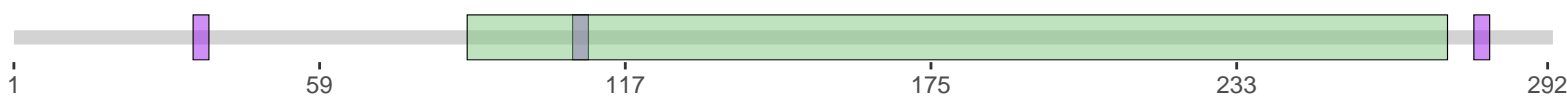


Gel Slice



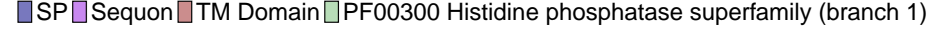
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ICFSSPISRAKTTAEIHWGKEEPLVFLDLSLKEAHLVLEGLRNEADAKRIYKRYEYTTWREDPNFQVDDVYPLQKLVGRAYEAWEEILLTPGENFLVTRHKSILRALICTPLGLGPERFREVDINNGLOVFKFNKGGEAMLHSLNMTAHMYTDHWHY

NbL02g20340.1 30S_ribosomal_protein_S5_chloroplastic [MW = 35.44 kDa]

No. of times detected



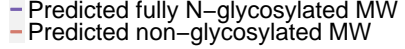
log(intensity)



Values from



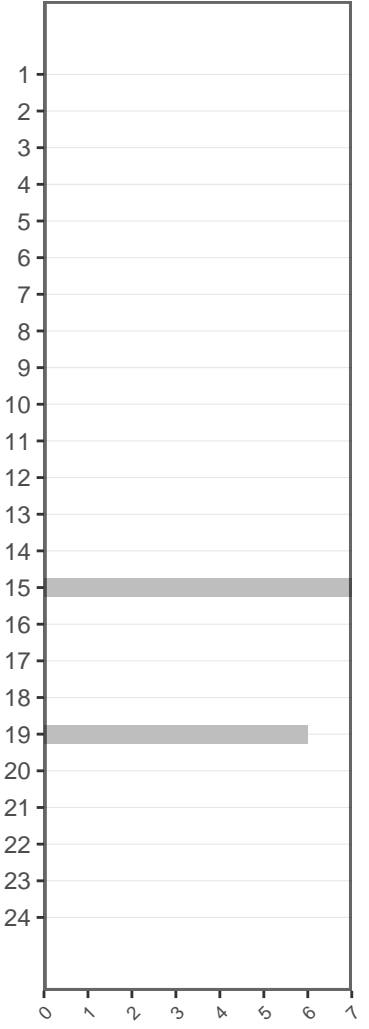
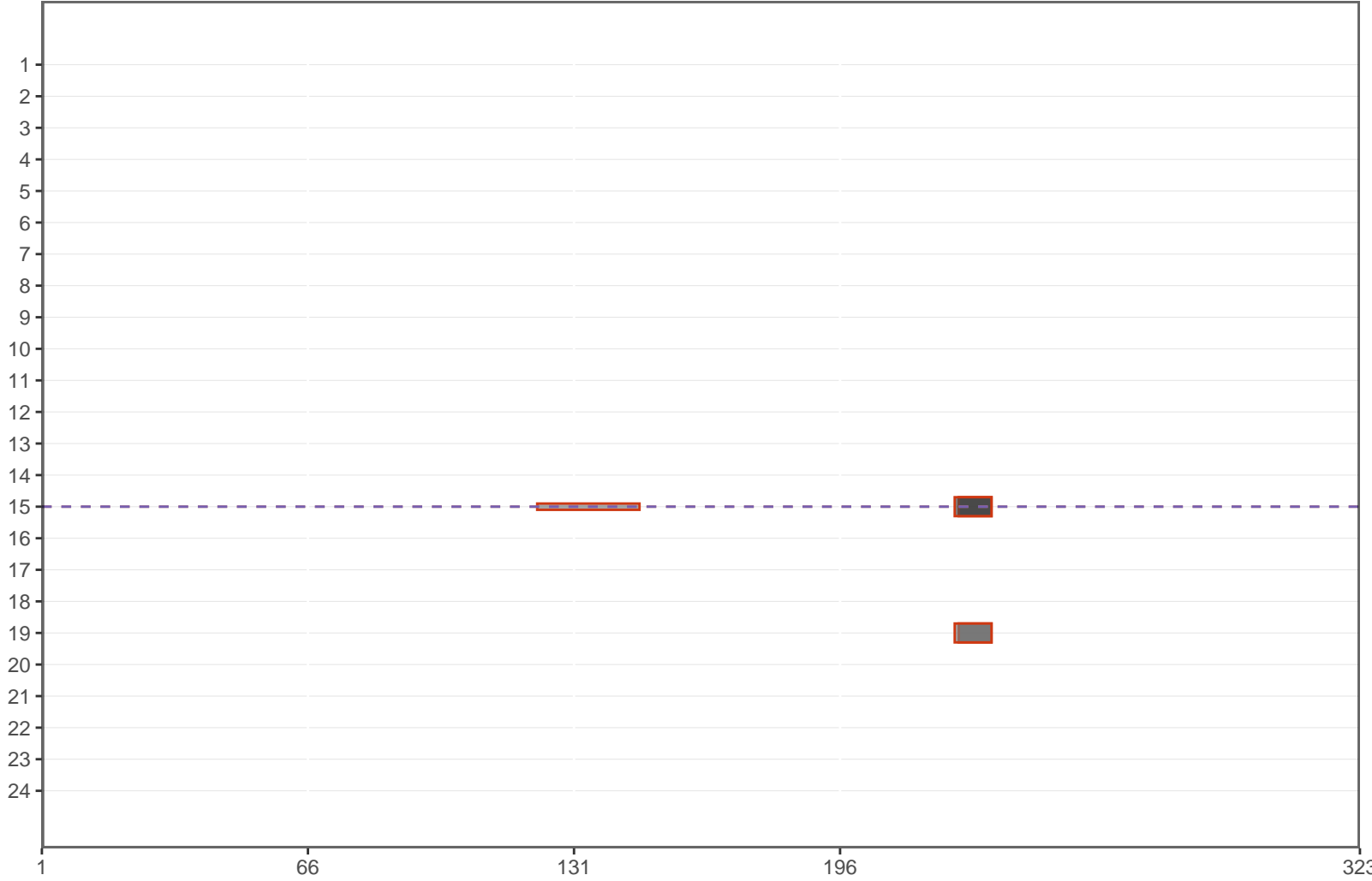
MW indication



Molecular weight

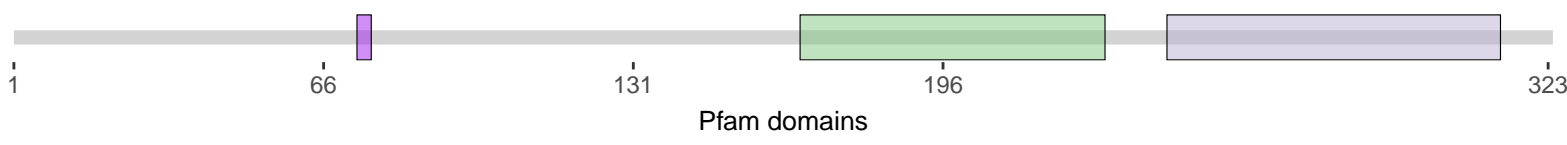


Gel Slice



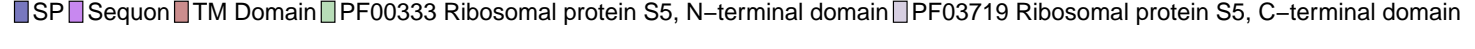
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

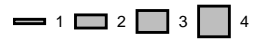


Protein sequence:

AFGKTKKEKAKDGFDERVVGVRVTRVYVWGGKQLHFRRAVVGDKKGGVGVGKAKEVAAVQKSAVNARRNVITVPMTKYLTFFHRSEGDFGARVMLRPAVPGTGVAGGAVRIVLEMAQVENALGKLGNNALNARATVVAVGQMRQFSEVAGERGFMEELW*

NbL02g20130.1 homeobox-DDT_domain_protein_RLT1 [MW = 188.29 kDa]

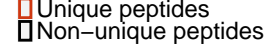
No. of times detected



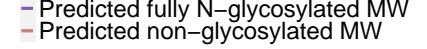
log(intensity)



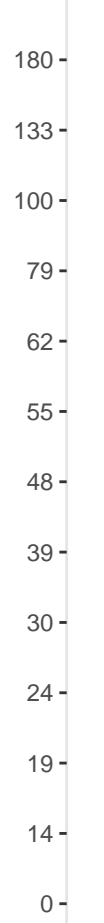
Values from



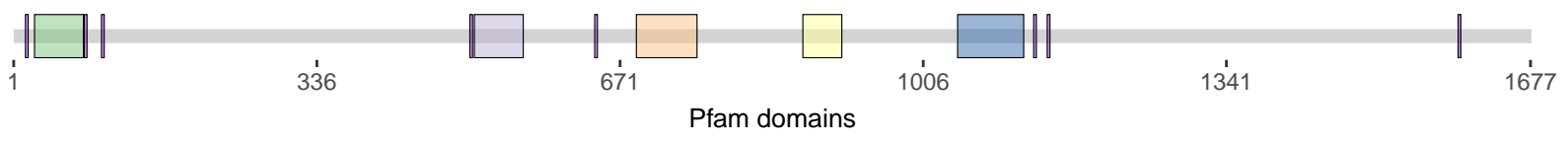
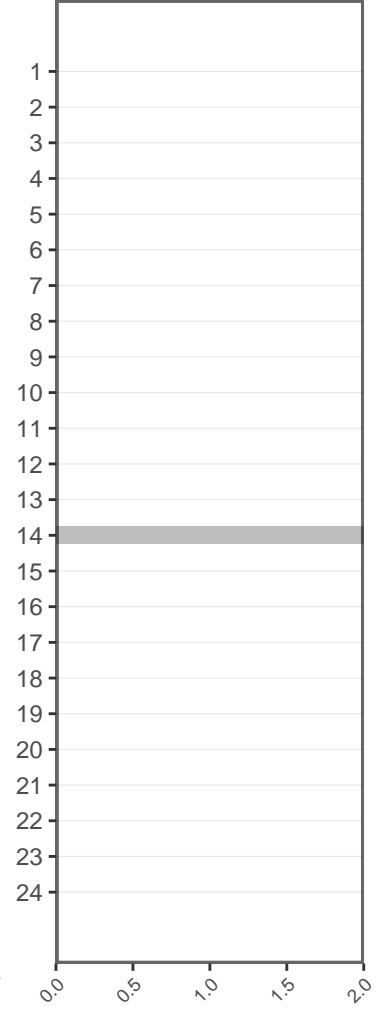
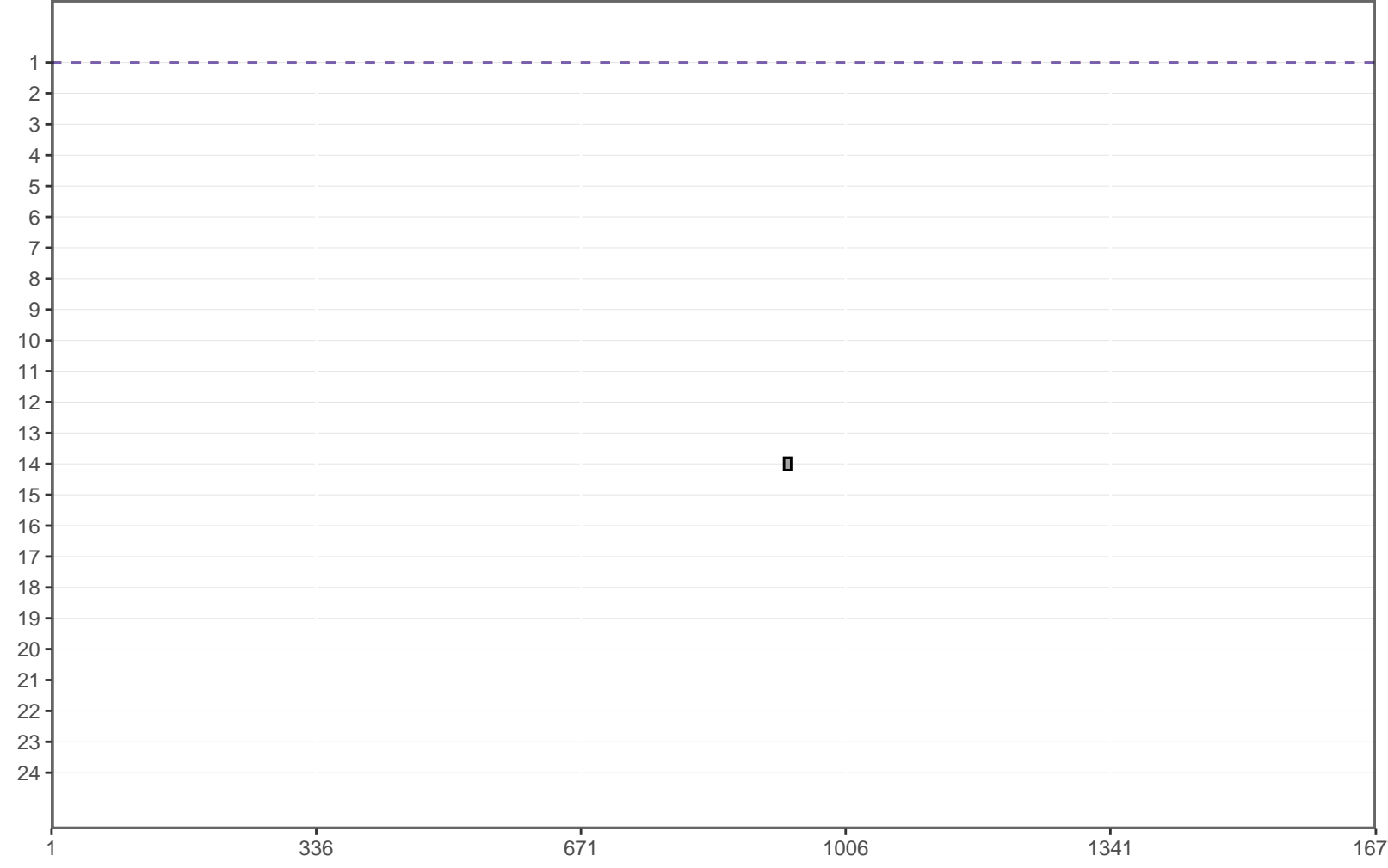
MW indication



Molecular weight



Gel Slice



Pfam Description

- SP
- TM Domain
- PF02791 DDT domain
- PF15612 WSTF, HB1, Itc1p, MBD9 motif 1
- Sequon
- PF00046 Homeodomain
- PF05066 HB1, ASXL, restriction endonuclease HTH domain
- PF15613 Williams-Beuren syndrome DDT (WSD), D-TOX E motif

Protein sequence:

ISILDTCLVNGKSKLSENEVGRIGVVDVADIEGSPGEGEIDESEKAGGPVWVGLTEGEYSOLCVVEERLNALVALGIANEGNIRVILEDRLDAAANALKKGMVAEAGLDKRRLEKEETNKFTDSEFNAAVEGSGPLGFFNPSKNGDTAPTPTTVVKDESAAVVDNINQNHFEESIAEKSSVAQETFMGELAIQPSGSGTAERSRMQLKFRGHKAEMVYVRSPLPLGGDRRRNRWYLFVWSSGSEDPGSGRIFVESPHGQWRLHDTEAFDGLLALDTRGWRSHLHMLQIEG

NbL02g19760.1 GDSL_esterase/lipase_At5g45920 [MW = 25.97 kDa]

No. of times detected



log(intensity)



Values from



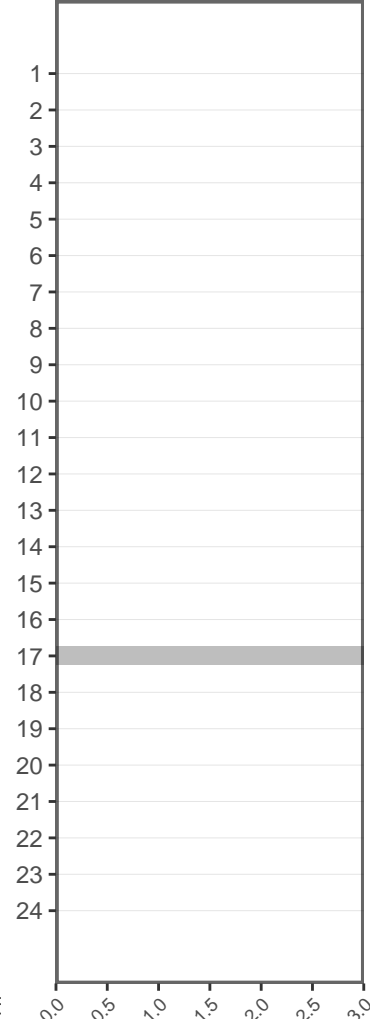
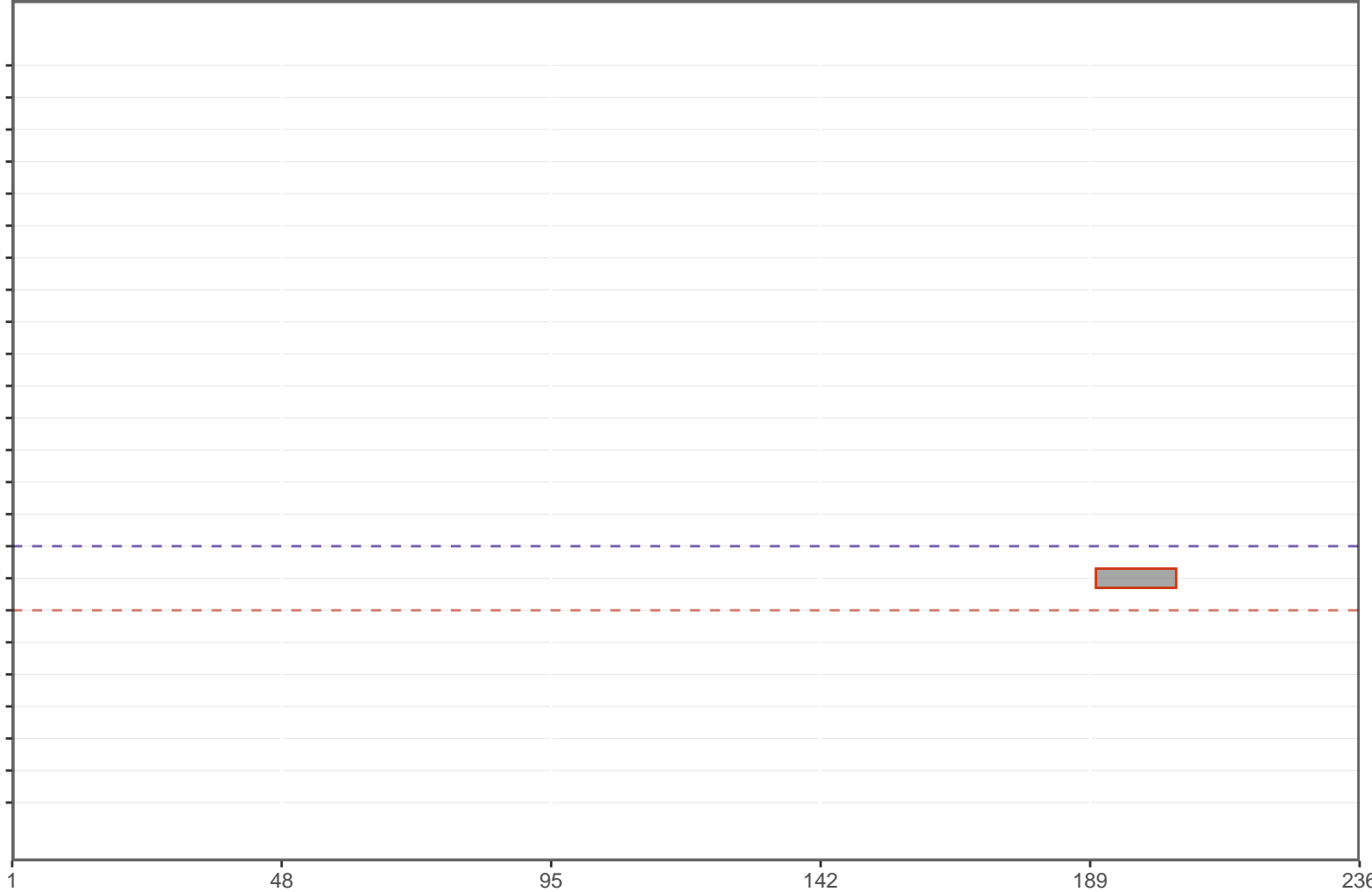
MW indication



Molecular weight



Gel Slice

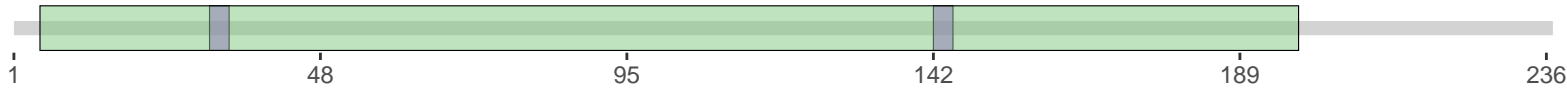


Peptide counts over 4 repeats

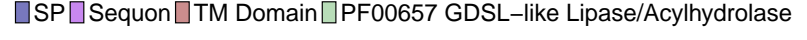
Protein length



Pfam domains



Pfam Description

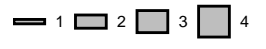


Protein sequence:

GRWPTTQVLSPPIDEPTRLLYPFMENHLGLBERTNETAGNYAKASLAWAEEGVLAVDLWTRMGGIPGWDTAGLSDGLHLGKGTGNEIFEEVVAALKKGLSVEALPVLPIVEIDPNDPLKFEGL

NbL02g19500.1 low-temperature-induced_cysteine_proteinase-like [MW - SP = 53.42 kDa]

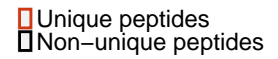
No. of times detected



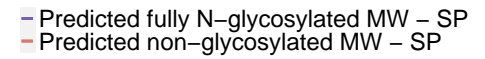
log(intensity)



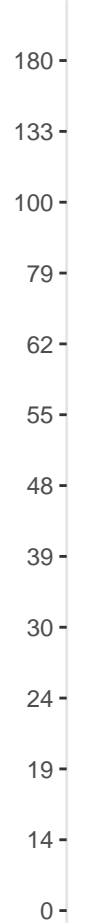
Values from



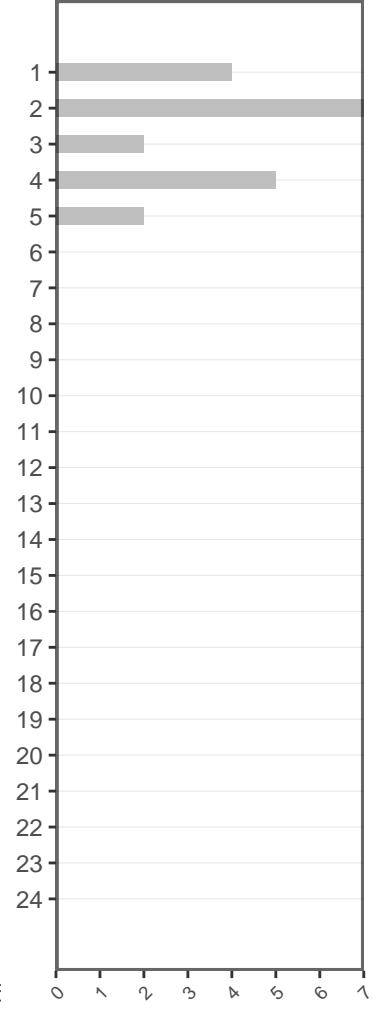
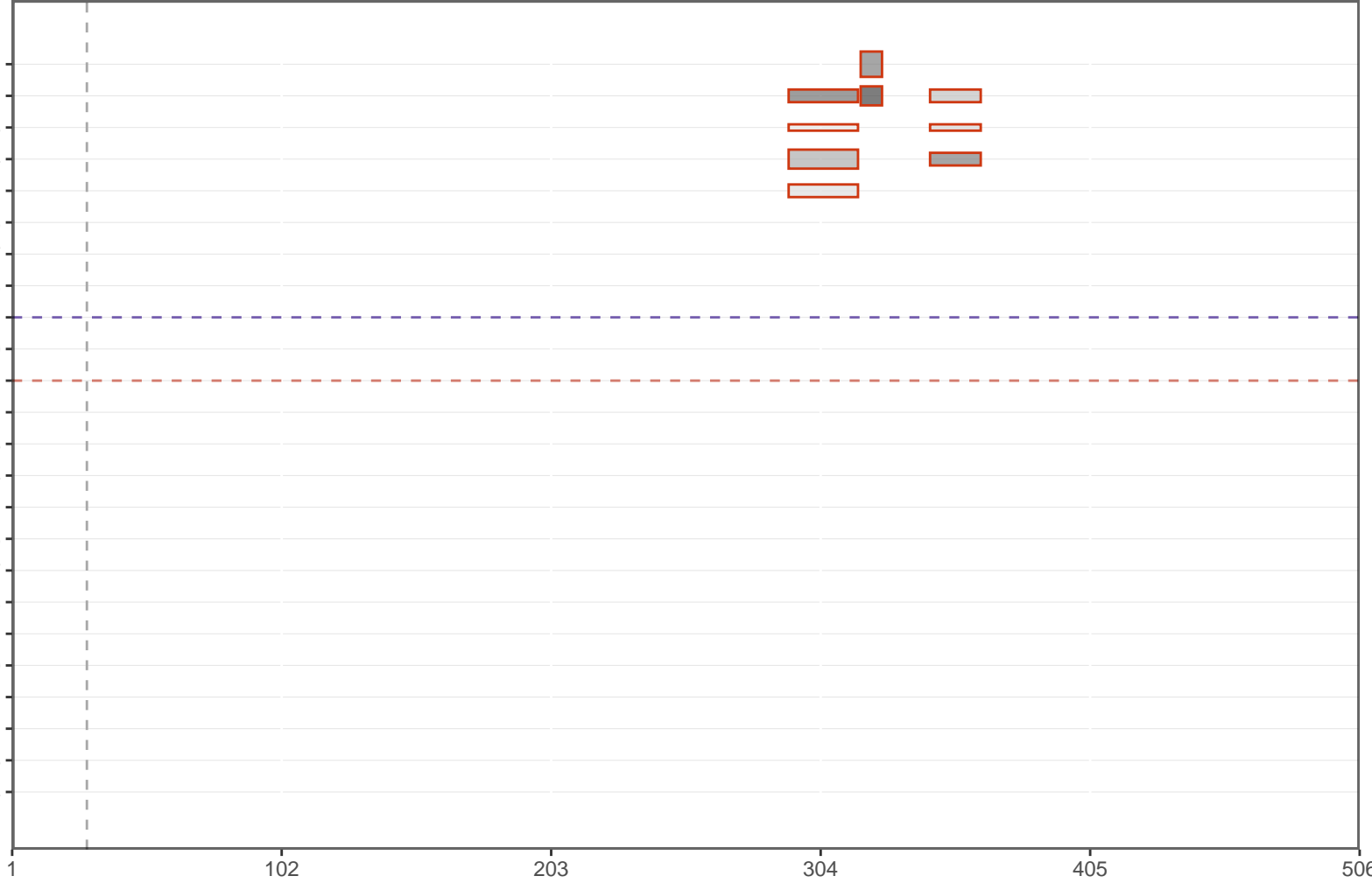
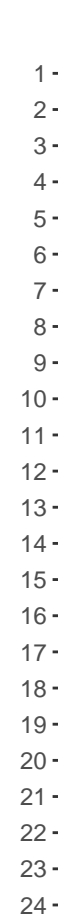
MW indication



Molecular weight

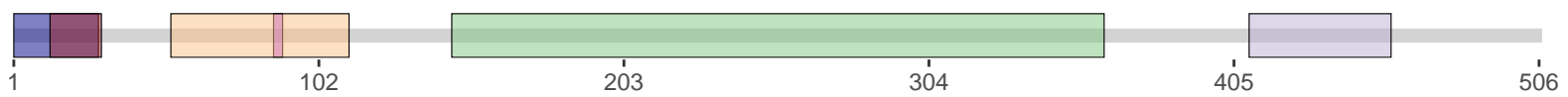


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CNYDKVNHKVTVDGVDVPEDENALLGAAADQPVSVADIGSLLDFQLYRGGIYDGCESNPDLSHLAVLVGYSKGGDDVWIKNSWGTTFWMEGVYRRTLYPLVGVCAINSLSAYPTKEASTAPSPVPSRWFPPPPPPPPPPPPPPPKPSECGDFYVCFEDQTCCEELVFGIGFQGGGCPYENGVCHGSEFCGADVPVGDVYEGLLGLKDRDNGVSEARKRRMAKHKLPWRANTEERDQTLKWRKHWAAMR

NbL02g19230.1 protein_HIGH_CHLOROPHYLL_FLUORESCENCE_PHENOTYPE_173_chloroplastic [MW = 66.16 kDa]

No. of times detected



log(intensity)



Values from



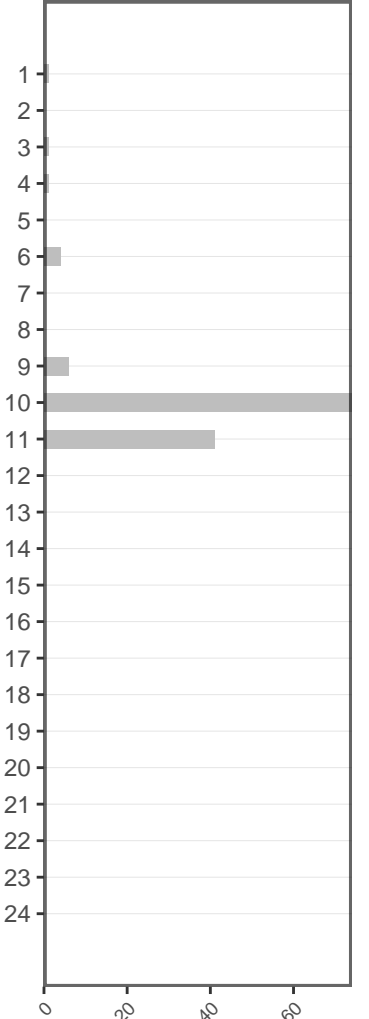
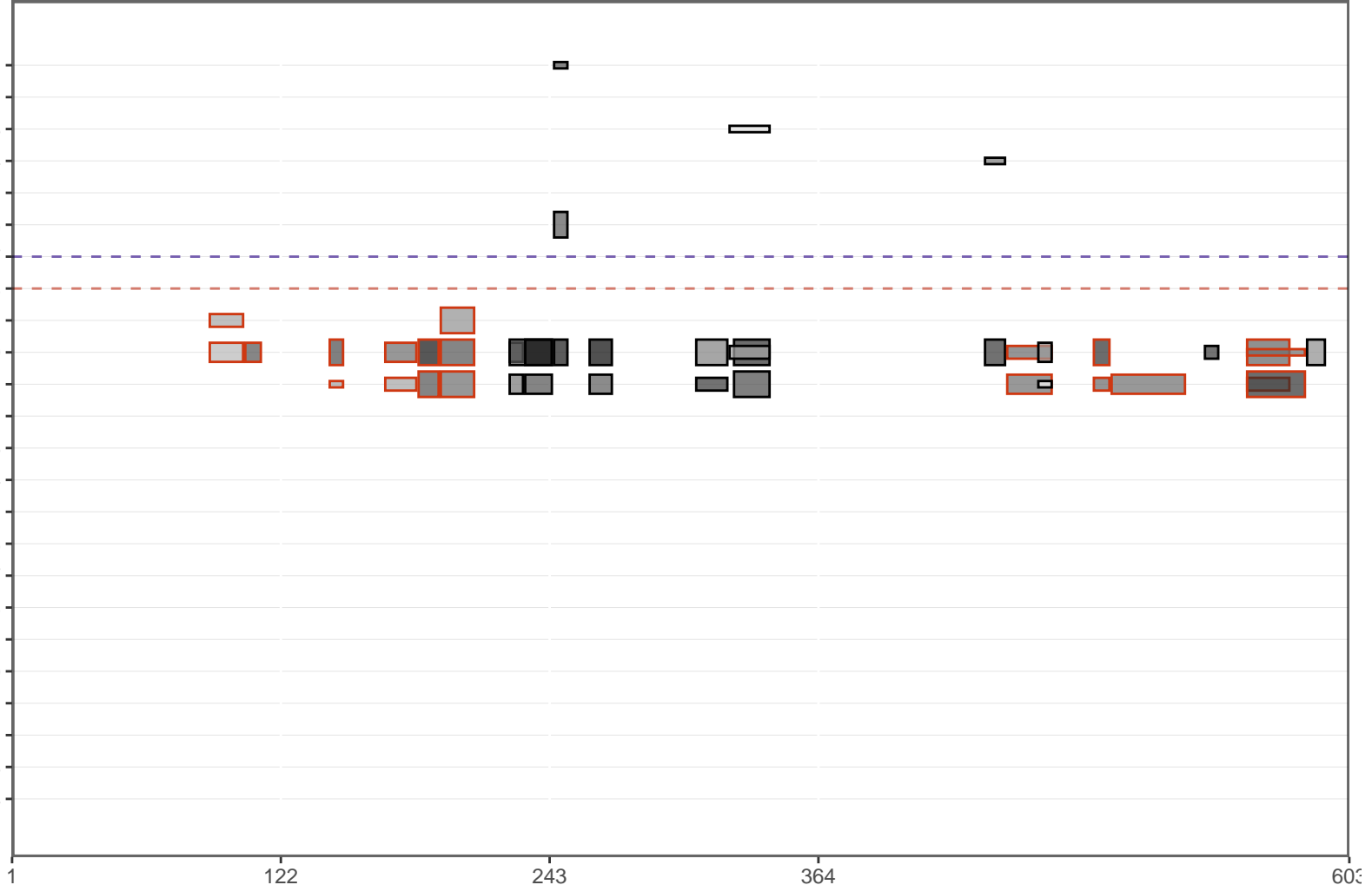
MW indication



Molecular weight

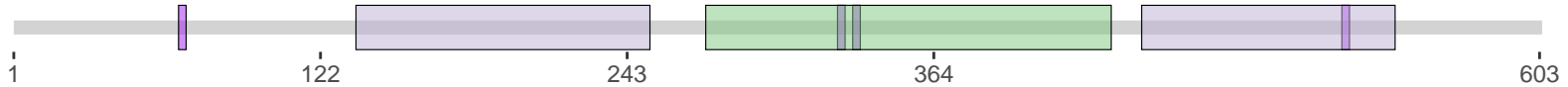


Gel Slice



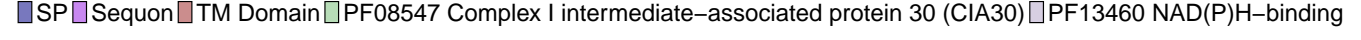
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SVSOSTTQIDLTGGENGSGPTGLFKGVVTTANNNGSFASIRTKNFSEPENLGAYDGLLELRKGGDRRYKLVRTSRDWDVAVDTLGSFDTEGWSVSLPFSRLRPIFRARVLDAPPDFDQMSLQLMFSKFFESDQGLNPTFKEGPFELPVGIRAVLKDPIRPFVHVSSAGVTRPERPGDLSKGPVAVLNKELGILTRFKLKGDEIRESGIPYIVRPAALTEEPAGADLFDQGDNTIKGKREEVARIGVAALKSPWAGDKTFEYKGVVFPFSEPTFVDPENPPLKDYNEYFK

NbL02g19210.1 probable_alphaalpha-trehalose-phosphate_synthase_[UDP-forming]_7 [MW = 96.77 kDa]

No. of times detected



log(intensity)



Values from



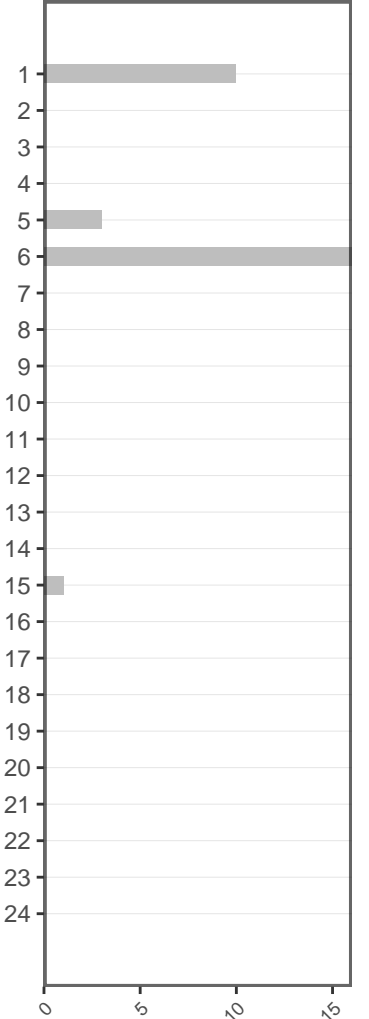
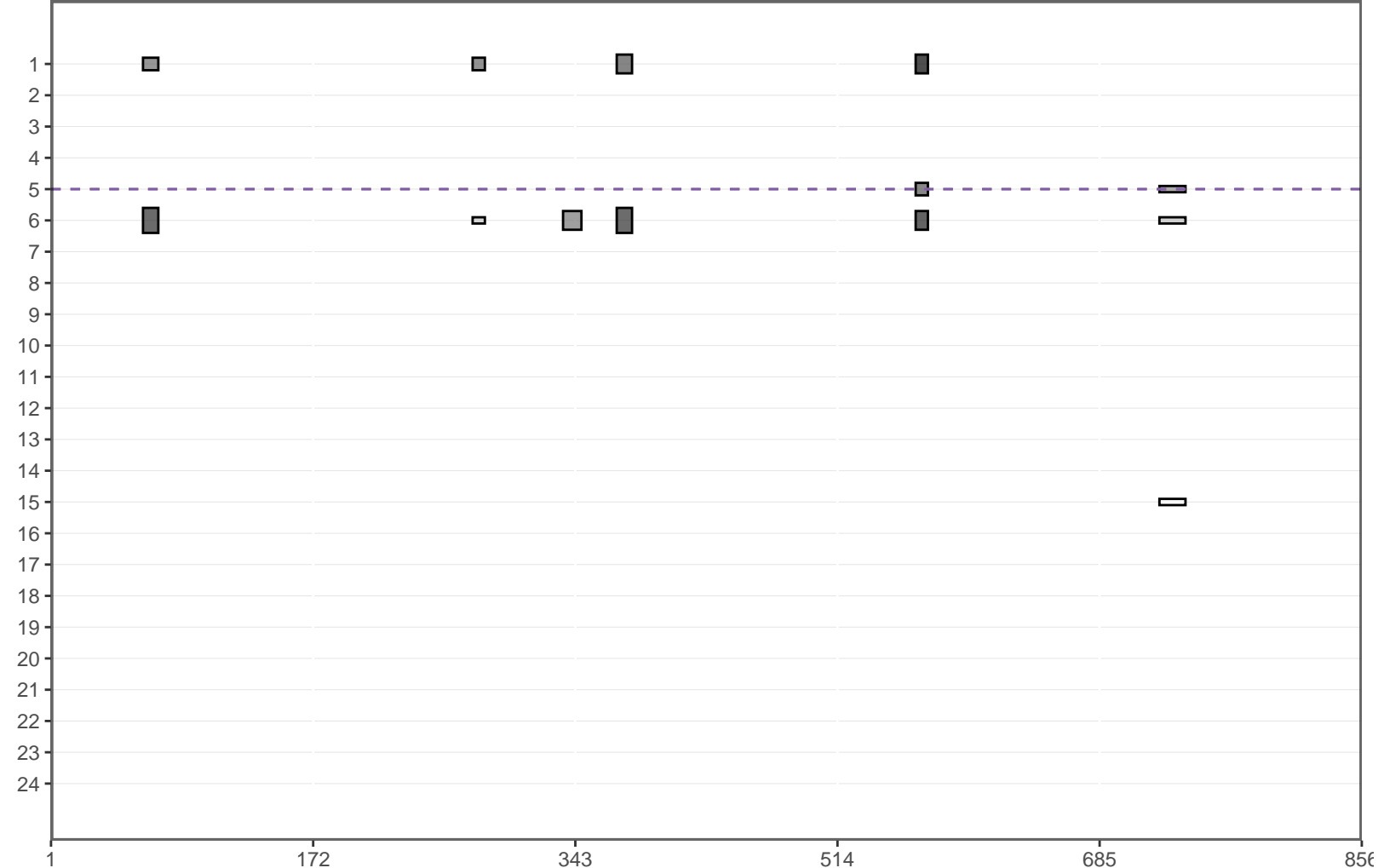
MW indication



Molecular weight



Gel Slice

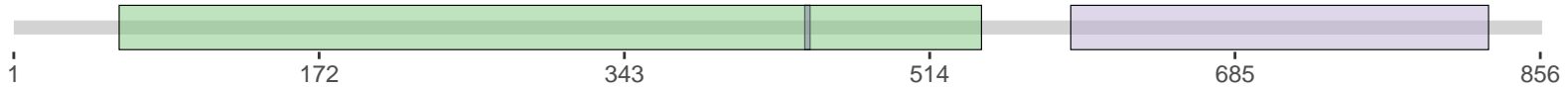


Protein length

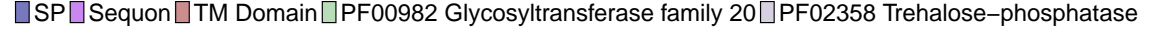


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

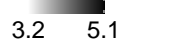
PVLSLERTAYTTVAEGVAVTAVRDGMNLTPEYIVSRGGIPGSDGTAESNGKKSMLIVSEFIFGSSPLSGAIRVNPWNVEATAEALNEAISMADAERLKHKHYKYLSTHDVAVVSRGFFQDLERTCKDFRRRQWGGIGLDFGRVVALDPNFRILSMQNVSYGSKAKNRALLEVDGTLMPQTSKIKVPSPEVHISINTLGGDERNTVFLVSGRGRDLSGRWVSPCEKLGIAAEHGFLRWSAHHKEVEVGGNSDFQWMMQAEPMKQGYTEATDGSYIETKESALVW

NbL02g19160.1 dihydroorotase_mitochondrial [MW = 43.11 kDa]

No. of times detected



log(intensity)



Values from



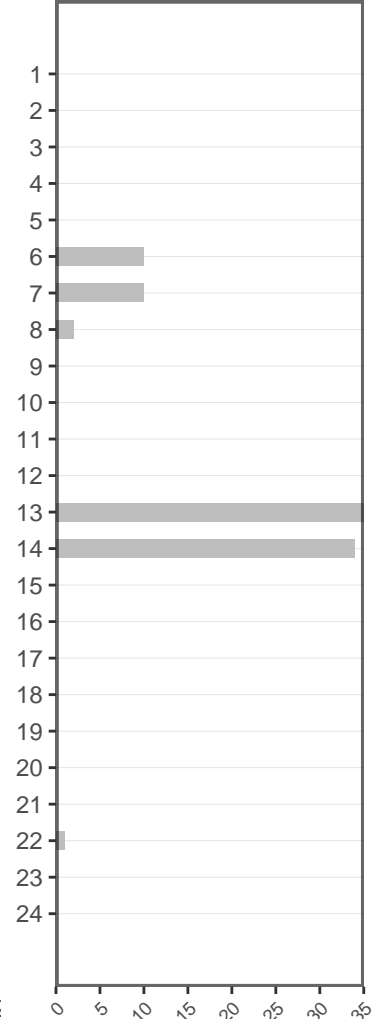
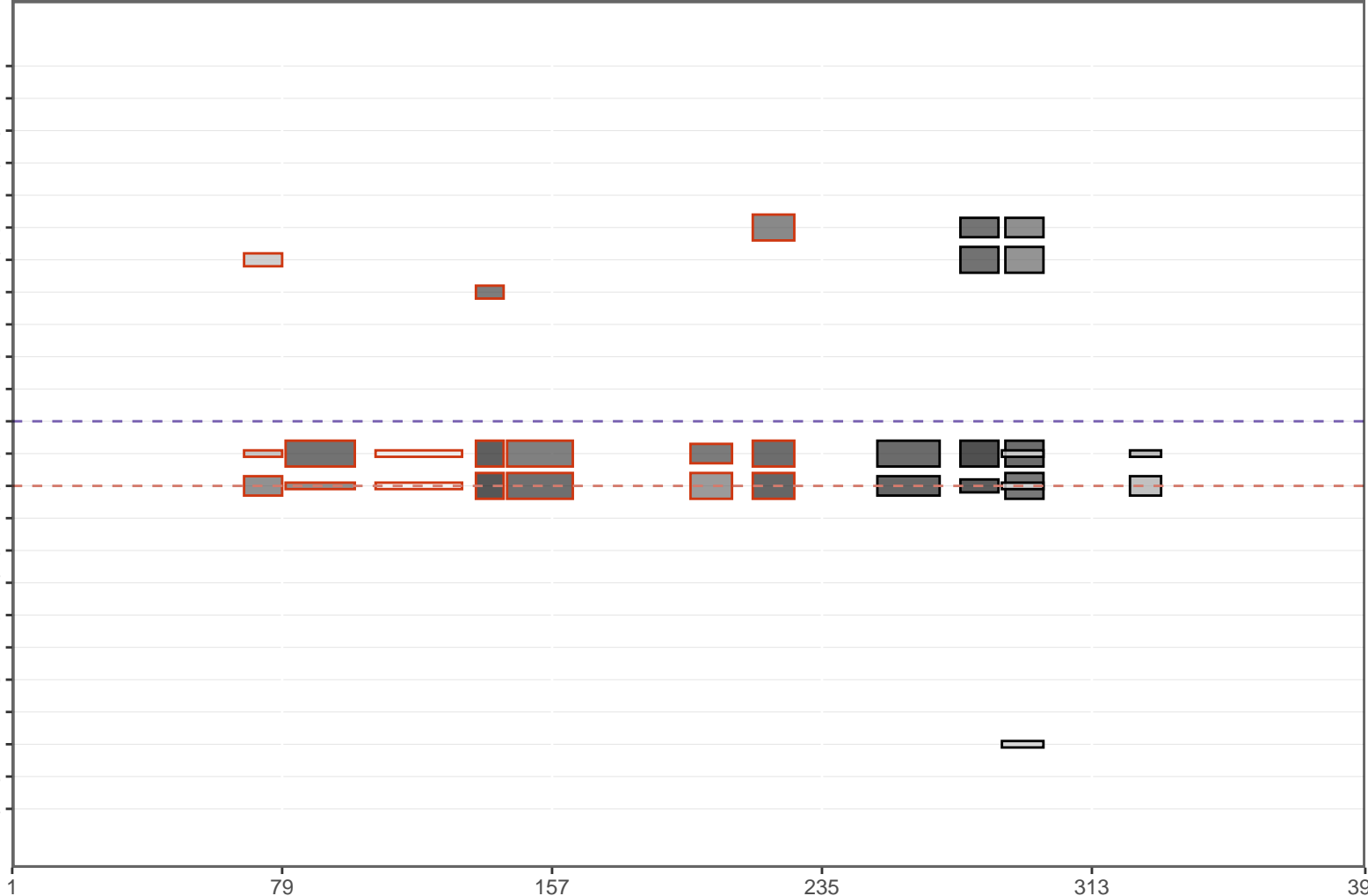
MW indication



Molecular weight

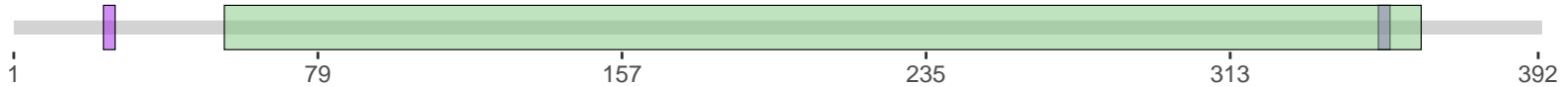


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TNPEYDFDREKVFEMVLSPLVQKFRLLKVMMEHVTMDAVKFEVSGTEGNVATYTPQHLVLRNLSLFGGGLGPHNYGLPLVKREIHRGALVSAVTSKSRFFLGTDSAPHRDRKKECGCGAGHNPVLSAVAKVFEQANLKLKLEAFTSFNPDFYGLPRNNEKIKLSKTPVWVPEFSVYASGDIVPMFAGEMLDLWLPPL

NbL02g18960.1 histidinol_dehydrogenase_chloroplastic [MW = 52.75 kDa]

No. of times detected



log(intensity)



Values from



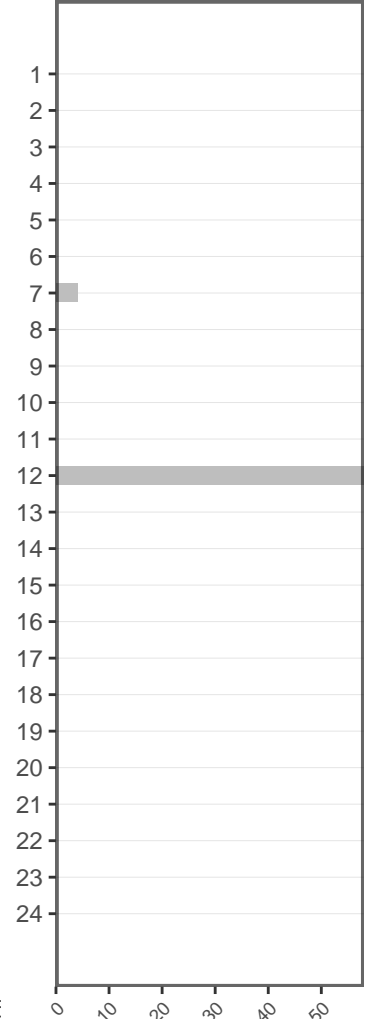
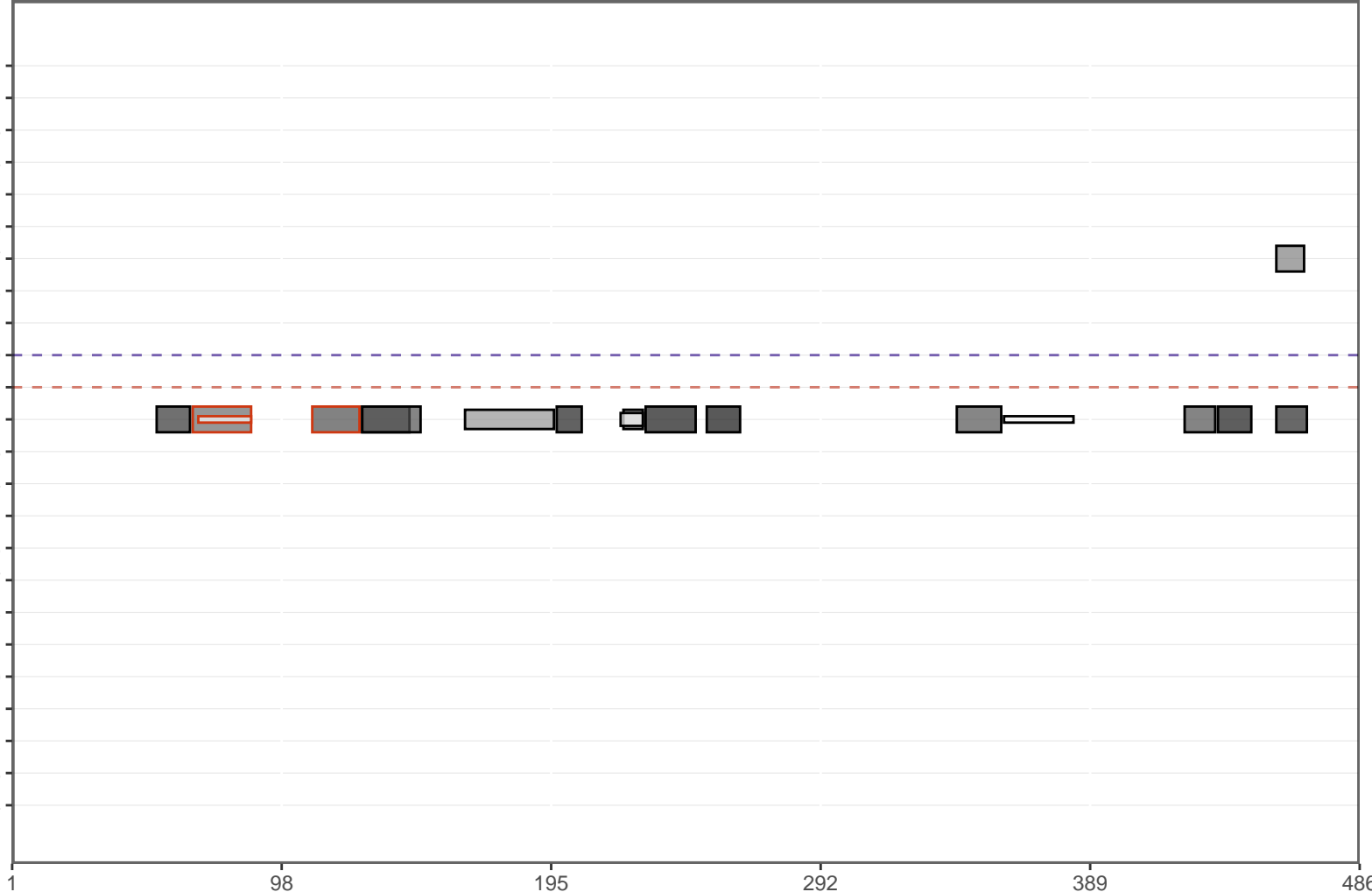
MW indication



Molecular weight

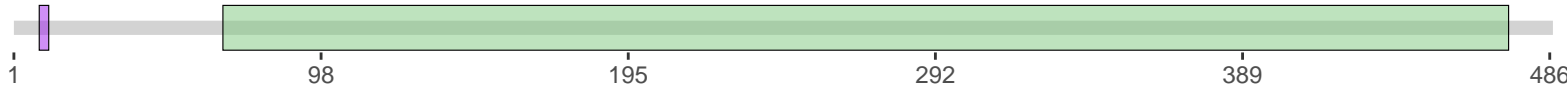


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

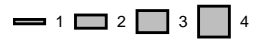


Protein sequence:

AQAISAMAWGTESGPKVEKYGPGNGVYTAAMKILQNSEAMVSDMPAGPSEVLIADKHSGFVVAADLLSGAEGFDG6GVVIAAGDDVDLNAIGEEIRKGGKALPRGEFALGALSHSETVLAARDMLEAIFSNMVAPEHLINVNEAEKWEIENAGSVFMGQWTFESVGDYASGTHVLPFTYGVARMYGGVBLDFKVTYVQSLEEGLRNLGPYVEKMAEVEGLDAHKRAVTLRLQDEARGISNR

NbL02g18950.1 probable_LRR_receptor-like_serine/threonine-protein_kinase_RFK1 [MW - SP = 109.82 kDa]

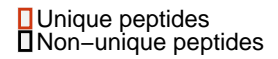
No. of times detected



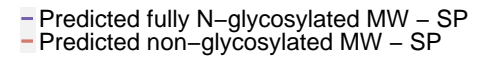
log(intensity)



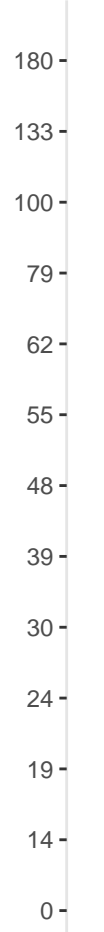
Values from



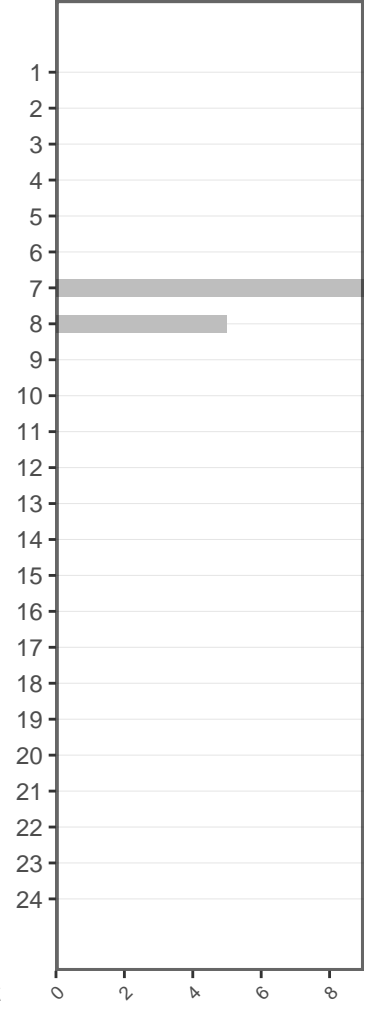
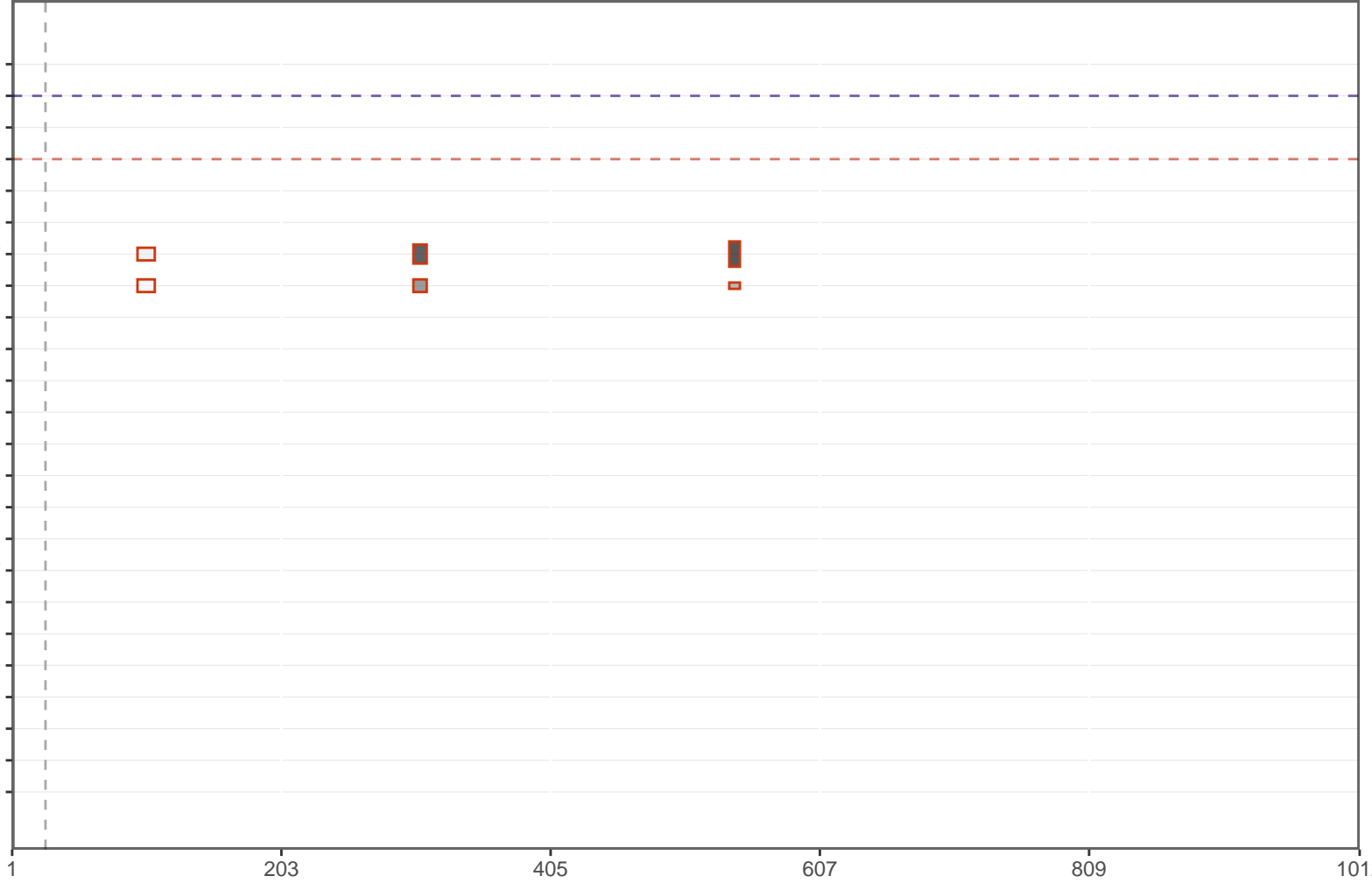
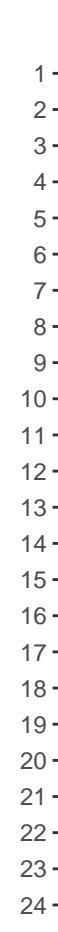
MW indication



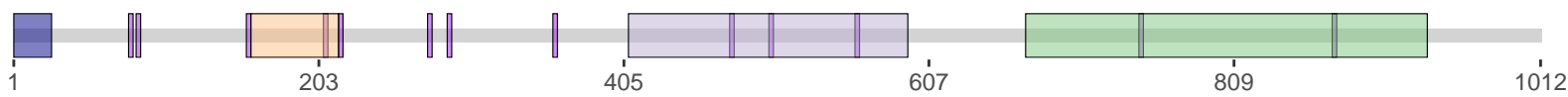
Molecular weight



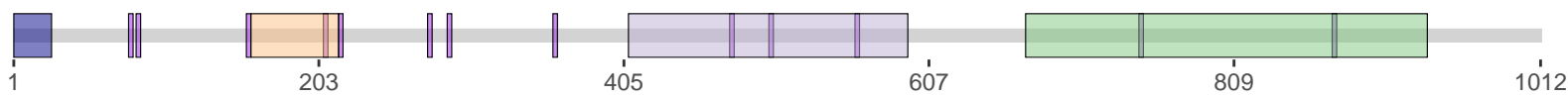
Gel Slice



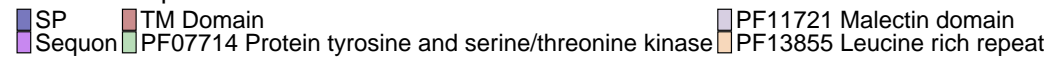
Protein length



Pfam domains



Pfam Description



Protein sequence:

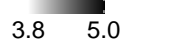
YCLENGNYVSLHFAEMFKEDHTFYNLGRRFVDYIDKLVWDFNEEEARGKRPVRRFNATVTDVLEIRLYWGKGTTRPLRQHYGALISAIVSDNFKFQSNEDRKTIVYVTVGLAAGITFFVLSLWVWGYLGRERKRRLDNLGVELQMVCFLLKQKAAIKNFDAFNKIGEGFGPQVYKGLPDGTLVWVKQLSOSKQGNREFLNEISTIGLQHPNLVYKLVHGGCIEADQLLVYEVLDNNSLAGALFQDRRLLEWATRFRLGLGIKGLAFVHEESSLKIVHRD

NbL02g18840.1 GDSL_esterase/lipase_At1g29670-like [MW = 40.83 kDa]

No. of times detected



log(intensity)



Values from



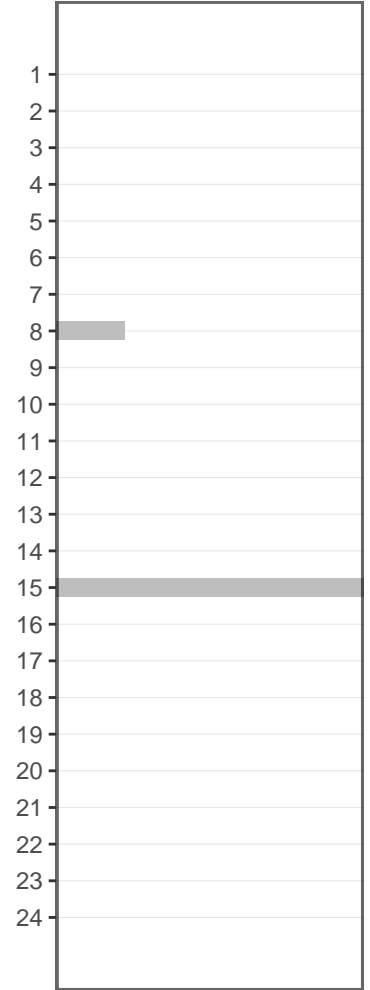
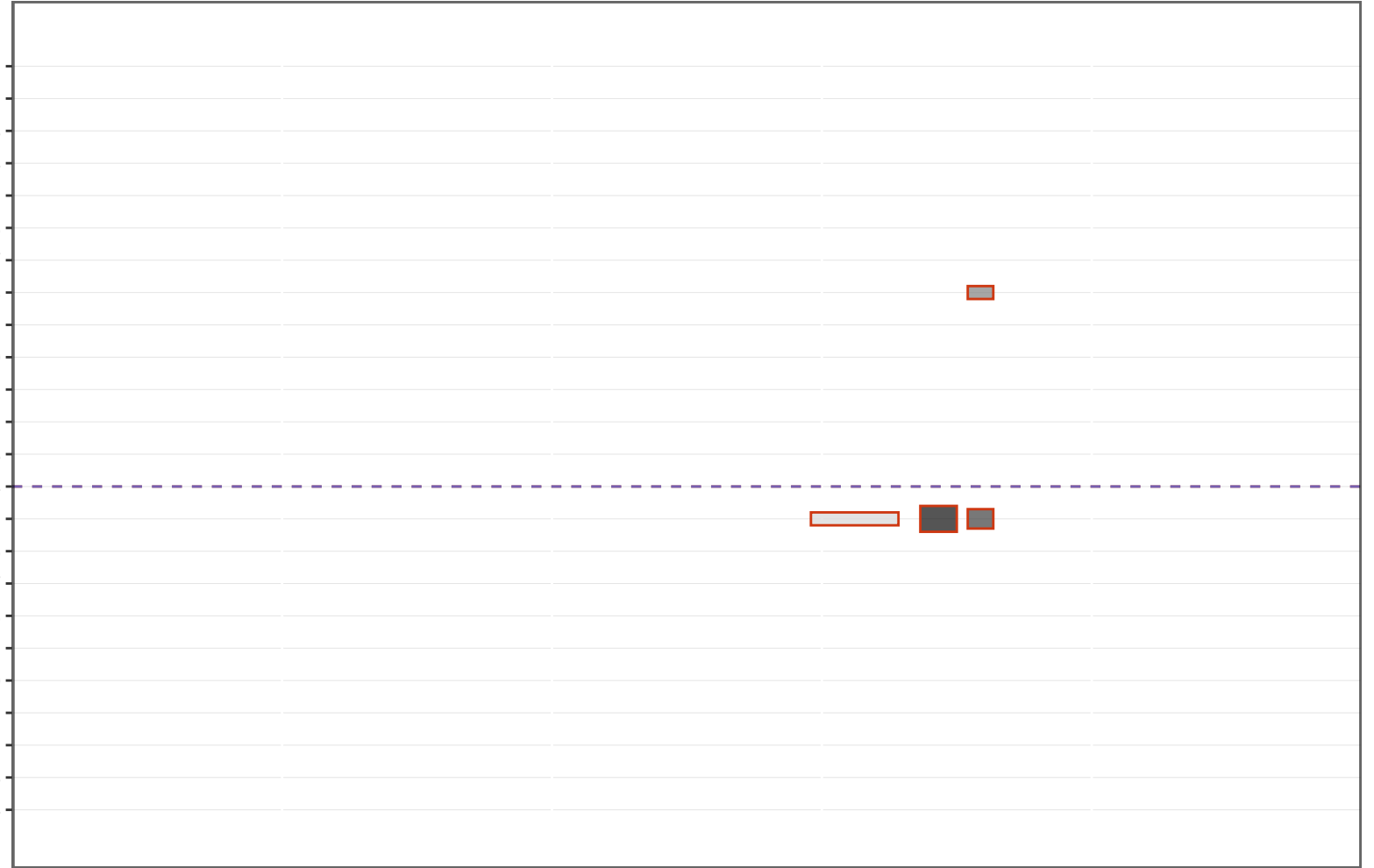
MW indication



Molecular weight



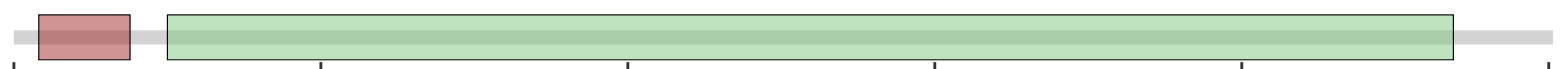
Gel Slice



Peptide counts over 4 repeats

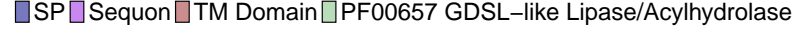


Protein length



Pfam domains

Pfam Description



Protein sequence:

SSNDYLNLYFMPLLYPTSGFTPDGVAHVLIQGYTQGLRLVYNGARKFVLIGVGGIGGSPNALAGNSPDGRTGVGRINAVANGLFNKALKVQNLNRTDPAKFFVDAVGFQGLQDNPFAFGLVETNAGCCGGRNNGDITLPPQRPGRNRNGYLFWDVDFHPTAAANIVVGRREYRAQKSSDAYFPDISRLAQL

NbL02g18830.1 GDSL_esterase/lipase_At5g45670-like [MW = 46.52 kDa]

No. of times detected



log(intensity)



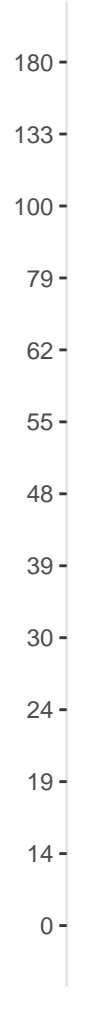
Values from



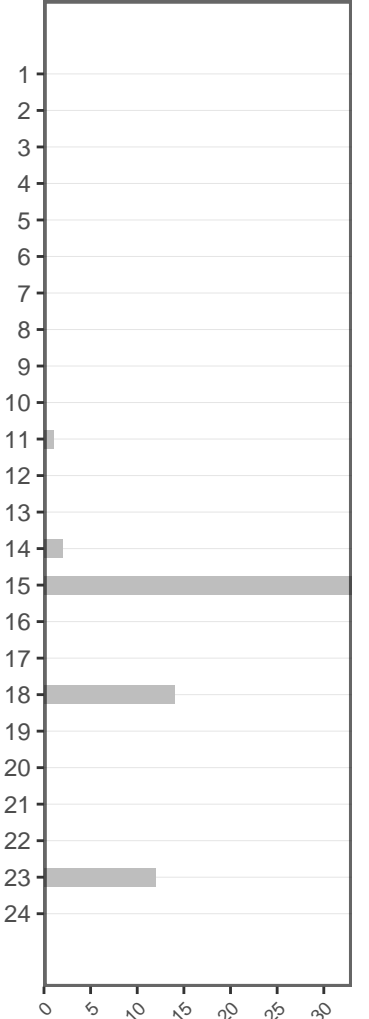
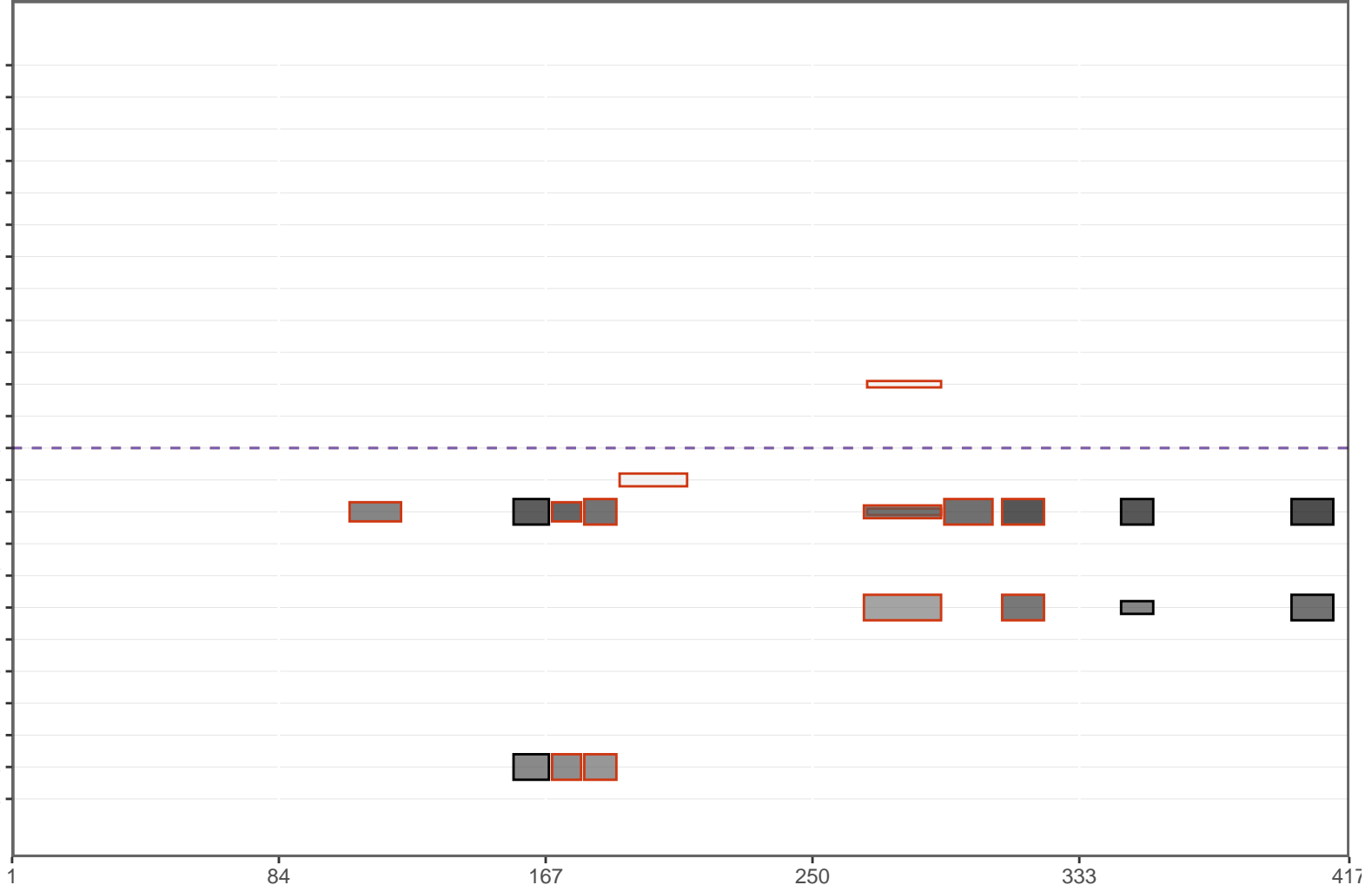
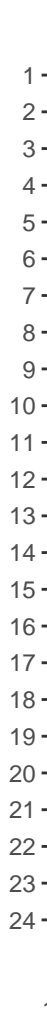
MW indication



Molecular weight

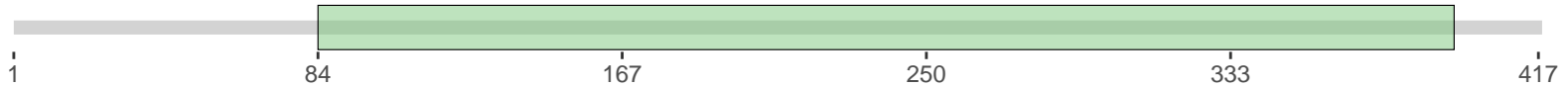


Gel Slice



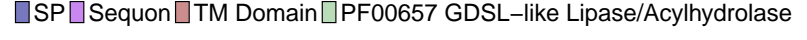
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

JILGDEASANNYSKGIYEVGLGSDNLYNNYFMPLYVSTRGQNPQYADVLIIGQVTOGLKTYDYGARKPVLIGVGGGSPNSLAGNRPDQKTAGNINAVANQLFNRLRGLVDDFNPTDPAKFIYINAYDFQDQIENPISAFGRVITNAGCCGVGRNNGGDTLPLGNPCERDDEYLFWDAFHPGEAANVIGRRBYRAERPSDEYVDFDRIQLGLV

NbL02g18800.1 subtilisin-like_protease_SBT5.3 [MW = 86.41 kDa]

No. of times detected



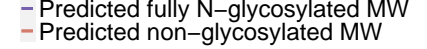
log(intensity)



Values from



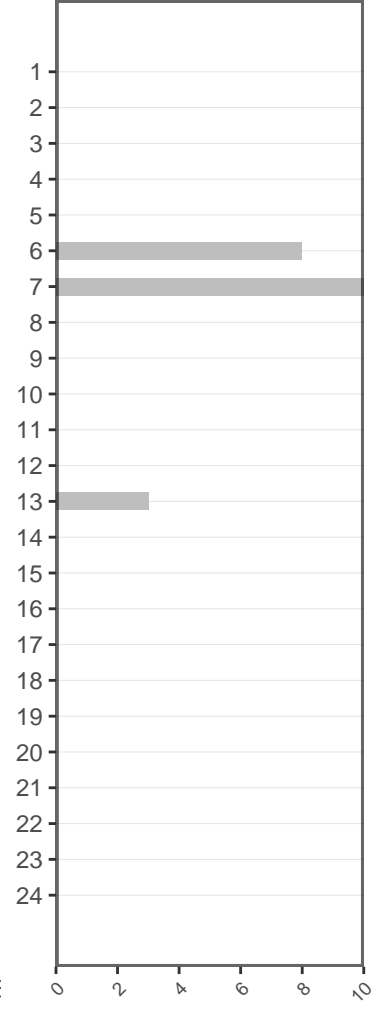
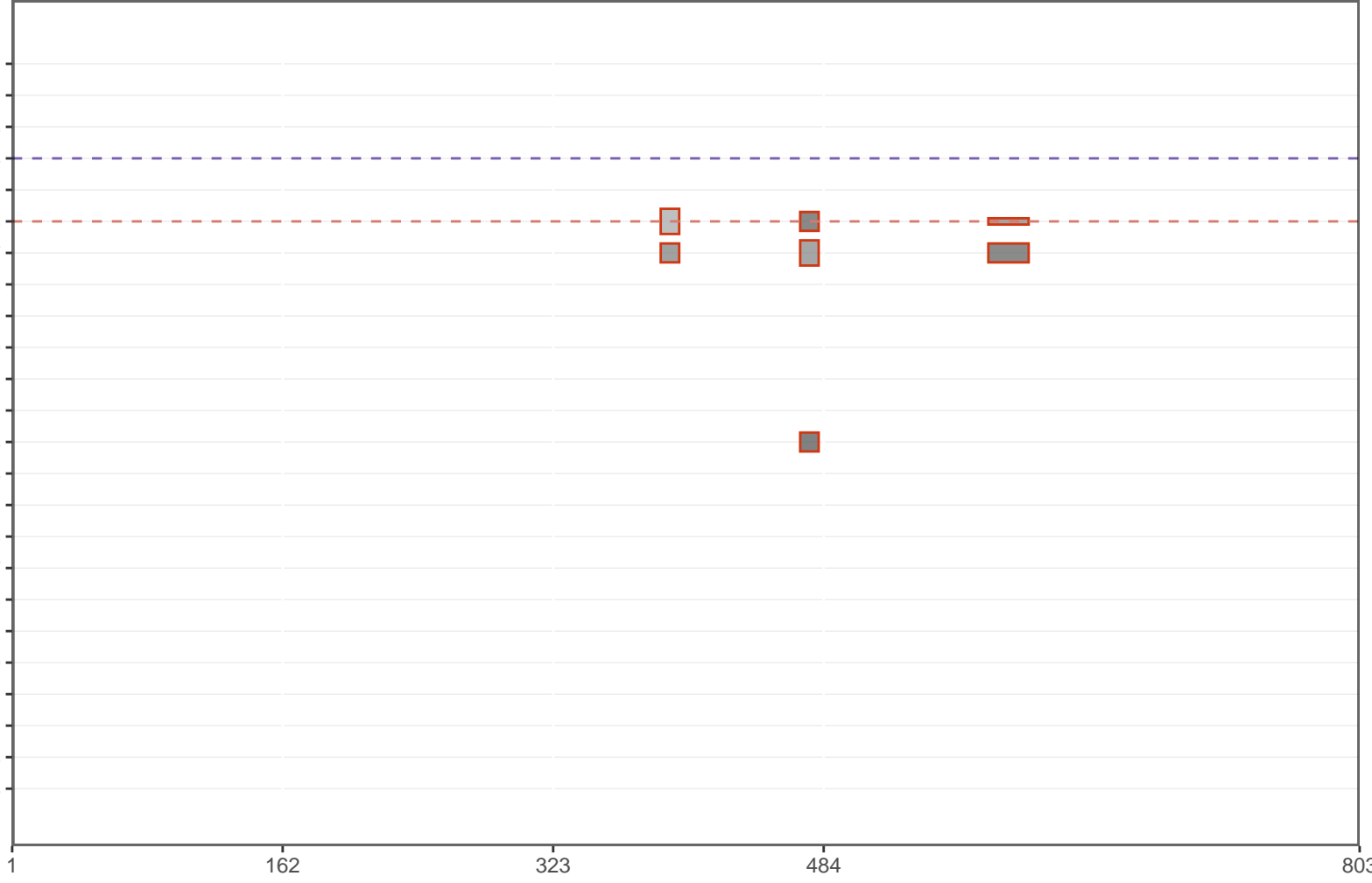
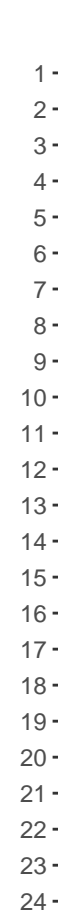
MW indication



Molecular weight



Gel Slice

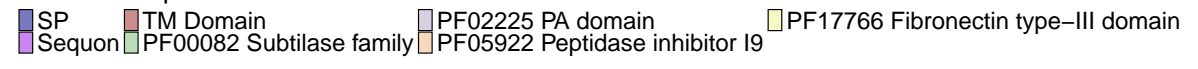


Protein length

Peptide counts over 4 repeats



Pfam Description



Protein sequence:

IPVVLQNGKFKMGQVTPPYKLEKMKMFLVYAGGVNSNVTKQVAGGGLPGLSPKAKGKIVDLRNGSTRVKGGEVVRAGGGIHLGNKANGAELVADPHFLPATAVDVYKSAVDLNLNYSKSPVAVVPAKTVLHSGKPPVYMASFTSRGPGSAVAPHILKPDITAPGLNLAAWGGGSEPTLDDIHRVVEYNIIGSTMSGCPHVGGAAALKAHPITWSSAARBSALITSAGLRNNVVEGQITDASGKPADPFQFGGGHFRPSKAADPGLVYDASVGDVLLFLCASGDKLDNE

NbL02g18780.1 subtilisin-like_protease_SBT5.3 [MW = 70.09 kDa]

No. of times detected



log(intensity)



Values from



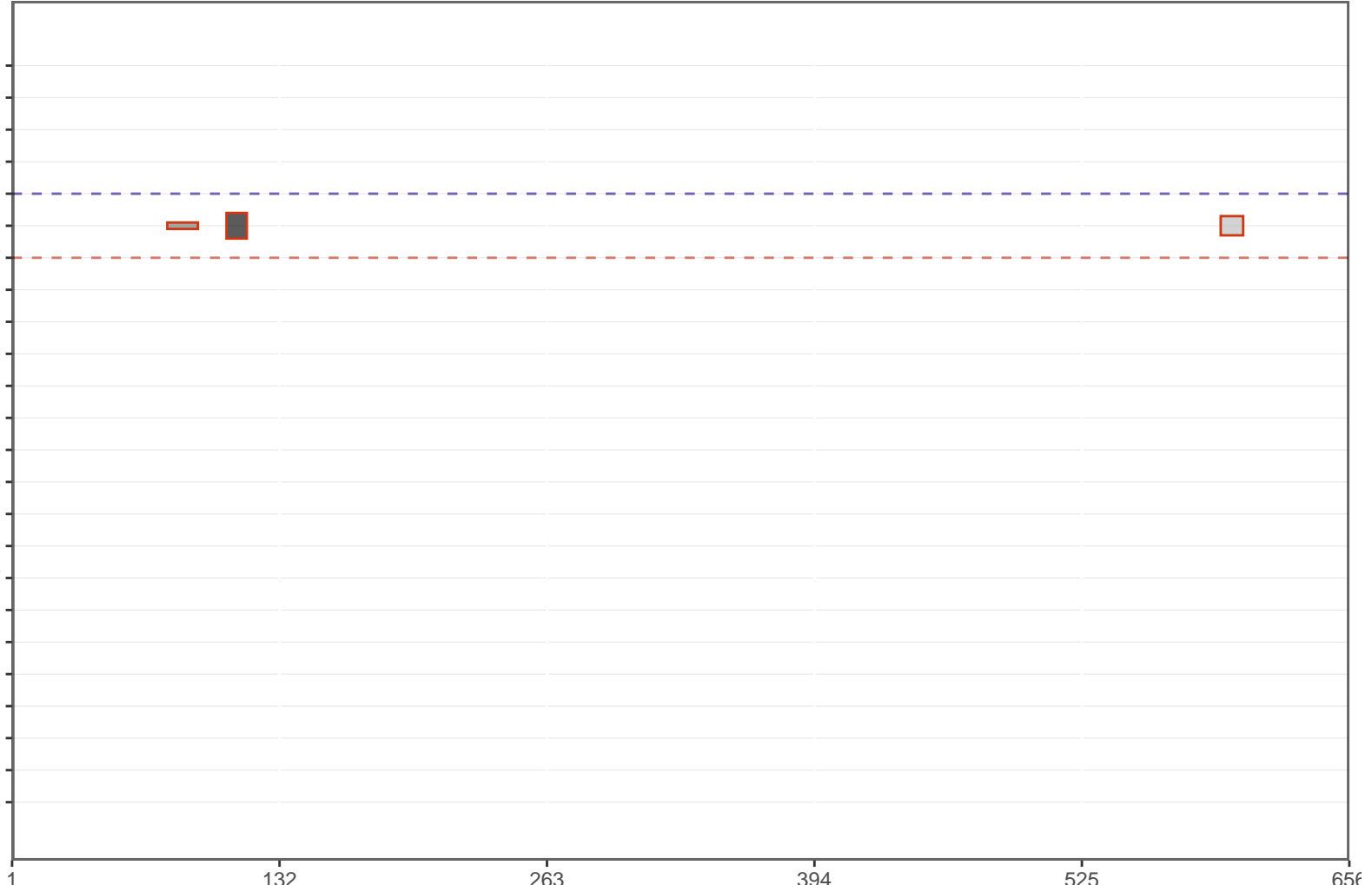
MW indication



Molecular weight

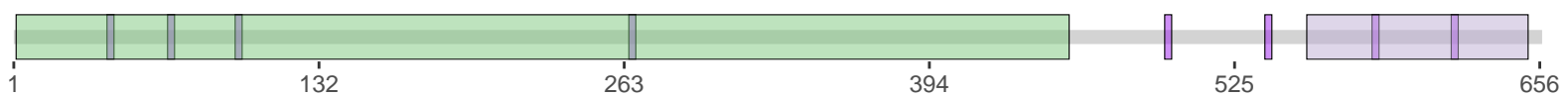


Gel Slice



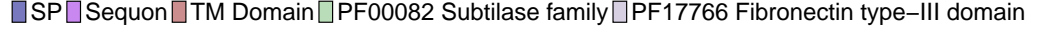
Peptide counts over 4 repeats

Protein length 1 132 263 394 525 656



Pfam domains

Pfam Description



Protein sequence:

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NbL02g18680.1 protein_SRG1-like [MW = 41.9 kDa]

No. of times detected



log(intensity)



Values from



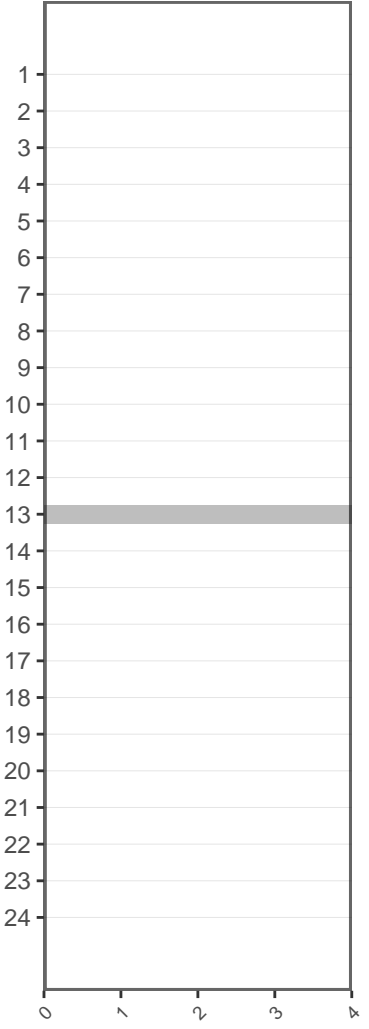
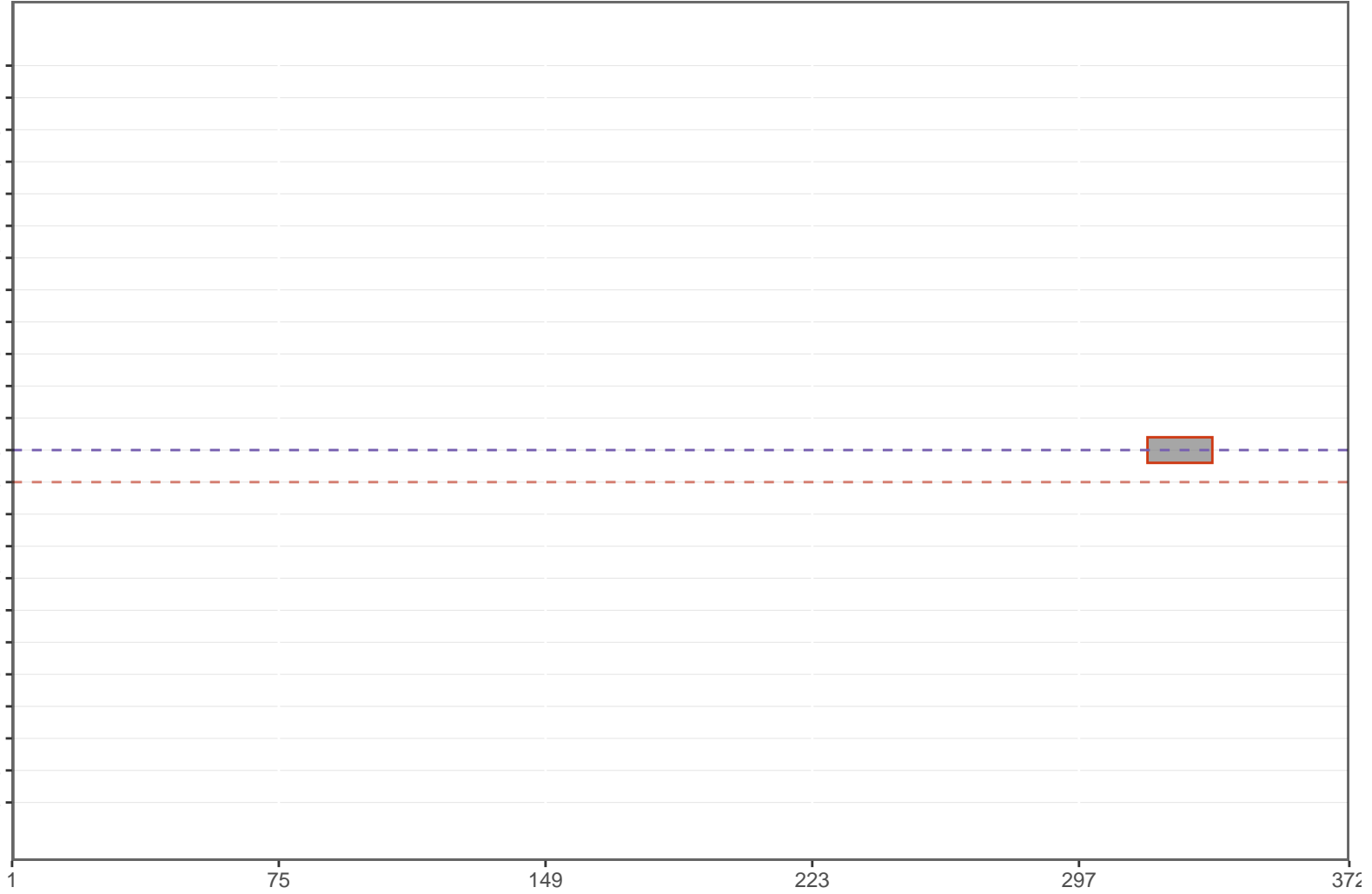
MW indication



Molecular weight



Gel Slice



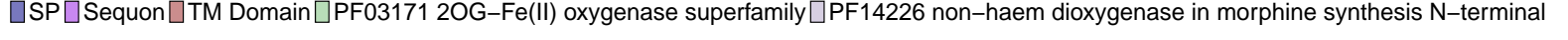
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LPLPFRFETVELVAELKTLALQINFAKALNDEEYMSLEFGEGMGAMRMNYYPPCPPEPEKVLGSLPHSDGVGLTLLQLNGMEGLGKDKGLWIPISPLNPAFINIGDLEIVTNGAYRSIEHRATVNNKKERLSATFYNPKLDGGIGPAPSIISSENTAKFKNGAADFRRGLFARKLKKKVLQVLRINVDNPAI

NbL02g18630.1 60S_ribosomal_protein_L32-1-like [MW = 19.71 kDa]

No. of times detected



log(intensity)



Values from



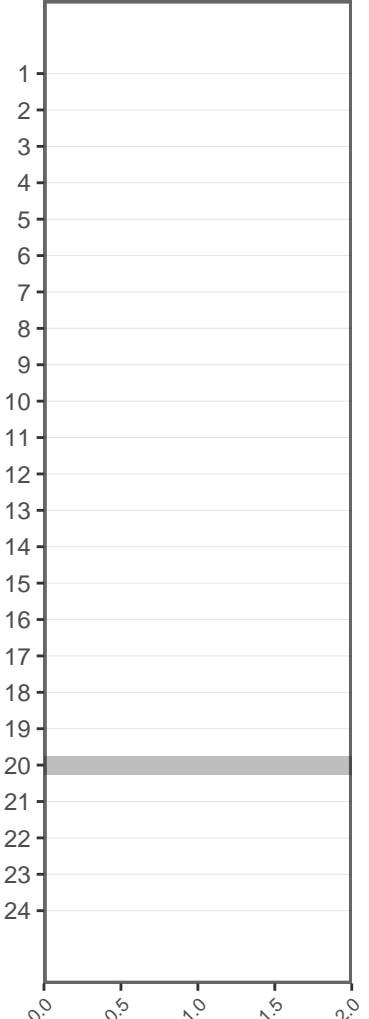
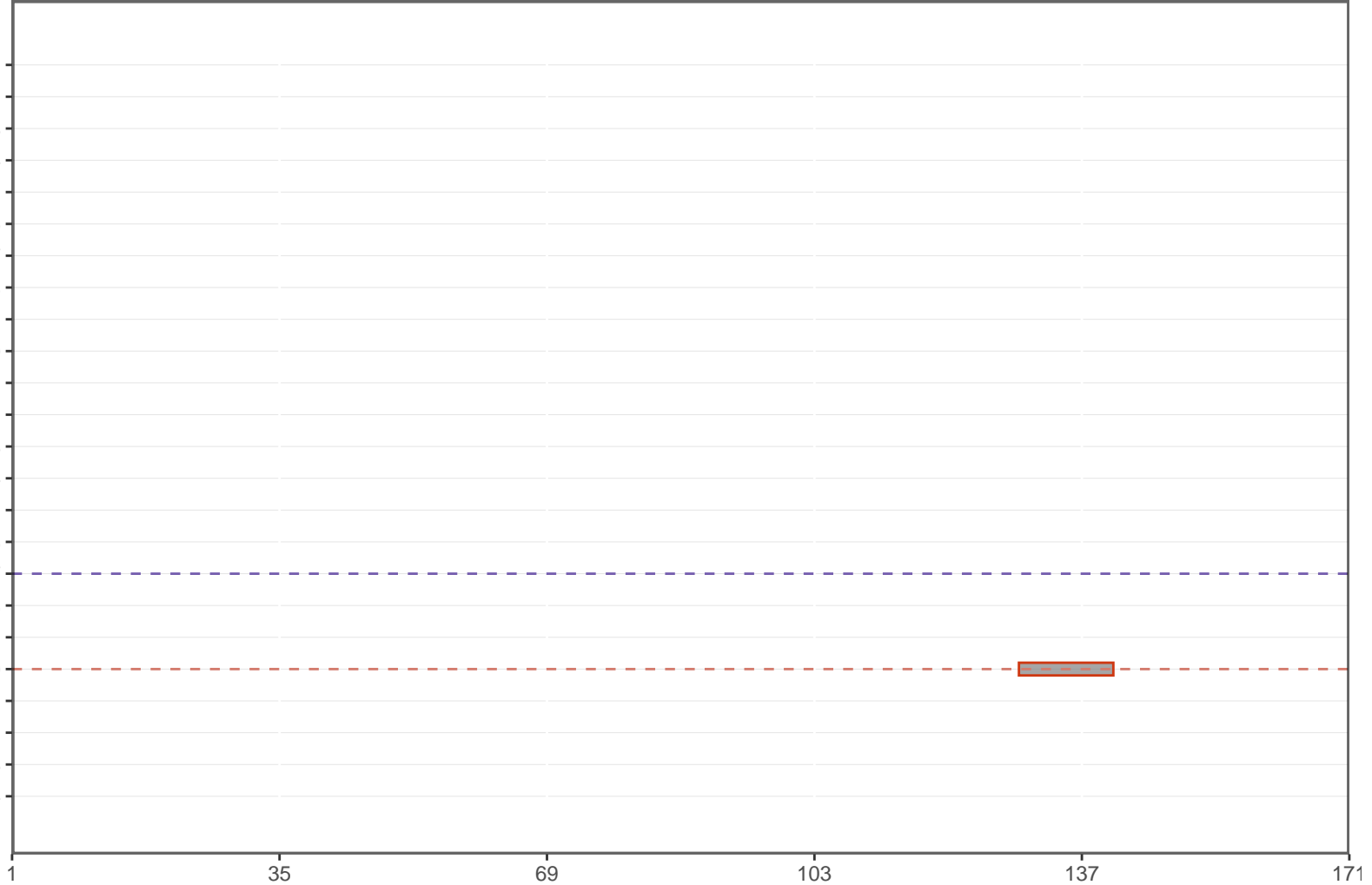
MW indication



Molecular weight

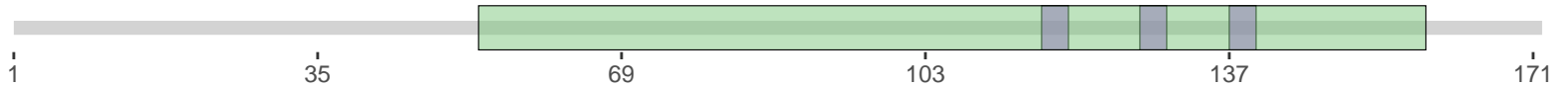


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KGIDSRVRRKFKYGGVLMFNGVGDNKRTRHYLPLNGFKKFLVHNASELDLLMHNRTGCAEIAHNVSTRKRKEVERAAQLDVAVTNKLARLRGQDEE

NbL02g18620.1 uncharacterized_LOC109210634 [MW = 80.67 kDa]

No. of times detected



log(intensity)



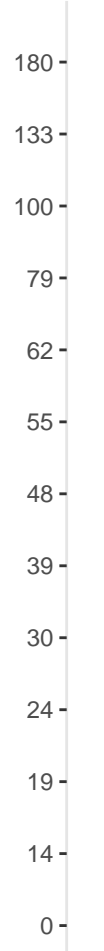
Values from



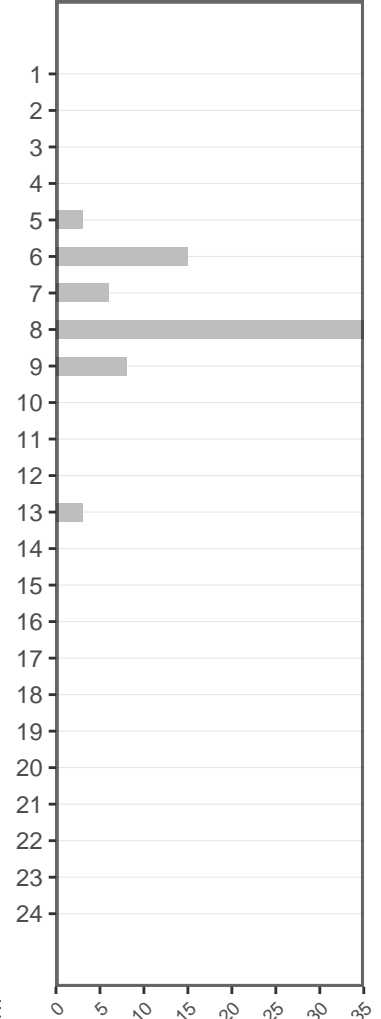
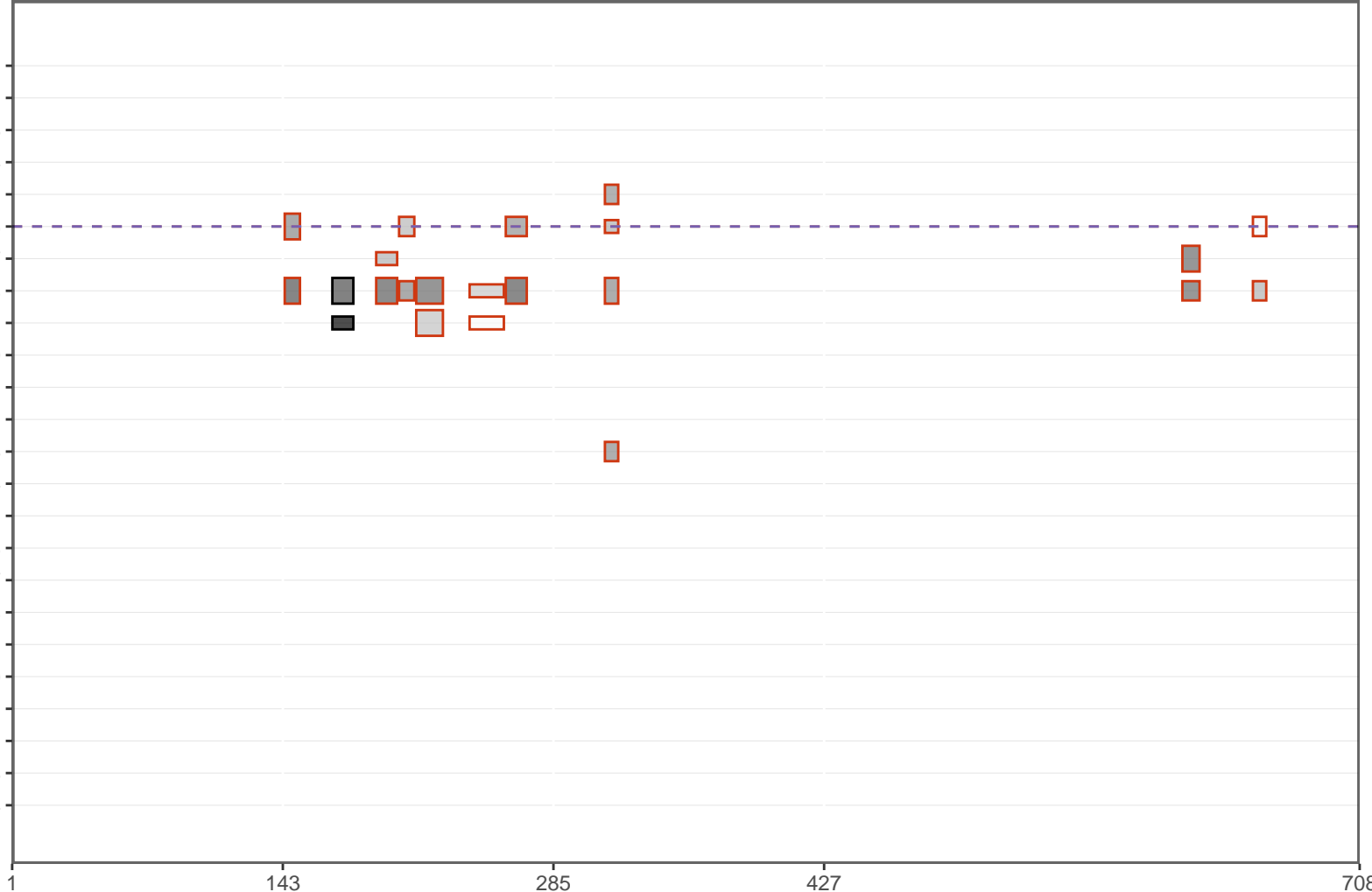
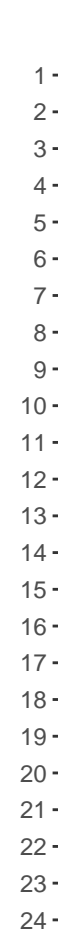
MW indication



Molecular weight



Gel Slice



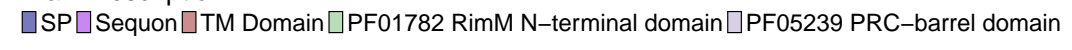
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

*OKRLIAAOKXLIHEMEGDHFRHGFYRGEKGRFLADQVHVNMSLGHALGNMKMPYKRWSEFPFVNALEVSNLTKGKFLSKENVERSSGCKVQEGDGRSLSSGNAVAIVLIGEMLGRSSPEHVGSHNNEIDIAHLHKALVDDSLRLIKMEDQLVPLVLPVPAEYIEYKGLDFIDHDFSNSEKWFLEEKLPVTVVSGEESKPKILMKSPWEIQPGSAGIVTLSSGNLLEHLHVMGVYEQVGSNGEYVNGEMLGGTSSRQANAGIQVTRDAGYSEERFN

NbL02g18490.1 DNA-binding_protein_DDB_G0278111-like [MW = 14.8 kDa]

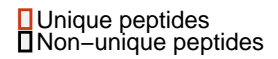
No. of times detected



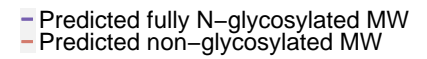
log(intensity)



Values from



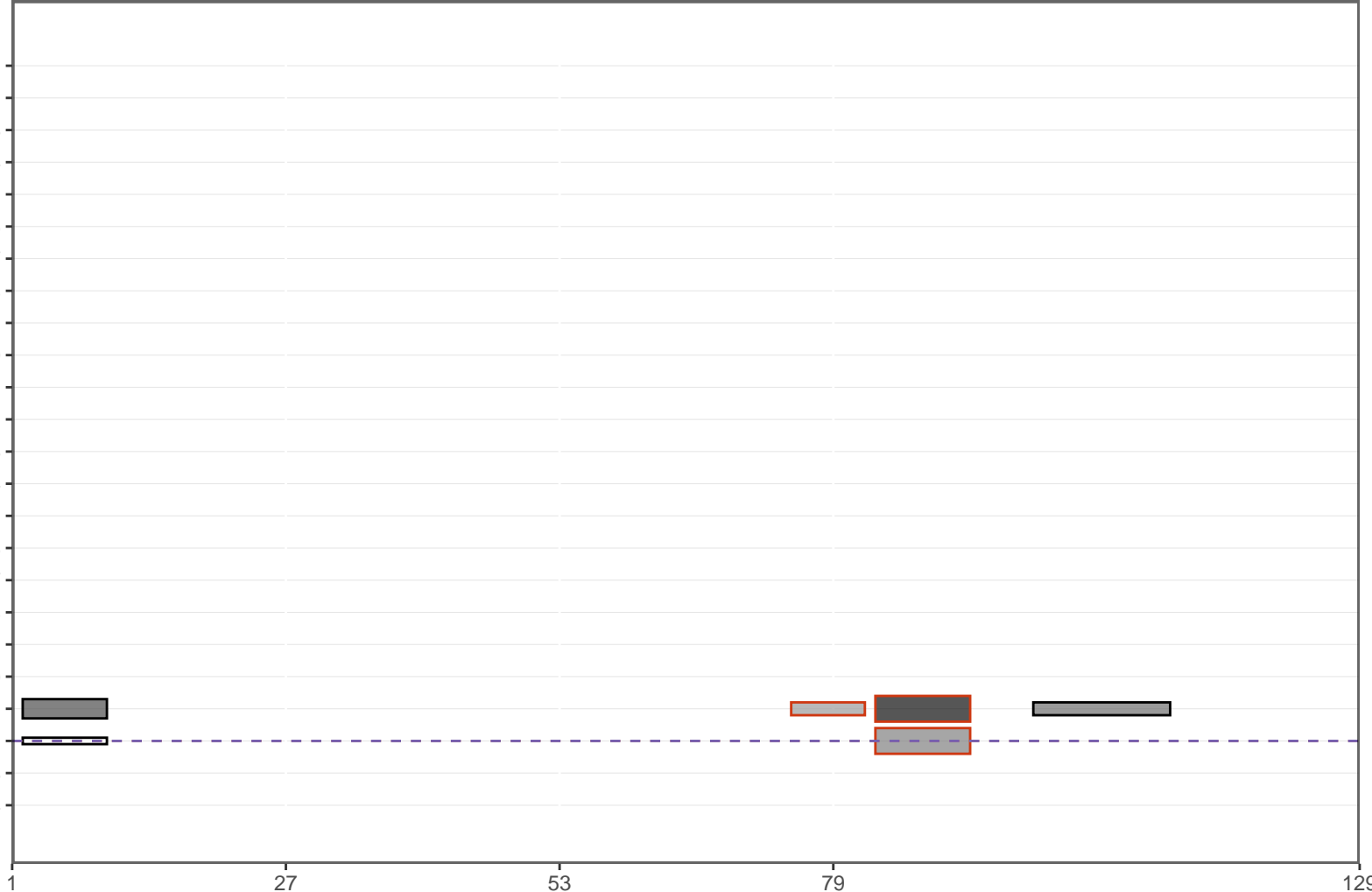
MW indication



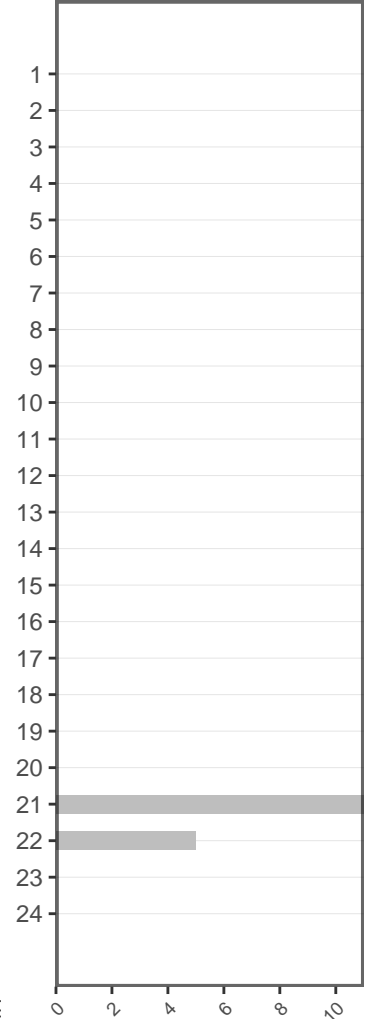
Molecular weight



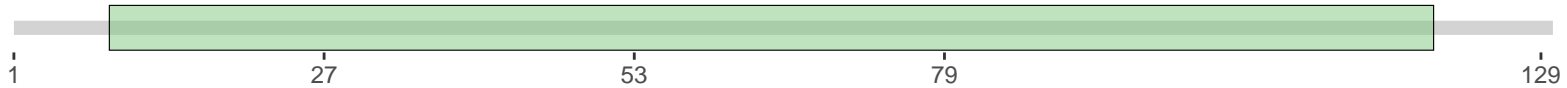
Gel Slice



Protein length

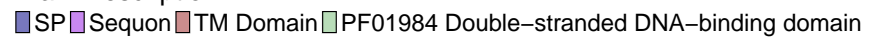


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

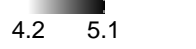
MLTQLSSEARARVARIALVPPKARGVEDVILRAAGYGGITEKVEEKLQLEGINFTGTFKGVTHRRRNVLDDDD

NbL02g18320.1 uncharacterized_protein_ycf23-like [MW = 33.91 kDa]

No. of times detected



log(intensity)



Values from



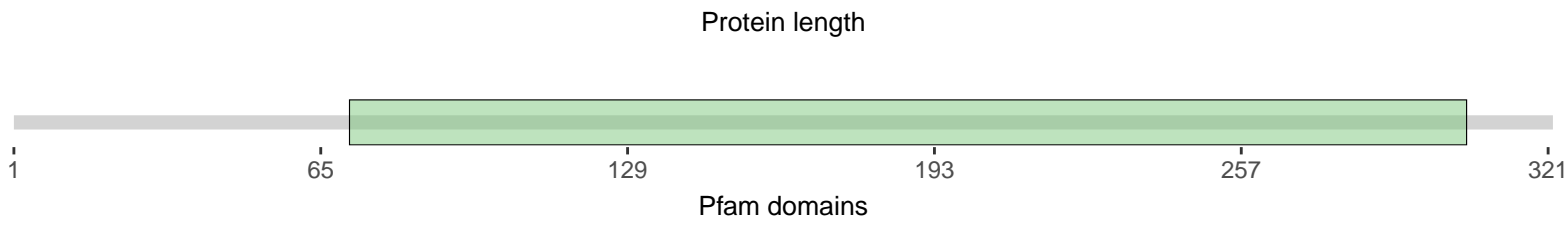
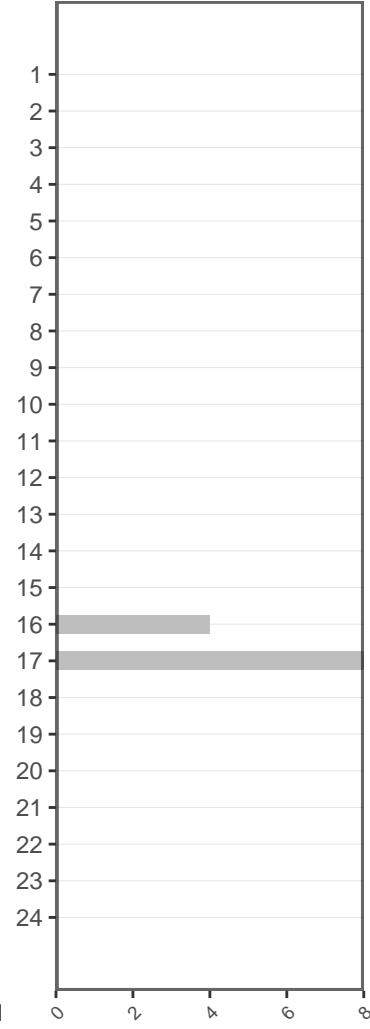
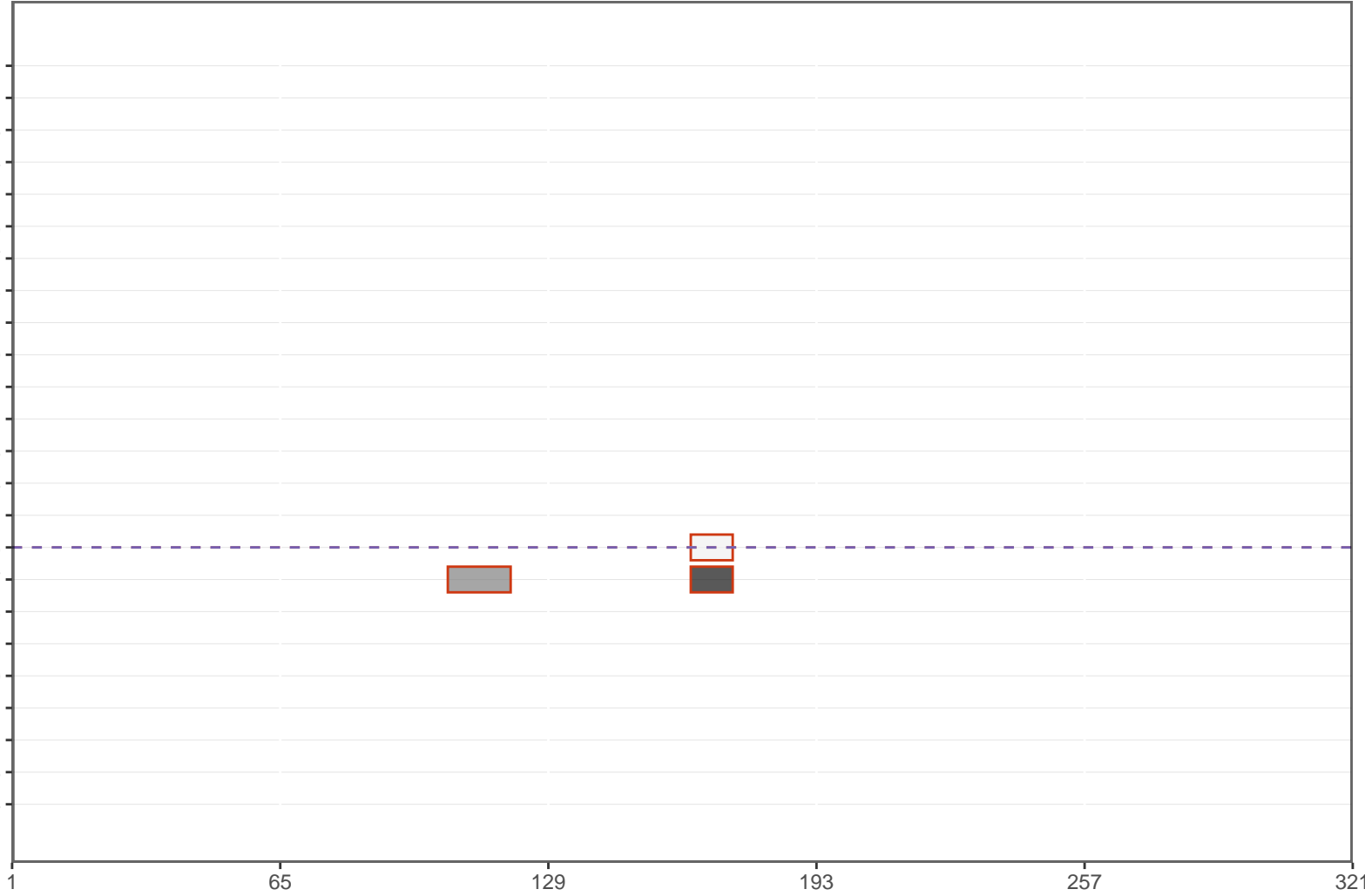
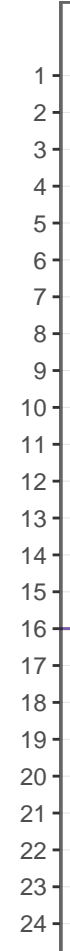
MW indication



Molecular weight



Gel Slice



Pfam Description
 ■ SP ■ Sequon ■ TM Domain ■ PF04481 Protein of unknown function (DUF561)

Protein sequence:

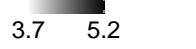
ALMVEIGNYDSFYENGLVFSPEQILKIKETKRILPLVTLVTVPHFLSLPDDQVLAELLEGEQVDIHTGEGKFSFSPKAGVLGLEKATPTLAAVSRVAVNIPVMGSSGLSAVTAPMAAAGAVGVSGAINKLNDQVWAMIAEVKSIANSLGLSTKTNLFEGSSLRLL

NbL02g18300.1 3-oxoacyl-[acyl-carrier-protein]_synthase_I_chloroplastic [MW = 49.98 kDa]

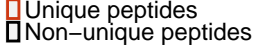
No. of times detected



log(intensity)



Values from



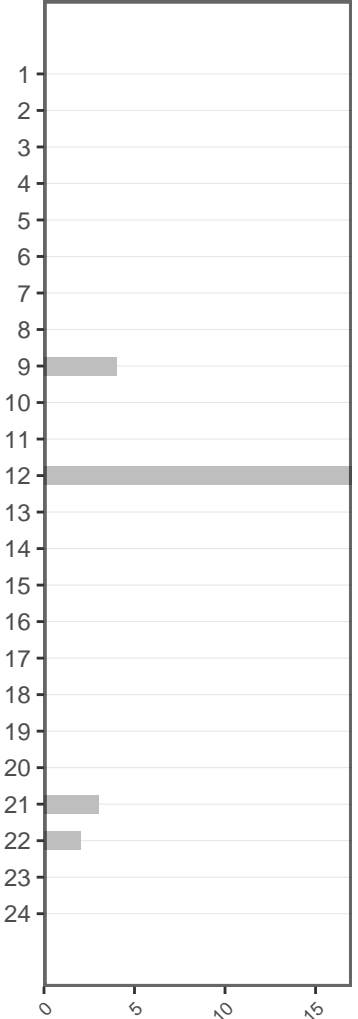
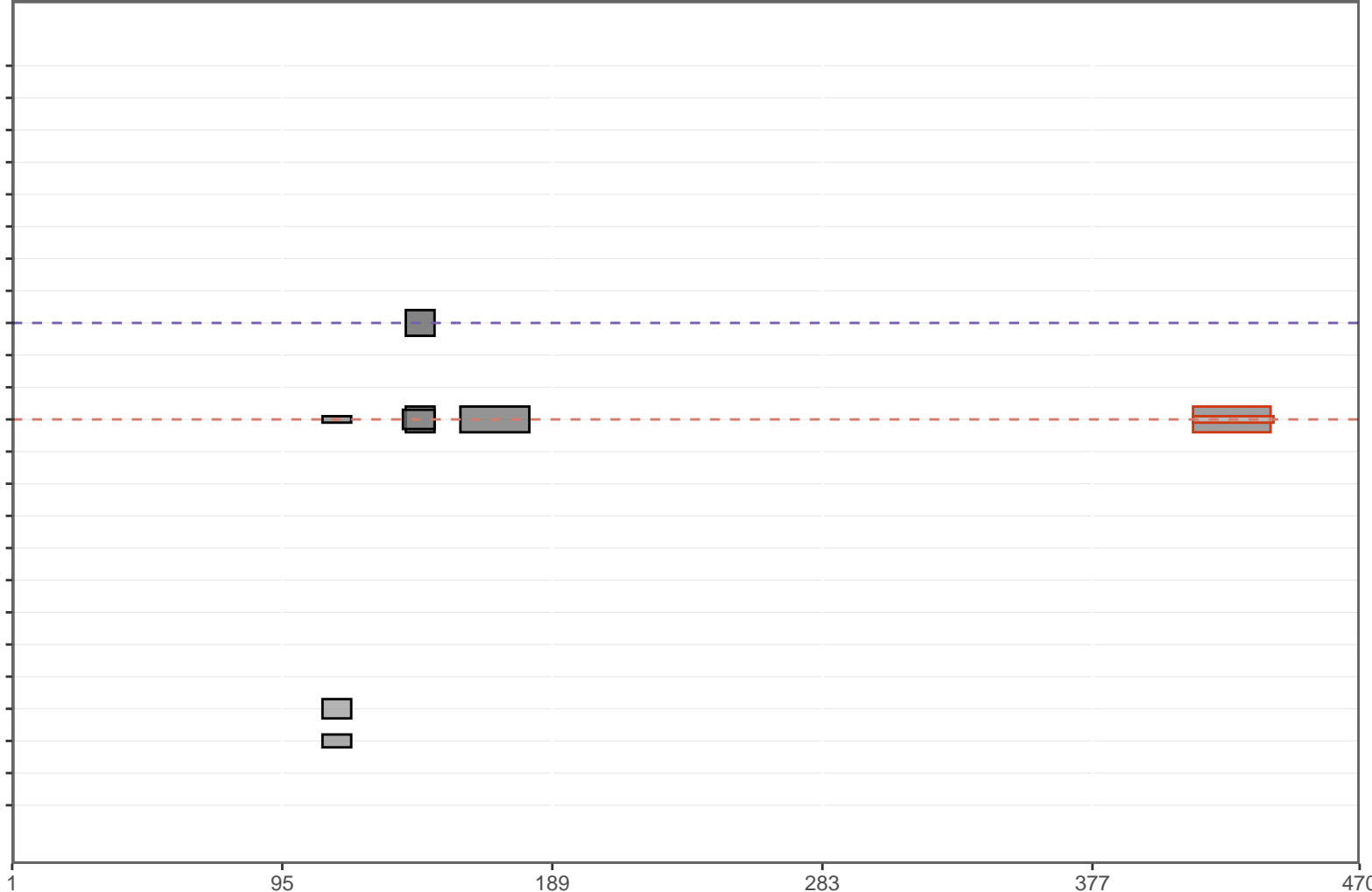
MW indication



Molecular weight

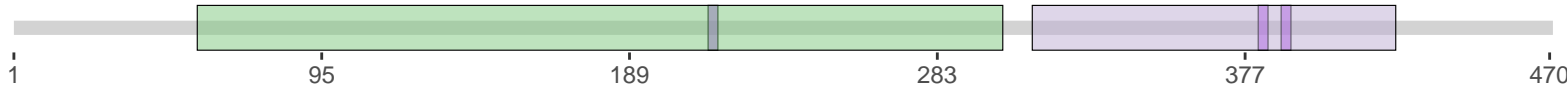


Gel Slice



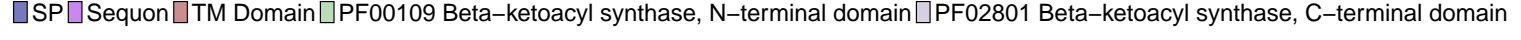
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NYCFYAAANHSRRGEADLMLAGGTEAIIPIGLGDFVACRALGQRNDPDTASRPWDKERDGFVMEGEGVLMESLEHAMKRGAPIAEVLGGAVNGDAHHMTDPRADLGVSSGIGSLEDAGVSPFEVNYNHAHMTSTVGDIAEIVNAKKVFKNTSGIKMNTKSMIGHGLGAAGGMEAMTVKAITGWWHPISINGFNPEPSVEFDTVPNKKGGHEVNVGDSNDFGFGGHNSVAVSAFKP

NbL02g18280.1 uncharacterized_protein_At2g34460_chloroplastic-like [MW = 27.29 kDa]

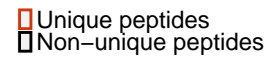
No. of times detected



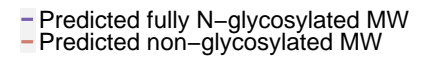
log(intensity)



Values from



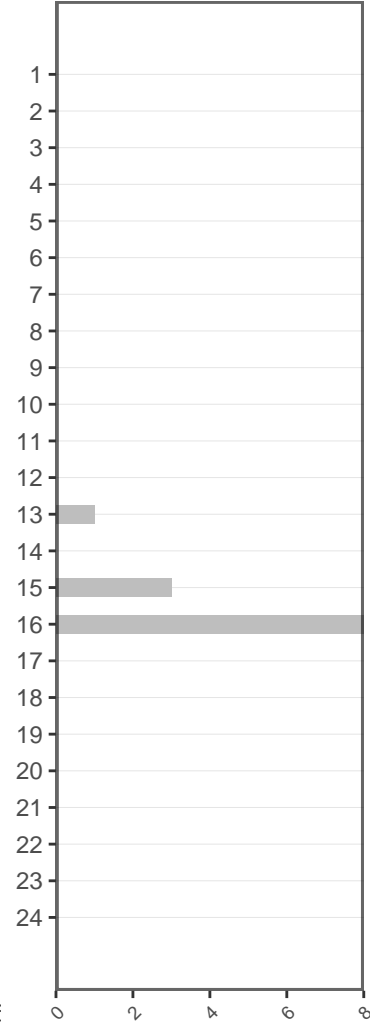
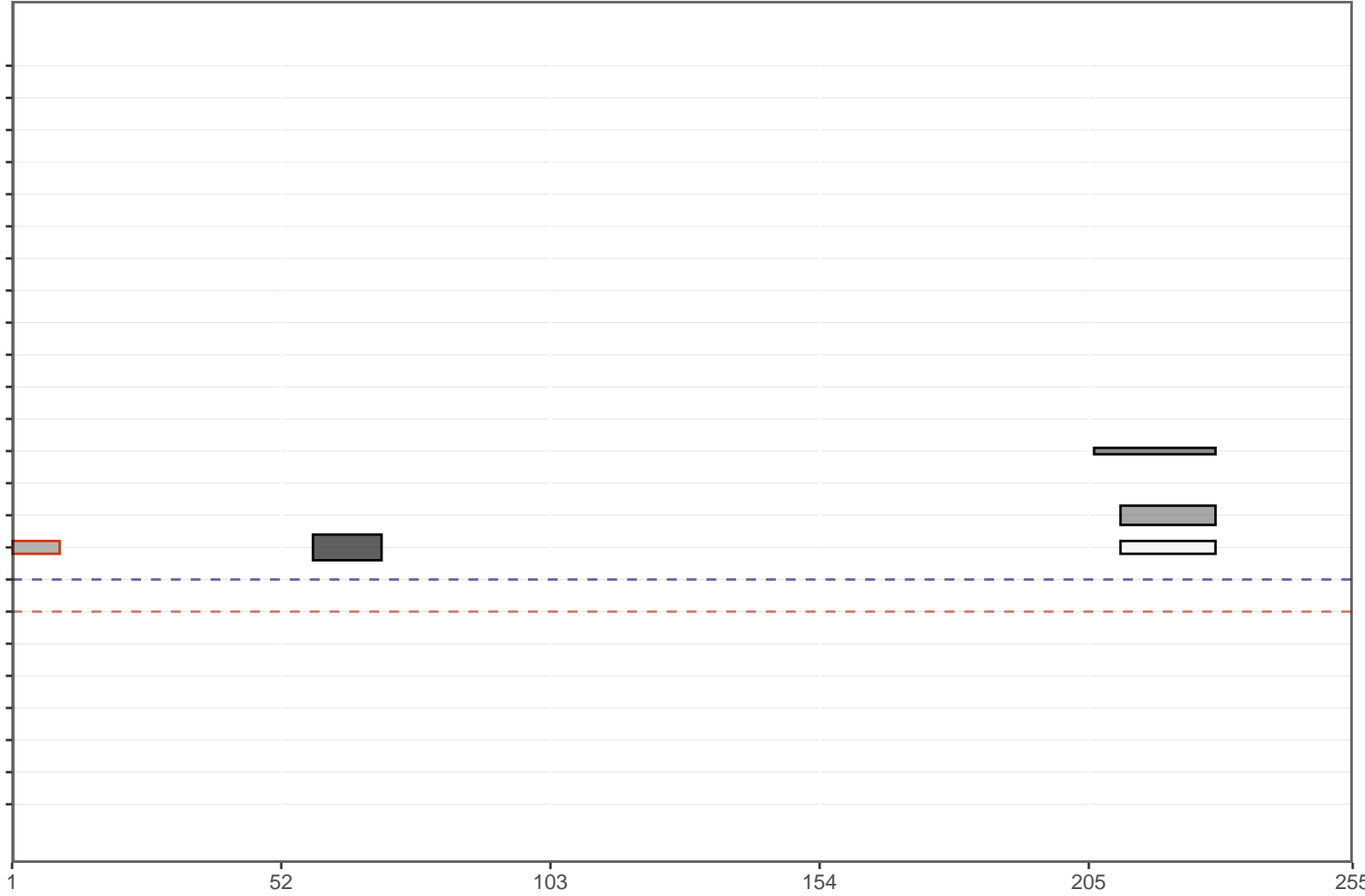
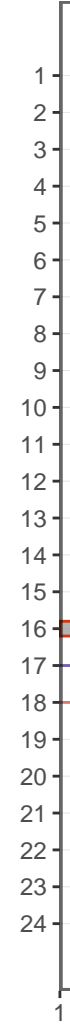
MW indication



Molecular weight

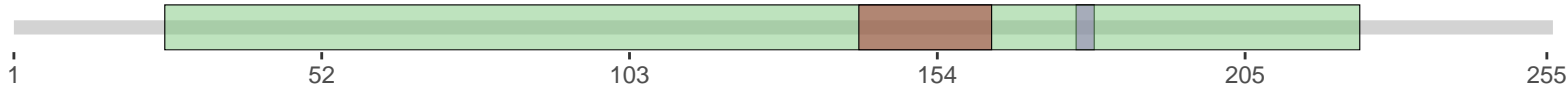


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL02g18210.1 60S_ribosomal_protein_L18a-like [MW = 21.41 kDa]

No. of times detected



log(intensity)



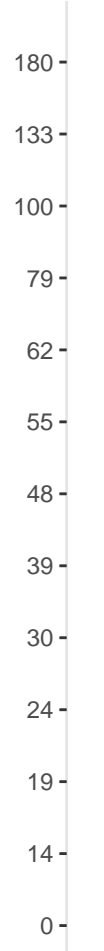
Values from



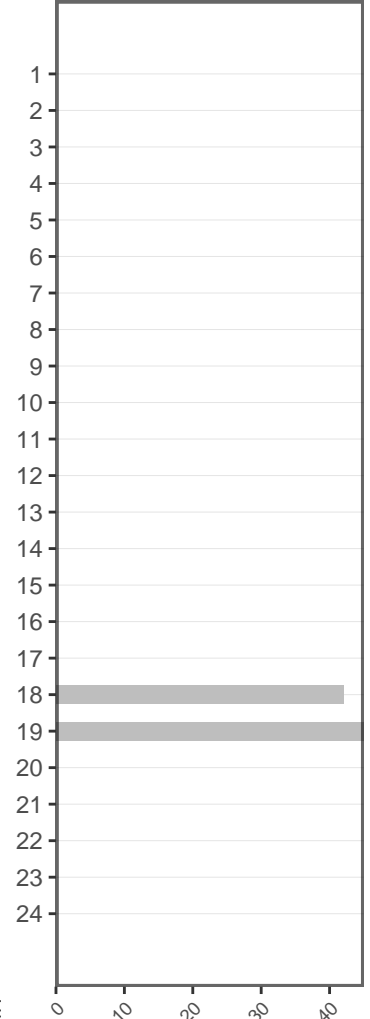
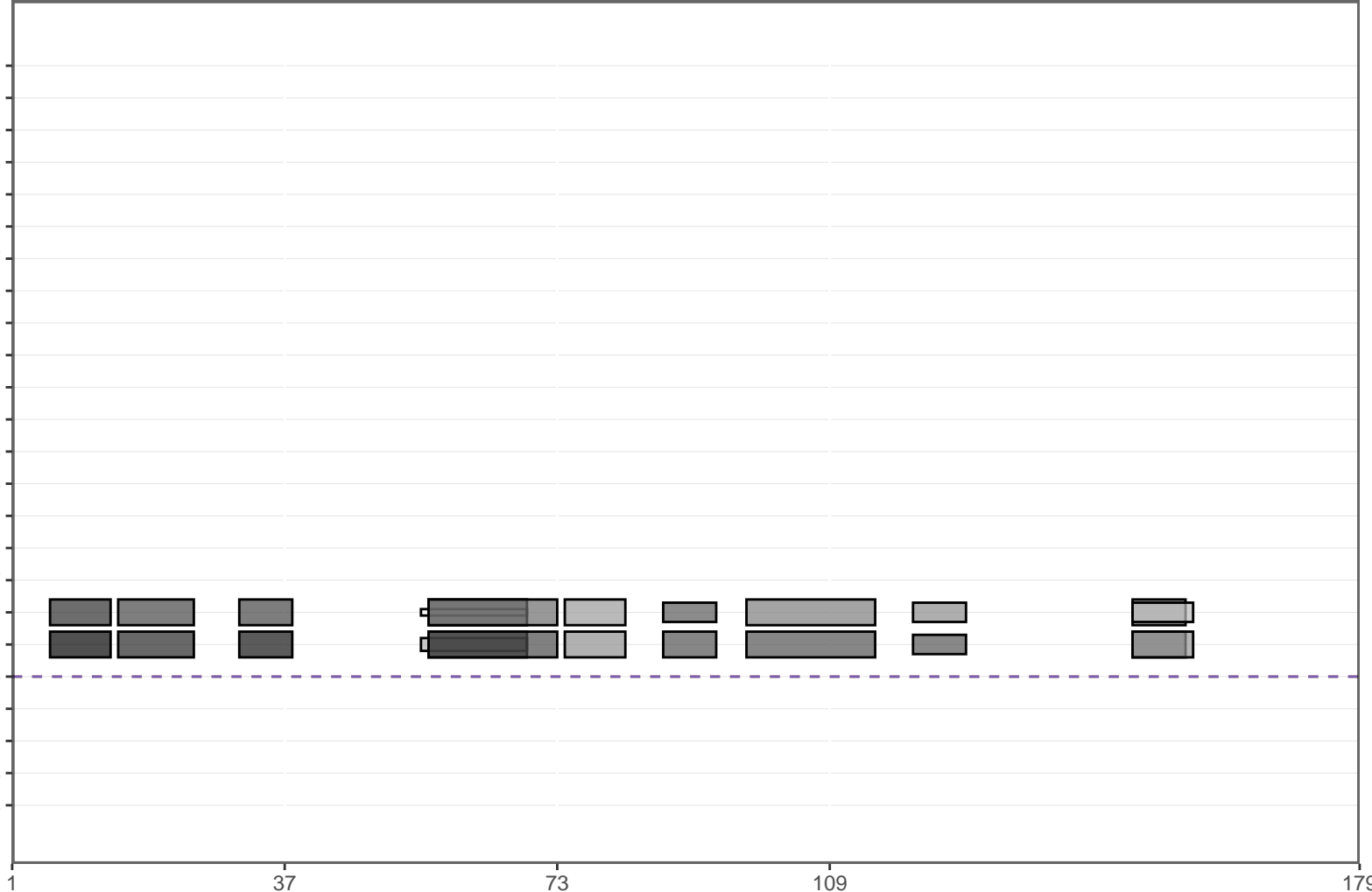
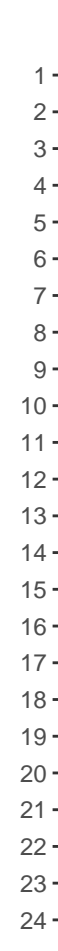
MW indication



Molecular weight

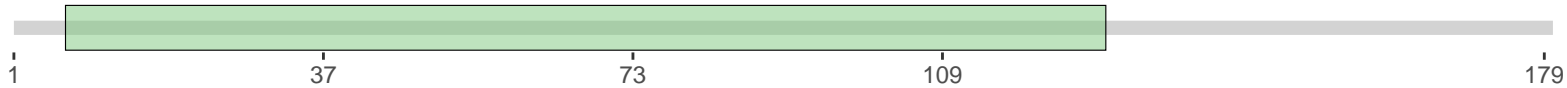


Gel Slice



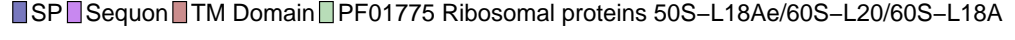
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

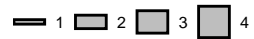


Protein sequence:

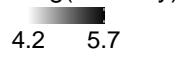
YVGIWLRYSRSTGVHNMVKEVRDFTLNGGVEQMVTETMASRHRVRRHHCIGIKTATPAKLRKRESTKQGFHDSKIKFPLVFKKVRPPSRKLTFTYKATRNPLFM

NbL02g18080.1 proteasome_subunit_alpha_type-5-like [MW = 26.07 kDa]

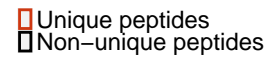
No. of times detected



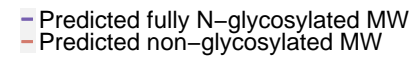
log(intensity)



Values from



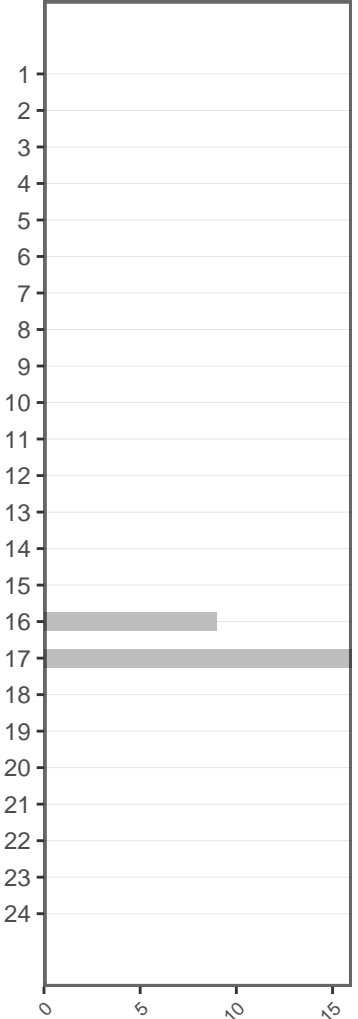
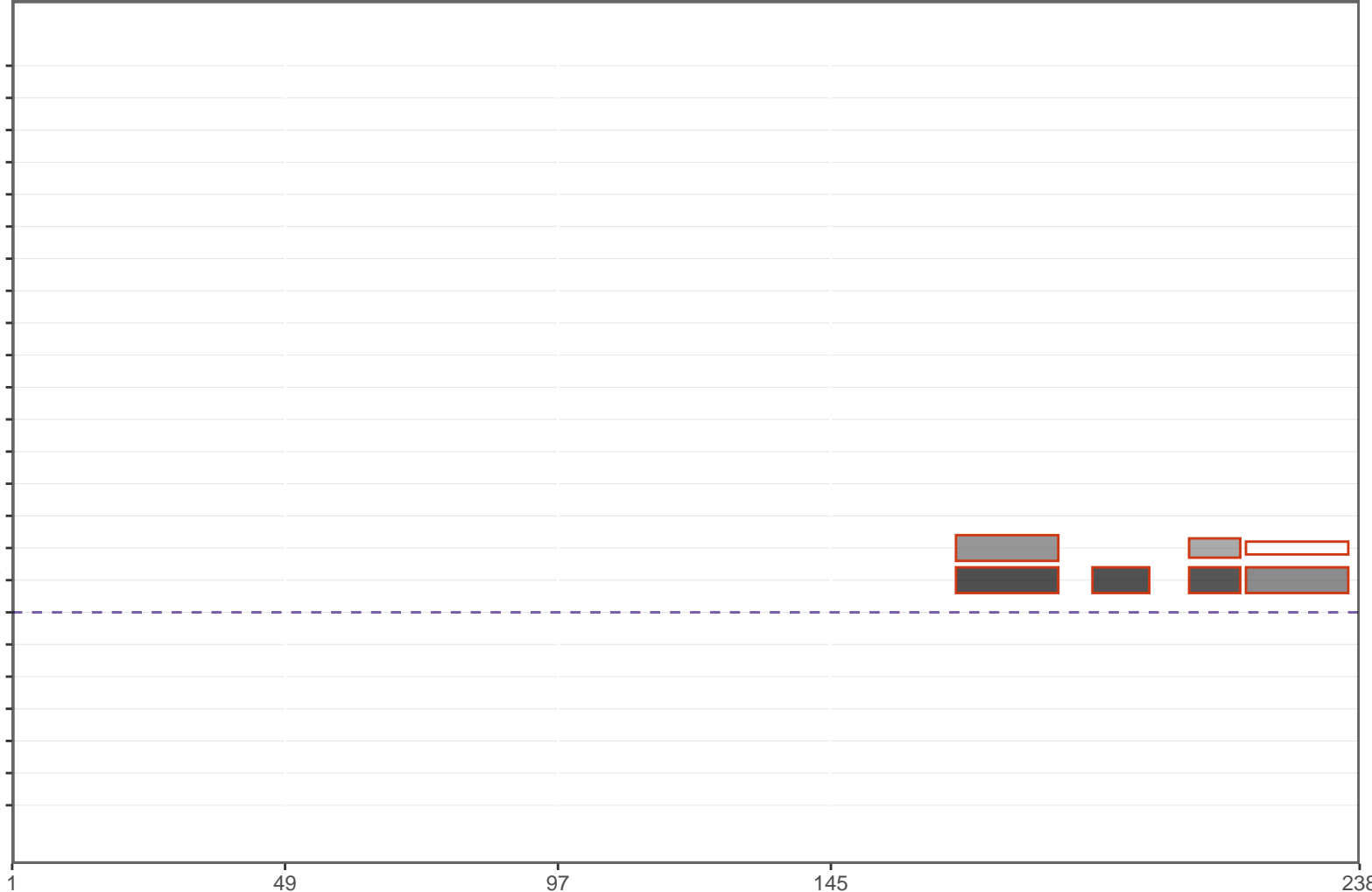
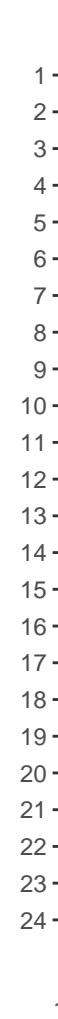
MW indication



Molecular weight



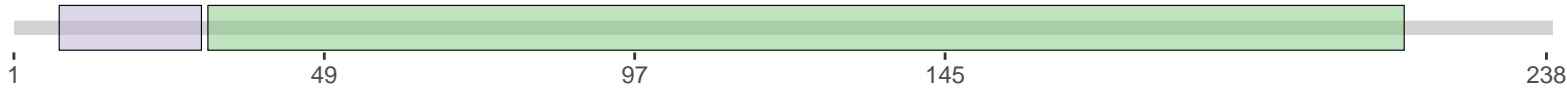
Gel Slice



Protein length

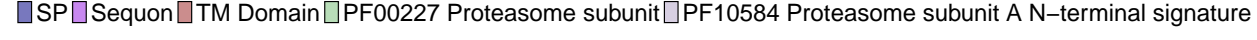


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ITVETSTOALCDLALRFEGDEEMSRFFGVSLIAGHDENGPSLYTDPGQTFWQGNAKAGSGSEGADSSLGEGHNKDLTKEAETIALSILKGVMEKVTDPNVDIARVSPFTHLYSPSEVEEIVRL*

NbL02g18070.1 uncharacterized_LOC109223617 [MW = 16.75 kDa]

No. of times detected



log(intensity)



Values from



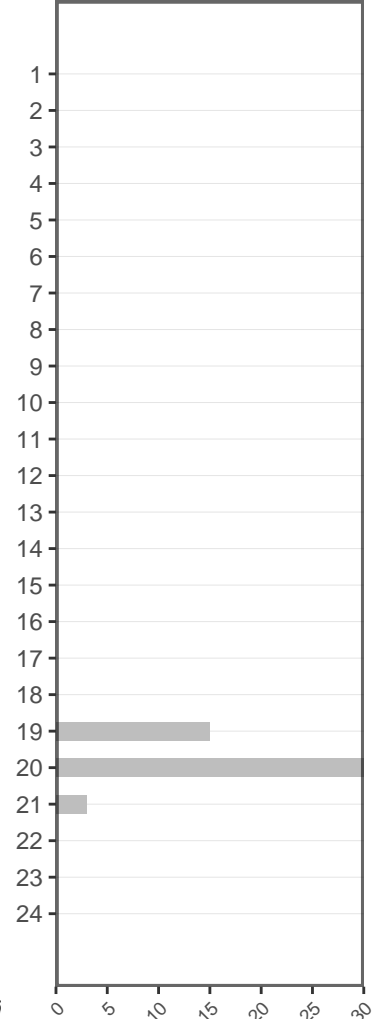
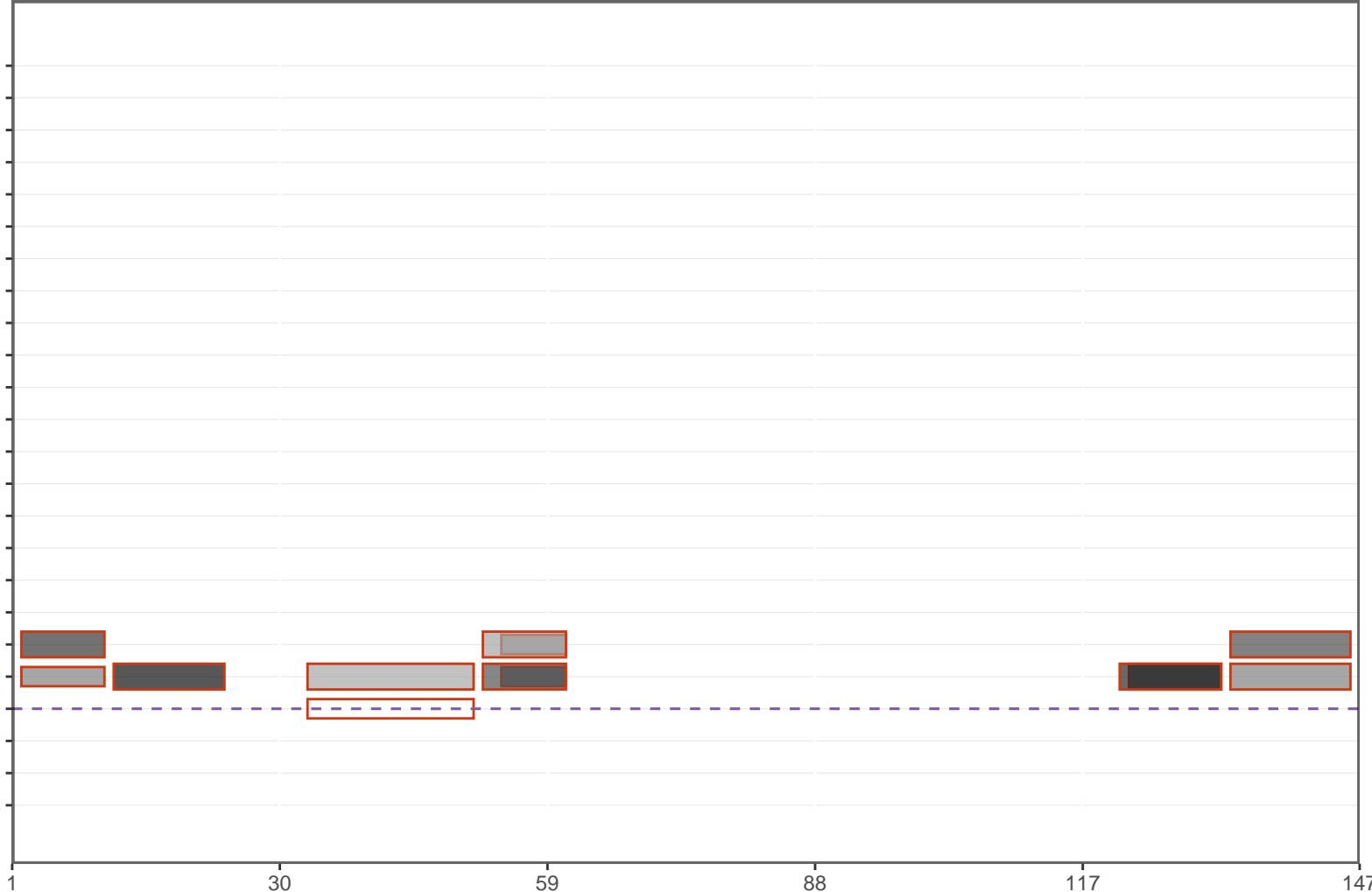
MW indication



Molecular weight

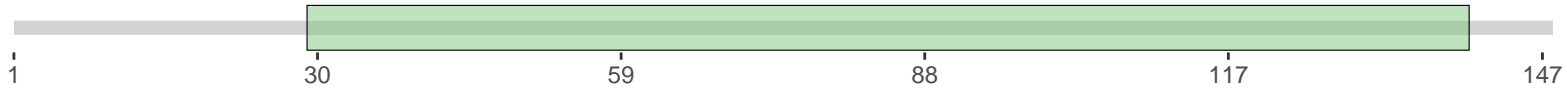


Gel Slice



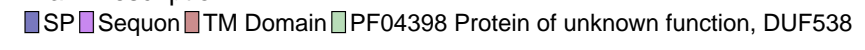
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

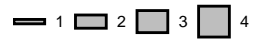


Protein sequence:

LKQKQAKKHFKYGGKLLWYDTEVTAIVEDRRMKKLTGVKSKELLWVTLSDISIGDPESKQKIFATAGLSRAVPIVSAFEEEEVEK*

NbL02g18000.1 40S_ribosomal_protein_S4 [MW = 34.99 kDa]

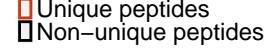
No. of times detected



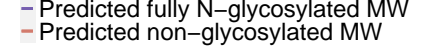
log(intensity)



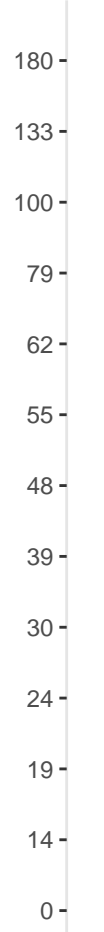
Values from



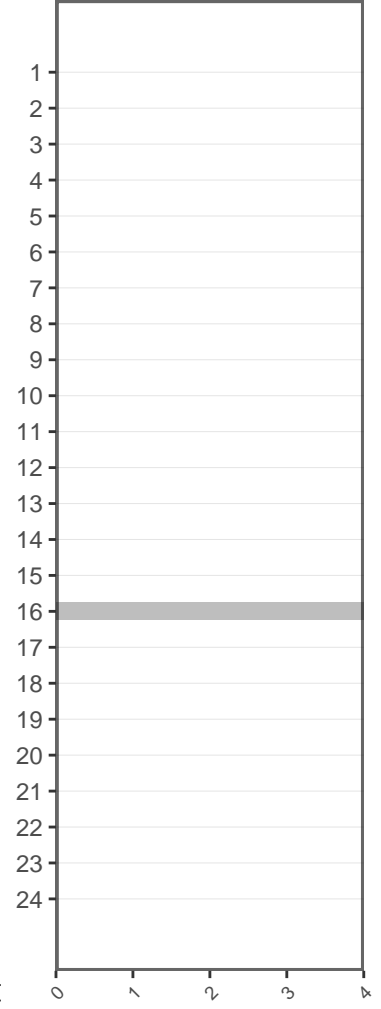
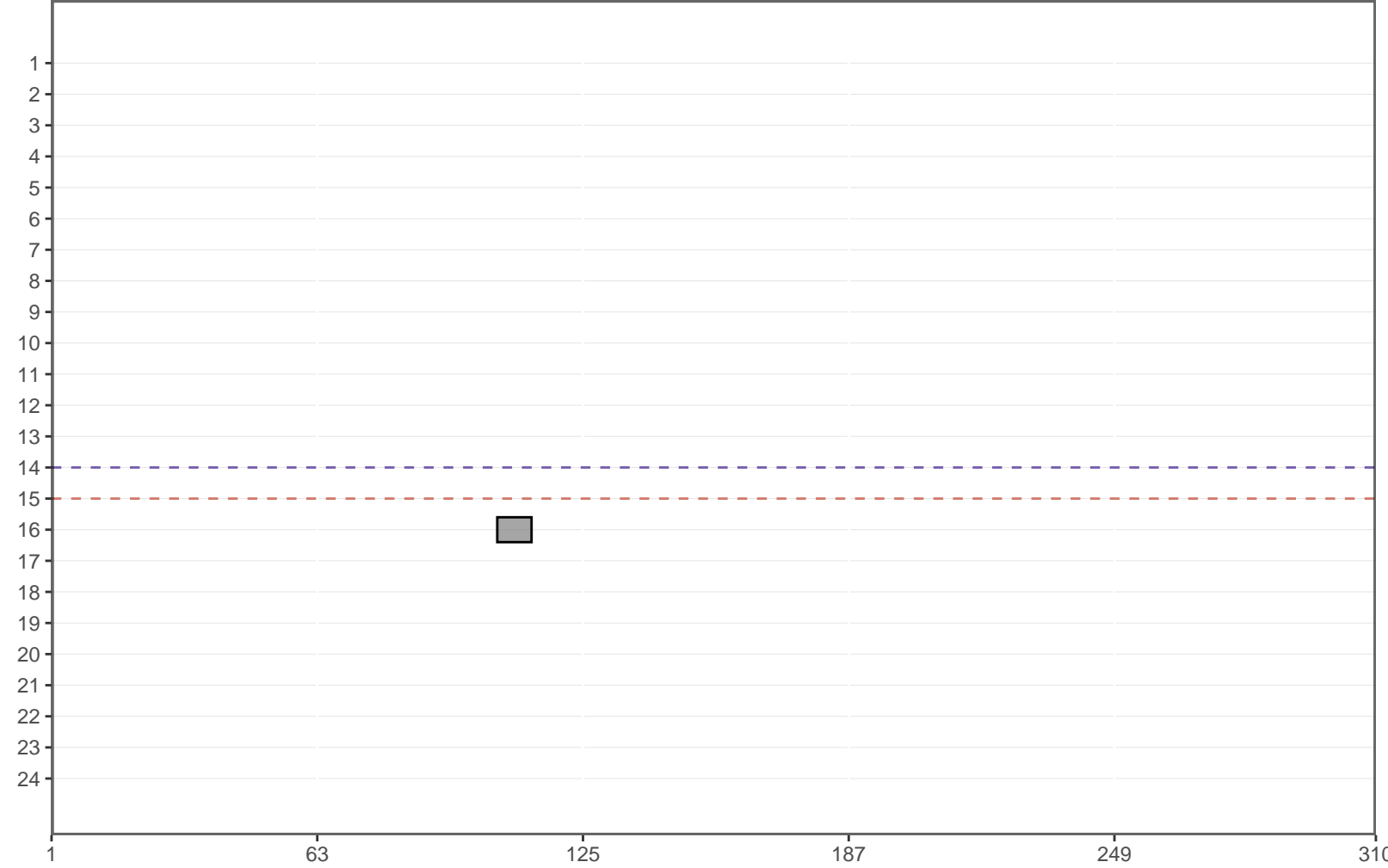
MW indication



Molecular weight



Gel Slice



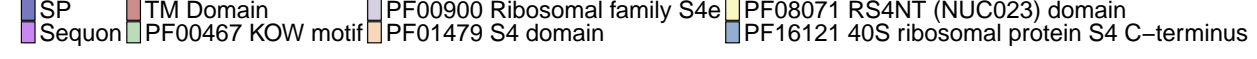
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NENFRLLYDTKGRFRHLHSLRDEEAKFKLGVREVFQGGKGIPIYNTYDGRTRIRYPDFLKAINDTKLDEENKIVDFIKFDVGNVVMVTGGRRNRGRVGVKIKREKHGGSFETHYHGIDALGHEFATRLGNVFTLGGKTKPWWLPLKGGKGLSHEEARKRLAAGSATAA

NbL02g17860.1 berberine_bridge_enzyme-like_13 [MW - SP = 58.95 kDa]

No. of times detected



log(intensity)



Values from



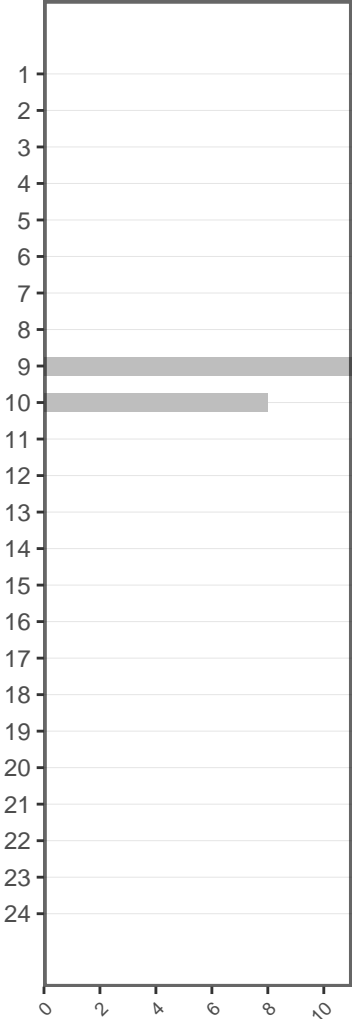
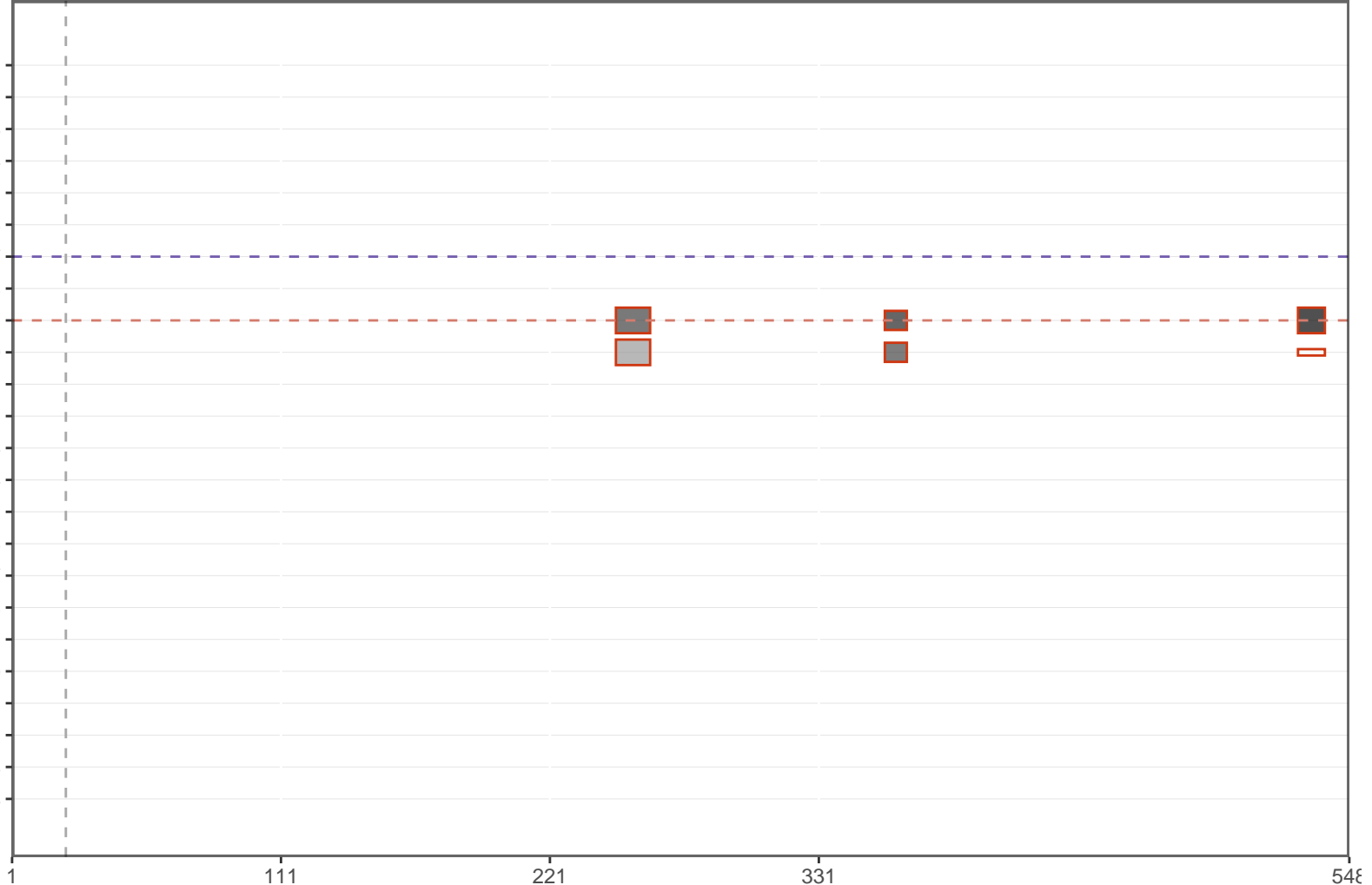
MW indication



Molecular weight



Gel Slice



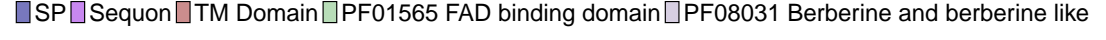
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

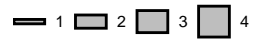


Protein sequence:

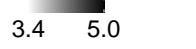
CTLEDGATKLYKYGQVADKIDNLFMRVYVAVERKDGKGEKTVGTAYNSLFLGKADRLLOTFMNESEFPELGLTKDKCTEMSWIESILVAGFPFKTPEILLGGKSTFRNFKYAKSDFKEPPEFGLGEMKRLLEEDSLMWNIPYGGMMANISEGETPFPHRKGVFKGQVYTLWTEFNGELATKHVDWRKLYNYMTSYASMFREAVVNYRDLGLGMNKNNSSEFVQASVWGANKYFKNNFNRLVEKTKVDPENFFKFEQSIFLPLTKRKGKQNI*

NbL02g17790.1 probable_LRR_receptor-like_serine/threonine-protein_kinase_At4g20940 [MW - SP = 113.27 kDa]

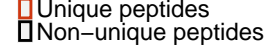
No. of times detected



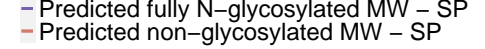
log(intensity)



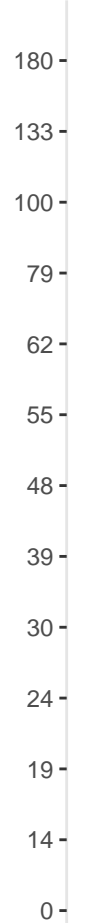
Values from



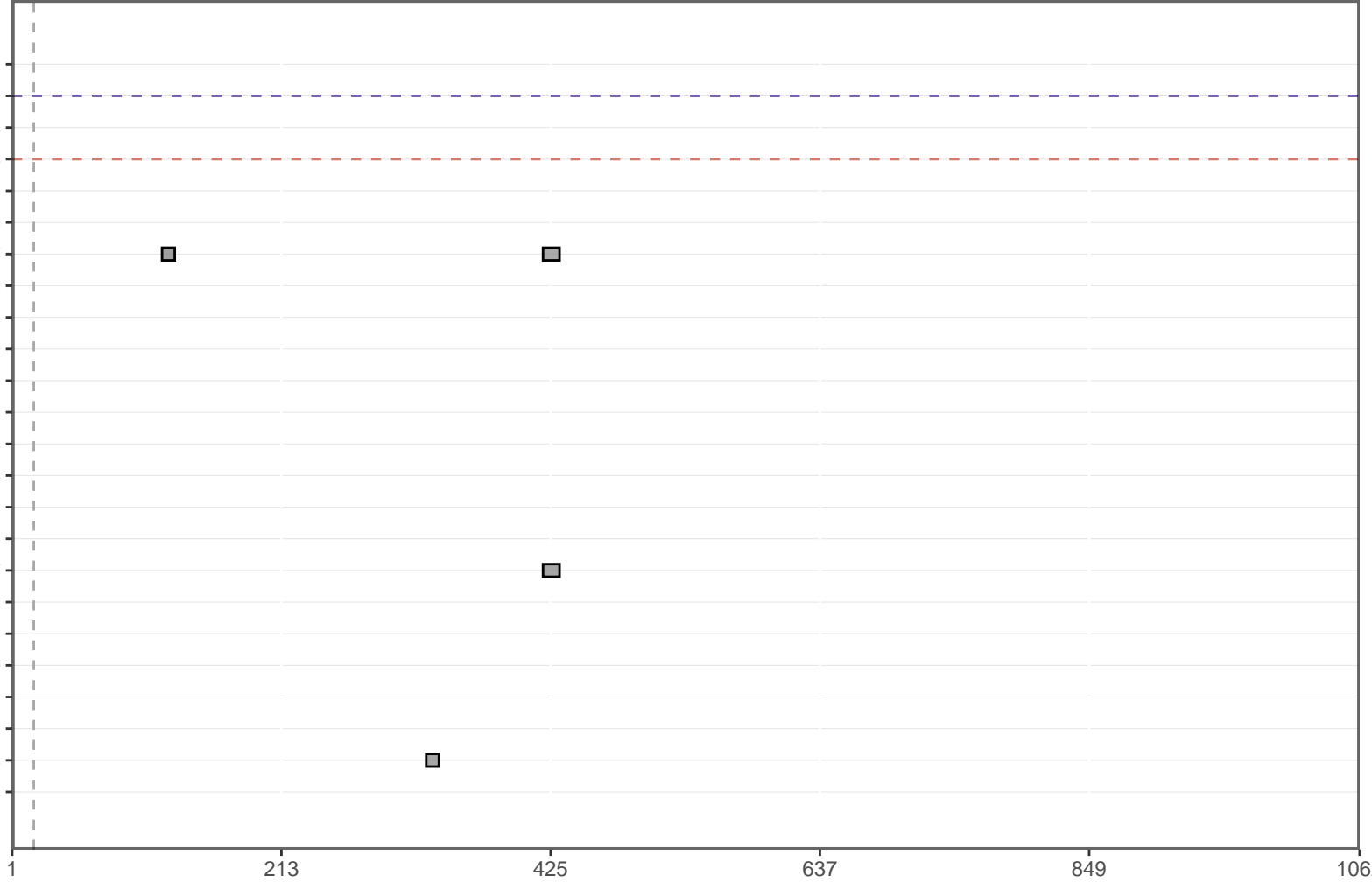
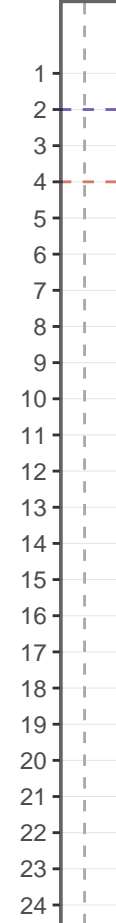
MW indication



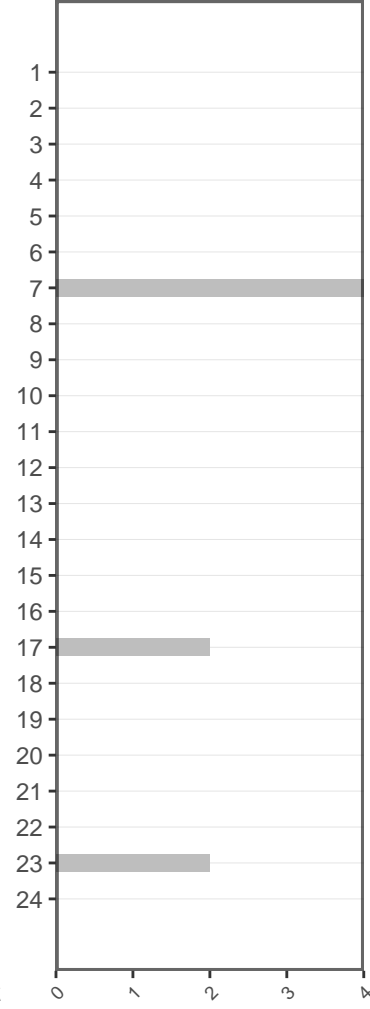
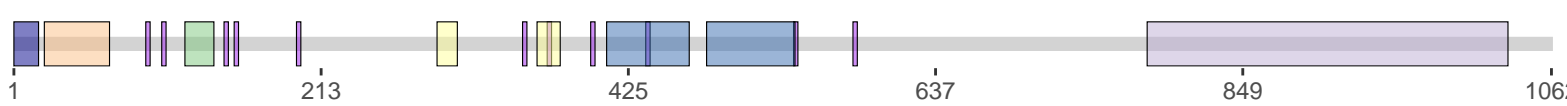
Molecular weight



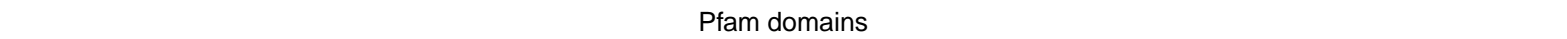
Gel Slice



Protein length

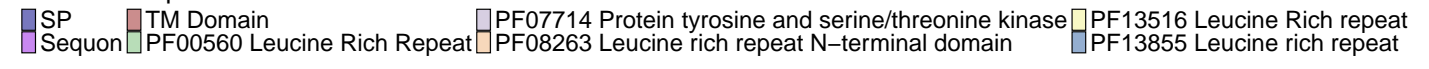


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

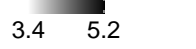
FPDEFDSLTLALLOLDIAGNFFSGELPFTSIDQVLSALTLSDIHSNHFITGPLKLNPLNGLSFNASLNDLSDGVYPENLRKFFLSSEFYPCNSGLGFNPPSGGSGAABAEADQKRSFKTIKVVHVAQVIALHLLLAIFMYYRAGRKPHQVTKRDVHHQAPSPHGVFSGREGTGDVYVAEQLMTRKGGSEIISPDEKMAAVTGFSPKSGSHFVSWSPESGGDEVAIENFARLDVRSPLRAGELYFLDITISFTPEELSRARKEVLRGSHGTSVYRATLENGLLTYKWLREGVAKC

NbL02g17710.1 probable_carboxylesterase_17 [MW = 37.61 kDa]

No. of times detected



log(intensity)



Values from



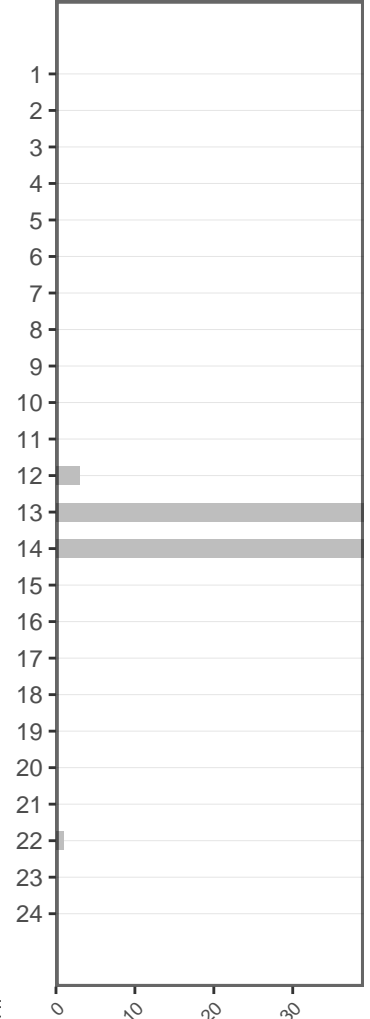
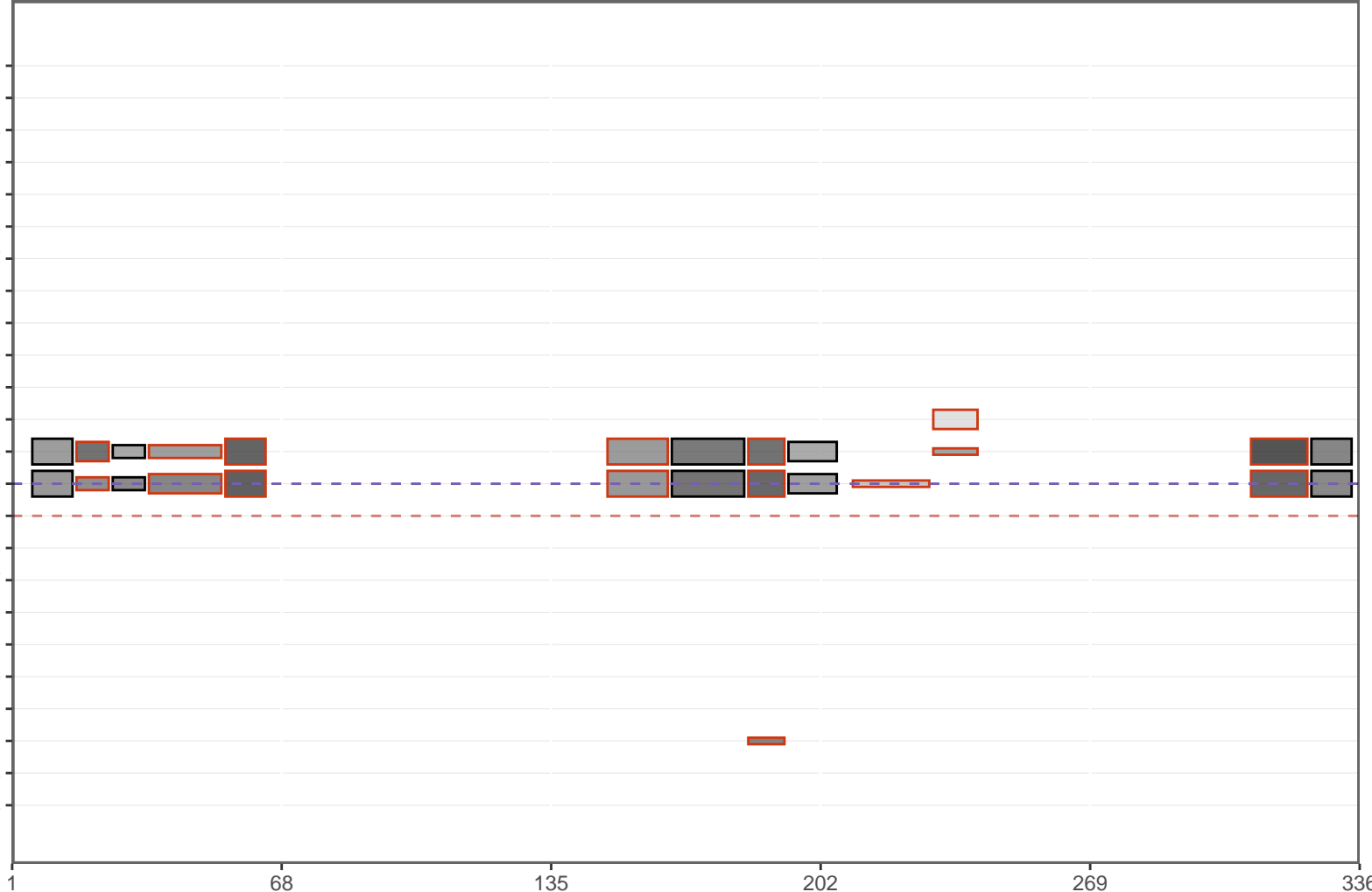
MW indication



Molecular weight

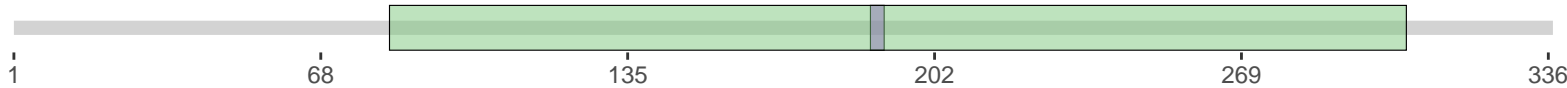


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

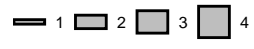


Protein sequence:

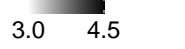
PVILNDYADFNRVFLUGDSGGNHWQAVRAGEENLSPMLRAGAIPIHPGFRVSRYSRKSSELEGEQTFLLDMVDKFLGLALPEGSNKDHPITGPMGEPQAVVEELKLPVLYVCMAEKDLKIDTEMEFYEAMNKGKDELVEFINGVGHSPYLNKIAVEMDPIVTASETKLYEVAEAFISQK

NbL02g17670.1 probable_choline_kinase_2 [MW = 40.55 kDa]

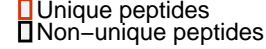
No. of times detected



log(intensity)



Values from



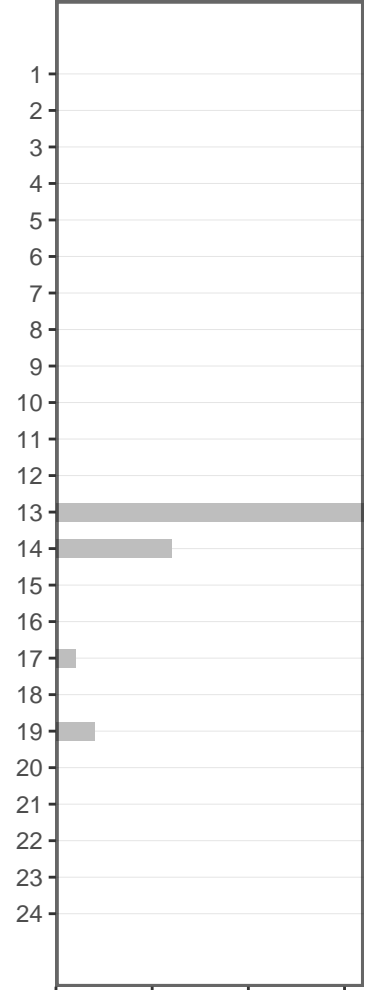
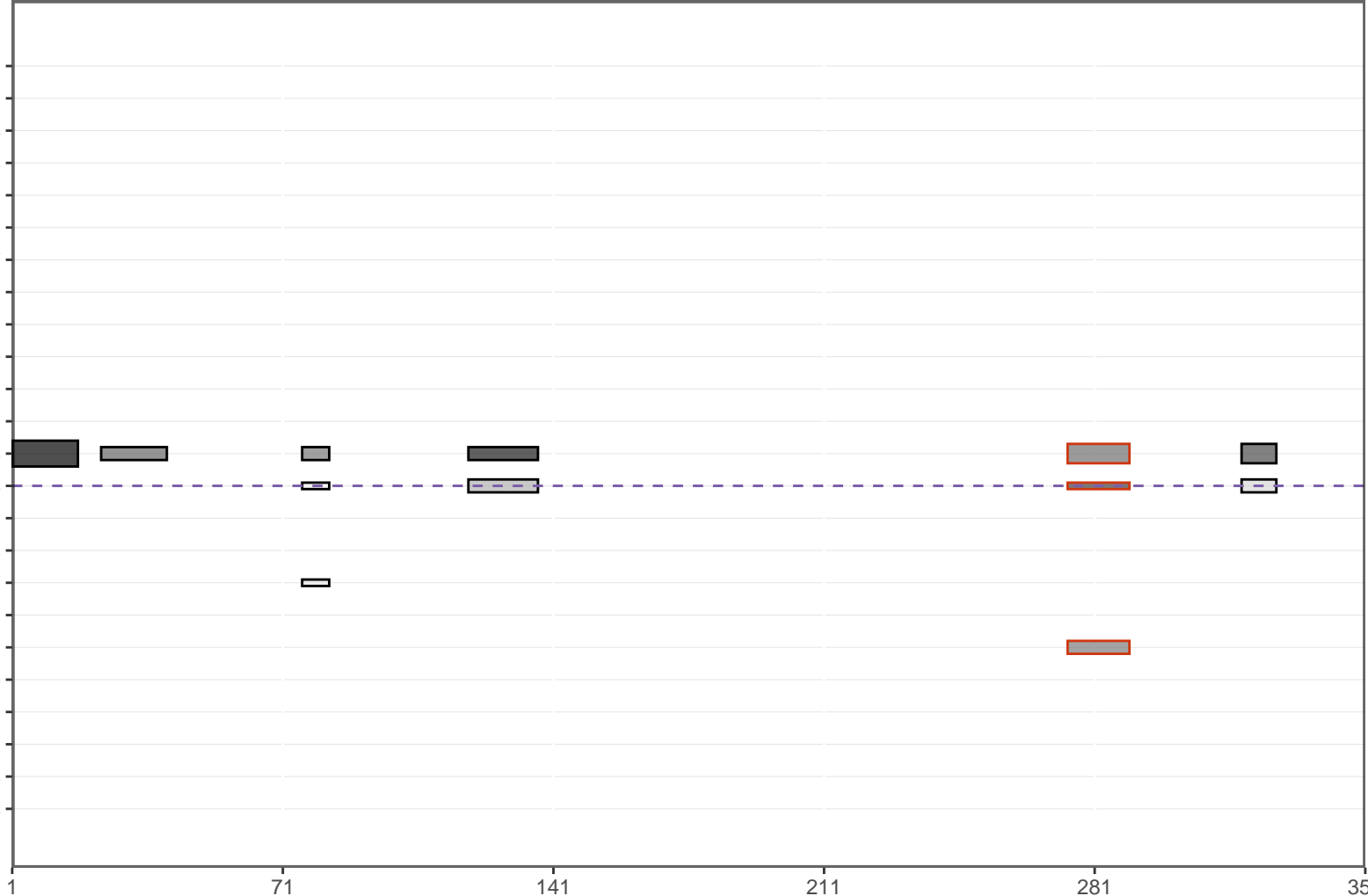
MW indication



Molecular weight

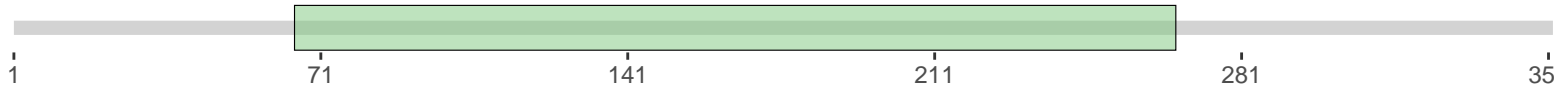


Gel Slice



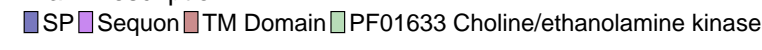
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

.INAVKRLASAEELKDFQLNHLVEVLSLEKSLAGNHLGSMGFHNDLQVGNIMMDEEIRSFITFDVEYAGYHNHAFDIANHFCEMVDYHTETPHIMDFSKYPLGLEERKFRFRALVSSGGSPSEGEELGKLAQVEKYLASHLFWGLWGHSHHVNKIDFNLEYARGRFGPIYWKPKPELLGSSGPKKGG

NbL02g17620.1 flavin-dependent_oxidoreductase_FOX2-like [MW = 62.15 kDa]

No. of times detected



log(intensity)



Values from



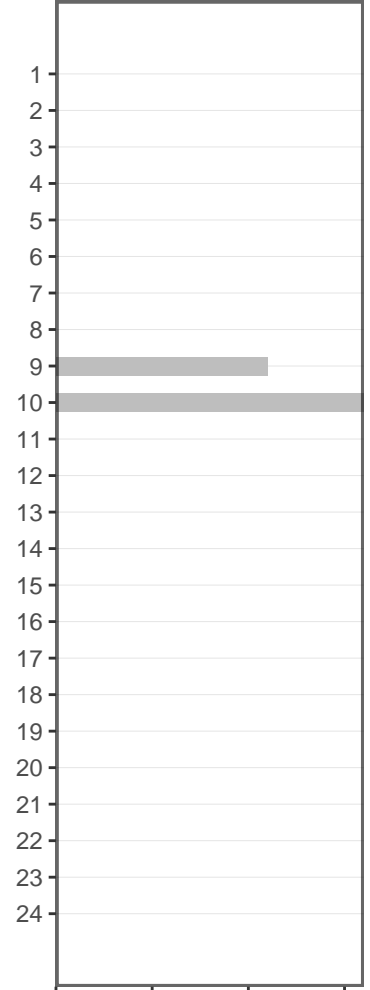
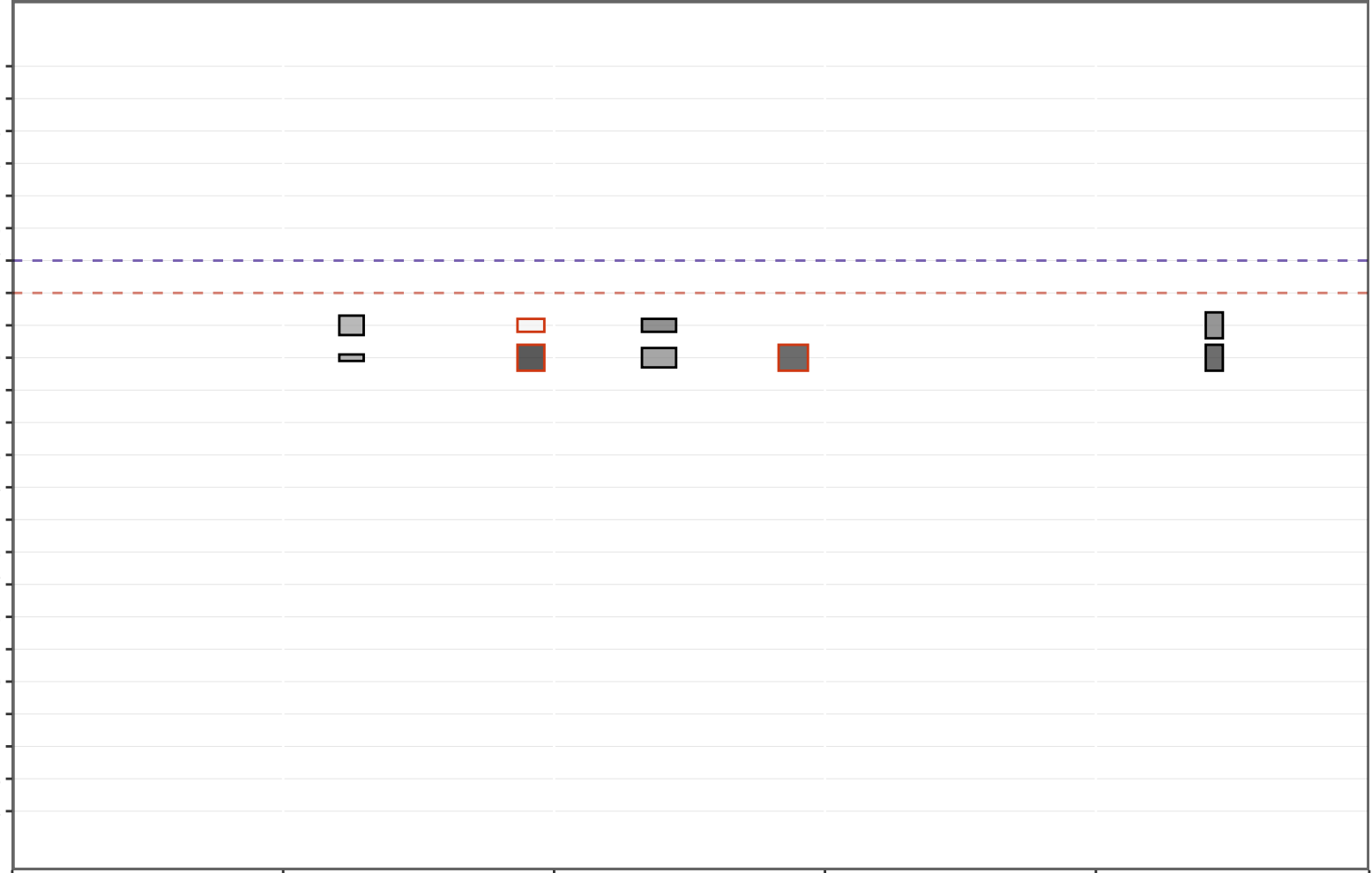
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

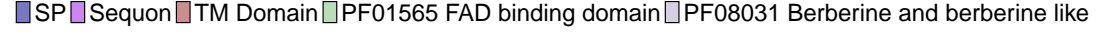


Protein length



Pfam domains

Pfam Description



Protein sequence:

TVPKLETGATKYLKWKQHWAKRDEDLFVRLVLTANSTKTKTKTQVAYQALFLGKTRDLHVMNHSPFELGLTGKDCVEMSWIESVYHAGVPSBKPEFLGKSLFPPNFKAKSDFLRIVFVPEGLDGMWKKFLEDDSPMMIWNPNVYGGMMKGIKSESSIFFHRKGVKIKQVLTQWTEGAKKSDKHNRWIRGLVEYMGTFVSKFPRKAVVNYRDLGLMNRNANSNPLEASVWGKKYFKNNYDRLLVAKTKVDPDNFFVHEGSLPLRLKVKGDKGKSLIIF

NbL02g17590.1 probable_ribose-5-phosphate_isomerase_4_chloroplastic [MW = 31.49 kDa]

No. of times detected



log(intensity)



Values from



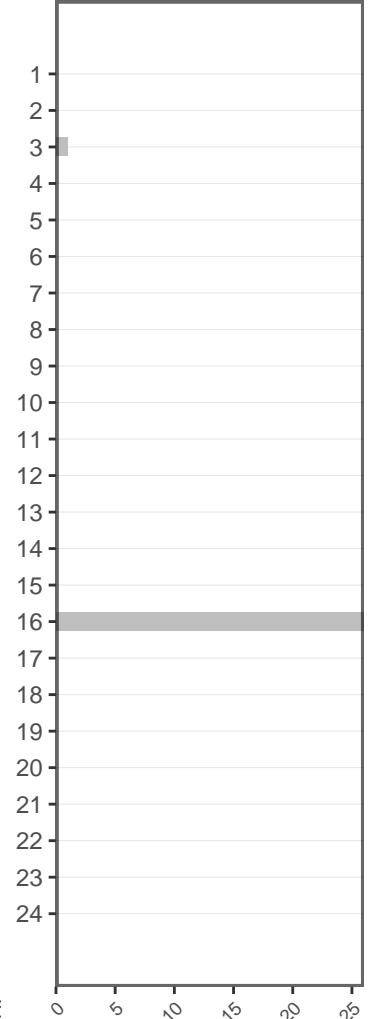
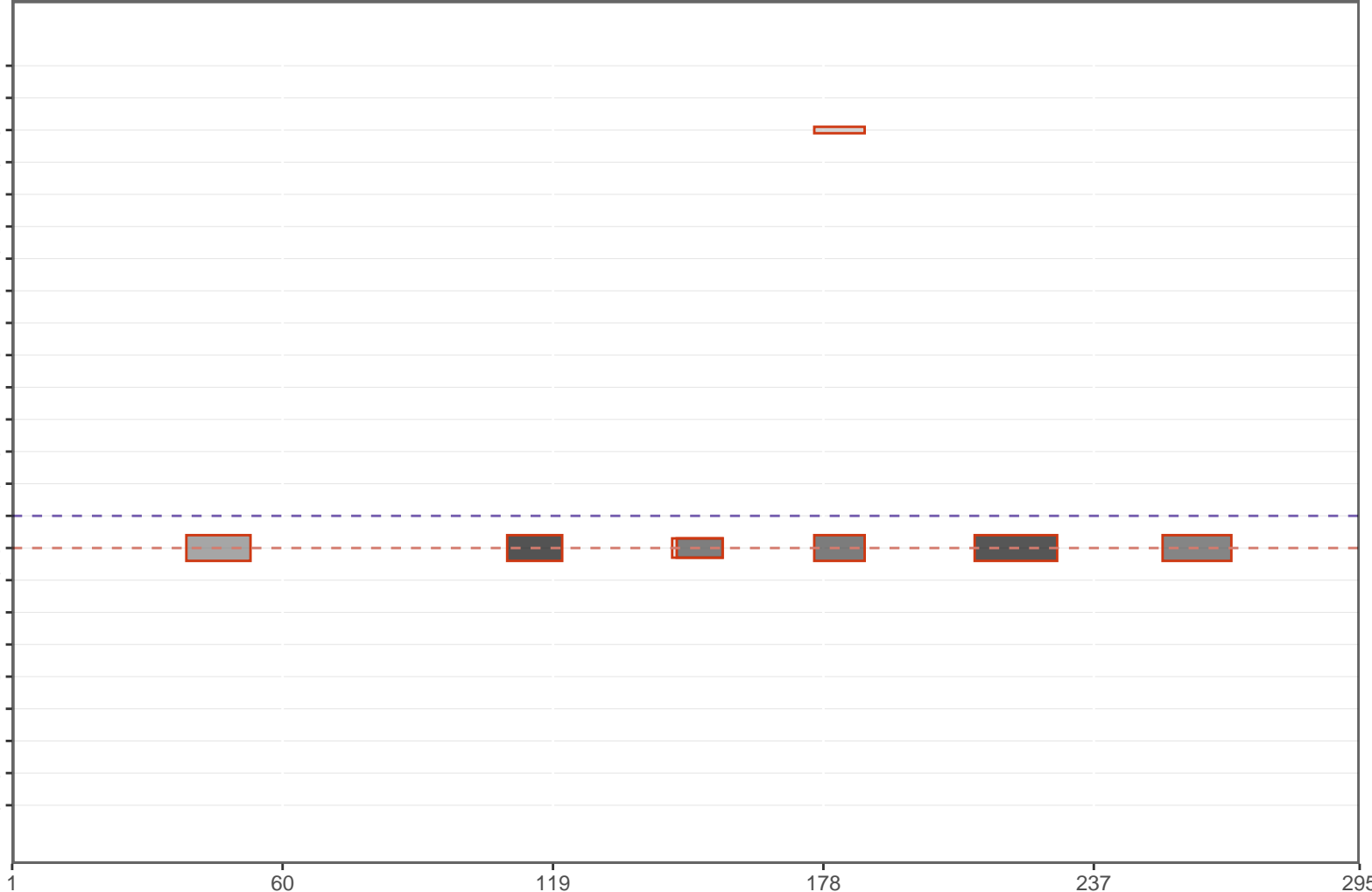
MW indication



Molecular weight

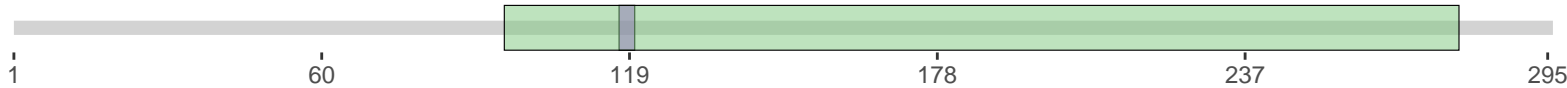


Gel Slice



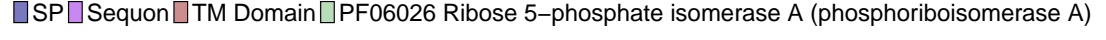
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TMEETLAIIGRRKRLGGDDSDIGEKIIEAADKLIKIKKPKGSDGSIPLKISVNWLETAEEIDKFLGDAEIVRRPPIAGPLGGDFLVTKEGHNLIDVFTSPMEISLVEVAKTLDDGIDGVVEHGVIFRNPCTARIVSENGLIADNTIEMESNL*

NbL02g17580.1 coatomer_subunit_epsilon-1-like [MW = 31.94 kDa]

No. of times detected



log(intensity)



Values from



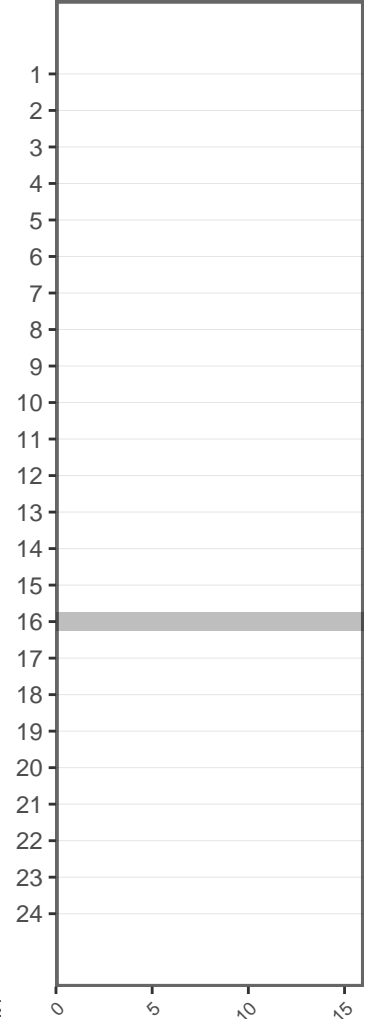
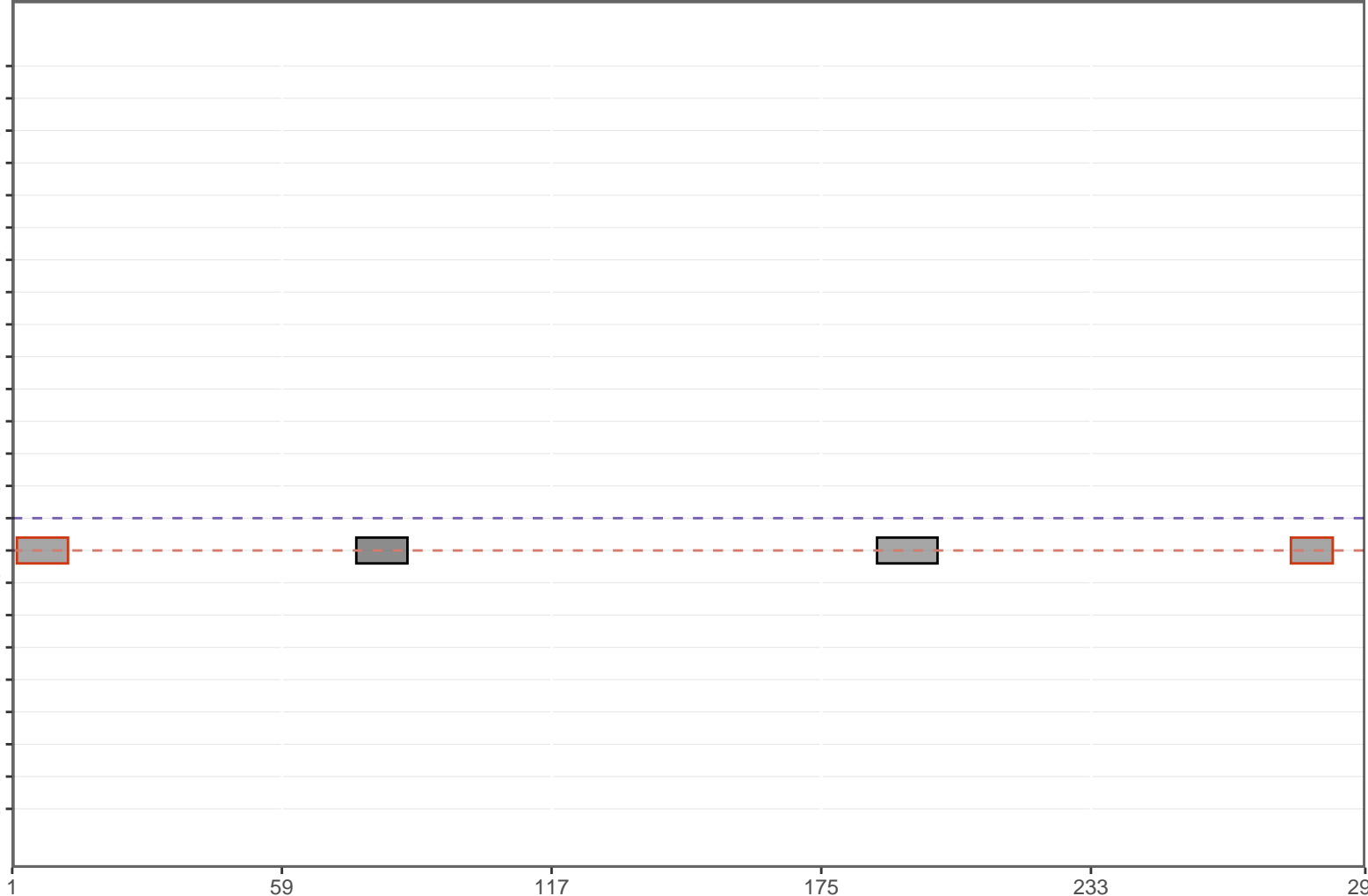
MW indication



Molecular weight

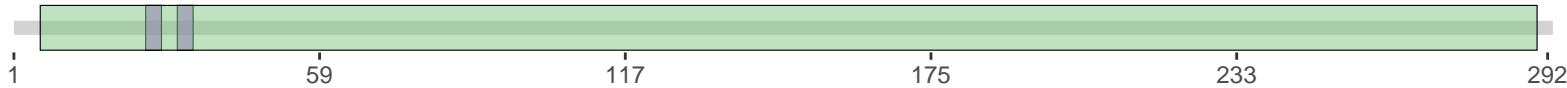


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MELIHALNVLQILKIMHRSDVAEKGLRIMQGVDEDHITLQLANAWLNLAVGGSKIGEAFLIFGDFSEKYMVMTSLNLNGKAVGDMHMGVDFEAETLLELALNKDADKDPETLANLVGSLHGLKPSARYLVNQLKLSHPDHALVKRAASAEESFDRAVGVVA

NbL02g17470.1 photosystem_I_reaction_center_subunit_III_chloroplasti-like [MW = 24.98 kDa]

No. of times detected



log(intensity)



Values from



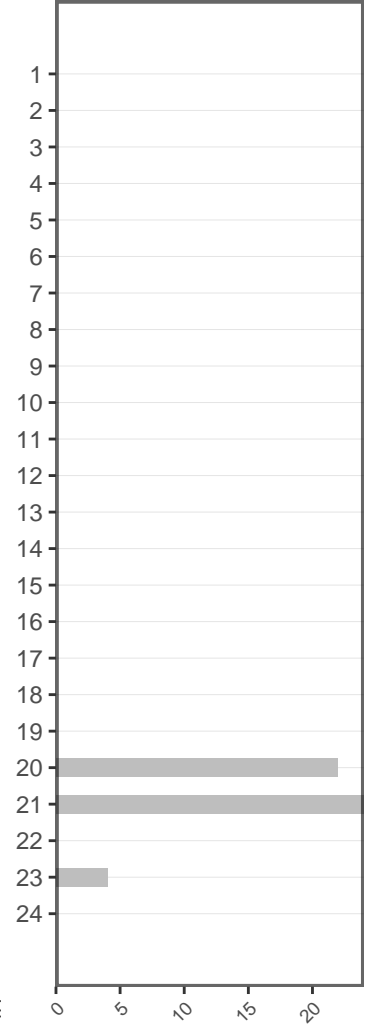
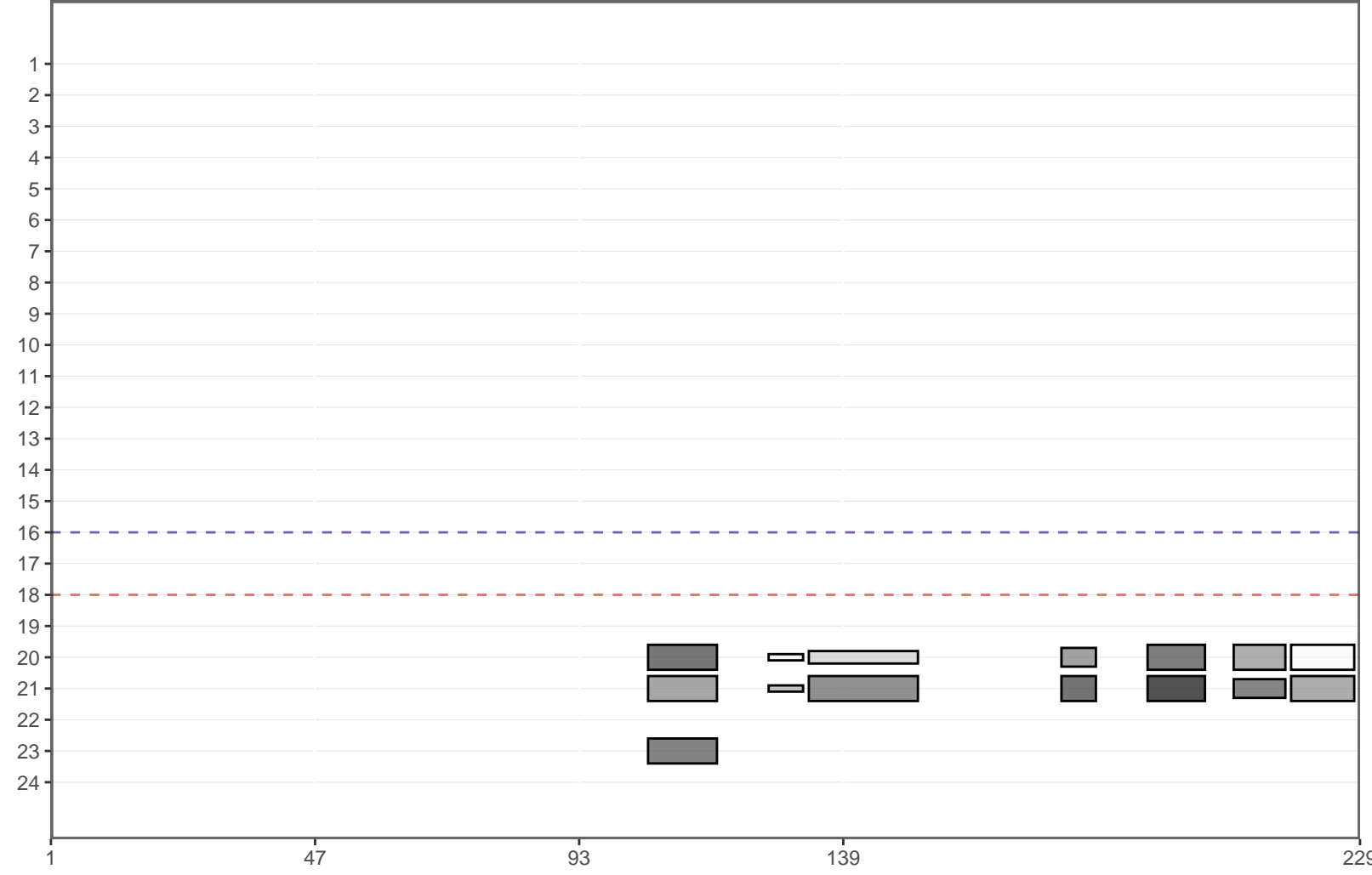
MW indication



Molecular weight

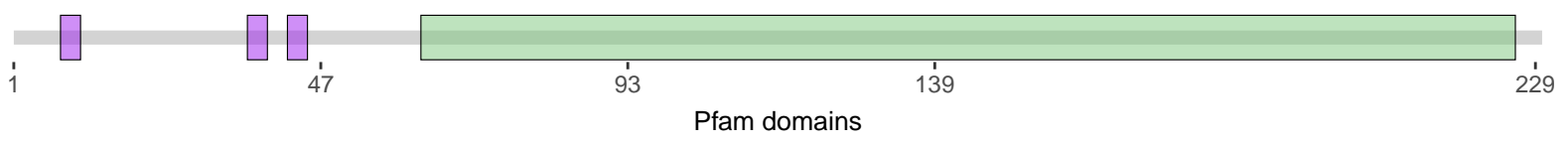


Gel Slice



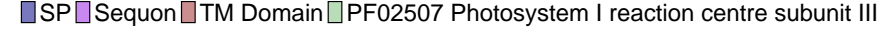
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SKLYAPDSAPLAKATVEKTRRFDMYGGKGLGGSDGLPHLVSGDQRHWGEFTTGGILFLVAGWGWVGRSYLAVRDQKPTMKEHIDVPLANKLWRGFSWPAVAVREFLNGELTQNF

NbL02g17430.1 haloacid_dehalogenase-like_hydrolase_domain-containing_protein_At3g48420 [MW = 41.48 kDa]

No. of times detected



log(intensity)



Values from



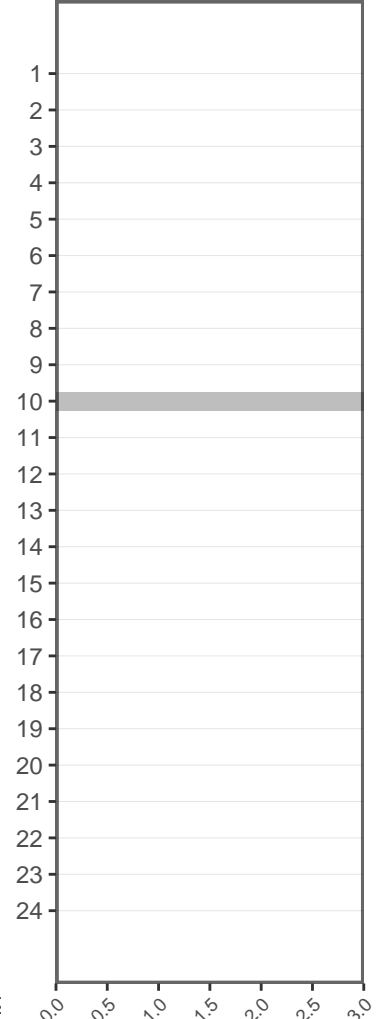
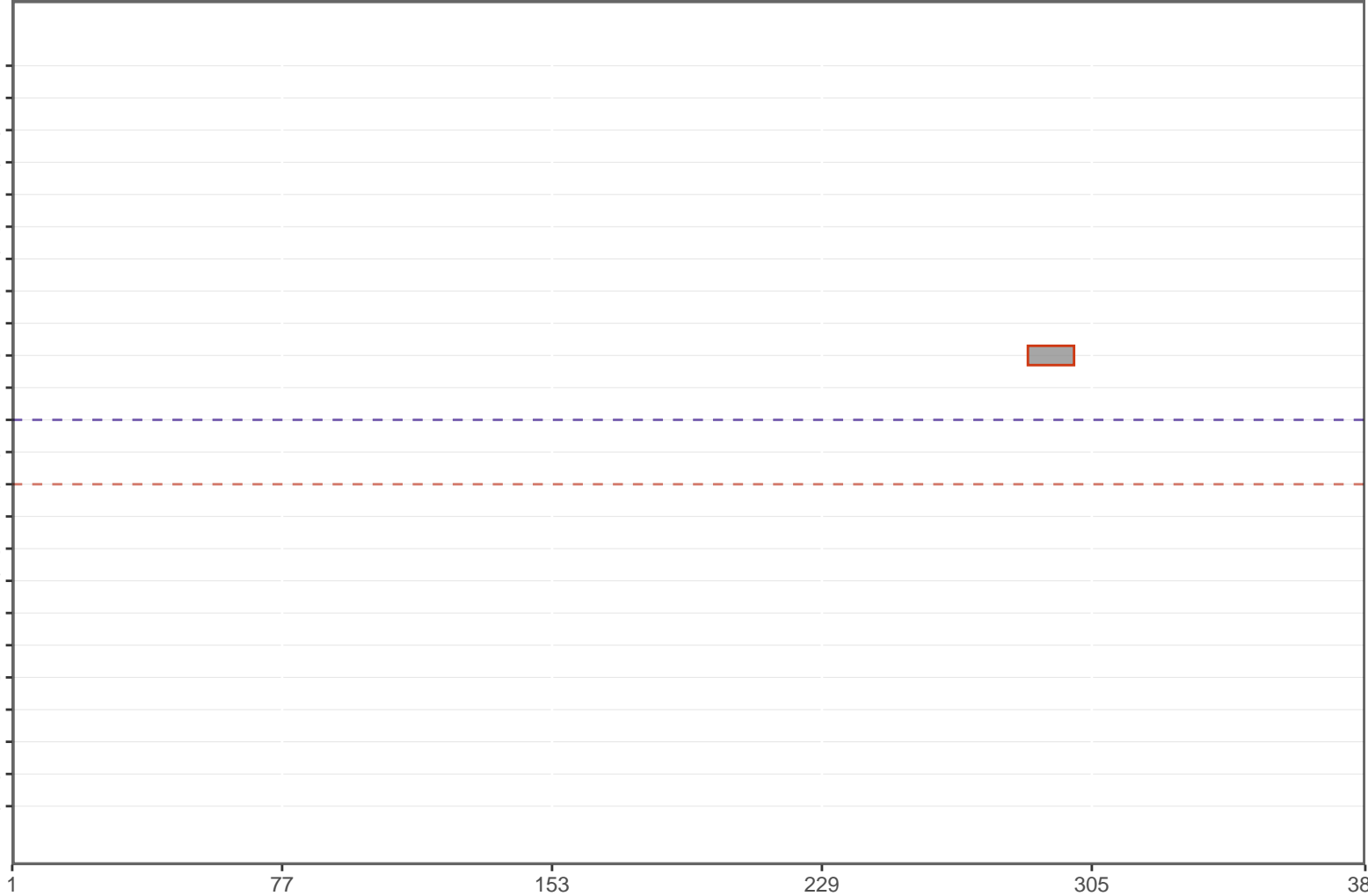
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

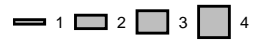
Pfam Description
 SP Sequon TM Domain

Protein sequence:

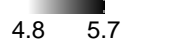
MSKSLPLRPDYEFIDEAYEEGVVPMILTSYKNGKGEKPARSIEKLGNDKMARIKLGMEEVKQGFYGLVFGGGVASDLGEQLAKARKAVSAEEQRIAEVASKMLKLVYDHTTSSSEEMKNVVAALRAGAEYANVPYDNGVWAGSGGVAEGERIGMDCVWVRSSSETARAFFPGAKAMDFGGGDLISRLRQIQGLDL

NbL02g17230.1 cathepsin_B-like [MW - SP = 36.66 kDa]

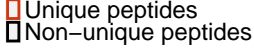
No. of times detected



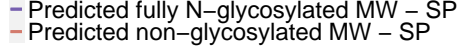
log(intensity)



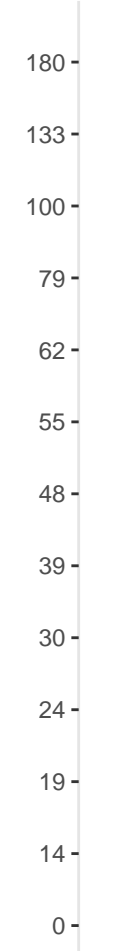
Values from



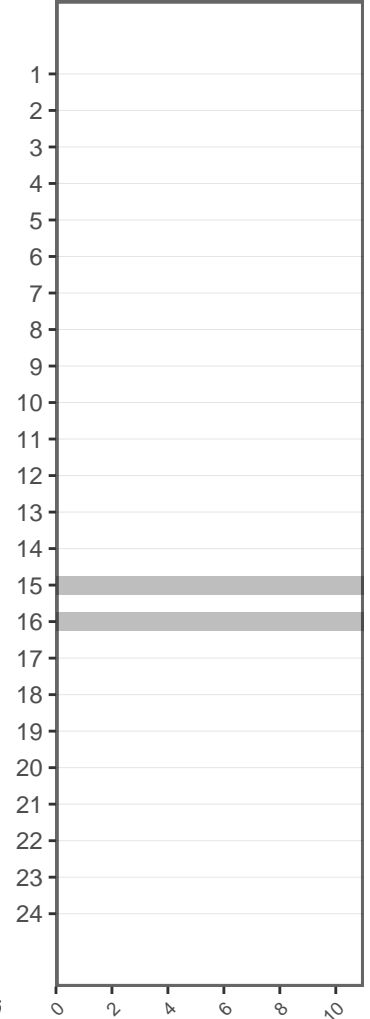
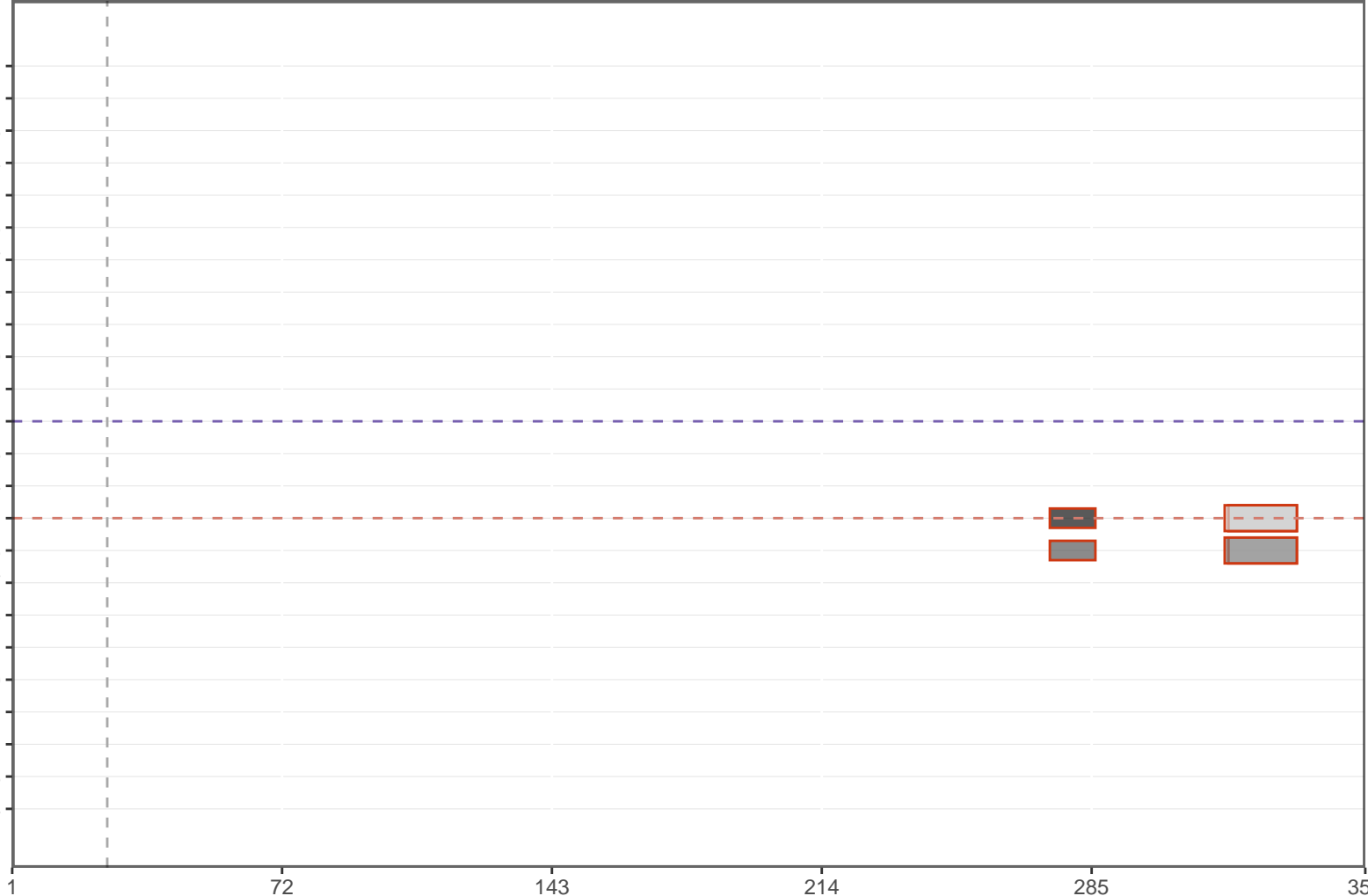
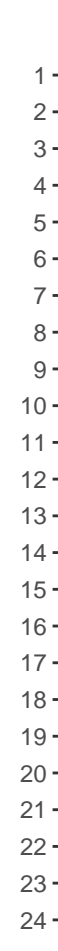
MW indication



Molecular weight

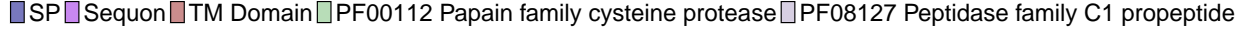


Gel Slice



Pfam domains

Pfam Description



Protein sequence:

GGGYPLQAWKYFVRLKGVVTDGDPYFDNEGSHPGCEPWPPTPKGHRKGVKGNLWISKKHFDGYNAYMISGDPHSIMTELYKNGPVEVFSFTVYEDFAHYKSGVYKHVTGDVVMGSHAVKLVGWTSEDDGEPYLLANGWNRKGVGGDGYFKIRKRTDCECEIEDEVVAGLPSARNLNMELDVSDAFLDAMV

NbL02g17190.1 phosphatase_IMPL1_chloroplastic-like [MW = 39.43 kDa]

No. of times detected



log(intensity)



Values from



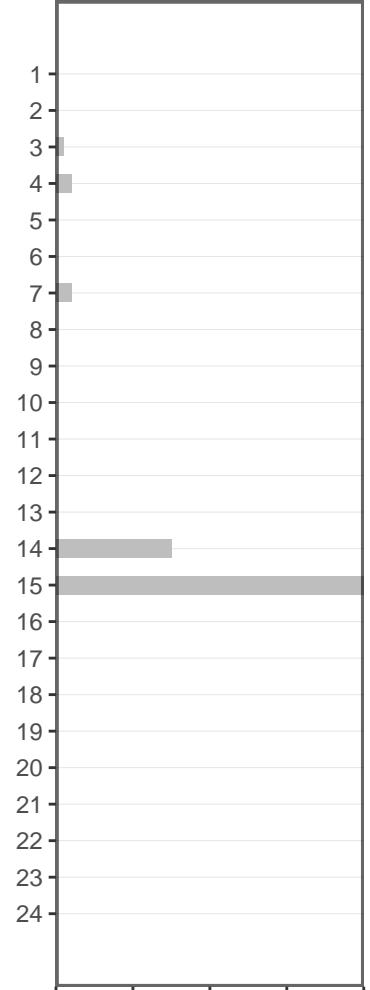
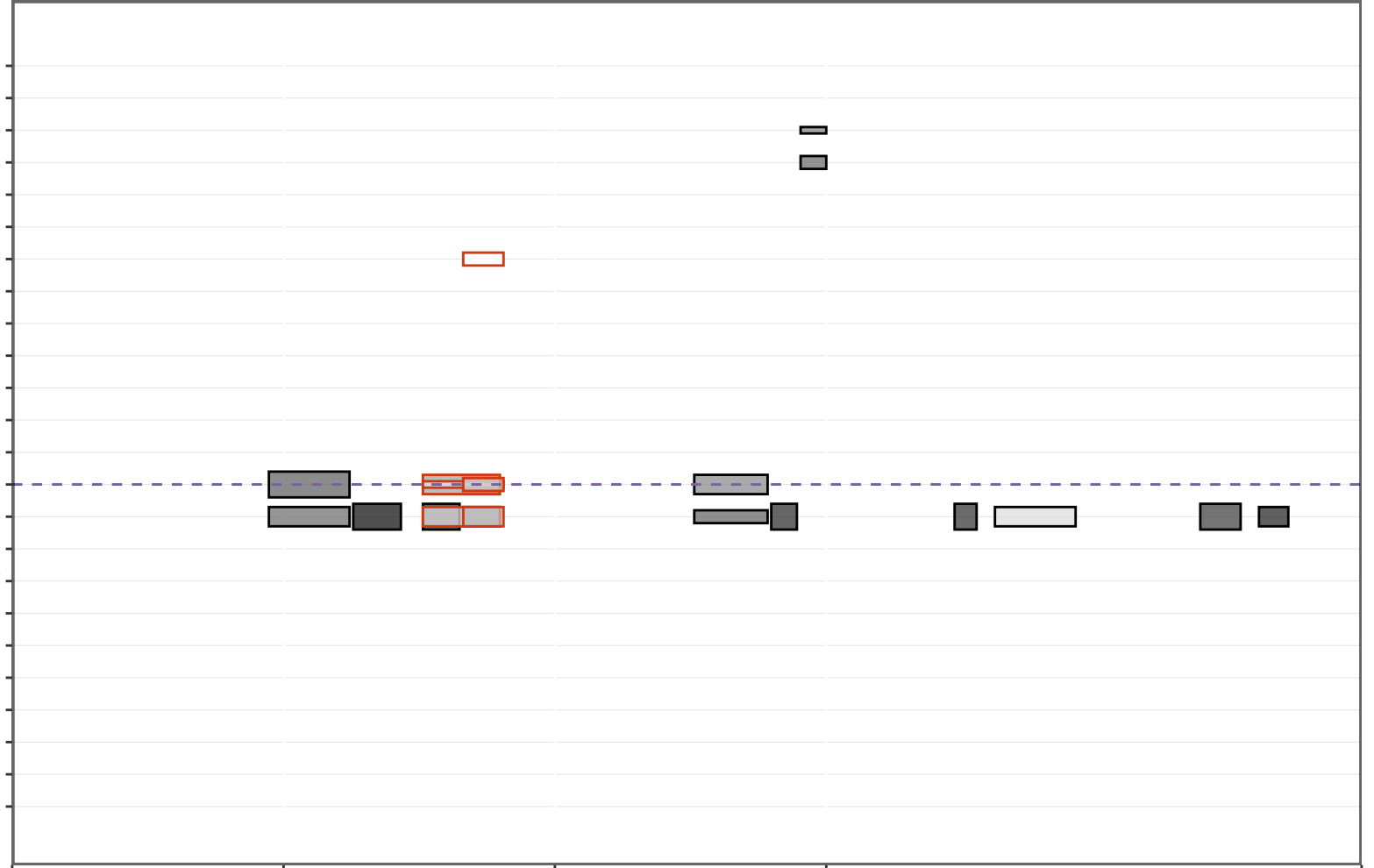
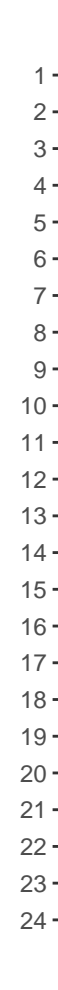
MW indication



Molecular weight



Gel Slice

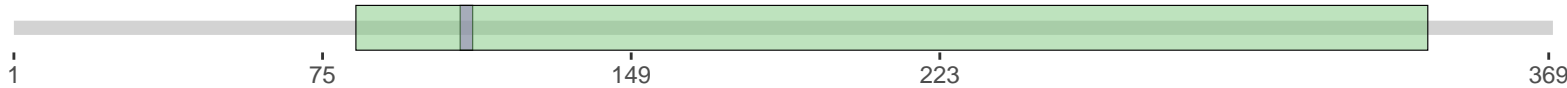


Protein length

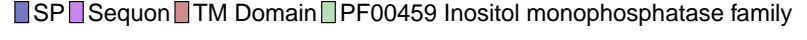
Peptide counts over 4 repeats



Pfam domains



Pfam Description

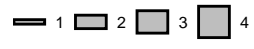


Protein sequence:

YPSFAVSYGVLFRRGKPAATVVEFGPMQWNRIFSAAGKGFANRKHVSGTKVEGELLVTFGGYDHDIPWATNMEFKDFDVRGRVRLGAAAVDMGHVAGIAEAVWEYRLKPWDAAGVLIIVEAGGTVSCMDGGKFSVDRSVLVSNGLLHAKLLEKIPRTENLAKKIDFSVWFKPENHYHTEV

NbL02g17160.1 cytochrome_c6_chloroplasmic [MW = 25.78 kDa]

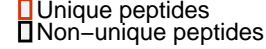
No. of times detected



log(intensity)



Values from



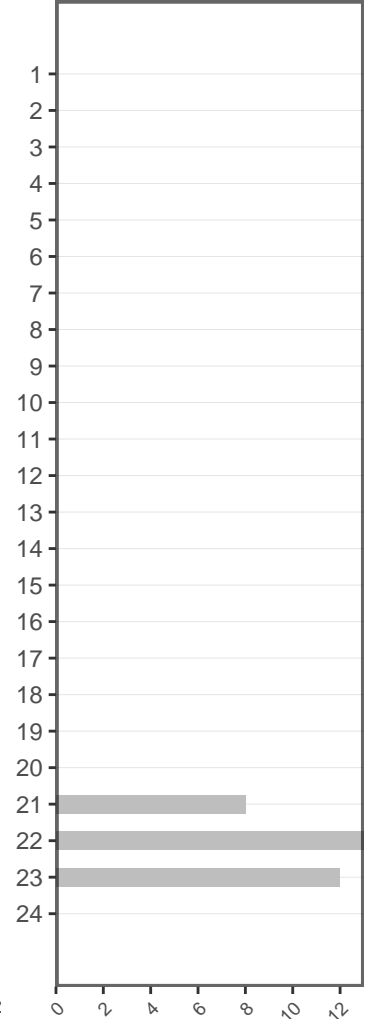
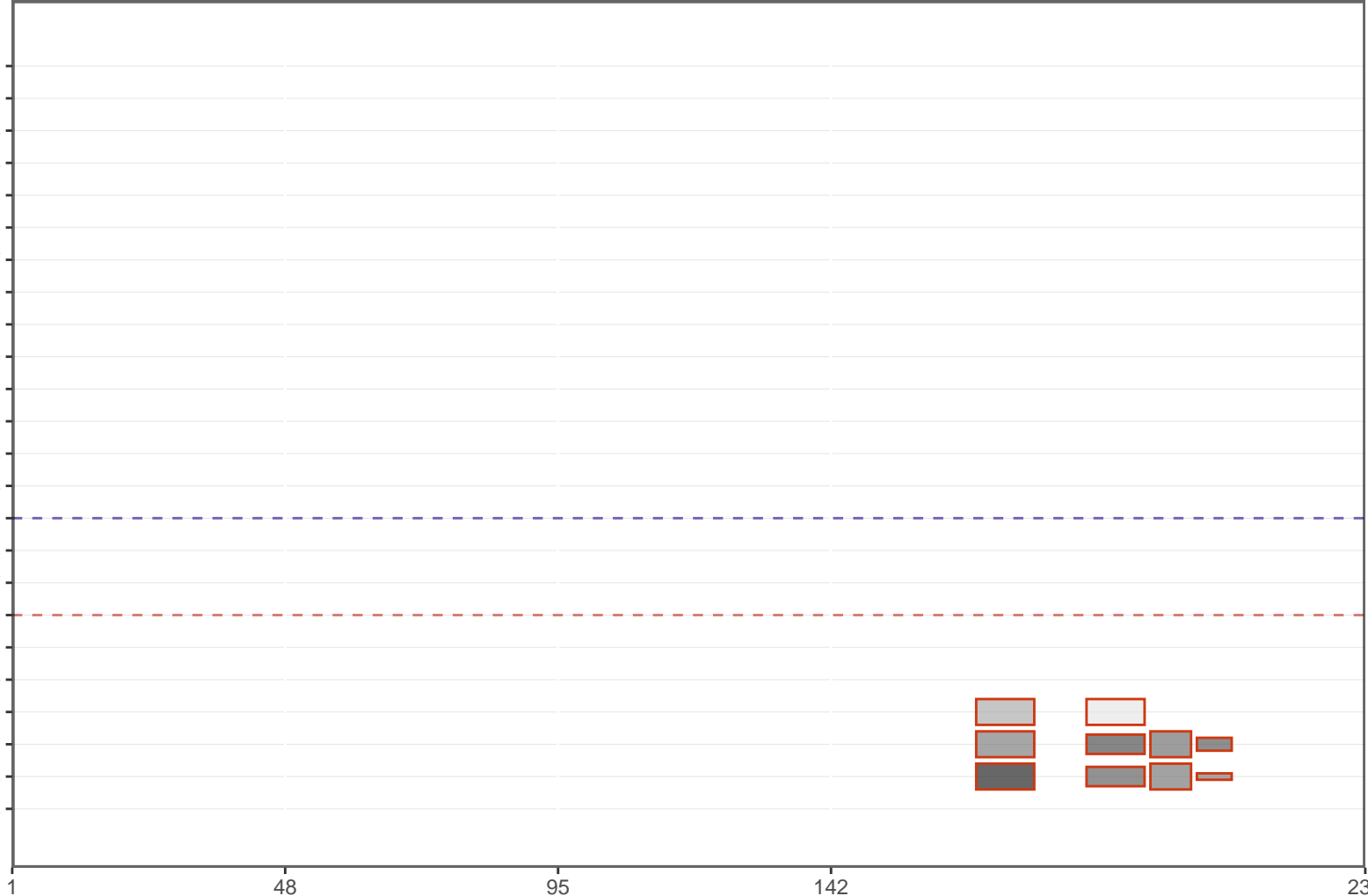
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

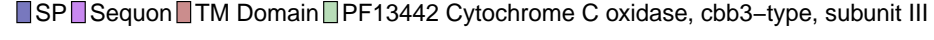


Protein length



Pfam domains

Pfam Description



Protein sequence:

.APPLMTALIAFSPYVPPVGVGTEIVQKGAALFSKACIGGHVGGNIQPGATFLKDLERNSADTEEEVRFVYKGRMPFGGNGTRGGCTFGRPLGGDEIKLVEFVKSGADGGWPKIENSGD

NbL02g17130.1 glutathionyl-hydroquinone_reductase_YqjG-like [MW = 41.25 kDa]

No. of times detected



log(intensity)



Values from



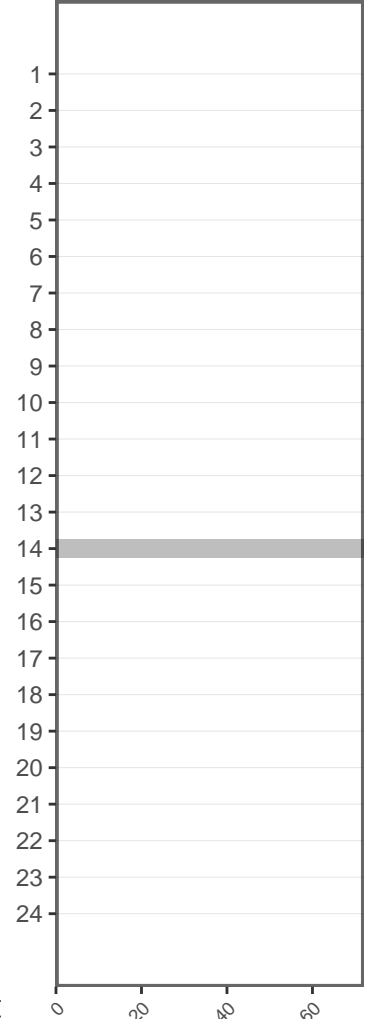
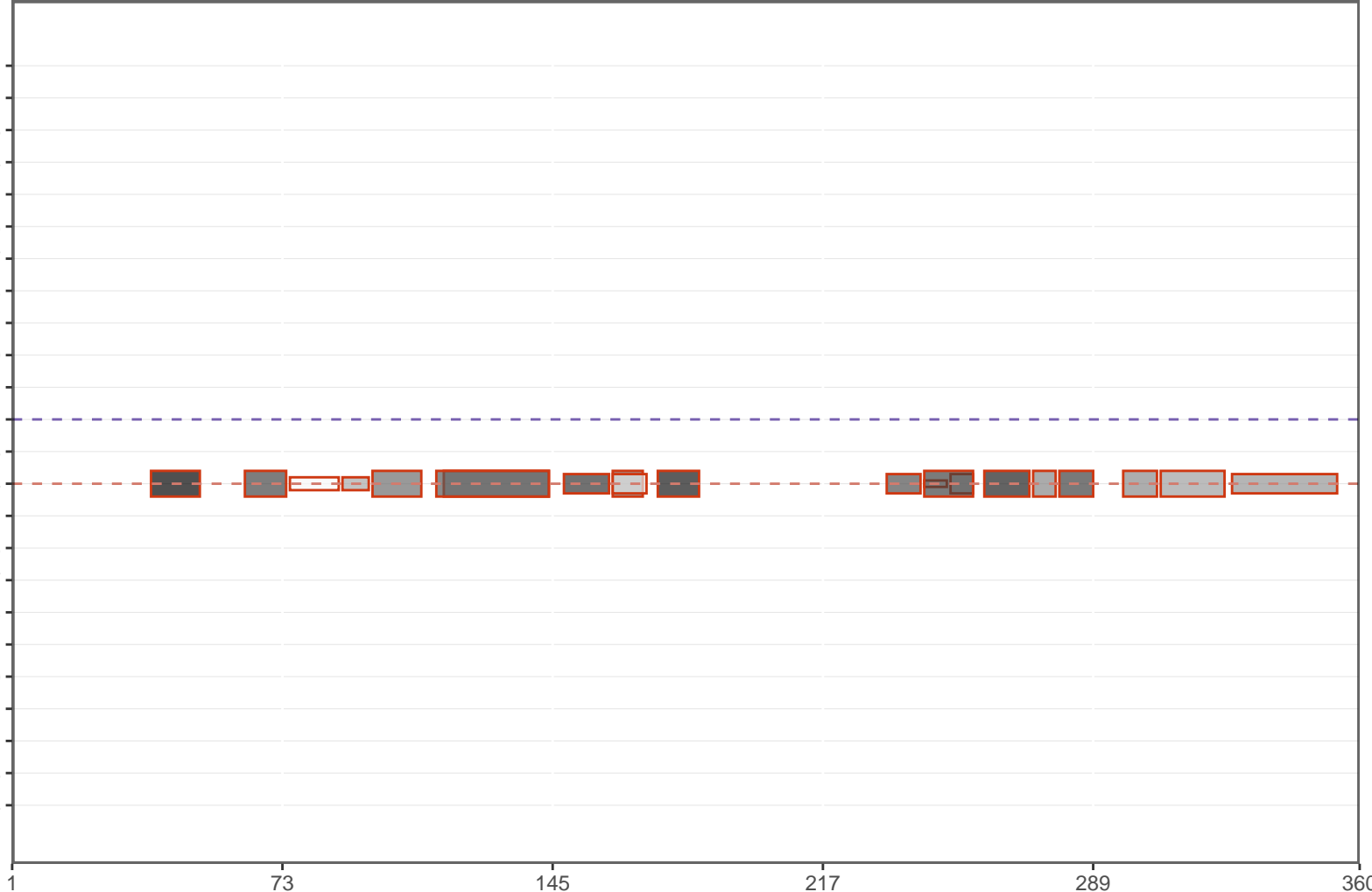
MW indication



Molecular weight

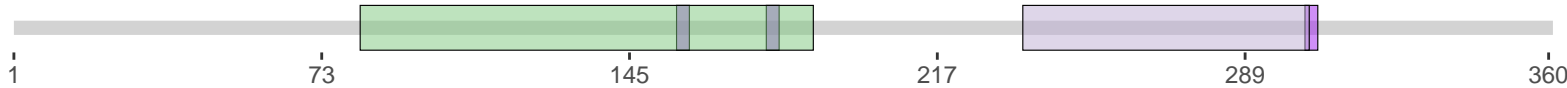


Gel Slice



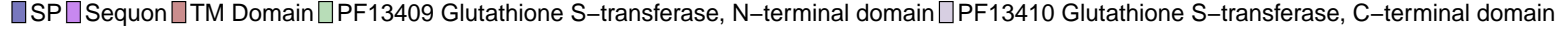
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

/LWDKLLKLTIVNNESSDIRMFENSEFNDSGNALDLYPPHLGGDINEEWYDGINGVYRGGFATKQEPYDEAVQKLYETLDKGMILSKGRFLCGDGVTEADIRLFTLIRFDEVAWVFXGNKLLREFPHLNYTKDFGIPGMSSTVNMHEIKKHYYGSHPTNPYGFQGPNDYSSPHIDREKFSK

NbL02g17080.1 50S_ribosomal_protein_L30-like [MW = 12.39 kDa]

No. of times detected



log(intensity)



Values from



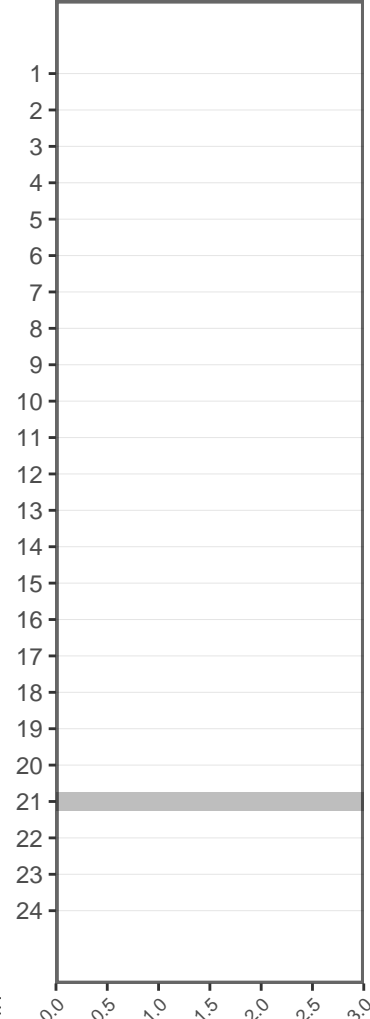
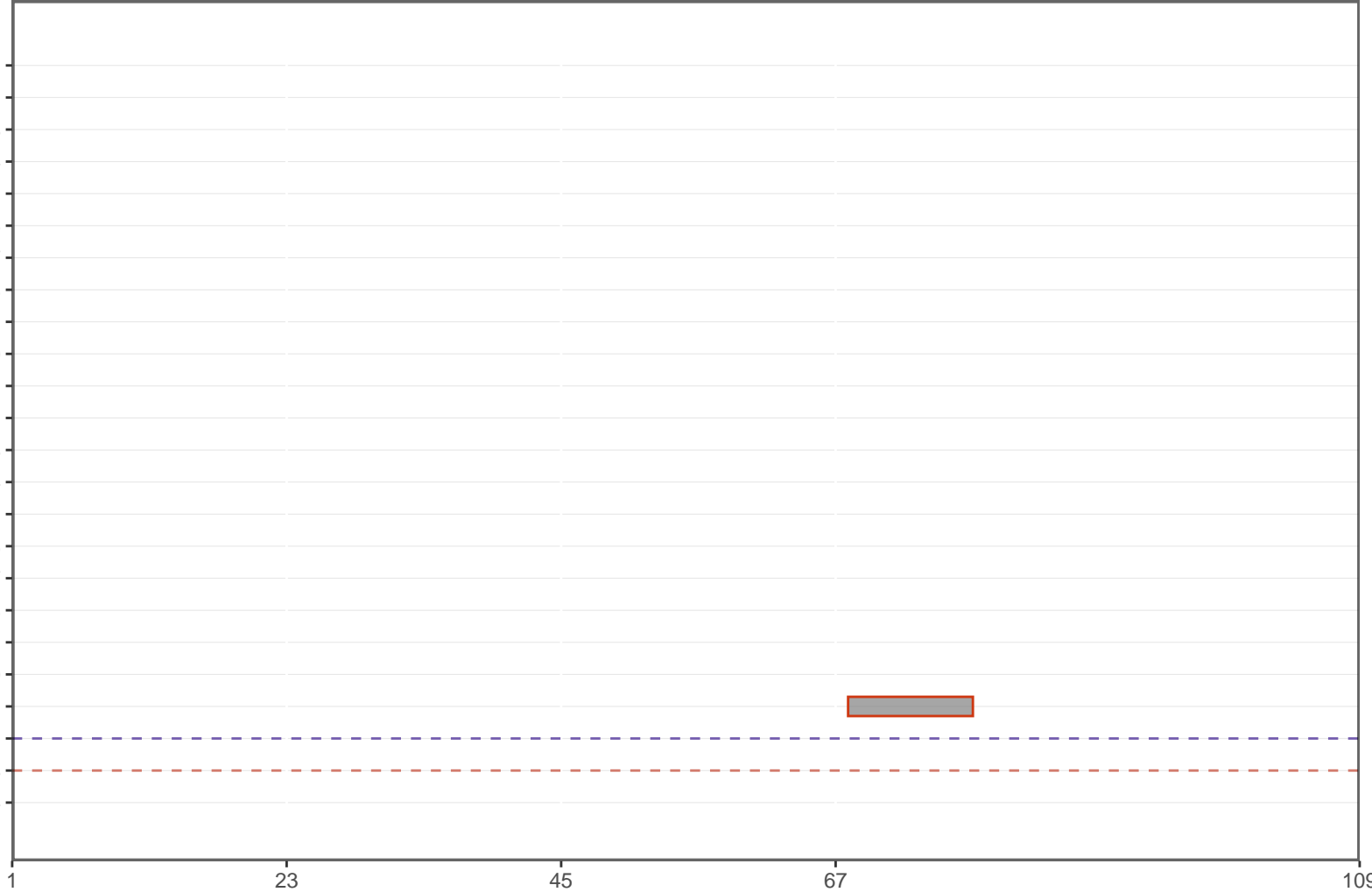
MW indication



Molecular weight



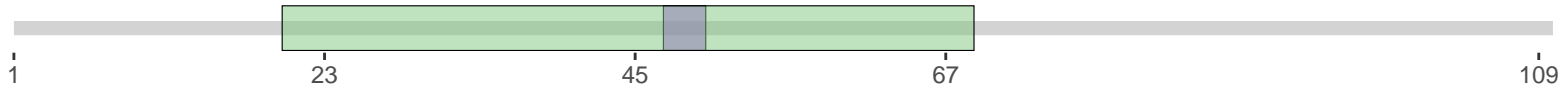
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

LRKCNRTVMRWNTPTVIRGMLGGVKRLVWVETEEMKARKEKLADHKAIRPLVNVNHAAPIADSVL*

NbL02g17040.1 14_kDa_zinc-binding_protein [MW = 19.69 kDa]

No. of times detected



log(intensity)



Values from



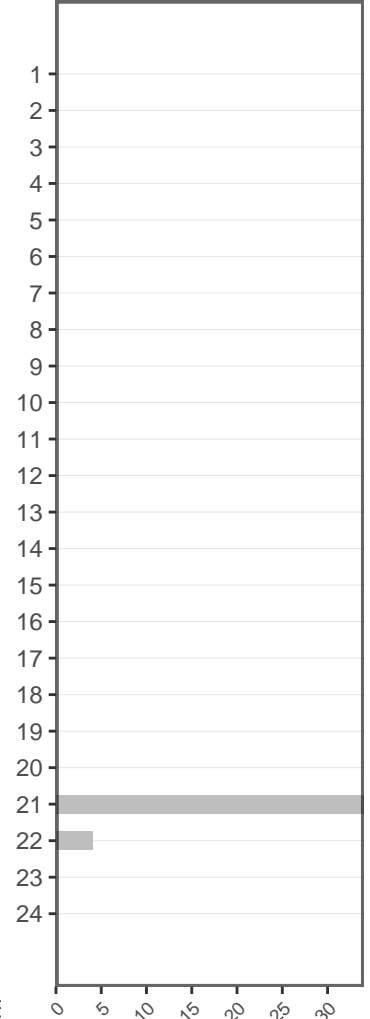
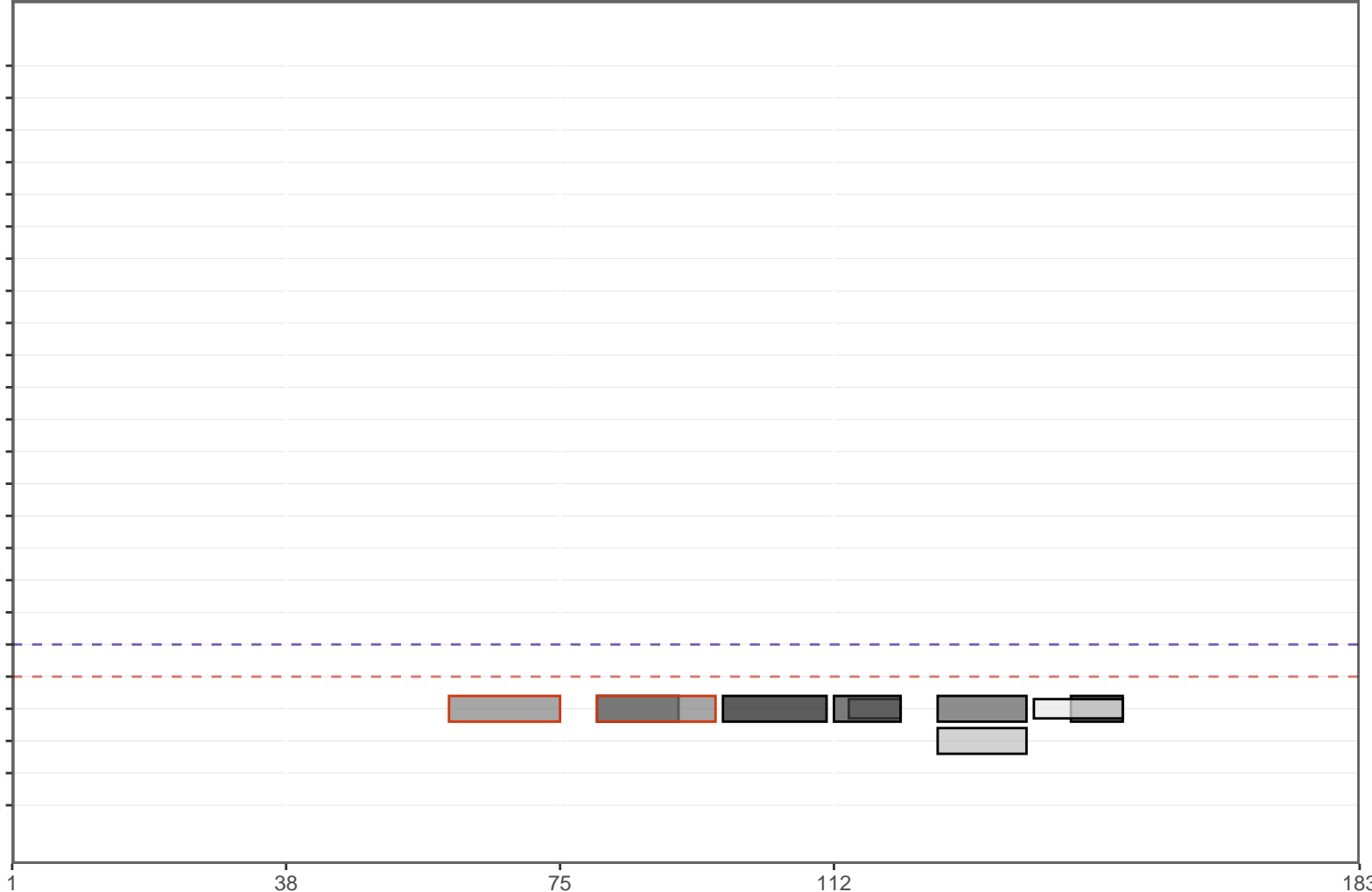
MW indication



Molecular weight

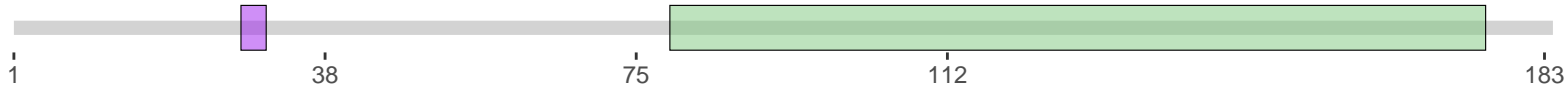


Gel Slice



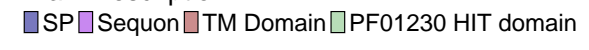
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

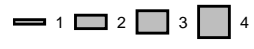


Protein sequence:

CEIPASVYVEDEKYLAFRDINPQAPVHVLVPLKLRDGLTELKKAQRHEDLGNLLVAAVIAEKEGIVDFRVLVNSGASAGQSVYHLHLVHGGRLKWPFG

NbL02g17020.1 tRNA_(guanine-N(7)-)-methyltransferase-like [MW = 32.8 kDa]

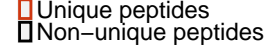
No. of times detected



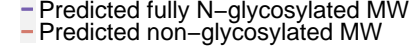
log(intensity)



Values from



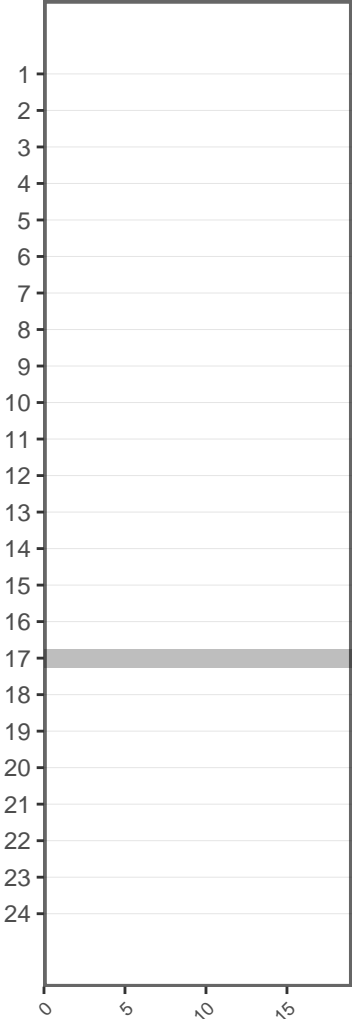
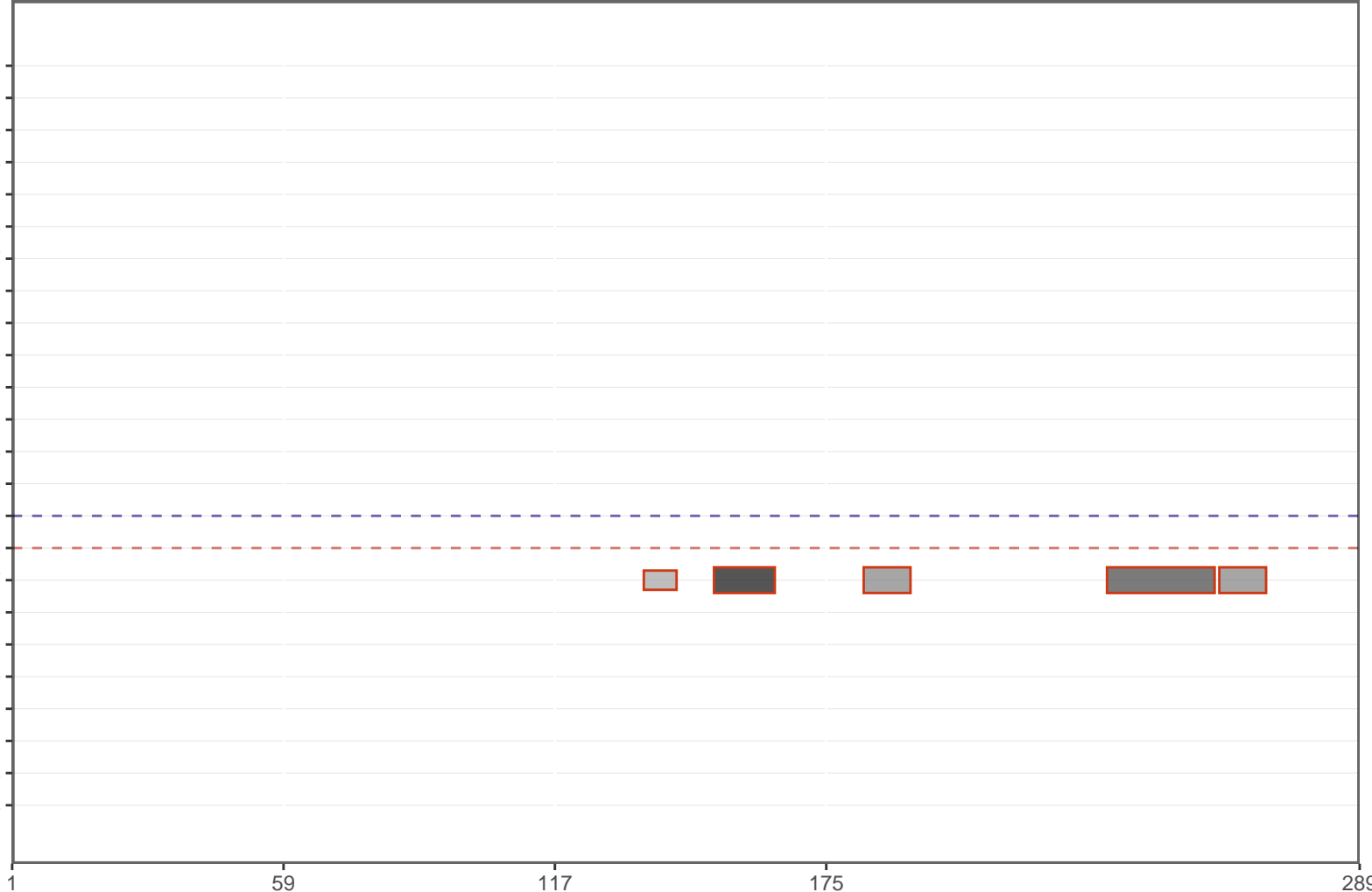
MW indication



Molecular weight



Gel Slice

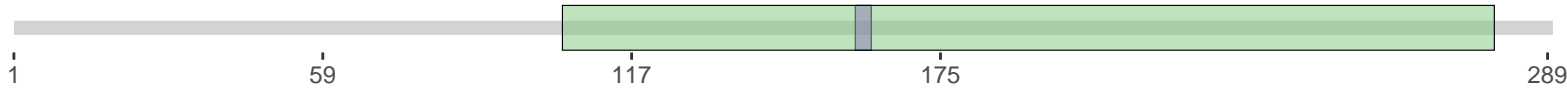


Peptide counts over 4 repeats

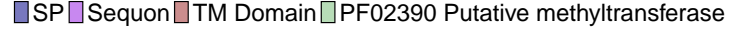
Protein length



Pfam domains



Pfam Description



Protein sequence:

VELRDKVTEYKERILGLRTTNPGGYQNVVYRTNEMKYIPNVFGKGLKQKMFLLFPDPHFKEKNHRRVRSFLLDEYAVYLVGGIYTTDVEELGEWMMKGLGELHPMFEPLTTELEADQVVKLLSTWEEGGKVARNDGGTFRVYRRIATH

NbL02g17010.1 pyrroline-5-carboxylate_reductase [MW = 28.93 kDa]

No. of times detected



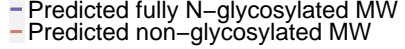
log(intensity)



Values from



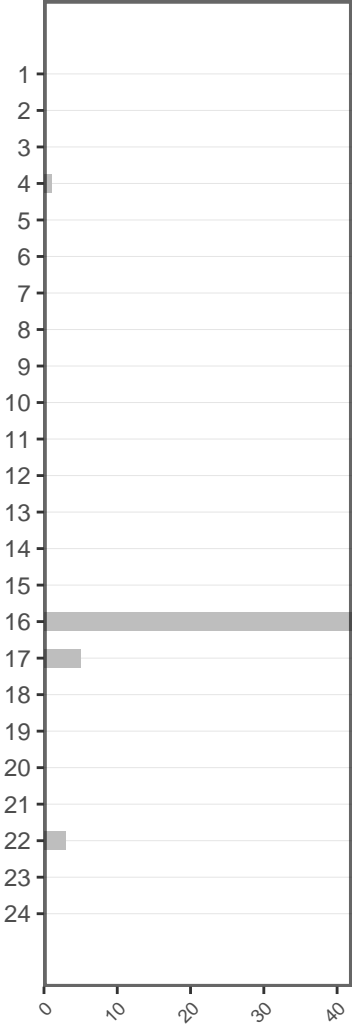
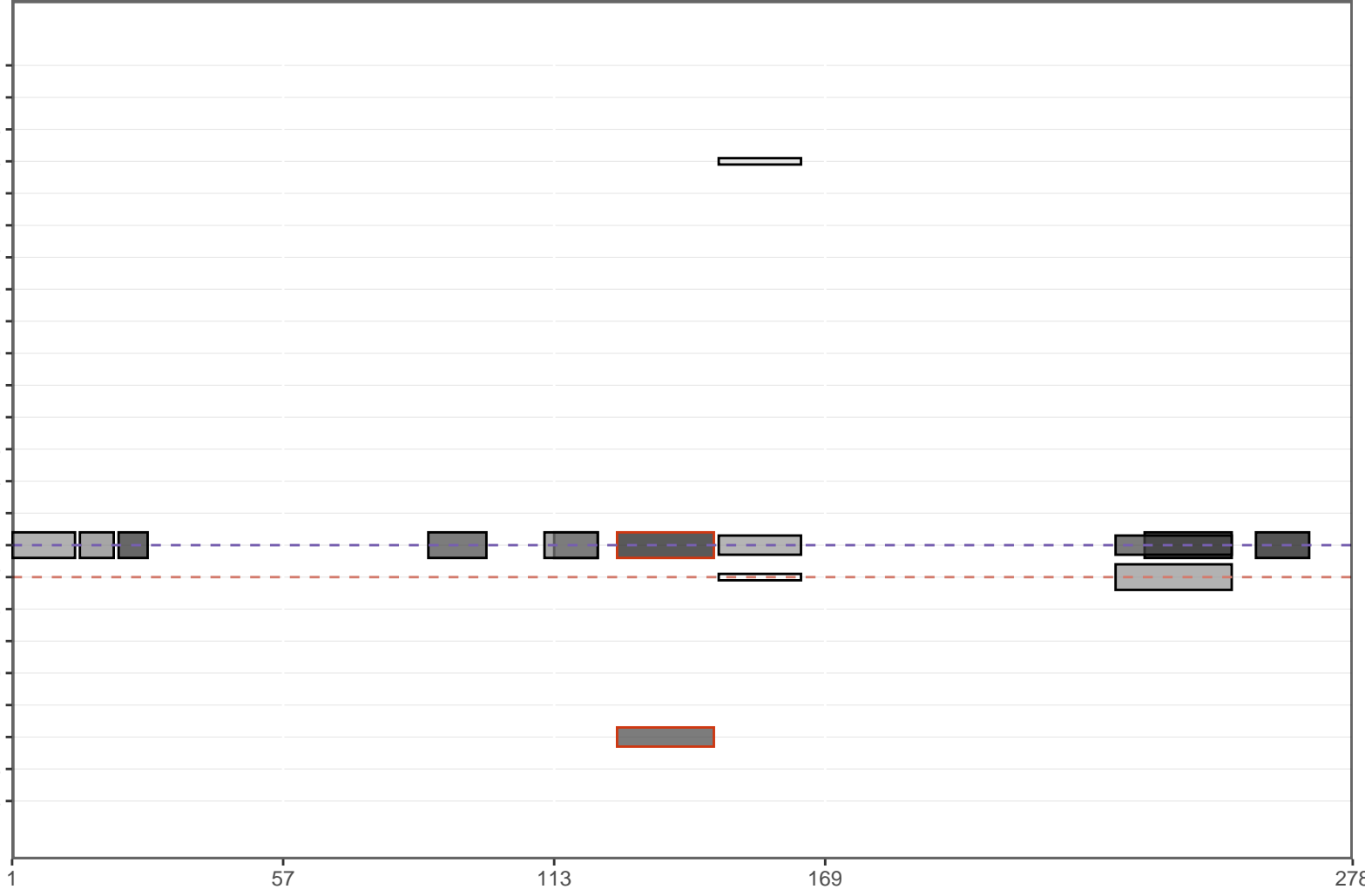
MW indication



Molecular weight

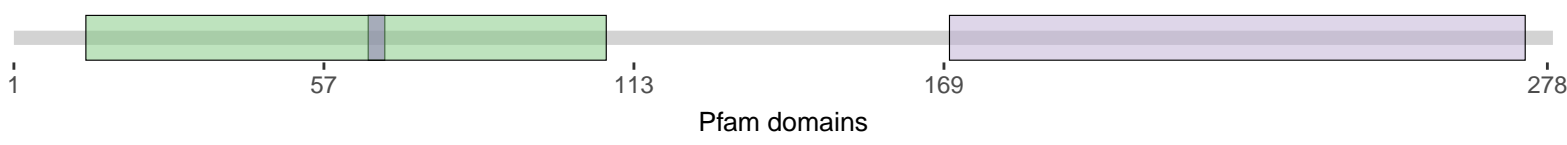


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

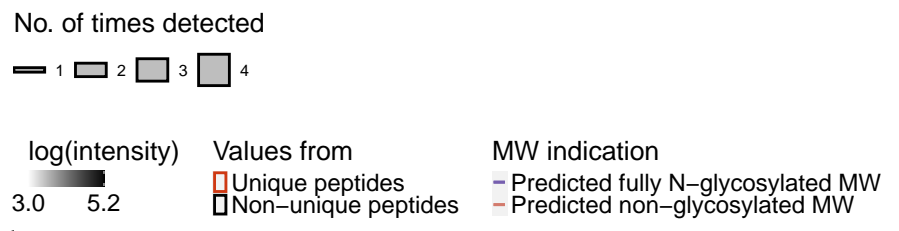
Pfam Description

- SP
- Sequon
- TM Domain
- PF03807 NADP oxidoreductase coenzyme F420-dependent
- PF14748 Pyrroline-5-carboxylate reductase dimerisation

Protein sequence:

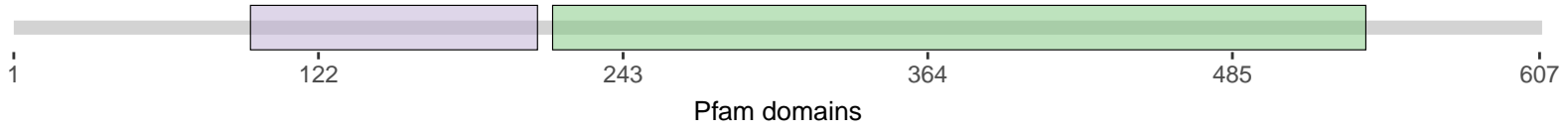
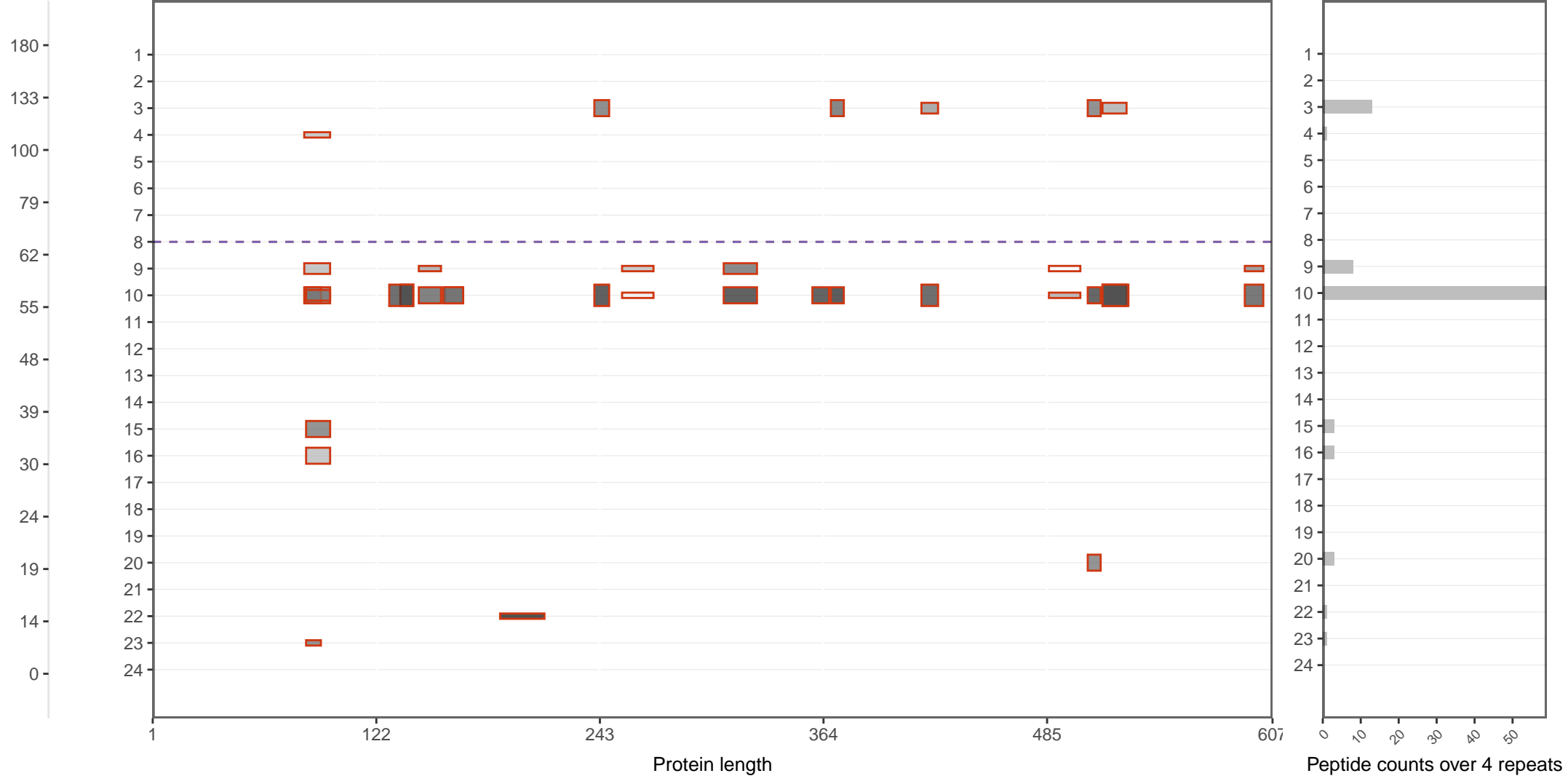
MPNTPSAVGDATVFTLGEKATTEDELISQLFSAIGKWRADENLFDVATGLSGSGPWFVLAELADGGVAAGLPRELALGLAAGTVLGAASMVWGMKHPGDKDDVASPGGTTAGIHELEKAGFRGLMNAVAAKRRELSDN

NbL02g16830.1 bifunctional_purine_biosynthesis_protein_PurH [MW = 66.14 kDa]



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain PF01808 AICARFT/IMPCHase bienzyme PF02142 MGS-like domain

Protein sequence:

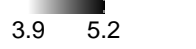
LRYPENPHKQALVAVVDKLSLSEVNAAGGATFVGHGKEMSYNNKLDADAAWNDVGEFNKPTQVYKHTNPGGVARDDGIEAYRLVAKADPVSAGFGVAFNVEDEALAKDIRREFRSPTDGETRMFYENVAPKYTEKLEVLKRGKSKTLRLEAKNKIKGLSLRGGGGVLAGDGDLTDPEDGFNVMSEKSPDENELNDQFALWLVKHKKNAMIAANNCLMGSGGGPNRRRESLRIMRKAGDEVKGAALASDAFFPFAWYDAVEEAGGGVSIIEPFGSGSRDKD

NbL02g16820.1 UDP-N-acetylglucosamine_diphosphorylase_1 [MW = 54.33 kDa]

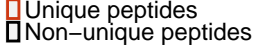
No. of times detected



log(intensity)



Values from



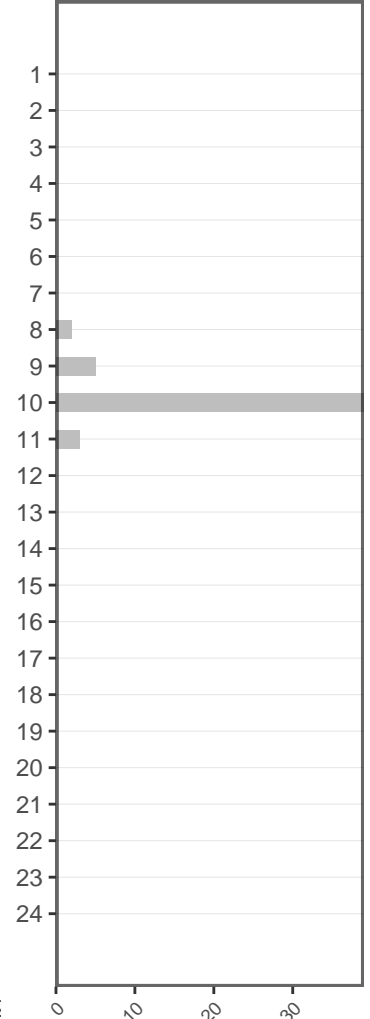
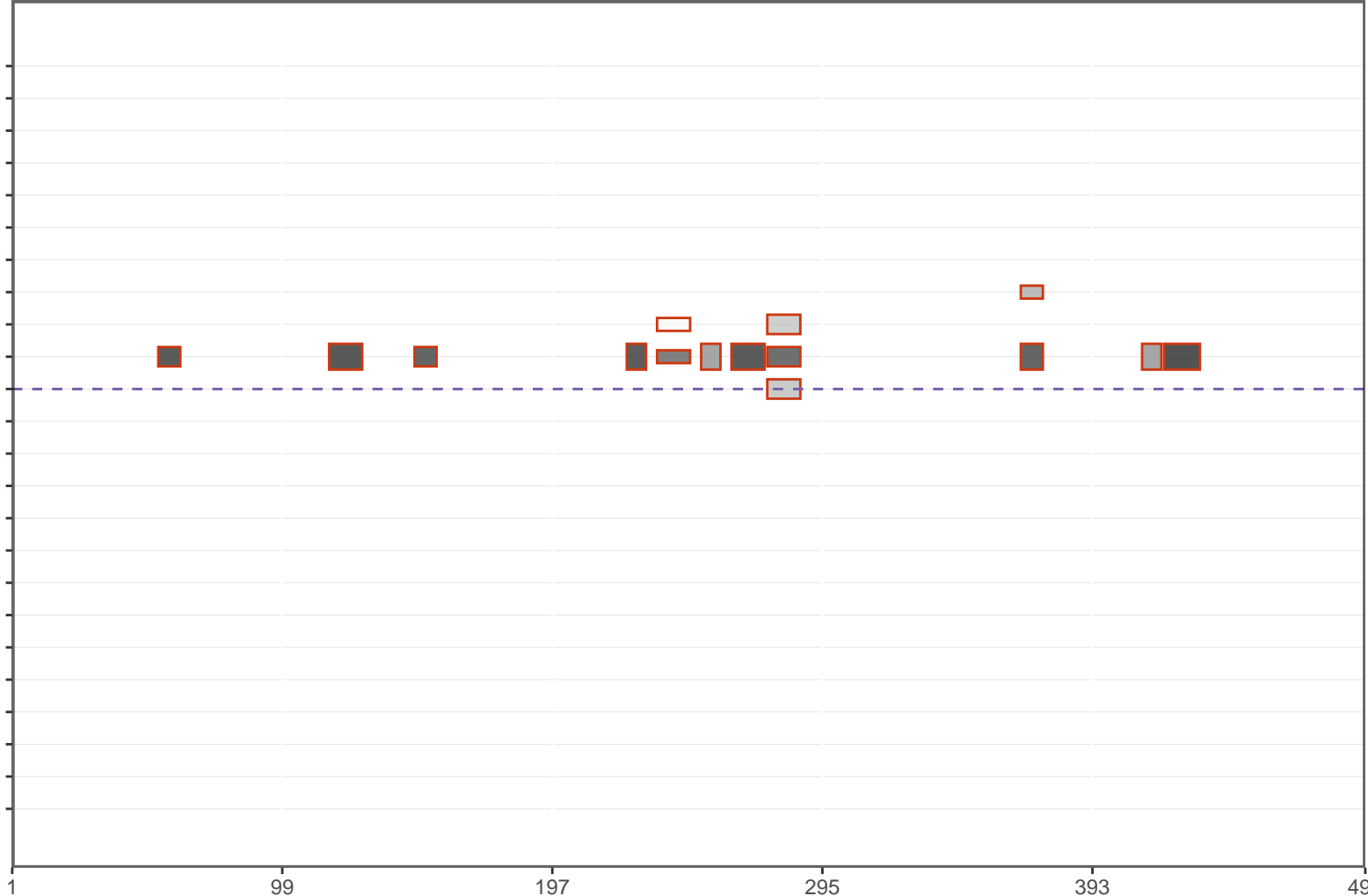
MW indication



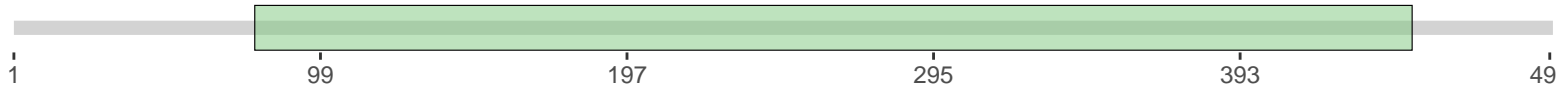
Molecular weight



Gel Slice



1 99 197 295 393 492



Pfam Description



Protein sequence:

KSPDQNGVYTLAKYRLLLEDMSNRGKIVDGVGDNALVRVADPTFLGYFDKGVSAAKVVRKAVYDQKGVYFVRGKGGPLAVVEVSELDPLCGAVNQGTRGLRFGWNSVGLHMFSLDFLNDVANGLEKDSVYHLAEKIPSHIGHTMGYKLEGRIFDAFFYPTPTALFEVYREEEFAPVKNANGANFDPDQARLLMLRLHTRWVAAGFLTHSVPLVATGVVEVPLGSGVAGENLEIKRGRTHAPGEISF

NbL02g16800.1 thioredoxin_O2_mitochondrial-like [MW = 21.88 kDa]

No. of times detected



log(intensity)



Values from



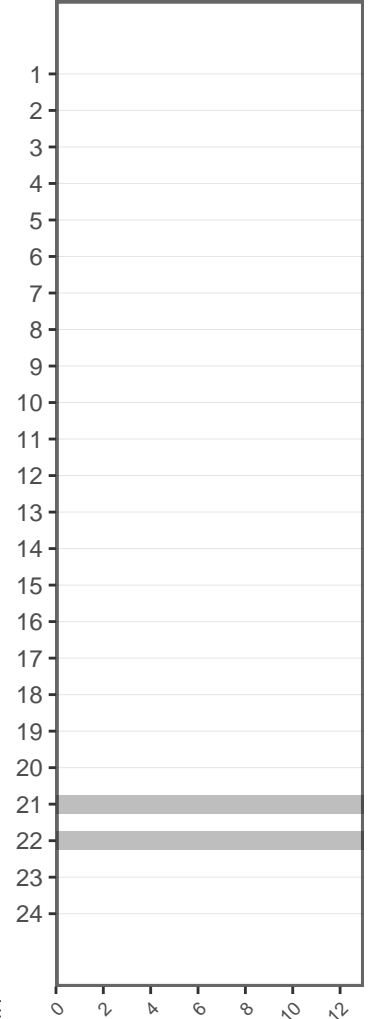
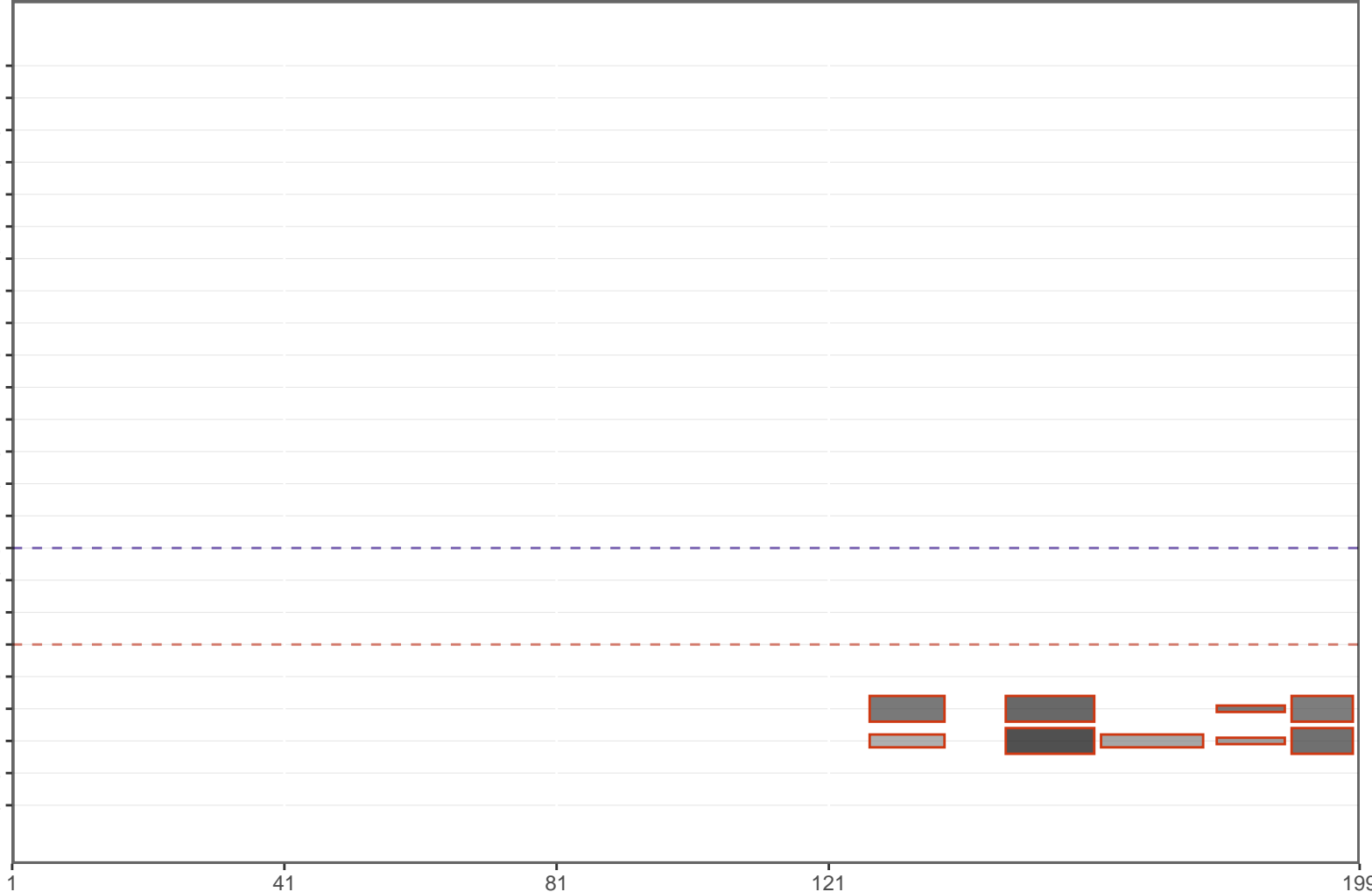
MW indication



Molecular weight



Gel Slice

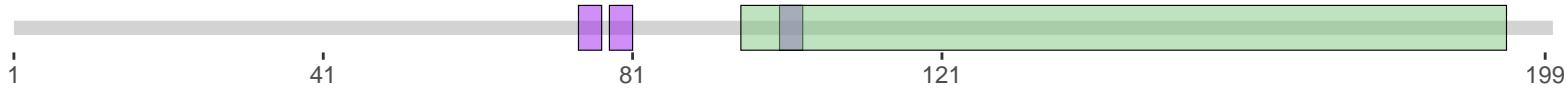


Peptide counts over 4 repeats

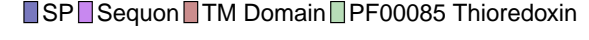
Protein length



Pfam domains



Pfam Description



Protein sequence:

IPSNVSISEECQFNFLRLKVDGSLPFIYETAWWGGPGRLLSPVIGQLSEKYPHVTYKVDIDKEGLGNALSKLNHVSPTLHFFFGNGKKTSEVIGADVGRLLKDTMEELVYK

NbL02g16530.1 acidic_endochitinase_Q [MW – SP = 25.06 kDa]

No. of times detected



log(intensity)



Values from



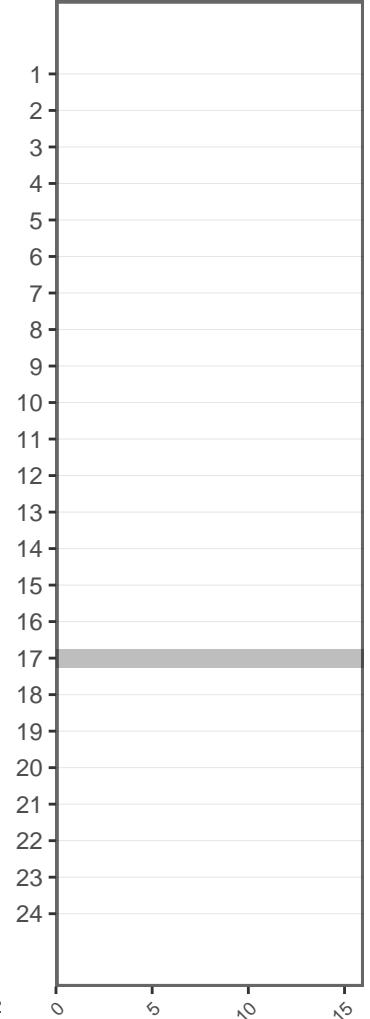
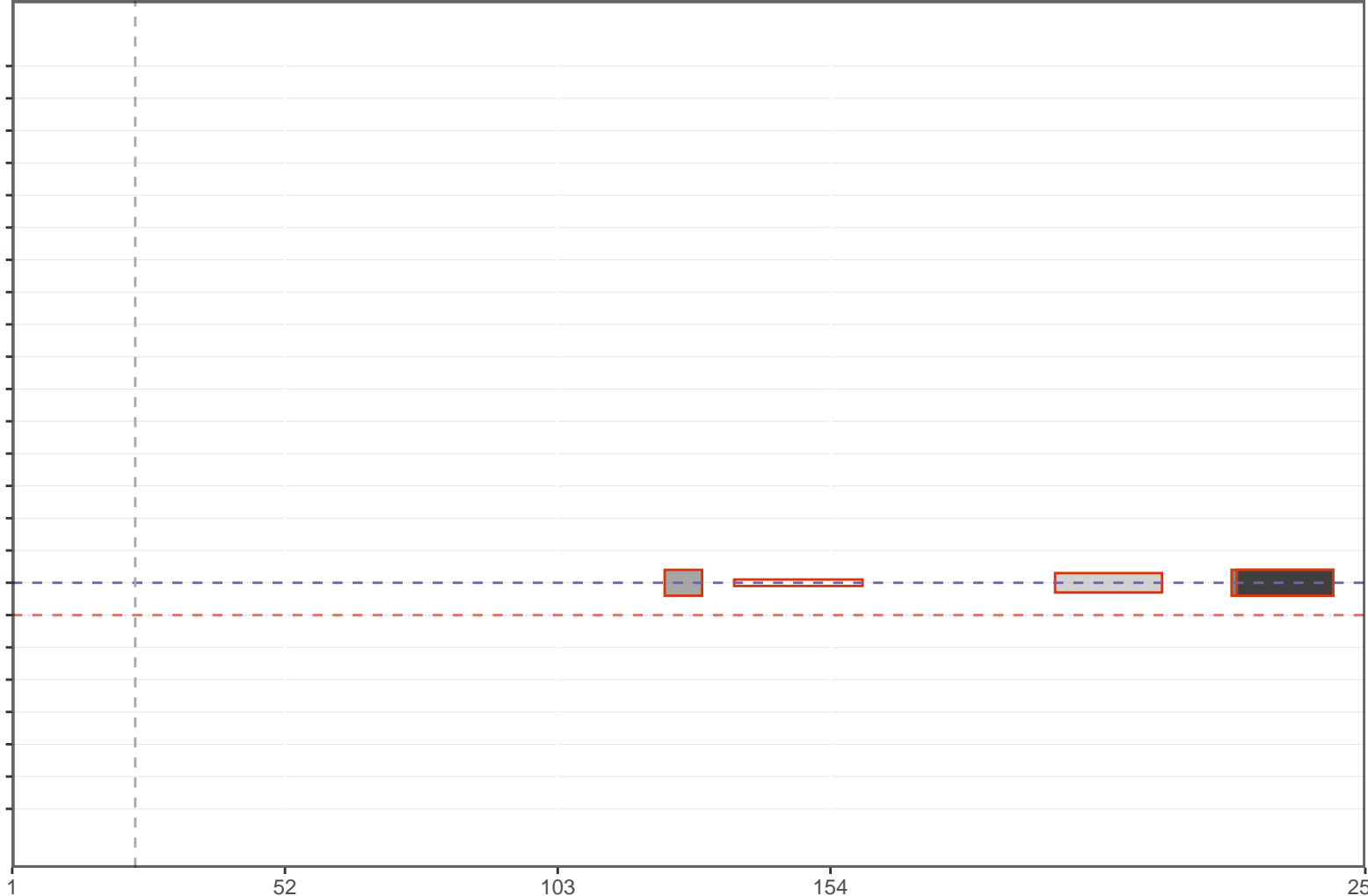
MW indication



Molecular weight



Gel Slice



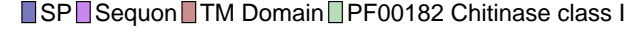
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

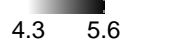
IQSERYYGRGPIQLTNRNNYKAGTAGDGLVNNPDLVATDATISFKTAIWFMTAGDNKPSSEHVIKGSWTPSAADGAANRVIPGYGVITNINNGGIECGMGRNDVAEDRIGYRRRYGGMLNVAFCENLDGYNQRNFAGQ

NbL02g16460.1 phosphoserine_aminotransferase_2_chloroplastic-like [MW = 50.78 kDa]

No. of times detected



log(intensity)



Values from



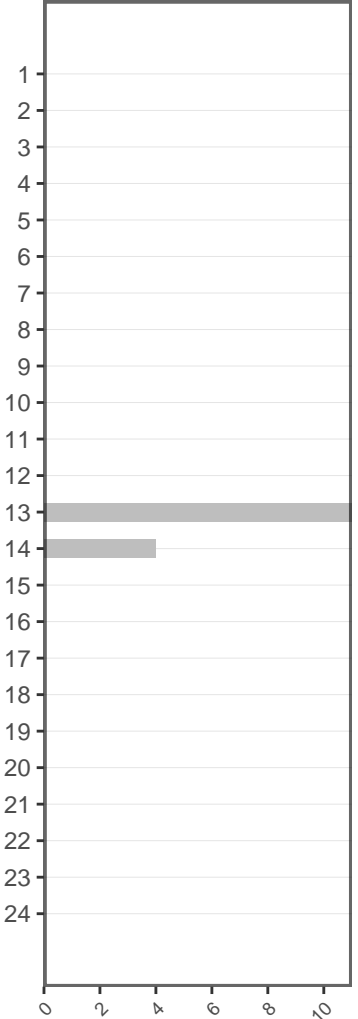
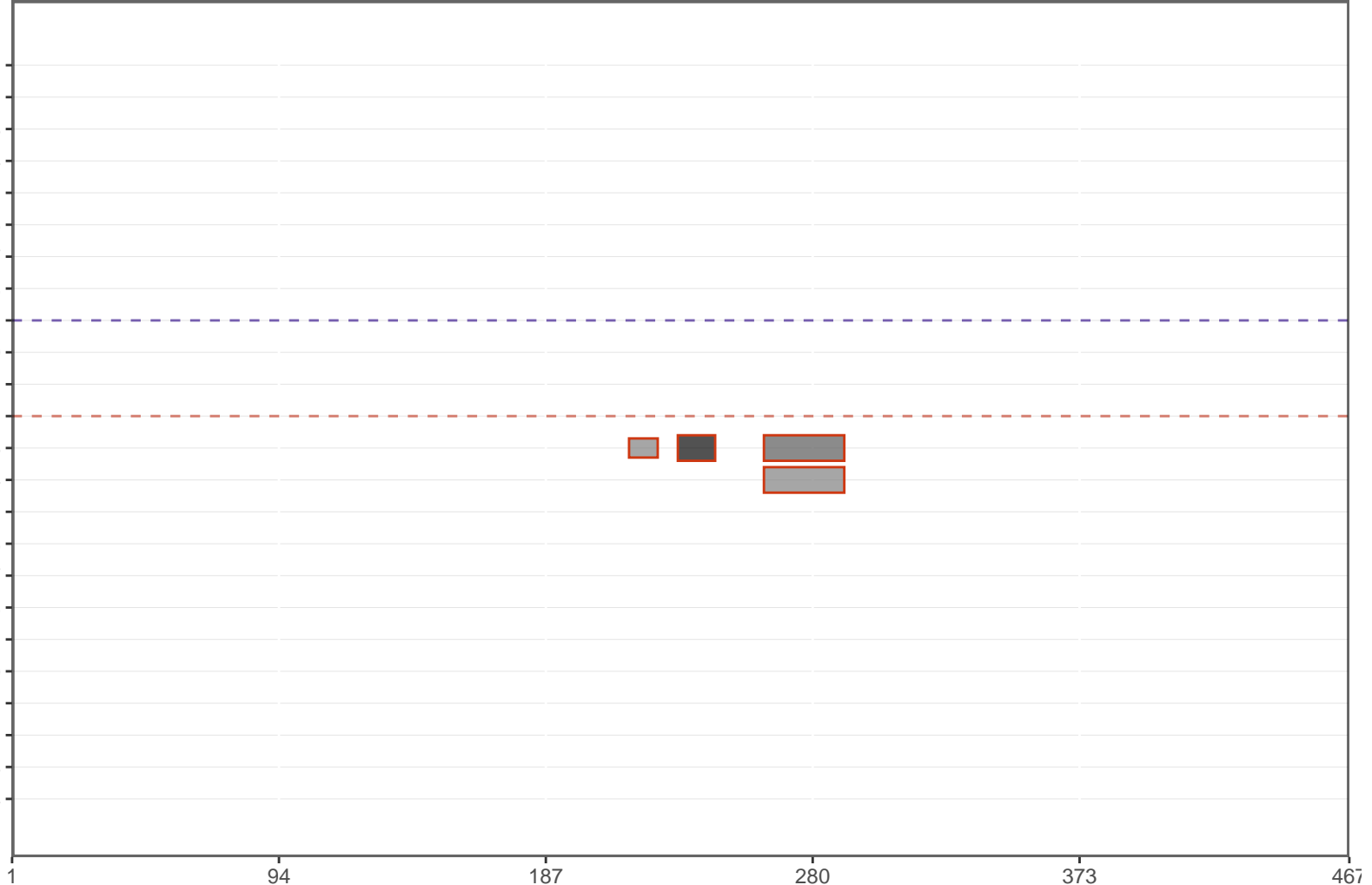
MW indication



Molecular weight



Gel Slice

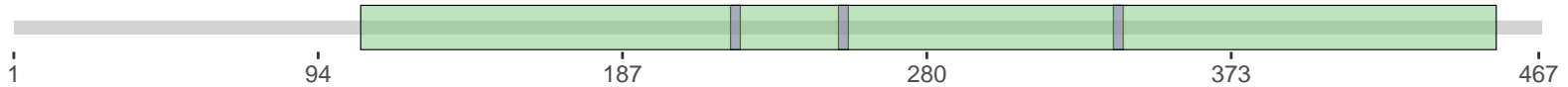


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VSVSGKSEKYYTKIPNFESLGGTTPGAKYLHICANETHIGVEFKDYPKPSNENTLIVADMSSNFGSKPVDVSKFGVYAGAKQNVSPSGVTVIRKDLGNAGESTPVMIDYKHAENNSLNTPTPGVGMGLVFEDELLADGGGLVEVEKNNKKAELIYNAIDSSNGFFRGPVEKSVRLMNVFTLAKPELEAEFVAAAAEKMAVQLKGRHSVGGMRASVYNAFLAGVEKLVAFMKDFQAQHA

NbL02g16430.1 ubiquitin_domain-containing_protein_DSK2b-like [MW = 60.17 kDa]

No. of times detected



log(intensity)



Values from



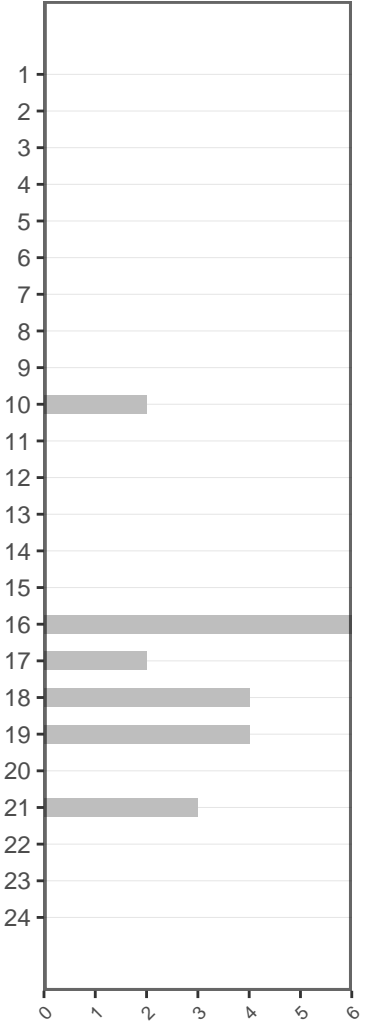
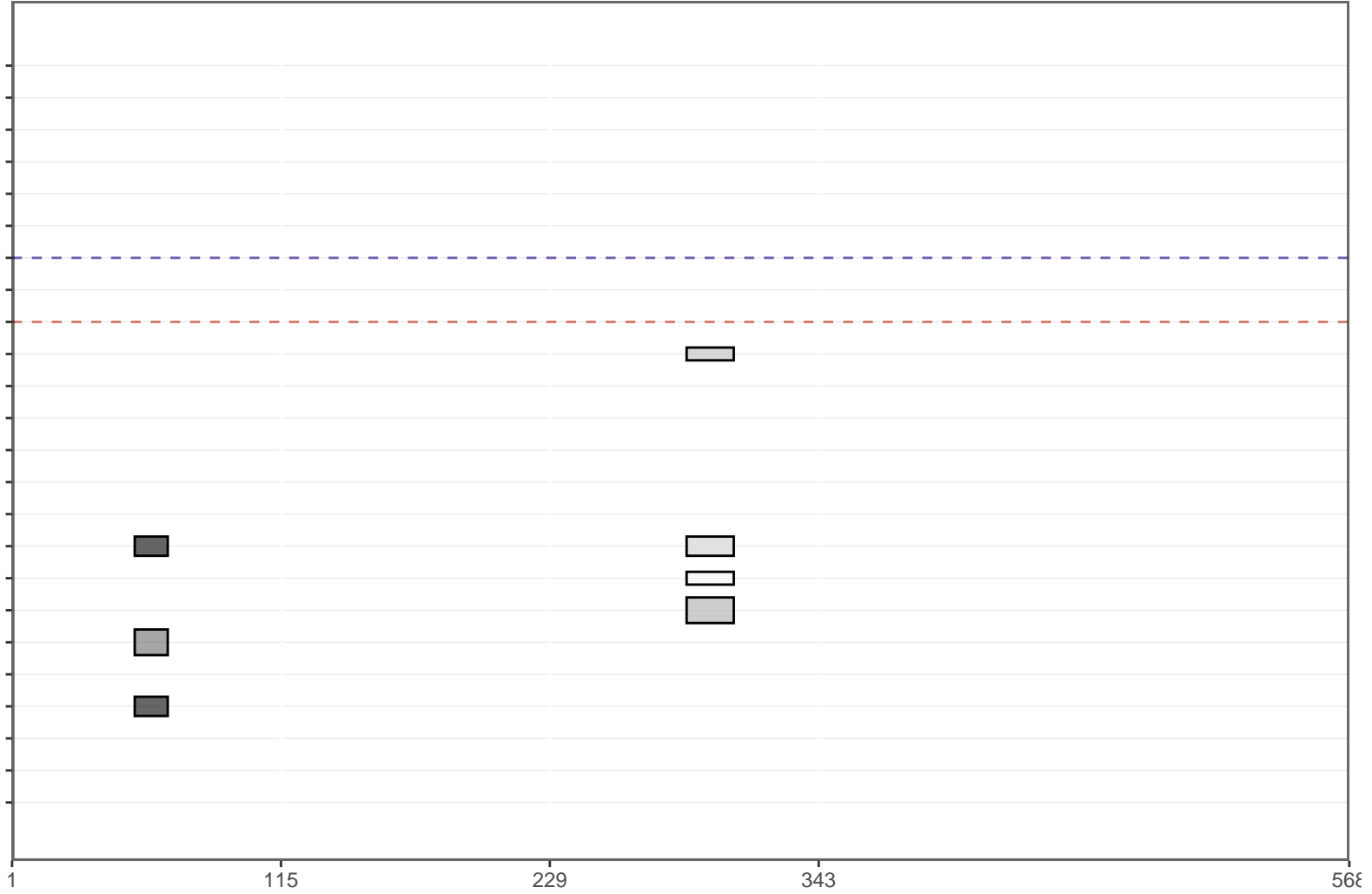
MW indication



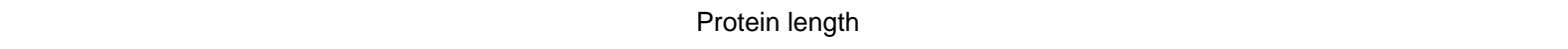
Molecular weight



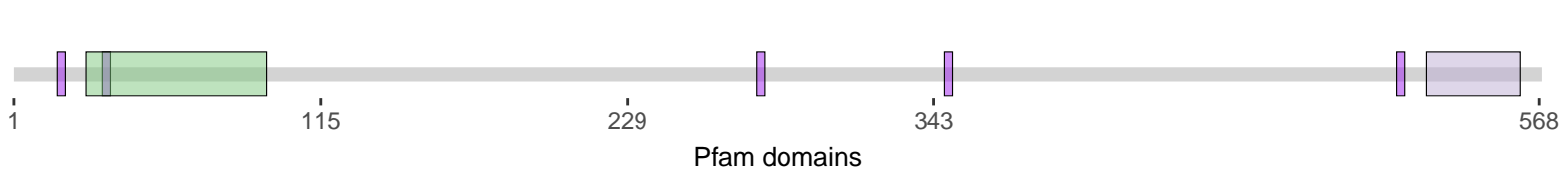
Gel Slice



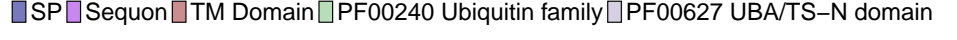
Protein length



Pfam domains



Pfam Description



Protein sequence:

IEPFLNATTMAGDARNDVGSNPFALLGAGGAGGGRVGSNPPPTGSSETTANTFVPTNPLNPNWASAGAGAGGNTTARENAAGETRAPSFAVLGGGLALPDLGMLGGMGGMPDAASLNGMGNPAGSGMMQGLLSNHQVMNQYLVQILGLNPQLRNMLDSNSHLREMMQNPFRQLTSPETMGQLMTFQGLL6QLGREGQTNPQGNAGGALENNIGMEMLMNMFQGLGSAGLGGVTRNRSNVPRPELVATQLVQLGDMGFFDTQENRALVATGNYL

NbL02g16410.1 catalase_isozyme_1 [MW = 56.91 kDa]

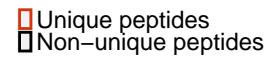
No. of times detected



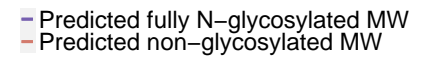
log(intensity)



Values from

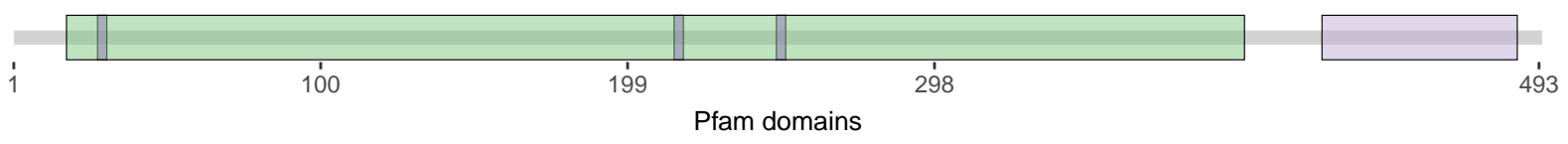
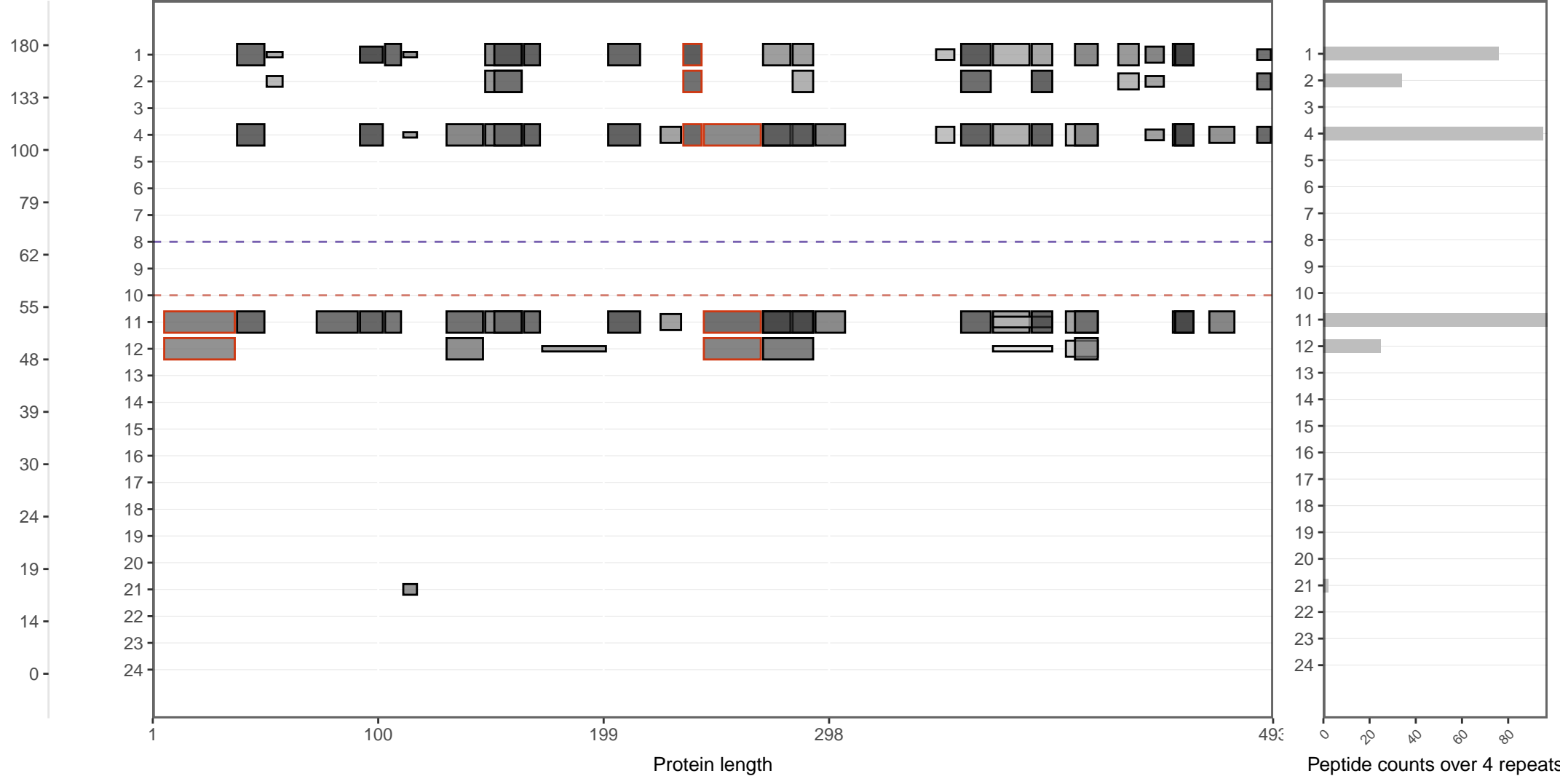


MW indication



Molecular weight

Gel Slice



Pfam Description



Protein sequence:

LSLLEEAARIGGANHSHATGQLYDSIAAGNYPEWKLFIGTMDPDHEDRFDFDPLDVTTKTWPEDLPLGFVGRVLVKNKDNFNENEQLAFQPSVIVPGVYVSDDKMLQTRIFSYSDTQRVRLGPNYLQLPANAPKGAHNNHYDGSMMFMHRDDEIDYFSPRYDQVRAEKNYFPSTMTGKREKQVQIKENFKQDGERVRSFTDQRGERFRRVVEALGDPRTYERISWISVWSDAQKSLGGKASRLNVRPSI

NbL02g16360.1 uncharacterized_LOC109214258 [MW = 115.58 kDa]

No. of times detected



log(intensity)



Values from



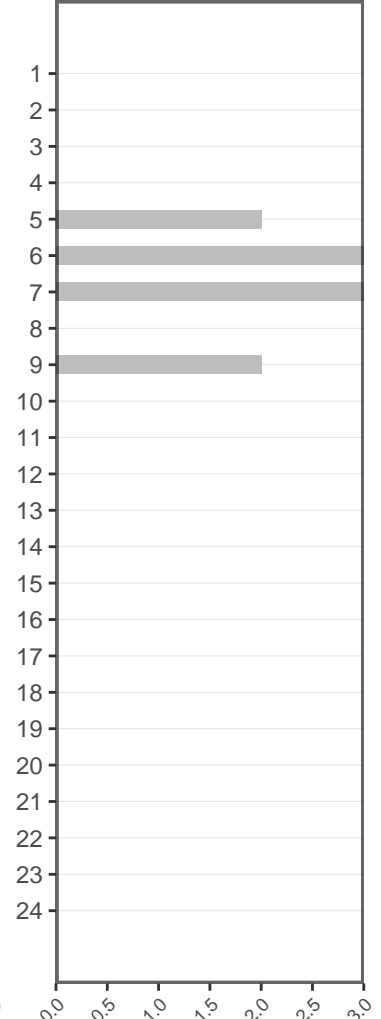
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains



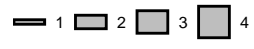
Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

LCILTSOLHLISGDDSGTVRYRKYKTEFFAPDTSFLSFQVSGKKGSNPIQGVKLVKVNAGVLSIGTSGESKYFAVSGDGGVYVLDSDSKTLVQTHIASEAGVISMQGNMCSGVHGFKNLIVVATKDSVLALETETGNILSPMVAHPKPKPRALFMQILDGOELSGRGLSISDGGIMIKGNSDNSAKQPVVLLQSEKALVYVSLHIVGGKQVYVKKFHSGLGQWASTEDSFEAGMLLFSNGKIEIRLPELGLLNETSVRGLMLSPPKANBIADHSKASKNGELIVDRD

NbL02g16260.1 epidermal_growth_factor_receptor_substrate_15-like_1 [MW = 130.55 kDa]

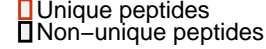
No. of times detected



log(intensity)



Values from



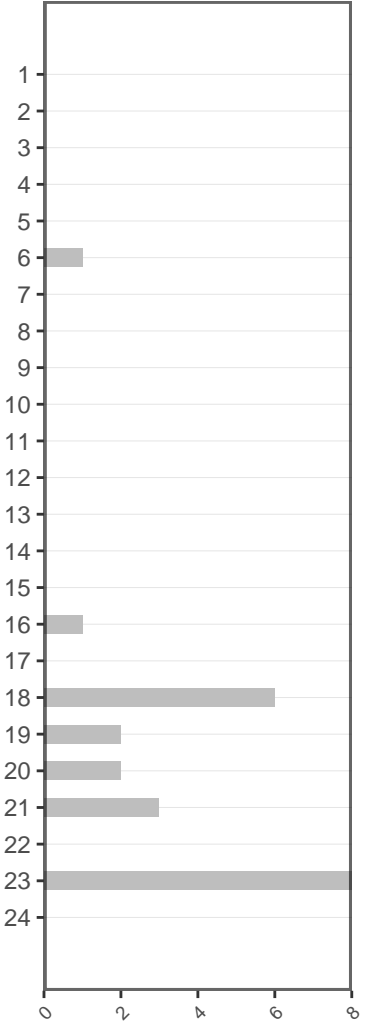
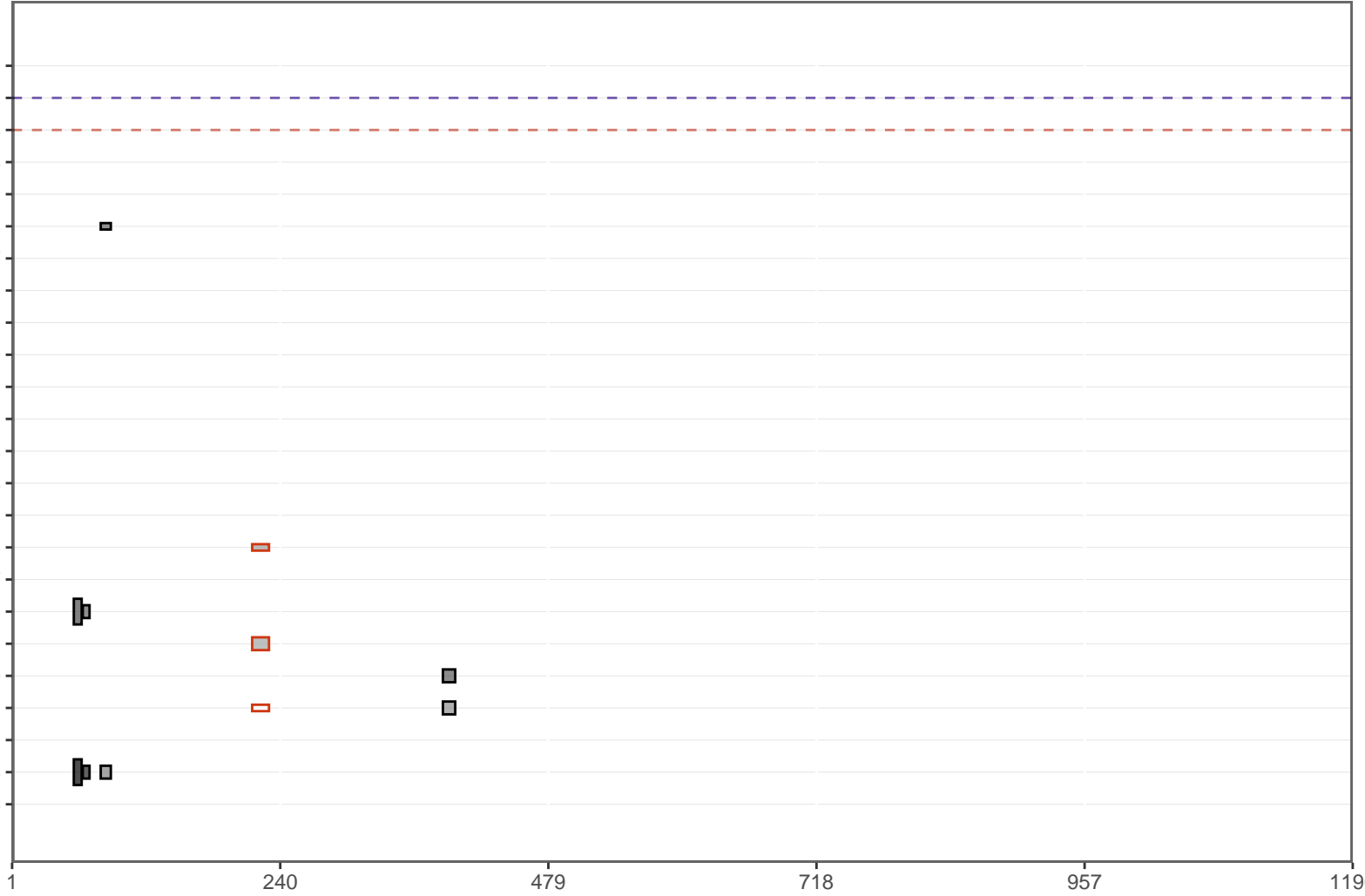
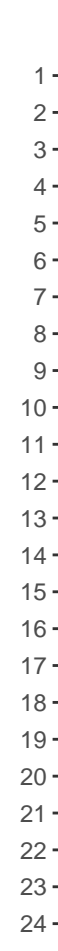
MW indication



Molecular weight



Gel Slice



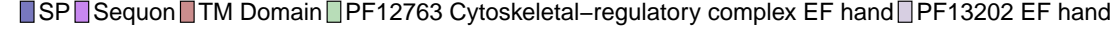
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

JLYKSRCCNRLNEIFRFTSADKKEVELLANKYEEKYKGTGDVASKLTFEEATFRDQEKMKELVKEIKVMDDGDKTGDGRASHQHTNLEELVKALNERKQTYGLRAKPTTLELFFGQVPGIGEGAAVDDEEVDKFEDEGFTFYKELTLDVKNVAPPKKESLVRKASPLDEDGAKSSADADTDKIDKVPNHGQAREVSDTTESAHGQGTARSPDTPSPRSNVAEVSFKEFQESMYKGVDFDGSPLAARPKDGFDSPLAAQDSERWGTESVFSDRGFDSEGW

NbL02g16160.1 thioredoxin_reductase_NTRB-like [MW = 40.23 kDa]

No. of times detected



log(intensity)



Values from



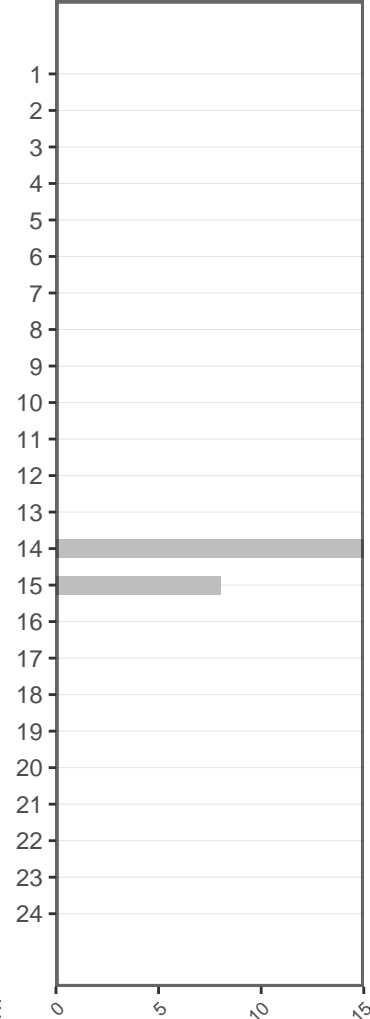
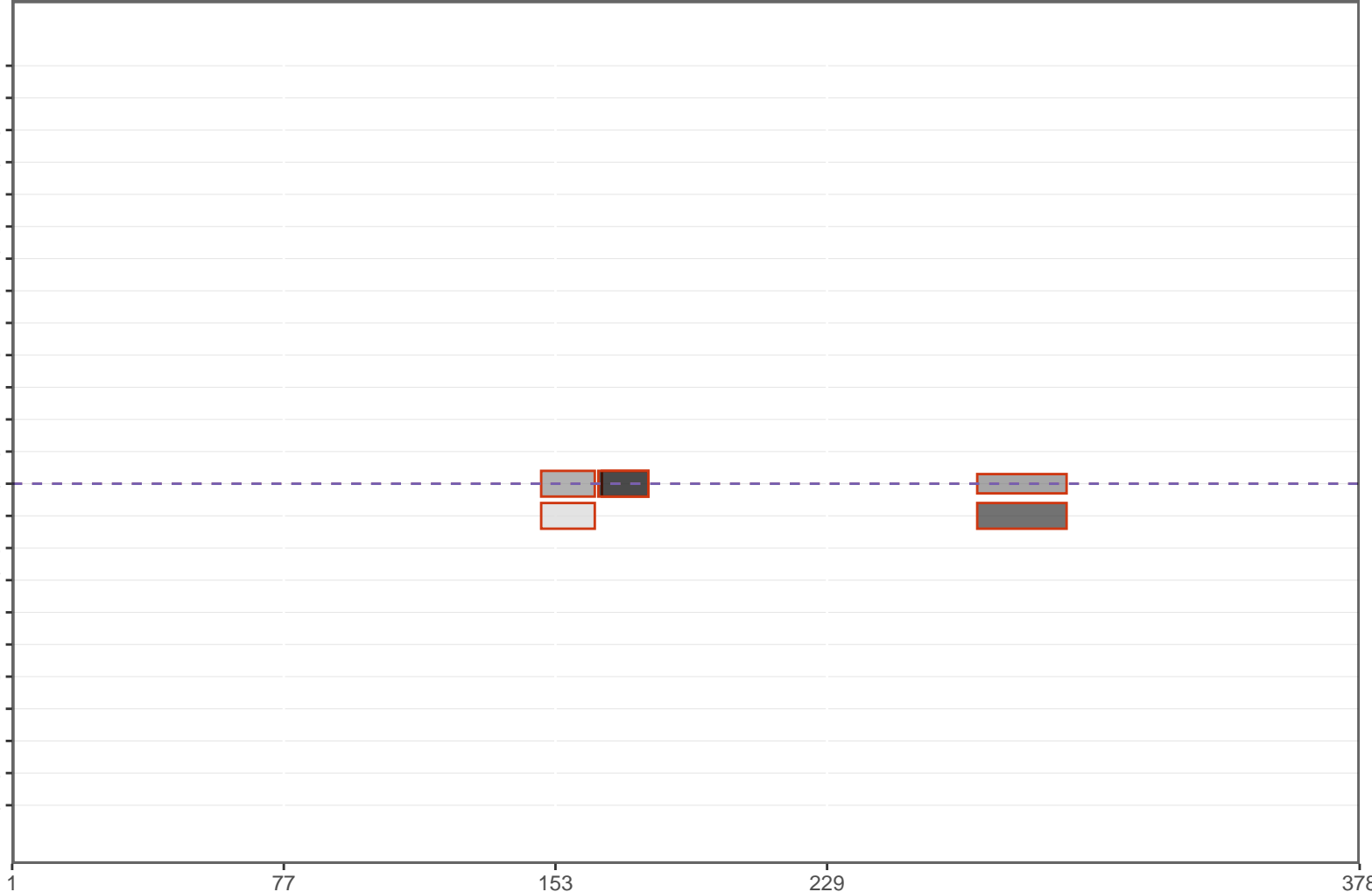
MW indication



Molecular weight



Gel Slice

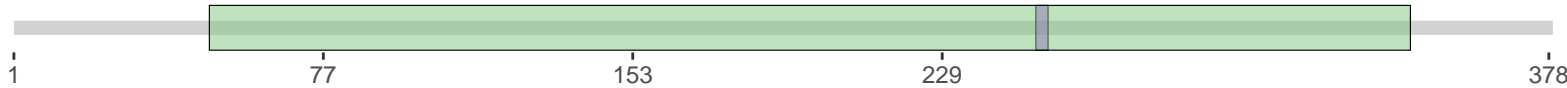


Peptide counts over 4 repeats

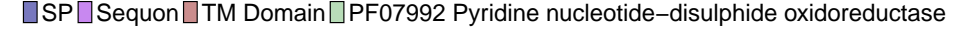
Protein length



Pfam domains



Pfam Description



Protein sequence:

NRGSAACVCDGAPFERNKPLAVGGGDBAMEEAFNLTKYGSKVYHRRDFRASKMDSRALSAPKIEVWNSBVVEAYGKLLGLKYNVVTGGVSDLVGVGLFFAAGHEPATKFLDGGLELSDGGVYVITNPGTFLFVSRGVFAAGVGVGDKKVRGATAGSGGNLPTCAPRGLVGLRDSDTROKSEKKNVVF

NbL02g16000.1 uncharacterized_LOC107769872 [MW = 19.96 kDa]

No. of times detected



log(intensity)



Values from



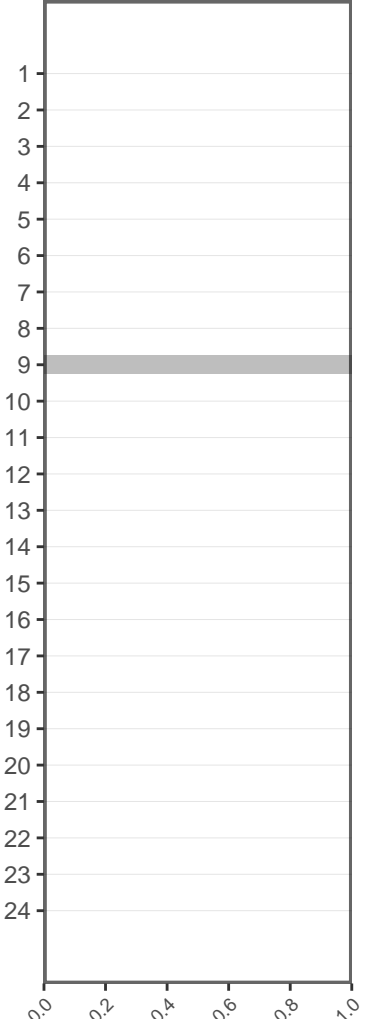
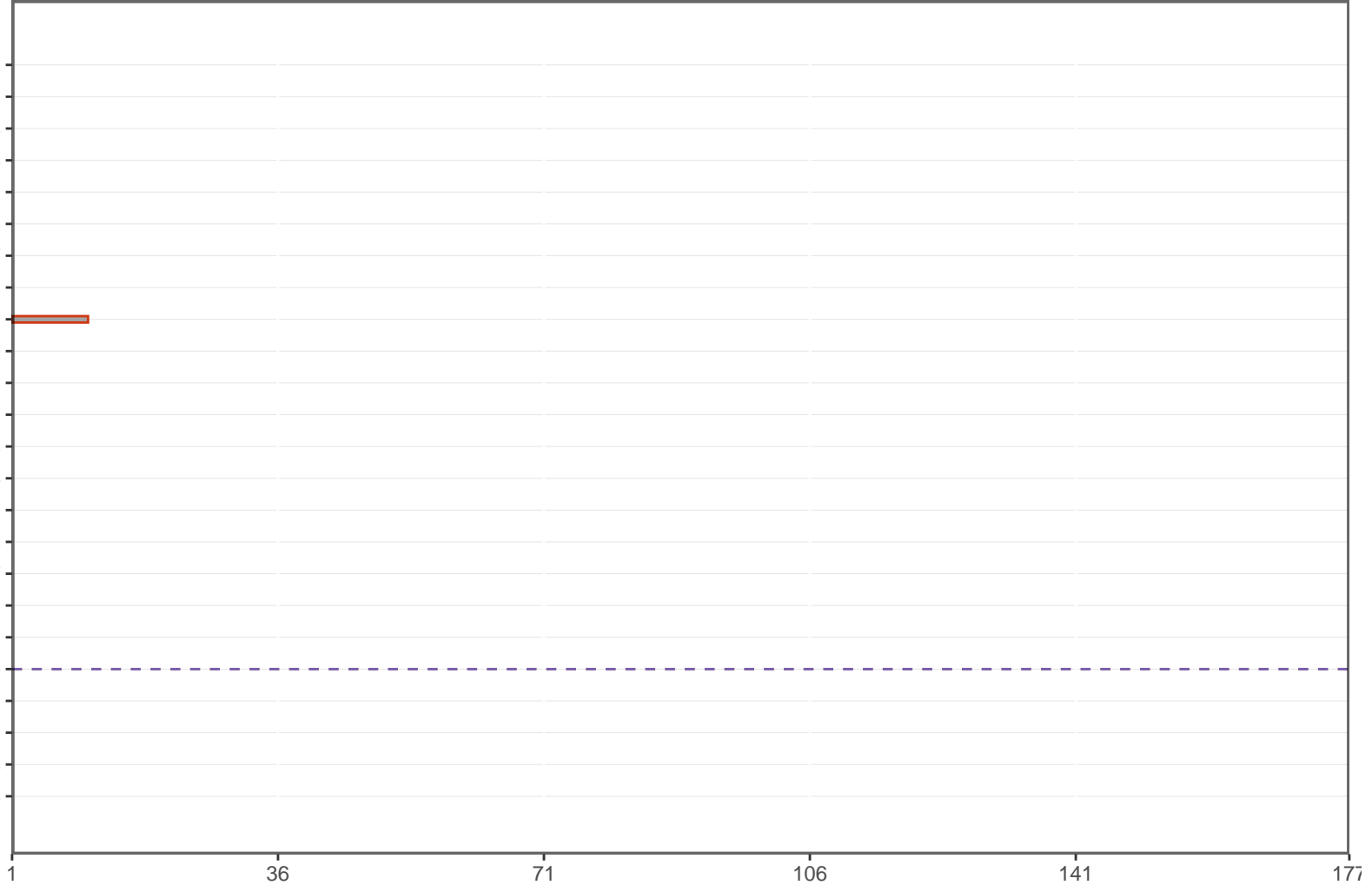
MW indication



Molecular weight

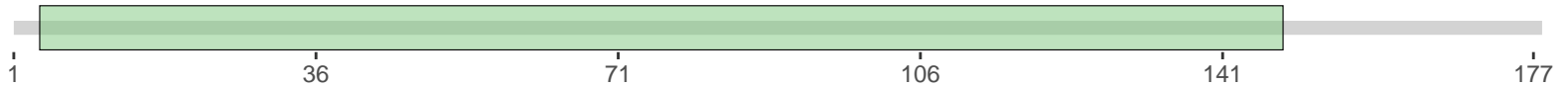


Gel Slice



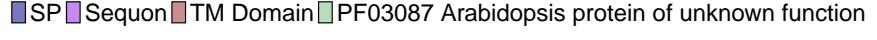
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

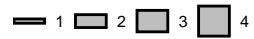


Protein sequence:

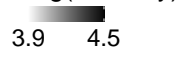
LTDDSYTRFTSFSSKIKRDAKRLALNLKGMDDAAWVPLLDADGDTWIRALREANAVGISTFQMLLFLGVPLDGFENALEATFRGLIRSRILLNLVLSG

NbL02g15860.1 DNA-directed_RNA_polymerase_II_subunit_1 [MW = 204.78 kDa]

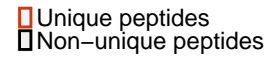
No. of times detected



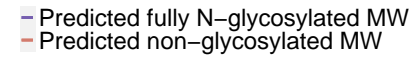
log(intensity)



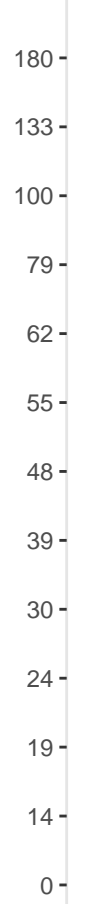
Values from



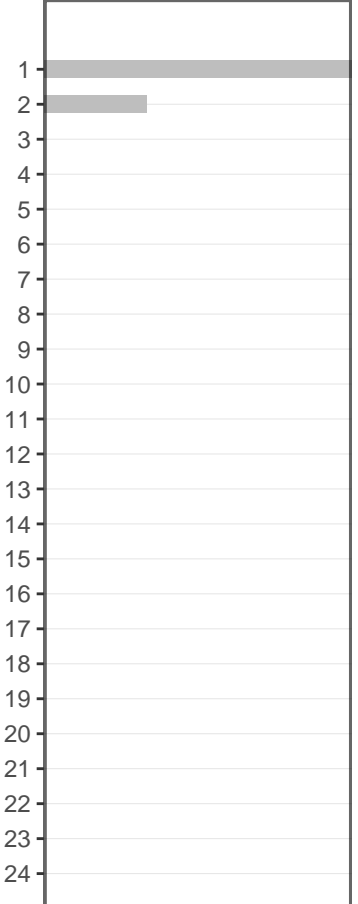
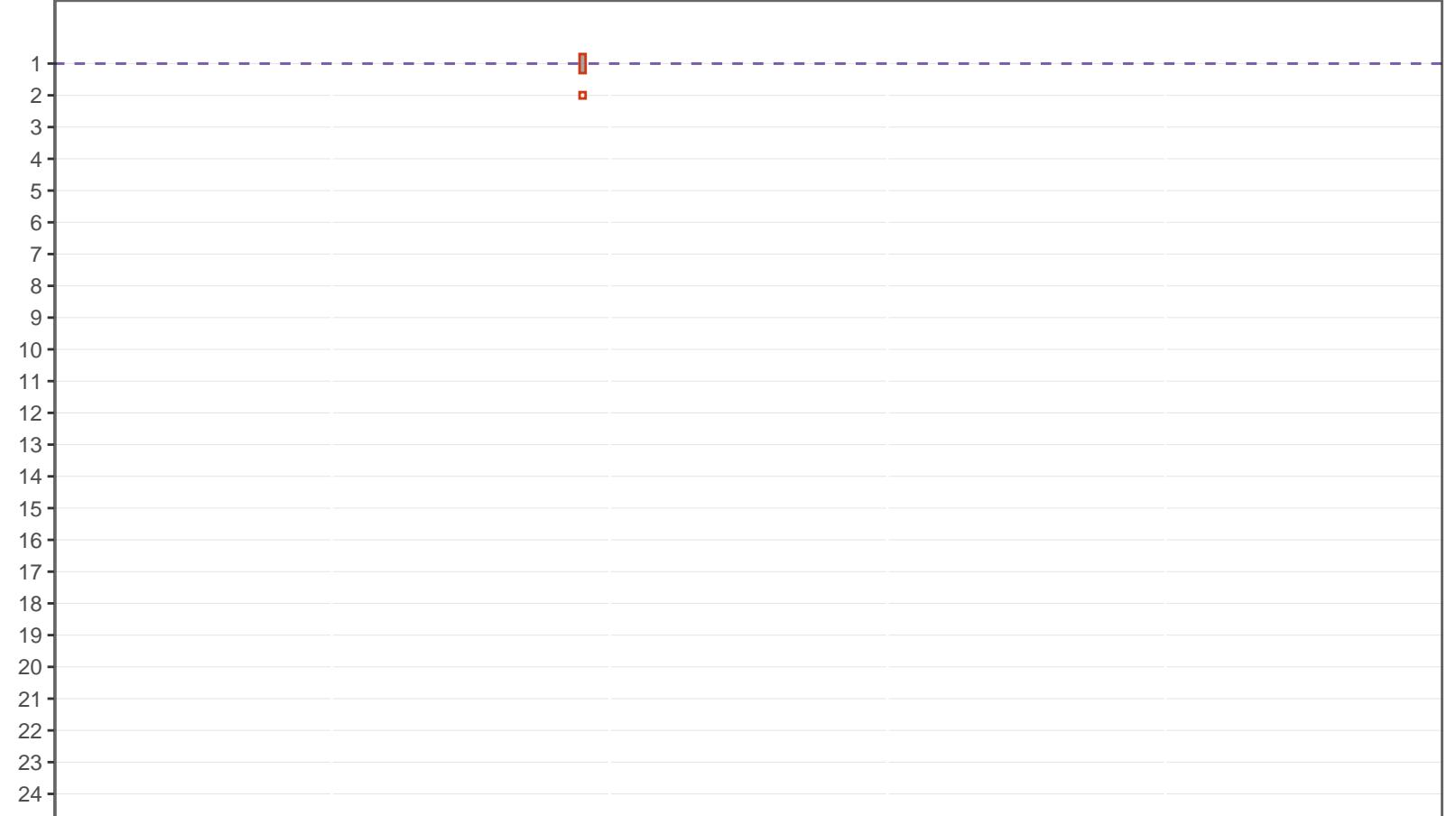
MW indication



Molecular weight

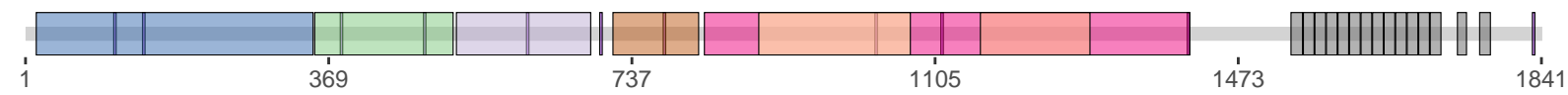


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- PF00623 RNA polymerase Rpb1, domain 2
- PF04992 RNA polymerase Rpb1, domain 6
- PF05000 RNA polymerase Rpb1, domain 4
- Sequon
- PF04983 RNA polymerase Rpb1, domain 3
- PF04997 RNA polymerase Rpb1, domain 1
- PF05001 RNA polymerase Rpb1 C-terminal repeat
- TM Domain
- PF04990 RNA polymerase Rpb1, domain 7
- PF04998 RNA polymerase Rpb1, domain 5

Protein sequence:

IAKSKTFDLYAYEIDDPNWNPVYMLPEAIEDLKTREIRSVFDVAEVKQLQADRLKLGTEFAWVTGDSNSWFLVWQRLVNLNAGTKFKIDFRRSDDMPMEIEVAWDKLOERLKVYPGDDVLSMEADKNTLFFNLRSALASKRYLHEYRLSREAFDWYVIGIESRFLQSLVAPGEMGCVAAQSGEPATQMTLNTFHVAGYSANNVLYGVPRLREINVAKKKTPSLVYLPKPEYKTKERAKTVQDALEYFTLRSVGTQTEVWYDPQPMSTLEEDVEFYKSYIEMPDDEIDP

NbL02g15790.1 ribulose_bisphosphate_carboxylase_large_chain [MW = 19.8 kDa]

No. of times detected



log(intensity)



Values from



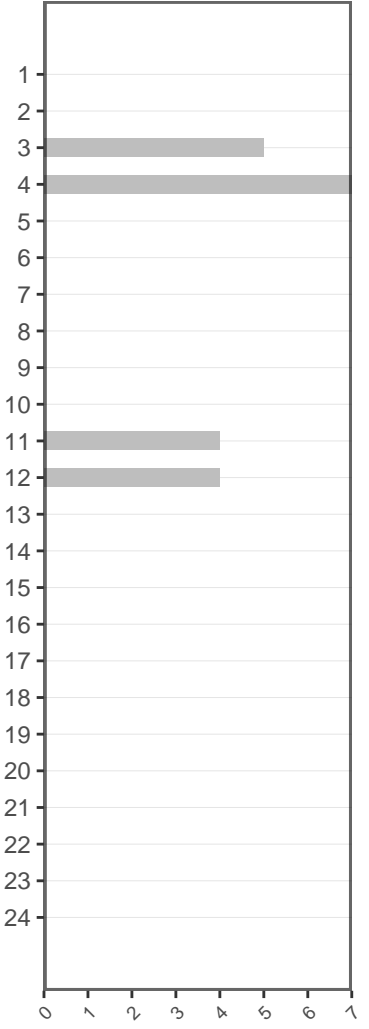
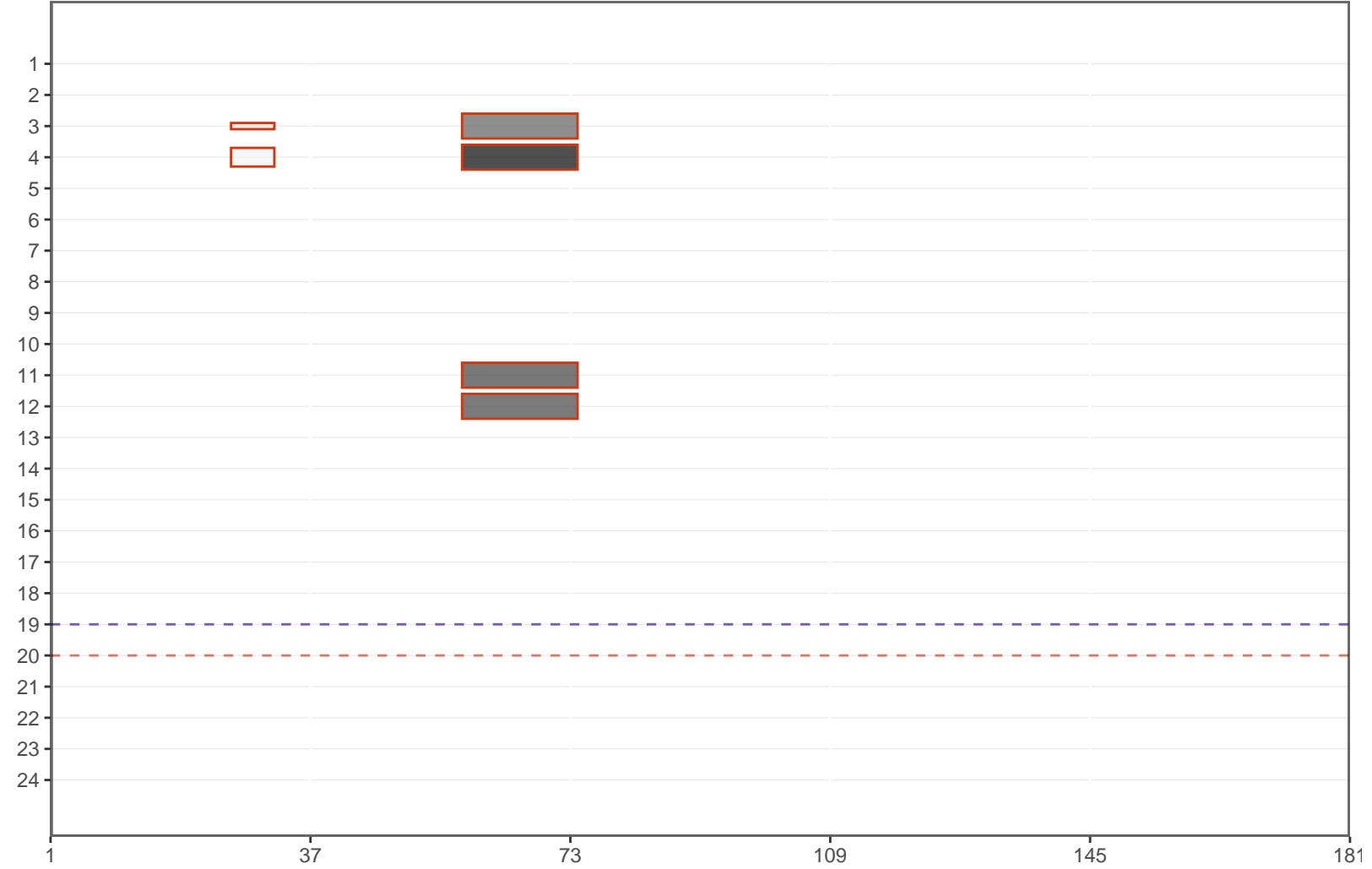
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

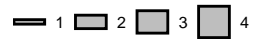
Pfam Description
 SP Sequon TM Domain

Protein sequence:

MFNFAAVDVLKSSILYRGRLEIPNGYVYFENRREGGQKVRWIKHLLDRMGFCDDKCFMNGDENFPAFKMTGARRSAEAVGGKNTSVEHSALESLRARI

NbL02g15770.1 aspartyl_protease_family_protein_1-like [MW - SP = 54.86 kDa]

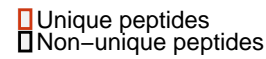
No. of times detected



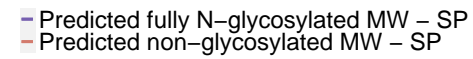
log(intensity)



Values from



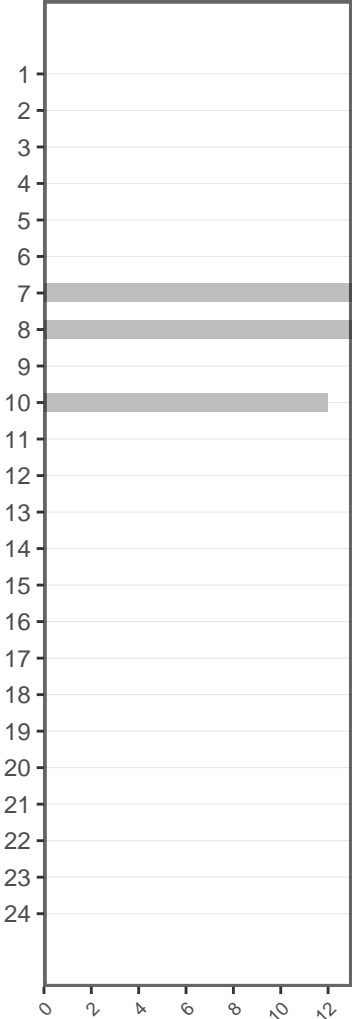
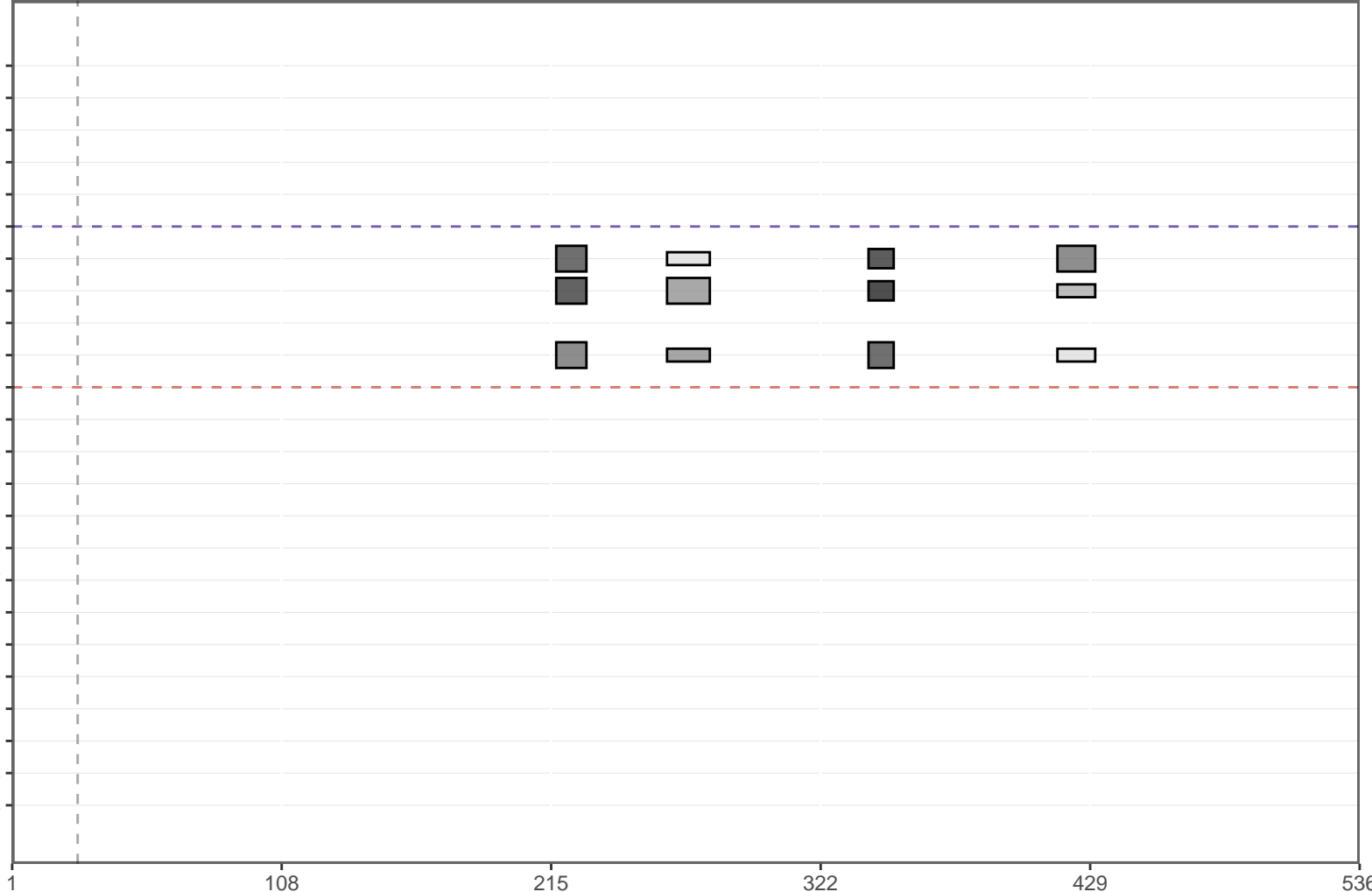
MW indication



Molecular weight

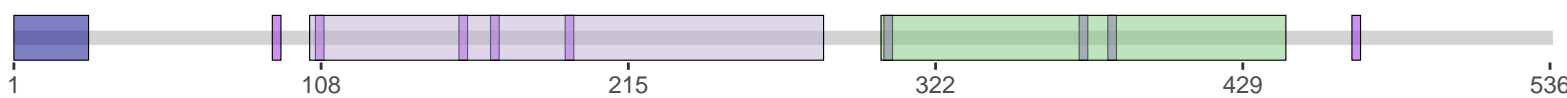


Gel Slice



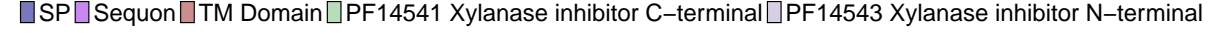
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

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NbL02g15750.1 uncharacterized_LOC109237051 [MW = 23.26 kDa]

No. of times detected



log(intensity)



Values from



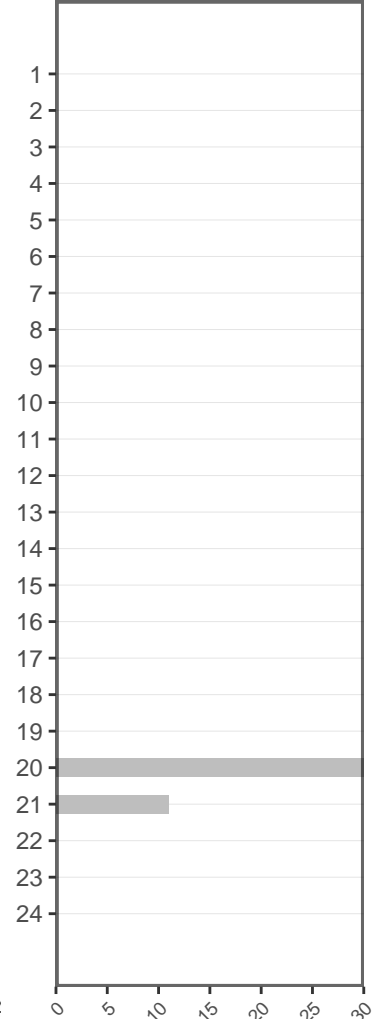
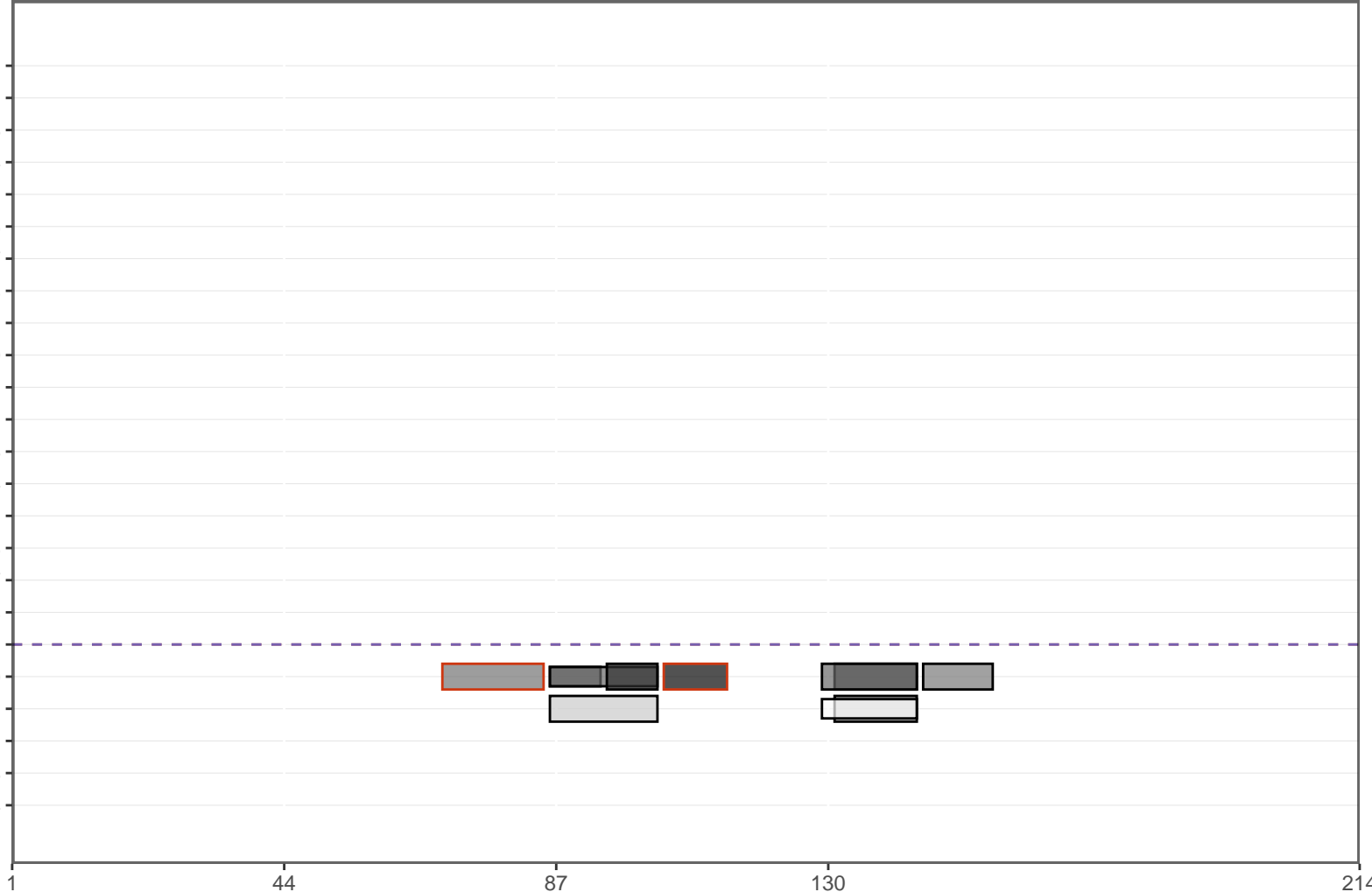
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains



Pfam Description
 SP Sequon TM Domain

Protein sequence:

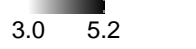
RNPYLSEGRQAAMATALANKYGADITVVVIDEKEKEAVPEHETQLASIRWHLSEGGYQEFKLLERLGEGRKPTAIGEADENMLDWVMSMEAIHGHVDANLAEFIPGVLLLL*

NbL02g15660.1 methionyl-tRNA_{formyltransferase}-like [MW = 39.08 kDa]

No. of times detected



log(intensity)



Values from



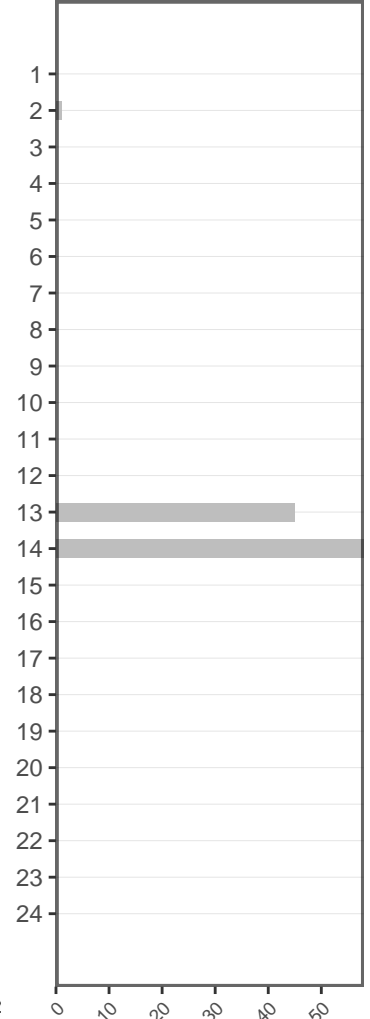
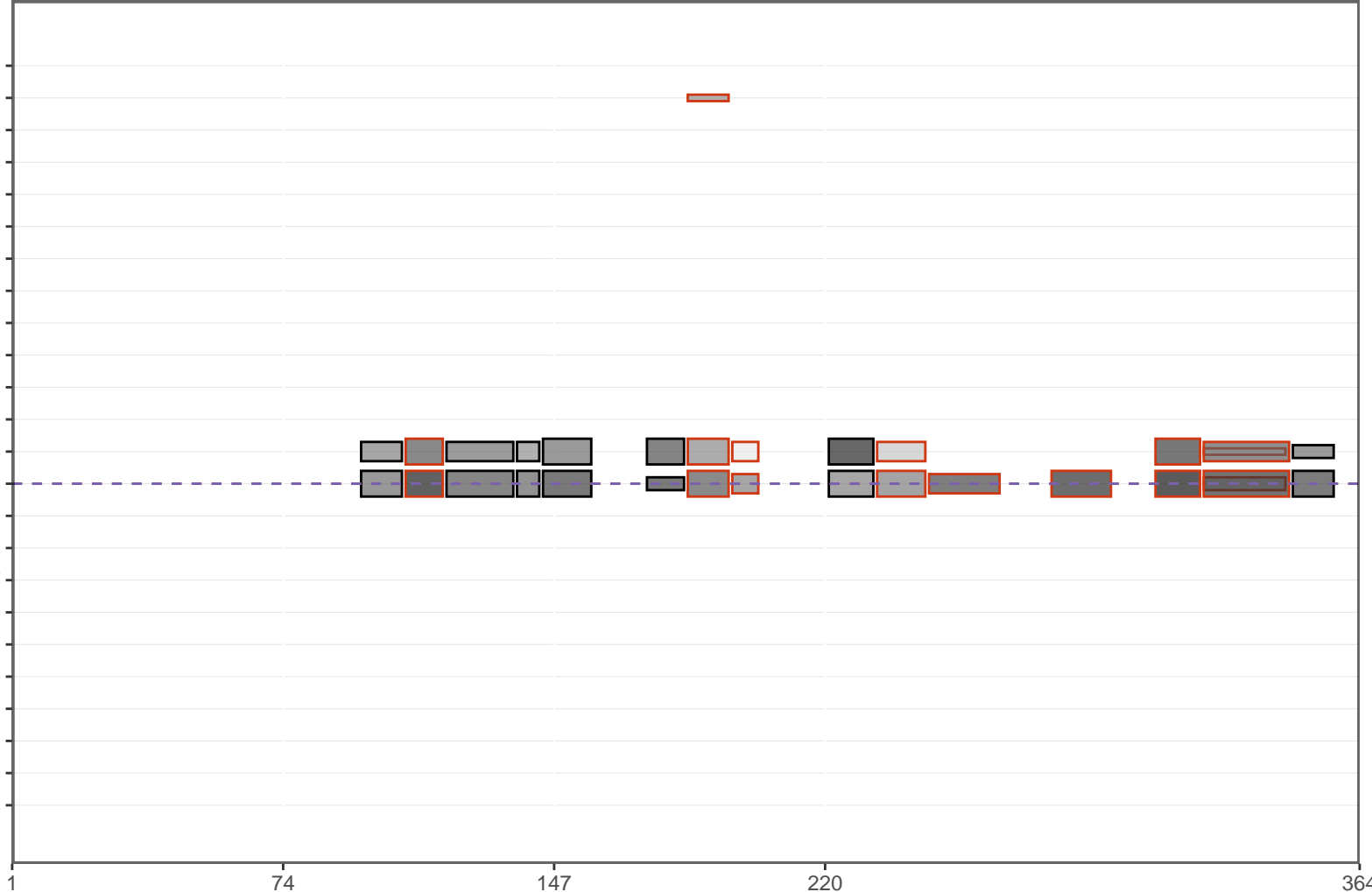
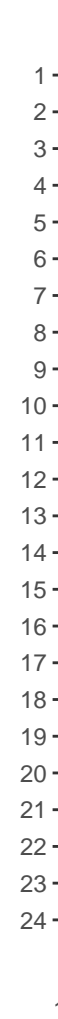
MW indication



Molecular weight

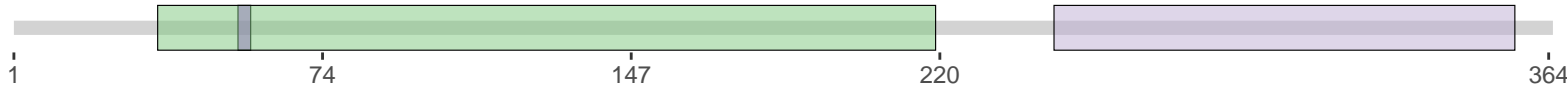


Gel Slice



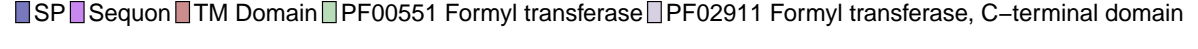
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

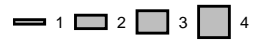


Protein sequence:

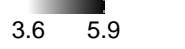
DSVYKETSGLAYTYRKLSDAGPIVALEIKVDDGKAPLDLDFALGSKLLRELPSIFDGSASGRAEDQDDSKATLAKITPEEHWLDFDEDAQVLIHKKVAFAGWPCTRARLIVDPSSGESSSELNIITRIYTGIRSGDIEANDVLFKGSILVPCGGDTALEVLEVDLPGKRAVNAASFVNLGRGLKKY

NbL02g15650.1 ATP-dependent_Clp_protease_proteolytic_subunit_3_chloroplastic-like [MW = 36.41 kDa]

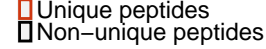
No. of times detected



log(intensity)



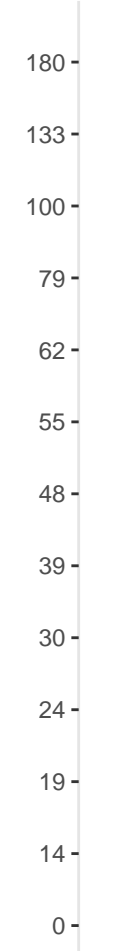
Values from



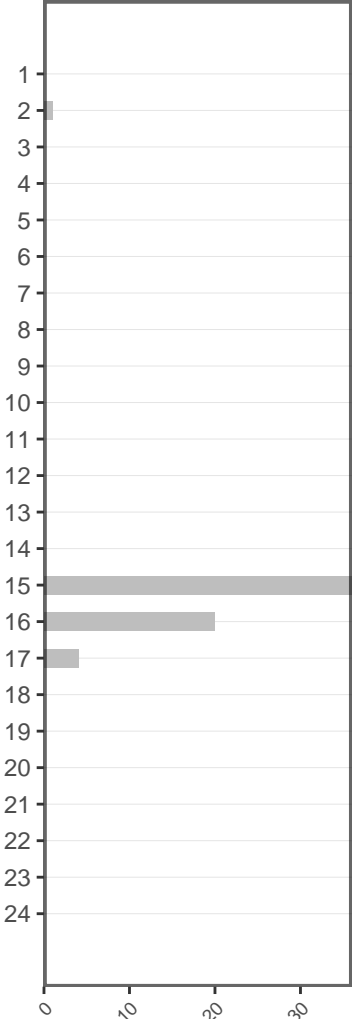
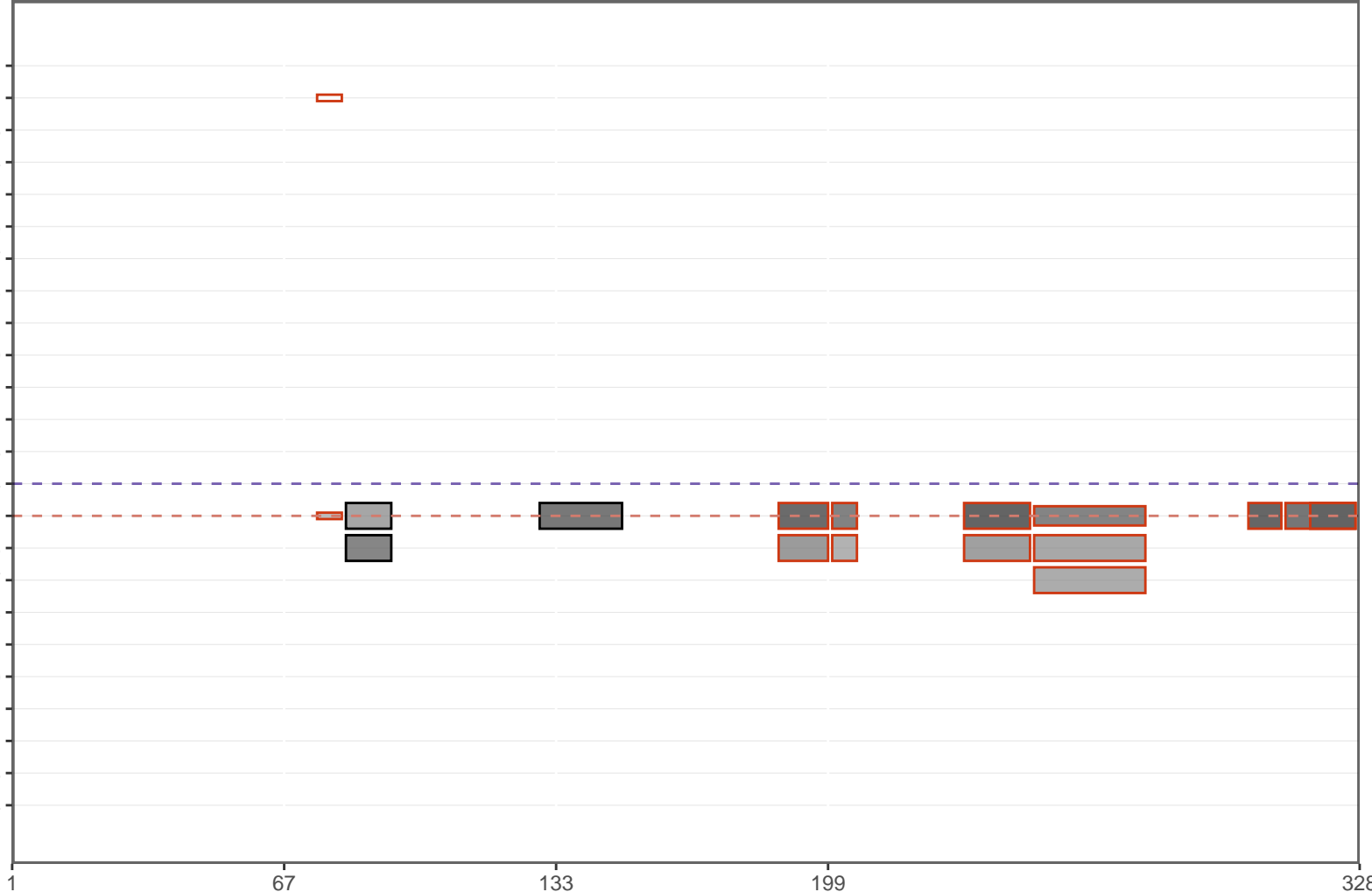
MW indication



Molecular weight



Gel Slice

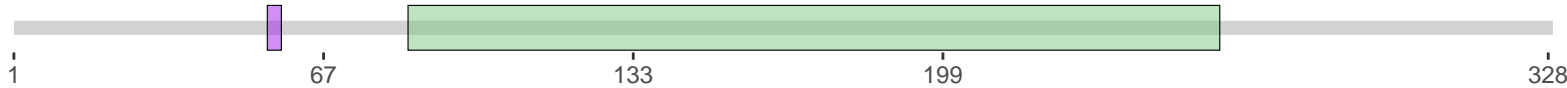


Protein length

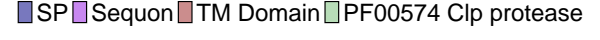


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ADVSTICMGLAASMGAFLLAGSGKGRVCMFNARVMIHQPLGTGGKATEMSIRIREMAYHKKLNKLSRITGKPEEKNEEDTDRDNFMNAWEKEVGLVDWIDDGKPLGLVPTADATAPKTRVYVDMVWIKIEGSKAKKLNLPSEERMLGTGVYSRGDDGKNEKQKDEAPSL*

NbL02g15540.1 2-hydroxyacyl-CoA_lyase [MW = 61.45 kDa]

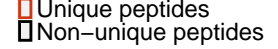
No. of times detected



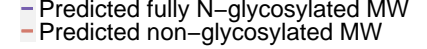
log(intensity)



Values from



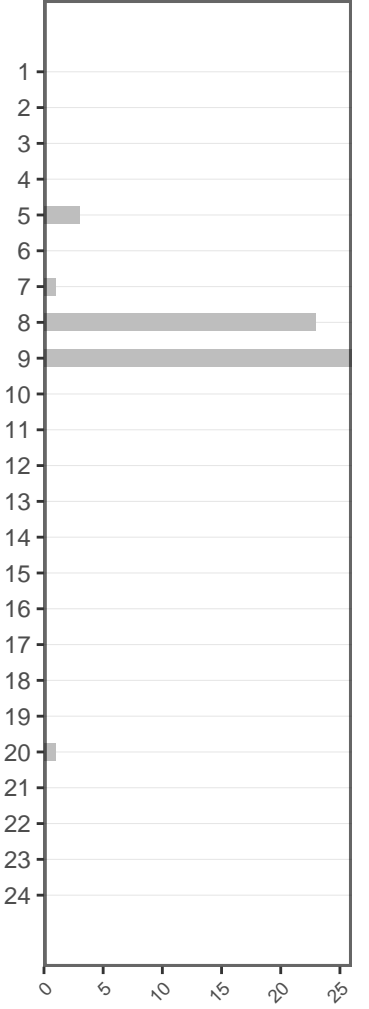
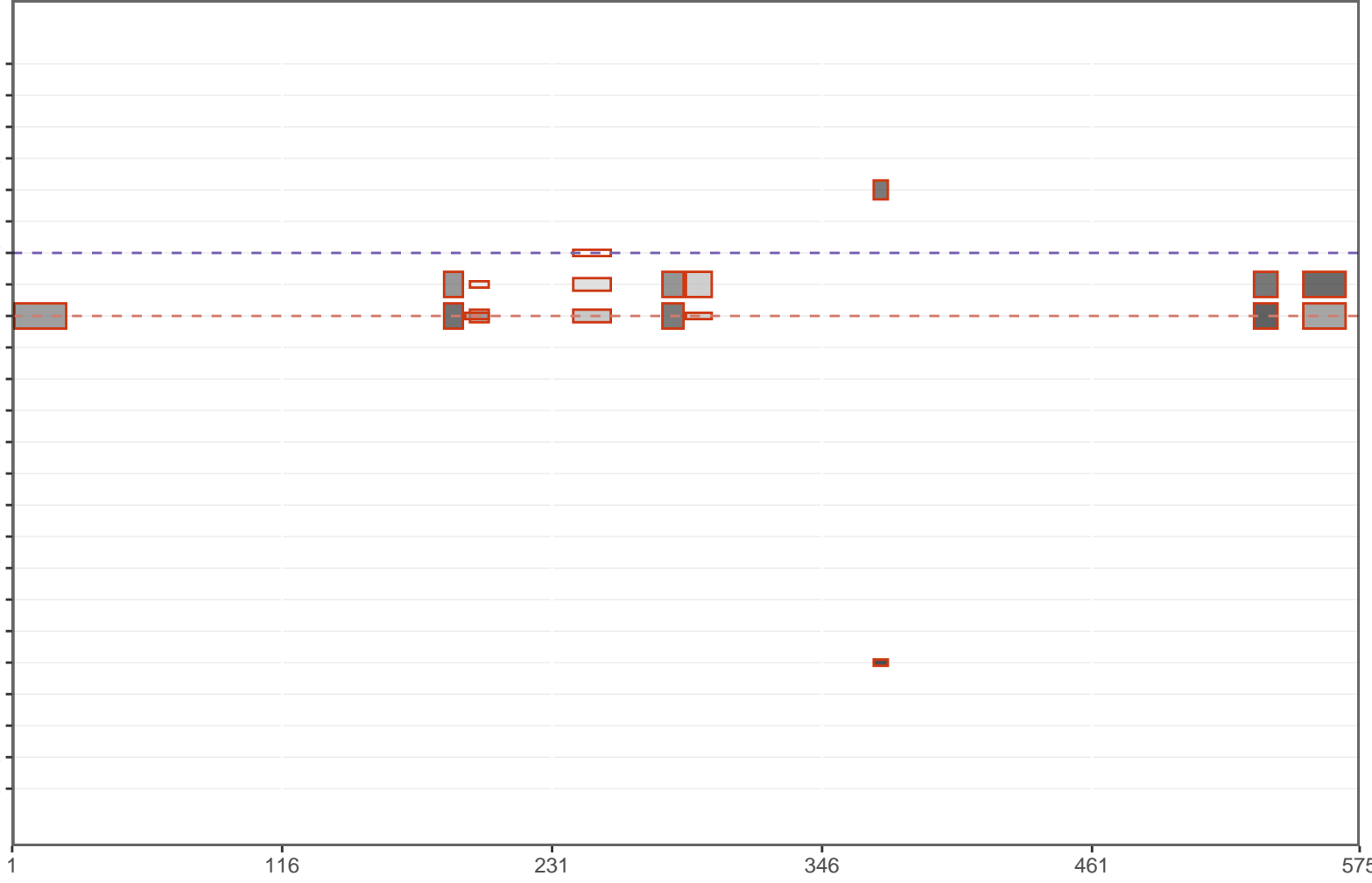
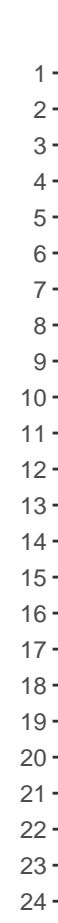
MW indication



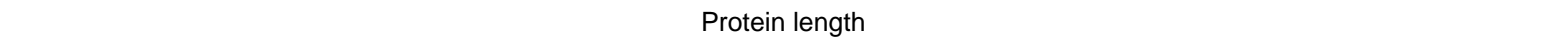
Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00205 Thiamine pyrophosphate enzyme, central domain
- PF02775 Thiamine pyrophosphate enzyme, C-terminal TPP binding domain
- PF02776 Thiamine pyrophosphate enzyme, N-terminal TPP binding domain

Protein sequence:

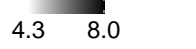
SKCDVALVIGARLNLWLFGEPPWWSKDFKFLVDVAEEIEIURKPLGLGVDATKVVEMLHKEIKDNFFLGLGKSHPPVEALAKKSKENVSKMEVQLAKDVPFNFMTMRIRHDMALGVSGPAPVVVSEGANMMDVGRVIVGTETPRRLDAGTWGTMGVGLGIAAAVAGPERLVVWEGDGGFGFSAMEVETLVRVQLFVWVWFNNGGVVGGDRRNPEETGPPYKEDRNPSTFVPGABYHLLIEAFGGKGYLWGTPEELRSALSESFSARKPWNVTIDPYGSESGR

NbL02g15180.1 ribulose_bisphosphate_carboxylase_small_chain_S41_chloroplastic-like [MW = 20.18 kDa]

No. of times detected



log(intensity)



Values from



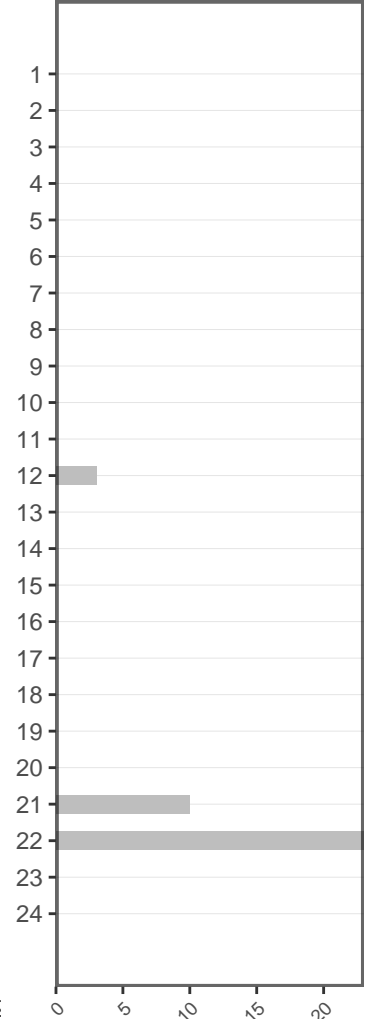
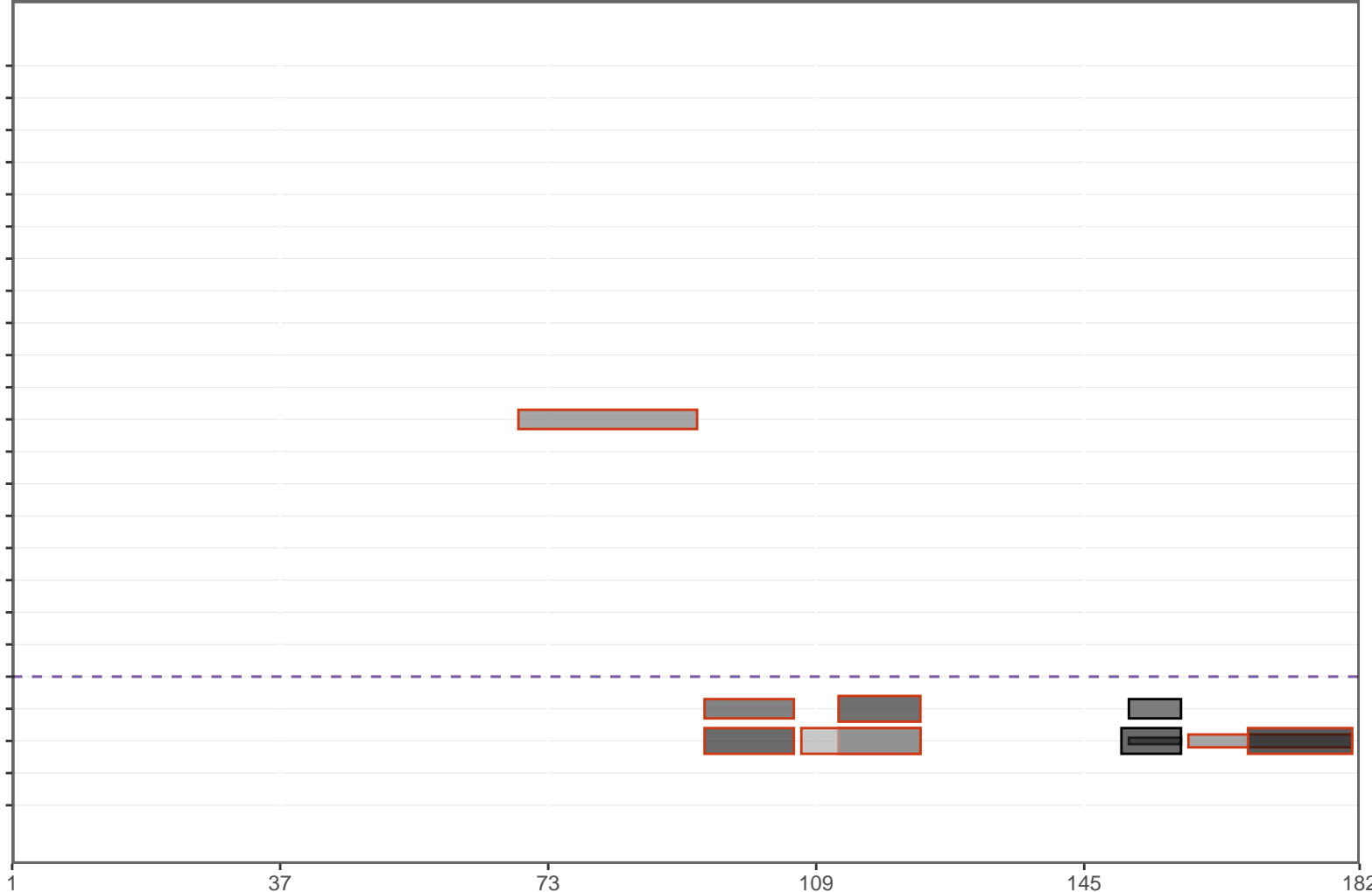
MW indication



Molecular weight

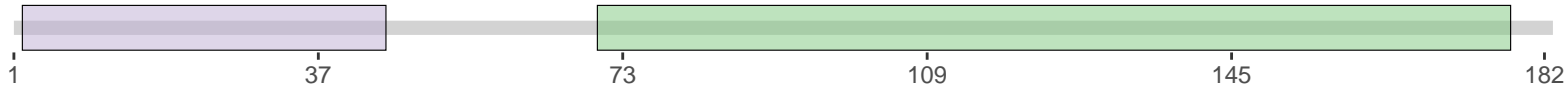


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

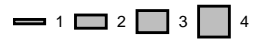
- SP
- Sequon
- TM Domain
- PF00101 Ribulose bisphosphate carboxylase, small chain
- PF12338 Ribulose-1,5-bisphosphate carboxylase small subunit

Protein sequence:

LSQELLSEVEYLKNGWVPCLEFETERGFVYREHHSRPGYVDRGRVWTKLPMFGGTDATQVLAEEVEAKKAVPQAWVRIGFDNVRQVQGISFIASKPEGYI

NbL02g15130.1 ubiquitin_receptor_RAD23d-like [MW = 41.21 kDa]

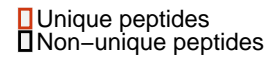
No. of times detected



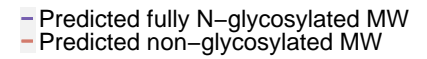
log(intensity)



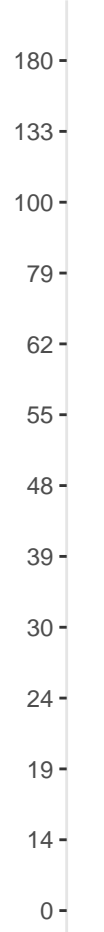
Values from



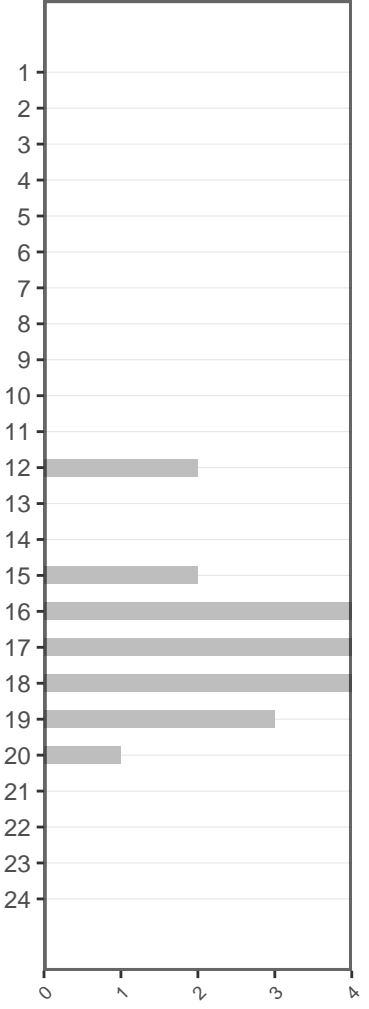
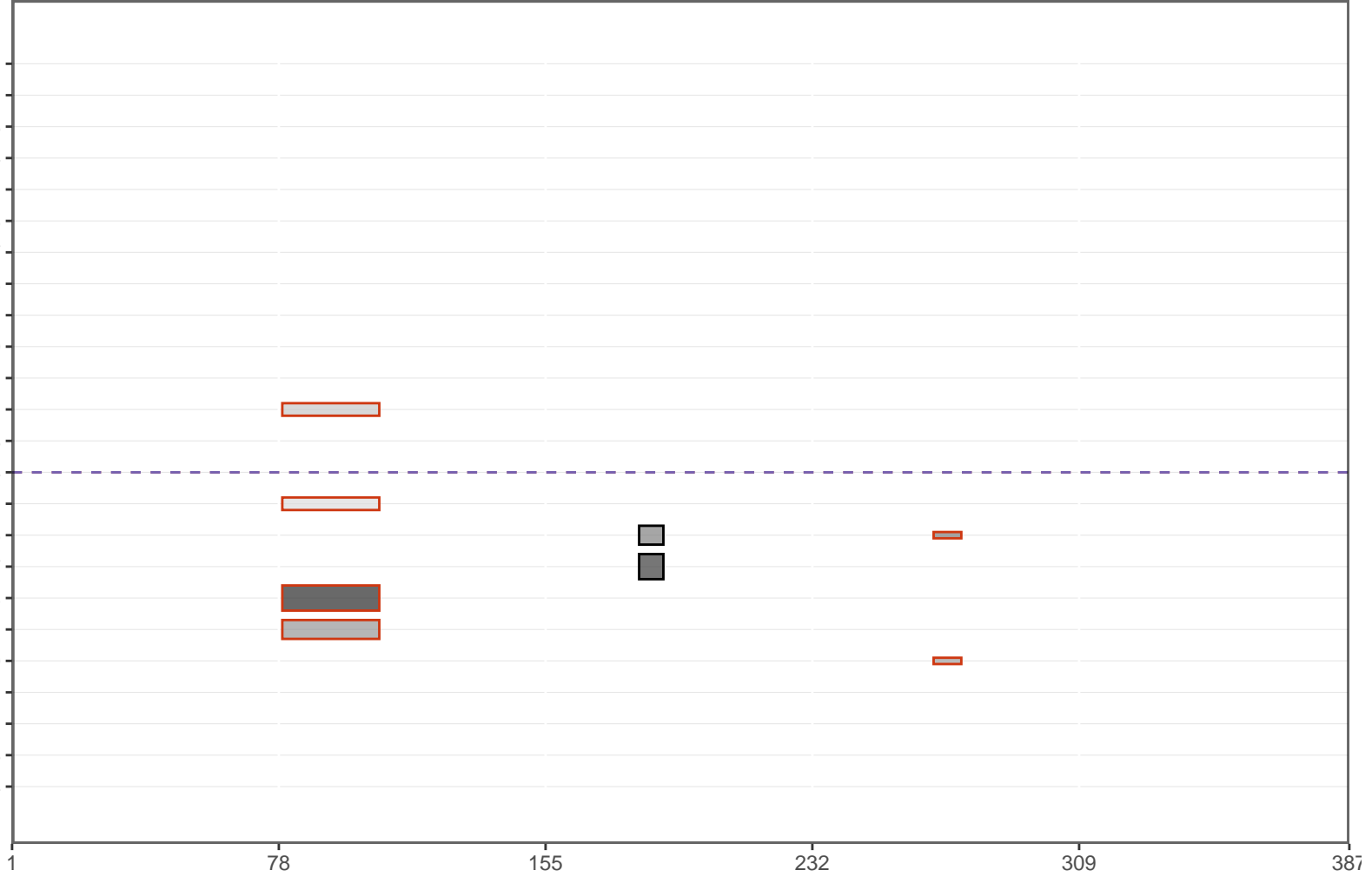
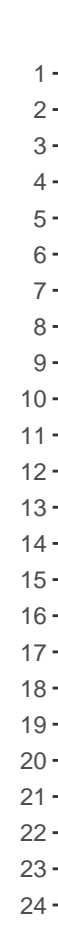
MW indication



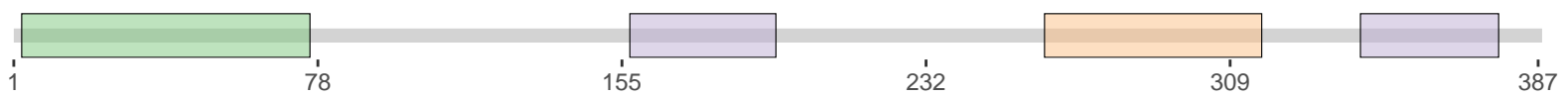
Molecular weight



Gel Slice

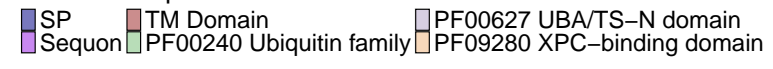


Protein length



Pfam domains

Pfam Description



Protein sequence:

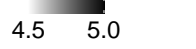
RAAYNPERAVDYLKSGIPEQAEIPFPAPTAATASGGAVNPSAGEAGQVWPSGGPNPLDLFPQVGLPNVGSNAGSGNLDRLNSPQALRTMVGANPQLQPMLELGGKGNPHLMRLQEHQPDFLRLINEPVEGGSAIGMAGAPQAVTVTPEREAEERLEAMGFDRALVLEVYFAGNKNKEELAANNLLDHHMEFDE

NbL02g15100.1 HEAT_repeat-containing_protein_5B [MW = 251.17 kDa]

No. of times detected



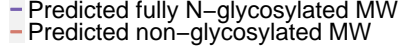
log(intensity)



Values from

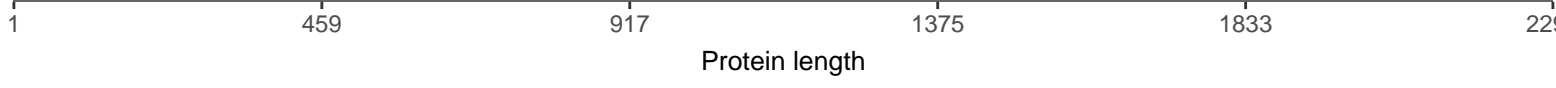


MW indication



Molecular weight

Gel Slice



Pfam Description
 ■ SP ■ Sequon ■ TM Domain

Protein sequence:

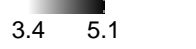
SGNDSSGLDCEAGLNYGDDDEDMVSSGNPTFDGVRGSHPIWLPFNKHLYRTRVFAAEGLSHLPAVGNKPAHFDAVALARKQPSGSPSSGDMVLLGLGELVSLAVQISTGFENMRPVGNLLSTIDKFGTLDPEFPCHLLEGGVQAQLVAVRTALDSSSGPALLEAGLQLATKILTKQKIVSRDGLAVKRIFSLGRPLNEFNLYVPSFAEWWGCKIKVRLTTHASLKKYTFAPLKNQKQVEQVDEVLALLPLFSVSSKILGHWLGLLKDQVYRTQSFQENWKPFLDGI

NbL02g15050.1 ultraviolet-B_receptor_UVR8-like [MW = 41.71 kDa]

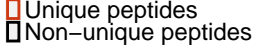
No. of times detected



log(intensity)



Values from



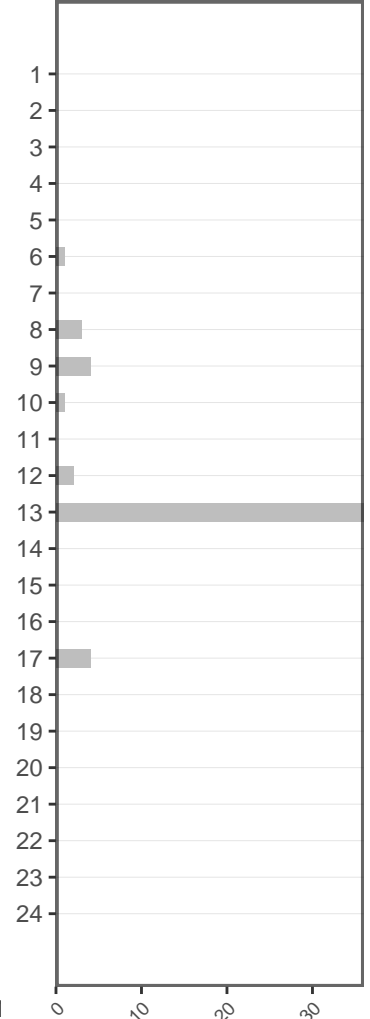
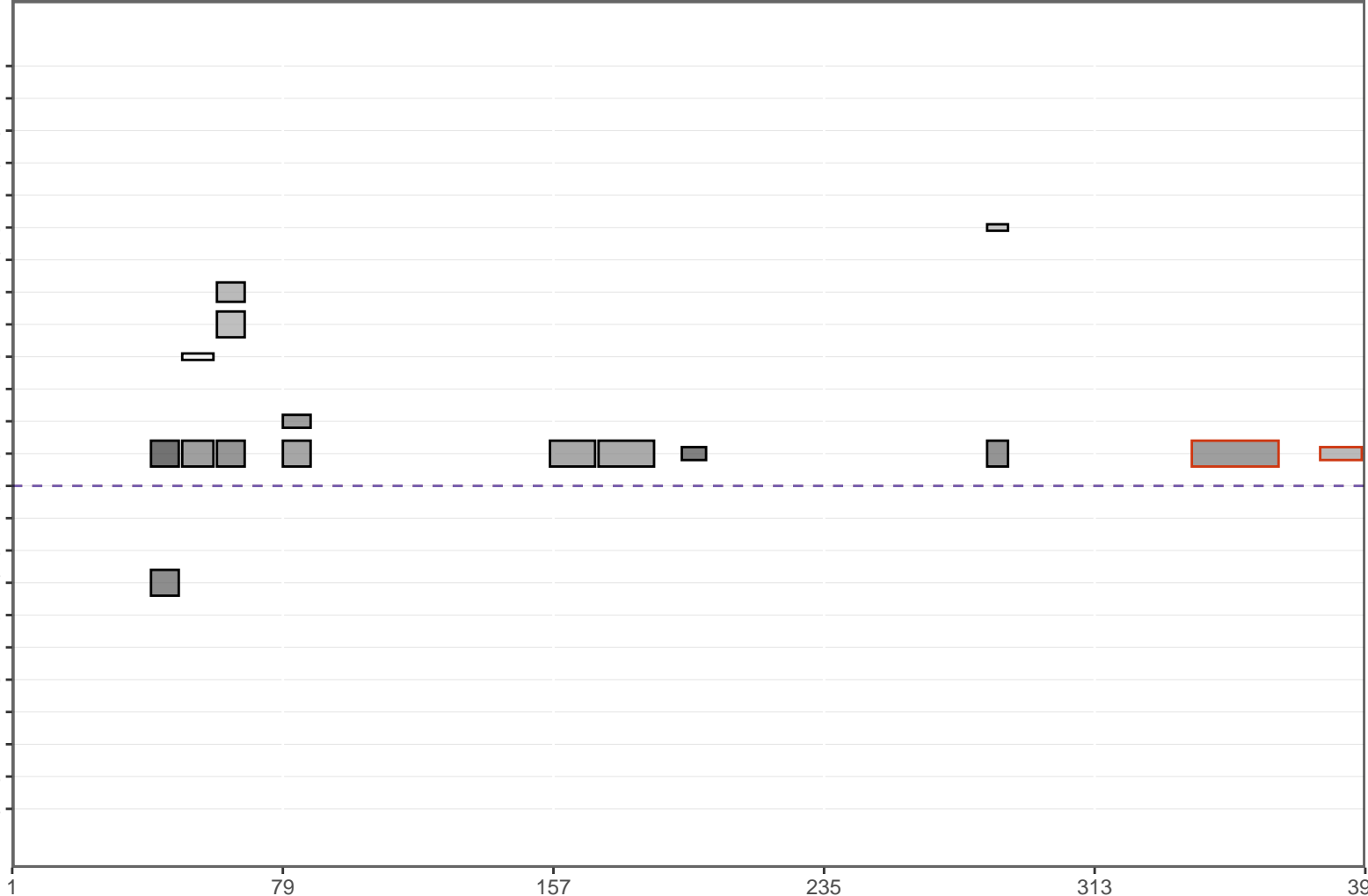
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

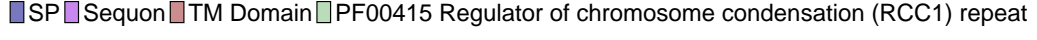
Protein length



Pfam domains



Pfam Description



Protein sequence:

SDIKQISTPVIRVOGLASVRLMVGAFHNLALLDDGLMAMWGNNEVYDGLGTGDTQPRRQPIAVQGLSGLTLVDMAAGDWHSAALDEGEVYVWGRGEHGRLLGFGDDKSKMVPQKVOLLAGENIVGVSDGGTHSVALTHDGRMFSFGRGRDHRLLGVRKVTTFGHPSEVPIPIPPPSDVSSTQGERWGAKLVAQGRHTLAVVEWQEESK

NbL02g15000.1 allene_oxide_cyclase_chloroplastic-like [MW = 26.18 kDa]

No. of times detected



log(intensity)



Values from



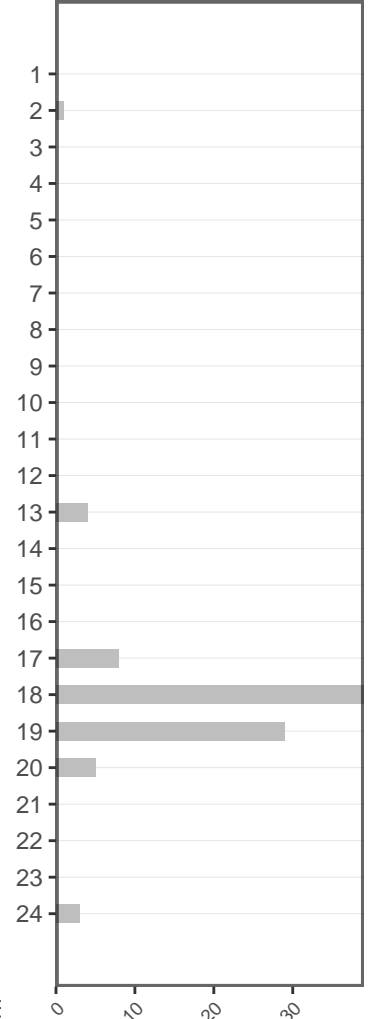
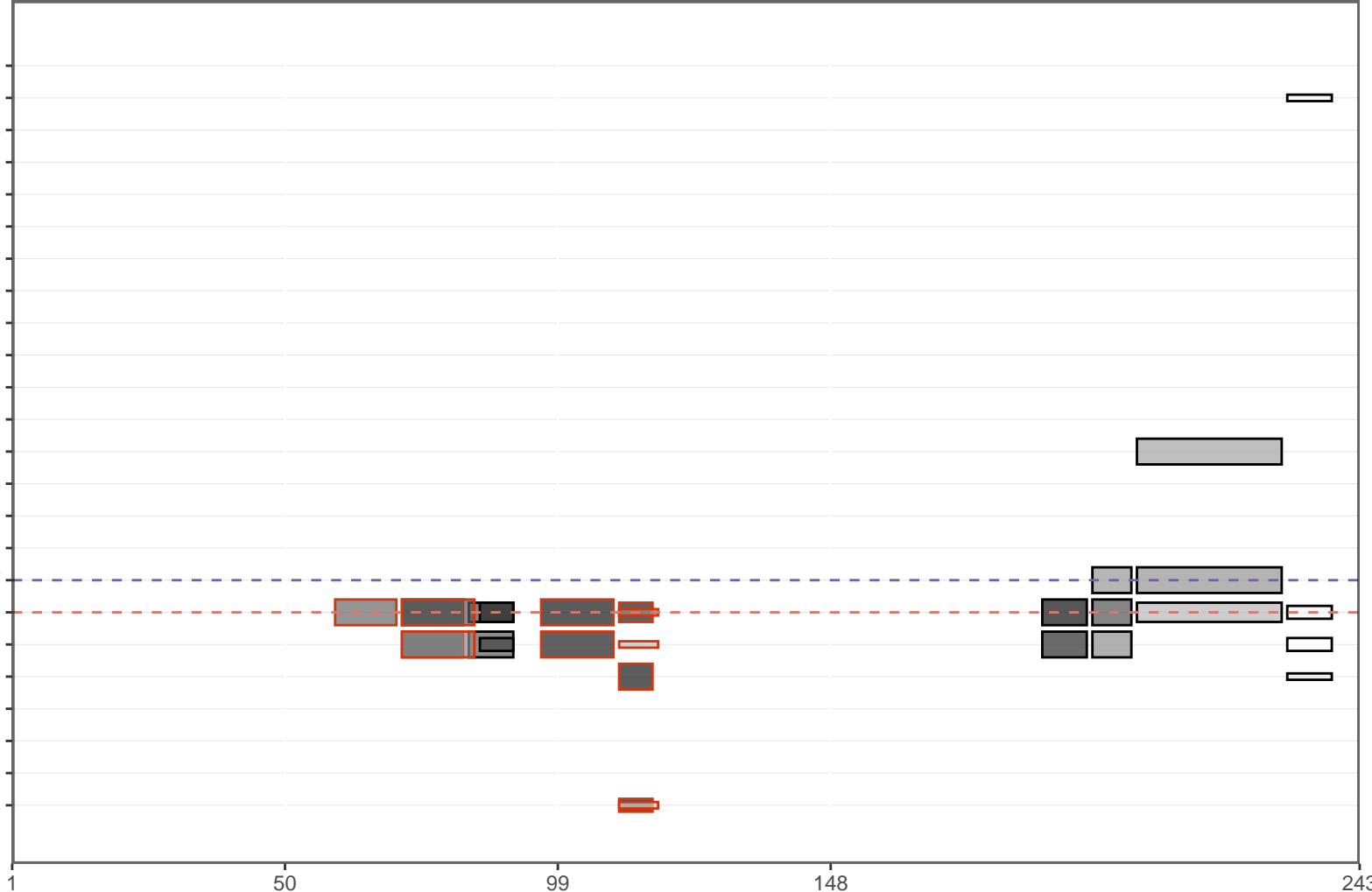
MW indication



Molecular weight

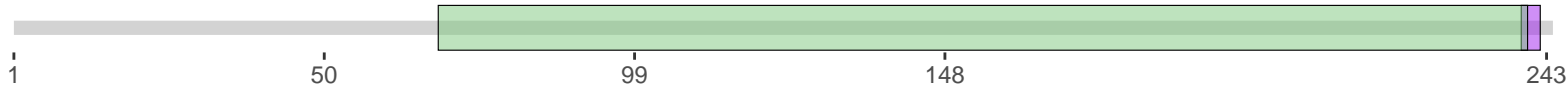


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

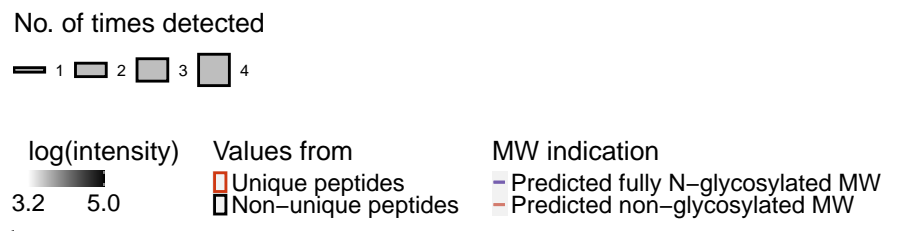
Pfam Description



Protein sequence:

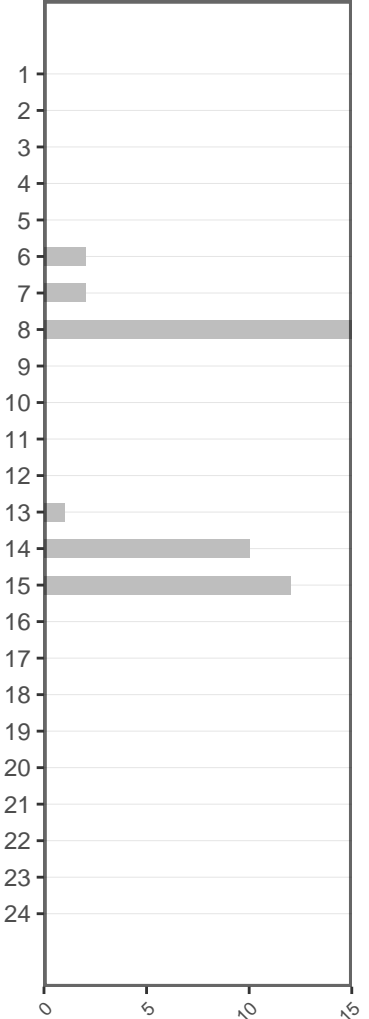
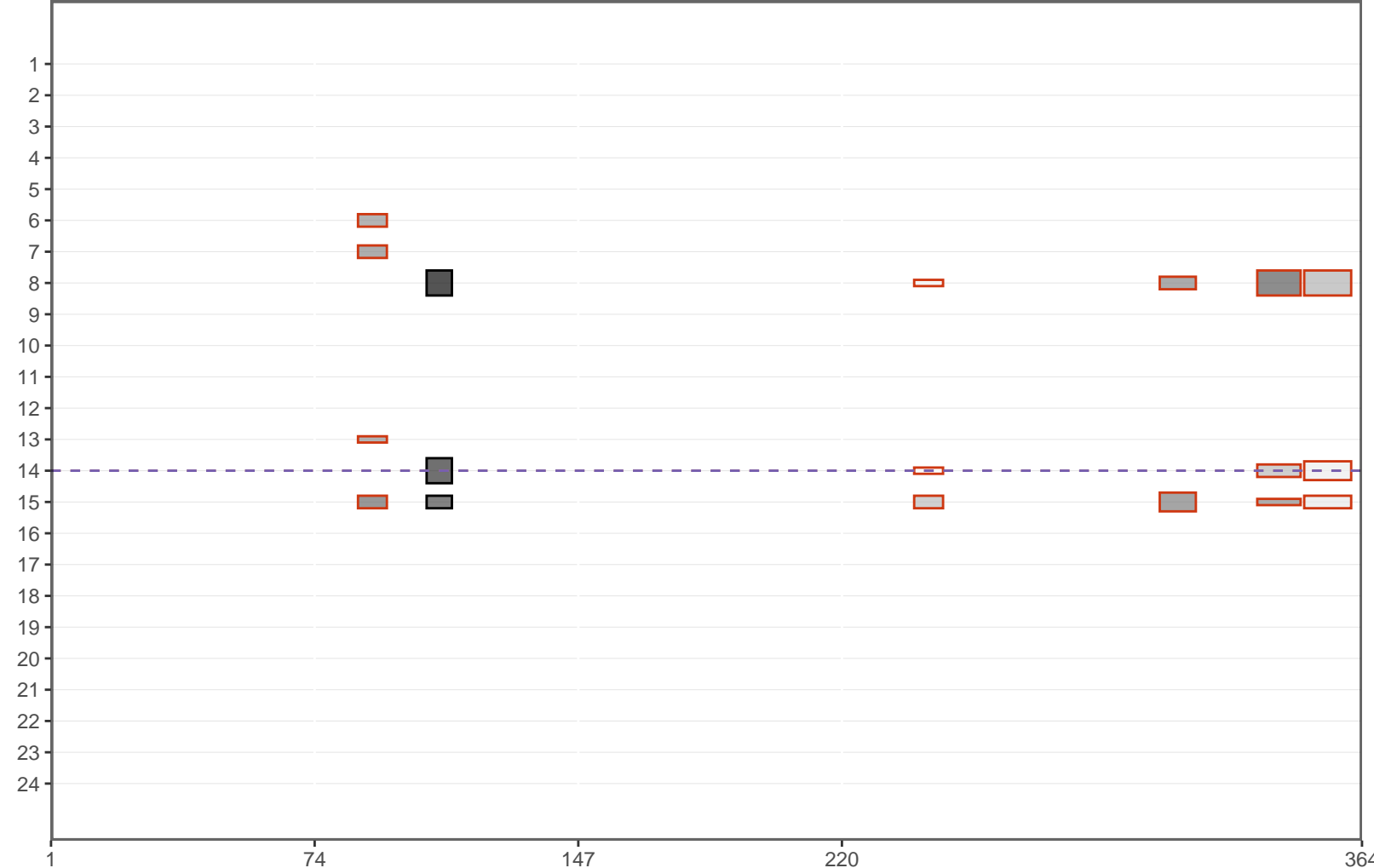
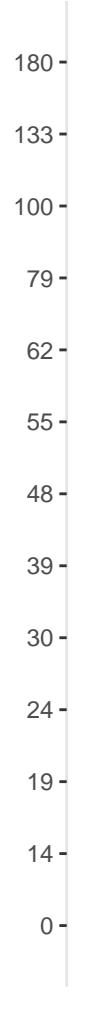
INKLYTGDLLKRRIGTAGLGLLRLKHEEEKKGRVYEANRSEYFQNYGHAVGGSYLTYEDSYLAVTGGGGIFAGVSGDGLGQIIFPKLFTFYLYLKGIDLPSELLVAVPPSPPTVEPPEAKKAGEAGATKKNFTN

NbL02g14970.1 geranylgeranyl_pyrophosphate_synthase_chloroplastic-like [MW = 39.56 kDa]

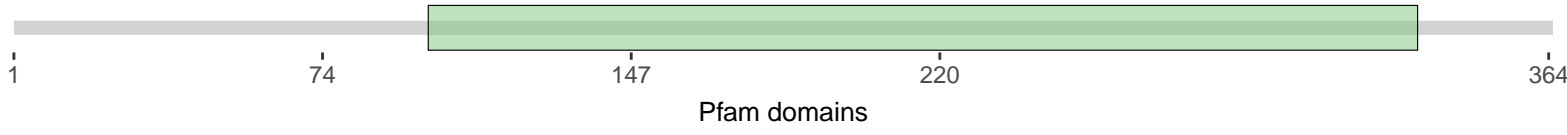


Molecular weight

Gel Slice



Protein length



Pfam Description
 SP Sequon TM Domain PF00348 Polyprenyl synthetase

Protein sequence:

ITNKKYGEDVAVLAGDALLALAFEHATQKGVPSHRVIRVVGELAKGICGAELVAGGVVDSIEGVSVDLKHLEFHLHKTAALEGGVVLGAILGWADDEEVEKLRKFAFGICGLLFGVDDILEVTKSSDQLGKTAQKDLVADKVTYKPLGIEKREFAEELNKEAQAQAGLAFDGGKAAPLALANVAVREN

NbL02g14740.1 F-box_protein_At5g49610-like [MW = 40.18 kDa]

No. of times detected



log(intensity)



Values from



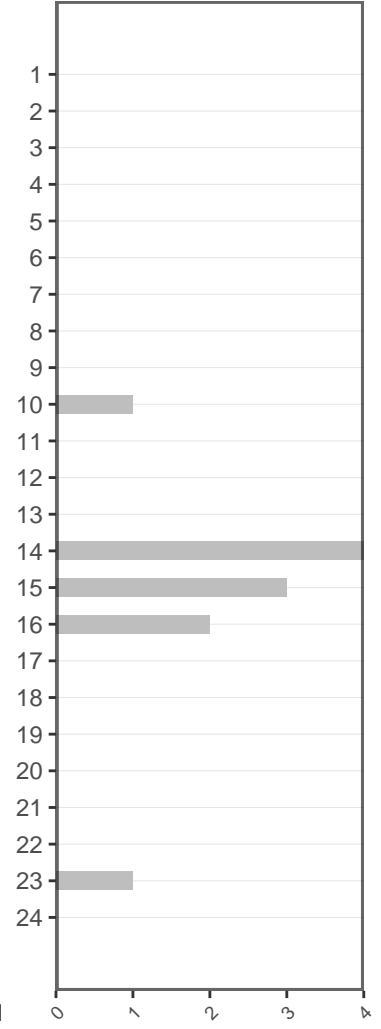
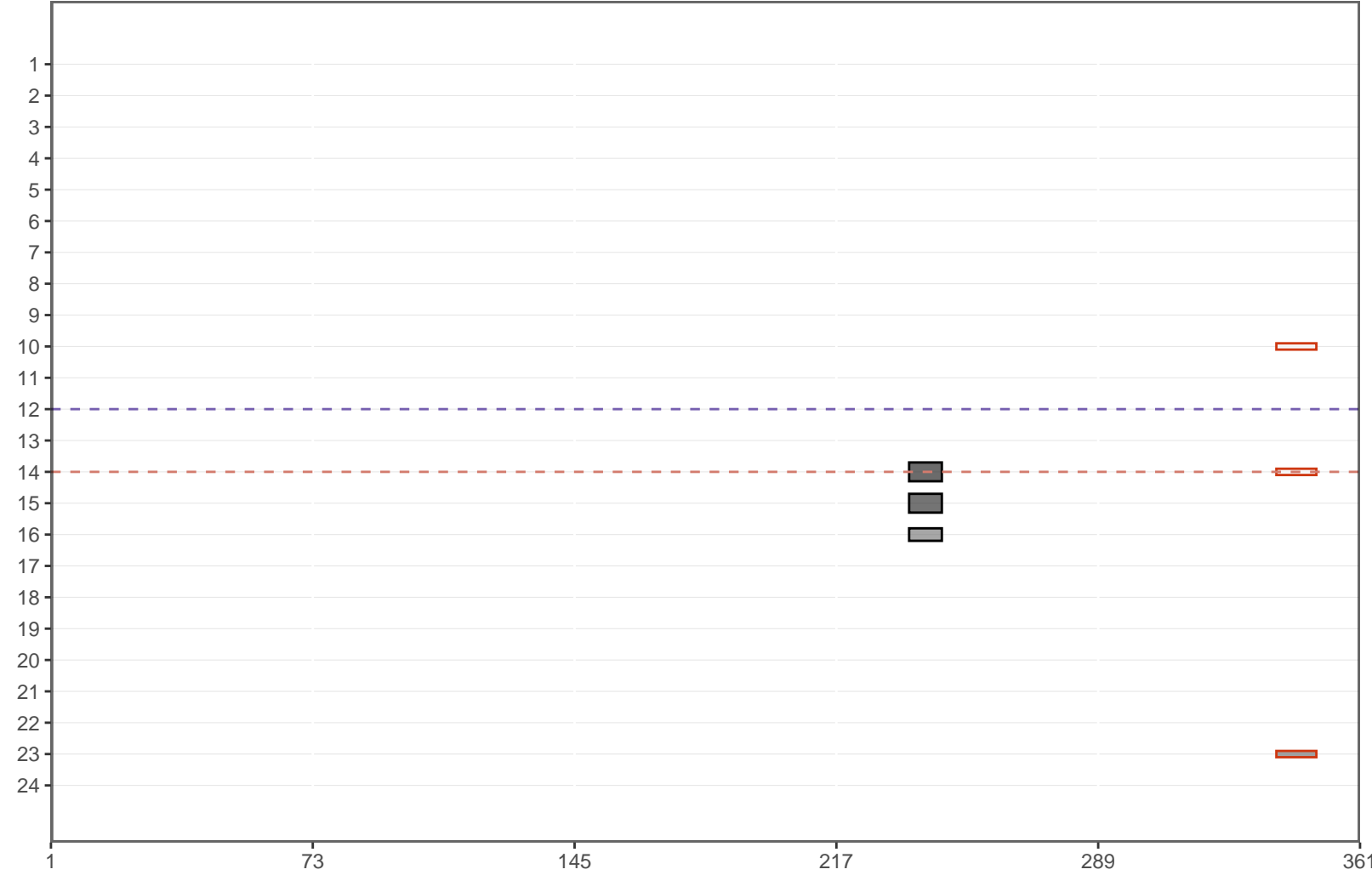
MW indication



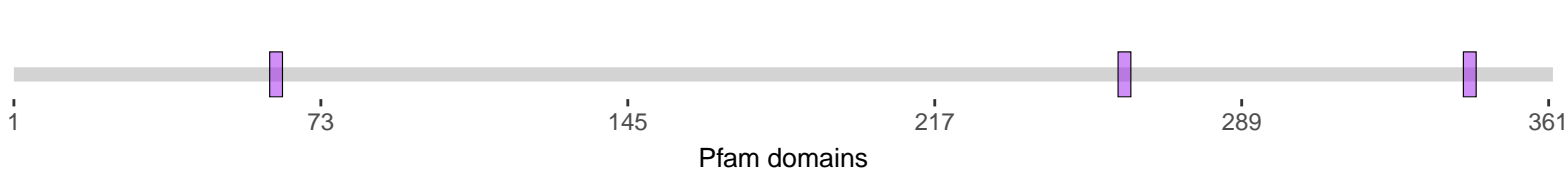
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

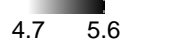
YKICAFPSDFDEATEFEVSSKEGTWEIAGEIGFGAWRVIPKSGVHVGVVYMMTTGSLAFDLTKERBQLLDVYARGLGVFSGKLGKCANVSGNRIIVYLTNAHNTMQMGSNTRMVESEKGGVLDKIVGDVARDYVSLVHVDGDMVHHSRERMYSYDFKSRATKAMENVEDIYMRGLFVYNNLVEL

NbL02g14680.1 succinate_dehydrogenase_[ubiquinone]_flavoprotein_subunit_1_mitochondrial [MW = 69.19 kDa]

No. of times detected



log(intensity)



Values from



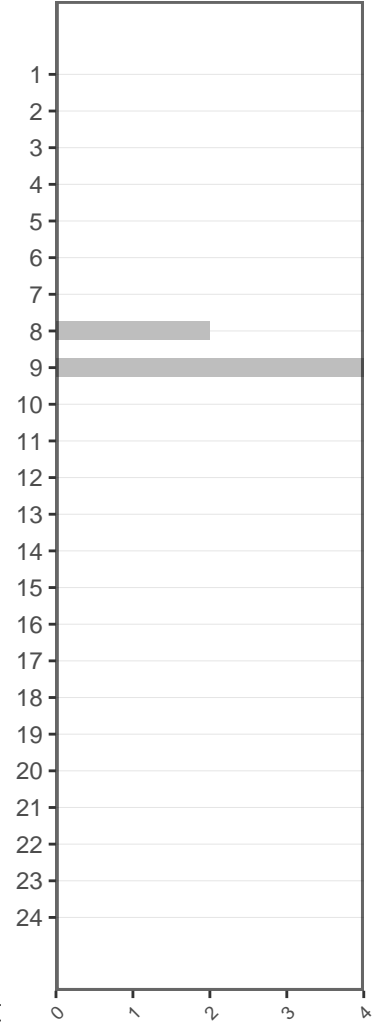
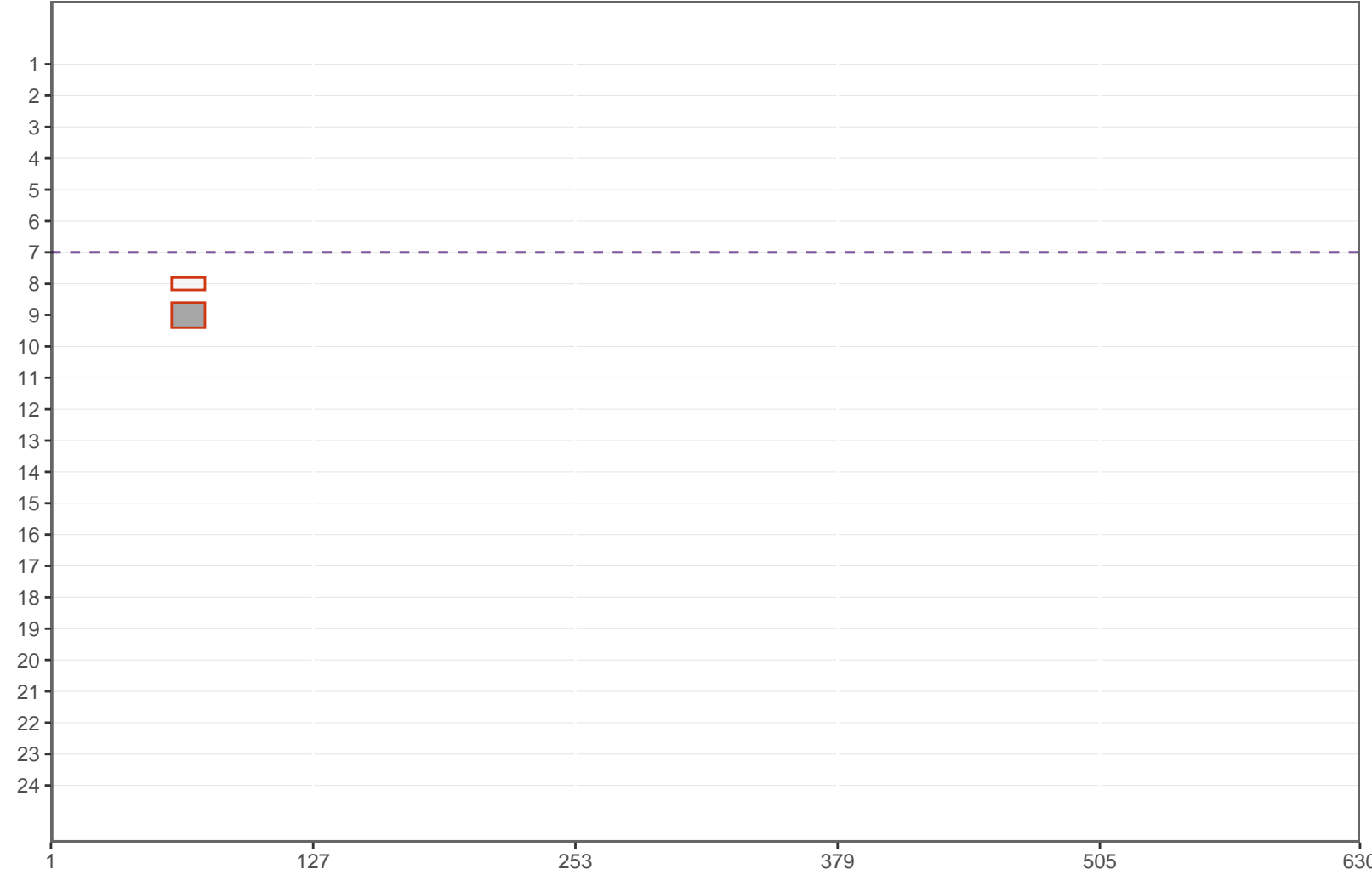
MW indication



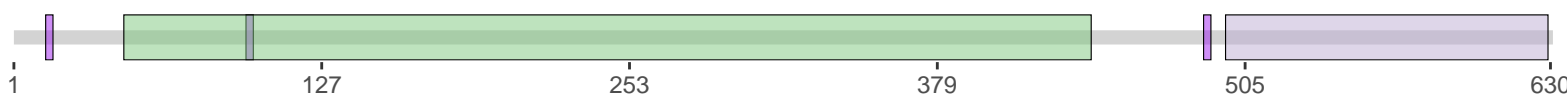
Molecular weight



Gel Slice

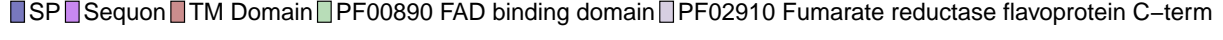


Protein length



Pfam domains

Pfam Description



Protein sequence:

SGILRNSEGERFMERYAPTANDLABRDVVRSMTEIREGRGKGLKDHVYHLNHLPEVLKERLPGISETAIFAGVDVTKRPIPLPTVYHNMGGIPTNYHGEVYTKGDNPDVAVPGLMAAGEAGCASVHGANRLGANBLDDIVVFRACANRWAEIQRPGENKPKLEKDGERITWALDKIRNSNGSLPTSKIRLNMQRVMGNNAVFRFTGETLEEGGQLDKTWESFHDVQLKDRBLWNSDUEIETLEENLINAGITMHSAEARKESRGAHAREDFTKRDEEKVMK

NbL02g14600.1 pyridine_nucleotide-disulfide_oxidoreductase_domain-containing_protein_2 [MW = 61.22 kDa]

No. of times detected



log(intensity)



Values from



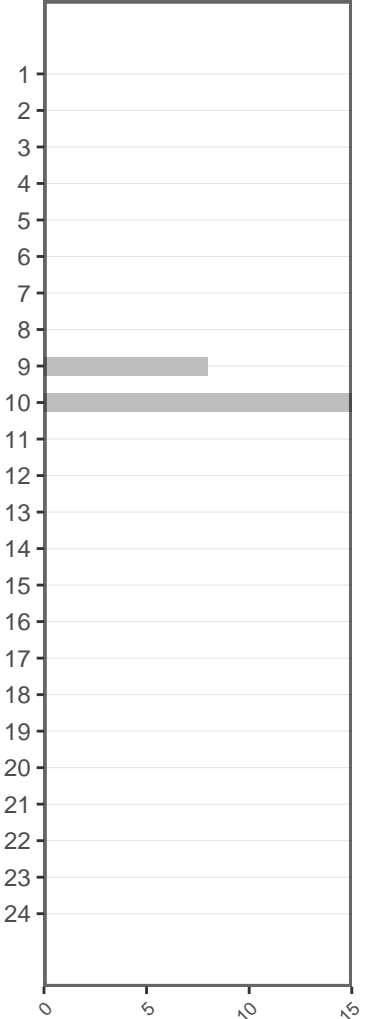
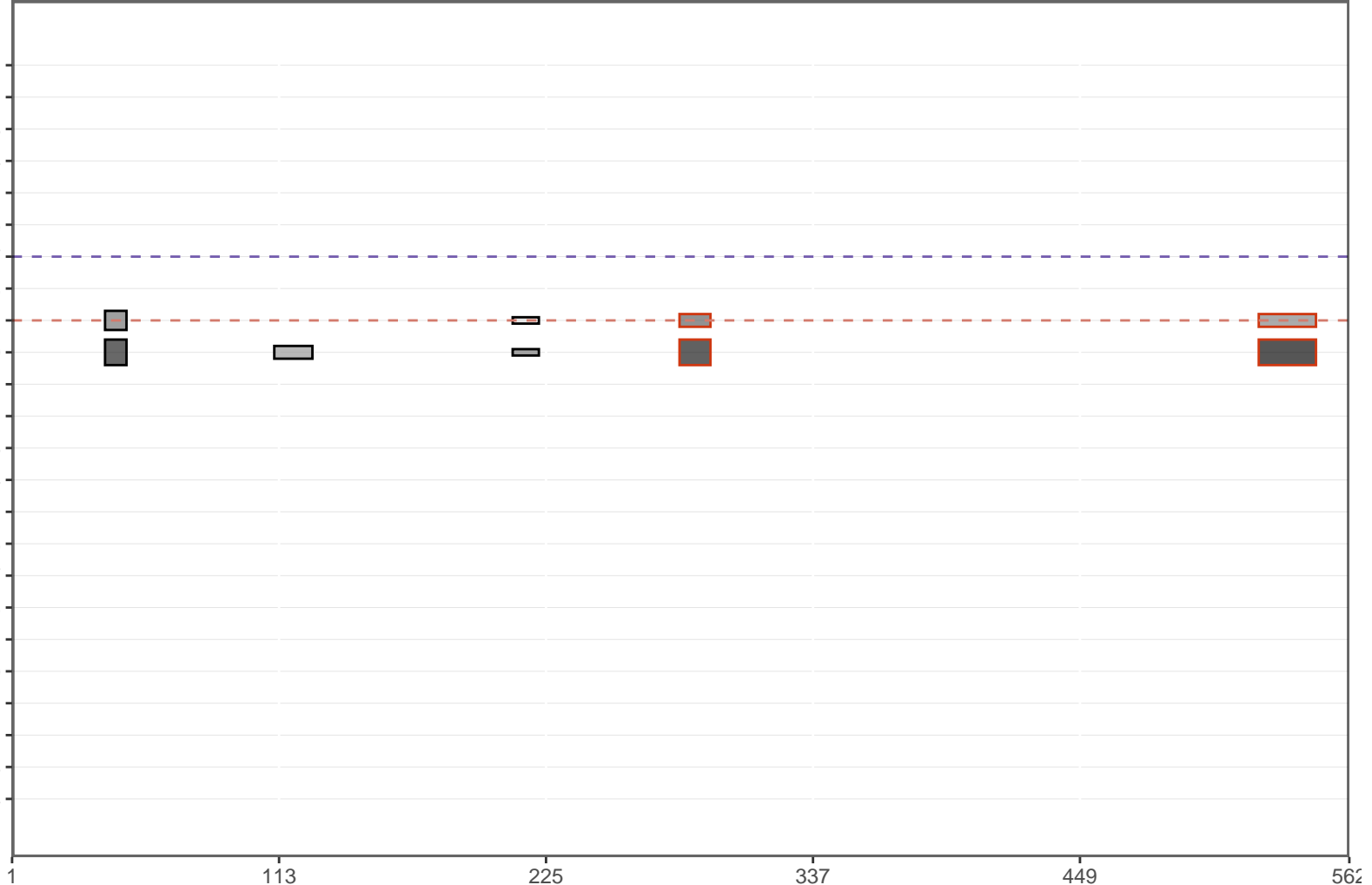
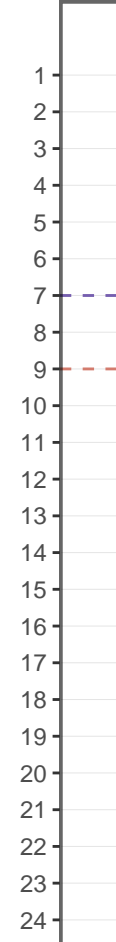
MW indication



Molecular weight

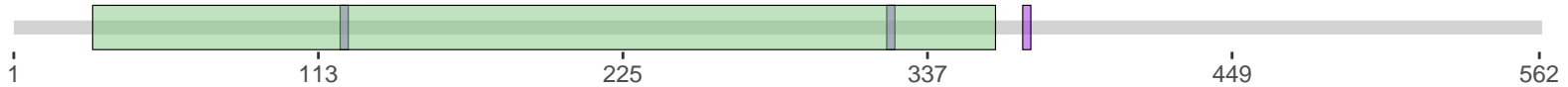


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SMGVSMAUAAAAKEAGATATNAEVSKLMEIDTGRVHGVMADGTLHSVLSGNATPKTFMQLPDDVLPDFHNAKSSDYRSATTKINLAVDGLPQFGCCNISHPDAQPHGSHTHIGPESMEEMHLAQAENGLPSRRRIEMTIPTVDFKTRSPGKHVIGLFIQYTPYKPGDGGWENFYRESFAGRFQSMIDVYAPGFS6SVHGVDMLTPPOLEREIGLTCGNFHGSMGLDLSFLMRPVKGSWNYRTPVEGLVCGSGAHPGGGVMGAPGRNAHVVIEDLQKS

NbL02g14440.1 uncharacterized_LOC109242336 [MW = 84.18 kDa]

No. of times detected



log(intensity)



Values from



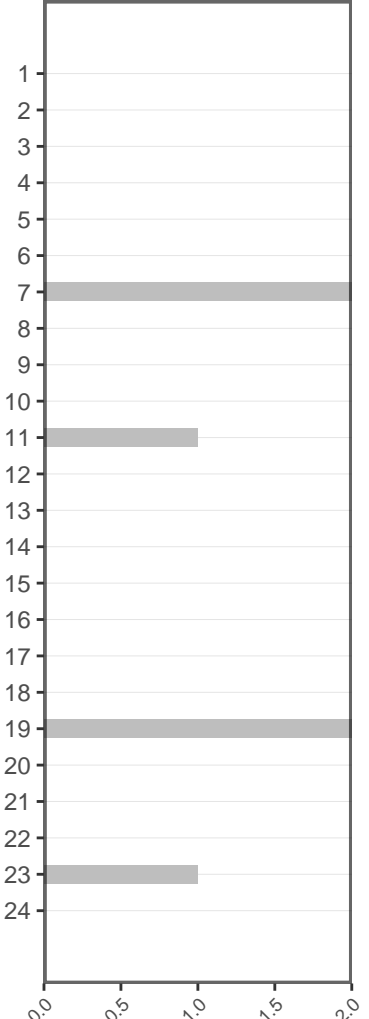
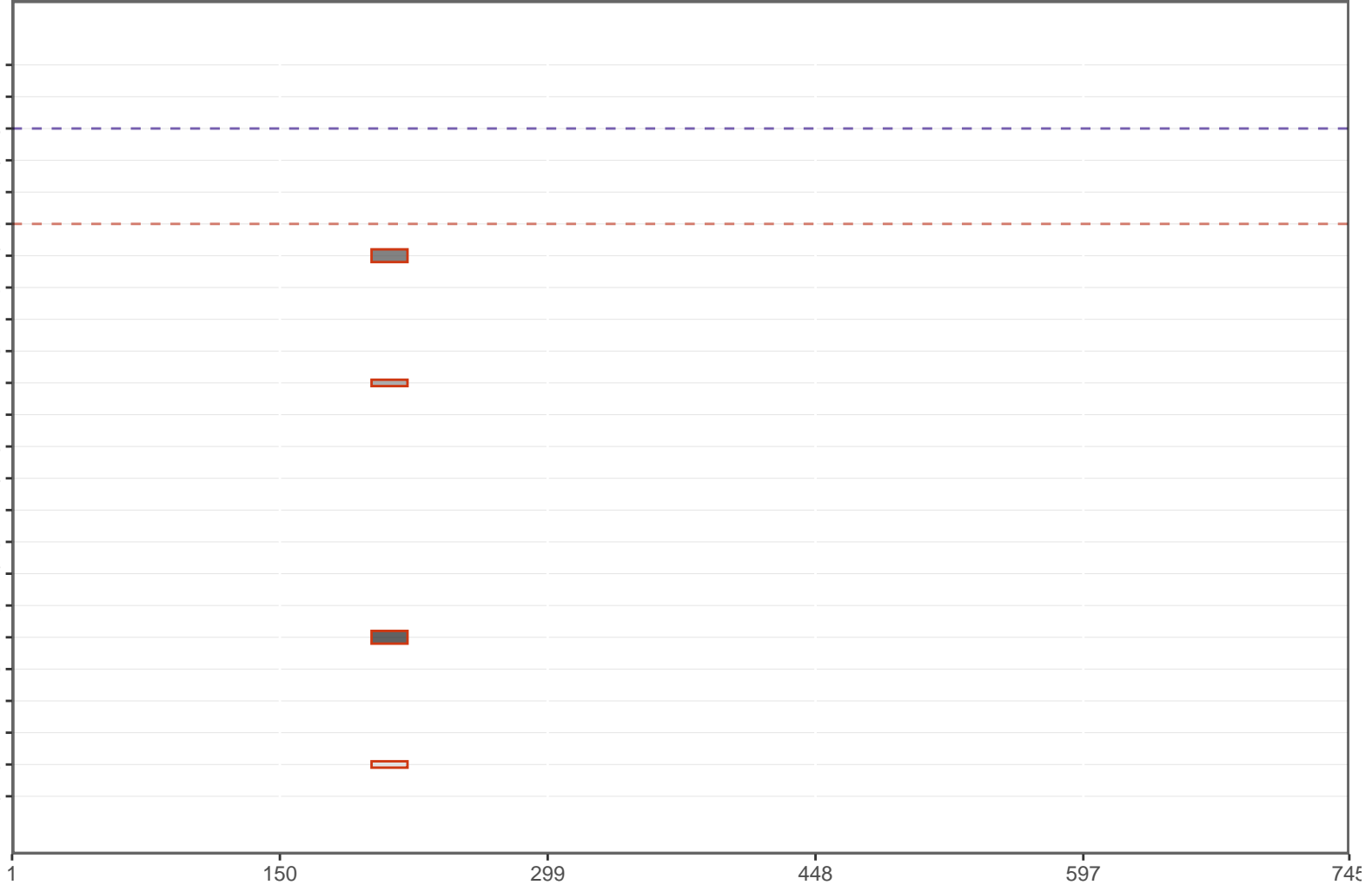
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains



Pfam Description
 SP Sequon TM Domain

Protein sequence:

SSCRTSRRESFPERGRPIDEALVIAKASIVIEBLRPFVADSYQPALEEFQHKKEALLKDLVSSNETFPQVLFMSPGSGGKRTLAIALLRREYGDACINSHLKYFQIKETRPMDVYVYVSSPHHELVNQLFENARVAIMAFYKIGISEVALTPEISRVNMAKDYKVVVLYNVDKAAENIGHLKWIMDCYSDACKHLGCEDDVSTLGSVNRTRKVVVELAAPVTHEIMKVLIEARKEDFELFMEFAAIAAKSKGNLRRRAIMALEACKAHNYPFAEDQPIGIVEDIYELAAELAL

NbL02g14360.1 beta-galactosidase_3 [MW - SP = 91.02 kDa]

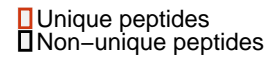
No. of times detected



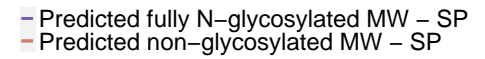
log(intensity)



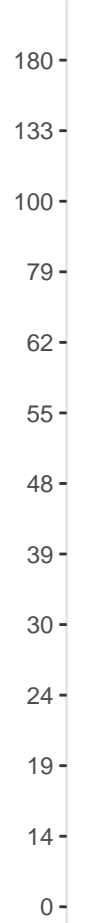
Values from



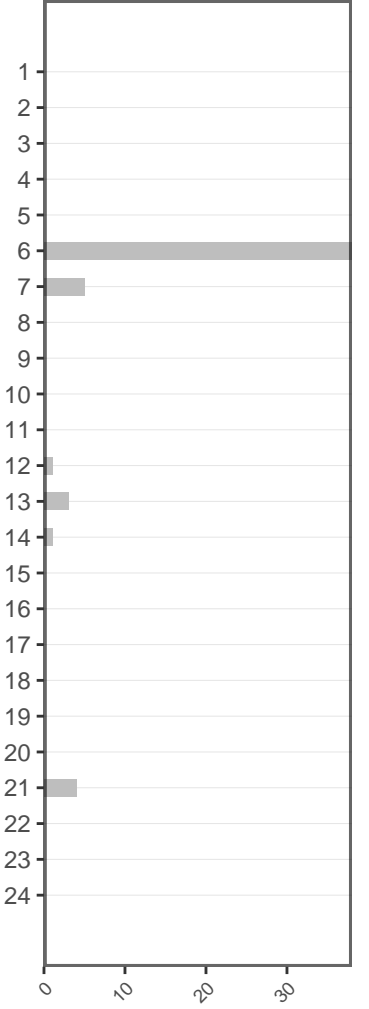
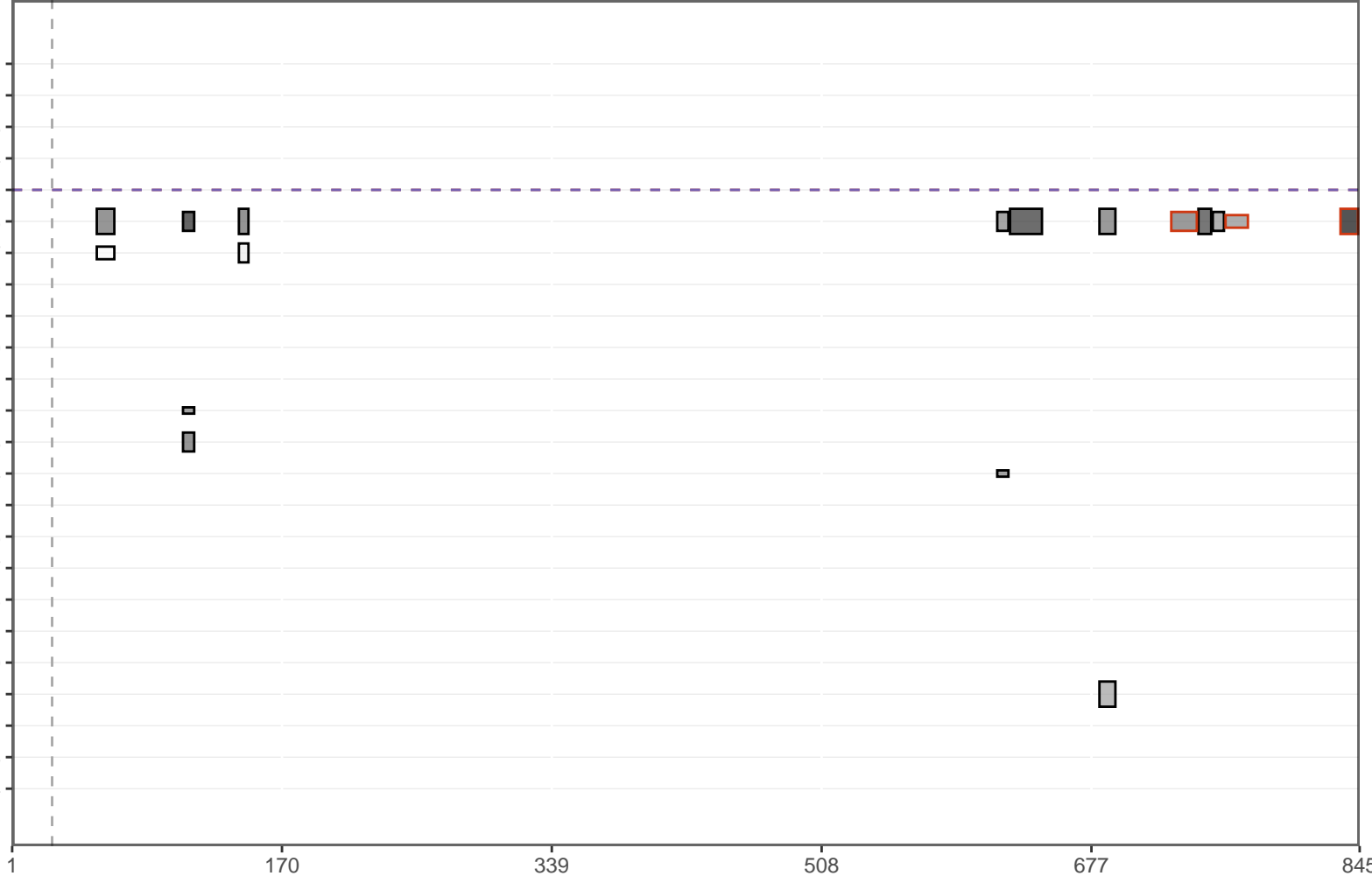
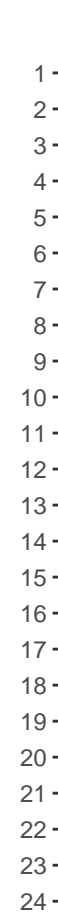
MW indication



Molecular weight

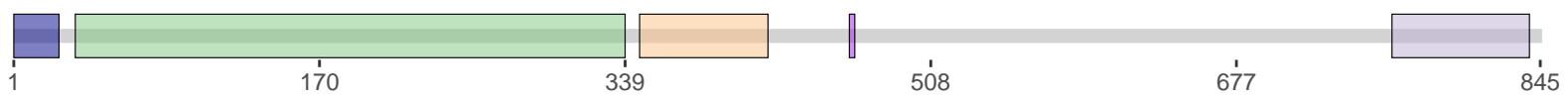


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VVFNATKVGVTSMEMLPINSEMLGWESEFNEDVSDALDDSSLRFRGFLLEQINVTRDTSQRLWYTFSDVSGSTESFLHGGELPFLVVESTGHALHVFINGDLSSGAFGSKNKNRRFVFKGKVLNLAGTNRHLLSVAWGLPNMGGHFFETWSTGVLGPAWHGLDQKWDLSLWAKWYVQVGLKGEAMNLVSPNGISAVDWMGGSLIAGRQGLPLWVKAVFNTPDGDEPLALDMSMKGQVWINGGSGRWTAYATGDCNGGHYSGNFRPKKGLGCGQPTQKYYHF

NbL02g14320.1 probable_ubiquitin-conjugating_enzyme_E2_18 [MW = 22.16 kDa]

No. of times detected



log(intensity)



Values from



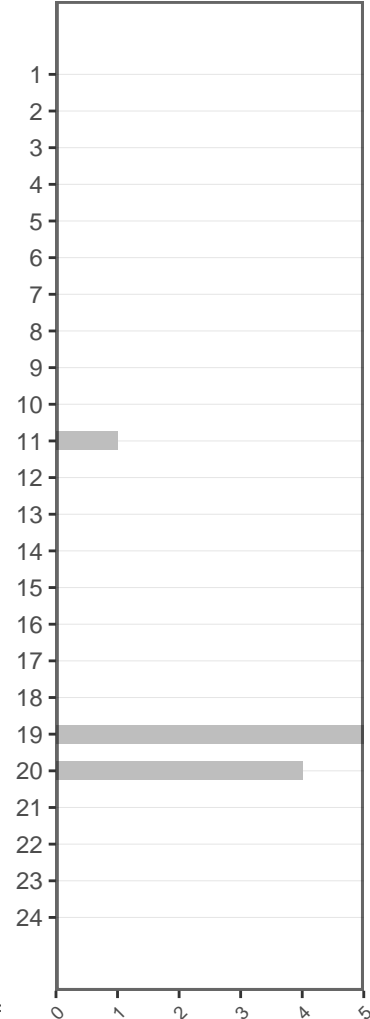
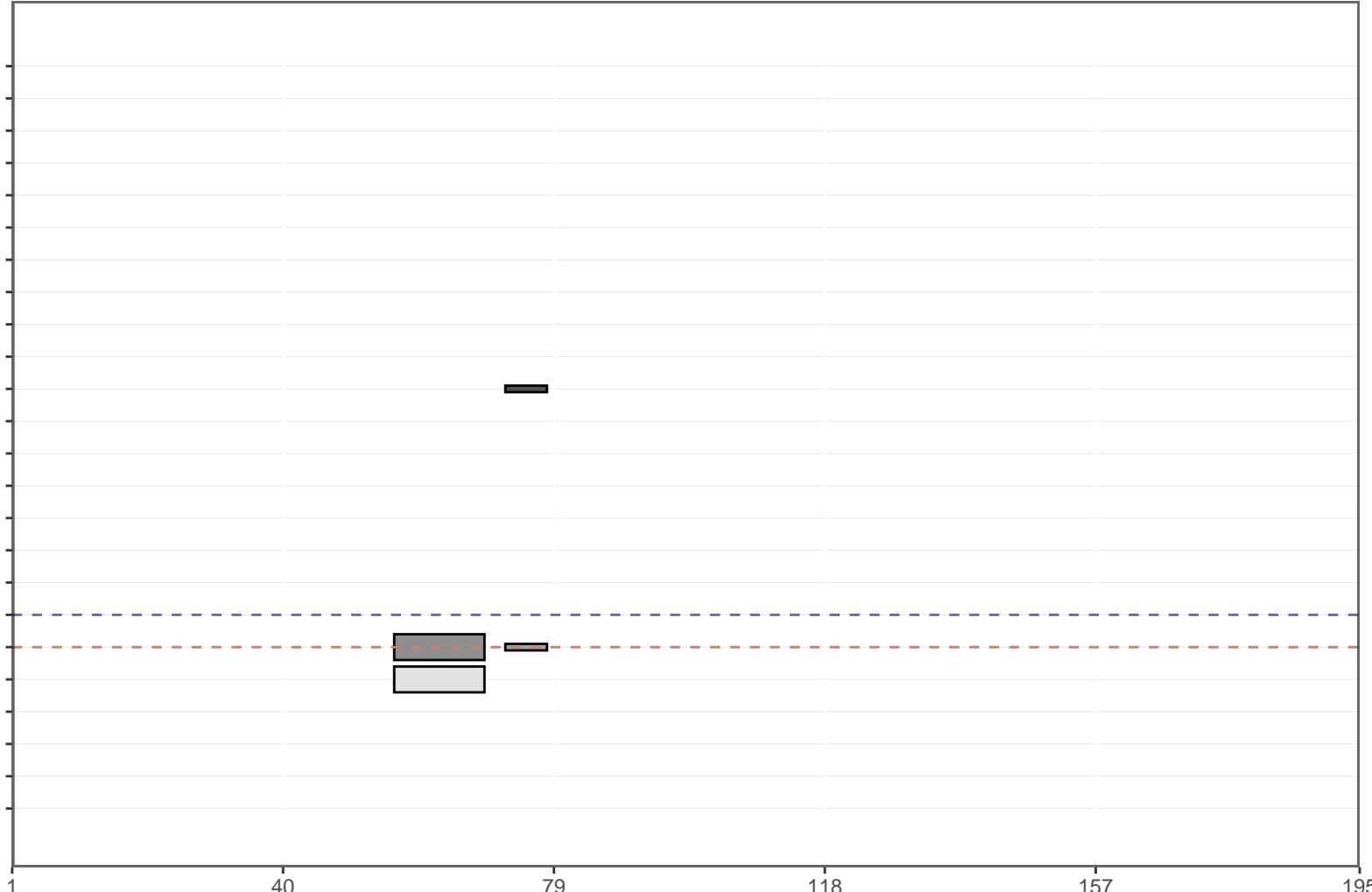
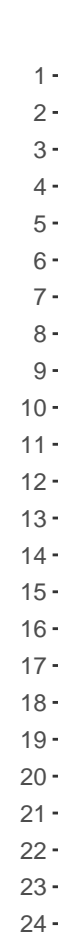
MW indication



Molecular weight

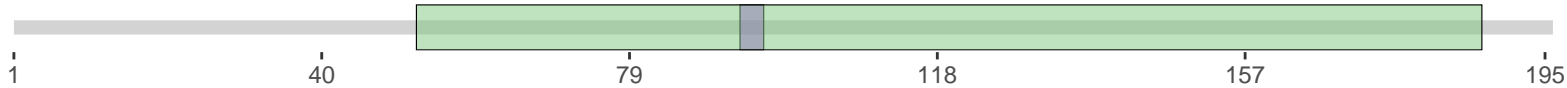


Gel Slice



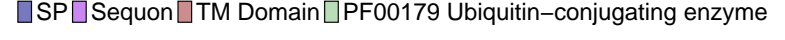
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MAPGTLVAVNETYQLGVDFPEHYFMEAPQVHFVPPALPHPHVYSGHGLDLVDSWPMFTVSSGIGLSMLSSSTVWQRPEQNDRIYVWNCRNGRSPKETRWWFHDQKV

NbL02g14240.1 abscisic_acid_and_environmental_stress-inducible_protein_TAS14-like [MW = 22.14 kDa]

No. of times detected



log(intensity)



Values from



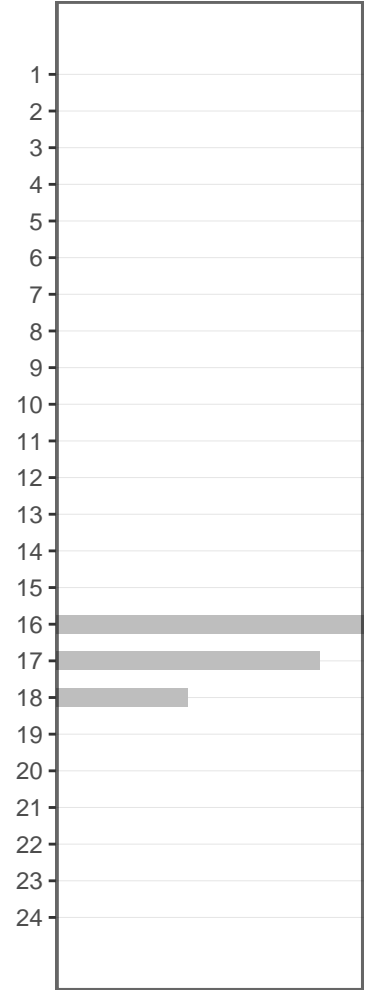
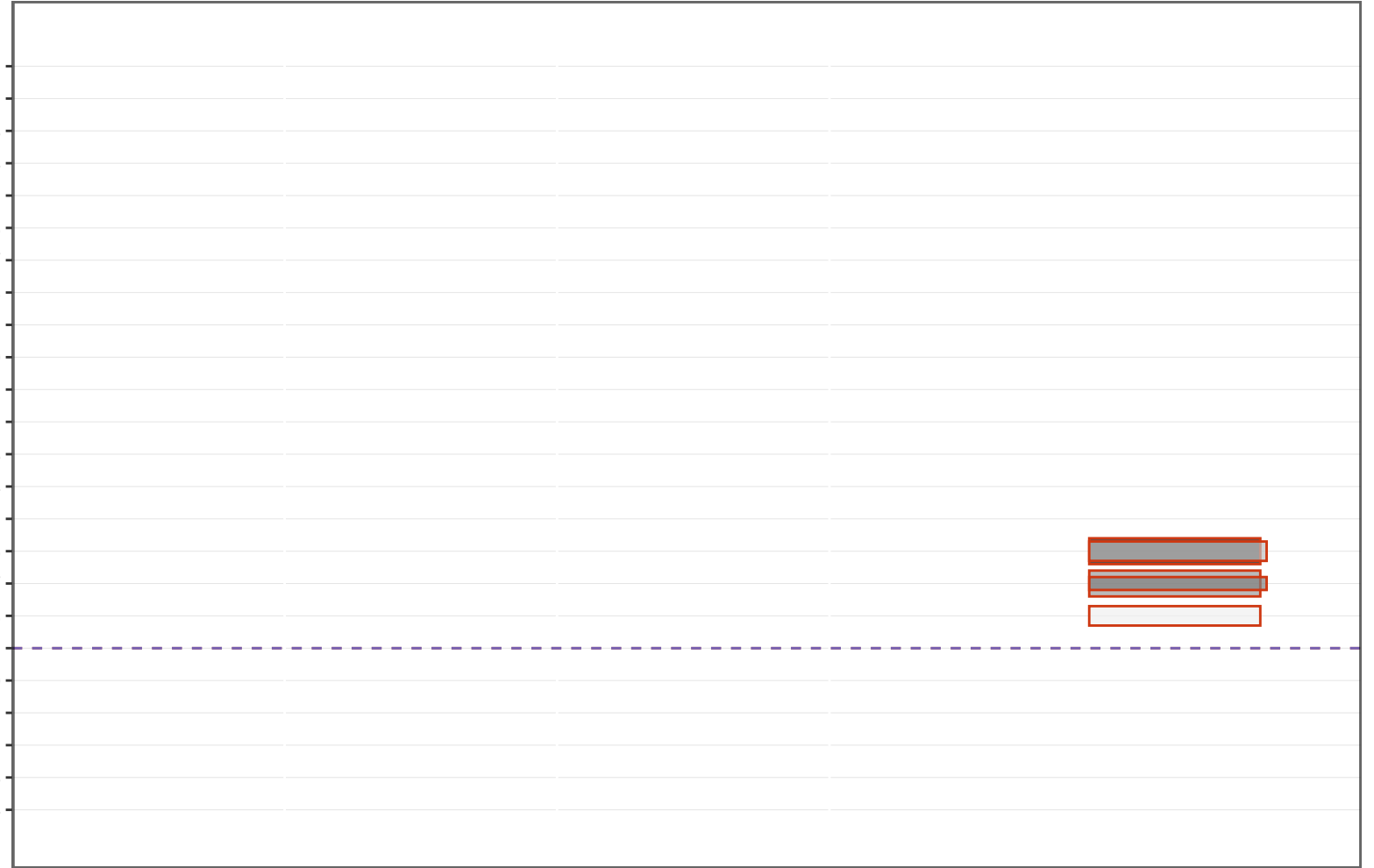
MW indication



Molecular weight



Gel Slice



Protein length

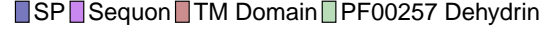


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IMGMGGEAYGTGGTGMGAMGGEYATGGTGMGMGTGGMHTQHHEGGQQLRRSDSSSSSEDDGEGGRARKGKEKIMKEMKPGGHAQDEGDDYNEGAQTYSYTEGGEKKGMMDKIKDKIPGMH

NbL02g13980.1 fructose-bisphosphate_aldolase_1_chloroplastic-like [MW = 42.75 kDa]

No. of times detected



log(intensity)



Values from



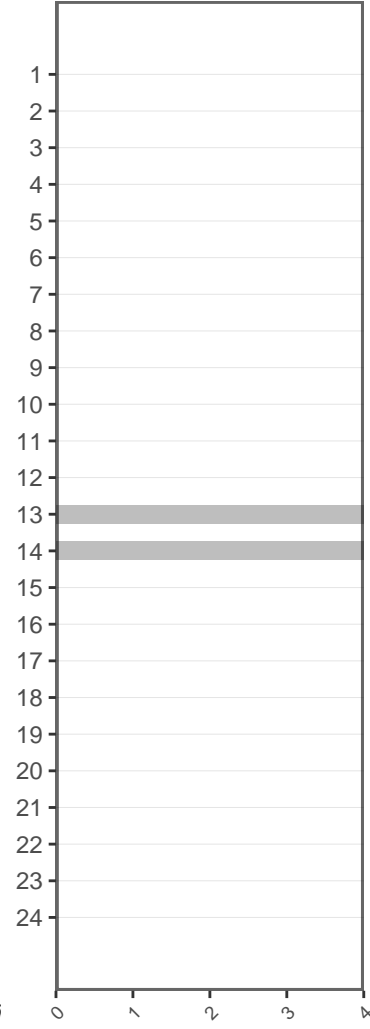
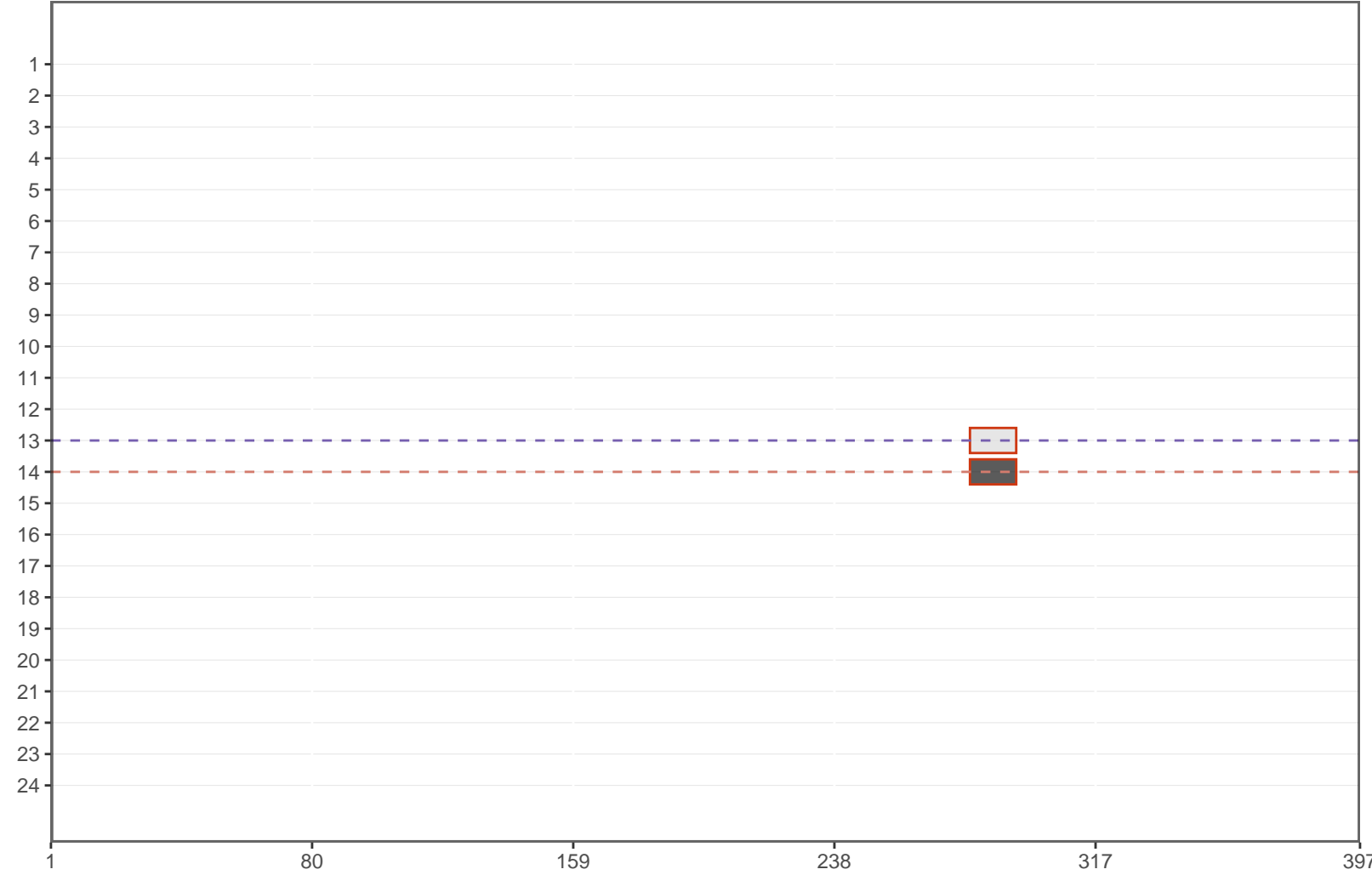
MW indication



Molecular weight



Gel Slice

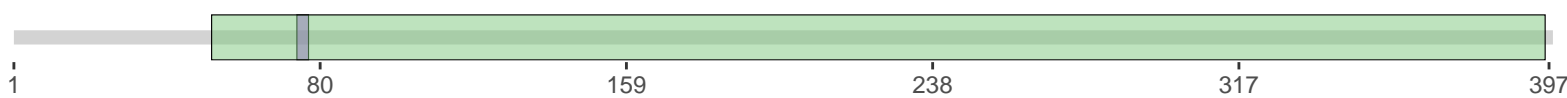


Protein length

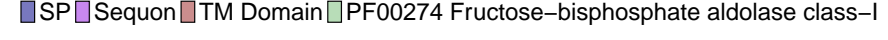


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

/V/SIPNGPSALVKEAAWGLARYVAISQDNLVPIPEPEILLDGEHNDIRTFEVAKKVVAEYFFVLAENNVMFEGILLKPEMVTPGAEGKERATPGQVADYTLNLRQRIPFVPGIMFLSGGGGSEVEATLNLNAMNGCPNPHWVSFSYARALQNTGLKTVGGRPENVAQGEALLVRAKANSLSAQLQKVTGEGESEEAANKGMFVKGYYV

NbL02g13710.1 naringenin2-oxoglutarate_3-dioxygenase [MW = 46.82 kDa]

No. of times detected



log(intensity)



Values from



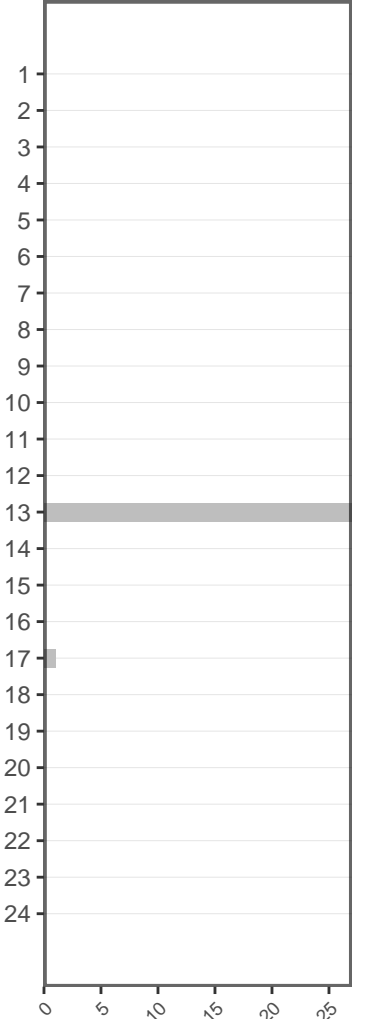
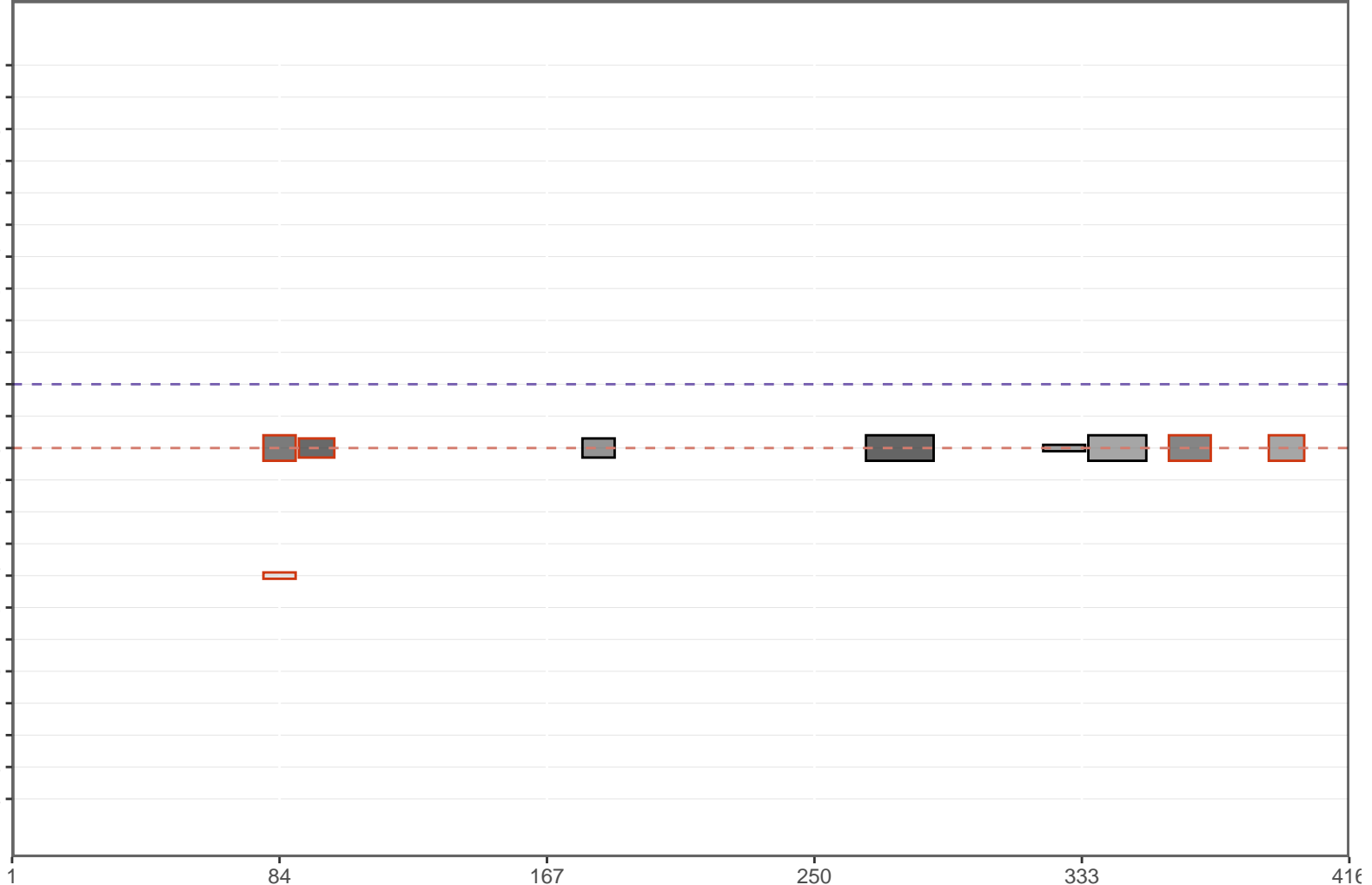
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF03171 2OG-Fe(II) oxygenase superfamily
- PF14226 non-haem dioxygenase in morphine synthesis N-terminal

Protein sequence:

KPEGIWVTKYSEKIMELAKLLEVLSEAMGLEKALTKACVMDQKVINFYKPGPDLTLGLKRHTDPTITLLDGGVGLQATKDKNGKWTWYQPVGAFVNLGDHGHFLSNRFRNADHQAVNSNSRSLSATFGNPAPEAVVPLKIREGEGKAVMDEPTTFAMRYRRKMSKDLALRKKIAKEGGQGAEEAAEKAKLETKEEHLA*

NbL02g13640.1 ferredoxin--NADP_reductase_leaf-type_isozyme_chloroplastic [MW = 29.03 kDa]

No. of times detected



log(intensity)



Values from



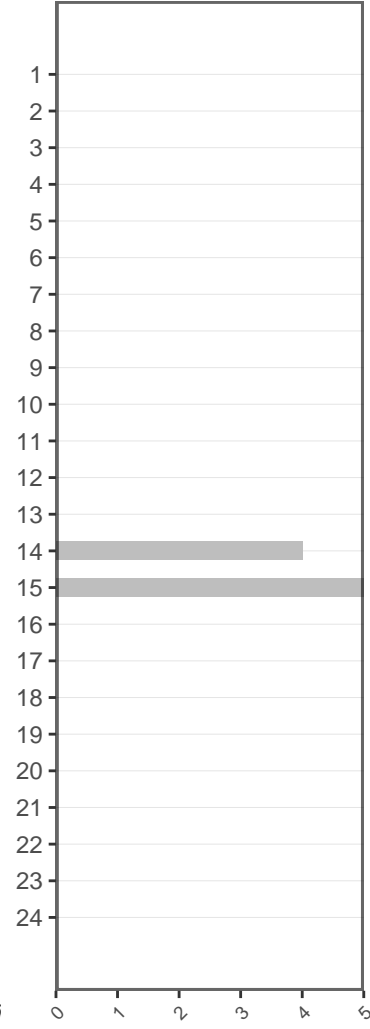
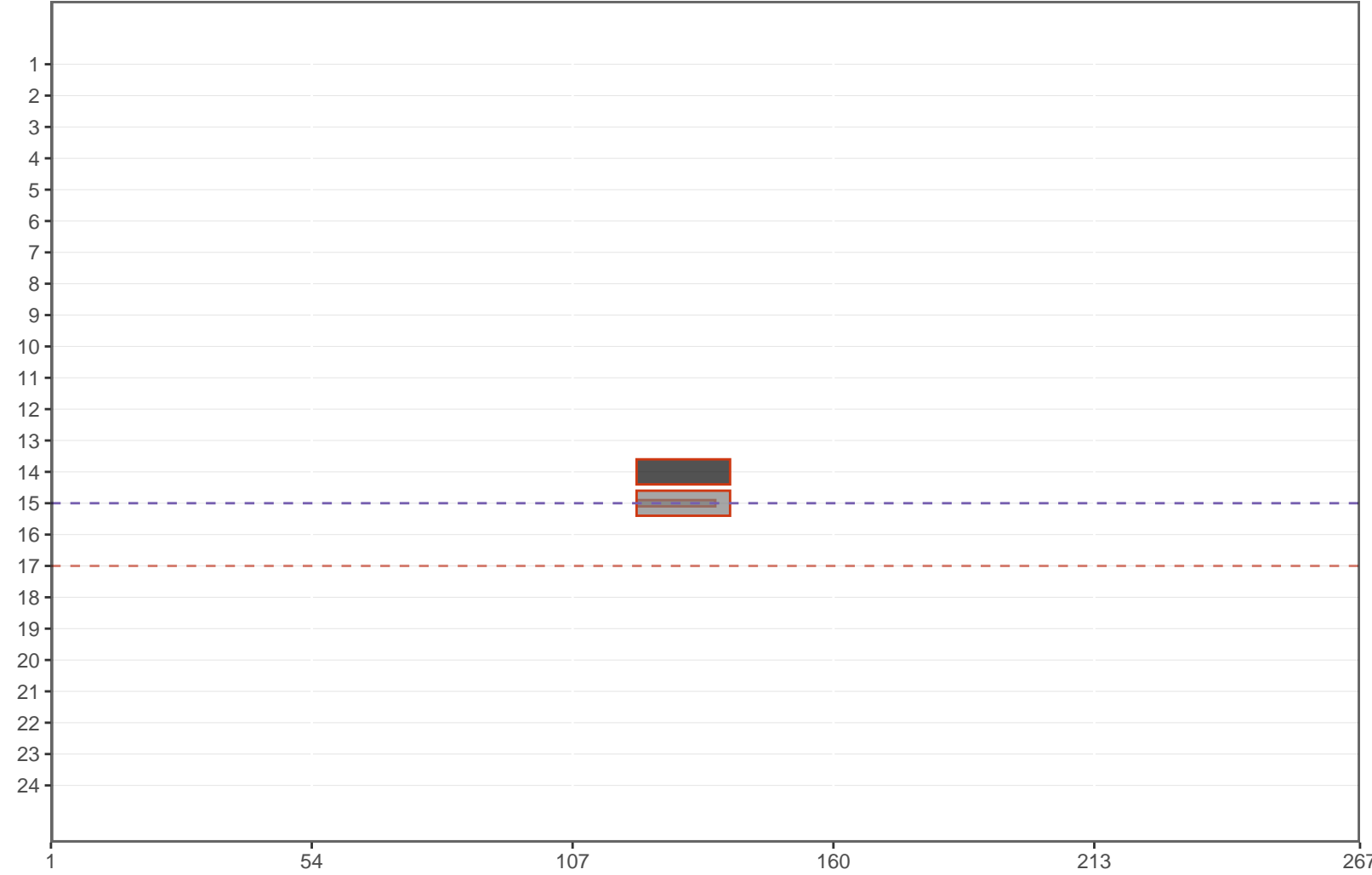
MW indication



Molecular weight

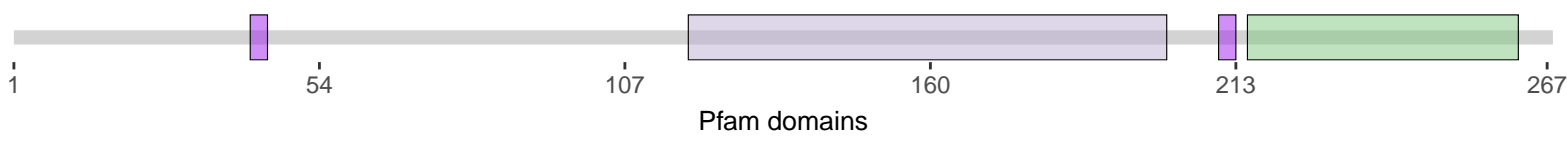


Gel Slice



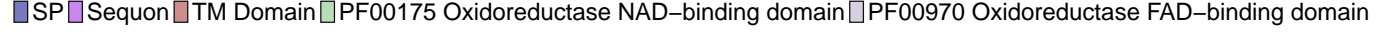
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

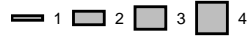


Protein sequence:

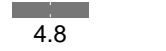
IGQSIQVADGVDAIEKPKRLRLYSASBALGDFGDDKTVSLGKRLVFTNDKGEVKGVCNFIIDGDKPGEVKTGPRVKEMLMPKDPNATVIMLATGTGIAPFRSLWKMFFEKHEKFKNGLAWFLVGVPTSSLLYKEVALI

NbL02g13580.1 26S_proteasome_non-ATPase_regulatory_subunit_4_homolog [MW = 42.39 kDa]

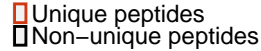
No. of times detected



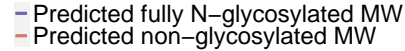
log(intensity)



Values from



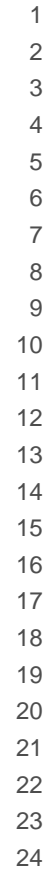
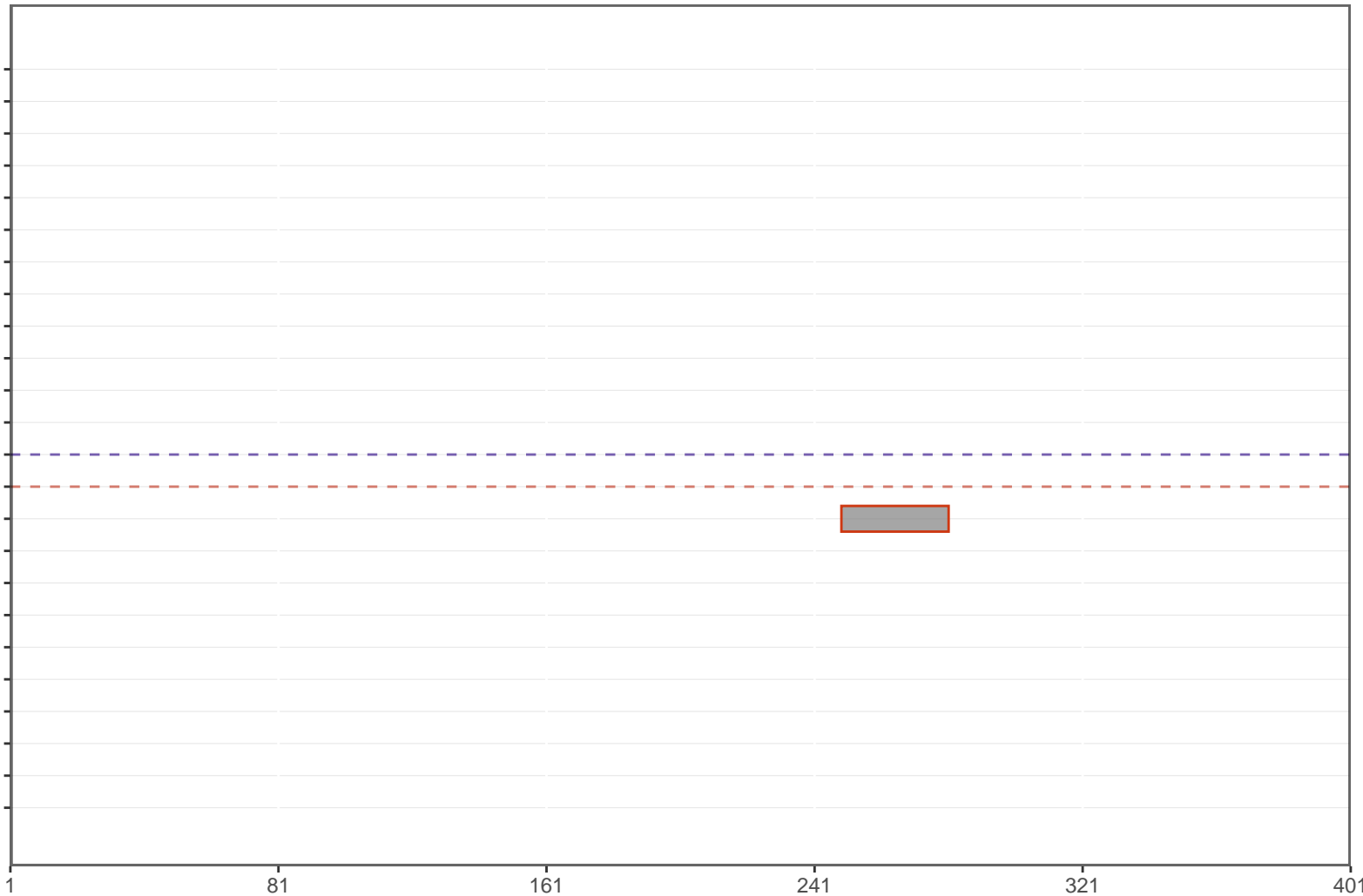
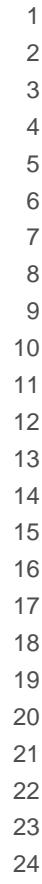
MW indication



Molecular weight



Gel Slice



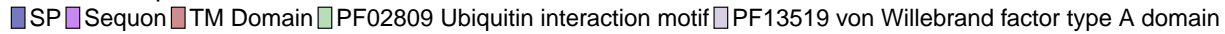
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SDGEGGSGFAAAMAAAAAGGVSGDFGVDPLDPELALALRVSMEEERARGEAANKKAAEETATGKGTGSETGQVTFMAENVAGTPEPENKATDLMEDENALLGQALAMEMDQASNVATRDITDMEAAEEDQDLALALQLSVGGSTNDGSGQTDMSKLLADGDFVSSILASLPGVDFPNDPFDVKLLASMGDGOSEKDKEDTDKQEKQK

NbL02g13570.1 alpha-mannosidase [MW - SP = 13.24 kDa]

No. of times detected



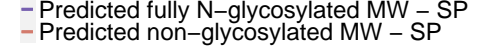
log(intensity)



Values from



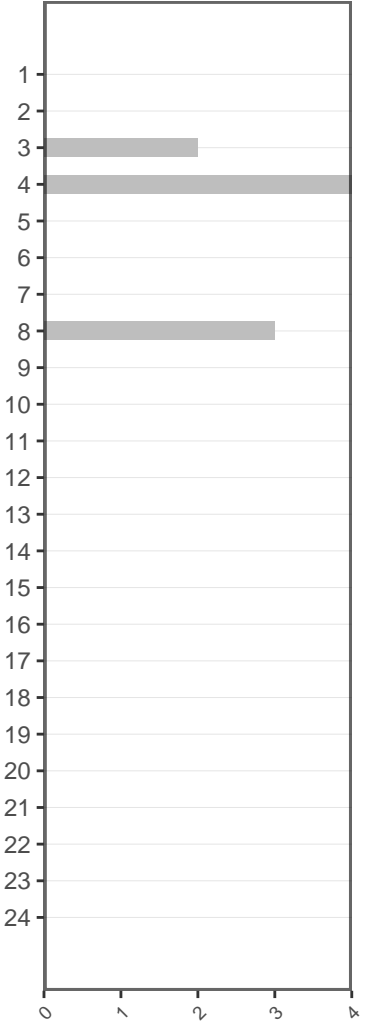
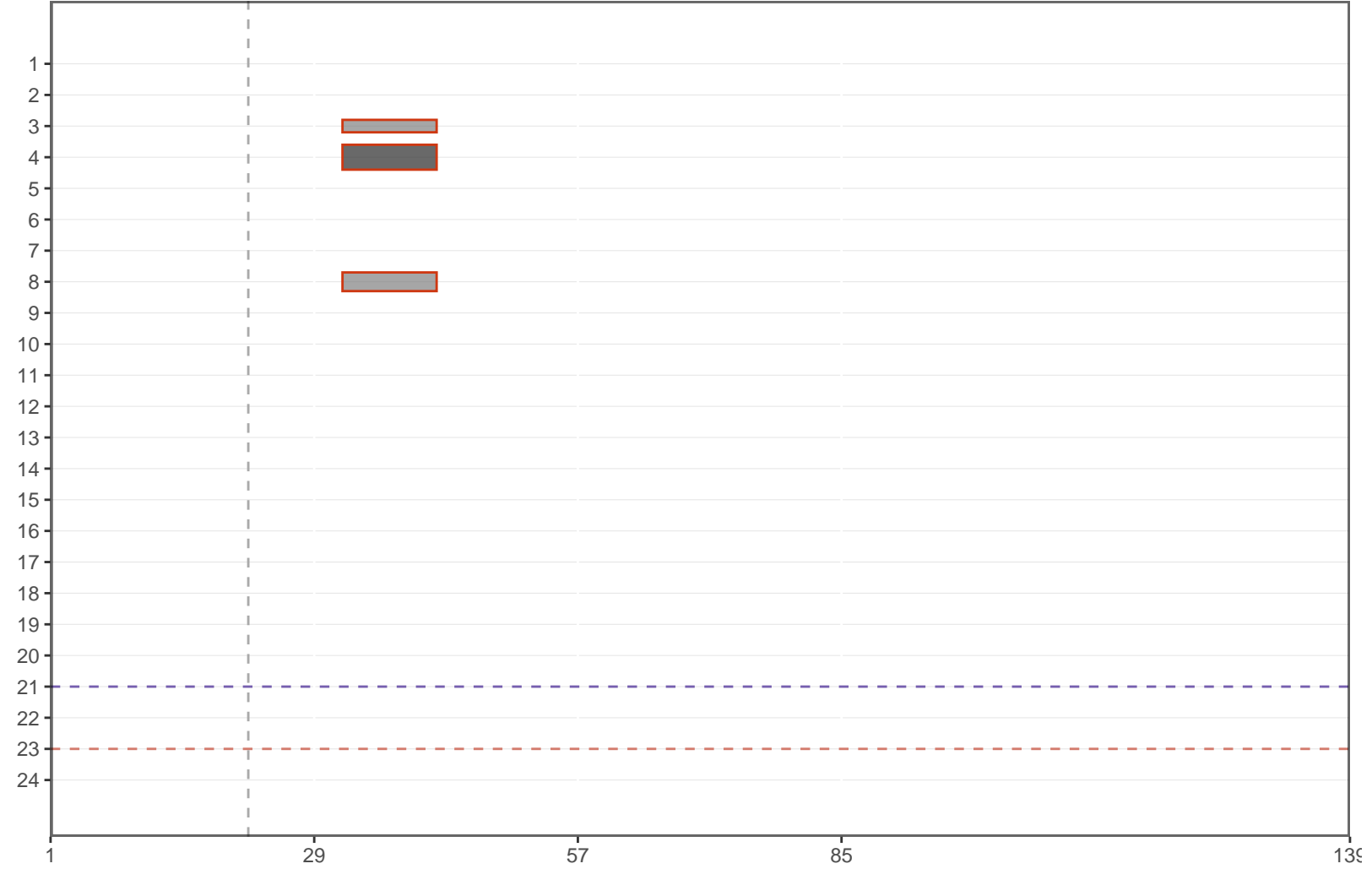
MW indication



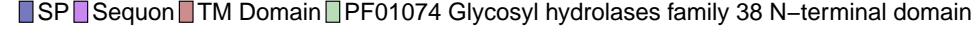
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

ILKTIQQYYVGSNFIQGGAEVENLVDGVVMSLRFRDPRKLLSLKWHFBIIVDTAKPRNSRRSEKPCFSWAGHKHWLVYAR1

NbL02g13470.1 3-dehydroquinase_chloroplastic [MW = 55.36 kDa]

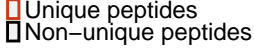
No. of times detected



log(intensity)



Values from



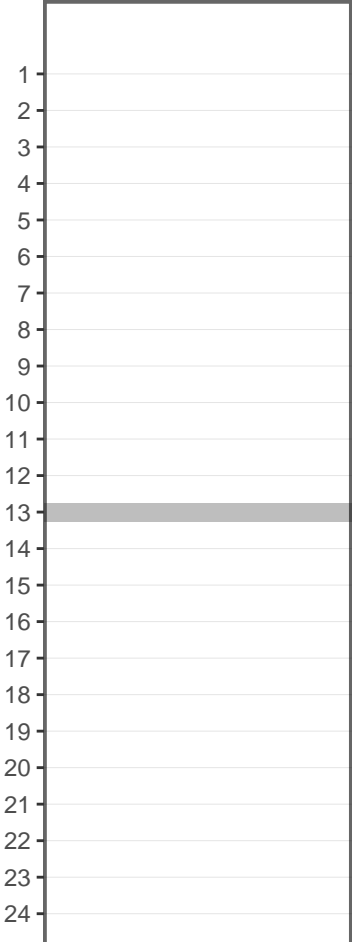
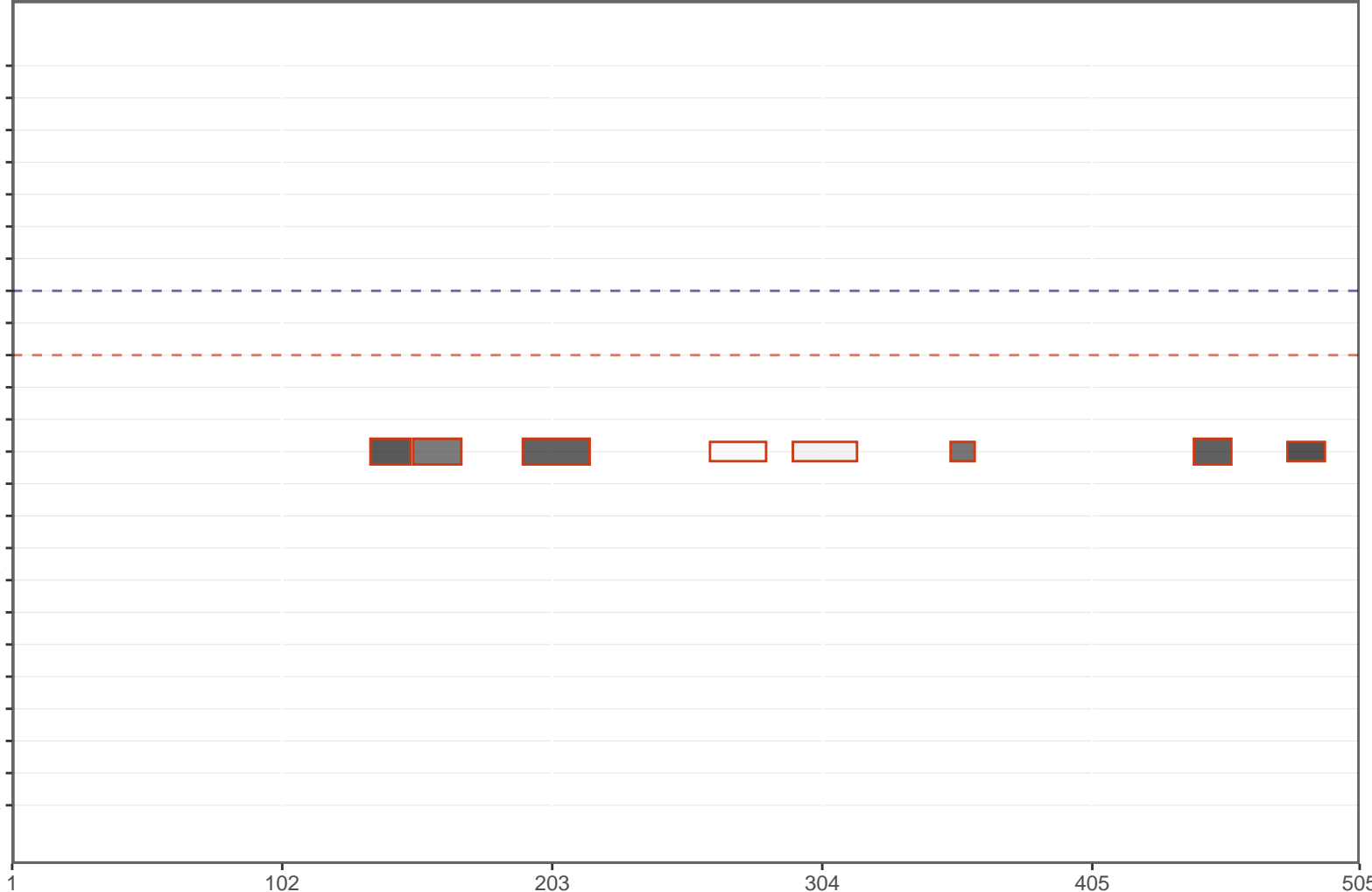
MW indication



Molecular weight

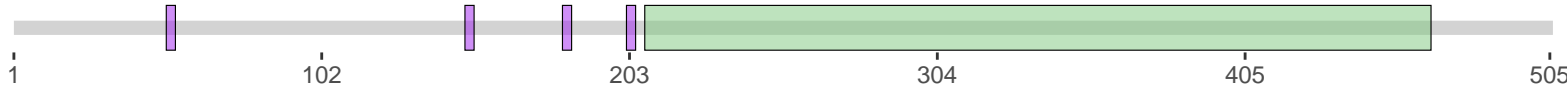


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

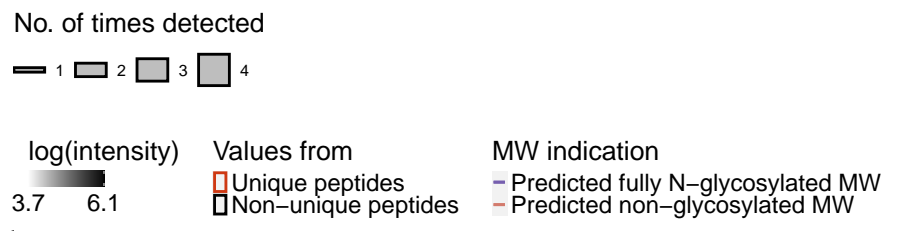
Pfam Description



Protein sequence:

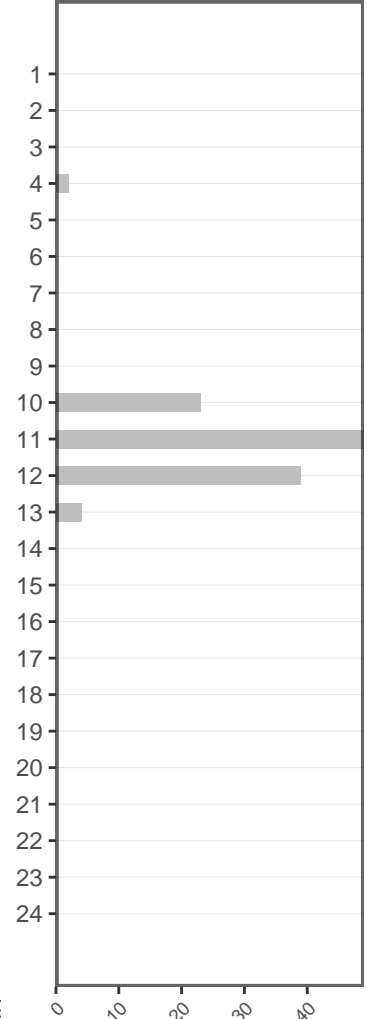
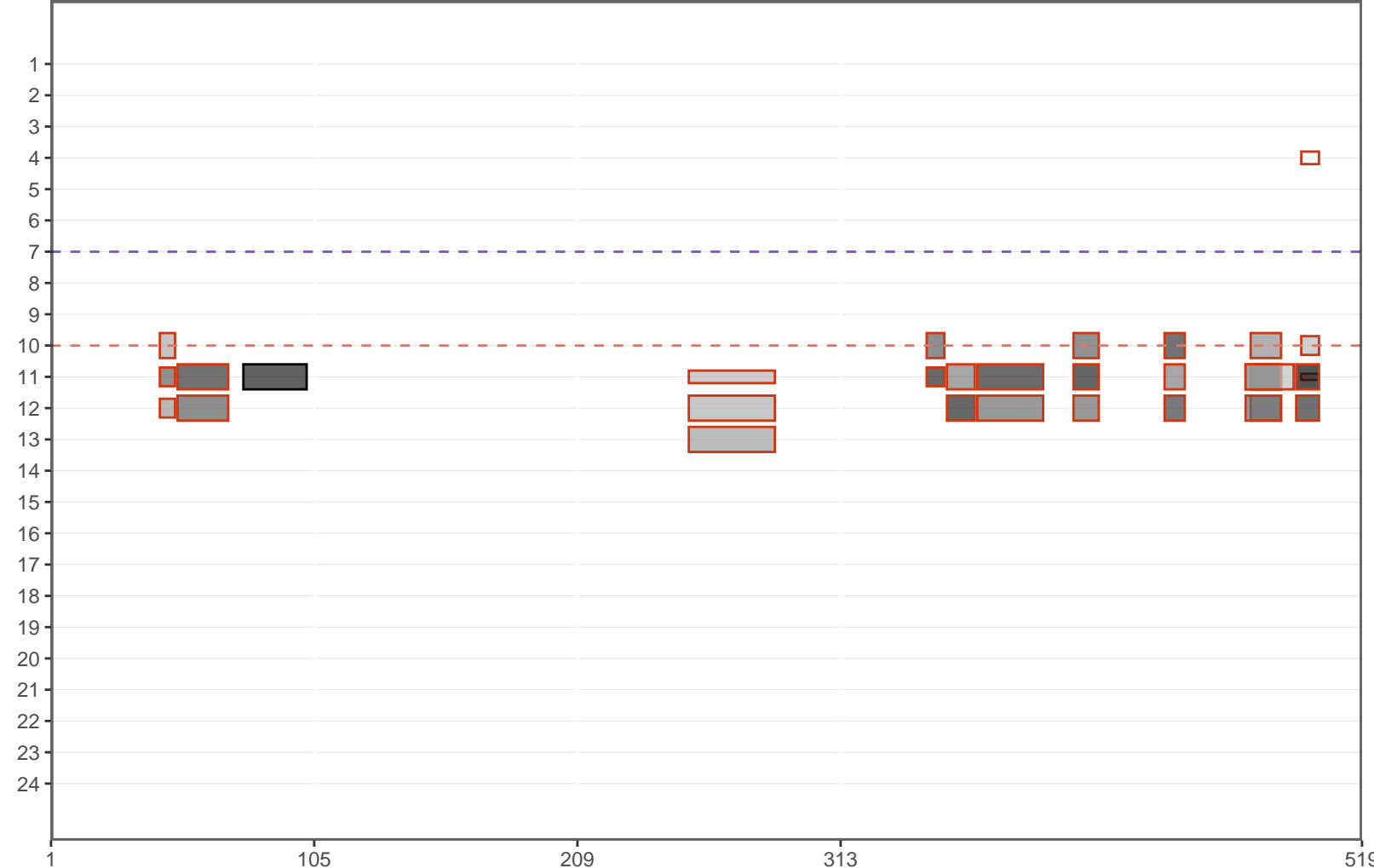
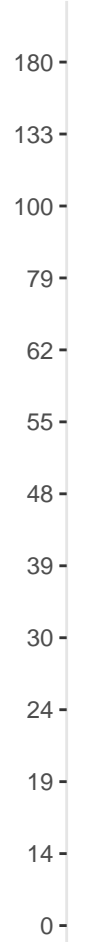
"VALGGVYGDICGYAASHYLRGVNFIPTTVMAGVDSVSGKTRINHPHGKMGAFYVQCVLVDLDTLDPRELASGLAEVHYKGLVDRDAEFFEWEQINMPLLLARPTAFTVAIKRSCENKAEVYSLDEKESGLRATLNLGHTFGHAVETGFGYGGWLLHGEAAVAGTVMVAVDMEHRLGWDDSLVQRVHNLGGAKLPTAPPETMTVMFKSMAVDKXVADGKLRLLKGLPLGNCVFTGDYDQKALDETLRAFSIS"

NbL02g13210.1 serine_hydroxymethyltransferase_mitochondrial-like [MW = 57.36 kDa]

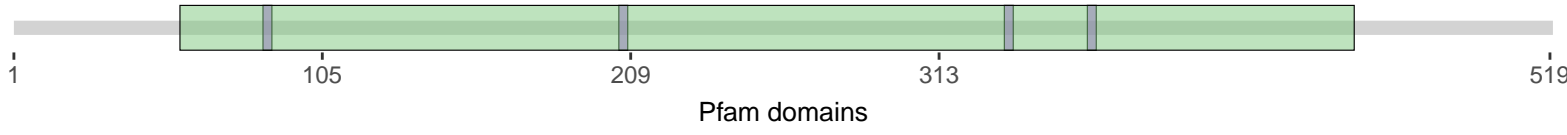


Molecular weight

Gel Slice



Protein length



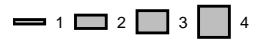
Pfam Description
 SP Sequon TM Domain PF00464 Serine hydroxymethyltransferase

Protein sequence:

V/C/D/K/Q/K/L/L/D/M/H/S/G/L/V/G/P/F/D/V/D/V/T/F/T/H/K/S/L/R/G/R/G/A/M/F/R/K/G/V/K/E/V/K/G/K/E/V/L/D/E/E/D/K/N/D/V/F/P/L/G/G/P/H/H/T/I/L/A/W/L/K/A/T/P/E/Y/K/V/G/E/Q/V/L/N/G/E/K/F/A/D/A/L/M/E/N/G/Y/E/L/V/S/G/S/T/E/H/L/V/L/N/L/K/N/K/G/D/G/S/R/V/K/E/L/E/A/V/H/A/A/N/K/N/T/V/P/G/V/S/A/M/V/P/G/R/M/G/T/L/S/R/G/V/E/E/D/V/K/V/A/E/F/D/A/W/K/L/V/K/K/A/E/T/G/T/L/K/D/F/V/T/L/G/S/S/A/P/K/E/I/N/K/L/R/H/D/V/E/Y/K/G/P/T/G/F/E/K/M/K/Y/N

NbL02g13200.1 probable_cytosolic_oligopeptidase_A [MW = 94.36 kDa]

No. of times detected



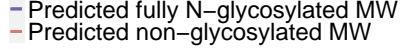
log(intensity)



Values from

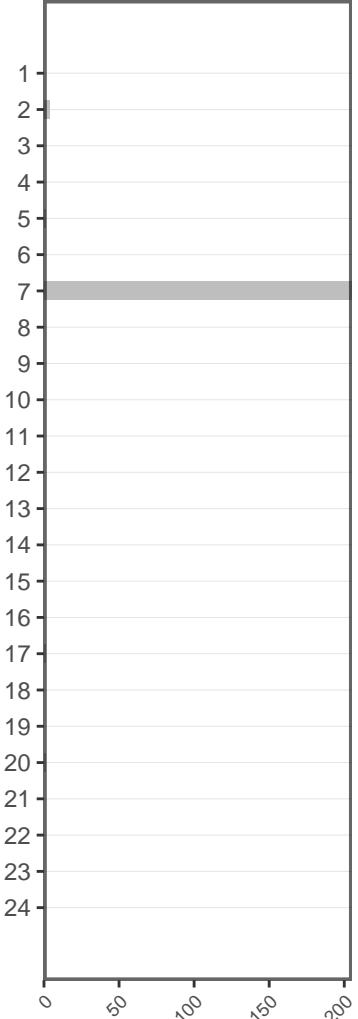
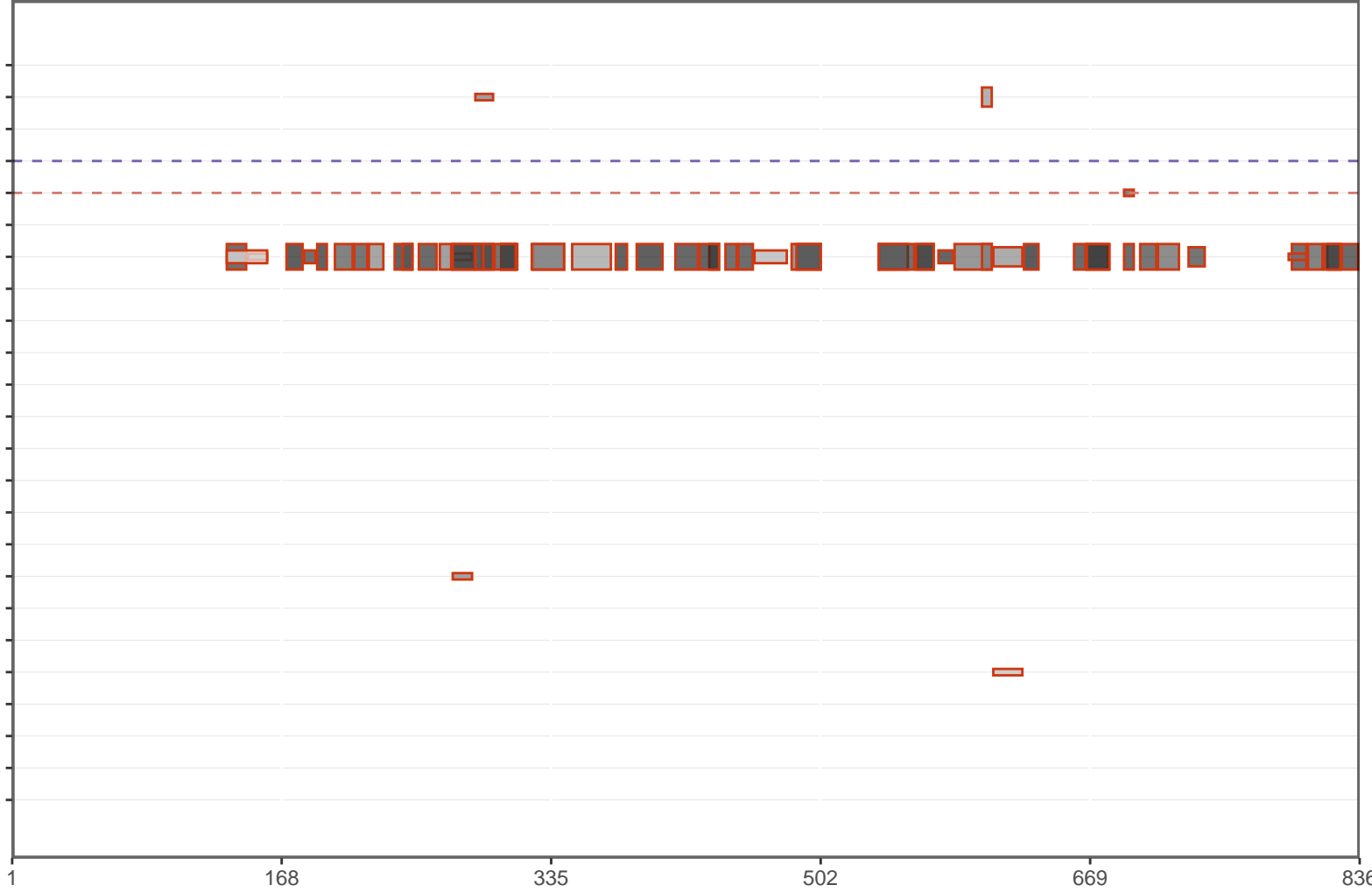
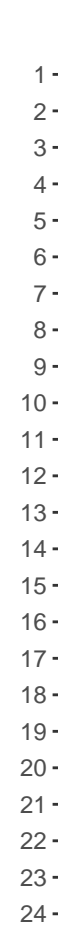


MW indication



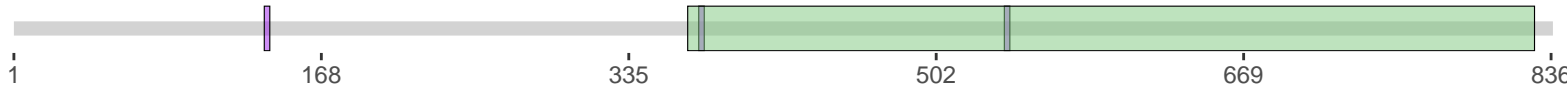
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LLGYNNAEVSMMKMATVQKAEELLEKLRRSSWDPWAKLEDLKFKQKSGAPEADLNHWDITFWSERLRREKYELENEELRPYFSLPRVMDGLFSLVLLFGINVEPADGLAPVWVNDVRFYRVNDSSGSPYAFYFDPVSRSEKRGGAWMDEVAWDSRVLGLDGSARLPAVHMVGNQMPVVGKPSLMTFRFVETVTFHEFGHALQHLMTKGDDEGLWAGRVEWDAVELPSQFMENWGYHRDITLMGIAKHHEGSELPEIYKLLTARTFRAGTISLRGLF

NbL02g13020.1 glutathione_S-transferase [MW = 23.8 kDa]

No. of times detected



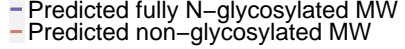
log(intensity)



Values from



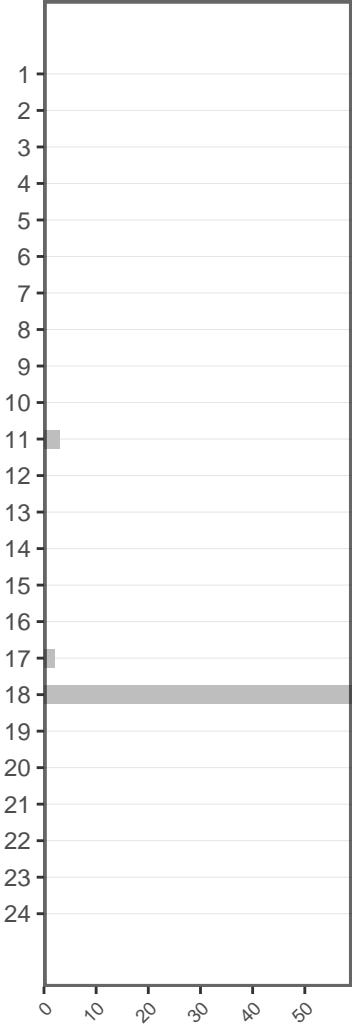
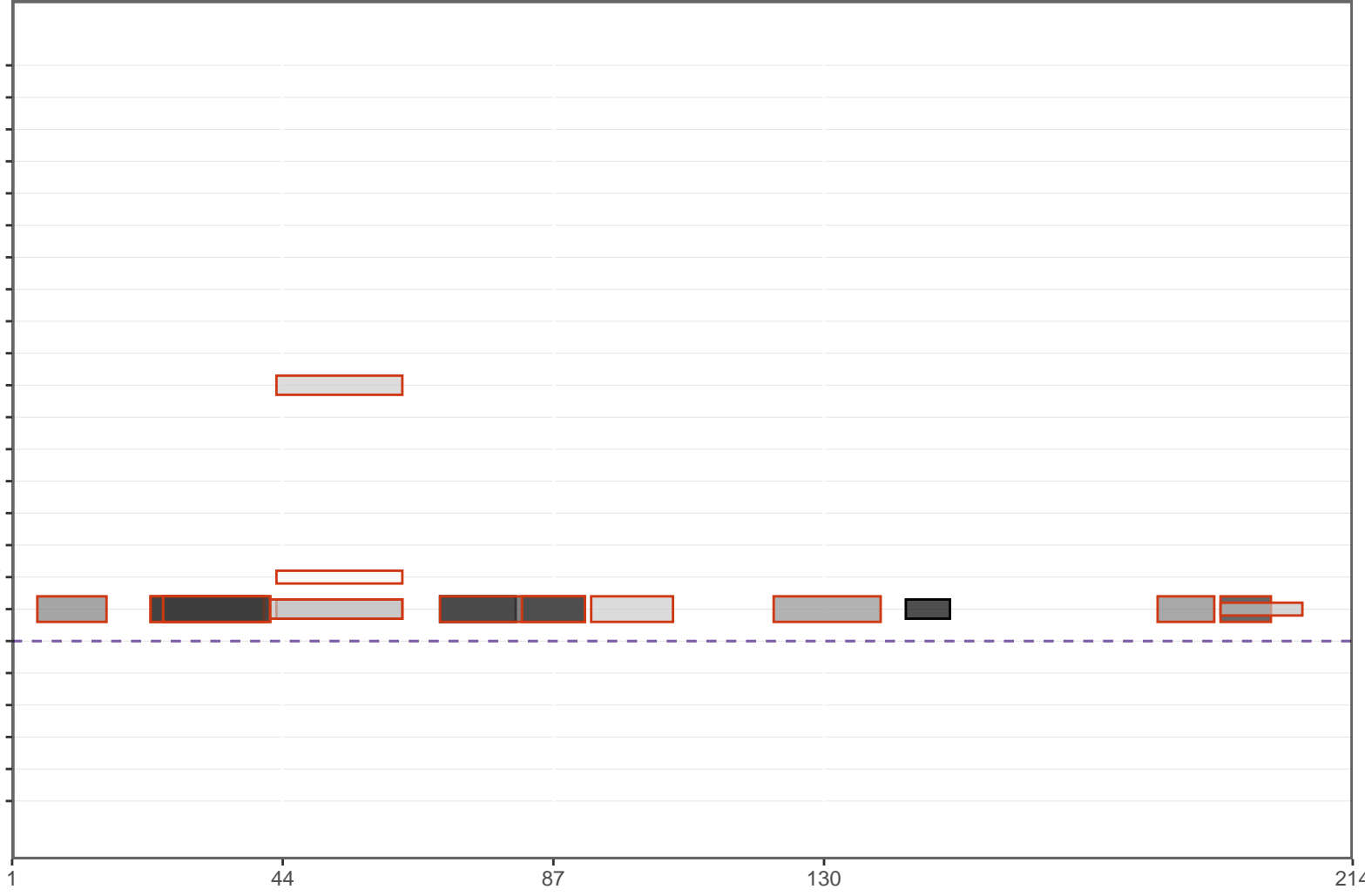
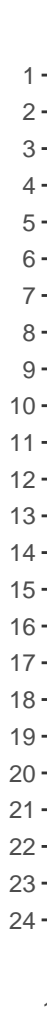
MW indication



Molecular weight

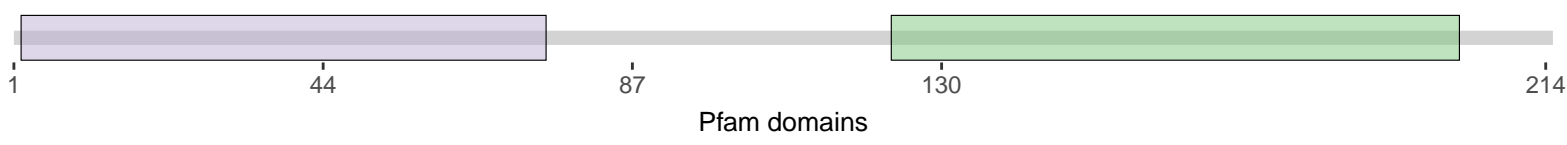


Gel Slice



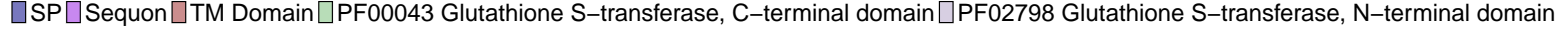
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IMSYVMEVSTYKFDPIGSKLGFELAWPKMGMVTDQAAVAENEKLGKLDVVEERLUKDKYLGGESFTLADLHAPVWVHYLMGTRKVKSLFDRPHVKKWAGADVGRFRWVKALELHKQ

NbL02g13010.1 uncharacterized_protein_Osl_027940 [MW = 21.58 kDa]

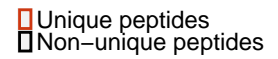
No. of times detected



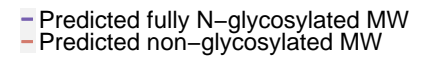
log(intensity)



Values from



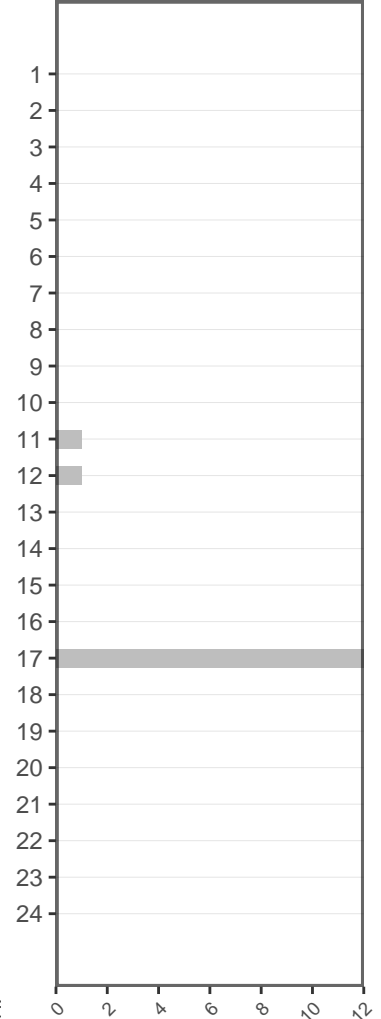
MW indication



Molecular weight



Gel Slice



Protein length

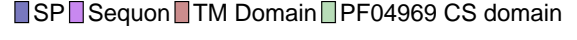


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IKLLHGDEKAPHYKVVQVWQVWVDEDDNDNTAAPGDFMNGMDFSKFGDMGMLGDDAMGDDLDSDSDDEEEVTKPSETVEGEPKGNKSVKGGAAEGKAAEAPSS

NbL02g12890.1 oxygen-evolving_enhancer_protein_1_chloroplastic-like [MW = 35.34 kDa]

No. of times detected



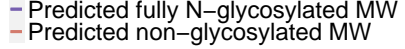
log(intensity)



Values from



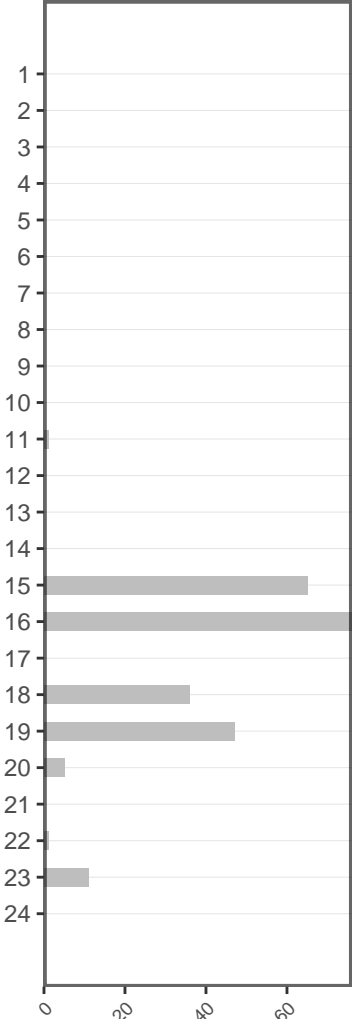
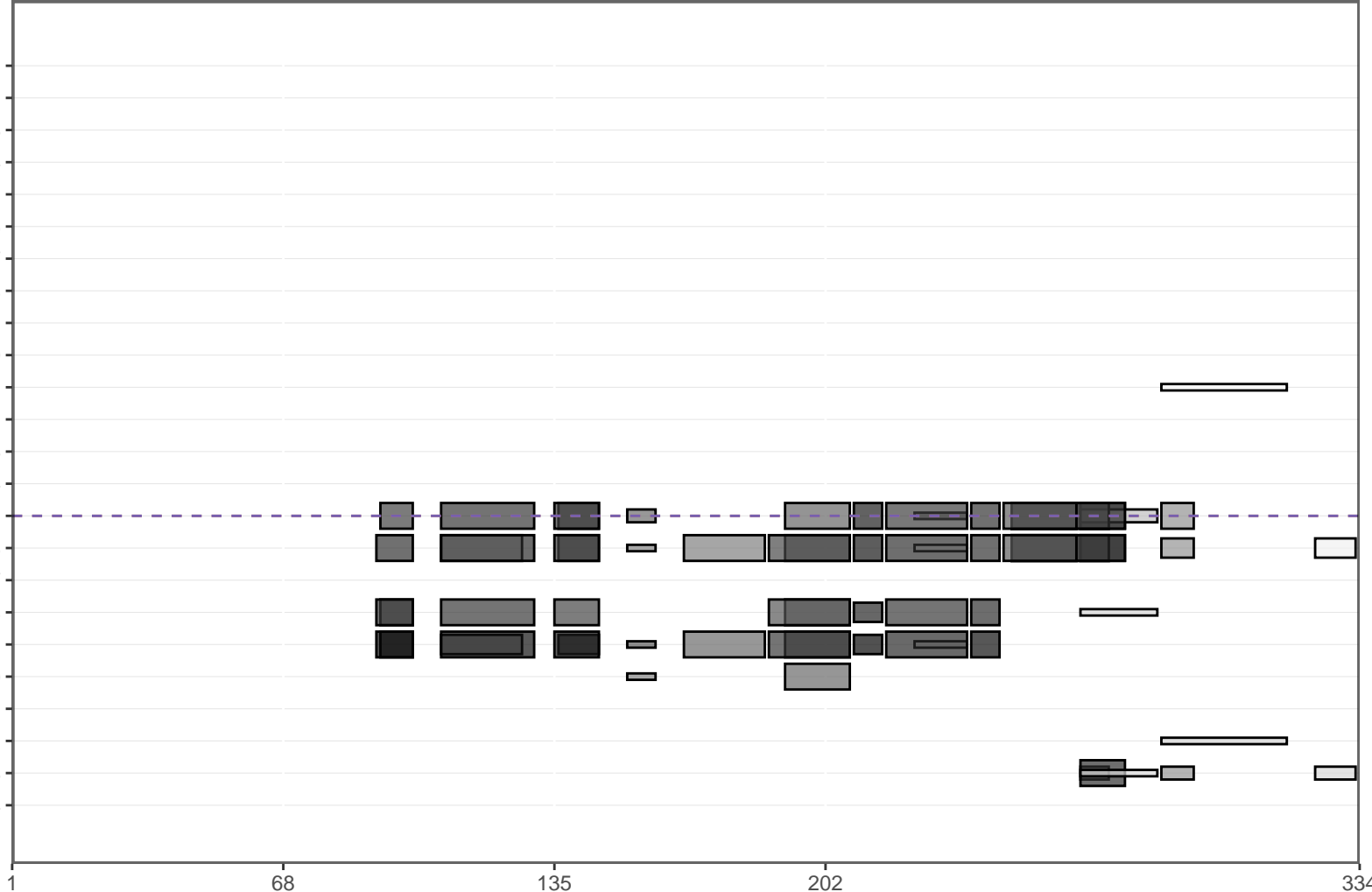
MW indication



Molecular weight

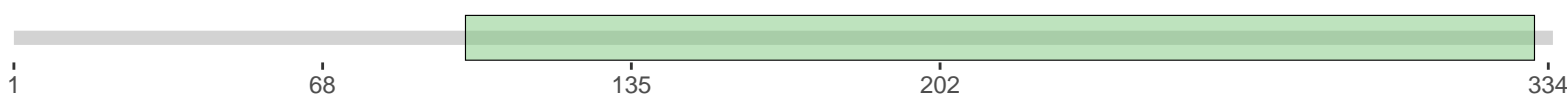


Gel Slice



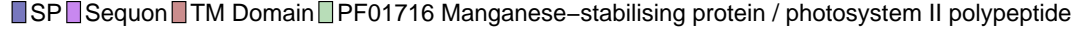
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

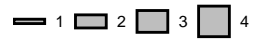


Protein sequence:

MAPPEFQKTKLMTLRYTLDEHGPFVSPDGTVKFEKDGDAVAATVQLPGGERVFFLFTKQLVAAGKPDGDFSGEFLVPSYRGSSFLDPKGRGGSTGYDVAVALPAGRRGDDEEKEKENKNTASSTGKITLVYTGKPKPETGEVIGVFESKQPSDGLGAKVPKDKKIGGVAQLDSE

NbL02g12820.1 5-oxoprolinase-like [MW = 137.99 kDa]

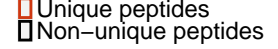
No. of times detected



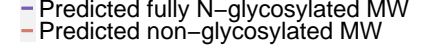
log(intensity)



Values from

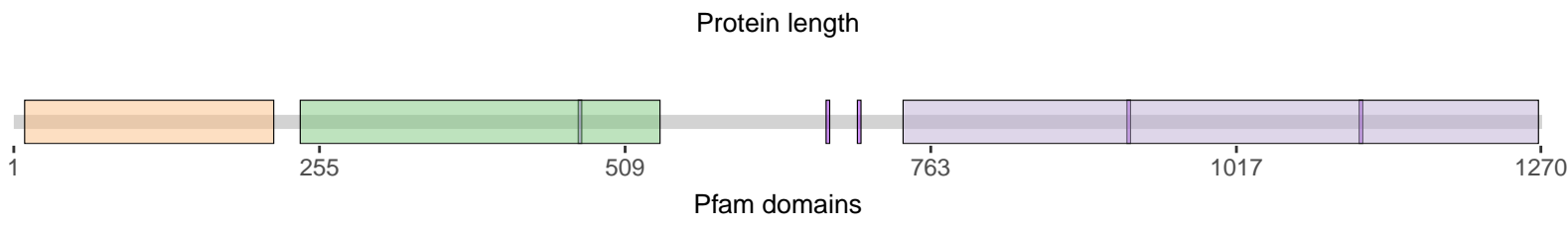
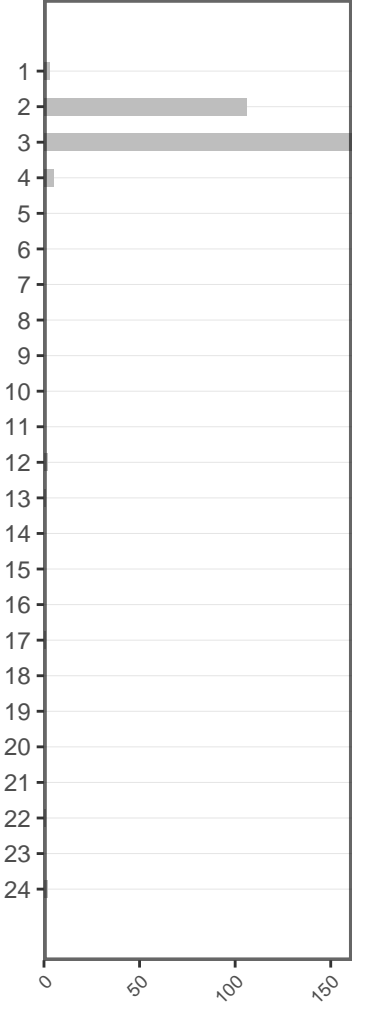
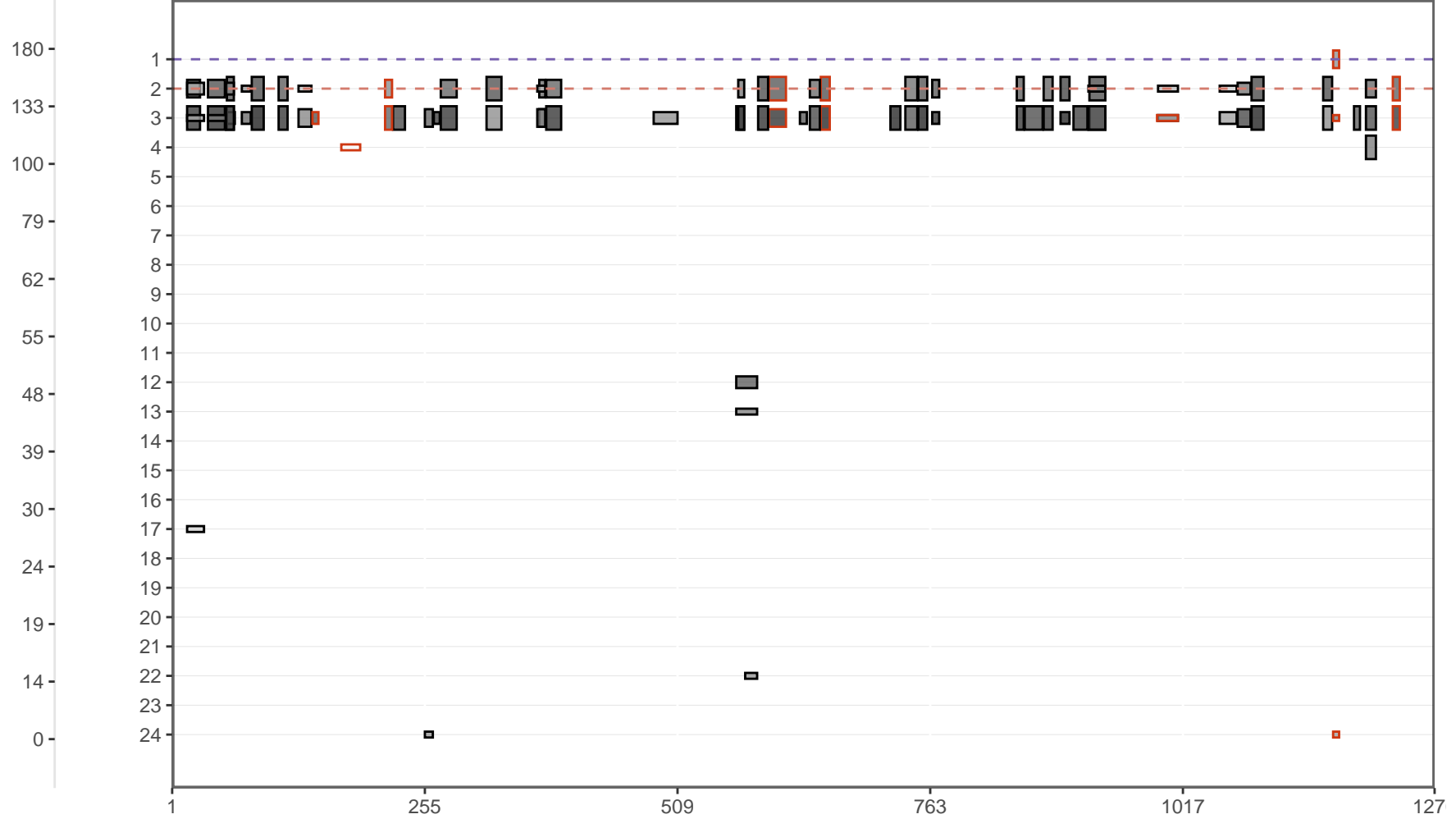


MW indication



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF01968 Hydantoinase/oxoprolinase
- PF02538 Hydantoinase B/oxoprolinase
- PF05378 Hydantoinase/oxoprolinase N-terminal region

Protein sequence:

EYGFILQNRNIVCGVIRVRGIVGVTNLRKRALDSSPGAPKIEGHYKVVYFGNGWINDTFLKLELNLAJGNVYVPGPMMNGNSTVIVPEPKAITRYGNIKIEIDSAINTAKVDEKAVDVGQLSIFNRFMGIAEGMGRITLQRTSISTNKKERLDFSCALFGPDGGLVNAAPHVPHLIGAMSSTVIRWQLKHWGDNLEGGDLVANKHPSAGGSHLPDITVITVFVFNKGRLIFVASRGRHIAEIGGITPGSMPPFSKFRWEEGAAKAFKLVKGTGTFQEEGRILRLRYPCSEESTHNPGT

NbL02g12380.1 uncharacterized_monothiol_glutaredoxin_ycf64-like [MW = 19.08 kDa]

No. of times detected



log(intensity)



Values from



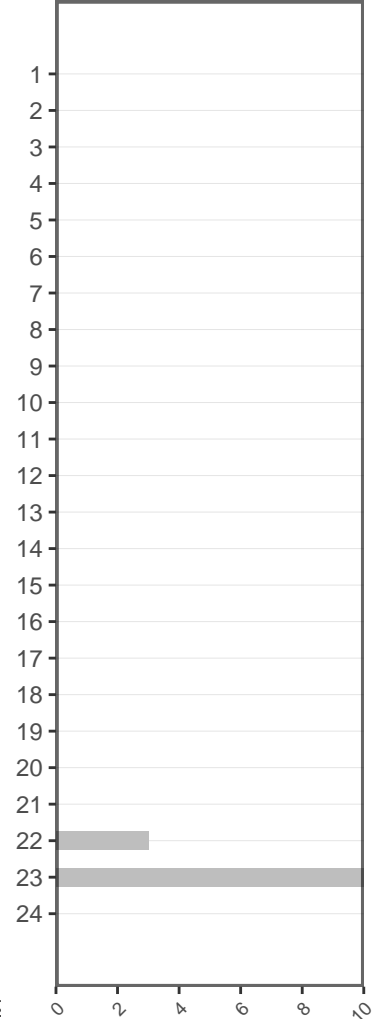
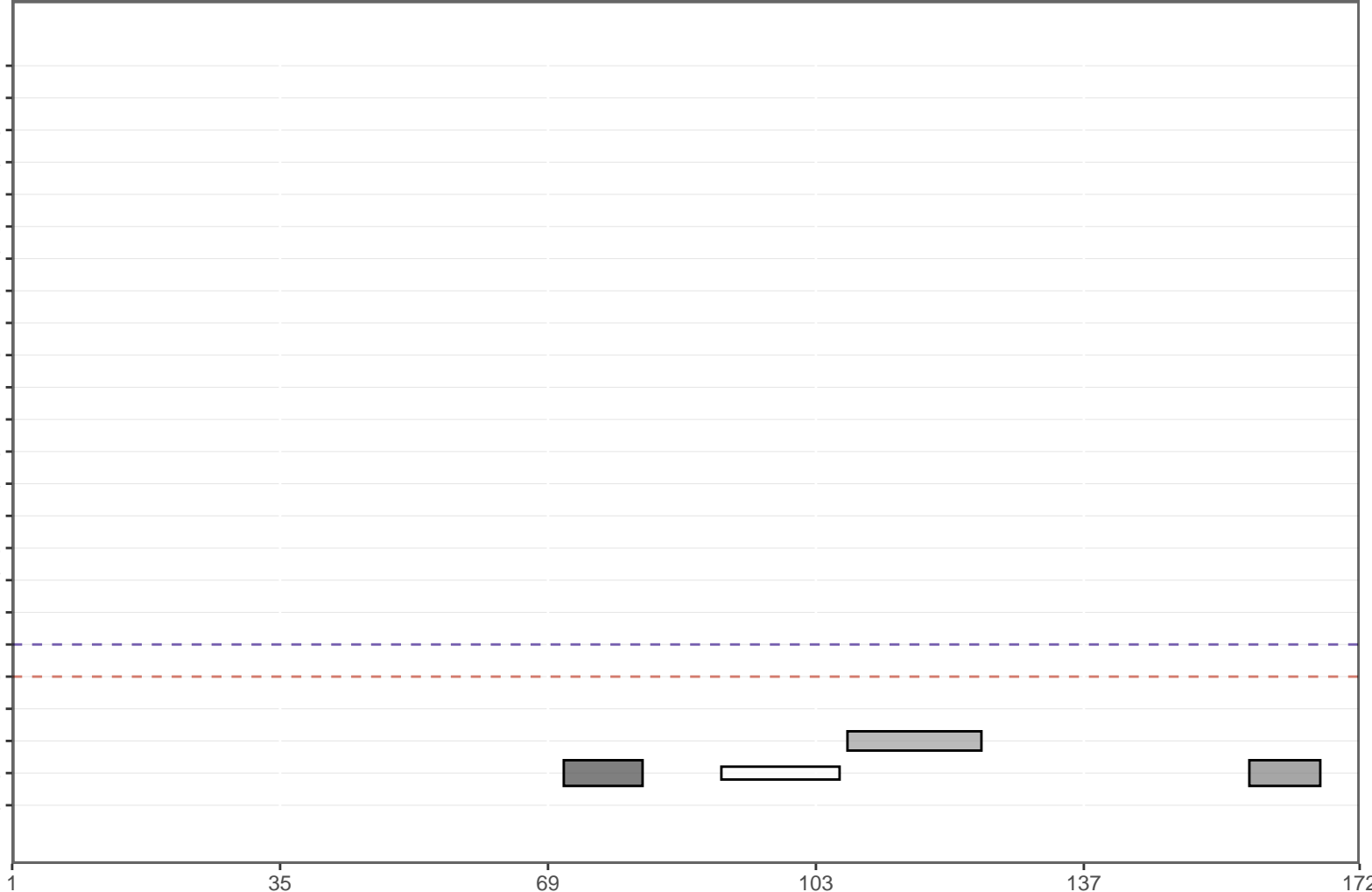
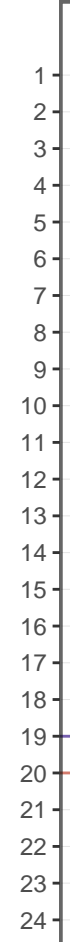
MW indication



Molecular weight



Gel Slice

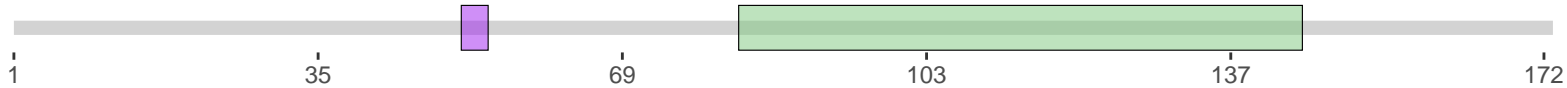


Peptide counts over 4 repeats

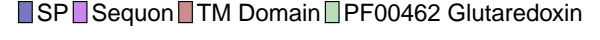
Protein length



Pfam domains



Pfam Description



Protein sequence:

DKIVVTSQKIVLFMKGTDFDGGGFSNTVQILKSLNAPFETNILENEALRGLKEYSSWPTFPQLYDGEFFGGDITVEAKYSGELGELLERTLGG

NbL02g12270.1 uncharacterized_LOC109215327 [MW = 22.24 kDa]

No. of times detected



log(intensity)



Values from



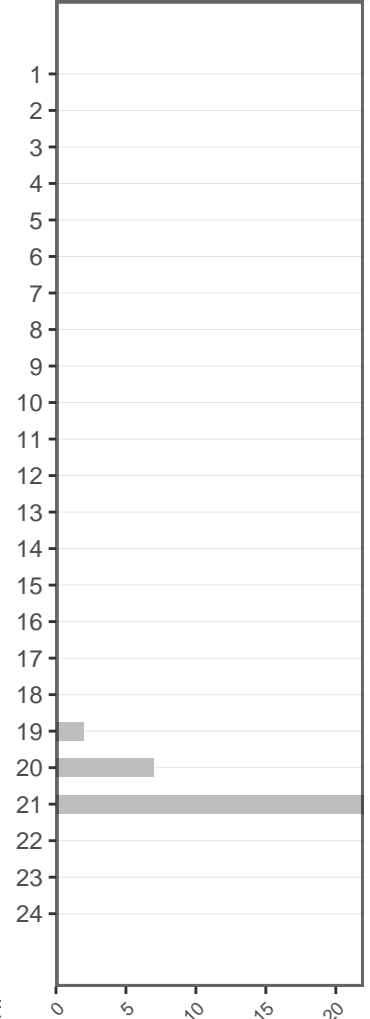
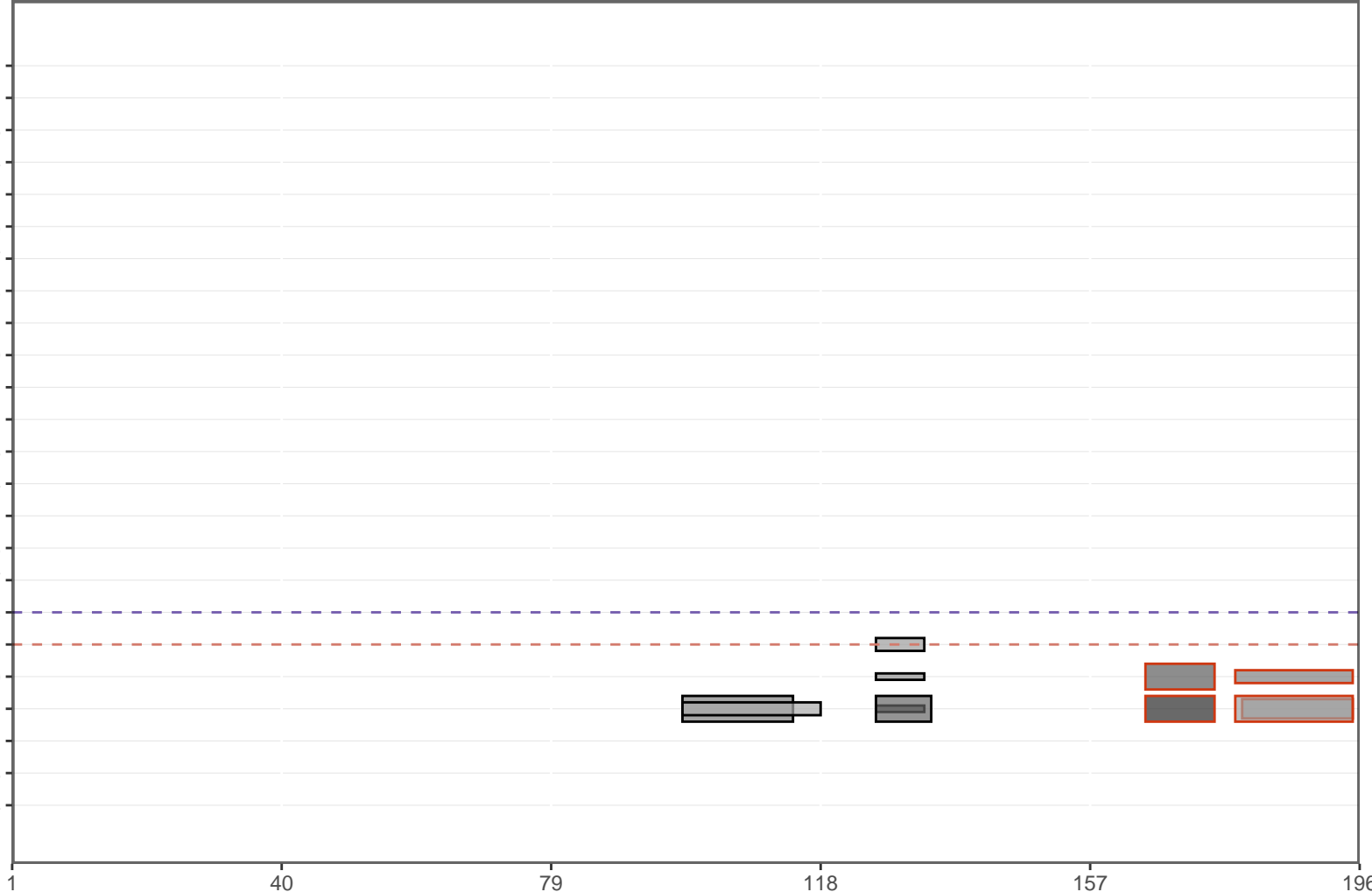
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ANANTLYFRSGYVWQVVDNEHEEHLVGRFRREVIRAGVQEQKRRRYFENKHDKLRKRSREAAKRNKRKRGPPRFSDDKQGEASKNRDDEGEDNWLFDGGLPYV

NbL02g12220.1 actin-histidine_N-methyltransferase [MW = 57.45 kDa]

No. of times detected



log(intensity)



Values from



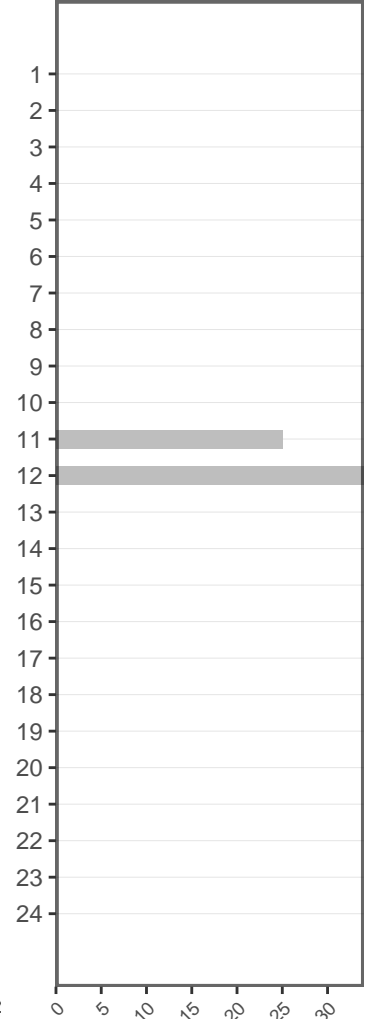
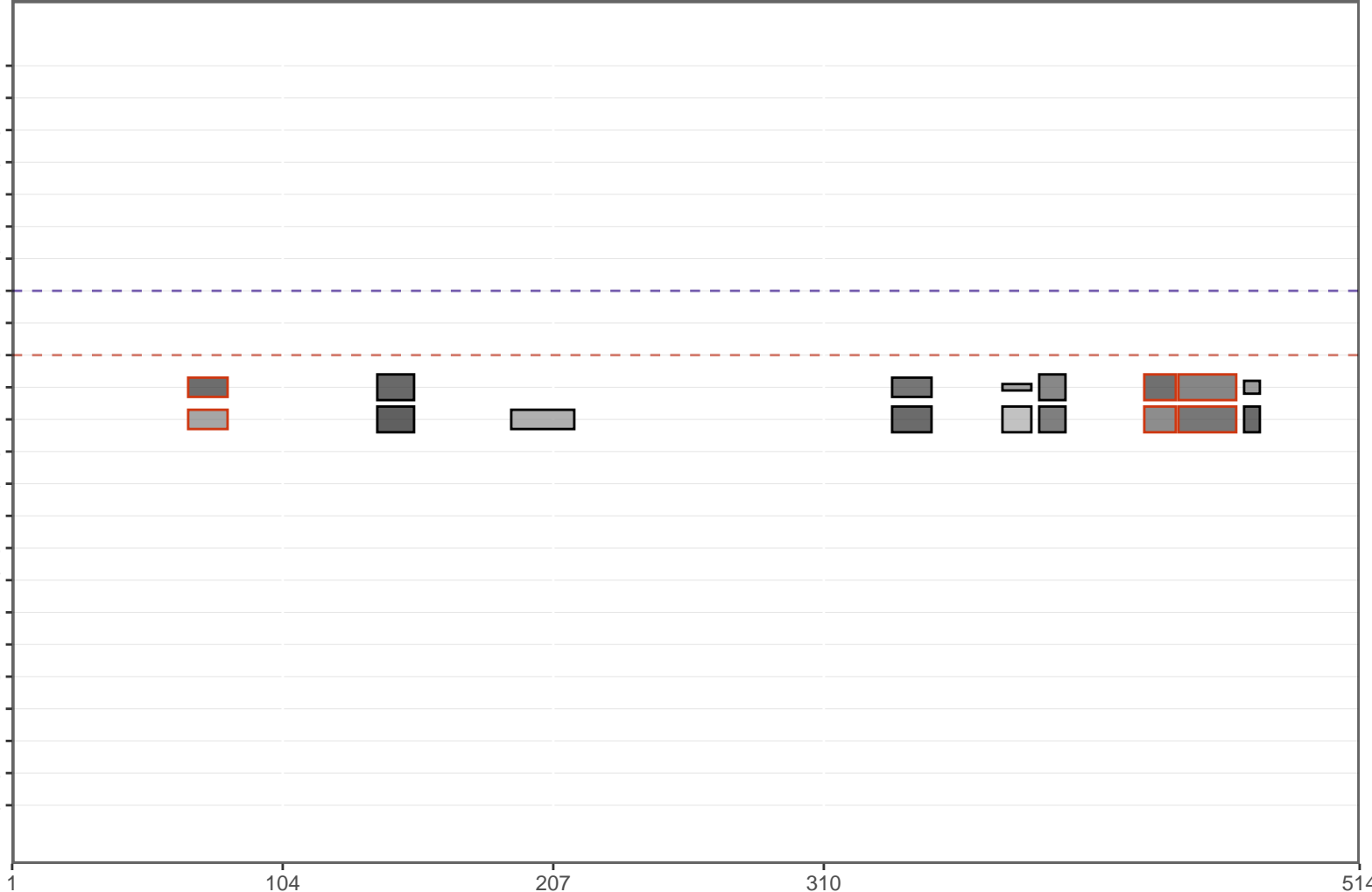
MW indication



Molecular weight



Gel Slice



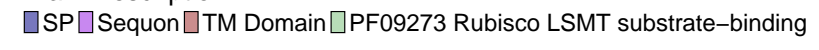
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IQYYPDITFAFPFEIKGAFVWQSDVHLEKQVSLARRFALVPLGPPLLSYGSNCRAMLATVDAVQLVDRVYSAGDPVWVCGPQNKLLINVFVDEENSVDRLMVEAALNTEDPQVQDKRLAQRNGKLSVGAFAVGVCKEREAVLEMLPVLRLGLVSDPSEMGTVLSGGGPGPSPCMERAVLGGLSDFEARLASVPTTLSDEBALLADTDMDPKRRVATGLVREKKILNAGLETTVNFINQLPDLGVSDPAPFAPTLK

NbL02g12080.1 carbonic_anhydrase_chloroplastic-like [MW = 28.63 kDa]

No. of times detected



log(intensity)



Values from



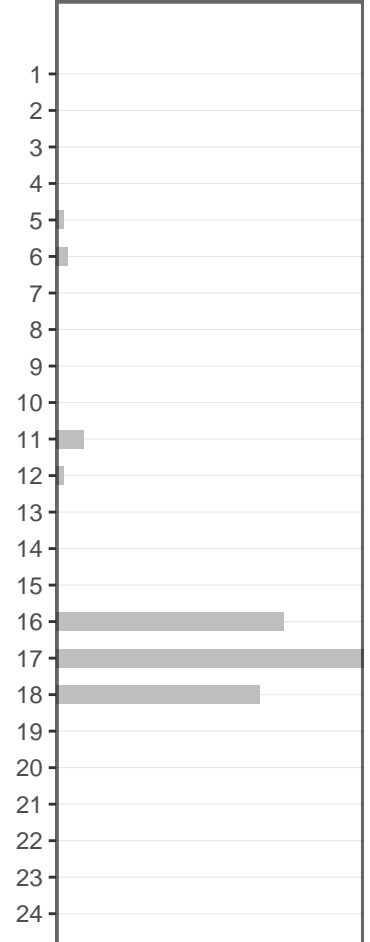
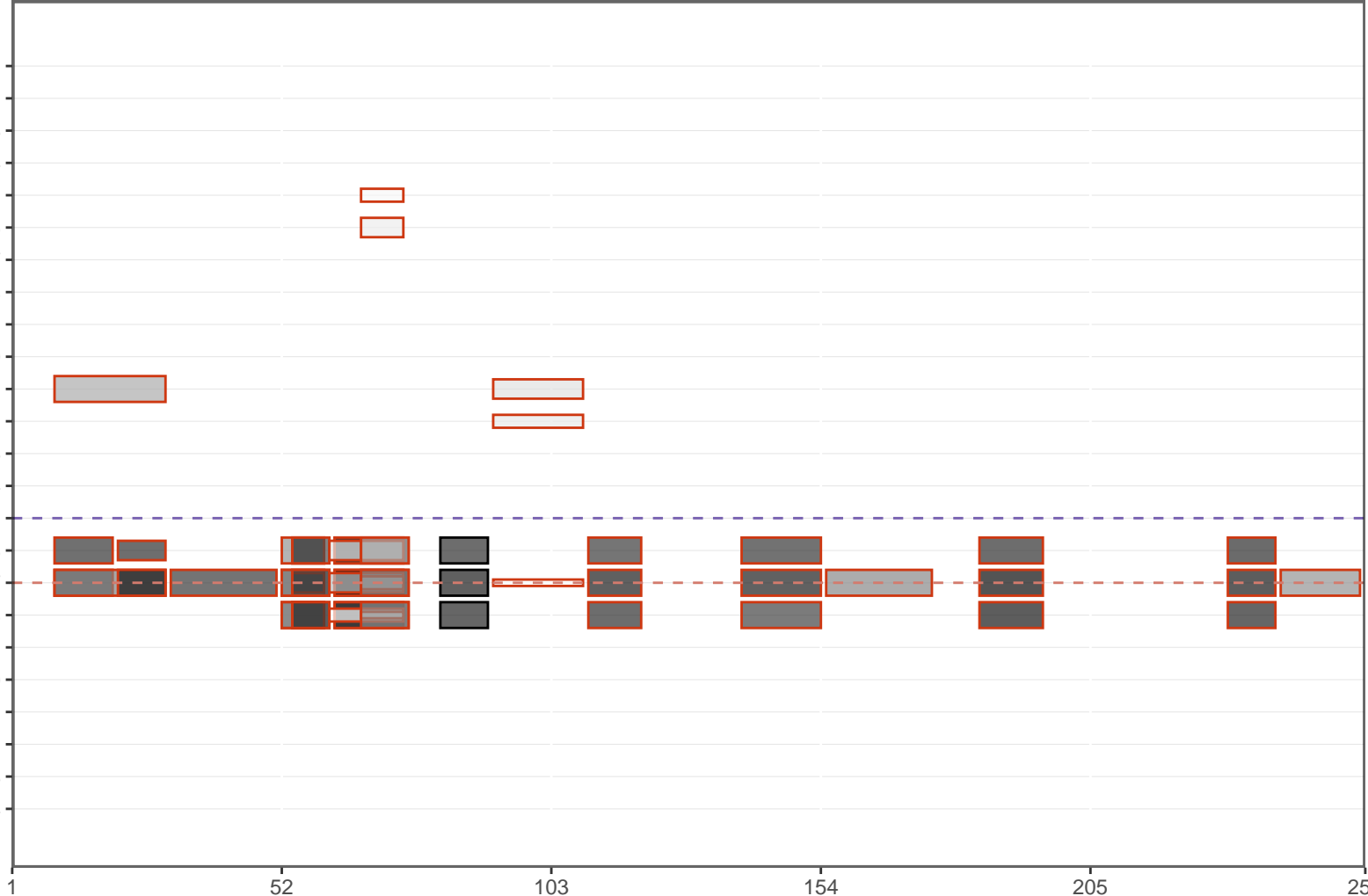
MW indication



Molecular weight

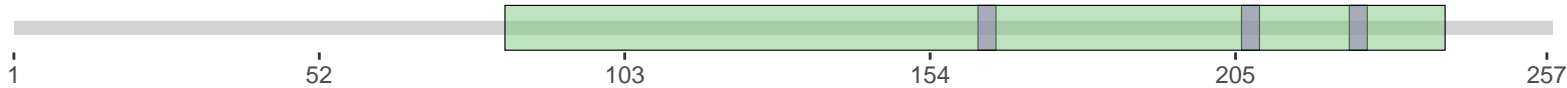


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

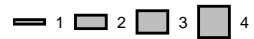


Protein sequence:

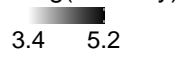
PPYDKTKYSGVCAIEHWLFLKVENLVIHGHSAAGGGKALMDLPENGGSESTDFIENWIKGLPAWAKVLAEHGDKTYEELKYQEMEAANNVSLANLFLYFVSDALVNTKLLKGGYDFEMEGKFEWGLNGLSHPHYV

NbL02g12060.1 putative_glucose-6-phosphate_1-epimerase [MW = 34.78 kDa]

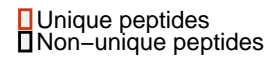
No. of times detected



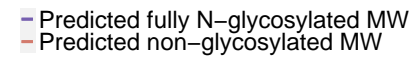
log(intensity)



Values from



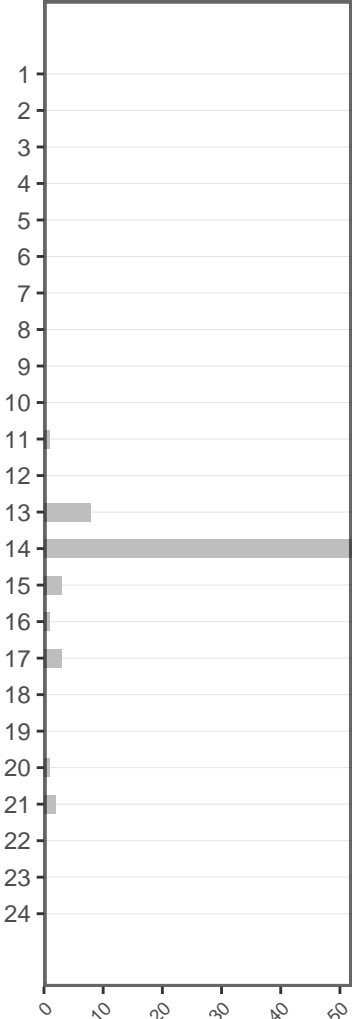
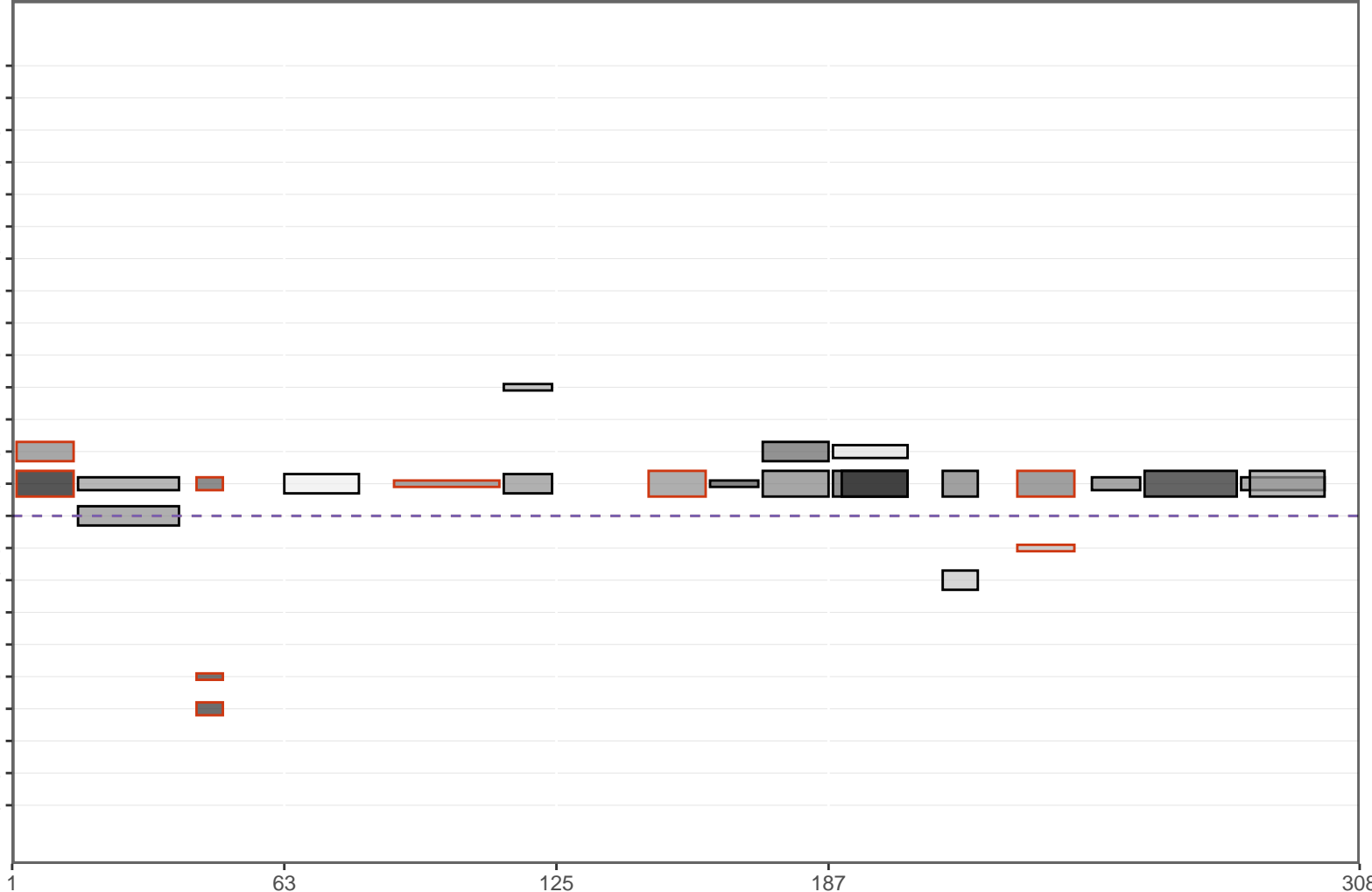
MW indication



Molecular weight

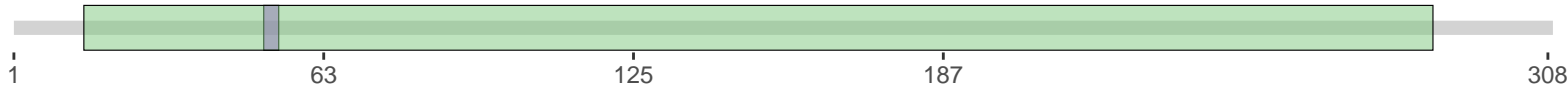


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IPRVINIDNKPFSFISLRINLYLSDISEVRRVEGLETLDFDNLQGRERYTEQADAITFDGSEDRVYLTPTKKAIDHEKRRFYVQKEGMLDAVWVNFVWNNKAKSLPOLGDEDKKMLGVDSAAVETPVLKPSSEWVKGRGELSTVSSBYGSGQLDPRKVLVGLA*

NbL02g11580.1 uncharacterized_LOC104228188 [MW = 20.53 kDa]

No. of times detected



log(intensity)



Values from



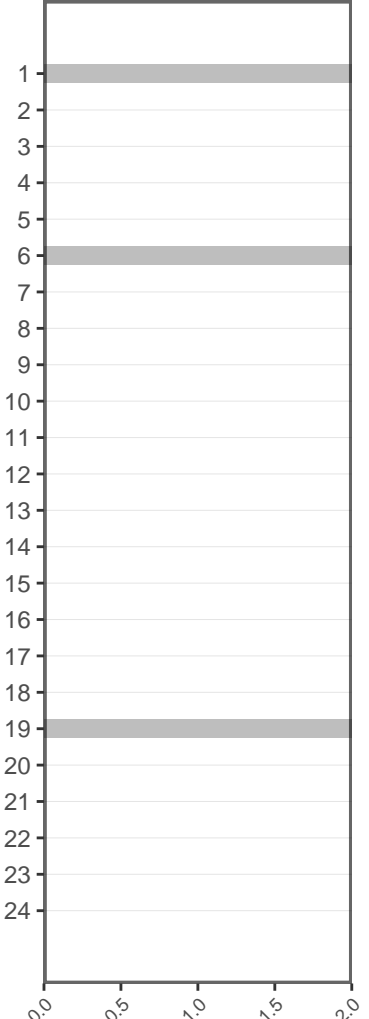
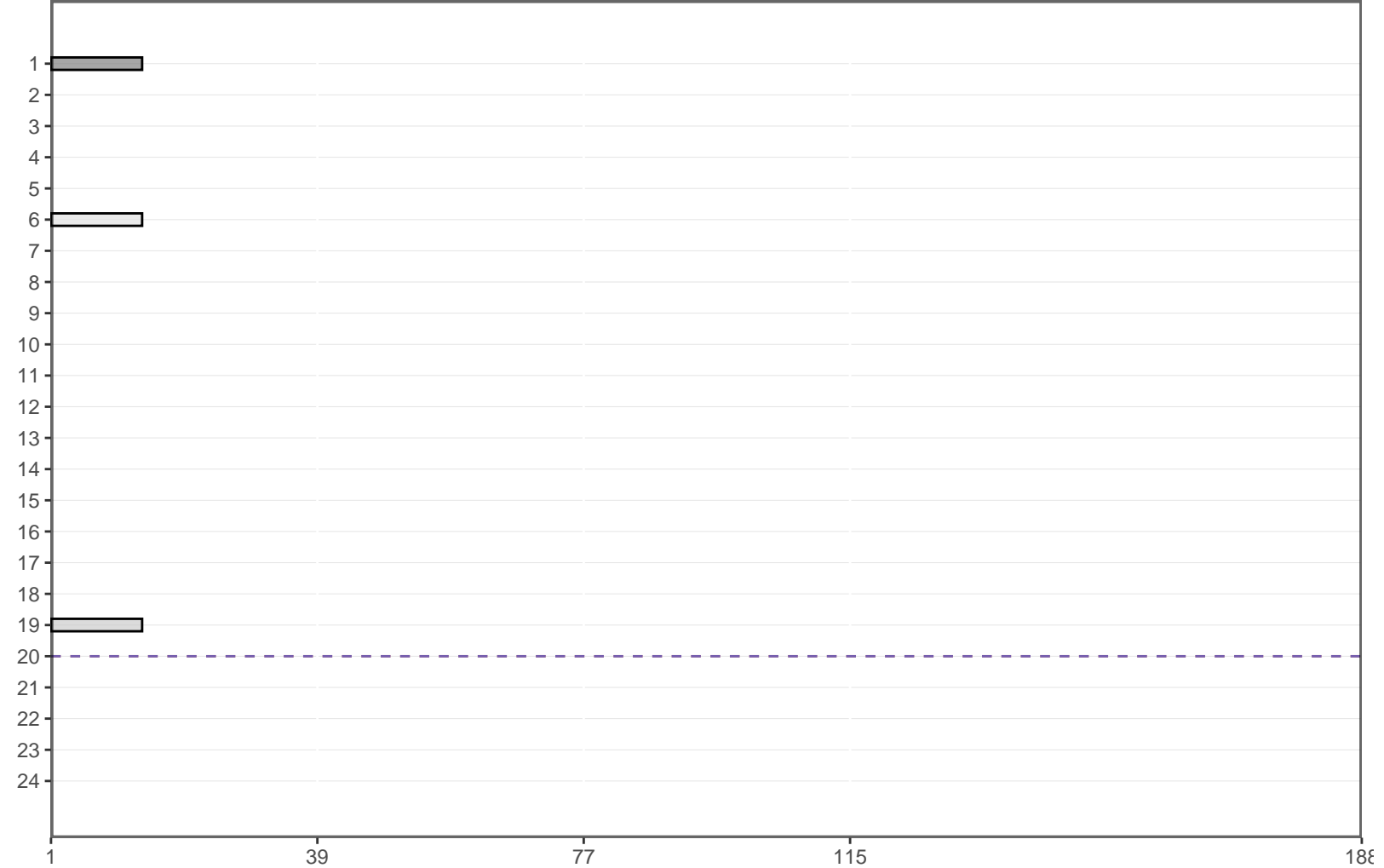
MW indication



Molecular weight



Gel Slice



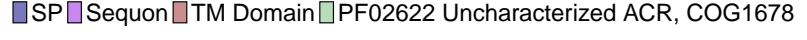
Protein length



Pfam domains



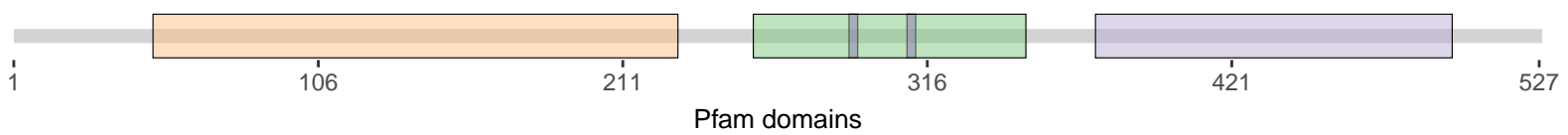
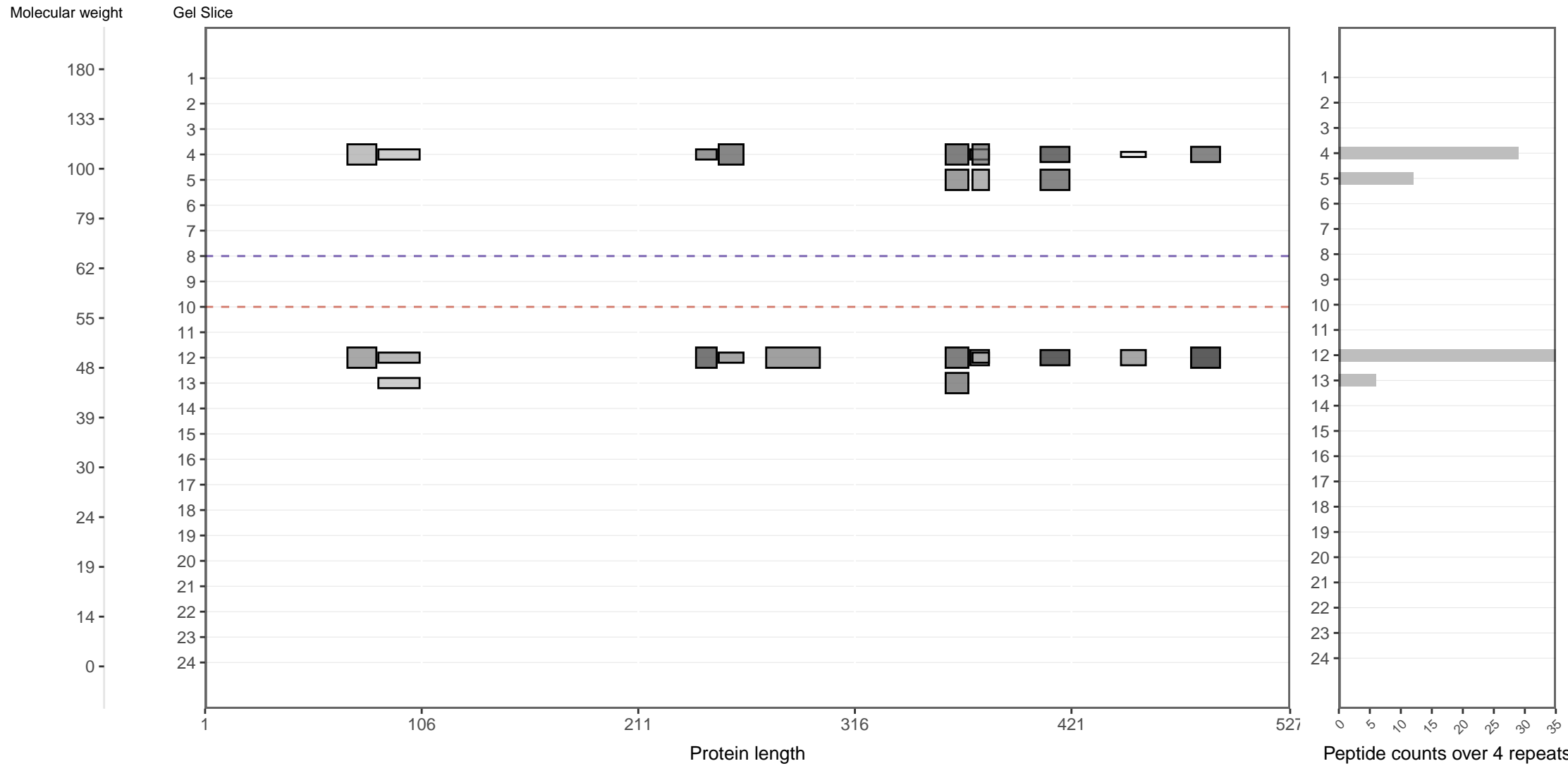
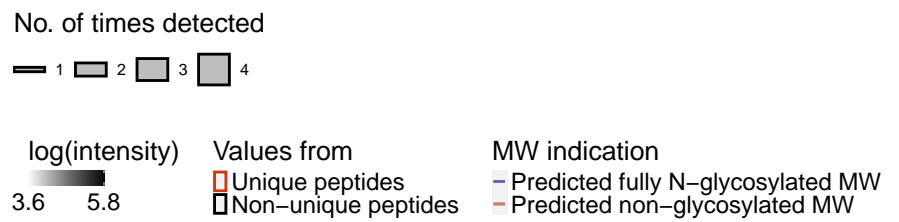
Pfam Description



Protein sequence:

IARLVAGEKALRSEEPSSVWNPDTVDLPPFWTIGKWAHTHEPEKGLIATEKLDGWHIFERTVALLLSMGNGPTGVILNRPSLVSIKEMR65VLGVRDLGE

NbL02g11570.1 UDP-glucose_6-dehydrogenase_3 [MW = 58.41 kDa]



Pfam Description

- SP
- TM Domain
- Sequon
- PF00984 UDP-glucose/GDP-mannose dehydrogenase family, central domain
- PF03720 UDP-glucose/GDP-mannose dehydrogenase family, UDP binding domain
- PF03721 UDP-glucose/GDP-mannose dehydrogenase family, NAD binding domain

Protein sequence:

TNLSAELSKLAAANFLAGRISSEVYVAMSALCEATGANVSGVWYAVGKDRIGPKFLNLSVDFGSSGQNDLNLVYCEINGLPEVAEYWKGVKINDYKTRFVNRVYVSMFNTVSGKRWVWLGFAFKDGTGTRTPMDVKGKLLGDKAKLSIVDPQVNEGQGRDLKMKFDWDFPLHLPMSPTTVKGVSVWWDVAITATKDAHVAVGLTEWDFKTLVDYKDYDNNMGKRFIFDGRNIVDEKLEIGFIVYSIGKPLDAILKMPWVA

NbL02g11490.1 ras_GTPase-activating_protein-binding_protein_2-like [MW = 50.32 kDa]

No. of times detected



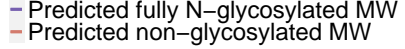
log(intensity)



Values from



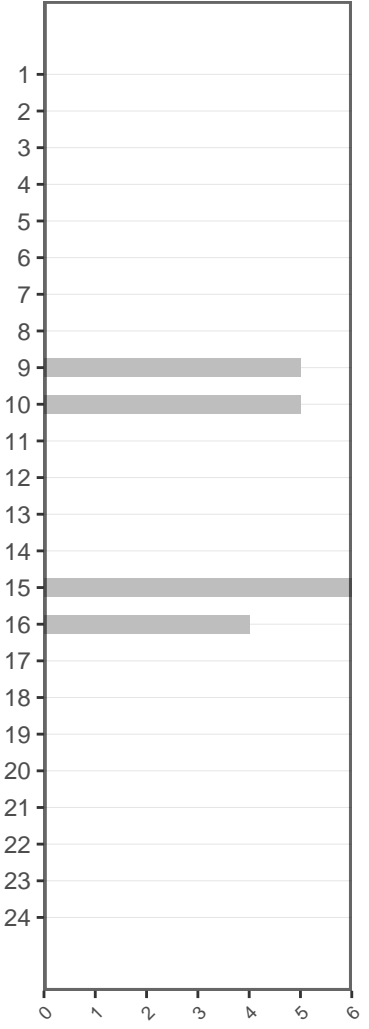
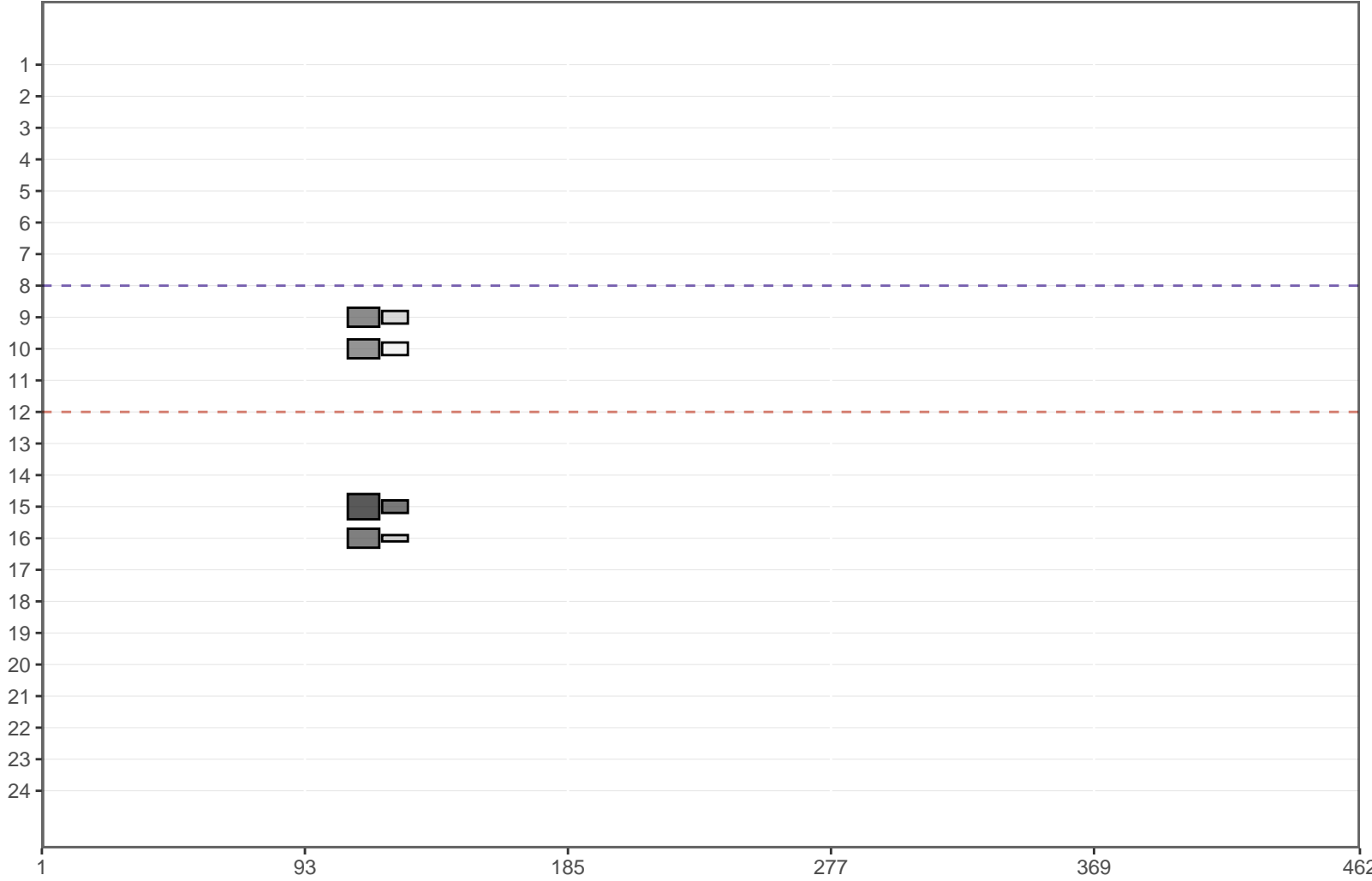
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

SP Sequon TM Domain PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) PF02136 Nuclear transport factor 2 (NTF2) domain

Protein sequence:

SENSVAQEDAPKKSYSASIVSSGTRKGFTRIVYPTNTRMAPKAVAKQPIAAVAGTFAPEASHPTVFNQTRVPEINDTEDEAEAGHSIVRNLPLOVTVAGLETFEKKFPIKGGGVGVVRENRGGGDFDFGVFEEDVSSMHSAGASPTTQGRGAVVEMKRTTTRVGEARGRFPPGRGGFRNDFRGRGNFGGGRVYGRNFEFGGRDFSGRGRGGGGRASEGVQGVRRGRGRGCGPQSSAPV

NbL02g11370.1 protein_FLX-like_2 [MW = 51.25 kDa]

No. of times detected



log(intensity)



Values from



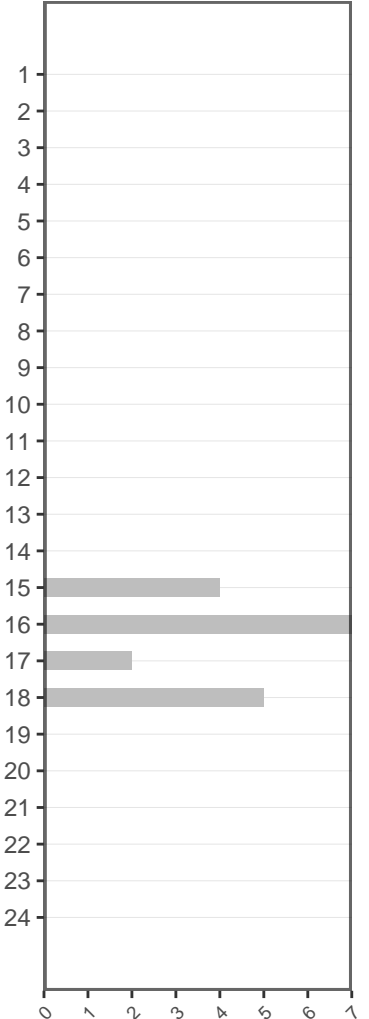
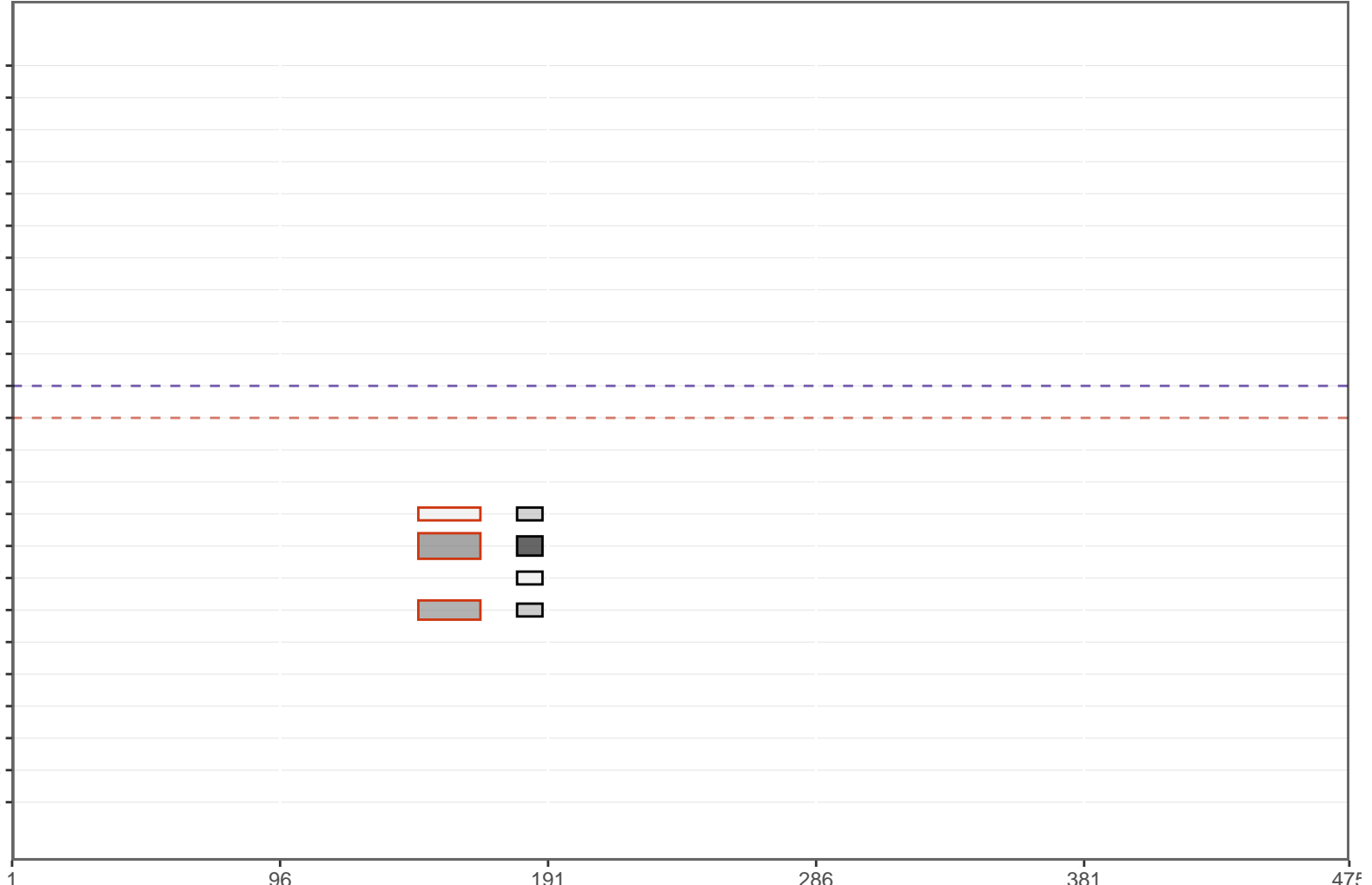
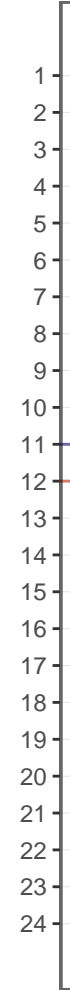
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

S L Q V M E K N Y M T M S R E V E K L R A E L N T E N S E R T G P Y G G A T G Y N E N D A A N N Y A G S N Y G D G Y G Y G R G P L P T A T N V G G W A V T S P R V G A G S V P R P N R P P Y D S S N M P G Y D A G R G M V P T G F G Y D A Q K G S A L A A E A D R G H G Y D T M K G P G Y D A G R A G Y E T Y G G P Y D G Y G A P V Y N A G R G S G Y D V R G S N Y D P A K A S N Y D A S N K G G V A T G G W A P M E N N P H S S T P P G H A G P G Y D A A A Q G S N P A R R

NbL02g11210.1 oxygen-evolving_enhancer_protein_1_chloroplastic [MW = 35.2 kDa]

No. of times detected



log(intensity)



Values from



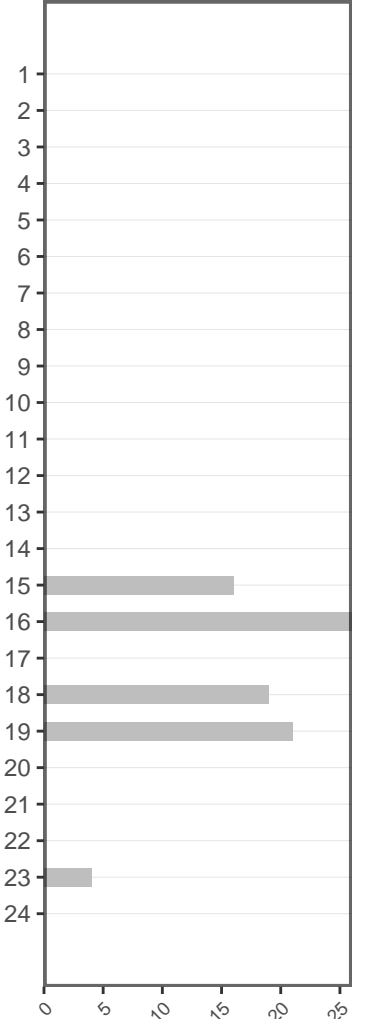
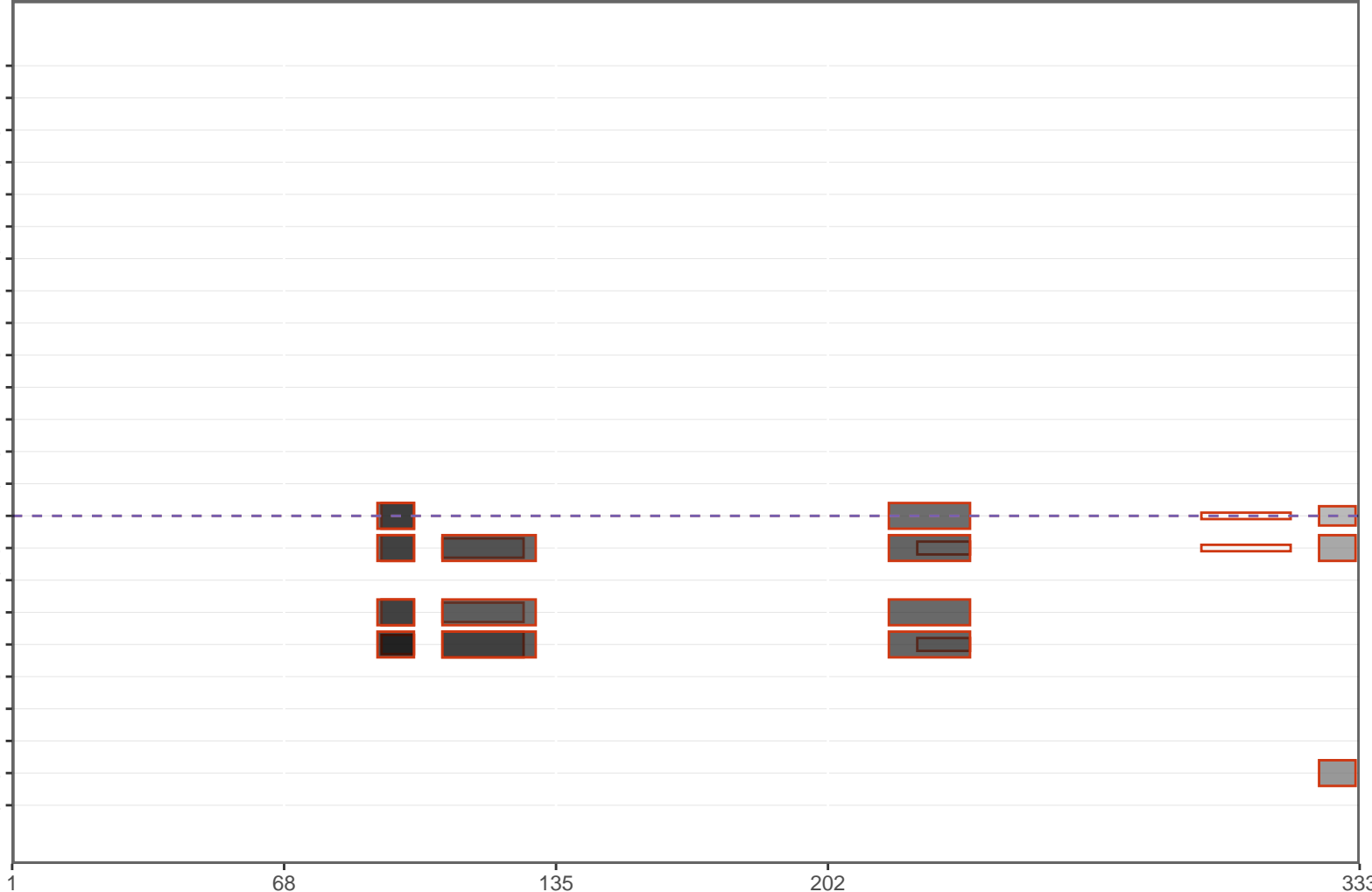
MW indication



Molecular weight

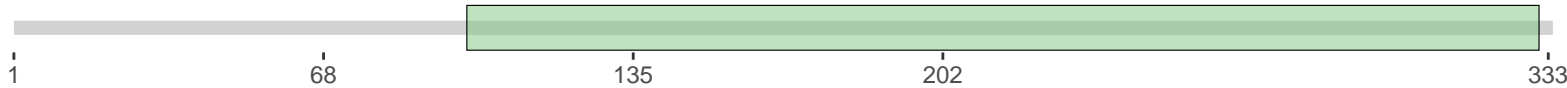


Gel Slice



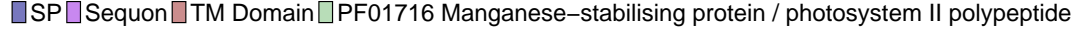
Protein length

Peptide counts over 4 repeats



Pfam domains

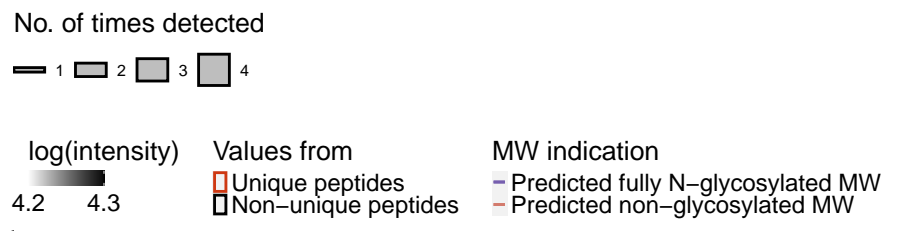
Pfam Description



Protein sequence:

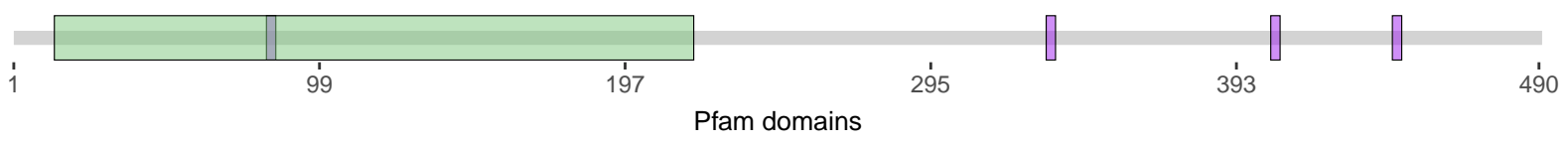
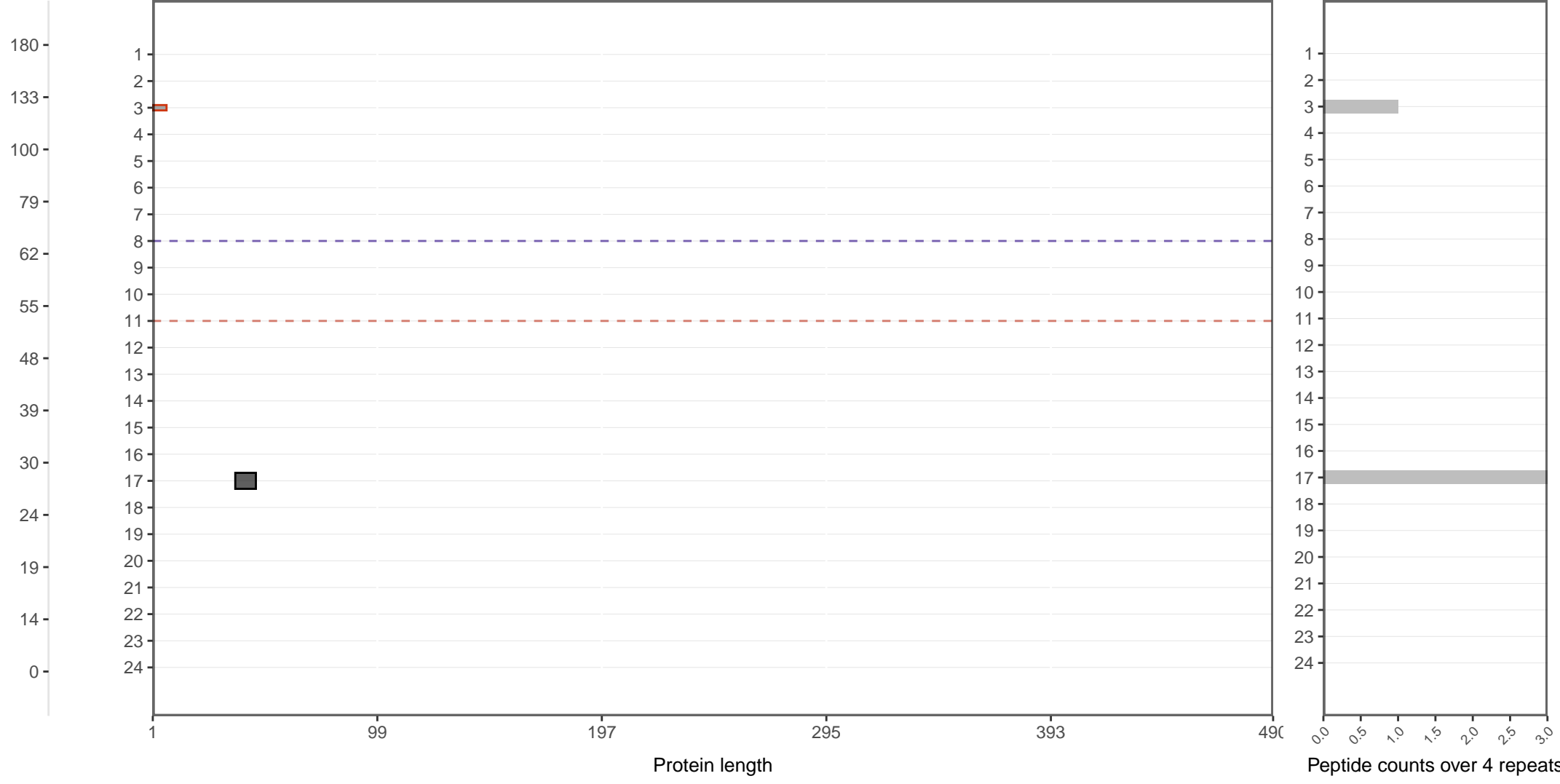
NAPPDFQTKLMTRLTYLDEIEGPFVEVSDGCTVKFEKNDGDAVFTVQLPQGERVPLFTTKQLVAGSKPEFSGSEFLVPSVRRGSSFLDPKGRGGSTGYDNALVMPAGRGDEEELKENVNTASSTGKFLVTVQSKPQTGEVGVGFESIQPSDTLGAHKVPKDVKDGIWYAGLE*

NbL02g11120.1 patatin-like_protein_2 [MW = 54.01 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF01734 Patatin-like phospholipase

Protein sequence:

MAPMDCXXMLVLSLGTGIGKEEKYSAVA656WGVLSWLYNNGASPLLDVFDGASADVDHLSMTMFGSLGNEKNYLRIGIPLKLIHFHNSNAIQGLNPNRPSRLGQRHRANVLFYVWAKPLDPETLFFP6GVPKQLGNSCLIPYSHINDIGSPRRNWFETNLFQPNQ6PLGYSISITQPGRFPVYCF5YLGNLWQYENLGPGLNATENLNLKLT6SGIRGHFGRPMDFG6DMLNGWQAAVFDQSTGNFC

NbL02g11050.1 L-ascorbate_oxidase_homolog [MW - SP = 57.39 kDa]

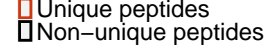
No. of times detected



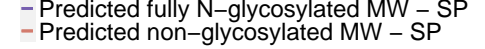
log(intensity)



Values from



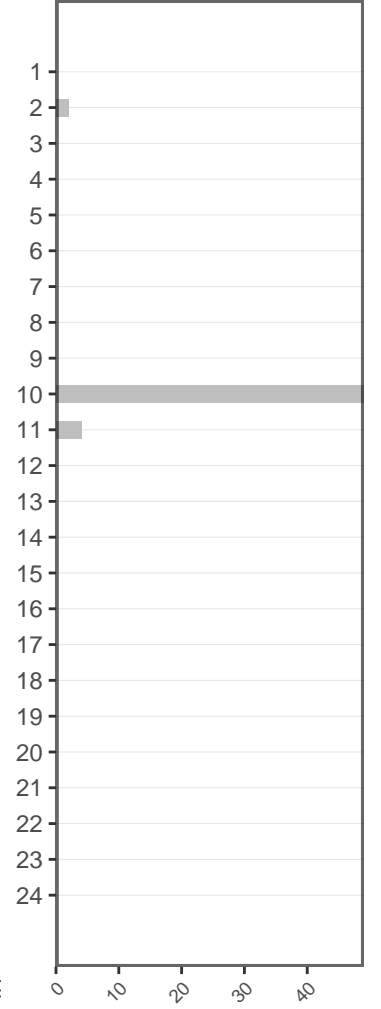
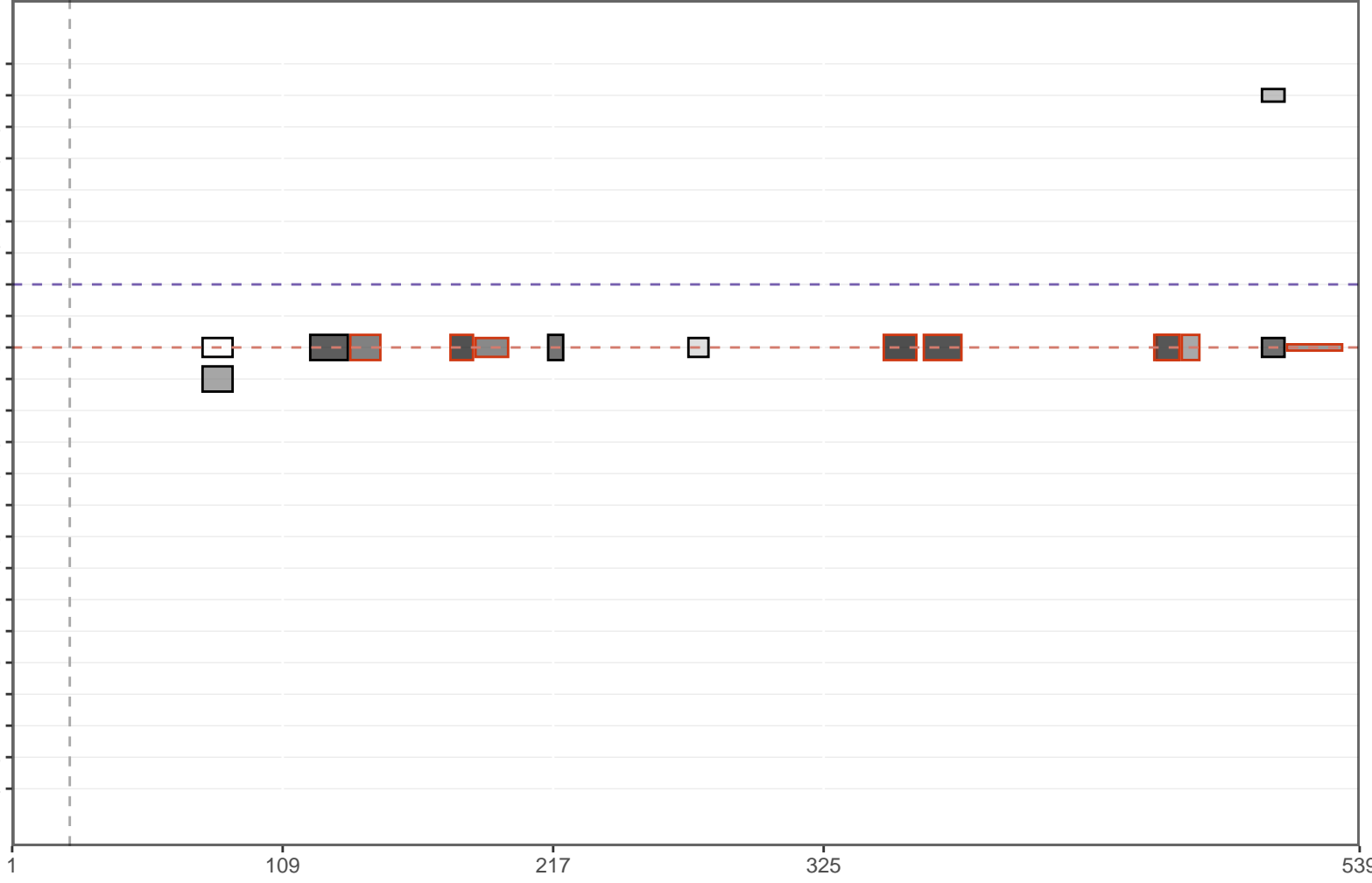
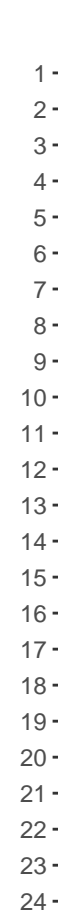
MW indication



Molecular weight

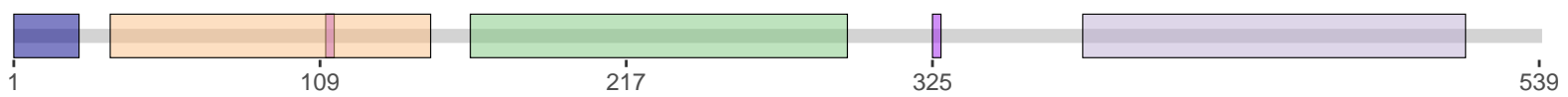


Gel Slice



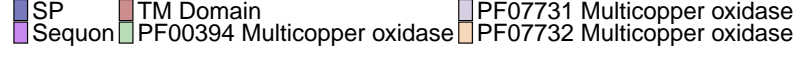
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LSLSLVTLDDPKDHYVMASRFFTTVLTAVLHHTNSGTPVSGPLPAGPDGDFQWBLMGARTFRWNLSTNAARPNPQGGFHYGKTPSRIVLANSAPLISGKGRVAVNSVSYNPDPPLKADHFNIPGVFSLNSIGTPTAASPISLTAVLPASLHEFLVFNQNNEDTVGSWHLGDYDFWVWFGGSGTWTQDSRKEYNLVDAIHRHTQGVYFKSWTAVVSLNCGMMNLRSAMWDRGLGGQVYLRVYNFTASLANEYDPTNALLGGKAVGRHP

NbL02g10900.1 probable_esterase_KAI2 [MW = 30.33 kDa]

No. of times detected



log(intensity)



Values from



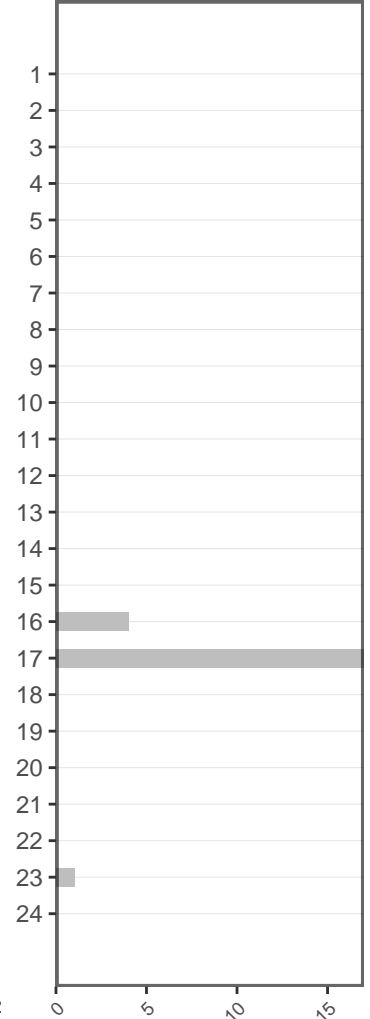
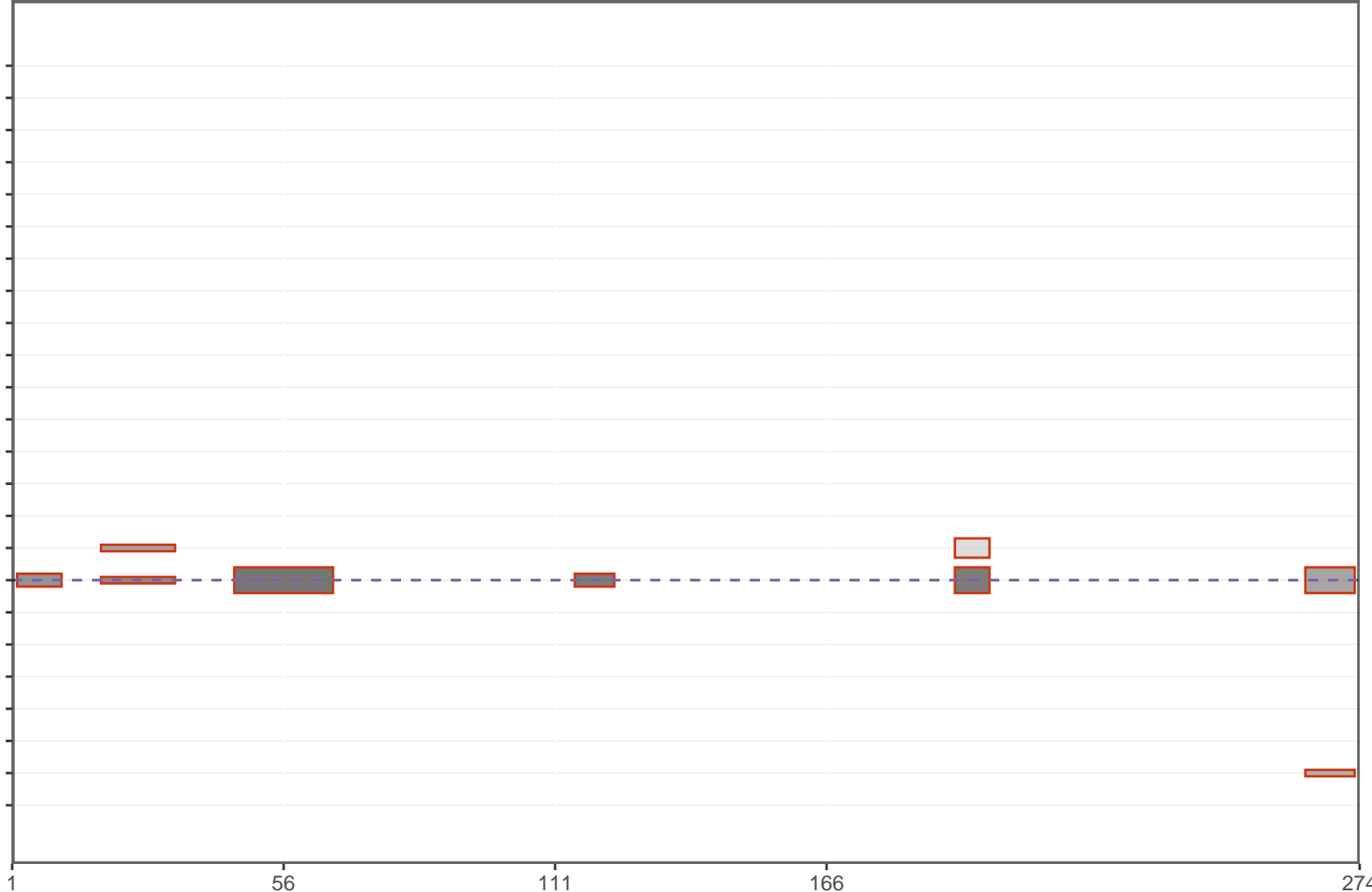
MW indication



Molecular weight

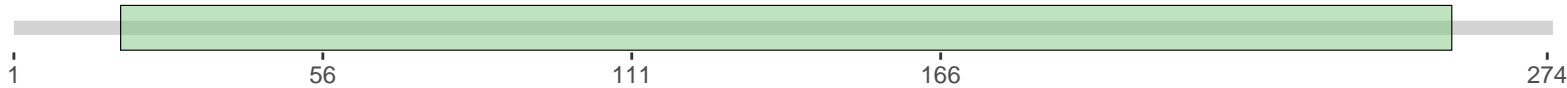


Gel Slice



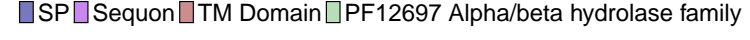
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

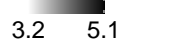
RFINTDDYGGFEKEDIDQLGSAAMESNKKWIDGFAPLVGGDMDSVAWDEFSRFLFNMRPDIALSVRTITFFDLRHFLESRVTVPCWHSKDLAVPVAVEYHGNLGGKSVIEVISTEGHLPQLSAPEVTVFVLLRHSHIDISDITV

NbL02g10850.1 casein_kinase_II_subunit_alpha-2-like [MW = 49.57 kDa]

No. of times detected



log(intensity)



Values from



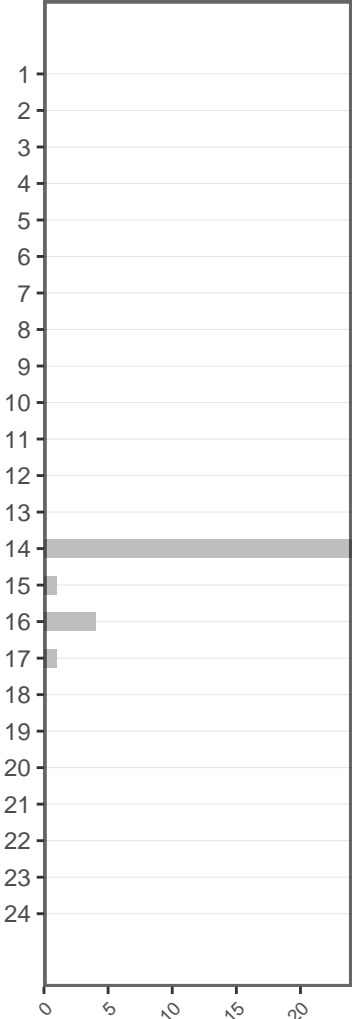
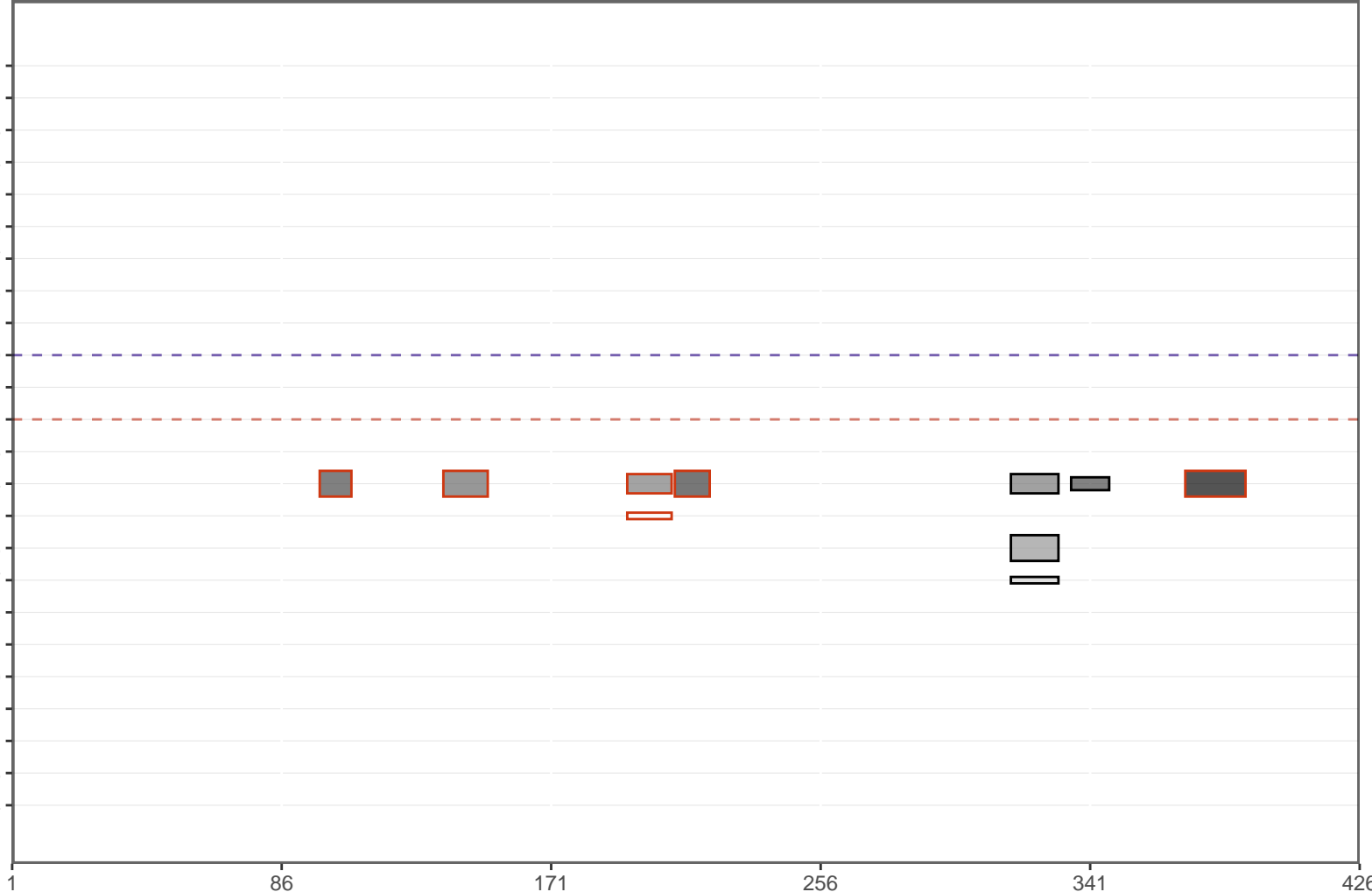
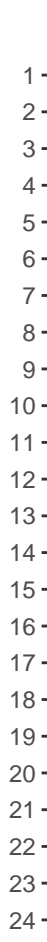
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

VVNTDFKLVLPNLSDFRYYVELLKALDYCHSGGIMHRDKPHNVMIDHDGRKLRIDWGLAEFYHPCKEYNNRVAQRVYKGPPELLVDLGGDYDLSLDWISLGGMFAGMFRKEPFYGHQNDVLDVQIAKILGTDLNSVLYNKVRLDPLLAALVGRHSRKPWRFINSENGHLACPEAVDFVDKLLRYDHDGRPTAKEAMAHFYFYPINAESSRIRTH

NbL02g10670.1 malate_dehydrogenase_glyoxysomal-like [MW = 37.95 kDa]

No. of times detected



log(intensity)



Values from



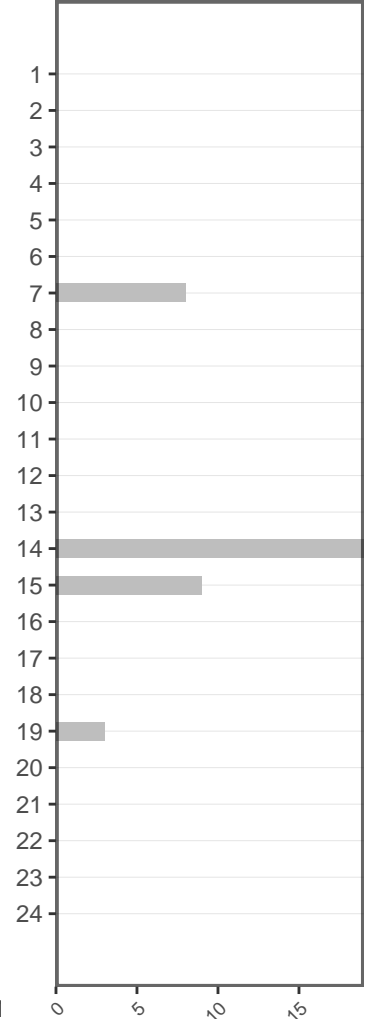
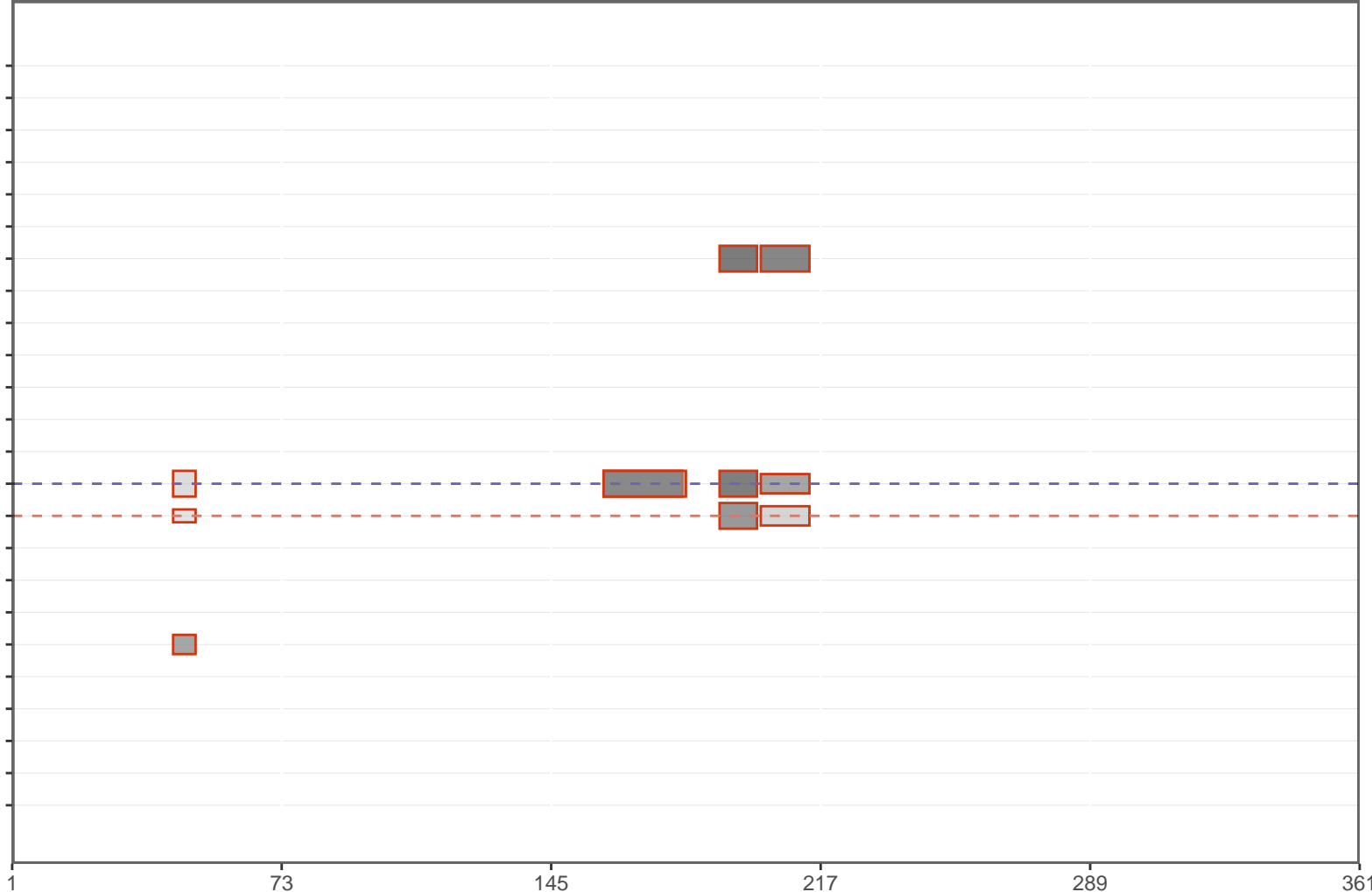
MW indication



Molecular weight



Gel Slice

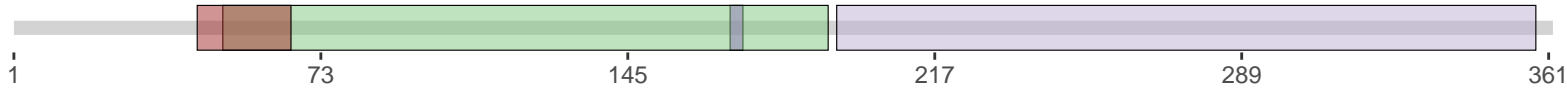


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF00056 lactate/malate dehydrogenase, NAD binding domain
- PF2866 lactate/malate dehydrogenase, alpha/beta C-terminal domain

Protein sequence:

VNSTYPAAEVYKAGTFDRRLRLLGVTMLDVRASSTFAEVLGLDPRVDVPPVGGHAGVTLPLLGGVWPPGQSTPEETEVYLSRIGNGGTEVVEAKAGAGGATLGMVAVAVKFADAGLHGLRGGAGVECAFVSSQVTELPPFAFKVRLGRNGVVEIPLGLPLNEVERSGLEKAKKELATSIQKGVNFVKK

NbL02g10610.1 serine_hydroxymethyltransferase_mitochondrial [MW = 57.17 kDa]

No. of times detected



log(intensity)



Values from



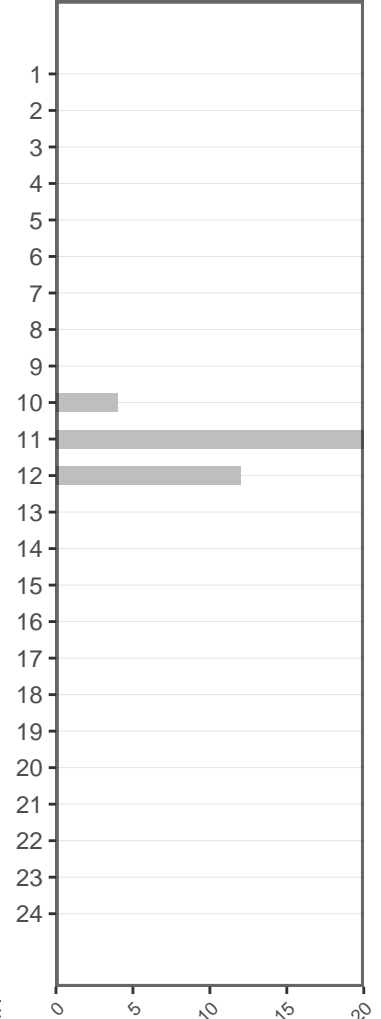
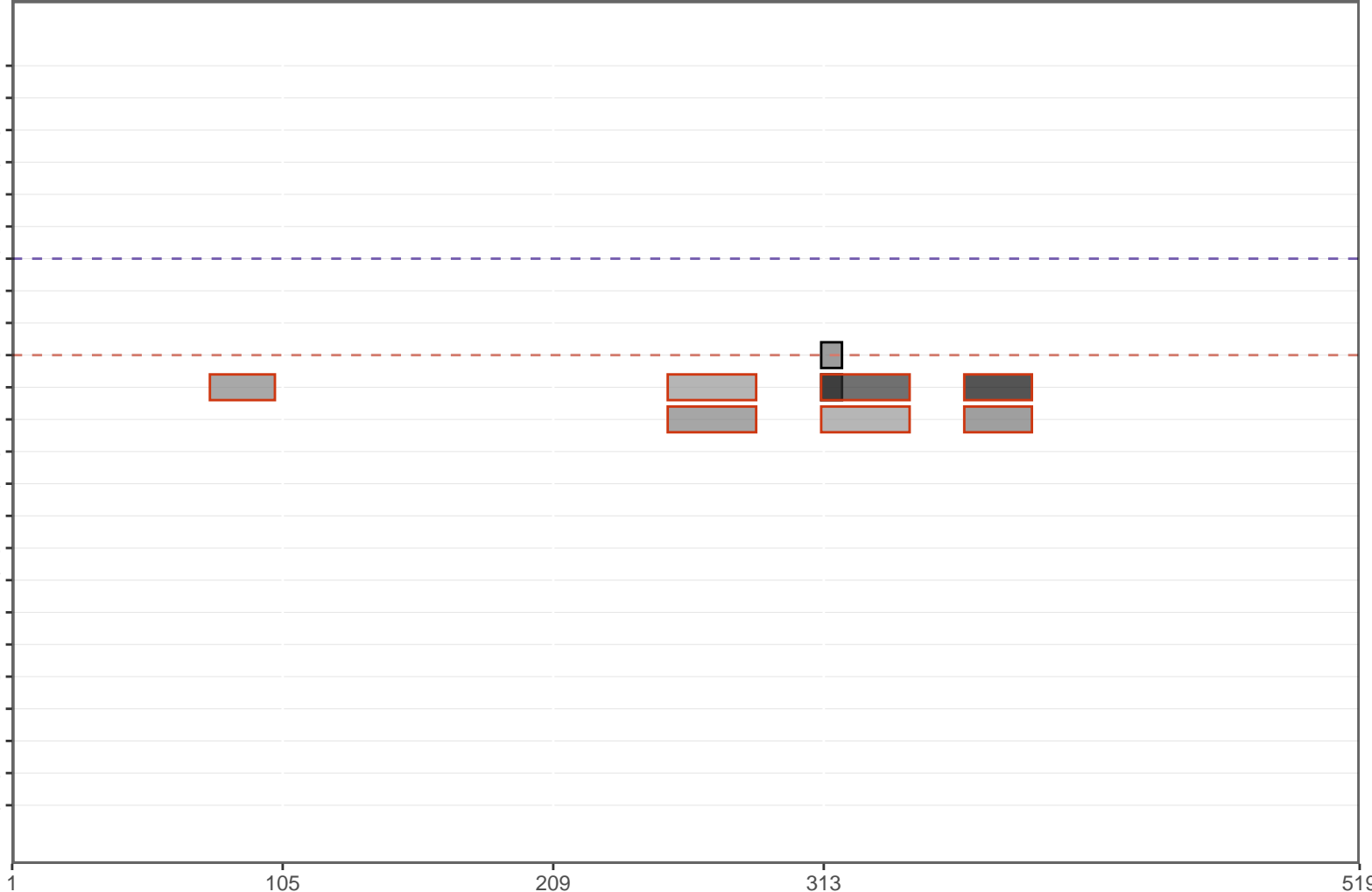
MW indication



Molecular weight

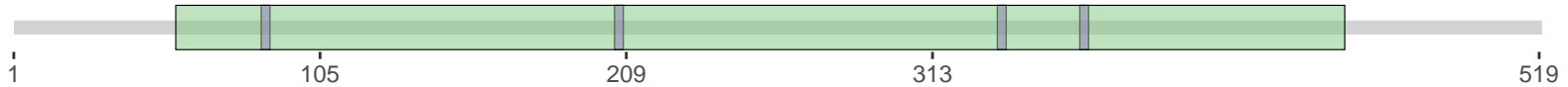


Gel Slice



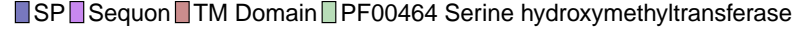
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

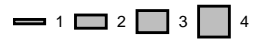


Protein sequence:

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NbL02g10390.1 ubiquitin_receptor_RAD23d-like [MW = 45.51 kDa]

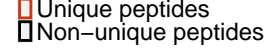
No. of times detected



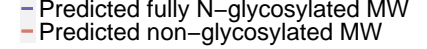
log(intensity)



Values from



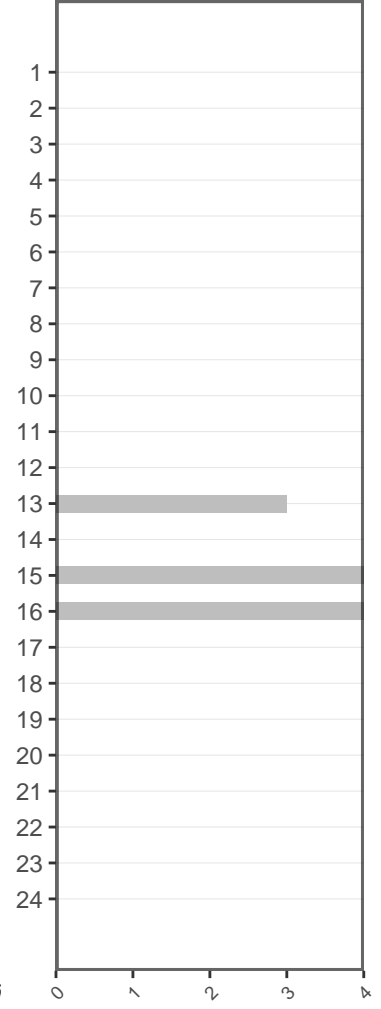
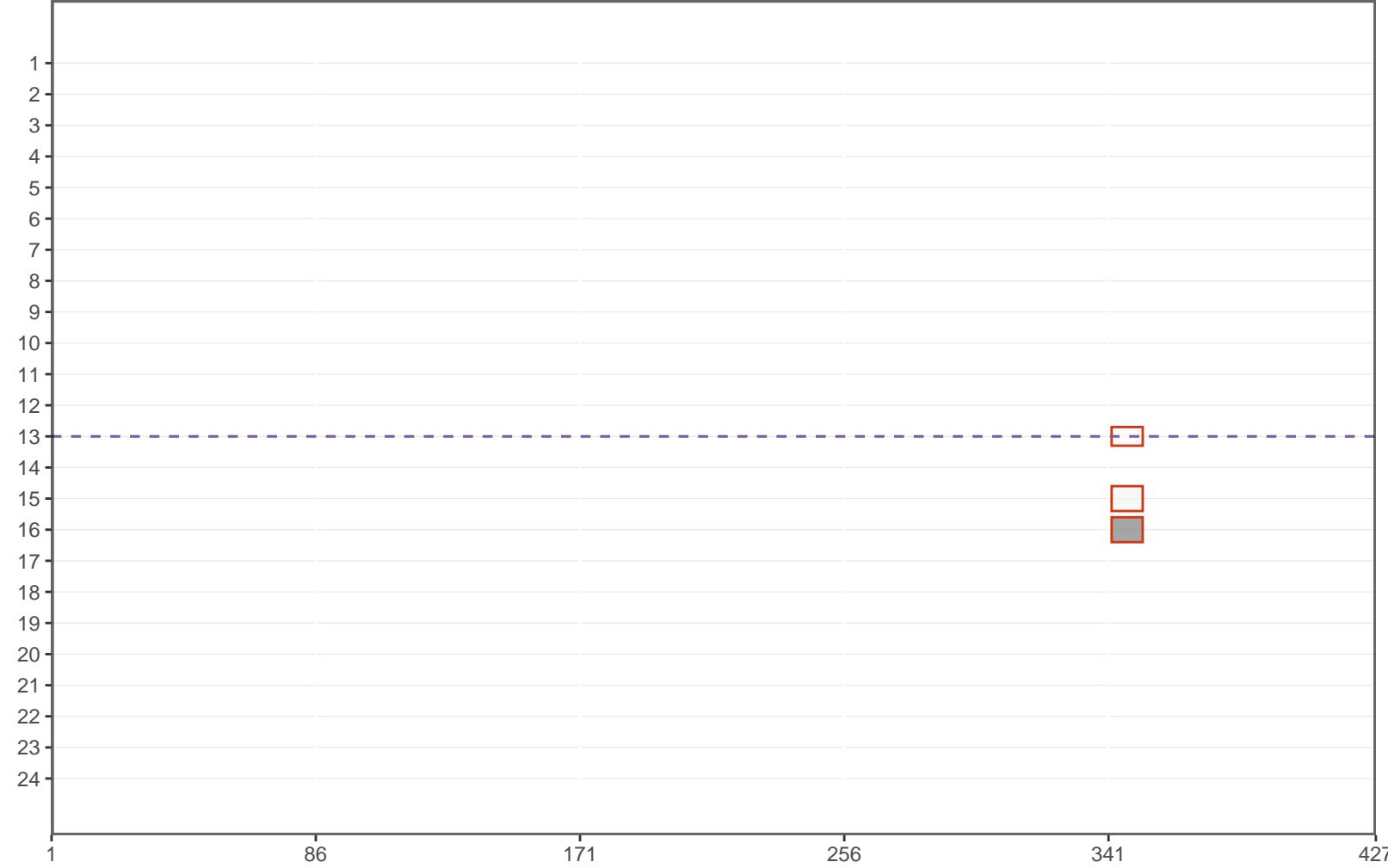
MW indication



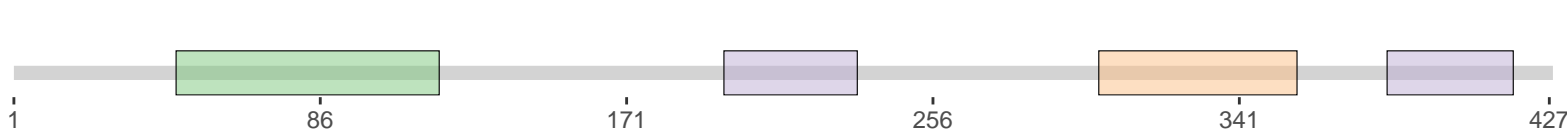
Molecular weight



Gel Slice

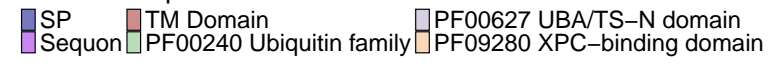


Protein length



Pfam domains

Pfam Description



Protein sequence:

DLLDGGGSVDRDTVIRALRAAFNFRERAEIYLVSGIPGAEIPAPAPAPAPARTSGGAVNPPVGSQRPVPSGGFNAFLDFPQGLPNVGSNAGAGNDFLNSPQFQALRAMVQANPQLQPMLEGKGNPQLMRHQDHQADFLRLINPEVEGEGNVPGGPAGAPQAVTVTPEREERLEAMGFDRALVGVFFAGNKNEELAAAYLLDHHMEFDE

NbL02g10380.1 T-complex_protein_1_subunit_zeta_1-like [MW = 58.84 kDa]

No. of times detected



log(intensity)



Values from



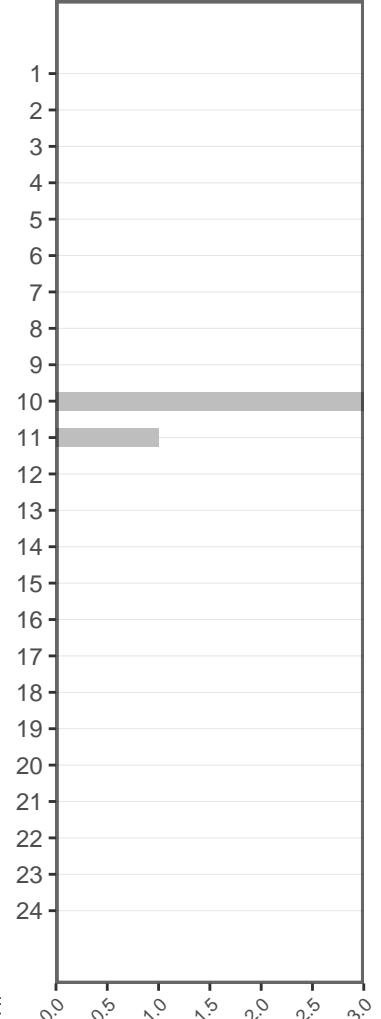
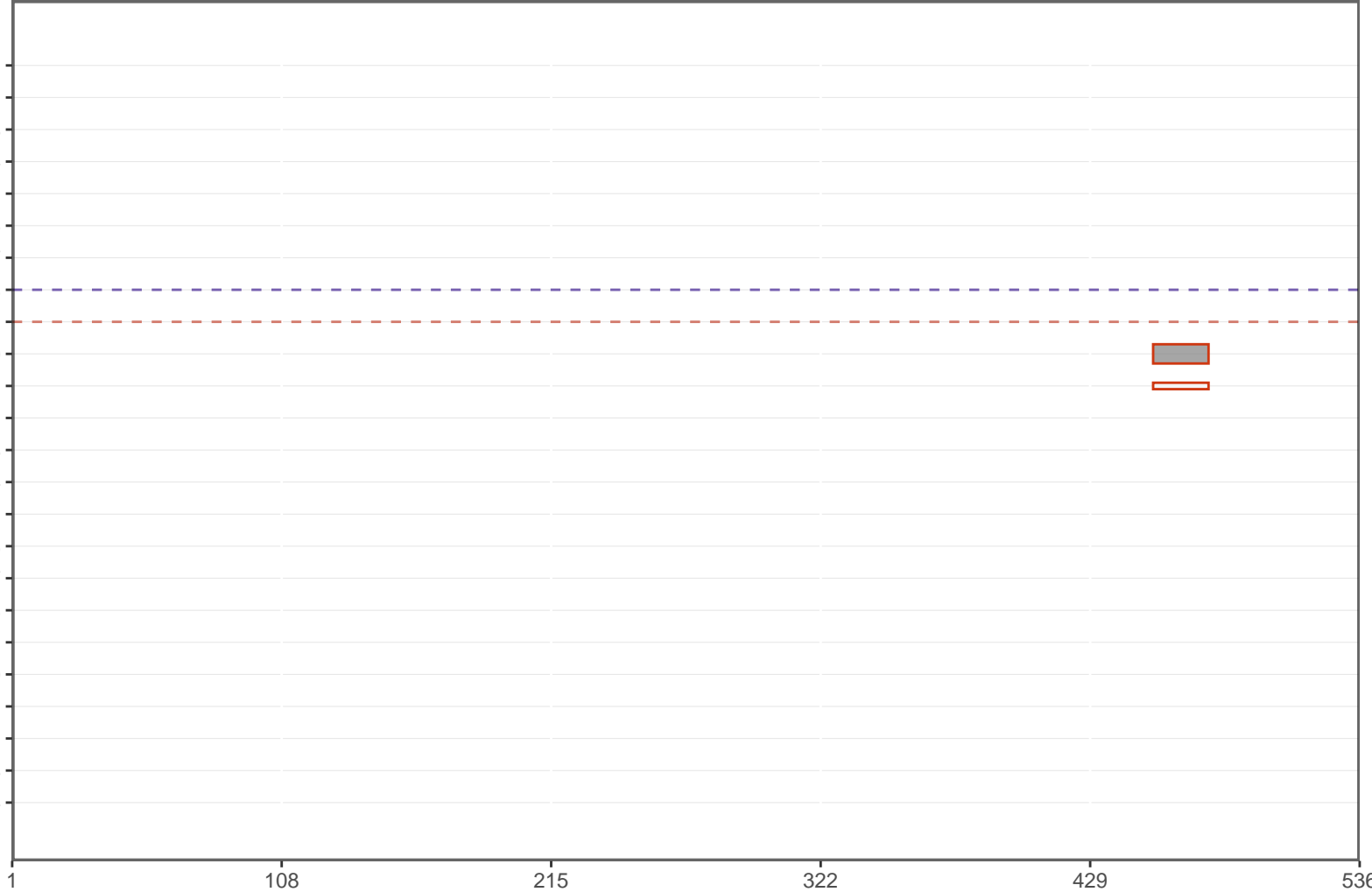
MW indication



Molecular weight



Gel Slice

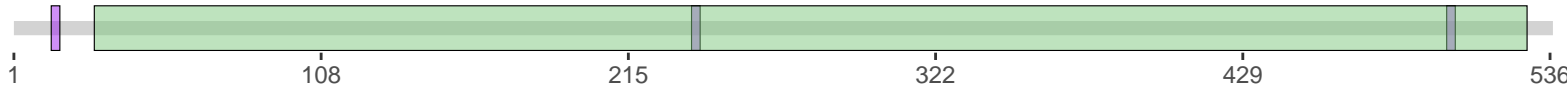


Protein length

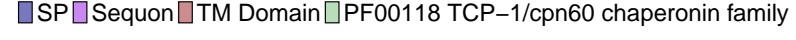


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

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NbL02g10360.1 14-3-3_protein_4 [MW = 29.43 kDa]

No. of times detected



log(intensity)



Values from



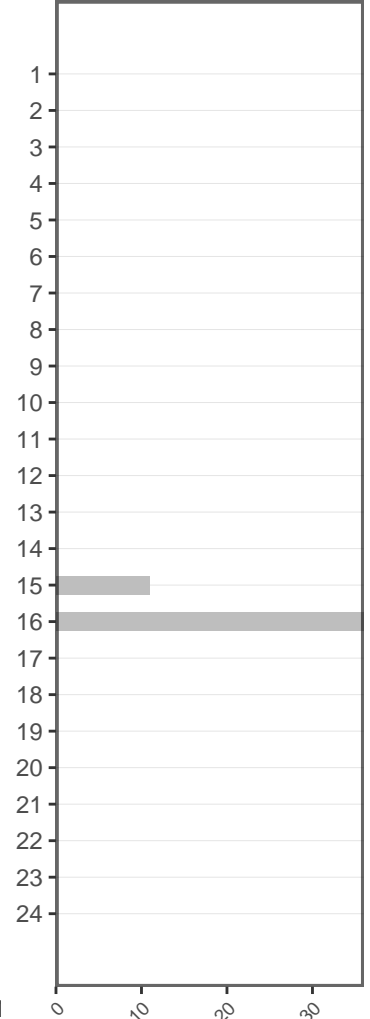
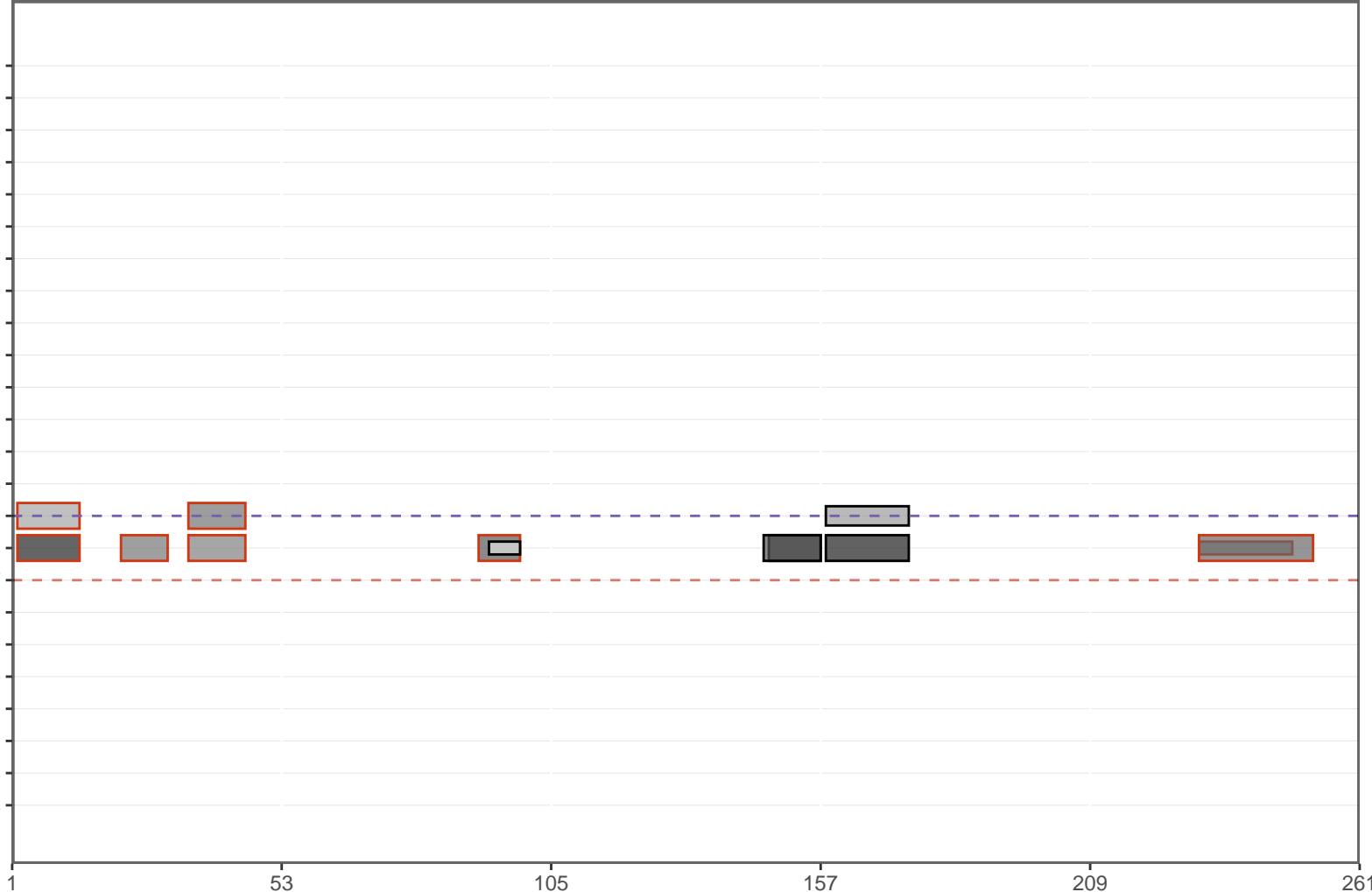
MW indication



Molecular weight

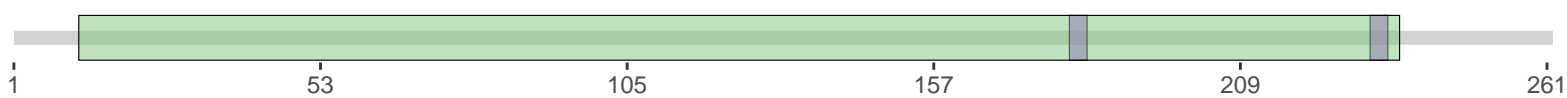


Gel Slice



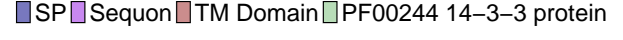
Peptide counts over 4 repeats

Protein length



Pfam domains

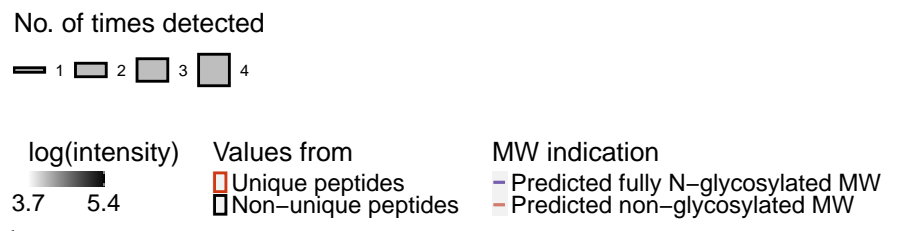
Pfam Description



Protein sequence:

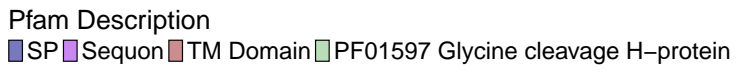
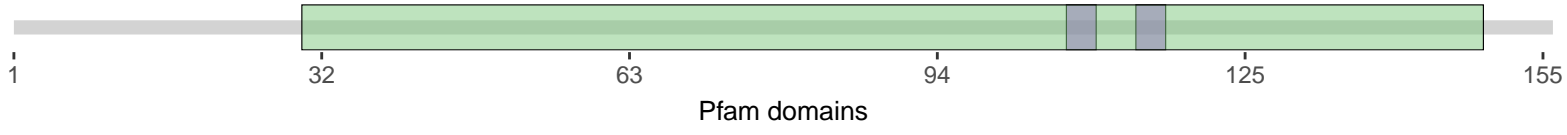
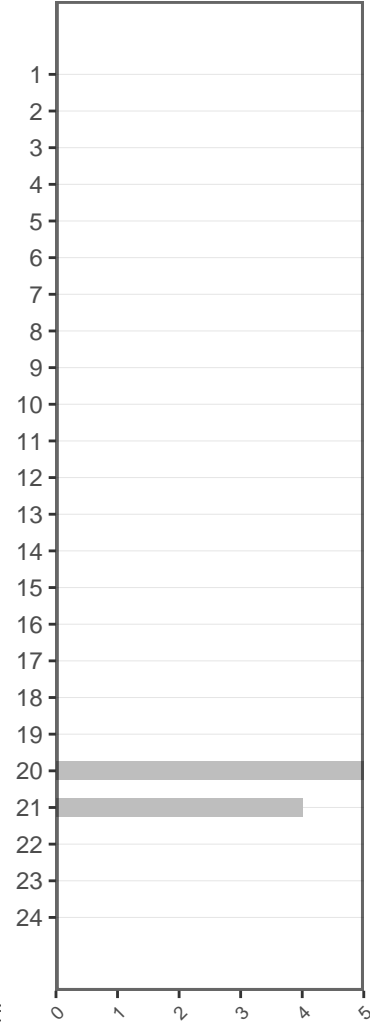
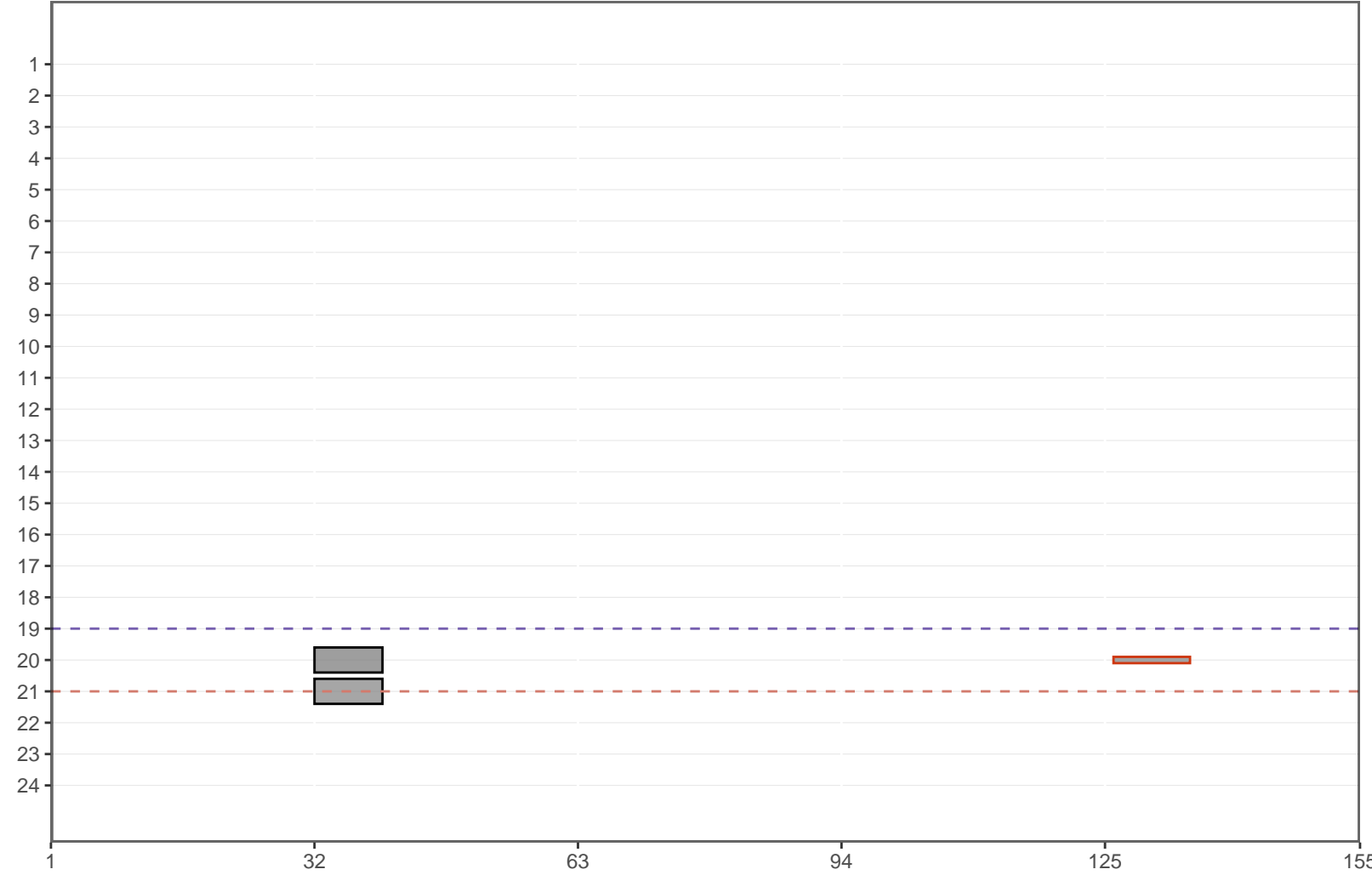
IAESKVFYLMKGGDHYRHLAEKFTGSEKKEAENTLLAWKSGADDALETALPHRILGLALNFVYFYEELNSPDRAGNLAKQAFDEANSELDLGEESYKDDSTLMOLLRDNLFWTSDNAEDAGDDIKKAPKHESGEGGGQ

NbL02g10210.1 glycine_cleavage_system_H_protein_2_mitochondrial-like [MW = 16.91 kDa]



Molecular weight

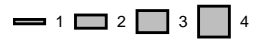
Gel Slice



Protein sequence:
 L L P E V G A S Y T O G S F G A V E G V K A T S D I N S F V G K V E V N E K L N D T P G L I N E S P Y G D G W I R V E I N N D E L K S L M D H D G V K F C E E E D A K H I

NbL02g09970.1 aspartic_proteinase-like [MW = 59.72 kDa]

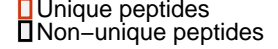
No. of times detected



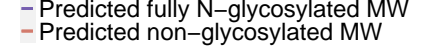
log(intensity)



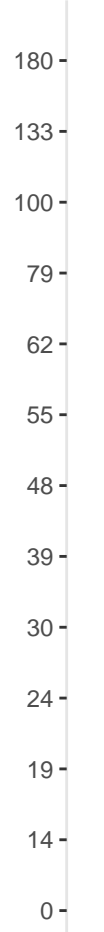
Values from



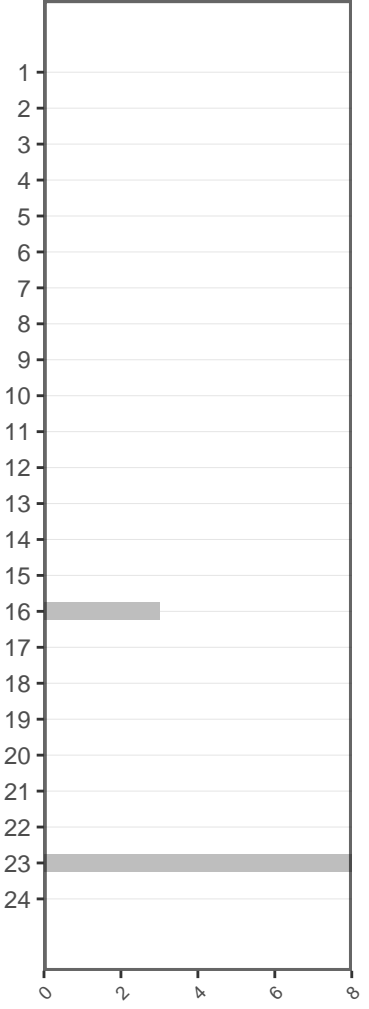
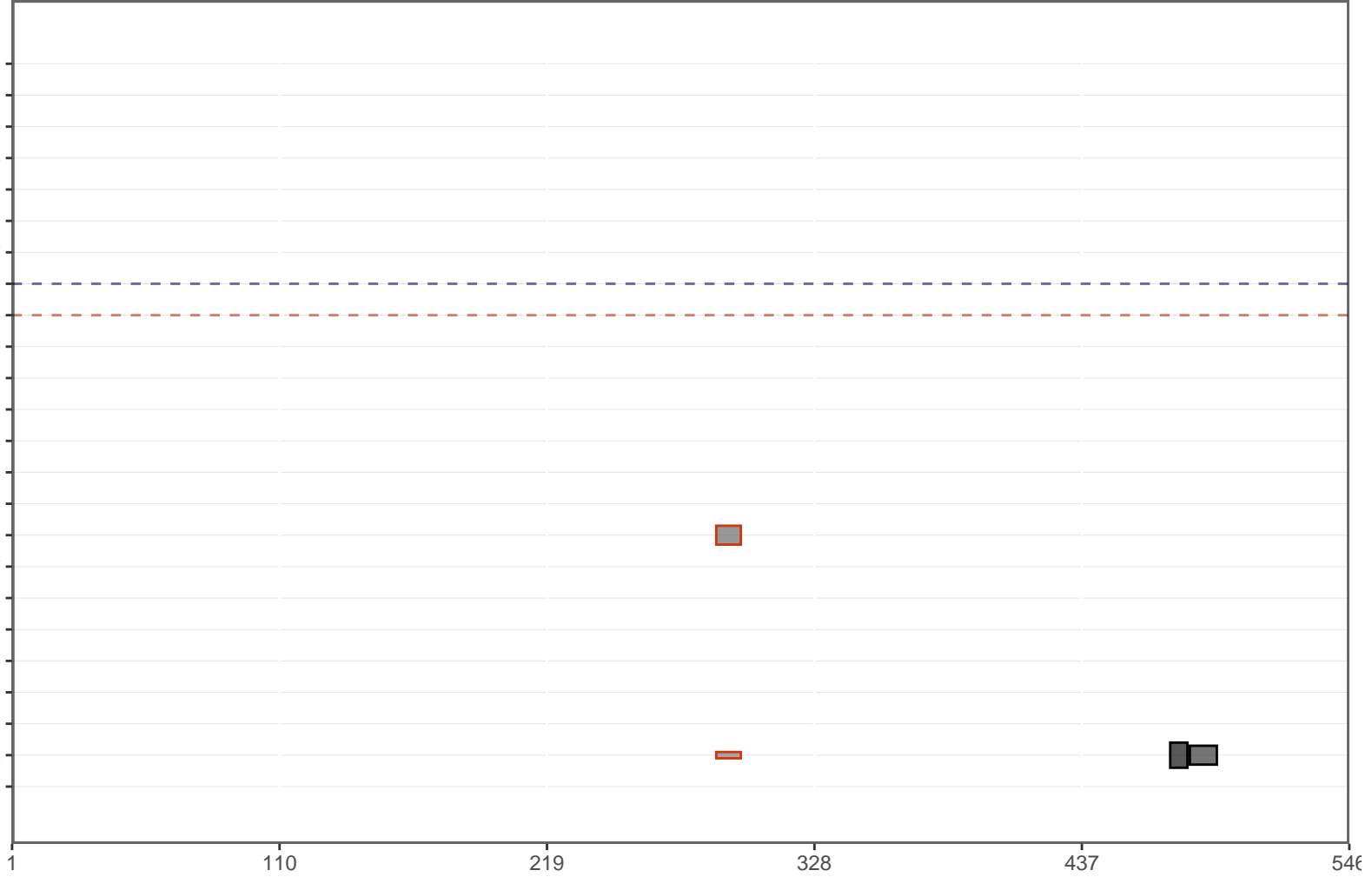
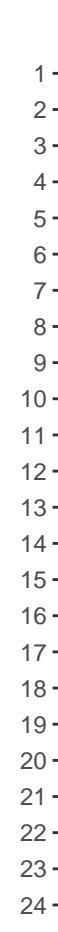
MW indication



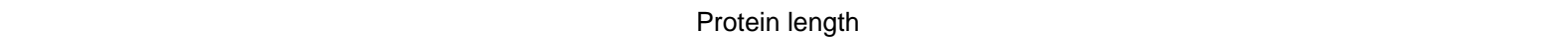
Molecular weight



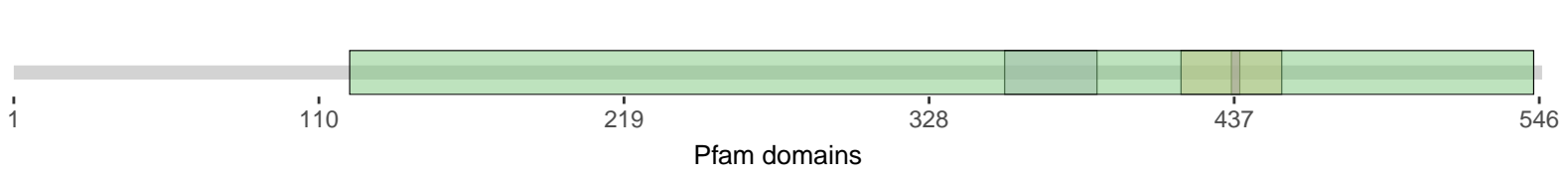
Gel Slice



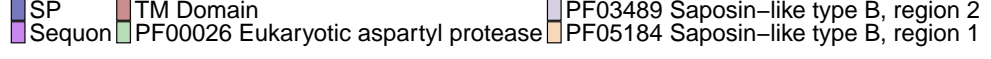
Protein length



Pfam domains



Pfam Description



Protein sequence:

MLNRYTEEECCGSEIVFGGVDPNHYKGETVYVPTGKGVWGFDMGDLIDGKATGVCEGGCSAAIDSGTSLLAGPTTSTMTNAGAGGVSSGQCKKVVVGVGGTIDMLLLAGADPKKICADVGVCTFDGKRVGVMGSEVVDKAGRSTGLQDGMCSGACEMAVWIMENLQGGNGTQDRLLNYYNELCERLPSPLGESAVDDCKLSMPKVSFTTSGKVFDFLSPNEVILKVGEGAKAQGGISGFTGLDIPRRRGLWILGDFMGRYHTVFDYGLRVGFAEA*

NbL02g09920.1 1-aminocyclopropane-1-carboxylate_oxidase [MW = 25.4 kDa]

No. of times detected



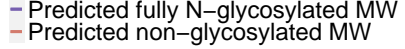
log(intensity)



Values from



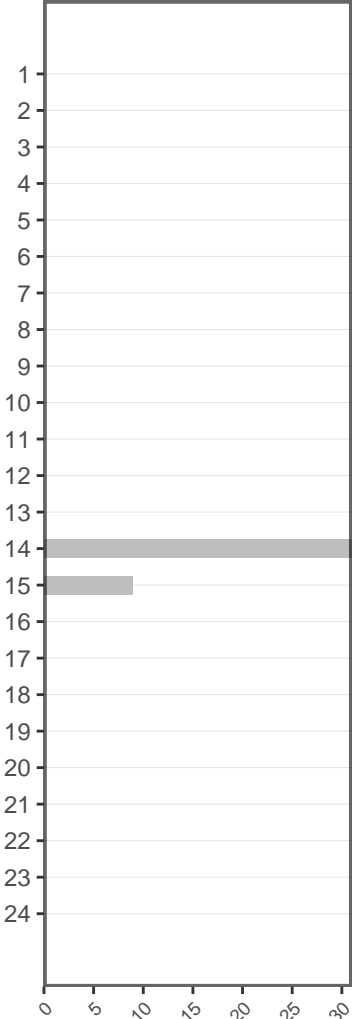
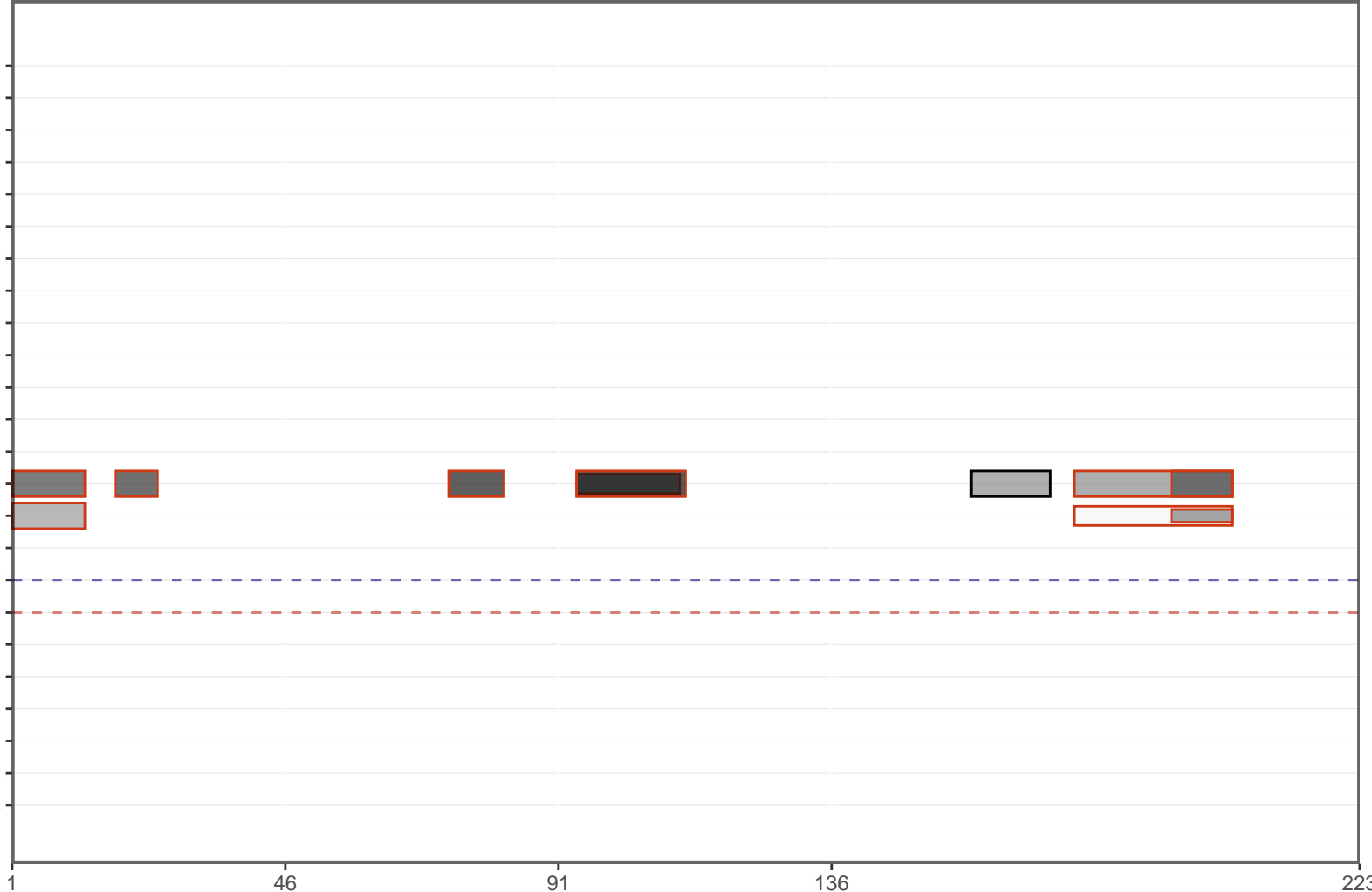
MW indication



Molecular weight



Gel Slice



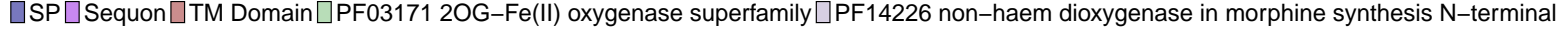
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

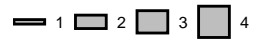


Protein sequence:

[SNISEVPLDLEHEYRKIMKEFAEKLEKLAEGQLLDLNGENLGLGDDGKAFYVSGKGFPTGTRVSNVPPCFKPKDLKGLRAHTDAGGILLFQDDKVGSLGLLKKDKKWDVPPMRHSVINLGDQLR]

NbL02g09570.1 RNA_polymerase_II_transcriptional_coactivator_KIWI-like [MW = 11.67 kDa]

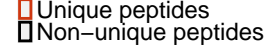
No. of times detected



log(intensity)



Values from



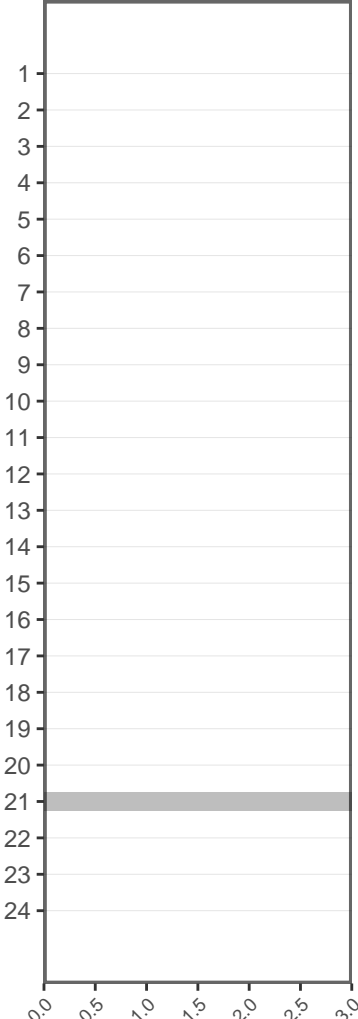
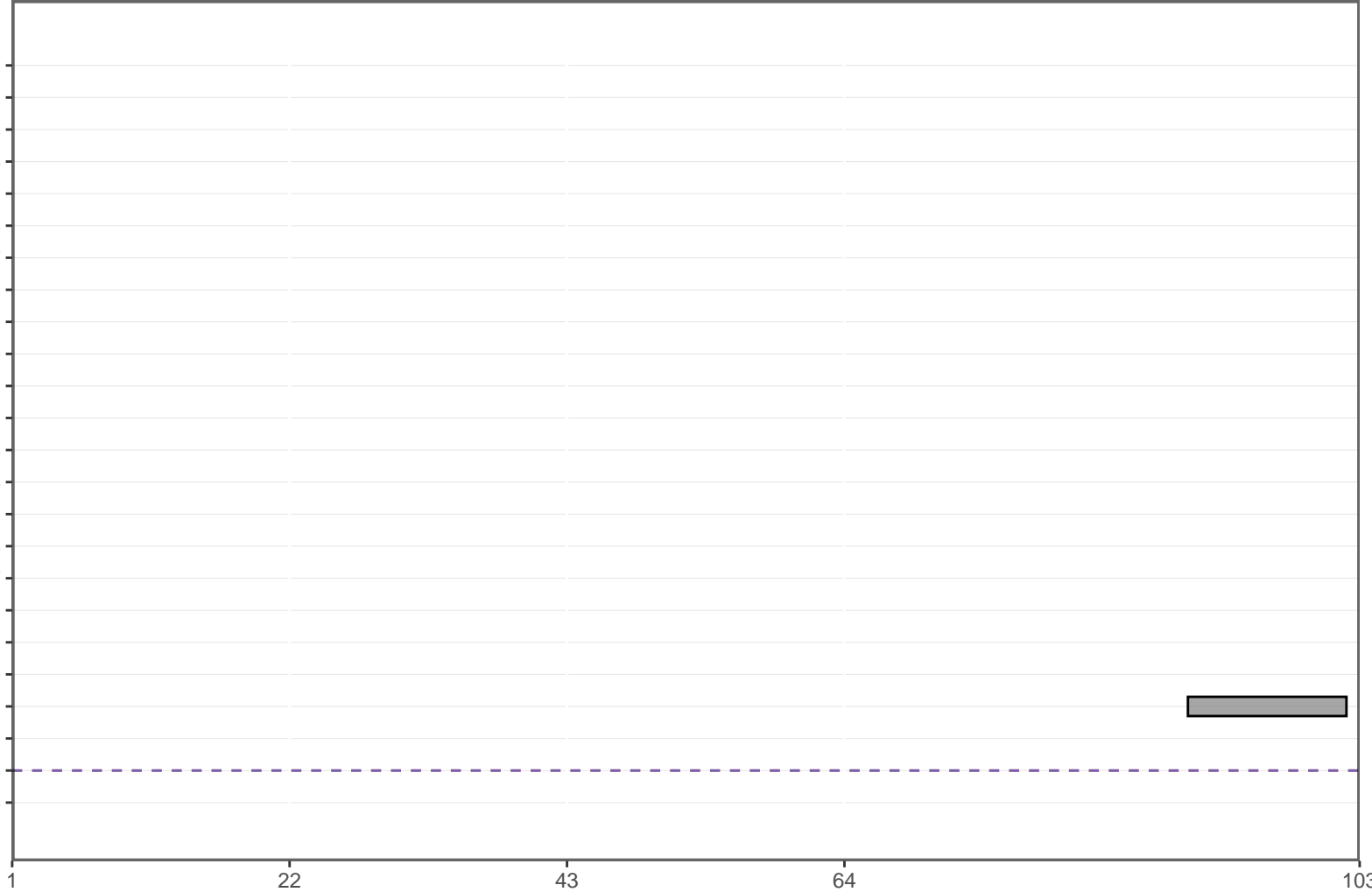
MW indication



Molecular weight



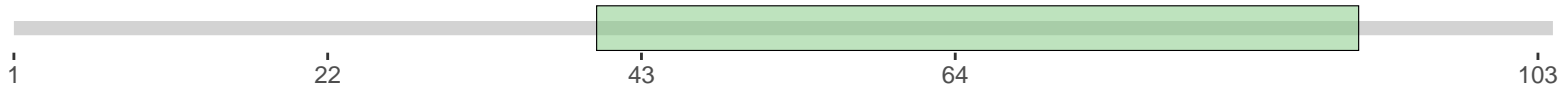
Gel Slice



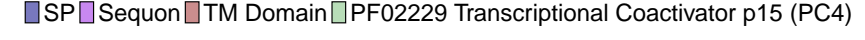
Protein length



Pfam domains



Pfam Description



Protein sequence:

VCEISKRRVSVREFGGKIMVDRIFYKDKGKMPGRKGIKLSMDGWNVLRHDAEDELVANS*

NbL02g09300.1 phosphopantetheine_adenylyltransferase [MW = 19.52 kDa]

No. of times detected



log(intensity)



Values from



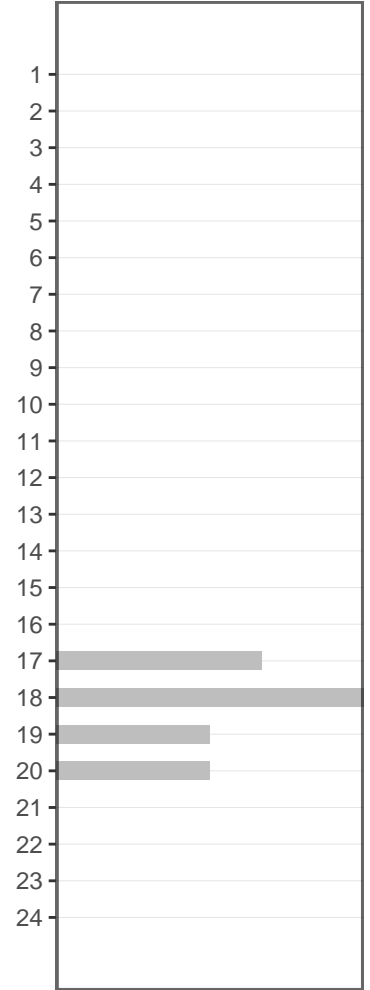
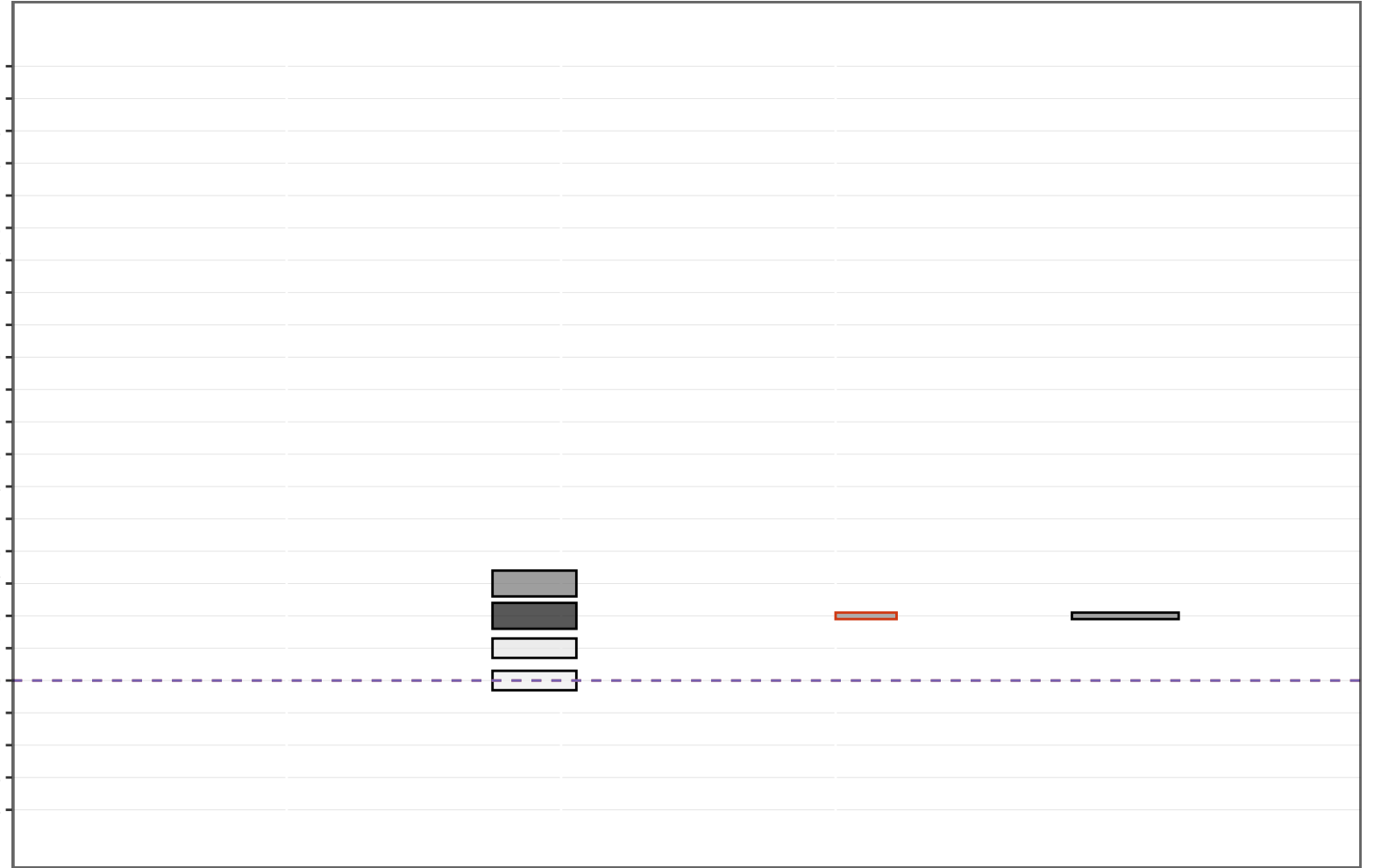
MW indication



Molecular weight



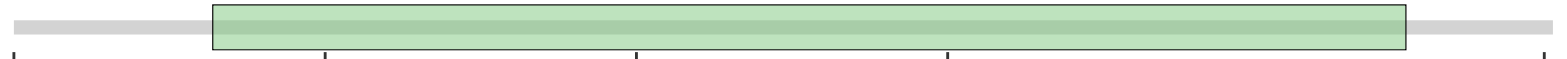
Gel Slice



Peptide counts over 4 repeats



Protein length



Pfam domains

Pfam Description



Protein sequence:

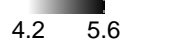
MCNVENYKSLKPELVVEAVPVVDVPGPSIDKNLEAVVSKETLPQGLVNRKRTERGLSQLKIEVVDLVSEESGDKLSSTALRKLAEKLRDHIPEGGQ

NbL02g09220.1 proteasome_subunit_beta_type-1 [MW = 24.69 kDa]

No. of times detected



log(intensity)



Values from



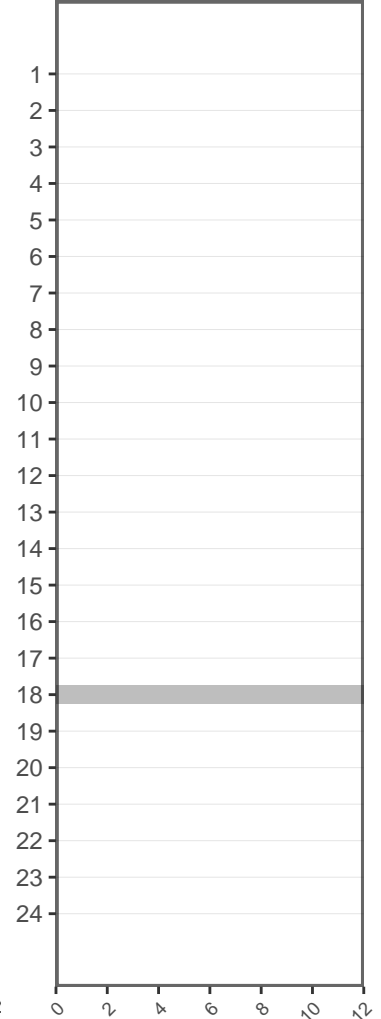
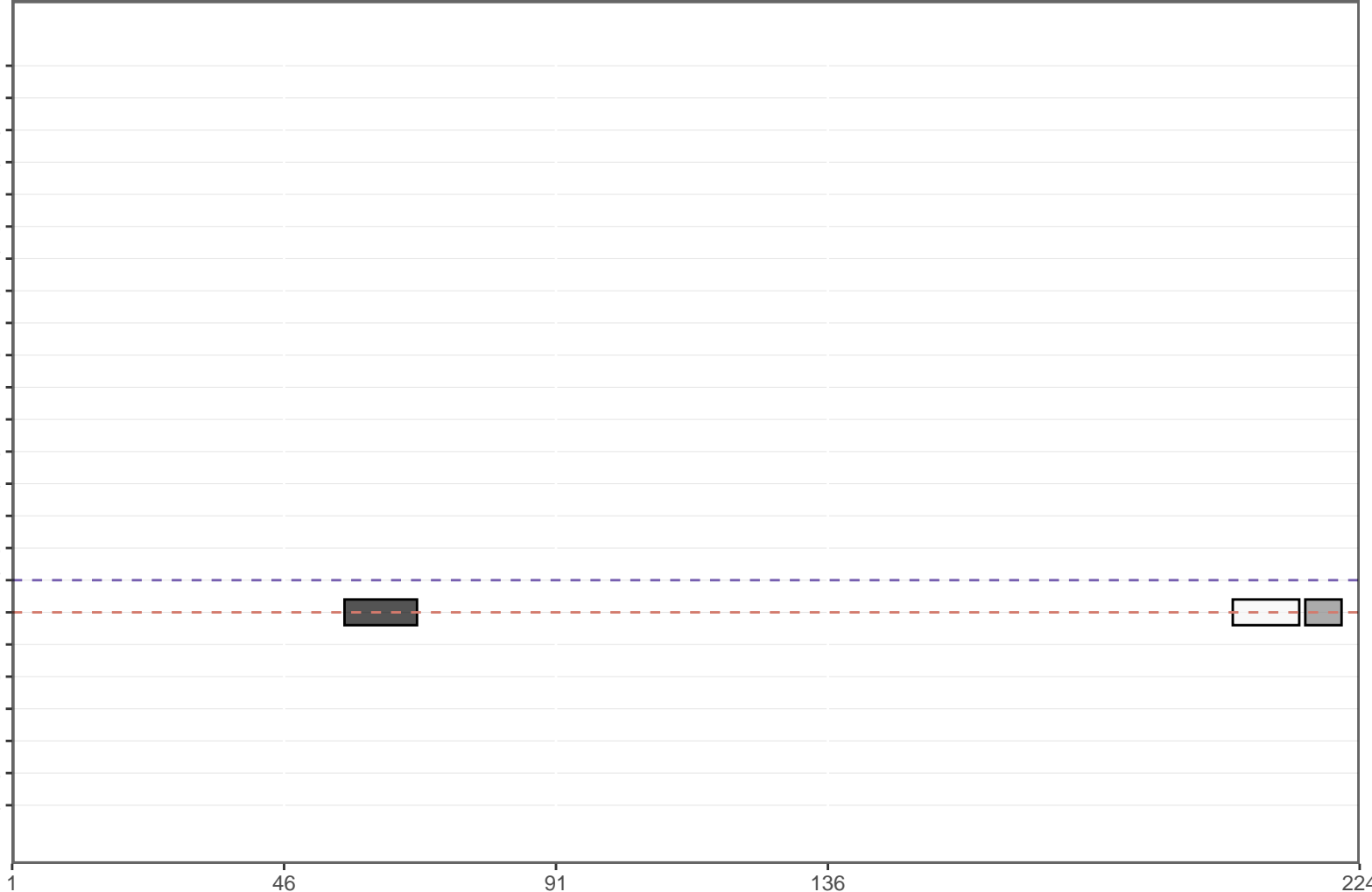
MW indication



Molecular weight



Gel Slice

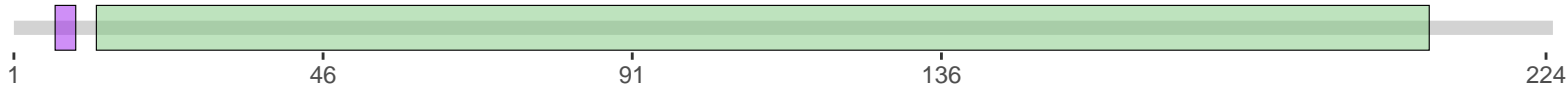


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LLSNTLYNRFFPYVFNVLGGDSEGKGCVFVFDVAVGSEYRIVGYSSGSGGSLMPLFDLNLKSPRLLLPAKDAVTPLSSEEAIDLVKTFGASATERDHYTGDRLIEVILNANGIRREEMELRKP

NbL02g09170.1 fructose-bisphosphate_aldolase_1_chloroplastic [MW = 42.55 kDa]

No. of times detected



log(intensity)



Values from



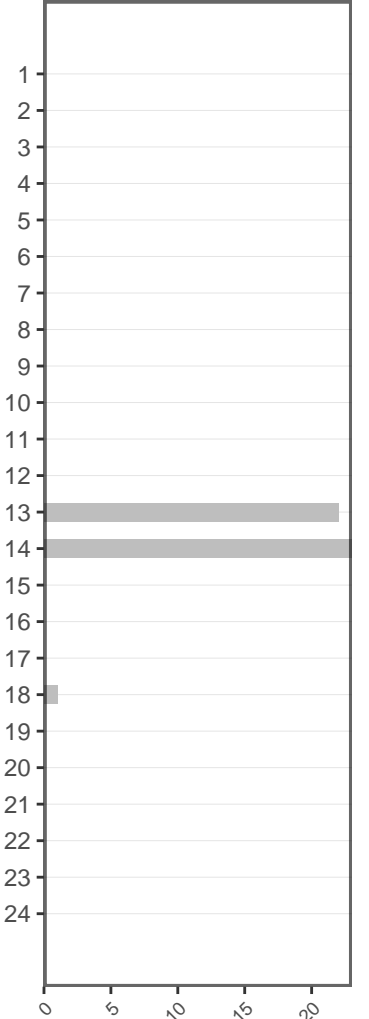
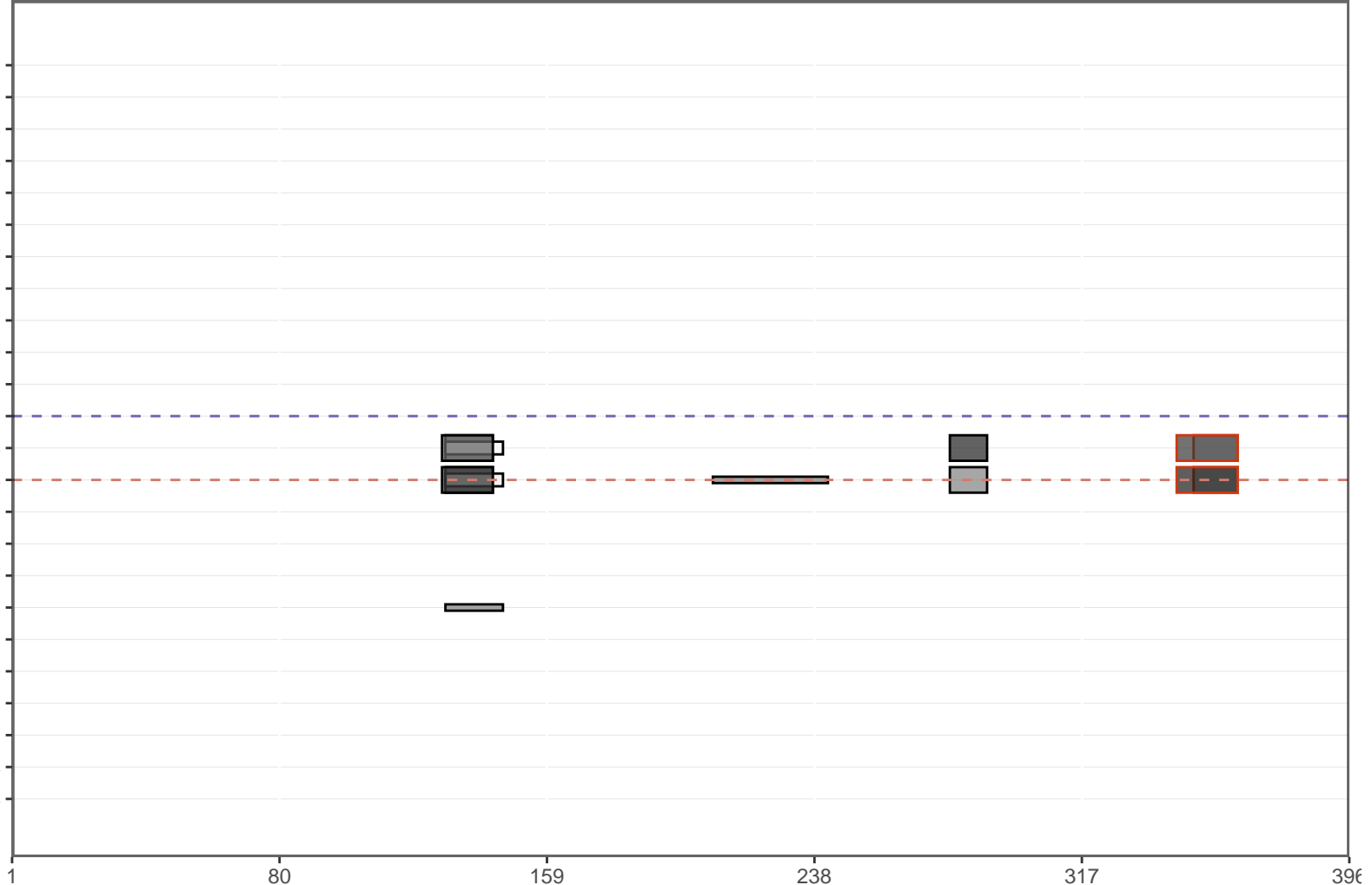
MW indication



Molecular weight

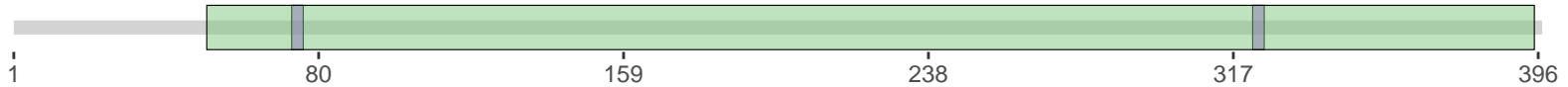


Gel Slice



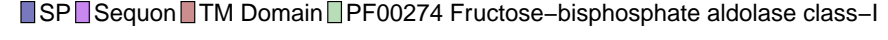
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL02g09100.1 nucleolin-like [MW = 135.26 kDa]

No. of times detected



log(intensity)



Values from



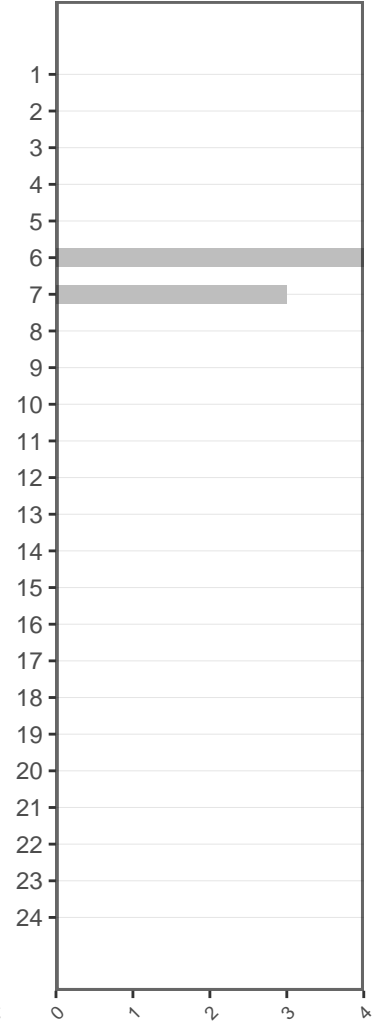
MW indication



Molecular weight



Gel Slice



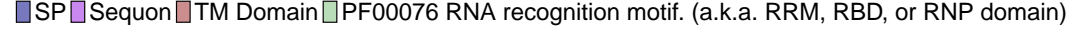
Protein length



Pfam domains



Pfam Description



Protein sequence:

E D T D K M K G K D I S F D E V G E D K E I A F A D G E N G E E F V E D G V P Q D Y E E A E A L D D E R A G L A A H A K E R M K R K E L E V F V G L D R D A V E E D L K R V F Q H K E V E I D V R M H R E V S T N K N G Y S F V K F A T K E G A S R A L S E M R N F V I R G K R G C T S P E E D N D T L F L G N I C N T W T K E A V R G K L K D Y G V E G V G S I N L V A D P K H E G L S R G F A L E F P C H T D A M T A Y K I L Q R P D V F G H P E R T A N V A F A E P L R D P D P E V M A G V K S V F I D G L F P Y W E E D C A R E K F K G F G N I R I L A R N M S T A K R K D F

NbL02g09080.1 peptidyl-prolyl_cis-trans_isomerase_Pin1-like [MW = 13.61 kDa]

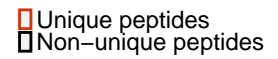
No. of times detected



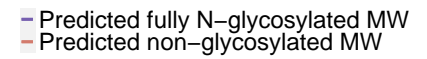
log(intensity)



Values from



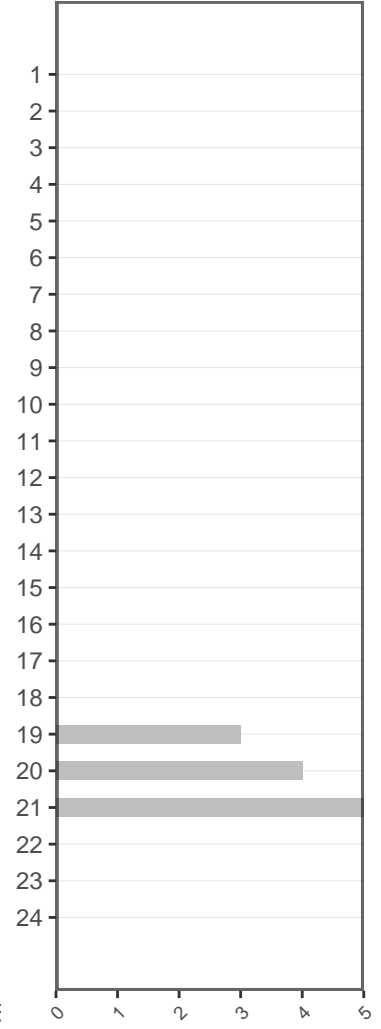
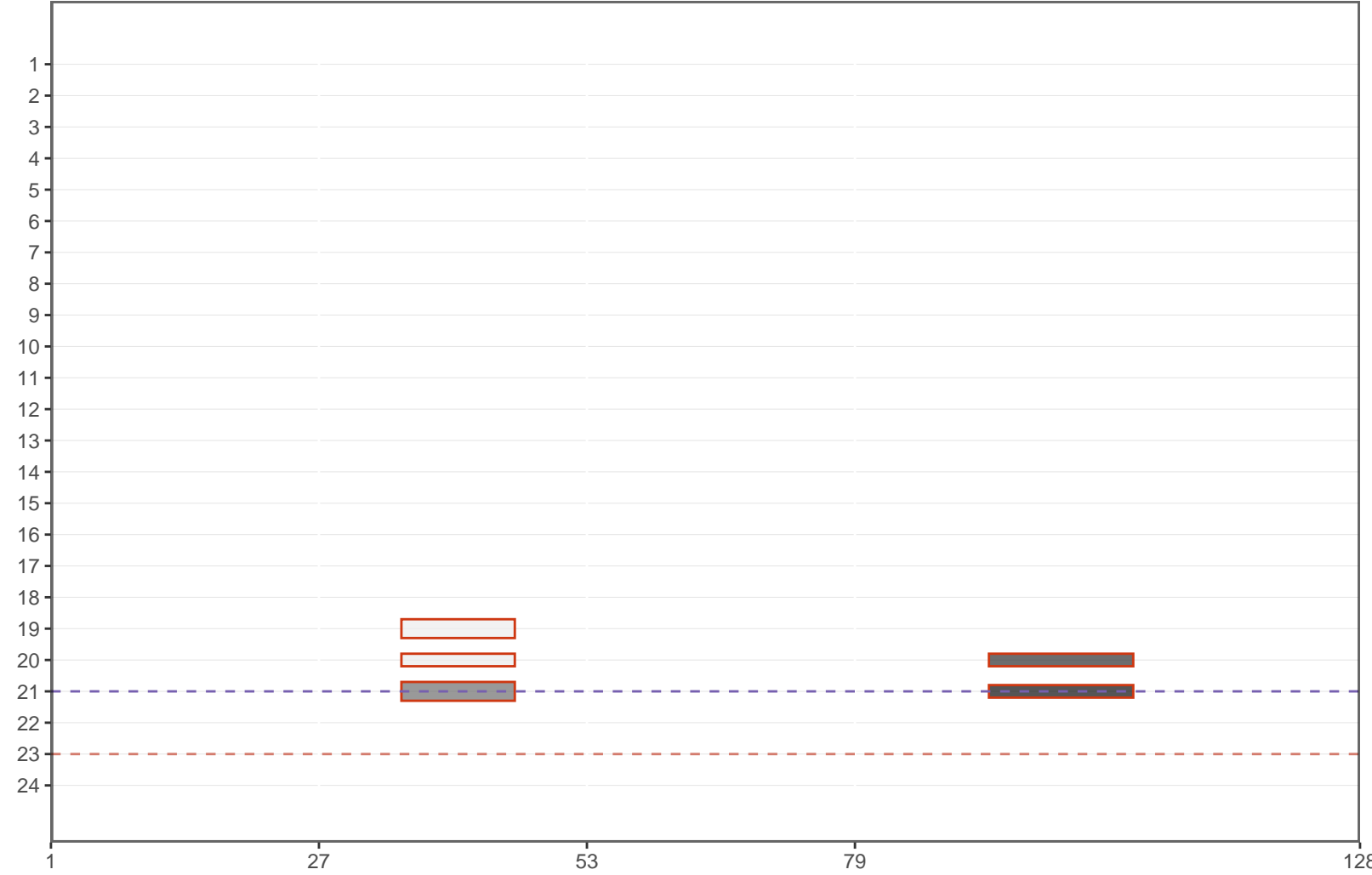
MW indication



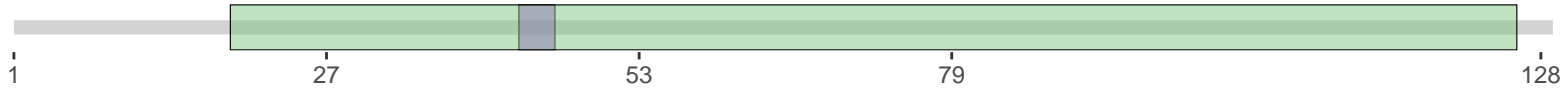
Molecular weight



Gel Slice

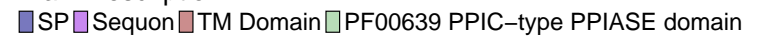


Protein length



Pfam domains

Pfam Description



Protein sequence:

/SQLKSLREDIVSGKAKFDVAATHSDGSSAKRGGDLGPFKGGQMKPFEEATYALKVGEISDIVETDSGVHKKRTA

NbL02g08840.1 anthocyanidin_3-O-glucosyltransferase_5-like [MW = 55.33 kDa]

No. of times detected



log(intensity)



Values from



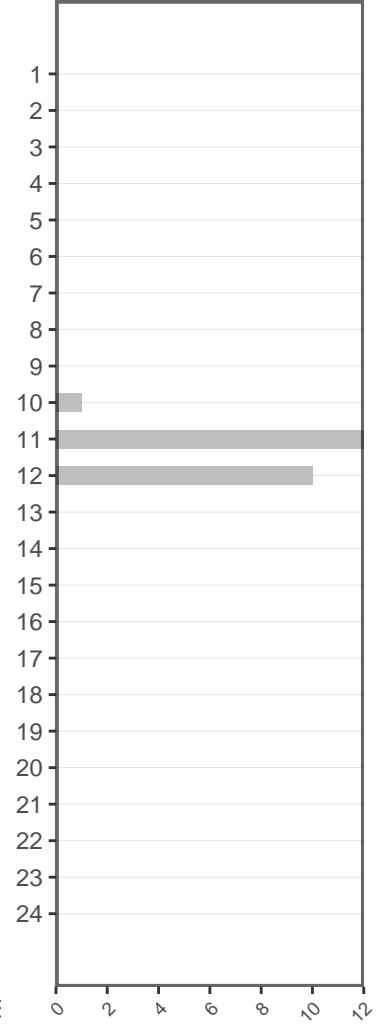
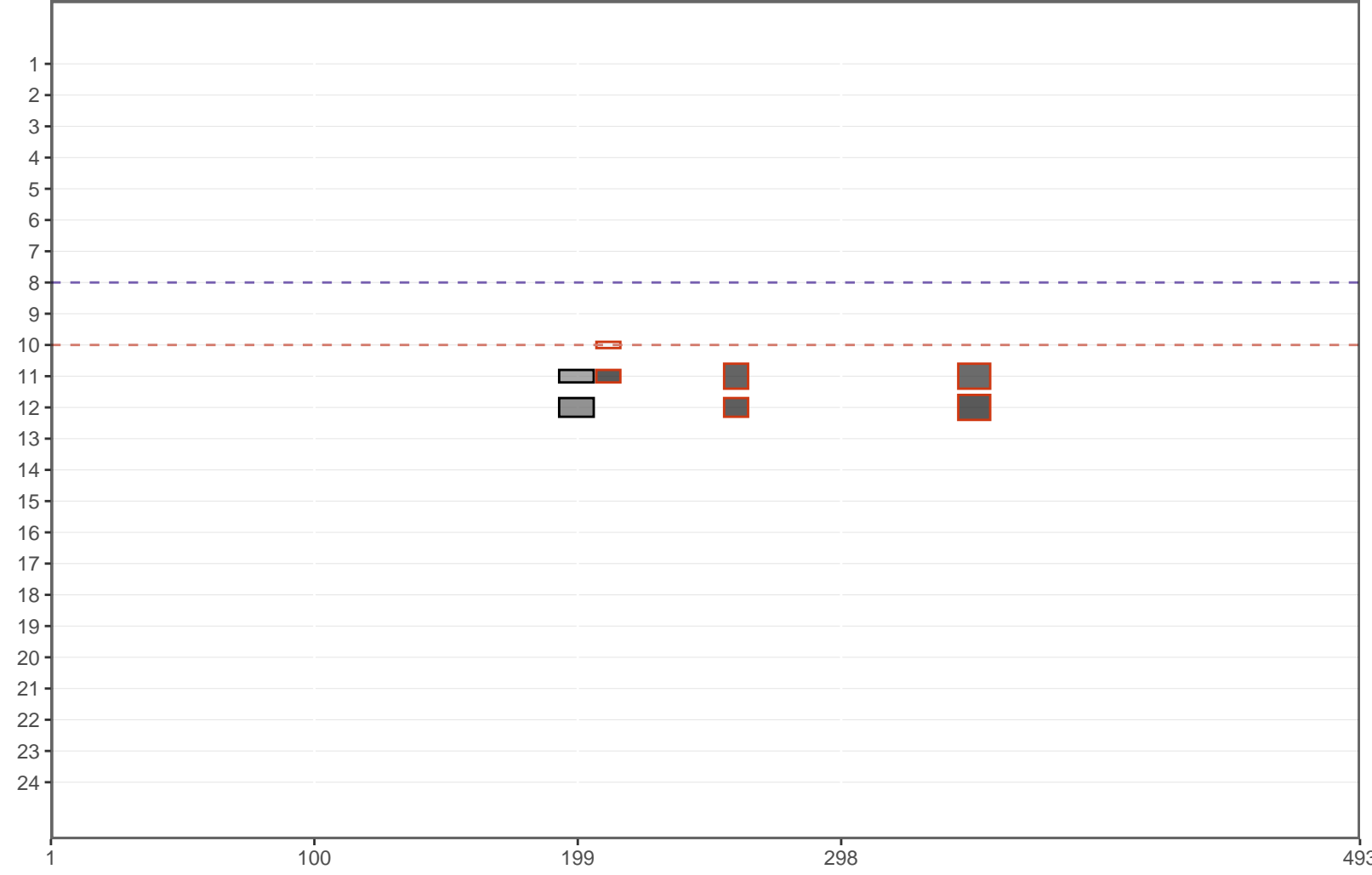
MW indication



Molecular weight



Gel Slice



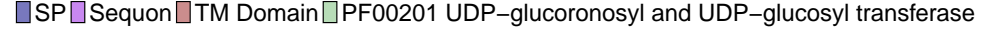
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ALRYNEKLRLLLVVFFPGLRKRKVEETLNDDEVQWLDKQNNESGLFVDFGSSGGLSTKQMTLAWGLLESDGQKFWVVRPPSDGADASAVLNSAGKDTFDMSEYLPDFLRTTRKDMGLVYPMWANGVEILSHSEVGGFLTHGQWNSYVESLITNGVPMIAWPLHAEQKMNAAALTEELGVARRFWLPTKLLKRRREEIGGMVRLMOTKEGRKIKKAKKLLKSAENALSDGGSSYNSICELVKDRSREL

NbL02g08390.1 protein_plastid_transcriptionally_active_16_chloroplast-like [MW = 54.4 kDa]

No. of times detected



log(intensity)



Values from

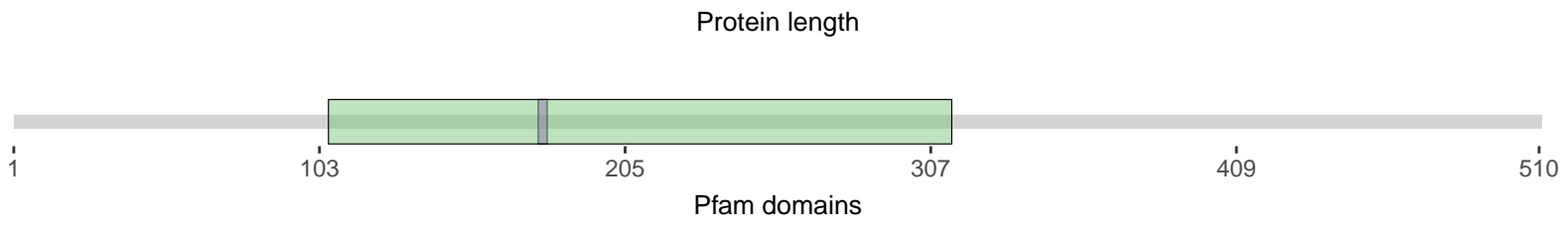
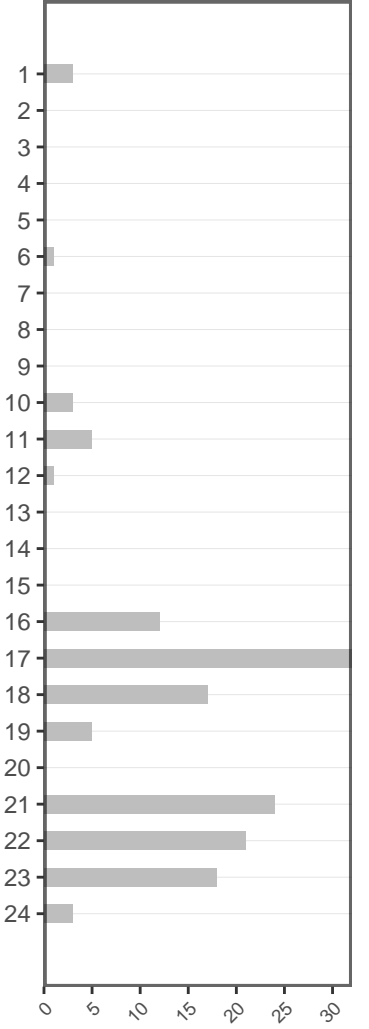
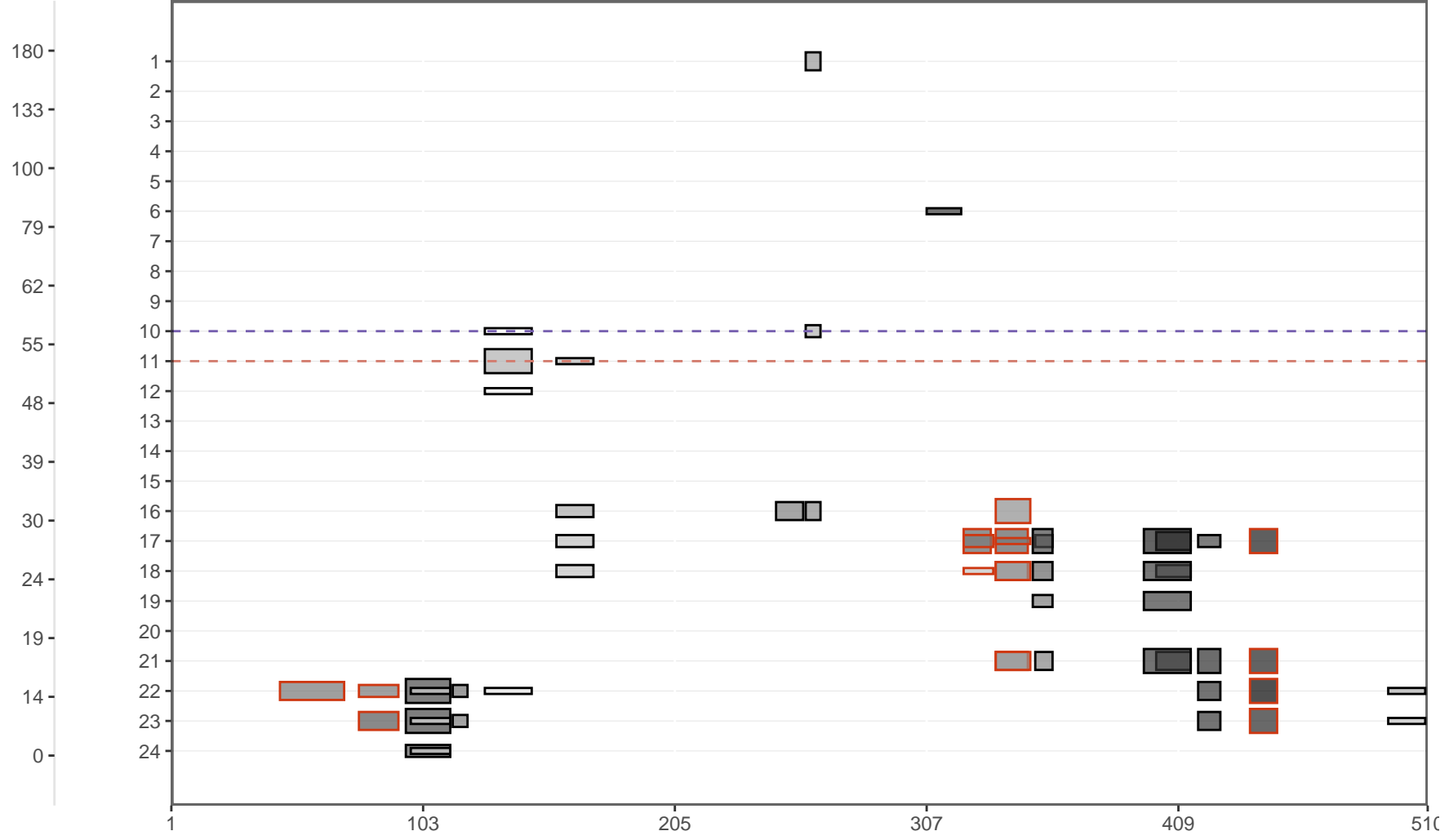


MW indication



Molecular weight

Gel Slice



Pfam Description
 ■ SP ■ Sequon ■ TM Domain ■ PF13460 NAD(P)H-binding

Protein sequence:

ILFSKSQLITTEFLGKIVETDWRVYTLKTLTSLTEDFSPSESSVNIIVSAEGSSAGENAYKVAKSELAKLVVDFNSNTAVAKNVVETFDPSBAKKTLDLFLSTPDEGRKRVKAAEALEKSKAAEEAARGAEGSKRDEEEVNRLEKQKAAKAVKAEAEKDSAAAGPVSFSLLDKAKGLSTGTFSEKLSGLKSAVKGKAGEESTQVATVRGQAKARNLPQKAVKSPRRKPFPAKKEAFKPKPKQZTETKTRKVFGLFGQGETVYVDD

NbL02g08250.1 40S_ribosomal_protein_S4-like [MW = 29.91 kDa]

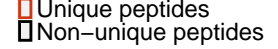
No. of times detected



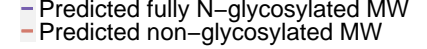
log(intensity)



Values from



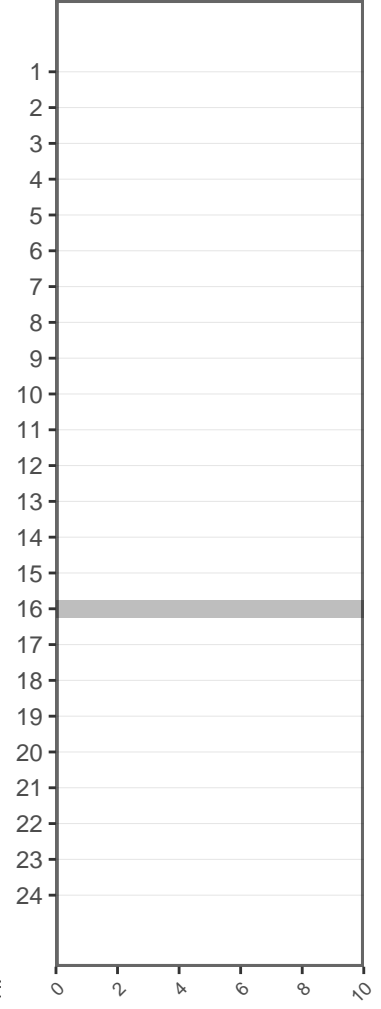
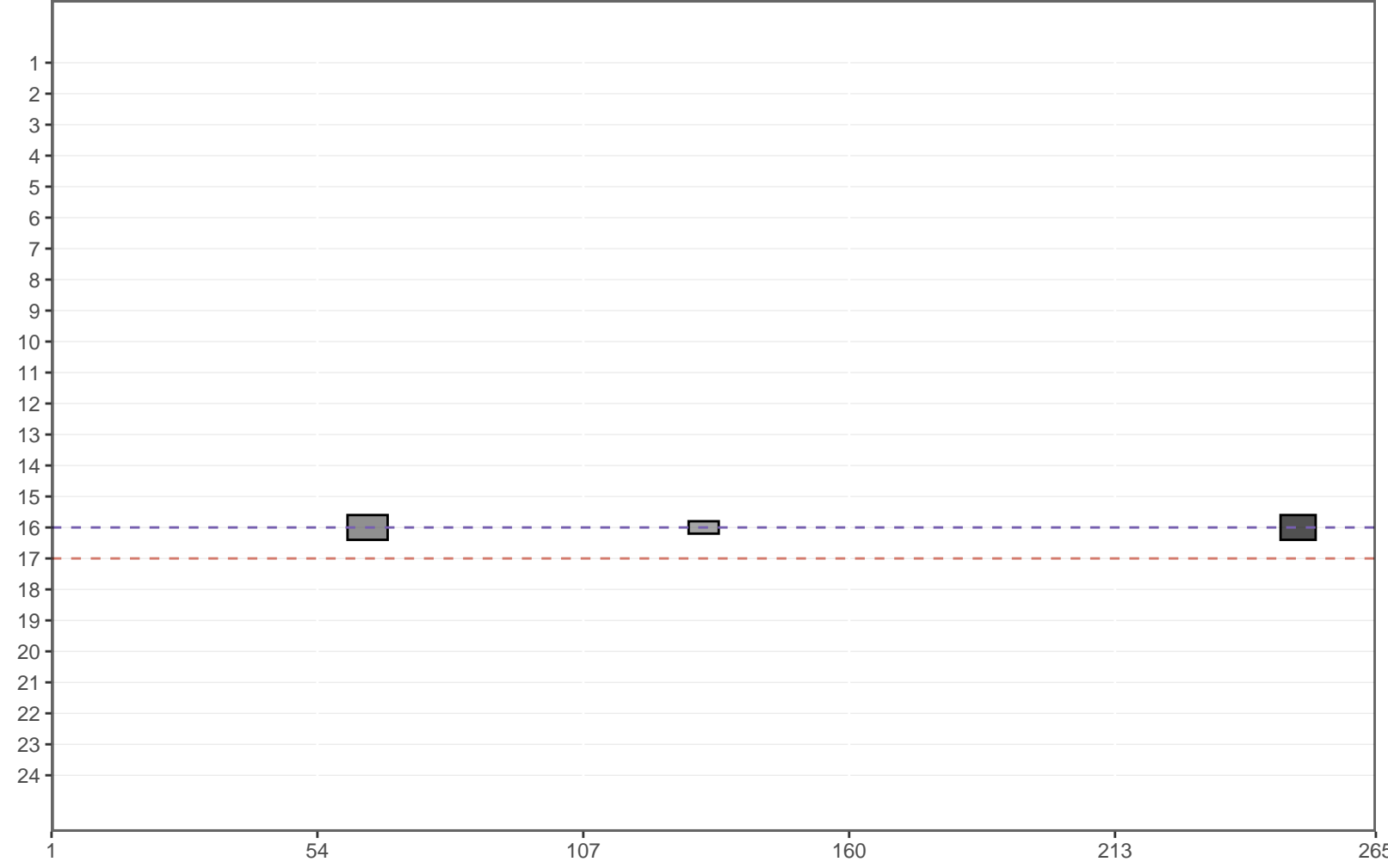
MW indication



Molecular weight

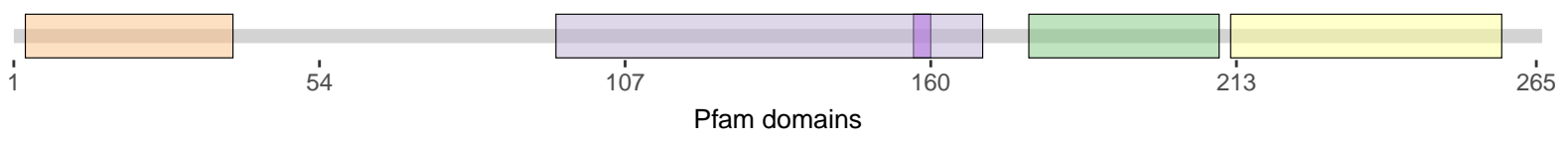


Gel Slice



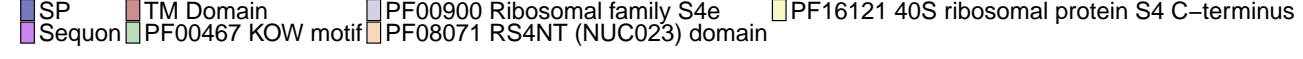
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AKFKLCKVRSVYFGGKGGIPVINTFYDGRTRVYDPDLKANDTKLDELSENKIVDFKFDVGNVMMVTGGRRNRGRVGVKNNREKHGGSFETVHDDALGHEFATRLGNVFTLGGTKFVYVSLPKGGKRLSIEEARKRLAAGSATVA

NbL02g08130.1 ERBB-3_BINDING_PROTEIN_1-like [MW = 39.64 kDa]

No. of times detected



log(intensity)



Values from



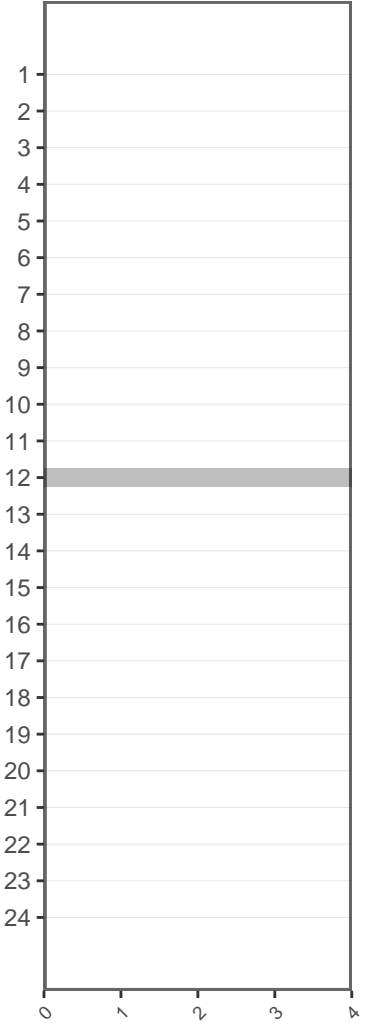
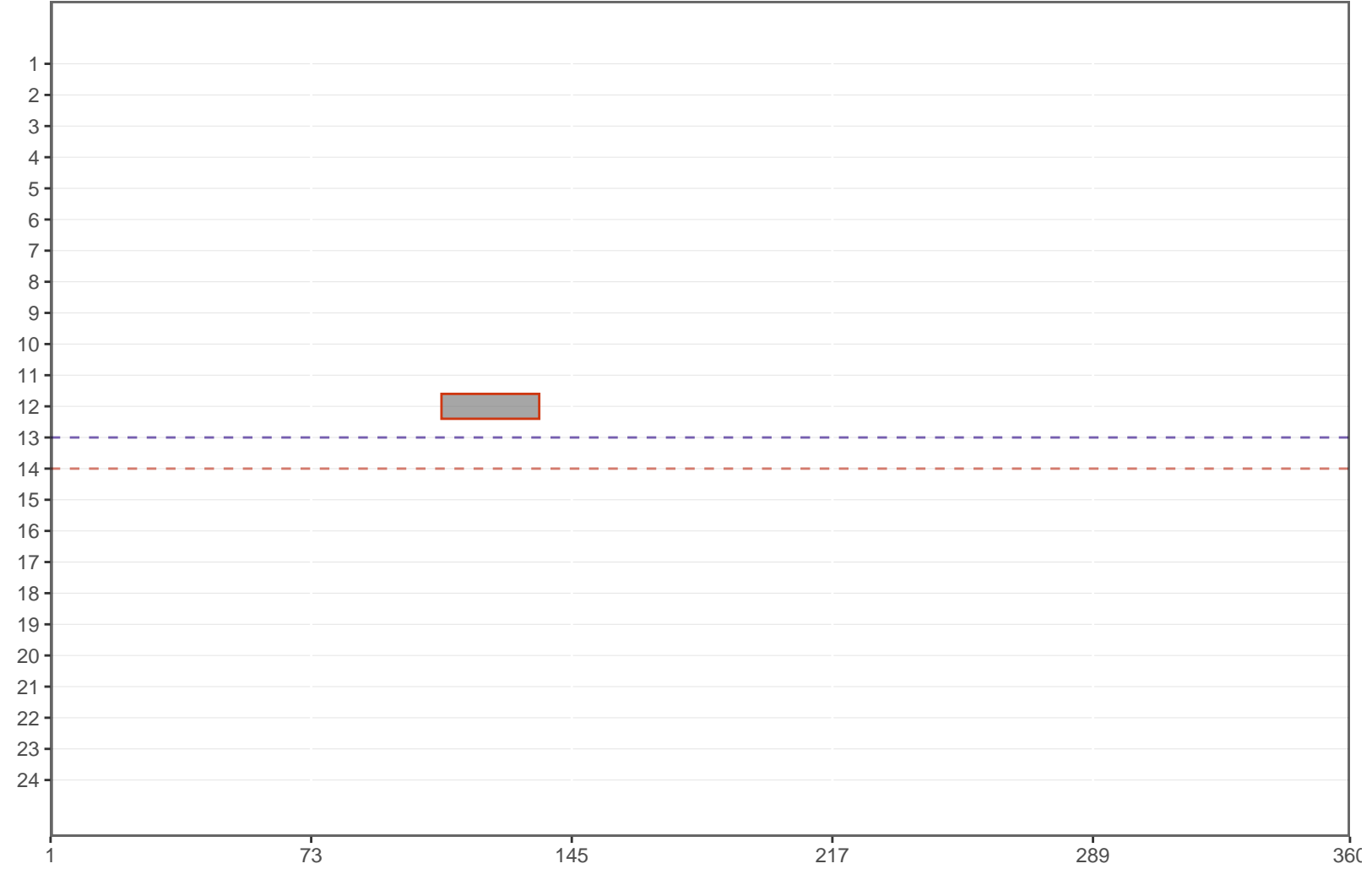
MW indication



Molecular weight

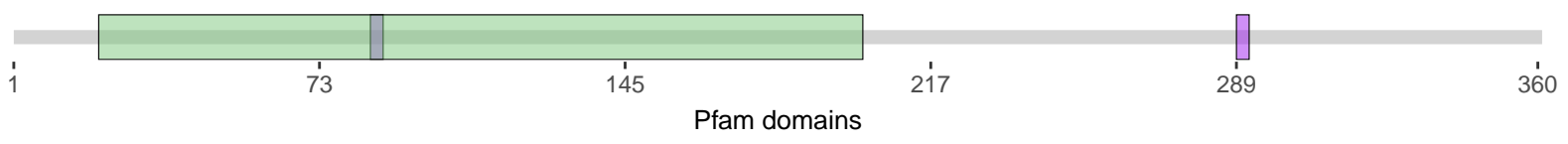


Gel Slice



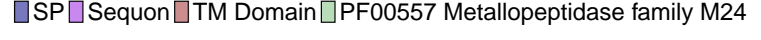
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AIQKVAAYDCKVIEGLSHGMKGFVIGNKPILLDEKGTTFYKRAVDKSHYLNKMKASRFIFSEISGKFPVMPFTARDLEKRAKRLGLVEGVNHELLGPVPLVLEKPGDVLVAHKFTVLLMPNGSDRITHTLGLGELKPAKTIIDDEPEIKTTLALPVGKKGKGGKPKKAKKSEKTEDESSQAEPMEGESNGAES

NbL02g08110.1 ran-binding_protein_1_homolog_c-like [MW = 24.04 kDa]

No. of times detected



log(intensity)



Values from



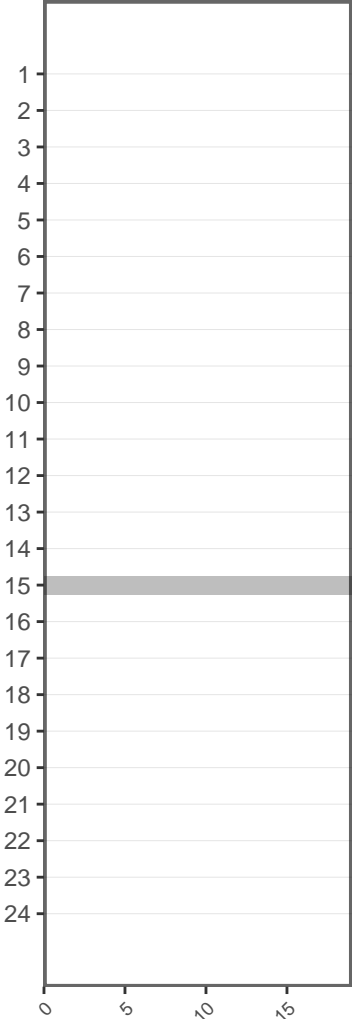
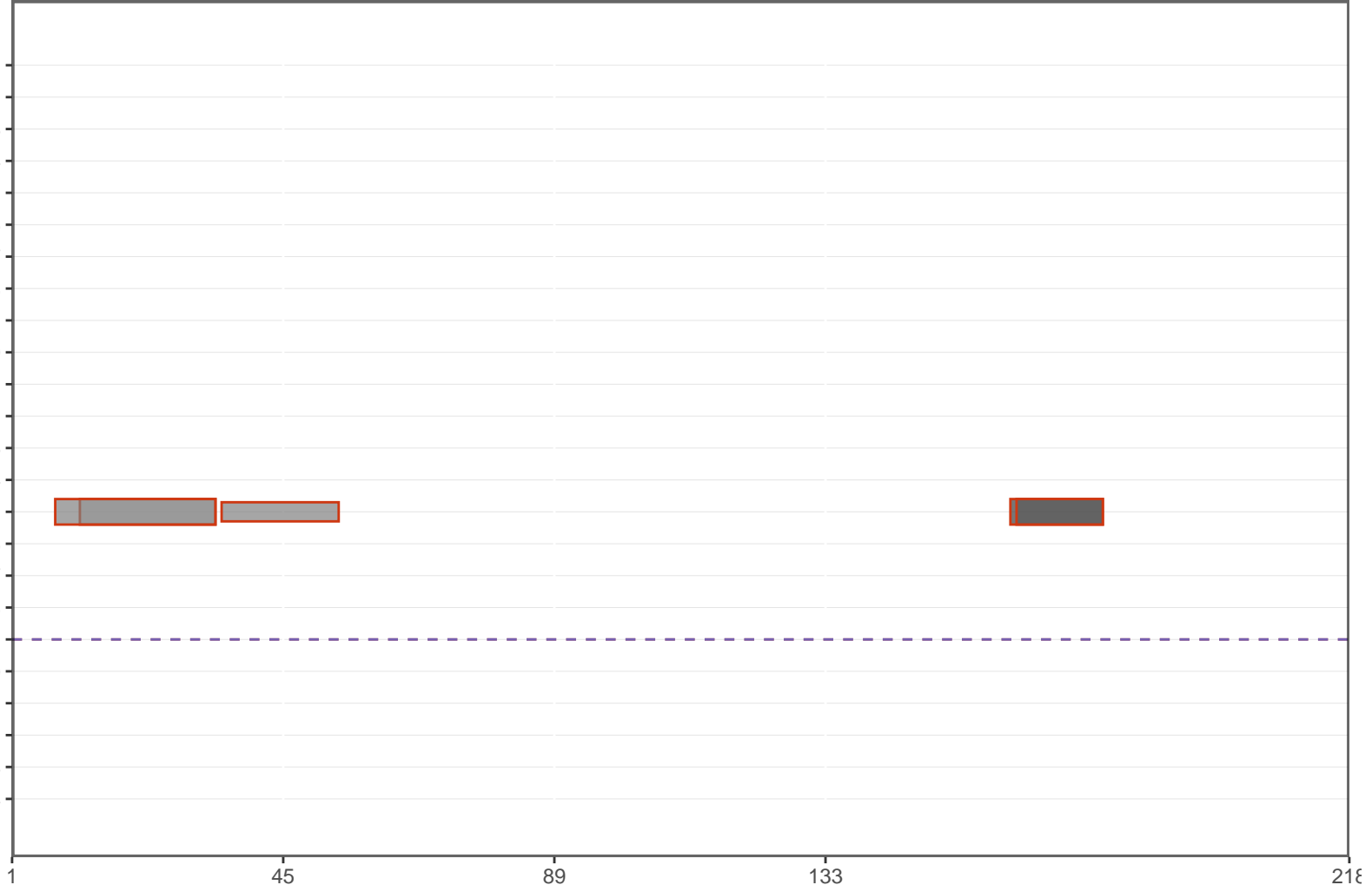
MW indication



Molecular weight



Gel Slice

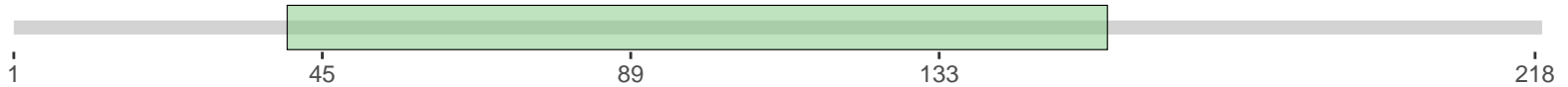


Protein length

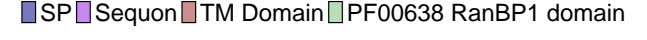


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KICANHLVLPMTLQEHAGNEKSGLWHPDFADGELKDELFLRFASIEKNGKSFMEMFQEVAESGQKVKVENEEDGSTAAGLLEKLSVEDKKGEEKSEDKTKEGDGKSGSPKDKTEKDESASA*

NbL02g08000.1 40S_ribosomal_protein_S26-3-like [MW = 14.51 kDa]

No. of times detected



log(intensity)



Values from



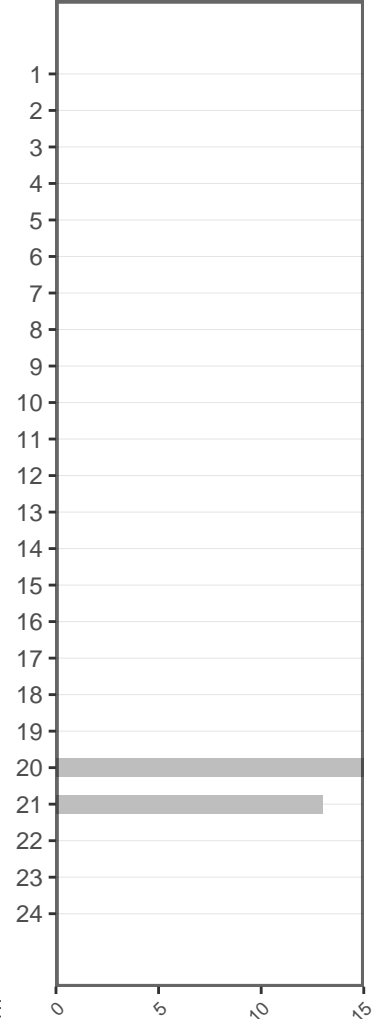
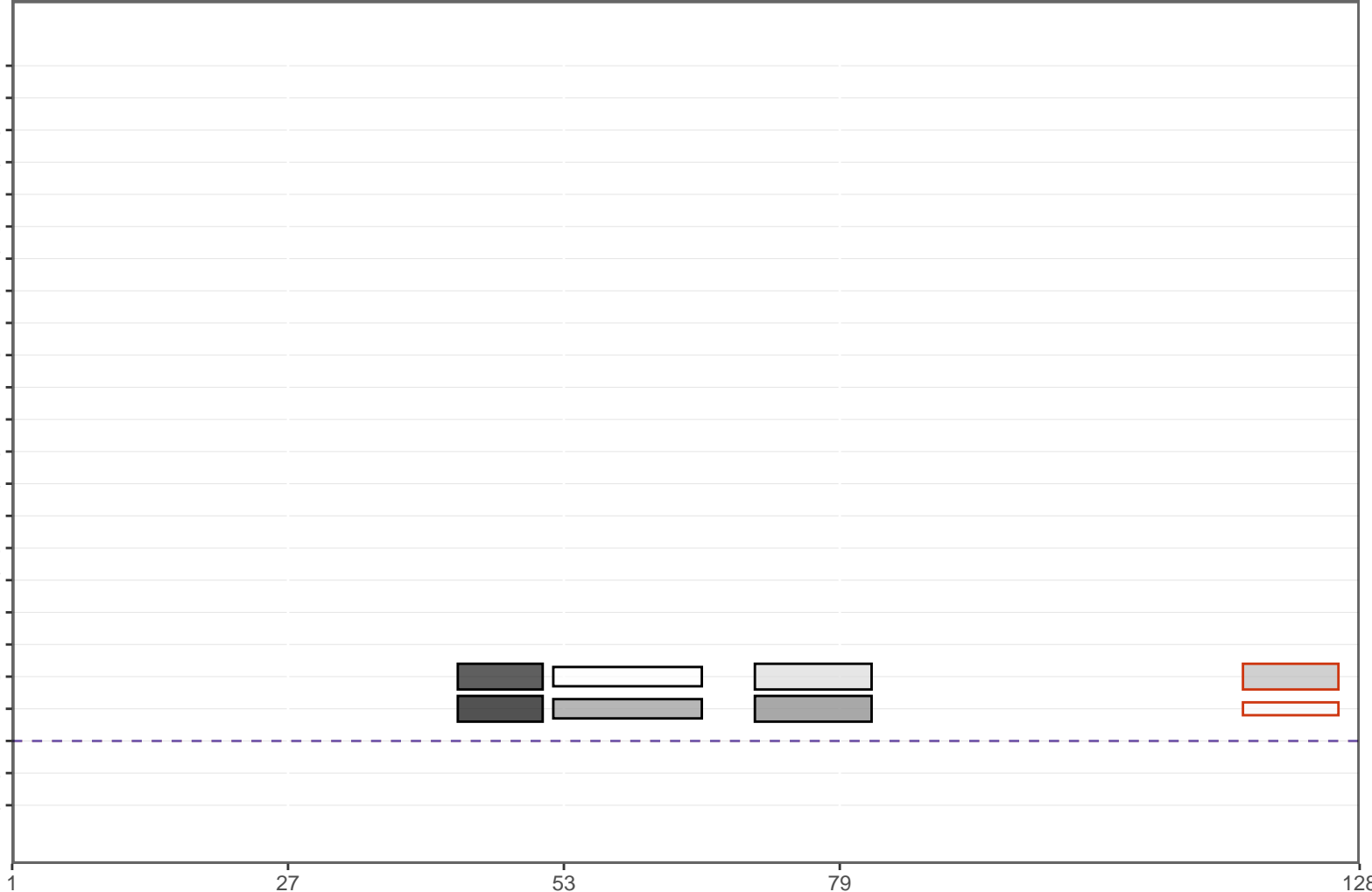
MW indication



Molecular weight

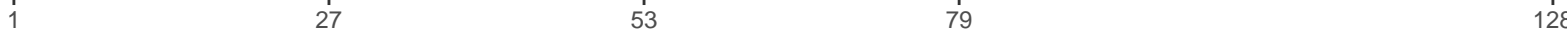


Gel Slice

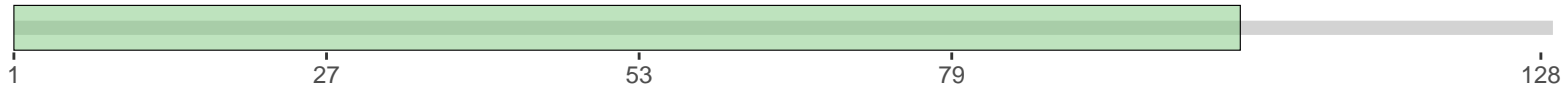


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

LDVGEACAFETYTLFRLVLMGIVGVGAHKKVWRVRSVTDRIIVREPPQFRFRPRDLPKFGDAPRPTGGAPAPRT

NbL02g07960.1 60S_ribosomal_protein_L10-like [MW = 24.78 kDa]

No. of times detected



log(intensity)



Values from



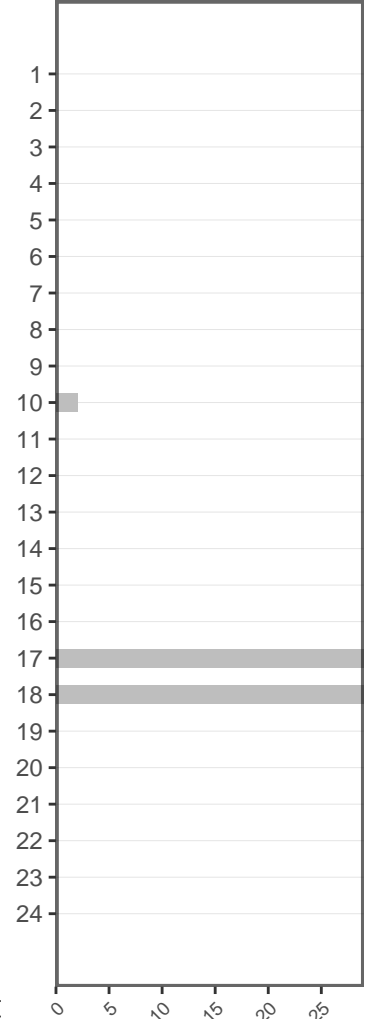
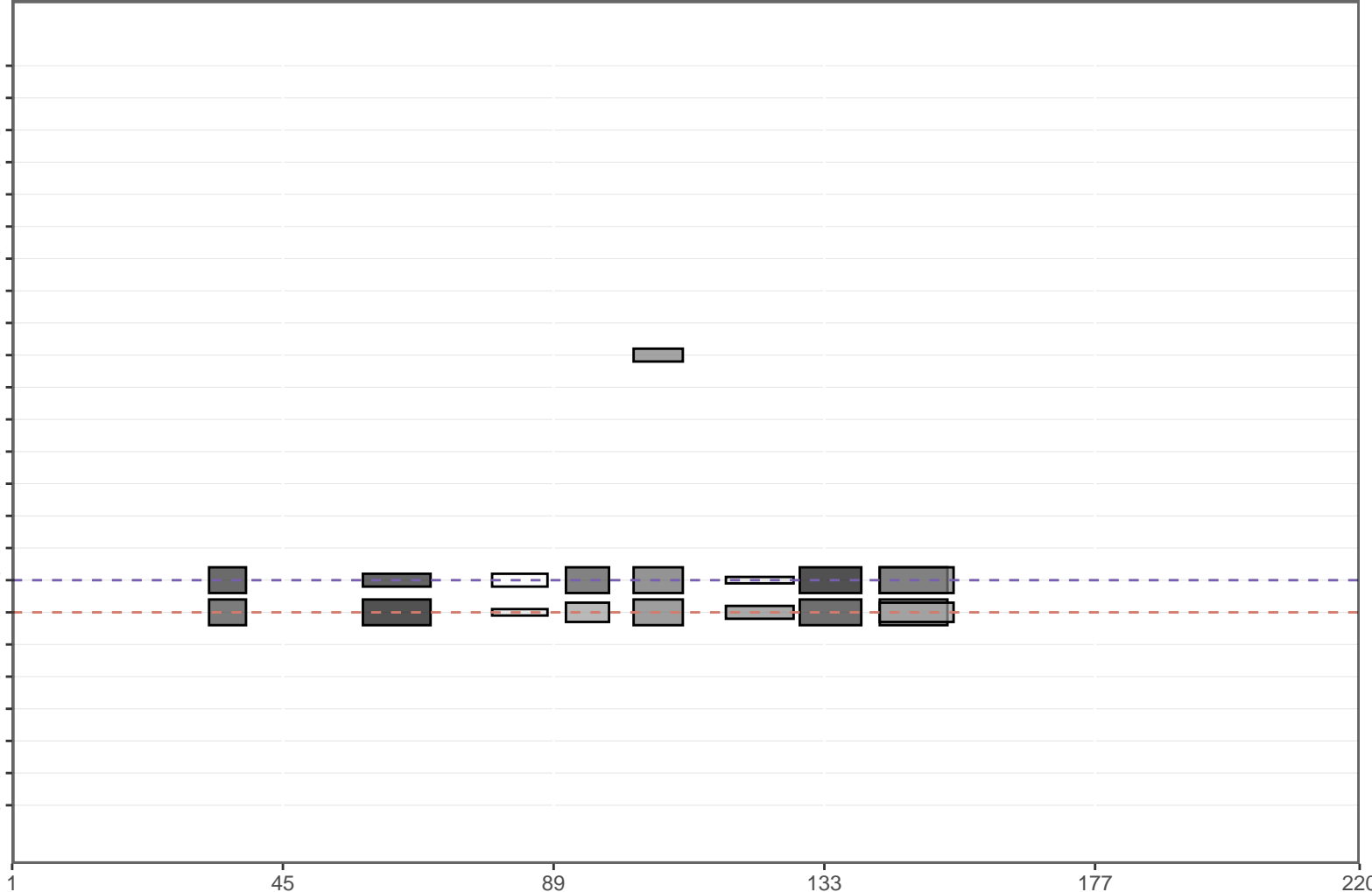
MW indication



Molecular weight

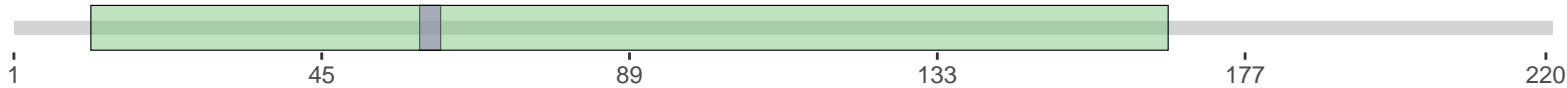


Gel Slice



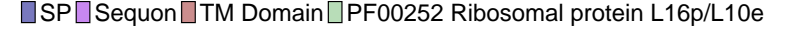
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RINKMLSCAGADRLGTGMRGAFKPGDGVCAARVAGVLLSVRKGKDGNNHAGEALRRAKFKFPGKQIVSRKVGFTKFRFDYLYKYKSENRIVPDGVNAKLLGGHGRLLAARDGPRAFLEAV

NbL02g07830.1 60S_ribosomal_protein_L5-like [MW = 34.45 kDa]

No. of times detected



log(intensity)



Values from



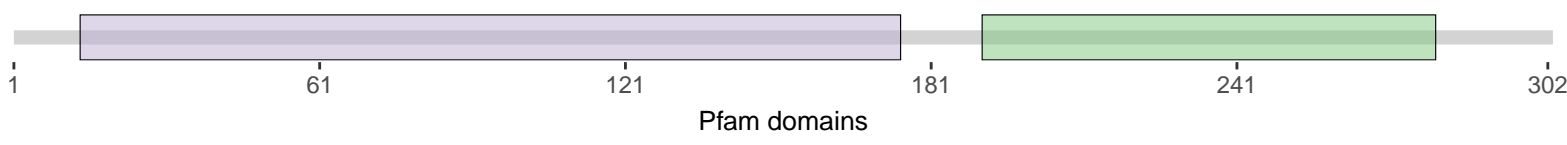
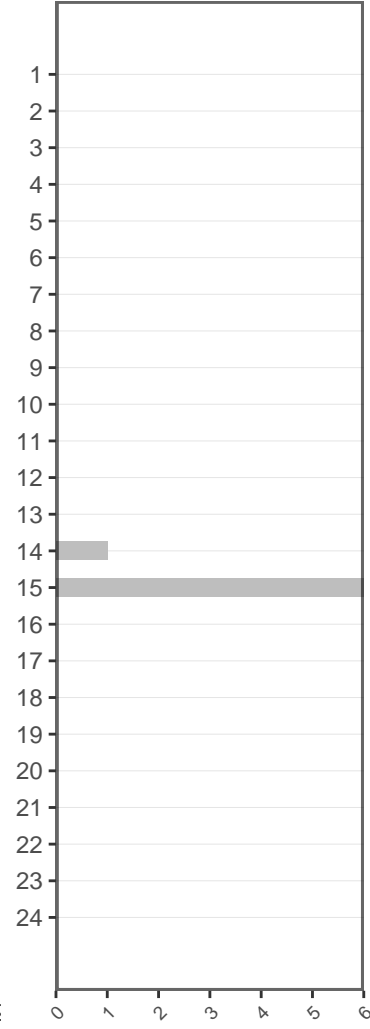
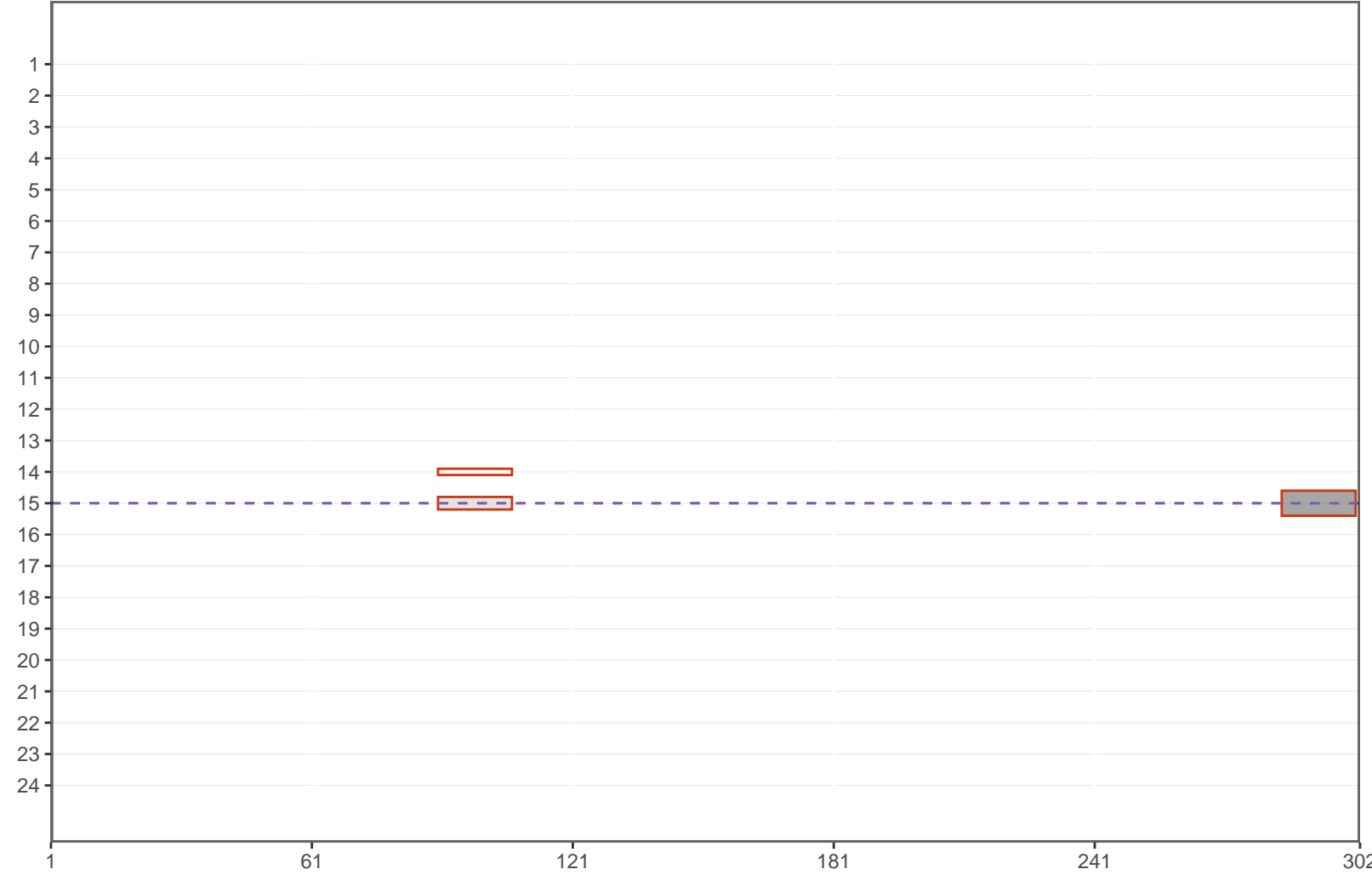
MW indication



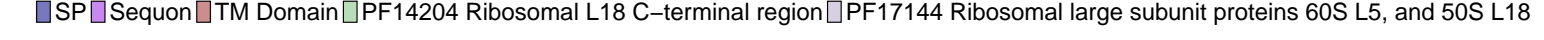
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

IPFRALLDGLVTRTTGNRVFGALKGALDGGIDPHSEKRFAGFGKDSKQLDGVHRKYYGGHVSAMKTLMEDEPEKYGSHFSEYIKTGLEADDEEMKKVHAIRADPSSKSKDKGPPKQKRVNLKGLTYDERKARUERLNALNAAAGNDDDEEDDD

NbL02g07730.1 cytochrome_b5-like [MW = 14.99 kDa]

No. of times detected



log(intensity)



Values from



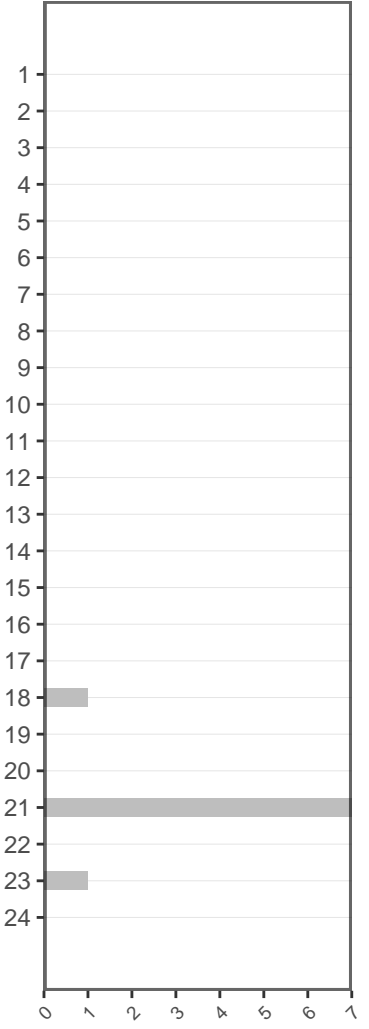
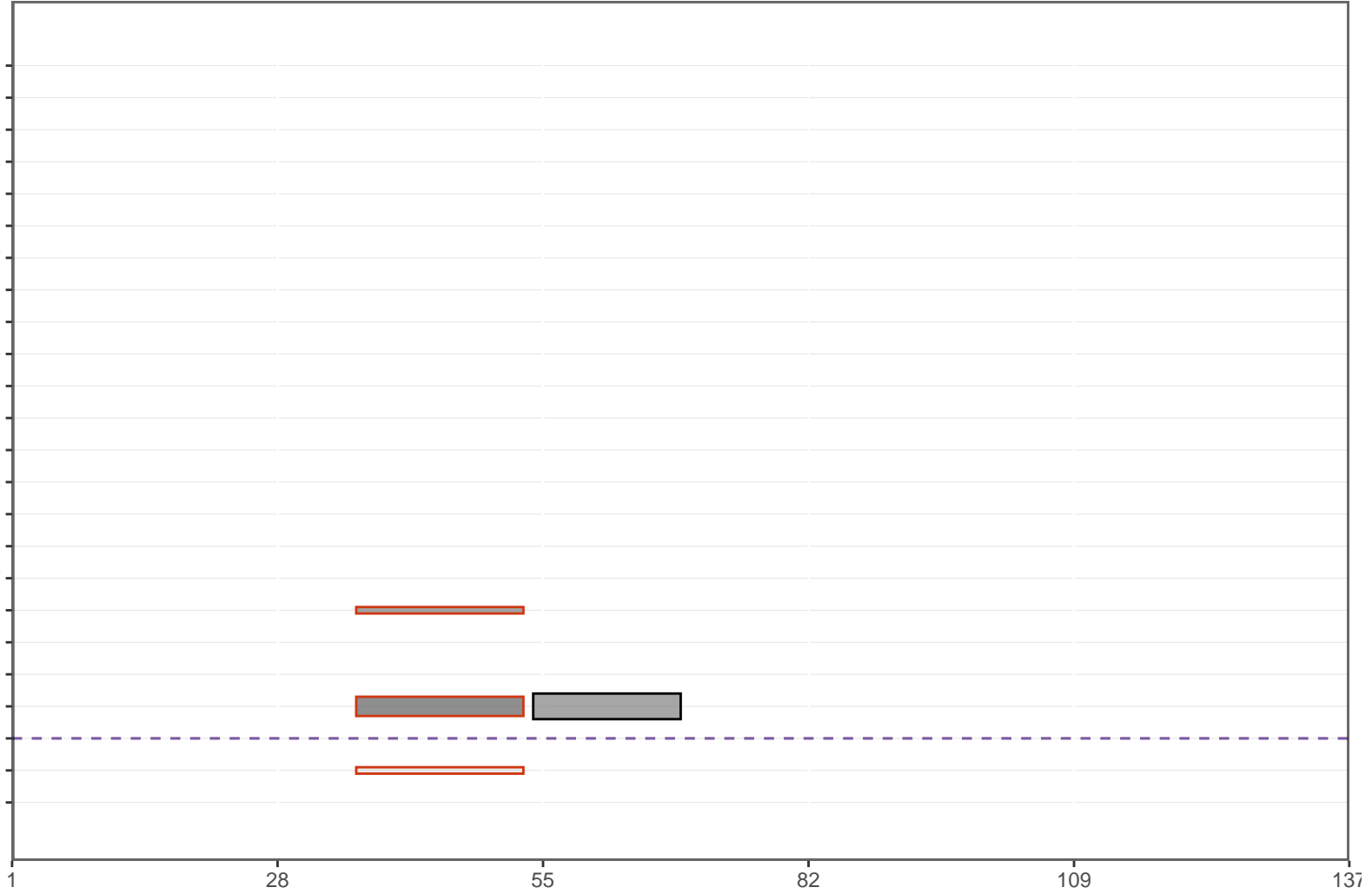
MW indication



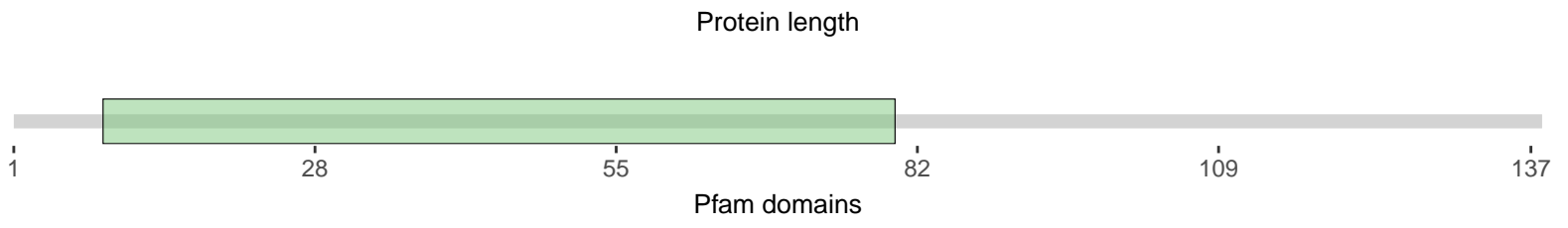
Molecular weight



Gel Slice

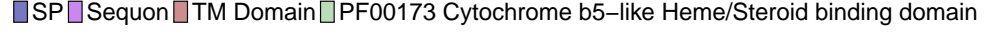


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DATDDFEDVGHSTSRAMLGEVYVGNDSATPRTKTYTPRNGPHVNDKTSSEFVKLLGFLVPLILGVAWGIRFYTKGGSAI

NbL02g07590.1 uncharacterized_LOC104215819 [MW = 16.63 kDa]

No. of times detected



log(intensity)



Values from



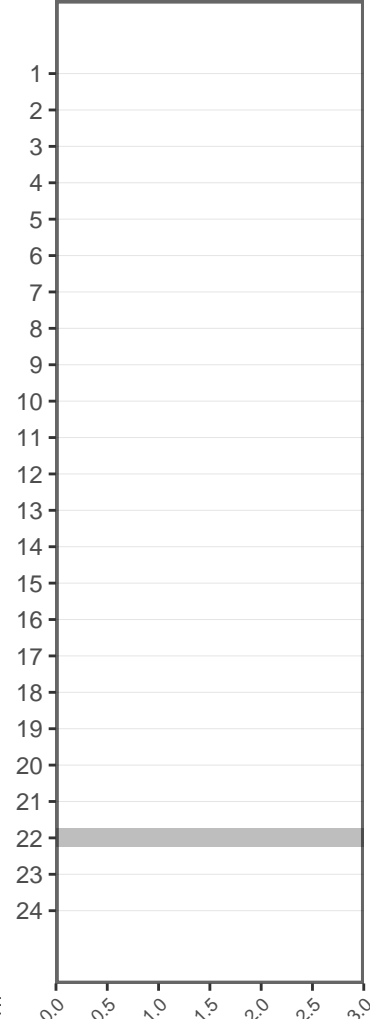
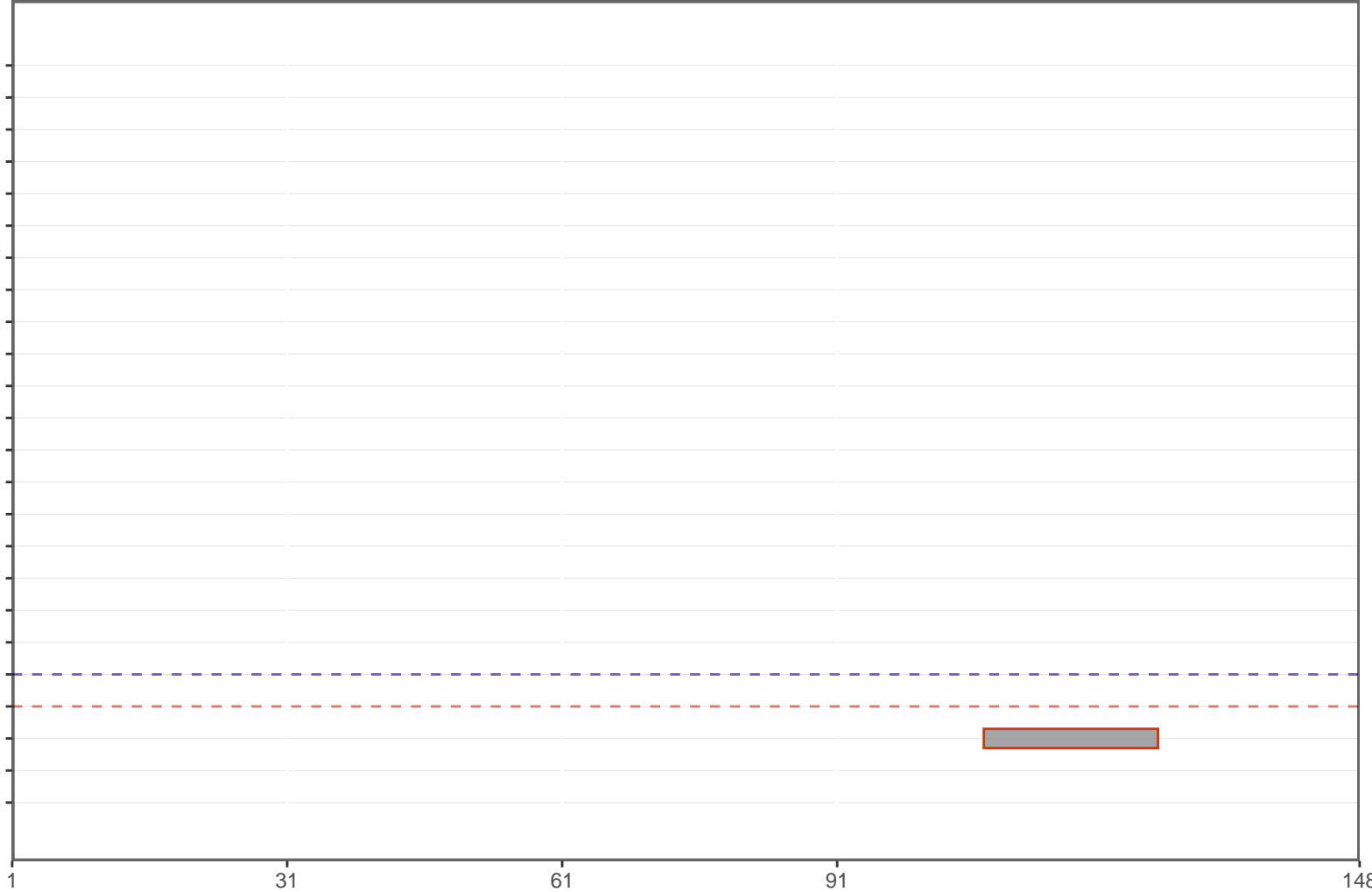
MW indication



Molecular weight



Gel Slice

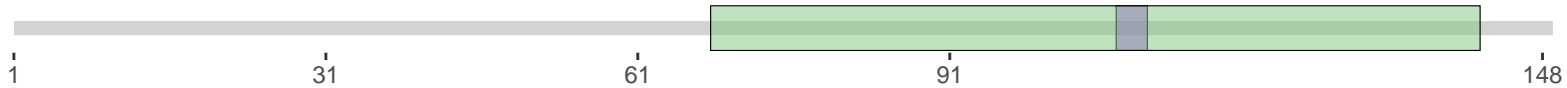


Peptide counts over 4 repeats

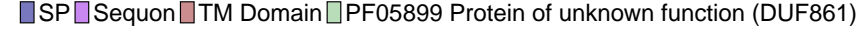
Protein length



Pfam domains



Pfam Description



Protein sequence:

ESQLNDLGIKSWPKWGGSPGKYLKFDAAETQYLLRGRKVKVYFNNSDDETFVFGAGDLVLPKGLSGTWSVWVAVDKHYKFD66

NbL02g07570.1 mitochondrial_import_receptor_subunit_TOM9-2 [MW = 11.13 kDa]

No. of times detected



log(intensity)



Values from



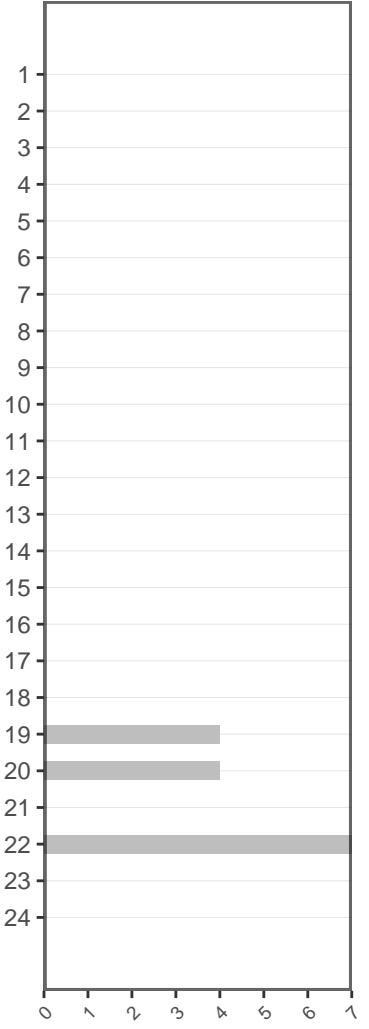
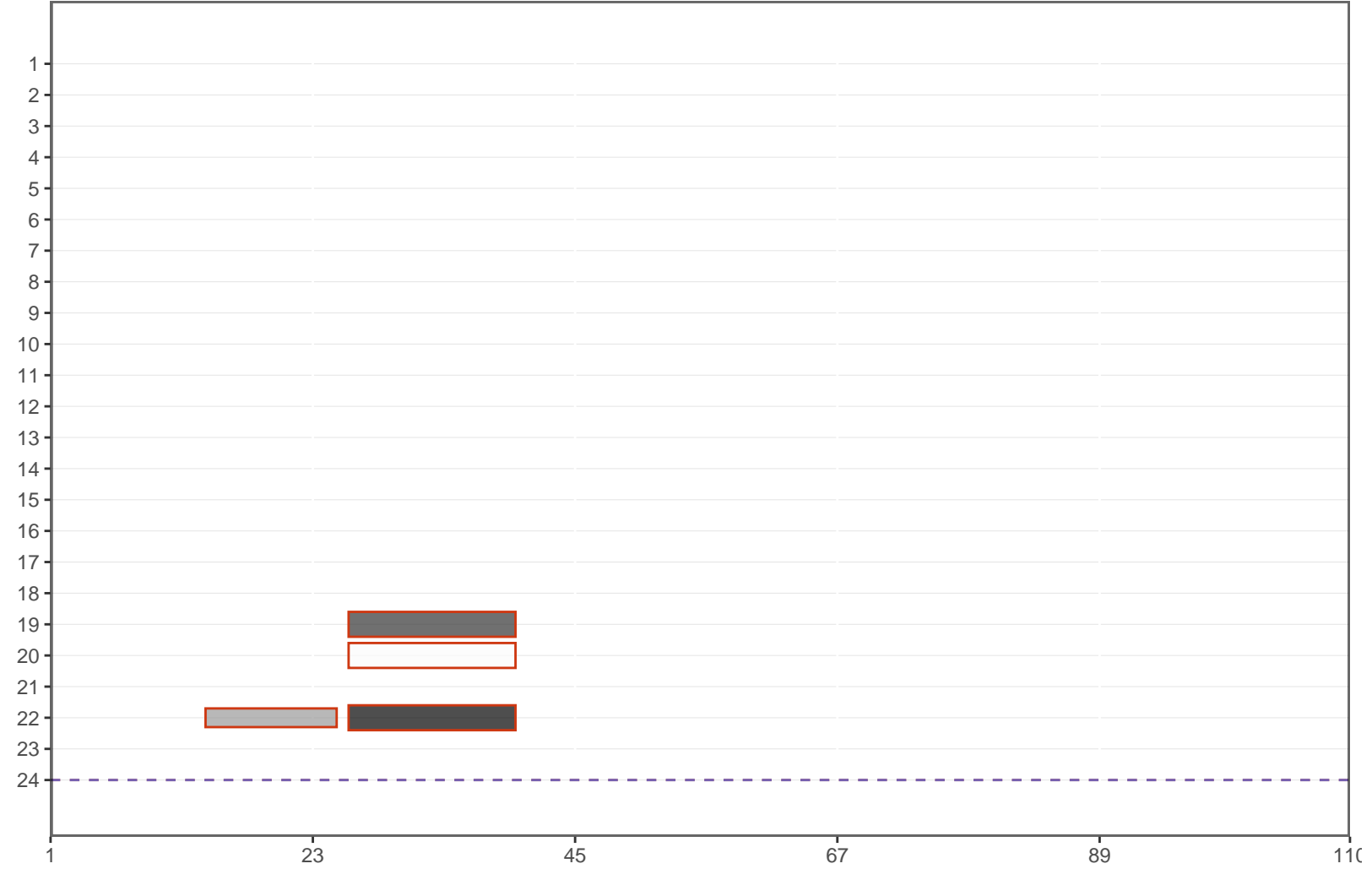
MW indication



Molecular weight

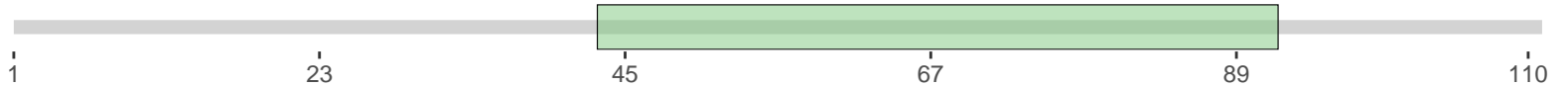


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

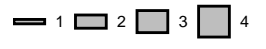


Protein sequence:

RAASDAALIAKLLKSTGKAAWIAGTFFLWVPLIEMDRDAGLFELELQASLLGTPPPPEAAGGRK

NbL02g07080.1 leucine-rich_repeat_receptor-like_serine/threonine-protein_kinase_BAM1 [MW - SP = 108.87 kDa]

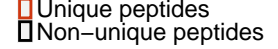
No. of times detected



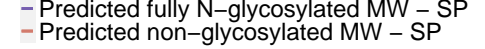
log(intensity)



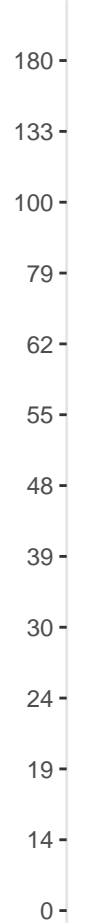
Values from



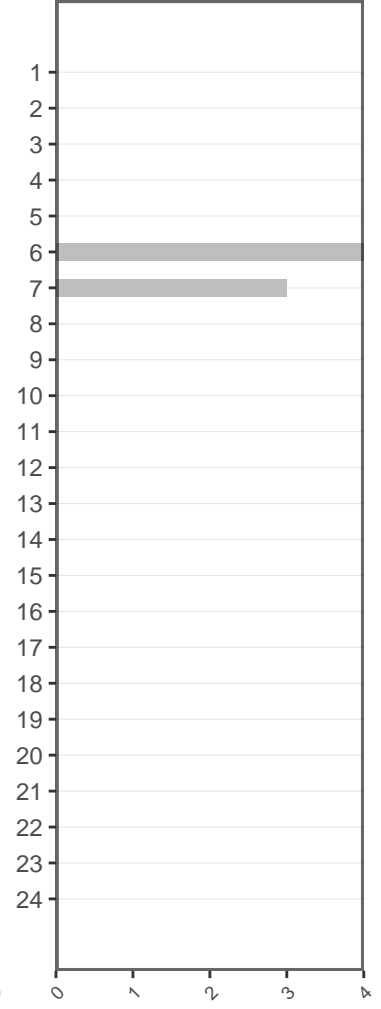
MW indication



Molecular weight



Gel Slice

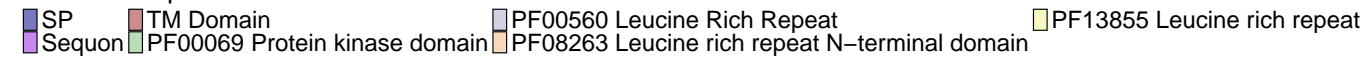


Protein length



Pfam domains

Pfam Description



Protein sequence:

QLSKIDFSHNDFGSPVPEISKQKLLFVDLGRNLQSGEIPTEIGMRILNLYNLGRNHLVGSIPPISEMQGLTSVDFBYNDFGLVPTGQGFYFNYSFLGNPDLOGPYLGPCKEGVYDGVGQPHQRGALSPMKLLLVGLLVGSIVFAVAIAIKARKLKAASEARAWKLTAFQRLDFTDGDVLDLQSLKEDNIGKGGAGVYKGVMPGGEHWAKRLLPAMSRGSEHDHGFNAEQTLGRIRRHIVRLLGFGSNHETNLLVVEYMPNGSLGEMLHGKKGHLLIWDTRYKAVI

NbL02g07010.1 probable_xyloglucan_endotransglucosylase/hydrolase_protein_6 [MW = 34.85 kDa]

No. of times detected



log(intensity)



Values from



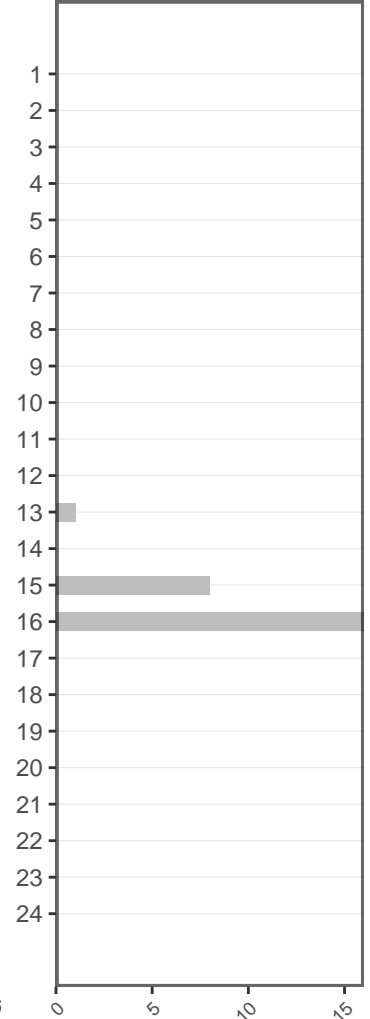
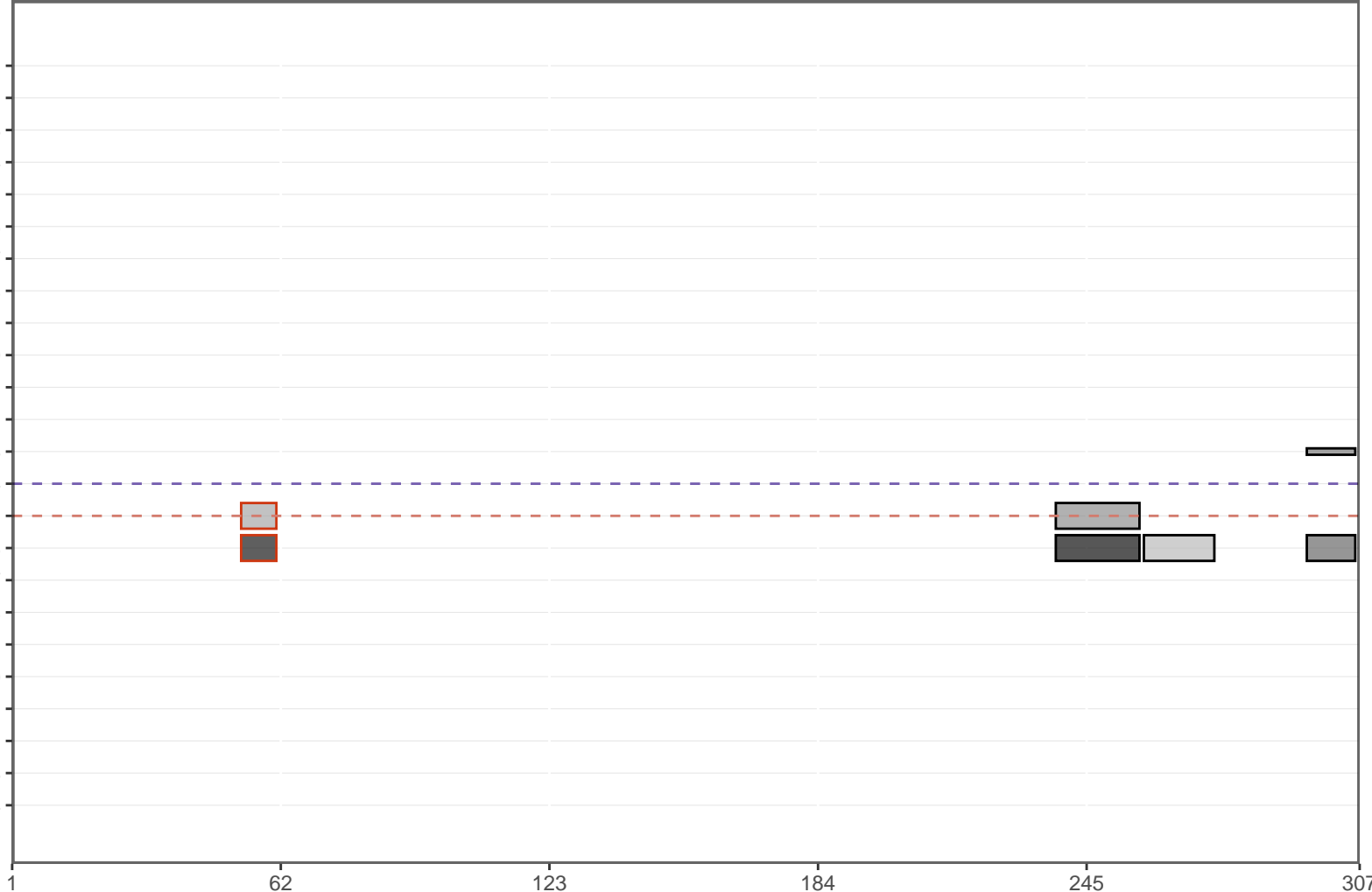
MW indication



Molecular weight



Gel Slice

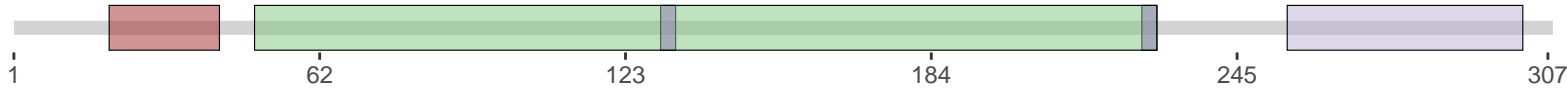


Peptide counts over 4 repeats

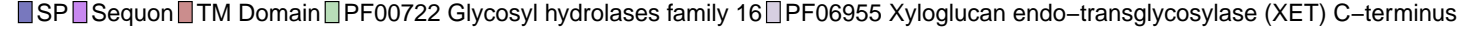
Protein length



Pfam domains



Pfam Description



Protein sequence:

1HGKDKERQVNLWFDPSADHFYFTLWNHHAVFYVDVPIRVRYKNNEAKGFFPKFQFMGVYSTLWEADDWATRGGLEKINWKSFPFYVYKDFDIEGGAMPNGASPNRNVWEGANYQQLSAVEARQYRWRMNHIMVGYCTKGRNFVPPPEGVAGI*

NbL02g07000.1 probable_xyloglucan_endotransglucosylase/hydrolase_protein_7 [MW - SP = 30.21 kDa]

No. of times detected



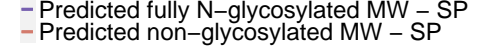
log(intensity)



Values from



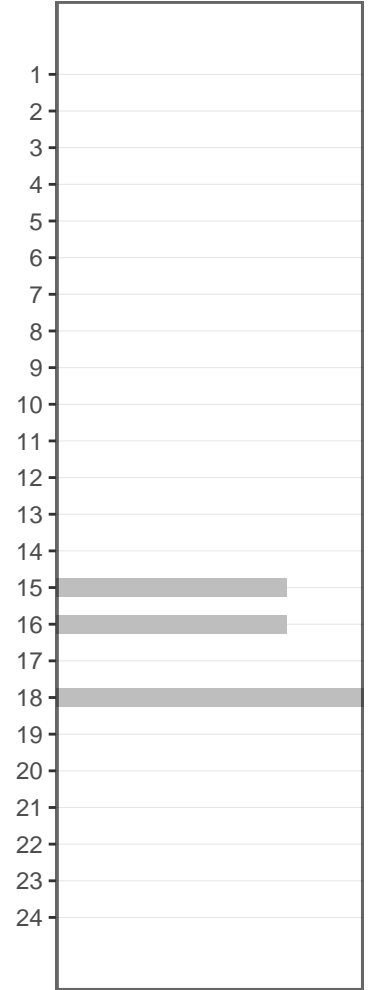
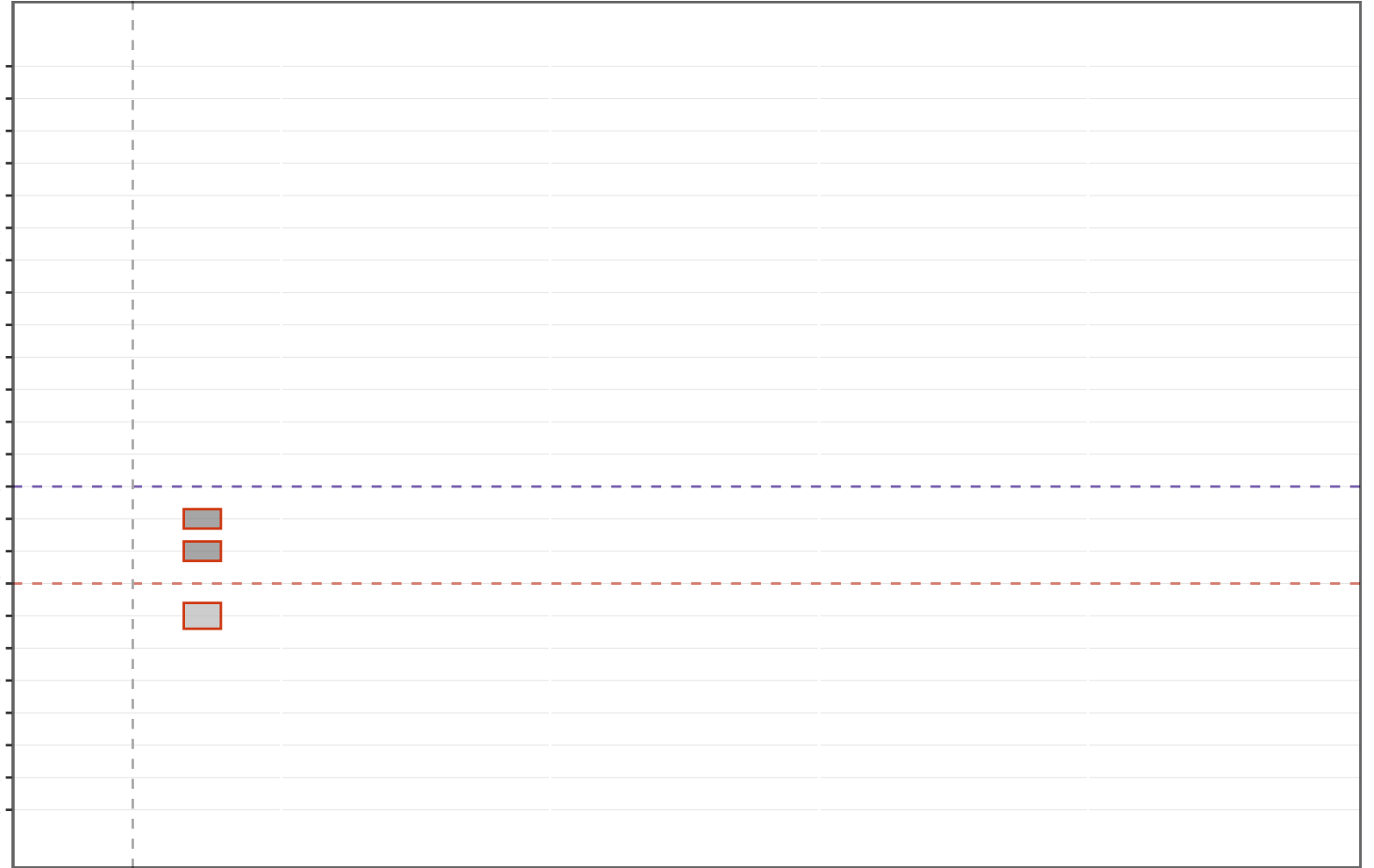
MW indication



Molecular weight



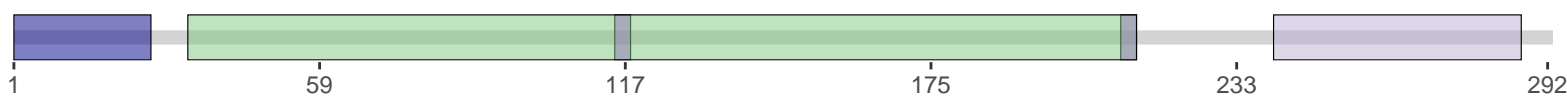
Gel Slice



Protein length

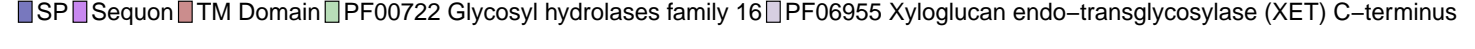


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

EGRINLVFDPSSADFHFTYTLWNHHTFTFYVDQVPIRVVKNNEAKGIPFKQPMGVYSTLWEADDWATRGGLEKINWEKSPFYWYKDFDEGGAMPGRNCAASNRINWEGANVQGLSAVEARQYRIVRINNHMYDYGTDKSRNPVPPRECVAIGI

NbL02g06680.1 ADP-ribosylation_factor-like_protein_8a [MW = 20.52 kDa]

No. of times detected



log(intensity)



Values from

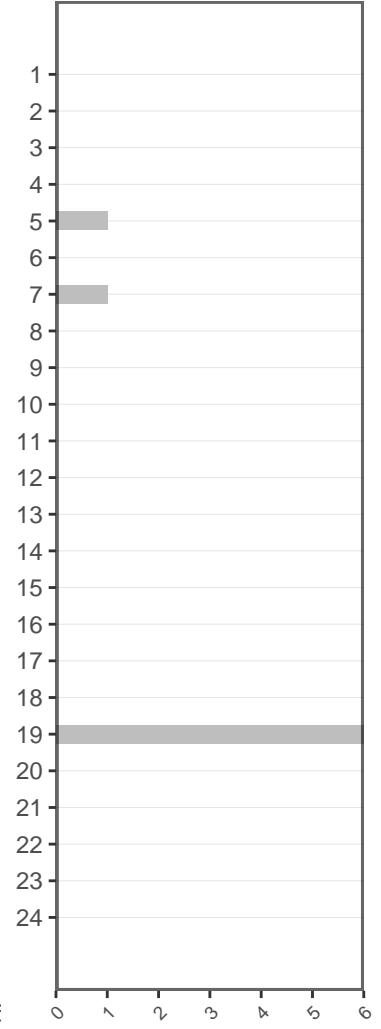
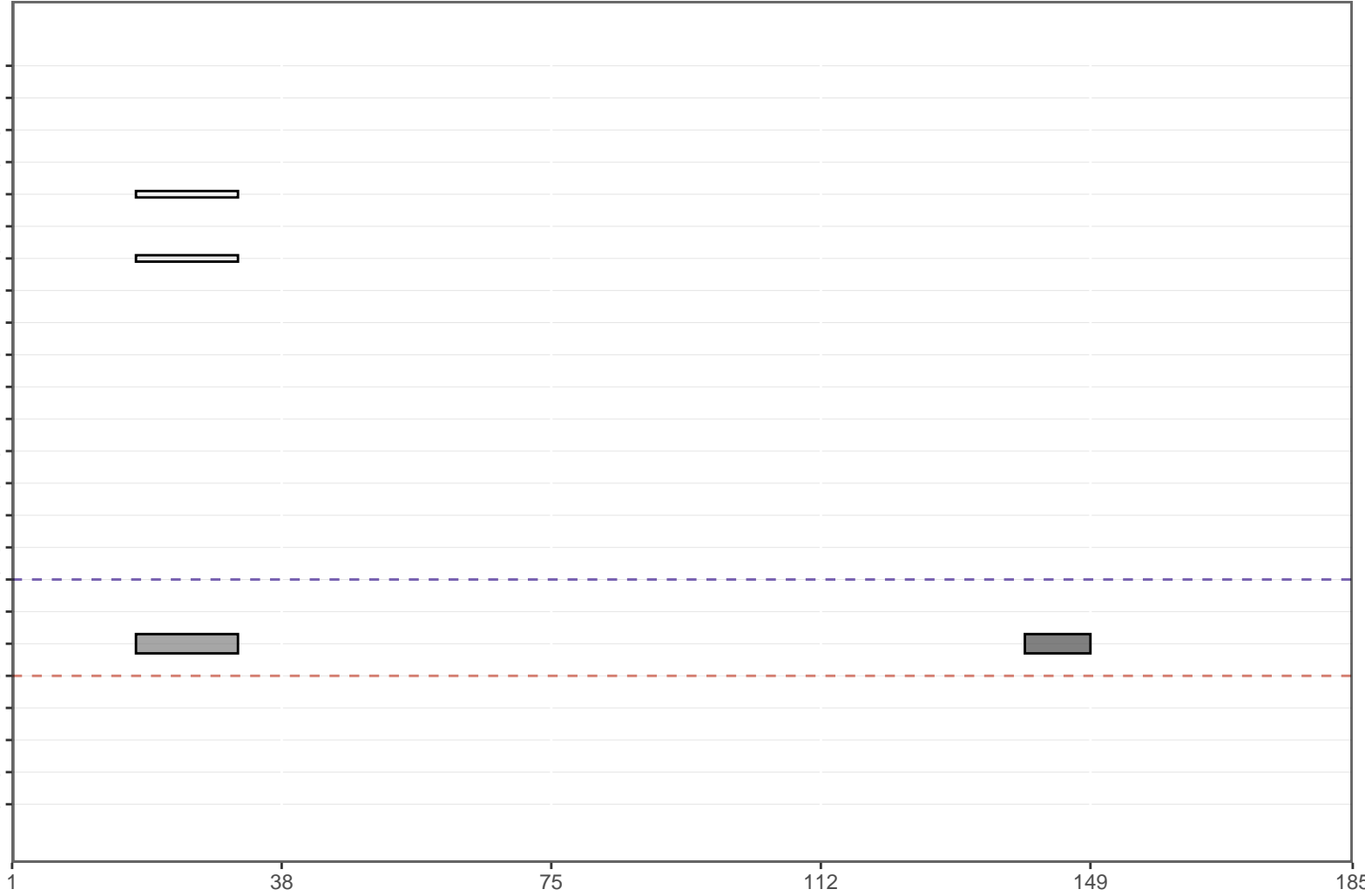
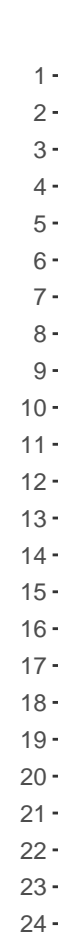
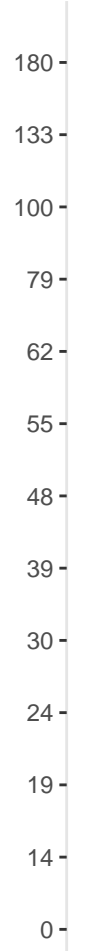


MW indication



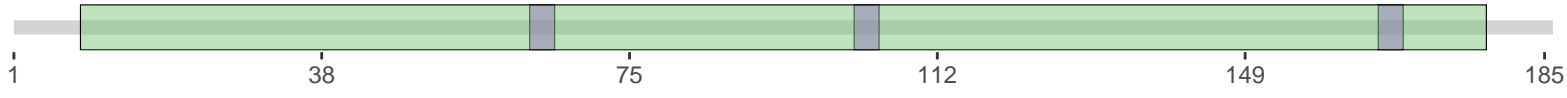
Molecular weight

Gel Slice



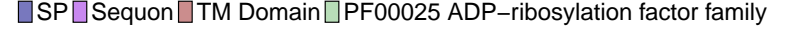
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SMWERYCRVA/SAAVVVDAADPDNLGISREHLDLLKPLSGIPLLVIGNKIDKPGVDSKGAALDQMLKSIDREVCQYMISGKSTNDSVHWLKHGKEK*

NbL02g06470.1 peroxidase_51-like [MW - SP = 33.23 kDa]

No. of times detected



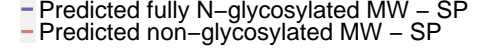
log(intensity)



Values from



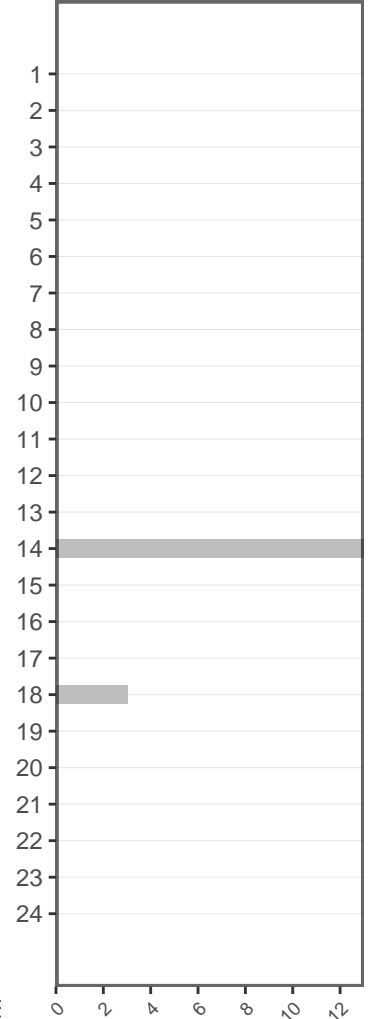
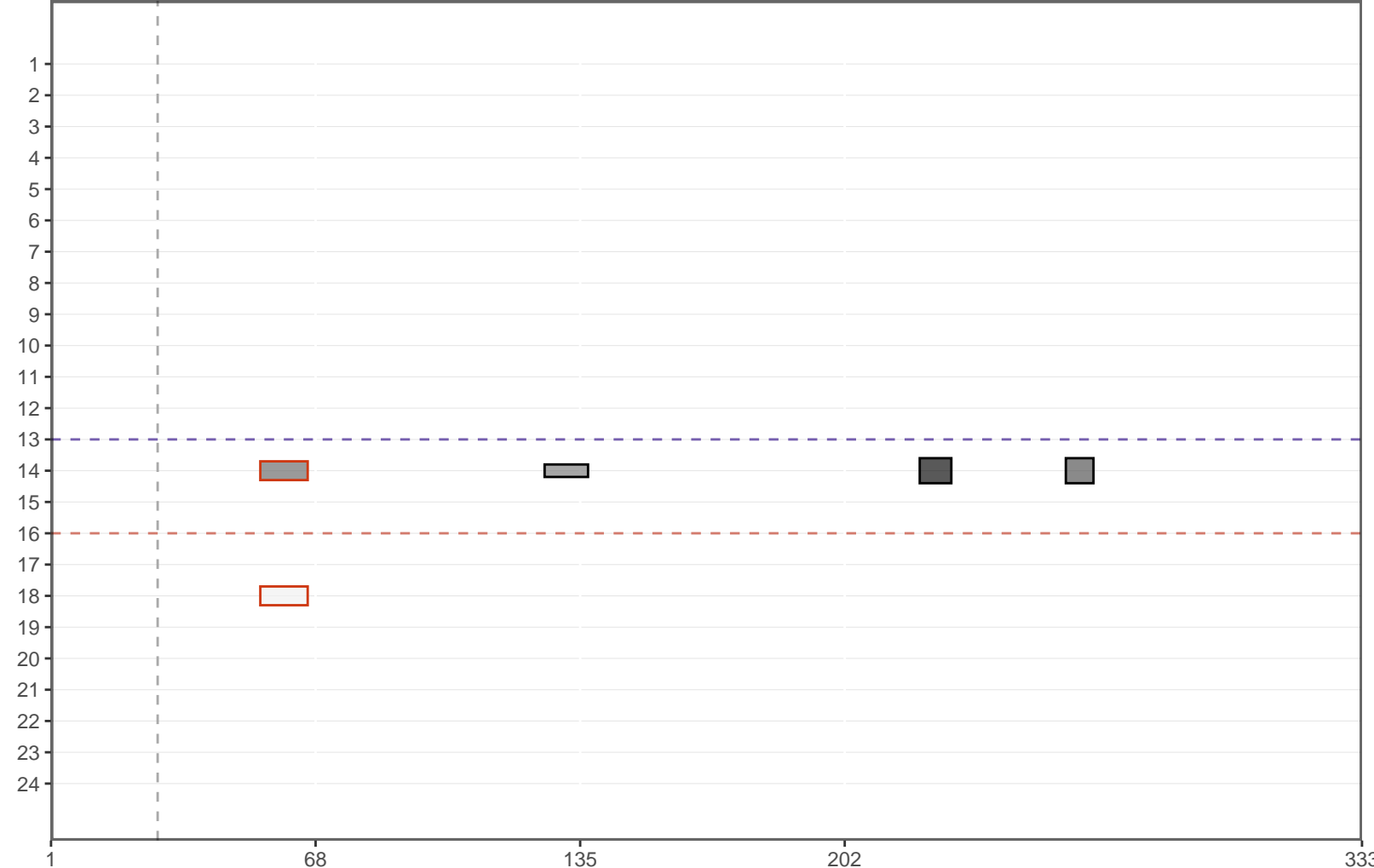
MW indication



Molecular weight

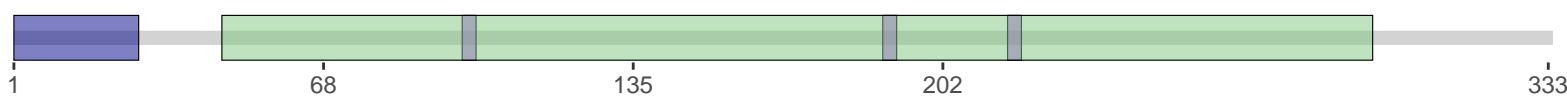


Gel Slice



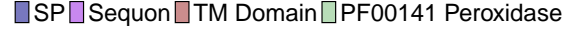
Peptide counts over 4 repeats

Protein length



Pfam domains

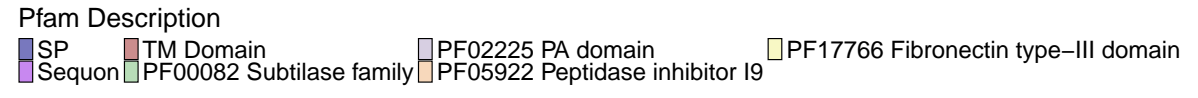
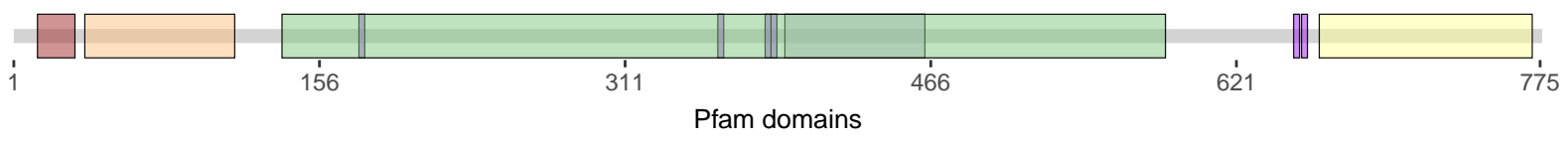
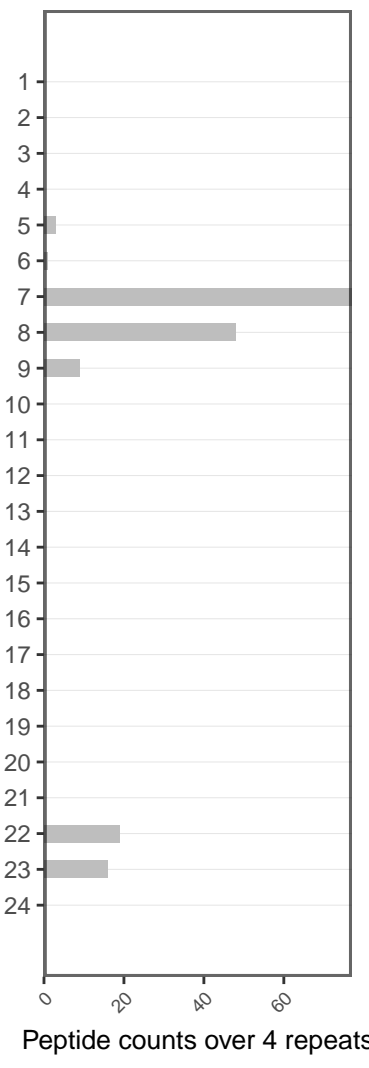
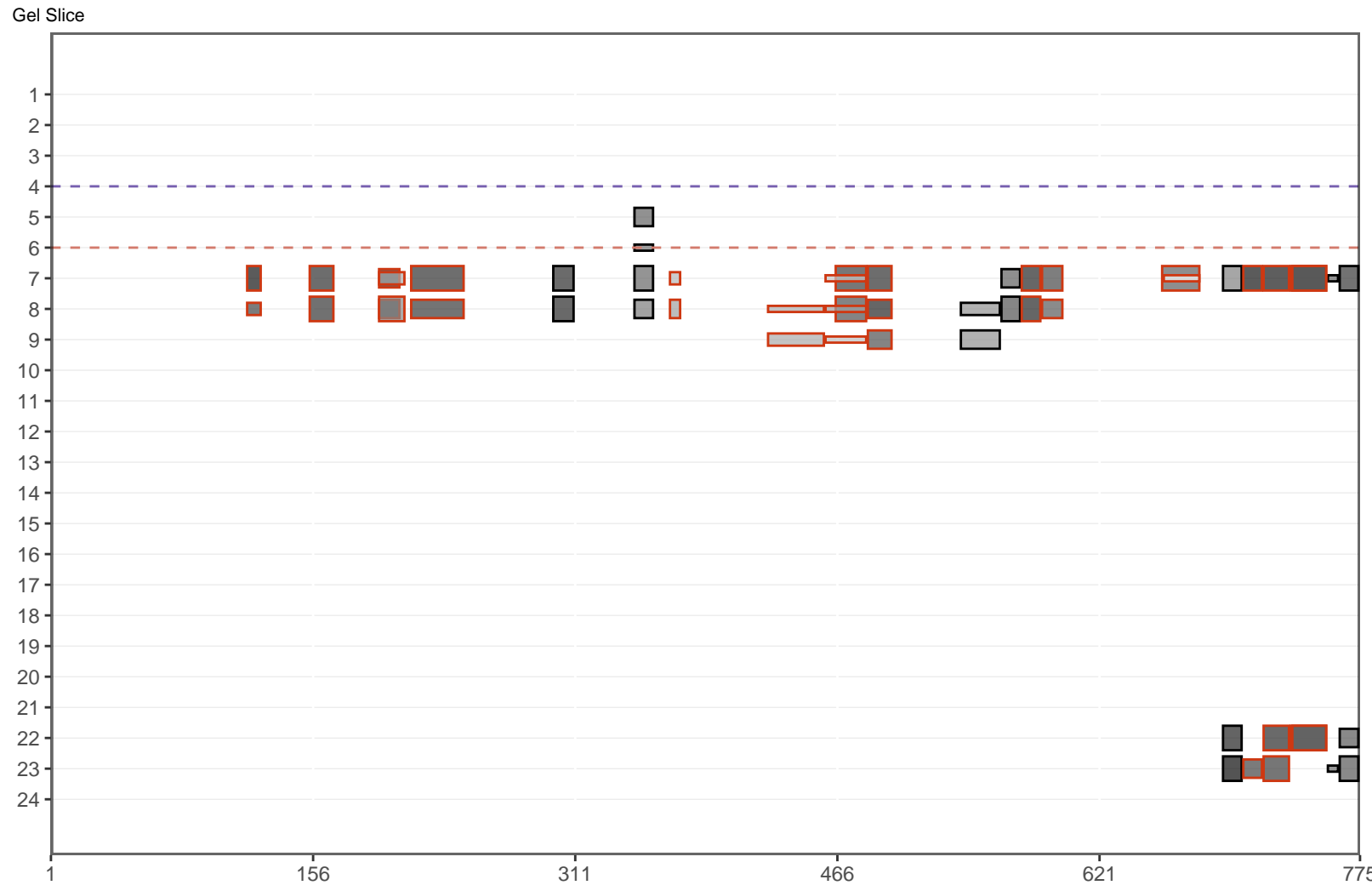
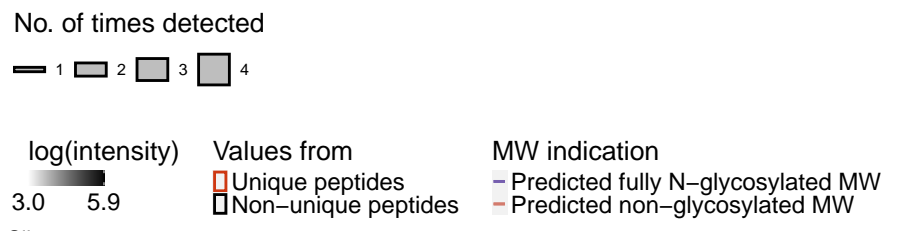
Pfam Description



Protein sequence:

.DGFSTKASNYEIGKLPKPTFFNLNGLNEMFASHLNGSDMIALSAHSHVGFSGKGFANRIYVNFSPKVPDPTLNGVYAAQLGMCPRNVDPRIANMDPKTPRPFENAFKNLGGMGLFTSDQVLYTDGRSKGTVDIWAASNSKAFGNAFVSAITKLGKRVGKVTGNGNRIKFDGGRFN

NbL02g06410.1 subtilisin-like_protease_SBT1.7 [MW = 81.95 kDa]



Protein sequence:
 *NQLPFVYAGNLSNVTNGNLSMTGTLPEKRWKGRKVLGDRGINARVQKGSVKAAGGAGMVLNTNANGEEELVADHLLPATAVSGKTDGAIIRDVLTSDENPTATLFEGETKVGIEPPIVAAFSSRGPNSITPELKPDIAPGVNLAGVTVGAVGPTGLEEDRRVGFENISGTEMSPHVSGLAALKGAHPVWSPNIRBALMTTAVTSYKNGGAGDGVSTGKRSTFFDHPGAGHVDVPSALNPLGLVYDITADDVNLFLGALDYTPSGISGLARRNFTGNEISKYSVTDLNYPS

NbL02g06340.1 probable_esterases_KAI2 [MW = 29.81 kDa]

No. of times detected



log(intensity)



Values from



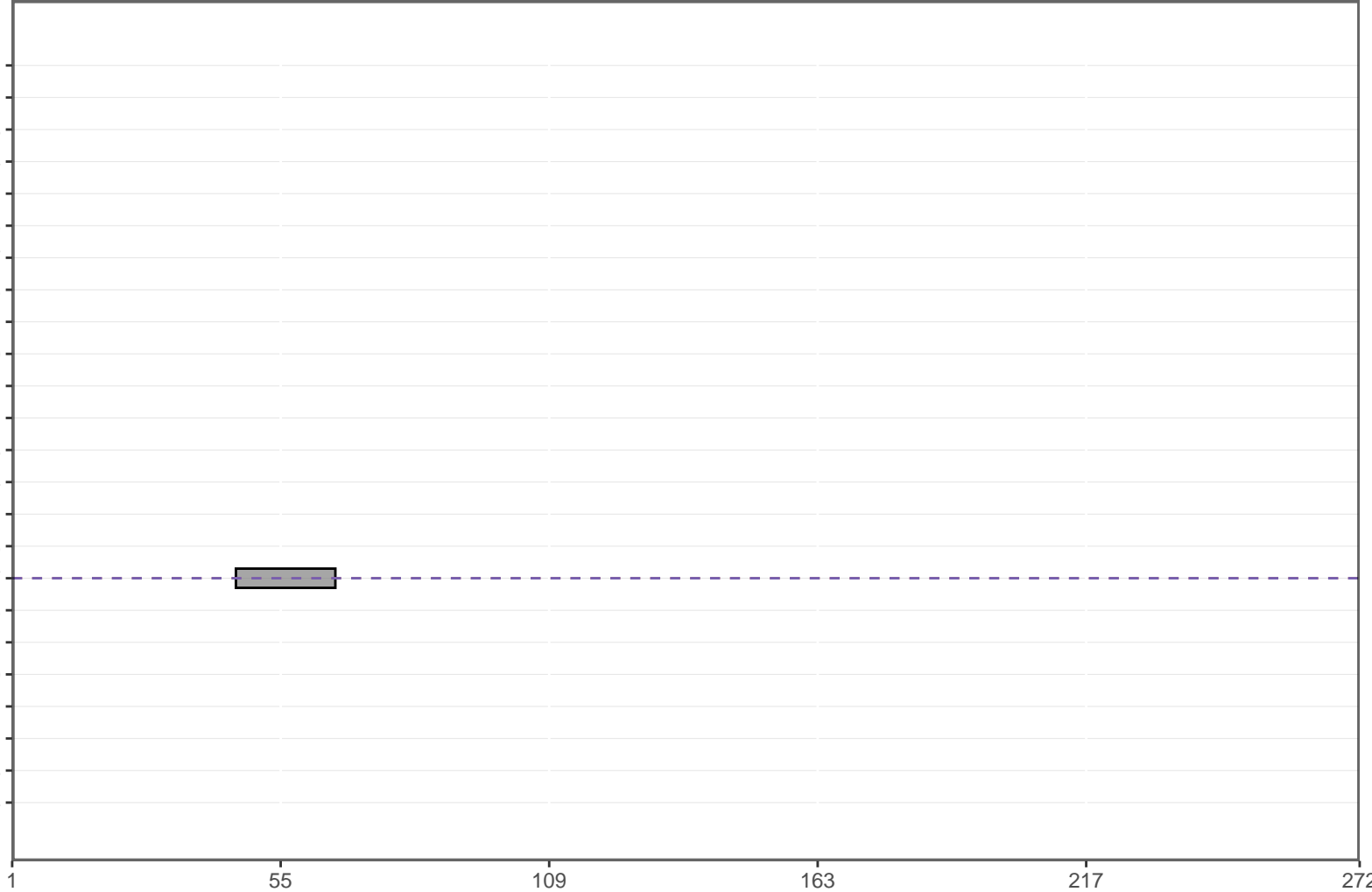
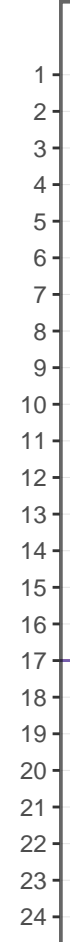
MW indication



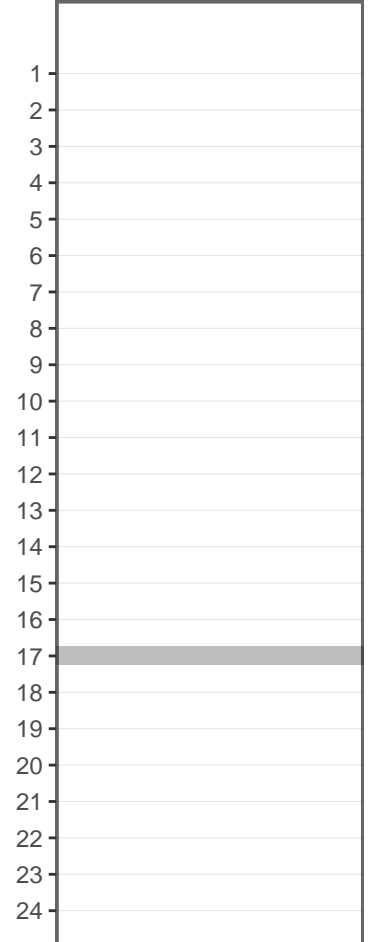
Molecular weight



Gel Slice



Protein length

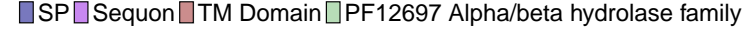


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

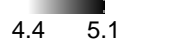
YLLNDYDYYGGFGEEDLDLQLEAMTSNKKAWGGGFAPLAVGGGDMDSVAVQEFGRITLFLNMRPDIALEVLQIFGSDLRHLPHVTVPCHIQSMKDLAVPVVAVSEYLHQNIGGGGSEVEMSTDGHLPQLGSSPDVVPVLLRHRVDAVD

NbL02g06000.1 caffeoyl-CoA_O-methyltransferase_4 [MW = 27.31 kDa]

No. of times detected



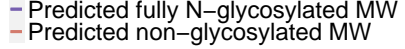
log(intensity)



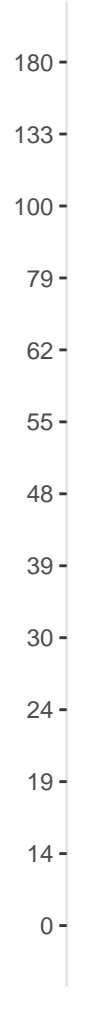
Values from



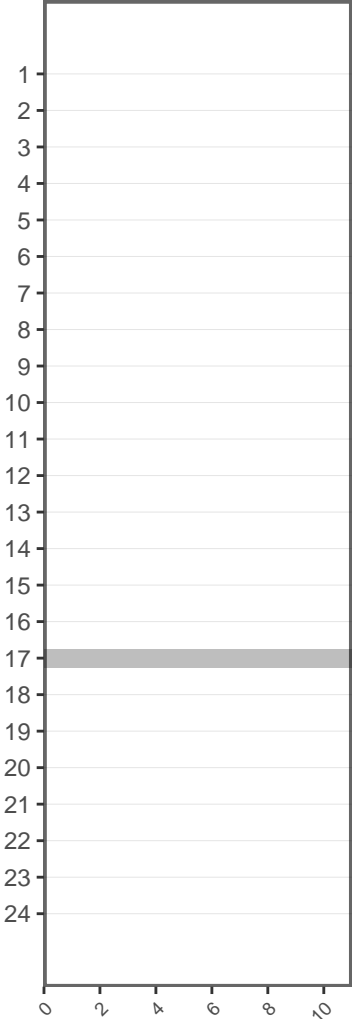
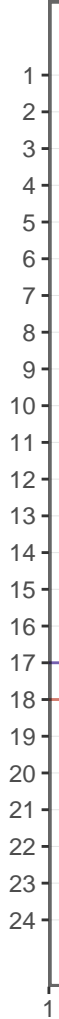
MW indication



Molecular weight



Gel Slice

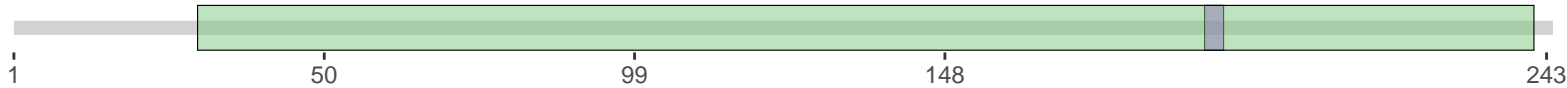


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

INRENYEIGLPVIEKAGLAHKIEFKEGPALVLDRIEMEDGKYHGSYDFVFDADKDNLYNHYKRUIIDLVKGGGLGVDNTLWNGSVVAPPDAFLRKYVRYRDFVLELNKALAADRSEIQGLPVGGDTLGRIT

NbL02g05960.1 nicotinate_phosphoribosyltransferase_2-like [MW = 62.91 kDa]

No. of times detected



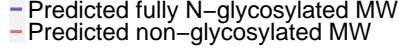
log(intensity)



Values from

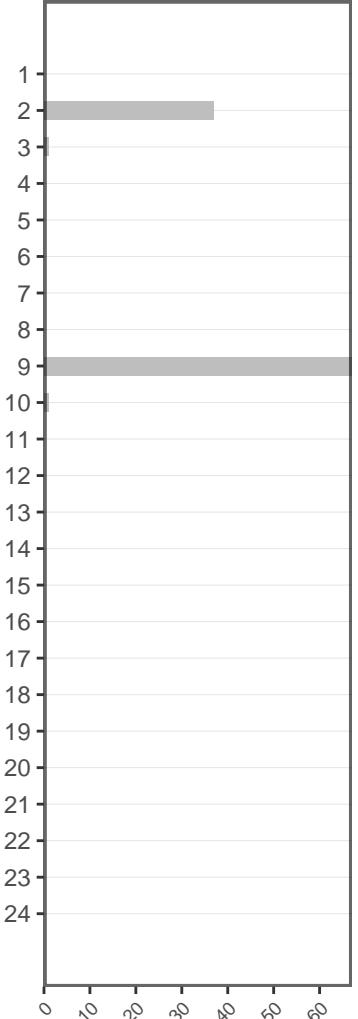
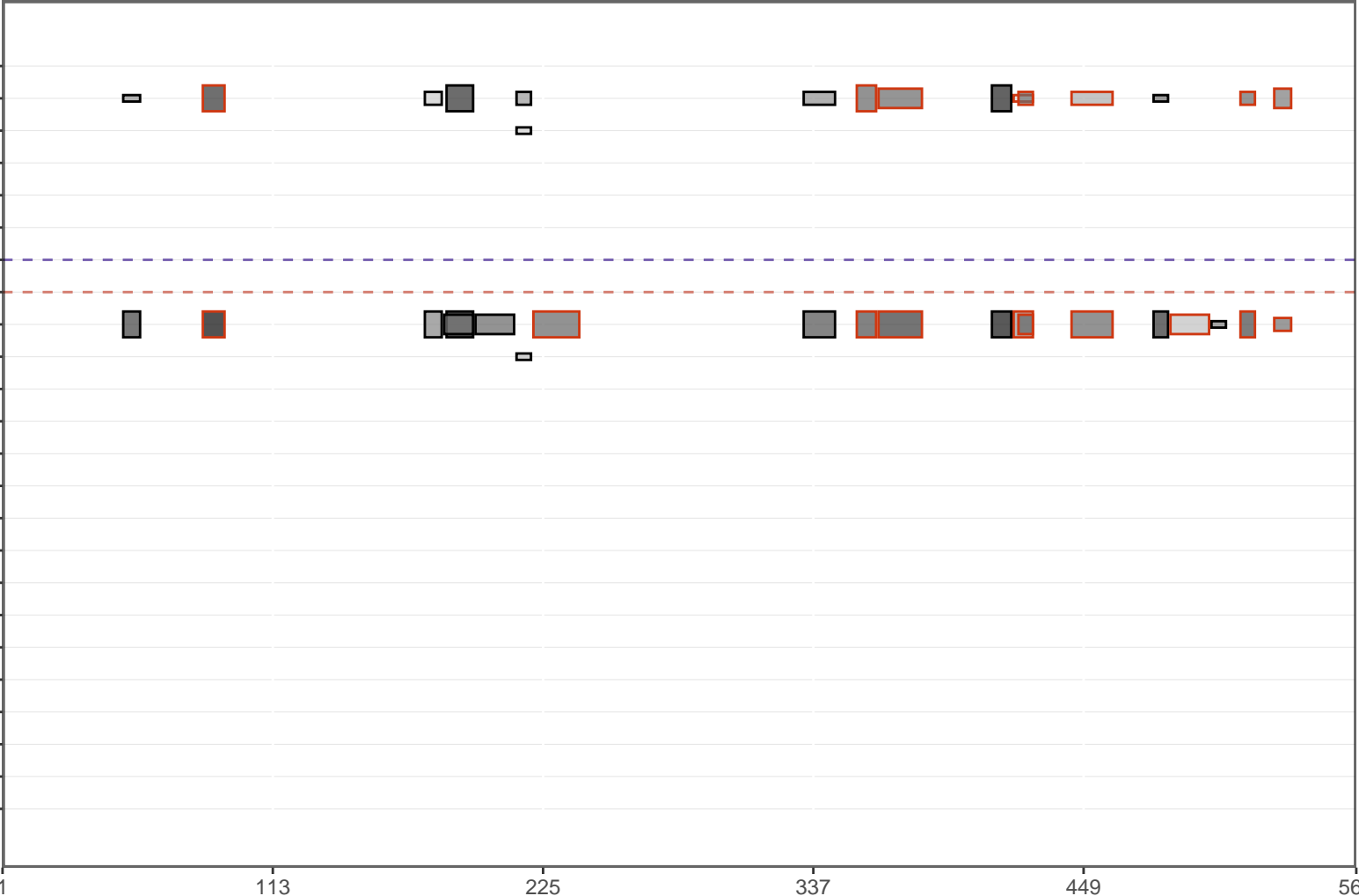
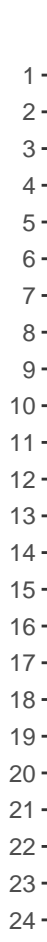


MW indication



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF17767 Nicotinate phosphoribosyltransferase (NAPRTase) N-terminal domain
- PF17956 Nicotinate phosphoribosyltransferase C-terminal domain

Protein sequence:

ILLGGFSETNQLSELAFTSVALAFPGGFLALVDYDVMRSGIPNFGAVALALNDLGYKAVGIRLDSGLAYGSGEARKFFRAIEKEFGLPGRKMNITASNDLNEETLBDALNKGHEVDFMFGDTHLVTDYQAAALGVFKLVEINNGPRKLSGSDVSKVSPICKKRYRLLYKCEGVALVDIMTGENEPQPKVGERILGRHPFSESKRAWVPPQRVEELLEGFWPGNSDQGTREDLPLKIEIRERIEGLQDKMRPDHMRRLNPTPKYQVGSYSAKLYDFHFLWLNAPVGLQ*

NbL02g05940.1 PI-PLC_X_domain-containing_protein_At5g67130-like [MW - SP = 42.09 kDa]

No. of times detected



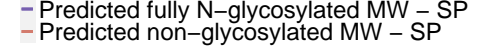
log(intensity)



Values from



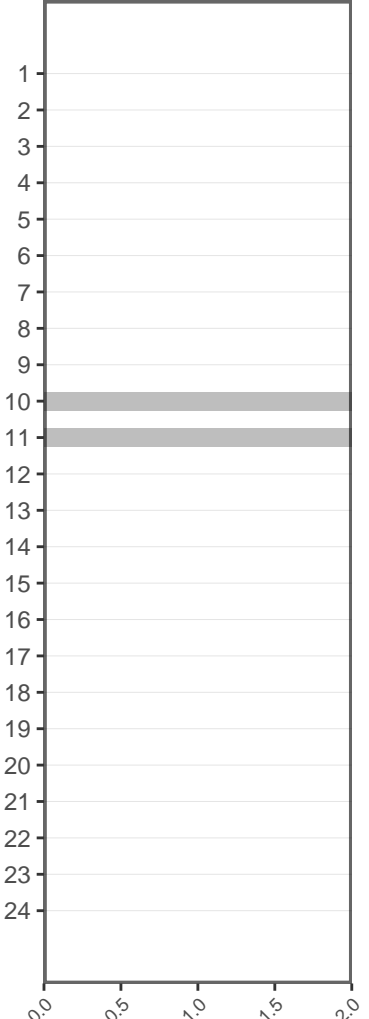
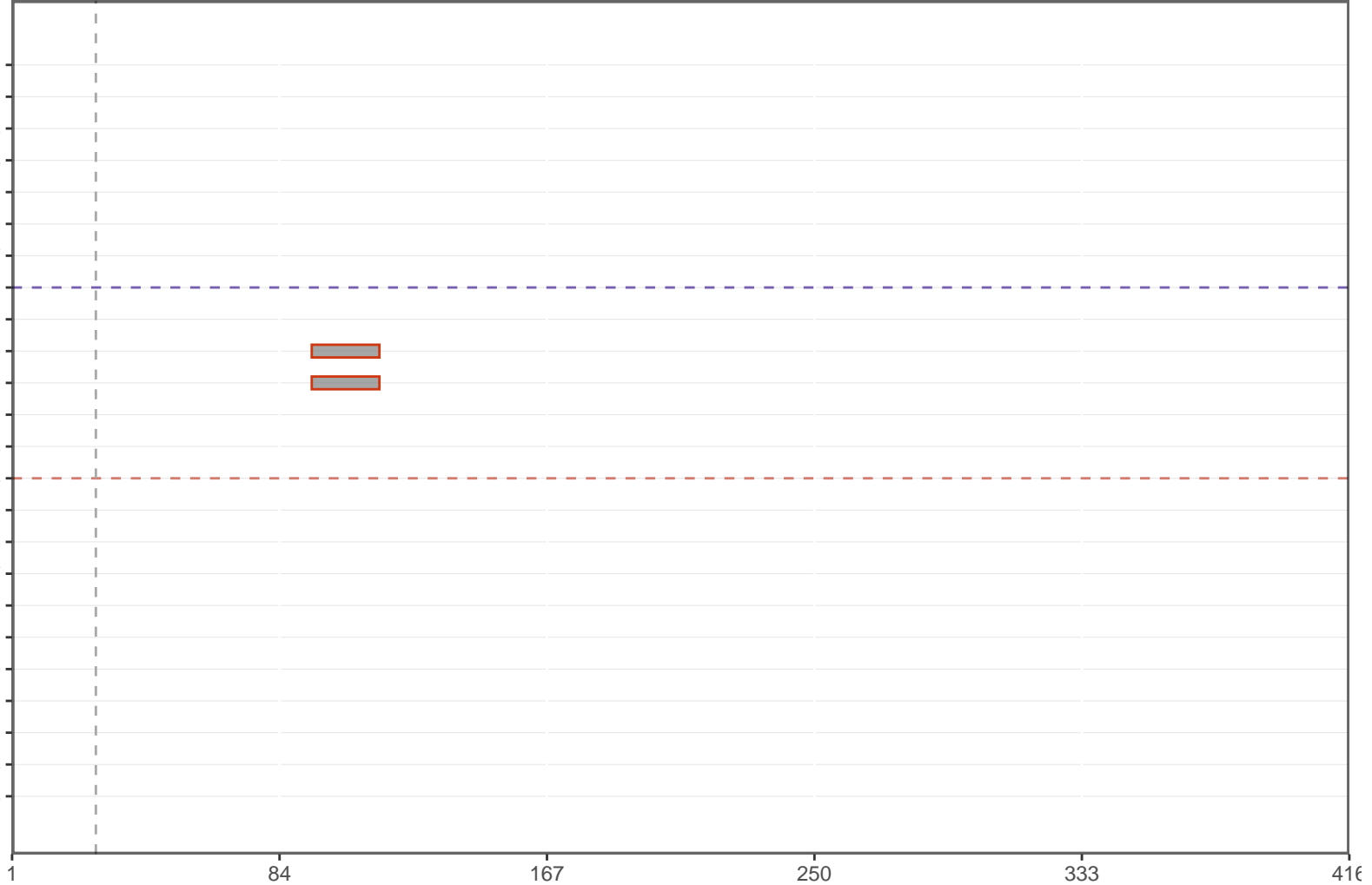
MW indication



Molecular weight



Gel Slice



Protein length

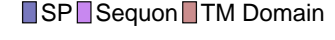


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

PVSRMPKQRKEDVPTVDDMAYKGNRQLVFTFSKSSKEASEGIAYEWRVYVENGYNNGMAYVGGCPREBESSPMTSSISLVLGNYPDNPNTAAGVDNSATLIMTKTKFEAAAGKRWPNFAVDYKQKSDGGGAPEAVDEANGQLACNGSSIAVQKASGTSHKKEAFMLSPFPFPAQATSGTGGDGNNEGNDNSHSRSLPLHWLGTIEVAALLLHA*

NbL02g05860.1 zeaxanthin_epoxidase_chloroplastic [MW = 72.59 kDa]

No. of times detected



log(intensity)



Values from



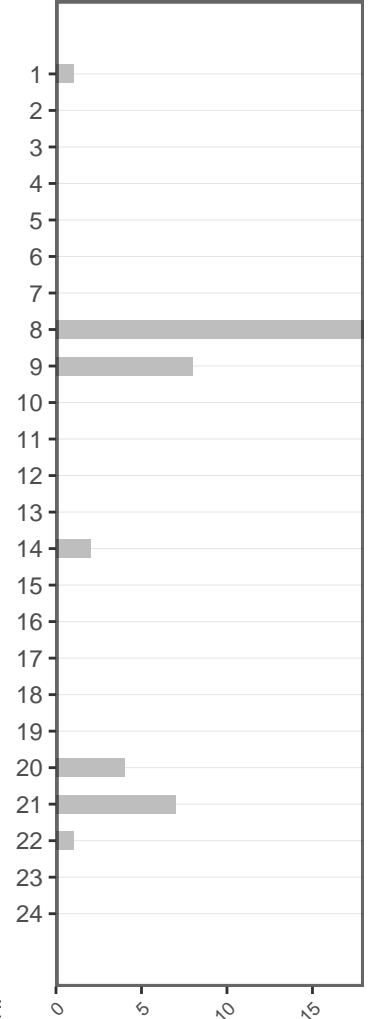
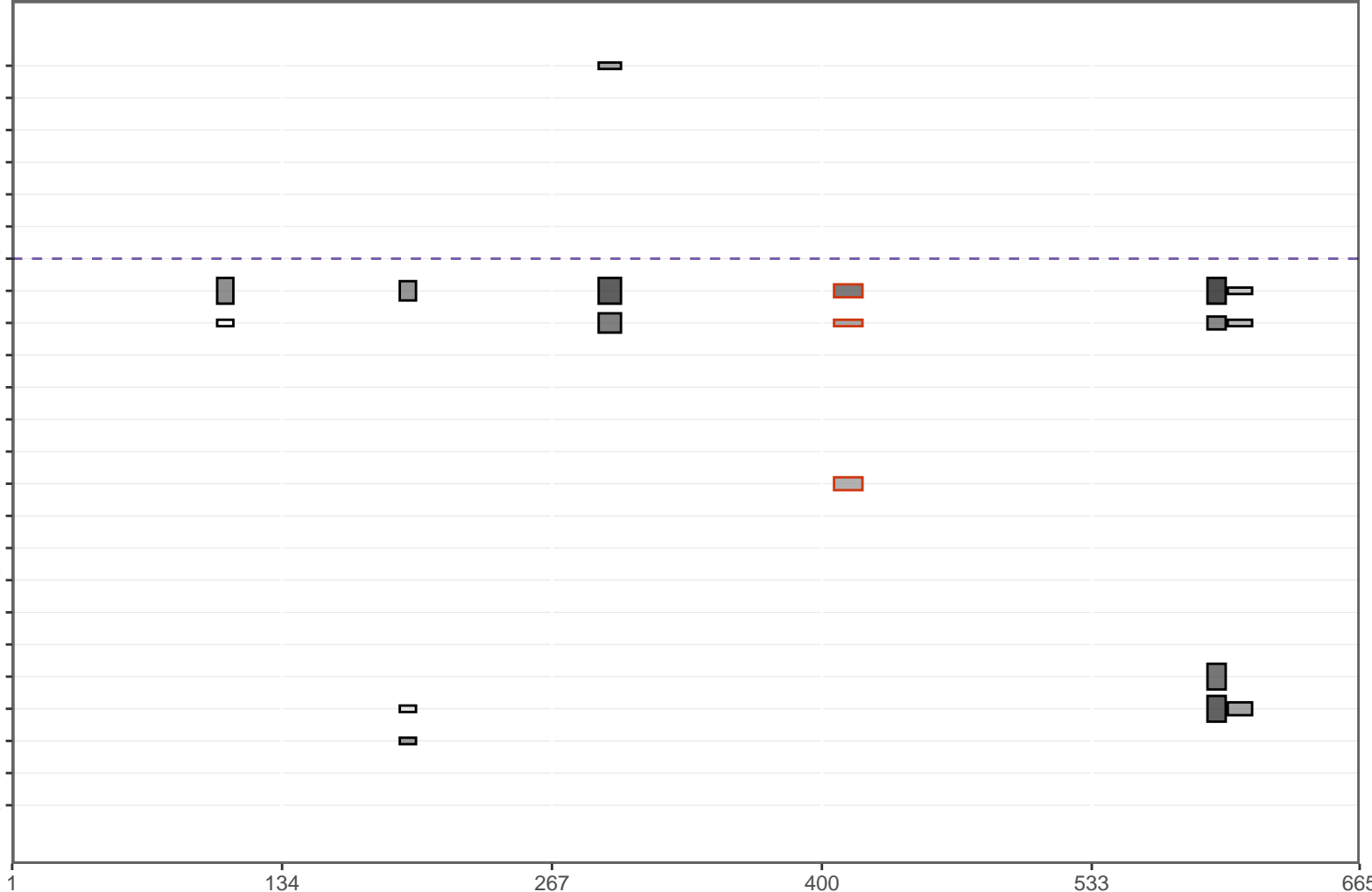
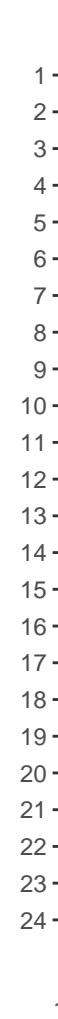
MW indication



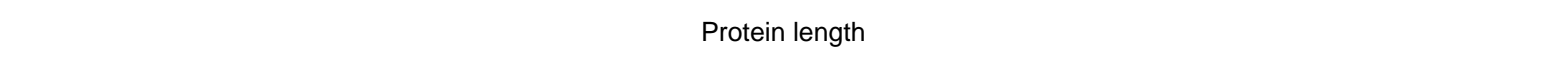
Molecular weight



Gel Slice

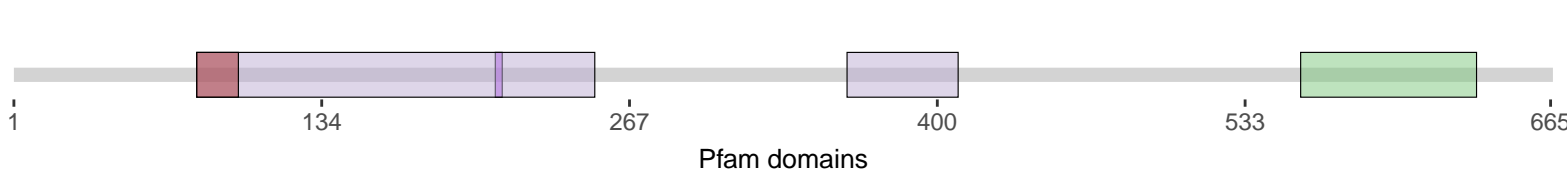


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KKARLLKFEIGWCINVDLWATDEDAILRRDYDRPPTFNWQKGRVTLFGDSVHAMQPNLGGGGMAEDVGLALELKNVSRSAEESGAVDIISLRVYESSRKLRVGVHIGLARMAAMASTYKAYLGVGLGFLSFKFRFHPGRVGGRRFDLGMPLMLGVLGNGENKLEGRIGHRLSEKANDLRNWFEDDALARATDAEWLLPAGSGNALEALLSRDEEMPTKGVSHVHTNIPGKSVVPLPGVSGMHARISYKGGAFFVTDLRSEHGTWITDNEGRI

NbL02g05810.1 high_mobility_group_B_protein_14 [MW = 18.56 kDa]

No. of times detected



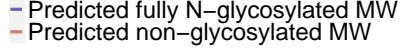
log(intensity)



Values from



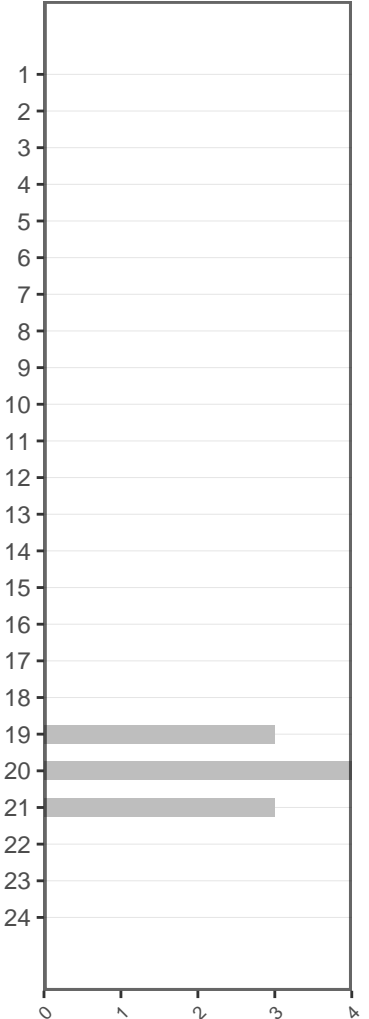
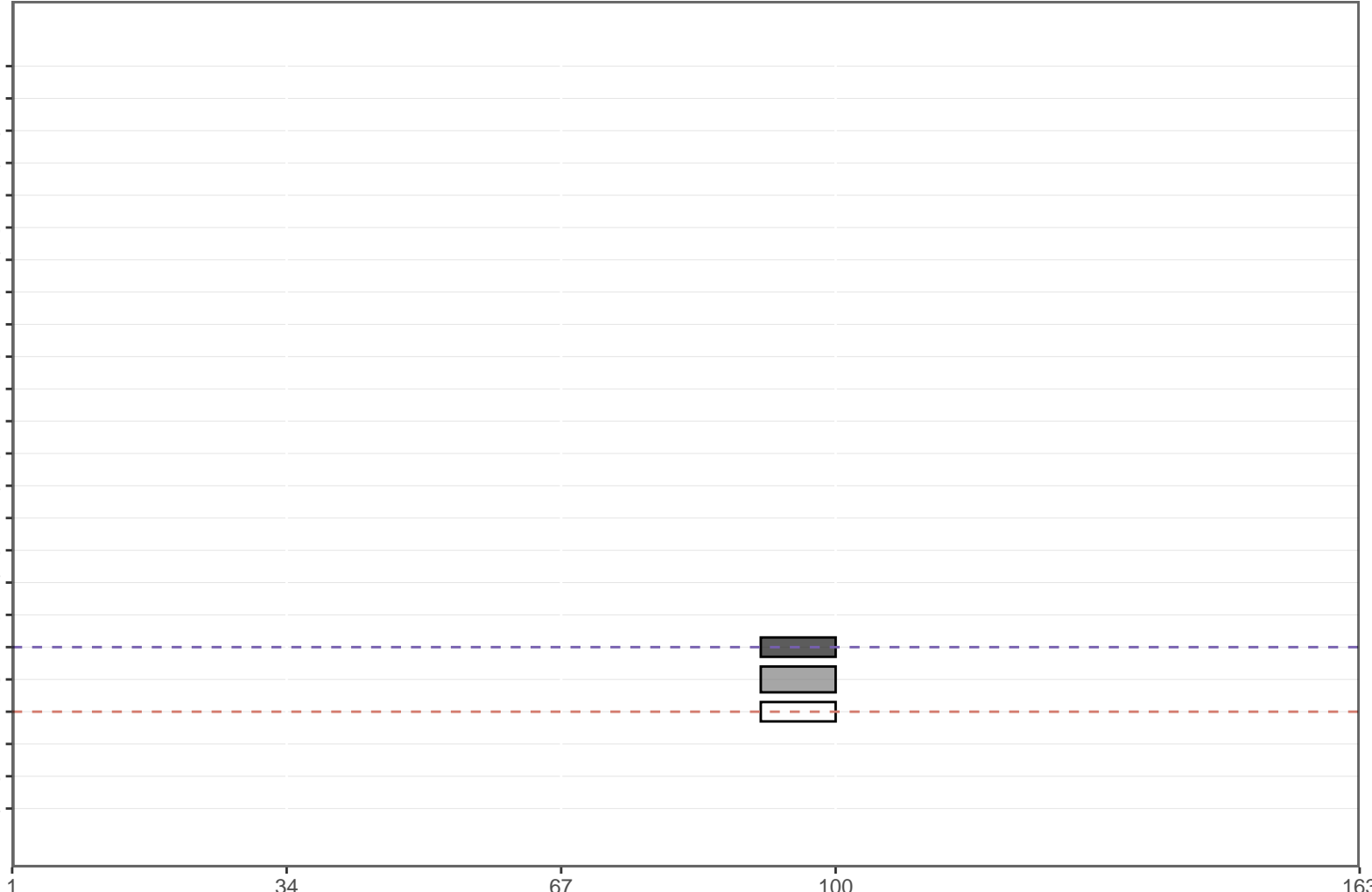
MW indication



Molecular weight



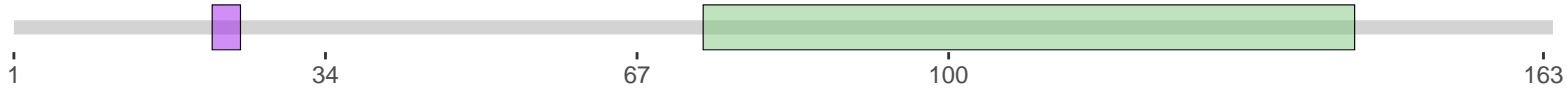
Gel Slice



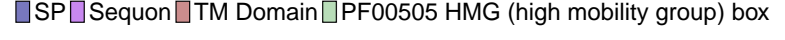
Protein length



Pfam domains



Pfam Description

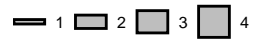


Protein sequence:

DAMKPKKPPPTAFFYFLIEDFRKFEQGNPDVKSMDVGVKADGGEKWKMTMYEEKVHYVDATENRREFDRAMADFNKRKESGEFOEFEEEDSDFEI

NbL02g05550.1 DNA_damage-binding_protein_1 [MW = 122.19 kDa]

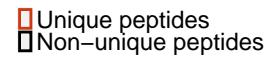
No. of times detected



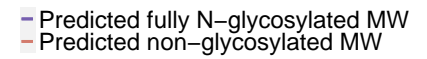
log(intensity)



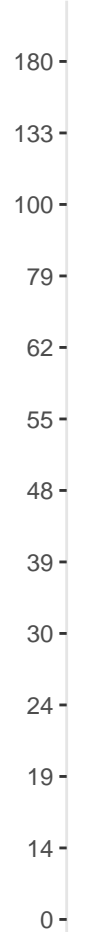
Values from



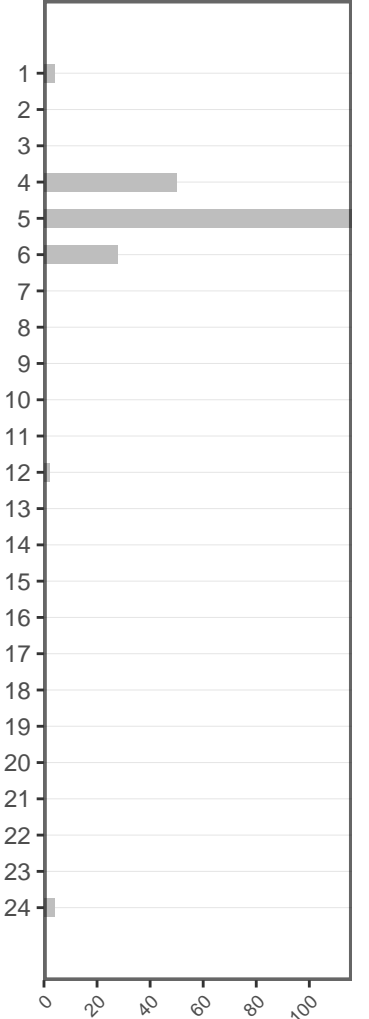
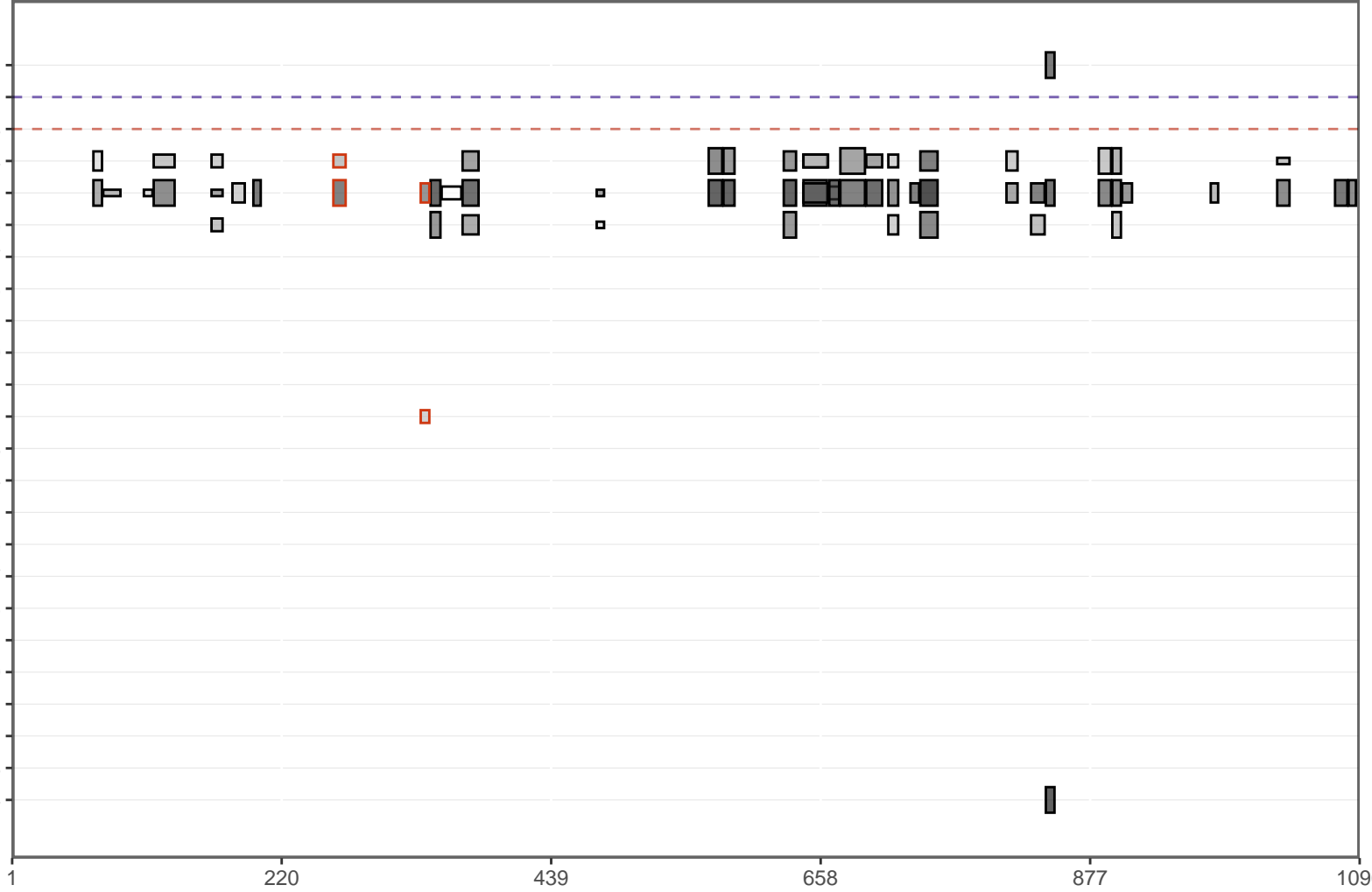
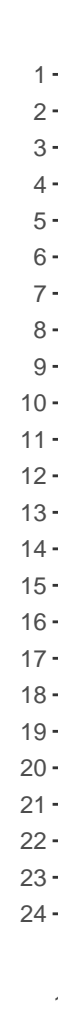
MW indication



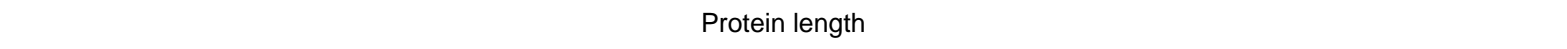
Molecular weight



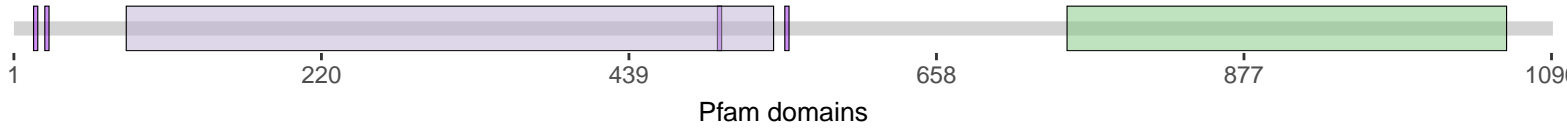
Gel Slice



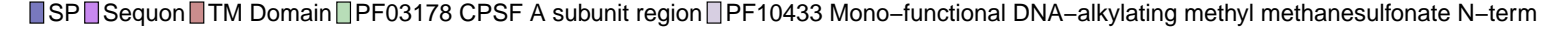
Protein length



Pfam domains



Pfam Description

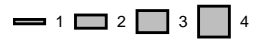


Protein sequence:

ISCLDINPGENPNYSGMAVGMWTDSEVRVYSLPDLNLTKEGLGGEIIPRSVLMGSEFEGISYLLCALGDGHLNLYLSMTGELTDRIKQVSLGTQPTLRTFSKADATHVFAASDRPTVYVSSNKLLYENVNLKEVSHMCPFNVAAPPDLSLAIAKEGELTGTIDEIKLHRSIPLGEHARRISHQEGTRTFALGVWYKTSNADDPVHFVRLDDQTFEFISYPLDQFEYGGSLGSGSFDSDSNYYVGVGTAVVMPPEENPTKGRILVRFVEDGKLGIAEKETKGAIVYSLNAF

NbL02g05500.1 40S_ribosomal_protein_S4-like [MW = 29.88 kDa]

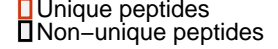
No. of times detected



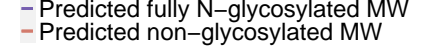
log(intensity)



Values from



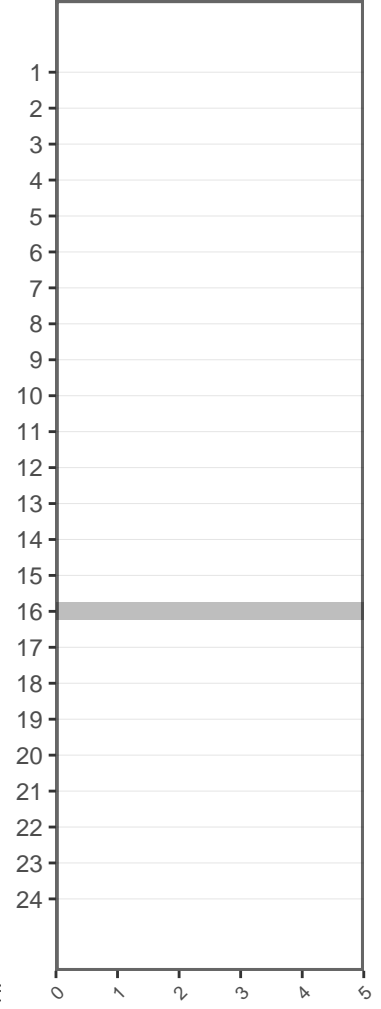
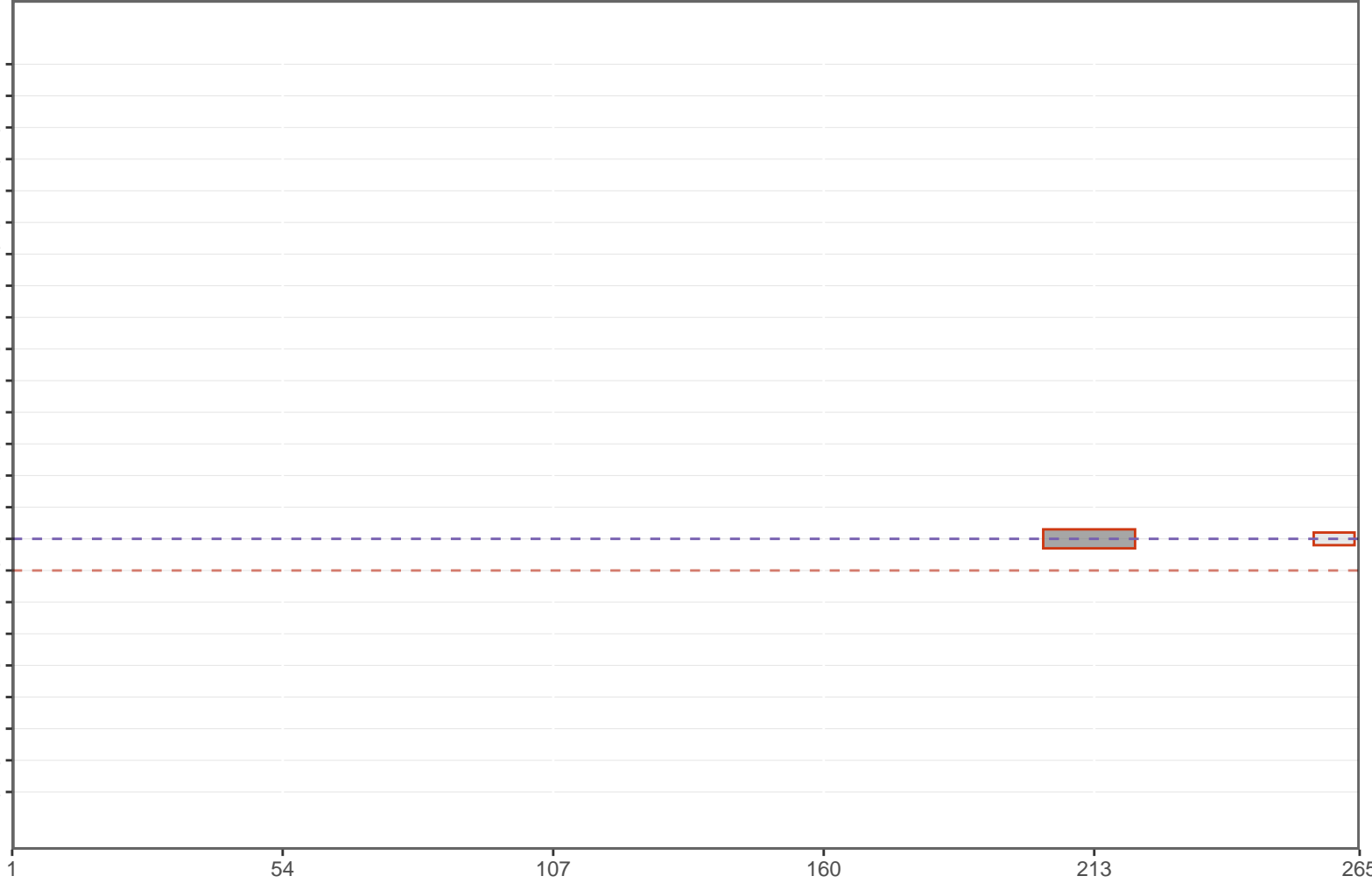
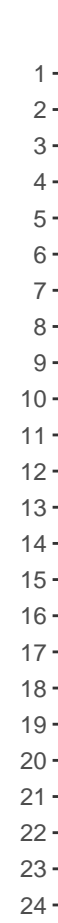
MW indication



Molecular weight



Gel Slice



Protein length

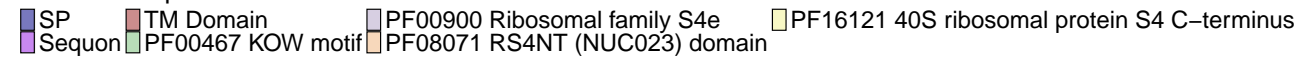


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

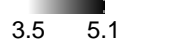
IAKFLCKVRSVYFGQKGFPLNTFYDGRTRIRYDPDLKANDTKLDLENKKIVDFKFDVGNVMMVTGGRRNRGRVGVKIKREKHKGSFETVHQDAGGHEFATRLGNVFLGKGTQKPVWLPKGGKIKLSIEEARKRLAAGSATTI

NbL02g05280.1 tubulin_beta_chain [MW = 57.69 kDa]

No. of times detected



log(intensity)



Values from



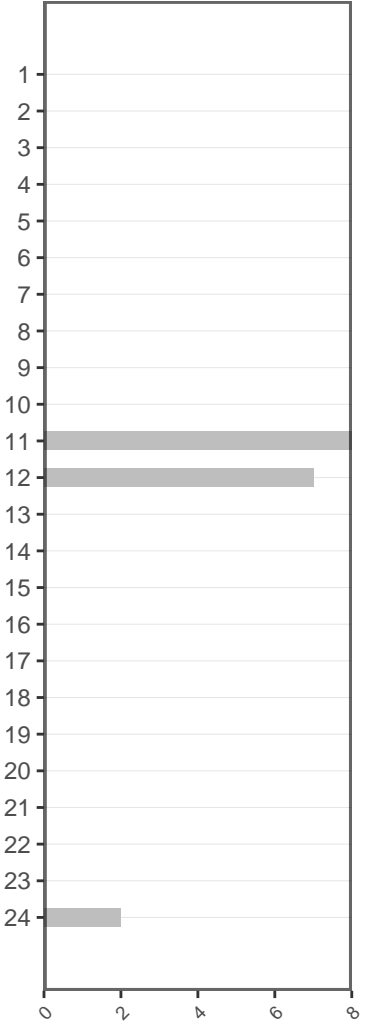
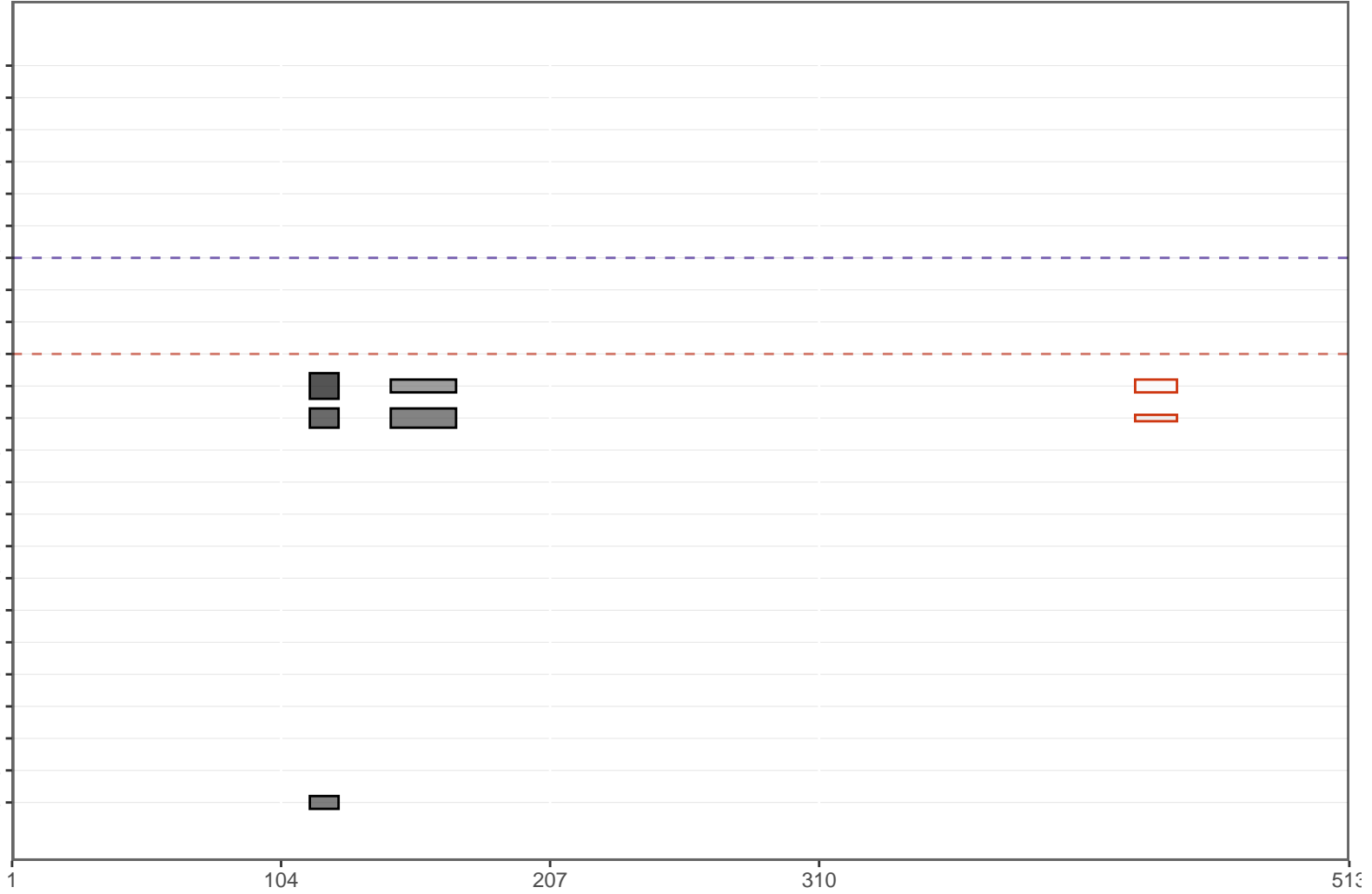
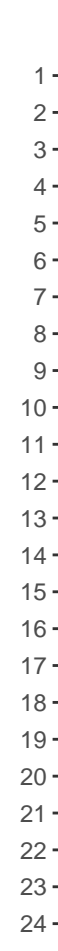
MW indication



Molecular weight

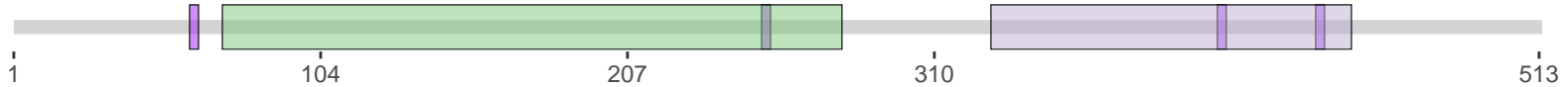


Gel Slice



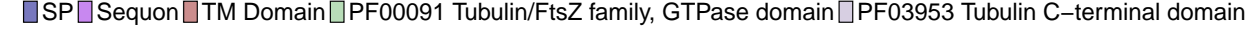
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DTVVEPYNATLSVYHQGVENADEGMVLENEALYDGFRTLKLSTPKFSGDLNHLISATMSGVTOGLRFFPQQLNSDLRKLAVNLPPFRLHFFMVGAPLTSRGGSLGVRALTVPELTQGMVDQAKNMKCAADPRHGRVLTASAMFRGKMTSEKVEDEQMLNVGNKNSGYSFVEWPNVWSSVDCDPPKGLKMASTFGNSTAIGEMFRRVSEGFTAMFRKAFLHWYTGEGMDMEFSEAEISNMNDLVAEYQQYGDATADDEVEEEEDDAW

NbL02g05270.1 probable_3-hydroxyisobutyrate_dehydrogenase_mitochondrial [MW = 43.88 kDa]

No. of times detected



log(intensity)



Values from



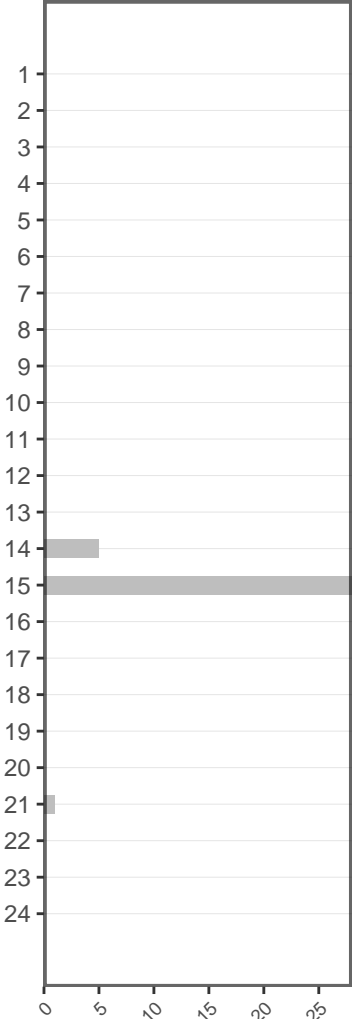
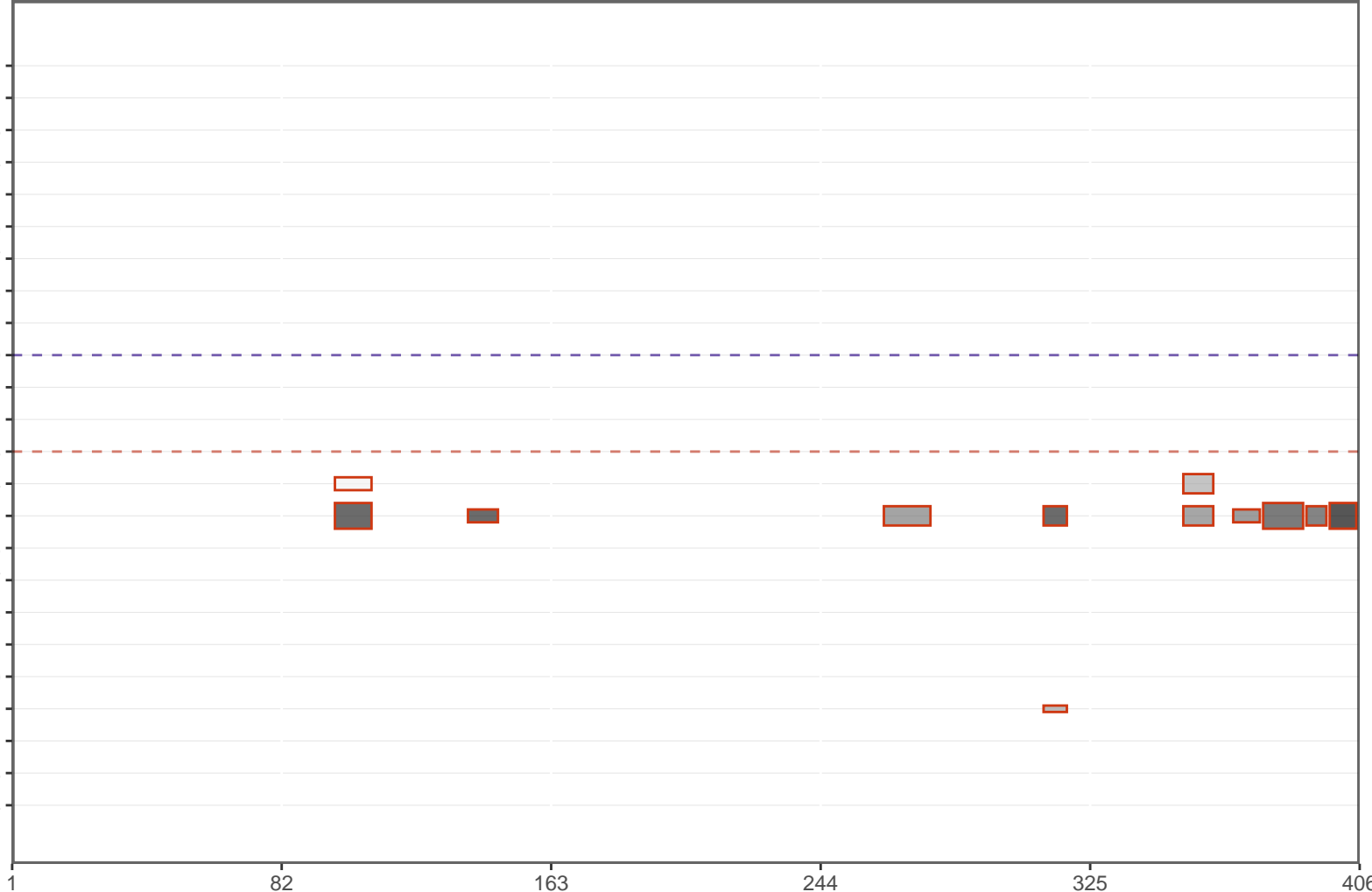
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF03446 NAD binding domain of 6-phosphogluconate dehydrogenase
- PF14833 NAD-binding of NADP-dependent 3-hydroxyisobutyrate dehydrogenase

Protein sequence:

STDPHTSRKYSADAGNGLHHRKDGWKTFRMLDAPVGGVLAENGTLTFMVGSTEEAYTAAPLFLSMGKNSIVGGGGGATANKICNNLAMAISMLGASEAFVLGGFGAASLTETKIFNASSARQWSSDTNPNVPGVMGVPSSRNIVGGFGASKLMAKDLNLAVASAKEIGLKPLTSGAENIFELGDNQHGAEKDFSSVFRVYVGGKDEQ

NbL02g05260.1 60S_ribosomal_protein_L35 [MW = 14.32 kDa]

No. of times detected



log(intensity)



Values from



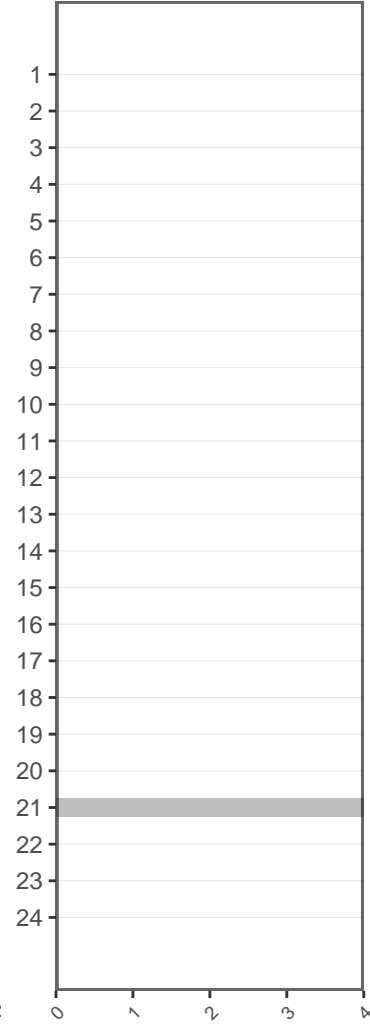
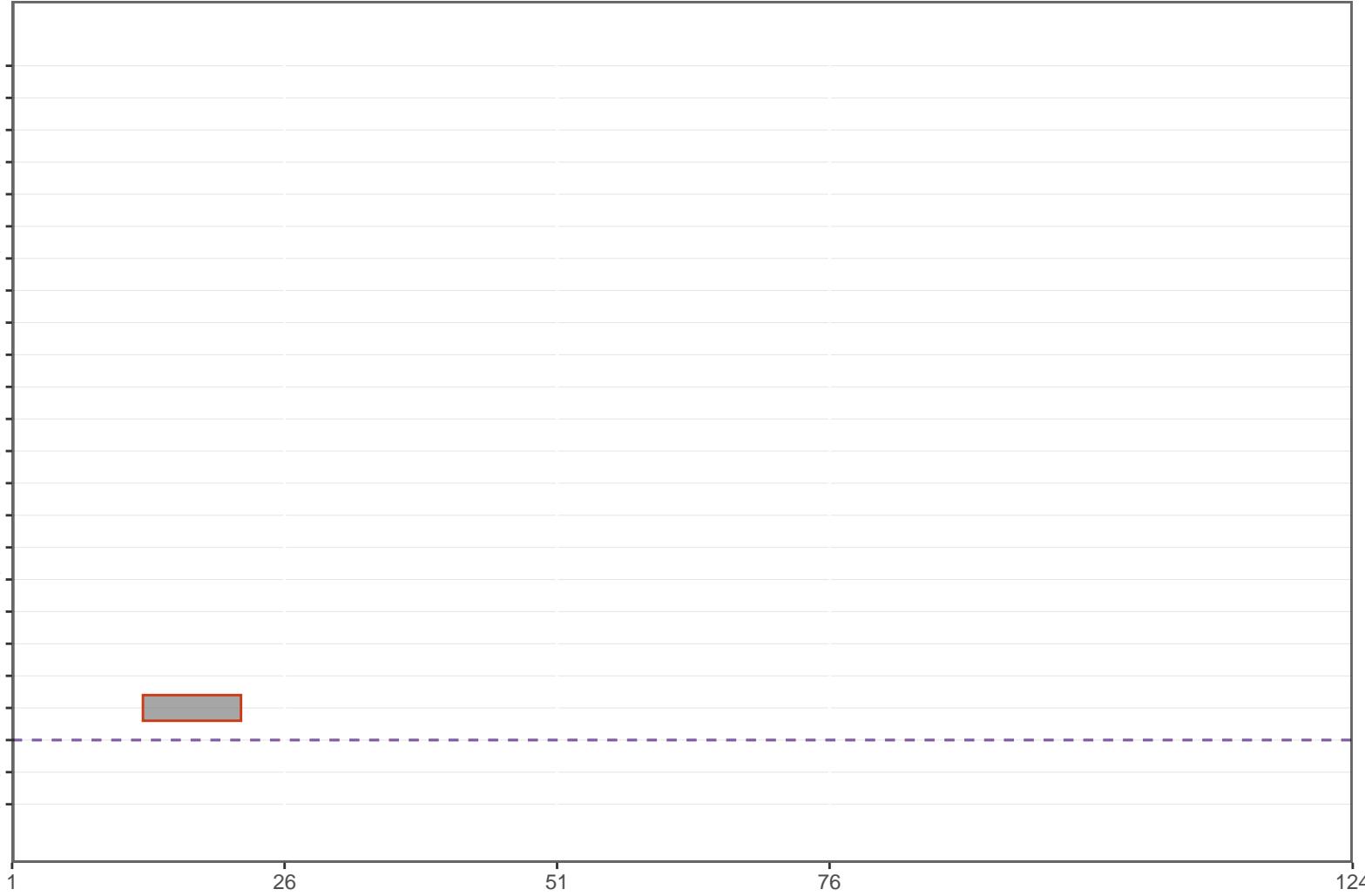
MW indication



Molecular weight

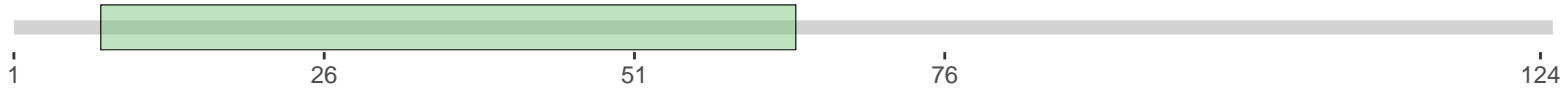


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

..VRLSIAQVLTVISGKQKTALEAEVKNKKYLPDLRPPKTRAIRRLTKHGASLKTEREKKKEMFFLRKQVAVV

NbL02g05220.1 actin-depolymerizing_factor_2-like [MW = 16.11 kDa]

No. of times detected



log(intensity)



Values from



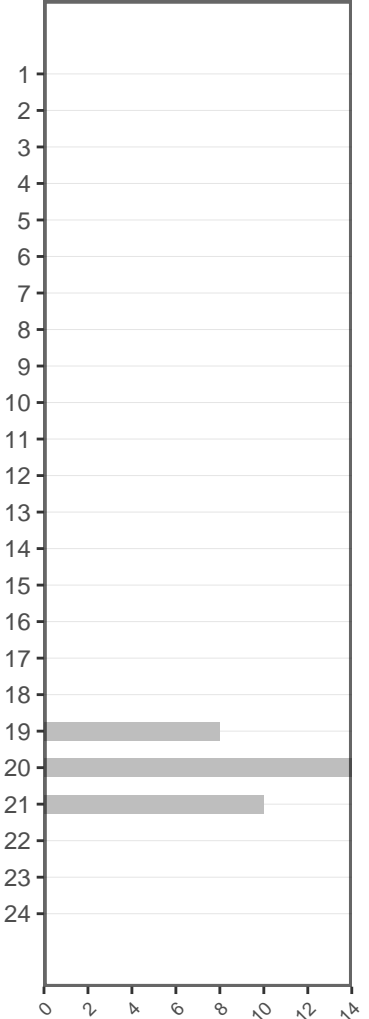
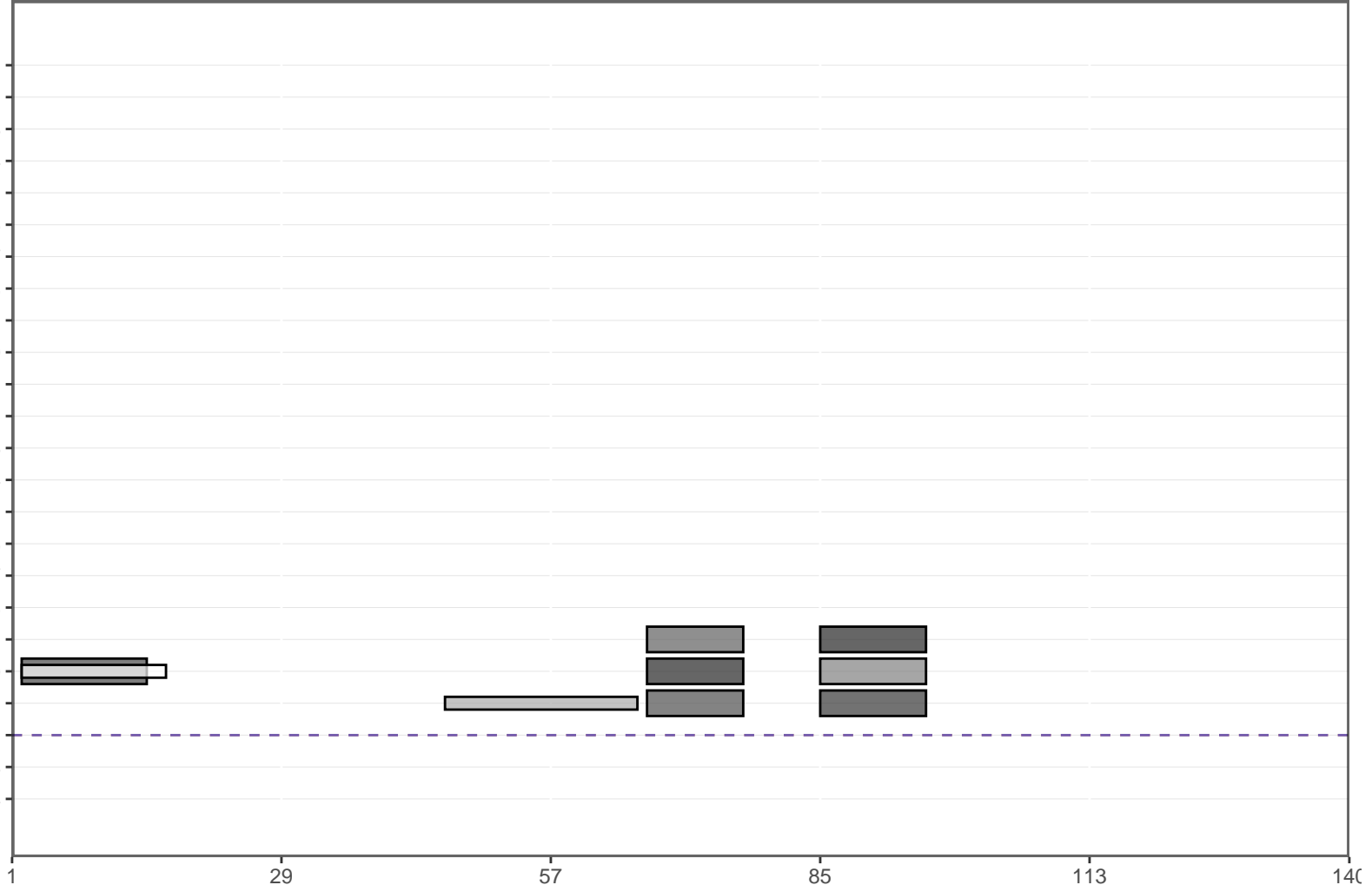
MW indication



Molecular weight



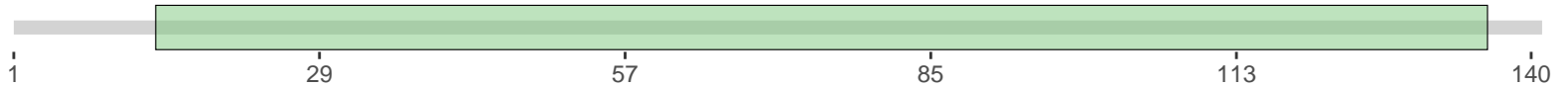
Gel Slice



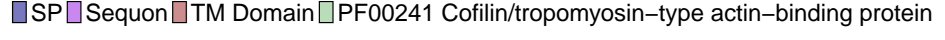
Protein length



Pfam domains



Pfam Description



Protein sequence:

CTHLPADECRVAVYDFDFLTKESVPKRIFIAWSPDTSKVRKMMYASSKDRFKRRELDGIGIELOATDPTMGLDFKGRAN

NbL02g05130.1 ferredoxin--NADP_reductase_root-type_isozyme_chloroplastic-like [MW = 41.91 kDa]

No. of times detected



log(intensity)



Values from



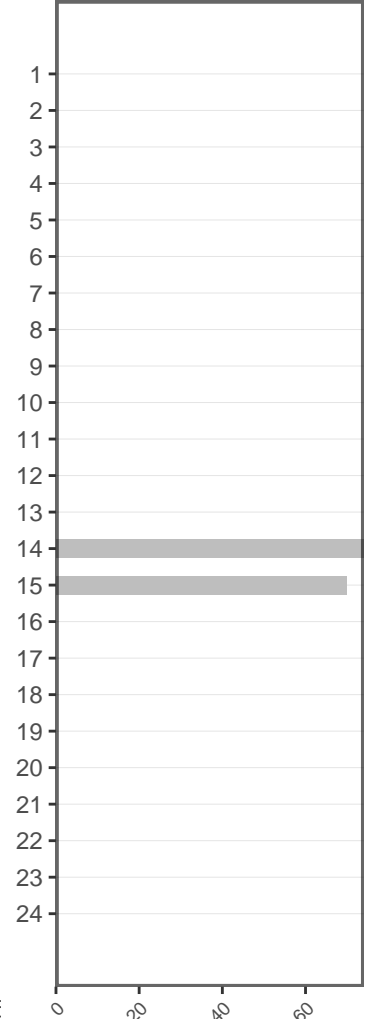
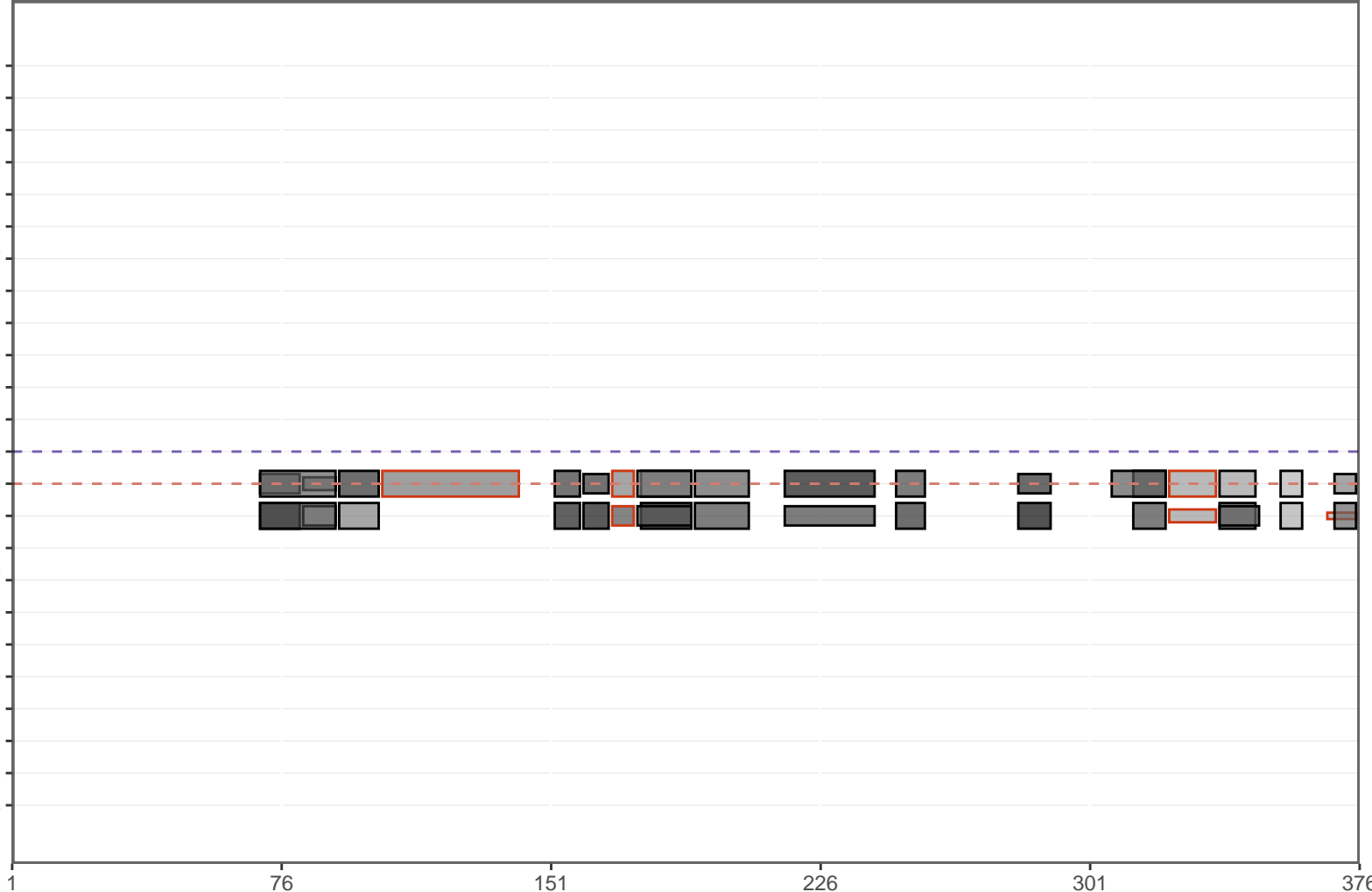
MW indication



Molecular weight



Gel Slice



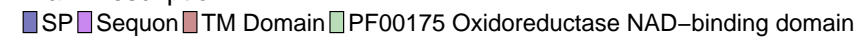
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

YYDPETGKEDPSKNGVCSNLFGLDGRKPGDKVKTGTPSGKMLLPEDNPNATHMGTGTGVAFPRGVLRRFMESGVPTKFNGLAWLFLGWANTDLSLLYDDEFTRYLNDYDGNFRYDRALSREQKNKGGKMYVDDKIEEYSDIEFKLLDEGAHMYFGLGKGMPPGGDTLKRVAERRGESWEQKLSLKKKNGQHWHEVY

NbL02g05080.1 C-factor [MW = 32.48 kDa]

No. of times detected



log(intensity)



Values from



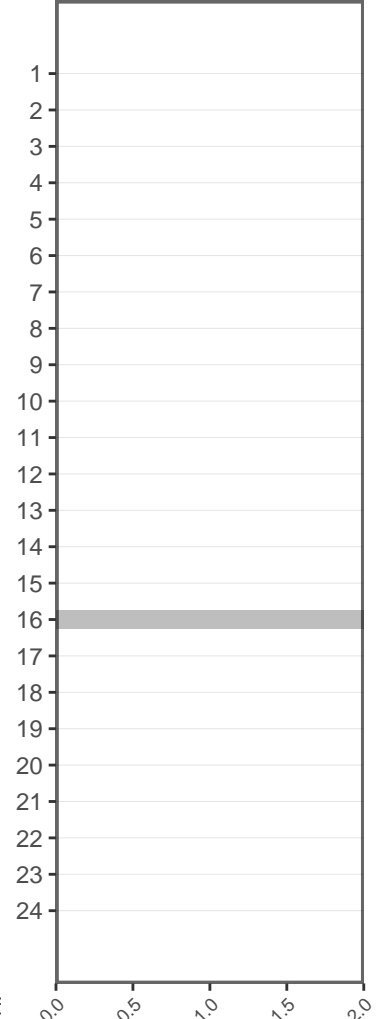
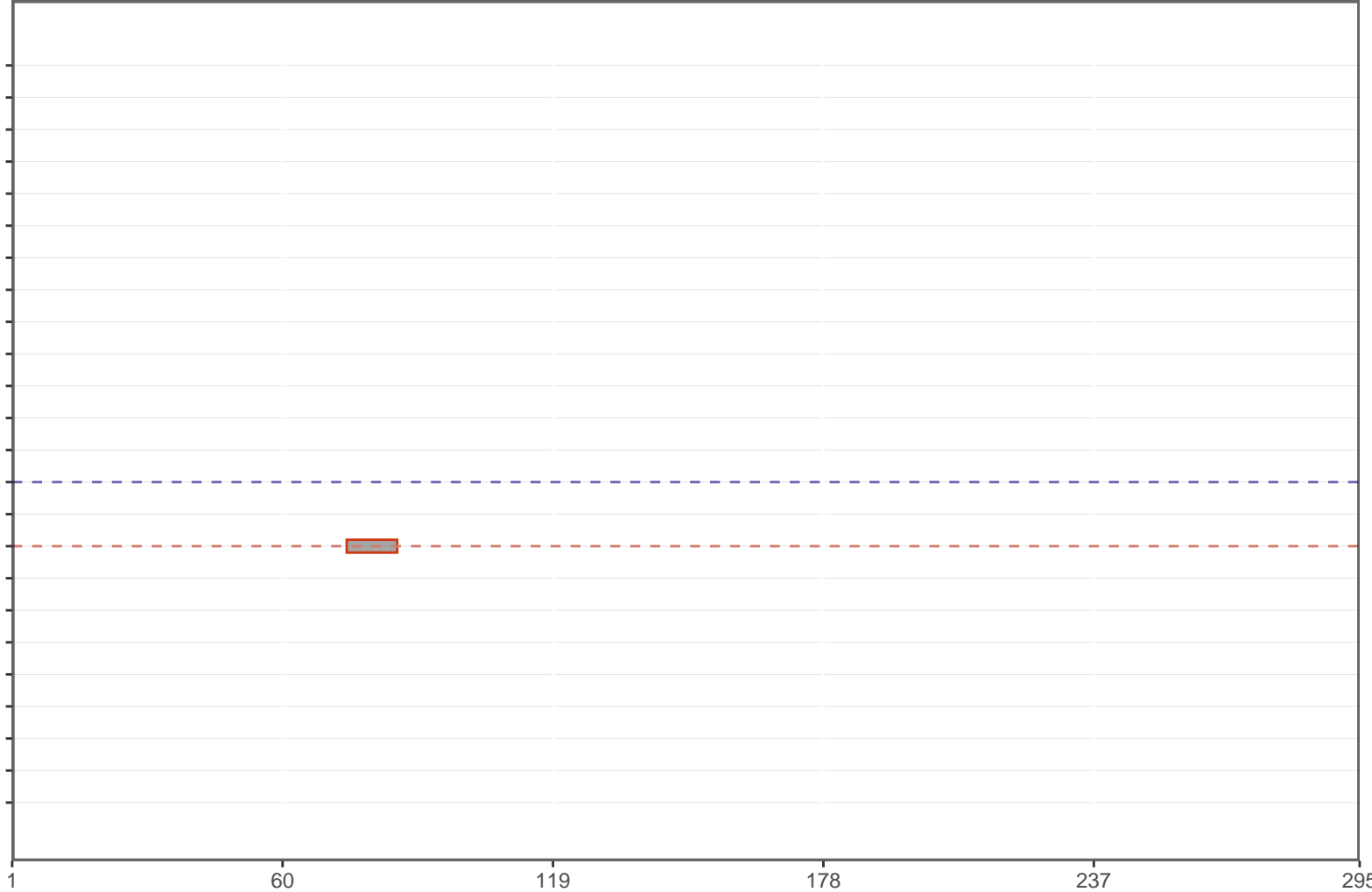
MW indication



Molecular weight

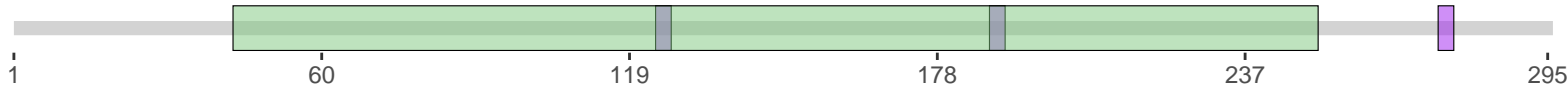


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VMPETTLISKVOREBLLLVADINAVGFLVIRKHMWPLKAGGGSGTDKDFAVANLSARVGGSDNLGGWHSYRAKTKALNQLTRNVAEFARKKDPICILLHPGTVDLSEKPFQRNVKPEKLTKEYSVQTLLEINNTKRBNGKFWAWDAGQIPW

NbL02g05060.1 obg-like_ATPase_1 [MW = 31.11 kDa]

No. of times detected



log(intensity)



Values from



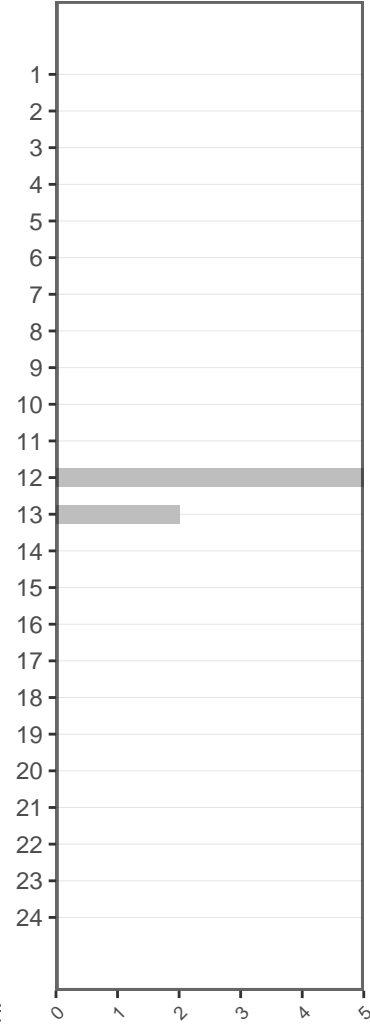
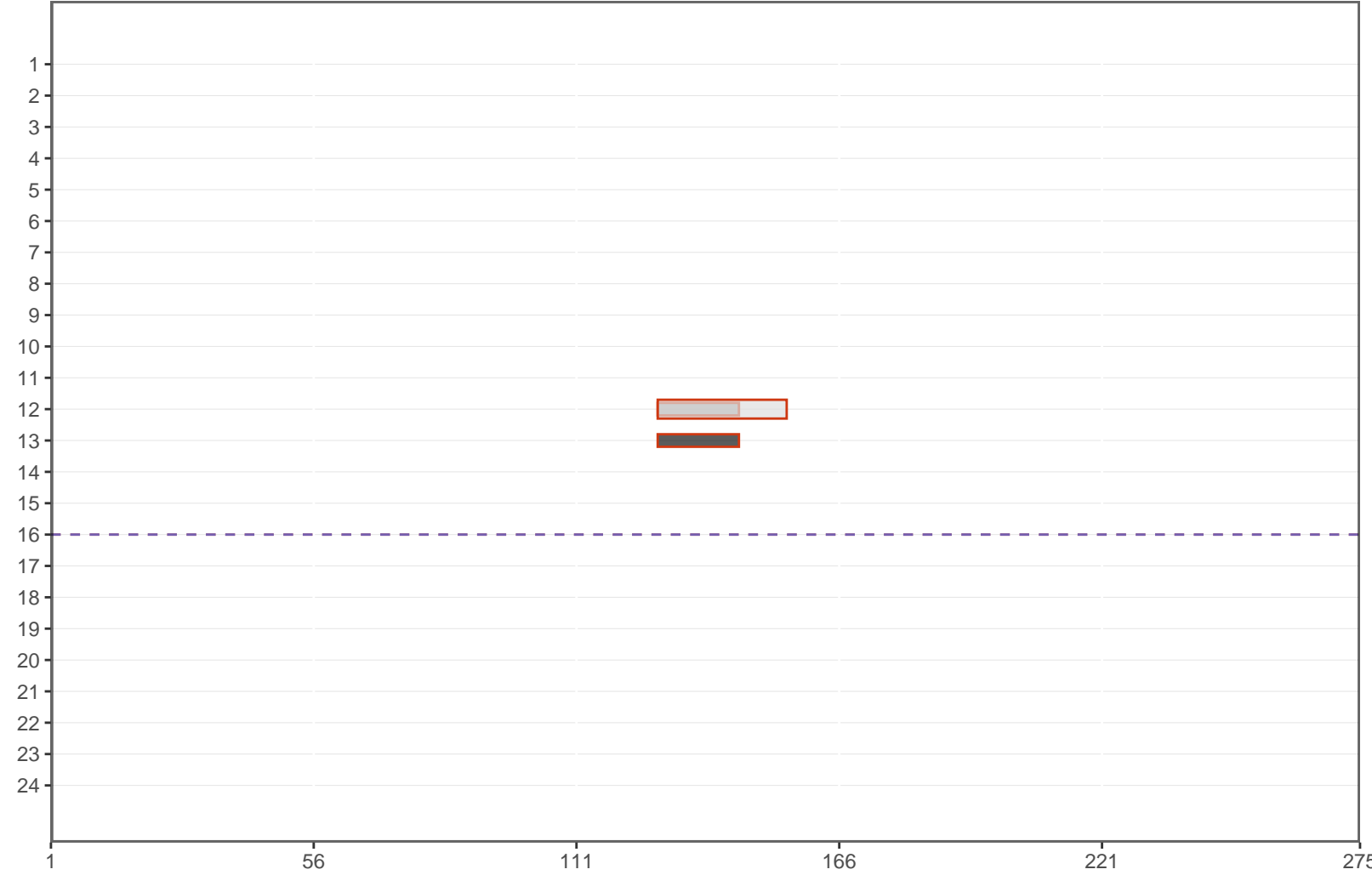
MW indication



Molecular weight

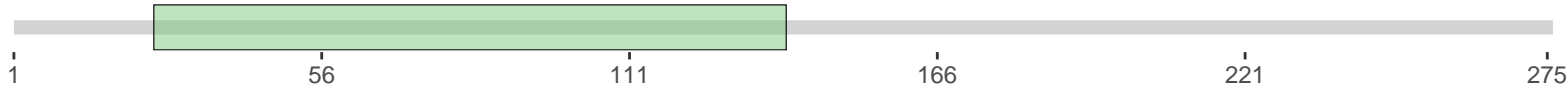


Gel Slice



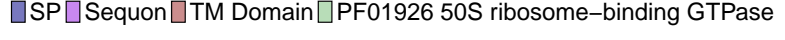
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

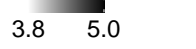
IVLRAFEDPDIHYVDNVDVPRDLRSEELRLKDFEMERRIEDLEKSMKRNDKQIKIEHLSLRVMSASLKEGDKIRLGDWKAADVFLNTFQLLTKAPVYLVNMMNEKDVARKKQKFLPKHAWVQEHGSGEIRPFSAAVRETLIGH

NbL02g05050.1 LRR_receptor-like_serine/threonine-protein_kinase_GHR1 [MW - SP = 112.79 kDa]

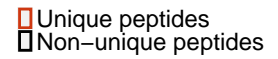
No. of times detected



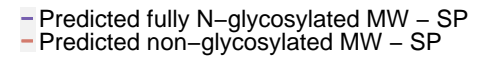
log(intensity)



Values from



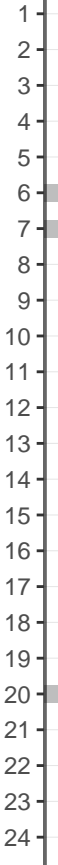
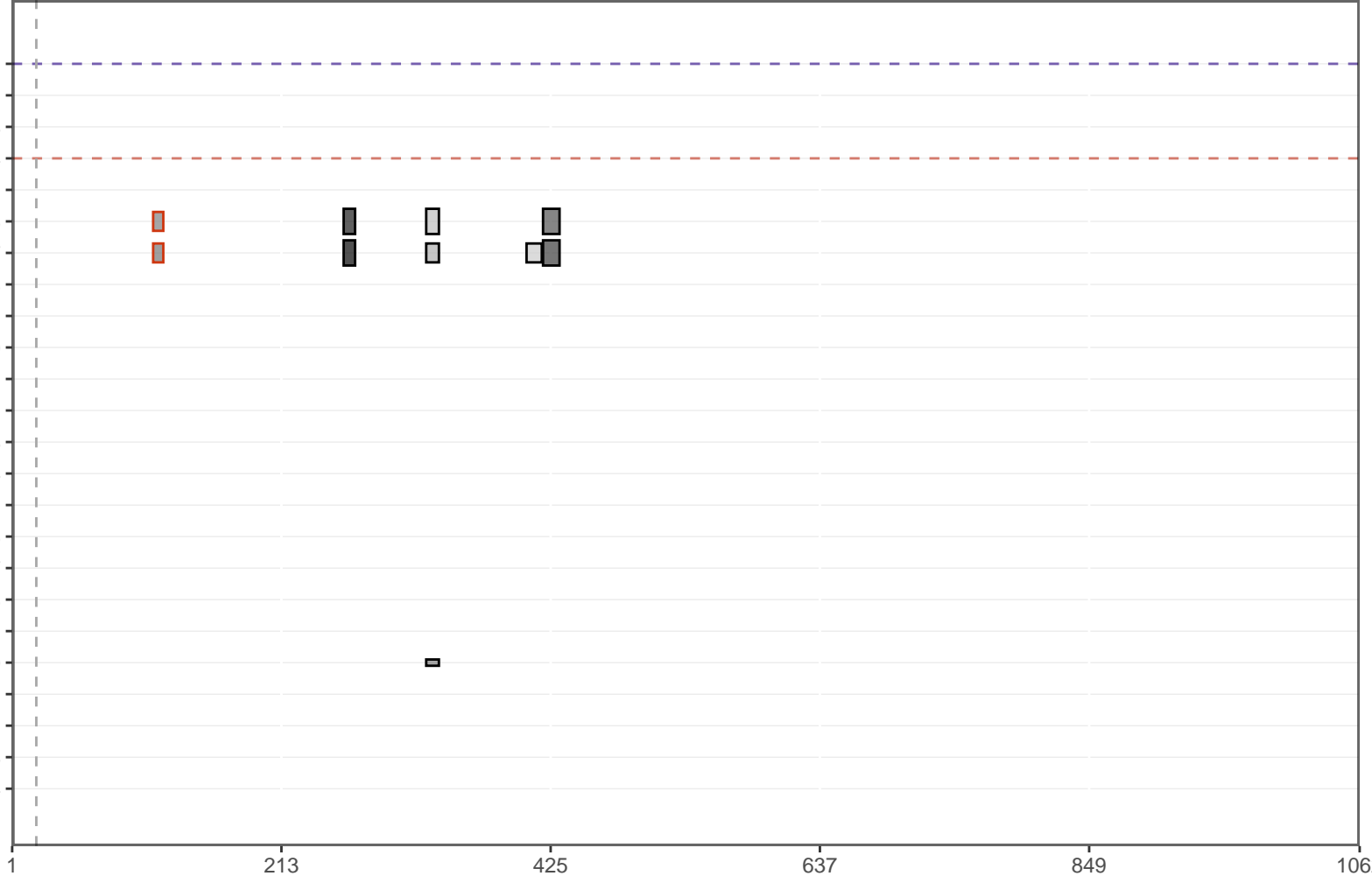
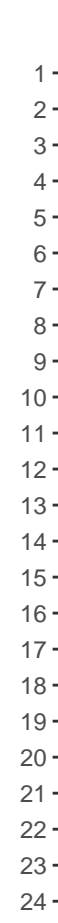
MW indication



Molecular weight

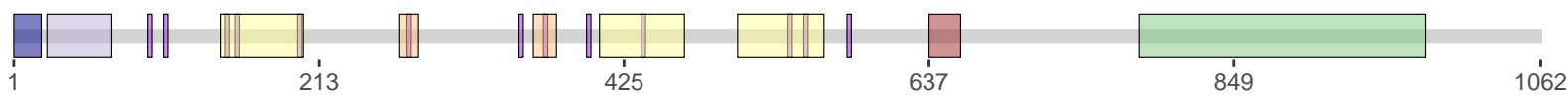


Gel Slice



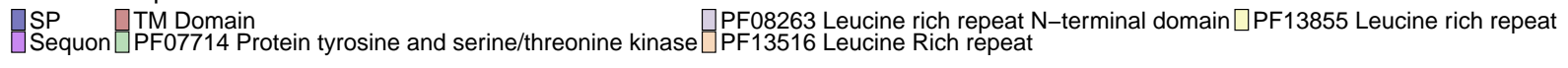
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

MDGFGSFTALQVLDIAGNNLGGSIPTSGHVSGLTSLDISENHFTGFLPKNLKNSLQSLNASLDFSGVVFQNLKRFPLSGFYQNSLQGFNPPSGGQAGSTENHRNKQLTKIKVIVAGVYVAIVLLAFIYLRAPRKPAQGMKKNVRRQAQSTPFAFSSREIVAGGVVYVAGQVATSRKASSSEHSPDCKMAATGFSRPSKASHFTWSPESGGDSYTAESLFRLLDVRPDPDLAGELYFLDQTSFTAELSRAPAEVLGRSSHGTEYKATLQNGLLLFYKWLREGVAKQRK

NbL02g04970.1 L-ascorbate_peroxidase_2_cytosolic [MW = 27.41 kDa]

No. of times detected



log(intensity)



Values from



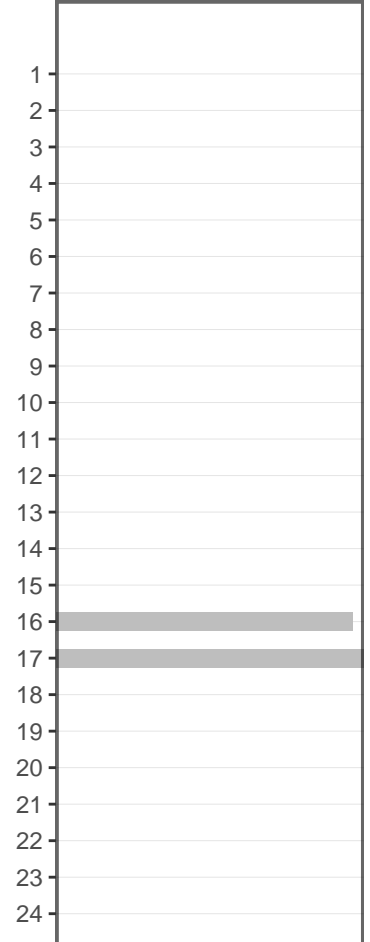
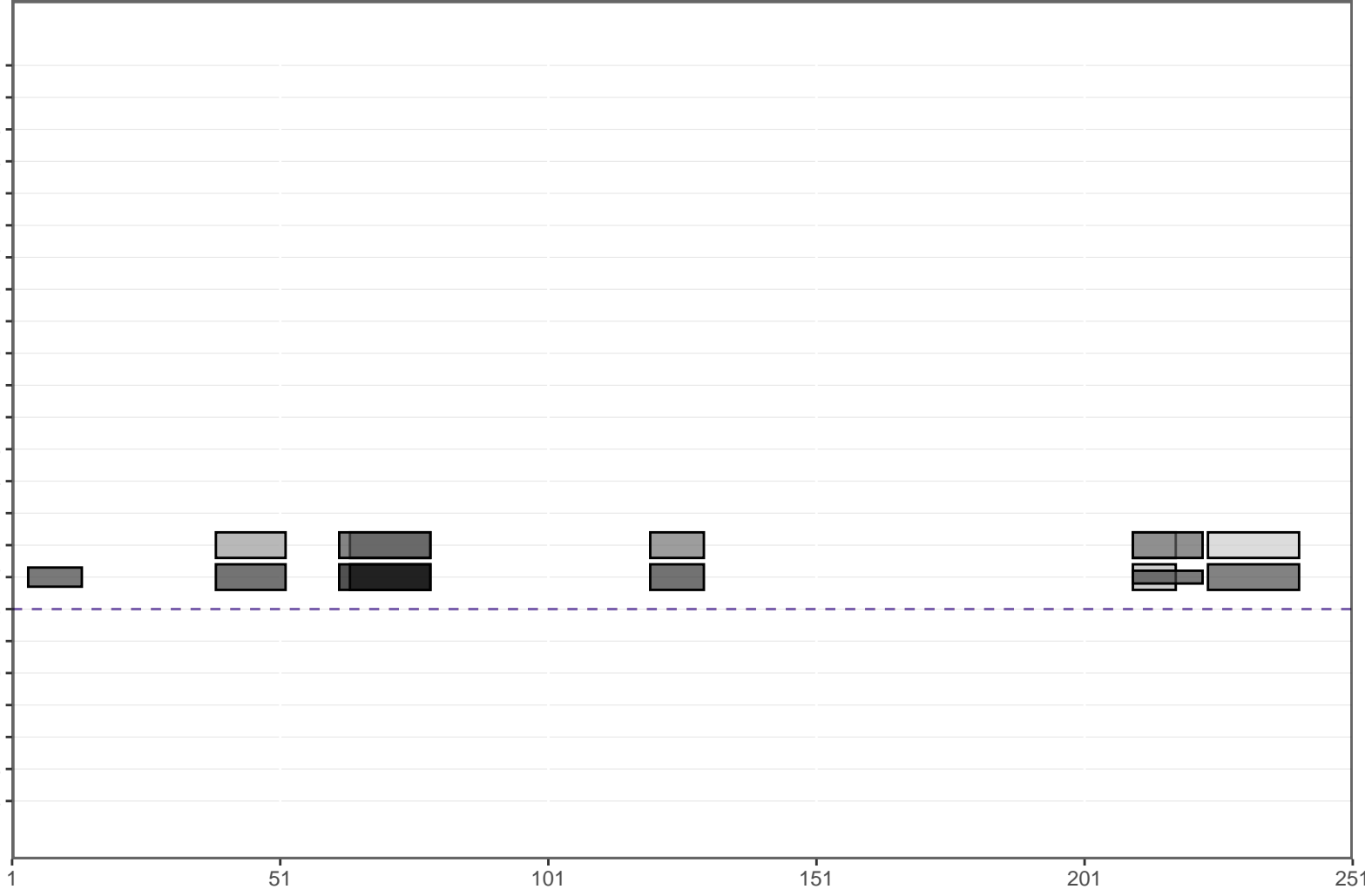
MW indication



Molecular weight



Gel Slice

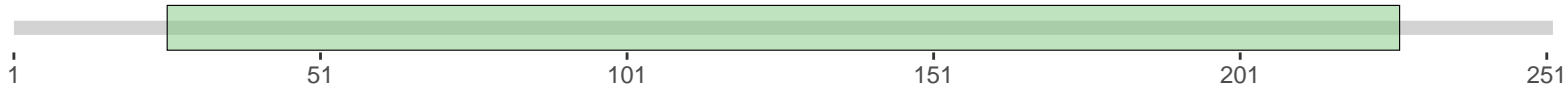


Peptide counts over 4 repeats

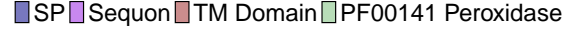
Protein length



Pfam domains



Pfam Description

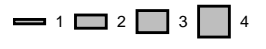


Protein sequence:

V/PFIPGREDKTEPPEVGRLPDQTKGSDHLRDVFVWQMGKSDKDIKVALGGGHTLGRCHKERSGFEGPWTFTNPLIFDNYFTLLSGEKEGLQLPBDKALLGDPAPFRPLVEKYAADEDFFADWAEHLKLSLGFRAEY

NbL02g04860.1 elongation_factor_1-alpha-like [MW = 49.3 kDa]

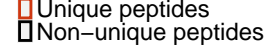
No. of times detected



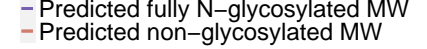
log(intensity)



Values from



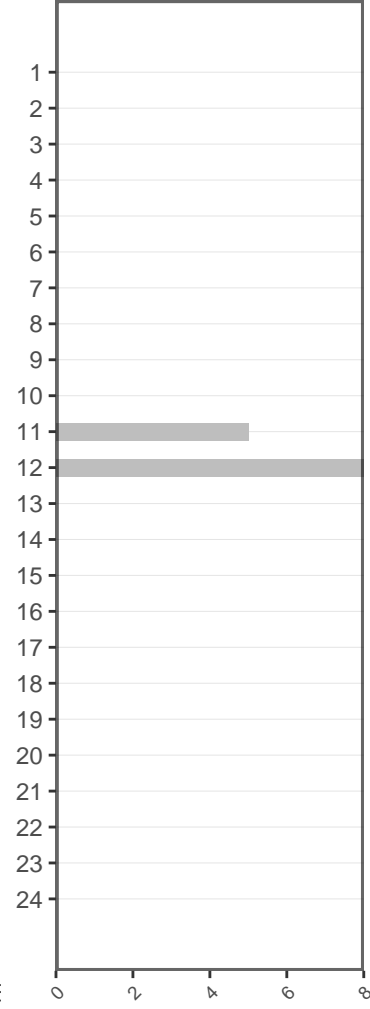
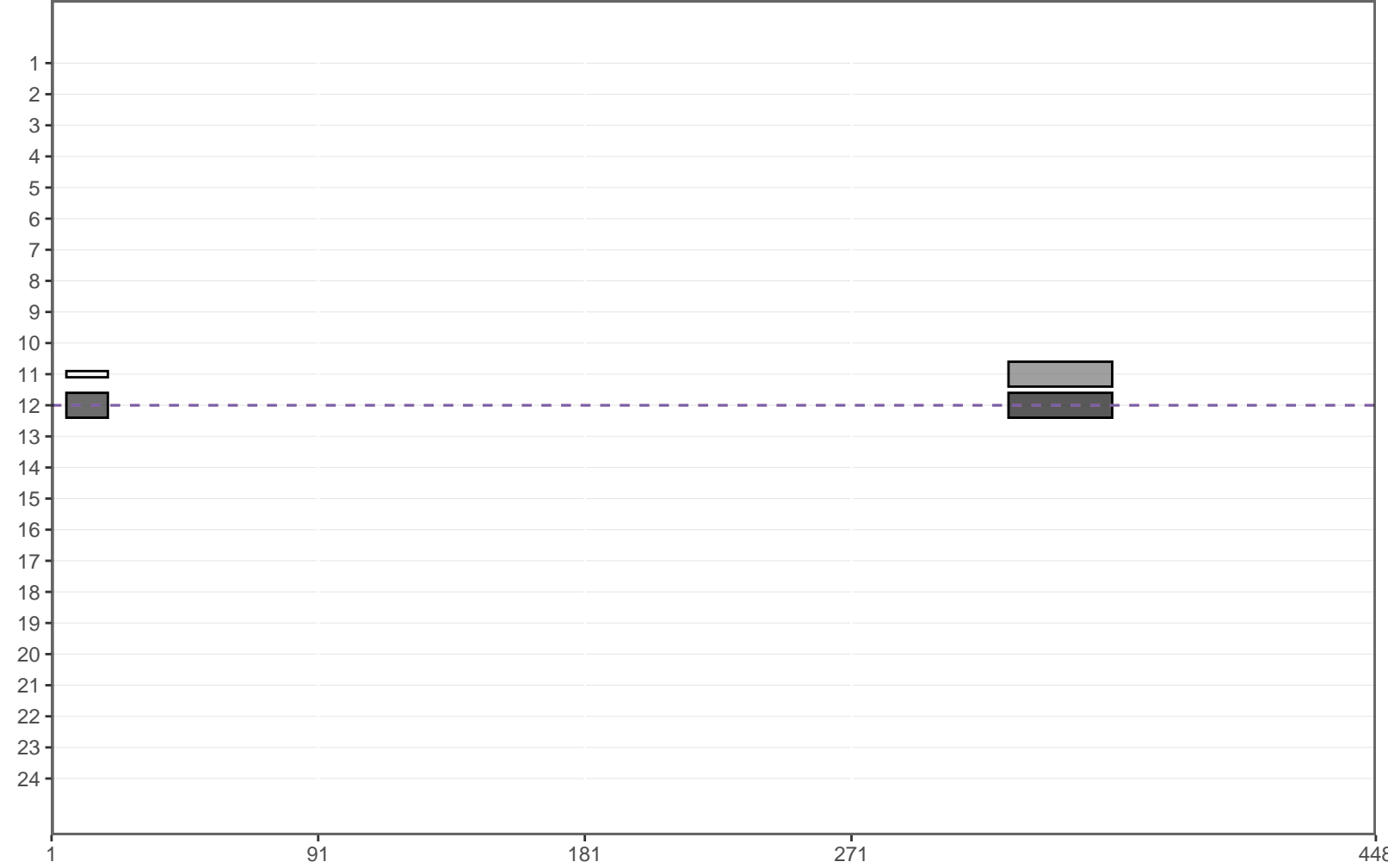
MW indication



Molecular weight

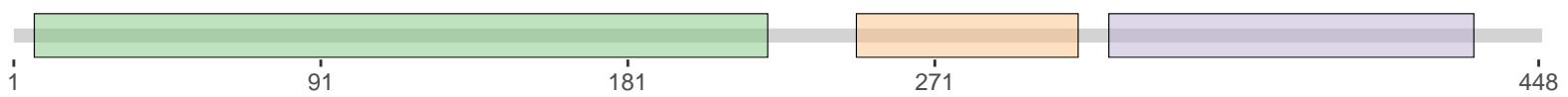


Gel Slice



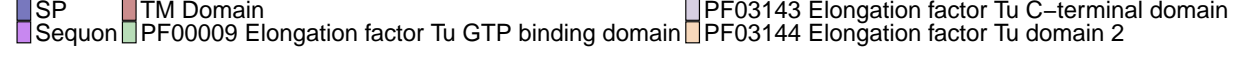
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

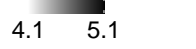
SPTLLEALDQNEPKRPTDKPLRLPLGQVYKIGKGTVPVGRVETGVLRKPMVYTFGPTQLTTEVKSVEMHHEALGQALPGDNVGFNKNVAVKDKLRGFAVSNKDDPAKGAASFSTGQVIMNHIPGGKNGVAPVLDGHTSHIAVKAFAELTKIDRRSGKELEKPKFKNGSDAGMVKMPTKPMVYVETTFSEYPLPLGRFAVRDMRGTVAWGVIKKNVKKDKPTGAKVTKAAGKKK

NbL02g04820.1 proteasome_subunit_beta_type-4 [MW = 27.88 kDa]

No. of times detected



log(intensity)



Values from



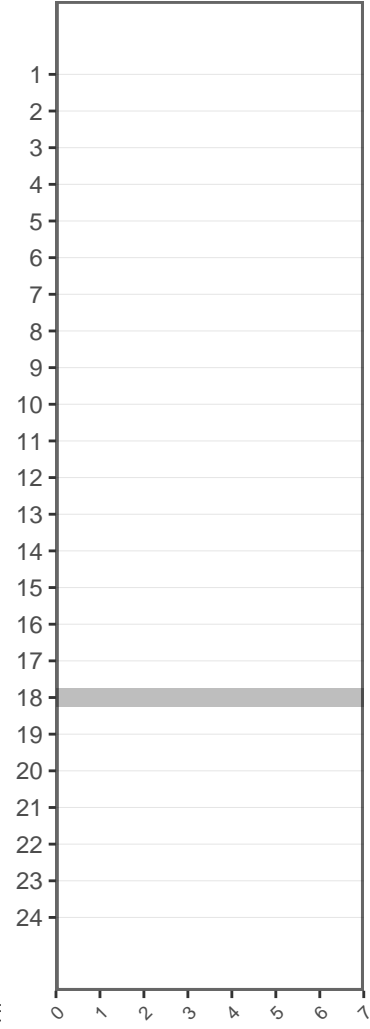
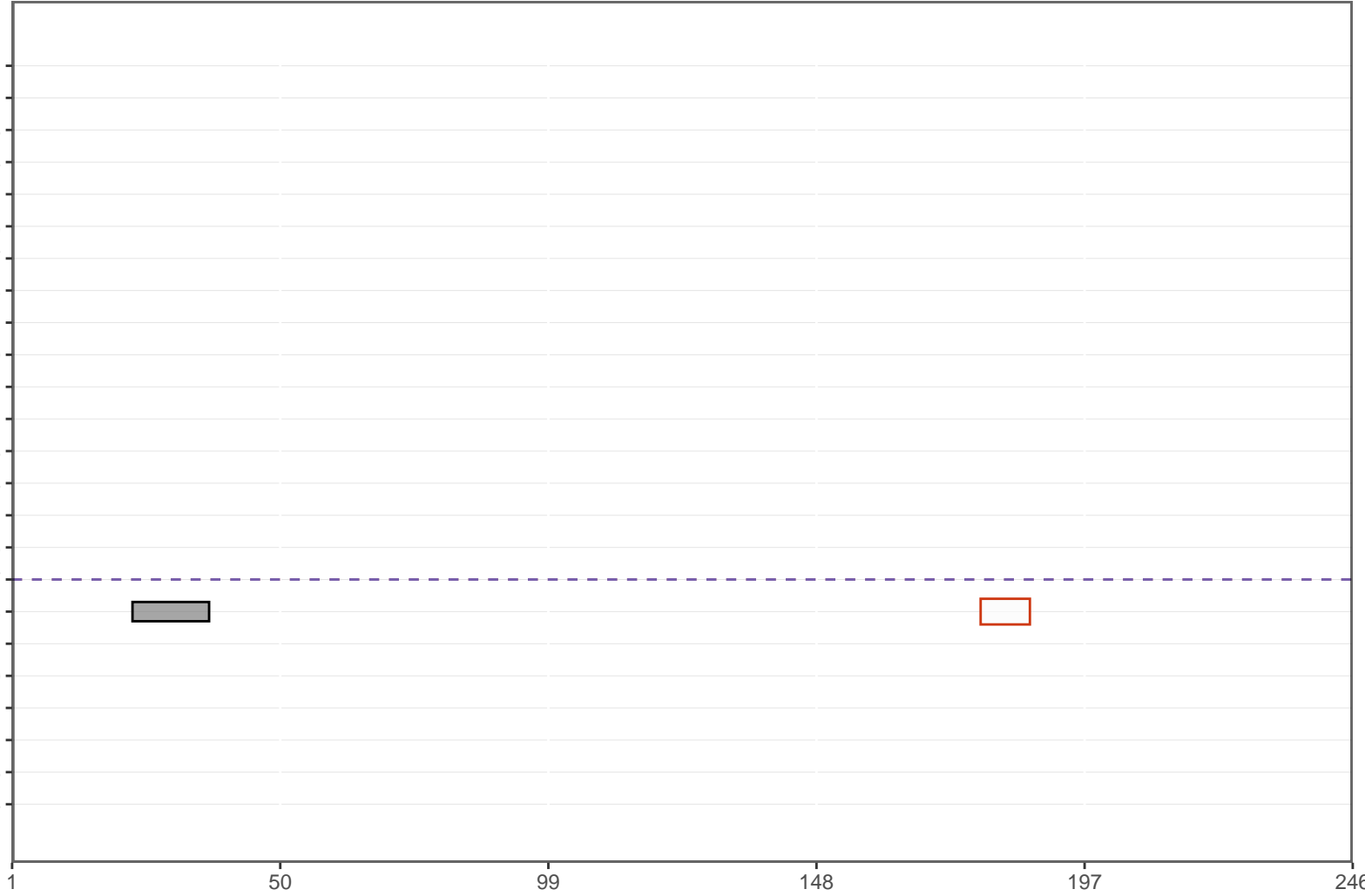
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

NYLTRMAYNRKINFLWNSLVLGGVKNQKYLGTVMIGVHYEDNHVATGFGNHLAKPIHDEWRDMSVEEGVLLKCKMRVLLYRDRBVAVKLGMGLDMLQLLLAETGTAASEFDFTSFYEGQIMVTPTMW

NbL02g04680.1 PIP2-4-like [MW = 30.73 kDa]

No. of times detected



log(intensity)



Values from

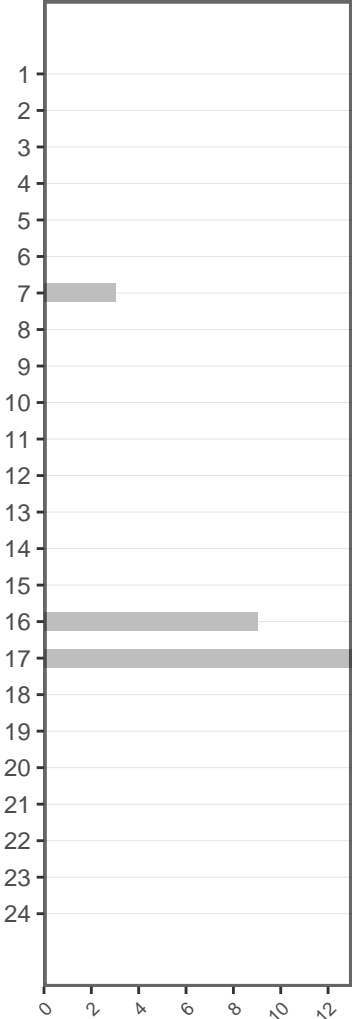
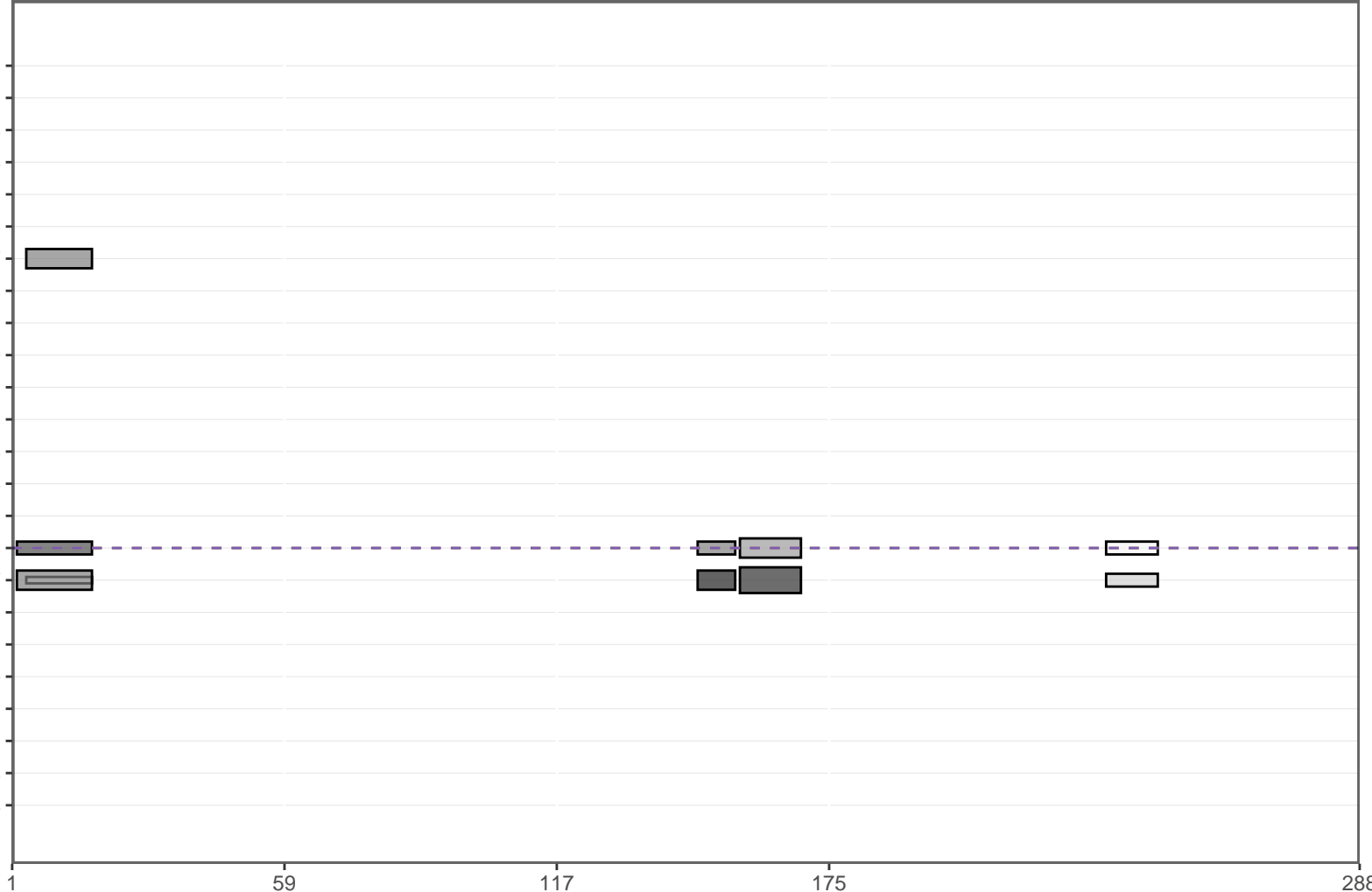
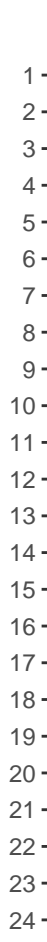


MW indication



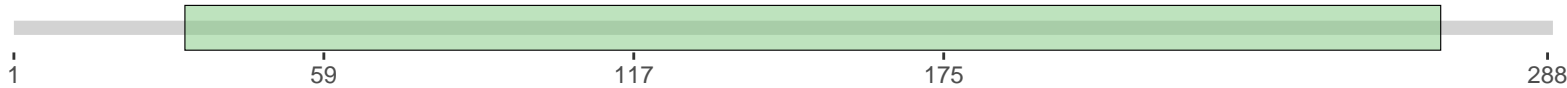
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

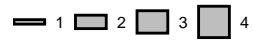


Protein sequence:

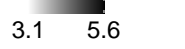
IQCLGALCGVGFVYKAFQSAIYVRYGGGANVMPGHHTKGVGLAEIGTFLVLYVTSATDPKRNARDSEHVPILAPLPIGFVFMVHLATIPITGTGINPARGFGAAVYVNHKAWDEHWFVWGFPGFAAAVYHQFILRAGAIAKLGFRSNAV

NbL02g04530.1 polyadenylate-binding_protein_8-like [MW = 70.46 kDa]

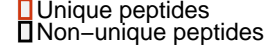
No. of times detected



log(intensity)



Values from



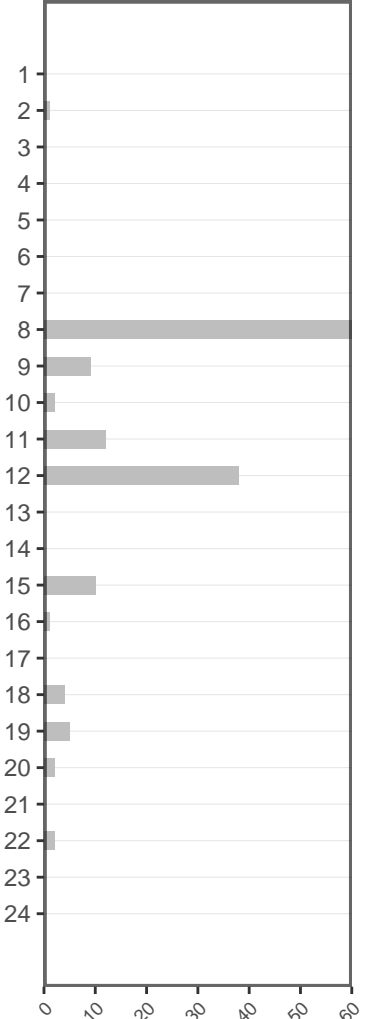
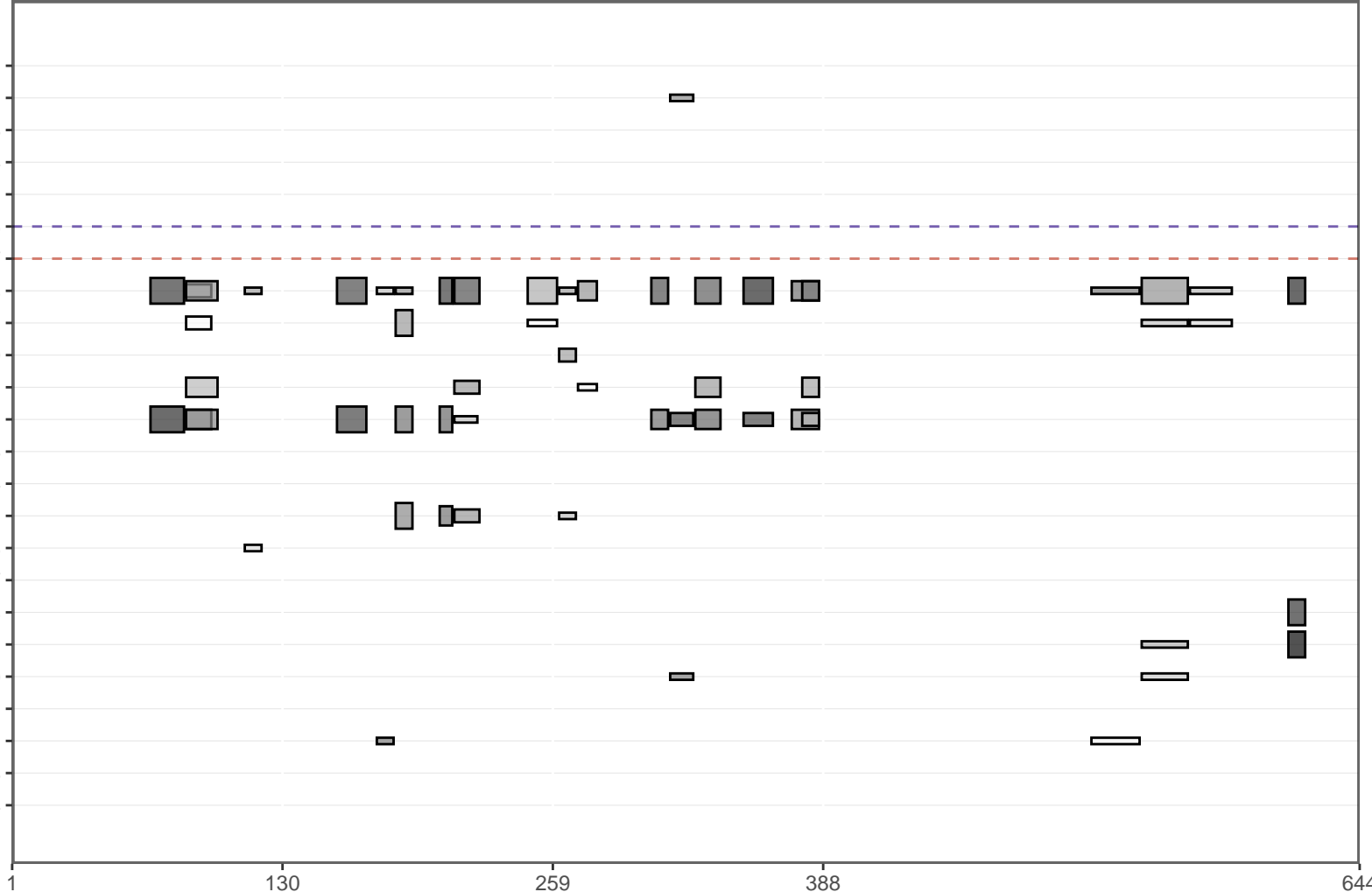
MW indication



Molecular weight



Gel Slice

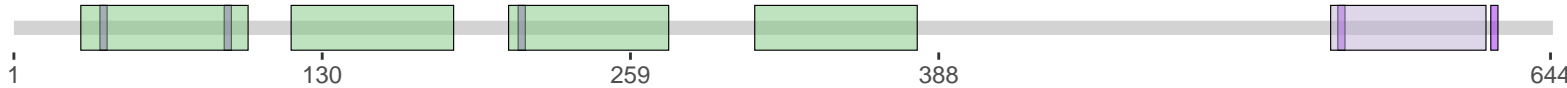


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- PF00658 Poly-adenylate binding protein, unique domain

Protein sequence:

LYIKNLDSDSDOKLKELFSPVGTTSKVMRDPGCVKSGGSEVAFSTPEEASRALSEMNKMMVSKPLVYALADRKEERRARLQAGFSGMRPMAAGSVAAPRMFMVPPGPGPLGGQIFYGGPPFMLPPGAFGYYGQQLVPGMRPGGPMNFEMPMVGGGGGGGRPGRRGGAVPLGGGGQVPLMGGQGMFPRGRGRYRYPGRGLPDGAFPGVGGGMFSPFYDGGGRVPRIPVGLATALANASPTGRTMLGENLYPLVEQLEPETAKYVTGMLLEMDGT

NbL02g04500.1 serine_carboxypeptidase-like [MW - SP = 53.97 kDa]

No. of times detected



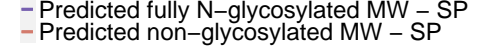
log(intensity)



Values from



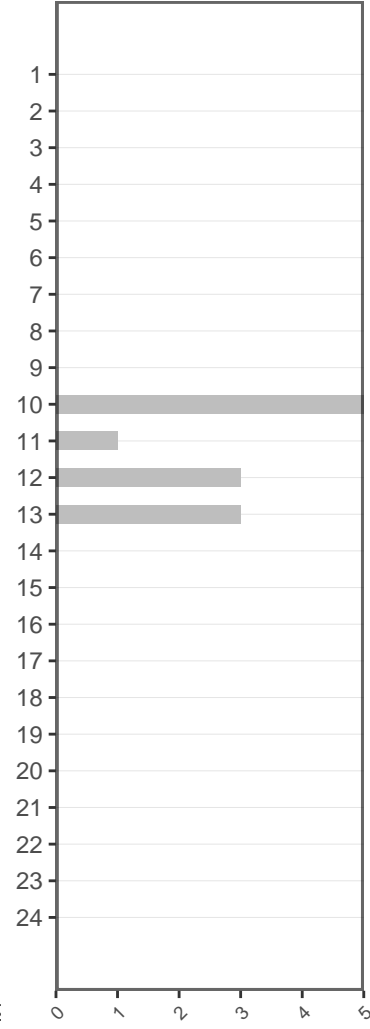
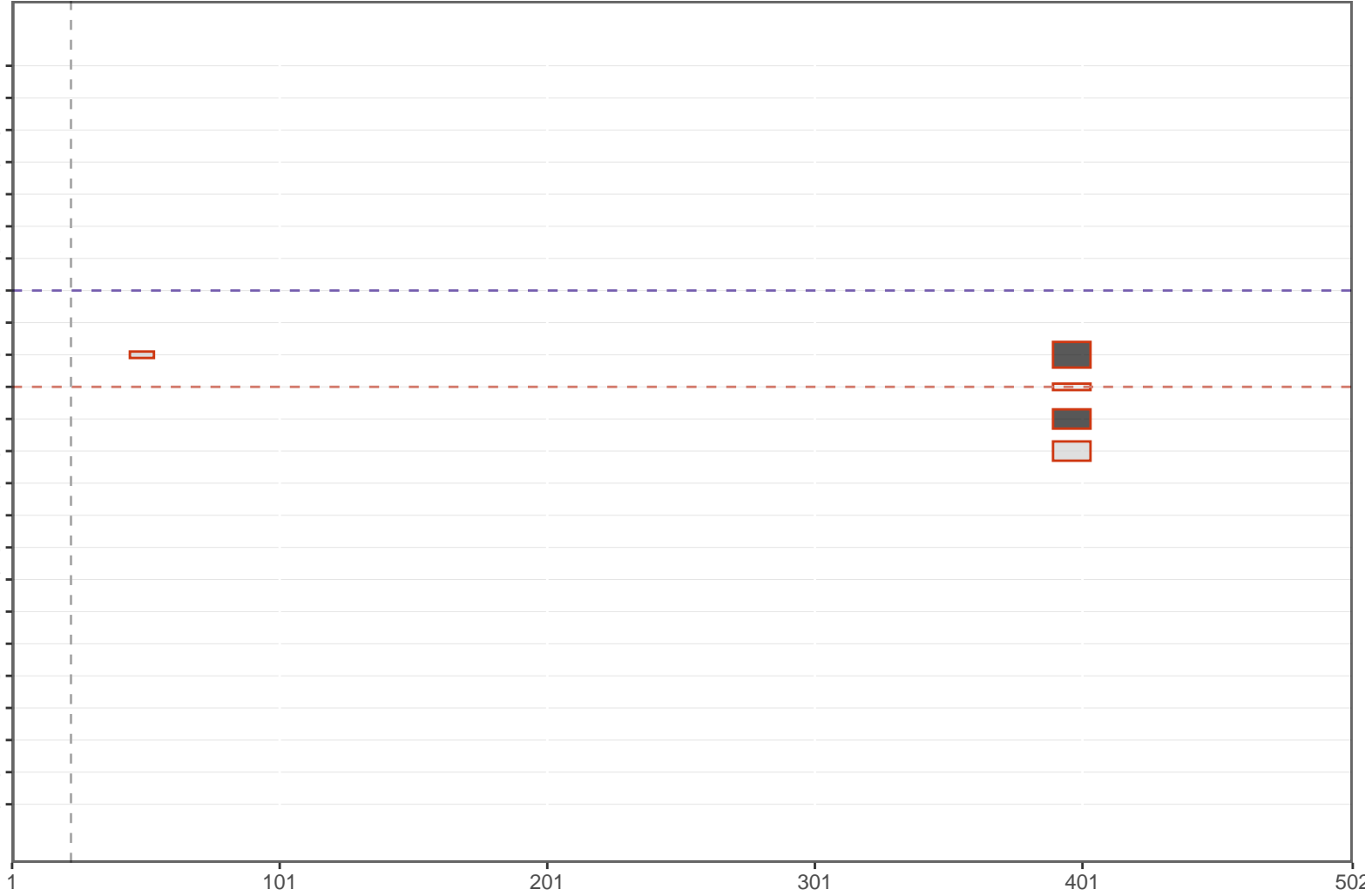
MW indication



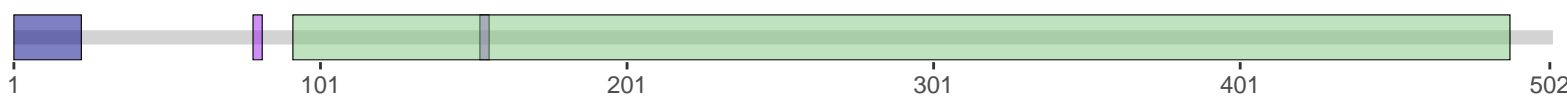
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

CGNKKKEGTHSLKGFAGNGLTFPEIHYKAYTDVALDMLRLLKADYNAIDKSYPKGGGARLRCGTDGSSAGMAAYLVCTSFNKMMDVYGDKNYDYVRKTKDGLGVDFSKMETLLNDEQVYKHALGVGGIDFVGSSTVYQAMQLDWMRNLEAGIPPLEDDIKLLVAGEYDLCGNLGNRWVWHAMEWSSGKDFGAAREVPETVDSGEKQKNGHSPFLKVKHDAGHMVPMGGPKAALEMGRWMDGKLSKEGHFAHM

NbL02g04360.1 aminopeptidase_M1 [MW = 99.26 kDa]

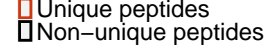
No. of times detected



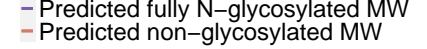
log(intensity)



Values from



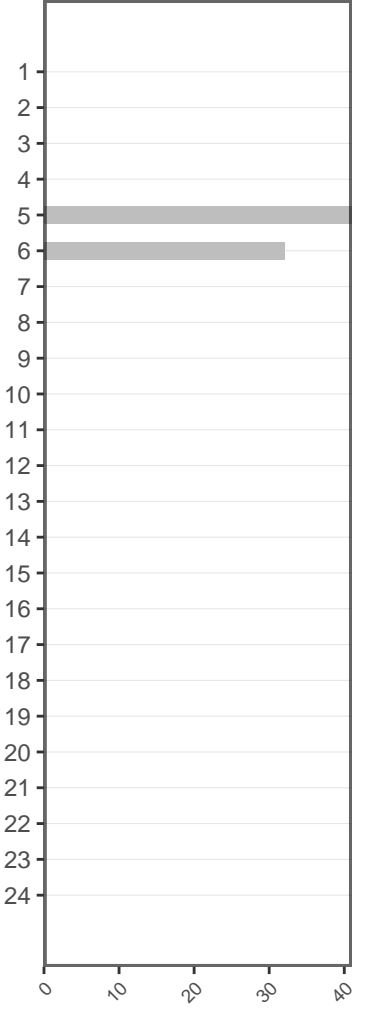
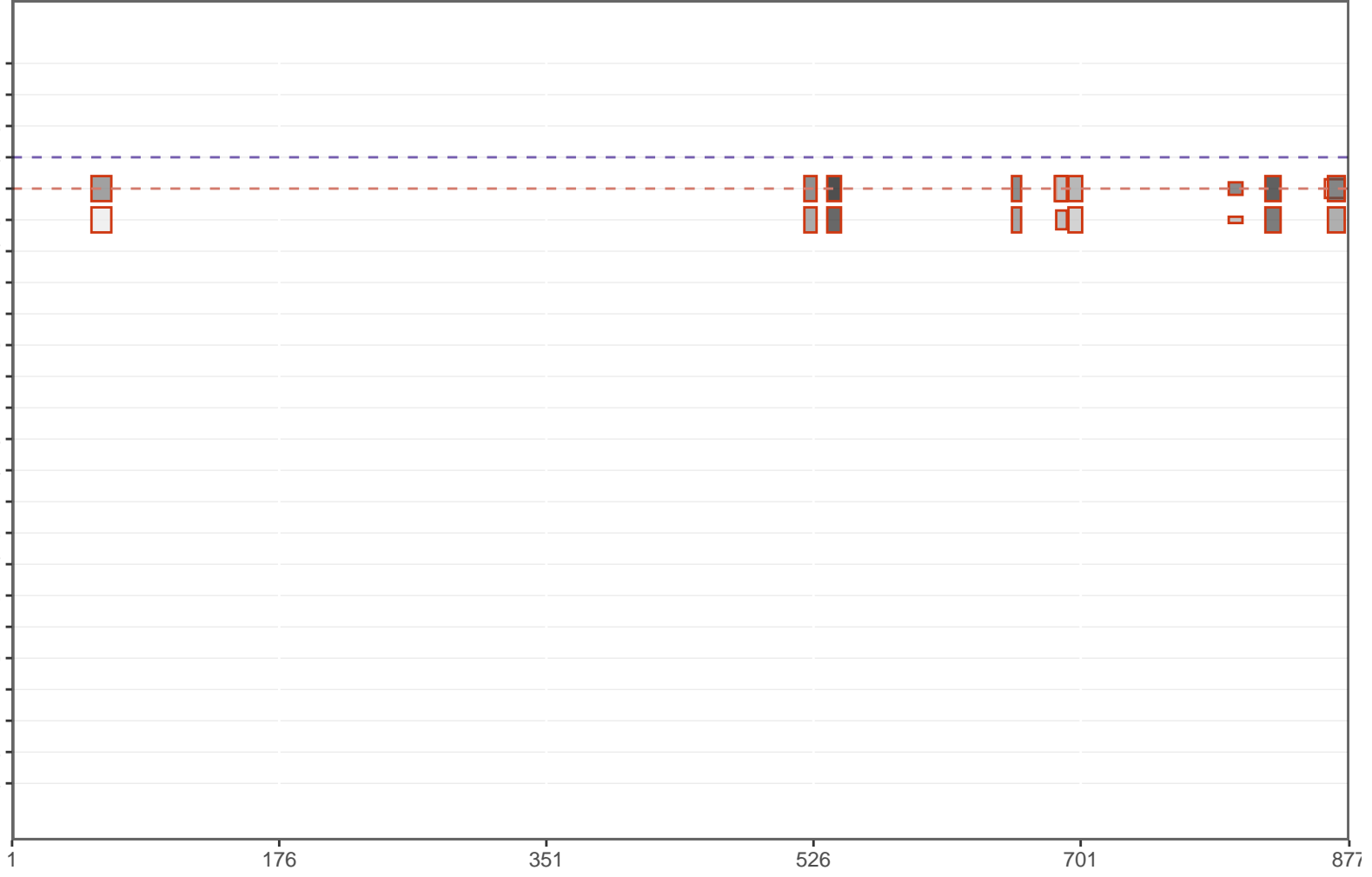
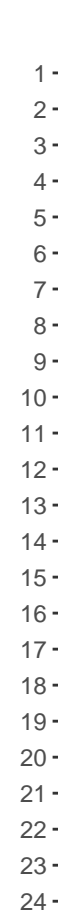
MW indication



Molecular weight

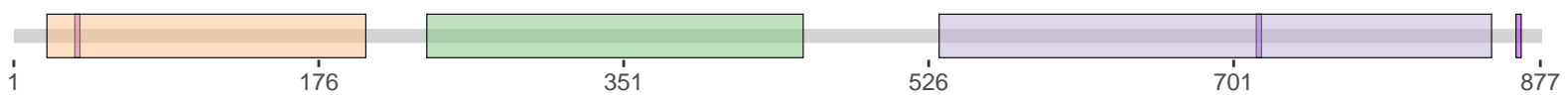


Gel Slice



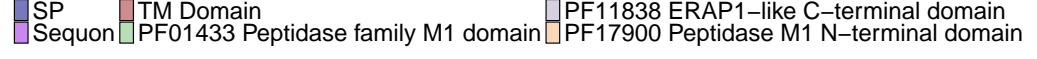
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CSNAKTEDLVSYVLSGEESEPPNMLMNSWTKGGGYPVYVVKIKDKQKLEGGTQIFLLSGSHGGGQWNPFLTCGGGYEVCKKFLMGEKSEALVDKLLSGSSKGNFPWIKVVEQTGFYRVYKVDDELSARLRYMESKGLSTNDKYGLDDGVALSMAGHGSLLSLLALMASFREELDTVLSNLISGYSYKRSIAADAVPDLKDHKLFNINLQFSAERLGGWDPKGGGERHLDMLRGELNVLAAFGHDETLEAIRRFHFLDNRNTALVPPDLRRAYVYVWQQRVYKSDR

NbL02g03980.1 21_kDa_protein-like [MW - SP = 19.1 kDa]

No. of times detected



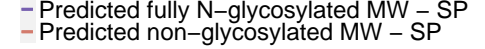
log(intensity)



Values from



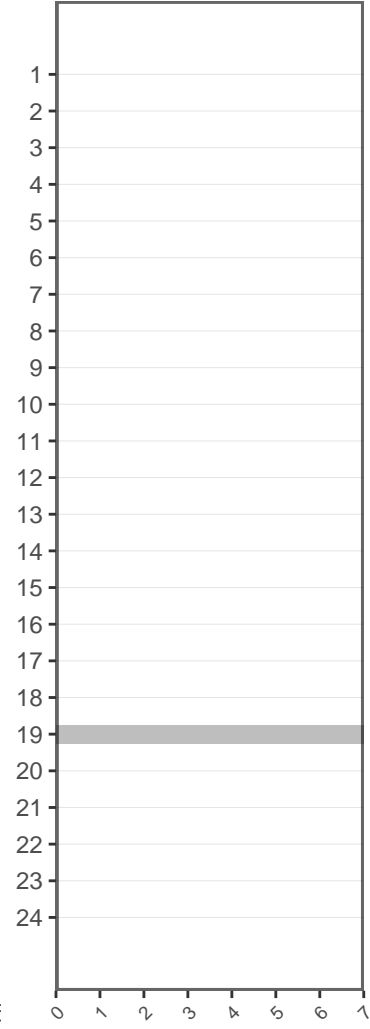
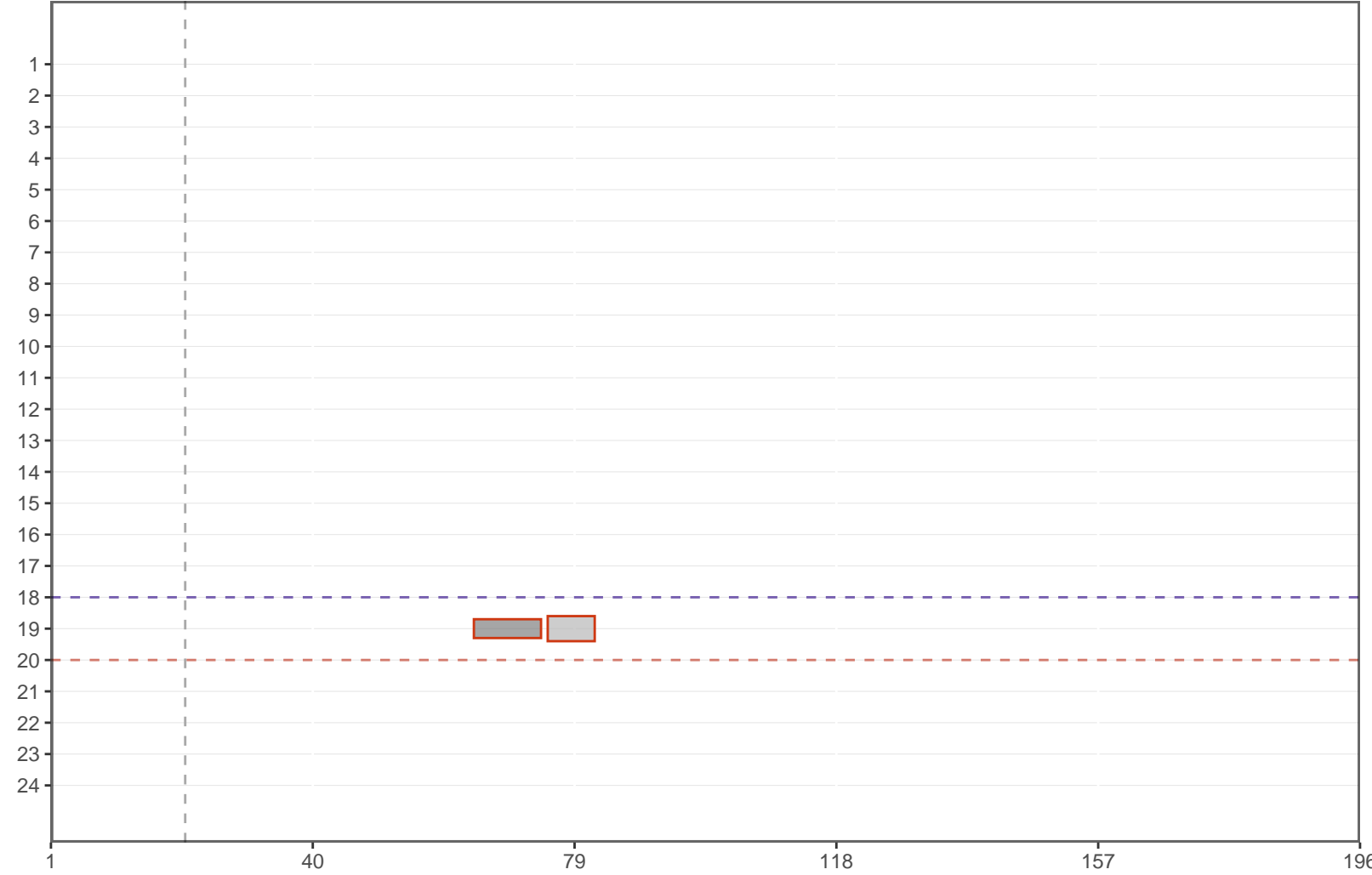
MW indication



Molecular weight

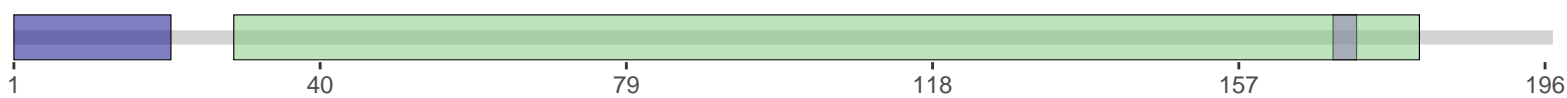


Gel Slice



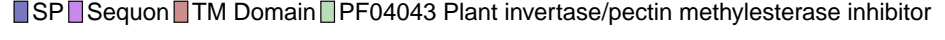
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

INSLKRRGRVALLDCVEGFDALDNLHNLSLGVLRKLSGQTFNDQMGVFTVLSAALTDSDTGLGGFDGRRRKGVKLLNRTNVGVMTSNALAVNLATTGPECLQNS

NbL02g03910.1 protein_MET1_chloroplastic [MW = 36.05 kDa]

No. of times detected



log(intensity)



Values from



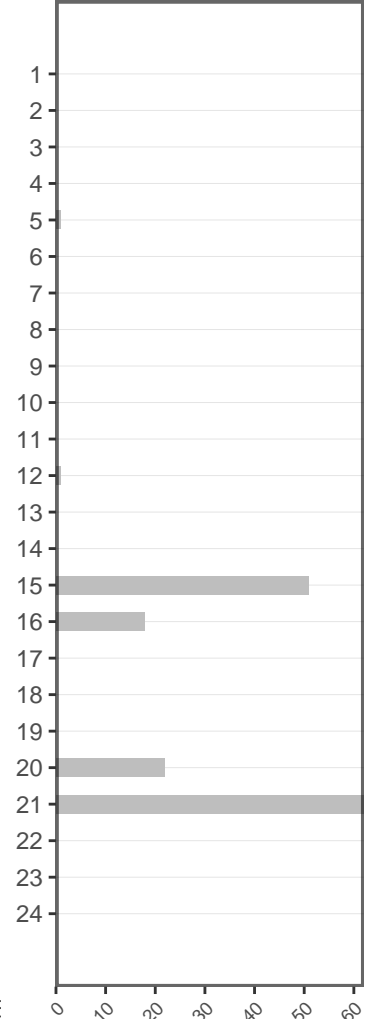
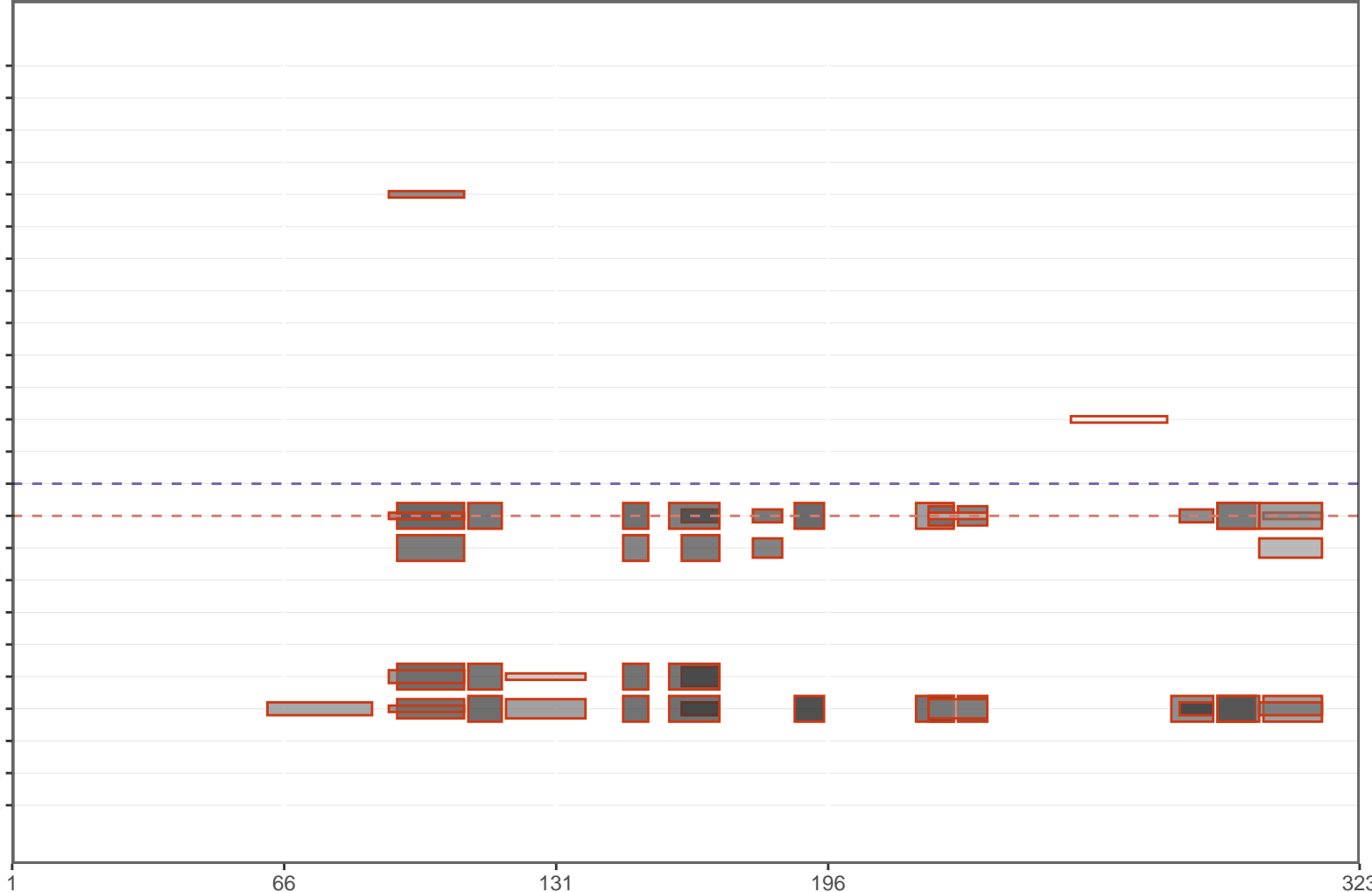
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

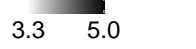
IPLLMAMKRYGKVEEAGELTEKIHRAERNAGFISDRVREIGLNTNARRKKEKREKDLREGLQLSKNGKYEEALEKFSVLGRPTGNAEAAWAGVYVWAGCYSKLNQLGAGLSALEDDAMDAGDFDFKRIKRTDPLANLRSDAYEPLMKKDFESFINENAINAKILFGFNK

NbL02g03890.1 lysine--tRNA_ligase_chloroplastic/mitochondrial [MW = 67.63 kDa]

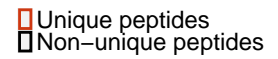
No. of times detected



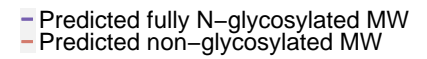
log(intensity)



Values from



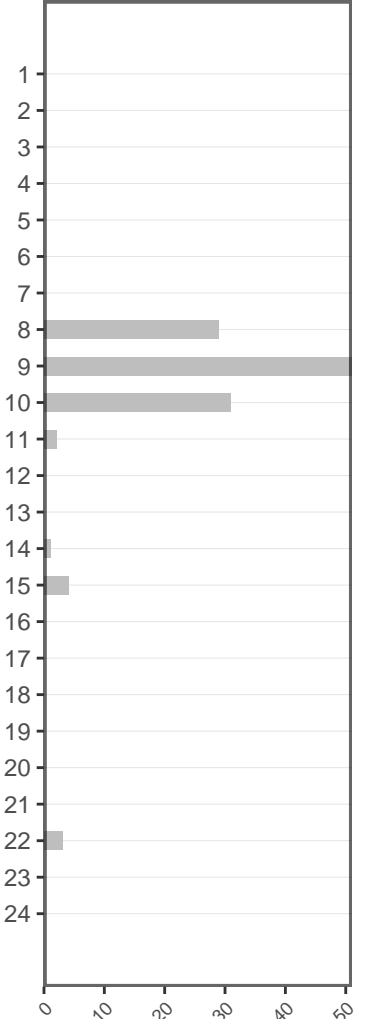
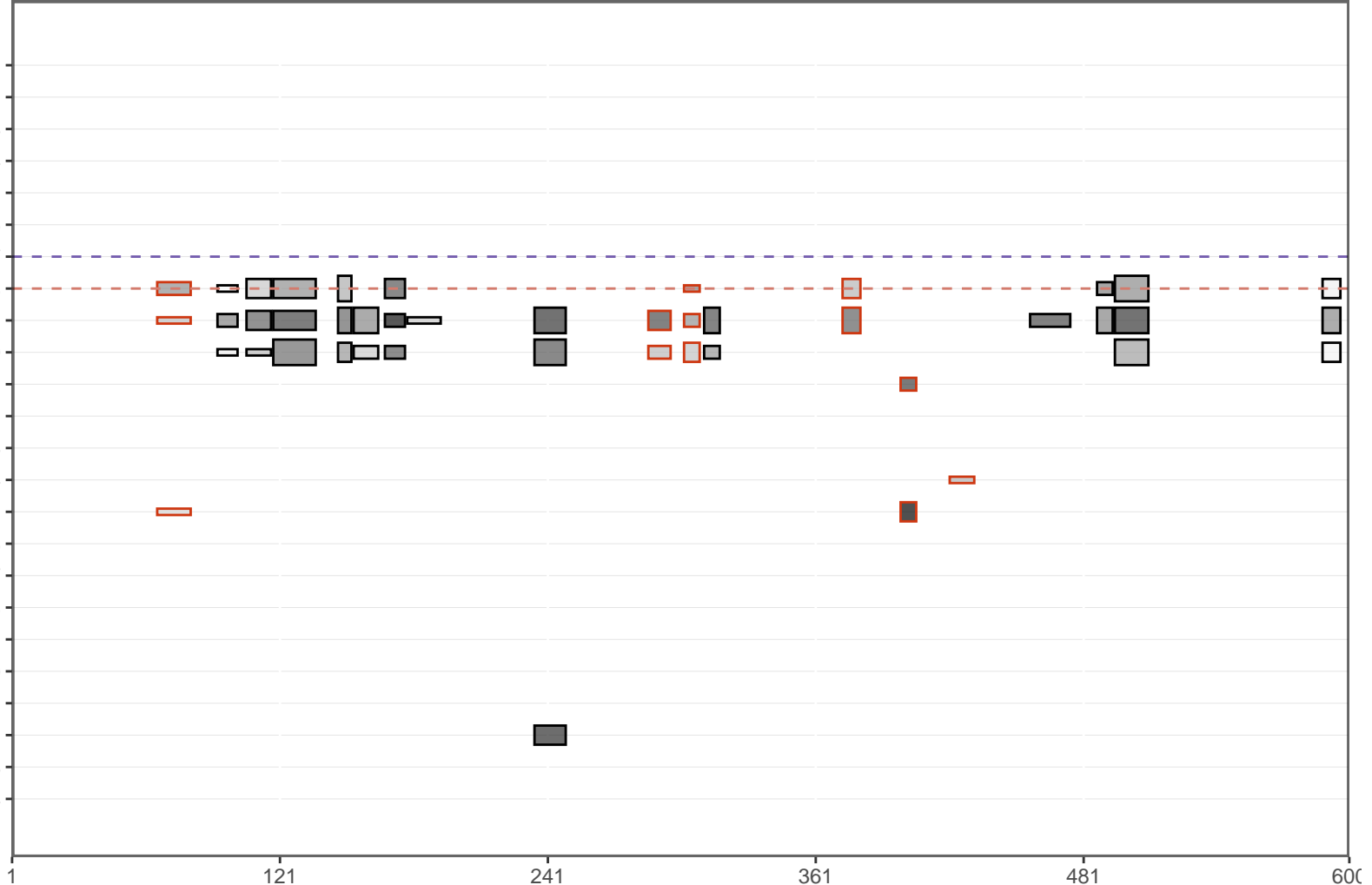
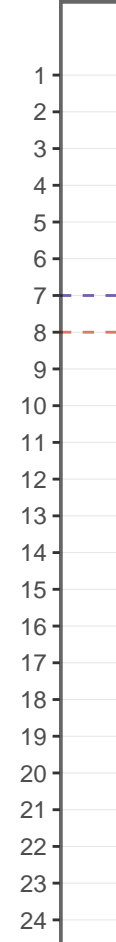
MW indication



Molecular weight

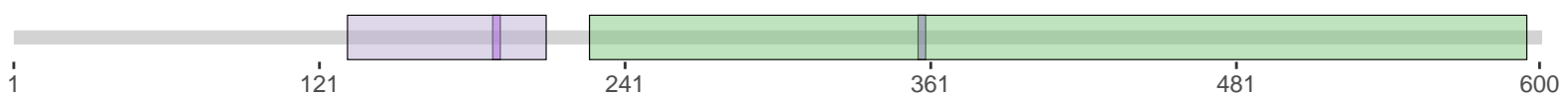


Gel Slice



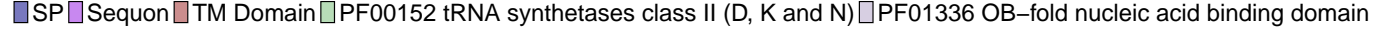
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PFITYNLSLGRDLYLRATELHKRMLVGFKEVYKIGRFRNEGISTRHNPEFTTIEYEAAYSDVSEMMNMTSEMTRCALVNGKLIHDVGGVNGICLERPWRRETMHNLVREATGIDFRNFGDOLKAAKEHSRKAIDLGDMDKGGSEACSGVGHLLNEVFEMLVPEKLGPTFVLDYPIESPLAKPHRHSGLTERFELFCIGRELNAFSELTPLDQRRRLLEEQVYKQHNENKKAASGLNKADADGGENKDDDDNSVEYVTLDEDFLTALEYGMPPASGMGLGIDRLVLLTI

NbL02g03870.1 isocitrate_dehydrogenase_[NADP] [MW = 46.78 kDa]

No. of times detected



log(intensity)



Values from



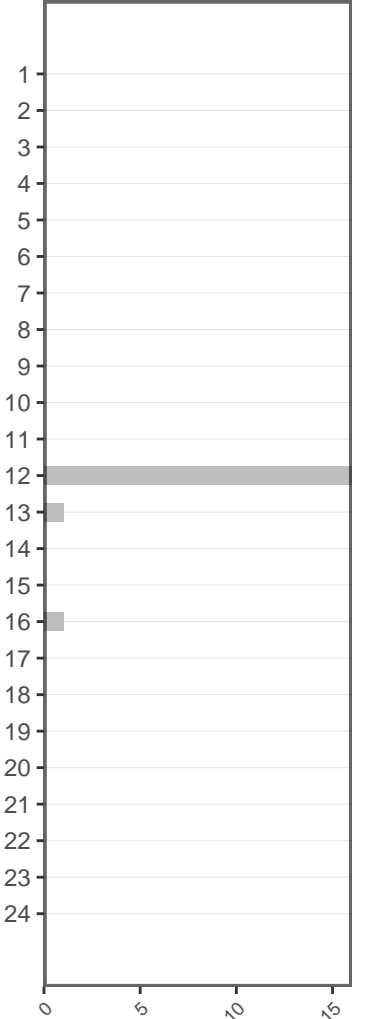
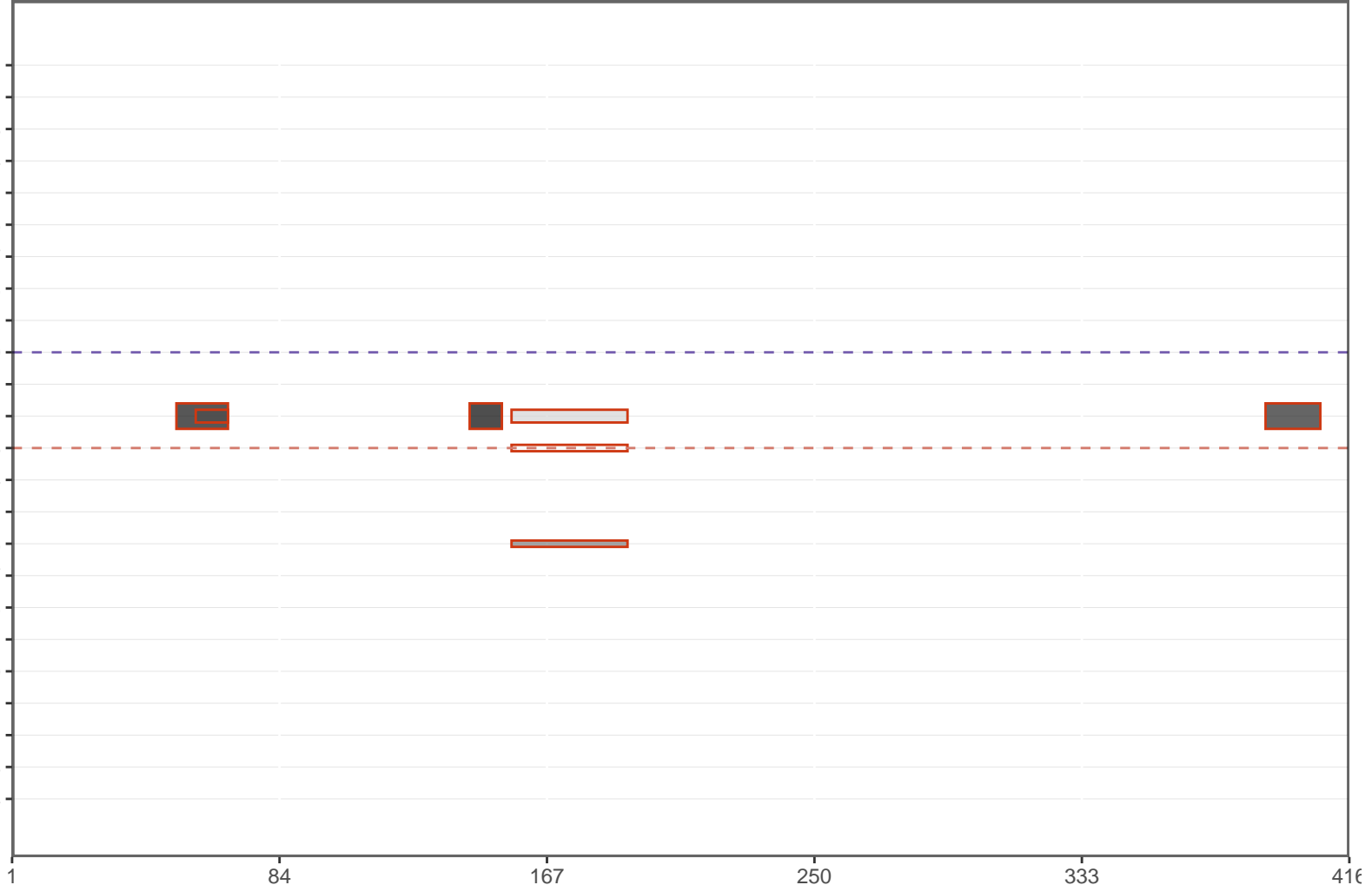
MW indication



Molecular weight

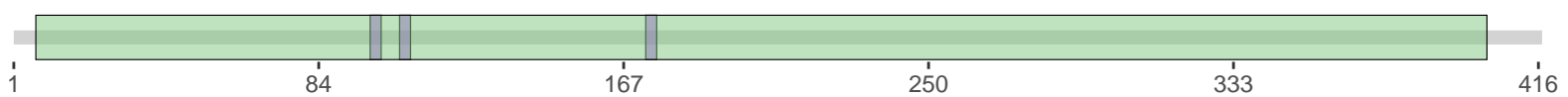


Gel Slice



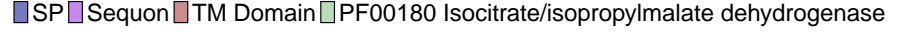
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ASMINMAYQKKWVPLSLSTKNTLKKYDGRFDFQVEVYEAHWKSKYEEAGWYEHRLDDMVAVALKSEGGYVWADKNYDGDVQSDFLAGDGLGSLGMLTSLVLCVDPDKTIEAEAAHGTVTRHYRHHQKGGSETNSIASIFAWTRGLAHRATLQIKNERLLDFTKLEAACIGAVESGKMTKDLALIHGSKLREHYLNTFEEDAWDELKARLLKAKA

NbL02g03800.1 UPF0061_protein_azo1574-like [MW = 43.09 kDa]

No. of times detected



log(intensity)



Values from



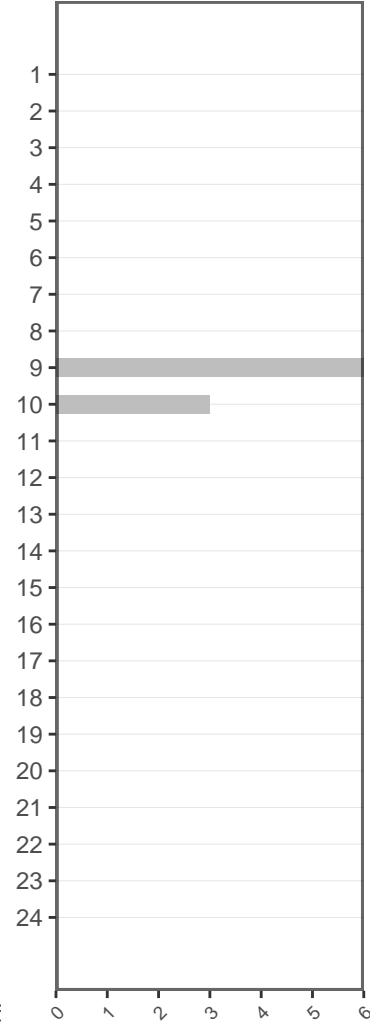
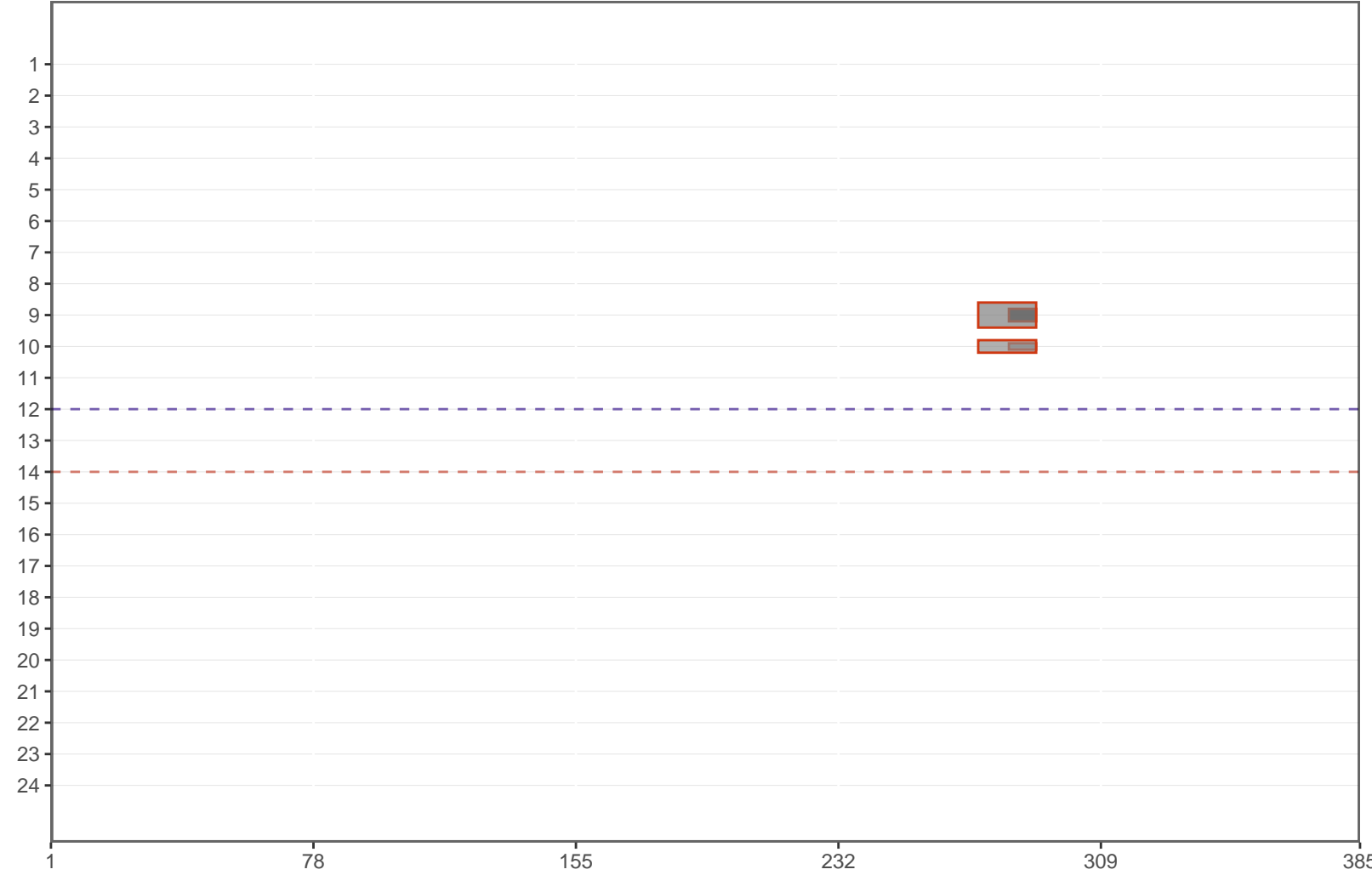
MW indication



Molecular weight



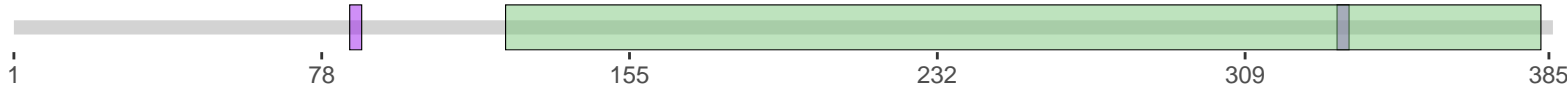
Gel Slice



1 78 155 232 309 385

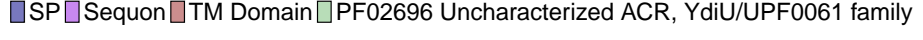
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AQNYYGHQFGQTVWAGQLGDGRATLGEVLNKSERVELQKAGKTPYSRFADGLAVLRSSREFLGSAMHSLGPTTRALGLVTTGKQVTRDMFVGDGPKDDPGAVGVAQGLRFGSYQLHARSGKQKLEIVRTLADVAIRHFFPHLELNMKKESIFSTGEEDDSAVDLTSENKYYAAWVVEVAERTASMARWGGVGFTH

NbL02g03750.1 enoyl-[acyl-carrier-protein]_reductase_[NADH]_chloroplastic-like [MW = 41.9 kDa]

No. of times detected



log(intensity)



Values from



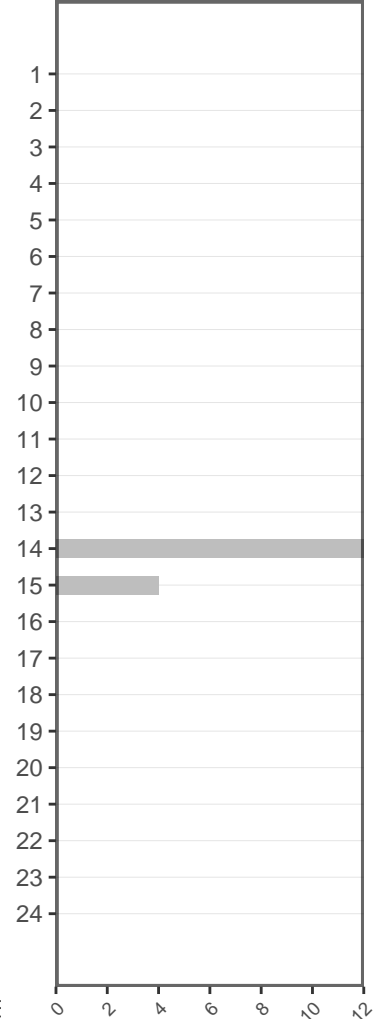
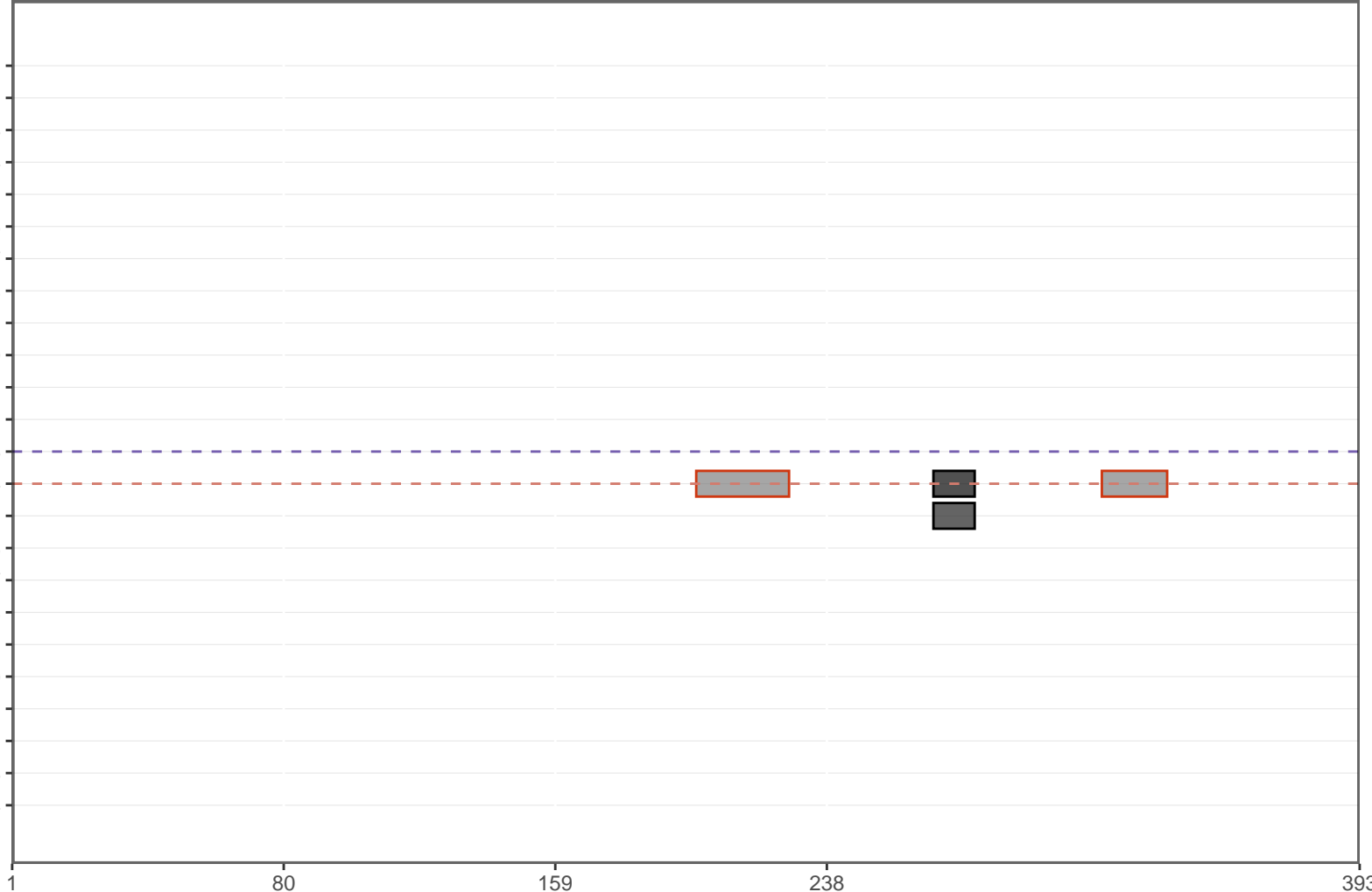
MW indication



Molecular weight



Gel Slice

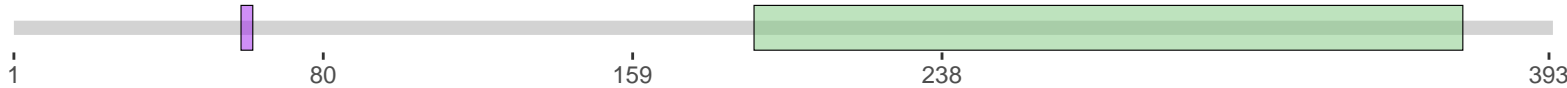


Protein length

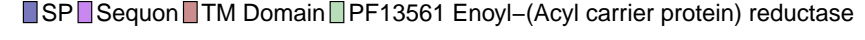


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

YAGSSKVTYSEVAESVKEDEFGSDILVHSLANGPEVTKPFLLETSRKGVLAASASGYSVYSLKHLFLPMNPGGSSISLTYASERHPGYGGGMSAKAALESQTRVLAFEAGRKKVRRVNTISAGPLRRAAKAIGFRIDMMDYVITNAPLQKELSADEVGNTAFLASPLASATGAVIYVQNLNMGVGVDSDFKDLNPKSEE

NbL02g03640.1 vacuolar_protein_sorting-associated_protein_26A [MW = 35.61 kDa]

No. of times detected



log(intensity)



Values from



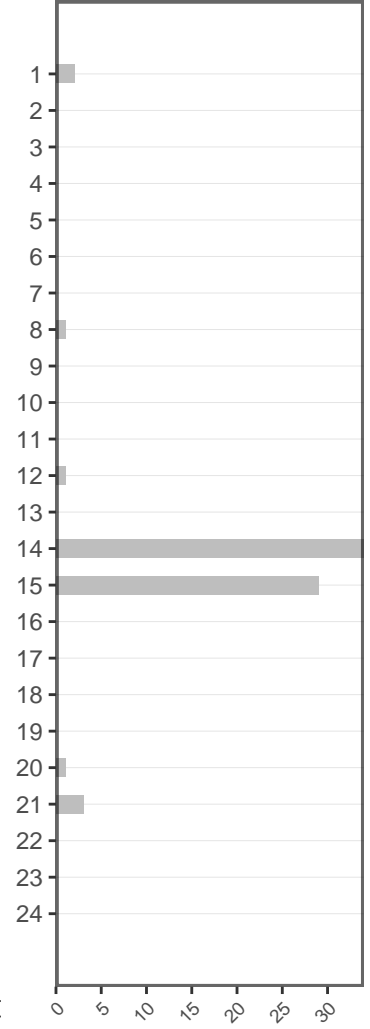
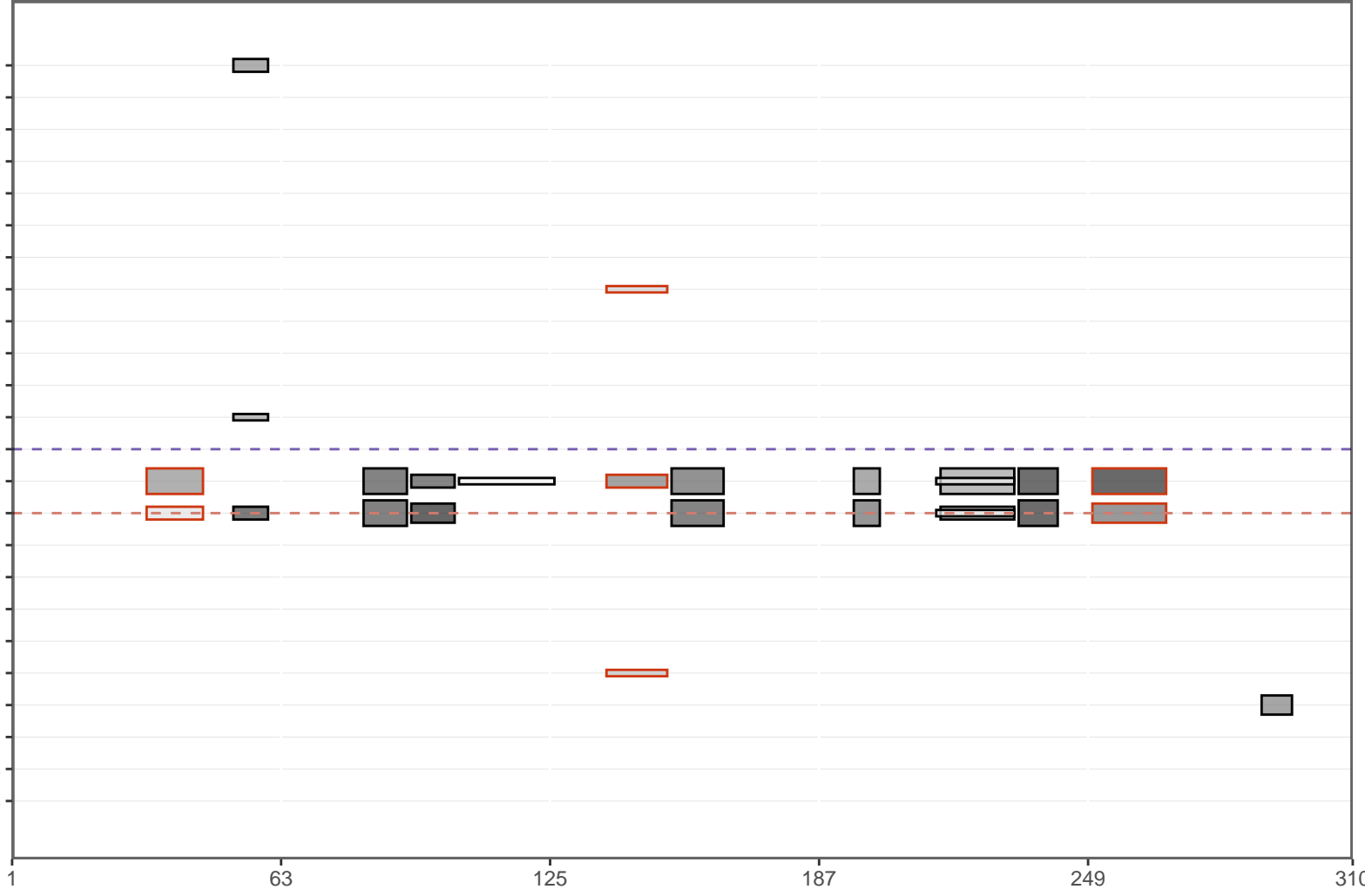
MW indication



Molecular weight

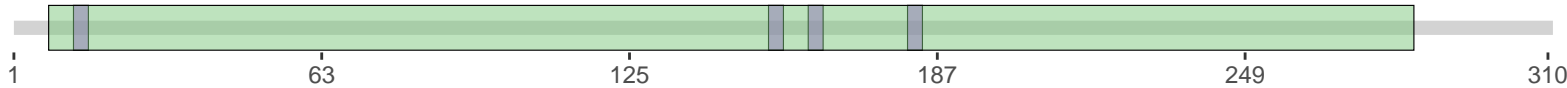


Gel Slice



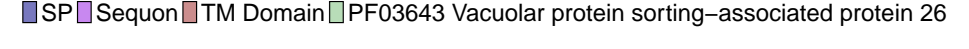
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GSIVEYDDFVVRNYSPPPSINISIKMEVIEDGLHIEFEYNKQKYLKQVIGIKYFLVIRIKINMDLEIRRRREGTGGANTHVETELAKFELMDGAPVRGESPRLFLSPVELTPTPHNNKFKVYKYLNLVLDDEDRRYFKQGEITMFLRLAETSVINGAVGA

NbL02g03290.1 ATP-dependent_6-phosphofructokinase_6-like [MW = 28.98 kDa]

No. of times detected



log(intensity)



Values from



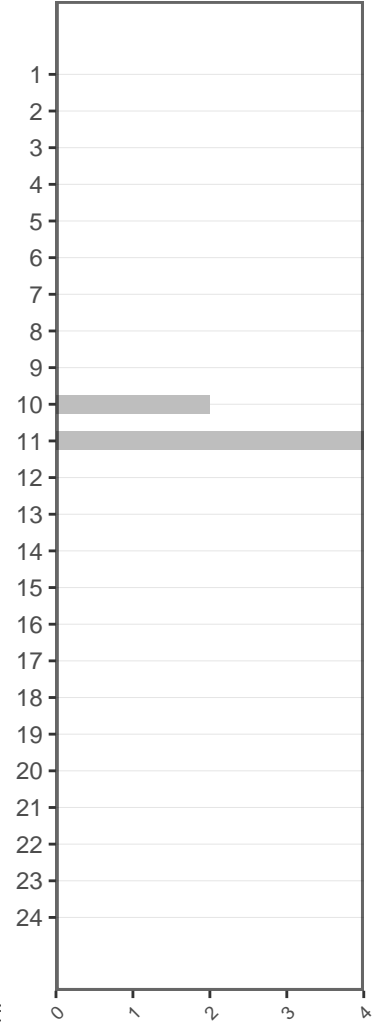
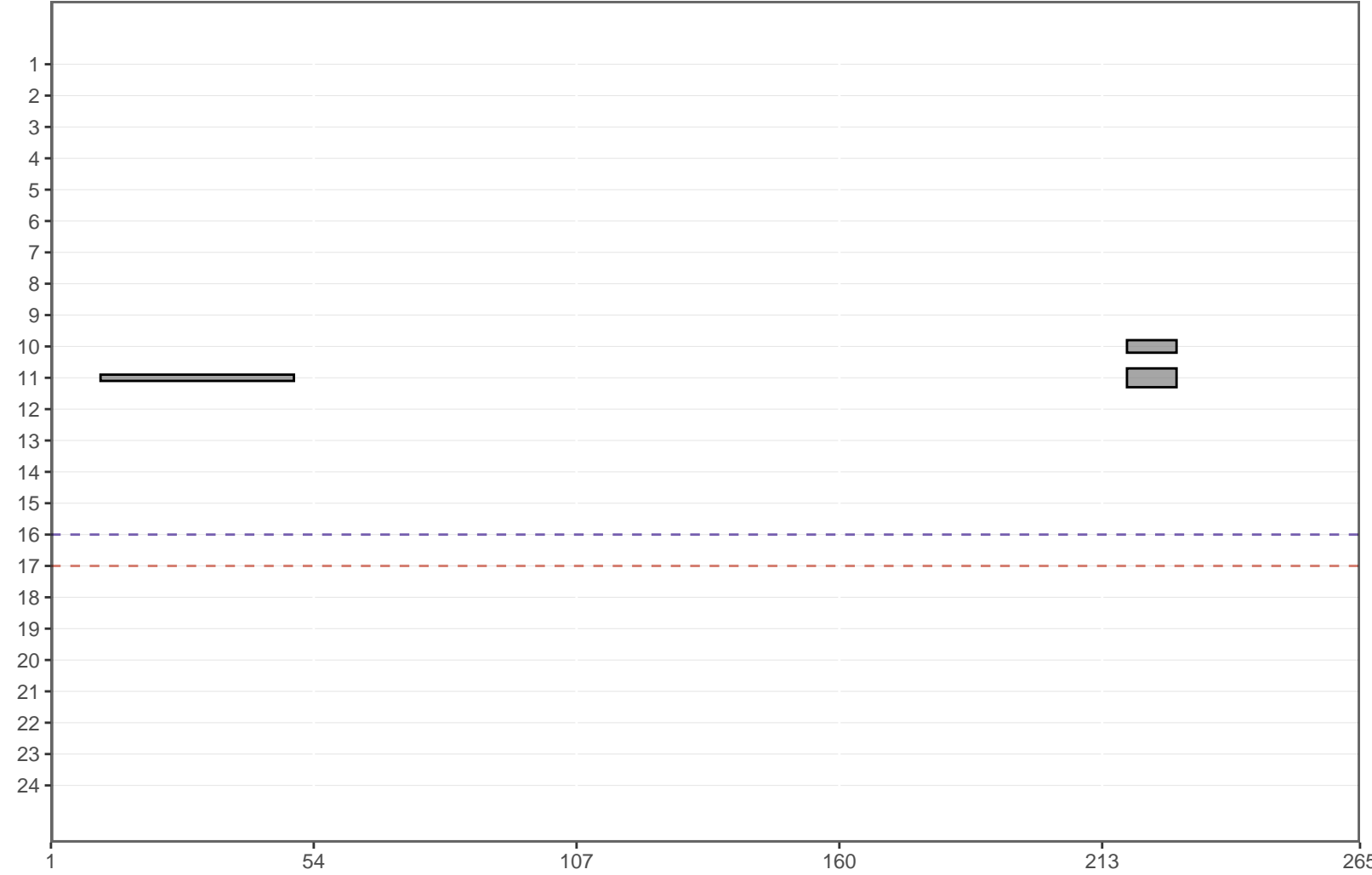
MW indication



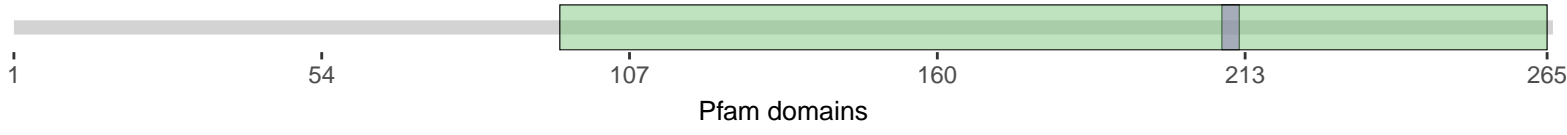
Molecular weight



Gel Slice



Peptide counts over 4 repeats



Pfam Description
 ■ SP ■ Sequon ■ TM Domain ■ PF00365 Phosphofructokinase

Protein sequence:

HHMYGVKRVMGIDGGYRGFYSKNIIFLTKVYVNDHHRKGGTILGTSRGGHVTKWVDSIQDQNGVYHGGDGTGRGAAVFEIIRRLGLNVSVAIGPIKTDNLDVRSFGFDSAVEEAGRAISAAHVEATFENGGLGLMLGR

NbL02g03270.1 acid_phosphatase_1_pseudogene [MW - SP = 27.87 kDa]

No. of times detected



log(intensity)



Values from



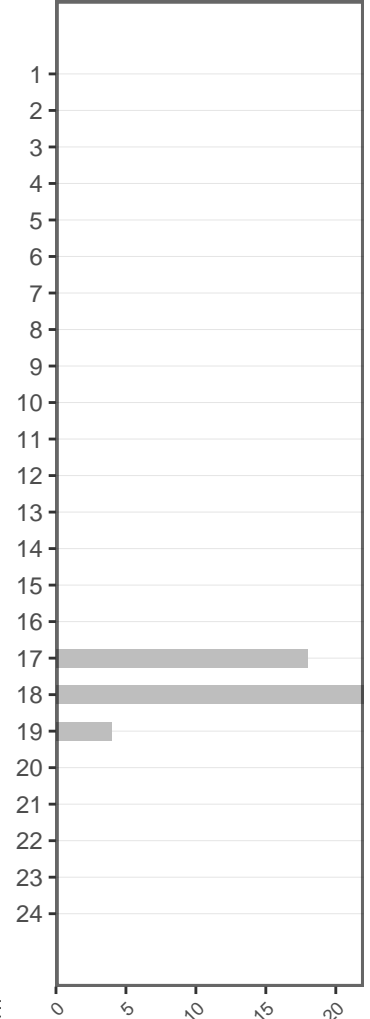
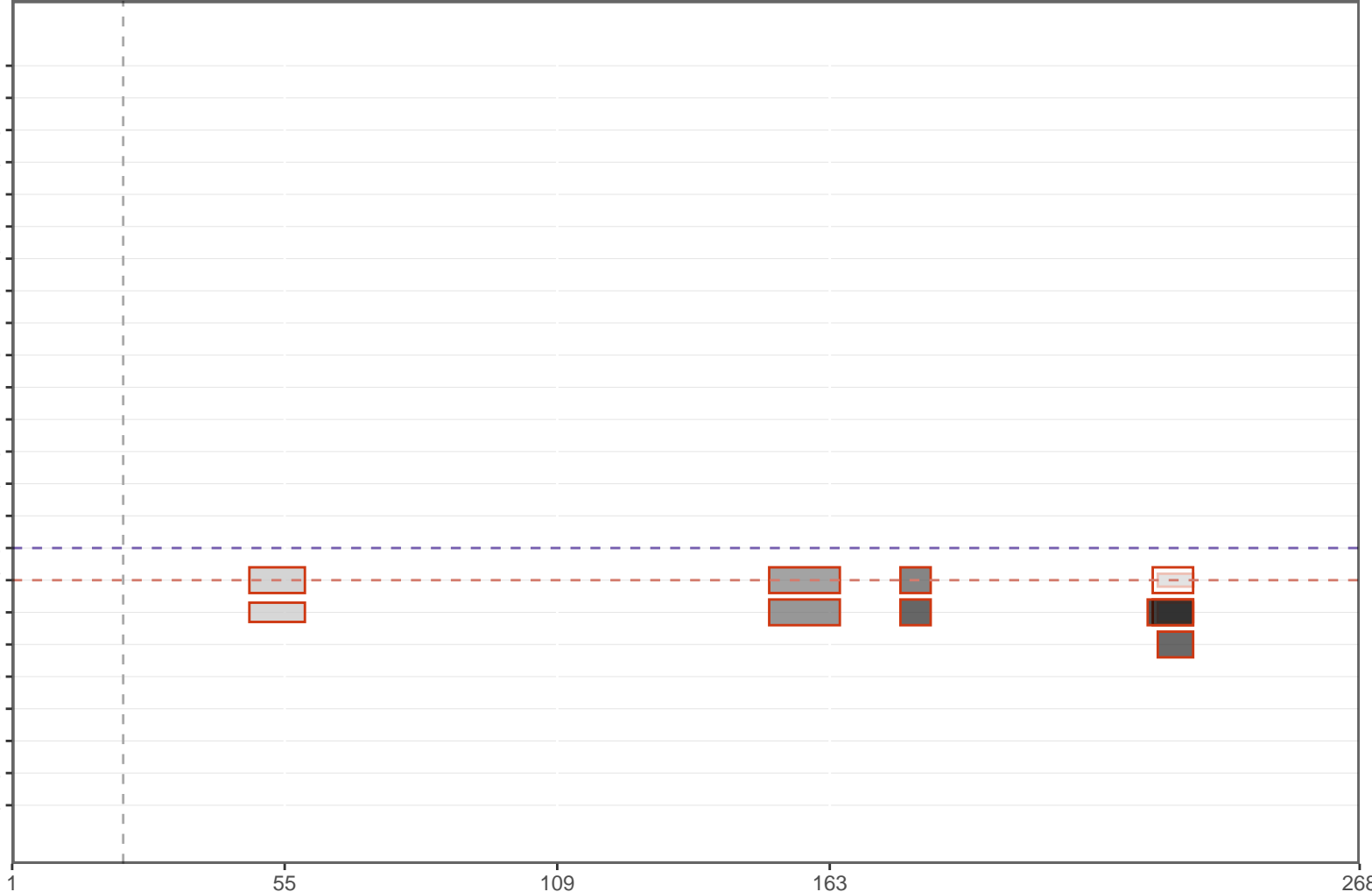
MW indication



Molecular weight



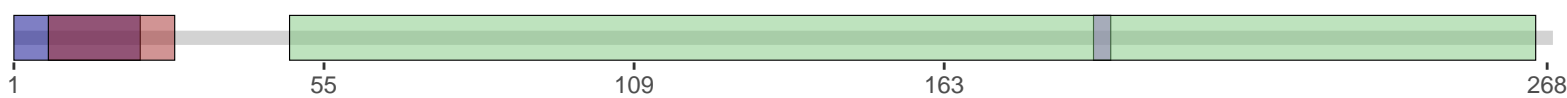
Gel Slice



Protein length

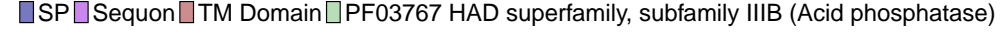


Peptide counts over 4 repeats



Pfam domains

Pfam Description

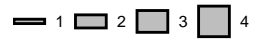


Protein sequence:

DIQETLLSNLPYYVTHGFGSEIFDEAFDKWVNEAEAPNAPPSLKLKELQGRGFRIFLITGRSELORNVTENKMYAGYENWERLILRGPSSDKGLATQYSEKRKELEDEGYRHGSSGGQWBYLNGFAVATRSFKLPNPMYYIA

NbL02g03250.1 phospholipase_D_alpha_1-like [MW = 92.3 kDa]

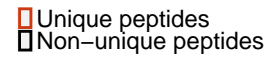
No. of times detected



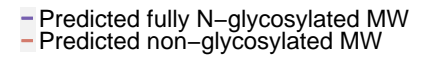
log(intensity)



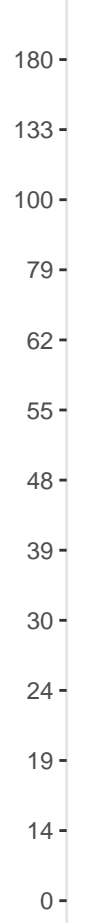
Values from



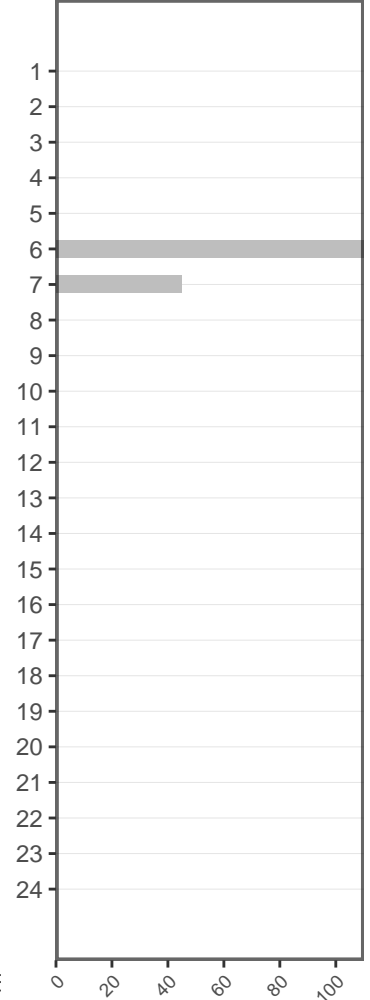
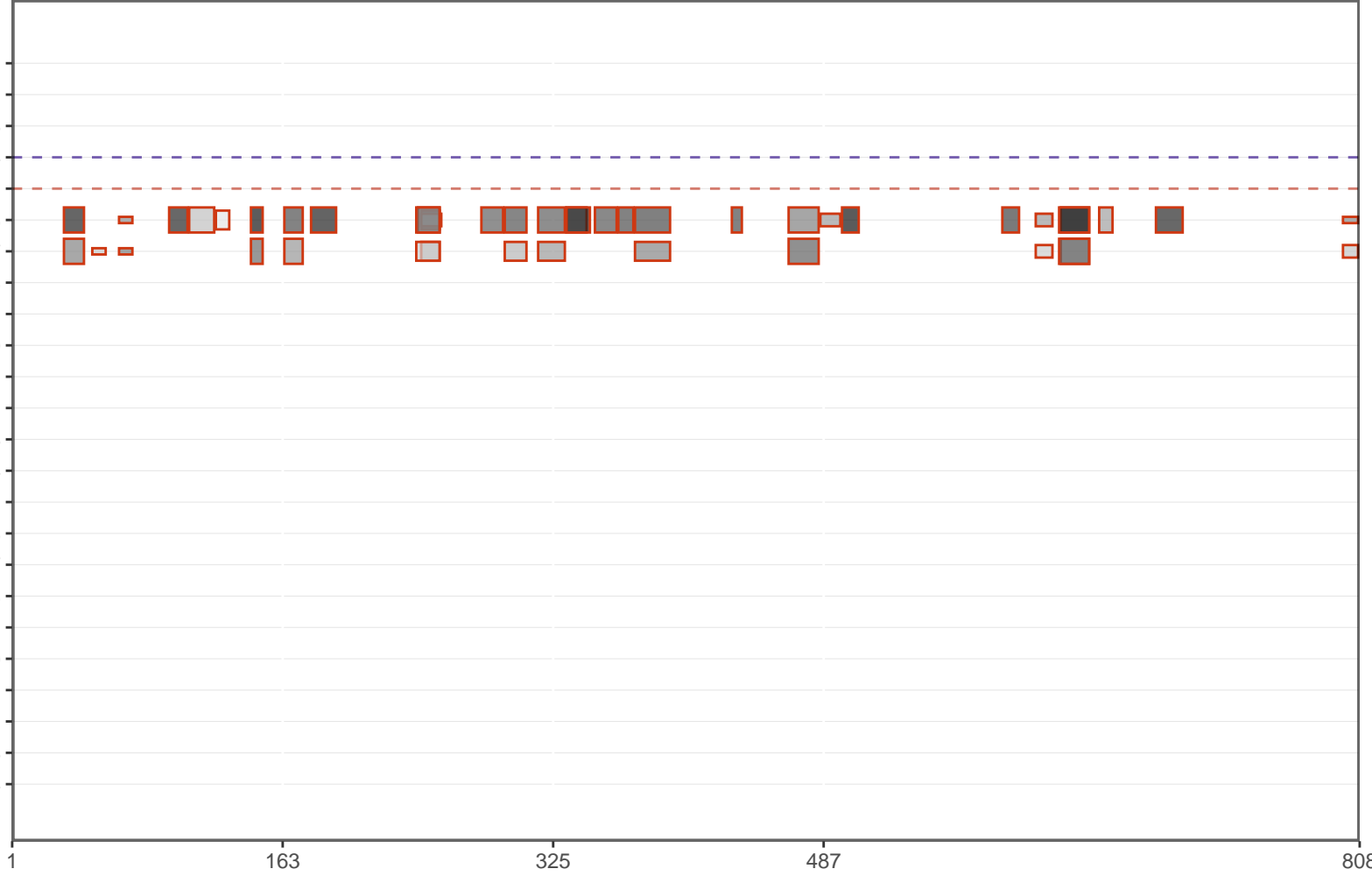
MW indication



Molecular weight

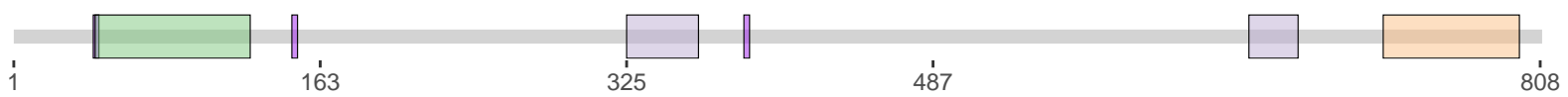


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

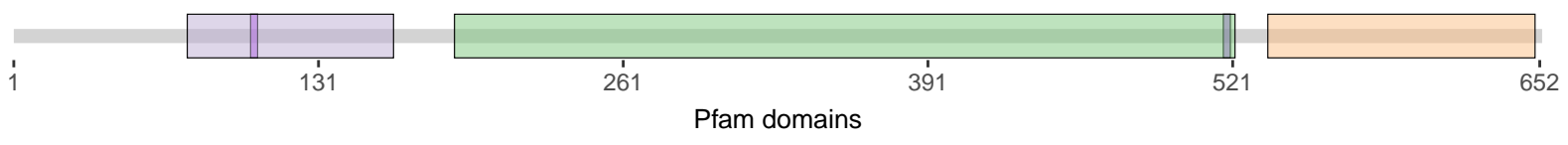
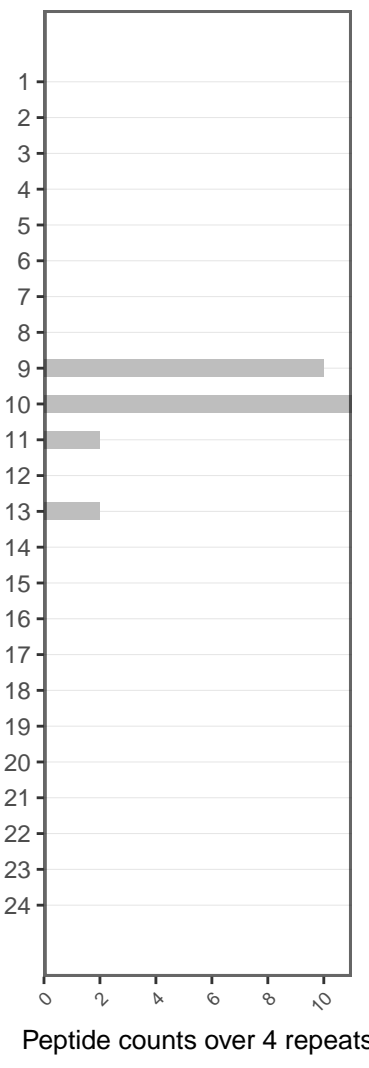
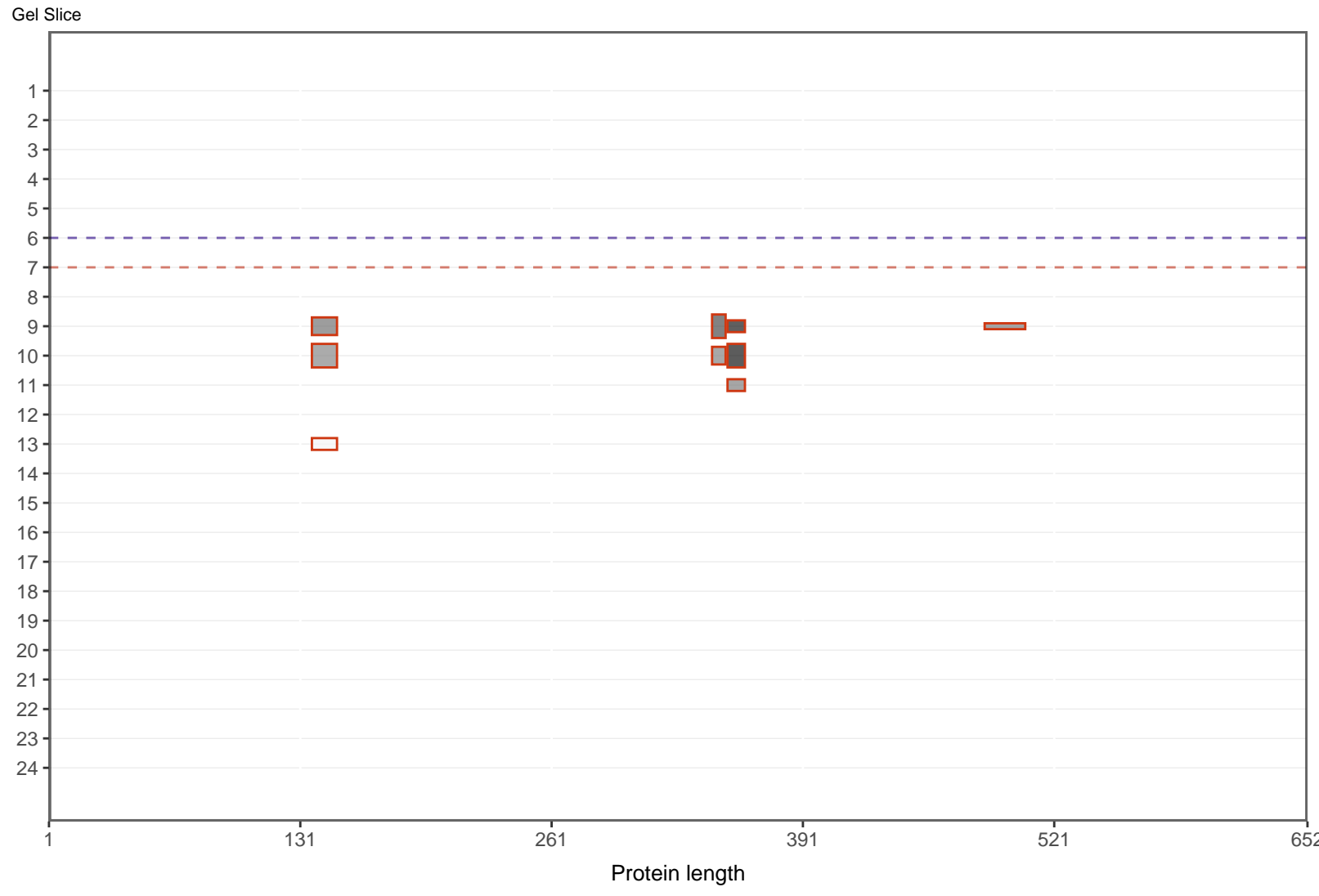
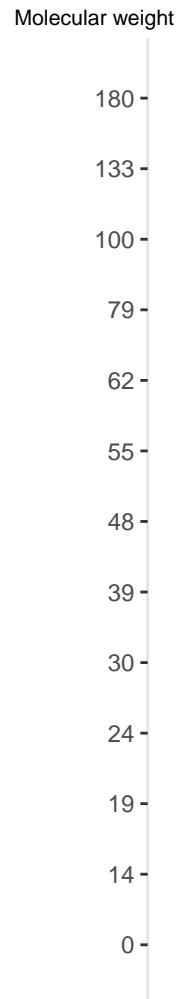
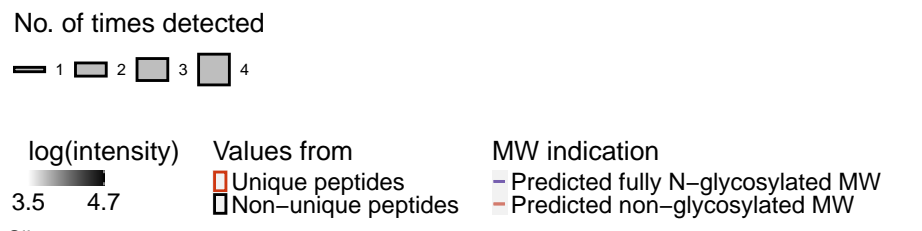
Pfam Description

- SP
- Sequon
- TM Domain
- PF00168 C2 domain
- PF00614 Phospholipase D Active site motif
- PF12357 Phospholipase D C terminal

Protein sequence:

SIQKGGPREPWIDHCRLEGPVWADVLYNFEQRWRKGGGKDLINLRIDINITPPSPVMYDQDITWVGVFRSDGGAAGFDPAPEAAKGLISGKDNIDRSIQDVAIARRAKHFVYIENGYFLGSSFWYSDKIDKEINALHLPKELSLKVKVSKIEAGERFTVYVYLLPMWPEGLFEGSGVQALDWRRTMRMMYTDHGALKVKGIANPKYLSFFDLGNRETAKGGEVEPSETPEPDSVVRAGEARRFMVYHAKMMVDEYKGSANQRSMGDARDSE

NbL02g03210.1 arginine--tRNA_ligase_chloroplastic/mitochondrial-like [MW = 73.54 kDa]

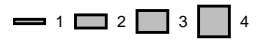


Protein sequence:

IEISREEFORVYERLIGVDLEEKGESEFYNPYIKAFNLNLYKGLHGESEGARVIFIEGKIPLVVKKDGGFNVASTDLAALWYRLNEEKADWIMVYTDVGGREHFEMFAAKLAGWLPLENNFPKASHVDFGLVGGDDKRFRTSTEVVXKLVLDLDEAKSRKLALEERKATEVWTADELEGTAEAVDVGAWKYADLKNRILNTYTFNFDMLSDKNGNTVYLLVYHARIGSIRKSGRDIIEELKVVGGVLAHQDERALGHLHGFPAENVEEAGINLPNLCCYLYLXLSDF

NbL02g03060.1 uncharacterized_LOC104114303 [MW = 302.25 kDa]

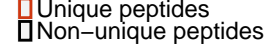
No. of times detected



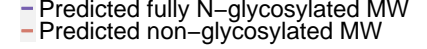
log(intensity)



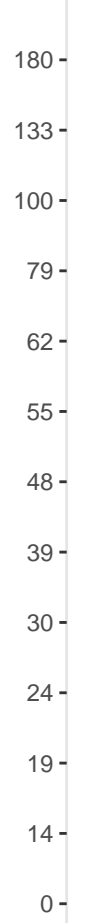
Values from



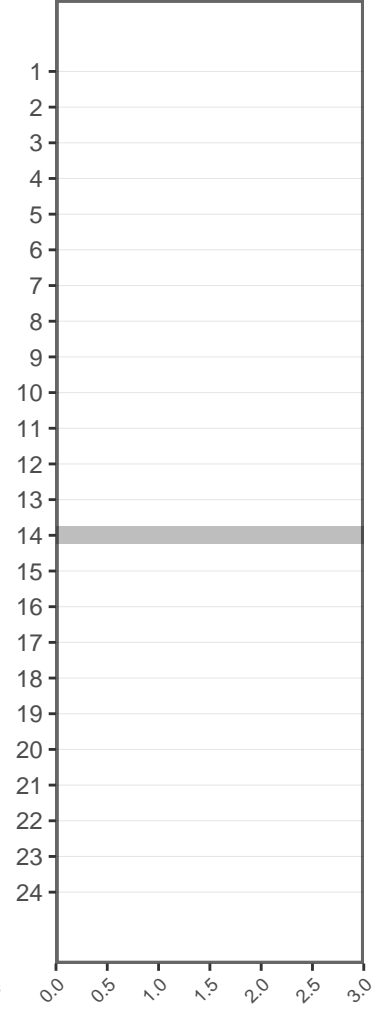
MW indication



Molecular weight

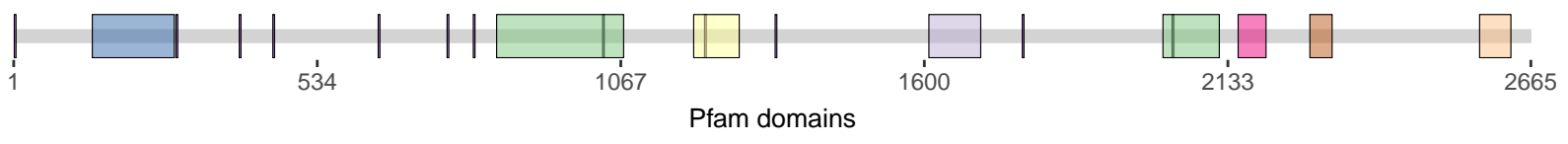


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Description

- PF00078 Reverse transcriptase (RNA-dependent DNA polymerase)
- PF03732 Retrotransposon gag protein
- PF13242 HAD-hyrolase-like
- PF13966 zinc-binding in reverse transcriptase
- PF14111 Domain of unknown function (DUF4283)
- PF17919 RNase H-like domain found in reverse transcriptase
- PF17921 Integrase zinc binding domain

Protein sequence:

IMAELCYNIVLERNSRFRNVSSEYGGOLLRNAYTGHRISLKFSLQFQHSPPGSSKPNELKFGTLNGIDELAETRRFKAWFLDQFGLVHDGKGPVPSAISTFTFSSEVSEFELGLRLKVVENVYGEADFILANGTEAAALPMKLEDEKLEGGAAKRIPIFVTEARALRVMPELRKVDALKVMDTVANSVTELTNSVESRMAQALEEIKRMINSGGNPVQNGSPVDRNEERIEPRAPRFENPHPTKNYRVDVHSRFDGTVLKDLGKYGKGFDDVVTPEEFKVKLVLSCKI

NbL02g03030.1 plastocyanin [MW = 17.01 kDa]

No. of times detected



log(intensity)



Values from



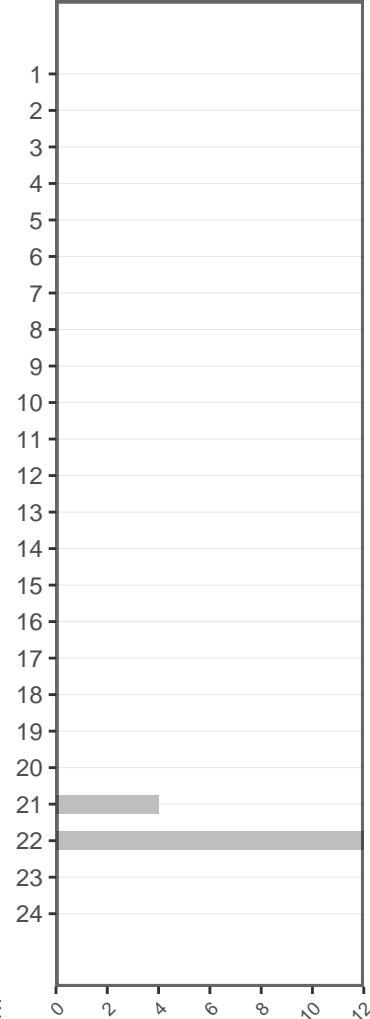
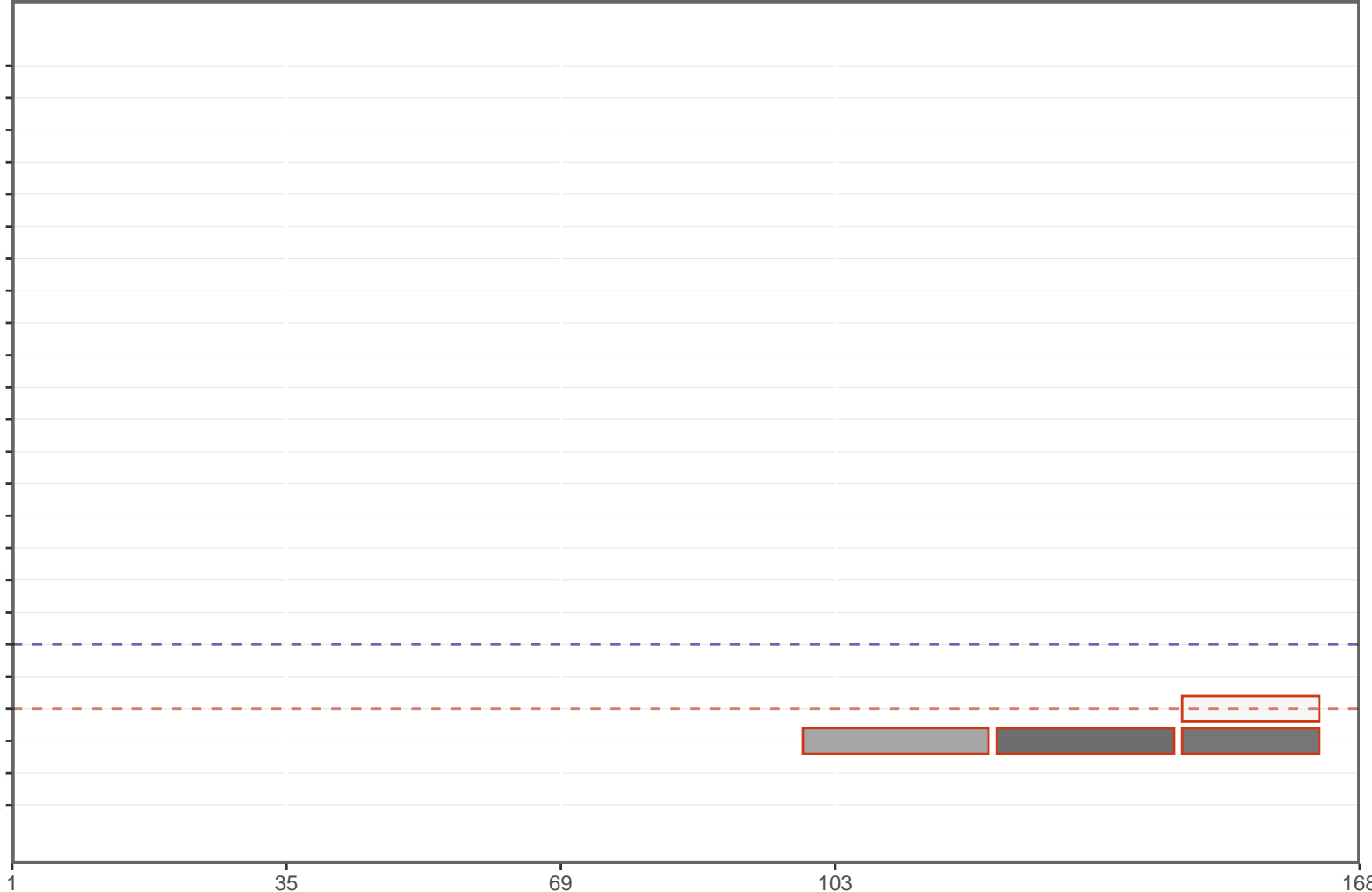
MW indication



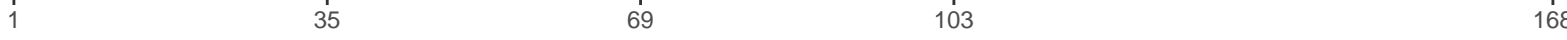
Molecular weight



Gel Slice



Protein length

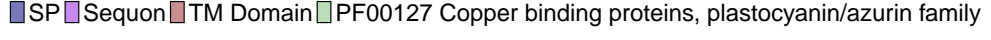


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

LGDDGSLAFVPGNFEVSGAGEKITFKNNAGFPHNVVFEDEIPSGVDASKIMSEEDLLNAPGETYVSLSEKGTYSFYCGPHOGAGMVGKVTN

NbL02g03010.1 uncharacterized_LOC109239937 [MW = 29.04 kDa]

No. of times detected



log(intensity)



Values from



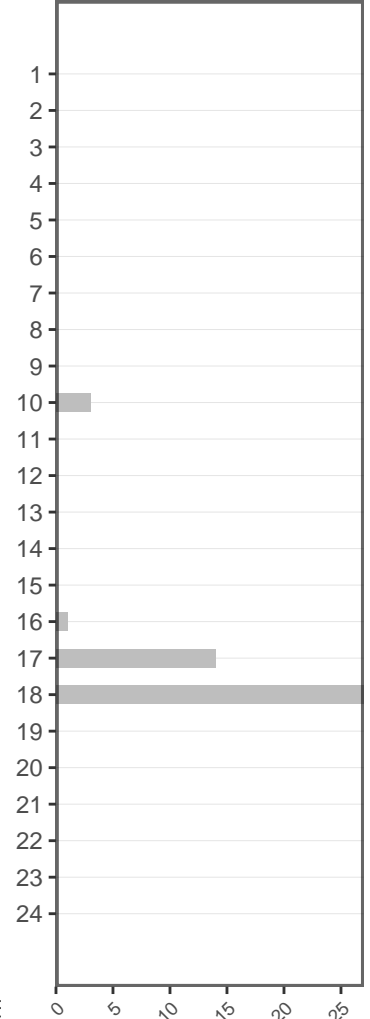
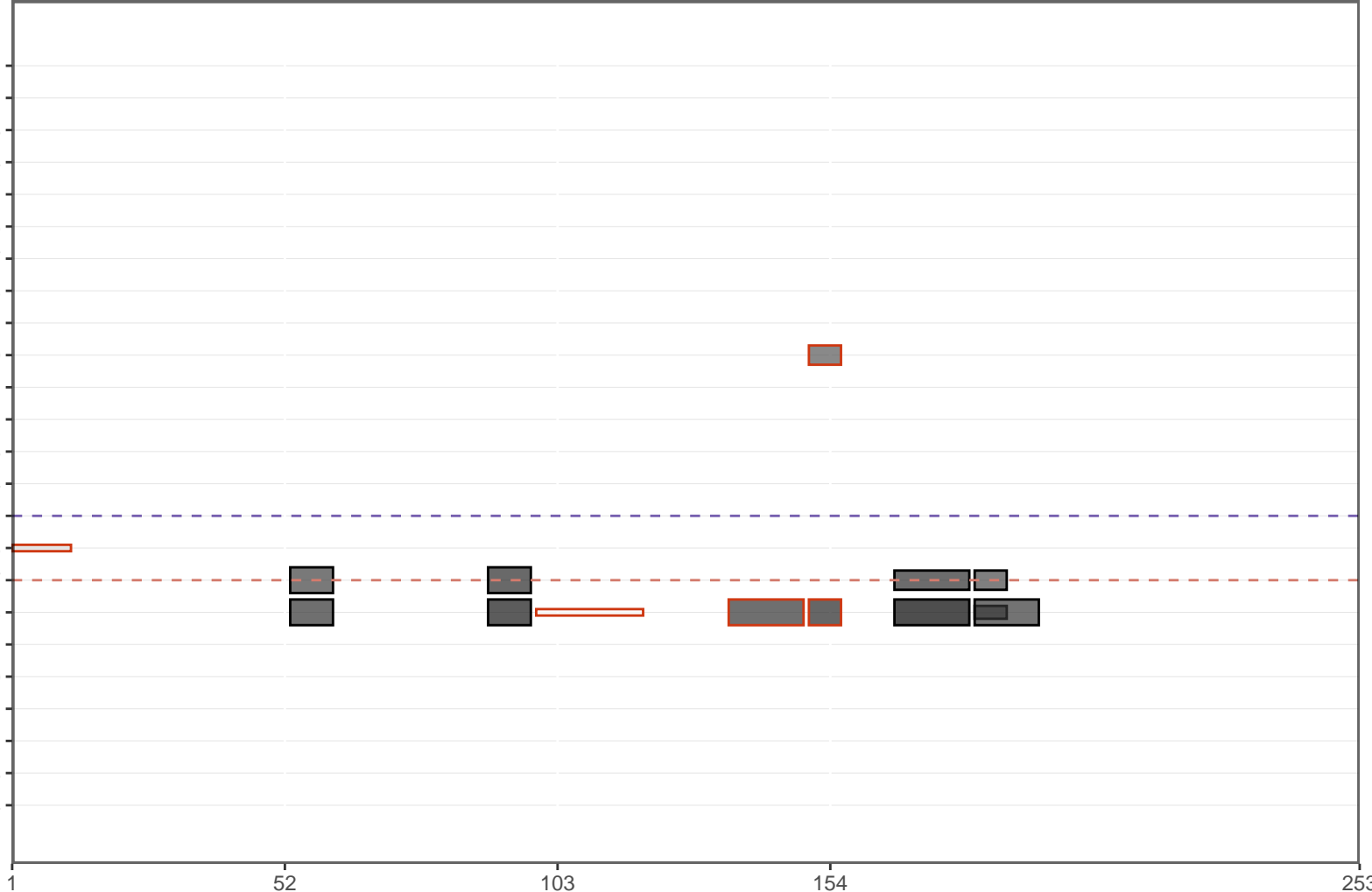
MW indication



Molecular weight

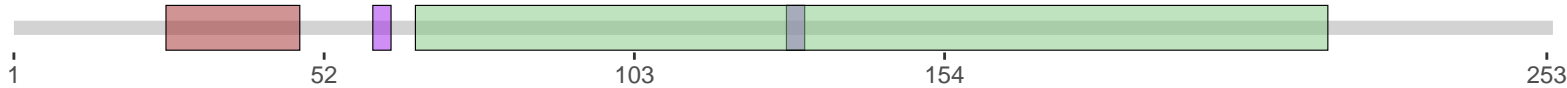


Gel Slice



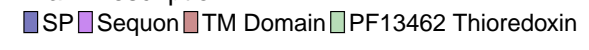
Protein length

Peptide counts over 4 repeats



Pfam domains

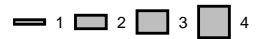
Pfam Description



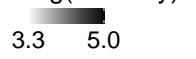
Protein sequence:

LTLSRALHVVNKLNASATYKLLSEFFDHQEDFYNAKATFDLBRASVVEKVARFETNAIGNSNVDYKAGFTDKTQDQTRLSFKYGCYKGVYGTFFFFVNGFPLPDAGSALDHWKRRVLDPLVHGGDTGRNYLLHFFL

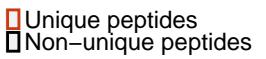
No. of times detected



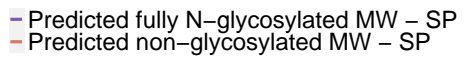
log(intensity)



Values from



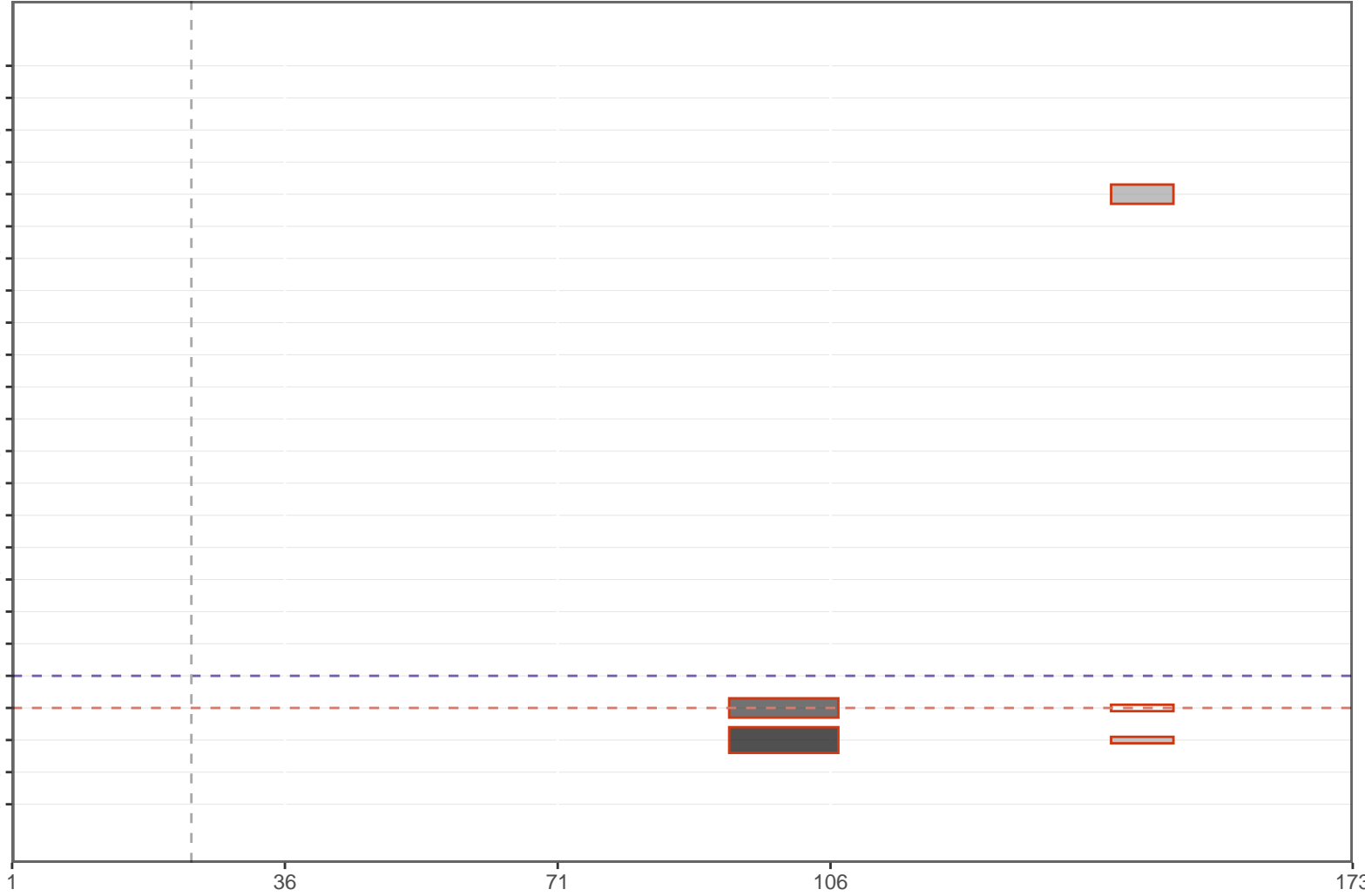
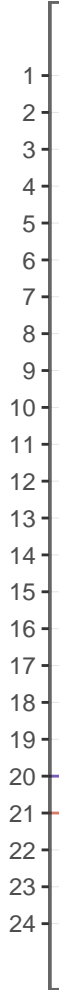
MW indication



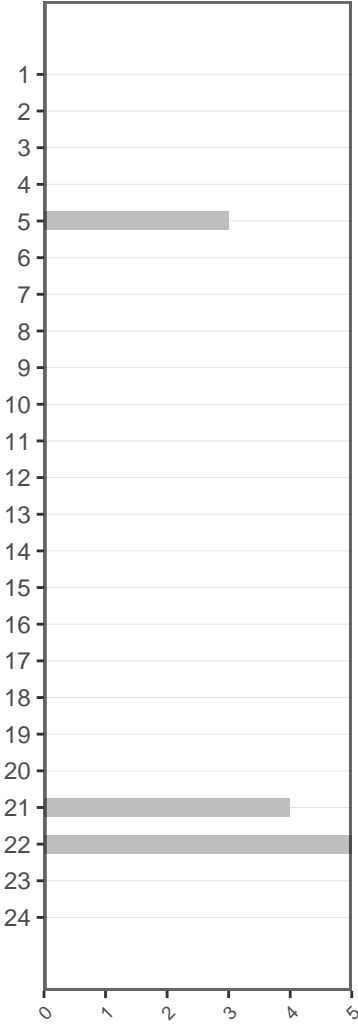
Molecular weight



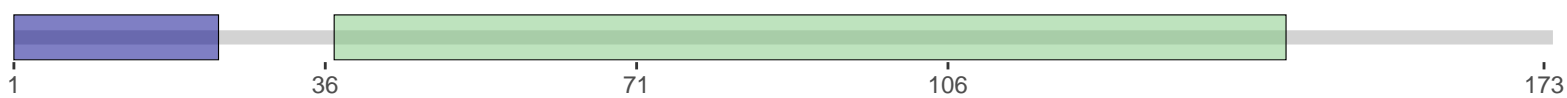
Gel Slice



Protein length

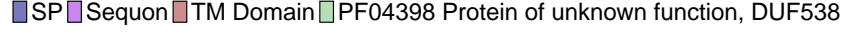


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YVVFQDQLVYYQKEIKGMKMGVGVSEVSGIGAKKLFVWVPTGIVNDEESHMERHVGFLSEKPAKDFETIPTCKNKGAKILFLGYDEDEWSEVLI

NbL02g02830.1 endoplasmin_homolog [MW - SP = 89.72 kDa]

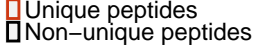
No. of times detected



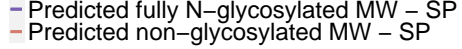
log(intensity)



Values from



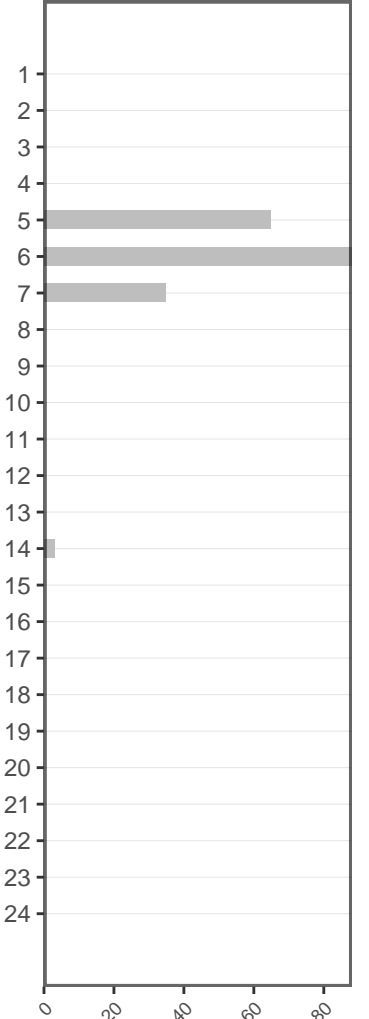
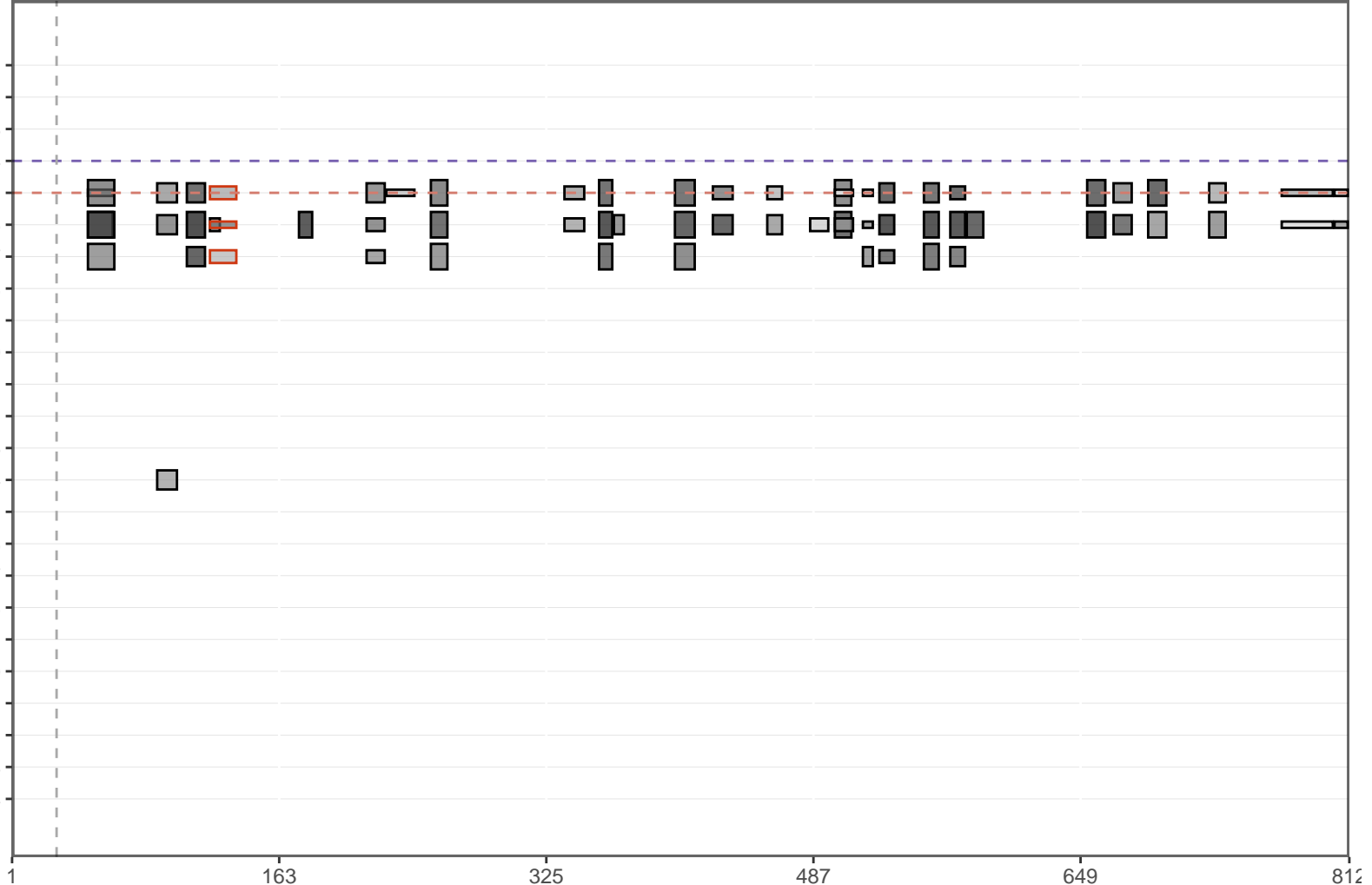
MW indication



Molecular weight

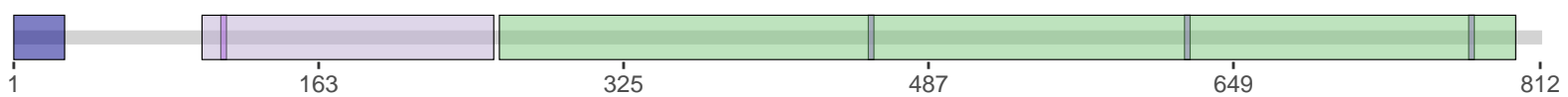


Gel Slice



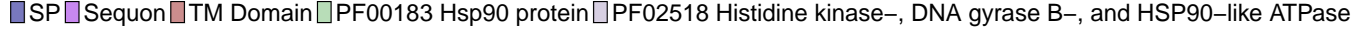
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CAVLFYPPKAPIDLVESYNNKSKGNLKLIVRRVRFISDFDELLPKYLKFLMLGLVDSDDTLPLNVSREMLGGHISLKTIKKLRKALDMIRKIAEDDPDESDKDKDIESSADNEKGGVAKVFNDFGKSVKLGIEDATNRRNLAKLRFETSKDGLTSLDQYISRMKAGQKDFVITGASKEGLEQSPFLERLTKNNYEVIFETDPVDEYLMGVMYEDHDKFQNVSKIEGLKLGKDSKAKELKESFKELTNWVKGALASDNDVDDKISNRLADTPDWVVTYSKYGWSANME

NbL02g02760.1 prolyl_endopeptidase-like [MW = 23.48 kDa]

No. of times detected



log(intensity)



Values from



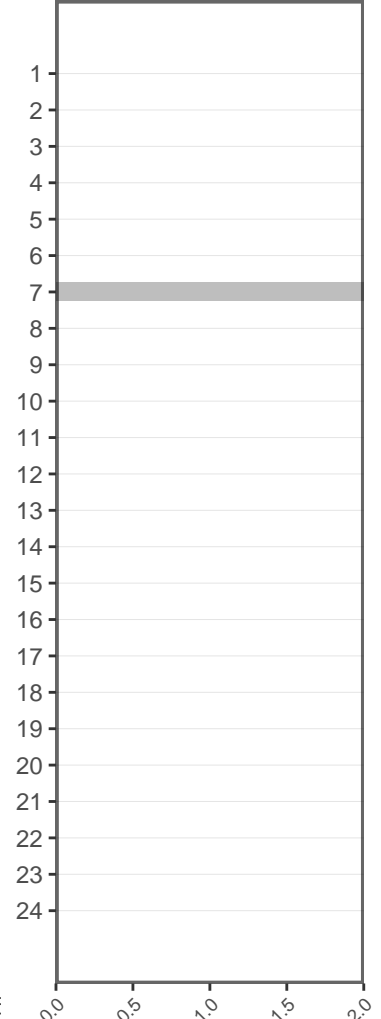
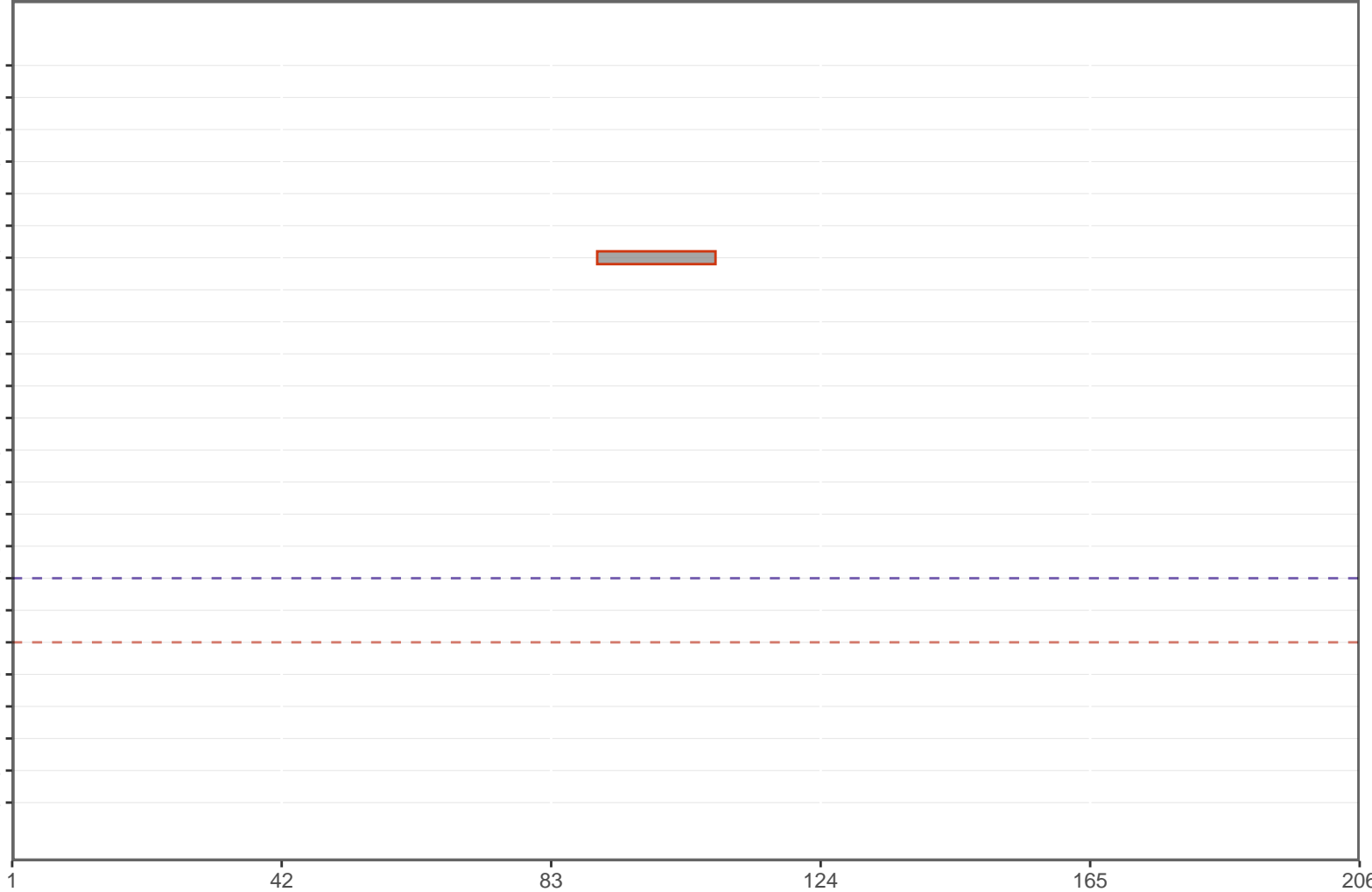
MW indication



Molecular weight



Gel Slice

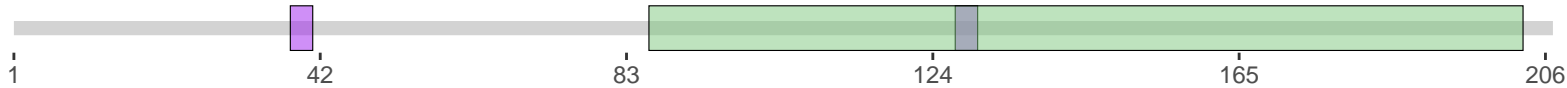


Protein length

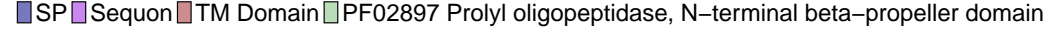


Peptide counts over 4 repeats

Pfam domains



Pfam Description

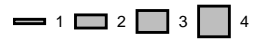


Protein sequence:

IESVVDNYHGVSVPDPYRWLEDDPDSSEETKEFVEKQVNLTDVSLKTKGTEKREKLEKTKLYDFPKYEVFRAGDKYFYFHNSGLGPKVLYVQDLSLGEPEVLLDPNTLSETGGH*

NbL02g02750.1 ATP-dependent_zinc_metalloprotease_FTSH_chloroplastic [MW = 76.59 kDa]

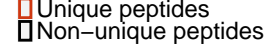
No. of times detected



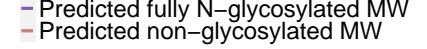
log(intensity)



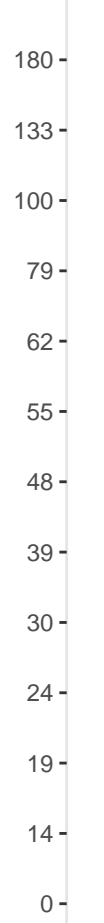
Values from



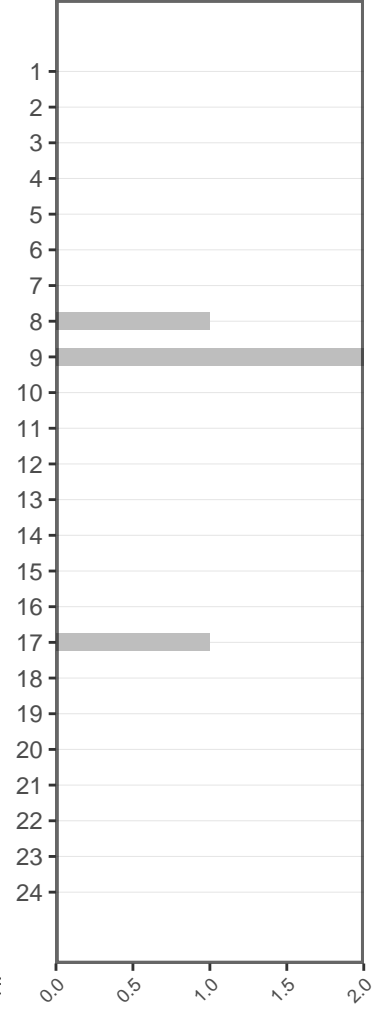
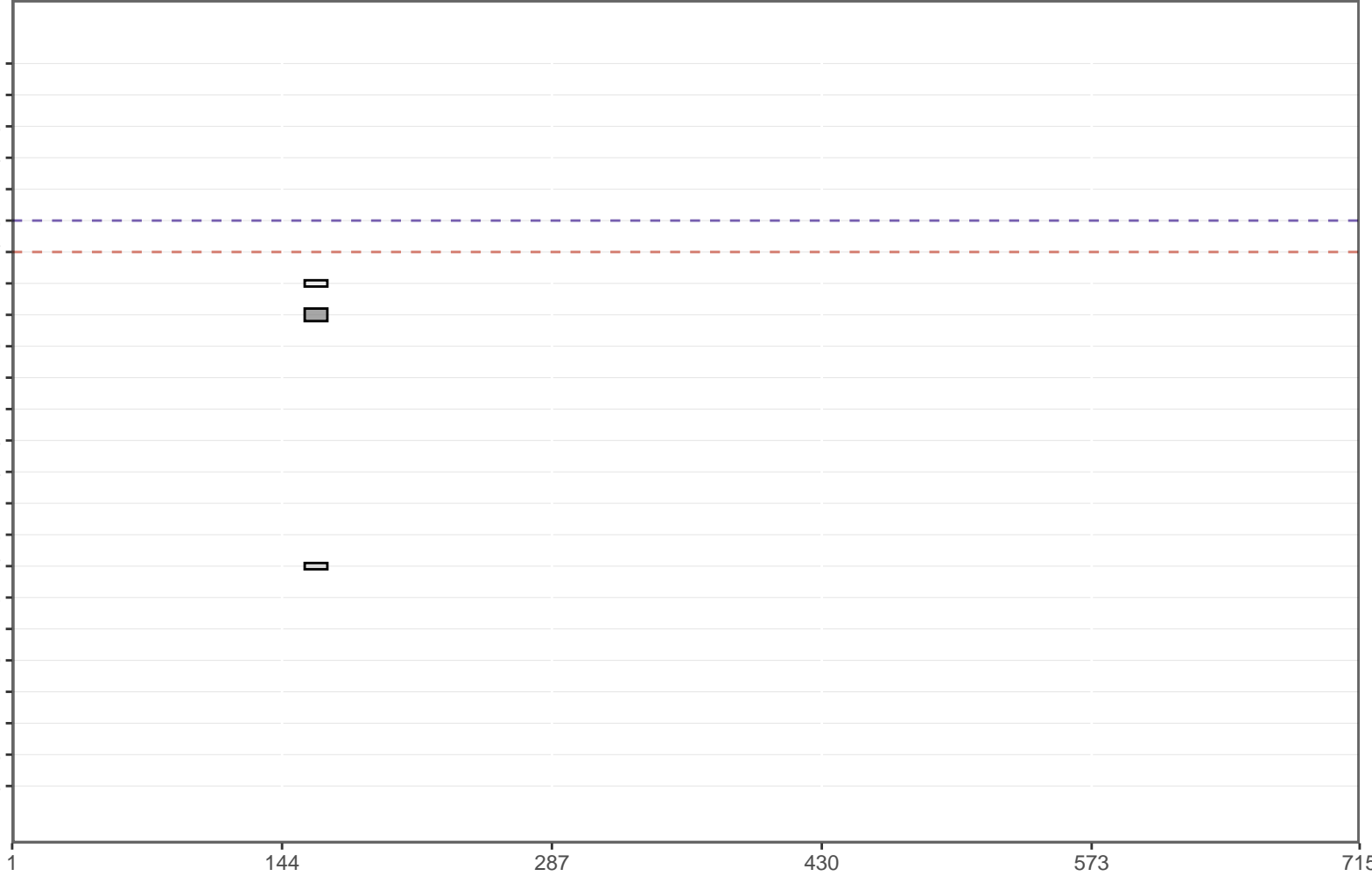
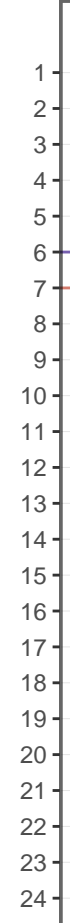
MW indication



Molecular weight



Gel Slice

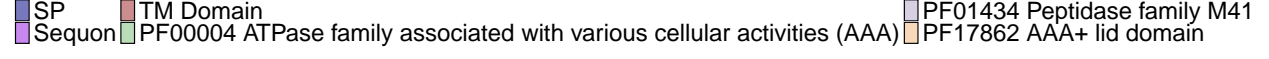


Protein length



Pfam domains

Pfam Description



Protein sequence:

DLFEAKSKAPCVFDEIDAVGRGRGAGLGGNDEREQTNLLTMDGFGSGNSGVVLAATNRPKVLDGALLRPGRFDRQVTADRPDVAGRVKLVHGRGKALAKVDFDKIARRTPGFTGADLGNLIMNEAAILARRDLKEIKGDISDALERIIAGPEKKNVAVSDEKKLVVHHEAGHALVGMPEYDPAKISIFRPGGAGLFTFFARSEERLESGLYSRVLNEMMAVALGGRVAEEVFGGDNVTTGASNDPMQVSRVARQMVERLGFSGKIQVAVUGGGGNPF

NbL02g02620.1 protein_TIC110_chloroplastic [MW = 112.44 kDa]

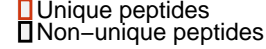
No. of times detected



log(intensity)



Values from



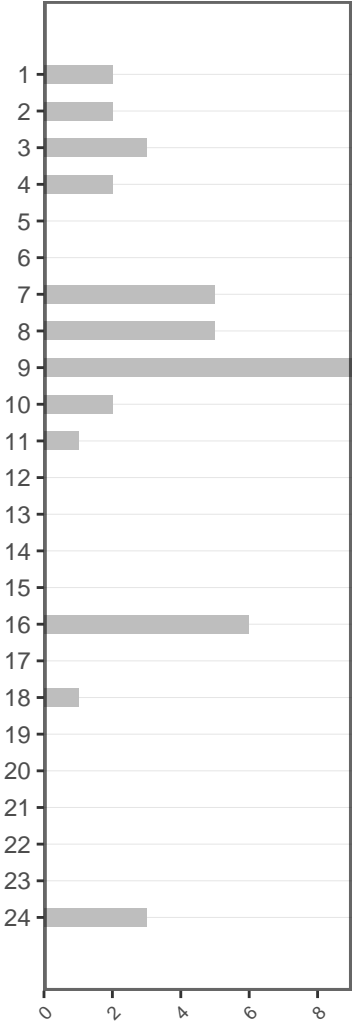
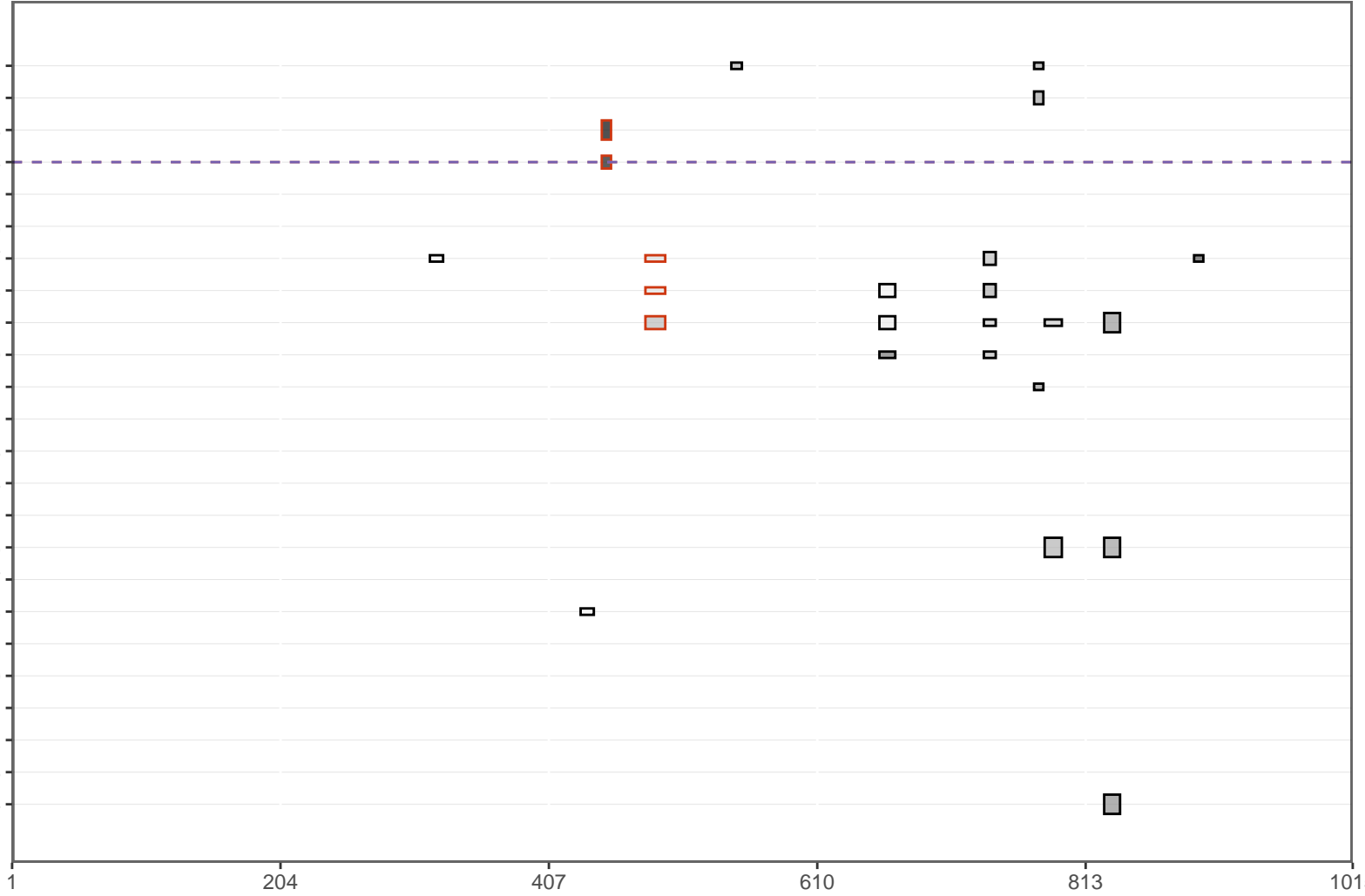
MW indication



Molecular weight

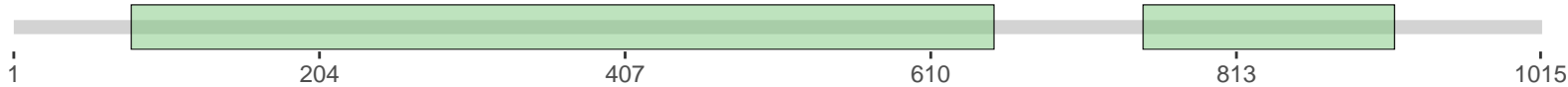


Gel Slice



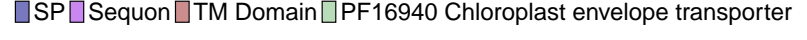
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISKAAYLQMLCEELESDPDKALGHEEYFRKLGKGLVADGELSDGDMKALERLGVMLGVPKQTVAAHADIDGSLFEKVKVEAAGVDGVDGDAEIKRVRKAAVGLRLTRVAMSIASKAVRKFIFRYSKARGSGSRTEGQAKELKMIAFNSLVTLGLVADIKGESSDTPPEEPKQEVQRTDEEDGGEWESLGRKAVKPKDNLKREIKGTESLKDGLPERDRADLYKTYLLFGLTGEVTRIPFGAGITTKKDDSEVVFSLGSLGILGLTDEIVEVHRSLAECAFROQAEVLA

NbL02g02550.1 CBS_domain-containing_protein_CBSX6 [MW = 15.2 kDa]

No. of times detected



log(intensity)



Values from



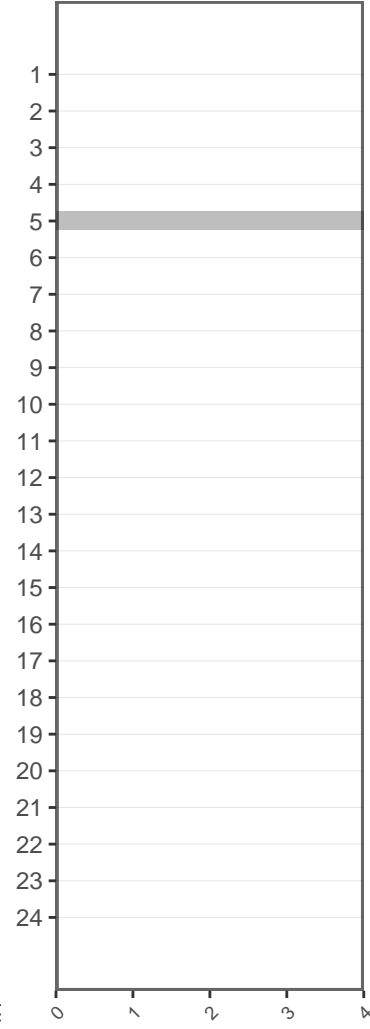
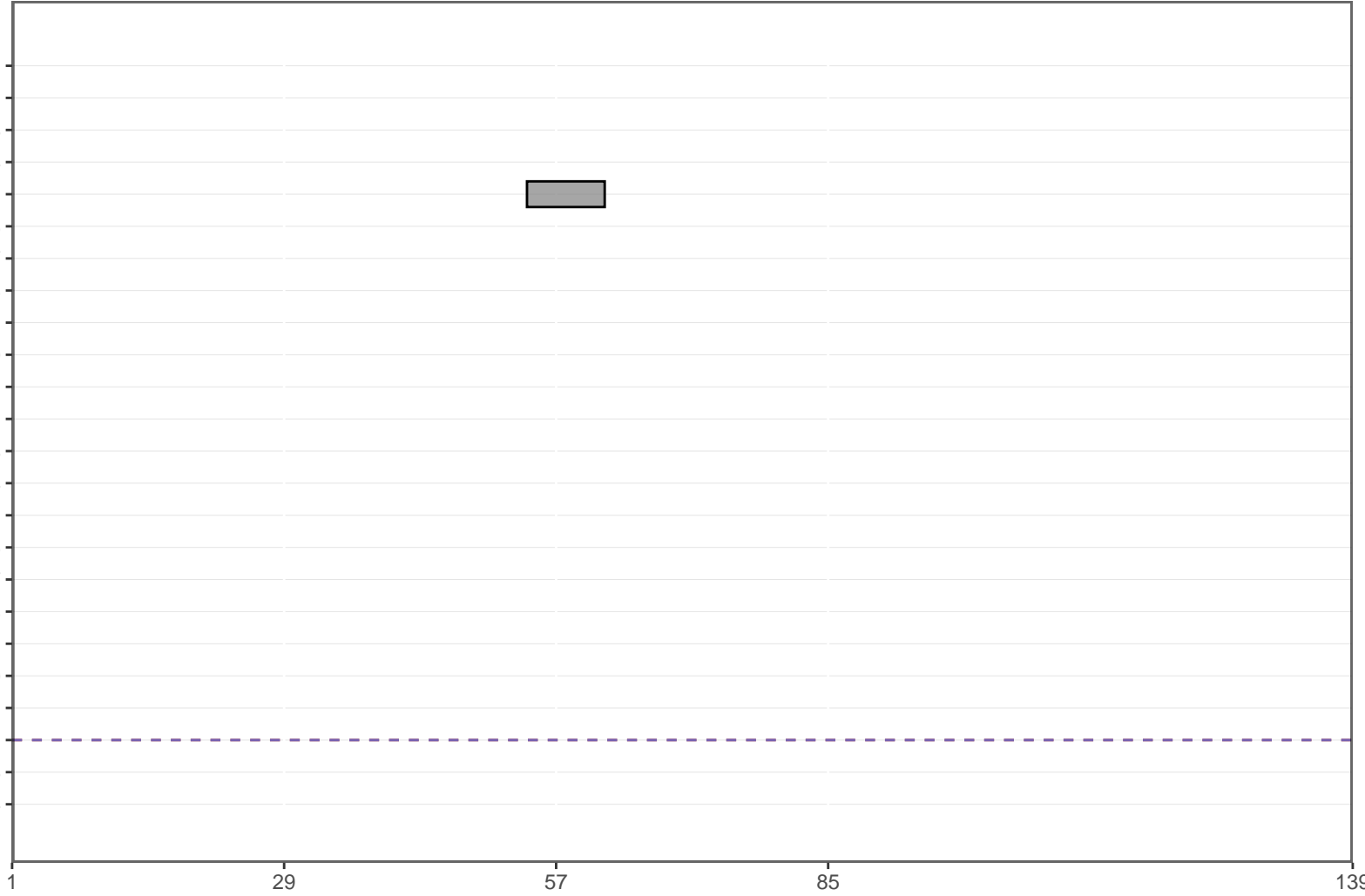
MW indication



Molecular weight



Gel Slice



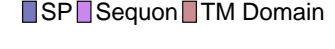
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

INSEMRARFVGLTSLGIVAFIAREEGIVDDEKAMKTPVSEVVVPPRLKLELPATRYNCAKRS66LLGGFMFDQGVY

NbL02g02390.1 violaxanthin_de-epoxidase_chloroplastic-like [MW = 54.59 kDa]

No. of times detected



log(intensity)



Values from



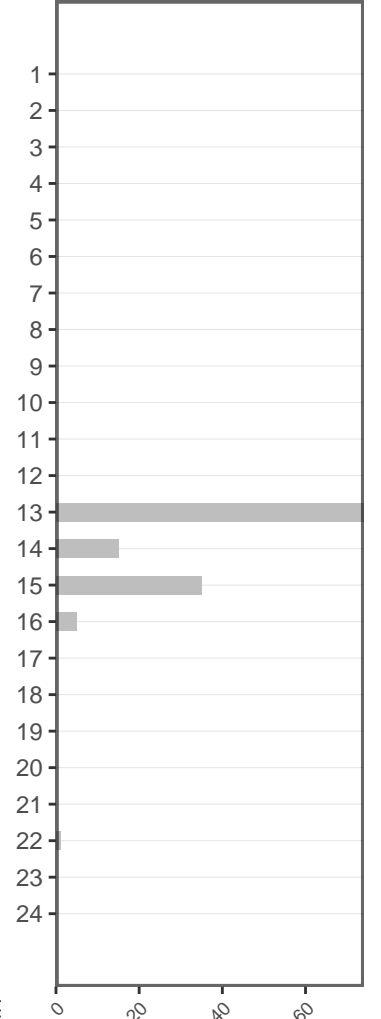
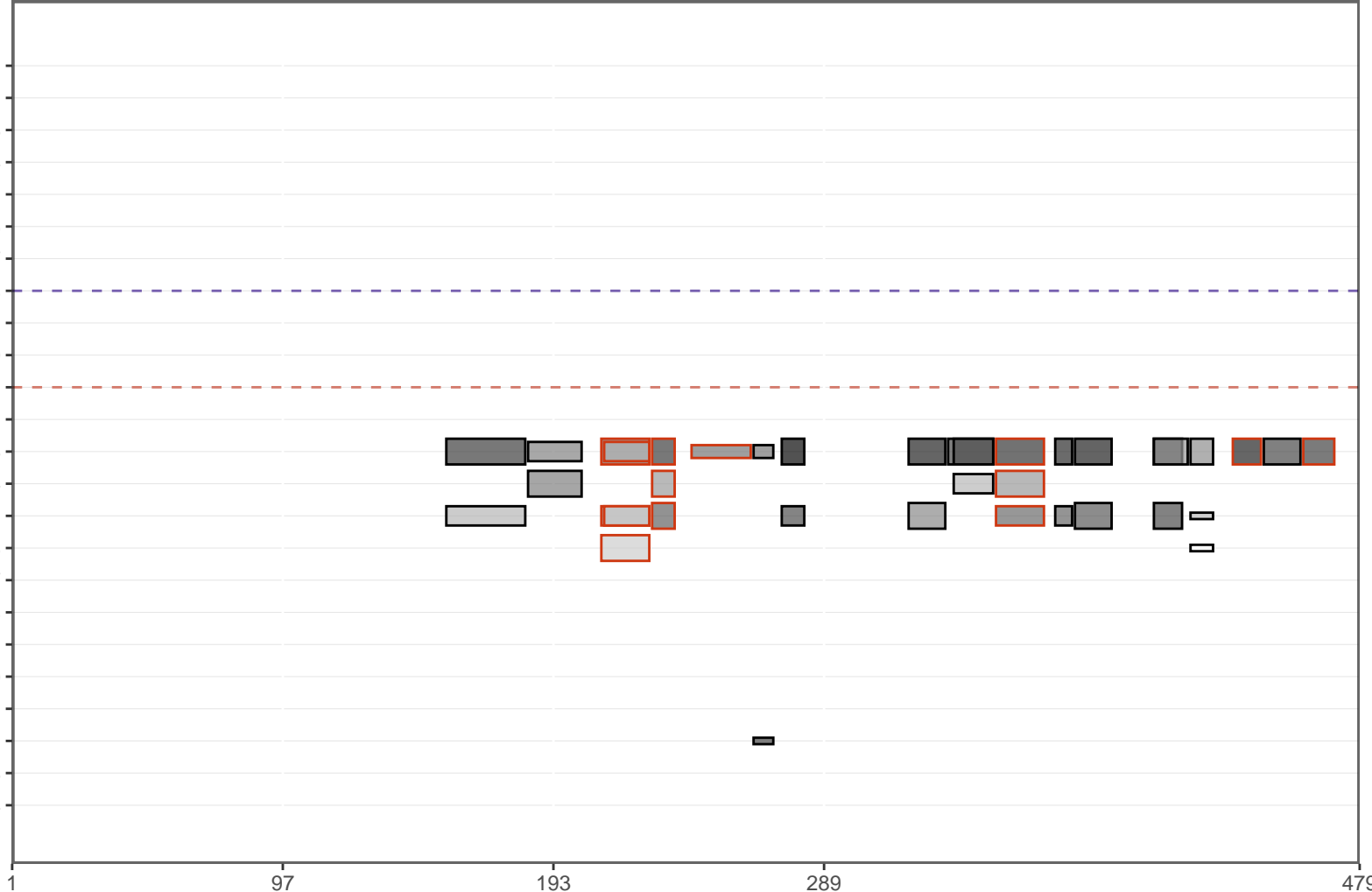
MW indication



Molecular weight

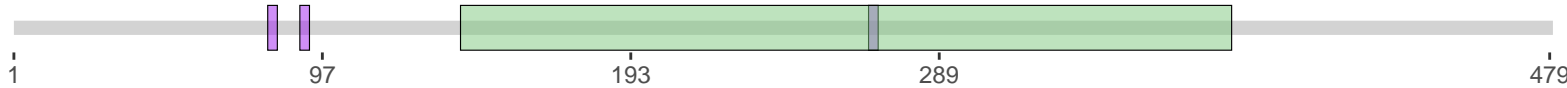


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

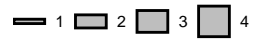
Pfam Description
 SP Sequon TM Domain PF07137 VDE lipocalin domain

Protein sequence:

KFDMDNDFSGKWFTRSLNPTFDADGDLHEFTEENKLVGLSWRIRTPDGGFFTRSAVQKFKVQDPKYPGLNHDNEYLYHYQDDWYLLSSKVENSPEDYHFYYKGRNDWDGYSAAVYTRSAVLFESIGPELQTAQKVGDFNTFRKTDNTGCGPEPLVLEKKEVVEEGERTIKVEEIEEVEKVRDKEVTLFSRLFEQFKELGQDEENFLRELSKEEMVLDGLKMEATEVEELFGRALPIRKLK

NbL02g02200.1 leukotriene_A-4_hydrolase_homolog [MW = 68.66 kDa]

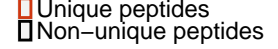
No. of times detected



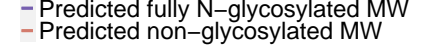
log(intensity)



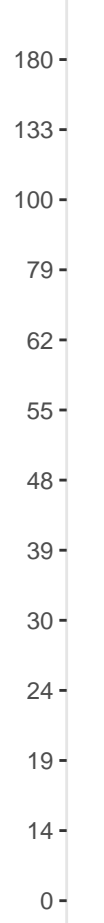
Values from



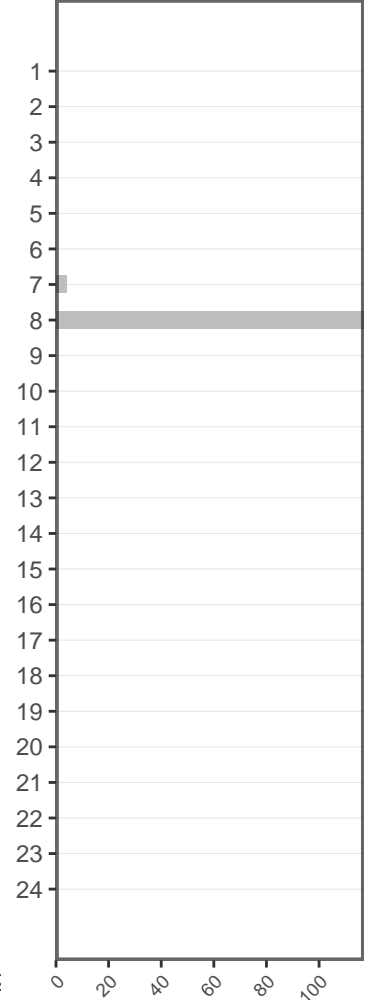
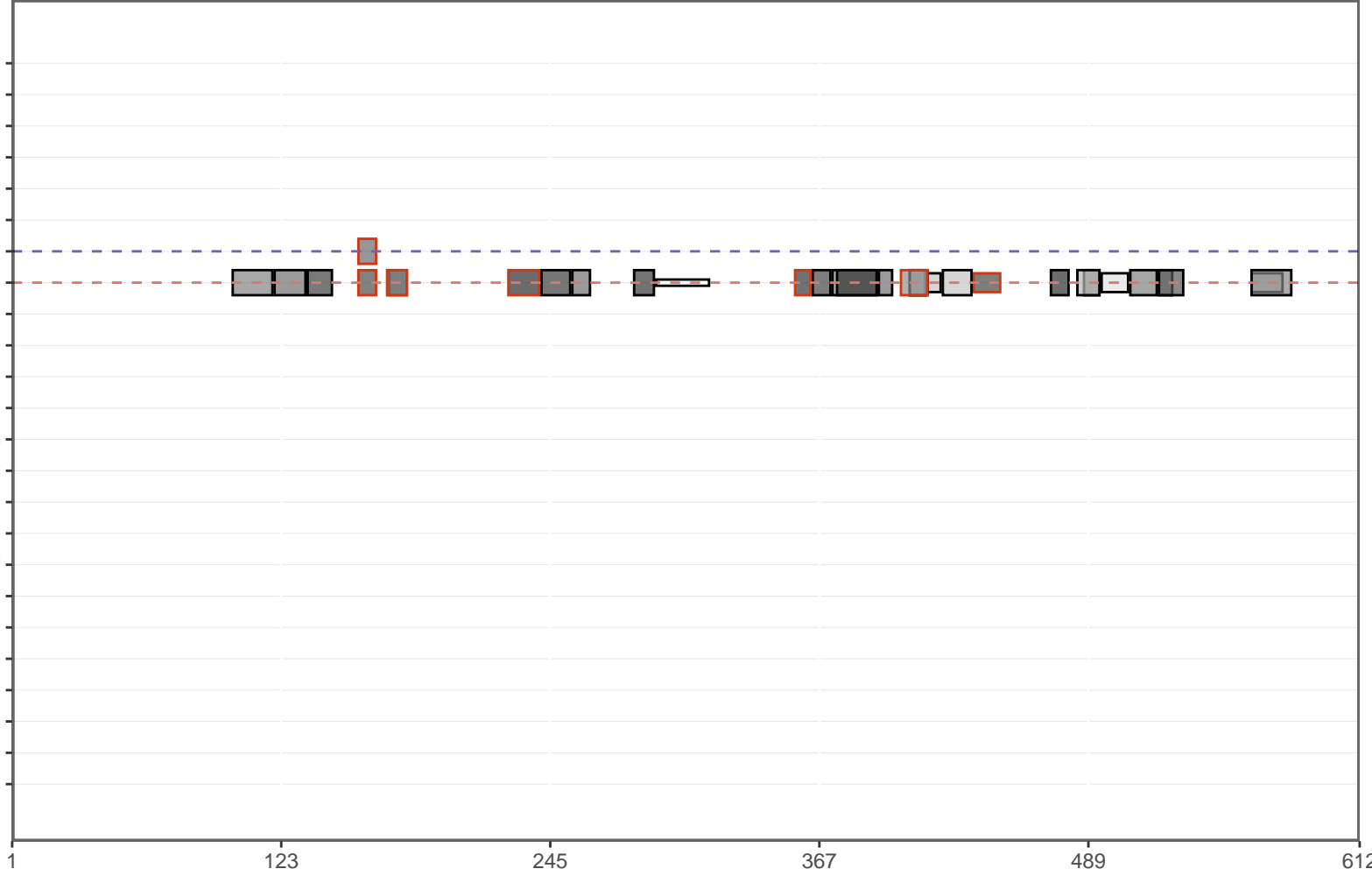
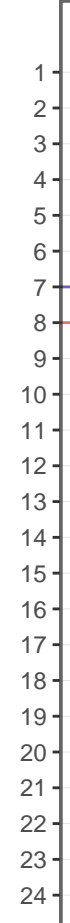
MW indication



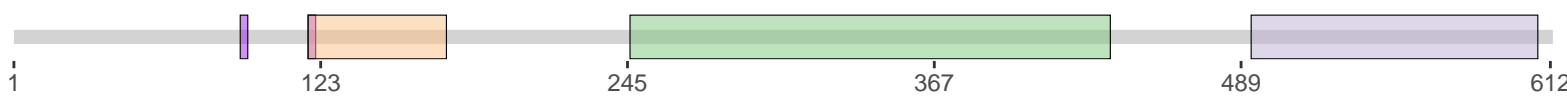
Molecular weight



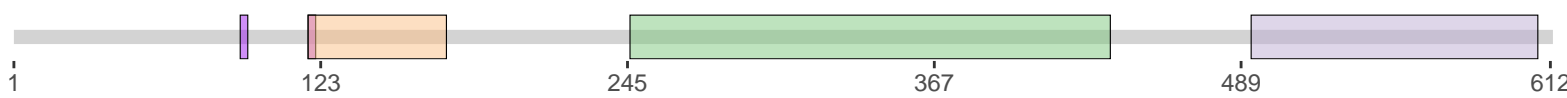
Gel Slice



Protein length



Pfam domains



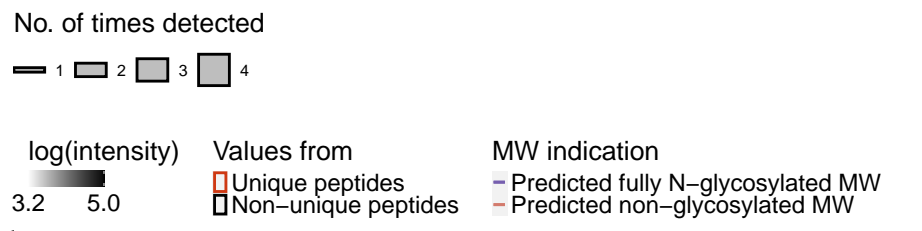
Pfam Description



Protein sequence:

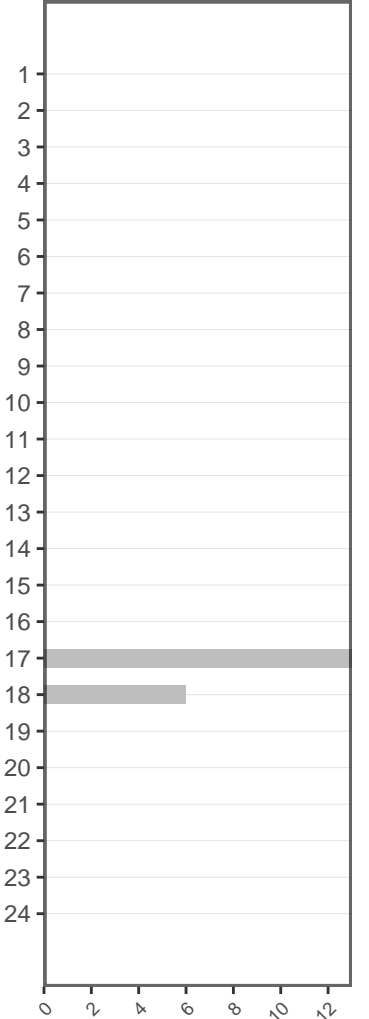
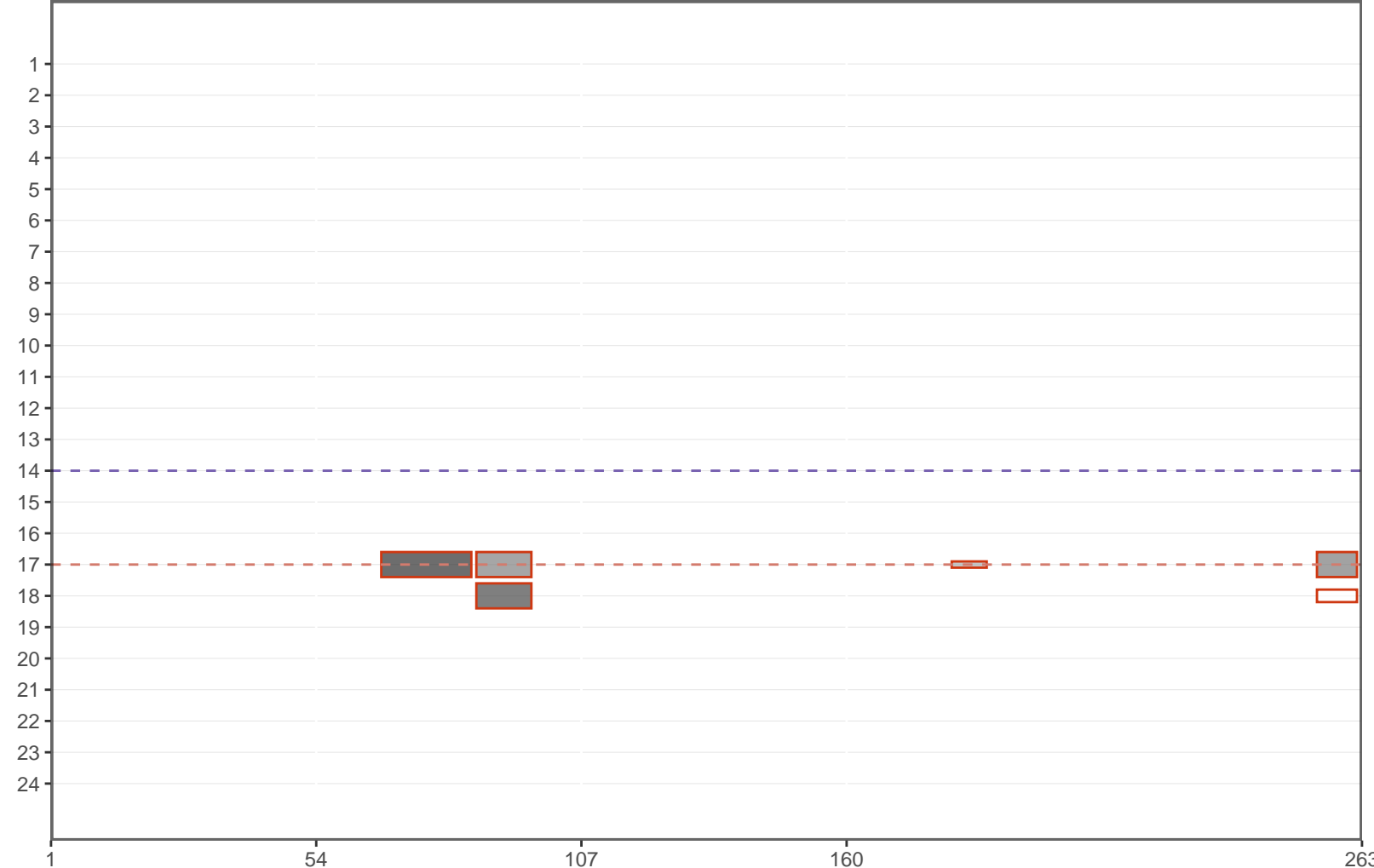
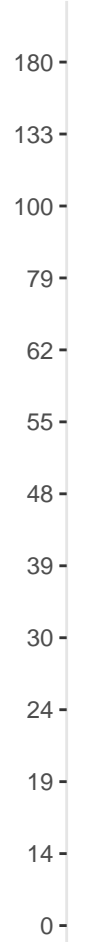
MASGQVVAHLELHSWGTGNLITNKNNDHFVWLNKGGFTTVAERRRIVEVQGEDAALNIGDVGWRLGIEEMERFKDMEFTLKTNGAGVDPDDVYSGVPYKGFQFLWRRIERIGRPAFDLKKYATFKFQSDTDMFLNFKADVPGIENIDKLVWTEGTGIPPDAMEFVSNYSKIVSLANEFKLGMPREDEVAADWKGGEWELVLENLPKSVEASQVTDALDARYHLLSEKDKVEVRAVFLGLAISARGRDYVGEVEKTKVEGRMKYLRPLVYALVGGAKKEEKAFARRVI

NbL02g02090.1 uncharacterized_LOC107785953 [MW = 29.08 kDa]



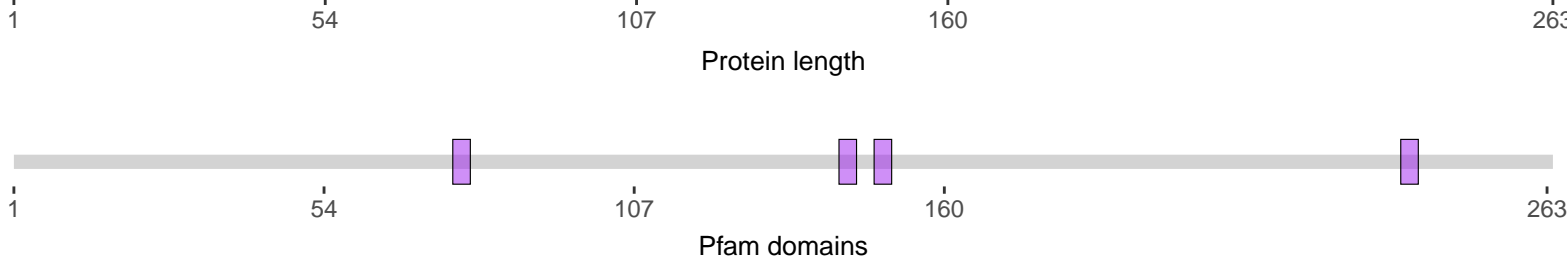
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains



Protein sequence:
 ILLSCGIPRFYIMQLKDRSLRFSNTHANVTGQLGSGIGNWVYLGWAKPQVDPADIKGARGEDWQSRGHFVPPWDEVQAFRISGPKFKILNHTGWHAGPLFTDQKMDFFNLELNNTNIVDHTHTDFINKNGVFLLDP

NbL02g02070.1 uncharacterized_LOC104220881 [MW = 184.43 kDa]

No. of times detected



log(intensity)



Values from



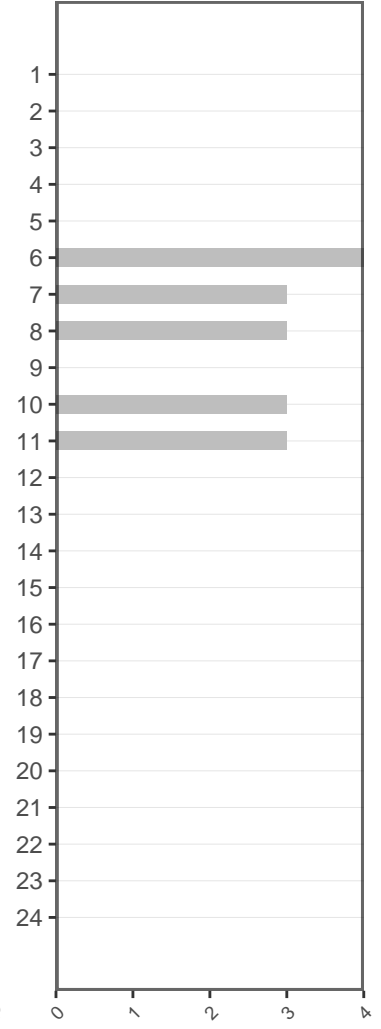
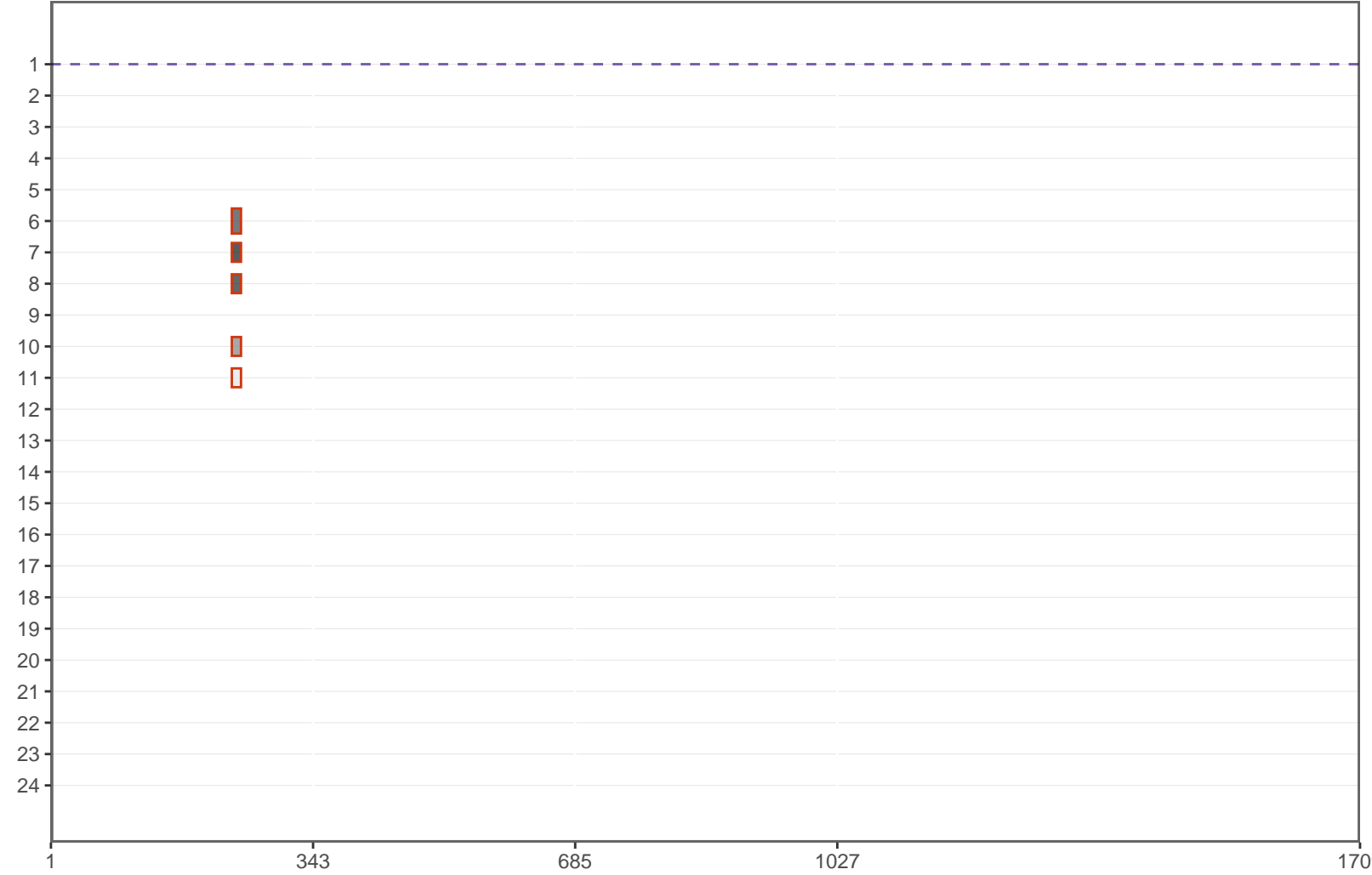
MW indication



Molecular weight



Gel Slice



Protein length

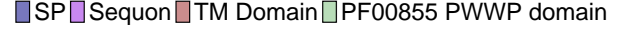


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

NAEGVSTRKHSDITKRESESTANQEGVVEHHILALEMDHEAGNAATADKMSGIEENFNVEGAIKSHYFTVNSGADVPPVVEETNFNVEGAIKSGYFTVNSGADVPPVVDGIVETYSKHTSNAETNGANNEYQDSSRADEGLVFHAHAEMKVDGPKGEVETGMSHTSNAETNGANNEYQDSSKADEGLVFRADAEMKVADEGEKGEVEKLNHADTAGESSEGGQKGTETEEVAEKTHAWMLNEKPVSLKMPGVLPPQGTDEEYISGDLWGVKVRSHIPWVPOQIFDPSD

NbL02g01760.1 isopentenyl-diphosphate_Delta-isomerase_I-like [MW = 33.19 kDa]

No. of times detected



log(intensity)



Values from



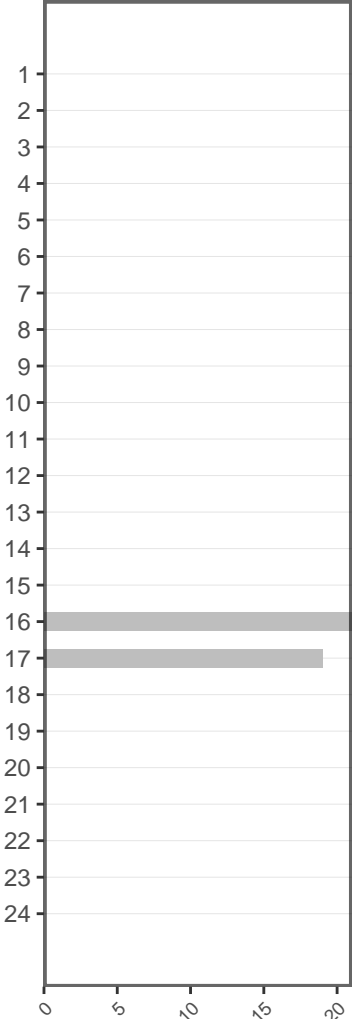
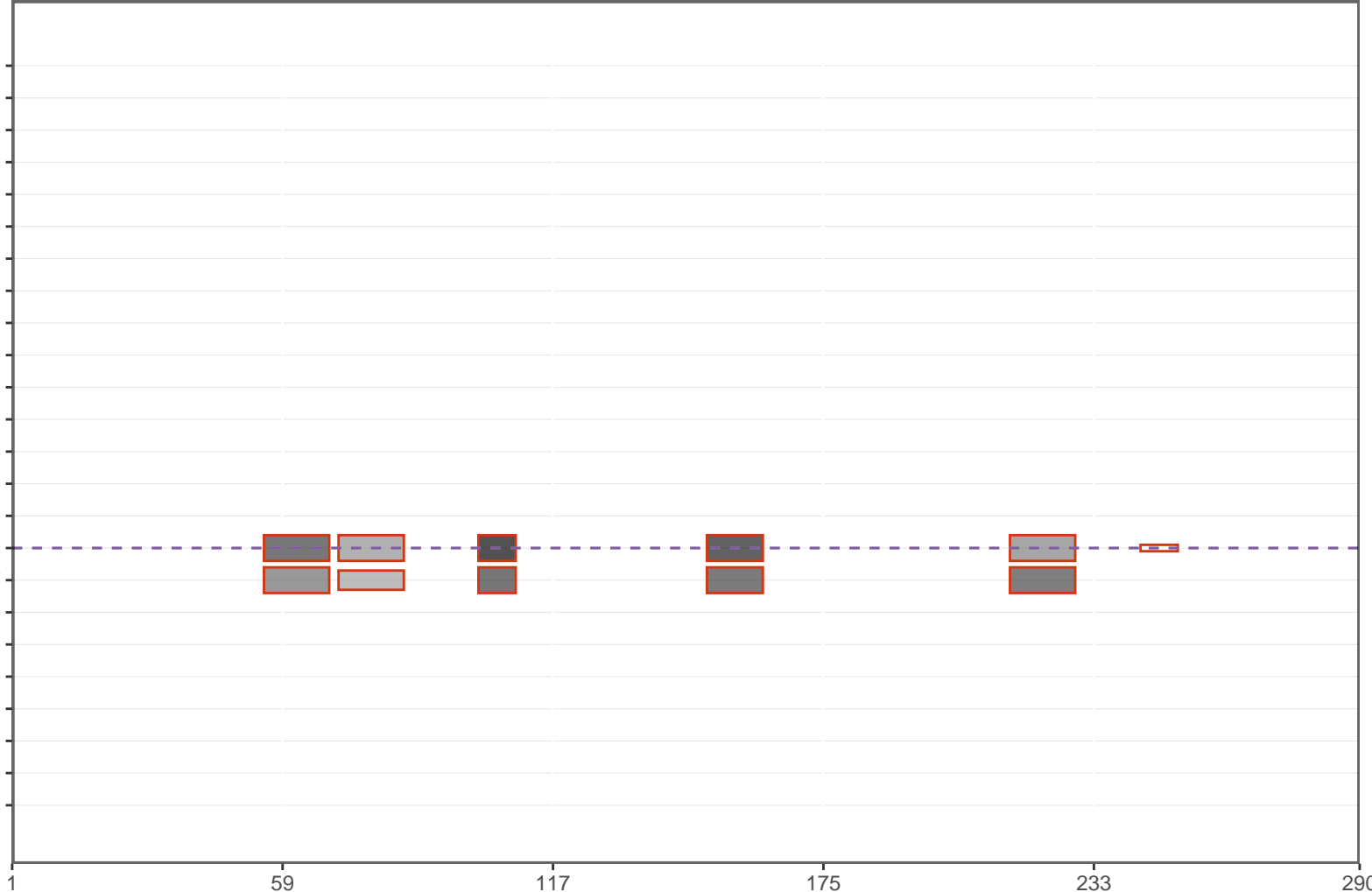
MW indication



Molecular weight



Gel Slice

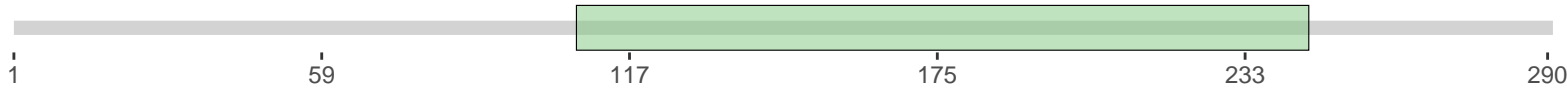


Protein length

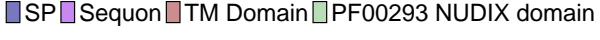


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

TFPLVWNTCCSIPLYRESELEEENLGVIRNAADRKLLDELGIPAEIVPVDQFTPLGRILYKAPSDGKWEHELDVLLFTVREVMKFPDVEADVWVYVNRQELKELRKADAGEGGLKLPVFRLLVDFNLFKRWVWHDLEKGTLEKVIDMKTHLFT

NbL02g01570.1 aspartate_aminotransferase_chloroplastic [MW = 50.72 kDa]

No. of times detected



log(intensity)



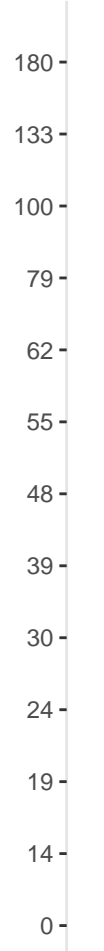
Values from



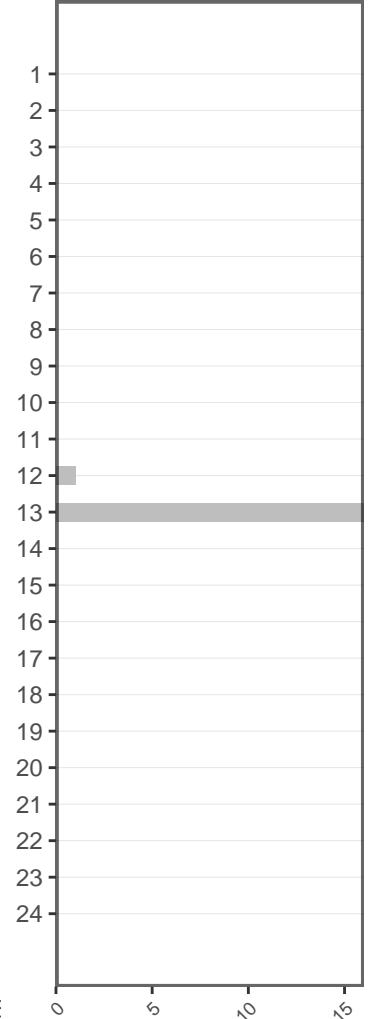
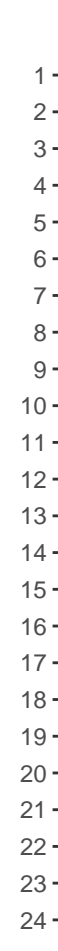
MW indication



Molecular weight

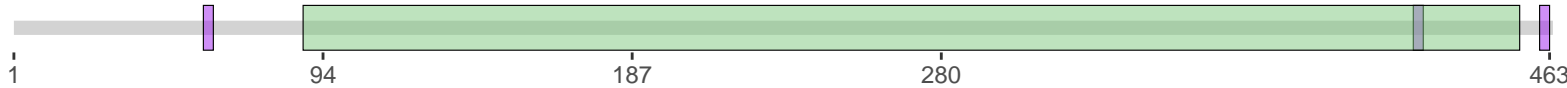


Gel Slice



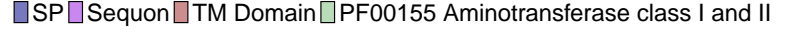
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

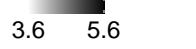
DFAGMIEDKAAPEGGFILLHGCAHPTGIPTTEGWEKIADVQENKHPFFDVAWGDFASGSLDEDASSVRLFAARGMELLVAGDYKNLGLYGERIGAINVLGSSADATRIVKSGLKRARPMYNNPPIHGARIVANVYGPPEFFDEWKGEMEMMAGRIKSVRQKLYDLSANDKSGDGYLYKDGIGMFSFTGLNKAQSENMFTNKWVHYMTKDGRIISLAGLSAANKDEYLAADIDVYVNS*

NbL02g01550.1 alanine--glyoxylate_aminotransferase_2_homolog_1_mitochondrial [MW = 26.13 kDa]

No. of times detected



log(intensity)



Values from



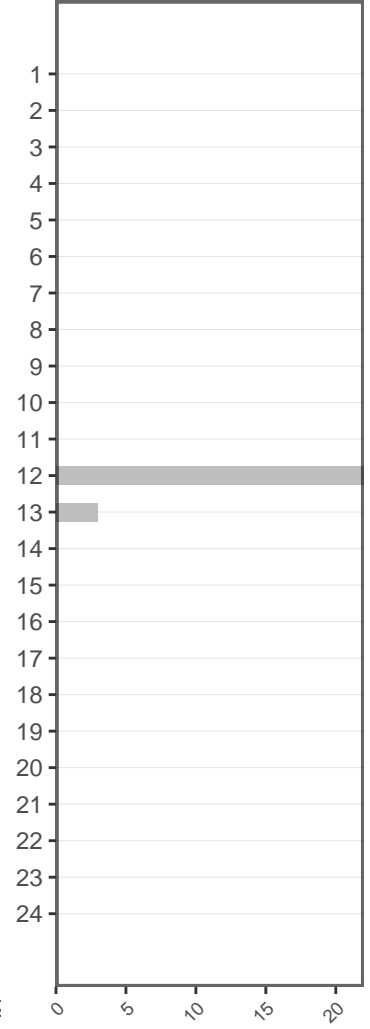
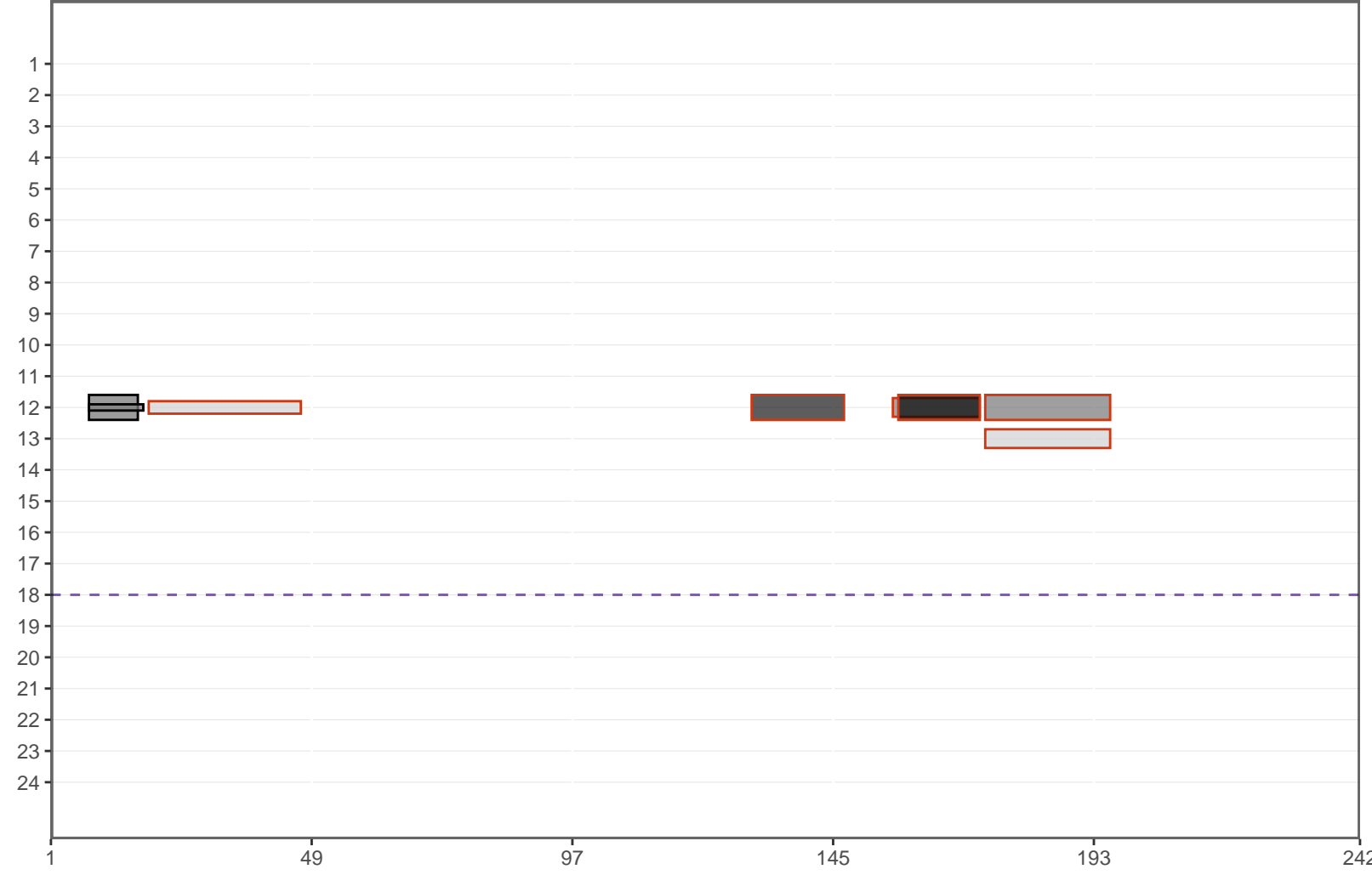
MW indication



Molecular weight

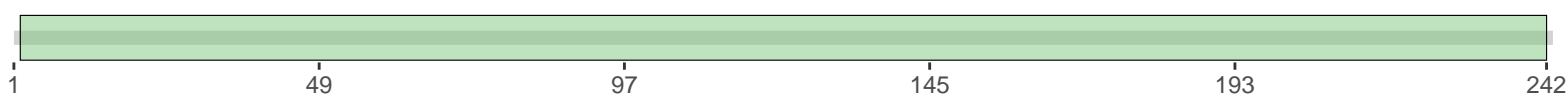


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

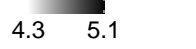
RNATHGGSANTIGLSTALNTWKYPIPDGEIHHVFNPNPYRQVFGSDAKRYAEDVGDHHDHGTSGKAWGFAETHQAGAGVAVELAPGYLALVYDIARKAGGVGIADEVDTGFGRTGSDVWFGTQGVFQNTMAK

NbL02g01540.1 alanine--glyoxylate_aminotransferase_2_homolog_1_mitochondrial [MW = 23.32 kDa]

No. of times detected



log(intensity)



Values from



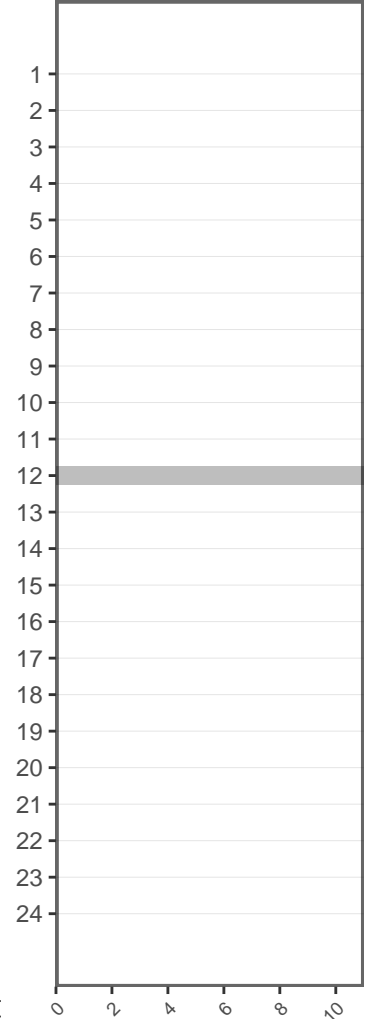
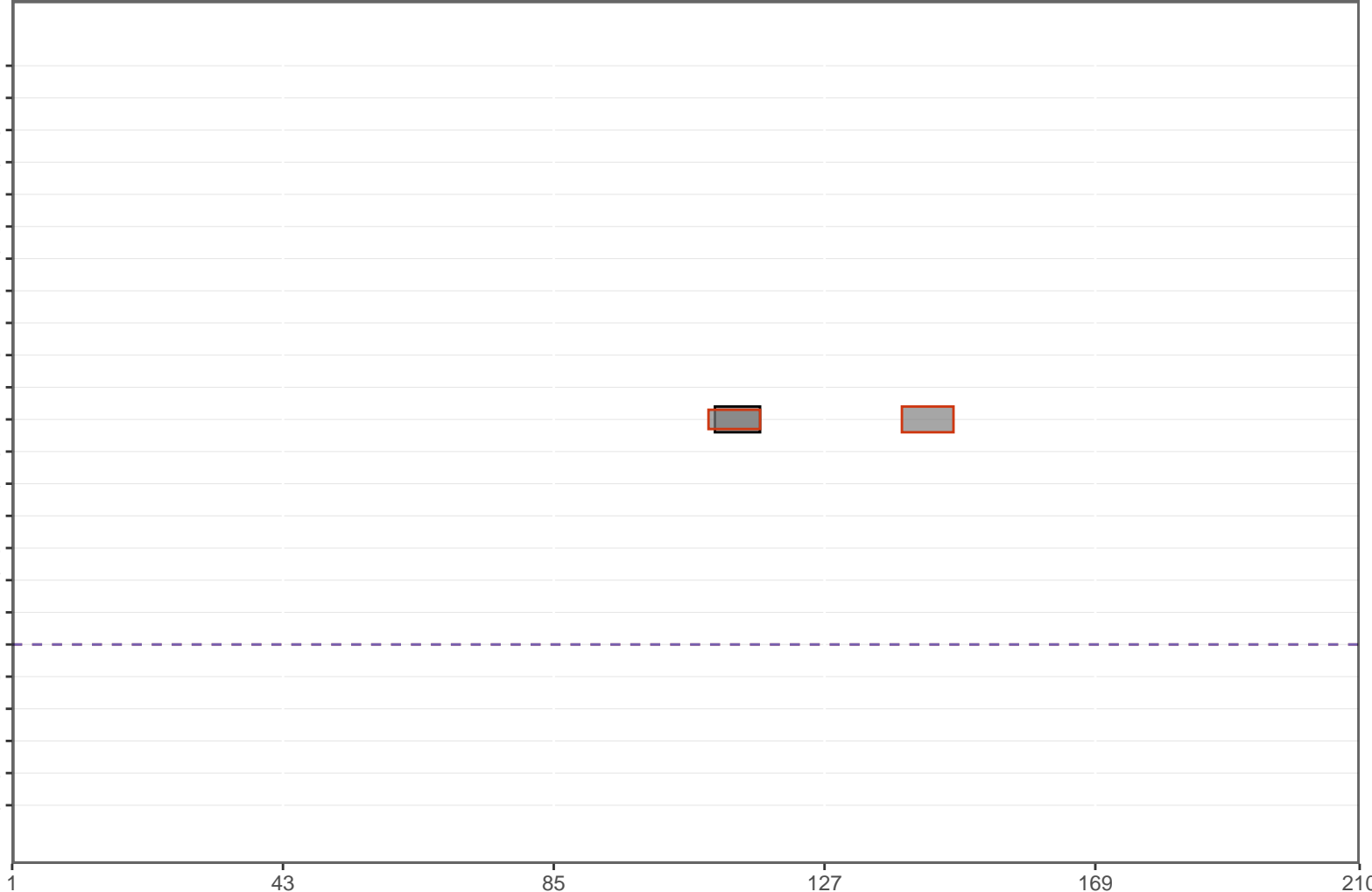
MW indication



Molecular weight



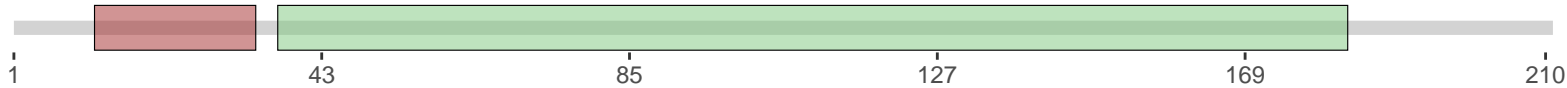
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ICAEVQSHLIGRLRDLGKRRHEIGDVRGRGLMVGIELVTRRKEKTPAKAETGVLEKLRFEGLVVGKGLHGNVFRKPPMFGKDDAGNLFTHWFNLRNFSWIPDLSIVENHFY*

NbL02g01370.1 L-ascorbate_oxidase [MW - SP = 61.46 kDa]

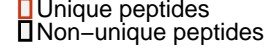
No. of times detected



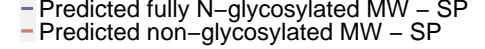
log(intensity)



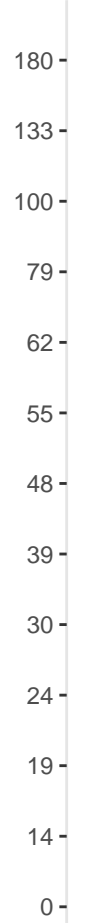
Values from



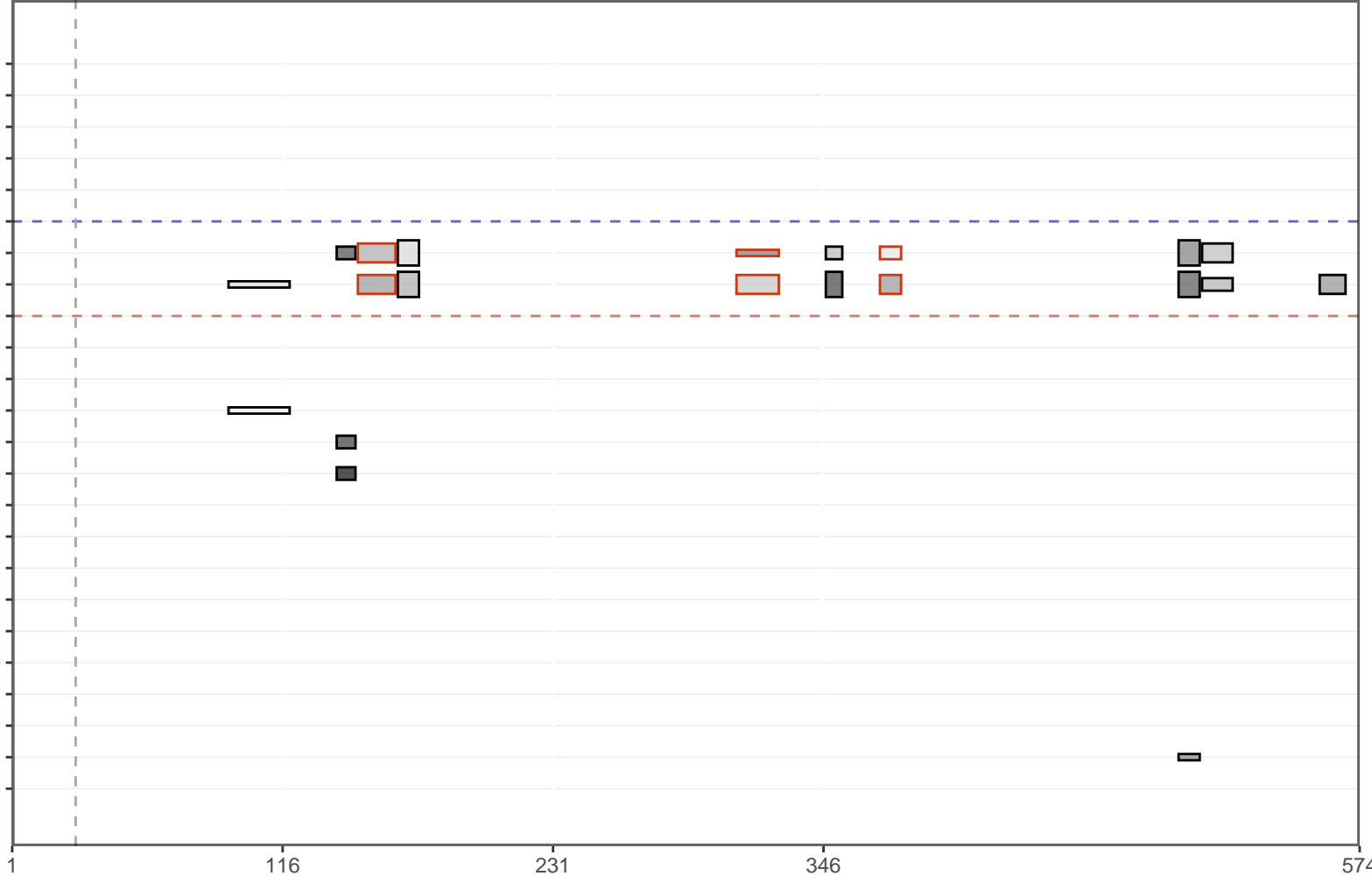
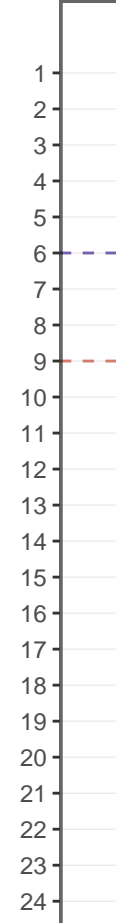
MW indication



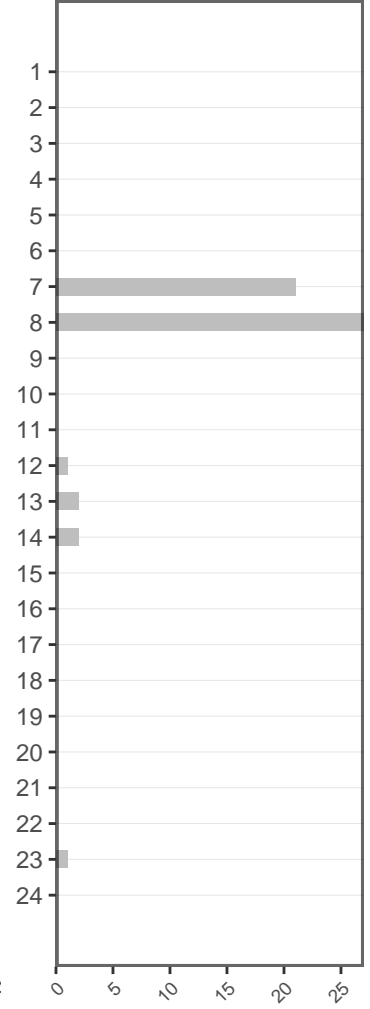
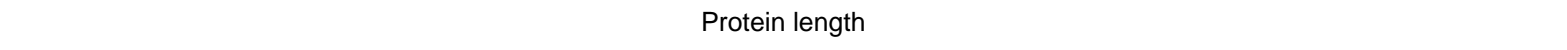
Molecular weight



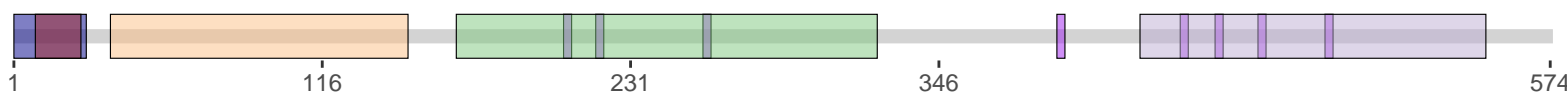
Gel Slice



Protein length

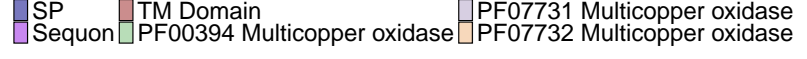


Peptide counts over 4 repeats



Pfam domains

Pfam Description

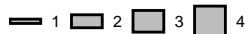


Protein sequence:

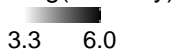
KLFLYSGETYSVLKAQDQPSRNYWASTKVRNRSATPNGLGIFTYYPNHPRRTPPTVPAGPHWANDAPRVAGSVAIKSHKDFHAPKTSDRIVMLNTGNRINGFVRSWVNVNFSNMPKHTPKLALKLHLLHTFEQTPPPENYHNENYDFISVQKNVWATTSNGIYRLKFTFTVDFILGNANTMFPNNSETHPWHLHGHDFFWVMGVNGKFNKGDIPKKNYLNIPIMKNTIPVHPYGVWTLRFQADNFGVWVAFHGHESHFFMGMGVVFEEGIDKVGKLPSTSMGCCD

NbL02g01350.1 bifunctional_aspartate_aminotransferase_and_glutamate/aspartate-prephenate_aminotransferase-like [MW = 51.59 kDa]

No. of times detected



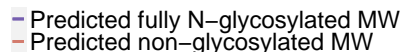
log(intensity)



Values from



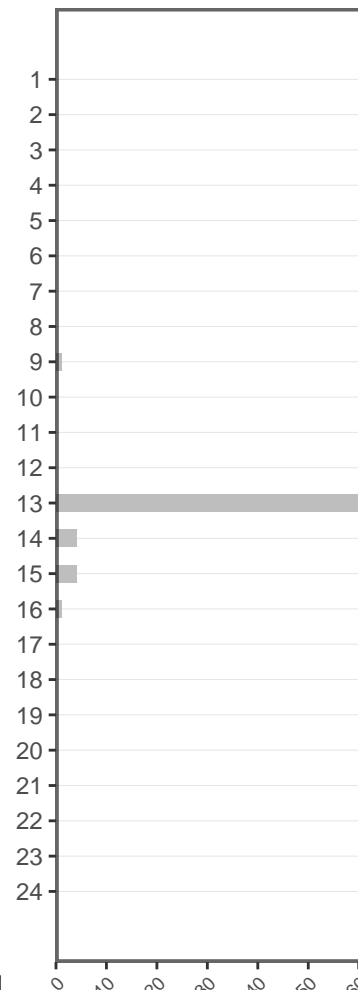
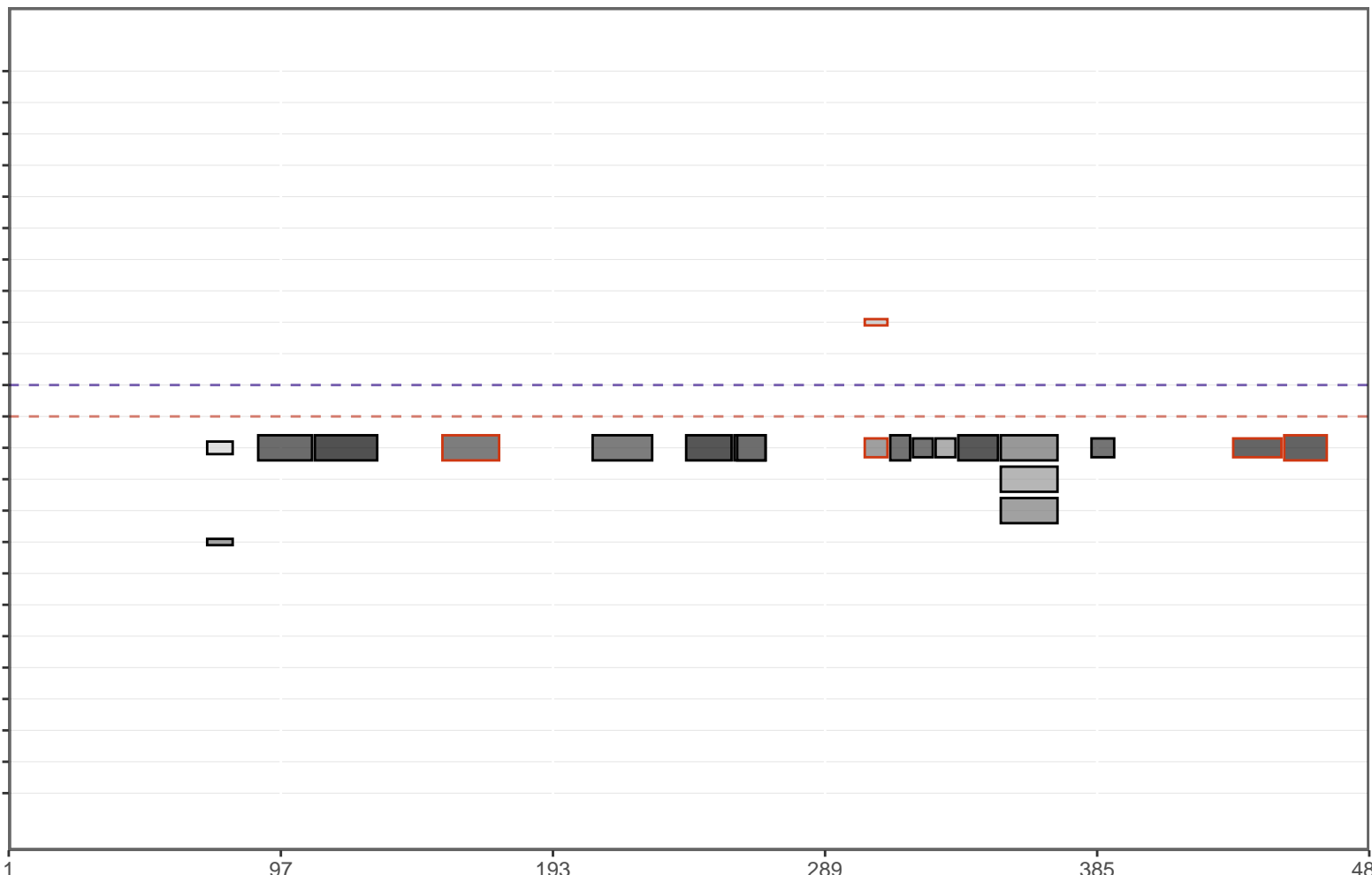
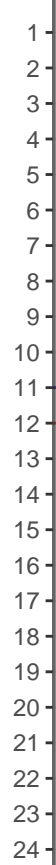
MW indication



Molecular weight



Gel Slice

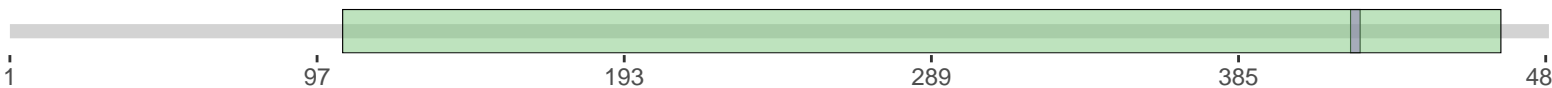


Protein length

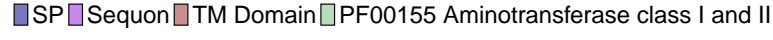
Peptide counts over 4 repeats

1 97 193 289 385 481

Pfam domains



Pfam Description



Protein sequence:

KLLESKLSKSRLLAGSPSNPTGQVYPRKLEEEAEIARHPRLVHDEIVEHIIYAPATHTEFASLPGMMDRRLTVNGFKAFAFMTGWRLLGVAGPKHFVSAQNKIGQGFTEGASISGKAQAAALGLGVYDGEAVATMVKAFRRERDDLVKSFGEIDGKIKSEPRGAFYLFIDL65YGVGVDFGSDNDESELGRYLLDKAQVALPGDAFGDDTCIRISVAASLSTLQAVERIKKALVTLRSHVPI

NbL02g01320.1 inositol-3-phosphate_synthase [MW = 56.39 kDa]

No. of times detected



log(intensity)



Values from

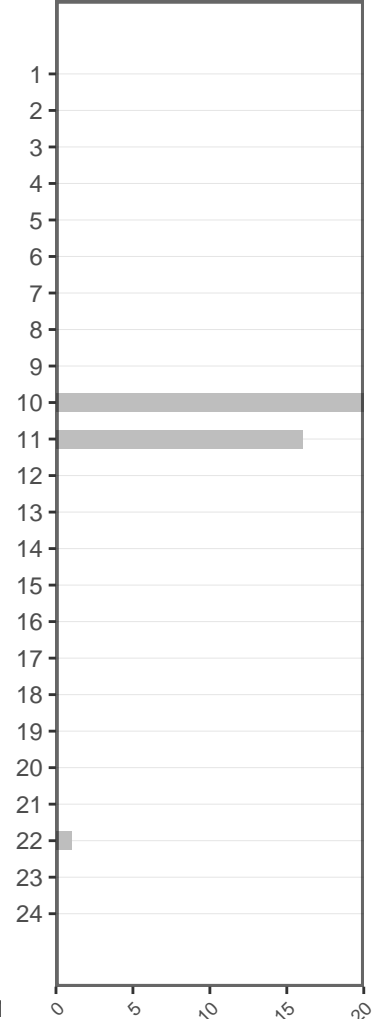
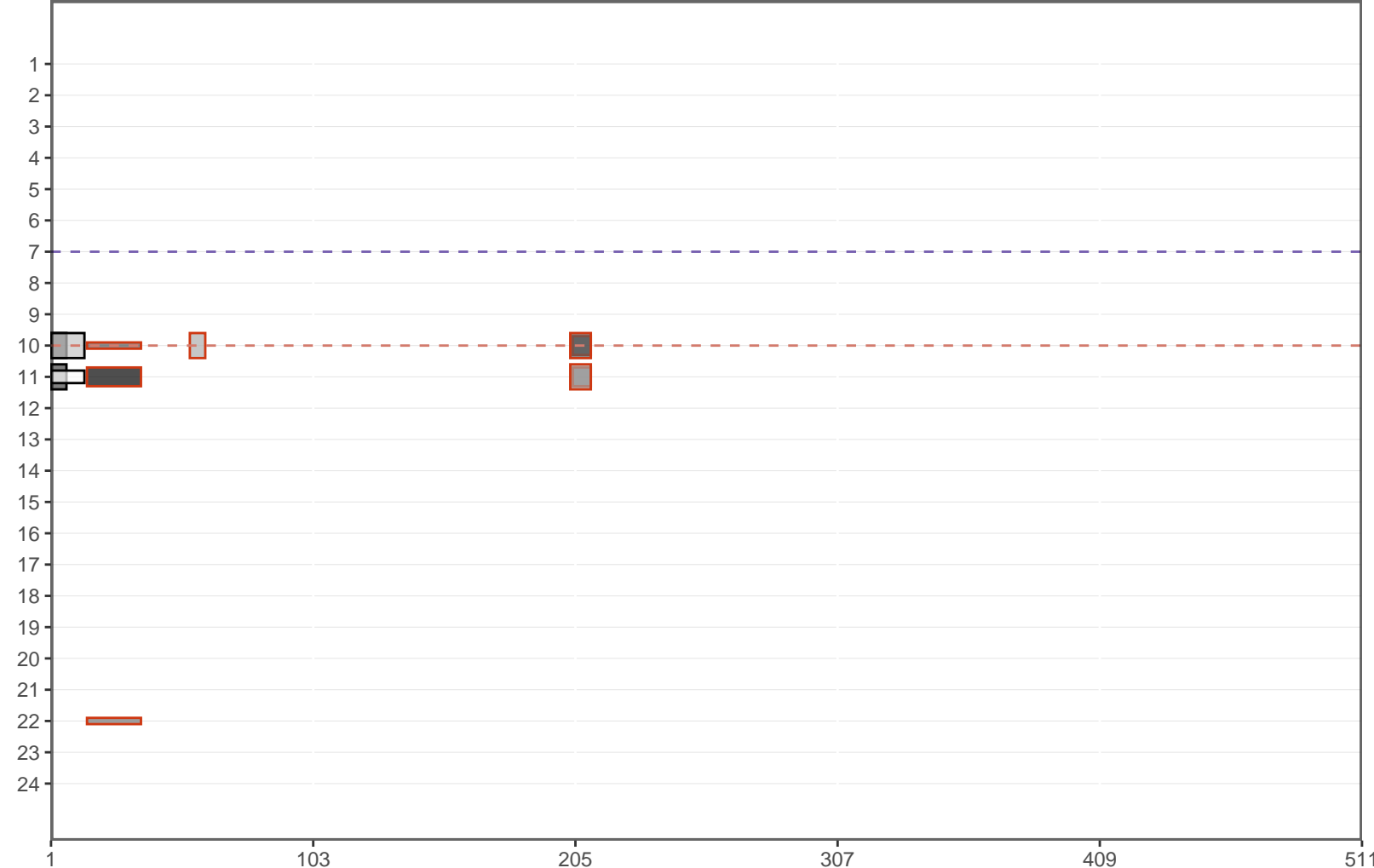
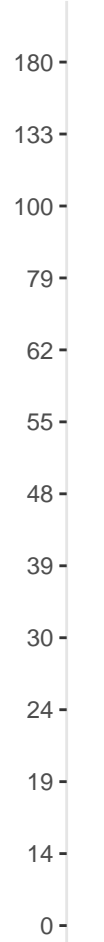


MW indication



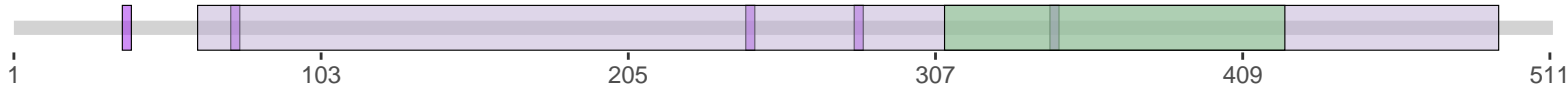
Molecular weight

Gel Slice



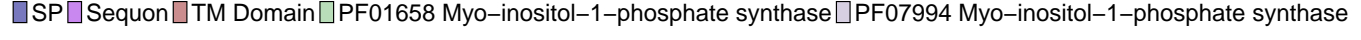
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

***GLNDTMEILFASVDRNEAIESPFLVAIGLENVPFINGSPQNTFVSGLDLAKRNLFGGDFKGGDTKMGKVLVDFLVGAGIKPTSVSYNHLGNDGMNLSGAPQTFRSKEIKENYDDMVSSNAILVEPGEHPDHVAVIKYVPYVGSKRAMDVEYSEIFMGGKNTVLHNTGEDSLLAIPILDVLLLAELSTRIGLKAEGEGKFKHSFHPWATLSVLTAKPLVPPGTFVVALSKGRAMLENLRADVGLAPENMILEYK

NbL02g01210.1 asparagine_synthetase_[glutamine-hydrolyzing]_2 [MW = 70.87 kDa]

No. of times detected



log(intensity)



Values from



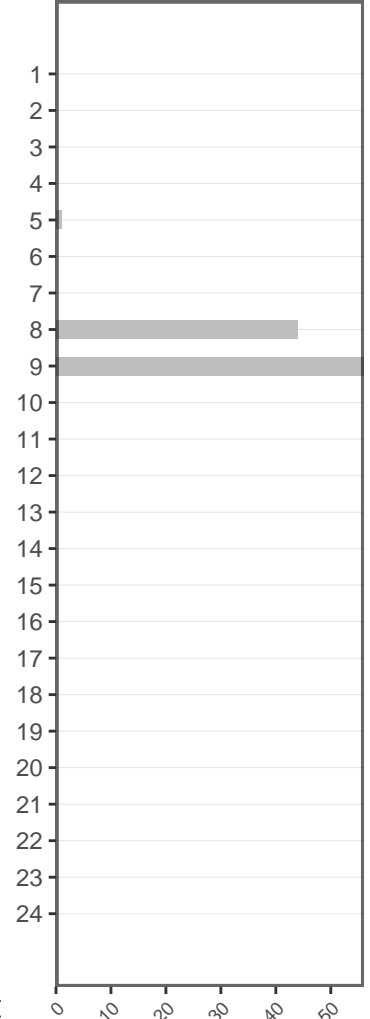
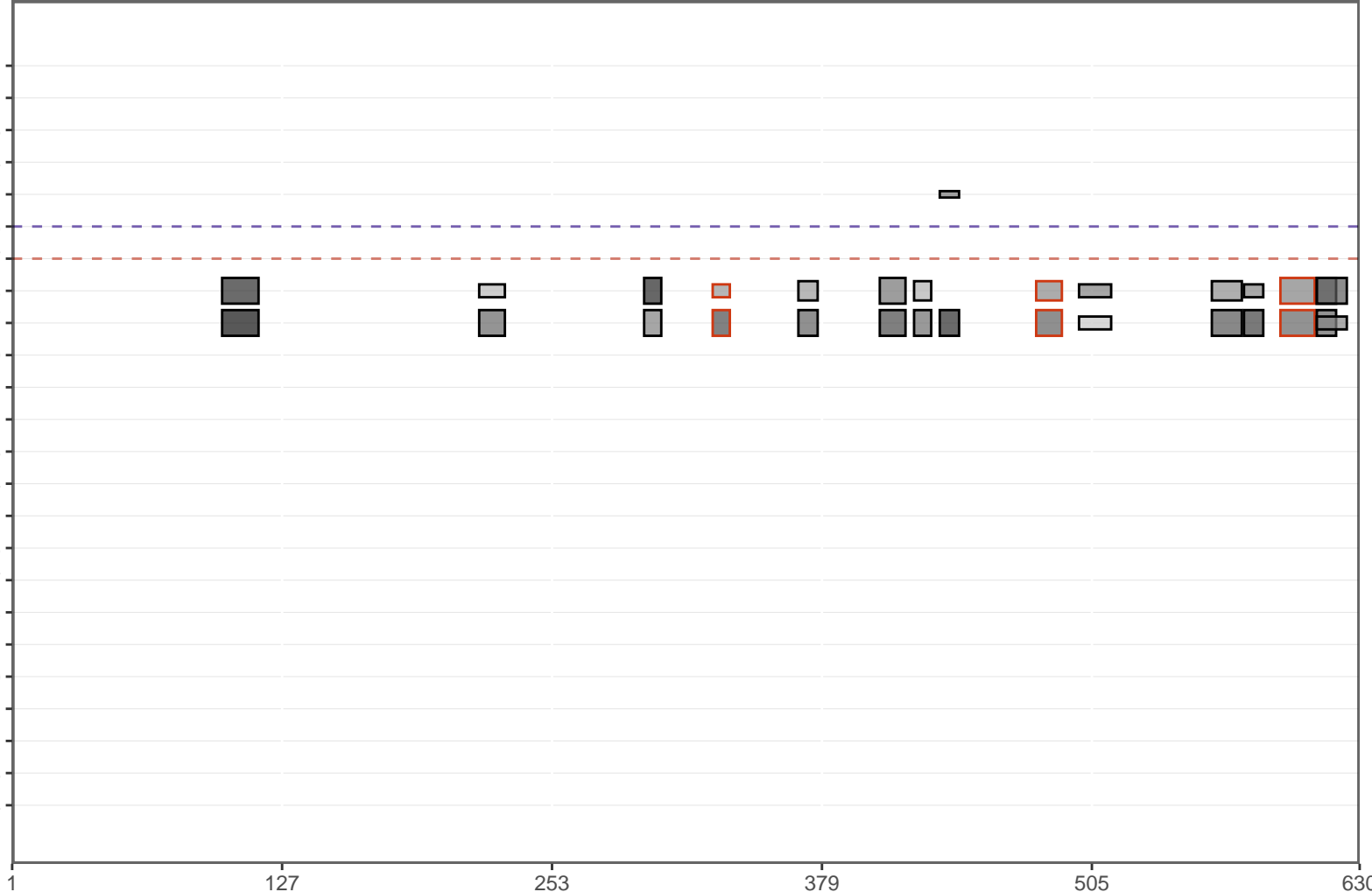
MW indication



Molecular weight



Gel Slice



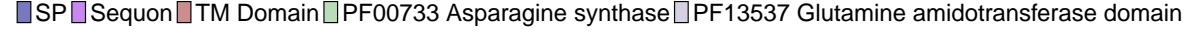
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

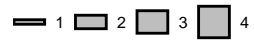


Protein sequence:

IRQVGSQLIHTFCVGLKGSPLKAKAREVADVPLGTRHHEHFHTVGEIGDALDEVIYHYETVDVTTIRASTPMLMSRKKKLGVMVLSGEGSDEIFGGYLYFHAKPKNKEEFHOETGRKKKAKHLYDGLRANKKSTSAWGVEARVPLDKERINVAMNIDPEWKMIRPDLGRIEKWVLRNFAFDGGNPNPLKPHLYRQKEGFSDGVDGYSWIDGLKDHASSLVSDGLMNTASFYVPHNPTTKEGYVYRIFERYFEPKNAARETVPGSPGSAAGSTAKAVEWBAVYSKNDLPSGRA

NbL02g01180.1 annexin_D2-like [MW = 35.91 kDa]

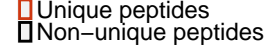
No. of times detected



log(intensity)



Values from



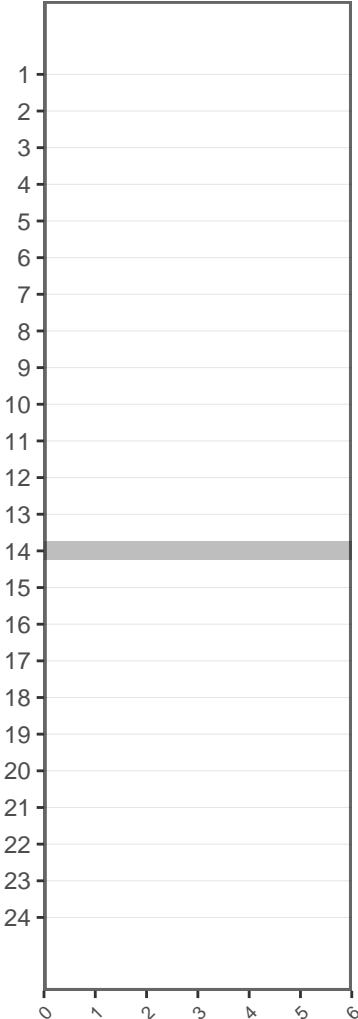
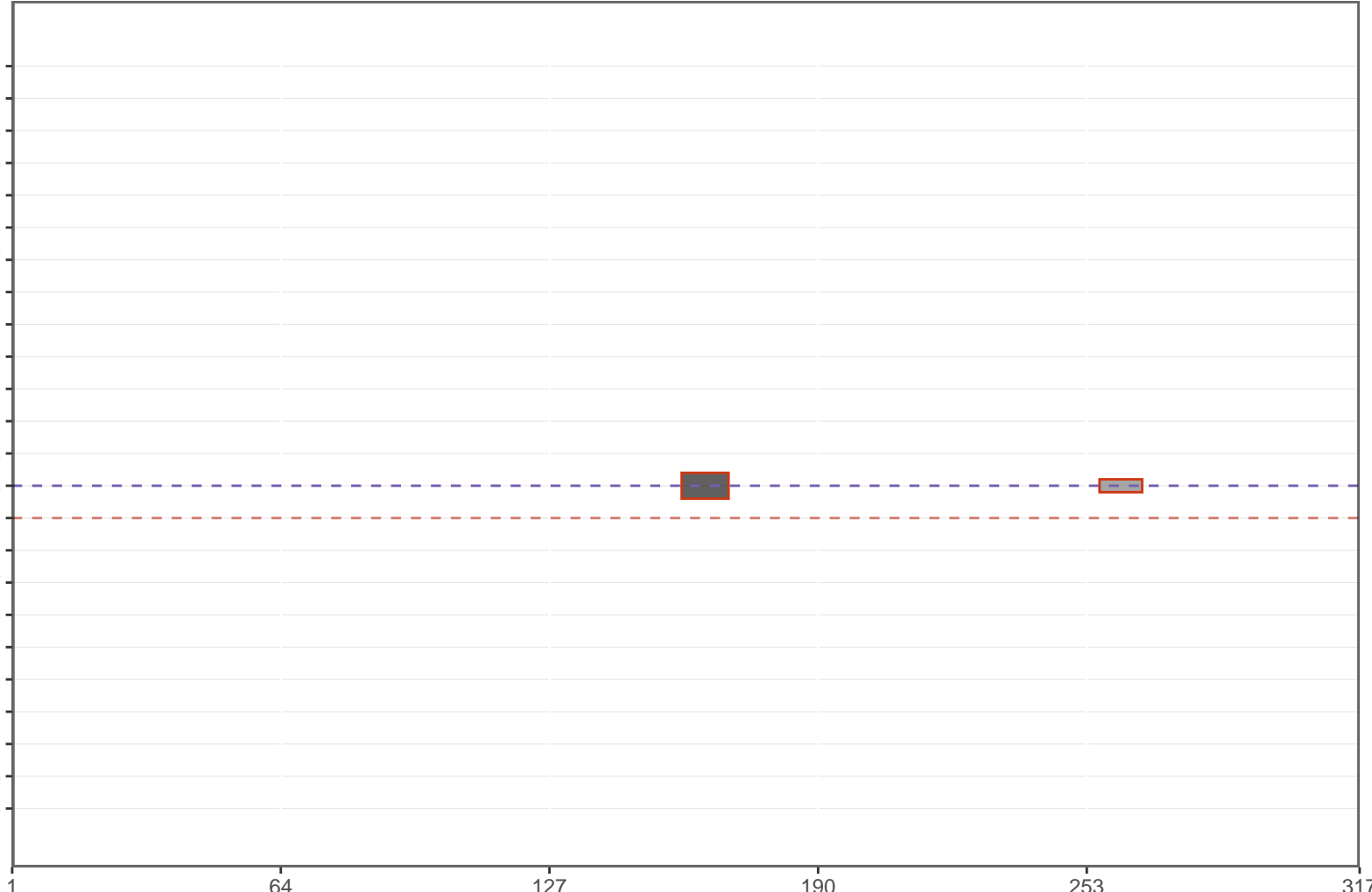
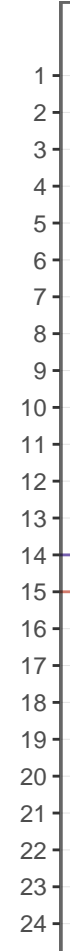
MW indication



Molecular weight



Gel Slice

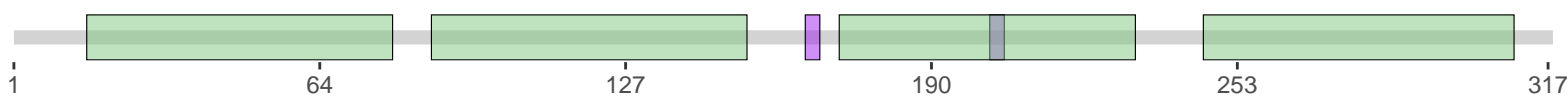


Protein length

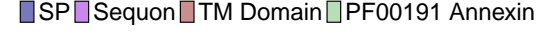


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

FRKLVPLVYAFRYEGEEVNTLARKENILHEKISDKAVNDELRIRISTRKAQLNATFNHYLDQHGNEINKDLETDSDDDEVYKILSAMIEGLKTPKPKYFEKVLRLGKGGAGTDEWDLFRVVTTRAEVDMERKEEYQKRNVSPLDRAMAGDTSGGYERMLLALIGHGDA*

NbL02g00700.1 transketolase_chloroplastic-like [MW = 79.86 kDa]

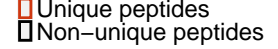
No. of times detected



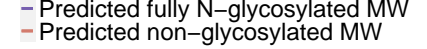
log(intensity)



Values from



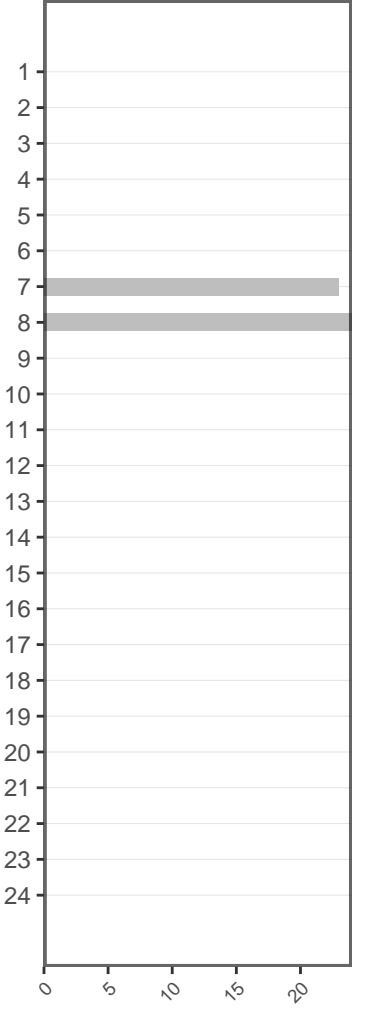
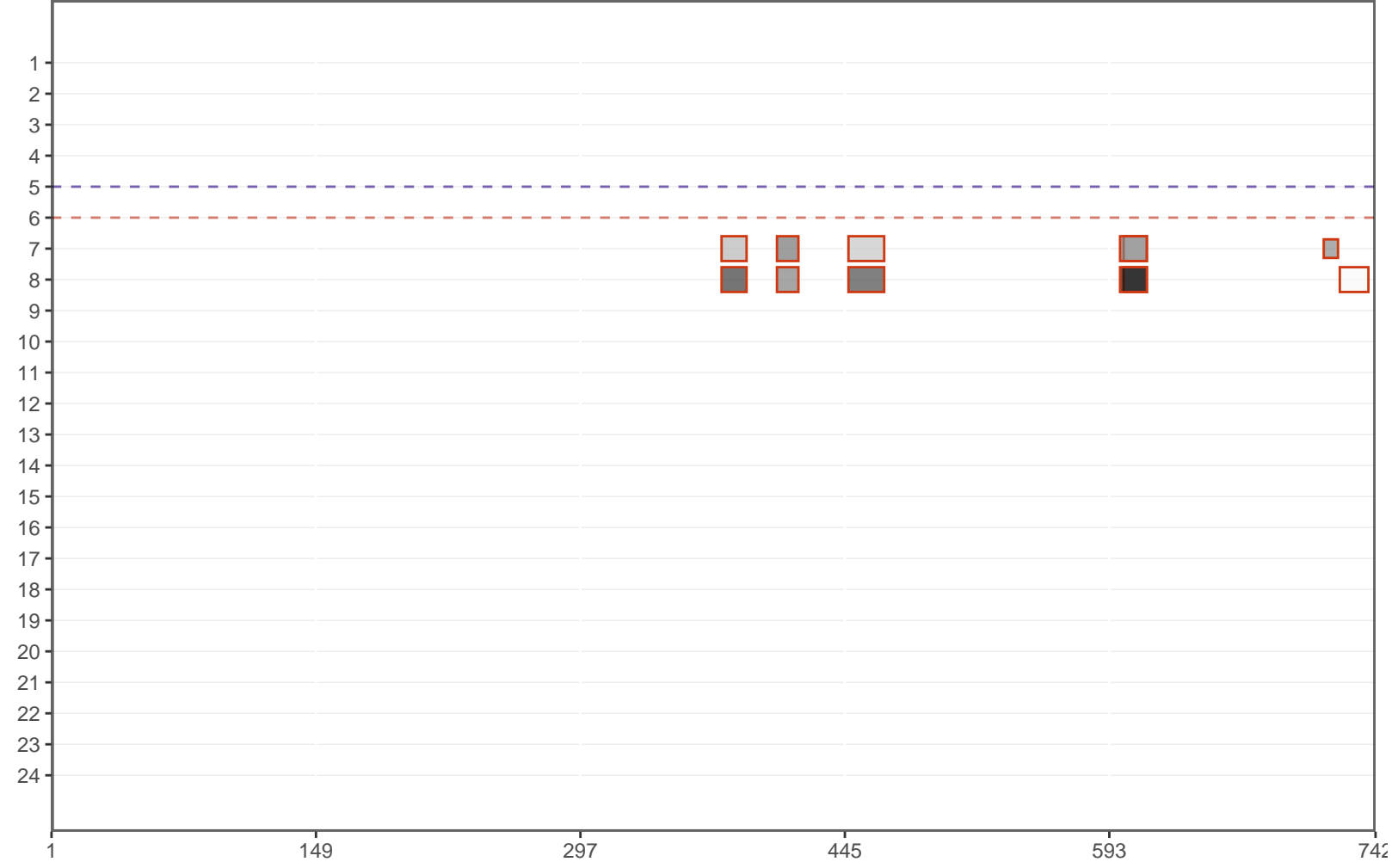
MW indication



Molecular weight



Gel Slice



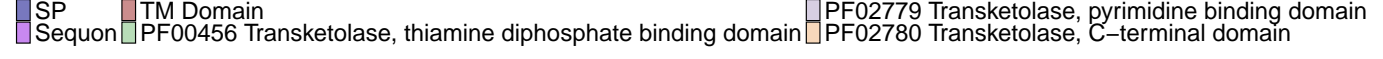
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IPYEPFHVPEDYKSHWSRHYPEGAALAGWNTKFAEYEKYPEEAELKSVITGELPGWKEKALPTYPESPADATRNLSGQNLNALAKVLPGLFGSADLASSNMTLKMFGDFQNKTPPEERNLRFQVREHMGAGNGLALHSDGLPVGATFFVFTDMRGAMRISALSEAGVYVMTHDEGLGLEDGDPHQPIEHLASFRAMPNLMFRPADGNETAGAYKMAVLRKIKTSPHLSRGLPQLTGGSSMEGAANGGVILSDNSSGNKPDVILGTGSELEIAVKAADLRP

NbL02g00300.1 uncharacterized_LOC109205733 [MW = 16.69 kDa]

No. of times detected



log(intensity)



Values from



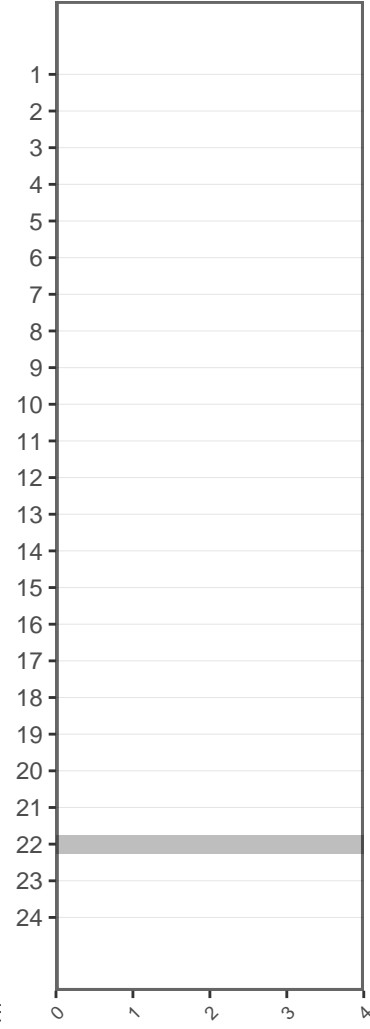
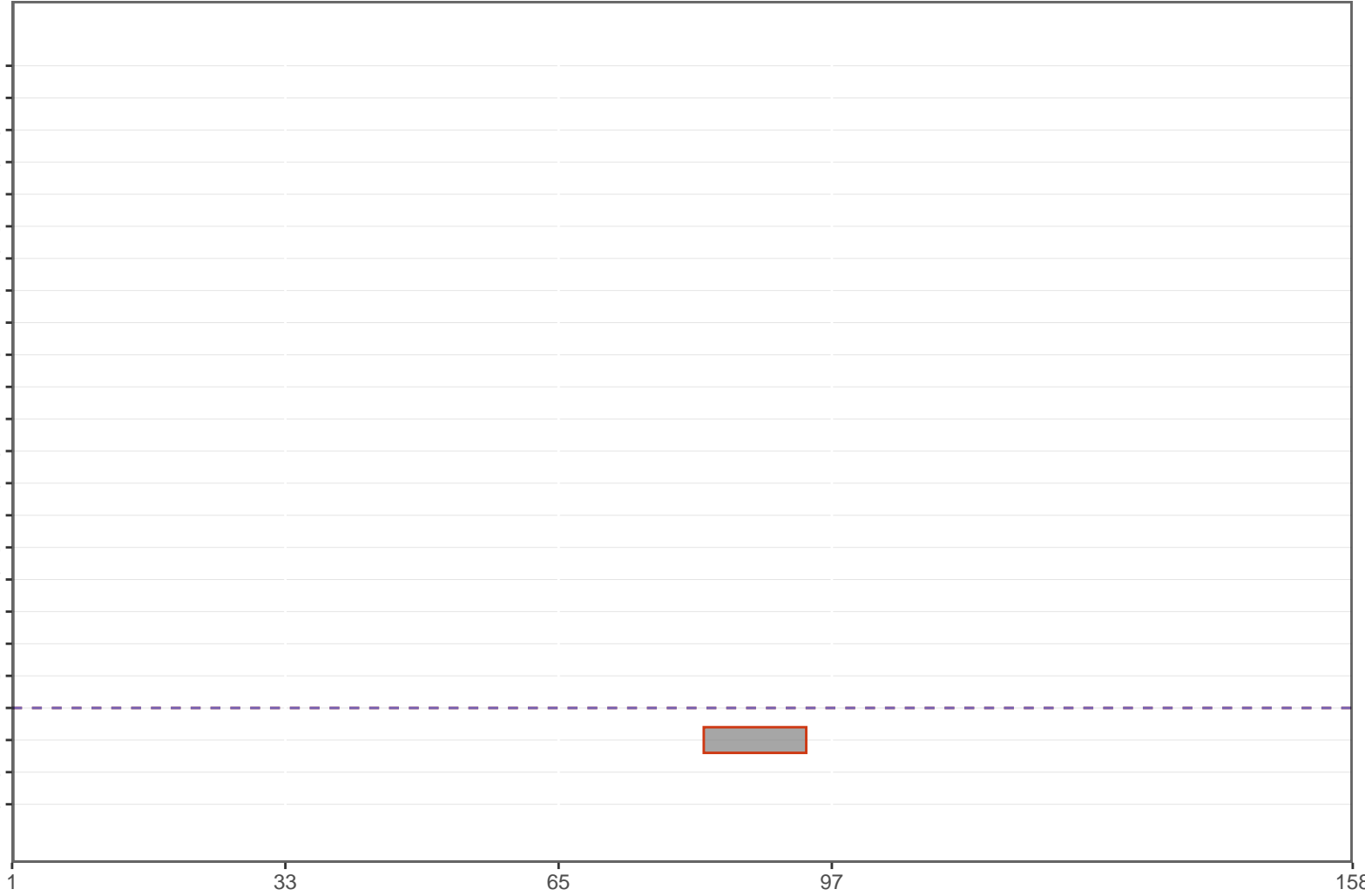
MW indication



Molecular weight



Gel Slice



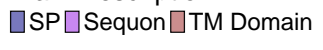
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IRCAEGGTQTVTRSGSTFVAPVQGEKESPALDDGGSGFPPRDDGGGGGGGGGGGNWKGFFFGFLAFLGFLKDGDEEGPYRDGRRR

NbL02g00260.1 4-alpha-glucanotransferase_chloroplastic/amyloplastic [MW = 65.29 kDa]

No. of times detected



log(intensity)



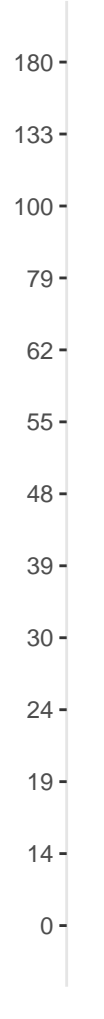
Values from



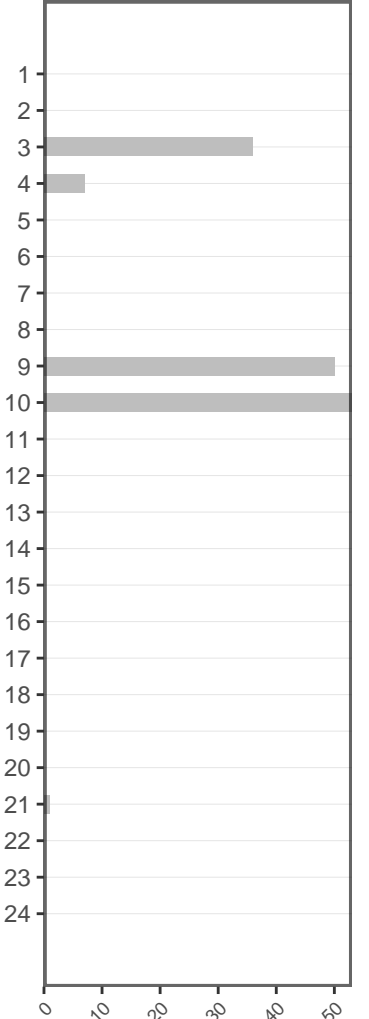
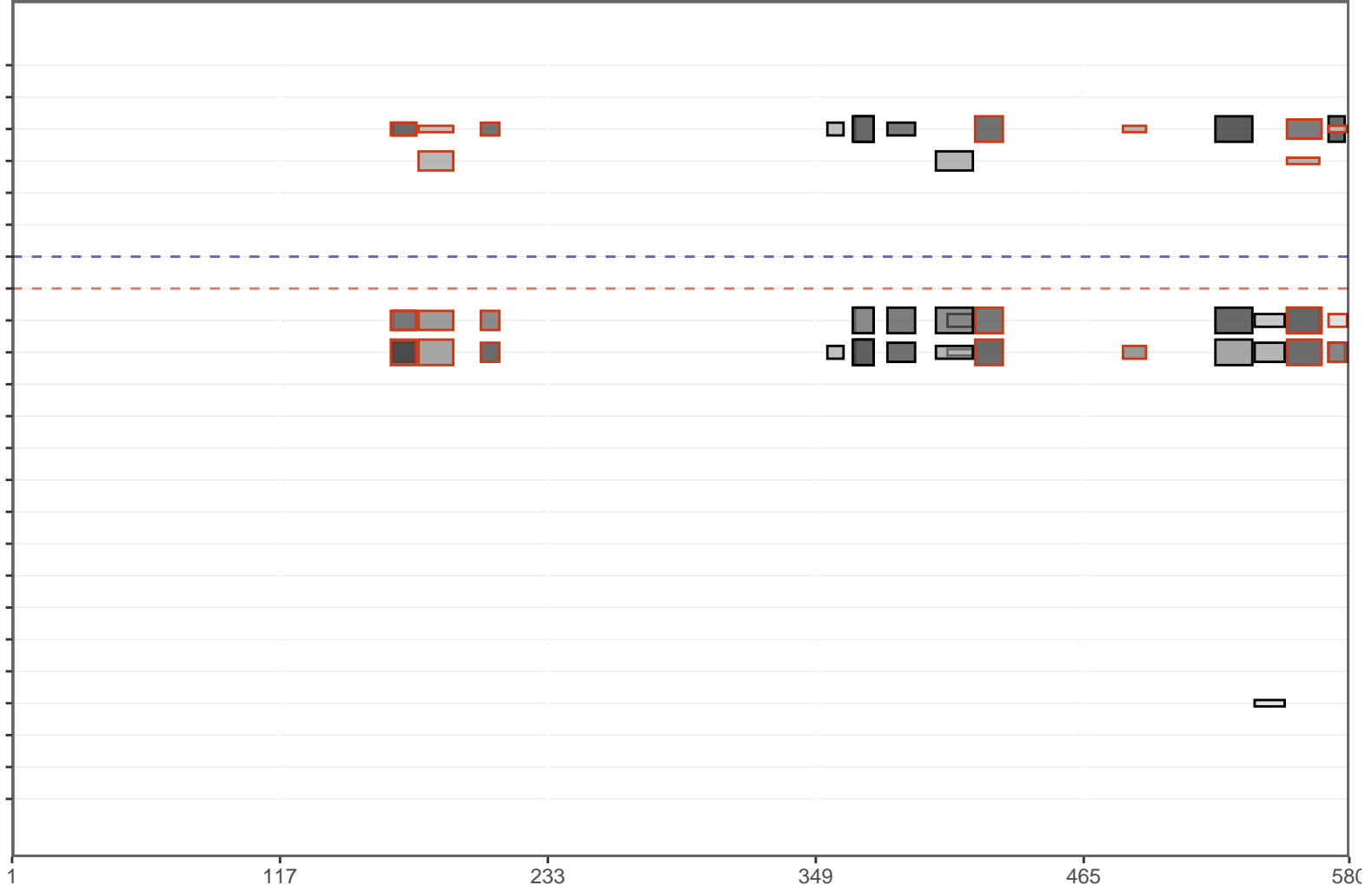
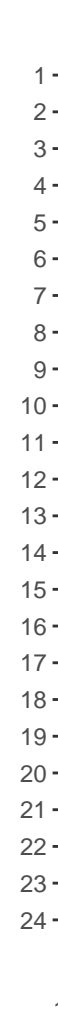
MW indication



Molecular weight

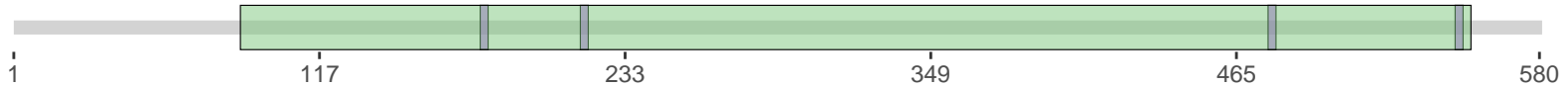


Gel Slice



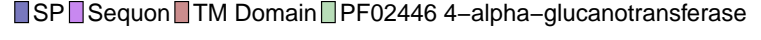
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

WQKVRDARSKGSGIMGDMPPYVGHHSADVWANKGFLNFKGFLVSGVPPDAFSETGDLWGSLYDWWAMEKDFGFSWWRIRRRATDLDFDFRDFHFRGFAFWVSEAKVAMLRGWKVGPKPLFDIAFQAVGKINIAEDLGVTKDYYQLRKGIEAPGMVLFQFGSGDAENPLPHINHEGNQVYYTGTHTDNDTRRGGWNLIPQEEKSNVLMYLENEEEIEISWGLIEAIVSBRVAWVPMQDVLGLGGEERMINPATGFGNWSWRIPSBTSTFDSLDEAKLIF

NbL02g00220.1 2-hydroxyisoflavanone_dehydratase-like [MW = 35.4 kDa]

No. of times detected



log(intensity)



Values from



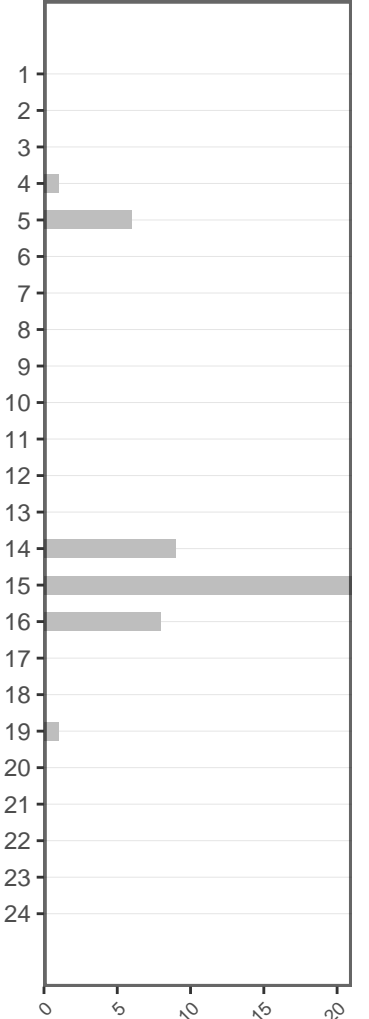
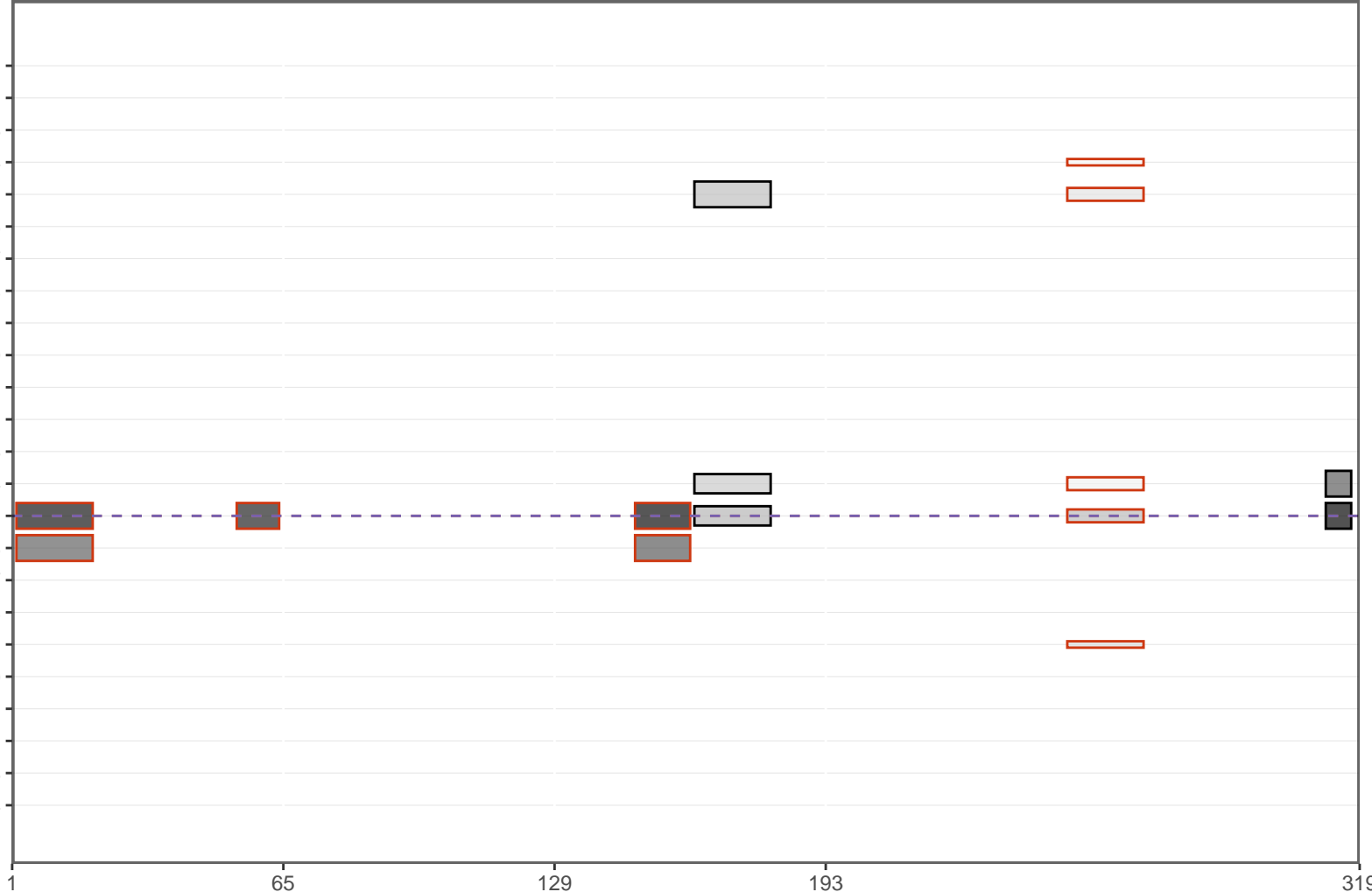
MW indication



Molecular weight

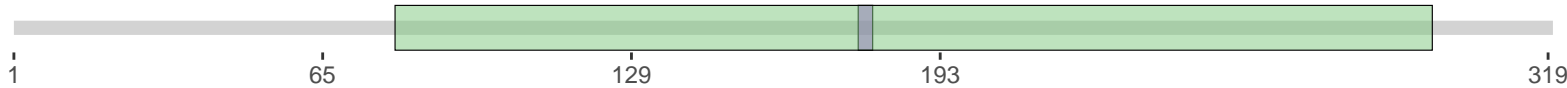


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KDAEPVIANHGDIDRLFIAGDSAGGNVFNMTMRVGRRELSITGVKLVGAIFRFFFLPEVENEGYKLVMTGPPREGGINSMPNVPSENGPBLSELGGRLFLGAGEKDELIPSEVSRFAEAVKNSGWKELEYIEVEGEGHGFGQANPETEKSKHLIKRMAFPIQRN

NbL02g00180.1 uncharacterized_LOC109214761 [MW = 44.02 kDa]

No. of times detected



log(intensity)



Values from



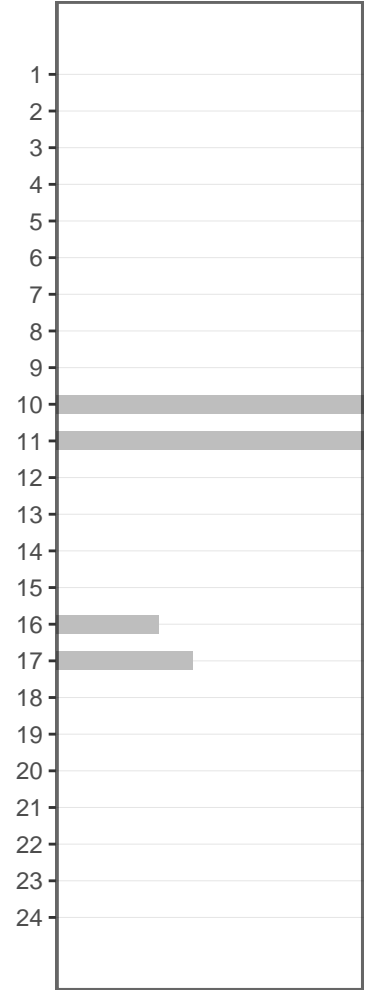
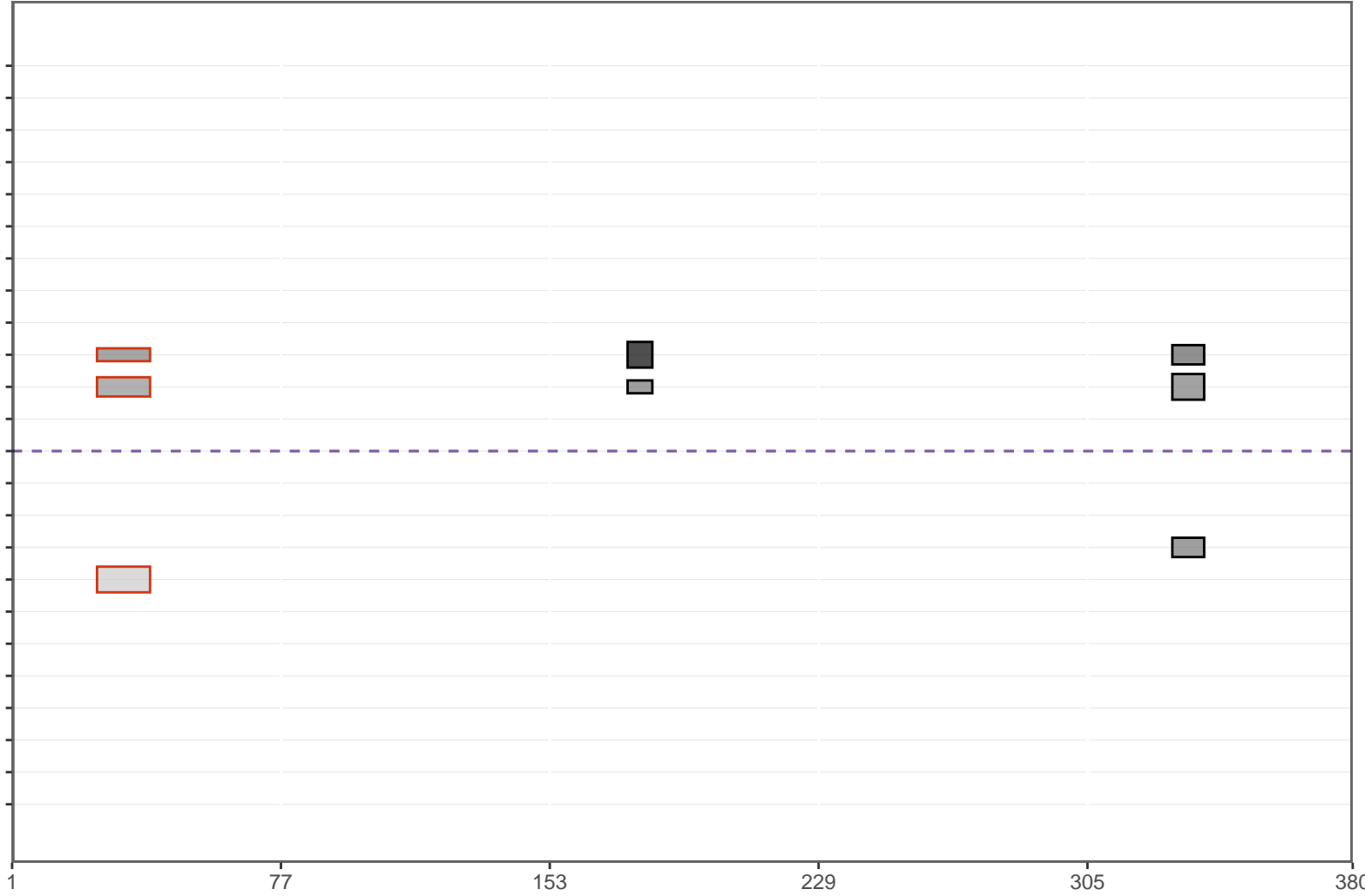
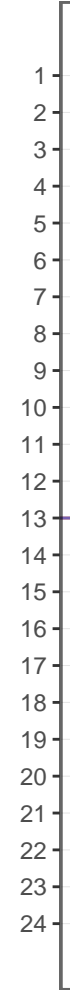
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

Protein length

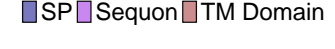
1 77 153 229 305 380

Protein length



Pfam domains

Pfam Description



Protein sequence:

IGINSVOREAEELPMKGMKMDWVPILENRESQVERLKSQIFLRGTRRAGLKHKLKLERVWKFVCLPYPYGFPAEDELGGSTVQLFPTPEPVFGDFWDFEPEEMADKLEAEELVADKDKDEFMEFVKEKVRGKKNRREARARKKAIGEMSEAKAAFGSMKFKYFYPMPSPDAPDVSQVKSPEINRYGKAHTVF

NbL02g00150.1 probable_inactive_receptor_kinase_At5g10020 [MW – SP = 112.58 kDa]

No. of times detected



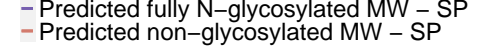
log(intensity)



Values from



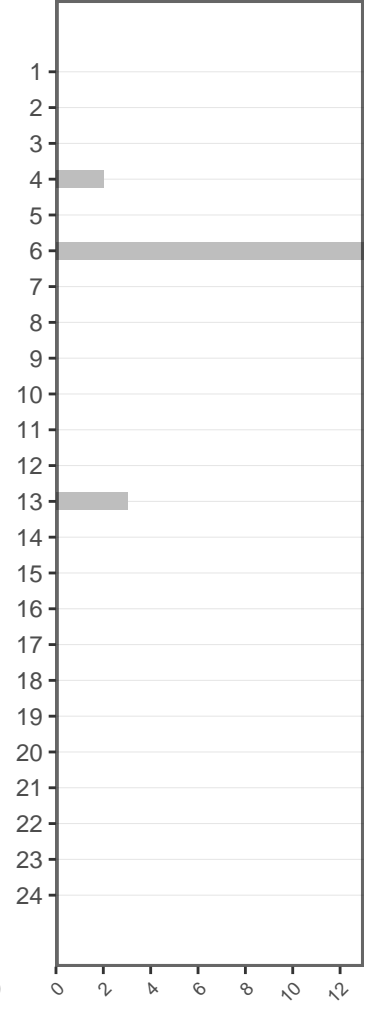
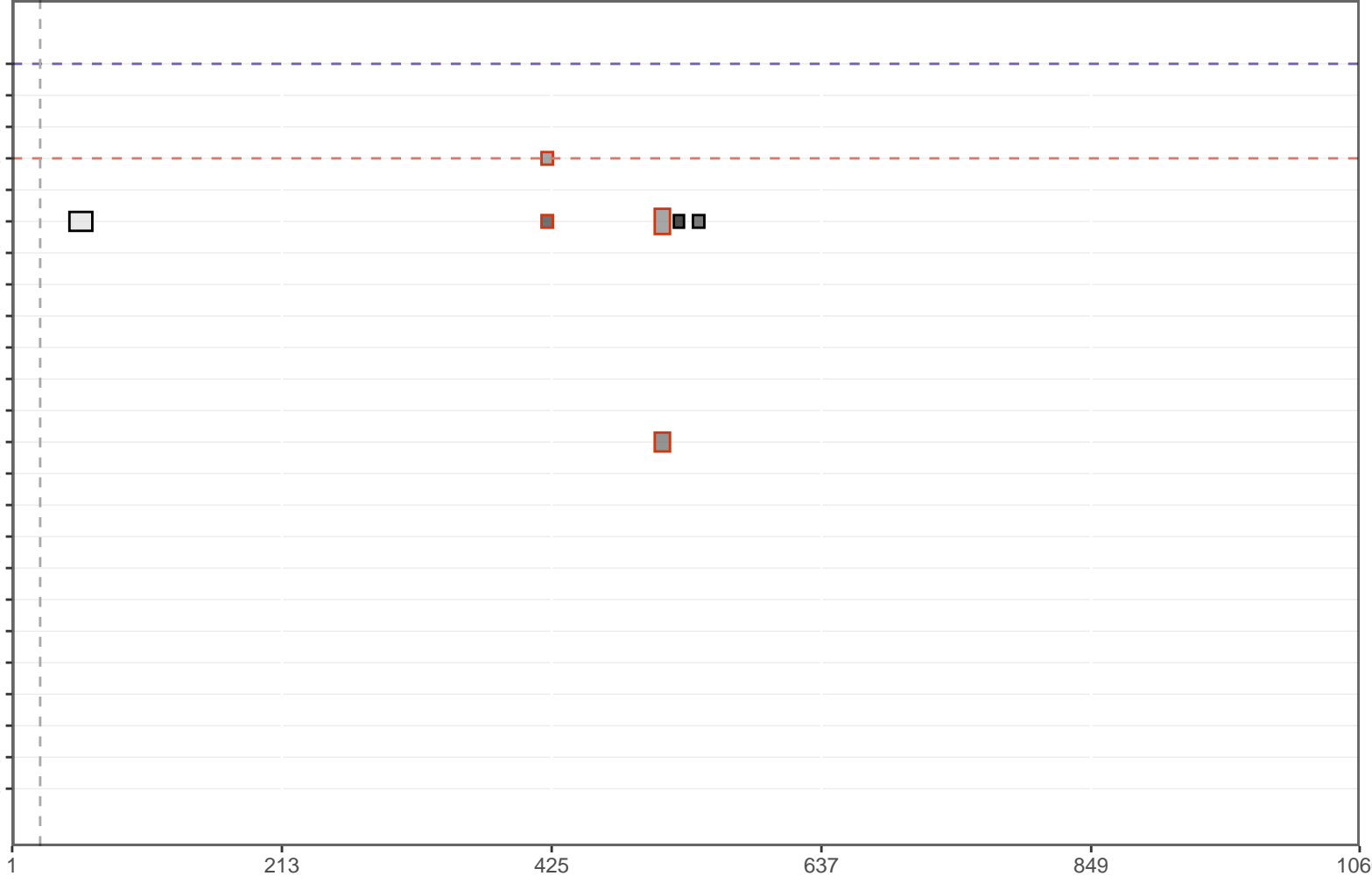
MW indication



Molecular weight

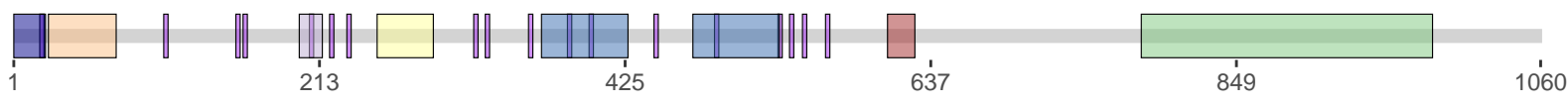


Gel Slice



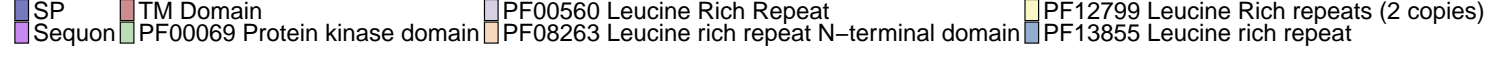
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

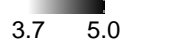
ILQLRSLSEFLDYSKNNFTGRIPENLSNLRVFNVSNDLGGTVFPLSKNFDSGFHPGNLLFLSNVWPHNNHGVDPGNSPRHHSKSKIKVAIVASVQALLMIAVFLFAVRRARAGDQRLRSGFNQGSAGADVILGRFNRRPAKFKHSGSEPPPTLSEFNHLLTNSGRLEGGIEGTEIEHVFPEGVTAGSATHTVANHPTSGRGPDPGSGSPRFDTIEGPVTLGVVSPDRLAGELFFMDGSLGFTAEELSGAPMEVLRGSHGTLKATLSSGIVLTWYLRV

NbL01g25400.1 chitinase-like_protein_1 [MW - SP = 33.32 kDa]

No. of times detected



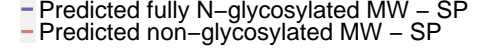
log(intensity)



Values from



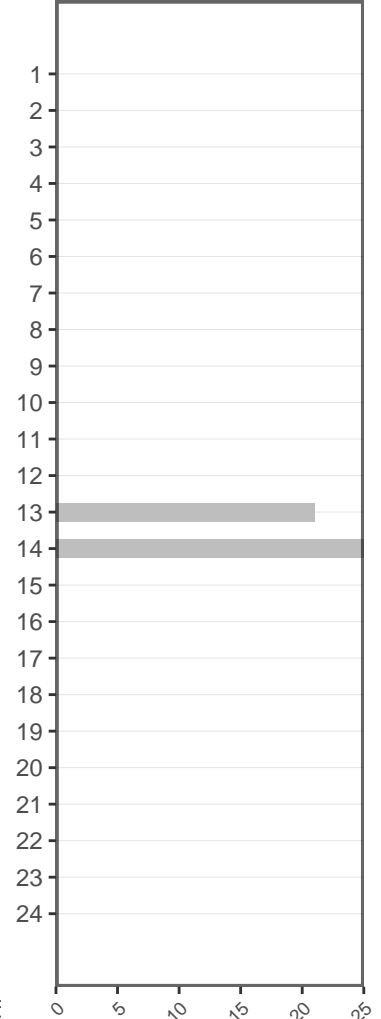
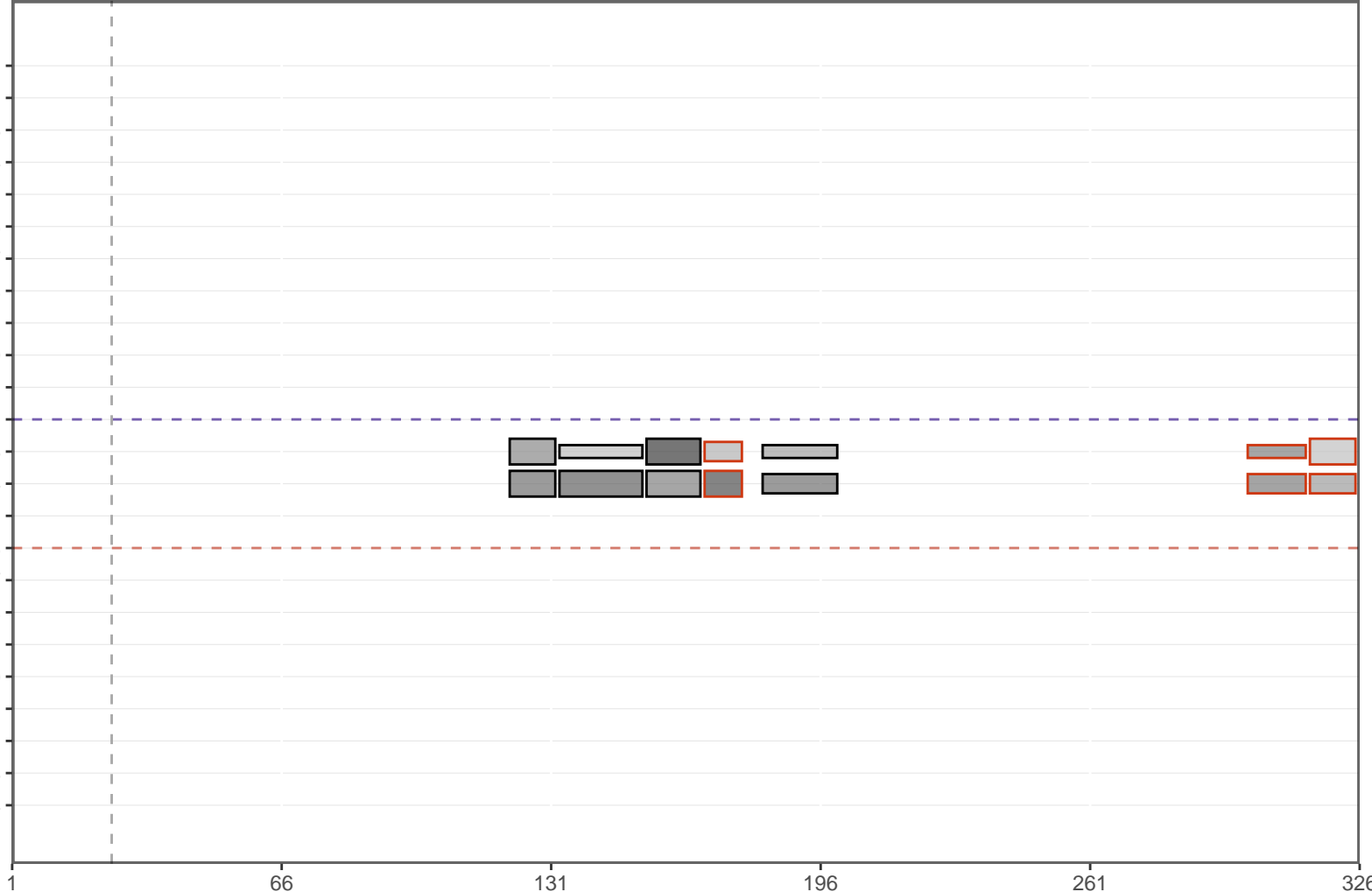
MW indication



Molecular weight



Gel Slice

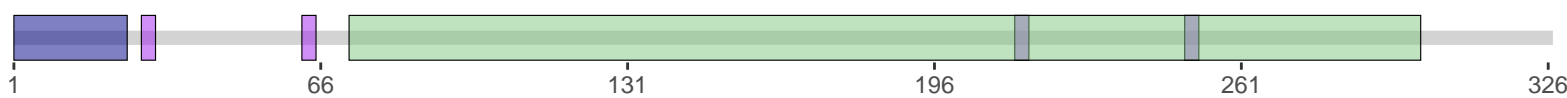


Protein length

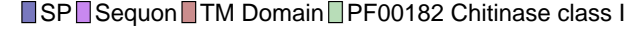


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KEMSPSDYCCDYFKLTVPTGARYYGRGALPIYNNYNGAIGEAALKLLDHPVEIQNATMAFGAAIWRWNPIMKRGGPSAHDAFVGNWKPDKNDLTKLPLPGFTTNNLYGDEVCGGGGVDGMNIIHFQYLEDLMGVGREEAGPHEVLTGGDQKAFNPSSASAAAS*

NbL01g25140.1 pirin-like_protein [MW = 36.71 kDa]

No. of times detected



log(intensity)



Values from



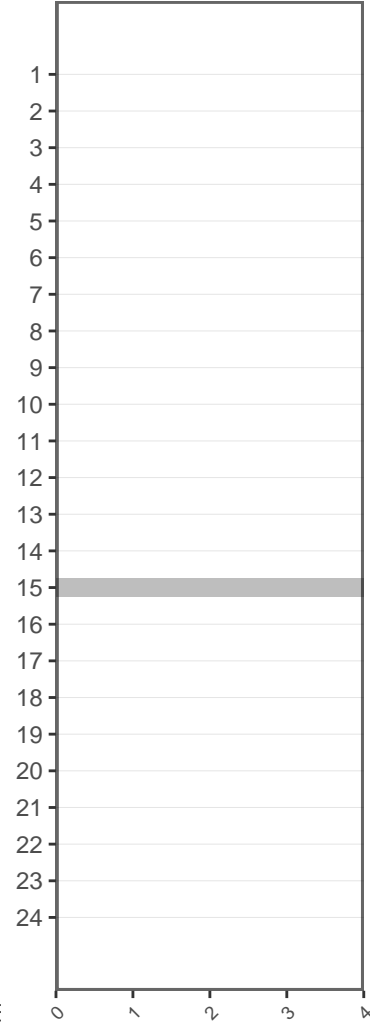
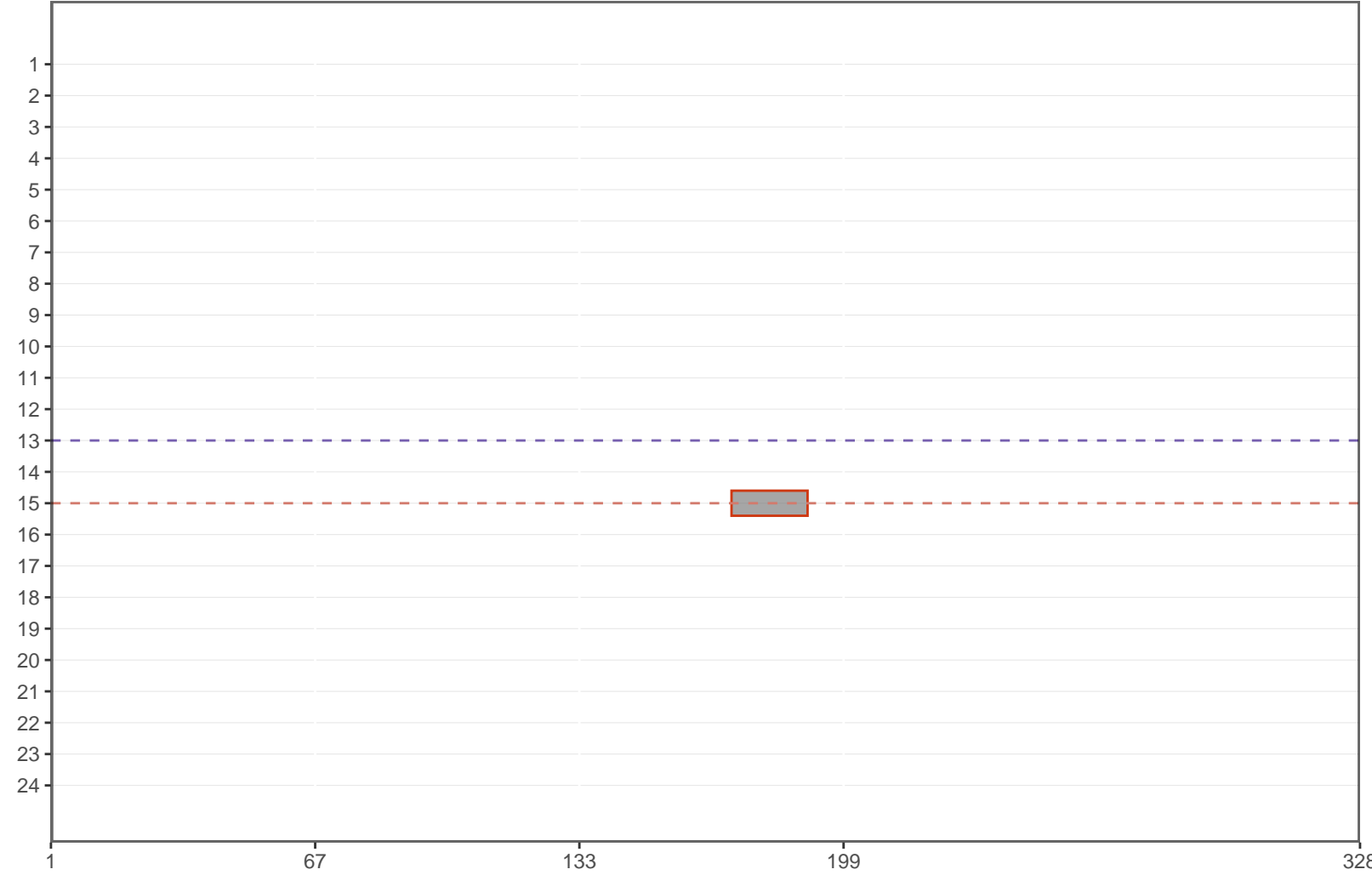
MW indication



Molecular weight

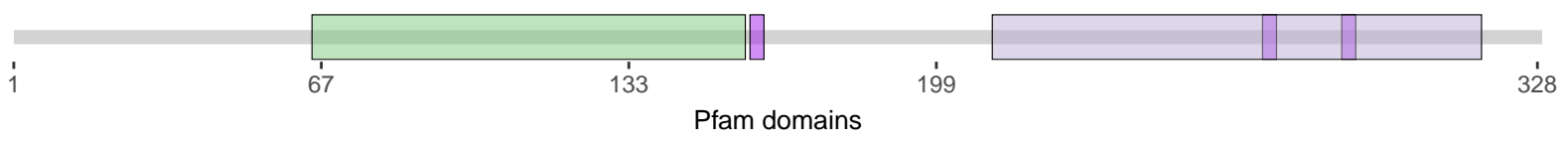


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IGLQLWNLSSRDKMEPRVYQELLNEIPTEAENEGVEVKIAGEAMGVQSPVYTRPTMTYLDFTLQPTSYHHQPTTRESWNAFVYVEGEGVFGIPNSGIPVAHHLGLVGPGEGLSVWVKSSKPLRFVLLGGQPNESVVGHHGPFVMSNGAEIDGTFEDVGYGKNGFENARYWRSGH

NbL01g25120.1 pirin-like_protein [MW = 32.34 kDa]

No. of times detected



log(intensity)



Values from



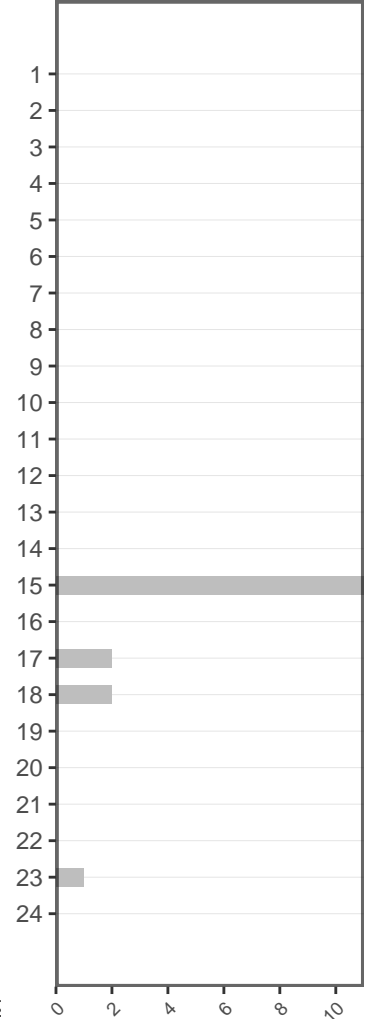
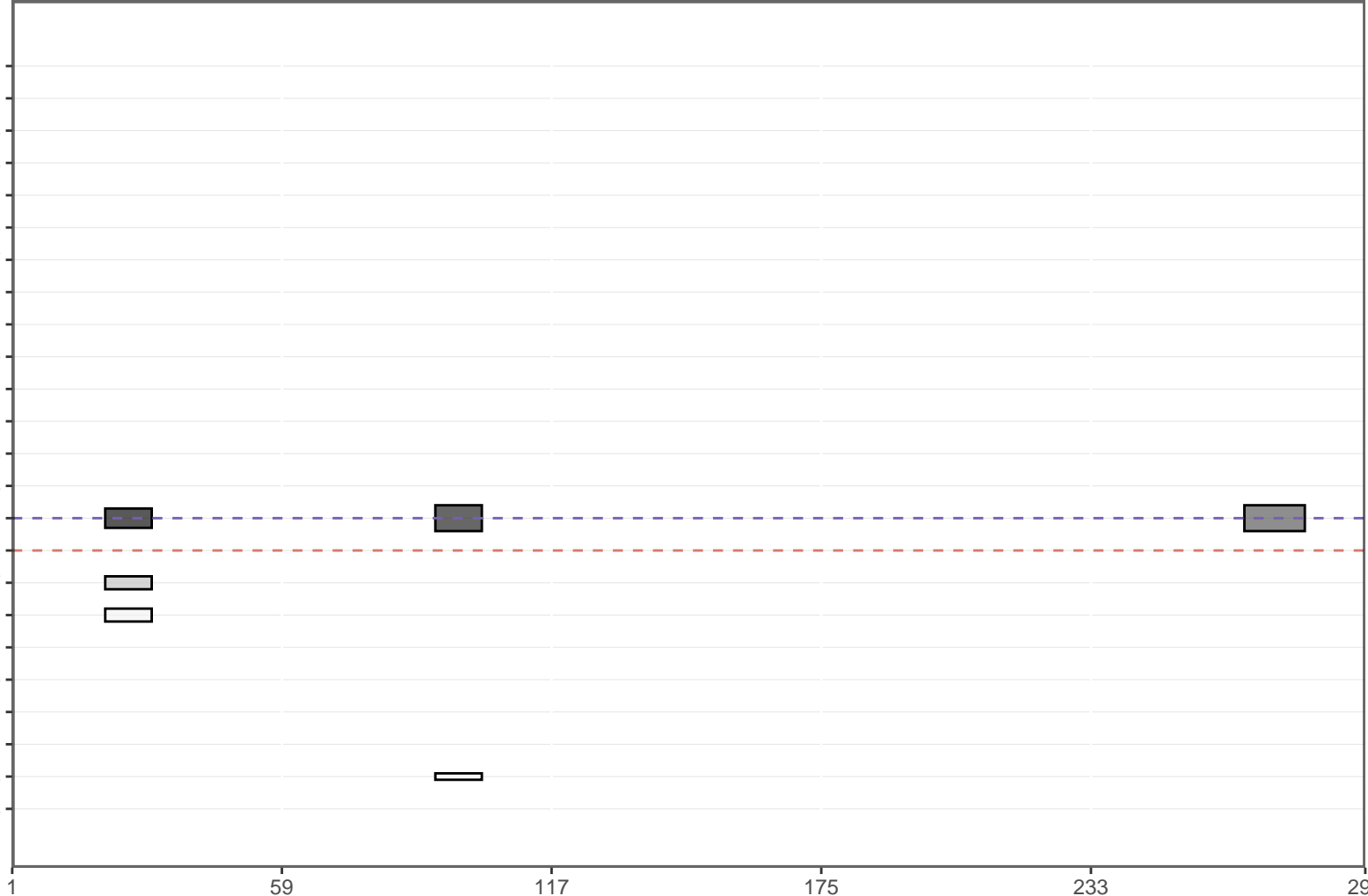
MW indication



Molecular weight



Gel Slice



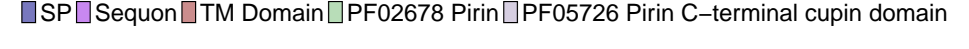
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEPRYQELLHLENPKAEKYGIVGVITIAEAMGVKSGVTRTPTMVLDFLTKPASEHKGPIPEBWSNSFYHIEGEGVFGSSDSTPTFAHQLVLPGEGLVWVWNSKPLRFVLVGGPINEPVAQYGPVMTKSEIMGAYGGVQLKNGFERARHWNSK

NbL01g25010.1 auxin-induced_protein_PCNT115 [MW = 38.51 kDa]

No. of times detected



log(intensity)



Values from



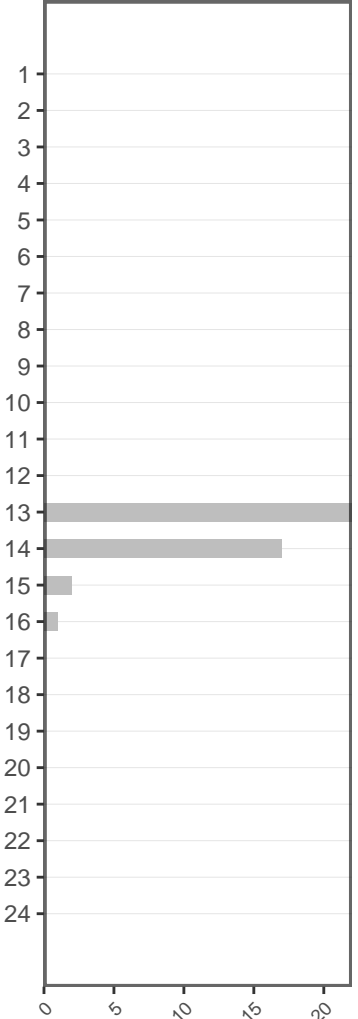
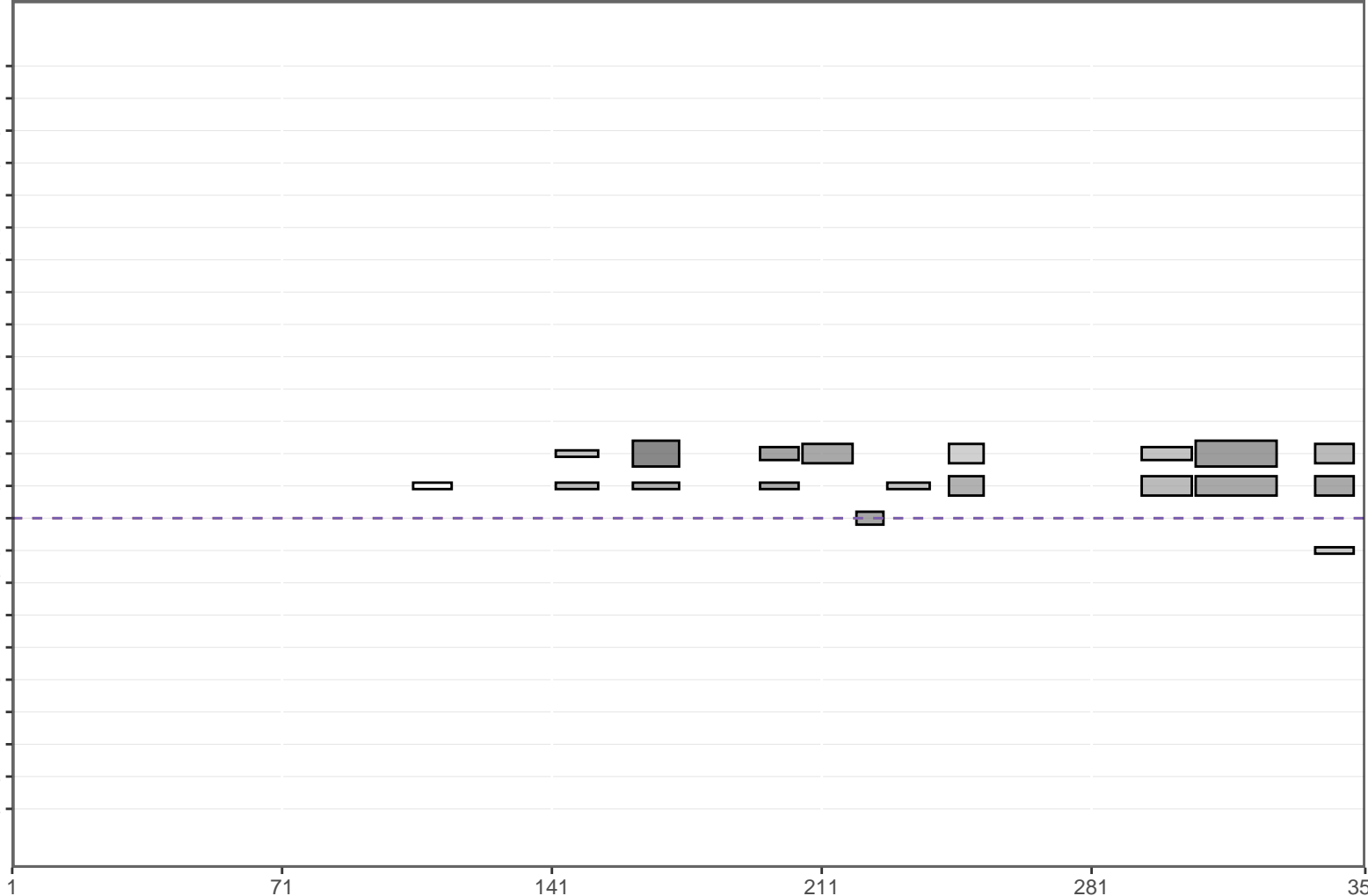
MW indication



Molecular weight

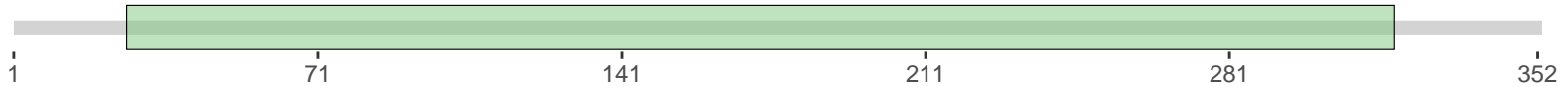


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IQLSEASASTIRRAHAWHPITAVQLEWLSWRDVEEIEIPTGRELGHIVWSPVLRGFLSSGPKLLEDMSNEDVRIKHLPRFQAENLEHNNKLVERICQGMARKGCTPSPGLALAWHHQGNQVCPPIGCTTNIENLNHIGALSIRLTSEDMAELESASDNVAGDQDRVIPGMSTYKNSSETPLSAWKTI

NbL01g25000.1 auxin-induced_protein_PCNT115-like [MW = 41.41 kDa]

No. of times detected



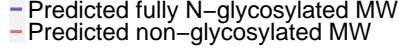
log(intensity)



Values from



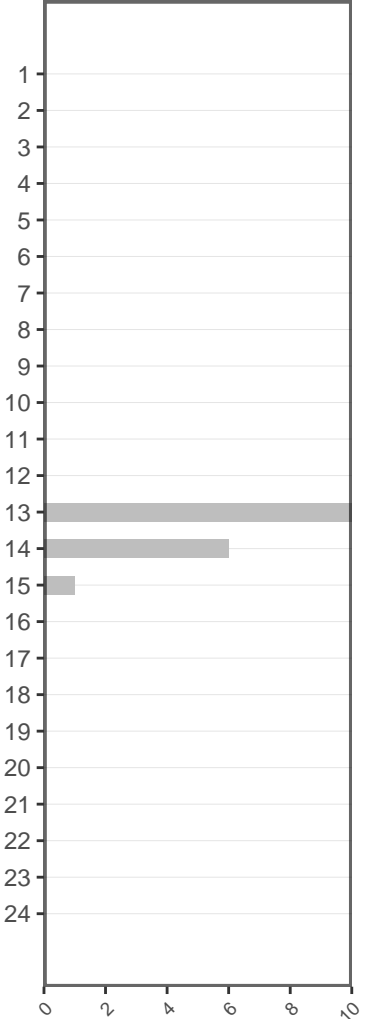
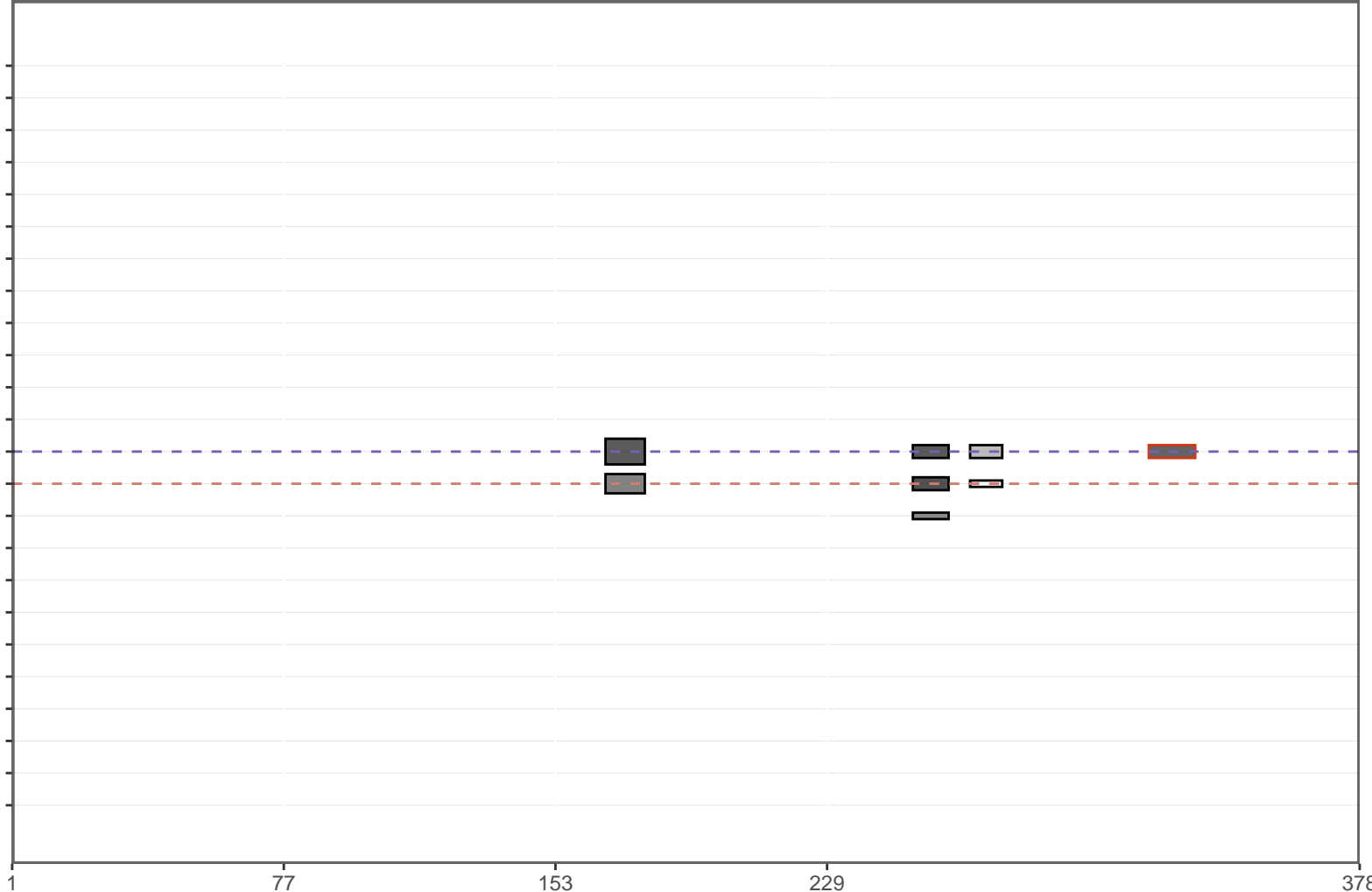
MW indication



Molecular weight

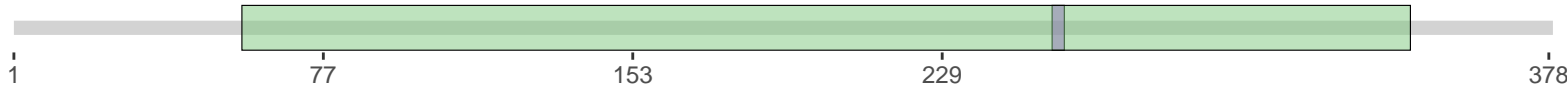


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

.KKLVEEGKIKYQLSEASASTIRRAHAWHTAVQLEWLSWRDVEEHNPTGRELIGIIVAYPLGRGLFSSGPKLLENLSNGDFRKHLPFRFQSDNLEHNKLYDRICGIAAKKGGCTPSGLALAWHHQGNDCGPIPGTTNIENLQNGNEALSIGKILTSDEMVELESASANAQGGDRVSSGASTYKDDSDTPPLSAWKATE

NbL01g24750.1 30S_ribosomal_protein_S1-like [MW = 42.62 kDa]

No. of times detected



log(intensity)



Values from



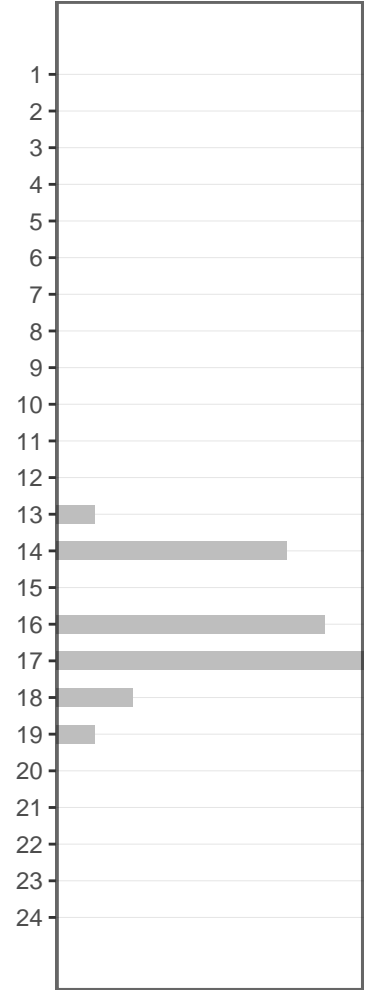
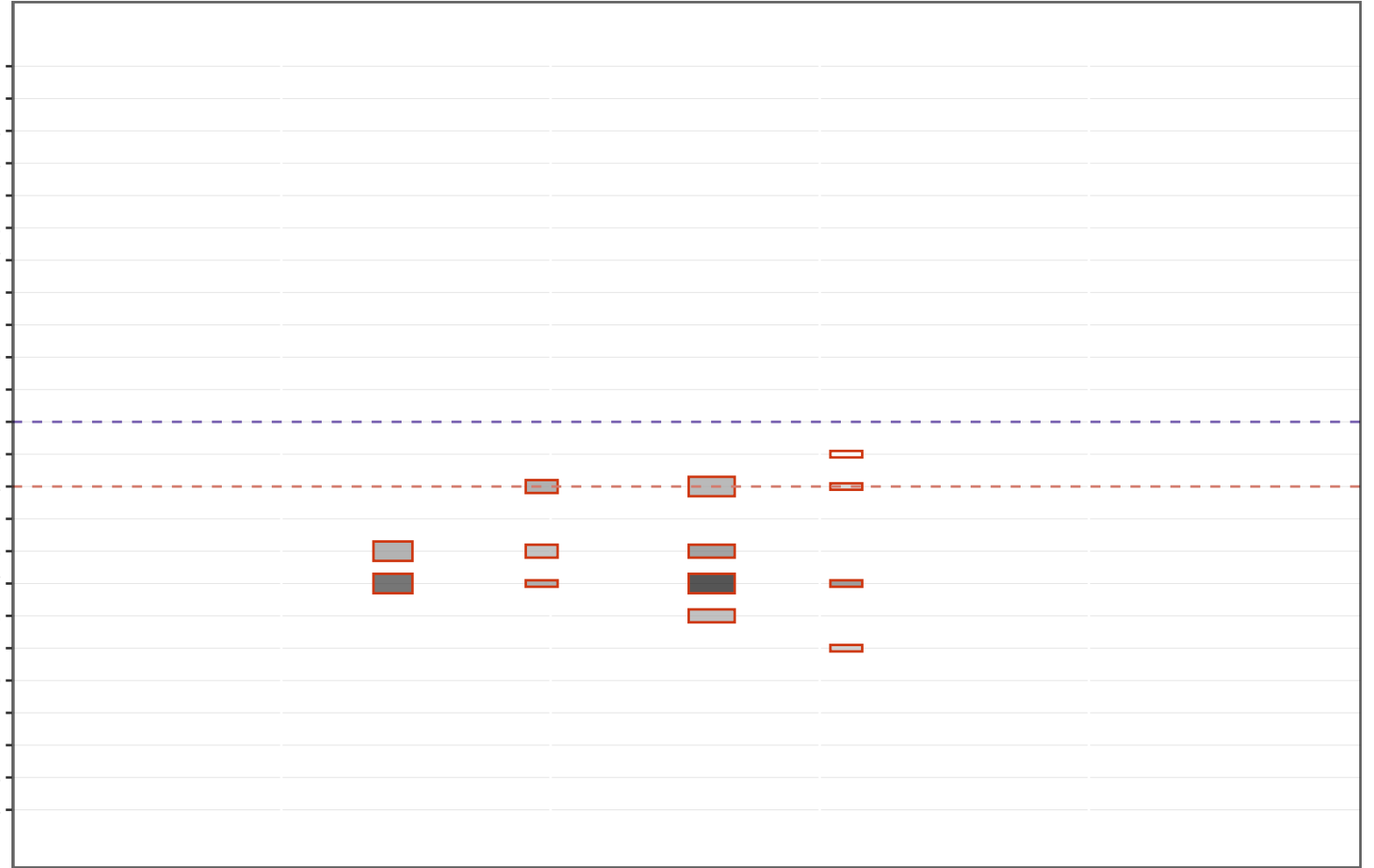
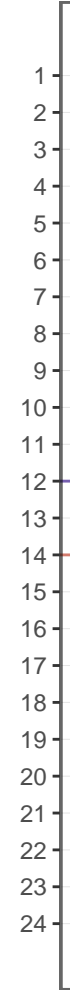
MW indication



Molecular weight



Gel Slice

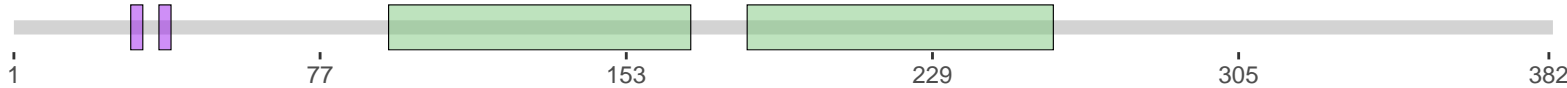


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SKFSYQINVGDFQARVGSVEEDYGFVHLRFPDGSYHLTGLVHVSEVSDLVHVDRLTEGGDQVRVKGINDREKSRITLSEKOLEEDPLLETLDKVIHKEAVDTNLSDDGCFVPEPLSGLETIEELMDEGSHVTITROGFEKRVVSGDLQVLVSNAPAGDGFLLARAGRQVDEKQLTSLDQEGKRALGRVLERVP

NbL01g24560.1 uncharacterized_LOC104096711 [MW = 101 kDa]

No. of times detected



log(intensity)



Values from



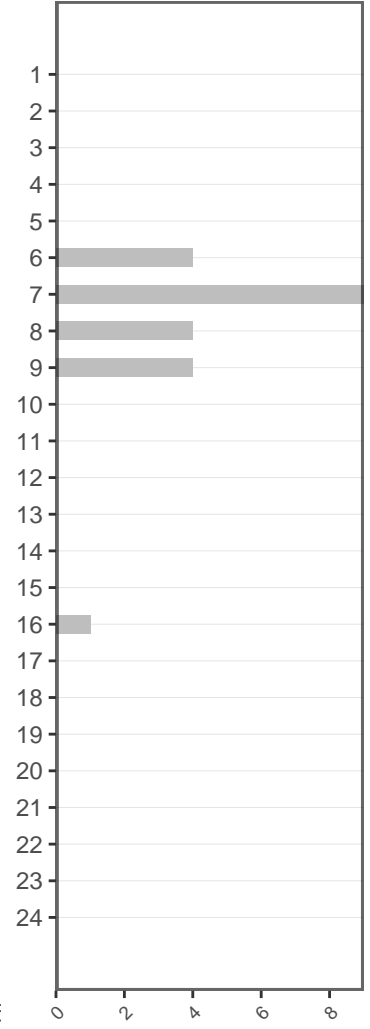
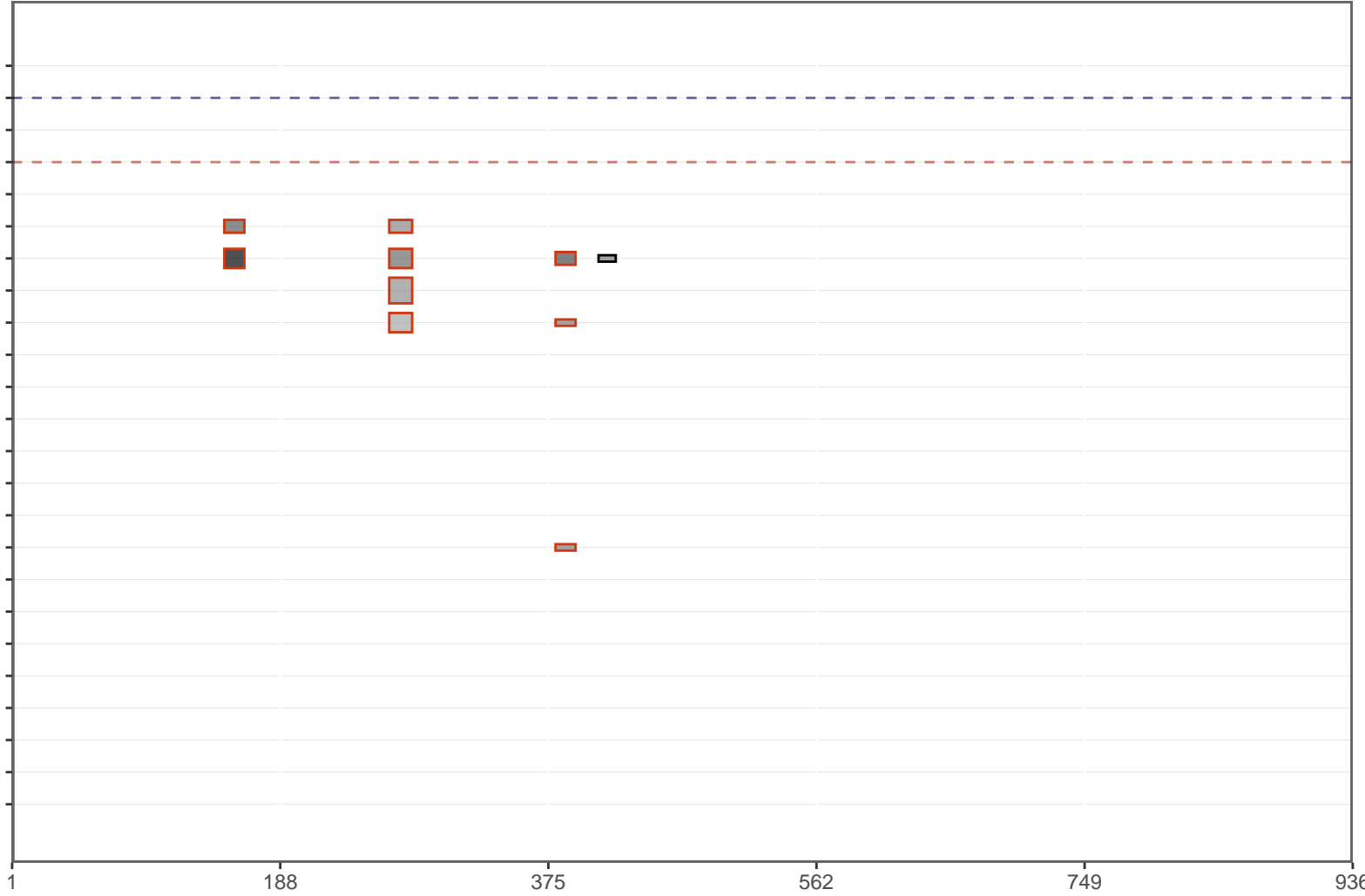
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

MDGDSLNSLPSGPTDHLMMNTFISGVKEAKGTTKVDVPIERTETIFSMEEENKDGHPENELLANKETTVDTSGLSEANGTTVTLGGSDHGEHEKARTEGQVAVGGETAKERSEENKRVFEQDKTICPVGGHSDRAIVTDTTVHEGRDEIFHEASEDSTVSNANAMPTSEGLDEKIBSDCKEPAQGLVDTDLKGRVVDNHNHAGDGKINATGVISSASLNKGNKIKGNNTVSAVDVSTN66SRADSLDANWGSVVLSTQ66STAVPDAEATDTRKLEPLQKPK1

NbL01g24550.1 protein_TIC_22-like_chloroplastic [MW = 36.45 kDa]

No. of times detected



log(intensity)



Values from



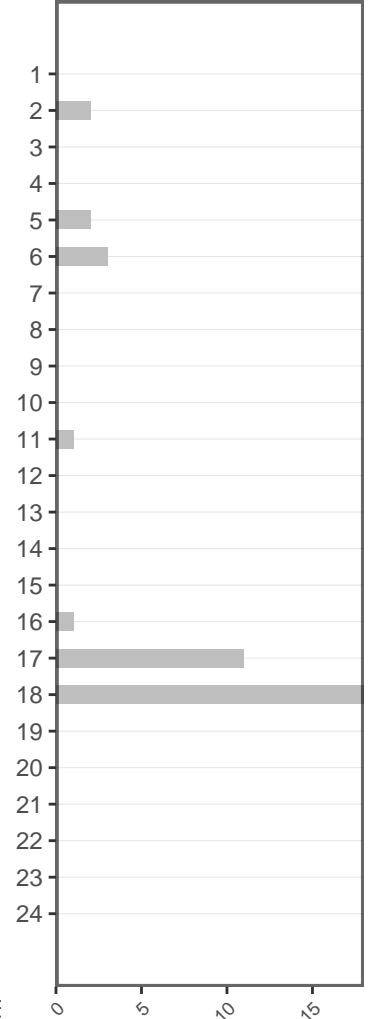
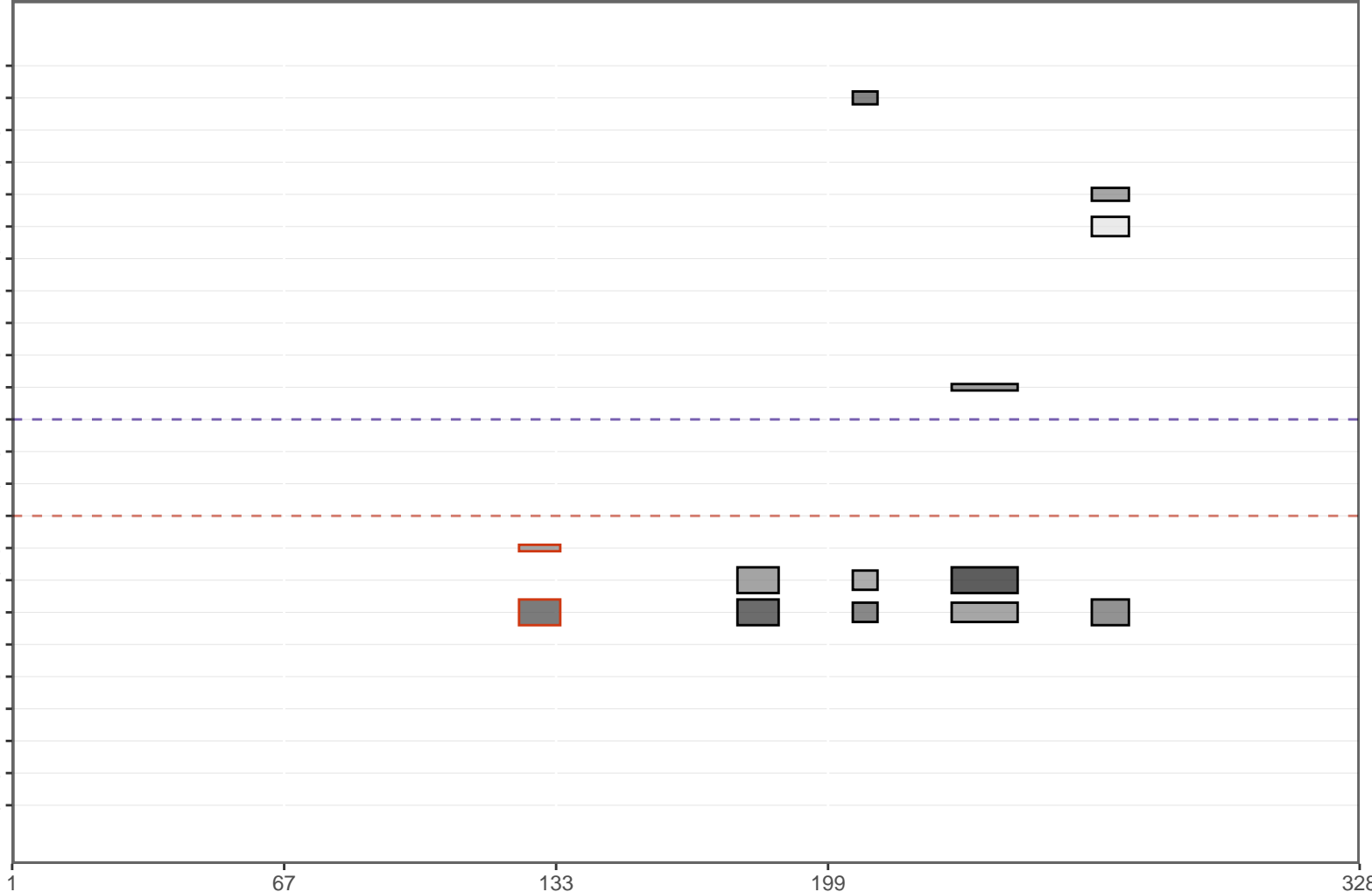
MW indication



Molecular weight

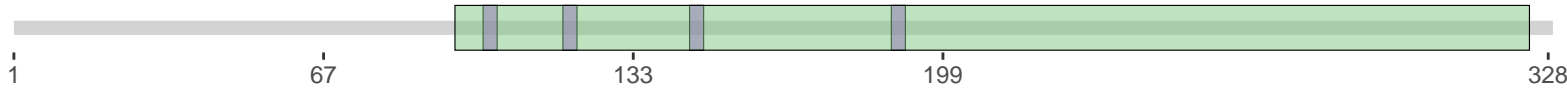


Gel Slice



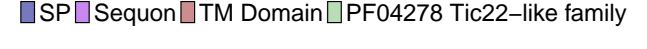
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

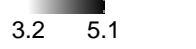
SGVSTGKILGLFCFSEADAEALRQGMESMDPTMRNGSRVAVPALNKVFKVDGVAFLPEASQVKNAMKERERTGTSDESFYGVVPGSRSLRNRVRFVFRKEDLENSLVRASGGGGRLNPKLKGDIQVAVLEDHGKMDTSTKWDVDFVPPGFDVSTHDSQK

NbL01g24500.1 crocetin_glucosyltransferase_chloroplastic-like [MW = 52.95 kDa]

No. of times detected



log(intensity)



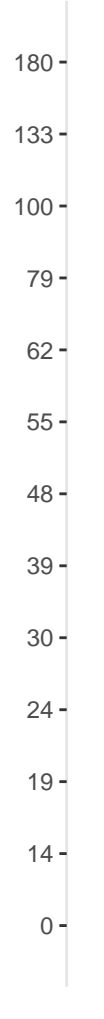
Values from



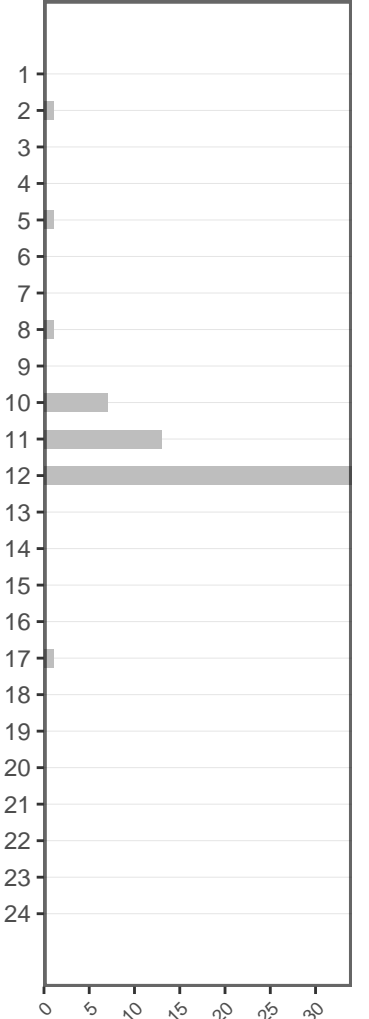
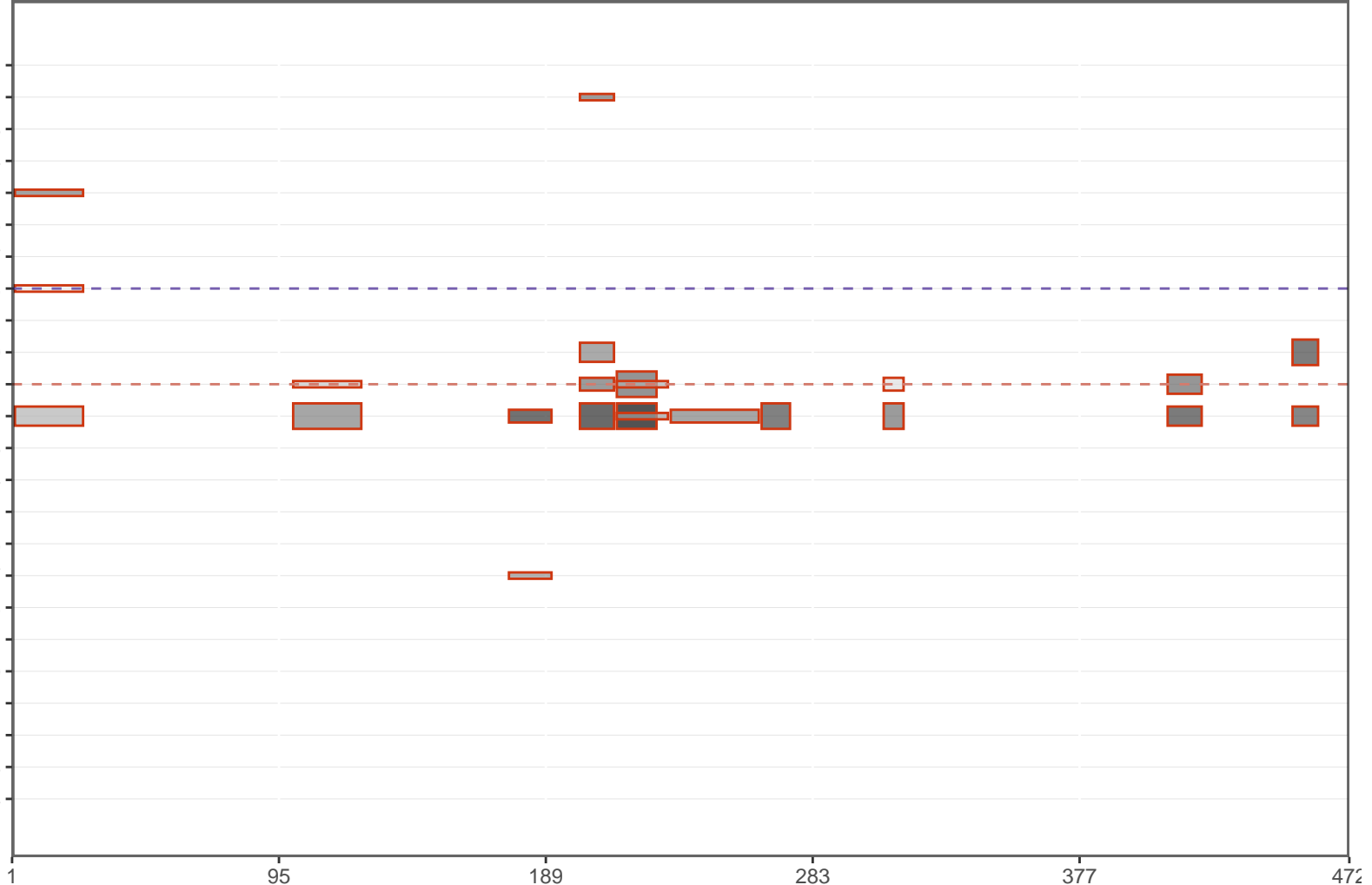
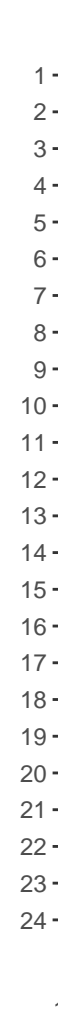
MW indication



Molecular weight



Gel Slice



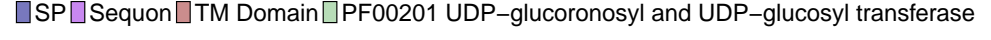
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ELKAIEKYNLIGIGLPSTFLDQKPLDSFAGDLFGKSNDSIEVLNKSANBSVYVIFSGLLNLKKNKKEEIAKGLIEKRPFLLWIRDOENKGGDEKEEELSGMMELEKGGKQKVPWGSQLEVLHPGLGPFVSHGQWNLSTLESLSGTGVVAFPHWTDGNTAAKLEIIVKIGVRLKKNEDGVVESEEIKRDIEMVMNSGKEGKEEMRRNAGKWKELAREAVKEGGSVMNLKAFVGEVGGKDC

NbL01g24450.1 receptor-like_kinase_TMK4 [MW - SP = 98.53 kDa]

No. of times detected



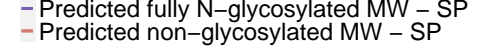
log(intensity)



Values from



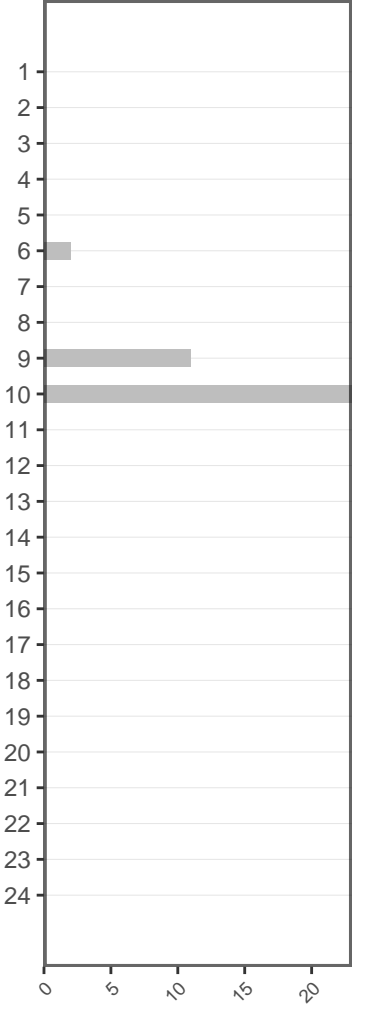
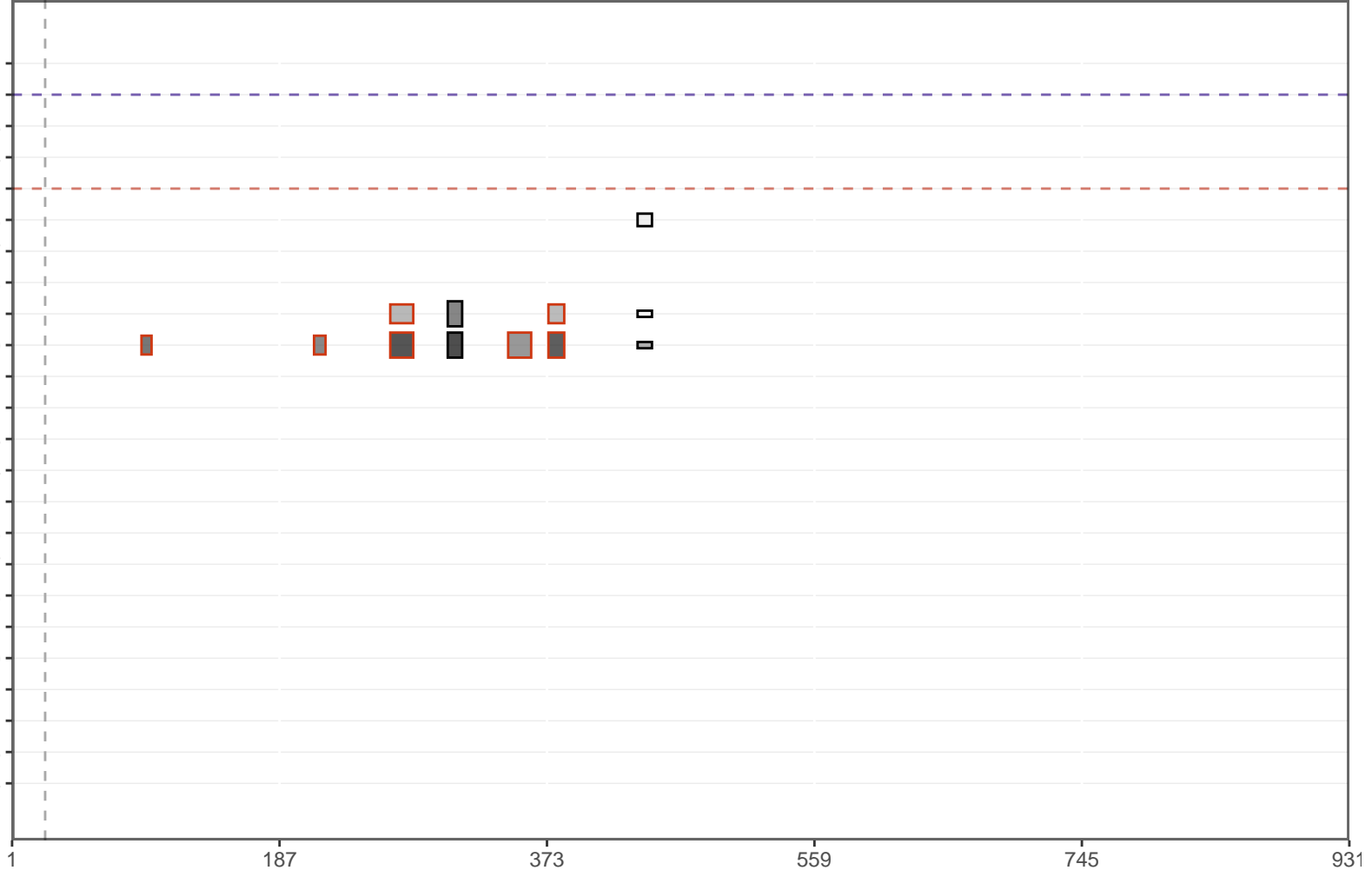
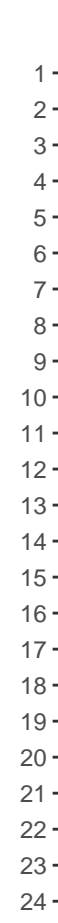
MW indication



Molecular weight

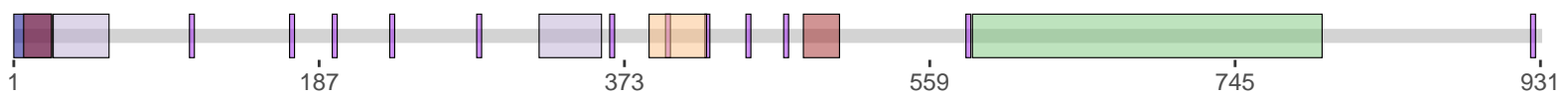


Gel Slice



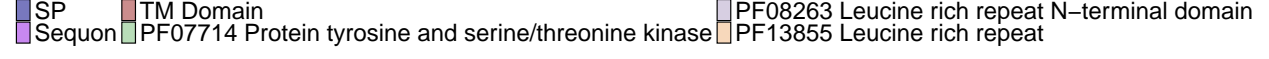
Protein length

Peptide counts over 4 repeats



Pfam domains

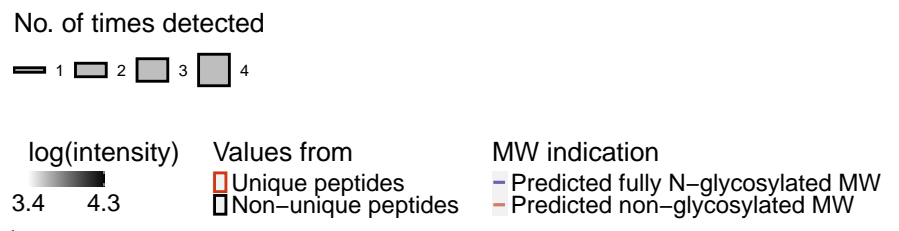
Pfam Description



Protein sequence:

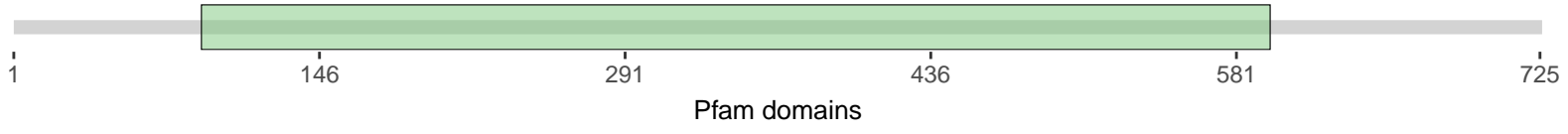
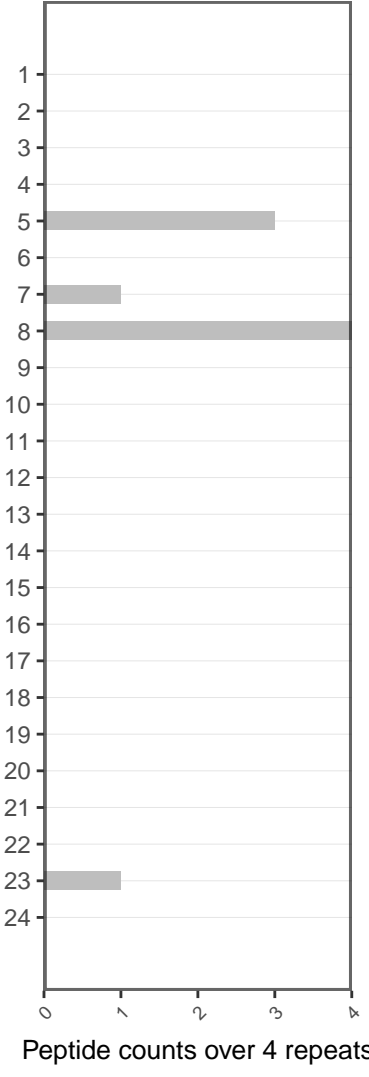
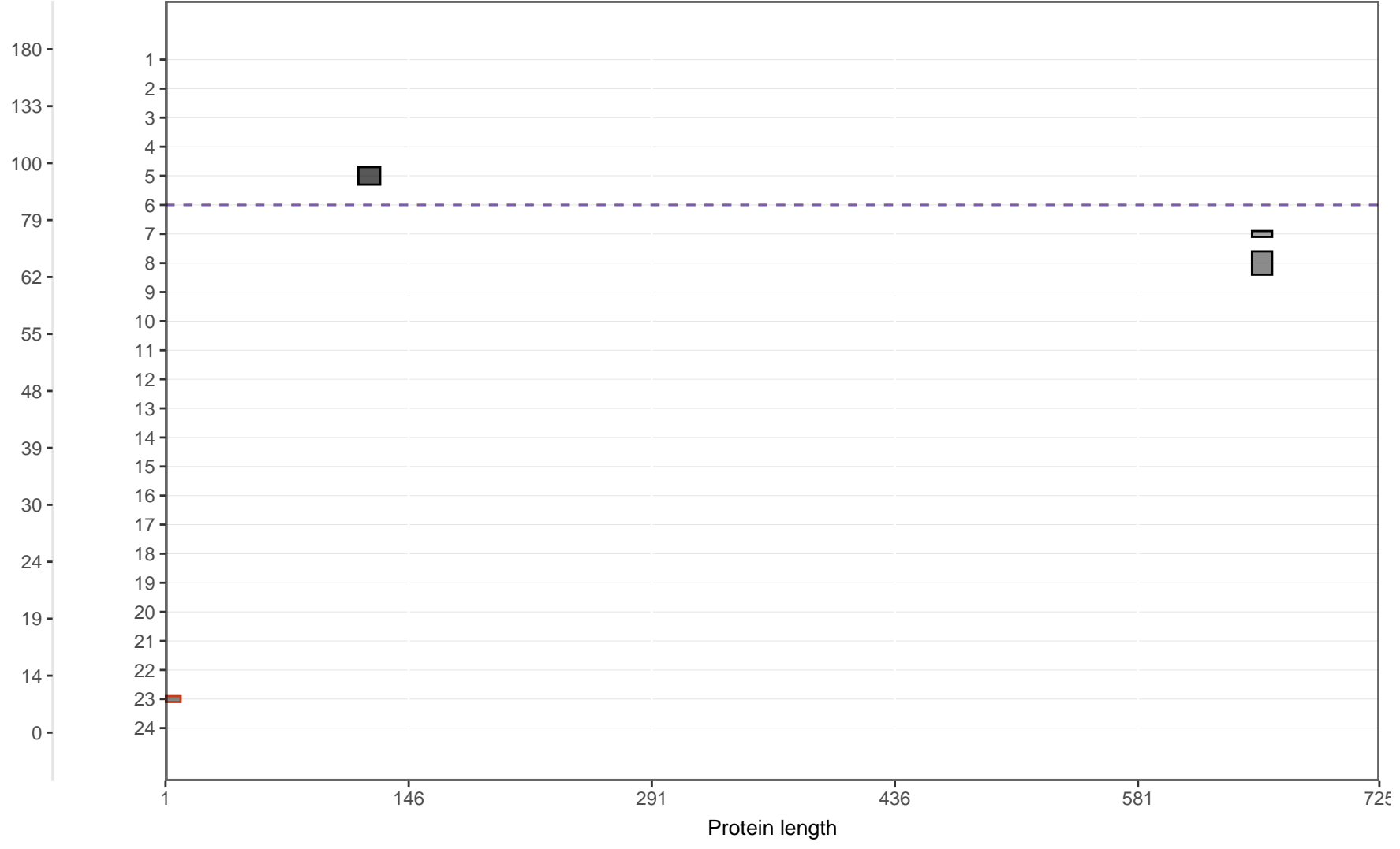
ISGGSGNSGSPDENSSGGKRPVBSAGMAGVVAIAVVFVLLVLFVYKCYLKRHRKFRGRVETPEKSNEMVAISSVPEVVGSGNGYTGVPSELGSGSGSDHEIPVFEGGKIAISQVLRQVTFNFSSENLVLRGGGFGVYVYKGEIHDGTRKAVKRMESGPFMGKNGMNEFQAEIIVLSKVRHRHLLVALLGSGVNGNERLLVVEYMPDGTLSQHLFEWQDFGYNPLTWKERVITLQVARGVEYVHSLAQGGFHRDLKPSNILLGDDLRAKAVDFGLVRNAPDGKYSVE

NbL01g24440.1 probable_acyl-activating_enzyme_16_chloroplastic [MW = 80.49 kDa]



Molecular weight

Gel Slice



Protein sequence:

EDLRRYQPNYLISVPLVYETLYSGILKQINSNSARKLIALFLRISIMAYMEAKRIYEGKLMKDKTQDPYVYVSLLEWLWARTAAALVPLHMLAKVIYKSHASIGISKAGVSGGSLSSRVKDFEAGKIQKNGYGLTESPVISARHPACNVLGSGVHPRIHVEYKIVNAETDEVLPFGSRGIVKARGFLVMKGYKXPLATKQADENGWLNFGDLGWAFDHSVGRSRKSGGVVLEGRANDTVLGTGENVEPSEIEAATGSSLHQIVVGGDORRLGAIIVPKKELLLA

NbL01g24400.1 selenium-binding_protein_1-like [MW = 53.62 kDa]

No. of times detected



log(intensity)



Values from



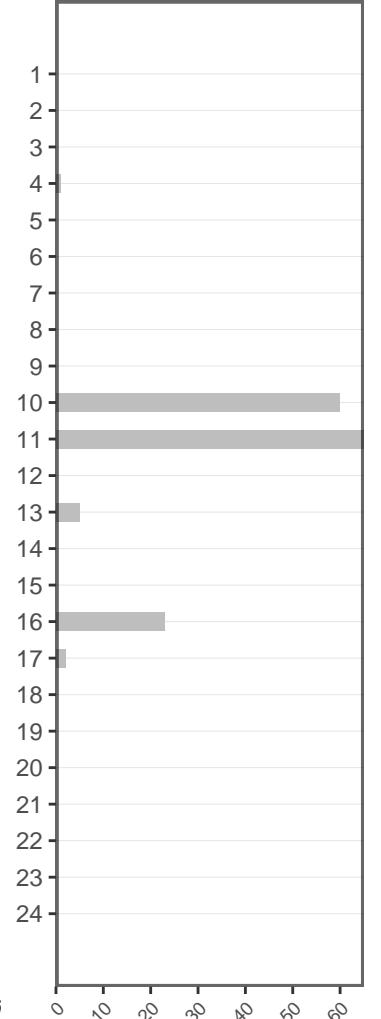
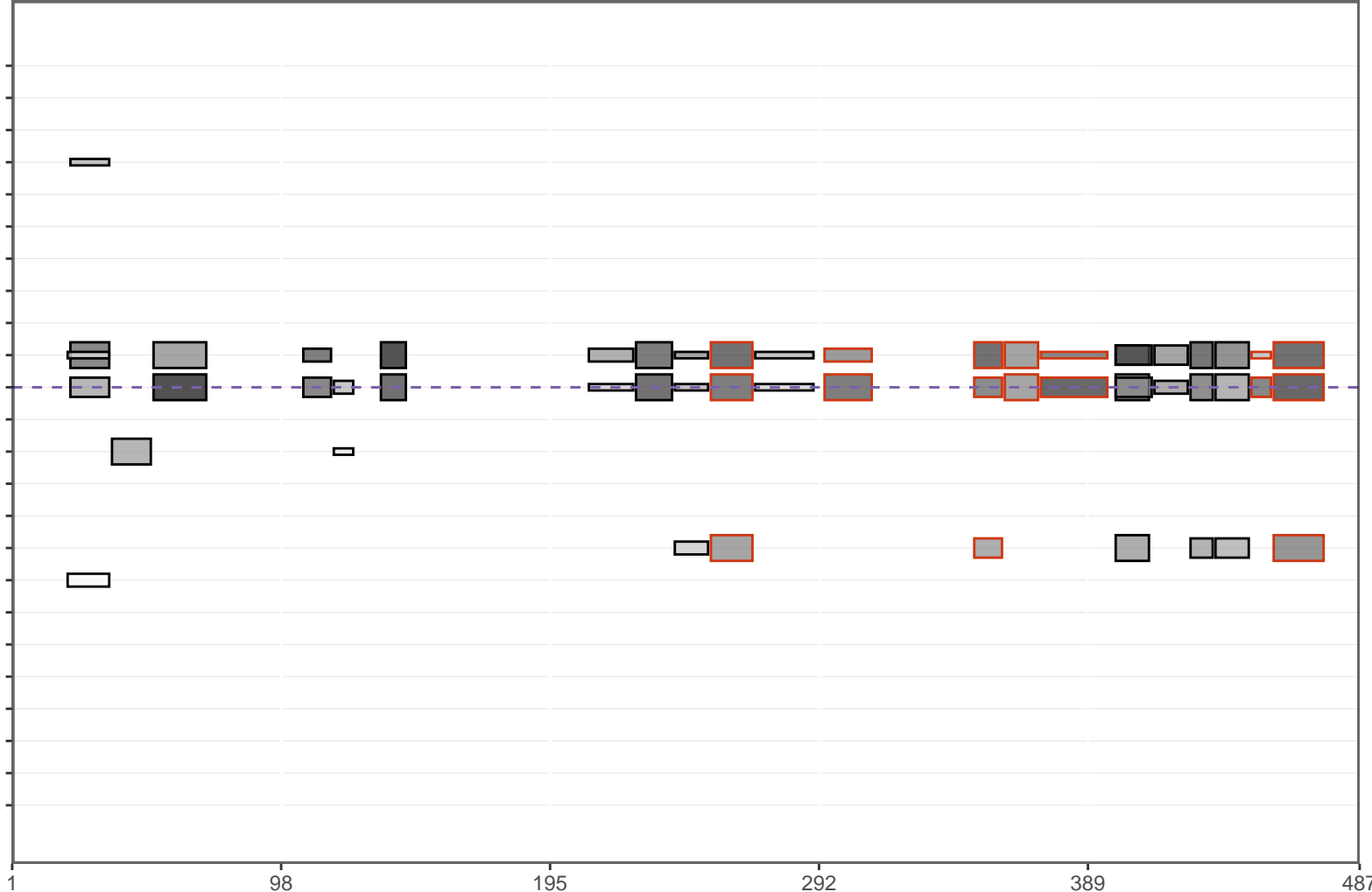
MW indication



Molecular weight

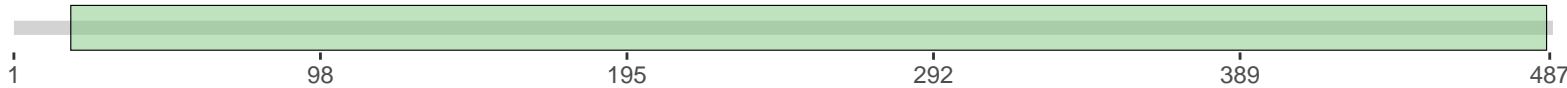


Gel Slice



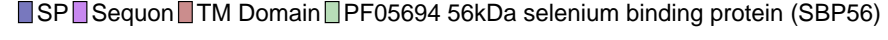
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

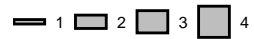


Protein sequence:

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NbL01g24330.1 NA [MW = 53.12 kDa]

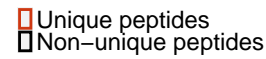
No. of times detected



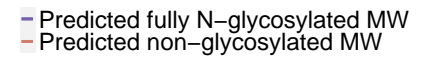
log(intensity)



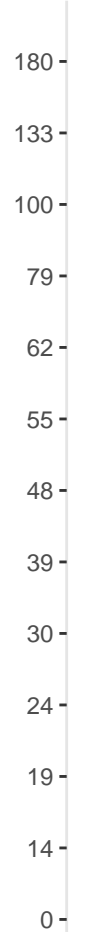
Values from



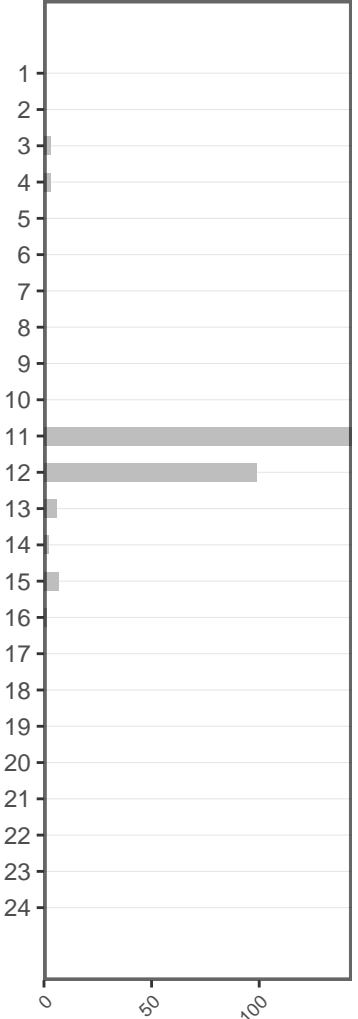
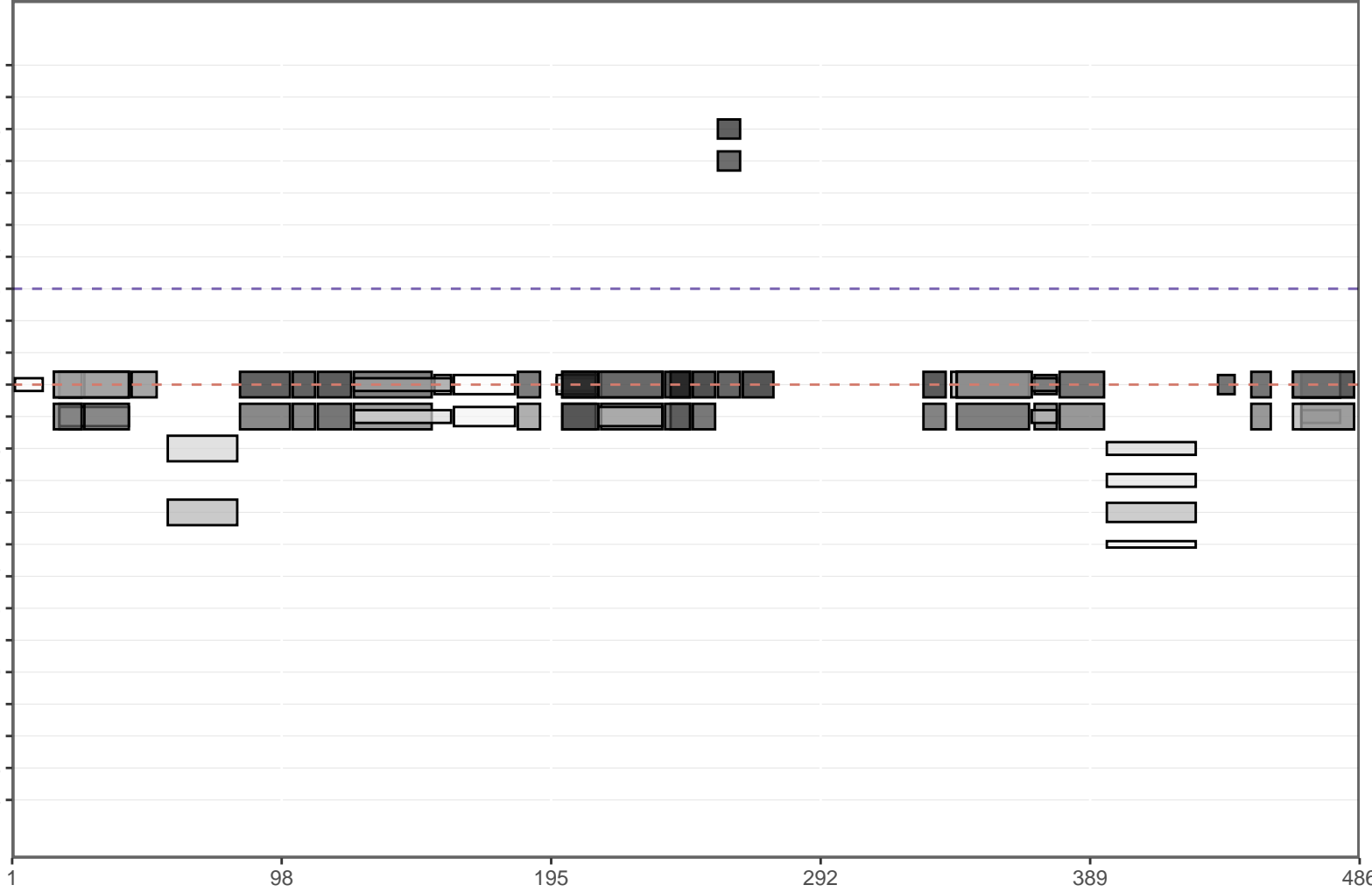
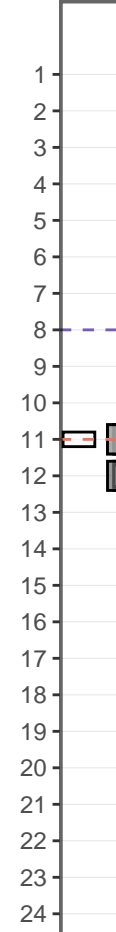
MW indication



Molecular weight

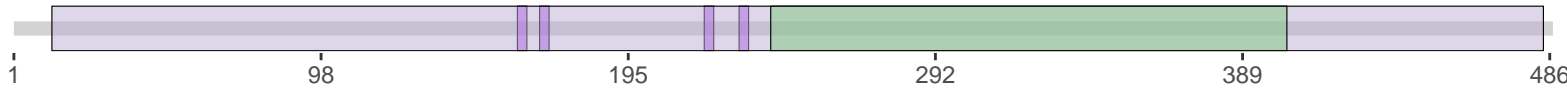


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00670 S-adenosyl-L-homocysteine hydrolase, NAD binding domain
- PF05221 S-adenosyl-L-homocysteine hydrolase

Protein sequence:

NDSVTKSKFDNLYGGRHSLFDGLMRATEENMIAKGVAVAGYGVGVKGGAAALKGAGARVIVTEIDFGCALGATMEGLGVLFLEDVSDVDVDFVFTTGGNDIMVDHMRKMKNNVAICNIGHFDNEIMLGETYPGVWRITIKPQTRRWVFPDINSQIIVLAEGRLMNLGGATGHPSEVMSGSFTNGVIAOLELWNEKSSGKYERKVVYLFKHLDEKVAALHLGKLGANLTQLSKDQADVSEVPEGPKPAHWRY

NbL01g24260.1 glycine-rich_RNA-binding_protein_4_mitochondrial-like [MW = 15.14 kDa]

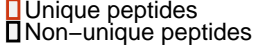
No. of times detected



log(intensity)



Values from



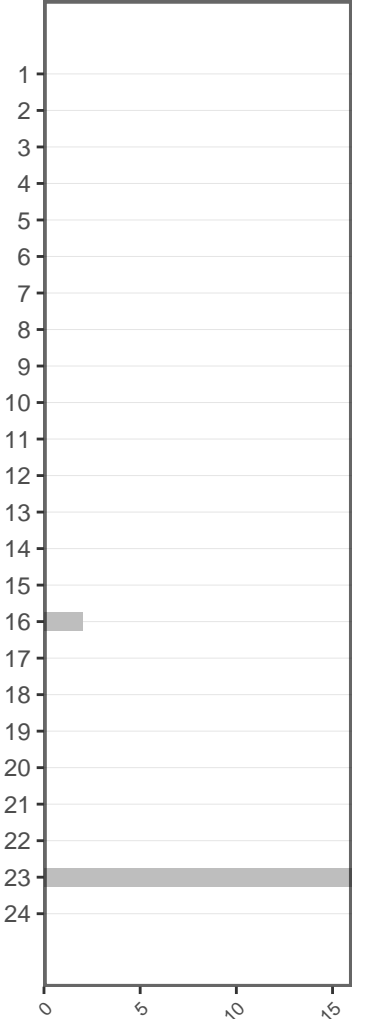
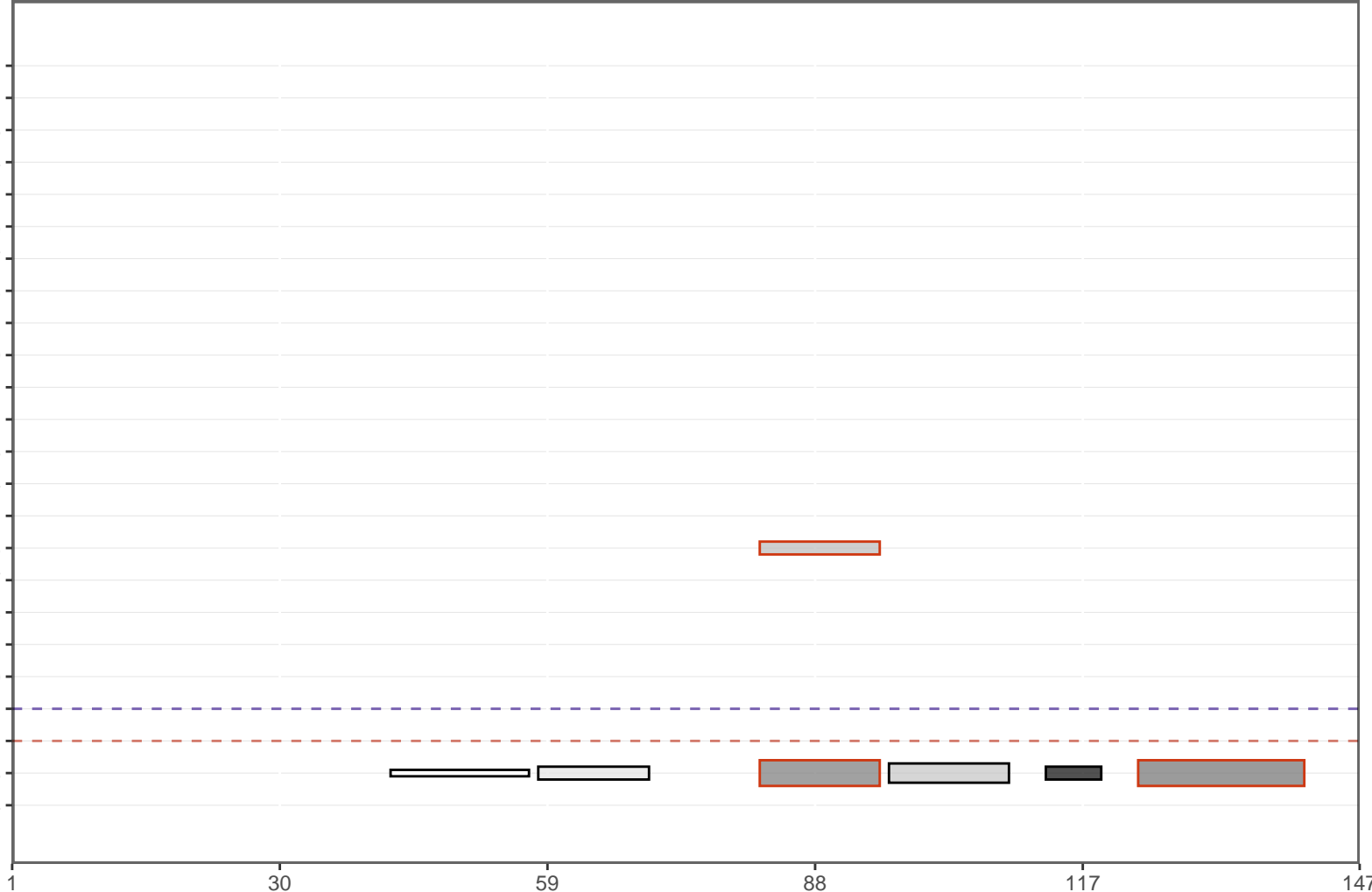
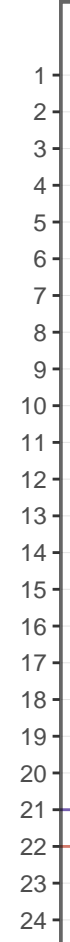
MW indication



Molecular weight

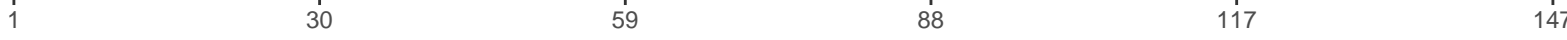


Gel Slice

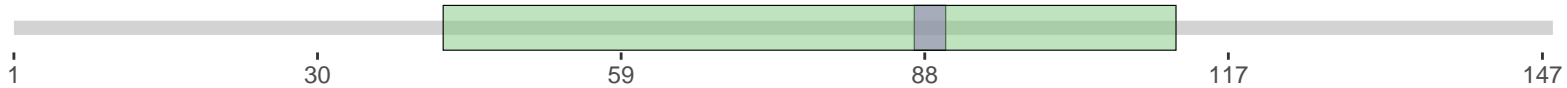


Peptide counts over 4 repeats

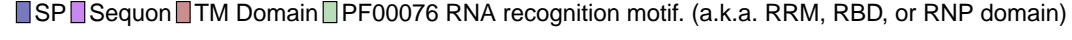
Protein length



Pfam domains



Pfam Description

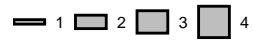


Protein sequence:

IGDVVDSKIVTDRDFTGRERGFVFNFTDGESEAKEAMTMDGDELNGRNRVSLAGERAPRISGGFGSGGGGGYGGGGYGGGRNDGF

NbL01g24250.1 protein_ECERIFERUM_26-like [MW = 47.9 kDa]

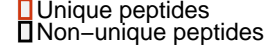
No. of times detected



log(intensity)



Values from



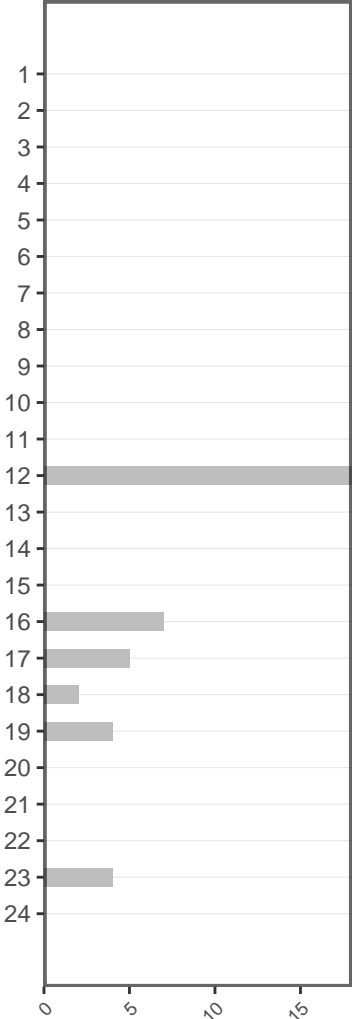
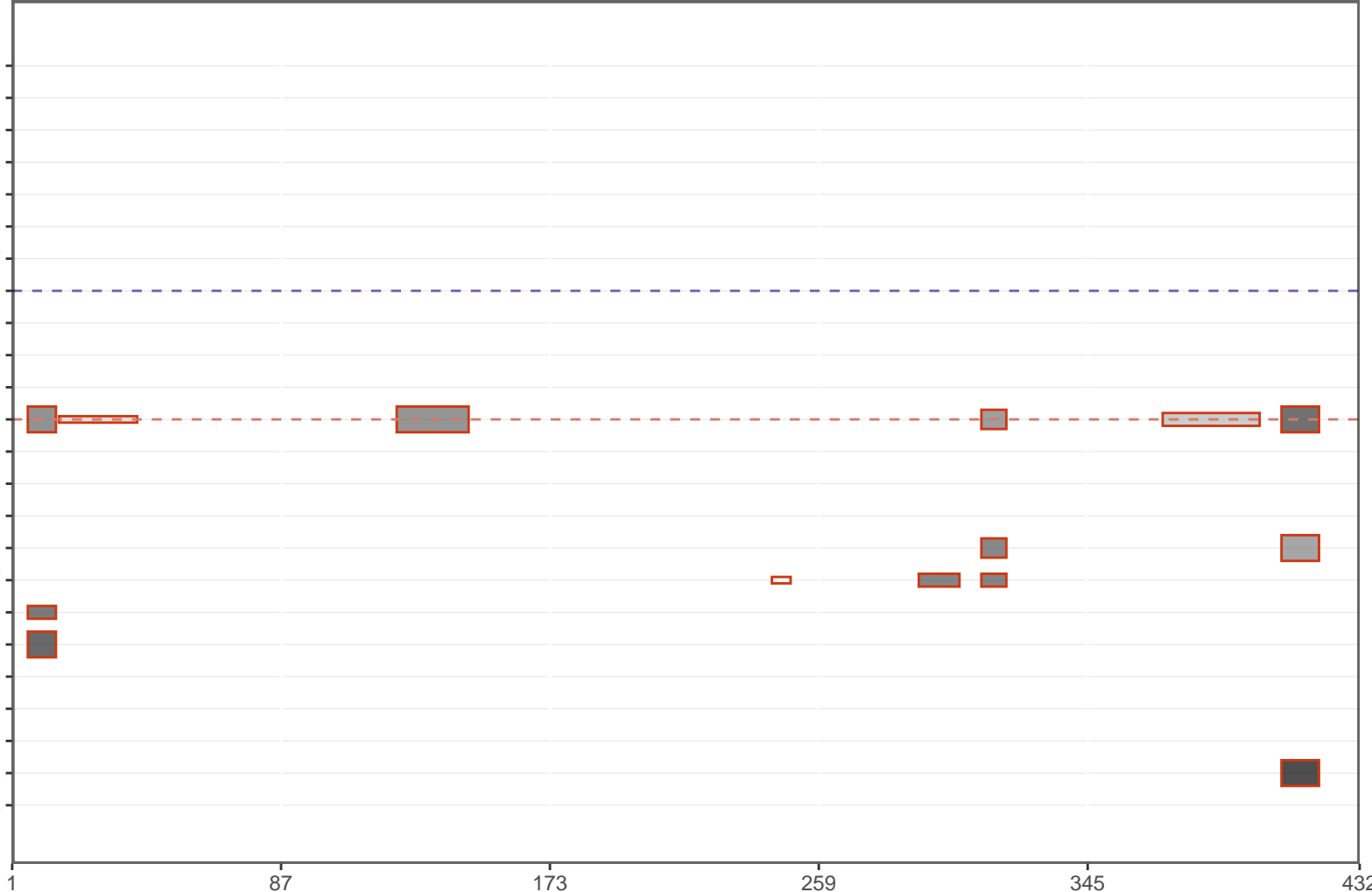
MW indication



Molecular weight



Gel Slice

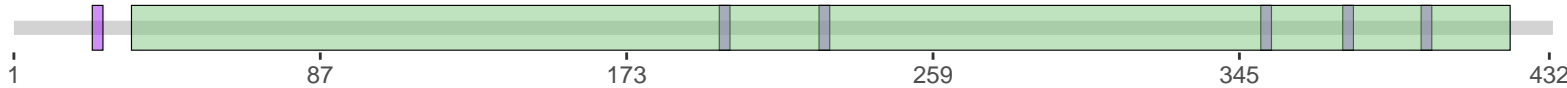
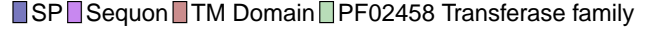


Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

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NbL01g24060.1 probable_sucrose-phosphate_synthase_2 [MW = 119.69 kDa]

No. of times detected



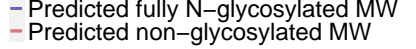
log(intensity)



Values from



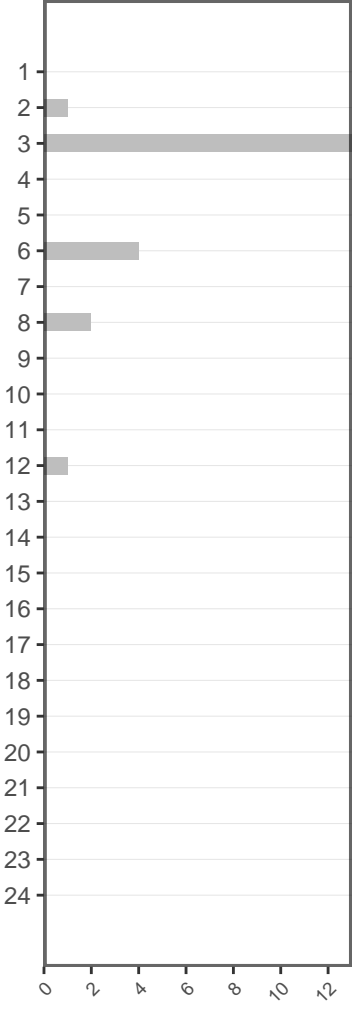
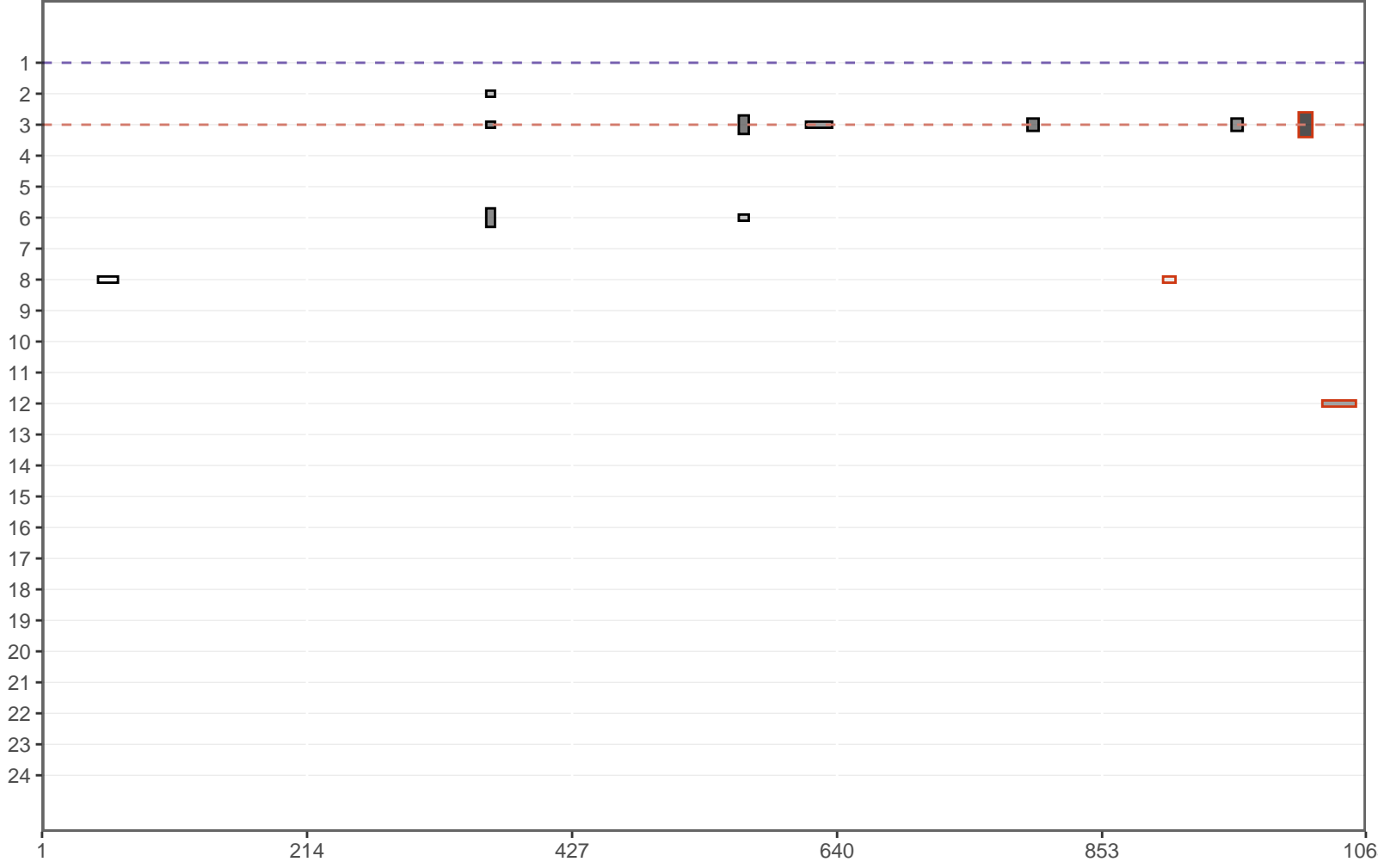
MW indication



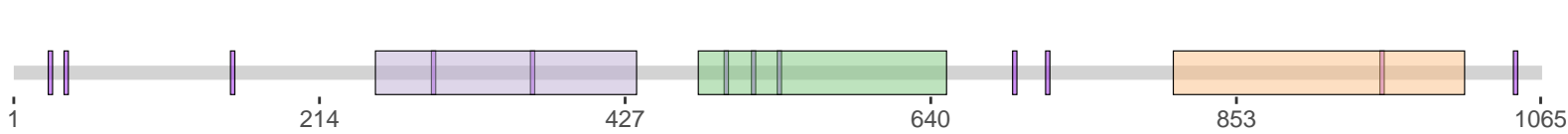
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

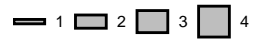


Protein sequence:

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NbL01g23940.1 purple_acid_phosphatase_15 [MW – SP = 59.96 kDa]

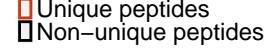
No. of times detected



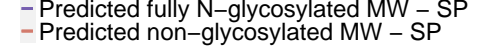
log(intensity)



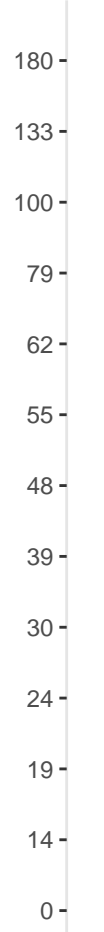
Values from



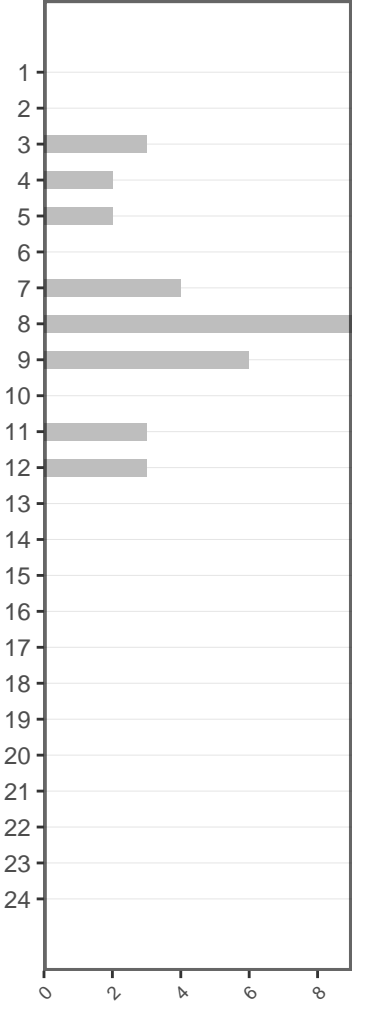
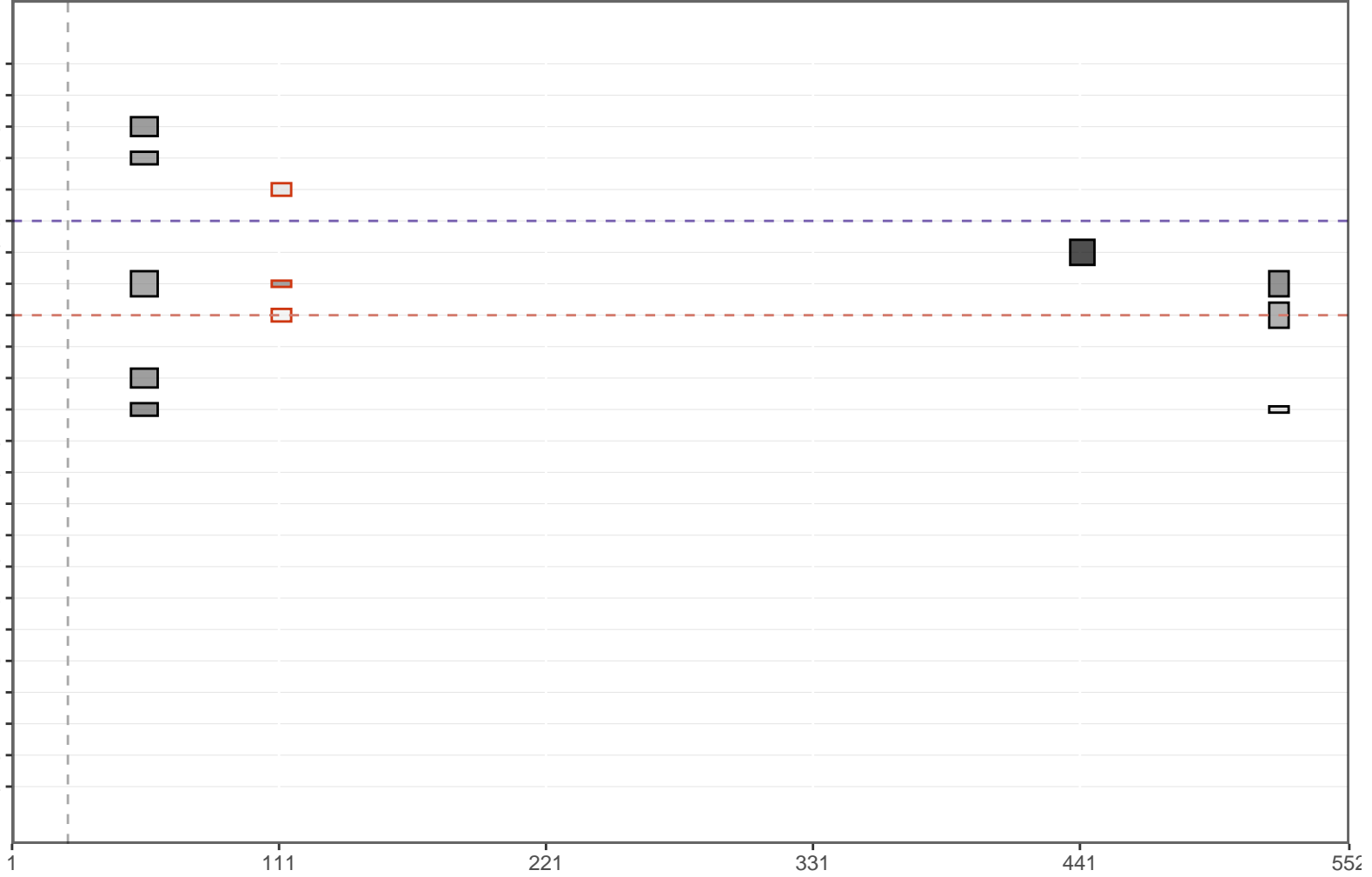
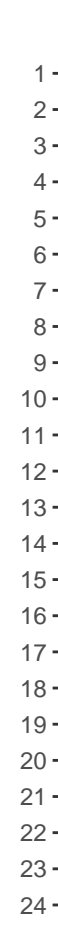
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL01g23810.1 glutathione_reductase_chloroplastic [MW = 58.52 kDa]

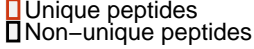
No. of times detected



log(intensity)



Values from

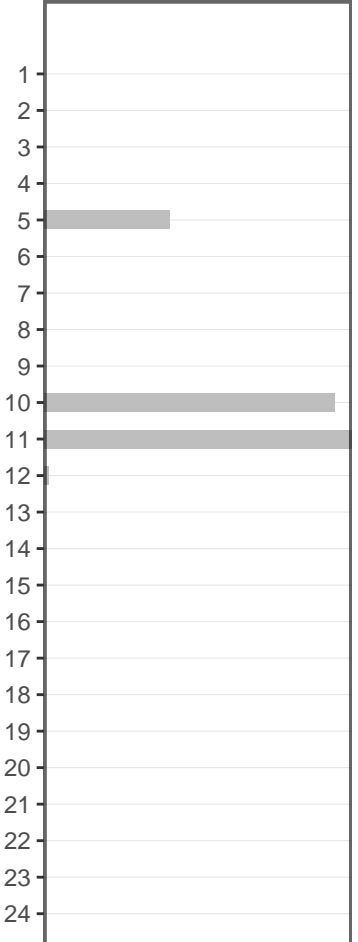
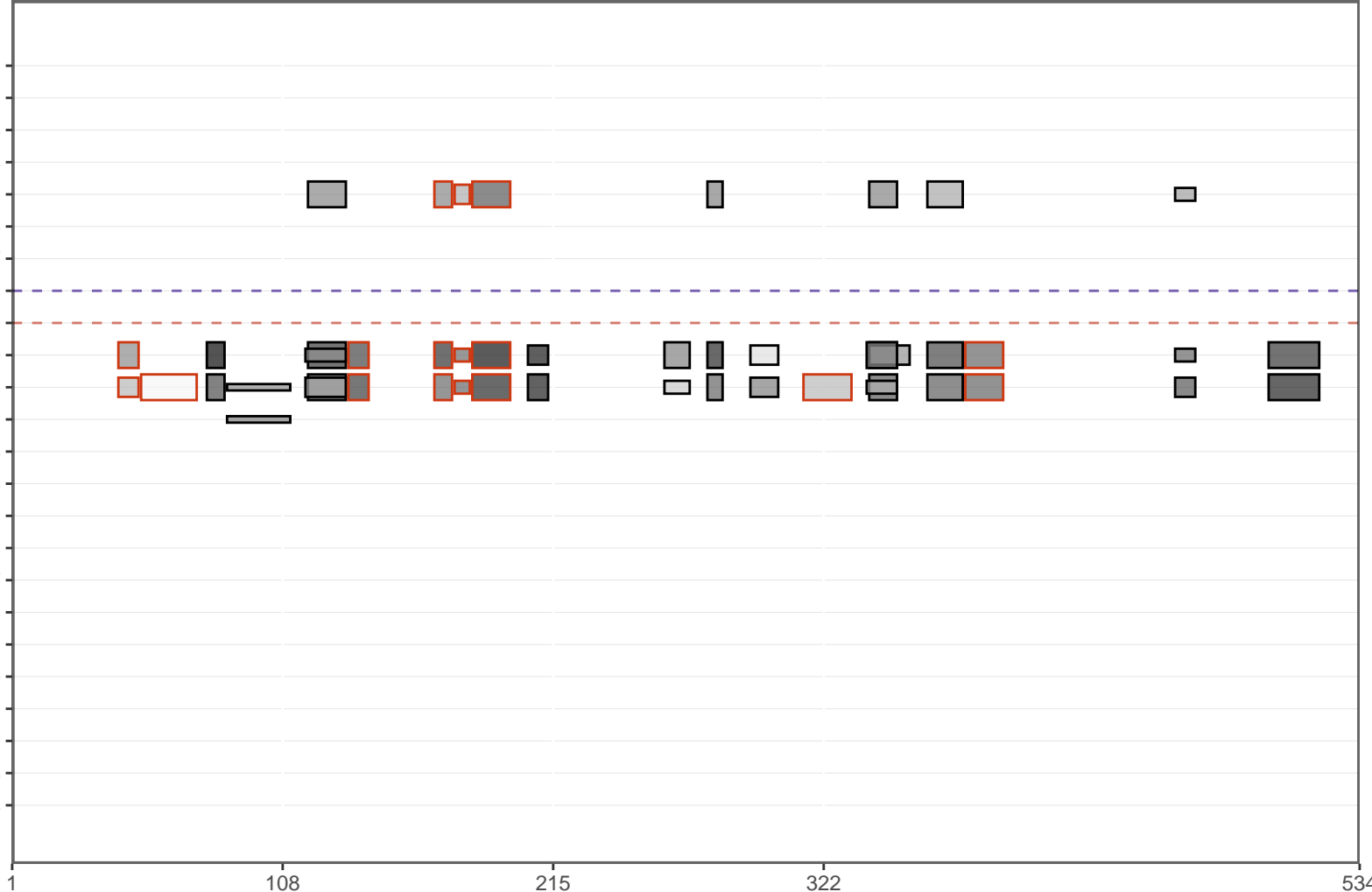
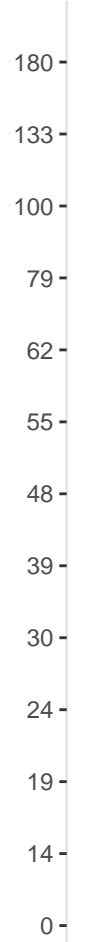


MW indication



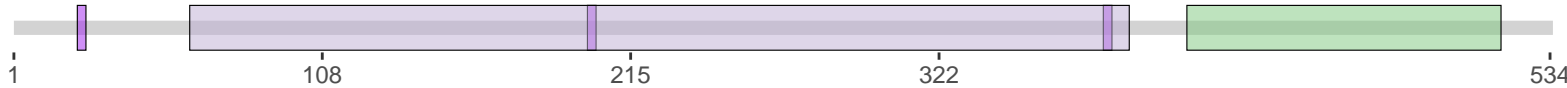
Molecular weight

Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

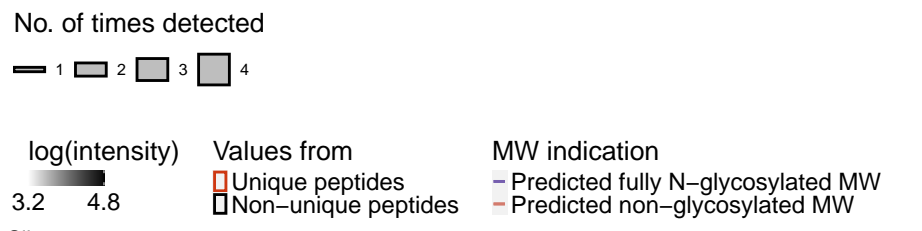
Pfam Description

- SP
- Sequon
- TM Domain
- PF02852 Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain
- PF07992 Pyridine nucleotide-disulphide oxidoreductase

Protein sequence:

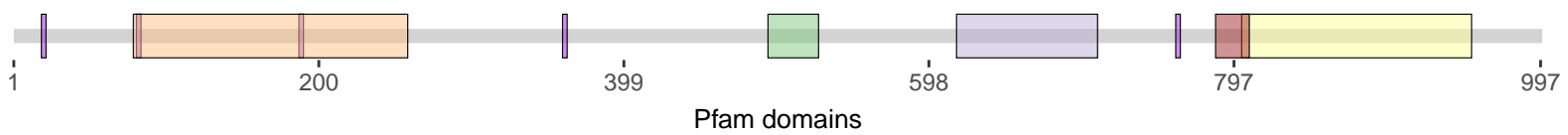
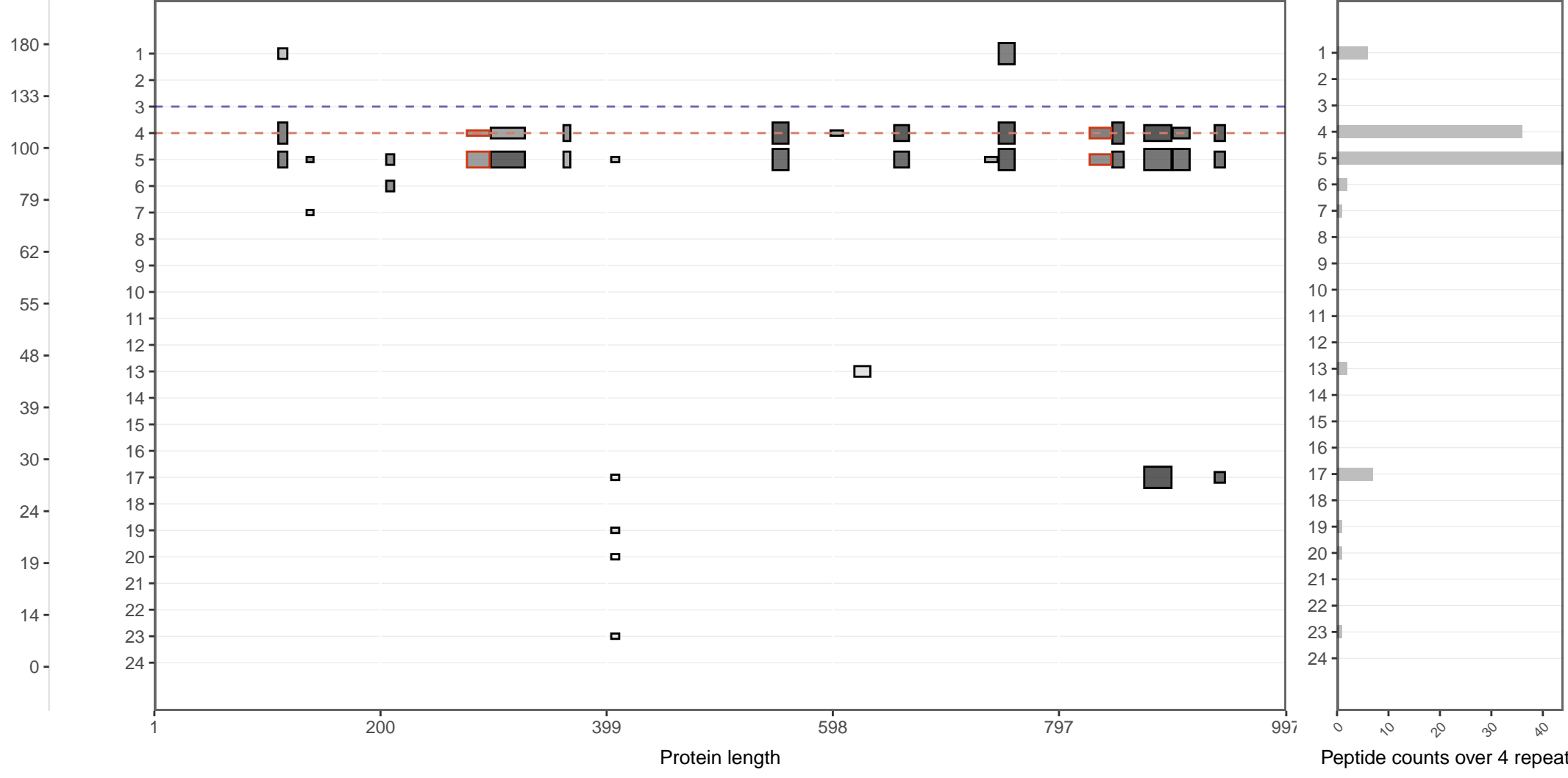
WRSGMGTVDLCLFRKELPLRIGFDDEMRAAWARNLEGRGTHMIPGTTTLEKTEKEDGKIVHTDHEVILADYVLFATGRLPNTRKLNLDWGVVELDKMAVVKVDEYSRTNVPWAWGDVTRNRMNLTVALMEGTGFAKTVFGGKPKPKDYLHHPGAVFGIIPPLVGLSEEAQEGVNGEVVYVSTFNPMNNTISGRGKEKVMKLVVEAETDKVLGASIGGPDPAEIMOGIAALKGGATKEQFDSTVGHIPSAAEFEVTRMRSETRRVSNSKRKTKLU---

NbL01g23710.1 26S_proteasome_non-ATPase_regulatory_subunit_1_homolog_A-like [MW = 108.01 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF01851 Proteasome/cyclosome repeat
- PF17781 RPN1/RPN2 N-terminal domain
- PF13646 HEAT repeats
- PF18004 26S proteasome regulatory subunit RPN2 C-terminal domain

Protein sequence:

STNVEVHQIACGLGLGLAALGTADEEDYDDIKNLYVDSAVAGEAAGIGMGLLMVGTASEKAGEMLAWHETQHEKIRGLGALTYVGRREEADTIEQMTDGGDPIRFGMVALALAVRGTANNKAIKQLLHFVSDVSDSDVRRRTAVLALGFVMSYSEPEGMPIRIVSLLSESYNPHVRYGAMAVGSGCAGTGLSEASISLERLFTSDVYDFVRRGALIAMAMVMQISEASDSRVGAFRRGLEKVLKHEDTMCKMGAILASGLDAGGRNVTKLLSKTKHDKITAVYGLAVI

NbL01g23610.1 pyruvate_kinase_isozyme_A_chloroplastic-like [MW = 65.22 kDa]

No. of times detected



log(intensity)



Values from



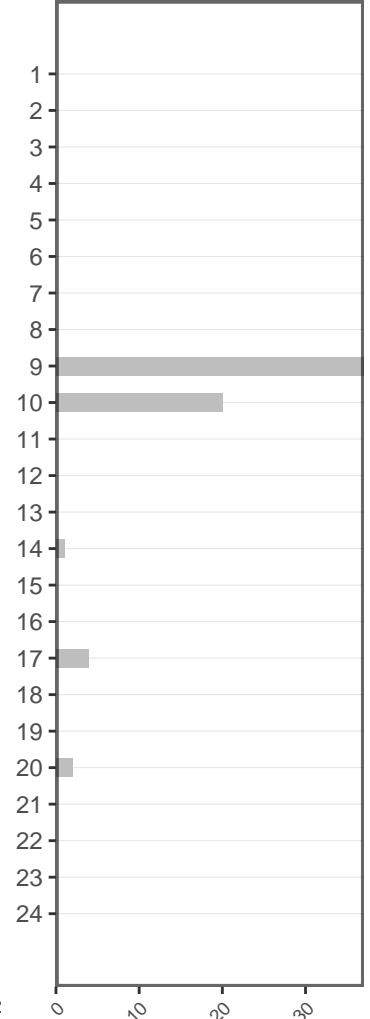
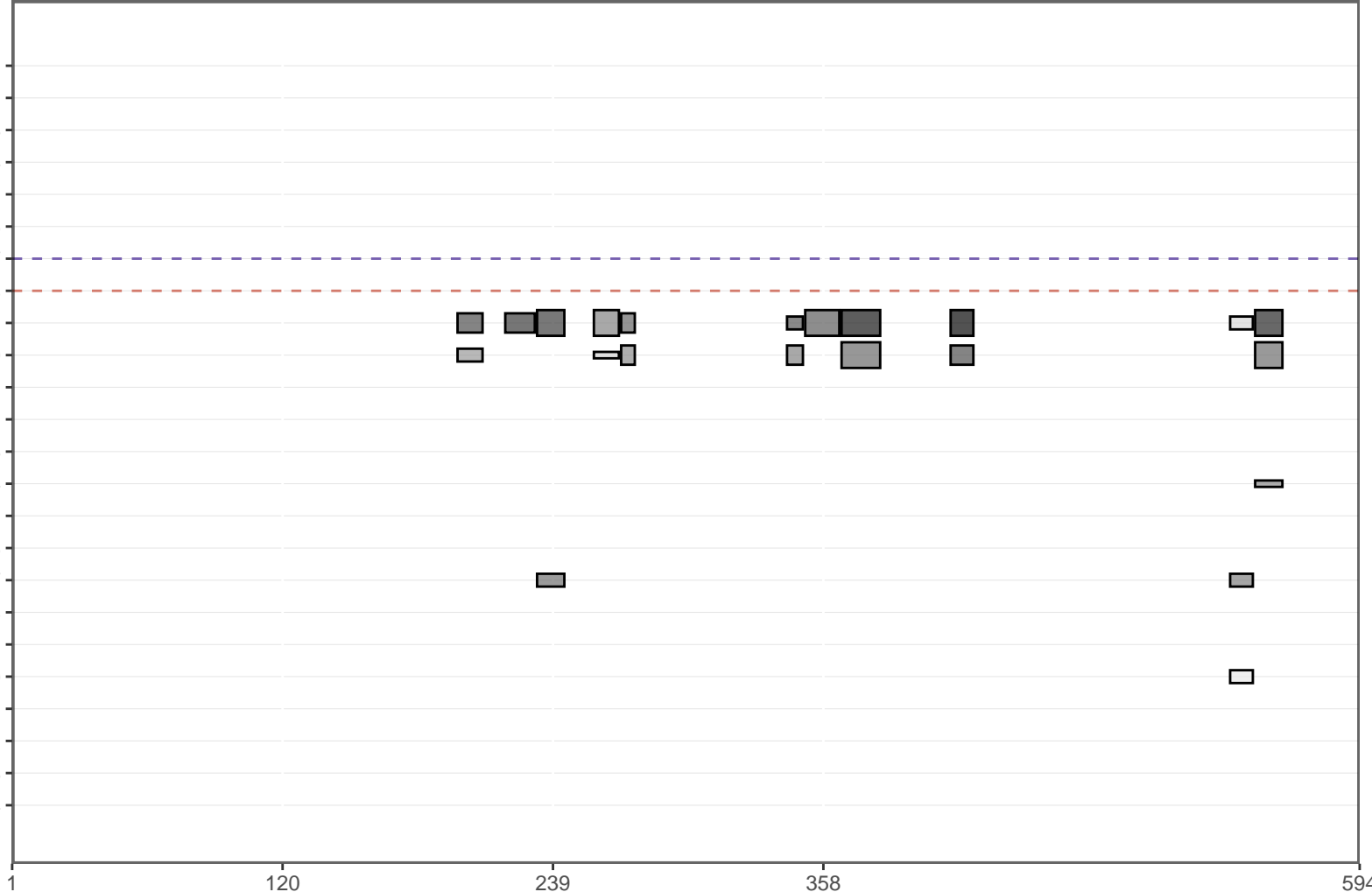
MW indication



Molecular weight

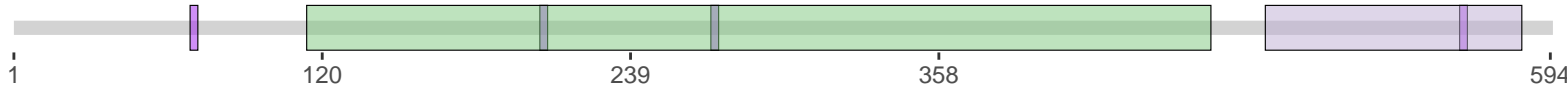


Gel Slice



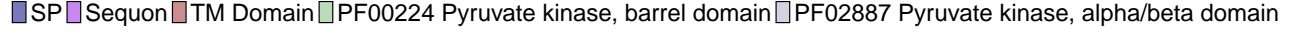
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL01g23580.1 GDP-mannose_35-epimerase_1 [MW = 42.92 kDa]

No. of times detected



log(intensity)



Values from



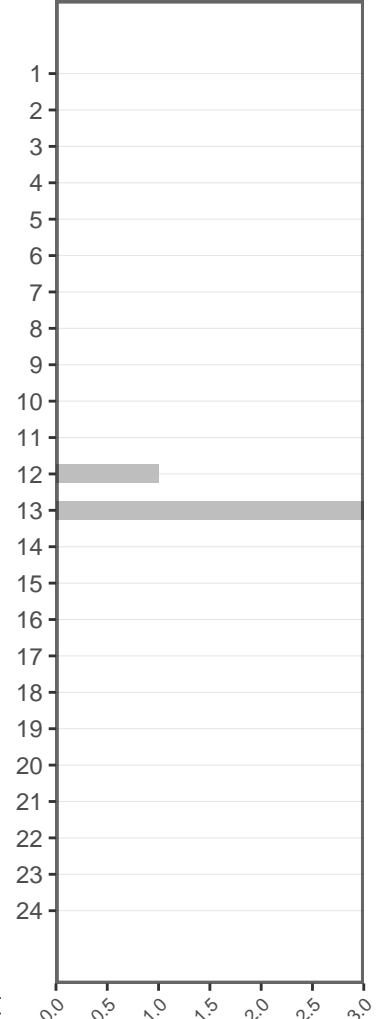
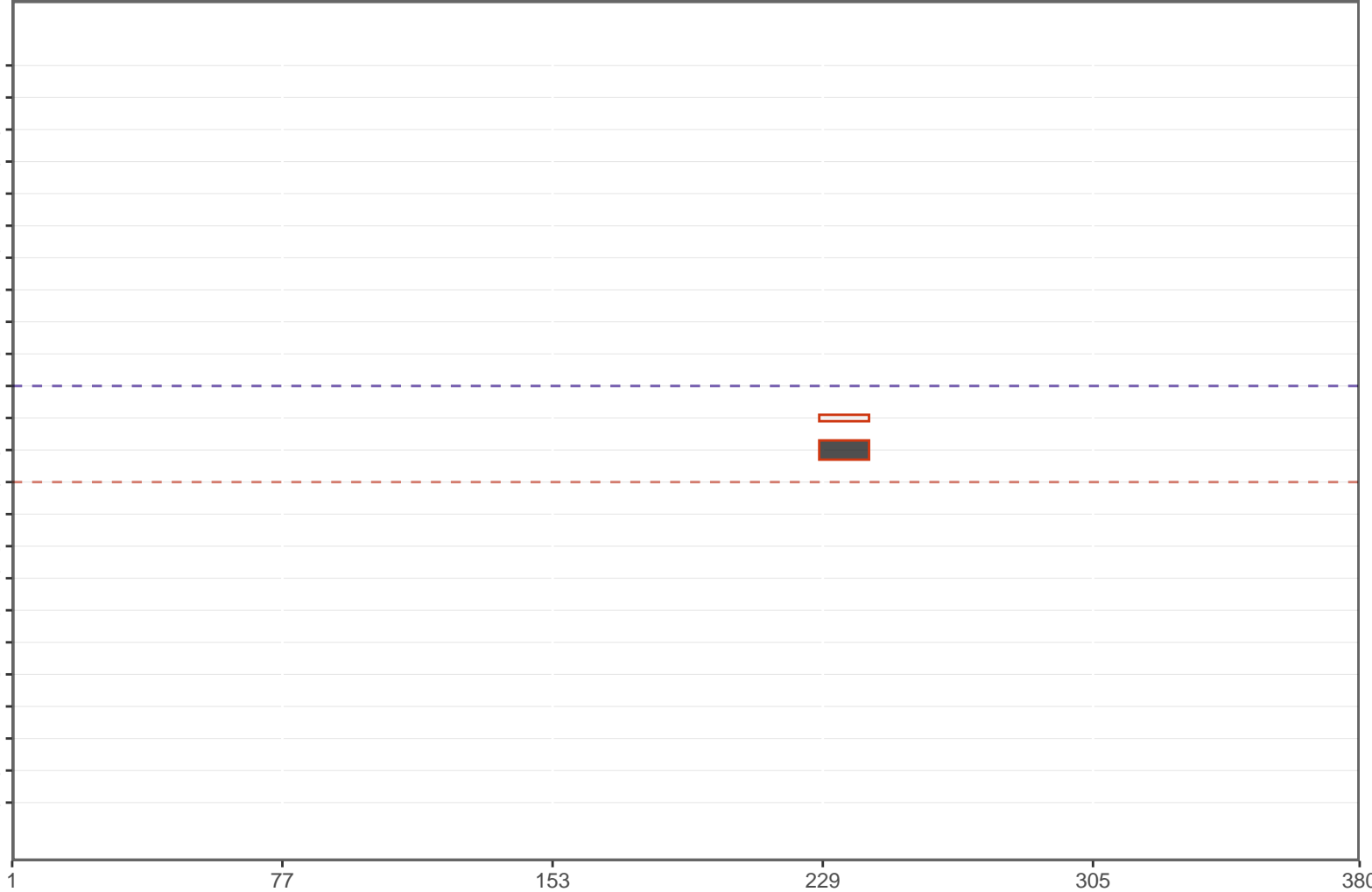
MW indication



Molecular weight



Gel Slice

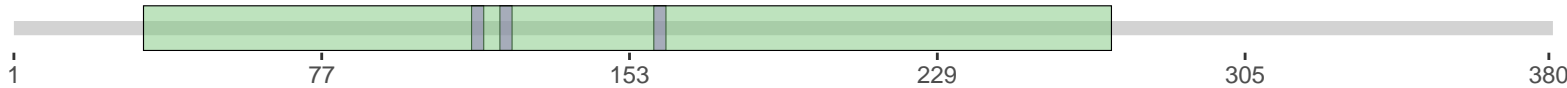


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

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NbL01g23460.1 NAD(P)H-quinone_oxidoreductase_subunit_N_chloroplastic [MW = 28.17 kDa]

No. of times detected



log(intensity)



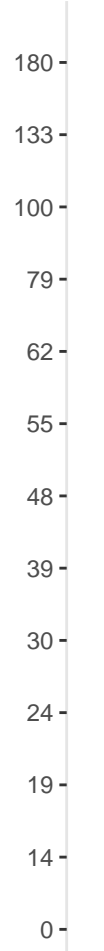
Values from



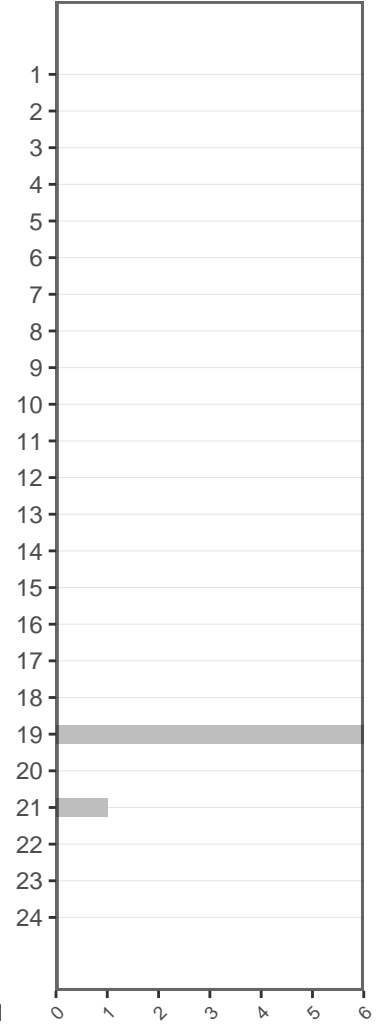
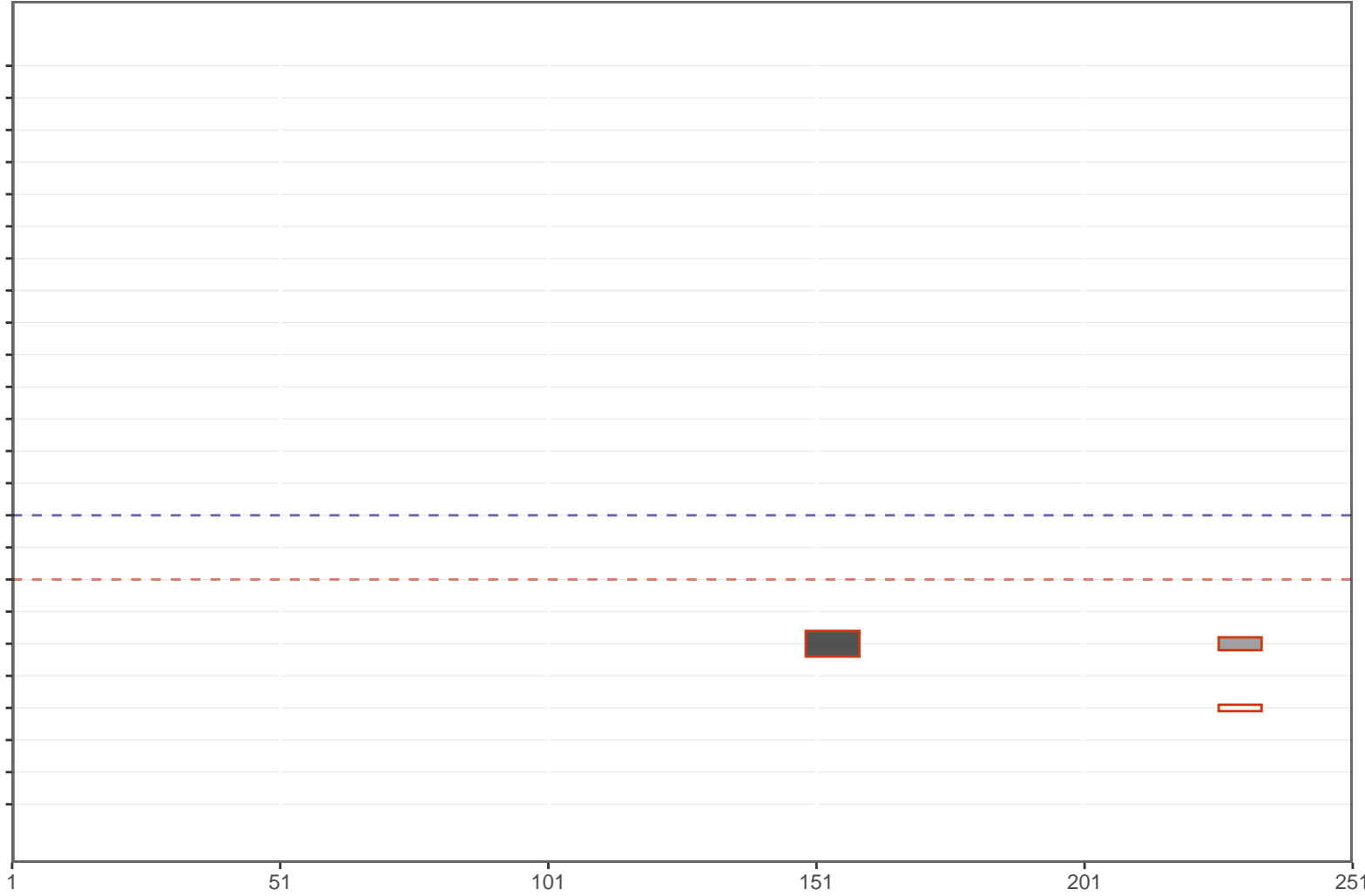
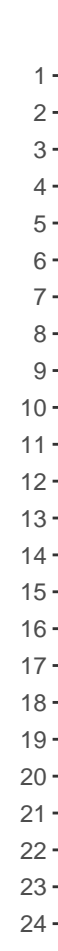
MW indication



Molecular weight

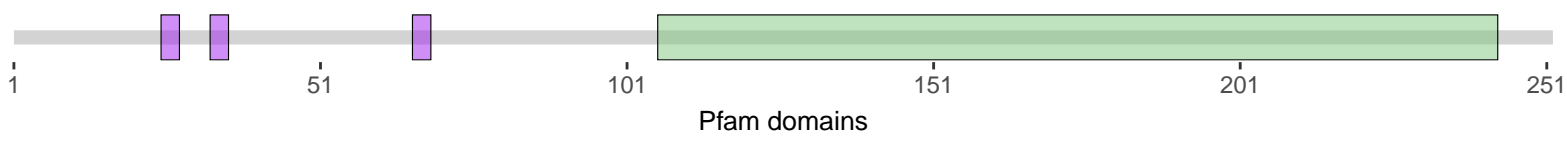


Gel Slice



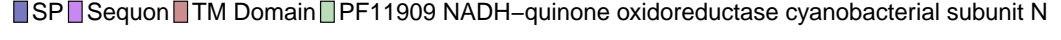
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEHKALAIYSPHEGGVEGRYLTRIKYGGYHFLDLSARGLGDPEFTLTKRHPVQNAHVGKGIARWYFFPEVDVRLLELFPNAKGLVWVIEAKVLKKAELGFLALLPLSRPKWVVAECGNWRKFMWPKLKEIAGLSGS

NbL01g23340.1 electron_transfer_flavoprotein_subunit_beta_mitochondrial-like [MW = 28.04 kDa]

No. of times detected



log(intensity)



Values from



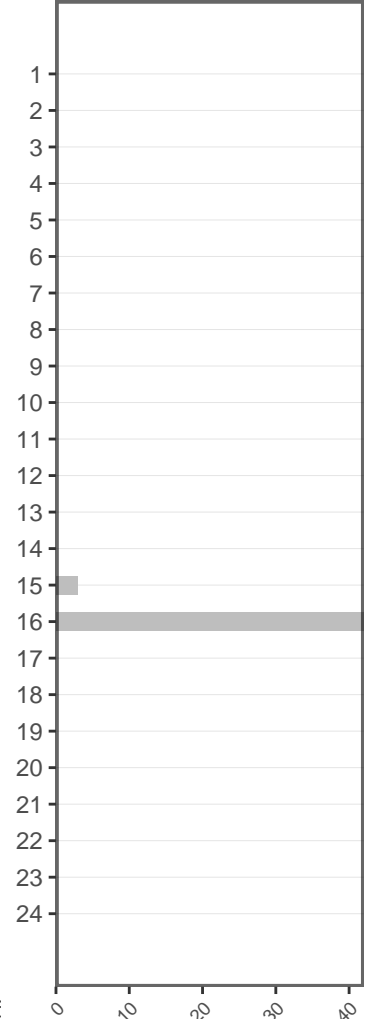
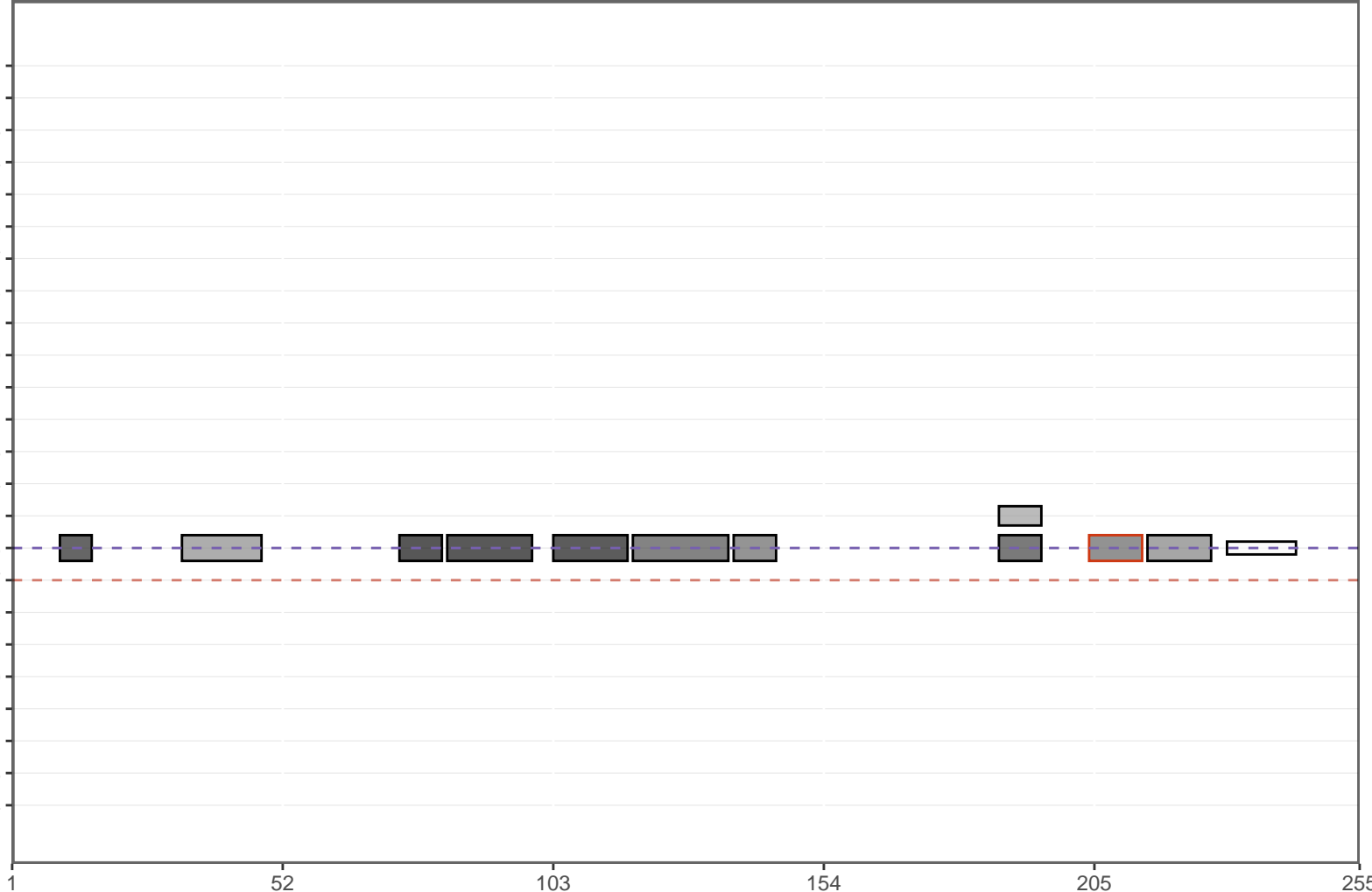
MW indication



Molecular weight

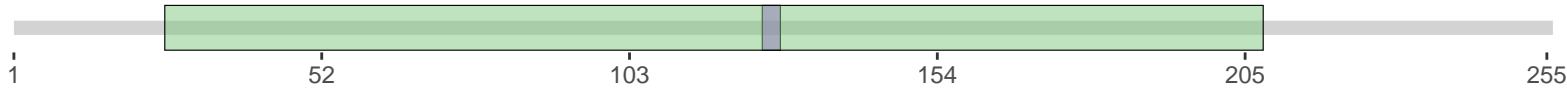


Gel Slice



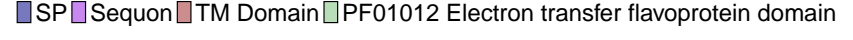
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL01g23220.1 DAG_protein_chloroplastic-like [MW = 28.61 kDa]

No. of times detected



log(intensity)



Values from



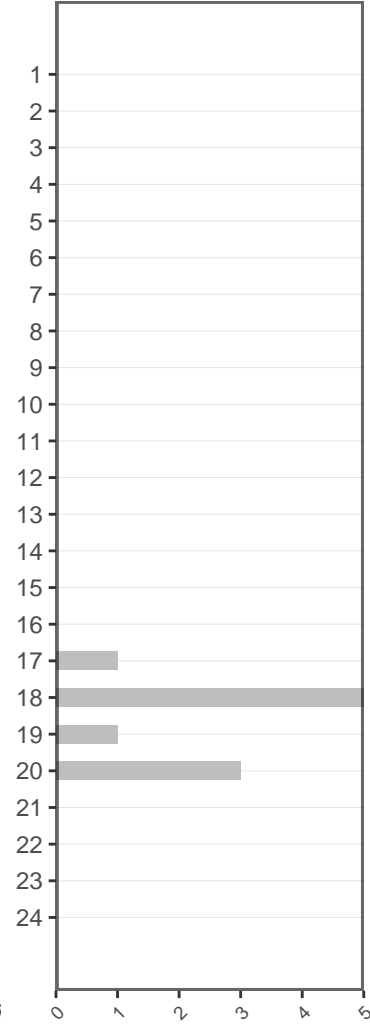
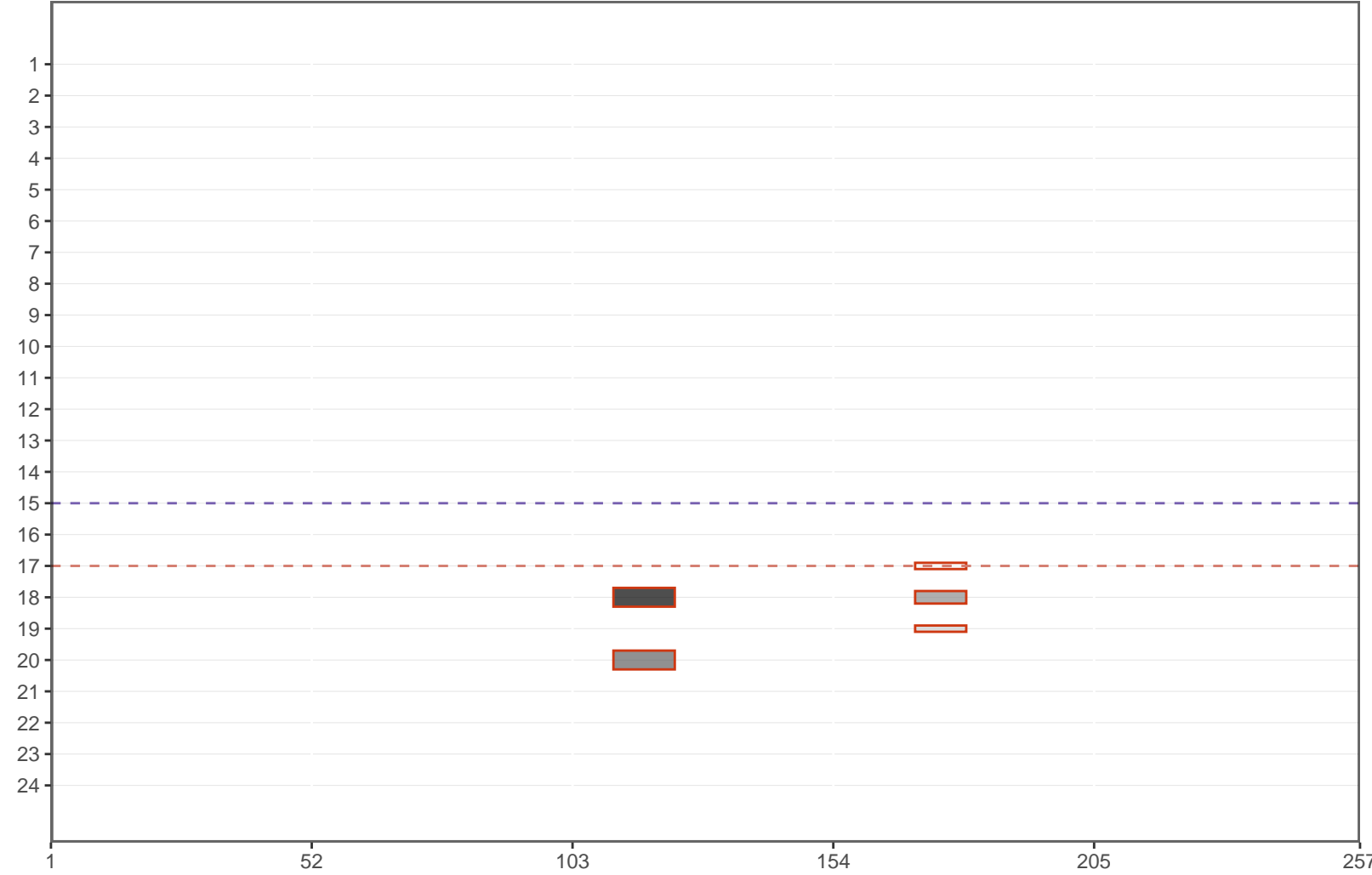
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

IEEEAOKKYSVSTFTYTGFGALISEELGKVKGLPGVLLVLPDGLVDPKDKYGGDLFVGGKVIHRPQYRFNONGSSRPRPRRYDRRREKMQVERREPIGRGAWTPNGQPPAGVSVGGGNFSGHTGGGPAAGGGGNSG

NbL01g23210.1 uncharacterized_transmembrane_protein_DDB_G0289901-like [MW = 52.7 kDa]

No. of times detected



log(intensity)



Values from



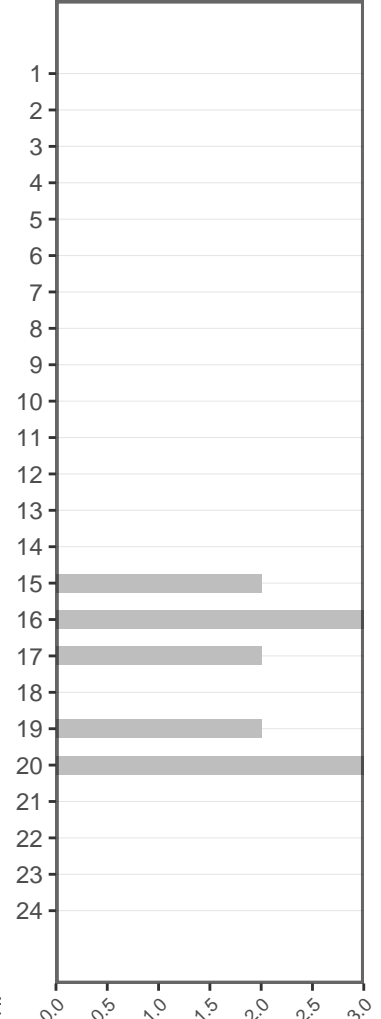
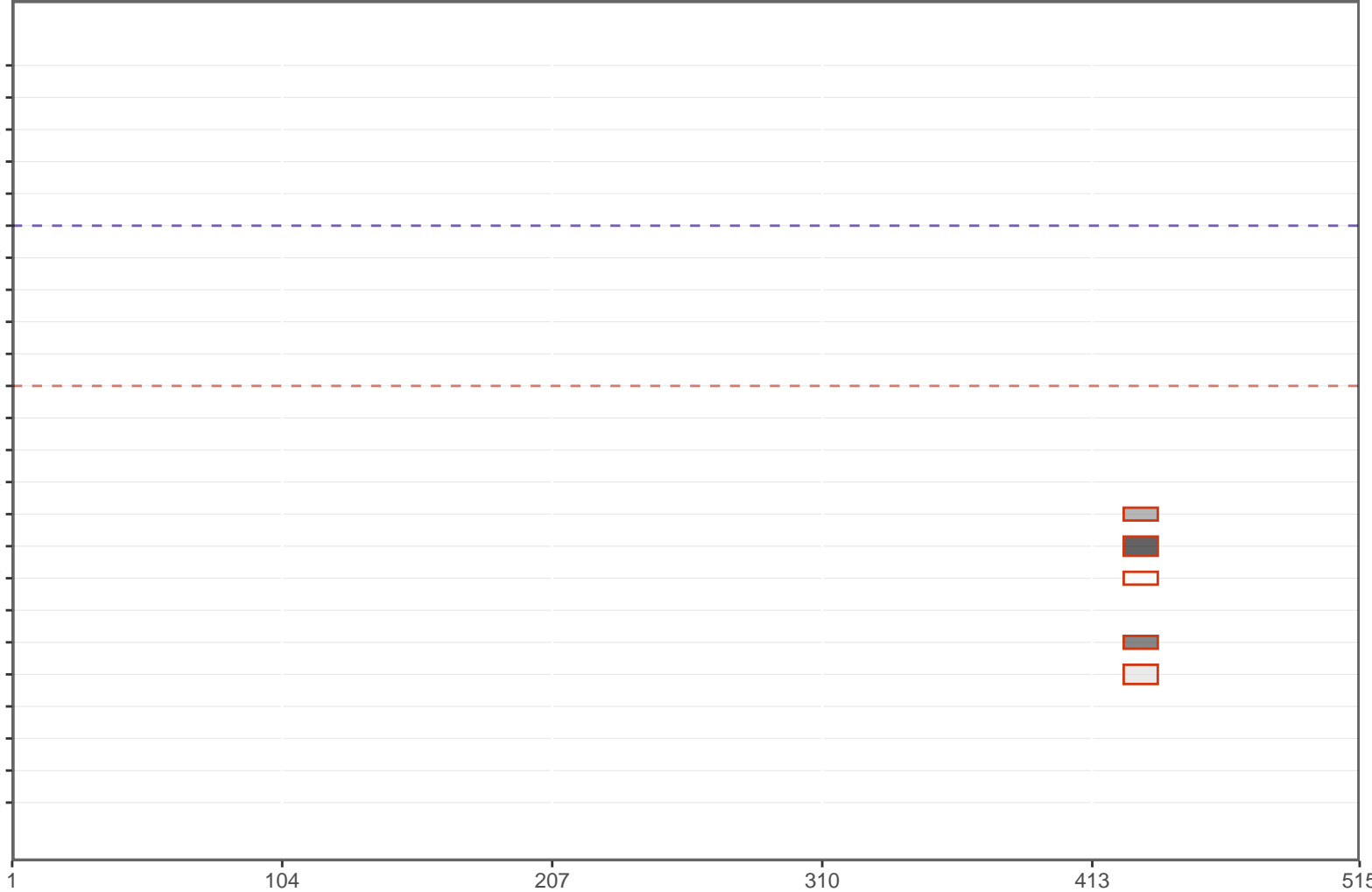
MW indication



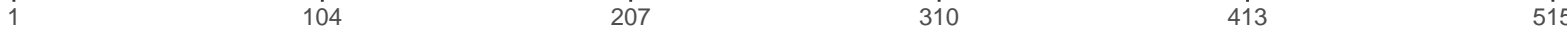
Molecular weight



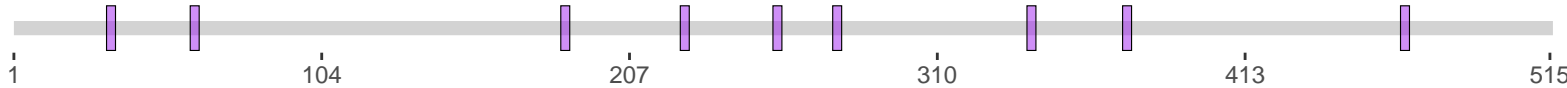
Gel Slice



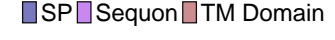
Protein length



Pfam domains



Pfam Description



Protein sequence:

SSGDNVFGDFQNTAKBGGSSGFGDFPFSTKNNASTGNSGSGGAYKVDVDFGFTNTGSGASATGSSGVDGDFGFTNTGSPATGSSGVDVDFSLFSSSTNASFGGAAGSGGSENGDFTGGDDWGFSEFVGNDSGTTLEGLPPFPAGVSAASKKNGMDNHKGGYADAKVLEWVWVILLEKAGDGDAGAMEVLSRASAGYKEVGEYKKAADVCTKYLEGDDKKNVSVLGRALLYESMEKVKLGAEDLRVTVMNIDPGRVARSSTHRLNKMAG*

NbL01g22830.1 ureidoglycolate_hydrolase [MW = 53.21 kDa]

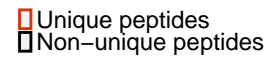
No. of times detected



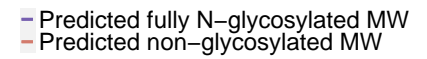
log(intensity)



Values from



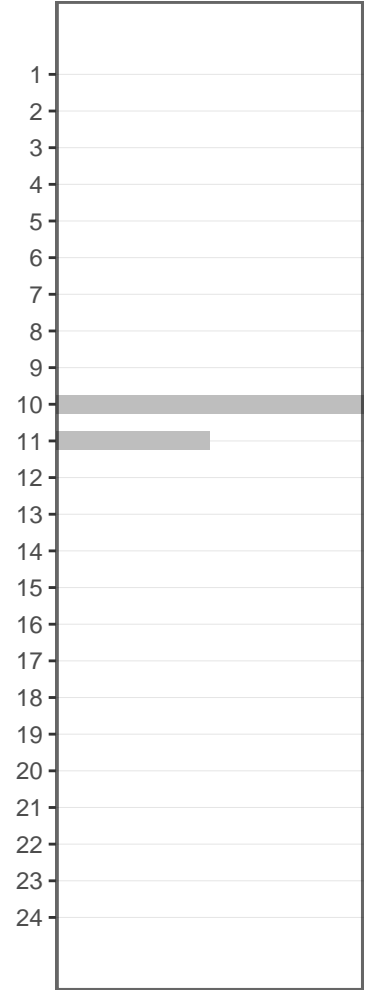
MW indication



Molecular weight

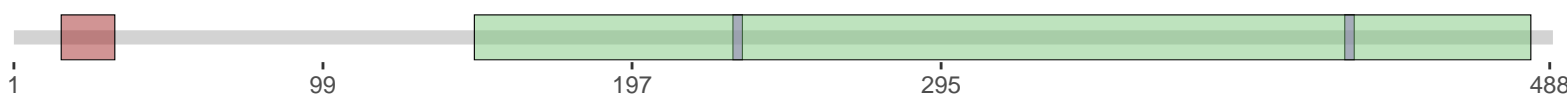


Gel Slice



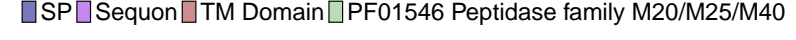
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description

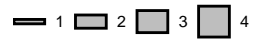


Protein sequence:

FSFEAAKFAQYGNKGDVFEVFLKKGYSFAFVELHEGGPILKEKETSIGVVTAAAPKIKVTFEGNGSHGAGALMPERNDAGLAAEALALAVEKHLEGGSDTGTVGLKLLHPGAINSPMAHLEIDTRIDDESRRLNVIENHIGSTLAAKRRKVMSEFEVNGDPPALSDSESTKATELACGELNTHKRMISRAYHDLFLMARISPMGMIFIPCKYKGSKPEEFSSVDDIANGVKVLAFLAKLSL

NbL01g22740.1 pleiotropic_drug_resistance_protein_1 [MW = 161.54 kDa]

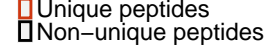
No. of times detected



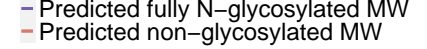
log(intensity)



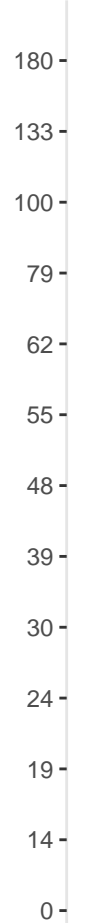
Values from



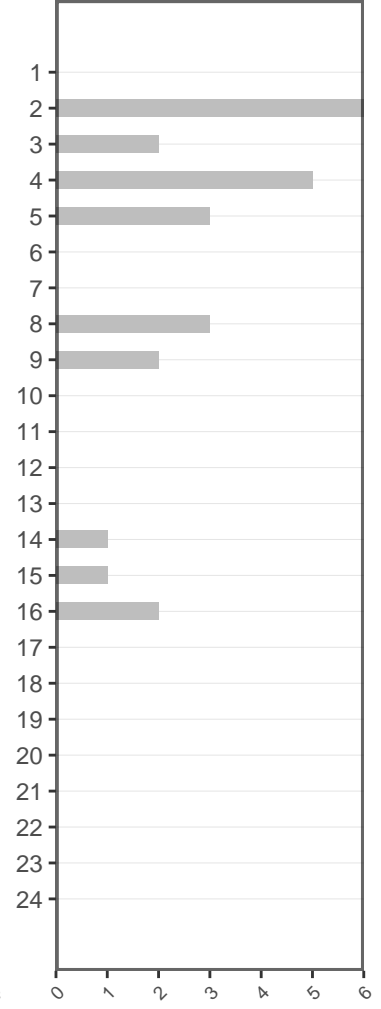
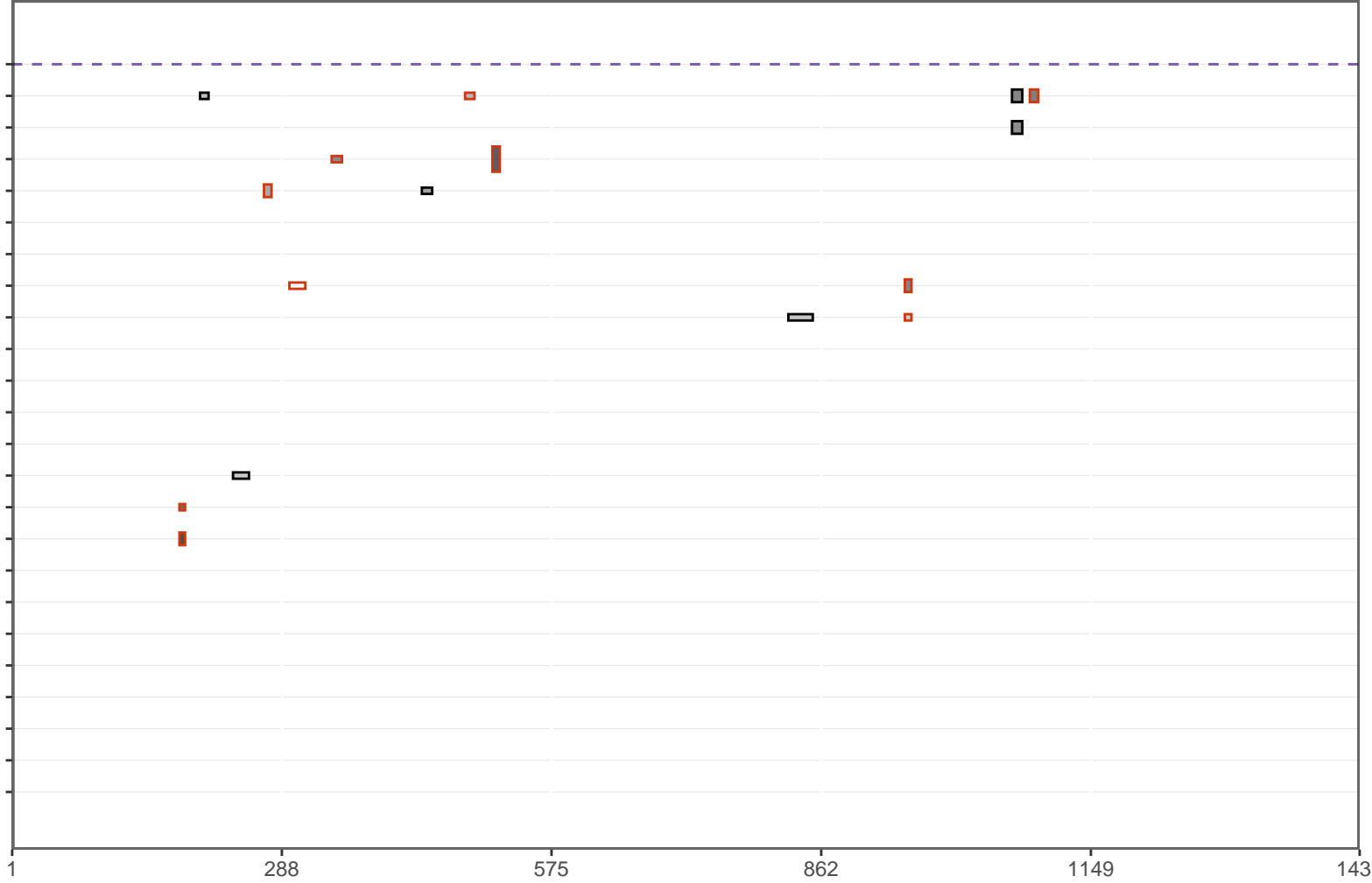
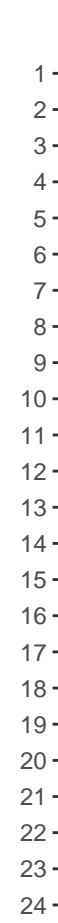
MW indication



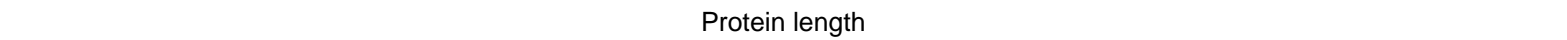
Molecular weight



Gel Slice



Protein length

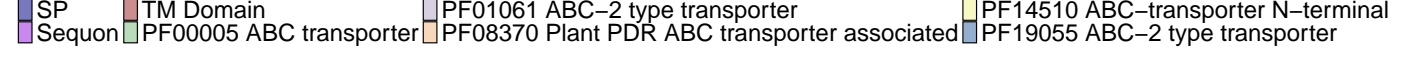


Peptide counts over 4 repeats



Pfam domains

Pfam Description

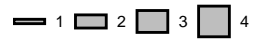


Protein sequence:

VTSPMMYSVNSILVNEFDGKWNHIVPGNETLIGATVVKSRGFFPEAVWWWIGVSGALVGFVWFNFGYSVALAYLNPFDPQAVLAEDGNAENAEVVSQGHSTDDGGDSISGSGNKKGMALFFEPHSITFDVAVSVVDMPOEMKEGGAGDRLLVLLKGVSGAFRPGVLTALMGVSGAKITLMDVLAQRKTGGYIDGDIRISGYPKKGKGFARISGQEGNDIHSPTVTVYESLIVSAWLRPDGDDEKTRKMFVDEVLMELVGLRLRSALVGLPGVNLSTEQRLTI

NbL01g22720.1 pleiotropic_drug_resistance_protein_1 [MW = 84.52 kDa]

No. of times detected



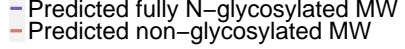
log(intensity)



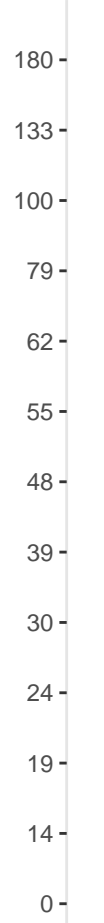
Values from



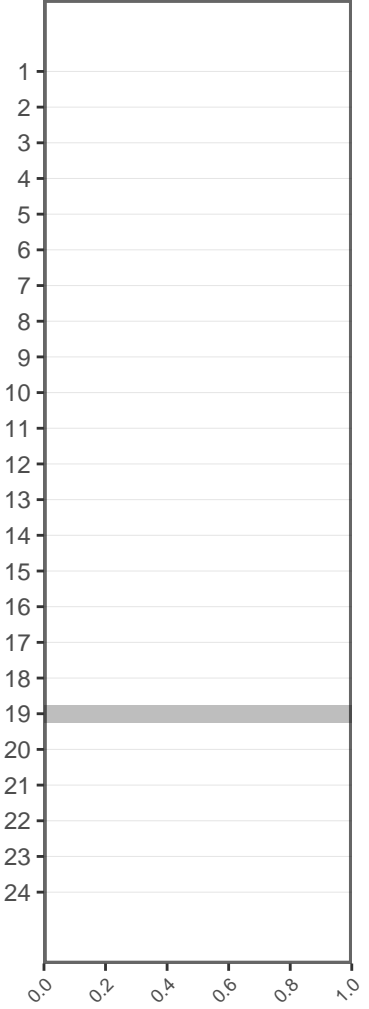
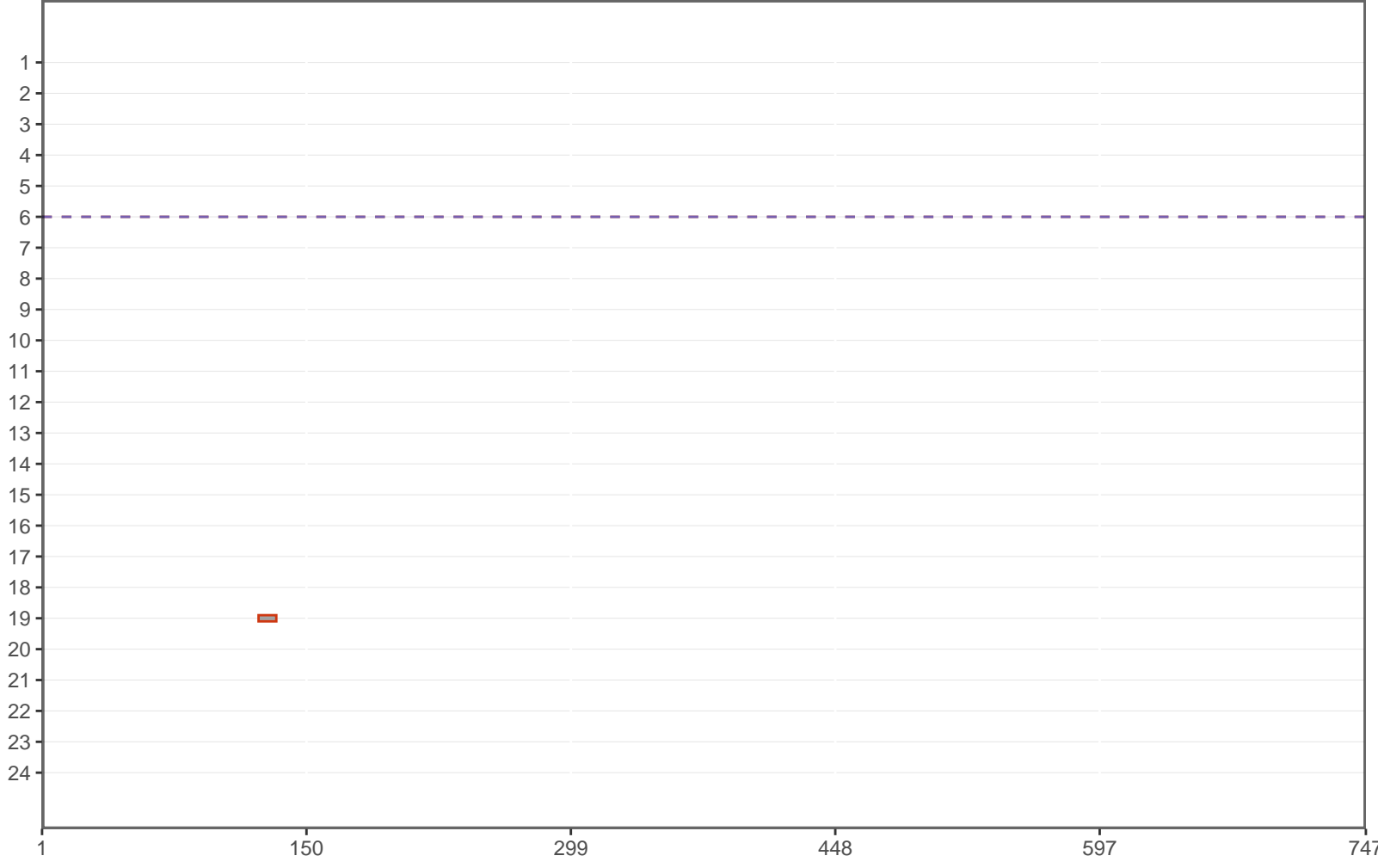
MW indication



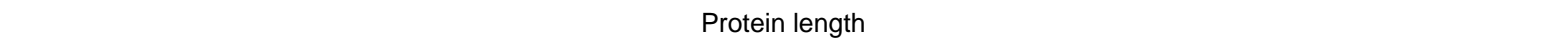
Molecular weight



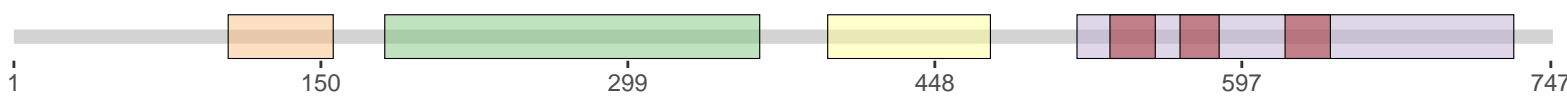
Gel Slice



Protein length

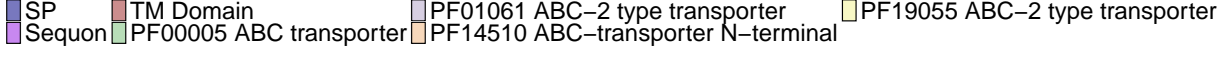


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

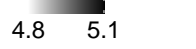
ADISTGLDSSSTTYGIVNSLKGQSVIRMGKGTALISLGLQPAPEYVNLFDHILLSDGQYVVEGPRDVLVEFFESMGFGKPERKGAADFLQEVTSKDKDGGVYVRRDPEYRFRFSKEFAEAVGSHVGRKVRDELATTFDKSKHPAALFTQKYGIGKROLKLVCTERELLMDGRNRFVYLFKFFQLLALMTMTFFFRTRKMRDPAEDGGYSGALFFVMMFMNGLSELMTLYKLVFYKQRDLFYKPSWAWAIPSWLKPVTRAEVGMWVFLFYVMGFDNIVGRFTKQFLLLLL

NbL01g22630.1 sm-like_protein_LSM5 [MW = 5.94 kDa]

No. of times detected



log(intensity)



Values from



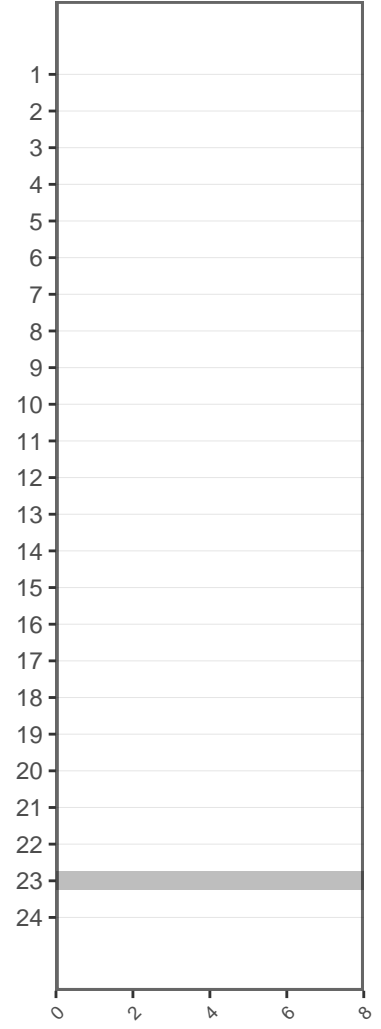
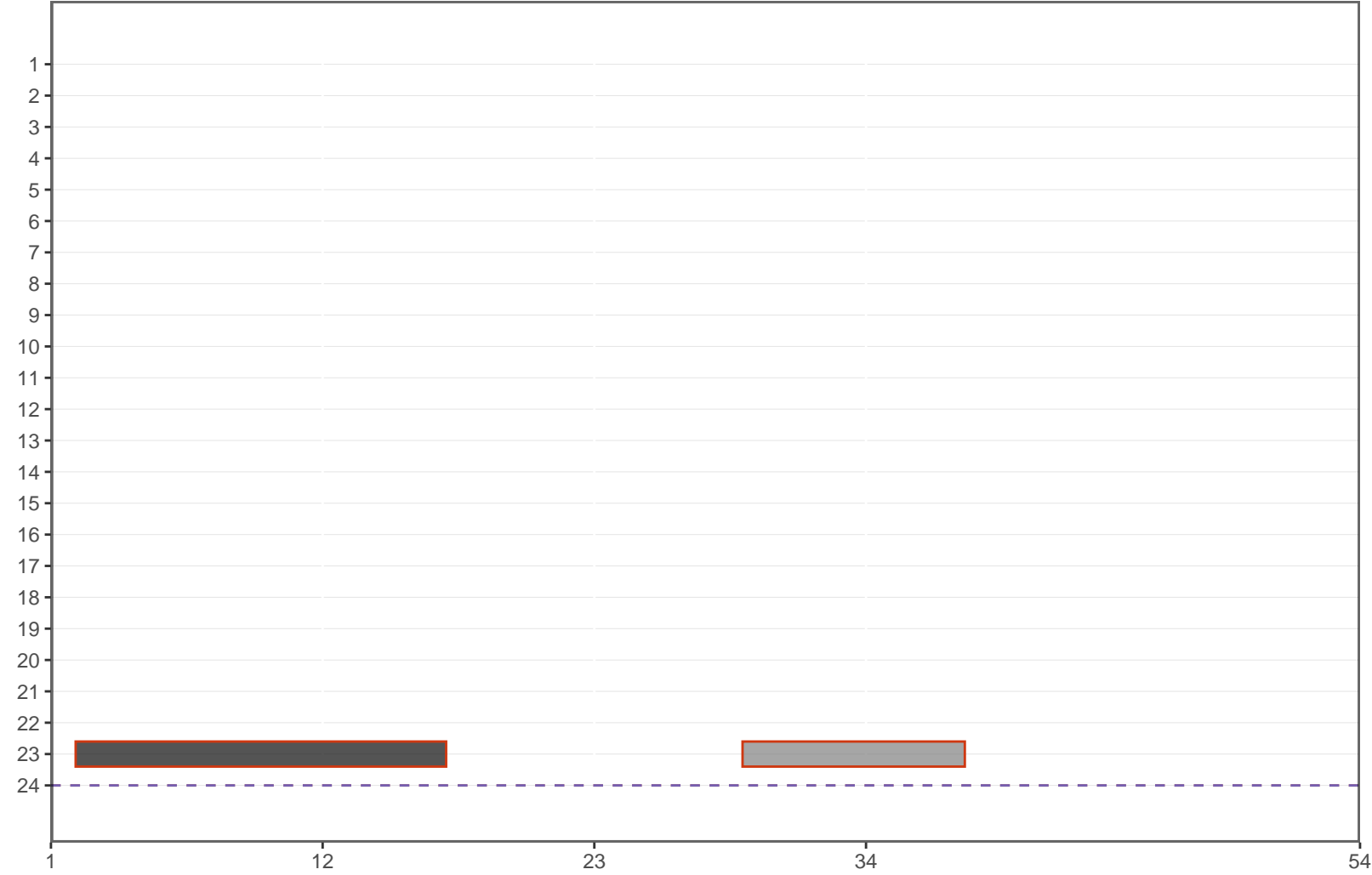
MW indication



Molecular weight



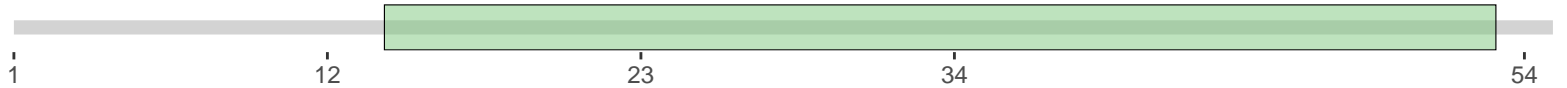
Gel Slice



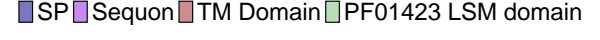
Protein length



Pfam domains



Pfam Description

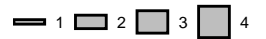


Protein sequence:

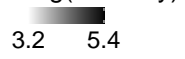
LIDRCIGSKIVYVMKGDKELVGTLRFDVYVMVLELVTE

NbL01g22610.1 3-ketoacyl-CoA_thiolase_2_peroxisomal [MW = 48.84 kDa]

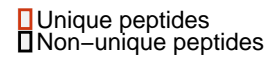
No. of times detected



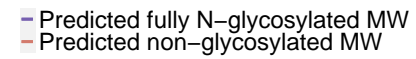
log(intensity)



Values from



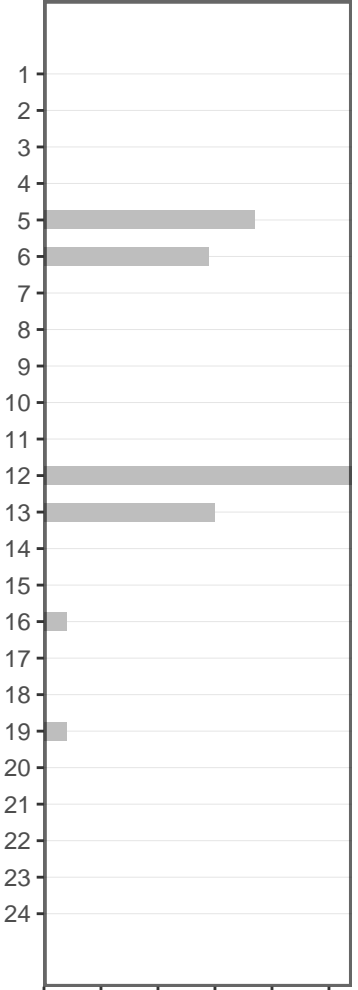
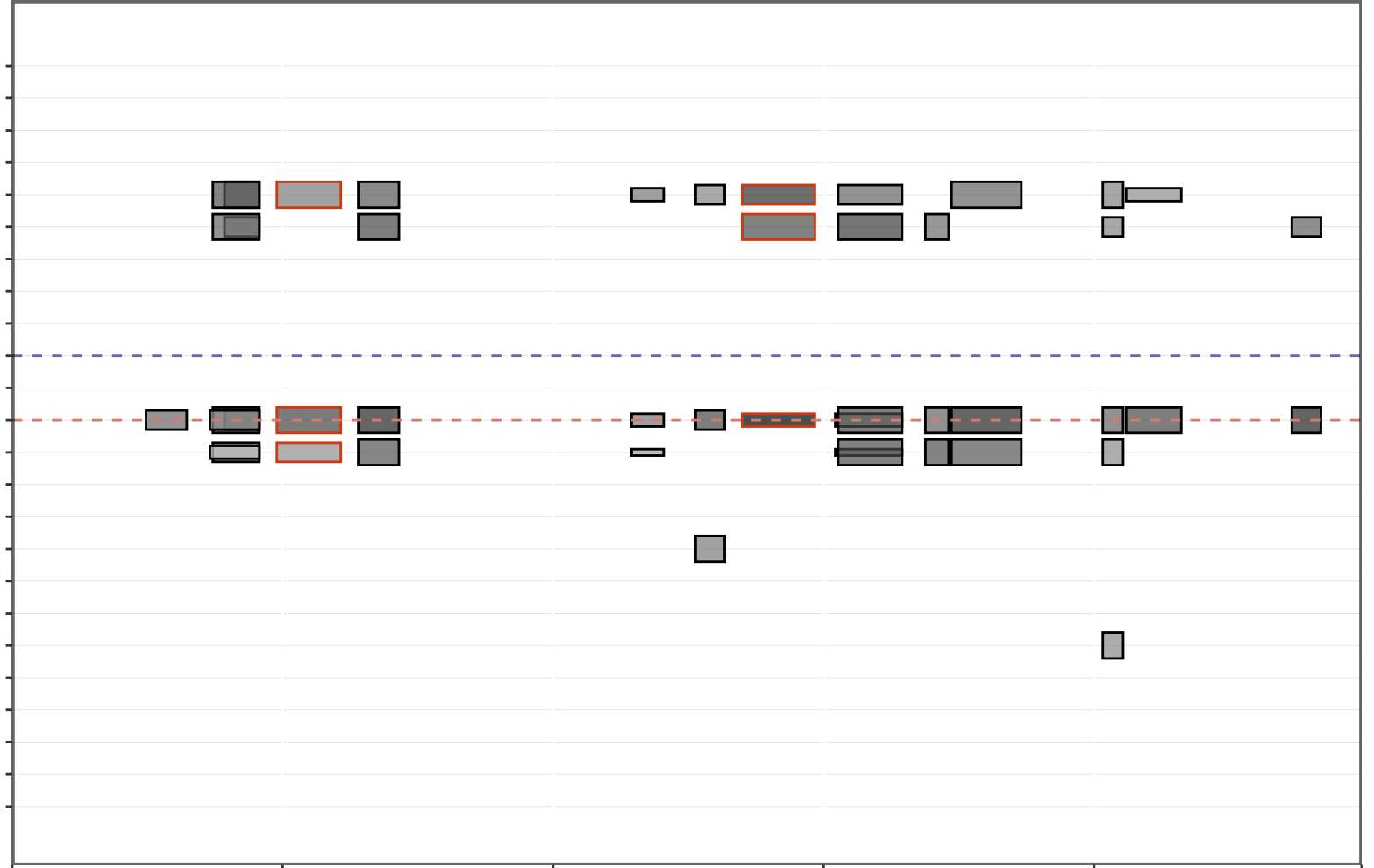
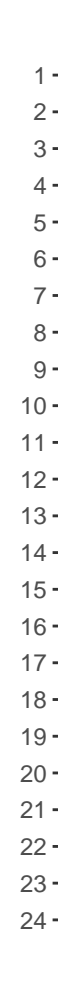
MW indication



Molecular weight



Gel Slice

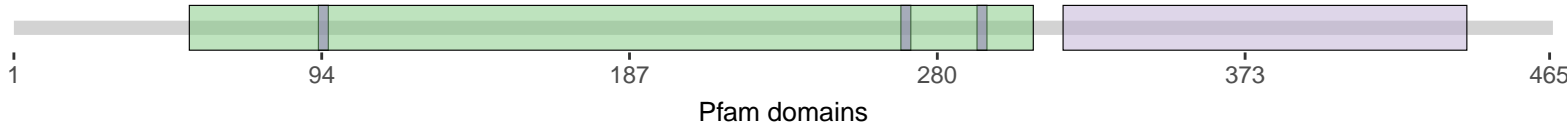
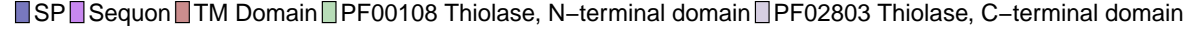


Protein length



Peptide counts over 4 repeats

Pfam Description



Protein sequence:

QAAVDSHRKAAALAAASGKFKRDEHPVPTKIVDPKTDGETPVTISVDDGIRPNAVSVDLAKLKPVKKSGTTTQAGNSGQVTDGAGAVLLMKRSLAMQKGLPLGVFRFTAAVGVDPAMGIGPWAIPAIAKVSAGLEEDLFEINEAFASGQVYVGRKLELDFPEKINNGSAMALGHPLGATGARGVATLLHEMKRRGKDRFGVSMCGTGMGAAVFERGDSGDELGNARKIGSHLLEKDAL

NbL01g22550.1 probable_pectate_lyase_8 [MW – SP = 46.54 kDa]

No. of times detected



log(intensity)



Values from



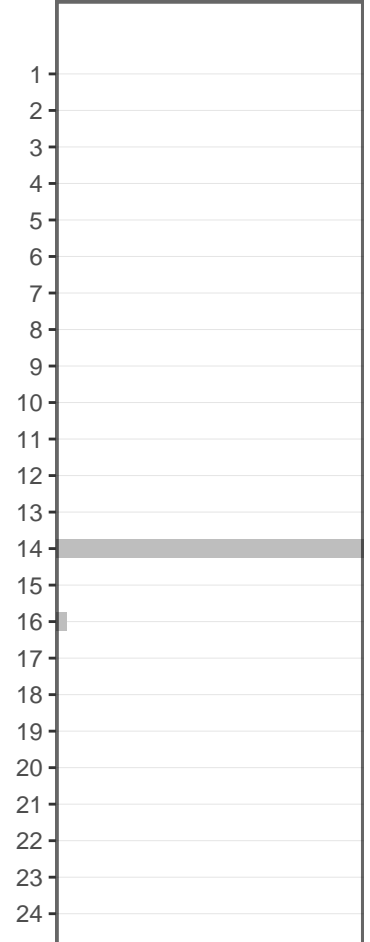
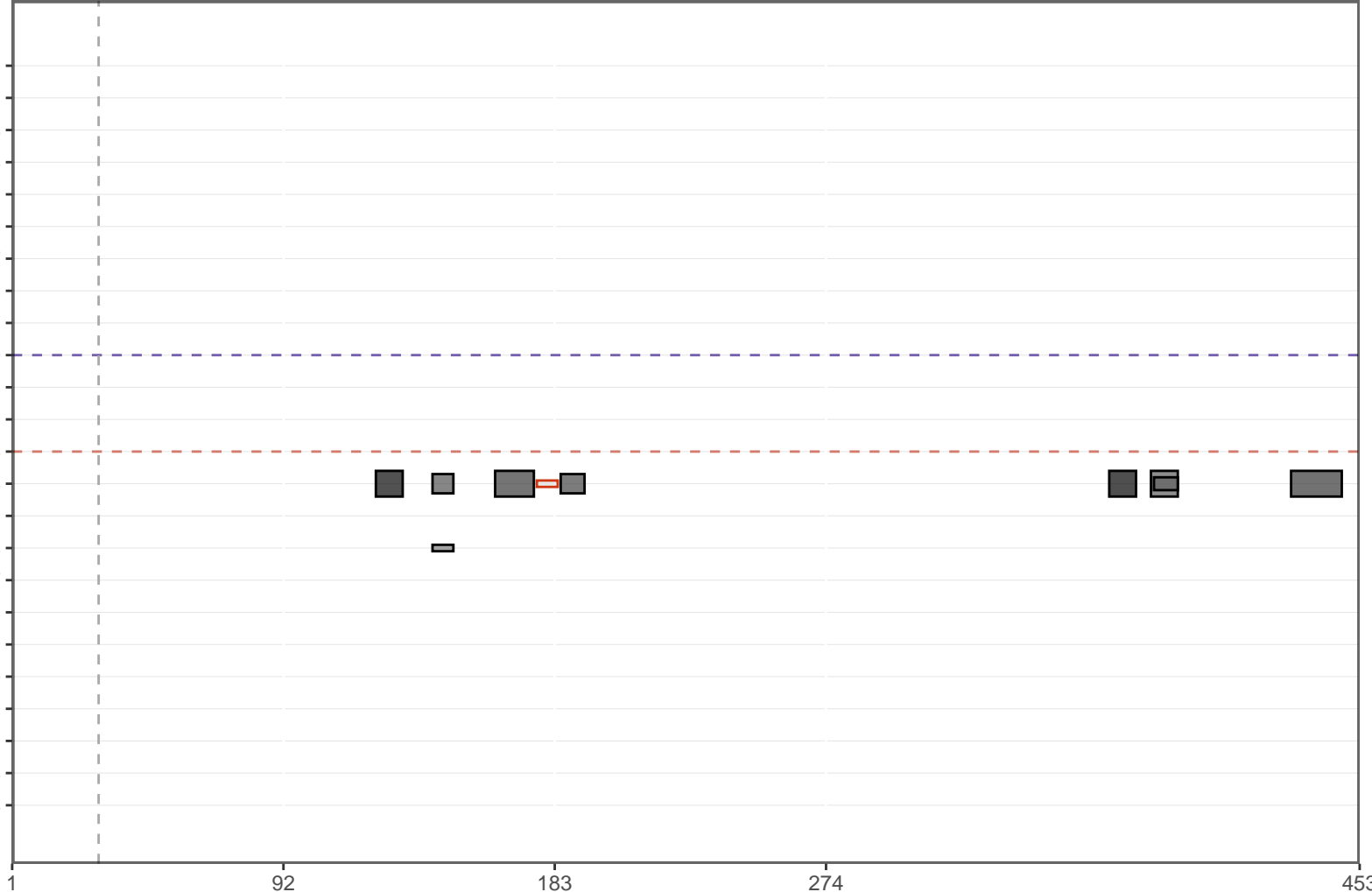
MW indication



Molecular weight



Gel Slice

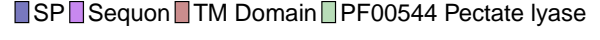


Peptide counts over 4 repeats



Pfam domains

Pfam Description

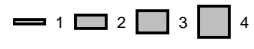


Protein sequence:

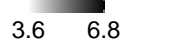
TNIIHQLHSHDCCKPTGNAMVRS6PHTGWRRTMADGDVAFVGG6SHWHDHNSLKHGADGLVDAMG6TATIEHNFANHNEVMLGH6DSYTRDKMGQVTHANHFGEGLGQRMPRGRHGYFHVYVNDYTHWEMVAIGGSANPTINGQGRYLAFTNPFKAEVTKRVDTAAGQWGWVWR6EGDMLNGAVFTPSGAGASASVARR6SLGAK66SMVGAITSAGPLACRR6RM6C

NbL01g22310.1 chaperonin_CPN60-2_mitochondrial [MW = 61.29 kDa]

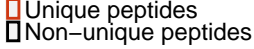
No. of times detected



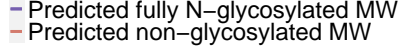
log(intensity)



Values from

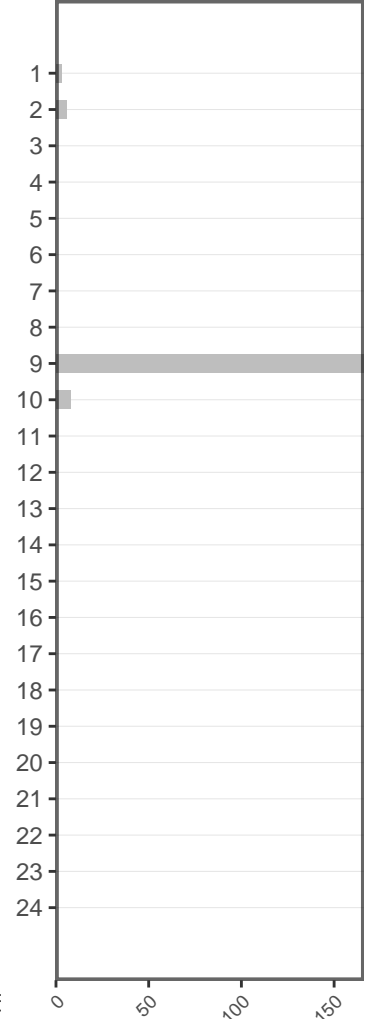
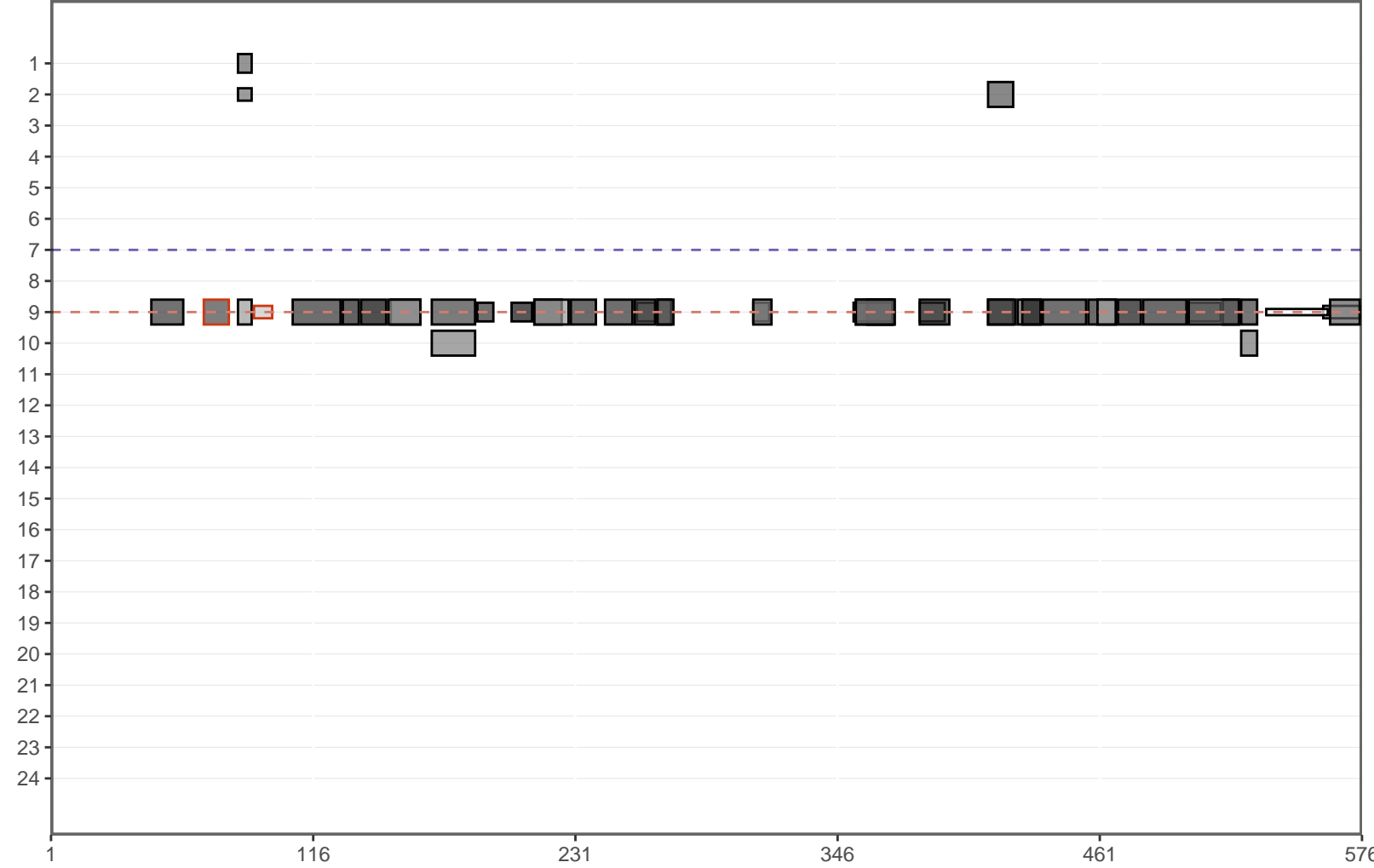
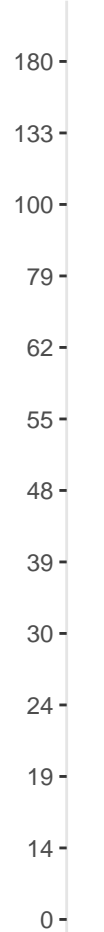


MW indication



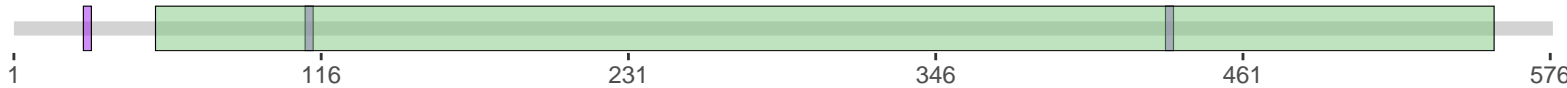
Molecular weight

Gel Slice



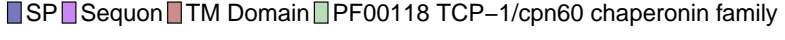
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KRQRLLVAEDVDSALATLNLNLRAGIKVCAKAPDFGNGRRKANLGDALITGGQVVTTELGLNIENVELEMLGCKKVAIKDDTIVLDGAGEKKEEGERCEQRSTIELTSDYDKLKERLAKIKSGGVAALIKGGASEAEVGEKDRVTDALNATKAAVEEGVPGGGVALLVAAKELDKLETANFDGKKGKGVQIKNALKTPVHTIASNAGVEGAAVVGKLLGGDDTLGYDAKAGEYVDMYKAGIDPLKVRTALVDAASVSLFTTEAVVLELFPKDEKTRPMGGGMGI

NbL01g22100.1 1_chloroplastic-like [MW = 64.38 kDa]

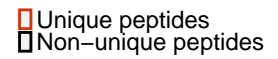
No. of times detected



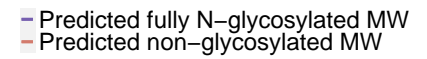
log(intensity)



Values from



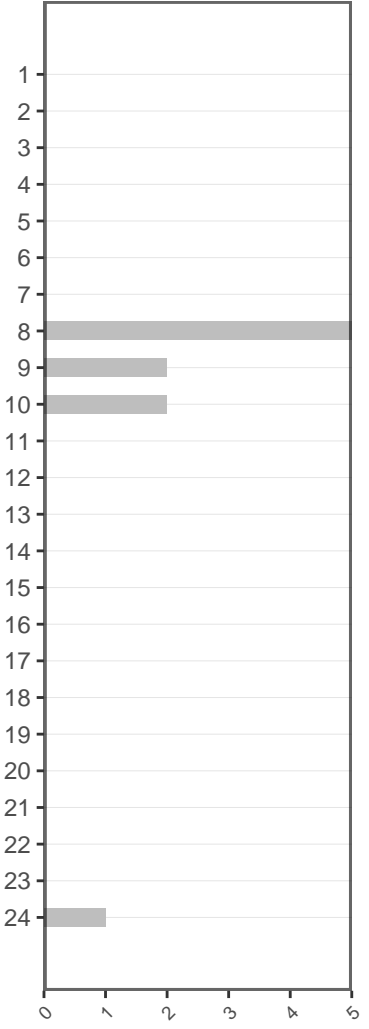
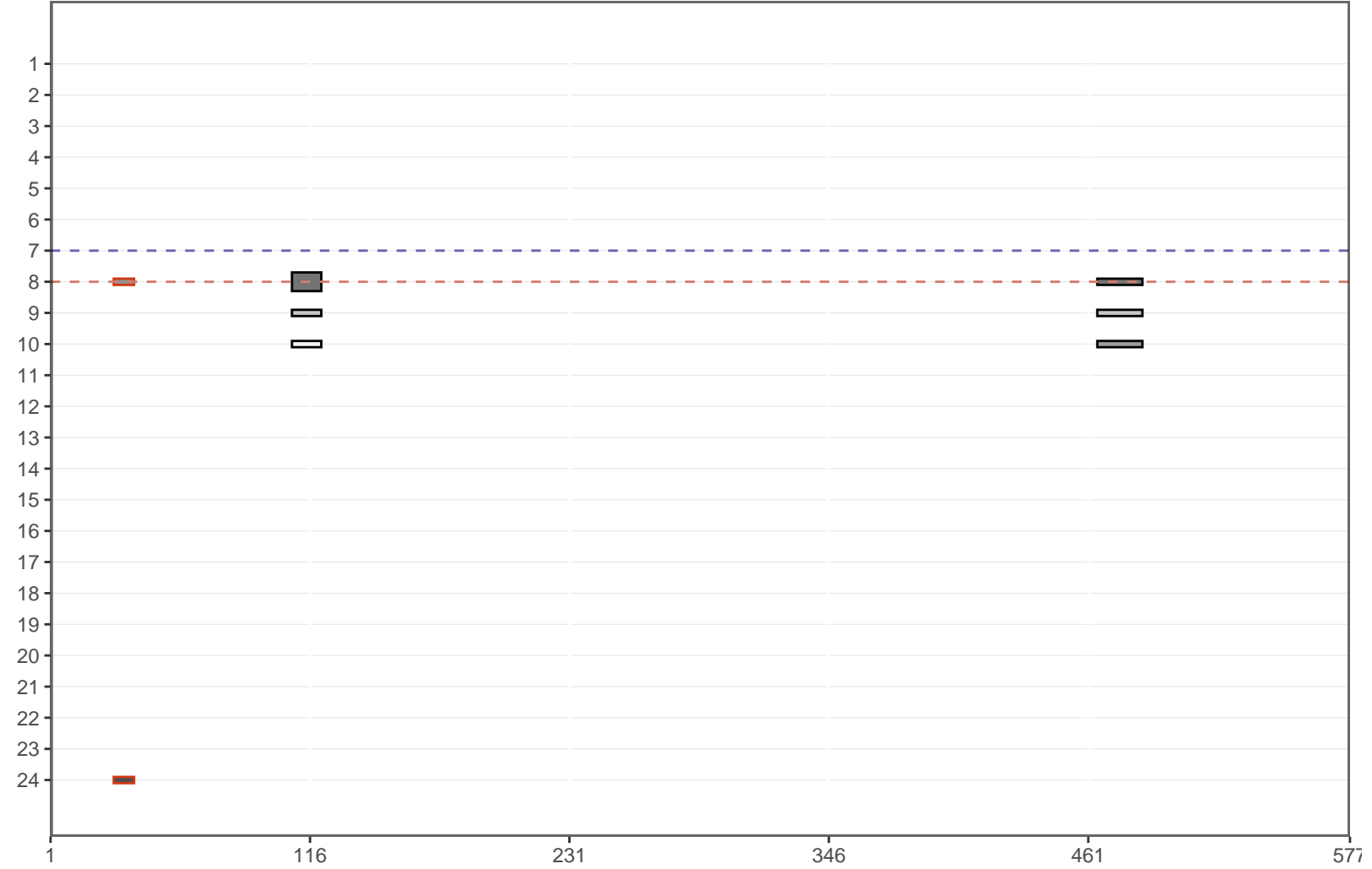
MW indication



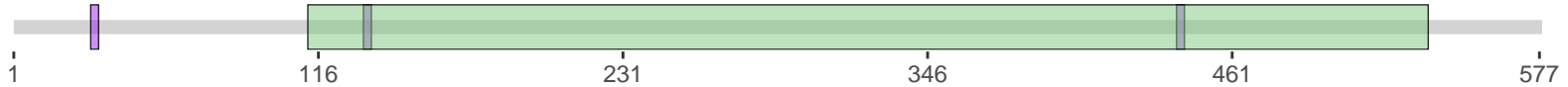
Molecular weight



Gel Slice

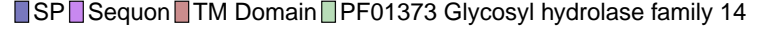


Protein length



Pfam domains

Pfam Description



Protein sequence:

YVGMGPAGELRYPSYPEQDGMWFFPGIGAFQGGSDKYMBLSKAAAEAFGKPEWGHSTFDAGHYNWPEDTNFFRKEGGWDDGGVGEFFLTWYSGMLLNIGERIGSAKAIFDDKGVKIEKIHGHVYGTIRSHAPELTAGYNYNTRFRDGYLPIAGMLARHGAFNFTGVEMRDHEGPGDAGCAPEKLVKRGVALATQGAQVPLAGENALPRYDDVAHEGILQASSLNIDGGSSDREMCAFTVLRMNPDLFHPDNWRRFVAFVKMKKEGKBHRCCOOLEGEAEHFV

NbL01g21920.1 glutamyl-tRNA(Gln)_amidotransferase_subunit_B_chloroplastic/mitochondrial [MW = 60.7 kDa]

No. of times detected



log(intensity)



Values from



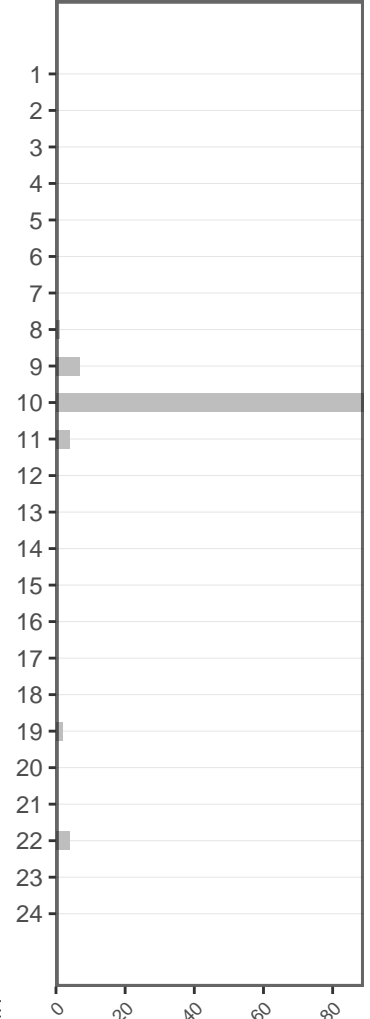
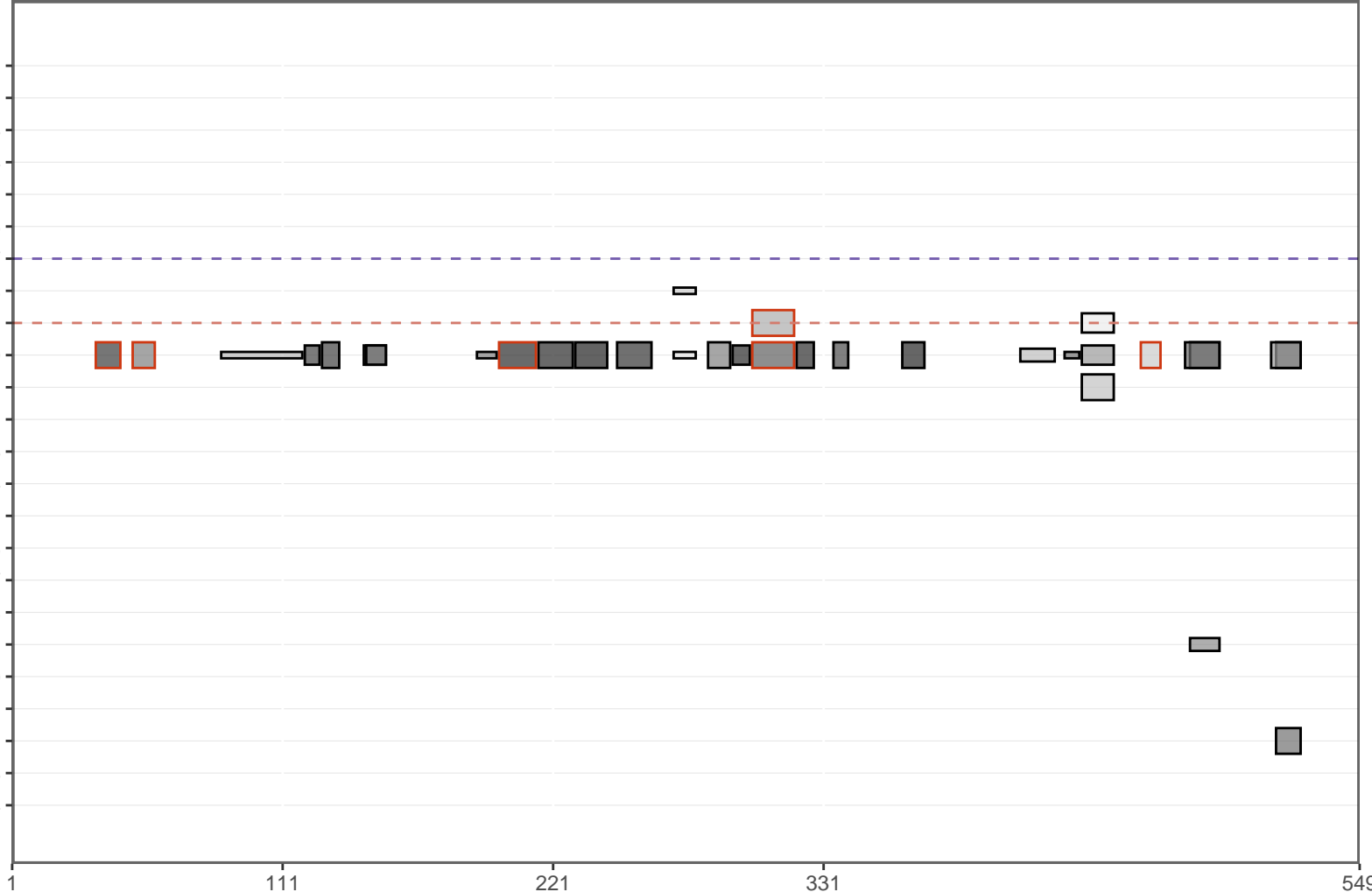
MW indication



Molecular weight

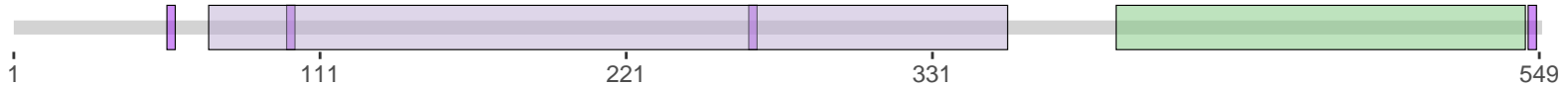


Gel Slice



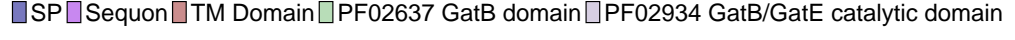
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

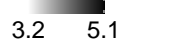
SLRCDVNSIVRPGGLEFGTIVEIKNLSFSBIVGRAADVEIGRQVLIHSGGGVDEIVGETRLIWEESGAKTVMRKKEGLADYRFFPEPLPGVLTLEEYVDNIRELSLPEVPEAKRRRYENKMLSGSDVLFLLANDMNIADFFDATAAGADVKLAANWIMSDIAAYMKNEKVTNEIKLSPQELGELASIKDGTISGKIKREIIVELMAMKGGTVKGLKIKEDLIVQIVDTAEIKMMDKVIADNPVKOLEQYRGGKTRKLOGFFAGGVMKESKGNKPKLLNKILLEKLNITS*

NbL01g21890.1 3-isopropylmalate_dehydratase_large_subunit_chloroplastic-like [MW = 55.26 kDa]

No. of times detected



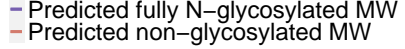
log(intensity)



Values from



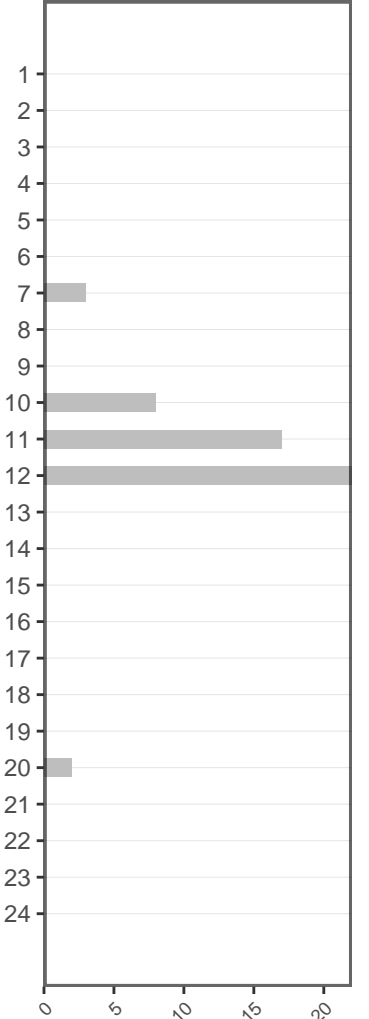
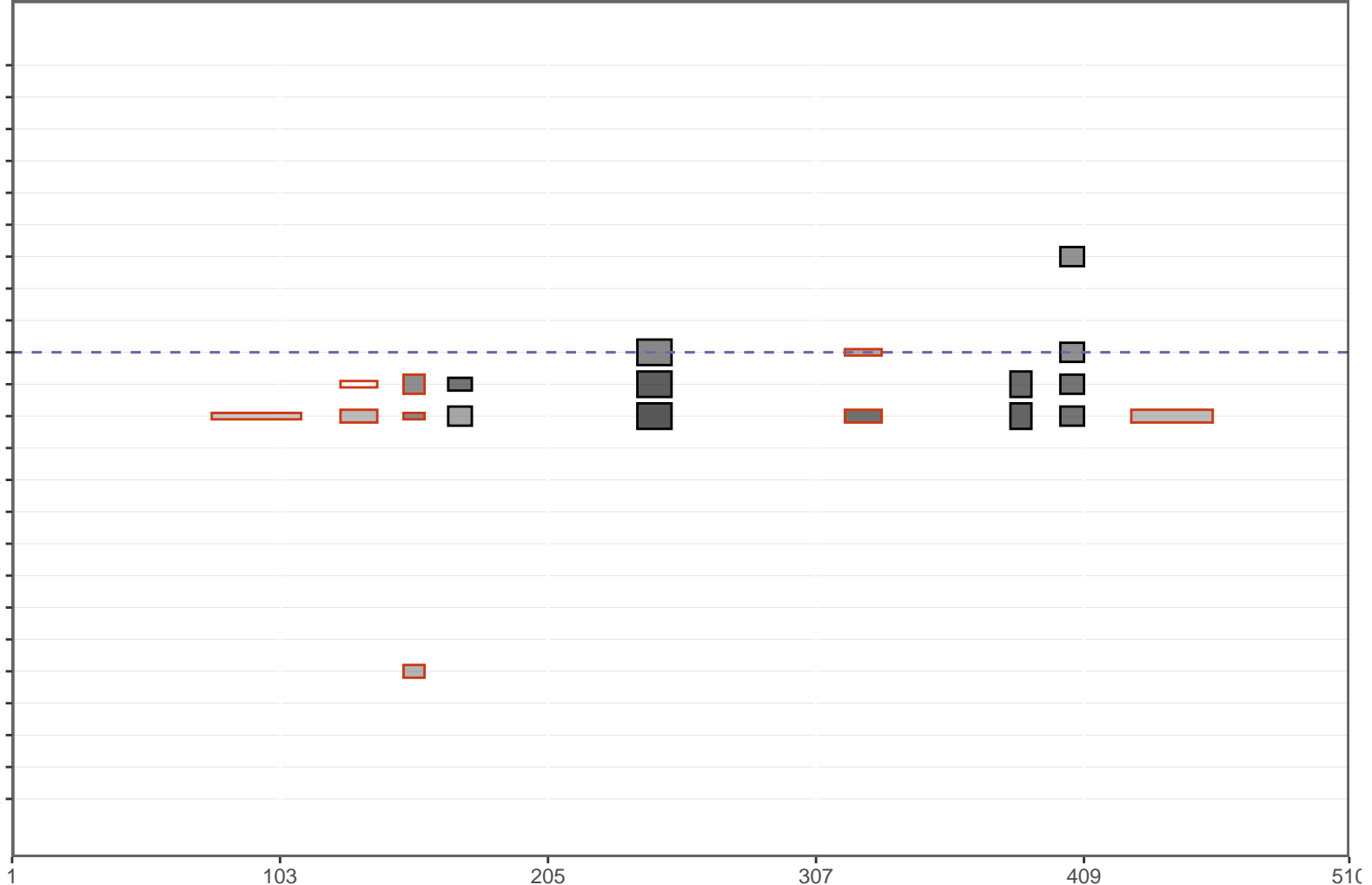
MW indication



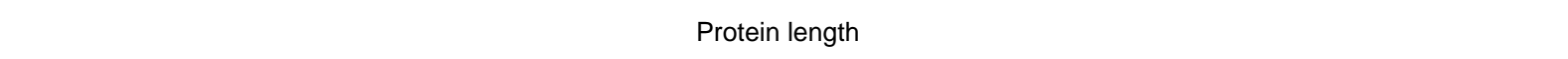
Molecular weight



Gel Slice

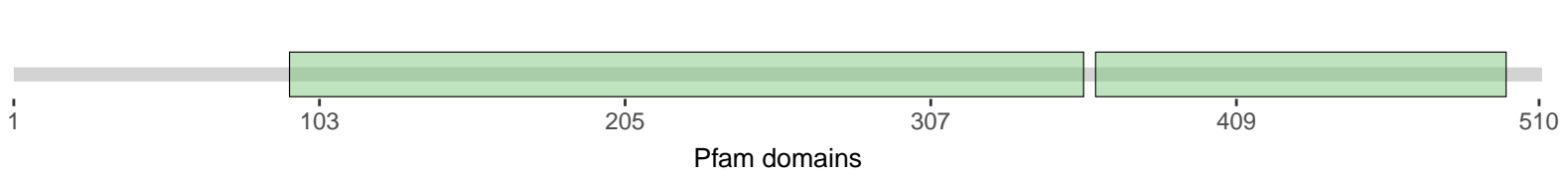


Protein length

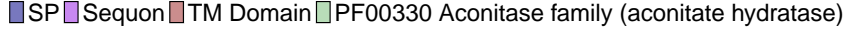


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IGEMPNYLLAXDLMLGHSSEISVAGATYKTMFEFAGTTVEISLMEERMTLGNMVEAGGKNVFPADKTTYDHLKDKTSVPEPVYSDGGARFLKEYRIDIKLEPLWAKPHSPDRALAREGKDKYKIDRVYHGSGTGKTEDFMSAAKFLASGKKVVPFTLVATRGVWMDIYSLPVPGSSGKTCSEIFQESGGCYEPASP6GGAGPGLPDTYGRLENEPKVCVSTTRNFPGRMGHEGGVLA8PYTAAASALTYVTDPRFLM

NbL01g21880.1 3-isopropylmalate_dehydratase_large_subunit-like [MW = 57.34 kDa]

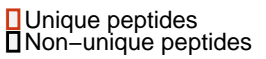
No. of times detected



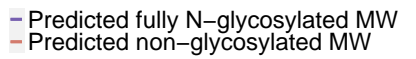
log(intensity)



Values from



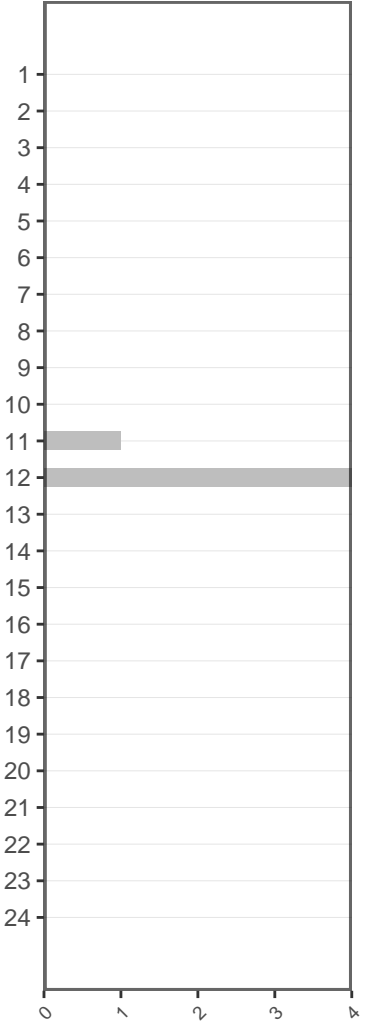
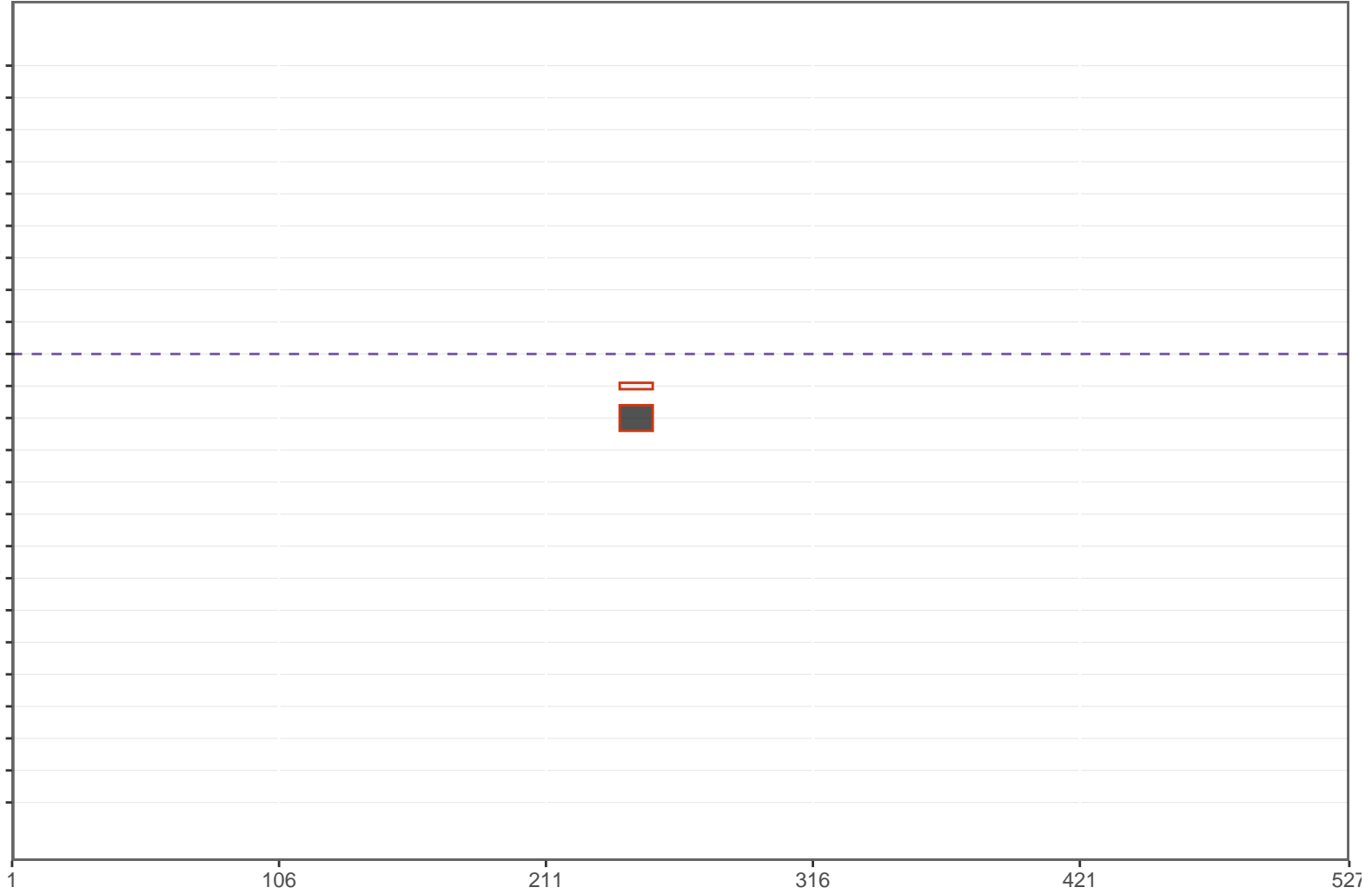
MW indication



Molecular weight

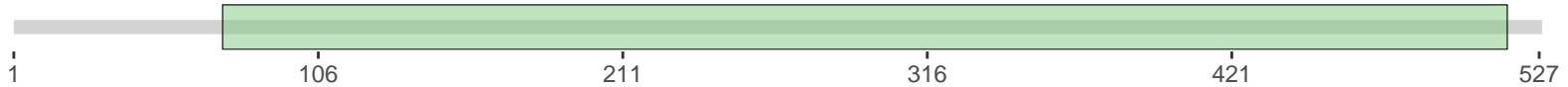


Gel Slice



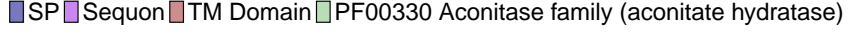
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LLAKDLMLQIGEIFVSGATYKTLFEPVSTVESLSGMEERMTLGNMVAEAGKNGVPTDKTYYDLKDKKTEVFPYVSDGGRFLKEYRIDSKLEPLAKPHSPDNRALAREGKDKKIDRVYIGSGCTGGKTEDFMAANKVFLASGKKIKVPTFLVPTQKWWMDVYTLFVPGSGGKTCGDFEEVCGCETPASPQAAACLGPGDPTVRLNRPKEITSSSRGNSLLQKGRVGVSTTNRFPGRMGHVEGGHLSAPVTAABALTGKVTDPREFLM---

NbL01g21830.1 RNA-binding_protein_CP33_chloroplastic [MW = 31.63 kDa]

No. of times detected



log(intensity)



Values from



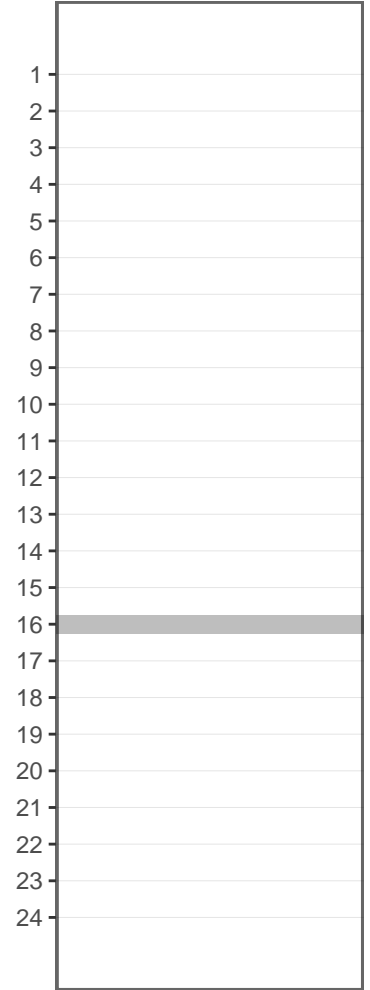
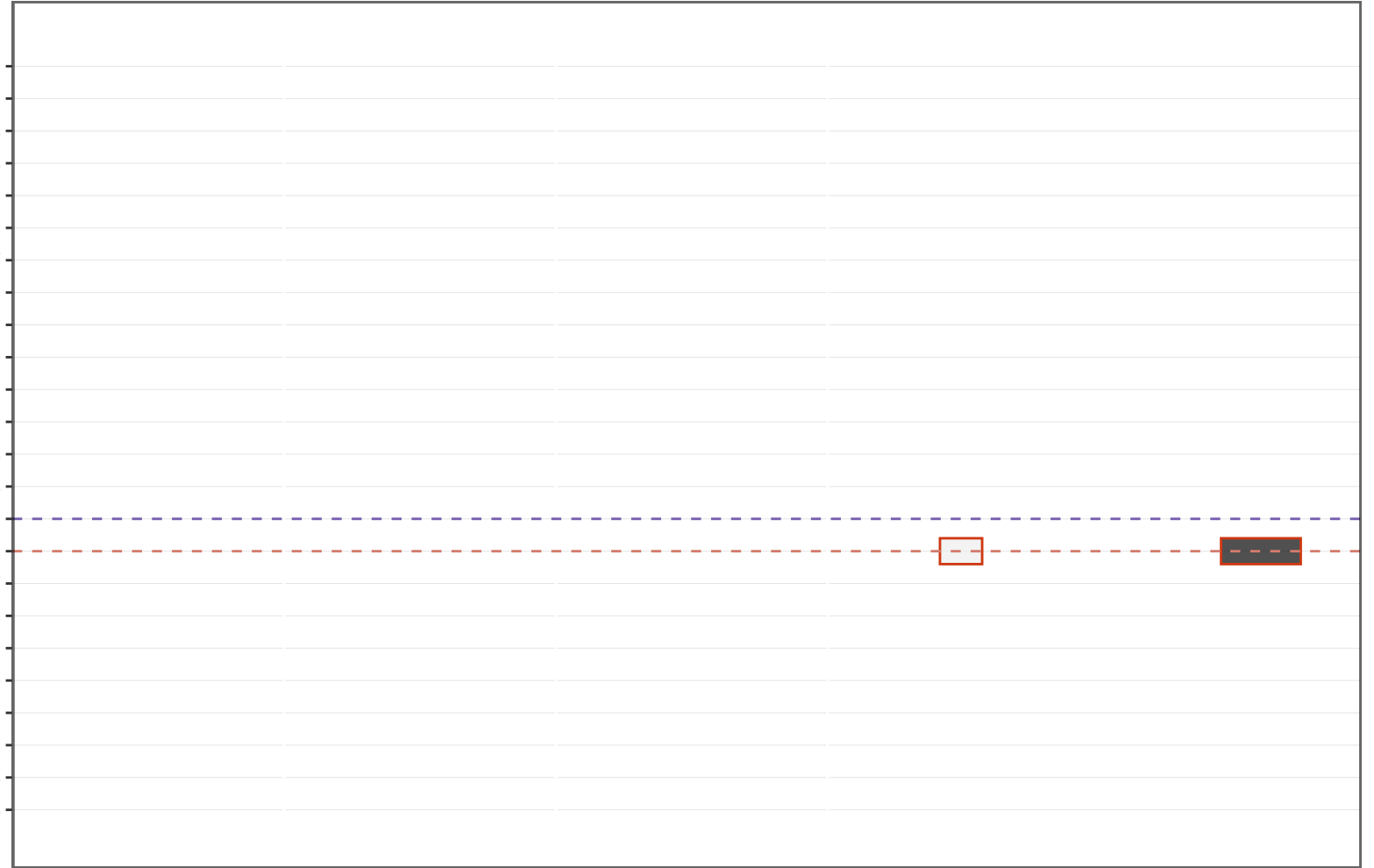
MW indication



Molecular weight



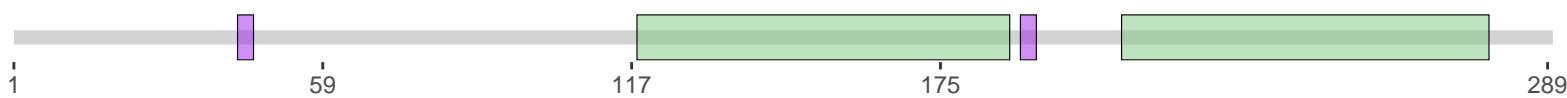
Gel Slice



Peptide counts over 4 repeats

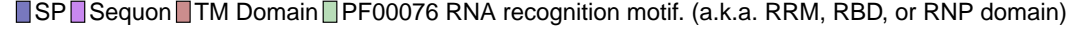
1 59 117 175 289

Protein length



Pfam domains

Pfam Description



Protein sequence:

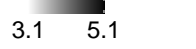
AGVGDYATPELVVYDRETEGKGRGFVYTMSELEDCKTVKINLDRREYGGRTLRVNFSGKPKPKPELVPETHEKLFVGNLAWSVTSESLAQAFQEGYGVVGARVLYDGETGRGRGYGVFVYENRQLENAIGNLNGVELDGRAVRISLAGGKKQ

NbL01g21770.1 succinate-semialdehyde_dehydrogenase_mitochondrial-like [MW = 55.47 kDa]

No. of times detected



log(intensity)



Values from



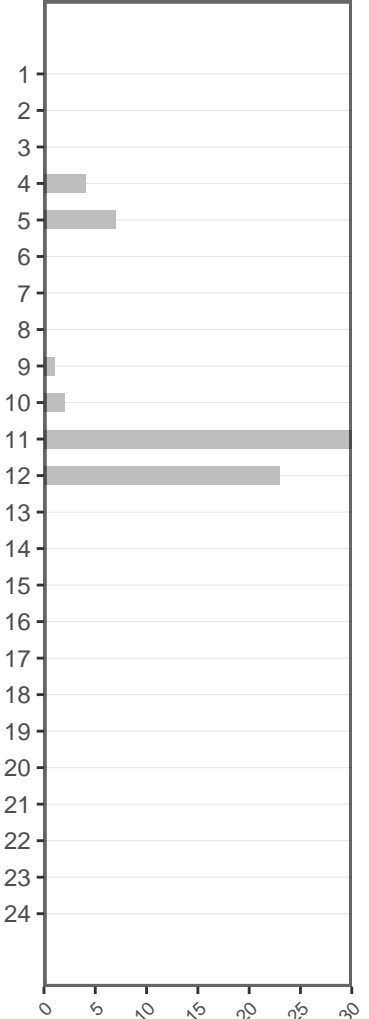
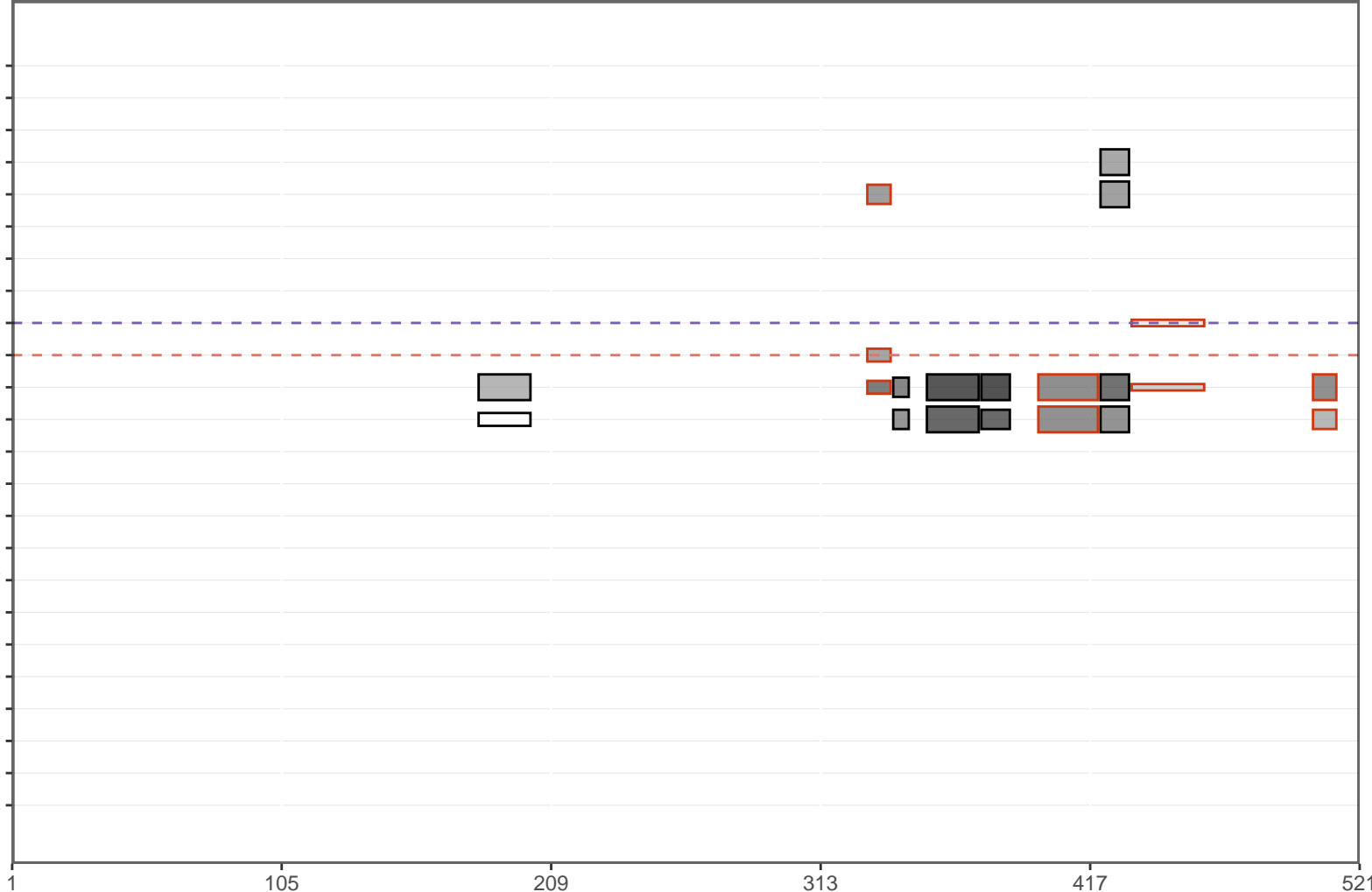
MW indication



Molecular weight

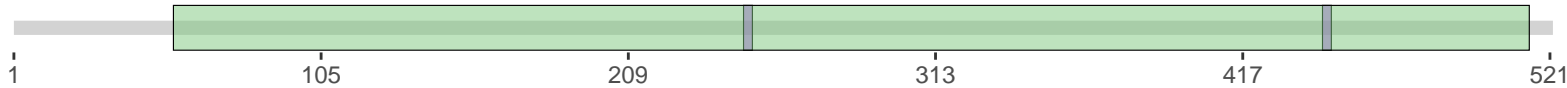


Gel Slice



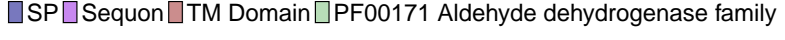
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

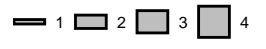


Protein sequence:

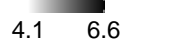
ASDIDGALLASPOVRKLTFTFGSTMVGKRLMAGAATVKKVSLLEGGNAPCHIFDDADIEVALKALATKFRINTGGTGVGNRILVGEIGYKFAFANAFANVQSMVYGDGFGSEGVGGPLINEAAVKKVYSEFVEDMTSKGAKVLVGGRKHSLSGMTFYEPYVTVGVNSEMLLRREEVFGVPLKFKTEEDAHMANDTNAAGLAWFSTNVORAWRVTEALEYGVGVNEGLVSTEVAPFGGVKQSGLRGREGSKYGLDVEYLEMKYVGLGMS*

NbL01g21750.1 glucose-6-phosphate_isomerase_cytosolic [MW = 63.67 kDa]

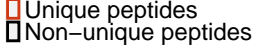
No. of times detected



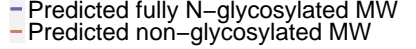
log(intensity)



Values from



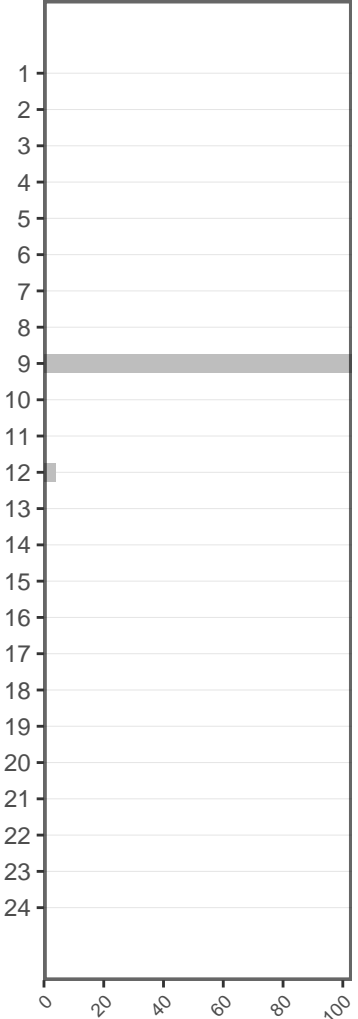
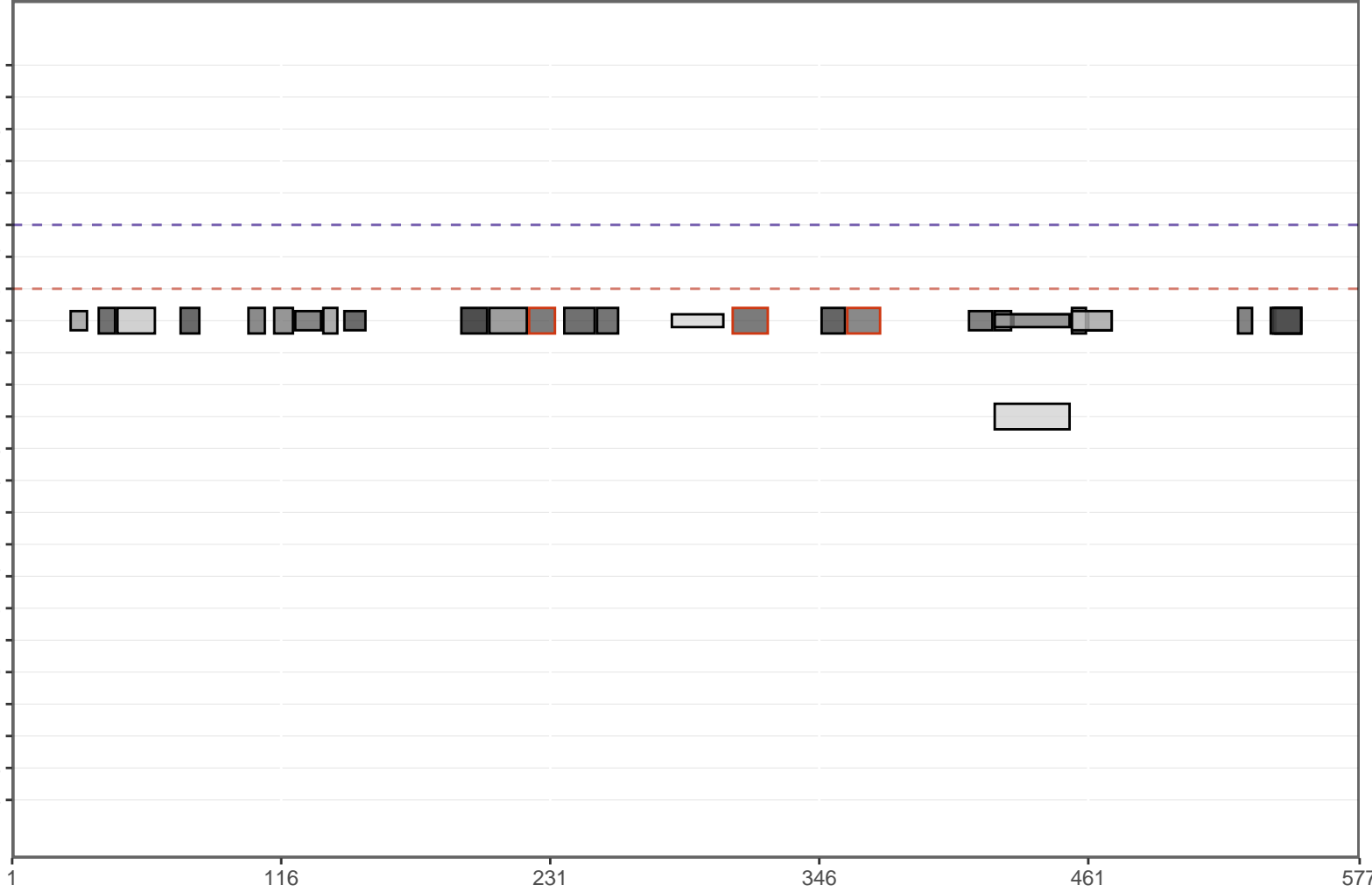
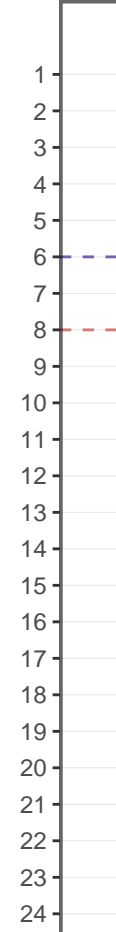
MW indication



Molecular weight

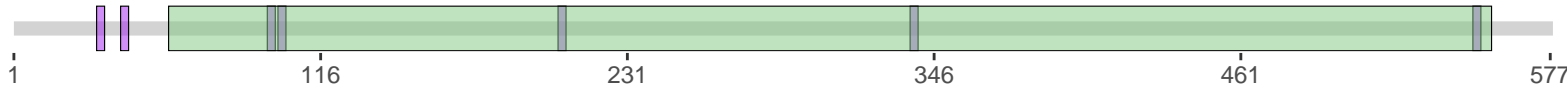


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DWVGGRYSVCSAVGVLPLSLGQYGFVKEFLKGSASVDQHFDSAPFEKNVPLVLLGLLGVNNSFLGYSARALPYSGALEKFTPHIQGVSMESNGKSGIDGVLPLVETGEIDFGEPGTNGGHSFYQLHGDGRVPCDFGIVYKGGQPVYLKDEVVSNHDELMSNFFAQDPAIAYGKTFEQLGKENVAEHLVSHKTFSGNRPBLSILLPSLNAYNIGQLLAIYEHRIWVQGFVWGINSDQGWVYELGKSLASQVRKQLHASKKGGSEVGFNFKTLITTYLEASADVPSD

NbL01g21720.1 pre-mRNA-processing_factor_19_homolog_1-like [MW = 56.56 kDa]

No. of times detected



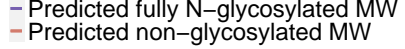
log(intensity)



Values from



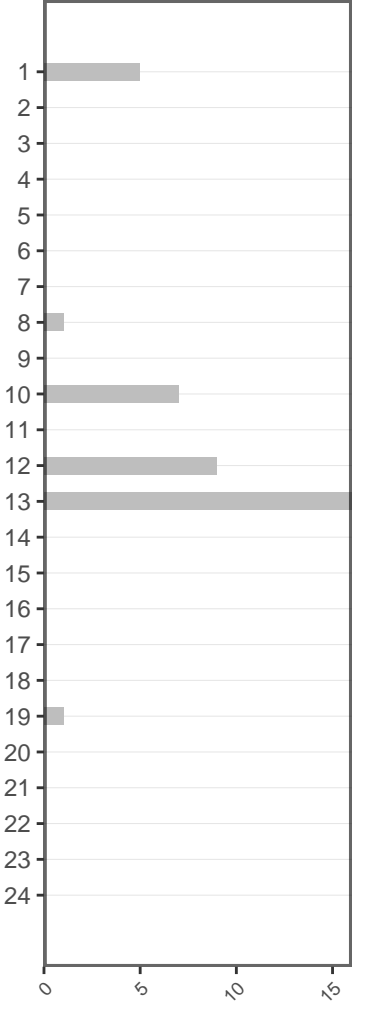
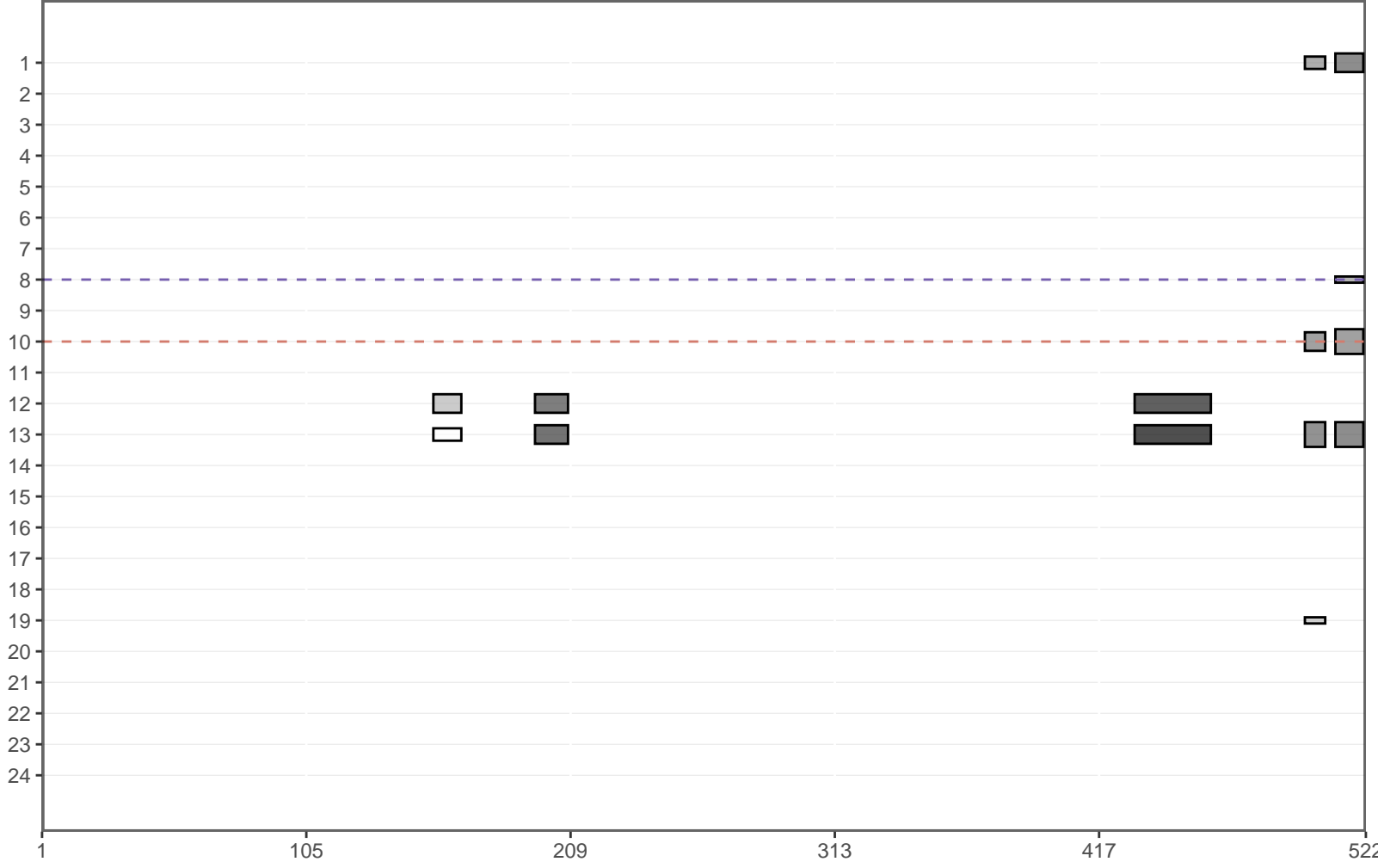
MW indication



Molecular weight

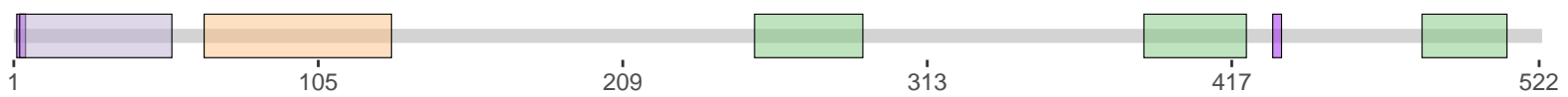


Gel Slice



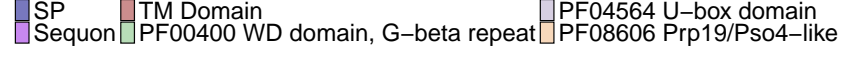
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

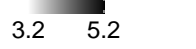
RPSGGIISTLSGHISKRVTSVKFASGEGLVSGSGADKTRVWQSSSENGAYDGRHLKDHAEVGAIVTHATNIVFVTAELDSTWGFYDLASGLGLAQVADATESEGYSAAFTPDGLLGTGTSGSLVKKWDVNSGANVARESDGHVGSVTAISFENGFLATAHDDGVLWDLRLKLNFRNFSLYDENTPTGSGVDFDHSGSYLALGGSDIRVFGVAGVKAENHKTLPDLGGTGKATGLKFGPDAKYIAVGSMDRNLRFGLPGEQMES

NbL01g21660.1 heterogeneous_nuclear_ribonucleoprotein_1-like [MW = 47.46 kDa]

No. of times detected



log(intensity)



Values from



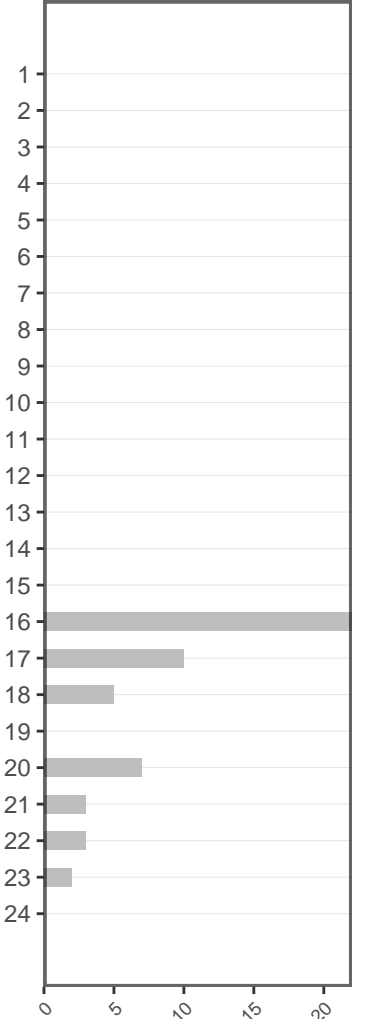
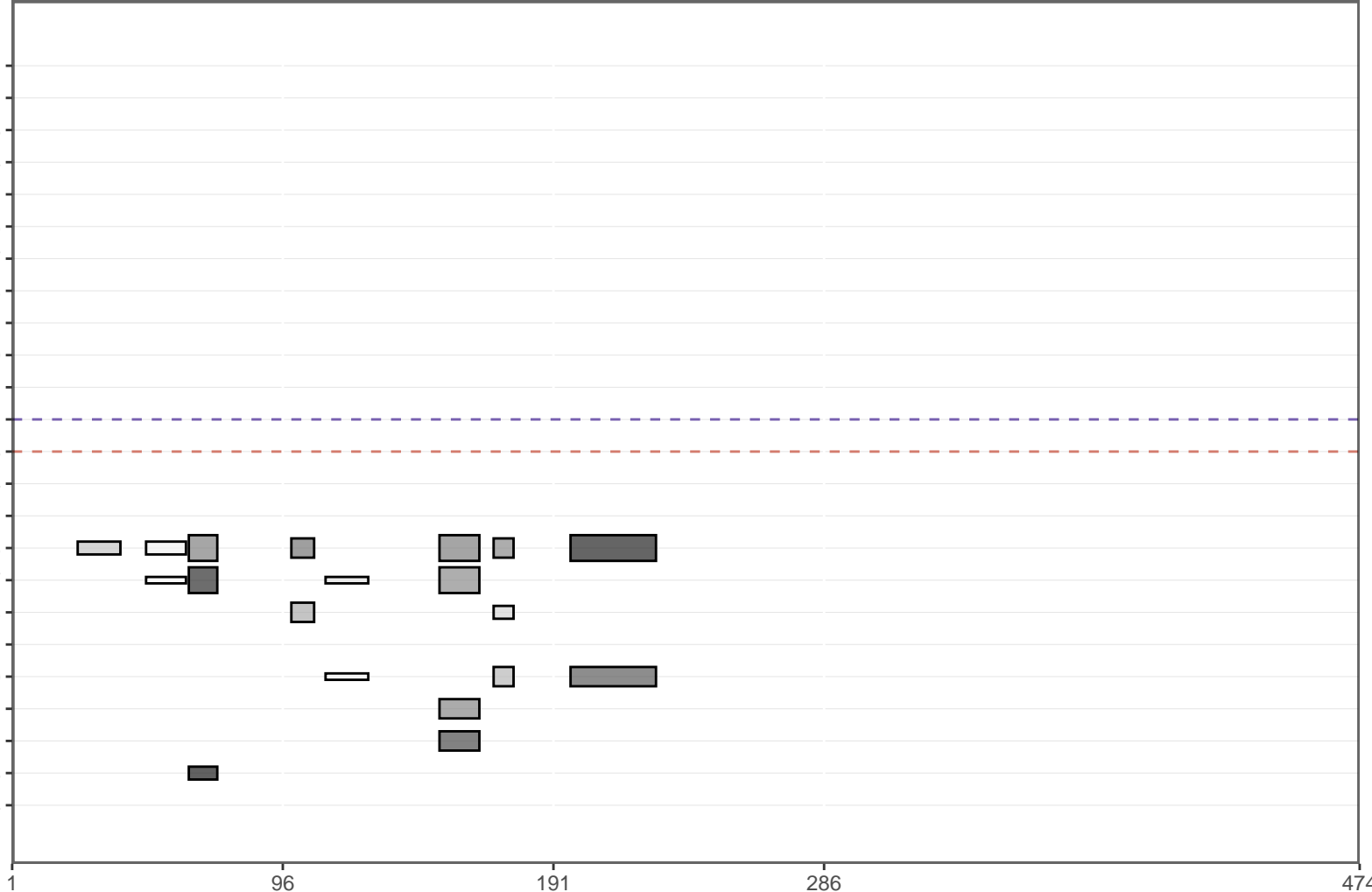
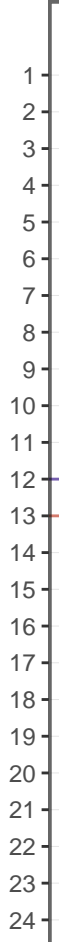
MW indication



Molecular weight



Gel Slice

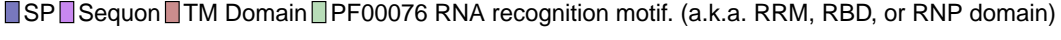


Protein length



Peptide counts over 4 repeats

Pfam Description



Protein sequence:

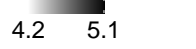
NR1M0SNPFGGYPG66GYPGYPG6NMGVGGYGGVGGANPFGYGSANPFGYGA...AANGNPNAPSTGYS6GFRGPRBTW6GAP6GYNVGYGNAPFWSANAGGGGCPA6GG66GPTGTTGTVGNQGYGGVAGNDGAVGNP6YGAVGRASGAP6GSPFVGG6AAGDMQ66GAGYVMS6GYPGDA6SN6YGNAAVRS6NS6G66GYPGAPFNGAHS6GAGYGG6YGGAP6RGA6GQ

NbL01g21610.1 protein_PROTON_GRADIENT_REGULATION_5_chloroplastic-like [MW = 12.91 kDa]

No. of times detected



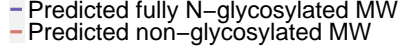
log(intensity)



Values from



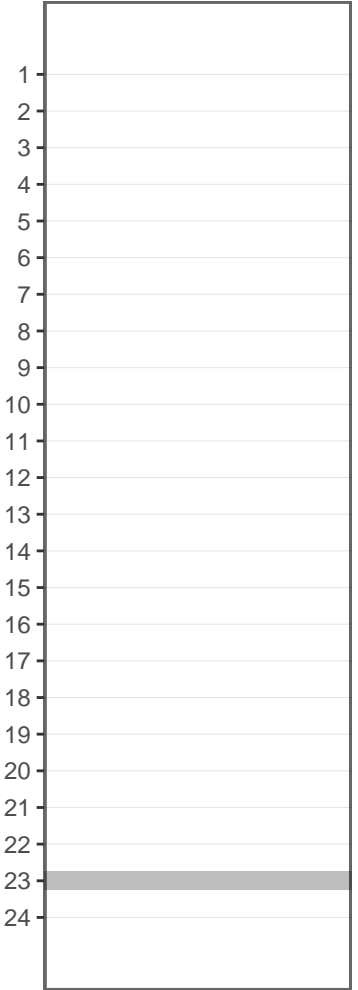
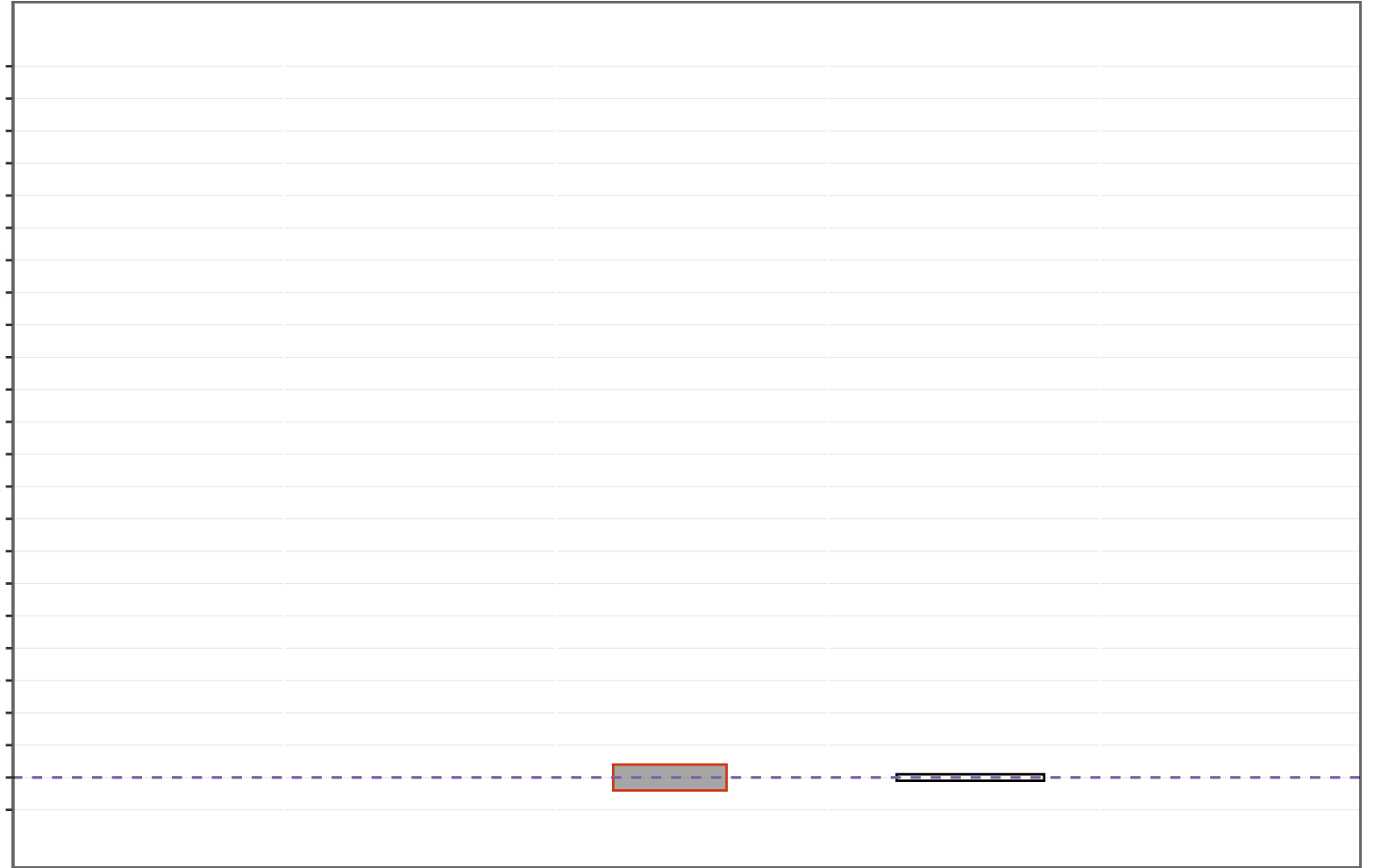
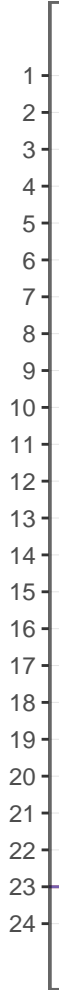
MW indication



Molecular weight



Gel Slice



Protein length

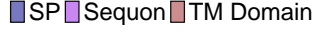


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IGINNDKGLFAPYVAVTRNIVGKRFNQLRKAALHSGVTEFCRIGADGKGRGGILRLAKKNGERLGLAV

NbL01g21570.1 acid_phosphatase_1-like [MW - SP = 27.01 kDa]

No. of times detected



log(intensity)



Values from

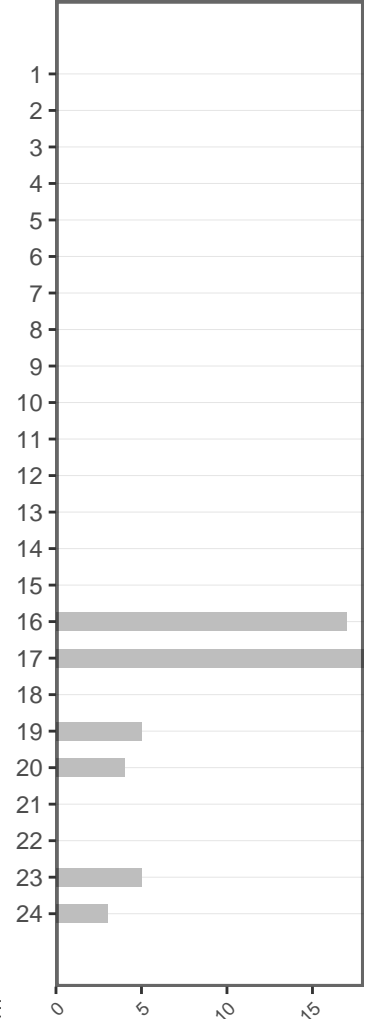
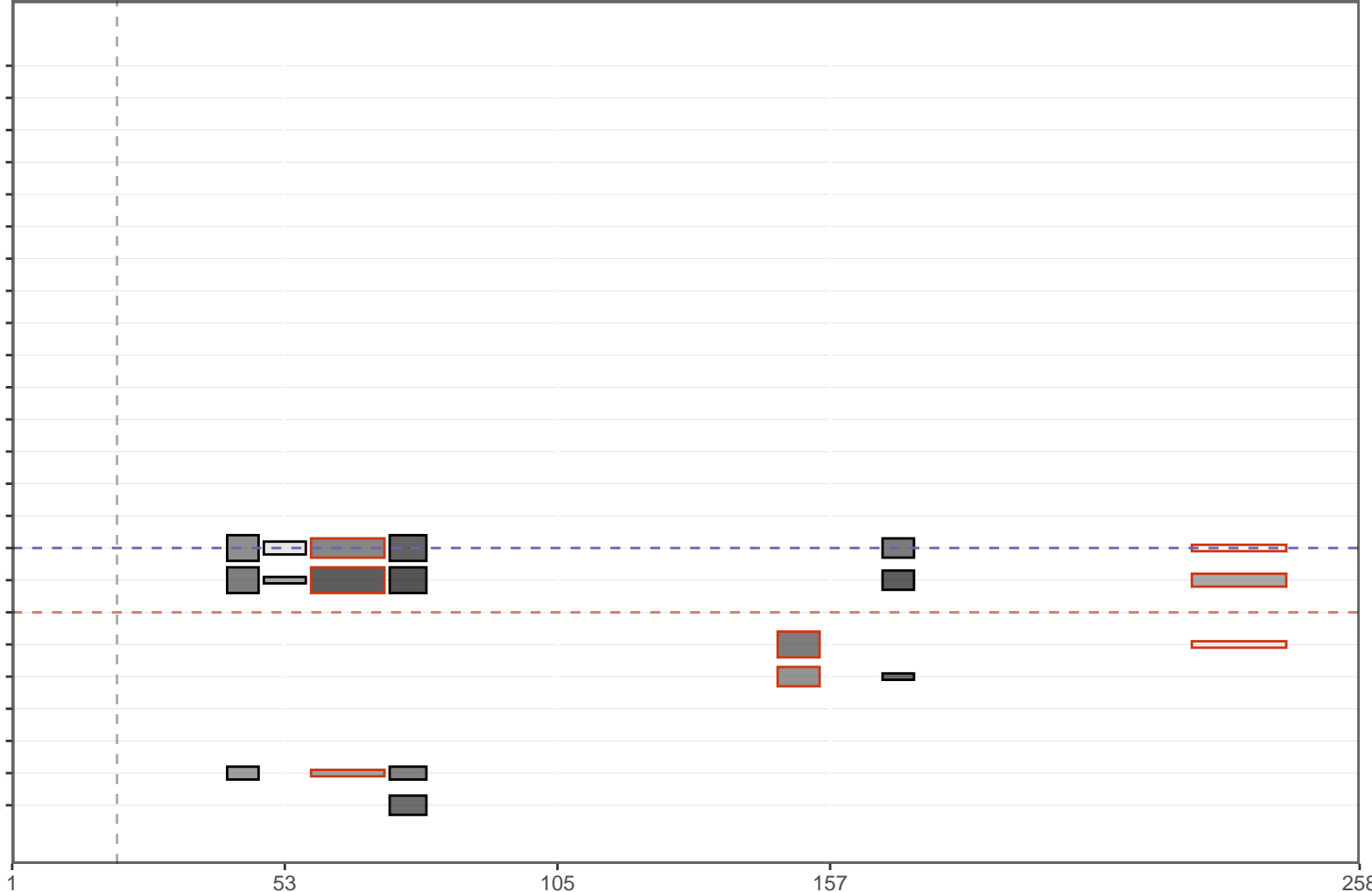
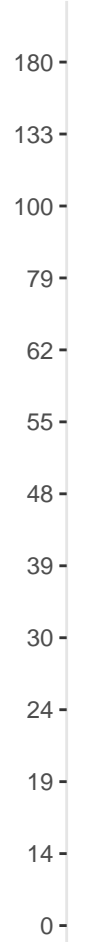


MW indication



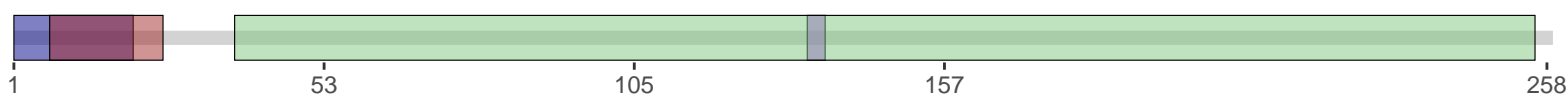
Molecular weight

Gel Slice



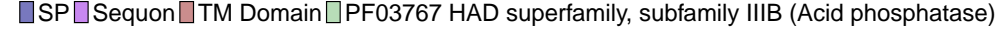
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

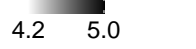
ITVPPYKQNGFGGKMLNVTSLSDWMDGGKGTALDHLKLFNHLKELGVKIFLVSRRKEHLRSPTDNLVHVGFVGTWLSULRGGDECKSADGGKAEVRSKLIKSGVRIILGVGDQWSSIEGLPEAKRTFKLNPFLYYVA

NbL01g21050.1 putative_germin-like_protein_2-1 [MW = 25.82 kDa]

No. of times detected



log(intensity)



Values from



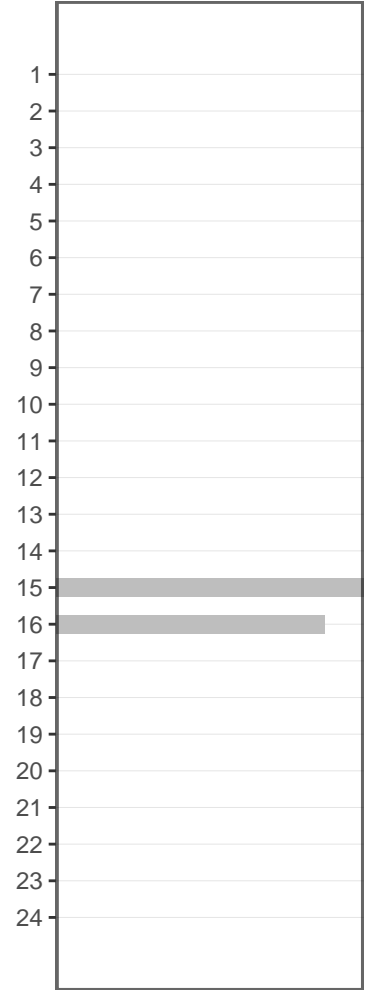
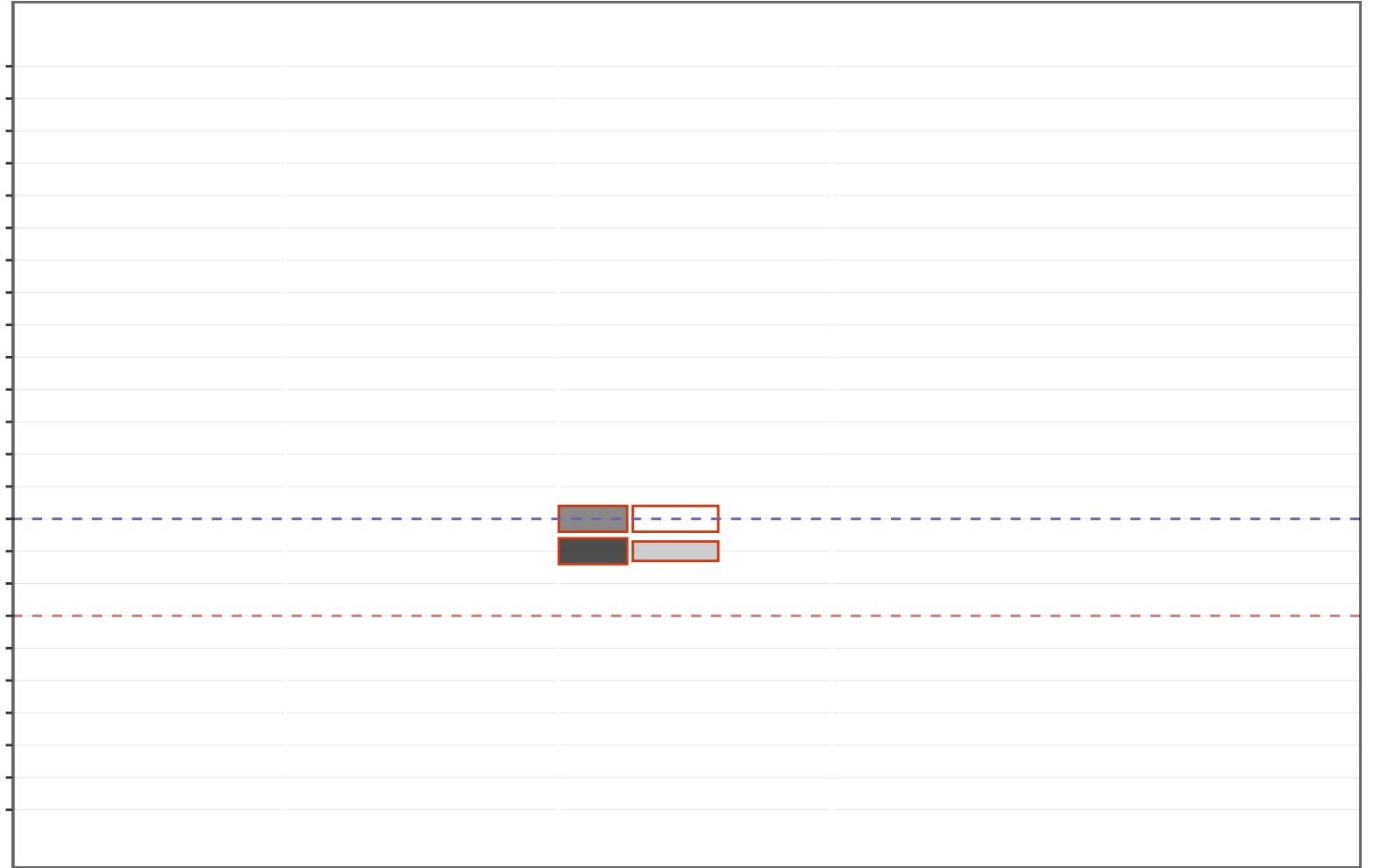
MW indication



Molecular weight

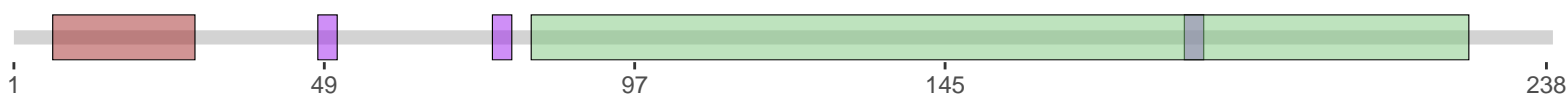


Gel Slice



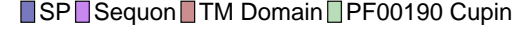
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IVRADVEFPLGISPHIRPGNEELRLLEGLVVAFTIPDQGNPKRLEFELINPGDVFVPGDLVHVDVNLGTTNTALSGFNQNPQVHMPPQLFGSNPPLDDVWKGFRLDKVVVEHLRAGFSKQ*

NbL01g20750.1 RNA-binding_protein_BRN1 [MW = 46.84 kDa]

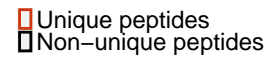
No. of times detected



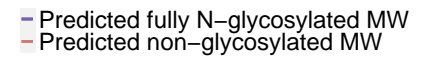
log(intensity)



Values from



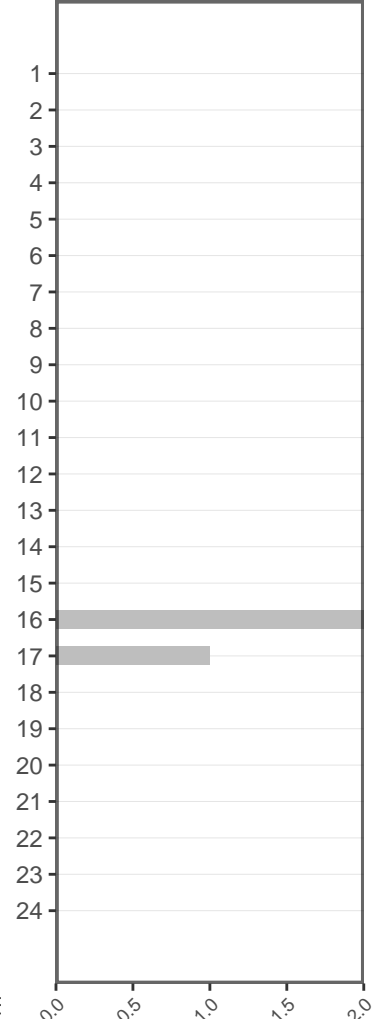
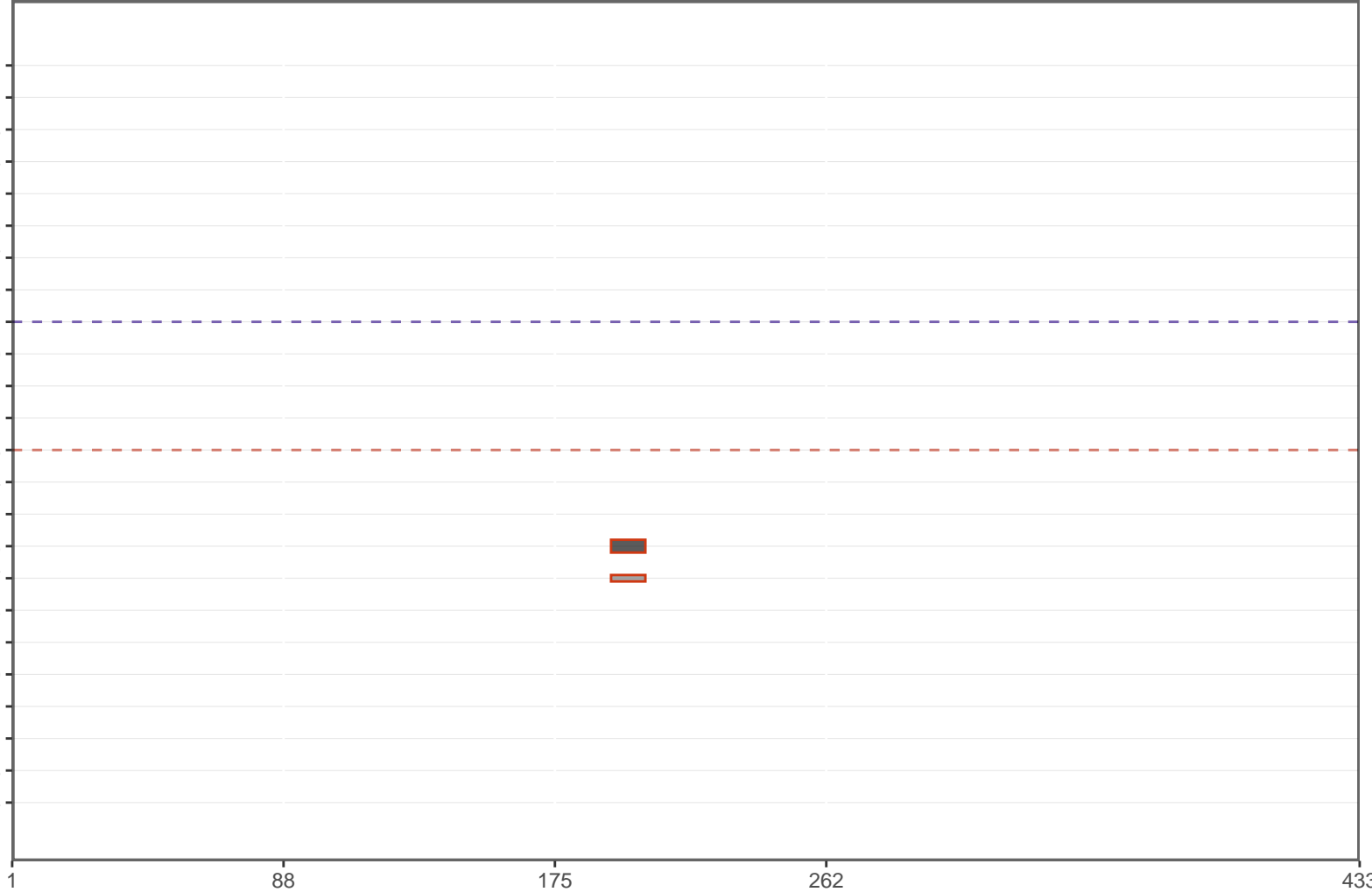
MW indication



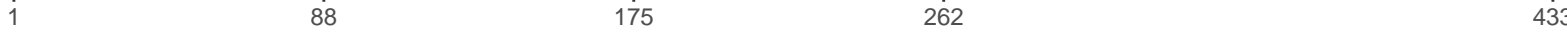
Molecular weight



Gel Slice



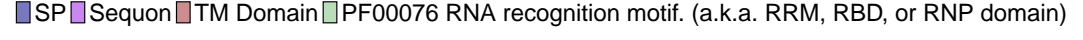
Protein length



Pfam domains



Pfam Description



Protein sequence:

HPSLFGALPMGYLMPKYNQYVGTPTGAYGLMQYRLPSVQNGPQFQNVPPINGASALRGAPDLEPGISPRNYSMEPSGVYGSAYFWPRLGLVPMFYAGDVMNARPPGSGPSPMPSTANHSAAASBVNSSTGGVVEGPPCANLFIYHIPQEFQDQDLANSFQFGRVLSAKVFDKATGVSKGFGFVYEDSPMAAGTAINMMNMGDLGSKKLVQLKRDNKGKHY

NbL01g20720.1 protease_Do-like_2_chloroplastic [MW = 68.01 kDa]

No. of times detected



log(intensity)



Values from



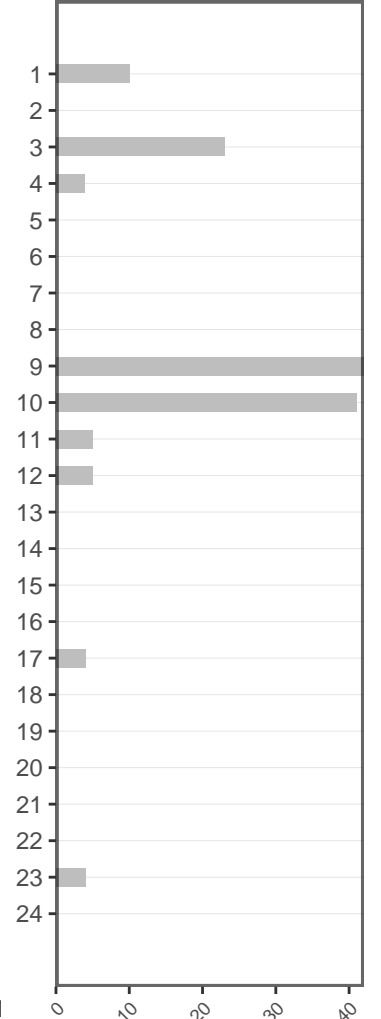
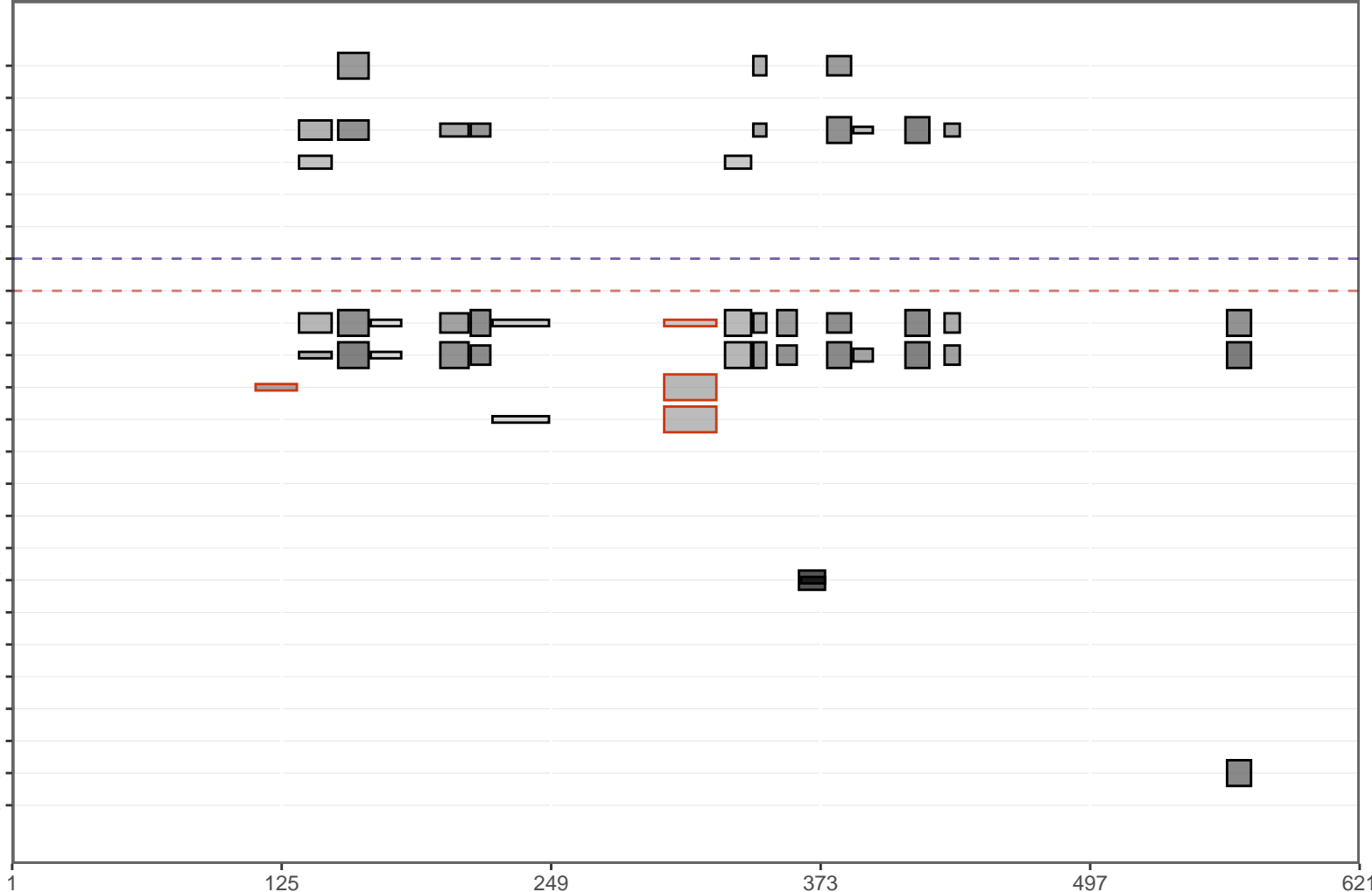
MW indication



Molecular weight



Gel Slice



Protein length

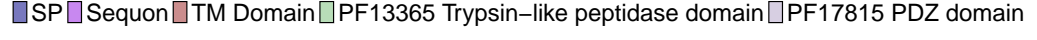


Peptide counts over 4 repeats

Pfam domains



Pfam Description

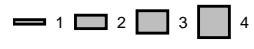


Protein sequence:

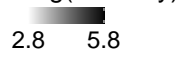
IGVAFQYRSDSETENGVYVFTTWSHFLEDEKRNKGYSGFPLGVLLQKLESPALRAQLKVPENEGVLRKVKVEPTSDVSNVLEKGGVHVSFDGVRIGGEGTVPFRSBAIRAFRYLISQKFTGDVAELGRAGEFMKVGALKPRVHLVPPVHEGGGPPVLAAGLFTPLSEPLGEECEEDSGLKLTARYSLAKFEGEGIVVLSGVLANEVNNGYEDISNEGILKINGTRIKNHHLAHLVDSCKDKYLVLEFEDNFLVLEREAWSASASIKDKYGPARESDLLEPYDPIRPD

NbL01g20600.1 NA [MW = 25.95 kDa]

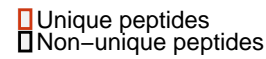
No. of times detected



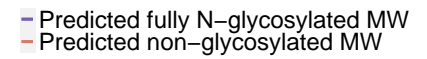
log(intensity)



Values from



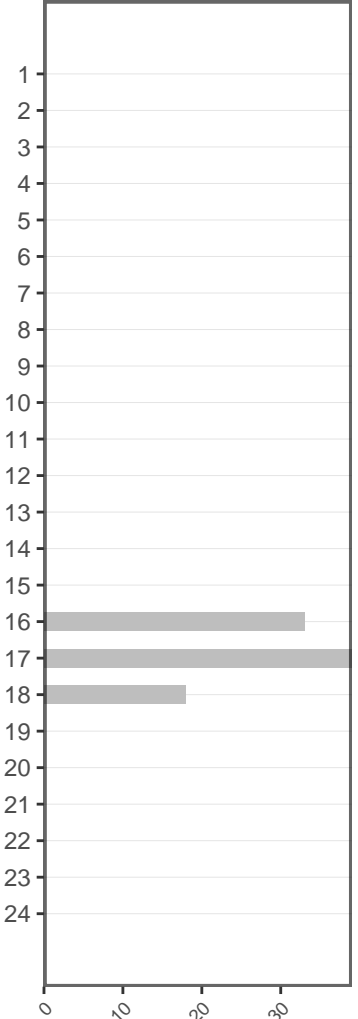
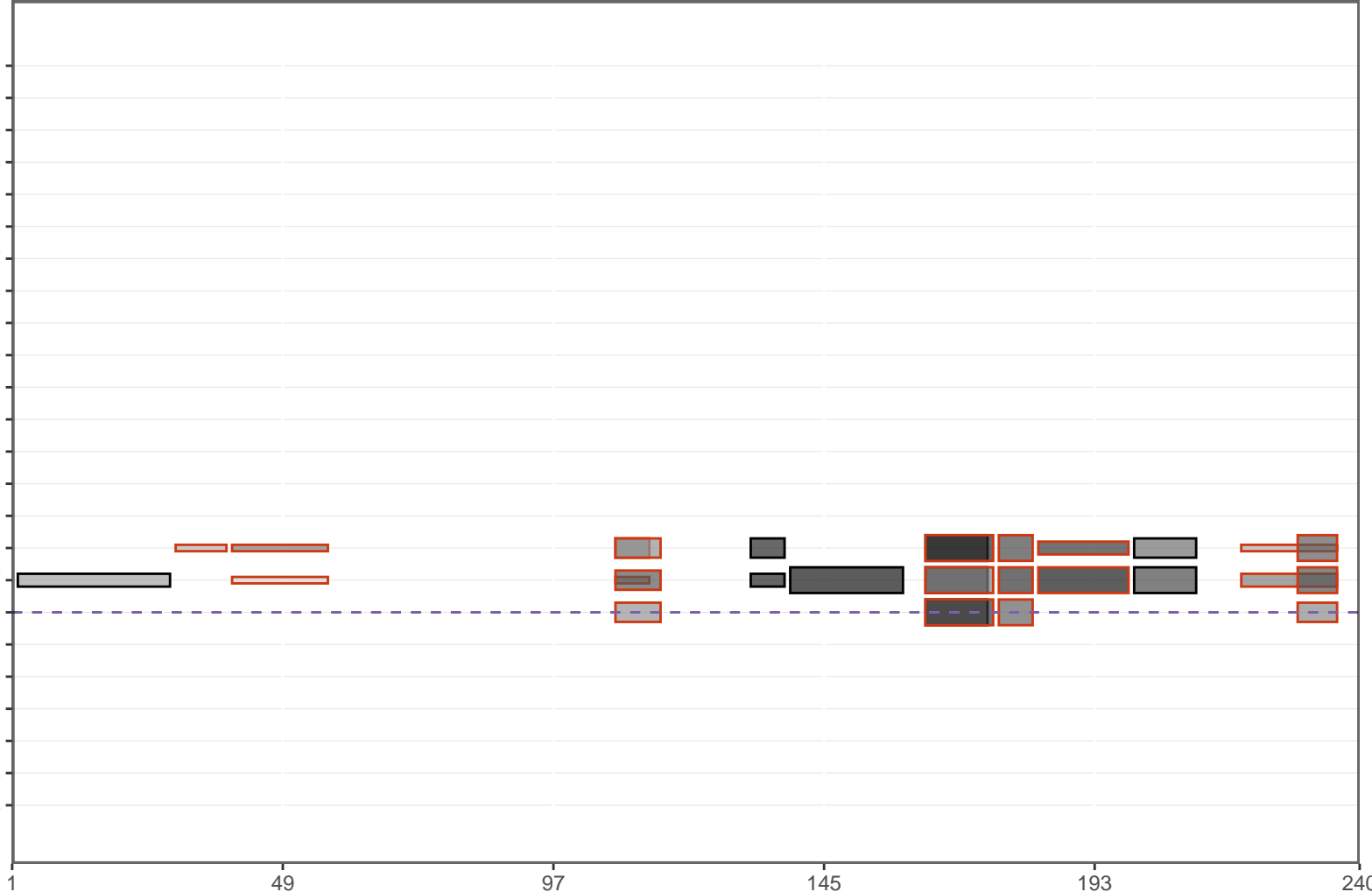
MW indication



Molecular weight

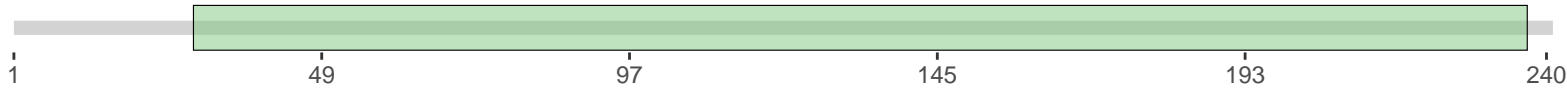


Gel Slice



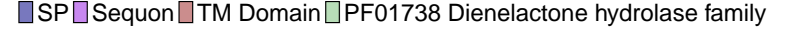
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

AKQVYSAIKDKIGISAVGAGFGWGANVAVQLAKSDDGAIVLHPSFVTVDDIKVKAIPALGAEIKRPPPELKGFEELGSKPEVDNFKVYIPQVAGWGTVRYDYDENKKVAGEAEAAHRMLLEWFTGHWK

NbL01g20580.1 sm-like_protein_LSM2 [MW = 14.5 kDa]

No. of times detected



log(intensity)



Values from



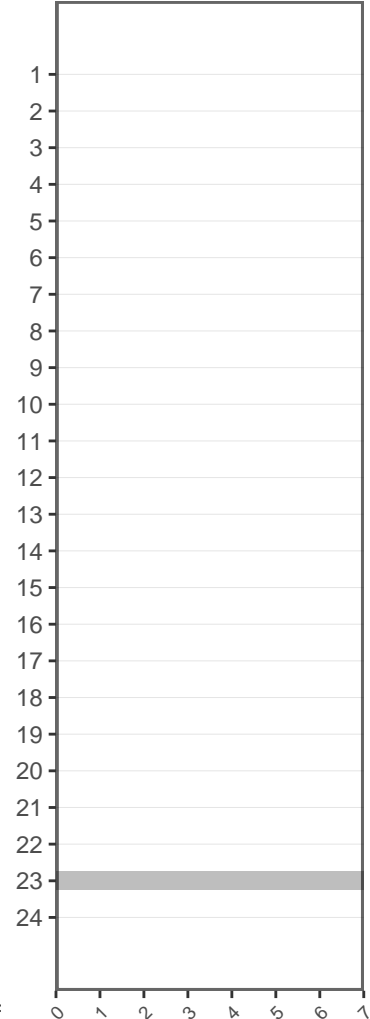
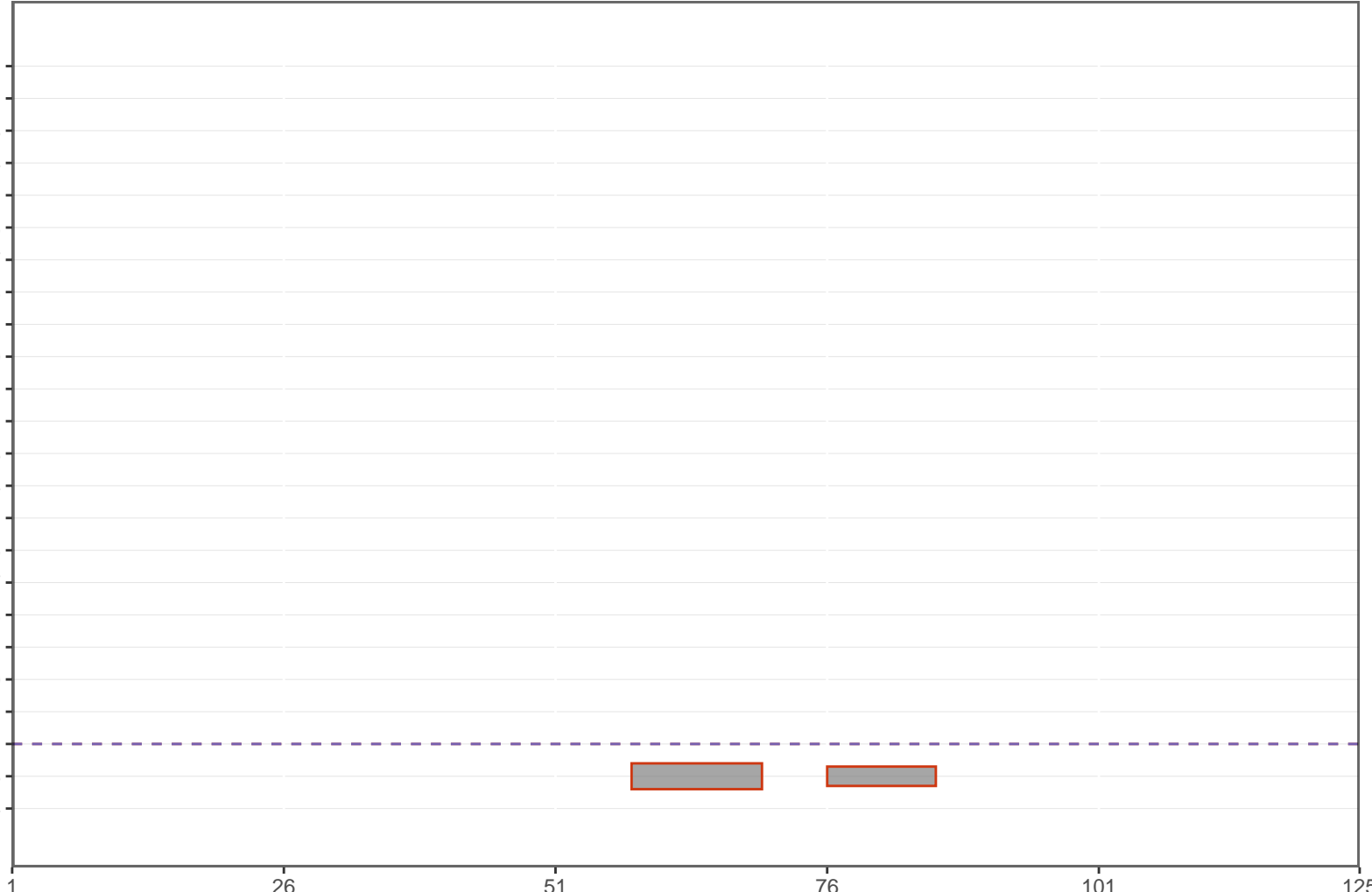
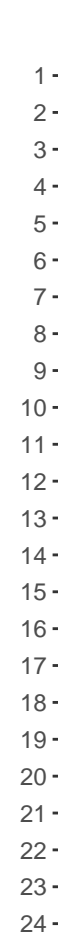
MW indication



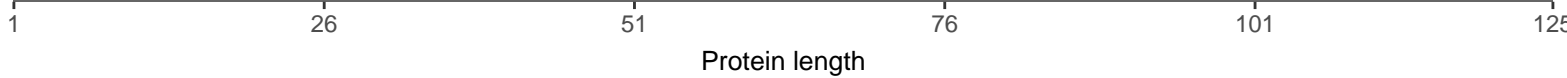
Molecular weight



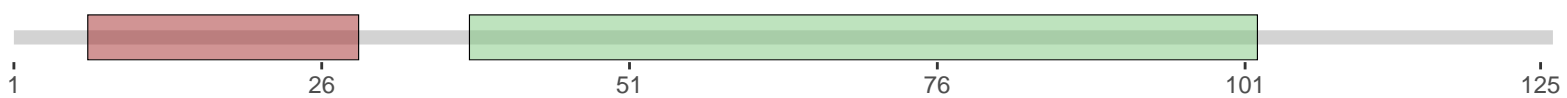
Gel Slice



Peptide counts over 4 repeats

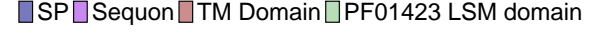


Protein length



Pfam domains

Pfam Description

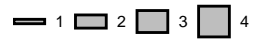


Protein sequence:

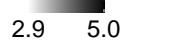
KNDLAIRGTLSHSVDQYLNKLENTFRVVDDEKYPHMKSVRNGFRIGSVVRYVQLPDDGVDELLHSDATREARRGG*

NbL01g20550.1 elongation_factor_Tu_mitochondrial [MW = 49.23 kDa]

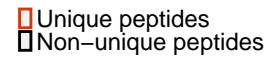
No. of times detected



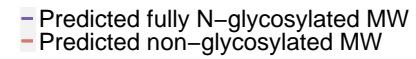
log(intensity)



Values from



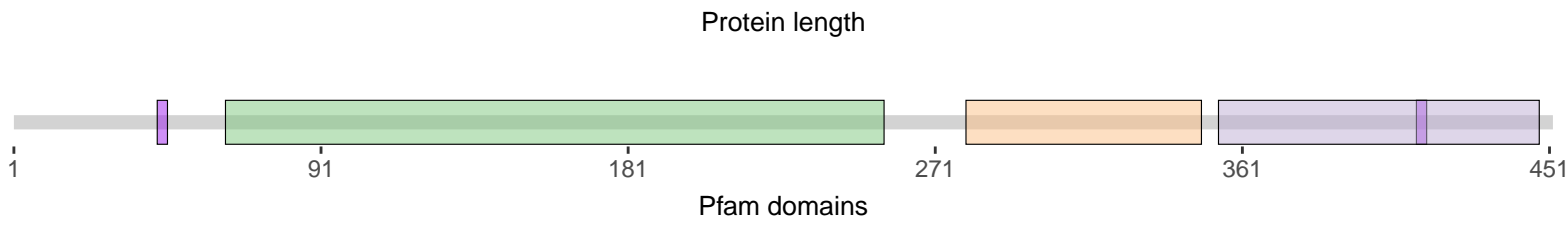
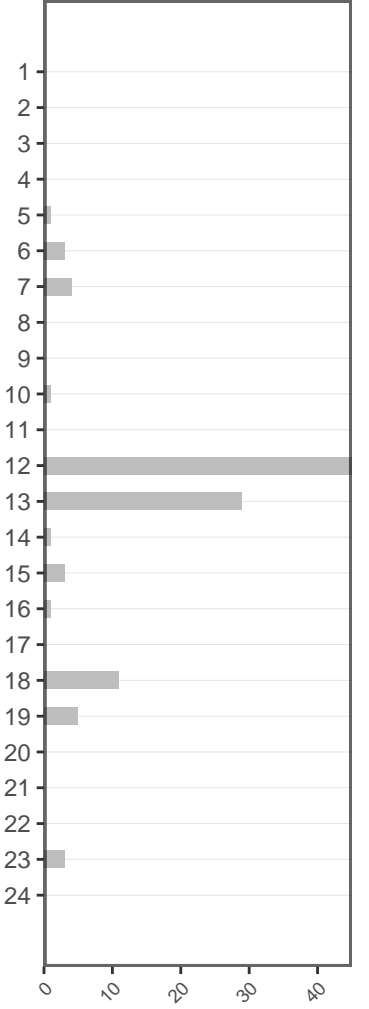
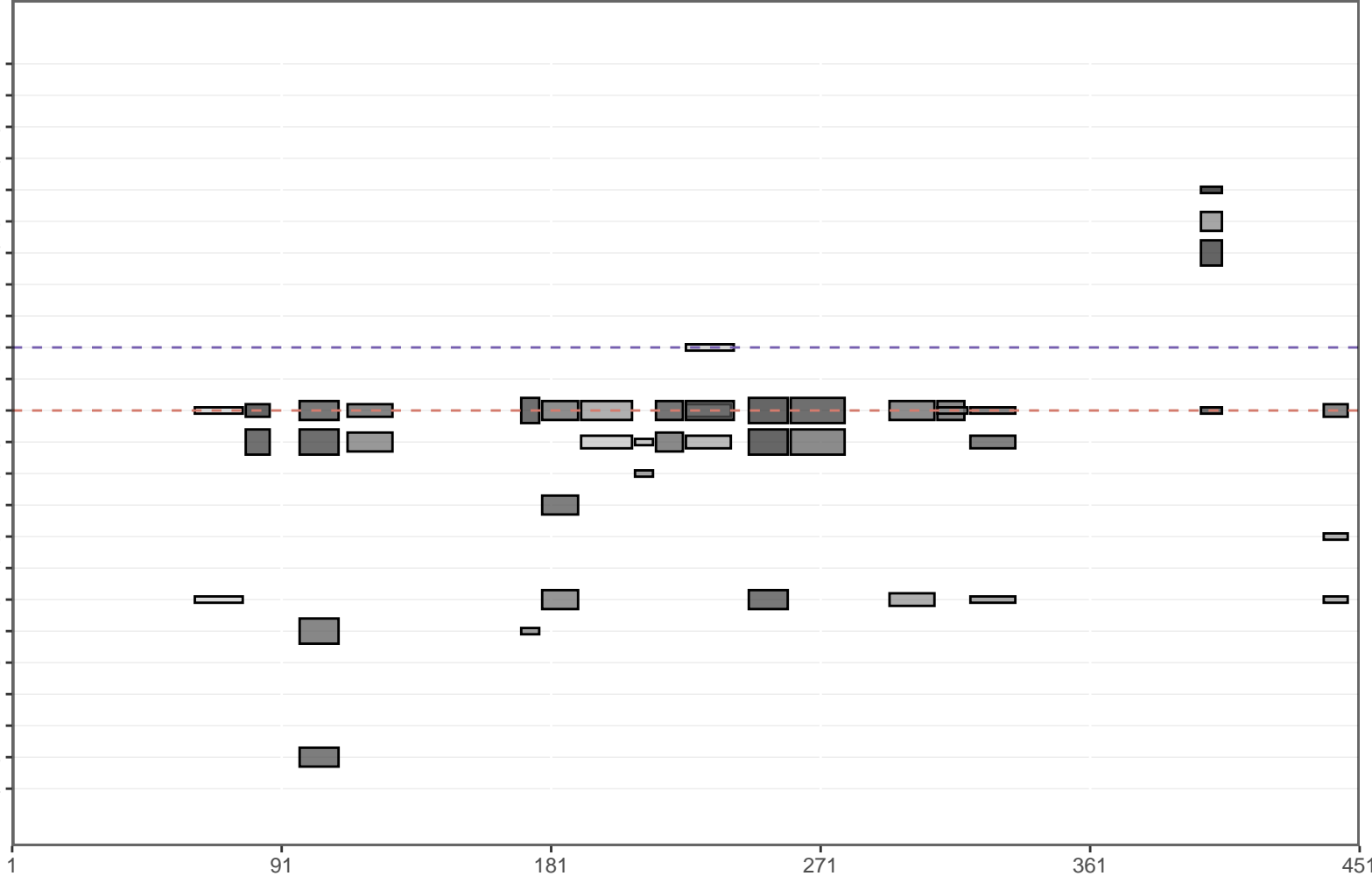
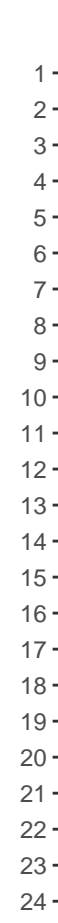
MW indication



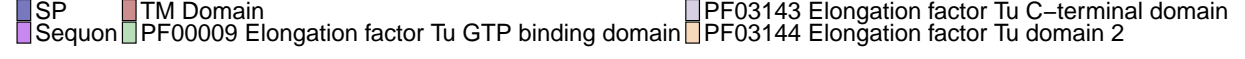
Molecular weight



Gel Slice



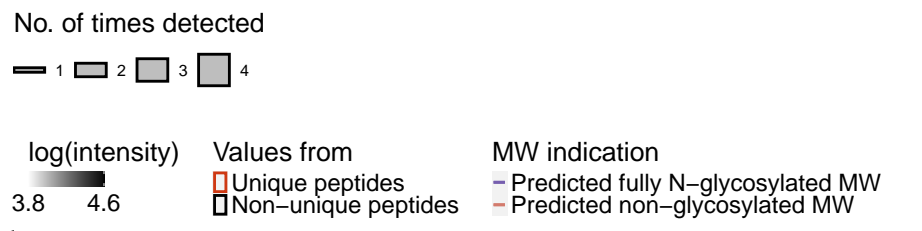
Pfam Description



Protein sequence:

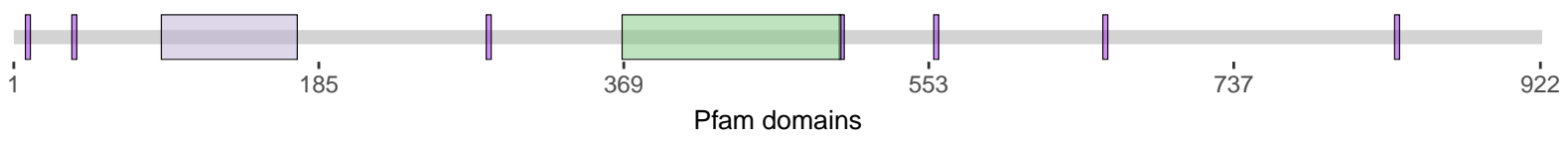
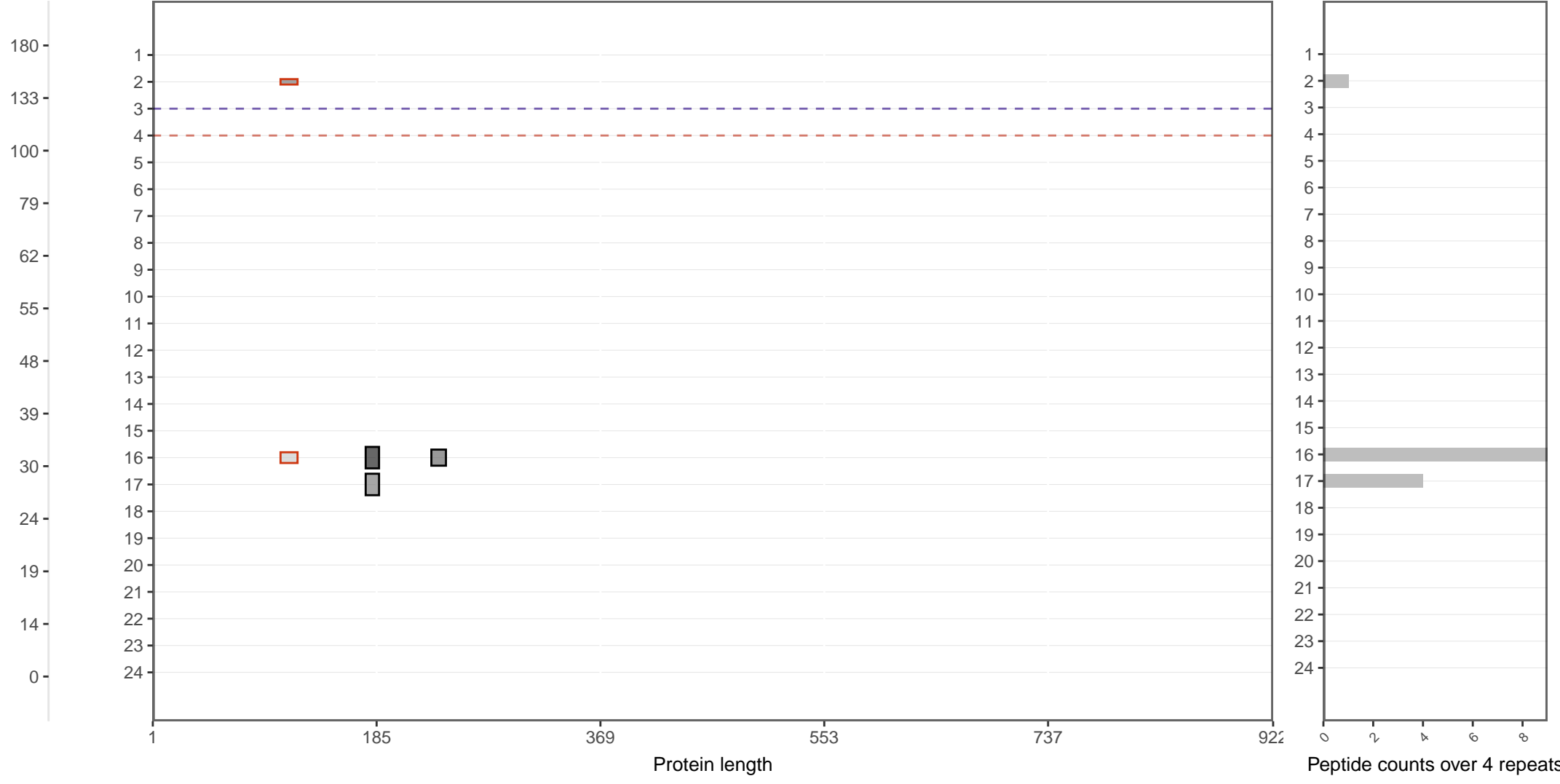
SFYKFPDCEIPRIIRGSEALBLOGTNEENKKAALKLMEAVDEVPDPVRQLDKPLFMPVEDVFSIOGRGTATGRVVEGGQKVGDDVEILGLMGGALKSTVTVGVEMFKKILDHGAAGNGLVLLLRGLKREDITRGMVAIKPGSVKTYKFKFAEIVLTKDEGGRTAFFSNVYRPGFYLRITADITGKVELPENWMMVMPGDNVYATFELISPVLPDAGRFALREGGRVYVAGVWVSKVLS*

NbL01g20300.1 probable_transmembrane_GTPase_FZO-like_chloroplastic [MW = 102.28 kDa]



Molecular weight

Gel Slice



Pfam Description

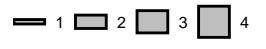
SP Sequon TM Domain PF01926 50S ribosome-binding GTPase PF02581 Thiamine monophosphate synthase

Protein sequence:

ORQQKLEEFYPRADLLFLVMSADRPLETESEVNFLLRYTQGWGKVVVFLKSDVYGNKGELEEAAGFIRENTGKLLNTDCLVLYPVSARLALAEAKLETDFDGLSGENRSGNDFHWKTKGFYEKLYLFLDASTGTGIERRMKLKGTPVAEQLVSEADQGLVREGCGAAGDGLLFLVEDVNSVKECTKLEIDSDLWKRGLVSMINSTGARVYRVLVEFTLQLSNVDLVTGVYFRGEKSTGMPTTSSQNDLGRAVLEGNLLGEYTKWLGGKRDQEGQFYKGSFEKVVIT

NbL01g20290.1 chloroplast_stem-loop_binding_protein_of_41_kDa_a_chloroplastic [MW = 44.17 kDa]

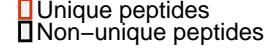
No. of times detected



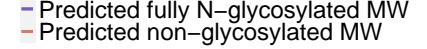
log(intensity)



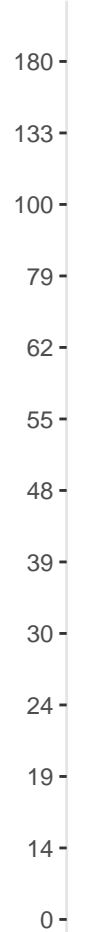
Values from



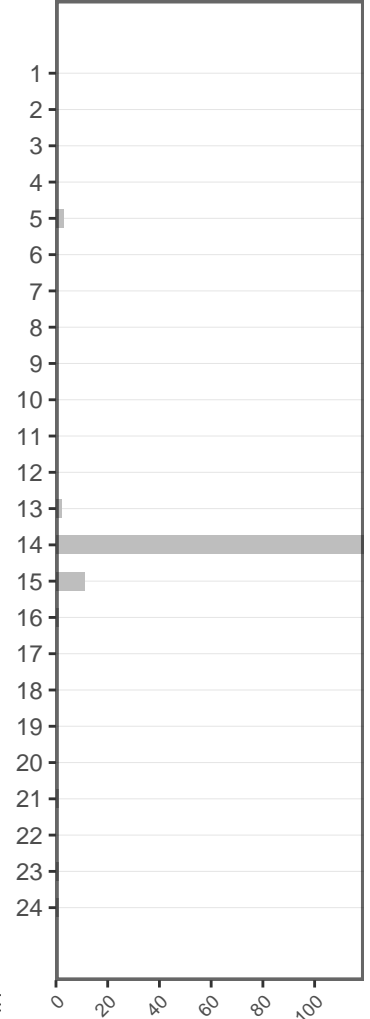
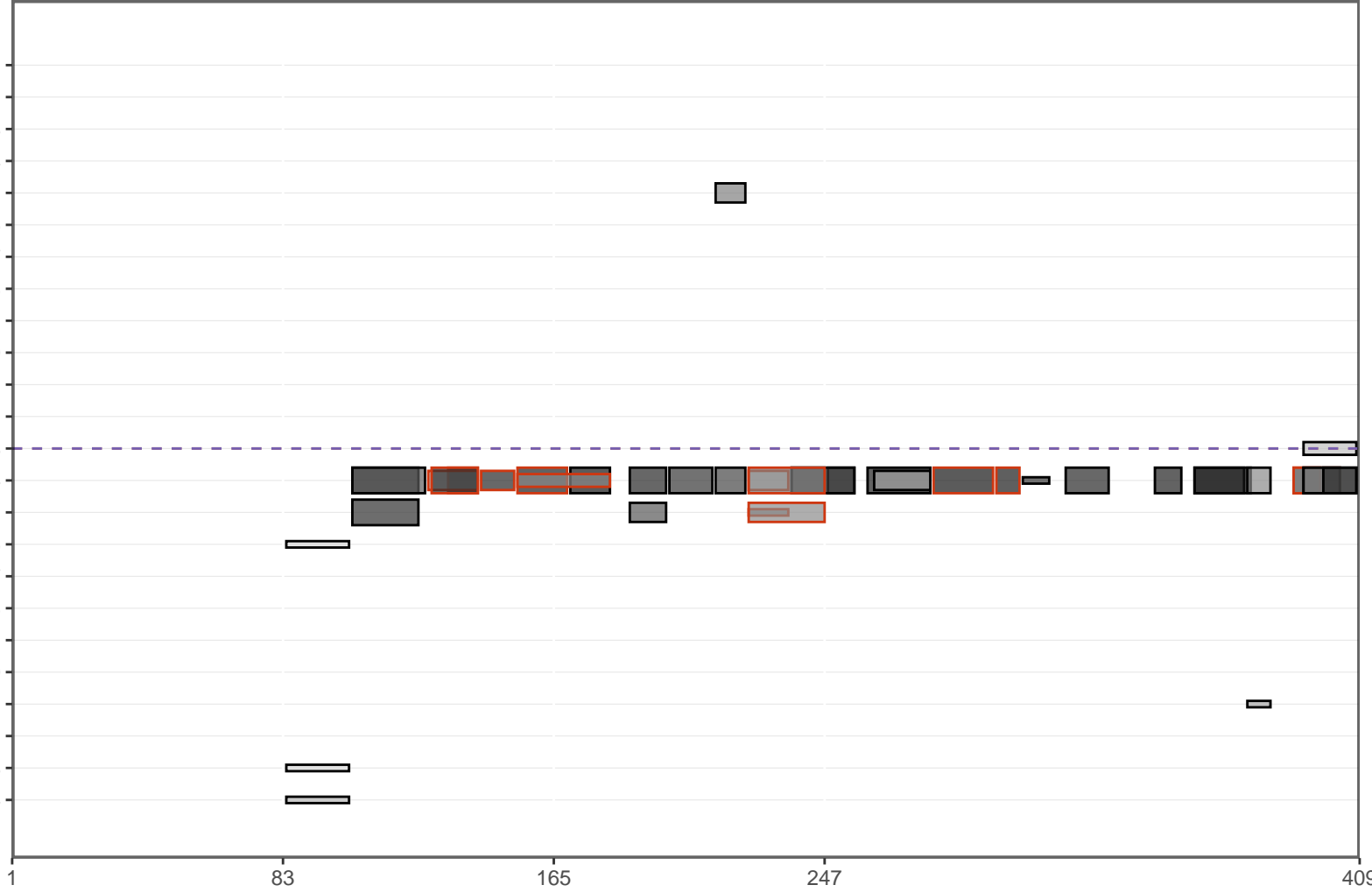
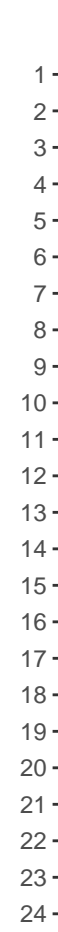
MW indication



Molecular weight

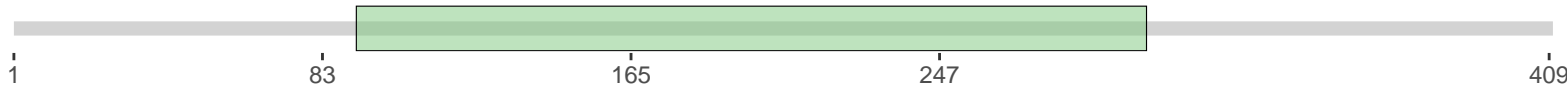


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ISAGIYKSTDEFPPIYMEGDVAKADAGHVGVEKYSFIDVWASFRPQVMGSSGNKDCDEEWFDRIVRGRPIVPIPGSGMQLTNAHVRLDLSMLTAVGNQPTAASGRIFNVSDRAVTLDMKMLCAKAAAGLSEVNHVDPKAVGVDAKAKFPFRNMFHYSEPRAAKEILGWSATTNLPEDLKERFDEYVYKGRDKEMKFELODKILEAKVPIVAA

NbL01g20280.1 RAN_GTPase-activating_protein_1-like [MW = 58.63 kDa]

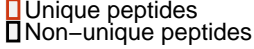
No. of times detected



log(intensity)



Values from



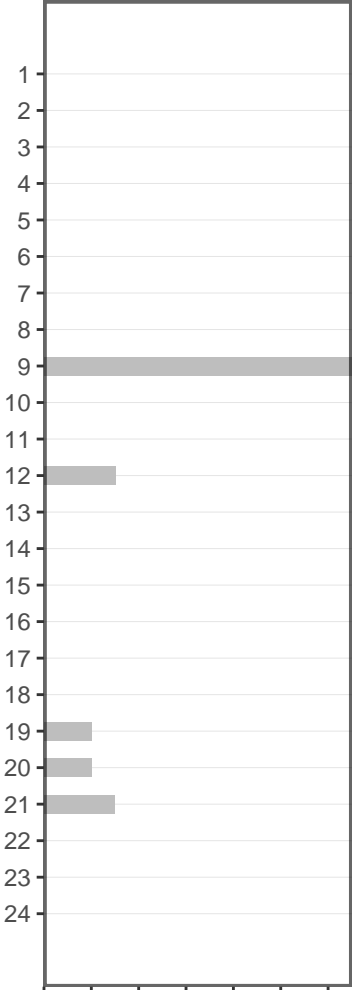
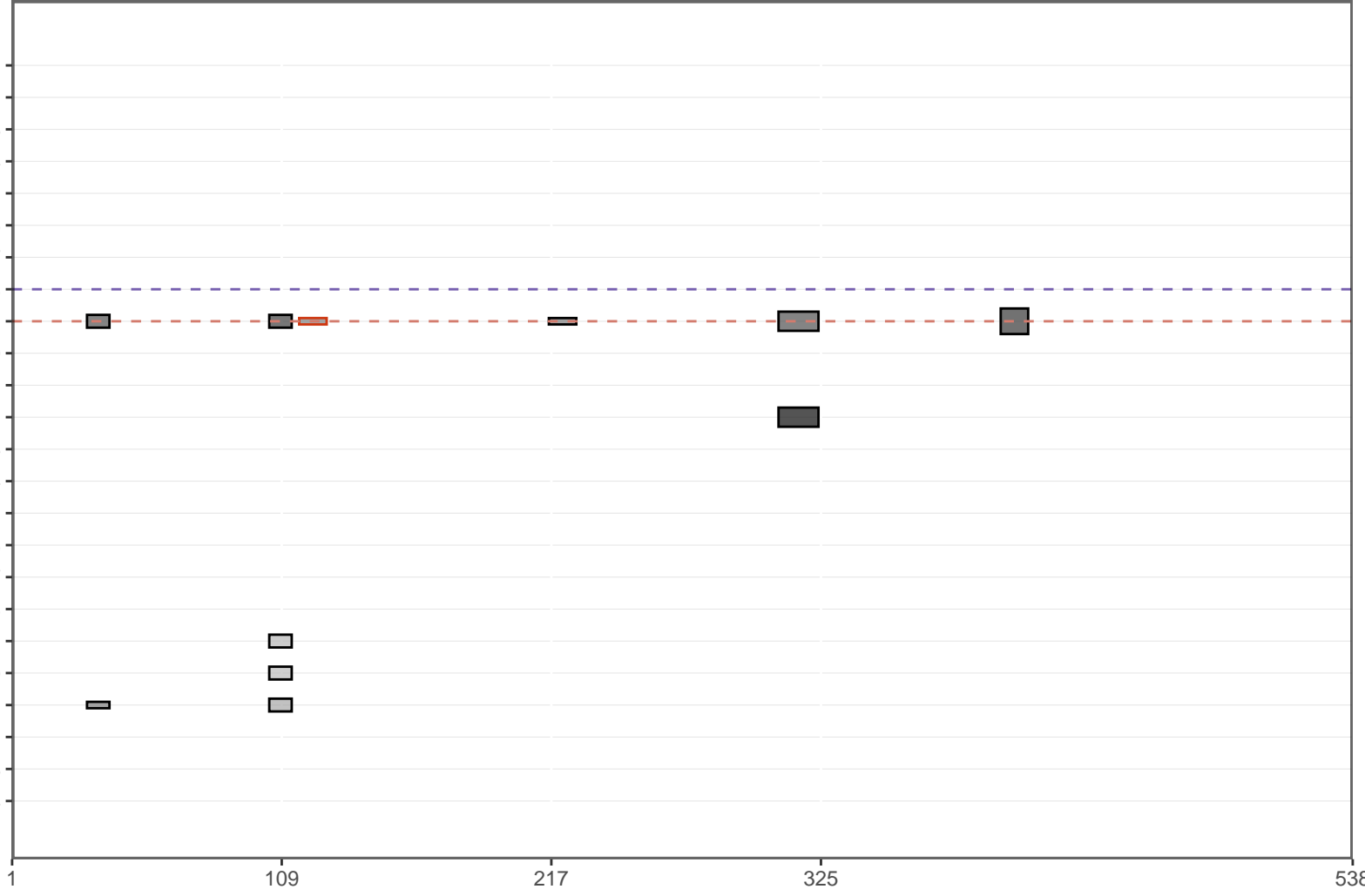
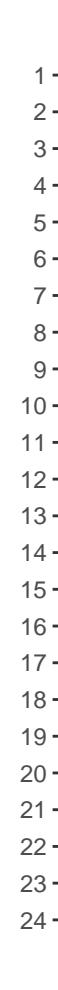
MW indication



Molecular weight

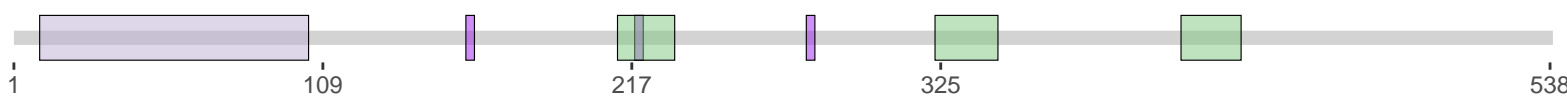


Gel Slice



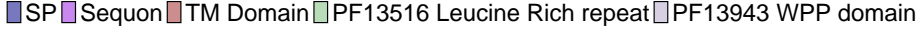
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IEAAQAVRELIPSTDAKRLRHFFHNMGTGDEGALISELKHSTALEDFRGSSTRVQSEGQVALSQALGEGRNKKLKLDRDMFGVEAGIALSKVALSIFSDSTERYLVNLEDEGSIALLKGGAPSLVLEMDGNDHTAKAAPVLAAGIAAKGFLTKLRLAENELKDEGALIAKALDDGHGGDELTDMSTNARRAGARGLAQAAVSKPQKVALSINGNFISDVGIDEVKDFNNSVNLGPLENDPEGEDEFEEEADEAEADNEVELETRKGLDKGEE---

NbL01g20230.1 ribosome-recycling_factor_chloroplastic-like [MW = 35.05 kDa]

No. of times detected



log(intensity)



Values from



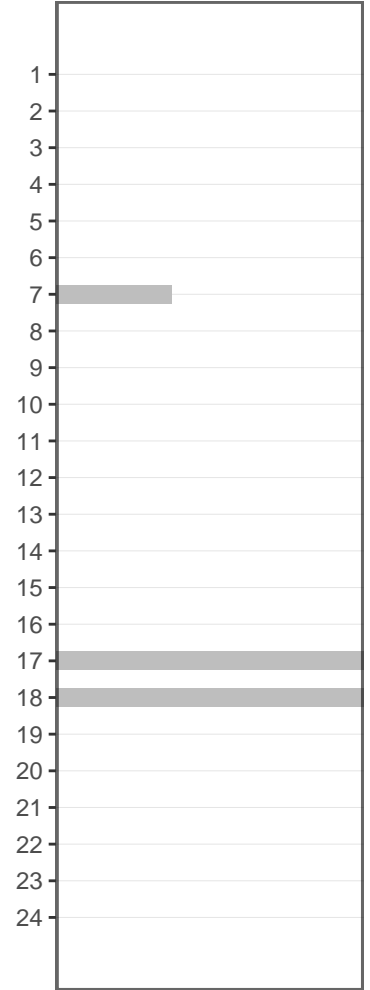
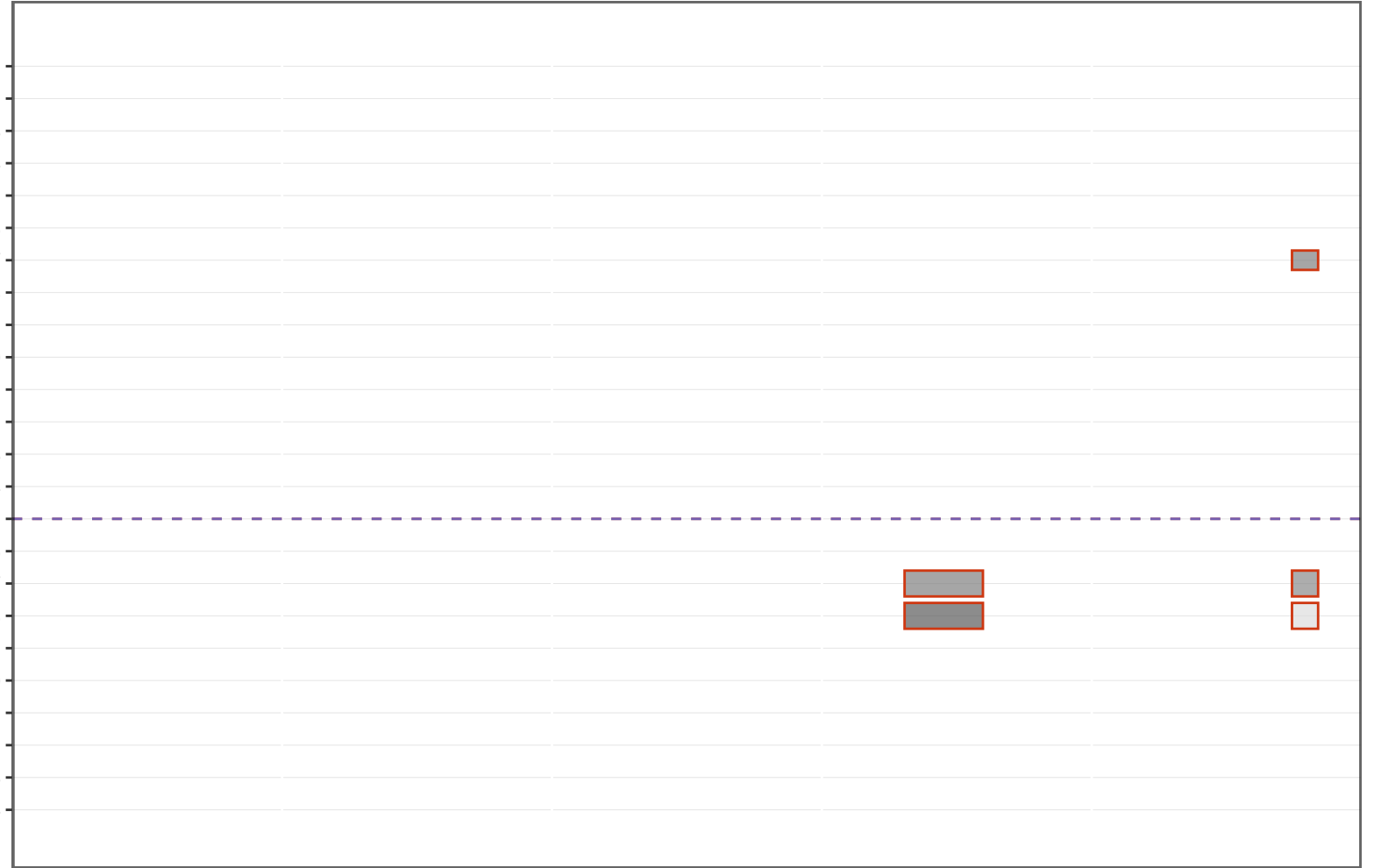
MW indication



Molecular weight



Gel Slice

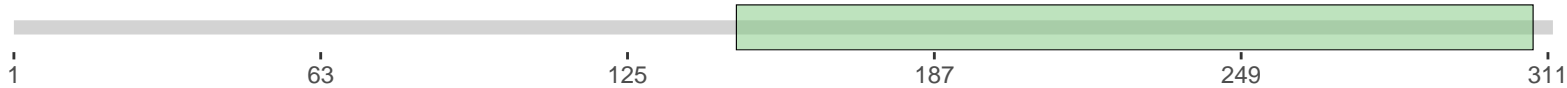


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

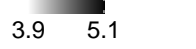
IQENVRSNFSRSRTGRASFMALDKIEVDVYGTPTVSLKGIAGIETPDSSELVQPYDKLSLKAIEKAAKNGSGLGAMFNNDEGEVIRMEVPLQTSDRRKEKLVSKGAEEGKVALNRNRDLAKAYEKEKEKLSLSEDNVYKDLSSDLGKVTDEYMKKVDVTFKQKEKELLTV

NbL01g20180.1 40S_ribosomal_protein_S24-1 [MW = 15.38 kDa]

No. of times detected



log(intensity)



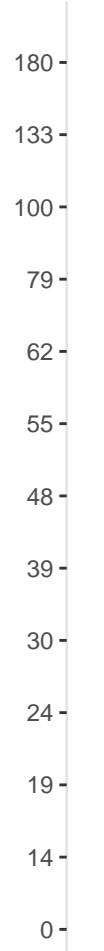
Values from



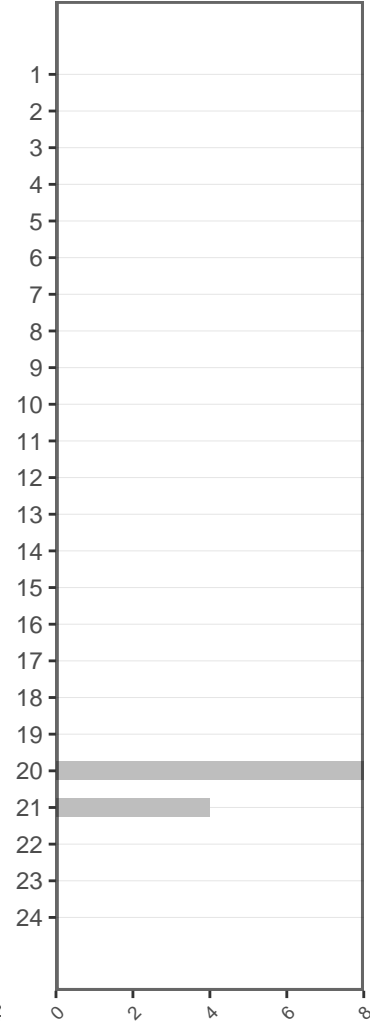
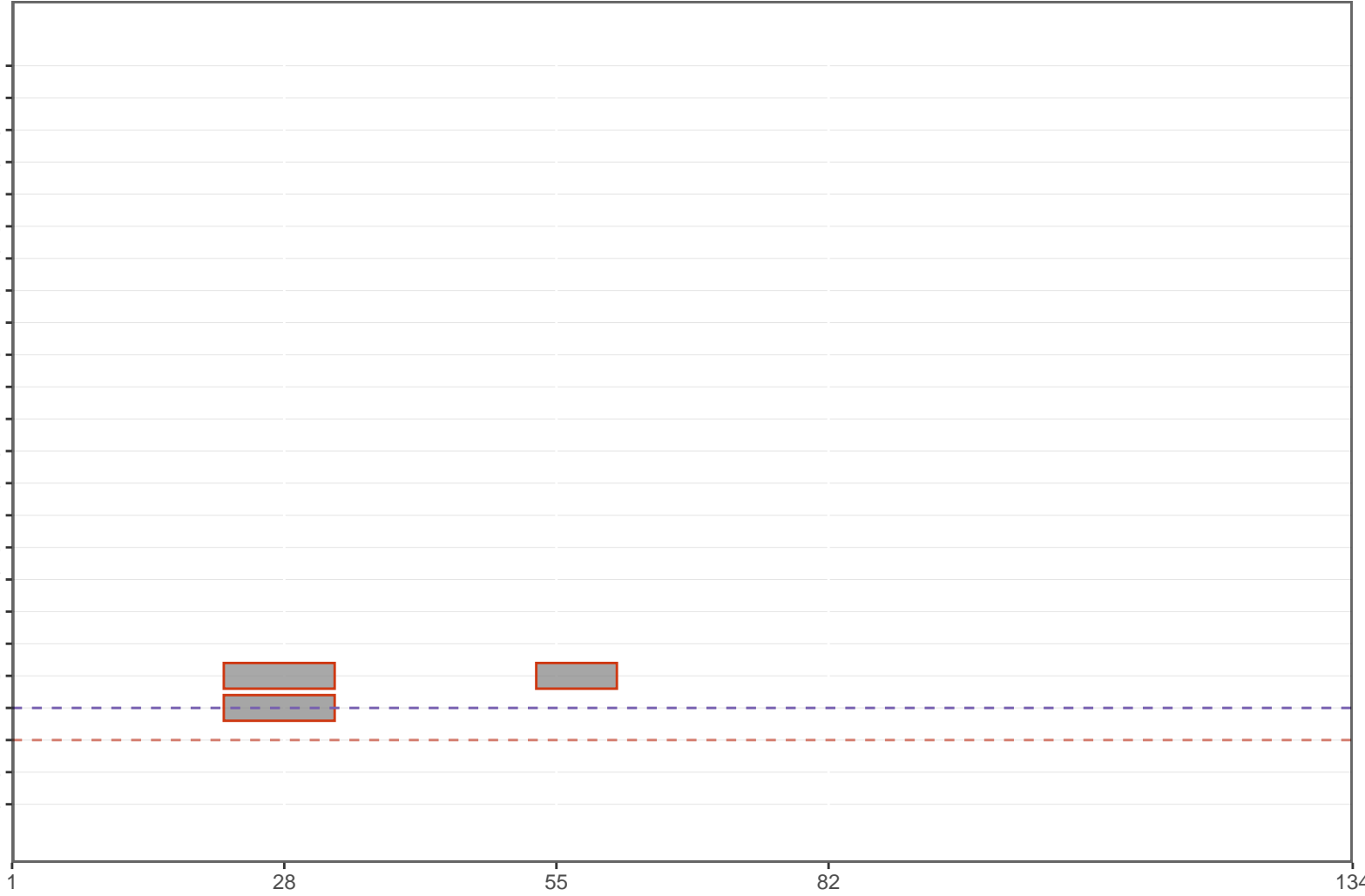
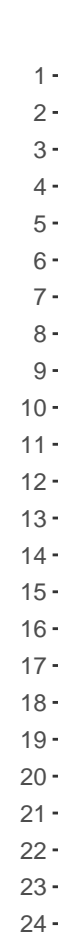
MW indication



Molecular weight



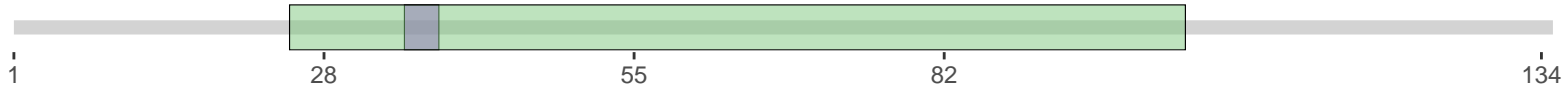
Gel Slice



Protein length



Pfam domains



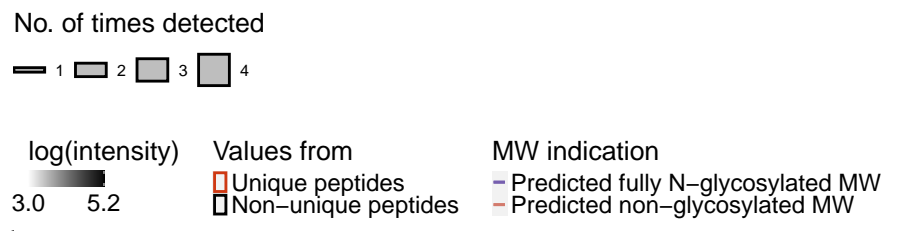
Pfam Description



Protein sequence:

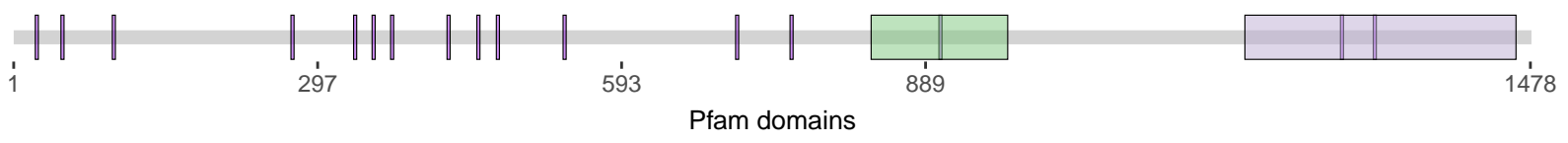
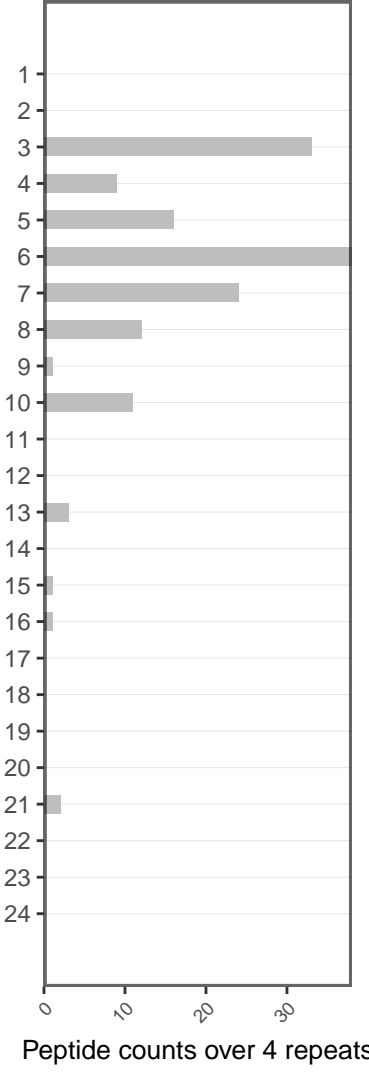
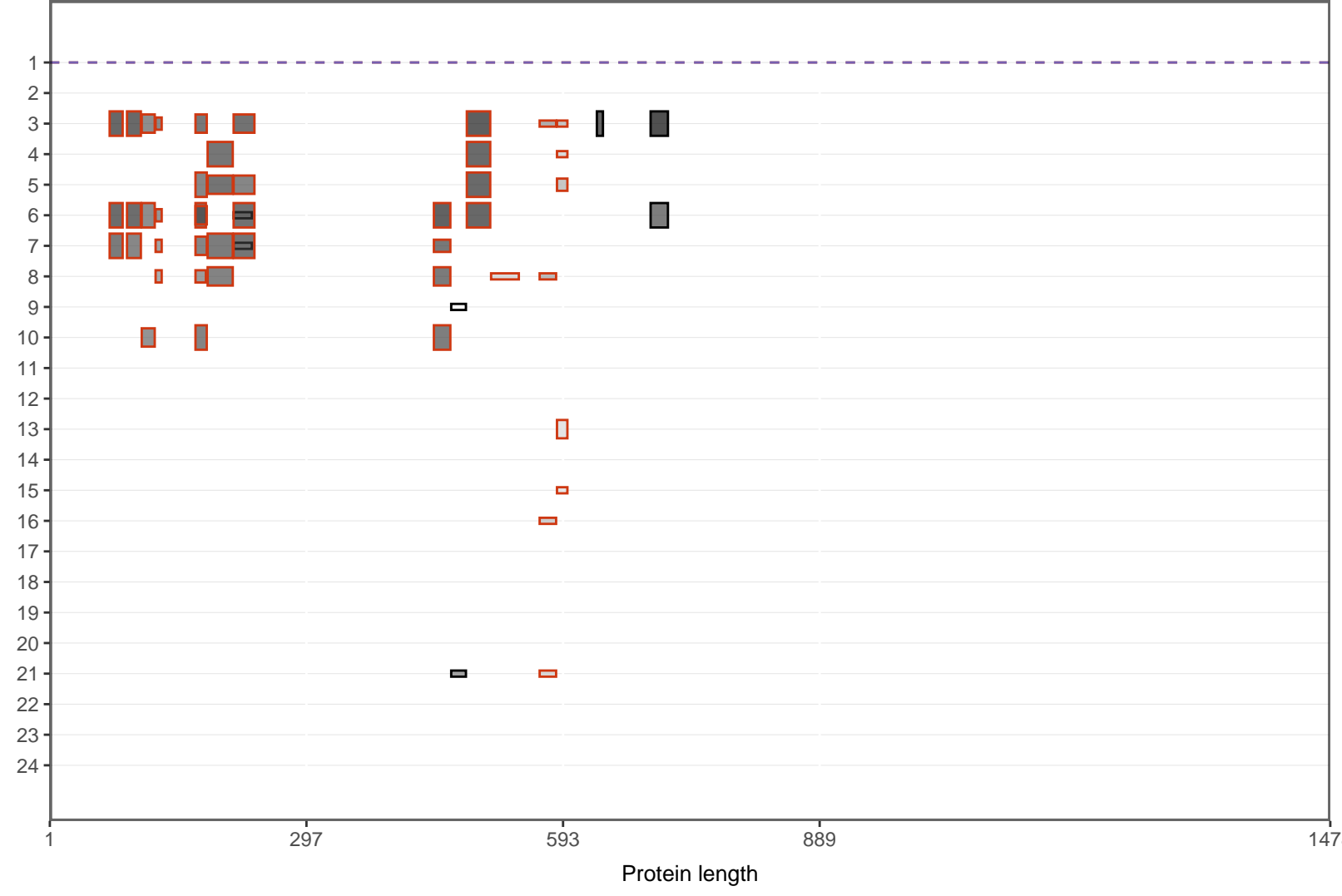
NAIFVFKFRTHFGGGKSTGFLGHDVENAKKVEPKVRLIRNGLDTKVEKSRKGMKERIKRRAKKVGVWTKAGDANKK

NbL01g19940.1 translocase_of_chloroplast_159_chloroplastic [MW = 158.11 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF04548 AIG1 family PF11886 Translocase of chloroplast 159/132, membrane anchor domain

Protein sequence:
 GLGSSLRSLRPAQPNRNLFTPS6LGNSEGENNLTTEEKKNKLEKLGQHRVXKFLRLHRLGLSSDESAAQVLYRLALMARRQNSLFLSLEAAKMRALGLEAEGEDLDFVYNIQVIGKSGVKGKATNIFGEEKTPINAFGNFTTSVKEIGVVEGVRRVDFTPGLKSGVMEQGNREVL6SANKFTKKRPPDFILYVDRLDQTRDLNLDLPMLKTTISGLGPSIWRBAVTLTHGASAPPDGP6SG6PL6YEVEVFTQRSHVQGG6IGAVGDLRMMSP6LNPVSLVENHPS

NbL01g19750.1 UDP-glucuronic_acid_decarboxylase_2-like [MW = 49.23 kDa]

No. of times detected



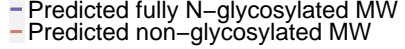
log(intensity)



Values from



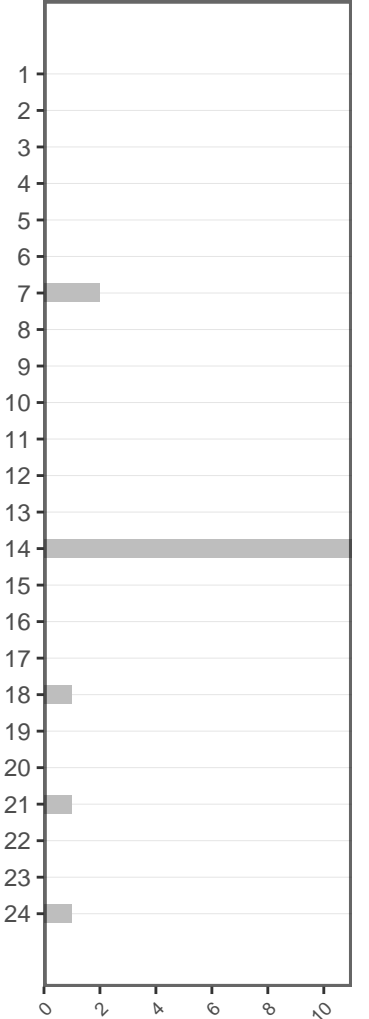
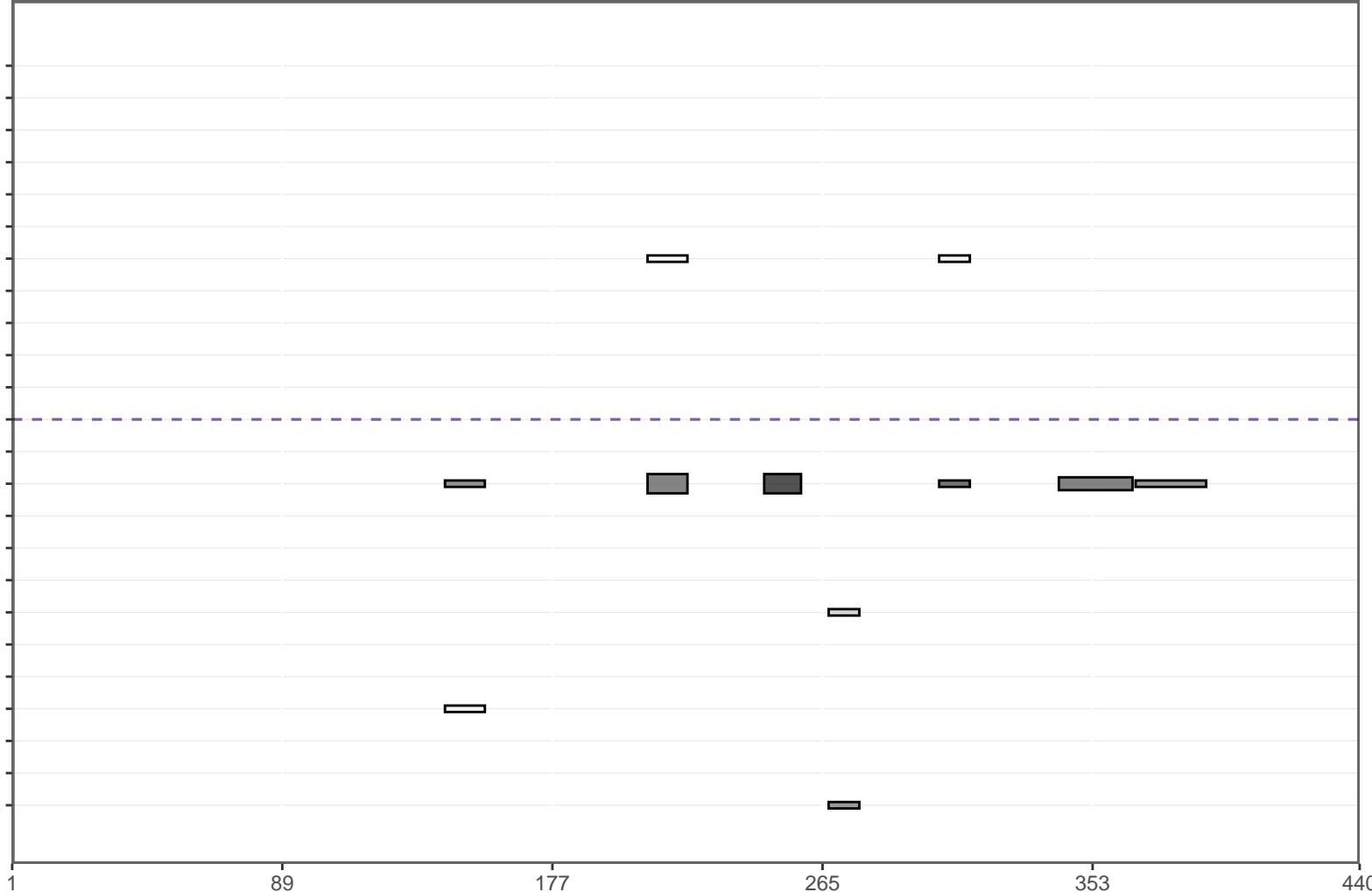
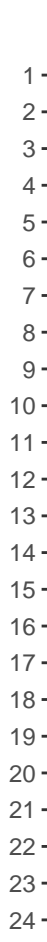
MW indication



Molecular weight



Gel Slice

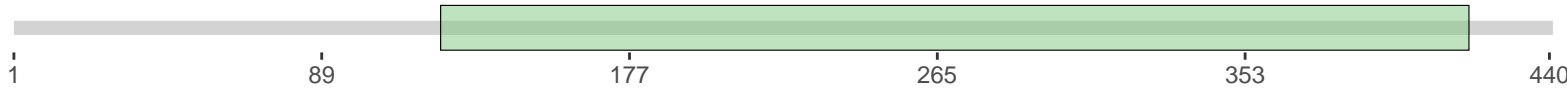


Peptide counts over 4 repeats

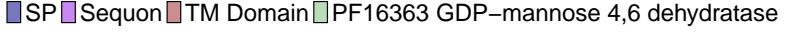
Protein length



Pfam domains



Pfam Description



Protein sequence:

/VGTLMMLGLAKRVGAFLLTSTSEVYVGDPLEHPQKETYWGNVNPVGRVRSYDEGKRTAETLMDYHRRGAGVEVRIARINFTYVGRMCDDGRVYGNFVQALRKLKMLPTLVYVGDGKQTRSFQYVSDLVLEGLMRLMEGEHVGFNLPNPGDEFMTELELAKVYGETIOPNAQIEFRPNTEDDPHKKRKPDSRAKELLGWEPKVALRKLGLPMMVQDFRGRIFADHKEDTSSATA

NbL01g19610.1 pectinesterase-like [MW = 64.5 kDa]

No. of times detected



log(intensity)



Values from



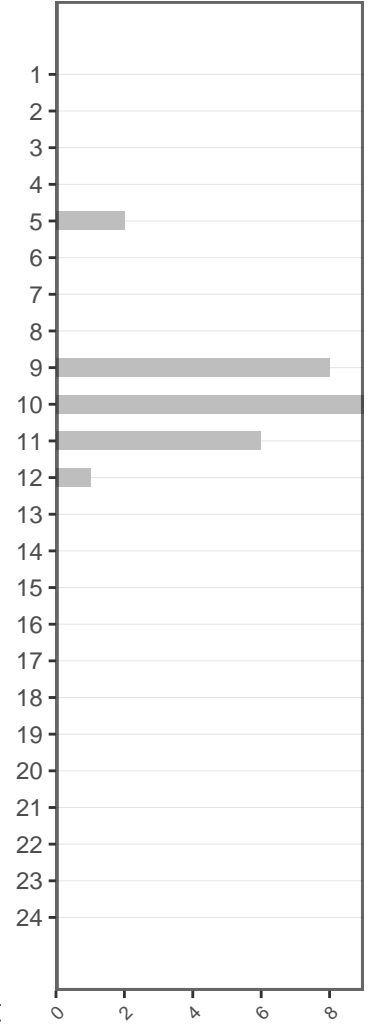
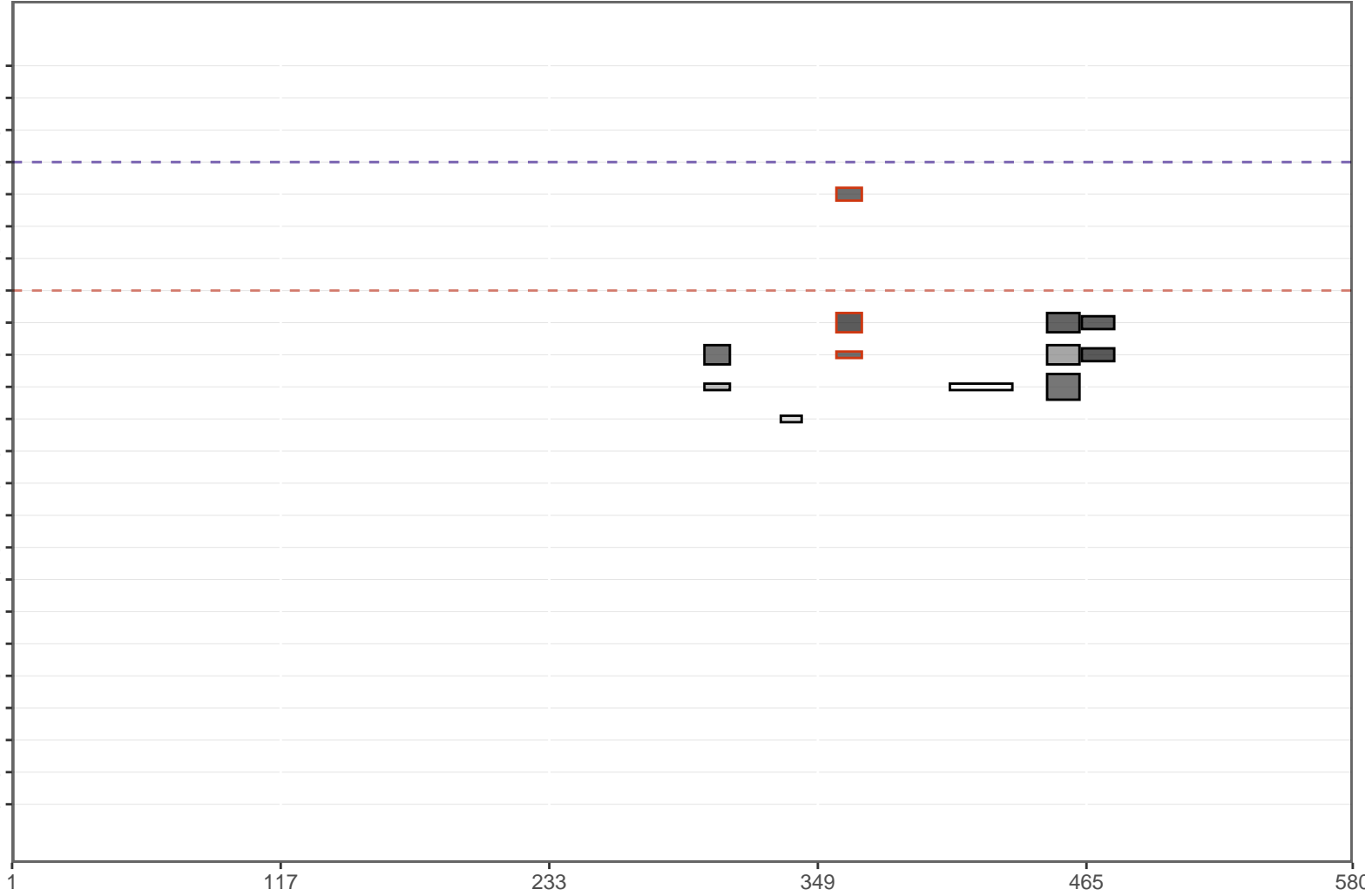
MW indication



Molecular weight

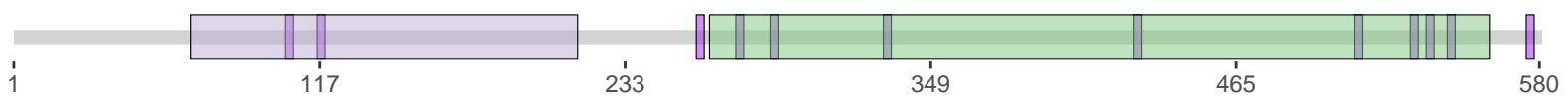


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

NEALSAAPNASRTRFVHKAGAYEYEVKRPMMFLDGGIGKTLKGNRNVVDGWTTFRSATVWVYGGFGFANGITFENFAGASKHQAVVRS68DLAFYGGSFVWQDTLWVHLRQFYRDCGVYGTVDFFGNAAVVFQNGSLVARKPNENGNIFTAGGREDPQNGTGISLNRKIAAALDLPVGG6FKNYGRPWKEYSRRTVM,LTHTGSLIEPAGLEWNGTTFALDLYVYGEYKNRGPGSNTSARVNW6GVYRWNNSAENGFTVGNFIEGKEVLPDTGFPFYLN

NbL01g19560.1 60S_ribosomal_protein_L19-1 [MW = 24.91 kDa]

No. of times detected



log(intensity)



Values from



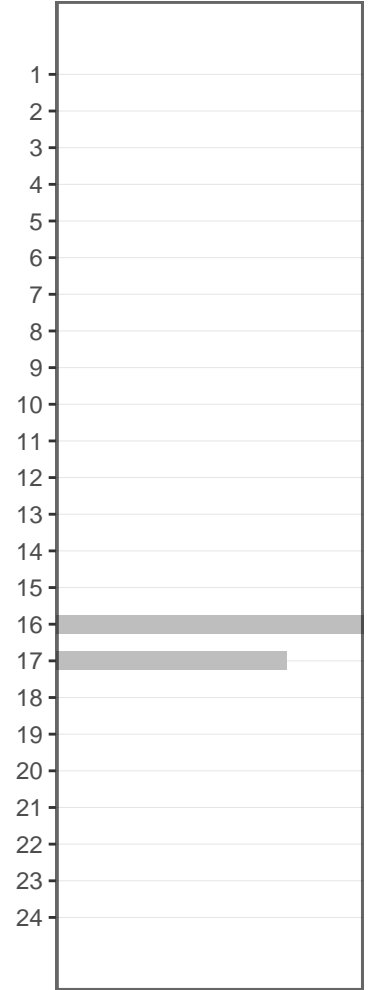
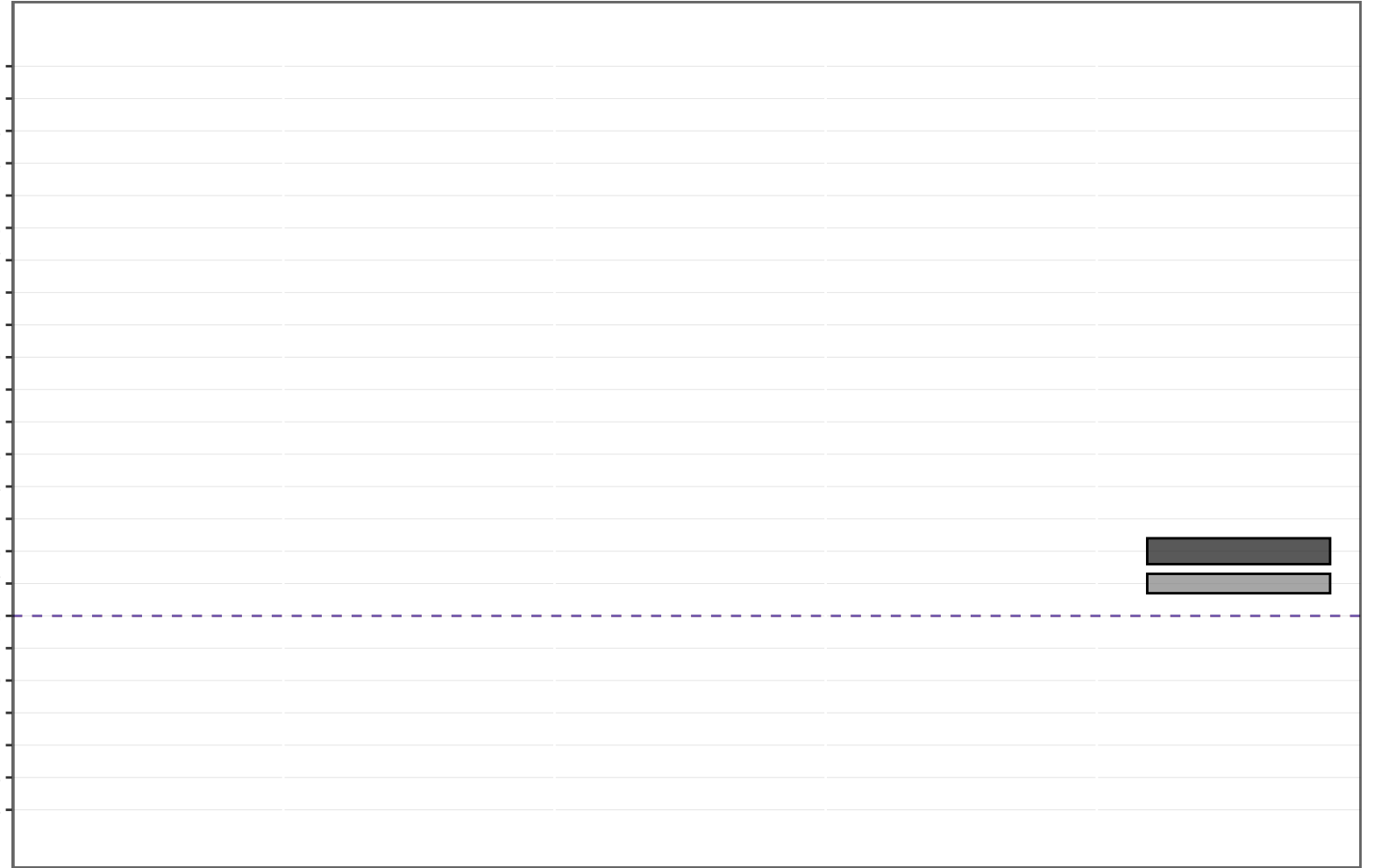
MW indication



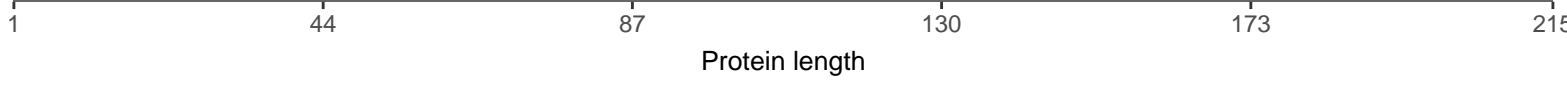
Molecular weight



Gel Slice

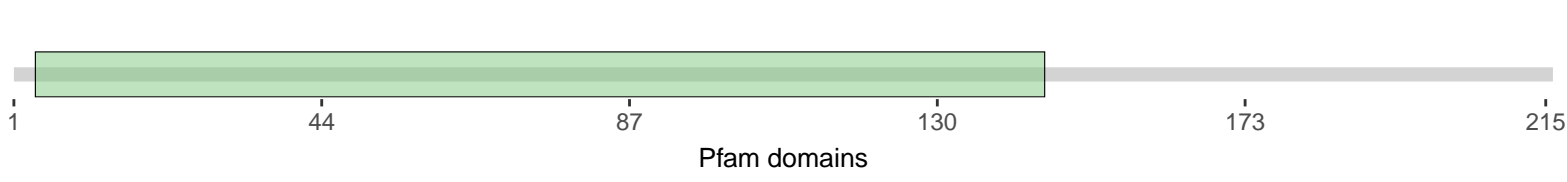


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

MRMRVLRRLRLKRYRESKIDRHIMYDMVMKGNVFNKRVLMEHHTKAEKAREKTLSDGFARAAKAKSERIKFARREERLAGDGPGERPVQVPAASATPQTADGGSKKSKK

NbL01g19540.1 probable_polygalacturonase [MW – SP = 47.54 kDa]

No. of times detected



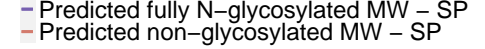
log(intensity)



Values from



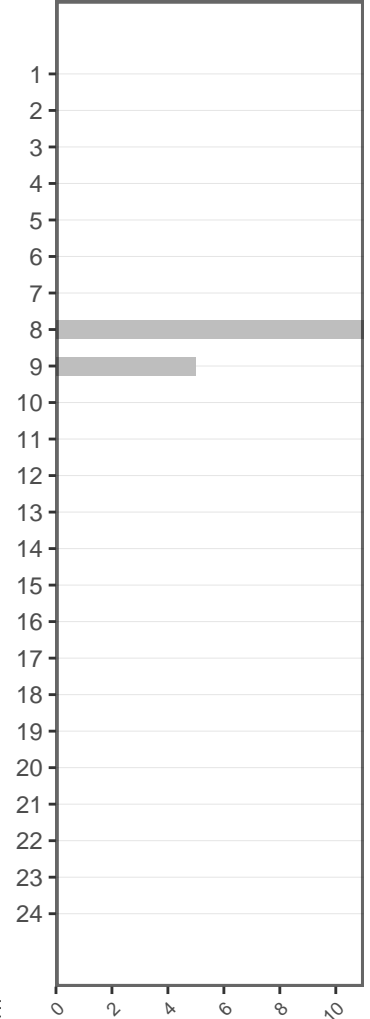
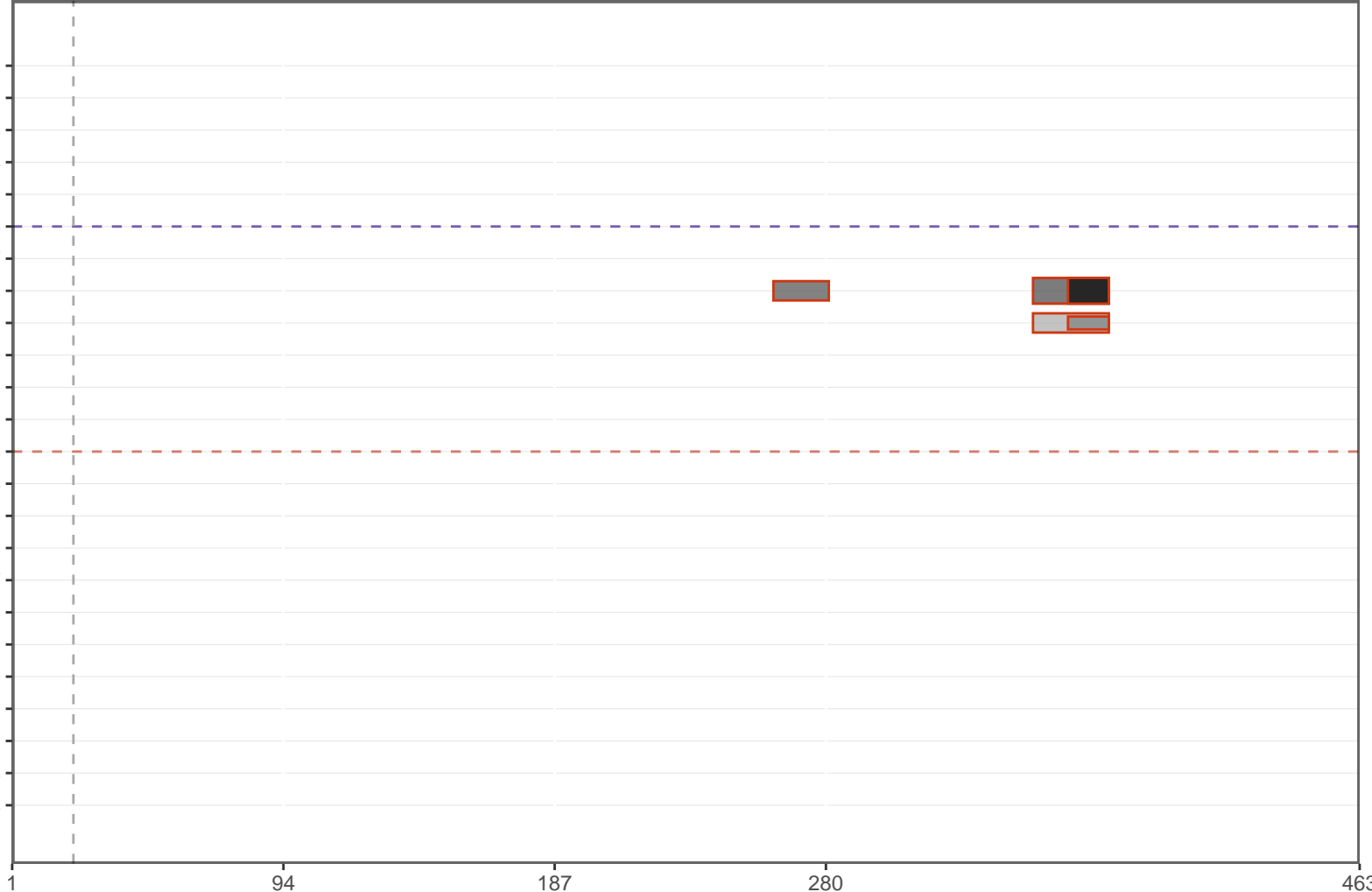
MW indication



Molecular weight

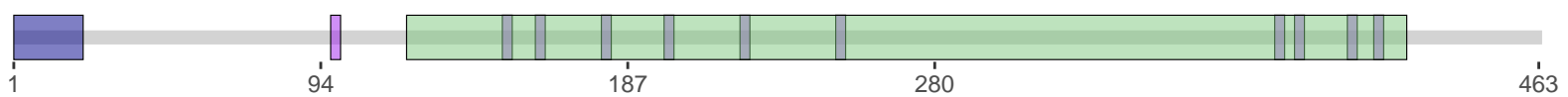


Gel Slice



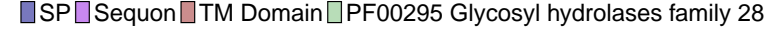
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VIQNLTVHSPDQSPYNTNGVFDPSSEHVCIEHNSITIGYDAVVLKSGWDEYGVGKPTSNVHRGVRLQSSAGSAWAFGSEMGGHNLVEHISLHDSLFGIDLKTARGGGYKDLMMNVAMENVGVGKATGVYDHPDEKYDPSGLPVVSGHTFKDIVGTNLSIAGNFTGLSESPFTGICLENISFSEISNLSTPWLQSDVWGGSENVFPEPCPELQGSFSSSSSAGFALPDPYKTEVAWL

NbL01g19170.1 tubulin-folding_cofactor_A [MW = 13.75 kDa]

No. of times detected



log(intensity)



Values from



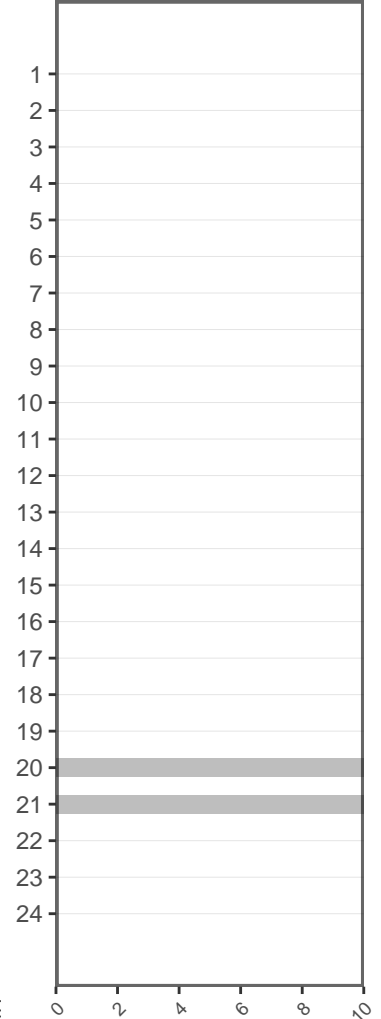
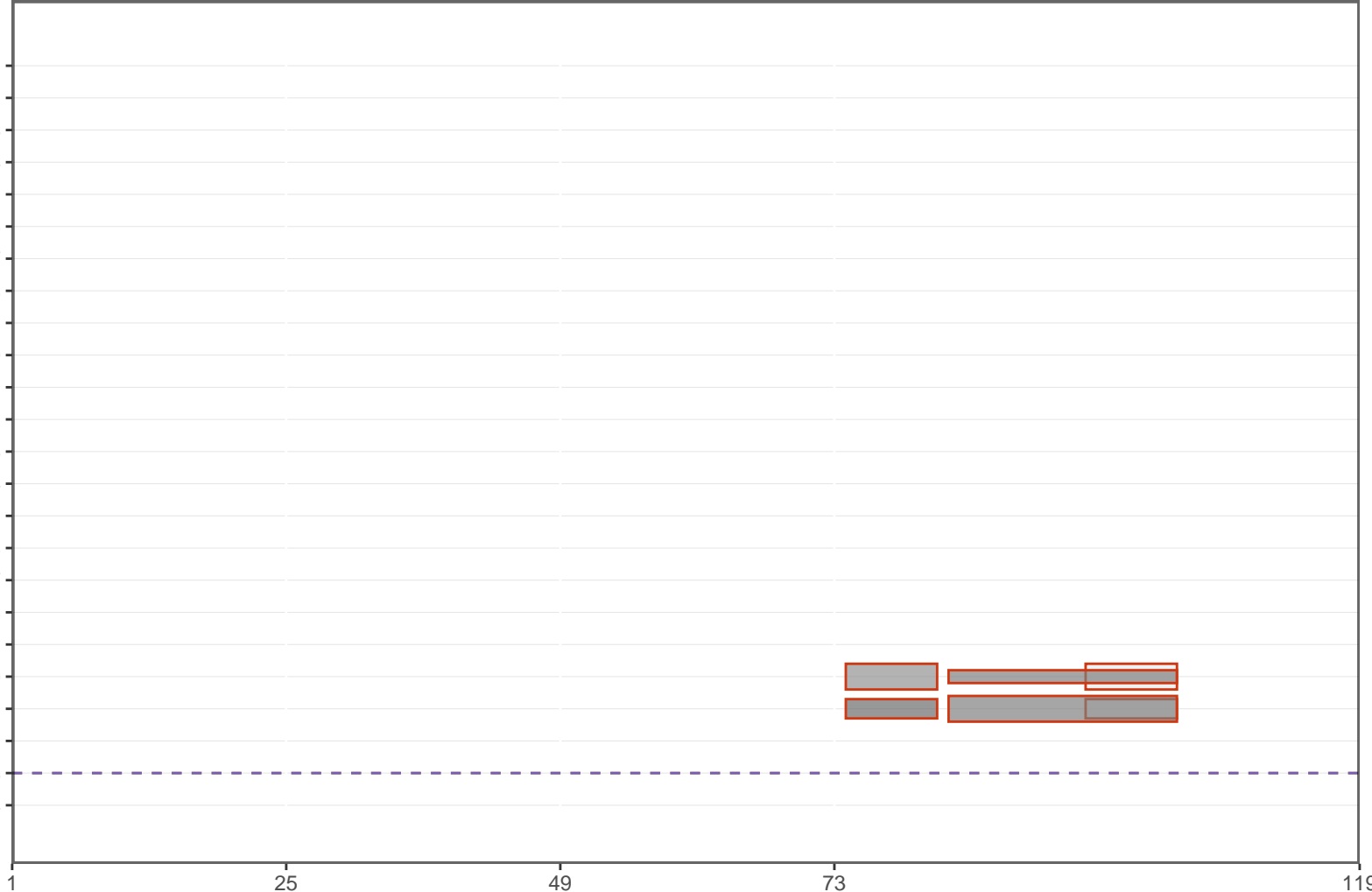
MW indication



Molecular weight



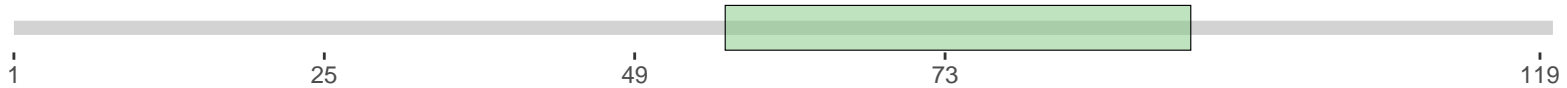
Gel Slice



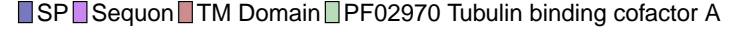
Protein length



Pfam domains



Pfam Description



Protein sequence:

LFSSCFWYRQENVAEGRMMVFDGRKRLEAAALDDKGAALVELEETDQKDGPEFEARTRADVEKLFESSEV*

NbL01g18990.1 40S_ribosomal_protein_S16-like [MW = 20.78 kDa]

No. of times detected



log(intensity)



Values from



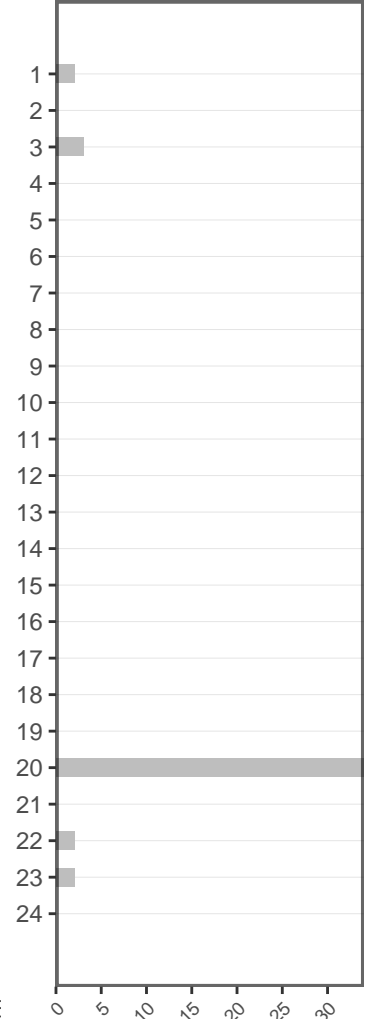
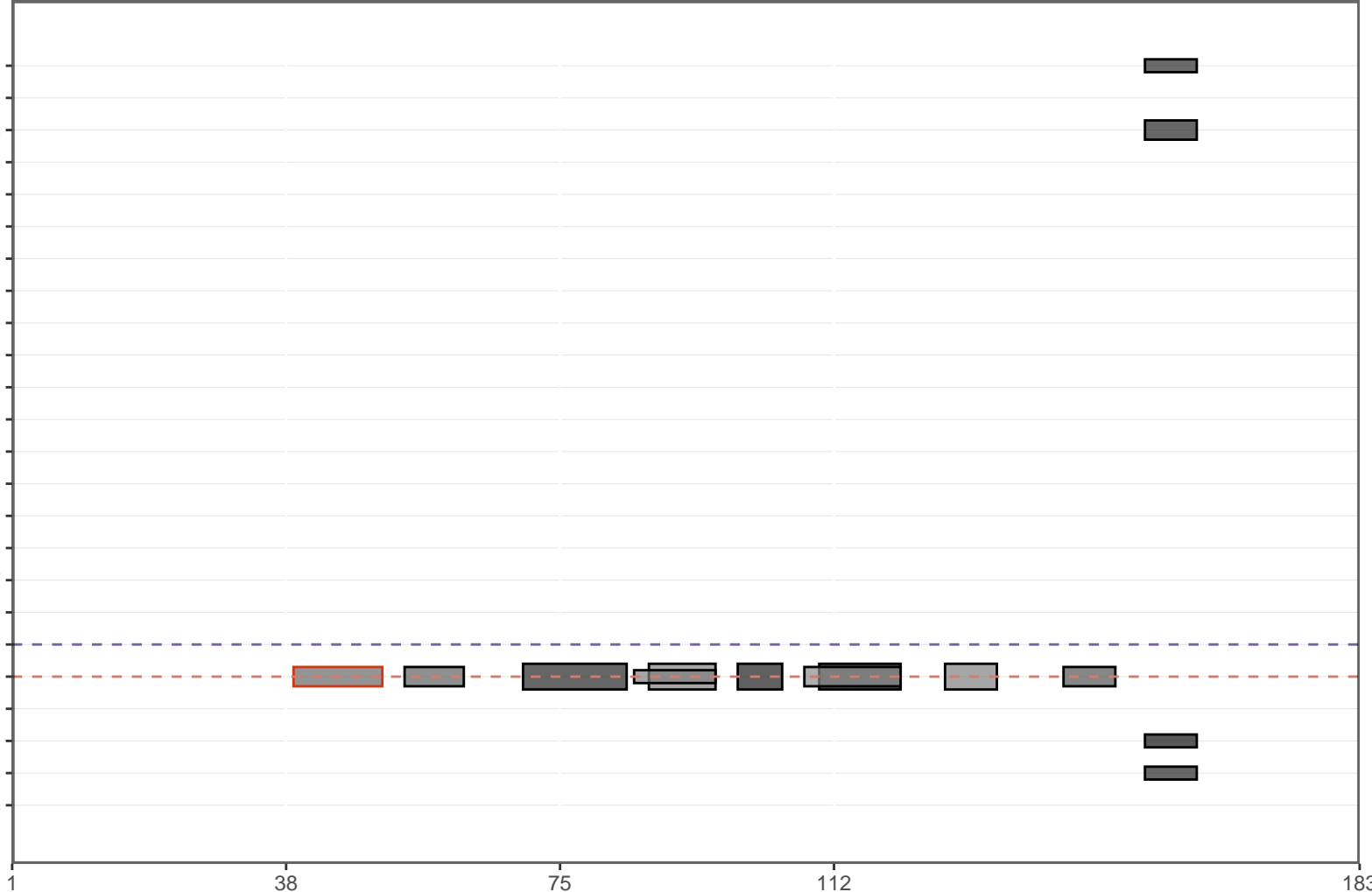
MW indication



Molecular weight

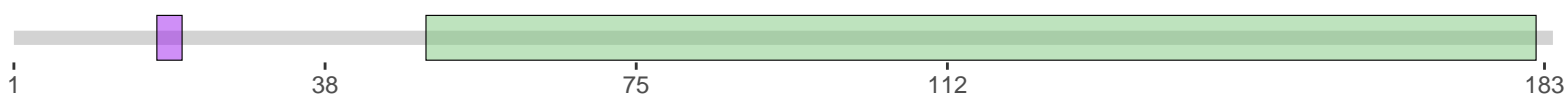


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IQPEILRYKAFEPILLGLGRHFRFAGVDMIRIRWGGGHTSGYAIRQSIKALVAFYQKYVDEGSKKEIKDLVRYDRTLVADPRRCEPKFKFGGRGARARFQKQYR

NbL01g18940.1 uncharacterized_LOC107810622 [MW = 32.17 kDa]

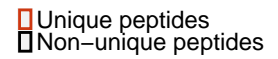
No. of times detected



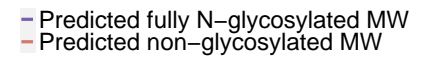
log(intensity)



Values from



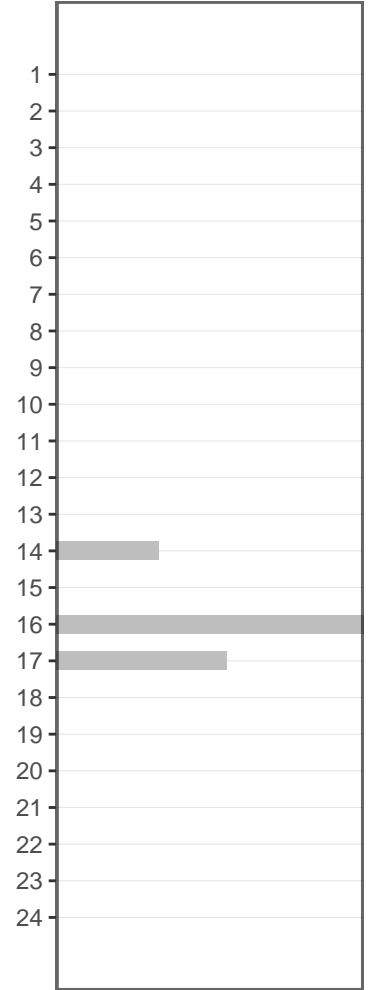
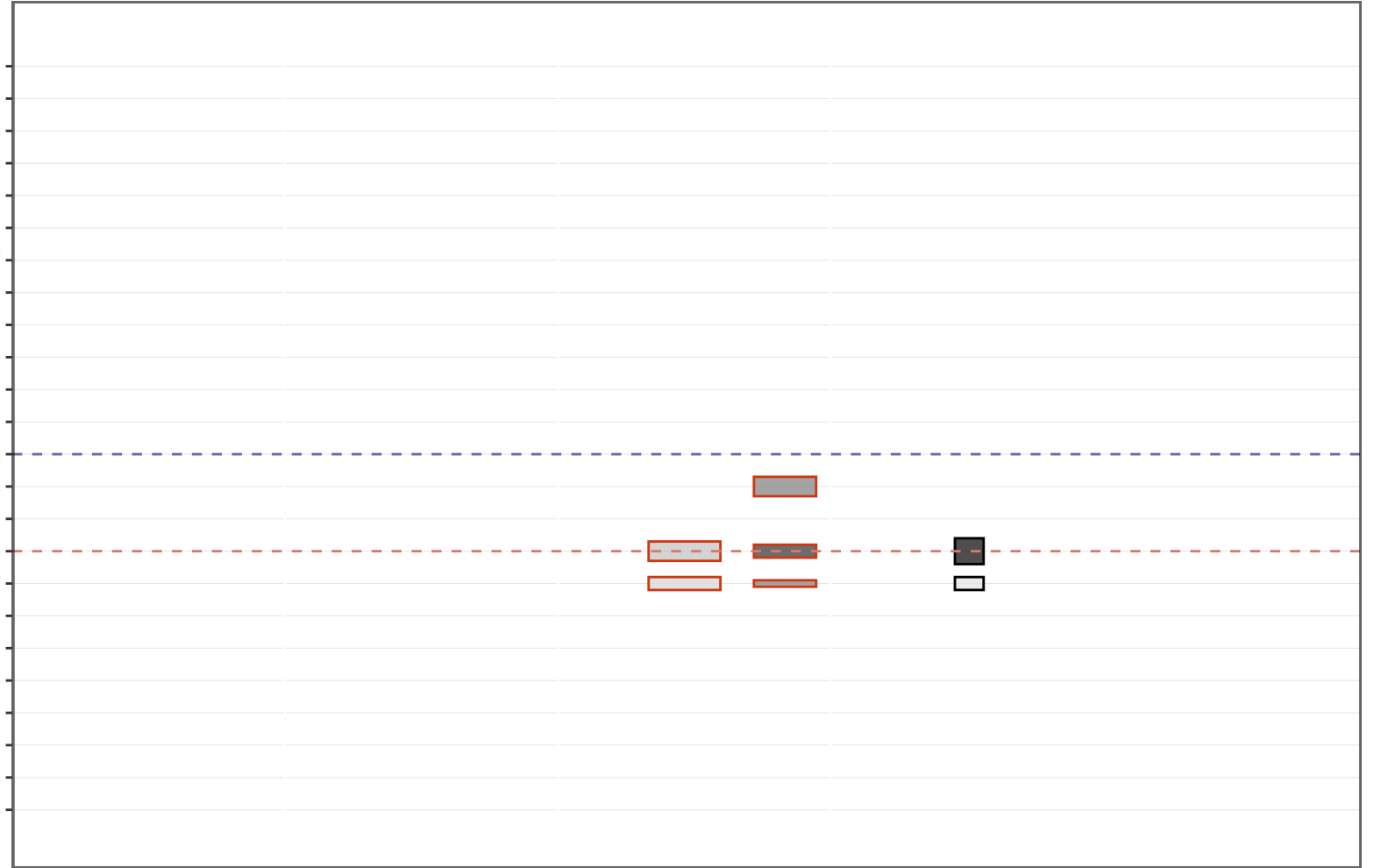
MW indication



Molecular weight



Gel Slice

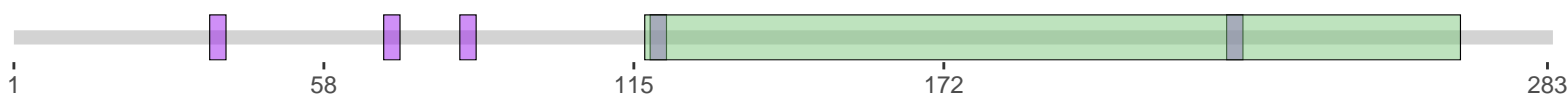


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description

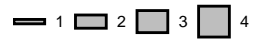


Protein sequence:

JDYERLADFIPLAVSGLLQKPEFNFAILLQISEGDLAFGLKFNAGKIVDQYEKDLDELPIGQRRIIEFKMVEGDFLFEGRKWSIEGQNPGEVKEHNSAAGQPFHTTVFVYVDVEPKLWLPVRIEGRLLCKEKTNLRFVREEAGKIVLTLSSVY

NbL01g18930.1 protein_transport_protein_SEC23-like [MW = 95.02 kDa]

No. of times detected



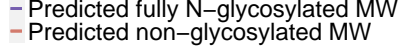
log(intensity)



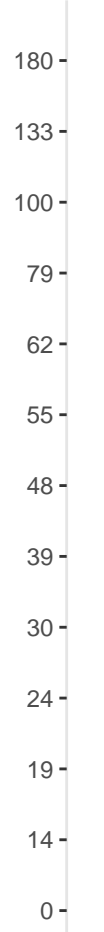
Values from



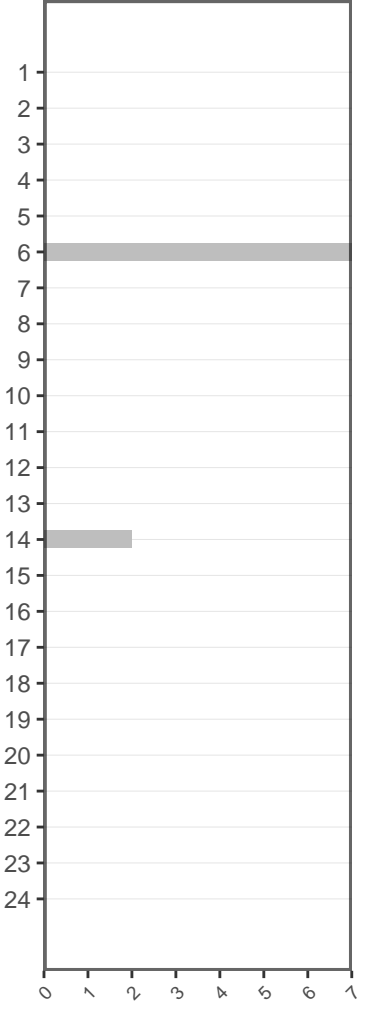
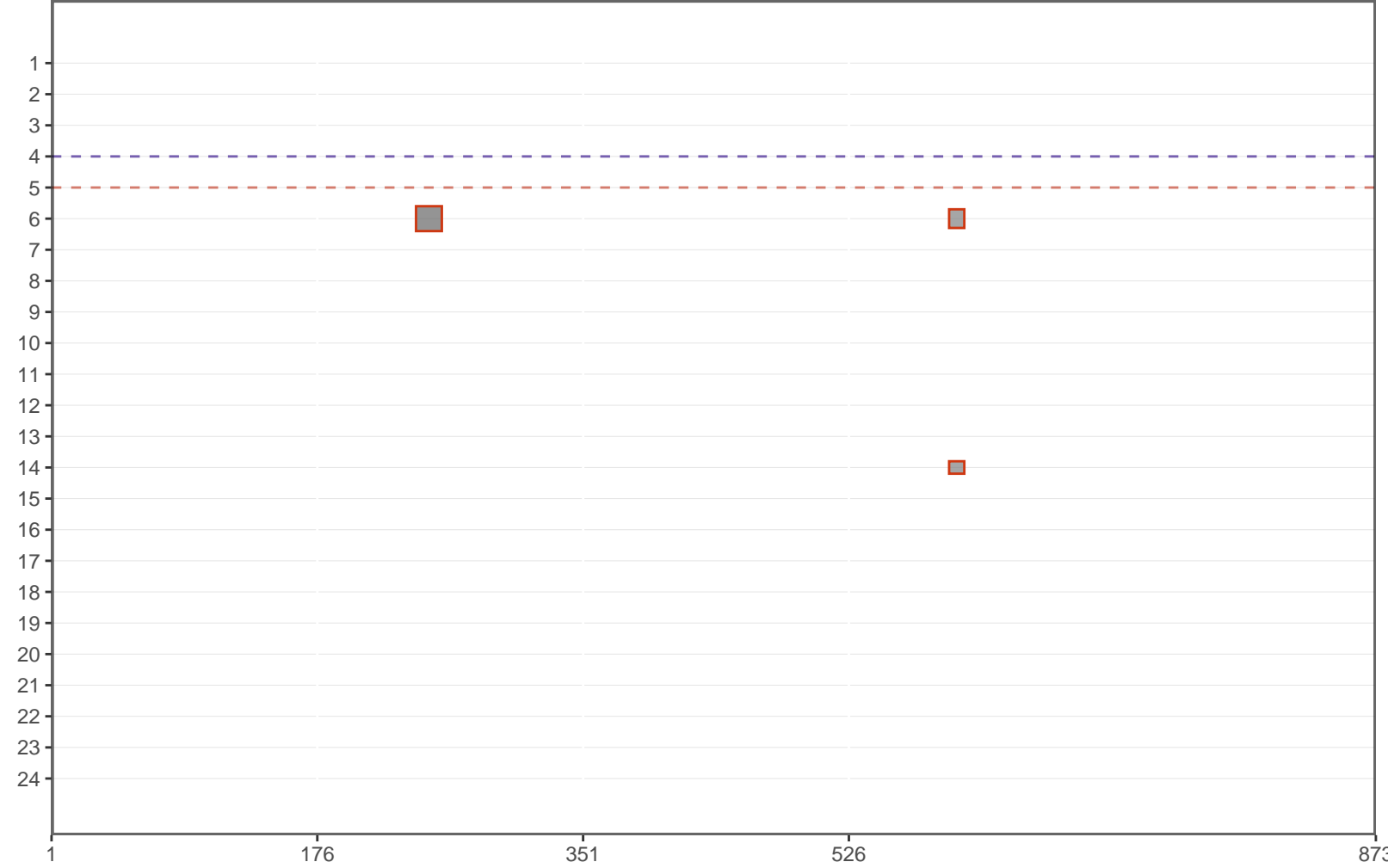
MW indication



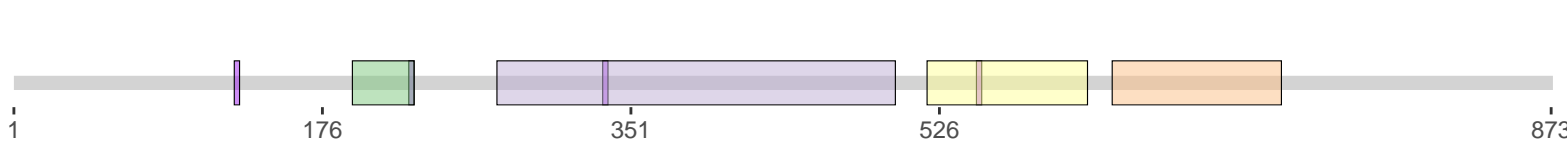
Molecular weight



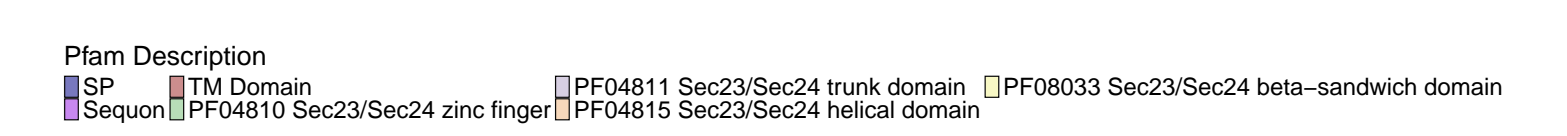
Gel Slice



Protein length



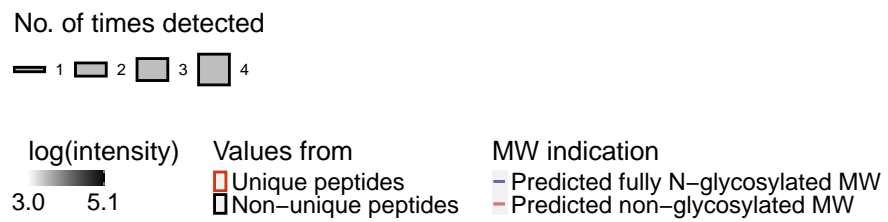
Pfam domains



Protein sequence:

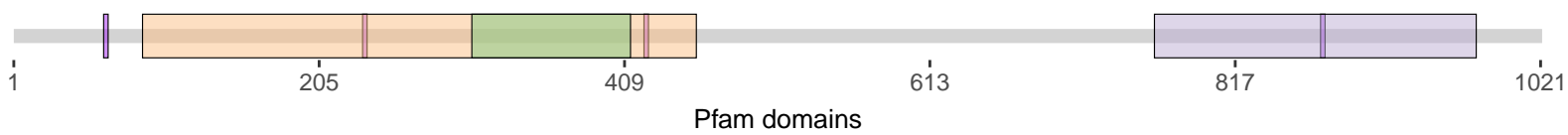
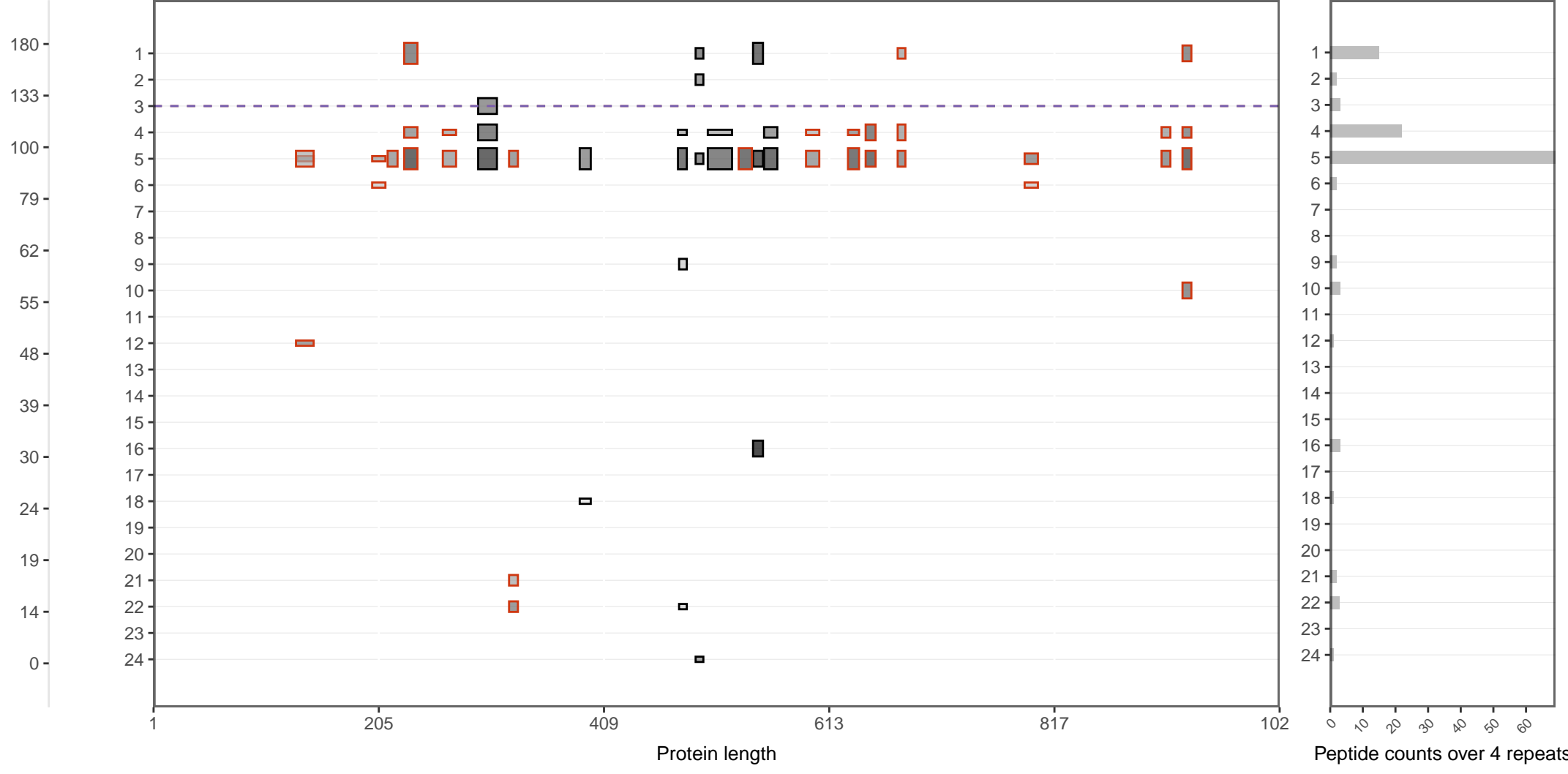
IGPNTCGPGSVPYBFSHPNVAHMEKSLKWMETLGRFAFRNNTVIDLCAAGTCFVRVPLQPLAKASGGVLLHDDDFGEAFQVNLGRASGRAAGSHGLLEVRGSEDFIVSGVIGPGEAAHVDNENETRNDDALVIQMLSVETQGSFALSMETKRIKRRDFVYFGFAKFSVDYVSGDITRIVTRLPRTVDSVSVSYLESVGDEVAVALIAKRTLRAKYANDALMFRVTVDERIKDITKFGSGMPKSKLYRFPRELSVLPPELLFHLRRGFLNGLIGHEDERSVLRNLFNAGFDL

NbL01g18920.1 protein_translocase_subunit_SECA1_chloroplastical [MW = 115.22 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP PF07516 SecA Wing and Scaffold domain
 Sequon TM Domain PF07517 SecA DEAD-like domain
 PF01043 SecA preprotein cross-linking domain

Protein sequence:

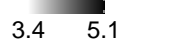
RMHIGGRPVLVGTTEVEGSDALSEQLREAGRHEVLAHPENVEREAIEVWQSGRLGAVTIATNMAGRGTDLHGGNAEFMARLKLREILMPRVAVRMEGVFVSAKPPKRTWKVYTESLFPICALGKEKTKLAEEVFAVFMWGTSLTELEAEERLSYSGEKGPIVQDEIVAKLRSAFLLEVRVYVYTEGEKKEAVSAGGLHVIGTERHESRRIDNQLRGRSGRGGDPGSSRFLLSELDNFRVFGDRIQGLMRAFRVDELPKEMTKALDEAGRKYENYFFDIRKOLF

NbL01g18890.1 protoporphyrinogen_oxidase_chloroplastic [MW = 59.65 kDa]

No. of times detected



log(intensity)



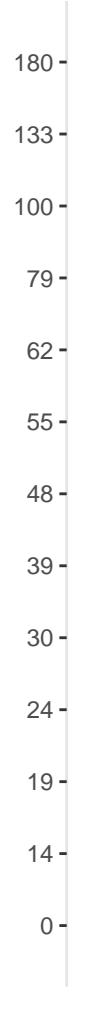
Values from



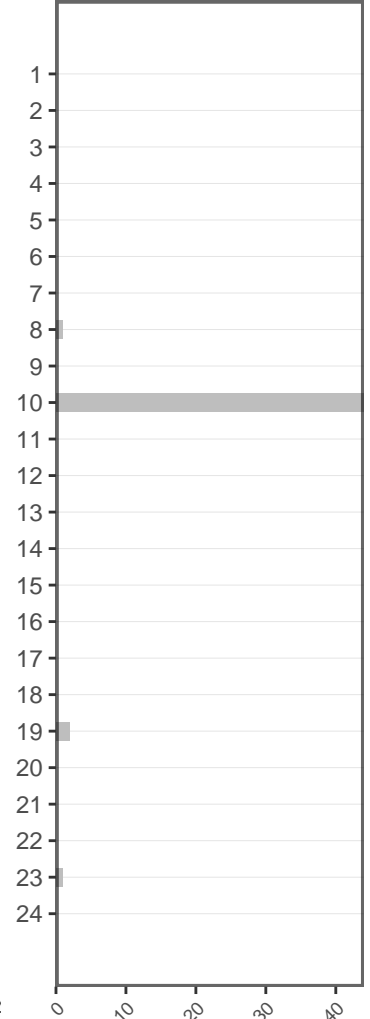
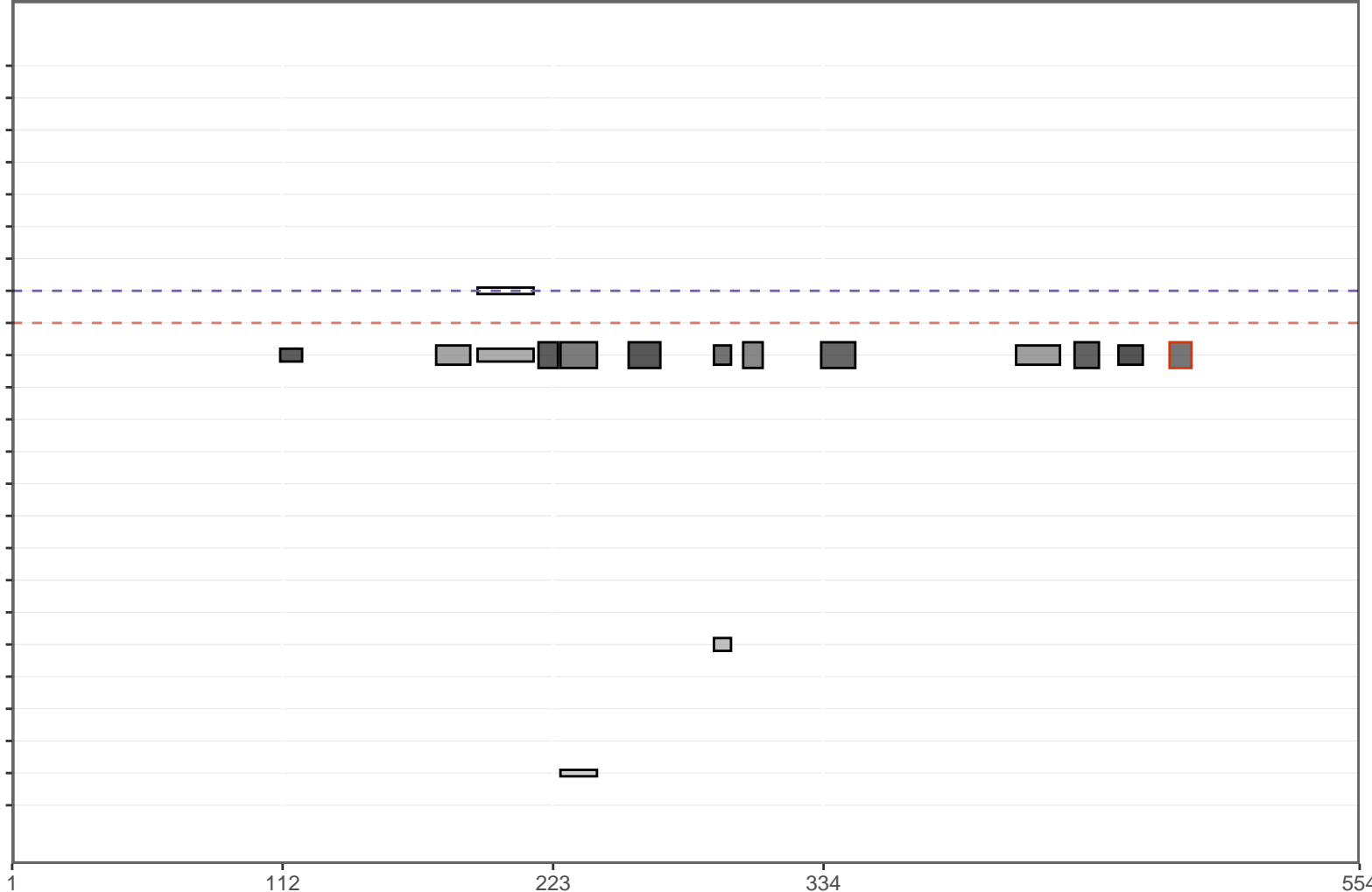
MW indication



Molecular weight

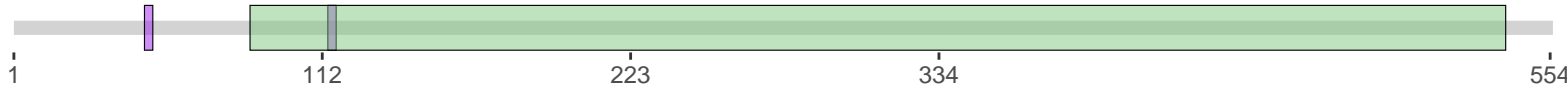


Gel Slice



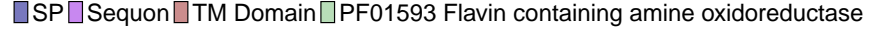
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IGGTFKAIKERSSTPKAPRDRPKPKPGQTVGSRFKRLRMLPDAISARLGGKLLGWKLSFTKSEKGGYRLETETPEGVVLLQGRSIVMTVPVYVWNLRLPWSAAADLGNFYPPVGVATVETVPGEARDERLVDGELKGFGLHPRRTGVEFLGTIVSSSFLNRPAPKRVLLLNHYGGAKNPEILSKTESQLVEVVDRLRKLMLKPKAQDPLVGVVIRVWPQAMPDFLVGHLDLSTAKAAMSDNGLGFLGGNYVSGVALGRGVGAYEVAISEVTGFLSRYAYK

NbL01g18700.1 probable_pre-mRNA-splicing_factor_ATP-dependent_RNA_helicase_DEAH2 [MW = 82.08 kDa]

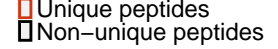
No. of times detected



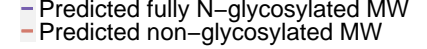
log(intensity)



Values from



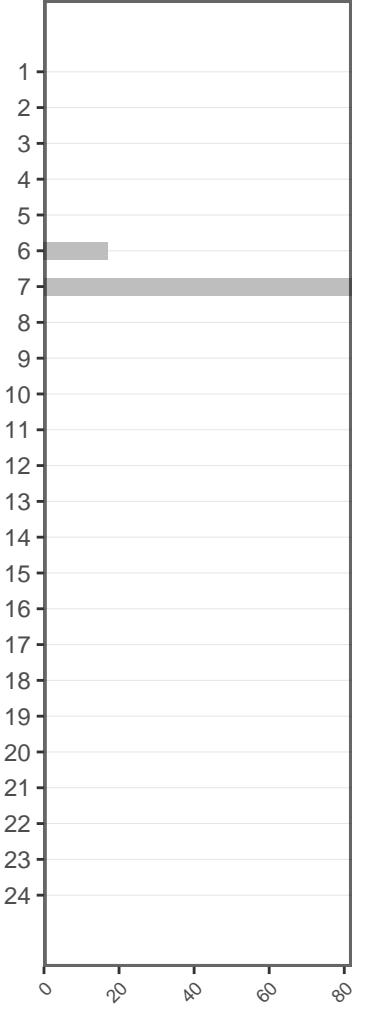
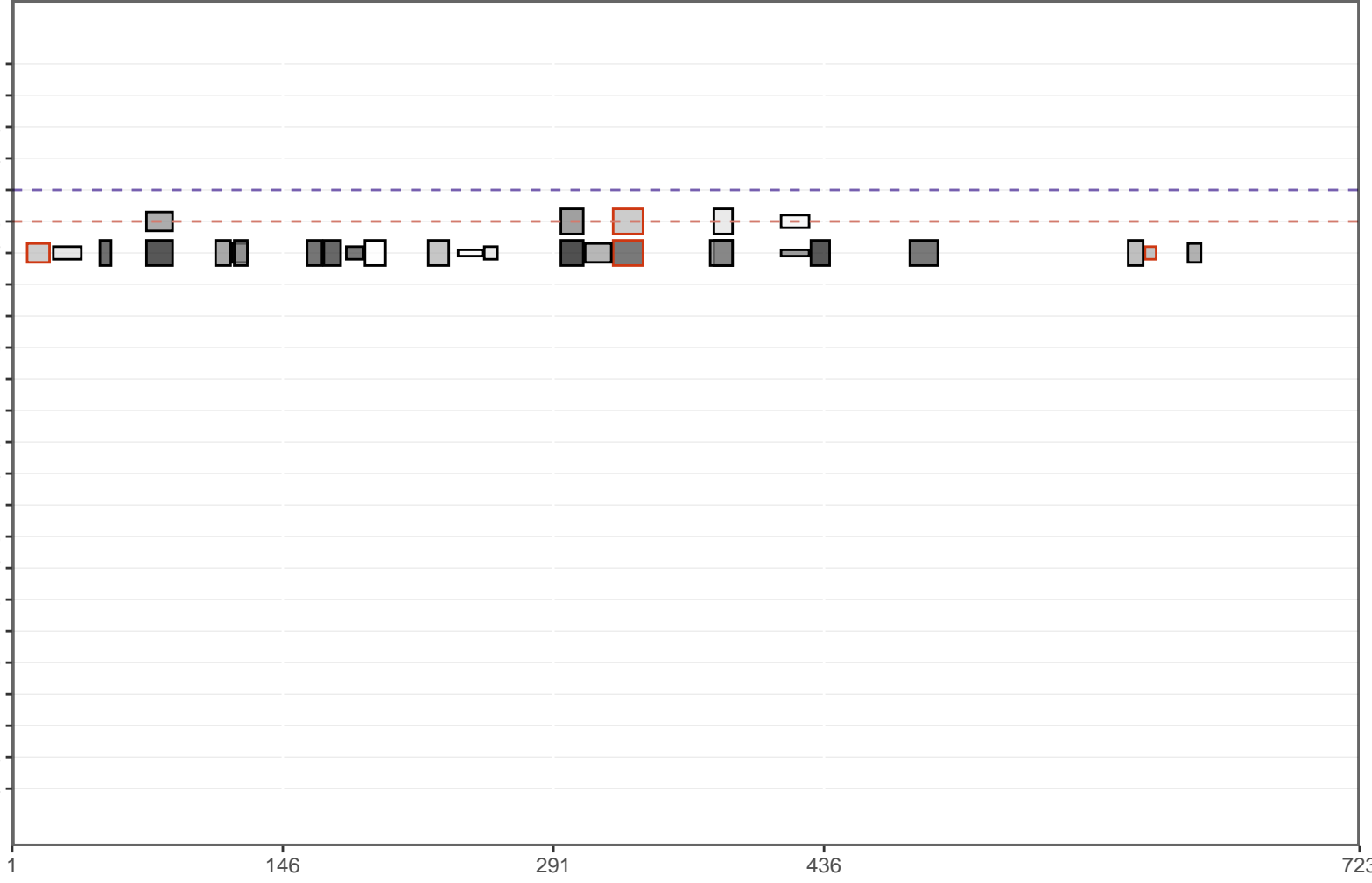
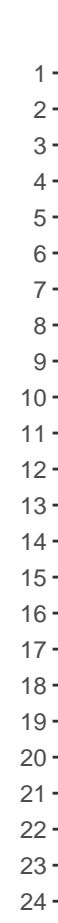
MW indication



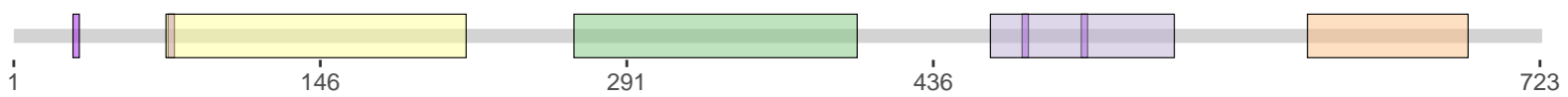
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

TSLTIDGIIVYIDPFGAKGKVVNFRVIRVESELLVSPISKASAHQRSGRAGRTPGPKGCFRLYTEKSFINDLGPQTYPEILRENLANITVLTLLKLGIDDLVHFDPMFAPETLMRALEVLNVLGALDDEGNLTRLGEMSEFPDQPMAMMLVVSSEFNCSNELISAMLSVPLNCFVPRREAGKKADEAKNRFHGDGDLTFLNYYHAYKNTEDPGQWYENFNGRAUKASDNVRRQLSRIMARFNKLCSTDFNERSDYYNIRKAMLAGYFMQVAHLERTGHYLTVKDNOV

NbL01g18690.1 long_chain_acyl-CoA_synthetase_1 [MW = 75.15 kDa]

No. of times detected



log(intensity)



Values from



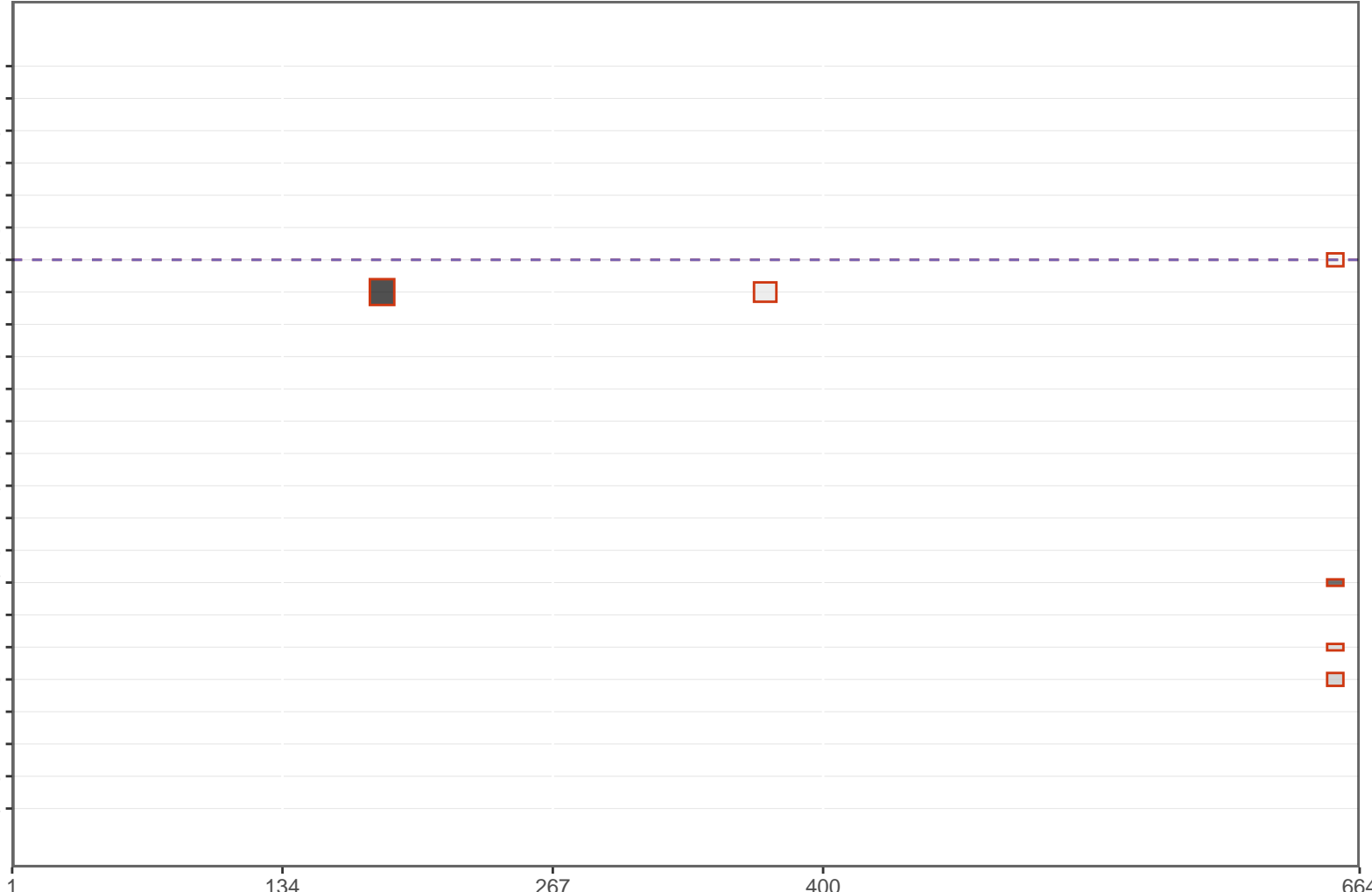
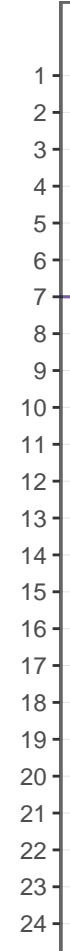
MW indication



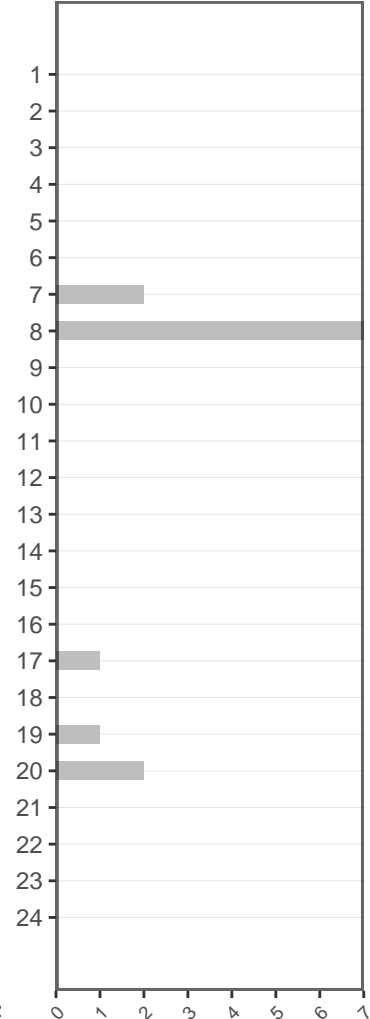
Molecular weight



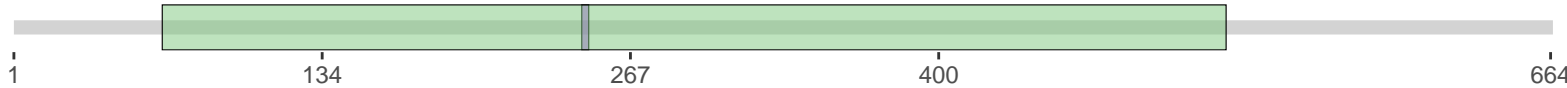
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

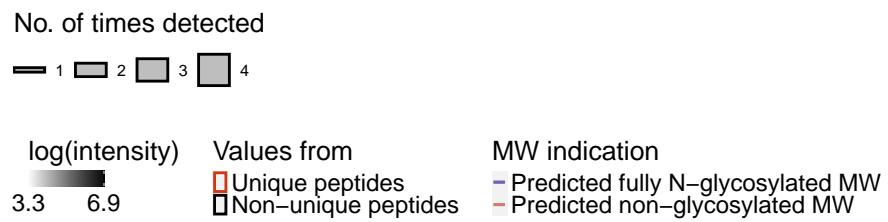
Pfam Description



Protein sequence:

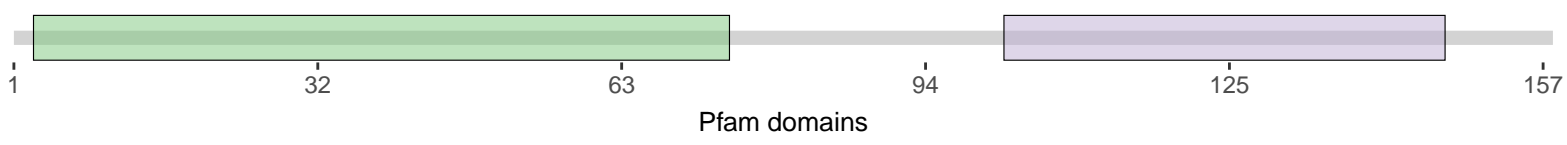
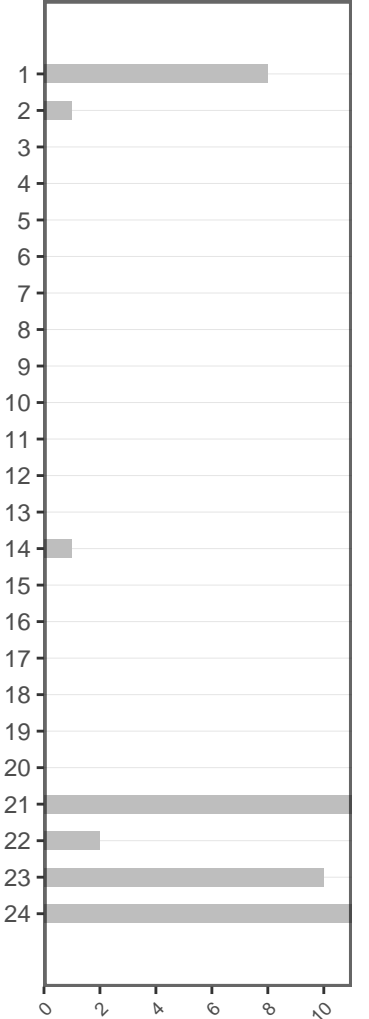
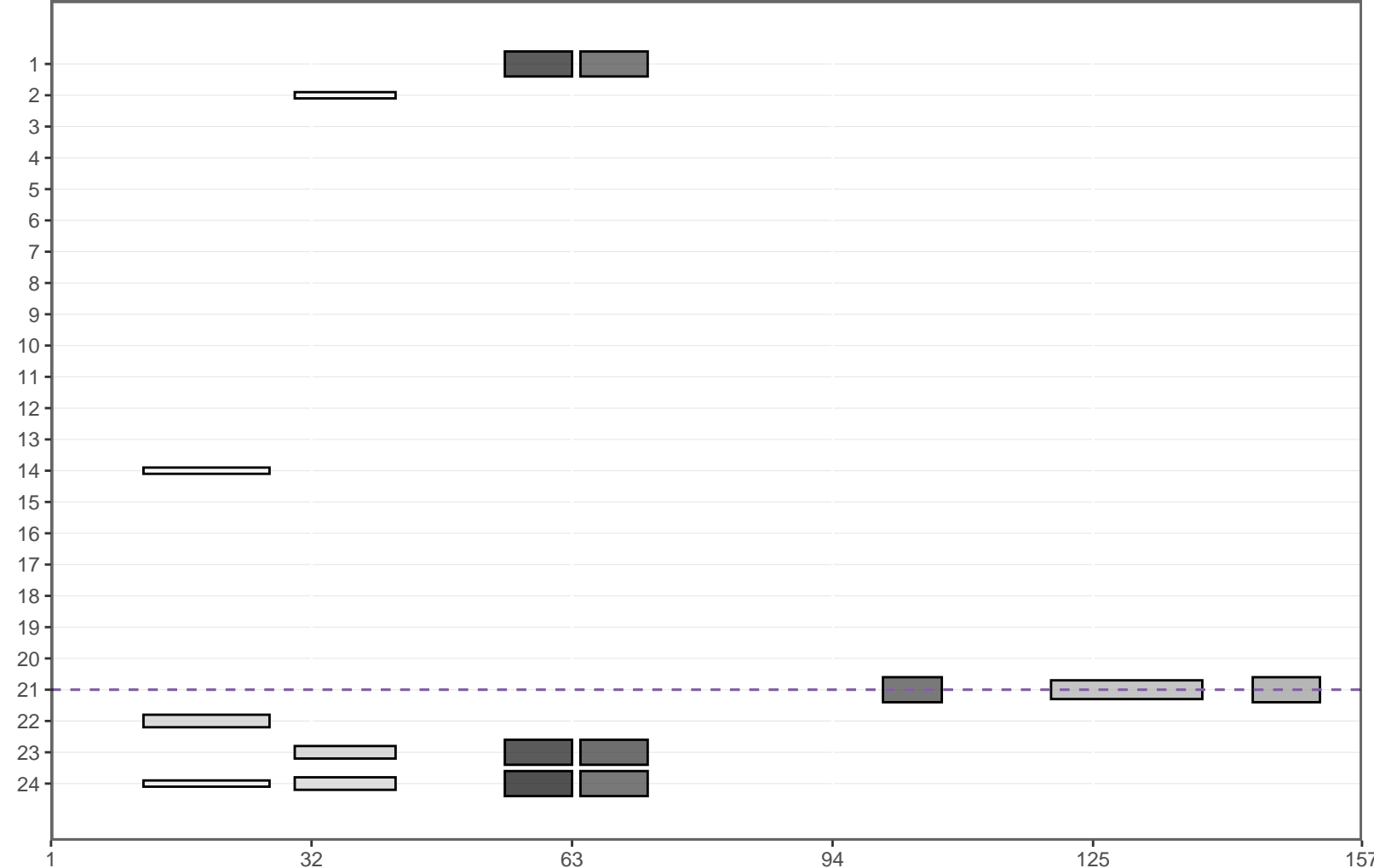
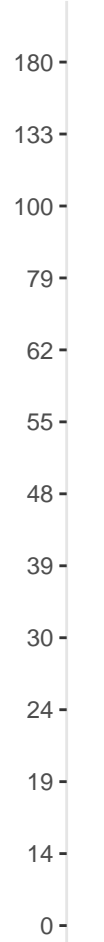
*LAGVPRVYEKHEGVKALGELNPFRRSMFHILNYKLLWMLGKYGKQYASPLADLLAFKWKVNRLLGGRIILVSGGAPLSTVEVEFLRVTSGGFVLOGYGLTETGSLATIGHPDEMMLGTVGPPFVTEVRLLEEVPDMGYHPLGGPRRGEICVRGRTAFTGGYKNGELTRVVKDGVWFHTGDGEMLPNGVYKIIDRKNVYKLSGGGEYVAMELEKYSIAPIEDWVYGGDFSNMLVAVVPHREGNTRKWKADGNGHKSGPELGLGELNHYLLELTAERKLRGF

NbL01g18620.1 ubiquitin-40S_ribosomal_protein_S27a [MW = 17.7 kDa]



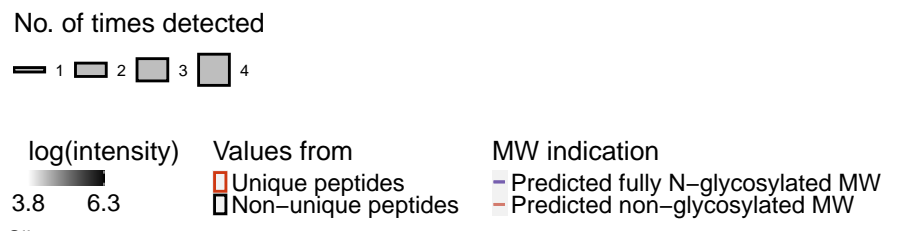
Molecular weight

Gel Slice



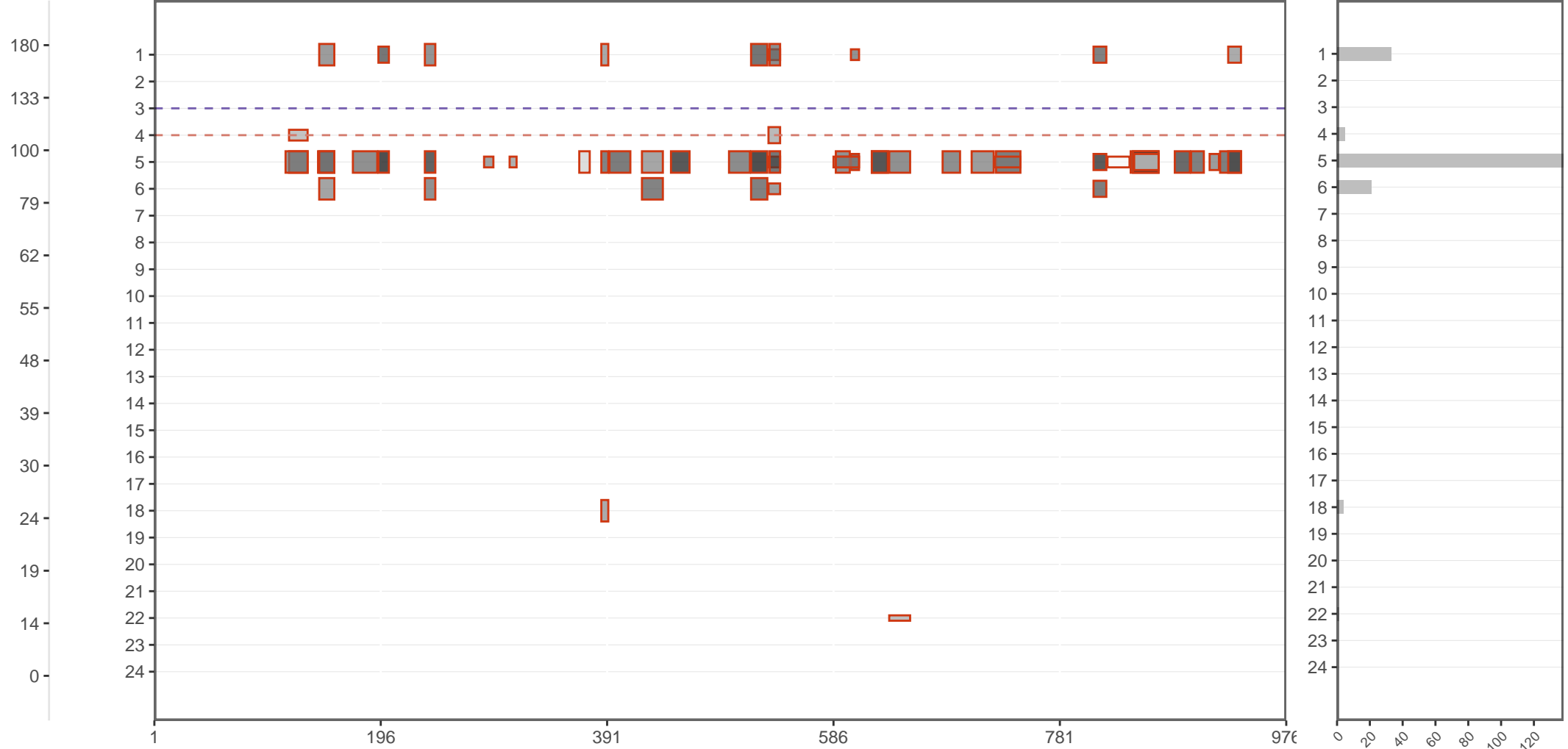
Protein sequence:
HLVLRRLRGGAXKRKKTKYTKPKKKKKKKKKVRLAVLQFYVVDGSGKVGRLRKEGPNAEQGGTFMANNFDRHYGKGGSTVYVKKAGAD

NbL01g18510.1 probable_glutamyl_endopeptidase_chloroplasmic [MW = 108.47 kDa]



Molecular weight

Gel Slice



Peptide counts over 4 repeats



Pfam Description
 SP Sequon TM Domain PF00326 Prolyl oligopeptidase family

Protein sequence:

VGDDTLALVYESWYKTRKVRVWSPGSENVNPHLFRDSEEDVSDPGSPMSRRTPAGTYVIAKVKKEDDDGDTYLLNGSGATPEGNPFLDLFDINTGSKERIRWQSNKEKYFETVALMSDDQKEGELSNKILKILTSKESKENTENTGYLLVSWPEKKKAGITNFPHPQLESLGKEMIRYGRKDGVLQATLTYLPPGYDPSRDKPLGLVWVYDFEFKSKDAASQVIRGSPNEFAGKGFPTSPFLWLARRFAVLSGPTIPIGEGDDEANDRVEQLVASEAAVEEVRIRGVDI

NbL01g18490.1 calvin_cycle_protein_CP12-2_chloroplastic-like [MW = 14.06 kDa]

No. of times detected



log(intensity)



Values from



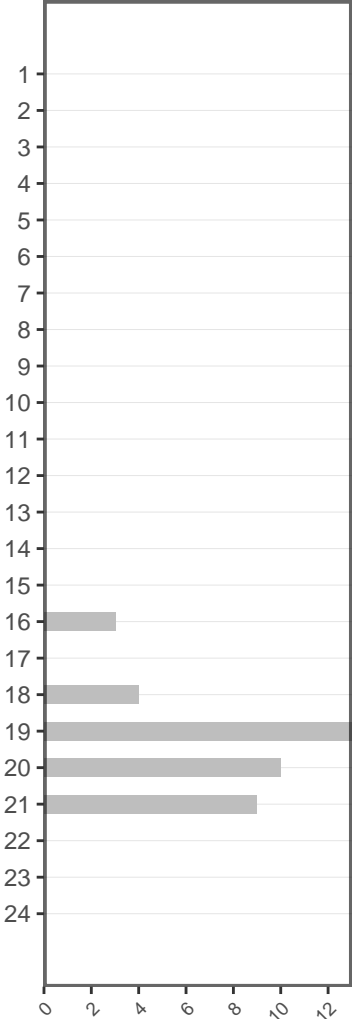
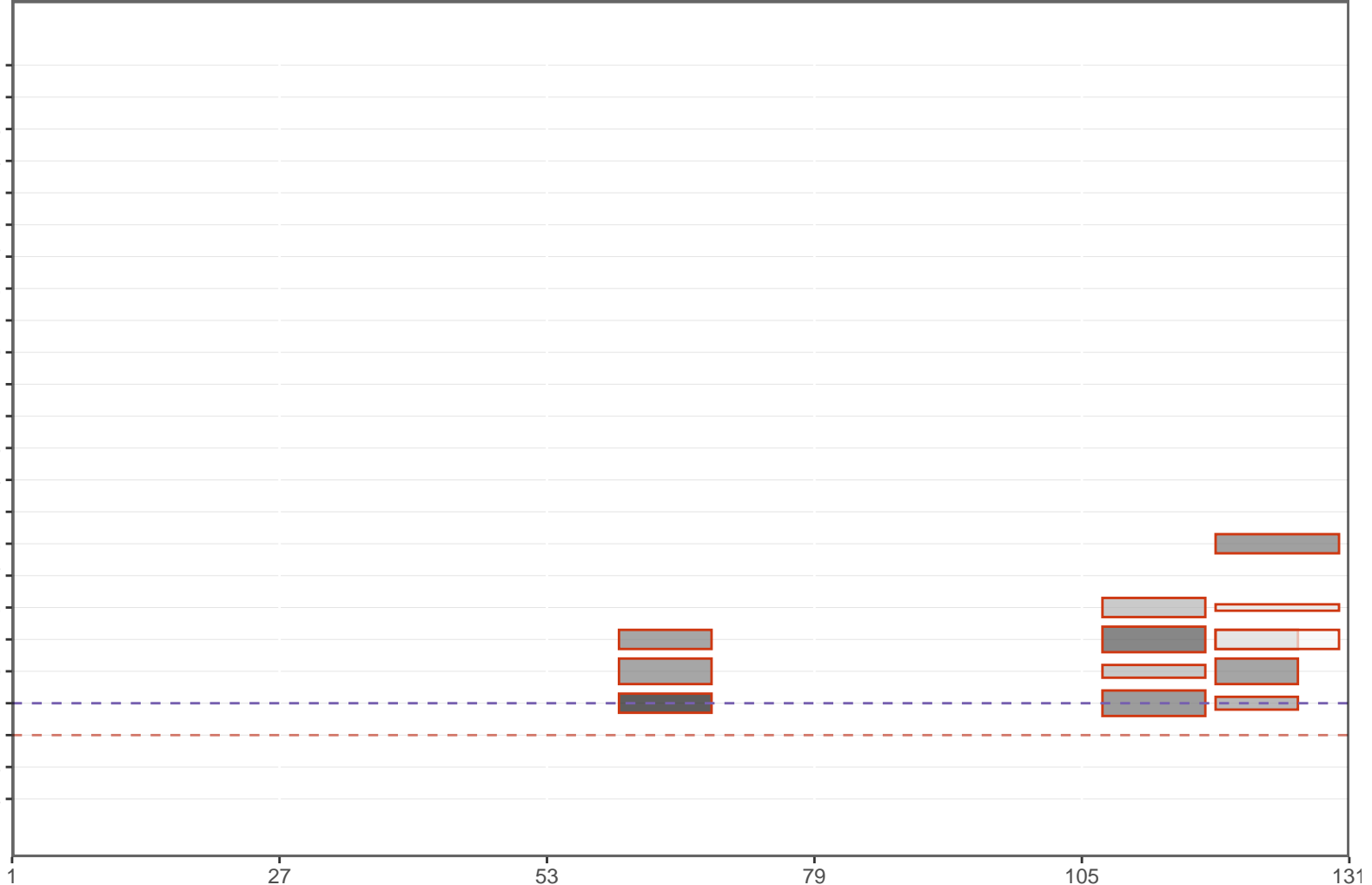
MW indication



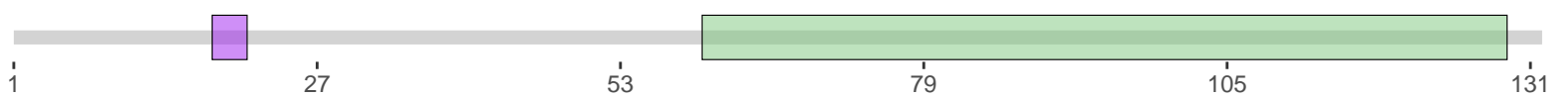
Molecular weight



Gel Slice

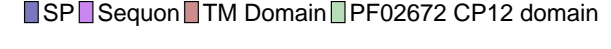


Protein length



Pfam domains

Pfam Description



Protein sequence:

SAAPDKLSDLVADSVKGAEEAGSENPASGEGCAAAWDDVEETSAAMASHARDKQKQNSDFLEGYCKENFETDECRVYDN

NbL01g18390.1 uncharacterized_LOC107787269 [MW = 18.71 kDa]

No. of times detected



log(intensity)



Values from



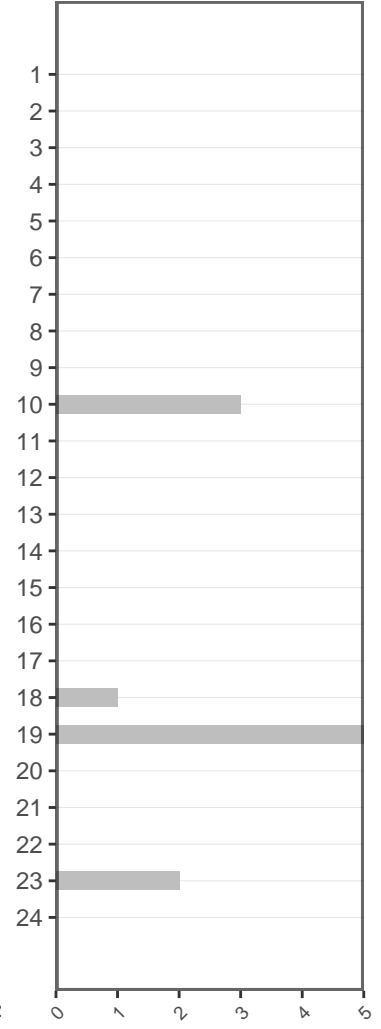
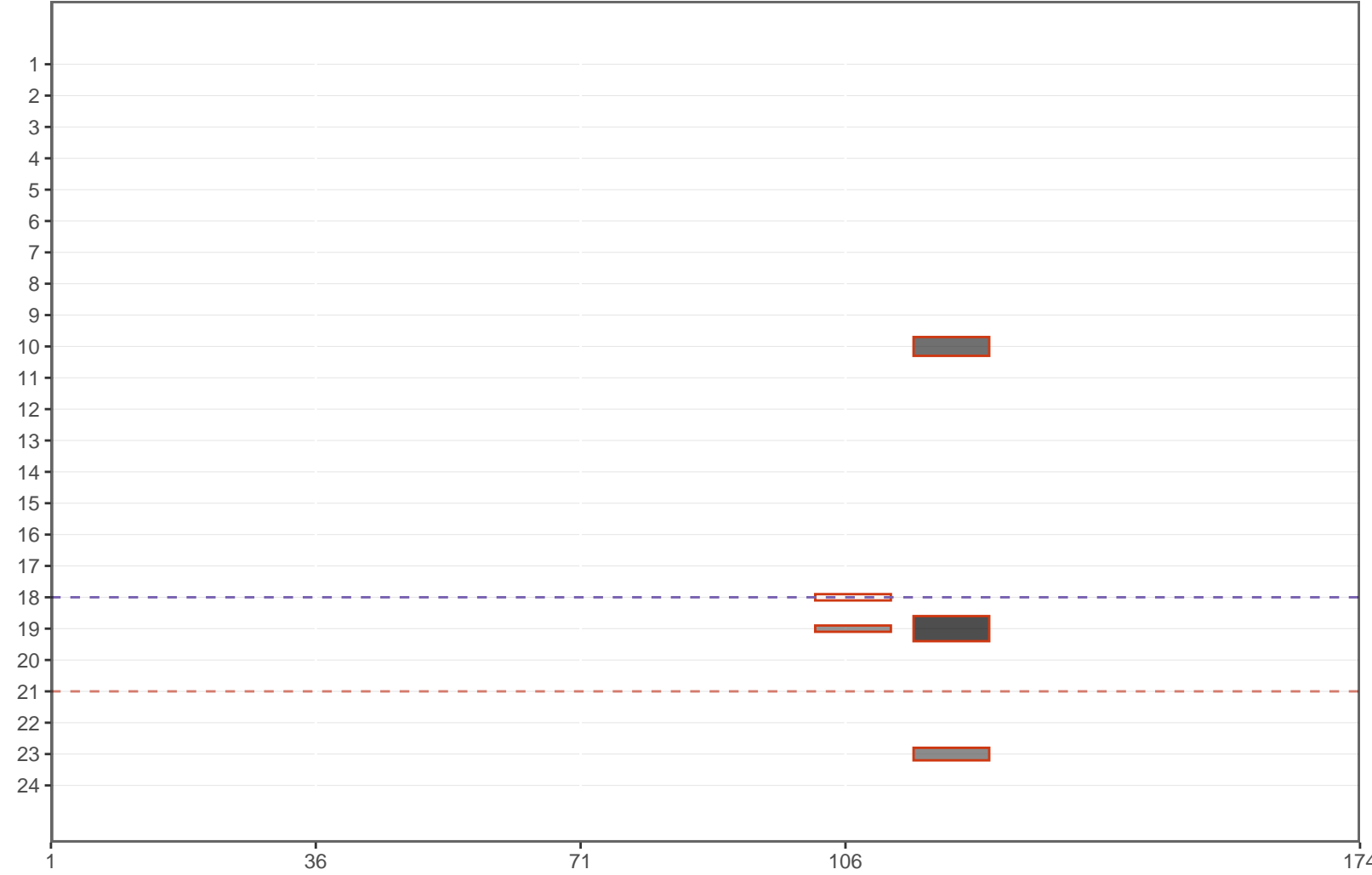
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

SELKLPDASVLLNSPQWVGYMTDHSRVAAMAENASRKRKRDINVSASTYPRSKIPKGTLPKMKNNVPEFGSGLVPPQLAGRSNVYTEDSKLFVKVQTPS

NbL01g18300.1 protein_transport_protein_Sec31A-like [MW = 121.97 kDa]

No. of times detected



log(intensity)



Values from



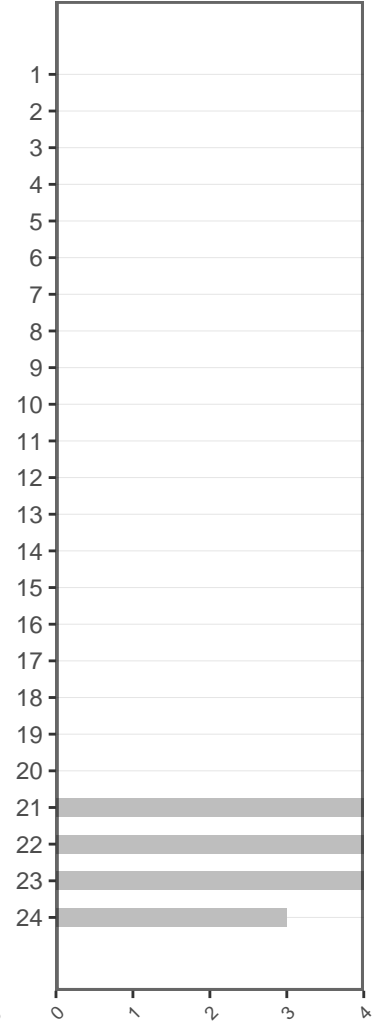
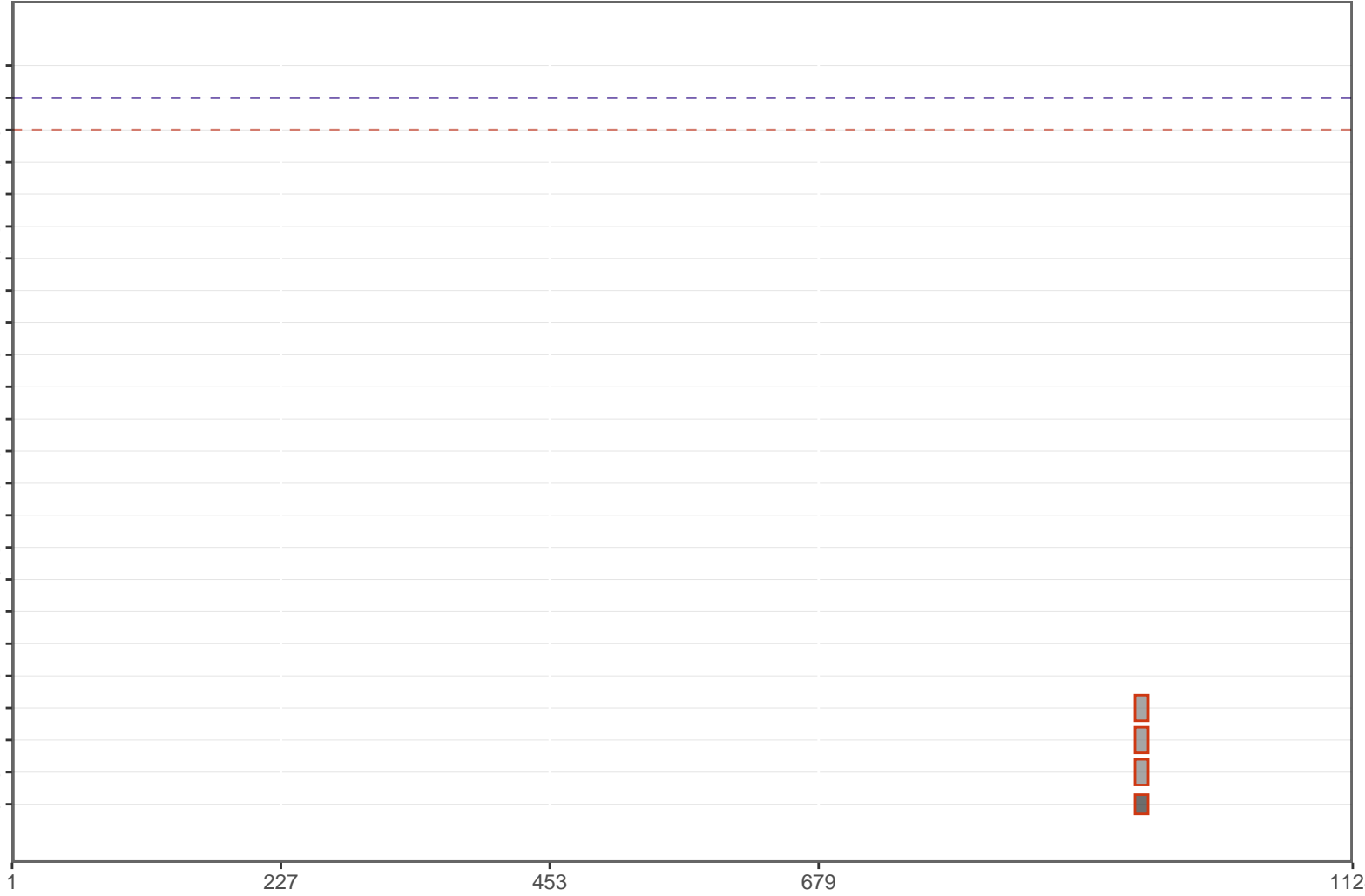
MW indication



Molecular weight

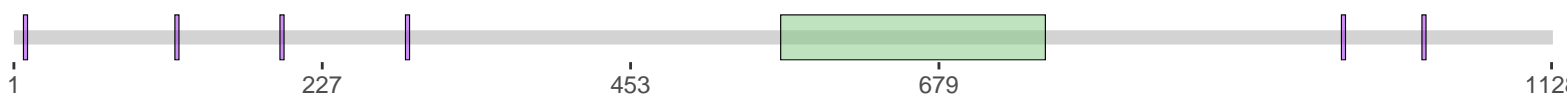


Gel Slice



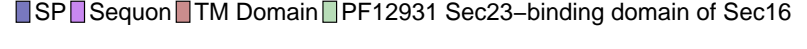
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DVQEEASDASFDFTVQRIALVGDGKVAWQIGSINRMADALVAHVGGASLWEGIRDGHKASGSSKLRVVAAMVNDMLMLVNRPLKQWKEFLALLGTFAPDQEWTSLSGDTLASRLLAAGETLPTFLCHYGAGNDKTIHWRSRLAEKRDKGKVVLLDGLDKMKTIVFALATGGKRFASLCKLLEKVAELASGGLLTAMEVYLLKMGSEELSPELTLRDRIALSTEPKWDKSKSMFQNSQLHSGGGYVADQGGYGMVDFTHYVPEGPKPKPQPSINSPIYENYQOPI

NbL01g18230.1 serine_carboxypeptidase-like_40 [MW = 33.34 kDa]

No. of times detected



log(intensity)



Values from



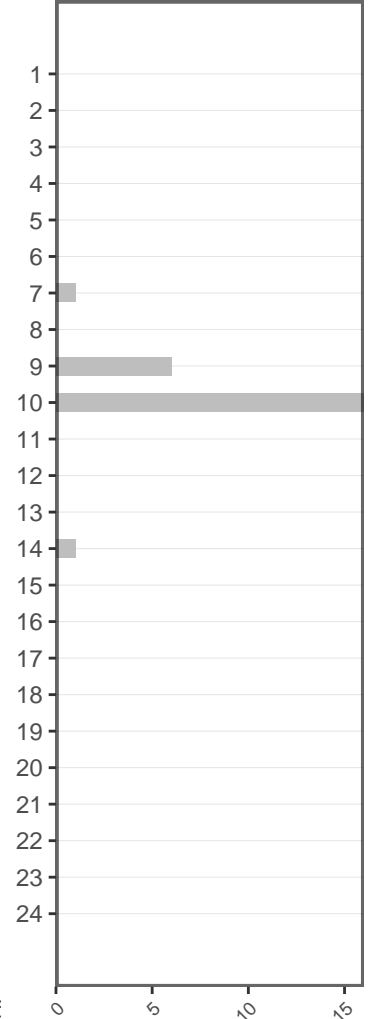
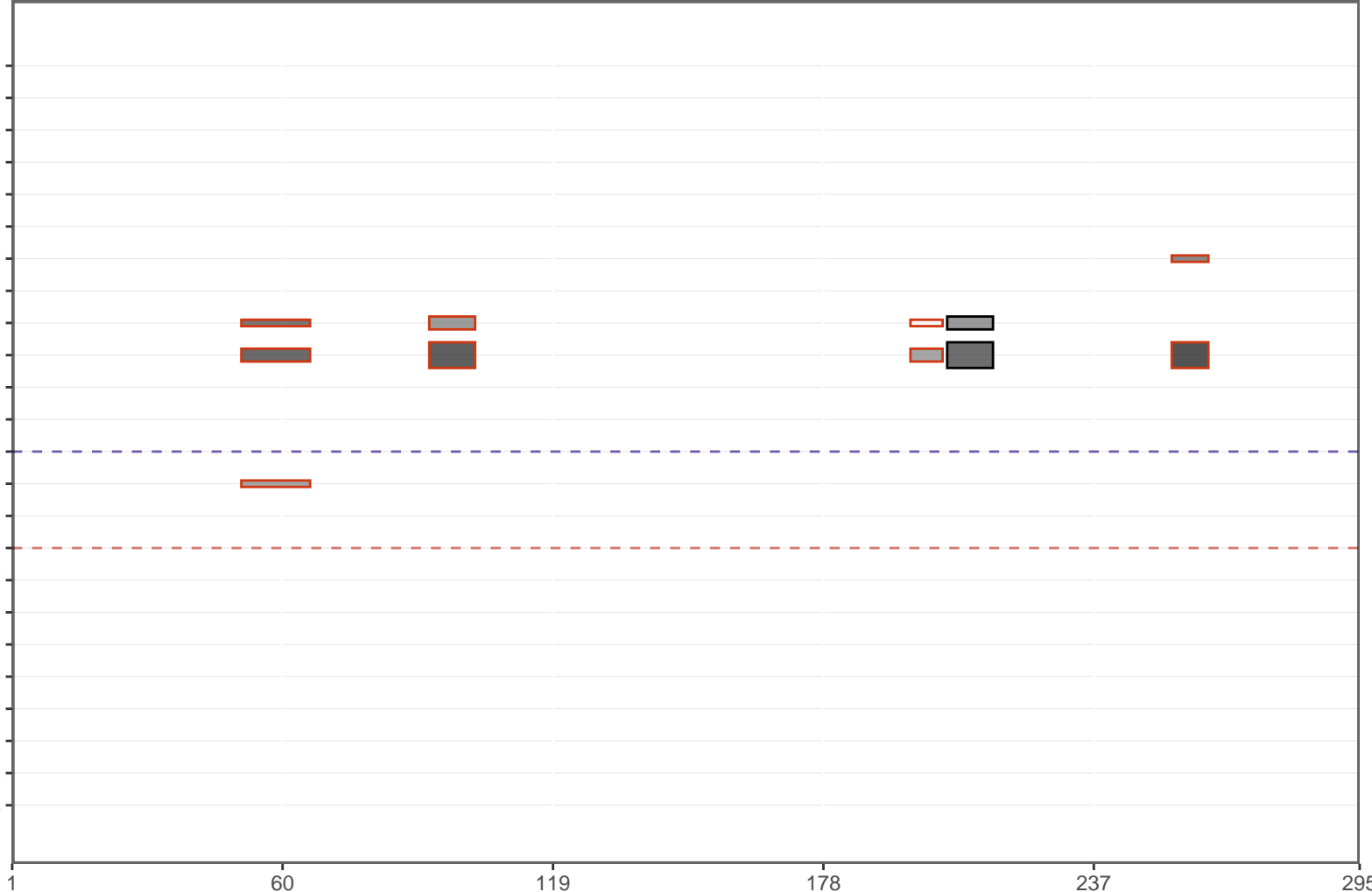
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PSLVDPCCSDYTYIANNRPDVGNAHANNVTKYKSNVGPCCGDAVLTNWFDSSTVPLLRREFMANGLRVWIFSGDIDGRVPTVSTKNSIKMKLPKTAWHIPWLSAEVGGYTVQVYKGMDFATVIRGTGHQVPEYEAARSLSLVMHFLAGTNLPDKHT

NbL01g18210.1 N-alpha-acetyltransferase_11-like [MW = 21.2 kDa]

No. of times detected



log(intensity)



Values from



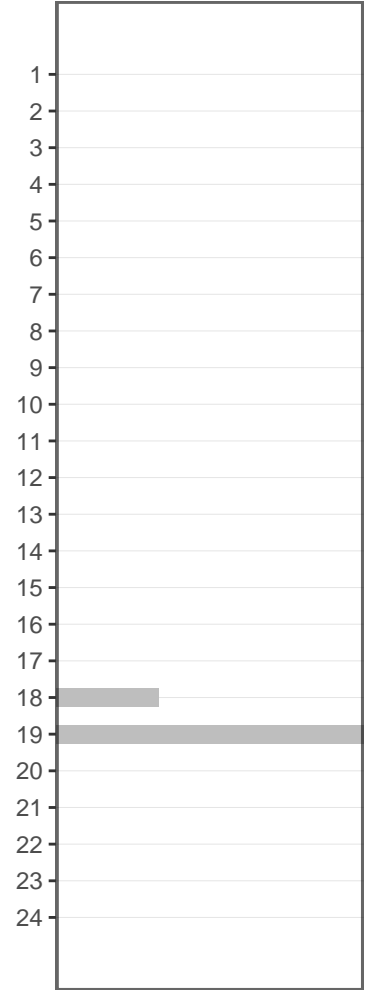
MW indication



Molecular weight



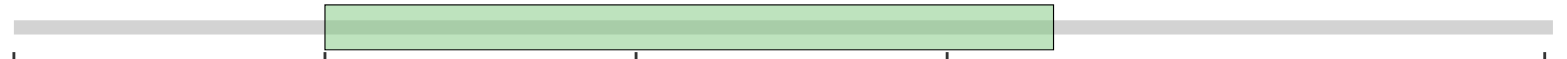
Gel Slice



Peptide counts over 4 repeats

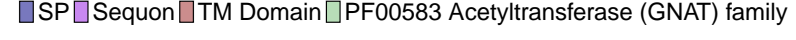
1 39 77 115 188

Protein length



Pfam domains

Pfam Description



Protein sequence:

KLGIATKLMTAACQNAMEQVFGAEYVSLHVRKSNRAAFKLYTETLGVKHDMEAKYVADGEDAVDMRKELKGRKHQDHHHHHHGGGGGSGEAKIGAKEGAAEAQAA*

NbL01g18140.1 subtilisin-like_protease [MW - SP = 79.9 kDa]

No. of times detected



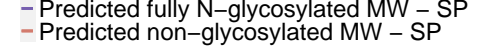
log(intensity)



Values from



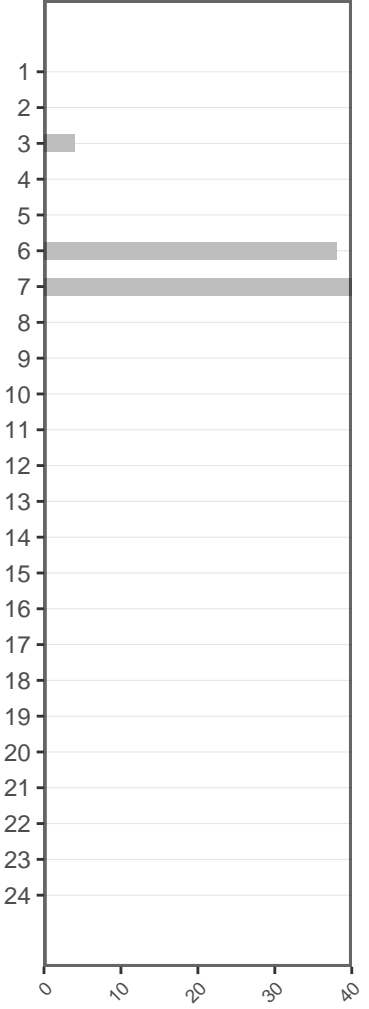
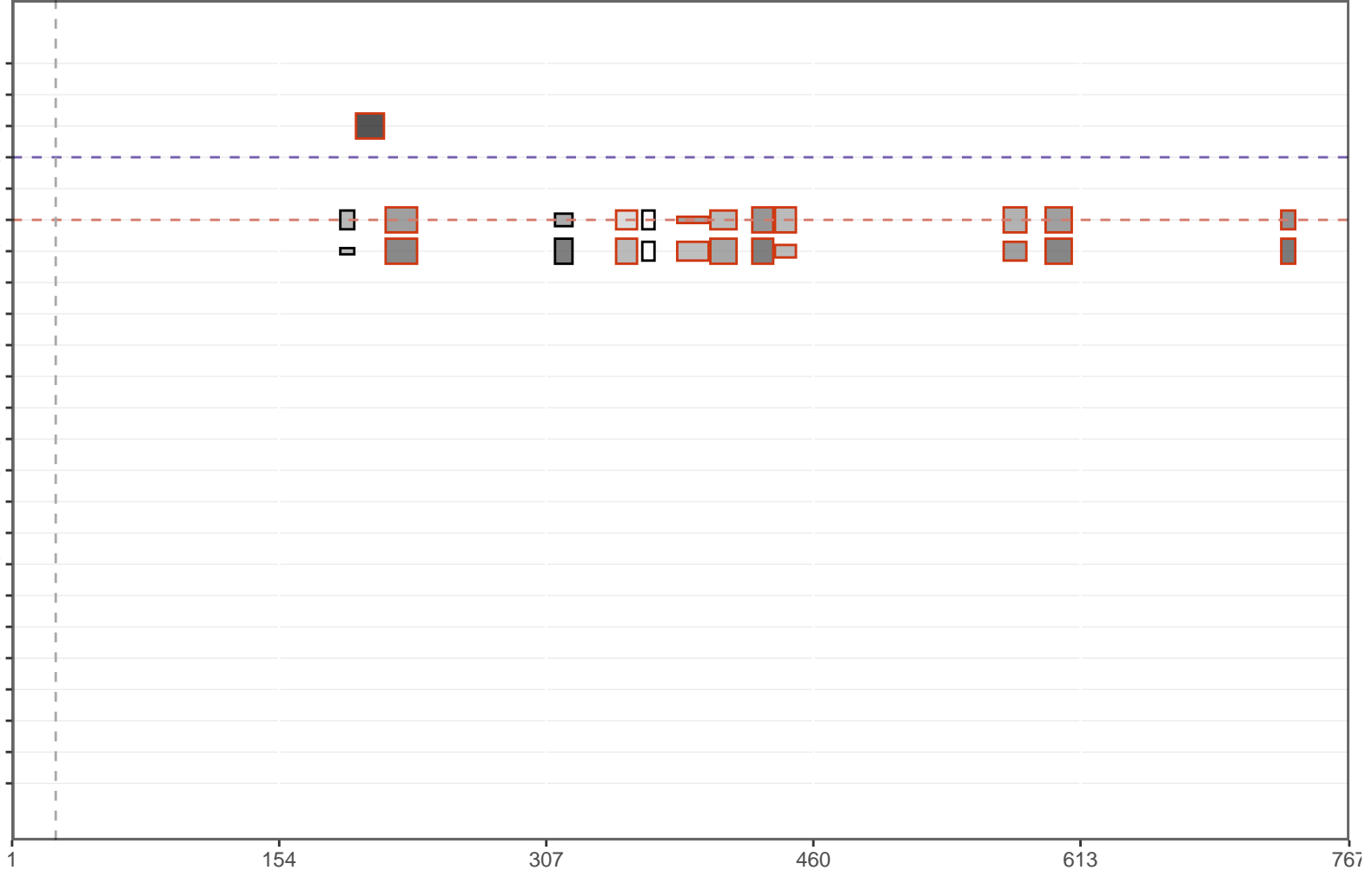
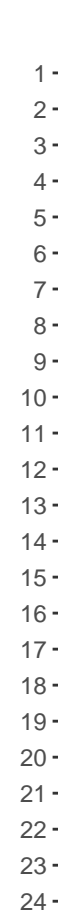
MW indication



Molecular weight

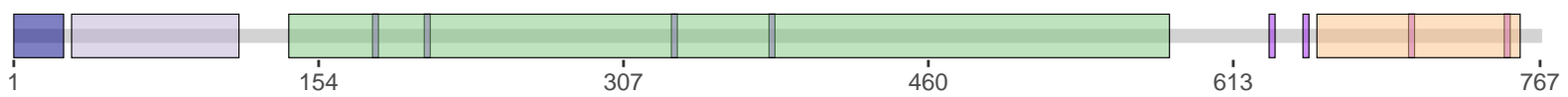


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

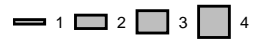


Protein sequence:

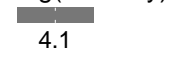
*ARAVKDSITYVYKNTFLADGNSSELL6QL6DPERTHHIGEDNGDFSDQMIRVTRARKAGIRISEDPGVFRSATFPNGVYVWKKEGKGVVYKNTVDPTATFTGQETVLDVTPAPVVAASBARGPSR6YLGAKPDLAPGVLLAAVPPVNFATGIGPNIEL6TDVILEEGTMAAPAAAGIAAMLKGAHPEWSPSAIRSAMMTADPLDNTFRKPKDSDNKAATPLDMSAGHYDPNRLDPGLVYDAPTPGDVYVNLGSLNFTTEEGKTIAR6SDNHN6N6R6ADLNYPSFYALYPLI

NbL01g18130.1 protein_RETICULATA-RELATED_4_chloroplastic-like [MW = 41.04 kDa]

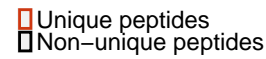
No. of times detected



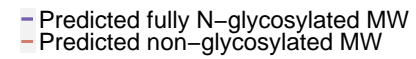
log(intensity)



Values from



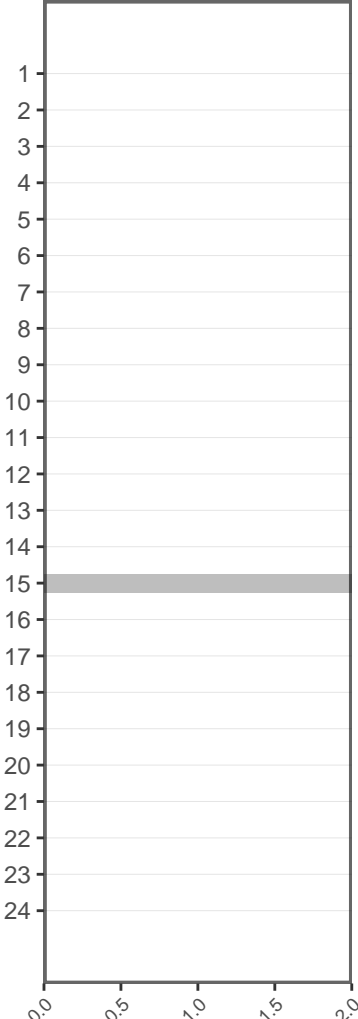
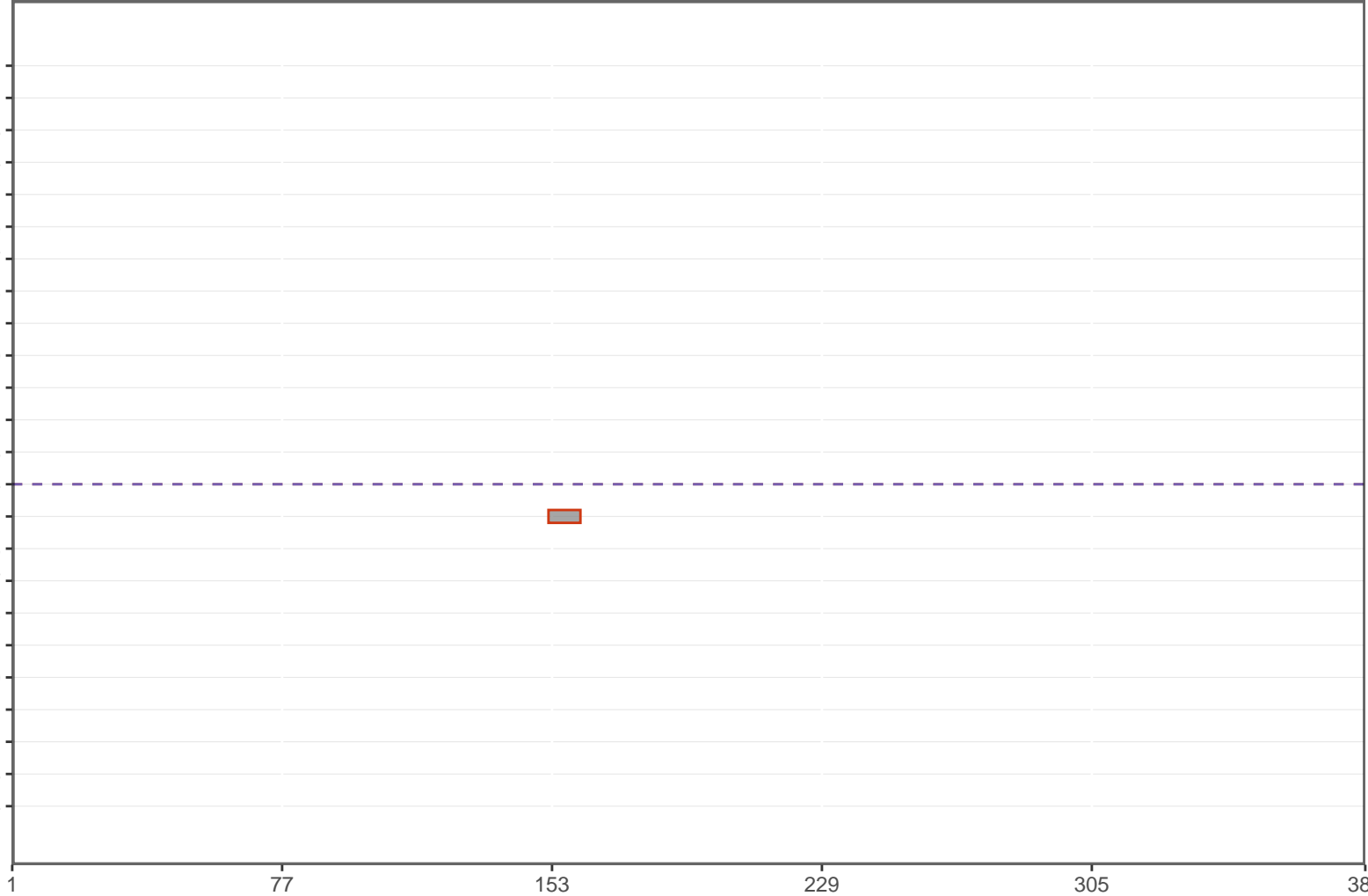
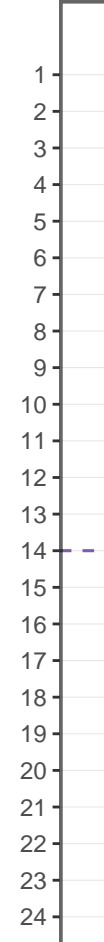
MW indication



Molecular weight

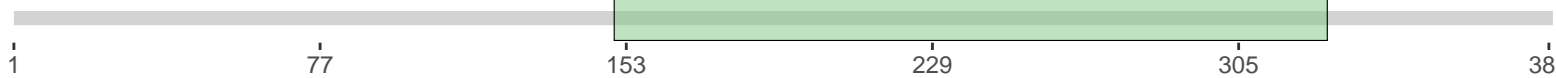


Gel Slice



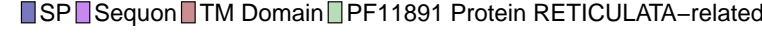
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LELEKRRNFKNLEDFVCAQVMAVAADFMILWLPAPFVILRPSLAIGAGLRIFFYQPDNAFGVYVLAGTSYTFLLGRIGAVIRNGAKLFAVGGSGASLGTGVYTNGLNARKAIDKTFAGEAEDLPILPTSAAYGVYMAVSNLRYQLAGVIEGRILEPLLHKHKLKALGDFVFRGTGNTFLGSLMWDFAFWIGIGRSGEKET

NbL01g18110.1 50S_ribosomal_protein_L1_chloroplastic [MW = 37.1 kDa]

No. of times detected



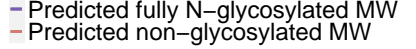
log(intensity)



Values from



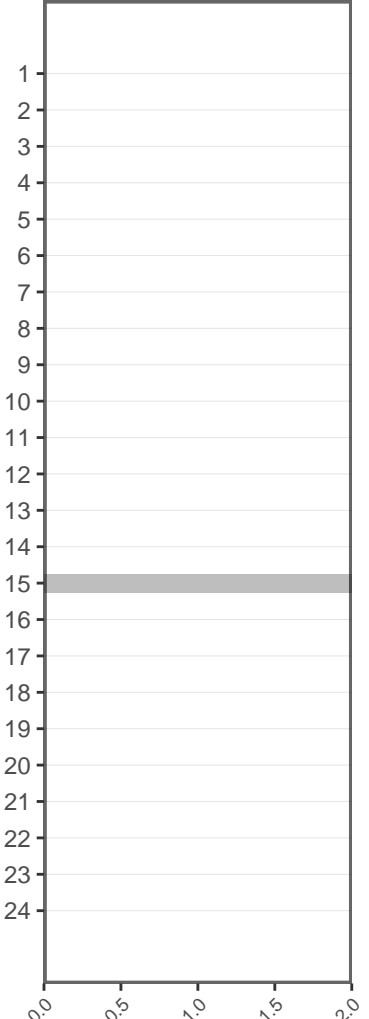
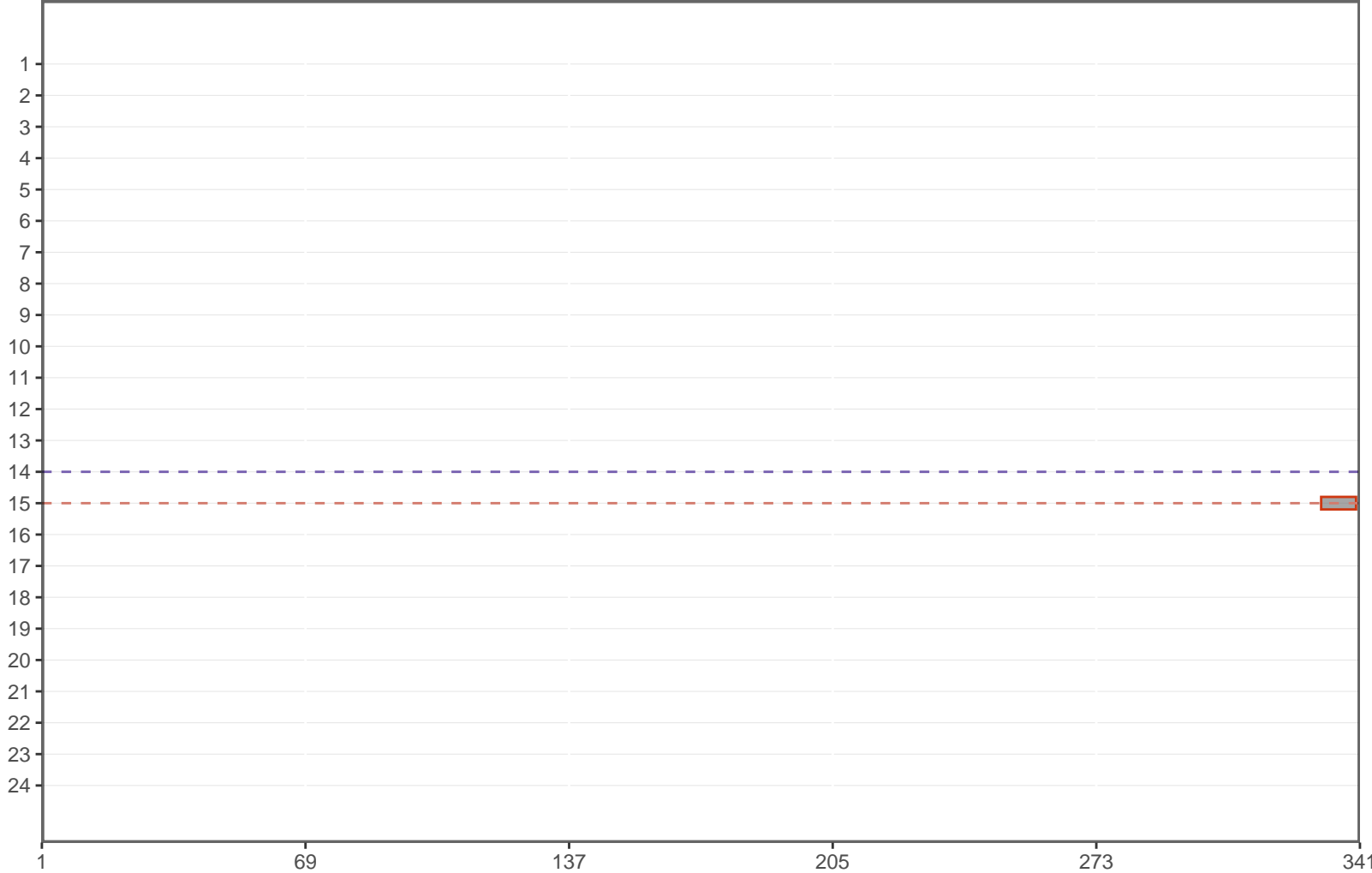
MW indication



Molecular weight

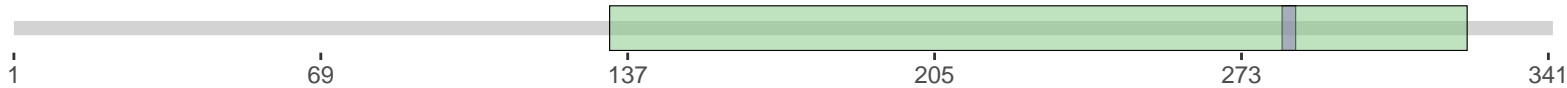


Gel Slice



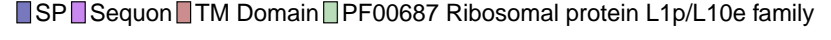
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IQQLRATVNLPKGTGGTVKWWLFDGKFDKAEAKNAGADLVGGEDLQEGKGGFMDFDLATPDMMPKVAWLSLGRILGPRGLMFPKAGTFTTNPGAEFFKQKVEVRAADKTVGHVLPFGKAFSEEDLINFIAAVKSIENKPGGAGGVVWKSAAHVGSMSMPSGIRLNVREMLEYKLPNT

NbL01g17920.1 uncharacterized_LOC104211372 [MW - SP = 37.65 kDa]

No. of times detected



log(intensity)



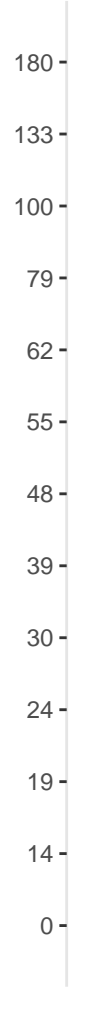
Values from



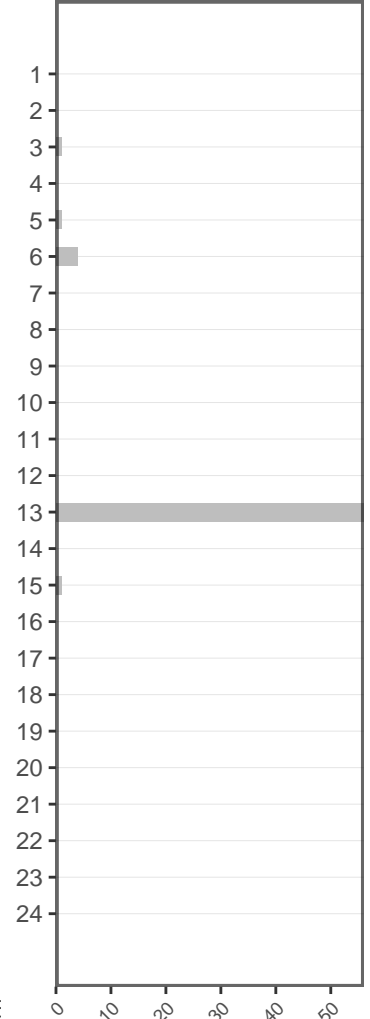
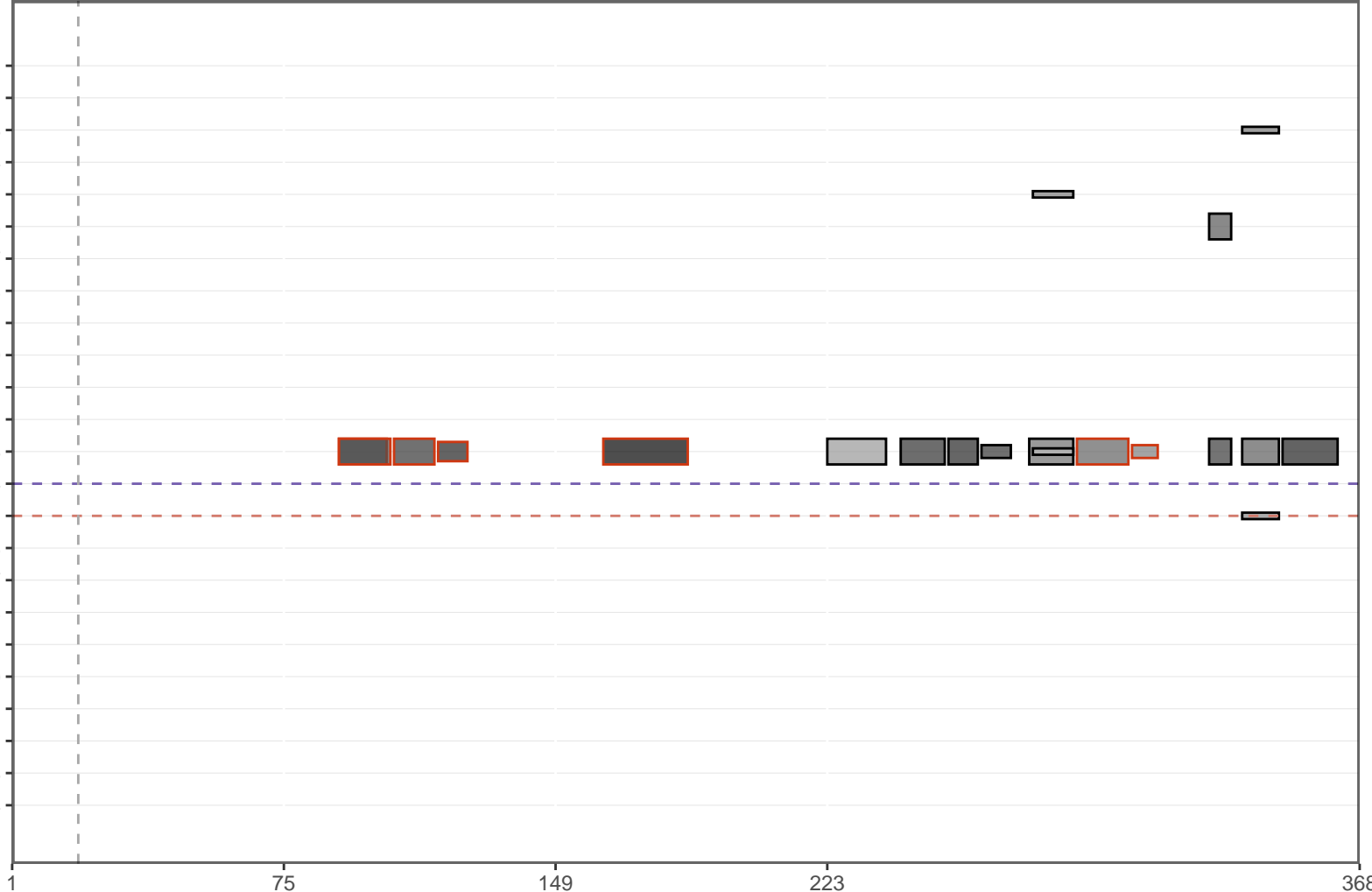
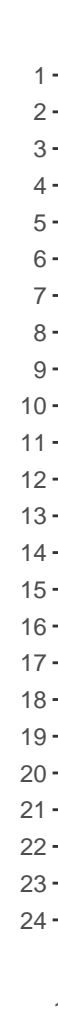
MW indication



Molecular weight

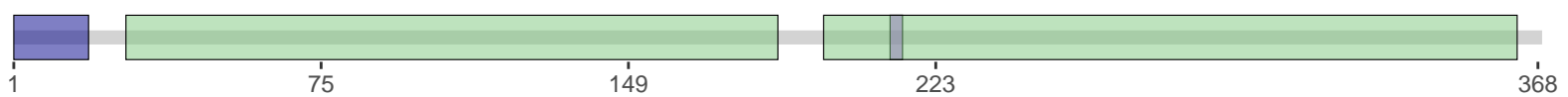


Gel Slice



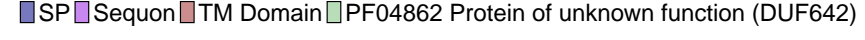
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

QEDPKCGPLLDAAVAKELFPQPTTRVNLVKNPGFEQPHLLNSHGVLLPPKGEDTSLPLPGWIEELKAVKFLDGAHFNVFFGRAAVELLAGRESAIGHRTVPKVYVAFYVGDANNGGCHGDMMEAFAAKETKVPKSGQKGSFKTVSKFKFTAIADRTTRITFYSGVYHTKINDYGLGCPVDEIKVTPW

NbL01g17560.1 thylakoid_luminal_19_kDa_protein_chloroplastic-like [MW = 26.68 kDa]

No. of times detected



log(intensity)



Values from



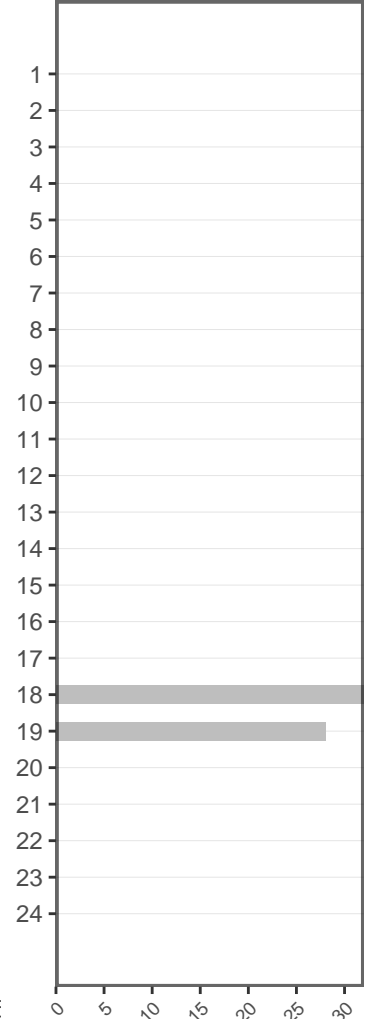
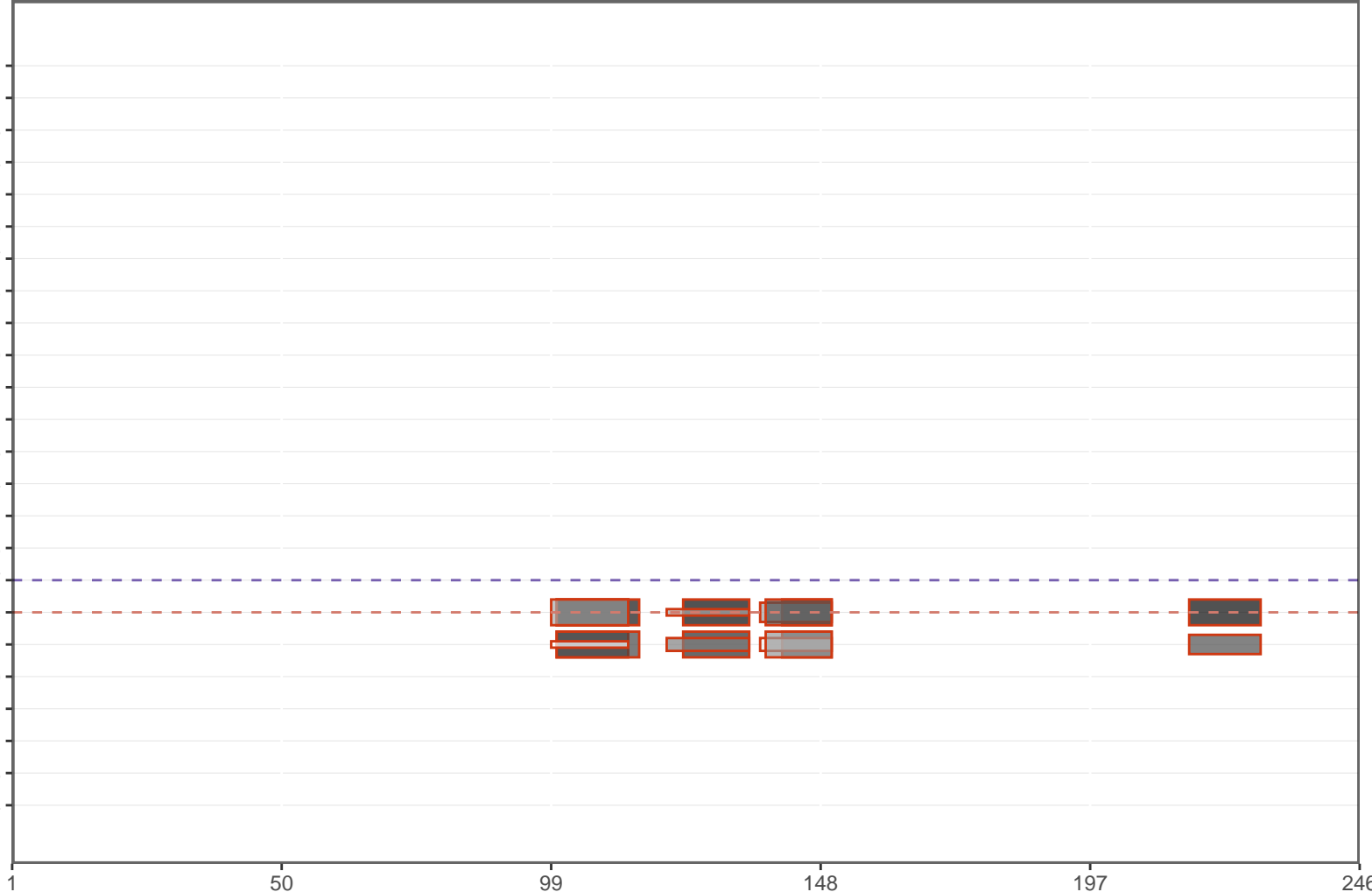
MW indication



Molecular weight



Gel Slice

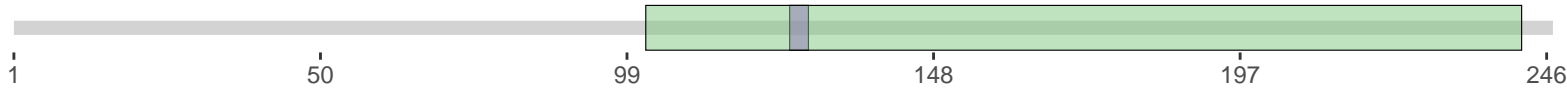


Peptide counts over 4 repeats

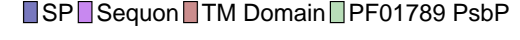
Protein length



Pfam domains



Pfam Description



Protein sequence:

VKERLVSKVEKGTNGTDFSEFYNPKKTEKEYLTVLAGFRQLAPKDAVNLNIALGDVNLGDIIANADSVTSEERKDENGQLYDVEIDGVAHSLITVCAKNNKYAHEVNAAPAEWKKDQDGLRHIIHQSFKTVG

NbL01g17470.1 uncharacterized_LOC109241047 [MW = 76.43 kDa]

No. of times detected



log(intensity)



Values from



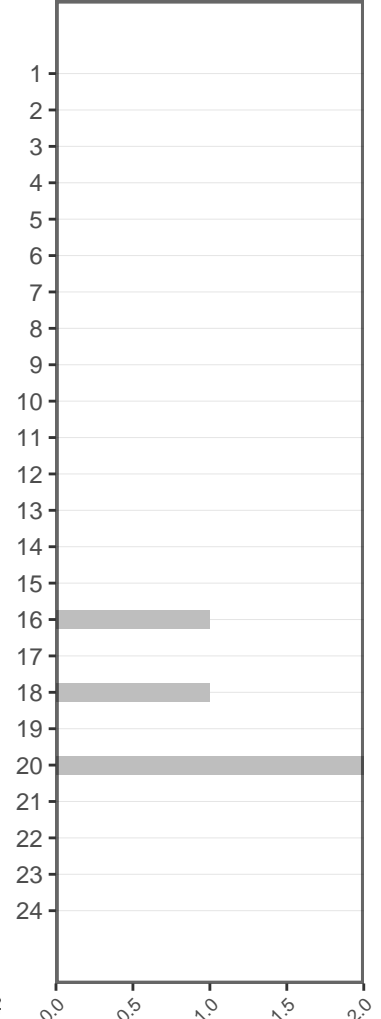
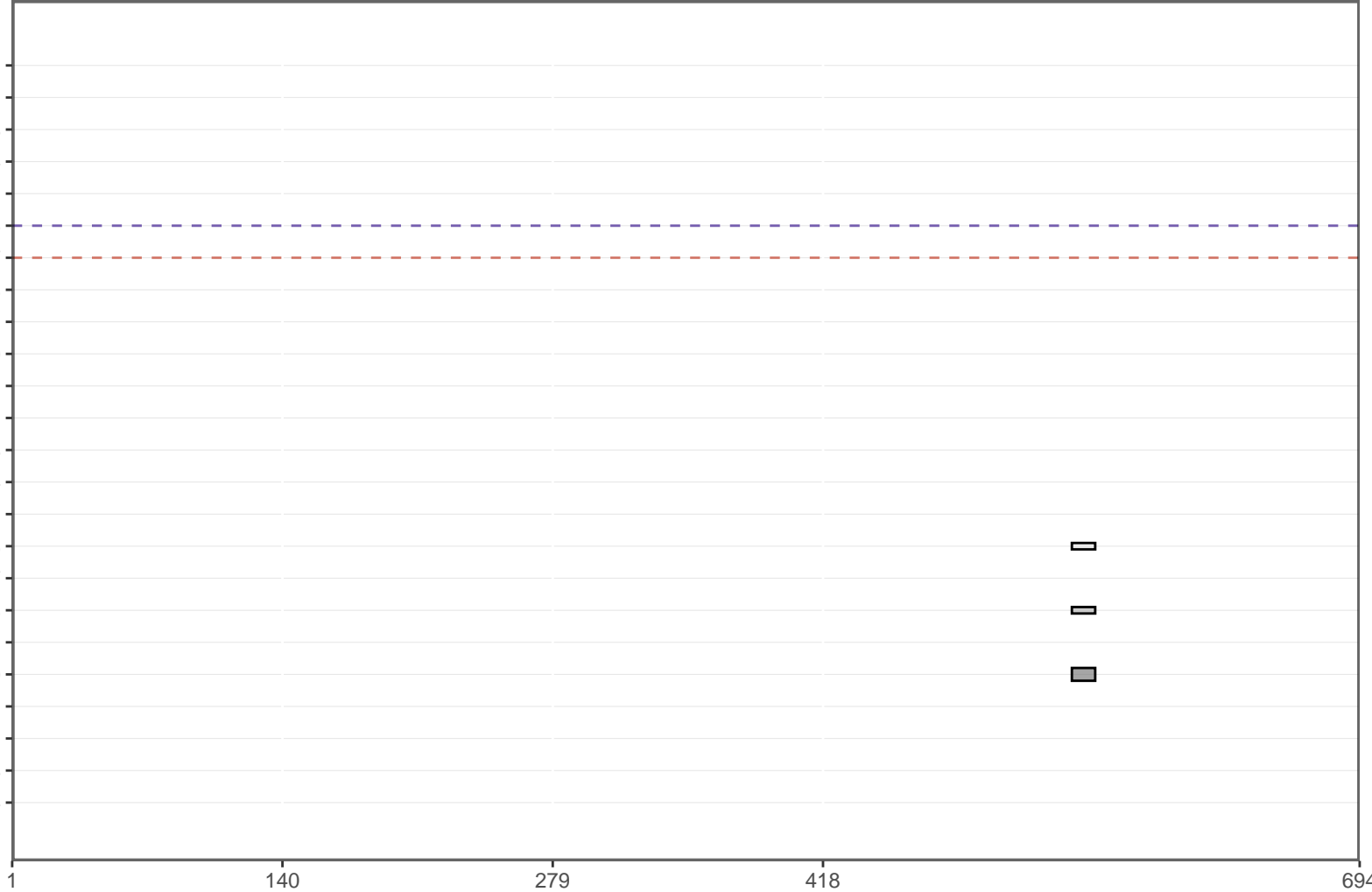
MW indication



Molecular weight



Gel Slice



Protein length

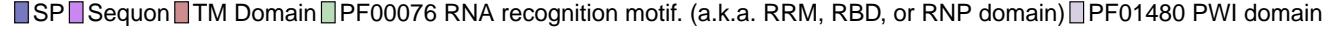


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

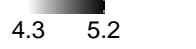
ISNYRQKRIGKSTLNDGTAWLYDSALDEEADHGINIVNKGAIDARTRTGAGFKNGKGETPLVVEYGVTVNANDLHKSQKDGDRPTFPAGAPHQPMVPLNVTWKSQVGEARQAALEREKGRSTLSESEGLANEPDMLTKESTNPIAVTNGNKVQVADTQKESGKTASINGLYSTGPTTEDADSRITFVNNVHFAATKDSLGRHFNKFGVLELVKVVILDTAATGGPKGSAVVEFMRKESAVNALELDGTSFMSRILKVVVKKSATPEAASVAVWVPRVTRAGPFAVSRFGVRFPPF

NbL01g17430.1 DNA-damage-repair/toleration_protein_DRT100-like [MW – SP = 36.63 kDa]

No. of times detected



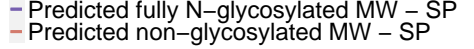
log(intensity)



Values from



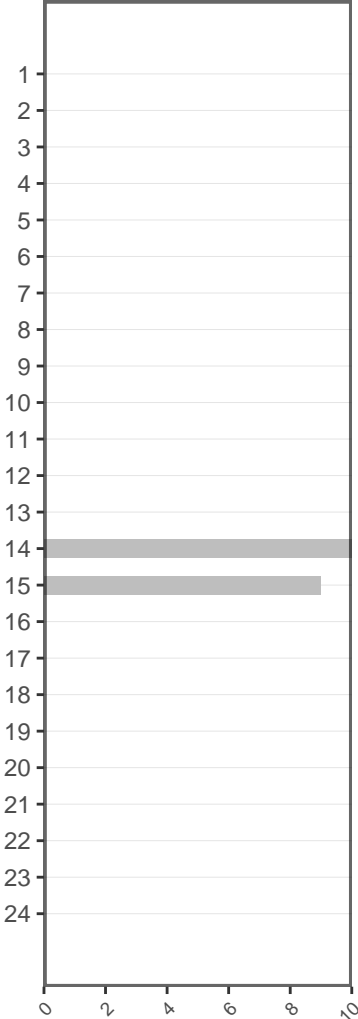
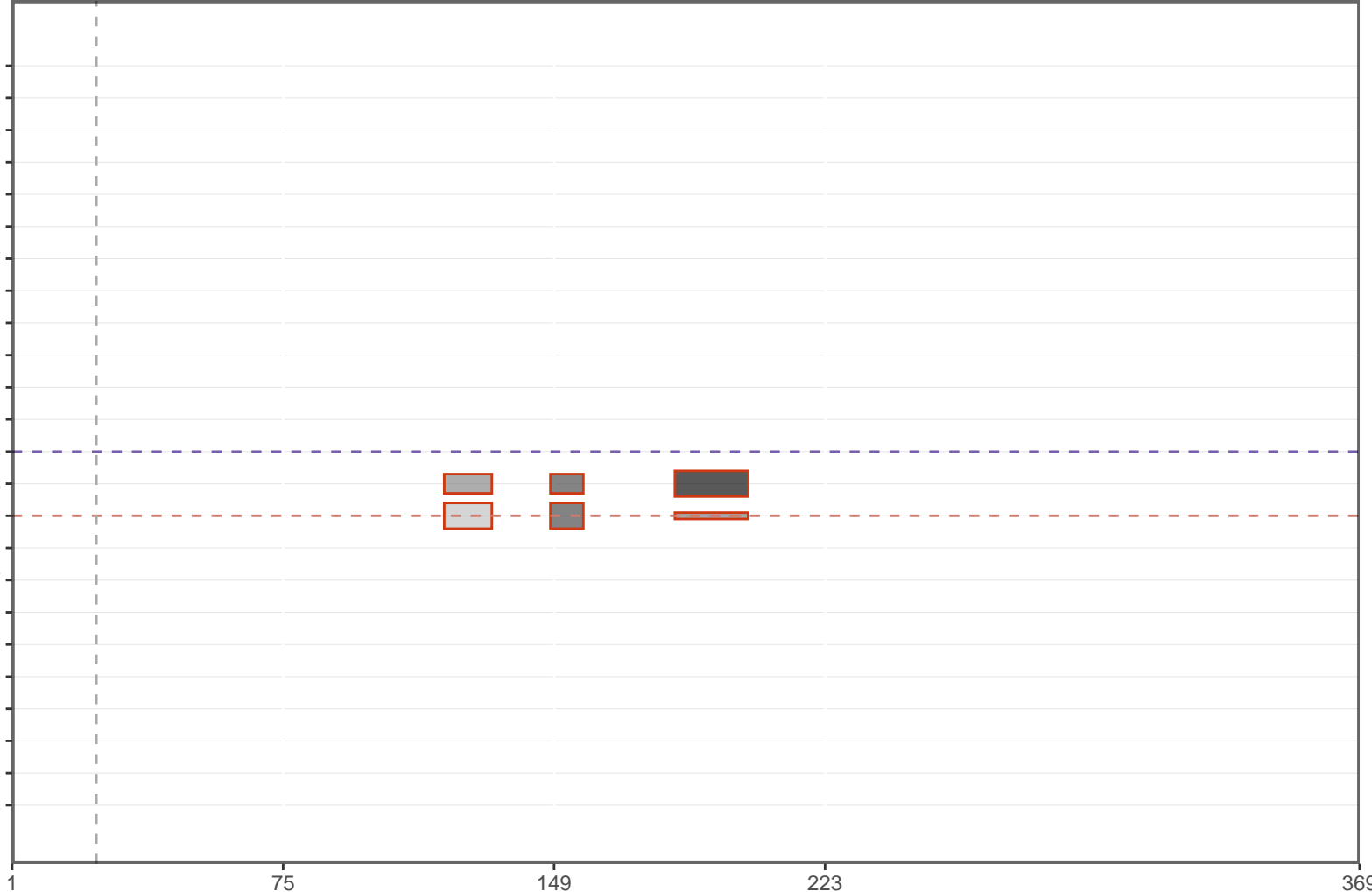
MW indication



Molecular weight



Gel Slice

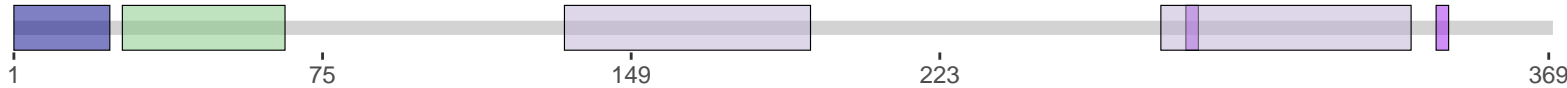


Protein length

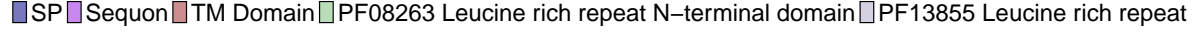


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

SIPGSIYVNLGKLMHLDLSEANGLGGEIPSDIGKLSMMSRALINKKIKTGGSPNSBIKLYRLADLDLAMNNGITGSPINQLGMPVLSLTLNLDENQLGSGSPTNLLSSPGLNINLNRNLEGLLPDVFSGSKTYFTHLDLSVNNLRGSPKSLASAKYVIGHLDLSVNHLOGPVPNGSFFDHLSEASSFNNDCLGGSPLRTG

NbL01g17240.1 siroheme_synthase [MW = 40.79 kDa]

No. of times detected



log(intensity)



Values from



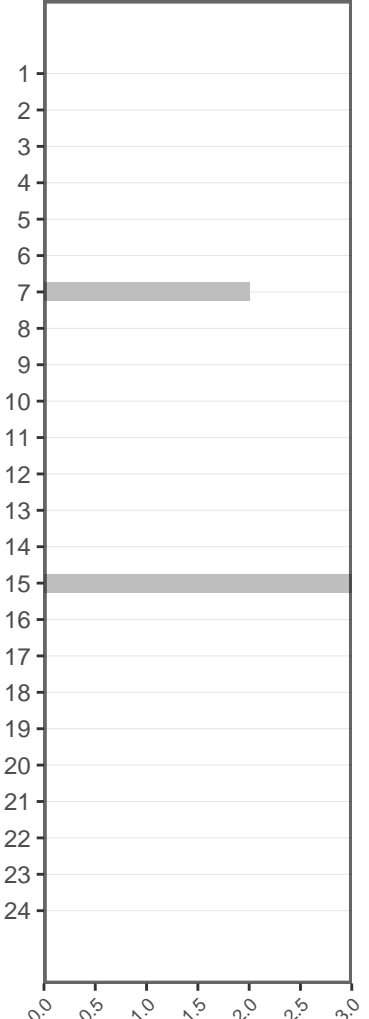
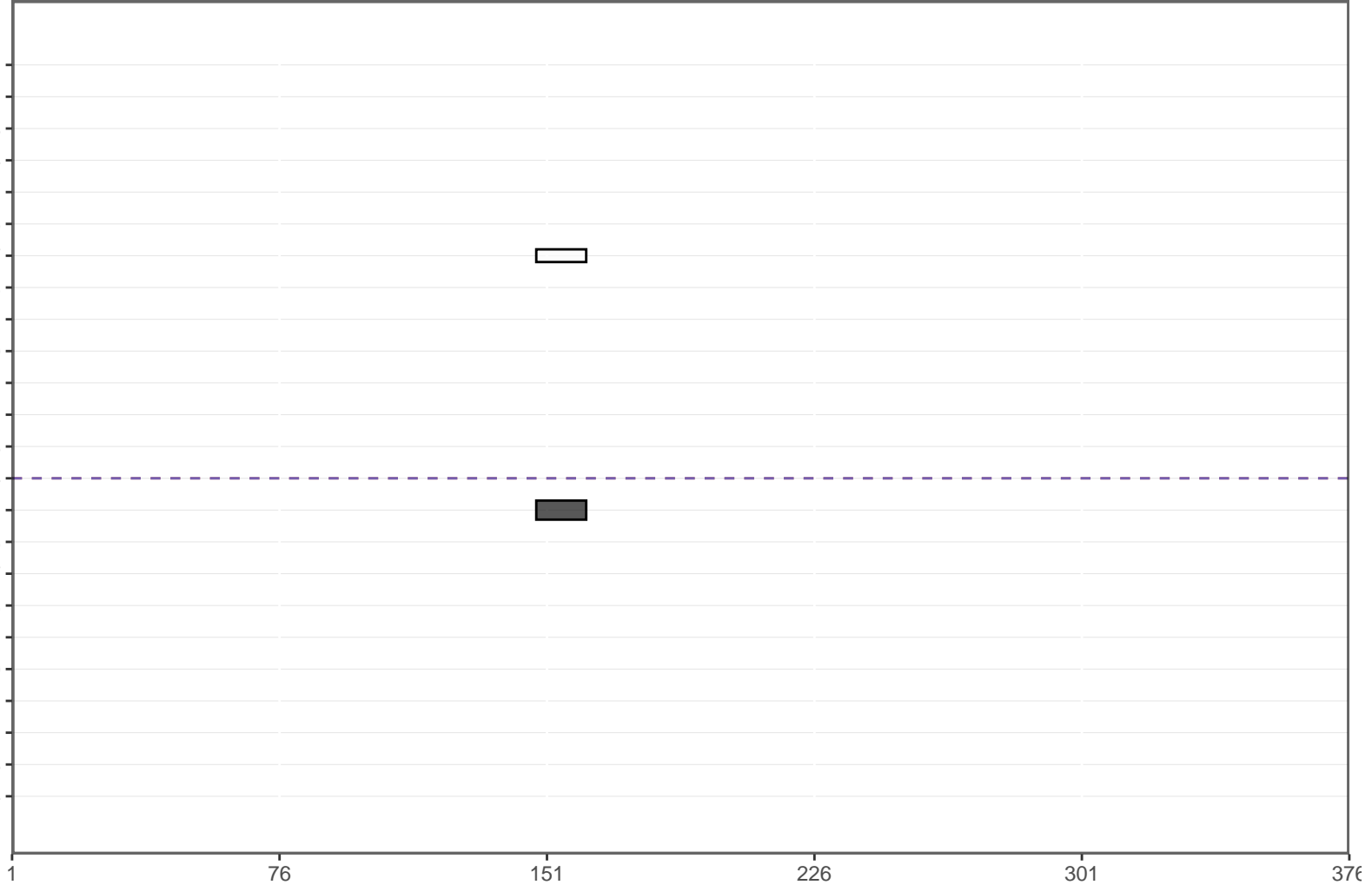
MW indication



Molecular weight



Gel Slice



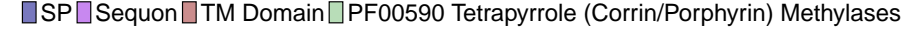
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

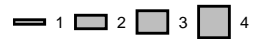


Protein sequence:

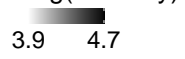
RTQEEHELLLSFAEAGANVRLKGGDPLVFRGGEMDFLQHGIGVQVPGITAAAGSIAELGFLTHRGIANSVRLTGHSRKGGADPLVAENAAADPDGTLVYVMGLSTLPLASLKHIGLFTDTPVAIERGTTDQGRMVFAELNLIANDIASNGLVSPFLIIEKVALESPLWPHSAEENPLVETRSSTNKVQ

NbL01g17060.1 citrate_synthase_mitochondrial [MW = 29.12 kDa]

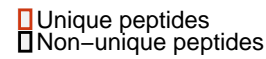
No. of times detected



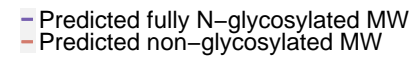
log(intensity)



Values from



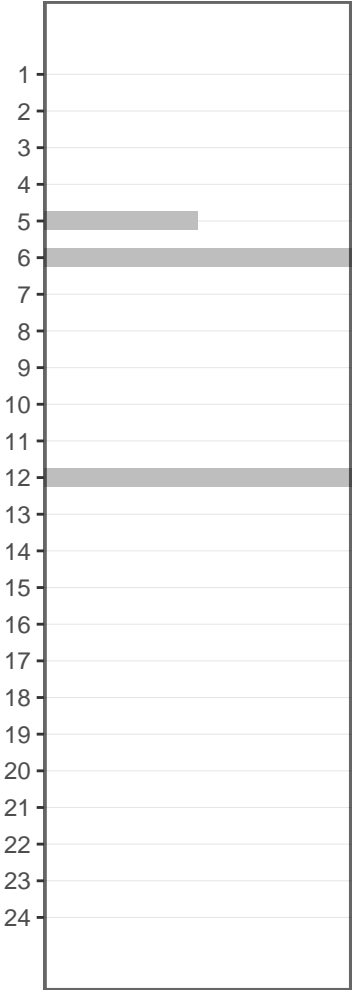
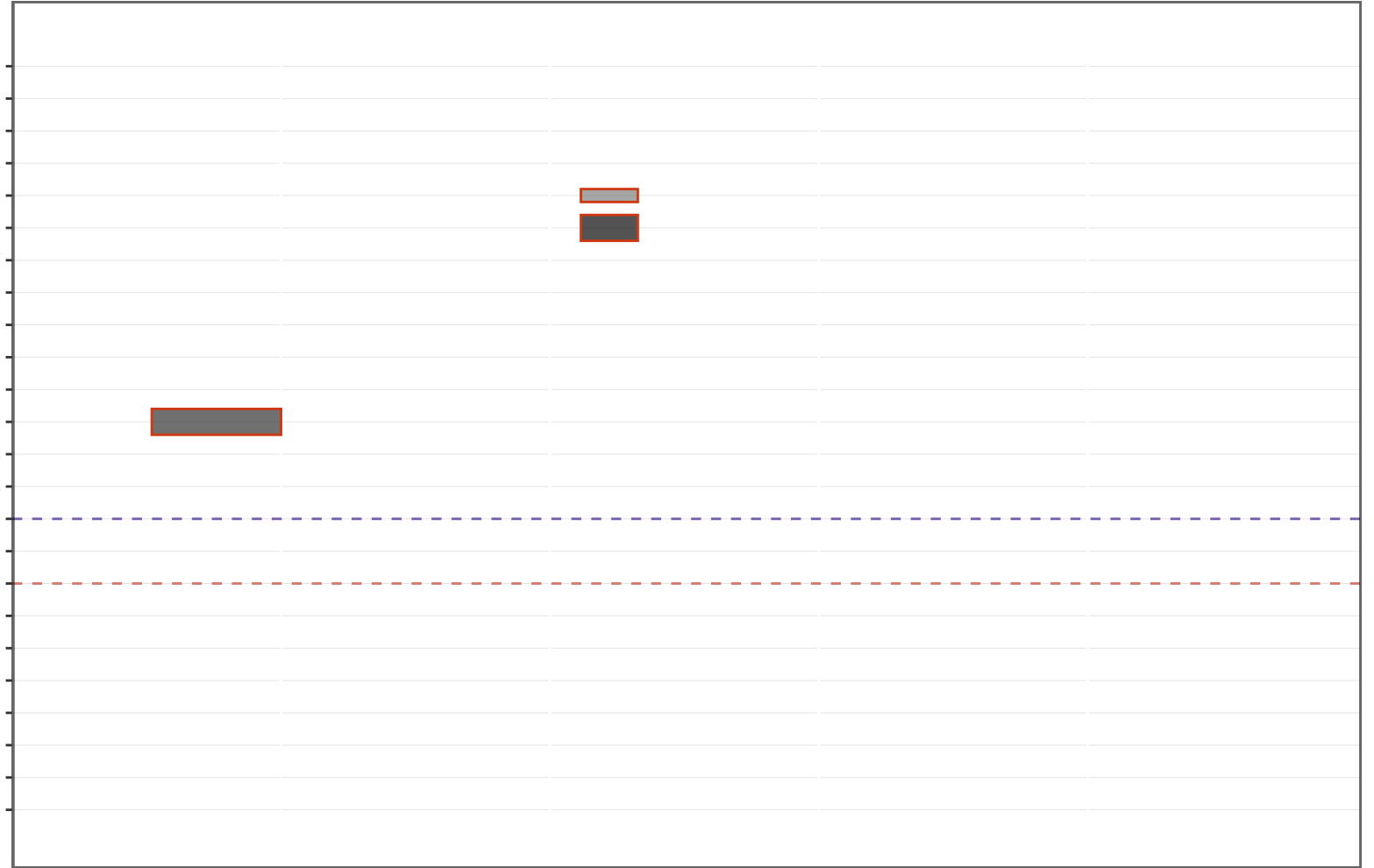
MW indication



Molecular weight



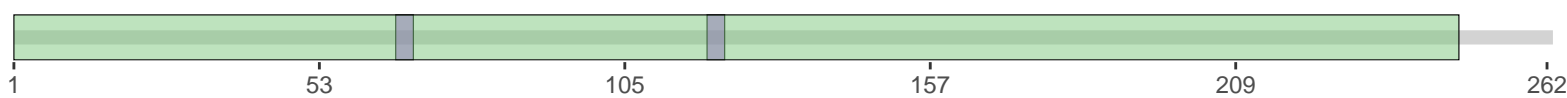
Gel Slice



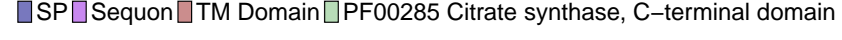
Protein length



Pfam domains



Pfam Description



Protein sequence:

INISKEQLKDIYVWIKLKGKIVVDFGFGHGLVLRKTDPRVYTDGREFALKHLPEDPLFQLVAKLYEVVPIITELGKVNPFVNDHSGVLLNLYGLTEARYYTVLFDVSRALGGSQLWDRALGLPLERPKVITMEWLENHCKKA*

NbL01g17020.1 uncharacterized_LOC104121022 [MW = 15.28 kDa]

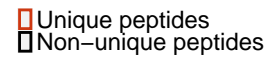
No. of times detected



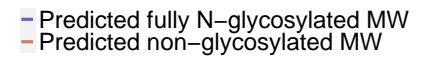
log(intensity)



Values from



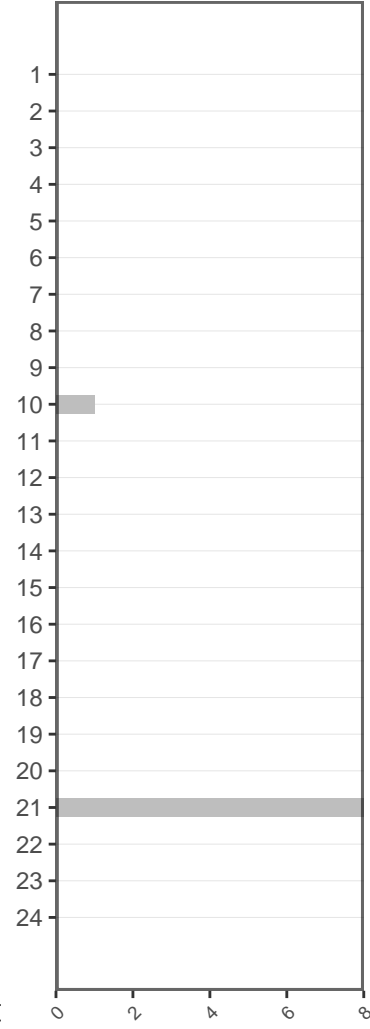
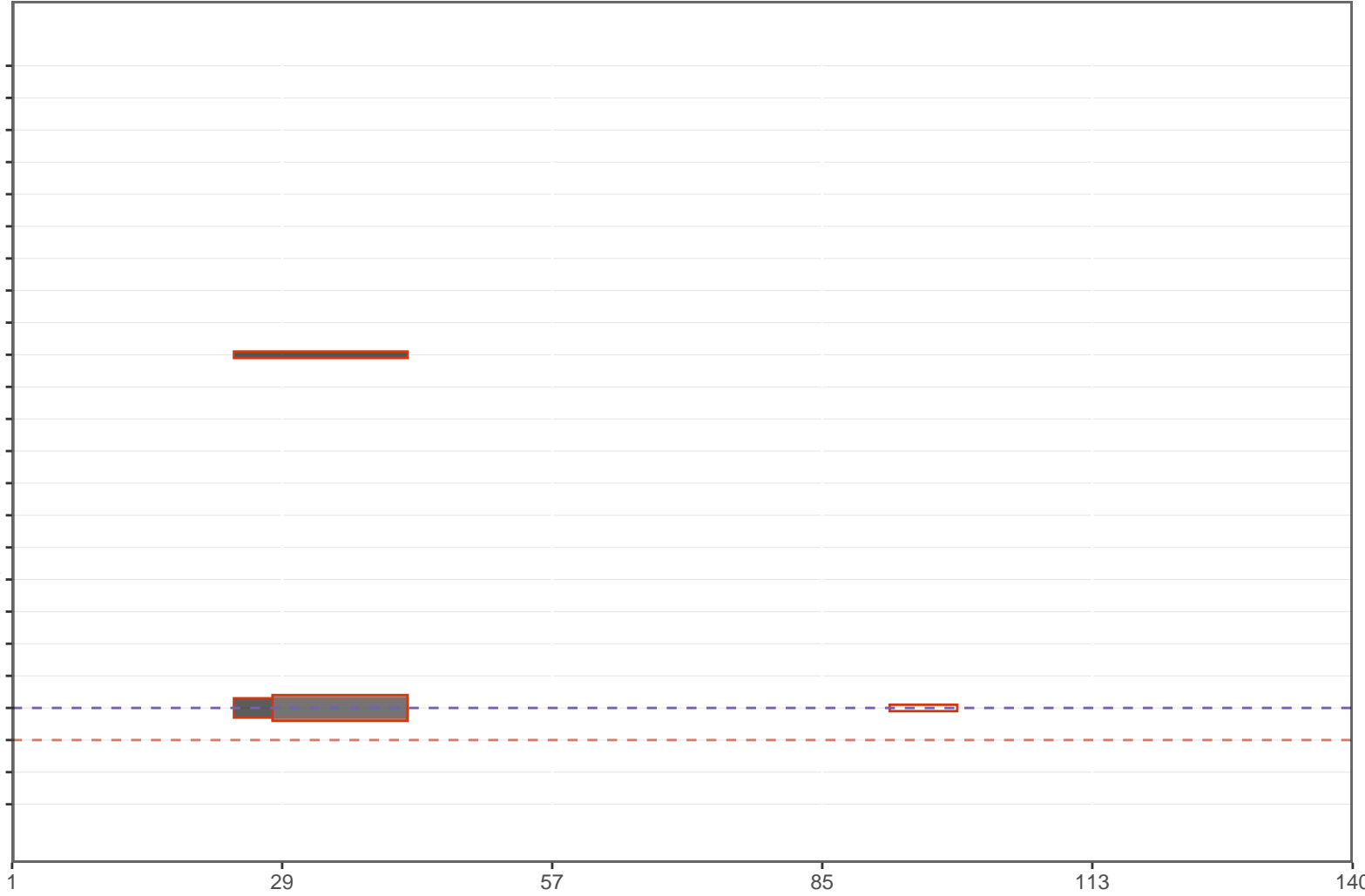
MW indication



Molecular weight

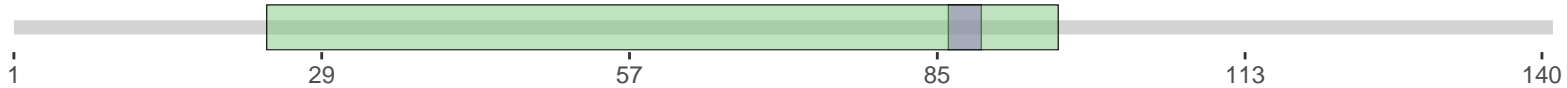


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

HFGVDVAASPEELTRLYDGFKEFKDGHNGTVDRQEFQENMRKIMLAADGLGSPQGMALDDSDGNLKGAAALEASKLPV

NbL01g16910.1 beta-hexosaminidase_2 [MW = 67.11 kDa]

No. of times detected



log(intensity)



Values from



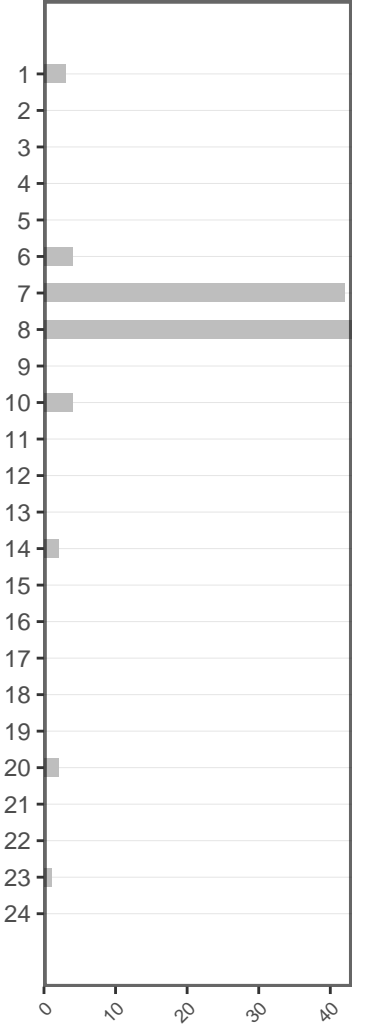
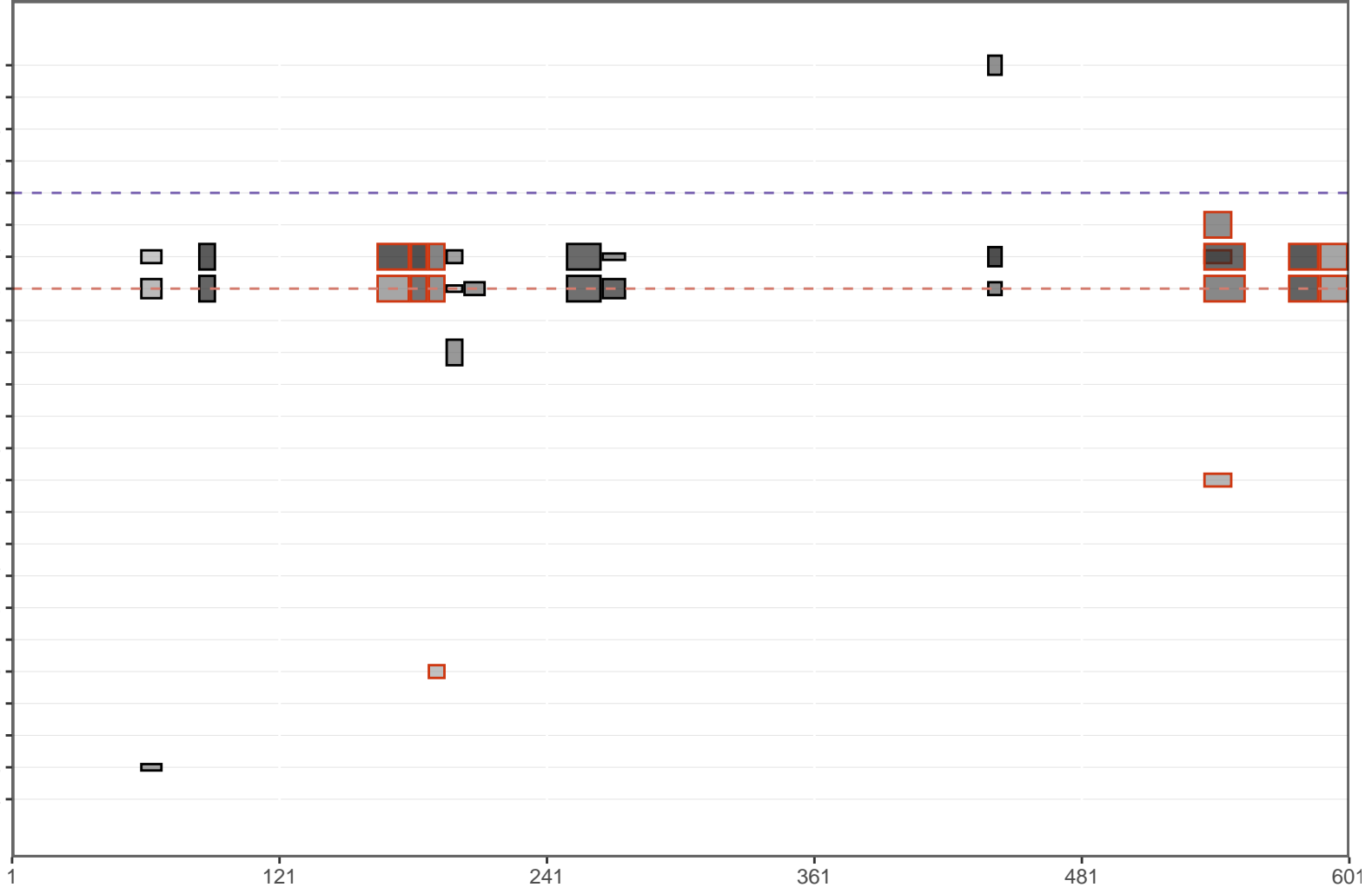
MW indication



Molecular weight

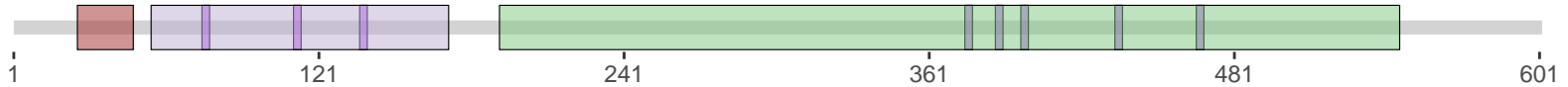


Gel Slice



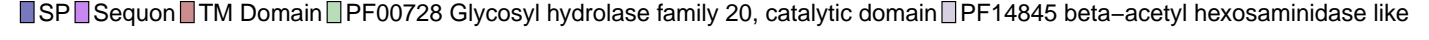
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

YPEIICANMFVYFPAASSPLAAEPFGTGLNPLSPKTYEVAKNVHDTIAMFPDLFLHGGADEINSAGWNTDPSIQKVASNGTLGQLEIFINNTLPEIISGLRIVVYWEEDVLSANVKNVPELLSPENVMQGTWVNGPNNKRLVTSQYRIVVSSADYYLLDGGHGSFVGNDRYDGPFGTDDGNGGSGWGGPKFTWETVYVYDITYGLTDEEAQLWGGVEALWSEGAQDSTVMDSRVWRPGSAMAETLWSGNRDETGMKRYAETDRLNEWRVYRMVARGIGAEPIQLV

NbL01g16900.1 non-specific_lipid-transfer_protein-like [MW - SP = 12.67 kDa]

No. of times detected



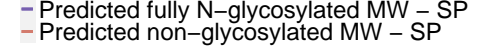
log(intensity)



Values from



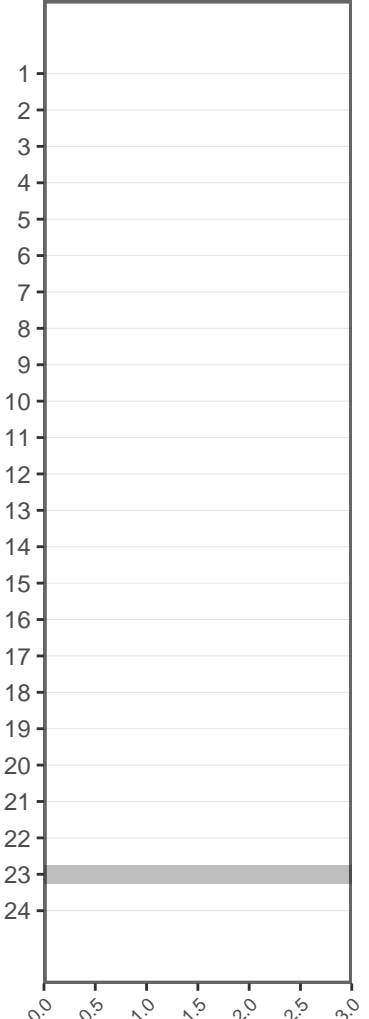
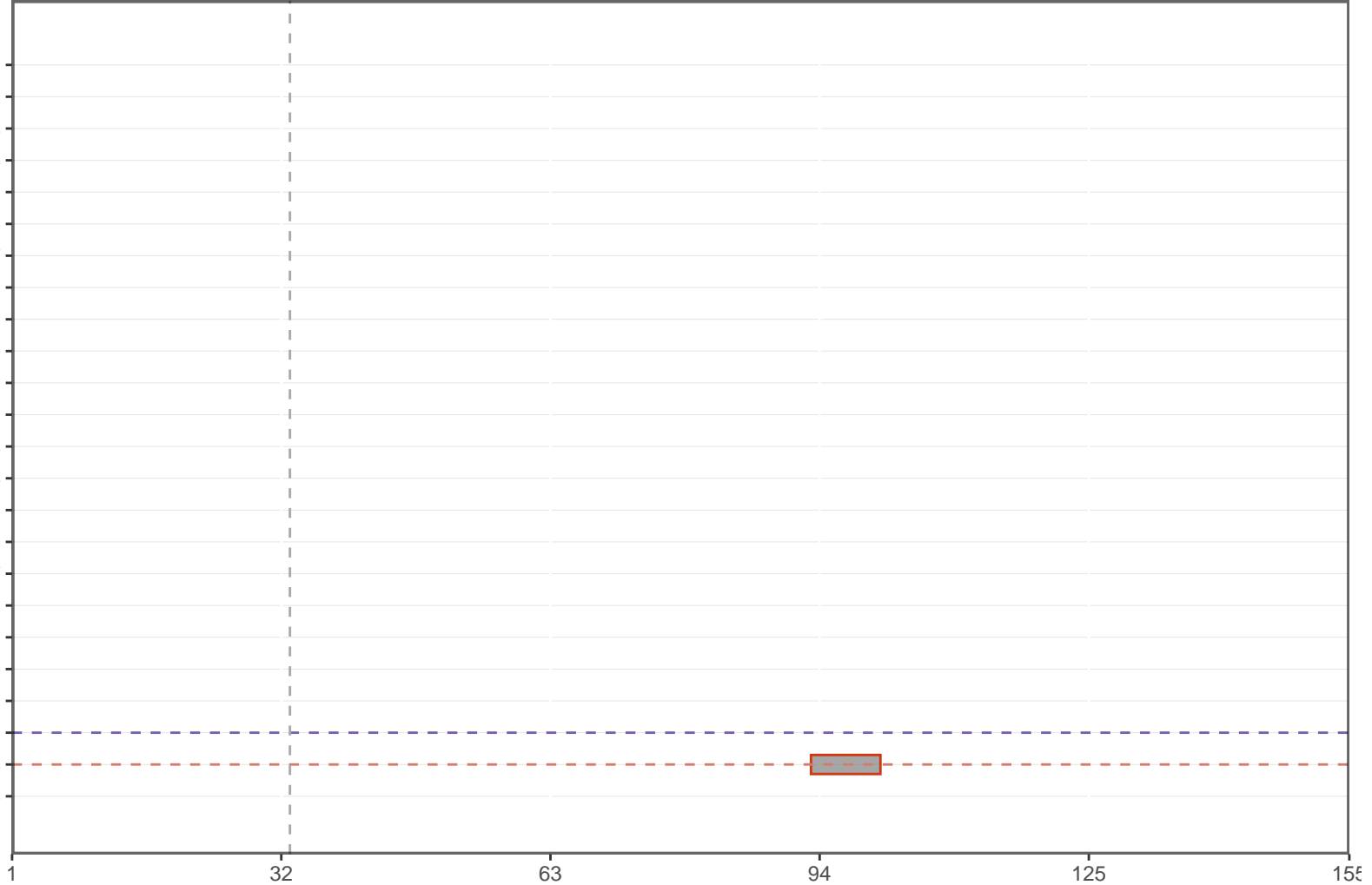
MW indication



Molecular weight



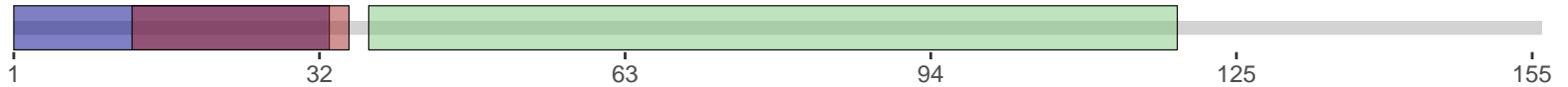
Gel Slice



Protein length

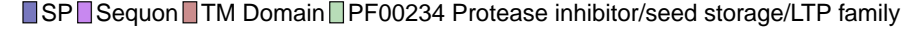


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CSLSGATSTTQDRQAACTGLKNAAGKVININAGLAKGLPGGGHLSFPISTVDCTKYYSFPPPPNPQKIFLSSSYLALWQKNFGLS*

NbL01g16880.1 uncharacterized_LOC109216616 [MW – SP = 44.3 kDa]

No. of times detected



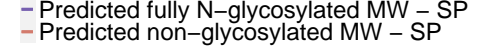
log(intensity)



Values from



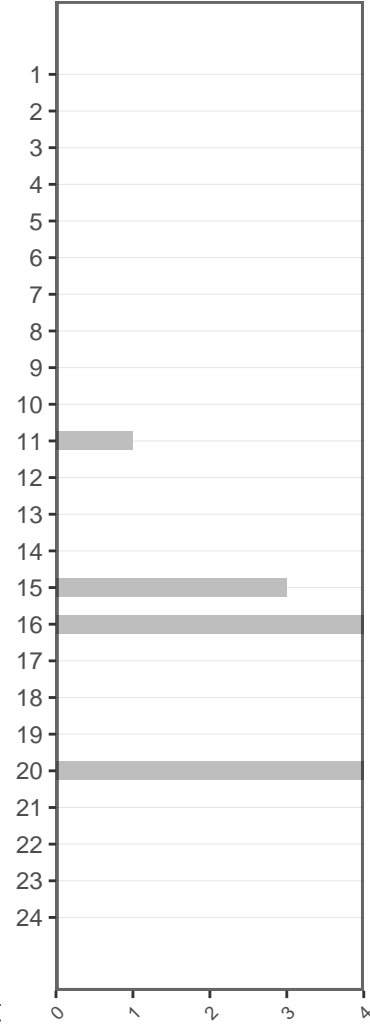
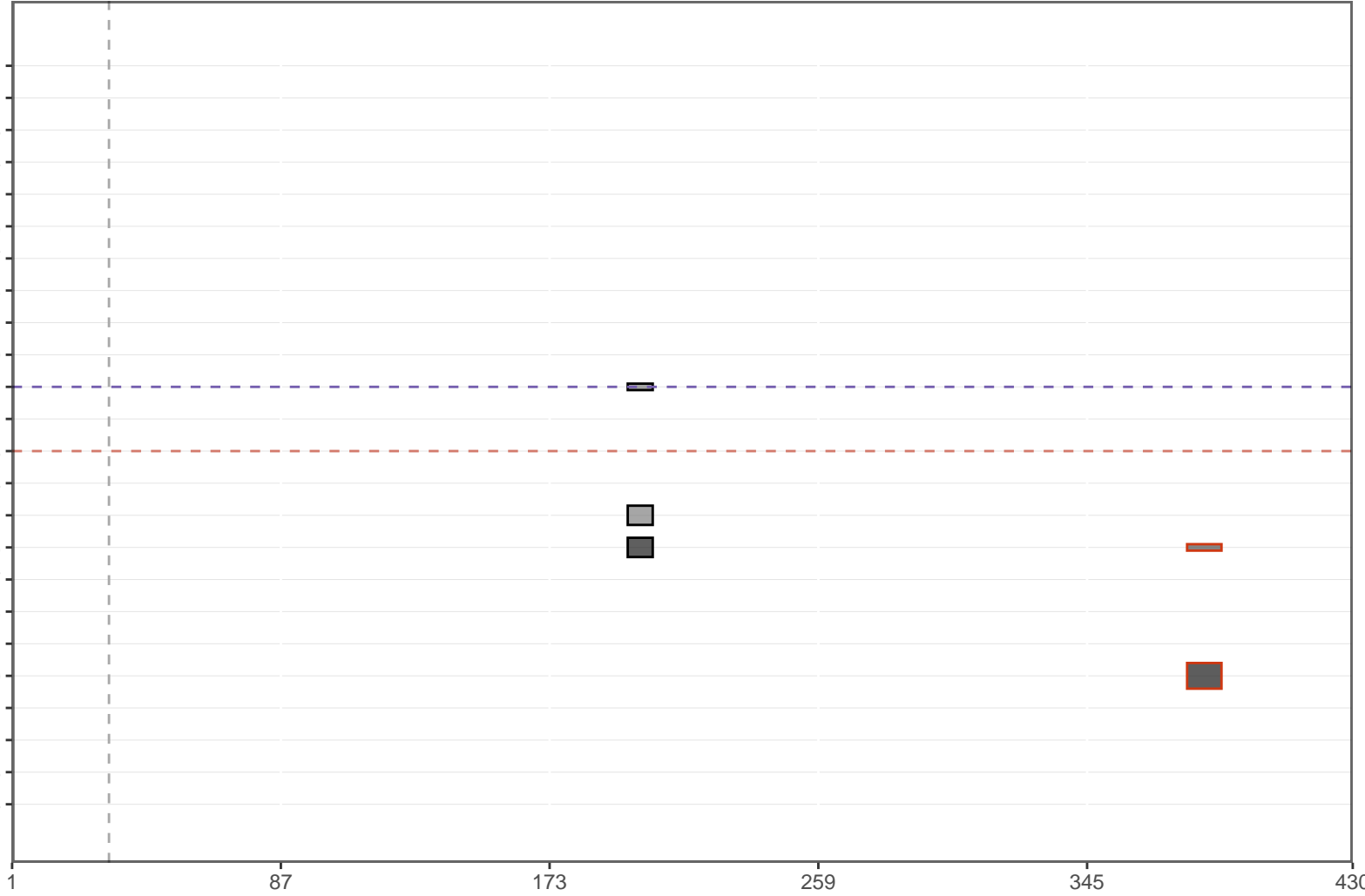
MW indication



Molecular weight



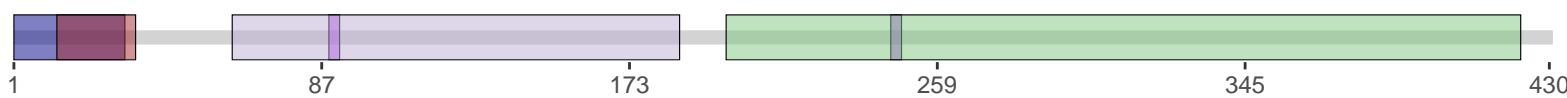
Gel Slice



Peptide counts over 4 repeats

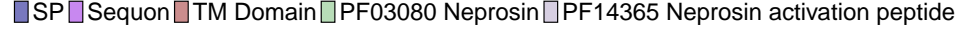
1 87 173 259 345 430

Protein length



Pfam domains

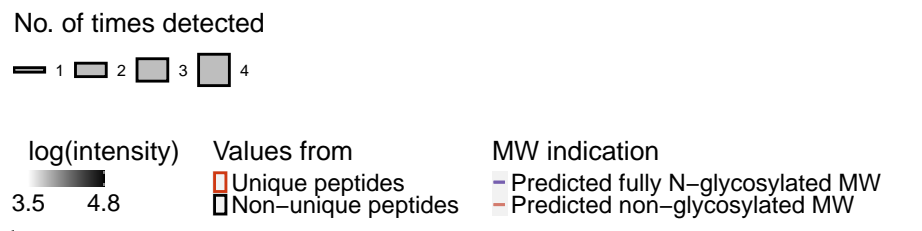
Pfam Description



Protein sequence:

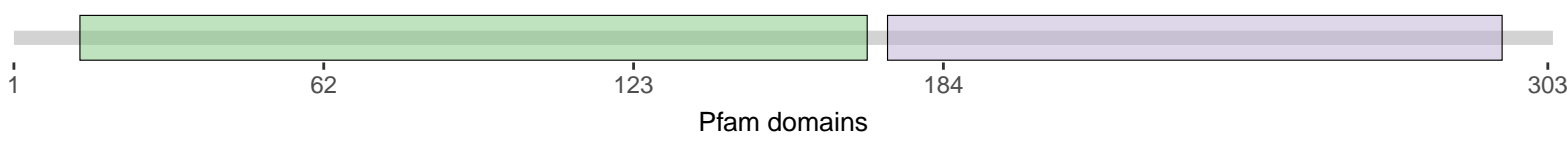
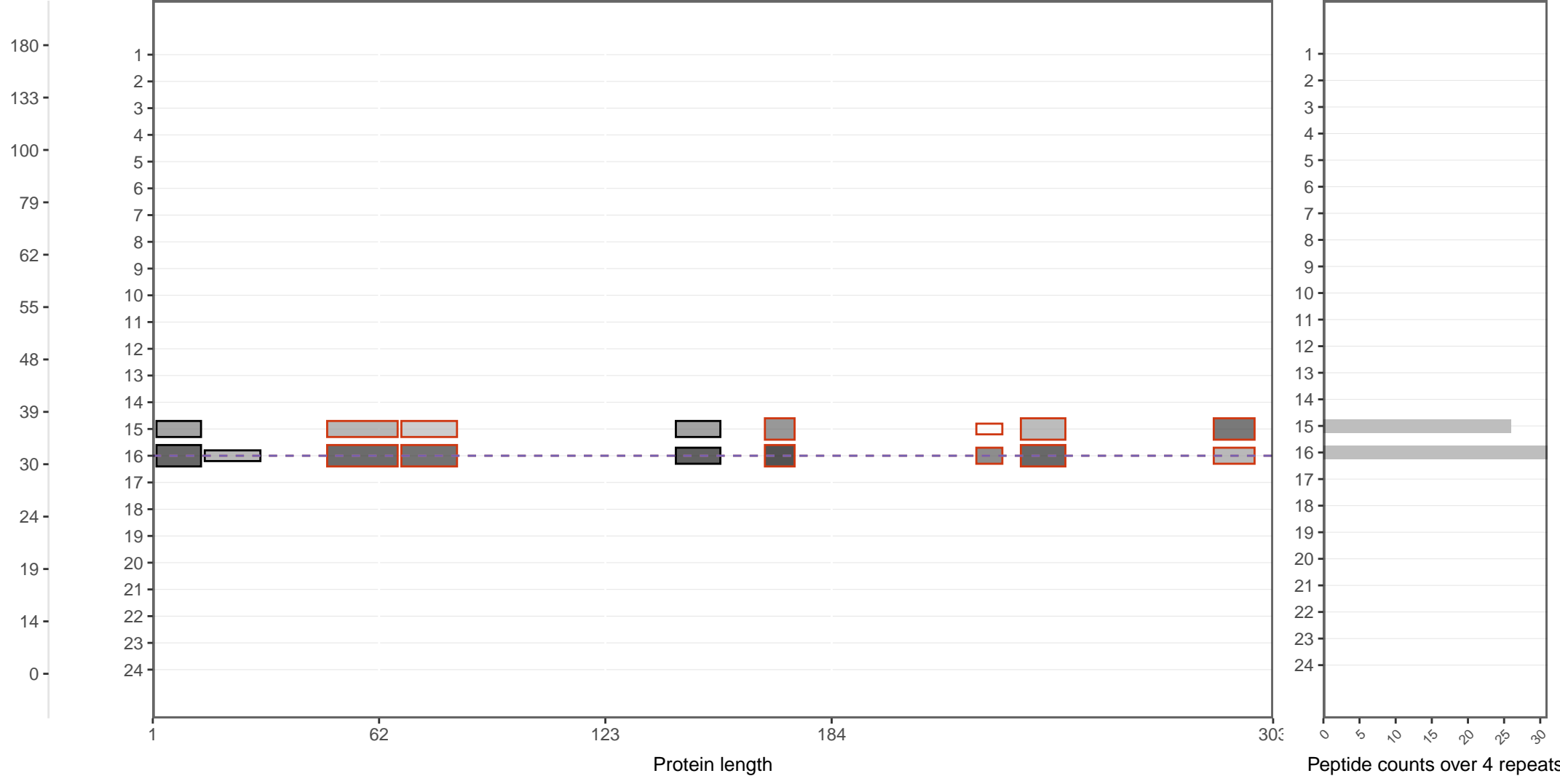
EPKIQDPNEFSLSQLWILGGGFDEDLNIEAGWGVSPDLVGDNINRIFFTYWTSDAYQATGCHYLLGGGFQINNEIMAGTISPLS6YHGSQYDISELWVKDPKQGNWMMGFGNDVYLYGHWYPLGFVYLTDSASMEWGGGEVNSESDGLHTTTQMGSGHFPPDEGFGKSSYFRNIQVVDGNSNLRAPQDLGIYTEDNNGYDVLGKNNQWGNVYFYGGPGRNENCP

NbL01g16810.1 probable_3-hydroxyisobutyrate_dehydrogenase-like_2_mitochondrial [MW = 31.65 kDa]



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF03446 NAD binding domain of 6-phosphogluconate dehydrogenase
- PF14833 NAD-binding of NADP-dependent 3-hydroxyisobutyrate dehydrogenase

Protein sequence:

SKLAIAGGNEDEVWVWIKPLFDVAGKVTFFVGGPKGGGSKIANQIVGGNLLGLSEGLVFADKAGLDMKFVEAKGGGAAGSKVMELFGERMIGRDFRPGGFTDVMWDLGMLGVGAEGGDDVWVLPQAALSKOLFSAIMVANGDGLGTGGLTIVIERINGK

NbL01g16640.1 glutathione_transferase_GST_23-like [MW = 25.99 kDa]

No. of times detected



log(intensity)



Values from



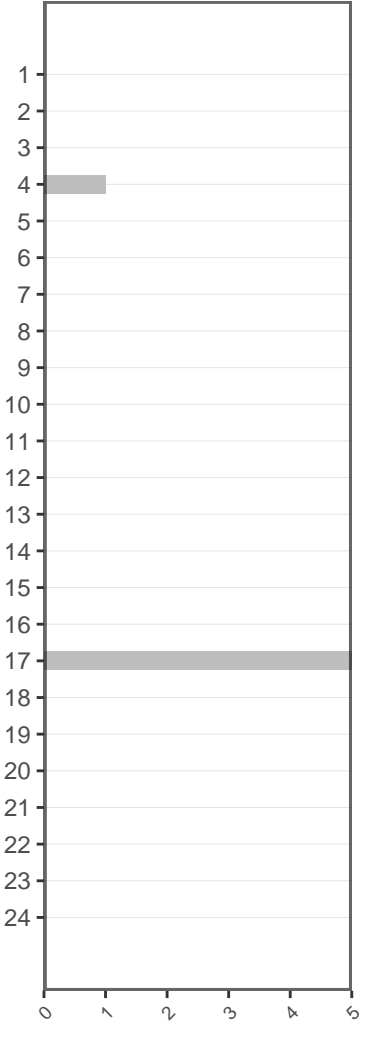
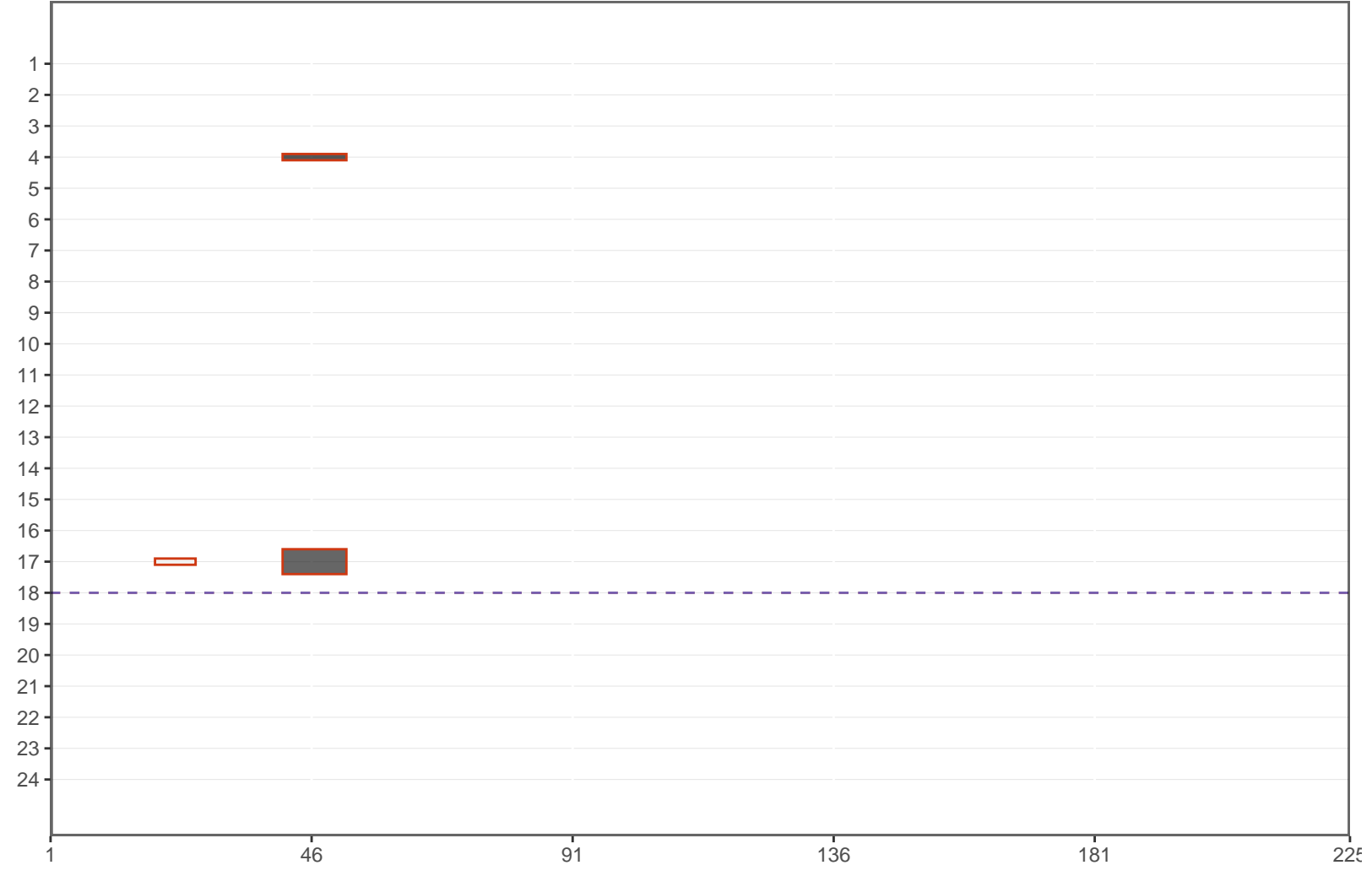
MW indication



Molecular weight

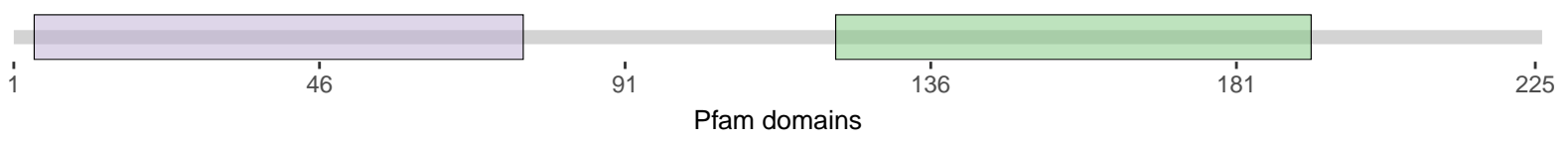


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00043 Glutathione S-transferase, C-terminal domain
- PF02798 Glutathione S-transferase, N-terminal domain

Protein sequence:

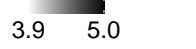
IGEEKLLPSMIVSYFTGGGNEKNKALGPWQNLLEELGKKEKFFGGEEIGYLDLSLGLWLVYLEDVFEFVIDLKFDAKLLLSAWMNFYDAPRIKEHWPRDKLVTRKQLLHENYQKAFAN*

NbL01g16540.1 DNA-directed_RNA_polymerases_II_IV_and_V_subunit_8B-like [MW = 16.84 kDa]

No. of times detected



log(intensity)



Values from



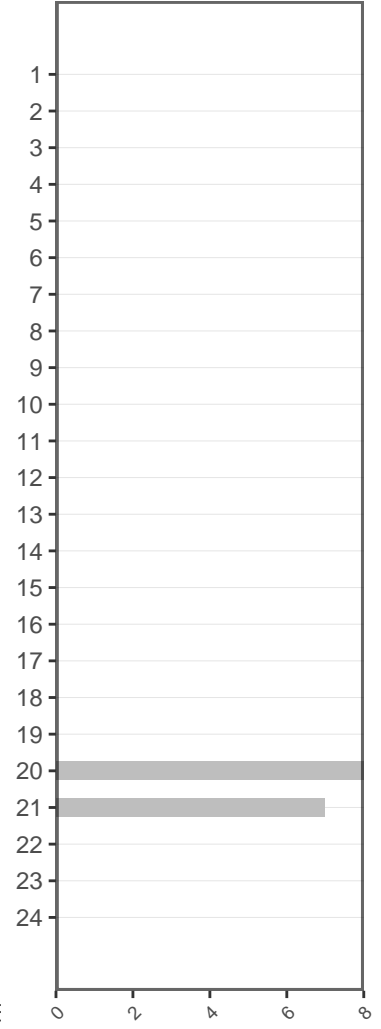
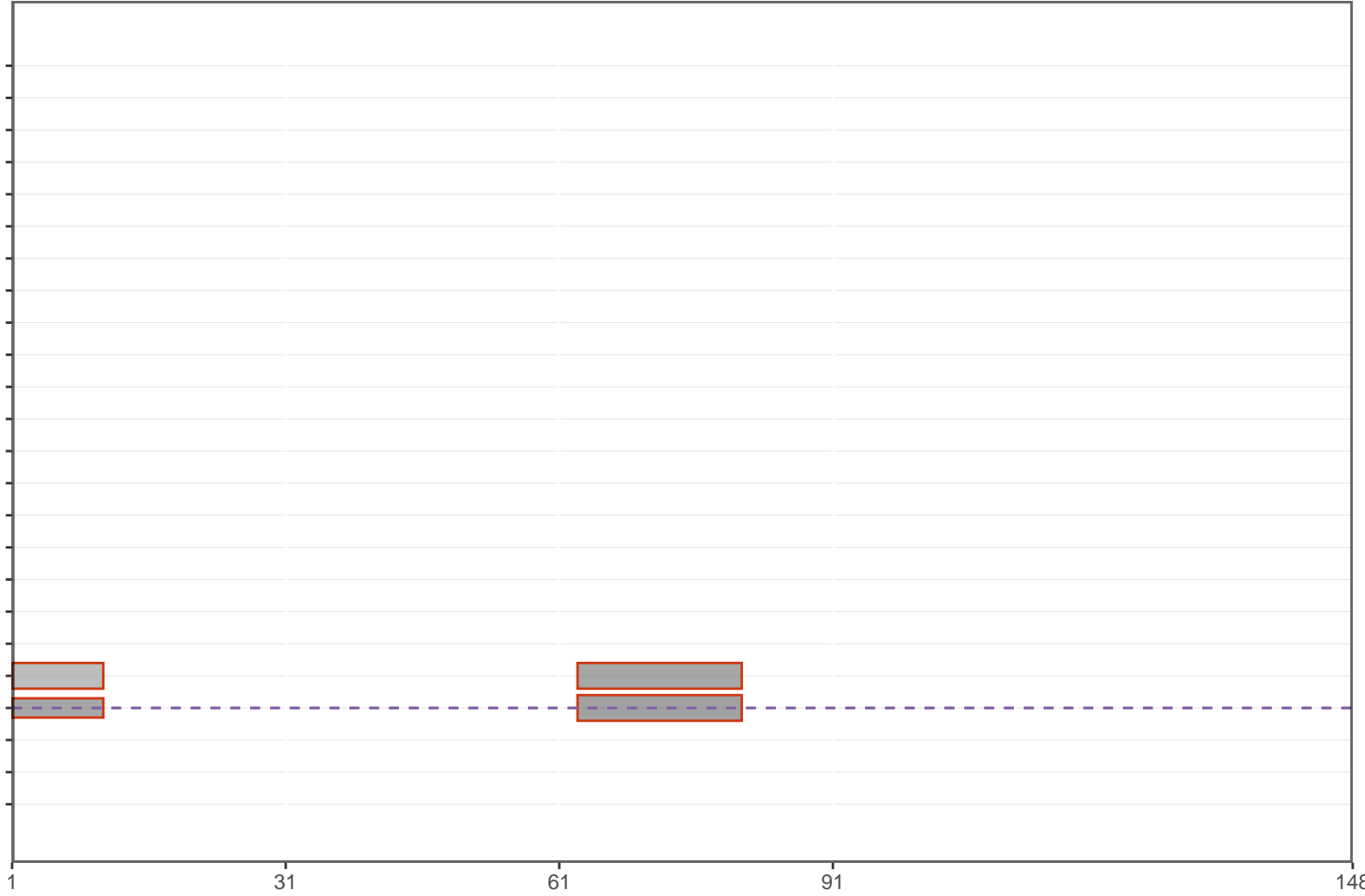
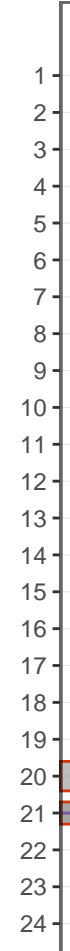
MW indication



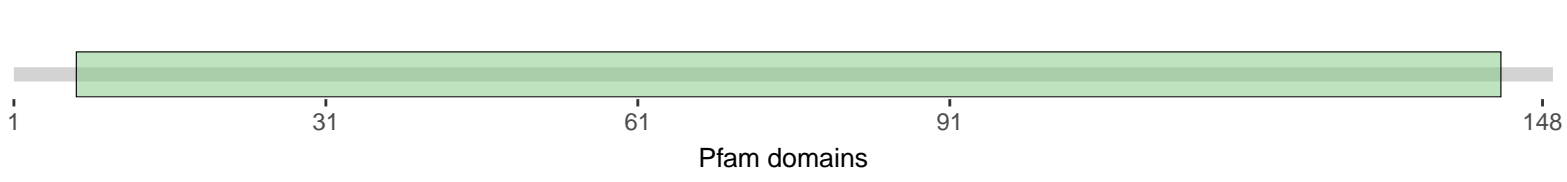
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

KTLLMDGSAVTSIHPPEGEQKSLADKFEYHWGLVYKVMSTSGPDKKVVVVSFGGLQLMLKSDPKVQKFKLDEKFLLLRKMTKV

NbL01g16510.1 uncharacterized_LOC109245038 [MW = 10.57 kDa]

No. of times detected



log(intensity)



Values from



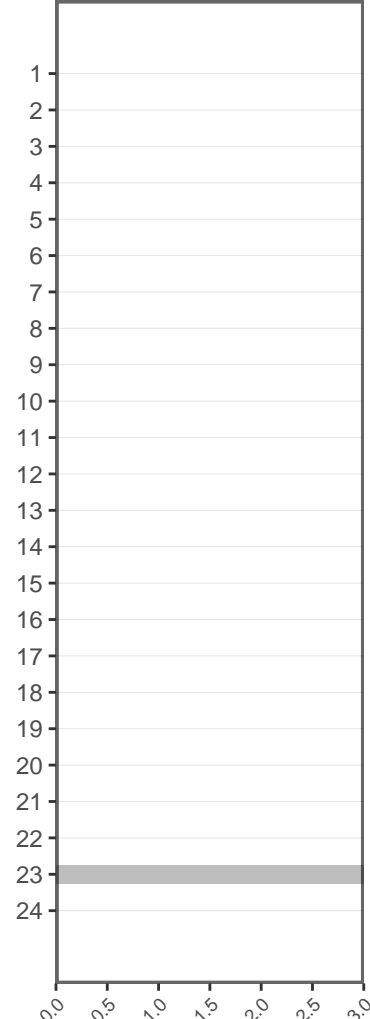
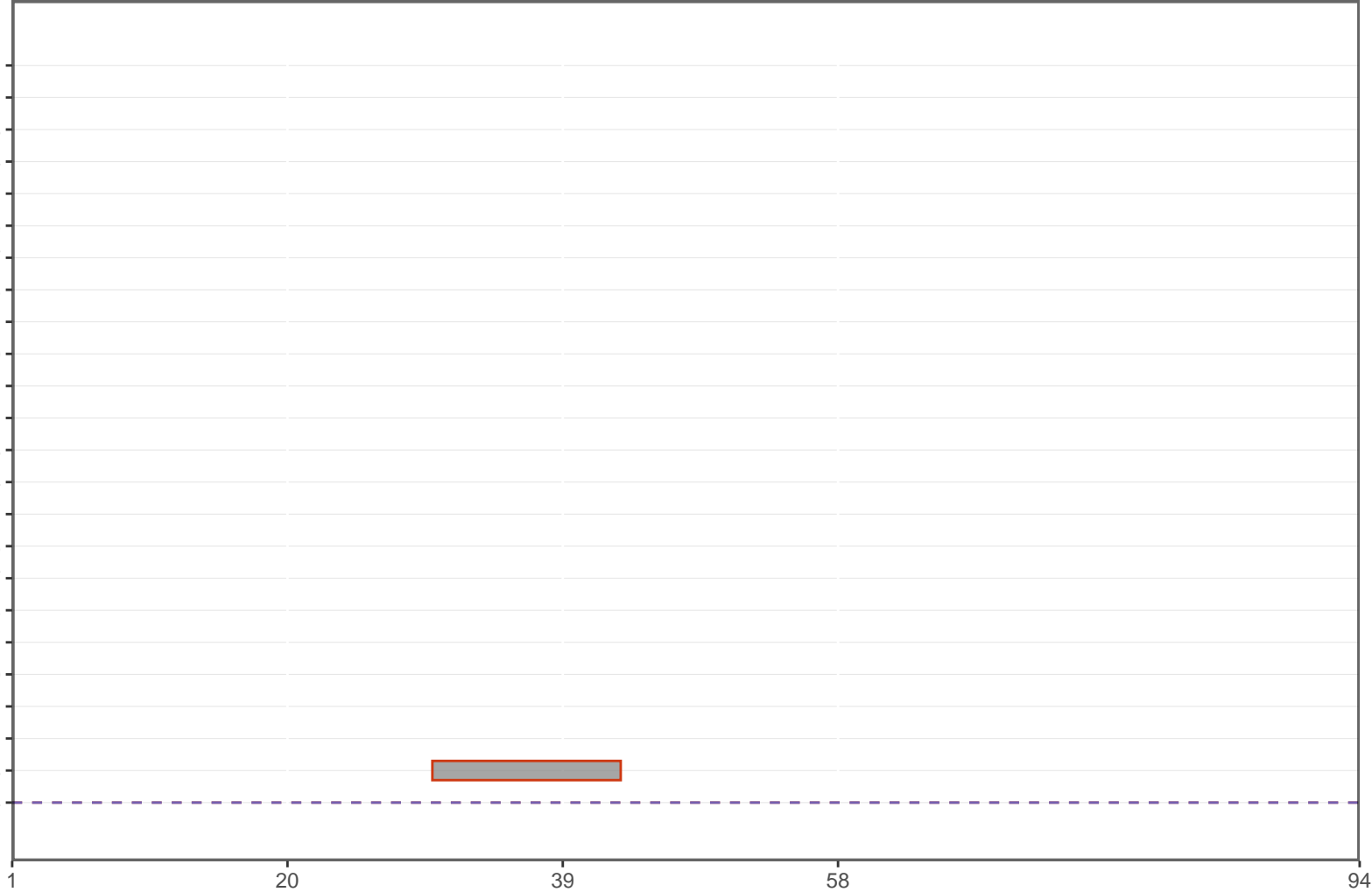
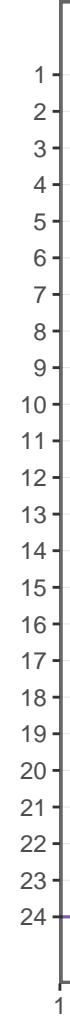
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

PALPLNLAARLQKSAEIVRAMFELGSEERLHNGDLDAAEYSLGRLRKEIPKHQVYQ*

NbL01g16400.1 protein_SCAI [MW = 69.82 kDa]

No. of times detected



log(intensity)



Values from



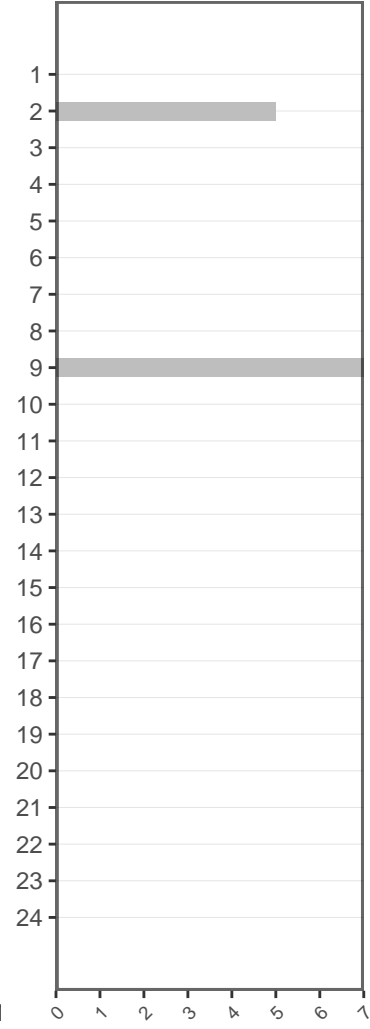
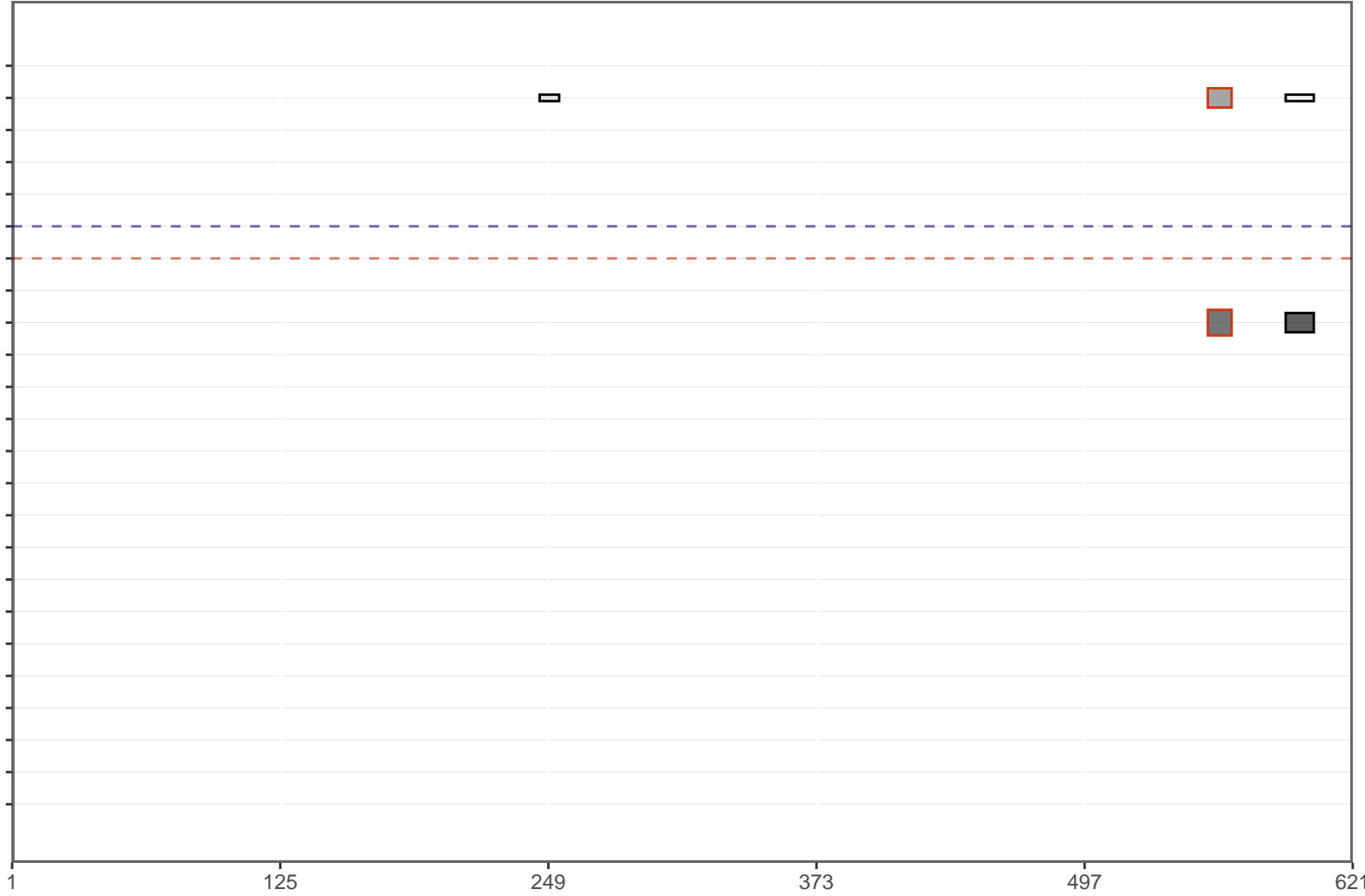
MW indication



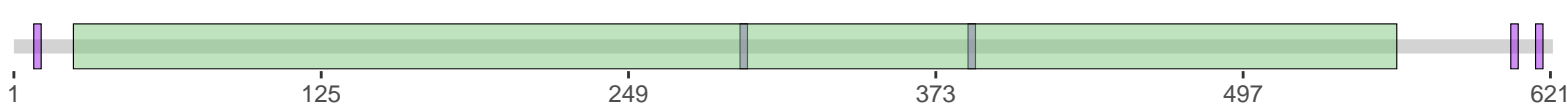
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

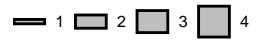


Protein sequence:

RVNYSDQISDPTLPNPKTKLYRQVPTNFLAVLATICEELSHDGVLLLVLSAAGSGGNFFSPPSHGAGRFMRRAVDLEATPTSGLSDFEIANNTSTREDGLTEGSGGNYHSGRGTGGVNGVYPCDLLPFTRRRLFLVHDSGGKAFKFTALSGSGEKEPVMALLSPHLPISAMDSRGRQPSGSLFTSFLTVPLGAFILMLGFTVSDNDMDMYGKAEKLLSSSLNEWGLLAAASDNLNPIVWSGTLGDPFLRRLRIFRFGRTALAIWPTFNKIEFLPEGIPGLPAVLPSSAACORTVL

NbL01g16380.1 nucleolar_GTP-binding_protein_1-like [MW = 77.8 kDa]

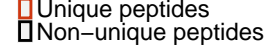
No. of times detected



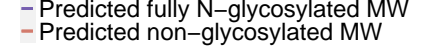
log(intensity)



Values from



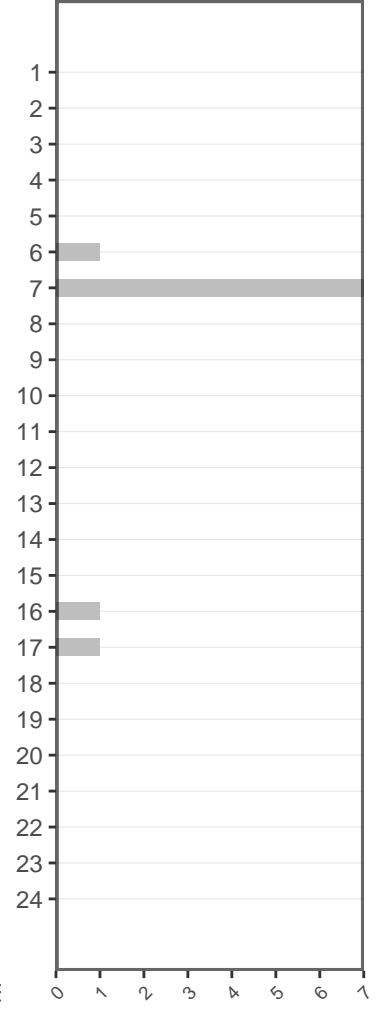
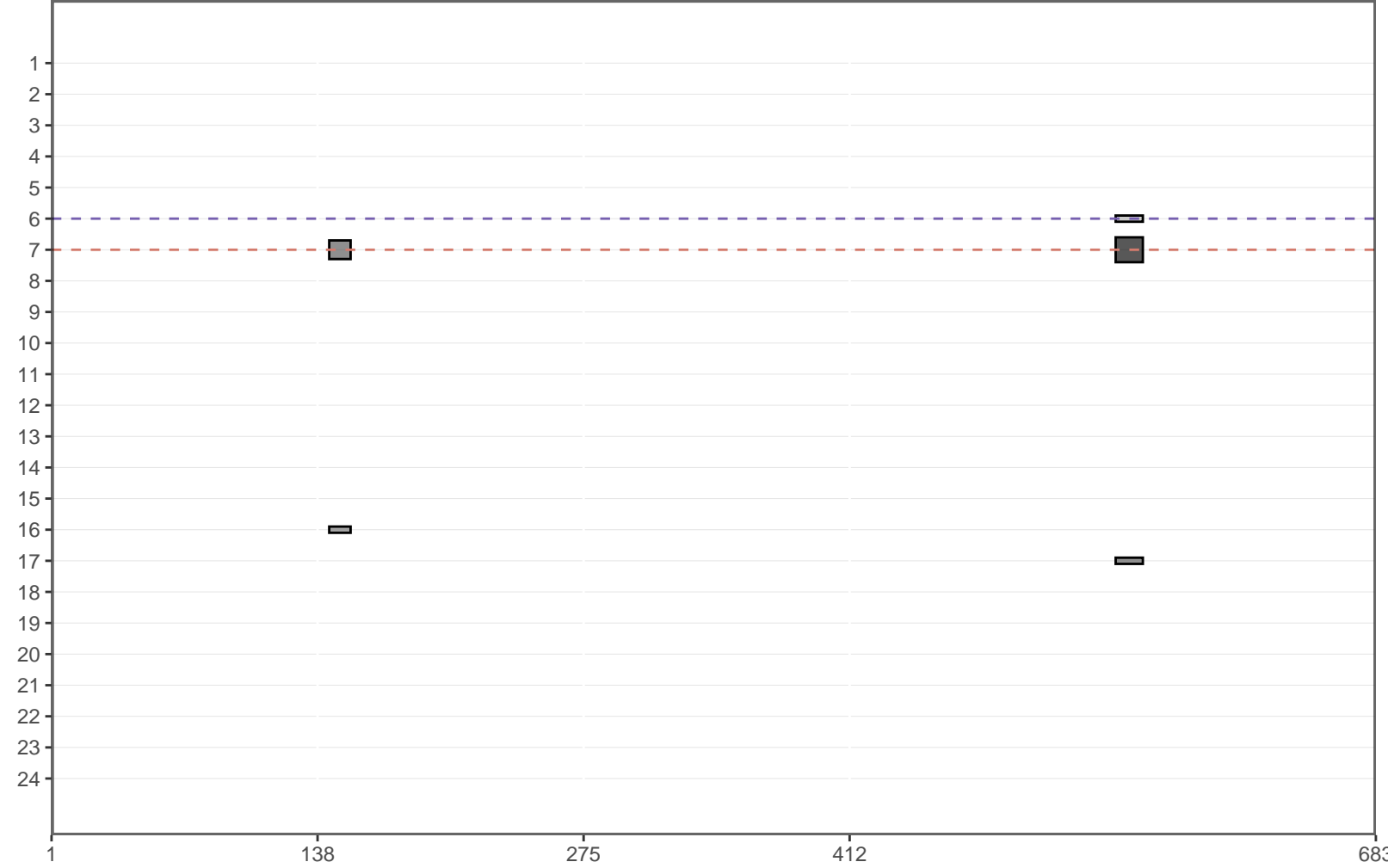
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF06858 Nucleolar GTP-binding protein 1 (NOG1)
- PF08155 NOGCT (NUC087) domain
- PF17835 NOG1 N-terminal helical domain

Protein sequence:

ISTLTEDGIVSYNAAGERLLNQRVELKMKKSLNDGLNRHFVAMPKPRDQKERFVGPQVLEARAKEAEADAQKQKRLERDLENENGGAGVYASLRKHVLLANEWKEQVMPFLDGHVYYDFDPDLQRLEELEREELRQDEEGDDDFEMDGVVELTPEEQALAEIRKQKSLHQHRIKQKTAESRPTVPRKFDNDKEFTSKRMGRQLSALGLDPTLAINPARSKSRGRKRERSRVERGGDDGKDMAMDVEITPNKGRRLRSLGIAARBRSRSRPPDEFVPG

NbL01g16360.1 uric_acid_degradation_bifunctional_protein_TTL [MW = 37.3 kDa]

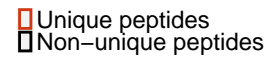
No. of times detected



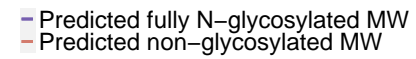
log(intensity)



Values from



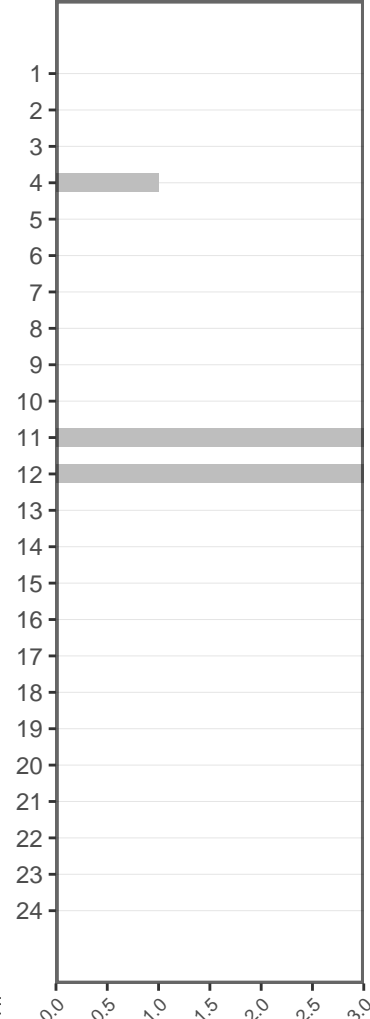
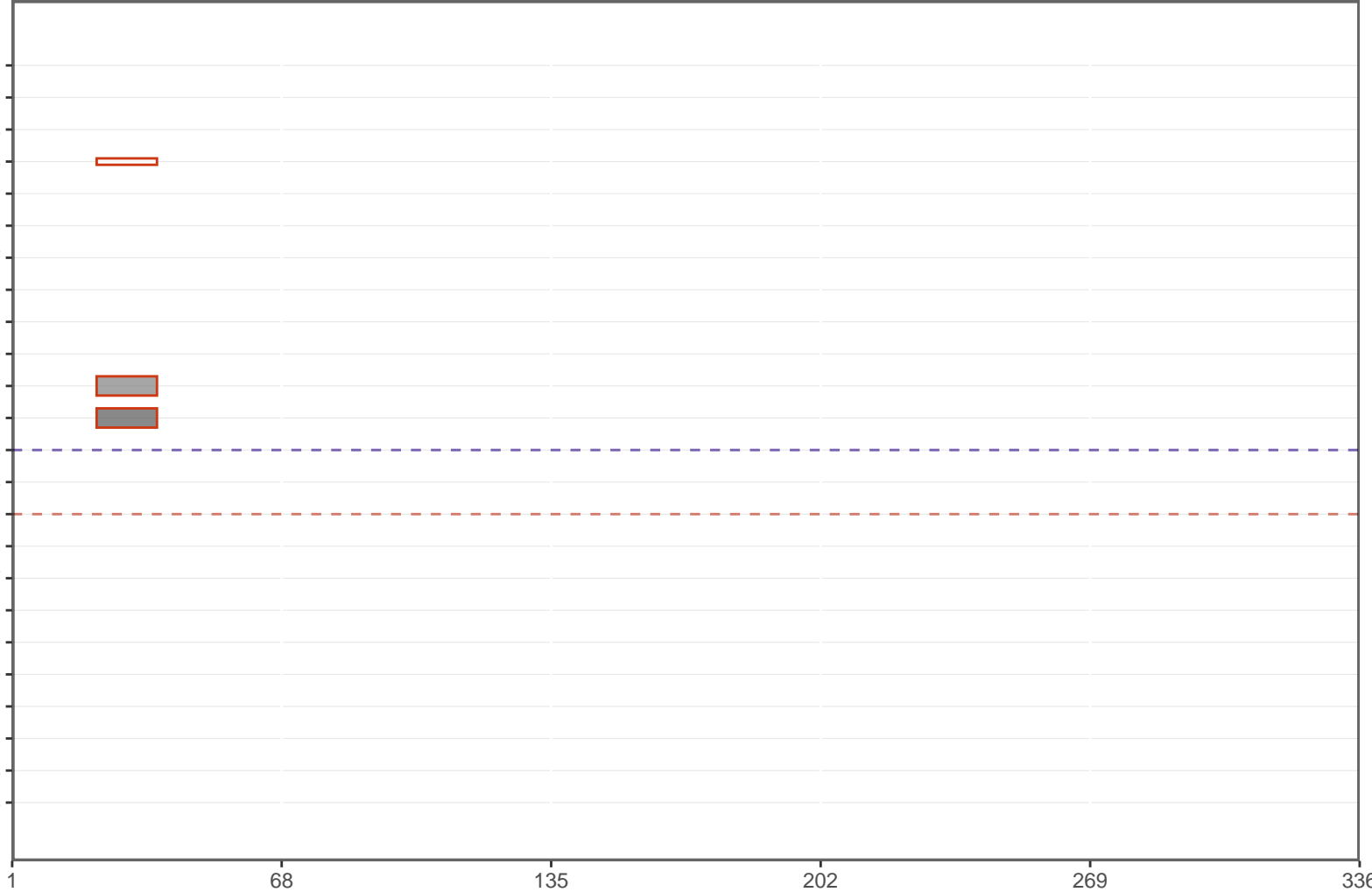
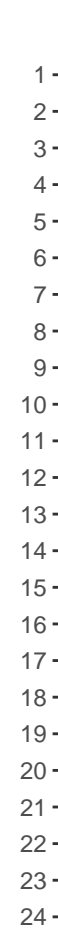
MW indication



Molecular weight



Gel Slice



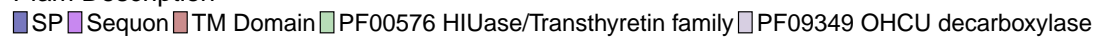
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RLAKLFADKADTAGTKIKSLARTNARKAEEDRVNIGAHILTAATGDAGAKPAHINRTRPPITTHVLDTERGCPNANGIEVQLEMWKKNGTRPQGFKANGGKWKVIGSATDKDGRGQLMMVLEALAPGIVRISFNTGEYIPDGFPPVIVGFEIREGKWDHFHVPLLLSFSTYRGE

NbL01g16350.1 3-hydroxyisobutyryl-CoA_hydrolase_1-like [MW = 42.61 kDa]

No. of times detected



log(intensity)



Values from



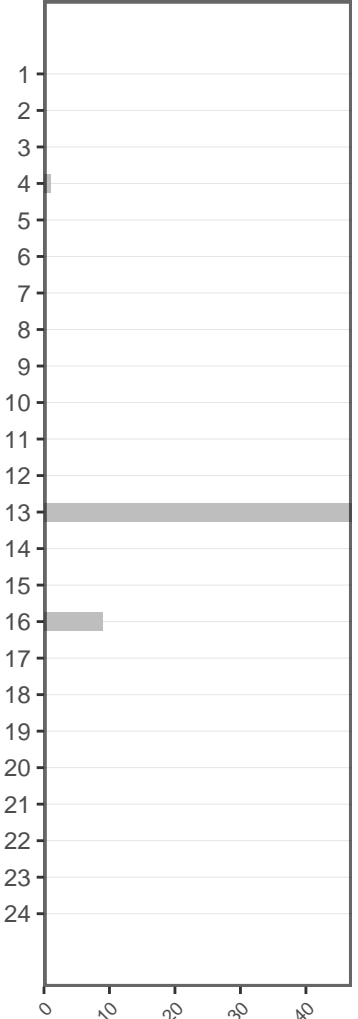
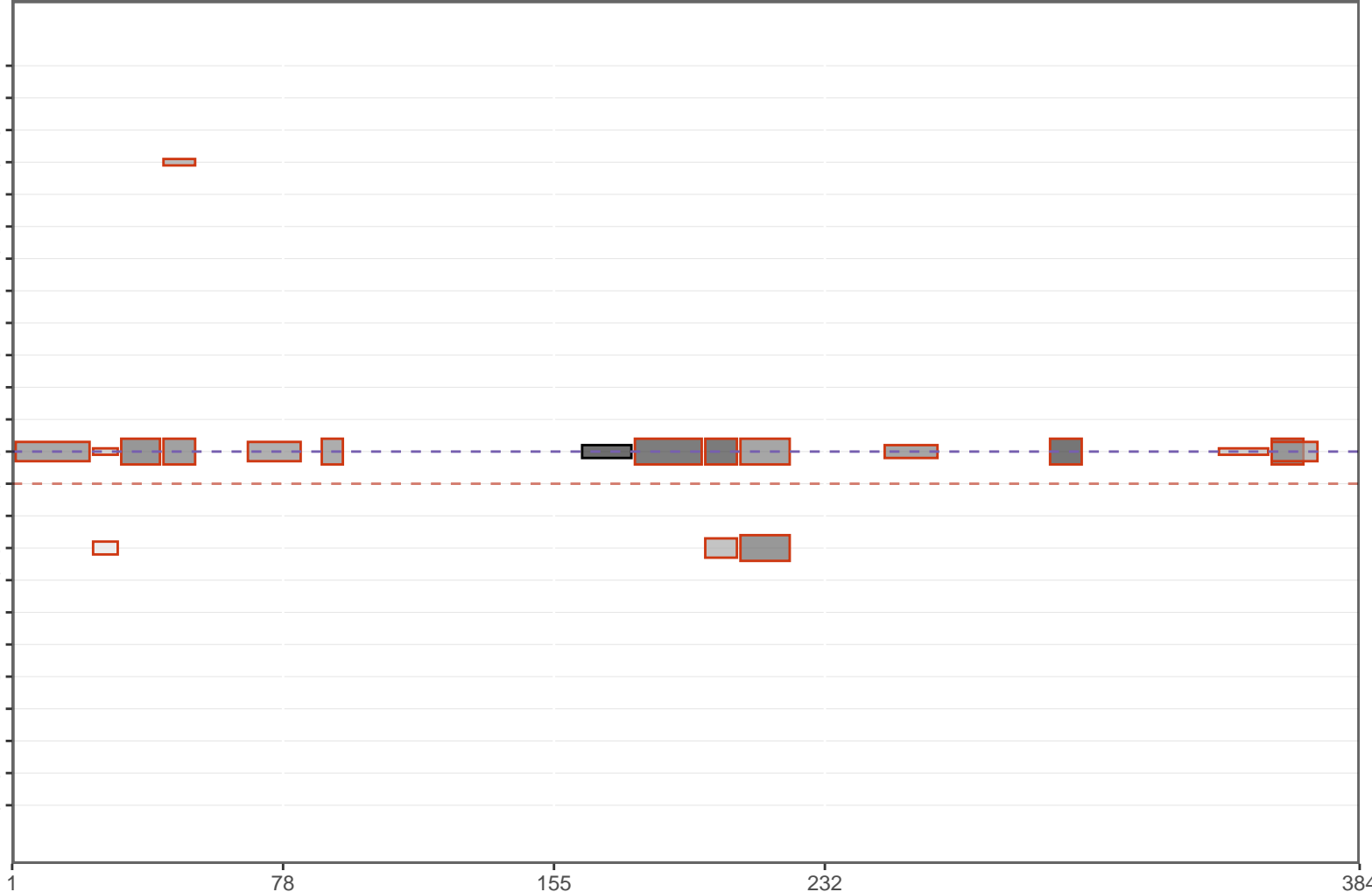
MW indication



Molecular weight

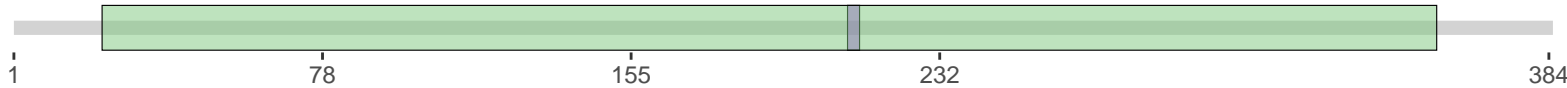


Gel Slice



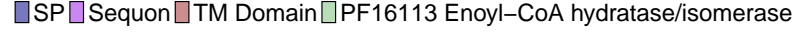
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RLDGAEMLACGLATHFVPSERLGLLEGLAVKWTSDPDVISTIRFSHPKLRKEGSSYHKMKIDRFSSRTVEHSALESEALNNDDWVSTHSLKKAAPTSLKLSLRIRREGRLGGVGSGLTREYRMVCHVLMGEFSKDFEFCGRALLIKDRNPKWEPRLDLIRDDVDYCFKNDDEDWEDLKLSPRNLPFYIAKL

NbL01g16140.1 UMP-CMP_kinase_3 [MW = 22.98 kDa]

No. of times detected



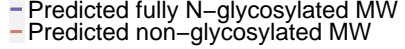
log(intensity)



Values from



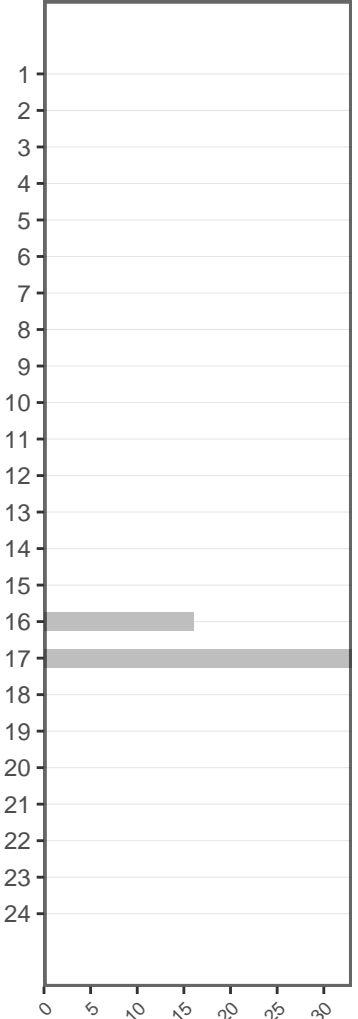
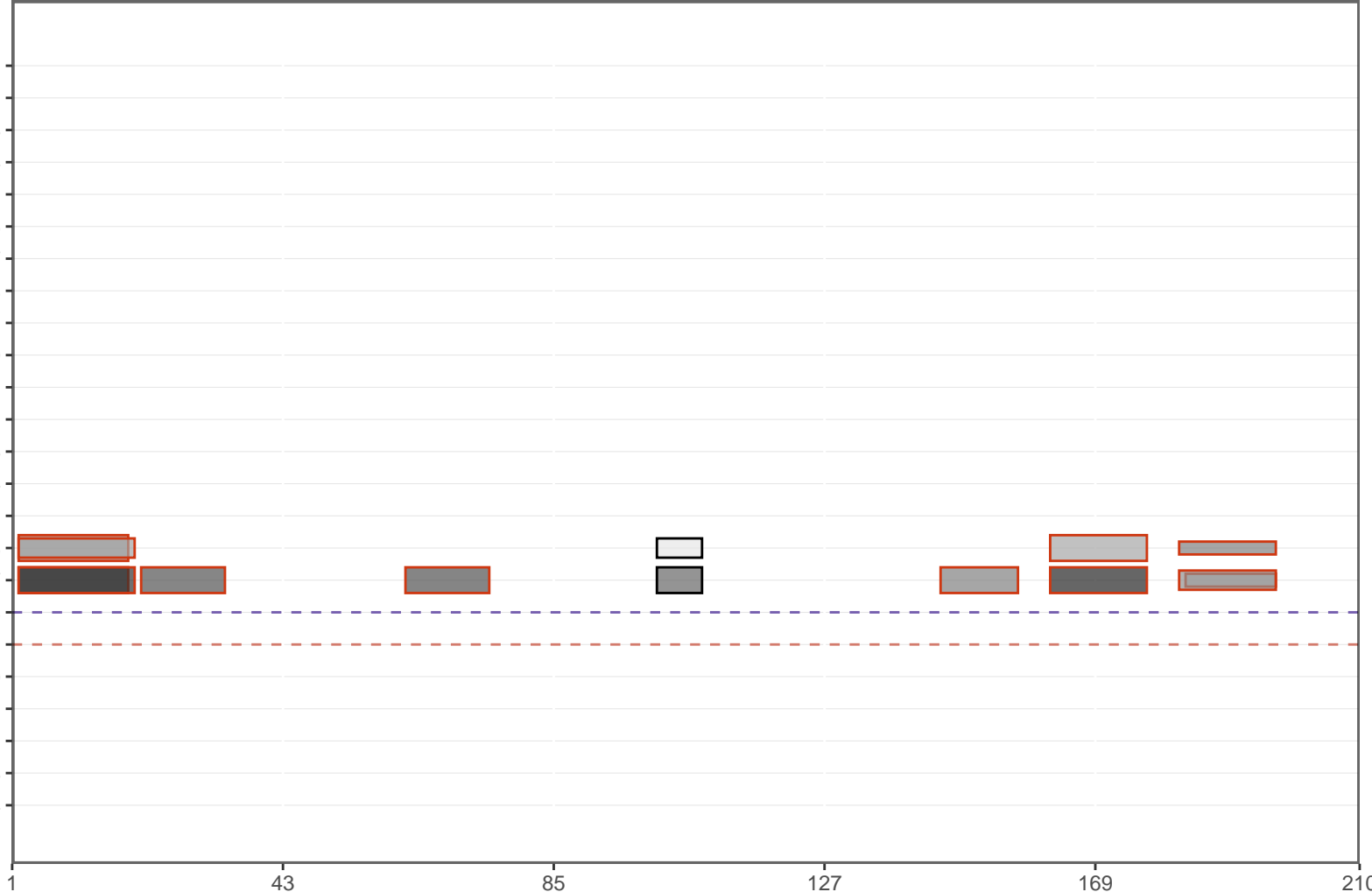
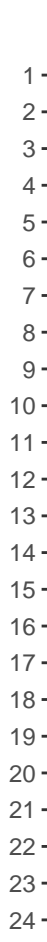
MW indication



Molecular weight

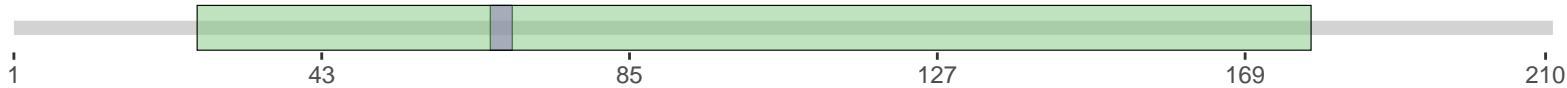


Gel Slice



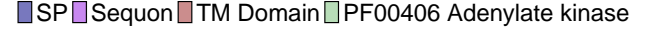
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AIDENGNCKFLIDGFFRNNEENRAAFESVTDGIEPEVLFDFDCEEEEMERRLLGRNNGREDNDTRKRFKVFLEGLPVIEYVNSKGVKRWIDAKPVGVEFAVKVAFVVEEVKY

NbL01g16040.1 acyl_carrier_protein_1_mitochondrial [MW = 13.75 kDa]

No. of times detected



log(intensity)



Values from



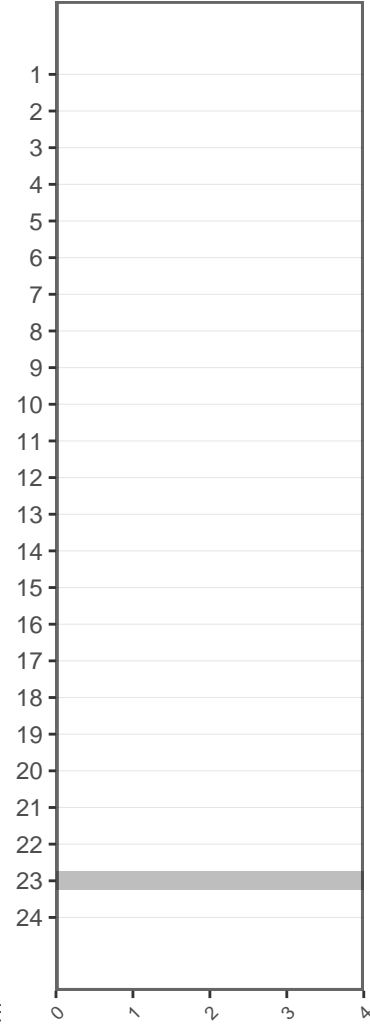
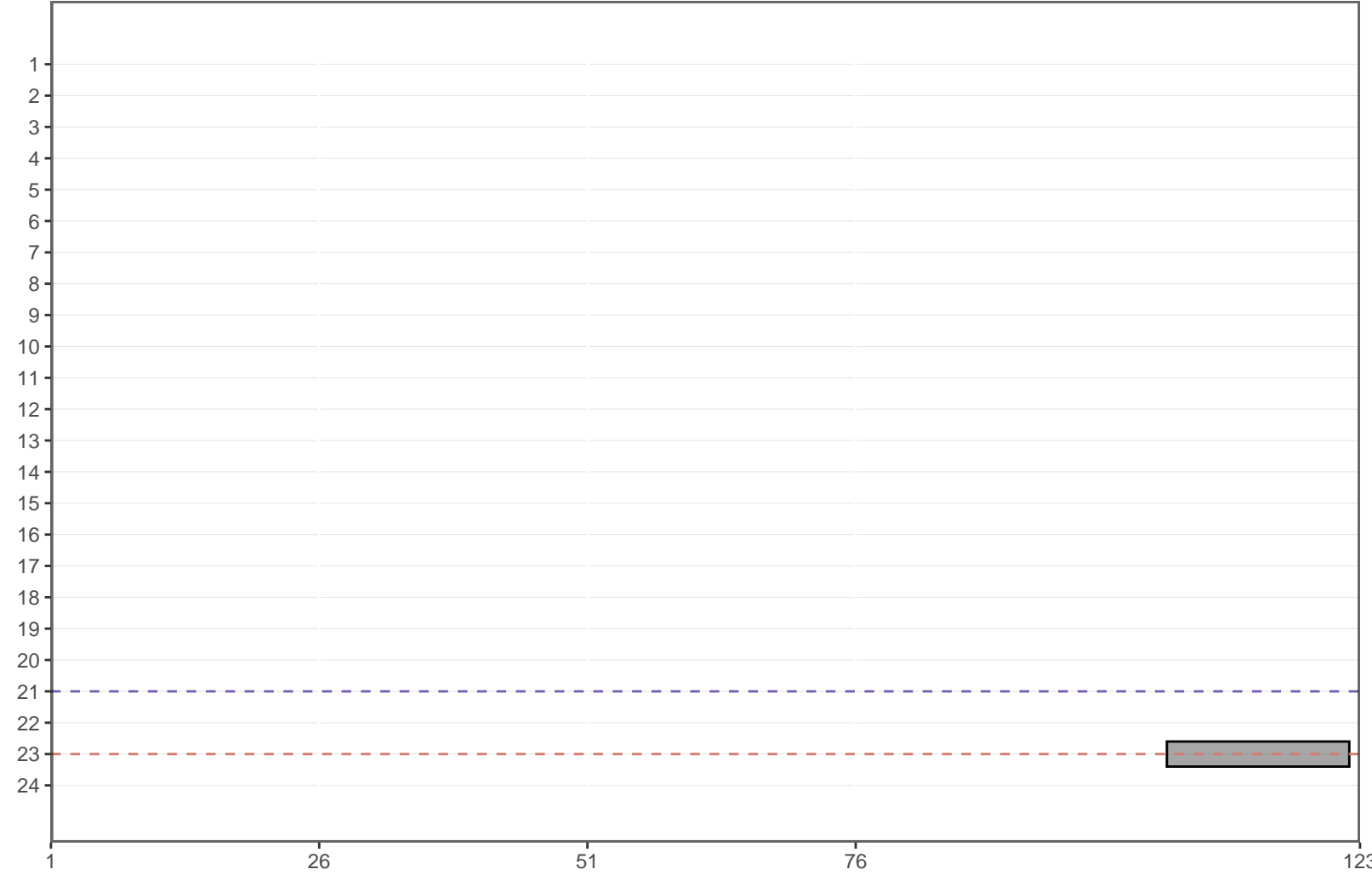
MW indication



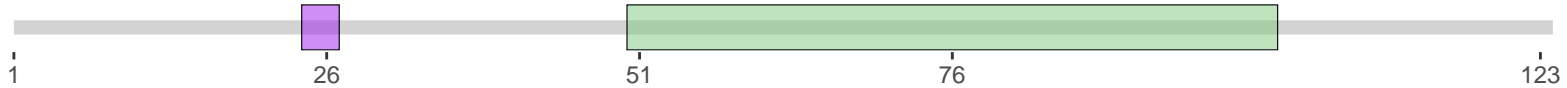
Molecular weight



Gel Slice

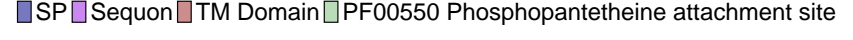


Protein length



Pfam domains

Pfam Description



Protein sequence:

IRVLDVVKCFPKVDPKIKVDFEYHFEKDLGLDLDLDTVEIVMALEEEFKLEIPDKEAVRIEGEHAIEYVNHFMSE

NbL01g15560.1 ras-related_protein_RABD2a-like [MW = 23.24 kDa]

No. of times detected



log(intensity)



Values from



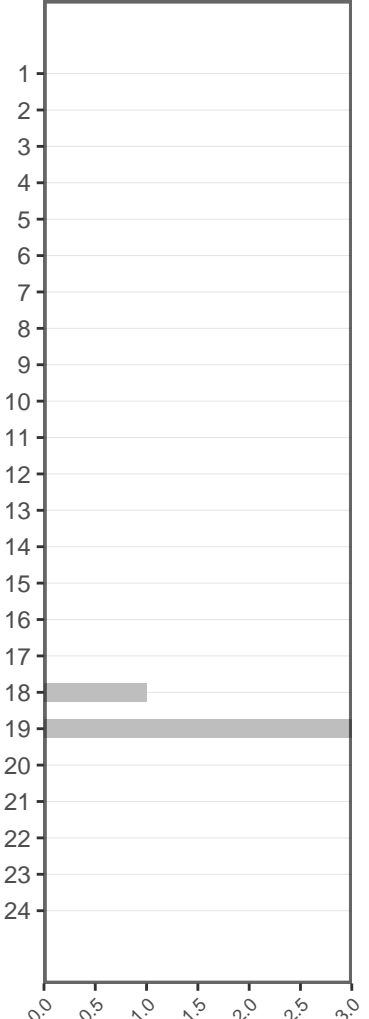
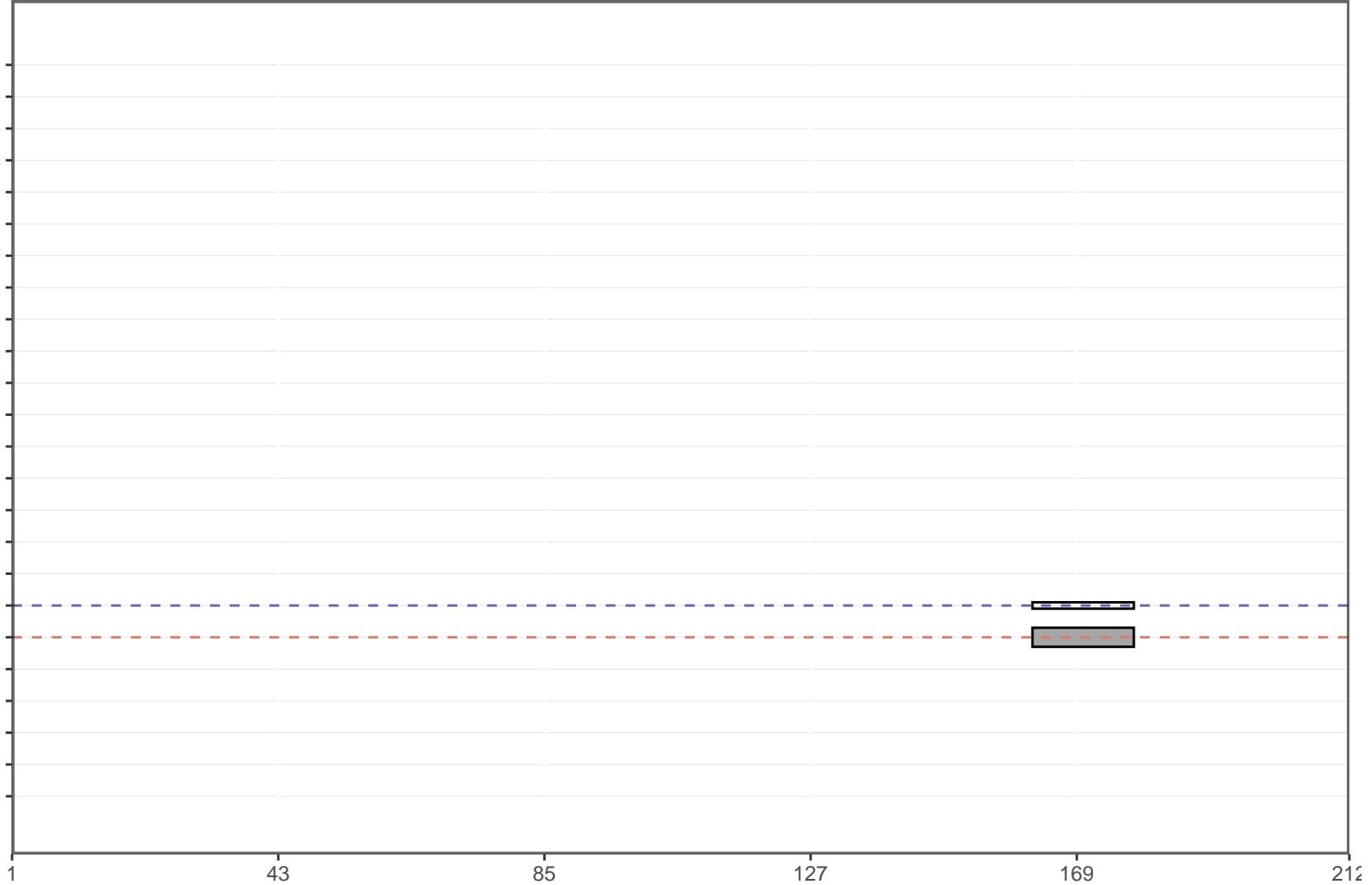
MW indication



Molecular weight



Gel Slice

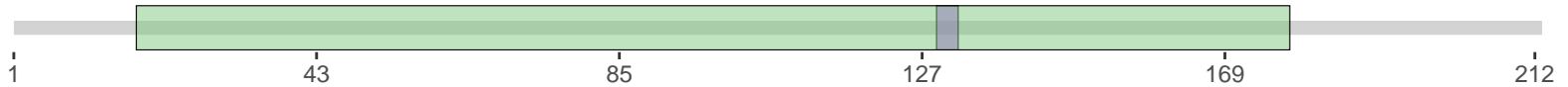


Protein length

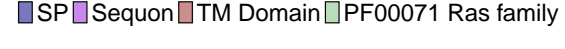


Peptide counts over 4 repeats

Pfam domains



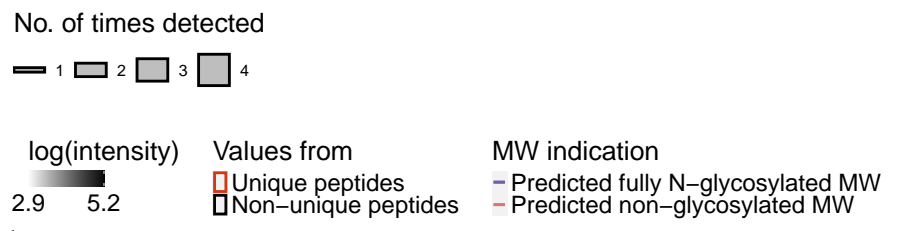
Pfam Description



Protein sequence:

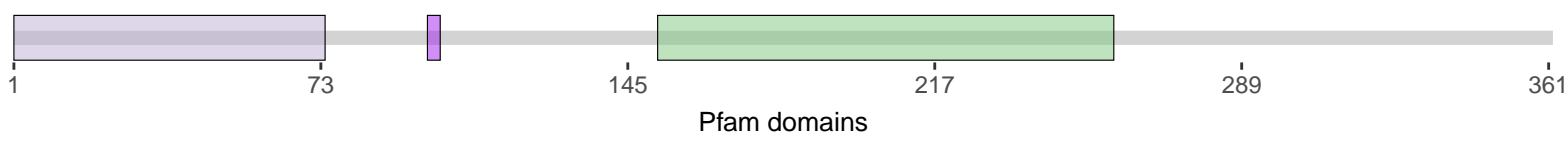
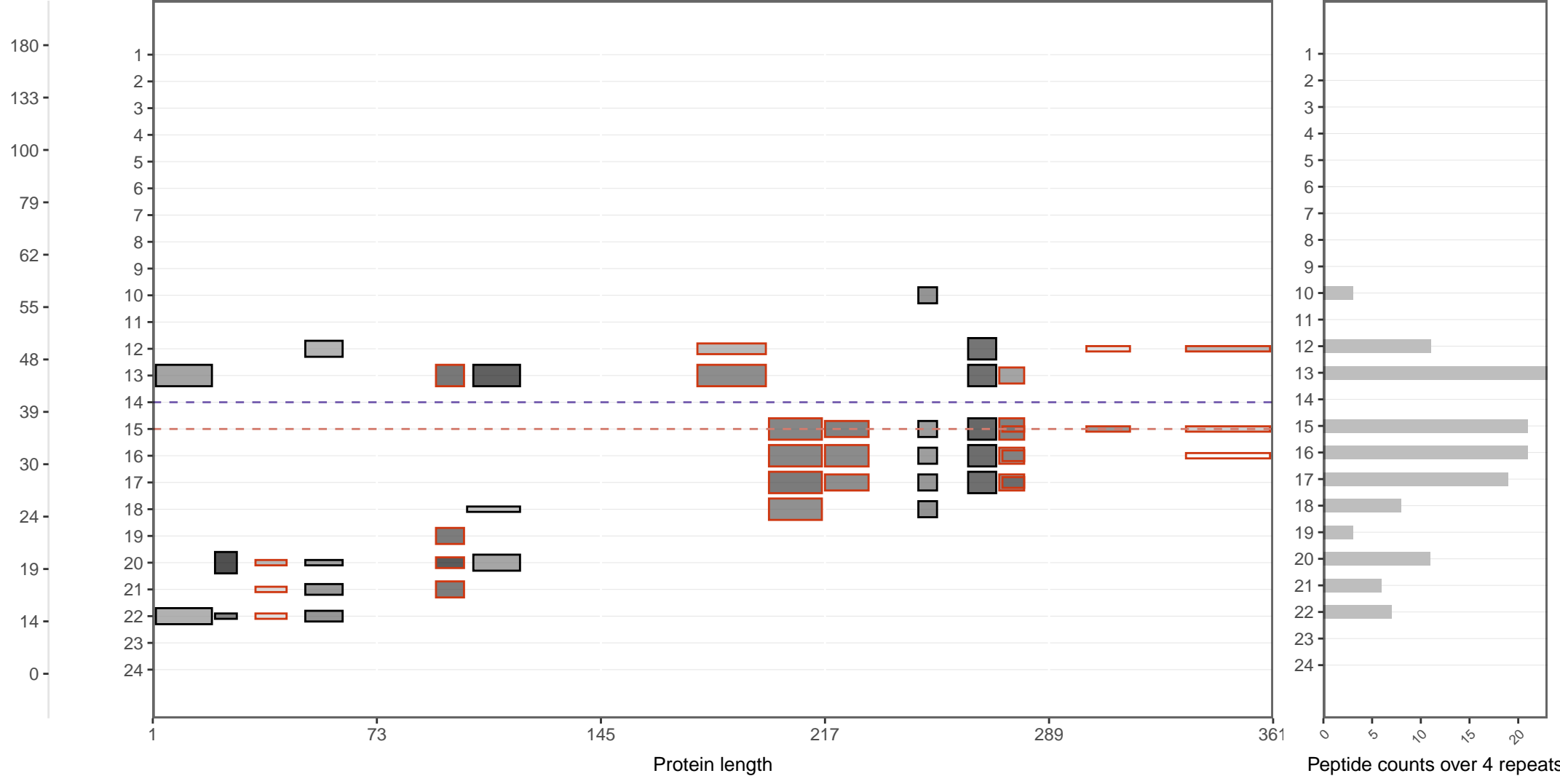
YDVTDOESFNIVKQWLEIGRVTFTNKNKILVGNKBDLTAIRVVSYETAKAFADKIGPFLKSAKDAISNVEQAFMMMTSARKNSMASQPATNTAKPPTVNIIRGGPVAQNSGGCCSS

NbL01g15550.1 plasminogen_activator_inhibitor_1_RNA-binding_protein-like [MW = 38.73 kDa]



Molecular weight

Gel Slice



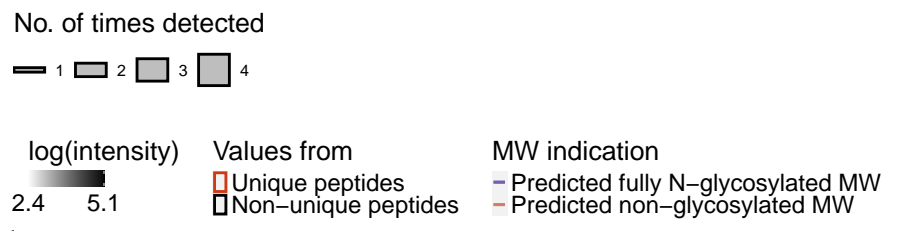
Pfam Description

SP Sequon TM Domain PF04774 Hyaluronan / mRNA binding family PF09598 Stm1

Protein sequence:

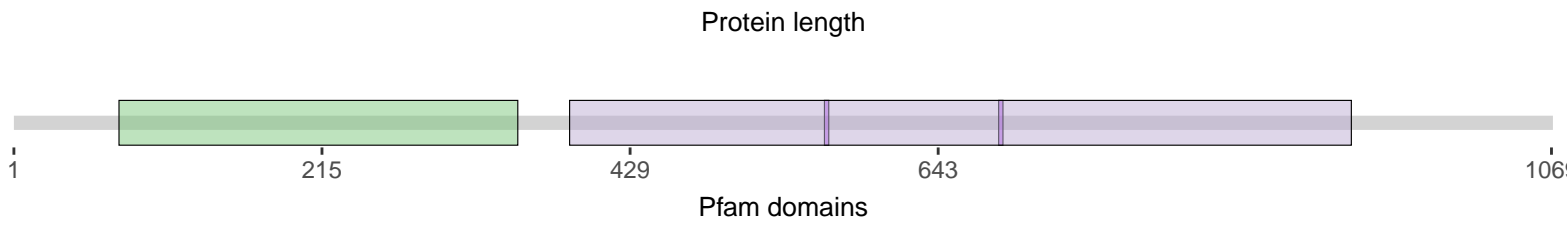
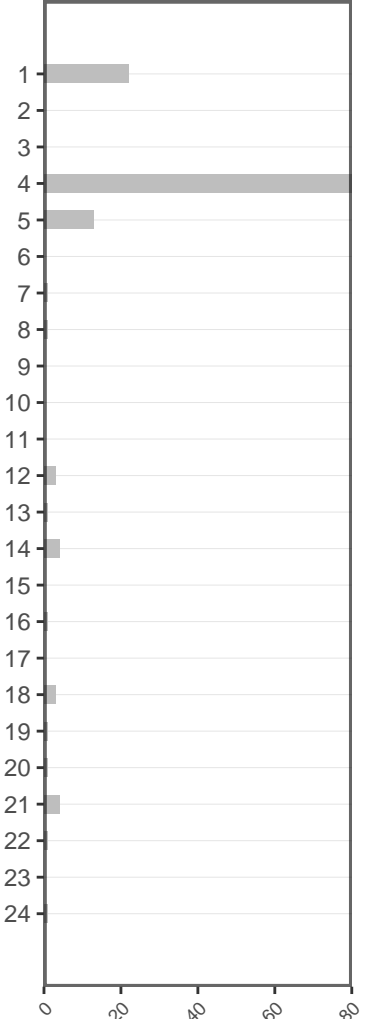
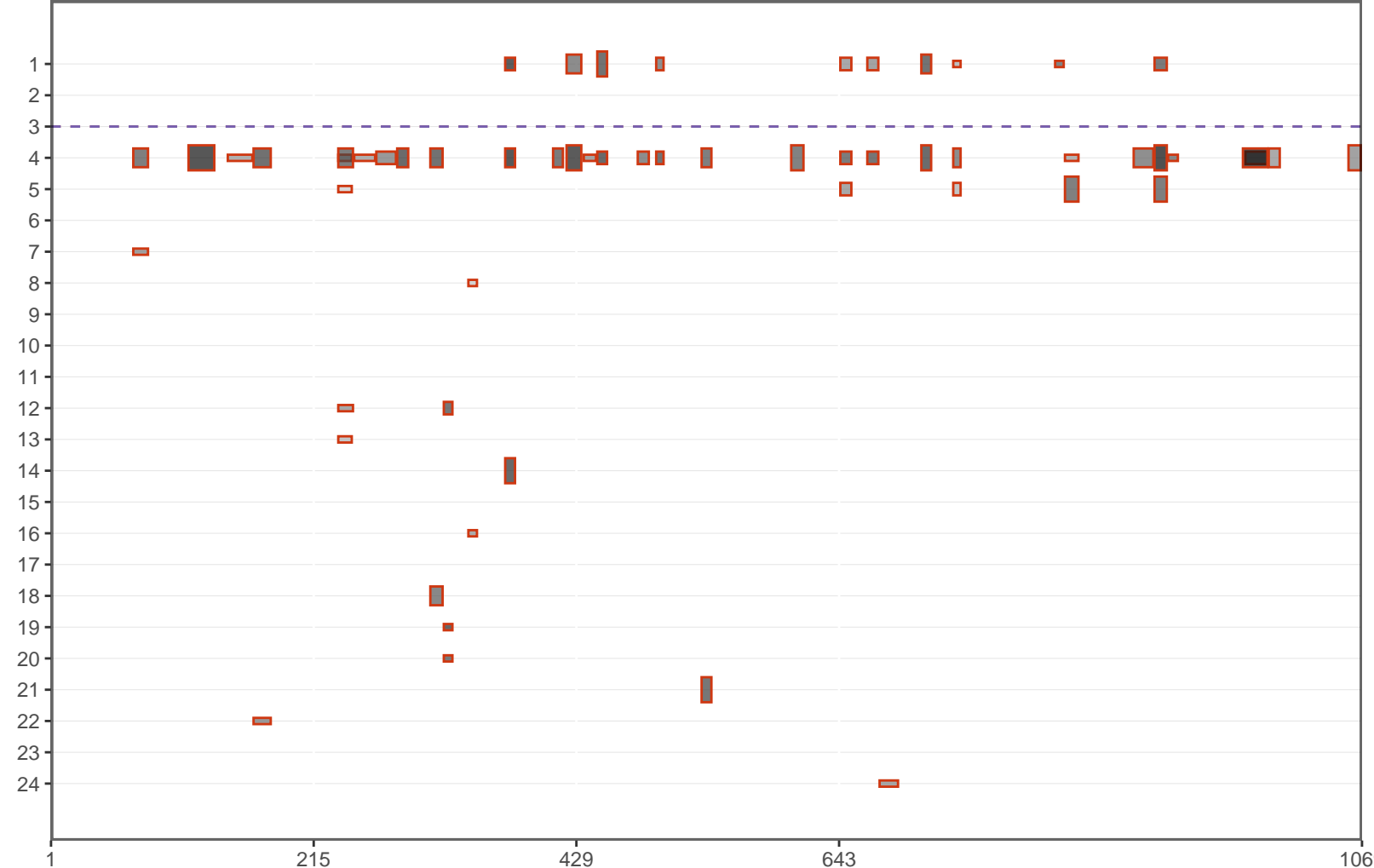
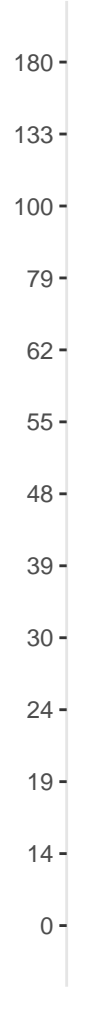
IEIKREGAGRGNGVSTGDADEVITQISDEIVANEKGNLNNAEKPSADGEAGDDKKENPVAAEADKEPENKEMTLEEYEVKLEEKRQALQALKTEERKYDTKFEFESMDQLSKKSSDDIFIKLGNPKDKRKEEAEKEKAKKAVSINEFLKPAEGERVYAPGGRGRGRGRGRGRGRGSGRGGADTTNVAEPPIEDPCHFTLGGK

NbL01g15540.1 glycine--tRNA_ligase_chloroplastic/mitochondrial_2 [MW = 119.77 kDa]



Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain PF02091 Glycyl-tRNA synthetase alpha subunit PF02092 Glycyl-tRNA synthetase beta subunit

Protein sequence:
 GIPIISDFPKSMRVNENAFSRIRWLAHGDVLPRIYAGVSGNIVSHGLRNPSTVKKLDAETIYANVMGSDAGLVVYKGRKKTMEHSNDAKSVHGHVMKSDLLDEVNVLVEAPLPVVGKFDSDFLPKELLIMVMQKHQRVYFAMTDENGLKLPYFITVWNGSDIKVYRKGNEAVLRAEFEDAKFFVEMDTRKRFSEFRPQKGLFHEKLGTMLDKMRIGNLVSEVGLSLGISEDKLKWQDAASLAMDALATAVWTEFTSLSGTMRHVALRDGYSEEIAEALFEIS

NbL01g15490.1 tRNA_wybutosine-synthesizing_protein_4 [MW = 38.9 kDa]

No. of times detected



log(intensity)



Values from



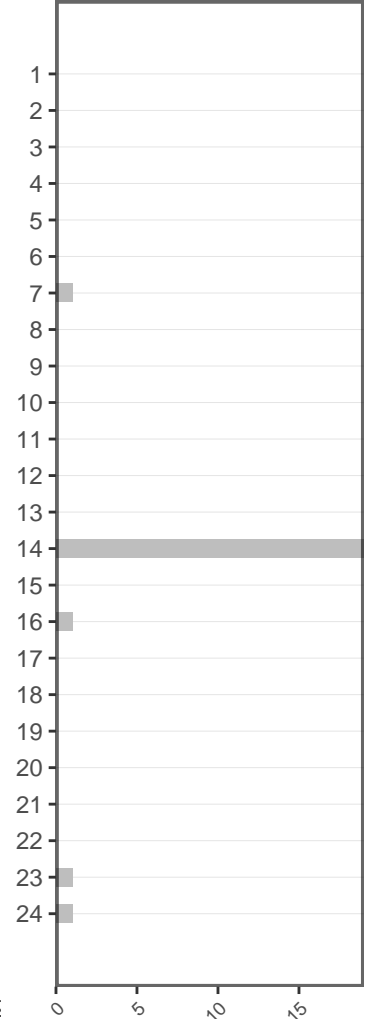
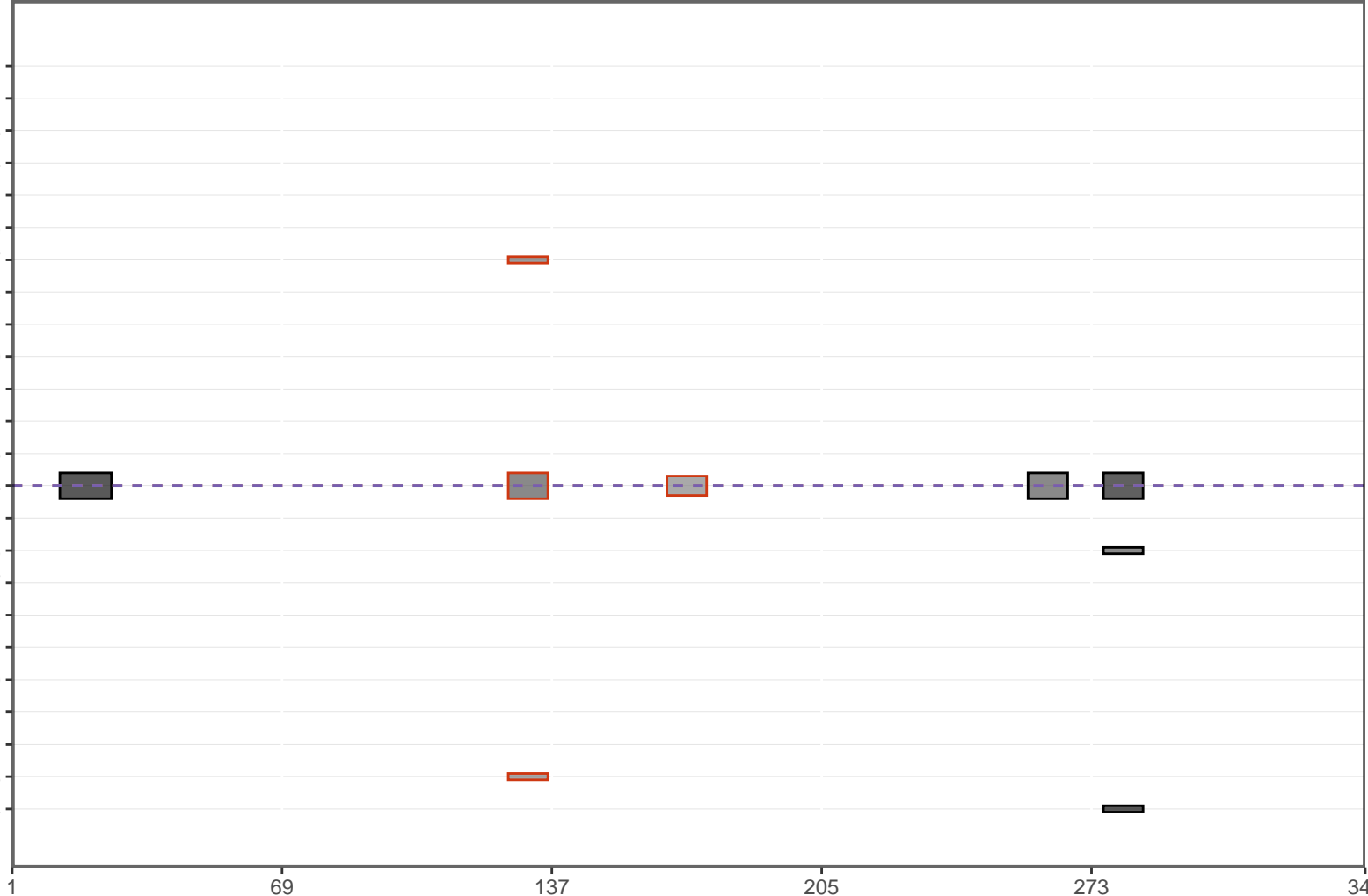
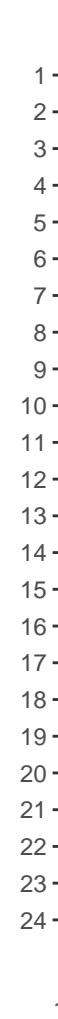
MW indication



Molecular weight

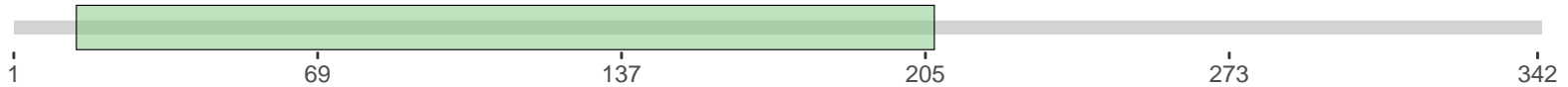


Gel Slice



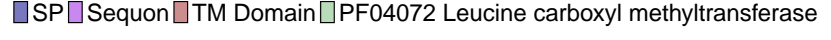
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL01g15190.1 nuclear_pore_complex_protein_NUP62-like [MW = 73.5 kDa]

No. of times detected



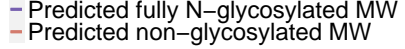
log(intensity)



Values from



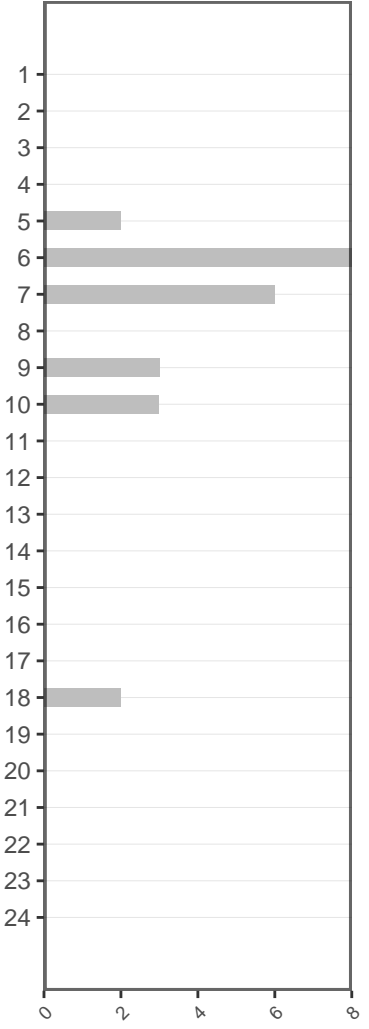
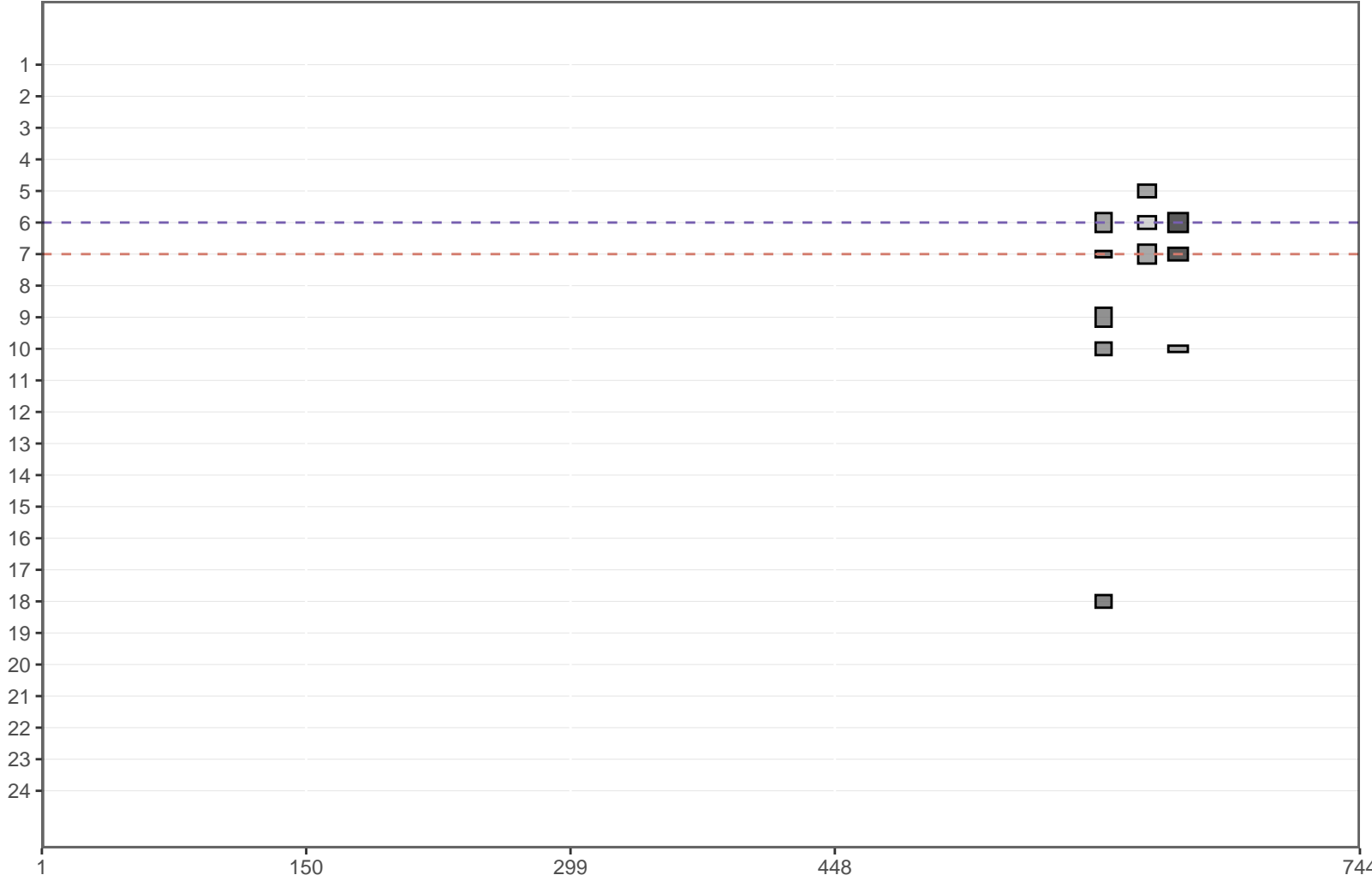
MW indication



Molecular weight



Gel Slice

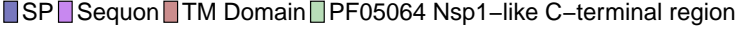


Protein length



Pfam domains

Pfam Description

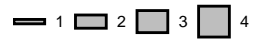


Protein sequence:

STSLSFSVTKGTGSSAAASGAPSLTAFPFSTSSAAASGATPVSKPAAGTGFSAISSLFSTVTTTTTGGTATATGTGSAVGTGTGTGSSLTFNPNAPSSAASTTSAAPTTFSSLSKKTGASTAALPFSFVPTTSGAATSAAPTSSALTVASSGTTSTVAATSTLALPSESTGKGVEEIKKQWNAELQERSANFRKQANAIADWKRILGNRDLRLLESEVGVVETQTSLERQLEIETHQEEVVKALQSMEEAADRIVKDERGVLDDEAASTRDMAYEQAEF

NbL01g15180.1 elongation_factor_G-2_mitochondrial-like [MW = 87.4 kDa]

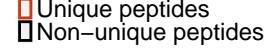
No. of times detected



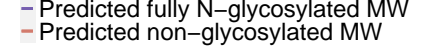
log(intensity)



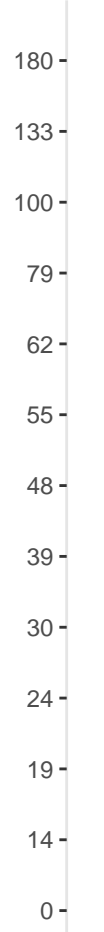
Values from



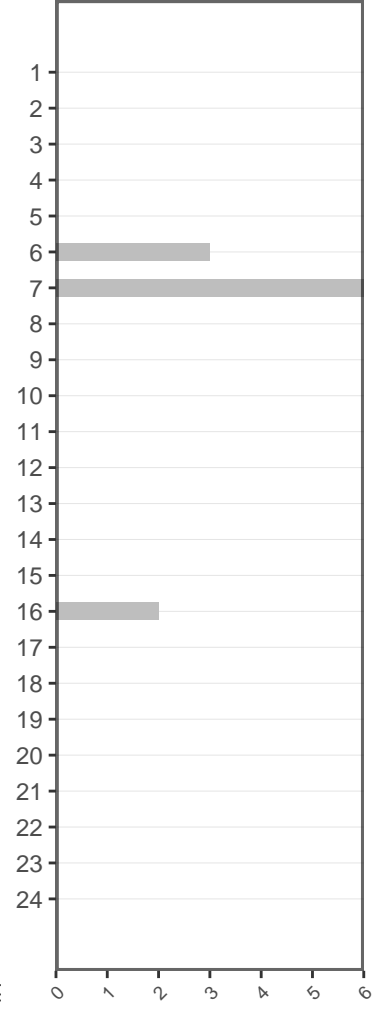
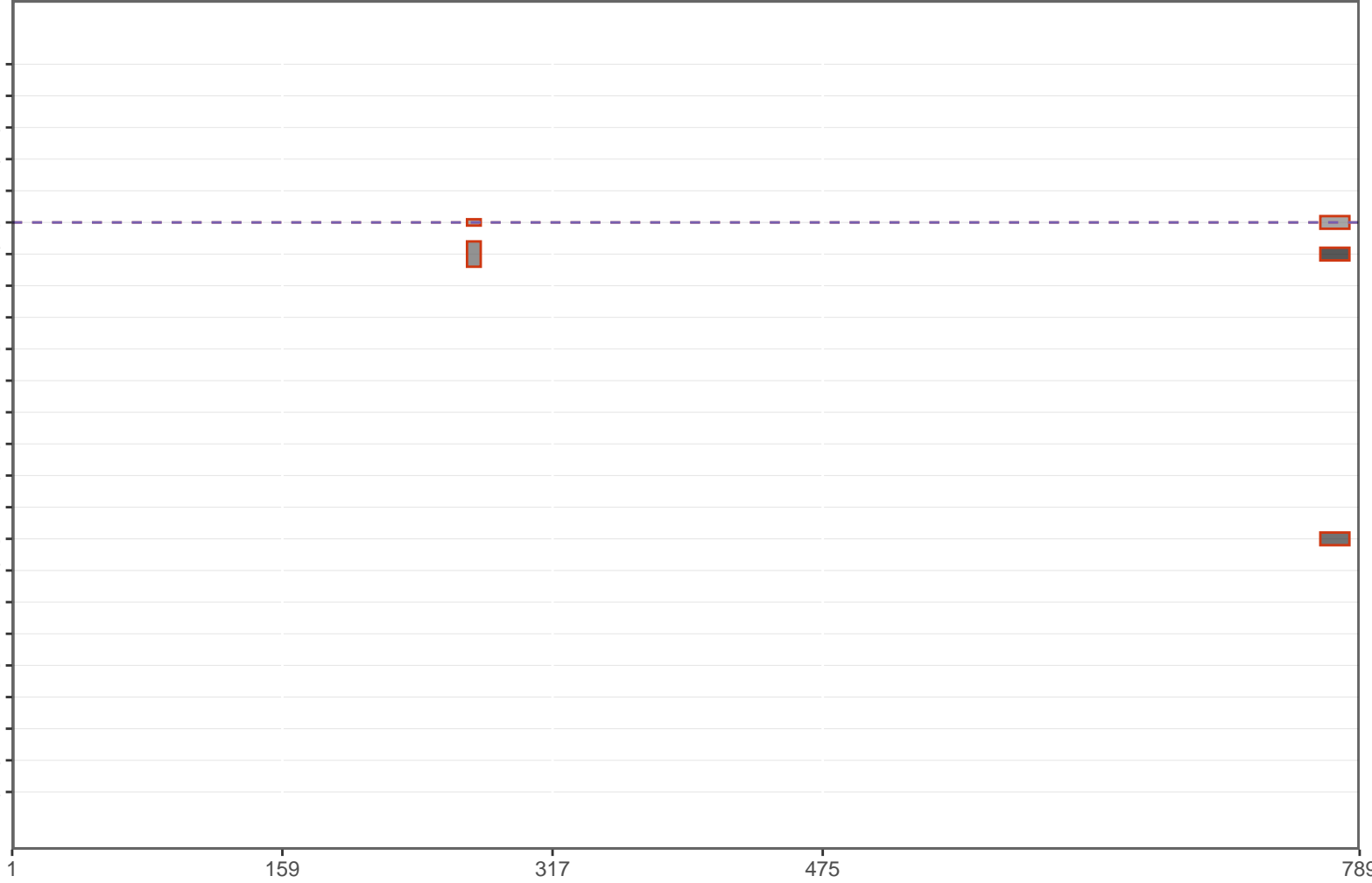
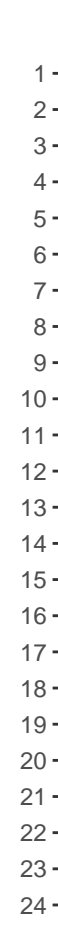
MW indication



Molecular weight

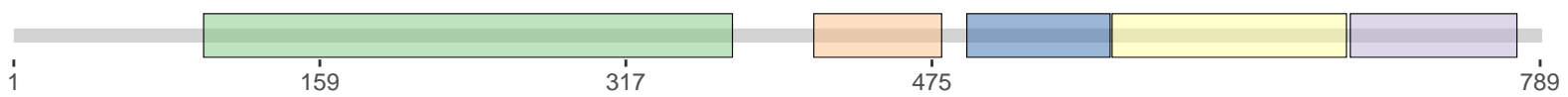


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00009 Elongation factor Tu GTP binding domain
- PF00679 Elongation factor G C-terminus
- PF03144 Elongation factor Tu domain 2
- PF03764 Elongation factor G, domain IV
- PF14492 Elongation Factor G, domain III

Protein sequence:

QTNLEKVTLCSPPTGALVAFKLEEGRFQGLTLYRIVEGVIRKGDFFINVNTGKRIRVPLRMHSNEMEDKGEAHAGQWVFGVDCASGDTFTDGGVYVYMTSMNVPEPVMASLAFVSVKDTGGGFSKALRFQREDPTFRVGLDAESGETISGMGELHLDYVERIRREYKVEAQVQKPRVNFRETTIKRADFDLHKHGSGGGGGYGRVIGYVEPLEGGSGKFFEDNMLVGGAPSNFVAKIEGFRFAANSGLGHIPVENIRVATDGNHIVDSSLELAFKLAS

NbL01g15170.1 3-hydroxyisobutyryl-CoA_hydrolase-like_protein_1_mitochondrial [MW = 45.06 kDa]

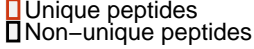
No. of times detected



log(intensity)



Values from



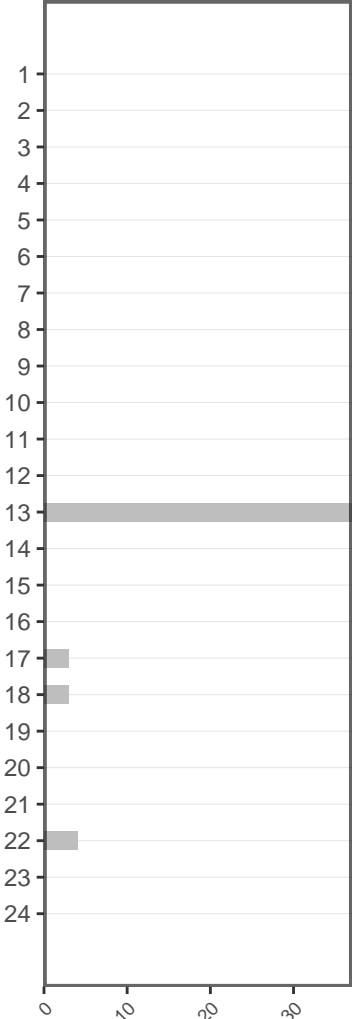
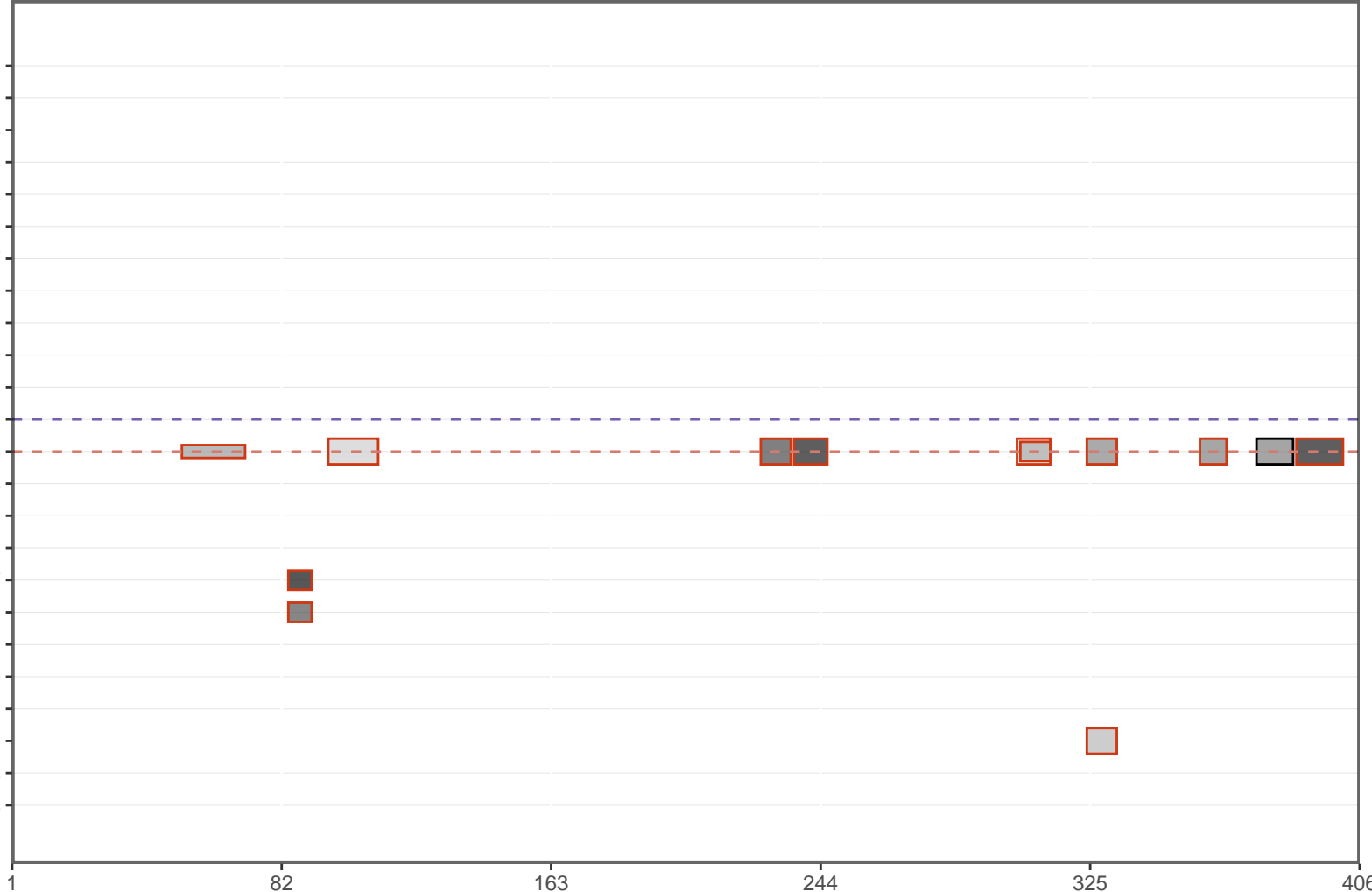
MW indication



Molecular weight

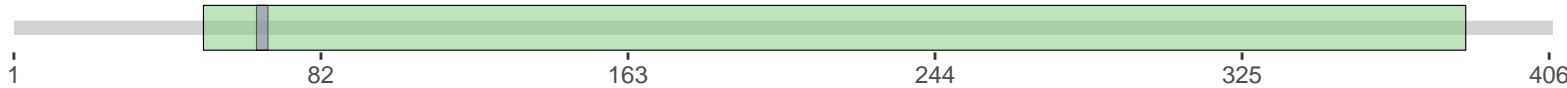


Gel Slice



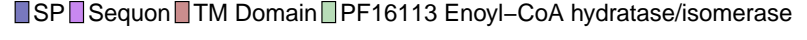
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LPQYLGEYLALTYGDKINGAEMISGGLATHYLSKAKLPLIEEGLGKLMTDGDPFVIERBLENGCGEVHPDPTFVLRHRIETLNGCFHDTVEEIDALEEBAANKQDAWCVSTLRKLGKETAPLGLKVLRSRIREGRHGTLDGGLREYRMSVQAFSGDITNDFCEGVRARLVRDFAPKWDPPFELDKVITDDMVDQVYFSRLTAFERFELELPTDQREAFY

NbL01g15160.1 malate_dehydrogenase_cytoplasmic-like [MW = 35.84 kDa]

No. of times detected



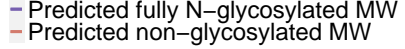
log(intensity)



Values from



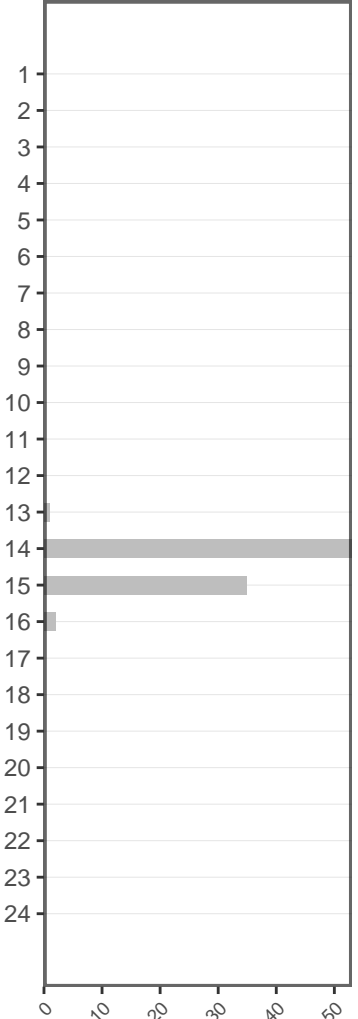
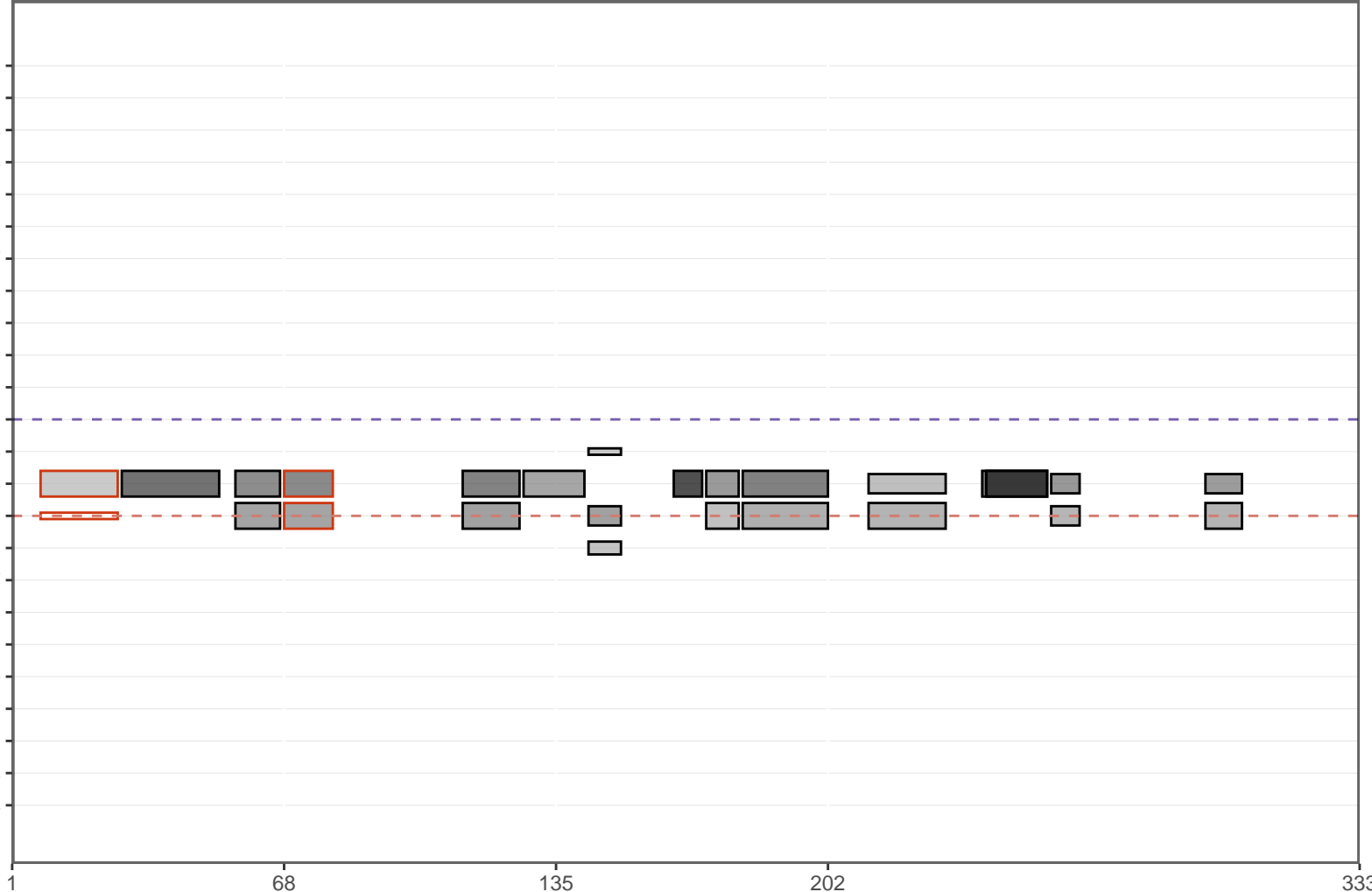
MW indication



Molecular weight



Gel Slice

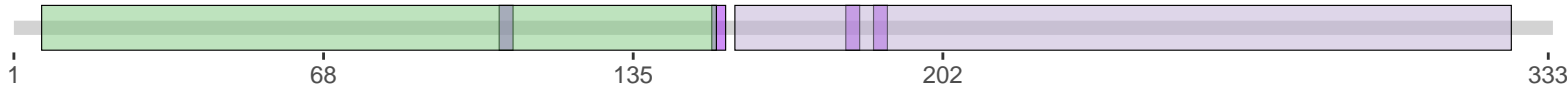


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description

- SP
- Sequon
- TM Domain
- PF00056 lactate/malate dehydrogenase, NAD binding domain
- PF02866 lactate/malate dehydrogenase, alpha/beta C-terminal domain

Protein sequence:

CLTRLDINRALGQIBERLNVHGGDKVNTWGNHSSTGYPDVNHATVKFTSGEKVRELVNDQWLNTEFFITVQGRGAANKARKLSALSAASSAGDHIRNIVLGTPTKGTWVSMGVYSDGSGYPPGLYSPFVTGKGEWISVQGLKIDFBRAMDATAKELIEKALVGLN*

NbL01g15120.1 T-complex_protein_1_subunit_alpha [MW = 59.14 kDa]

No. of times detected



log(intensity)



Values from

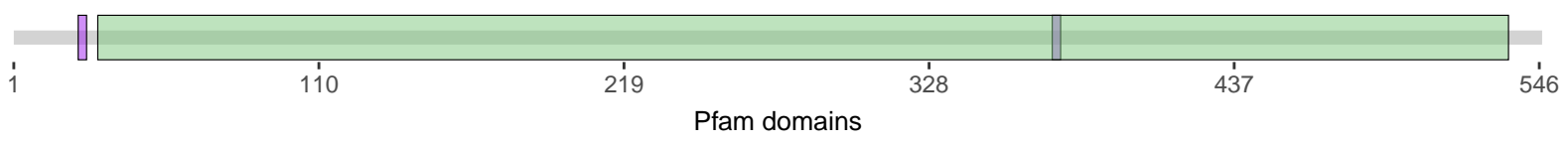
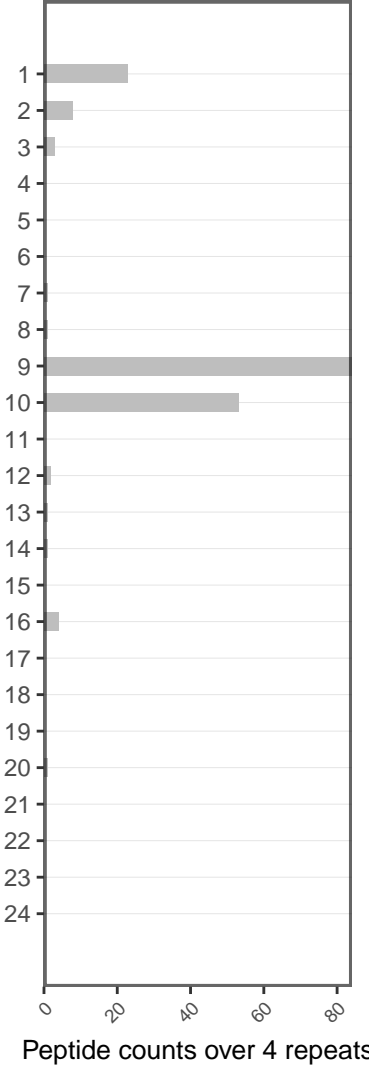
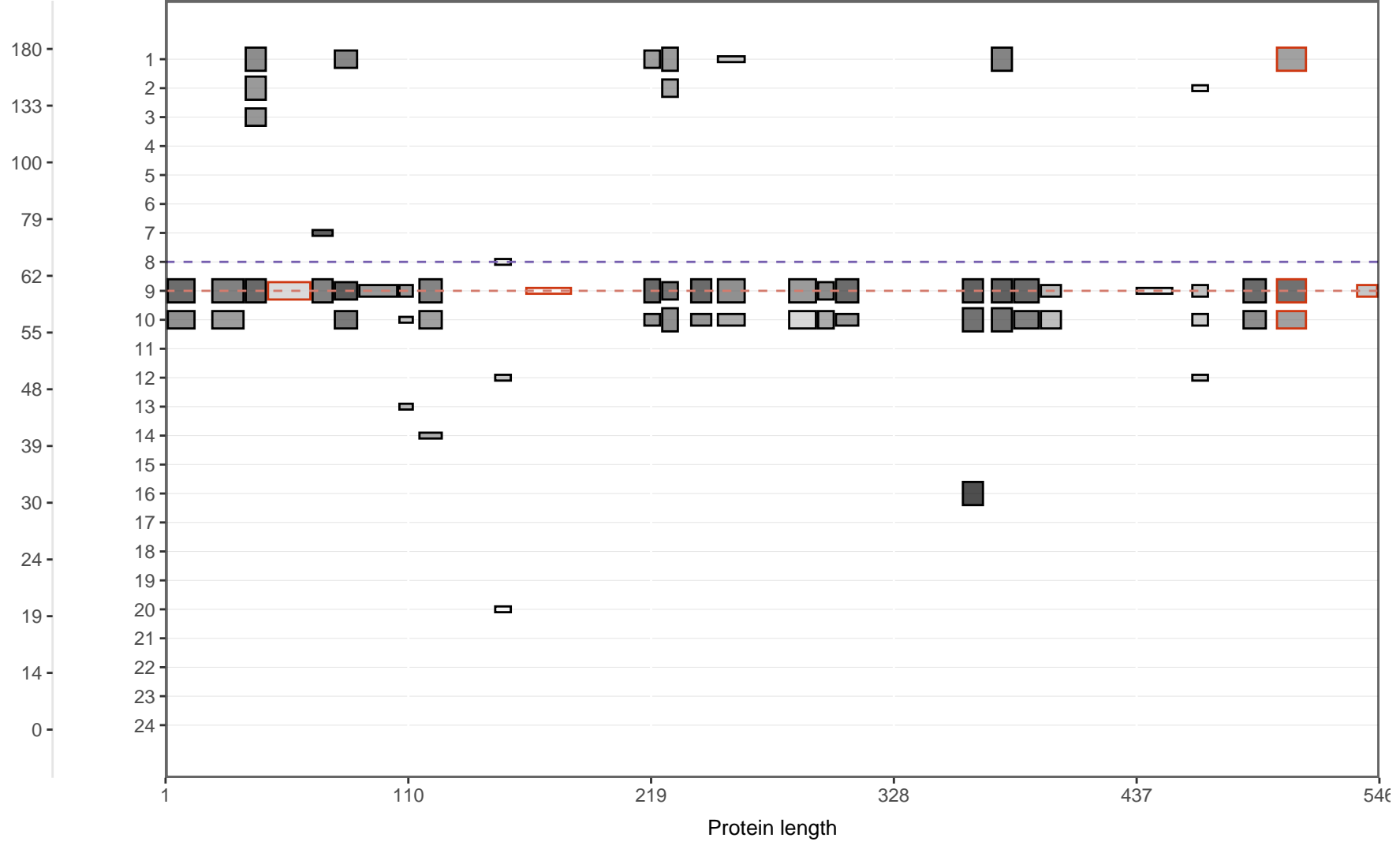


MW indication

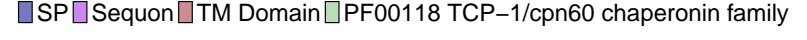


Molecular weight

Gel Slice



Pfam Description



Protein sequence:

DPRELERRQREADMTKERIGKLLSAGANVYVLSKGGDDMALKYFVEAGAVRRVRKEDLRHWAKATGATVSTFADMEGEETTFEPILLGHAEVEVVEERIAADDVVWVGTNRNSSVSLIRGANDFMLDEMERALHDALGVKRTLESTTVVAGGGVAEALGVYLELATTLSGREGLAMQFAESLLVFPKVLNNAAKDSDDLKVRKSRGSHYLAGTKADKKHLSGSMGLDLAKGTVRNMLEAGVIEPAMGKWKIIGFATEAAITLIRIDDMIRLVKVDENGDQD

NbL01g14870.1 ATP_synthase_subunit_O_mitochondrial-like [MW = 26.42 kDa]

No. of times detected



log(intensity)



Values from



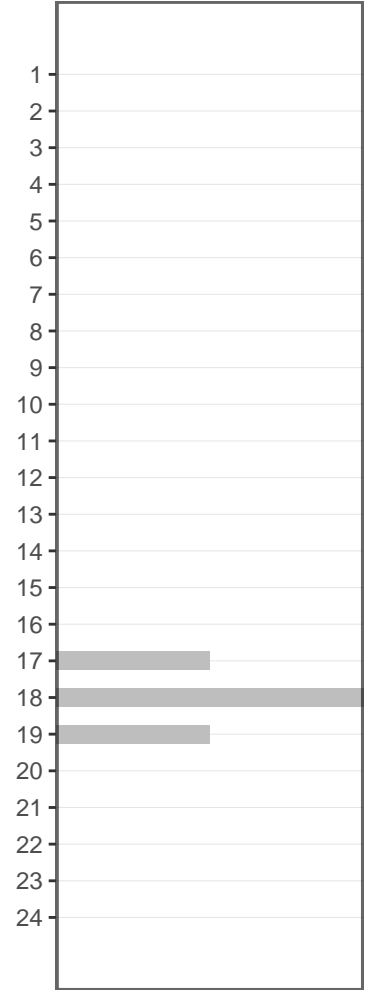
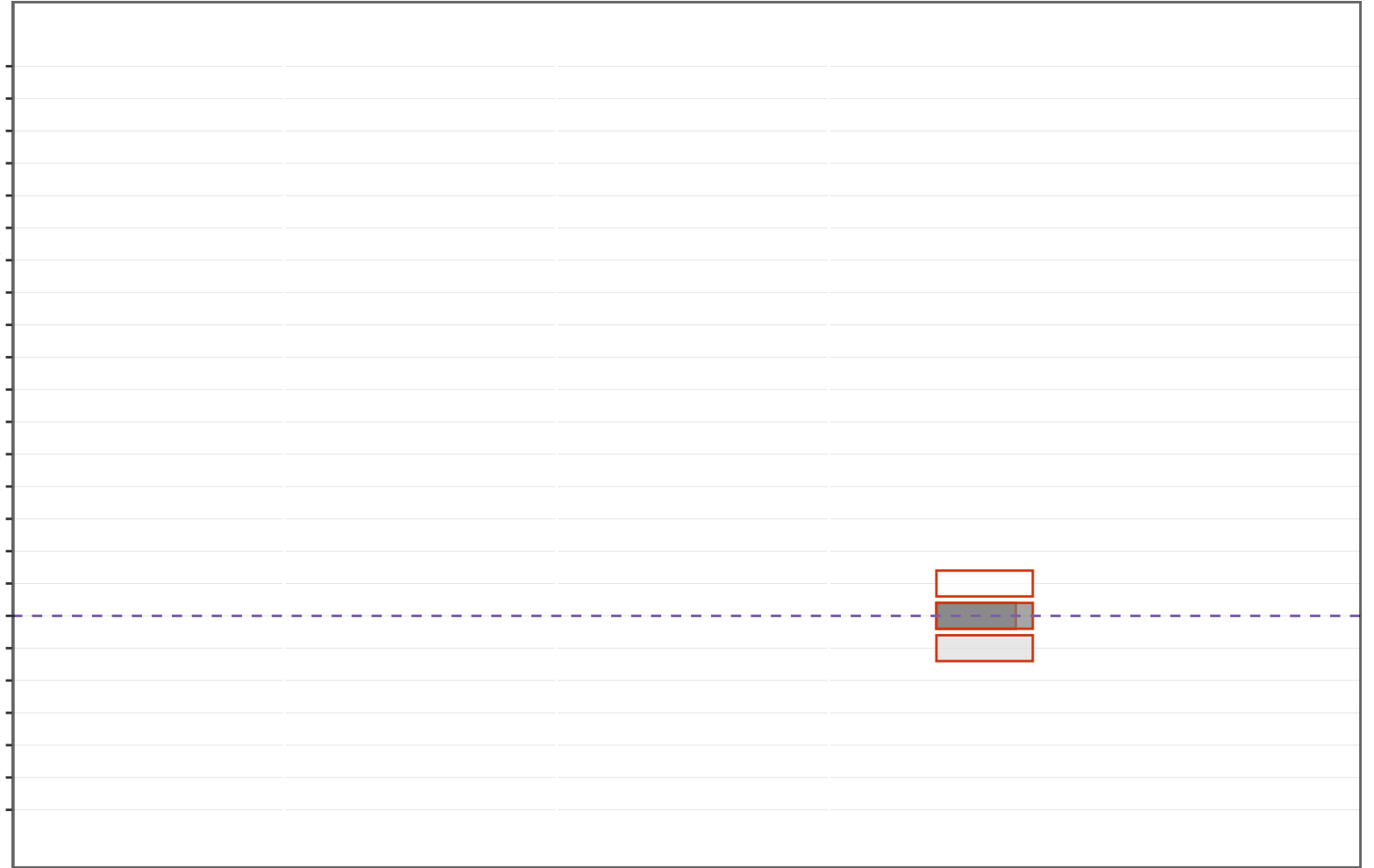
MW indication



Molecular weight



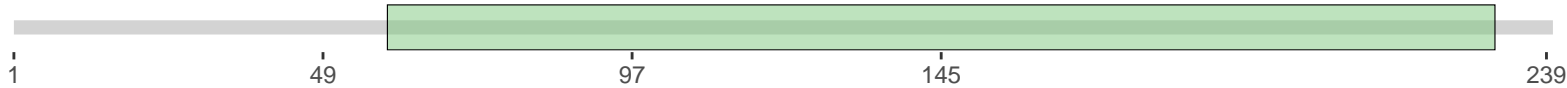
Gel Slice



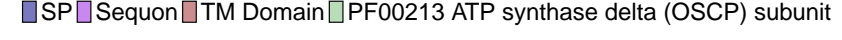
Protein length



Pfam domains



Pfam Description

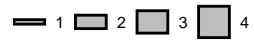


Protein sequence:

IVPTDTRVKAISDCAGANFGDLTRNFLVLAENGRLLKHIDIAKRAELTMAHKGELKATVTVVPLPPEEEKELKELTGDVMGKGGKWNIEQKIDPSLGGVIEFGQKVFDMISIRTRAROMERLLKEPLNF

NbL01g14860.1 polyadenylate-binding_protein_2-like [MW = 22.23 kDa]

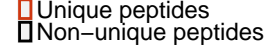
No. of times detected



log(intensity)



Values from



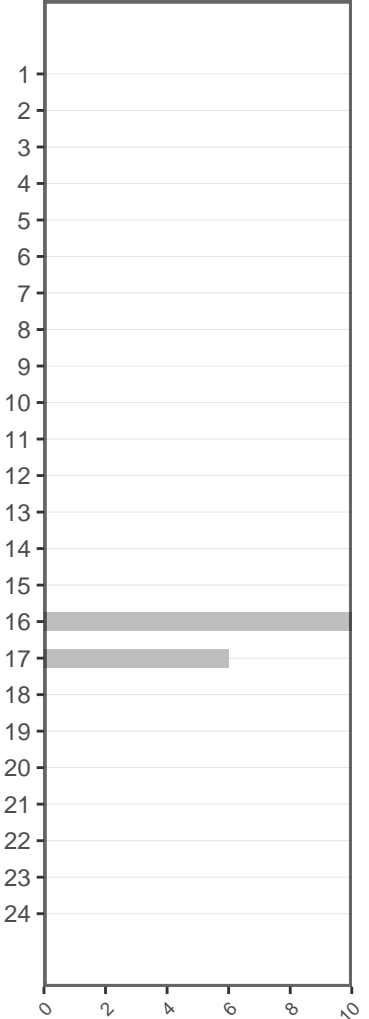
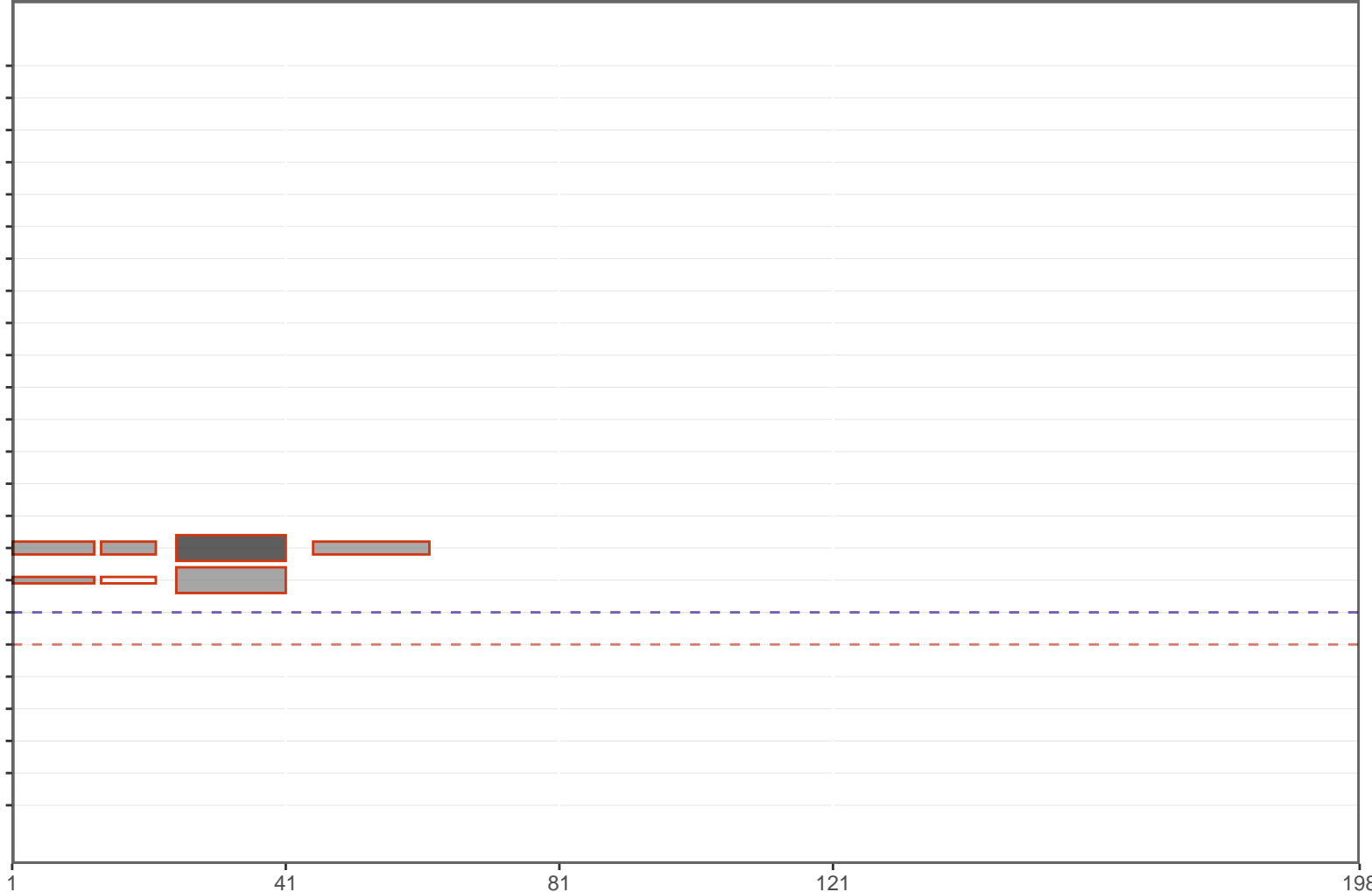
MW indication



Molecular weight



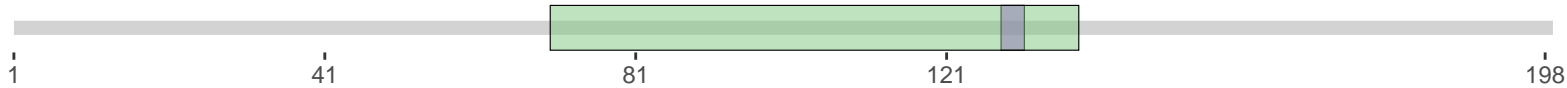
Gel Slice



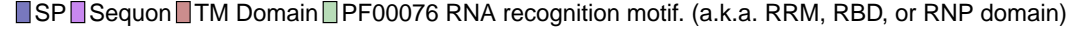
Protein length



Pfam domains



Pfam Description



Protein sequence:

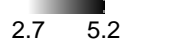
IQHFGACGTYNRVTRTRNFGGPKGWVVEFLEAEAVGEALLNESELHGROIKVSAKRTNVPGMQGFARRRPNPYMGFRGQTRFIPAPVYFSGYGGKVPRARAPMRYSPYF

NbL01g14840.1 protein_EXORDIUM-like_2 [MW - SP = 29.18 kDa]

No. of times detected



log(intensity)



Values from



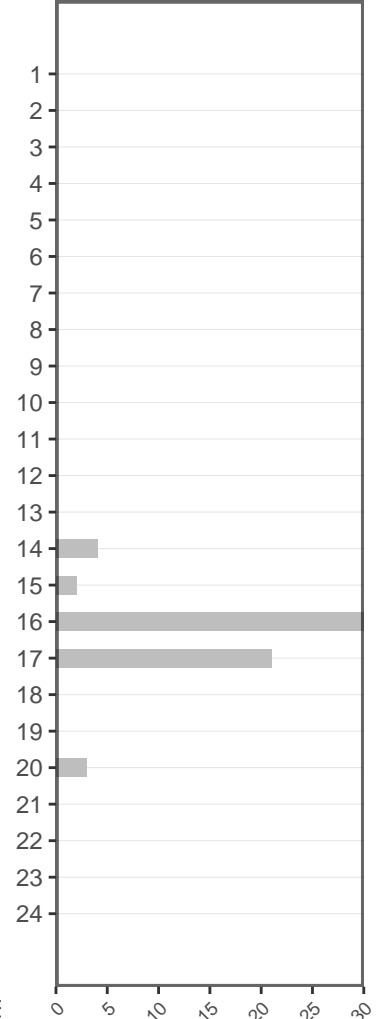
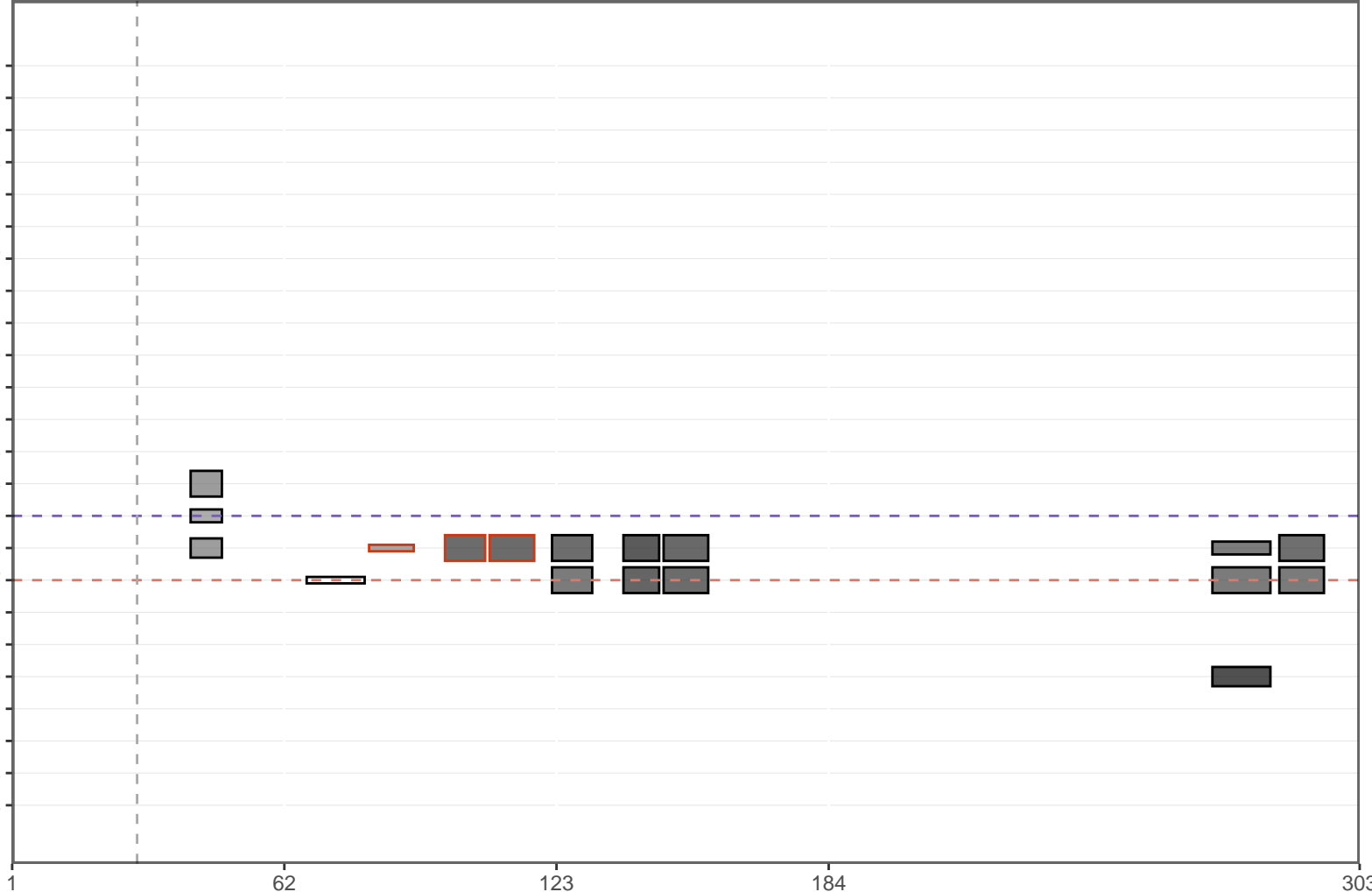
MW indication



Molecular weight



Gel Slice



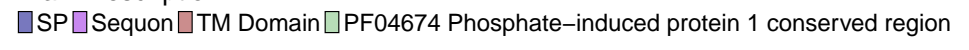
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LVLTKADVFEVGFCEMRGDTGHSRGMRFYAWVWVNGNETGQAGGGAWFFHQPYPGQTPPLVAPNSDGVGDMINVATVLAQTVTPNPNNGYFDGDPATAPLEAVSAGCTGMFGSGSEYRPGVGVLDKSTGASVYNAHGVNGRRLLPMMWDPKASGSLV

NbL01g14600.1 peroxidase_N1 [MW = 38.4 kDa]

No. of times detected



log(intensity)



Values from



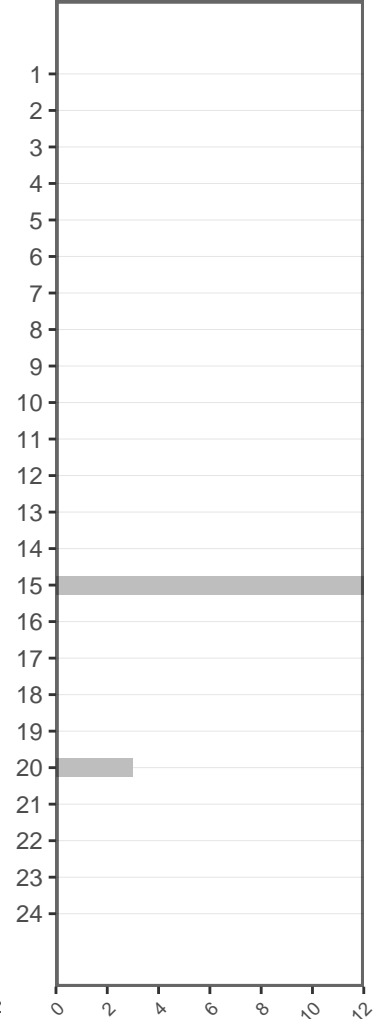
MW indication



Molecular weight



Gel Slice

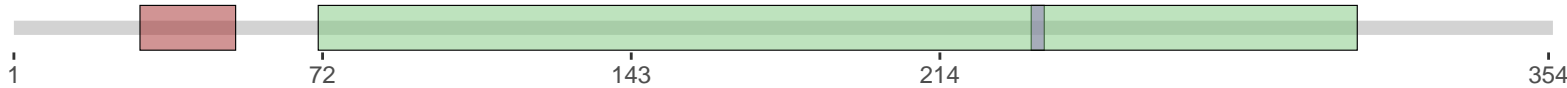


Peptide counts over 4 repeats

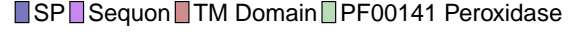
Protein length



Pfam domains



Pfam Description



Protein sequence:

SVPTGRDRGRVSRADAAANLPAFFEDVDGKGFLEKLNFGDVALTGATHTGTAGCAVIRDLRFNFTGCPDPSIDATFLPQLRALCPNGDASRRVGLDTPGAVNFDTSYFANLNRGVLESDDKLVTDASTRFVQRFVGRGLLGLTFGVDFGRSMVMMMSNEVKTGTNGEIRKVCAN

NbL01g14580.1 uncharacterized_LOC104221519 [MW = 18.92 kDa]

No. of times detected



log(intensity)



Values from



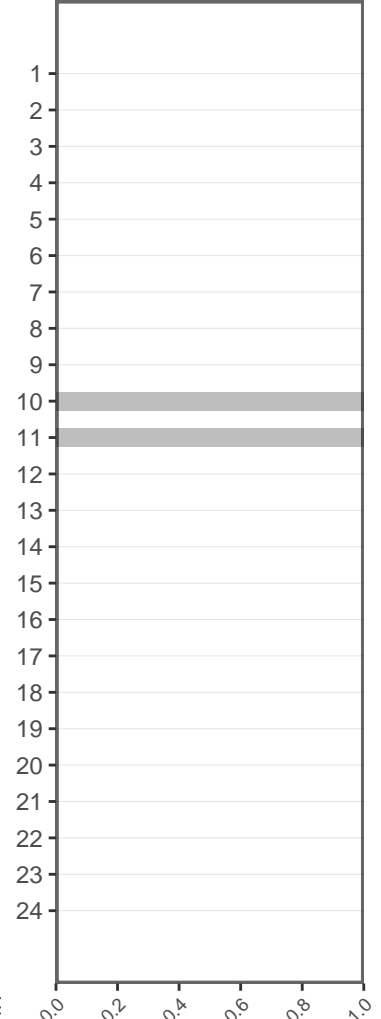
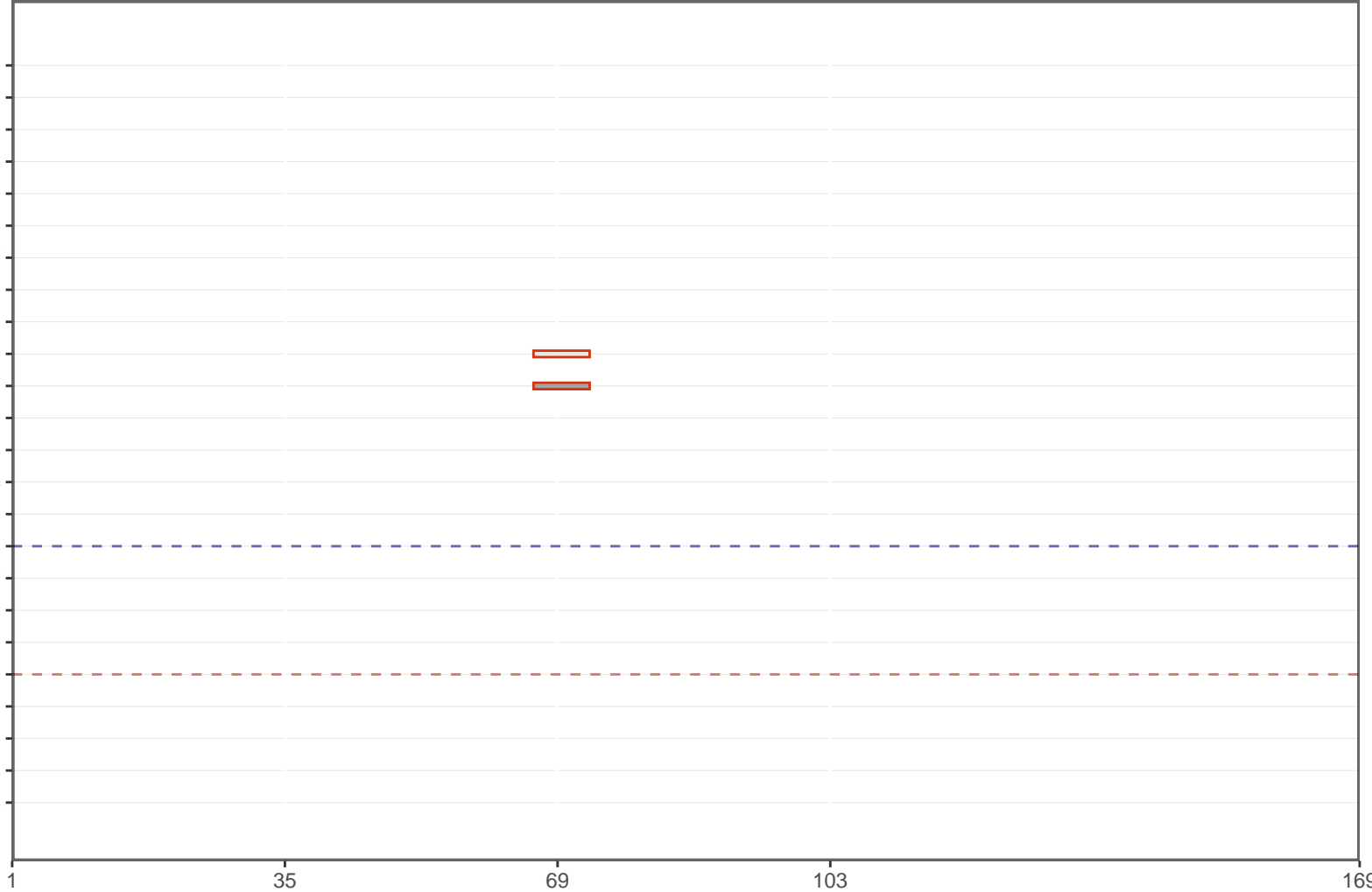
MW indication



Molecular weight



Gel Slice



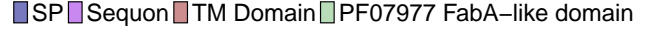
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

1ELRYPAFPPTVMDINQIREILPHRFPELLVDRVIEYNPQVSAWIKNVTINDNFFPGHFPERPIMPQVLMVEIGEVLTLOELLLLGLGFYLRVLRVY

NbL01g14560.1 probable_protein_phosphatase_2C_62 [MW = 86.59 kDa]

No. of times detected



log(intensity)



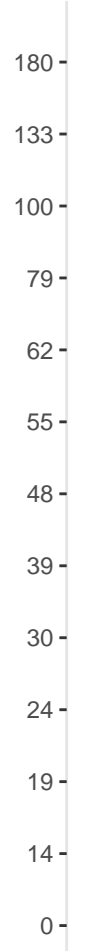
Values from



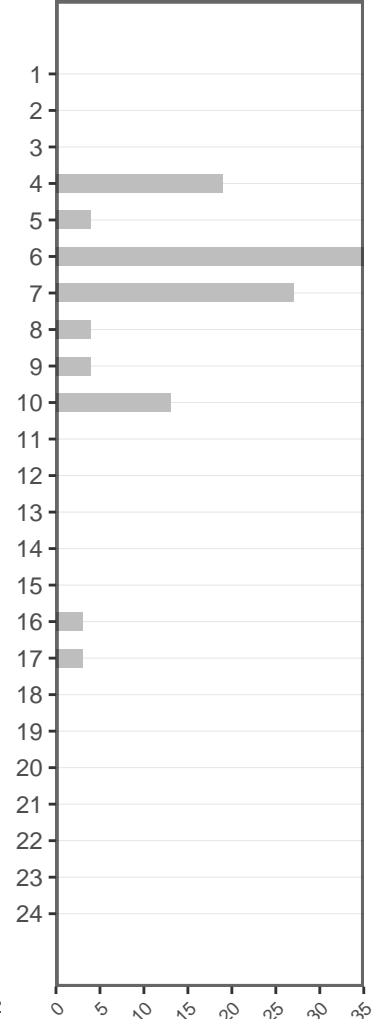
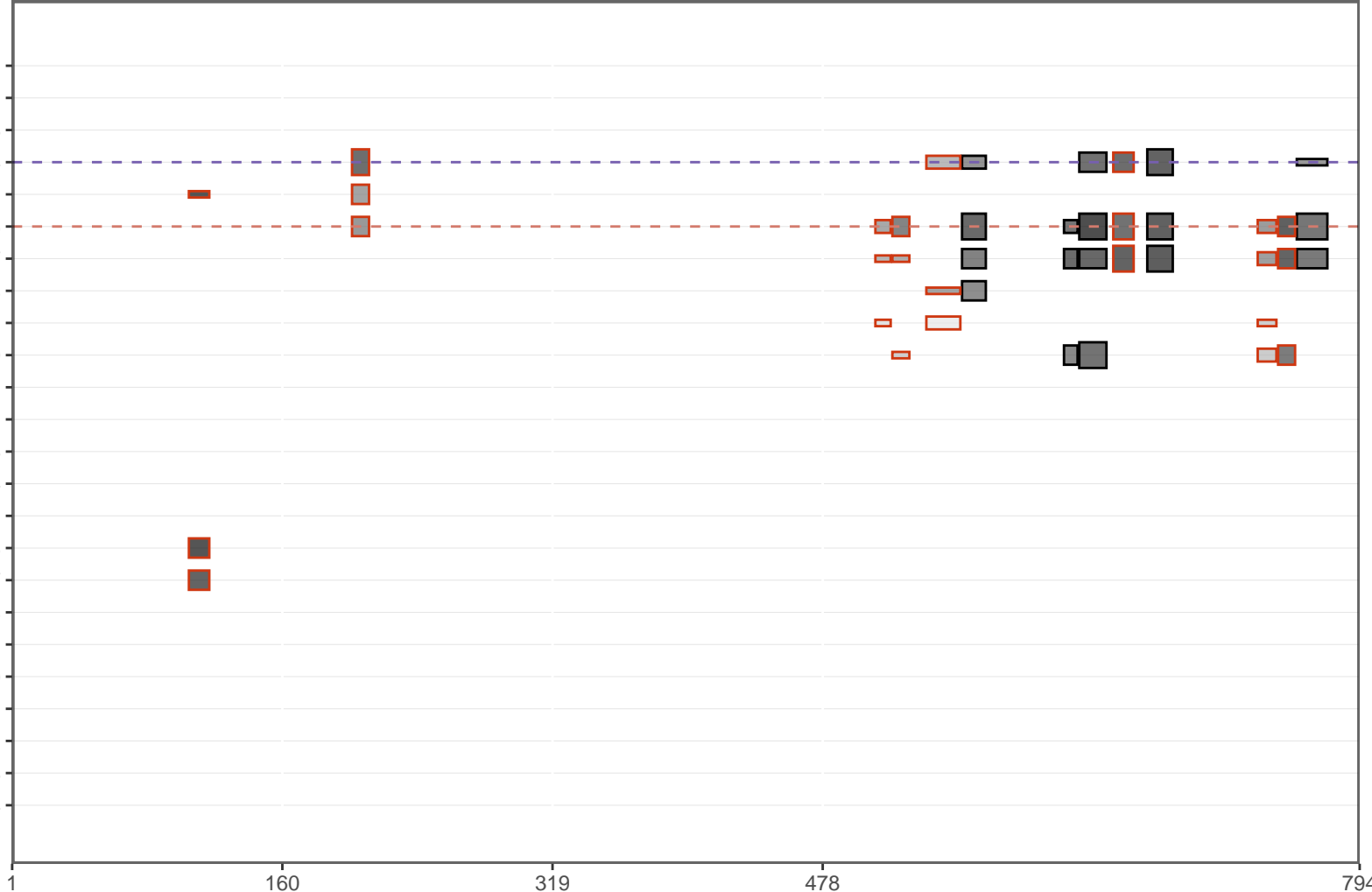
MW indication



Molecular weight



Gel Slice



Protein length

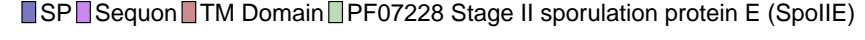


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VPEENLENETYVDEISFENADRIHLSIDAEDLSTQVLSLENDGDTLTFNFSGEDTDDGASGKGTFRKDSDEANVIEVMPLEPMLAAEPLDEEVDHNLTSSENEEGESPLSPEENLPLSLVEAEKKAENENVEVREISGHEVVEDRSEANGSSKAMPKELHLSGGATLLEYPSPKALTGHEAFVADGKWLGVADGVGWSLEGGSDKGYAKELMQNSEGIVSGGDNDLDFPKQVNLNLSVSKTDSGSGSTALAHFDGKDLRVANGDGGFIIRNGSVYRKSSPMLHEFLI

NbL01g14500.1 cytochrome_f [MW = 24.69 kDa]

No. of times detected



log(intensity)



Values from



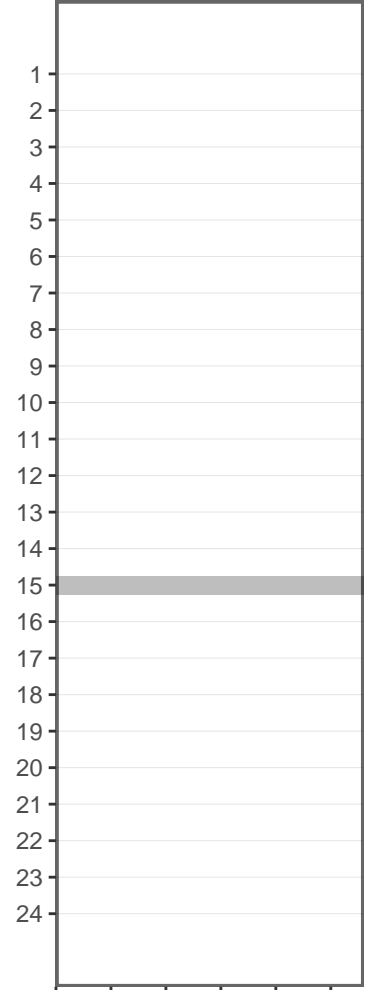
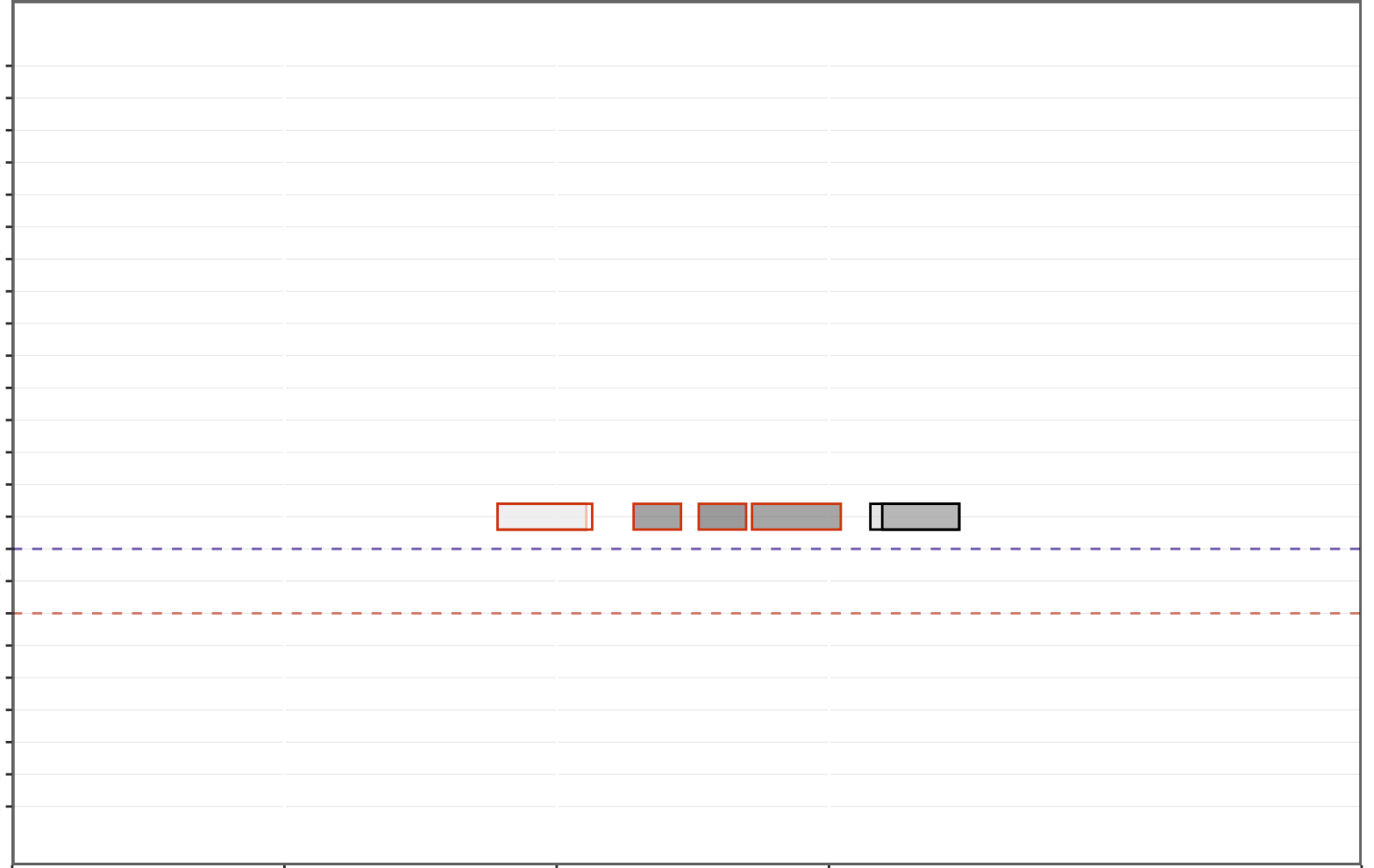
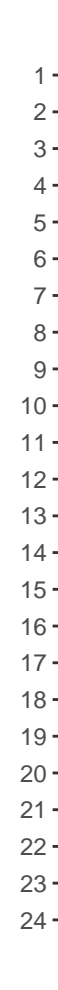
MW indication



Molecular weight

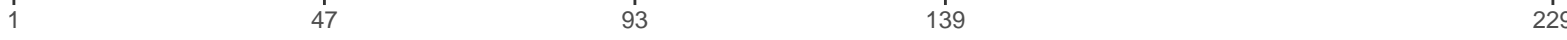


Gel Slice

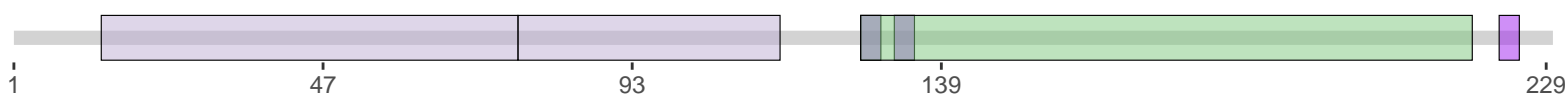


Peptide counts over 4 repeats

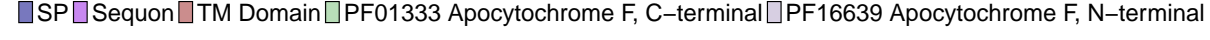
Protein length



Pfam domains



Pfam Description



Protein sequence:

/HFLKYPIYVGNRGRGQYFDGSKSNFTVYNATAAGIVKIRKEKGGYETITDASDGRGVVDIIPQPELLVSEGESKFDQLTNSFNVGGFGGGDAEIVLQDPLRVQGLLFTGPHNVSSDVF

NbL01g14480.1 beta-xyloridase/alpha-L-arabinofuranosidase_2-like [MW - SP = 80.98 kDa]

No. of times detected



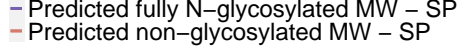
log(intensity)



Values from



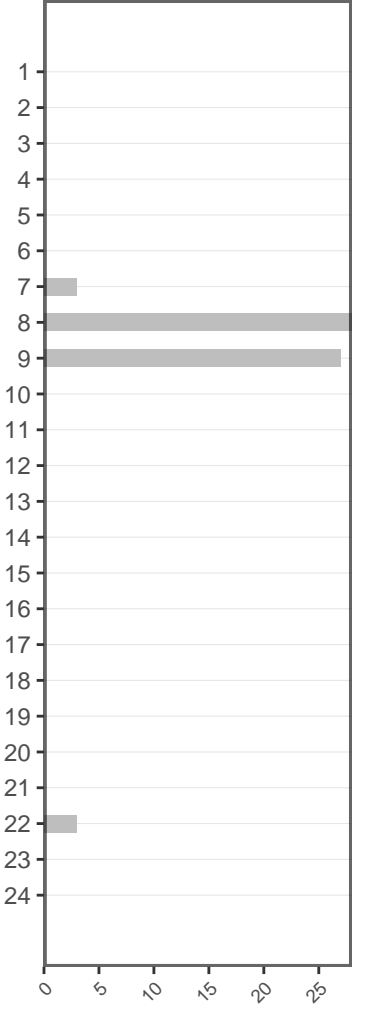
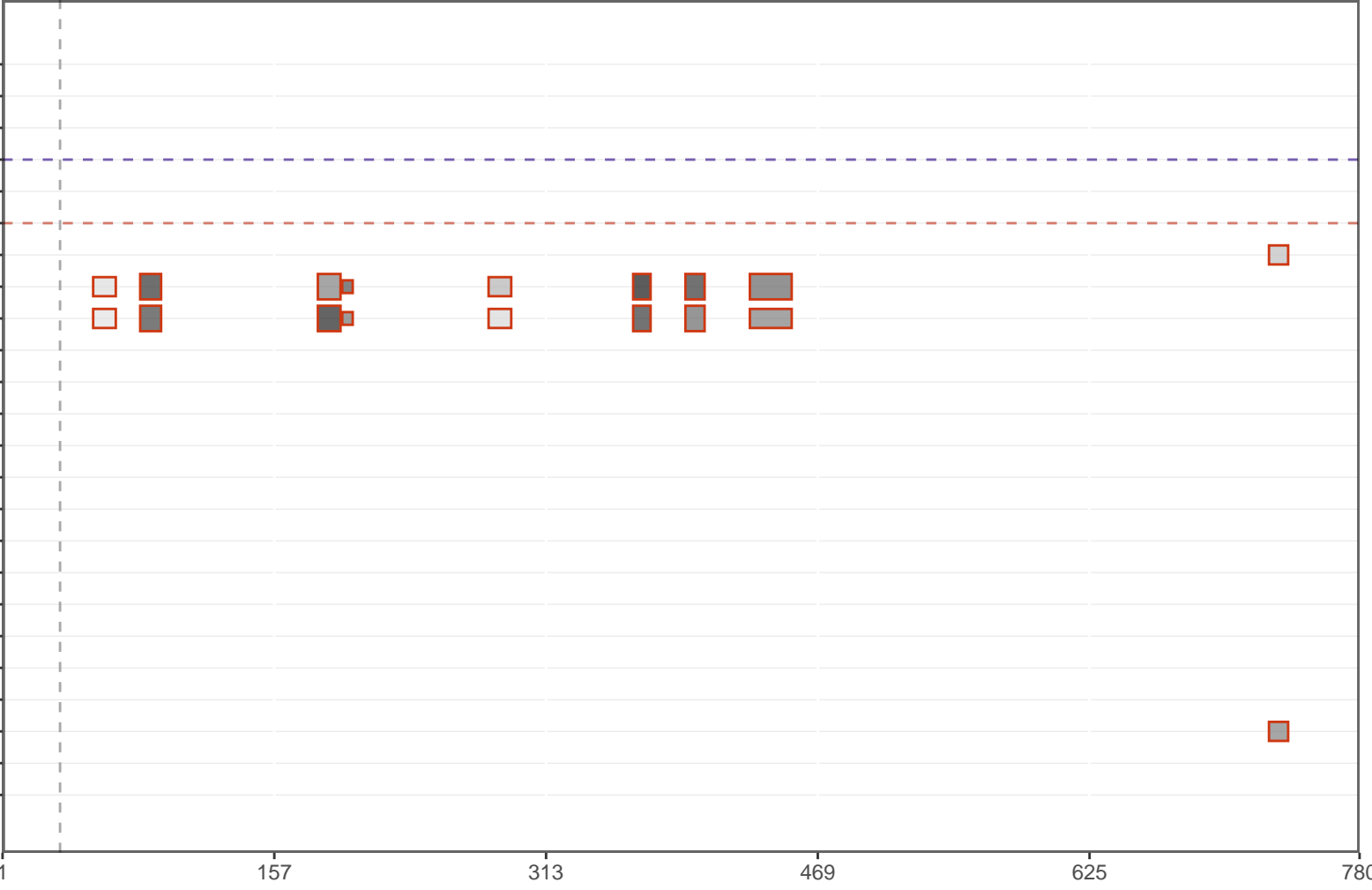
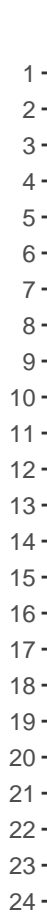
MW indication



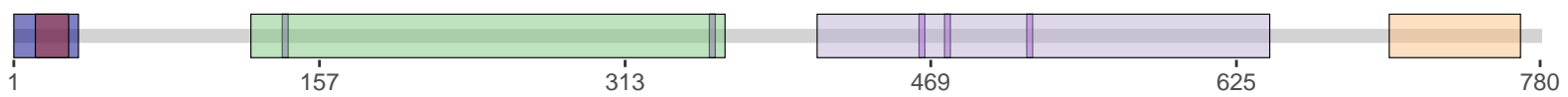
Molecular weight



Gel Slice

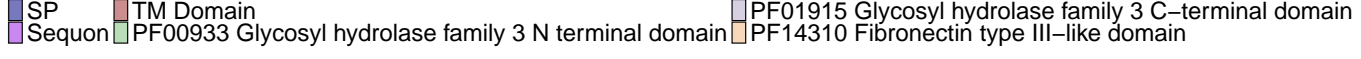


Protein length



Pfam domains

Pfam Description



Protein sequence:

IFFDGDPKNIAYGSLGPKDVGSPHEHGLAREAARGGIVLLKNSAGSLPLSPKSIKSLAVGPNANVGVNMGVSEGTGPKLITPLQGLNASVTVVHPGQFNASVSGDPLADDAKKAADAAVAVVVGSDQSIERSKDRVNFLLPGQGGSLFTEVASVSKGPIVILVIMSGGMDVQFAVDNPKVTSVAVHGFPGEDGGALADIFGYYNPGRPLMTWVPGVADKVMETNMMRFPDKTGFPRGRVRFYKGPVFVNFQDGLVSNYKHHLVQAPKYVSPLEEAGACI

NbL01g14440.1 phosphatidylserine_decarboxylase_proenzyme_2-like [MW = 71.83 kDa]

No. of times detected



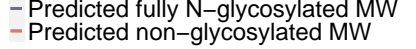
log(intensity)



Values from



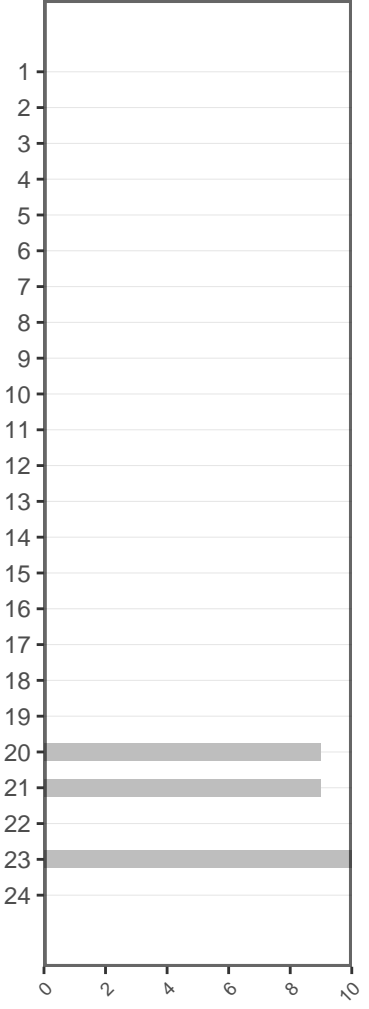
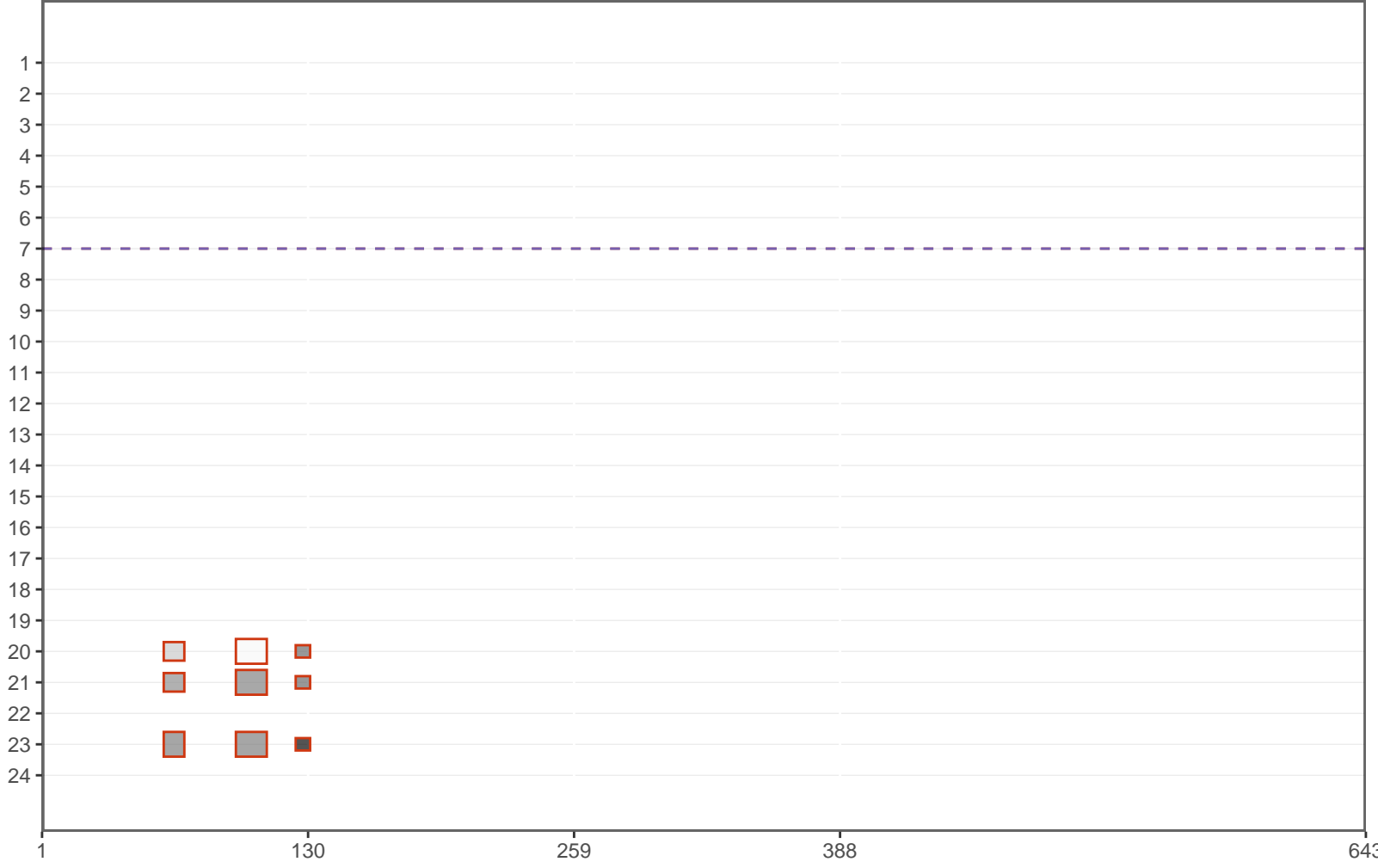
MW indication



Molecular weight



Gel Slice

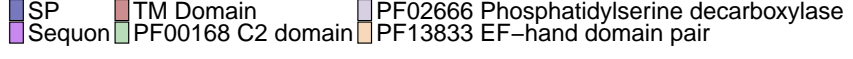


Protein length



Pfam domains

Pfam Description



Protein sequence:

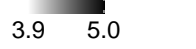
ISSGVWFKLSEVWVFSTYDGLRSGSAGHILVYDRKKRRLVEEHDNRKLVSMRAHYGKFLGLMDNGAKELRSLSEKQKQKMDSAEAKKIFNFIKGLGQNMDEVKYPLKQKFTNFEFFRRLKPGARPIAFIERDDIAVCAADGRLLMVFNSVADSRFVWKGKRFQKGLLQNEACGSAFVNGALVIFRLAPQGVHRFHFVPGTIEKFEIPGGLYTVNPIAWNSKYGNVFTENKRVYSISIEYFGKVAEVAIGATMVGSGINFRKEGQVYKKGDFRQYFSFGGSTVICVFI

NbL01g14370.1 glycine-rich_RNA-binding_protein_RZ1A-like [MW = 22.3 kDa]

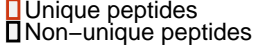
No. of times detected



log(intensity)



Values from



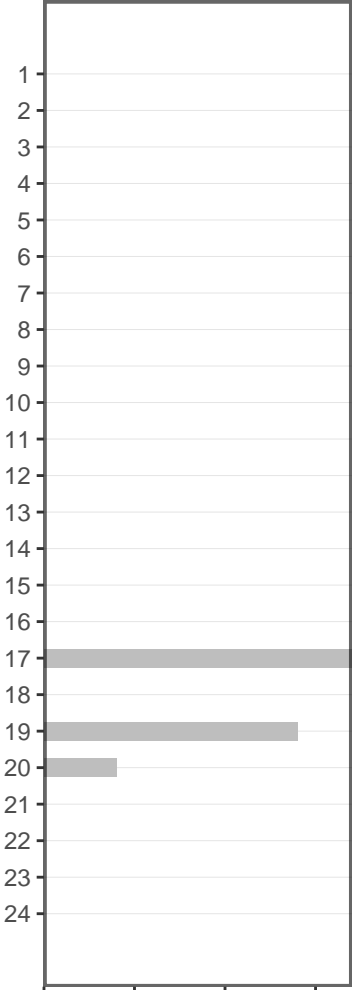
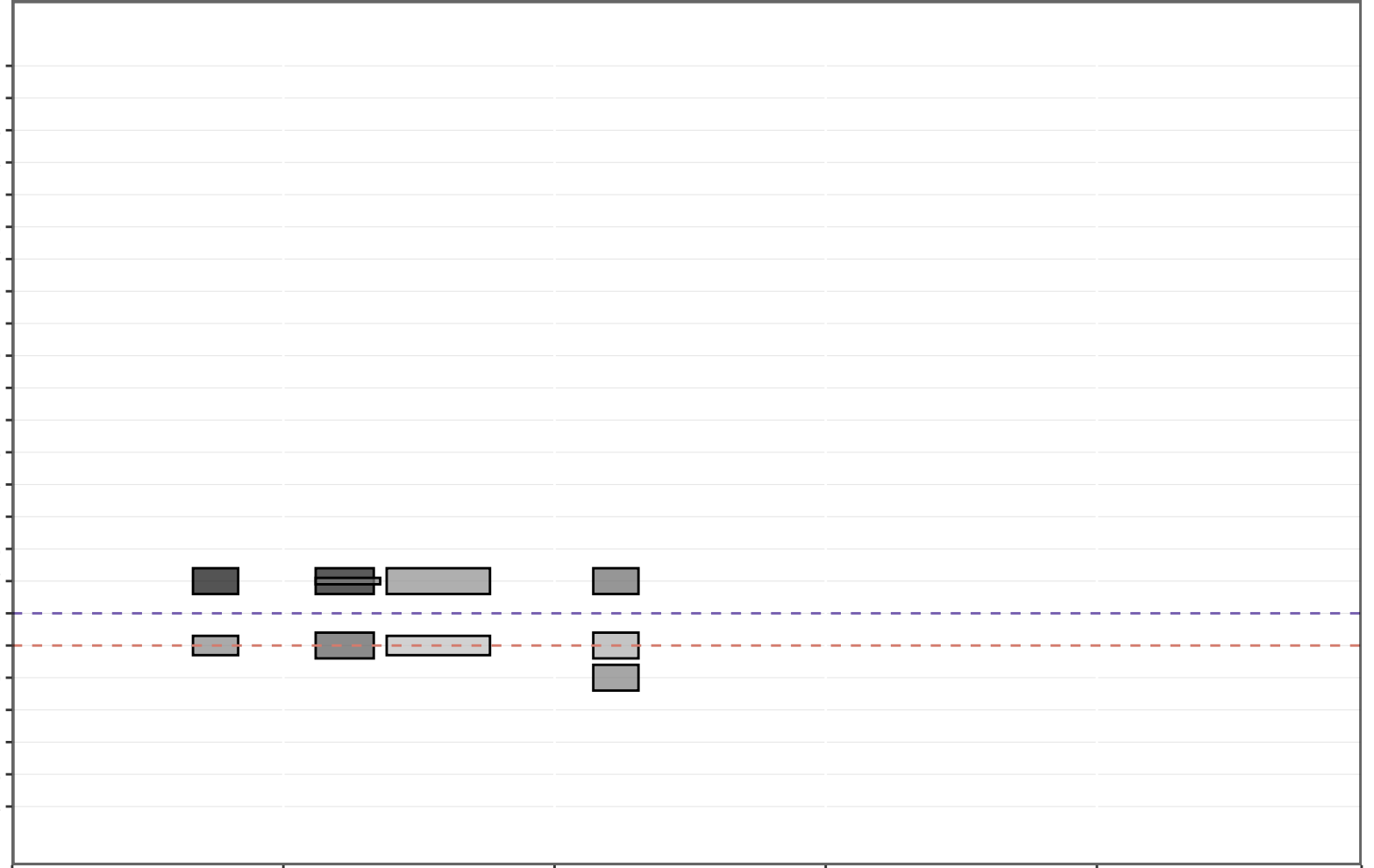
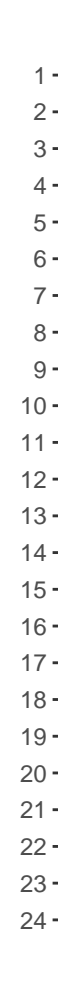
MW indication



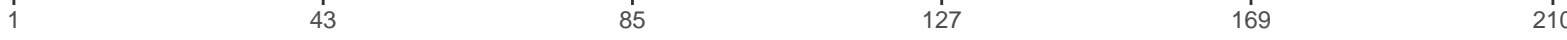
Molecular weight



Gel Slice



Protein length

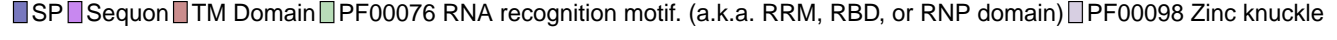


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IPRDRDRGRDRDRGRDRYGGGRSGGGGDFNCGKPKHFARECPSEGGGRGRYGGGGGGGGSGGSGYGPDRNGDRYGRSGRGGGGGRGGGRFSDRSGFYEARRSSGGSRAG

NbL01g14330.1 actin-101 [MW = 41.66 kDa]

No. of times detected



log(intensity)



Values from



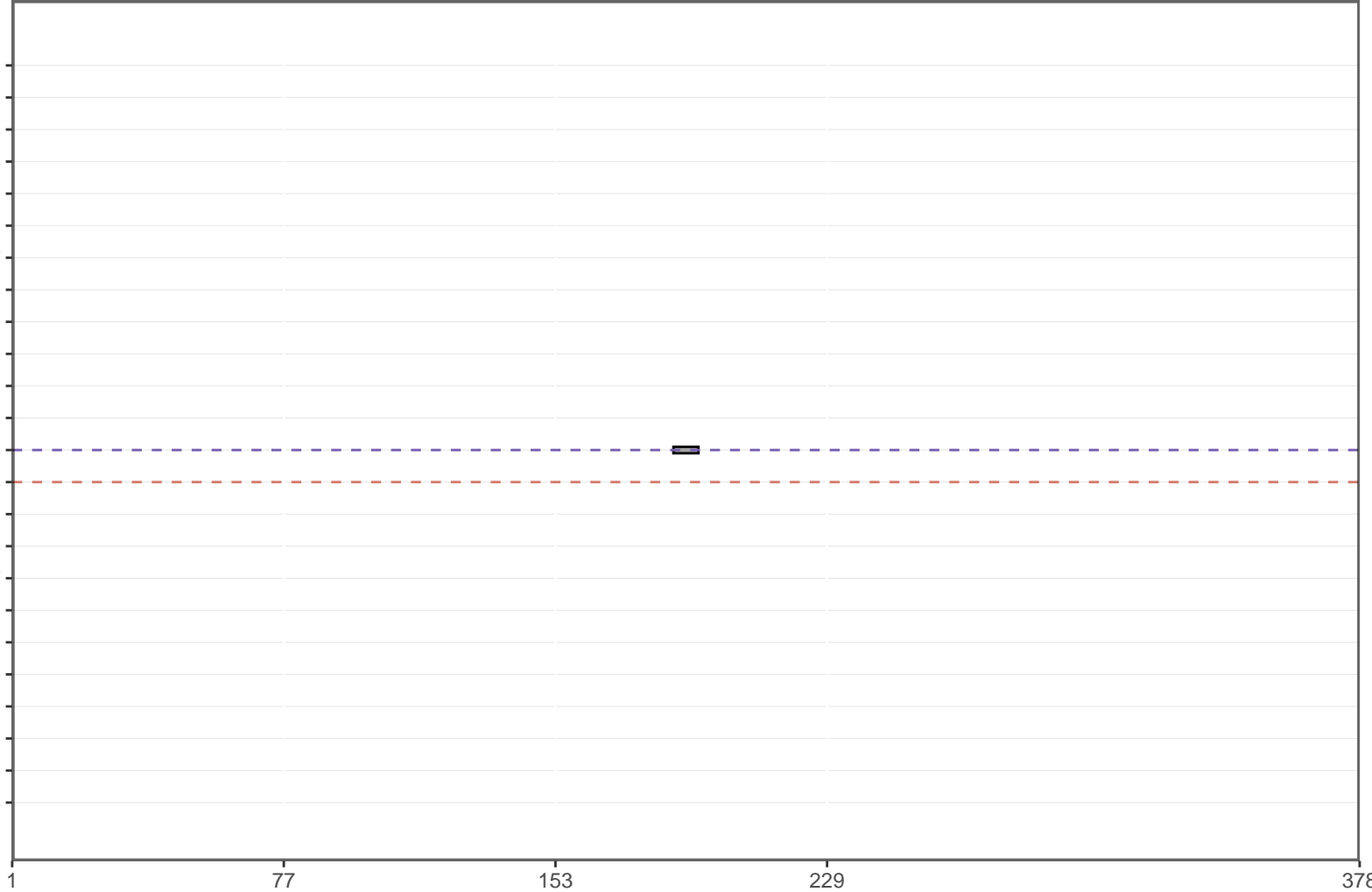
MW indication



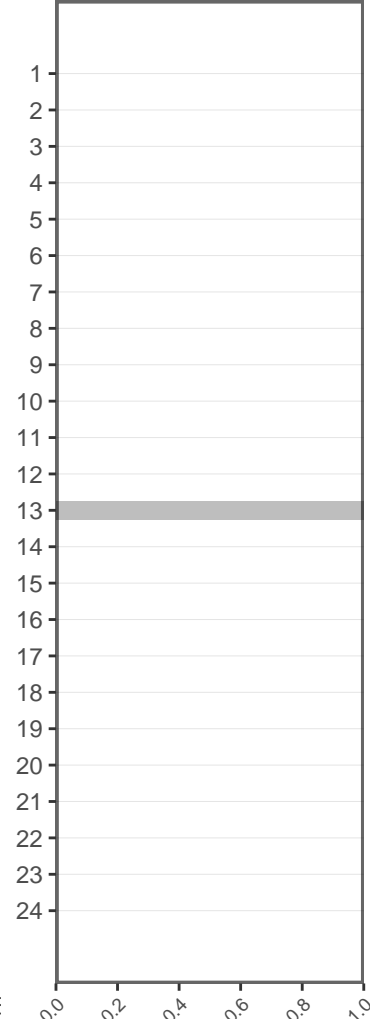
Molecular weight



Gel Slice



Protein length

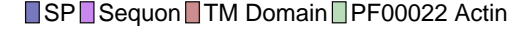


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PHALRLDLAQRDLFDCLMLKTERGYSFTTSAERREIVRDVKEKLYALDYEQELETAKSSSSVEKSYELPDGGVITIGSERFRCPREVLFGPRLVGMEEAGIHETTYNSIMKGDVDRKDLVGNVLSGGTTFMFGIADRMSKEITALPSSMKIKVVAAPPERKYSVWGGGSLASLSTFQQMWTKGEYDESGPSVHRKCF

NbL01g14180.1 60S_ribosomal_protein_L3 [MW = 44.45 kDa]

No. of times detected



log(intensity)



Values from



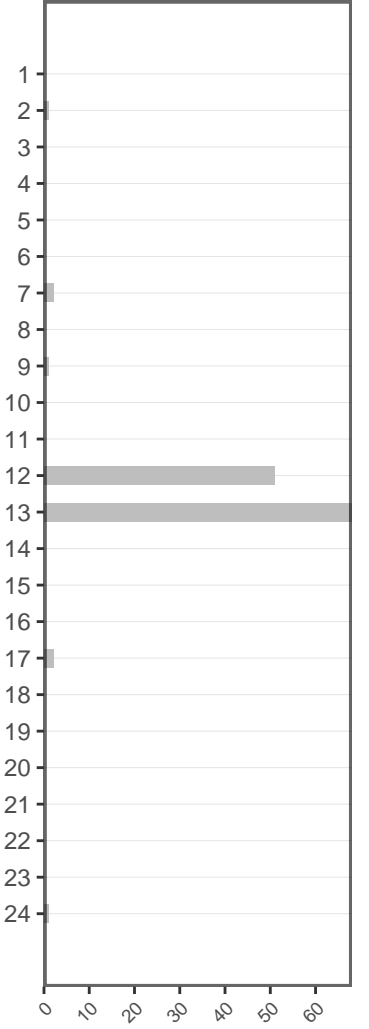
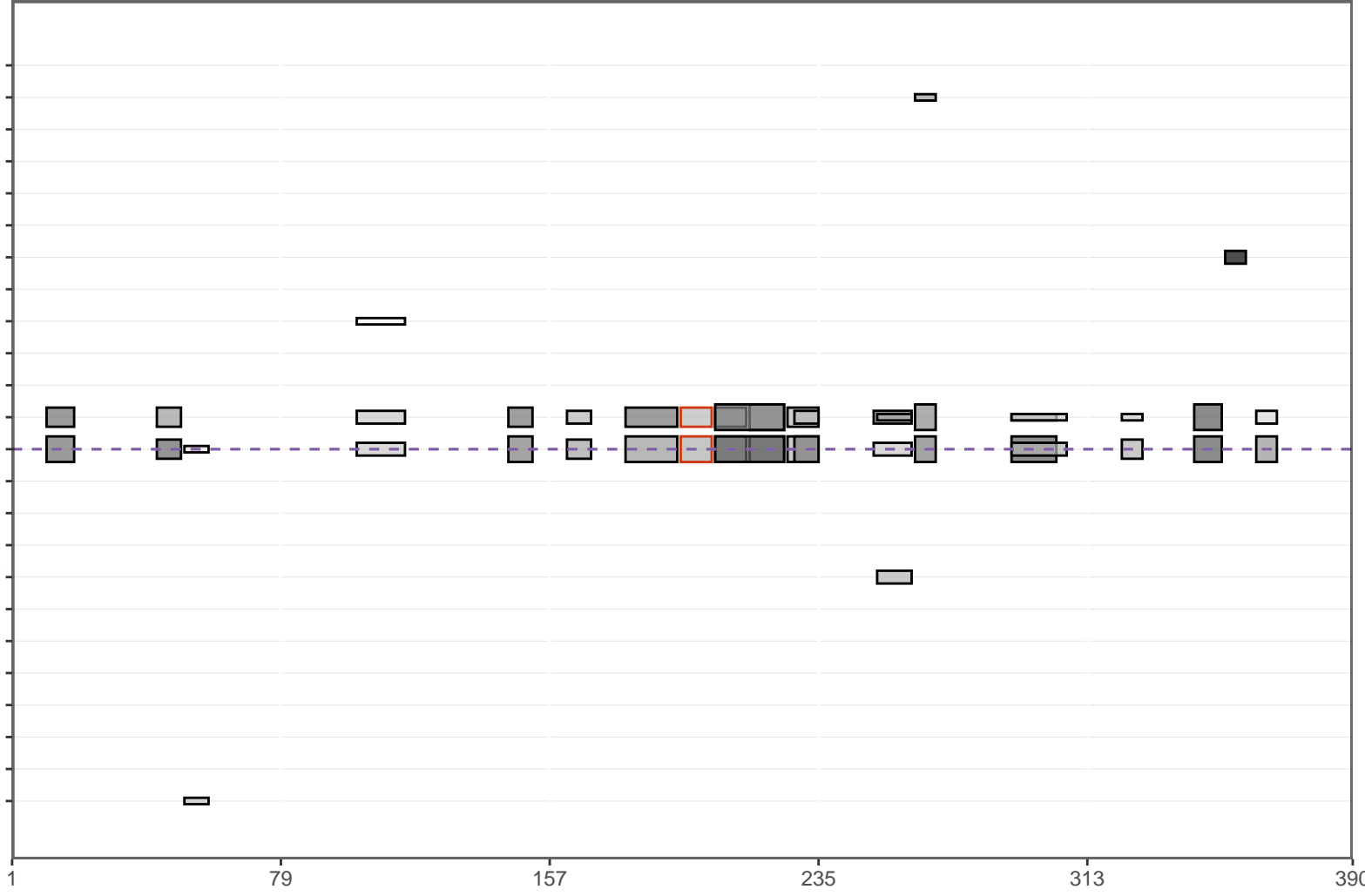
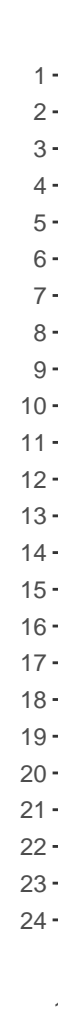
MW indication



Molecular weight

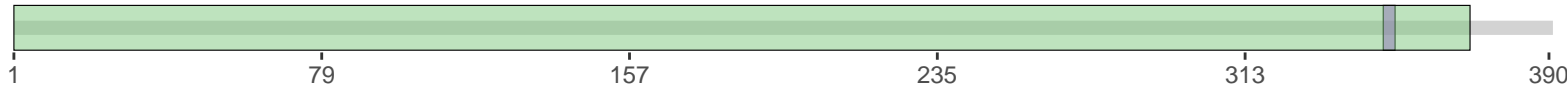


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEIQVNGGTAQKVFAYSFEKGVPEVDAVFKQKDEMDIDHGVTKGKGVYVTRWGVYTRLPKRTVRLRGLKQVADGSAWHPRVSYTVARAGQNGYVHRTEMNKKVYKLGKAGGESHAAITDFDRTKEIKTPMAGGFHYGVVKKDDVLLIKGGCVSPKPKVTVLRGSLNGTSRVAALEEIKLKFDTSSKFGHGRFQTQEKQKPYGRKAY

NbL01g14110.1 WD-40_repeat-containing_protein_MSI1 [MW = 48.37 kDa]

No. of times detected



log(intensity)



Values from



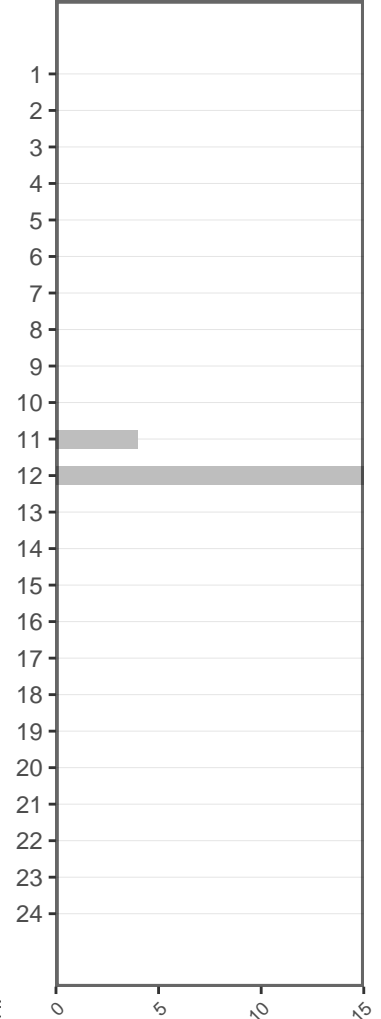
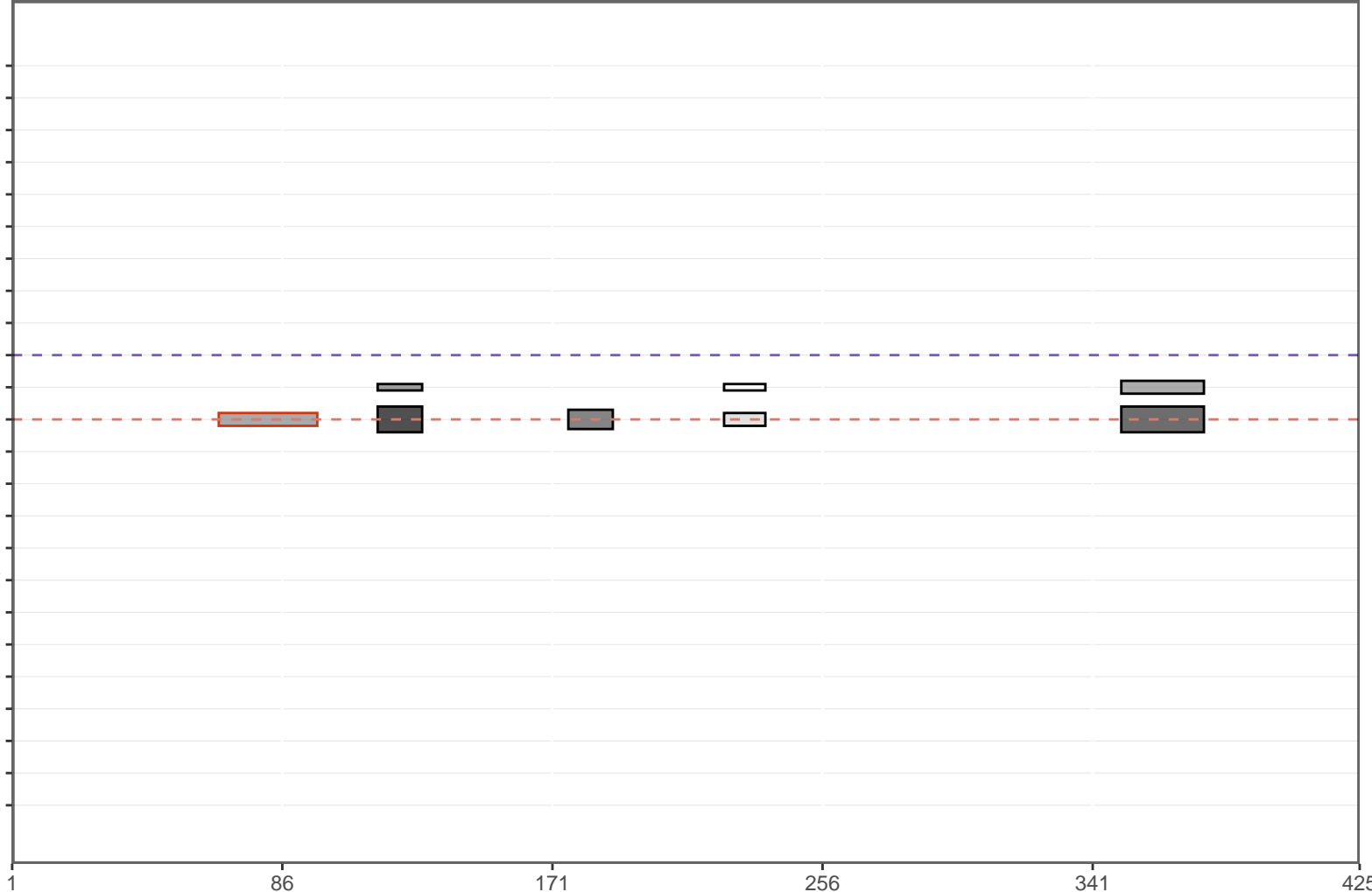
MW indication



Molecular weight



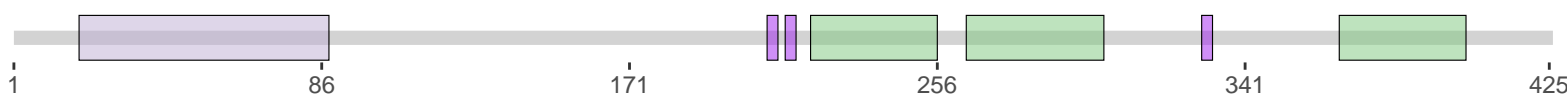
Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description

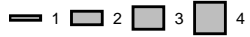


Protein sequence:

SDADCLVDINATPKNSLSLDMQIFKIHGVEEDVAWHLRHEVLFSGVGGDDQYLHWDLRTPSVTKPIGSAVAHQSEVNLQAFNPFNEWVATGDTKTKYKFLDLRKRISTALHTLDCHEEYFDQVWPKNETLASGCLGRRLMVDLSRIDEEGTPEDAEDGPELFFHGGHTRKSGDFSWNPCEDDVVAASVAEDNLGHWQMAENIYHDEDDLPGDDATKAPL

NbL01g14050.1 basic_blue_protein [MW - SP = 10.4 kDa]

No. of times detected



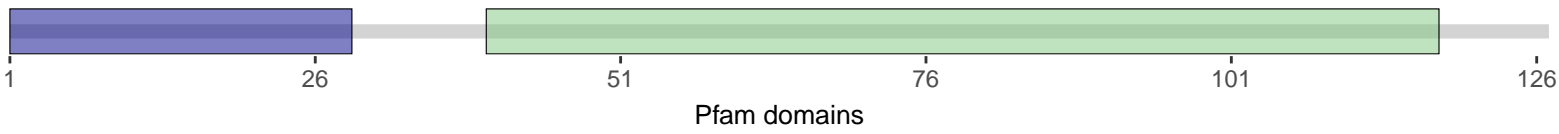
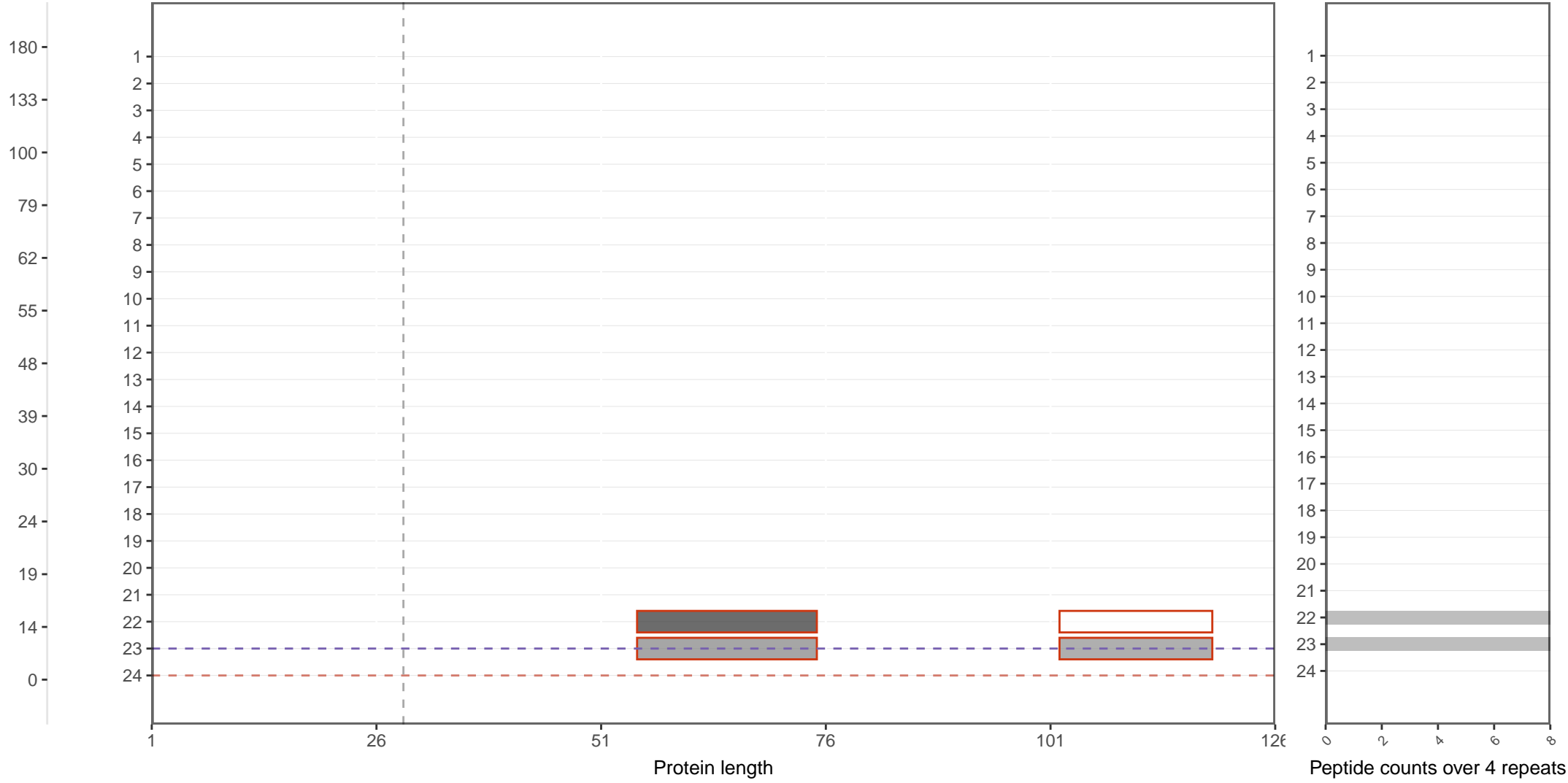
log(intensity)
4.7 5.4

Values from
Unique peptides (red outline)
Non-unique peptides (grey outline)

MW indication
Predicted fully N-glycosylated MW - SP (blue dashed line)
Predicted non-glycosylated MW - SP (red dashed line)

Molecular weight

Gel Slice



Pfam Description

SP Sequon TM Domain PF02298 Plastocyanin-like domain

Protein sequence:

GKRFKAGDLAFNYPGAAHNNVNNKAGVNSGRTRPGEKVYNNKGGDKIKLVKGGNYFICNFAGHCEGGMKIVFASL

NbL01g13880.1 ankyrin_repeat_domain-containing_protein_2B-like [MW = 37.19 kDa]

No. of times detected



log(intensity)



Values from



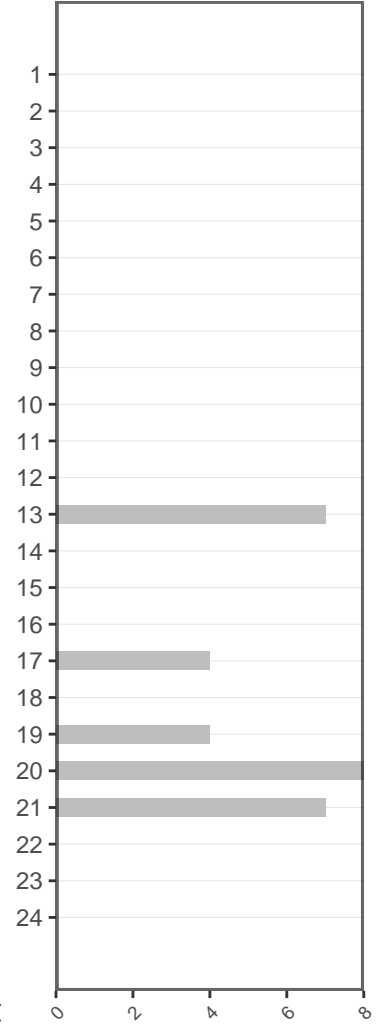
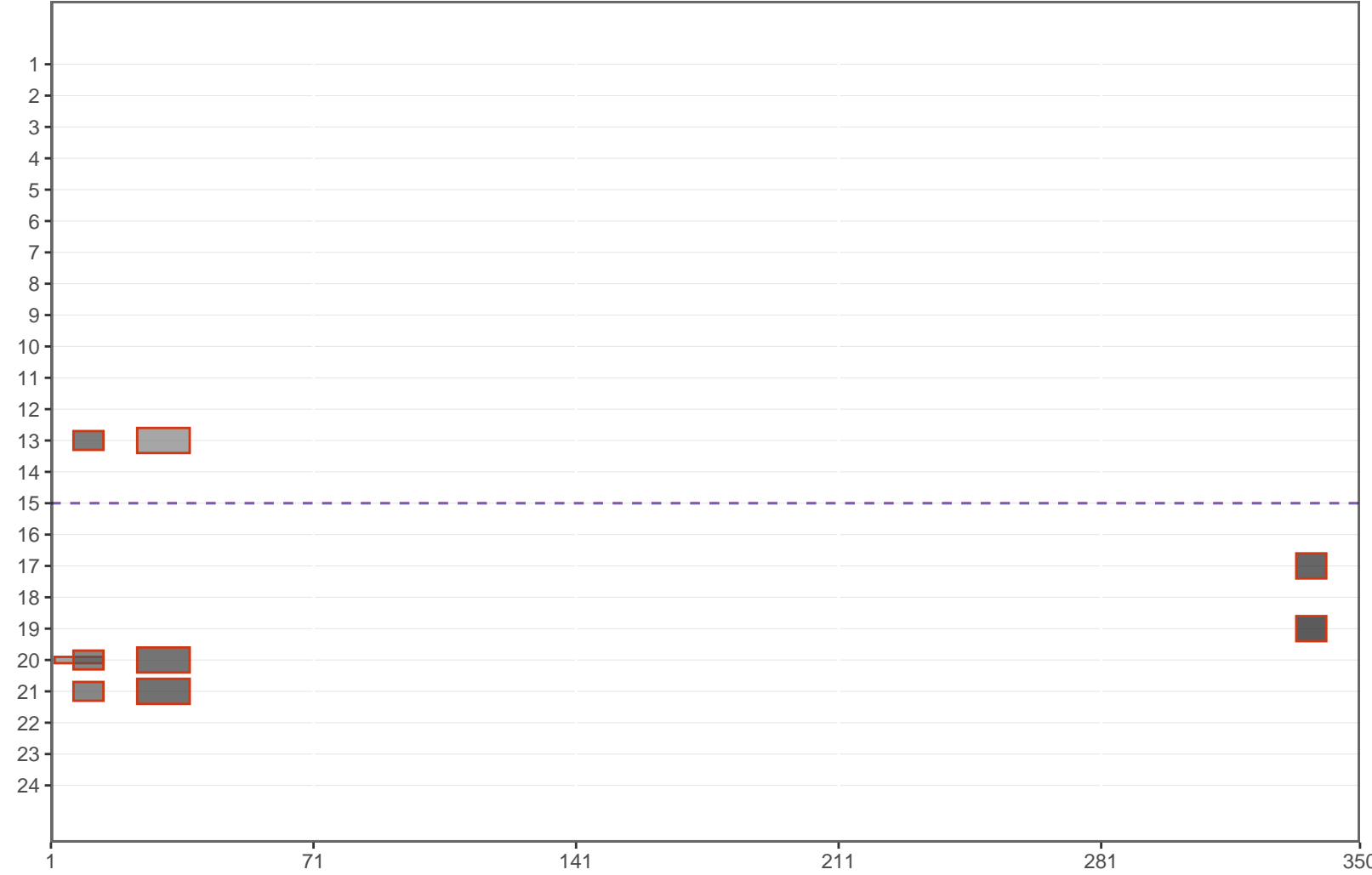
MW indication



Molecular weight

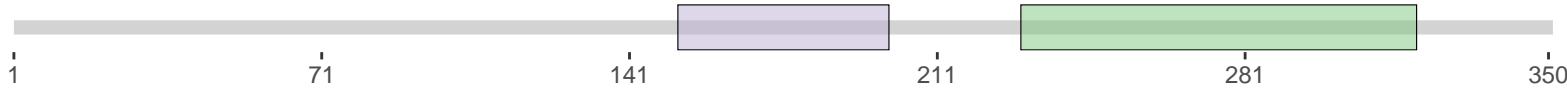


Gel Slice



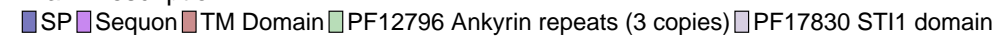
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IRKEDPSLKPILLEIEEGGGPAMMRVYNDGELTKKIGKAMGFAAGGEGATSAIPGTDTEEEANEDESIVHQGASVGDALGLKAALTAGAKDKDEEDSEGRTALHFACGGYGEVKAGILLLENGAVDVALDKNKNTALHYAAGYGRKEGVALLLENGAAVTLQNLGDKTPREVAKLNGDEEVKLEKDKVFL

NbL01g13780.1 UDP-glucose:glycoprotein_glycosyltransferase [MW - SP = 182.79 kDa]

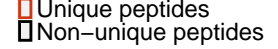
No. of times detected



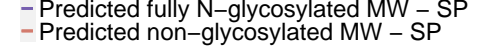
log(intensity)



Values from

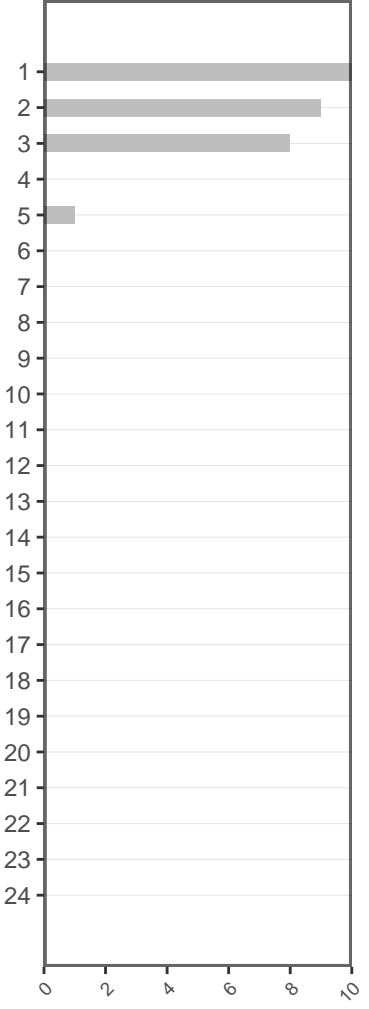
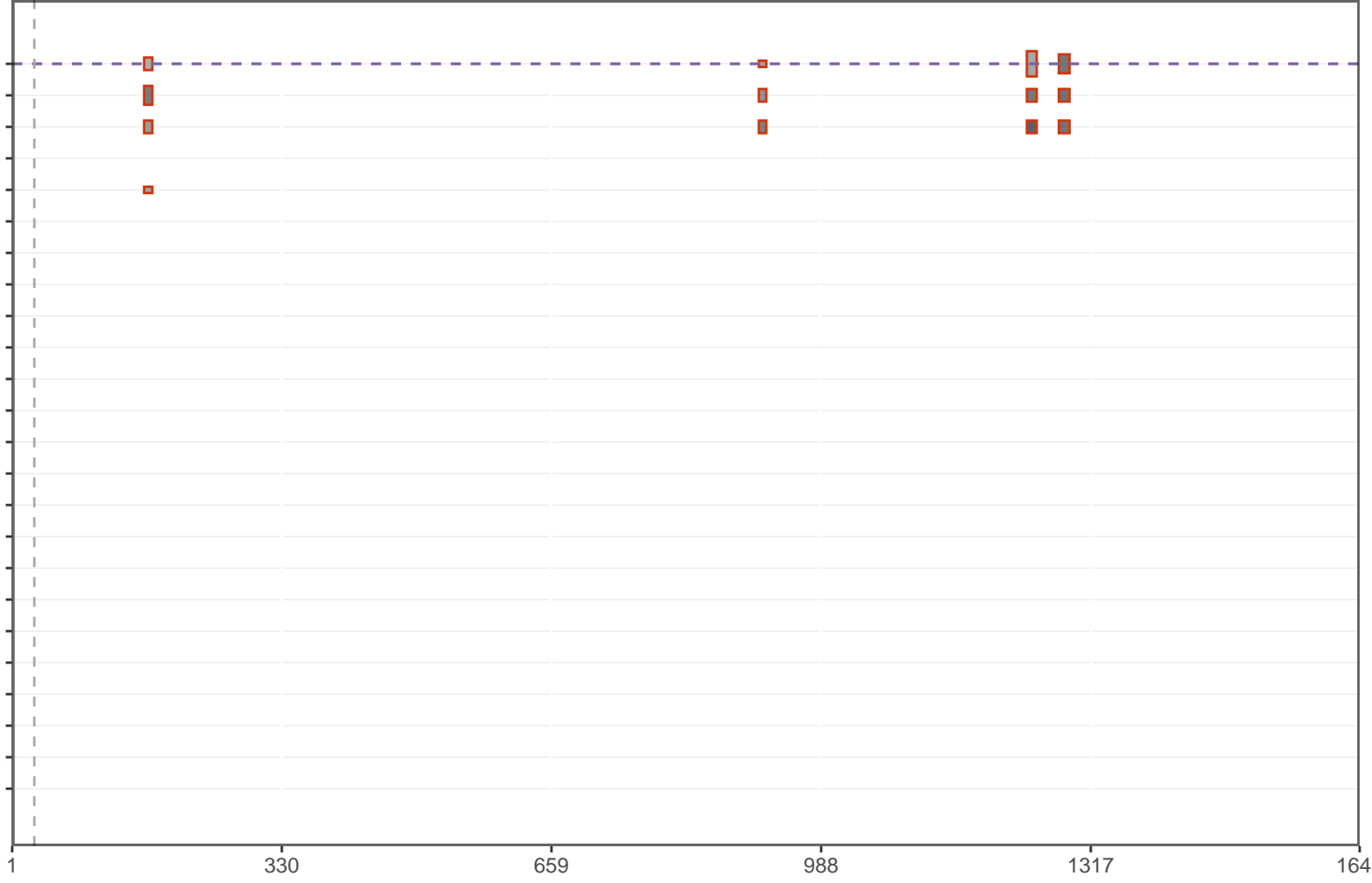
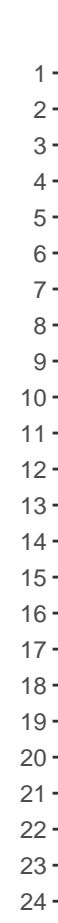
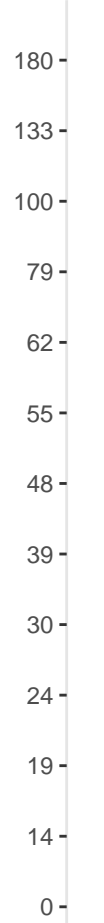


MW indication



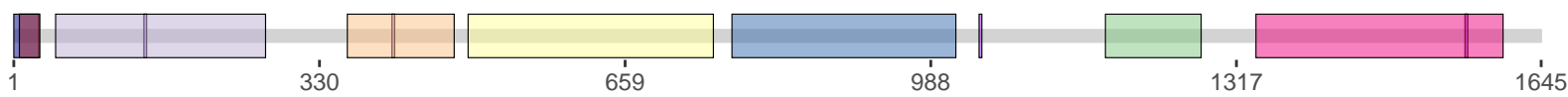
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Seuon
- TM Domain
- PF06427 UDP-glucose:Glycoprotein Glucosyltransferase
- PF18400 Thioredoxin-like domain
- PF18401 Thioredoxin-like domain
- PF18402 Thioredoxin-like domain
- PF18403 Thioredoxin-like domain
- PF18404 Glucosyltransferase 24

Protein sequence:

MRLLREGHYLYMAGTTTGRGLGVFNLSLDPHSFLFMKVFGITASSYGHKKGVLFQLDQICSFYEHNMHATSAGPESEAEFLDKVFEFLANSNGLSGKLGKLSGLTDEKLRMLNKKVGTFLFGGVGLVYGANAVITNTRVIGLVGDATFLSHDLGLESLEFQGRKHVEIEEYKVEDIDPDMALTSKFISSIVMVEVSSIMRDRK66EGARFELL5AKYSAVVLENESSIHDAVDPL66FGQKLSGLLRLLSKSRP5MRLNINPMS6LVDLPLKKNRYRYVPTLDDFSSTD

NbL01g13750.1 serine_hydroxymethyltransferase_7-like [MW = 65.53 kDa]

No. of times detected



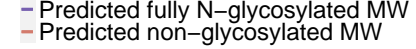
log(intensity)



Values from



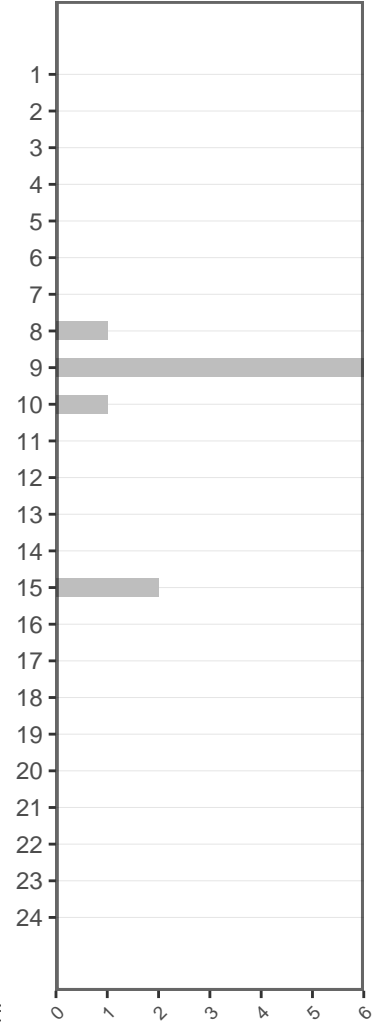
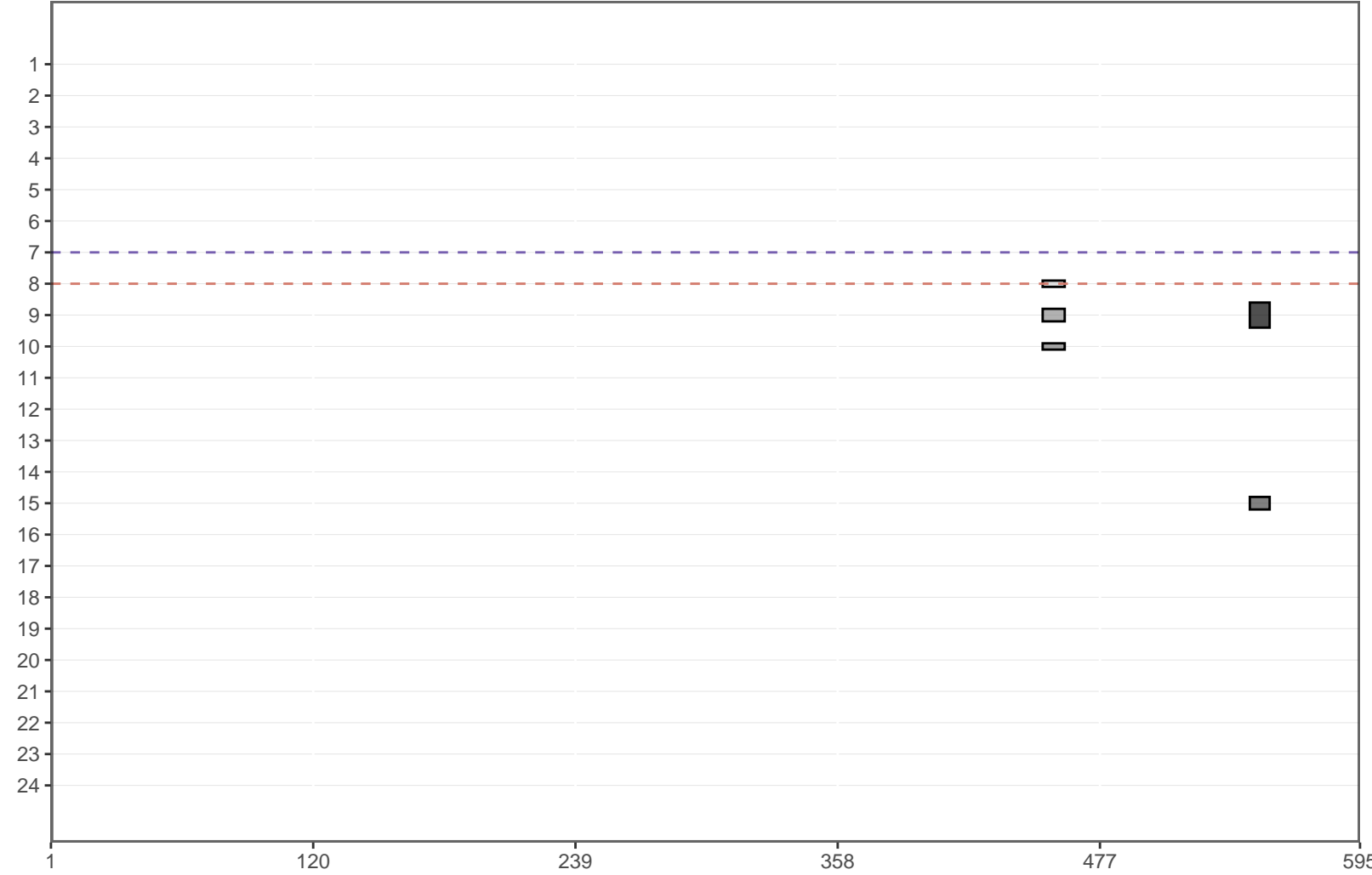
MW indication



Molecular weight



Gel Slice



1 120 239 358 477 595

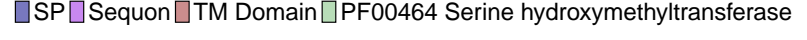
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SYKVDPTGGYYDFKLEERALDFRPHLGGGSSYPREWDYAKFRGADKQGAALLGDMAQISGLAAKEGASPFYDQDVTSFTTKSLRGRGGIFFYRKGSKPRKRGLLNQGSGGDKYDFEERKFAVFPALGGGPHNHHAAALAKGVATPEVKTVMQGVKRNAGLAAALLRRNGRLVTGGTDNHMLLDLRLNGLTGKFKVDELGHITLNVKVMVFDNGSITPGGVRIGTRMTSRGGIENDFETTFDILLKAQITNSVQREHGKLVKFLKGLNNKDVIELR1

NbL01g13700.1 thiamine_biosynthetic_bifunctional_enzyme_TH1_chloroplastic-like [MW = 60.72 kDa]

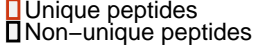
No. of times detected



log(intensity)



Values from



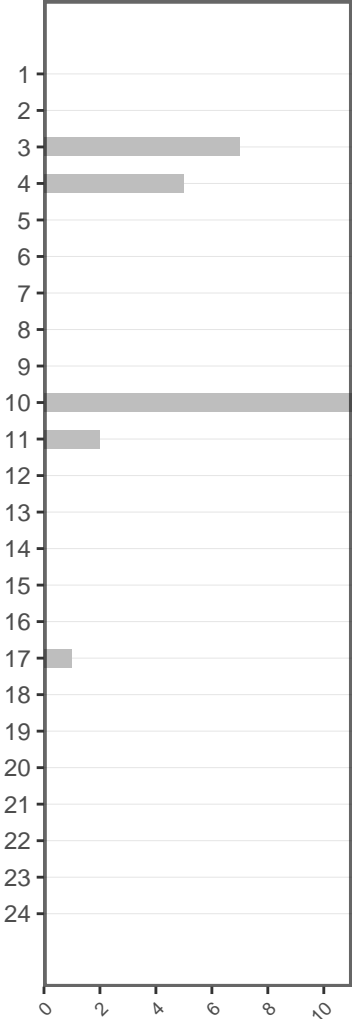
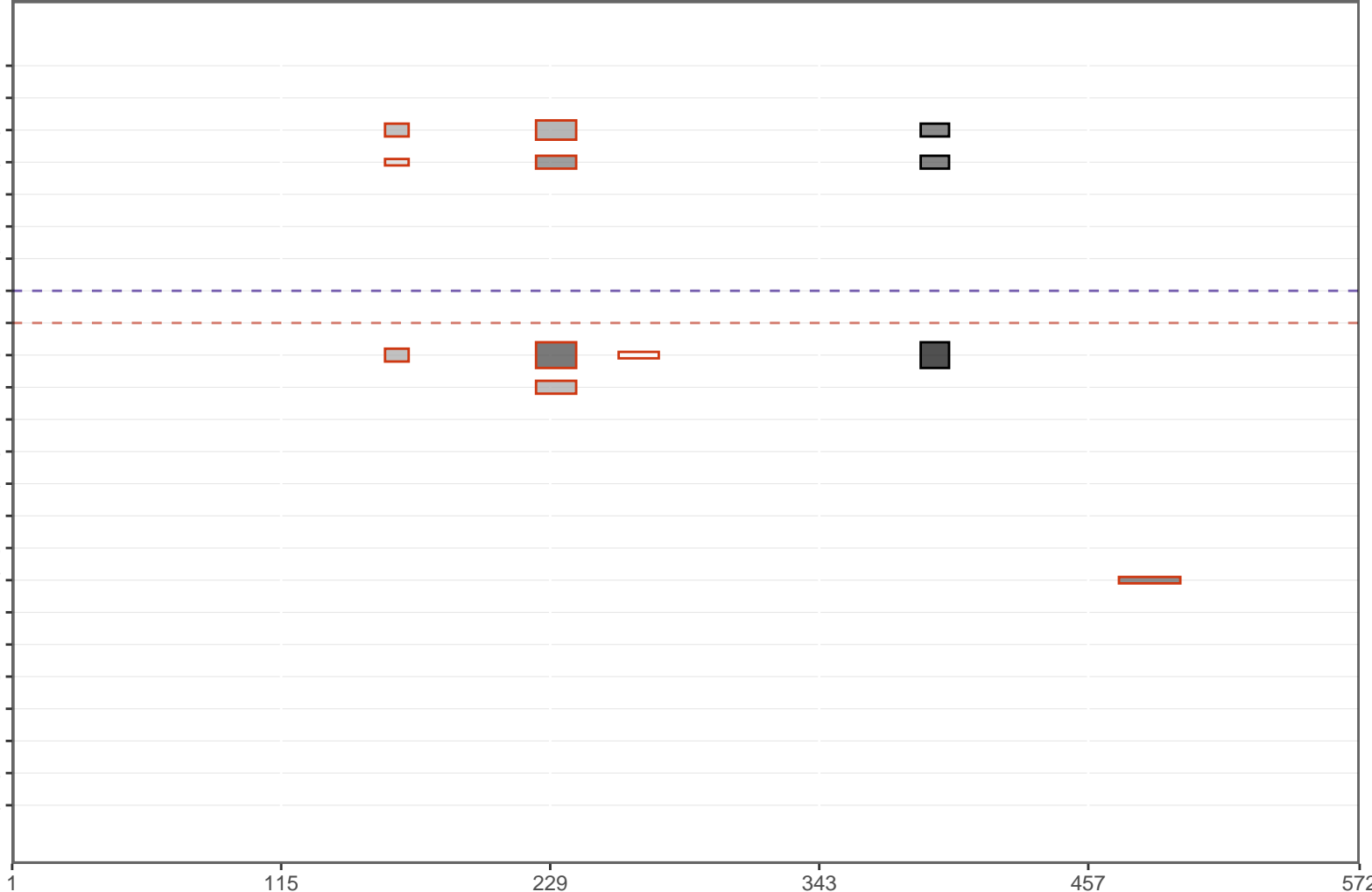
MW indication



Molecular weight



Gel Slice

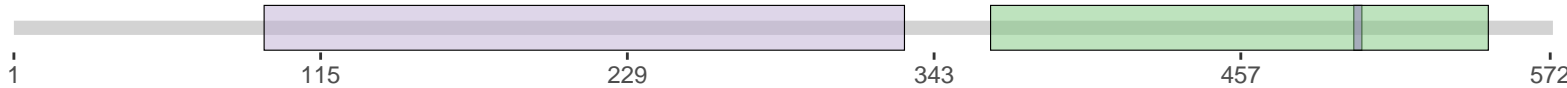


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description

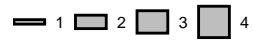


Protein sequence:

DGKDFYFRSSRIMPTNTHGTGGLASSIAAELAKGQMLSAVKVAKHYEAALESYSKNVILGGGRGPMIDHLKLNKSNVGRFFDQDLFLVAVTDRMKNRWSRSIVDAVKAIEGGASHIQLEKEVETSDFLEAAKACLKIKGRVHGVPLINDRIDVALASDADGVHGGQSDMPHAAARALLGPDKIGVSGKTEPHAGQAWLGDADHGGGGVYPTNTKENKKTIGLGLKAVKLSKLPVVAWGGIGIPNAQAVMGLGVNLIKGVAVVSAVDFREGVLTETRLKLELVKE

NbL01g13690.1 kinase_SRK2A [MW = 40.88 kDa]

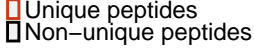
No. of times detected



log(intensity)



Values from



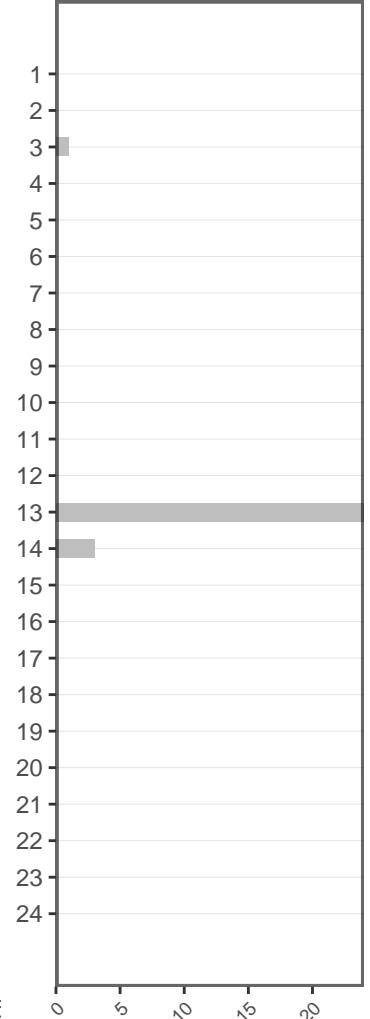
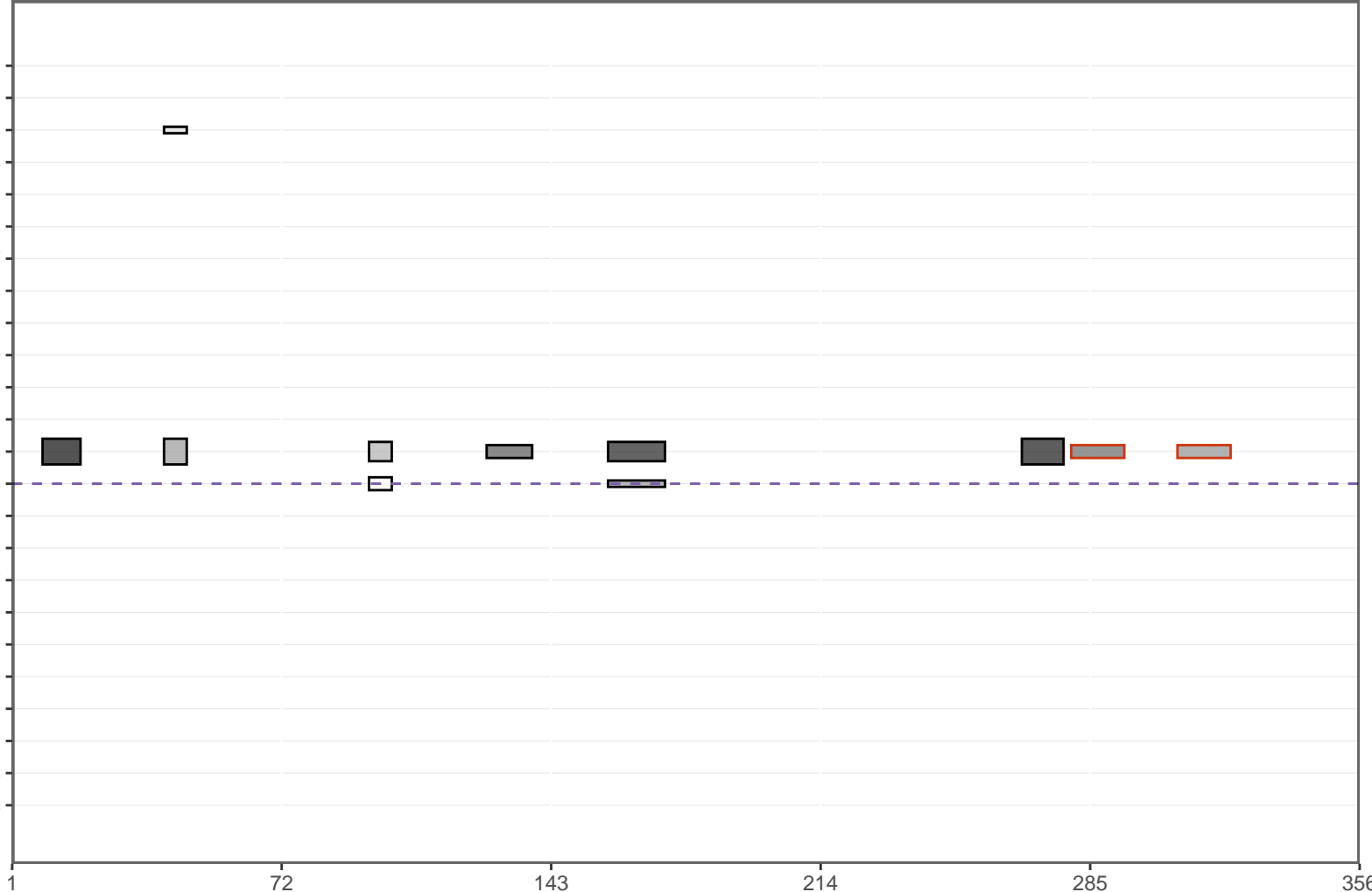
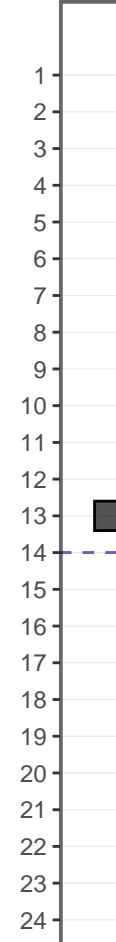
MW indication



Molecular weight

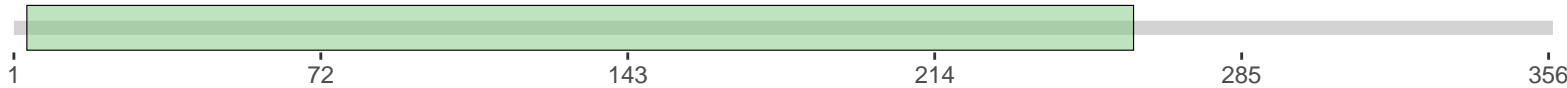


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AFEVLSRREYDQKLAADVWISGCVTLVMLVAYPFDEGDPKFRKTKQRIMAVQYKIPDVIYHSGDCRHLGRIFVANFRRTIKKIKHPWFLNLPRLTEAQAQAYYRRENPTTFLSGLSVEIMKIVAEAKTPAPSRVSGFGWGGEEEEKEKGGVVEEGEDEEEDEVEYKQVGAHESGVEVLT

NbL01g13610.1 ubiquitin-like_domain-containing_CTD_phosphatase [MW = 38.74 kDa]

No. of times detected



log(intensity)



Values from



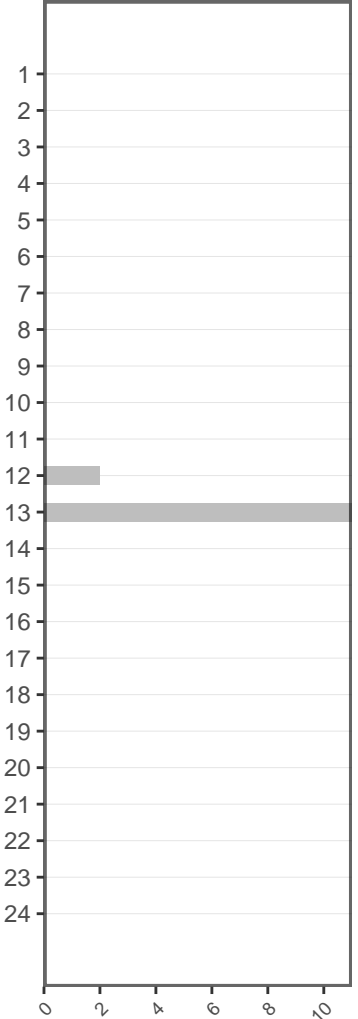
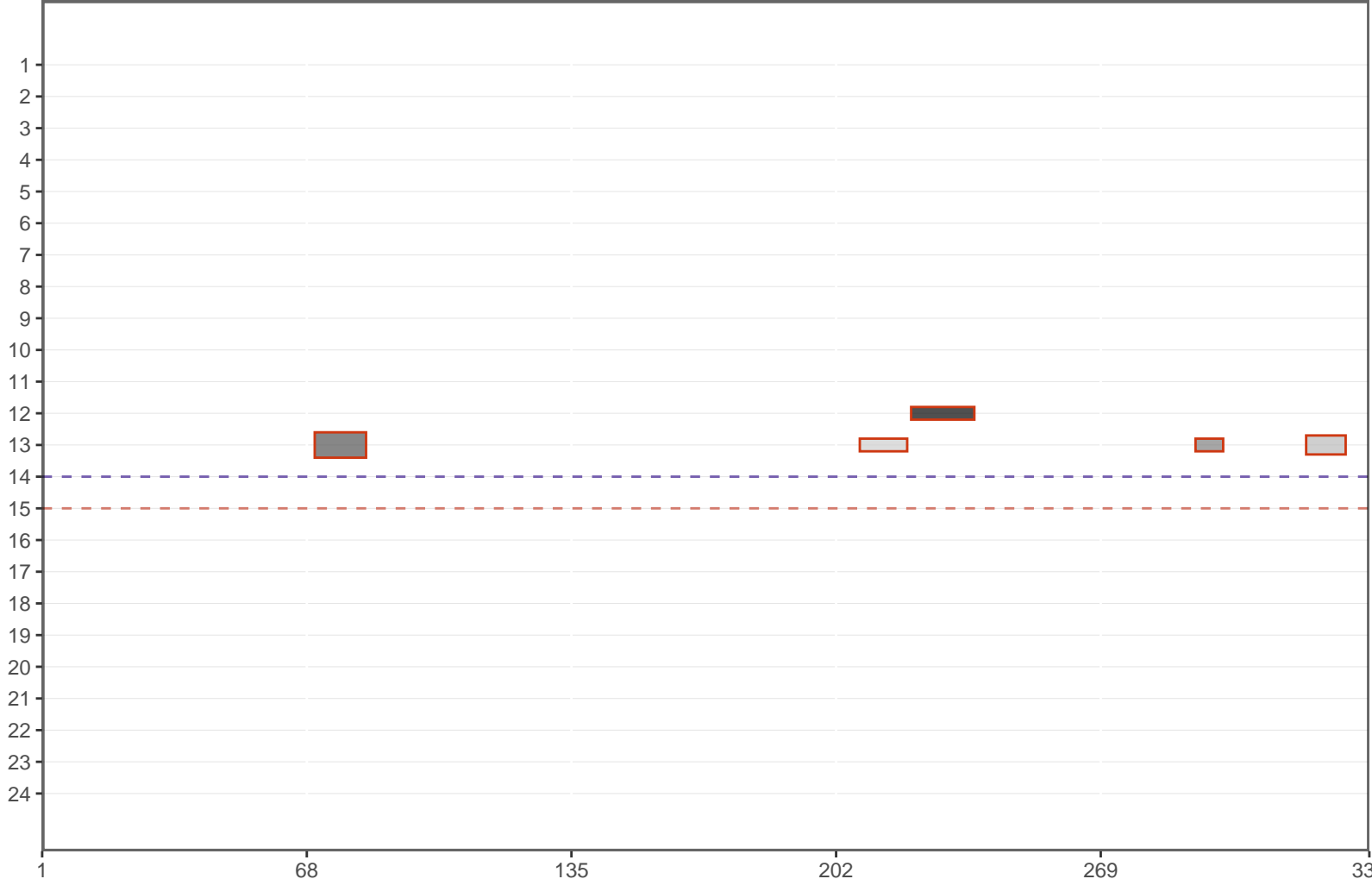
MW indication



Molecular weight

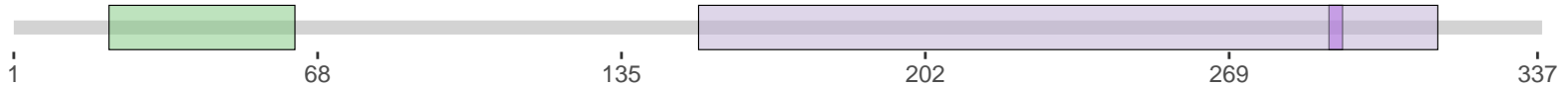


Gel Slice



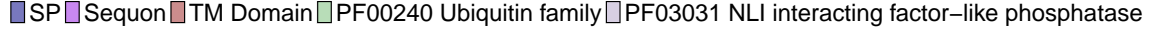
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IDYTLTDHRSIAENPLGLMRPKLHEFLSAWAAYEDIMWISATSMKWVELKMGGLGVLDPHYKATALLDHHMAMITVQSDRYGVFDCKPLGLIWAHFFPEFYSPKNTMFDGLRRNFVAMPQNGLVKPKFKAHANRSTGELMKLFGYLLAAADLDVSVLDHKHWESFNEIDNPKRRRH*

NbL01g13550.1 ATP_phosphoribosyltransferase_2_chloroplastic-like [MW = 43.01 kDa]

No. of times detected



log(intensity)



Values from



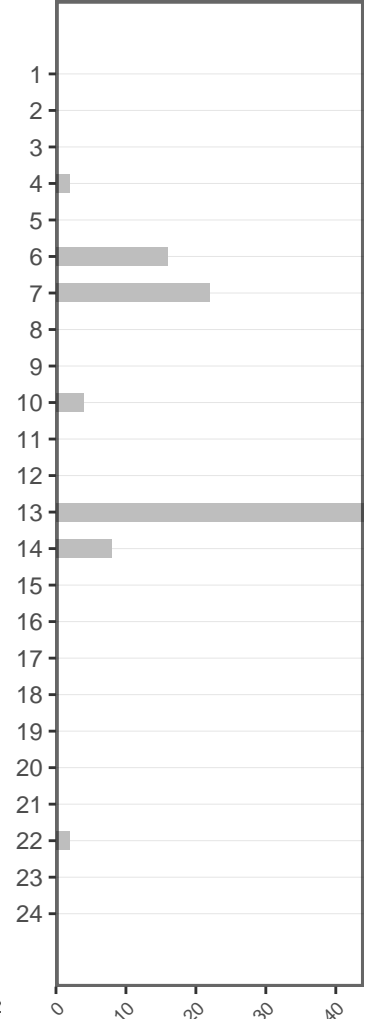
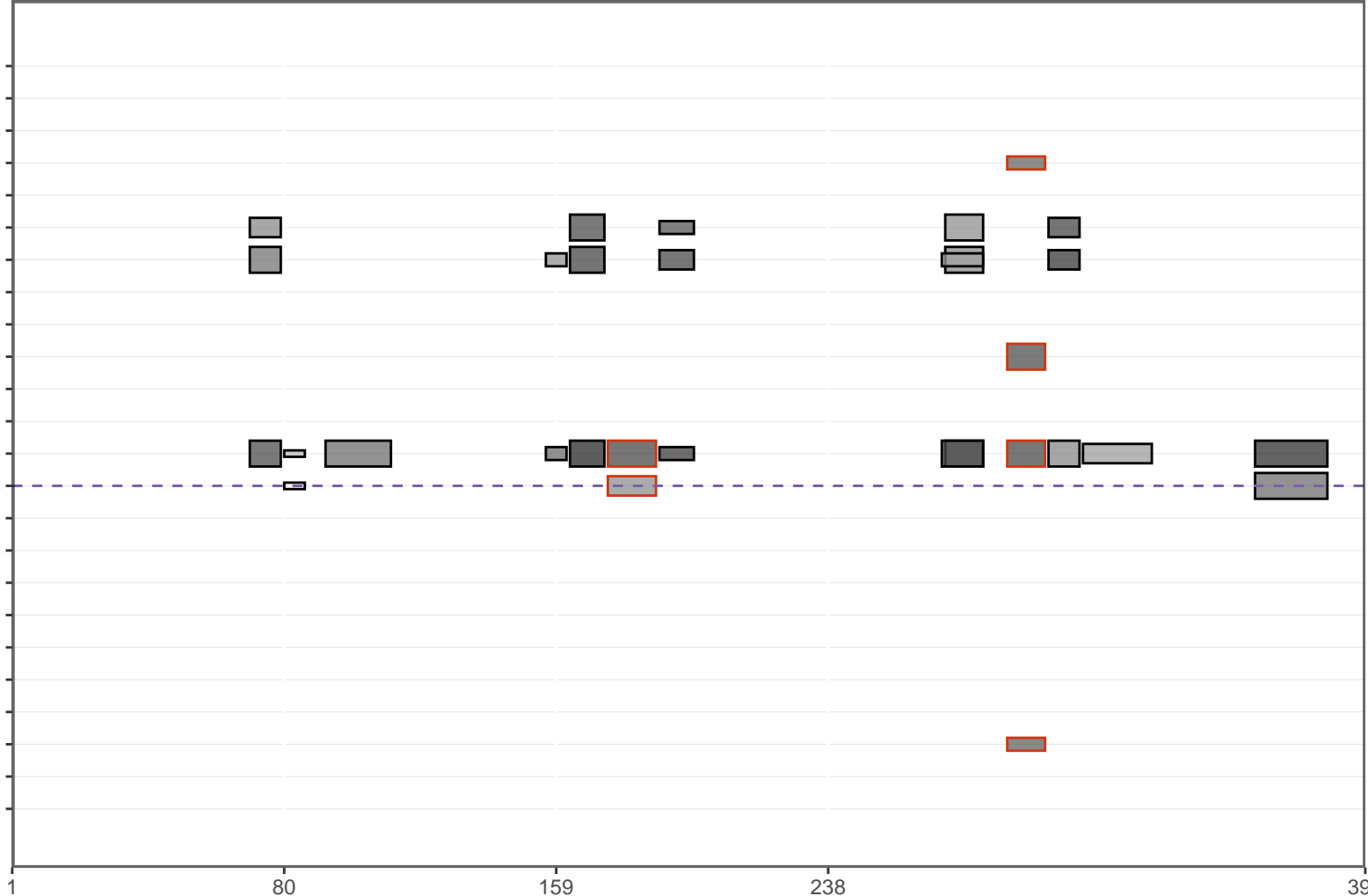
MW indication



Molecular weight

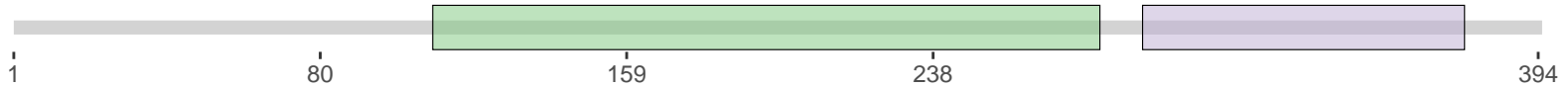


Gel Slice



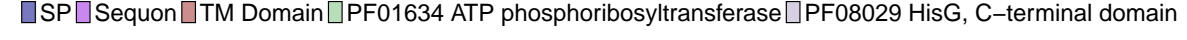
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TPEPLRWATGFTYLGPKFMKNDGLKHVTFSTADGALEAAPMGIADAVDLVSSGDTLRNLIKIEEGGILEGDAVLVGRKSLMQRKGLDTHHEMLERLEAHLRAIGQFTVTANMRGSSAEAEERILSGTSLGSLGGPTVSPVFKRDRGRVTADYFAIVGVKPKALYKSVQGLRAIGSSGVLSPLTYFDEETPRWRQLLEMLGL

NbL01g13530.1 nifU-like_protein_2_chloroplastic [MW = 26.35 kDa]

No. of times detected



log(intensity)



Values from



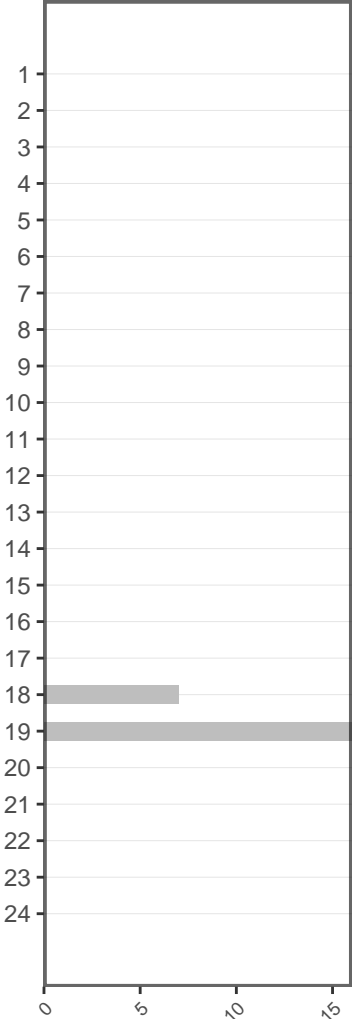
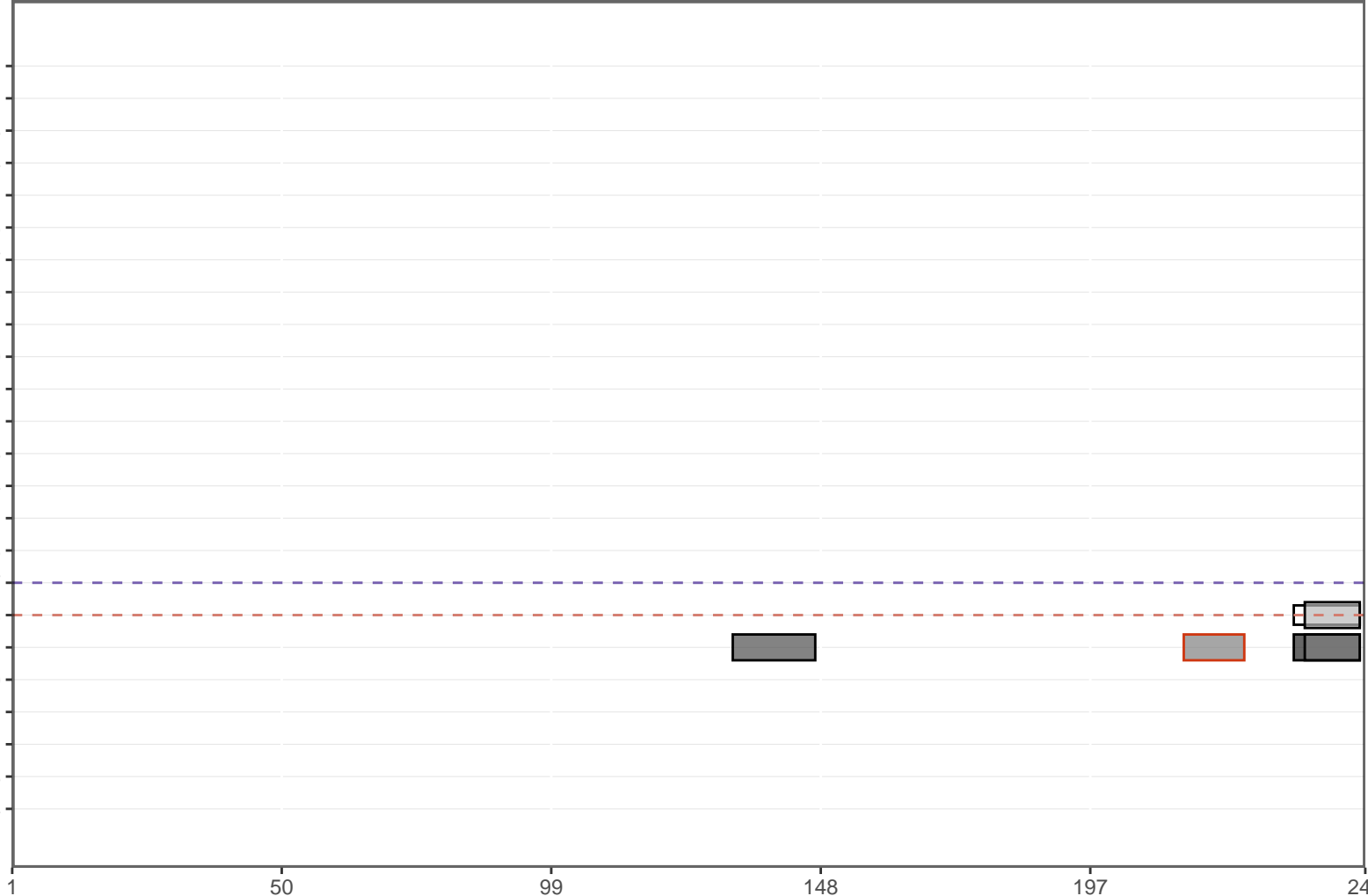
MW indication



Molecular weight



Gel Slice

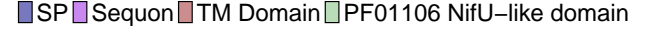


Peptide counts over 4 repeats

Protein length

Pfam domains

Pfam Description



Protein sequence:

IPYLIADGGNVALIKKIDGNVWLKLGAGGSCPSVVTMLGIERRLMKPFIVWEAVPDEETGLELNEENEKVLLEIRPYLVGAAGGSLLEWEEPIKVRITGPAAGVMTVRVAVTQKLRKIPMAAVQLQ*

NbL01g13380.1 60S_ribosomal_protein_L3-2 [MW = 44.4 kDa]

No. of times detected



log(intensity)



Values from



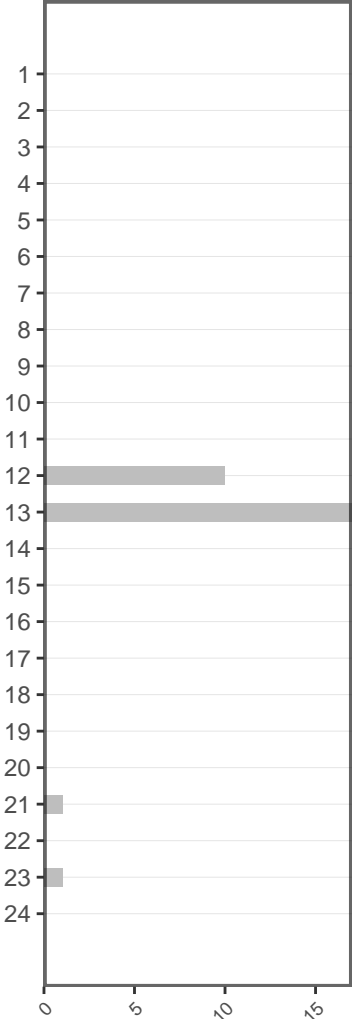
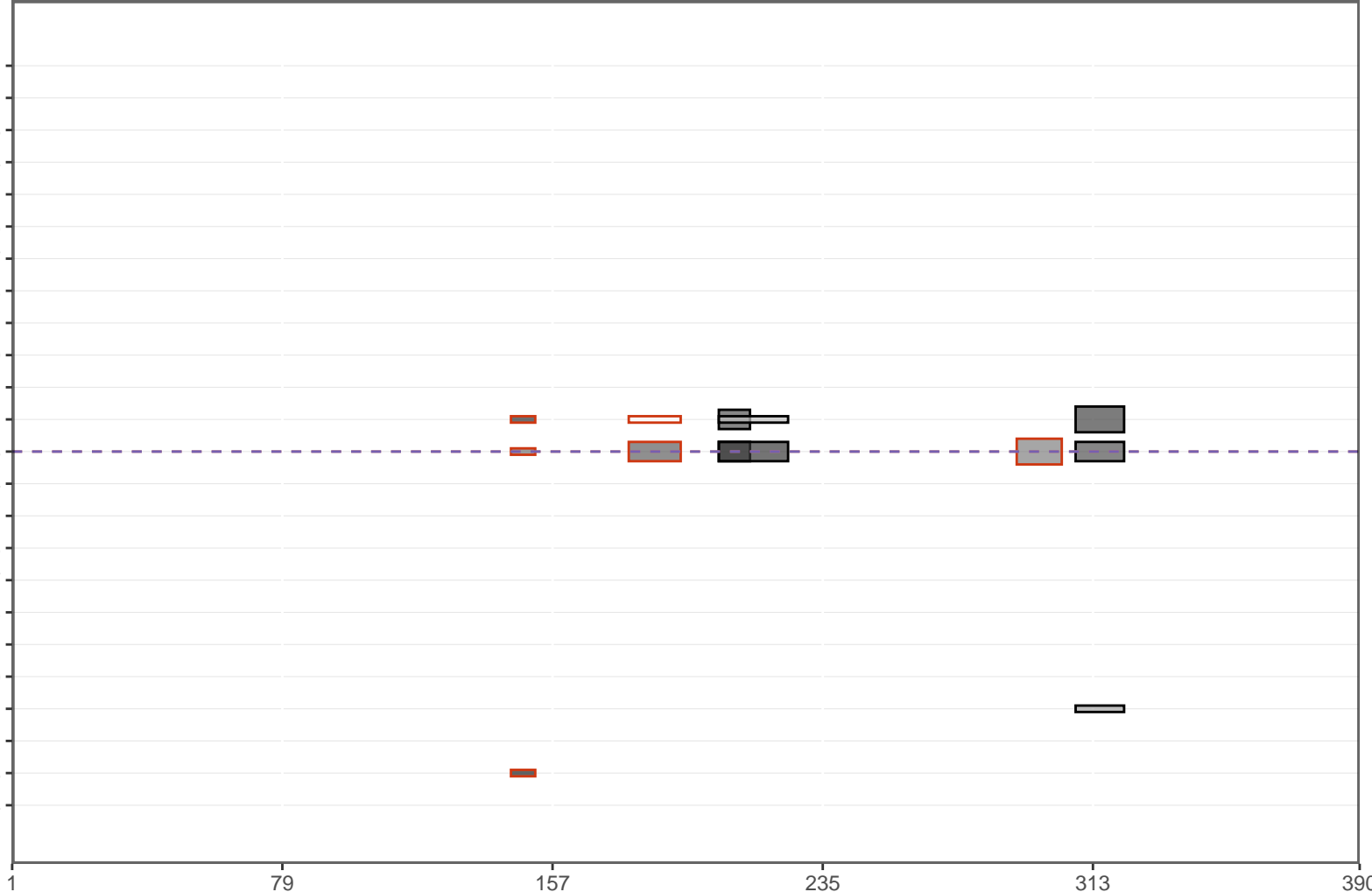
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

LMELIQNGGDVADKVDYAVGFFKDFVDFMFKQNDMDIDGVTYKGGKGFVTRWGVTRLPKTRHRLGRKAVGAWHPARVSVTVARAGNGYHRTLELNKKVYRLGKAGDGHSAITDFDRTEKDDTPMAGGFPHYGVKEDFLIKGGCGVPPKRVVTLRGLLNGTGRVALEEIKLFDTSKFGHGRFQTTGQEKAKFYGRLLKA

NbL01g13370.1 50S_ribosomal_protein_L4_chloroplastic [MW = 34.37 kDa]

No. of times detected



log(intensity)



Values from



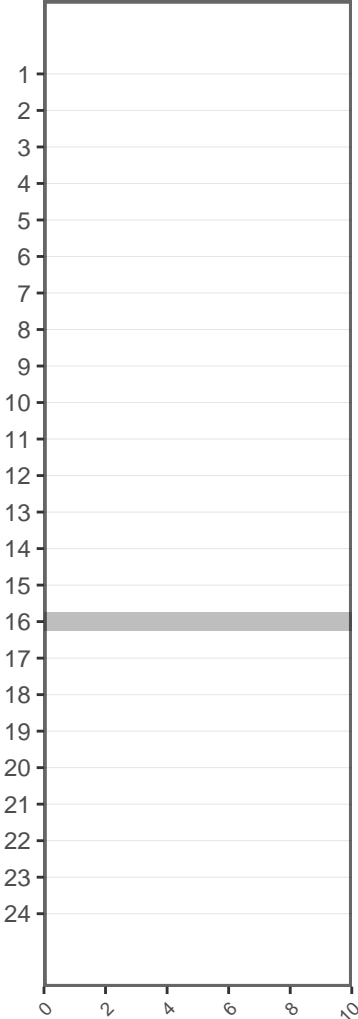
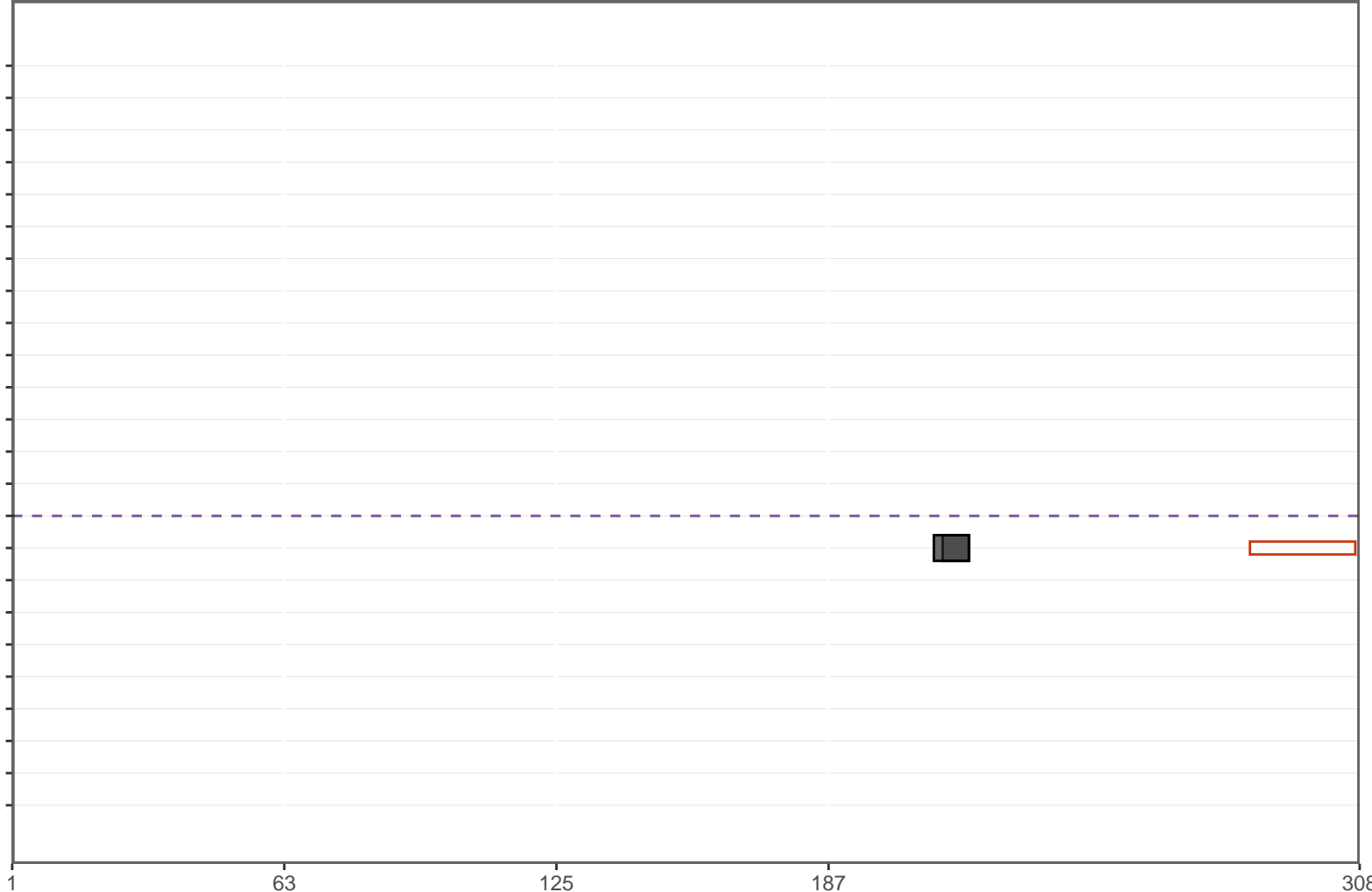
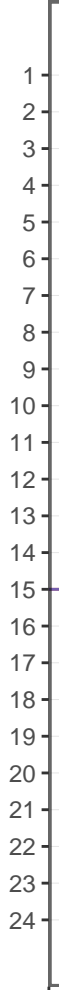
MW indication



Molecular weight

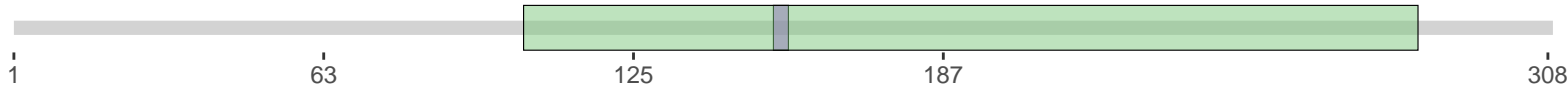


Gel Slice



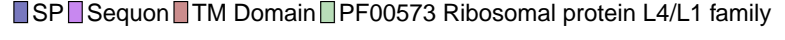
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

KTGRARRGNSRTRPLRPGGGVVFGRPKKDWKVKINNKERLAIGTALSSASENTIVVEEFNDKFEKPKTKFELMRRVWGLDPKEKSLFLMTEVSDNVLSSRNIGTKMLTRPTLNLFDLIDSEKLVTKSAVDFLNERYGDENEWEDEGGEINDDGGAEESSE

NbL01g13340.1 coatomer_subunit_delta-like [MW = 58.02 kDa]

No. of times detected



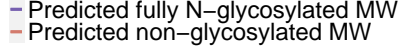
log(intensity)



Values from



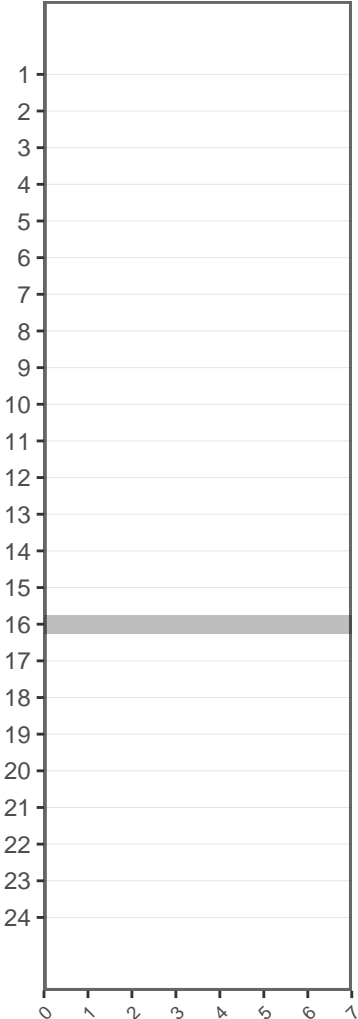
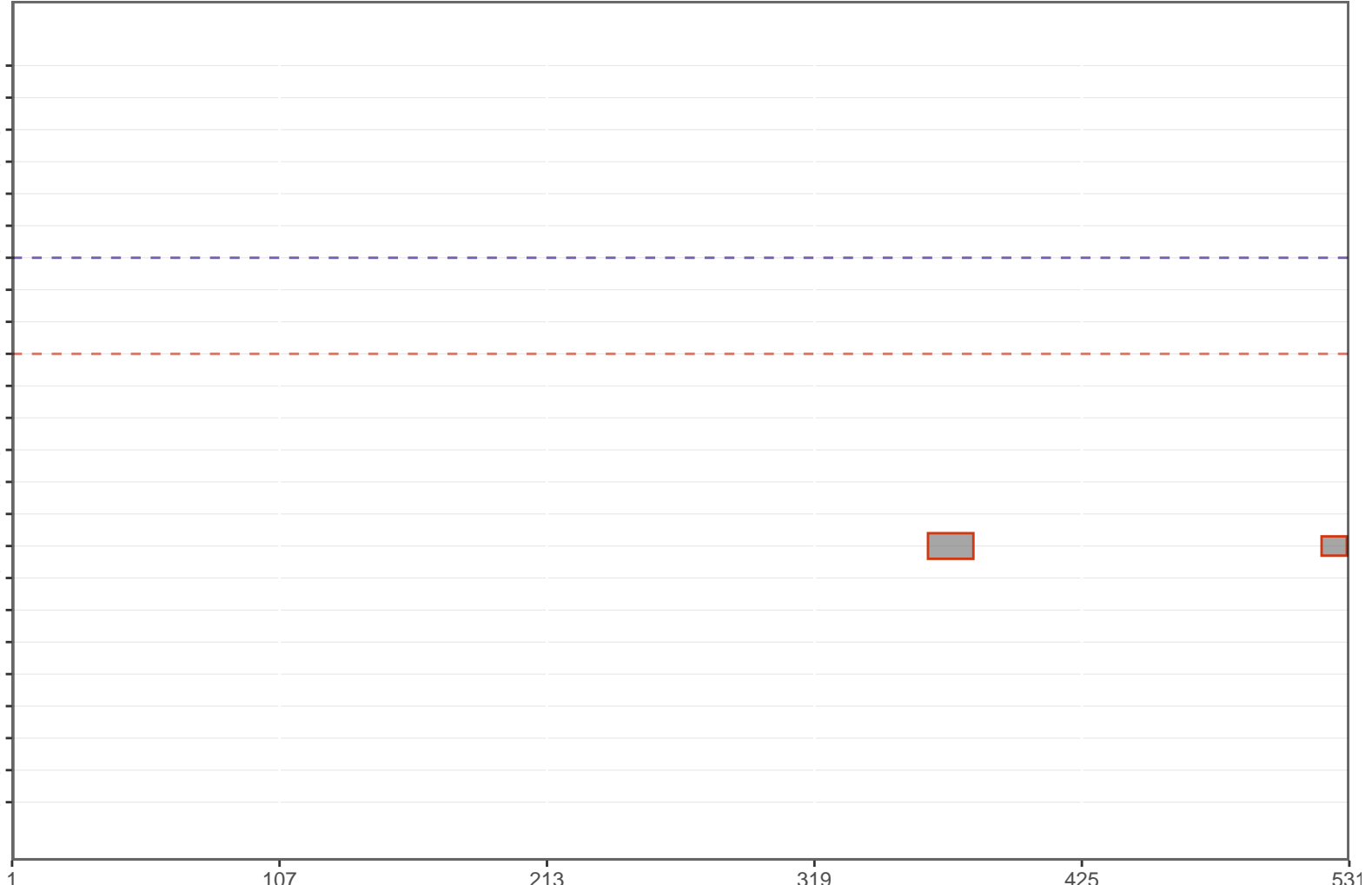
MW indication



Molecular weight



Gel Slice



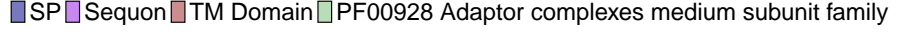
Protein length

Peptide counts over 4 repeats



Pfam domains

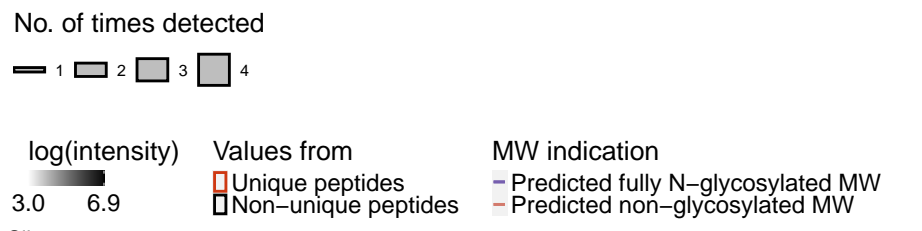
Pfam Description



Protein sequence:

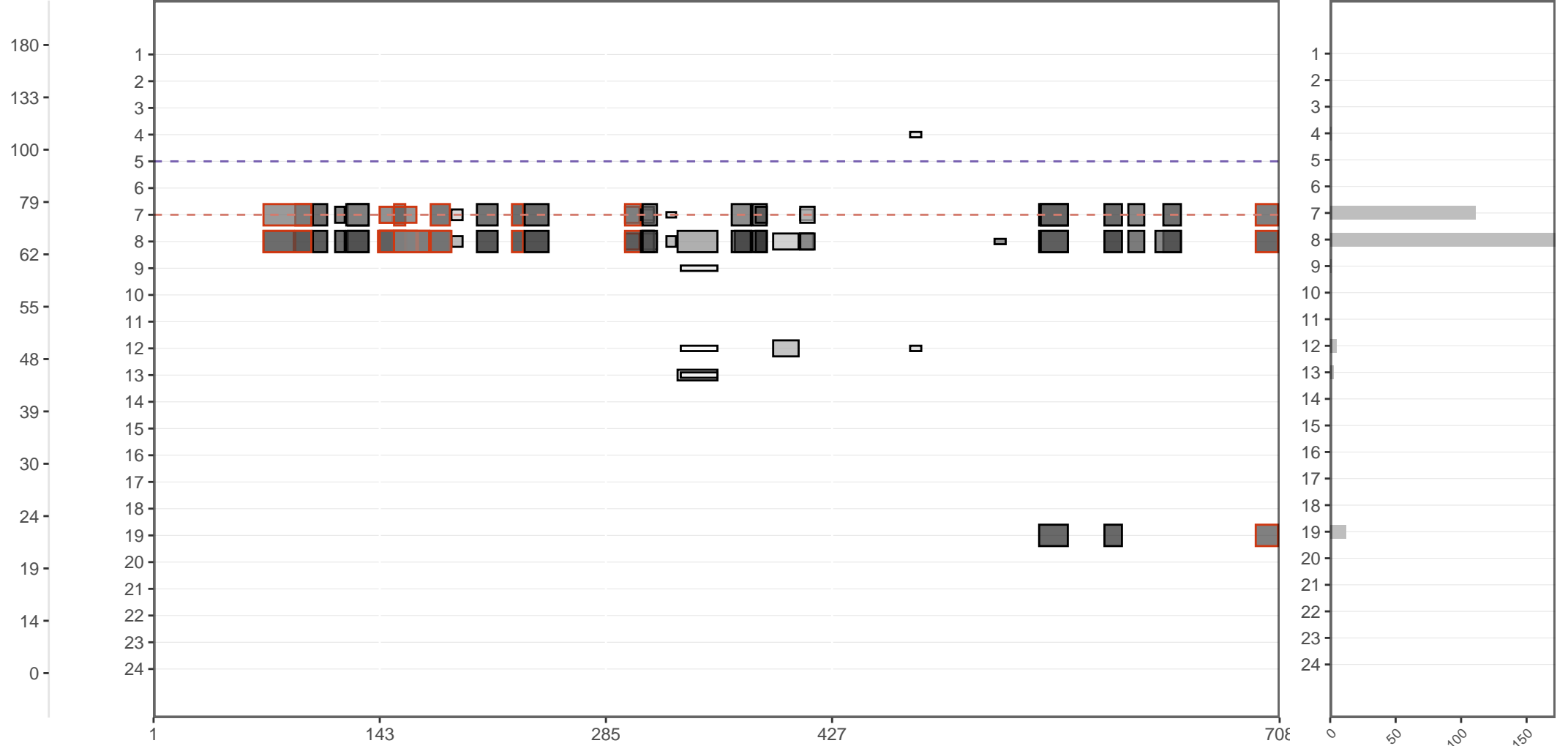
DKTNGFLESLSKAEGEVVEEDVRRPBGIGAKRFAAALPTDPIVLTVEEKINVTLKRDGGVSNFDVGGTLSLGLNGEDAFIQVGIETSGNPKLFTKHPNMNKELFSENENLGLKDFNRPPTTGGGGDGVLLLRWRMGTADESILPTINGWPEVSGSEFYVNEIETPAGIDLGNVYVIEVPLPALREAPNVGGIDGEWRVDFRNVLEWVLLDINSNGCGVLEFVVPADPQVFFPISARFTASRFSDLKYYNLPIKGGTPKHSGRTQLSTETFYQVV

NbL01g13320.1 stromal_70_kDa_heat_shock-related_protein_chloroplastic [MW = 75.32 kDa]



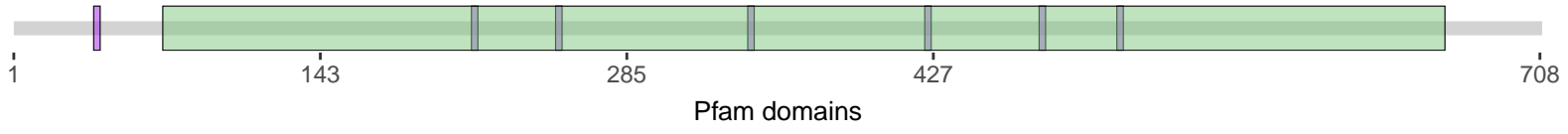
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

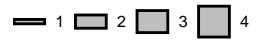


Protein sequence:

INSLPFTATADGPKYHETTRKGFEEGLDLDRLKTPVQNSLRQKLSFSDIDEVLVGGSTRIPWQDELKRLGKDPNVTVPDVEVAGAAVAGVLAGVSDVLLDVTPLGILETLLGGVMTKIPRNTLPTSKSEVFSTADGGTSVEINVLGGEREFVRDNKLSGFRLDGIPPAFRGVPGQIEVKFDIDANGILSVTAIDKGTGKKQDIFITGASTLPGDVEVRMVKAEERFAGEDEKRNDAIDTRNGADGAVVQTEKQLKELGDKVPGPVKKEVAKLGLKEKASGG

NbL01g13260.1 acetolactate_synthase_1_chloroplastic [MW = 59.9 kDa]

No. of times detected



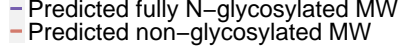
log(intensity)



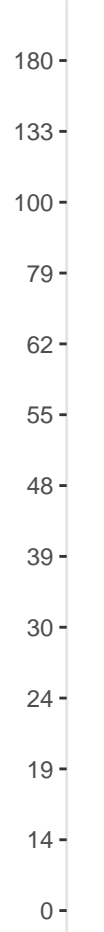
Values from



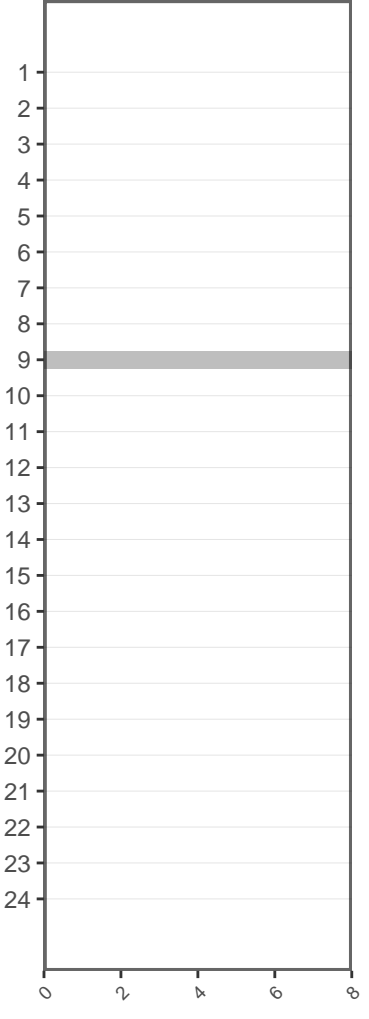
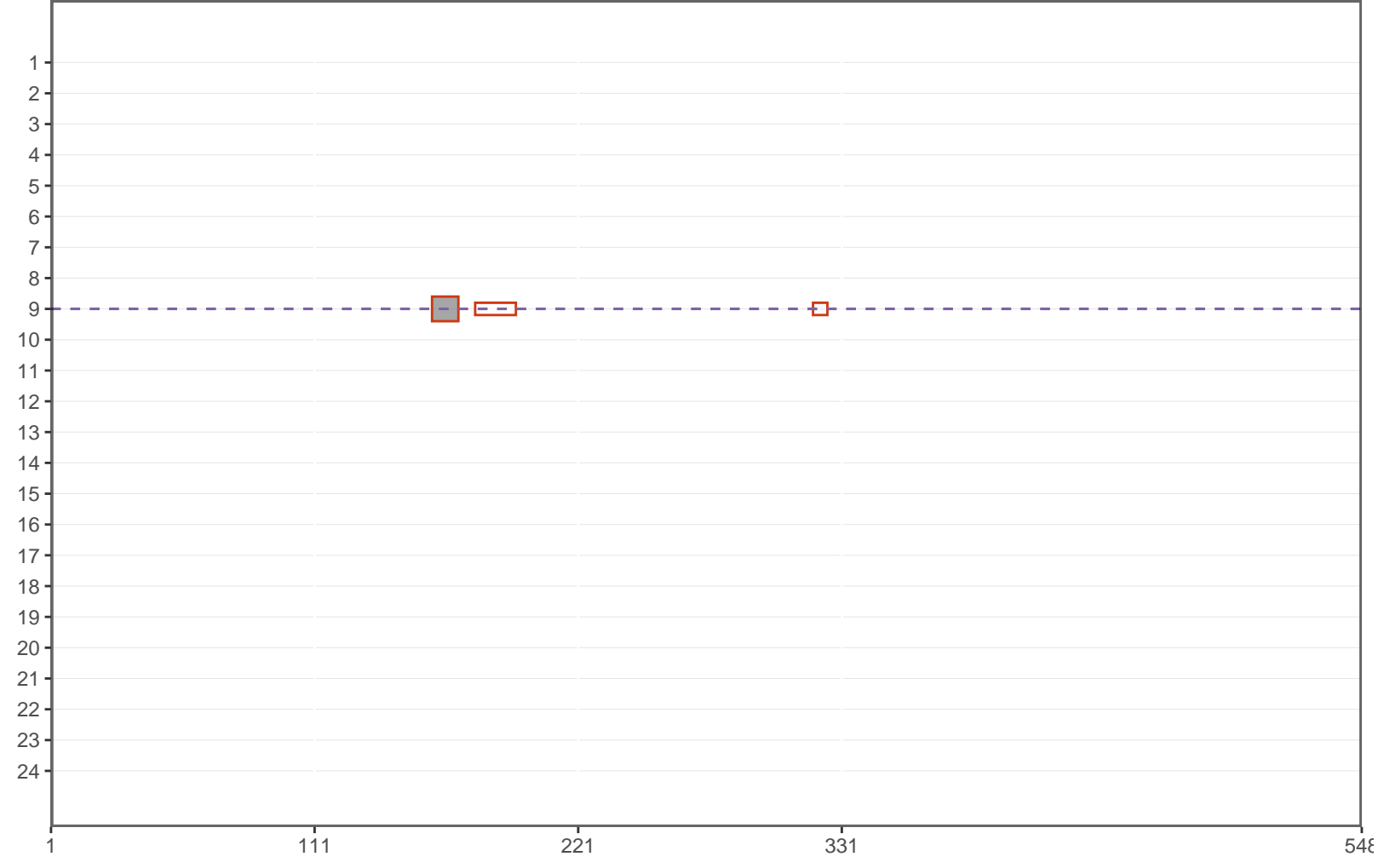
MW indication



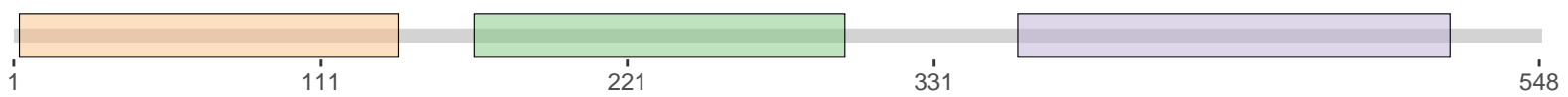
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00205 Thiamine pyrophosphate enzyme, central domain
- PF02775 Thiamine pyrophosphate enzyme, C-terminal TPP binding domain
- PF02776 Thiamine pyrophosphate enzyme, N-terminal TPP binding domain

Protein sequence:

FASRAKIVYHIDISAEIGKNGKPHVSGADRLALQGLNSLSEKEGKLLDFSAWRGELMEKQKWKHPFNKTFGDMPDQYVAVGLDELTSNGAHSITGVGQHQMAWAQYKRYKPRQVLTGGGLGAMGFLPAAGAAVGRPDEVVVDDGGGFMNVQELATIKVENLPIKMLLNQHLGMVVQWEDRFYKANRAHTYLGKNSNEAIEFPMKFAEAGGVPAARVTRDDLRRAAQKMLDTPGPKLDDVWPHQEHVLPMPISGGAFKQVTEGGRISY*

NbL01g13060.1 uncharacterized_LOC107796198 [MW = 52.54 kDa]

No. of times detected



log(intensity)



Values from



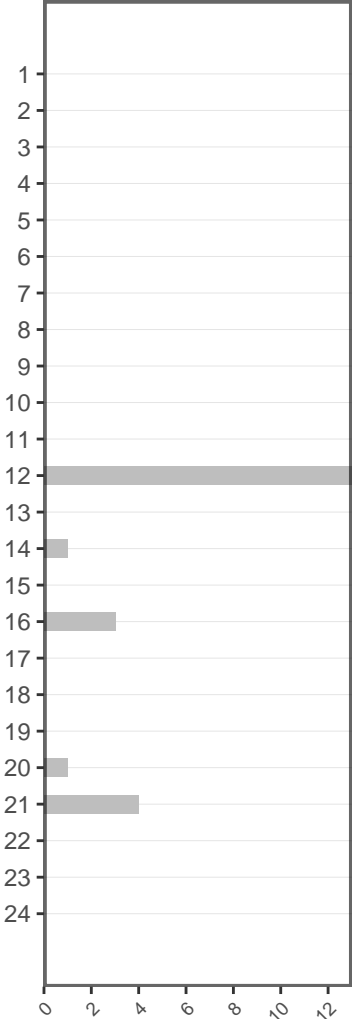
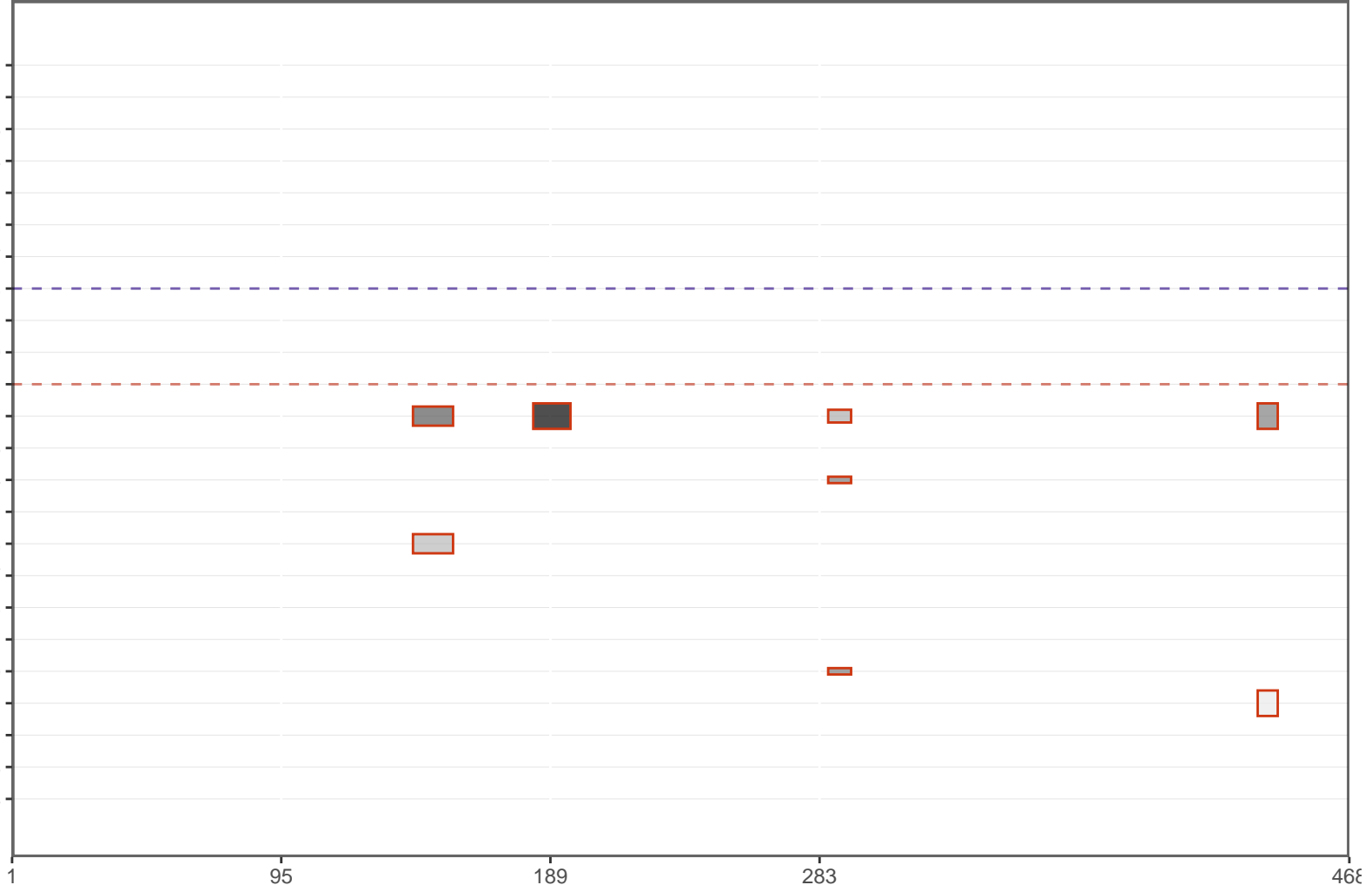
MW indication



Molecular weight



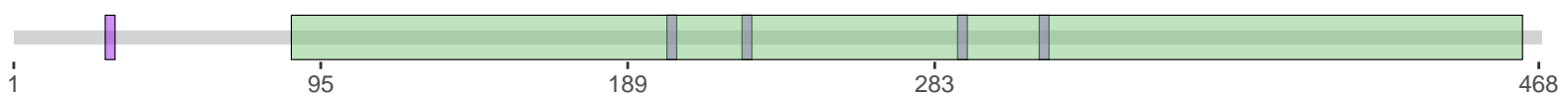
Gel Slice



Protein length

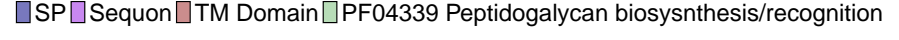


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FNVSSLIHTPTANSEWRKLEEKFLGRIGMQYHWKRNRYKSFDEFLMDMKGSKRKNRIGERRKKSAGNVTMKRLRGVEIKASHWDTFYKFRNTDNKRWGTAVLTRDFHQMDSARMGDNLVVAEEGDELVAALNLGGDTLVGRVWGLPGAYANLHFEADYVQAEAAEELNLGTVVEAGAGGCHKGRGYMPVTTYSCHYVLDDEFRRVFDDFLIVRESAGVKVIMLLGGDGFPEKNVWSI

NbL01g13000.1 survival_of_motor_neuron-related-splicing_factor_30 [MW = 33.32 kDa]

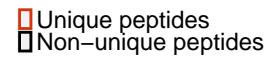
No. of times detected



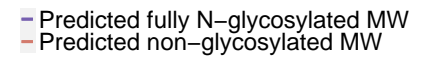
log(intensity)



Values from



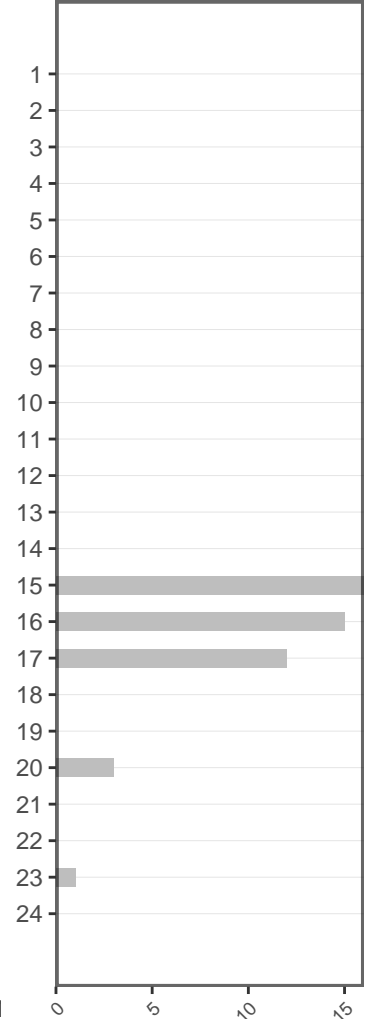
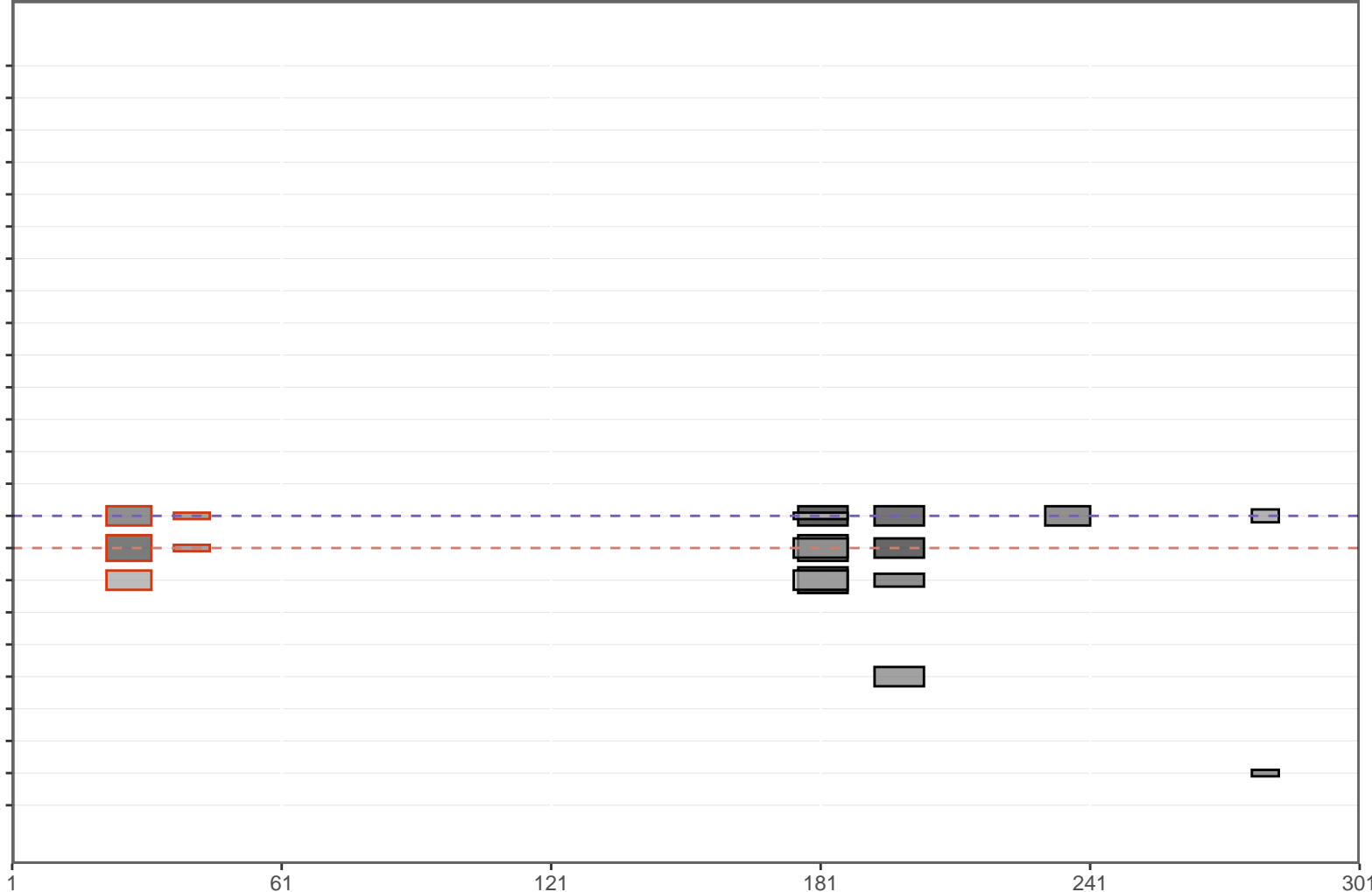
MW indication



Molecular weight

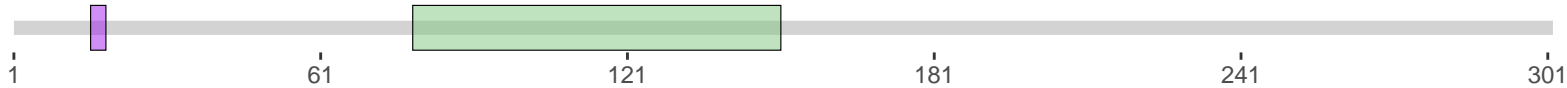


Gel Slice



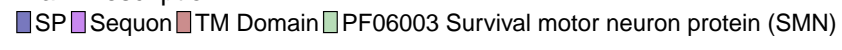
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

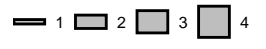


Protein sequence:

IGNKEEVDHANRPLDQEGFVPLVLEAEKIAEATKQALKRRIAGAAADVDQSRFLPAKLLIDPNDPEVDKAAAKRKHAFKSKVRIEQLVAGNKRQNAWQDFQSTKGGTKKVFVFSGRKRRESIFKSPEDPHGKGVYTGSGKGLTFQRRKHLHLKGANAEASDEI

NbL01g12920.1 methionine_S-methyltransferase-like [MW = 121.29 kDa]

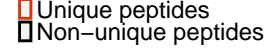
No. of times detected



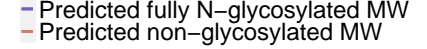
log(intensity)



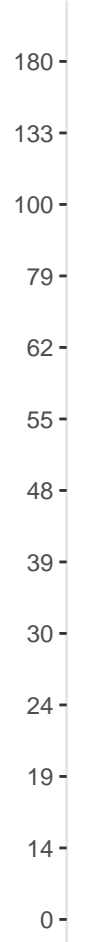
Values from



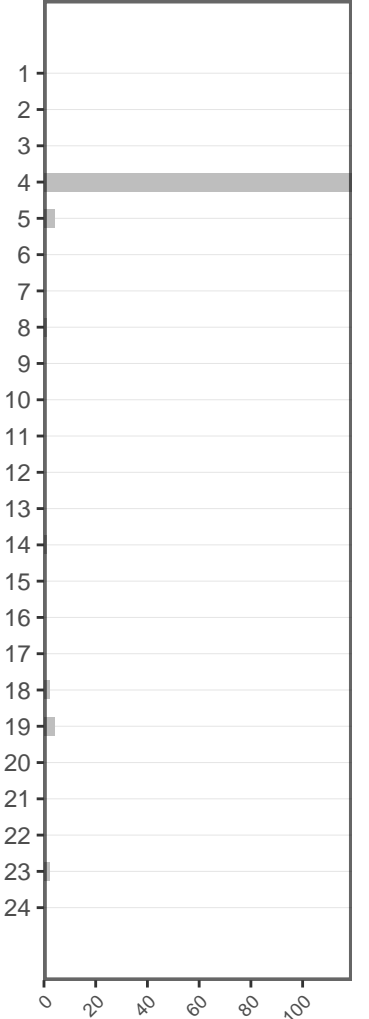
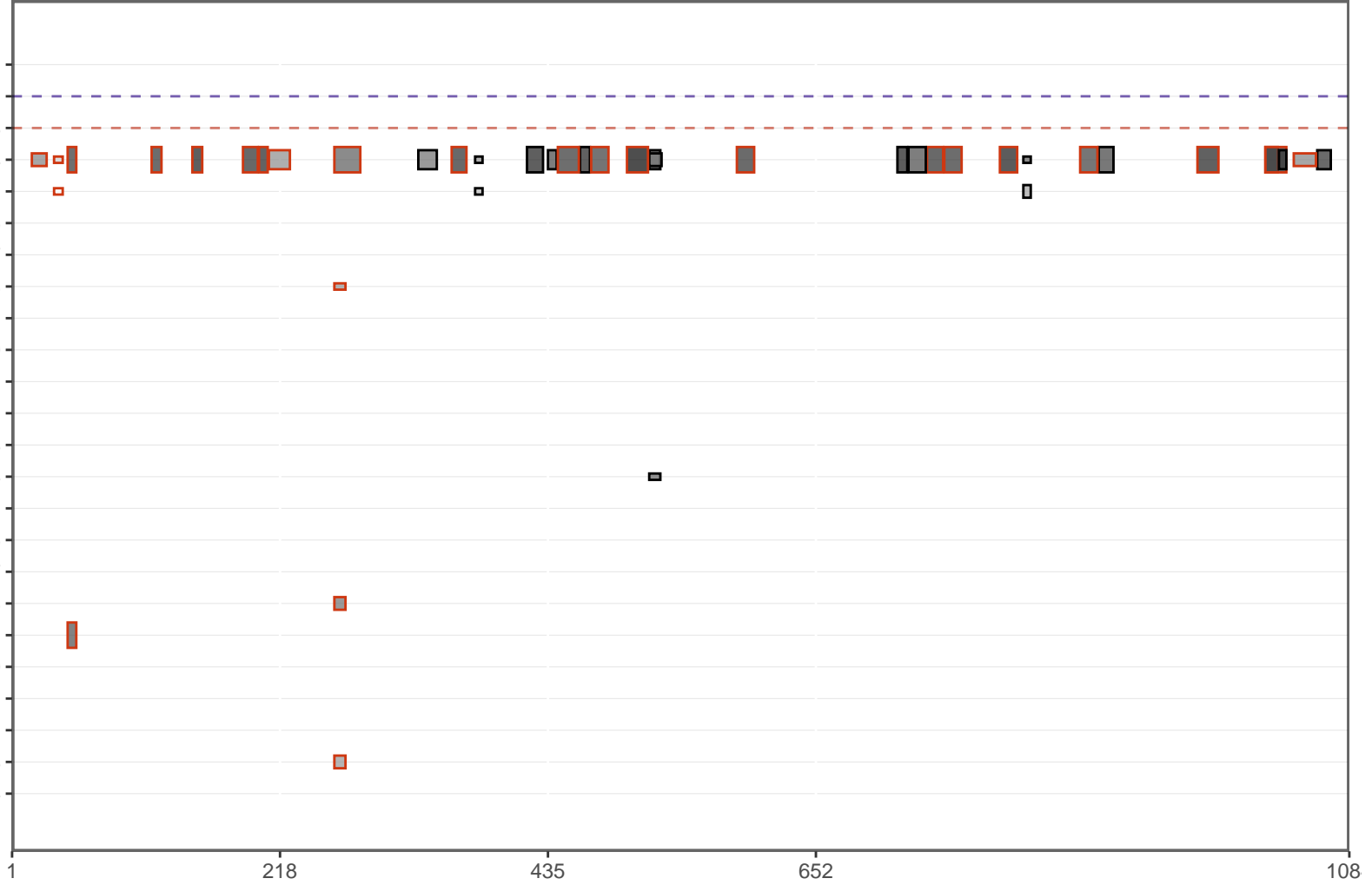
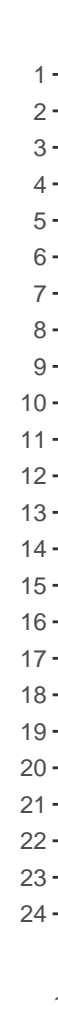
MW indication



Molecular weight



Gel Slice



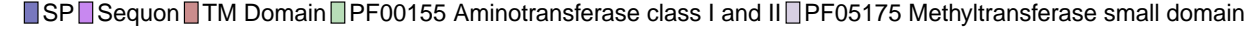
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KPQVVTGMAQFSEVTS65FEYLLDTREIGRFLFVD60DFEL66LPSKNGVLFKARTSLPSHAARIGGLWNGVYSDLEVAFVISEDKTYKALSKTMEELGQNTAL69YYYGOLFHELLAFQLSDRHPPAREAEKELKAKMGFFPSV65SVLNHAELEVD65DLNHHMDV66GFLPPTPKAAAFESGFVRGNIAESEIDVTSNRQLME65SYGFFPTNSKTEFFVADCPALF68KLVGGHHEGGTLGFFM68NG65VSAANFVKANAVIPTSP68EGFKLTKTQTVESFLKTN

NbL01g12820.1 2-C-methyl-D-erythritol_4-phosphate_cytidylyltransferase_chloroplastic [MW = 34.25 kDa]

No. of times detected



log(intensity)



Values from



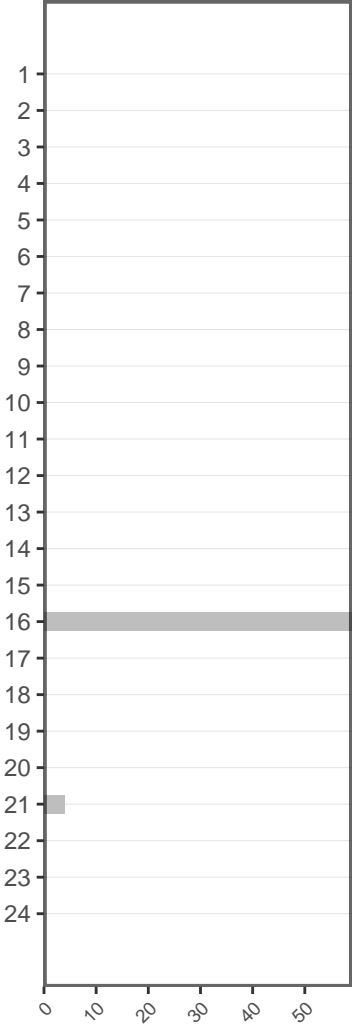
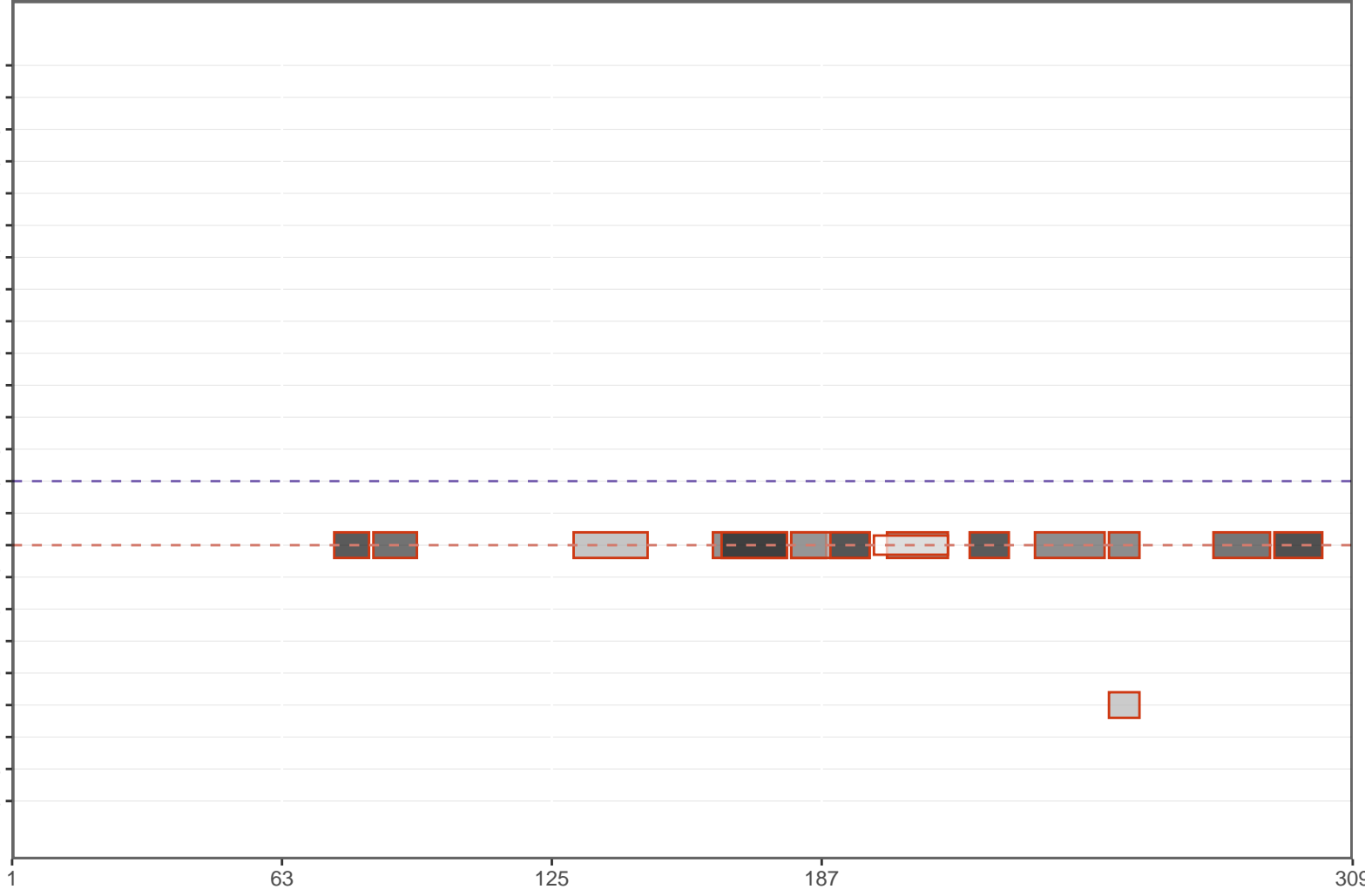
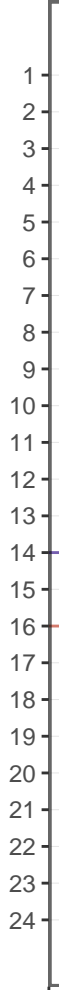
MW indication



Molecular weight

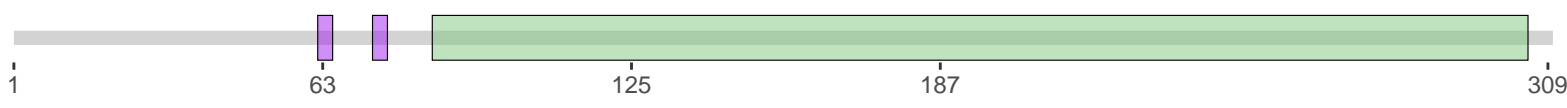


Gel Slice



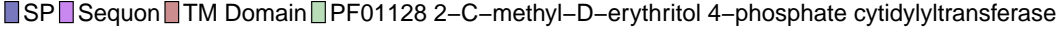
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DIFEDAKENIVYKLFALPGKERGDEVYVGLGEVDNSKLVGHDSARPLVWTEDEVKVLKDGWLVSAALVGVPAKATKEANSESFVVKTLDRKTLVEMQTPQVVKPELLKKGFEVLRREGLEVTDQVSEVHEHUKHPVYITEGYSYTKVYTPDQLLAERLNTEE

NbL01g12760.1 cinnamoyl-CoA_reductase_1 [MW = 35.66 kDa]

No. of times detected



log(intensity)



Values from



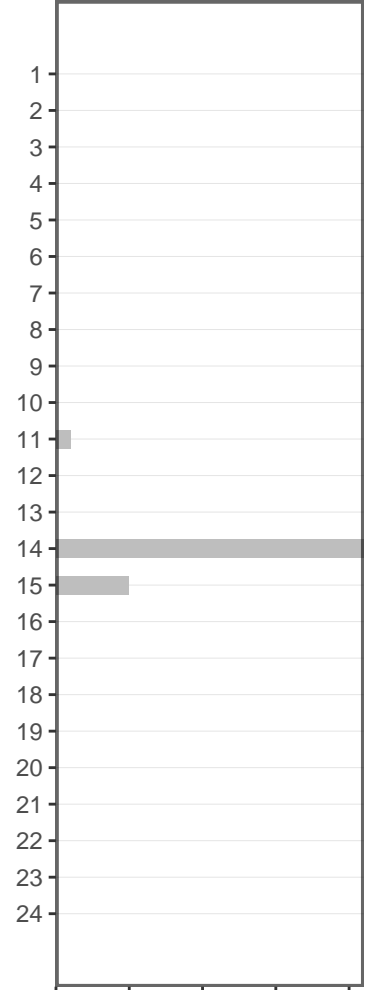
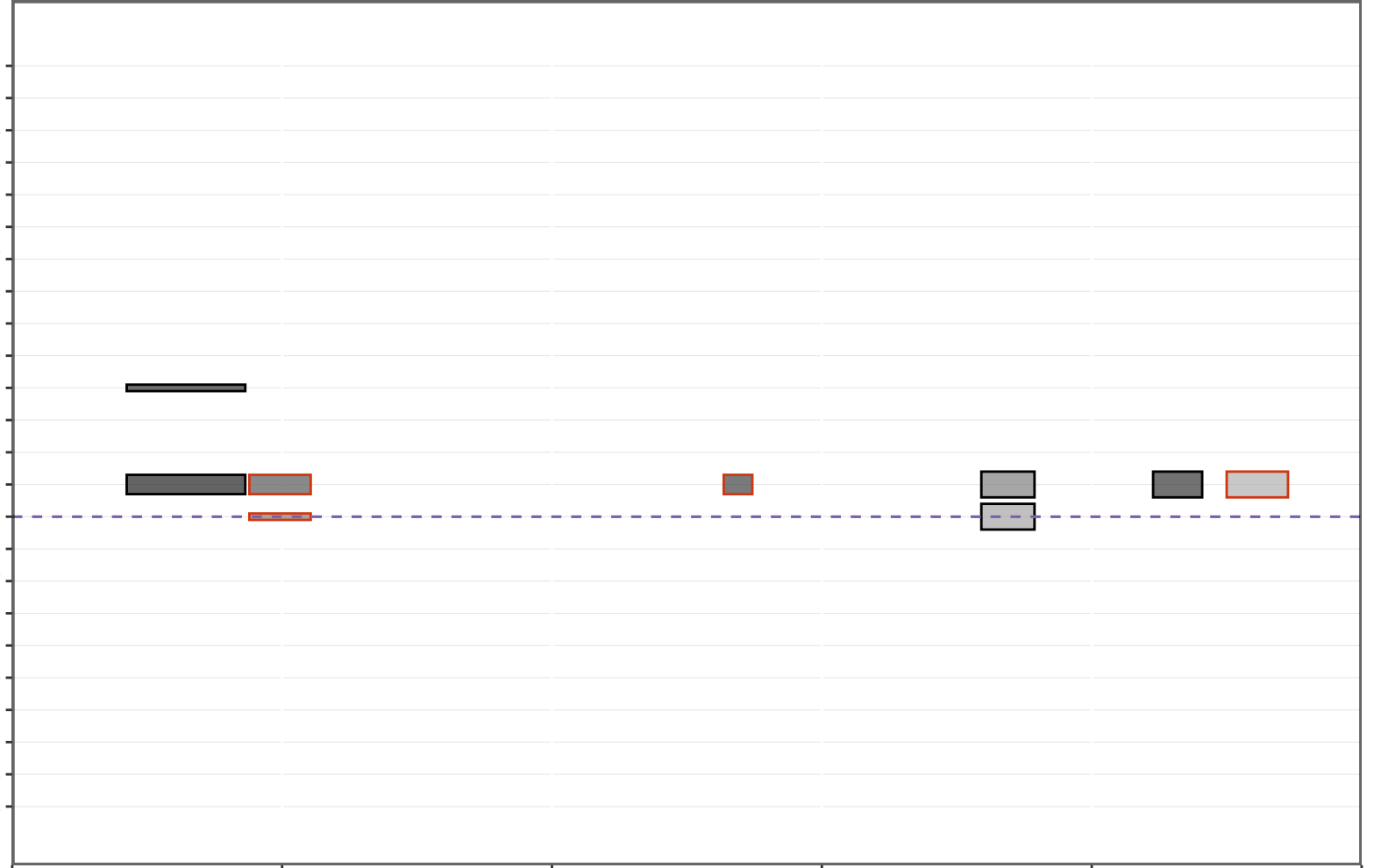
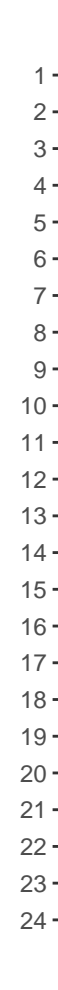
MW indication



Molecular weight



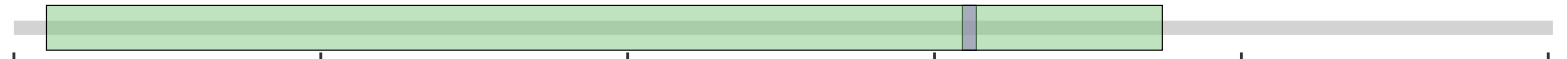
Gel Slice



Peptide counts over 4 repeats

1 67 133 199 265 331

Protein length



Pfam domains

Pfam Description



Protein sequence:

DLDYCKSRQKYYFVVKTLAEKAWFEFAEKNGLDVWAINPATGLGQLLQPLNASCALGQLLGGSTDGEYHVLGAVHVKDVAKQILFESPHASGRHLGTNGYQFGDFAEVSKLYPEFFPIRFTGETQPLVGGKDAKKLIDLGLVFTVEDAVRDTVYSLKAKGFLKQGGN

NbL01g12560.1 NADPH:adrenodoxin_oxidoreductase_mitochondrial [MW = 57.74 kDa]

No. of times detected



log(intensity)



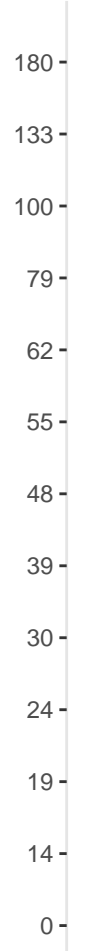
Values from



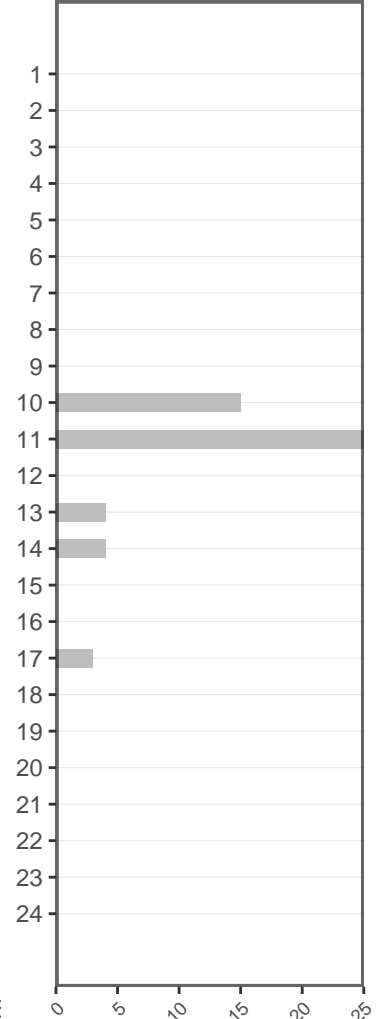
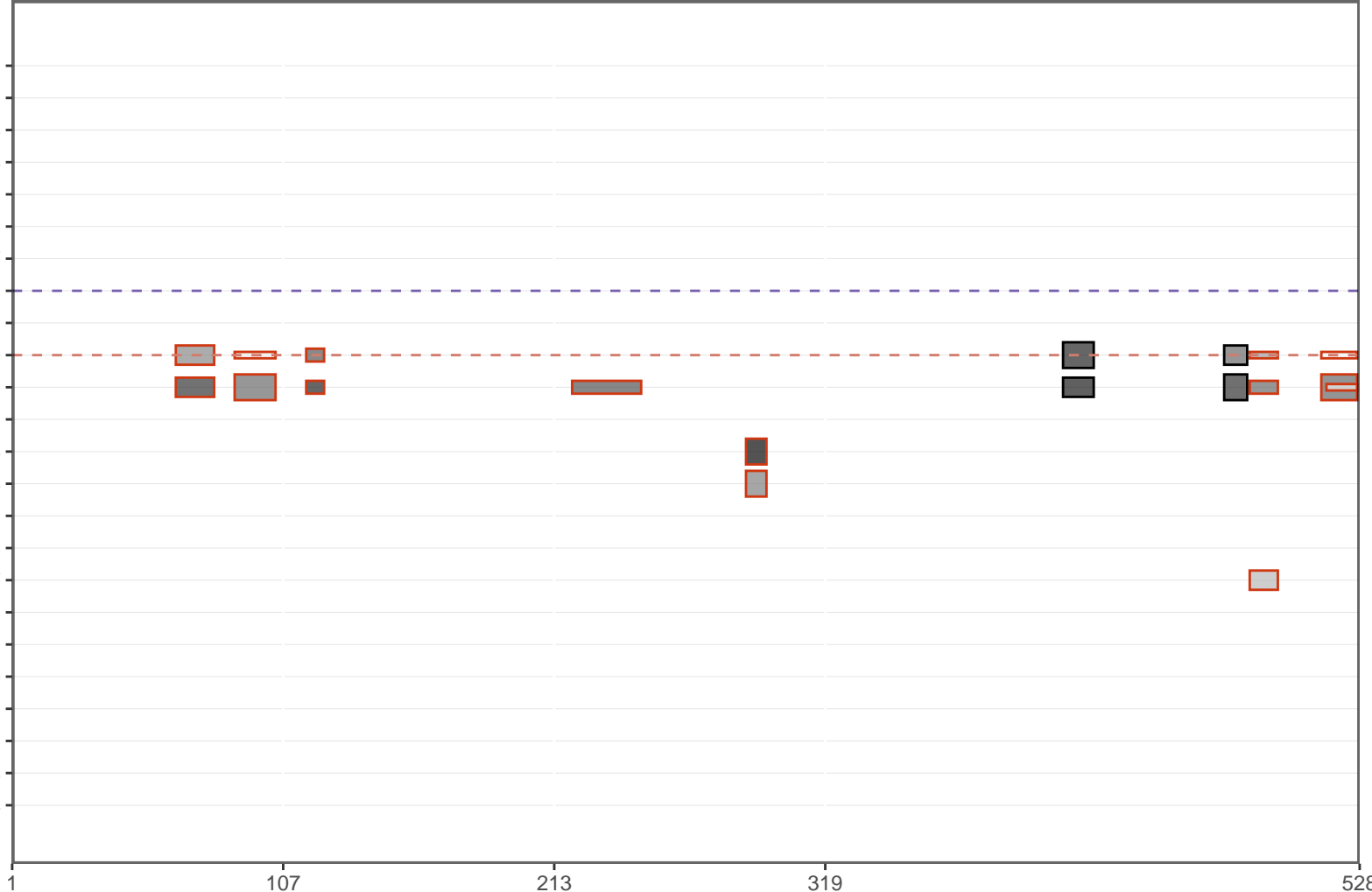
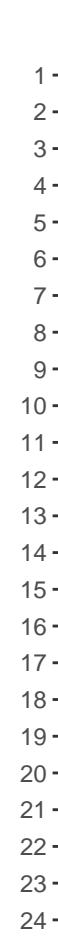
MW indication



Molecular weight



Gel Slice



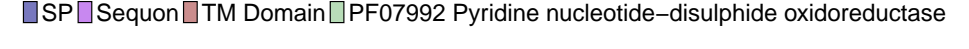
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

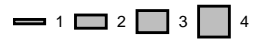


Protein sequence:

GRRGAQAATAKELREVLGKDLFIEQGADLSKTPDAEELKSNRIKRRHLLSKAATSAASVCSGPGQKELHFVFFRKPRFLESDCRGSHVAGLRLERTLKEDAGSGRQAVGTGLFDEMEGGLVLSKSVGKSRPVDGLPFDHKKGVNPNVQGRVLSAASGQDALVEKGLVYQGWLKRPTGHIATNLYCAEETVAISIEDVQGGLYTSSGSLKPKRGREGLLQLLDSRNINVPFGGWENIDSEKRRGSLKPKREKLTAWGELLEVAIK

NbL01g12380.1 cyprosin-like [MW - SP = 52.45 kDa]

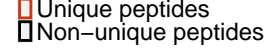
No. of times detected



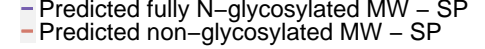
log(intensity)



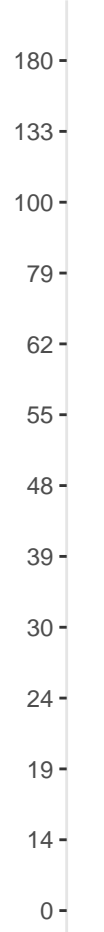
Values from



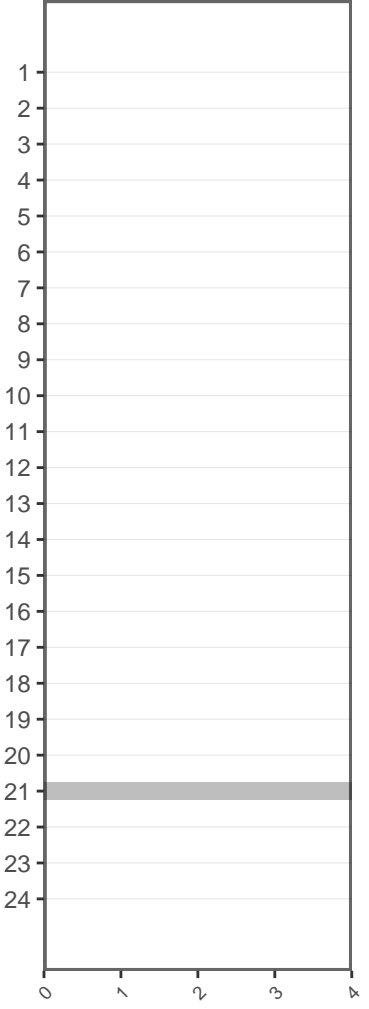
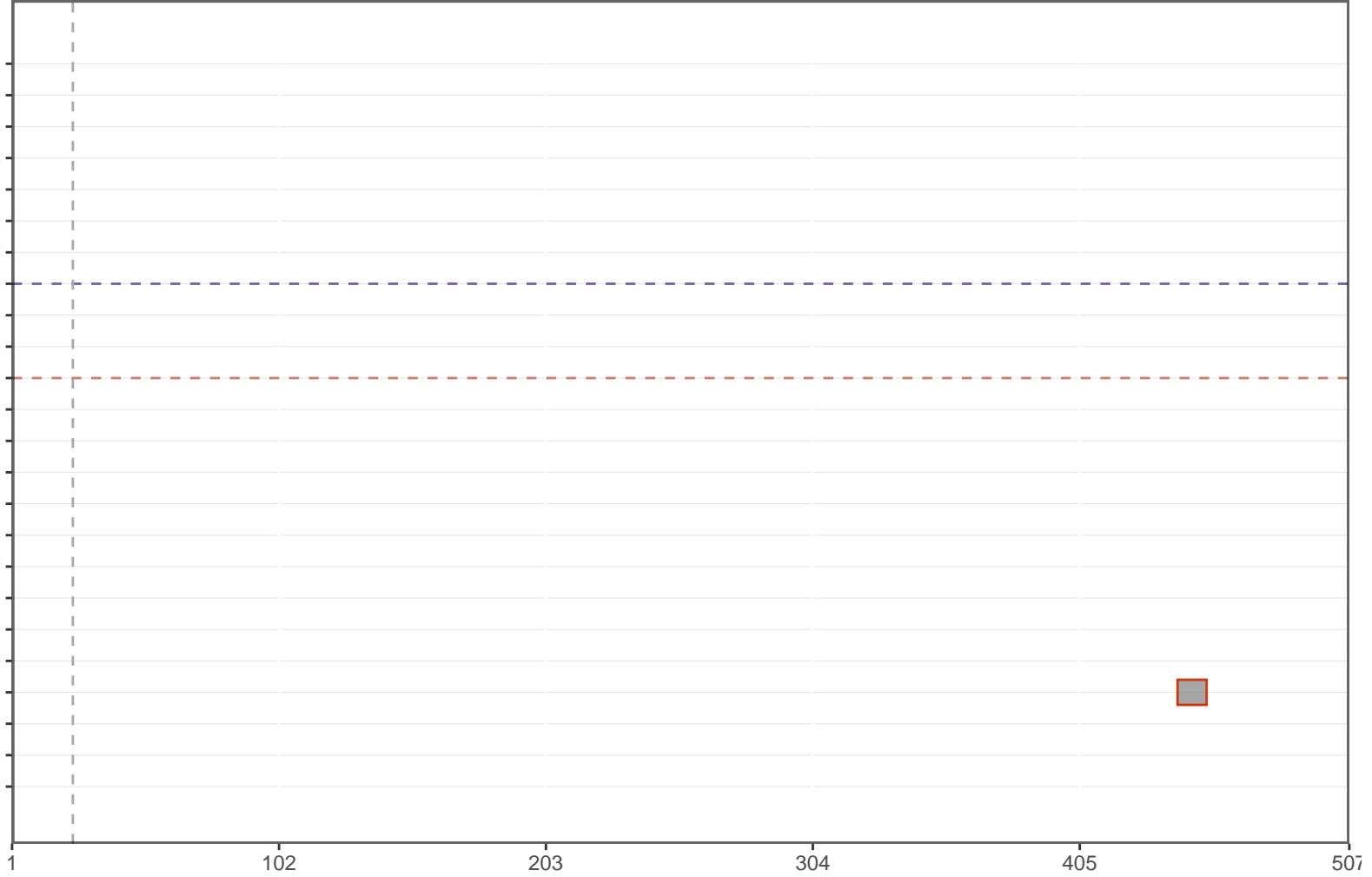
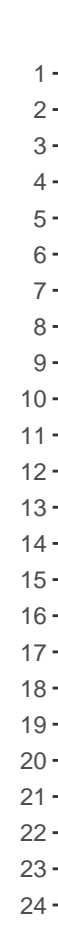
MW indication



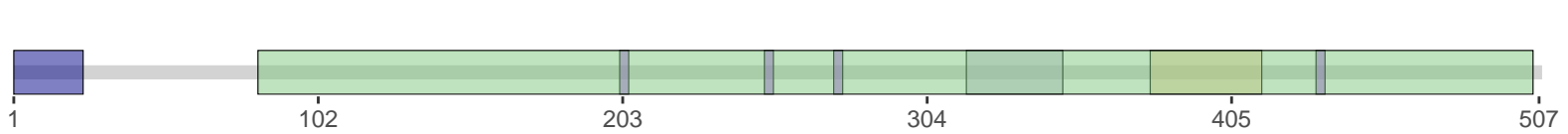
Molecular weight



Gel Slice



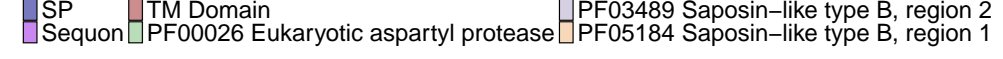
Protein length



Pfam domains



Pfam Description



Protein sequence:

/DSNHFKGNHTYVPLTQKGYWGFMDLFGNASTGVGAGGAAVDSGTSLLAGPTTVVQINHAAGAEVVSMECKTVSQYGVEMWNLVSGVRRPQVGSAGLGVFNAGAHVGSNIRTVVERETEGSSVGEAPLGTADCEMAVAVMGNOLKQKQKTKERVLEVYNQLGKLPSPFMGESVVDGSMIALFNFTFKDKAVVLPDQYLVKVGEGITIGMBSGFAALDVPPRPFVWLDGVFMGVYHTVFDYGNERLGFAEAV

NbL01g12350.1 pentatricopeptide_repeat-containing_protein_At3g53700_chloroplastic-like [MW = 82.13 kDa]

No. of times detected



log(intensity)



Values from



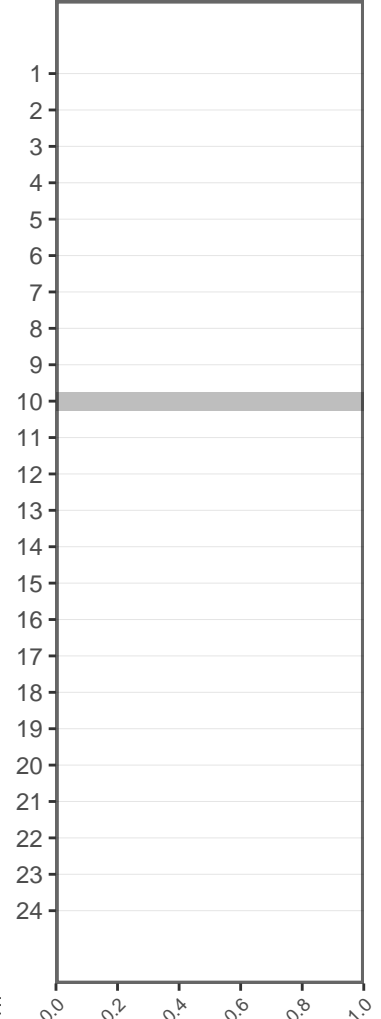
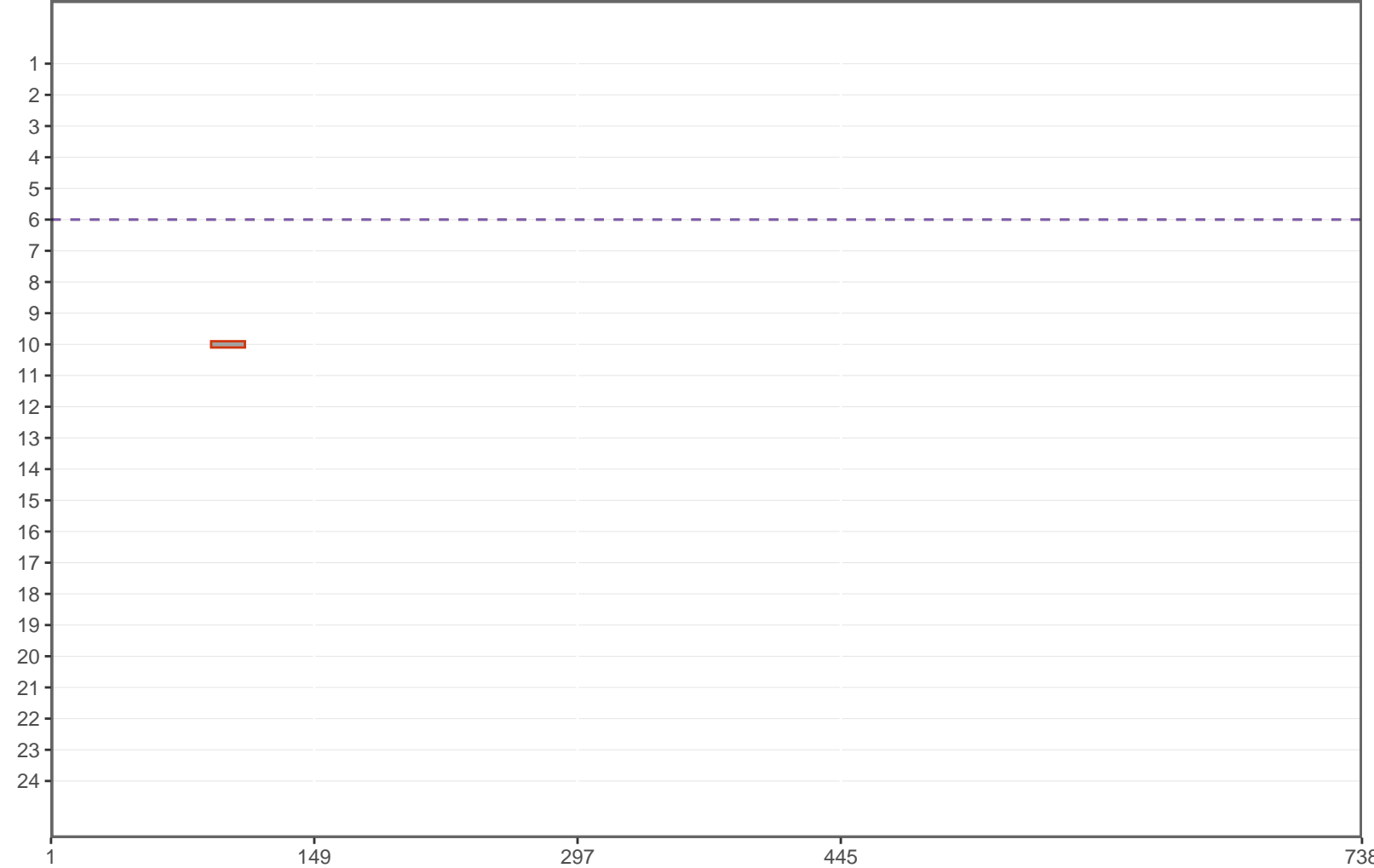
MW indication



Molecular weight



Gel Slice

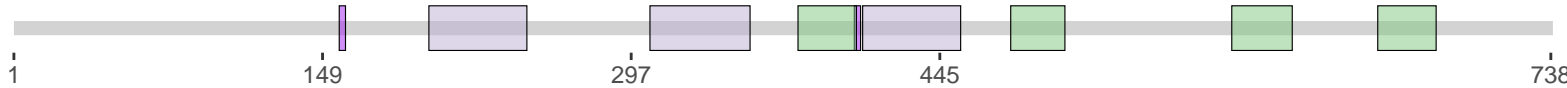


Protein length

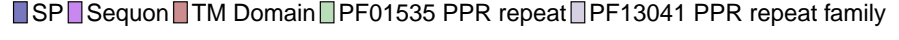


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

MLSEAKFNDKEVAEVLVFNALLEAFNDGTFSAEDLFDMLERNFTDGHSWNIMIRYMCQNEKLDALKYLARMTVSSVSDSSTYSALHGNKLGEGEDALALYHFRKAGFDLVSVAQIEGLGHEKIQEAAEVEFGFMSTKRNFLGSSGFDKLMKGLCTSGVWGRAKLLPLAYSGTLSSTAAYNNLGGFLSRASDLFVLSRMVINGCTLDGETYGLIRGIMTSLGNEKCALFDQMLGRGLSDSETLAELELVWNGVHMLSSDKLVSESEVDSAY

NbL01g12230.1 ATP-citrate_synthase_alpha_chain_protein_2 [MW = 46.85 kDa]

No. of times detected



log(intensity)



Values from



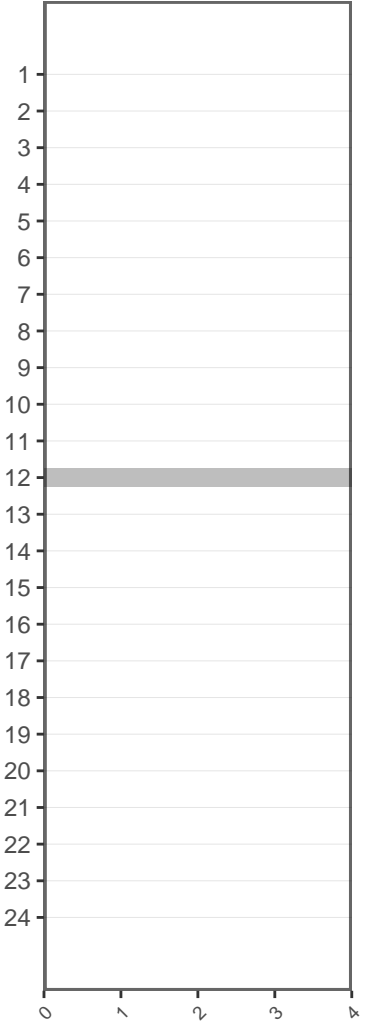
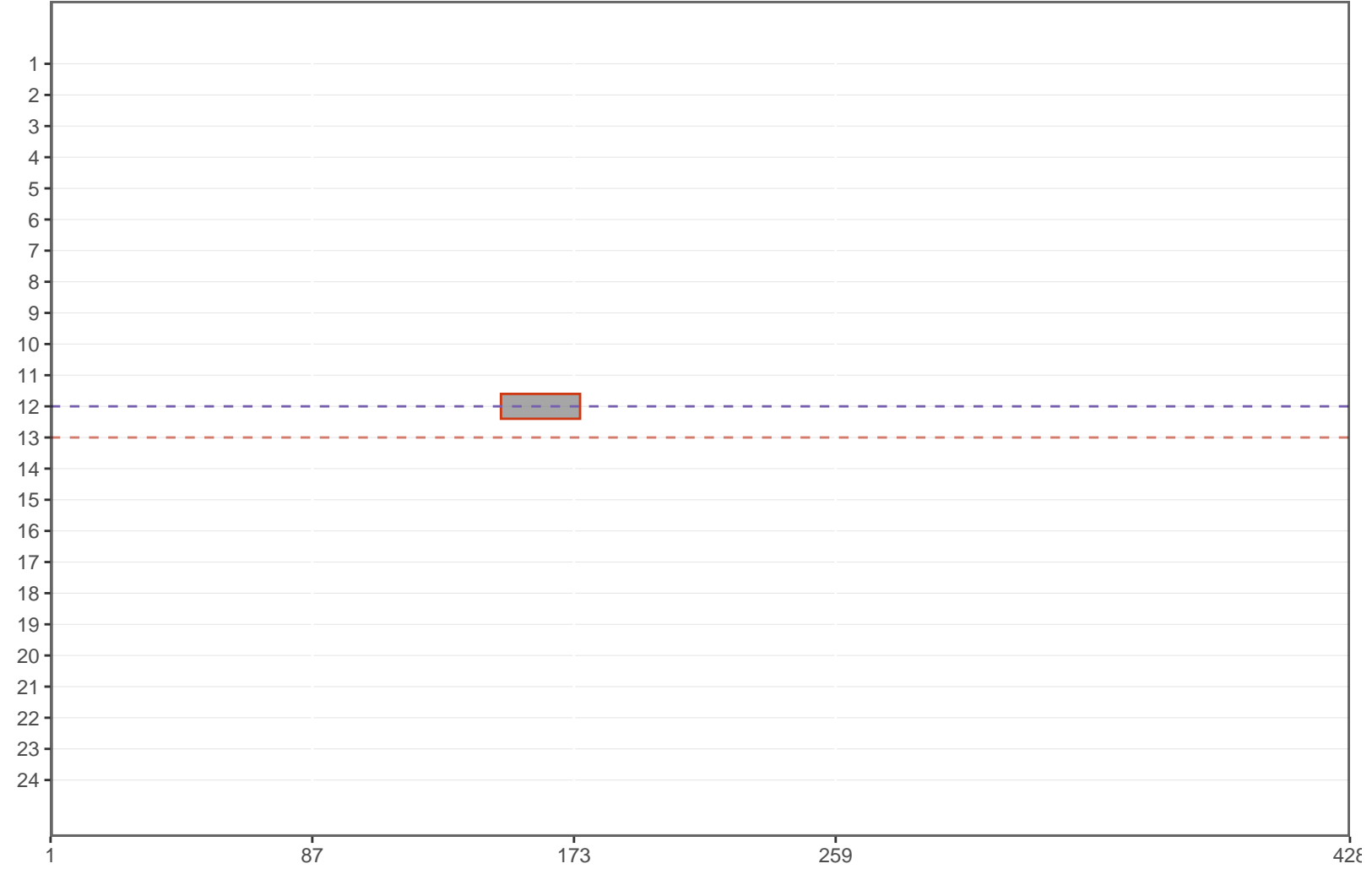
MW indication



Molecular weight



Gel Slice



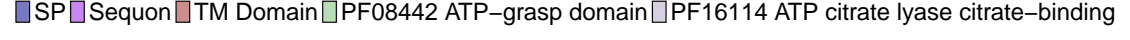
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TLVNGDPYPLDMRGELEDDTAFRNFKWGSIEFPLPFGRLVSPTEFHSLEDEKTSASLKFVLYNPKGRIMTMVAGGGAEVYADTVGDLGAYELGNVAEYSGAPNEEEVLYQVAVLDGATANPQGRKRALVGGGIANFTDVAATFNHGRALREKAKLKAAGMHVYVRGGPNYQTLAKMRALGEELGVPLEVYGPATMTGICKRAIDIMSEASVCF

NbL01g12150.1 pyrrolidone-carboxylate_peptidase-like [MW = 23.92 kDa]

No. of times detected



log(intensity)



Values from



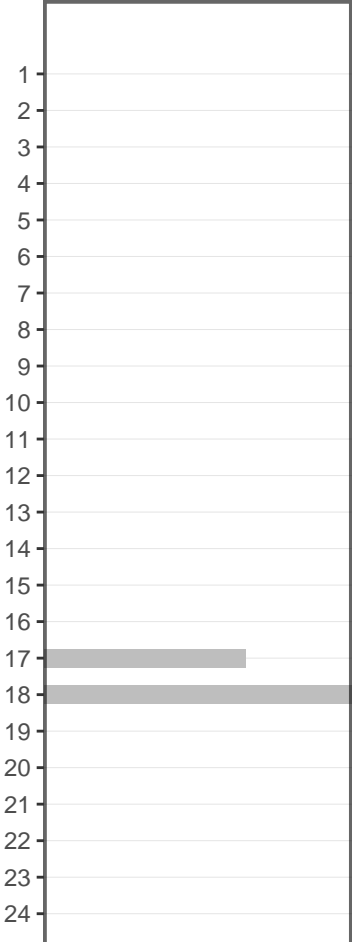
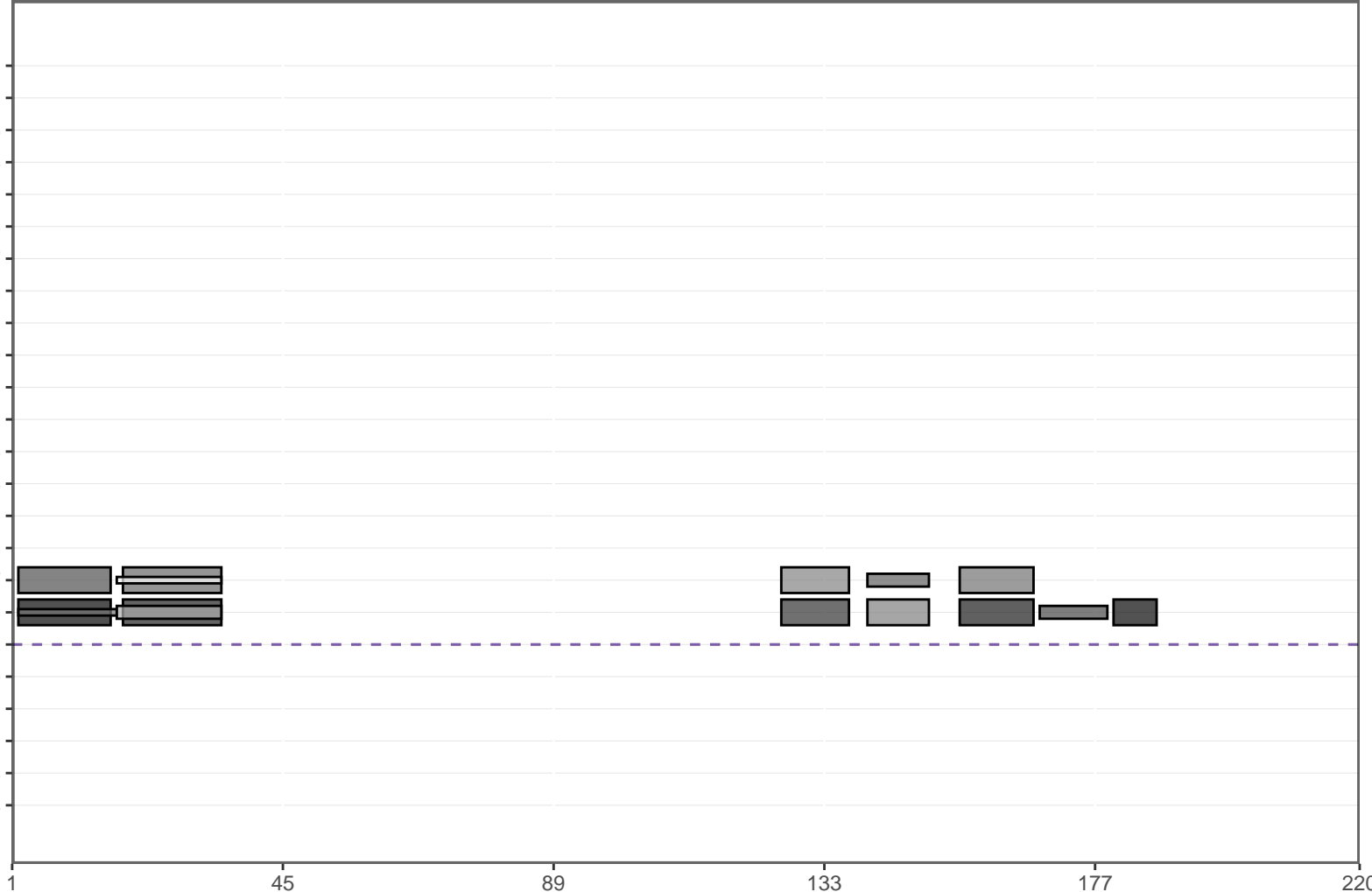
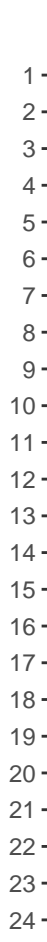
MW indication



Molecular weight



Gel Slice

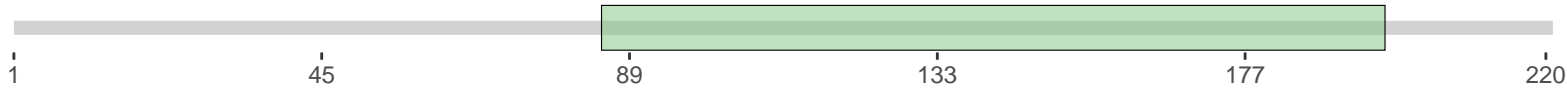


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description



Protein sequence:

IGATMFAIENQAVNEATFRGPDMEWPKQVPIVHADGAISRKREIPLVEETIKVLAAMGVEVMTSDDAGRFCVNYVYHSLRFAEQNGIRSLFVHPLFLTDEETQMDFASLLEVLASLY

NbL01g12120.1 GDSL_esterase/lipase_At1g09390 [MW - SP = 37.13 kDa]

No. of times detected



log(intensity)



Values from



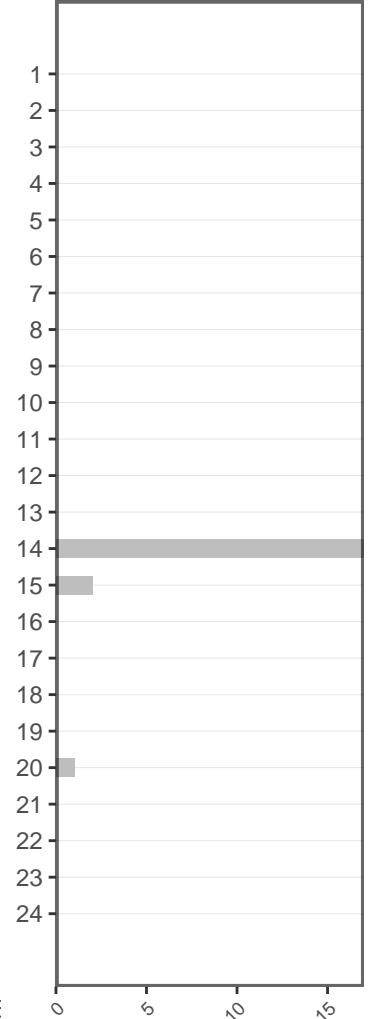
MW indication



Molecular weight



Gel Slice



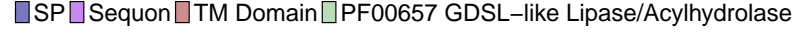
Protein length

Peptide counts over 4 repeats



Pfam domains

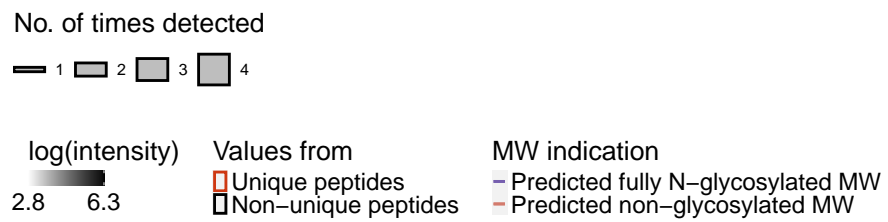
Pfam Description



Protein sequence:

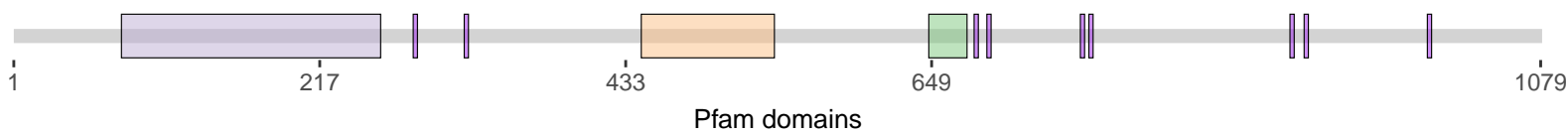
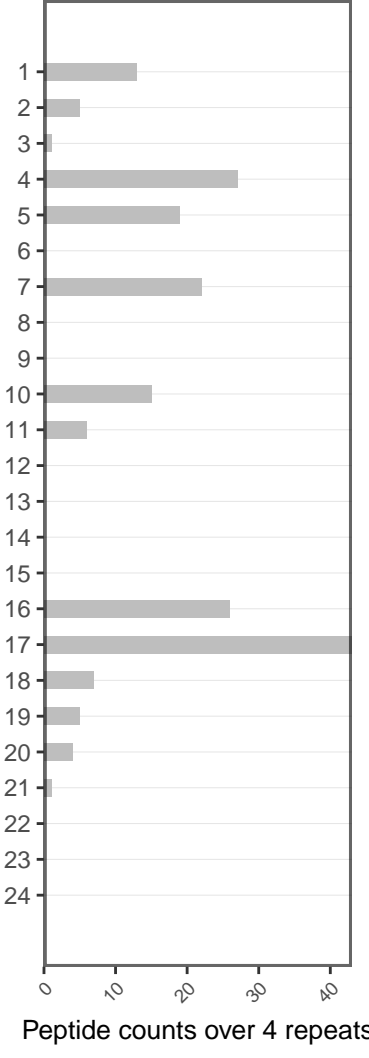
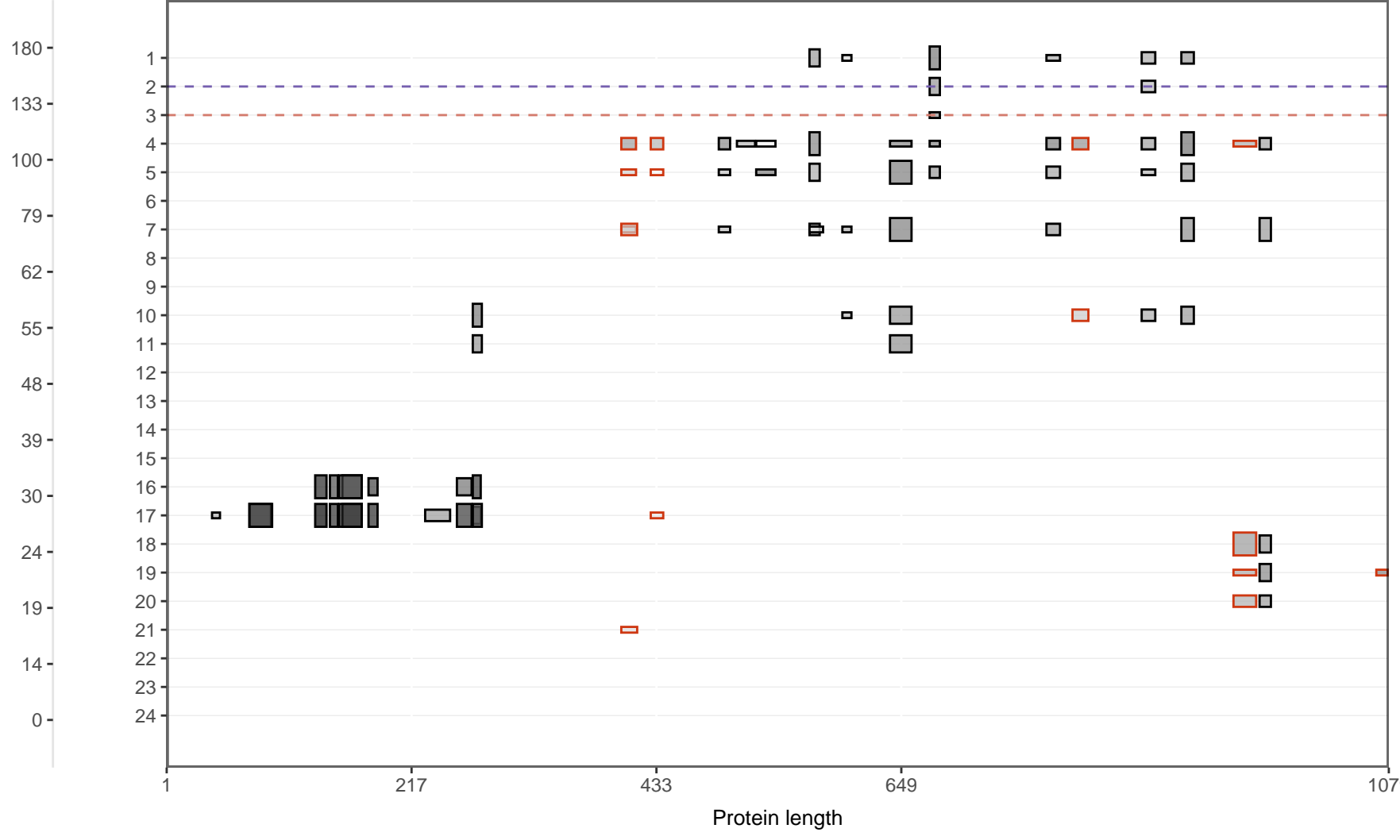
IAQDFAKNMPYIEVAKMPSFTEIKNAQVYSGGGRKFWVHTGPGGPKLTVQKVSDDLDPHGGLASVNSAAKLFNEGLRHVDGELGSEMDDATVYVDIWAQKDLNSENAYGFSNPLMAGCGYGGPPVWYRKGVYGGHPGVGVGSEVSEFISWDGVHTETANRVAASKLSTEYSTRIGDFDFCH

NbL01g11980.1 NHL_repeat-containing_protein_2 [MW = 117.18 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP (blue) TM Domain (red) PF13419 Haloacid dehalogenase-like hydrolase (grey)
 Sequon (purple) PF01436 NHL repeat (green) PF13905 Thioredoxin-like (orange)

Protein sequence:

WPTFALGPNGLKLAQMGEGHRKDKLQVLAALLFYGRKKLIDSTPIPLRLEKNNDRLLTSPKLFKPKGLAVDLNLRLFISDGNHNRIVTDLEGNFLVGVSGTGAEGLRDGNDFDATTFRPQGLAVNAKNNLVAIDTENHALRVIDFVNETVRLTLAGNGTKGSDVEGGGTGTADLNSPVDVCFEPENGIYHAMAAGHQHWVHETSGGVTRAFSGNGFERNQNNGS66TNTSFAQPGSLSRDLKKEAVAD666SRVADLRTFGSRLLAGGPRMAENLFXFGDHDG

NbL01g11880.1 uncharacterized_LOC109210159 [MW = 20.11 kDa]

No. of times detected



log(intensity)



Values from



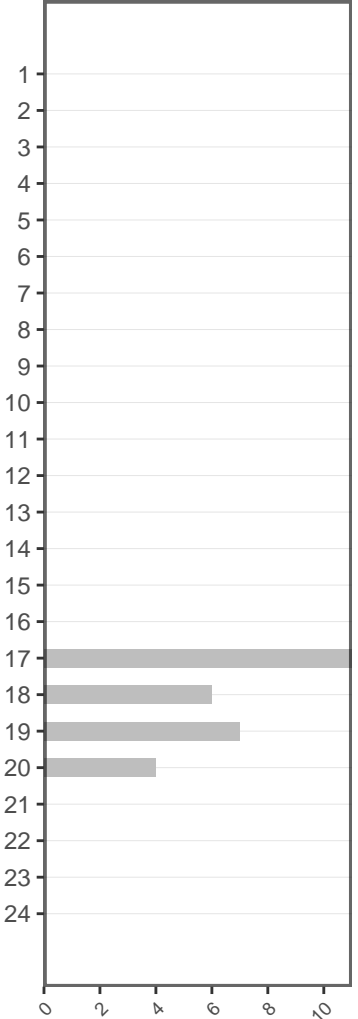
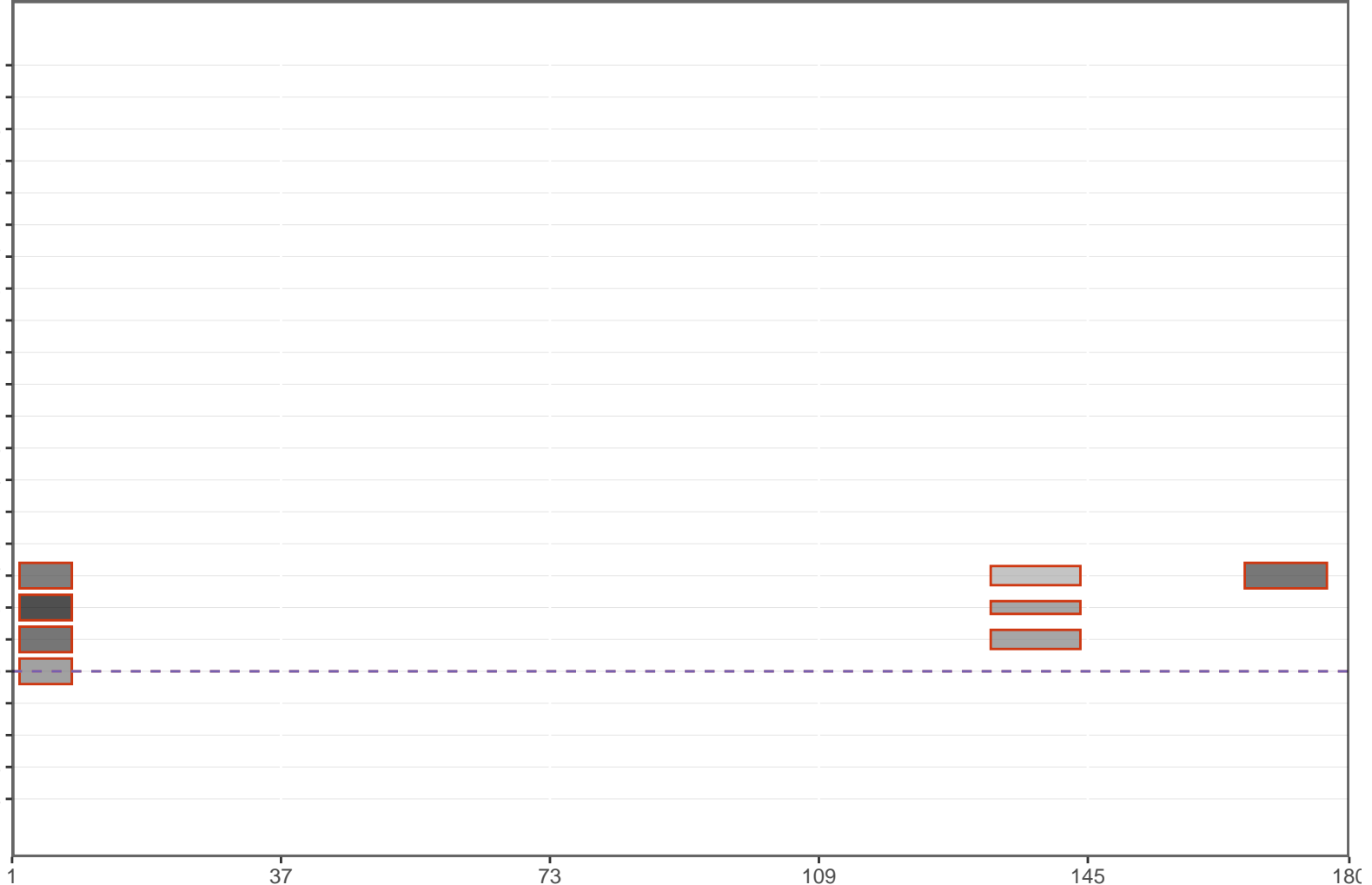
MW indication



Molecular weight

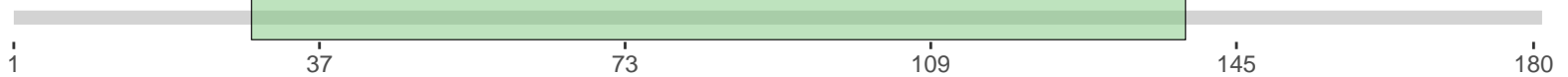


Gel Slice



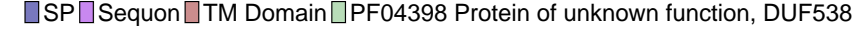
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SVQYGEYTAIVEQNKIKKLTGVKAKELLMLTLEIGVDDPDTGKHKFKATSGLSRITFFVSAFEIDVTRKKEEKVEEVNEVNNKENKEVHPAAVAEEVKEV

NbL01g11870.1 uncharacterized_LOC107830650 [MW = 37.8 kDa]

No. of times detected



log(intensity)



Values from



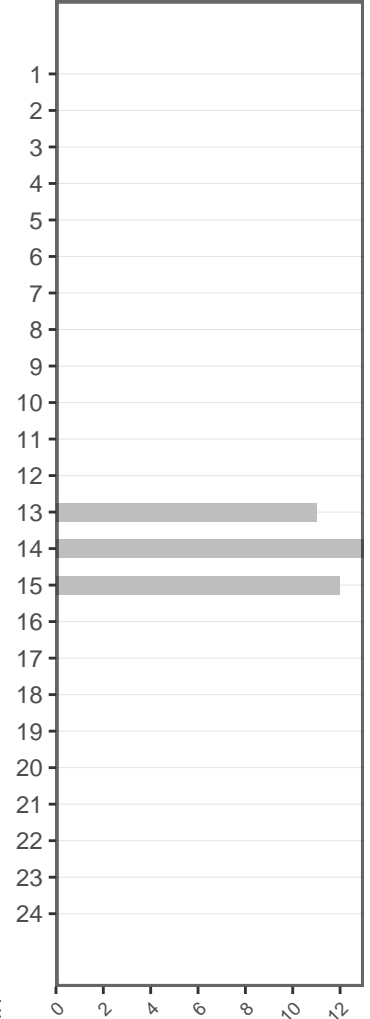
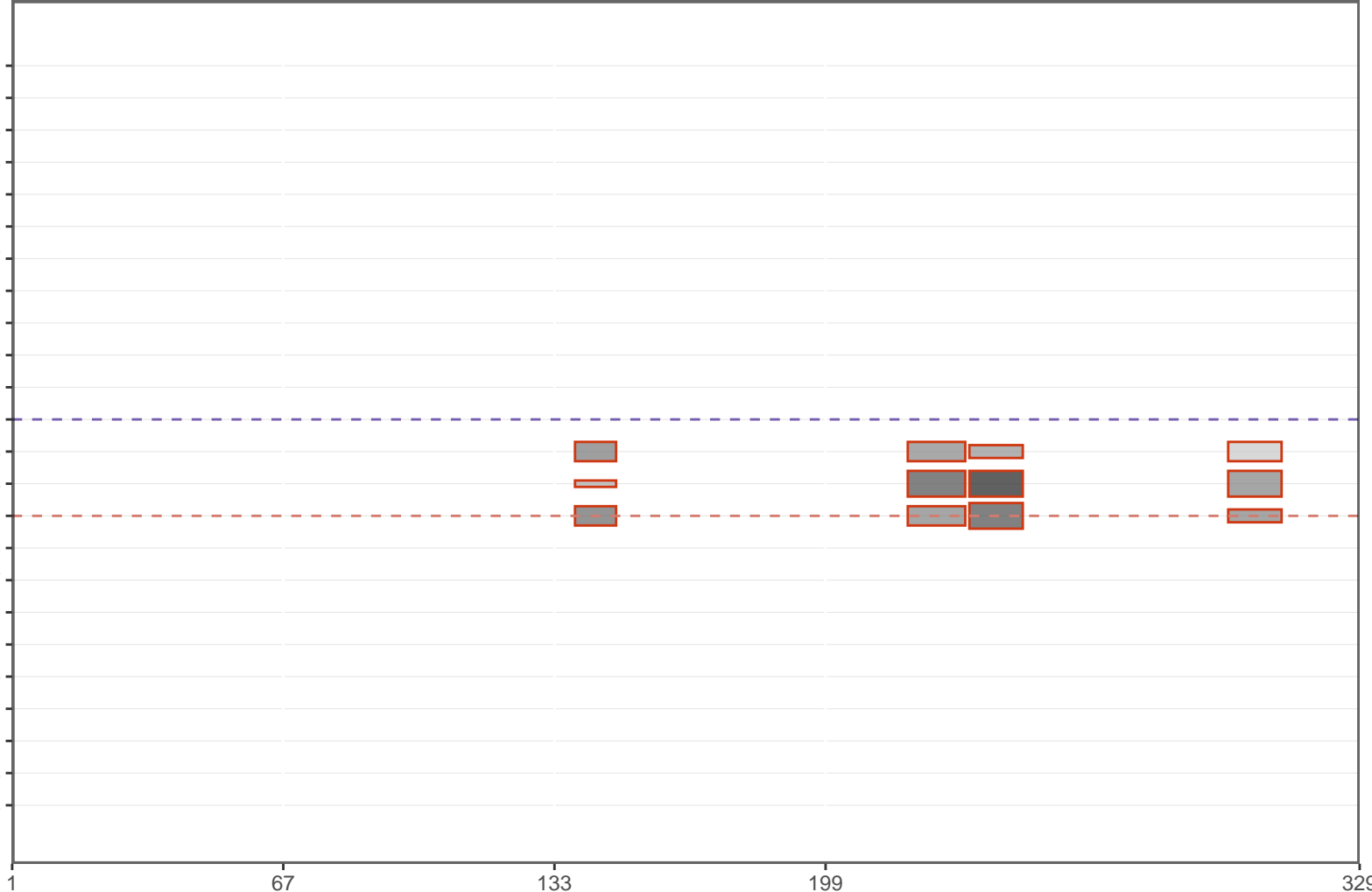
MW indication



Molecular weight

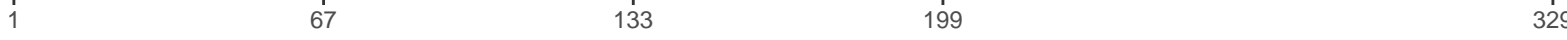


Gel Slice



Peptide counts over 4 repeats

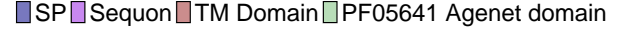
Protein length



Pfam domains



Pfam Description



Protein sequence:

EWANGKVTPTPLGGGEGDEDEVEETLASTDKPSNDAAENFSEGLIVEVSSDEEGFEGAWFAATVAVLLDNGNLYEYQNLRNDDDTAFLEAEADRLVVRPRRPDIPGPFKSFVLEEDVALYNDGIVWVGVSKVKGGRYRVGFKGNNELEFNHADLRJLHLDWINGKWVTPSGALK

NbL01g11820.1 trafficking_protein_particle_complex_subunit_4 [MW = 16.02 kDa]

No. of times detected



log(intensity)



Values from



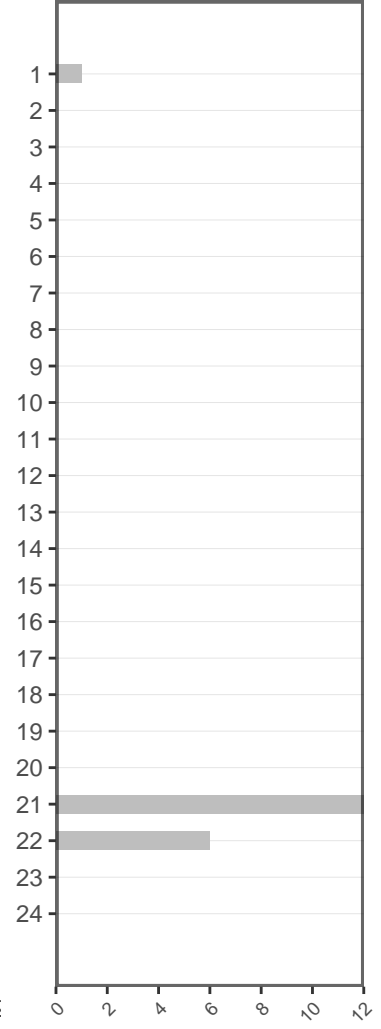
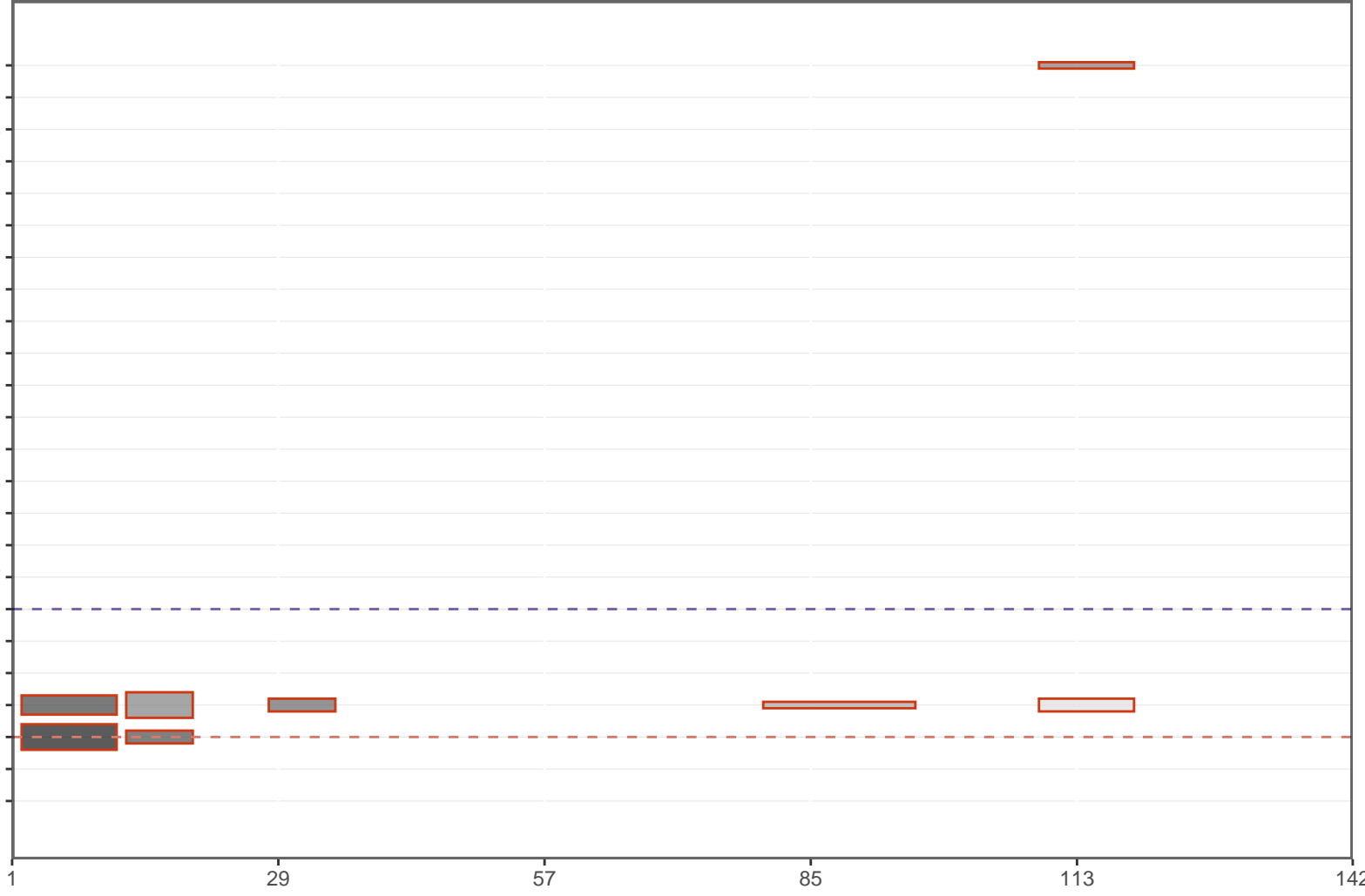
MW indication



Molecular weight

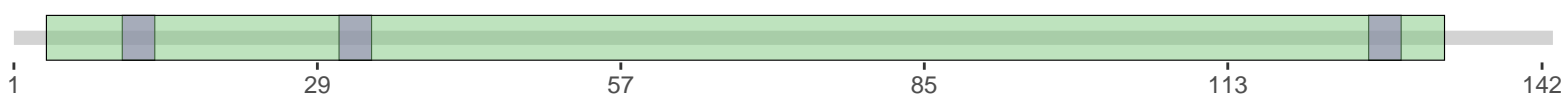


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SIELLDQNFDLHCFQSLGTGKFFVWGEPSLHMEBLKYYVELYTDVWLNKPFYEMEMPIRCELFQNLGDAVQKDRVALLGR*

NbL01g11810.1 ABC_transporter_I_family_member_20-like [MW = 36.67 kDa]

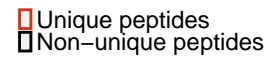
No. of times detected



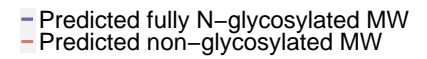
log(intensity)



Values from



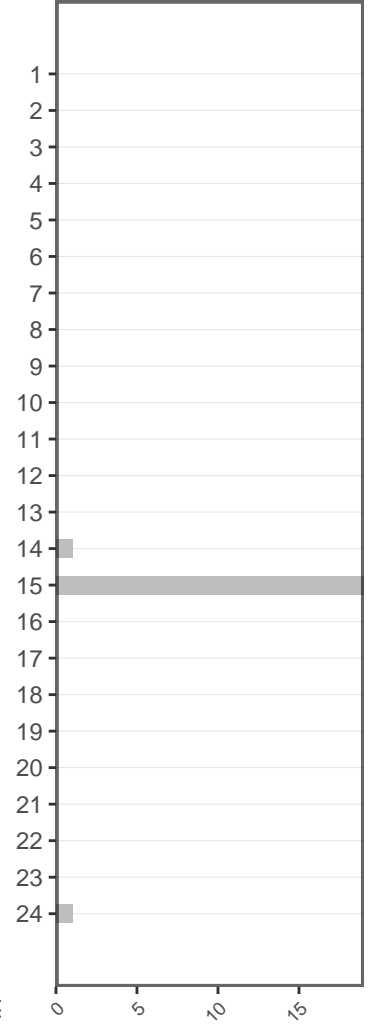
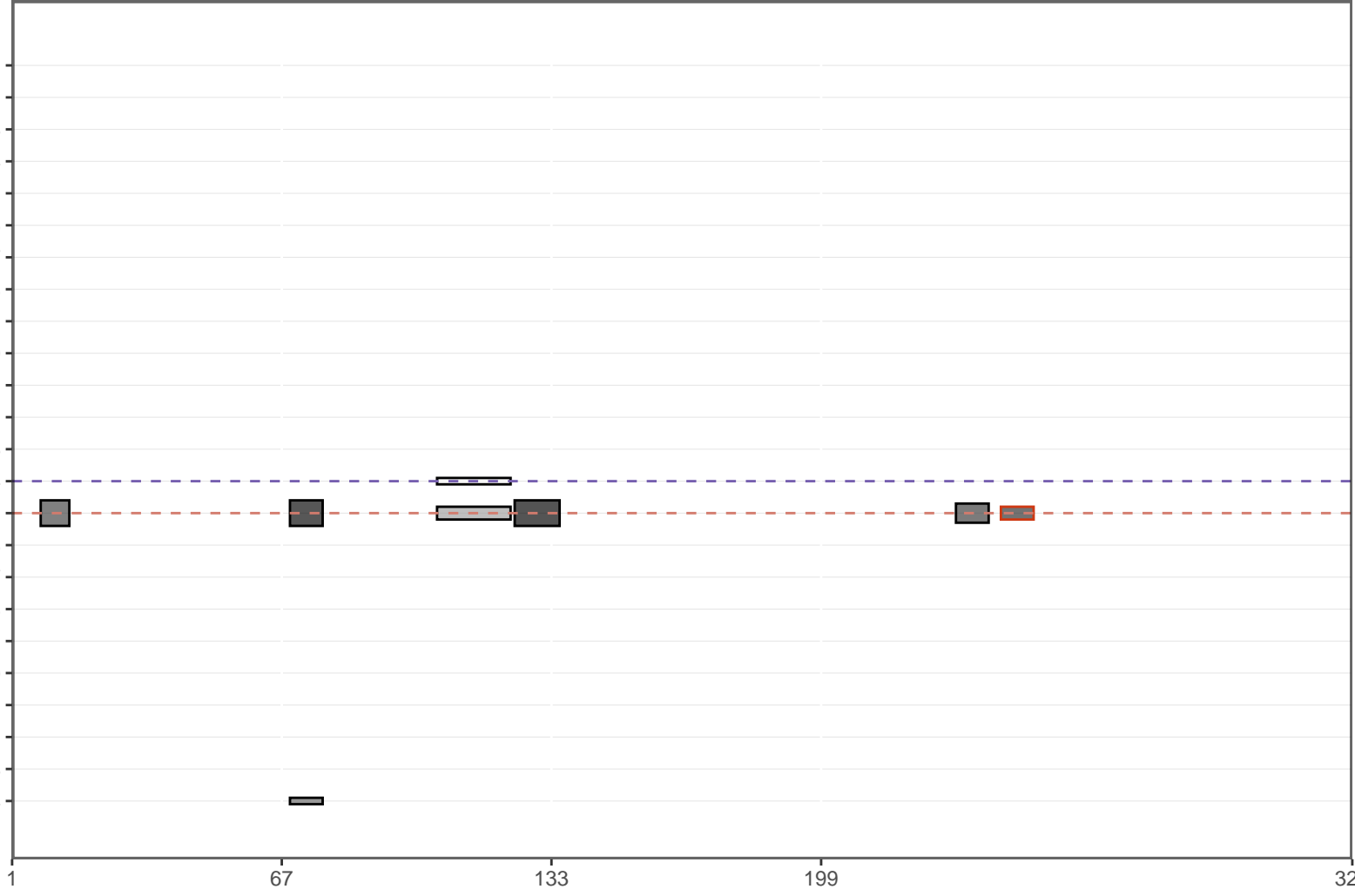
MW indication



Molecular weight

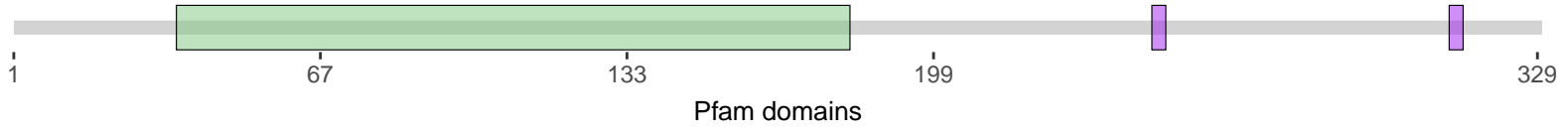


Gel Slice



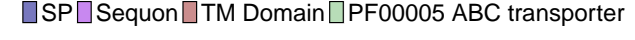
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

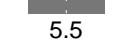
KASDQRRRVQICMGLLKPKFKVLLLEDFVLDLGLARADLLKFLSKKEGEERGATIIYATHFDGLENWPSHMLYVAHGKLGALAMPMDKVKKEIENISMLMRTVESWLKKEDEERKRKRKAKKGLPEYKQKVEGSRVGDPAARAAARPLNGWAGRLNNTIAGEENFVLSNRVLR

NbL01g11760.1 60S_ribosomal_protein_L36-2-like [MW = 12.36 kDa]

No. of times detected



log(intensity)



Values from



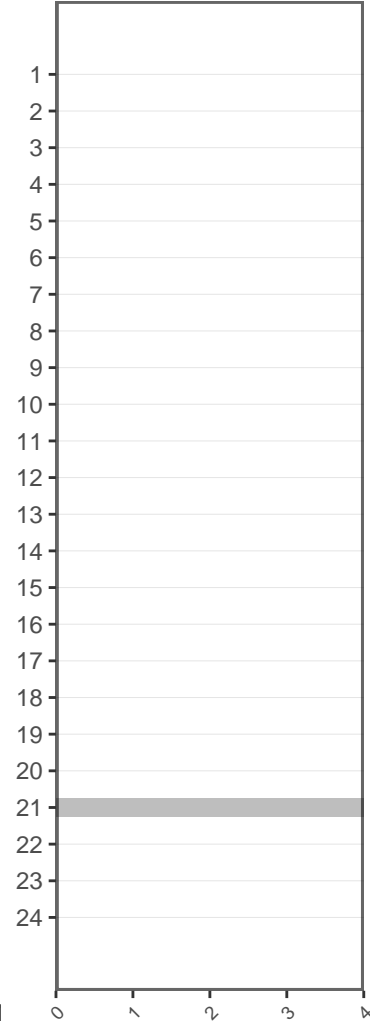
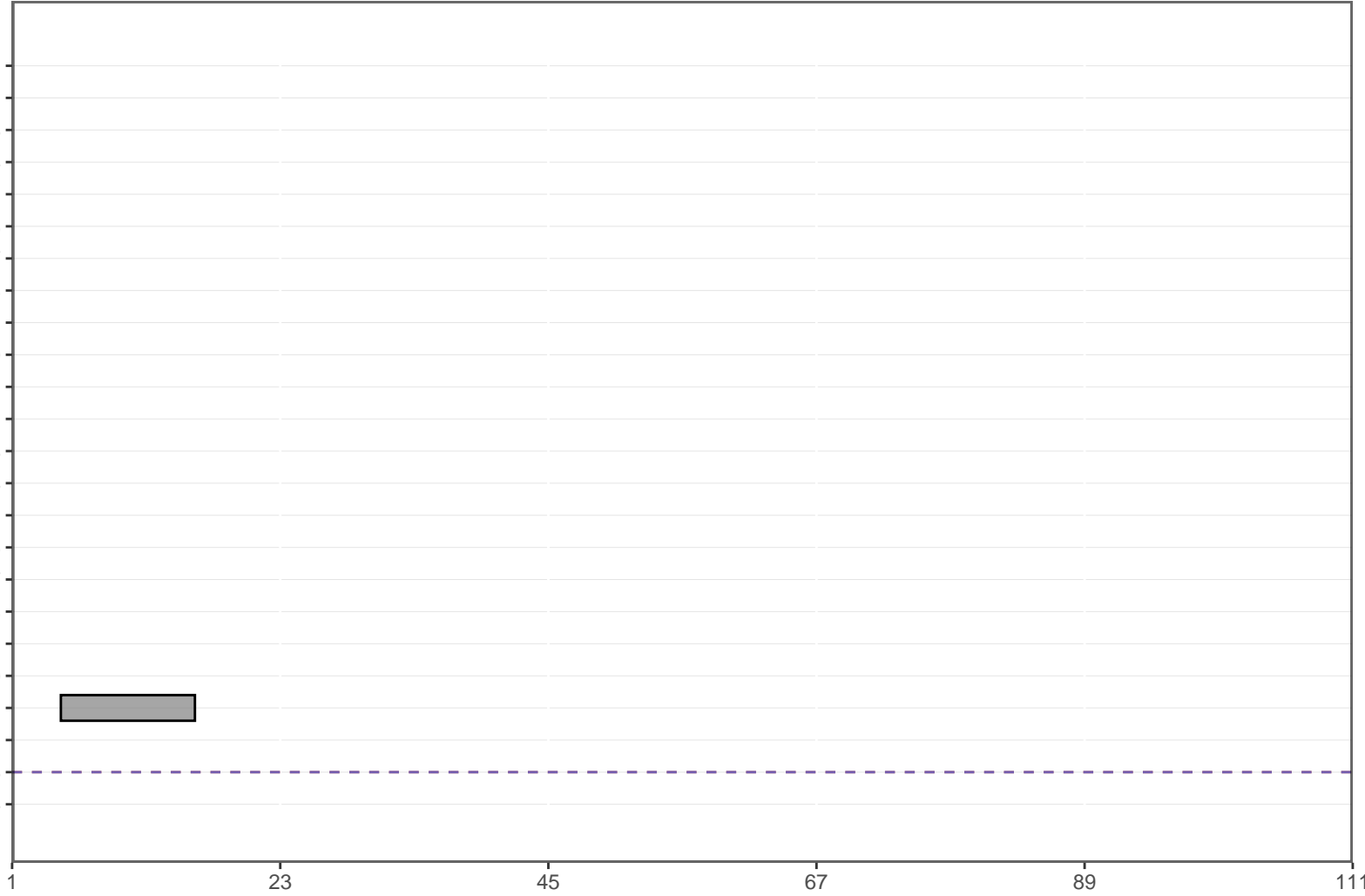
MW indication



Molecular weight

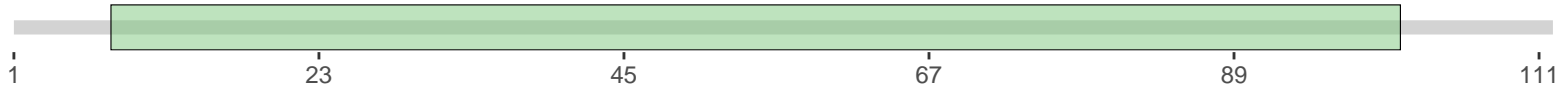


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FVRSLSREVAIGFAPYEKRITELLKVGKDKRAIKVAKRKLGTGHRANKKREEMSVLRKMRATGGGKKK

NbL01g11620.1 iron-sulfur_assembly_protein_IscA-like_2_mitochondrial [MW = 16.95 kDa]

No. of times detected



log(intensity)



Values from



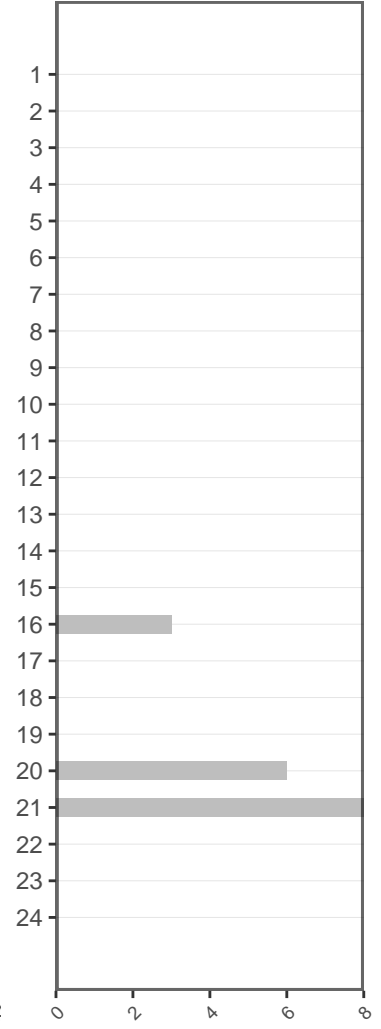
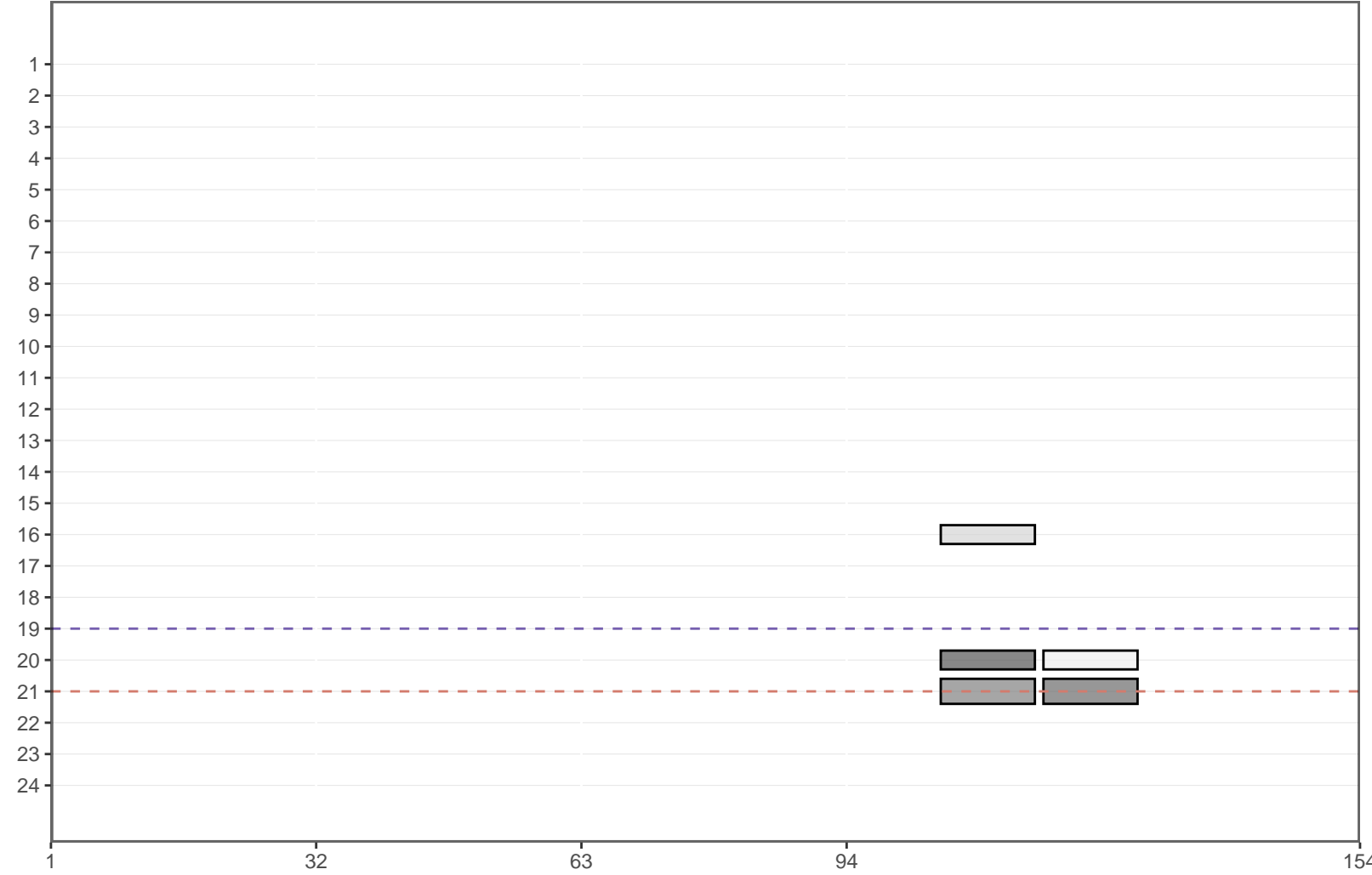
MW indication



Molecular weight



Gel Slice



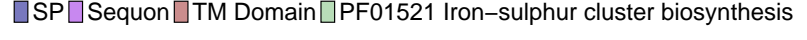
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KEKMLRLSVEAGGGSGFGYEFSLDDGTNEDDRIFERAGVKLVVNVVYDFVKGATVDYVEELURSAFQVSTNPSAVGGGCKSEFMKQ

NbL01g11590.1 calreticulin [MW - SP = 44.24 kDa]

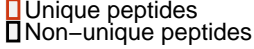
No. of times detected



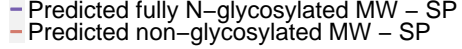
log(intensity)



Values from



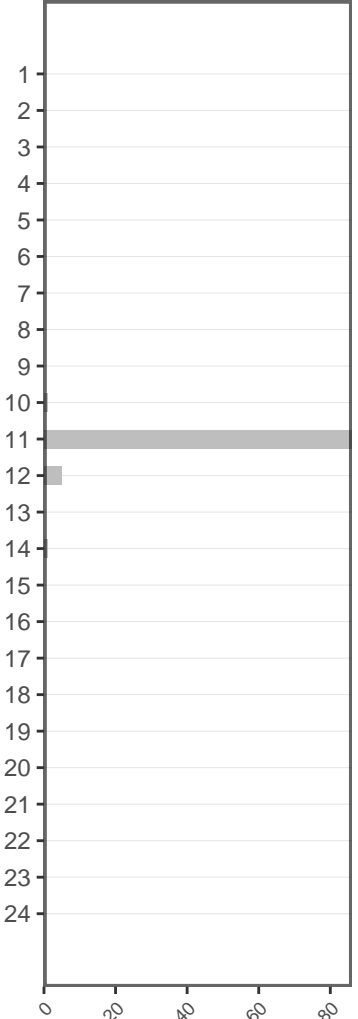
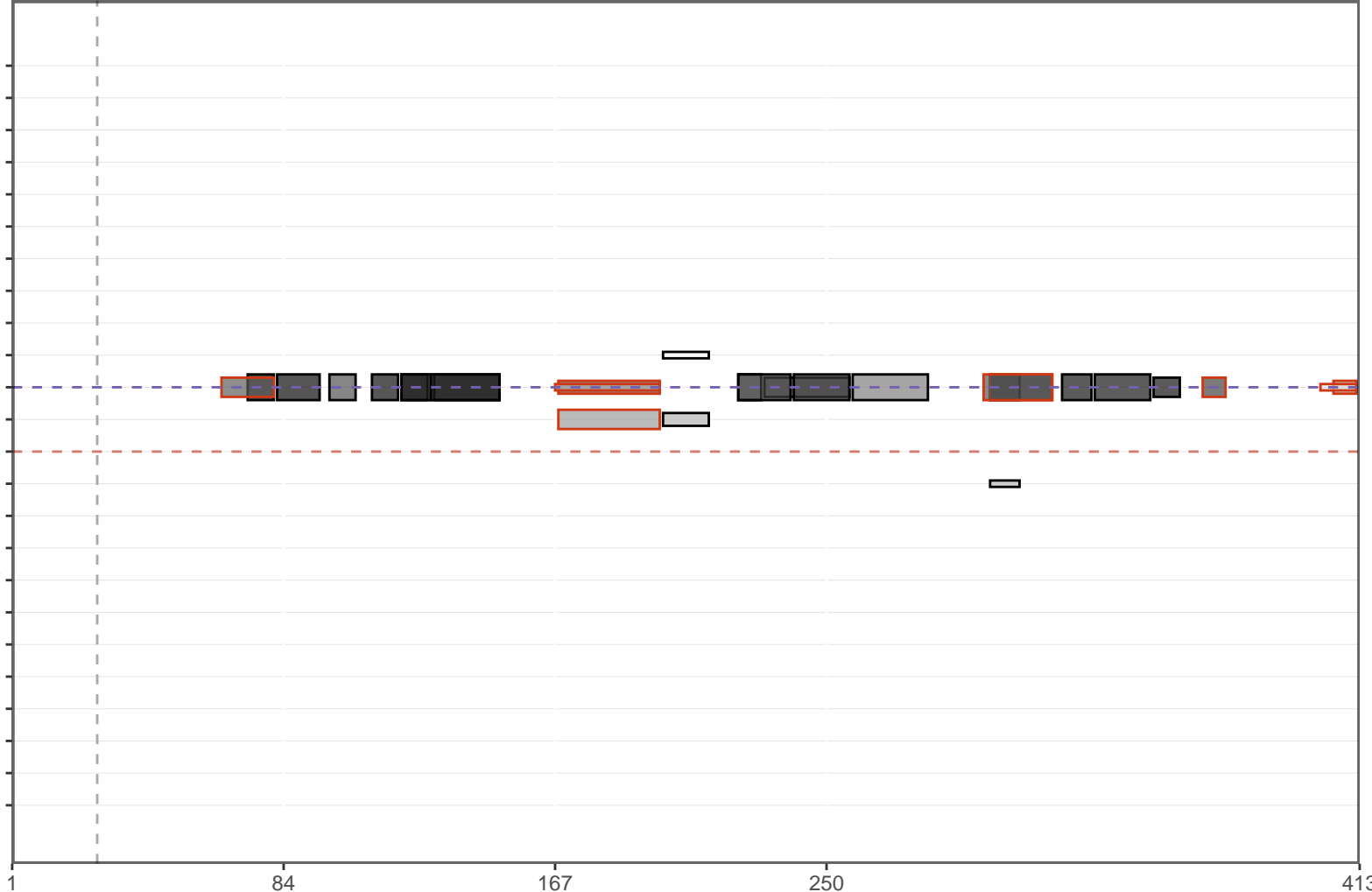
MW indication



Molecular weight

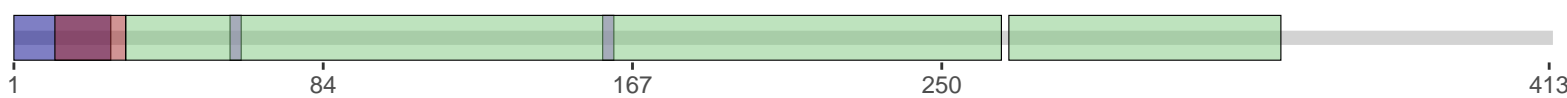


Gel Slice



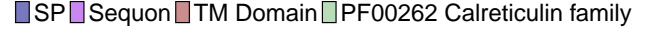
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DNVEKOSGLYSDWDLPPKTKDPSAKKPEDWDEKFEFDIDPEKDFEGYDDPEEITFDPAANKPEDWDEDEGEWTAFTIPNPEYKGPWPKFKKINPNYKKGKAPLIDNPPDKDDPLVYFPLKLYGVELWQVKGSTLFDNIVIGDDPEYKAAAEETWGGKDAEKAFAEEAKREDEESKDFADSDAEEDDSDADDKESKDEAHDEL

NbL01g11550.1 dihydrolipoyl_dehydrogenase_2_chloroplastic-like [MW = 60.59 kDa]

No. of times detected



log(intensity)



Values from

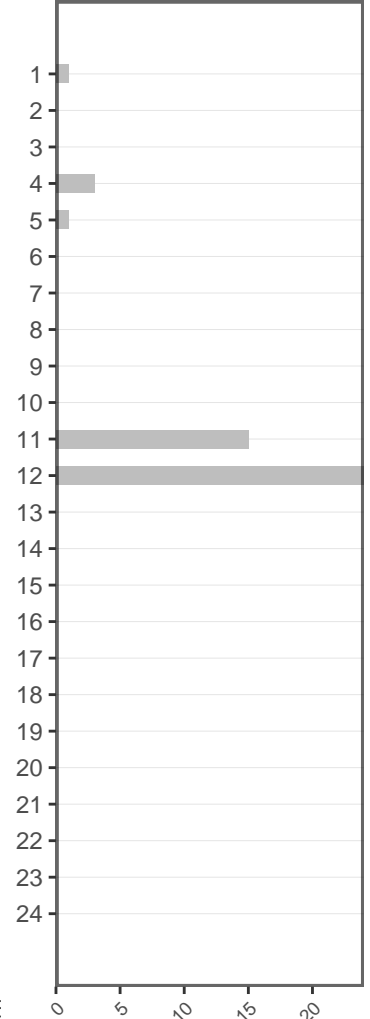
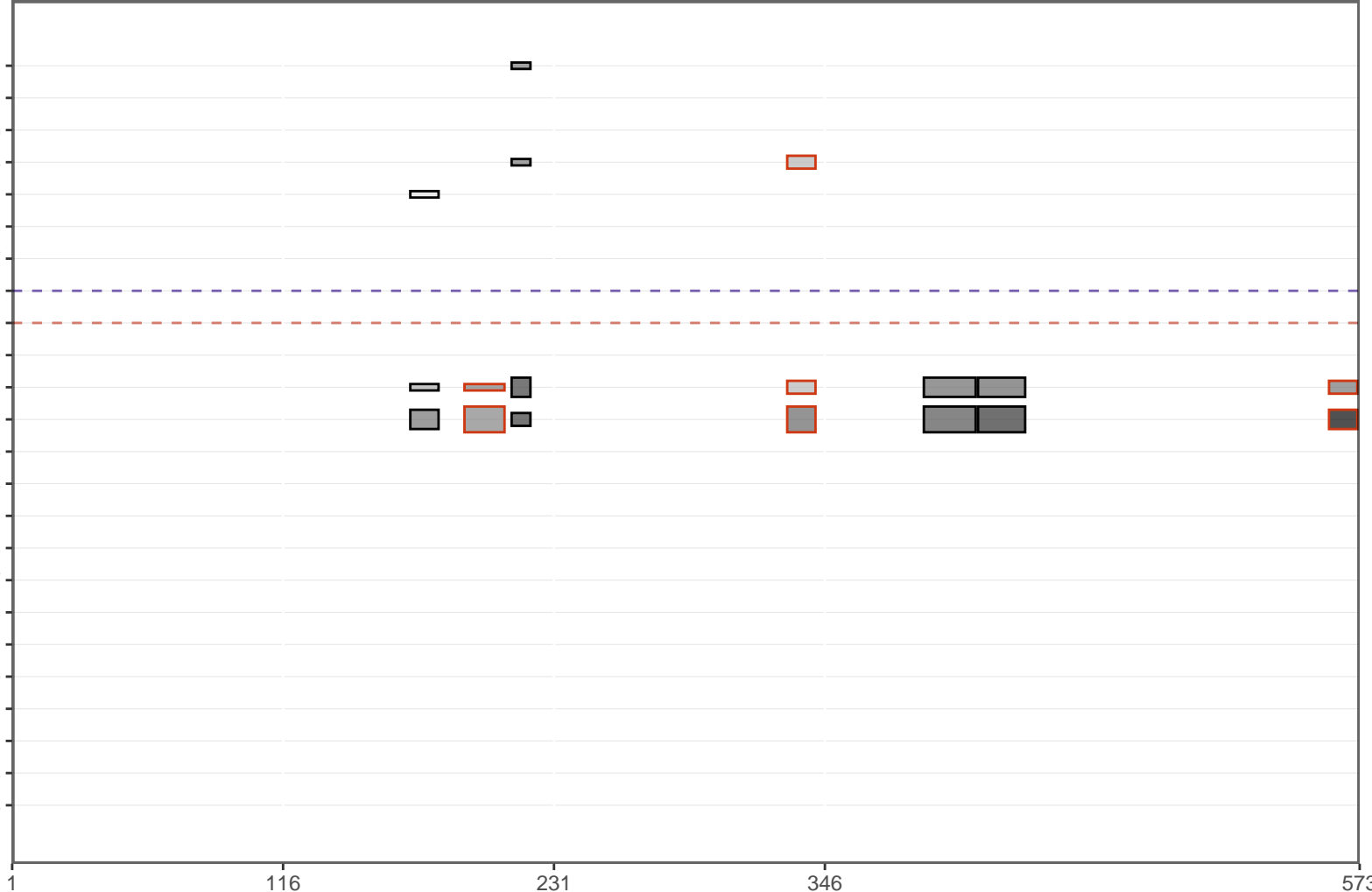
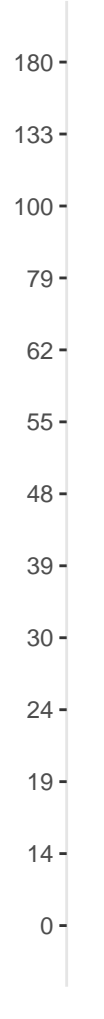


MW indication



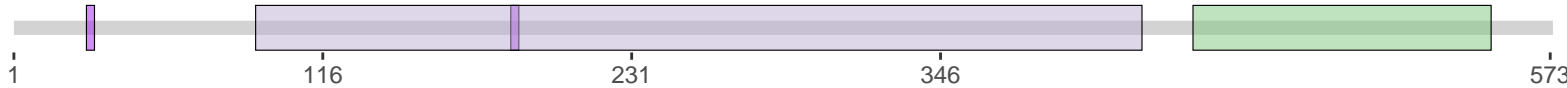
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

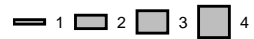
- SP
- Sequon
- TM Domain
- PF02852 Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain
- PF07992 Pyridine nucleotide-disulphide oxidoreductase

Protein sequence:

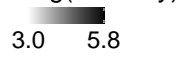
EFSDY TALGSEYTFVEALDQLMPGDFPEIKLAGRVLNRPKIDYHTGVFASKITFANDGKPVITLIDAKTKELKDTLEVDALAIATGRAPFTGLGLENINVTGRGFVDERMDVIDANGELVPHLYCGDANGKMMLAHAASADGIVVEQVGTGKDHILNHLISPAAGFTHPHESIMVGLTEPQAREKAEKEGFEIGIAKTSFKANTKALAENEGEGIAKMYRPDNGEILGVHFGMHAADLHEASNAIMGTRHDKKFAVAHAPTLSEVIDELFKAAVKVKAHTSSPYTEPVA

NbL01g11510.1 probable_protein_disulfide-isomerase_A6 [MW - SP = 37.02 kDa]

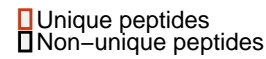
No. of times detected



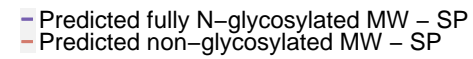
log(intensity)



Values from



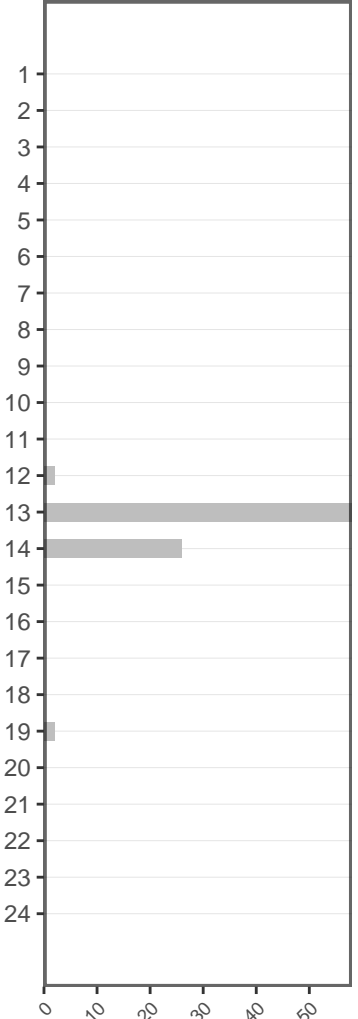
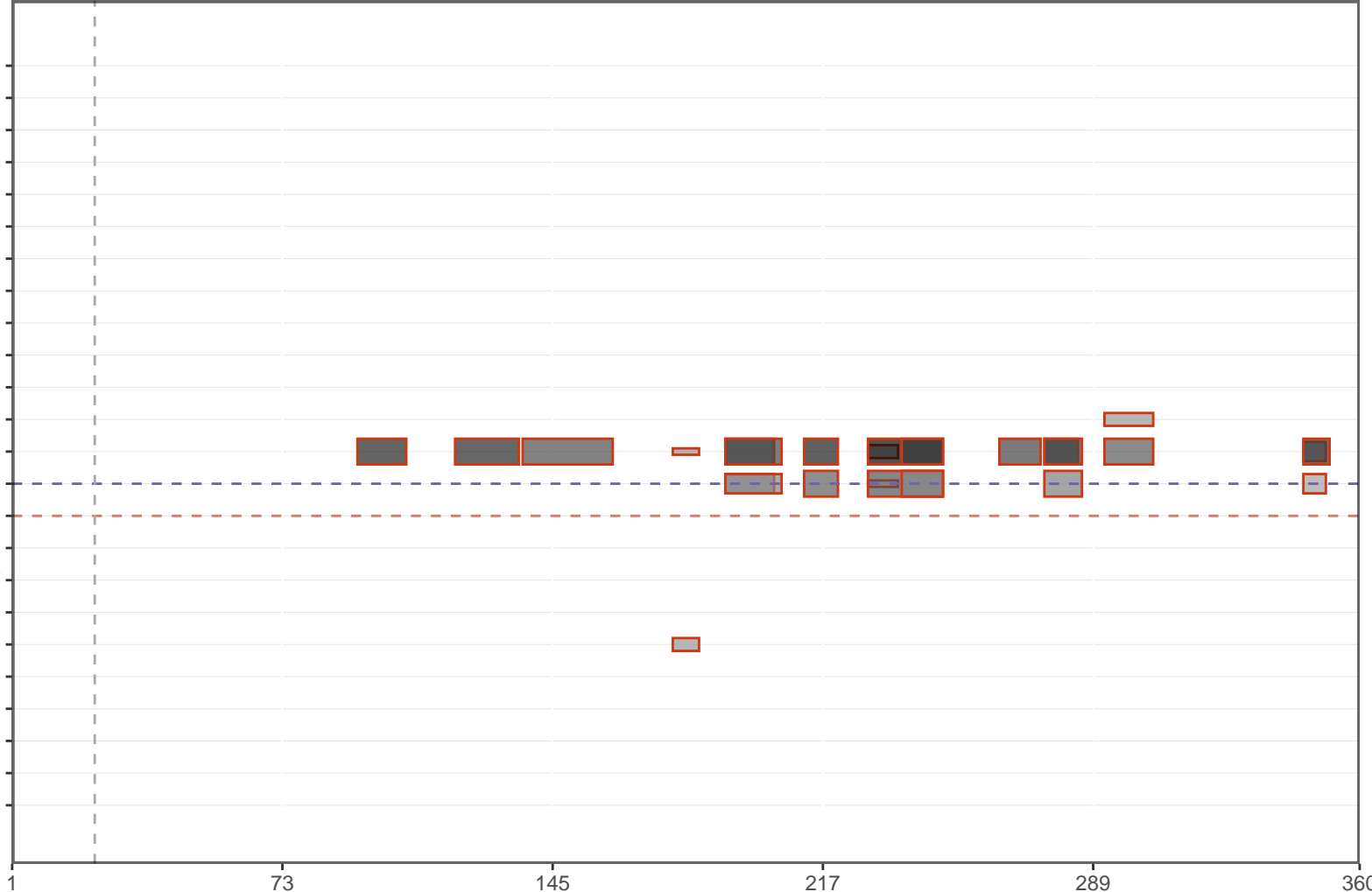
MW indication



Molecular weight

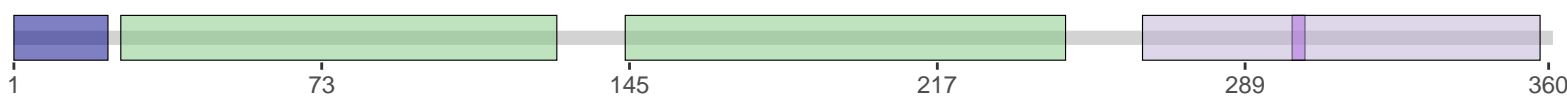


Gel Slice



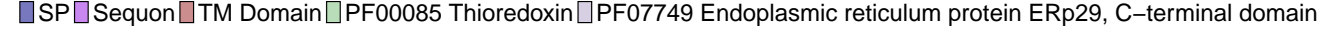
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

YAPVCHGHCNLAHYEKVATAFKQEEGVIANLADAKHRLDLGKYGVSQFPTLKFPPKGNKAGEDVDGGRDLDDFVNFINEKSGTSRDSKGGFTSKGGIVELDTLVKEFVSATNEEKKALLSKMEDEAGKLNLSAARYGKIYLVKAKSMKMGADYARNEIGRLERMLAKSISPAKSEDFTLKKNLATA

NbL01g11210.1 topless-related_protein_3-like [MW = 124.46 kDa]

No. of times detected



log(intensity)



Values from



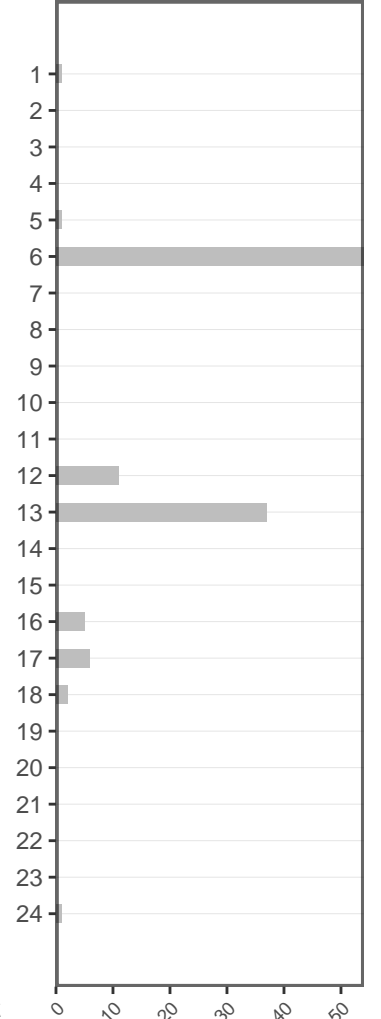
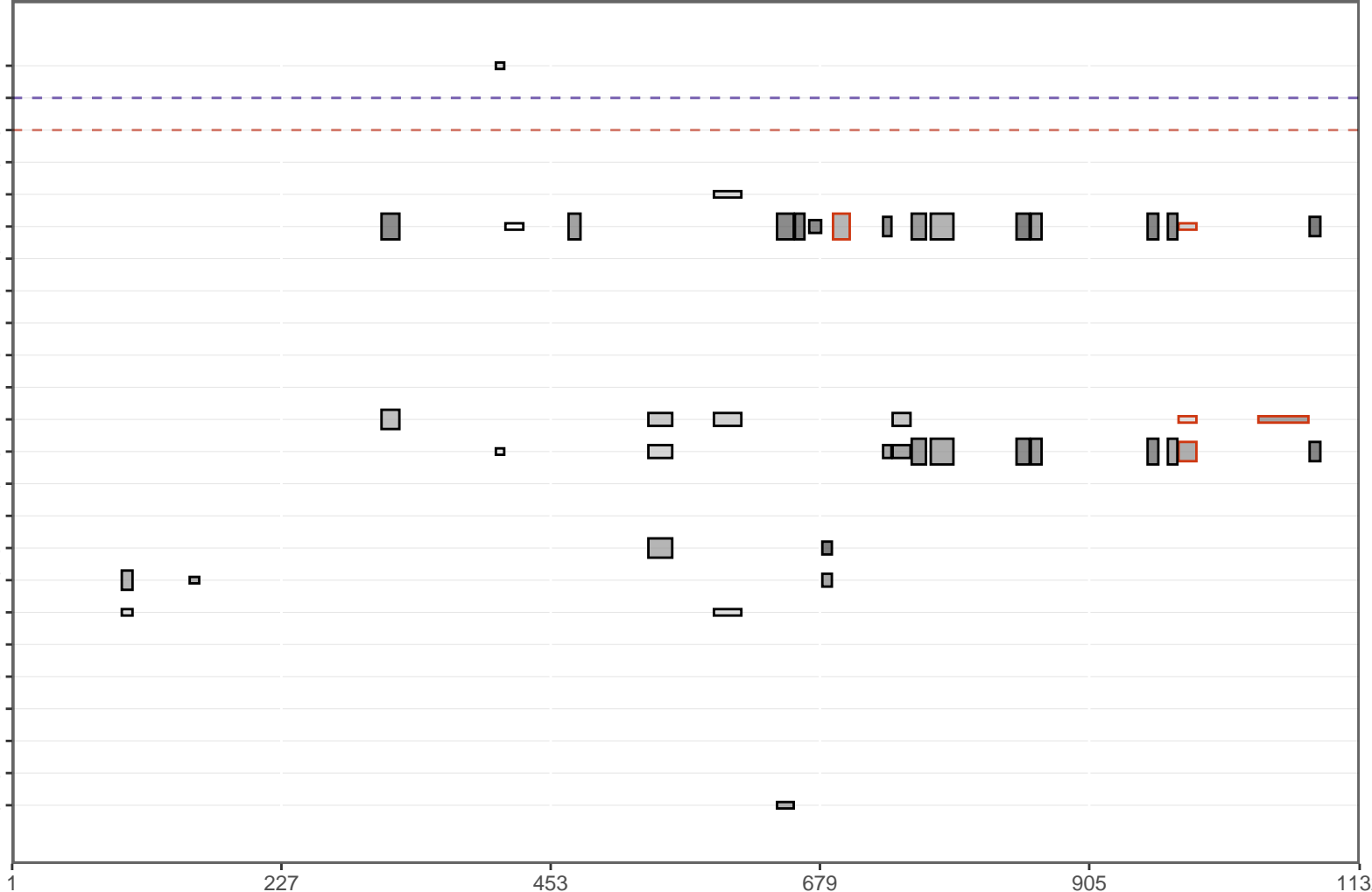
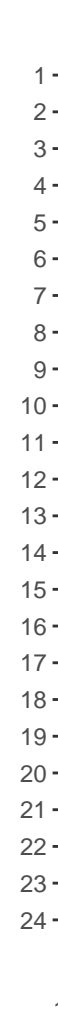
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

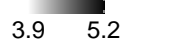
ILFSCGTGKEGDSFLVEWNESEGAIKRITYTGRFRKKEAGVYGFDTTGNHFLAVGEDSGQKFRWDMDSINLITDADGGLPRLRFRNKEGNLAVTTADNGKIKLGNAGMRRLRTRVEAPFEALRSPHEAAIKAGSGSVNPTVFNKVERRSGSPFRPRLPGLNGVDSVPRMEKPRLEEDVSDKAKPWLQTEILDGAGGRMVTMPESDSDSNKVARLLYNTNSGVGVLALGSGSTGKLLWVWARNEQNPESGKATANKVYVPHHWGPNISGLLMANDVSGVNLLEAVPCIALSKNDK

NbL01g11190.1 deoxyuridine_5'-triphosphate_nucleotidohydrolase [MW = 24.67 kDa]

No. of times detected



log(intensity)



Values from



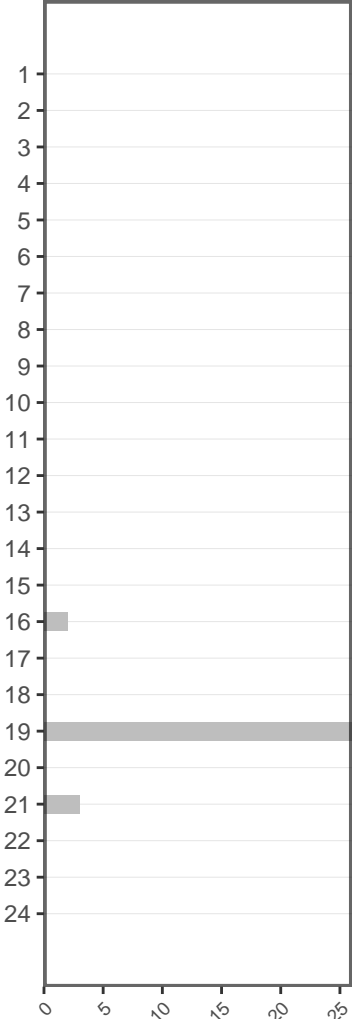
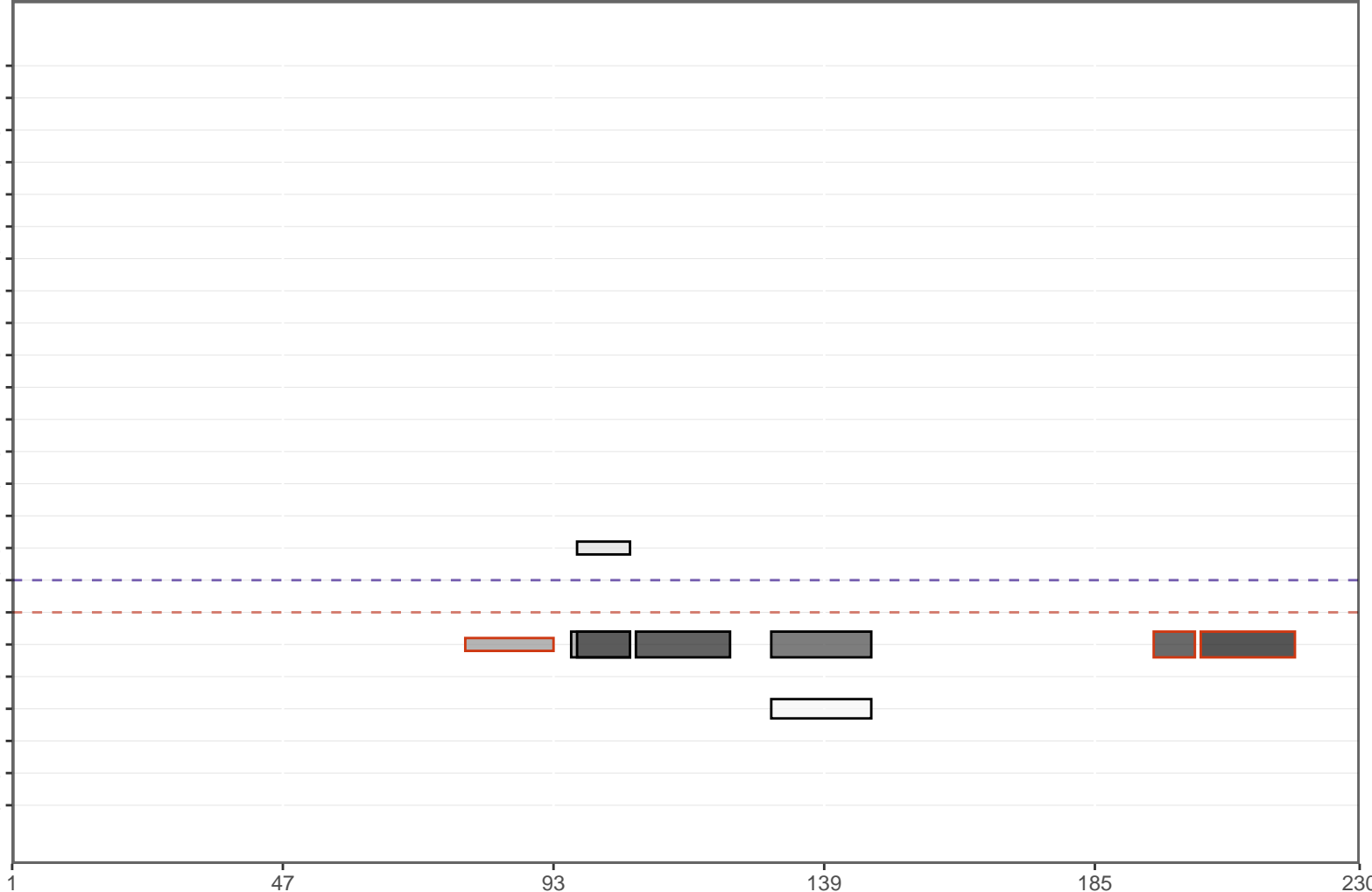
MW indication



Molecular weight



Gel Slice

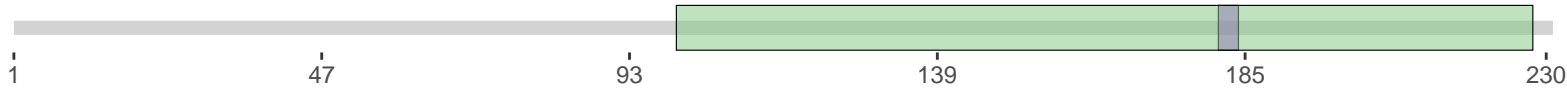


Protein length

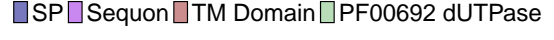


Peptide counts over 4 repeats

Pfam domains



Pfam Description

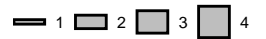


Protein sequence:

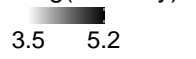
VLPSSASPLSAGYDLSSAAEAKVPRGKALIFDLSIAVPGGAVARIAPRGLAWKHSDVAGVGDADYRGRPGVGLFNHSDVDFEWAGDRIMQLHKVTPDVEEVDLDSFVRSGGFGSTGV

NbL01g11080.1 bifunctional_epoxide_hydrolase_2-like [MW = 35.58 kDa]

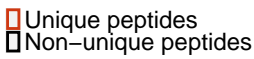
No. of times detected



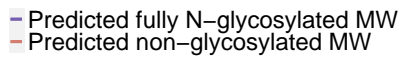
log(intensity)



Values from

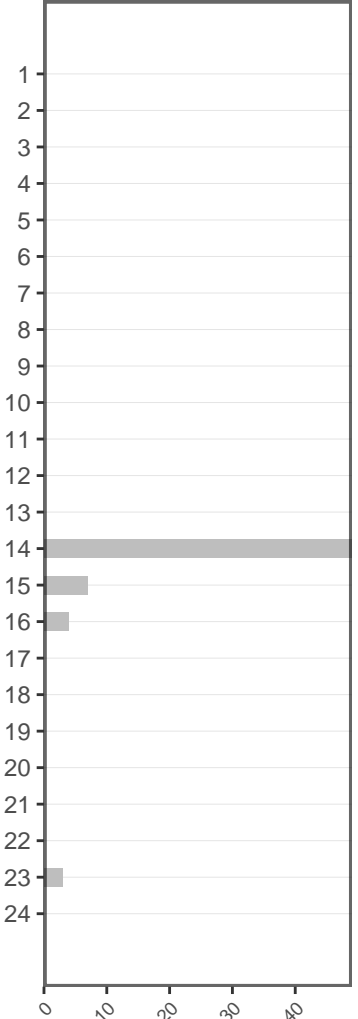
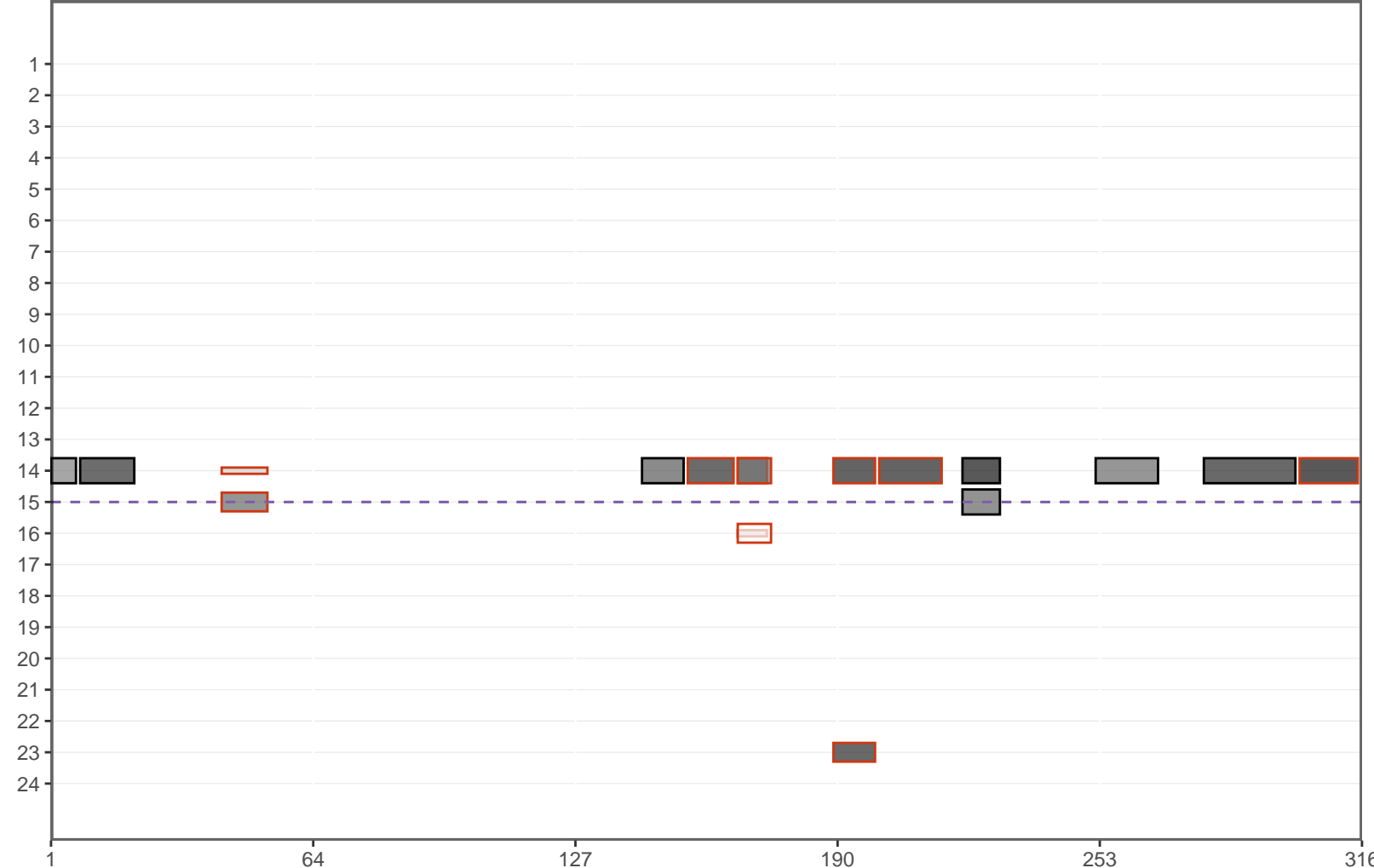
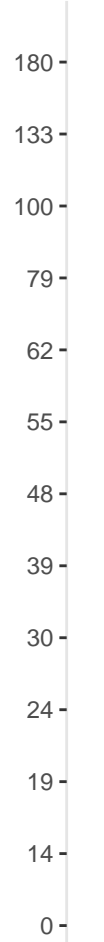


MW indication



Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

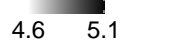
SDDYMCRFQDPGMEEEIANYGSEVLRKILTRKPKPPLPKGSPFGISFDKSLPRLGGDGLNYSTKFDRIKFTGLNYYRALDLNVELTAAWFGAKVYVFKFMVGEGLVYVTFPGMEYVHGGGFRKDVPLMDEDAVVMGAAHFRNGERAGEINSHYDFNKF

NbL01g11070.1 60S_ribosomal_protein_L18-2-like [MW = 26 kDa]

No. of times detected



log(intensity)



Values from



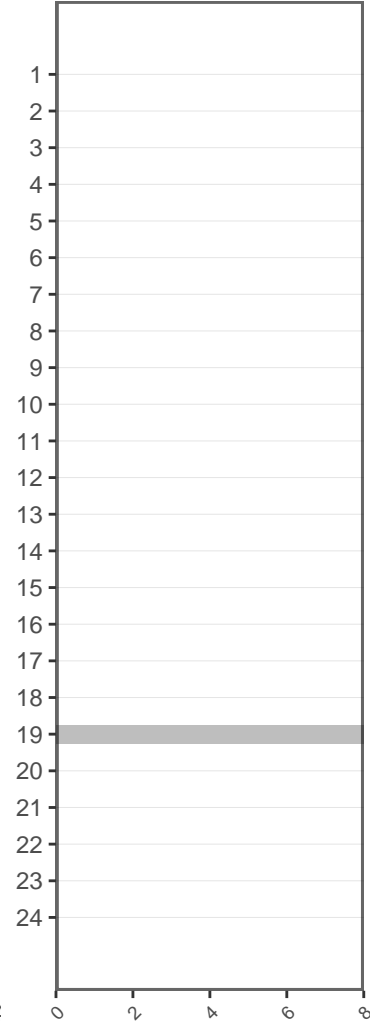
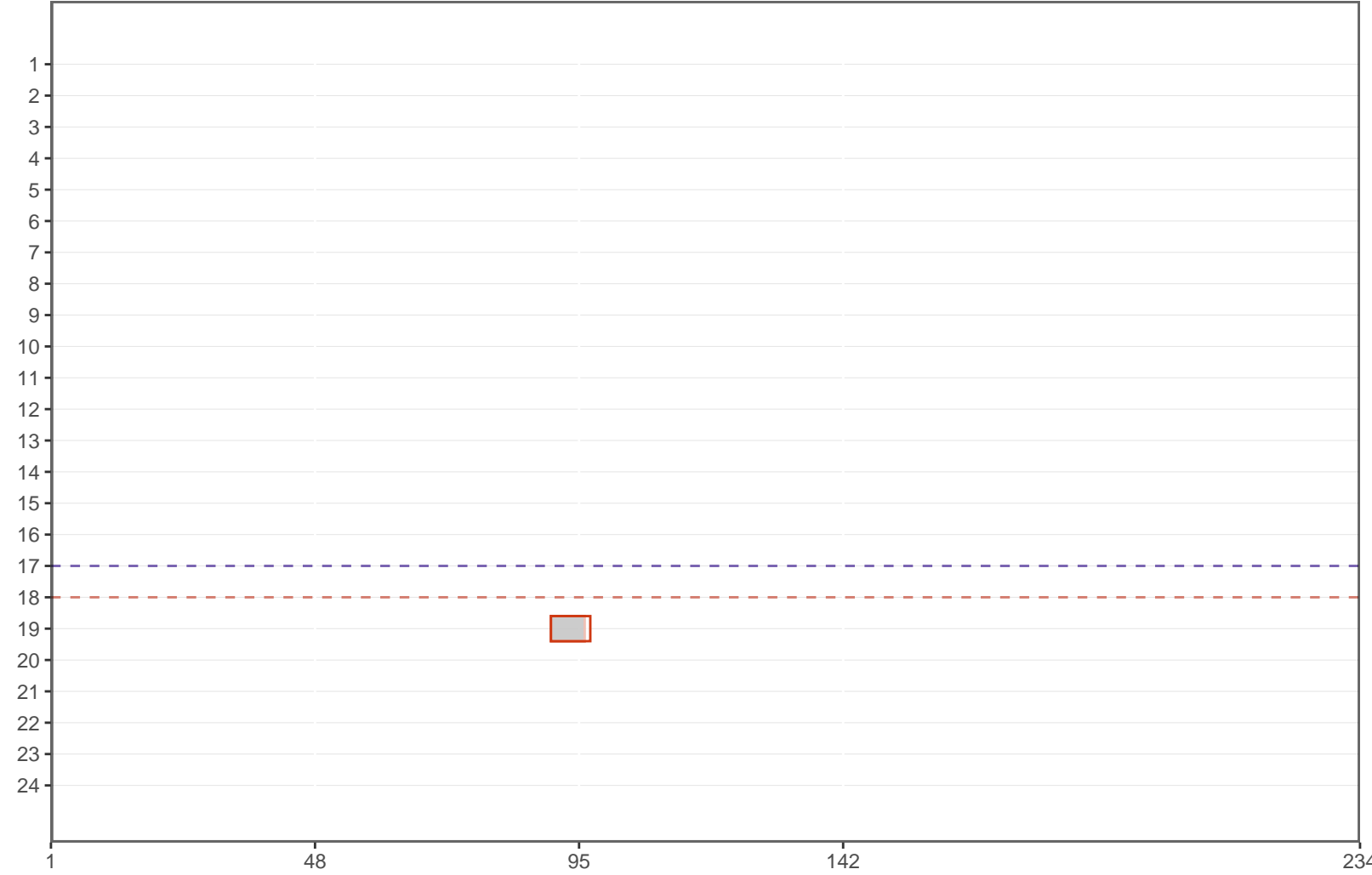
MW indication



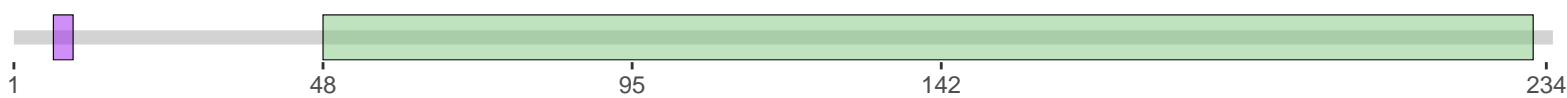
Molecular weight



Gel Slice



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKPPLSLRLSLSVYAKGKEDKVVVVGITFDNRAVEVPAIKVGLRFITKARARIEKAGGEGCLTFDGLALRAPLGONTLLLRGPKNAEAVKHFGAPGVPHSHTKPFVIRGKGRKFERARGRNRSRGGYKA

NbL01g11060.1 malignant_T-cell-amplified_sequence_1_homolog [MW = 21.49 kDa]

No. of times detected



log(intensity)



Values from



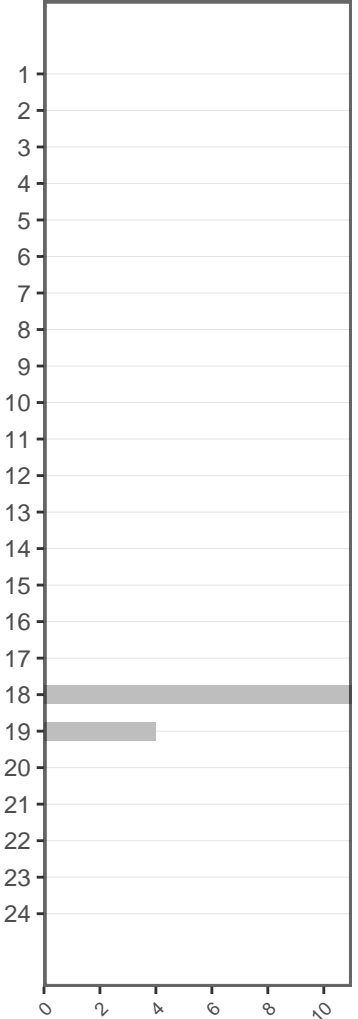
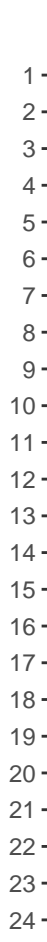
MW indication



Molecular weight



Gel Slice

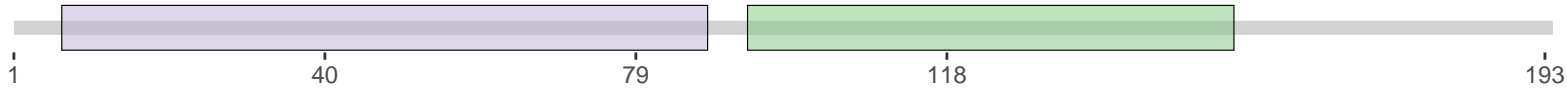


Protein length

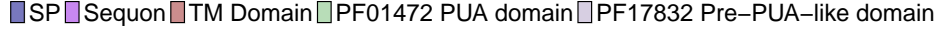


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

HOYPSIMKQLQVDRGAKFKVLSGANIMCPGLTSPGGALDDEVGAEPTVAIMAEQKHALAIGFTKMSAKEGGSTRELIVFQIRLLMMASGRVSDWIELEWKMTMFFFKK

NbL01g11000.1 auxin-repressed_12.5_kDa_protein-like [MW = 13.71 kDa]

No. of times detected



log(intensity)



Values from



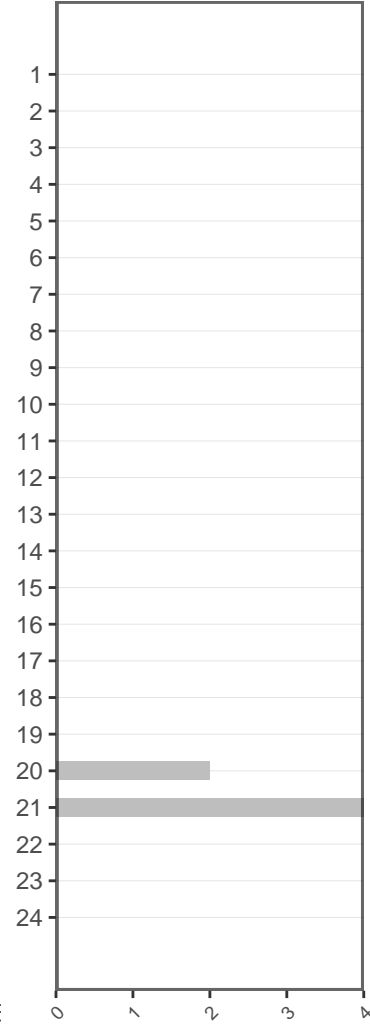
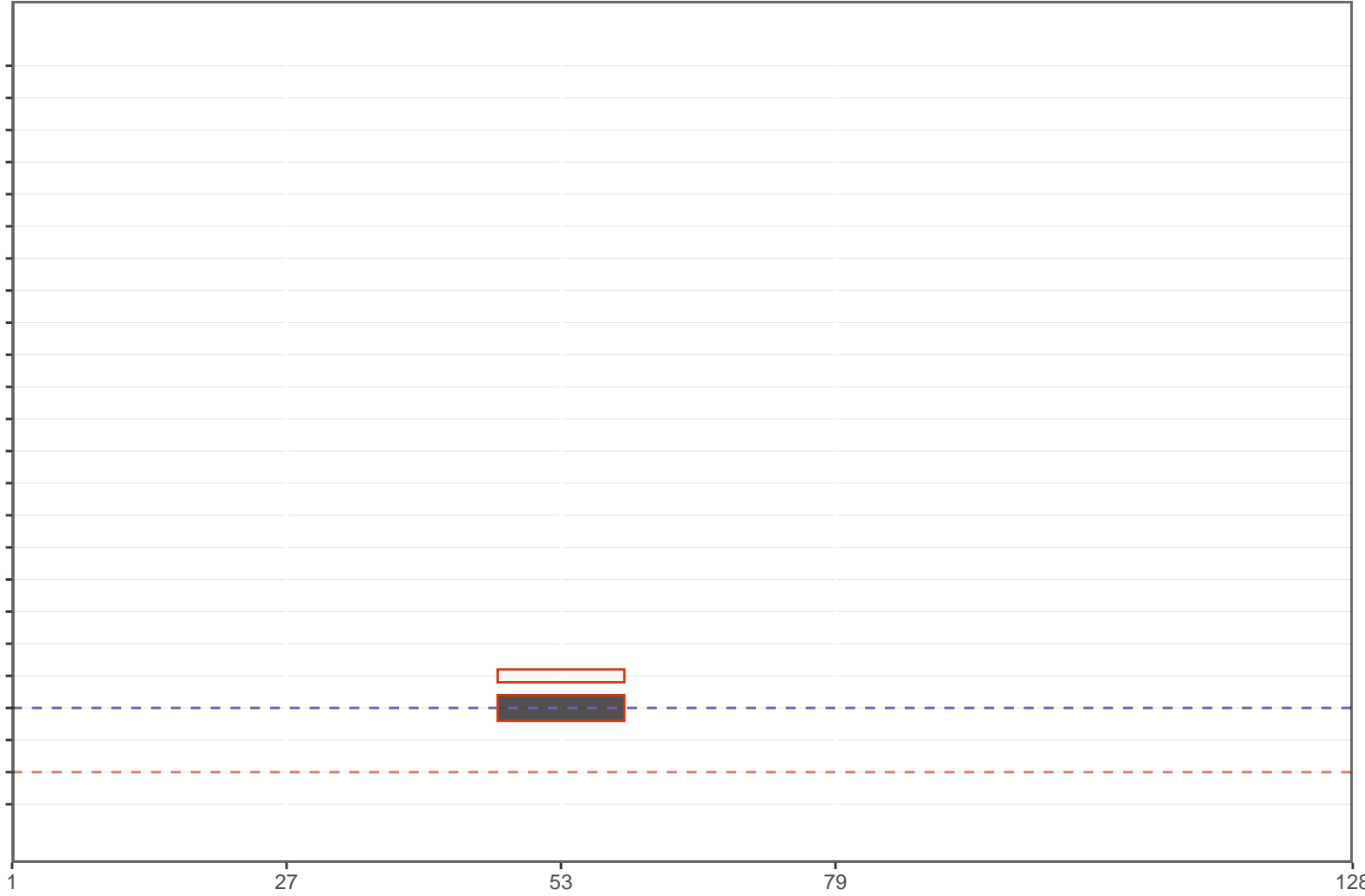
MW indication



Molecular weight

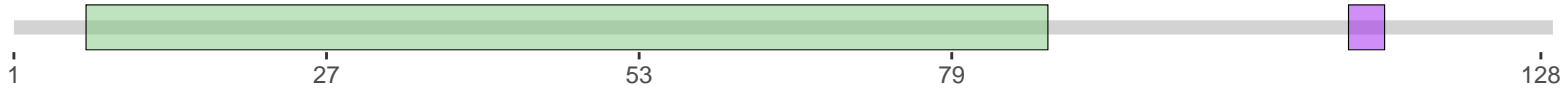


Gel Slice



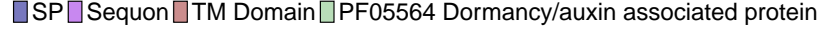
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

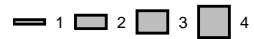


Protein sequence:

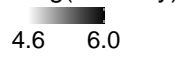
IASSSDAIVRVRTSMVKKPPGGNRRDPPVSPMGTTTPVSPFAGAGGREAVHSRRRBFANENASGGVSPRSPRPFDL

NbL01g10880.1 ATP-dependent_Clp_protease_proteolytic_subunit-related_protein_3_chloroplastic [MW = 35.77 kDa]

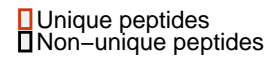
No. of times detected



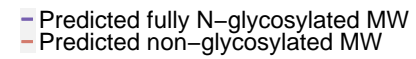
log(intensity)



Values from



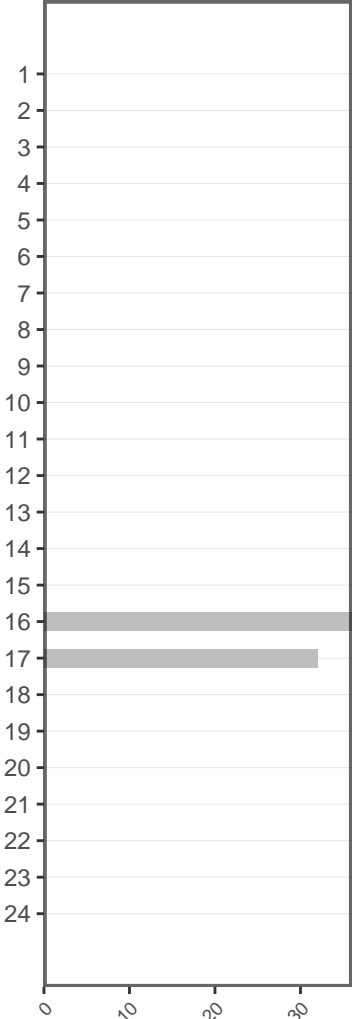
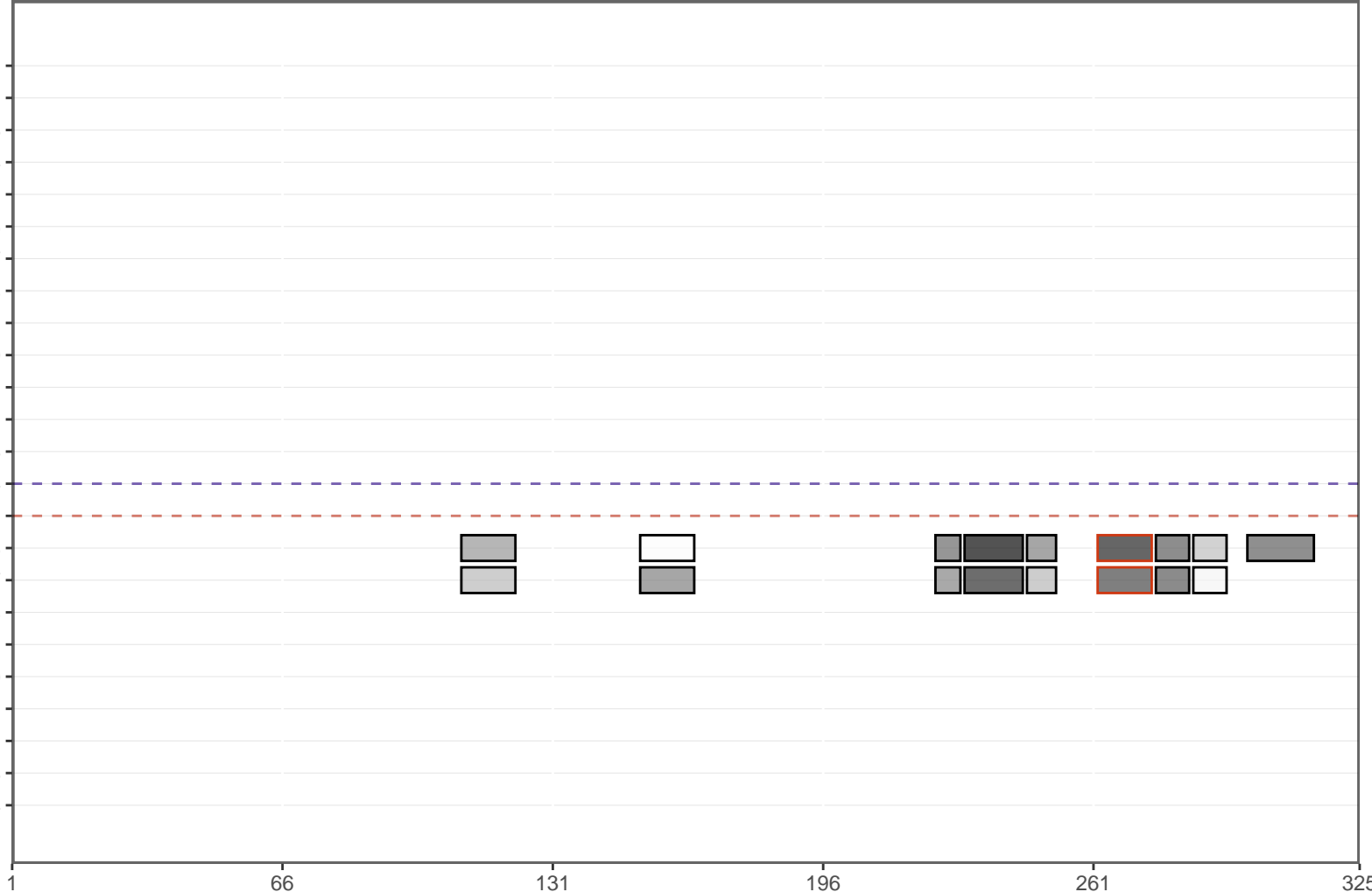
MW indication



Molecular weight

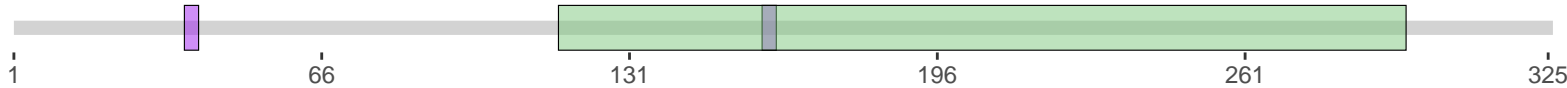


Gel Slice



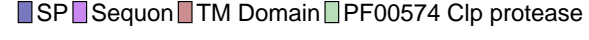
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DPKPEFLYINISGTFRDDGETVGMETEGFAIYDAMMLKLNKIHVAGAAIGGACILLAAAGSKGRFMMHAKAMIQPRVPSGLMPASGVDFIRAKEVINRDLVLLAKHTENSEEAWANMRRPFYMDATRRAREFGVIDKILWRGGEGIMADVSAPEQWDKNAGKVDAP

NbL01g10850.1 40S_ribosomal_protein_S10-1-like [MW = 20.06 kDa]

No. of times detected



log(intensity)



Values from



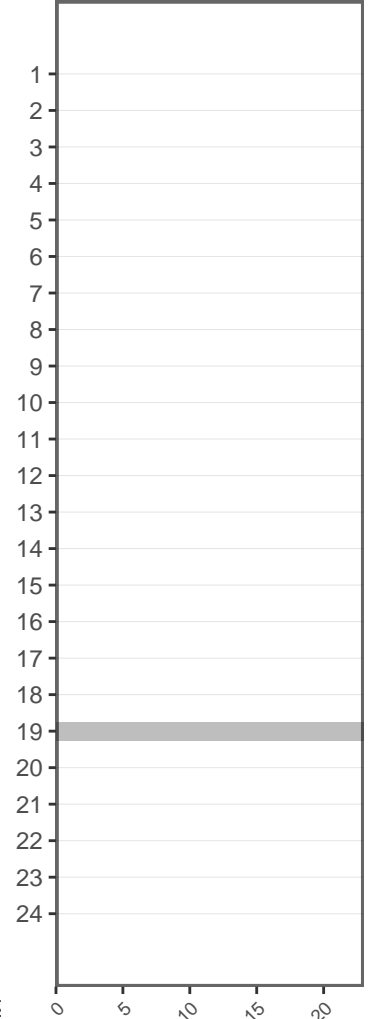
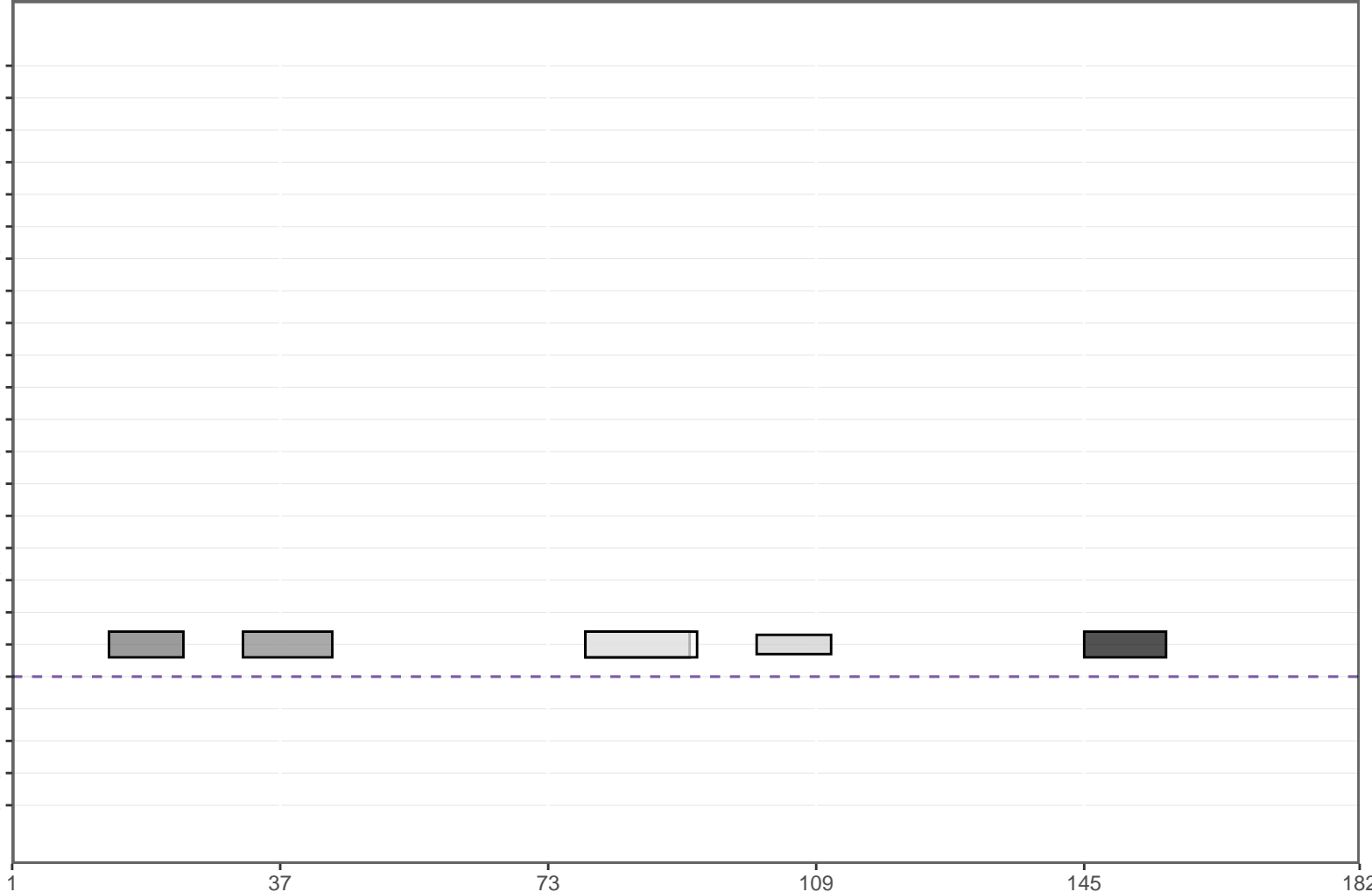
MW indication



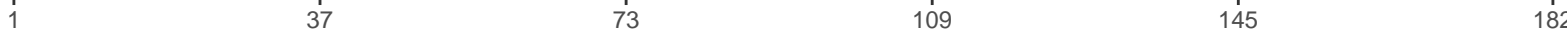
Molecular weight



Gel Slice

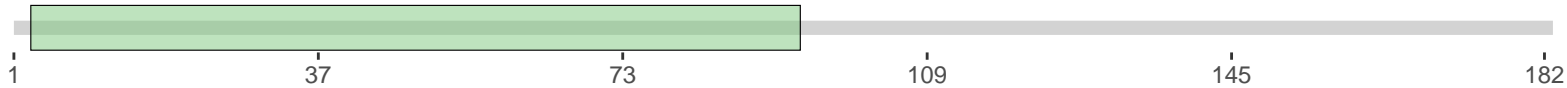


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ILPSEIVYATLTKSAMPVLRPMGGPPGDRPRGRPRFEGDPRFRFEGDREGYRAGPRGPPGEGFGEKGGAPADVQVFRGSGGRPGFGRGSGGGFAGAPPSSSF*

NbL01g10820.1 xyloglucan_endotransglucosylase/hydrolase_protein [MW – SP = 31.68 kDa]

No. of times detected



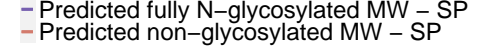
log(intensity)



Values from



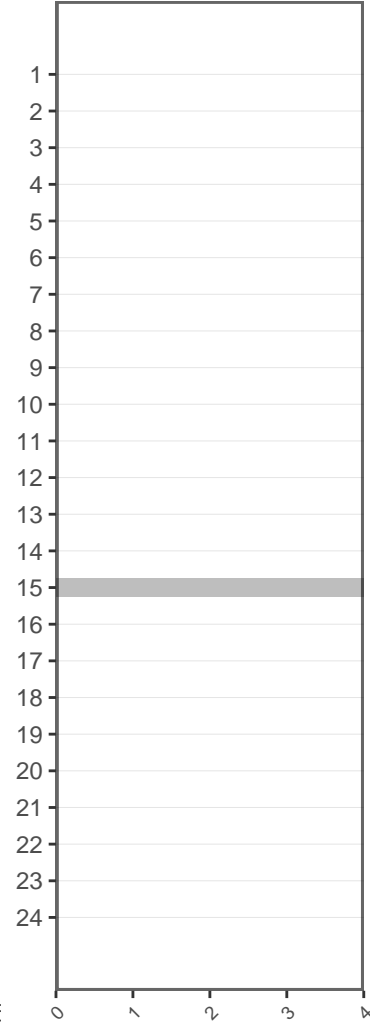
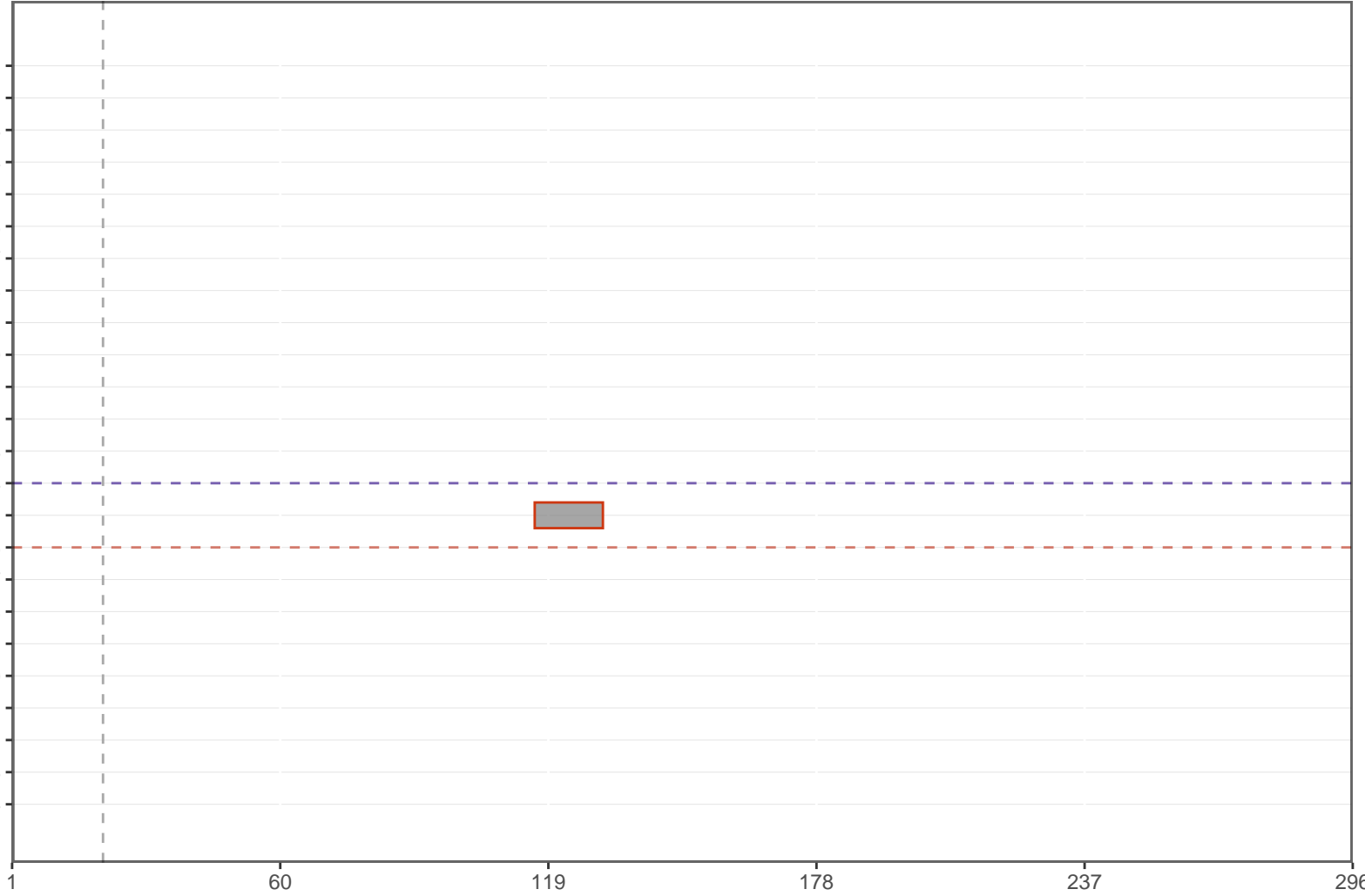
MW indication



Molecular weight

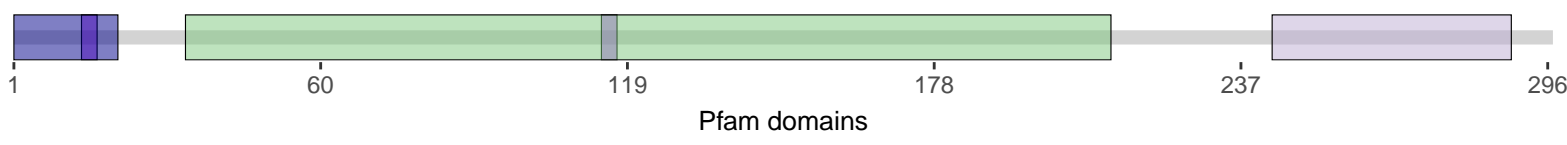


Gel Slice



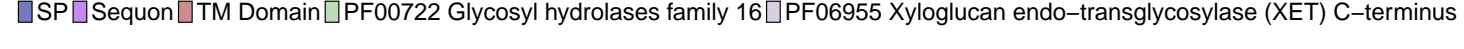
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

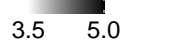
SRILYLFDPKGYHEKSVLWNTFGVIFVDVPIRAFKNKDLGVNFFNPKMYSSLWDADDDWATRGGLEKTDWNSNAPFTASYSFHVDSGEAATPQEVGVQVNTKGMRRWDDKAFQDLDALGVRRLLRWRRQKYTYNYGTDKRRYPTLPPEGTQDRDI

NbL01g10780.1 glutathione_S-transferase_U7-like [MW = 25.67 kDa]

No. of times detected



log(intensity)



Values from



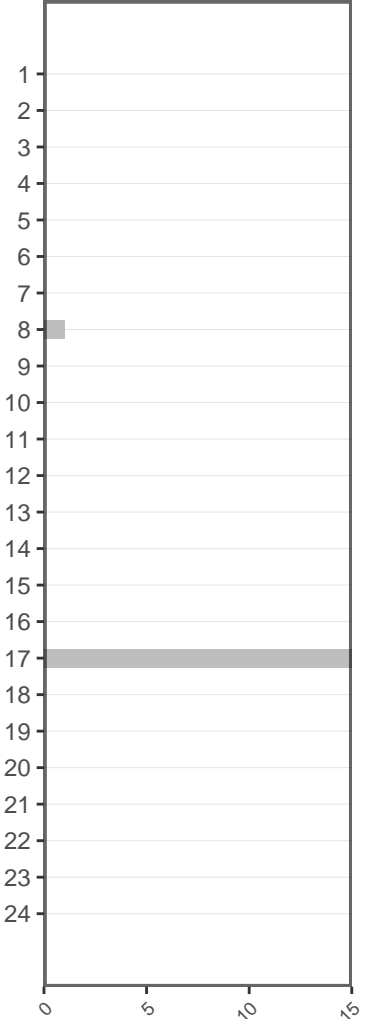
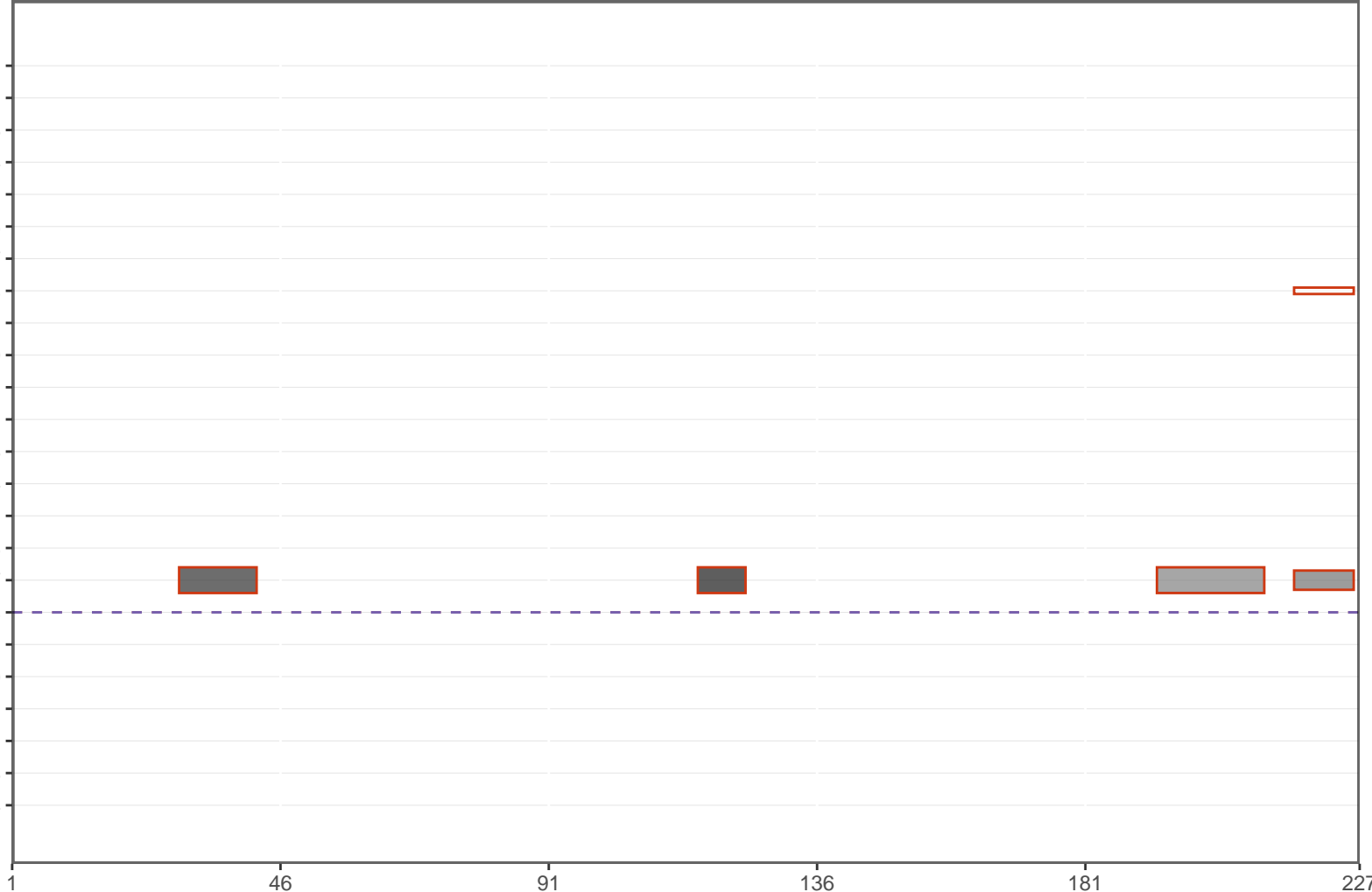
MW indication



Molecular weight



Gel Slice



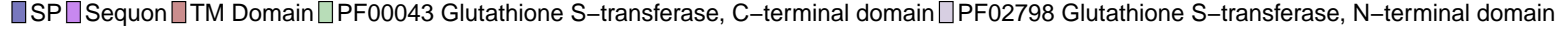
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

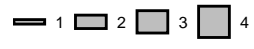


Protein sequence:

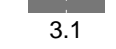
VFIDGKFYEAANKKAFSSGSKAEVDNVAEGLQLLEGGITGKFKFGGEGHYDVIWGWYWFQYVEEVEGFKAMDSKEYPOLNNAWIKNFQVFLIQGLPKPDDWKAFFKGFKDAALADTV

NbL01g10730.1 histone_H2A.1 [MW = 15.53 kDa]

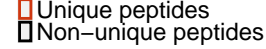
No. of times detected



log(intensity)



Values from



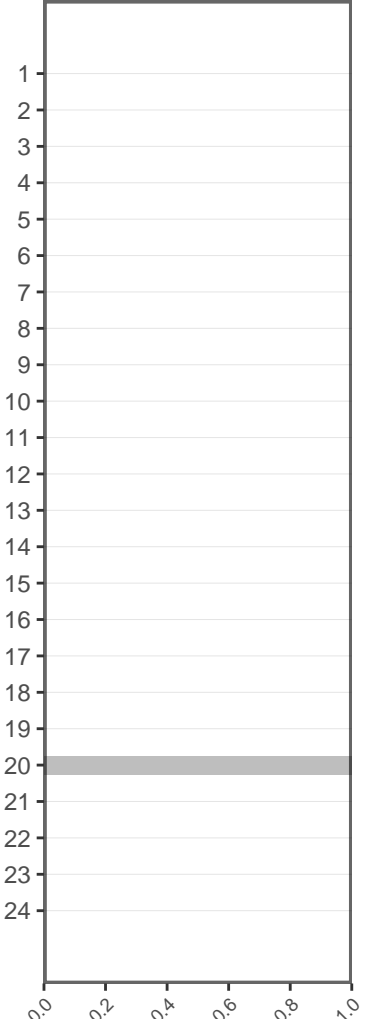
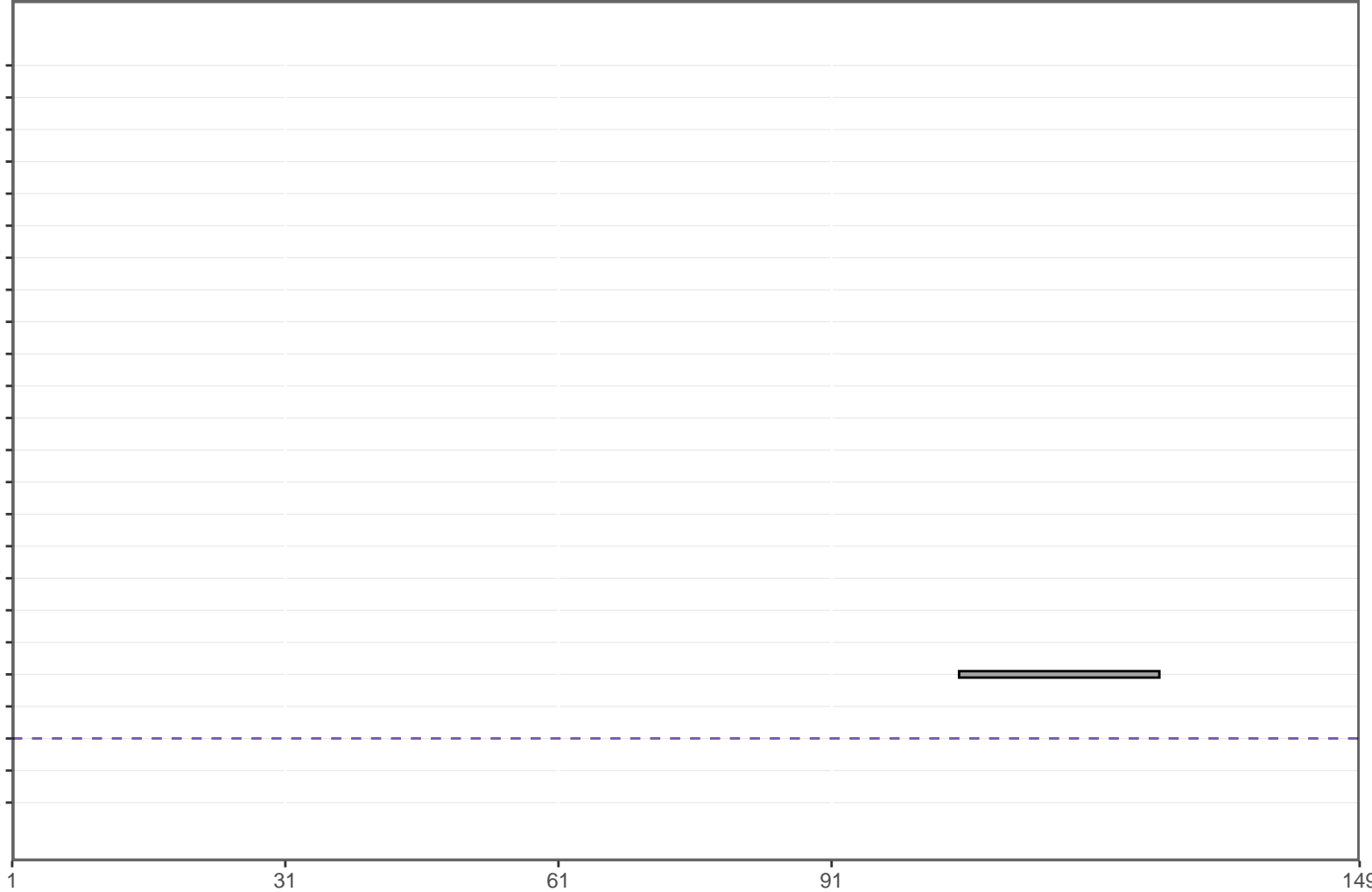
MW indication



Molecular weight



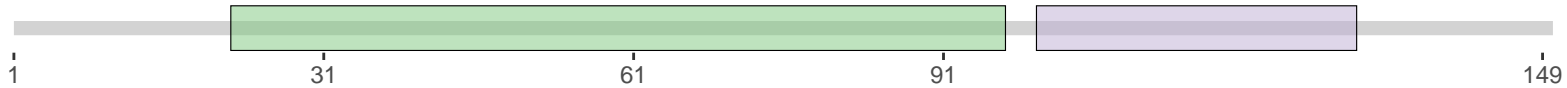
Gel Slice



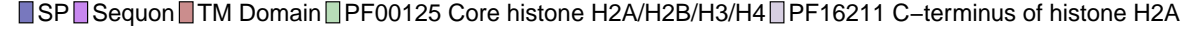
Protein length



Pfam domains



Pfam Description



Protein sequence:

AAVLEYLAEEVLELAGNAARDNKKSRIPRHVLLAVRNDEELGKLLGGVTIASGGVLFNINPVLKPKTAIVEEKASKPKATKSPKKA*

NbL01g10720.1 autophagy-related_protein_18a-like [MW = 48.98 kDa]

No. of times detected



log(intensity)



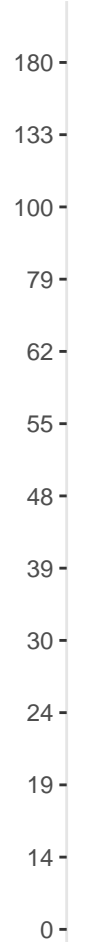
Values from



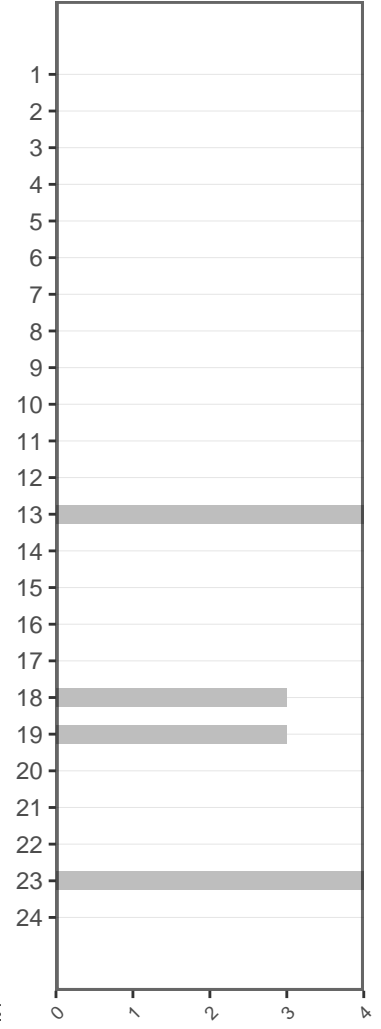
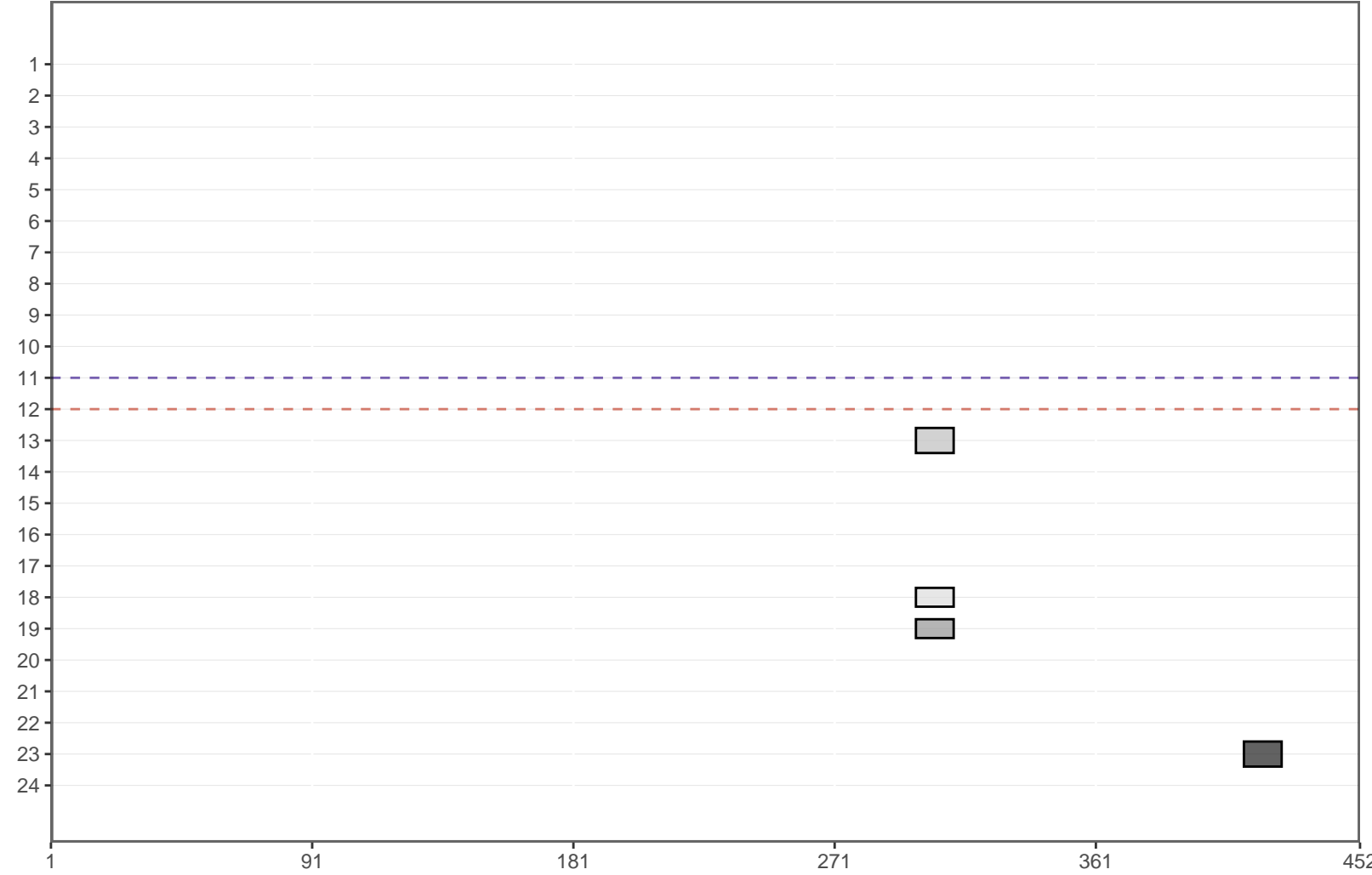
MW indication



Molecular weight



Gel Slice



1 91 181 271 361 452

Protein length

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24



Pfam domains

Pfam Description



Protein sequence:

FADLLKLIHQIETVANPKGLCEVSGVSGMMLVCPGLQKGGVVRVEHYAKRTKFMAMHDSRIVCFALTINGRLLATASKGTLRVRFNTLDGSLVGEVRRGADRREIYSLAFSSTAGWLAVSDDKGTWYVFNLIKVDGSAVGVDRPRGASESNATSPSAVSHLSFRIGVLPKYFSSEWVSWQFRLEGLQHVFGHQKNTVILGMDGGSFVROGFDAAAGGEMTLEHHSFLKPEENP

NbL01g10540.1 probable_linoleate_9S-lipoxygenase_5 [MW = 97.51 kDa]

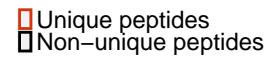
No. of times detected



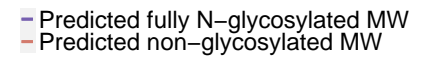
log(intensity)



Values from



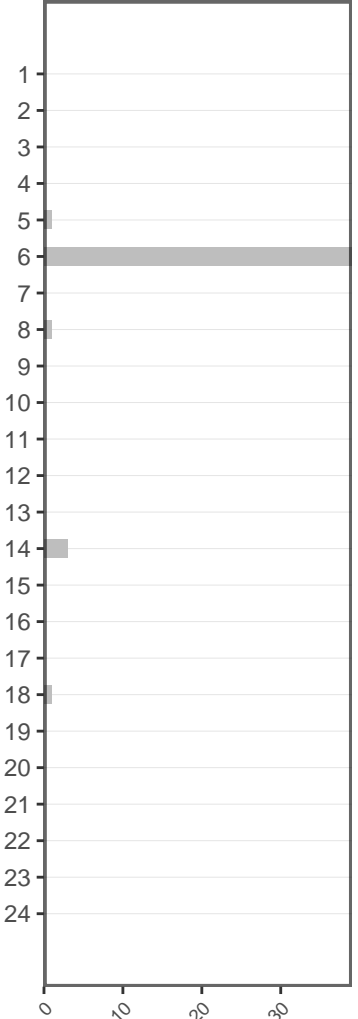
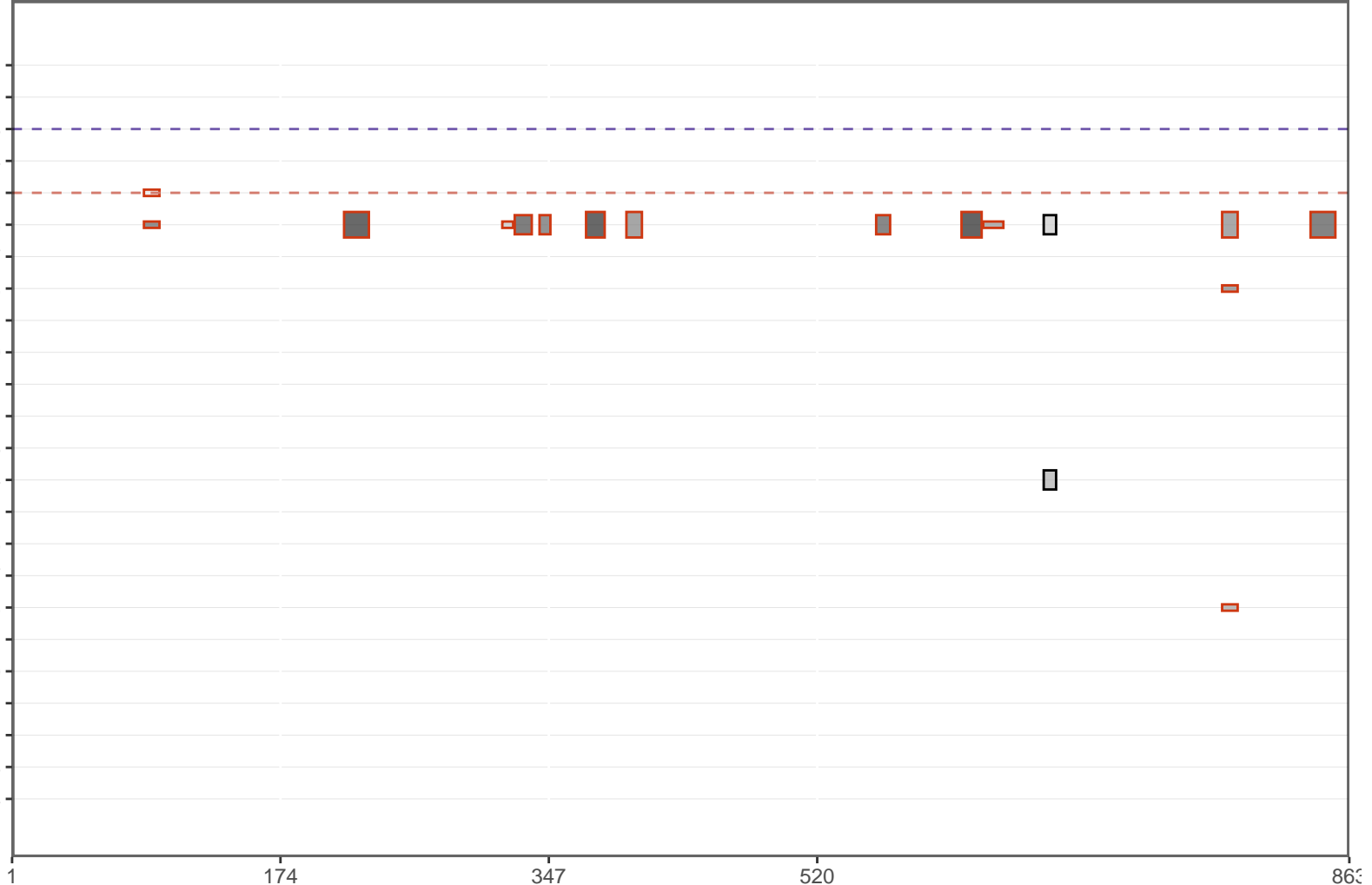
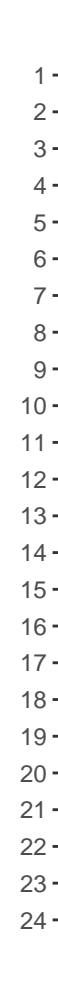
MW indication



Molecular weight

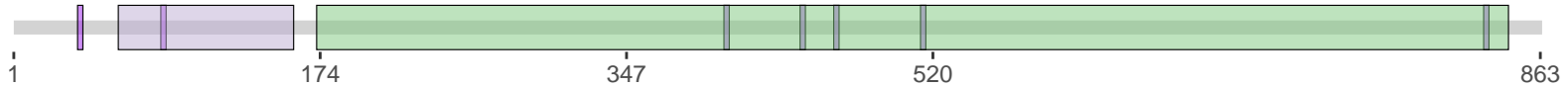


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TDEAKTNKLFILNHDLMFPLRRINTSTDTKTYASRTLFLFGDNGTLKPLAIELSLPHPDGDDGFAVSKVYTPADGGVEGSIWGLAKAYAAVNDGSGVHQLISHVINTHVAIEFPYATNRQLSTLHPYKLLHPHFRETMINNALARQLINGGGLLELTVFRAKYEMEMSAVYKDWVFFPEQALPTDLKRGVAVEDSSPHGRLLKGDYFPYAVDGLKIWSAKSWTEYGNYYYKSDDAVQKDTLEQAWWKLREEGHGDKKDEPWPKMGTVQELDSCITTIWIASLHA

NbL01g10510.1 probable_Xaa-Pro_aminopeptidase_P [MW = 80.29 kDa]

No. of times detected



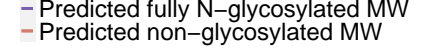
log(intensity)



Values from



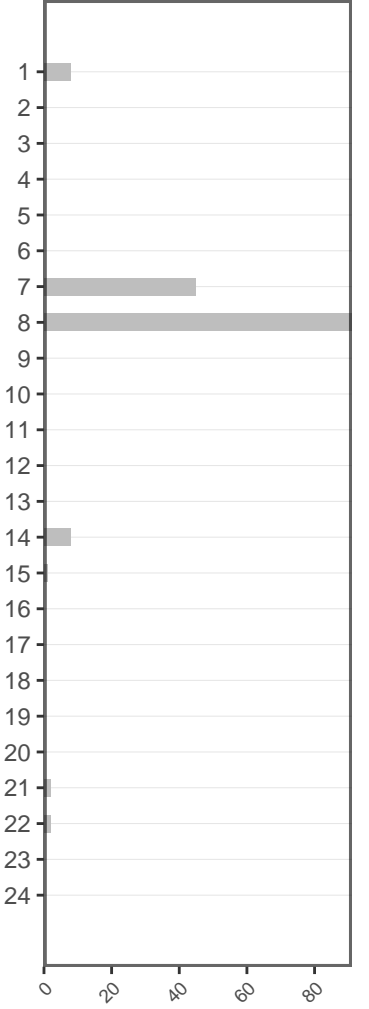
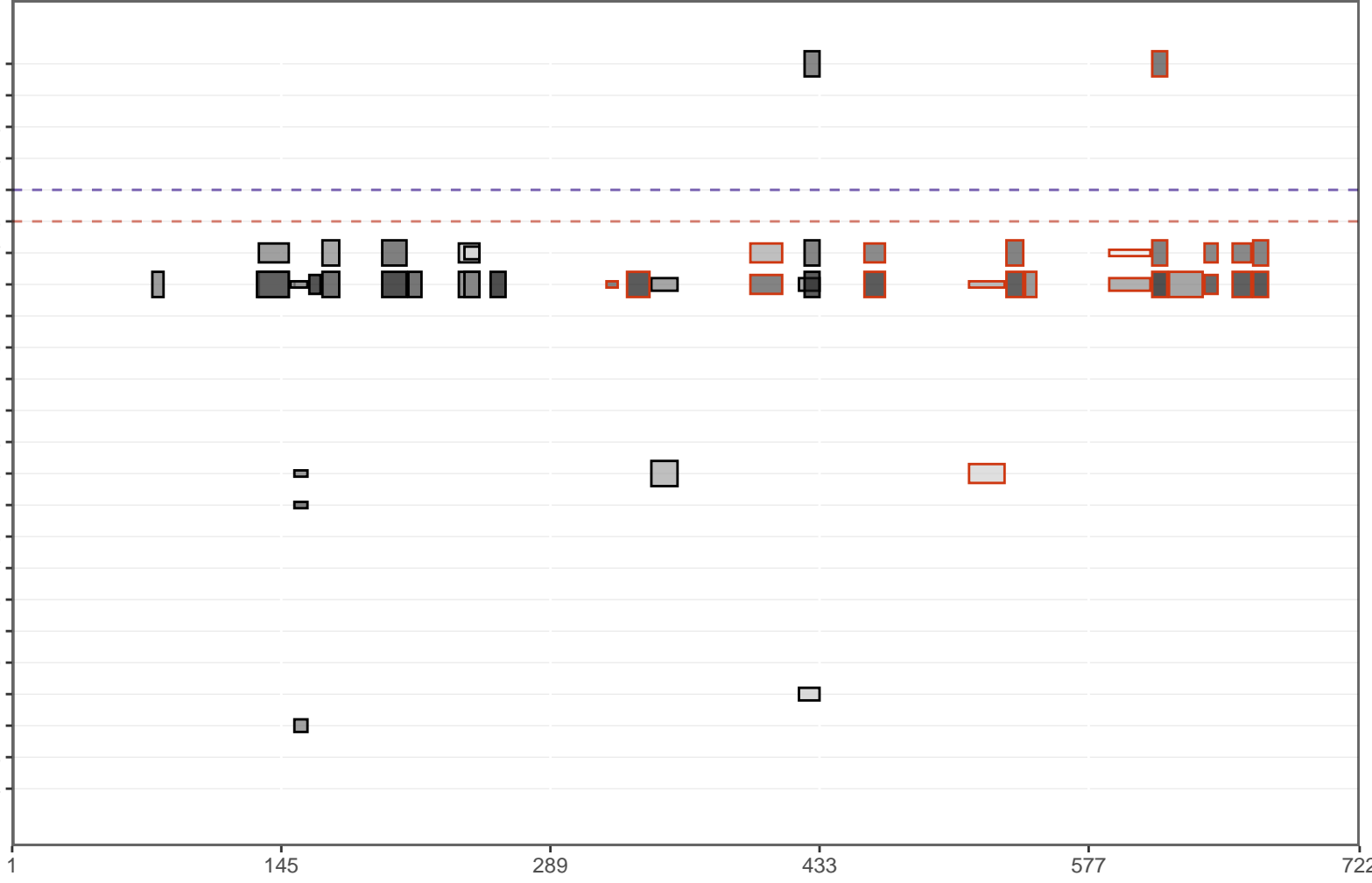
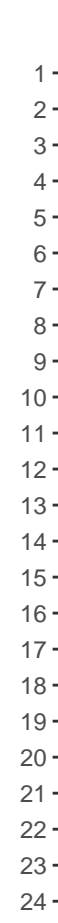
MW indication



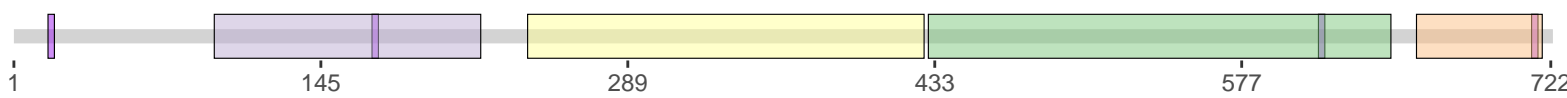
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

IESLSAAKGAKLWLDTSSEVNAANVSEAGYKYPWNSATKSRKIKTANLDVNDQSGGSGAVYRSGSPVSLRKAQKNDALLEGMRNGHLRDAALAAQFWWLEDEIQRNVLTEVEVADKLEFRSHQDGFSDTSFDTSISGGGANGAIHKKPEPDGSGVVDGKELFLDGGGGYDGTTRITRVHFGEPGAREREGFTFVLRGGHALDQAVFPENTPQFVLDATFARSLWKVGLDNRHGTGTHGVAALNVHEGPHSIFRFGNMFLLRGMVSNPEGYEDHDFGIRENI

NbL01g10500.1 long_chain_acyl-CoA_synthetase_6_peroxisomal [MW = 77.1 kDa]

No. of times detected



log(intensity)



Values from



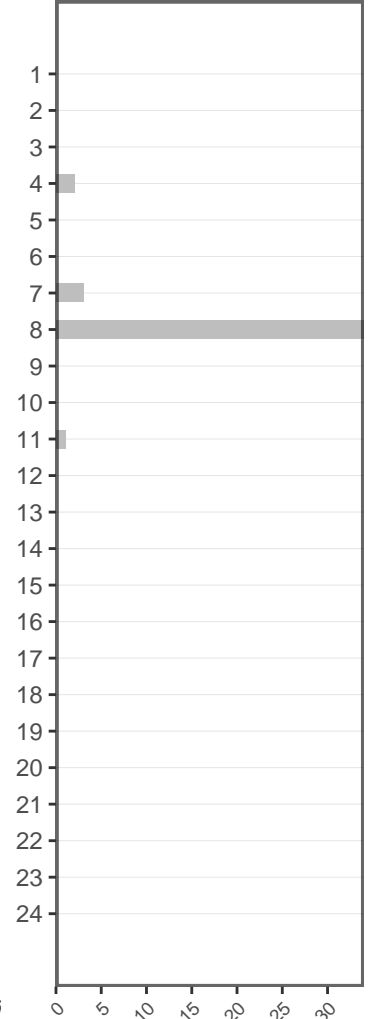
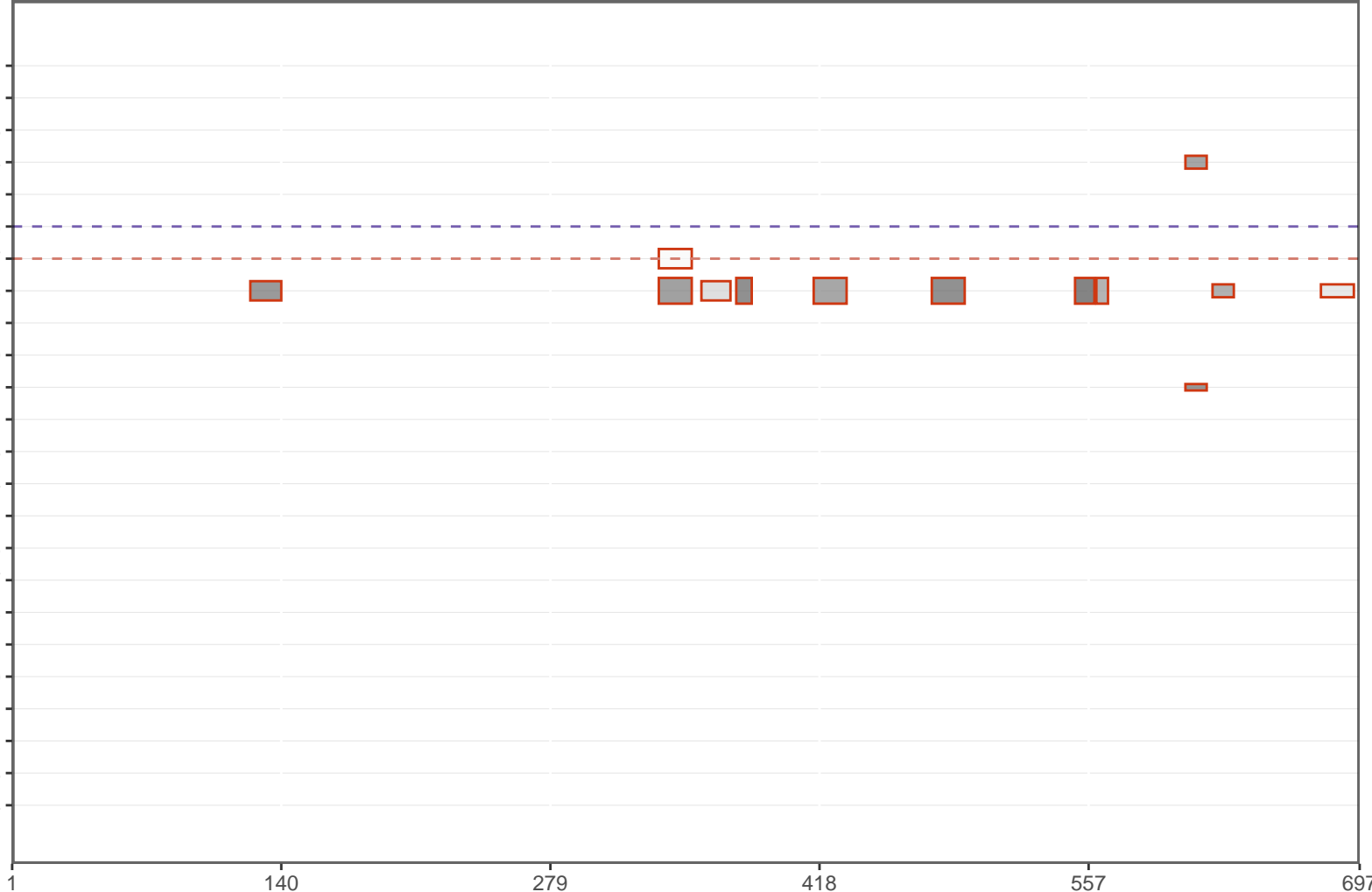
MW indication



Molecular weight

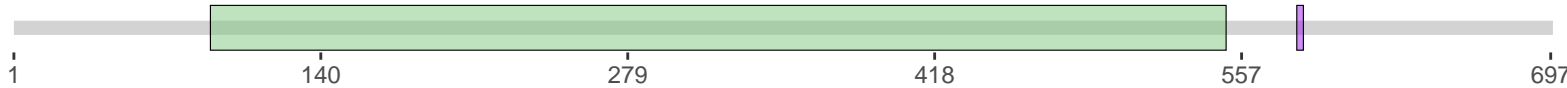


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

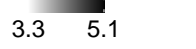
DDLATLRPTIFSSVPRLLNRYVAGFTNAGTSGLLKGRFLNFAAYNSKKGAVMMGRKPSMADRLLVFNKIKDKLGGRRVRLMTSGASPLSPDVMFLRVFGGLVMEGYGMETETSGVSSMDSDLLTGHVGSFNPAGEIKLVDPENMYSYTSBEDQPHPRGEIGVIRGPIIFEGYKXDEVQTRFVDEIDGGWLHTGDGILWLPGGRLKIDRKNFKLAGGGEYIAPEKIEVYAKGKFAVQGFVYGDGDFNSBLVAWVGVPEPDKFEKAWASGEGHYEELGGLGIDPRKAAVLAEMDAVGI

NbL01g10480.1 mannosylglycoprotein_endo-beta-mannosidase [MW = 110.56 kDa]

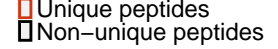
No. of times detected



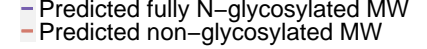
log(intensity)



Values from



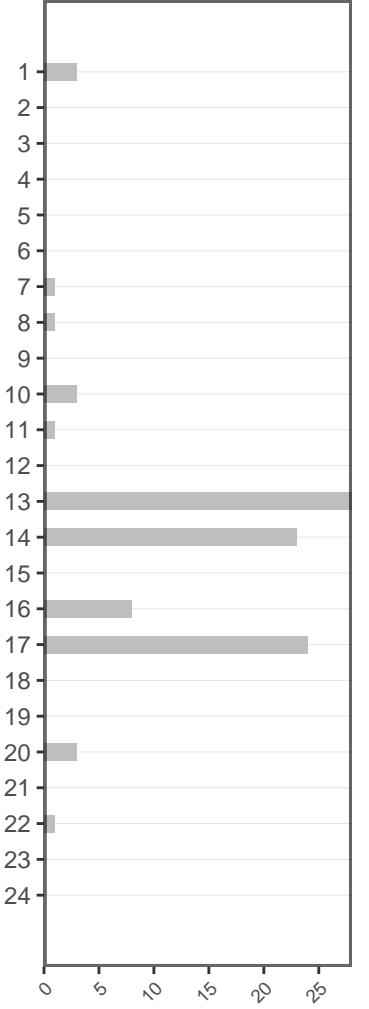
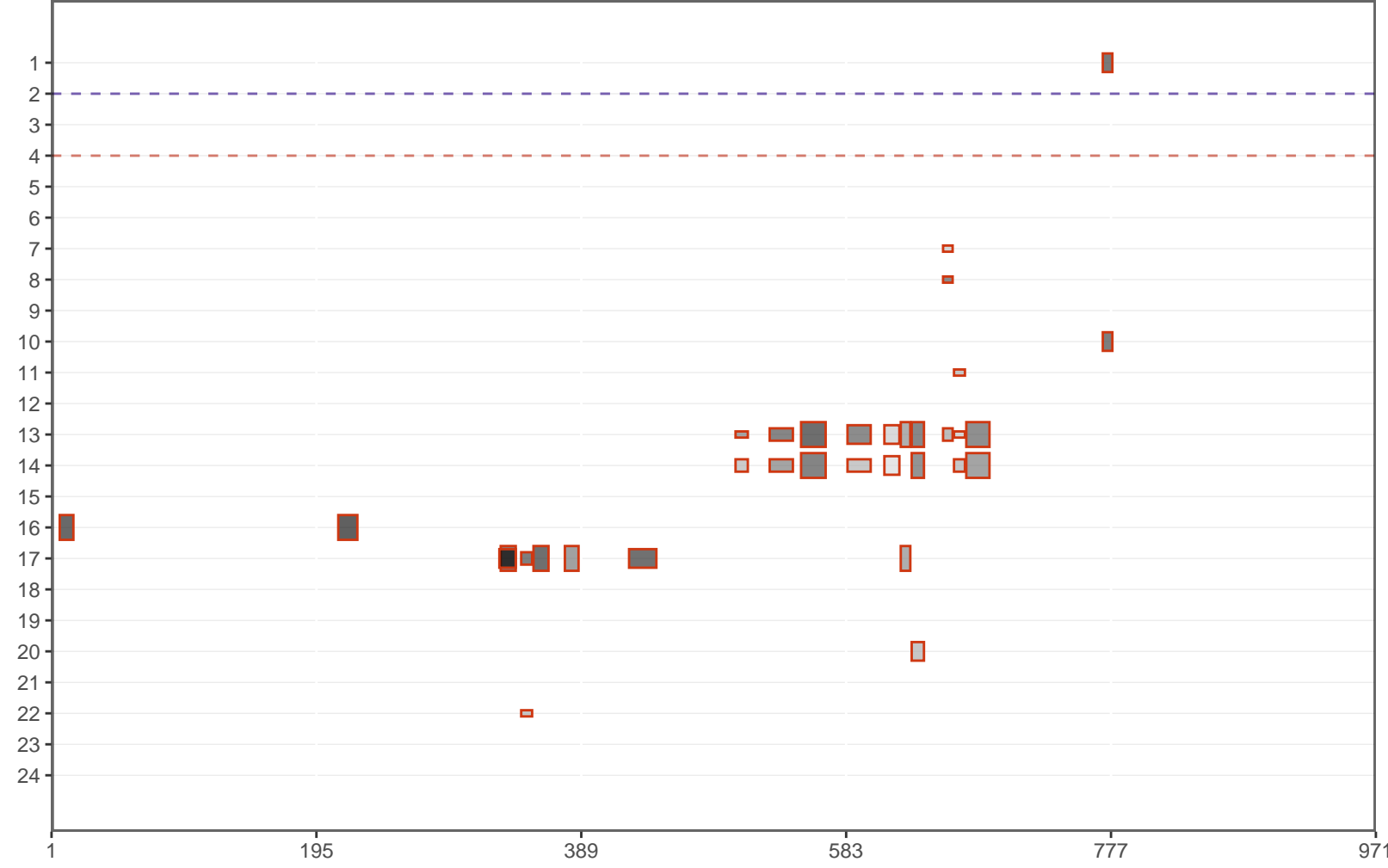
MW indication



Molecular weight

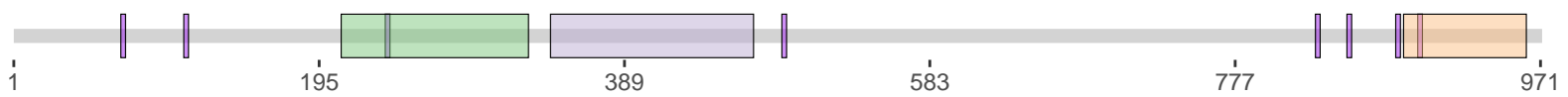


Gel Slice



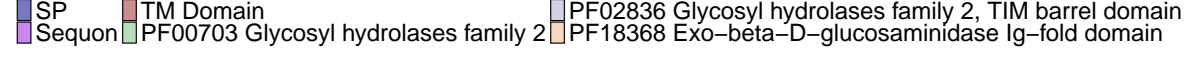
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

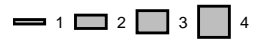


Protein sequence:

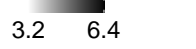
NALKNDLQLHPYFMKENDSGSATTPLVLDKPSGHLGSTRVYVGGSMWDGFDGKGDFTDGPVEIKGNPEDFFRHDIYKYGFNPEVGNVGMPLAATIRATMPPEGWQPLFKLSDGYSIEEVPNPNWYHKYIPYKPKGKVDQGLSYGTPKDLDDFDLKAQLNHYVQYRALLEGWTSGMMSKYTGVALWKTQNPWTGLRGDFYDHLHDGDTAGFYGGRSAAEPIHWQLNLATYSIEVNTMSEELPNVAIEASIWDLGEGEPYKTSKELTVPPKKTSTTEMKYPKSKNPK

NbL01g10330.1 serine--tRNA_ligase-like [MW = 51.07 kDa]

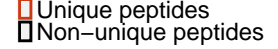
No. of times detected



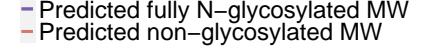
log(intensity)



Values from

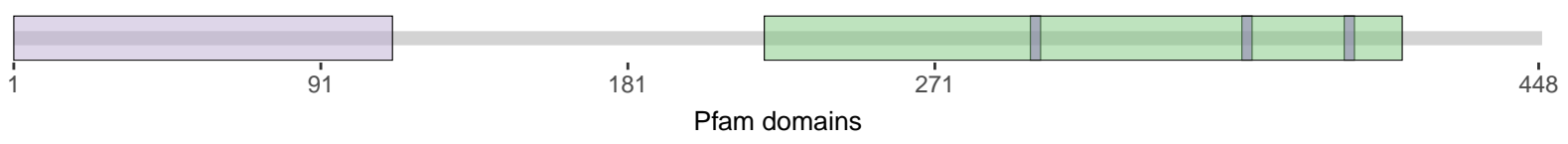
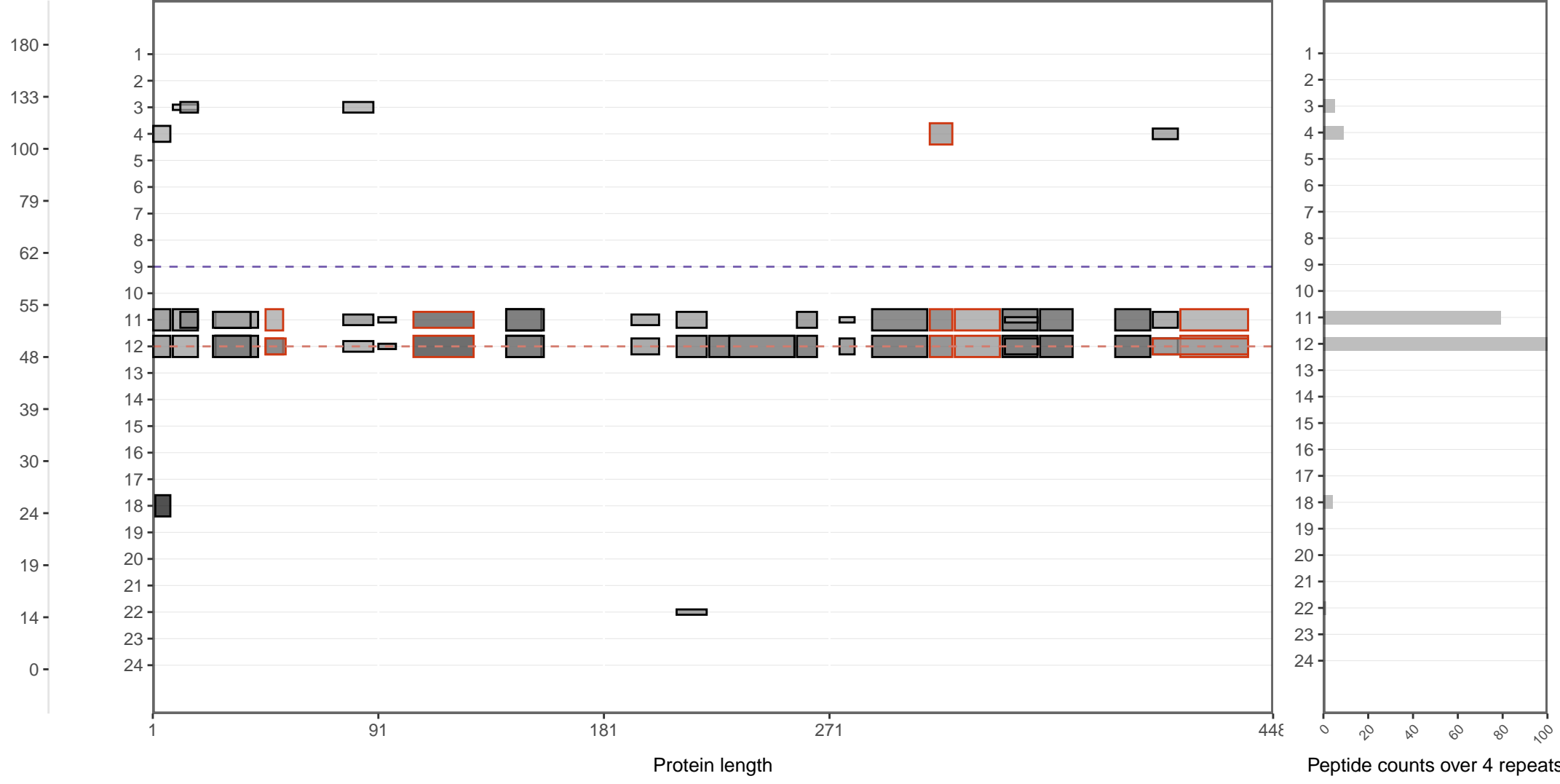


MW indication



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF00587 tRNA synthetase class II core domain (G, H, P, S and T)
- PF02403 Seryl-tRNA synthetase N-terminal domain

Protein sequence:

DLAQDFEELYKYVTGEGDDKYLATAEGLGAYHLDDWIHPGQLPLRYAGYSBGFRIKESGSRDITLGFIRVHQFERKVEGQFLTSPNGDSWDHHEEMKNSEFFQKIKIPYQIVSISGALNDAANAAKYYDLEGWYPAISSTYRELVSQGNQTDYQSRKLEIRFGQKKNQEGAKGVYHLLNSTLTATERTICOLENNKREGDGVPEIPVLRPYMDGVTFMFGQTFPAKEAGKQKKA*

NbL01g10290.1 glucose_and_ribitol_dehydrogenase_homolog_1 [MW = 31.73 kDa]

No. of times detected



log(intensity)



Values from



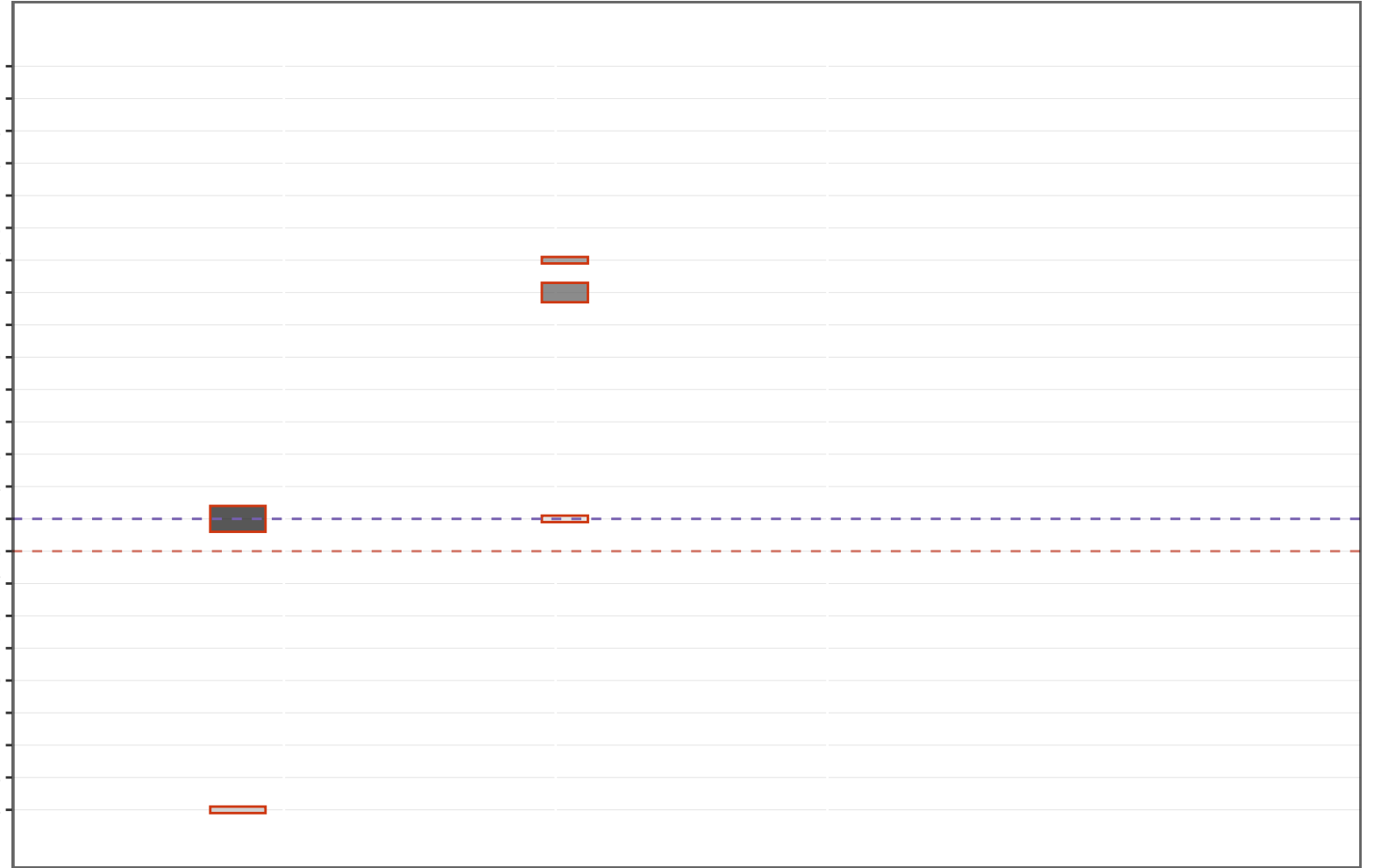
MW indication



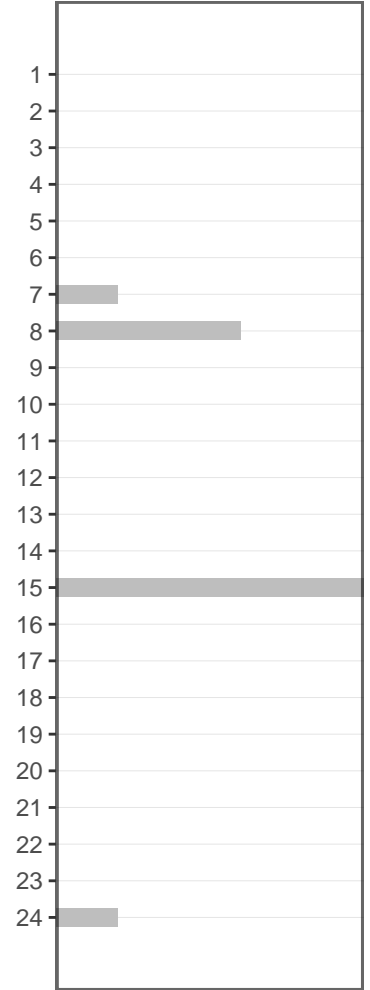
Molecular weight



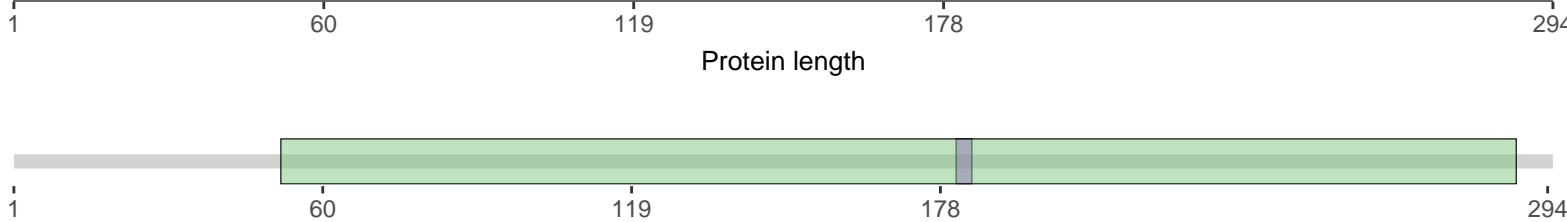
Gel Slice



Protein length

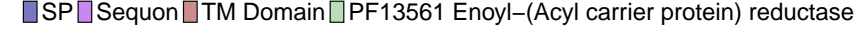


Peptide counts over 4 repeats



Pfam domains

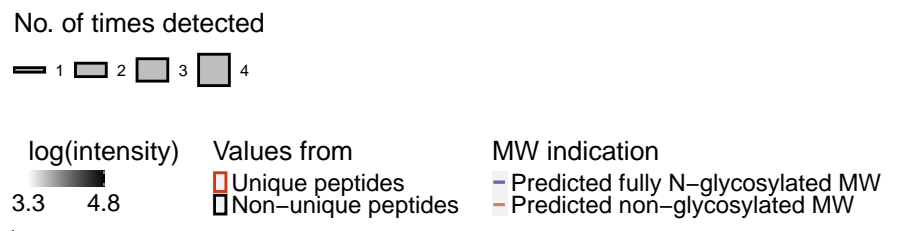
Pfam Description



Protein sequence:

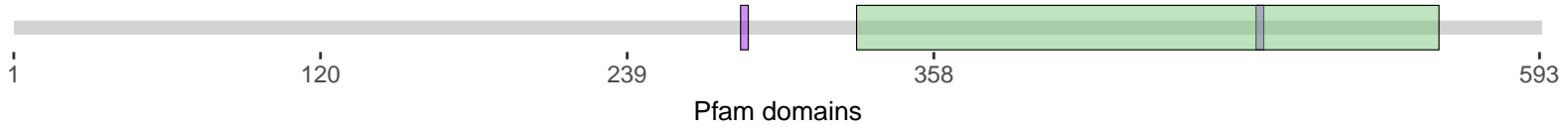
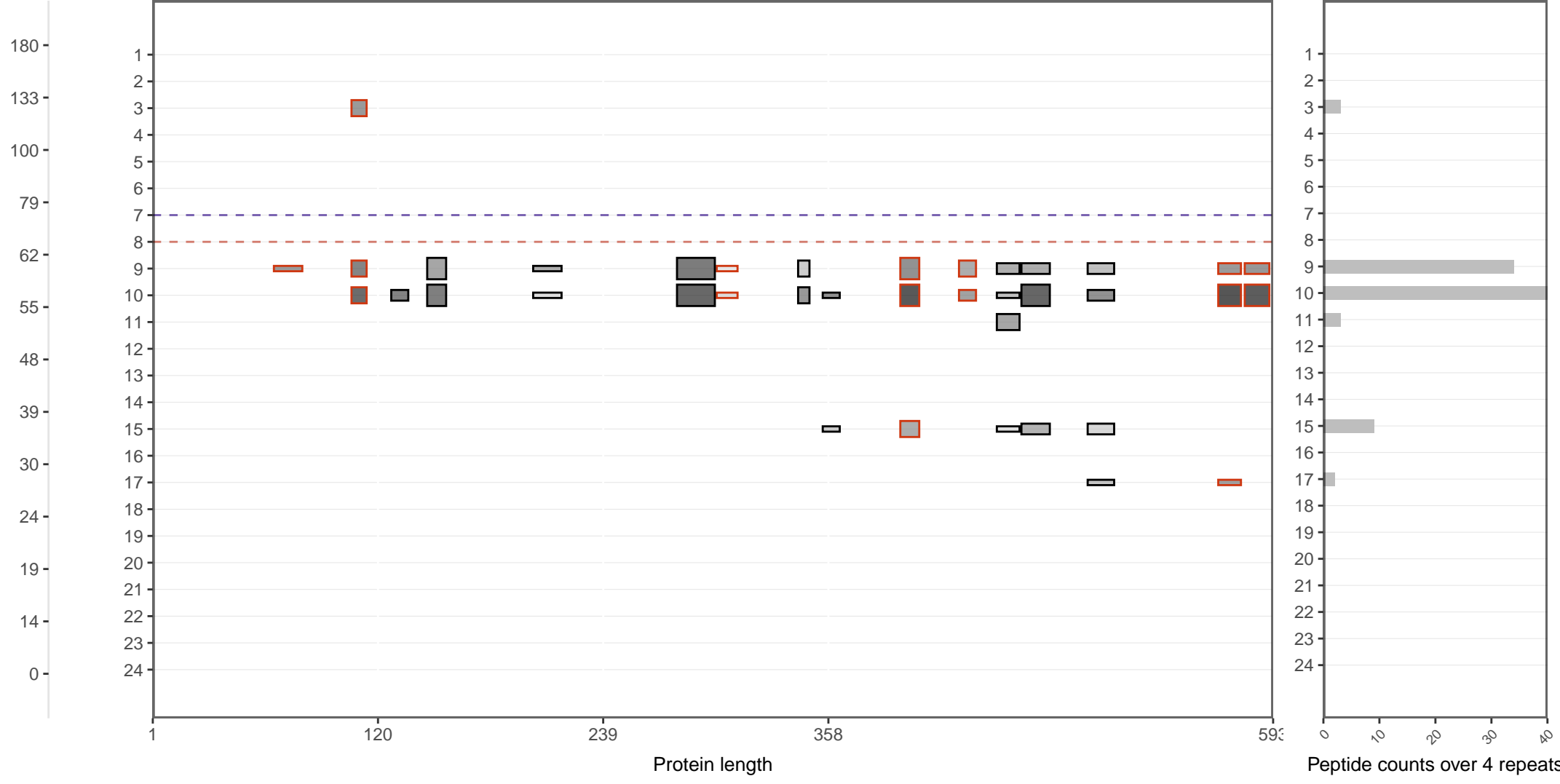
VNNAAEQYATSVSEINEERLERVFRFTNFDFYFVTRHAKHMKEGSSINTTSVYAYKGNAKLLDYATKGANVAFTRGLALGLVERGRVNGVAPGRHWTLPIPAFTFEEGANFGKQVPMKRAGQREVAPSIVFLASSPSSVYSGQVHPNGGTVA*

NbL01g10140.1 branched-chain-amino-acid_aminotransferase-like_protein_1 [MW = 66.4 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF01063 Amino-transferase class IV

Protein sequence:

ISTLPHSLPVPANNEKLLWVGGDEVRETAKVSVFDSVVOGGDAWVEGLRVYGGKLFKLEEHLDRLFDSAKALAFSNVPTREEVKEAIFKTLITNGMFDNAHRIKTLTRGKKVTSGMSPSFNRYGGTLVLAEWKPPVYDNEKGMVLTATRRNPNKLDKHHNNLLNLLKIEGNAAGADDAWMLDKDGYVSETNATNLFVKKKGRVYTPHADYGLPGITRATVMEVLNENFVLEERRILSEFTADEVWTTGTMGELSPVAKIDGRHGDGRVGPITOTLQNAVYKLA

NbL01g10120.1 GDSL_esterase/lipase_At1g54790 [MW - SP = 42.82 kDa]

No. of times detected



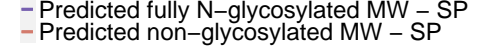
log(intensity)



Values from



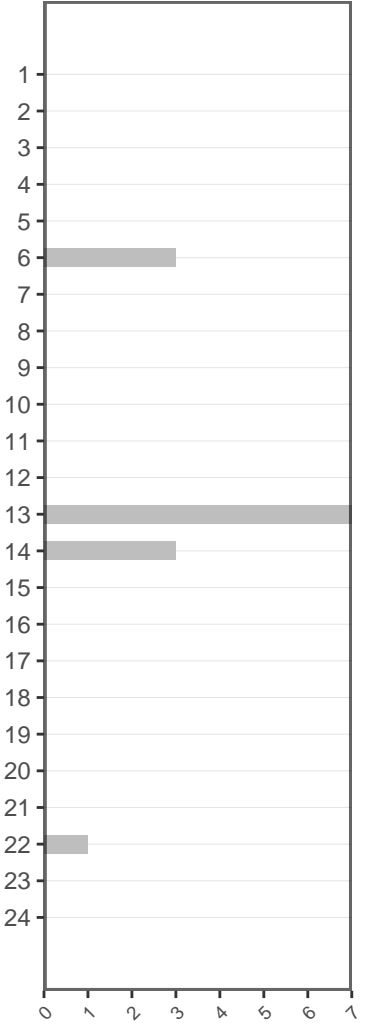
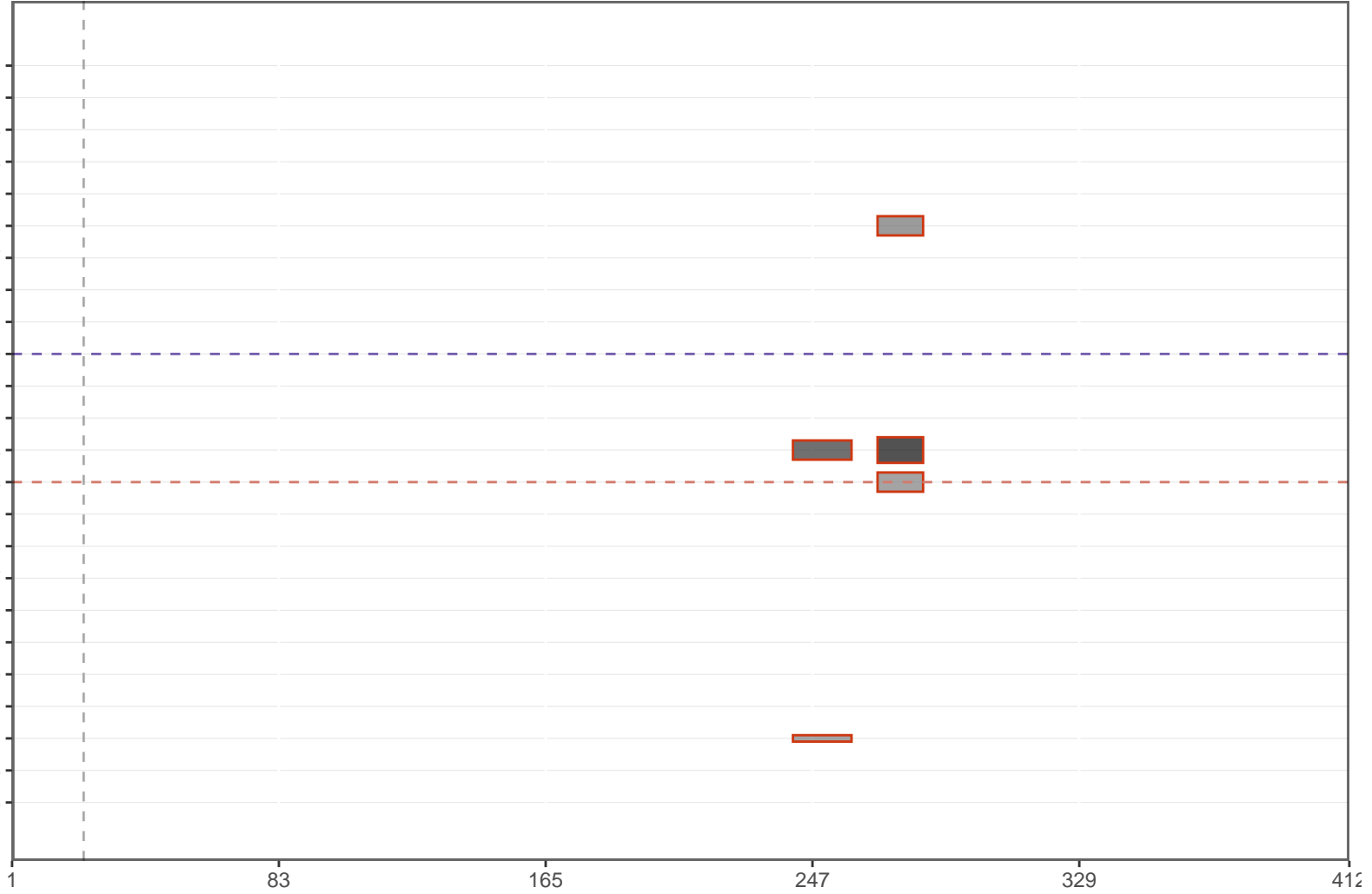
MW indication



Molecular weight



Gel Slice

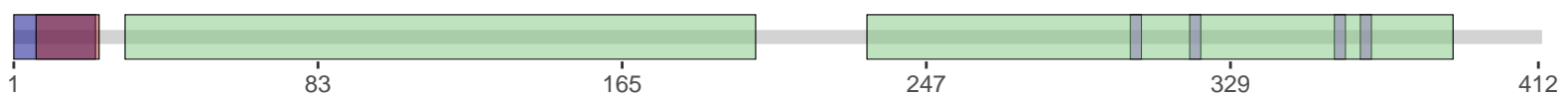


Protein length

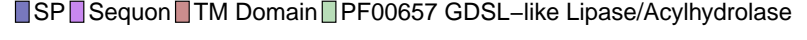


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

VFEDGVYKSNRRLGRTPVVIKRSKLVSVFLTSQRVYELGARFNVAHNTGRLGGLGQNAKFGTDSKLDLGGVSEHNGAAKILNLGVALCKKLGSGVADANTHVDFTKSNLIANYRYGFEGPLMAGDGYGGPPLNVDNRVADGLTKVHDGNNVTAKANDSSEYINWDGHHYTETANGFVASGLTKYSDPPFDKMPFLKLPK

NbL01g10080.1 glutathione_synthetase_chloroplastic [MW = 64.25 kDa]

No. of times detected



log(intensity)



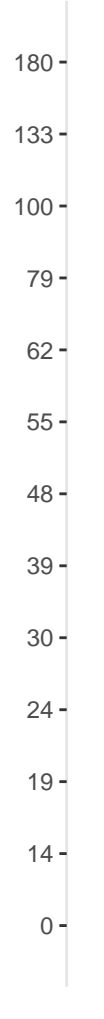
Values from



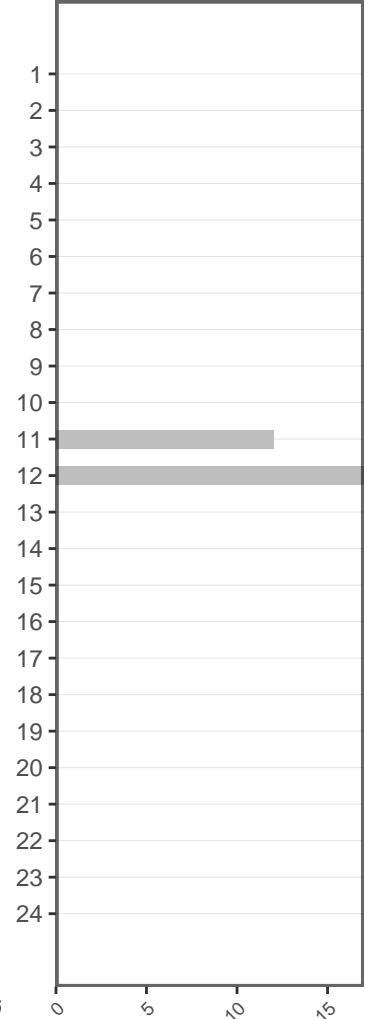
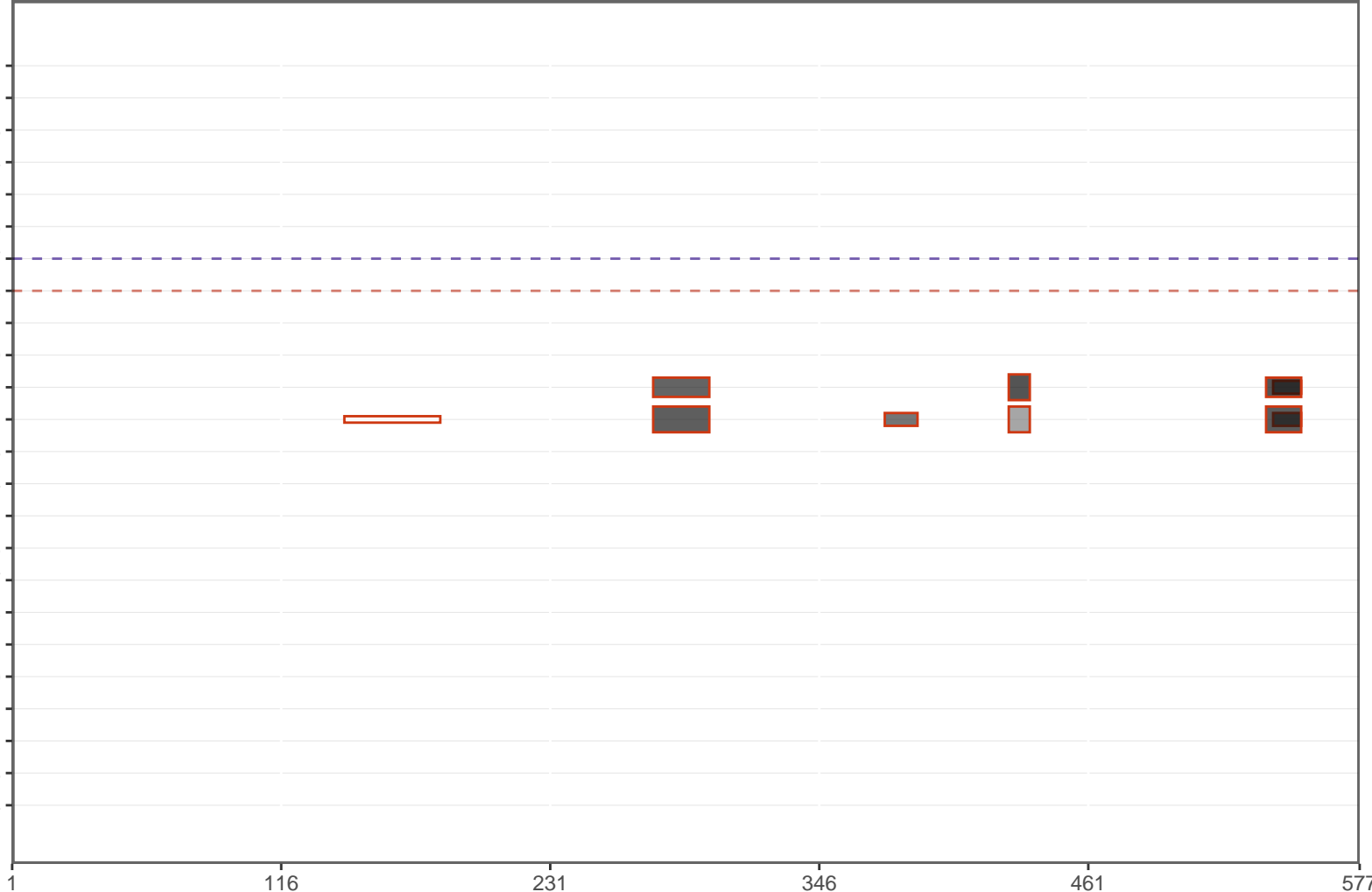
MW indication



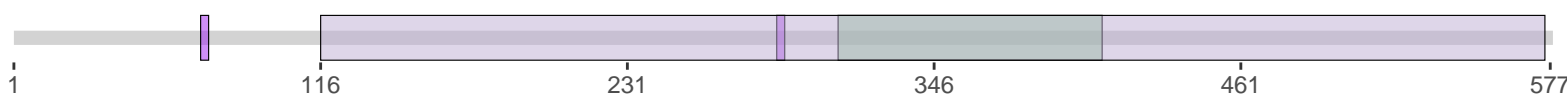
Molecular weight



Gel Slice

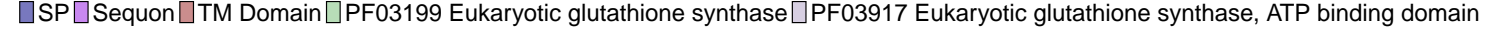


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CIALDPKIPNTNSVNGFADALAKAWNEYGDPRVAVMFVYGAEEERNMVDQHWLSASLGEKHQVTTTRKTLAEIDAGDELLEDGTLVVDGEAWVNYFRAGYAPSDVHSESEWKAARLLMEQSRVAKGSPSISYHLAGTKKIGGELAKPNVLERFLENKDDVAKLKRKGFAGLWLSDESDTVKDAERPVLVVMKPKRQEGGNNYGEDKKEALLKLGKEGTGSDAFILMQRIFPTVSHSLMREGIPHKEGTISELGYGYTLRNEKEVLNGQSGYLMRTKVSSNEGGVAGFA

NbL01g10030.1 broad-range_acid_phosphatase_DET1-like [MW = 34.49 kDa]

No. of times detected



log(intensity)



Values from



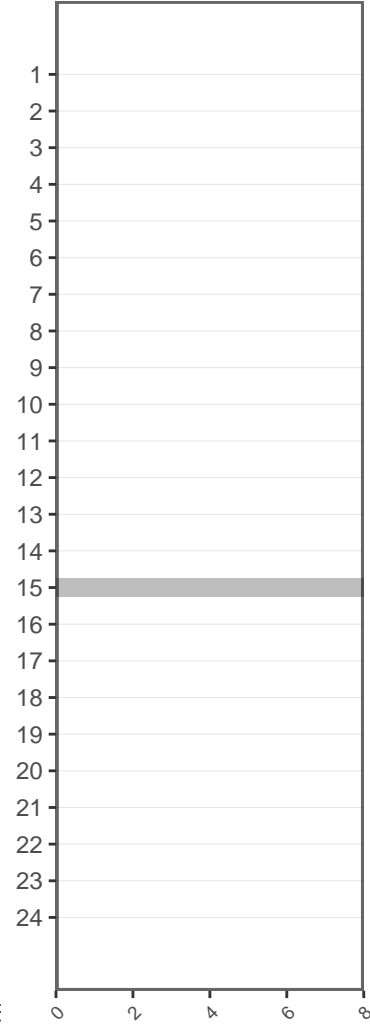
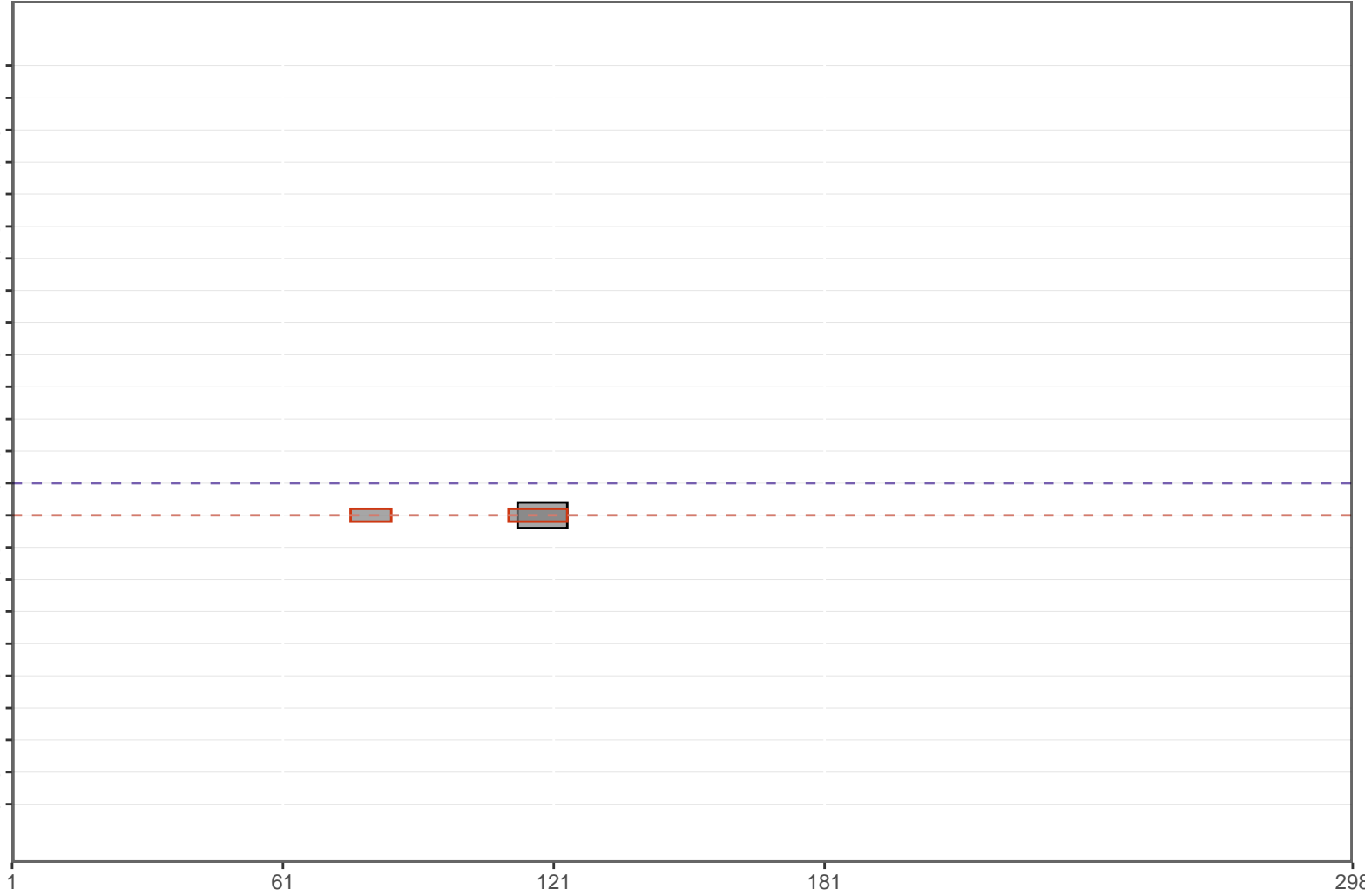
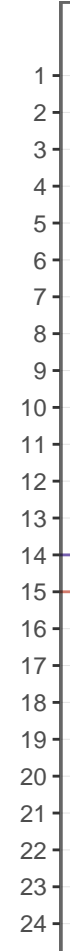
MW indication



Molecular weight

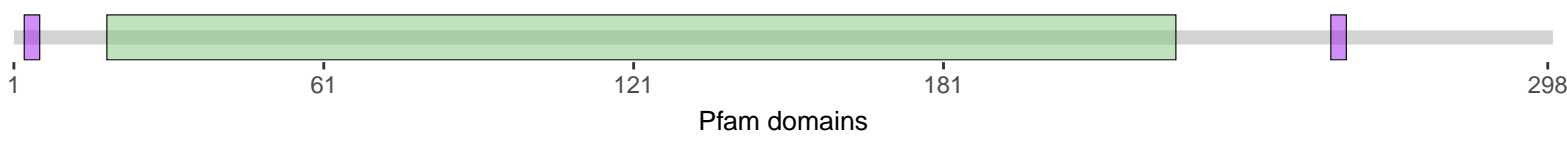


Gel Slice

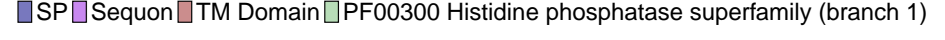


Protein length

Peptide counts over 4 repeats



Pfam Description



Protein sequence:

FYRFPFGESADVDRVSHFLESLWRDVMNRHHDPNDELNLVISHGLASRFLMKWFKWTFVGFYLNLLNGEFRVMELGAGGEVSLAVHSHDEEMLEWGLPEMIADQKWRANAARIGSLNDHGPTFLDAFFDHLTDSNDEDEGDKGNLGLP

NbL01g09900.1 4-hydroxy-tetrahydrodipicolinate_reductase_1_chloroplast-like [MW = 36.26 kDa]

No. of times detected



log(intensity)



Values from



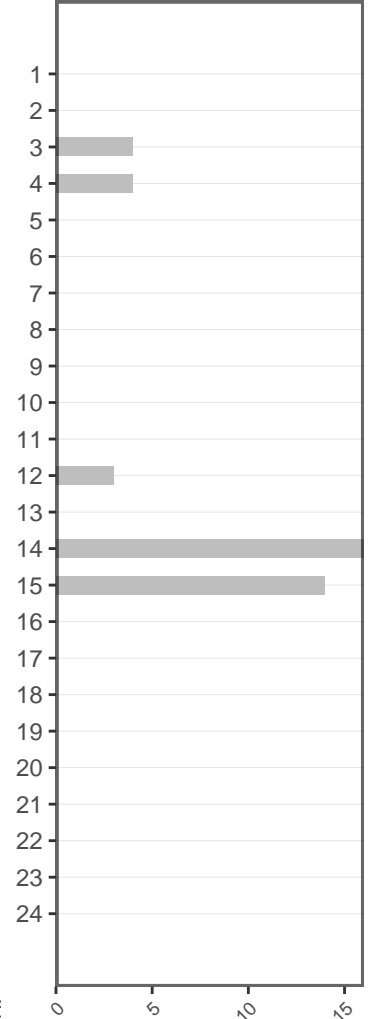
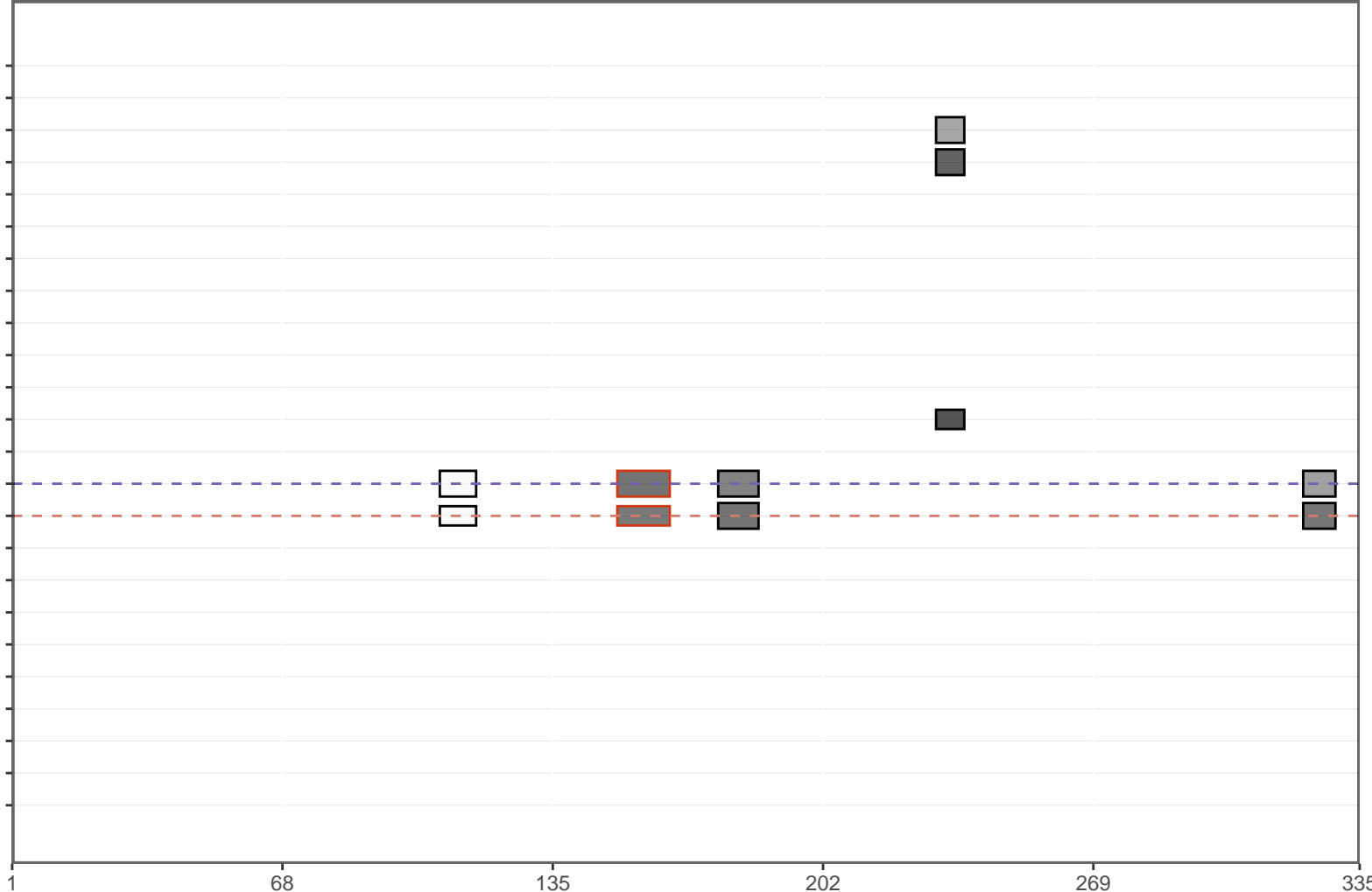
MW indication



Molecular weight

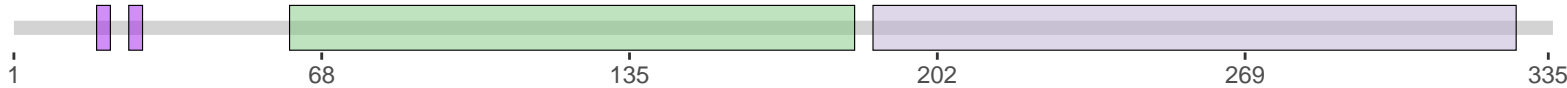


Gel Slice



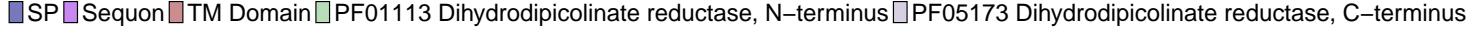
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VMGTTGGDREKLYKTVADSKVYAVISPMGKGVVAFLAAMEIMAEQFPGAFSGYTLQVMEHQASKLDTGGTAKAVISGFQKLGVSFDLDEVLKRPDKGVEMVGVPEEHLLGHAFHMHVHTSPDGSVSEFEFGHNVQGRSHVAGETVDAILFLAKVKLKEEKRIYDMIDLREGNMR

NbL01g09760.1 translation_initiation_factor_eIF-2B_subunit_epsilon [MW = 81.99 kDa]

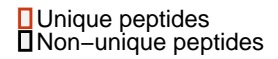
No. of times detected



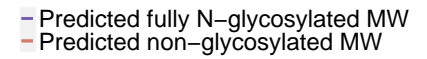
log(intensity)



Values from



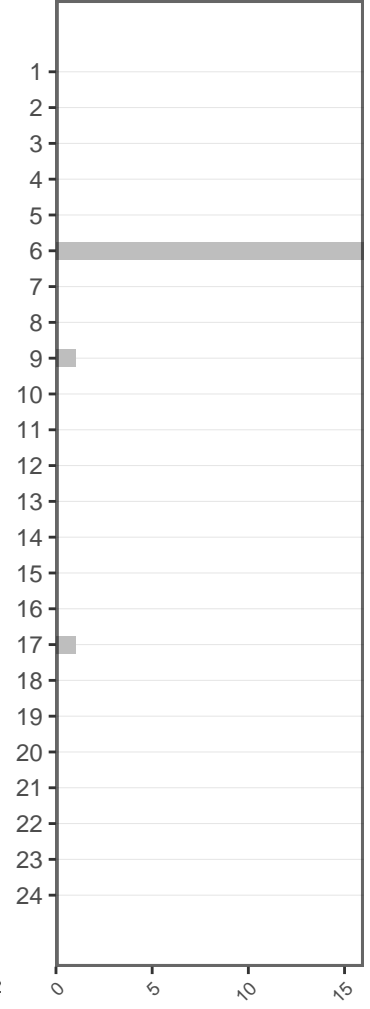
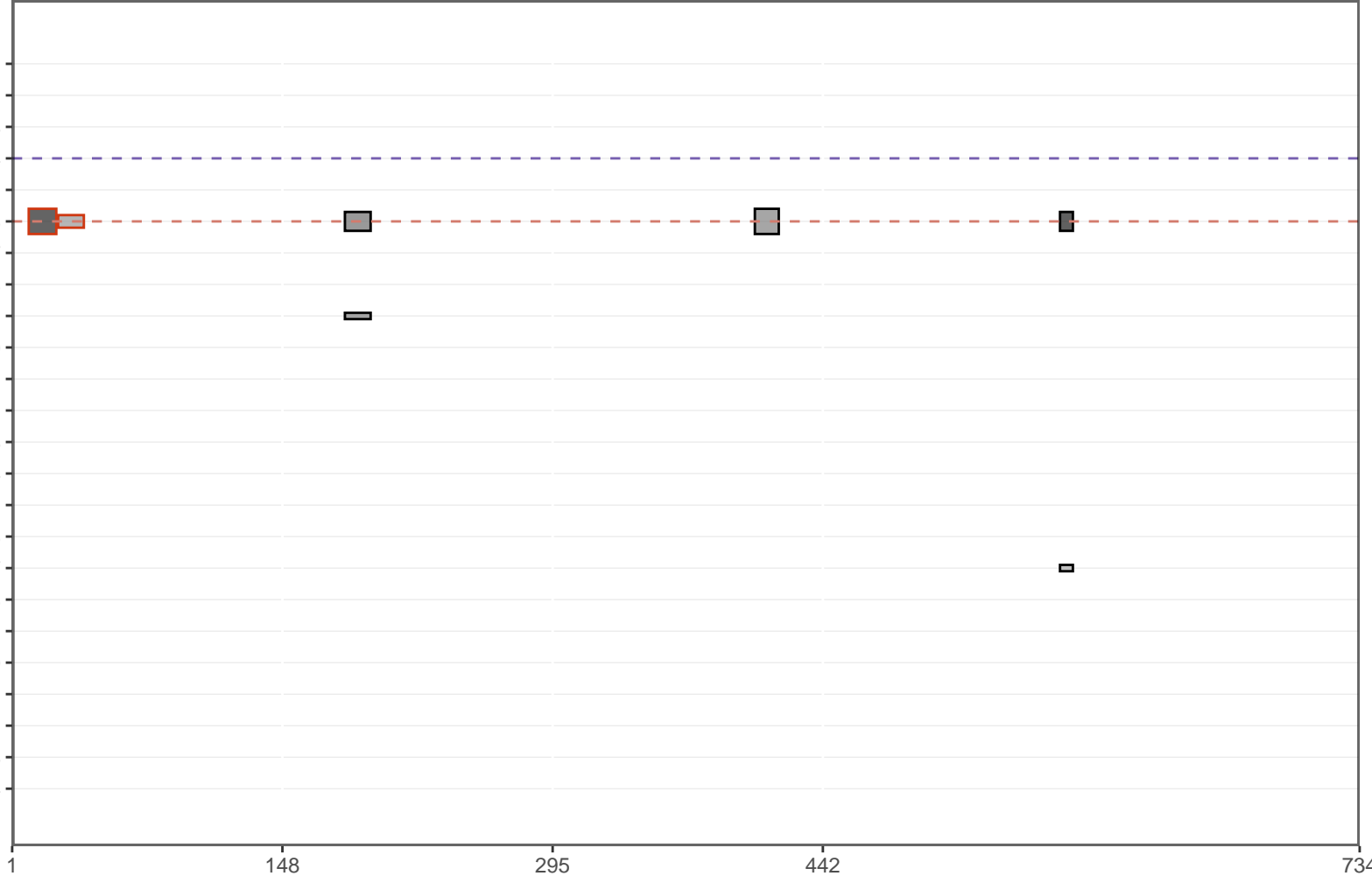
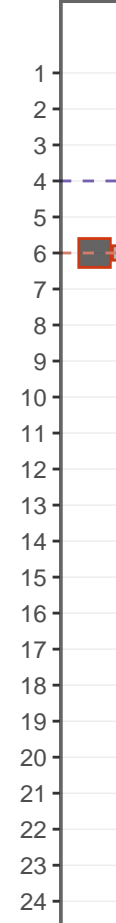
MW indication



Molecular weight

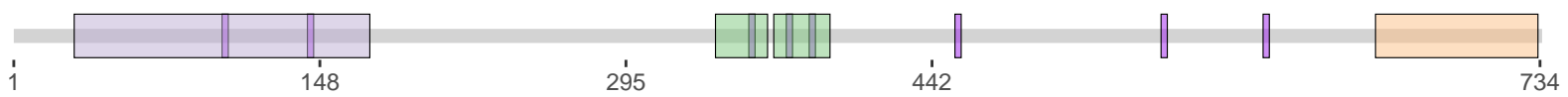


Gel Slice



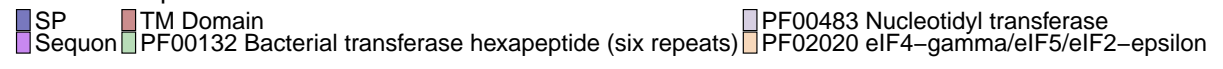
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

INTEISNIVGEGGGSGSNVTEGGYWHNVTEEDGCKLHSIVDGGVTMKGGAALEPQVLSFRVYVGRNPLVPAYSKVSFLGGPKQDSDEELLEVDNNSGGITSPSSGDTLDELNEEERTELAESGQYEYVDGGVGFVLISEGGGQEEWRHSVAPIPVQKLVGMQITNDEADSNEDGTFLLPSPGELGPDITNDSNEDGEDTRDDSVIFEREVEATFORAVEEVEVTEHIVLELVNLRISVNYMTSADGAGALFYVMKALDAPHDSPIELVNNVATAVKKVKKLKYLYI

NbL01g09670.1 translation_initiation_factor_IF-2-like [MW = 62.24 kDa]

No. of times detected



log(intensity)



Values from



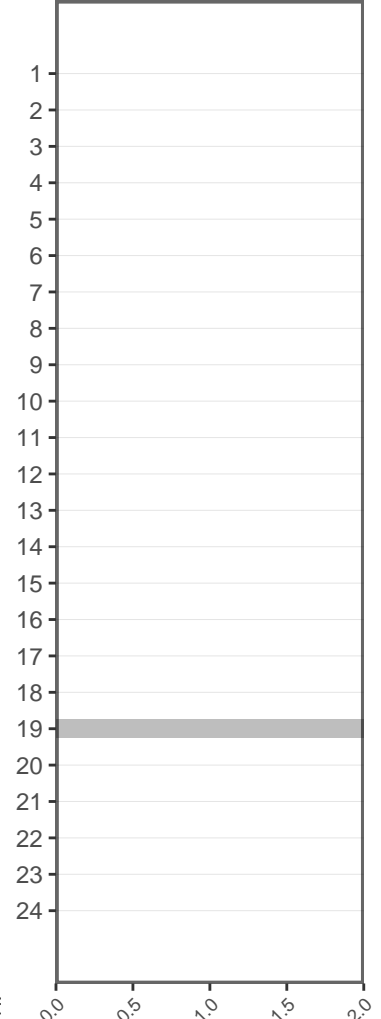
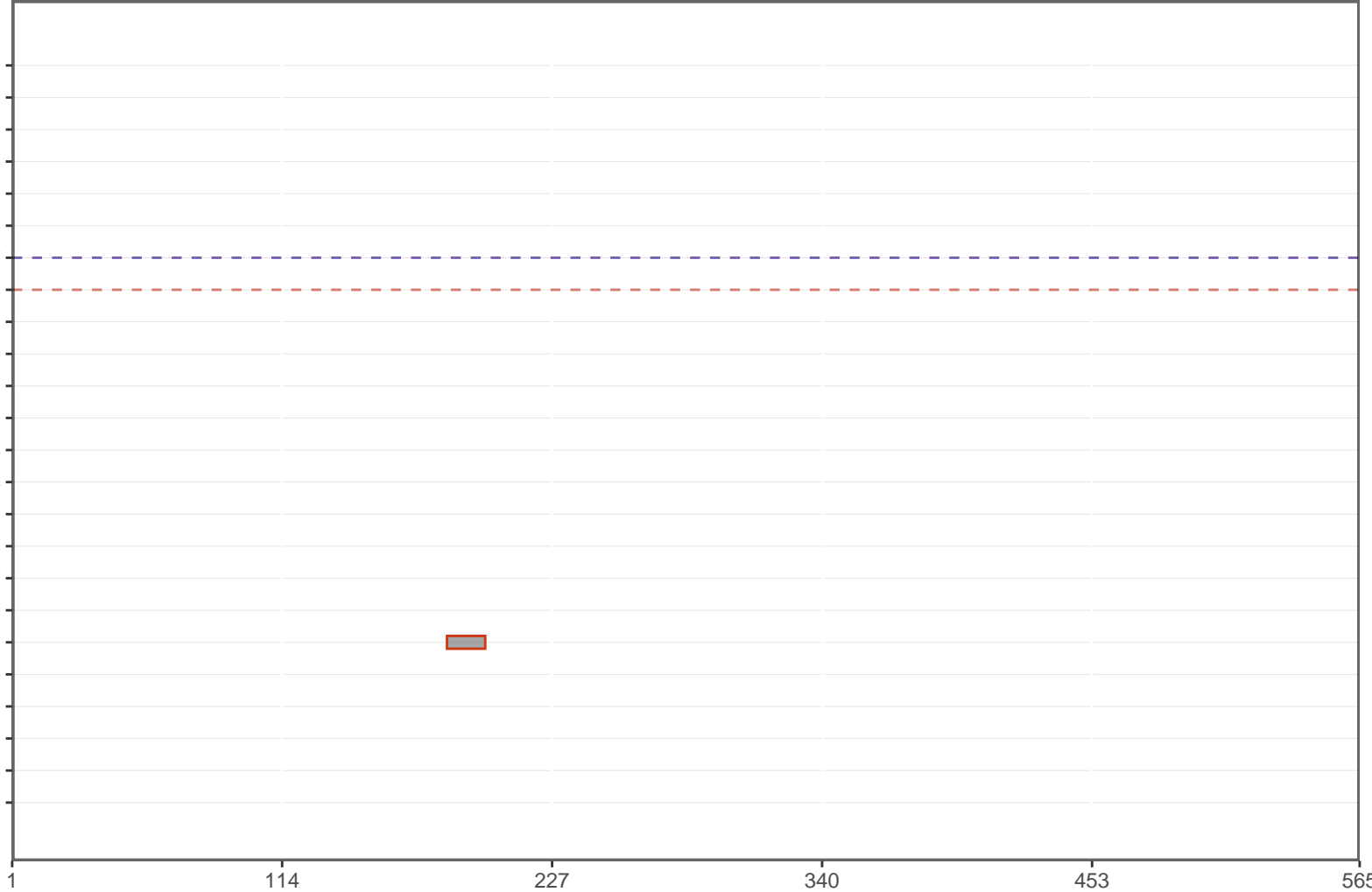
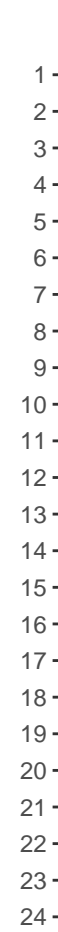
MW indication



Molecular weight



Gel Slice



Protein length

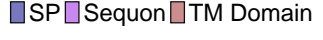


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

IKKAVQLSRHSDDGGGGGGGGGRGVGFRGGRGGRGAMGRGRGRGRGRGRGRGVRRDENEDDLESDFVLGDNADGEMANKLGFETMNTLAEAFEGEMASRVLSPFMDDAVEALHTNMMCEPEVLMGDFESNPDIKPPISLRDALEKMKPFLMAVEGKDGDEWEKVEETMETVPLMKKEVDVYSGPDRVTAKGGQDELERAKTTPQSAPNPKRFEHAWLSLQVYVQLVCFNSLSLRMKKQVETSEFFELDIANWKNERHLSH1KRXEKLTYTR

NbL01g09660.1 uncharacterized_N-acetyltransferase_p20-like [MW = 19.37 kDa]

No. of times detected



log(intensity)



Values from



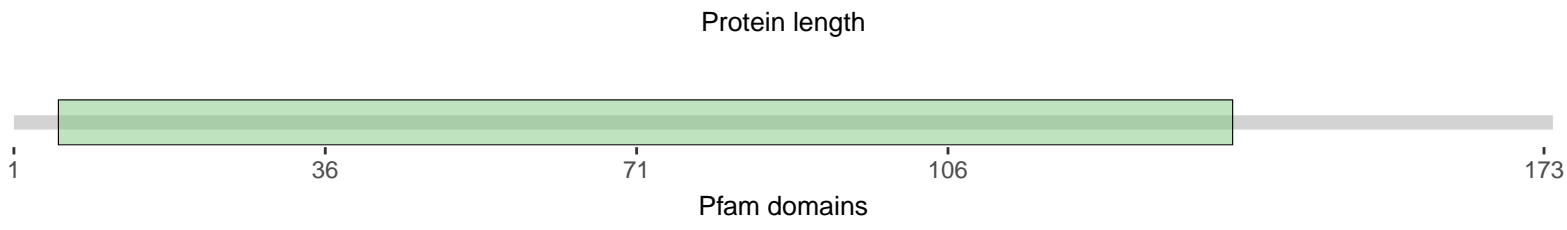
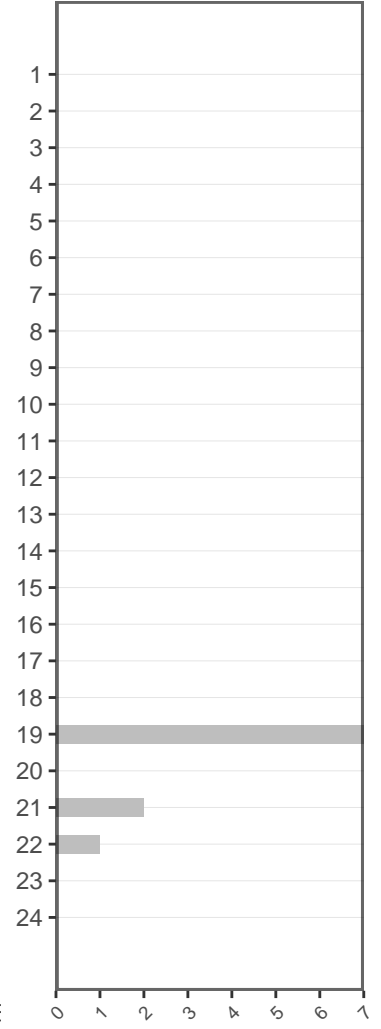
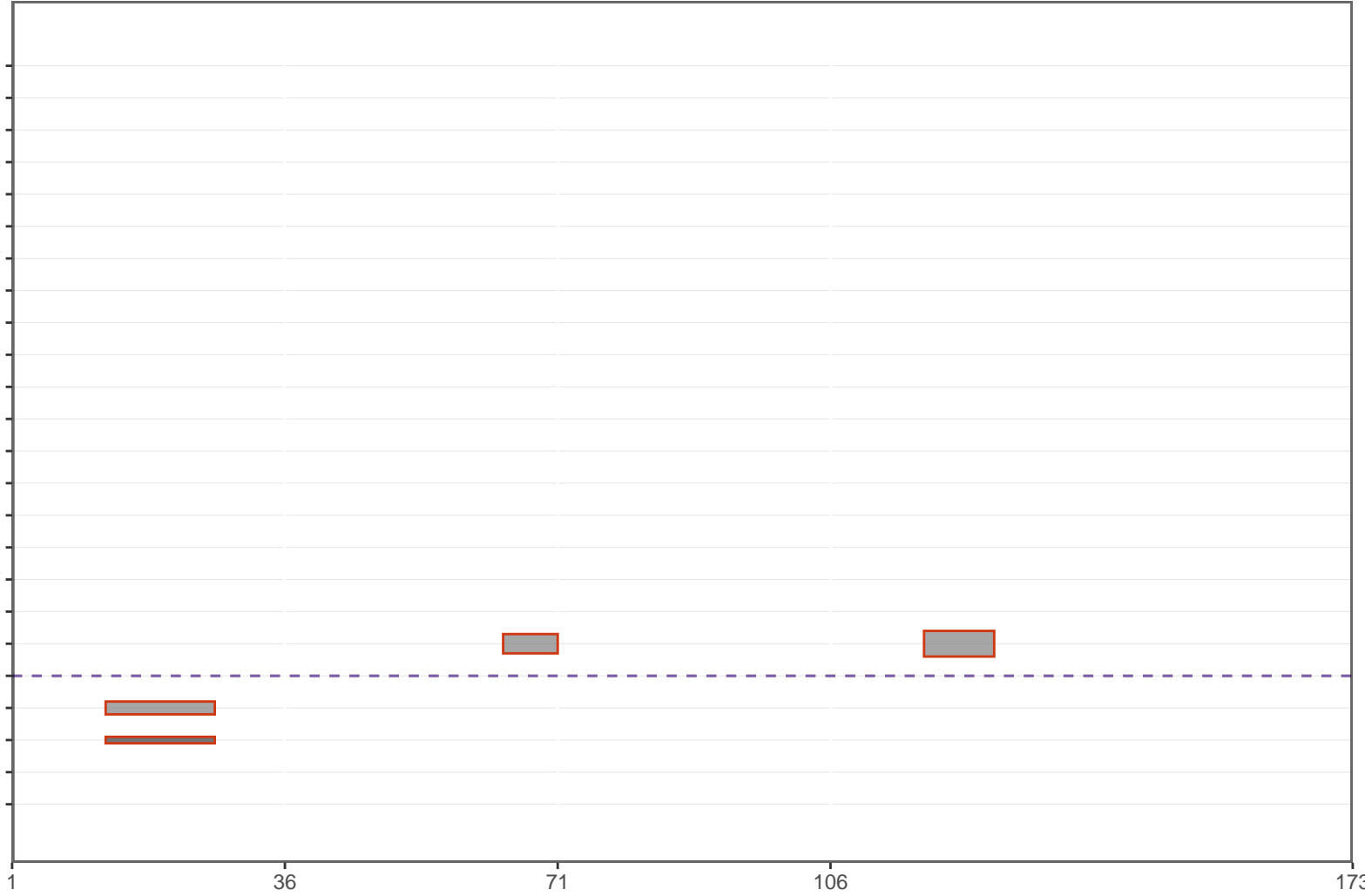
MW indication



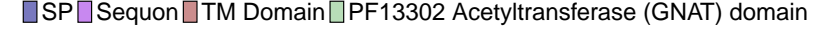
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

SDDKCRAEIGYLAAEYWGQGITPKAKMAMPLIFSDPEVRLGALSDANNRASHRVLEKAGFYKMGFRKYYFKGKDKVLYGLLSTDPHLHP

NbL01g09640.1 deoxyuridine_5'-triphosphate_nucleotidohydrolase-like [MW = 18.36 kDa]

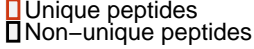
No. of times detected



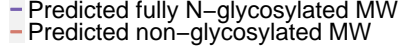
log(intensity)



Values from

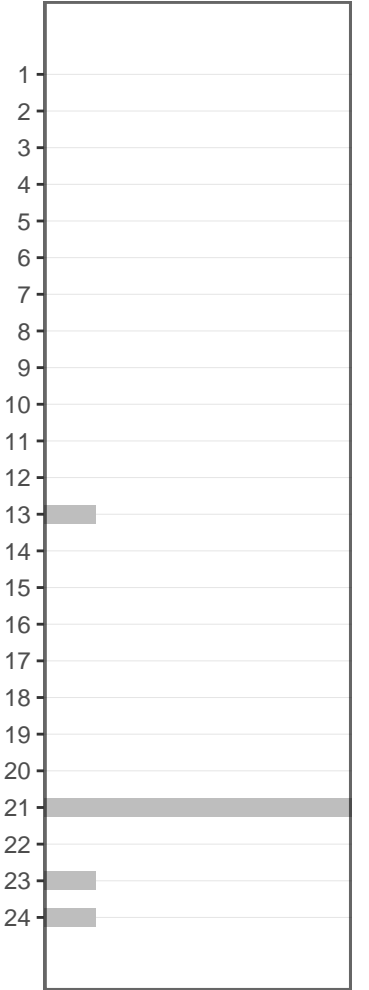
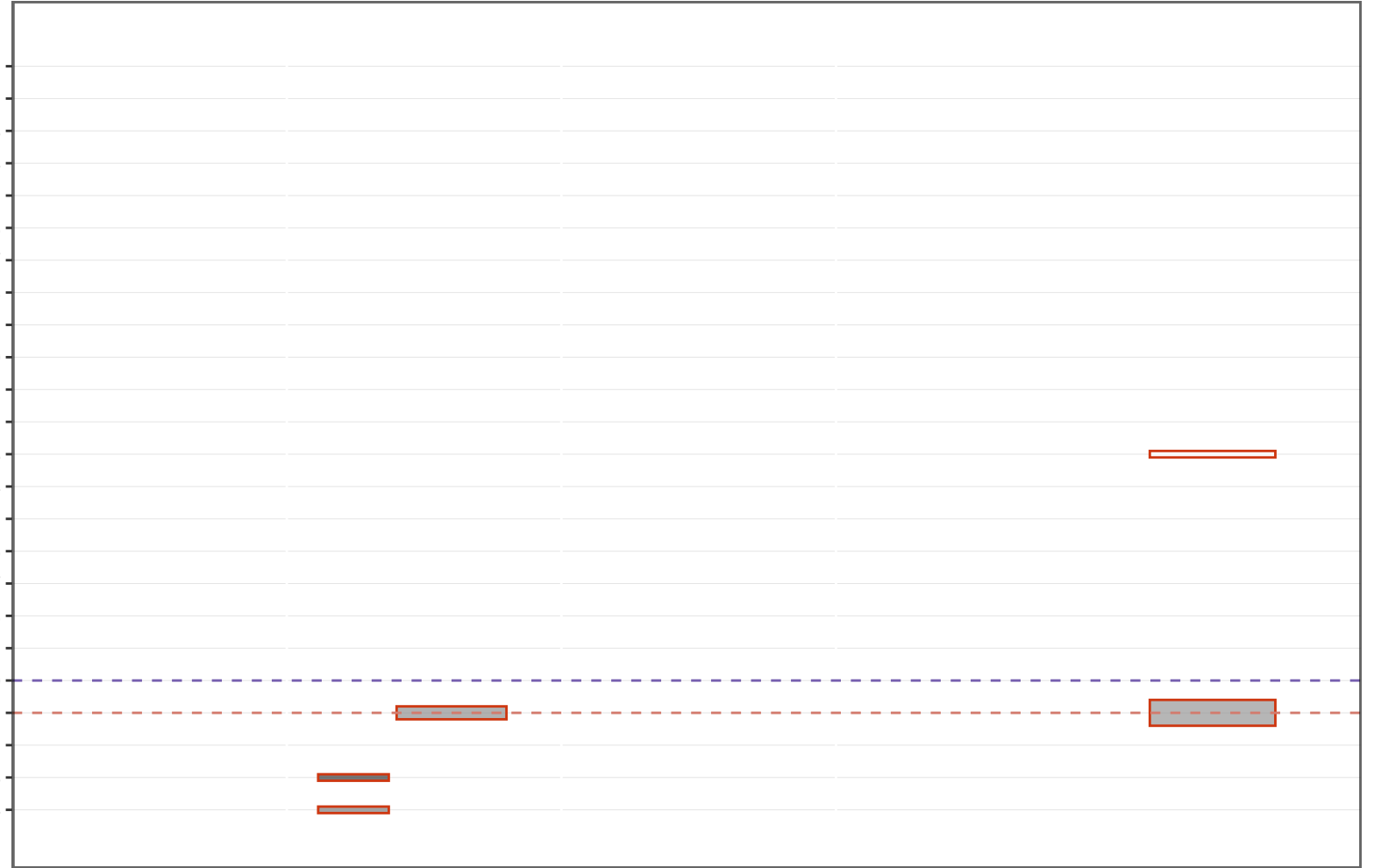


MW indication



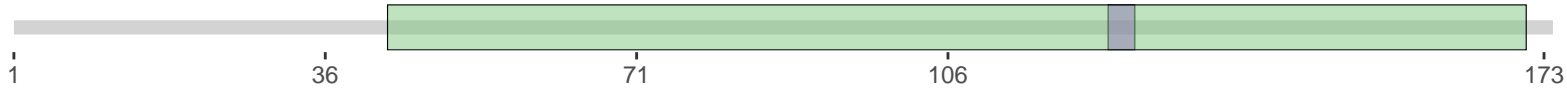
Molecular weight

Gel Slice



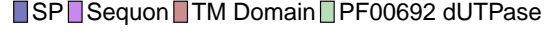
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CAVPTDLSIAVPEGFVAPAPRGLTWHSDVAGAGVIDADYRGRPGVILFNHSDVDFEVKGDRIAGLIEKINIPDVEEVDLSTVIRGSGGFGSTGV

NbL01g09630.1 cysteine_synthase-like [MW = 34.57 kDa]

No. of times detected



log(intensity)



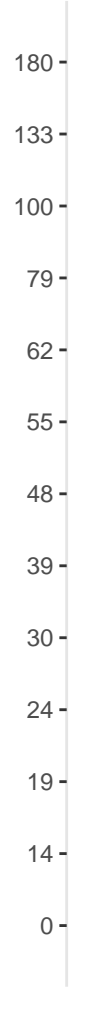
Values from



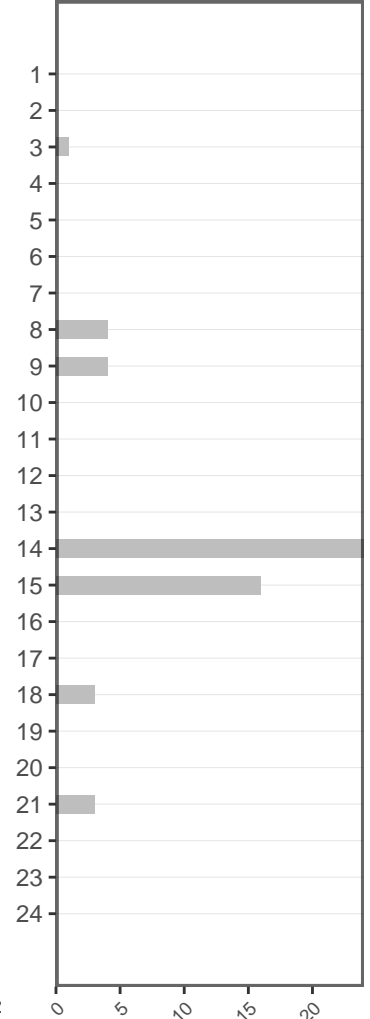
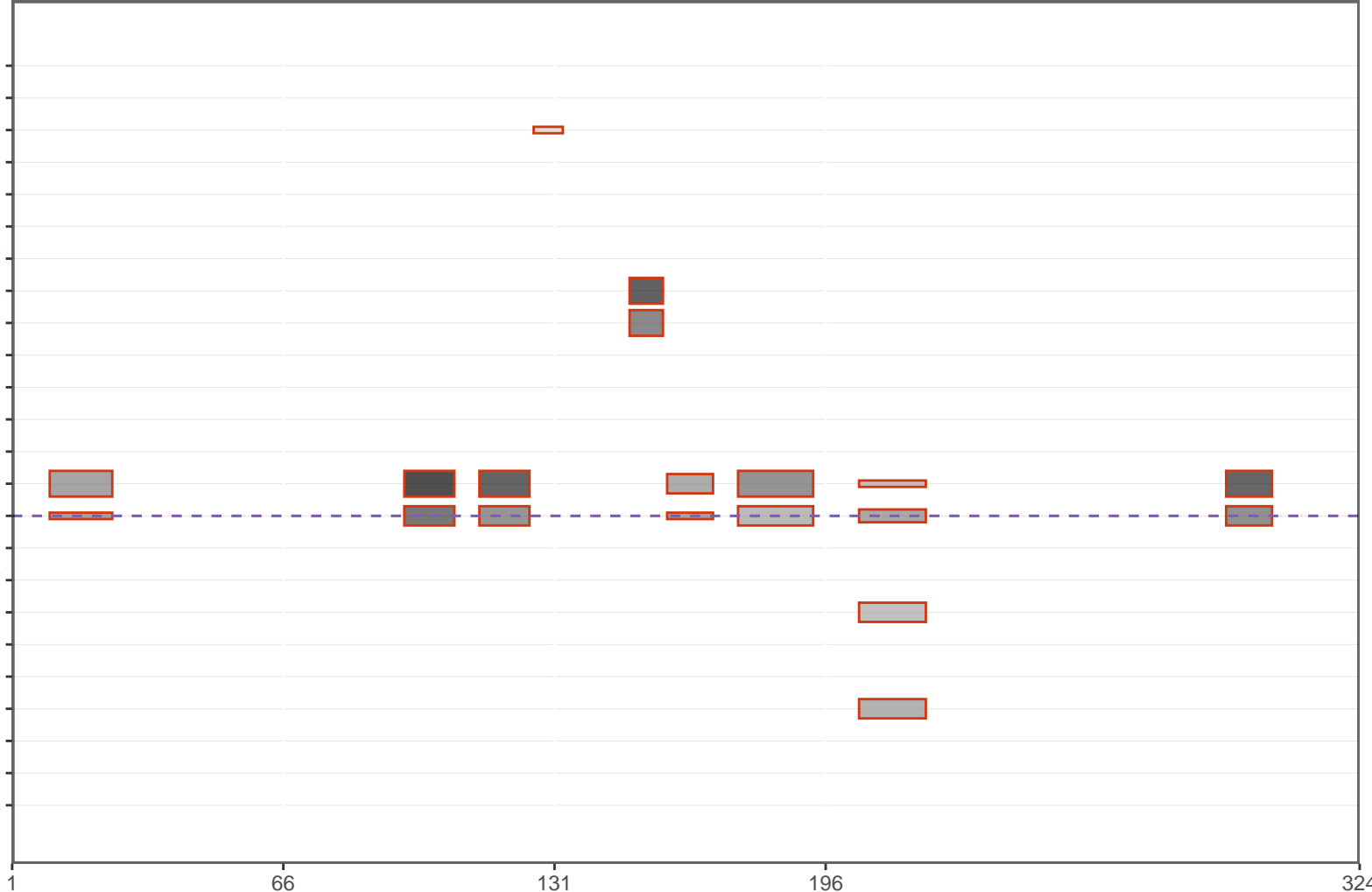
MW indication



Molecular weight

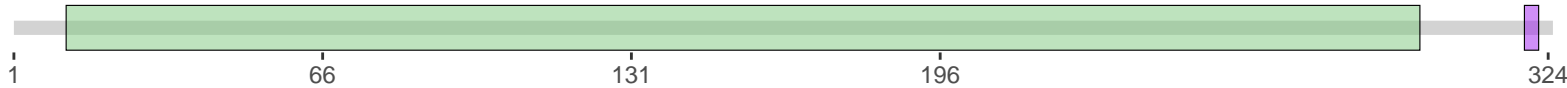


Gel Slice



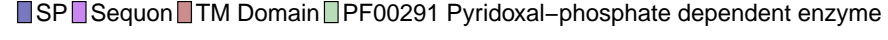
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

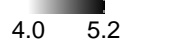
JFENPANPKIHYETGTGPEWIKSTGGKVDIFAGIGTGGTGTGAGRFLKEKPFEMKVIYGIPTENALLNGGKGPHKIGIGAGFVPLVLDLDELVLQVSSDEAIEMTKLLAWKEGLLVGISGAAAAAIVKAVKPKENAGKLVIFPSPGERYLSTVLFDSIRIEEVENMTFE

NbL01g09600.1 guanine_deaminase-like [MW = 20.33 kDa]

No. of times detected



log(intensity)



Values from

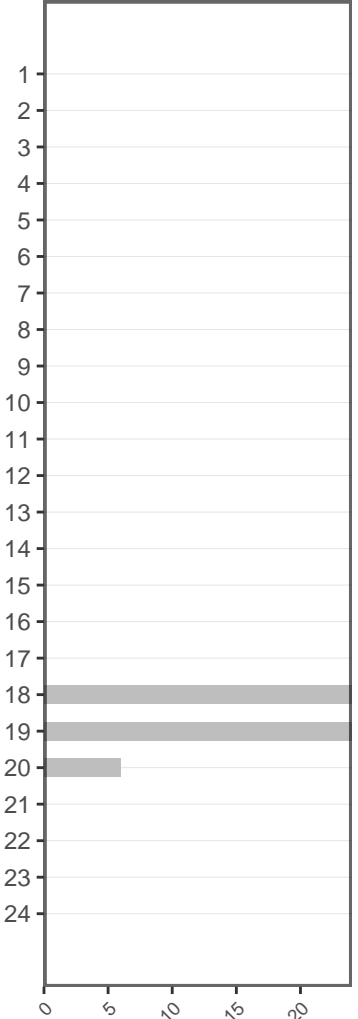
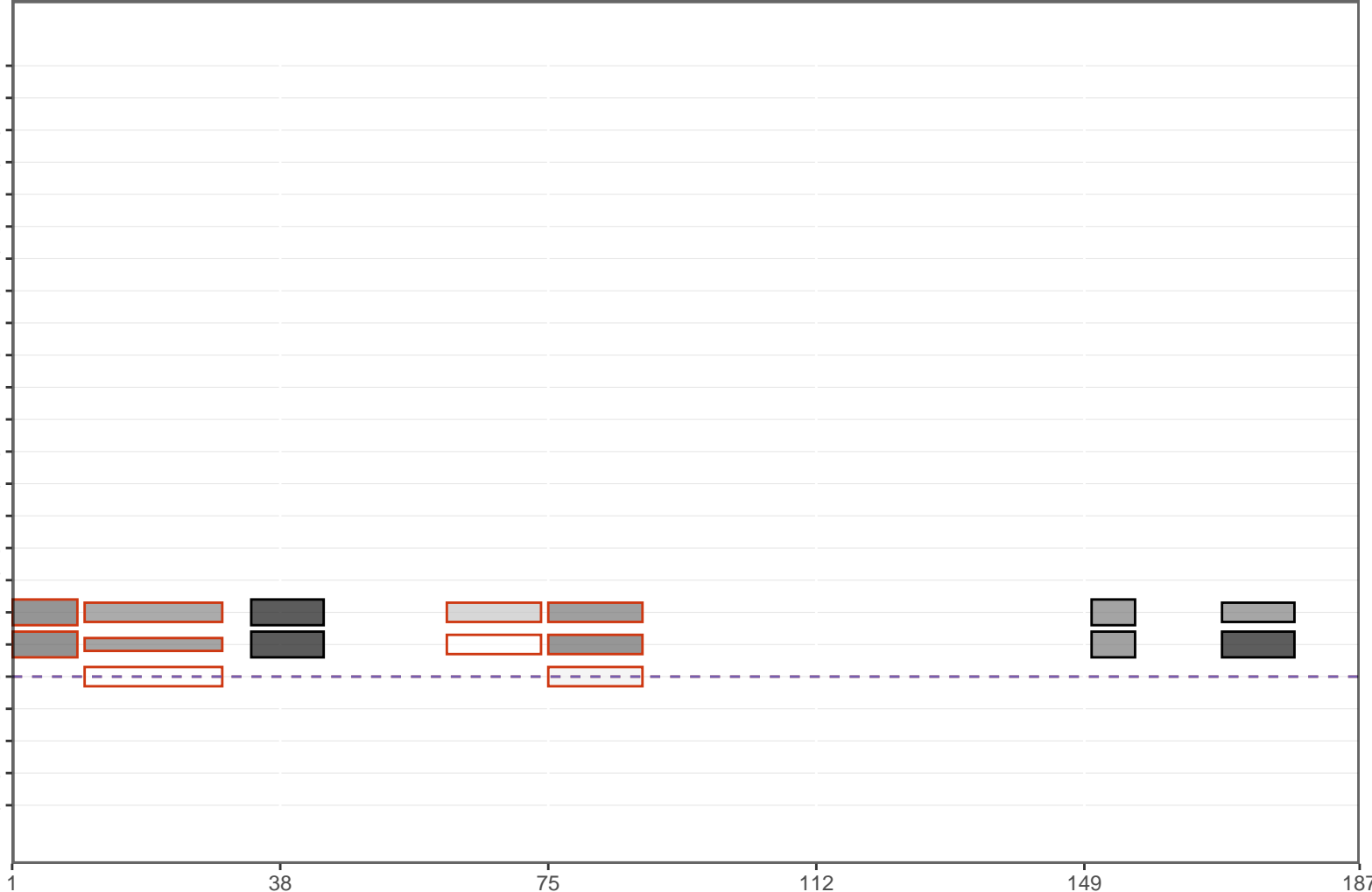
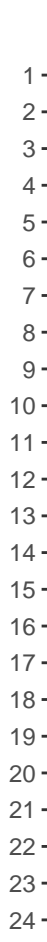
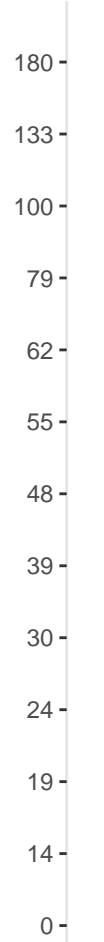


MW indication



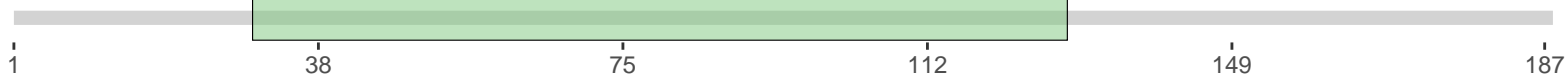
Molecular weight

Gel Slice



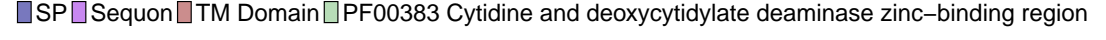
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

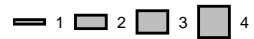


Protein sequence:

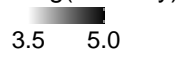
PTAHAEVTAVREAGKRLNRFELSDGEHVASCEPQPMFGAHLRSRIKRLVYGAKAEAAIAGFDIADALRGTFYKQAKLEIKKADGKALAEQVFEKTKKFTYV

NbL01g09550.1 nudix_hydrolase_20_chloroplastic-like [MW = 40.69 kDa]

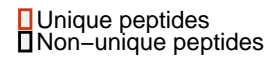
No. of times detected



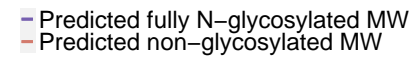
log(intensity)



Values from



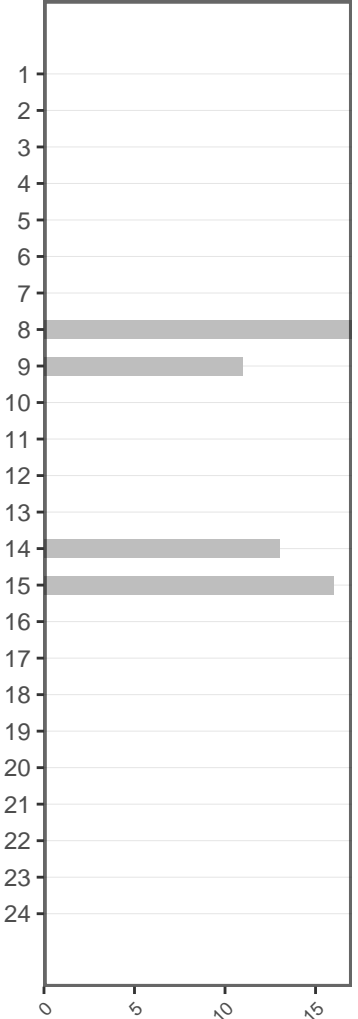
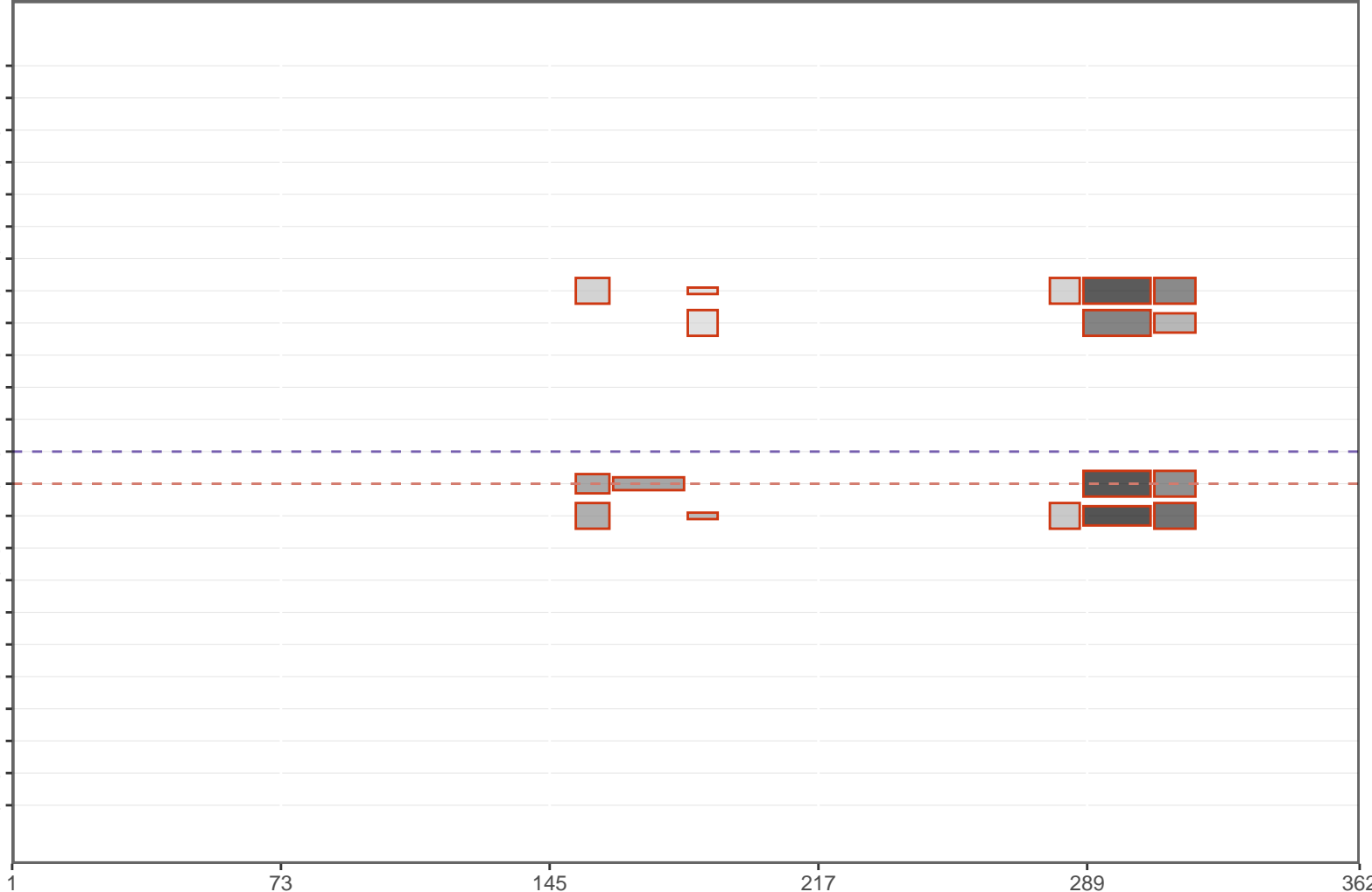
MW indication



Molecular weight

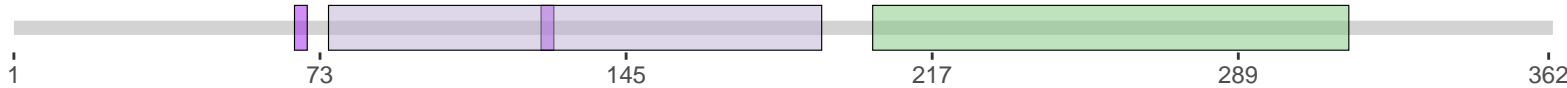


Gel Slice



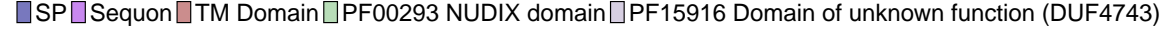
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SAFGEPVFFSLERAAAPYFGIKAVGHMISGVVEKNDQKFLWLAKRSATKSTVPGMLDHLVAGGLPHGISGGENVYKECKEEAGIPRSIRGAVPPGVAVSIDIEGYRMRKRDVLCYDYLKPAEGFVPHNEDGEVESEFRLLVPTQVANVRSASFFKANGNLIHFLFRHGIVRPEEFQYLLRLOSLSKSGGCS

NbL01g09540.1 zeta-carotene_desaturase_chloroplastic/chromoplastic [MW = 59.06 kDa]

No. of times detected



log(intensity)



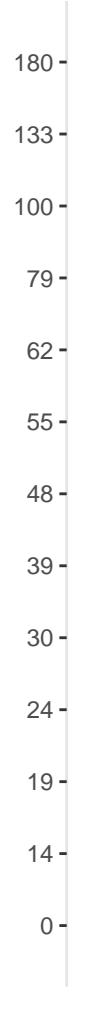
Values from



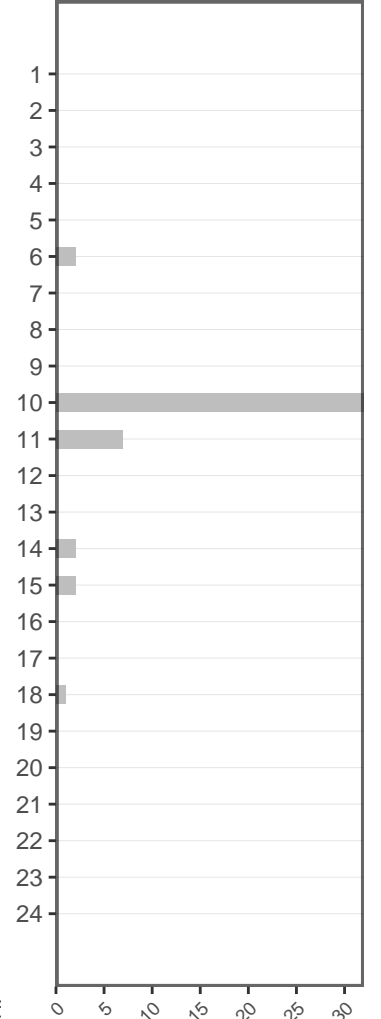
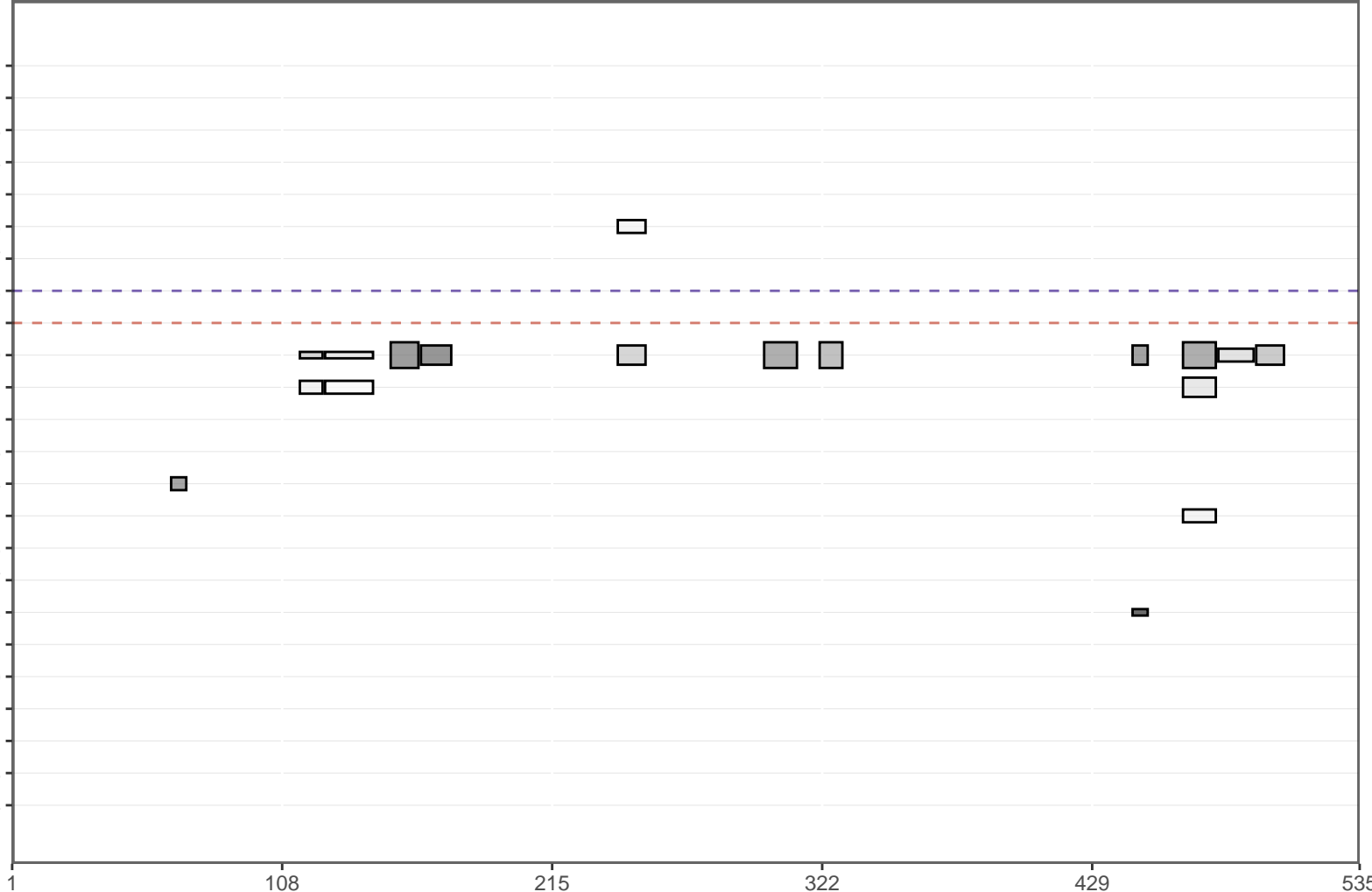
MW indication



Molecular weight



Gel Slice

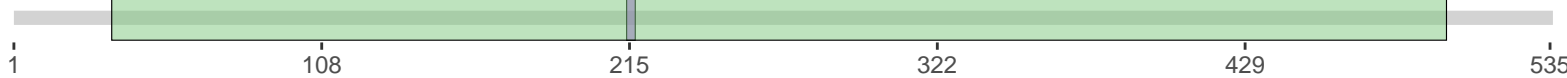


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ILDKGGRFHLRWGGREVLVETSSDGMVYVSGLAMSKATQKVKVADAYVAAGDVPKIKRLVPOKWELEFFDNVYKLVGVVAVVQLRVNNGWDTLQDLERSRQLKRLNLLYTPDAFSGFADLALASPEDYKIEGGSLQGVLTGDDYMPFLNDEIKRVSKGVLSLFRSSGGLEVTWSSVYKIGDGLYREGPKKPRFPDQKTPVENFFLAGSVTKQDHDSDMEGATLGGSGASAVVCDAGENLVALRKKIATAESNEIEDVSVSDELGLV

NbL01g09530.1 phototropin-2-like [MW = 107.8 kDa]

No. of times detected



log(intensity)



Values from



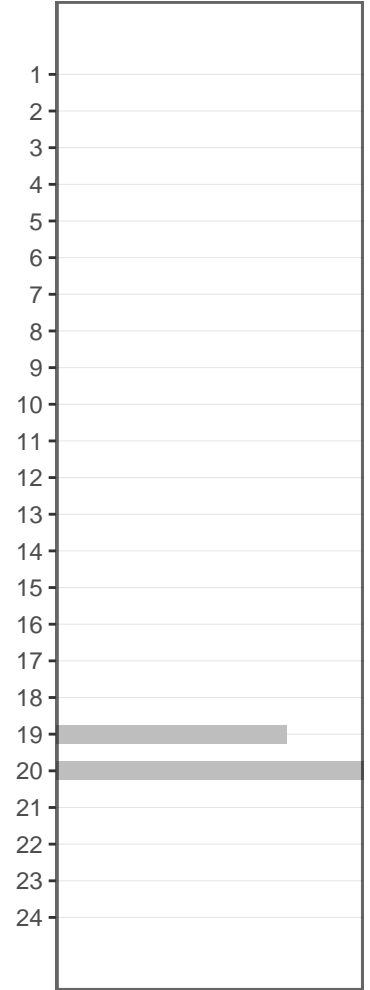
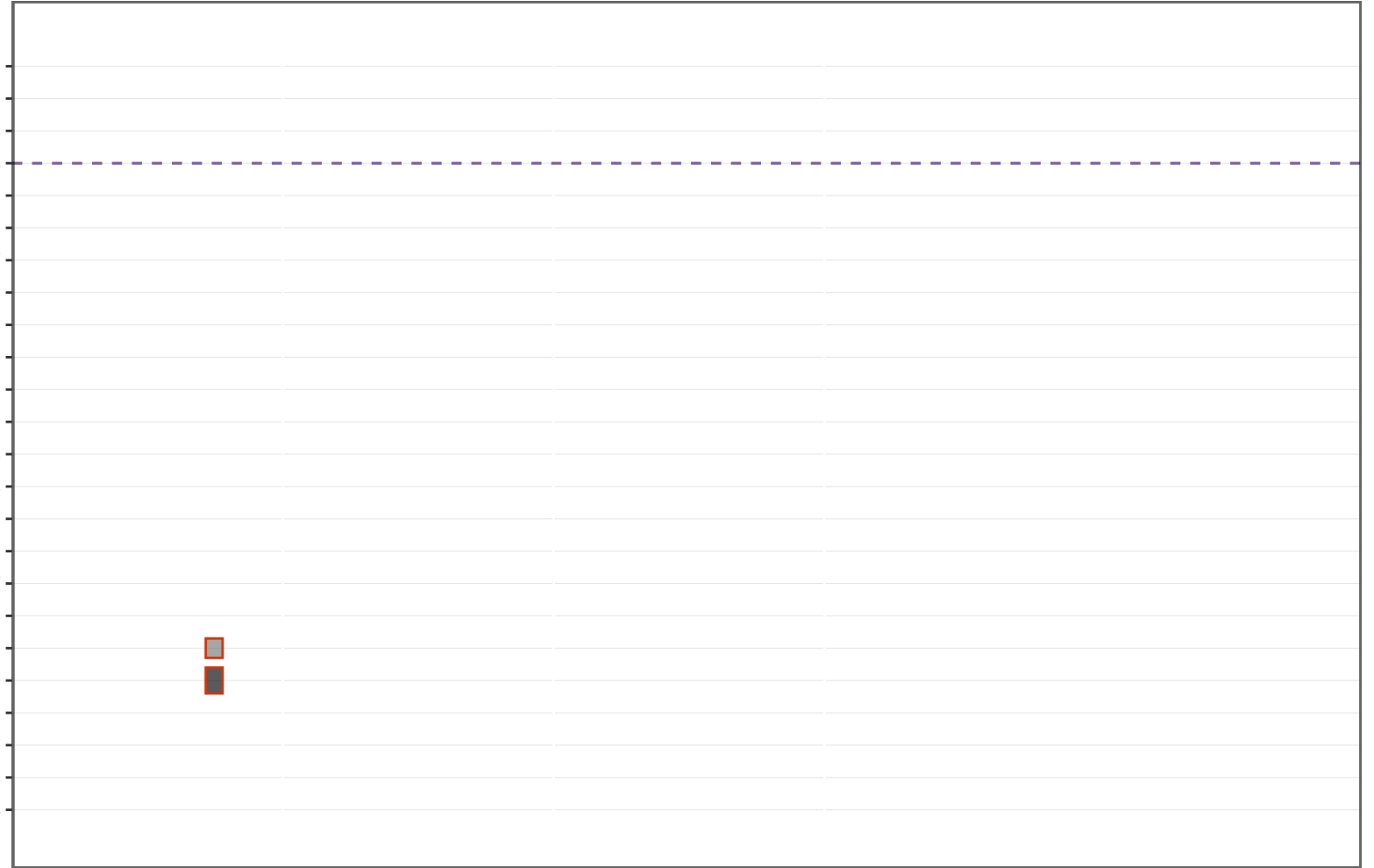
MW indication



Molecular weight



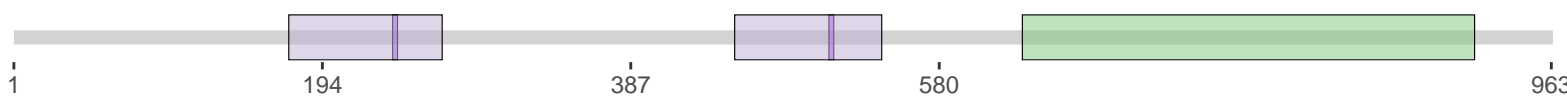
Gel Slice



Peptide counts over 4 repeats

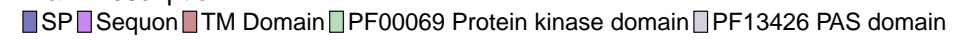
1 194 387 580 963

Protein length



Pfam domains

Pfam Description



Protein sequence:

FLLELYTRREELGNGRFLGSPEDQATVQKIRDAIREGRETIVQLINYSKSGKFWLHFLGPMRDQKQELQHFVIGVLDGSDHLEFLRNRLSEQTEGSSAKLYKATAENVDEAVRELFDANSKPEDLWALHSGKPYPRPHKRDSSALWTAQKQTANGERIGLNFKPVRLGGDGTGSEVHLKELKGTGELFAMKAMDKSMLNRNKVHRACVEREIALLDHPLPALYSFQDTETHVQLTDFDQGGELFALLDRQPMNIFKEESARFYAAEVLEGLVHCLGIITYRDKPE

NbL01g09450.1 multisubstrate_pseudouridine_synthase_7 [MW = 83.47 kDa]

No. of times detected



log(intensity)



Values from

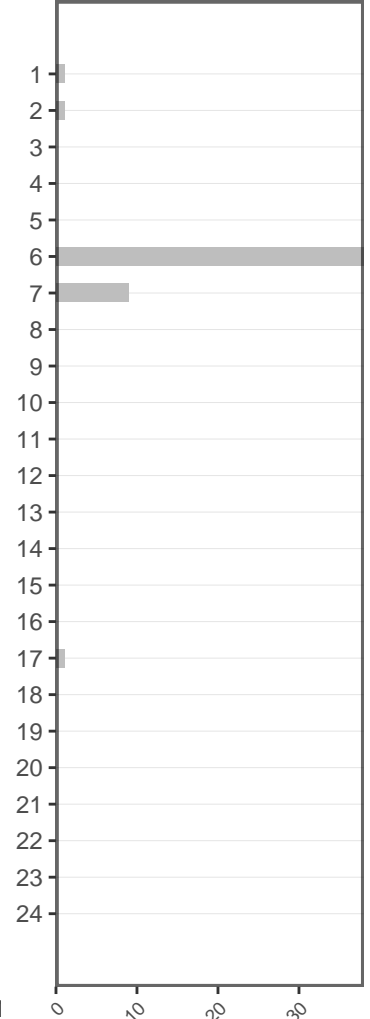
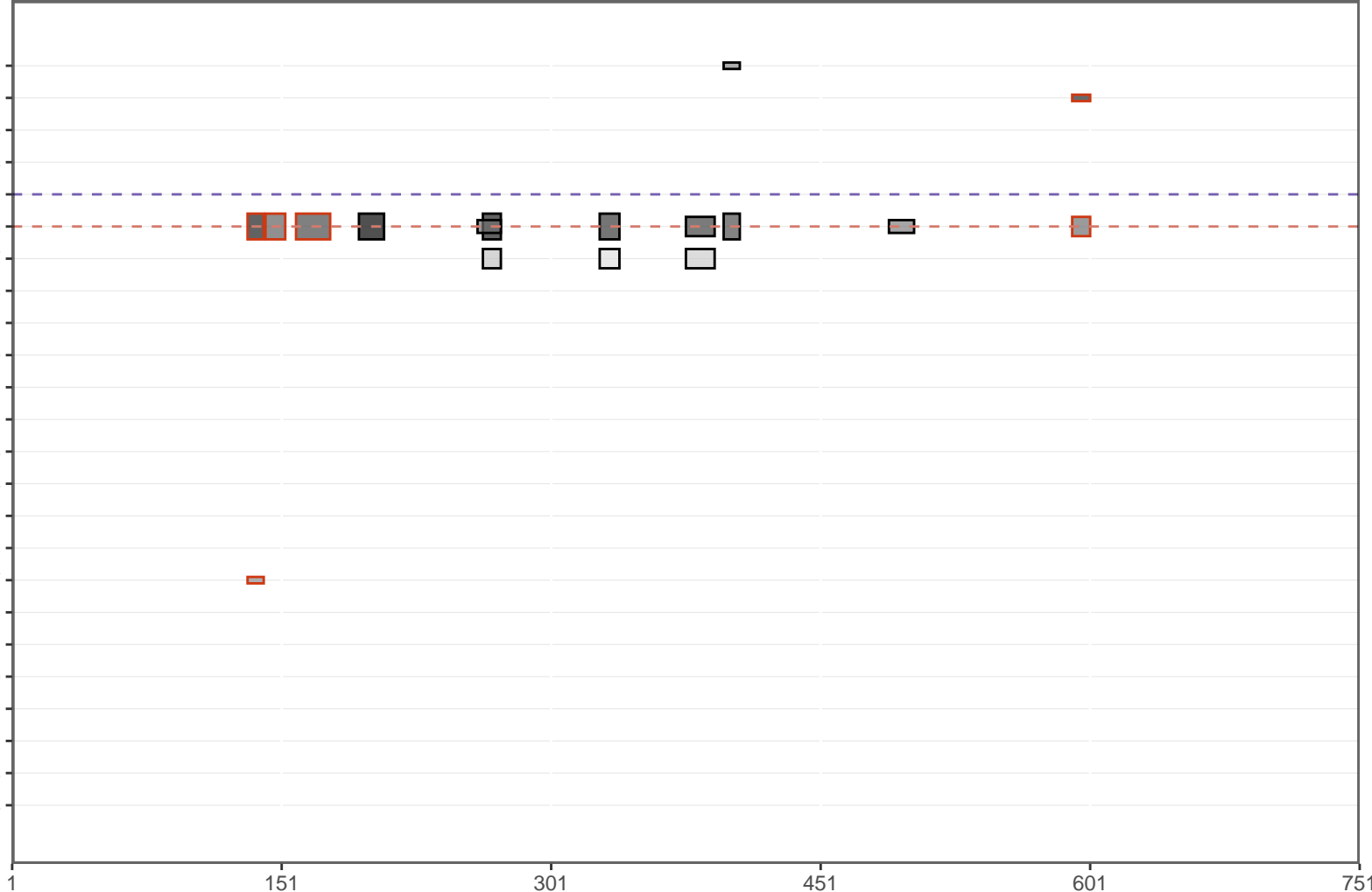


MW indication



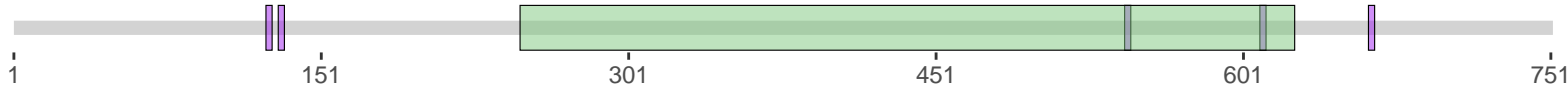
Molecular weight

Gel Slice



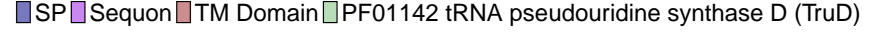
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IEHGFNYFGLRFGSSVPTHLGALLRGEWKAASVLSLIDPREGKKAISTVREYKESGDTGTLRQLPRHLAERAILQGLKSPNGLGALKGIPRTLMMYVHVGQSLWNHAAASMRVQKHGFDQVYLGDLVYSKQPKETKTFVAAGEDVNGNEMDDYSLNLDSETDPPFEKKNISYKAAINEEDLISGDTYRIEDVLLFLPQSRVYVPSNDIGEYVGDLAGKDGSLTETAHKKEKFSITMTGAVRRVFGKPKDFEWELLGYTDGTIPLAETDFDAKSKKSKYREE

NbL01g09390.1 probable_ribose-5-phosphate_isomerase_3_chloroplastic [MW = 30.36 kDa]

No. of times detected



log(intensity)



Values from



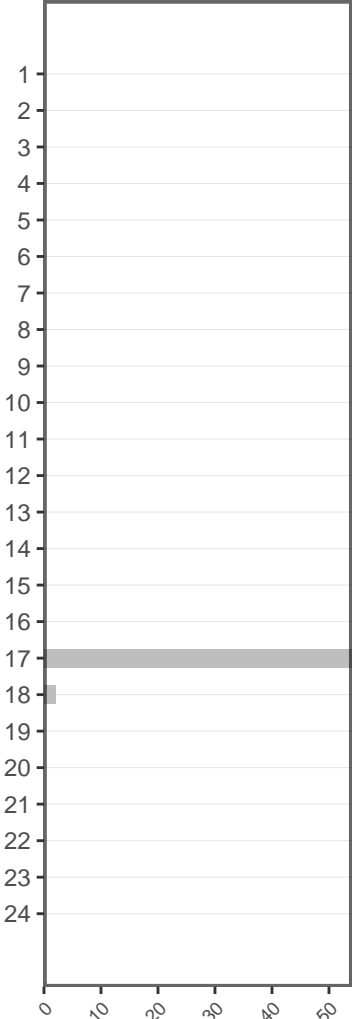
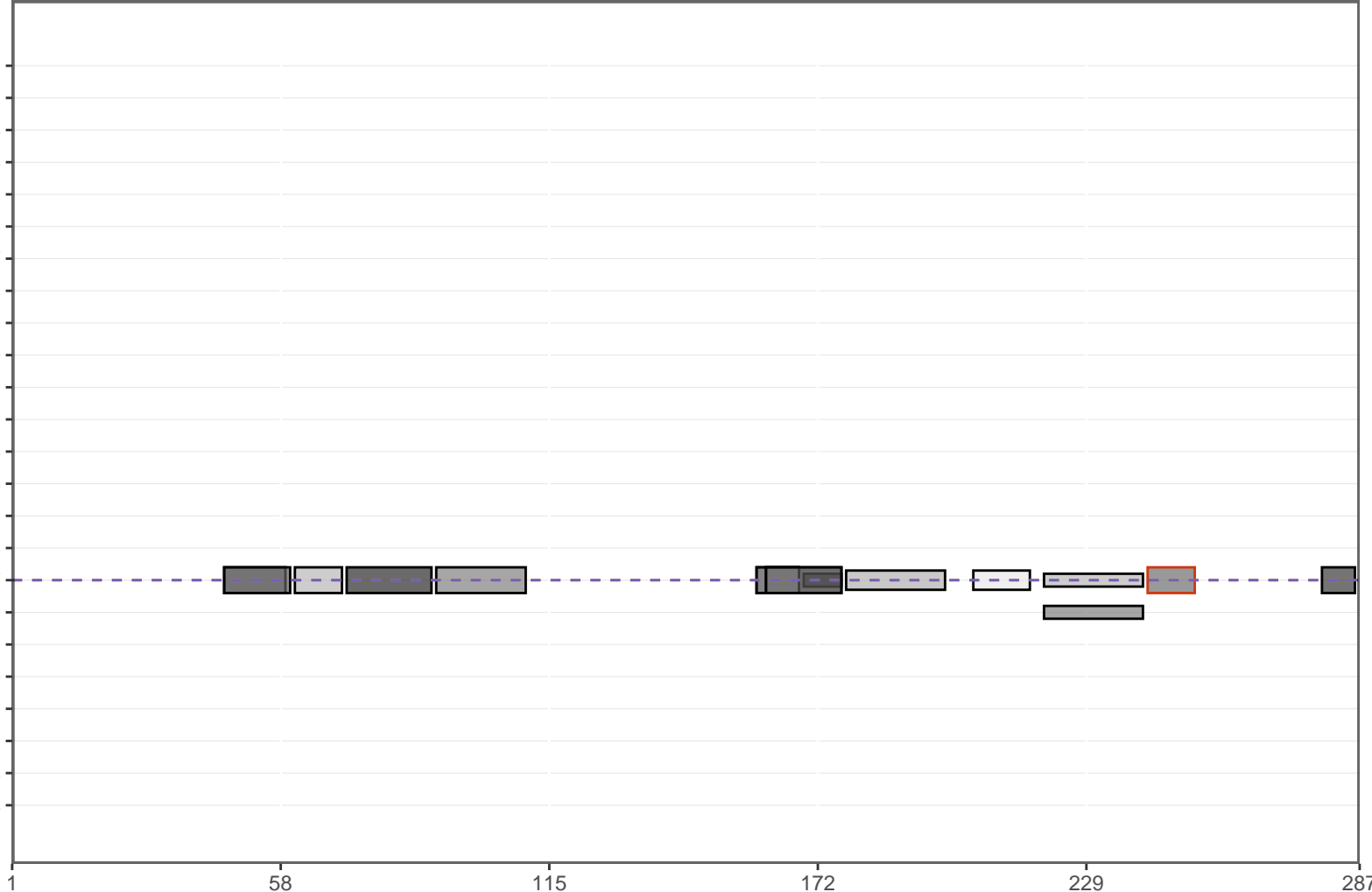
MW indication



Molecular weight

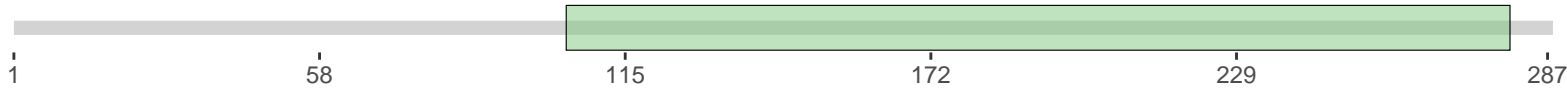


Gel Slice



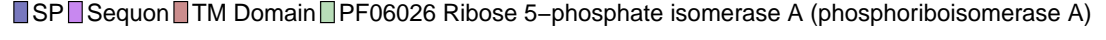
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SLAIDGAEVDFPNLNLVWGRGSGALLREKMMVEASDKFVWVDDSKLVSLGSGSLAMPVEVDFGWKYNLVRIGELFKAEGVDKLRVDDNGKPYVTDNSNYVDLYFKTRPDRSAAAGKEIAALEGVVEHGLFLDMTAVIAGKEGVSVGSK

NbL01g09380.1 PITH_domain-containing_protein_At3g04780 [MW = 19.65 kDa]

No. of times detected



log(intensity)



Values from



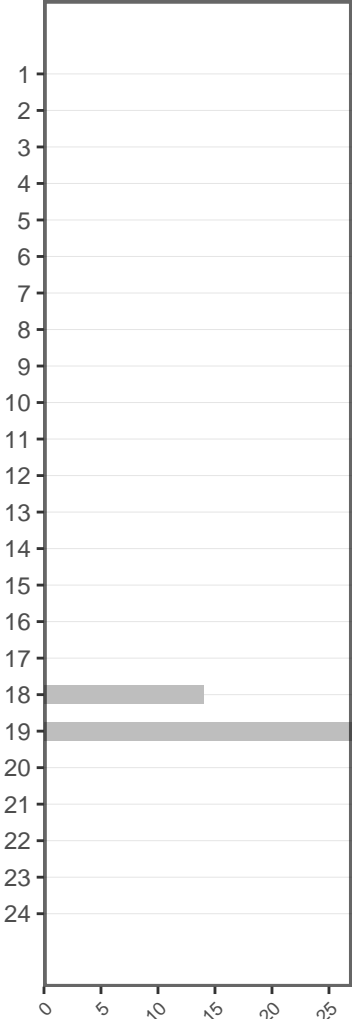
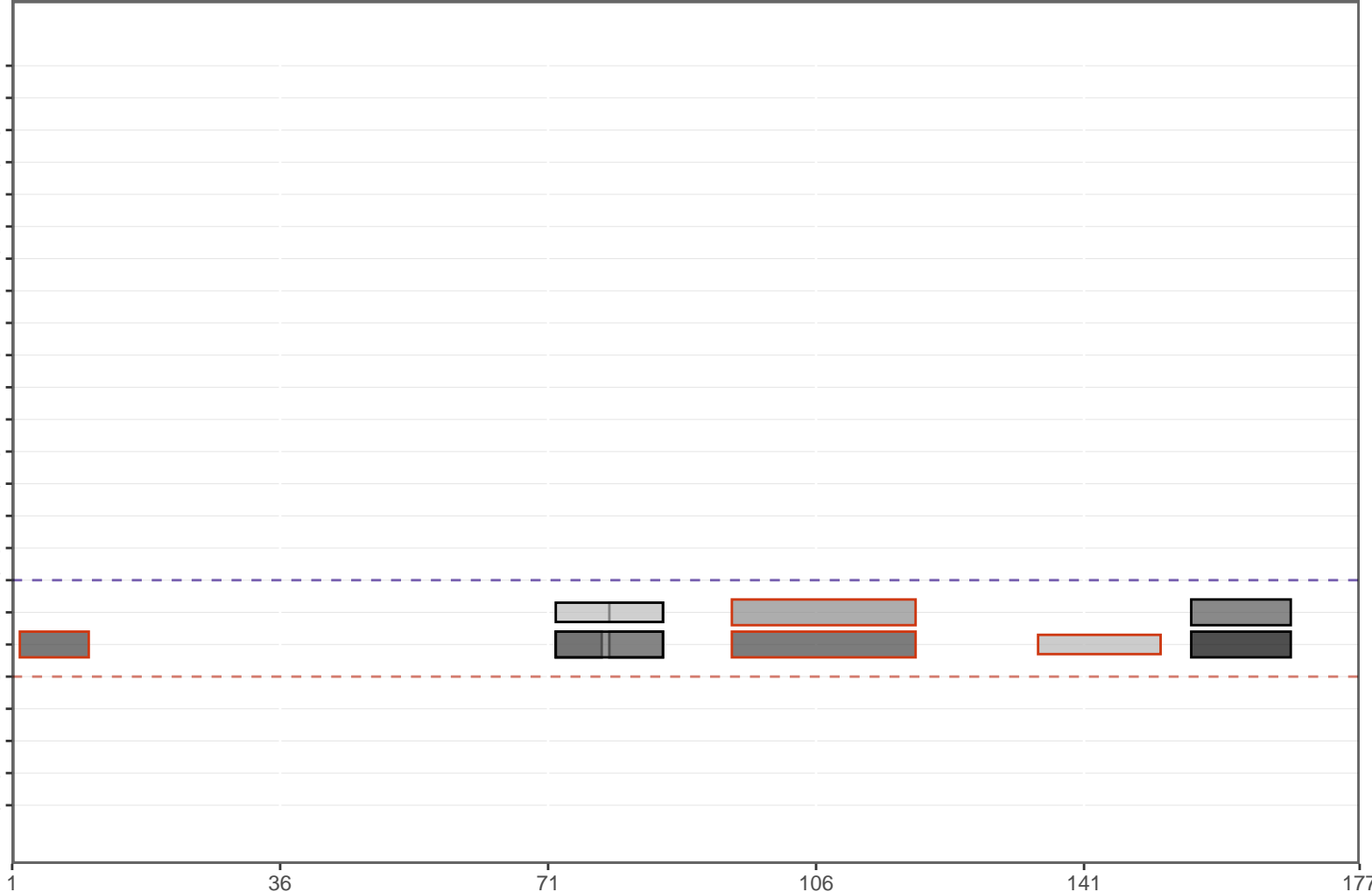
MW indication



Molecular weight



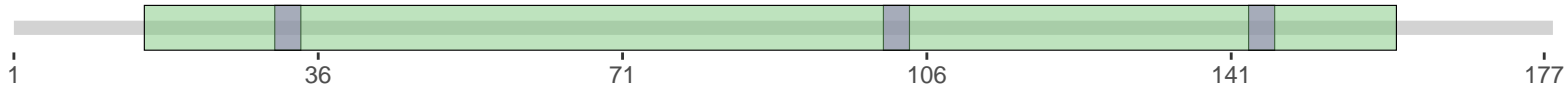
Gel Slice



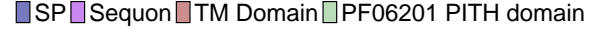
Protein length



Pfam domains



Pfam Description



Protein sequence:

FVIKGPEEEGPKTVLIFGNKEHMGFSNVDYPPSDTAVLSEDLKGGKPVLLKYYKFGNVRBVTIFIEDNGSDSELTAVKQIVLYGTTVETDMKGLKIEDH

NbL01g09320.1 uncharacterized_LOC104217073 [MW = 36.25 kDa]

No. of times detected



log(intensity)



Values from



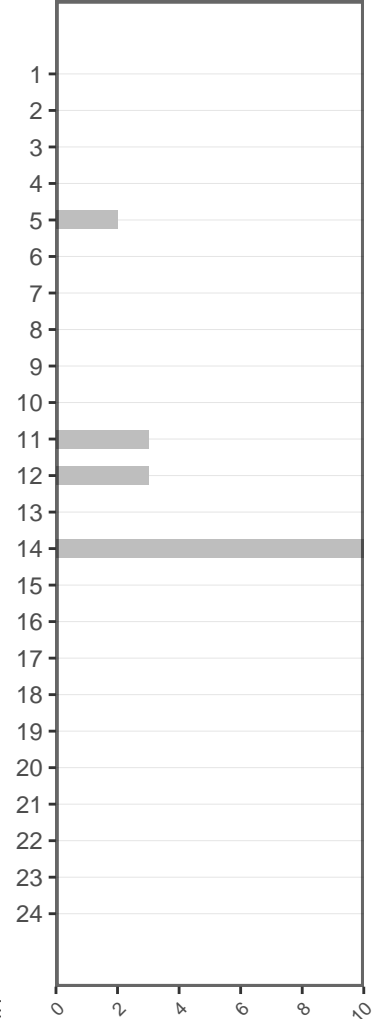
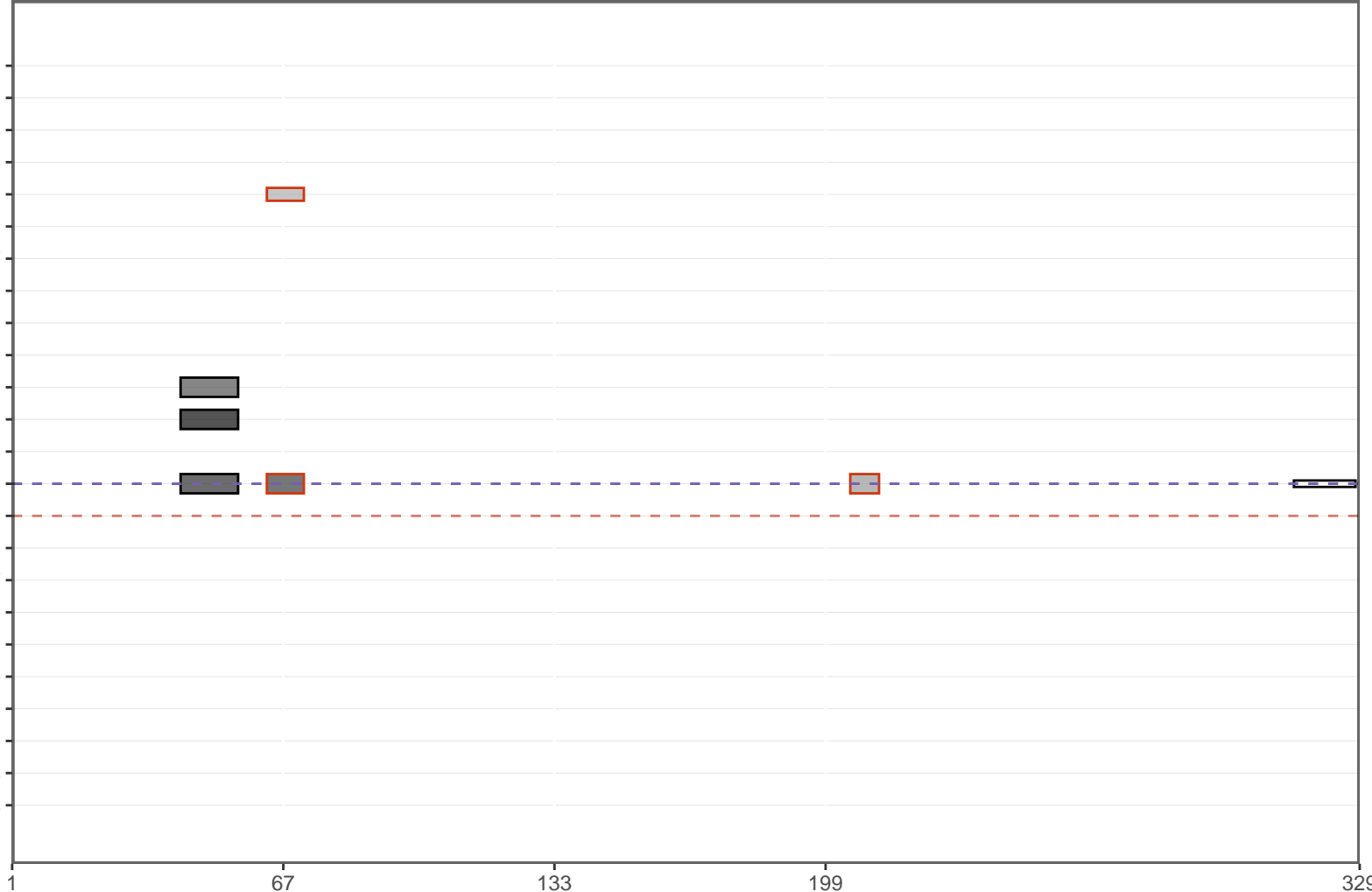
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

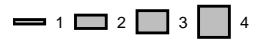
Pfam Description
 SP Sequon TM Domain

Protein sequence:

MGVEMGPPLSEFFLLGDLKSHGAEDELDGGAGFAHLLGPVLQELADALAKNPVAVVQKRNNGSKLRKVLADEKQLRETVKIMQEKQDEKDPSPNKDVIRQLKLEKNGASLGLPLKNDKVVLLYDVLGDMENKGTDAASDKDELIVFLKDKLEKFAAGLEVNPFTFDLEN

NbL01g09310.1 GDP-mannose_35-epimerase_1-like [MW = 42.53 kDa]

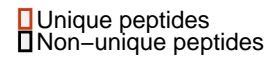
No. of times detected



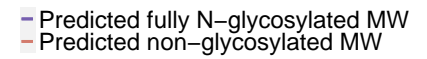
log(intensity)



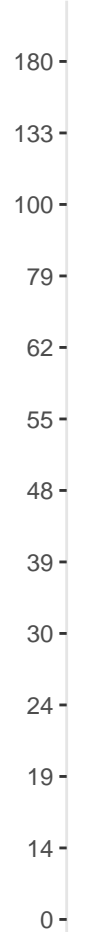
Values from



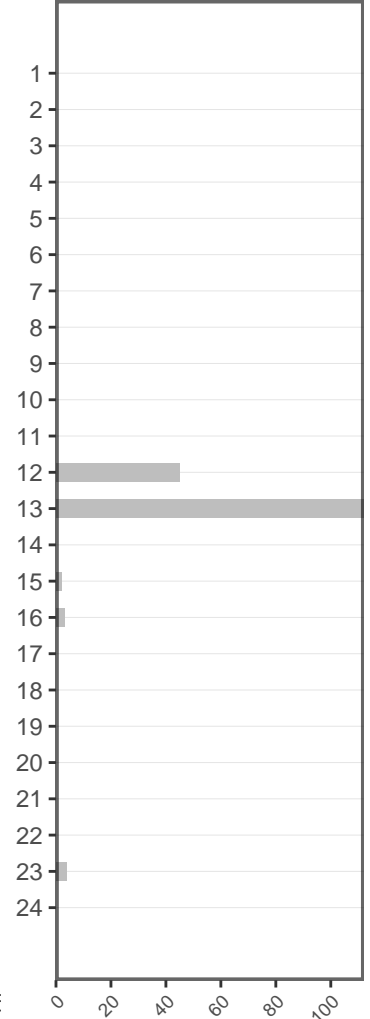
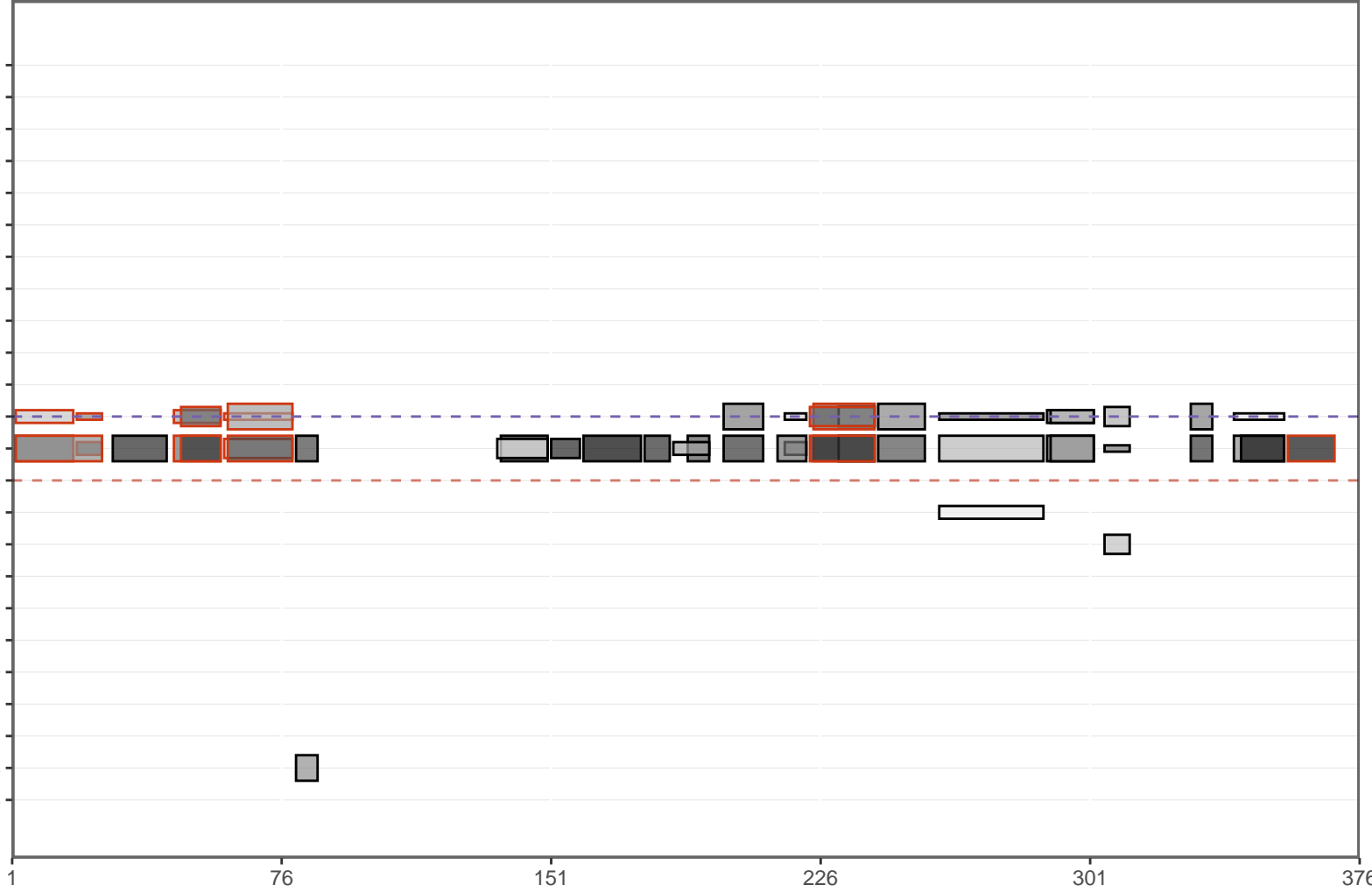
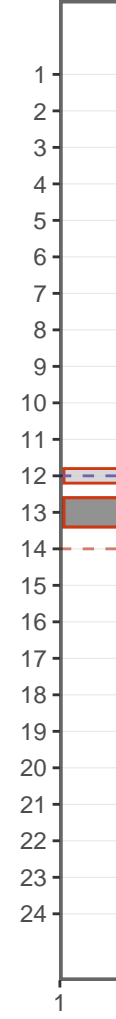
MW indication



Molecular weight

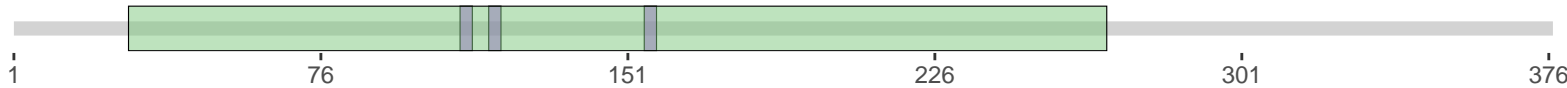


Gel Slice



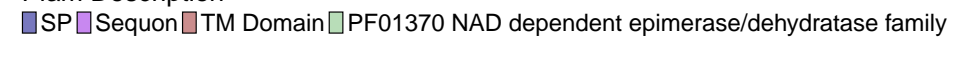
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IKLATELCKIYKDFGIEGRGRFHNYFFPGTAVKGGREKAPAFGRKAGTAVQKFEFMWGDGLGTRSFSTFIDEQVEGVLRILTKSDRFEPVNIQSDQEMVSNMEMEMVLSFEDKLPKHHPCGPEGRGRNSDNLKEKLGWAPTMLKDKGLRITYFWIKIEGIEKESQGVNANHYGSSKVVGTGAPVELGSLRAADGKE

NbL01g09280.1 sec-independent_protein_translocase_protein_TATA_chloroplastic-like [MW = 16.27 kDa]

No. of times detected



log(intensity)



Values from



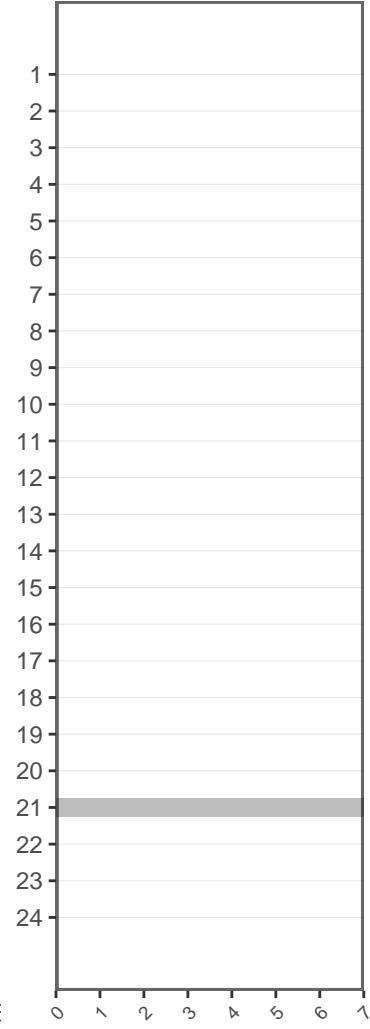
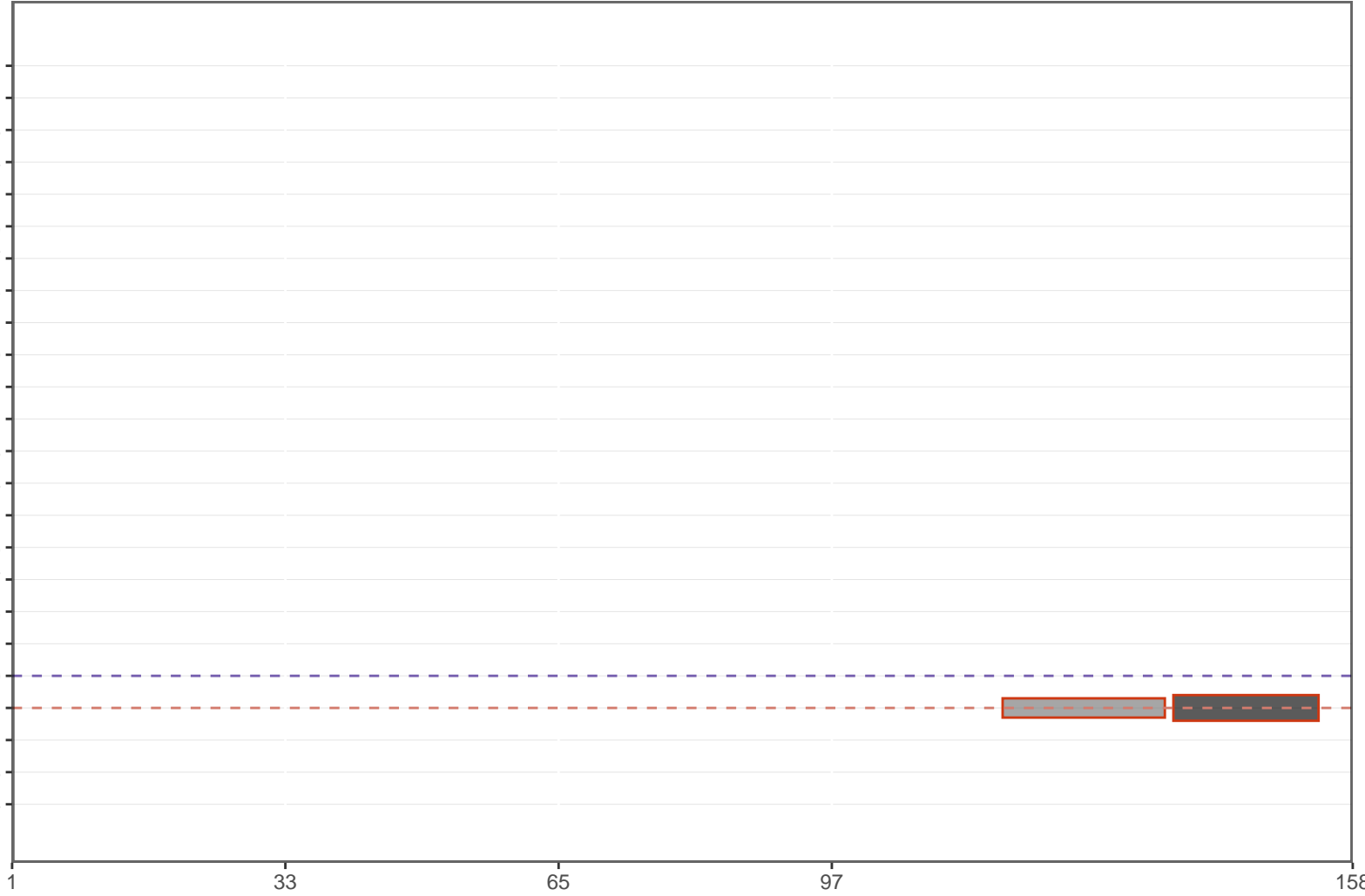
MW indication



Molecular weight

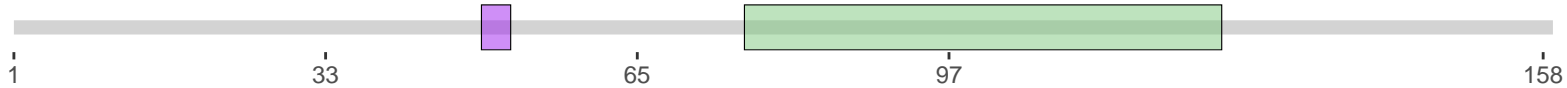


Gel Slice



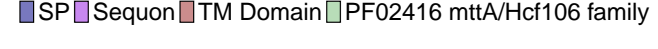
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ILSCNCLFGLGYPPELVMAGVWALVFGPKQLPEVGRIGIKTKVKSFGQAAKFEFETELKKEPEASAEPTAEKAMEASGEKQDITVSSIKSSP

NbL01g09270.1 probable_prefoldin_subunit_4 [MW = 14.83 kDa]

No. of times detected



log(intensity)



Values from



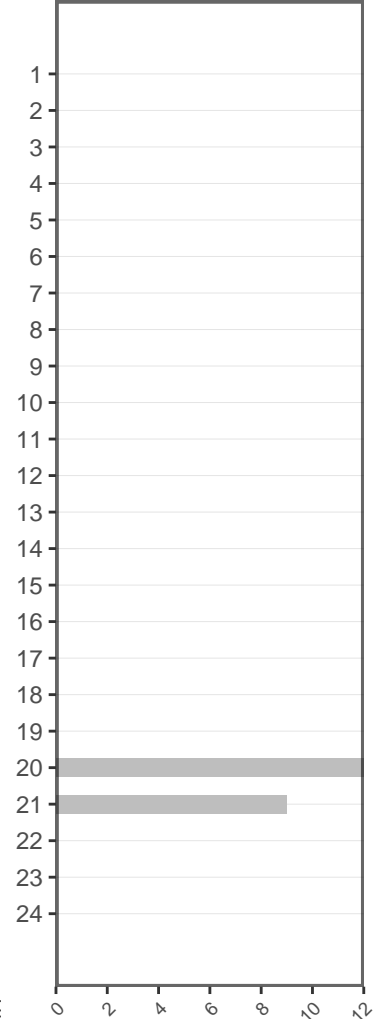
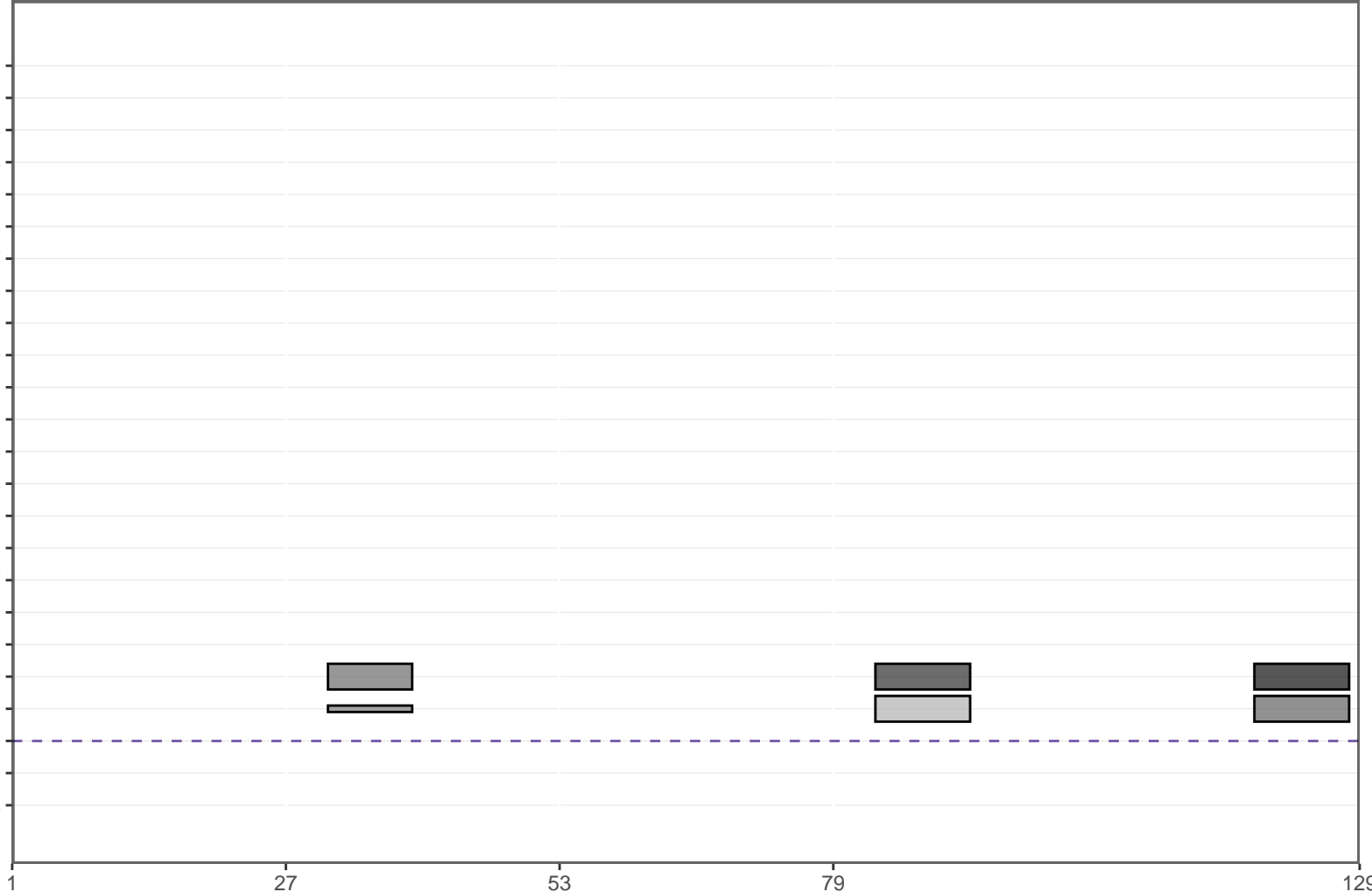
MW indication



Molecular weight

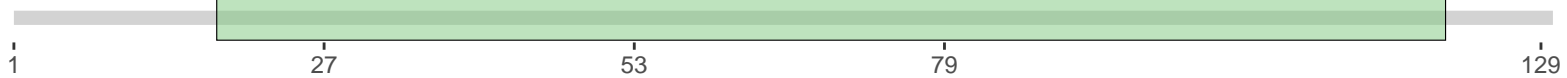


Gel Slice



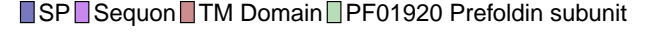
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DASNELILTDEEIVRFQKGEVFAHVPKKEEVEGRINMQEVTAKNLEKLEEEKETVVGQMAELKKILYGFKDSINLEED*

NbL01g09230.1 wound-induced_protein_WIN1 [MW - SP = 19.69 kDa]

No. of times detected



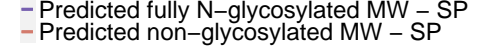
log(intensity)



Values from



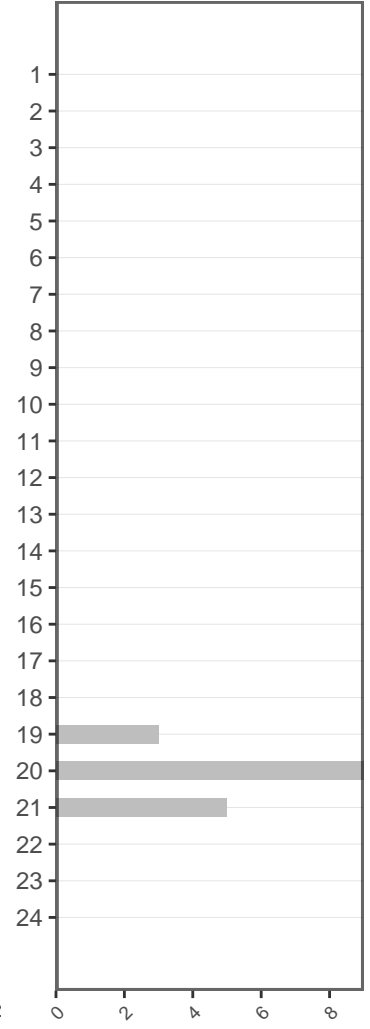
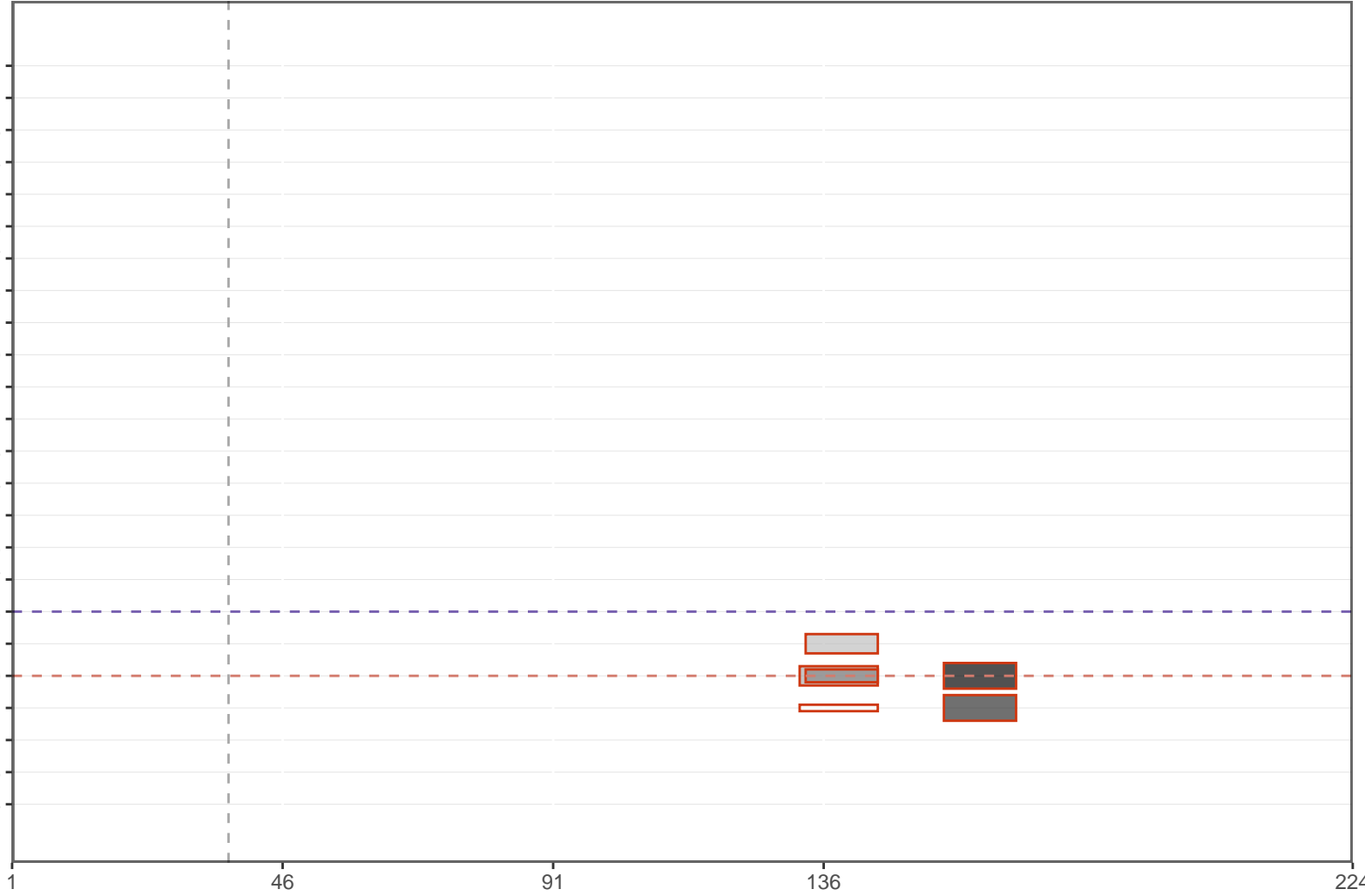
MW indication



Molecular weight



Gel Slice



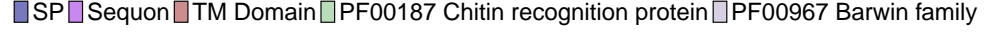
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

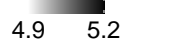
1HYNPNVGVWDLVAVSAVGETWDSGNKPLAWRRKYGWTFAGFPGVPRGRD56GKLRVNTGTGAGTTRVIVDQCGNSGLEDLDVNVFRQLDTDRGNRGRHLVNYEFVNGGDMNVALVSPVQKE

NbL01g09210.1 pathogenesis-related_protein_PR-4A [MW - SP = 13.63 kDa]

No. of times detected



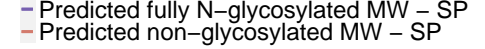
log(intensity)



Values from



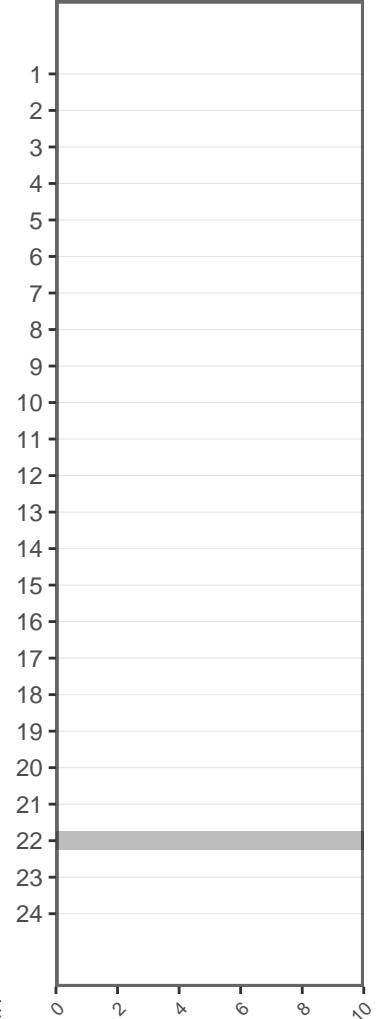
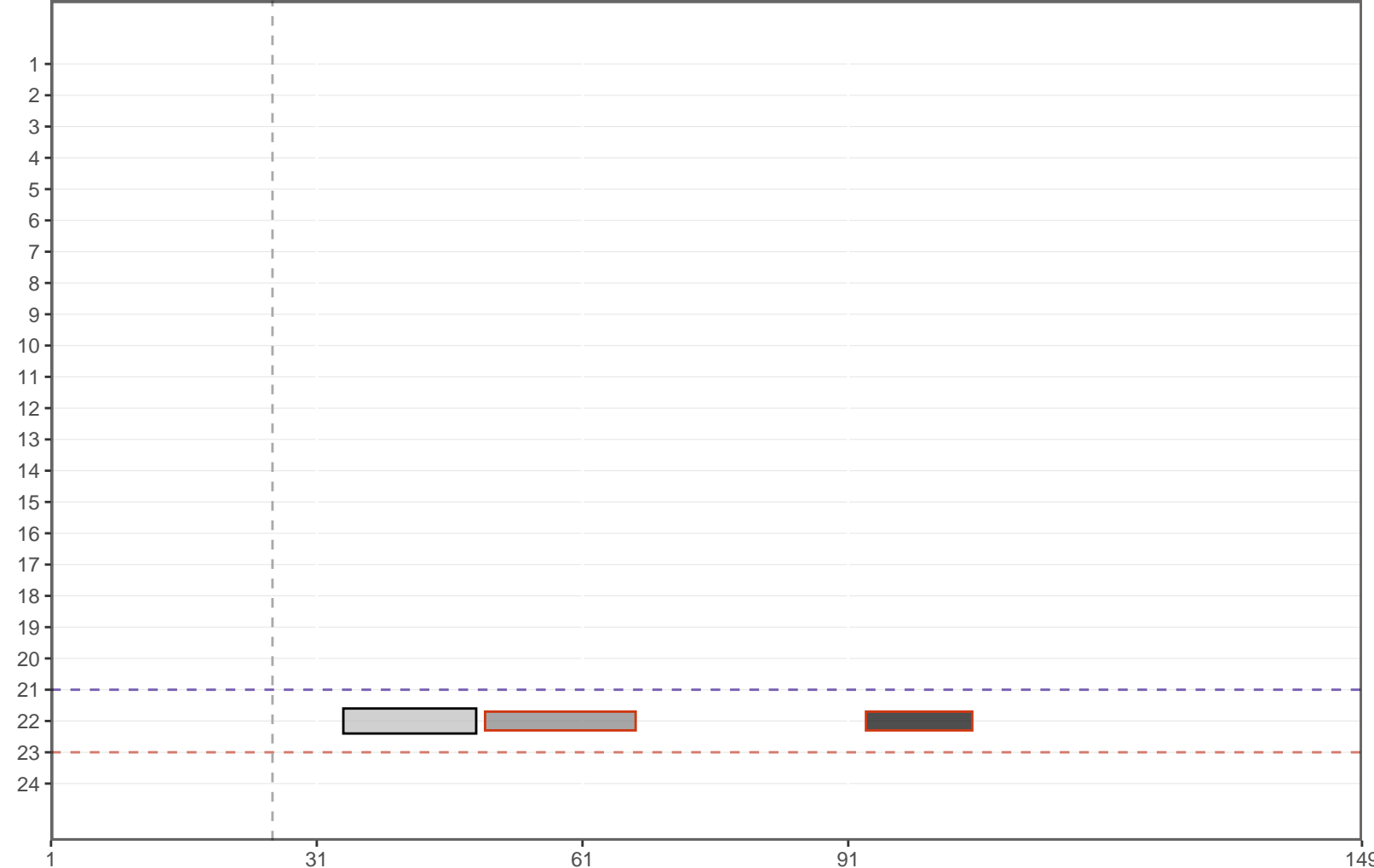
MW indication



Molecular weight



Gel Slice

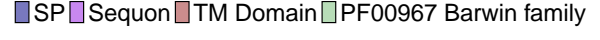


Protein length



Pfam domains

Pfam Description



Protein sequence:

PLTWRQKYGVWTFQDMAGPQGGSDSGRGLRVINTGTGTQTVRVRVDDGRNGGLDLENVFNQLDTRNGVYGGHLLVWYEFNGDD*

NbL01g09160.1 uncharacterized_LOC104210129 [MW = 53.57 kDa]

No. of times detected



log(intensity)



Values from



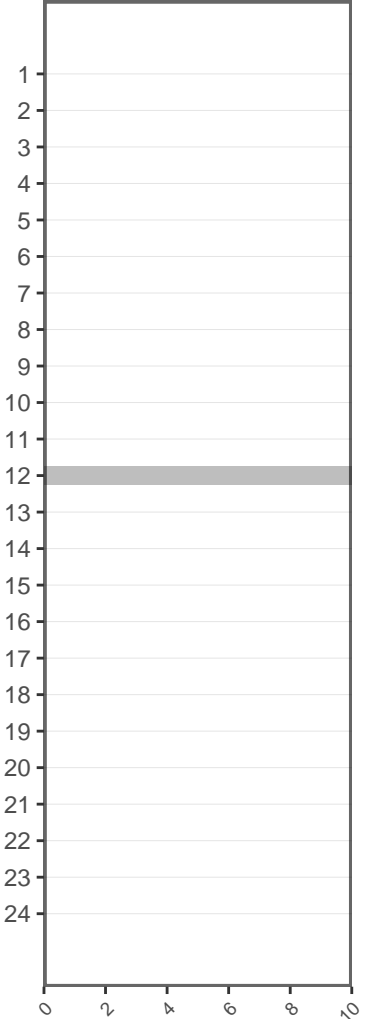
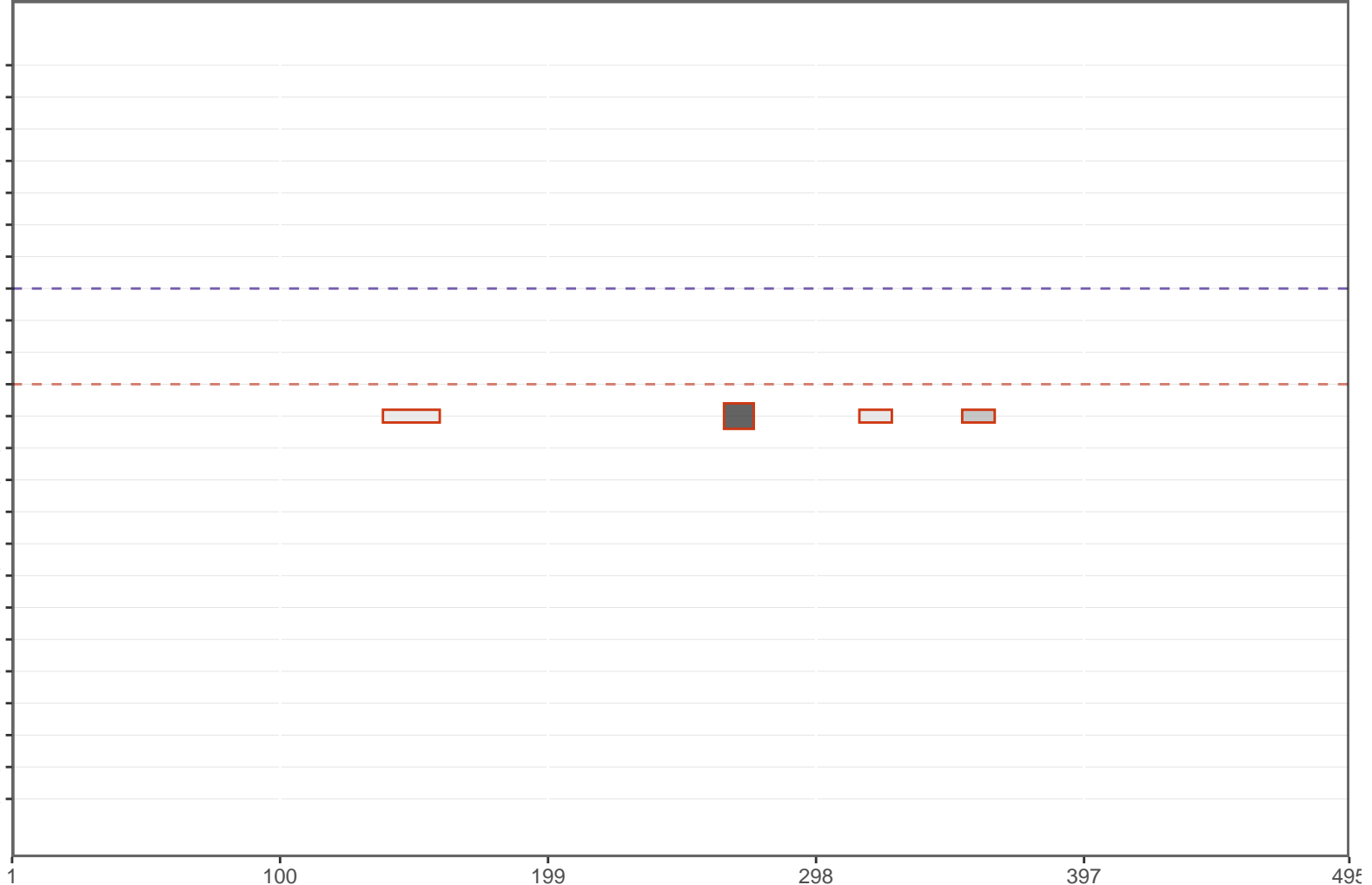
MW indication



Molecular weight



Gel Slice



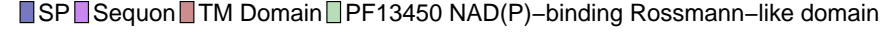
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

GTWHLSEKXPCGGDAIVAHNGKCANRLLASGGLPLIARQMKRLELSPWALLAAFEDPLPTAVNAEELPFEGAFVKGVEVSWMANNKHLGRDSGGQCVTFSTAFAGKQNKVQGESIPWTAERVKEAMLEGGVEKALGLSKNSLORPFYTRLGLWGAAALPTNTPGVPCGDFPRGRAGICGDWLLGSSVEAANISGIALADHADYFEGGGPCSDDEFVAGLHDDYKPLGGHDGGFPLEYVDGTTKFPALTLAT

NbL01g09120.1 Fanconi_anemia_group_D2_protein_homolog [MW = 166.81 kDa]

No. of times detected



log(intensity)



Values from



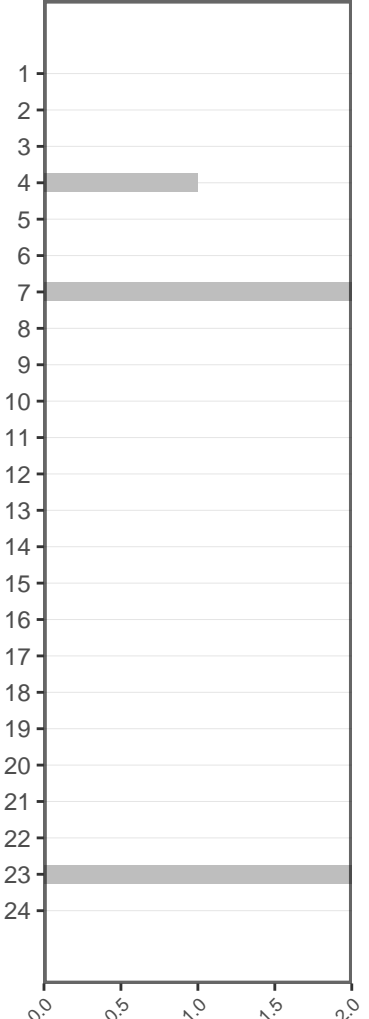
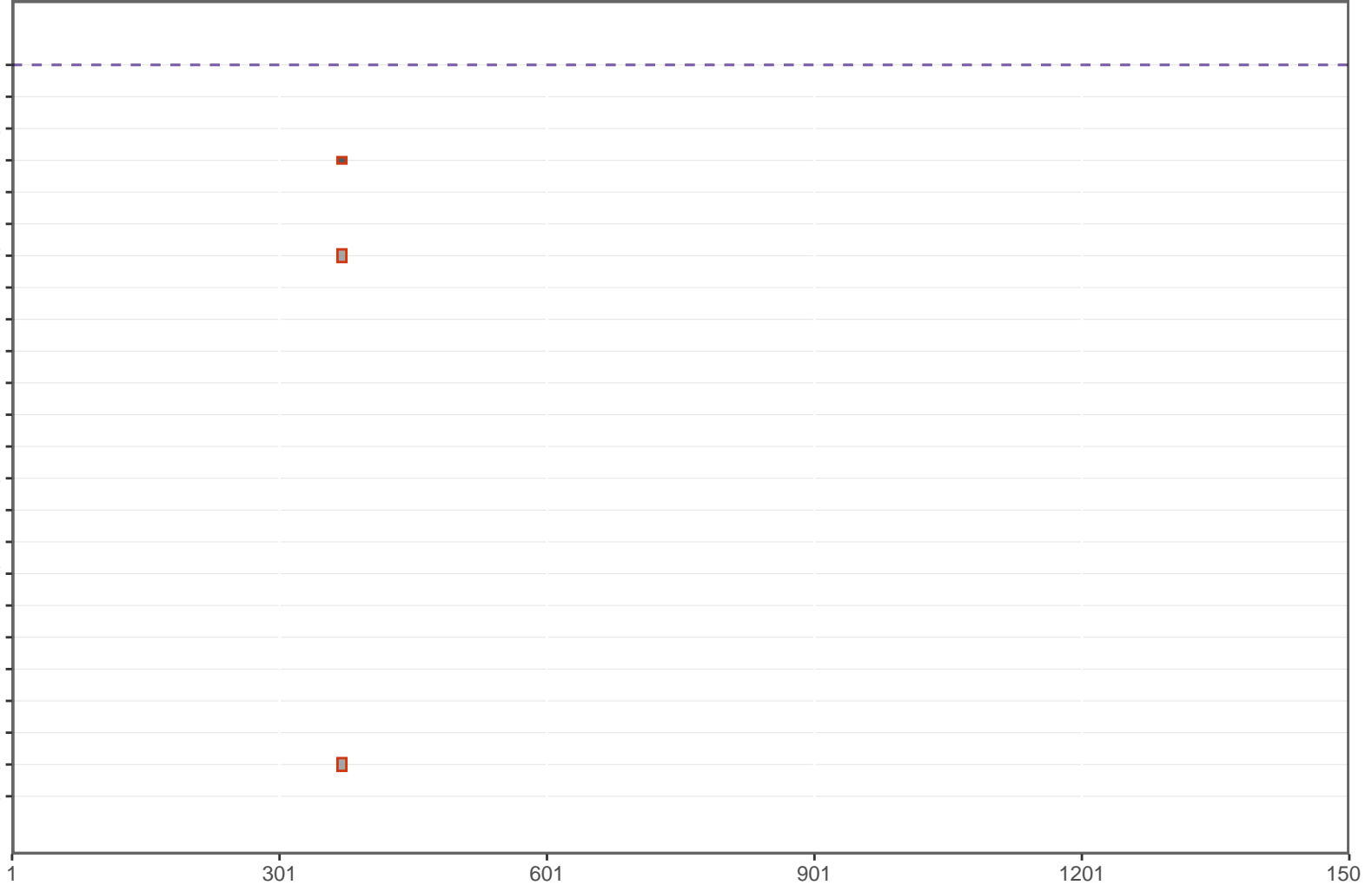
MW indication



Molecular weight

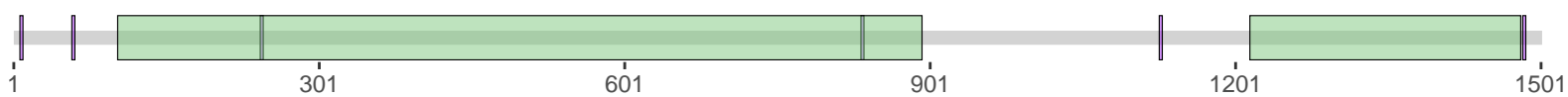


Gel Slice



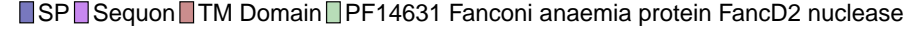
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

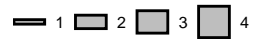


Protein sequence:

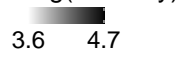
SLAGDALLGCPHLPSSKFFSEPLWGLSGLGKQKQHILSLVYAAWNLRELLNAFGTQAVNECDFSGATREEFKLFKRLRNLFLESLNLNLSLRQGLSLPELQPHLESLNQLNDRDGEIKNEHGNNGNGLSGKKEKTSQASLTDGKLRQPTMVLKAKAGVPSGDEPVSRSPTGCKSGSAPEPESGSLNLRNSKIPANVDVSTAVEHVEADRYKFRPLLLDGFALFGKTDGSDGADPASELPLGLVLRDLNLRKLEDFSPRRHILVRRMSVPPAFGEMKVFIEFSKQF

NbL01g09040.1 flowering_locus_K_homology_domain-like [MW = 53.82 kDa]

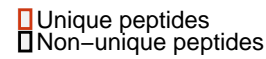
No. of times detected



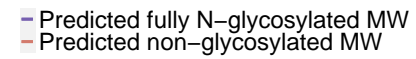
log(intensity)



Values from



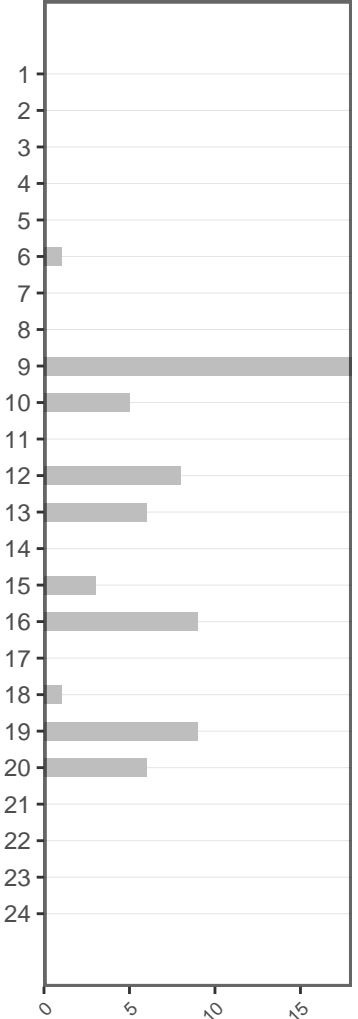
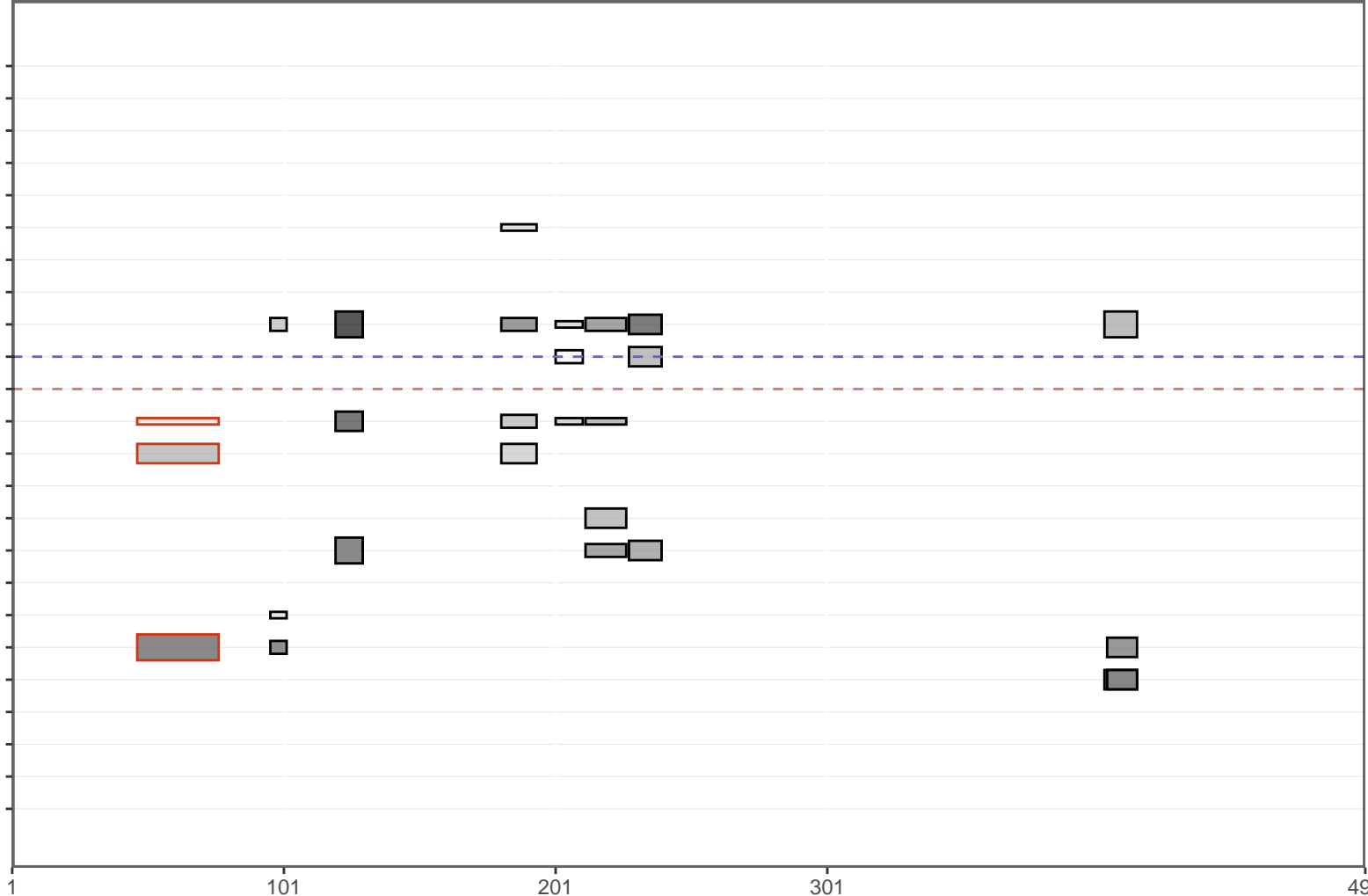
MW indication



Molecular weight

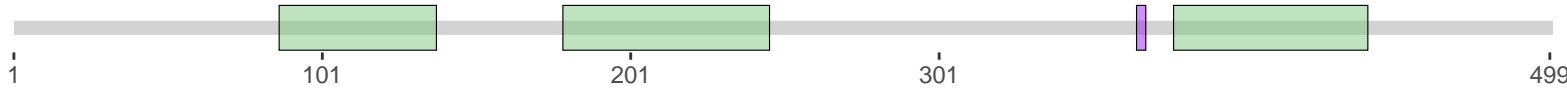


Gel Slice



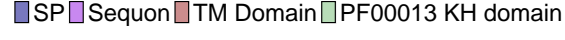
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

/HKAVELIANLRKFLVDRISIPVFEQMGMNPNPVEHMPRRQSGWGPQQGAFPPSAVGGPGYGSNPHFMPRRSRQHDYYPADMPSPRQHDYAPVDMPPPLEKQPHGDISAVGREAPMSMHSSENNNTAAPSITQITQHMGIPLSYADAVIGTNGASISYIRRRVSGATVITQETRGVYVPEMTVEISGTASGVGTAGGLVQNFMDAGAPAGAGTAPPADGGYNSYGAAPTSMYSAPTNPNGVPGGGSYGSGVGTNYGVY

NbL01g09000.1 retinoblastoma-binding_protein_5_homolog [MW = 58.07 kDa]

No. of times detected



log(intensity)



Values from



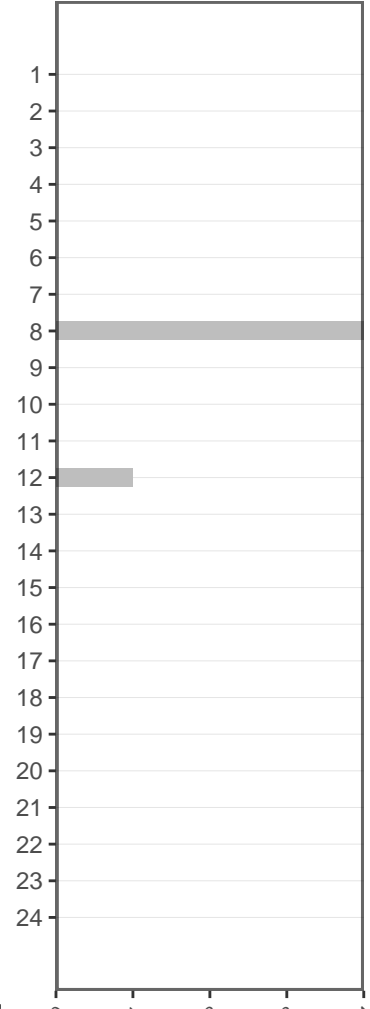
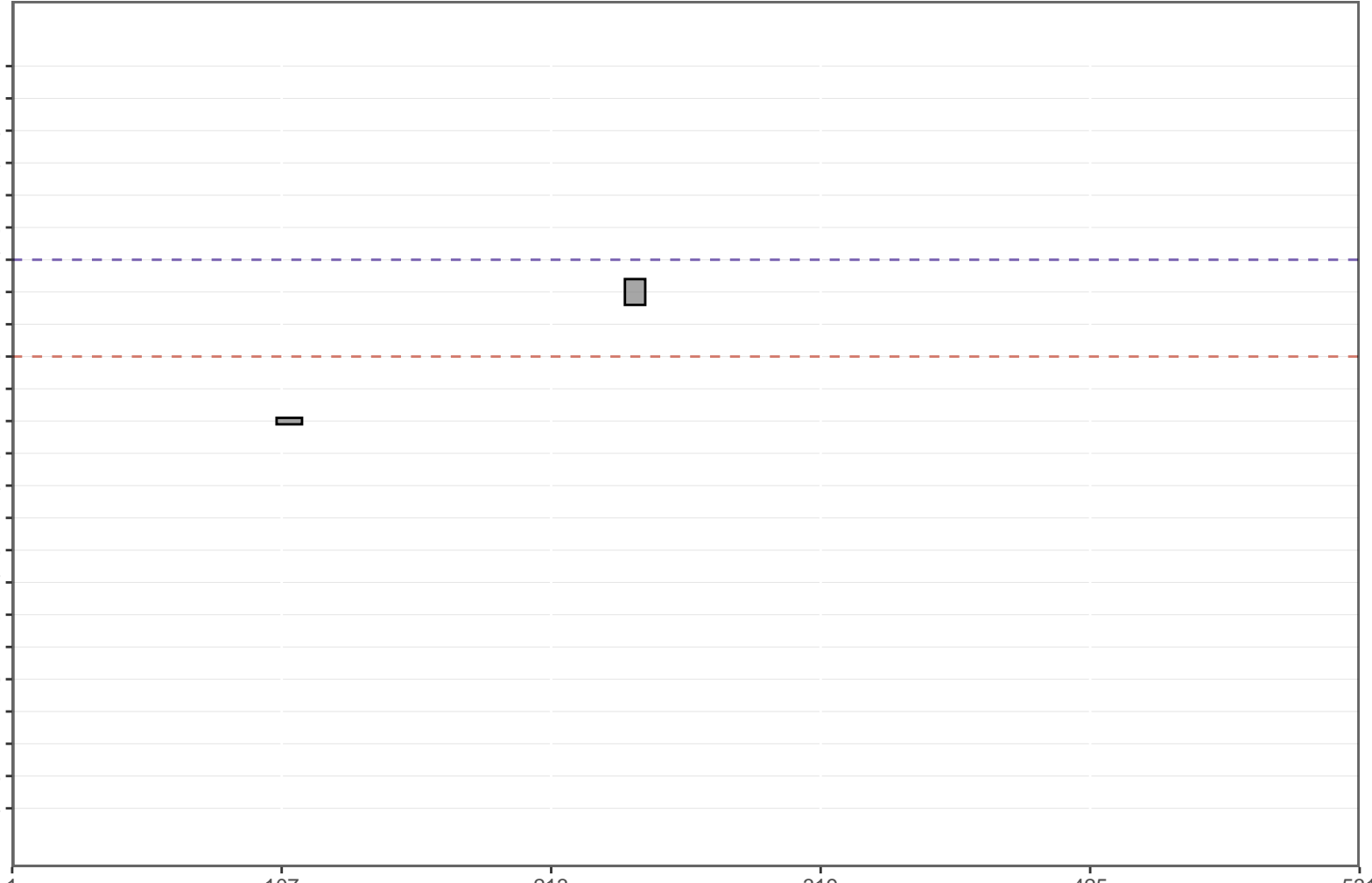
MW indication



Molecular weight

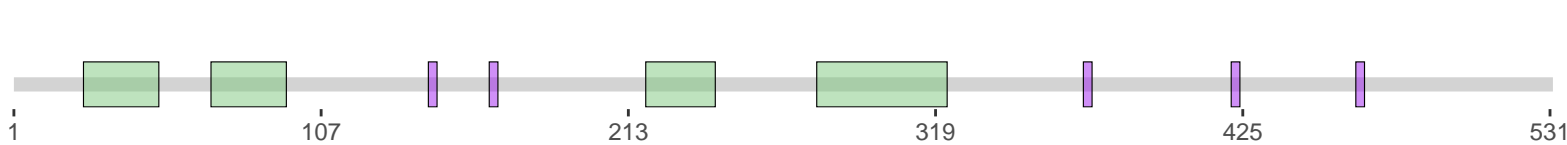


Gel Slice

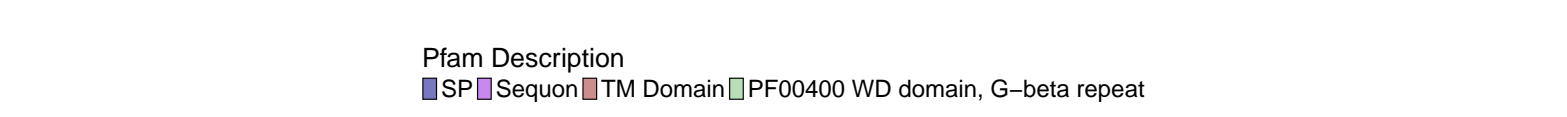


Peptide counts over 4 repeats

Protein length



Pfam domains



Pfam Description

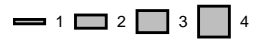


Protein sequence:

DEATNDLNELEGVFNKAVGAGGLALFRFQDSVTRVHWKAPCFSGDGEWVVGSGANKGDKYVWDRAGHLWLEGPKEAIDLAWHPVHPVSVSLAGVYVWAKDYTENWSAFAPDFKLEENEYVEREDEFDLNPEIEKVKESDANEDEDIDKGVENDSTFSQSDMSQGEIGFLPADPDPAPFEGQKGVGSTSKLGEENSGSPEEAGQNGGVNHESSPFEGEDTGTTCVKKRKRKPKSEKYLELQAEKVKKPSGKTKPSGKHGN---

NbL01g08920.1 proline--tRNA_ligase [MW = 60.88 kDa]

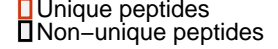
No. of times detected



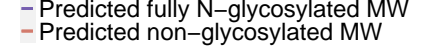
log(intensity)



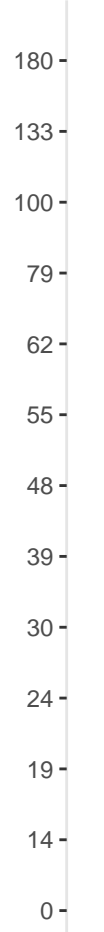
Values from



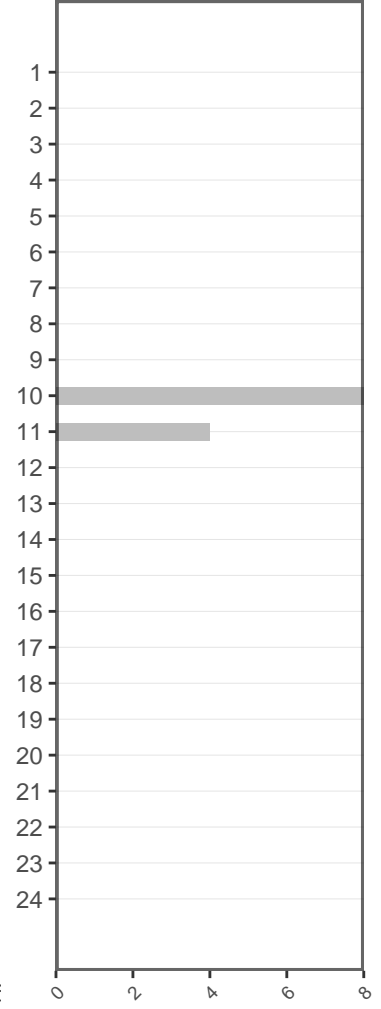
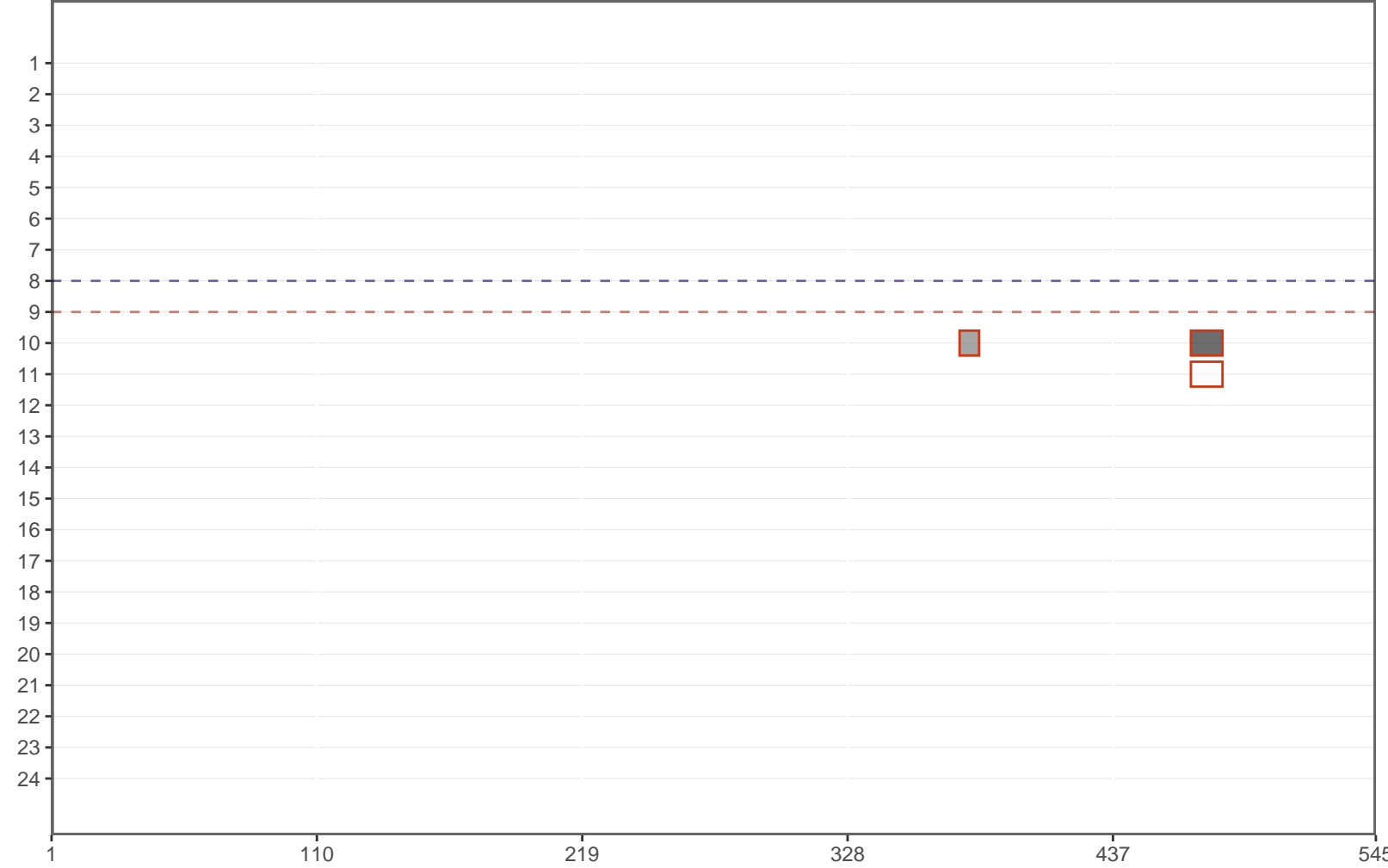
MW indication



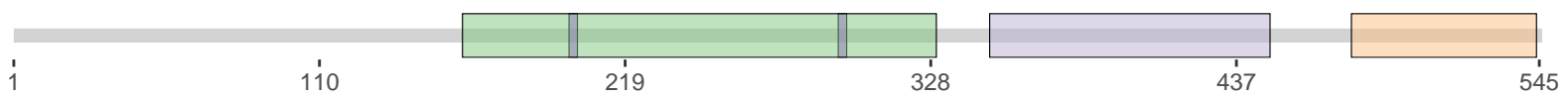
Molecular weight



Gel Slice

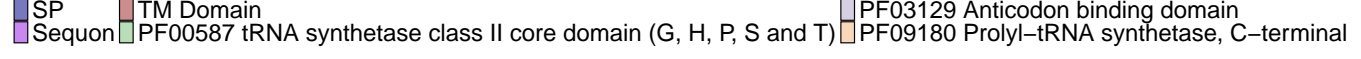


Protein length



Pfam domains

Pfam Description



Protein sequence:

VETFDASRTYTIEMMGDRKALGAGTSHNLGGNFRSFRNFQFTDENGGQRGHVWQTSWAISFRVGGIMTHGGDAGLLLPRLAPVQVWVPIWKKNEKTGVLTAASSSVKGTLAGAGIKVDDTDGRTPGWKNFVEMKGVPLRIEIGPRDVSSTVVISRRDVPKGGKGVFGSMEPSSLVAVVIDKLNEVQSSLERATFRDSDNIVDVSSEYKELKELAIADGHWARGPWSASDEEELKVEETGATIRGFFPEQEGPKGLMTFGNSADEVAIFKSY*

NbL01g08750.1 protein_MAINTENANCE_OF_PSII_UNDER_HIGH_LIGHT_1 [MW = 25.79 kDa]

No. of times detected



log(intensity)



Values from



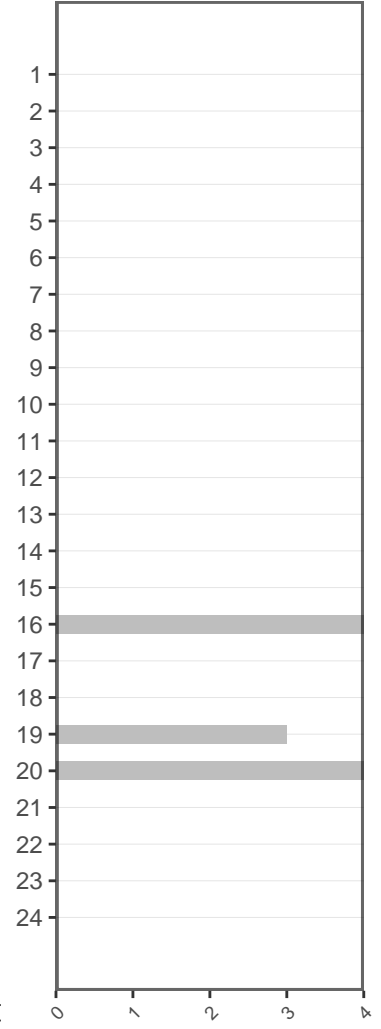
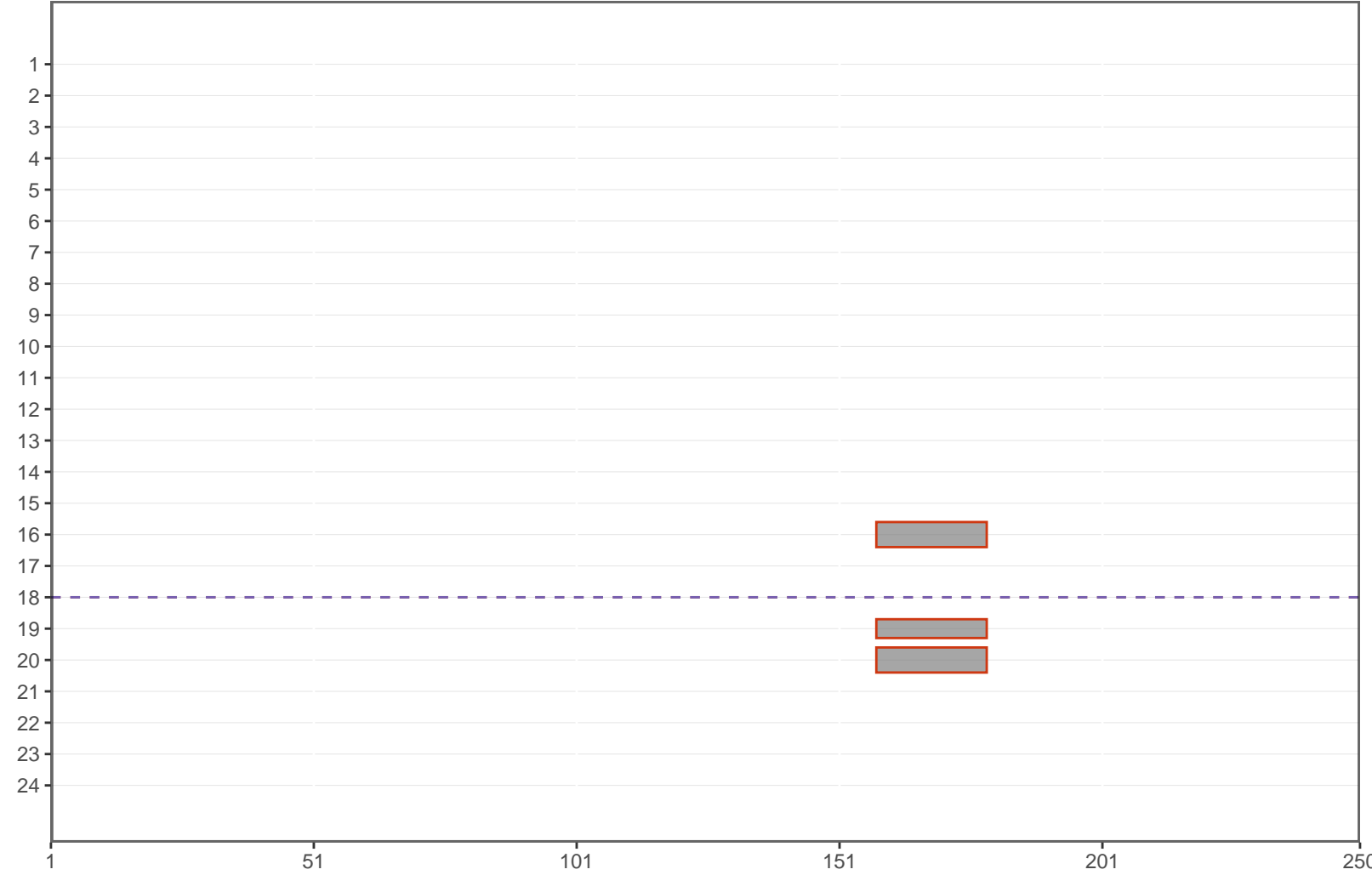
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

AVYYAESAISSGSGAGFTSDGAENTAAAGIALISLAAASBILQVGNKSPRPVGTMEVGGPRLSYKFKRPVEIVGASVAPETEAPTAPEVAGASVAETEAPTAPEVESSALEAPAPQVEVQSEAPQDTSSSSSDVSI

NbL01g08710.1 40S_ribosomal_protein_S20-2-like [MW = 13.73 kDa]

No. of times detected



log(intensity)



Values from



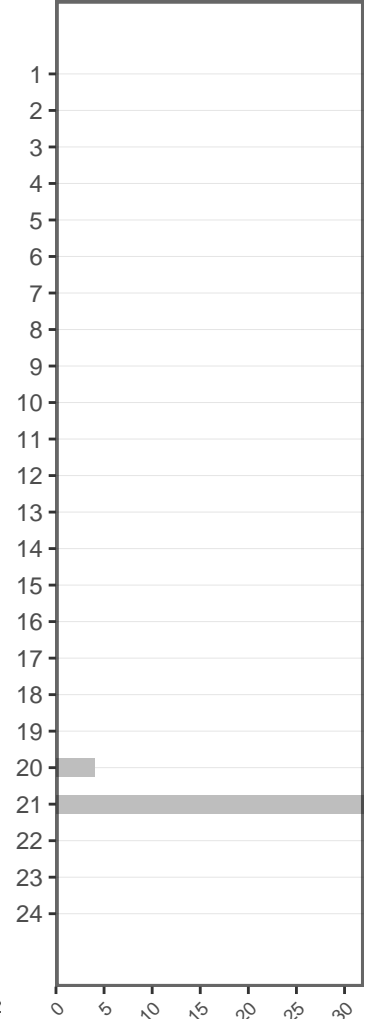
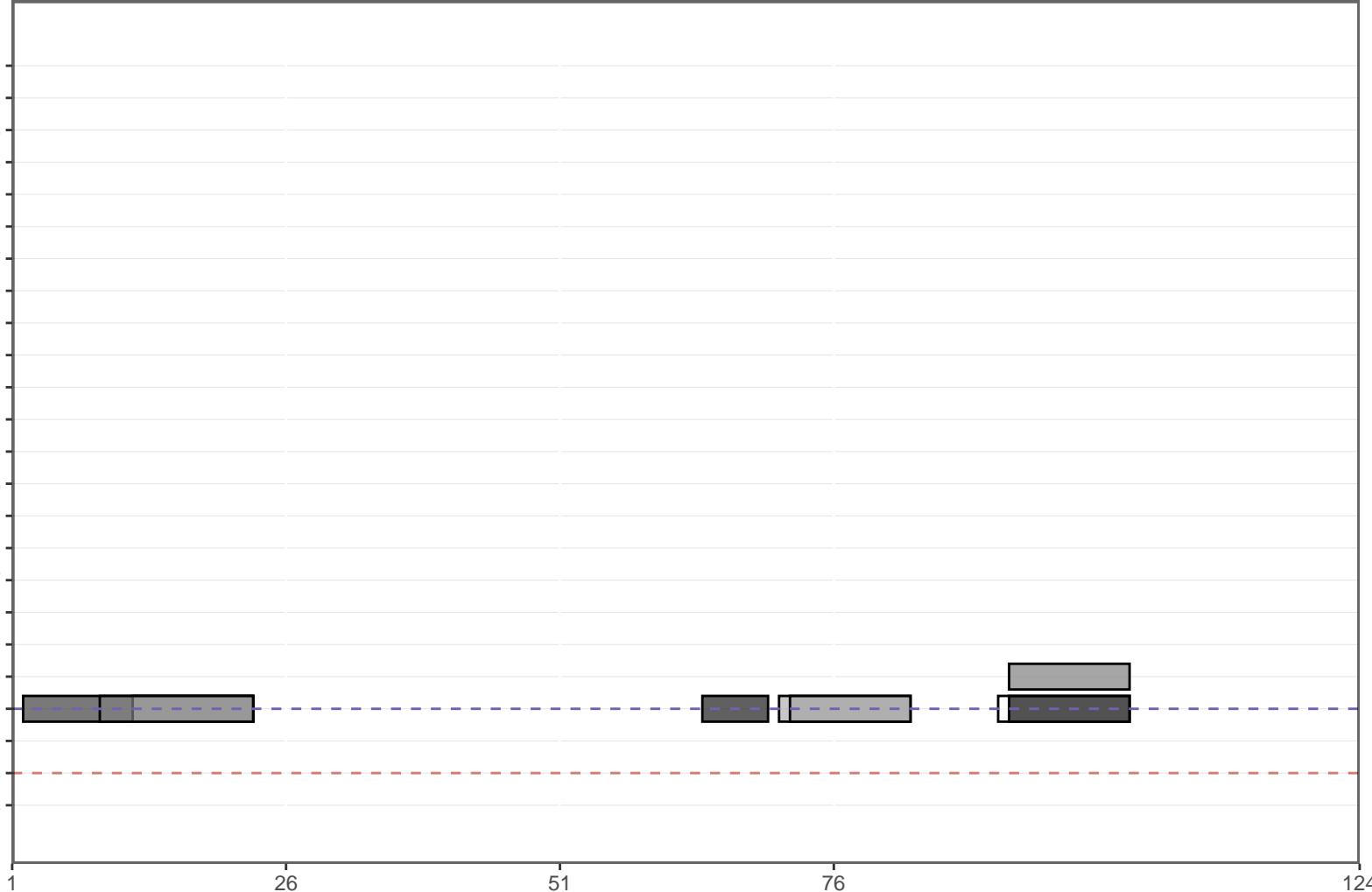
MW indication



Molecular weight

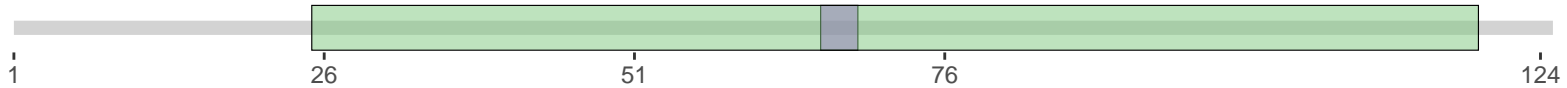


Gel Slice



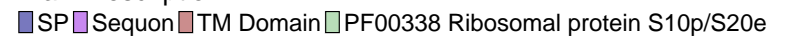
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

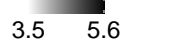
DKRLRVKGPVRLMPTKVALNITFRKSPGGEGTNTWDRFELRVHRVDFLSSADVWKGITSTIEPQVEVEVTIAD*

NbL01g08660.1 peptidyl-prolyl_cis-trans_isomerase_CYP22-like [MW = 20.59 kDa]

No. of times detected



log(intensity)



Values from



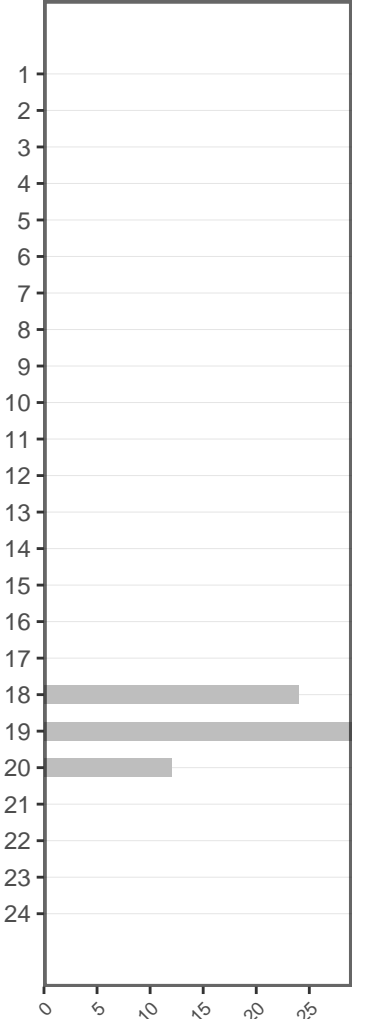
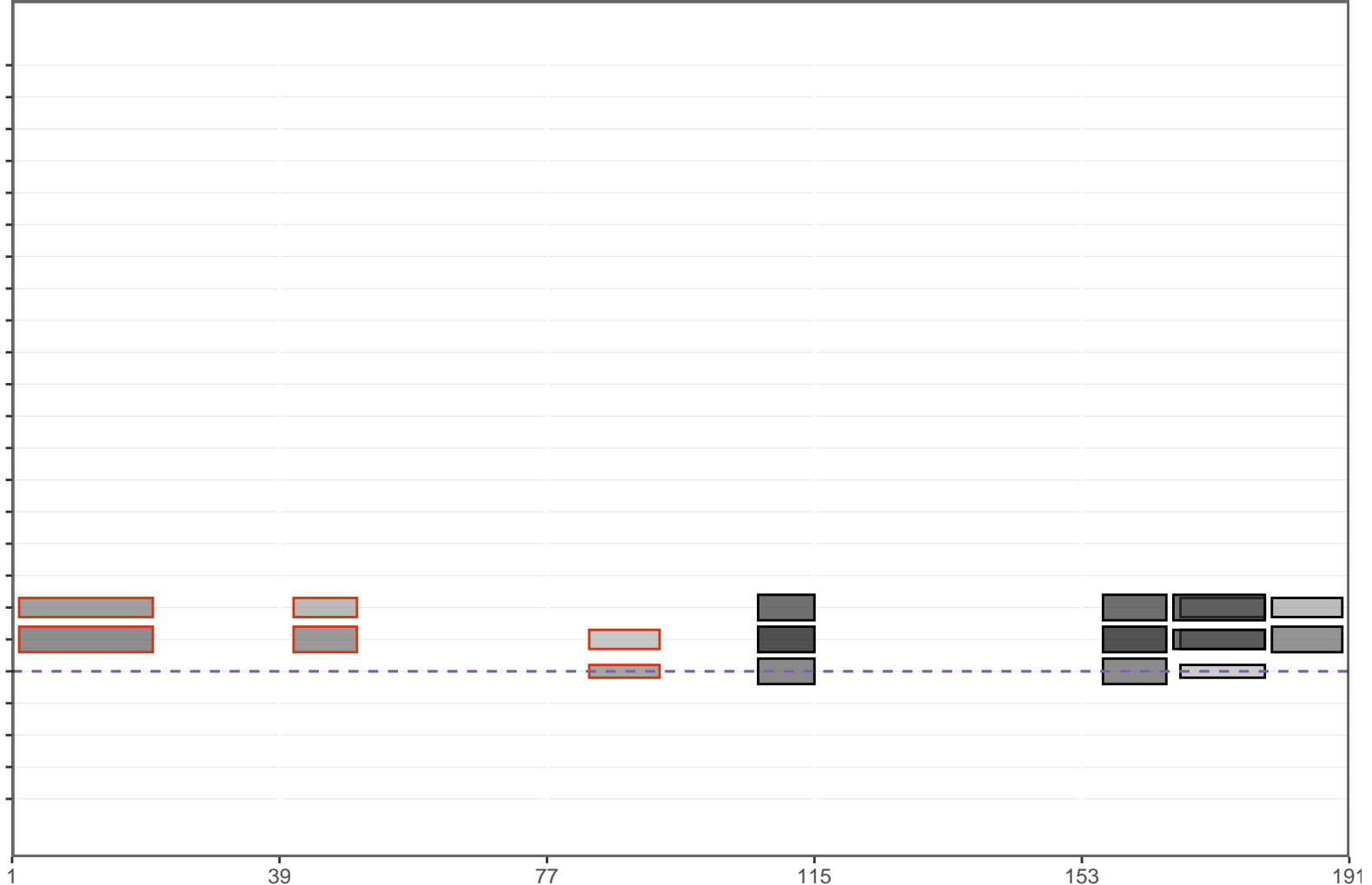
MW indication



Molecular weight

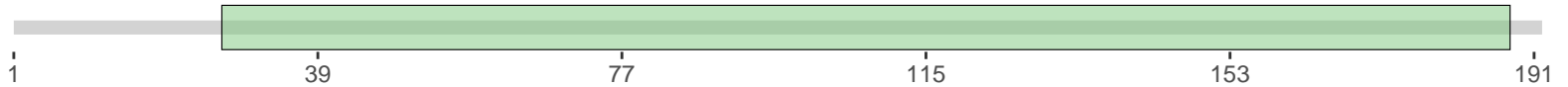


Gel Slice



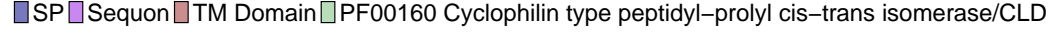
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IFMIGGDFLKGDGSGGVSHGSKFEDENFIKHTGPGLLSMANGSPNTNSGGFFVTGAKCDWLGNKHVYFGRVLDGGLLVVRKIENVAWGANNKPKLADMAEGGEM

NbL01g08600.1 aspartyl_protease_AED3-like [MW = 49.6 kDa]

No. of times detected



log(intensity)



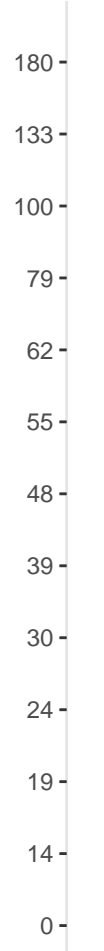
Values from



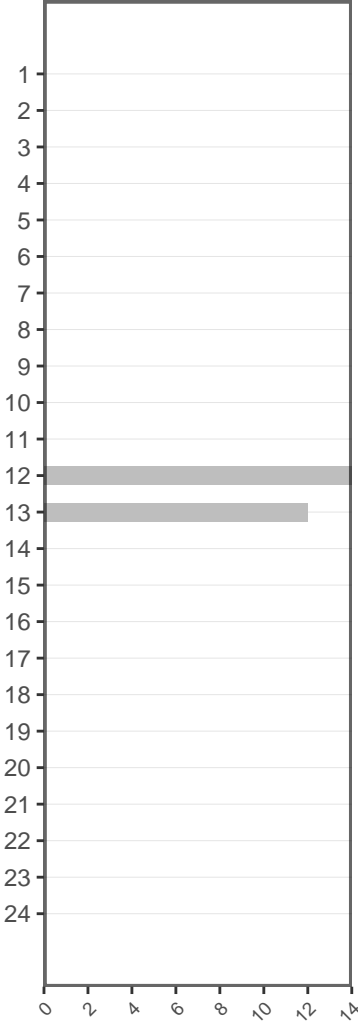
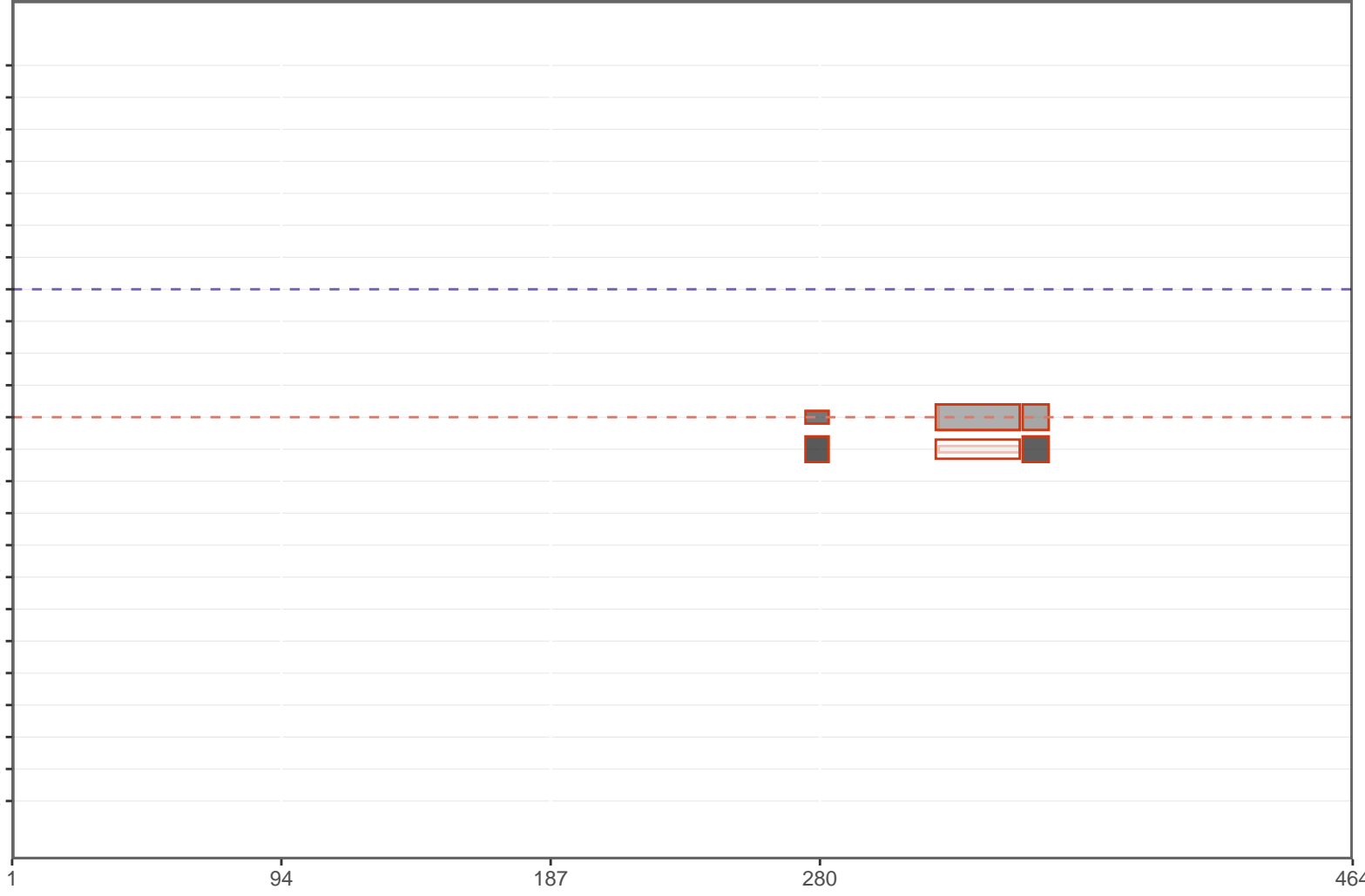
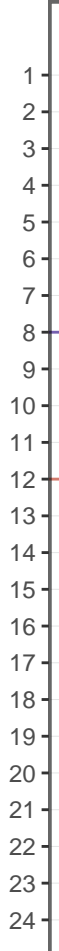
MW indication



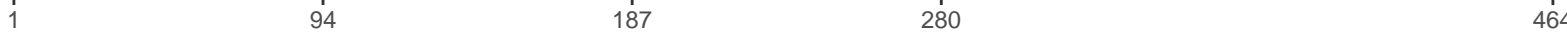
Molecular weight



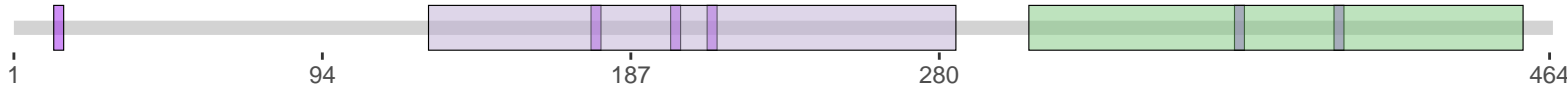
Gel Slice



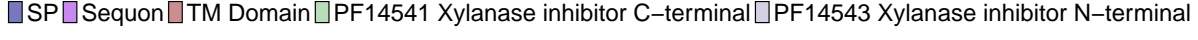
Protein length



Pfam domains



Pfam Description



Protein sequence:

STDVPSYTGCVKATGSSAPPOGLLGLGRPLSLFSGTQSHYQSTFFSVGLPBYKSNFAGTFLRLGPNGGPKRIKTTQLLRNPRR6SFYVNLVGVKVGSRIVDIPPSALAFNPTTGAGTIDSGTVFTRLVESAYTAVKNEFRFRMRGNTVTSLGGFDGTGTVPTPTITLTFAGMNVTLPGDNFLIR6666TTLAMASPADPNVSNLVNANWGGQNHRLFDVYNEKLGVAETCS

NbL01g08580.1 NAD(P)H:quinone_oxidoreductase-like [MW = 21.68 kDa]

No. of times detected



log(intensity)



Values from



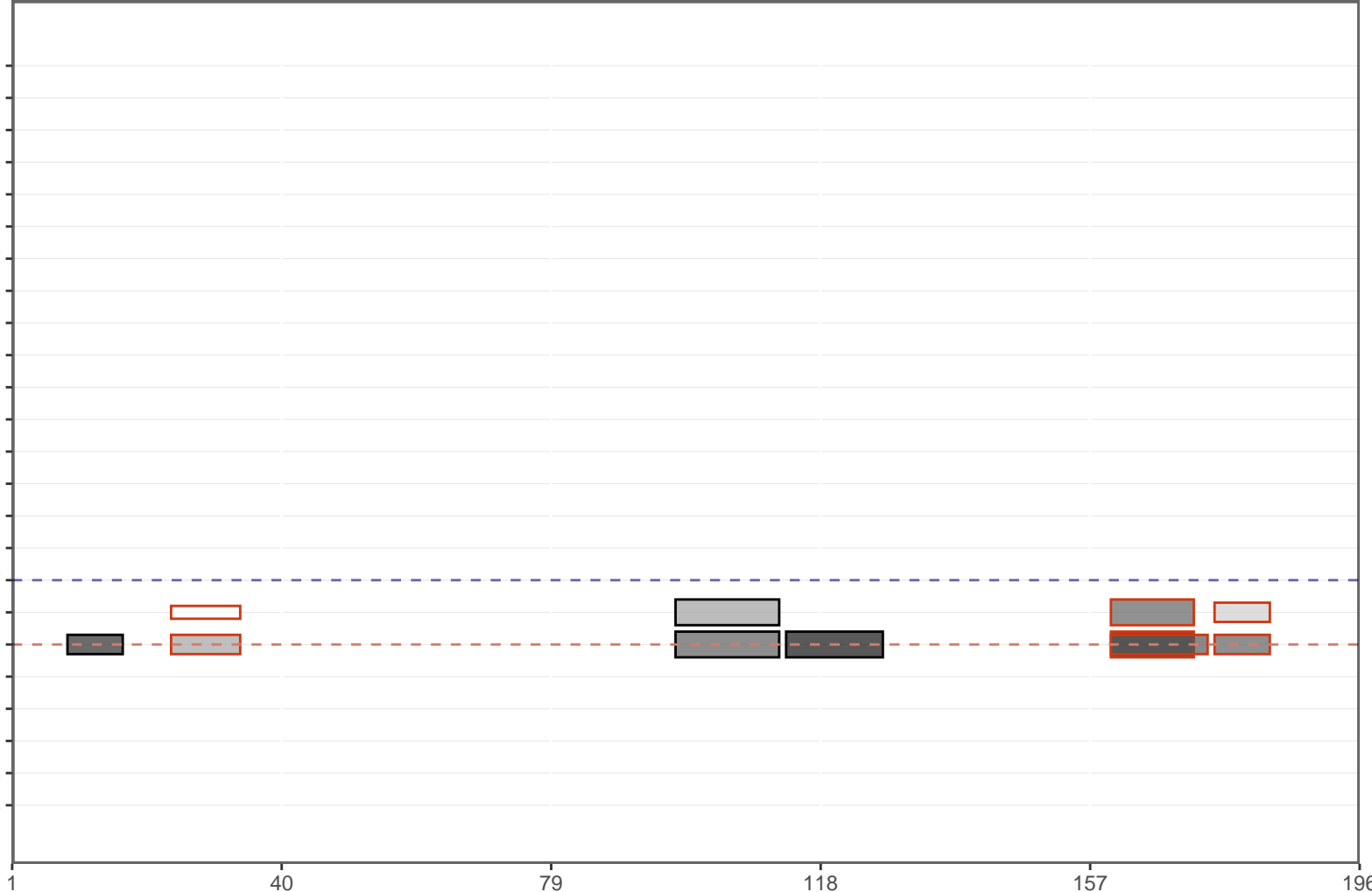
MW indication



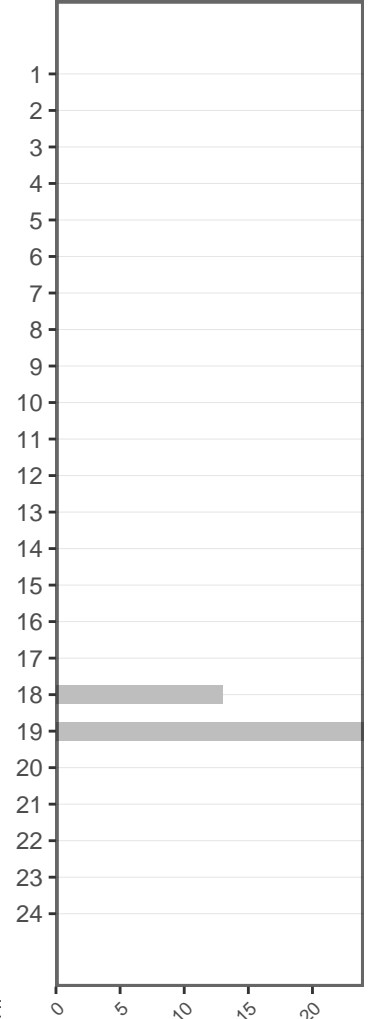
Molecular weight



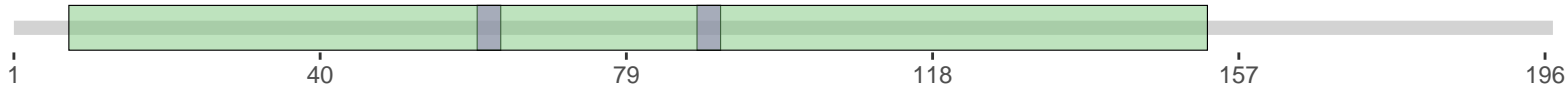
Gel Slice



Protein length

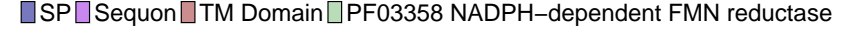


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

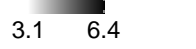
EYNYSVTGPLKNSDQWASRPNNWGDKAAAVSAGGNFGGGRSHYHLRQIGYDHLFINKPEFFLNAFELPKPKFDGGVLTDEESKNRKEVLLVLAFAFLRLKGLKSE

NbL01g08560.1 NAD(P)H:quinone_oxidoreductase [MW = 21.94 kDa]

No. of times detected



log(intensity)



Values from



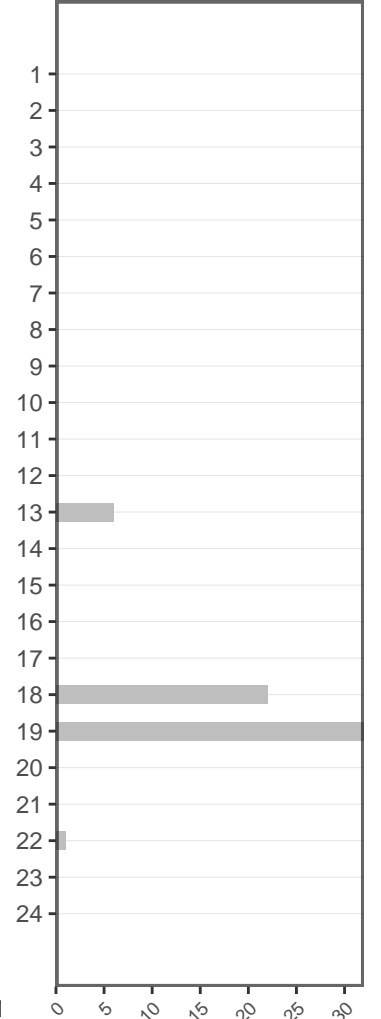
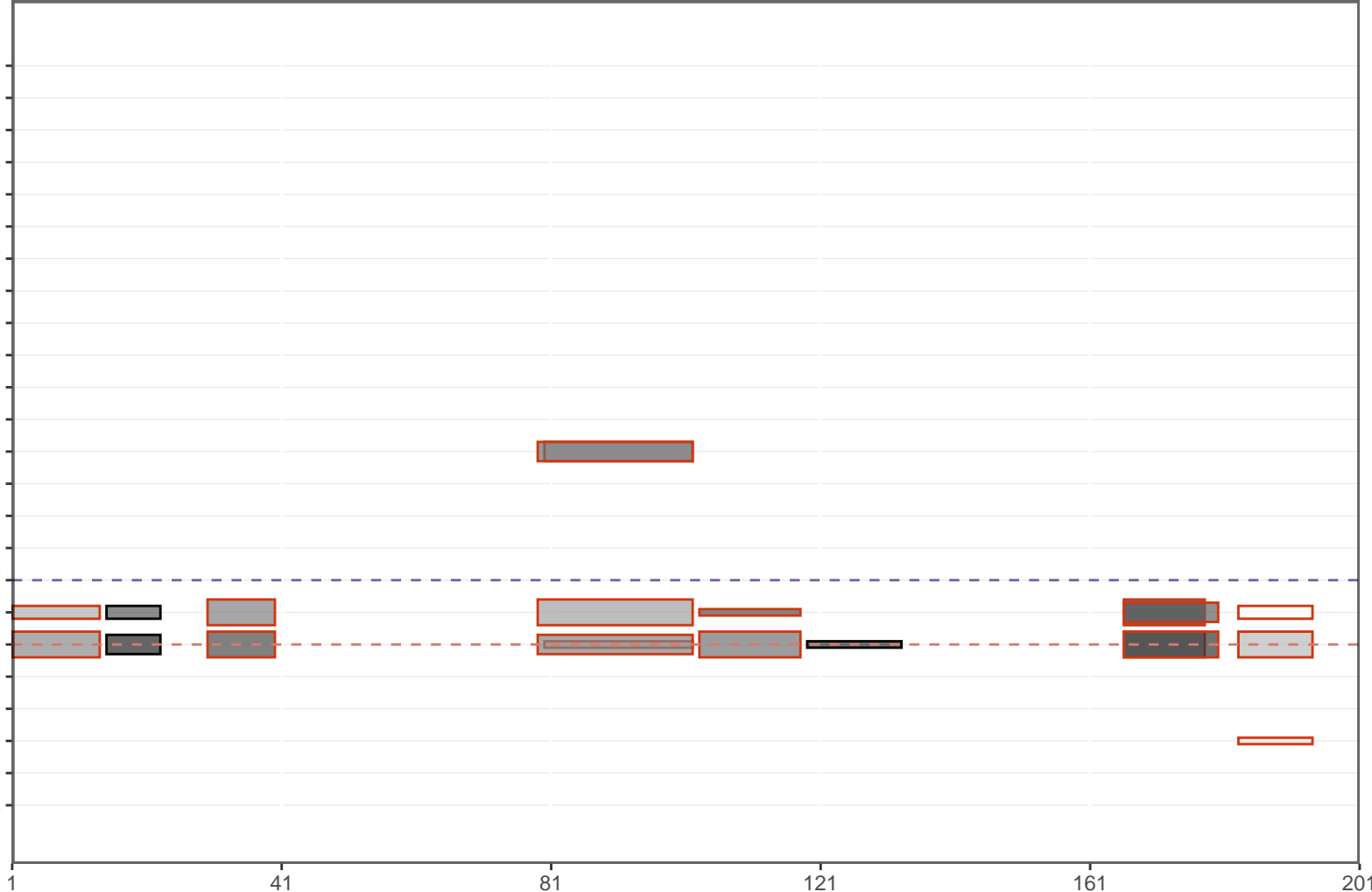
MW indication



Molecular weight

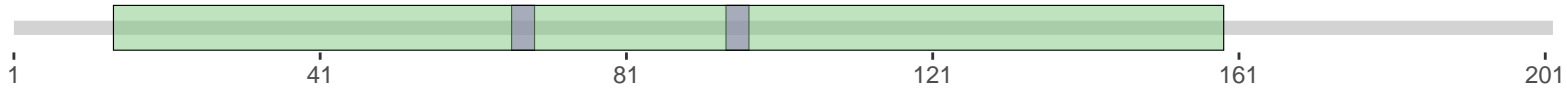


Gel Slice



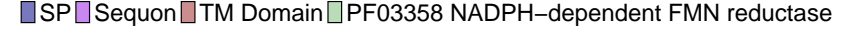
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

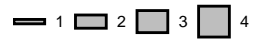


Protein sequence:

ASPEYNSVITGPLKNAIDWASRPFNWADKAAAVSAGGGFGGGRAGYHLRQIGVYLDLHFINKPEFFLNAFQPPSKFDSGDVLTDEETKQKIKALLGLGAFTRLKKGKE

NbL01g08040.1 clustered_mitochondria_protein_homolog [MW = 209.8 kDa]

No. of times detected



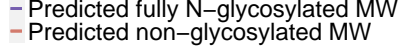
log(intensity)



Values from

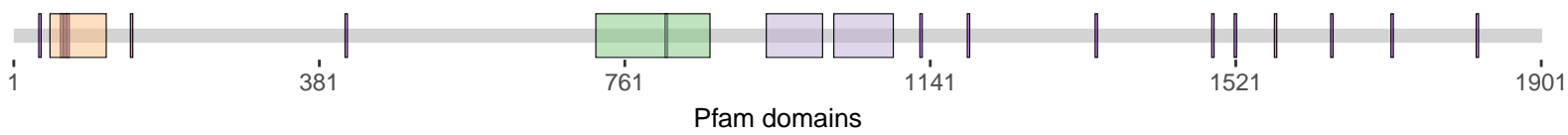
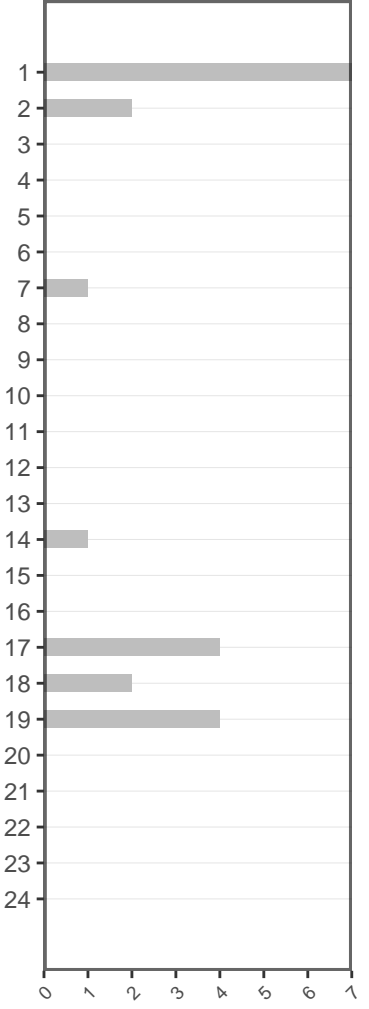
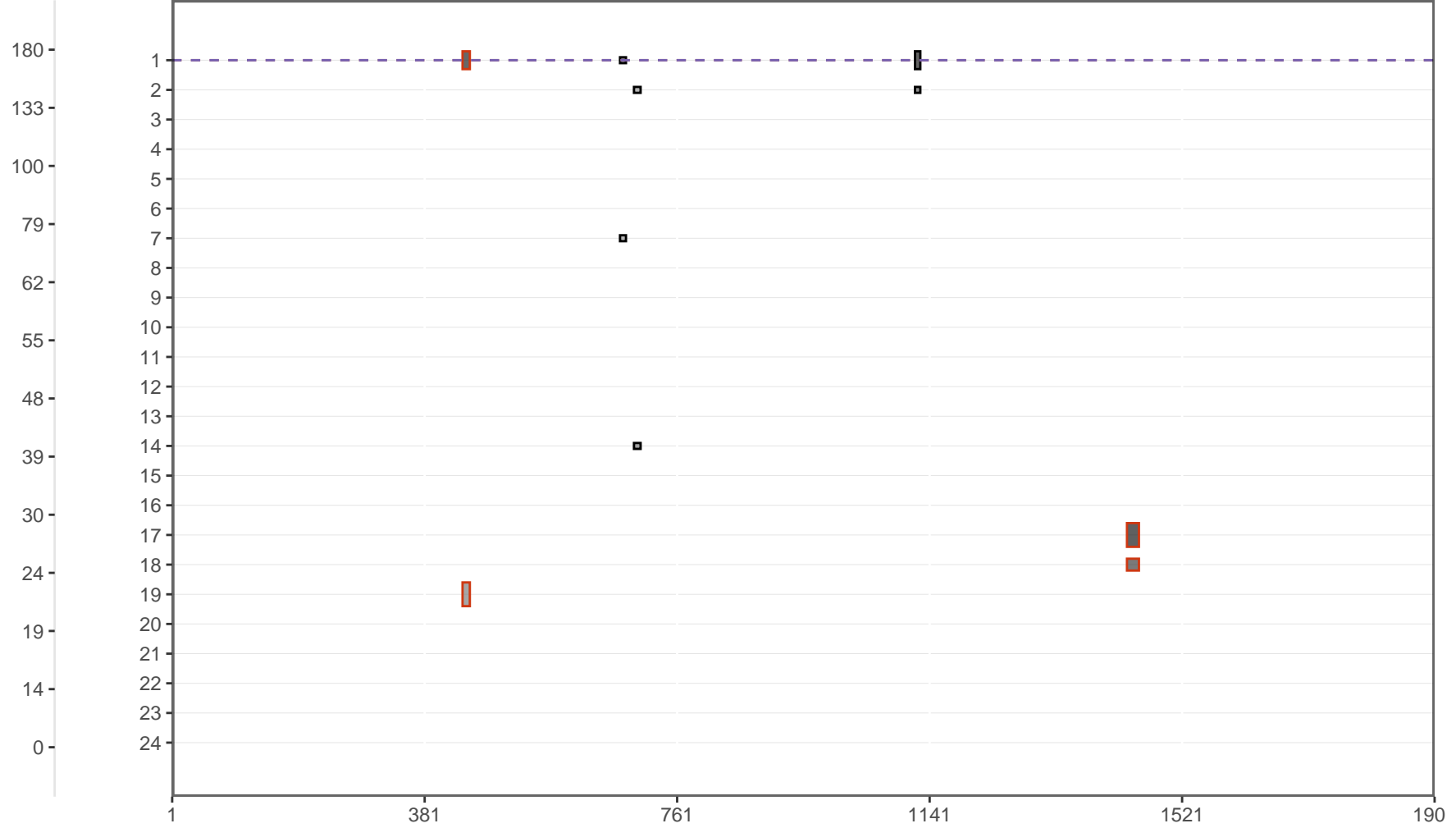


MW indication



Molecular weight

Gel Slice



Pfam Description

- SP
- Sequon
- TM Domain
- PF12807 Translation initiation factor eIF3 subunit 135
- PF13424 Tetratricopeptide repeat
- PF15044 Mitochondrial function, CLU-N-term

Protein sequence:

IAYSLLAIVLYHTGDFNGATRYGKALGINERELGLEHDHPTMKSVDLAVFYRRLQHTLAKLYKRALYKLLHTGGPSHPNTATYINWAMMEEGLGKLVHVALRKLKALKGNKGLLGPDHQTAASYHAMALESLMEAYPLSVQHEGFTLQILRAKLPDDLRTQDAAWLEVFESKAFEGQEAARNGTKPDSIASKGLHLSVSDLLGVNPNPDAKGRDYGSKRKGFSYKAFISQVKGSGDGSNVTSPN6DTPK6VLKEESDEEKHVEDHTDPHPOMNLEFPDVTYKFI

NbL01g07800.1 jasmonic_acid-amido_synthetase_JAR1-like [MW = 67.33 kDa]

No. of times detected



log(intensity)



Values from



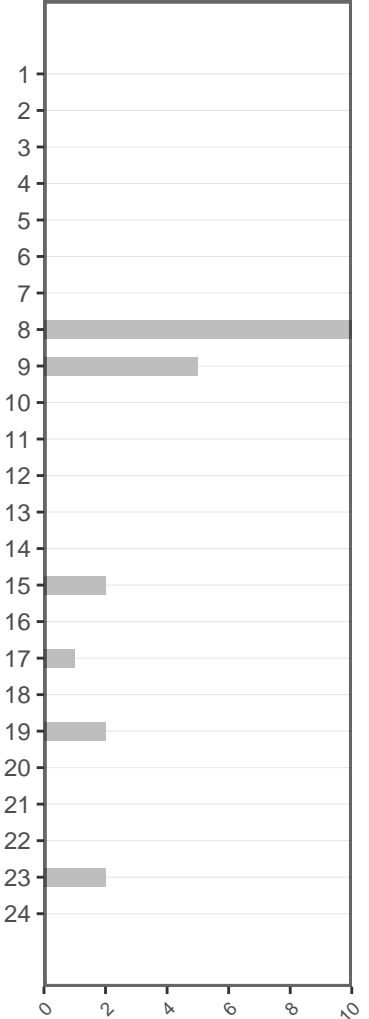
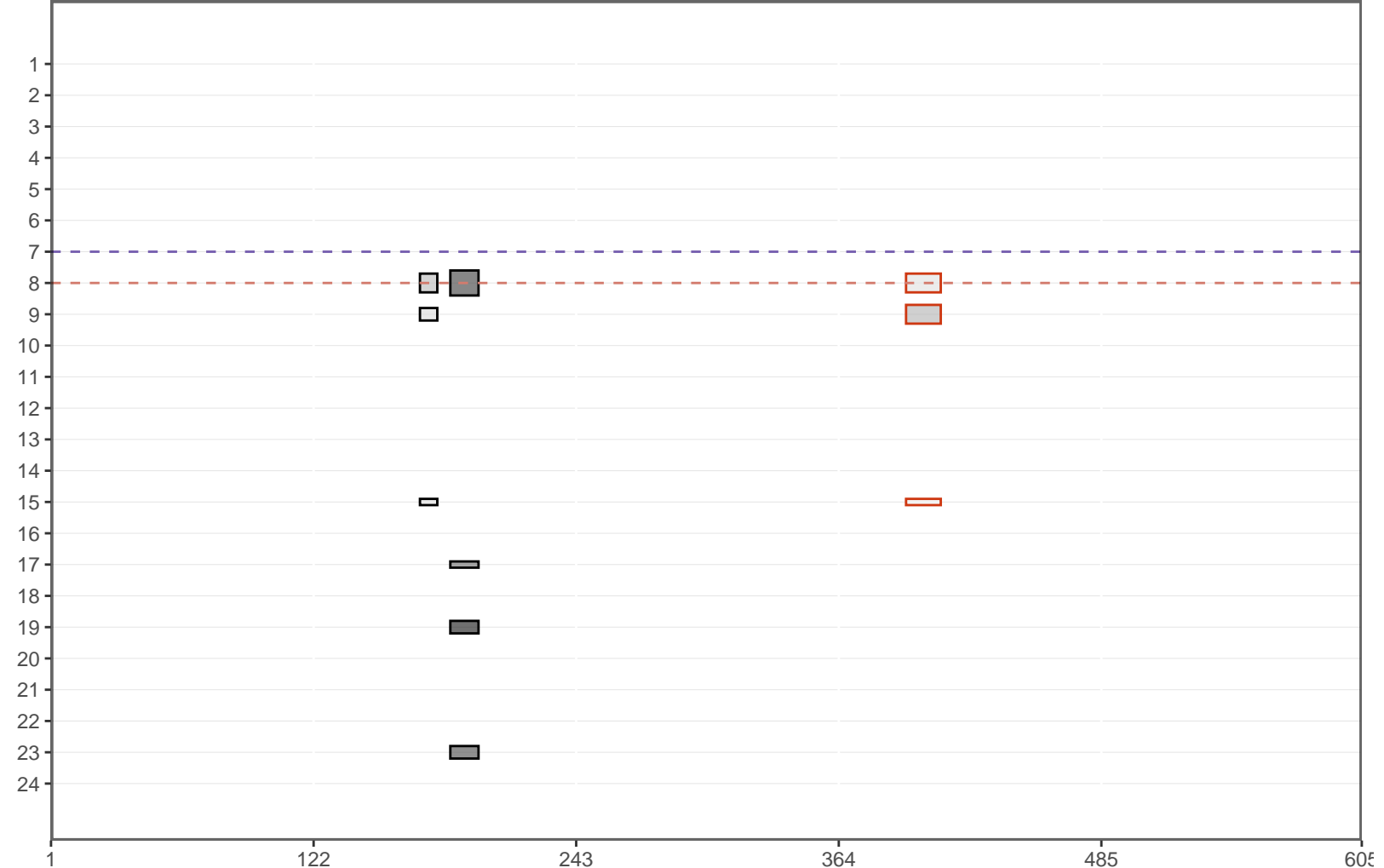
MW indication



Molecular weight

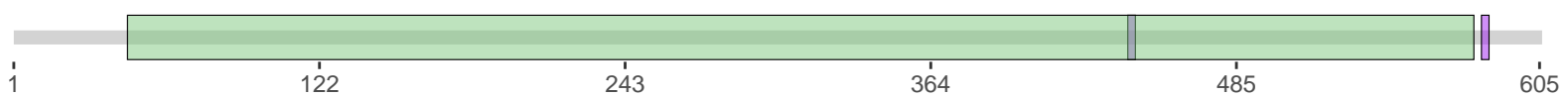


Gel Slice



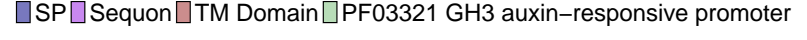
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SKLLKDPDEQADTFRRKGGSLNHWGLIPVFNKAVYVGMVTSMEPYLKLRLHYAGELPLGADHYGSSSEGWGANVVKPLPELVYAVLPLNGVYEFIPLRGDLGVEPTPVGLAEVKGEEYEVNVTNFAGLVRYRLGVDVYKIKGFHNATPELQFGRNLLSINIKNTKEDLGLAVEAAKLLVNEKSEVVDFTSHVWVAADPGHVVVFWVELSGEASDETLQEGCNLQKSFVDVMDYLGSRKANAGALELRVAKRGTFRHKLDHFVGLGGAVSGFKTPRCVGFNPSTI

NbL01g07710.1 exosome_complex_component_RRP41_homolog [MW = 26.62 kDa]

No. of times detected



log(intensity)



Values from



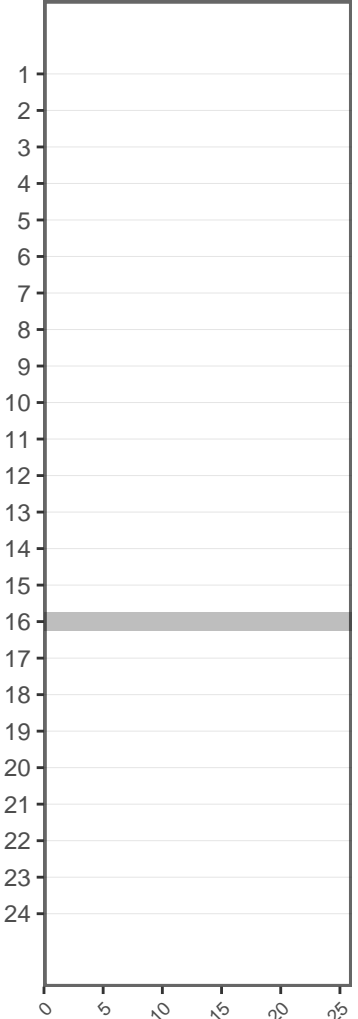
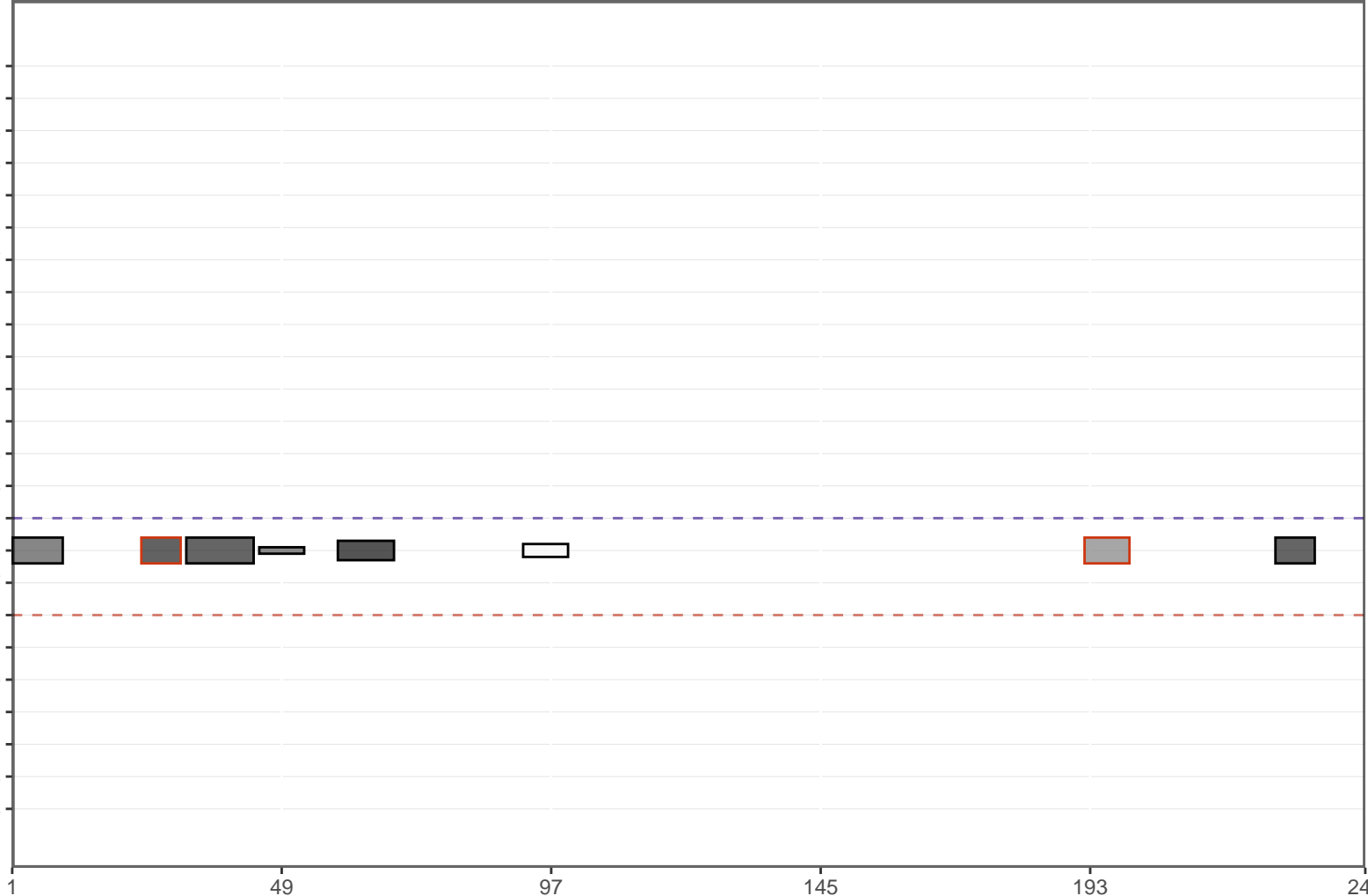
MW indication



Molecular weight

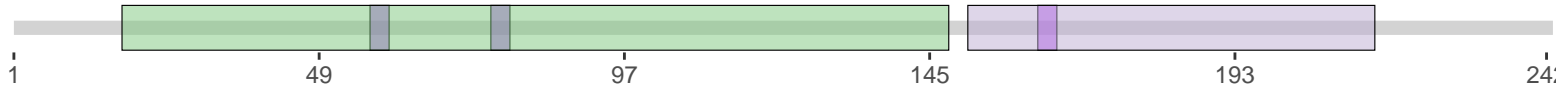


Gel Slice



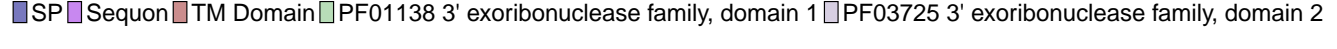
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

ACILTHLMRPSQIDIFVGVLGADGGTRFAGINAATLALADAGFMRDLVTRSGAGYLNSTPLLENNKLEDSAGGPDVTVGLPKLKHVTLIGMDKLPIDTFETVMQLAVEGGKAVESVIREILLENTKKLEIRRGV

NbL01g07670.1 uncharacterized_LOC107820362 [MW = 27.55 kDa]

No. of times detected



log(intensity)



Values from



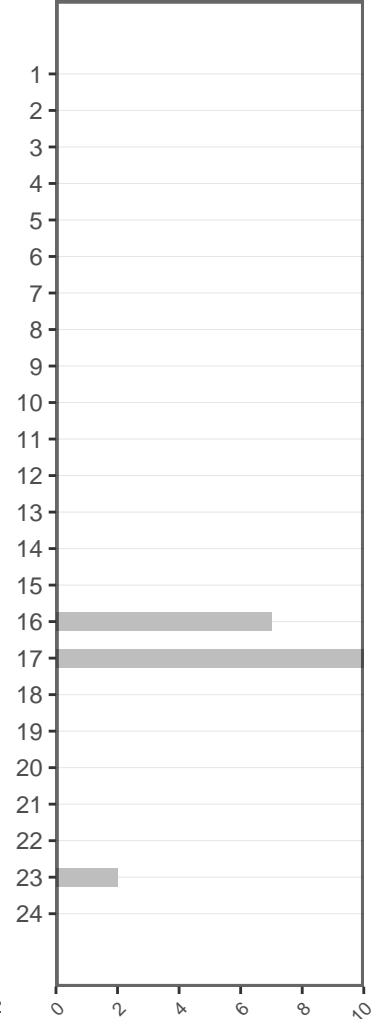
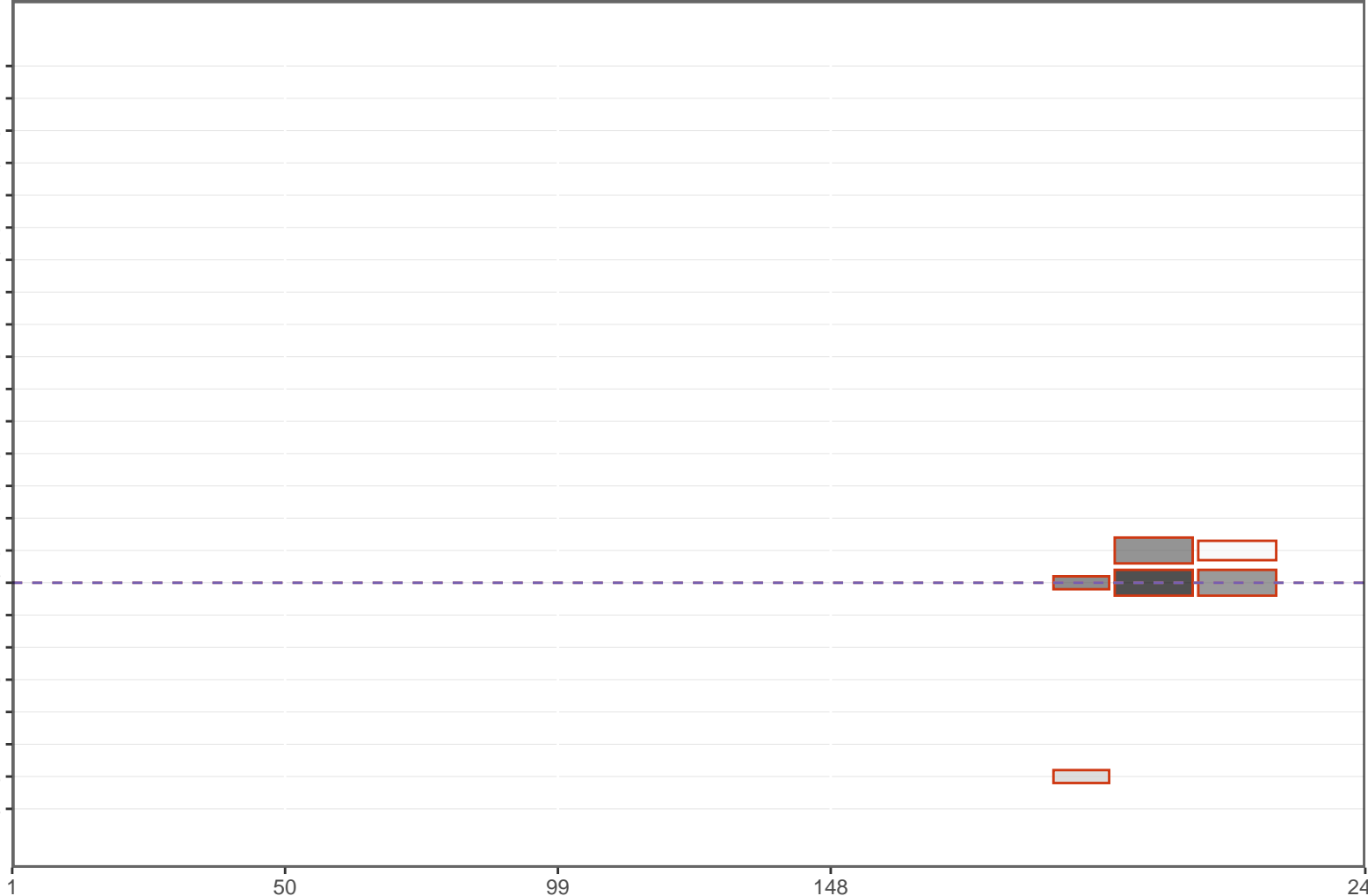
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description
■ SP ■ Sequon ■ TM Domain

Protein sequence:

IRDEELKXKXKXKKEFANFVPIGPPGLDHLGLVDEKLPKYEMTVEDGRRLAKEYSRVLMRKHRRGRQAAESTLLRLKKEAIEALPENLKAALIPDLTFPPVNRFRMATLTPPEIEGVEKVAANKSSAKEKLR

NbL01g07660.1 eukaryotic_translation_initiation_factor_1A-like [MW = 16.32 kDa]

No. of times detected



log(intensity)



Values from



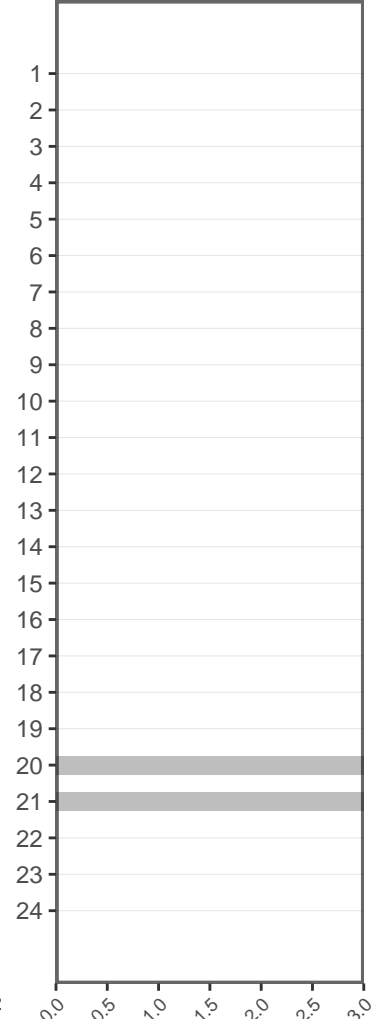
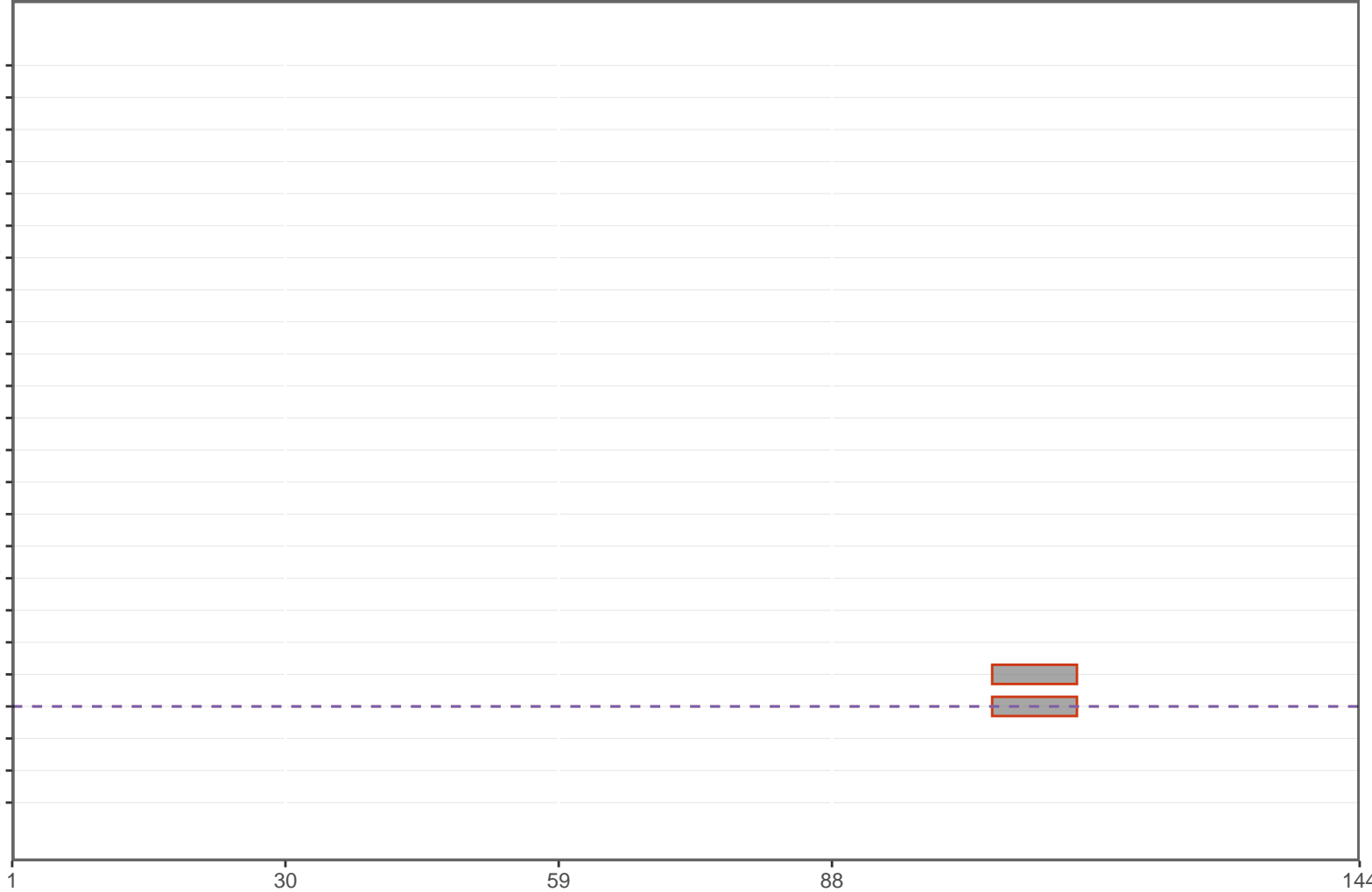
MW indication



Molecular weight

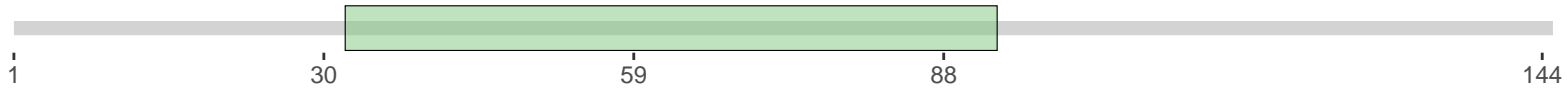


Gel Slice



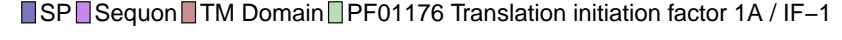
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

RLCHIRGKMRKKVWVAAGDILVGLRDYGDQKADVILKMPDEARLLKAYGELPESTRLNEVGLDEEDDGGDDVIEFEDEDIKI*

NbL01g07470.1 desiccation_protectant_protein_Lea14_homolog [MW = 18.52 kDa]

No. of times detected



log(intensity)



Values from



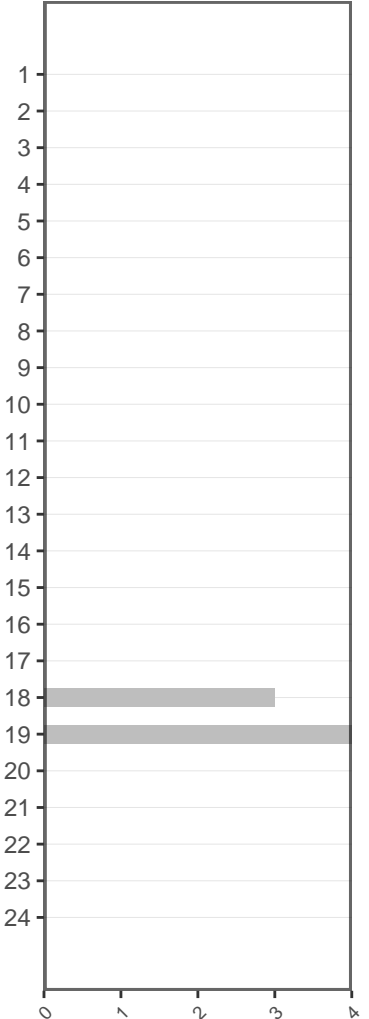
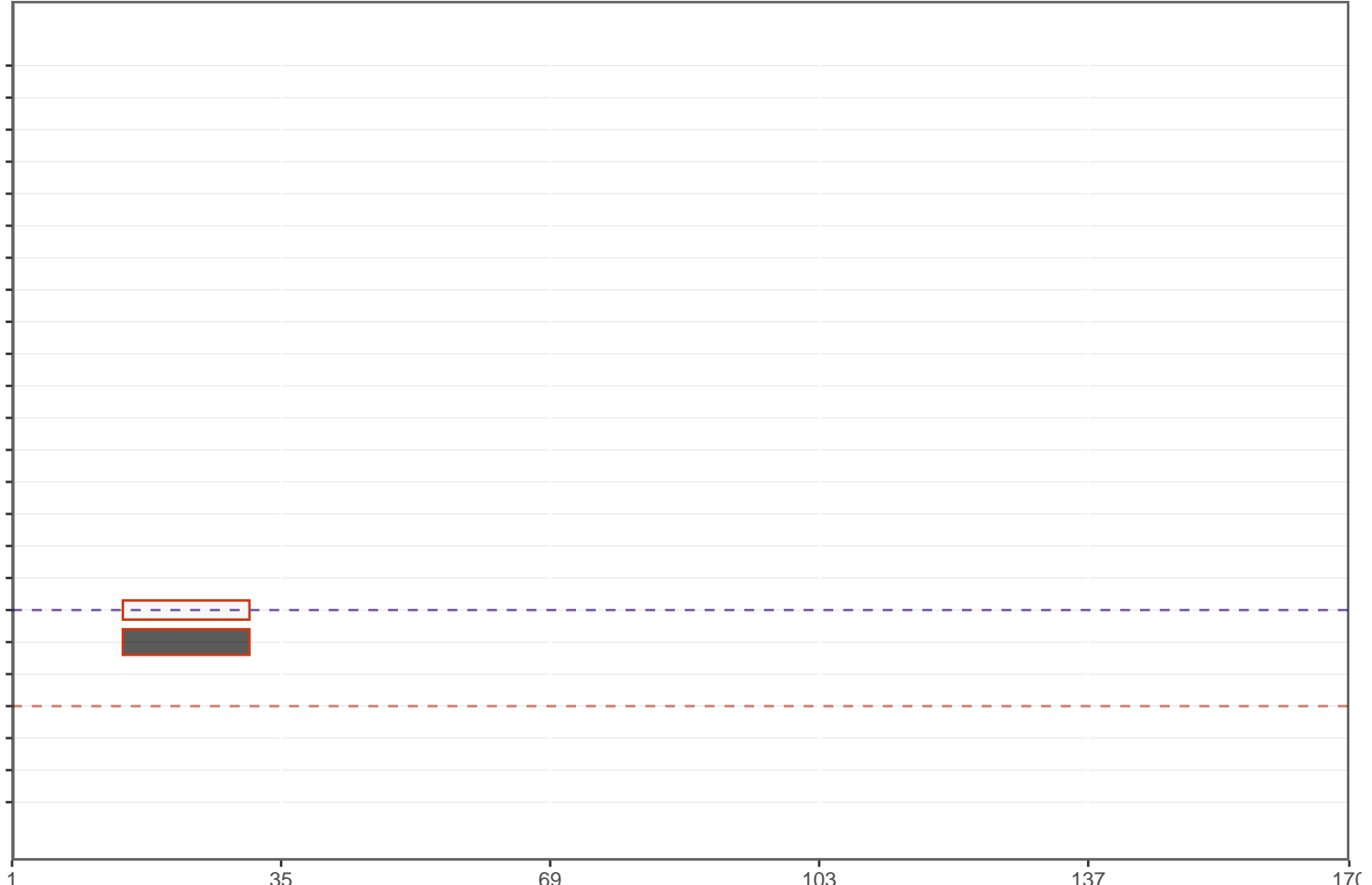
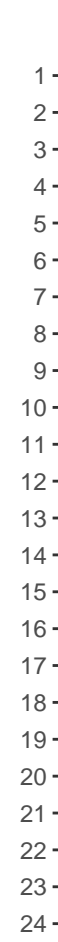
MW indication



Molecular weight



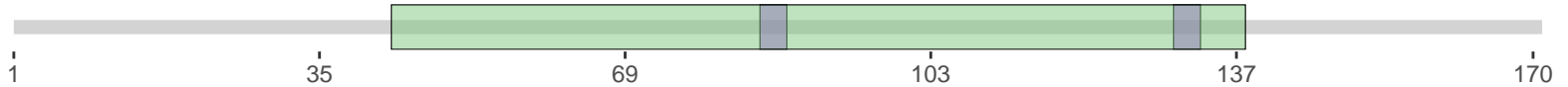
Gel Slice



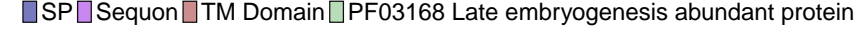
Protein length



Pfam domains



Pfam Description

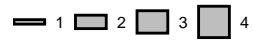


Protein sequence:

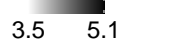
IGRIDPQGNKANDSTMLDVPVQVPHSVLLSLVLDLGGDWDIDDTLELGLHDLPLVGNFTPLSYSGEYKLPFLSDLWGTGKEEDEKEDPTKVEP

NbL01g07460.1 proline_aminopeptidase-like [MW = 57.49 kDa]

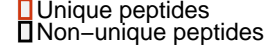
No. of times detected



log(intensity)



Values from



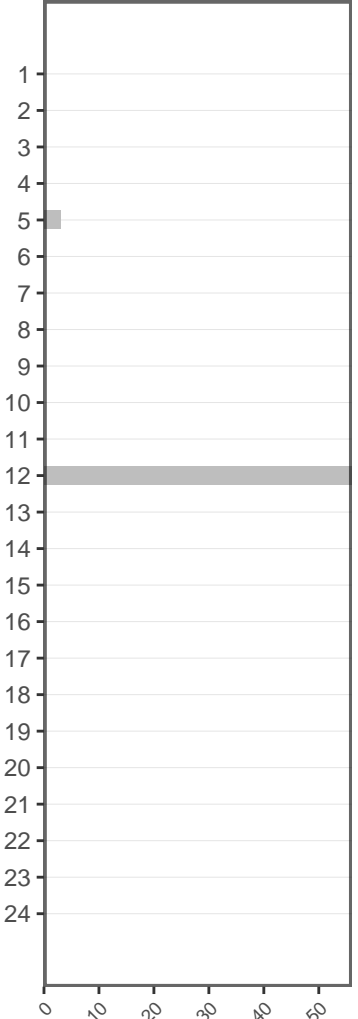
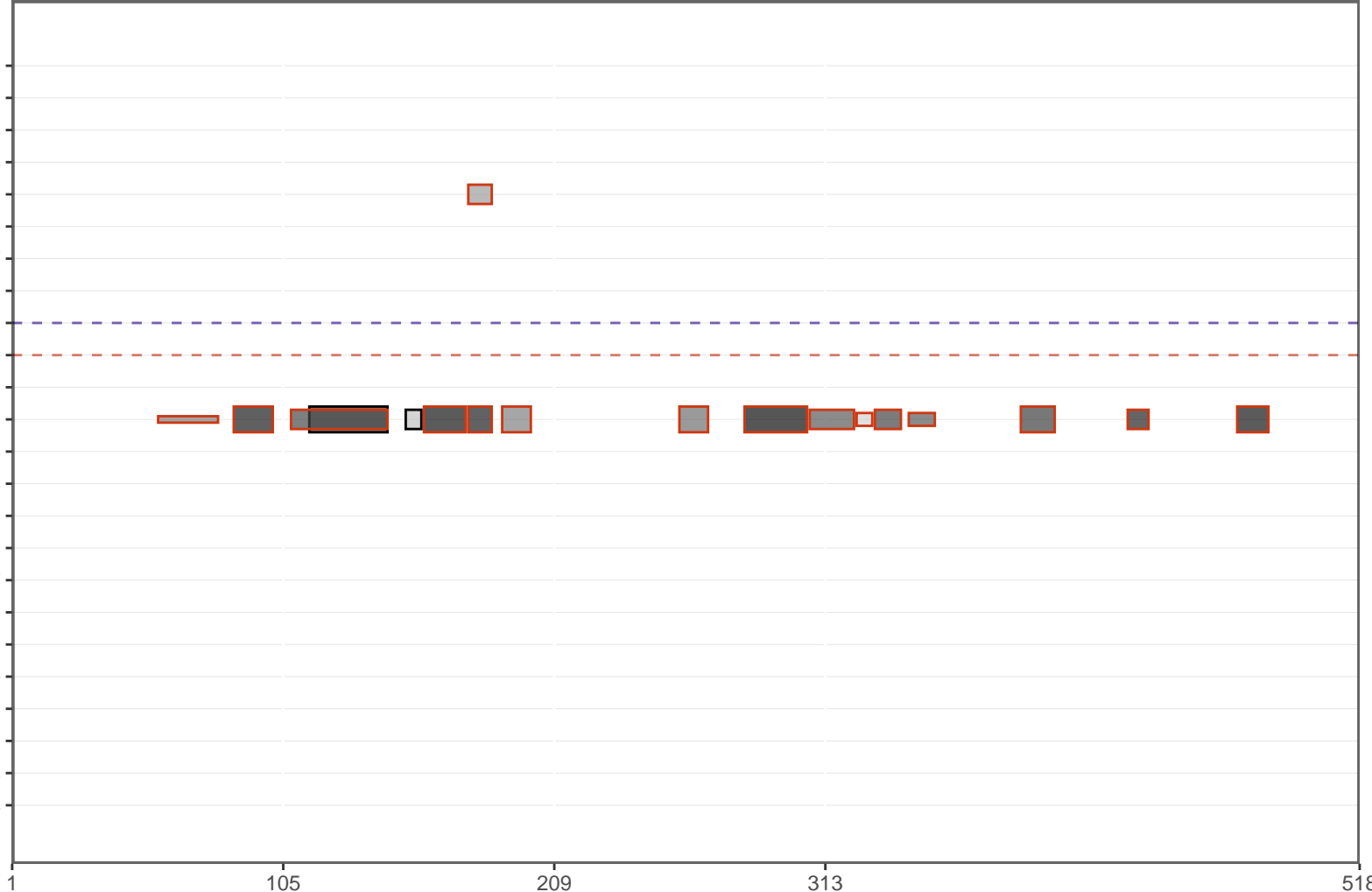
MW indication



Molecular weight

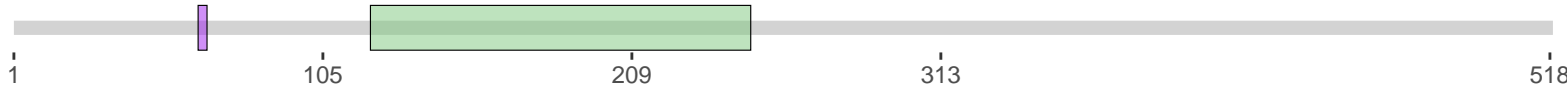


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

KGCTADAVYRAGFEQLMHQNEKYYKRFQDIEVRDKVNYLAESEGGGLPLPSGGILTRGLGLLGLGSGSNGFERLHYLFFERVWDSVVGAKRRISDFLNAVIERWAFDANPLVALLHESVYQDGSLLWSAHRRAENENKFDIEAAKGGSPVLTGEMIFWLFDEVHALRPFKDAAGLAEKKWPSLYDIALKDKNVVPAWAAVYEDMNVNFKLSMETASQAIGRLWITNEYMHHSGLRDAGSKVLDHLMLNKKPLP

NbL01g07280.1 succinate_dehydrogenase_[ubiquinone]_iron-sulfur_subunit_2_mitochondrial-like [MW = 31.15 kDa]

No. of times detected



log(intensity)



Values from



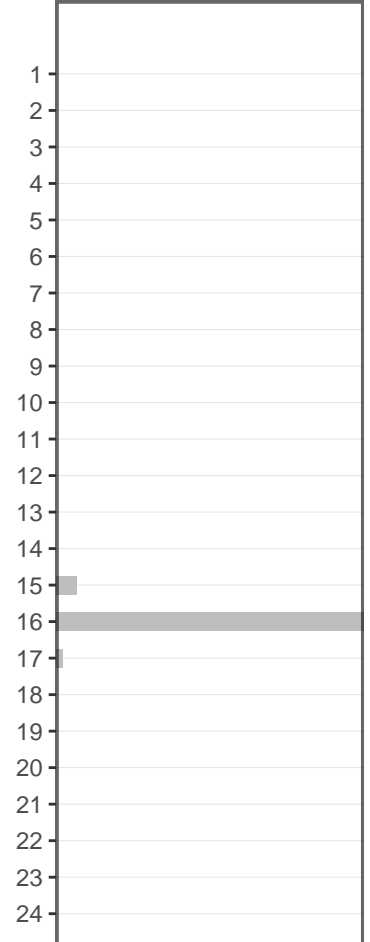
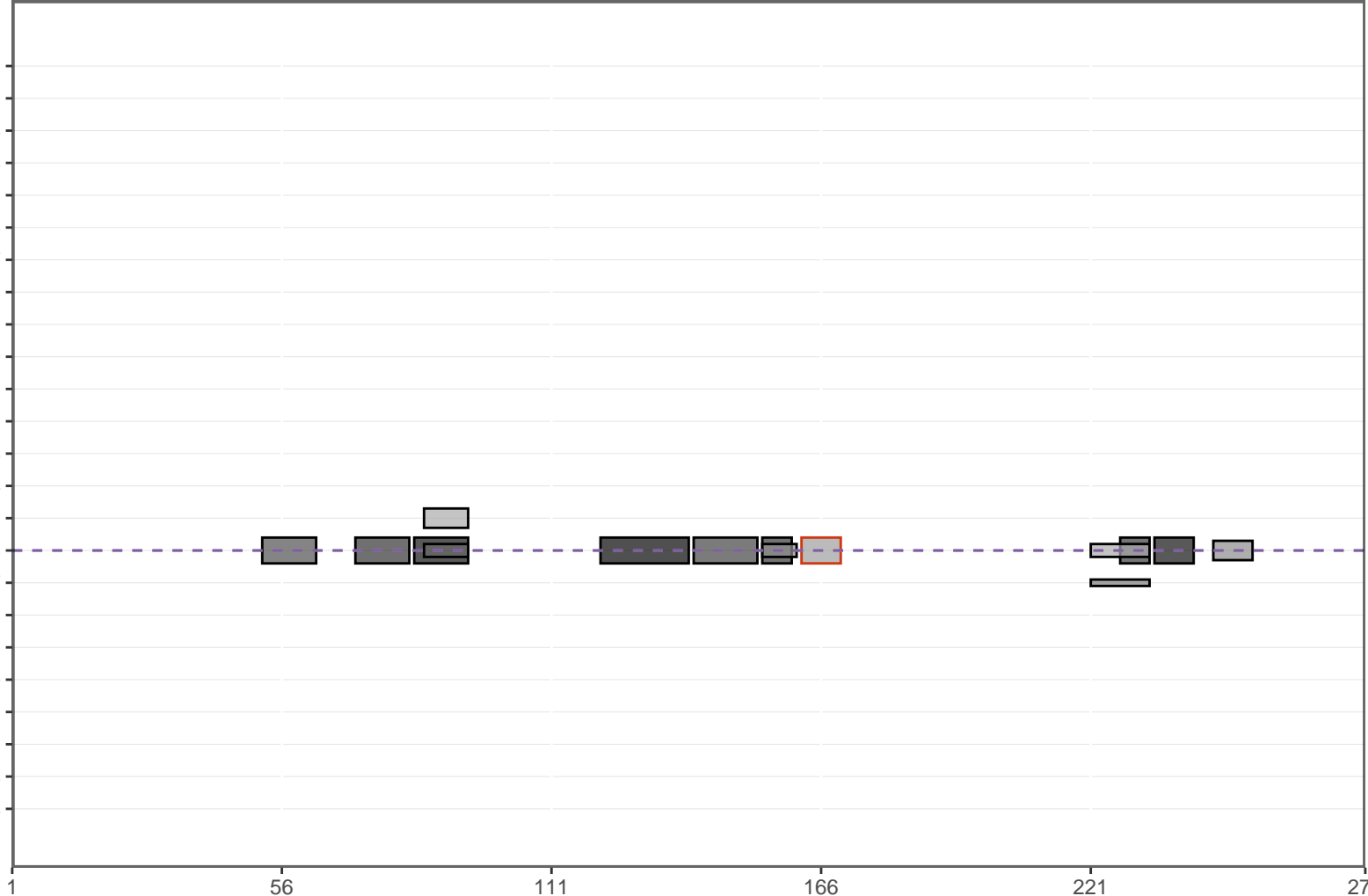
MW indication



Molecular weight

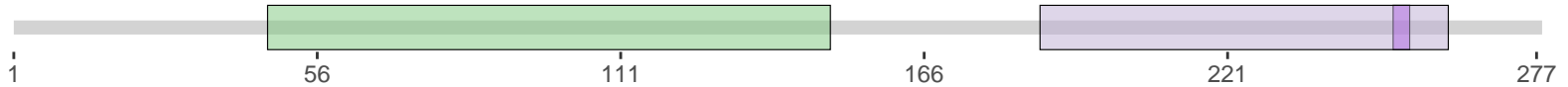


Gel Slice



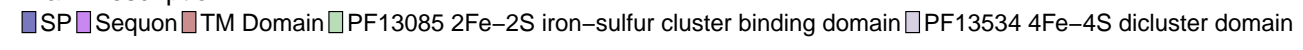
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

STITPLIMFVKDLVDMFNFDNYKSIPIWLRKRTPTPTGKPIQGSKDRRAKLDGMVEICLCAAGSTGCPVYWWNPESVLPAAALHANRRWMDGRDEVTQERLDVANDFKLYRCHTLNGSRACPKGLNPGKHQNKRLLEAS*

NbL01g07120.1 bifunctional_L-3-cyanoalanine_synthase/cysteine_synthase_2_mitochondrial [MW = 39.41 kDa]

No. of times detected



log(intensity)



Values from

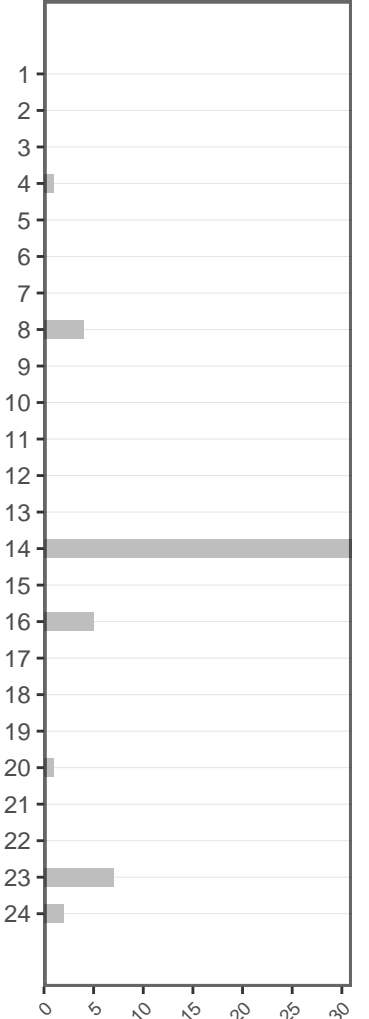
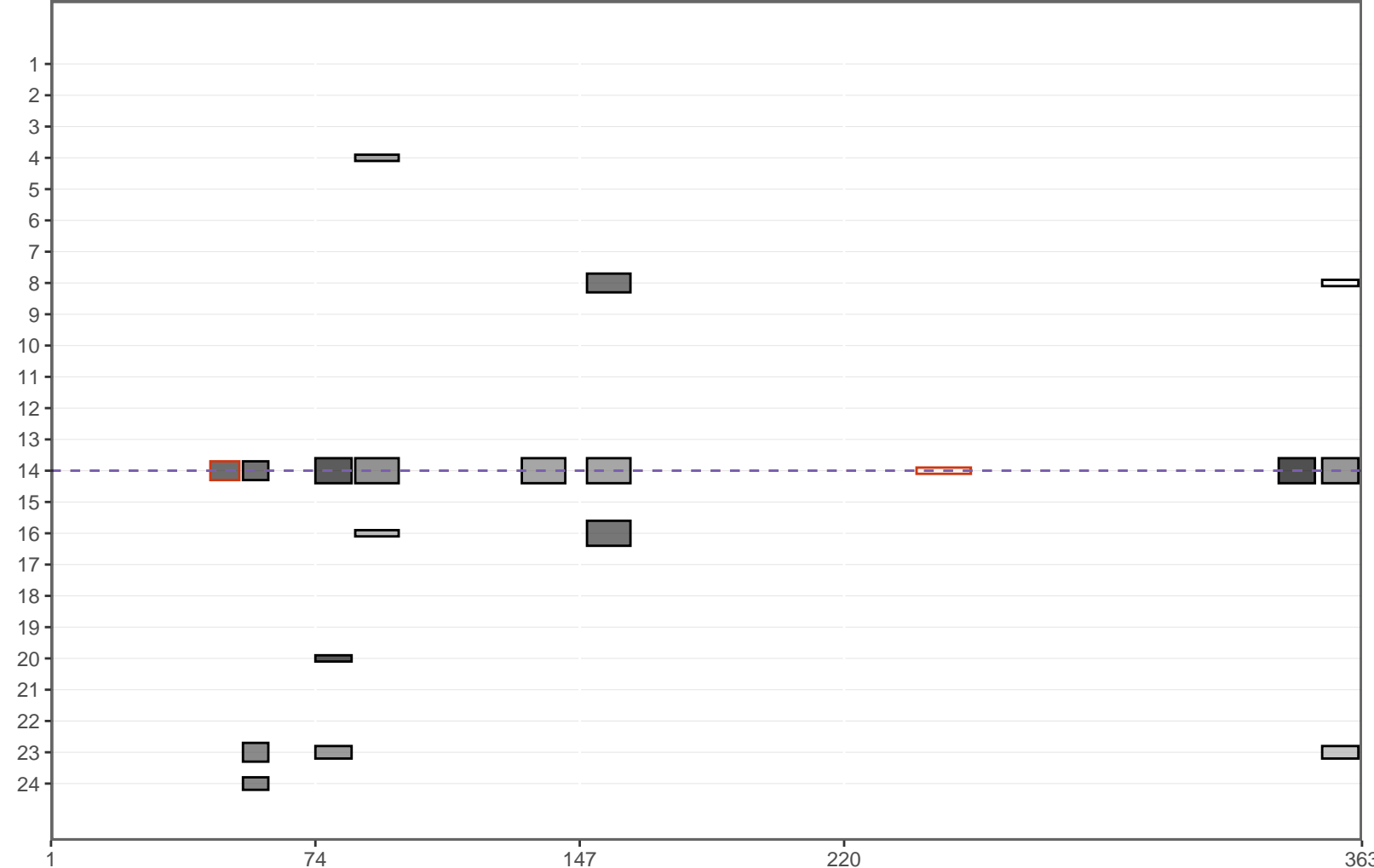
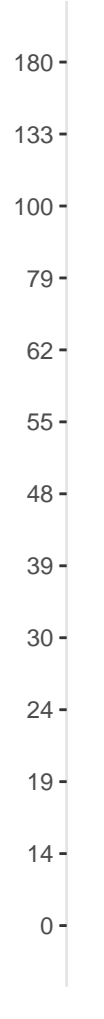


MW indication



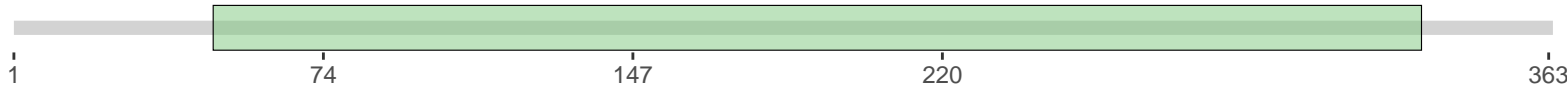
Molecular weight

Gel Slice



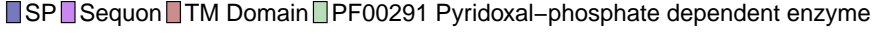
Protein length

Peptide counts over 4 repeats



Pfam domains

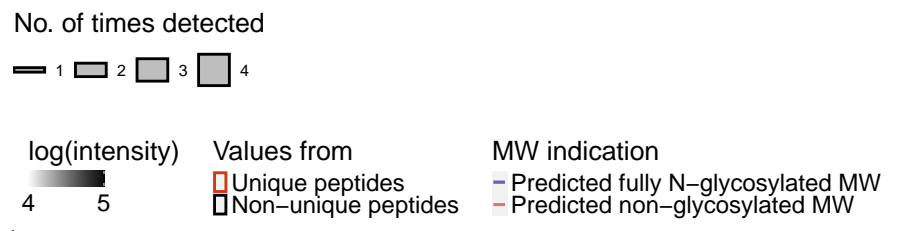
Pfam Description



Protein sequence:

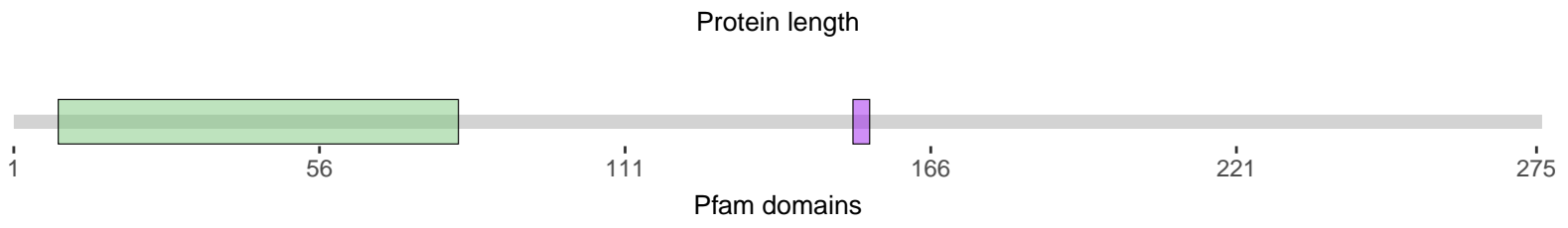
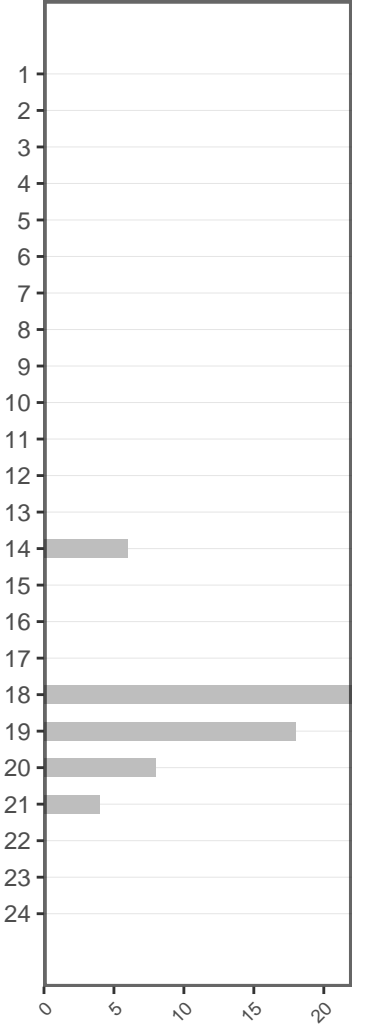
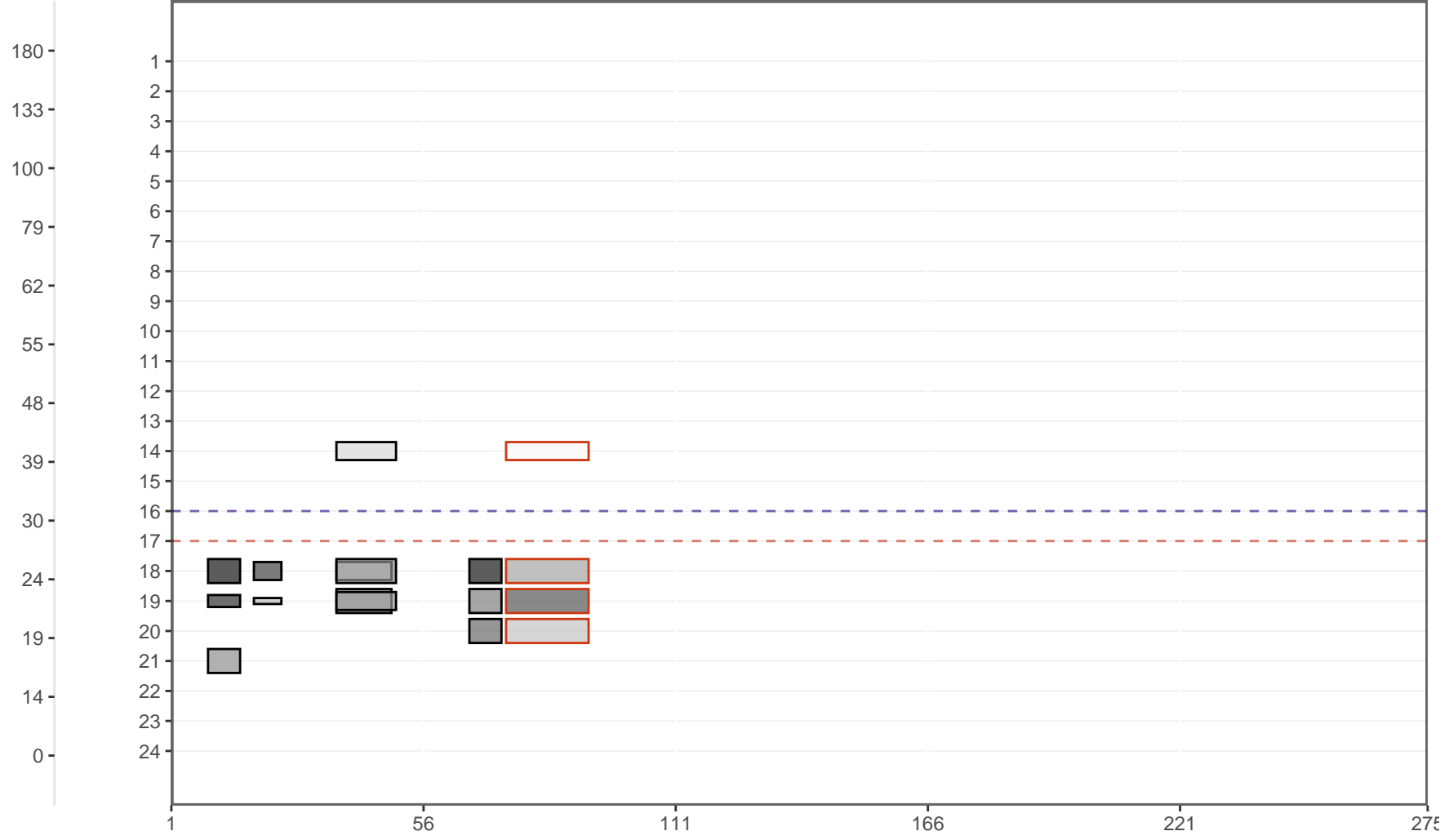
AYDLDLETPNFMIGQGFNPNFQHFHETTPGEIWEETGGNVDFVMDGIGGGTVSGVGVYKSKNPNVKGVGEFTESNVLNGGKPGPHHTGNGVGRKPDLDMDIMEEVLVMSSEDAVNMARELAVKEGLMVGISGGANTVAALQLAGKPKNGKLVTRHASFGERLYLSSVLYGDLRKEAENMQRVSVQ

NbL01g06840.1 small_nuclear_ribonucleoprotein-associated_protein_B'-like [MW = 28.91 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain PF01423 LSM domain

Protein sequence:
 VRLGGGAPGMMQFQSRFPFNVEAPFNMYRPPVMRPPGGPPMGMQRPGFPPFMAAPPFQFRPGGPPQFPFQFGRPMVPPFPMRGRPPRPPGAPRPPMGGPPGPPRPPMPPPPGGGVVYVGRPRGMPPPPGNGQ

NbL01g06830.1 acyl-CoA_thioesterase_2-like [MW = 49.12 kDa]

No. of times detected



log(intensity)



Values from



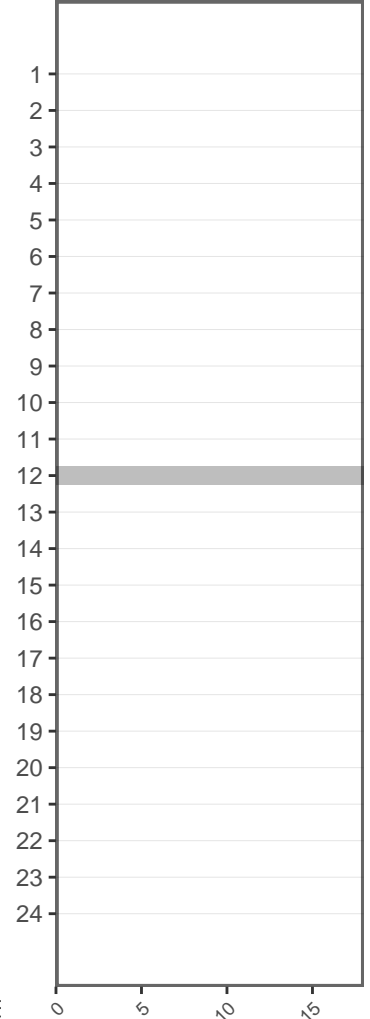
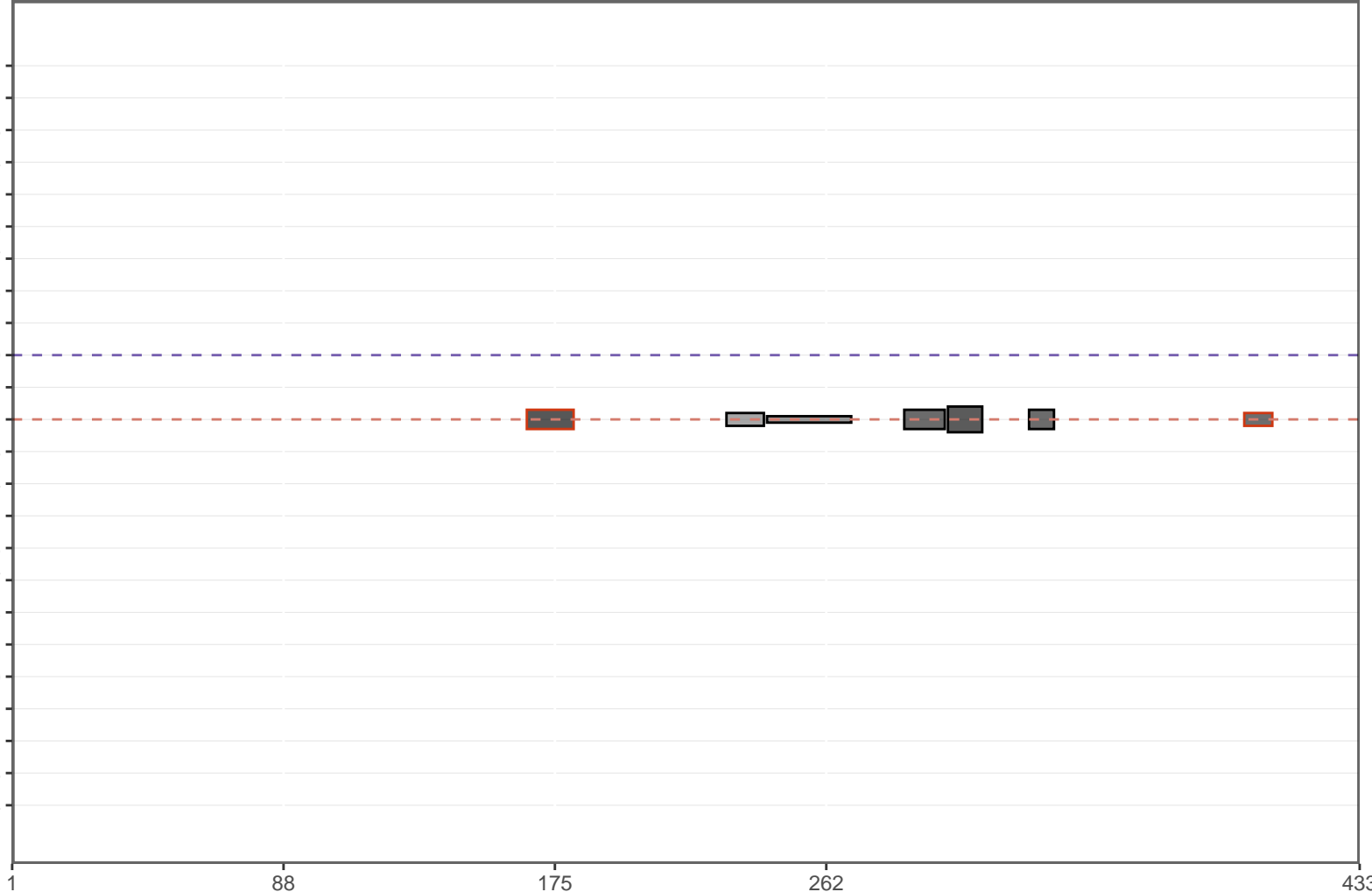
MW indication



Molecular weight

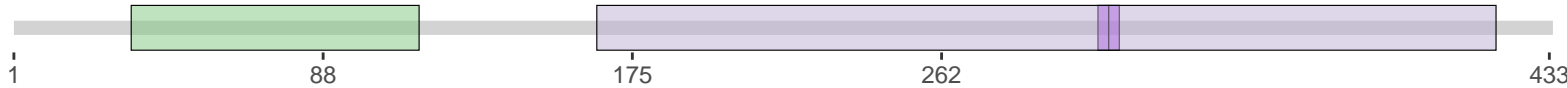


Gel Slice



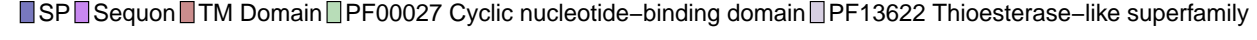
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

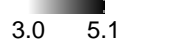
P1YQVYRVRDCKSATRRVDAIKGNVIFLLASFDKDEDFDHDGQAQMPDVPDPELLEMEQLREMRKTDPLRPRTRYRNKVAATANEVWPIERIFGEPNNATNGKSPPLRFWFRAGKGLSDGDLHRCVAAFASDLIFLTVSLNPHRKKDKTSEVSLDHSMMWHRFRADDDWLFVITSPAAYNARGFVSGEMFNKQELVLSLQEGQLRFRKPPSVRPKL

NbL01g06800.1 riboflavin_biosynthesis_protein_PYRD_chloroplastic [MW = 47.85 kDa]

No. of times detected



log(intensity)



Values from



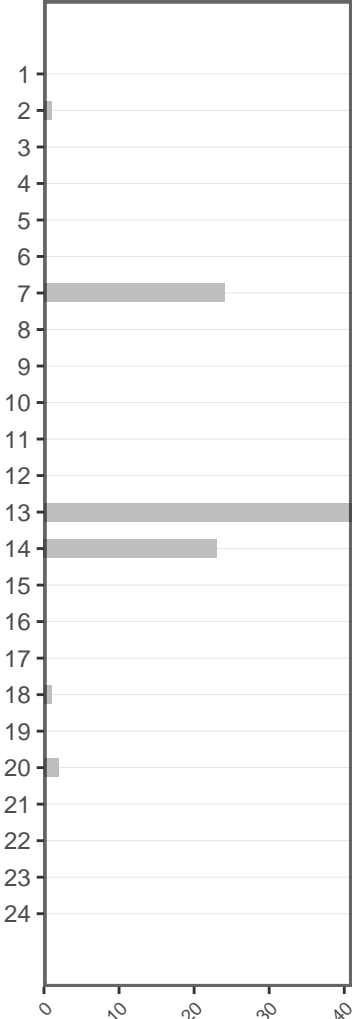
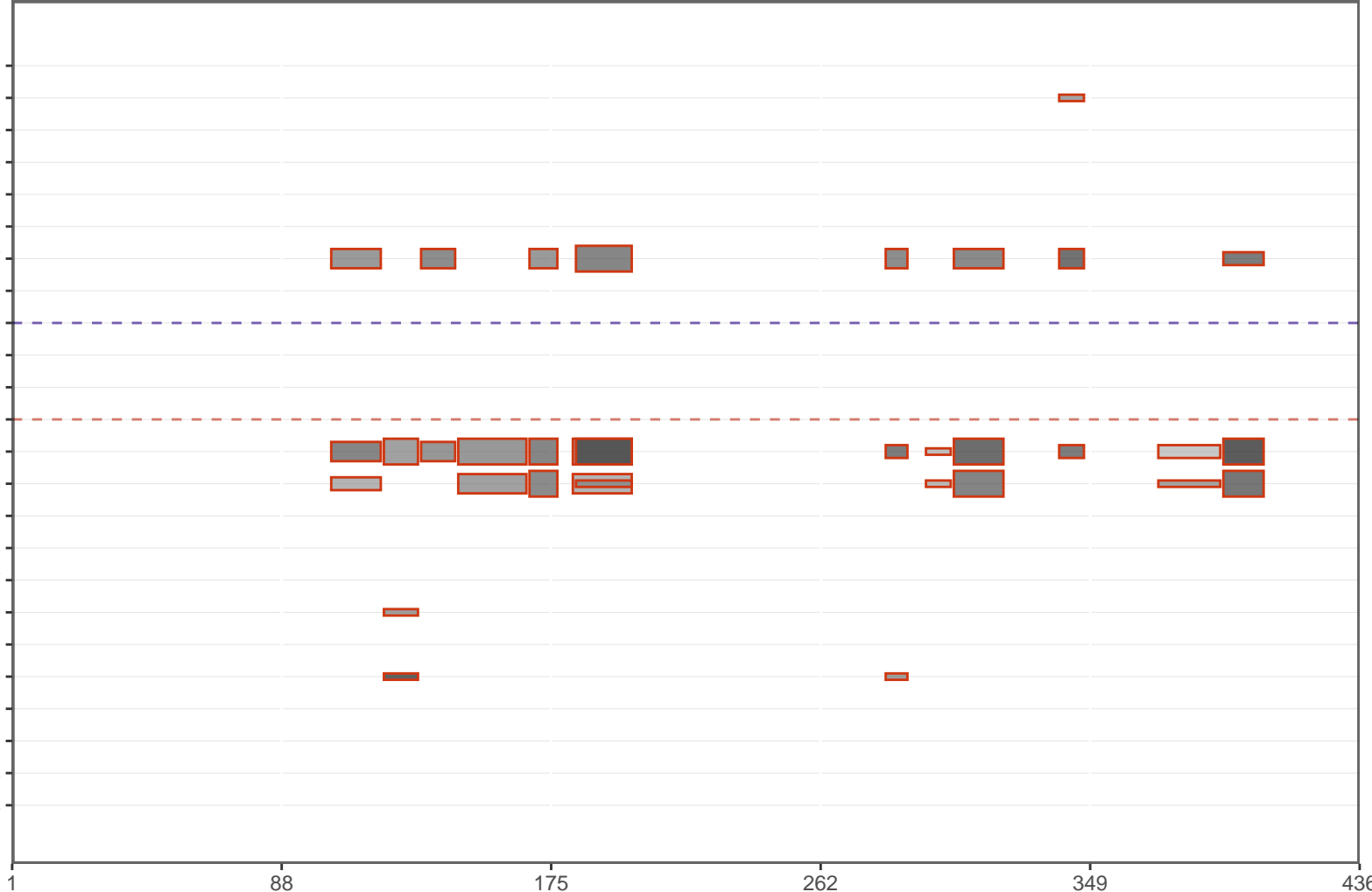
MW indication



Molecular weight



Gel Slice



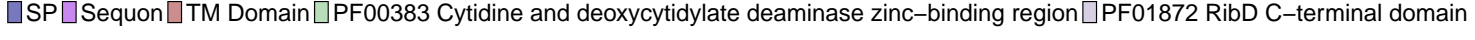
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IDAIGIEVITGVVEEELGRKLNKAVHGMITGKPFVTLRYSLVDDGDFSNLGEVMEGGYHKKLQEVDAVIVSLLSKNYSVLSKKEPCAKGKPLQVLAASDLSLQPLVADTDTSTKTFISNEITVKLEASDRGIETVTERMINLTALEHCKRGGKGVMLDLRGNSTDFEELGEGFEQNFQKVVIVLPLGGSGKEAFKHMGGNRRLLKILTSRTLGGSLLEGYF

NbL01g06780.1 uncharacterized_LOC107784826 [MW = 74.58 kDa]

No. of times detected



log(intensity)



Values from



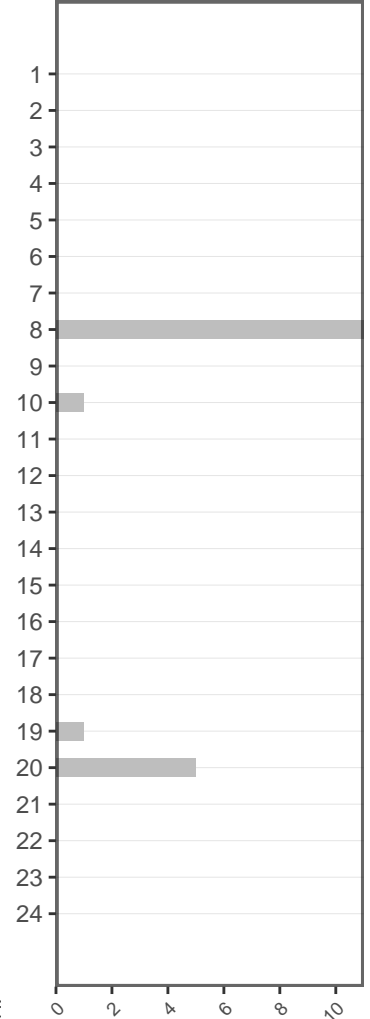
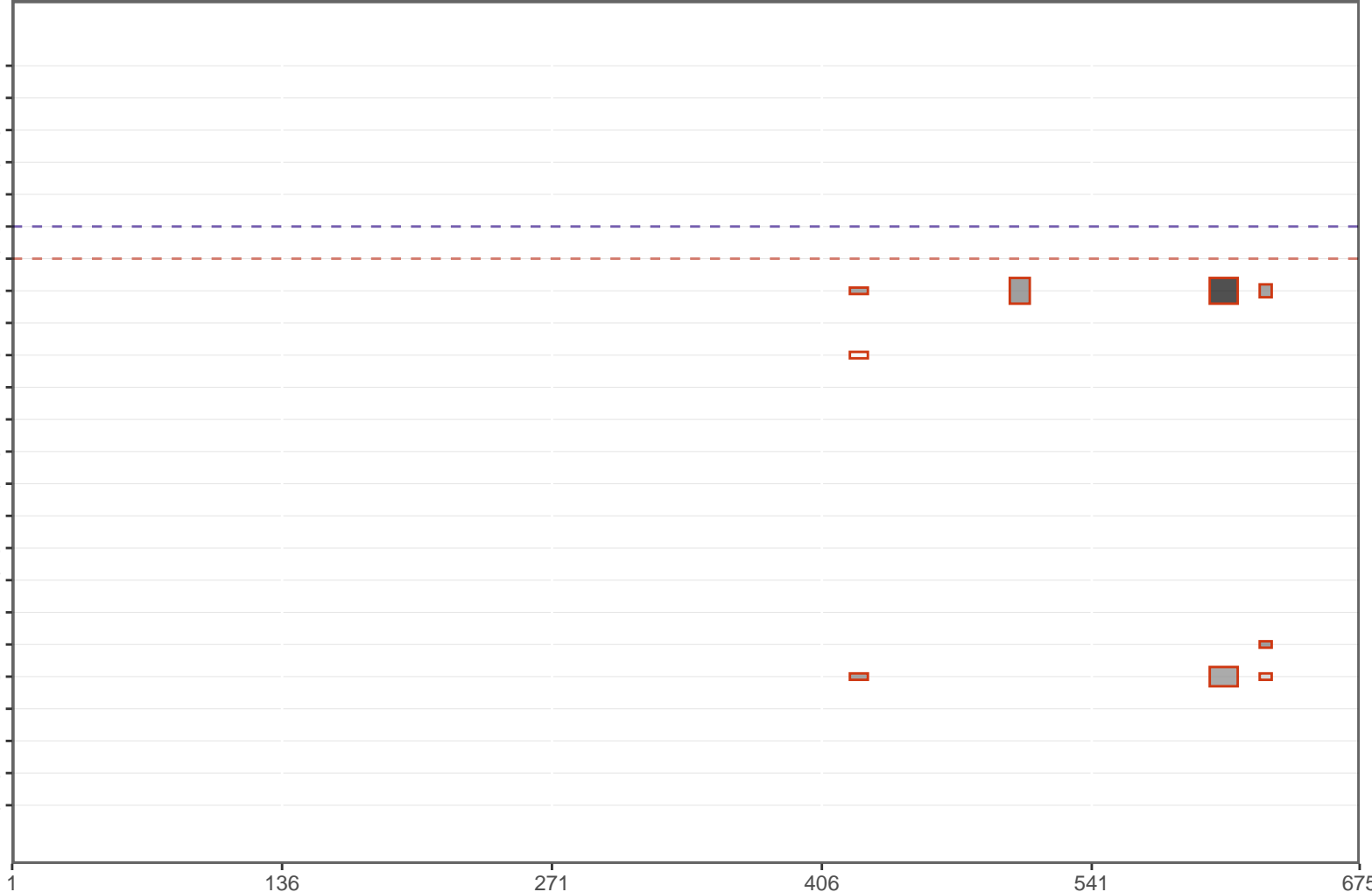
MW indication



Molecular weight



Gel Slice

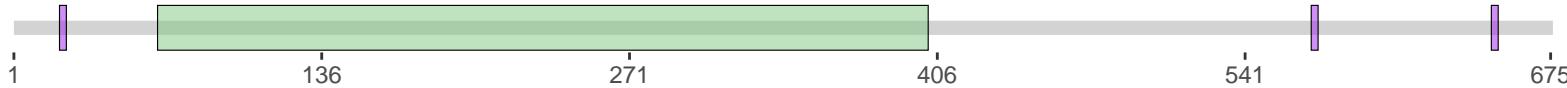


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

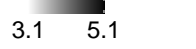
SYITPDVYVDFQDVSFQTLSSKVLGAGAKPSASAPTKLLLLASKDKGKVGWGEISYGGYGGVAKRAKADFLVRWMEVEVGTGTTNKLFSYHGLDSLKAASIDEDLPRDGDRLRMDDGLFEFEEGAAHFKFIALYTNQPRAGGGGISTGHKKEILEKALVKKRDKVQVHVTYTRNKMGGSDMASPKDMQTSFHFDEVLRSPIETETALNKKEGAPQQLSPAPHERKIPLYDAHRSRAGDKGDDLNFSLIPYFPDIERLKKIVTOEWKVKVVARLLNP6SFPTSGDIERRDK

NbL01g06650.1 protein_pleiotropic_regulatory_locus_1-like [MW = 53.4 kDa]

No. of times detected



log(intensity)



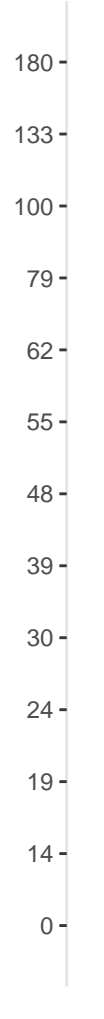
Values from



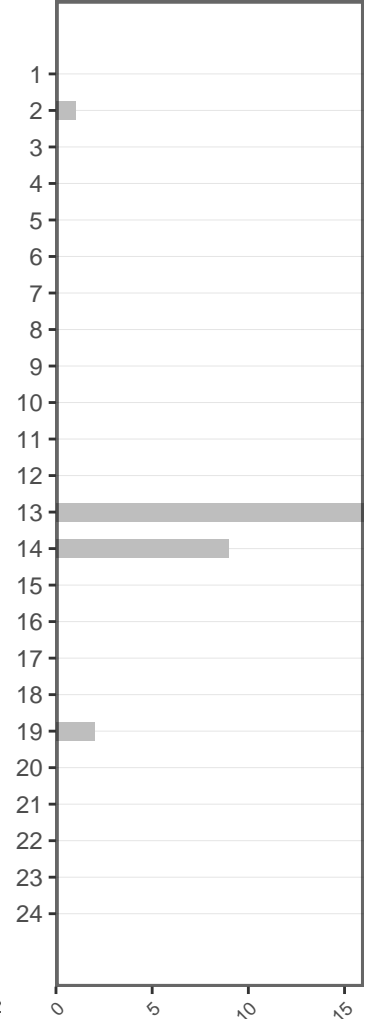
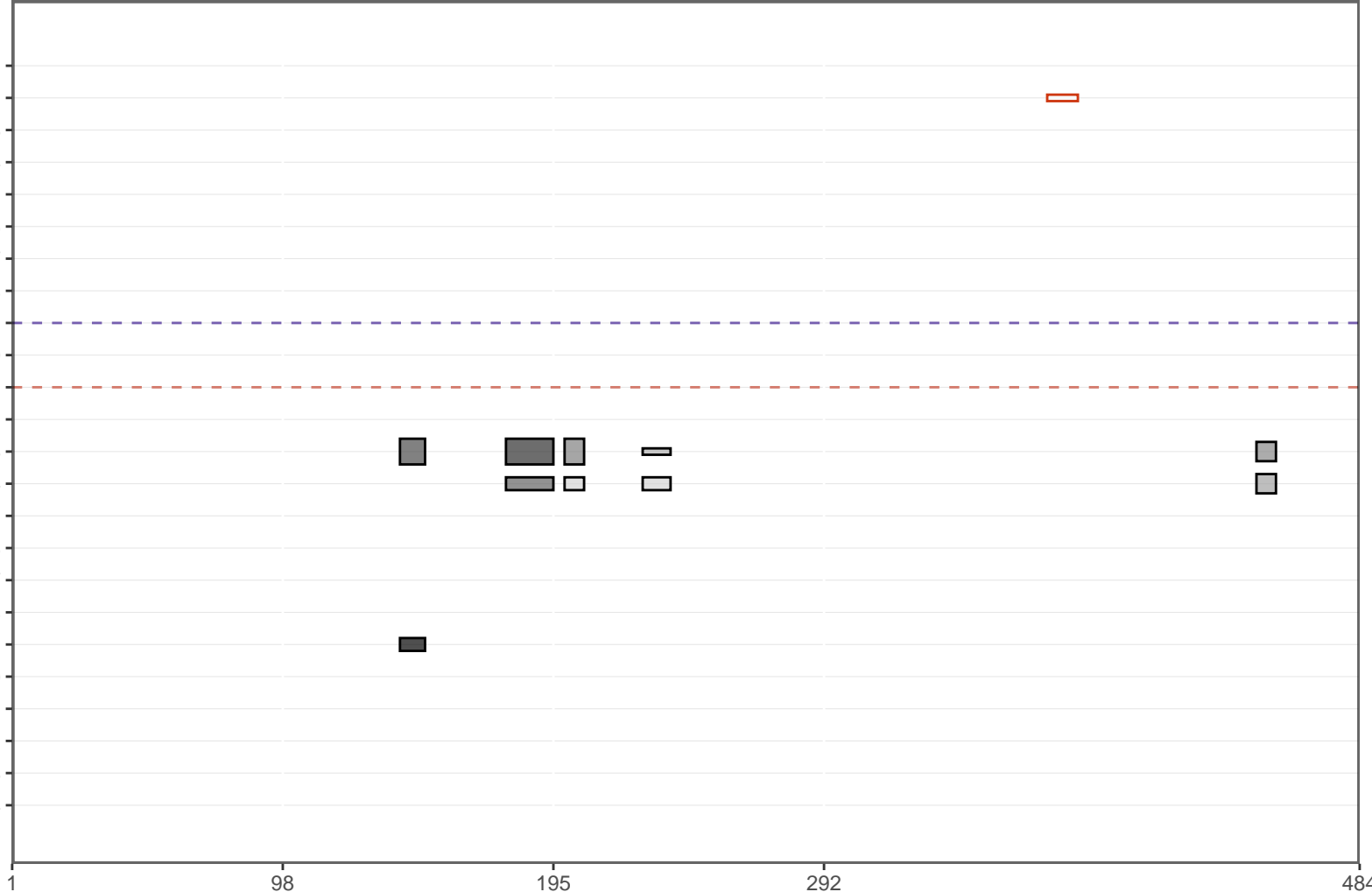
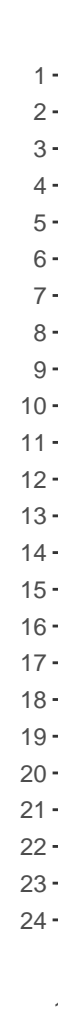
MW indication



Molecular weight

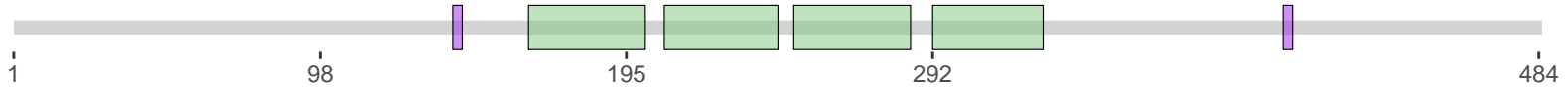


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IFSAGDGLLVKCYDELEGNKVRISYHGLGGVYGLALHPTIDILFTGGRDVGVRVWDRSRMQRHALSEGHNTVCGVFTFRMPDQVITGSHDSTIKFWDLRVYKGTMTALTHHKKGVRRAMAGHPTEDGCFASASADNKKFNLKPGELHNMLSGGKTVNANAVNDGGVMTATGGDNGSMVFTGDWISGHNFQGGSTVQPGSLDSEAGIYALTYDMTGRUSISEADKTKMMKKEDEATPETHPLHFKPKDRIIRF

NbL01g06600.1 K(+)_efflux_antipporter_2_chloroplastic-like [MW = 130.34 kDa]

No. of times detected



log(intensity)



Values from



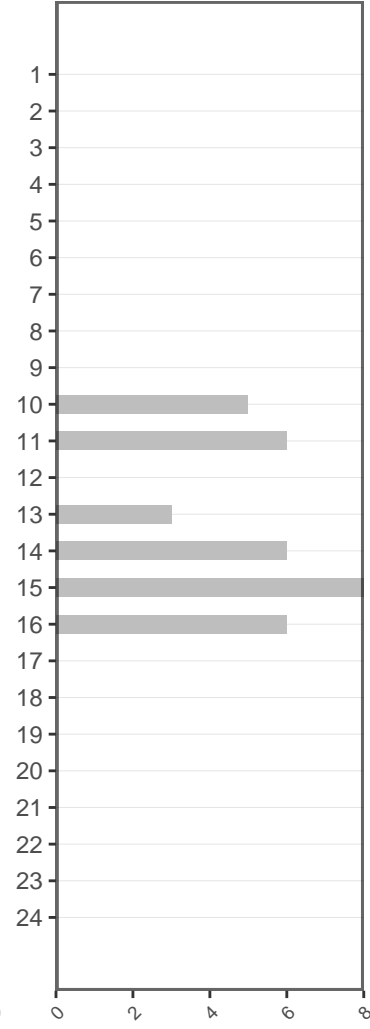
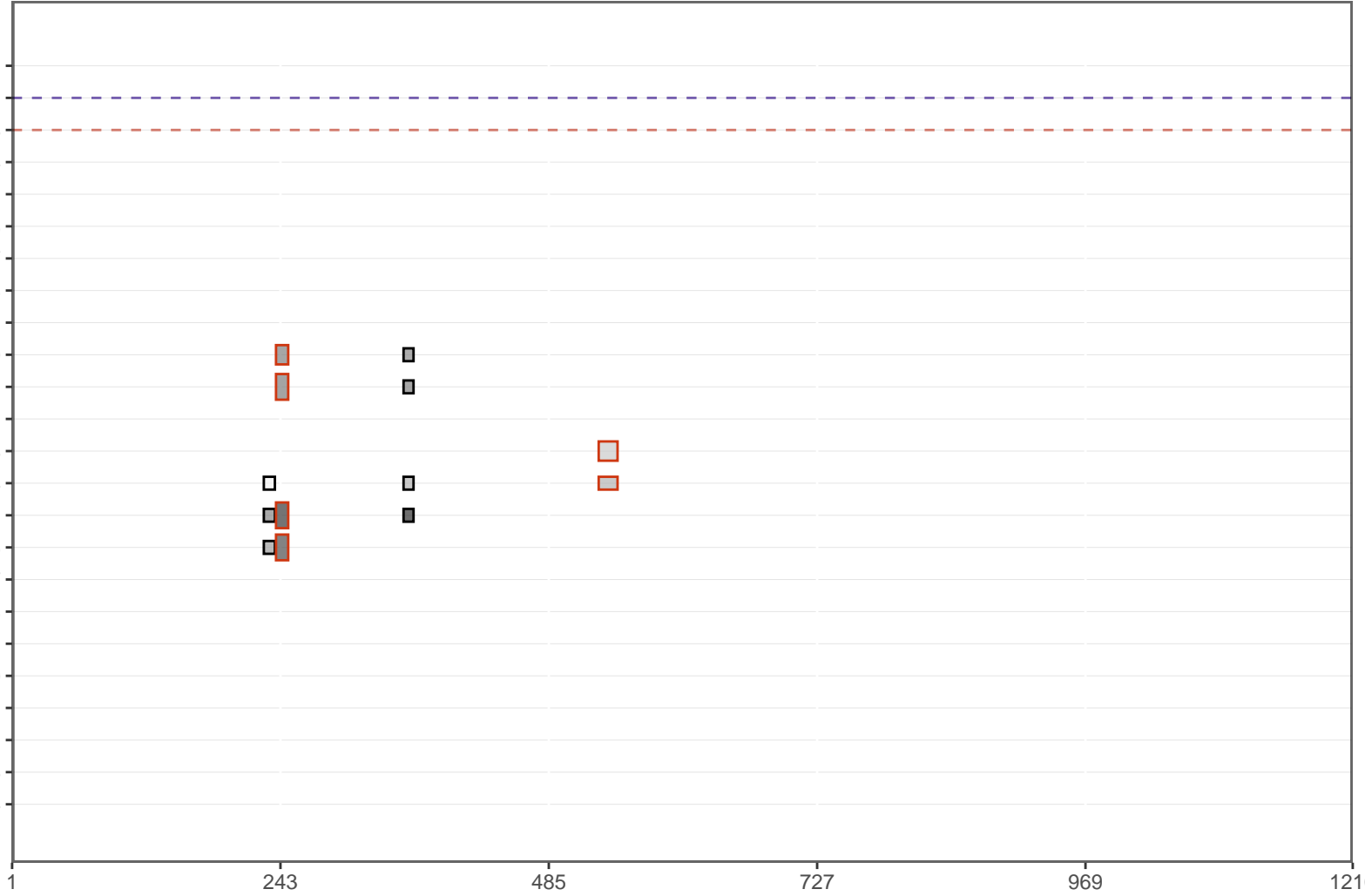
MW indication



Molecular weight



Gel Slice

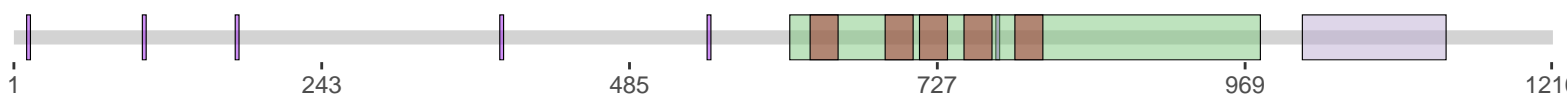


Protein length

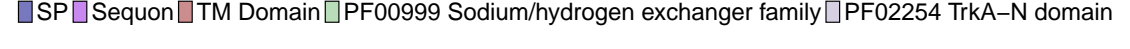


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

KLPEKLTLMELPHOENEEASLFDMLWLLLSAVVVFQKIPGGSPVLGVLAAGLISPYGLSIRRHVHGTAAAEFQVFLFNIGLLESVERLSMKKVVFGLGTAQVLVAVVYGLVAHFAAGGAPMAVIGNGLSSTAVVLQVLRGEGESTSRHGRATFVLLFGDLAVVLLILPLSPNSKGGVGFGAIAELGLAAVKAVATAHAGRLLLRPIYKQIAENQNAEFSANTLVILGTSLLTARAGLSMALGAFIAGLLLAETEFSLQVEGDAPYRGLLLGLFFMTVC

NbL01g06540.1 (+)-neomenthol_dehydrogenase-like [MW = 33.37 kDa]

No. of times detected



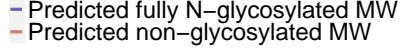
log(intensity)



Values from



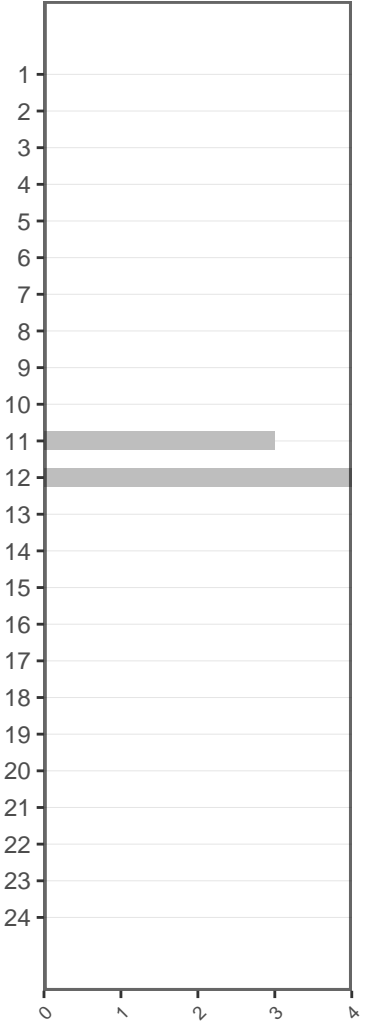
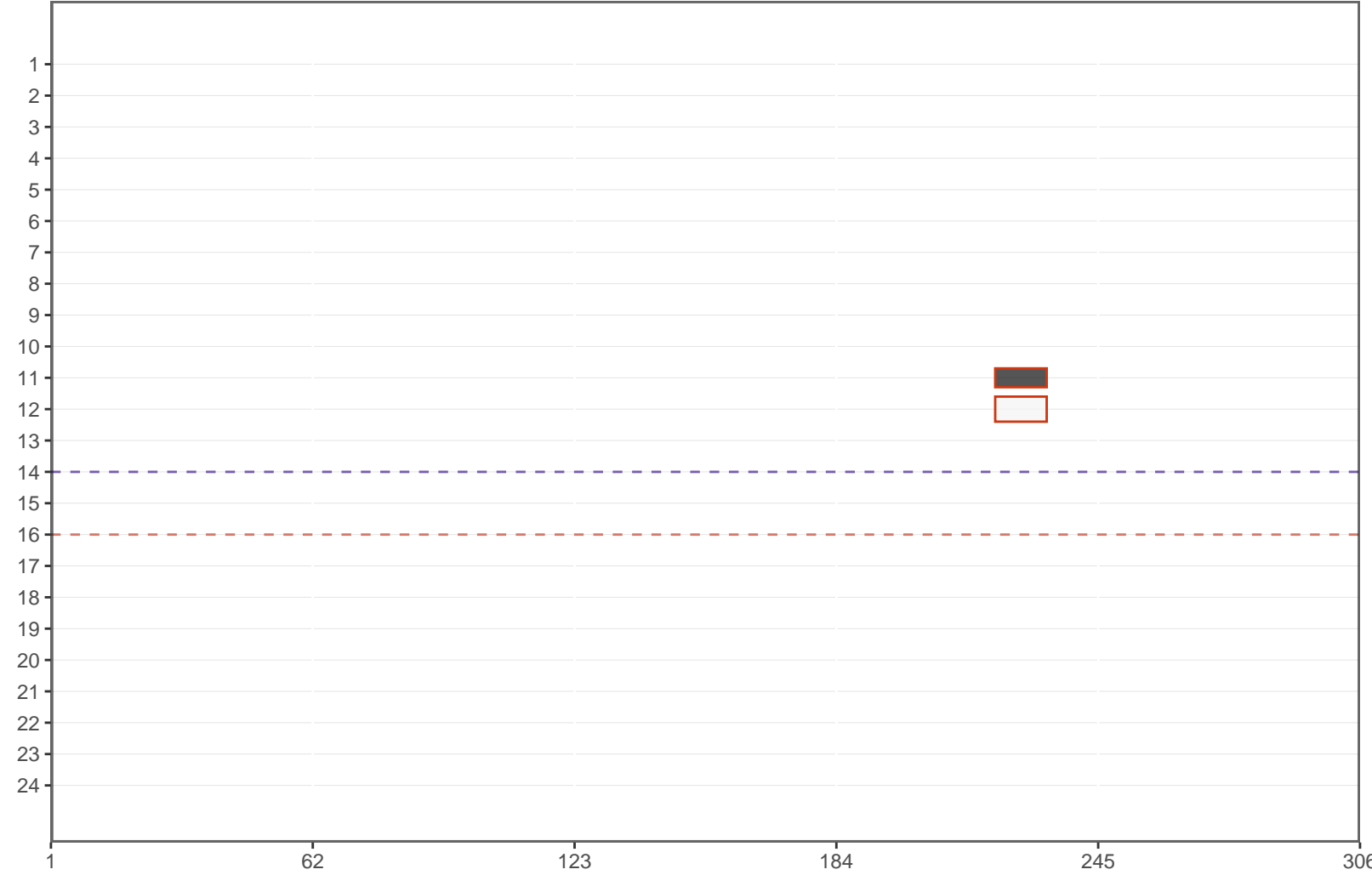
MW indication



Molecular weight

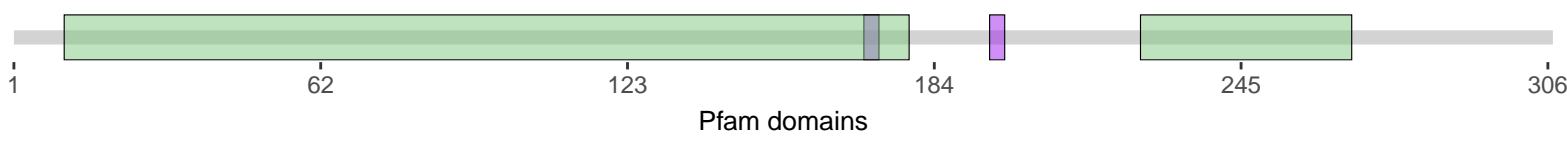


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CLQTNYYGVKRMTEAFPLLLKLSKSPRNVNVS6SMGRLLKLNLEHWAKGLVSDSENTEENKDEVEIEQHLRDYKENALQAKDWPLMSAVILSKAMNNAVGRVMAKKHMSIQINCICPGFVKTMTFNNSGLSIEQGAESFVALLALGPHGGP6GFFVRRKKVSSSL

NbL01g06520.1 (+)-neomenthol_dehydrogenase-like [MW = 34.8 kDa]

No. of times detected



log(intensity)



Values from



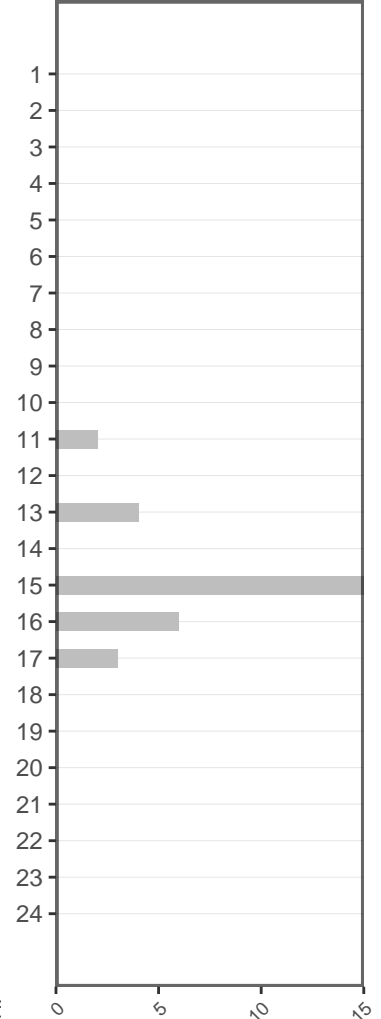
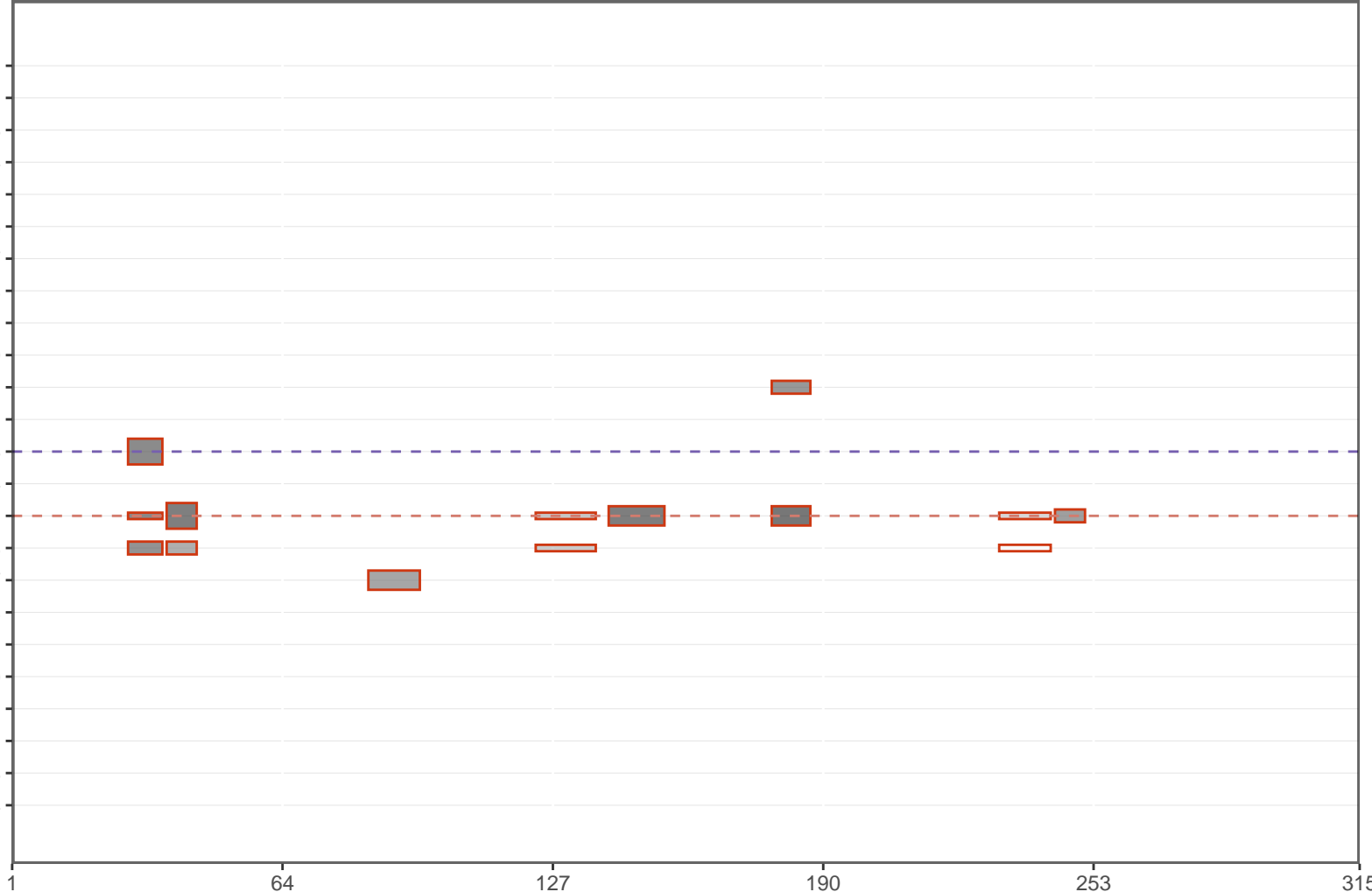
MW indication



Molecular weight

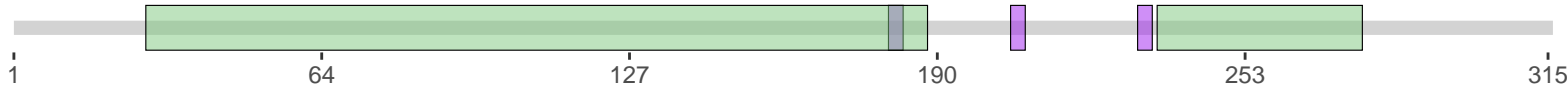


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

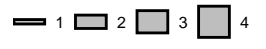


Protein sequence:

AGECLKTNYYGAKGMIGELLPLLGFSDFRIVNVSIVGKLEHVRNEWAVGVLSADNLTERRVDEVLAFLQDLKDLGDMETKNWSLIFFWYTLKSKAMNAYTRILAKKYPSSLINDVCPDYVYKDTMTINDGKLVVEEGAESPVWLLALPKGGPQKRYFNRIKEVDFP

NbL01g06490.1 NAD-dependent_malic_enzyme_59_kDa_isoform_mitochondrial [MW = 66.31 kDa]

No. of times detected



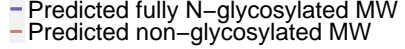
log(intensity)



Values from

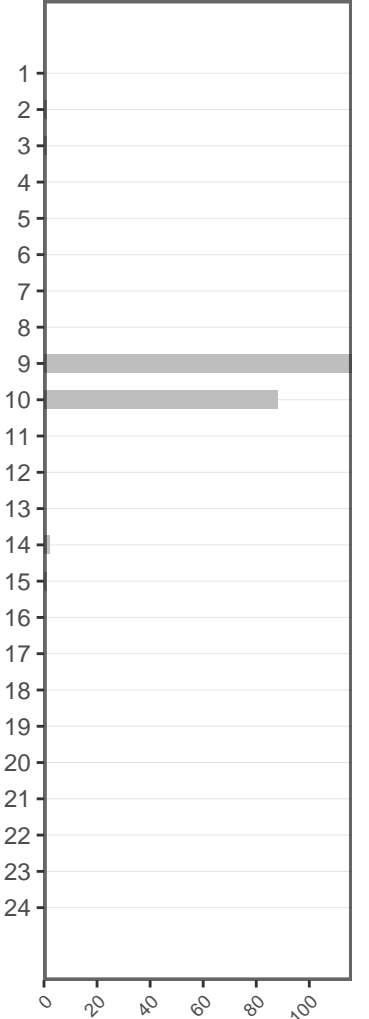
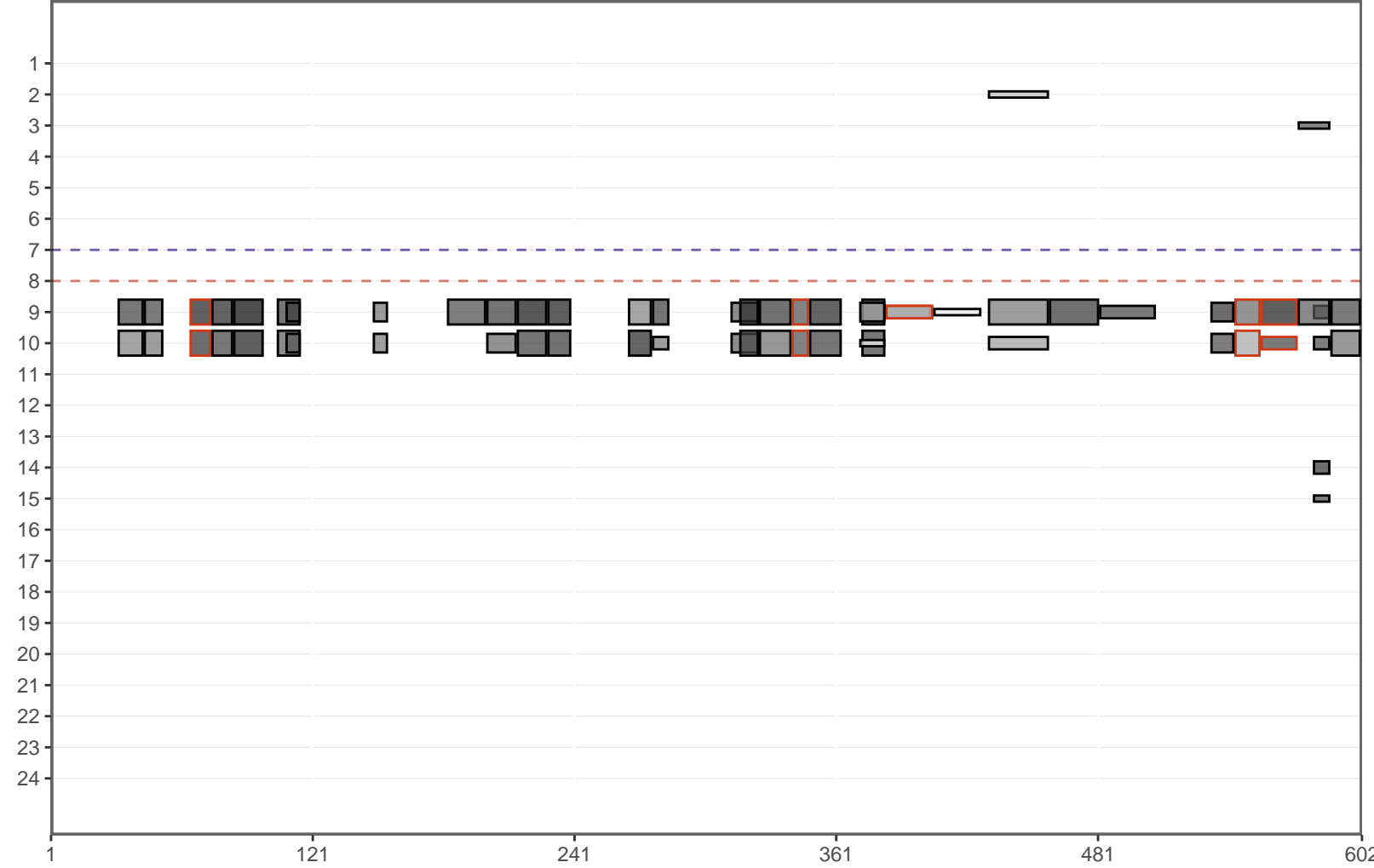


MW indication



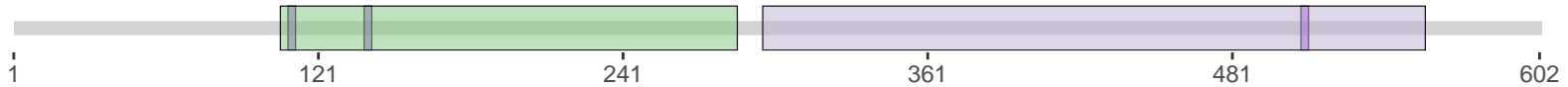
Molecular weight

Gel Slice



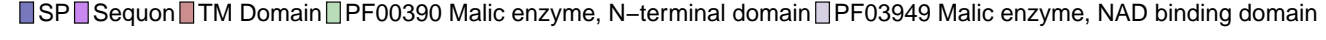
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KFCMFNDIOIGTAGVALAGLLGTVRAGRPLTDFANFKVIVAGAGSAGLGVKMLQAVSRMAGPSADPHFFLLDKNGLTKRDKDIPALPFAKAAHEIEGLGLGEGAGLLEIVKVKRPHVLLGLGSDVGGFHEEVLRAMREGSDVSRPAFAMSNPTNAECCPVDAFKLAGENIVFASGFFENVDLGNKIKHVNQANNMYLFPDGLGALLSGARNISDTMLEAAEGLASYSMSDDEIKRGLYPSINDRDTAEVGAAVLRRAVAEDLAEGHGDV/GARELQHSKEE

NbL01g06380.1 synaptotagmin-4 [MW = 55.92 kDa]

No. of times detected



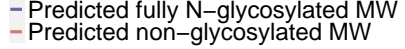
log(intensity)



Values from



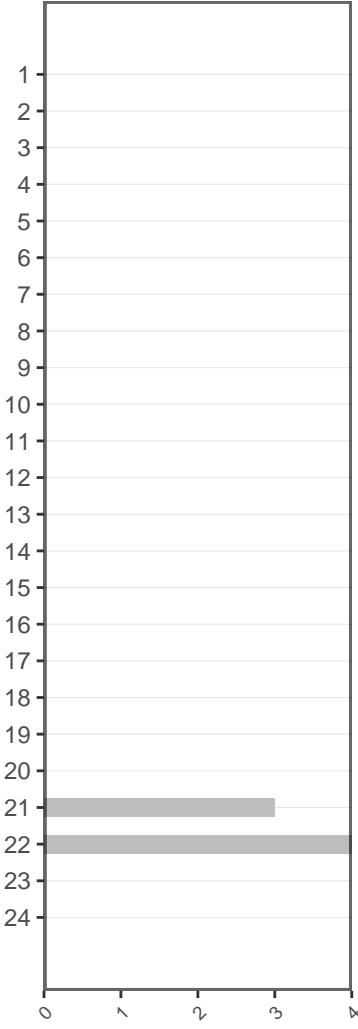
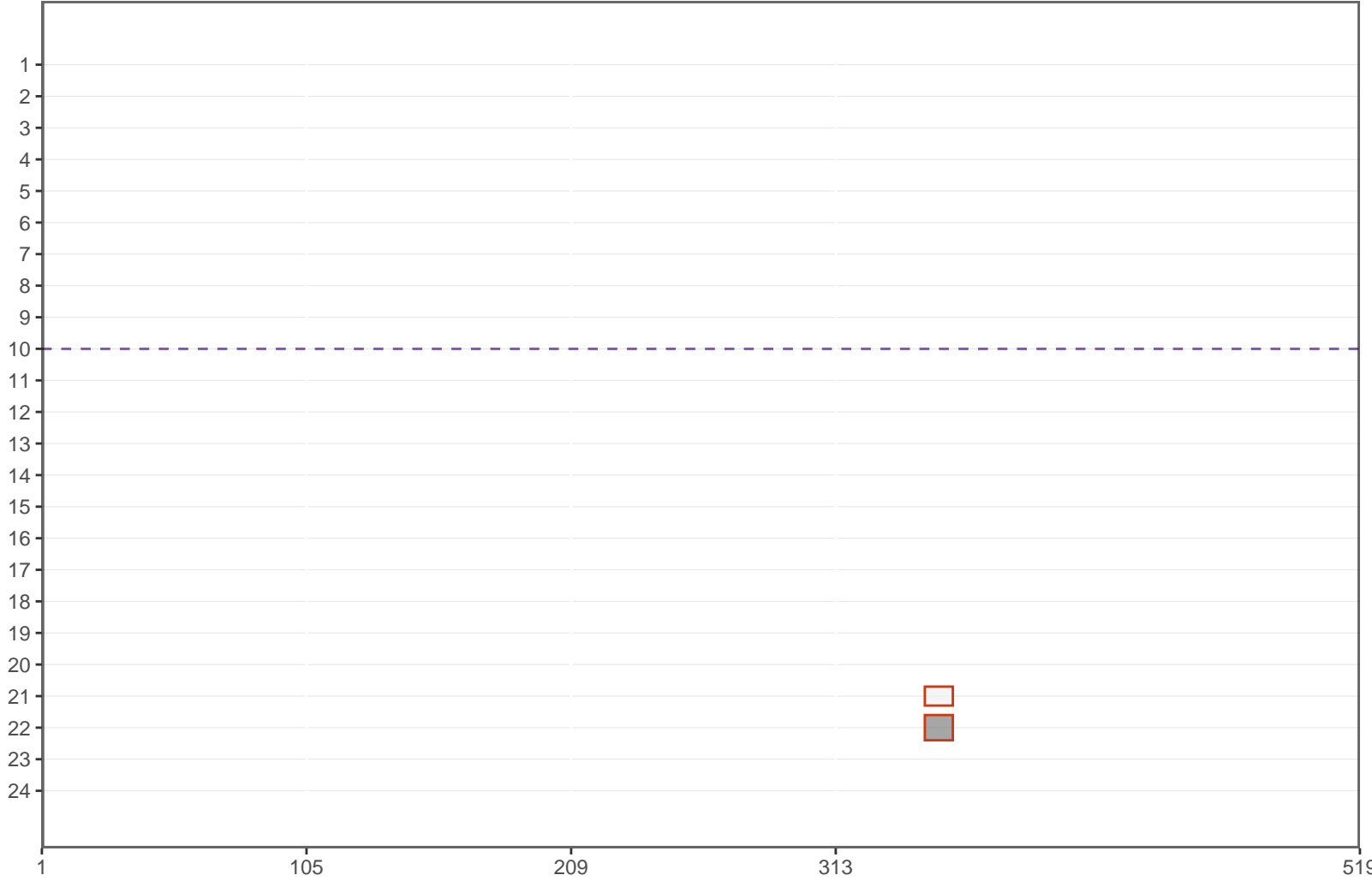
MW indication



Molecular weight

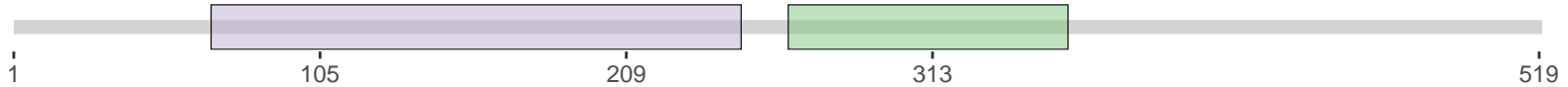


Gel Slice



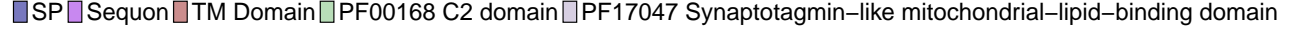
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SGVPYDTSDELKPDGKLVIVTWANGLKHEMIGKSDPAVVVIRPLFKVTKTKIDNNLNPAVWDGTFELIAEDKETSGLVEVFDKDVGGDQRMGAKLPLNELVAAAKEIELRLPLKMLKVKDKDKDGTTRKVLVHEFNKEEGLAALAEAEKALEERKLLKSEGVIGSTMALDGAASLVGGVSLVGTGLGAGVGLVGTGVGAGVGVSSGFGAVVSGLSKAGKFMGRFTFTSSKKKSGSSTPVAISIGENGGAKPLKTYLANTD

NbL01g06310.1 histone_deacetylase_complex_subunit_SAP18-like [MW = 17.76 kDa]

No. of times detected



log(intensity)



Values from



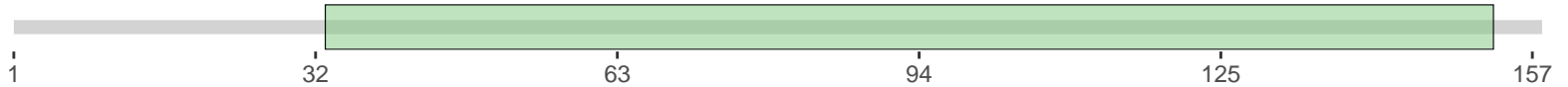
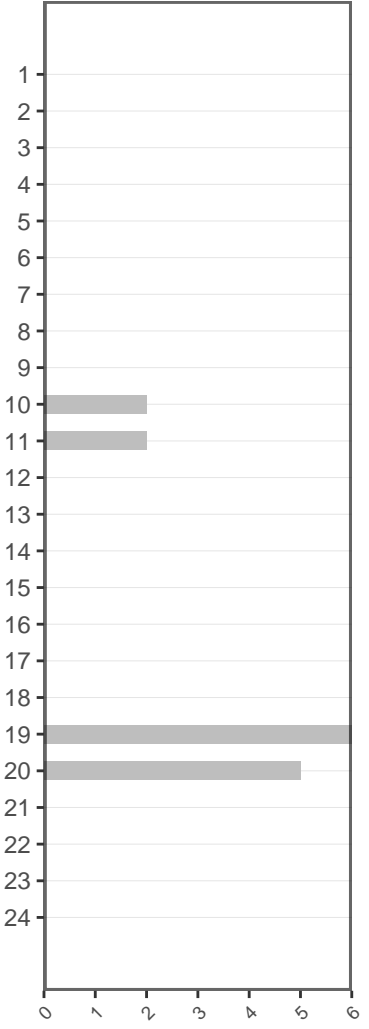
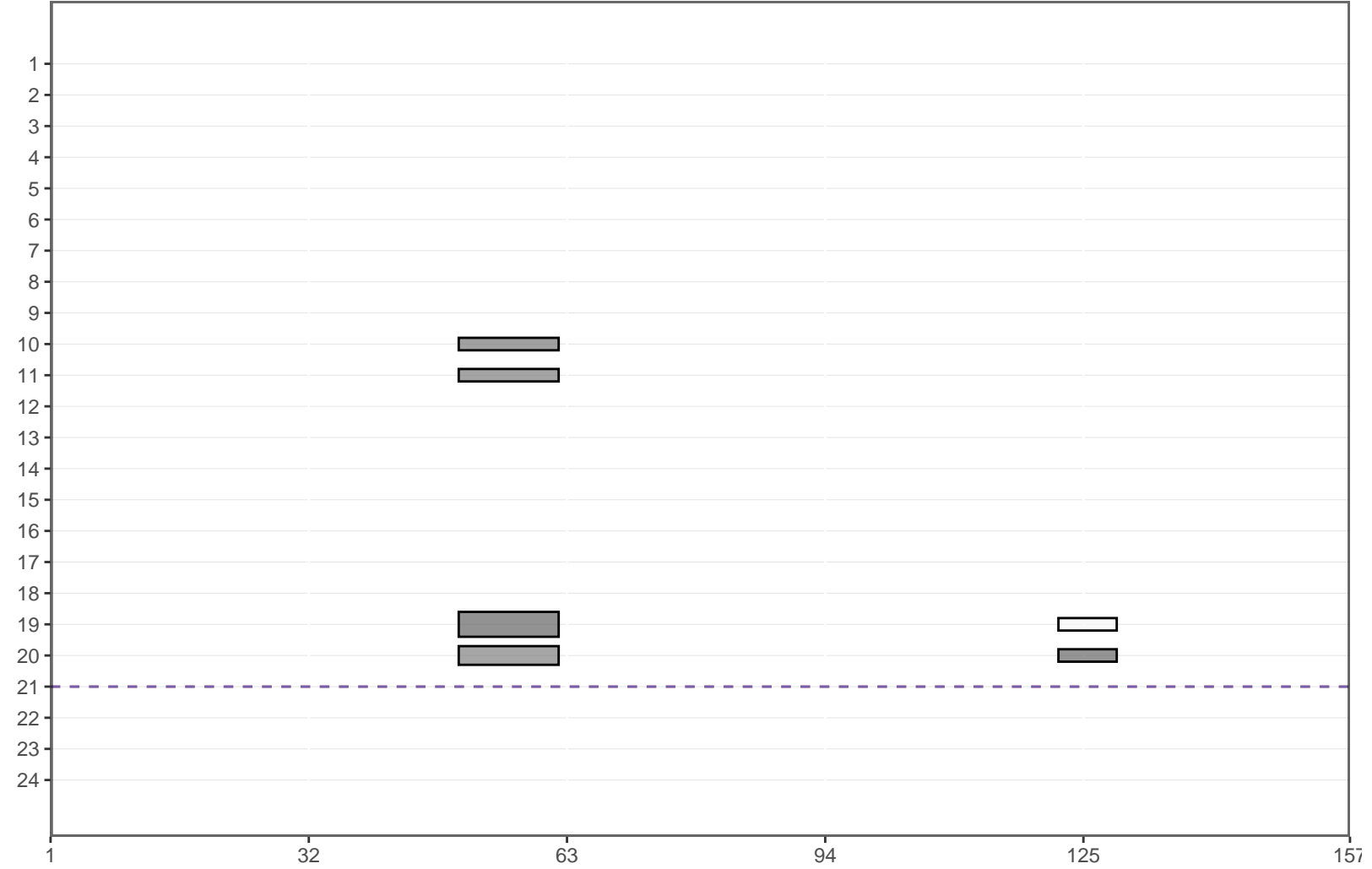
MW indication



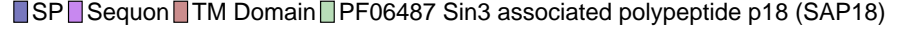
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

EPKDEVOYITWMDATLRELTDLWKEVPEARRRDAELSFVYVDPKGRFRVREVRGTYEYVNGRRPDSGSKLDELKFGIDWLDVAITFQI

NbL01g05960.1 COP9_signalosome_complex_subunit_1 [MW = 50.28 kDa]

No. of times detected



log(intensity)



Values from



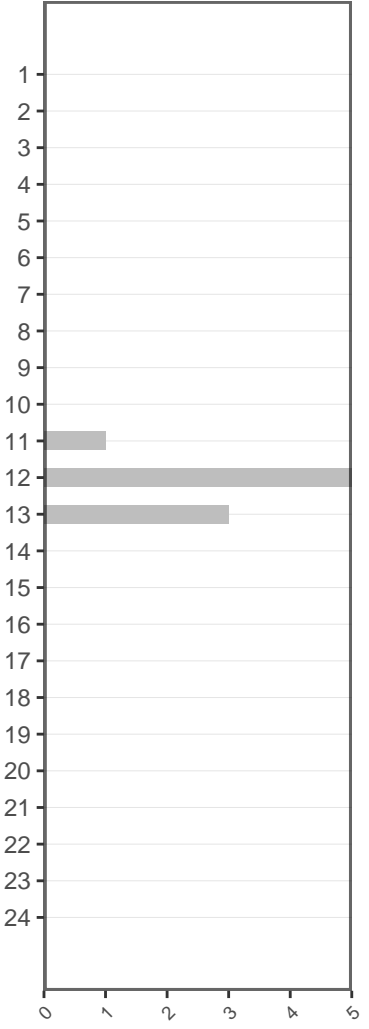
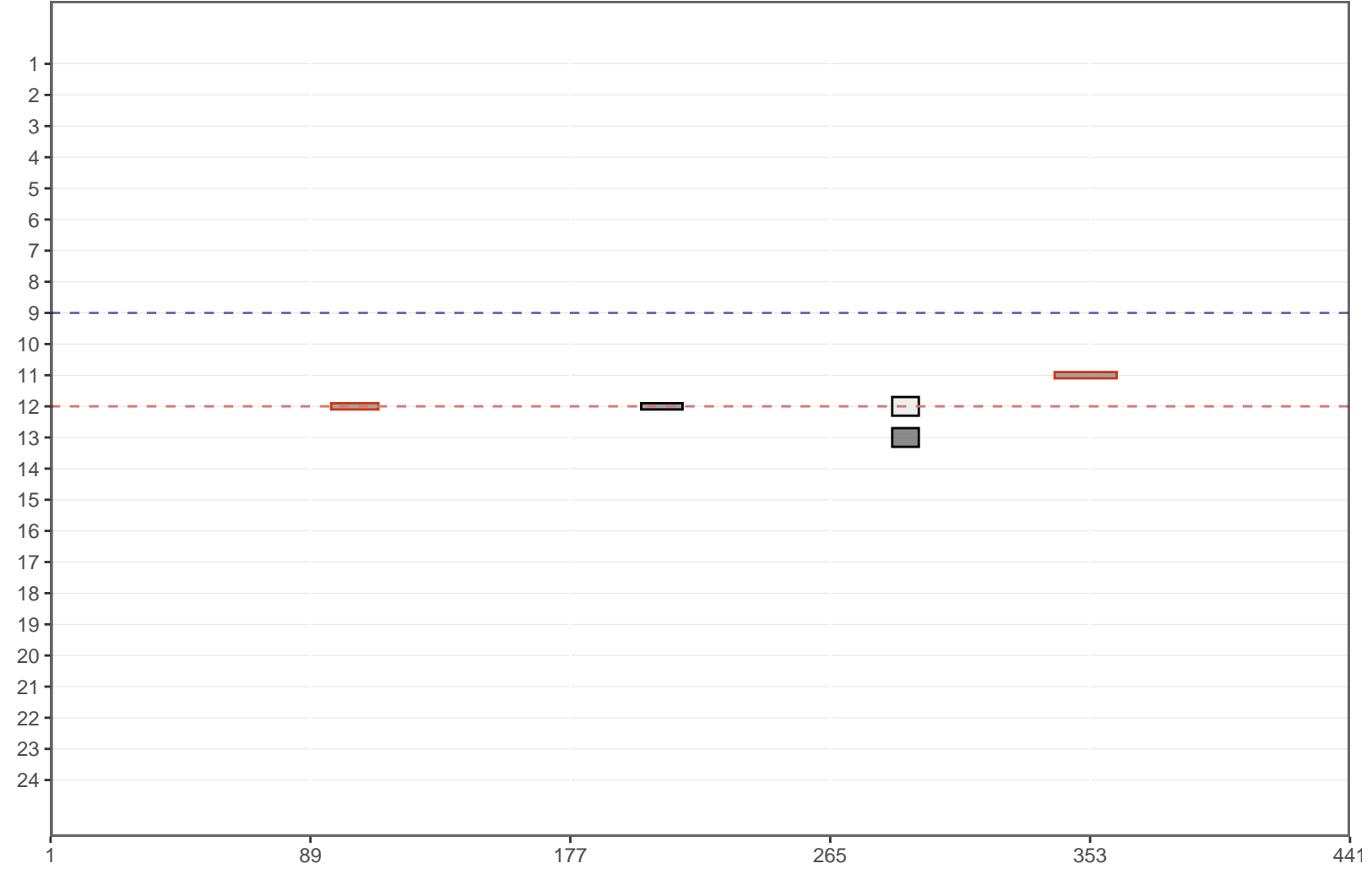
MW indication



Molecular weight

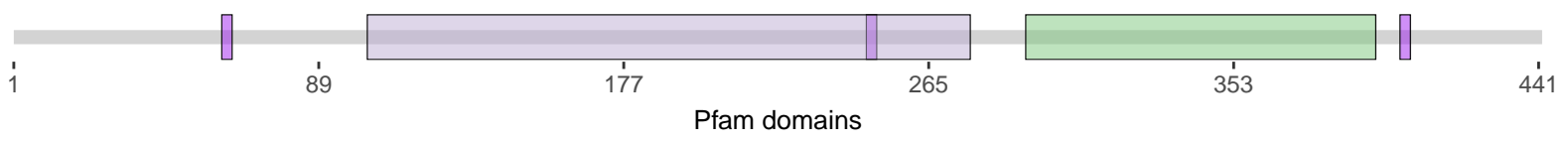


Gel Slice



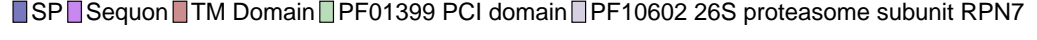
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

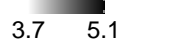
DALESLTVAKLRCAAGLANLEAKKYLAAARKFLEVSPELGNNYTEVAAGDVAIVYGGGLCALASDFRAELKSKVDNINFRNLELVEPEIRELHDFTYSHYAGLEVLEGNLKKANLLLDHLEHDHVTETYDQIRNKALQYTHPFVSVLDNMMANAPKTSVAGLEKELEALFTDNGDARIDSHNKLRYRHADQRNATFGKVLQGTGREFRDVREMLLRANLKHHEHLRASRKH*

NbL01g05840.1 uncharacterized_LOC107827105 [MW = 19.53 kDa]

No. of times detected



log(intensity)



Values from



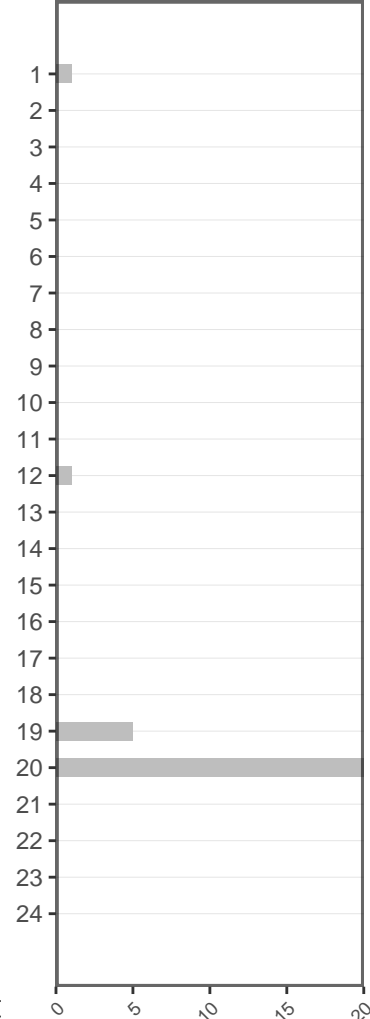
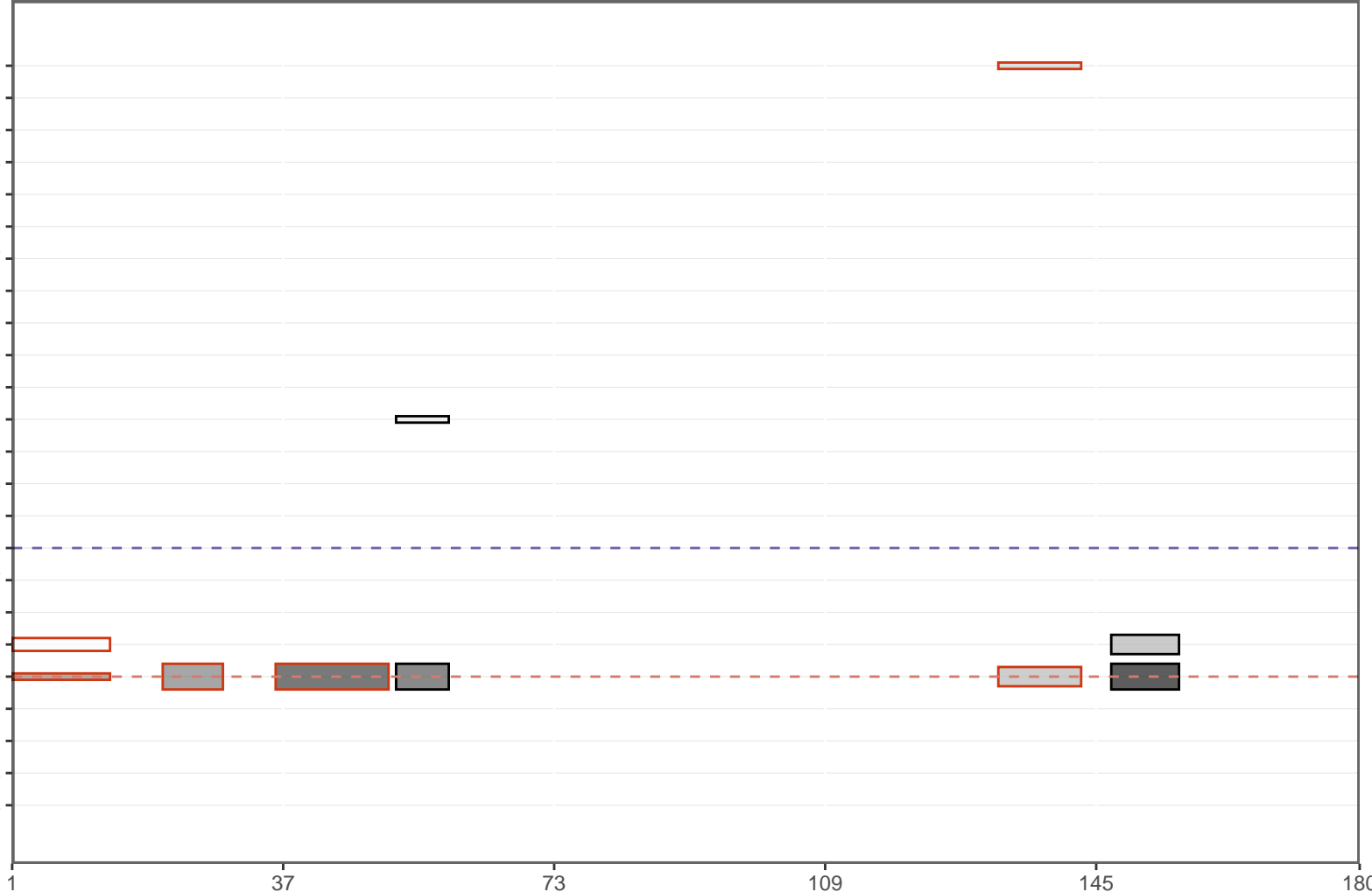
MW indication



Molecular weight

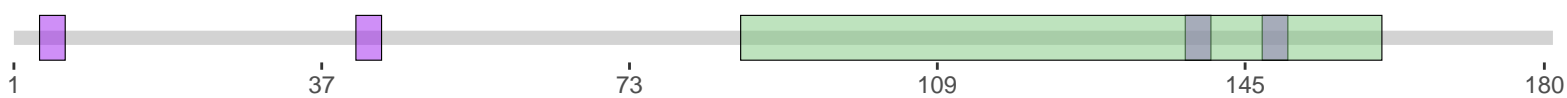


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

.SVKPPIMNYGSLHGGAAGVDFVRIATGARTVIGKDKELFLGELSHLYLGGASRNAEIVNATVIRSGRNLTVAVDFRVKDEKLYSHATFYHMPVASL

NbL01g05810.1 fasciclin-like_arabinogalactan_protein_8 [MW - SP = 41.49 kDa]

No. of times detected



log(intensity)



Values from



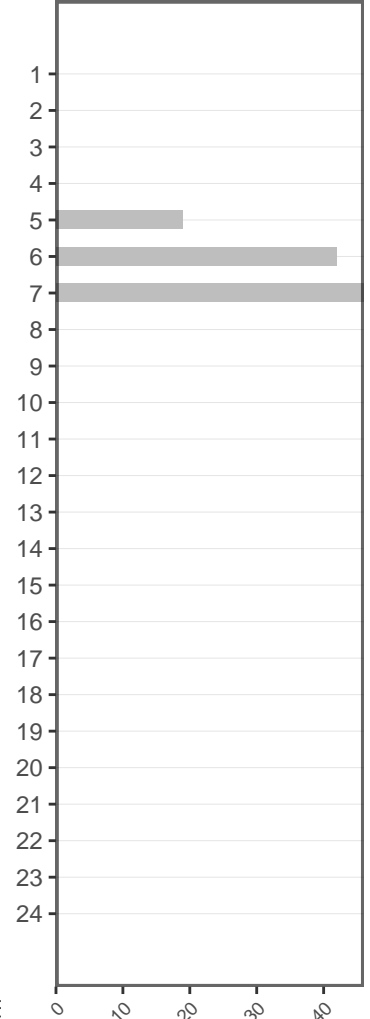
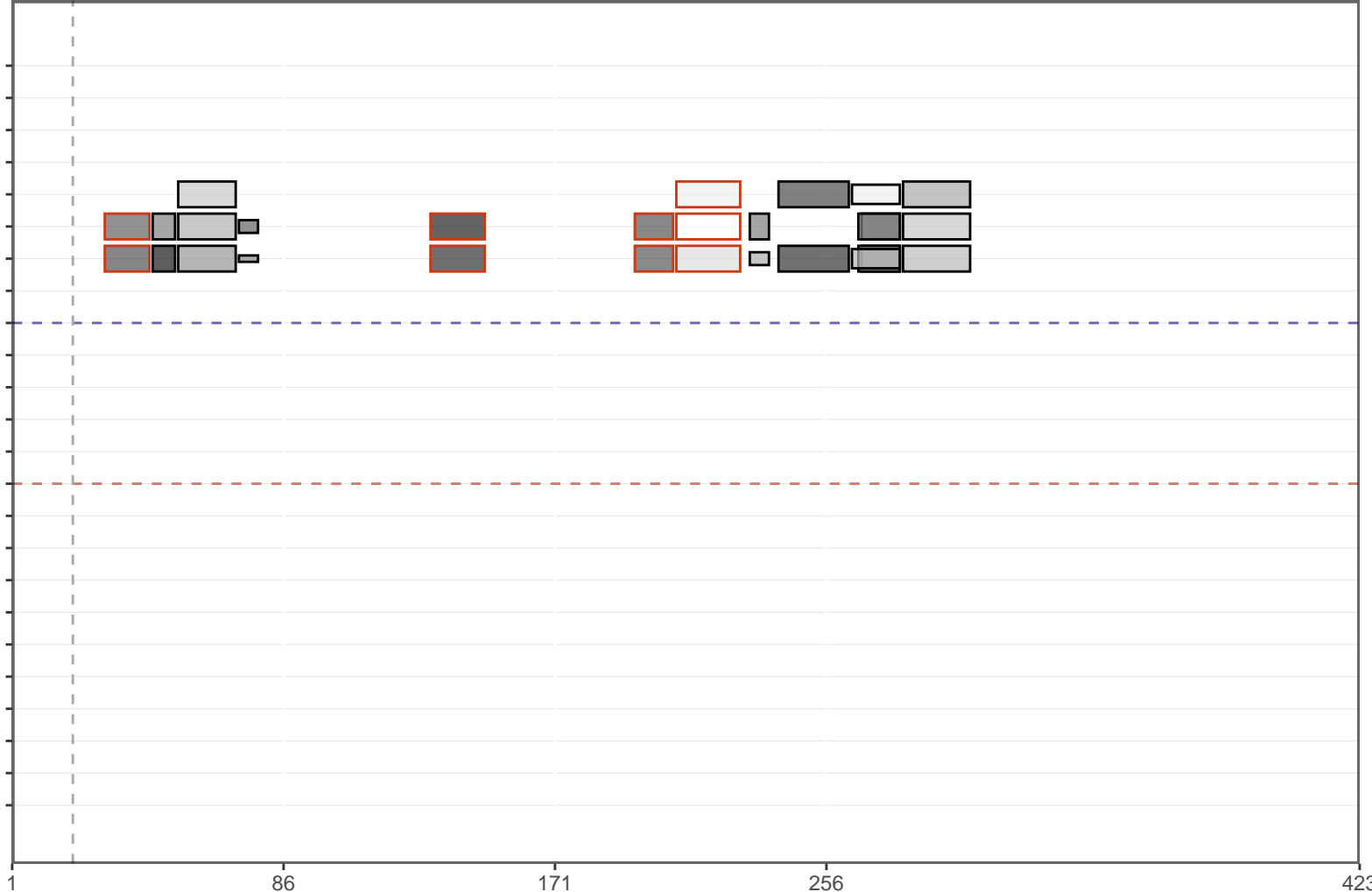
MW indication



Molecular weight



Gel Slice



Protein length

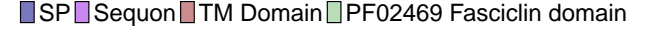


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

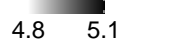
IQSSVLYKTYQTAAATGLTFVAFNDFEAFKGGKVPDLNKLKAEVWVSLGGYHVPSTYPTIGLTKTKNDPISFLATNGASKYDLASASTAGDQVLTDTGVDSSRIATWIDSTFFQITFDVDSVLLFPEELFGKSGSPAPQCPAPETSPSPAPGASPGPAPGASPPMMSPPAPPTTSSPAGAPADGPAADSENSTAKKNAGNINAPALLKVLTVGVSVVSYLSP

NbL01g05620.1 uncharacterized_LOC107773275 [MW = 25.32 kDa]

No. of times detected



log(intensity)



Values from



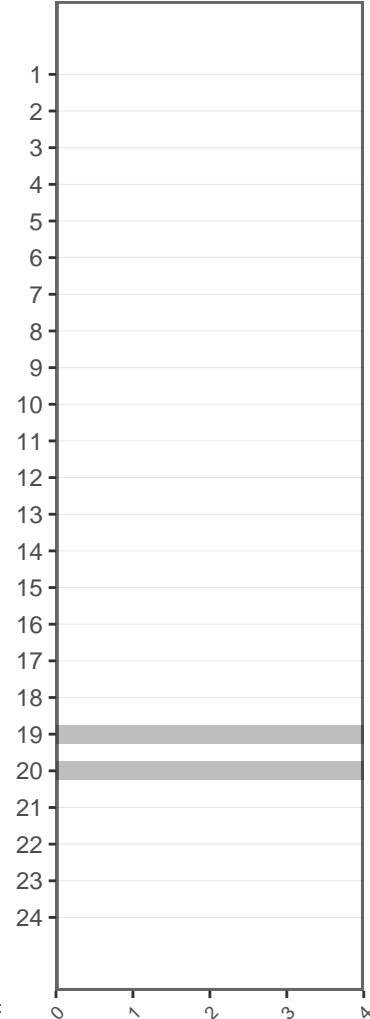
MW indication



Molecular weight



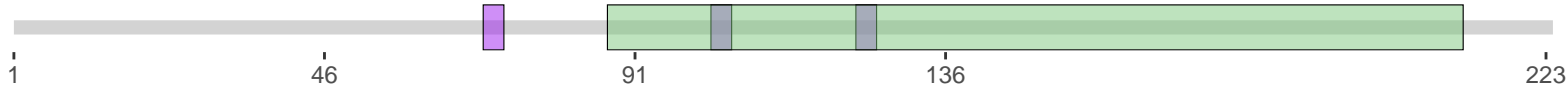
Gel Slice



Peptide counts over 4 repeats

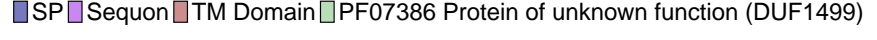


Protein length



Pfam domains

Pfam Description



Protein sequence:

ISENSDSAHYAPPWVWVNPPEGRKGNVREKAMEELLGVKSTPKPKFSPKIAEMKDDVYRVEYESPLGFVDDMEFWFPPGKKSIVQYRBSASRLGNVDFDANRRKRAKRLRLELKKGWASEDTV

NbL01g05470.1 tRNA_2'-phosphotransferase_1-like [MW = 33.61 kDa]

No. of times detected



log(intensity)



Values from



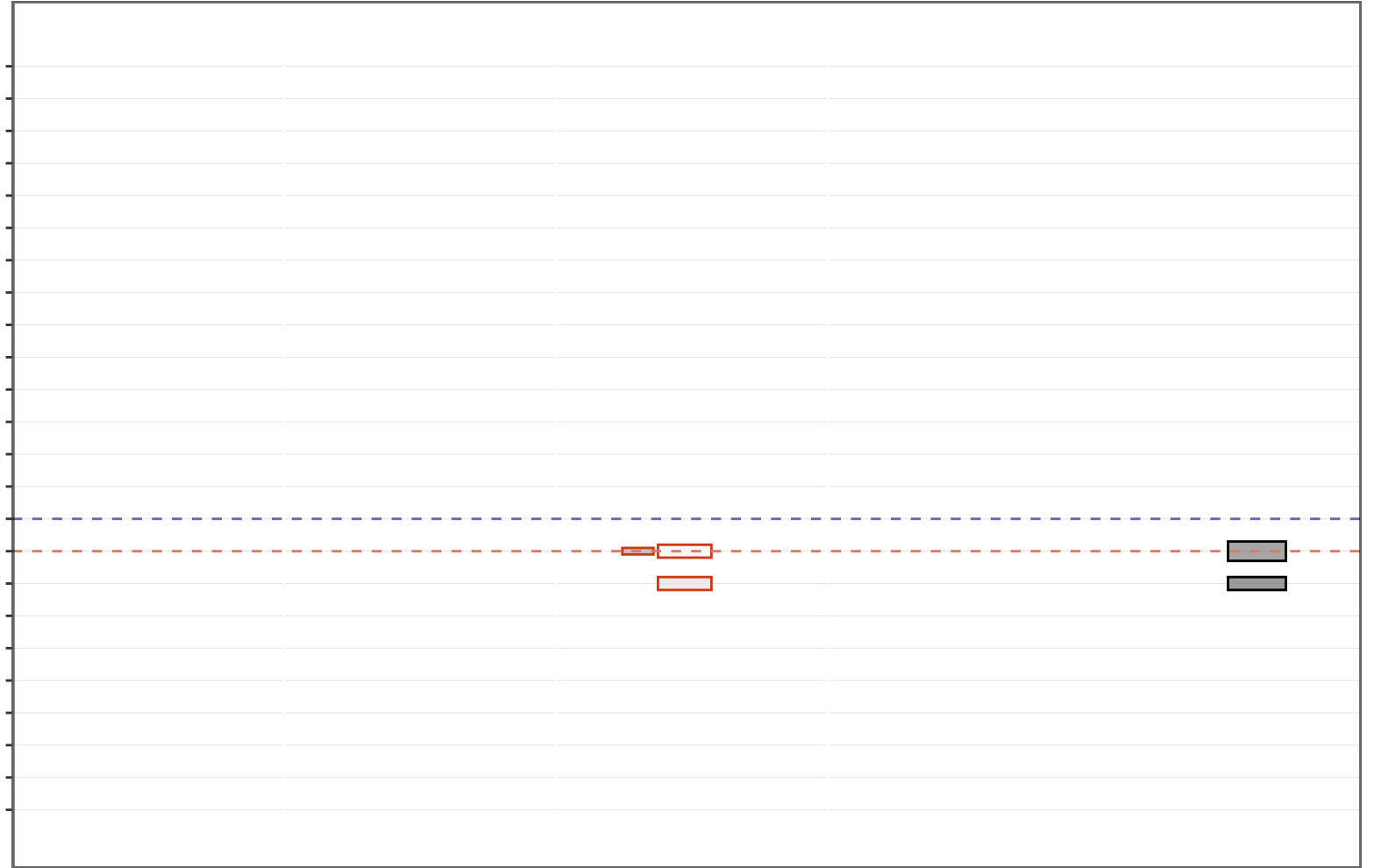
MW indication



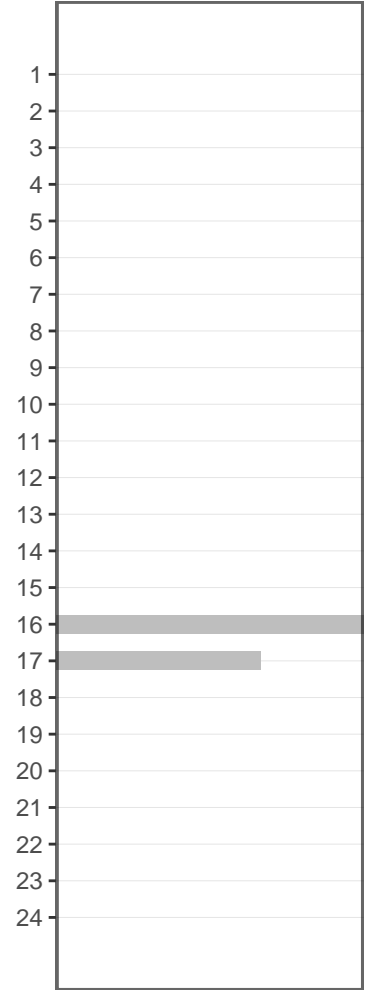
Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

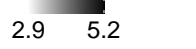
TFANVPLRSHYVDVKEAVGKDKGRFGLEENGELLIRANGHTVKIVETESLKKPLSADEVVGVHGTYYKNLESILEHGLKRMKRLHVFHSCGLPTDGEVIGSMRRDNNVJFLDVRRALEDGMKLYISDNRVILTEGFDGAVPVYKFEKVEEWPDRKPLPL

NbL01g05450.1 3-phosphoshikimate_1-carboxyvinyltransferase_1_chloroplastic [MW = 55.79 kDa]

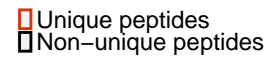
No. of times detected



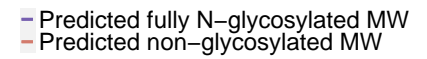
log(intensity)



Values from



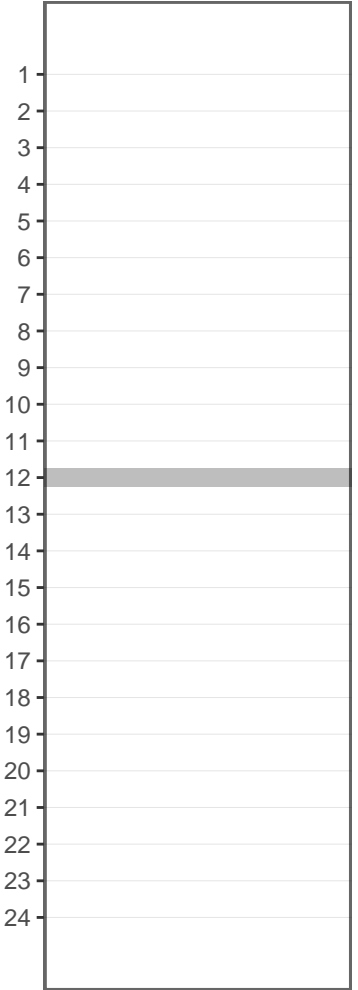
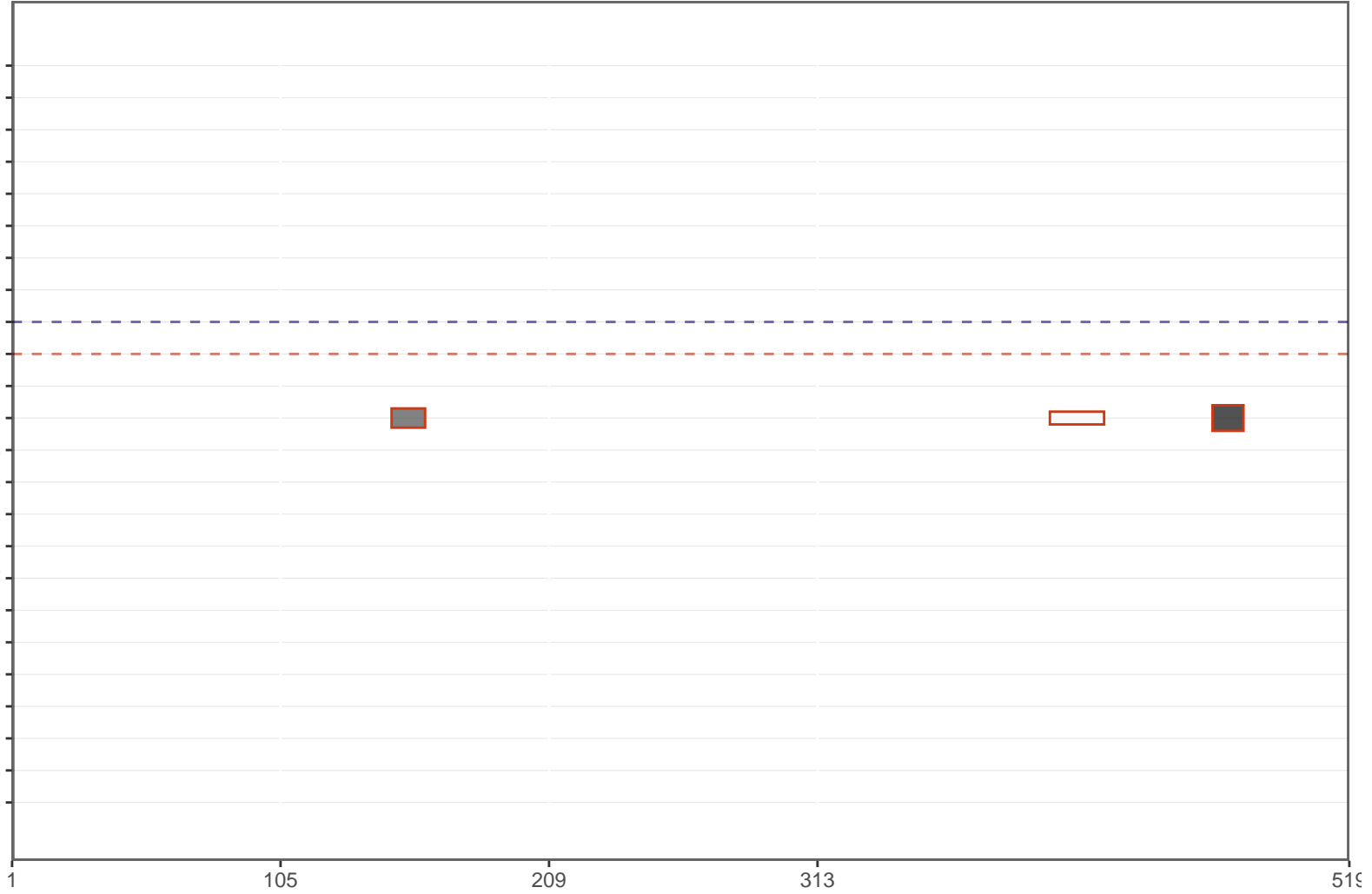
MW indication



Molecular weight



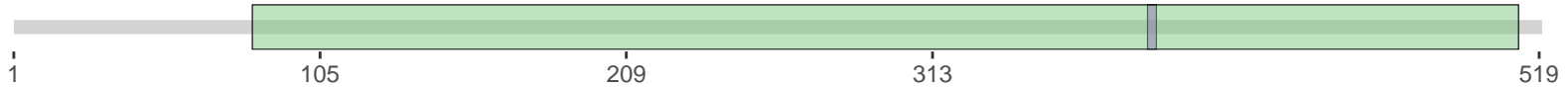
Gel Slice



Peptide counts over 4 repeats

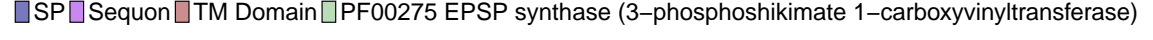
1 105 209 313 519

Protein length



Pfam domains

Pfam Description



Protein sequence:

SGSISSOYLTAALLMAFLALGDVEIEIDKLVPPYVEMTLKLMERFGVSEVHTSSWDFLVRGGGKHYKSPGKAVYEGDASSASYFLAGAATGGTFTYVEGGCTSSLGGDVNFAEVLKMKMGAEVTVTENSIVTKGPPRNSGGMHLRAVDVNMNKKMPQVMTLAVVAFADGFTAIRDVAASWRVKETERMIAICTELRKLGATVEGSDGHTTPEKLSVTEIDTYDQHRMAMAFSLAACADVPVTKDQPGCTRKTRFPNFDVLAQGYSKH

NbL01g05350.1 methionine_aminopeptidase_1A-like [MW = 43.49 kDa]

No. of times detected



log(intensity)



Values from



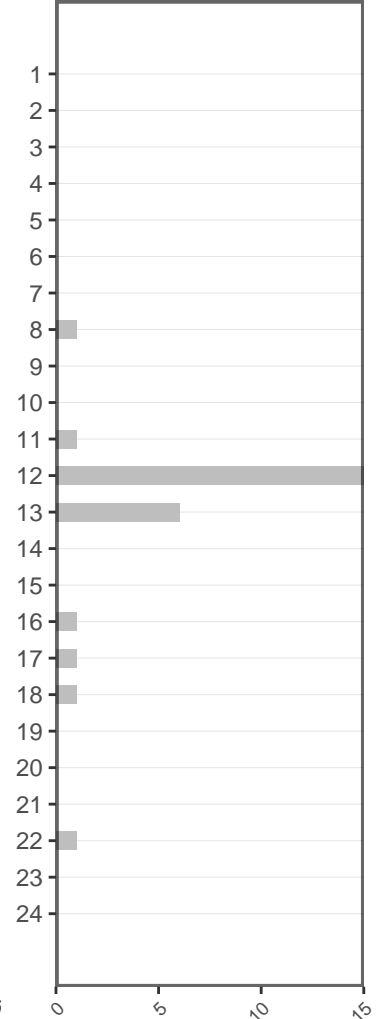
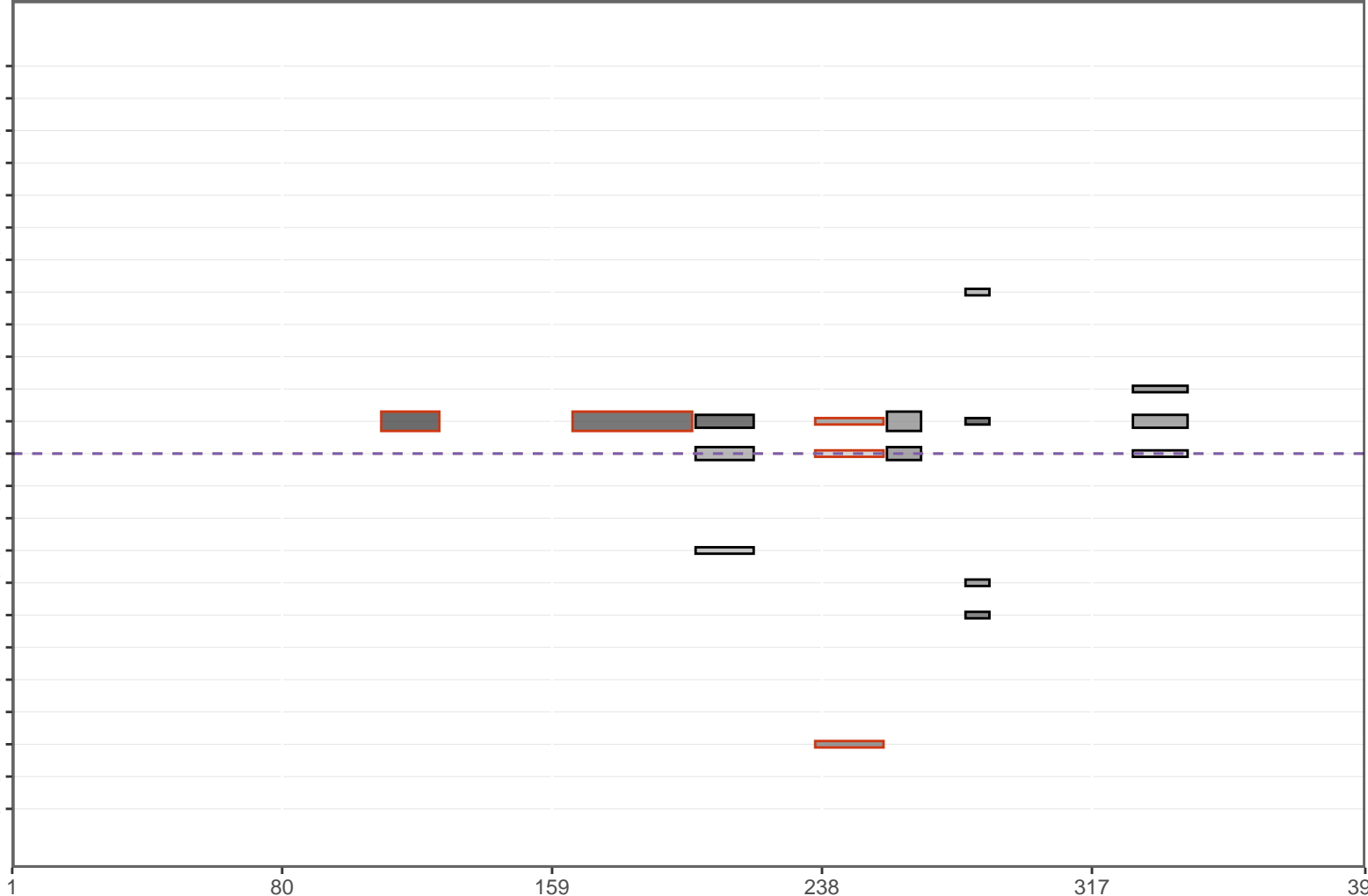
MW indication



Molecular weight

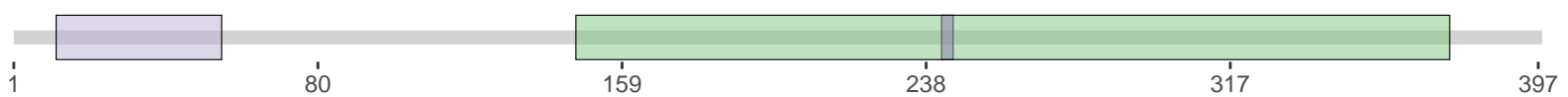


Gel Slice



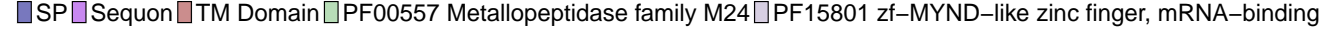
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

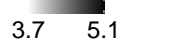
AGAYPSPLNYHFFPKSGGTSVNEVGHGIPDARKLEDGDVNVVDYTFYKGVHGDNLNETFFVGNVDEASDRLVGDTYEGLKASVAKPGVRFREIGEVNIRHSLGSLVWVSKYDGHGIGELFCAPNPHYSRKNVAVGVMAAGQFTTIEPMINAGVWRDRMWPDGWTA/TADGKREAGDFEHLV/TETDGEVLTARLPTSPKVFPPAL65

NbL01g05070.1 uncharacterized_LOC104217986 [MW = 27.44 kDa]

No. of times detected



log(intensity)



Values from



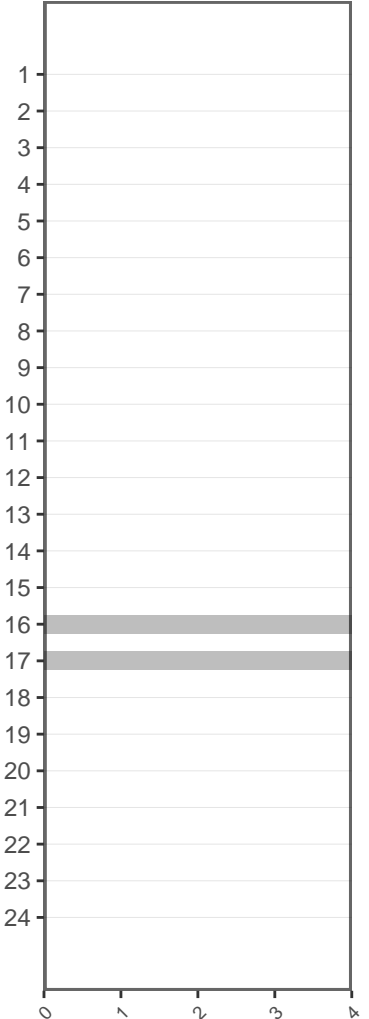
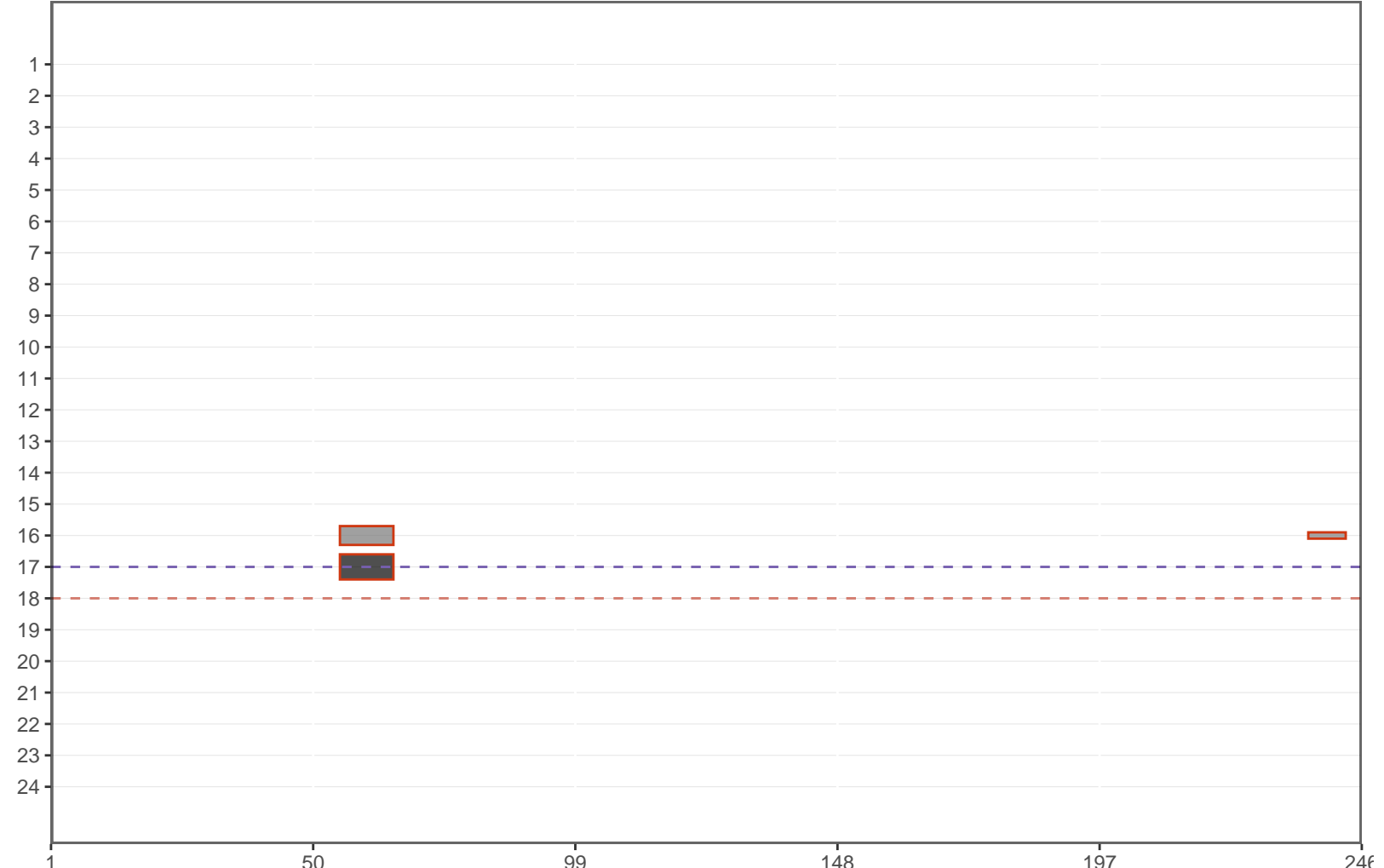
MW indication



Molecular weight

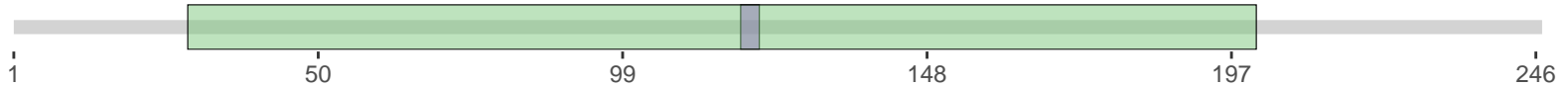


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MLEKEQNVTIRKDDVDGHDGHSFGDEGDNFVDMWNNKIGFLVVGACTDGVLDVFGSTLSAKNRGFLGLEEVVWYDGGCATDFDFAVARINTKDISPHQGLMHHVGLYMAKERGAKIAREVDFNSLKKP

NbL01g05060.1 fructose-16-bisphosphatase_class_1-like [MW = 44.81 kDa]

No. of times detected



log(intensity)



Values from



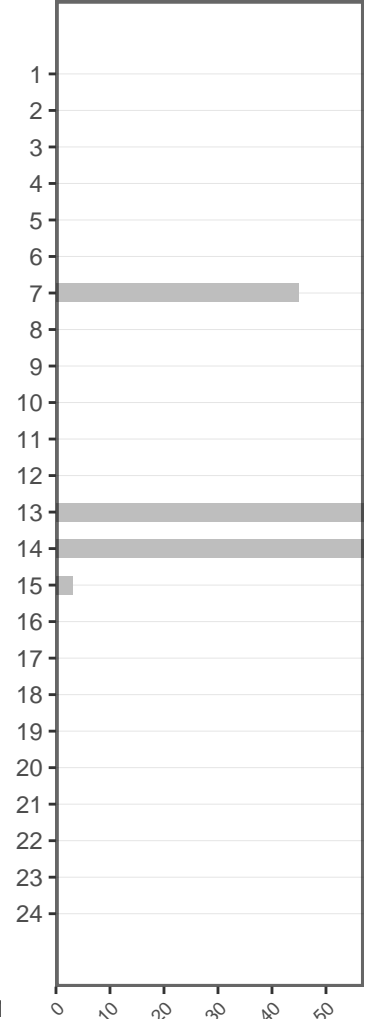
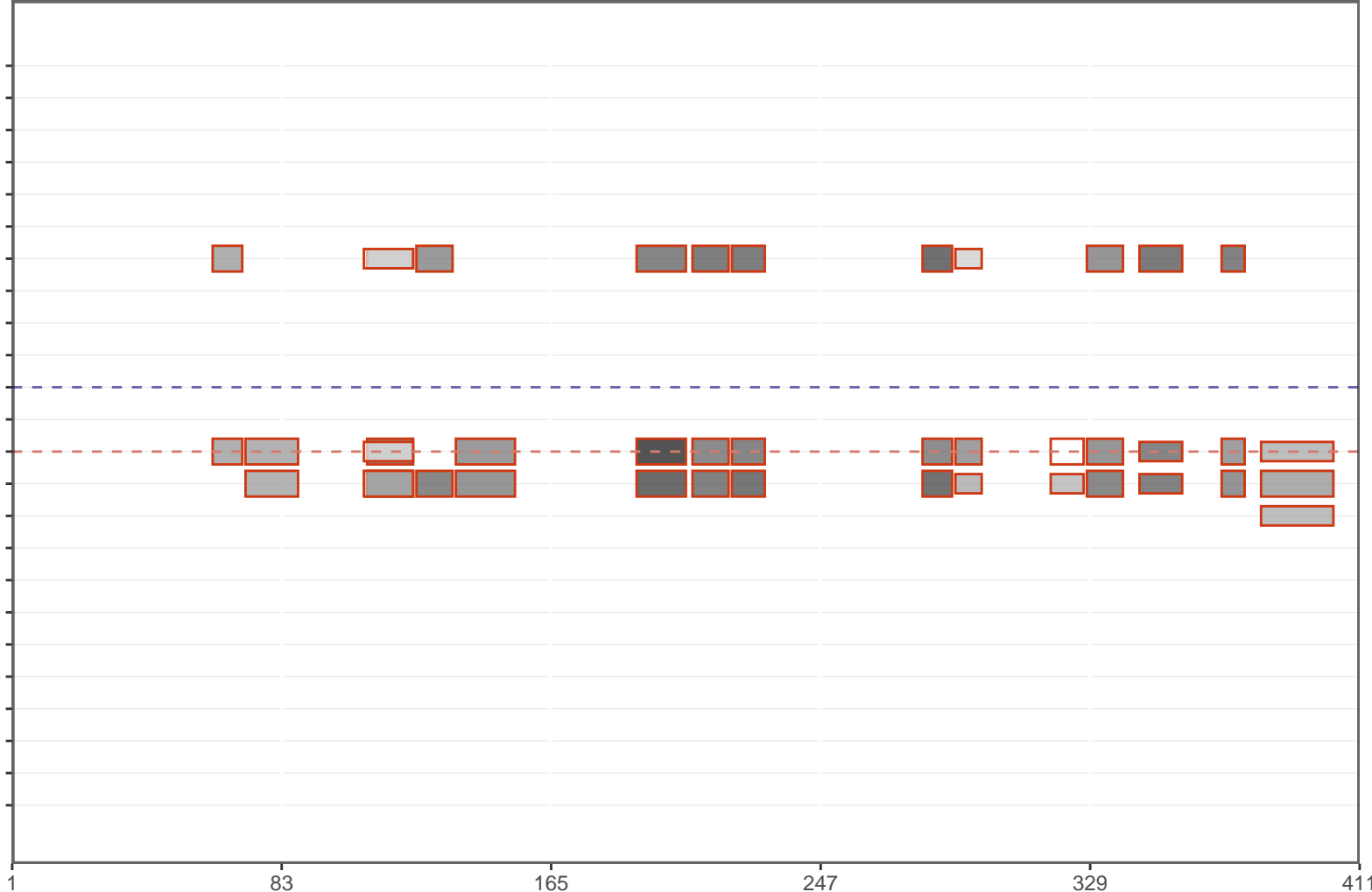
MW indication



Molecular weight

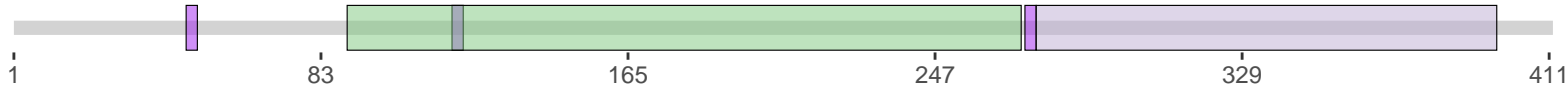


Gel Slice



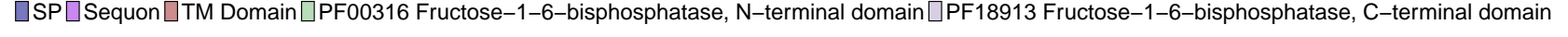
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IDASIPDTGTFGIYKRLVEIDHLPVEEKASLNLGGGAKLIAAAVLYSBSATLGCASFSGGTHAFTLDDHTTGDGFLTHFNISPPRGGQVYVNDARYFDWPEGLRQYDITRQGGKHKPKYSARYKIGSLVADFHRTLLYGGVAMNPRDHLRLVVEANPLSFLAEKAGGRGGDKNRLISGIPKVLHQRLLFLFGSSDDDEELGGYGDVQGVKVPFGYDV

NbL01g04990.1 methylmalonate-semialdehyde_dehydrogenase_[acylating]_mitochondrial [MW = 56.83 kDa]

No. of times detected



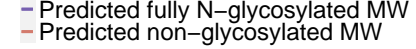
log(intensity)



Values from



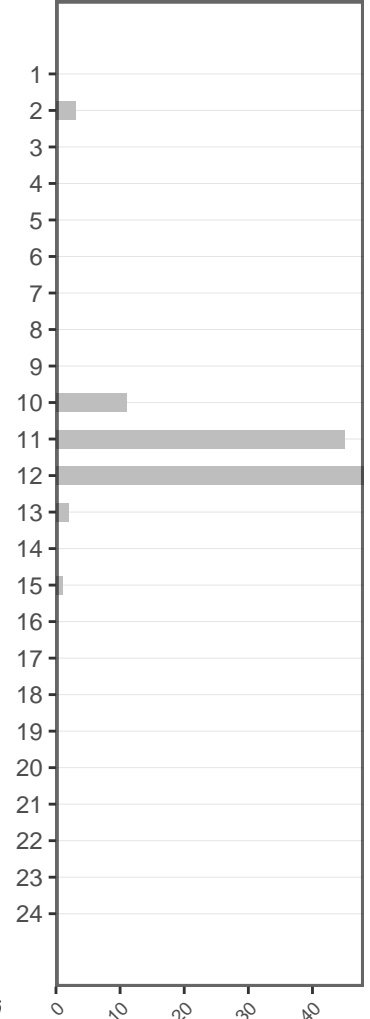
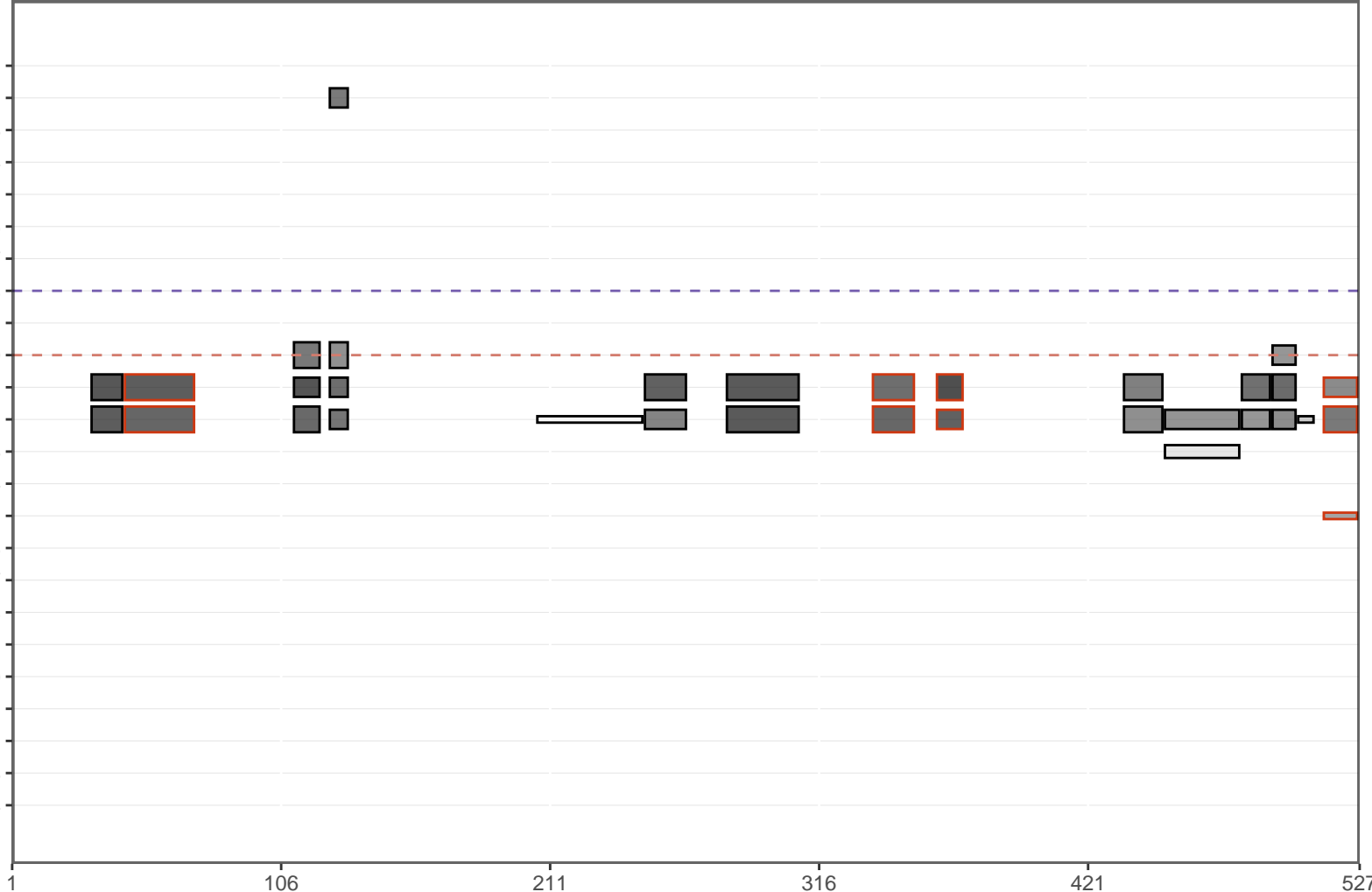
MW indication



Molecular weight

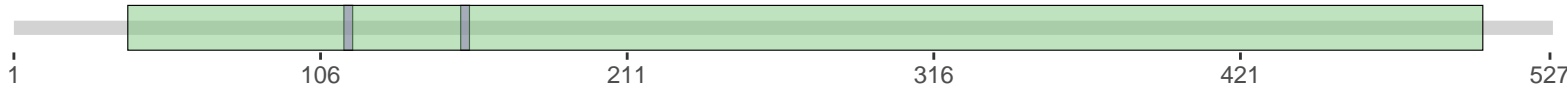


Gel Slice



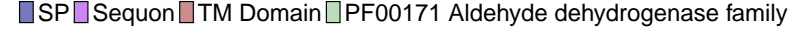
Protein length

Peptide counts over 4 repeats



Pfam domains

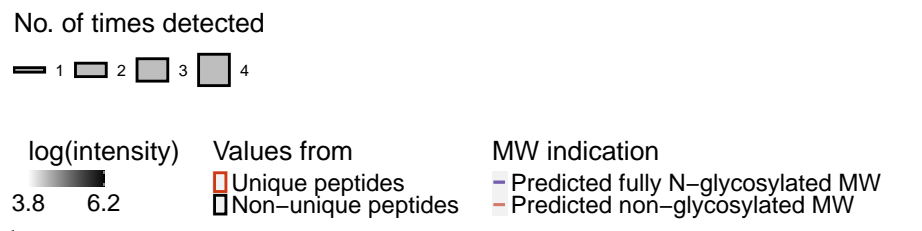
Pfam Description



Protein sequence:

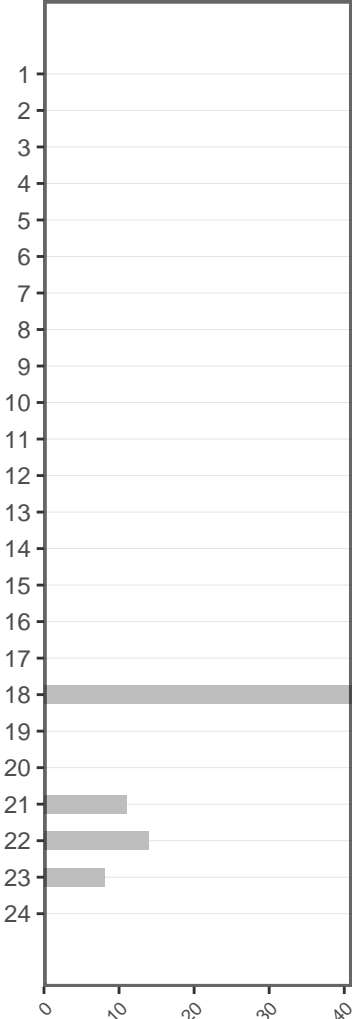
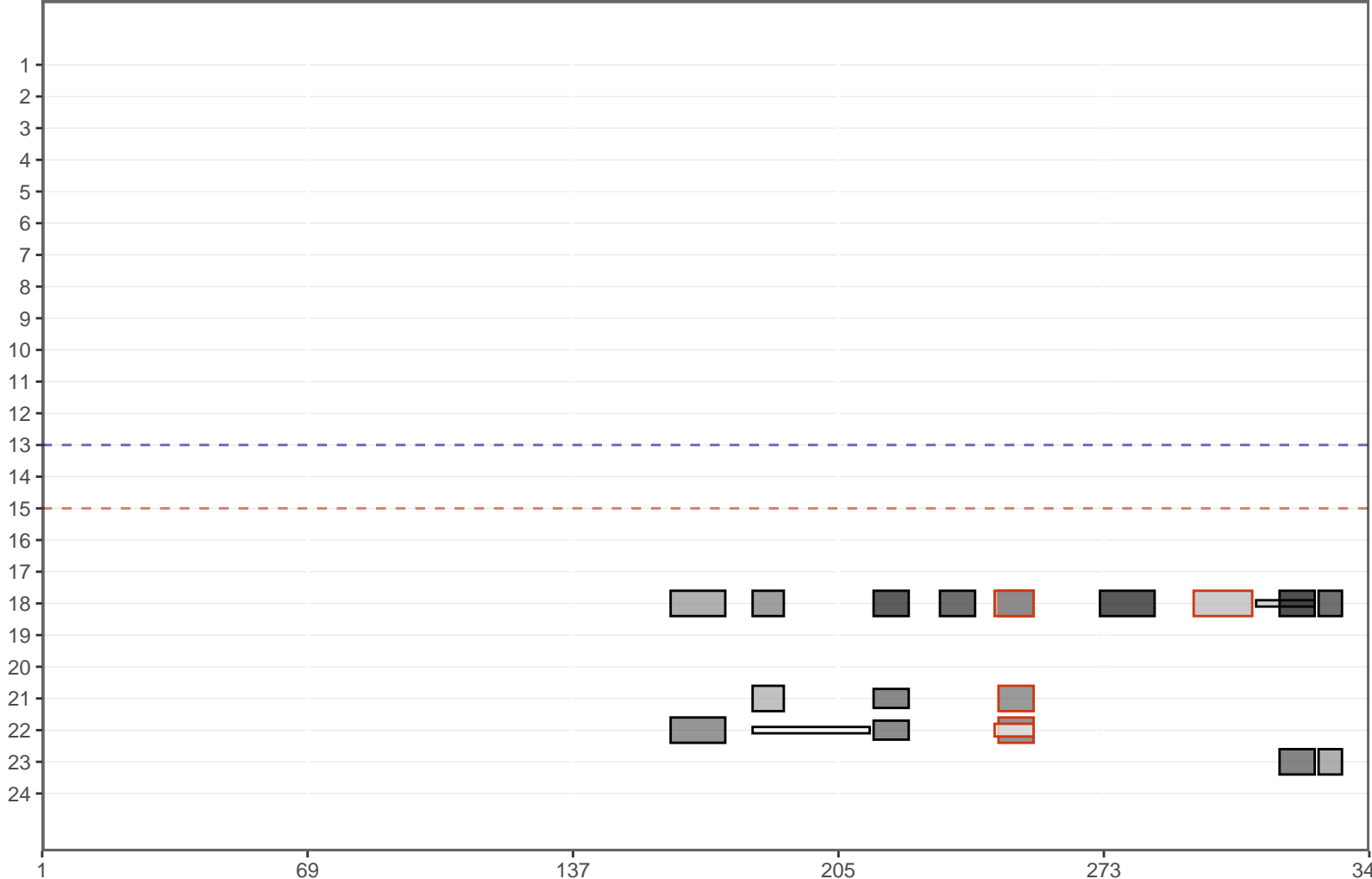
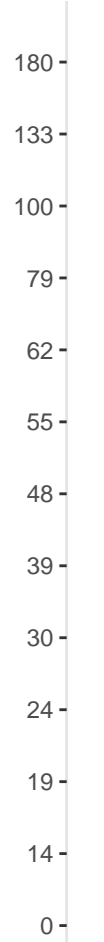
VGSNAGMIHYARASAKGRVDSNGAKNHGVAMPDANIDSTVNLVAAGFGAAGGRGMALSTVVFVGDGKPVWEKLLERAKALKVSGGTEFNADLGPVWIKQAKERVCRLLVQSDSDSARLLLDGRDVPVPGYEKGNFVGPPLSGVTPDMDCYKEEFGPLUQMDSNLEAINVNNKIKWGNGAAIFFTSGVAARKFQTEIEAGGVGINPVPVPLFFSFTGSKAFAGDNLFYKAGVGFYTGKTKTQGWKDLRGSGSVSLAMPTSGK---

NbL01g04970.1 psbP_domain-containing_protein_1_chloroplastic-like [MW = 38.28 kDa]



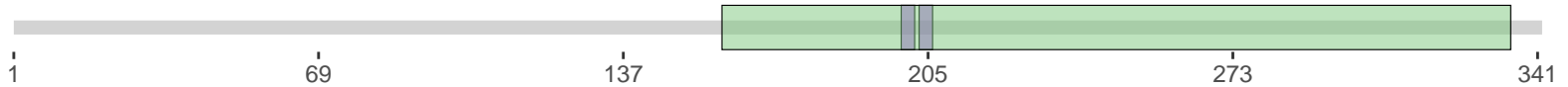
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

SP Sequon TM Domain PF01789 PsbP

Protein sequence:

IFREYIDTFDGYSFMYPRNWNQVRGAGDIFFRDPLVLDENLSMNISSPSSAYKSVEDLGPPEKAGKGVLRQYLTFEMSTRLGVRRSSVLSASSRVAADGGKLYEVEVNNKSWANNELVAMPDQRRVRLWEVDRIYVLSVGVENNDLYELRHGTPEKTFDEESDRAMDSEFRVAKIEV

NbL01g04860.1 glutamate--tRNA_ligase_chloroplastic/mitochondrial [MW = 63.37 kDa]

No. of times detected



log(intensity)



Values from



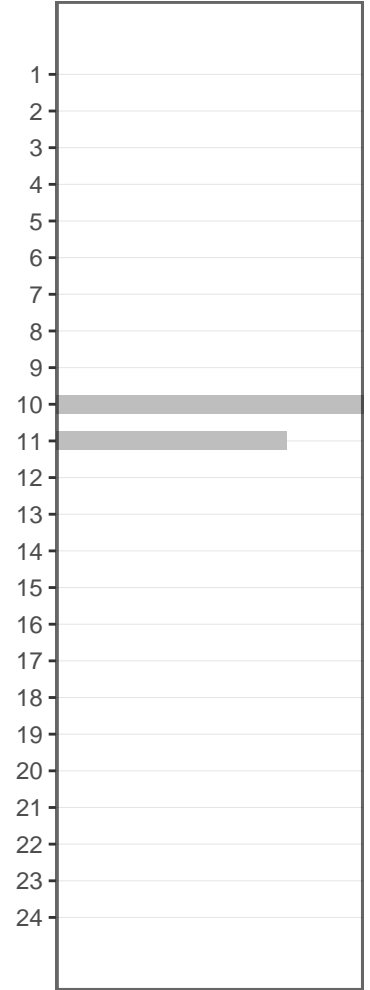
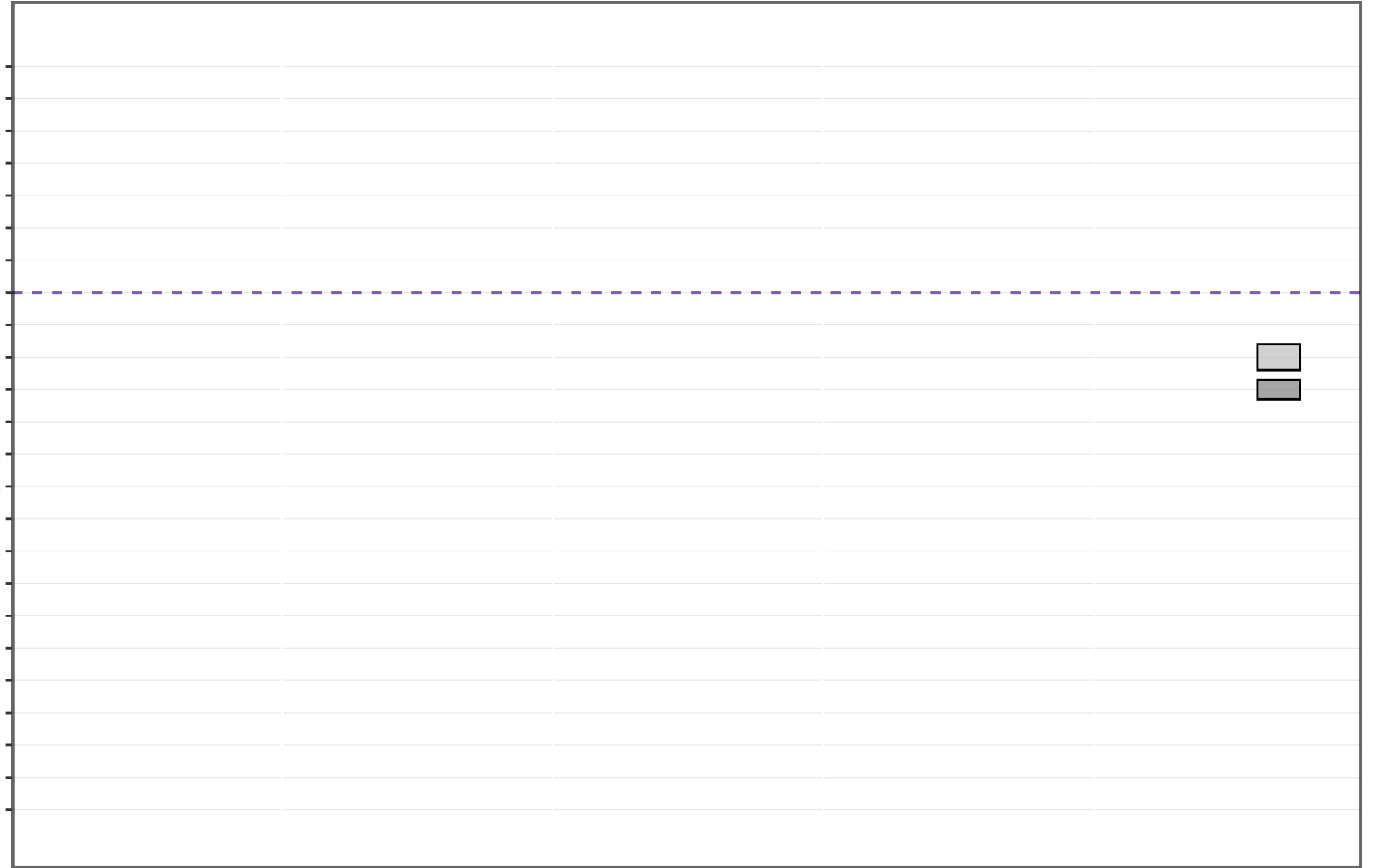
MW indication



Molecular weight



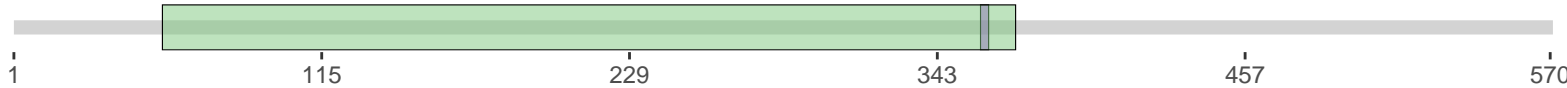
Gel Slice



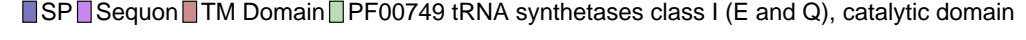
Protein length



Pfam domains



Pfam Description

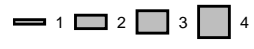


Protein sequence:

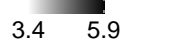
.PNTLRQALLTYKALGFPMPHFVHLSLAPDRSKLKRKHGATSVGDFRDMGSLPQAMVNYLALLGWDDGTENEFFLEQLVEKFTIERVWKSQGAIFDSTKLRLWMMNGDHLRSLPSEELRIGERWKGAGITTESGGIFQDALLKDKDGLTDSKALSSLLSYPLVETLASAEKPLEEDGVSEVAKSLLAAVDSGELSGALAEQGPQWQKWKWVNFGLKLRKKGKSLFMPFLVLTQKLRHDPDGLATTALYKAGTSGSVWPDQAGVTFDELRKLRREVQVESFSDVPLSAC

NbL01g04850.1 aminoacylase-1 [MW = 52.27 kDa]

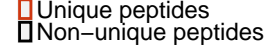
No. of times detected



log(intensity)



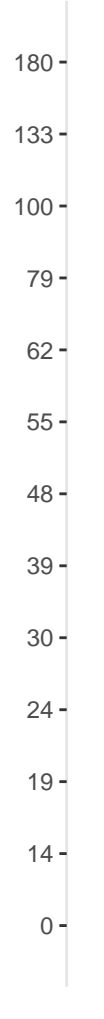
Values from



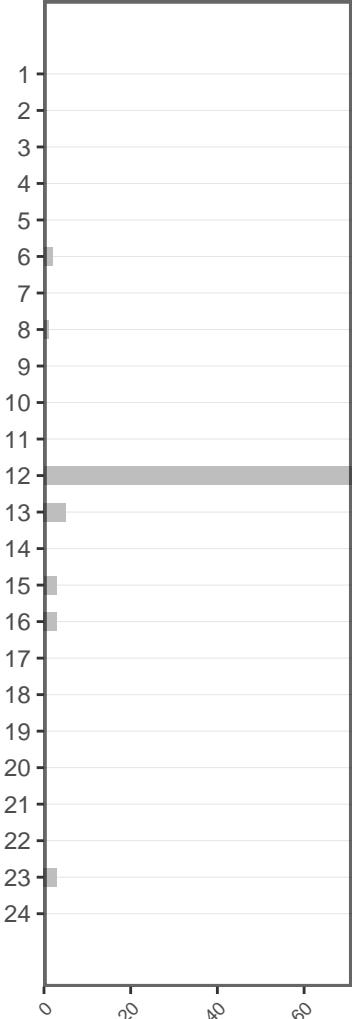
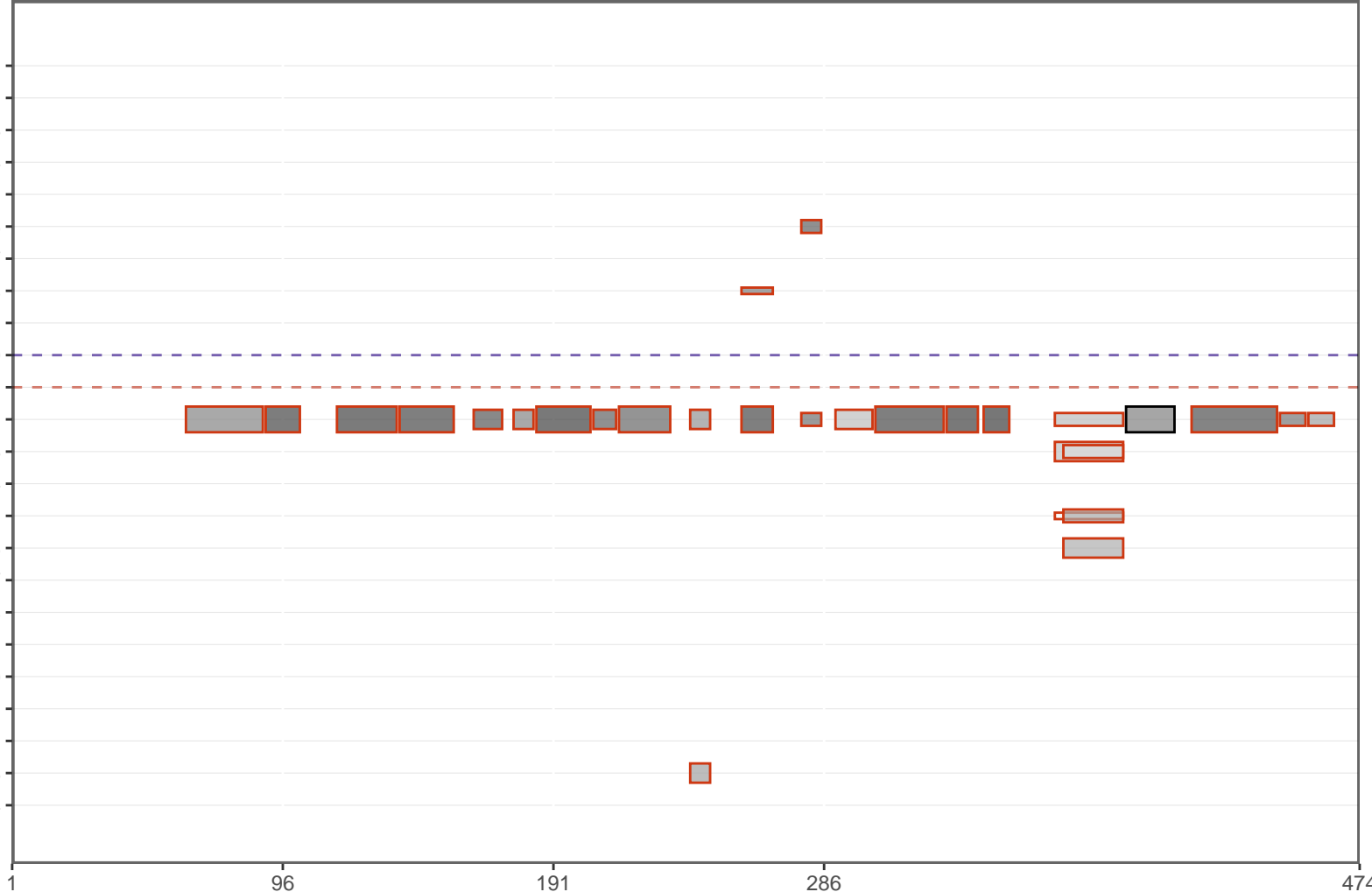
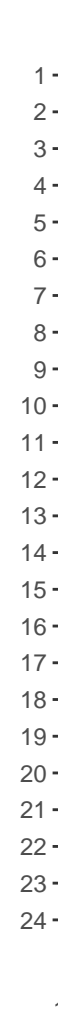
MW indication



Molecular weight

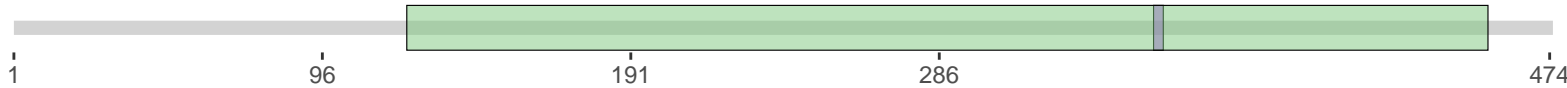


Gel Slice



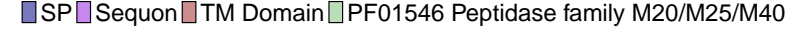
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PSPTENYRAFYGERSPFWLWVAVGAPGHGAKLYDNSAMENLKVETRRFRRAAGFDLWVAGLKAEGEIVSNMVLKAGTSPSPGFVMMNIGPBEAAGDFDIRVPTADGASLEKRIAEVWAPSRNMTFEFKQKQVSNVNDKFORFPAITAVDGSNIAWVWALLEEIVKANAGVQKPEIFPASTDARYFRERGLPAIGFSPMANTPILLHDHNEFLNKDEYLVGGIDVYGSKTVASVIEHPRDEASREEL

NbL01g04840.1 uncharacterized_protein_At2g17340-like [MW = 40.69 kDa]

No. of times detected



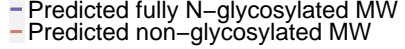
log(intensity)



Values from



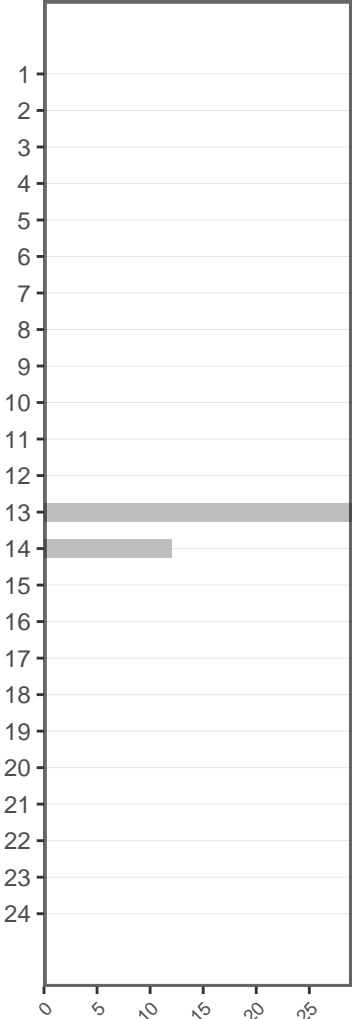
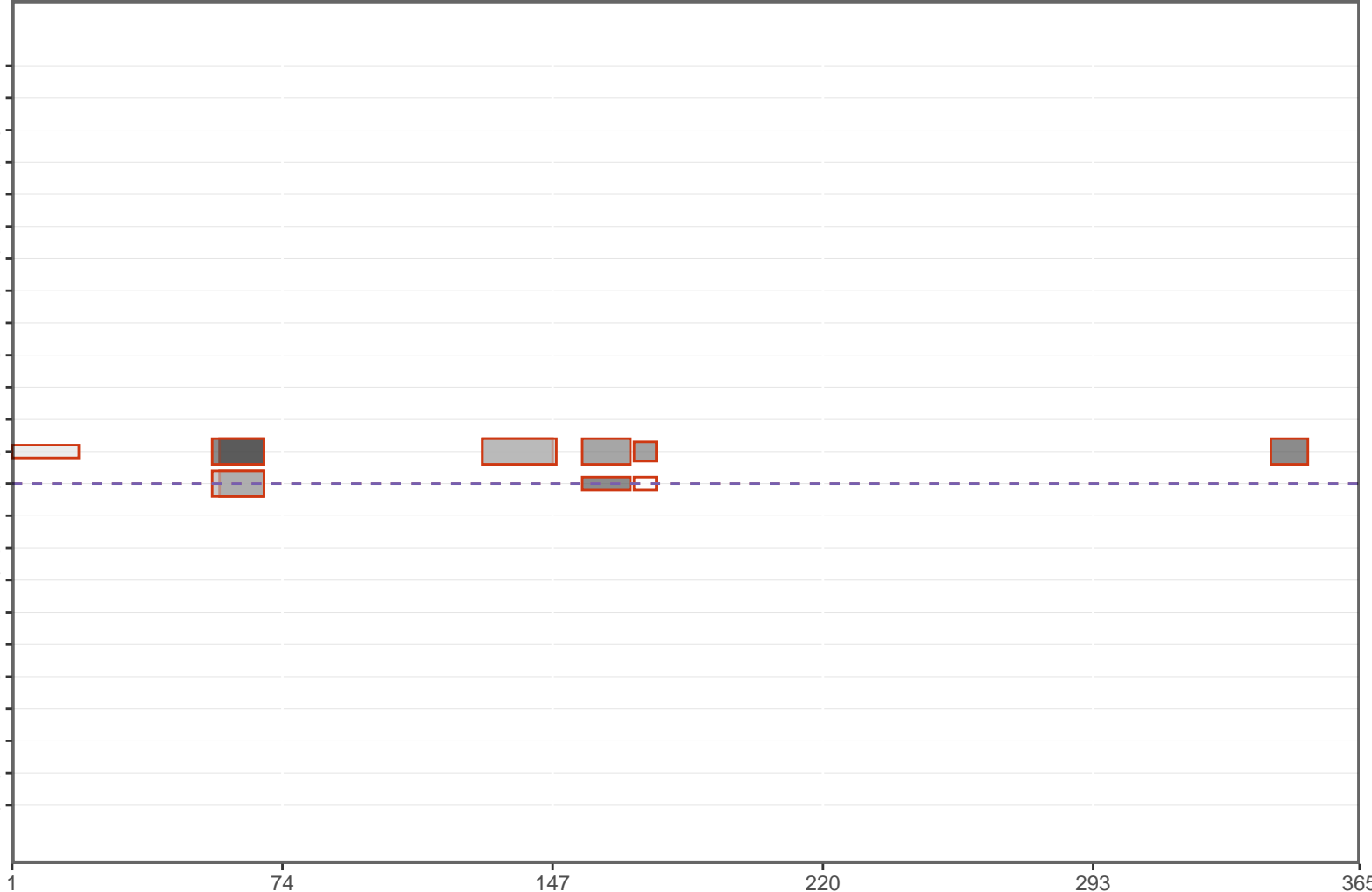
MW indication



Molecular weight

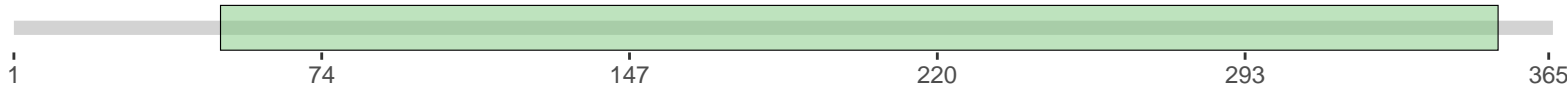


Gel Slice



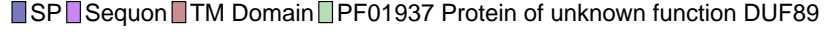
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AKLAELFSRDGISFLAAGENLVRPPWIDMDTFITLKRKSKWKAIVFDNBSGADHILGILPFARELLRHGTQHLAANDLPSINDVYTHELVEISKLDKDEHKIKLVGVDTSNLLVANSNDLPLVILMGISPELAYLASDADVILEGMRGIETNLVAGFKDSDSKIGMVAHPEVAEFLGGRLYDGVFKYNEIMET

NbL01g04800.1 homoserine_kinase-like [MW = 38.42 kDa]

No. of times detected



log(intensity)



Values from



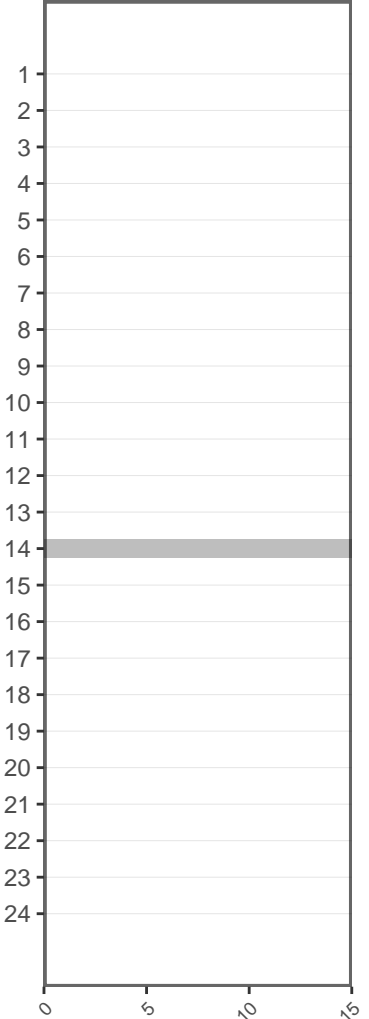
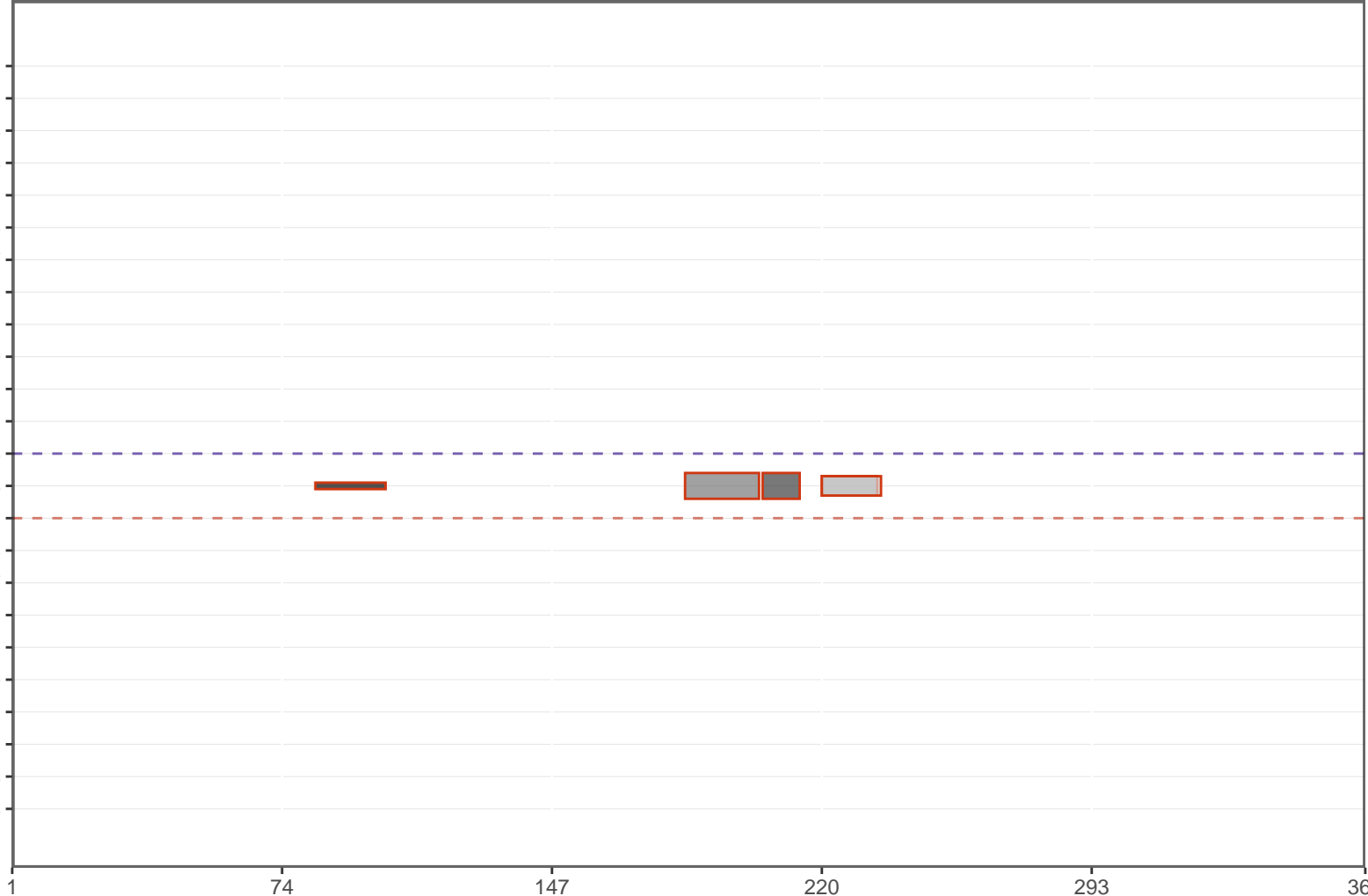
MW indication



Molecular weight



Gel Slice

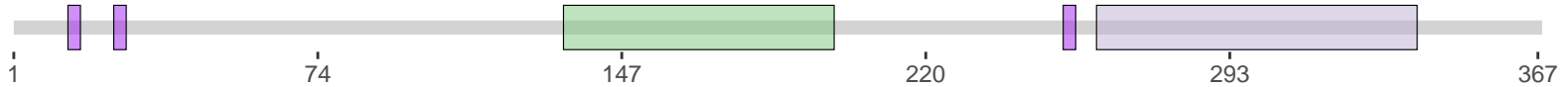


Protein length

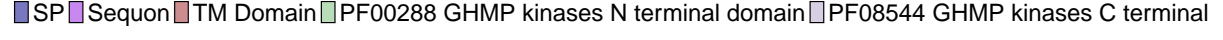


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ILVLAGLESESKVSGYHMDNAPNMGDFVLRBYDPLELHQLKFPHEKEFFVWLNPEFEAPTQKMRRAALPQGITMESHHWNSGAAALVAWVLOGDLSEVLGKALSDSDKIVRRAPLIPGMEGVKVVMEAGAGGCTISGAGPTAVWTDNEEKREIGRGRMVEAFKKEGNLKSEAMVKKLDRVGARLVSSDPR

NbL01g04700.1 metal-independent_phosphoserine_phosphatase [MW = 25.64 kDa]

No. of times detected



log(intensity)



Values from



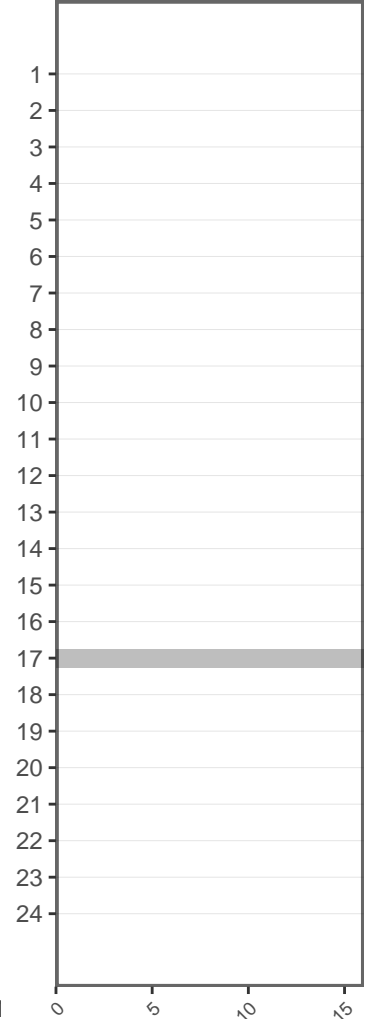
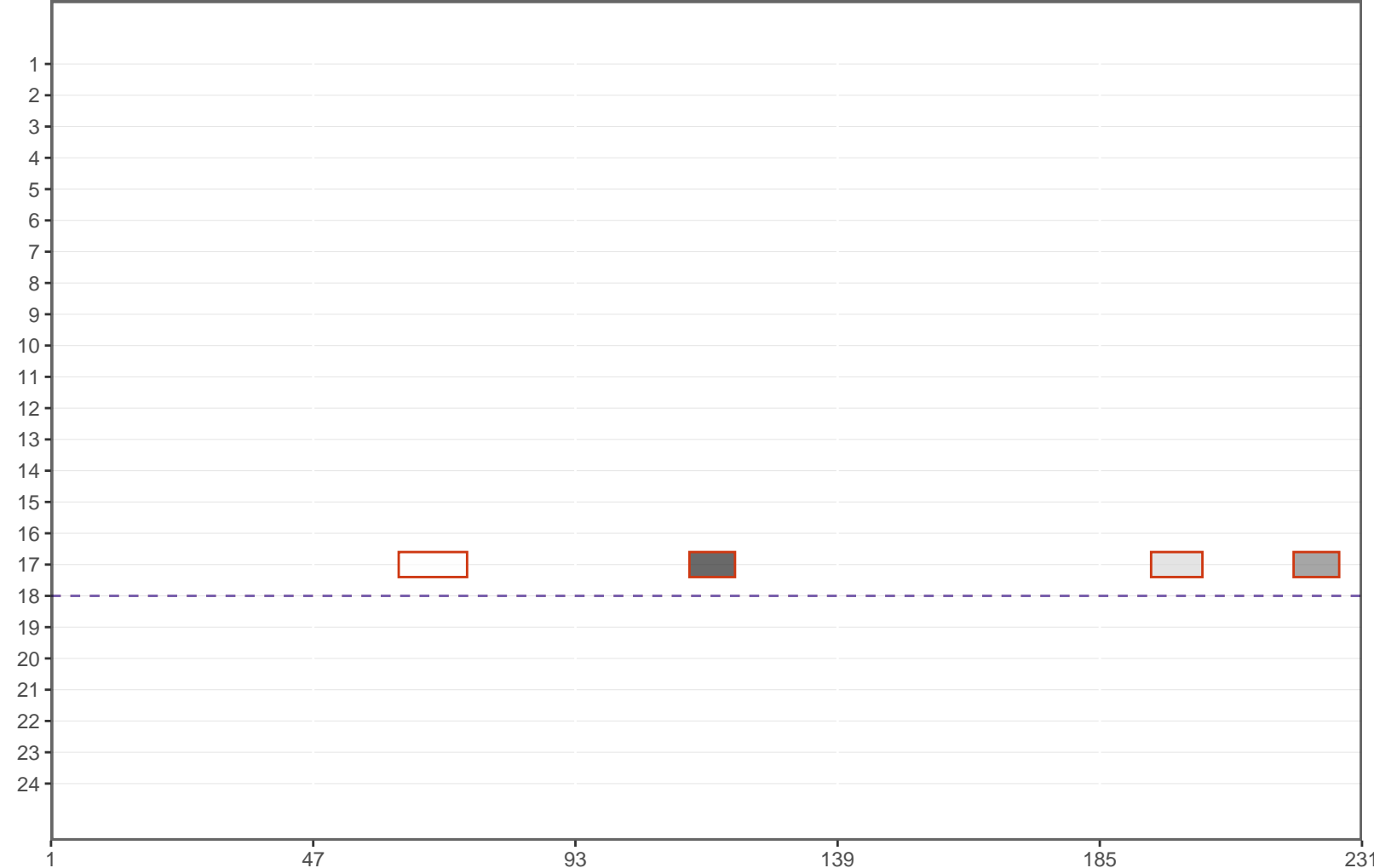
MW indication



Molecular weight

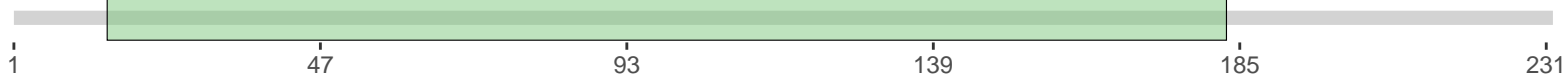


Gel Slice



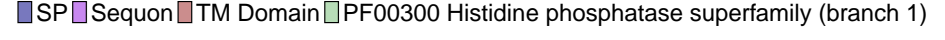
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

DMVLEDLRERFTGPRVELKSHDKYPRDIALDEKDFPMQPDGSGVADVSRILTSALINMESQFGGCTVLLVSHGDPLOIFQTVLNAAKDYKGGCENDLFSRVGAVKIPQVLSGHRFALGTGELRQVY

NbL01g04690.1 SEC1_family_transport_protein_SLY1-like [MW = 69.54 kDa]

No. of times detected



log(intensity)



Values from



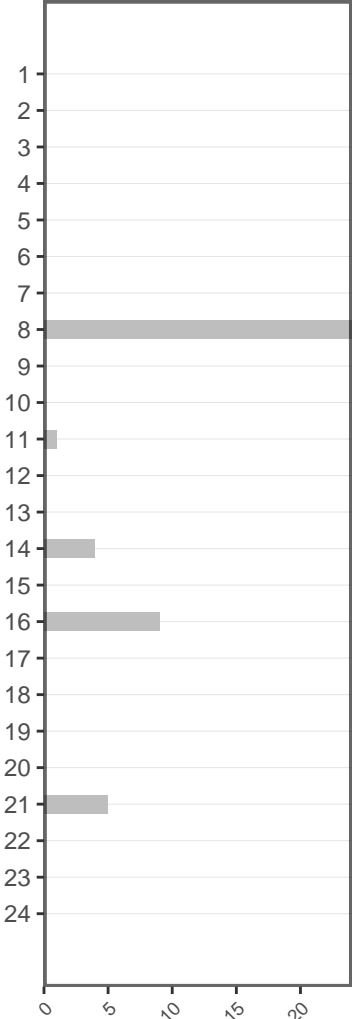
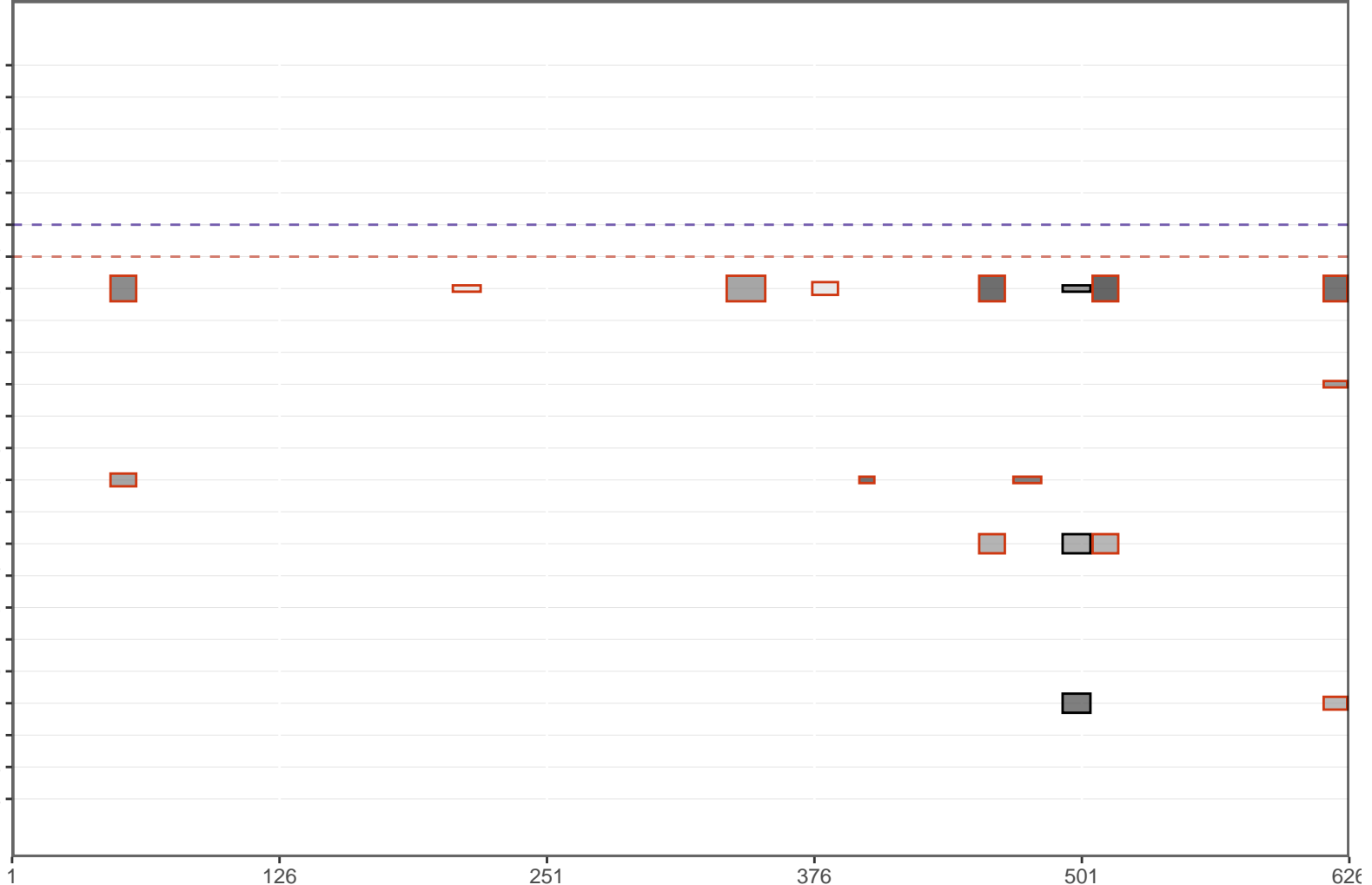
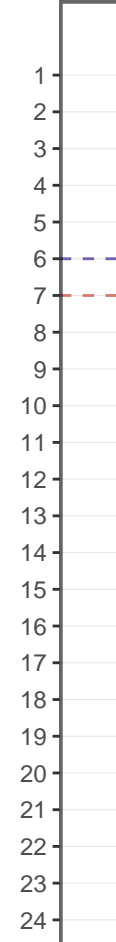
MW indication



Molecular weight

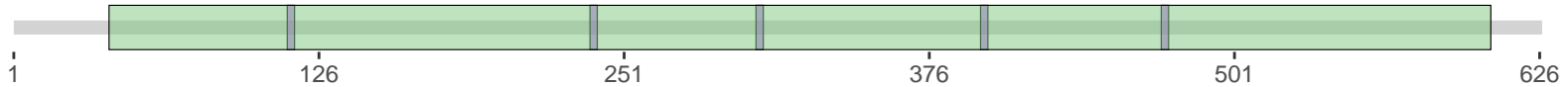


Gel Slice



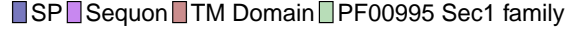
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

VTANVSLFPEVAVIEESGLNKKYKDKVEVNRKRTGGNAGAEFDGTDLIGNKTHLMNVAWNSLPFELTERKQVVDKHTNATVLLGEIKERSLDSYAKNESDMVVGADRNLELGLRGTQVDKLRFAIMYLISTESLPGSEVEMETALRESEVDTTAFQYKIKKSLNVSLSANSASRENVDWAEKLYGGISAVTAGVKNLLSSDHLQLGRITVEALMEGKPNPEIDSYVLDRAPRKSSSGMSSSHLKGPFKEAVFMGGGNVVEVGSLSGLASRQDFVQIVYGTTEL

NbL01g04650.1 lysM_domain-containing_GPI-anchored_protein_2 [MW - SP = 35.32 kDa]

No. of times detected



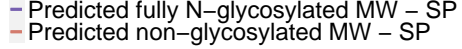
log(intensity)



Values from



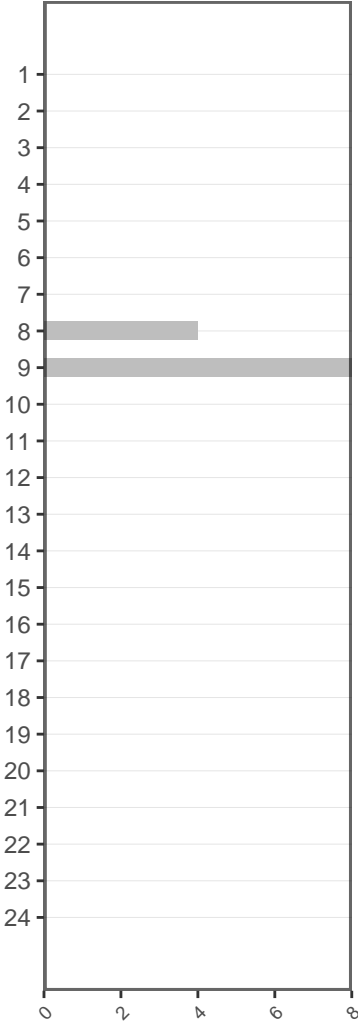
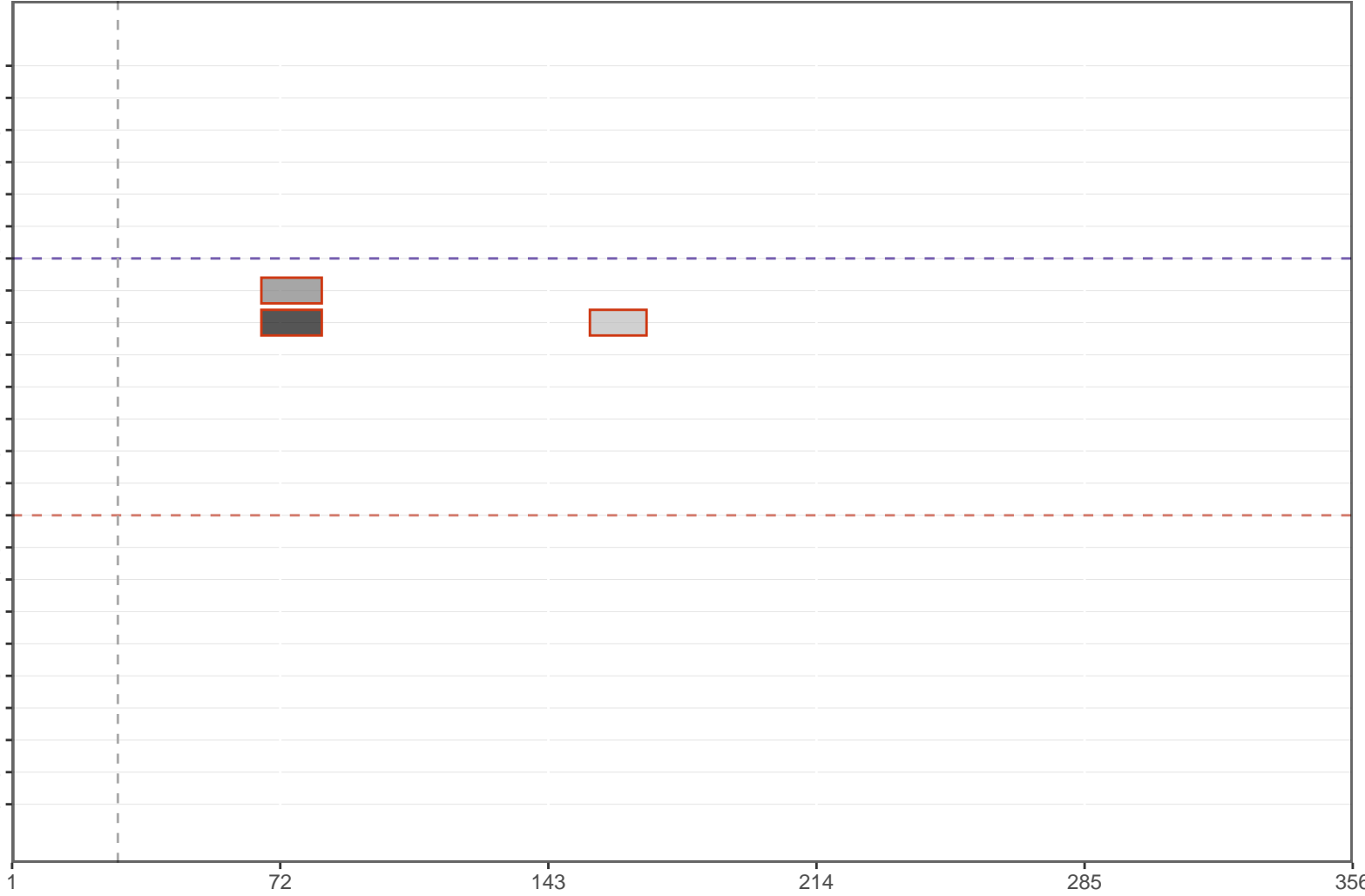
MW indication



Molecular weight

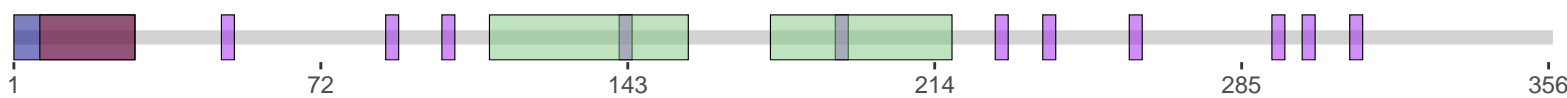


Gel Slice



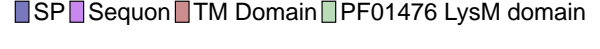
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SEKVVYHGHLVAAGNTVDIAAGQVNVVGGDTLLKLNGLSDPKELAGSVLVDPLKADQGMVNTSLDPLVNDTVVFTAAANDVACKGDAANKWFLQQGPSQKSKLWKSGLMGGGLDSFYHGNTSPDCNSTTGAVAGVSNQTFITFTSTGSGTGRNTASDMRSGTWRWNILVAHLLASVLR*

NbL01g04600.1 uncharacterized_protein_ycf39-like [MW = 43.89 kDa]

No. of times detected



log(intensity)



Values from



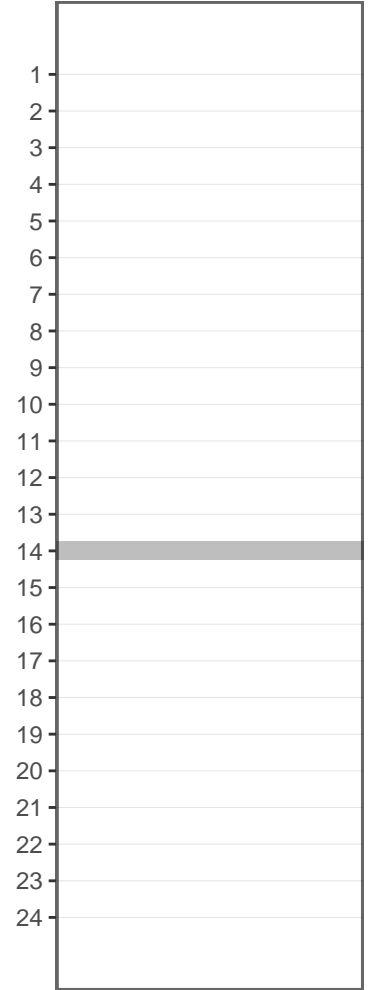
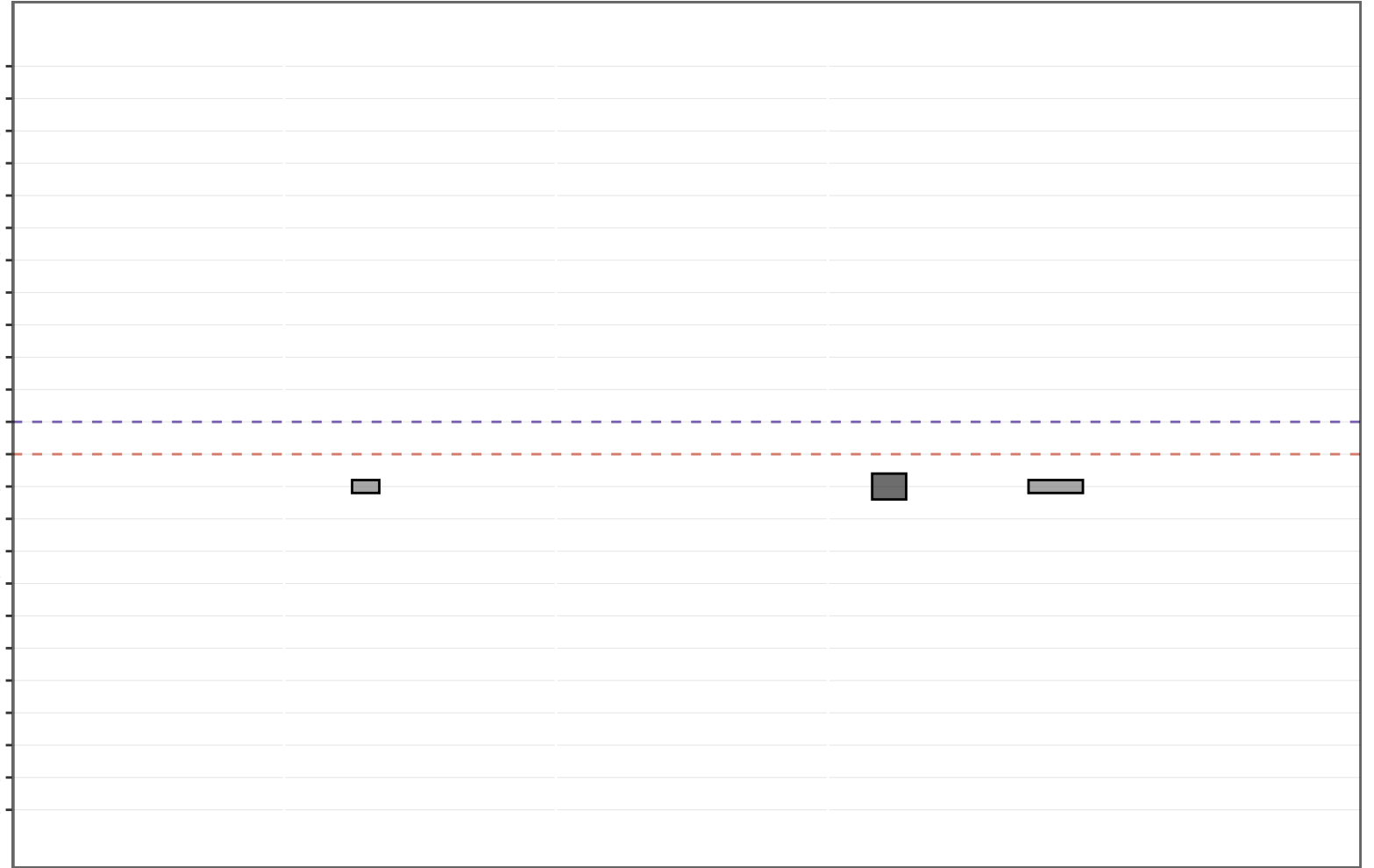
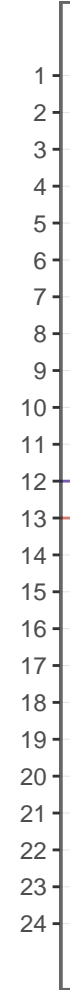
MW indication



Molecular weight

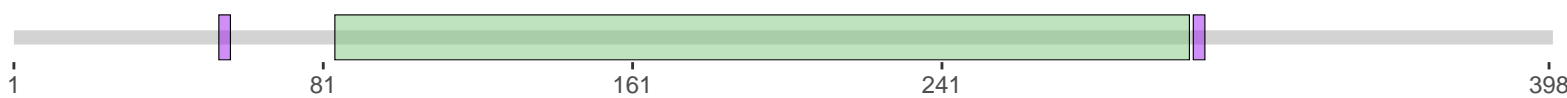


Gel Slice



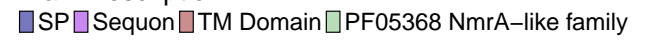
Peptide counts over 4 repeats

Protein length



Pfam domains

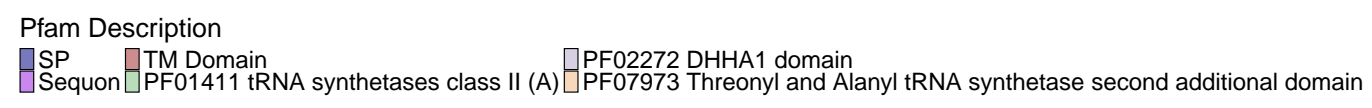
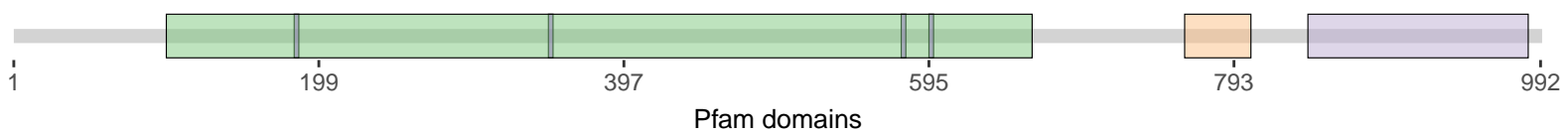
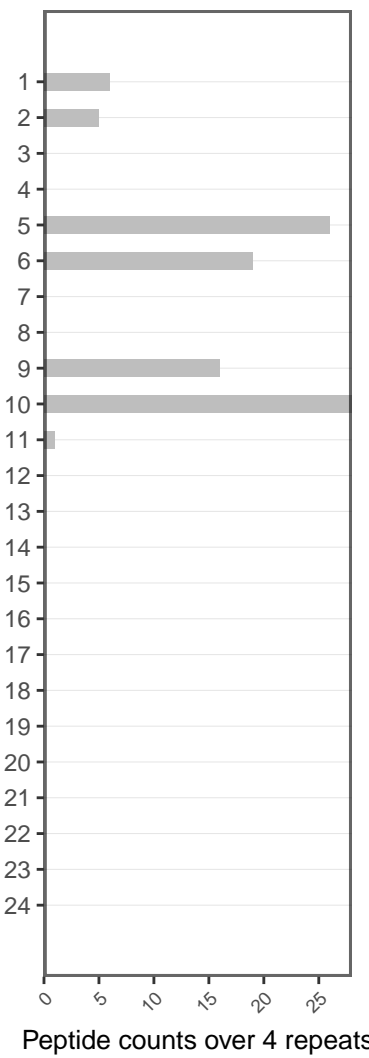
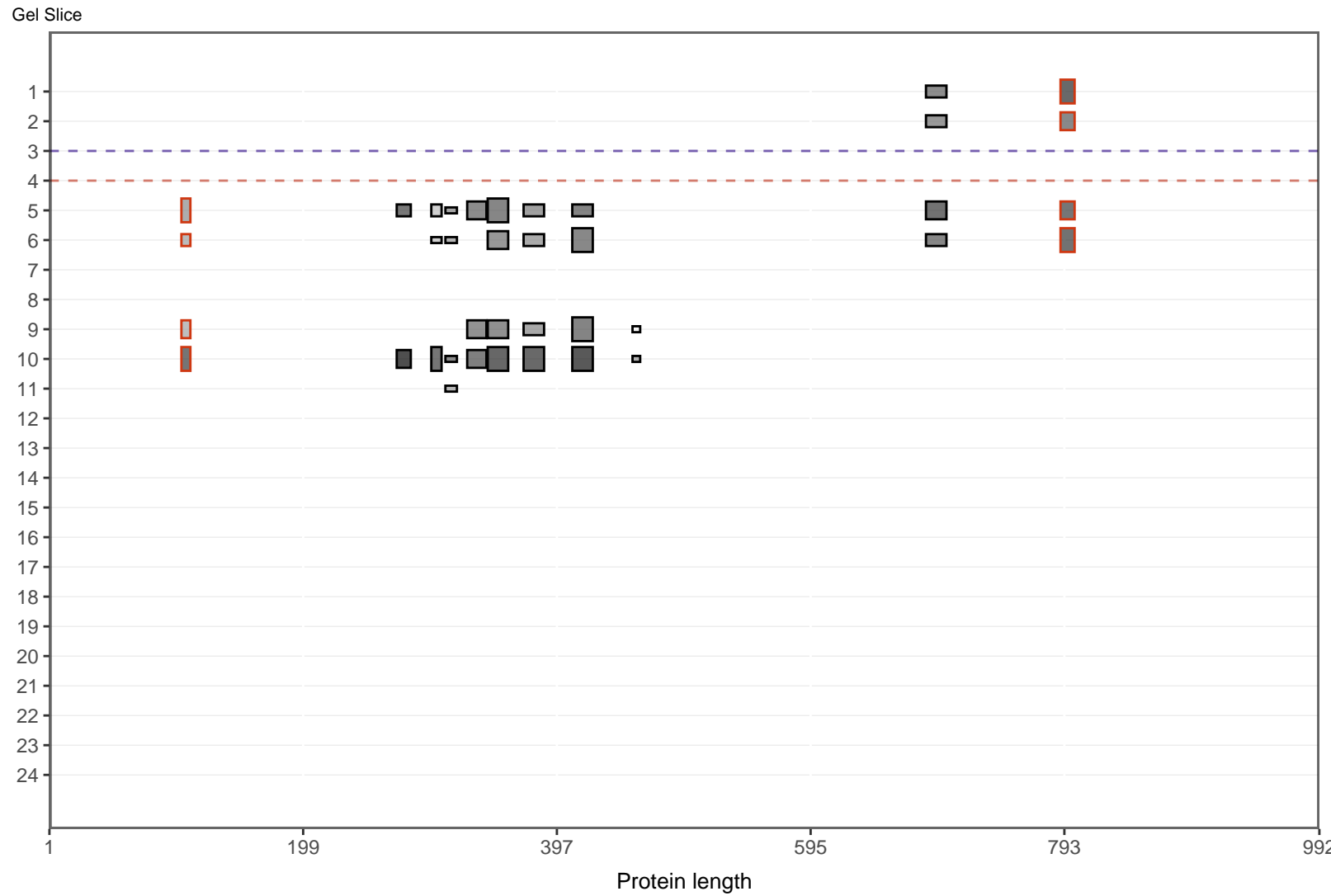
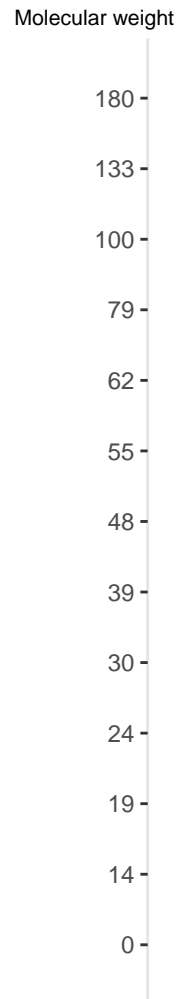
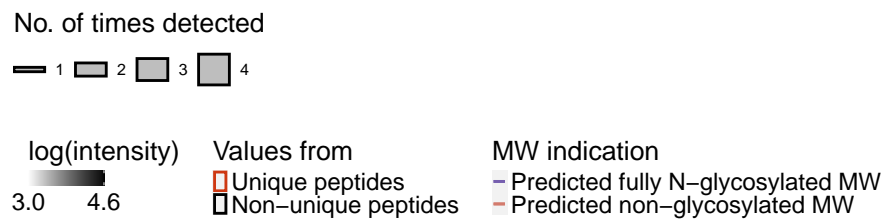
Pfam Description



Protein sequence:

MFSSINCDKHPVPLMEKIKYOTEKFLRDSGLNHVAVIRLGGFMAGLIGQVWPLEEKSVWGTDPATRIAWMDTGQIALRTFIALRNENINGKLLTFAGPRAWTTGSEVTLGERLAGQDANVTFVPSVLRILTRQLRLEFVWTDVADRLAFSEVLTSDTVFVPMETYSLLGVDAKGVSELEKYLGDVFTNLKRLKDKKAGSGKGTDFP

NbL01g04530.1 alanine--tRNA_ligase_chloroplastic/mitochondrial [MW = 109.18 kDa]



Protein sequence:

APCMSGKDAFLVLYDTYGFPEITNEWEAERGIGDMNSFDIEMEKGRGLGSAHSDTVLGVENGANLAEDIPDTEFLGYNTRLSKAVVEGLLVNGSPVAQVSKSGSEVEILLNRTPFAESGGGGDNGFLYMMEAENEQGTVEIKDVAQKSMGNFVHKGTITTEGMEVREVEAAVDASLRGRRAVHHHTATHLQSAKRVIGQETSQAGSLVAFDRLLRFDNFHRLDQKKEVEIEGLNHWIGDAWLETKVMSLTDAKRDGAIAMFGEKYGEQVRRVVEVPGVSMELCGGT

NbL01g04470.1 coiled-coil_domain-containing_protein_124-like [MW = 27.1 kDa]

No. of times detected



log(intensity)



Values from



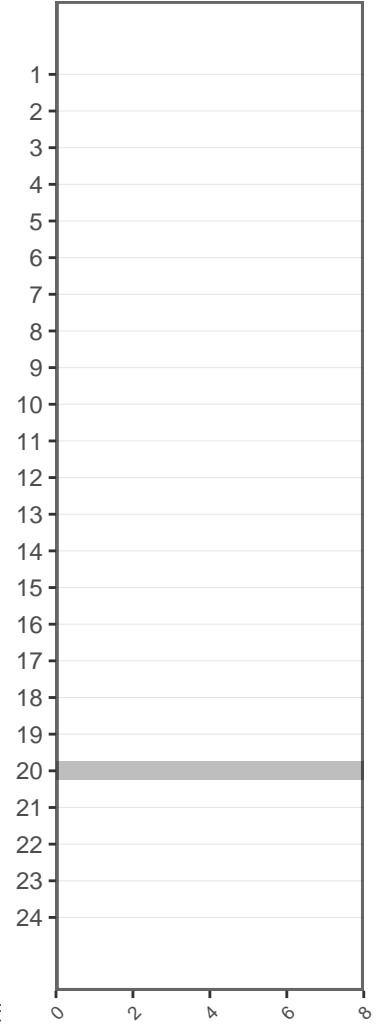
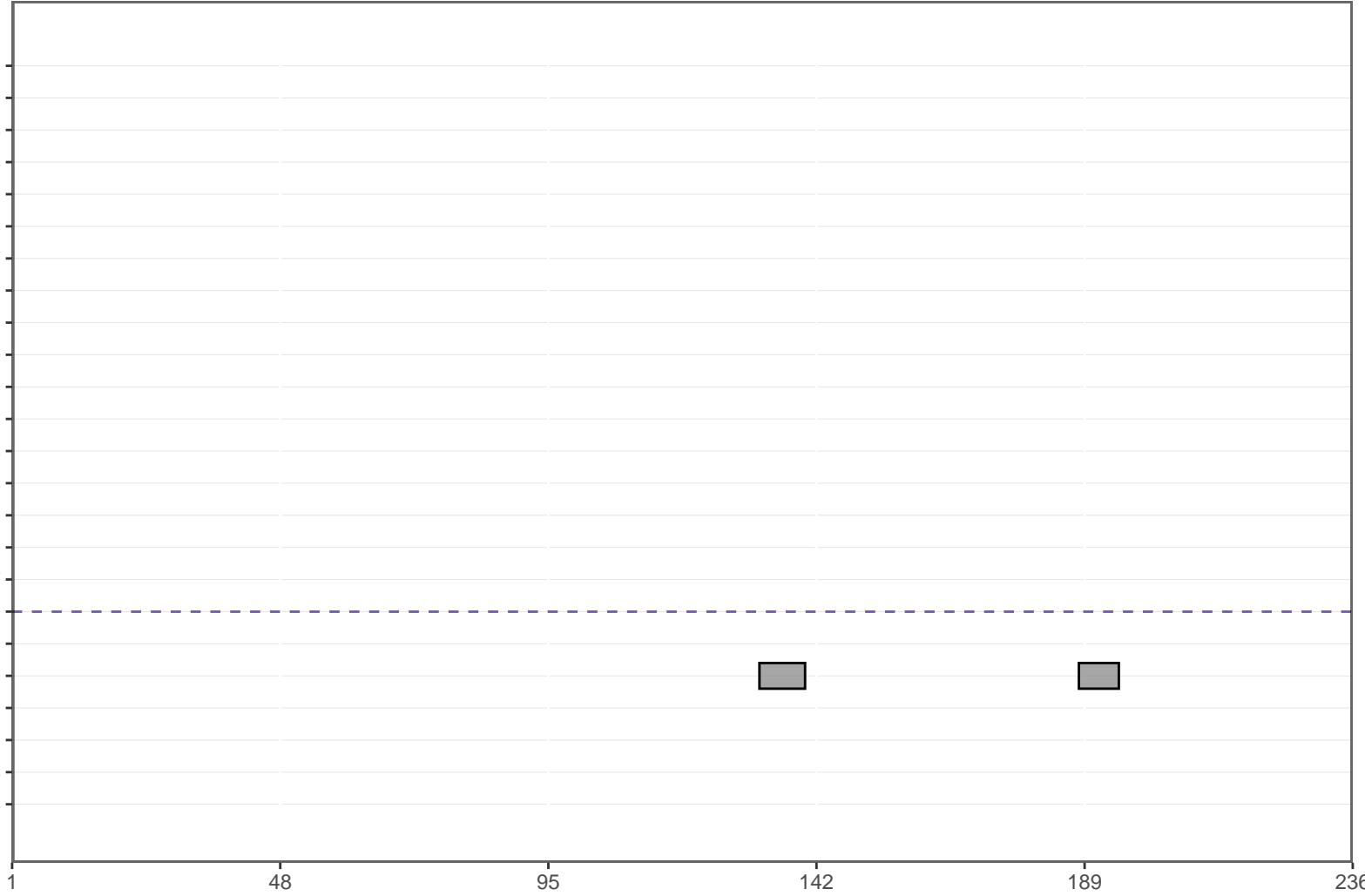
MW indication



Molecular weight

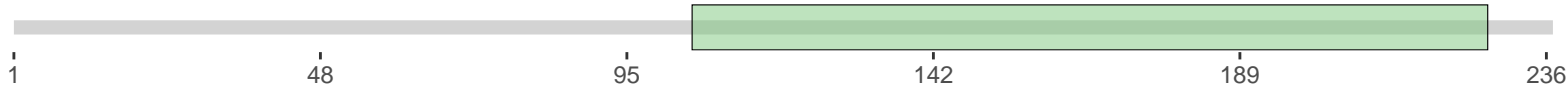


Gel Slice



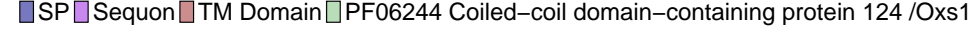
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TEAELRRRKEEEQVALANKAEENRRGSRMAEEVEEYKTVLVFNRRDDSGIEASTVDDIASLSAISDSLPPDRHPEKRLRAAFKAFEEAELRVLKEEKPGLTHGYKDLWKLWKKSPDPLNGINLRCTLC

NbL01g04130.1 SKP1-like_protein_1A [MW = 17.6 kDa]

No. of times detected



log(intensity)



Values from



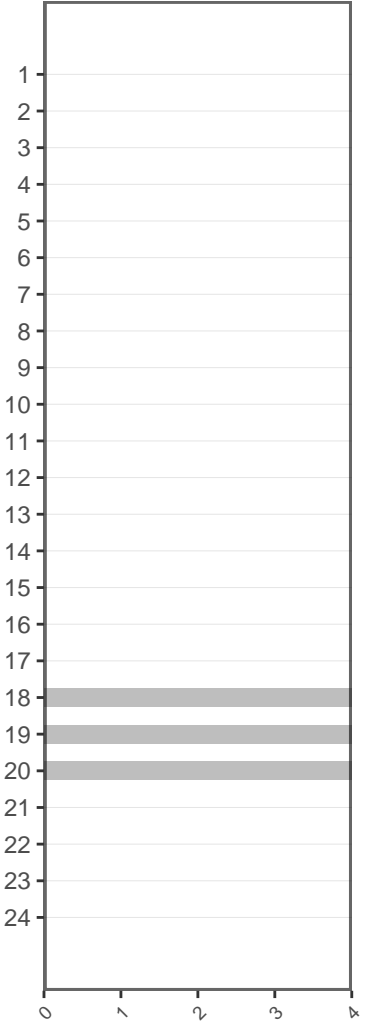
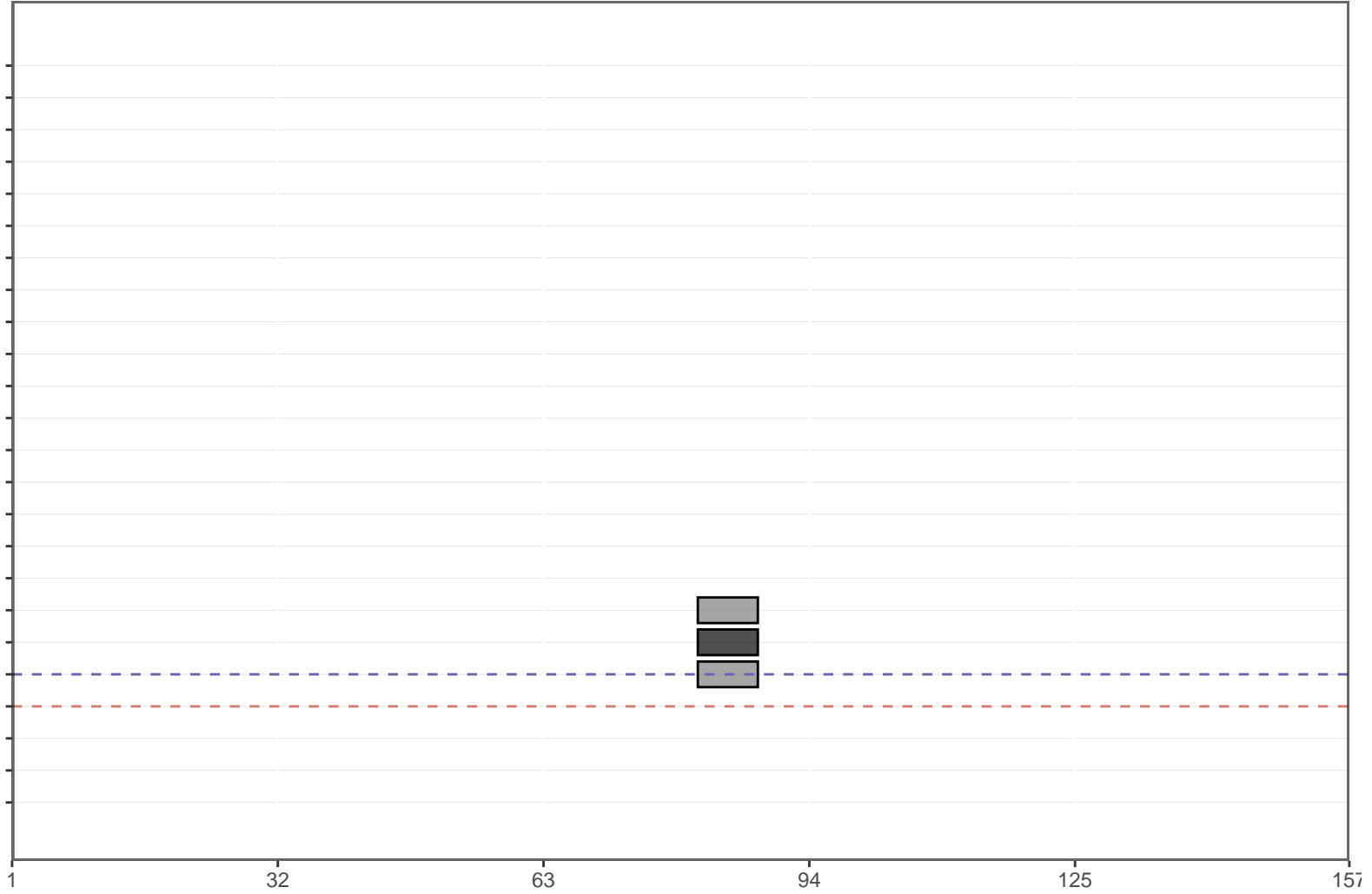
MW indication



Molecular weight



Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

WAAKTDKASEDDKIKFADDFVKVVDGATLFDLHAANYLNKIKLLDGTGQVADMIGKTPREIRKTFNKINDFTPEEEEEVRRNEMWAFI

NbL01g04120.1 UDP-glycosyltransferase_73C2-like [MW = 54.83 kDa]

No. of times detected



log(intensity)



Values from



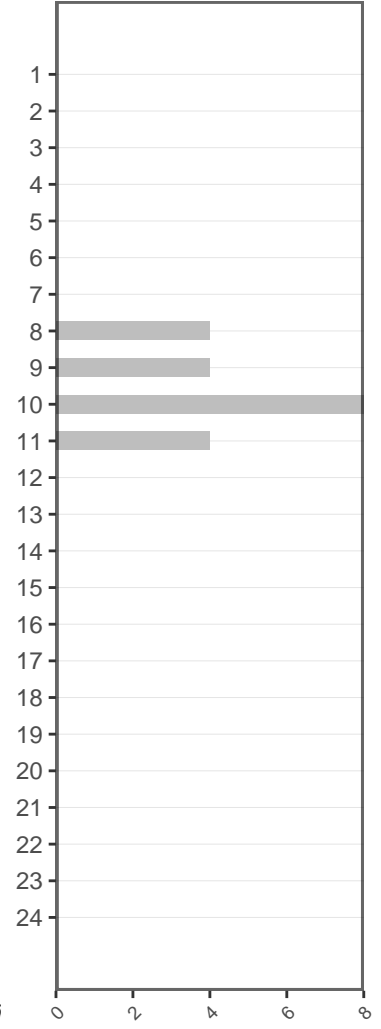
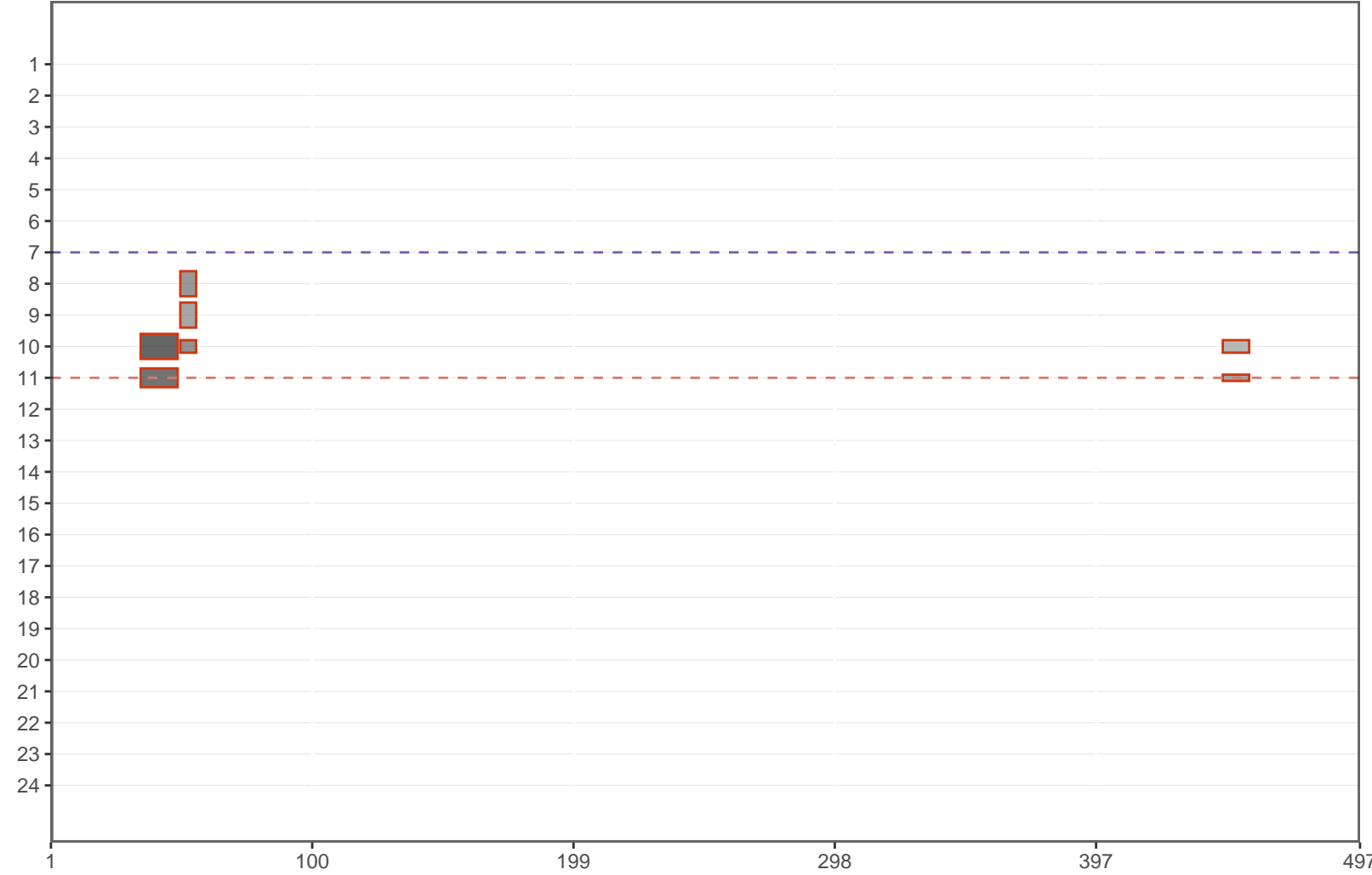
MW indication



Molecular weight



Gel Slice



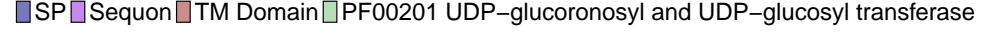
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

CARGGKWCYCPVSLGAKENEDLVTRGNKTAISNGDCLKWLDFETESVYVYVSLGSLRALTVAQMVLELGLGLEENRPFVWVLLGGSDKLNLEKWLLENGFEERKERGVLRGWPAPQVLLSHFPAAGGVATHCGWNETLEGISAGLPMVTFPLFAEGFQNEKLVGVKIGVSLGVKVPVKKWGDDEENVGVLLKDDVKKALDKLMDGEEGQVRRTKAKELGELAKKAFEGGGSSVYVNLTSUEDIEQQNHKDK

NbL01g04110.1 glycerate_dehydrogenase [MW = 42.3 kDa]

No. of times detected



log(intensity)



Values from



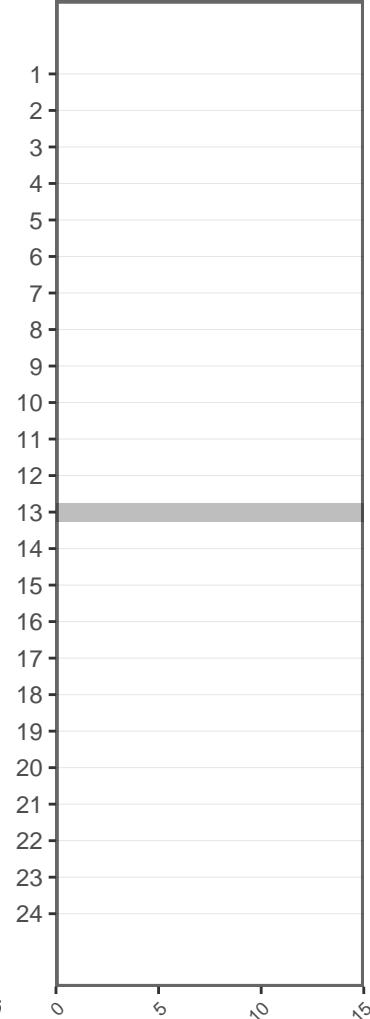
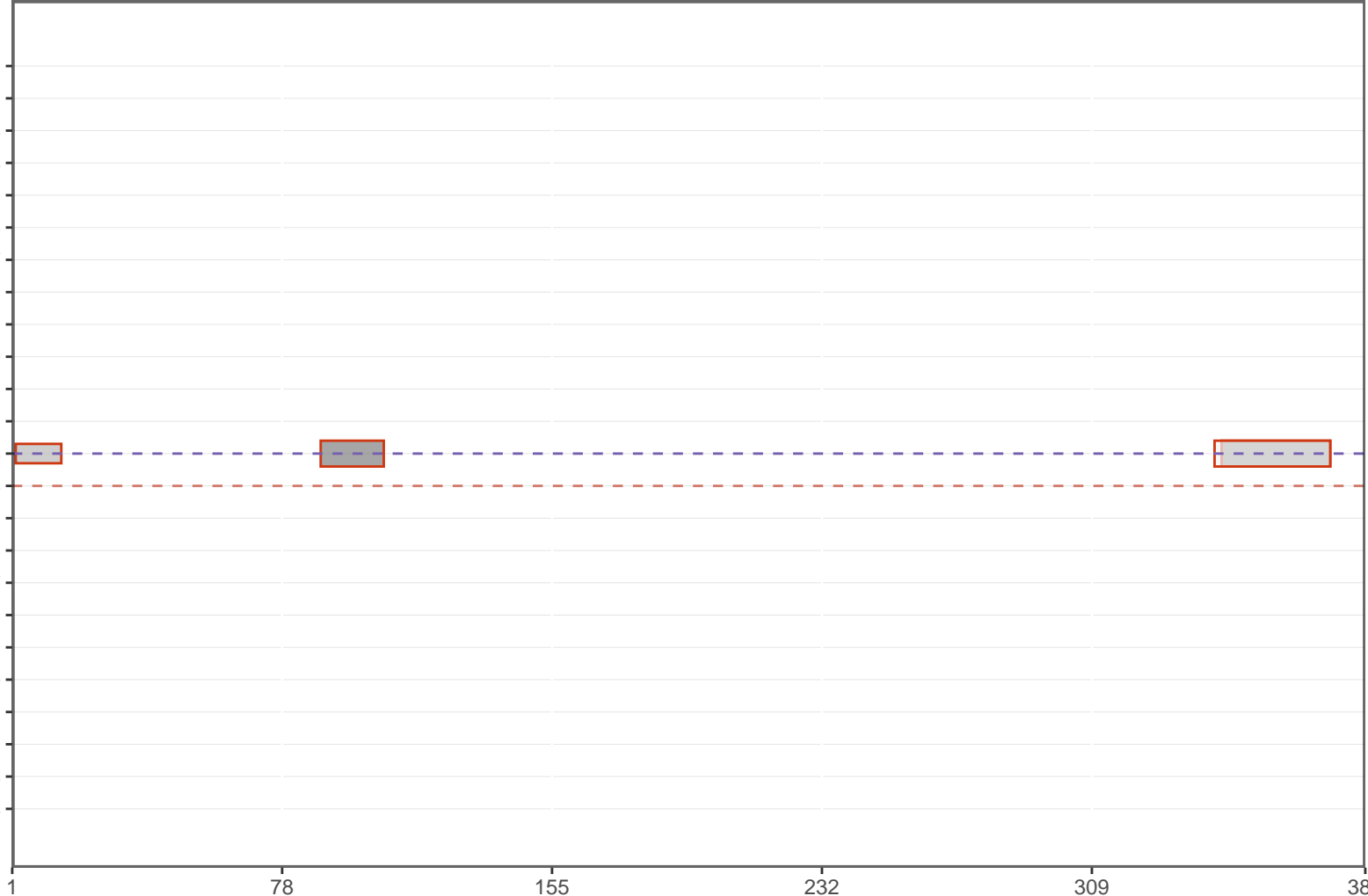
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP Sequon
- TM Domain
- PF00389 D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain
- PF02826 D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain

Protein sequence:

IRRMIEGFKXINLNYDYLQDTRLEKFKVYGGFLKASGGQPVTKRRAASMEIEVLRADYHSHLPDQKTTYHVNKERLMMKKEALVNGRGPVDEVALVEHLRENPMFRVGLDFEDEPYMKPGLADMKNVAVVPHIASASQVTRGEMTFLAALNVLGKIKGYVWVGNPNVDAFLNENSGPRAGPVSINKTLGLPVSKL

NbL01g04040.1 WD-40_repeat-containing_protein_MSI2-like [MW = 45.1 kDa]

No. of times detected



log(intensity)



Values from



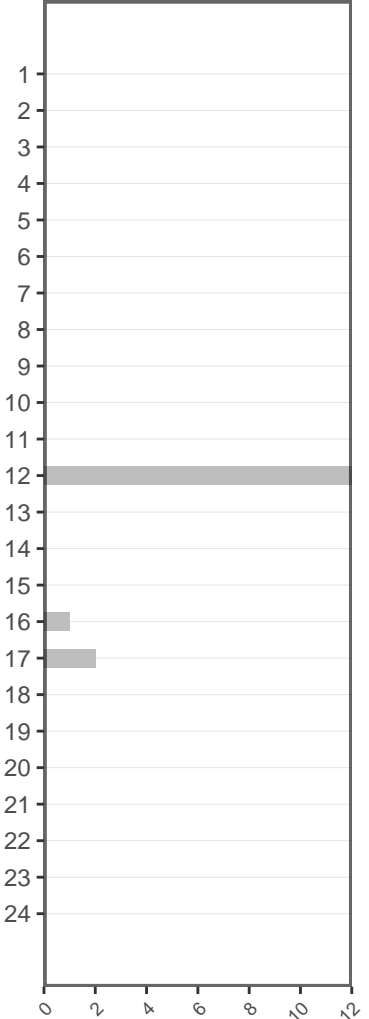
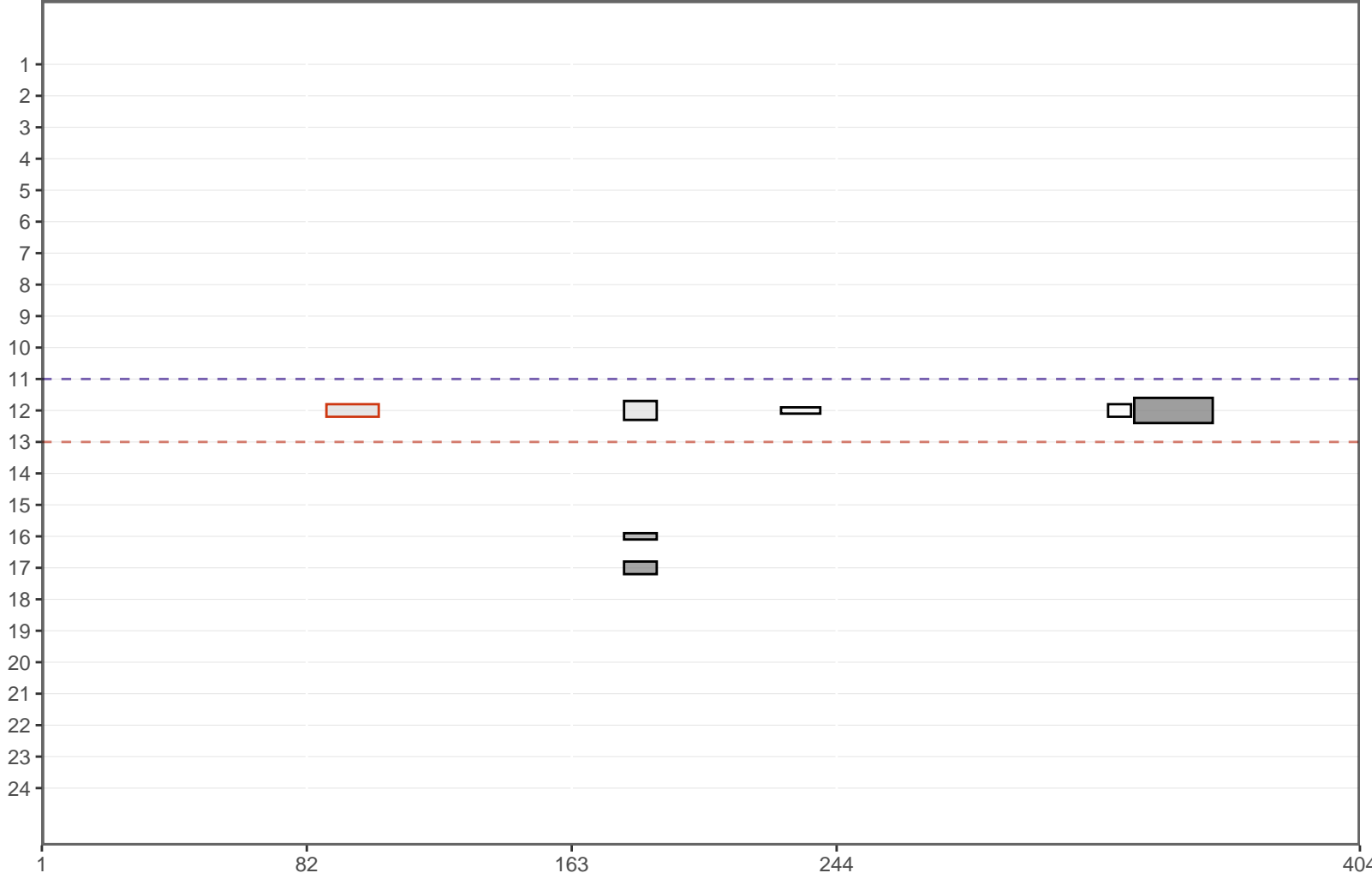
MW indication



Molecular weight

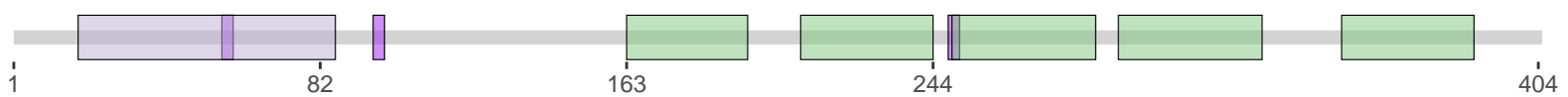


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

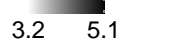
ICLLVDV/SAMPQNKVLLAHRFEYEEHADVVDV/SWHPKNEILFGVGGDCRLIWDLRTNKGSHVWVHEKAVNGLSFNSYNEWLLATASDSDTVGLFDLRKLGSTPLHVFVGHTEDEVFQVEVDPNHTVLIASSAGDRRLMVDLNRIGDEQLEGEAEDGPSSELLFSGHGHKARISDFWVWKNPEPWIISVAEDNTGIVWGMAESIYRDDDDNGDC

NbL01g03750.1 vacuolar-sorting_receptor_3-like [MW - SP = 66.85 kDa]

No. of times detected



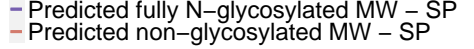
log(intensity)



Values from

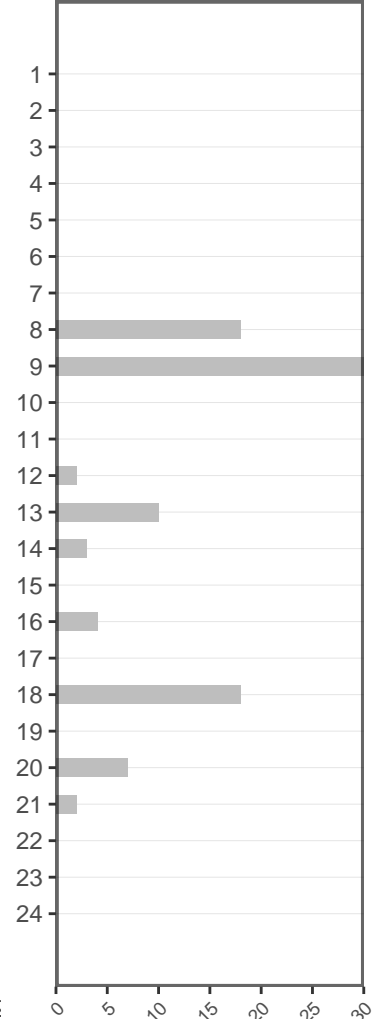
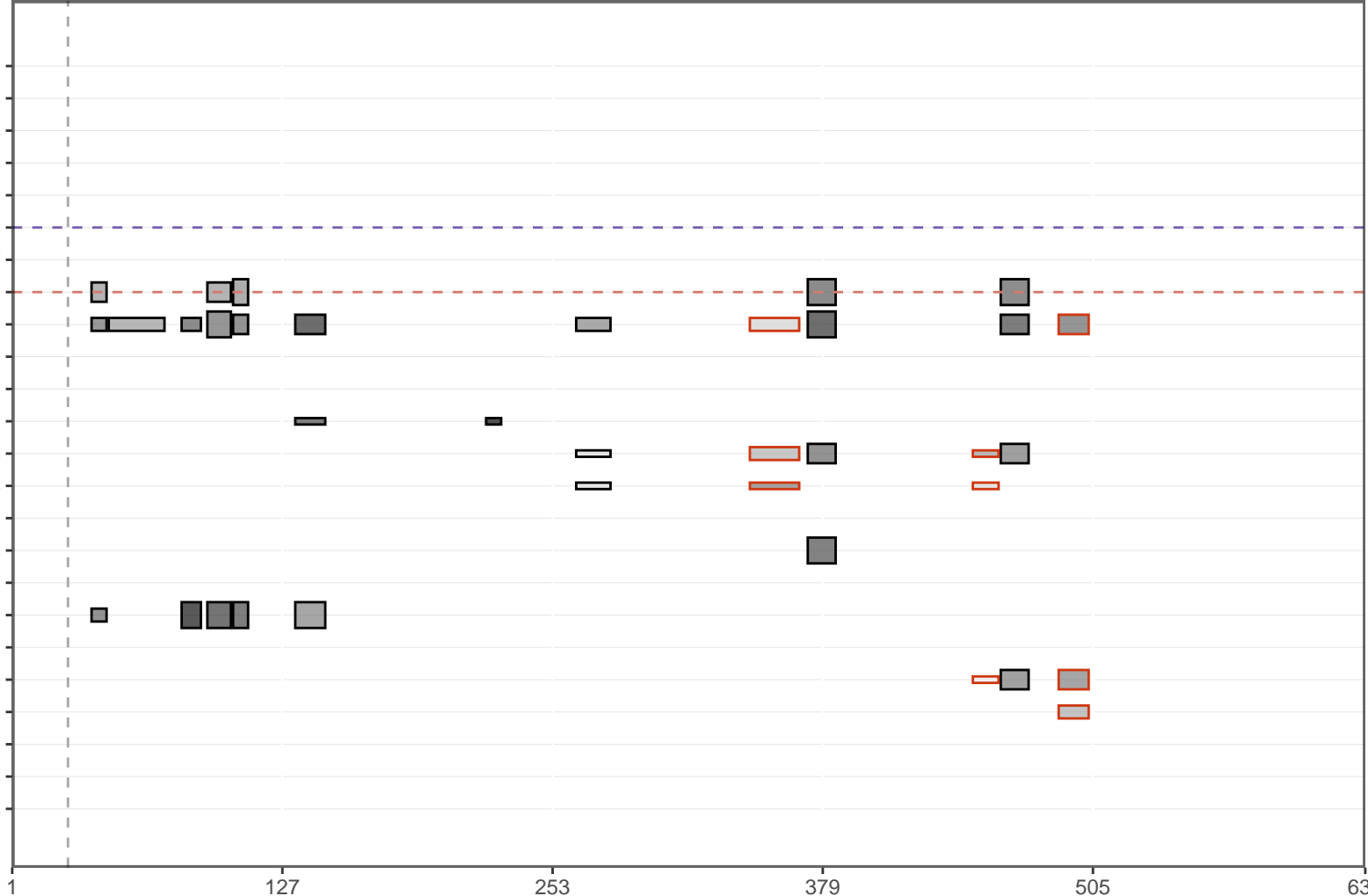
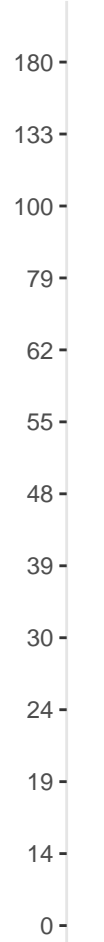


MW indication



Molecular weight

Gel Slice



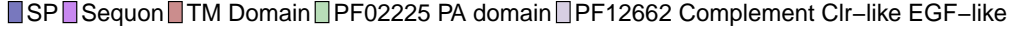
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

WVDTDFQRCPLMEKKNYKKEGADGVKSLGLDLRRIKIEKMGMDPNADENPNVLEEQDAQVKGKTRGDTLPLFLVNNRQVYRGLKLEKAVLKAAGFEETTERPVQLSDQVETNEGRDNGNNGGQWKAANTACKDTRFRGRVGECPVAVDGVGFKGDGYSBSGATSGPGRKALNNGGWHDRDGHHTYSAGVDNEEGKAGAPPPGFKGDGVNSCEDVDECEKKAADGCPGESSGKNTWGSVYEGSGSGLLYRHDHTGDISKRAAREVKSAAVAWVAIIGLAMAGGG

NbL01g03710.1 mitotic_checkpoint_protein_BUB3.1-like [MW = 37.8 kDa]

No. of times detected



log(intensity)



Values from



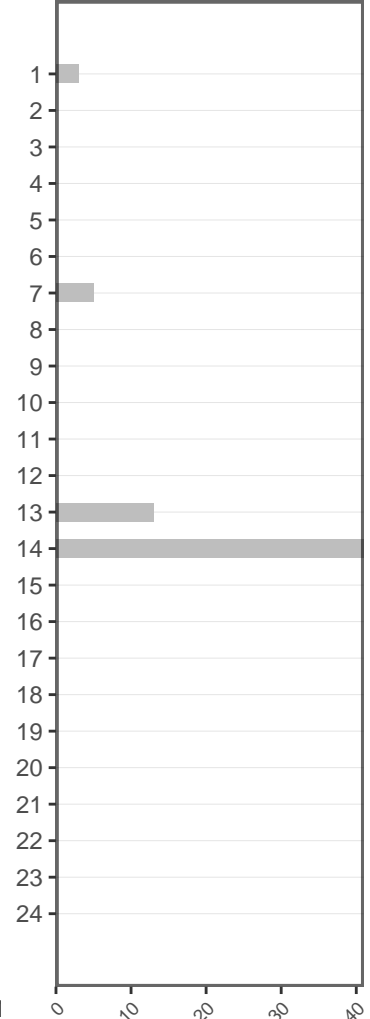
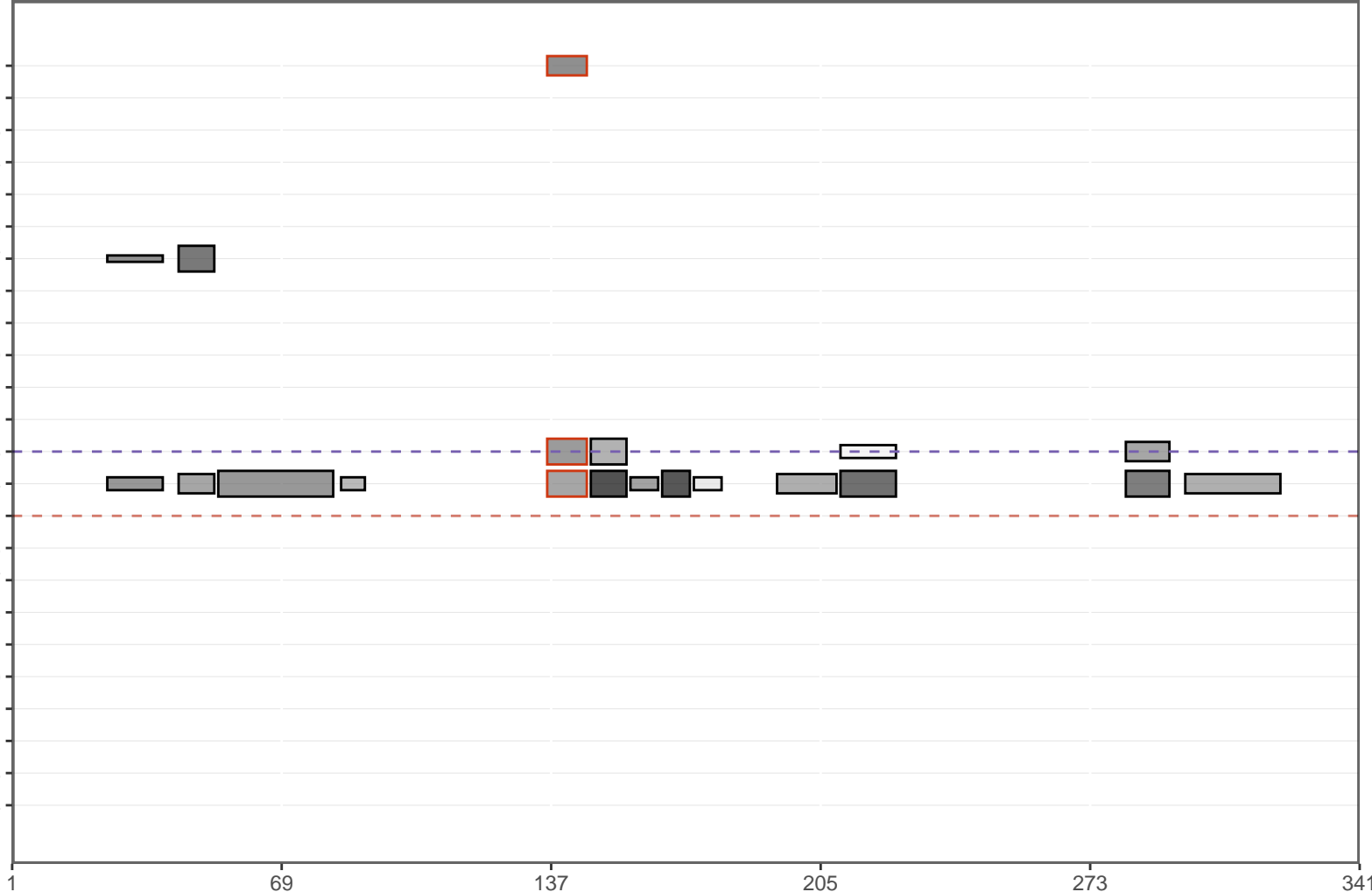
MW indication



Molecular weight

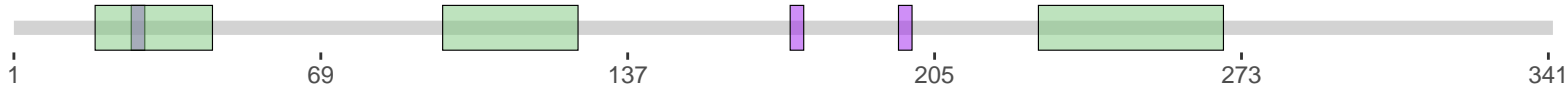


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

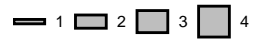


Protein sequence:

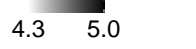
LVWATGRHYNYDLRINMSGPEGRREBSLKYGTGRVRCYVNGTGVALLSSVEGRVAMEFFDLSEAGDGSKKYAFKGRKTEAGRDVYVPVAIAFHPHYGTATGGDGGYVNWVDGNNKKRLYQPKYPSIAALFSRDRGLLAWASSYTFEEEGEKPHEDAIIRSEVNEVEVKPKVLPNPTT

NbL01g03620.1 somatic_embryogenesis_receptor_kinase_2-like [MW = 31.7 kDa]

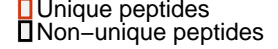
No. of times detected



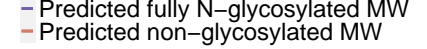
log(intensity)



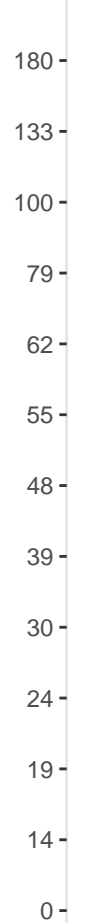
Values from



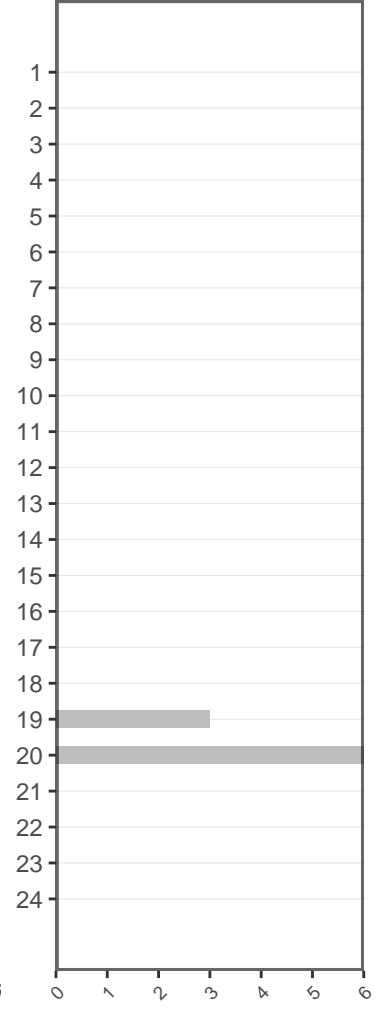
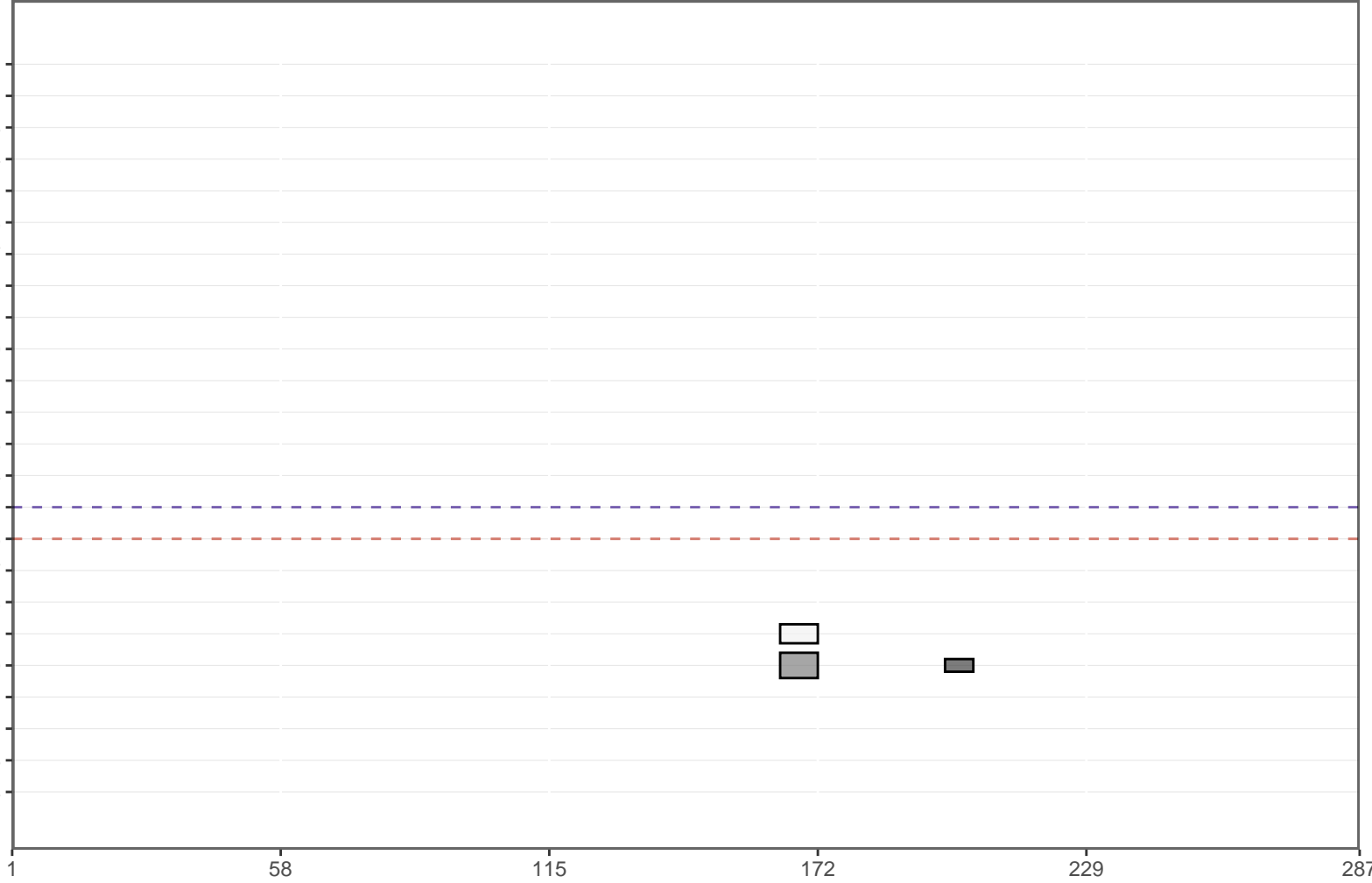
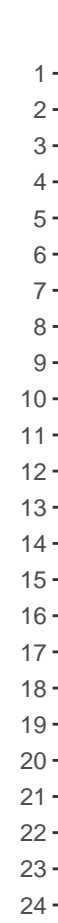
MW indication



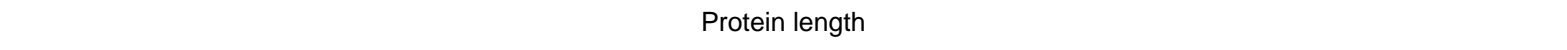
Molecular weight



Gel Slice

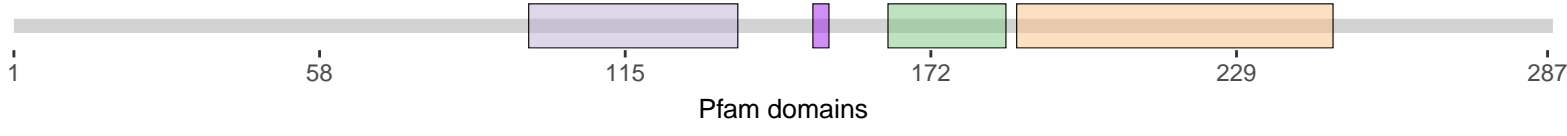


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

HITCDSSNHYRRLDLDGNTNSGTLGPELGEKKNLYLELYRNNGIGKPKELGNLENLSMDLVGNRFEGNPKSFAALKELRFLRLNDNKLTFGSIPELTLPLNKKVFDVSNNDLGGTIPVDGPFQSGFFMGEFAHNRNLNGPELKLGLAPVDFGDK

NbL01g03580.1 protein_TR11-like [MW = 21.96 kDa]

No. of times detected



log(intensity)



Values from



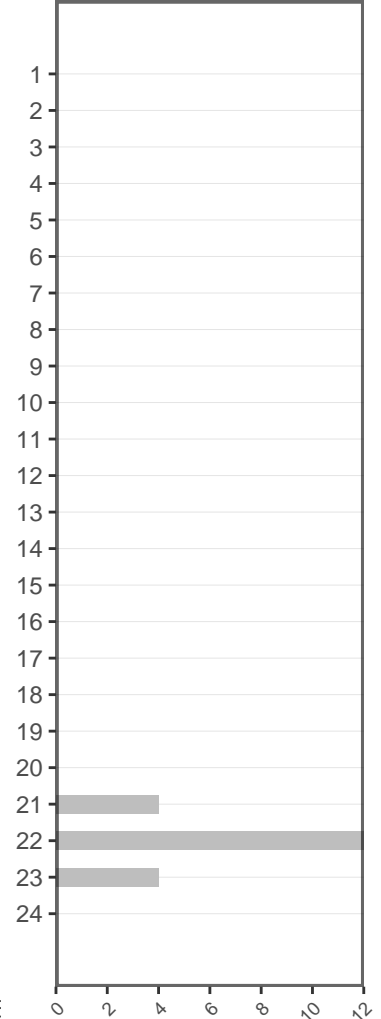
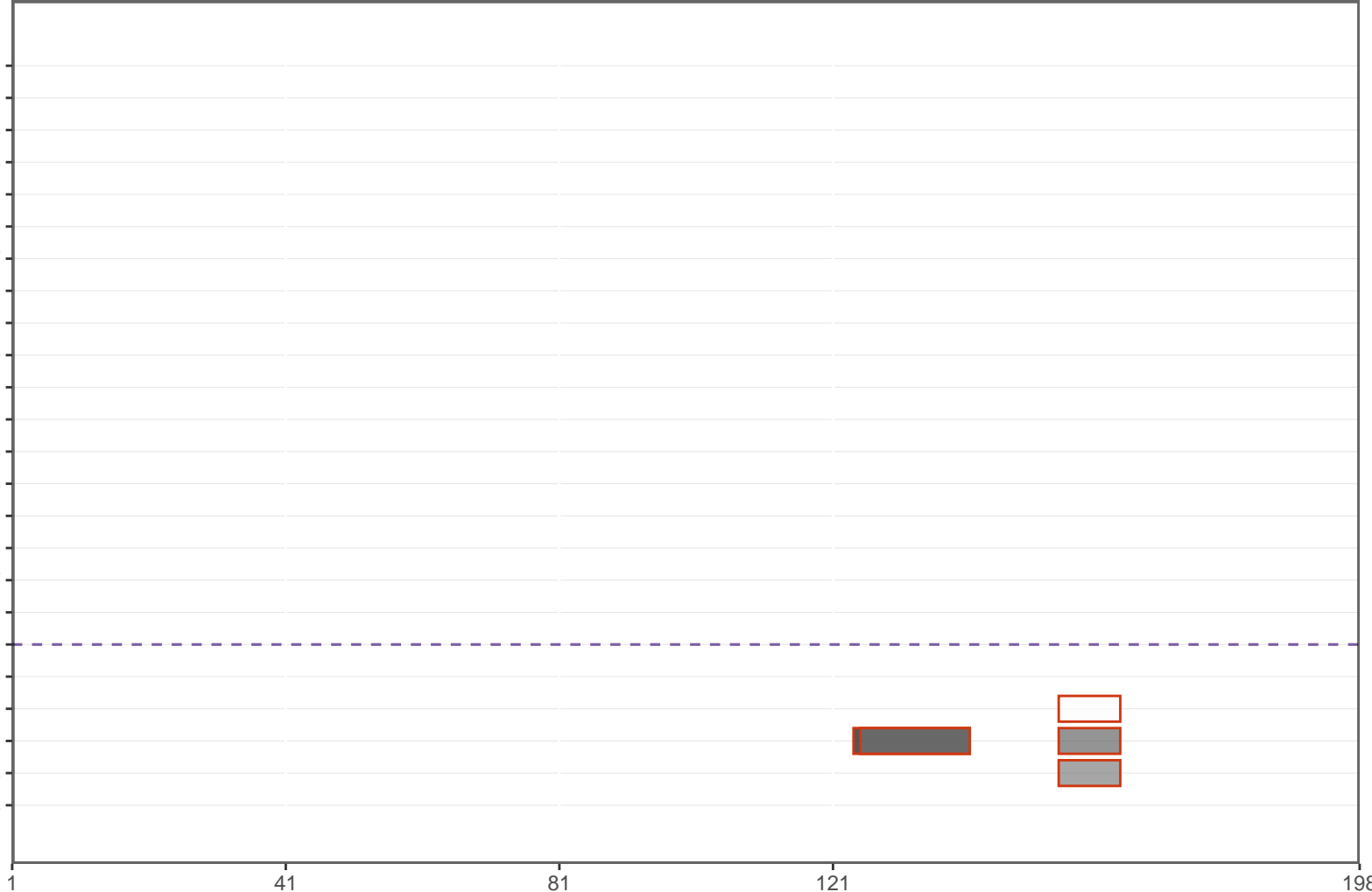
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

AAHIANLRTRVMVFATTSKPVATEPKREPRGIMKRRVSPEMQAFVGGIAEIPRTQALKLVAHAKENNLGDPGNKVVICDEKLNIFPKDRVGFLEIAGLISPHLW*

NbL01g03470.1 TIP41-like_protein [MW = 34.62 kDa]

No. of times detected



log(intensity)



Values from



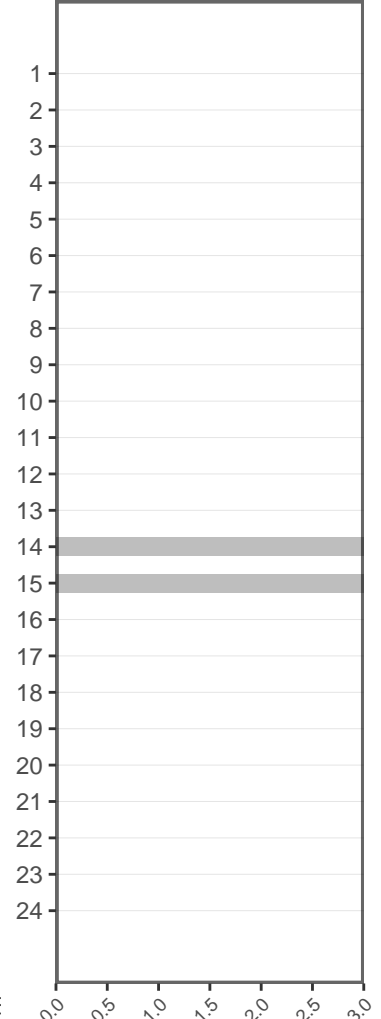
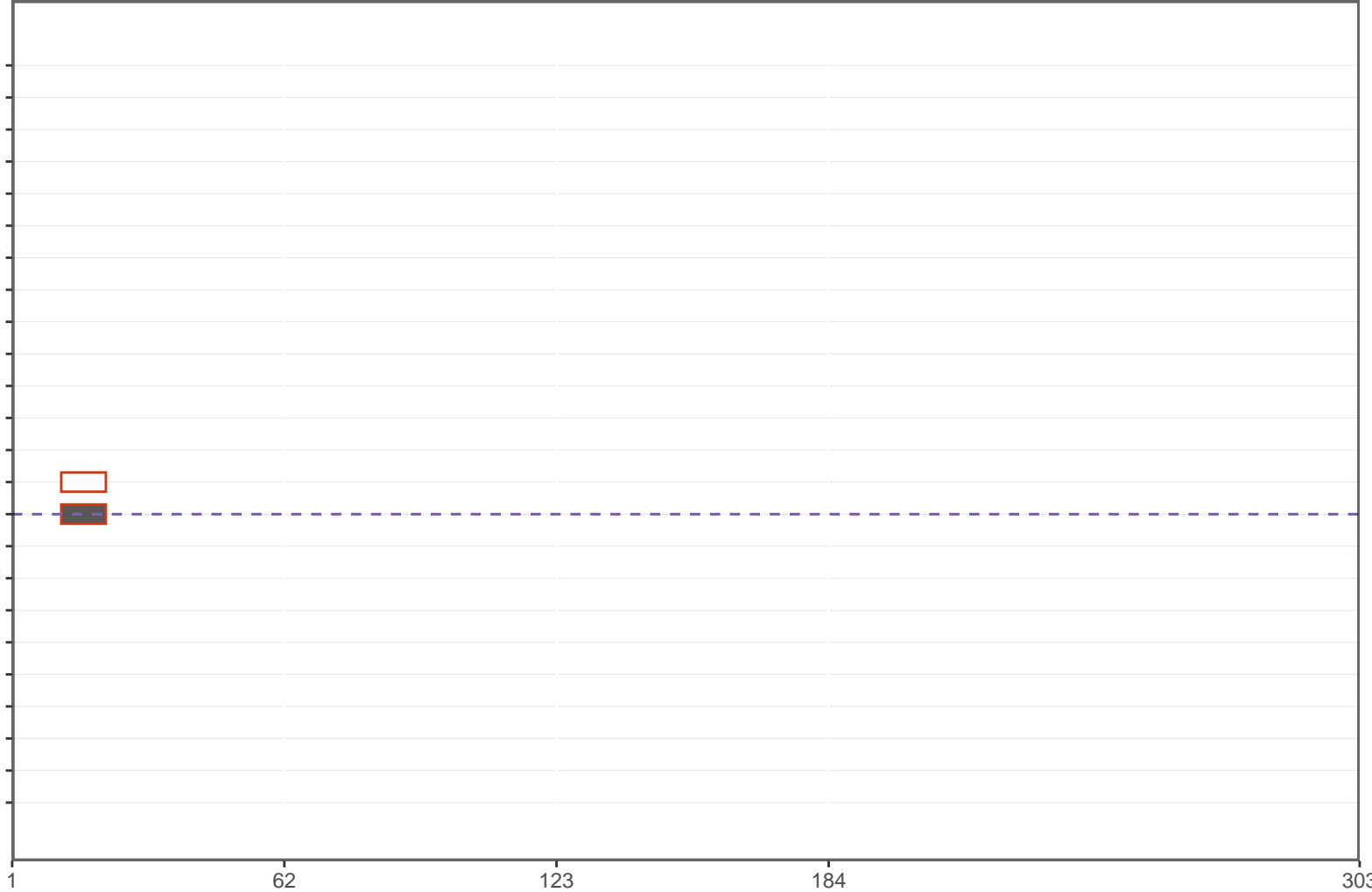
MW indication



Molecular weight



Gel Slice

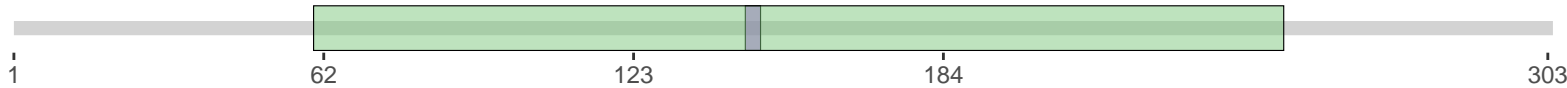


Peptide counts over 4 repeats

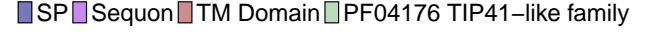
Protein length



Pfam domains



Pfam Description

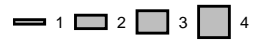


Protein sequence:

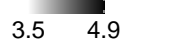
AERVROLNSNSSCBLQWEDCTEKIDVLALASKEPLFYDEIHLVEDELAQNGHSLTVKVRVMPSPGWFLLLRFVLRVQVLMRLRDTRLHCLFGDHHMKSVLRRESCVREATFGLSGKQYPSDGAAYSDPTSERLPIIMQKTKLSEIPCWVGLYSDTDGDKDS

NbL01g03400.1 methylthioribose_kinase [MW = 47.81 kDa]

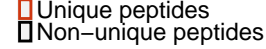
No. of times detected



log(intensity)



Values from



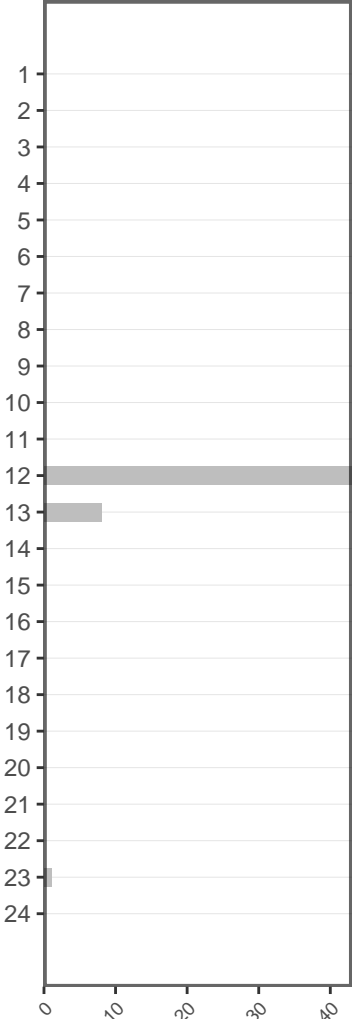
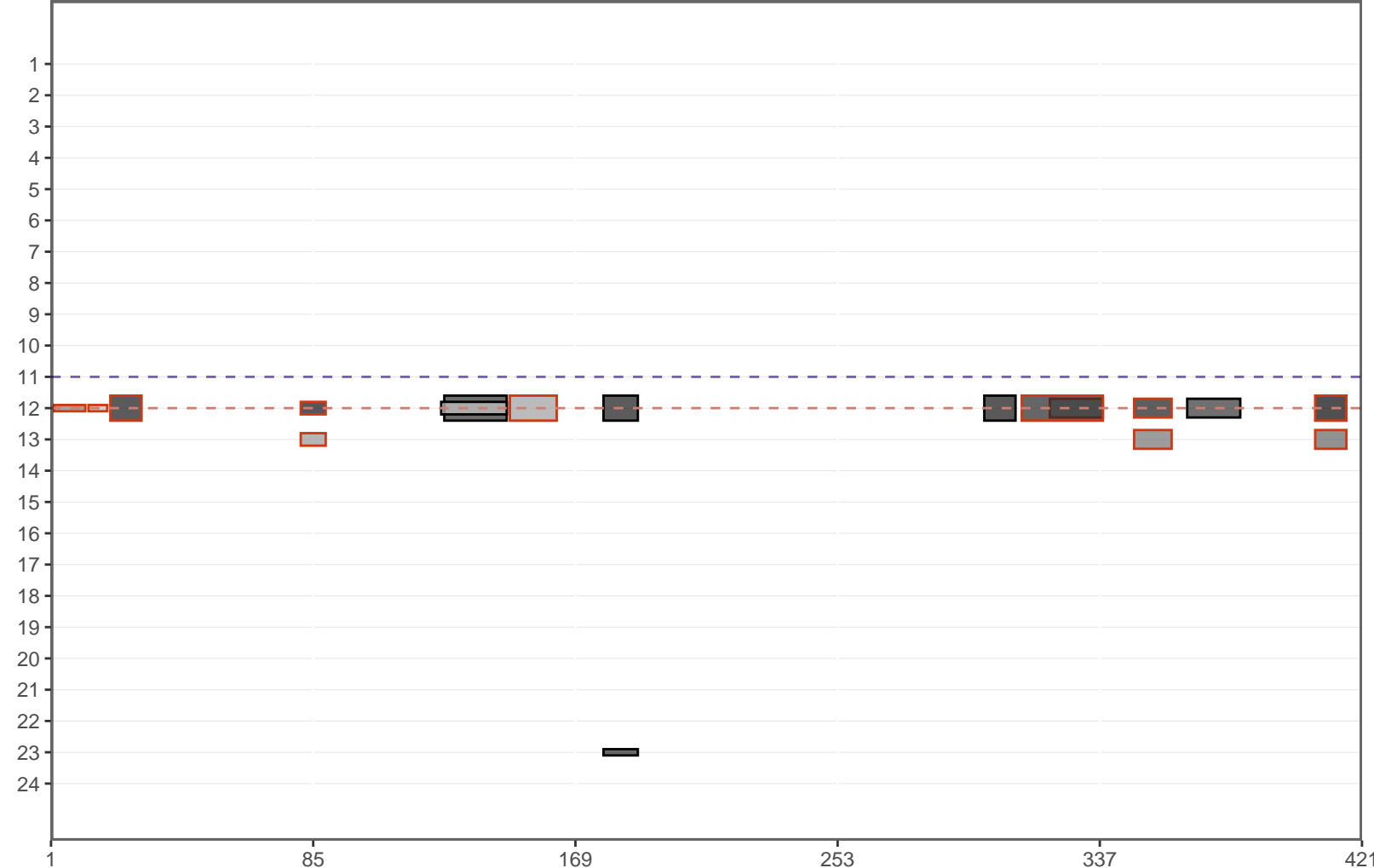
MW indication



Molecular weight

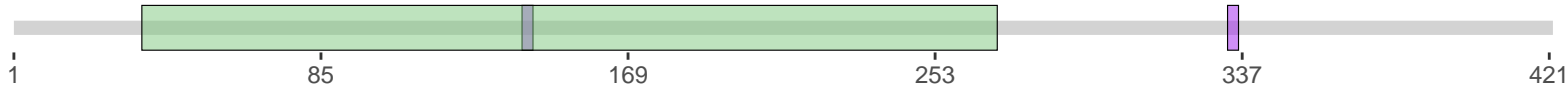


Gel Slice



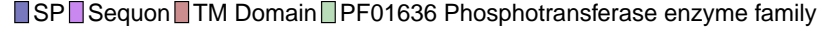
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PYLDDAEAVRKNDGLKIEVAELKSKFGRAGALHGDHHTGSLMTGQSTQVDFEFAYFGPMGFDGAFIGNLILAYFGDGDHADQANDRKYKVVWIKTITETWLNFKHKLALWDEHKDGPGEALFPEYNNTELRELVTGQKYMKELFEDTLFGGAKMIRRVGVVAHVDFEESKDAARADGERRALNGAKKIKERRNWSIEEIVSTIEKHVLDQ

NbL01g03340.1 probable_cinnamyl_alcohol_dehydrogenase_2 [MW = 38.77 kDa]

No. of times detected



log(intensity)



Values from



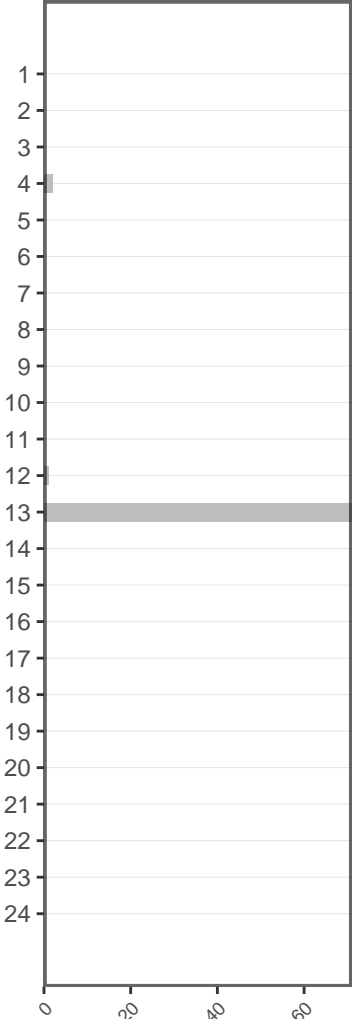
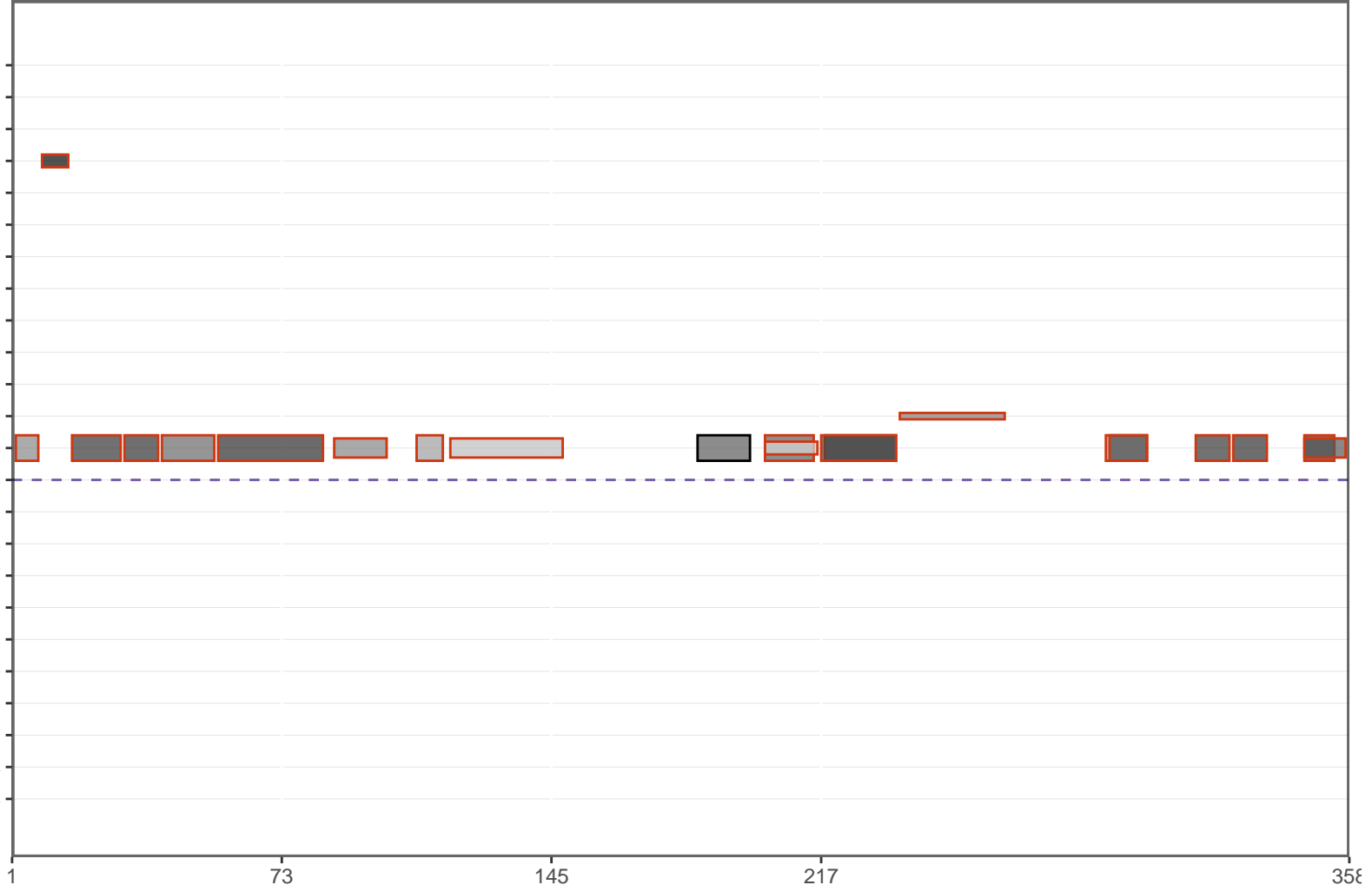
MW indication



Molecular weight

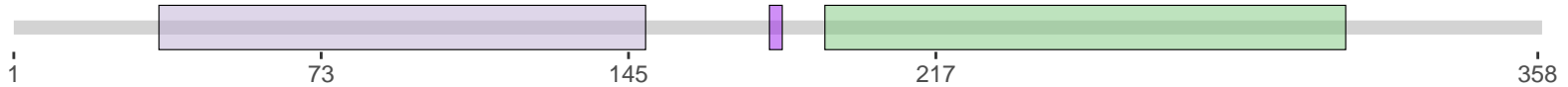


Gel Slice



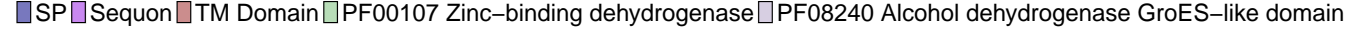
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

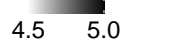
CAGITVYSPLNIFGFNGLRGGILGLGGVGHMGVIAKAMGHVTVISSKPKRGEALEHLGADDYVSSDTDKMGEAASLSLHDITVPVGHPLPEYLSLLKIDGKILMGVINTPLQFISPMMLGRKSTGSGFSGMKETEKMLFQKEKGVTSQIEKMDVNTMERLEKNDVRYRFVVDVAGSKLDQ*

NbL01g03260.1 cyclase-like_protein_2 [MW - SP = 28.11 kDa]

No. of times detected



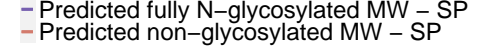
log(intensity)



Values from



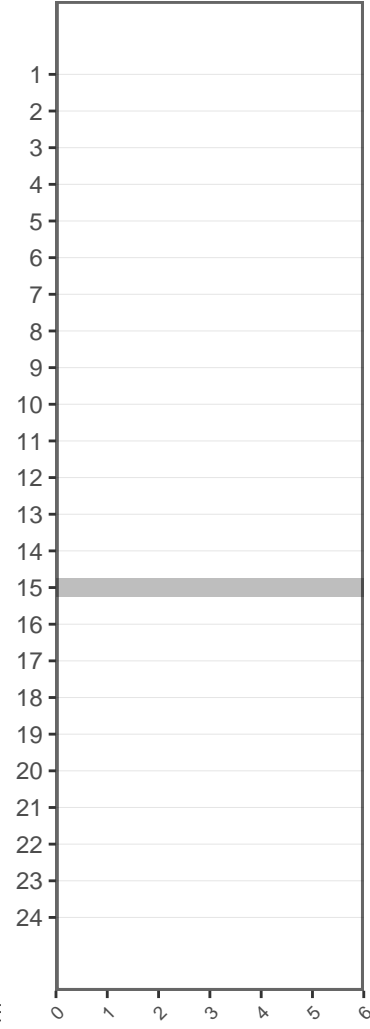
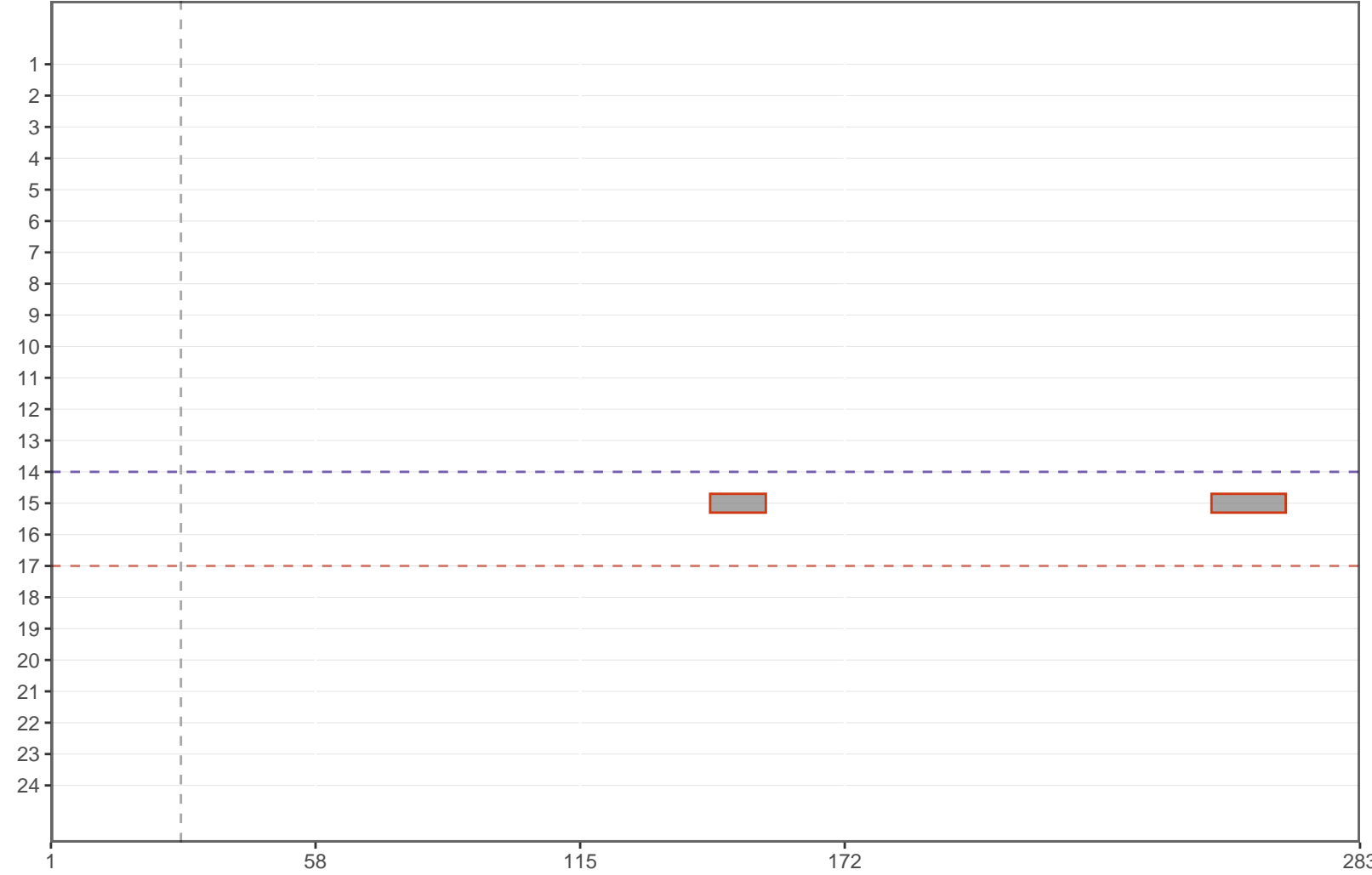
MW indication



Molecular weight



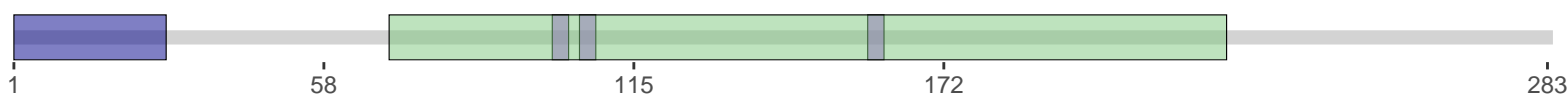
Gel Slice



Protein length

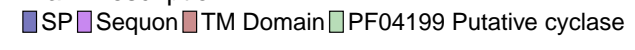


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

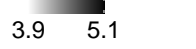
YAEYYDAGFDYDLSLRLVNLGPNLVDPKDKLITADVMQSLHPKGVKRVLFRLLNTDRRLMMKKAFDTEYVGFMKDAGWLVNTDKLVGIDYLSVAWFDLIPSHLVFLKSEIILVEGLKLDDETGIVHHCLPLRLLAGEGSPRGLIK

NbL01g03160.1 glucosyltransferase [MW = 53.56 kDa]

No. of times detected



log(intensity)



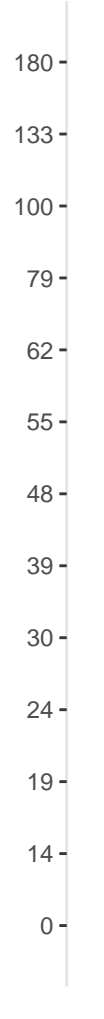
Values from



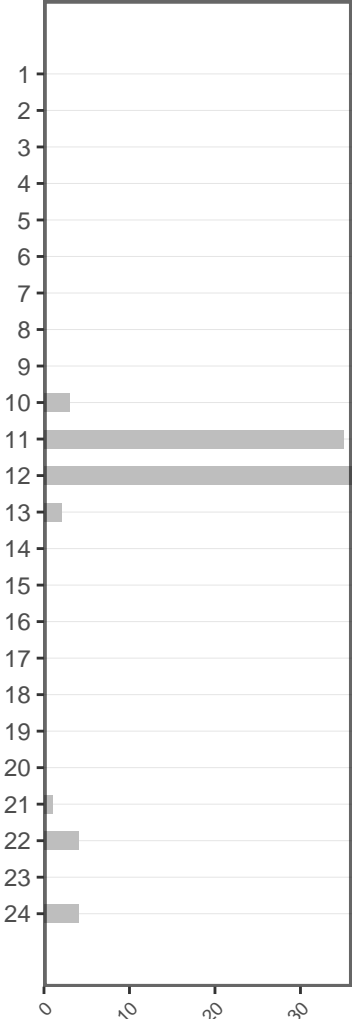
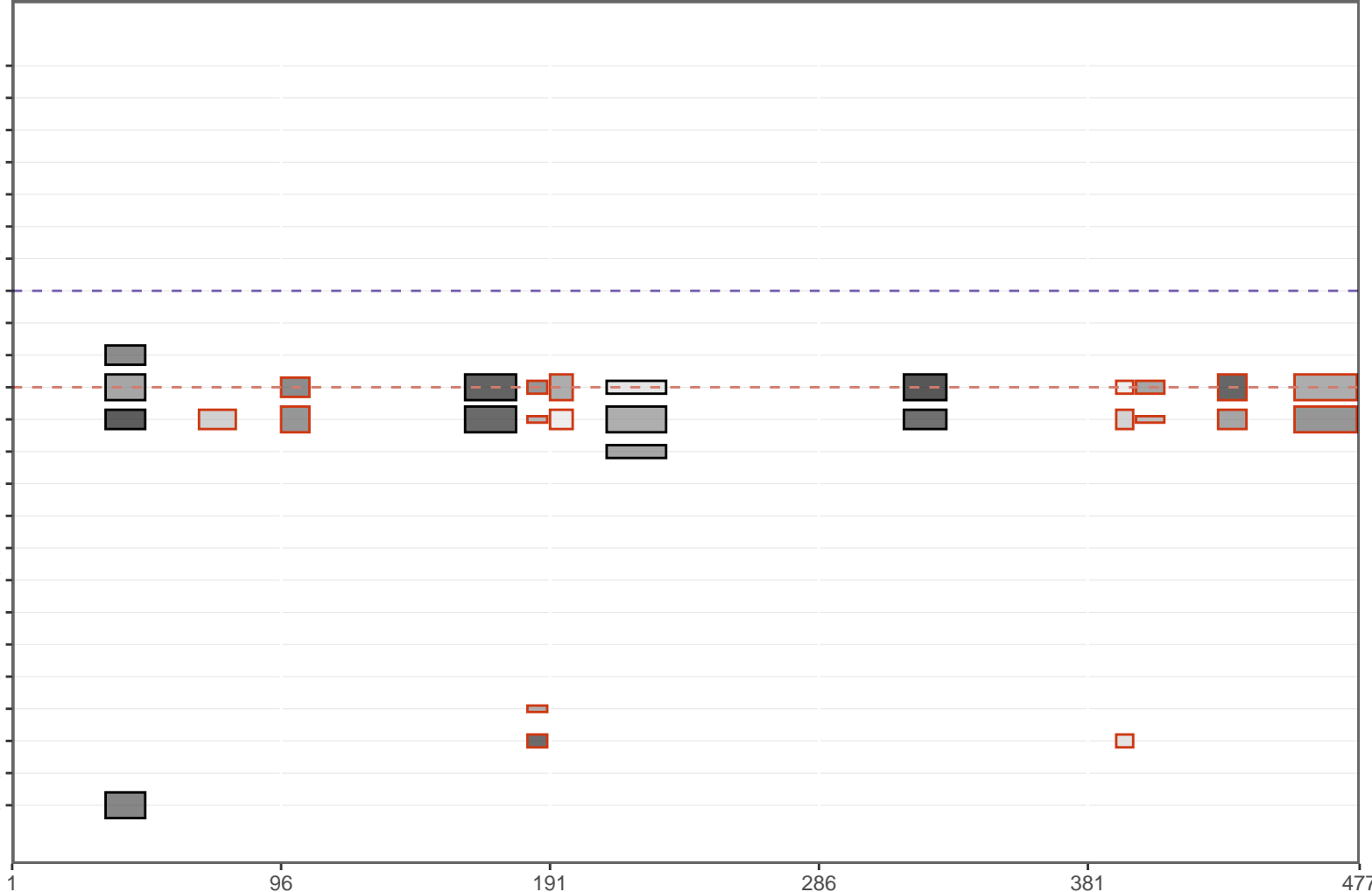
MW indication



Molecular weight

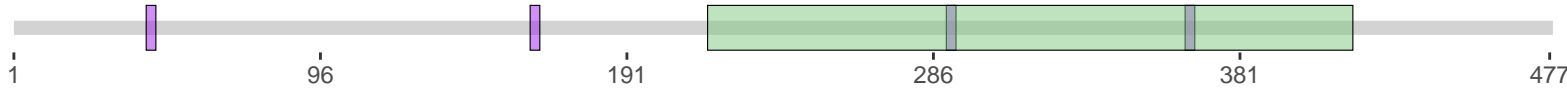


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

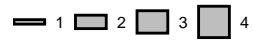


Protein sequence:

HYTKYLGRRAWAGPLGMCNRDIDVKAERKKSIDKHECLKWLDSKPKSIVVYIGFGSVANFTAGQLHELAMGIEASGDFWVVRTELNDWDLPEGFEERTKEKGLIRGWAPQVLLDHEBVGAFVTHGQWNSLLEGVSGGVPMTWVFPVFAEGFNEKLVTVLKTGAGVSGQWRRSASEGVKREAIKAKKRVMSSEADGFRNRAKAYKEMATKAEIKGGSSVYGLTLLLEDISTYSSDHI

NbL01g03130.1 polyadenylate-binding_protein_8-like [MW = 71.81 kDa]

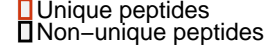
No. of times detected



log(intensity)



Values from



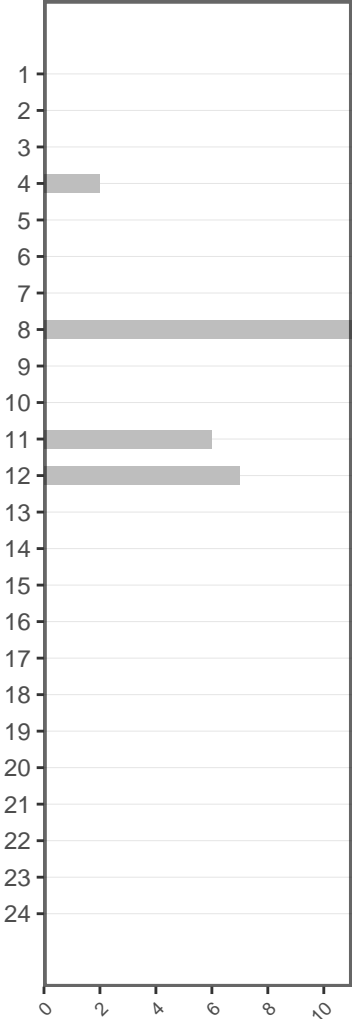
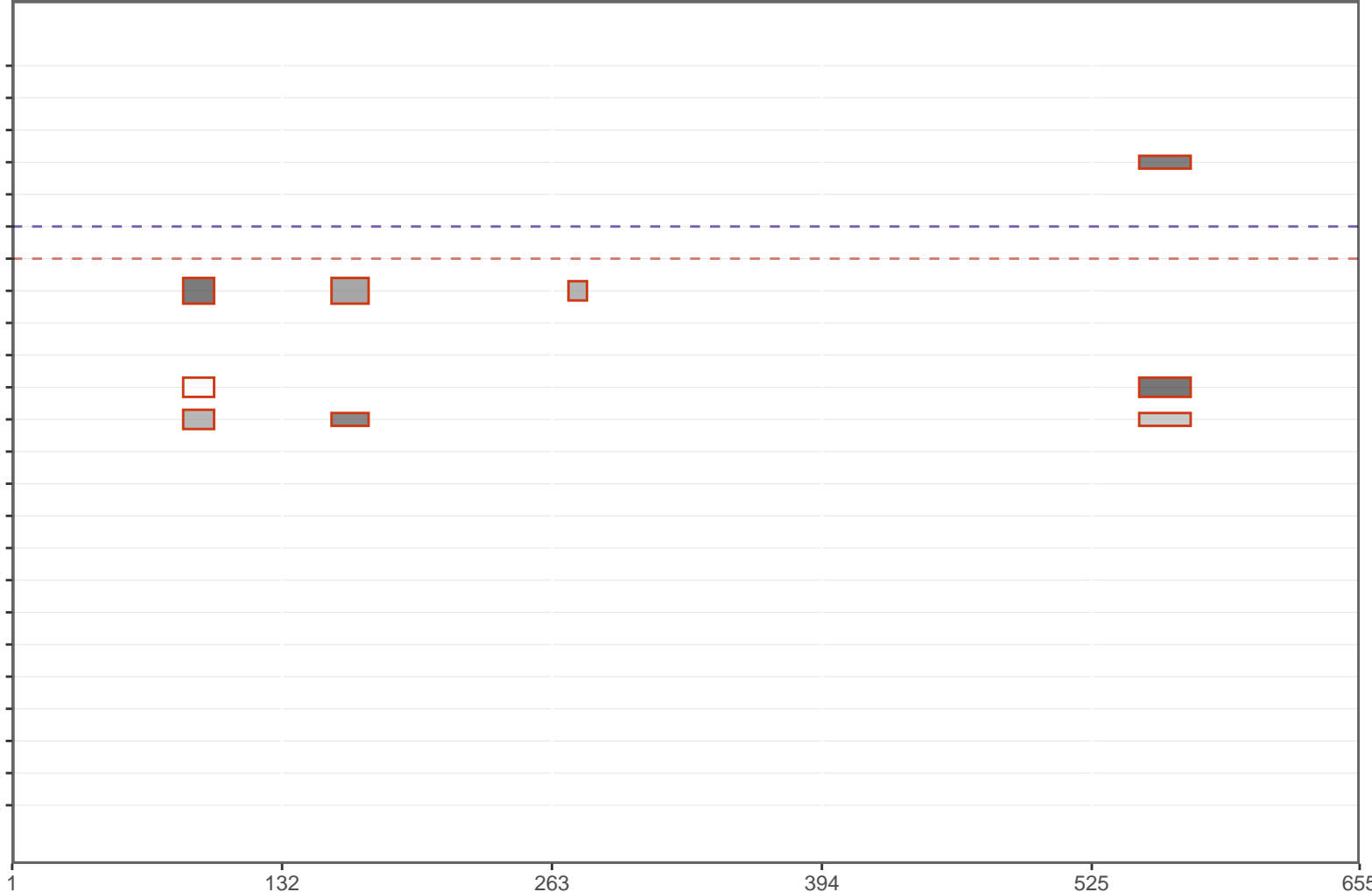
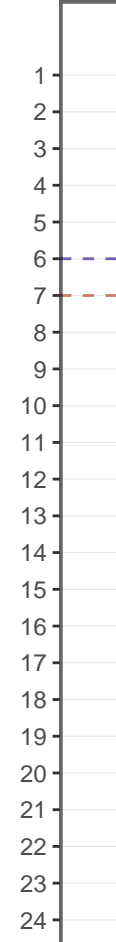
MW indication



Molecular weight

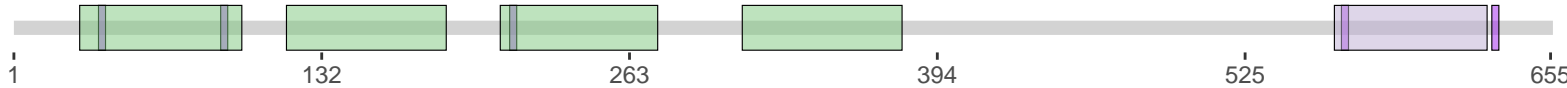


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

- SP
- Sequon
- TM Domain
- PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- PF00658 Poly-adenylate binding protein, unique domain

Protein sequence:

DSISDEKLEKLFSPVGTTFSSKVMRDPDGVKSGGSEVAFSTPEEASRALSEMNKGMVSKPLVYALAGRKEERRARLGAQFSGMRPIAMASSVAPRPMYVPPGPGGLGGQIFYGPPMLPPQVNRRAAGFYGGQLVPMRPGGGPMPNFMPVYGGGGGQRRPGRGGVPLGGGGPVLMDQQGMFPRGRGVYRYPGRGLPDGGFFGVGGGMFSPYDMGGMPVRDAGVQPIFVGLATALANASPTQRMLGENLYPLVEGLEPETAAYVTGMLL

NbL01g03090.1 filament-like_plant_protein_7 [MW = 96.15 kDa]

No. of times detected



log(intensity)



Values from



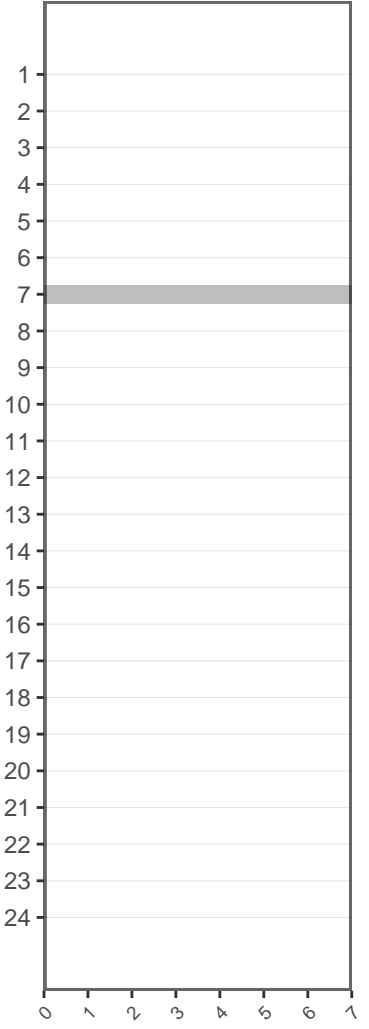
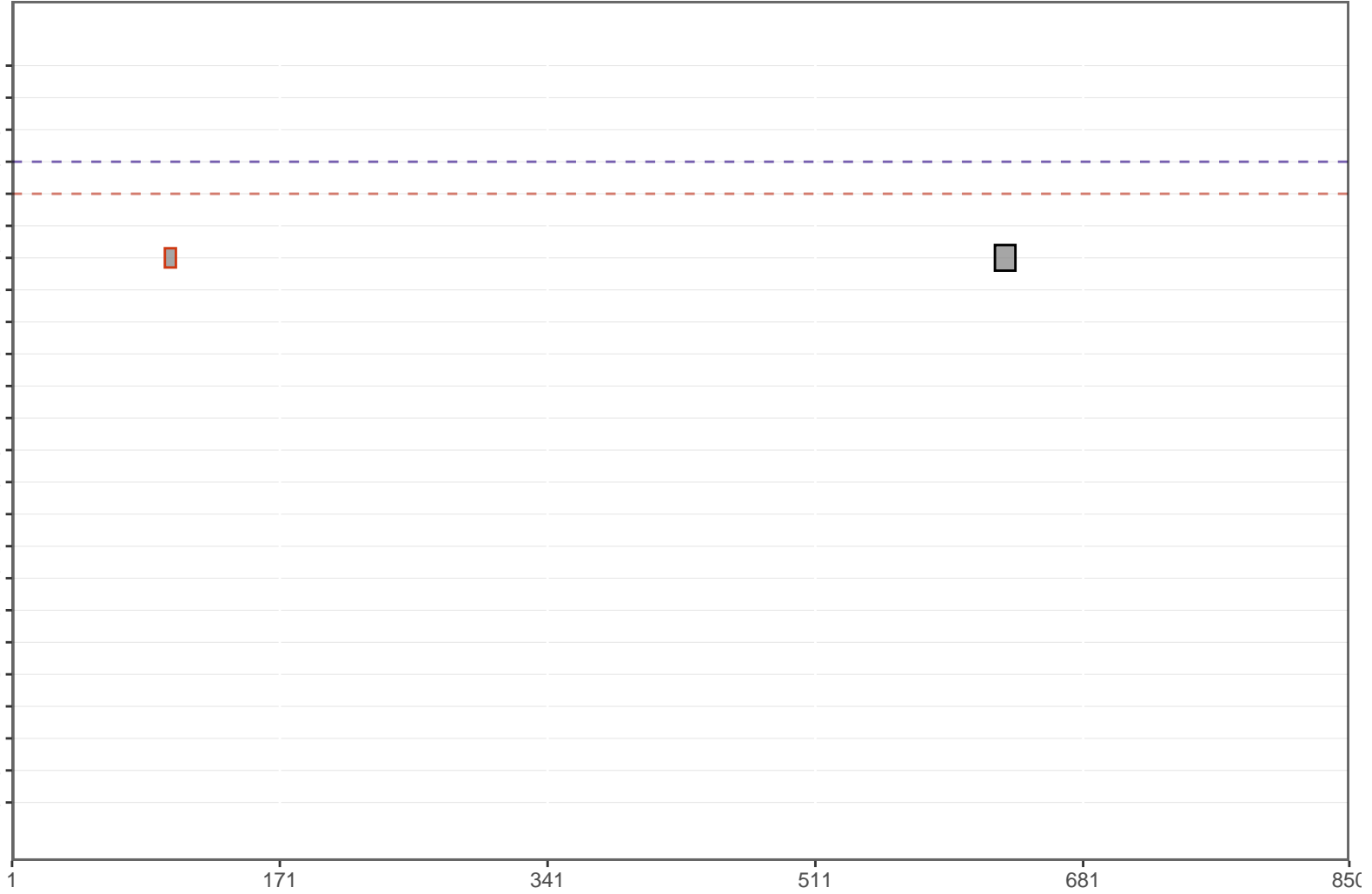
MW indication



Molecular weight

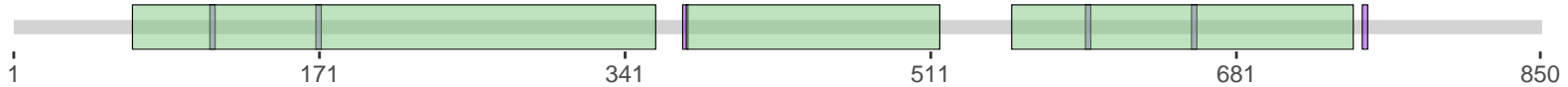


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

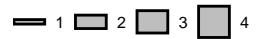


Protein sequence:

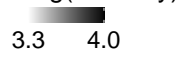
LAIVADSTIGSSYPPEQDLSLDELSDSRIETHGHQIDSTGKELVYKGGVLDYDLGMEVGGDGLLKRSPNWLHEILKIMEGSHVYKKGIDELIEDIRVALHSVTPPTGTPSELLPISGFTTWKSPVTFPKMQSLTFEPQSMGQVISELEKHLIQEENERLKAENSMKSSNKDQVQKLVVYKNGENLANELKGGQGGVSLRAELEEVKESKRIMMEDLMENKGINEDLDLTGLTVTKVWLNETQKLSLSELEVEDRSHCCDEEGTGLLEGLQLEGITANPTSDNMDKGI

NbL01g03060.1 caffeoyl-CoA_O-methyltransferase_6 [MW = 27.74 kDa]

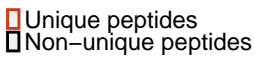
No. of times detected



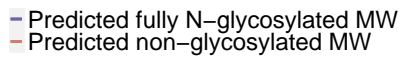
log(intensity)



Values from



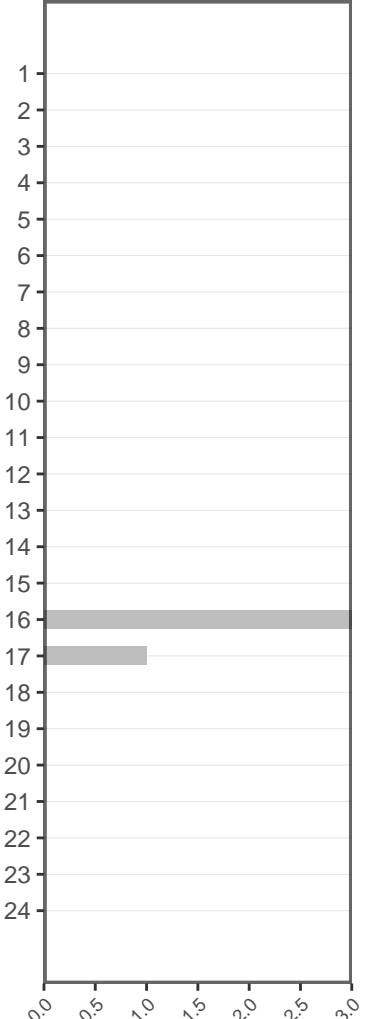
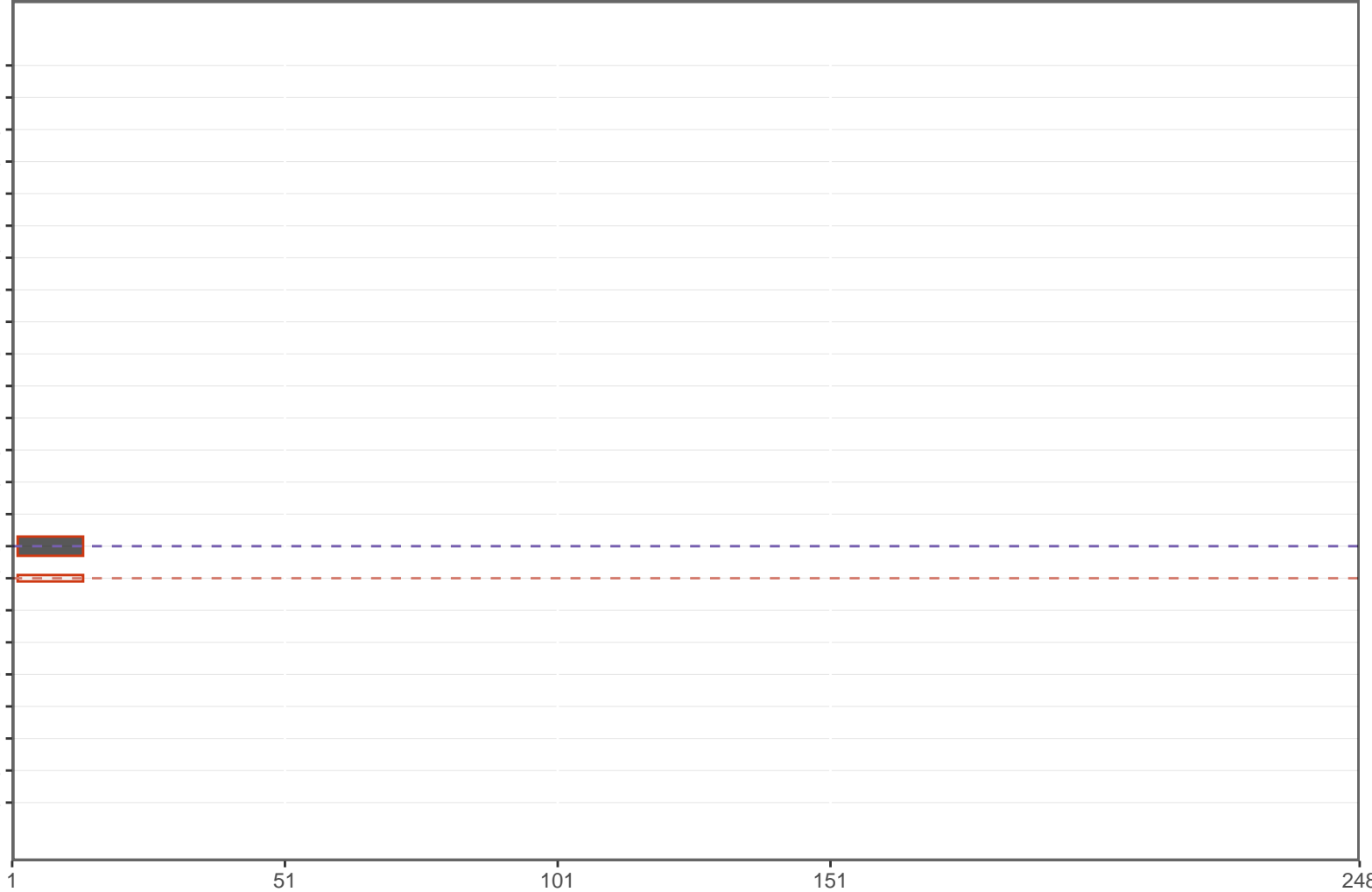
MW indication



Molecular weight



Gel Slice

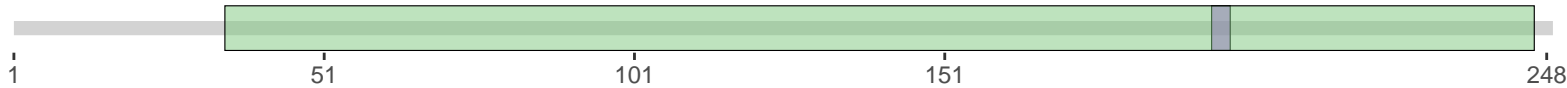


Protein length



Peptide counts over 4 repeats

Pfam domains



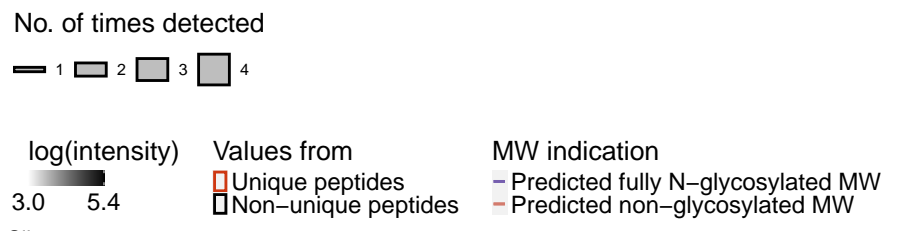
Pfam Description



Protein sequence:

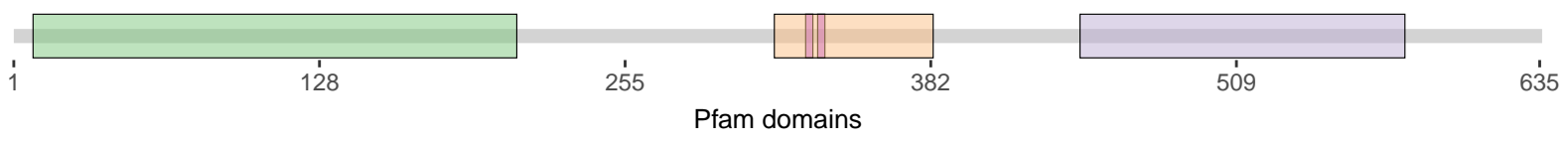
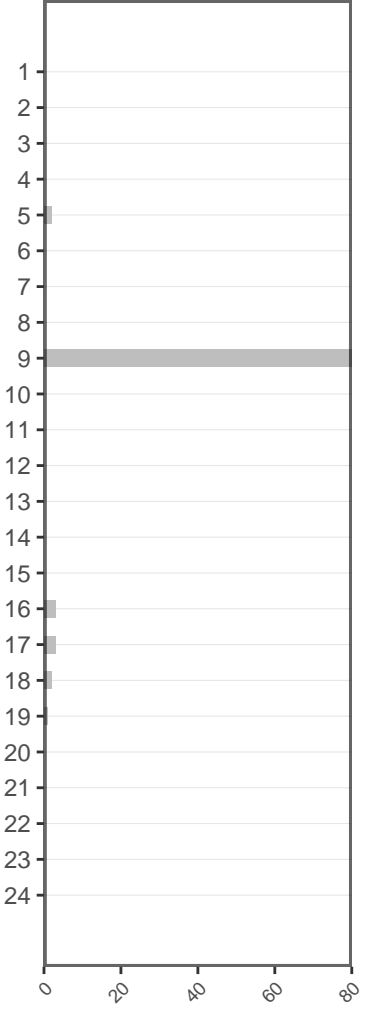
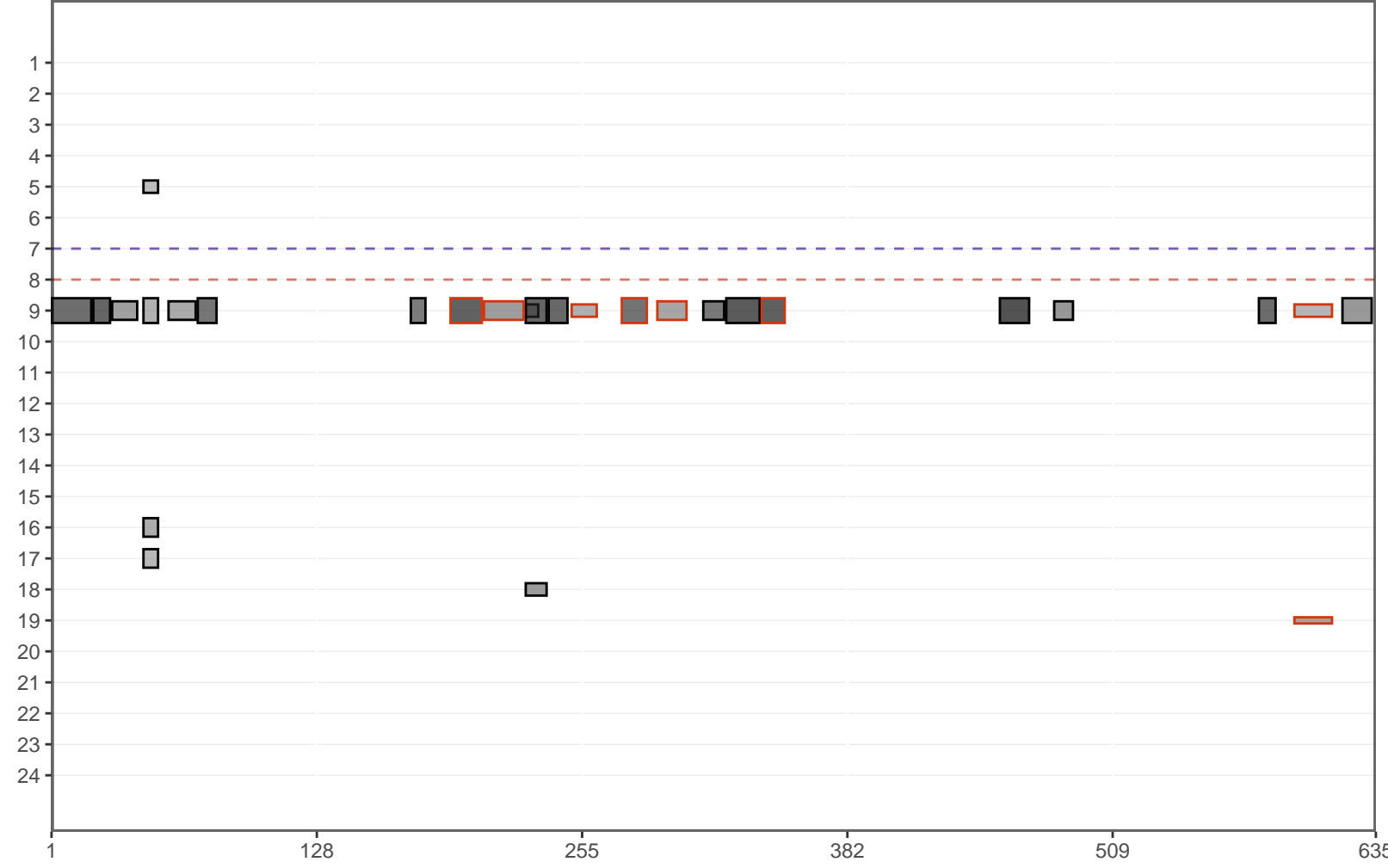
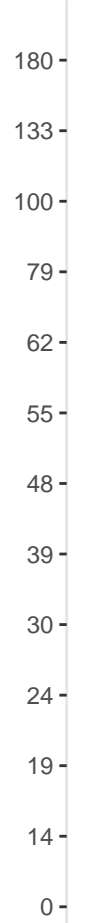
MDINRENYEIGLPVQKAGVAKIDFREGPALPVLQDLMEEDKNNHGTDFDFVDAKDKNYINHKRIELVYGGVGGYDNTLWNGSVAAPPDAPMRKYVRYRDFLELNKALAADPRIEICMLPVGGDITLGRRIE

NbL01g02850.1 probable_quinone_oxidoreductase [MW = 68.33 kDa]



Molecular weight

Gel Slice



Protein sequence:

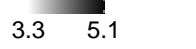
ATRIVRTALRLPLKPDHLLKVVYAGVNASDVFNFSSGRVYFSGDNDIASRLPLDSGFVAGIAAGDAVKNLKGMPAAMTFGGVYAEFVTVFVQGHLPKAPPEVLAAMLTGSLTASALEKAAQMGESGVVAVTAAAGGTGGFVAGLAKLSGNTVATCGGTEKAKLLKDLGVDRIYDKYENKAVLKEFFPKGVIVVYVESVGGEMFDGLNALAVYGRLLVIGMISGVGGEHGWPRNYPGICEKLLAKSOTVAGFFLVGYAHLWQEHLDRLVNFSSGKLKAIIDPKYQFGLHSI

NbL01g02790.1 EKC/KEOPS_complex_subunit_TPRKB [MW = 18.69 kDa]

No. of times detected



log(intensity)



Values from



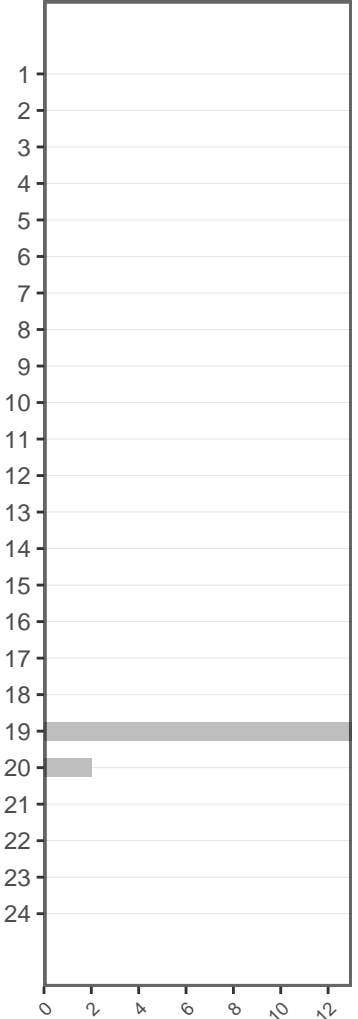
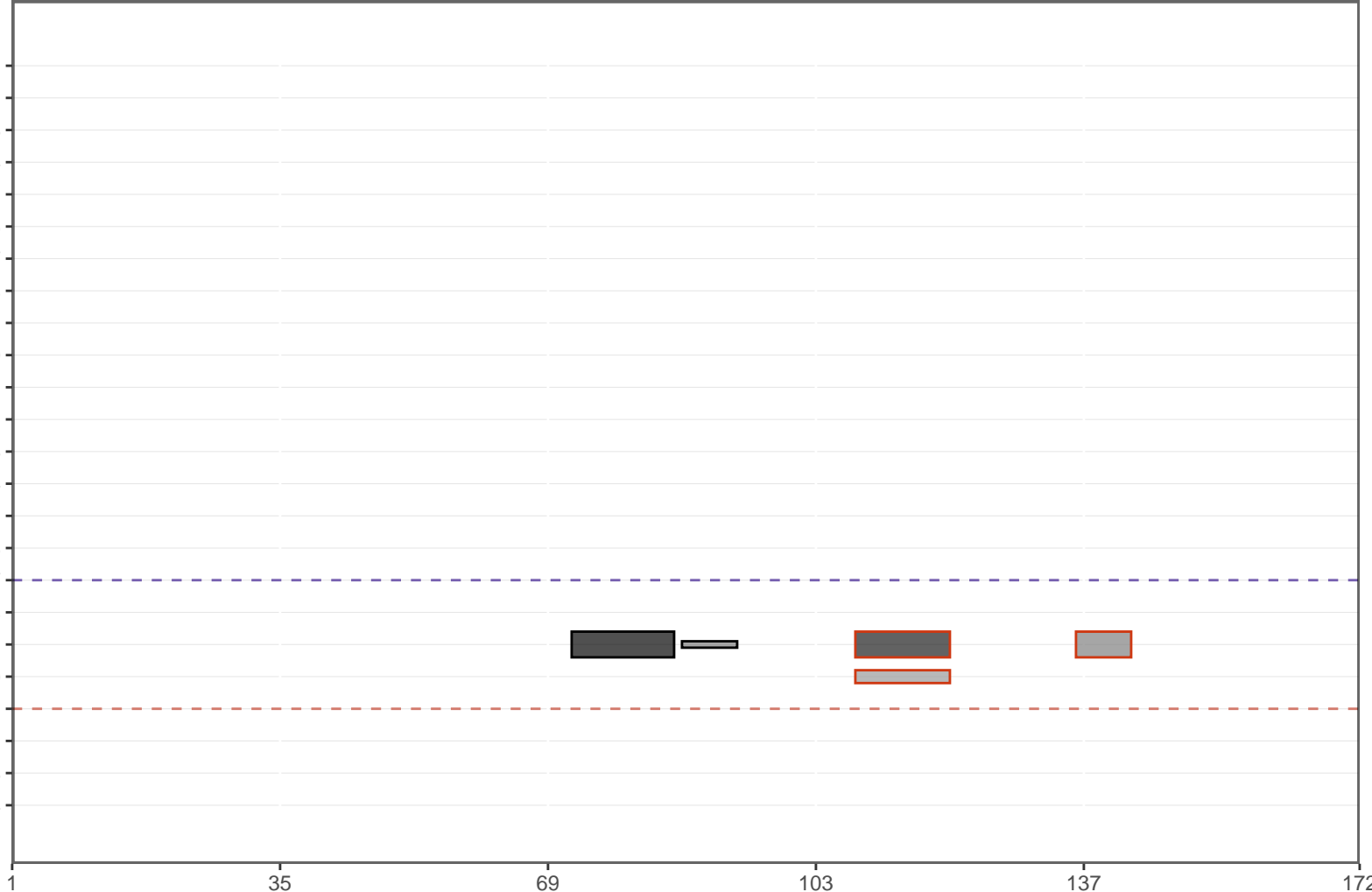
MW indication



Molecular weight

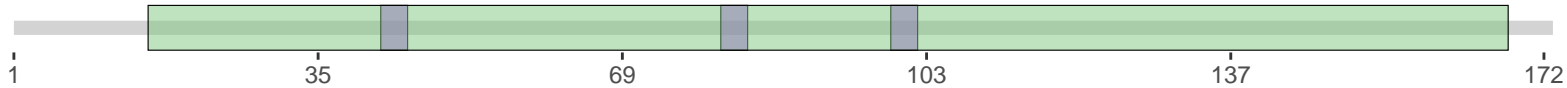


Gel Slice



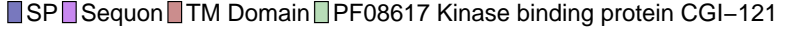
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

TLHSELYVNYSGSKHSESLKRGDADNTSEVLAARFGALADEMVAWEKLVNGKEIDLELEQRINGADQKQHYKISLELEISLADATGRIIARDAL*

NbL01g02710.1 ferredoxin--nitrite_reductase_chloroplastic-like [MW = 68.22 kDa]

No. of times detected



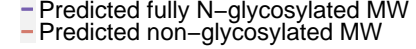
log(intensity)



Values from



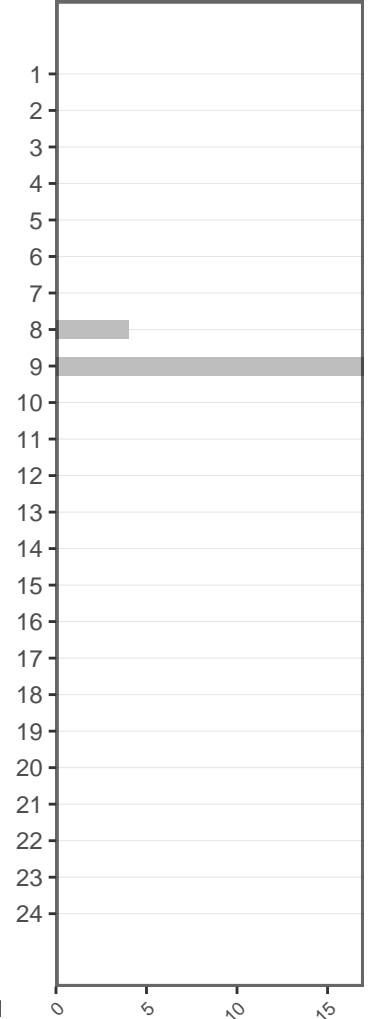
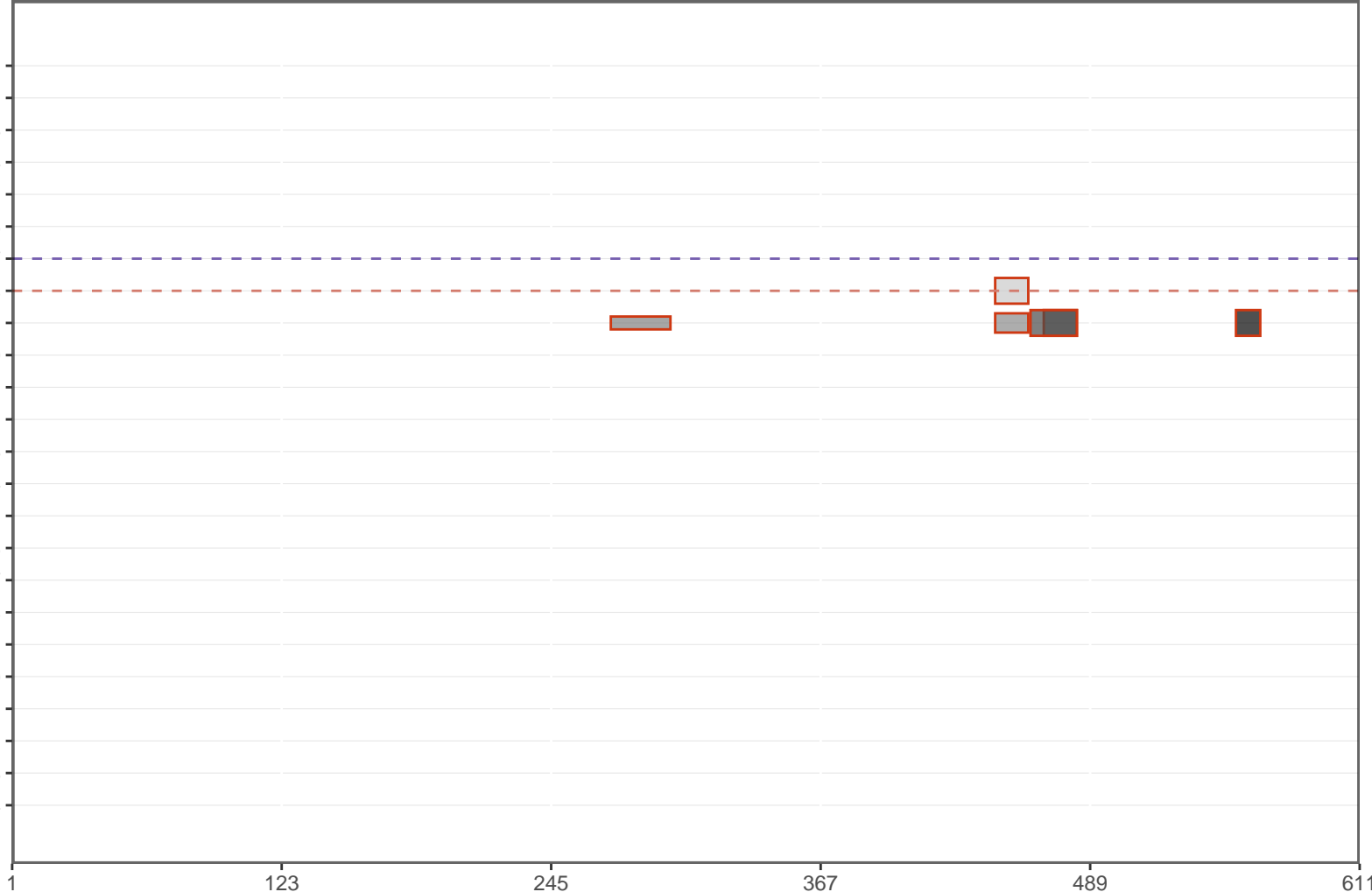
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

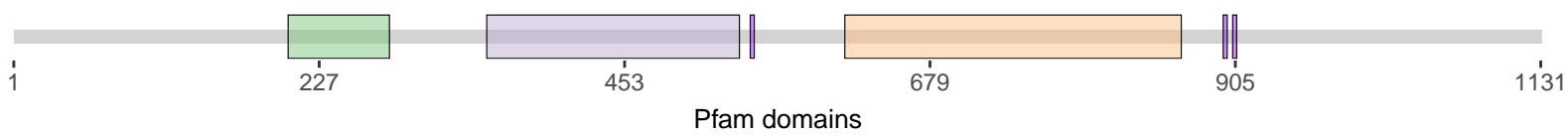
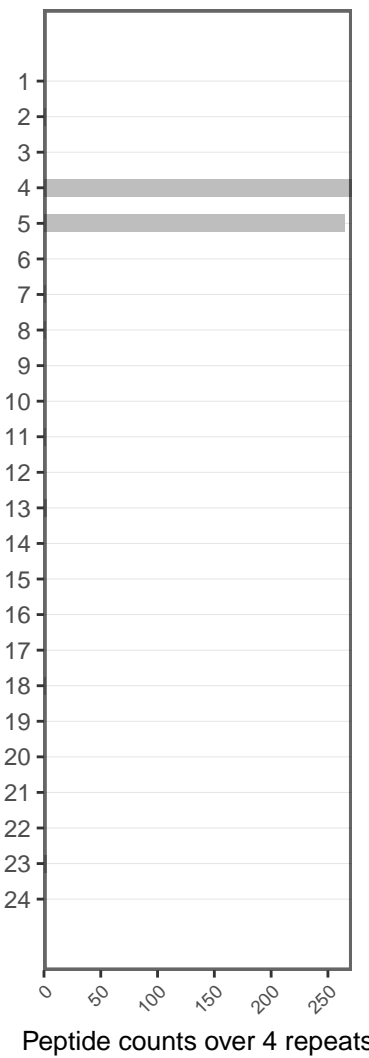
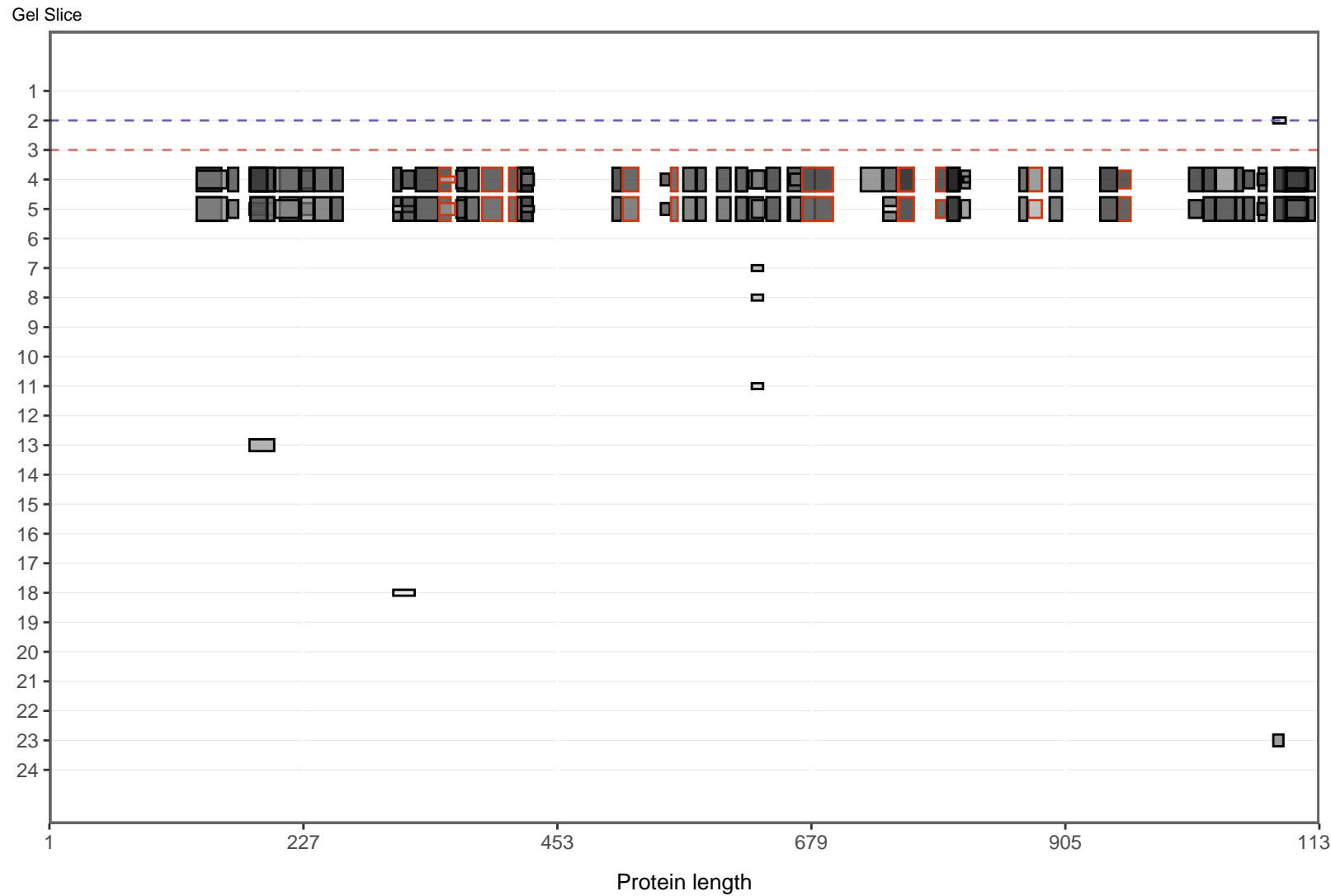
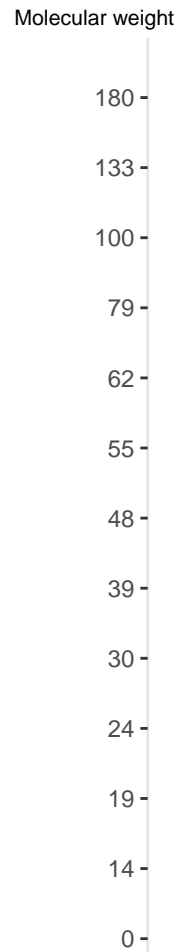
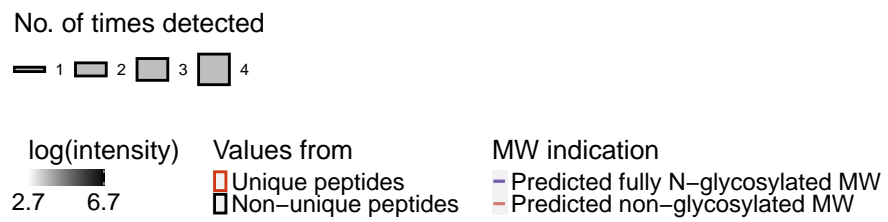
Pfam Description

- SP
- Sequon
- TM Domain
- PF01077 Nitrite and sulphite reductase 4Fe-4S domain
- PF03460 Nitrite/Sulfite reductase ferredoxin-like half domain

Protein sequence:

*MPATKDGRFGFNLSVGGFFSAKRQDEAIFLDWIPADDDVVPVKKALEAFRDLAGFRGNRQKGRMMWLDLGLGVGFRAEVEKRPMPQGLERASPEDLVQKHWRERRVGLVHPQKQEGEYFGLHPIVGRVADDDMLARLADEYVSGSEIRLTVQGNMVPNIENKIEALLKEPVLSEAFSPDPLMKGLVAGTQNGFGGQAIETKARLKITEEVQRQVSLTKPVRMHWTFGPNTCAGQVQWADIGFMGLTRDKNKKTVEGADVFLGRRIGSDSHLGEVYKAVPCDD

NbL01g02640.1 presequence_protease_1_chloroplastic/mitochondrial-like [MW = 127.3 kDa]



- Pfam Description**
- SP
 - Sequon
 - TM Domain
 - PF00675 Insulinase (Peptidase family M16)
 - PF05193 Peptidase M16 inactive domain
 - PF08367 Peptidase M16C associated

Protein sequence:
 GLALMLRSIGKWIYDMDFPEFLKYKPLKALKARIAKEGSKAVFAPLDQYILRNPHRTVEMQPDFKASREEEKEKFLDKVYKASMTGDELARATHRLKKGTEPDPPEALKSVPSLSLGDIPREPTHVPTVEVSDINGKVKLRLHDLFTNDVLYAEVDFDMSSLSKGLLPLVPLFGSLLEMGTKDLDFVGLNGLIRKTKGGISFYPTTSVVRGKVEPCKIVRGGKAMSGRTRDGLFNLRVLDGVLDNDHKRFKQFVSGSRARMENLRKGGHSAASRMGAKLVNAG

NbL01g02630.1 2-hydroxyisoflavanone_dehydratase-like [MW = 35.3 kDa]

No. of times detected



log(intensity)



Values from



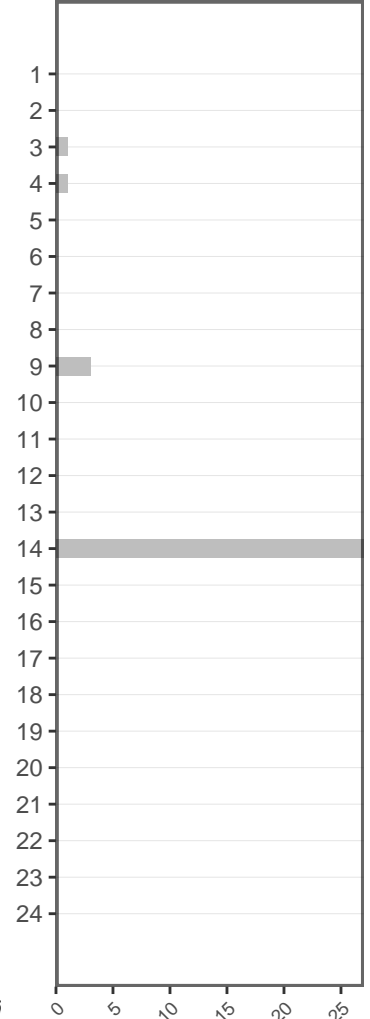
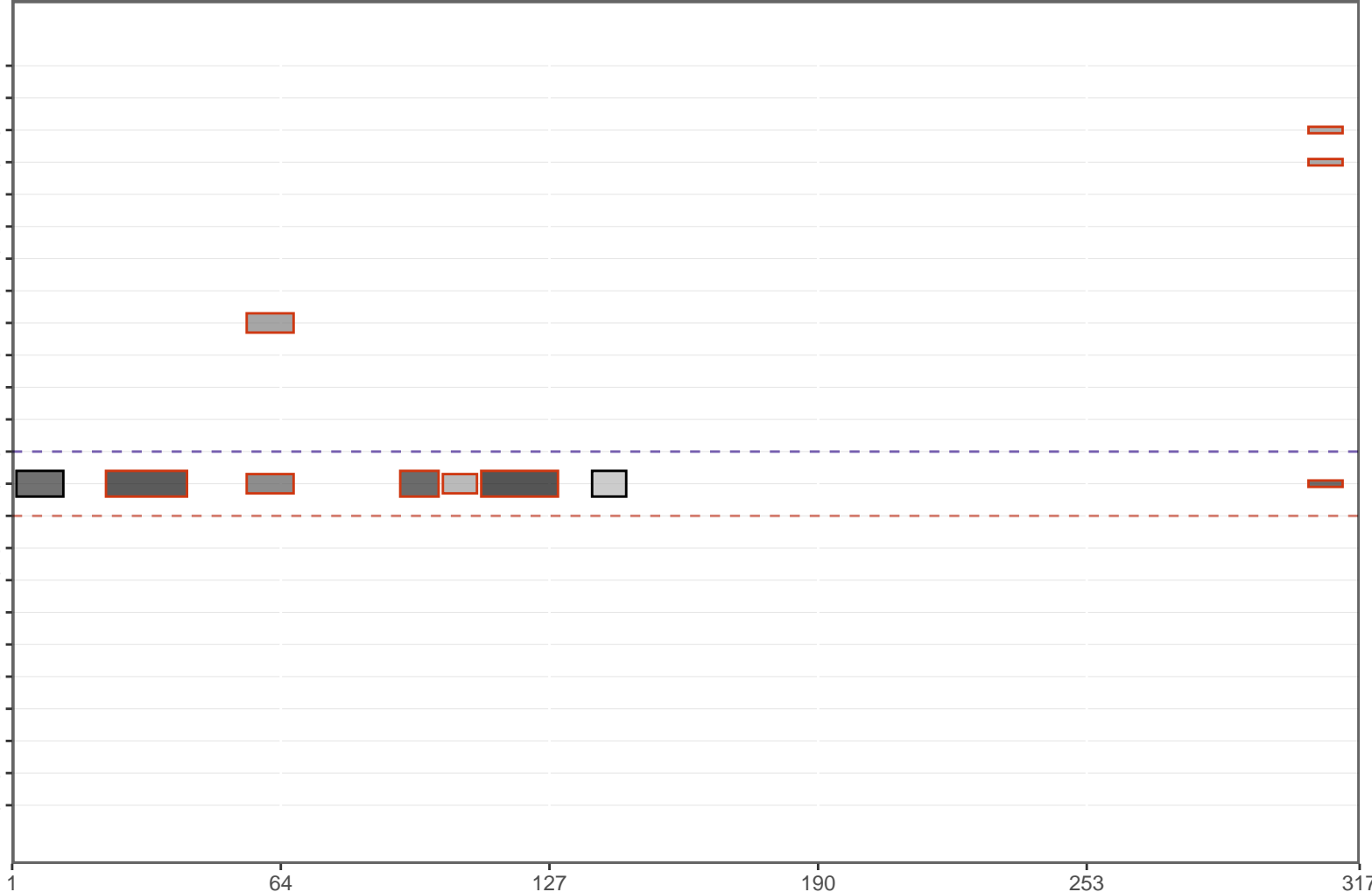
MW indication



Molecular weight

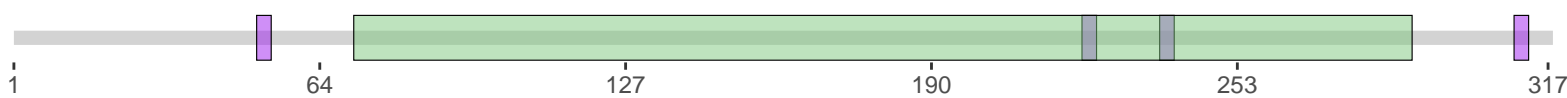


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

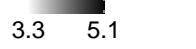
HADLNHYFFGDSAGANAHNAIRVGLKLNGLKIDGIFLAGPYFVWGIUDIGEAEENLDGKNYIEKLVAFAPNSGGLDDPVMNPEKDPNLSLGGDKVLYVWAGKPLKYRGLYKELLESKGGWGTVEVVEIKDEEHVFLHFAPTSEANMVLKKLASFLNDSKLR

NbL01g02620.1 probable_carboxylesterase_12 [MW = 34.86 kDa]

No. of times detected



log(intensity)



Values from



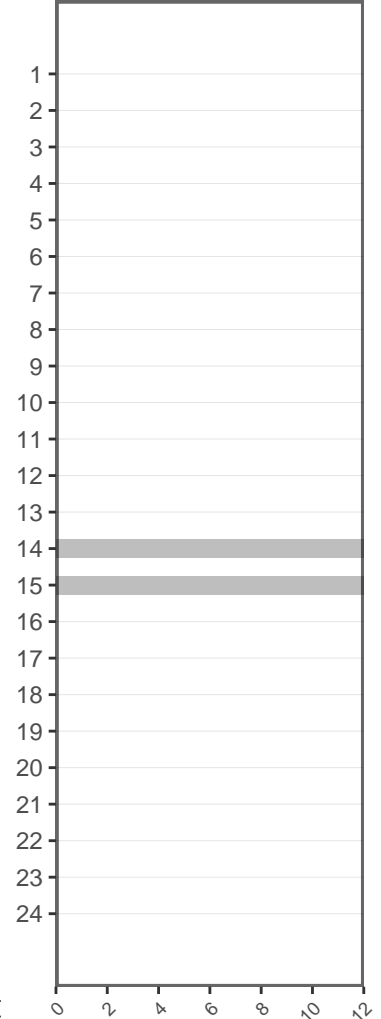
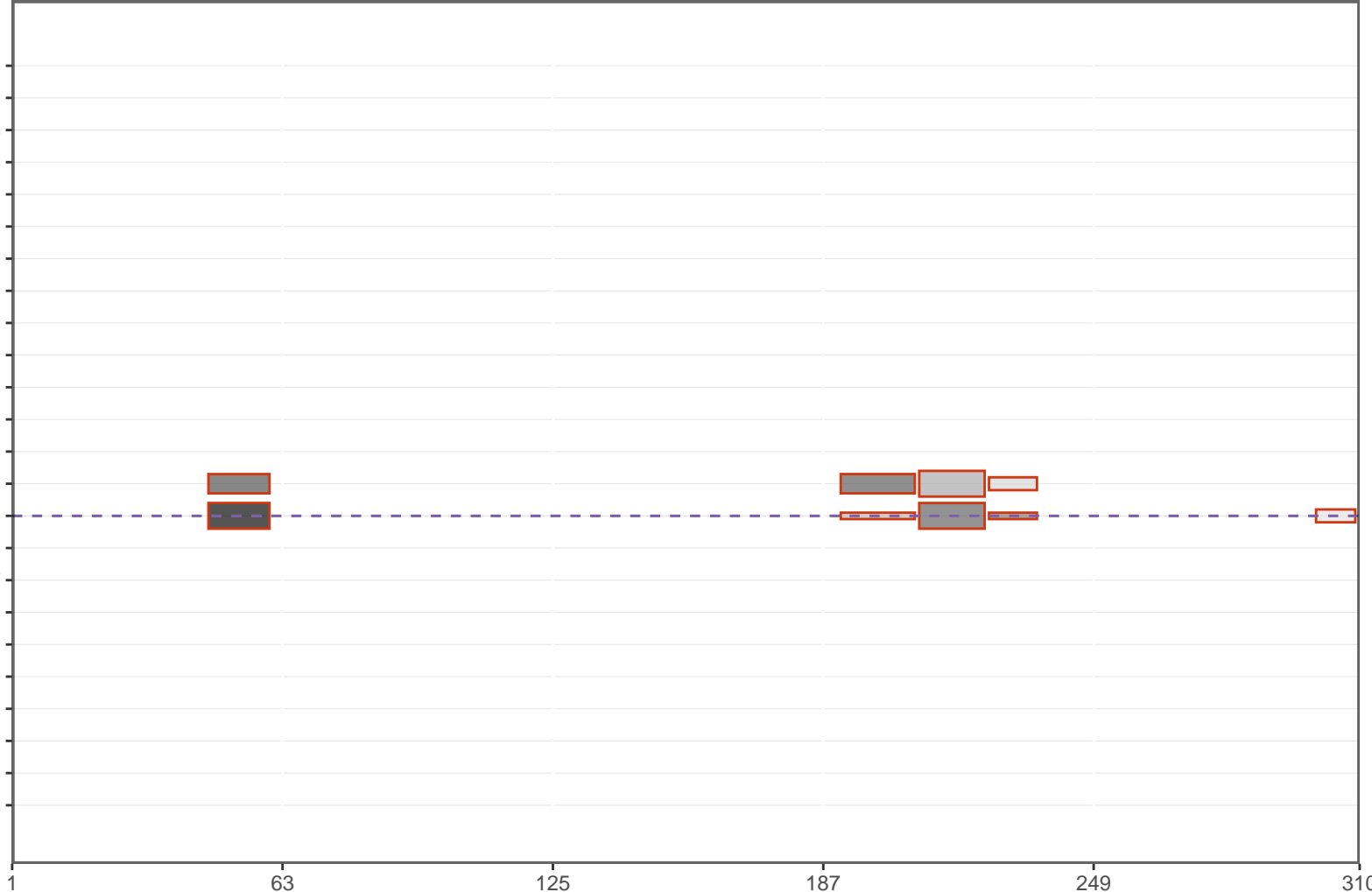
MW indication



Molecular weight

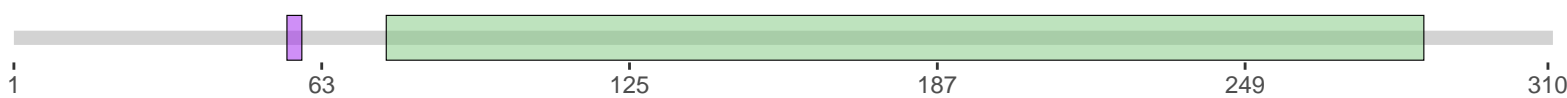


Gel Slice



Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

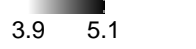
IGTEPWLGSHADFSRFLAGDSAGANAHNMMMGASVDEKLDGGLKLVGMALHPYFGNNGPDRIRWISYOCPEPNTDPRFRPAHPSLLKSLKIVCSKILGTGKDFIRDRGWTFYEALKKGGVWGEVEKETEGETEEHVFHIVFTPTCDKAKALMKWLADFFQGGSS

NbL01g02610.1 2-hydroxyisoflavanone_dehydratase-like [MW = 43.46 kDa]

No. of times detected



log(intensity)



Values from



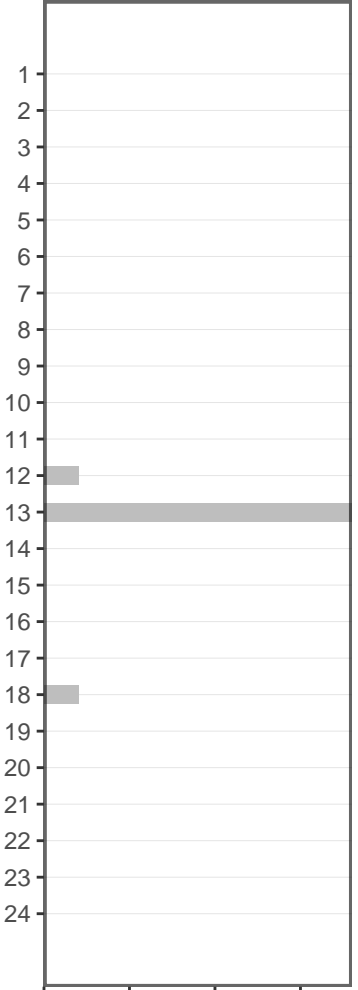
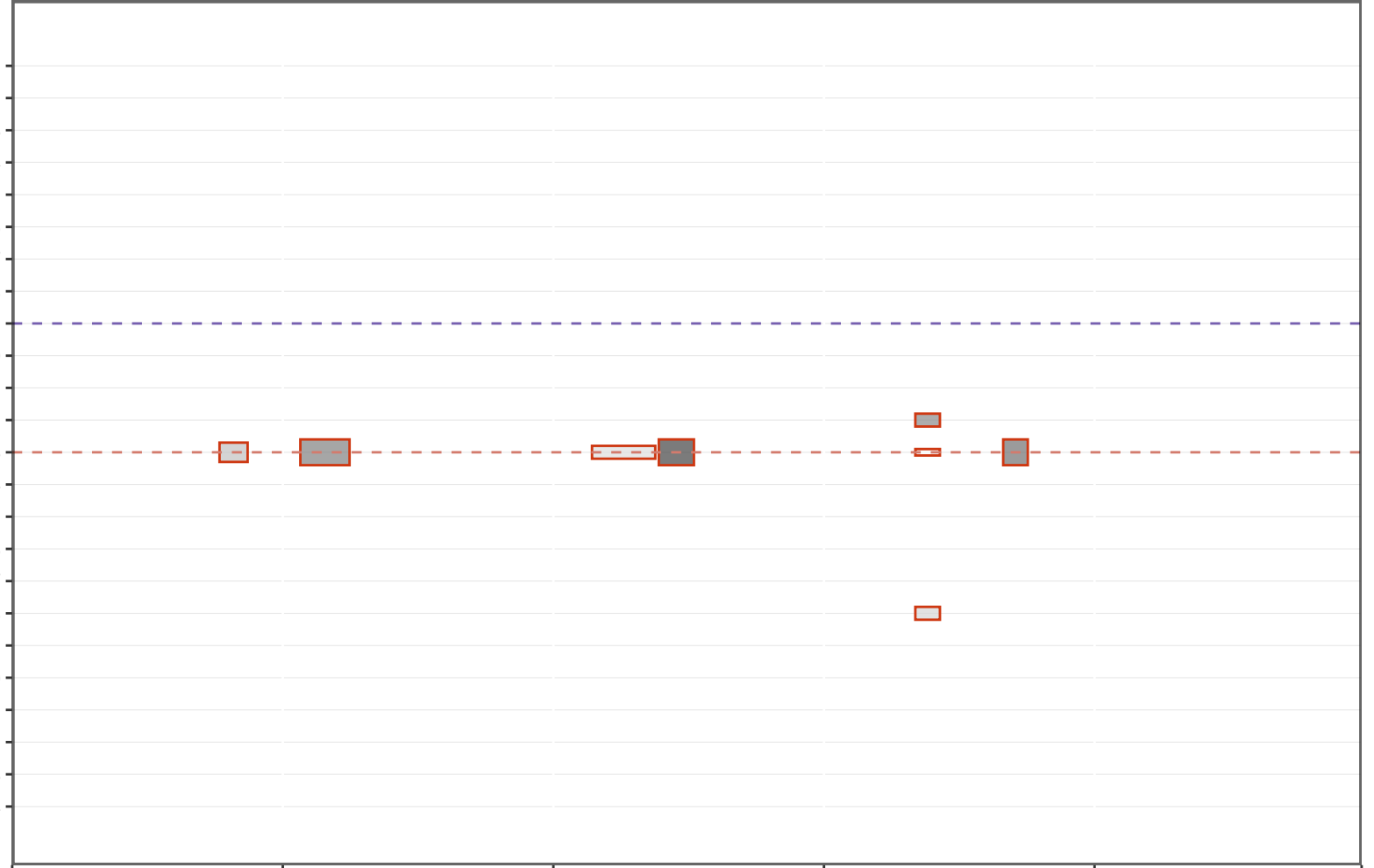
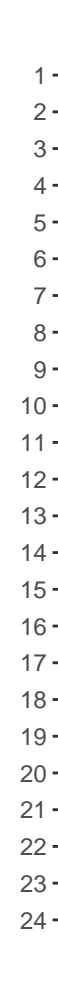
MW indication



Molecular weight

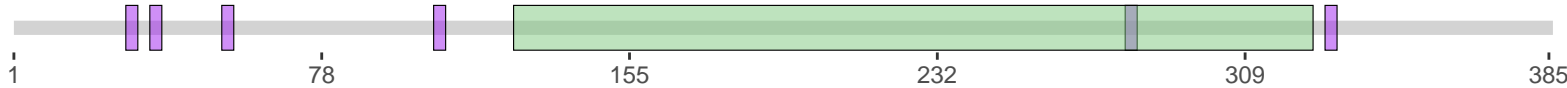


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

AKVVEGGTDPVWIKGHADFGRVYVLAGDSAGANAHNMMVRVSEESHFRPLIGMALIDPFYFGNDKDPDLWNYLGPKTTGTYDPRFNPAHPMLLSKINGSKVLCVGTAGKDFLRDRAWTYIYENLKKSGWVGEVDMKEIEGEDHVFHLYNGTSEKANALMKKSVVDFVYDDSDGHHVNLGSKVSEFSMSLIFAFNLFDCVYKSSP

NbL01g02600.1 probable_carboxylesterase_2 [MW = 33.84 kDa]

No. of times detected



log(intensity)



Values from



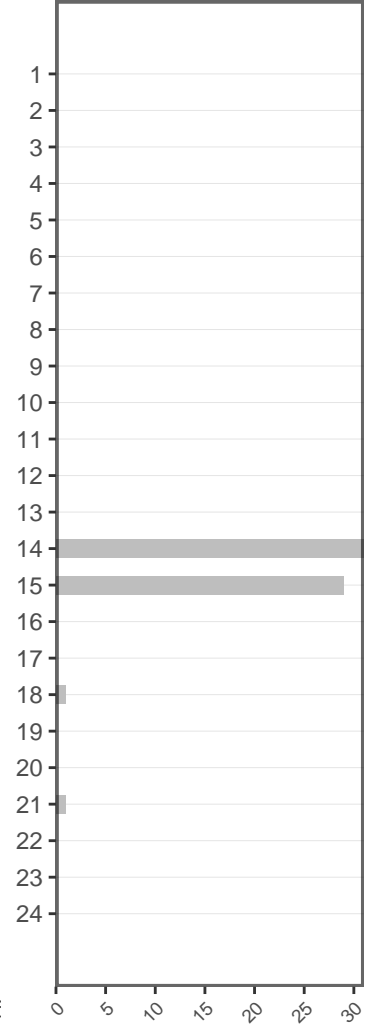
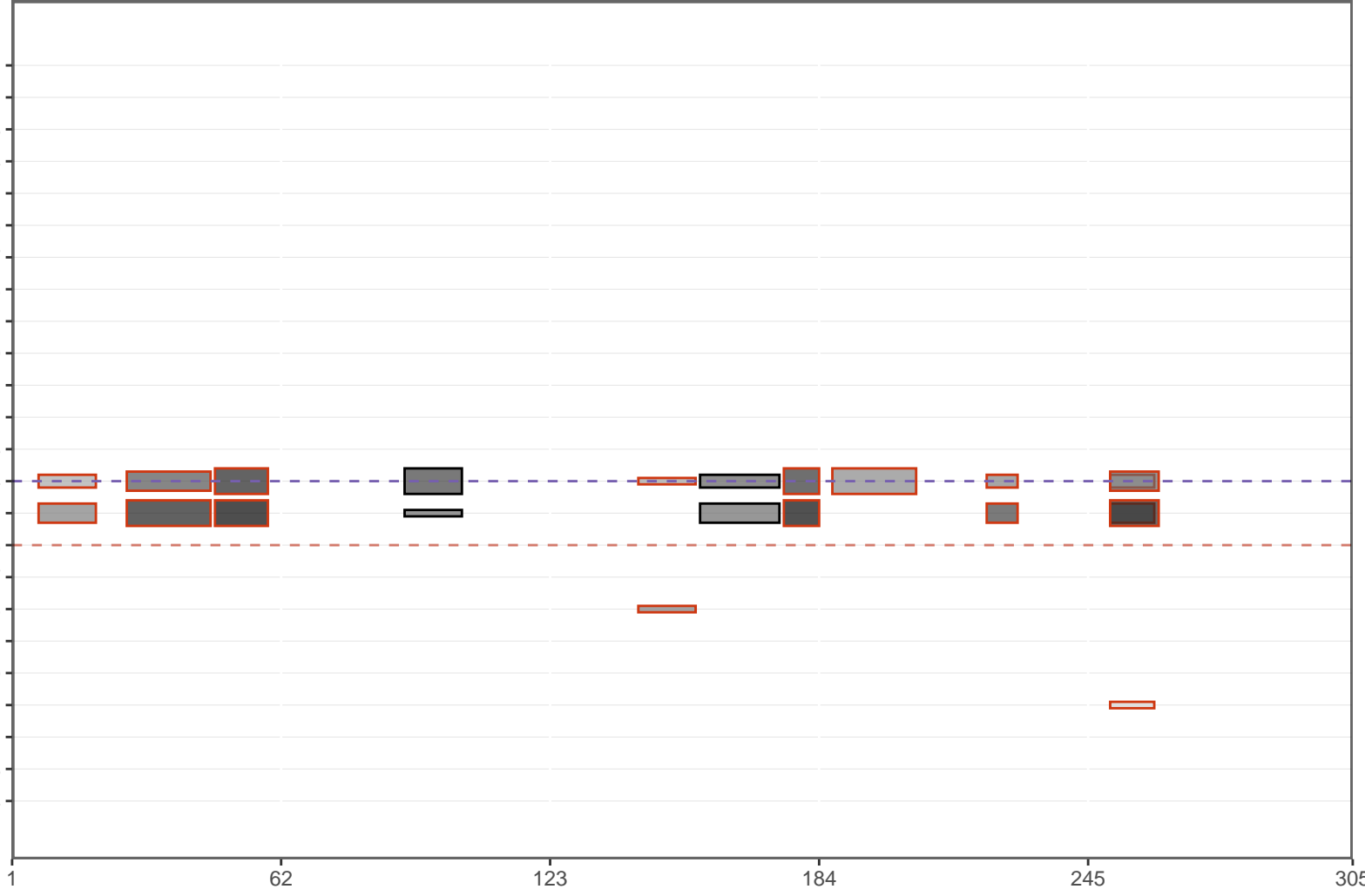
MW indication



Molecular weight

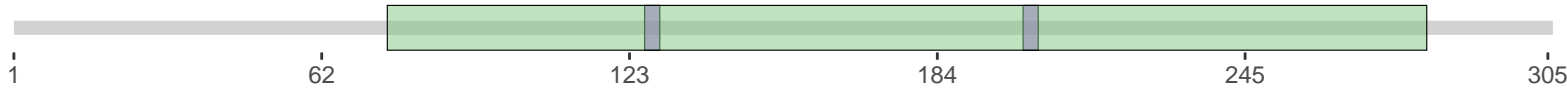


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

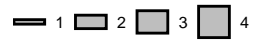


Protein sequence:

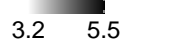
IKGPESWLENEYADFGKVFIGGESAGANANDWARAGVSDLDLKVKILGLYLWHPYFGVENDTLYKLCPTDTGGGFEDPRVNPILLDRPKSMAGKVKVFLVAEKDFLKEGTMNYYEGLKXSEWNGELEIMETKSGEGHCFHFIPMSEKAWALMDKLVDFLRKD*

NbL01g02580.1 polyadenylate-binding_protein_RBP47 [MW = 46.86 kDa]

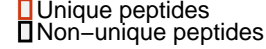
No. of times detected



log(intensity)



Values from



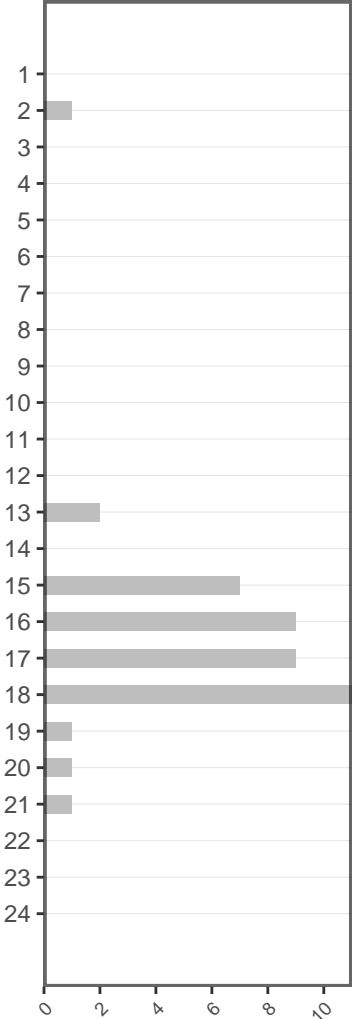
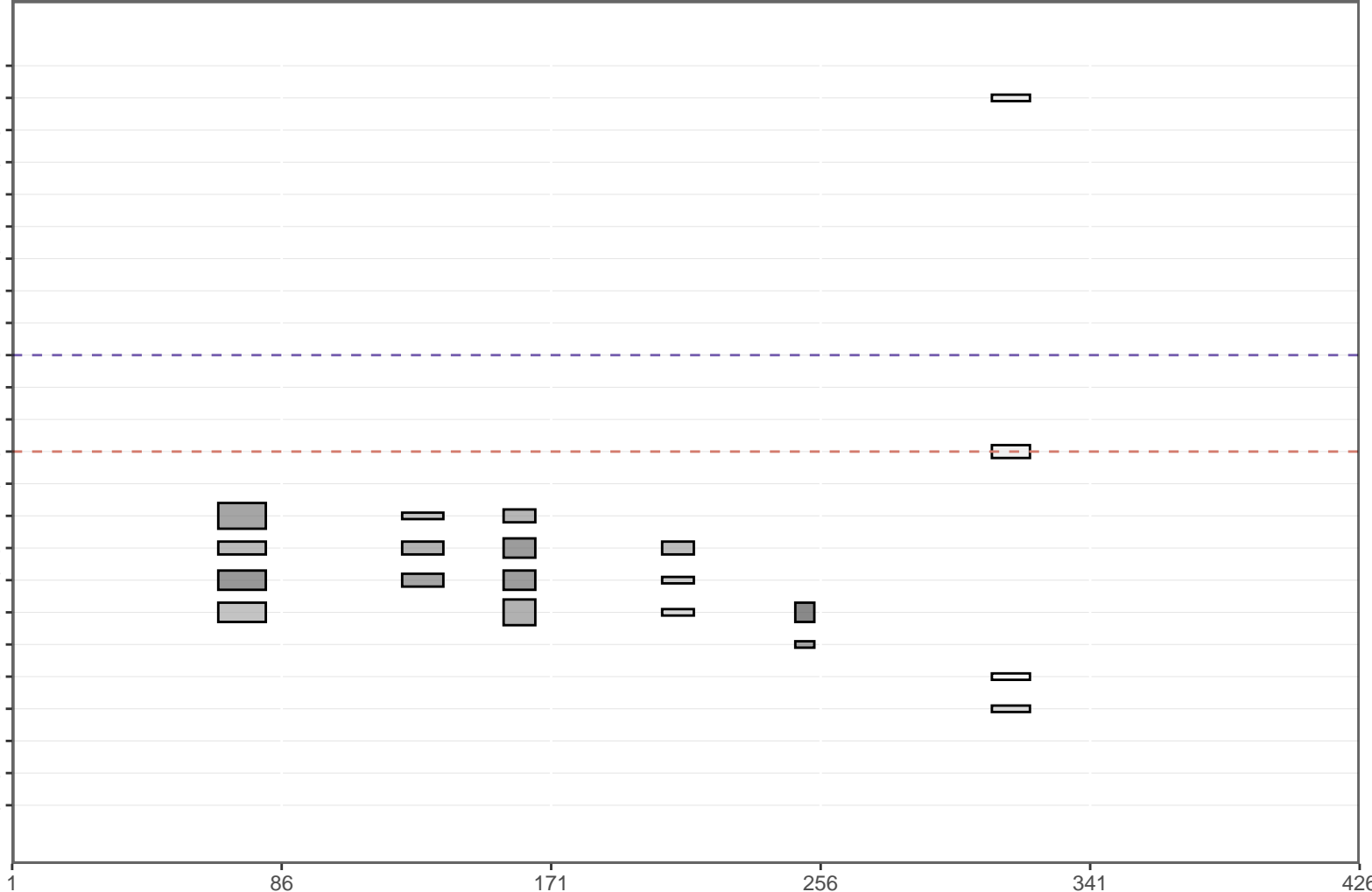
MW indication



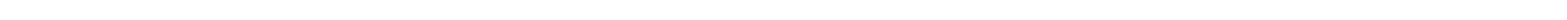
Molecular weight



Gel Slice

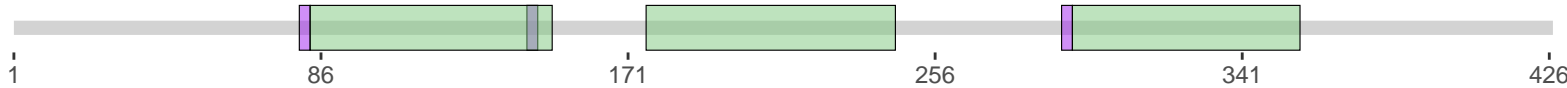


Protein length

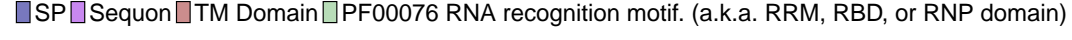


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

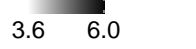
/PSLKGAQVYVDANTGHSKGYGFVRFQDESERRAMTEMNGVYVGSRRAMRIGVATPKKPSAQQGVYSSQAVLSSGYSANGAAPHQSGQDQSDSNTFTFVGGLDSEVTDDELRQSFNQFGEVYVSKIFPKGKCGFVGFEDRSAGEAIQKLSGAHGKQAVRLSWGRSPNKGMRITDSSGQWNGGYNRGRNYGGVGYGTSQEDSGMYTGAAYGASISNGYGNHGQPVSI

NbL01g02560.1 serine_carboxypeptidase-like_26 [MW = 56.27 kDa]

No. of times detected



log(intensity)



Values from



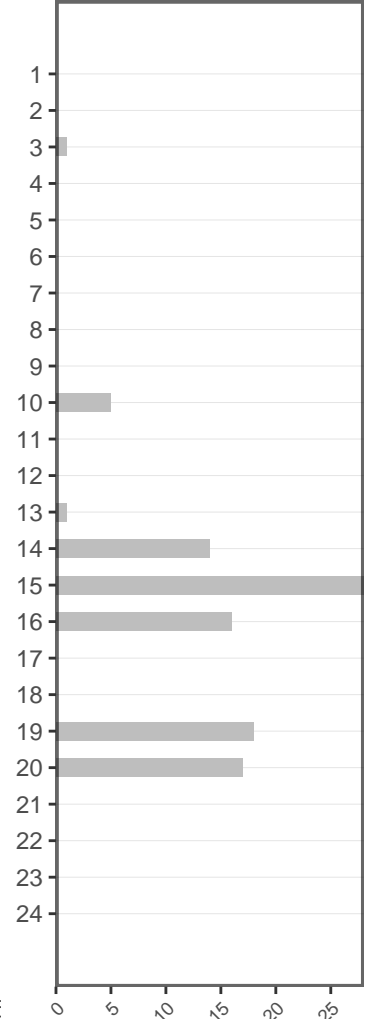
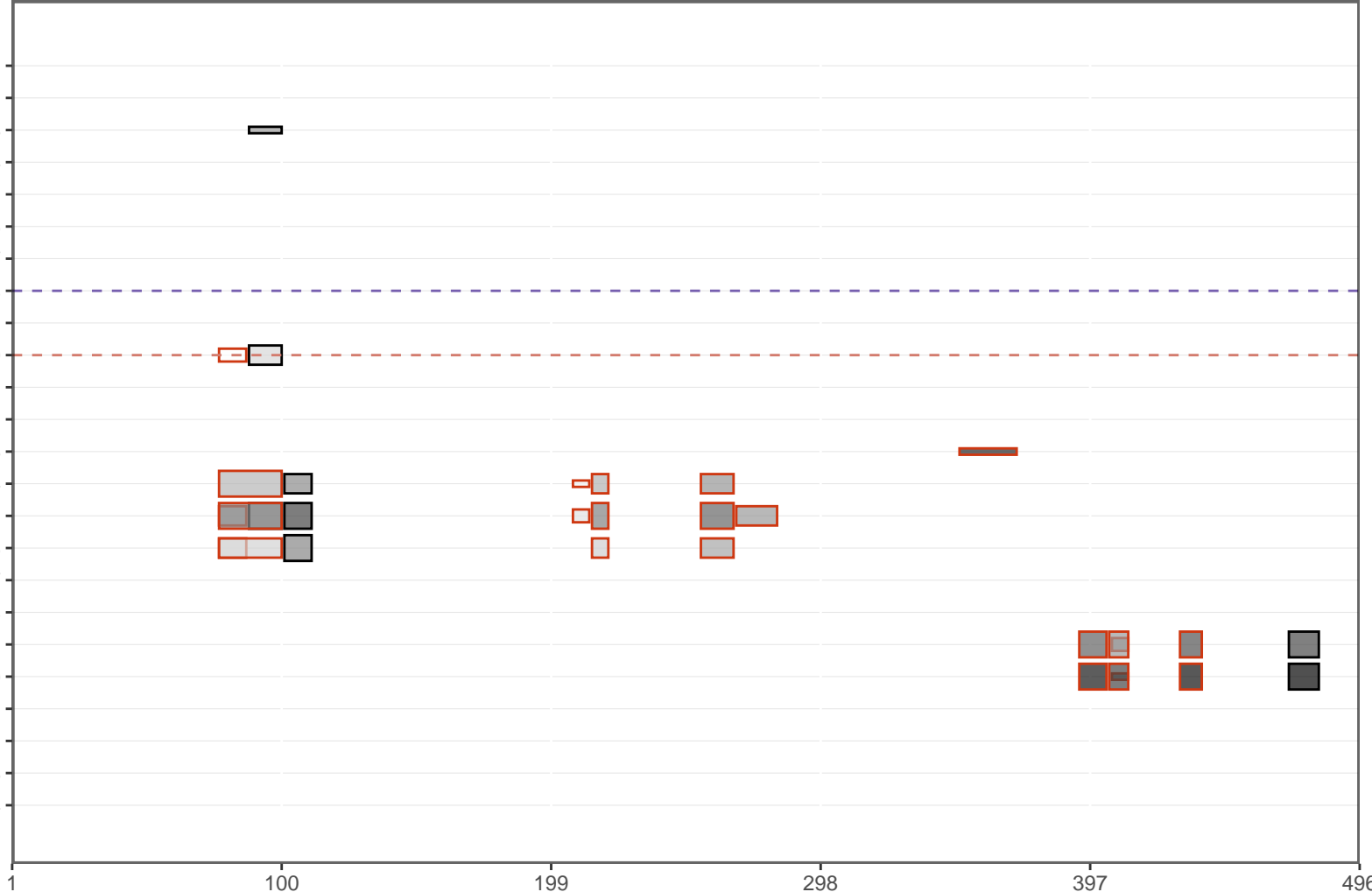
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

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NbL01g02240.1 CCG-binding_protein_1 [MW = 23.08 kDa]

No. of times detected



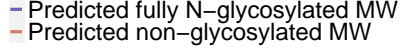
log(intensity)



Values from



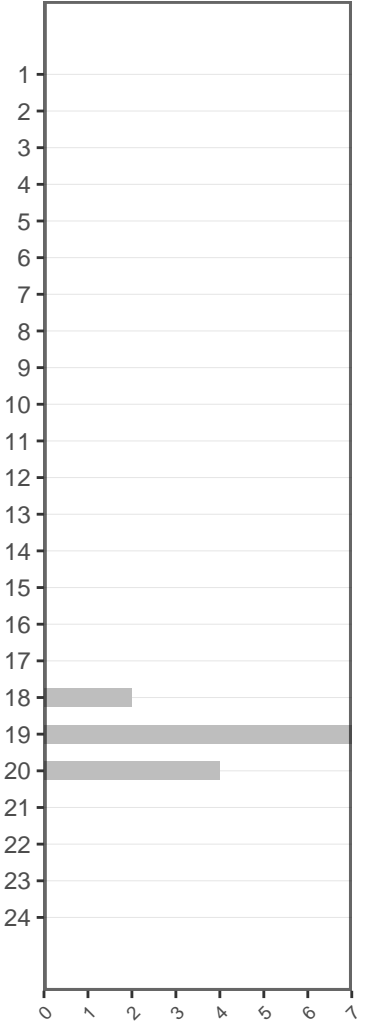
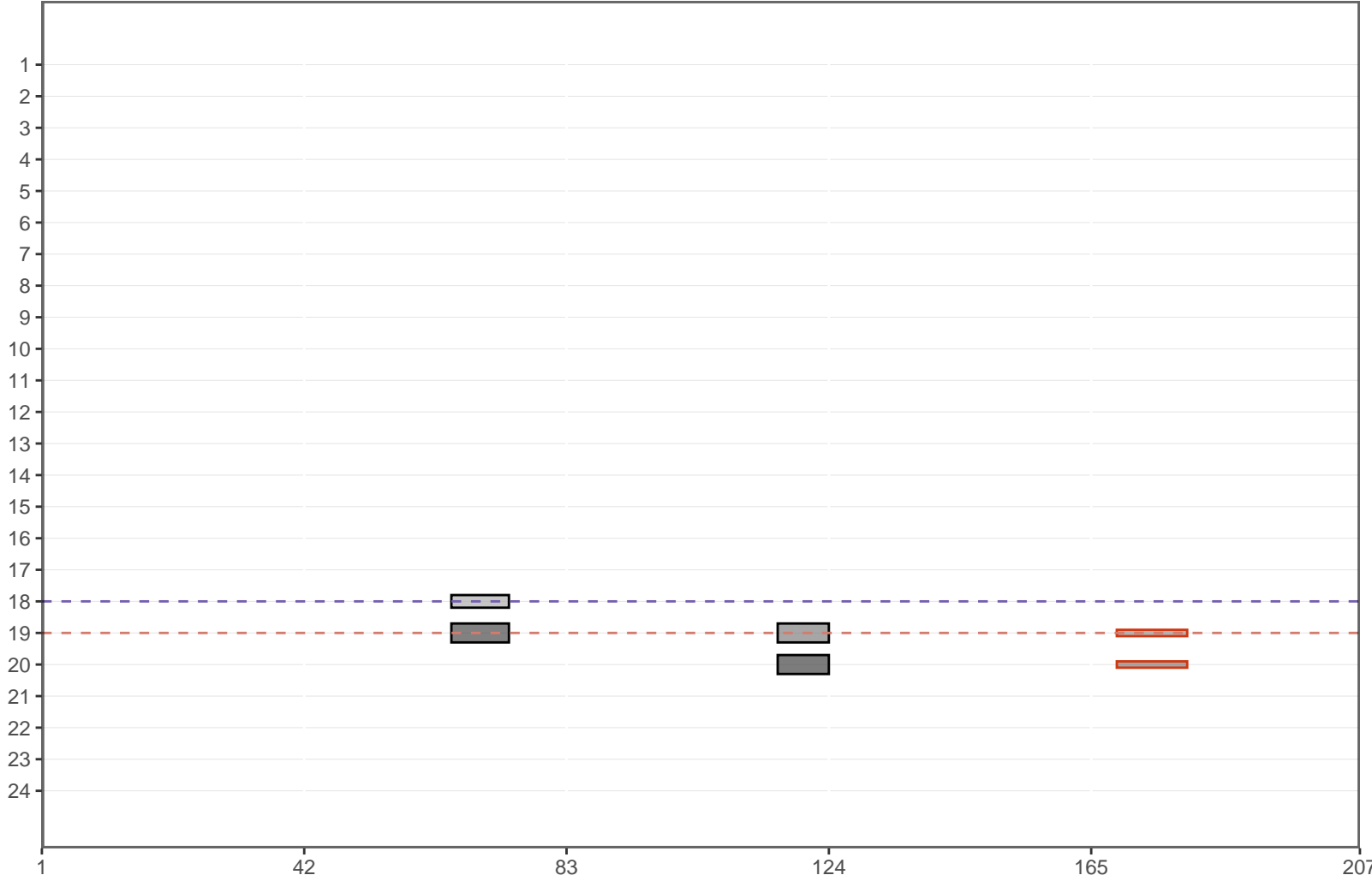
MW indication



Molecular weight



Gel Slice

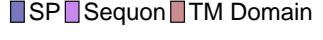


Protein length



Pfam domains

Pfam Description



Protein sequence:

ISCVQAYFELKDLLEKAPKKEEVEERLIGAGGVKTLUGLHGVSMDHKKAKRKRKSTHMANLEEKWAPGPIVDGLPKTRLEEEENKMKMPDSFTRLLRAKGTHPVWYSALDVF

NbL01g02140.1 proteasome_assembly_chaperone_2 [MW = 30.54 kDa]

No. of times detected



log(intensity)



Values from



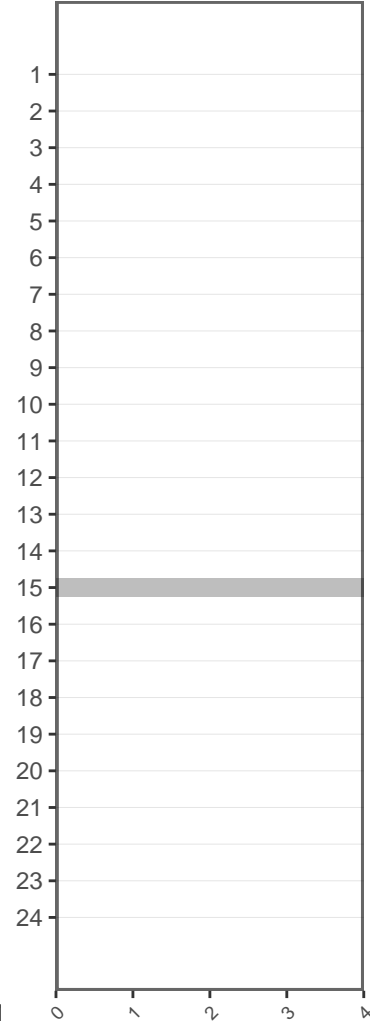
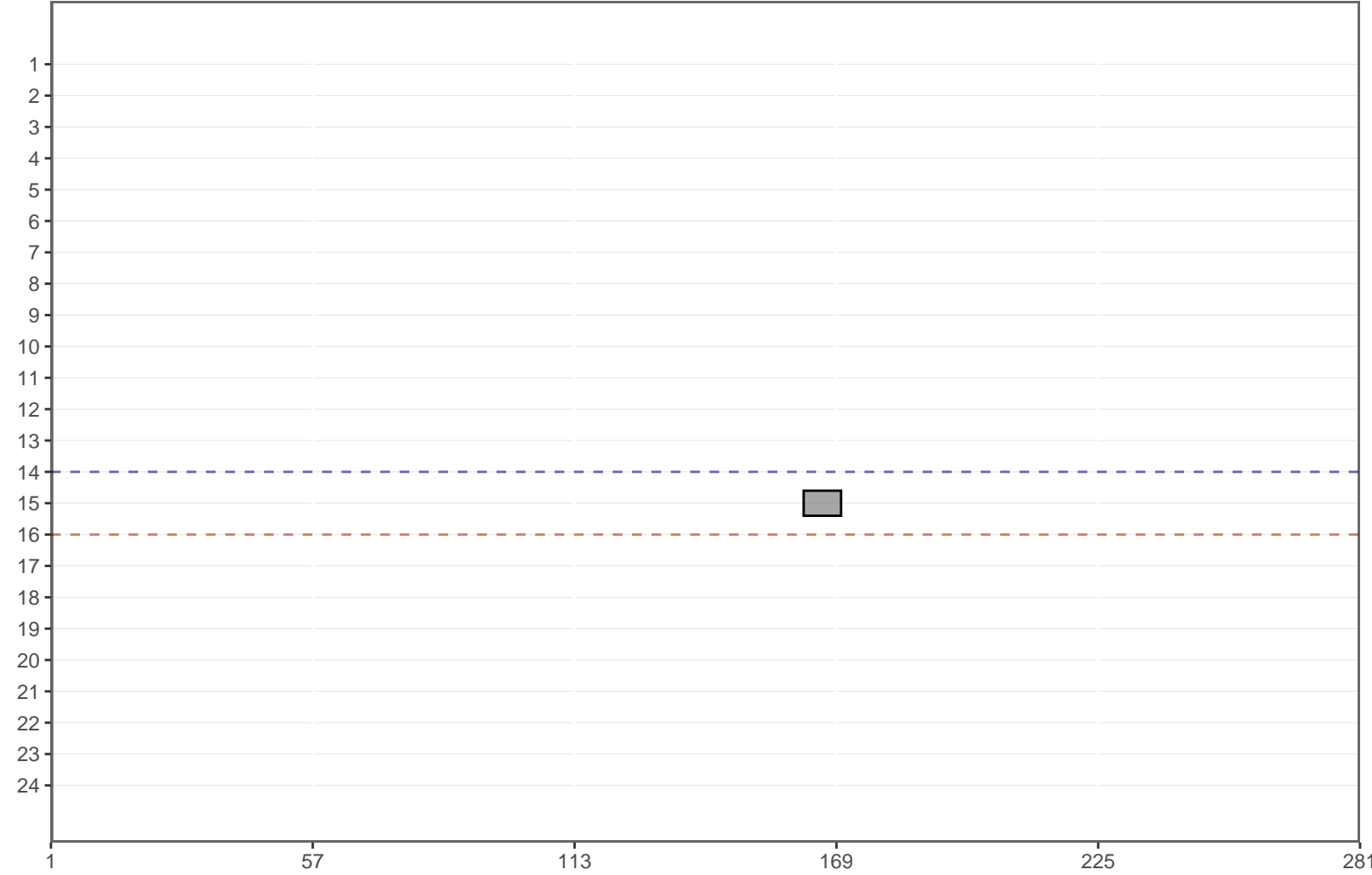
MW indication



Molecular weight

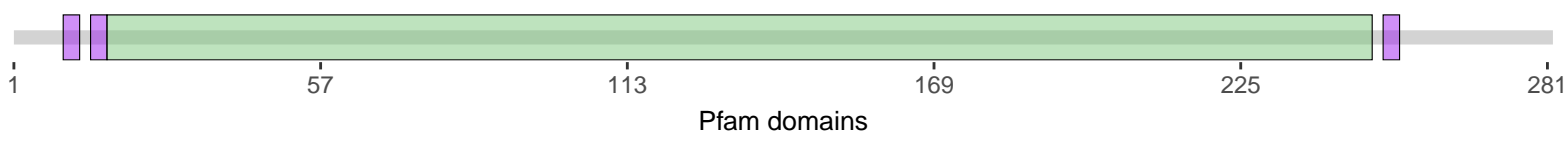


Gel Slice



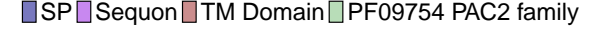
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

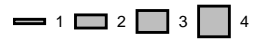


Protein sequence:

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NbL01g02110.1 phosphoribosylamine--glycine_ligase-like [MW = 54.98 kDa]

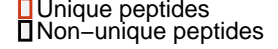
No. of times detected



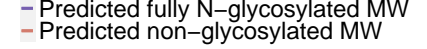
log(intensity)



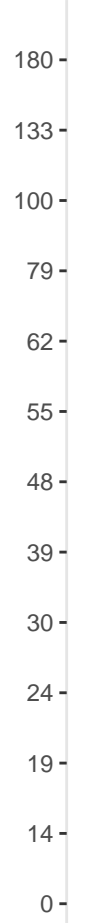
Values from



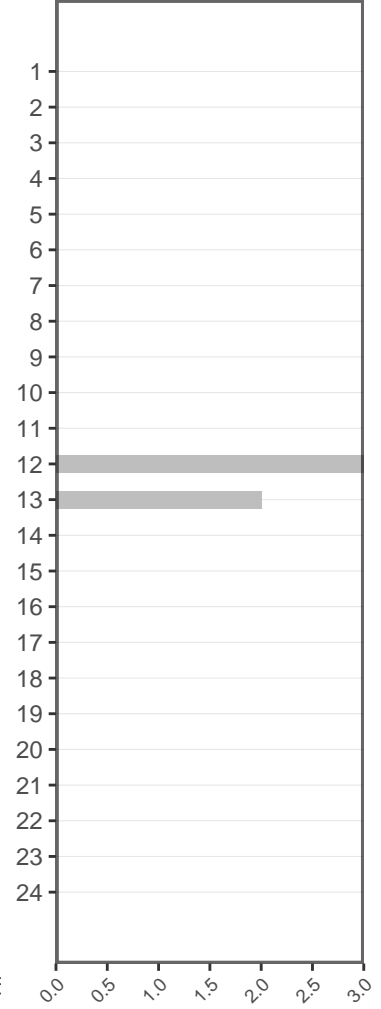
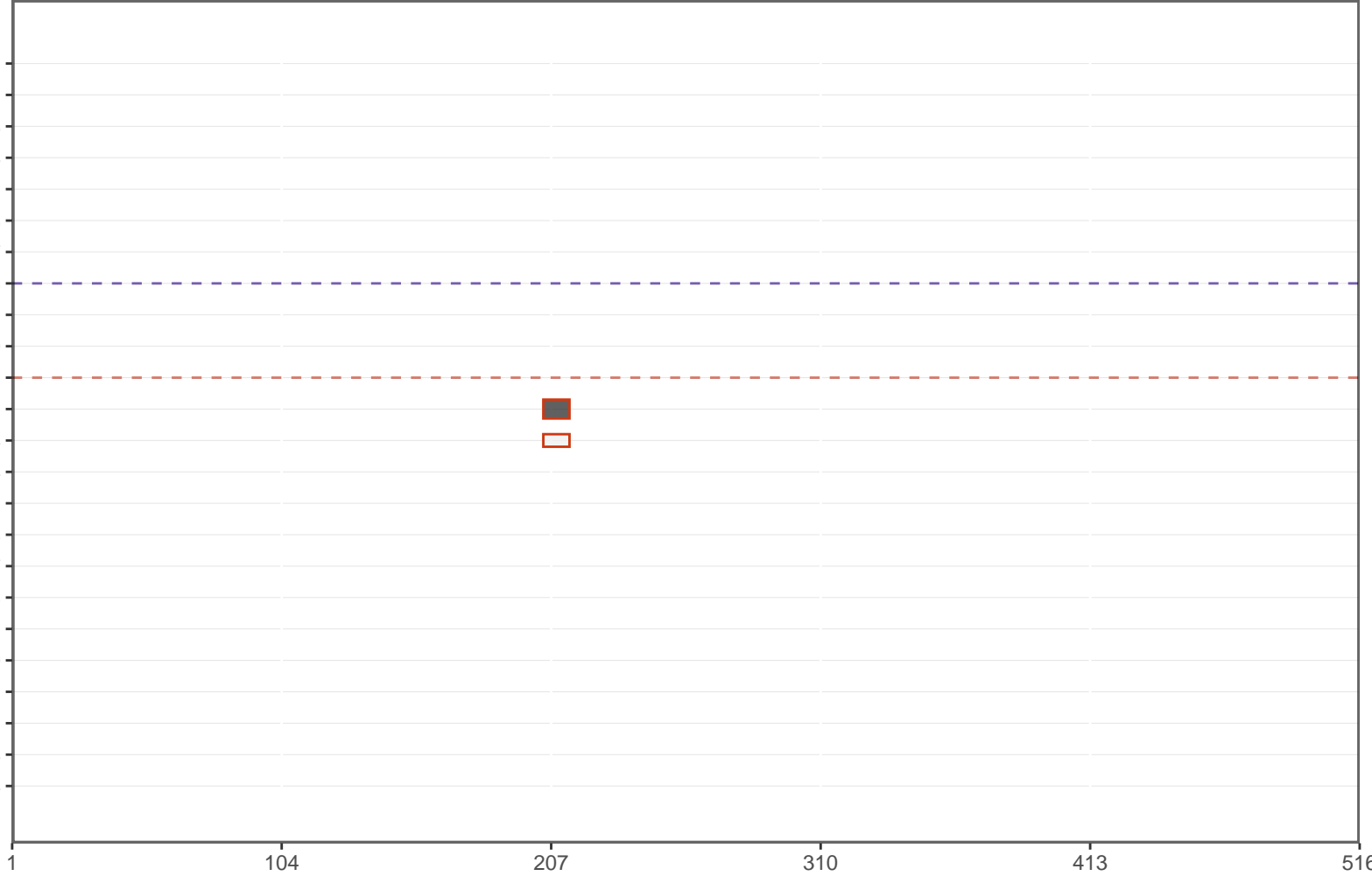
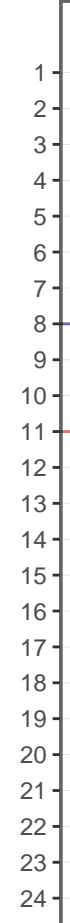
MW indication



Molecular weight

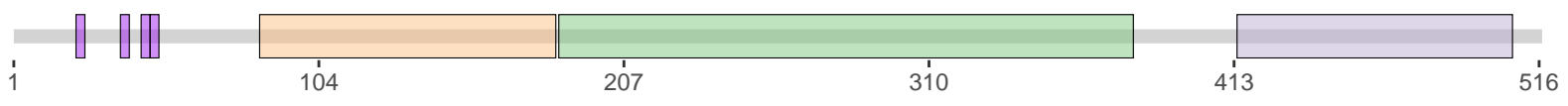


Gel Slice



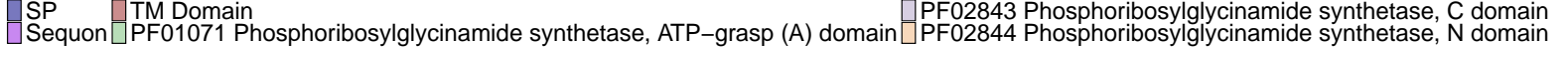
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

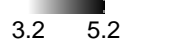
EAVDSMLVENVFGSAGSRVVEEYLEEGEASFFALVDGEHAPLESAGDHRKRVGGDGTGPNITGDMGAVSPAPVTKELQGVVMESHFFTVKGMTTEEGKFFVGLVYAGLMIKKTFGFFLQVNVRFQDPEGGVLMVRLESQVLEVLAACRGKLRGVSLDWSHGEMAVVMAASKGYPGYQKGTVHKLEEAEGVAPSVKVFHAGTAFDADGNFATGGRVLSGVTKGKEDLEEARDRVAQVAEQISWPGGPFYRDIGWRALPHKQYS

NbL01g01930.1 tyrosine--tRNA_ligase_1_cytoplasmic-like [MW = 46.3 kDa]

No. of times detected



log(intensity)



Values from



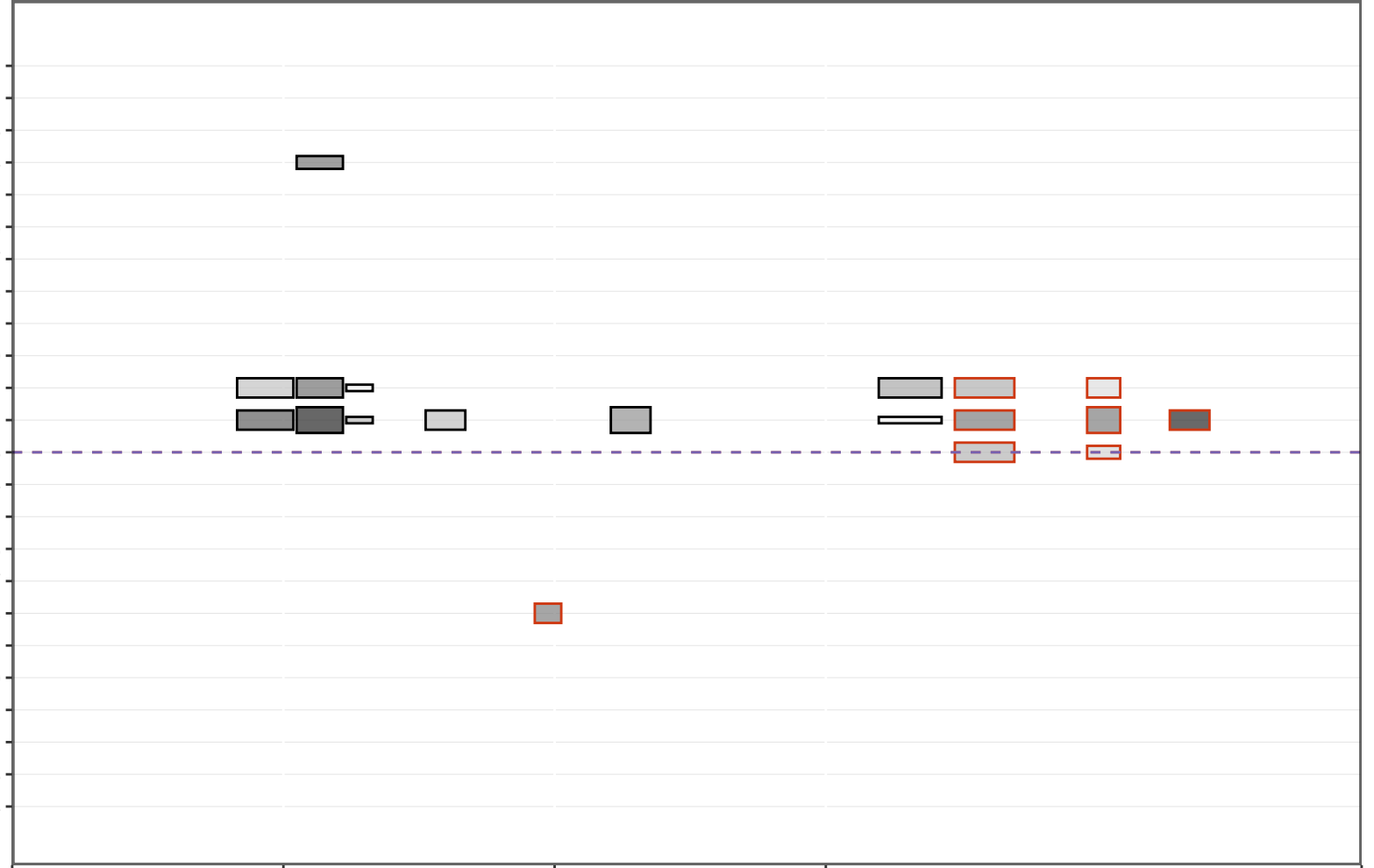
MW indication



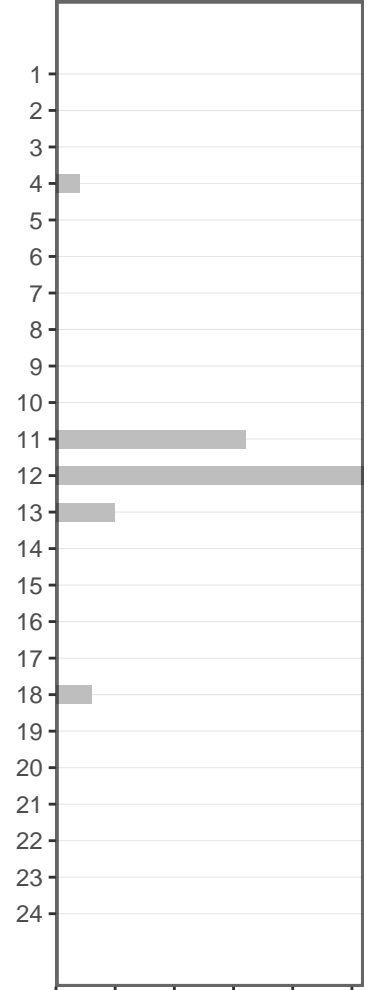
Molecular weight



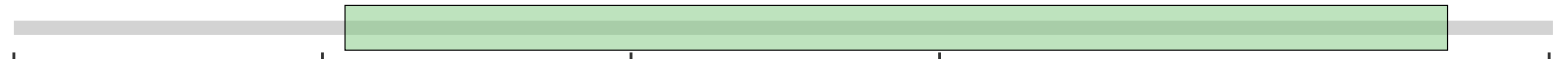
Gel Slice



Protein length

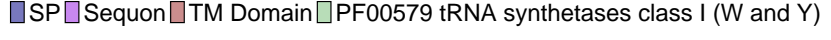


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DIARRNKLPRILRCQIMGRBEQDELTAQIFVPCMGKADIFLKKADIGQLGMDQRKVVNVLAREYGDGDKRKNKPLSHMLPLGLGEGGEMKSKDPS66IYMEDEEAEVNLKRRKAFQFPKVAEKVPCLEKRYVYLPWFNEFKIERIAENGDKTYWFEELAADYESGKLPADLKPALSKAANKILQPVDRHFRNDGKAKDLMKRVRKSRVTR

NbL01g01760.1 ras-related_protein_RABG3f [MW = 23 kDa]

No. of times detected



log(intensity)



Values from



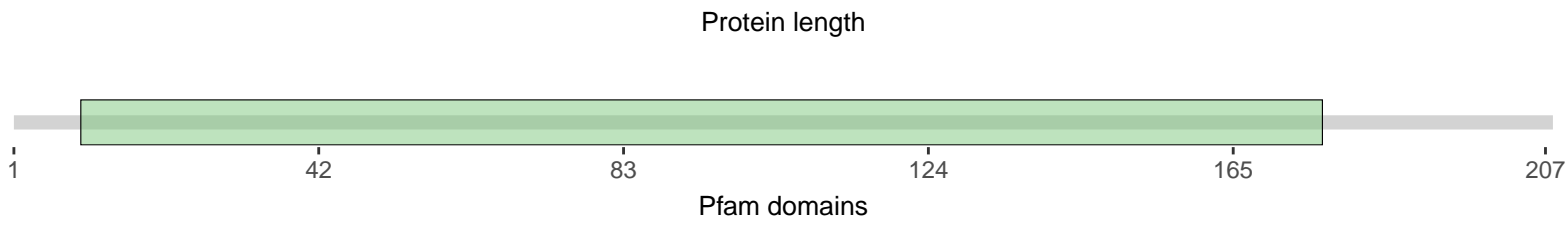
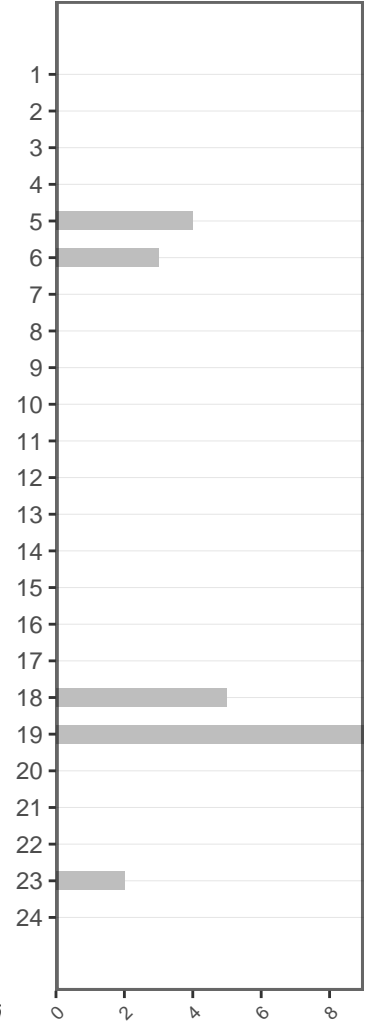
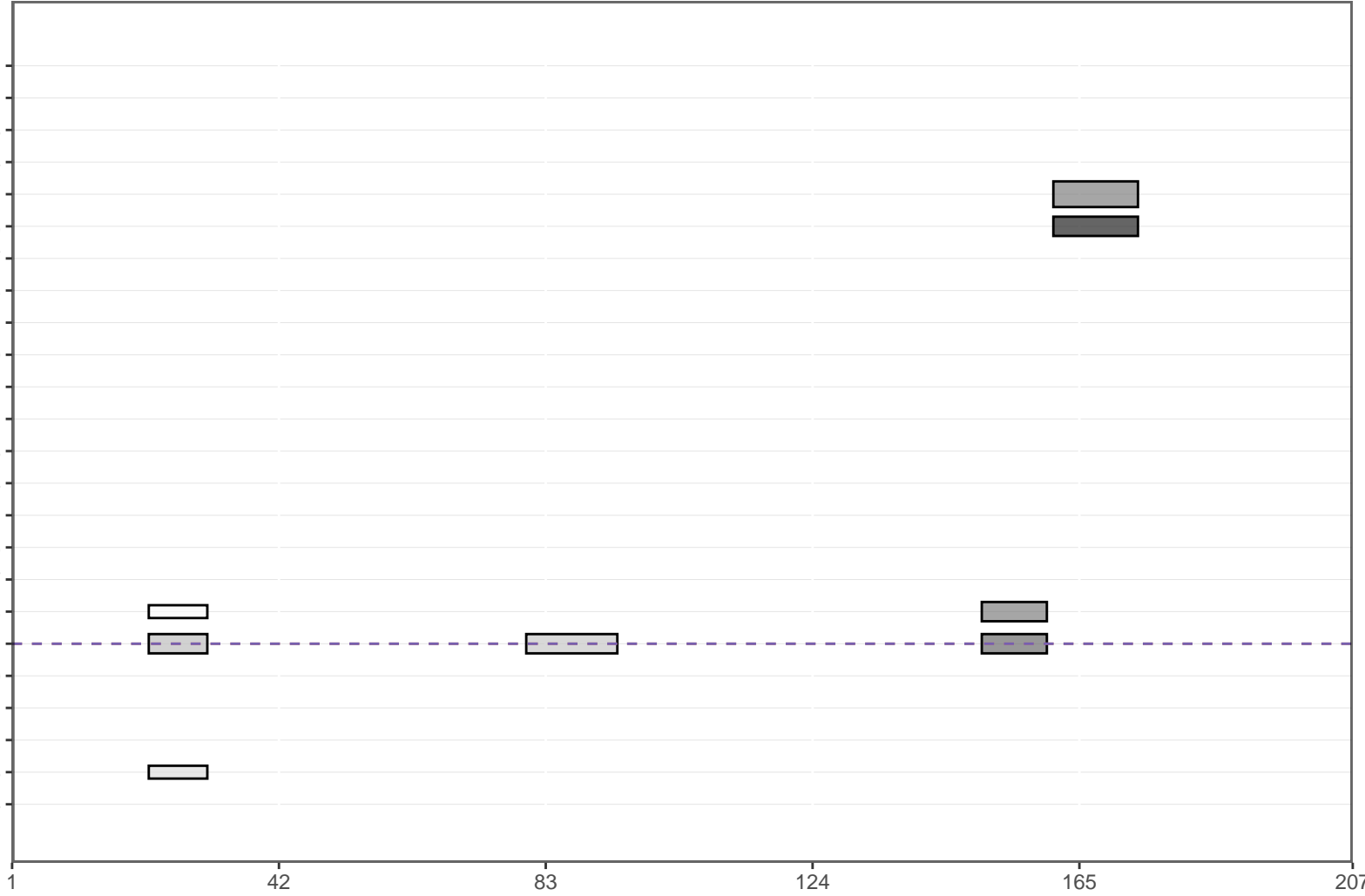
MW indication



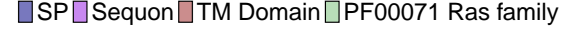
Molecular weight



Gel Slice



Pfam Description



Protein sequence:

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NbL01g01740.1 coatomer_subunit_gamma [MW = 98.06 kDa]

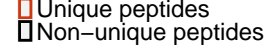
No. of times detected



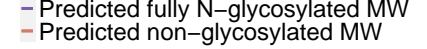
log(intensity)



Values from



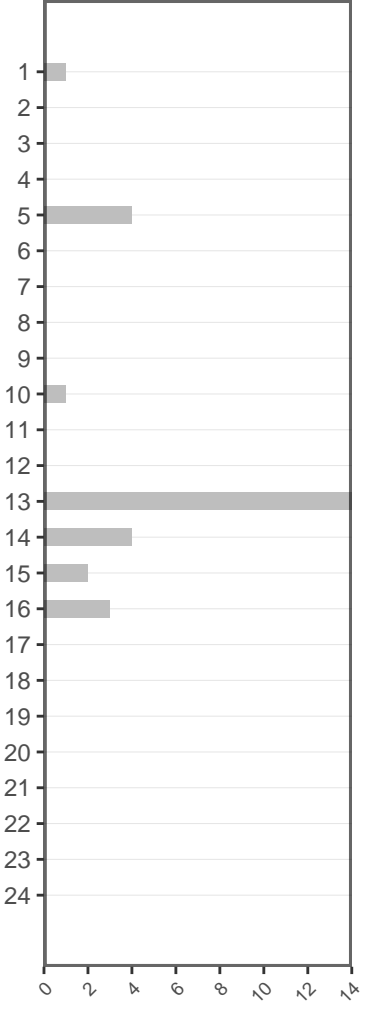
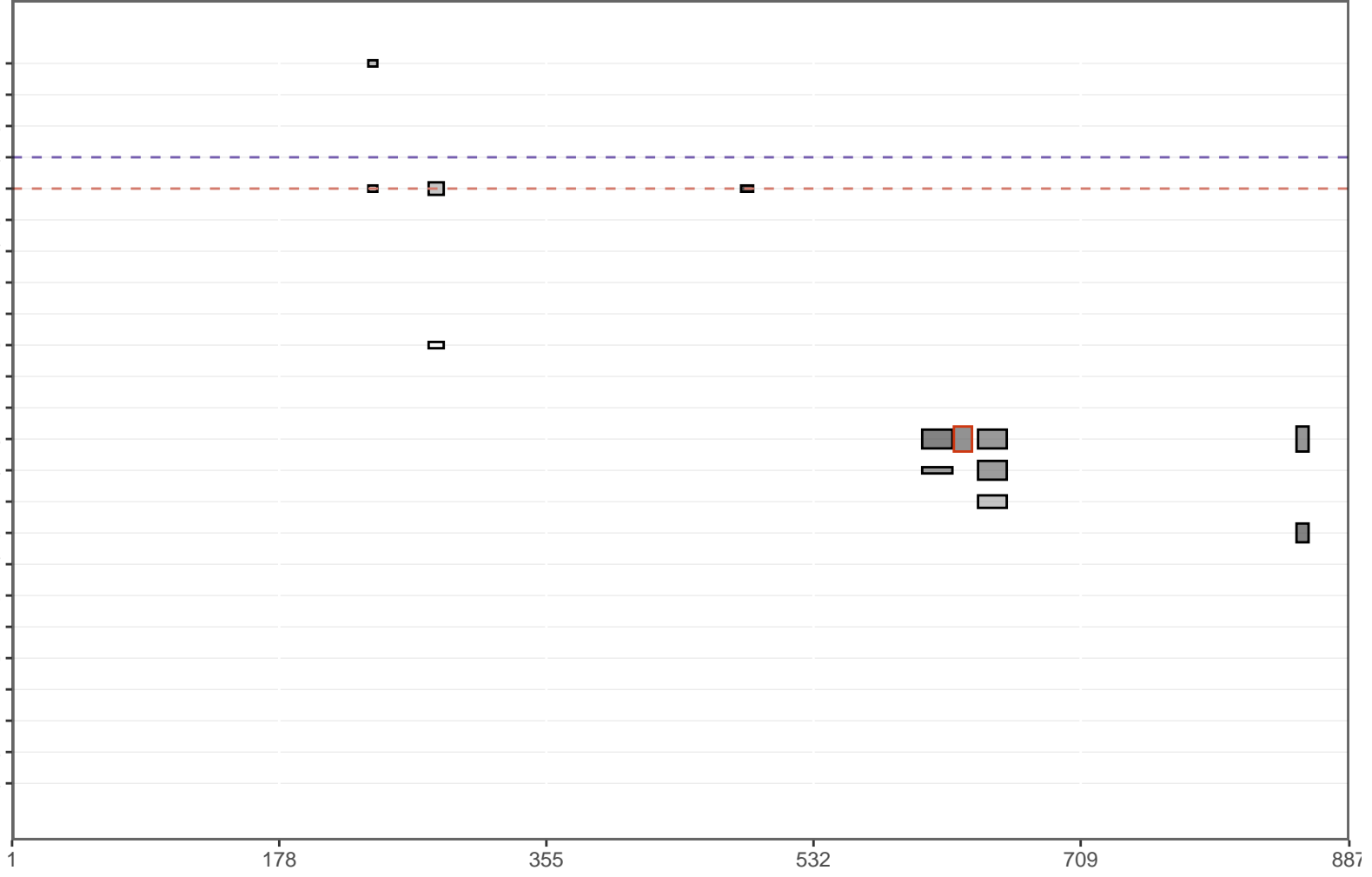
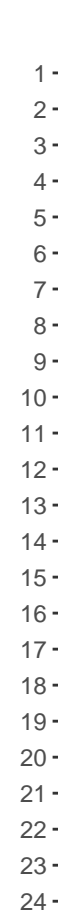
MW indication



Molecular weight



Gel Slice



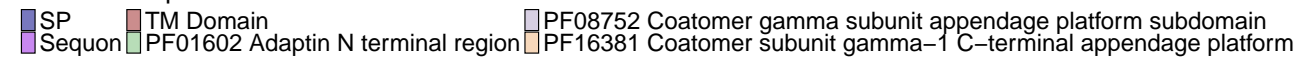
Protein length

Peptide counts over 4 repeats



Pfam domains

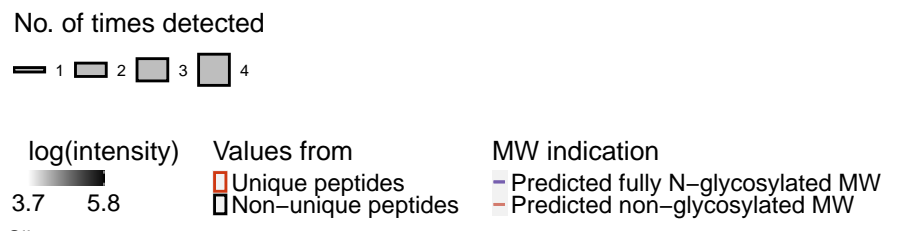
Pfam Description



Protein sequence:

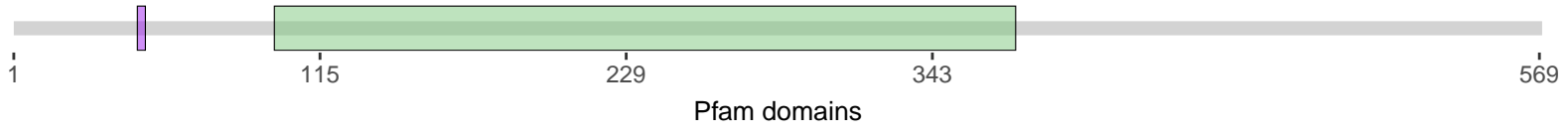
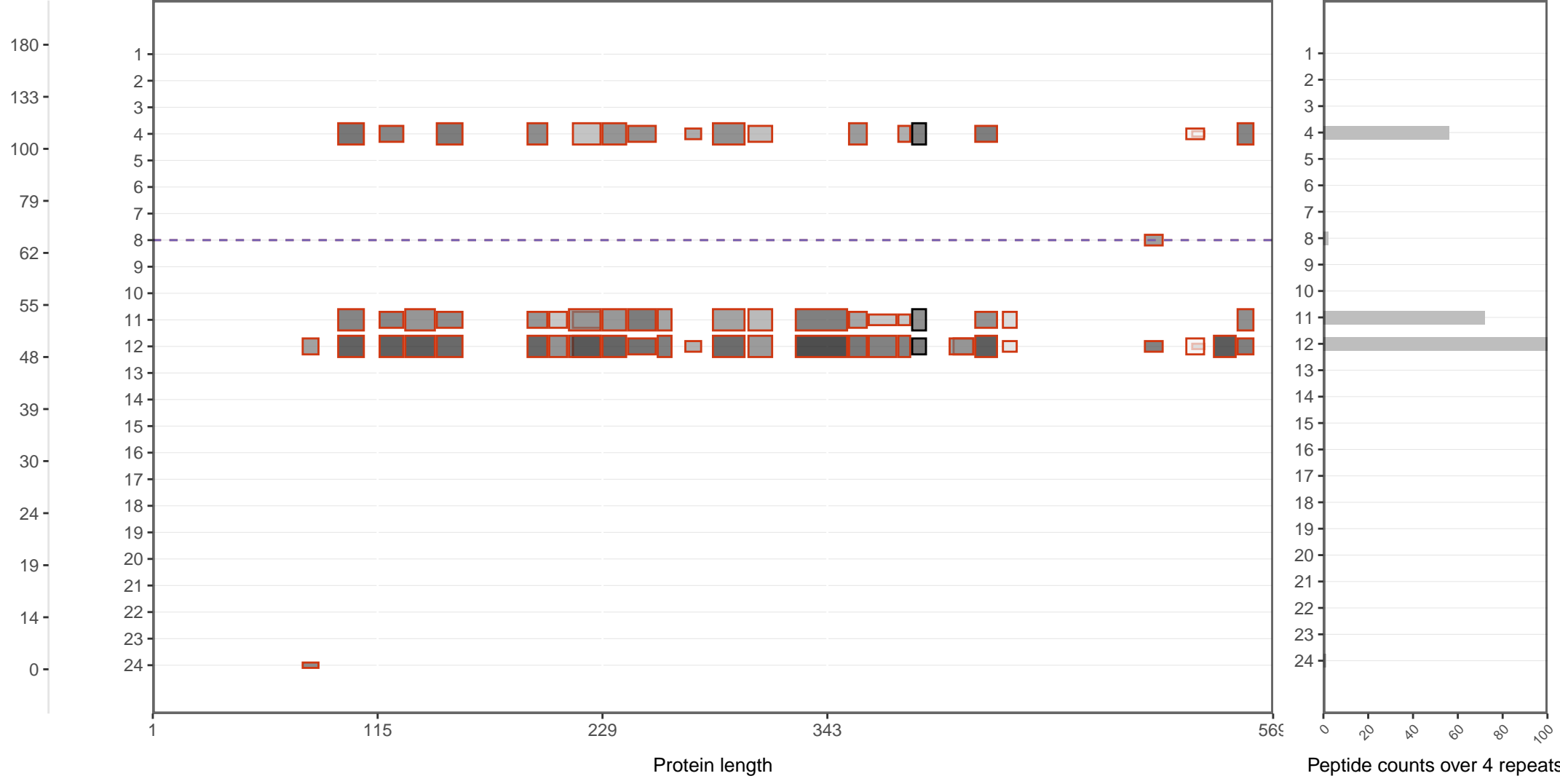
AKEGGLLHLCFEIEDGEFTYLSGHLFLGNEGPKTSQPKVIRVYVNRVILENATVRSASVSLAKFGALVDLSLKRIFVLLKROLFDSDDEVDRATLVLNLTGGDGAIVETDEEVEKFLFGLGVPVLTNLETSLKNYKPEEFPDHSVPEKVKSGQPLSEKKAQKPKTGLAAPPVAPTSTVDAYERLLSSPEFTSFGKLFKSAAPVELTEAETEWWVNVKHNFDNHVFGVNGTNTIPEQLLENVTVVDASEAEFSEVASKPLKGLPVDTGDTFAVEKPEGVPAVQKFS

NbL01g01540.1 glucose-1-phosphate_adenylyltransferase_large_subunit_1 [MW = 63.07 kDa]



Molecular weight

Gel Slice



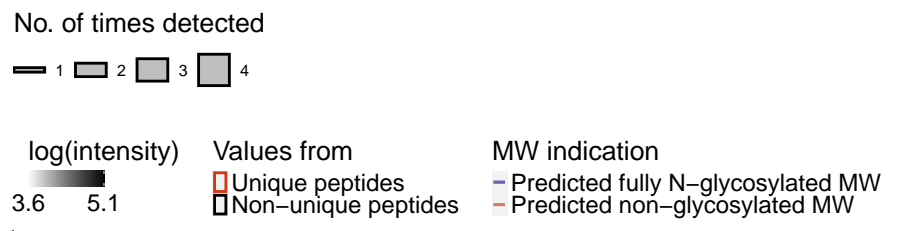
Pfam Description

- SP
- Sequon
- TM Domain
- PF00483 Nucleotidyl transferase

Protein sequence:

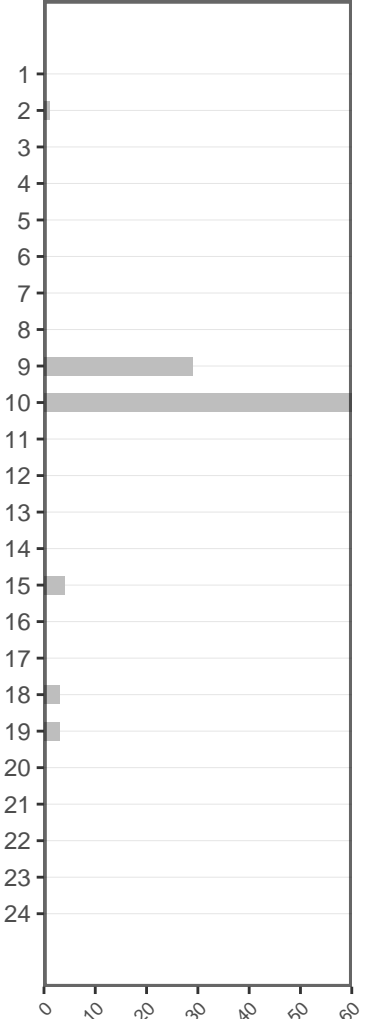
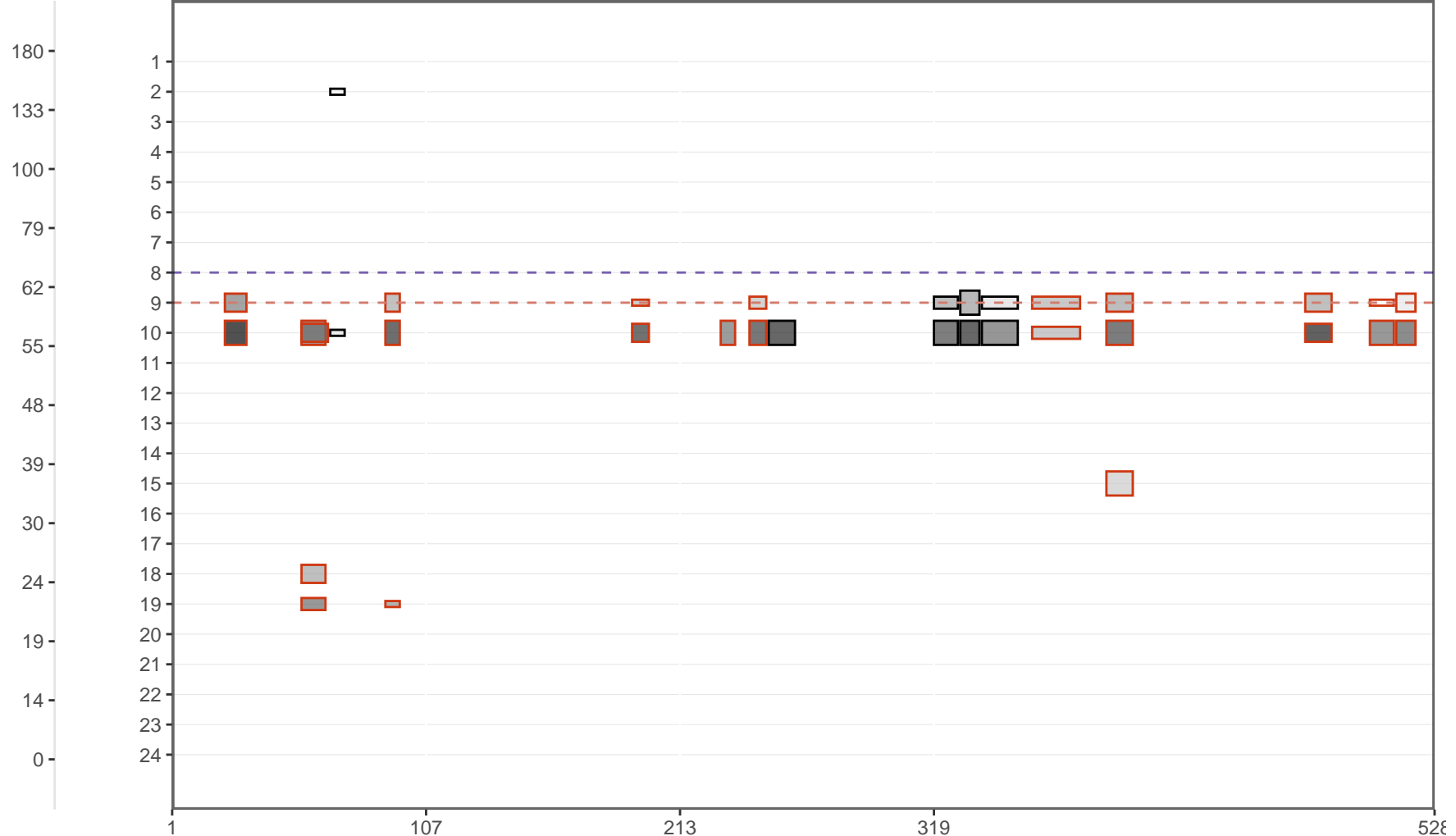
GRVYQFAEKPKGFDLKKAMQVDTFLGLSPQEAKRSPYASMGVYVFKTDVLLKLLKWRVPTANDFQSEHPLAINEHNVGAYFRDQWEDIGTKSFYDANLALTAESGPKFEFYDKPTPTYSRFLPPTKIDNCKIKDAISHGFLREGSDVHSVIGERLRDQGVELKVCMLNGLYFLSMQNAFFLHFLVRYGPTQTFVLLPFQDGLMGGADYVQTESEIASLAEKGKVPMSGIGENTKIRNCHDKNAKIGKQVWIMNKDGVKEADRPEDGFYRAGLTVAEKATKDGTVI*

NbL01g01530.1 bifunctional_dihydrofolate_reductase-thymidylate_synthase-like [MW = 58.93 kDa]



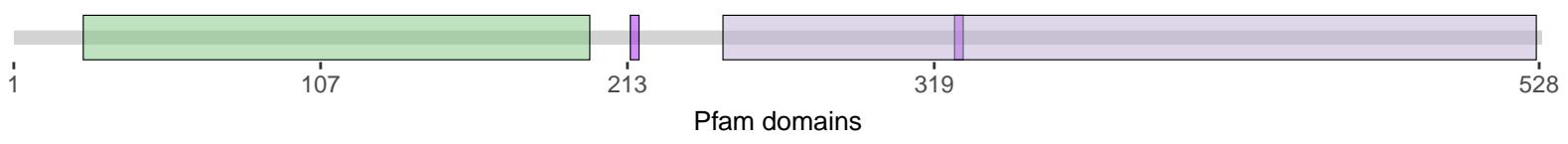
Molecular weight

Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam Description
 SP Sequon TM Domain PF00186 Dihydrofolate reductase PF00303 Thymidylate synthase

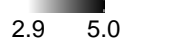
Protein sequence:
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NbL01g01390.1 SUMO-activating_enzyme_subunit_2 [MW = 72.67 kDa]

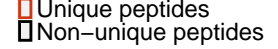
No. of times detected



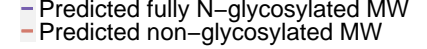
log(intensity)



Values from



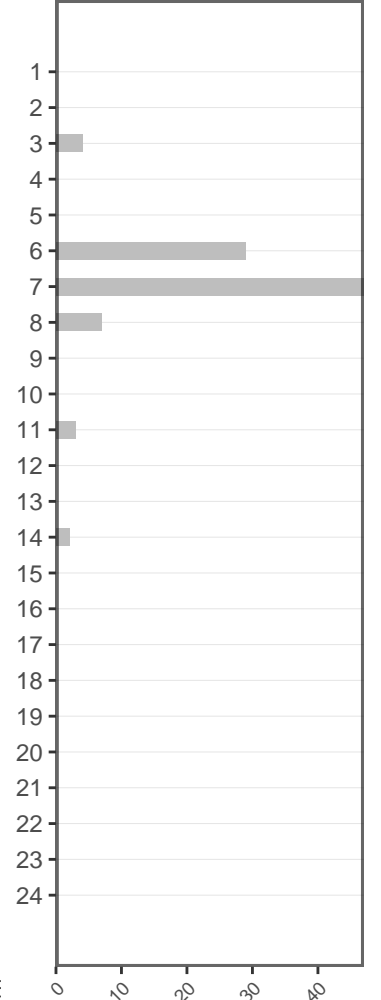
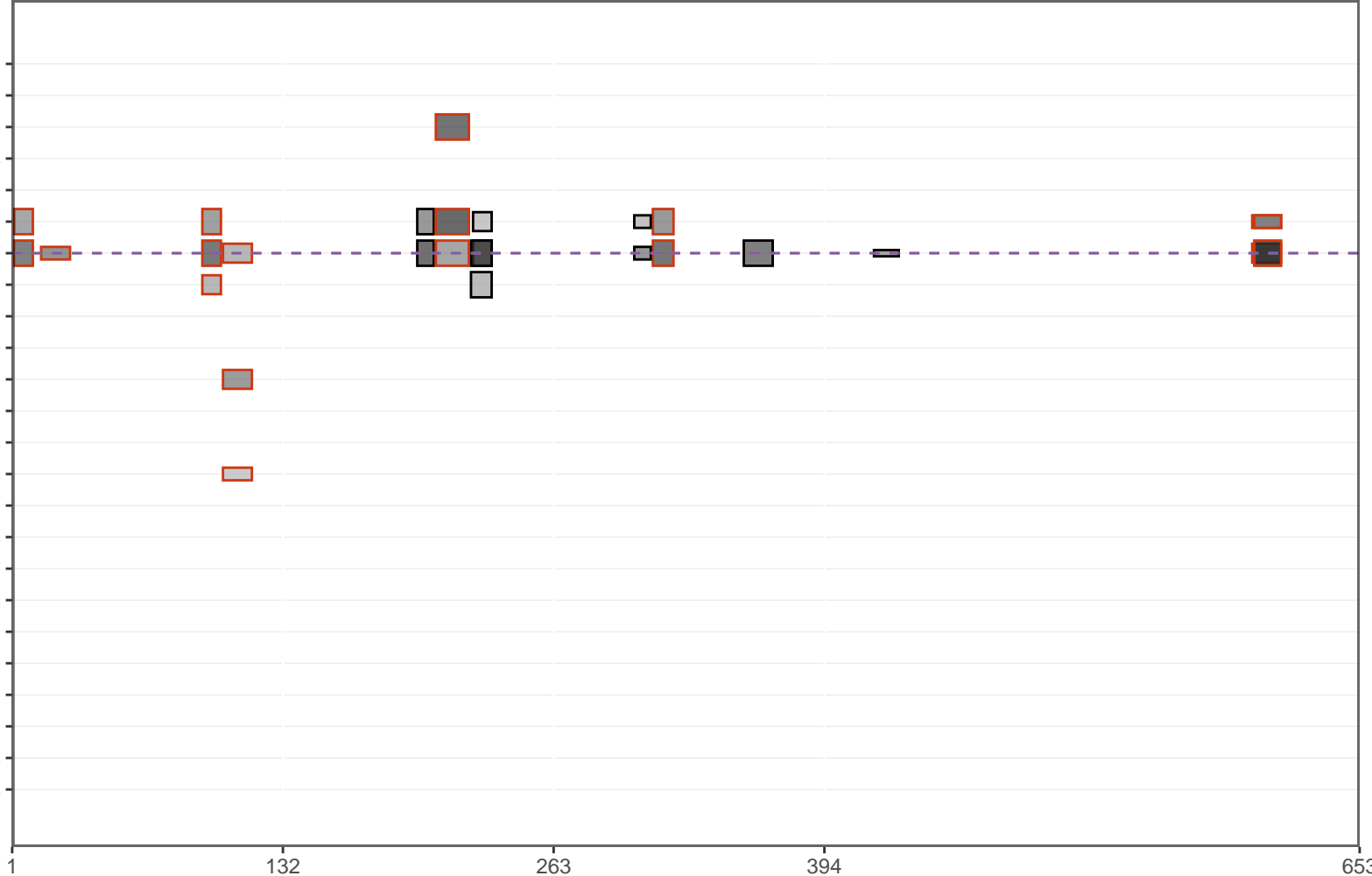
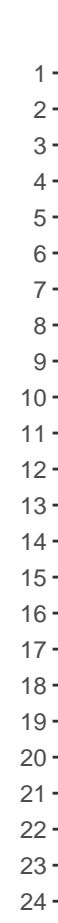
MW indication



Molecular weight



Gel Slice



Protein length

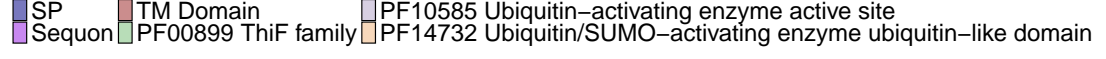


Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

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NbL01g01340.1 probable_receptor_protein_kinase_TMK1 [MW – SP = 98.75 kDa]

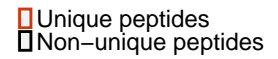
No. of times detected



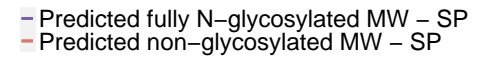
log(intensity)



Values from



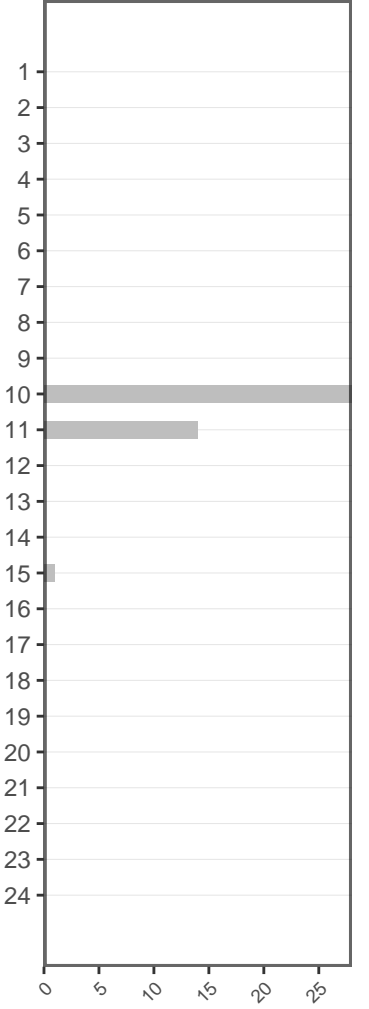
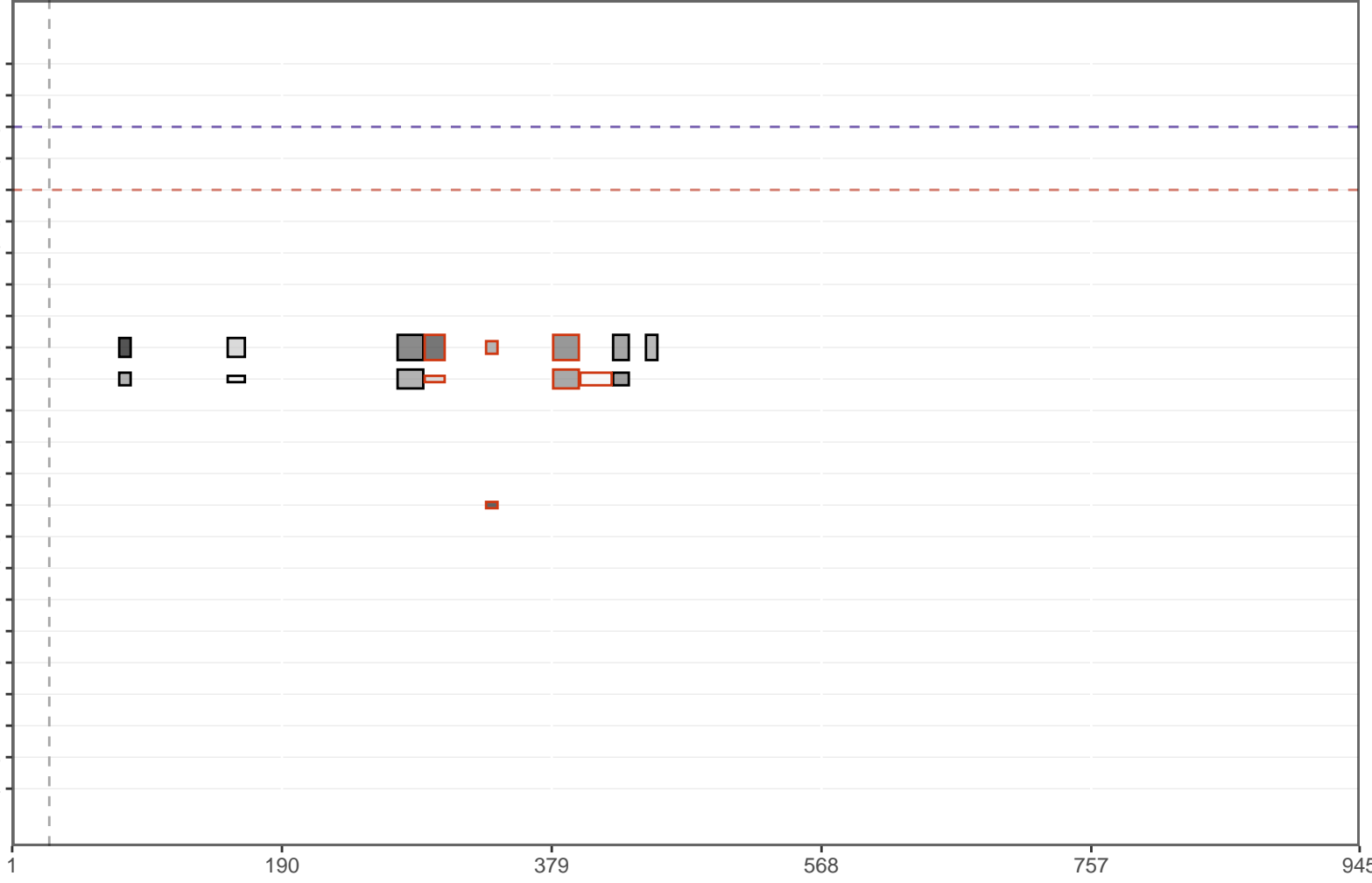
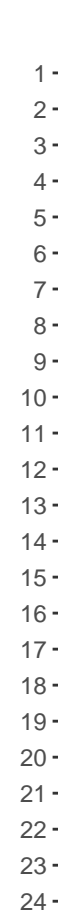
MW indication



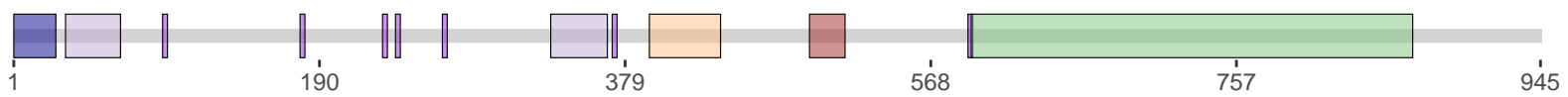
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

STPSGSTPGSSDGGGGGGTHATGGKKSSTGVAVGVHGVGVCAAVVLAGLFLYGLYRTHKIKRSGRVGSPHTVVIHPHSHSGSDGDAWKTAGSRVNGDGGSSAPGDLHVEAGNMVHSIQVLRDVTNFKKWLGRGGFGTYVYKGLHDGTHKMAVWRMEGGVMTKGLDEFKSEIATVTRHRHLVTLGVLGDNEIRLLVVEYMPQGTLSRVLFNWKKEGLKPLEWTRRLTALDVARGVYHLHGLAQQGDFIHRDLKPSKILLGGDMRAKVAQDFGLVRLAFDQGA!

NbL01g01330.1 beta-galactosidase_3-like [MW - SP = 81.74 kDa]

No. of times detected



log(intensity)



Values from



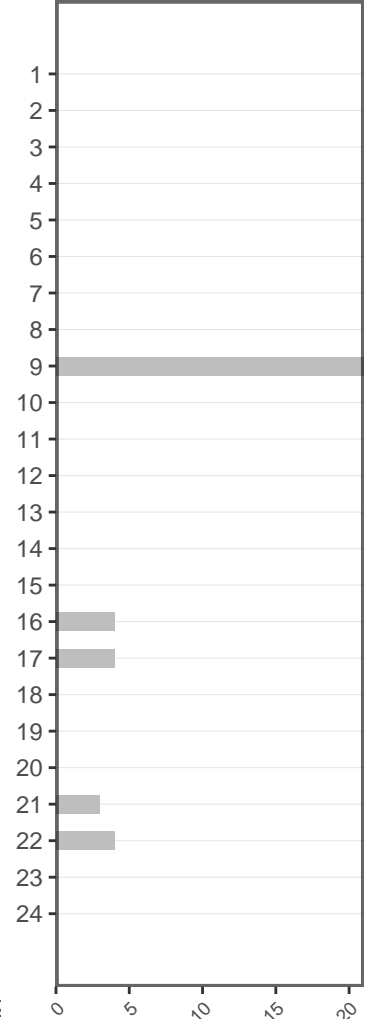
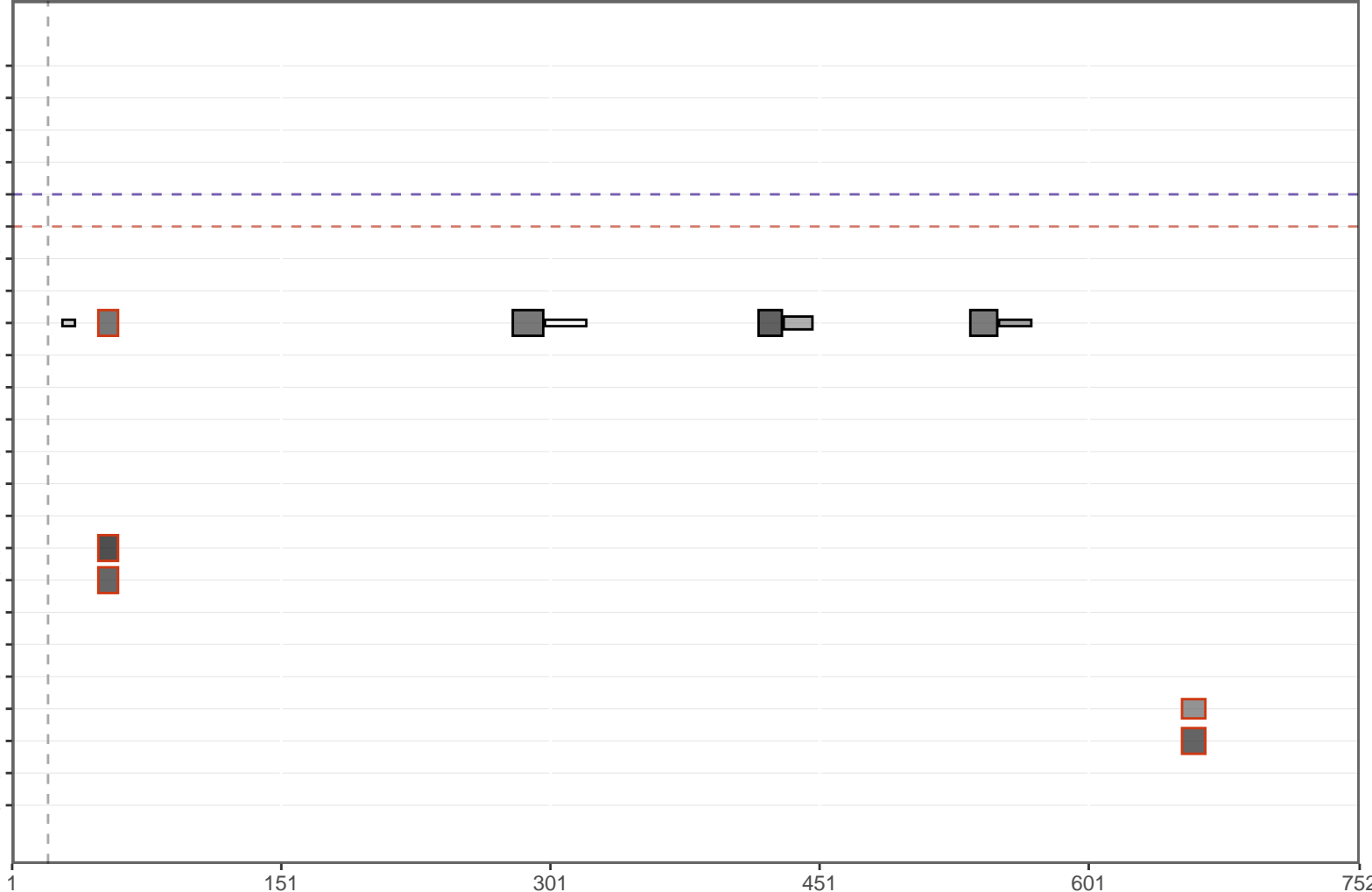
MW indication



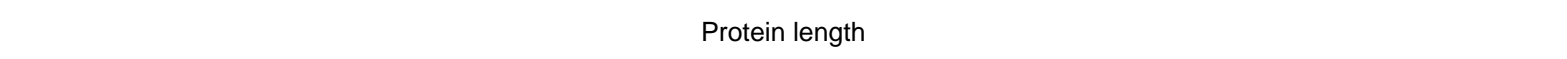
Molecular weight



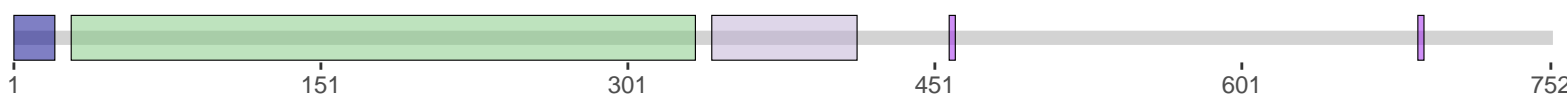
Gel Slice



Protein length

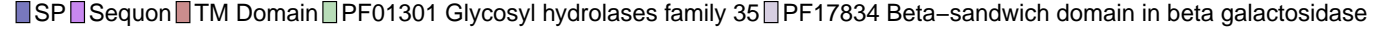


Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ISGICAAFLNFIHLTSPNIVTFRHSHYDLPPWBSILPDDKKNVYNTARVGVKTSNAGMLPFTNQLRITWETFSBEDVSTIDADSKLTVGLLEQLNVTFRDTSQDYLWYTTVEISSAESFLHRGHILTLTVDSAGHALVFNIGRLSGGVYGNRENRRVYFTTGGVNLHAGINRISLLEWVGLPNNGARVETWSTGVLGPVLLHGLDKGPRDLSWQKWSYQVWVFLVLMMLHLRGLTTLNVAFAQVGLRGEAMNLDSPNVAADWVGGSLIARQRPLTWYKYVYTNAPRGSD

NbL01g01310.1 purple_acid_phosphatase_2-like [MW - SP = 50.88 kDa]

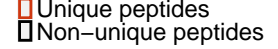
No. of times detected



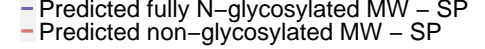
log(intensity)



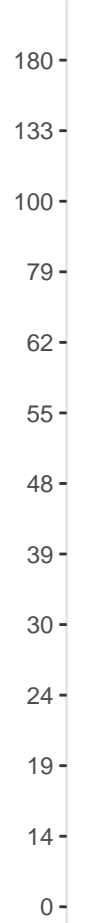
Values from



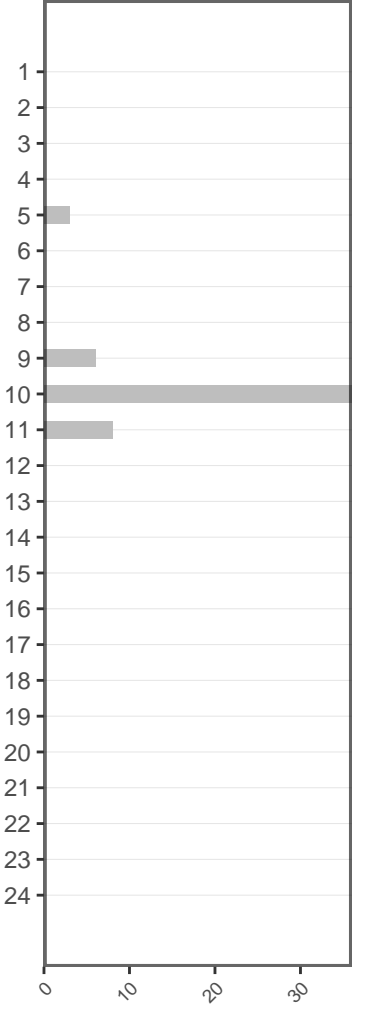
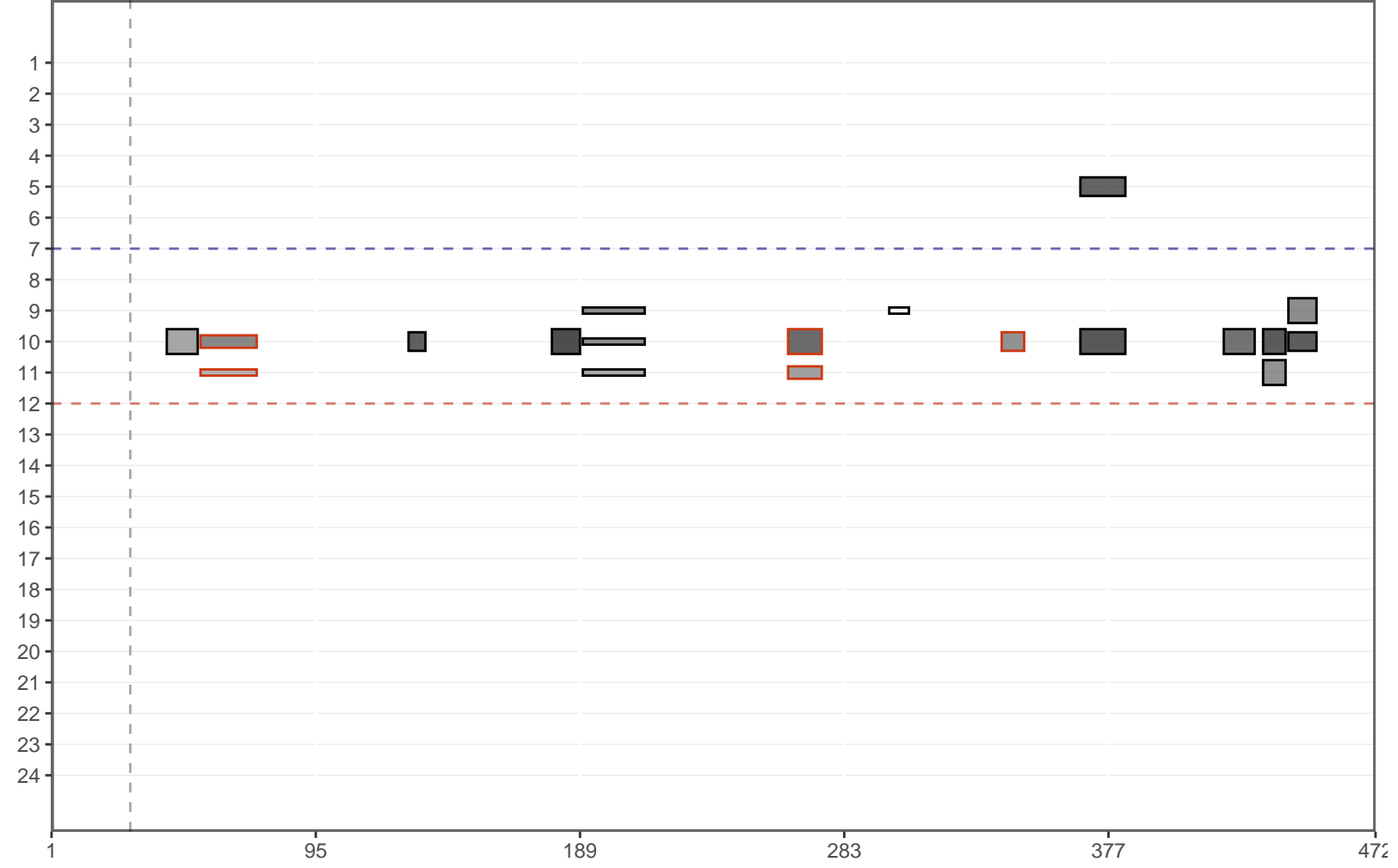
MW indication



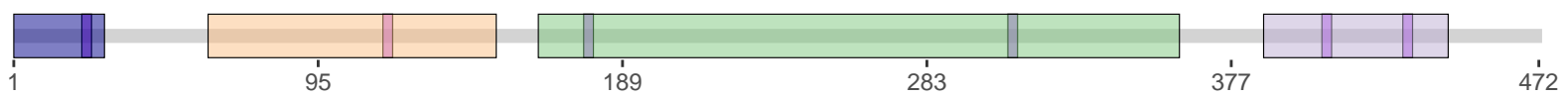
Molecular weight



Gel Slice



Protein length



Pfam domains

Pfam Description



Protein sequence:

STAYQPIWVTAQNIHEIDFAPEIGETKPKFKPVTIRHYHVPYRASDSTPLWYGVKRASAVHILSSVSAVKGKYPQKWLLEELPKVNRTEPWLVLVHSPWVNYHNYHMEGETMRVMEYEPWFKYKVDVIFAGHHAVERTERISNWAYNVNGECTPIRDSAPYVTHGGDGNLEGLATNMTPEPQVYSAFREAQFGHATLAKNRTHAYVSWIRNDDGYVWEADKIWNINRINPVDSEMALVQ

NbL01g01290.1 cysteine_protease_RD19A-like [MW - SP = 38.07 kDa]

No. of times detected



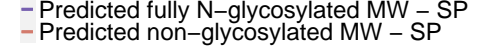
log(intensity)



Values from



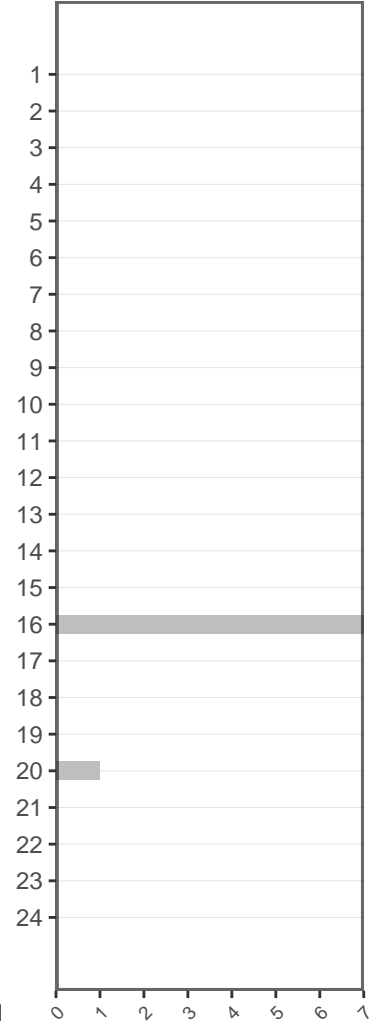
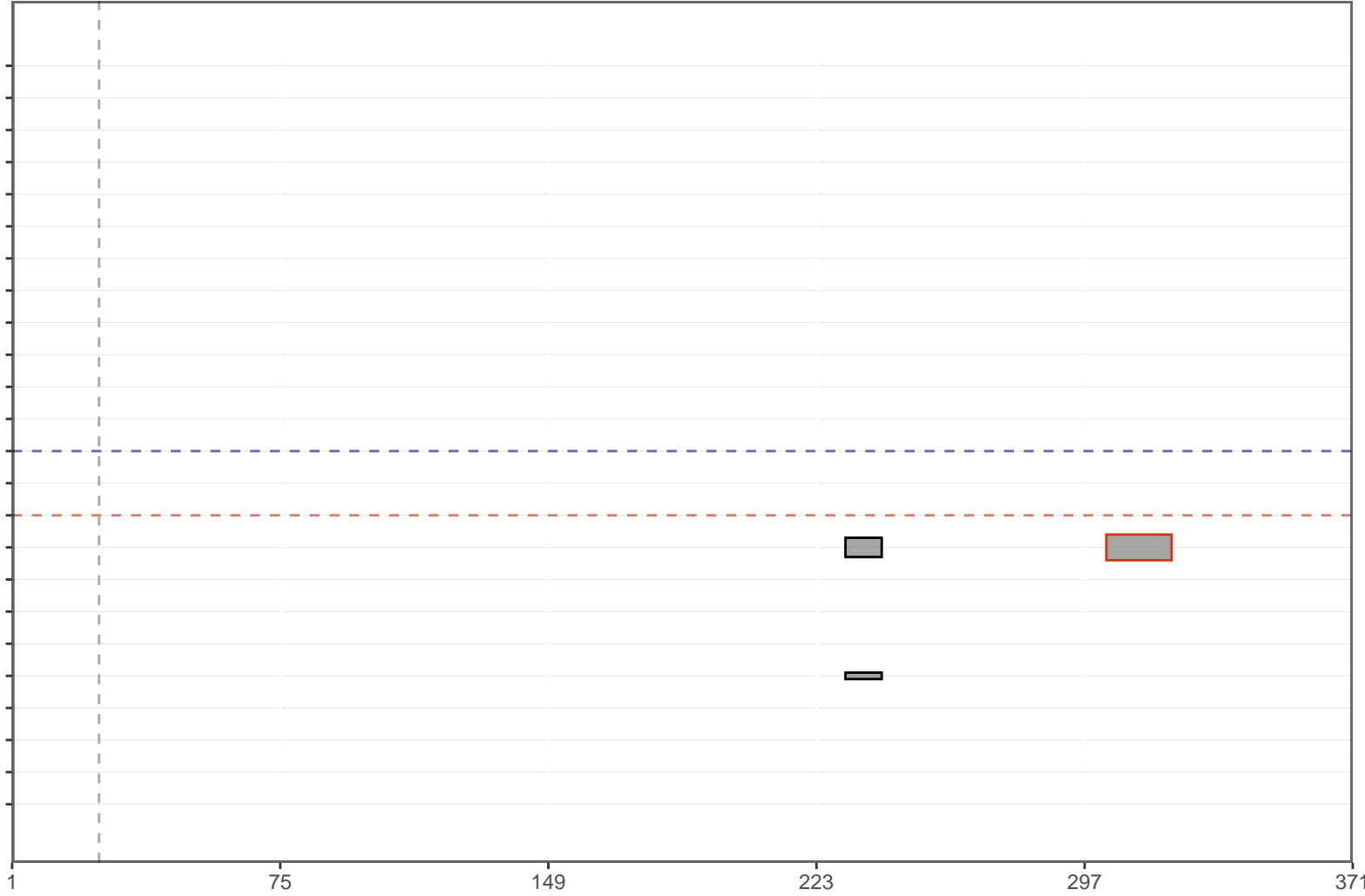
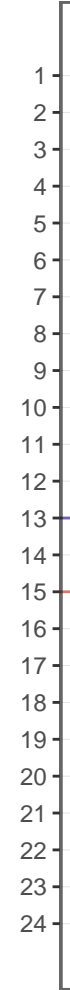
MW indication



Molecular weight



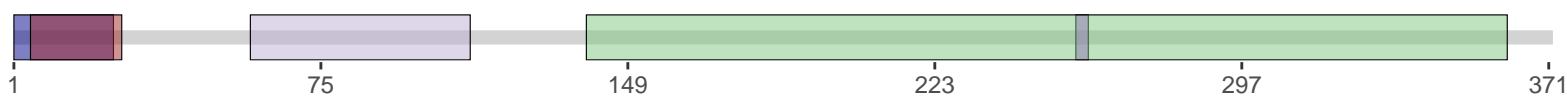
Gel Slice



Protein length

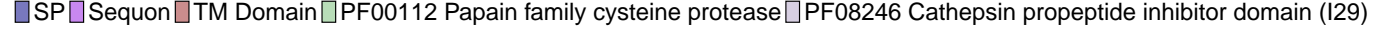


Peptide counts over 4 repeats



Pfam domains

Pfam Description

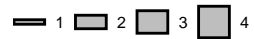


Protein sequence:

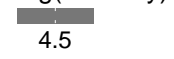
SAANYLSTGKLRRLSEGLVDDGHEGDPPEEKDSCDAGCNGGLMNSAFETYLKAGSLMREEDPYPTGDRGTCKFDNTKAAKVAKVFVSVLDEEGHAAALVKNKGLPAAVAINAVFMDTYVGGVSGPFIHCKNLDHGVALLVGYGTGFSPIRMKEKPYVWIKNSWGEKVGNGYKIKGRGRNVGVDGSMVSTVAAVSTSSH

NbL01g01280.1 V-type_proton_ATPase_subunit_a2-like [MW = 92.56 kDa]

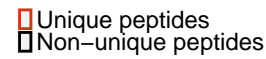
No. of times detected



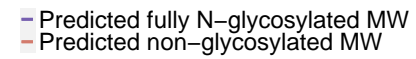
log(intensity)



Values from



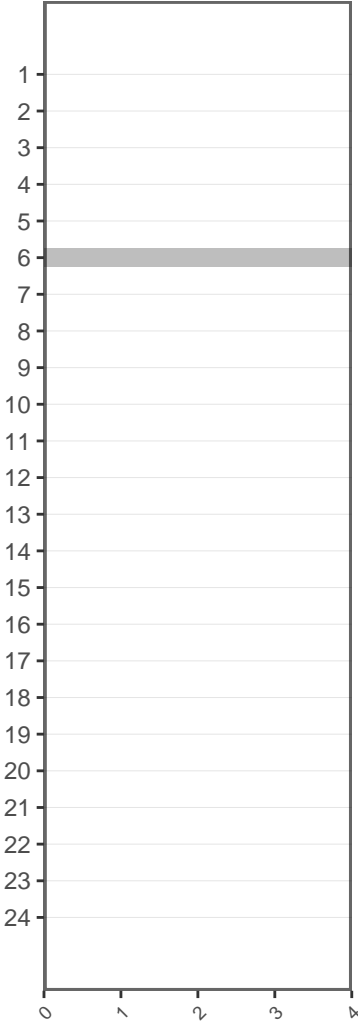
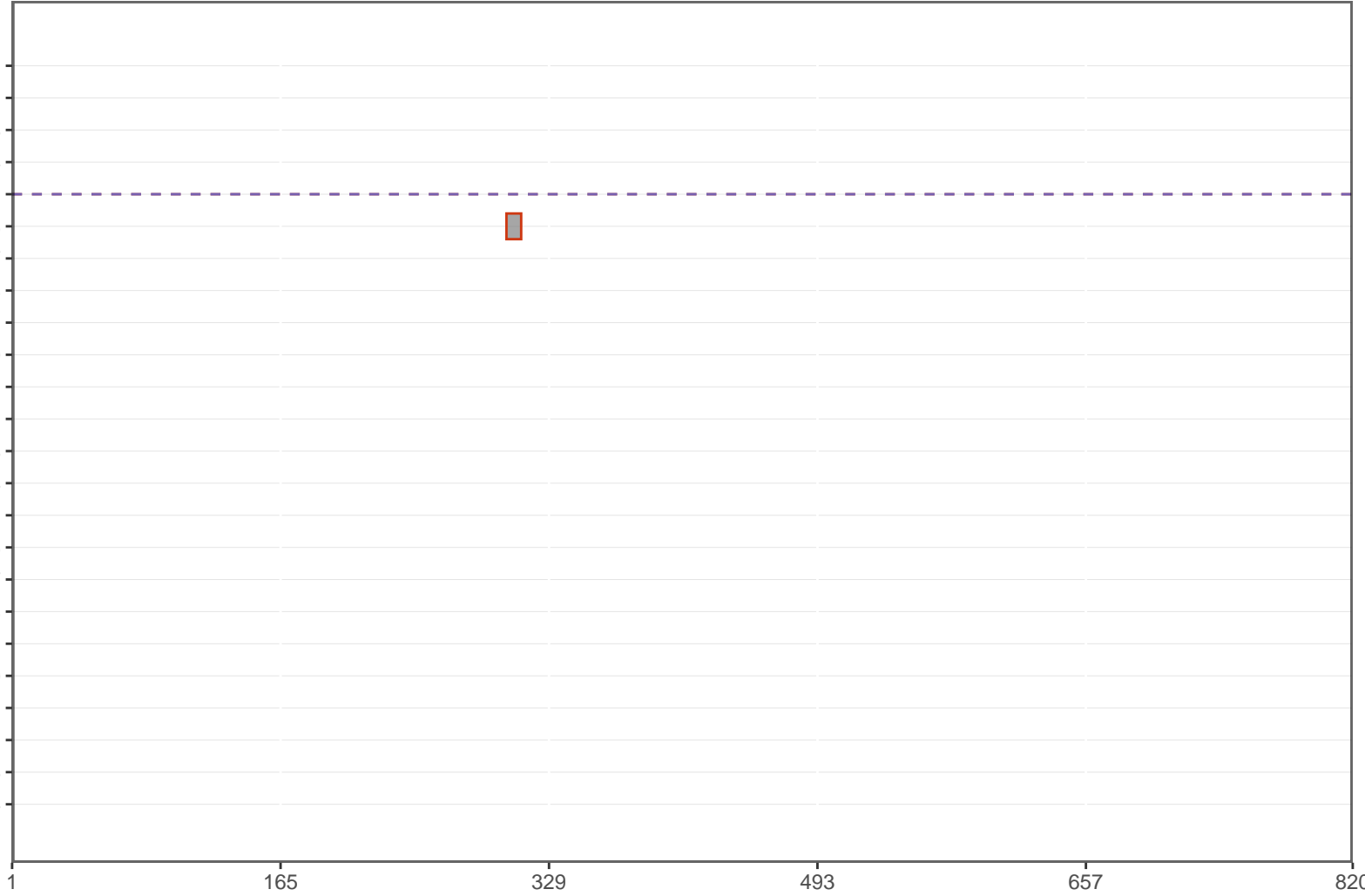
MW indication



Molecular weight

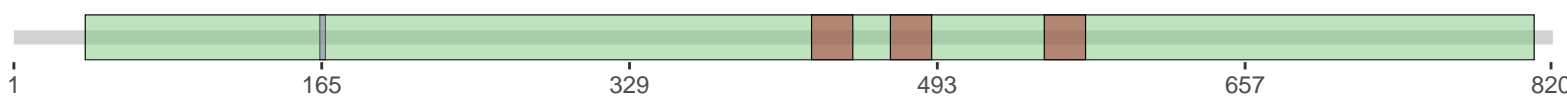


Gel Slice



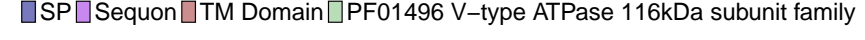
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

SSFOEIVDAYGVAKYQGANFGVYVITFPFLFAVFMFGDWHGHCILLATLFLIREKILSSQKLGDMEMTFGGRYVIFMMSLFSIVTGLYNEFFSVPFELFGRSAYGCRDPRDSTAGLKVPRDTPYFGVDPWVHGTRSELPLVNLKMKMKGILLGVADQNLGFLSFFNALFRSGINWQGFYQIFLNALFGYLEVLIWVWGTGSKADLYHVMYMFSLPTDELGENLFAQOKTTQVLLFRSALVWPWMLFKPFLKQKQHERHGGQVYALGEAEESLLVSSDSE

NbL01g01250.1 uncharacterized_LOC104113315 [MW – SP = 39.6 kDa]

No. of times detected



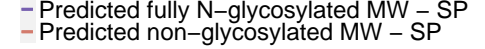
log(intensity)



Values from



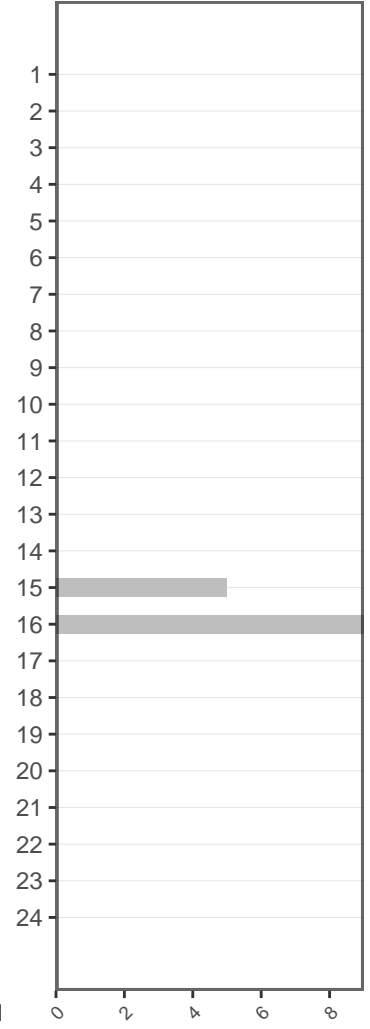
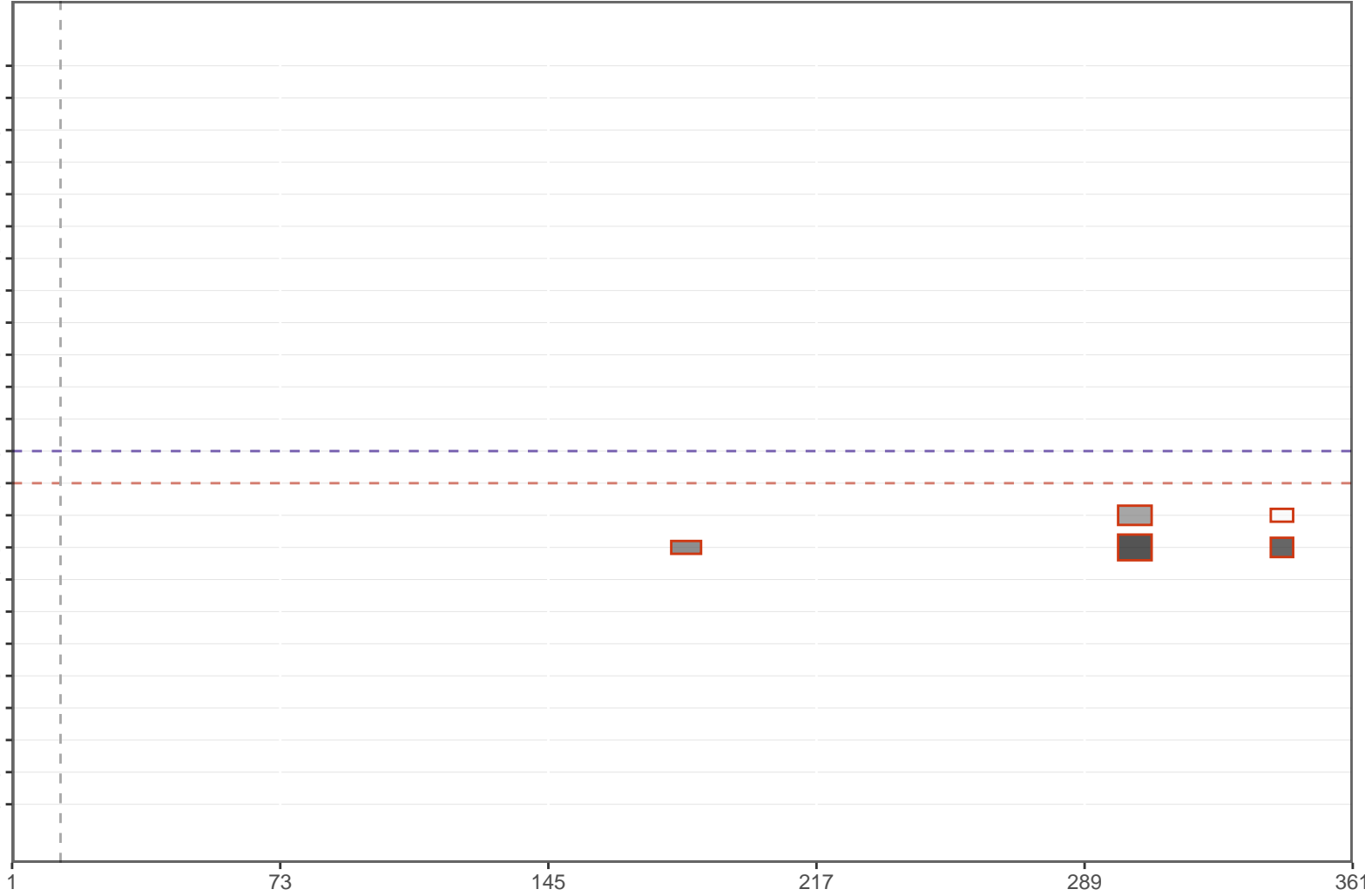
MW indication



Molecular weight



Gel Slice



Protein length

Pfam domains

Pfam Description
 SP Sequon TM Domain

Protein sequence:

RLVHKTKKIDSDSTVLAIALEPVLVEVEEHWVPRDPEALSLMEKEINQREGEGLDEGFLSEVNAQLRQAANKDGGKPLGEMLQKVLGLVSRVLSKRSVYAKKNEVLSKAEQFLSEKIKAPEEEVWNLIDGMYGKGDISPEELVYWKIKRMERTLIRTEGGYQQRVLEIYLVKGLGEARSLIKVLDG

NbL01g01210.1 uncharacterized_LOC104090505 [MW = 28.12 kDa]

No. of times detected



log(intensity)



Values from



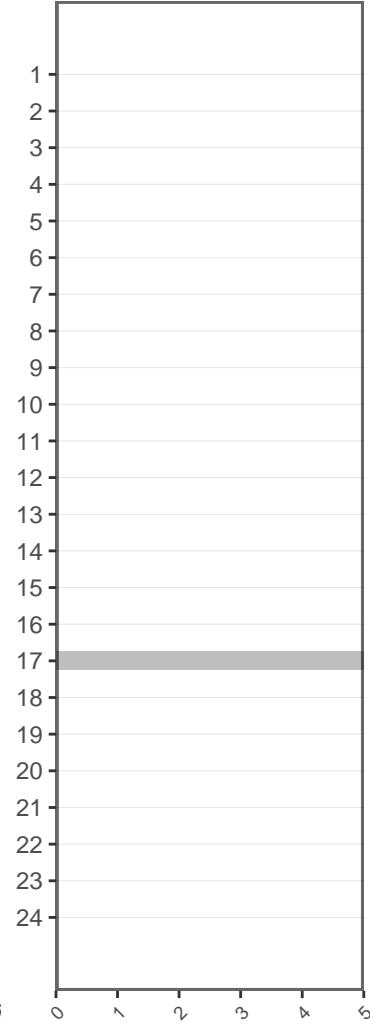
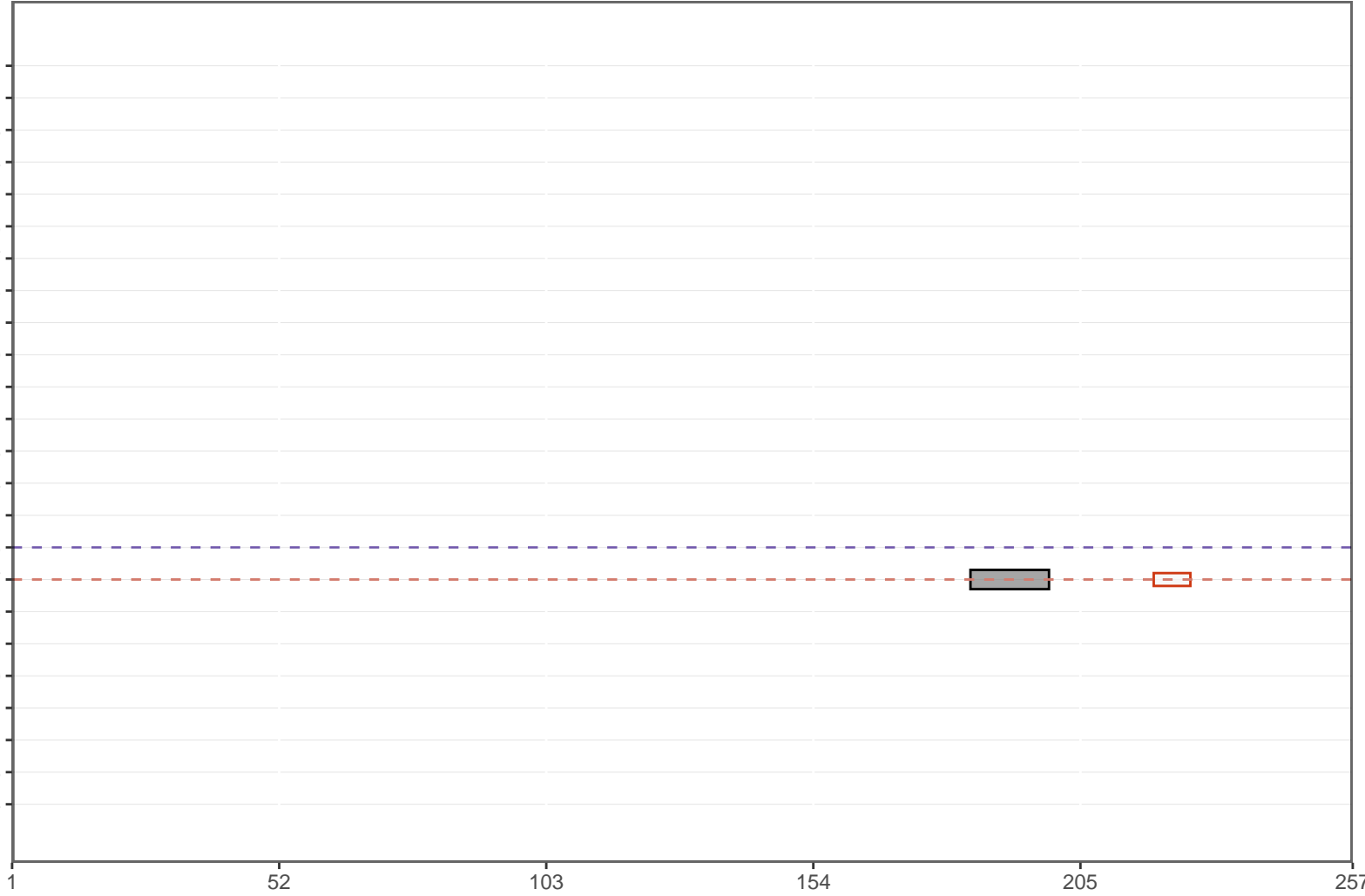
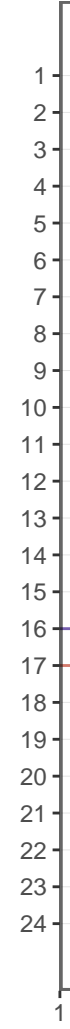
MW indication



Molecular weight

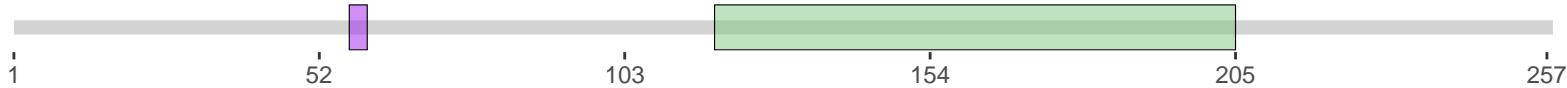


Gel Slice



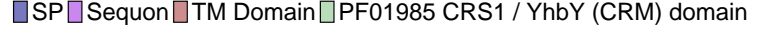
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SLTVKKEKELASVHSLGKRLKSGGVKSGVTSVFAFDLTELAEANELLKLIKHGTGPGGELDDVVKHLEETAGSVVVGQIGRTVLYRPSVTKLKAEEKKKGQNAFMRRKGVAAKGGFESKGGVPKPVARGRGSSRV

NbL01g01190.1 40S_ribosomal_protein_S11 [MW = 17.68 kDa]

No. of times detected



log(intensity)



Values from



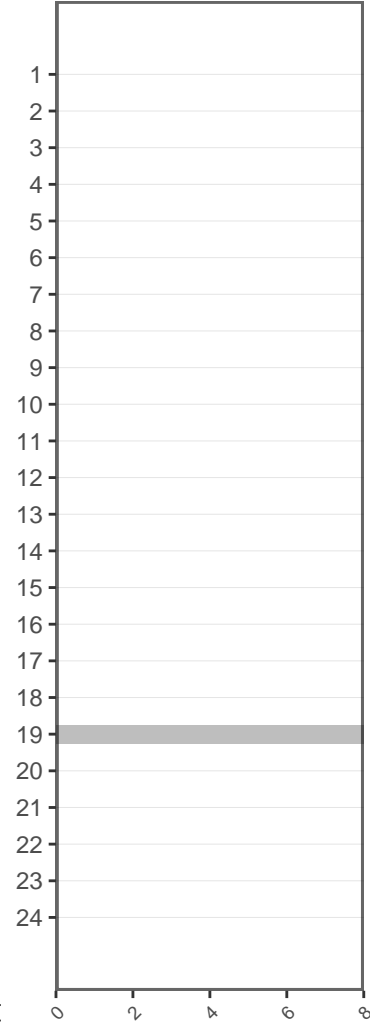
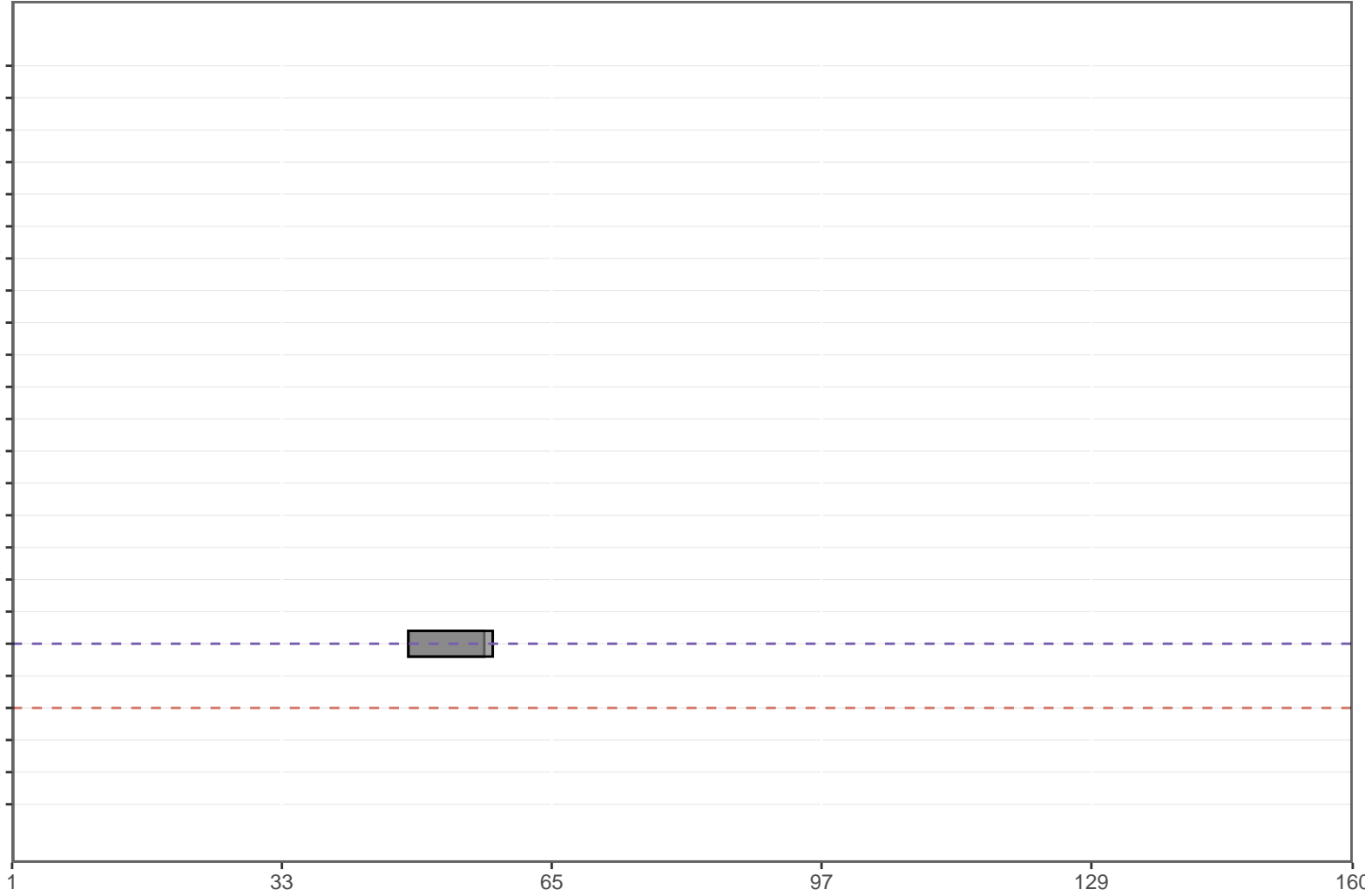
MW indication



Molecular weight

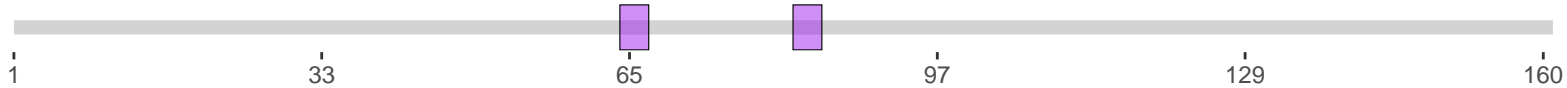


Gel Slice



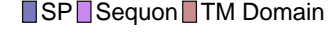
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

SIRGRILAGTCHSAMNRTIWRRLVHVKYQRYEKRHNSIPFHSIPCFRVRKEGDHVIIGDCRPLEKTVRFNLUKVIPIGSAAGGKKAFTM

NbL01g01130.1 fructose-bisphosphate_aldolase_1_chloroplastic-like [MW = 42.8 kDa]

No. of times detected



log(intensity)



Values from



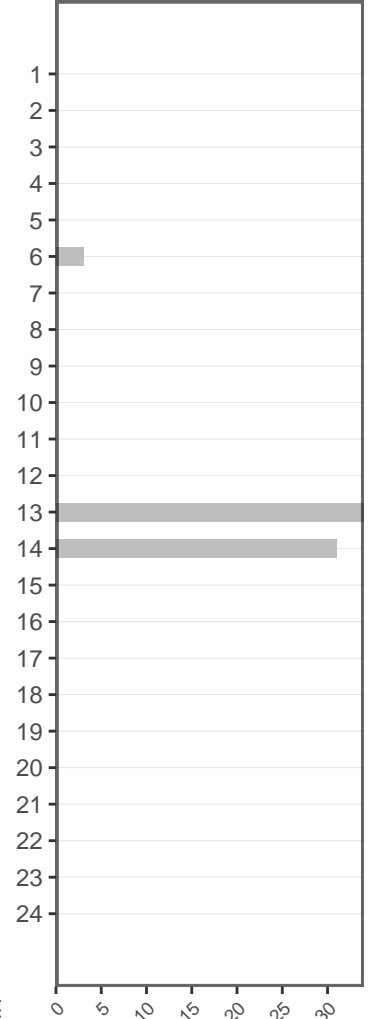
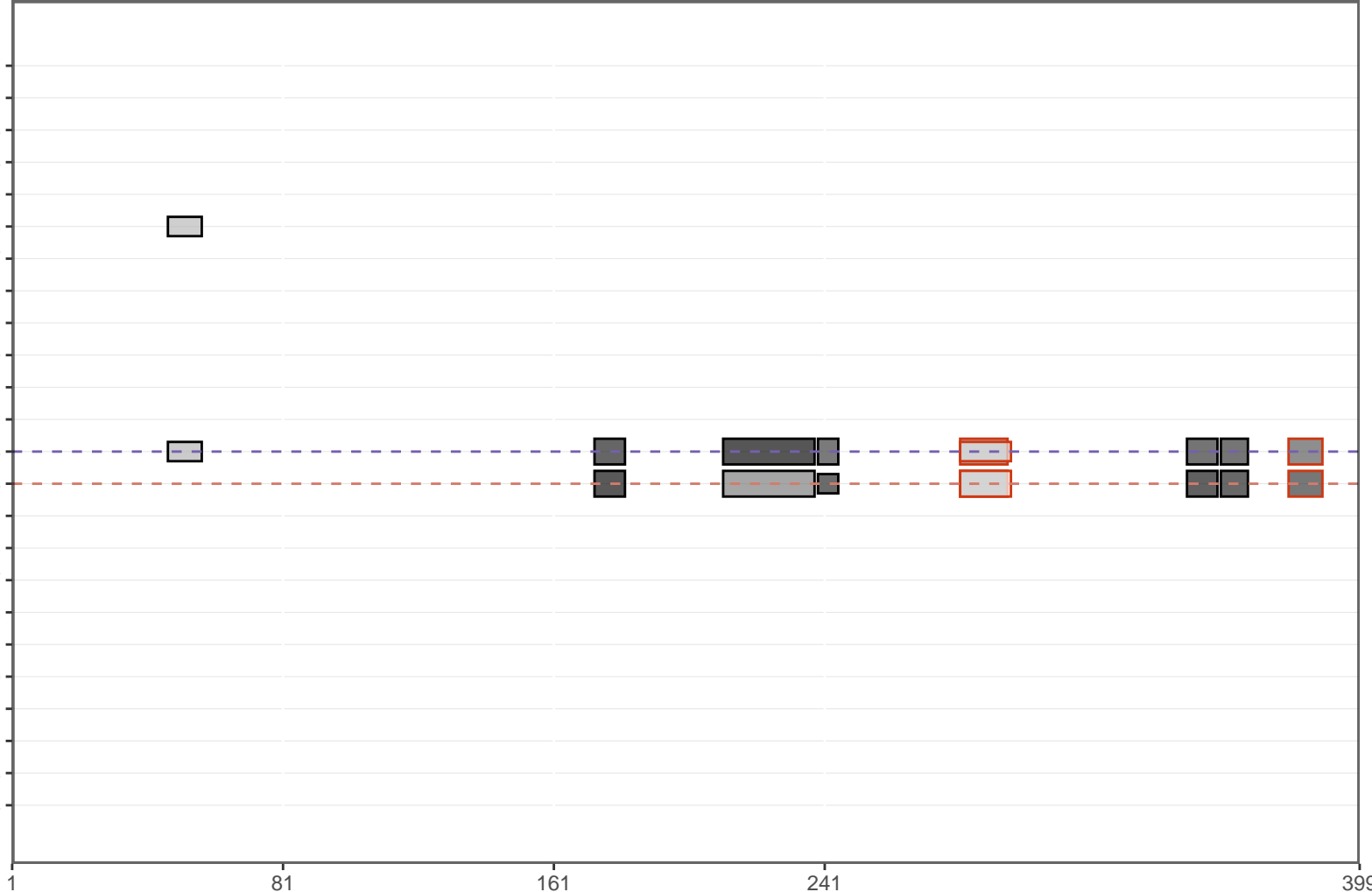
MW indication



Molecular weight

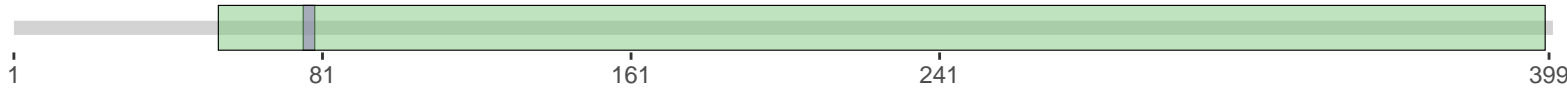


Gel Slice



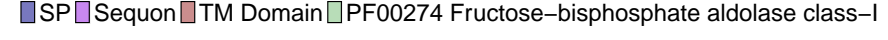
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

TVVSPYNGPSALAVKEAAWGLRVAASGGDGLVPIVEPELLEDGHEGIDRTFEVAGKWAEVFEVLAENNVMEFGLKPSMVTFGAECRDRTPQGVADYTLSELKRRIPPAVPGMFLSGGGSEVEATLNLNMMNGAFNPWHVFSFYARALQNTGLKTKTWGGPENKAAQDALLTRAKANSLADGLKYSGGESDEAKQGMFVKGVVY

NbL01g01040.1 NADP-dependent_D-sorbitol-6-phosphate_dehydrogenase-like [MW = 34.64 kDa]

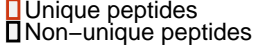
No. of times detected



log(intensity)



Values from



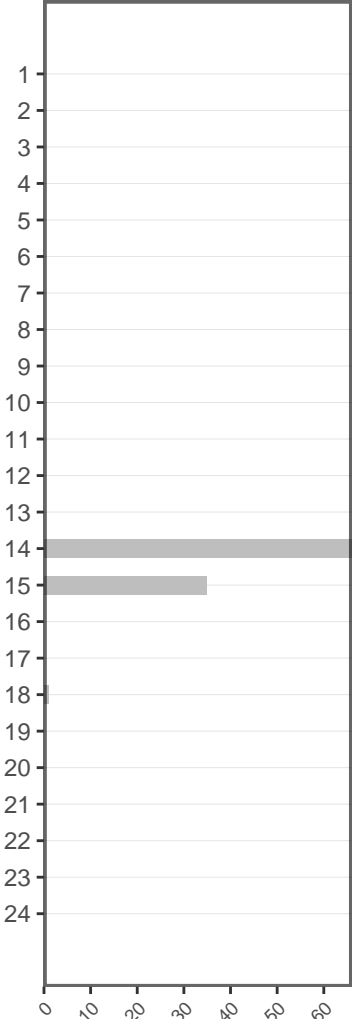
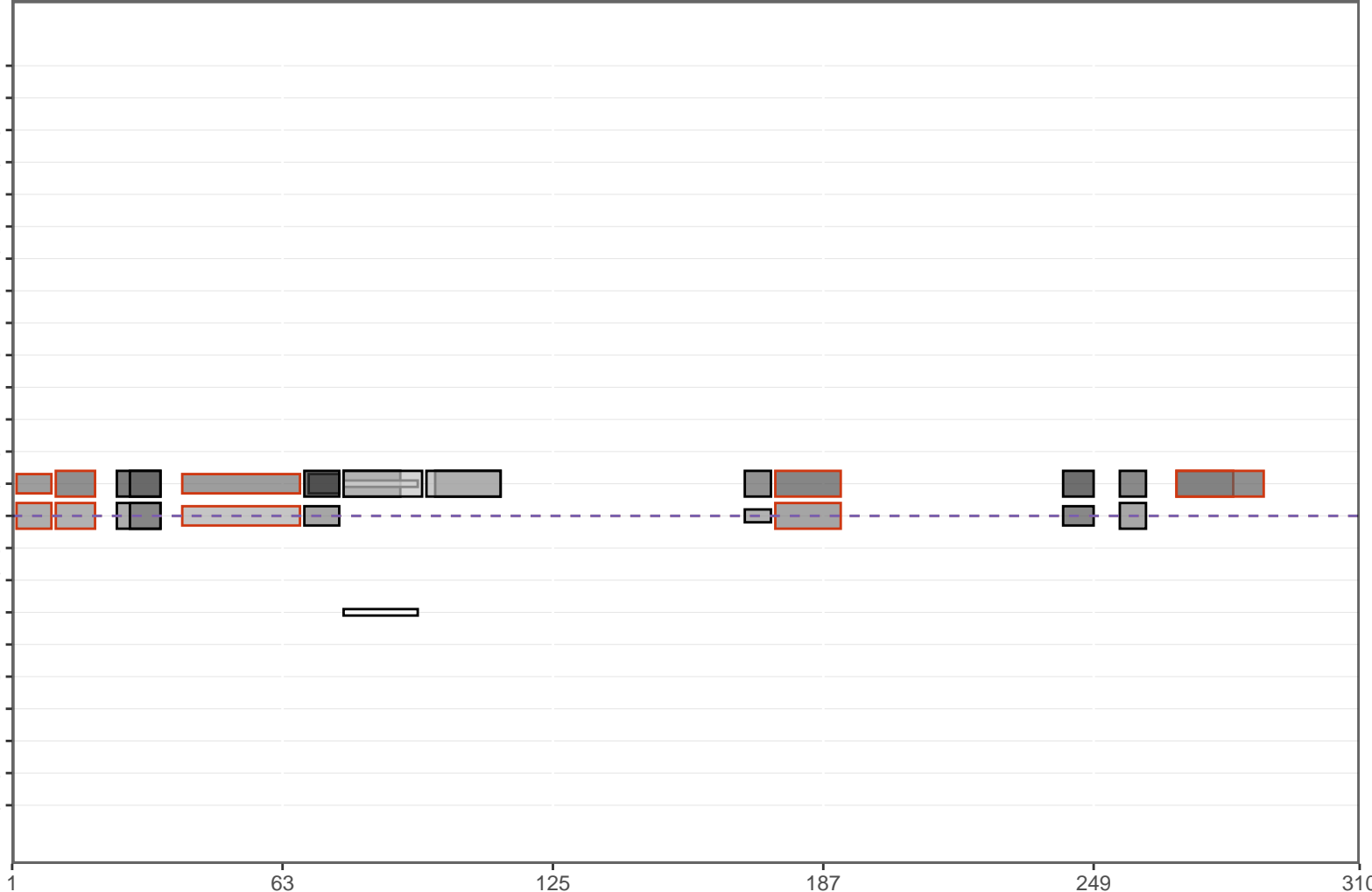
MW indication



Molecular weight

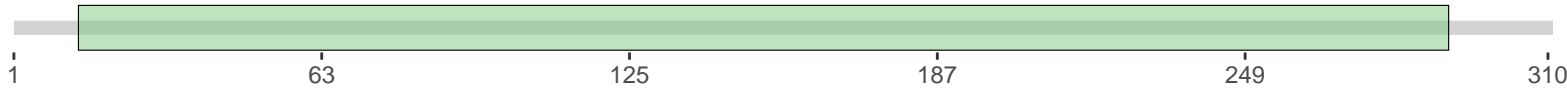


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IHAMENLSGLVHSGIGENYDFLTRDGLAVSKVKNQIETHPYFQRSLVKFGQKHGICVTAHTPLGGAANTEWFGVSGLEDPAKGLAEKWKTKVAGVYLRVWGIQRNTVYVPSKSLERLGENFNILDFELTKEDMDLVKSLDKYRTNGPAKFWGIDLV*

NbL01g01000.1 tRNA-dihydrouridine(47)_synthase_[NAD(P)(+)]-like [MW = 78.35 kDa]

No. of times detected



log(intensity)



Values from



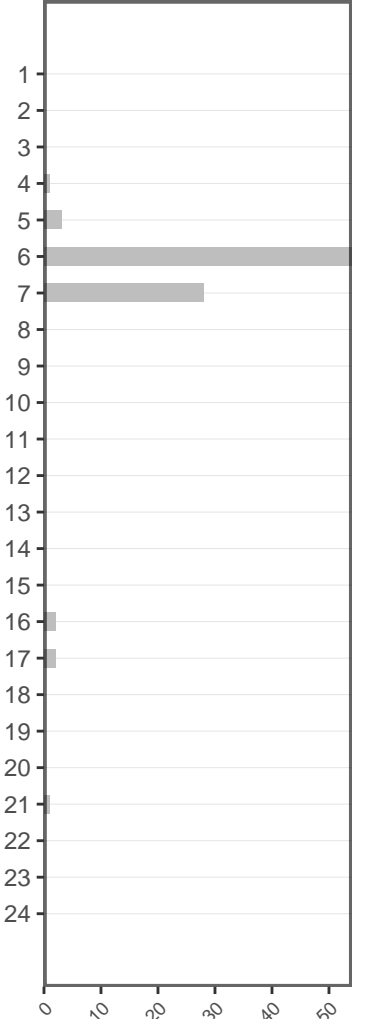
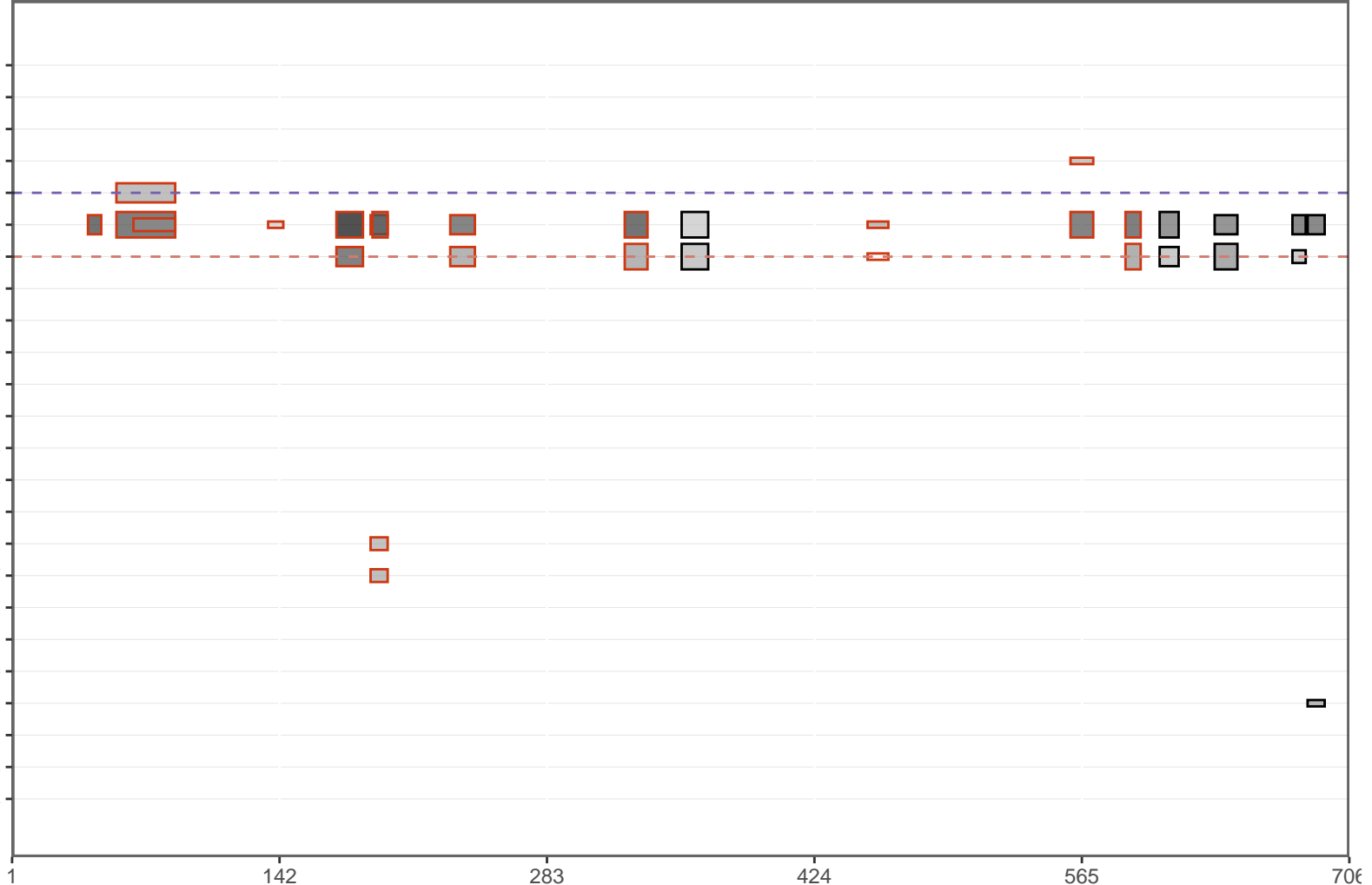
MW indication



Molecular weight

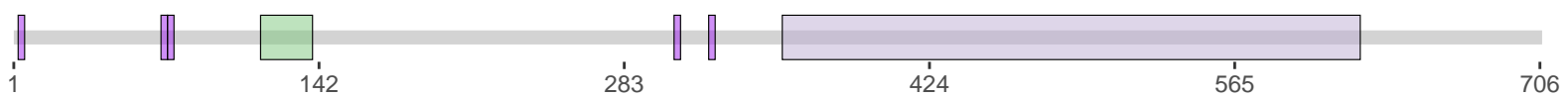


Gel Slice



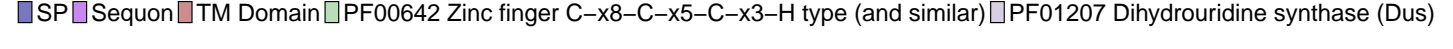
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KLHPREKILDFRDKLFLAPLTTVGNLFFRRVGVKVLGADVTSSEMMAMGTLNIGGQASEWALLRRHSEENLFGVQIGAVPDTVTKTVELIEGGQGVDFIDNMGCPIDVWVNGAGSALLTKPTRMKGVVEASATVDIPVTKVTVAVFEQKNRISLADIGNWGATAVTHGRGRQDRYKSLADWDVHYGGVGRAPKSLQVLGNQGVFXYLEWNNKHKTDSPELSTGMARGALIKFWIFTEKEQKHWDITSGERLDLKDVARFGLHVGSDSKGVETTRHFLLEWLSYTCF

NbL01g00990.1 amidophosphoribosyltransferase_chloroplastic-like [MW – SP = 61.8 kDa]

No. of times detected



log(intensity)



Values from



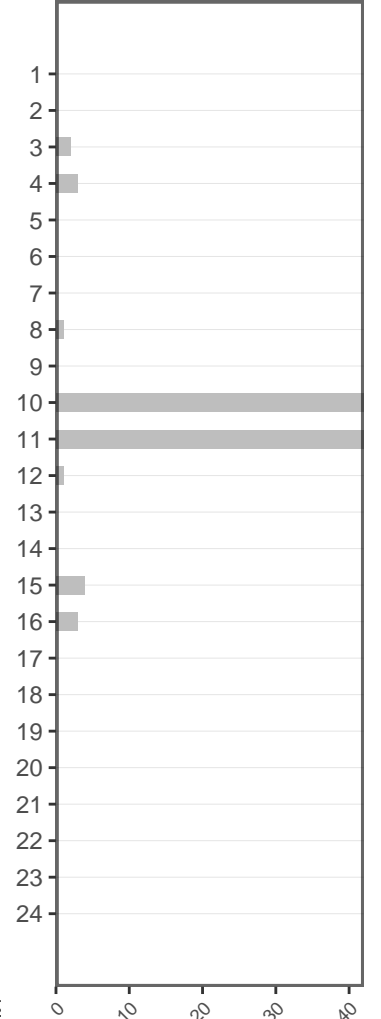
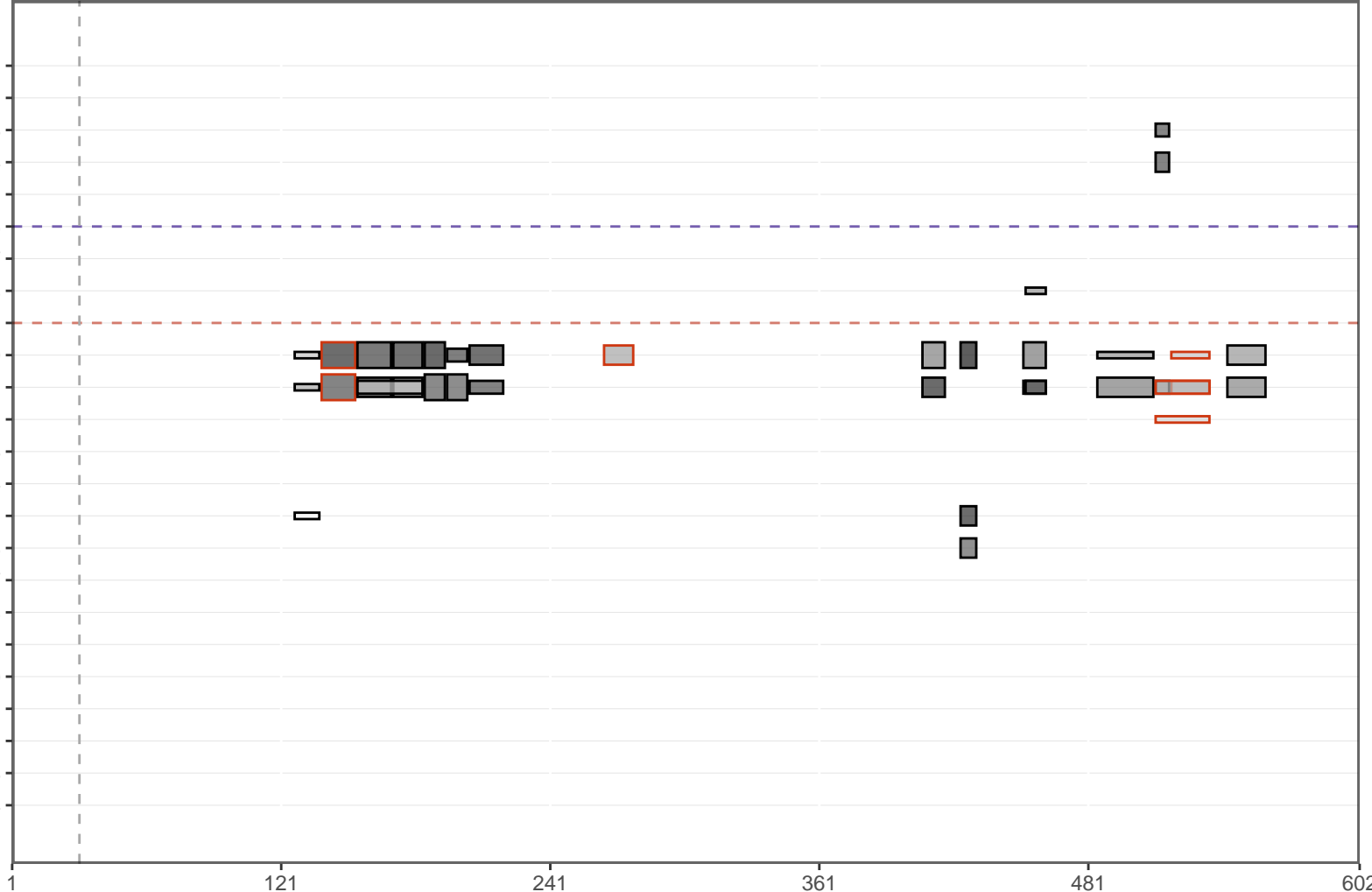
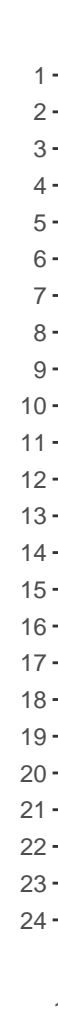
MW indication



Molecular weight

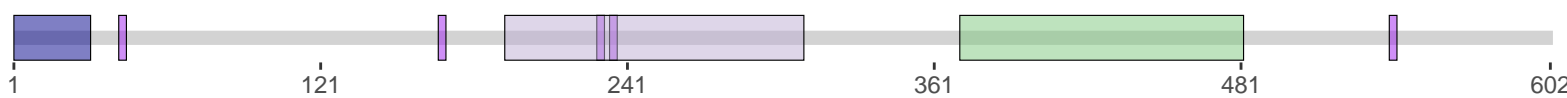


Gel Slice



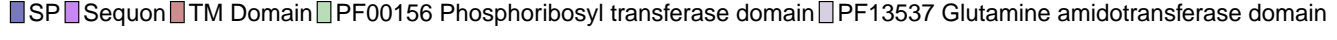
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

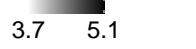
RPLVMGRRSNGAVFASSETCALDUEATYERIEVSPGEVWVVDKDGVSIGLMPHPERRSGIFEHYFALPNSVYVFRGSVYESSRRAFGEELATEAPVEGDVWVAVPDSGVAAALGVAKAGVFPDQGLRSHYVGRTFIEPQKIRDFGVKLLKLSVRAVLEGRKRVVVDSDVIRGTTSSKIVRLLKEAGAEVHMRIASPHIAGVYGVDTFSSDELINRMSVEEIKERFGSDSLAFLPIDSLNKLKLGNDKSFQVYCFSGNYPVEPTGKVRIGDFMDDGLSGMDSDDGWL

NbL01g00980.1 peptidyl-prolyl_cis-trans_isomerase_Pin1 [MW = 12.95 kDa]

No. of times detected



log(intensity)



Values from



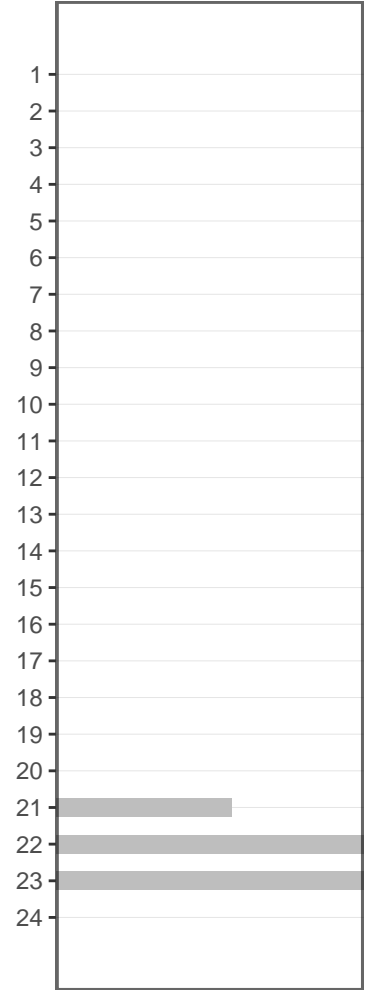
MW indication



Molecular weight



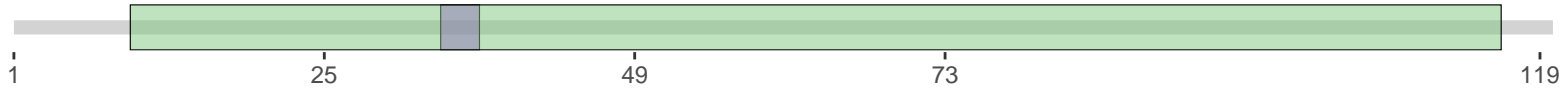
Gel Slice



Protein length



Pfam domains



Pfam Description



Protein sequence:

AFRDIIISGSKFEDVASRFSDCGSAKRGGDLGPFGRGOMQKPFEDKTFALKVGEISDHDTDGGVHLRTG

NbL01g00870.1 pentatricopeptide_repeat-containing_protein_MRL1_chloroplastic [MW = 123.04 kDa]

No. of times detected



log(intensity)



Values from



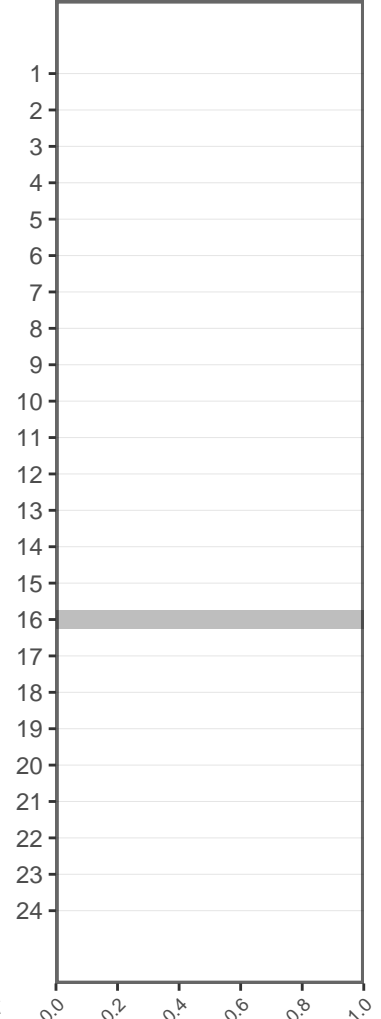
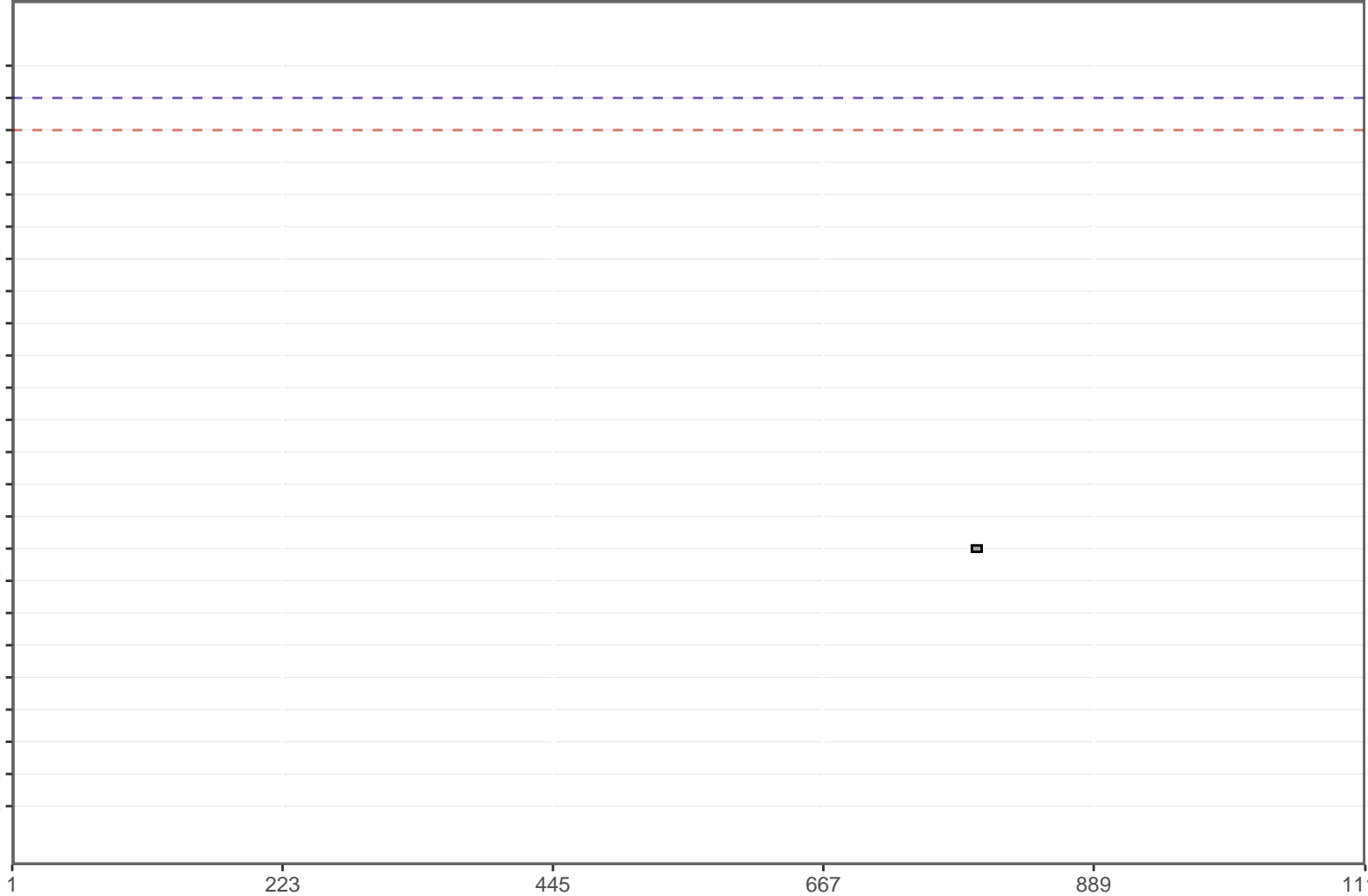
MW indication



Molecular weight

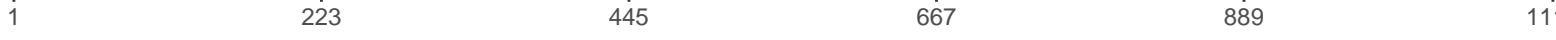


Gel Slice

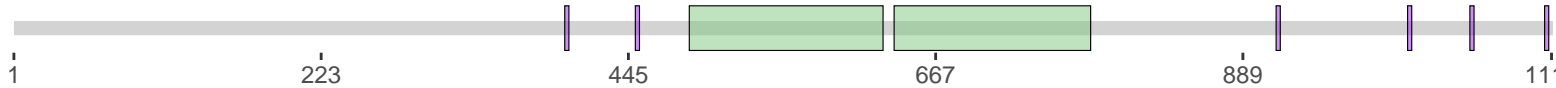


Peptide counts over 4 repeats

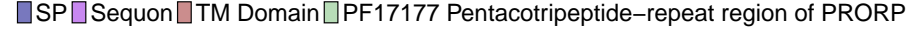
Protein length



Pfam domains



Pfam Description



Protein sequence:

EVYHEMVAAGVEPNNTYTGALDGGAKAGVAKAFGAYGMRSKNWPDRVVFNALTAGGGGSAVDRAFDVLSSEMKAEARPIEPDQITGALMKAGANAGQVDRALDYYRMDIKYDKGTAEVYTIWNCDCGNGNWFDFARSYDDMTRKGVYVPEMFISALVDVAGHAGKLEDAFVLEEARTKGNVGSMSYSSLMGAGSNKNNWQKALELYEEDVGVKVKPTVSMNNALVTLGDADQVYKALEIFSEMKRVDLGPNTITYYFTLLVASEKDELEIDGLMLLSHAKKDG

NbL01g00850.1 5'-methylthioadenosine/S-adenosylhomocysteine_nucleosidase_2 [MW = 27.78 kDa]

No. of times detected



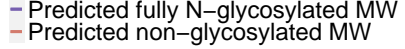
log(intensity)



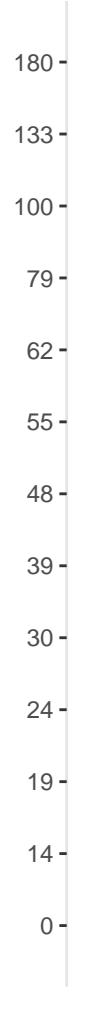
Values from



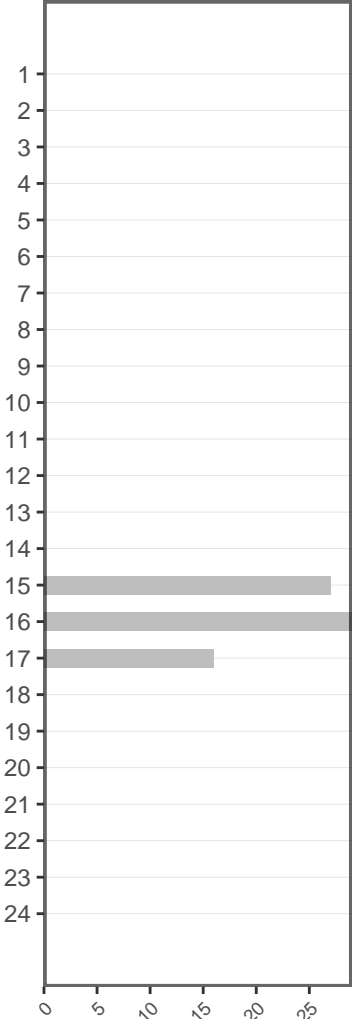
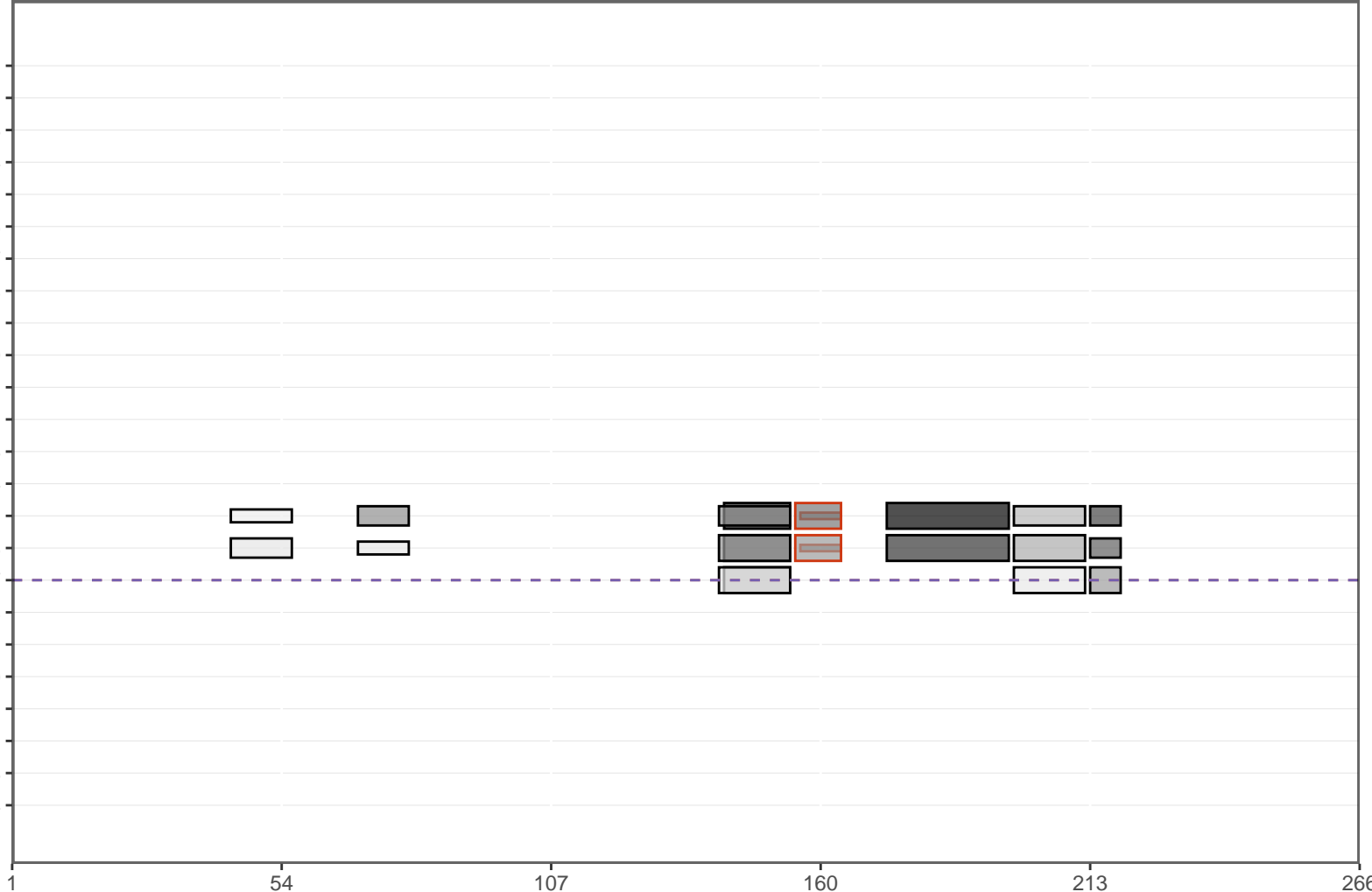
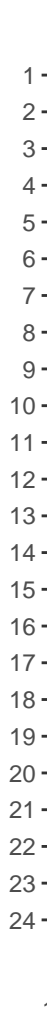
MW indication



Molecular weight

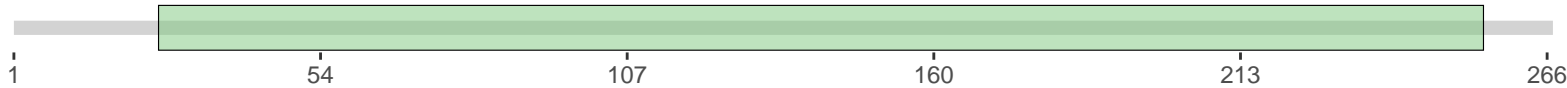


Gel Slice



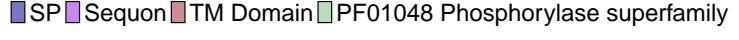
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IAKGASIGDVFLLASEVAFHRRRIPPFVDFYGVGSRKAFATPNLLKELNKKVGLKSTGDSLEMSFMDSEASVNDATVYKDMEGAAWVYADLLKVPVIFLKAATVDVGGDKPTAEFLQNLAAVTAALDGTATLVDCISGKGLSDU

NbL01g00810.1 triosephosphate_isomerase_chloroplastic [MW = 34.78 kDa]

No. of times detected



log(intensity)



Values from



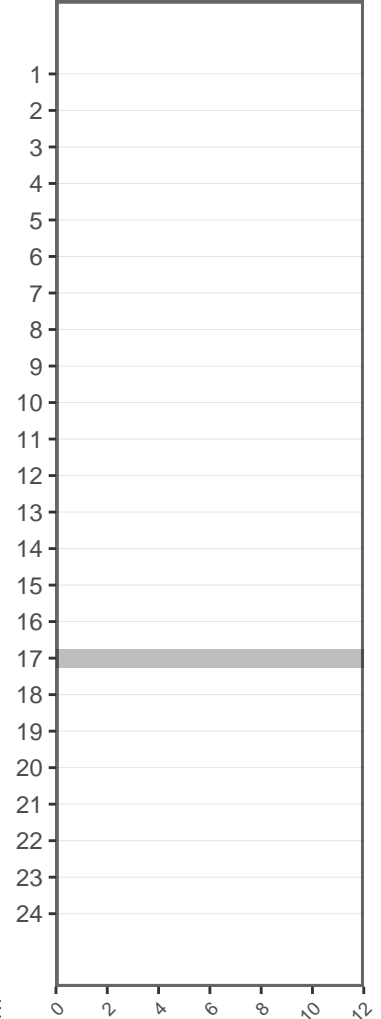
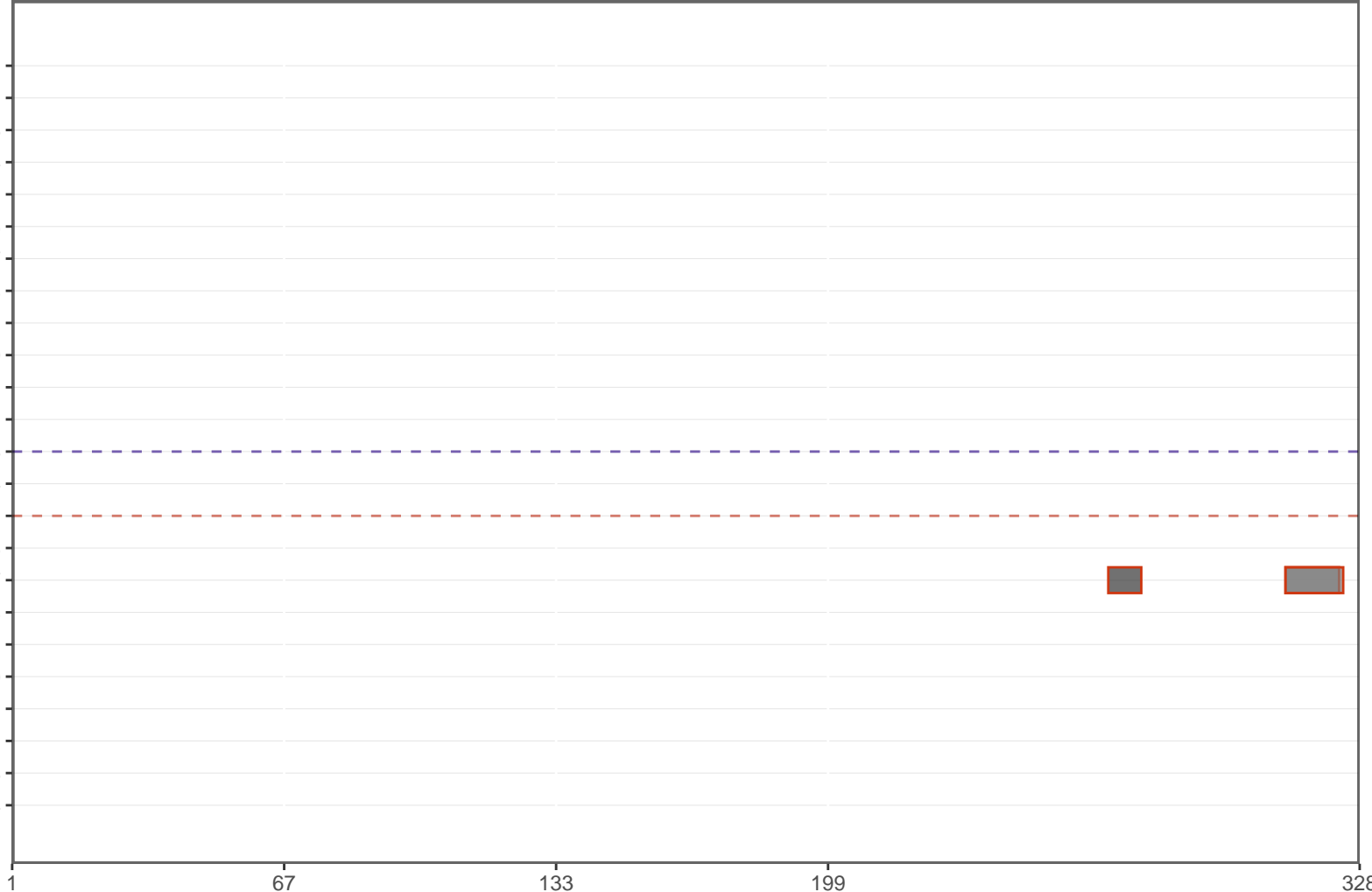
MW indication



Molecular weight



Gel Slice

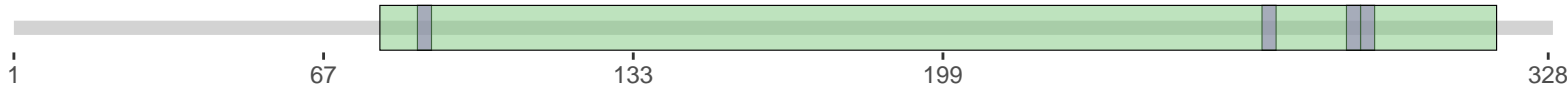


Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

ESVVEQLKDLGCKWVILGHERRHVGENDERFKKAAVALSQGVGVVIAGIGELLOEREAGKTFDVFQGLKAFADALPGWBNVAIAYEPIVAWIGTKVAGPEQAGEVHAAVREVLTKNVASDVASKTRIRYGGVNGVNGS6SLAKKEDIDGFLVGGASLKGTEFATINSVTSKVA*

NbL01g00760.1 peptidyl-prolyl_cis-trans_isomerase-like [MW = 18.1 kDa]

No. of times detected



log(intensity)



Values from



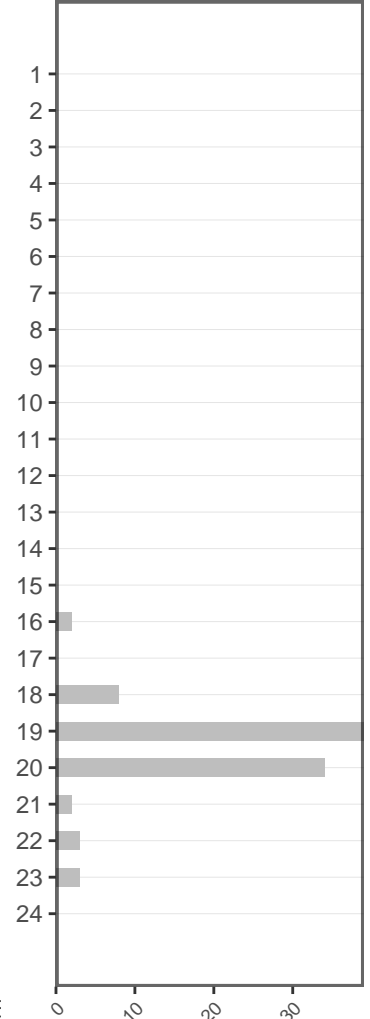
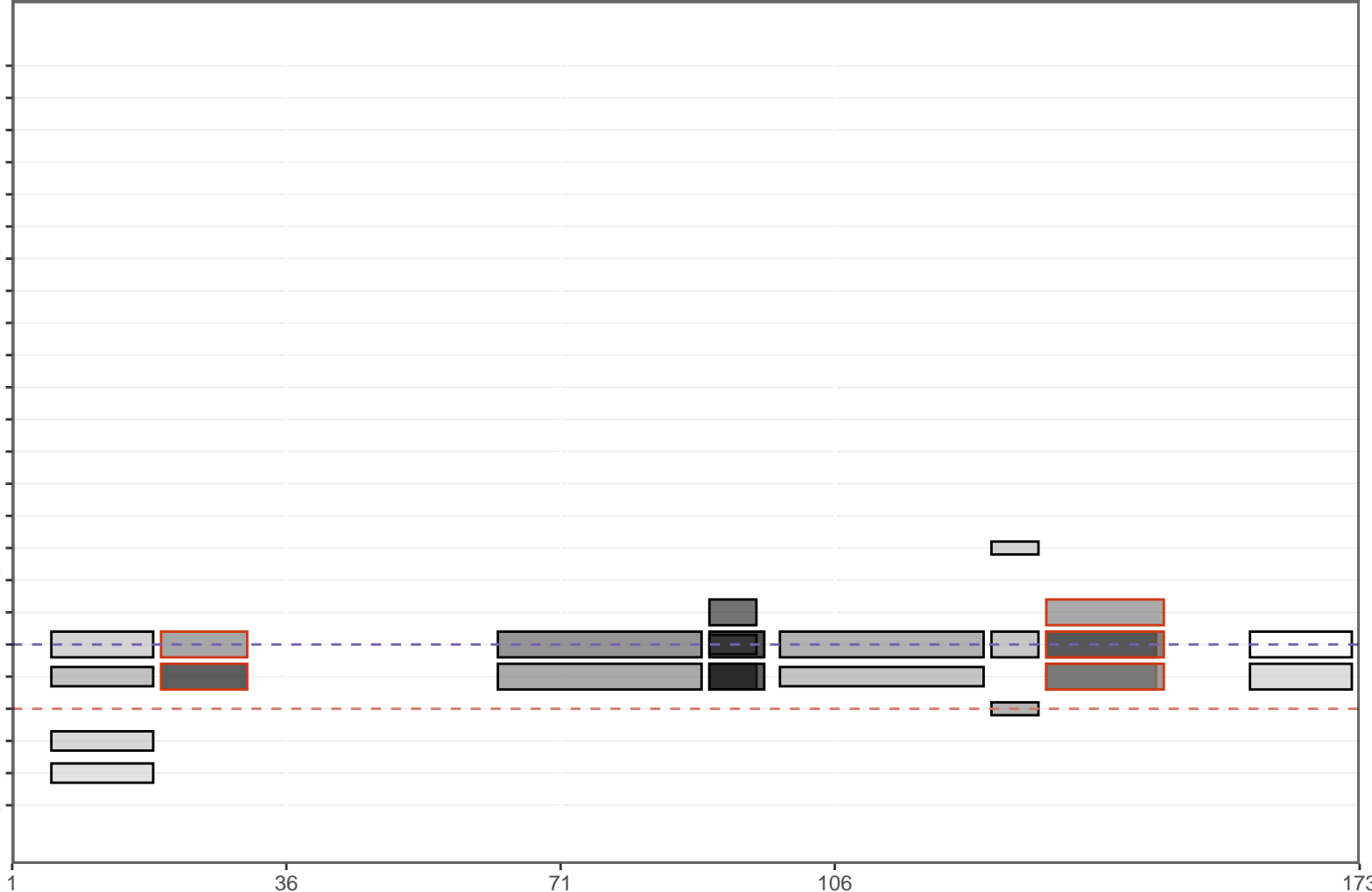
MW indication



Molecular weight

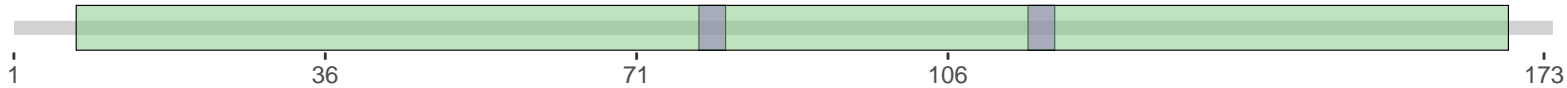


Gel Slice



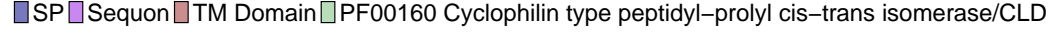
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

FTAGNGTGGESISYGAKFADENFKRKHHTGPGLEMANAGPGTNGSGOFFRKTAKTEWLDGKHVVFQGVVVEGYDVRKKAEEAVGSGGRGKRPVVIADGGGLG

NbL01g00700.1 translocase_of_chloroplast_120_chloroplastic-like [MW = 152 kDa]

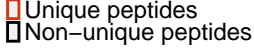
No. of times detected



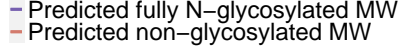
log(intensity)



Values from



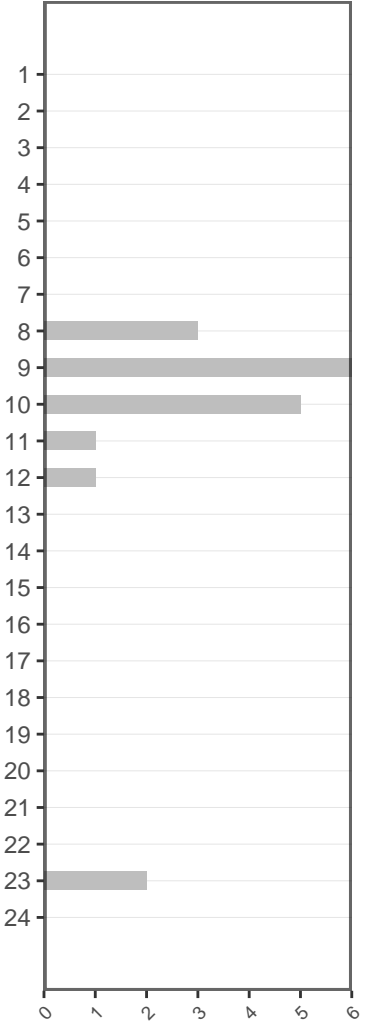
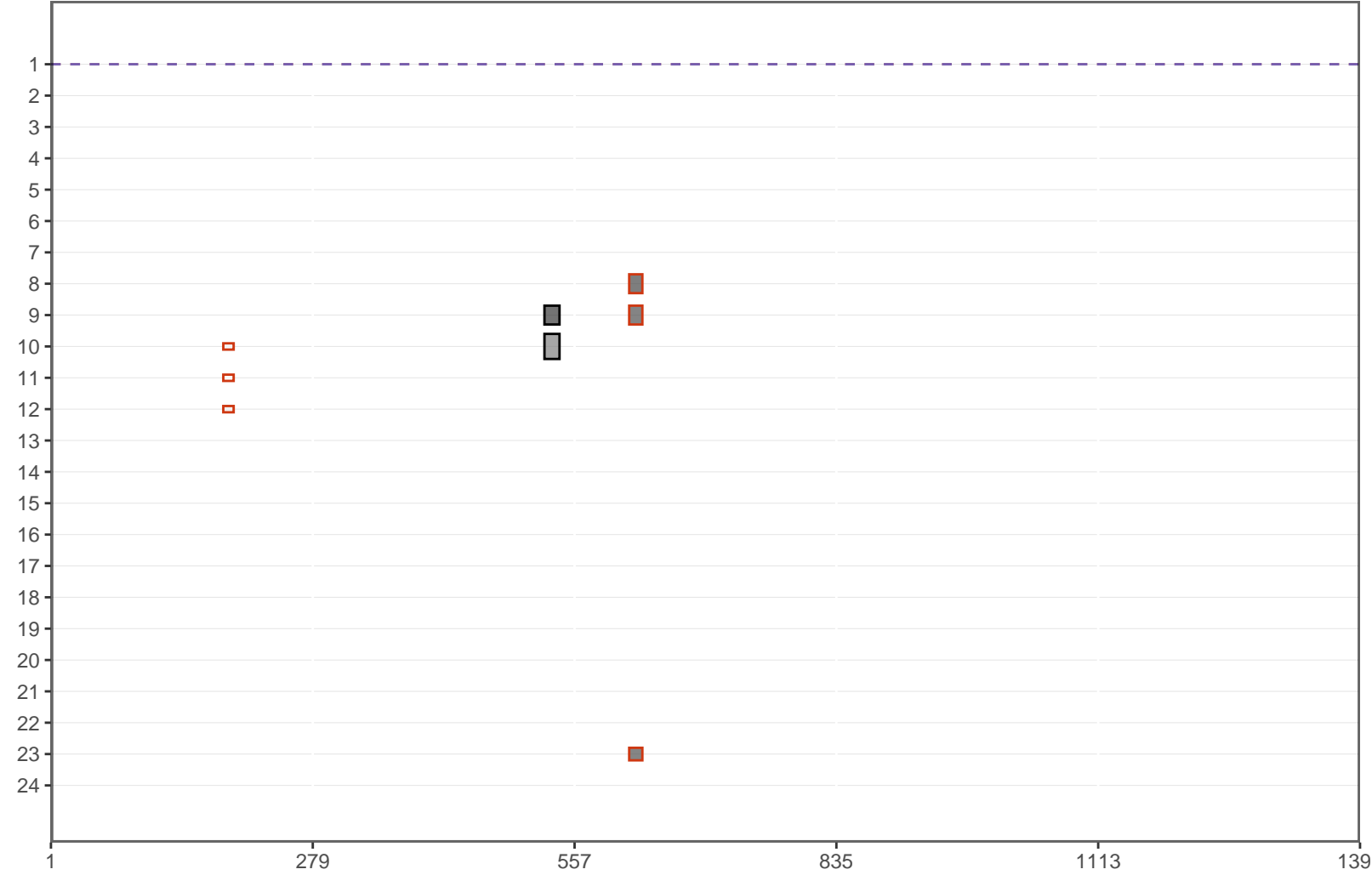
MW indication



Molecular weight



Gel Slice



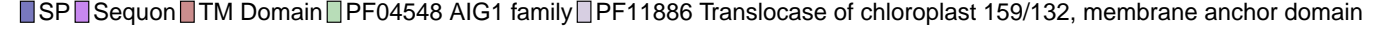
Protein length



Pfam domains



Pfam Description



Protein sequence:

ADEYDREKLCMRVXFLRLAHLGGTPHNVYAGVYLRGLAEQLRGRSGSRVAASFRASMAAEQLEAAGDEPLDFSGTIMVLGKTVGKSAFNIFDEVWFGTDAFLGKTVGQVGVGTVDGKVRVDTPLGLLPSWSDQRGNELQGVKRFNKTPDPIVLYDLRLDMQSRDYGMLPLRTITEIFGPGSIWFNAIVLTHAAGAPFGNGTFTVDMFVTRQSHVVDGARRGAAGDMRLMNPVSLVENHSAGRTNRAGGRVLPNGGQWKPILLLSFASKLAE

NbL01g00640.1 thaumatin-like_protein_1b [MW = 41.31 kDa]

No. of times detected



log(intensity)



Values from



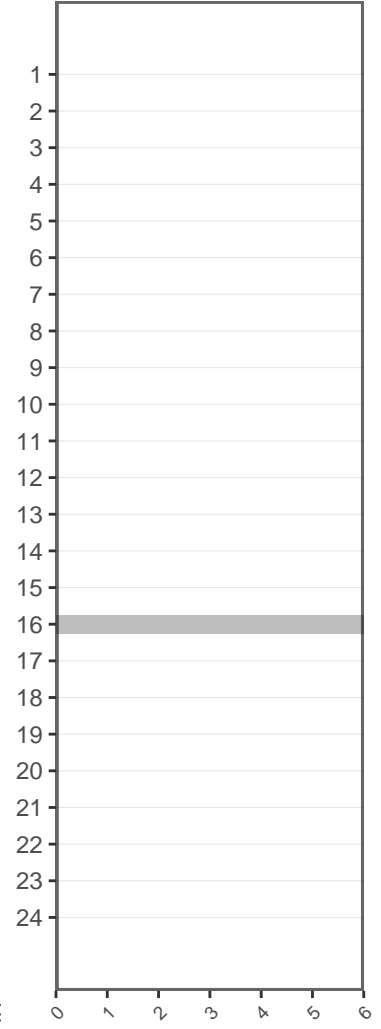
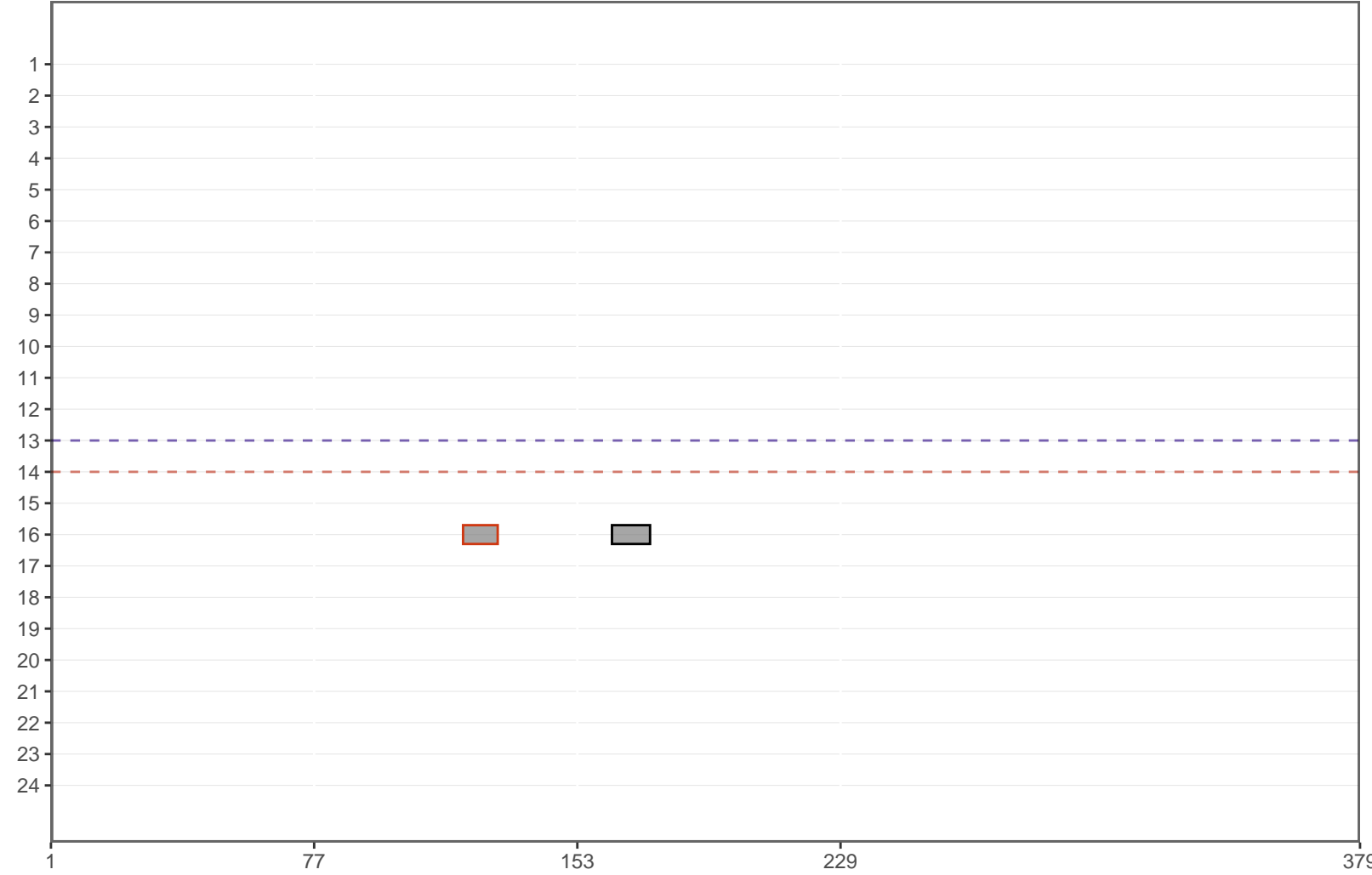
MW indication



Molecular weight



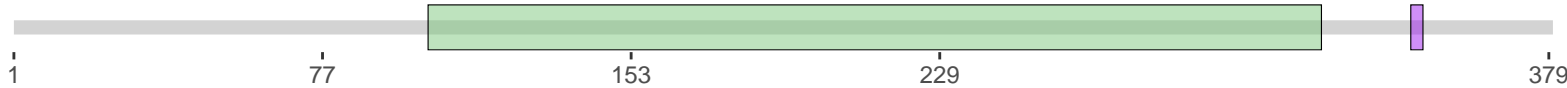
Gel Slice



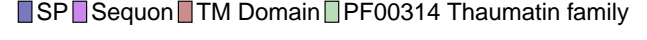
Protein length



Pfam domains



Pfam Description



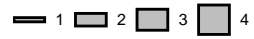
Protein sequence:

AGGGAIIPATLAEFTLNGDGGDFYVSLVDGYNLPLMLVAKGSTRGGGSATGGLVDLNGACPRDLRVASGKSHSEVGGKSAQLAFNDPIYCGSESHNTPDQGPVYSLFFKHACPRGYSVAYDDKSTFTFCASADYLIIFGLPYTSMKVLGLRKPDELPLVNTMMYGRHHRGGESSIRPELLHPYGVSNLHL*

NbL01g00540.1

L-ascorbate_peroxidase_3_peroxisomal_(LOC104249656)_transcript_variant_X1_mRNA_XM_009806132.1_PREDICTED:_Nicotiana_sylvestris_L-
[MW = 35.39 kDa]

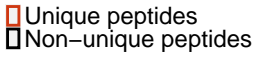
No. of times detected



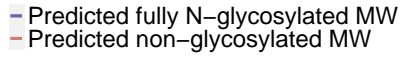
log(intensity)



Values from

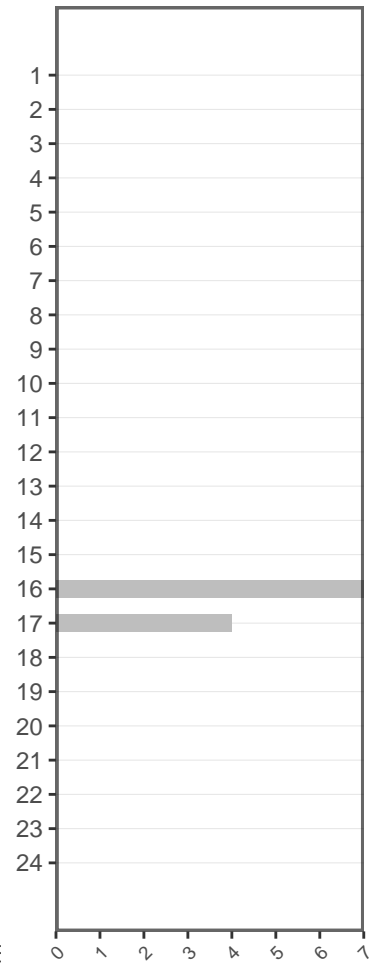
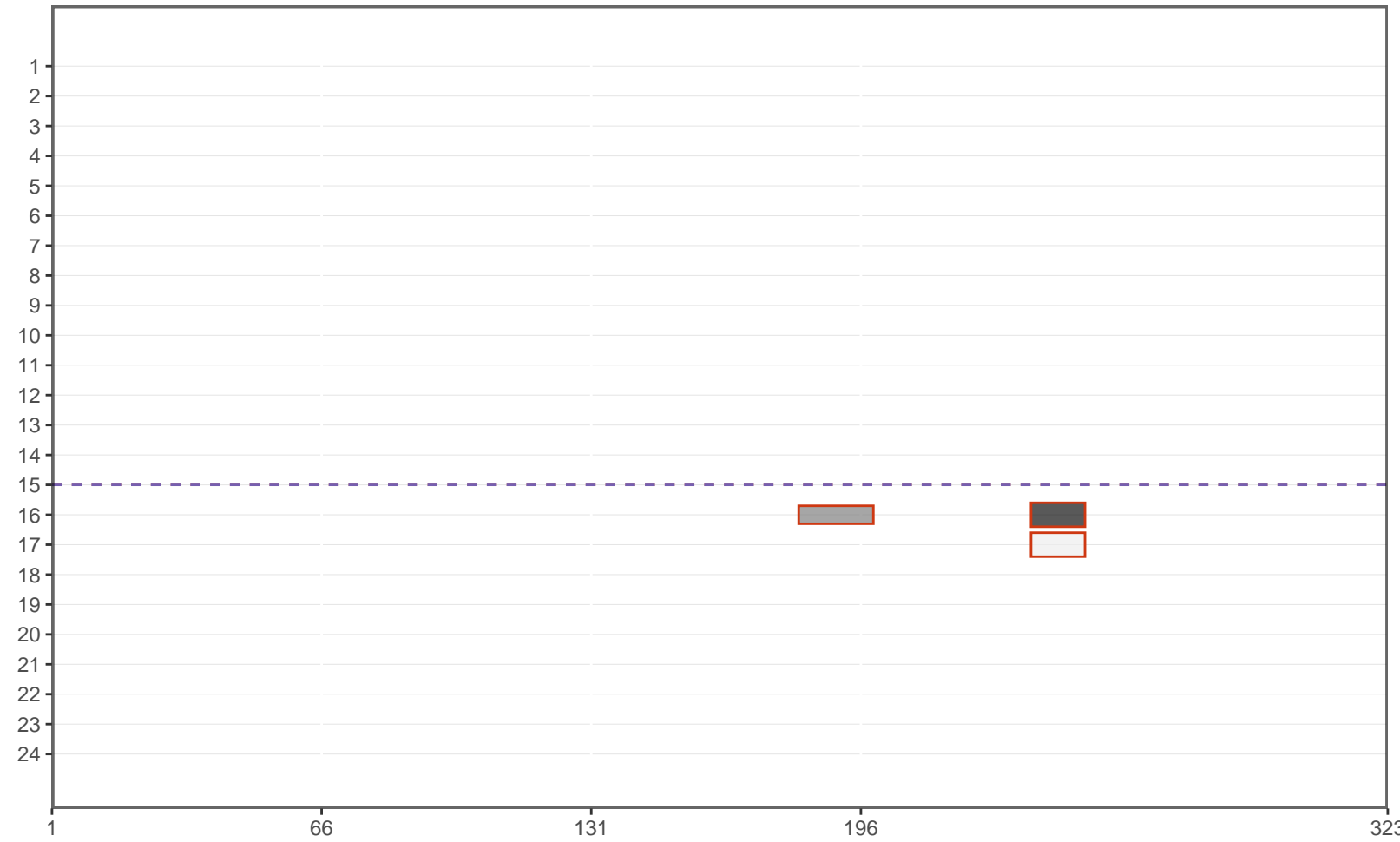
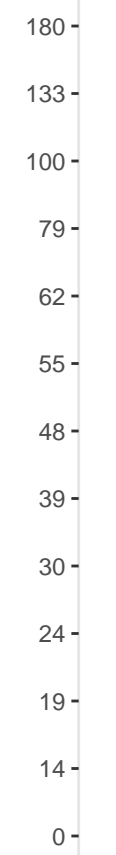


MW indication



Molecular weight

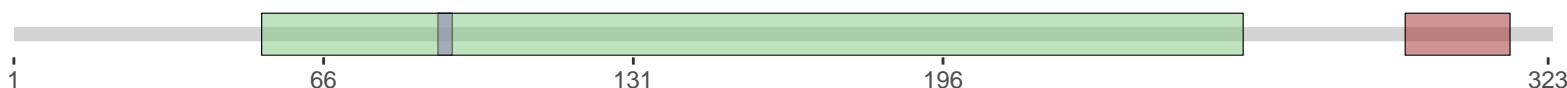
Gel Slice



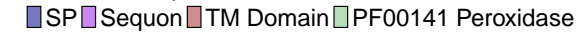
Protein length



Pfam domains



Pfam Description



Protein sequence:

GRKDSVSPKEGREPDMAKGGVPHLKDVFYRMGLSDIEDIALSGGHTLGRAPHERSGFDSPWTKELKFDNSYFVELLKGESQLLKPDTDALLDDPEFRGVYELVAKDEDAFFRDWVSHKKLSELGFTPSGGSKATVRDGTLAGSAGVGVVAAVVALSYWYEVKRMK

NbL01g00220.1 L-galactose_dehydrogenase [MW = 34.92 kDa]

No. of times detected



log(intensity)



Values from



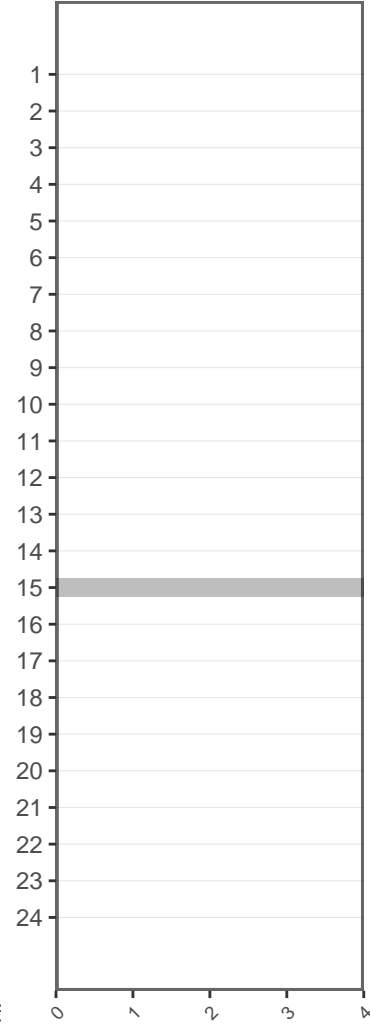
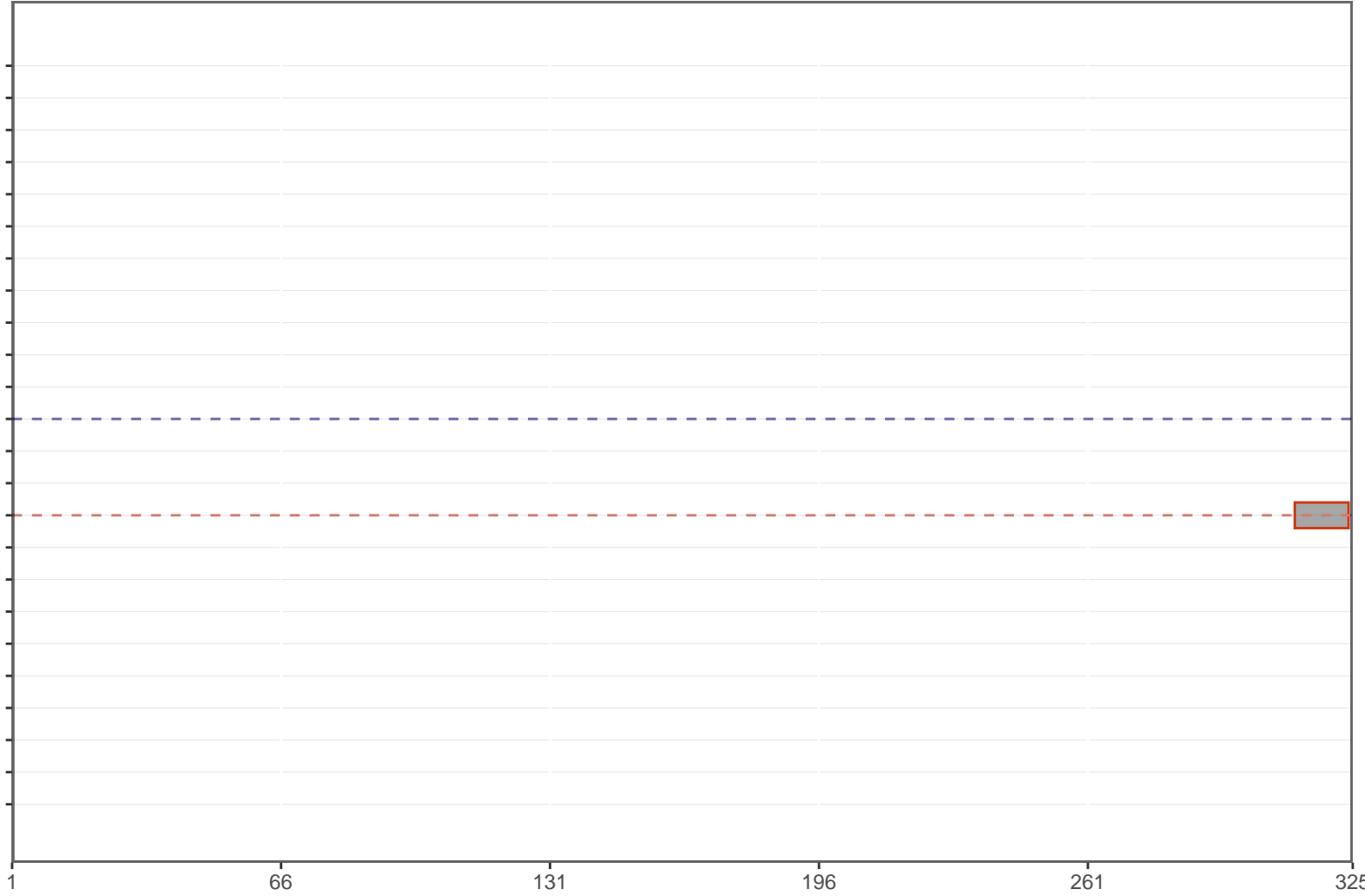
MW indication



Molecular weight

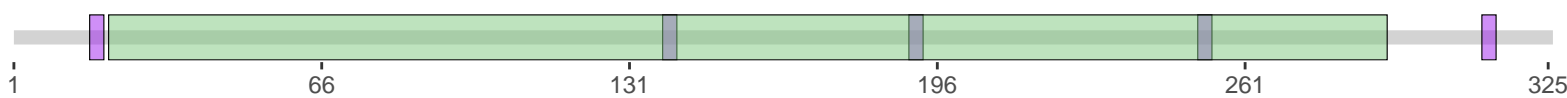


Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

KQAGKIRFGITGLPLGFFVYLDKRVPRGTVEVILVYGHYGINDTLEDPLVYLSKGVGVISASFLAMQLLTEADAFVHWPASSELKAAADRAAVDHCCKGKGNKIKLALGYSLANTDISVLYGMKSVKEVEENGALELATAGMDEETLSSEITDLKPKVKNQSWPSSGQQLFY

NbL01g00180.1 peptide_methionine_sulfoxide_reductase_B5-like [MW = 22.45 kDa]

No. of times detected



log(intensity)



Values from



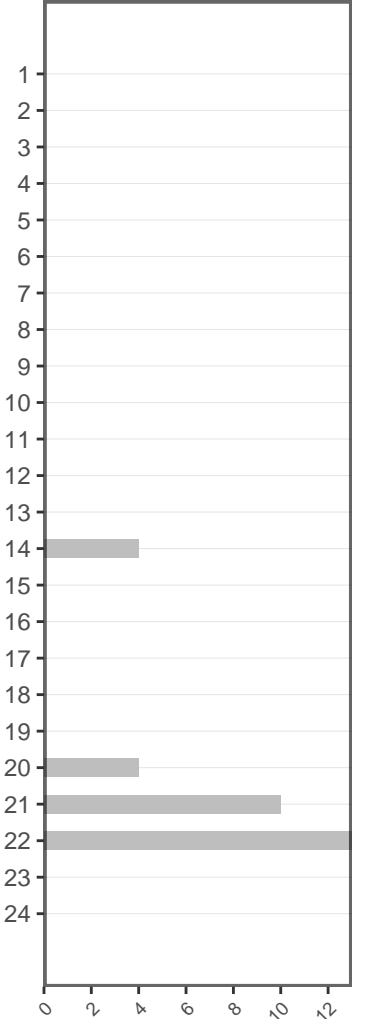
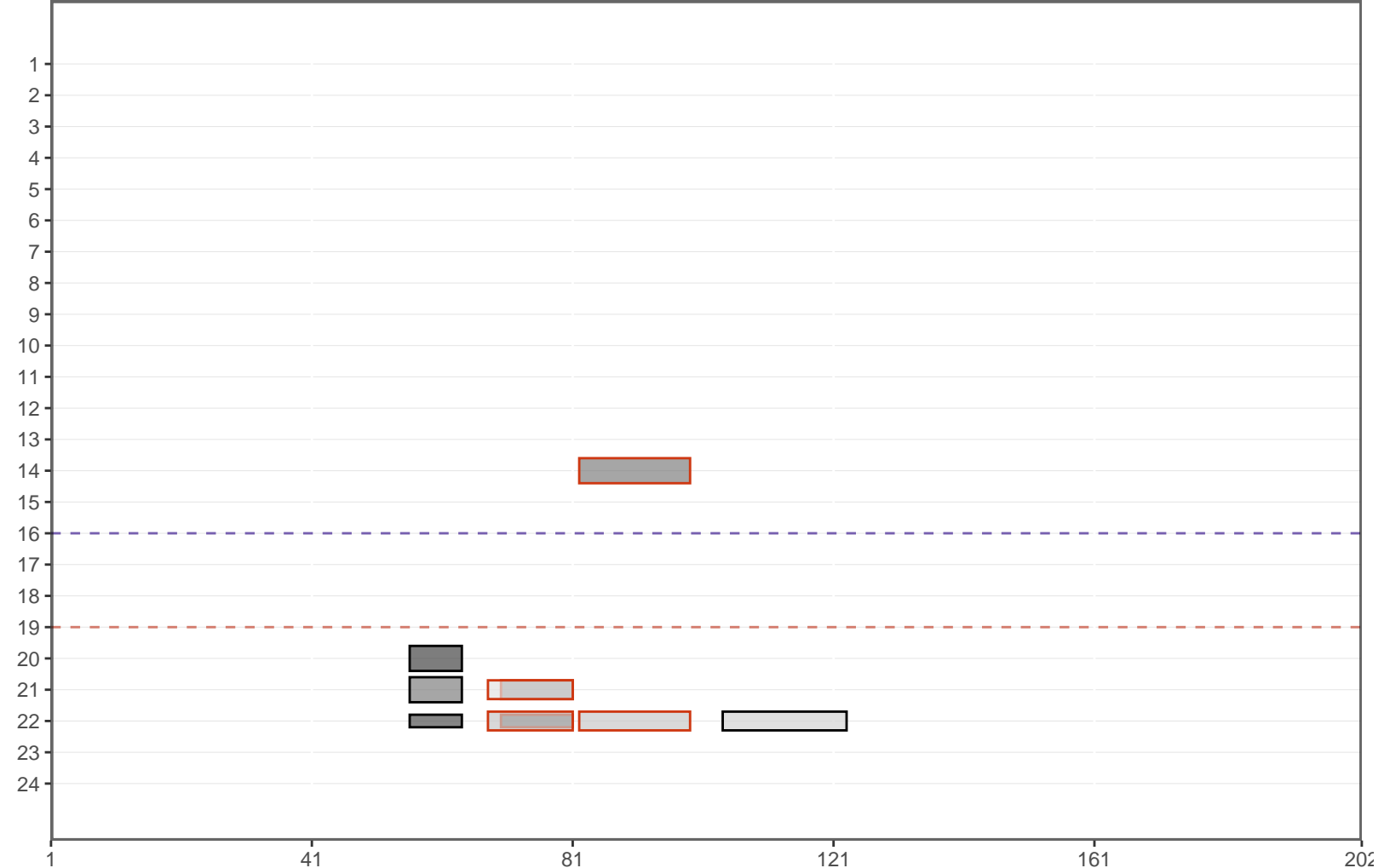
MW indication



Molecular weight

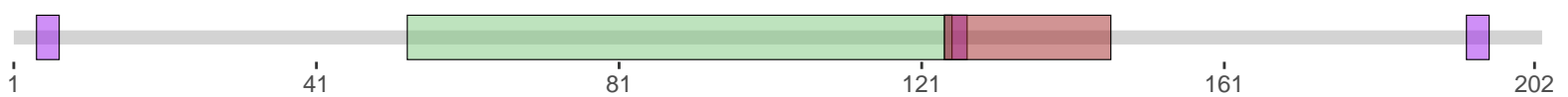


Gel Slice



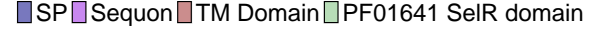
Protein length

Peptide counts over 4 repeats



Pfam domains

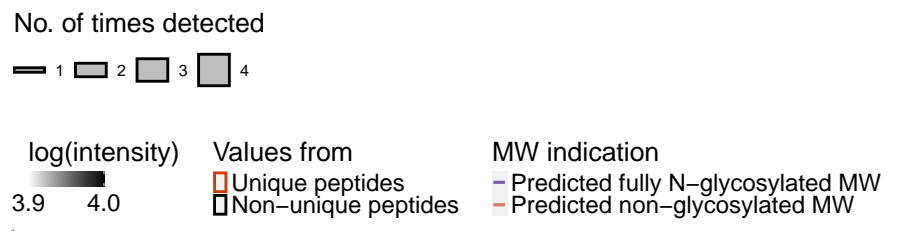
Pfam Description



Protein sequence:

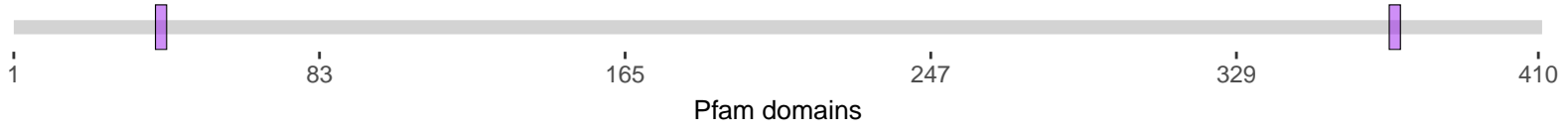
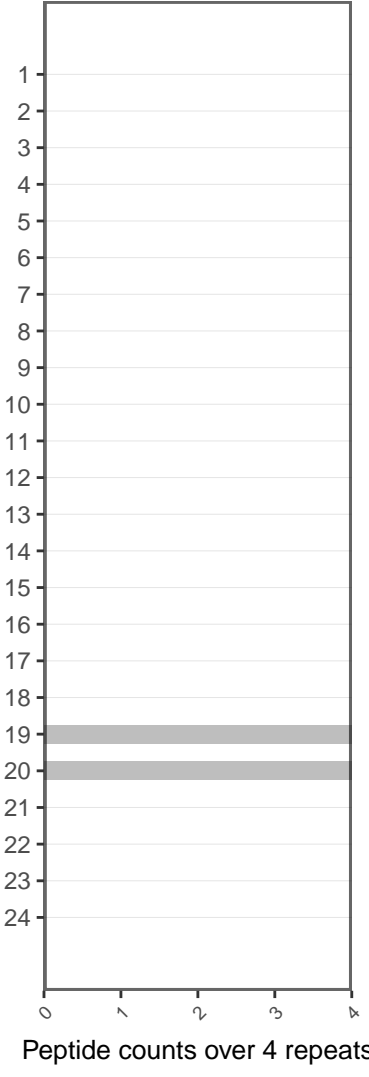
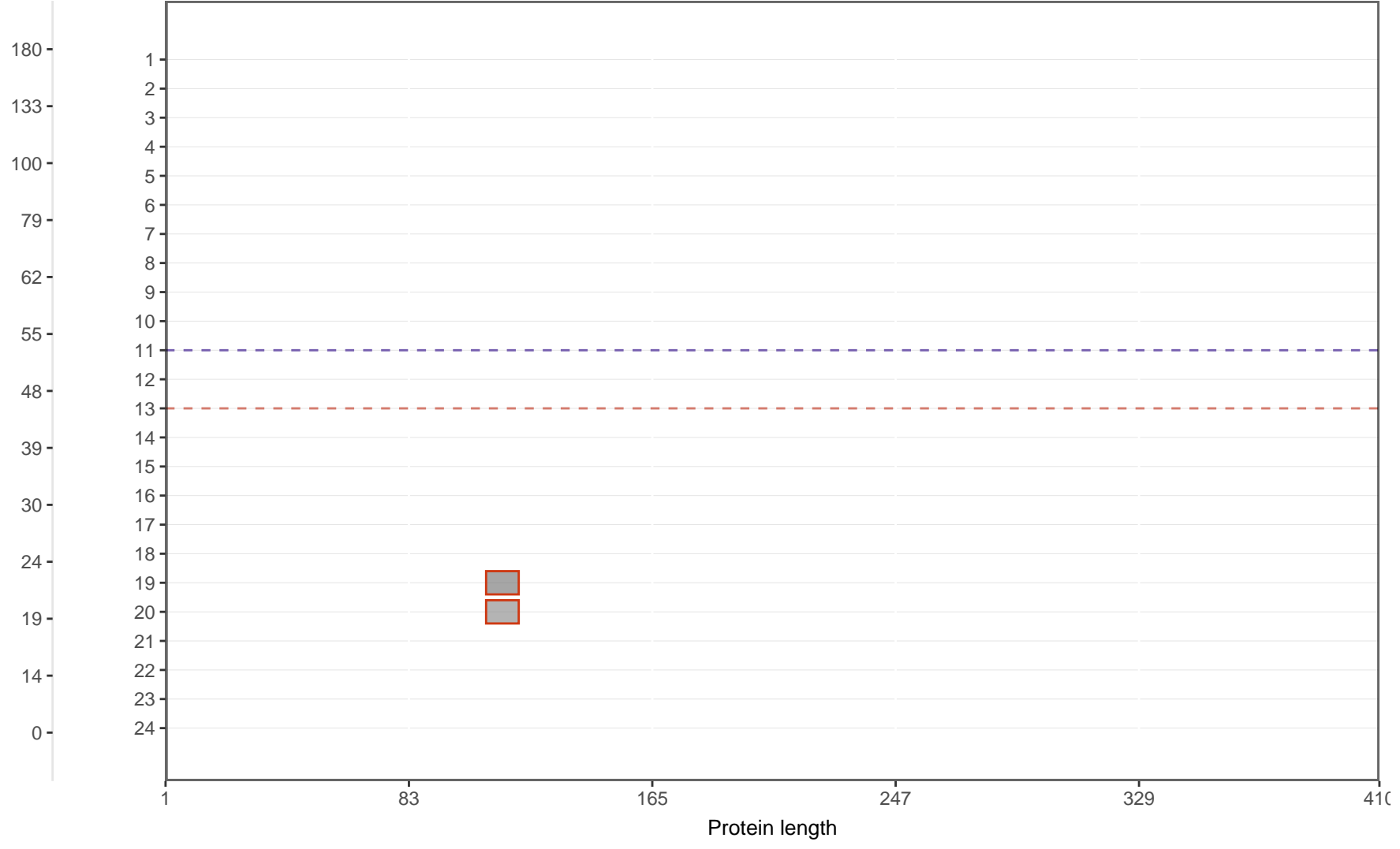
TYLCAGCCTPLYSATKFNSPGQWPFVEGLPQAINRNVFSSHFASLFFFNFLNFRLEVHGSFSGFDNSAALTLEMSALSTFTLLELLKCTKQEGKNSGFPPLHN

NbL01g00100.1 multiple_organelar_RNA_editing_factor_1_mitochondrial-like [MW = 46.08 kDa]



Molecular weight

Gel Slice



Pfam Description
 SP Sequon TM Domain

Protein sequence:

SNRPRRGPQFOGNGNYGPHSPQGNFGPPQGAFAAGQNGYAAAGPFPQNGFGRVYSPAGQNGYSGDQYPPPPQGYSAFGSPQGNYSQGNPLPQQGYEAPQNVPSGWNHSGPQGSFSPQGNYSQGGAGDPVHQTPLGSSPQGNWNSGQGRGDSRQYQVWYNSQEGQGNYSQGRDGRVWPPERGRFRGNHGHWHFEGRGRGNQR

NbL00g03500.1 stromal_70_kDa_heat_shock-related_protein_chloroplastic [MW = 46.85 kDa]

No. of times detected



log(intensity)



Values from



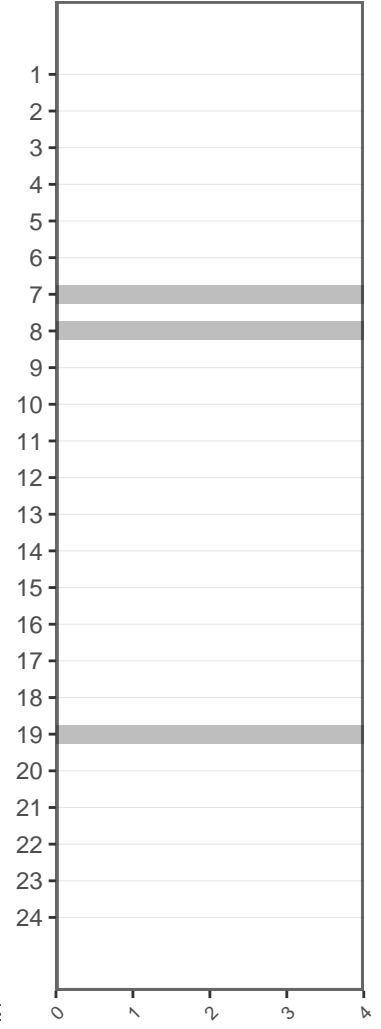
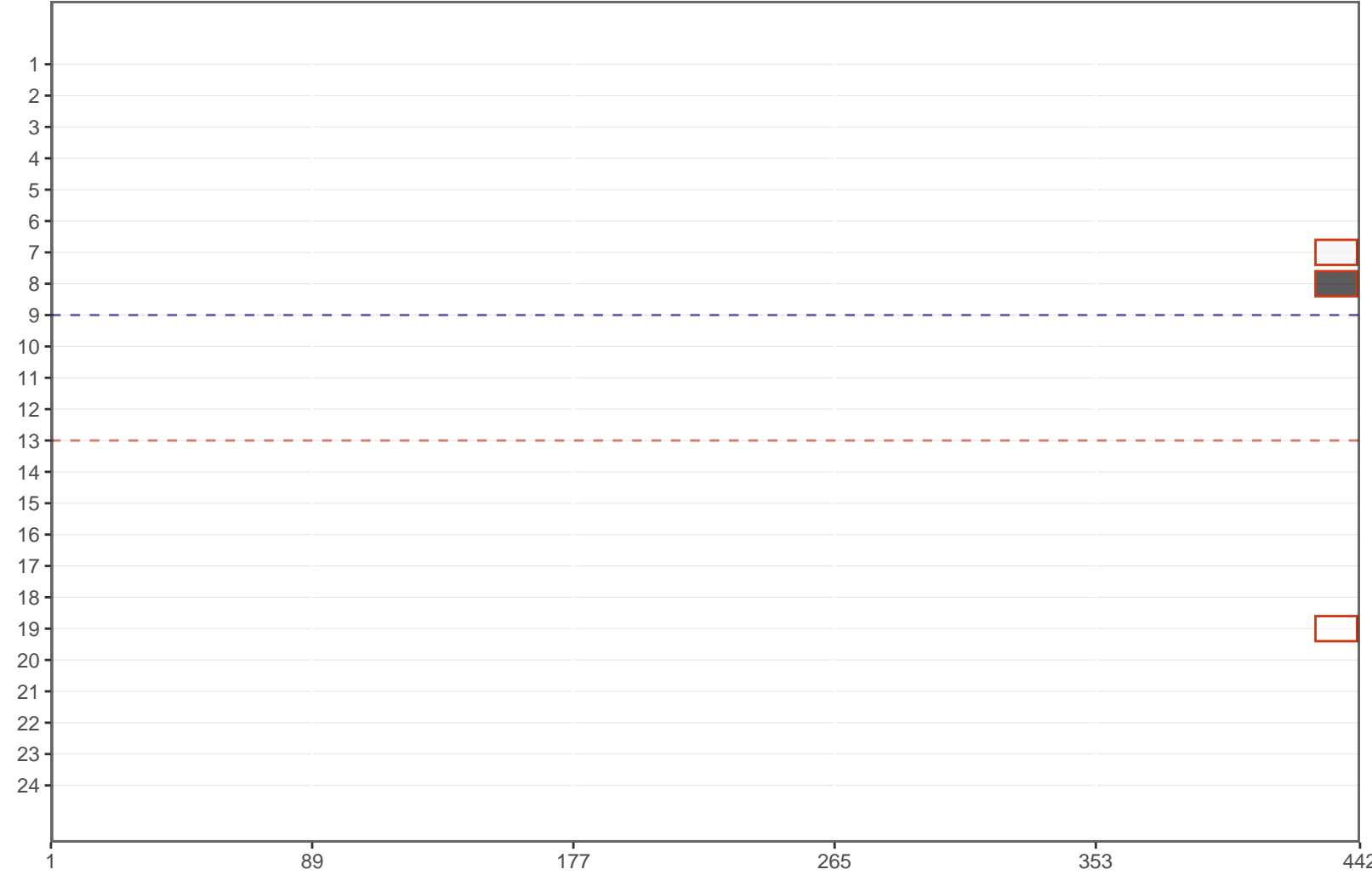
MW indication



Molecular weight

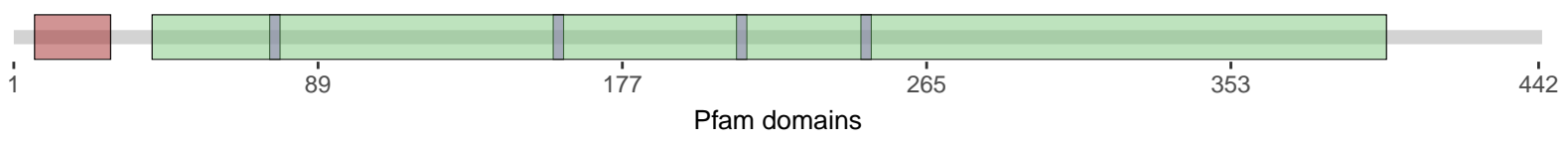


Gel Slice



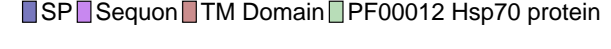
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

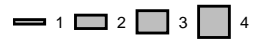


Protein sequence:

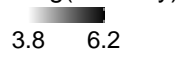
TSKSEVFTAAADGGTSVEINLQGEREFVRNKLKSGFRLLDGIIPAPRQVPPQIEVKFDIDANGILSVTAIDKGTGKQNDITFGASTLPGDEVERMVEAEERFAQEDKEKRDIDTRNGADSVVYQTEKQLKELGDKVPPGPKKEVKAHLGELKEAISGSGTQTMKDMAMALNDEVMQLGGSLYQPGAGAAAPGAPAPQDSAGPSSESSGKPGDGVDAIDFTDSEK

NbL00g03310.1 DNA-directed_RNA_polymerase_subunit_beta" [MW = 140.46 kDa]

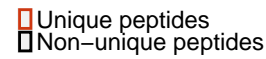
No. of times detected



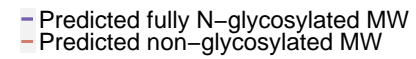
log(intensity)



Values from



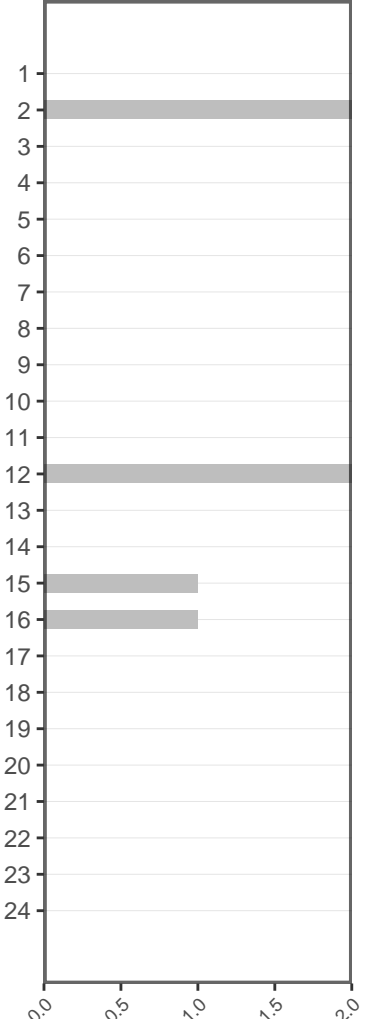
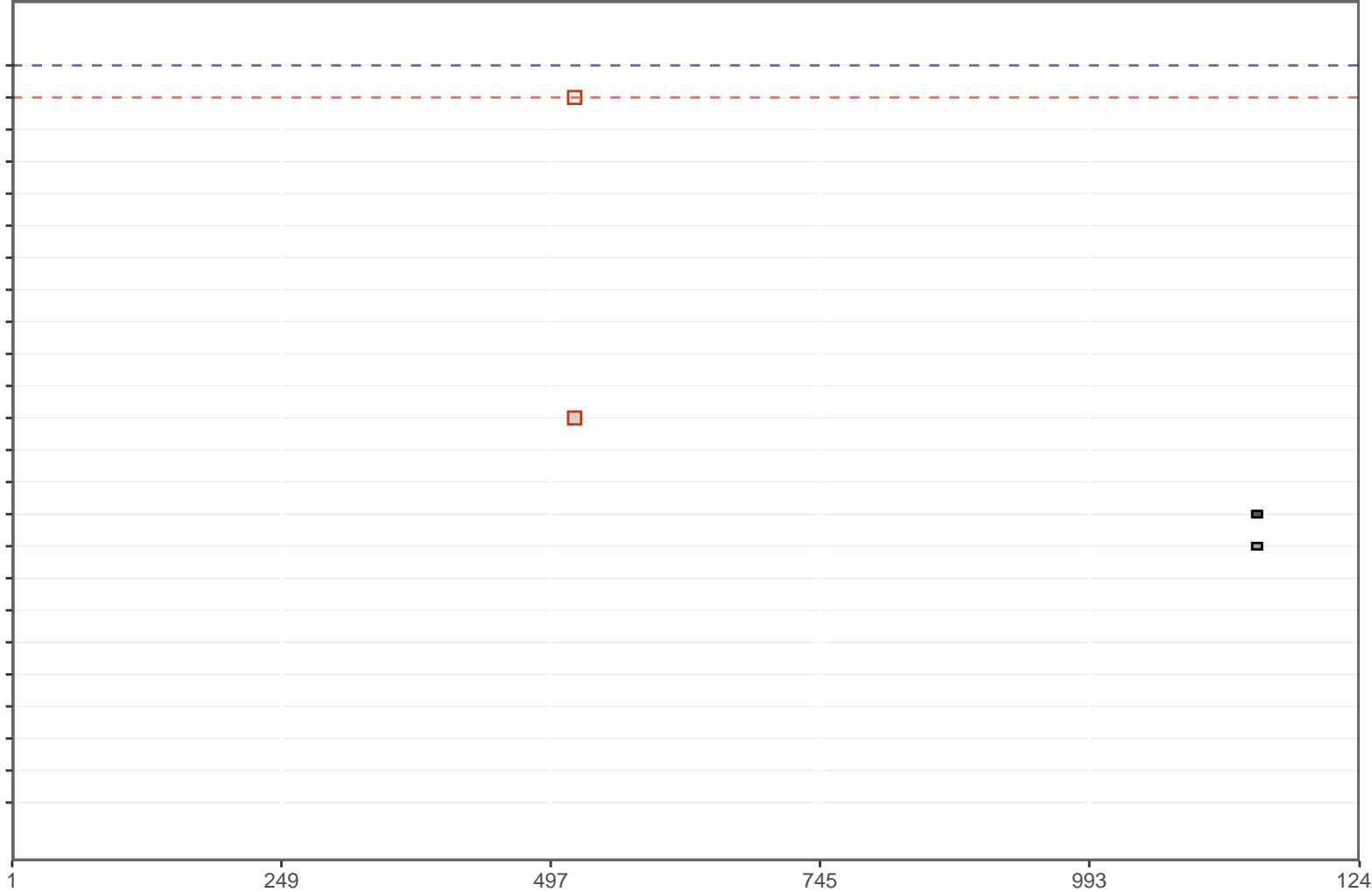
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

IPVNGIFRNSILVFDPRVYRKSGGIKYGTVEHSHVKKEDLLEVRGVKEFRPKYQMKVDRFFPEEIVHLPQ66SIMVRNNSVGVDTQITLNLRSRGLVYRVERKKRIELKIFSGDHFPGETGKSRHTGVLLPPTGTRKRSKESKVKVWYVQRTFRKQKFFLVLRPLVTVYETDGINLATLFPDPLQERDNLVQLRINNYLYLGNKPKRIGSDTSGIQLVRTGLVWVWQDQKSG66CEARASPVERTNGLRHFLLRNVLKSPHVGKRNDFGSGLLSDNSGDCI

NbL00g03000.1 putative_deoxyribonuclease_TATDN1 [MW = 19.35 kDa]

No. of times detected



log(intensity)



Values from



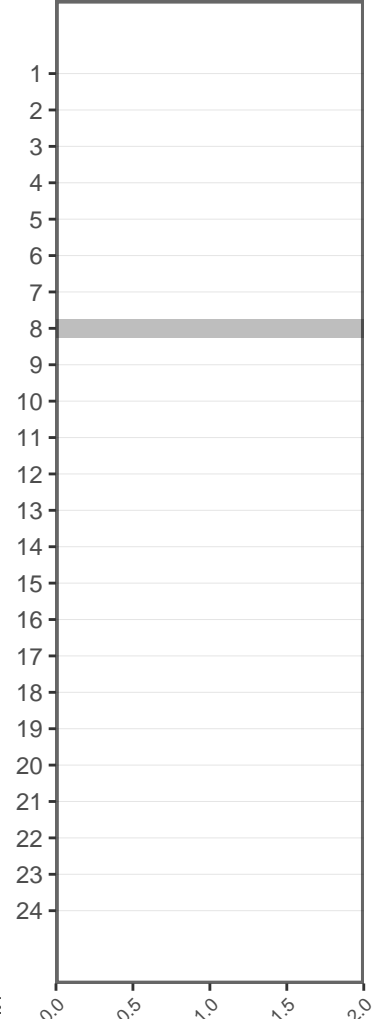
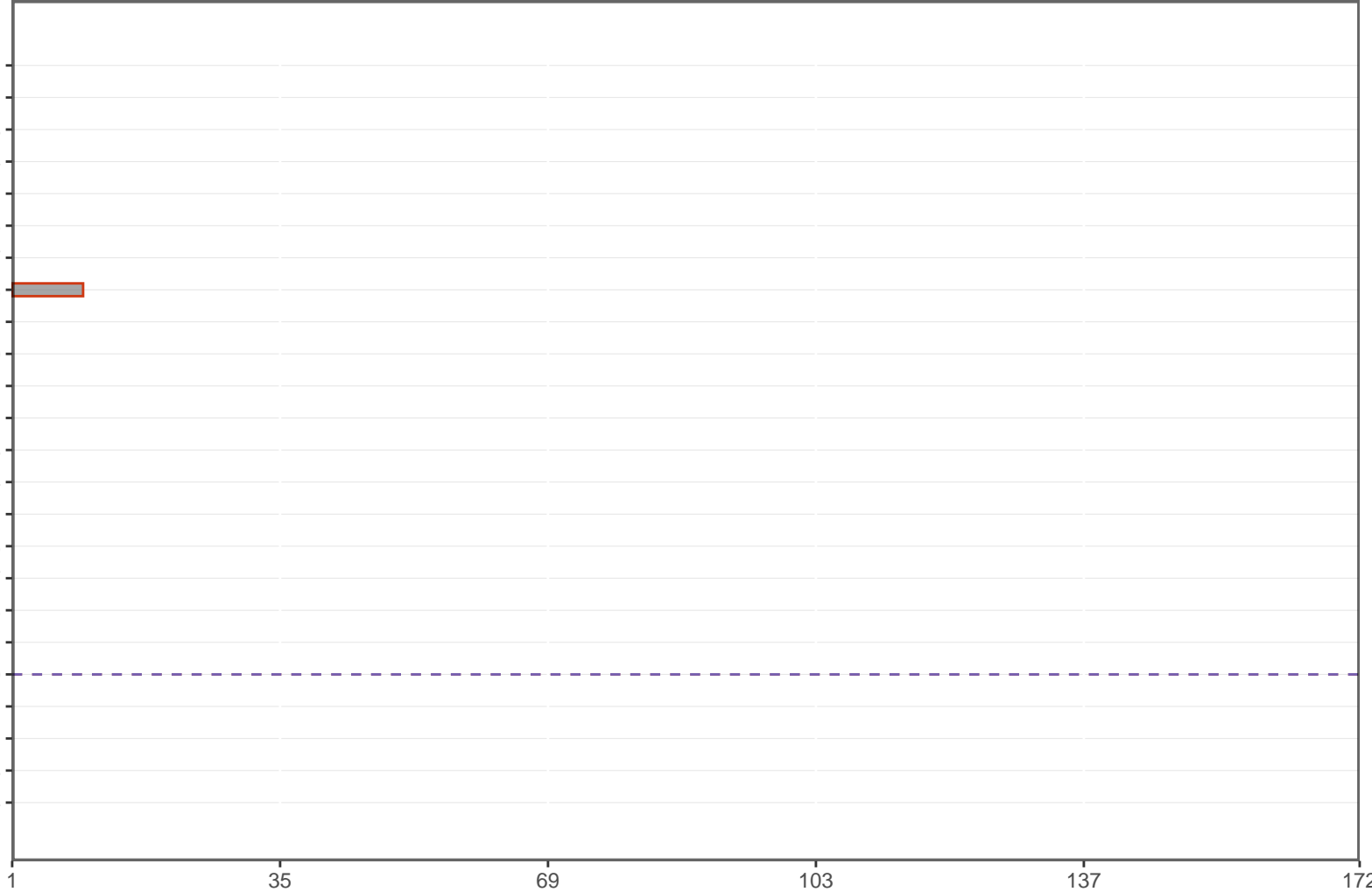
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DSPYCDIKNSHAGSHFVMSWSPSNKKERHDGEGLVKGRNEFQLVRGVLEWAGTKGTFDDGLGKTLVHNTGRVFFPYDLDSAAEALLVSGREAICKKPS

NbL00g02860.1 cathepsin_B-like [MW - SP = 39.32 kDa]

No. of times detected



log(intensity)



Values from



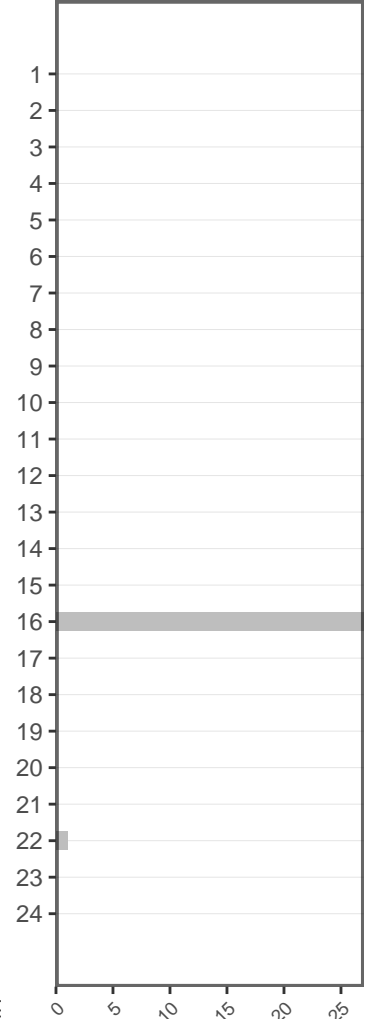
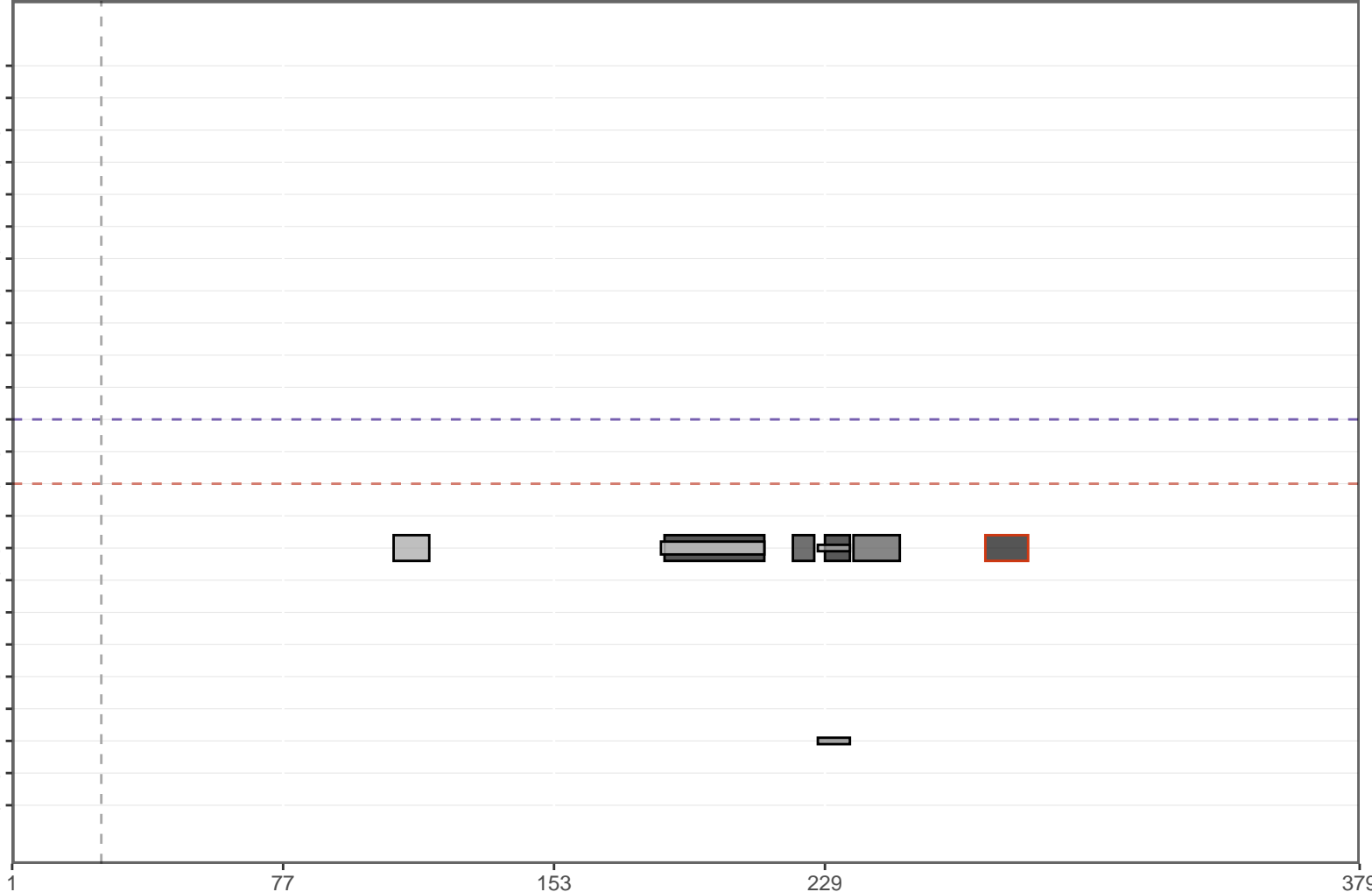
MW indication



Molecular weight

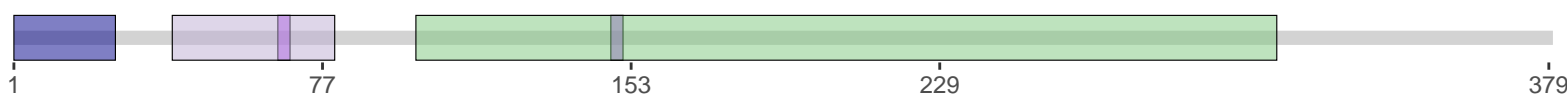


Gel Slice



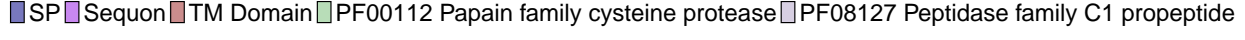
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

IRRGVYTECDPYFDNEGCGHPGQEGVYPTPKQGRKGVKENLWGGKSKYGVNAVRHIDPHSIMTEYKNGPVEVSFTVYEDFAHKYKGGVYKHIGQSMGSHVAKLIGWGTSEGGEDWLLANSDWNRGWGDVCTLFSPPAFYVGGPHQPRGCKSESPEGGGKFLGSMGLGVLETTLSPKGRKGVVHTLPRPW

NbL00g02820.1 transaldolase [MW = 28.28 kDa]

No. of times detected



log(intensity)



Values from



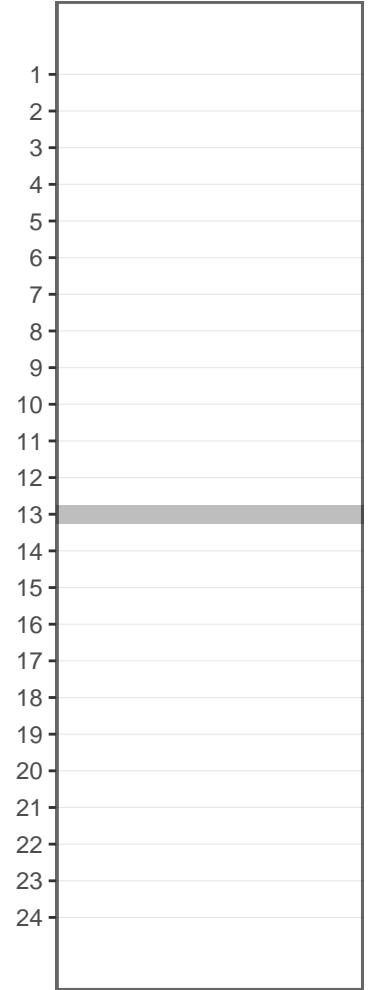
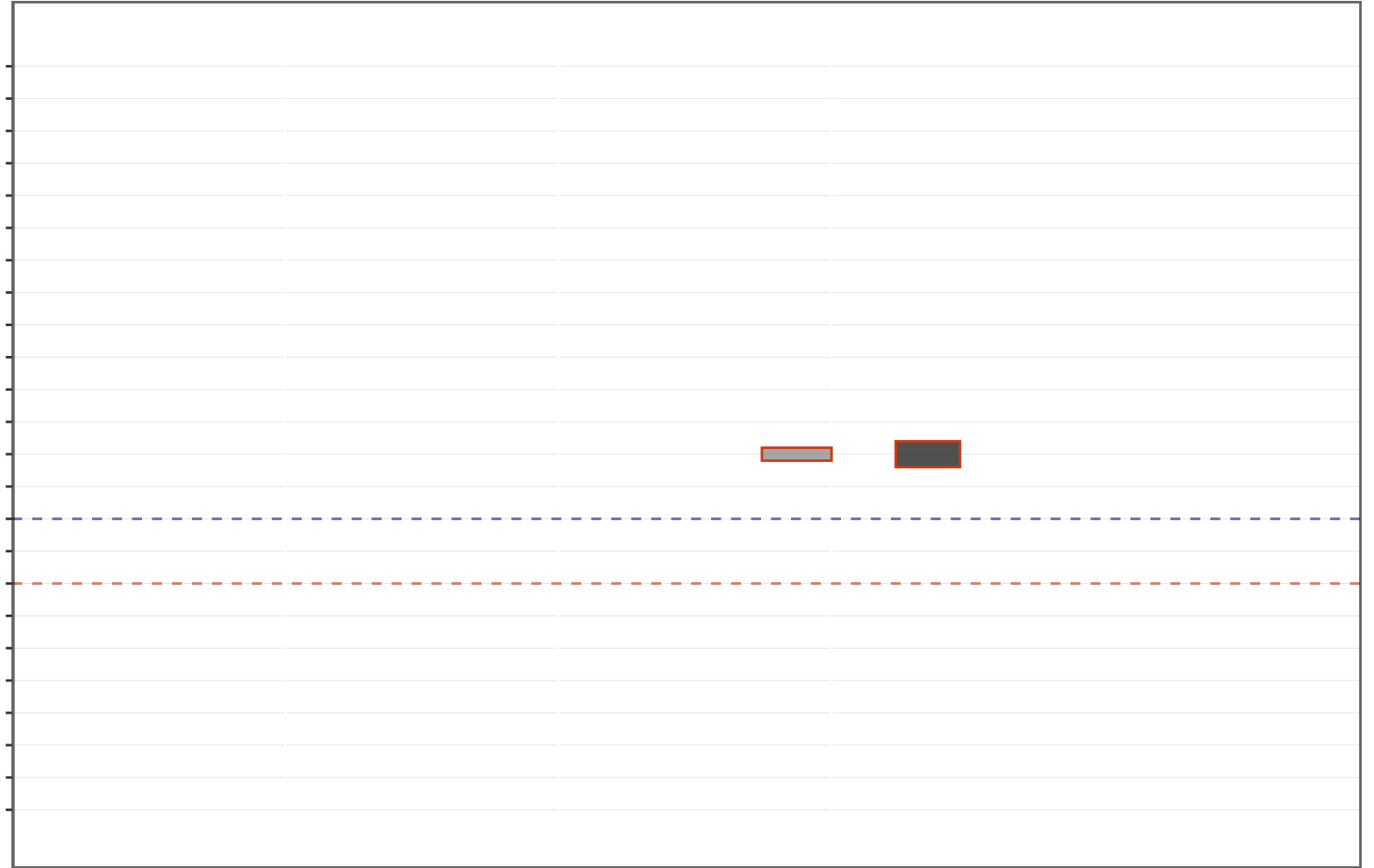
MW indication



Molecular weight



Gel Slice



Peptide counts over 4 repeats

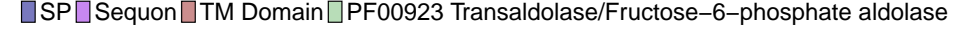


Protein length



Pfam domains

Pfam Description



Protein sequence:

SSTVYKRTTLIDLYERGGSPWYDNLGRPTDLLPLIESGVRGVTSENPIFQKAISTSNAYNEGFRDLVQAGKDESYVWELVYKDIQDAKLFESIVDKTDGADGYYVSEVSPRLAEDTKGTVEAAKWLHKLVPMGI

NbL00g02050.1 ubiquitin-conjugating_enzyme_E2_7-like [MW = 18.95 kDa]

No. of times detected



log(intensity)



Values from



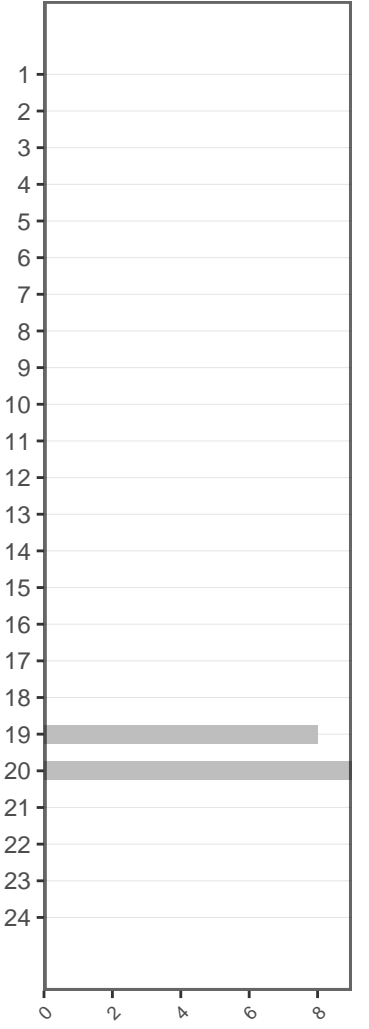
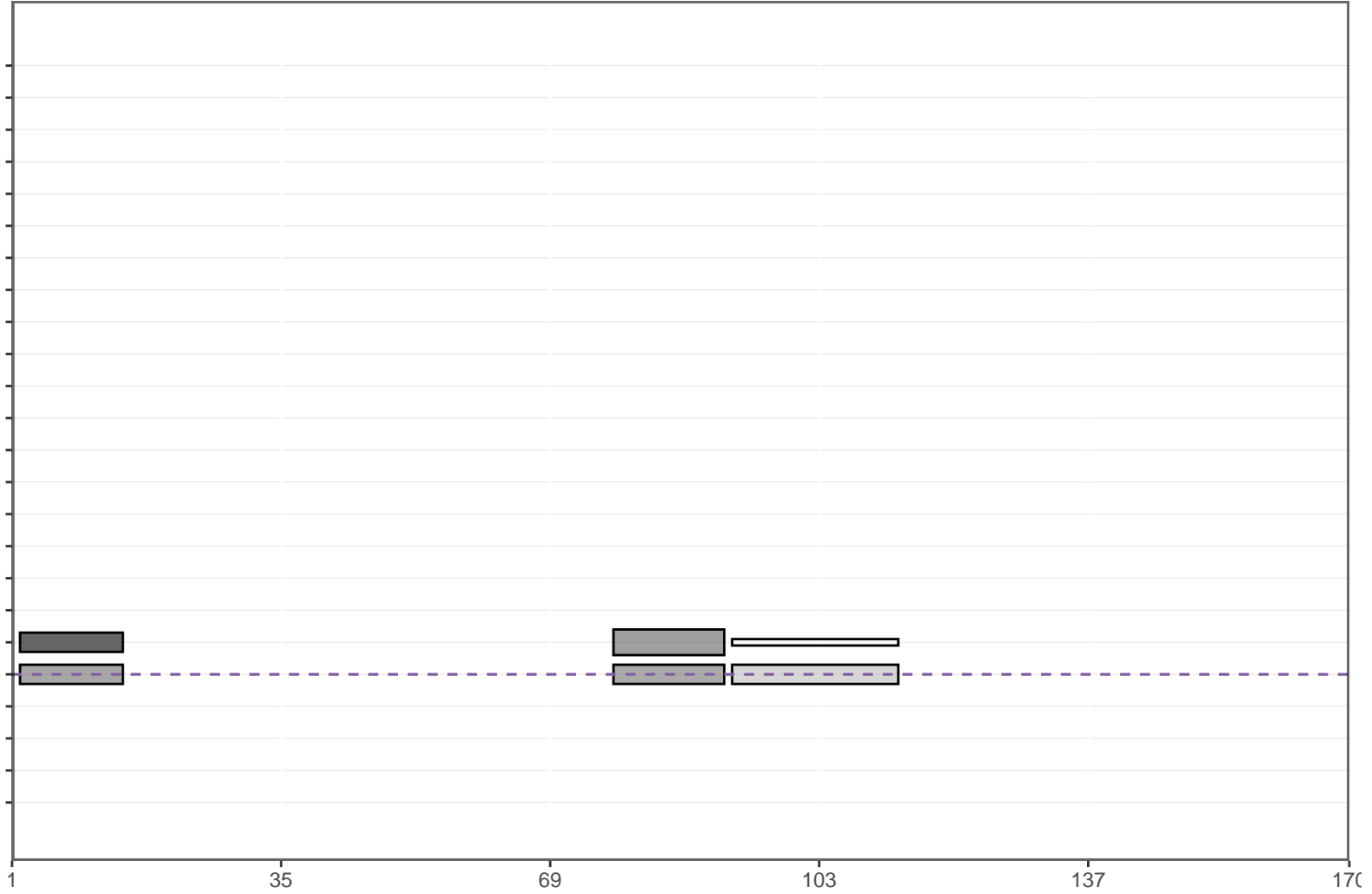
MW indication



Molecular weight

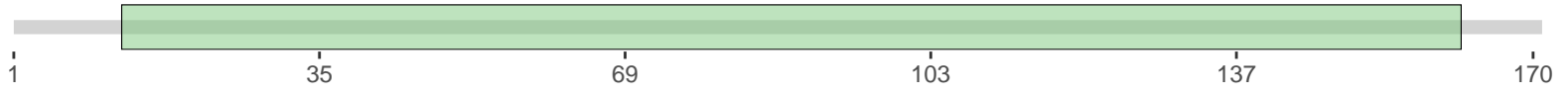


Gel Slice



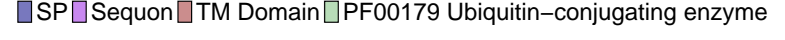
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

PPTVRFITDIIWIPNIVYSDGKVGIGILHPPGDDPNGYELASERWSPVHTVESIVLHISMLSSPNDESPNVEAAKEWREKRFENKRVSRQVRRSGEIP

NbL00g01620.1 uncharacterized_LOC107788871 [MW = 23.73 kDa]

No. of times detected



log(intensity)



Values from



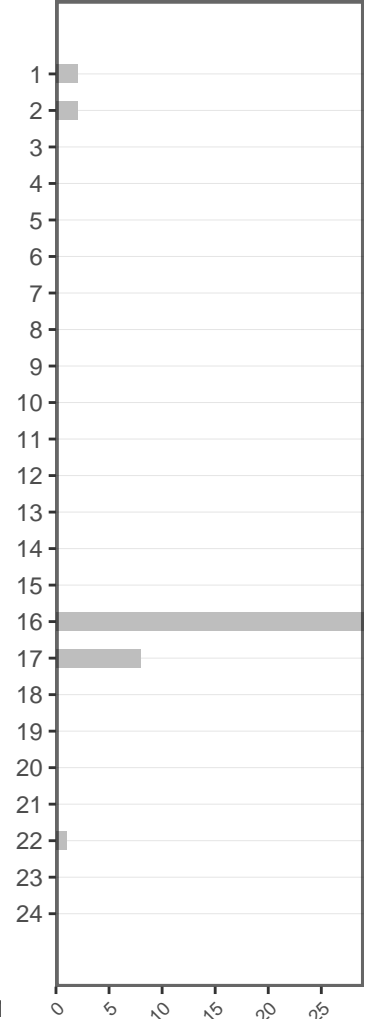
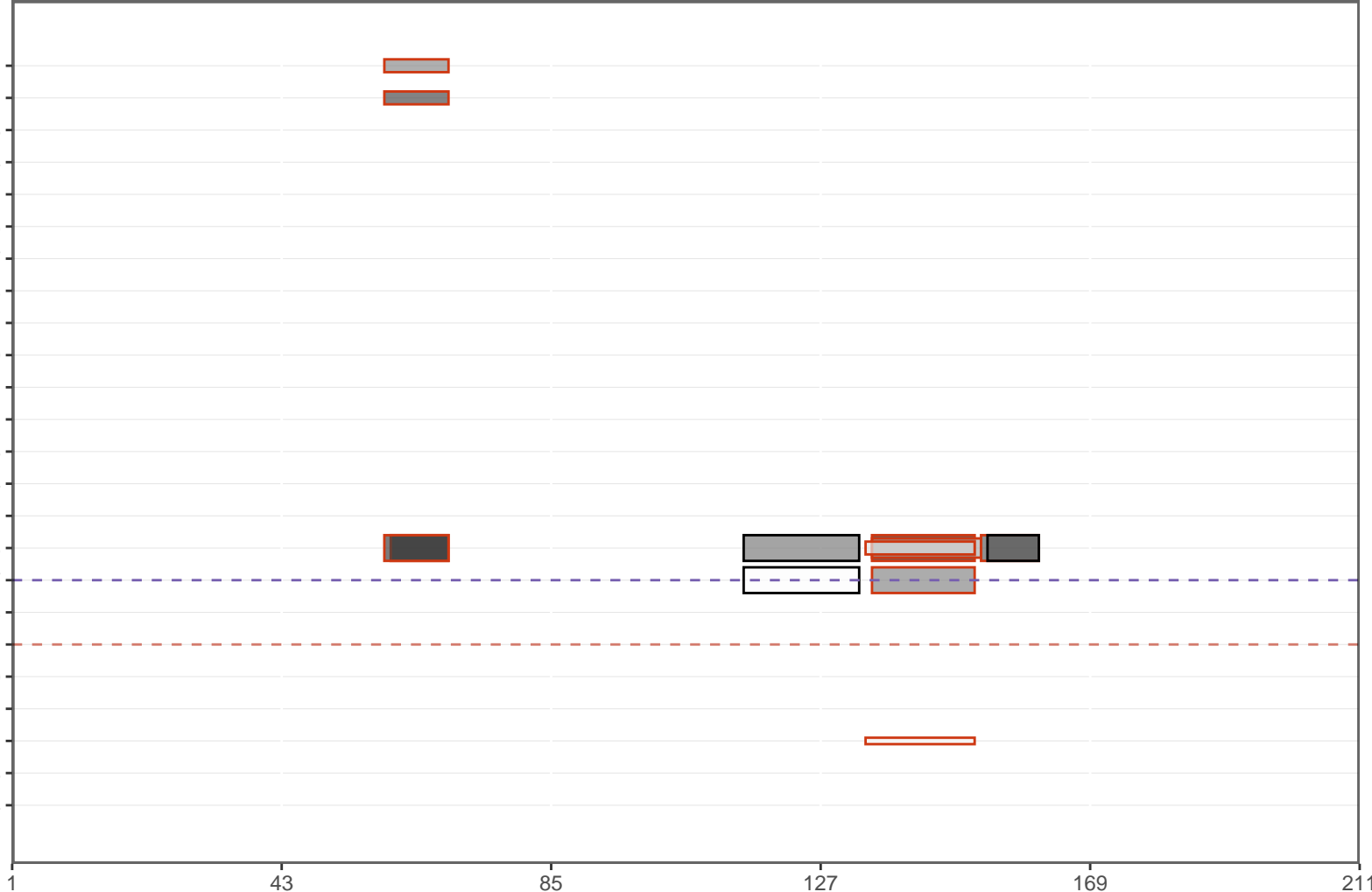
MW indication



Molecular weight

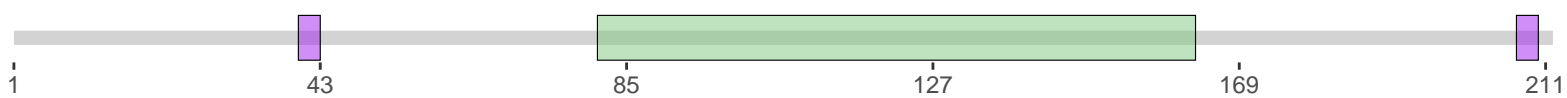


Gel Slice



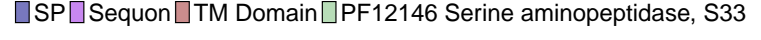
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description

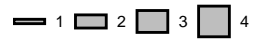


Protein sequence:

DFYTMVNLVAAMEKEGIVFRDFPPNGSESGFGVGNVREADDLHSHVEYFNGANRKYIVLGLHSGKGVSTFAKSGVYVESILCTVKKRFRTRNYGALGSFFSWVFGCGDITP

NbL00g01610.1 DNA-directed_RNA_polymerase_subunit_beta-like [MW = 123.55 kDa]

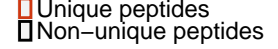
No. of times detected



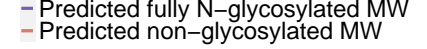
log(intensity)



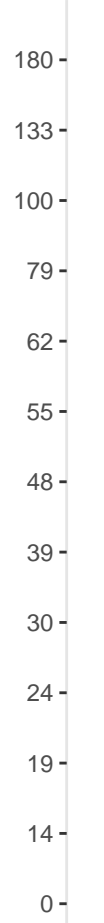
Values from



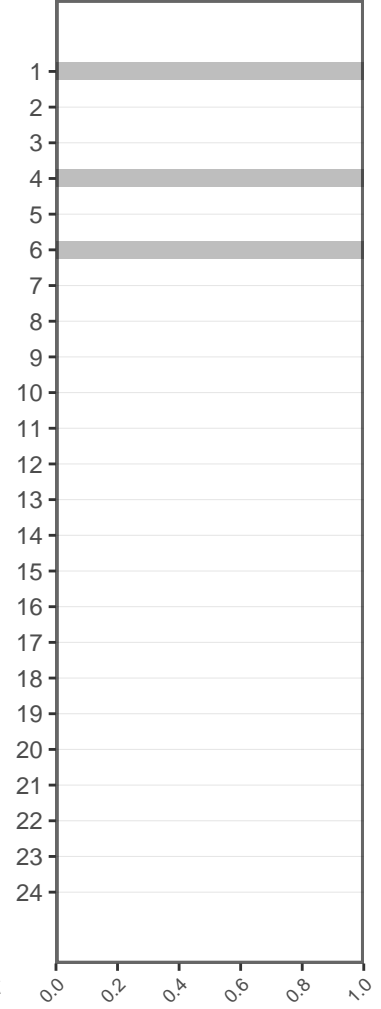
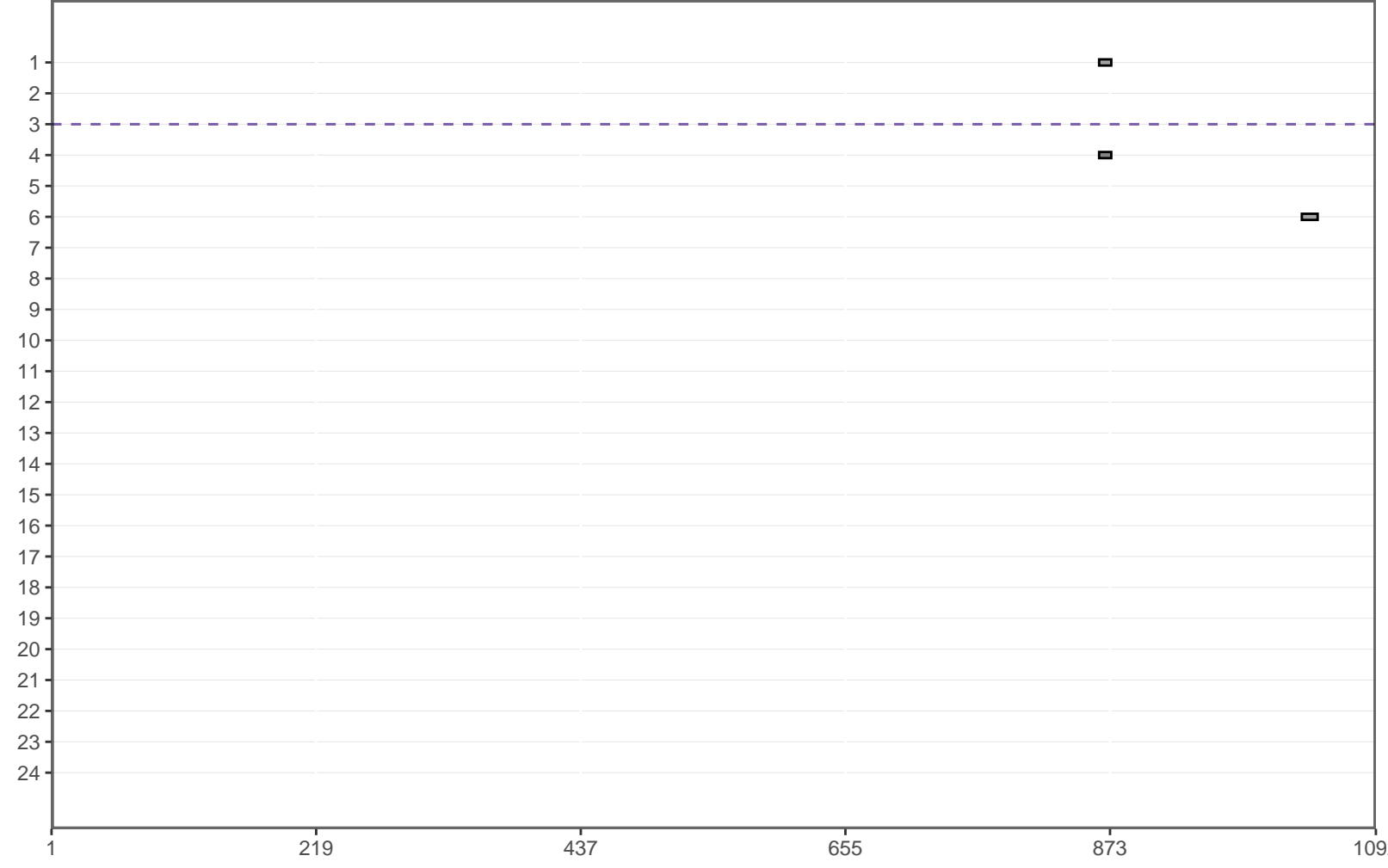
MW indication



Molecular weight



Gel Slice



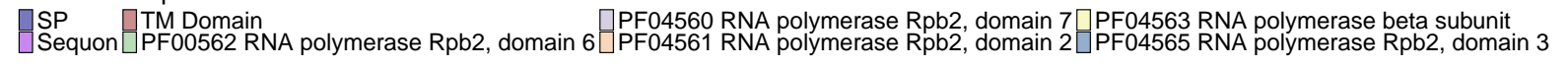
Protein length



Pfam domains



Pfam Description



Protein sequence:

LSFQRDEYYMVAAGNSLALNDGQEEGVWPRRYRQGEFLTAWEGVHLRSIFFQYFEGASLPIFIEHNDANRALMSNMQRQAVPLRSEKIGVGTGLERQAALDGGALAAEREGVVYNTDKLLAGNGDLGILVYQRSNNFTMHHQKGVPRGKCKKGGQLADGATVGGELAGKNVLAWMPWEGVNSBEDVLSERLVYEDHTSFKIRKYEIQHTVTSGGPEKVTNEPHLEAHLRLNLDKNGIVMLGSWVETGDNLVGLTPOVWKESSVAPEDRLRALGIC

NbL00g01400.1 ras-related_protein_RABF1 [MW = 21.57 kDa]

No. of times detected



log(intensity)



Values from



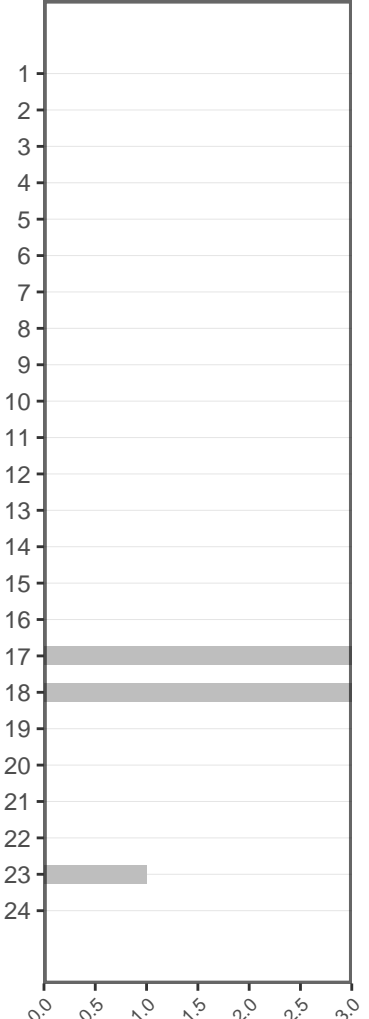
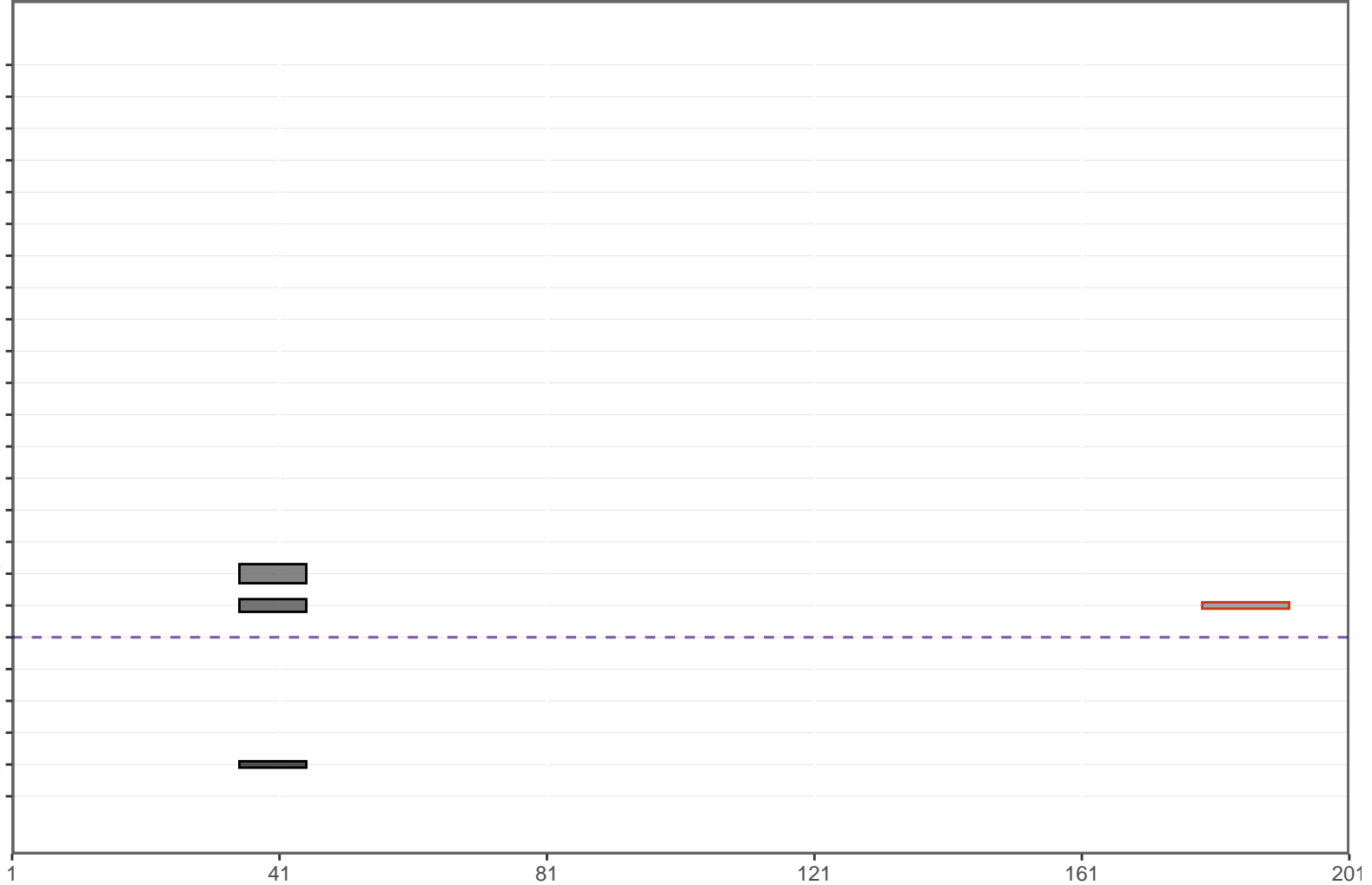
MW indication



Molecular weight

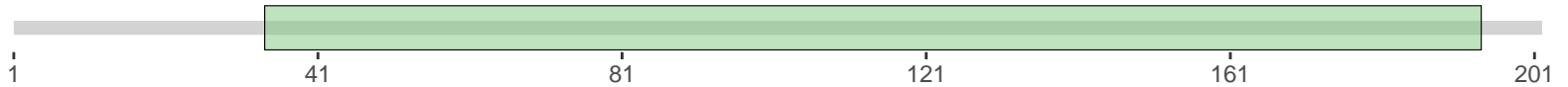


Gel Slice



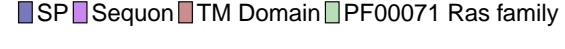
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

MDTADGQERYALALAPLYRGAEEVAVVYDTSPEFSAKAGVWKELOKHGSPDIVMALVGNKADLHEKREVTTQDGDCAEKNMGFFIETSAKTADNINGLFEEIAKRLPRPSAA*

NbL00g01300.1 50S_ribosomal_protein_L2-A_chloroplastic [MW = 30.01 kDa]

No. of times detected



log(intensity)



Values from



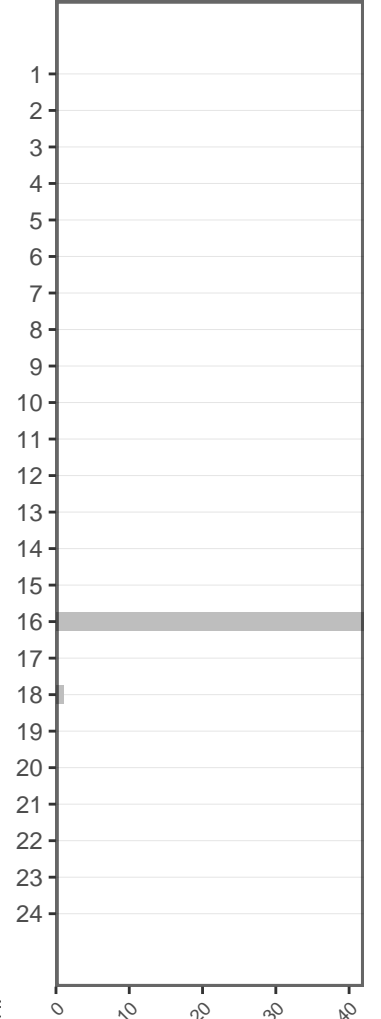
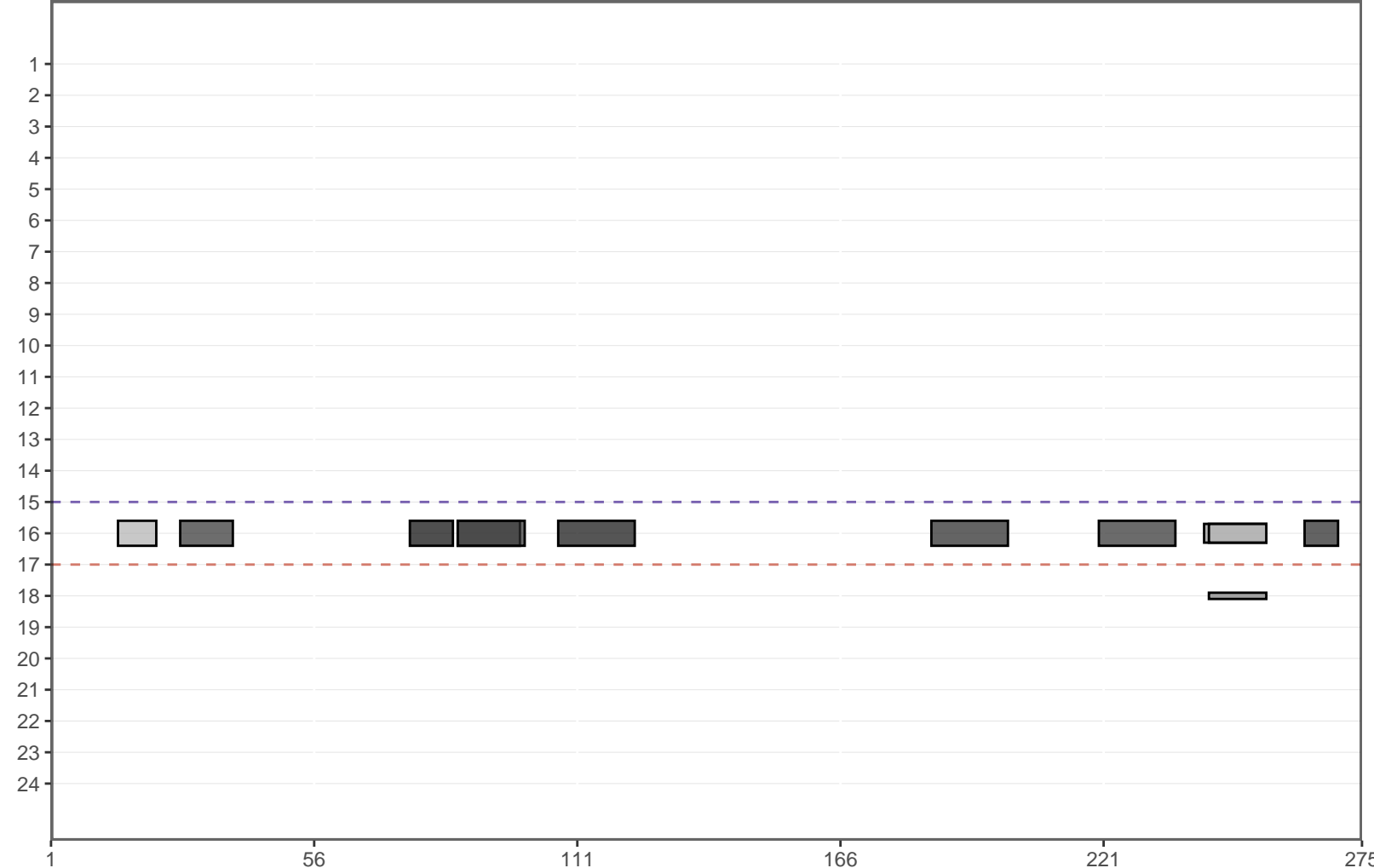
MW indication



Molecular weight

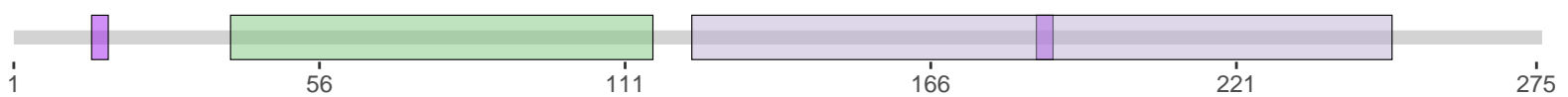


Gel Slice



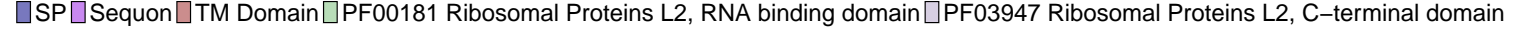
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

ALPLTDMPLGTAIINIEITLGGKGGALARAAGAVAKLAKKEGKTSATLNLPSGGEVRLISKNSGTSATGGVGNVGVNGKSLGRAGSKRWLGRKRPVVRGVVANNPVDHPHGSGGEGRAPIGRKKPTTPWGVYALGRRSRKRKRYSDNLILRRRK

NbL00g00910.1 protein_IN2-1_homolog_B-like [MW = 33.24 kDa]

No. of times detected



log(intensity)



Values from



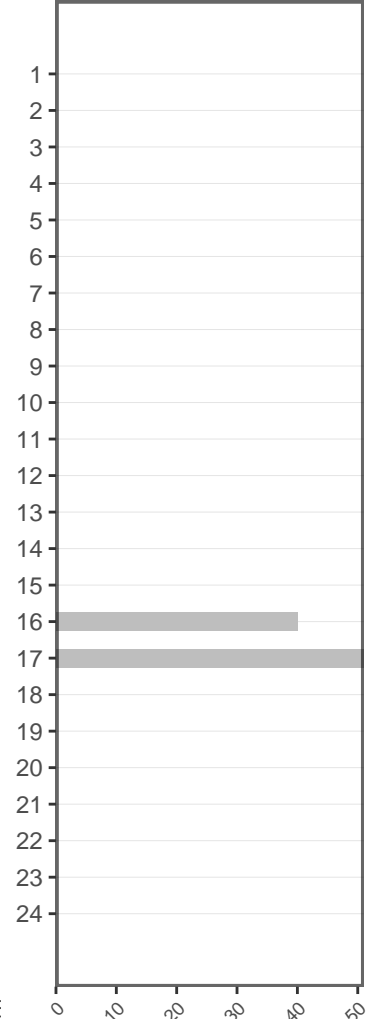
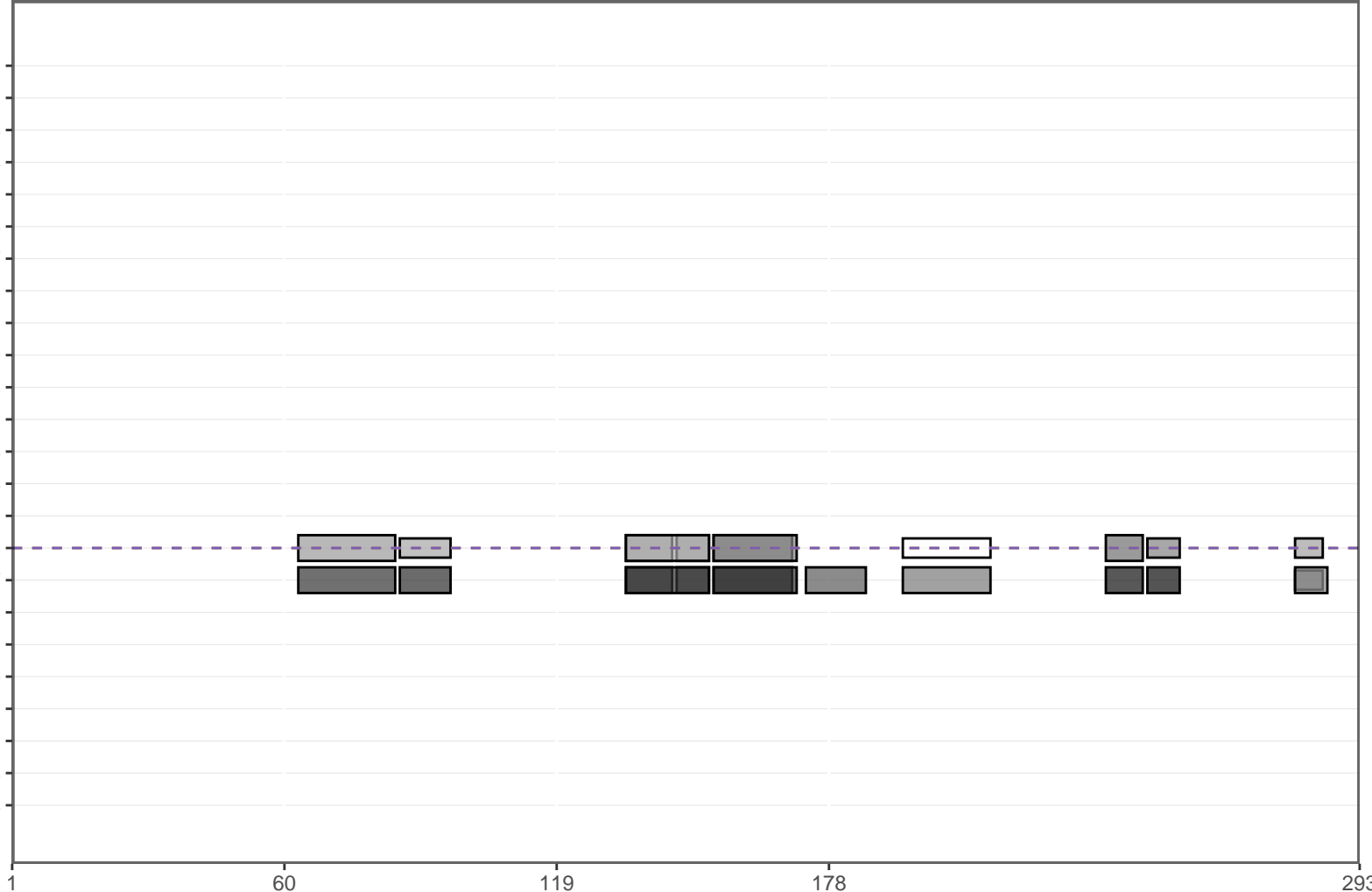
MW indication



Molecular weight

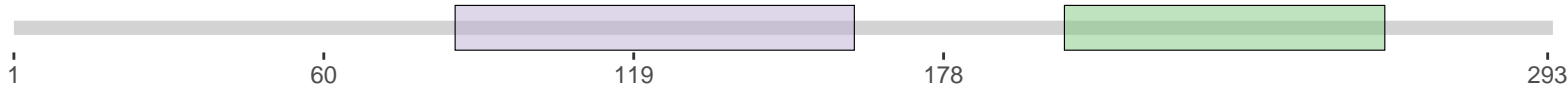


Gel Slice



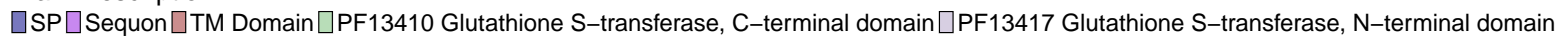
Peptide counts over 4 repeats

Protein length



Pfam domains

Pfam Description



Protein sequence:

VPSLEHNNNEVYKGGEMDLIRYHDSNFEKPSLFPDDPKRKFQEMFHSFDSFYKAVISSFKEDTANDANAAFDSIETLSKFDVGGPFFLGTFRSLVDIYAWPIERFQPFLLDQKNFDITTRGRSKLAAWEEEMNGIEAVTVYTKRNKELLESYKRFSGV

NbL00g00890.1 ras-related_protein_RABE1a [MW = 23.76 kDa]

No. of times detected



log(intensity)



Values from



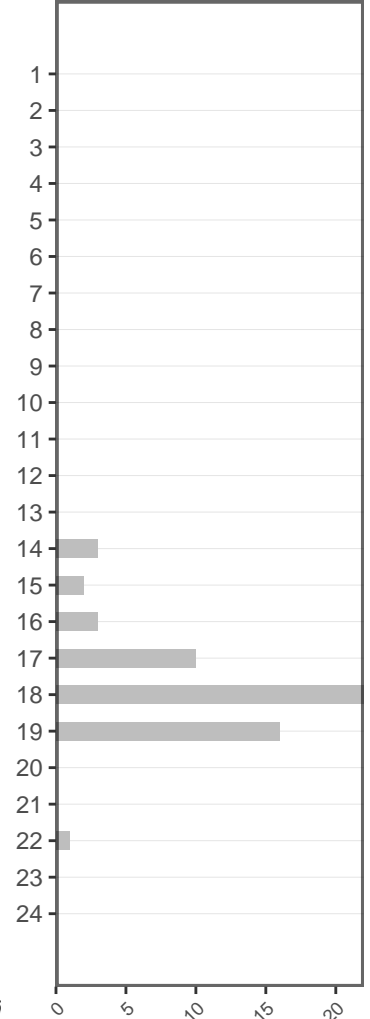
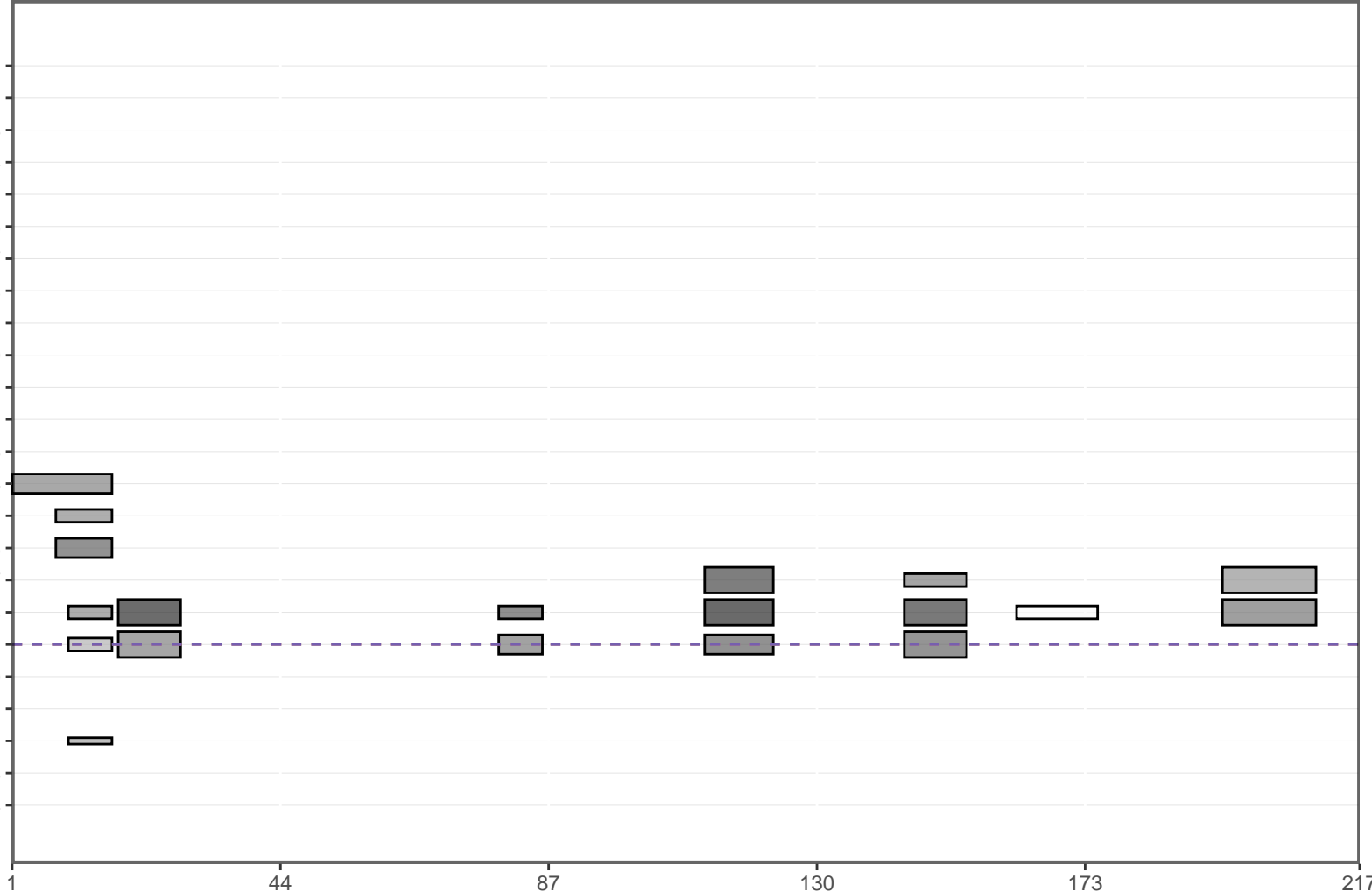
MW indication



Molecular weight

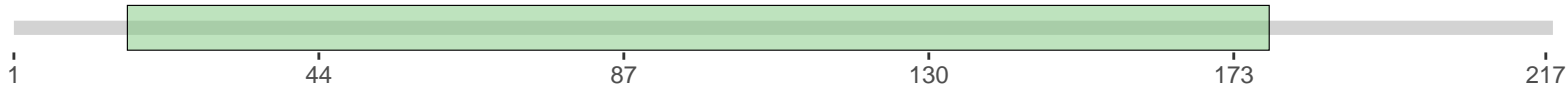


Gel Slice



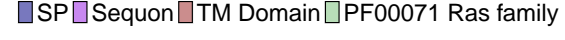
Protein length

Peptide counts over 4 repeats



Pfam domains

Pfam Description



Protein sequence:

DESSFNIRNWRNEGHASDNVKNLGVNKADMDSEKRAVPTSKGGALAEVGIKFFETSAKTNLNVQVFFSARDIKRGLADTDSKAEPSTLKNQPDAGAGGGAQKSAAGGSE

NbL00g00550.1 heat_shock_cognate_70_kDa_protein_2-like [MW = 71.01 kDa]

No. of times detected



log(intensity)



Values from



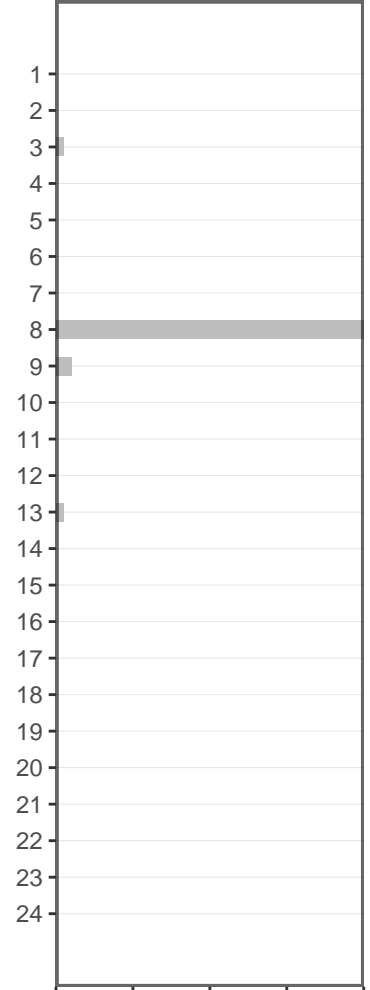
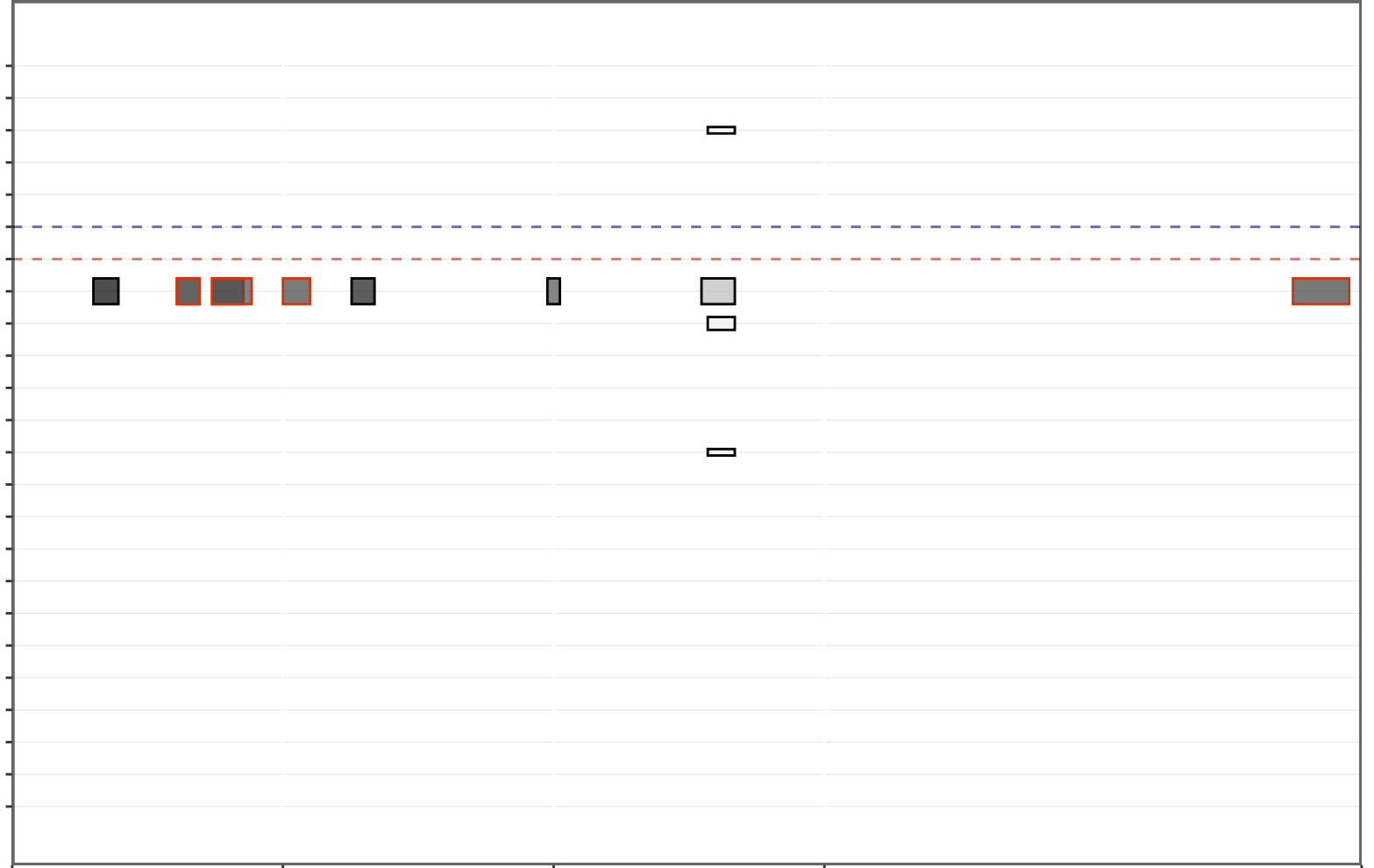
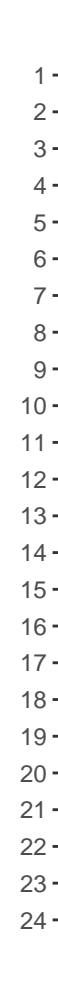
MW indication



Molecular weight



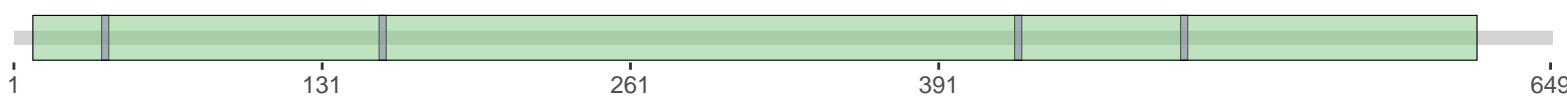
Gel Slice



Peptide counts over 4 repeats

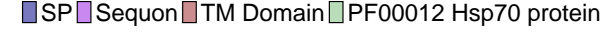
1 131 261 391 649

Protein length



Pfam domains

Pfam Description



Protein sequence:

IDLFRKCMPEVYKGLRDAKMKSTVHIVLVGGSTRIPKVKQLLQDFNGKELCKSNPGEAWYGAAVGAAALSGEGNEKVGDLLLDTPLSLGLGTAGGVMVTLIPRNTIPIPTKKEQVFTSYSDNGPQVLIQVYVEGERARTRDNNLLGKFEKSGFPAPRGGVPIQTVCFDDIDANGLNVSAEKDTTGGKNTITNDKGRLSKEIEKIMVGEAEKYKAEDEEHKKVKAANALENAYNMRNTIKDKEKSLSPDDKKKIEDAIDQAIWLDENGLAEDEFEDKMKELKESIC

NbL00g00360.1 glutelin_type-B_2-like [MW = 38.19 kDa]

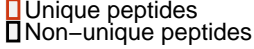
No. of times detected



log(intensity)



Values from



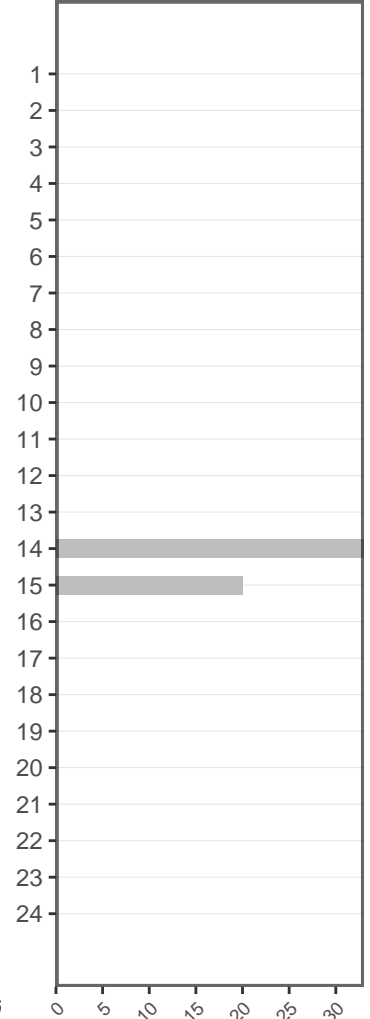
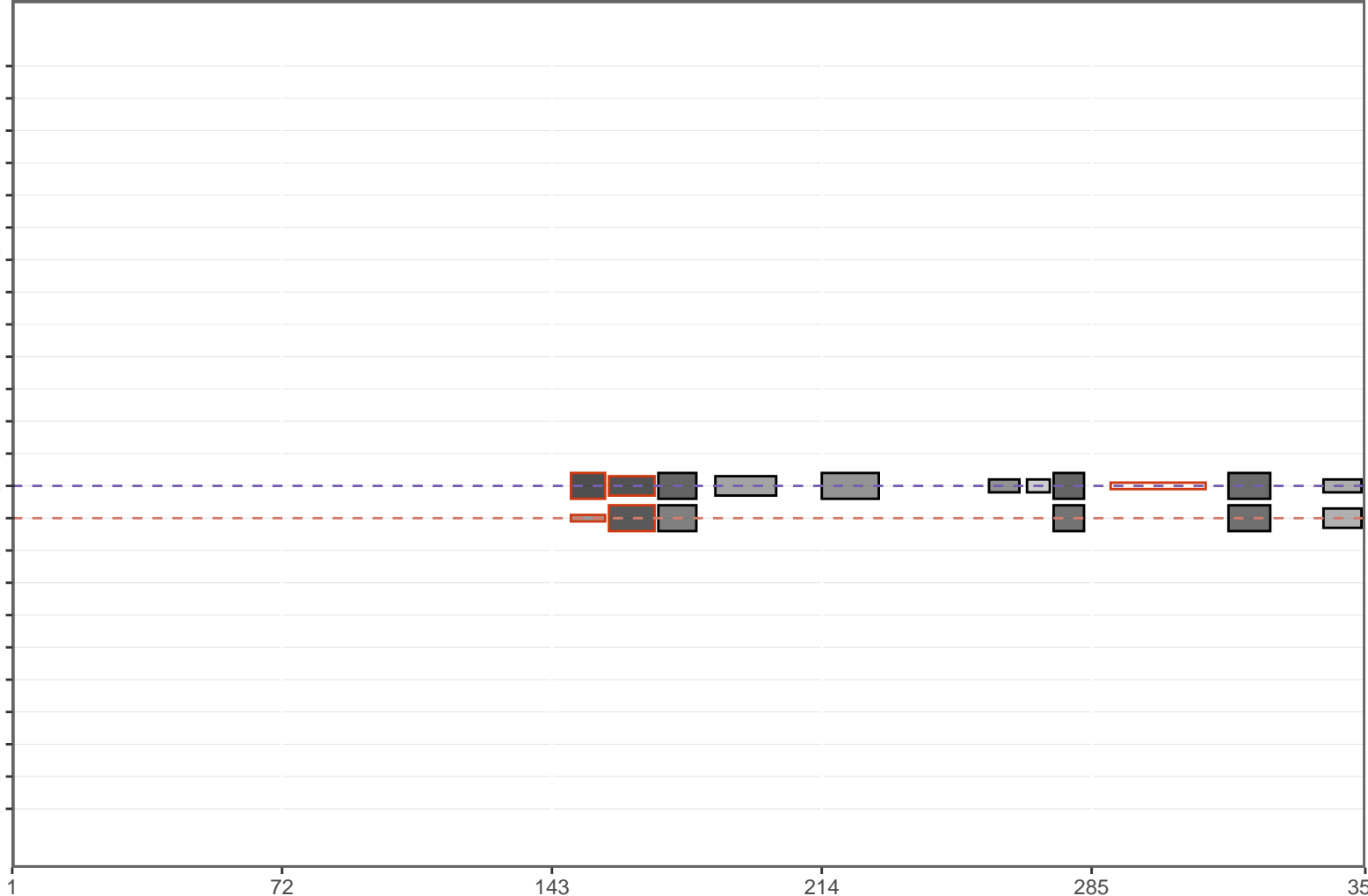
MW indication



Molecular weight



Gel Slice



Protein length



Peptide counts over 4 repeats

Pfam domains



Pfam Description



Protein sequence:

CGIVKLDAGFQMPFEPKGGHRDGMVNLGELFLEVDKDKGGKVVVNLTKNPLVIGSEVLGADLVRINGSAMCSGFSGDSALGVTVYRGGSRGVGVGPDGKRVLETHKAGNLFVPRFFVYVKIGDPDGMDFSIITFNPIFHLAGRTSVVKALSPQVLGAAPKVEADVEKGFSEKRTAEIFFPPN

NbL00g00330.1 photosystem_II_CP43_reaction_center_protein-like [MW = 14.98 kDa]

No. of times detected



log(intensity)



Values from



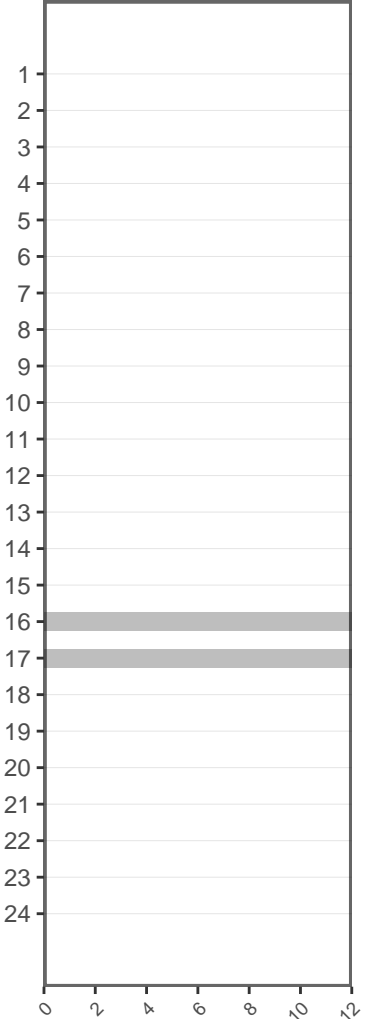
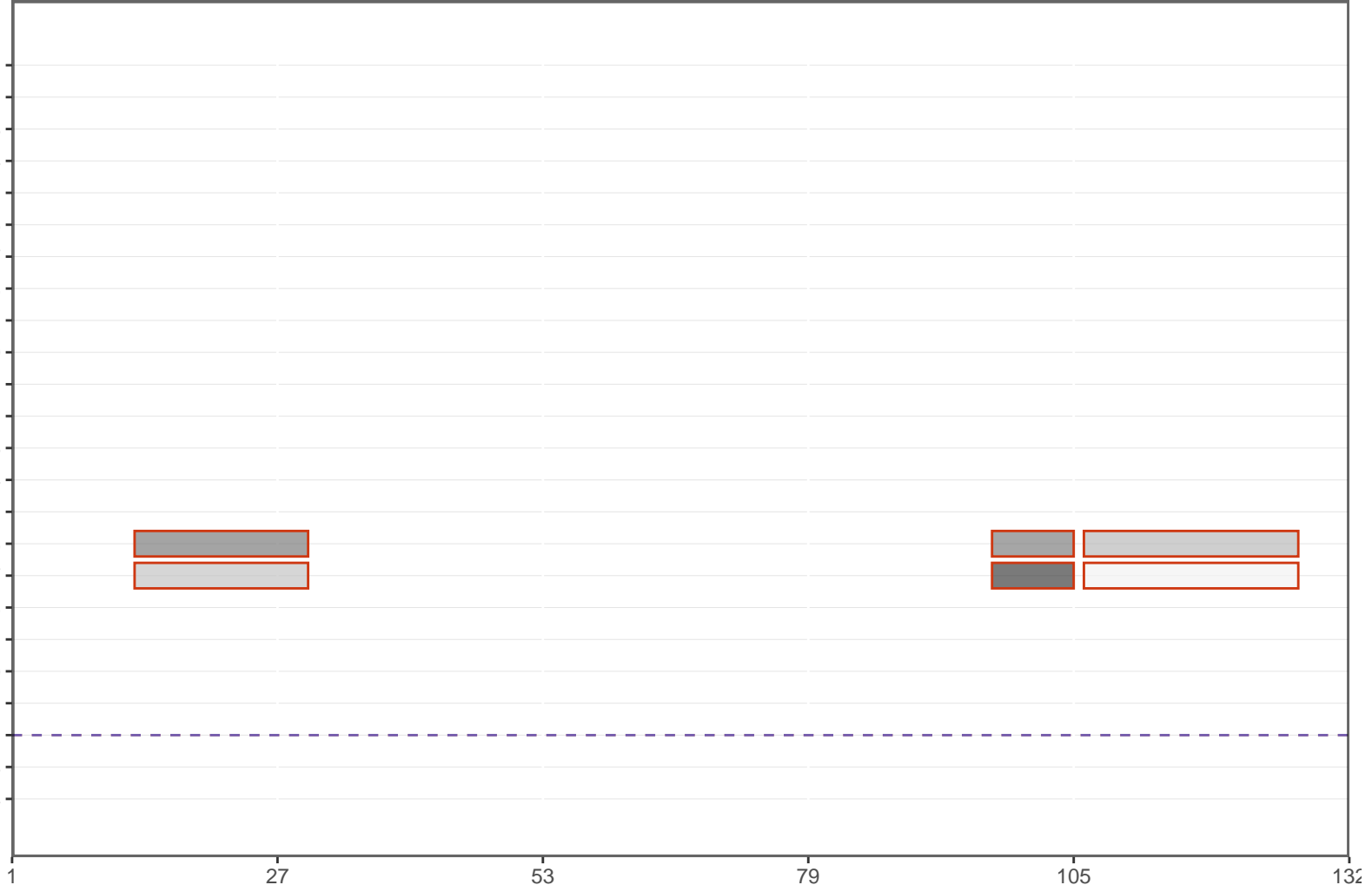
MW indication



Molecular weight



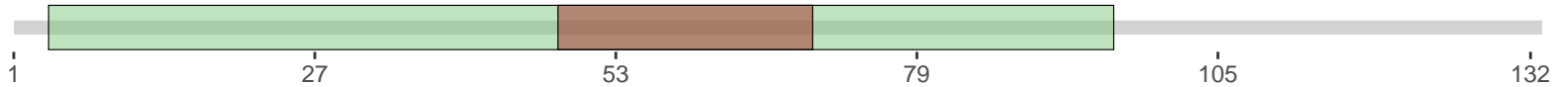
Gel Slice



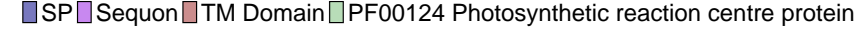
Protein length



Pfam domains



Pfam Description



Protein sequence:

VPVTLQVMSALGVVGLALNLRVDFVSGEIRAAEDPEFETFYTKNILLNEGIRAWMAQDQPHENLFFEEVLRGNAL

NbL00g00250.1 GTPase_Der [MW = 72.38 kDa]

No. of times detected



log(intensity)



Values from



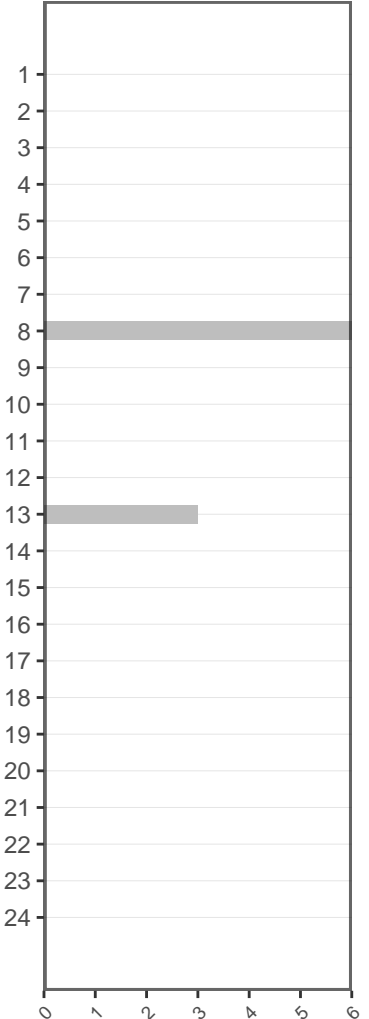
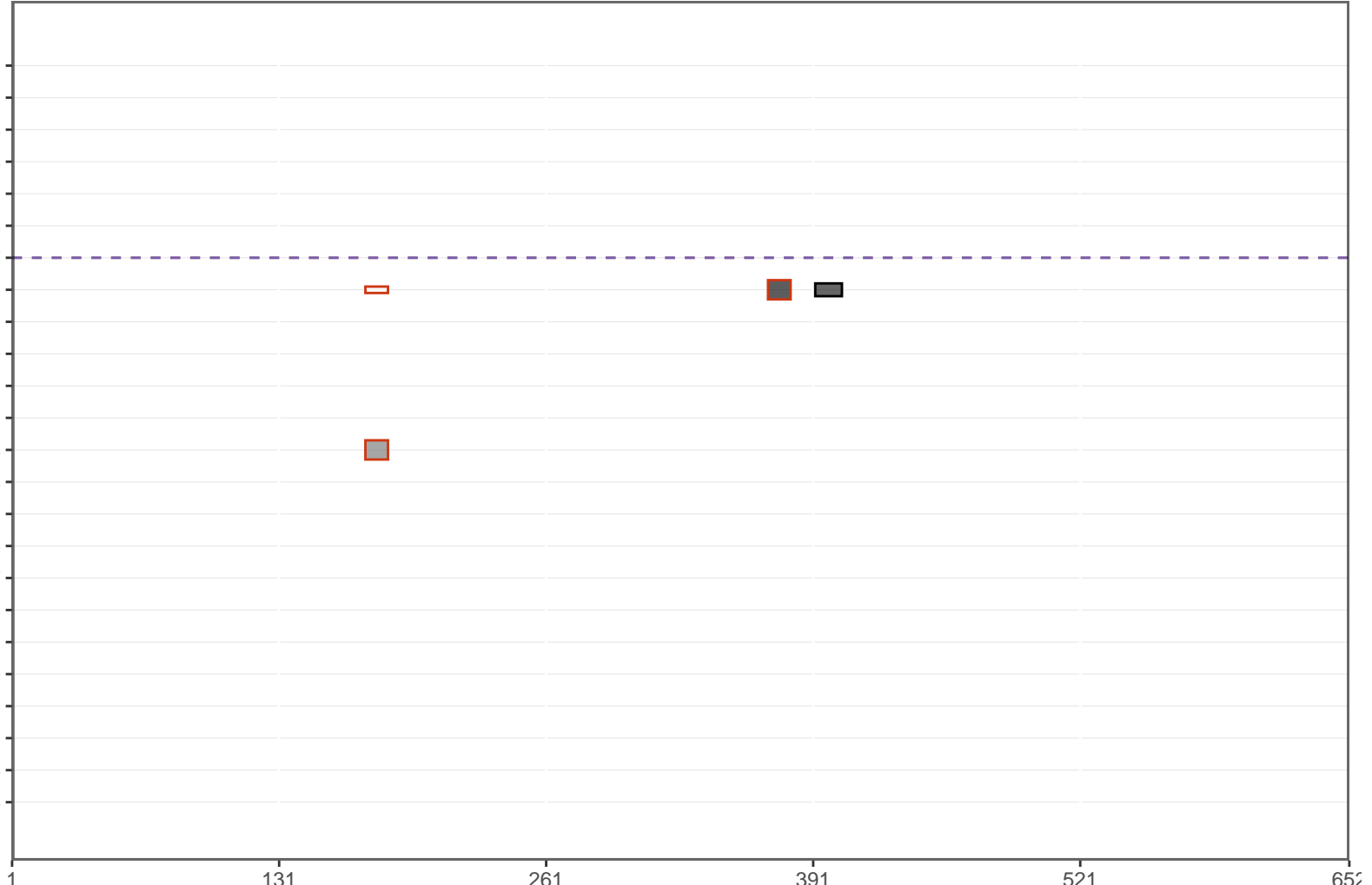
MW indication



Molecular weight



Gel Slice



Protein length

Peptide counts over 4 repeats



Pfam domains

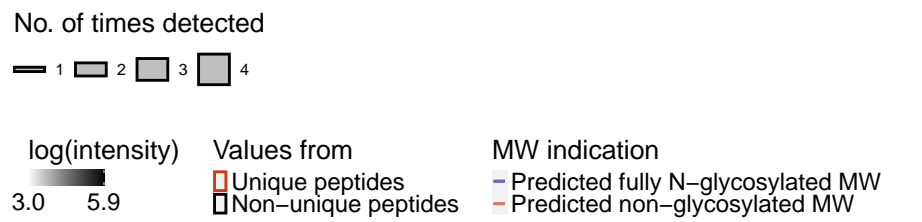
Pfam Description

- SP
- Sequon
- TM Domain
- PF01926 50S ribosome-binding GTPase
- PF14714 KH-domain-like of EngA bacterial GTPase enzymes, C-terminal

Protein sequence:

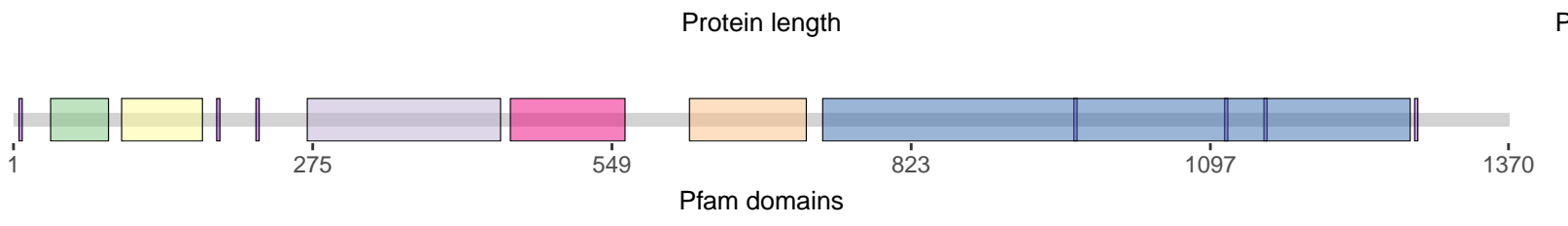
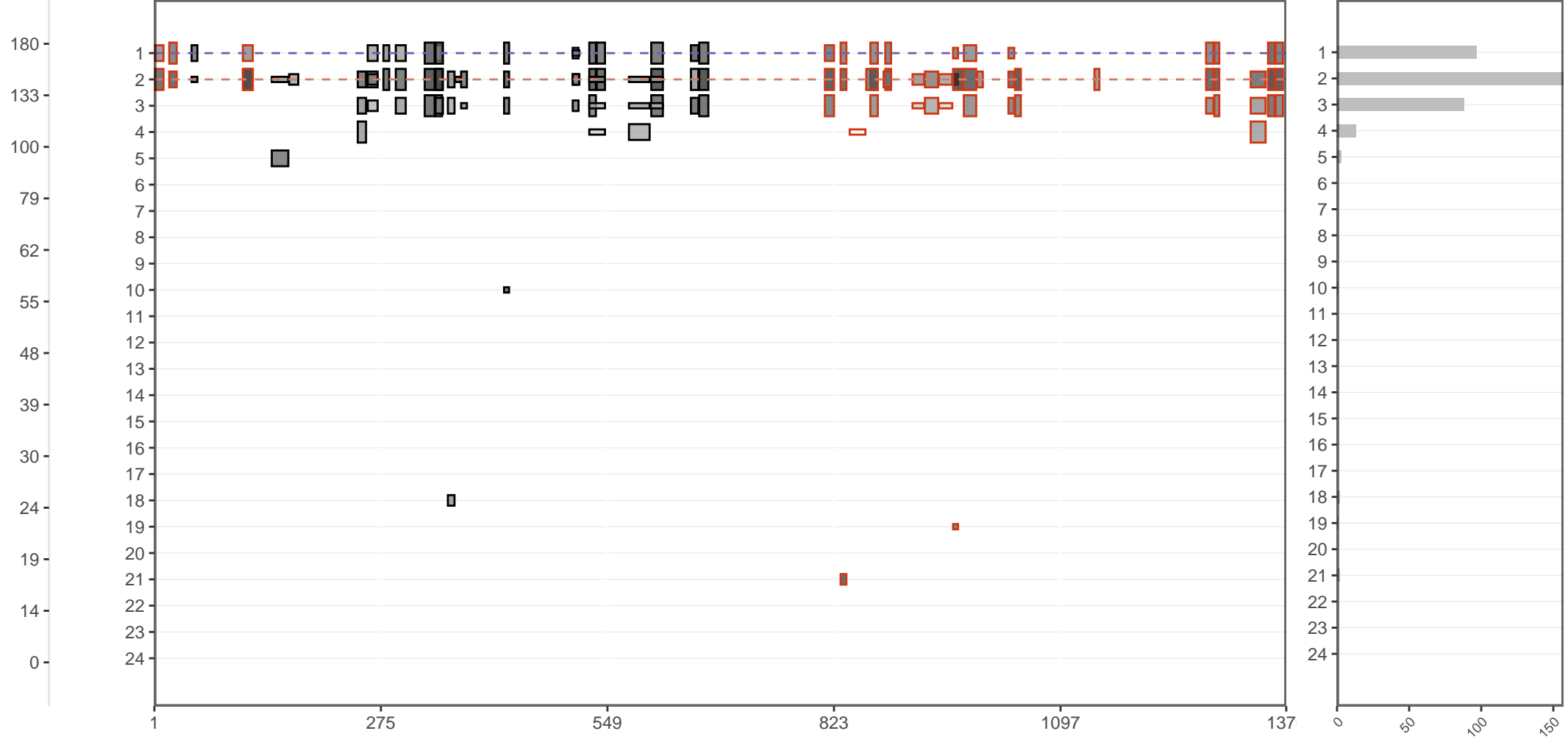
ILGFDLPISALSGTGTGVALDLVGGKIKVEEPEYLEEENVYPAIIVGRPNVNGKSLNALVGENRTIVSPVGGTRDMDTEFTGSDGKFRLLDTAGIRKAAVAAGSGSPEALVNGAFRAIRRRSDVVALVIEAAMGTEGDKIAERIEKGGKGLVWKKWDTPFNKNGGETTVFYEEEDVRRKVRKLSWAPVYGTAMAGHSEVKIWAATAAWEKERBRLTALNGVYREAAFKAPRTRGGKRGVYVYSTQAARRPDTFFVFNDAKLFSETYRRYMEKQLRMSAGFAGTP

NbL00g00230.1 xanthine_dehydrogenase_1-like [MW = 150.4 kDa]



Molecular weight

Gel Slice



- PF00941 FAD binding domain in molybdopterin dehydrogenase
- PF01799 [2Fe-2S] binding domain
- PF03450 CO dehydrogenase
- PF01315 Aldehyde oxidase and xanthine dehydrogenase, a/b hammerhead domain
- PF02738 Molybdopterin-binding domain of aldehyde dehydrogenase

Protein sequence:

NMVGPIVTDDELFAIVFVTGGVGGVGVVADTHEENAKLAARKVHVEYEDLPVLSIEDAIGANSHYHPTARGLTKGDEGGFGSGGGDNIIEGEVIRVGGDGHFYLEPGGLTWTVDSGNEVHMISSTGAPQKHQKVVSGVGLFMSKVVQKTRIGGGFGGKETRSAFLAAVAWPSYLLDRPVKLLDRDIDMMISGGRHSLGKVVYGFINDGKVLALDLRIYENAGNSLDLSLWLERAMFHSNHYEIRNMRVNGAVGETNFPNSATFRGGPQCLIAENVIERIA