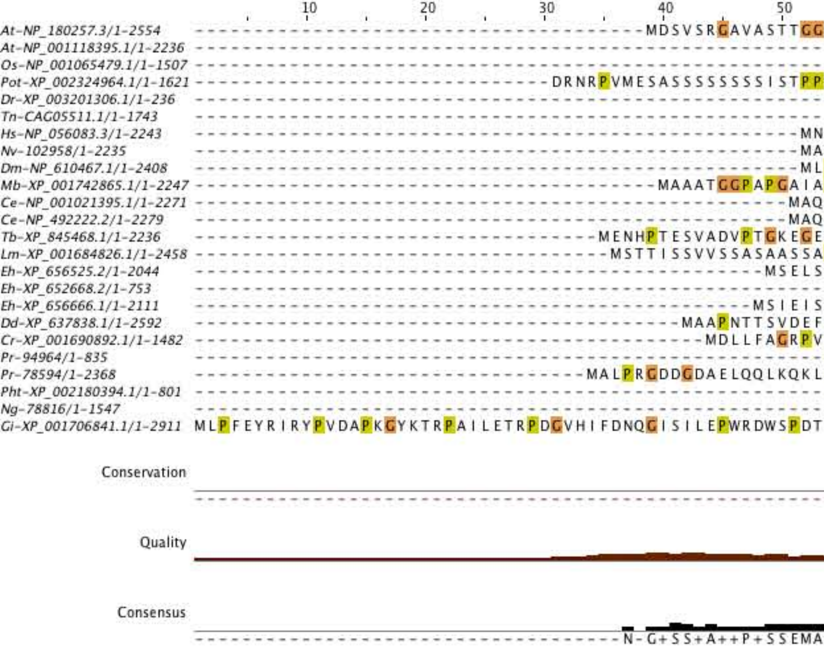

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At-NP_001118395.1/1-2236  -----------------------------------------------------
Os-NP_001065479.1/1-1507  -----------------------------------------------------
Pot-XP_002324964.1/1-1621 ------------------------------DRNRPVMESASSSSSSSSISTPP
Dr-XP_003201306.1/1-236   -----------------------------------------------------
Tn-CAG05511.1/1-1743      -----------------------------------------------------
Hs-NP_056083.3/1-2243     ---------------------------------------------------MN
Nv-102958/1-2235          ---------------------------------------------------MA
Dm-NP_610467.1/1-2408     ---------------------------------------------------ML
Mb-XP_001742865.1/1-2247  ---------------------------------------MAAATGGPAPGAIA
Ce-NP_001021395.1/1-2271  --------------------------------------------------MAQ
Ce-NP_492222.2/1-2279     --------------------------------------------------MAQ
Tb-XP_845468.1/1-2236     ----------------------------------MENHPTESVADVPTGKEGE
Lm-XP_001684826.1/1-2458  -----------------------------------MSTTISSVVSSASAASSA
Eh-XP_656525.2/1-2044     ------------------------------------------------MSELS
Eh-XP_652668.2/1-753      -----------------------------------------------------
Eh-XP_656666.1/1-2111     -----------------------------------------------MSIEIS
Dd-XP_637838.1/1-2592     -----------------------------------------MAAPNTTSVDEF
Cr-XP_001690892.1/1-1482  -------------------------------------------MDLLFAGRPV
Pr-94964/1-835            -----------------------------------------------------
Pr-78594/1-2368           ---------------------------------MALPRGDDGDAELQQLKQKL
Pht-XP_002180394.1/1-801  -----------------------------------------------------
Ng-78816/1-1547           -----------------------------------------------------
Gi-XP_001706841.1/1-2911  MLPFEYRIRYPVDAPKGYKTRPAILETRPDGVHIFDNQGISILEPWRDWSPDT

Conservation
                          -----------------------------------------------------

Quality

Consensus
                          ------------------------------------N-G+SS+A++P+SSEMA
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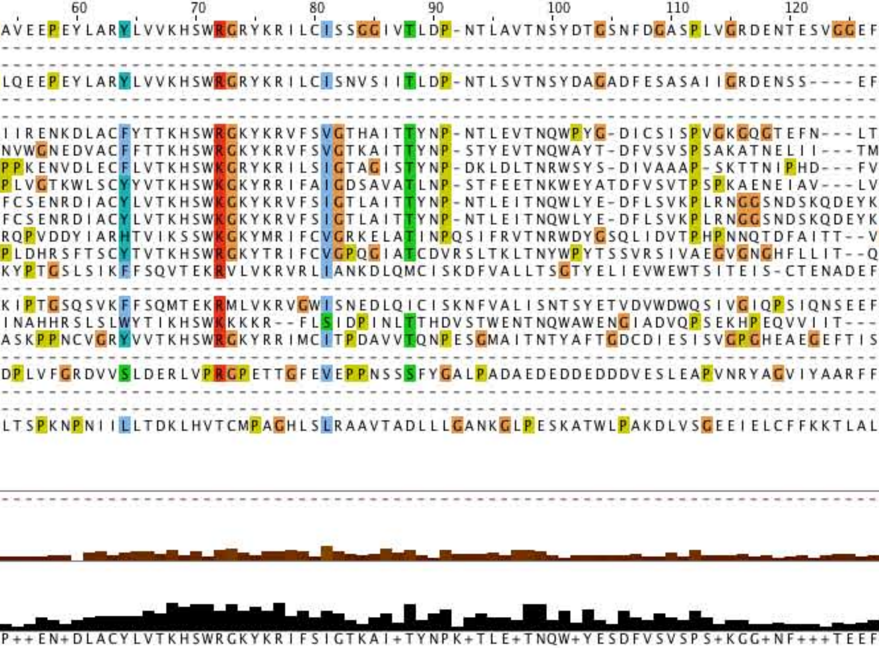

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--------------------------------------------------------------------------
--------------------------------------------------------------------------
IIRENKDLACFYTTKHSWRGKYKRVFSVGTHAITTYNP-NTLEVTNQWPYG-DICSISPVGKGQGTEFN---LT
NVWGNEDVACFFTTKHSWRGKYKRVFSVGTKAITTYNP-STYEVTNQWAYT-DFVSVSPSAKATNELII---TM
PPKENVDLECFLVTKHSWKGRYKRILSIGTAGISTYNP-DKLDLTNRWSYS-DIVAAAP-SKTTNIPHD---FV
PLVGTKWLSCYYVTKHSWKGKYRRIFAIGDSAVATLNP-STFEETNKWEYATDFVSVTPSPKAENEIAV---LV
FCSENRDIACYLVTKHSWKGKYKRVFSIGTLAITTYNP-NTLEITNQWLYE-DFLSVKPLRNGGSNDSKQDEYK
FCSENRDIACYLVTKHSWKGKYKRVFSIGTLAITTYNP-NTLEITNQWLYE-DFLSVKPLRNGGSNDSKQDEYK
RQPVDDYIARHTVIKSSWKGKYMRIFCVGRKELATINPQSIFRVTNRWDYGSQLIDVTPHPNNQTDFAITT--V
PLDHRSFTSCYTVTKHSWRGKYTRIFCVGPQGIATCDVRSLTKLTNYWPYTSSVRSIVAEGVGNGHFLLIT--Q
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--------------------------------------------------------------------------
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--------------------------------------------------------------------------
--------------------------------------------------------------------------
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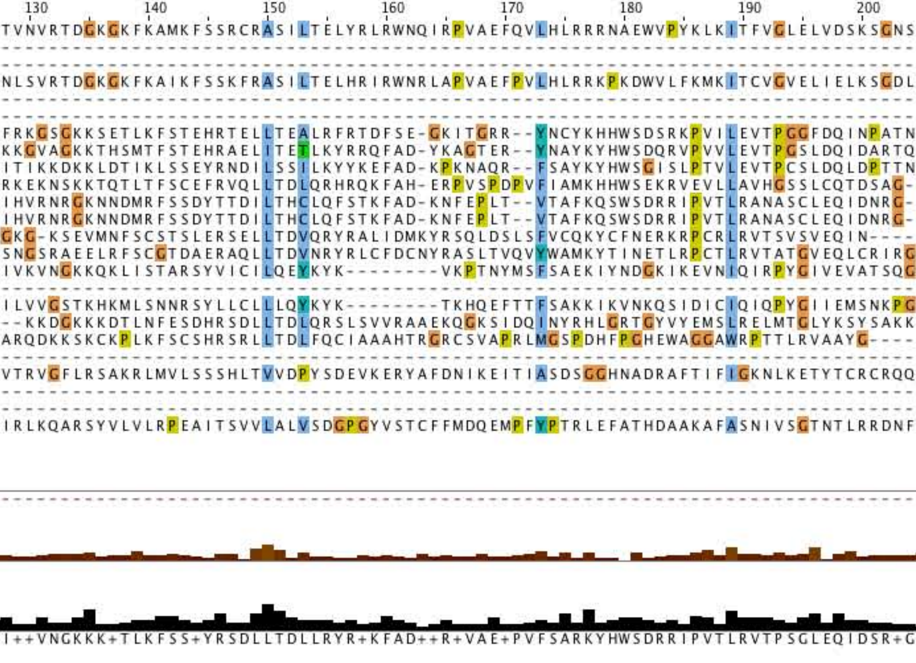

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-----------------------------------------------------------------------------
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-----------------------------------------------------------------------------
-----------------------------------------------------------------------------
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RKEKNSKKTQTLTFSCEFRVQLLTDLQRHRQKFAH-ERPVSPDPVFIAMKHHWSEKRVEVLLAVHGSSLCQTDSAG-
IHVRNRGKNNDMRFSSDYTTDILTHCLQFSTKFAD-KNFEPLT--VTAFKQSWSDRRIPVTLRANASCLEQIDNRG-
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SNGSRAEELRFSCGTDAERAQLLTDVNRYRLCFDCNYRASLTVQVYWAMKYTINETLRPCTLRVTATGVEQLCRIRG
IVKVNGKKQKLISTARSYVICILQEYKYK---------VKPTNYMSFSAEKIYNDGKIKEVNIQIRPYGIVEVATSQG
-----------------------------------------------------------------------------
ILVVGSTKHKMLSNNRSYLLCLLLQYKYK---------TKHQEFTTFSAKKIKVNKQSIDICIQIQPYGIIEMSNKPG
--KKDGKKKDTLNFESDHRSDLLTDLQRSLSVVRAAEKQGKSIDQINYRHLGRTGYVYEMSLRELMTGLYKSYSAKK
ARQDKKSKCKPLKFSCSHRSRLLTDLFQCIAAAHTRGRCSVAPRLMGSPDHFPGHEWAGGAWRPTTLRVAAYG----
-----------------------------------------------------------------------------
VTRVGFLRSAKRLMVLSSSHLTVVDPYSDEVKERYAFDNIKEITIASDSGGHNADRAFTIFIGKNLKETYTCRCRQQ
-----------------------------------------------------------------------------
-----------------------------------------------------------------------------
IRLKQARSYVLVLRPEAITSVVLALVSDGPGYVSTCFFMDQEMPFYPTRLEFATHDAAKAFASNIVSGTNTLRRDNF

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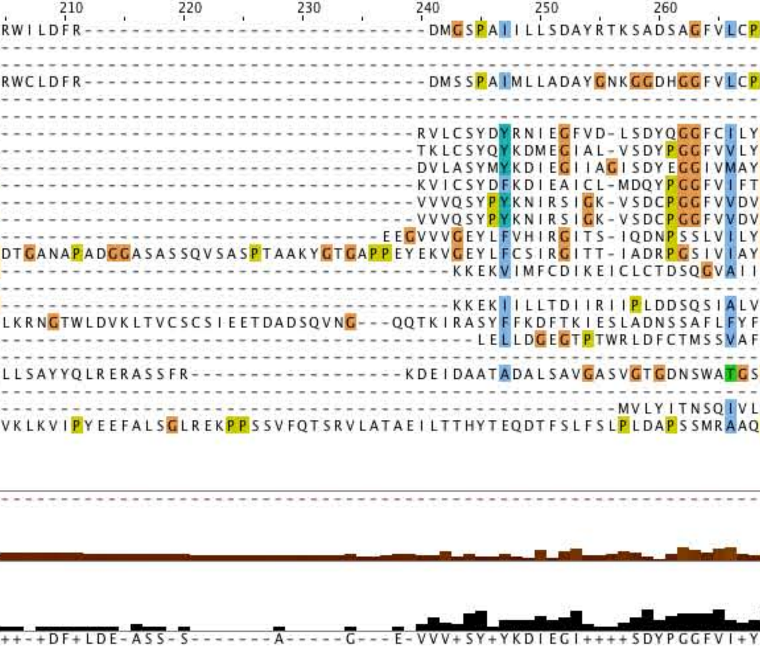

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----------------------------------------------------------------
RWCLDFR-----------------------------DMSSPAIMLLADAYGNKGGDHGGFVLCP
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-----------------------------------TKLCSYQYKDMEGIAL-VSDYPGGFVVLY
-----------------------------------DVLASYMYKDIEGIIAGISDYEGGIVMAY
-----------------------------------KVICSYDFKDIEAICL-MDQYPGGFVIFT
-----------------------------------VVVQSYPYKNIRSIGK-VSDCPGGFVVDV
-----------------------------------VVVQSYPYKNIRSIGK-VSDCPGGFVVDV
--------------------------------EEGVVVGEYLFVHIRGITS-IQDNPSSLVILY
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----------------------------------------------------------------
--------------------------------------KKEKIILLTDIIRIIPLDDSQSIALV
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----------------------------------------LELLDGEGTPTWRLDFCTMSSVAF
----------------------------------------------------------------
LLSAYYQLRERASSFR------------------KDEIDAATADALSAVGASVGTGDNSWATGS
----------------------------------------------------------------
----------------------------------------------------MVLYITNSQIVL
VKLKVIPYEEFALSGLREKPPSSVFQTSRVLATAEILTTHYTEQDTFSLFSLPLDAPSSMRAAQ

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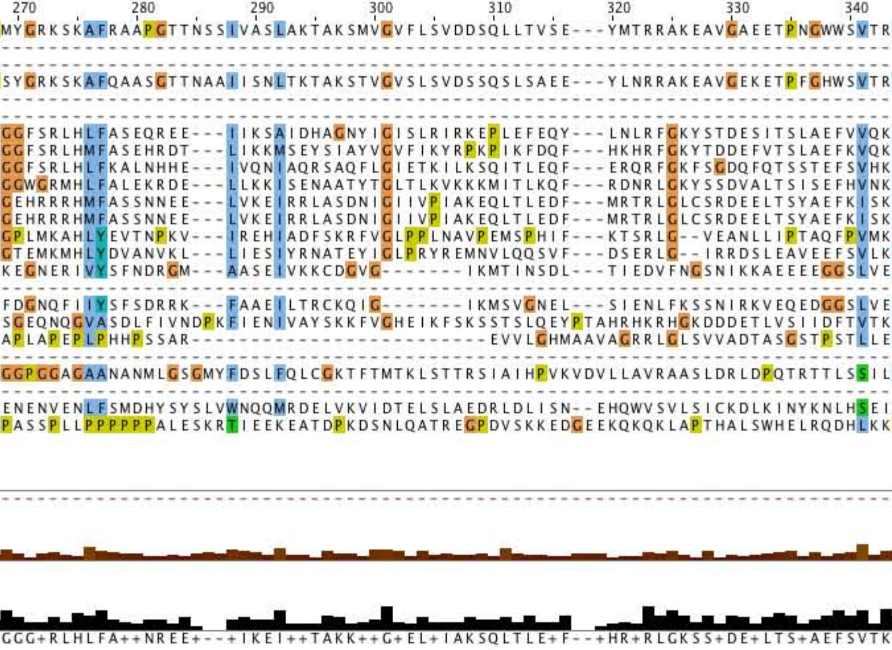

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---------------------------------------------------------------------------
---------------------------------------------------------------------------
SYGRKSKAFQAASGTTNAAIISNLTKTAKSTVGVSLSVDSSQSLSAEE---YLNRRAKEAVGEKETPFGHWSVTR
---------------------------------------------------------------------------
---------------------------------------------------------------------------
GGFSRLHLFASEQREE---IIKSAIDHAGNYIGISLRIRKEPLEFEQY---LNLRFGKYSTDESITSLAEFVVQK
GGFSRLHMFASEHRDT---LIKKMSEYSIAYVGVFIKYRPKPIKFDQF---HKHRFGKYTDDEFVTSLAEFKVQK
GGFSRLHLFKALNHHE---IVQNIAQRSAQFLGIETKILKSQITLEQF---ERQRFGKFSGDQFQTSSTEFSVHK
GGWGRMHLFALEKRDE---LLKKISENAATYTGLTLKVKKKMITLKQF---RDNRLGKYSSDVALTSISEFHVNK
GEHRRRHMFASSNNEE---LVKEIRRLASDNIGIIVPIAKEQLTLEDF---MRTRLGLCSRDEELTSYAEFKISK
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GPLMKAHLYEVTNPKV---IREHIADFSKRFVGLPPLNAVPEMSPHIF---KTSRLG--VEANLLIPTAQFPVMK
GTEMKMHLYDVANVKL---LIESIYRNATEYIGLPRYREMNVLQQSVF---DSERLG--IRRDSLEAVEEFSVLK
KEGNERIVYSFNDRGM---AASEIVKKCDGVG-------IKMTINSDL---TIEDVFNGSNIKKAEEEEGGSLVE
---------------------------------------------------------------------------
FDGNQFIIYSFSDRRK---FAAEILTRCKQIG-------IKMSVGNEL---SIENLFKSSNIRKVEQEDGGSLVE
SGEQNQGVASDLFIVNDPKFIENIVAYSKKFVGHEIKFSKSSTSLQEYPTAHRHKRHGKDDDETLVSIIDFTVTK
APLAPEPLPHHPSSAR-------------------------EVVLGHMAAVAGRRLGLSVVADTASGSTPSTLLE
---------------------------------------------------------------------------
GGPGGAGAANANMLGSGMYFDSLFQLCGKTFTMTKLSTTRSIAIHPVKVDVLLAVRAASLDRLDPQTRTTLSSIL
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ENENVENLFSMDHYSYSLVWNQQMRDELVKVIDTELSLAEDRLDLISN--EHQWVSVLSICKDLKINYKNLHSEI
PASSPLLPPPPPPALESKRTIEEKEATDPKDSNLQATREGPDVSKKEDGEEKQKQKLAPTHALSWHELRQDHLKK



---------------------------------------------------------------------------




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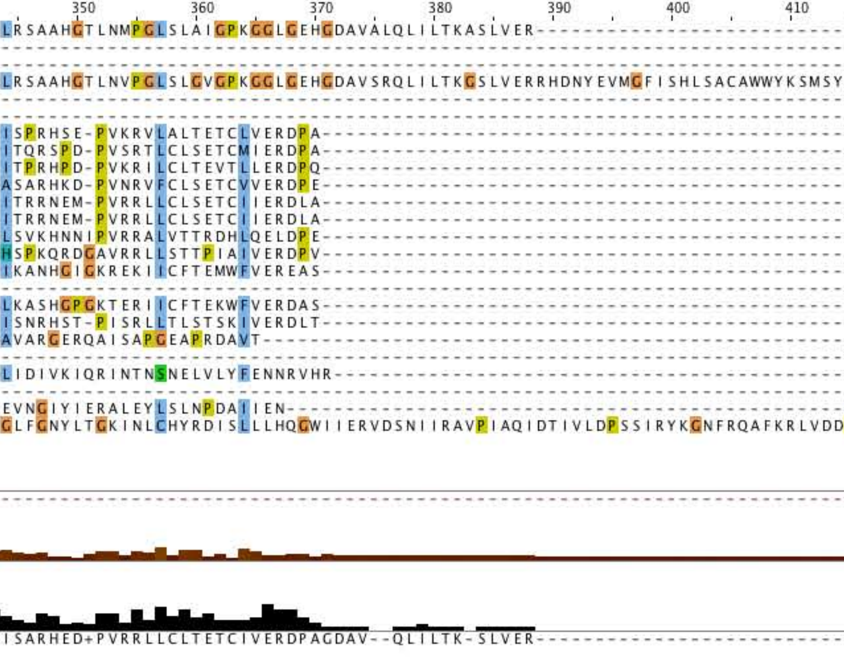

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-----------------------------------------------------------------------
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-----------------------------------------------------------------------
-----------------------------------------------------------------------
ISPRHSE-PVKRVLALTETCLVERDPA--------------------------------------------
ITQRSPD-PVSRTLCLSETCMIERDPA--------------------------------------------
ITPRHPD-PVKRILCLTEVTLLERDPQ--------------------------------------------
ASARHKD-PVNRVFCLSETCVVERDPE--------------------------------------------
ITRRNEM-PVRRLLCLSETCIIERDLA--------------------------------------------
ITRRNEM-PVRRLLCLSETCIIERDLA--------------------------------------------
LSVKHNNIPVRRALVTTRDHLQELDPE--------------------------------------------
HSPKQRDGAVRRLLSTTPIAIVERDPV--------------------------------------------
IKANHGIGKREKIICFTEMWFVEREAS--------------------------------------------
-----------------------------------------------------------------------
LKASHGPGKTERIICFTEKWFVERDAS--------------------------------------------
ISNRHST-PISRLLTLSTSKIVERDLT--------------------------------------------
AVARGERQAISAPGEAPRDAVT-------------------------------------------------
-----------------------------------------------------------------------
LIDIVKIQRINTNSNELVLYFENNRVHR-------------------------------------------
-----------------------------------------------------------------------
EVNGIYIERALEYLSLNPDAIIEN-----------------------------------------------
GLFGNYLTGKINLCHYRDISLLLHQGWIIERVDSNIIRAVPIAQIDTIVLDPSSIRYKGNFRQAFKRLVDD

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ISARHED+PVRRLLCLTETCIVERDPAGDAV--QLILTK-SLVER--------------------------
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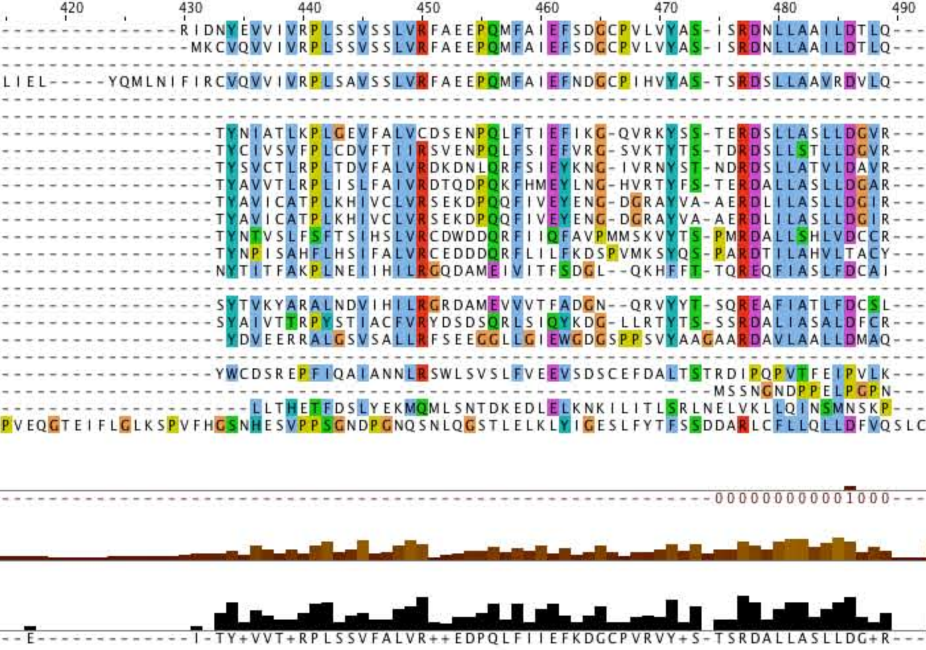

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----------------MKCVQVVIVRPLSSVSSLVRFAEEPQMFAIEFSDGCPVLVYAS-ISRDNLLAAILDTLQ---
------------------------------------------------------------------------------
LIEL-----YQMLNIFIRCVQVVIVRPLSAVSSLVRFAEEPQMFAIEFNDGCPIHVYAS-TSRDSLLAAVRDVLQ---
------------------------------------------------------------------------------
------------------------------------------------------------------------------
------------------TYNIATLKPLGEVFALVCDSENPQLFTIEFIKG-QVRKYSS-TERDSLLASLLDGVR---
------------------TYCIVSVFPLCDVFTIIRSVENPQLFSIEFVRG-SVKTYTS-TDRDSLLSTLLDGVR---
------------------TYSVCTLRPLTDVFALVRDKDNLQRFSIEYKNG-IVRNYST-NDRDSLLATVLDAVR---
------------------TYAVVTLRPLISLFAIVRDTQDPQKFHMEYLNG-HVRTYFS-TERDALLASLLDGAR---
------------------TYAVICATPLKHIVCLVRSEKDPQQFIVEYENG-DGRAYVA-AERDLILASLLDGIR---
------------------TYAVICATPLKHIVCLVRSEKDPQQFIVEYENG-DGRAYVA-AERDLILASLLDGIR---
------------------TYNTVSLFSFTSIHSLVRCDWDDQRFIIQFAVPMMSKVYTS-PMRDALLSHLVDCCR---
------------------TYNPISAHFLHSIFALVRCEDDDQRFLILFKDSPVMKSYQS-PARDTILAHVLTACY---
------------------NYTITFAKPLNEIIHILRGQDAMEIVITFSDGL--QKHFFT-TQREQFIASLFDCAI---
------------------------------------------------------------------------------
------------------SYTVKYARALNDVIHILRGRDAMEVVVTFADGN--QRVYYT-SQREAFIATLFDCSL---
------------------SYAIVTTRPYSTIACFVRYDSDSQRLSIQYKDG-LLRTYTS-SSRDALIASALDFCR---
-------------------YDVEERRALGSVSALLRFSEEGGLLGIEWGDGSPPSVYAAGAARDAVLAALLDMAQ---
------------------------------------------------------------------------------
------------------YWCDSREPFIQAIANNLRSWLSVSLFVEEVSDSCEFDALTSTRDIPQPVTFEIPVLK---
------------------------------------------------------------MSSNGNDPPELPGPN---
---------------------LLTHETFDSLYEKMQMLSNTDKEDLELKNKILITLSRLNELVKLLQINSMNSKP---
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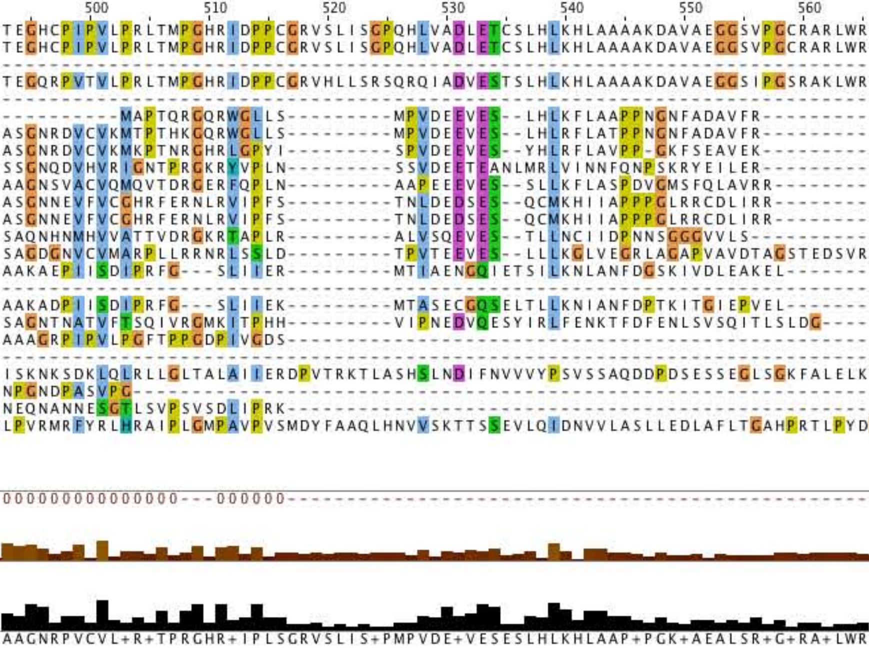

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-------------------------------------------------------------------------
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ASGNRDVCVKMTPTHKGQRWGLLS---------MPVDEEVES--LHLRFLATPPNGNFADAVFR---------
ASGNRDVCVKMKPTNRGHRLGPYI---------SPVDEEVES--YHLRFLAVPP-GKFSEAVEK---------
SSGNQDVHVRIGNTPRGKRYVPLN---------SSVDEETEANLMRLVINNFQNPSKRYEILER---------
AAGNSVACVQMQVTDRGERFQPLN---------AAPEEEVES--SLLKFLASPDVGMSFQLAVRR--------
ASGNNEVFVCGHRFERNLRVIPFS---------TNLDEDSES--QCMKHIIAPPPGLRRCDLIRR--------
ASGNNEVFVCGHRFERNLRVIPFS---------TNLDEDSES--QCMKHIIAPPPGLRRCDLIRR--------
SAQNHNMHVVATTVDRGKRTAPLR---------ALVSQEVES--TLLNCIIDPNNSGGGVVLS----------
SAGDGNVCVMARPLLRRNRLSSLD---------TPVTEEVES--LLLKGLVEGRLAGAPVAVDTAGSTEDSVR
AAKAEPIISDIPRFG---SLIIER---------MTIAENGQIETSILKNLANFDGSKIVDLEAKEL-------
-------------------------------------------------------------------------
AAKADPIISDIPRFG---SLIIEK---------MTASECGQSELTLLKNIANFDPTKITGIEPVEL-------
SAGNTNATVFTSQIVRGMKITPHH---------VIPNEDVQESYIRLFENKTFDFENLSVSQITLSLDG----
AAAGRPIPVLPGFTPPGDPIVGDS-------------------------------------------------
-------------------------------------------------------------------------
ISKNKSDKLQLRLLGLTALAIIERDPVTRKTLASHSLNDIFNVVVYPSVSSAQDDPDSESSEGLSGKFALELK
NPGNDPASVPG--------------------------------------------------------------
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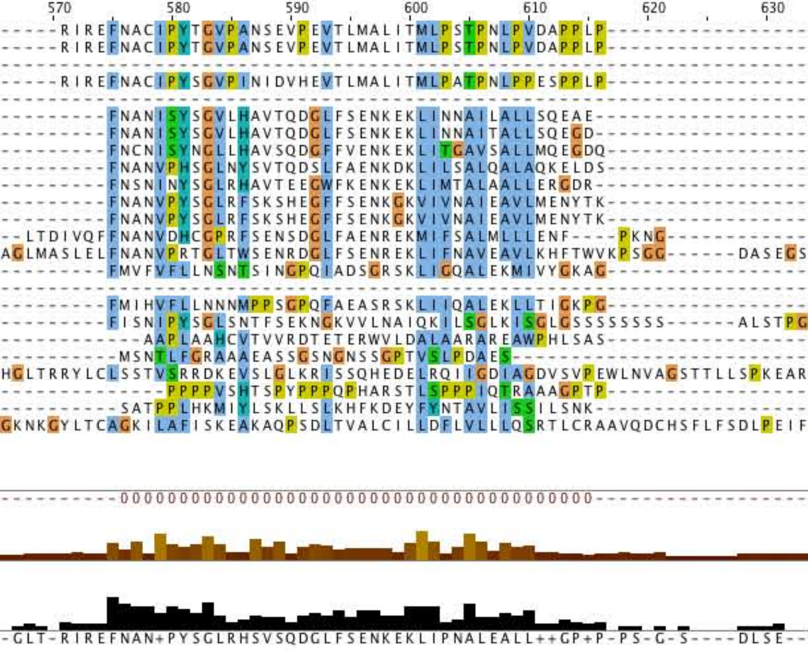

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---------FNSNINYSGLRHAVTEEGWFKENKEKLIMTALAALLERGDR-----------------
---------FNANVPYSGLRFSKSHEGFFSENKGKVIVNAIEAVLMENYTK----------------
---------FNANVPYSGLRFSKSHEGFFSENKGKVIVNAIEAVLMENYTK----------------
--LTDIVQFFNANVDHCGPRFSENSDGLFAENREKMIFSALMLLLENF----PKNG------------
AGLMASLELFNANVPRTGLTWSENRDGLFSENREKLIFNAVEAVLKHFTWVKPSGG------DASEGS
---------FMVFVFLLNSNTSINGPQIADSGRSKLIGQALEKMIVYGKAG-----------------
--------------------------------------------------------------------
---------FMIHVFLLNNNMPPSGPQFAEASRSKLIIQALEKLLTIGKPG-----------------
---------FISNIPYSGLSNTFSEKNGKVVLNAIQKILSGLKISGLGSSSSSSSS------ALSTPG
------------AAPLAAHCVTVVRDTETERWVLDALAARAREAWPHLSAS-----------------
----------MSNTLFGRAAAEASSGSNGNSSGPTVSLPDAES-------------------------
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--------------PPPPVSHTSPYPPPQPHARSTLSPPPIQTRAAAGPTP-----------------
----------SATPPLHKMIYLSKLLSLKHFKDEYFYNTAVLISSILSNK------------------
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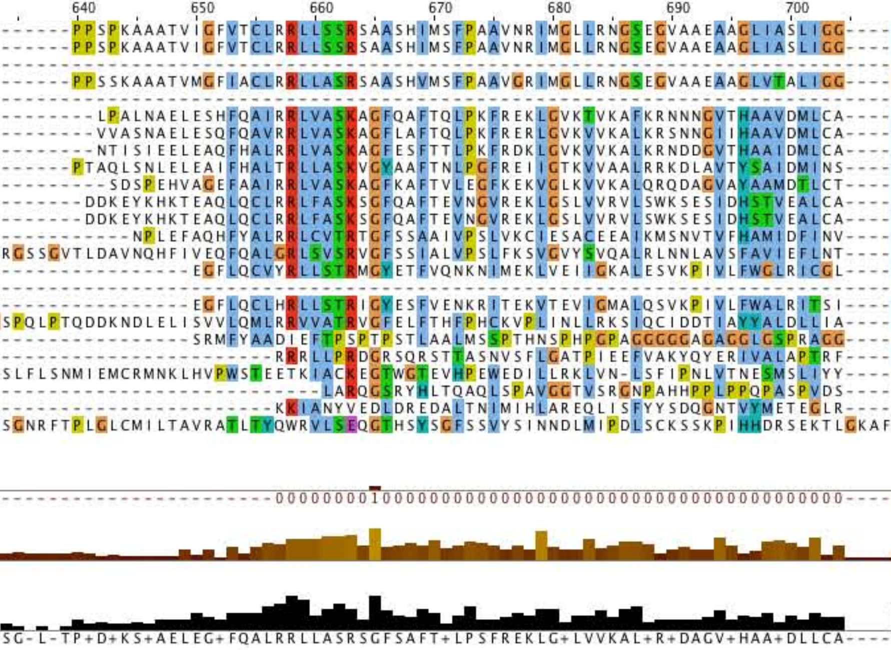

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-----------NPLEFAQHFYALRRLCVTRTGFSSAAIVPSLVKCIESACEEAIKMSNVTVFHAMIDFINV----
RGSSGVTLDAVNQHFIVEQFQALGRLSVSRVGFSSIALVPSLFKSVGVYSVQALRLNNLAVSFAVIEFLNT----
----------------EGFLQCVYRLLSTRMGYETFVQNKNIMEKLVEIIGKALESVKPIVLFWGLRICGL----
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----------------EGFLQCLHRLLSTRIGYESFVENKRITEKVTEVIGMALQSVKPIVLFWALRITSI----
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-----------------------KKIANYVEDLDREDALTNIMIHLAREQLISFYYSDQGNTVYMETEGLR----
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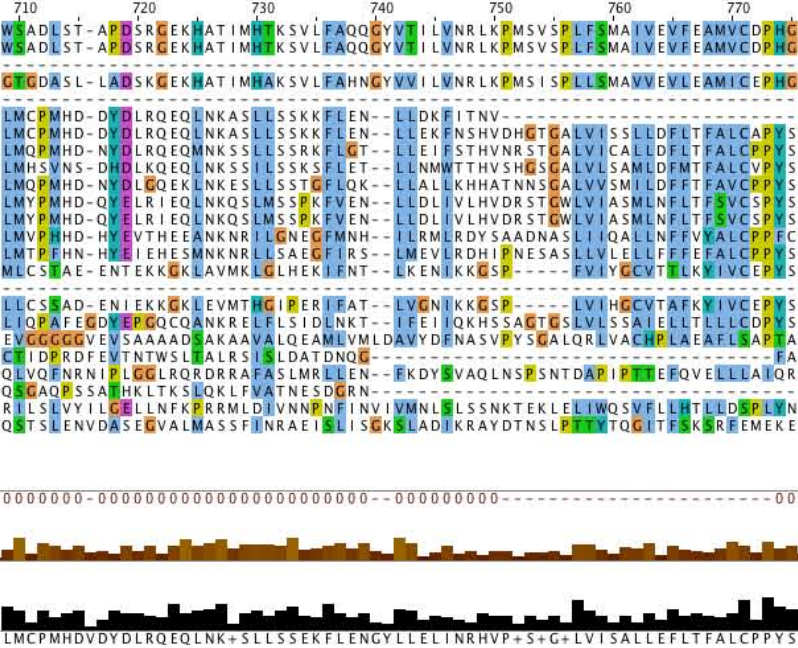

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LIQPAFEGDYEPGQCQANKRELFLSIDLNKT--IFEIIQKHSSAGTGSLVLSSAIELLTLLLCDPYS
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CTIDPRDFEVTNTWSLTALRSISLDATDNQG----------------------------------FA
QLVQFNRNIPLGGLRQRDRRAFASLMRLLEN--FKDYSVAQLNSPSNTDAPIPTTEFQVELLLAIQR
QSGAQPSSATHKLTKSLQKLFVATNESDGRN------------------------------------
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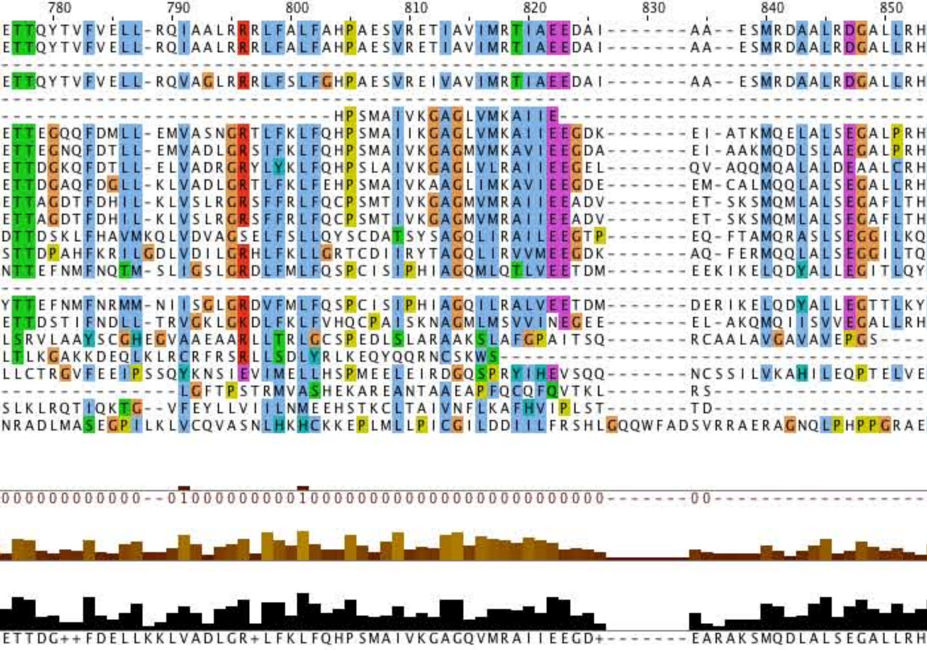

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---------------LGFTPSTRMVASHEKAREANTAAEAPFQCQFQVTKL-------RS------------------
SLKLRQTIQKTG--VFEYLLVIILNMEEHSTKCLTAIVNFLKAFHVIPLST-------TD------------------
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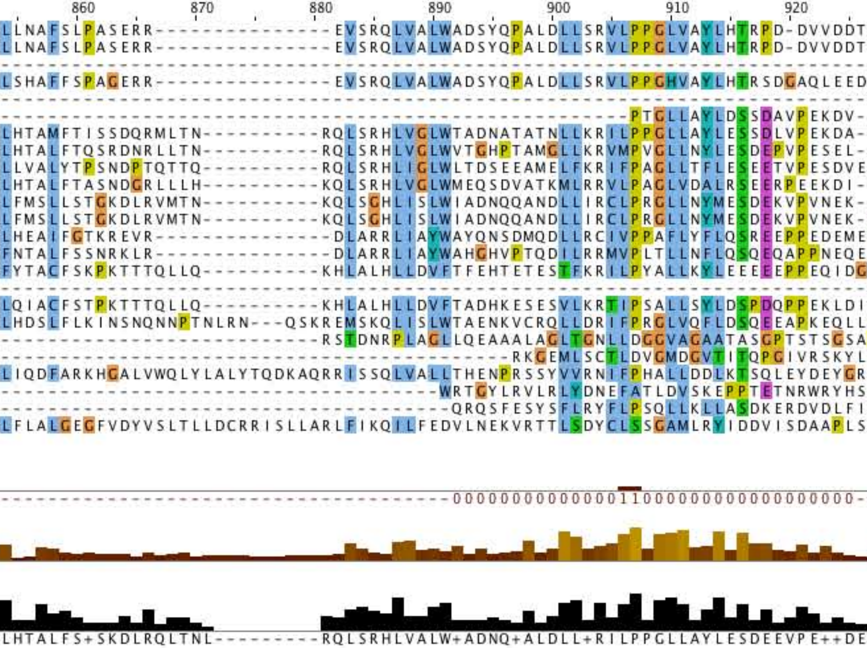

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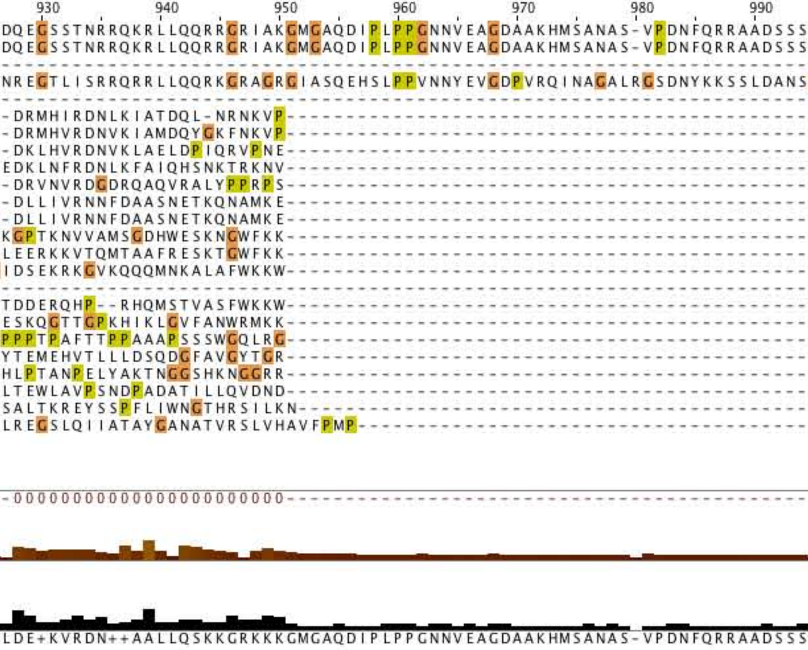

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-DRVNVRDGDRQAQVRALYPPRPS--------------------------------------------
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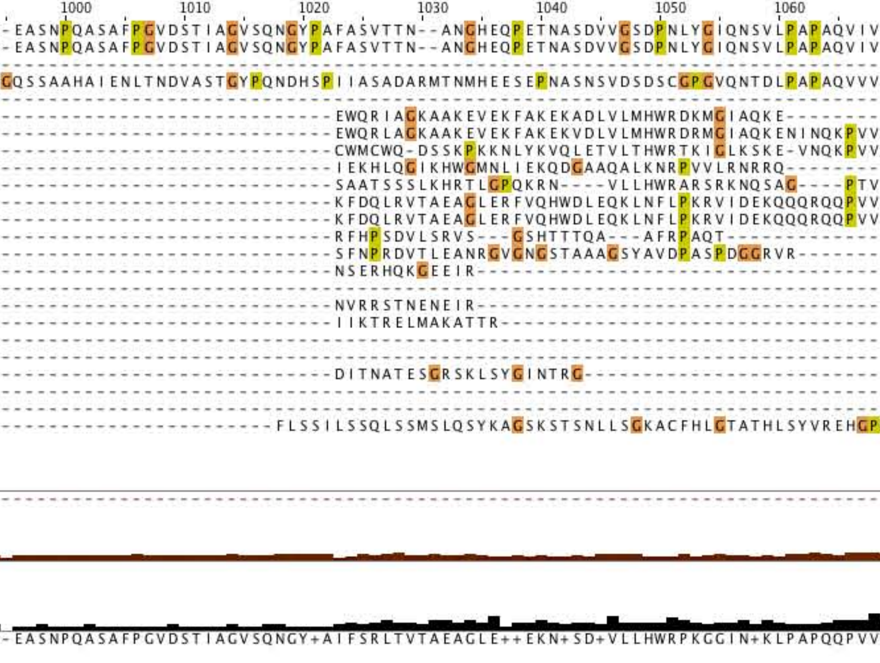

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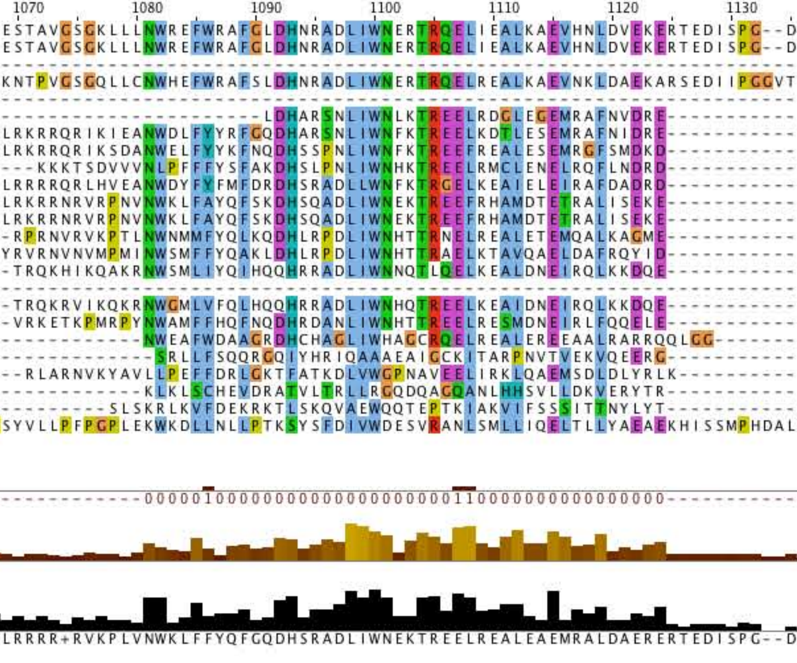

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---------SLSKRLKVFDEKRKTLSKQVAEWQQTEPTKIAKVIFSSSITTNYLYT-----------
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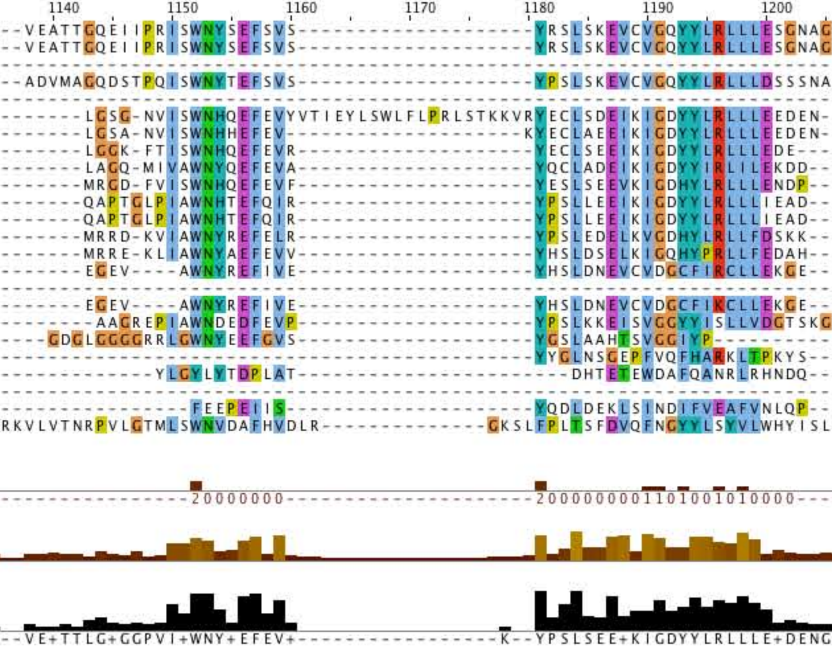

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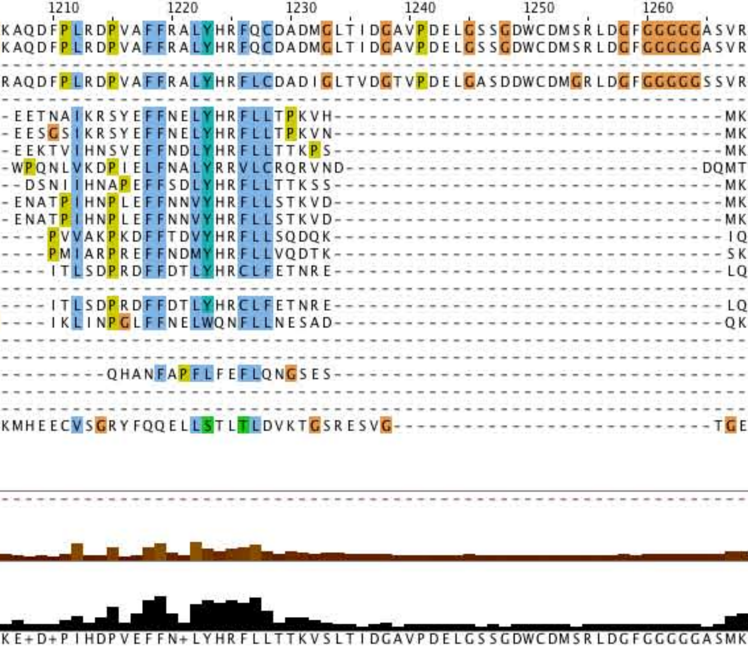

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---------------------------------------------------------------
---------------------------------------------------------------
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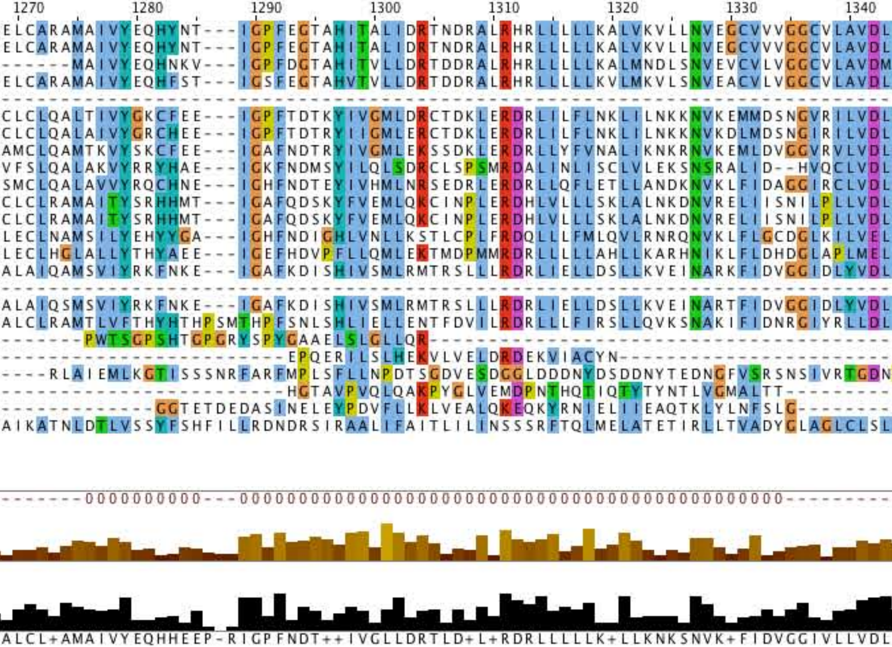

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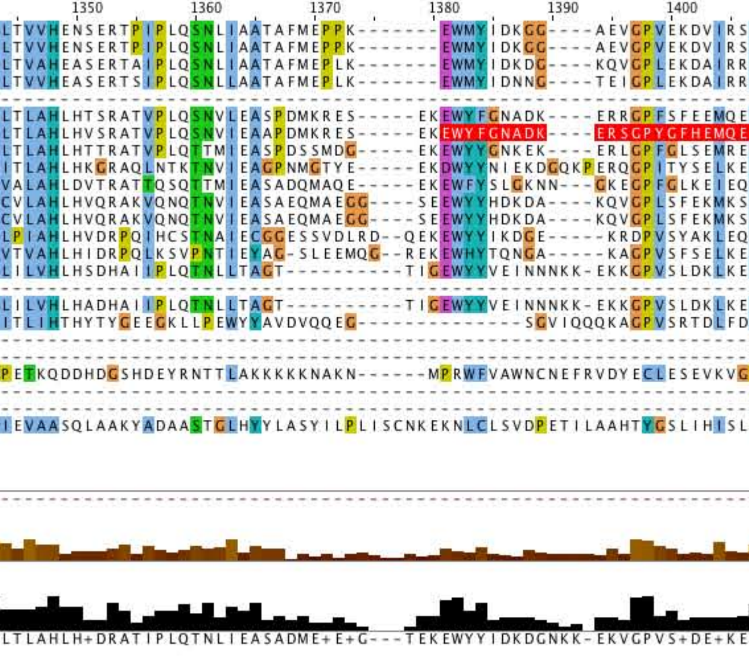

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LILVHLHSDHAIIPLQTNLLTAGT----------TIGEWYYVEINNNKK-EKKGPVSLDKLKE
---------------------------------------------------------------
LILVHLHADHAIIPLQTNLLTAGT----------TIGEWYYVEINNNKK-EKKGPVSLDKLKE
ITLIHTHYTYGEEGKLLPEWYYAVDVQQEG--------------SGVIQQQKAGPVSRTDLFD
---------------------------------------------------------------
---------------------------------------------------------------
PETKQDDHDGSHDEYRNTTLAKKKKKNAKN------MPRWFVAWNCNEFRVDYECLESEVKVG
---------------------------------------------------------------
---------------------------------------------------------------
IEVAASQLAAKYADAASTGLHYYLASYILPLISCNKEKNLCLSVDPETILAAHTYGSLIHISL

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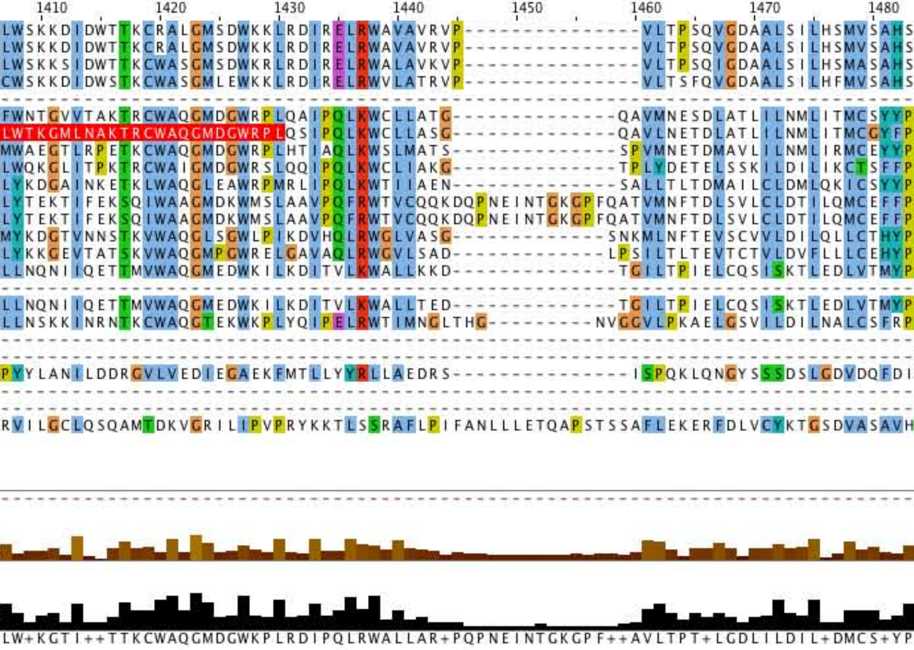

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LWSKKSIDWTTKCWASGMSDWKRLRDIRELRWALAVKVP----------------VLTPSQIGDAALSILHSMASAHS
CWSKKDIDWSTKCWASGMLEWKKLRDIRELRWVLATRVP----------------VLTSFQVGDAALSILHFMVSAHS
-------------------------------------------------------------------------------
FWNTGVVTAKTRCWAQGMDGWRPLQAIPQLKWCLLATG-------------QAVMNESDLATLILNMLITMCSYYP
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LYKDGAINKETKLWAQGLEAWRPMRLIPQLKWTIIAEN-------------SALLTLTDMAILCLDMLQKICSYYP
LYTEKTIFEKSQIWAAGMDKWMSLAAVPQFRWTVCQQKDQPNEINTGKGPFQATVMNFTDLSVLCLDTILQMCEFFP
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MYKDGTVNNSTKVWAQGLSGWLPIKDVHQLRWGLVASG------------SNKMLNFTEVSCVVLDILQLLCTHYP
LYKKGEVTATSKVWAQGMPGWRELGAVAQLRWGVLSAD------------LPSILTLTEVTCTVLDVFLLLCEHYP
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LLNSKKINRNTKCWAQGTEKWKPLYQIPELRWTIMNGLTHG---------NVGGVLPKAELGSVILDILNALCSFRP
-------------------------------------------------------------------------------
-------------------------------------------------------------------------------
PYYLANILDDRGVLVEDIEGAEKFMTLLYYRLLAEDRS---------------ISPQKLQNGYSSSDSLGDVDQFDI
-------------------------------------------------------------------------------
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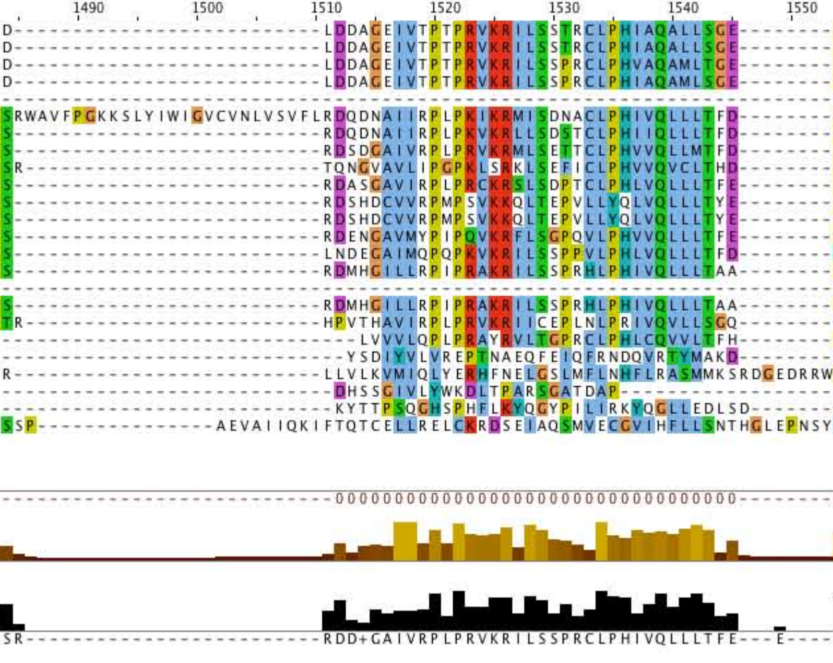

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SRWAVFPGKKSLYIWIGVCVNLVSVFLRDQDNAIIRPLPKIKRMISDNACLPHIVQLLLTFD--------
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S--------------------------RDSDGAIVRPLPRVKRMLSETTCLPHVVQLLMTFD--------
SR-------------------------TQNGVAVLIPGPKLSRKLSEFICLPHVVQVCLTHD--------
S--------------------------RDASGAVIRPLPRCKRSLSDPTCLPHLVQLLLTFE--------
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S--------------------------RDENGAVMYPIPQVKRFLSGPQVLPHVVQLLLTFE--------
S--------------------------LNDEGAIMQPQPKVKRILSSPPVLPHLVQLLLTFD--------
S--------------------------RDMHGILLRPIPRAKRILSSPRHLPHIVQLLLTAA--------
----------------------------------------------------------------------
S--------------------------RDMHGILLRPIPRAKRILSSPRHLPHIVQLLLTAA--------
TR-------------------------HPVTHAVIRPLPRVKRIICEPLNLPRIVQVLLSGQ--------
------------------------------LVVVLQPLPRAYRVLTGPRCLPHLCQVVLTFH--------
-----------------------------YSDIYVLVREPTNAEQFEIQFRNDQVRTYMAKD--------
R--------------------------LLVLKVMIQLYERHFNELGSLMFLNHFLRASMMKSRDGEDRRW
----------------------------DHSSGIVLYWKDLTPARSGATDAP------------------
----------------------------KYTTPSQGHSPHFLKYQGYPILIRKYQGLLEDLSD-------
SSP---------------AEVAIIQKIFTQTCELLRELCKRDSEIAQSMVECGVIHFLLSNTHGLEPNSY

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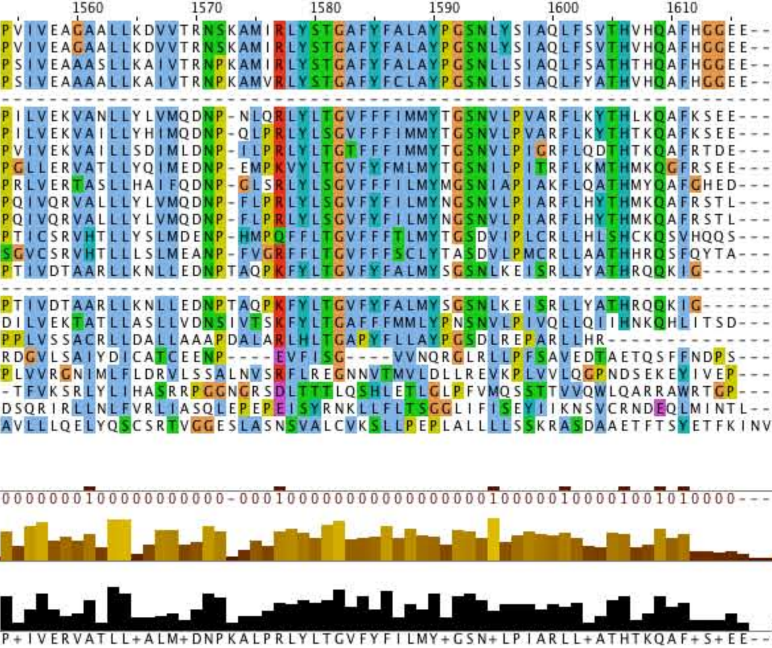

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PVIVEKVAILLSDIMLDNP-ILPRLYLTGTFFFIMMYTGSNVLPIGRFLQDTHTKQAFRTDE---
PGLLERVATLLYQIMEDNP-EMPKVYLTGVFYFMLMYTGSNILPITRFLKMTHMKQGFRSEE---
PRLVERTASLLHAIFQDNP-GLSRLYLSGVFFFILMYMGSNIAPIAKFLQATHMYQAFGHED---
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-----------------------------------------------------------------
PTIVDTAARLLKNLLEDNPTAQPKFYLTGVFYFALMYSGSNLKEISRLLYATHRQQKIG------
DILVEKTATLLASLLVDNSIVTSKFYLTGAFFFMMLYPNSNVLPIVQLLQIIHNKQHLITSD---
PPLVSSACRLLDALLAAAPDALARLHLTGAPYFLLAYPGSDLREPARLLHR--------------
RDGVLSAIYDICATCEENP----EVFISG----VVNQRGLRLLPFSAVEDTAETQSFFNDPS---
PLVVRGNIMLFLDRVLSSALNVSRFLREGNNVTMVLDLLREVKPLVVLQGPNDSEKEYIVEP---
-TFVKSRLYLIHASRRPGGNGRSDLTTTLQSHLETLGLPFVMQSSTTVVQWLQARRAWRTGP---
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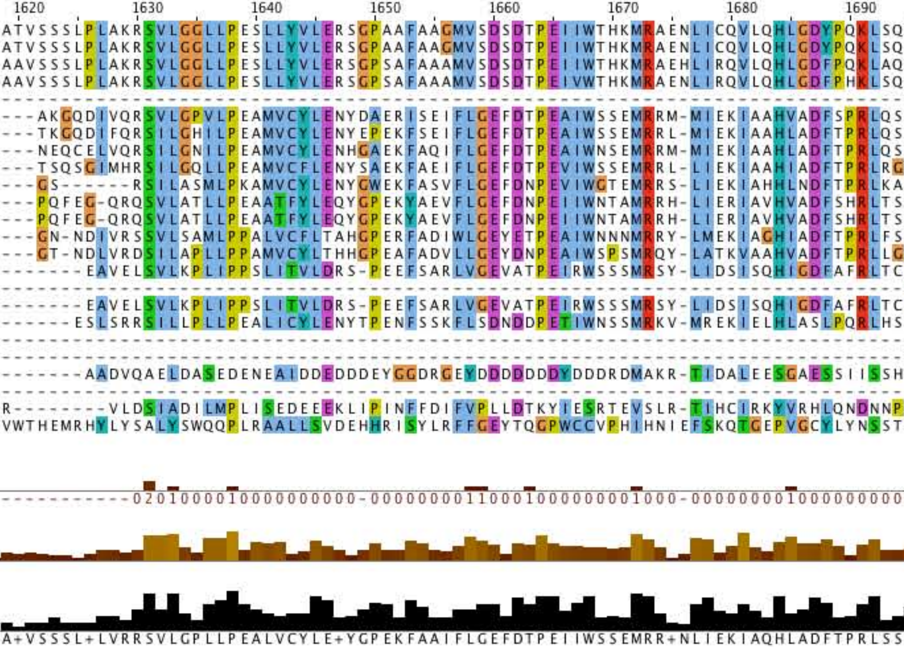

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---NEQCELVQRSILGNILPEAMVCYLENHGAEKFAQIFLGEFDTPEAIWNSEMRRM-MIEKIAAHLADFTPRLQS
---TSQSGIMHRSILGQLLPEAMVCFLENYSAEKFAEIFLGEFDTPEVIWSSEMRRL-LIEKIAAHIADFTPRLRG
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---GT-NDLVRDSILAPLLPPAMVCYLTHHGPEAFADVLLGEYDNPEAIWSPSMRQY-LATKVAAHVADFTPRLLG
-------EAVELSVLKPLIPPSLITVLDRS-PEEFSARLVGEVATPEIRWSSSMRSY-LIDSISQHIGDFAFRLTC
----------------------------------------------------------------------------
-------EAVELSVLKPLIPPSLITVLDRS-PEEFSARLVGEVATPEIRWSSSMRSY-LIDSISQHIGDFAFRLTC
------ESLSRRSILLPLLPEALICYLENYTPENFSSKFLSDNDDPETIWNSSMRKV-MREKIELHLASLPQRLHS
----------------------------------------------------------------------------
----------------------------------------------------------------------------
-------AADVQAELDASEDENEAIDDEDDDEYGGDRGEYDDDDDDDYDDDRDMAKR-TIDALEESGAESSIISSH
----------------------------------------------------------------------------
R--------VLDSIADILMPLISEDEEEKLIPINFFDIFVPLLDTKYIESRTEVSLR-TIHCIRKYVRHLQNDNNP
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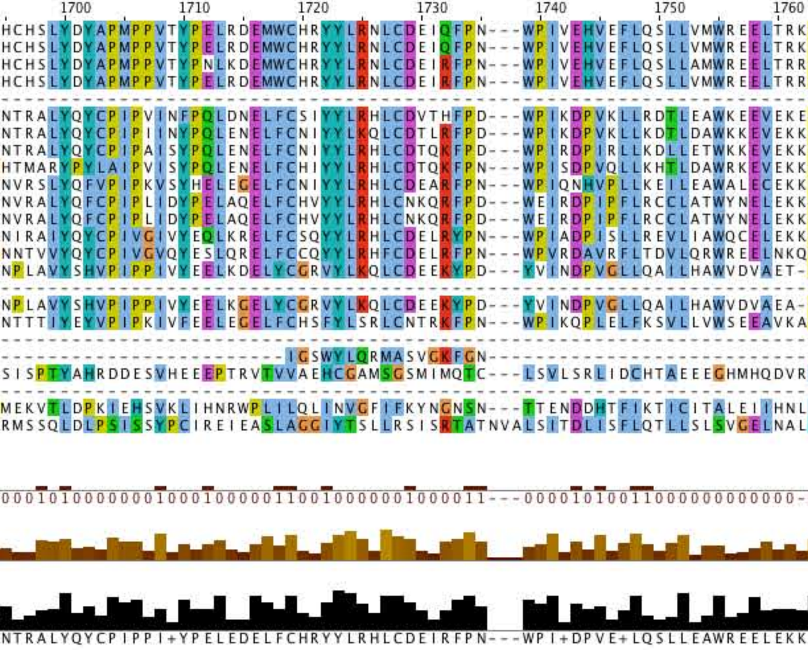

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------------------------IGSWYLQRMASVGKFGN---------------------------
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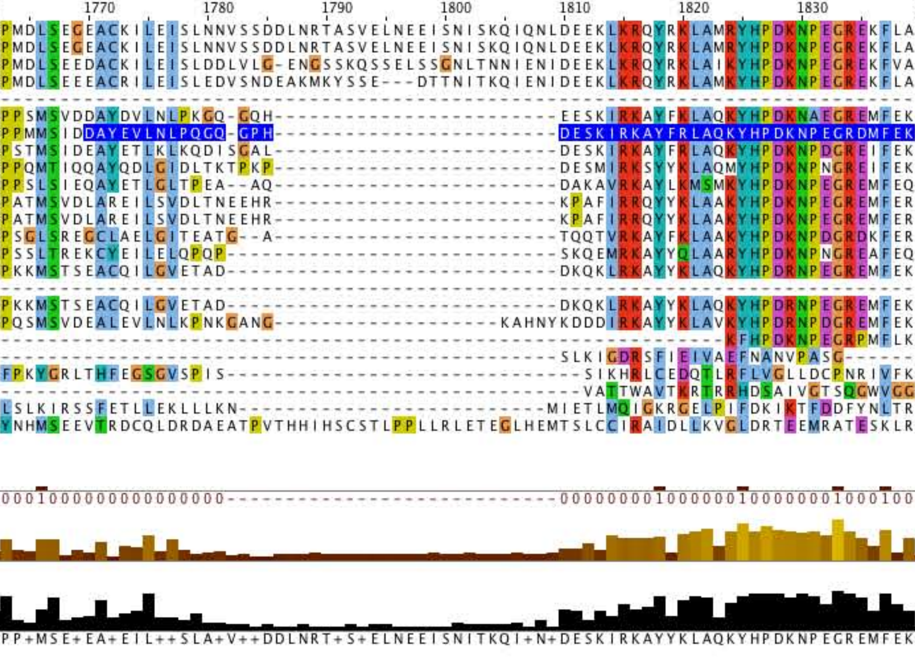

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-----------------------------------------------------------------------------
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PPMMSIDDAYEVLNLPQGQ-GPH------------------------DESKIRKAYFRLAQKYHPDKNPEGRDMFEK
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PPQMTIQQAYQDLGIDLTKTPKP------------------------DESMIRKSYYKLAQMYHPDKNPNGREIFEK
PPSLSIEQAYETLGLTPEA--AQ------------------------DAKAVRKAYLKMSMKYHPDKNPEGREMFEQ
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-------------------------------------------------------------KFHPDKNPEGRPMFLK
-----------------------------------------------------------------------------
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FPKYGRLTHFEGSGVSPIS------------------------------SIKHRLCEDQTLRFLVGLLDCPNRIVFK
-------------------------------------------------VATTWAVTKRTRRHDSAIVGTSQGWVGG
LSLKIRSSFETLLEKLLLKN--------------------------MIETLMQIGKRGELPIFDKIKTFDDFYNLTR
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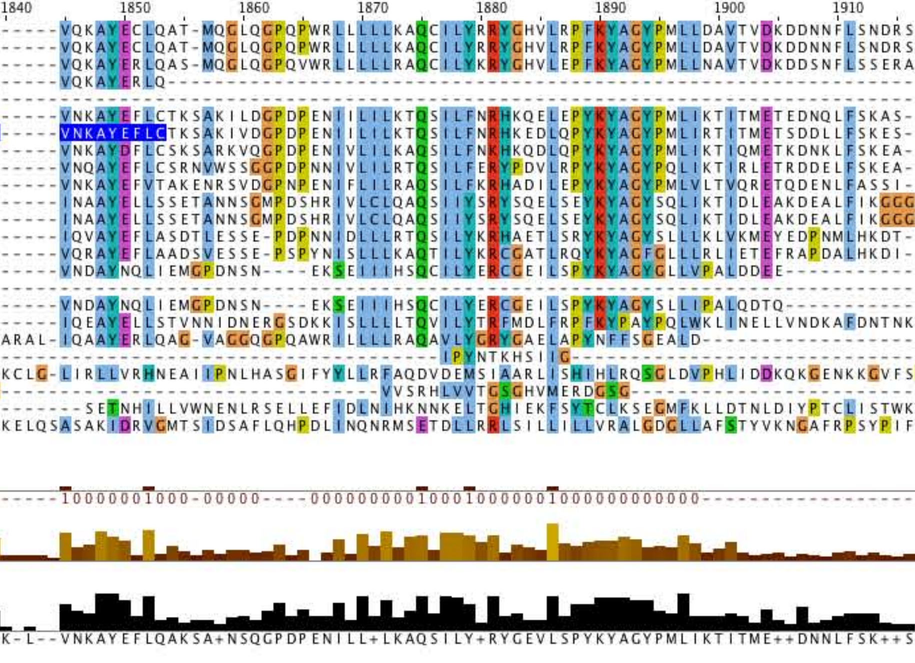

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-----VNDAYNQLIEMGPDNSN----EKSEIIIHSQCILYERCGEILSPYKYAGYGLLVPALDDEE-----------
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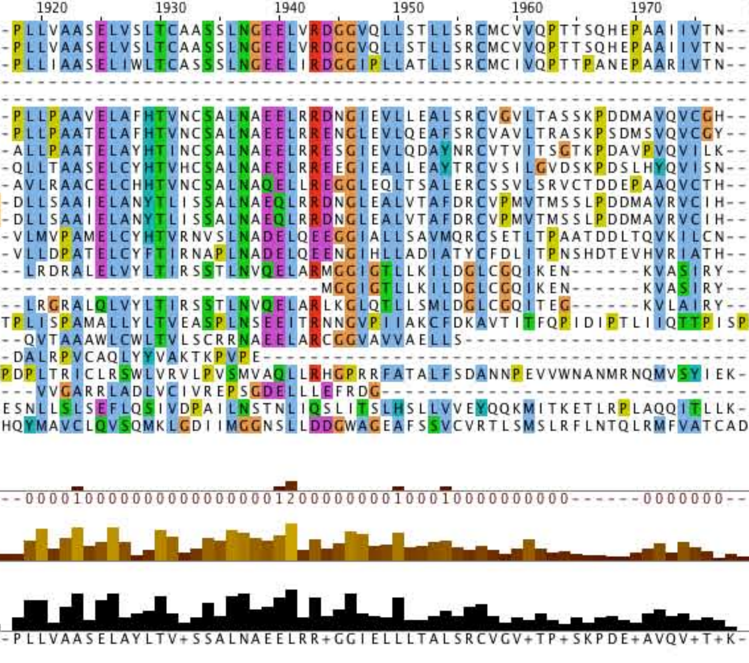

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-PLLIAASELIWLTCASSSLNGEELIRDGGIPLLATLLSRCMCIVQPTTPANEPAARIVTN--
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-ALLPAATELAYHTINCSALNAEELRRESGIEVLQDAYNRCVTVITSGTKPDAVPVQVILK--
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-AVLRAACELCHHTVNCSALNAQELLREGGLEQLTSALERCSSVLSRVCTDDEPAAQVCTH--
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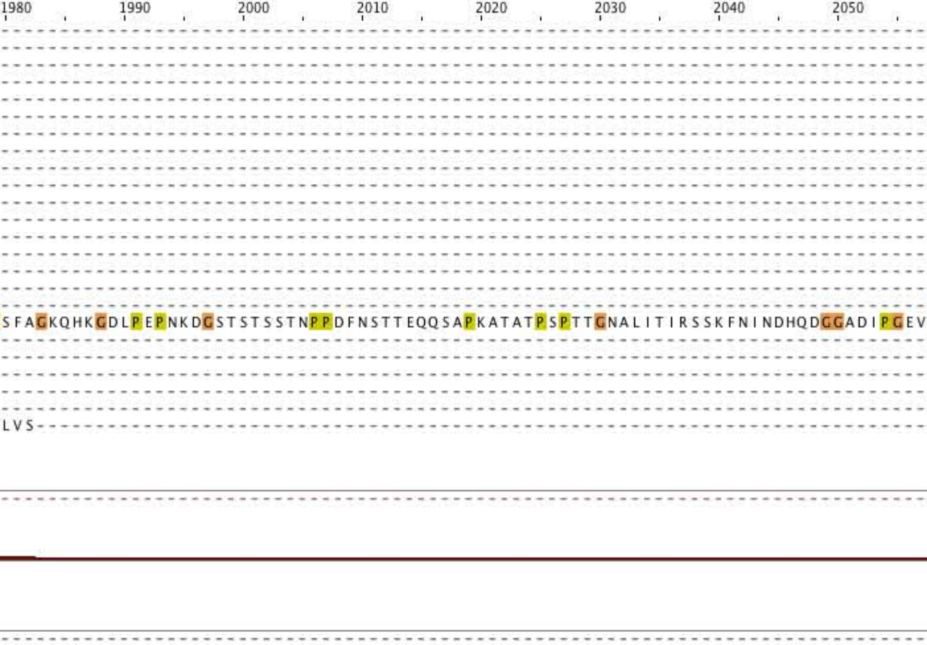

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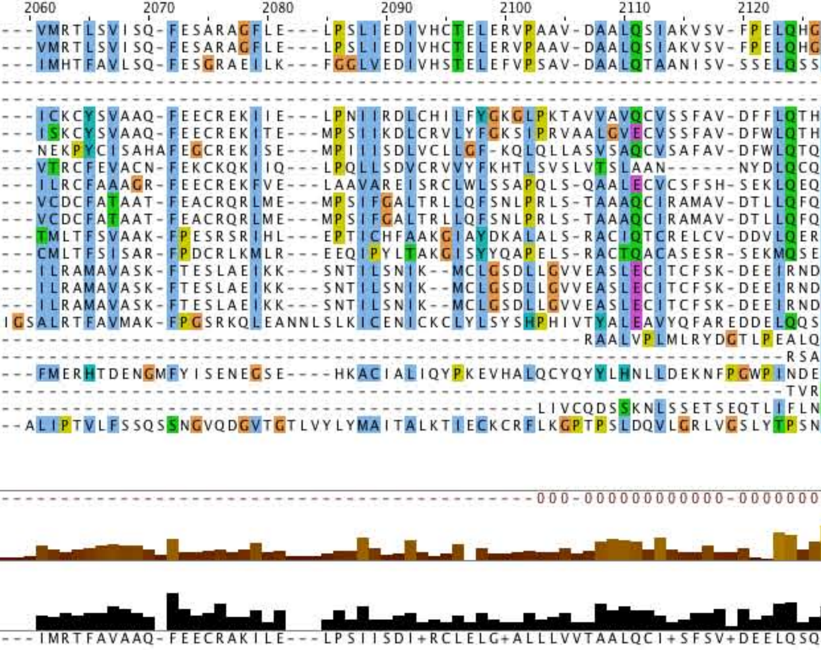

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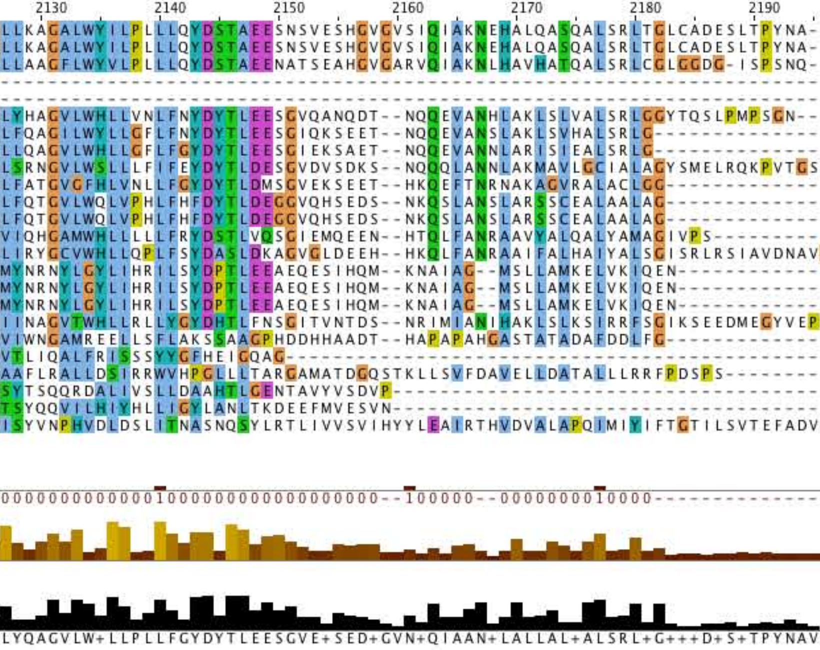

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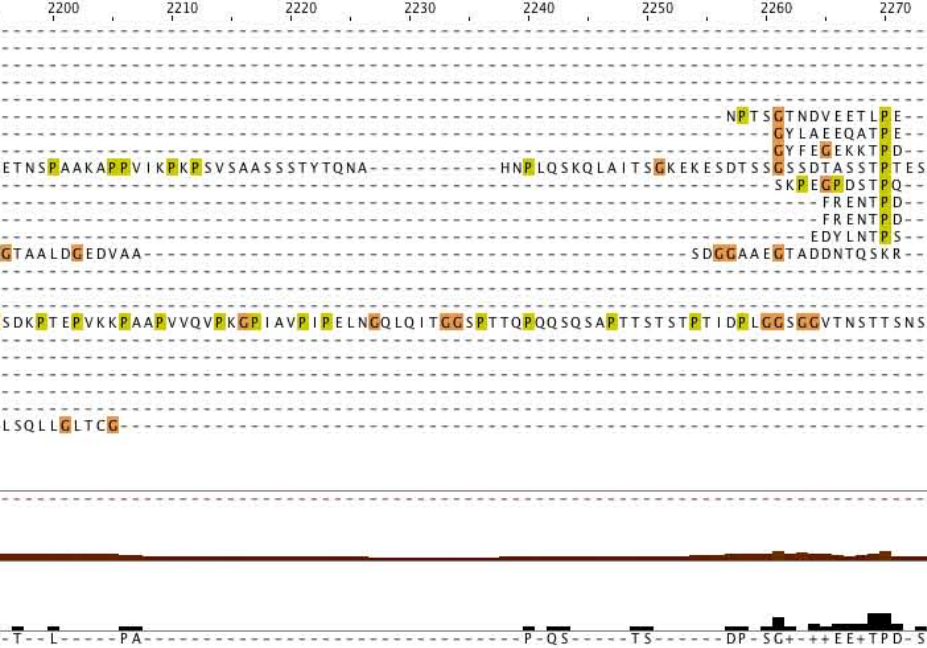
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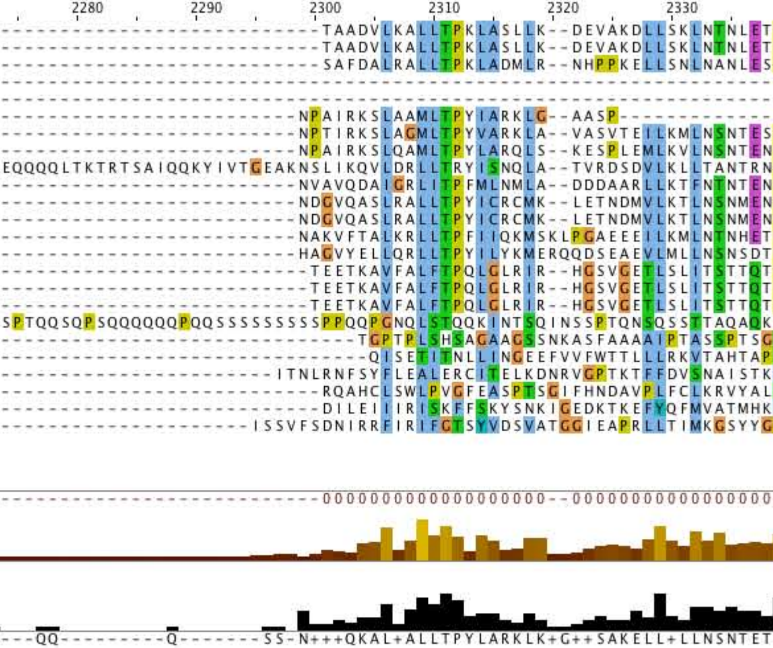

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-----------------------------------------------------------------
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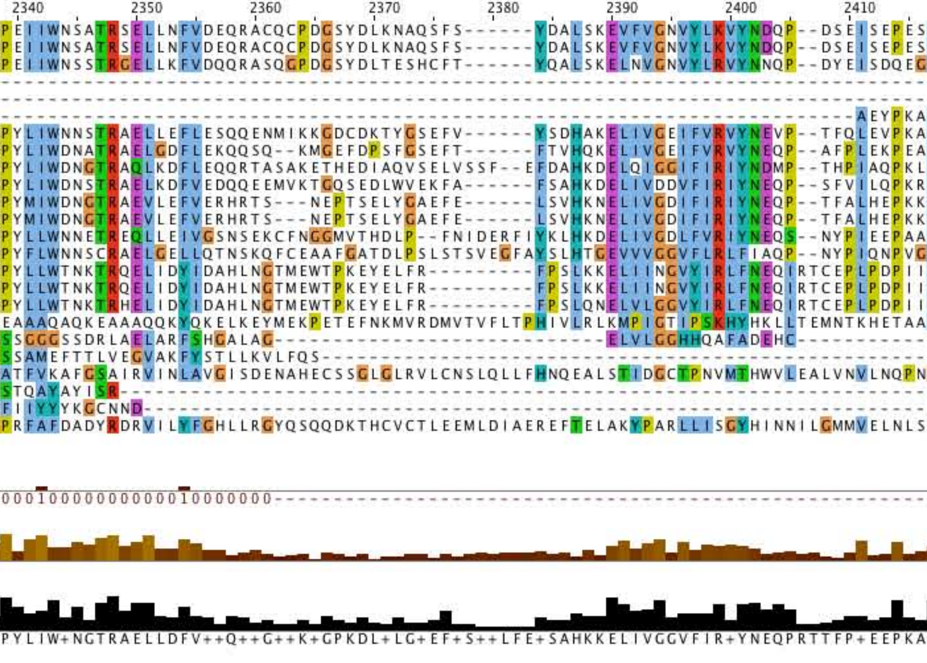

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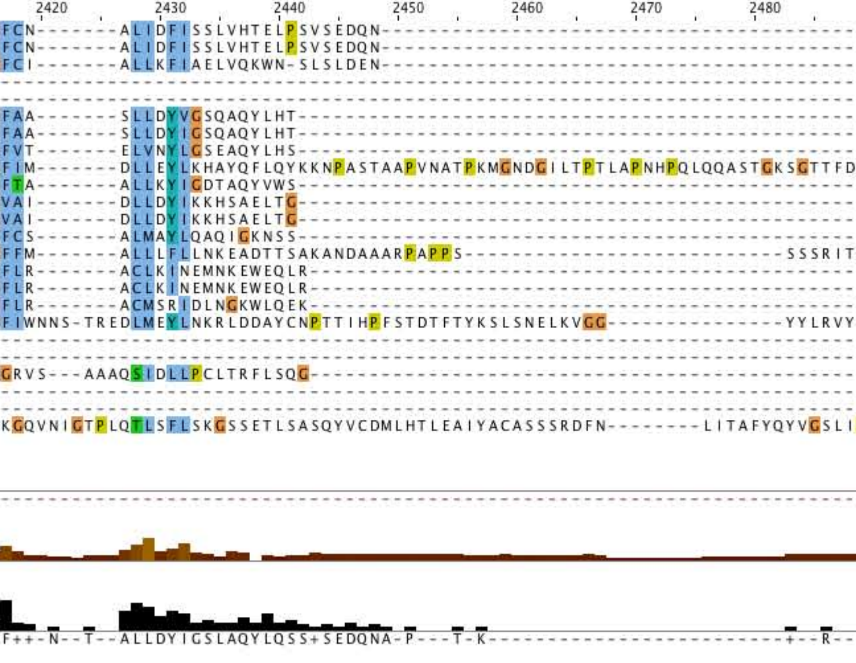

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------------------------------------------------------------------------
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FAA-------SLLDYIGSQAQYLHT-----------------------------------------------
FVT-------ELVNYLGSEAQYLHS-----------------------------------------------
FIM-------DLLEYLKHAYQFLQYKKNPASTAAPVNATPKMGNDGILTPTLAPNHPQLQQASTGKSGTTFD
FTA-------ALLKYIGDTAQYVWS-----------------------------------------------
VAI-------DLLDYIKKHSAELTG-----------------------------------------------
VAI-------DLLDYIKKHSAELTG-----------------------------------------------
FCS-------ALMAYLQAQIGKNSS-----------------------------------------------
FFM-------ALLLFLLNKEADTTSAKANDAAARPAPPS---------------------------SSSRIT
FLR-------ACLKINEMNKEWEQLR----------------------------------------------
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------------------------------------------------------------------------
GRVS---AAAQSIDLLPCLTRFLSQG----------------------------------------------
------------------------------------------------------------------------
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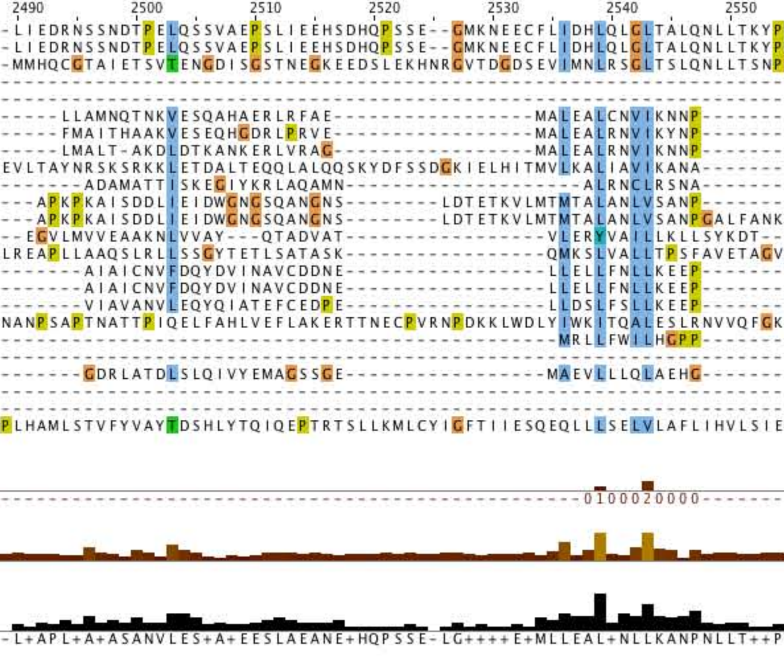

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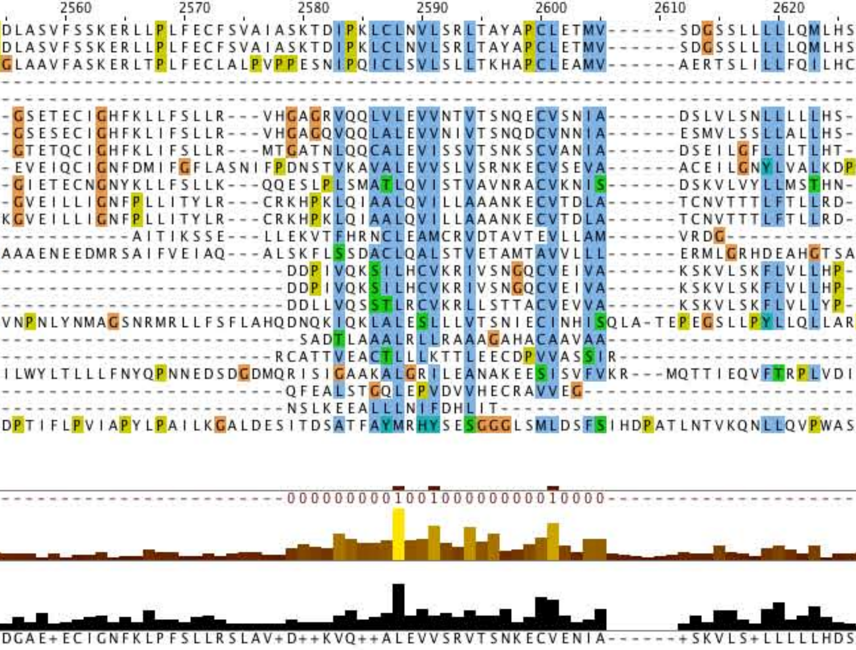

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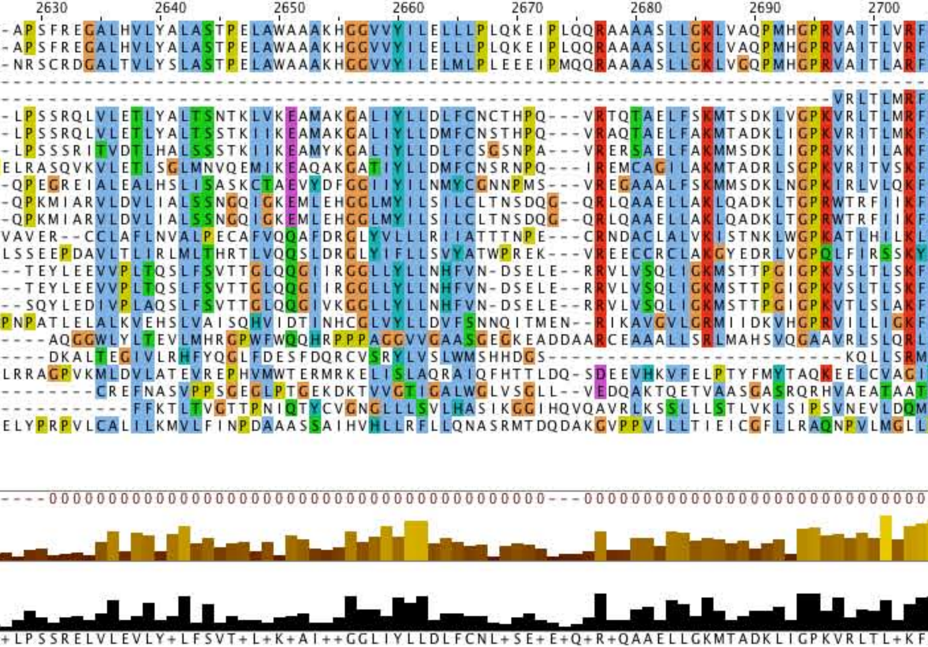

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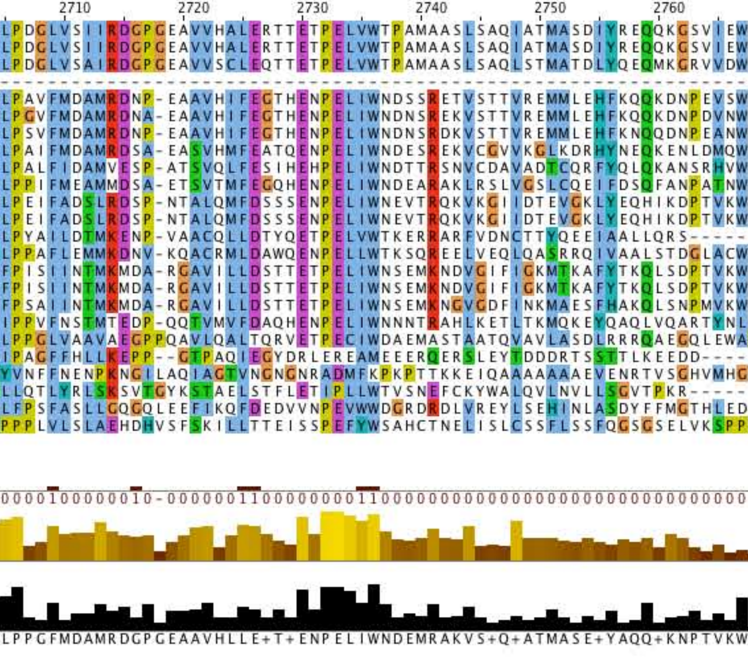

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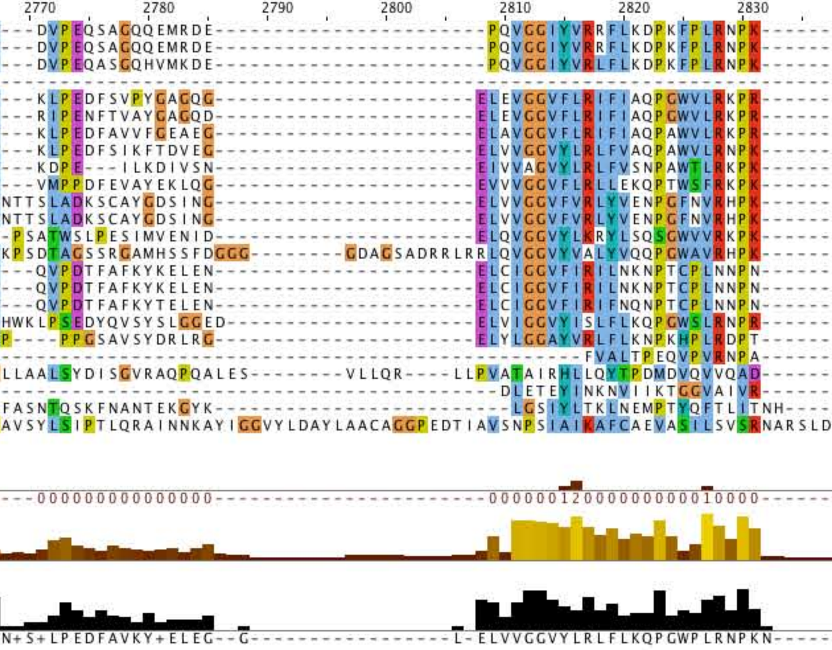

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P----PPGSAVSYDRLRG----------------------ELYLGGAYVRLFLKNPKHPLRDPT------
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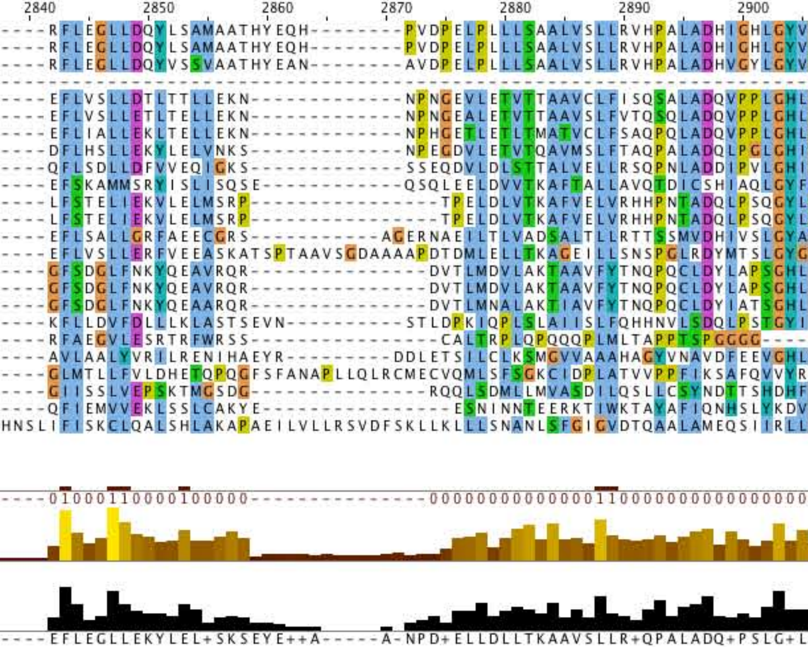

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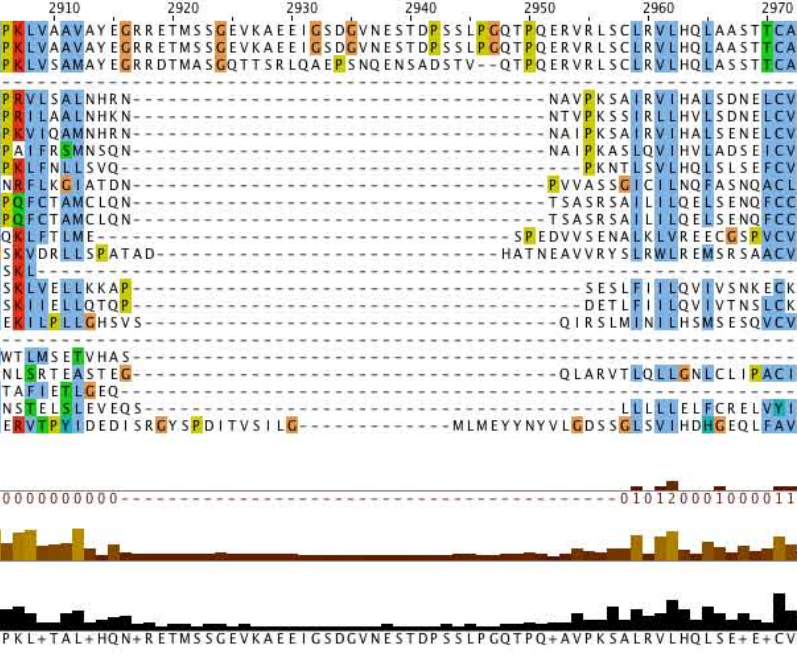

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SKL----------------------------------------------------------------
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TAFIETLGEQ---------------------------------------------------------
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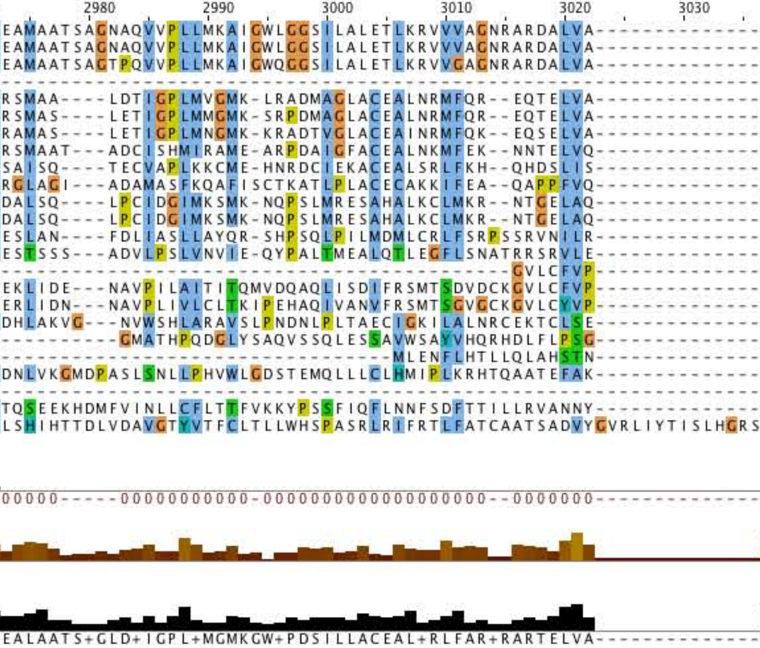

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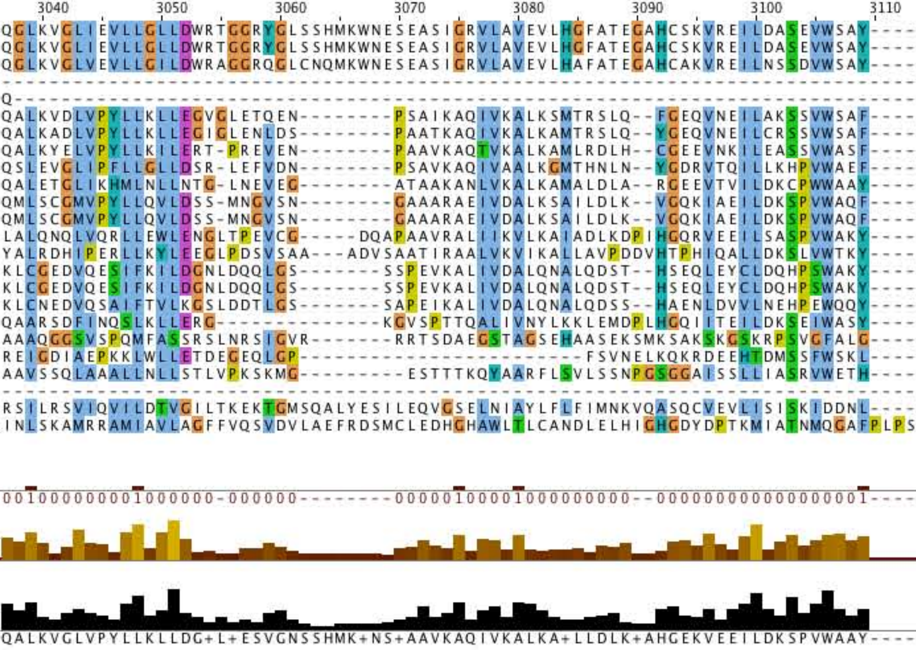

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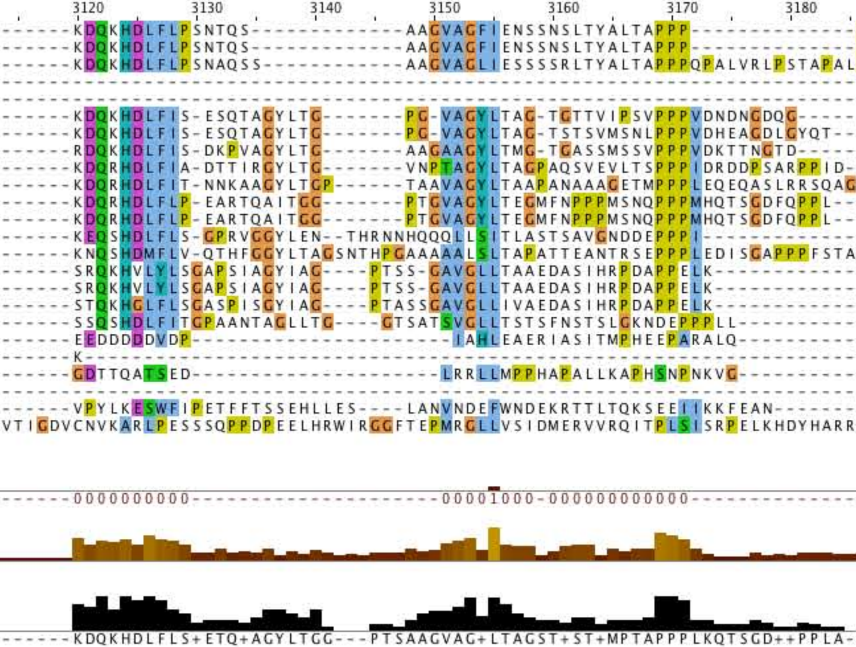

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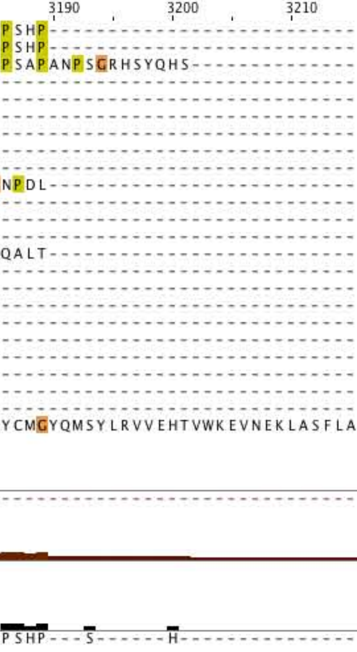

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